#Supplementary Table 4 - all mutations and short insertion/deletions in all cases

Patient ID	Biopsy Time Point	Hugo Symbol	Entrez Gene Id	NCBI Build	Chr	Start position	End position	Variant Classification	Variant Type	Reference Allele	Tumor Allele	Number of alterate reads	Number of reference reads	cDNA Change	Codon Change	Protein Change
Pat_04	Pre-Treatment	KIAA0562	9731	37	1	3765332	3765332	Missense_Mutation	SNP	G	A	7	24	c.127C>T	c.(127-129)CCA>TCA	p.P43S
Pat_04	Pre-Treatment	SPSB1	80176	37	1	9416327	9416327	Missense_Mutation	SNP	C	T	4	19	c.377C>T	c.(376-378)TCT>TTT	p.S126F
Pat_04	Pre-Treatment	TNFRSF8	943	37	1	12164438	12164438	Missense_Mutation	SNP	G	A	10	75	c.271G>A	c.(271-273)GAC>AAC	p.D91N
Pat_04	Pre-Treatment	VPS13D	55187	37	1	12343000	12343000	Missense_Mutation	SNP	C	T	14	96	c.4841C>T	c.(4840-4842)TCC>TTC	p.S1614F
Pat_04	Pre-Treatment	PRAMEF6	440561	37	1	13001331	13001331	Missense_Mutation	SNP	C	T	14	363	c.352G>A	c.(352-354)GAA>AAA	p.E118K
Pat_04	Pre-Treatment	CLCNKA	1187	37	1	16351312	16351312	Missense_Mutation	SNP	C	T	8	43	c.284C>T	c.(283-285)TCC>TTC	p.S95F
Pat_04	Pre-Treatment	ACTL8	81569	37	1	18152898	18152898	Missense_Mutation	SNP	G	A	5	67	c.985G>A	c.(985-987)GAG>AAG	p.E329K
Pat_04	Pre-Treatment	CAMK2N1	55450	37	1	20810152	20810152	Missense_Mutation	SNP	G	A	13	71	c.227C>T	c.(226-228)CCT>CTT	p.P76L
Pat_04	Pre-Treatment	CSMD2	114784	37	1	34276436	34276436	Missense_Mutation	SNP	G	A	13	113	c.1234C>T	c.(1234-1236)CCC>TCC	p.P412S
Pat_04	Pre-Treatment	SFPQ	6421	37	1	35656483	35656483	Missense_Mutation	SNP	A	T	7	41	c.1131T>A	c.(1129-1131)AAT>AAA	p.N377K
Pat_04	Pre-Treatment	CSF3R	1441	37	1	36939068	36939068	Missense_Mutation	SNP	G	A	7	107	c.641C>T	c.(640-642)TCC>TTC	p.S214F
Pat_04	Pre-Treatment	GRIK3	2899	37	1	37291235	37291235	Missense_Mutation	SNP	C	T	3	28	c.1723G>A	c.(1723-1725)GGG>AGG	p.G575R
Pat_04	Pre-Treatment	DNALI1	7802	37	1	38022543	38022543	Missense_Mutation	SNP	A	G	6	53	c.14A>G	c.(13-15)AAC>AGC	p.N5S
Pat_04	Pre-Treatment	DNALI1	7802	37	1	38023207	38023207	Missense_Mutation	SNP	C	T	20	88	c.151C>T	c.(151-153)CGG>TGG	p.R51W
Pat_04	Pre-Treatment	CYP4X1	260293	37	1	47514288	47514288	Nonsense_Mutation	SNP	G	A	19	106	c.1259G>A	c.(1258-1260)TGG>TAG	p.W420*
Pat_04	Pre-Treatment	PODN	127435	37	1	53542998	53542998	Missense_Mutation	SNP	C	A	19	98	c.862C>A	c.(862-864)CTG>ATG	p.L288M
Pat_04	Pre-Treatment	LRRC42	115353	37	1	54432030	54432030	Missense_Mutation	SNP	C	T	15	75	c.989C>T	c.(988-990)CCT>CTT	p.P330L
Pat_04	Pre-Treatment	C8B	732	37	1	57422517	57422517	Missense_Mutation	SNP	C	T	19	136	c.316G>A	c.(316-318)GAA>AAA	p.E106K
Pat_04	Pre-Treatment	UBE2U	148581	37	1	64671364	64671364	Missense_Mutation	SNP	G	A	5	89	c.109G>A	c.(109-111)GAA>AAA	p.E37K
Pat_04	Pre-Treatment	SERBP1	26135	37	1	67881007	67881007	Missense_Mutation	SNP	A	G	11	85	c.1012T>C	c.(1012-1014)TCG>CCG	p.S338P
Pat_04	Pre-Treatment	RPE65	6121	37	1	68896804	68896804	Missense_Mutation	SNP	G	A	10	49	c.1394C>T	c.(1393-1395)TCA>TTA	p.S465L
Pat_04	Pre-Treatment	LRRIQ3	127255	37	1	74507480	74507480	Missense_Mutation	SNP	G	A	9	47	c.1135C>T	c.(1135-1137)CCT>TCT	p.P379S
Pat_04	Pre-Treatment	C1orf173	127254	37	1	75037778	75037778	Missense_Mutation	SNP	C	T	9	70	c.3616G>A	c.(3616-3618)GAA>AAA	p.E1206K
Pat_04	Pre-Treatment	C1orf173	127254	37	1	75039017	75039017	Missense_Mutation	SNP	C	T	15	113	c.2377G>A	c.(2377-2379)GGG>AGG	p.G793R
Pat_04	Pre-Treatment	SLC44A5	204962	37	1	75679418	75679418	Missense_Mutation	SNP	G	A	17	107	c.1934C>T	c.(1933-1935)TCT>TTT	p.S645F
Pat_04	Pre-Treatment	NEXN	91624	37	1	78392256	78392256	Missense_Mutation	SNP	G	A	7	35	c.647G>A	c.(646-648)CGA>CAA	p.R216Q
Pat_04	Pre-Treatment	NEXN	91624	37	1	78401698	78401698	Missense_Mutation	SNP	T	G	5	30	c.1442T>G	c.(1441-1443)ATT>AGT	p.I481S
Pat_04	Pre-Treatment	CLCA4	22802	37	1	87025664	87025664	Missense_Mutation	SNP	G	A	6	44	c.209G>A	c.(208-210)AGA>AAA	p.R70K
Pat_04	Pre-Treatment	CDC7	8317	37	1	91967356	91967356	Nonsense_Mutation	SNP	T	A	4	65	c.83T>A	c.(82-84)TTA>TAA	p.L28*
Pat_04	Pre-Treatment	OLFML3	56944	37	1	114523090	114523090	Missense_Mutation	SNP	C	T	15	42	c.251C>T	c.(250-252)TCC>TTC	p.S84F
Pat_04	Pre-Treatment	CD2	914	37	1	117303169	117303169	Nonsense_Mutation	SNP	G	A	11	66	c.528G>A	c.(526-528)TGG>TGA	p.W176*
Pat_04	Pre-Treatment	HSD3B1	3283	37	1	120056726	120056727	Missense_Mutation	DNP	GG	AA	11	64	c.580_581GG>AA	c.(580-582)GGA>AAA	p.G194K
Pat_04	Pre-Treatment	NBPF10	100132406	37	1	145327549	145327550	Missense_Mutation	DNP	AT	TC	6	34	.4331_4332AT>T	c.(4330-4332)AAT>ATC	p.N1444I
Pat_04	Pre-Treatment	ECM1	1893	37	1	150482203	150482203	Missense_Mutation	SNP	C	T	24	133	c.188C>T	c.(187-189)TCT>TTT	p.S63F
Pat_04	Pre-Treatment	HRNR	388697	37	1	152192982	152192982	Missense_Mutation	SNP	C	T	13	93	c.1123G>A	c.(1123-1125)GGA>AGA	p.G375R
Pat_04	Pre-Treatment	FLG	2312	37	1	152279644	152279644	Missense_Mutation	SNP	C	T	20	152	c.7718G>A	c.(7717-7719)AGT>AAT	p.S2573N
Pat_04	Pre-Treatment	SPRR2G	6706	37	1	153122531	153122531	Missense_Mutation	SNP	G	A	23	173	c.56C>T	c.(55-57)CCC>CTC	p.P19L
Pat_04	Pre-Treatment	NPR1	4881	37	1	153654983	153654983	Missense_Mutation	SNP	G	A	8	47	c.1181G>A	c.(1180-1182)GGA>GAA	p.G394E
Pat_04	Pre-Treatment	NUP210L	91181	37	1	154061958	154061958	Missense_Mutation	SNP	G	A	32	203	c.2300C>T	c.(2299-2301)CCA>CTA	p.P767L
Pat_04	Pre-Treatment	PKLR	5313	37	1	155262980	155262980	Missense_Mutation	SNP	G	A	16	134	c.1424C>T	c.(1423-1425)ACC>ATC	p.T475I
Pat_04	Pre-Treatment	PAQR6	79957	37	1	156215359	156215359	Missense_Mutation	SNP	G	A	8	61	c.479C>T	c.(478-480)TCC>TTC	p.S160F
Pat_04	Pre-Treatment	IQGAP3	128239	37	1	156518436	156518436	Missense_Mutation	SNP	G	A	6	65	c.1930C>T	c.(1930-1932)CCC>TCC	p.P644S
Pat_04	Pre-Treatment	OR10K1	391109	37	1	158435715	158435715	Missense_Mutation	SNP	C	T	22	108	c.364C>T	c.(364-366)CGC>TGC	p.R122C

Pat_04	Pre-Treatment	OR10Z1	128368	37	1	158576979	158576979	Missense_Mutation	SNP	C	T	16	111	c.751C>T	c.(751-753)CAT>TAT	p.H251Y
Pat_04	Pre-Treatment	FCER1A	2205	37	1	159273945	159273945	Missense_Mutation	SNP	G	A	9	90	c.304G>A	c.(304-306)GAA>AAA	p.E102K
Pat_04	Pre-Treatment	FCER1A	2205	37	1	159275948	159275948	Missense_Mutation	SNP	G	A	7	75	c.502G>A	c.(502-504)GTT>ATT	p.V168I
Pat_04	Pre-Treatment	APCS	325	37	1	159558454	159558454	Missense_Mutation	SNP	G	A	9	62	c.628G>A	c.(628-630)GAA>AAA	p.E210K
Pat_04	Pre-Treatment	FCRL6	343413	37	1	159779306	159779306	Missense_Mutation	SNP	C	T	9	38	c.719C>T	c.(718-720)TCC>TTC	p.S240F
Pat_04	Pre-Treatment	SLAMF9	89886	37	1	159923915	159923915	Missense_Mutation	SNP	G	A	10	58	c.13C>T	c.(13-15)CCT>TCT	p.P5S
Pat_04	Pre-Treatment	SLAMF1	6504	37	1	160616672	160616672	Missense_Mutation	SNP	T	C	4	31	c.64A>G	c.(64-66)AGC>GGC	p.S22G
Pat_04	Pre-Treatment	ILDR2	387597	37	1	166927005	166927006	Splice_Site	DNP	CC	TT	7	51	c.379_splice	c.e2+1	p.D127_splice
Pat_04	Pre-Treatment	ADCY10	55811	37	1	167839549	167839549	Missense_Mutation	SNP	C	T	5	40	c.1562G>A	c.(1561-1563)GGA>GAA	p.G521E
Pat_04	Pre-Treatment	F5	2153	37	1	169495256	169495256	Splice_Site	SNP	C	T	4	31	c.5600_splice	c.e18-1	p.G1867_splice
Pat_04	Pre-Treatment	FMO1	2326	37	1	171254520	171254520	Missense_Mutation	SNP	G	A	6	36	c.1436G>A	c.(1435-1437)GGA>GAA	p.G479E
Pat_04	Pre-Treatment	C1orf9	51430	37	1	172522463	172522463	Missense_Mutation	SNP	T	C	16	108	c.241T>C	c.(241-243)TCT>CCT	p.S81P
Pat_04	Pre-Treatment	PAPPA2	60676	37	1	176680981	176680981	Missense_Mutation	SNP	C	T	16	122	c.3662C>T	c.(3661-3663)TCA>TTA	p.S1221L
Pat_04	Pre-Treatment	ANGPTL1	9068	37	1	178820285	178820285	Missense_Mutation	SNP	C	T	15	85	c.1455G>A	c.(1453-1455)ATG>ATA	p.M485I
Pat_04	Pre-Treatment	LHX4	89884	37	1	180243389	180243389	Missense_Mutation	SNP	G	A	13	79	c.848G>A	c.(847-849)GGA>GAA	p.G283E
Pat_04	Pre-Treatment	FAM129A	116496	37	1	184792417	184792417	Missense_Mutation	SNP	C	T	7	54	c.869G>A	c.(868-870)GGA>GAA	p.G290E
Pat_04	Pre-Treatment	PTGS2	5743	37	1	186645203	186645203	Missense_Mutation	SNP	G	C	22	190	c.1084C>G	c.(1084-1086)CGT>GGT	p.R362G
Pat_04	Pre-Treatment	PTGS2	5743	37	1	186648489	186648489	Missense_Mutation	SNP	G	A	8	40	c.134C>T	c.(133-135)ACC>ATC	p.T45I
Pat_04	Pre-Treatment	CFH	3075	37	1	196715001	196715001	Missense_Mutation	SNP	C	T	8	76	c.3365C>T	c.(3364-3366)TCA>TTA	p.S1122L
Pat_04	Pre-Treatment	CFHR5	81494	37	1	196953127	196953127	Missense_Mutation	SNP	C	T	5	47	c.290C>T	c.(289-291)TCT>TTT	p.S97F
Pat_04	Pre-Treatment	F13B	2165	37	1	197032172	197032172	Missense_Mutation	SNP	A	C	18	101	c.80T>G	c.(79-81)TTT>TGT	p.F27C
Pat_04	Pre-Treatment	ZBTB41	360023	37	1	197168712	197168712	Missense_Mutation	SNP	G	A	9	40	c.892C>T	c.(892-894)CCT>TCT	p.P298S
Pat_04	Pre-Treatment	PTPRC	5788	37	1	198700830	198700830	Missense_Mutation	SNP	G	A	15	89	c.1943G>A	c.(1942-1944)GGA>GAA	p.G648E
Pat_04	Pre-Treatment	CAMSAP1L1	23271	37	1	200816379	200816379	Missense_Mutation	SNP	C	T	6	59	c.1184C>T	c.(1183-1185)CCT>CTT	p.P395L
Pat_04	Pre-Treatment	MAPKAPK2	9261	37	1	206904574	206904574	Missense_Mutation	SNP	C	T	7	57	c.859C>T	c.(859-861)CCC>TCC	p.P287S
Pat_04	Pre-Treatment	C4BPA	722	37	1	207288861	207288861	Splice_Site	SNP	G	A	13	45	c.428_splice	c.e4+1	p.G143_splice
Pat_04	Pre-Treatment	CD34	947	37	1	208061265	208061265	Missense_Mutation	SNP	C	T	5	12	c.976G>A	c.(976-978)GAA>AAA	p.E326K
Pat_04	Pre-Treatment	INTS7	25896	37	1	212115237	212115237	Missense_Mutation	SNP	G	A	25	136	c.2818C>T	c.(2818-2820)CGC>TGC	p.R940C
Pat_04	Pre-Treatment	CENPF	1063	37	1	214818698	214818698	Missense_Mutation	SNP	C	G	12	78	c.5785C>G	c.(5785-5787)CAA>GAA	p.Q1929E
Pat_04	Pre-Treatment	CENPF	1063	37	1	214819239	214819239	Nonsense_Mutation	SNP	C	G	9	27	c.6326C>G	c.(6325-6327)TCA>TGA	p.S2109*
Pat_04	Pre-Treatment	CENPF	1063	37	1	214819542	214819542	Missense_Mutation	SNP	C	G	2	13	c.6629C>G	c.(6628-6630)TCT>TGT	p.S2210C
Pat_04	Pre-Treatment	USH2A	7399	37	1	215848705	215848705	Missense_Mutation	SNP	C	T	14	105	c.12548G>A	c.(12547-12549)GGA>GAA	p.G4183E
Pat_04	Pre-Treatment	USH2A	7399	37	1	215848928	215848928	Missense_Mutation	SNP	C	T	5	36	c.12325G>A	c.(12325-12327)GAG>AAG	p.E4109K
Pat_04	Pre-Treatment	C1orf65	164127	37	1	223568129	223568129	Missense_Mutation	SNP	G	A	4	20	c.1312G>A	c.(1312-1314)GAC>AAC	p.D438N
Pat_04	Pre-Treatment	LEFTY1	10637	37	1	226075325	226075325	Missense_Mutation	SNP	G	A	3	26	c.511C>T	c.(511-513)CAC>TAC	p.H171Y
Pat_04	Pre-Treatment	NID1	4811	37	1	236142388	236142388	Missense_Mutation	SNP	C	T	9	36	c.3529G>A	c.(3529-3531)GAT>AAT	p.D1177N
Pat_04	Pre-Treatment	ERO1LB	56605	37	1	236399699	236399699	Splice_Site	SNP	C	T	10	50	c.506_splice	c.e7-1	p.D169_splice
Pat_04	Pre-Treatment	EDARADD	128178	37	1	236590728	236590728	Missense_Mutation	SNP	G	A	8	27	c.197G>A	c.(196-198)CGA>CAA	p.R66Q
Pat_04	Pre-Treatment	FMN2	56776	37	1	240370756	240370756	Missense_Mutation	SNP	C	T	16	133	c.2644C>T	c.(2644-2646)CCT>TCT	p.P882S
Pat_04	Pre-Treatment	NLRP3	114548	37	1	247588630	247588630	Missense_Mutation	SNP	G	A	5	14	c.1885G>A	c.(1885-1887)GAA>AAA	p.E629K
Pat_04	Pre-Treatment	OR2M3	127062	37	1	248366913	248366913	Missense_Mutation	SNP	C	T	19	214	c.544C>T	c.(544-546)CCC>TCC	p.P182S
Pat_04	Pre-Treatment	AKR1C2	1646	37	10	5040933	5040933	Missense_Mutation	SNP	C	T	8	58	c.454G>A	c.(454-456)GAG>AAG	p.E152K
Pat_04	Pre-Treatment	PRKCQ	5588	37	10	6539184	6539184	Missense_Mutation	SNP	C	T	20	133	c.572G>A	c.(571-573)CGA>CAA	p.R191Q
Pat_04	Pre-Treatment	FAM171A1	221061	37	10	15296720	15296720	Missense_Mutation	SNP	C	T	4	11	c.577G>A	c.(577-579)GGA>AGA	p.G193R
Pat_04	Pre-Treatment	FAM188A	80013	37	10	15879309	15879309	Missense_Mutation	SNP	G	A	19	79	c.470C>T	c.(469-471)TCG>TTG	p.S157L
Pat_04	Pre-Treatment	NEBL	10529	37	10	21141577	21141577	Missense_Mutation	SNP	C	T	4	13	c.905G>A	c.(904-906)CGA>CAA	p.R302Q
Pat_04	Pre-Treatment	SPAG6	9576	37	10	22653876	22653876	Missense_Mutation	SNP	T	G	5	46	c.216T>G	c.(214-216)AAT>AAG	p.N72K

Pat_04	Pre-Treatment	KIAA1217	56243	37	10	24508702	24508702	Missense_Mutation	SNP	G	A	11	57	c.218G>A	c.(217-219)CGA>CAA	p.R73Q
Pat_04	Pre-Treatment	ARMC4	55130	37	10	28151512	28151512	Missense_Mutation	SNP	C	T	4	16	c.2650G>A	c.(2650-2652)GAA>AAA	p.E884K
Pat_04	Pre-Treatment	ANKRD30A	91074	37	10	37430948	37430948	Missense_Mutation	SNP	C	G	4	52	c.955C>G	c.(955-957)CCA>GCA	p.P319A
Pat_04	Pre-Treatment	ANKRD30A	91074	37	10	37442579	37442579	Missense_Mutation	SNP	G	A	7	123	c.1619G>A	c.(1618-1620)GGA>GAA	p.G540E
Pat_04	Pre-Treatment	GDF10	2662	37	10	48426748	48426748	Missense_Mutation	SNP	G	A	14	82	c.1259C>T	c.(1258-1260)TCC>TTC	p.S420F
Pat_04	Pre-Treatment	C10orf71	118461	37	10	50531497	50531497	Missense_Mutation	SNP	C	T	6	37	c.907C>T	c.(907-909)CCC>TCC	p.P303S
Pat_04	Pre-Treatment	OGDHL	55753	37	10	50944432	50944432	Missense_Mutation	SNP	C	T	14	127	c.2725G>A	c.(2725-2727)GAG>AAG	p.E909K
Pat_04	Pre-Treatment	PCDH15	65217	37	10	55582222	55582222	Missense_Mutation	SNP	G	A	4	10	c.5264C>T	c.(5263-5265)CCT>CTT	p.P1755L
Pat_04	Pre-Treatment	PCDH15	65217	37	10	55582895	55582895	Missense_Mutation	SNP	C	T	8	63	c.4591G>A	c.(4591-4593)GAA>AAA	p.E1531K
Pat_04	Pre-Treatment	BICC1	80114	37	10	60566860	60566860	Missense_Mutation	SNP	A	C	21	81	c.2318A>C	c.(2317-2319)AAG>ACG	p.K773T
Pat_04	Pre-Treatment	FAM13C	220965	37	10	61029693	61029693	Missense_Mutation	SNP	C	T	7	66	c.769G>A	c.(769-771)GCC>ACC	p.A257T
Pat_04	Pre-Treatment	ANK3	288	37	10	61835412	61835412	Missense_Mutation	SNP	C	T	3	27	c.5227G>A	c.(5227-5229)GAA>AAA	p.E1743K
Pat_04	Pre-Treatment	ANK3	288	37	10	61835855	61835855	Missense_Mutation	SNP	G	A	15	100	c.4784C>T	c.(4783-4785)TCC>TTC	p.S1595F
Pat_04	Pre-Treatment	ADAMTS14	140766	37	10	72511379	72511379	Missense_Mutation	SNP	C	T	4	32	c.2573C>T	c.(2572-2574)CCC>CTC	p.P858L
Pat_04	Pre-Treatment	LIPF	8513	37	10	90435380	90435380	Missense_Mutation	SNP	G	A	10	46	c.854G>A	c.(853-855)GGA>GAA	p.G285E
Pat_04	Pre-Treatment	CYP26A1	1592	37	10	94836867	94836867	Missense_Mutation	SNP	C	T	5	26	c.1300C>T	c.(1300-1302)CCA>TCA	p.P434S
Pat_04	Pre-Treatment	GPR120	338557	37	10	95335855	95335855	Missense_Mutation	SNP	C	T	8	78	c.575C>T	c.(574-576)TCG>TTG	p.S192L
Pat_04	Pre-Treatment	CYP2C18	1562	37	10	96447650	96447650	Missense_Mutation	SNP	G	A	10	96	c.292G>A	c.(292-294)GGA>AGA	p.G98R
Pat_04	Pre-Treatment	CYP2C8	1558	37	10	96802823	96802823	Missense_Mutation	SNP	C	T	7	26	c.973G>A	c.(973-975)GAA>AAA	p.E325K
Pat_04	Pre-Treatment	INA	9118	37	10	105048248	105048248	Missense_Mutation	SNP	C	T	11	109	c.1322C>T	c.(1321-1323)TCC>TTC	p.S441F
Pat_04	Pre-Treatment	PCGF6	84108	37	10	105106997	105106997	Missense_Mutation	SNP	G	A	4	46	c.671C>T	c.(670-672)CCT>CTT	p.P224L
Pat_04	Pre-Treatment	TAF5	6877	37	10	105147305	105147305	Missense_Mutation	SNP	C	T	12	63	c.2035C>T	c.(2035-2037)CCC>TCC	p.P679S
Pat_04	Pre-Treatment	CCDC147	159686	37	10	106160585	106160585	Missense_Mutation	SNP	C	T	6	40	c.1963C>T	c.(1963-1965)CTC>TTC	p.L655F
Pat_04	Pre-Treatment	AFAP1L2	84632	37	10	116075447	116075447	Nonsense_Mutation	SNP	G	A	3	13	c.484C>T	c.(484-486)CAG>TAG	p.Q162*
Pat_04	Pre-Treatment	HTRA1	5654	37	10	124248449	124248449	Missense_Mutation	SNP	A	T	11	122	c.504A>T	c.(502-504)AAA>AAT	p.K168N
Pat_04	Pre-Treatment	DMBT1	1755	37	10	124336068	124336068	Missense_Mutation	SNP	G	A	34	150	c.437G>A	c.(436-438)GGC>GAC	p.G146D
Pat_04	Pre-Treatment	DMBT1	1755	37	10	124351788	124351788	Missense_Mutation	SNP	G	A	29	199	c.2177G>A	c.(2176-2178)GGA>GAA	p.G726E
Pat_04	Pre-Treatment	DMBT1	1755	37	10	124358589	124358589	Missense_Mutation	SNP	G	A	11	86	c.3256G>A	c.(3256-3258)GAA>AAA	p.E1086K
Pat_04	Pre-Treatment	C10orf120	399814	37	10	124457694	124457694	Missense_Mutation	SNP	C	T	11	60	c.563G>A	c.(562-564)AGG>AAG	p.R188K
Pat_04	Pre-Treatment	MKI67	4288	37	10	129901363	129901363	Missense_Mutation	SNP	G	A	16	101	c.8741C>T	c.(8740-8742)CCC>CTC	p.P2914L
Pat_04	Pre-Treatment	CDHR5	53841	37	11	618803	618803	Missense_Mutation	SNP	T	C	3	119	c.1756A>G	c.(1756-1758)ATG>GTG	p.M586V
Pat_04	Pre-Treatment	MUC5B	727897	37	11	1158952	1158952	Missense_Mutation	SNP	G	A	8	50	c.1130G>A	c.(1129-1131)GGG>GAG	p.G377E
Pat_04	Pre-Treatment	MUC5B	727897	37	11	1159051	1159051	Missense_Mutation	SNP	C	T	9	53	c.1229C>T	c.(1228-1230)TCC>TTC	p.S410F
Pat_04	Pre-Treatment	OR52K2	119774	37	11	4471474	4471474	Missense_Mutation	SNP	G	A	9	49	c.905G>A	c.(904-906)CGT>CAT	p.R302H
Pat_04	Pre-Treatment	OR52K1	390036	37	11	4510305	4510305	Missense_Mutation	SNP	G	A	14	75	c.175G>A	c.(175-177)GAA>AAA	p.E59K
Pat_04	Pre-Treatment	OR51E2	81285	37	11	4703494	4703494	Missense_Mutation	SNP	G	A	5	29	c.448C>T	c.(448-450)CGC>TGC	p.R150C
Pat_04	Pre-Treatment	OR51B2	79345	37	11	5344611	5344611	Missense_Mutation	SNP	G	A	8	34	c.917C>T	c.(916-918)TCT>TTT	p.S306F
Pat_04	Pre-Treatment	DCHS1	8642	37	11	6647528	6647528	Missense_Mutation	SNP	C	T	3	18	c.6448G>A	c.(6448-6450)GGA>AGA	p.G2150R
Pat_04	Pre-Treatment	OR10A4	283297	37	11	6898467	6898467	Missense_Mutation	SNP	G	C	10	67	c.589G>C	c.(589-591)GAA>CAA	p.E197Q
Pat_04	Pre-Treatment	OR10A6	390093	37	11	7949304	7949304	Missense_Mutation	SNP	C	T	15	109	c.906G>A	c.(904-906)ATG>ATA	p.M302I
Pat_04	Pre-Treatment	OR10A6	390093	37	11	7949711	7949711	Missense_Mutation	SNP	G	A	3	21	c.499C>T	c.(499-501)CCC>TCC	p.P167S
Pat_04	Pre-Treatment	NLRP10	338322	37	11	7982236	7982236	Missense_Mutation	SNP	C	T	13	60	c.923G>A	c.(922-924)CGT>CAT	p.R308H
Pat_04	Pre-Treatment	LMO1	4004	37	11	8251941	8251941	Missense_Mutation	SNP	C	T	17	109	c.136G>A	c.(136-138)GAA>AAA	p.E46K
Pat_04	Pre-Treatment	SLC6A5	9152	37	11	20658828	20658828	Missense_Mutation	SNP	G	A	5	57	c.1848G>A	c.(1846-1848)ATG>ATA	p.M616I
Pat_04	Pre-Treatment	NELL1	4745	37	11	20949942	20949942	Missense_Mutation	SNP	G	A	30	147	c.914G>A	c.(913-915)CGA>CAA	p.R305Q
Pat_04	Pre-Treatment	SYT13	57586	37	11	45265844	45265844	Missense_Mutation	SNP	C	T	7	72	c.1040G>A	c.(1039-1041)CGA>CAA	p.R347Q
Pat_04	Pre-Treatment	PHF21A	51317	37	11	46098346	46098346	Missense_Mutation	SNP	G	A	17	80	c.112C>T	c.(112-114)CAT>TAT	p.H38Y

Pat_04	Pre-Treatment	LRP4	4038	37	11	46896442	46896442	Missense_Mutation	SNP	G	A	13	127	c.4138C>T	c.(4138-4140)CCT>TCT	p.P1380S
Pat_04	Pre-Treatment	LOC440040	440040	37	11	49597970	49597970	Missense_Mutation	SNP	G	A	10	36	c.83G>A	c.(82-84)GGG>GAG	p.G28E
Pat_04	Pre-Treatment	OR4C6	219432	37	11	55433183	55433183	Nonsense_Mutation	SNP	C	T	5	91	c.541C>T	c.(541-543)CAG>TAG	p.Q181*
Pat_04	Pre-Treatment	OR5L2	26338	37	11	55594988	55594988	Missense_Mutation	SNP	G	A	20	159	c.294G>A	c.(292-294)ATG>ATA	p.M98I
Pat_04	Pre-Treatment	OR8K3	219473	37	11	56086408	56086408	Missense_Mutation	SNP	C	T	5	26	c.626C>T	c.(625-627)TCA>TTA	p.S209L
Pat_04	Pre-Treatment	OR5M8	219484	37	11	56258200	56258200	Missense_Mutation	SNP	G	A	5	22	c.647C>T	c.(646-648)TCC>TTC	p.S216F
Pat_04	Pre-Treatment	OR5AP2	338675	37	11	56409825	56409825	Missense_Mutation	SNP	C	T	10	58	c.91G>A	c.(91-93)GGA>AGA	p.G31R
Pat_04	Pre-Treatment	SERPING1	710	37	11	57373665	57373665	Missense_Mutation	SNP	C	T	16	152	c.868C>T	c.(868-870)CTC>TTC	p.L290F
Pat_04	Pre-Treatment	OR6Q1	219952	37	11	57799199	57799199	Missense_Mutation	SNP	C	T	15	111	c.775C>T	c.(775-777)CTT>TTT	p.L259F
Pat_04	Pre-Treatment	OR5AN1	390195	37	11	59132740	59132740	Missense_Mutation	SNP	G	A	9	55	c.809G>A	c.(808-810)AGC>AAC	p.S270N
Pat_04	Pre-Treatment	OR4D11	219986	37	11	59271557	59271557	Missense_Mutation	SNP	G	A	28	166	c.509G>A	c.(508-510)GGA>GAA	p.G170E
Pat_04	Pre-Treatment	SCGB1D1	10648	37	11	61960872	61960872	Missense_Mutation	SNP	G	A	5	36	c.245G>A	c.(244-246)GGA>GAA	p.G82E
Pat_04	Pre-Treatment	EML3	256364	37	11	62377131	62377131	Missense_Mutation	SNP	G	A	14	217	c.604C>T	c.(604-606)CCT>TCT	p.P202S
Pat_04	Pre-Treatment	TTC9C	283237	37	11	62502877	62502877	Missense_Mutation	SNP	G	A	3	41	c.262G>A	c.(262-264)GTG>ATG	p.V88M
Pat_04	Pre-Treatment	SLC22A25	387601	37	11	62931333	62931333	Missense_Mutation	SNP	T	A	20	70	c.1607A>T	c.(1606-1608)AAT>ATT	p.N536I
Pat_04	Pre-Treatment	NPAS4	266743	37	11	66190283	66190283	Missense_Mutation	SNP	C	T	17	98	c.569C>T	c.(568-570)GCT>GTT	p.A190V
Pat_04	Pre-Treatment	NPAS4	266743	37	11	66192379	66192379	Missense_Mutation	SNP	C	T	15	100	c.2018C>T	c.(2017-2019)TCC>TTC	p.S673F
Pat_04	Pre-Treatment	ACTN3	89	37	11	66325562	66325562	Missense_Mutation	SNP	C	T	5	21	c.1193C>T	c.(1192-1194)TCG>TTG	p.S398L
Pat_04	Pre-Treatment	GPR152	390212	37	11	67219541	67219541	Missense_Mutation	SNP	C	T	5	32	c.655G>A	c.(655-657)GCC>ACC	p.A219T
Pat_04	Pre-Treatment	SHANK2	22941	37	11	70331654	70331654	Missense_Mutation	SNP	G	A	8	88	c.4744C>T	c.(4744-4746)CCC>TCC	p.P1582S
Pat_04	Pre-Treatment	SHANK2	22941	37	11	70349008	70349008	Missense_Mutation	SNP	C	T	11	100	c.2090G>A	c.(2089-2091)GGC>GAC	p.G697D
Pat_04	Pre-Treatment	ARHGEF17	9828	37	11	73073768	73073768	Missense_Mutation	SNP	C	T	10	64	c.4985C>T	c.(4984-4986)TCC>TTC	p.S1662F
Pat_04	Pre-Treatment	CNTN5	53942	37	11	99827585	99827585	Missense_Mutation	SNP	G	A	13	76	c.721G>A	c.(721-723)GAA>AAA	p.E241K
Pat_04	Pre-Treatment	MMP13	4322	37	11	102826054	102826054	Missense_Mutation	SNP	C	T	21	103	c.289G>A	c.(289-291)GGG>AGG	p.G97R
Pat_04	Pre-Treatment	DDI1	414301	37	11	103908697	103908697	Missense_Mutation	SNP	G	A	5	34	c.1147G>A	c.(1147-1149)GAA>AAA	p.E383K
Pat_04	Pre-Treatment	ARHGAP20	57569	37	11	110485305	110485305	Missense_Mutation	SNP	C	T	19	87	c.610G>A	c.(610-612)GAC>AAC	p.D204N
Pat_04	Pre-Treatment	PPP2R1B	5519	37	11	111613299	111613299	Missense_Mutation	SNP	G	A	11	48	c.1645C>T	c.(1645-1647)CGC>TGC	p.R549C
Pat_04	Pre-Treatment	BCO2	83875	37	11	112064712	112064712	Missense_Mutation	SNP	G	A	5	45	c.628G>A	c.(628-630)GAA>AAA	p.E210K
Pat_04	Pre-Treatment	NCAM1	4684	37	11	113102999	113102999	Missense_Mutation	SNP	C	T	8	63	c.1072C>T	c.(1072-1074)CGG>TGG	p.R358W
Pat_04	Pre-Treatment	HTR3A	3359	37	11	113860388	113860388	Missense_Mutation	SNP	C	T	18	91	c.1454C>T	c.(1453-1455)TCC>TTC	p.S485F
Pat_04	Pre-Treatment	APOA4	337	37	11	116692155	116692155	Missense_Mutation	SNP	C	T	28	172	c.619G>A	c.(619-621)GAA>AAA	p.E207K
Pat_04	Pre-Treatment	POU2F3	25833	37	11	120139927	120139927	Nonsense_Mutation	SNP	C	T	3	37	c.106C>T	c.(106-108)CGA>TGA	p.R36*
Pat_04	Pre-Treatment	SORL1	6653	37	11	121425911	121425911	Missense_Mutation	SNP	G	A	5	59	c.2455G>A	c.(2455-2457)GGA>AGA	p.G819R
Pat_04	Pre-Treatment	OR8G2	26492	37	11	124095851	124095851	Missense_Mutation	SNP	C	T	37	180	c.454C>T	c.(454-456)CAC>TAC	p.H152Y
Pat_04	Pre-Treatment	OR8B8	26493	37	11	124310962	124310962	Missense_Mutation	SNP	G	A	6	50	c.20C>T	c.(19-21)TCC>TTC	p.S7F
Pat_04	Pre-Treatment	STT3A	3703	37	11	125472736	125472736	Missense_Mutation	SNP	C	T	12	74	c.310C>T	c.(310-312)CAT>TAT	p.H104Y
Pat_04	Pre-Treatment	NTM	50863	37	11	132016408	132016408	Missense_Mutation	SNP	G	A	4	23	c.400G>A	c.(400-402)GTA>ATA	p.V134I
Pat_04	Pre-Treatment	ENO2	2026	37	12	7026828	7026828	Missense_Mutation	SNP	C	T	8	64	c.394C>T	c.(394-396)CGC>TGC	p.R132C
Pat_04	Pre-Treatment	CD163L1	283316	37	12	7586282	7586282	Missense_Mutation	SNP	C	T	22	93	c.133G>A	c.(133-135)GAT>AAT	p.D45N
Pat_04	Pre-Treatment	CD163	9332	37	12	7635262	7635262	Missense_Mutation	SNP	C	T	17	106	c.3224G>A	c.(3223-3225)CGA>CAA	p.R1075Q
Pat_04	Pre-Treatment	AICDA	57379	37	12	8757868	8757868	Missense_Mutation	SNP	C	T	5	25	c.370G>A	c.(370-372)GAG>AAG	p.E124K
Pat_04	Pre-Treatment	PIK3C2G	5288	37	12	18699326	18699326	Missense_Mutation	SNP	C	T	3	15	c.3427C>T	c.(3427-3429)CCA>TCA	p.P1143S
Pat_04	Pre-Treatment	PDE3A	5139	37	12	20766384	20766384	Missense_Mutation	SNP	G	A	7	35	c.1019G>A	c.(1018-1020)GGA>GAA	p.G340E
Pat_04	Pre-Treatment	IAPP	3375	37	12	21526270	21526270	Splice_Site	SNP	G	A	6	41	c.-14_splice	c.e2-1	
Pat_04	Pre-Treatment	TM7SF3	51768	37	12	27128554	27128554	Missense_Mutation	SNP	G	A	10	22	c.1325C>T	c.(1324-1326)TCG>TTG	p.S442L
Pat_04	Pre-Treatment	ARID2	196528	37	12	46243512	46243512	Missense_Mutation	SNP	T	C	29	222	c.1865T>C	c.(1864-1866)GTT>GCT	p.V622A
Pat_04	Pre-Treatment	OR8S1	341568	37	12	48920268	48920268	Missense_Mutation	SNP	C	T	3	47	c.854C>T	c.(853-855)TCC>TTC	p.S285F

Pat_04	Pre-Treatment	SPATS2	65244	37	12	49918579	49918579	Missense_Mutation	SNP	C	T	24	142	c.1226C>T	c.(1225-1227)CCT>CTT	p.P409L
Pat_04	Pre-Treatment	FAM186B	84070	37	12	49992716	49992716	Missense_Mutation	SNP	T	C	9	33	c.2186A>G	c.(2185-2187)AAC>AGC	p.N729S
Pat_04	Pre-Treatment	SMARCD1	6602	37	12	50492520	50492521	Missense_Mutation	DNP	CC	TT	7	64	.1416_1417CC>T	414-1419)AACCCA>AATT	p.P473S
Pat_04	Pre-Treatment	GPD1	2819	37	12	50501428	50501428	Missense_Mutation	SNP	G	A	28	163	c.691G>A	c.(691-693)GGA>AGA	p.G231R
Pat_04	Pre-Treatment	DIP2B	57609	37	12	51112507	51112507	Missense_Mutation	SNP	C	T	5	37	c.2867C>T	c.(2866-2868)TCC>TTC	p.S956F
Pat_04	Pre-Treatment	KRT73	319101	37	12	53012103	53012103	Missense_Mutation	SNP	C	T	22	171	c.206G>A	c.(205-207)GGA>GAA	p.G69E
Pat_04	Pre-Treatment	KRT76	51350	37	12	53169247	53169247	Missense_Mutation	SNP	G	A	20	84	c.740C>T	c.(739-741)TCA>TTA	p.S247L
Pat_04	Pre-Treatment	RARG	5916	37	12	53605618	53605619	Missense_Mutation	DNP	CC	TT	4	25	.1206_1207GG>A	204-1209)ATGGAG>ATAA	.402_403ME>I
Pat_04	Pre-Treatment	SP7	121340	37	12	53722944	53722945	Missense_Mutation	DNP	GG	AA	7	98	c.281_282CC>TT	c.(280-282)CCC>CTT	p.P94L
Pat_04	Pre-Treatment	OR6C6	283365	37	12	55688815	55688815	Missense_Mutation	SNP	C	T	9	29	c.202G>A	c.(202-204)GAA>AAA	p.E68K
Pat_04	Pre-Treatment	OR6C75	390323	37	12	55759078	55759078	Missense_Mutation	SNP	C	T	16	108	c.184C>T	c.(184-186)CGG>TGG	p.R62W
Pat_04	Pre-Treatment	AGAP2	116986	37	12	58135698	58135698	Nonsense_Mutation	SNP	G	A	24	126	c.157C>T	c.(157-159)CGA>TGA	p.R53*
Pat_04	Pre-Treatment	AVIL	10677	37	12	58203639	58203639	Missense_Mutation	SNP	C	T	12	55	c.796G>A	c.(796-798)GAG>AAG	p.E266K
Pat_04	Pre-Treatment	C12orf66	144577	37	12	64588160	64588160	Missense_Mutation	SNP	G	A	6	42	c.800C>T	c.(799-801)GCC>GTC	p.A267V
Pat_04	Pre-Treatment	GRIP1	23426	37	12	66911727	66911727	Missense_Mutation	SNP	G	A	9	61	c.532C>T	c.(532-534)CGT>TGT	p.R178C
Pat_04	Pre-Treatment	TRHDE	29953	37	12	72771887	72771887	Missense_Mutation	SNP	C	T	9	57	c.1166C>T	c.(1165-1167)TCC>TTC	p.S389F
Pat_04	Pre-Treatment	KCNC2	3747	37	12	75441969	75441969	Missense_Mutation	SNP	C	T	32	186	c.1744G>A	c.(1744-1746)GAT>AAT	p.D582N
Pat_04	Pre-Treatment	NAV3	89795	37	12	78516155	78516156	Missense_Mutation	DNP	GG	AA	10	95	.4185_4186GG>A	183-4188)GAGGTC>GAA	p.V1396I
Pat_04	Pre-Treatment	LRRIQ1	84125	37	12	85517918	85517918	Missense_Mutation	SNP	G	A	15	47	c.3628G>A	c.(3628-3630)GAA>AAA	p.E1210K
Pat_04	Pre-Treatment	TMCC3	57458	37	12	94975716	94975716	Missense_Mutation	SNP	G	A	4	62	c.677C>T	c.(676-678)TCC>TTC	p.S226F
Pat_04	Pre-Treatment	TMPO	7112	37	12	98938042	98938043	Nonsense_Mutation	DNP	GG	AA	8	56	c.698_699GG>AA	c.(697-699)TGG>TAA	p.W233*
Pat_04	Pre-Treatment	MYBPC1	4604	37	12	102061659	102061659	Missense_Mutation	SNP	C	T	4	14	c.2485C>T	c.(2485-2487)CTC>TTC	p.L829F
Pat_04	Pre-Treatment	STAB2	55576	37	12	104131460	104131460	Missense_Mutation	SNP	C	T	16	90	c.5599C>T	c.(5599-5601)CTC>TTC	p.L1867F
Pat_04	Pre-Treatment	SELPLG	6404	37	12	109017999	109017999	Missense_Mutation	SNP	C	T	5	31	c.85G>A	c.(85-87)GAG>AAG	p.E29K
Pat_04	Pre-Treatment	MAPKAPK5	8550	37	12	112308962	112308962	Missense_Mutation	SNP	C	T	17	122	c.557C>T	c.(556-558)ACC>ATC	p.T186I
Pat_04	Pre-Treatment	NOS1	4842	37	12	117696239	117696239	Missense_Mutation	SNP	C	T	6	26	c.2494G>A	c.(2494-2496)GAA>AAA	p.E832K
Pat_04	Pre-Treatment	WDR66	144406	37	12	122437800	122437800	Missense_Mutation	SNP	G	A	14	64	c.3185G>A	c.(3184-3186)GGG>GAG	p.G1062E
Pat_04	Pre-Treatment	PITPNM2	57605	37	12	123475211	123475211	Missense_Mutation	SNP	G	A	4	42	c.2450C>T	c.(2449-2451)GCC>GTC	p.A817V
Pat_04	Pre-Treatment	TMEM132B	114795	37	12	126135239	126135239	Missense_Mutation	SNP	G	A	7	45	c.1639G>A	c.(1639-1641)GAA>AAA	p.E547K
Pat_04	Pre-Treatment	TMEM132B	114795	37	12	126137083	126137083	Missense_Mutation	SNP	G	C	8	79	c.1996G>C	c.(1996-1998)GCT>CCT	p.A666P
Pat_04	Pre-Treatment	ZNF140	7699	37	12	133682816	133682816	Missense_Mutation	SNP	G	A	23	132	c.953G>A	c.(952-954)CGA>CAA	p.R318Q
Pat_04	Pre-Treatment	GJB6	10804	37	13	20797567	20797567	Missense_Mutation	SNP	G	A	40	198	c.53C>T	c.(52-54)ACC>ATC	p.T18I
Pat_04	Pre-Treatment	KL	9365	37	13	33629411	33629411	Missense_Mutation	SNP	C	T	13	44	c.1558C>T	c.(1558-1560)CCC>TCC	p.P520S
Pat_04	Pre-Treatment	C13orf23	80209	37	13	39602432	39602432	Missense_Mutation	SNP	G	A	3	28	c.301C>T	c.(301-303)CGT>TGT	p.R101C
Pat_04	Pre-Treatment	KIAA0564	23078	37	13	42263512	42263512	Missense_Mutation	SNP	A	G	9	42	c.4109T>C	c.(4108-4110)GTT>GCT	p.V1370A
Pat_04	Pre-Treatment	DACH1	1602	37	13	72134038	72134038	Missense_Mutation	SNP	C	T	3	17	c.1349G>A	c.(1348-1350)AGA>AAA	p.R450K
Pat_04	Pre-Treatment	POTEG	404785	37	14	19553531	19553531	Missense_Mutation	SNP	G	A	5	214	c.115G>A	c.(115-117)GGC>AGC	p.G39S
Pat_04	Pre-Treatment	OR4K2	390431	37	14	20345124	20345124	Missense_Mutation	SNP	C	T	12	111	c.698C>T	c.(697-699)TCA>TTA	p.S233L
Pat_04	Pre-Treatment	OR4K1	79544	37	14	20404138	20404138	Missense_Mutation	SNP	C	T	17	78	c.313C>T	c.(313-315)CAC>TAC	p.H105Y
Pat_04	Pre-Treatment	OR4K13	390433	37	14	20502223	20502224	Nonsense_Mutation	DNP	CG	TA	7	59	c.694_695CG>TA	c.(694-696)CGA>TAA	p.R232*
Pat_04	Pre-Treatment	OR10G3	26533	37	14	22038587	22038587	Missense_Mutation	SNP	C	A	6	43	c.289G>T	c.(289-291)GGC>TGC	p.G97C
Pat_04	Pre-Treatment	OR4E2	26686	37	14	22133562	22133562	Missense_Mutation	SNP	G	A	30	165	c.266G>A	c.(265-267)AGA>AAA	p.R89K
Pat_04	Pre-Treatment	AKAP6	9472	37	14	33291502	33291502	Missense_Mutation	SNP	G	A	4	25	c.4483G>A	c.(4483-4485)GAG>AAG	p.E1495K
Pat_04	Pre-Treatment	AKAP6	9472	37	14	33292790	33292790	Missense_Mutation	SNP	G	A	5	44	c.5771G>A	c.(5770-5772)GGG>GAG	p.G1924E
Pat_04	Pre-Treatment	RALGAPA1	253959	37	14	36217895	36217895	Missense_Mutation	SNP	G	A	10	38	c.1147C>T	c.(1147-1149)CTC>TTC	p.L383F
Pat_04	Pre-Treatment	SSTR1	6751	37	14	38679634	38679634	Missense_Mutation	SNP	C	T	15	77	c.1040C>T	c.(1039-1041)GCG>GTG	p.A347V
Pat_04	Pre-Treatment	TRAPPC6B	122553	37	14	39623414	39623414	Splice_Site	SNP	C	T	5	15	c.351_splice	c.e4+1	p.K117_splice

Pat_04	Pre-Treatment	C14orf105	55195	37	14	57947409	57947409	Missense_Mutation	SNP	C	T	9	42	c.559G>A	c.(559-561)GAC>AAC	p.D187N
Pat_04	Pre-Treatment	C14orf37	145407	37	14	58605719	58605719	Missense_Mutation	SNP	G	A	10	71	c.358C>T	c.(358-360)CCC>TCC	p.P120S
Pat_04	Pre-Treatment	ADAM21	8747	37	14	70924389	70924389	Missense_Mutation	SNP	C	T	13	124	c.173C>T	c.(172-174)CCT>CTT	p.P58L
Pat_04	Pre-Treatment	DCAF4	26094	37	14	73425449	73425449	Missense_Mutation	SNP	C	T	28	131	c.1424C>T	c.(1423-1425)TCC>TTC	p.S475F
Pat_04	Pre-Treatment	MLH3	27030	37	14	75516045	75516045	Missense_Mutation	SNP	C	T	8	32	c.314G>A	c.(313-315)AGT>AAT	p.S105N
Pat_04	Pre-Treatment	NRXN3	9369	37	14	79432412	79432412	Missense_Mutation	SNP	G	A	11	41	c.1321G>A	c.(1321-1323)GAA>AAA	p.E441K
Pat_04	Pre-Treatment	C14orf145	145508	37	14	81302605	81302605	Missense_Mutation	SNP	G	A	23	117	c.1001C>T	c.(1000-1002)TCC>TTC	p.S334F
Pat_04	Pre-Treatment	GALC	2581	37	14	88417058	88417058	Missense_Mutation	SNP	A	C	3	32	c.1196T>G	c.(1195-1197)CTT>CGT	p.L399R
Pat_04	Pre-Treatment	ATG2B	55102	37	14	96783592	96783592	Missense_Mutation	SNP	G	A	8	30	c.3100C>T	c.(3100-3102)CGT>TGT	p.R1034C
Pat_04	Pre-Treatment	AK7	122481	37	14	96912921	96912921	Missense_Mutation	SNP	C	T	9	62	c.847C>T	c.(847-849)CAT>TAT	p.H283Y
Pat_04	Pre-Treatment	C14orf177	283598	37	14	99183486	99183486	Missense_Mutation	SNP	G	A	11	48	c.253G>A	c.(253-255)GAA>AAA	p.E85K
Pat_04	Pre-Treatment	OR4N4	283694	37	15	22383010	22383010	Missense_Mutation	SNP	G	A	16	104	c.538G>A	c.(538-540)GAT>AAT	p.D180N
Pat_04	Pre-Treatment	GOLGA8DP	100132979	37	15	22709716	22709716	Splice_Site	SNP	C	T	10	93	c.172_splice	c.e10-1	p.V58_splice
Pat_04	Pre-Treatment	MAGEL2	54551	37	15	23890470	23890470	Missense_Mutation	SNP	G	A	10	70	c.611C>T	c.(610-612)CCC>CTC	p.P204L
Pat_04	Pre-Treatment	NDN	4692	37	15	23932346	23932346	Missense_Mutation	SNP	C	T	6	35	c.19G>A	c.(19-21)GAT>AAT	p.D7N
Pat_04	Pre-Treatment	GABRB3	2562	37	15	26825489	26825489	Nonsense_Mutation	SNP	G	T	10	107	c.659C>A	c.(658-660)TCG>TAG	p.S220*
Pat_04	Pre-Treatment	GABRB3	2562	37	15	27184461	27184461	Nonsense_Mutation	SNP	C	T	17	61	c.123G>A	c.(121-123)TGG>TGA	p.W41*
Pat_04	Pre-Treatment	TRPM1	4308	37	15	31318400	31318401	Missense_Mutation	DNP	CC	TT	4	32	.3504_3505GG>A	502-3507)CGGGAG>CGA	p.E1169K
Pat_04	Pre-Treatment	FMN1	342184	37	15	33261588	33261588	Missense_Mutation	SNP	C	T	24	186	c.1645G>A	c.(1645-1647)GAG>AAG	p.E549K
Pat_04	Pre-Treatment	CHRM5	1133	37	15	34355453	34355453	Missense_Mutation	SNP	C	T	35	182	c.535C>T	c.(535-537)CCA>TCA	p.P179S
Pat_04	Pre-Treatment	C15orf53	400359	37	15	38990511	38990511	Missense_Mutation	SNP	G	A	6	51	c.305G>A	c.(304-306)GGA>GAA	p.G102E
Pat_04	Pre-Treatment	JMJD7-PLA2G4B	8681	37	15	42138213	42138213	Nonsense_Mutation	SNP	G	A	7	39	c.1568G>A	c.(1567-1569)TGG>TAG	p.W523*
Pat_04	Pre-Treatment	SPTBN5	51332	37	15	42173383	42173383	Missense_Mutation	SNP	G	A	5	26	c.2402C>T	c.(2401-2403)CCC>CTC	p.P801L
Pat_04	Pre-Treatment	ZFP106	64397	37	15	42743893	42743893	Missense_Mutation	SNP	C	T	8	36	c.508G>A	c.(508-510)GGC>AGC	p.G170S
Pat_04	Pre-Treatment	TGM5	9333	37	15	43527730	43527730	Missense_Mutation	SNP	C	T	9	53	c.1651G>A	c.(1651-1653)GAT>AAT	p.D551N
Pat_04	Pre-Treatment	TUBGCP4	27229	37	15	43668311	43668311	Missense_Mutation	SNP	C	T	49	140	c.94C>T	c.(94-96)CCT>TCT	p.P32S
Pat_04	Pre-Treatment	FBN1	2200	37	15	48808466	48808466	Missense_Mutation	SNP	G	A	16	133	c.1241C>T	c.(1240-1242)CCT>CTT	p.P414L
Pat_04	Pre-Treatment	SHC4	399694	37	15	49176530	49176530	Missense_Mutation	SNP	T	A	8	45	c.755A>T	c.(754-756)AAA>ATA	p.K252I
Pat_04	Pre-Treatment	TRPM7	54822	37	15	50888521	50888521	Missense_Mutation	SNP	G	A	13	31	c.3221C>T	c.(3220-3222)CCA>CTA	p.P1074L
Pat_04	Pre-Treatment	GCNT3	9245	37	15	59910526	59910526	Missense_Mutation	SNP	C	T	10	54	c.89C>T	c.(88-90)TCT>TTT	p.S30F
Pat_04	Pre-Treatment	ZNF609	23060	37	15	64968294	64968294	Missense_Mutation	SNP	C	T	9	78	c.3241C>T	c.(3241-3243)CCC>TCC	p.P1081S
Pat_04	Pre-Treatment	MAP2K1	5604	37	15	66729162	66729162	Missense_Mutation	SNP	C	T	13	63	c.370C>T	c.(370-372)CCG>TCG	p.P124S
Pat_04	Pre-Treatment	LBXCOR1	390598	37	15	68125575	68125576	Missense_Mutation	DNP	CC	TT	5	67	.2651_2652CC>T	c.(2650-2652)GCC>GTT	p.A884V
Pat_04	Pre-Treatment	STRA6	64220	37	15	74487802	74487802	Nonsense_Mutation	SNP	C	T	4	18	c.438G>A	c.(436-438)TGG>TGA	p.W146*
Pat_04	Pre-Treatment	NRG4	145957	37	15	76301551	76301551	Missense_Mutation	SNP	G	A	24	72	c.94C>T	c.(94-96)CCA>TCA	p.P32S
Pat_04	Pre-Treatment	SCAPER	49855	37	15	76726576	76726576	Missense_Mutation	SNP	C	T	17	105	c.3154G>A	c.(3154-3156)GGA>AGA	p.G1052R
Pat_04	Pre-Treatment	AP3B2	8120	37	15	83350179	83350179	Missense_Mutation	SNP	G	A	5	45	c.514C>T	c.(514-516)CTC>TTC	p.L172F
Pat_04	Pre-Treatment	ADAMTSL3	57188	37	15	84566668	84566668	Missense_Mutation	SNP	G	A	10	90	c.1526G>A	c.(1525-1527)CGC>CAC	p.R509H
Pat_04	Pre-Treatment	POLG	5428	37	15	89870446	89870446	Missense_Mutation	SNP	G	A	8	104	c.1385C>T	c.(1384-1386)TCG>TTG	p.S462L
Pat_04	Pre-Treatment	PDIA2	64714	37	16	333362	333362	Missense_Mutation	SNP	G	A	4	40	c.193G>A	c.(193-195)GAA>AAA	p.E65K
Pat_04	Pre-Treatment	IFT140	9742	37	16	1636207	1636207	Missense_Mutation	SNP	C	T	14	88	c.1079G>A	c.(1078-1080)AGC>AAC	p.S360N
Pat_04	Pre-Treatment	PRSS22	64063	37	16	2905608	2905608	Missense_Mutation	SNP	A	C	16	78	c.526T>G	c.(526-528)TGG>GGG	p.W176G
Pat_04	Pre-Treatment	C16orf68	79091	37	16	8722796	8722796	Nonsense_Mutation	SNP	C	T	10	52	c.343C>T	c.(343-345)CAG>TAG	p.Q115*
Pat_04	Pre-Treatment	MYH11	4629	37	16	15818560	15818560	Missense_Mutation	SNP	C	T	14	115	c.4060G>A	c.(4060-4062)GAG>AAG	p.E1354K
Pat_04	Pre-Treatment	ACSM5	54988	37	16	20441100	20441100	Missense_Mutation	SNP	G	A	6	50	c.1102G>A	c.(1102-1104)GAA>AAA	p.E368K
Pat_04	Pre-Treatment	ACSM5	54988	37	16	20442640	20442640	Nonsense_Mutation	SNP	T	G	13	84	c.1305T>G	c.(1303-1305)TAT>TAG	p.Y435*
Pat_04	Pre-Treatment	ACSM2B	348158	37	16	20570625	20570625	Missense_Mutation	SNP	G	A	7	40	c.322C>T	c.(322-324)CGT>TGT	p.R108C

Pat_04	Pre-Treatment	ADCY7	113	37	16	50339482	50339482	Missense_Mutation	SNP	G	A	21	88	c.1664G>A	c.(1663-1665)GGG>GAG	p.G555E
Pat_04	Pre-Treatment	SALL1	6299	37	16	51173753	51173753	Missense_Mutation	SNP	G	A	8	55	c.2380C>T	c.(2380-2382)CCC>TCC	p.P794S
Pat_04	Pre-Treatment	NLRC5	84166	37	16	57059817	57059817	Missense_Mutation	SNP	C	T	9	63	c.962C>T	c.(961-963)CCA>CTA	p.P321L
Pat_04	Pre-Treatment	ELMO3	79767	37	16	67236560	67236560	Missense_Mutation	SNP	C	T	9	41	c.1588C>T	c.(1588-1590)CGC>TGC	p.R530C
Pat_04	Pre-Treatment	LCAT	3931	37	16	67974168	67974168	Missense_Mutation	SNP	G	A	8	46	c.962C>T	c.(961-963)TCA>TTA	p.S321L
Pat_04	Pre-Treatment	MLKL	197259	37	16	74719425	74719425	Missense_Mutation	SNP	G	A	11	29	c.779C>T	c.(778-780)CCC>CTC	p.P260L
Pat_04	Pre-Treatment	COTL1	23406	37	16	84600458	84600458	Missense_Mutation	SNP	G	T	7	36	c.422C>A	c.(421-423)ACG>AAG	p.T141K
Pat_04	Pre-Treatment	CTU2	348180	37	16	88778062	88778062	Missense_Mutation	SNP	C	T	10	61	c.302C>T	c.(301-303)GCC>GTC	p.A101V
Pat_04	Pre-Treatment	SERPINF2	5345	37	17	1657799	1657799	Missense_Mutation	SNP	G	A	13	90	c.1447G>A	c.(1447-1449)GAT>AAT	p.D483N
Pat_04	Pre-Treatment	OR1G1	8390	37	17	3029911	3029911	Missense_Mutation	SNP	G	A	6	43	c.935C>T	c.(934-936)TCC>TTC	p.S312F
Pat_04	Pre-Treatment	SPNS3	201305	37	17	4352673	4352673	Missense_Mutation	SNP	A	G	3	15	c.914A>G	c.(913-915)AAC>AGC	p.N305S
Pat_04	Pre-Treatment	ASGR2	433	37	17	7017463	7017463	Missense_Mutation	SNP	G	A	18	95	c.97C>T	c.(97-99)CCC>TCC	p.P33S
Pat_04	Pre-Treatment	SENP3	26168	37	17	7473708	7473709	Missense_Mutation	DNP	CC	TT	4	69	.1376_1377CC>T	c.(1375-1377)CCC>CTT	p.P459L
Pat_04	Pre-Treatment	C17orf68	80169	37	17	8132180	8132181	Missense_Mutation	DNP	GG	AA	3	14	.3251_3252CC>T	c.(3250-3252)GCC>GTT	p.A1084V
Pat_04	Pre-Treatment	PFAS	5198	37	17	8169252	8169253	Missense_Mutation	DNP	CC	TT	11	44	.2618_2619CC>T	c.(2617-2619)TCC>TTT	p.S873F
Pat_04	Pre-Treatment	USP43	124739	37	17	9596484	9596484	Missense_Mutation	SNP	C	T	3	29	c.1394C>T	c.(1393-1395)TCT>TTT	p.S465F
Pat_04	Pre-Treatment	MYH8	4626	37	17	10323496	10323496	Missense_Mutation	SNP	G	A	5	46	c.49C>T	c.(49-51)CCC>TCC	p.P17S
Pat_04	Pre-Treatment	MYH1	4619	37	17	10419317	10419317	Missense_Mutation	SNP	C	T	19	138	c.431G>A	c.(430-432)CGA>CAA	p.R144Q
Pat_04	Pre-Treatment	MYH2	4620	37	17	10432122	10432122	Missense_Mutation	SNP	C	T	13	65	c.3629G>A	c.(3628-3630)GGG>GAG	p.G1210E
Pat_04	Pre-Treatment	MYH2	4620	37	17	10436665	10436665	Missense_Mutation	SNP	C	T	15	82	c.2378G>A	c.(2377-2379)CGA>CAA	p.R793Q
Pat_04	Pre-Treatment	MYH3	4621	37	17	10545802	10545802	Missense_Mutation	SNP	A	G	7	96	c.1820T>C	c.(1819-1821)GTT>GCT	p.V607A
Pat_04	Pre-Treatment	DNAH9	1770	37	17	11775104	11775104	Splice_Site	SNP	G	A	9	40	c.10242_splice	c.e52+1	p.K3414_splice
Pat_04	Pre-Treatment	RICH2	9912	37	17	12832325	12832325	Missense_Mutation	SNP	G	A	4	34	c.544G>A	c.(544-546)GAA>AAA	p.E182K
Pat_04	Pre-Treatment	MPRIP	23164	37	17	17062245	17062245	Missense_Mutation	SNP	G	A	3	39	c.1975G>A	c.(1975-1977)GTC>ATC	p.V659I
Pat_04	Pre-Treatment	TOP3A	7156	37	17	18194301	18194301	Missense_Mutation	SNP	A	T	9	64	c.1322T>A	c.(1321-1323)TTC>TAC	p.F441Y
Pat_04	Pre-Treatment	EPN2	22905	37	17	19237275	19237275	Missense_Mutation	SNP	C	T	6	25	c.1634C>T	c.(1633-1635)CCC>CTC	p.P545L
Pat_04	Pre-Treatment	FLJ40504	284085	37	17	26604047	26604047	Nonsense_Mutation	SNP	C	T	5	28	c.428G>A	c.(427-429)TGG>TAG	p.W143*
Pat_04	Pre-Treatment	PHF12	57649	37	17	27233933	27233933	Missense_Mutation	SNP	G	A	31	158	c.2621C>T	c.(2620-2622)TCG>TTG	p.S874L
Pat_04	Pre-Treatment	NUFIP2	57532	37	17	27613355	27613355	Missense_Mutation	SNP	G	A	11	49	c.1657C>T	c.(1657-1659)CCC>TCC	p.P553S
Pat_04	Pre-Treatment	SLFN11	91607	37	17	33690601	33690601	Missense_Mutation	SNP	C	T	19	149	c.226G>A	c.(226-228)GAT>AAT	p.D76N
Pat_04	Pre-Treatment	SLFN13	146857	37	17	33768054	33768054	Missense_Mutation	SNP	G	A	20	74	c.2254C>T	c.(2254-2256)CCT>TCT	p.P752S
Pat_04	Pre-Treatment	SLFN12L	342615	37	17	33802424	33802424	Missense_Mutation	SNP	T	A	3	22	c.1372A>T	c.(1372-1374)ATA>TTA	p.I458L
Pat_04	Pre-Treatment	CASC3	22794	37	17	38319744	38319744	Missense_Mutation	SNP	C	T	10	51	c.796C>T	c.(796-798)CCT>TCT	p.P266S
Pat_04	Pre-Treatment	KRT10	3858	37	17	38975078	38975078	Missense_Mutation	SNP	G	A	10	33	c.1709C>T	c.(1708-1710)TCT>TTT	p.S570F
Pat_04	Pre-Treatment	KRT34	3885	37	17	39535652	39535652	Missense_Mutation	SNP	G	A	47	99	c.955C>T	c.(955-957)CGC>TGC	p.R319C
Pat_04	Pre-Treatment	HAP1	9001	37	17	39881183	39881183	Missense_Mutation	SNP	C	T	99	217	c.1786G>A	c.(1786-1788)GAA>AAA	p.E596K
Pat_04	Pre-Treatment	CD300LG	146894	37	17	41930375	41930375	Missense_Mutation	SNP	G	A	21	42	c.475G>A	c.(475-477)GGA>AGA	p.G159R
Pat_04	Pre-Treatment	CRHR1	1394	37	17	43898765	43898765	Missense_Mutation	SNP	C	T	29	82	c.286C>T	c.(286-288)CGC>TGC	p.R96C
Pat_04	Pre-Treatment	MAPT	4137	37	17	44060753	44060753	Missense_Mutation	SNP	G	A	3	21	c.583G>A	c.(583-585)GAC>AAC	p.D195N
Pat_04	Pre-Treatment	ITGB3	3690	37	17	45369775	45369775	Missense_Mutation	SNP	G	A	40	68	c.1531G>A	c.(1531-1533)GAA>AAA	p.E511K
Pat_04	Pre-Treatment	HOXB5	3215	37	17	46669678	46669678	Missense_Mutation	SNP	C	T	49	126	c.703G>A	c.(703-705)GAG>AAG	p.E235K
Pat_04	Pre-Treatment	CACNA1G	8913	37	17	48669445	48669445	Nonsense_Mutation	SNP	C	T	9	37	c.2902C>T	c.(2902-2904)CAG>TAG	p.Q968*
Pat_04	Pre-Treatment	ABCC3	8714	37	17	48745099	48745099	Nonsense_Mutation	SNP	G	A	16	30	c.1616G>A	c.(1615-1617)TGG>TAG	p.W539*
Pat_04	Pre-Treatment	ANKFN1	162282	37	17	54403614	54403614	Missense_Mutation	SNP	G	A	25	54	c.95G>A	c.(94-96)AGG>AAG	p.R32K
Pat_04	Pre-Treatment	TBX4	9496	37	17	59560825	59560825	Missense_Mutation	SNP	C	T	14	31	c.1586C>T	c.(1585-1587)TCC>TTC	p.S529F
Pat_04	Pre-Treatment	MED13	9969	37	17	60088215	60088215	Missense_Mutation	SNP	G	A	17	43	c.1663C>T	c.(1663-1665)CCT>TCT	p.P555S
Pat_04	Pre-Treatment	ACE	1636	37	17	61560491	61560491	Missense_Mutation	SNP	C	T	43	130	c.1444C>T	c.(1444-1446)CGT>TGT	p.R482C

Pat_04	Pre-Treatment	ABCA5	23461	37	17	67270238	67270238	Nonsense_Mutation	SNP	G	A	7	19	c.2626C>T	c.(2626-2628)CAG>TAG	p.Q876*
Pat_04	Pre-Treatment	C17orf28	283987	37	17	72947703	72947703	Missense_Mutation	SNP	C	T	5	10	c.2329G>A	c.(2329-2331)GAC>AAC	p.D777N
Pat_04	Pre-Treatment	SUMO2	6613	37	17	73178912	73178913	Missense_Mutation	DNP	GG	AT	3	8	c.17_18CC>AT	c.(16-18)CCC>CAT	p.P6H
Pat_04	Pre-Treatment	ASPSCR1	79058	37	17	79954390	79954390	Missense_Mutation	SNP	C	T	4	8	c.601C>T	c.(601-603)CCC>TCC	p.P201S
Pat_04	Pre-Treatment	LAMA1	284217	37	18	7015798	7015798	Missense_Mutation	SNP	G	A	22	156	c.3049C>T	c.(3049-3051)CCC>TCC	p.P1017S
Pat_04	Pre-Treatment	CTAGE1	64693	37	18	19996208	19996208	Missense_Mutation	SNP	C	T	10	72	c.1567G>A	c.(1567-1569)GGA>AGA	p.G523R
Pat_04	Pre-Treatment	LAMA3	3909	37	18	21404431	21404431	Missense_Mutation	SNP	C	T	14	85	c.2473C>T	c.(2473-2475)CCA>TCA	p.P825S
Pat_04	Pre-Treatment	DSC2	1824	37	18	28648063	28648063	Missense_Mutation	SNP	C	T	10	64	c.2624G>A	c.(2623-2625)CGA>CAA	p.R875Q
Pat_04	Pre-Treatment	DSG3	1830	37	18	29052358	29052358	Missense_Mutation	SNP	G	A	6	54	c.2009G>A	c.(2008-2010)GGA>GAA	p.G670E
Pat_04	Pre-Treatment	DSG2	1829	37	18	29101149	29101149	Missense_Mutation	SNP	G	A	13	71	c.466G>A	c.(466-468)GAA>AAA	p.E156K
Pat_04	Pre-Treatment	ASXL3	80816	37	18	31324838	31324838	Missense_Mutation	SNP	G	A	8	72	c.5026G>A	c.(5026-5028)GAC>AAC	p.D1676N
Pat_04	Pre-Treatment	LIPG	9388	37	18	47109952	47109953	Missense_Mutation	DNP	CC	TT	9	101	.1184_1185CC>T	c.(1183-1185)ACC>ATT	p.T395I
Pat_04	Pre-Treatment	CTDP1	9150	37	18	77474496	77474496	Missense_Mutation	SNP	C	T	4	32	c.1036C>T	c.(1036-1038)CAT>TAT	p.H346Y
Pat_04	Pre-Treatment	RANBP3	8498	37	19	5923844	5923844	Nonsense_Mutation	SNP	G	A	5	35	c.1078C>T	c.(1078-1080)CAG>TAG	p.Q360*
Pat_04	Pre-Treatment	PNPLA6	10908	37	19	7607951	7607951	Missense_Mutation	SNP	T	A	8	50	c.1616T>A	c.(1615-1617)ATT>AAT	p.I539N
Pat_04	Pre-Treatment	KIAA1543	57662	37	19	7677786	7677786	Missense_Mutation	SNP	G	A	8	25	c.2407G>A	c.(2407-2409)GAC>AAC	p.D803N
Pat_04	Pre-Treatment	CD209	30835	37	19	7810698	7810698	Missense_Mutation	SNP	A	G	5	164	c.454T>C	c.(454-456)TGG>CGG	p.W152R
Pat_04	Pre-Treatment	MUC16	94025	37	19	8966784	8966784	Missense_Mutation	SNP	T	A	3	9	c.43169A>T	.(43168-43170)GAC>GT	p.D14390V
Pat_04	Pre-Treatment	MUC16	94025	37	19	9056502	9056502	Missense_Mutation	SNP	G	A	10	84	c.30944C>T	c.(30943-30945)GCT>GTT	p.A10315V
Pat_04	Pre-Treatment	MUC16	94025	37	19	9073306	9073306	Missense_Mutation	SNP	C	A	18	78	c.14140G>T	.(14140-14142)GGG>TG	p.G4714W
Pat_04	Pre-Treatment	MUC16	94025	37	19	9075757	9075757	Missense_Mutation	SNP	C	T	8	11	c.11689G>A	c.(11689-11691)GTT>ATT	p.V3897I
Pat_04	Pre-Treatment	MUC16	94025	37	19	9086149	9086149	Missense_Mutation	SNP	C	T	6	28	c.5666G>A	c.(5665-5667)GGA>GAA	p.G1889E
Pat_04	Pre-Treatment	CARM1	10498	37	19	11024650	11024650	Missense_Mutation	SNP	C	T	13	22	c.767C>T	c.(766-768)TCG>TTG	p.S256L
Pat_04	Pre-Treatment	ZNF788	388507	37	19	12223831	12223831	Missense_Mutation	SNP	G	A	13	18	c.1469G>A	c.(1468-1470)CGA>CAA	p.R490Q
Pat_04	Pre-Treatment	ZNF20	7568	37	19	12243437	12243437	Nonsense_Mutation	SNP	G	A	36	109	c.1564C>T	c.(1564-1566)CGA>TGA	p.R522*
Pat_04	Pre-Treatment	RFX1	5989	37	19	14093039	14093039	Missense_Mutation	SNP	G	T	4	19	c.515C>A	c.(514-516)GCT>GAT	p.A172D
Pat_04	Pre-Treatment	ILVBL	10994	37	19	15226693	15226693	Missense_Mutation	SNP	G	A	6	24	c.1582C>T	c.(1582-1584)CTC>TTC	p.L528F
Pat_04	Pre-Treatment	RASAL3	64926	37	19	15564018	15564018	Missense_Mutation	SNP	G	A	6	14	c.2570C>T	c.(2569-2571)TCC>TTC	p.S857F
Pat_04	Pre-Treatment	OR10H2	26538	37	19	15839265	15839266	Missense_Mutation	DNP	CC	TT	19	37	c.412_413CC>TT	c.(412-414)CCA>TTA	p.P138L
Pat_04	Pre-Treatment	USHBP1	83878	37	19	17369091	17369091	Missense_Mutation	SNP	C	T	14	59	c.1150G>A	c.(1150-1152)GAA>AAA	p.E384K
Pat_04	Pre-Treatment	SSBP4	170463	37	19	18542851	18542852	Missense_Mutation	DNP	CC	TT	3	22	c.607_608CC>TT	c.(607-609)CCT>TTT	p.P203F
Pat_04	Pre-Treatment	HAPLN4	404037	37	19	19369386	19369386	Missense_Mutation	SNP	G	A	8	58	c.763C>T	c.(763-765)CGC>TGC	p.R255C
Pat_04	Pre-Treatment	CILP2	148113	37	19	19654548	19654549	Missense_Mutation	DNP	GG	AA	45	180	.1194_1195GG>A	192-1197)GAGGAC>GAA	p.D399N
Pat_04	Pre-Treatment	GMIP	51291	37	19	19745413	19745413	Missense_Mutation	SNP	G	A	23	184	c.1987C>T	c.(1987-1989)CCC>TCC	p.P663S
Pat_04	Pre-Treatment	ZNF208	7757	37	19	22156029	22156029	Missense_Mutation	SNP	G	A	7	16	c.1507C>T	c.(1507-1509)CAT>TAT	p.H503Y
Pat_04	Pre-Treatment	ZNF208	7757	37	19	22171587	22171587	Missense_Mutation	SNP	A	G	26	71	c.128T>C	c.(127-129)CTG>CCG	p.L43P
Pat_04	Pre-Treatment	ZNF257	113835	37	19	22270877	22270877	Missense_Mutation	SNP	G	A	5	24	c.325G>A	c.(325-327)GAG>AAG	p.E109K
Pat_04	Pre-Treatment	ZNF536	9745	37	19	30935299	30935299	Missense_Mutation	SNP	C	T	4	15	c.830C>T	c.(829-831)ACC>ATC	p.T277I
Pat_04	Pre-Treatment	SIPA1L3	23094	37	19	38655182	38655182	Missense_Mutation	SNP	C	T	14	81	c.3844C>T	c.(3844-3846)CAC>TAC	p.H1282Y
Pat_04	Pre-Treatment	LRFN1	57622	37	19	39798424	39798424	Missense_Mutation	SNP	C	T	4	15	c.2165G>A	c.(2164-2166)CGC>CAC	p.R722H
Pat_04	Pre-Treatment	LGALS14	56891	37	19	40197259	40197259	Missense_Mutation	SNP	C	T	40	238	c.38C>T	c.(37-39)TCC>TTC	p.S13F
Pat_04	Pre-Treatment	FCGBP	8857	37	19	40364385	40364385	Missense_Mutation	SNP	G	A	10	72	c.14257C>T	c.(14257-14259)CCT>TCT	p.P4753S
Pat_04	Pre-Treatment	CEACAM21	90273	37	19	42091803	42091803	Missense_Mutation	SNP	G	A	19	102	c.805G>A	c.(805-807)GAT>AAT	p.D269N
Pat_04	Pre-Treatment	PSG3	5671	37	19	43243017	43243017	Missense_Mutation	SNP	C	T	36	290	c.289G>A	c.(289-291)GGA>AGA	p.G97R
Pat_04	Pre-Treatment	PSG6	5675	37	19	43414992	43414992	Missense_Mutation	SNP	G	A	25	145	c.446C>T	c.(445-447)TCC>TTC	p.S149F
Pat_04	Pre-Treatment	EXOC3L2	90332	37	19	45716515	45716515	Missense_Mutation	SNP	C	T	8	15	c.1042G>A	c.(1042-1044)GAG>AAG	p.E348K
Pat_04	Pre-Treatment	DHX34	9704	37	19	47856918	47856918	Nonsense_Mutation	SNP	C	T	4	31	c.631C>T	c.(631-633)CAG>TAG	p.Q211*

Pat_04	Pre-Treatment	CPT1C	126129	37	19	50195561	50195561	Missense_Mutation	SNP	G	A	9	67	c.52G>A	c.(52-54)GGG>AGG	p.G18R
Pat_04	Pre-Treatment	KLK6	5653	37	19	51462539	51462539	Missense_Mutation	SNP	G	A	4	49	c.616C>T	c.(616-618)CAC>TAC	p.H206Y
Pat_04	Pre-Treatment	ZNF160	90338	37	19	53577477	53577477	Missense_Mutation	SNP	C	T	9	44	c.187G>A	c.(187-189)GGG>AGG	p.G63R
Pat_04	Pre-Treatment	BIRC8	112401	37	19	53793465	53793465	Missense_Mutation	SNP	G	A	5	20	c.163C>T	c.(163-165)CCT>TCT	p.P55S
Pat_04	Pre-Treatment	ZNF331	55422	37	19	54081132	54081132	Missense_Mutation	SNP	G	A	6	53	c.1318G>A	c.(1318-1320)GAA>AAA	p.E440K
Pat_04	Pre-Treatment	PRKCG	5582	37	19	54395828	54395828	Missense_Mutation	SNP	C	T	4	18	c.752C>T	c.(751-753)TCC>TTC	p.S251F
Pat_04	Pre-Treatment	CACNG7	59284	37	19	54416194	54416194	Missense_Mutation	SNP	G	A	4	46	c.109G>A	c.(109-111)GAA>AAA	p.E37K
Pat_04	Pre-Treatment	LILRB2	10288	37	19	54782149	54782149	Missense_Mutation	SNP	G	A	14	94	c.1223C>T	c.(1222-1224)TCT>TTT	p.S408F
Pat_04	Pre-Treatment	NLRP9	338321	37	19	56243785	56243785	Missense_Mutation	SNP	C	T	23	138	c.1412G>A	c.(1411-1413)GGA>GAA	p.G471E
Pat_04	Pre-Treatment	ZNF776	284309	37	19	58265313	58265313	Missense_Mutation	SNP	C	T	8	53	c.815C>T	c.(814-816)TCA>TTA	p.S272L
Pat_04	Pre-Treatment	CMPK2	129607	37	2	6991588	6991588	Missense_Mutation	SNP	G	A	3	34	c.1219C>T	c.(1219-1221)CGT>TGT	p.R407C
Pat_04	Pre-Treatment	TAF1B	9014	37	2	10059864	10059864	Missense_Mutation	SNP	C	T	4	45	c.1480C>T	c.(1480-1482)CTT>TTT	p.L494F
Pat_04	Pre-Treatment	APOB	338	37	2	21230175	21230175	Missense_Mutation	SNP	G	A	4	24	c.9565C>T	c.(9565-9567)CCT>TCT	p.P3189S
Pat_04	Pre-Treatment	APOB	338	37	2	21232704	21232704	Missense_Mutation	SNP	C	T	9	56	c.7036G>A	c.(7036-7038)GAG>AAG	p.E2346K
Pat_04	Pre-Treatment	APOB	338	37	2	21234639	21234639	Missense_Mutation	SNP	C	T	15	98	c.5101G>A	c.(5101-5103)GGG>AGG	p.G1701R
Pat_04	Pre-Treatment	APOB	338	37	2	21260958	21260958	Missense_Mutation	SNP	C	T	6	52	c.409G>A	c.(409-411)GAA>AAA	p.E137K
Pat_04	Pre-Treatment	C2orf16	84226	37	2	27801613	27801613	Missense_Mutation	SNP	G	A	5	36	c.2174G>A	c.(2173-2175)GGG>GAG	p.G725E
Pat_04	Pre-Treatment	ZNF512	84450	37	2	27844168	27844169	Missense_Mutation	DNP	CC	TT	5	48	.1544_1545CC>T	c.(1543-1545)CCC>CTT	p.P515L
Pat_04	Pre-Treatment	XDH	7498	37	2	31596764	31596764	Missense_Mutation	SNP	G	A	6	47	c.1661C>T	c.(1660-1662)CCC>CTC	p.P554L
Pat_04	Pre-Treatment	TTC27	55622	37	2	32983371	32983371	Missense_Mutation	SNP	C	T	5	34	c.1465C>T	c.(1465-1467)CTT>TTT	p.L489F
Pat_04	Pre-Treatment	SOS1	6654	37	2	39237821	39237821	Missense_Mutation	SNP	A	G	7	30	c.2414T>C	c.(2413-2415)GTT>GCT	p.V805A
Pat_04	Pre-Treatment	SRBD1	55133	37	2	45808918	45808918	Nonsense_Mutation	SNP	G	A	3	29	c.847C>T	c.(847-849)CAG>TAG	p.Q283*
Pat_04	Pre-Treatment	GTF2A1L	11036	37	2	48960051	48960051	Missense_Mutation	SNP	C	T	22	116	c.1349C>T	c.(1348-1350)TCG>TTG	p.S450L
Pat_04	Pre-Treatment	CD207	50489	37	2	71062706	71062706	Missense_Mutation	SNP	G	A	7	64	c.106C>T	c.(106-108)CCG>TCG	p.P36S
Pat_04	Pre-Treatment	SLC4A5	57835	37	2	74452032	74452032	Missense_Mutation	SNP	C	T	4	39	c.3229G>A	c.(3229-3231)GAA>AAA	p.E1077K
Pat_04	Pre-Treatment	CTNNA2	1496	37	2	80801392	80801392	Missense_Mutation	SNP	G	A	16	152	c.1846G>A	c.(1846-1848)GTG>ATG	p.V616M
Pat_04	Pre-Treatment	TEKT4	150483	37	2	95541342	95541342	Missense_Mutation	SNP	G	A	11	85	c.946G>A	c.(946-948)GAA>AAA	p.E316K
Pat_04	Pre-Treatment	VWA3B	200403	37	2	98846646	98846646	Nonsense_Mutation	SNP	C	T	5	29	c.2284C>T	c.(2284-2286)CAG>TAG	p.Q762*
Pat_04	Pre-Treatment	AFF3	3899	37	2	100170815	100170815	Missense_Mutation	SNP	C	T	21	168	c.3517G>A	c.(3517-3519)GAC>AAC	p.D1173N
Pat_04	Pre-Treatment	PDCL3	79031	37	2	101183064	101183064	Missense_Mutation	SNP	G	A	13	87	c.106G>A	c.(106-108)GAG>AAG	p.E36K
Pat_04	Pre-Treatment	WASH2P	375260	37	2	114355096	114355097	Missense_Mutation	DNP	CC	TT	3	30	c.473_474CC>TT	c.(472-474)TCC>TTT	p.S158F
Pat_04	Pre-Treatment	CNTNAP5	129684	37	2	125671785	125671785	Missense_Mutation	SNP	G	A	9	42	c.3841G>A	c.(3841-3843)GAA>AAA	p.E1281K
Pat_04	Pre-Treatment	TUBA3D	113457	37	2	132240324	132240324	Missense_Mutation	SNP	C	T	29	251	c.1256C>T	c.(1255-1257)TCT>TTT	p.S419F
Pat_04	Pre-Treatment	THSD7B	80731	37	2	137872735	137872735	Missense_Mutation	SNP	C	T	7	48	c.1148C>T	c.(1147-1149)TCT>TTT	p.S383F
Pat_04	Pre-Treatment	RIF1	55183	37	2	152315402	152315403	Missense_Mutation	DNP	CC	TT	5	66	.2933_2934CC>T	c.(2932-2934)TCC>TTT	p.S978F
Pat_04	Pre-Treatment	NEB	4703	37	2	152483656	152483656	Missense_Mutation	SNP	C	T	8	68	c.9478G>A	c.(9478-9480)GAT>AAT	p.D3160N
Pat_04	Pre-Treatment	NEB	4703	37	2	152522767	152522767	Missense_Mutation	SNP	G	A	37	178	c.4868C>T	c.(4867-4869)ACC>ATC	p.T1623I
Pat_04	Pre-Treatment	GALNT5	11227	37	2	158152976	158152976	Missense_Mutation	SNP	C	T	4	40	c.1948C>T	c.(1948-1950)CCT>TCT	p.P650S
Pat_04	Pre-Treatment	LY75	4065	37	2	160628523	160628523	Missense_Mutation	SNP	C	T	14	53	c.5461G>A	c.(5461-5463)GTA>ATA	p.V1821I
Pat_04	Pre-Treatment	DPP4	1803	37	2	162875748	162875748	Missense_Mutation	SNP	C	T	9	52	c.1283G>A	c.(1282-1284)GGA>GAA	p.G428E
Pat_04	Pre-Treatment	SCN9A	6335	37	2	167129097	167129097	Missense_Mutation	SNP	C	T	7	30	c.3130G>A	c.(3130-3132)GAA>AAA	p.E1044K
Pat_04	Pre-Treatment	XIRP2	129446	37	2	168099400	168099400	Missense_Mutation	SNP	C	T	7	32	c.1498C>T	c.(1498-1500)CGT>TGT	p.R500C
Pat_04	Pre-Treatment	XIRP2	129446	37	2	168100876	168100876	Missense_Mutation	SNP	C	A	6	61	c.2974C>A	c.(2974-2976)CAA>AAA	p.Q992K
Pat_04	Pre-Treatment	MYO3B	140469	37	2	171259392	171259392	Missense_Mutation	SNP	G	A	12	92	c.2164G>A	c.(2164-2166)GAT>AAT	p.D722N
Pat_04	Pre-Treatment	HOXD3	3232	37	2	177036364	177036364	Missense_Mutation	SNP	C	T	15	98	c.661C>T	c.(661-663)CGG>TGG	p.R221W
Pat_04	Pre-Treatment	PRKRA	8575	37	2	179300872	179300872	Missense_Mutation	SNP	C	T	4	32	c.784G>A	c.(784-786)GAT>AAT	p.D262N
Pat_04	Pre-Treatment	TTN	7273	37	2	179584992	179584992	Splice_Site	SNP	C	T	3	21	c.19646_splice	c.e78-1	p.E6549_splice

Pat_04	Pre-Treatment	TTN	7273	37	2	179638691	179638691	Missense_Mutation	SNP	G	A	15	98	c.7204C>T	c.(7204-7206)CAC>TAC	p.H2402Y
Pat_04	Pre-Treatment	COL5A2	1290	37	2	189916129	189916129	Missense_Mutation	SNP	G	A	6	38	c.2848C>T	c.(2848-2850)CAT>TAT	p.H950Y
Pat_04	Pre-Treatment	COL5A2	1290	37	2	189917690	189917690	Missense_Mutation	SNP	C	T	4	31	c.2608G>A	c.(2608-2610)GGA>AGA	p.G870R
Pat_04	Pre-Treatment	SLC40A1	30061	37	2	190428819	190428819	Missense_Mutation	SNP	C	T	10	32	c.893G>A	c.(892-894)GGA>GAA	p.G298E
Pat_04	Pre-Treatment	AOX1	316	37	2	201515720	201515720	Missense_Mutation	SNP	G	T	8	39	c.2871G>T	c.(2869-2871)AAG>AAT	p.K957N
Pat_04	Pre-Treatment	PIKFYVE	200576	37	2	209169680	209169680	Missense_Mutation	SNP	C	T	14	67	c.1579C>T	c.(1579-1581)CAT>TAT	p.H527Y
Pat_04	Pre-Treatment	PIKFYVE	200576	37	2	209219937	209219937	Missense_Mutation	SNP	C	T	13	56	c.6205C>T	c.(6205-6207)CCG>TCG	p.P2069S
Pat_04	Pre-Treatment	MAP2	4133	37	2	210557907	210557907	Missense_Mutation	SNP	C	T	5	50	c.1013C>T	c.(1012-1014)TCG>TTG	p.S338L
Pat_04	Pre-Treatment	ACADL	33	37	2	211074927	211074927	Missense_Mutation	SNP	C	T	5	101	c.596G>A	c.(595-597)GGA>GAA	p.G199E
Pat_04	Pre-Treatment	MYL1	4632	37	2	211179727	211179727	Missense_Mutation	SNP	C	T	20	92	c.40G>A	c.(40-42)GCT>ACT	p.A14T
Pat_04	Pre-Treatment	CPS1	1373	37	2	211525356	211525356	Missense_Mutation	SNP	C	T	11	56	c.3904C>T	c.(3904-3906)CCT>TCT	p.P1302S
Pat_04	Pre-Treatment	C2orf62	375307	37	2	219221619	219221620	Missense_Mutation	DNP	GG	TA	7	96	c.12_13GG>TA	.(10-15)AAGGTT>AATAT	p.4_5KV>NI
Pat_04	Pre-Treatment	WNT10A	80326	37	2	219754924	219754924	Missense_Mutation	SNP	C	T	8	19	c.595C>T	c.(595-597)CCC>TCC	p.P199S
Pat_04	Pre-Treatment	CCDC108	255101	37	2	219874711	219874711	Missense_Mutation	SNP	C	T	4	20	c.4405G>A	c.(4405-4407)GAG>AAG	p.E1469K
Pat_04	Pre-Treatment	SP100	6672	37	2	231380144	231380144	Missense_Mutation	SNP	C	T	8	37	c.2429C>T	c.(2428-2430)ACC>ATC	p.T810I
Pat_04	Pre-Treatment	ALPP	250	37	2	233246398	233246398	Missense_Mutation	SNP	C	T	3	24	c.1501C>T	c.(1501-1503)CCC>TCC	p.P501S
Pat_04	Pre-Treatment	UGT1A10	54575	37	2	234545275	234545275	Missense_Mutation	SNP	G	A	19	97	c.107G>A	c.(106-108)AGT>AAT	p.S36N
Pat_04	Pre-Treatment	UGT1A10	54575	37	2	234545511	234545511	Missense_Mutation	SNP	G	T	7	55	c.343G>T	c.(343-345)GGT>TGT	p.G115C
Pat_04	Pre-Treatment	LRRFIP1	9208	37	2	238664828	238664828	Missense_Mutation	SNP	G	A	3	21	c.745G>A	c.(745-747)GAG>AAG	p.E249K
Pat_04	Pre-Treatment	RBM44	375316	37	2	238725794	238725794	Missense_Mutation	SNP	G	A	5	50	c.235G>A	c.(235-237)GAG>AAG	p.E79K
Pat_04	Pre-Treatment	FERMT1	55612	37	20	6064715	6064715	Missense_Mutation	SNP	C	T	11	33	c.1690G>A	c.(1690-1692)GAG>AAG	p.E564K
Pat_04	Pre-Treatment	PAK7	57144	37	20	9561213	9561213	Missense_Mutation	SNP	G	A	10	92	c.569C>T	c.(568-570)TCC>TTC	p.S190F
Pat_04	Pre-Treatment	SEL1L2	80343	37	20	13936742	13936742	Missense_Mutation	SNP	C	T	3	15	c.94G>A	c.(94-96)GAA>AAA	p.E32K
Pat_04	Pre-Treatment	SLC24A3	57419	37	20	19566085	19566085	Missense_Mutation	SNP	G	A	15	118	c.509G>A	c.(508-510)GGG>GAG	p.G170E
Pat_04	Pre-Treatment	GZF1	64412	37	20	23346126	23346126	Missense_Mutation	SNP	A	G	9	51	c.1106A>G	c.(1105-1107)CAC>CGC	p.H369R
Pat_04	Pre-Treatment	NINL	22981	37	20	25439044	25439044	Missense_Mutation	SNP	G	A	13	67	c.3818C>T	c.(3817-3819)GCC>GTC	p.A1273V
Pat_04	Pre-Treatment	TTLL9	164395	37	20	30497607	30497607	Missense_Mutation	SNP	G	A	9	33	c.386G>A	c.(385-387)GGA>GAA	p.G129E
Pat_04	Pre-Treatment	PHF20	51230	37	20	34526957	34526957	Missense_Mutation	SNP	C	T	6	62	c.2639C>T	c.(2638-2640)TCC>TTC	p.S880F
Pat_04	Pre-Treatment	C20orf132	140699	37	20	35738689	35738689	Missense_Mutation	SNP	G	A	19	100	c.2914C>T	c.(2914-2916)CCC>TCC	p.P972S
Pat_04	Pre-Treatment	TOX2	84969	37	20	42635337	42635337	Missense_Mutation	SNP	C	T	7	72	c.343C>T	c.(343-345)CCT>TCT	p.P115S
Pat_04	Pre-Treatment	PABPC1L	80336	37	20	43559174	43559175	Missense_Mutation	DNP	CC	TT	24	168	.1046_1047CC>T	c.(1045-1047)GCC>GTT	p.A349V
Pat_04	Pre-Treatment	SEMG2	6407	37	20	43851853	43851853	Missense_Mutation	SNP	C	T	4	46	c.1580C>T	c.(1579-1581)TCT>TTT	p.S527F
Pat_04	Pre-Treatment	RBPJL	11317	37	20	43936864	43936864	Missense_Mutation	SNP	G	A	12	33	c.104G>A	c.(103-105)AGG>AAG	p.R35K
Pat_04	Pre-Treatment	SLC13A3	64849	37	20	45188756	45188756	Nonsense_Mutation	SNP	G	A	28	226	c.1714C>T	c.(1714-1716)CAG>TAG	p.Q572*
Pat_04	Pre-Treatment	FAM65C	140876	37	20	49204357	49204357	Missense_Mutation	SNP	C	T	8	41	c.2722G>A	c.(2722-2724)GAA>AAA	p.E908K
Pat_04	Pre-Treatment	CASS4	57091	37	20	55033439	55033439	Missense_Mutation	SNP	C	T	4	36	c.1997C>T	c.(1996-1998)CCT>CTT	p.P666L
Pat_04	Pre-Treatment	LIPI	149998	37	21	15535839	15535839	Nonsense_Mutation	SNP	G	A	10	64	c.970C>T	c.(970-972)CAA>TAA	p.Q324*
Pat_04	Pre-Treatment	NCAM2	4685	37	21	22910264	22910264	Missense_Mutation	SNP	G	A	3	12	c.2500G>A	c.(2500-2502)GAC>AAC	p.D834N
Pat_04	Pre-Treatment	KRTAP13-2	337959	37	21	31744348	31744348	Missense_Mutation	SNP	C	T	9	36	c.184G>A	c.(184-186)GAG>AAG	p.E62K
Pat_04	Pre-Treatment	RUNX1	861	37	21	36171700	36171700	Missense_Mutation	SNP	C	T	18	102	c.784G>A	c.(784-786)GGA>AGA	p.G262R
Pat_04	Pre-Treatment	KCNJ6	3763	37	21	39087056	39087056	Missense_Mutation	SNP	T	C	9	55	c.404A>G	c.(403-405)AAC>AGC	p.N135S
Pat_04	Pre-Treatment	DSCAM	1826	37	21	41539173	41539173	Missense_Mutation	SNP	G	A	10	69	c.2990C>T	c.(2989-2991)TCA>TTA	p.S997L
Pat_04	Pre-Treatment	PRDM15	63977	37	21	43259872	43259872	Missense_Mutation	SNP	G	A	20	104	c.1829C>T	c.(1828-1830)CCC>CTC	p.P610L
Pat_04	Pre-Treatment	TFF1	7031	37	21	43783369	43783369	Missense_Mutation	SNP	G	A	6	34	c.233C>T	c.(232-234)CCA>CTA	p.P78L
Pat_04	Pre-Treatment	TRPM2	7226	37	21	45798932	45798932	Missense_Mutation	SNP	C	T	11	84	c.1067C>T	c.(1066-1068)TCG>TTG	p.S356L
Pat_04	Pre-Treatment	C21orf29	54084	37	21	45949798	45949798	Missense_Mutation	SNP	C	T	4	18	c.673G>A	c.(673-675)GCC>ACC	p.A225T
Pat_04	Pre-Treatment	DGCR8	54487	37	22	20073602	20073602	Missense_Mutation	SNP	C	T	5	42	c.116C>T	c.(115-117)CCC>CTC	p.P39L

Pat_04	Pre-Treatment	UBE2L3	7332	37	22	21947243	21947243	Missense_Mutation	SNP	C	T	9	33	c.121C>T	c.(121-123)CCT>TCT	p.P41S
Pat_04	Pre-Treatment	C22orf43	51233	37	22	23959845	23959845	Splice_Site	SNP	C	T	4	49	c.437_splice	c.e7-1	p.C146_splice
Pat_04	Pre-Treatment	CABIN1	23523	37	22	24459467	24459467	Missense_Mutation	SNP	G	A	34	207	c.1742G>A	c.(1741-1743)GGA>GAA	p.G581E
Pat_04	Pre-Treatment	UPB1	51733	37	22	24906761	24906761	Missense_Mutation	SNP	G	A	18	78	c.409G>A	c.(409-411)GAA>AAA	p.E137K
Pat_04	Pre-Treatment	PES1	23481	37	22	30980371	30980371	Missense_Mutation	SNP	G	A	5	25	c.611C>T	c.(610-612)CCC>CTC	p.P204L
Pat_04	Pre-Treatment	SLC5A1	6523	37	22	32498055	32498055	Missense_Mutation	SNP	G	T	4	33	c.1496G>T	c.(1495-1497)CGT>CTT	p.R499L
Pat_04	Pre-Treatment	BPIL2	254240	37	22	32810372	32810372	Missense_Mutation	SNP	G	A	15	59	c.1442C>T	c.(1441-1443)TCC>TTC	p.S481F
Pat_04	Pre-Treatment	NCF4	4689	37	22	37273776	37273776	Missense_Mutation	SNP	C	T	3	20	c.931C>T	c.(931-933)CGT>TGT	p.R311C
Pat_04	Pre-Treatment	CSF2RB	1439	37	22	37326728	37326728	Missense_Mutation	SNP	T	A	4	29	c.868T>A	c.(868-870)TCC>ACC	p.S290T
Pat_04	Pre-Treatment	SOX10	6663	37	22	38374125	38374125	Missense_Mutation	SNP	T	C	4	6	c.446A>G	c.(445-447)GAC>GGC	p.D149G
Pat_04	Pre-Treatment	MGAT3	4248	37	22	39884316	39884316	Missense_Mutation	SNP	C	T	9	79	c.964C>T	c.(964-966)CCG>TCG	p.P322S
Pat_04	Pre-Treatment	SAMM50	25813	37	22	44364653	44364653	Missense_Mutation	SNP	C	T	17	92	c.277C>T	c.(277-279)CTT>TTT	p.L93F
Pat_04	Pre-Treatment	TUBGCP6	85378	37	22	50656440	50656440	Missense_Mutation	SNP	G	A	4	25	c.5275C>T	c.(5275-5277)CCT>TCT	p.P1759S
Pat_04	Pre-Treatment	SRGAP3	9901	37	3	9027574	9027574	Missense_Mutation	SNP	C	T	7	54	c.2929G>A	c.(2929-2931)GAA>AAA	p.E977K
Pat_04	Pre-Treatment	C3orf24	115795	37	3	10146112	10146112	Missense_Mutation	SNP	C	T	13	104	c.347G>A	c.(346-348)GGG>GAG	p.G116E
Pat_04	Pre-Treatment	ATP2B2	491	37	3	10370737	10370737	Missense_Mutation	SNP	G	T	11	56	c.3493C>A	c.(3493-3495)CAT>AAT	p.H1165N
Pat_04	Pre-Treatment	SLC6A11	6538	37	3	10858146	10858146	Missense_Mutation	SNP	G	A	5	28	c.196G>A	c.(196-198)GAG>AAG	p.E66K
Pat_04	Pre-Treatment	KCNH8	131096	37	3	19436767	19436767	Missense_Mutation	SNP	G	A	22	77	c.1141G>A	c.(1141-1143)GAG>AAG	p.E381K
Pat_04	Pre-Treatment	RARB	5915	37	3	25611288	25611288	Missense_Mutation	SNP	C	T	4	28	c.509C>T	c.(508-510)TCG>TTG	p.S170L
Pat_04	Pre-Treatment	NEK10	152110	37	3	27332853	27332853	Missense_Mutation	SNP	T	C	4	21	c.1505A>G	c.(1504-1506)AAT>AGT	p.N502S
Pat_04	Pre-Treatment	STAC	6769	37	3	36534652	36534652	Missense_Mutation	SNP	C	T	5	30	c.697C>T	c.(697-699)CTT>TTT	p.L233F
Pat_04	Pre-Treatment	SCN5A	6331	37	3	38645271	38645271	Missense_Mutation	SNP	C	T	15	67	c.1822G>A	c.(1822-1824)GAC>AAC	p.D608N
Pat_04	Pre-Treatment	SCN11A	11280	37	3	38949439	38949439	Splice_Site	SNP	C	T	4	26	c.1473_splice	c.e10+1	p.K491_splice
Pat_04	Pre-Treatment	XIRP1	165904	37	3	39228008	39228008	Missense_Mutation	SNP	C	T	5	73	c.2929G>A	c.(2929-2931)GAC>AAC	p.D977N
Pat_04	Pre-Treatment	CYP8B1	1582	37	3	42916636	42916637	Missense_Mutation	DNP	CC	TT	6	49	c.672_673GG>AA	670-675)CGGGAG>CGAA	p.E225K
Pat_04	Pre-Treatment	SLC6A20	54716	37	3	45801369	45801369	Nonsense_Mutation	SNP	G	A	19	93	c.1609C>T	c.(1609-1611)CAA>TAA	p.Q537*
Pat_04	Pre-Treatment	FYCO1	79443	37	3	46021220	46021220	Missense_Mutation	SNP	G	A	5	81	c.265C>T	c.(265-267)CGC>TGC	p.R89C
Pat_04	Pre-Treatment	SMARCC1	6599	37	3	47727558	47727558	Missense_Mutation	SNP	A	C	27	165	c.1366T>G	c.(1366-1368)TCA>GCA	p.S456A
Pat_04	Pre-Treatment	DHX30	22907	37	3	47888205	47888206	Missense_Mutation	DNP	CC	TT	4	35	.1643_1644CC>T	c.(1642-1644)CCC>CTT	p.P548L
Pat_04	Pre-Treatment	CELSR3	1951	37	3	48667522	48667523	Missense_Mutation	DNP	GG	AA	11	75	11609_11610CC>	c.(11608-11610)TCC>TTT	p.S3870F
Pat_04	Pre-Treatment	DOCK3	1795	37	3	51350306	51350306	Missense_Mutation	SNP	G	A	4	16	c.3226G>A	c.(3226-3228)GAA>AAA	p.E1076K
Pat_04	Pre-Treatment	ROBO2	6092	37	3	77657012	77657012	Missense_Mutation	SNP	C	T	5	35	c.3200C>T	c.(3199-3201)TCC>TTC	p.S1067F
Pat_04	Pre-Treatment	OR5H1	26341	37	3	97852001	97852001	Missense_Mutation	SNP	C	T	13	41	c.460C>T	c.(460-462)CTT>TTT	p.L154F
Pat_04	Pre-Treatment	OR5H14	403273	37	3	97868569	97868569	Missense_Mutation	SNP	C	T	19	135	c.340C>T	c.(340-342)CTC>TTC	p.L114F
Pat_04	Pre-Treatment	SENP7	57337	37	3	101086756	101086756	Missense_Mutation	SNP	G	A	9	64	c.896C>T	c.(895-897)TCC>TTC	p.S299F
Pat_04	Pre-Treatment	MORC1	27136	37	3	108682434	108682434	Nonsense_Mutation	SNP	G	A	3	11	c.2626C>T	c.(2626-2628)CAA>TAA	p.Q876*
Pat_04	Pre-Treatment	CD96	10225	37	3	111296349	111296349	Missense_Mutation	SNP	G	A	21	127	c.544G>A	c.(544-546)GAA>AAA	p.E182K
Pat_04	Pre-Treatment	STXBP5L	9515	37	3	120957925	120957925	Missense_Mutation	SNP	C	T	7	27	c.1292C>T	c.(1291-1293)TCT>TTT	p.S431F
Pat_04	Pre-Treatment	STXBP5L	9515	37	3	121100155	121100155	Missense_Mutation	SNP	C	T	3	29	c.2435C>T	c.(2434-2436)TCC>TTC	p.S812F
Pat_04	Pre-Treatment	STXBP5L	9515	37	3	121132090	121132090	Missense_Mutation	SNP	G	A	14	84	c.3106G>A	c.(3106-3108)GAA>AAA	p.E1036K
Pat_04	Pre-Treatment	GOLGB1	2804	37	3	121413651	121413651	Nonsense_Mutation	SNP	G	A	12	150	c.5704C>T	c.(5704-5706)CAA>TAA	p.Q1902*
Pat_04	Pre-Treatment	SEMA5B	54437	37	3	122634315	122634315	Missense_Mutation	SNP	G	A	10	66	c.1960C>T	c.(1960-1962)CCA>TCA	p.P654S
Pat_04	Pre-Treatment	MYLK	4638	37	3	123457826	123457826	Missense_Mutation	SNP	C	T	10	24	c.506G>A	c.(505-507)CGA>CAA	p.R169Q
Pat_04	Pre-Treatment	TF	7018	37	3	133475789	133475789	Missense_Mutation	SNP	C	T	8	58	c.806C>T	c.(805-807)ACC>ATC	p.T269I
Pat_04	Pre-Treatment	TRIM42	287015	37	3	140407128	140407128	Missense_Mutation	SNP	G	A	12	96	c.1604G>A	c.(1603-1605)CGA>CAA	p.R535Q
Pat_04	Pre-Treatment	PLS1	5357	37	3	142430803	142430803	Missense_Mutation	SNP	C	G	20	116	c.1844C>G	c.(1843-1845)ACG>AGG	p.T615R
Pat_04	Pre-Treatment	MED12L	116931	37	3	150883728	150883728	Missense_Mutation	SNP	C	T	4	50	c.1453C>T	c.(1453-1455)CAT>TAT	p.H485Y

Pat_04	Pre-Treatment	IFT80	57560	37	3	160075309	160075309	Missense_Mutation	SNP	T	A	5	49	c.607A>T	c.(607-609)ATT>TTT	p.I203F
Pat_04	Pre-Treatment	PRKCI	5584	37	3	170009711	170009711	Missense_Mutation	SNP	T	A	6	31	c.1273T>A	c.(1273-1275)TTA>ATA	p.L425I
Pat_04	Pre-Treatment	MFN1	55669	37	3	179082192	179082192	Missense_Mutation	SNP	C	T	8	40	c.644C>T	c.(643-645)ACG>ATG	p.T215M
Pat_04	Pre-Treatment	DCUN1D1	54165	37	3	182683508	182683508	Missense_Mutation	SNP	G	A	11	60	c.37C>T	c.(37-39)CGT>TGT	p.R13C
Pat_04	Pre-Treatment	LAMP3	27074	37	3	182853615	182853615	Missense_Mutation	SNP	G	A	67	432	c.1007C>T	c.(1006-1008)TCC>TTC	p.S336F
Pat_04	Pre-Treatment	EHHADH	1962	37	3	184911242	184911242	Missense_Mutation	SNP	G	A	7	59	c.944C>T	c.(943-945)TCT>TTT	p.S315F
Pat_04	Pre-Treatment	ETV5	2119	37	3	185797804	185797804	Missense_Mutation	SNP	G	A	5	21	c.452C>T	c.(451-453)CCC>CTC	p.P151L
Pat_04	Pre-Treatment	KNG1	3827	37	3	186460017	186460017	Missense_Mutation	SNP	C	T	14	74	c.1832C>T	c.(1831-1833)TCC>TTC	p.S611F
Pat_04	Pre-Treatment	MUC4	4585	37	3	195515915	195515915	Missense_Mutation	SNP	C	T	4	41	c.2536G>A	c.(2536-2538)GAA>AAA	p.E846K
Pat_04	Pre-Treatment	ADD1	118	37	4	2930044	2930045	Missense_Mutation	DNP	CC	TT	3	24	.2008_2009CC>T	c.(2008-2010)CCC>TTC	p.P670F
Pat_04	Pre-Treatment	SLC2A9	56606	37	4	9943645	9943645	Missense_Mutation	SNP	C	T	12	53	c.706G>A	c.(706-708)GGA>AGA	p.G236R
Pat_04	Pre-Treatment	KCNIP4	80333	37	4	20852291	20852291	Splice_Site	SNP	C	T	3	21	c.113_splice	c.e2-1	p.D38_splice
Pat_04	Pre-Treatment	ANAPC4	29945	37	4	25382044	25382044	Missense_Mutation	SNP	C	T	8	45	c.178C>T	c.(178-180)CCA>TCA	p.P60S
Pat_04	Pre-Treatment	FRYL	285527	37	4	48542086	48542086	Splice_Site	SNP	C	T	5	18	c.6296_splice	c.e47-1	.G2099_splic
Pat_04	Pre-Treatment	UGT2B10	7365	37	4	69693142	69693142	Missense_Mutation	SNP	T	A	18	102	c.1183T>A	c.(1183-1185)TTT>ATT	p.F395I
Pat_04	Pre-Treatment	MTTP	4547	37	4	100521808	100521808	Missense_Mutation	SNP	G	A	4	70	c.1154G>A	c.(1153-1155)AGC>AAC	p.S385N
Pat_04	Pre-Treatment	ENPEP	2028	37	4	111397871	111397871	Missense_Mutation	SNP	C	T	16	92	c.301C>T	c.(301-303)CAC>TAC	p.H101Y
Pat_04	Pre-Treatment	ENPEP	2028	37	4	111397893	111397893	Missense_Mutation	SNP	C	T	19	116	c.323C>T	c.(322-324)CCC>CTC	p.P108L
Pat_04	Pre-Treatment	FAT4	79633	37	4	126367498	126367498	Missense_Mutation	SNP	G	A	8	77	c.7244G>A	c.(7243-7245)GGA>GAA	p.G2415E
Pat_04	Pre-Treatment	PCDH18	54510	37	4	138442599	138442599	Missense_Mutation	SNP	C	T	12	52	c.2992G>A	c.(2992-2994)GAT>AAT	p.D998N
Pat_04	Pre-Treatment	SLC10A7	84068	37	4	147214126	147214126	Missense_Mutation	SNP	G	A	8	24	c.728C>T	c.(727-729)TCT>TTT	p.S243F
Pat_04	Pre-Treatment	PET112L	5188	37	4	152609912	152609912	Missense_Mutation	SNP	C	T	5	32	c.1201G>A	c.(1201-1203)GAA>AAA	p.E401K
Pat_04	Pre-Treatment	DCHS2	54798	37	4	155157307	155157307	Missense_Mutation	SNP	C	T	18	80	c.7132G>A	c.(7132-7134)GAT>AAT	p.D2378N
Pat_04	Pre-Treatment	FGA	2243	37	4	155507312	155507313	Missense_Mutation	DNP	CC	TT	13	133	.1268_1269GG>A	c.(1267-1269)GGG>GAA	p.G423E
Pat_04	Pre-Treatment	SH3RF1	57630	37	4	170057764	170057764	Missense_Mutation	SNP	G	A	9	35	c.773C>T	c.(772-774)TCG>TTG	p.S258L
Pat_04	Pre-Treatment	SORBS2	8470	37	4	186545315	186545315	Missense_Mutation	SNP	G	A	8	51	c.1256C>T	c.(1255-1257)CCC>CTC	p.P419L
Pat_04	Pre-Treatment	LPCAT1	79888	37	5	1494881	1494881	Missense_Mutation	SNP	G	A	9	83	c.427C>T	c.(427-429)CCT>TCT	p.P143S
Pat_04	Pre-Treatment	SEMA5A	9037	37	5	9063103	9063103	Missense_Mutation	SNP	C	T	10	70	c.2414G>A	c.(2413-2415)CGG>CAG	p.R805Q
Pat_04	Pre-Treatment	DNAH5	1767	37	5	13701415	13701415	Missense_Mutation	SNP	C	T	8	69	c.13469G>A	.(13468-13470)GGA>GA	p.G4490E
Pat_04	Pre-Treatment	DNAH5	1767	37	5	13714558	13714558	Missense_Mutation	SNP	C	T	19	119	c.13081G>A	c.(13081-13083)GAT>AAT	p.D4361N
Pat_04	Pre-Treatment	DNAH5	1767	37	5	13871769	13871769	Missense_Mutation	SNP	C	T	6	30	c.3502G>A	c.(3502-3504)GAA>AAA	p.E1168K
Pat_04	Pre-Treatment	TRIO	7204	37	5	14498726	14498726	Missense_Mutation	SNP	C	T	17	124	c.8309C>T	c.(8308-8310)TCG>TTG	p.S2770L
Pat_04	Pre-Treatment	CDH18	1016	37	5	19544029	19544029	Missense_Mutation	SNP	C	T	7	56	c.1339G>A	c.(1339-1341)GAC>AAC	p.D447N
Pat_04	Pre-Treatment	CDH9	1007	37	5	26906133	26906133	Missense_Mutation	SNP	G	A	9	152	c.746C>T	c.(745-747)TCT>TTT	p.S249F
Pat_04	Pre-Treatment	AGXT2	64902	37	5	35010230	35010230	Missense_Mutation	SNP	C	T	16	68	c.1213G>A	c.(1213-1215)GAA>AAA	p.E405K
Pat_04	Pre-Treatment	C9	735	37	5	39341321	39341321	Missense_Mutation	SNP	C	T	15	141	c.403G>A	c.(403-405)GAA>AAA	p.E135K
Pat_04	Pre-Treatment	HEATR7B2	133558	37	5	41038915	41038915	Missense_Mutation	SNP	G	A	5	21	c.2137C>T	c.(2137-2139)CCC>TCC	p.P713S
Pat_04	Pre-Treatment	HCN1	348980	37	5	45267313	45267313	Missense_Mutation	SNP	C	T	17	81	c.1661G>A	c.(1660-1662)CGA>CAA	p.R554Q
Pat_04	Pre-Treatment	IL31RA	133396	37	5	55203220	55203220	Missense_Mutation	SNP	C	T	4	51	c.1286C>T	c.(1285-1287)TCT>TTT	p.S429F
Pat_04	Pre-Treatment	BDP1	55814	37	5	70785458	70785458	Missense_Mutation	SNP	T	A	6	43	c.1441T>A	c.(1441-1443)TTA>ATA	p.L481I
Pat_04	Pre-Treatment	MAP1B	4131	37	5	71494189	71494190	Missense_Mutation	DNP	CC	TT	13	71	.5007_5008CC>T	005-5010)CACCCT>CATT	p.P1670S
Pat_04	Pre-Treatment	FAM169A	26049	37	5	74100362	74100362	Missense_Mutation	SNP	C	T	12	105	c.868G>A	c.(868-870)GAA>AAA	p.E290K
Pat_04	Pre-Treatment	PDE8B	8622	37	5	76714110	76714110	Missense_Mutation	SNP	C	G	6	92	c.1968C>G	c.(1966-1968)GAC>GAG	p.D656E
Pat_04	Pre-Treatment	VCAN	1462	37	5	82875858	82875858	Missense_Mutation	SNP	C	T	13	87	c.9940C>T	c.(9940-9942)CGT>TGT	p.R3314C
Pat_04	Pre-Treatment	VCAN	1462	37	5	82876246	82876246	Missense_Mutation	SNP	G	A	3	27	c.10184G>A	.(10183-10185)AGG>AA	p.R3395K
Pat_04	Pre-Treatment	GPR98	84059	37	5	89949427	89949427	Missense_Mutation	SNP	C	T	10	22	c.4036C>T	c.(4036-4038)CCC>TCC	p.P1346S
Pat_04	Pre-Treatment	CAST	831	37	5	96062522	96062522	Missense_Mutation	SNP	G	A	6	49	c.46G>A	c.(46-48)GAA>AAA	p.E16K

Pat_04	Pre-Treatment	CAST	831	37	5	96093305	96093305	Missense_Mutation	SNP	C	T	8	61	c.1531C>T	c.(1531-1533)CTT>TTT	p.L511F
Pat_04	Pre-Treatment	CHD1	1105	37	5	98192317	98192317	Missense_Mutation	SNP	G	A	7	30	c.4900C>T	c.(4900-4902)CAC>TAC	p.H1634Y
Pat_04	Pre-Treatment	MAN2A1	4124	37	5	109200786	109200786	Missense_Mutation	SNP	G	A	10	90	c.3221G>A	c.(3220-3222)GGG>GAG	p.G1074E
Pat_04	Pre-Treatment	STARD4	134429	37	5	110837710	110837710	Missense_Mutation	SNP	C	T	23	93	c.232G>A	c.(232-234)GAT>AAT	p.D78N
Pat_04	Pre-Treatment	SHROOM1	134549	37	5	132160400	132160400	Missense_Mutation	SNP	G	A	10	62	c.1148C>T	c.(1147-1149)CCC>CTC	p.P383L
Pat_04	Pre-Treatment	PCDHA1	56147	37	5	140167451	140167451	Missense_Mutation	SNP	G	A	22	138	c.1576G>A	c.(1576-1578)GAG>AAG	p.E526K
Pat_04	Pre-Treatment	PCDHA2	56146	37	5	140176383	140176383	Nonsense_Mutation	SNP	C	T	14	94	c.1834C>T	c.(1834-1836)CAG>TAG	p.Q612*
Pat_04	Pre-Treatment	PCDHA3	56145	37	5	140180999	140180999	Missense_Mutation	SNP	G	A	23	142	c.217G>A	c.(217-219)GAC>AAC	p.D73N
Pat_04	Pre-Treatment	PCDHA4	56144	37	5	140187313	140187313	Missense_Mutation	SNP	G	A	7	30	c.541G>A	c.(541-543)GAA>AAA	p.E181K
Pat_04	Pre-Treatment	PCDHA5	56143	37	5	140201564	140201564	Missense_Mutation	SNP	G	C	32	132	c.204G>C	c.(202-204)AAG>AAC	p.K68N
Pat_04	Pre-Treatment	PCDHA7	56141	37	5	140214360	140214360	Missense_Mutation	SNP	C	T	18	200	c.392C>T	c.(391-393)CCG>CTG	p.P131L
Pat_04	Pre-Treatment	PCDHB4	56131	37	5	140502392	140502392	Missense_Mutation	SNP	G	A	8	68	c.812G>A	c.(811-813)GGA>GAA	p.G271E
Pat_04	Pre-Treatment	PCDHB6	56130	37	5	140530635	140530635	Missense_Mutation	SNP	G	A	5	26	c.797G>A	c.(796-798)AGA>AAA	p.R266K
Pat_04	Pre-Treatment	PCDHB16	57717	37	5	140562587	140562587	Missense_Mutation	SNP	G	T	7	24	c.453G>T	c.(451-453)GAG>GAT	p.E151D
Pat_04	Pre-Treatment	PCDHGA1	56114	37	5	140712562	140712562	Missense_Mutation	SNP	C	T	24	215	c.2311C>T	c.(2311-2313)CCC>TCC	p.P771S
Pat_04	Pre-Treatment	PCDHGA3	56112	37	5	140725366	140725366	Missense_Mutation	SNP	C	T	12	80	c.1766C>T	c.(1765-1767)ACC>ATC	p.T589I
Pat_04	Pre-Treatment	PCDHGA3	56112	37	5	140725489	140725489	Missense_Mutation	SNP	G	A	7	67	c.1889G>A	c.(1888-1890)CGA>CAA	p.R630Q
Pat_04	Pre-Treatment	TCERG1	10915	37	5	145843320	145843320	Missense_Mutation	SNP	C	T	44	174	c.1099C>T	c.(1099-1101)CGT>TGT	p.R367C
Pat_04	Pre-Treatment	PPP2R2B	5521	37	5	145969685	145969685	Missense_Mutation	SNP	G	A	20	99	c.1157C>T	c.(1156-1158)GCT>GTT	p.A386V
Pat_04	Pre-Treatment	JAKMIP2	9832	37	5	147024427	147024427	Missense_Mutation	SNP	C	T	4	54	c.1069G>A	c.(1069-1071)GAA>AAA	p.E357K
Pat_04	Pre-Treatment	GRIA1	2890	37	5	153077667	153077667	Missense_Mutation	SNP	G	A	17	88	c.1198G>A	c.(1198-1200)GAT>AAT	p.D400N
Pat_04	Pre-Treatment	CCNJL	79616	37	5	159686764	159686764	Missense_Mutation	SNP	G	A	16	99	c.439C>T	c.(439-441)CGG>TGG	p.R147W
Pat_04	Pre-Treatment	ODZ2	57451	37	5	167420031	167420031	Missense_Mutation	SNP	G	A	12	94	c.1030G>A	c.(1030-1032)GTT>ATT	p.V344I
Pat_04	Pre-Treatment	SLIT3	6586	37	5	168175380	168175380	Missense_Mutation	SNP	C	T	5	54	c.2197G>A	c.(2197-2199)GAG>AAG	p.E733K
Pat_04	Pre-Treatment	FOXI1	2299	37	5	169535146	169535146	Missense_Mutation	SNP	C	T	10	36	c.668C>T	c.(667-669)TCC>TTC	p.S223F
Pat_04	Pre-Treatment	EIF4E1B	253314	37	5	176072457	176072457	Missense_Mutation	SNP	G	A	10	32	c.554G>A	c.(553-555)GGG>GAG	p.G185E
Pat_04	Pre-Treatment	ZFP2	80108	37	5	178358462	178358462	Missense_Mutation	SNP	G	A	10	49	c.148G>A	c.(148-150)GAA>AAA	p.E50K
Pat_04	Pre-Treatment	KAAG1	353219	37	6	24358066	24358066	Missense_Mutation	SNP	G	A	12	22	c.199G>A	c.(199-201)GGA>AGA	p.G67R
Pat_04	Pre-Treatment	OR2B3	442184	37	6	29054557	29054557	Missense_Mutation	SNP	C	T	4	27	c.469G>A	c.(469-471)GTG>ATG	p.V157M
Pat_04	Pre-Treatment	HLA-DOA	3111	37	6	32975249	32975249	Missense_Mutation	SNP	C	T	43	152	c.452G>A	c.(451-453)GGC>GAC	p.G151D
Pat_04	Pre-Treatment	BRPF3	27154	37	6	36169418	36169418	Missense_Mutation	SNP	C	T	3	15	c.1319C>T	c.(1318-1320)TCC>TTC	p.S440F
Pat_04	Pre-Treatment	YIPF3	25844	37	6	43480605	43480605	Missense_Mutation	SNP	C	T	3	17	c.674G>A	c.(673-675)GGC>GAC	p.G225D
Pat_04	Pre-Treatment	MEP1A	4224	37	6	46777273	46777273	Missense_Mutation	SNP	G	A	23	92	c.379G>A	c.(379-381)GGG>AGG	p.G127R
Pat_04	Pre-Treatment	CRISP2	7180	37	6	49663558	49663558	Missense_Mutation	SNP	C	T	8	65	c.595G>A	c.(595-597)GGA>AGA	p.G199R
Pat_04	Pre-Treatment	PGK2	5232	37	6	49754814	49754814	Missense_Mutation	SNP	C	T	8	55	c.87G>A	c.(85-87)ATG>ATA	p.M29I
Pat_04	Pre-Treatment	FAM83B	222584	37	6	54735177	54735177	Missense_Mutation	SNP	G	A	12	80	c.133G>A	c.(133-135)GAA>AAA	p.E45K
Pat_04	Pre-Treatment	BMP5	653	37	6	55623909	55623909	Nonsense_Mutation	SNP	C	T	9	51	c.1109G>A	c.(1108-1110)TGG>TAG	p.W370*
Pat_04	Pre-Treatment	BEND6	221336	37	6	56879993	56879993	Missense_Mutation	SNP	G	A	12	53	c.361G>A	c.(361-363)GGT>AGT	p.G121S
Pat_04	Pre-Treatment	PHF3	23469	37	6	64413499	64413499	Missense_Mutation	SNP	C	T	4	30	c.3305C>T	c.(3304-3306)TCT>TTT	p.S1102F
Pat_04	Pre-Treatment	COL9A1	1297	37	6	70990558	70990558	Missense_Mutation	SNP	C	T	3	14	c.932G>A	c.(931-933)GGA>GAA	p.G311E
Pat_04	Pre-Treatment	KCNQ5	56479	37	6	73904661	73904661	Missense_Mutation	SNP	G	A	7	50	c.2323G>A	c.(2323-2325)GAA>AAA	p.E775K
Pat_04	Pre-Treatment	GJA10	84694	37	6	90605358	90605358	Missense_Mutation	SNP	G	A	4	34	c.1171G>A	c.(1171-1173)GAC>AAC	p.D391N
Pat_04	Pre-Treatment	C6orf167	253714	37	6	97702456	97702456	Missense_Mutation	SNP	G	A	8	17	c.1096C>T	c.(1096-1098)CGC>TGC	p.R366C
Pat_04	Pre-Treatment	SIM1	6492	37	6	100841729	100841729	Missense_Mutation	SNP	G	A	7	36	c.1204C>T	c.(1204-1206)CAT>TAT	p.H402Y
Pat_04	Pre-Treatment	REV3L	5980	37	6	111688989	111688989	Missense_Mutation	SNP	G	A	11	91	c.6002C>T	c.(6001-6003)CCA>CTA	p.P2001L
Pat_04	Pre-Treatment	ROS1	6098	37	6	117662685	117662685	Nonsense_Mutation	SNP	G	A	10	59	c.4780C>T	c.(4780-4782)CAG>TAG	p.Q1594*
Pat_04	Pre-Treatment	MAN1A1	4121	37	6	119522499	119522499	Missense_Mutation	SNP	C	T	6	28	c.1130G>A	c.(1129-1131)CGA>CAA	p.R377Q

Pat_04	Pre-Treatment	PTPRK	5796	37	6	128306900	128306900	Missense_Mutation	SNP	G	A	5	52	c.3214C>T	c.(3214-3216)CCT>TCT	p.P1072S
Pat_04	Pre-Treatment	SYNE1	23345	37	6	152583252	152583252	Missense_Mutation	SNP	C	T	6	49	c.18887G>A	c.(18886-18888)AGA>AAA	p.R6296K
Pat_04	Pre-Treatment	SYNE1	23345	37	6	152706973	152706973	Missense_Mutation	SNP	C	T	5	39	c.8488G>A	c.(8488-8490)GAA>AAA	p.E2830K
Pat_04	Pre-Treatment	MYCT1	80177	37	6	153043059	153043059	Missense_Mutation	SNP	C	T	14	104	c.379C>T	c.(379-381)CGC>TGC	p.R127C
Pat_04	Pre-Treatment	LPA	4018	37	6	161022099	161022099	Missense_Mutation	SNP	C	T	10	71	c.2977G>A	c.(2977-2979)GAT>AAT	p.D993N
Pat_04	Pre-Treatment	PACRG	135138	37	6	163510440	163510440	Missense_Mutation	SNP	G	A	10	40	c.613G>A	c.(613-615)GGG>AGG	p.G205R
Pat_04	Pre-Treatment	TCP10L2	401285	37	6	167591993	167591993	Missense_Mutation	SNP	C	T	22	138	c.620C>T	c.(619-621)CCC>CTC	p.P207L
Pat_04	Pre-Treatment	MAD1L1	8379	37	7	2265161	2265161	Missense_Mutation	SNP	G	A	5	25	c.175C>T	c.(175-177)CGT>TGT	p.R59C
Pat_04	Pre-Treatment	ACTB	60	37	7	5568184	5568184	Missense_Mutation	SNP	C	T	9	54	c.530G>A	c.(529-531)CGT>CAT	p.R177H
Pat_04	Pre-Treatment	DNAH11	8701	37	7	21730448	21730448	Missense_Mutation	SNP	C	T	33	133	c.6011C>T	c.(6010-6012)CCG>CTG	p.P2004L
Pat_04	Pre-Treatment	DNAH11	8701	37	7	21827019	21827019	Missense_Mutation	SNP	G	A	6	31	c.9763G>A	c.(9763-9765)GTT>ATT	p.V3255I
Pat_04	Pre-Treatment	STK31	56164	37	7	23830450	23830450	Missense_Mutation	SNP	G	A	12	48	c.2645G>A	c.(2644-2646)CGA>CAA	p.R882Q
Pat_04	Pre-Treatment	NPC1L1	29881	37	7	44579280	44579280	Missense_Mutation	SNP	C	T	7	58	c.716G>A	c.(715-717)GGG>GAG	p.G239E
Pat_04	Pre-Treatment	WBSCR17	64409	37	7	71135003	71135003	Missense_Mutation	SNP	G	A	22	49	c.1313G>A	c.(1312-1314)AGG>AAG	p.R438K
Pat_04	Pre-Treatment	BAZ1B	9031	37	7	72865214	72865215	Missense_Mutation	DNP	GG	AA	22	138	.3542_3543CC>T	c.(3541-3543)TCC>TTT	p.S1181F
Pat_04	Pre-Treatment	MAGI2	9863	37	7	77756606	77756606	Missense_Mutation	SNP	G	A	24	252	c.3331C>T	c.(3331-3333)CCC>TCC	p.P1111S
Pat_04	Pre-Treatment	PCLO	27445	37	7	82538294	82538294	Missense_Mutation	SNP	C	T	5	53	c.13336G>A	c.(13336-13338)GAT>AAT	p.D4446N
Pat_04	Pre-Treatment	PCLO	27445	37	7	82544905	82544905	Missense_Mutation	SNP	G	A	9	62	c.12397C>T	c.(12397-12399)CGT>TGT	p.R4133C
Pat_04	Pre-Treatment	PCLO	27445	37	7	82578956	82578956	Missense_Mutation	SNP	C	T	18	186	c.10948G>A	c.(10948-10950)GAT>AAT	p.D3650N
Pat_04	Pre-Treatment	PCLO	27445	37	7	82580479	82580479	Missense_Mutation	SNP	G	A	3	25	c.9425C>T	c.(9424-9426)TCA>TTA	p.S3142L
Pat_04	Pre-Treatment	PCLO	27445	37	7	82582341	82582341	Missense_Mutation	SNP	C	T	6	60	c.7928G>A	c.(7927-7929)GGA>GAA	p.G2643E
Pat_04	Pre-Treatment	PCLO	27445	37	7	82764798	82764798	Missense_Mutation	SNP	G	A	5	57	c.2068C>T	c.(2068-2070)CCA>TCA	p.P690S
Pat_04	Pre-Treatment	ABCB1	5243	37	7	87175304	87175304	Missense_Mutation	SNP	G	A	13	95	c.1762C>T	c.(1762-1764)CGT>TGT	p.R588C
Pat_04	Pre-Treatment	AKAP9	10142	37	7	91712907	91712907	Nonsense_Mutation	SNP	C	T	7	73	c.8584C>T	c.(8584-8586)CAG>TAG	p.Q2862*
Pat_04	Pre-Treatment	HEPACAM2	253012	37	7	92826842	92826842	Missense_Mutation	SNP	G	A	3	23	c.1094C>T	c.(1093-1095)TCC>TTC	p.S365F
Pat_04	Pre-Treatment	HEPACAM2	253012	37	7	92844875	92844875	Missense_Mutation	SNP	T	A	15	71	c.554A>T	c.(553-555)AAT>ATT	p.N185I
Pat_04	Pre-Treatment	ARPC1B	10095	37	7	98984382	98984382	Missense_Mutation	SNP	G	A	19	127	c.139G>A	c.(139-141)GAG>AAG	p.E47K
Pat_04	Pre-Treatment	TRIM4	89122	37	7	99490070	99490070	Missense_Mutation	SNP	G	A	35	258	c.1219C>T	c.(1219-1221)CGT>TGT	p.R407C
Pat_04	Pre-Treatment	STAG3	10734	37	7	99787166	99787166	Missense_Mutation	SNP	C	T	39	88	c.814C>T	c.(814-816)CCA>TCA	p.P272S
Pat_04	Pre-Treatment	C7orf61	402573	37	7	100061186	100061186	Missense_Mutation	SNP	G	A	6	40	c.187C>T	c.(187-189)CCA>TCA	p.P63S
Pat_04	Pre-Treatment	MYL10	93408	37	7	101266307	101266307	Missense_Mutation	SNP	C	T	11	57	c.319G>A	c.(319-321)GAG>AAG	p.E107K
Pat_04	Pre-Treatment	RELN	5649	37	7	103113269	103113269	Missense_Mutation	SNP	C	T	10	52	c.10373G>A	.(10372-10374)CGA>CAA	p.R3458Q
Pat_04	Pre-Treatment	RELN	5649	37	7	103180703	103180703	Missense_Mutation	SNP	G	A	12	100	c.6871C>T	c.(6871-6873)CTT>TTT	p.L2291F
Pat_04	Pre-Treatment	RELN	5649	37	7	103629593	103629593	Missense_Mutation	SNP	C	T	15	61	c.211G>A	c.(211-213)GGA>AGA	p.G71R
Pat_04	Pre-Treatment	BCAP29	55973	37	7	107258776	107258776	Missense_Mutation	SNP	C	T	5	43	c.694C>T	c.(694-696)CGT>TGT	p.R232C
Pat_04	Pre-Treatment	TFEC	22797	37	7	115596807	115596807	Missense_Mutation	SNP	C	T	10	69	c.308G>A	c.(307-309)GGA>GAA	p.G103E
Pat_04	Pre-Treatment	MET	4233	37	7	116339706	116339706	Missense_Mutation	SNP	G	A	13	76	c.568G>A	c.(568-570)GAC>AAC	p.D190N
Pat_04	Pre-Treatment	NRF1	4899	37	7	129349000	129349000	Missense_Mutation	SNP	C	T	26	237	c.692C>T	c.(691-693)CCC>CTC	p.P231L
Pat_04	Pre-Treatment	NRF1	4899	37	7	129394921	129394921	Missense_Mutation	SNP	G	A	9	78	c.1412G>A	c.(1411-1413)GGA>GAA	p.G471E
Pat_04	Pre-Treatment	CPA1	1357	37	7	130023244	130023244	Missense_Mutation	SNP	G	A	8	52	c.496G>A	c.(496-498)GGC>AGC	p.G166S
Pat_04	Pre-Treatment	MEST	4232	37	7	130138283	130138283	Missense_Mutation	SNP	G	A	12	81	c.500G>A	c.(499-501)CGG>CAG	p.R167Q
Pat_04	Pre-Treatment	PLXNA4	91584	37	7	132193185	132193185	Missense_Mutation	SNP	C	T	7	66	c.268G>A	c.(268-270)GAG>AAG	p.E90K
Pat_04	Pre-Treatment	CREB3L2	64764	37	7	137567192	137567192	Missense_Mutation	SNP	C	T	16	102	c.1453G>A	c.(1453-1455)GAG>AAG	p.E485K
Pat_04	Pre-Treatment	TMEM213	155006	37	7	138486131	138486131	Missense_Mutation	SNP	G	A	4	20	c.142G>A	c.(142-144)GAG>AAG	p.E48K
Pat_04	Pre-Treatment	TBXAS1	6916	37	7	139717589	139717589	Missense_Mutation	SNP	C	T	13	142	c.1624C>T	c.(1624-1626)CAC>TAC	p.H542Y
Pat_04	Pre-Treatment	BRAF	673	37	7	140453136	140453137	Missense_Mutation	DNP	AC	TT	31	71	.1798_1799GT>A	c.(1798-1800)GTG>AAG	p.V600K
Pat_04	Pre-Treatment	TAS2R38	5726	37	7	141673021	141673021	Missense_Mutation	SNP	G	A	5	50	c.469C>T	c.(469-471)CTC>TTC	p.L157F

Pat_04	Pre-Treatment	TAS2R39	259285	37	7	142881106	142881106	Missense_Mutation	SNP	A	G	5	53	c.595A>G	c.(595-597)ACA>GCA	p.T199A
Pat_04	Pre-Treatment	FAM131B	9715	37	7	143053747	143053747	Nonsense_Mutation	SNP	G	A	39	224	c.895C>T	c.(895-897)CGA>TGA	p.R299*
Pat_04	Pre-Treatment	FAM131B	9715	37	7	143056030	143056030	Nonsense_Mutation	SNP	C	T	6	52	c.272G>A	c.(271-273)TGG>TAG	p.W91*
Pat_04	Pre-Treatment	OR2A5	393046	37	7	143747858	143747858	Missense_Mutation	SNP	C	T	30	196	c.364C>T	c.(364-366)CGG>TGG	p.R122W
Pat_04	Pre-Treatment	SSPO	23145	37	7	149509361	149509362	Missense_Mutation	DNP	GG	AA	3	16	.9759_9760GG>A	57-9762)GGGGGA>GGA	p.G3254R
Pat_04	Pre-Treatment	ZNF862	643641	37	7	149544869	149544869	Missense_Mutation	SNP	C	T	5	14	c.287C>T	c.(286-288)CCC>CTC	p.P96L
Pat_04	Pre-Treatment	ACCN3	9311	37	7	150747192	150747192	Splice_Site	SNP	G	A	16	70	c.535_splice	c.e2-1	p.I179_splice
Pat_04	Pre-Treatment	GBX1	2636	37	7	150846152	150846152	Missense_Mutation	SNP	C	T	53	393	c.616G>A	c.(616-618)GAA>AAA	p.E206K
Pat_04	Pre-Treatment	CSMD1	64478	37	8	2820770	2820770	Nonsense_Mutation	SNP	C	T	19	115	c.9431G>A	c.(9430-9432)TGG>TAG	p.W3144*
Pat_04	Pre-Treatment	RP1L1	94137	37	8	10465655	10465655	Missense_Mutation	SNP	C	T	17	122	c.5953G>A	c.(5953-5955)GAG>AAG	p.E1985K
Pat_04	Pre-Treatment	MSR1	4481	37	8	15978011	15978011	Missense_Mutation	SNP	C	T	32	194	c.1138G>A	c.(1138-1140)GAA>AAA	p.E380K
Pat_04	Pre-Treatment	NAT2	10	37	8	18258373	18258373	Missense_Mutation	SNP	C	T	6	43	c.860C>T	c.(859-861)TCC>TTC	p.S287F
Pat_04	Pre-Treatment	SLC18A1	6570	37	8	20028976	20028976	Missense_Mutation	SNP	C	T	18	95	c.754G>A	c.(754-756)GAG>AAG	p.E252K
Pat_04	Pre-Treatment	PHYHIP	9796	37	8	22084457	22084457	Missense_Mutation	SNP	C	T	13	73	c.247G>A	c.(247-249)GAG>AAG	p.E83K
Pat_04	Pre-Treatment	PIWIL2	55124	37	8	22211798	22211798	Missense_Mutation	SNP	T	A	20	87	c.2672T>A	c.(2671-2673)CTT>CAT	p.L891H
Pat_04	Pre-Treatment	ADAM28	10863	37	8	24193049	24193049	Missense_Mutation	SNP	G	A	8	37	c.1462G>A	c.(1462-1464)GAT>AAT	p.D488N
Pat_04	Pre-Treatment	ADAM7	8756	37	8	24350704	24350704	Missense_Mutation	SNP	G	A	10	26	c.1804G>A	c.(1804-1806)GGC>AGC	p.G602S
Pat_04	Pre-Treatment	EBF2	64641	37	8	25708119	25708119	Missense_Mutation	SNP	C	T	13	91	c.1687G>A	c.(1687-1689)GGA>AGA	p.G563R
Pat_04	Pre-Treatment	EBF2	64641	37	8	25718744	25718744	Splice_Site	SNP	T	C	11	61	c.1165_splice	c.e13-1	p.D389_splice
Pat_04	Pre-Treatment	TEX15	56154	37	8	30701904	30701904	Missense_Mutation	SNP	C	T	19	123	c.4630G>A	c.(4630-4632)GAA>AAA	p.E1544K
Pat_04	Pre-Treatment	ANK1	286	37	8	41550683	41550683	Missense_Mutation	SNP	C	T	23	88	c.3569G>A	c.(3568-3570)GGA>GAA	p.G1190E
Pat_04	Pre-Treatment	PXDNL	137902	37	8	52321545	52321545	Missense_Mutation	SNP	G	A	5	58	c.2639C>T	c.(2638-2640)TCA>TTA	p.S880L
Pat_04	Pre-Treatment	PXDNL	137902	37	8	52321663	52321663	Missense_Mutation	SNP	G	A	3	28	c.2521C>T	c.(2521-2523)CCT>TCT	p.P841S
Pat_04	Pre-Treatment	PCMTD1	115294	37	8	52733153	52733153	Nonsense_Mutation	SNP	T	A	5	184	c.832A>T	c.(832-834)AGA>TGA	p.R278*
Pat_04	Pre-Treatment	RP1	6101	37	8	55539678	55539678	Missense_Mutation	SNP	C	T	6	20	c.3236C>T	c.(3235-3237)CCA>CTA	p.P1079L
Pat_04	Pre-Treatment	XKR4	114786	37	8	56015146	56015146	Missense_Mutation	SNP	G	A	4	11	c.98G>A	c.(97-99)GGA>GAA	p.G33E
Pat_04	Pre-Treatment	CSPP1	79848	37	8	68007843	68007843	Missense_Mutation	SNP	C	T	10	34	c.931C>T	c.(931-933)CGT>TGT	p.R311C
Pat_04	Pre-Treatment	C8orf34	116328	37	8	69358567	69358567	Missense_Mutation	SNP	C	T	3	25	c.221C>T	c.(220-222)TCC>TTC	p.S74F
Pat_04	Pre-Treatment	C8orf34	116328	37	8	69434034	69434034	Missense_Mutation	SNP	G	A	3	42	c.508G>A	c.(508-510)GAA>AAA	p.E170K
Pat_04	Pre-Treatment	KCNB2	9312	37	8	73849835	73849835	Missense_Mutation	SNP	C	T	31	232	c.2245C>T	c.(2245-2247)CCG>TCG	p.P749S
Pat_04	Pre-Treatment	ZFHX4	79776	37	8	77618289	77618289	Nonsense_Mutation	SNP	C	T	3	21	c.1966C>T	c.(1966-1968)CAG>TAG	p.Q656*
Pat_04	Pre-Treatment	TPD52	7163	37	8	80976726	80976726	Missense_Mutation	SNP	C	T	17	98	c.242G>A	c.(241-243)AGA>AAA	p.R81K
Pat_04	Pre-Treatment	PMP2	5375	37	8	82357197	82357197	Missense_Mutation	SNP	C	T	4	31	c.101G>A	c.(100-102)GGA>GAA	p.G34E
Pat_04	Pre-Treatment	RGS22	26166	37	8	101075717	101075717	Missense_Mutation	SNP	C	T	9	50	c.1279G>A	c.(1279-1281)GGA>AGA	p.G427R
Pat_04	Pre-Treatment	SNX31	169166	37	8	101629886	101629886	Missense_Mutation	SNP	C	T	10	70	c.394G>A	c.(394-396)GAA>AAA	p.E132K
Pat_04	Pre-Treatment	CSMD3	114788	37	8	113301606	113301606	Missense_Mutation	SNP	G	C	17	152	c.9136C>G	c.(9136-9138)CCT>GCT	p.P3046A
Pat_04	Pre-Treatment	ZHX2	22882	37	8	123964603	123964603	Missense_Mutation	SNP	C	T	11	51	c.853C>T	c.(853-855)CCT>TCT	p.P285S
Pat_04	Pre-Treatment	FAM83A	84985	37	8	124195392	124195392	Missense_Mutation	SNP	C	T	12	76	c.296C>T	c.(295-297)TCC>TTC	p.S99F
Pat_04	Pre-Treatment	ADCY8	114	37	8	132051738	132051738	Missense_Mutation	SNP	G	A	5	30	c.842C>T	c.(841-843)ACC>ATC	p.T281I
Pat_04	Pre-Treatment	COL22A1	169044	37	8	139845361	139845361	Missense_Mutation	SNP	C	T	10	59	c.766G>A	c.(766-768)GAA>AAA	p.E256K
Pat_04	Pre-Treatment	ZNF16	7564	37	8	146157650	146157650	Missense_Mutation	SNP	G	A	15	135	c.523C>T	c.(523-525)CCT>TCT	p.P175S
Pat_04	Pre-Treatment	KDM4C	23081	37	9	7174607	7174607	Nonsense_Mutation	SNP	C	T	20	102	c.3049C>T	c.(3049-3051)CAA>TAA	p.Q1017*
Pat_04	Pre-Treatment	FREM1	158326	37	9	14841507	14841507	Missense_Mutation	SNP	C	T	4	38	c.1819G>A	c.(1819-1821)GAA>AAA	p.E607K
Pat_04	Pre-Treatment	CDKN2A	1029	37	9	21971186	21971186	Nonsense_Mutation	SNP	G	A	3	18	c.172C>T	c.(172-174)CGA>TGA	p.R58*
Pat_04	Pre-Treatment	ANXA2P2	304	37	9	33625005	33625005	Missense_Mutation	SNP	G	A	4	37	c.734G>A	c.(733-735)AGG>AAG	p.R245K
Pat_04	Pre-Treatment	FAM75A6	389730	37	9	43627750	43627751	Missense_Mutation	DNP	CC	TT	37	238	c.936_937GG>AA	(934-939)ATGGAA>ATAA	.312_313ME>I
Pat_04	Pre-Treatment	FOXD4L5	653427	37	9	70177790	70177790	Missense_Mutation	SNP	C	T	6	73	c.194G>A	c.(193-195)GGC>GAC	p.G65D

Pat_04	Pre-Treatment	APBA1	320	37	9	72131466	72131466	Missense_Mutation	SNP	C	T	3	7	c.661G>A	c.(661-663)GAC>AAC	p.D221N
Pat_04	Pre-Treatment	MAMDC2	256691	37	9	72785420	72785420	Missense_Mutation	SNP	G	C	11	64	c.1524G>C	c.(1522-1524)GAG>GAC	p.E508D
Pat_04	Pre-Treatment	TRPM3	80036	37	9	73233959	73233959	Missense_Mutation	SNP	C	T	6	41	c.2146G>A	c.(2146-2148)GAA>AAA	p.E716K
Pat_04	Pre-Treatment	TMC1	117531	37	9	75445446	75445446	Splice_Site	SNP	G	A	5	35	c.2208_splice	c.e22+1	p.M736_splice
Pat_04	Pre-Treatment	PCSK5	5125	37	9	78601135	78601135	Missense_Mutation	SNP	C	T	14	85	c.385C>T	c.(385-387)CCC>TCC	p.P129S
Pat_04	Pre-Treatment	PCSK5	5125	37	9	78804019	78804019	Missense_Mutation	SNP	C	T	5	45	c.2390C>T	c.(2389-2391)GCT>GTT	p.A797V
Pat_04	Pre-Treatment	PRUNE2	158471	37	9	79322383	79322383	Missense_Mutation	SNP	C	T	3	34	c.4807G>A	c.(4807-4809)GAG>AAG	p.E1603K
Pat_04	Pre-Treatment	PRUNE2	158471	37	9	79326139	79326139	Missense_Mutation	SNP	C	T	3	23	c.1051G>A	c.(1051-1053)GAA>AAA	p.E351K
Pat_04	Pre-Treatment	GRIN3A	116443	37	9	104449125	104449125	Missense_Mutation	SNP	G	A	9	27	c.1057C>T	c.(1057-1059)CGT>TGT	p.R353C
Pat_04	Pre-Treatment	OR13F1	138805	37	9	107266743	107266743	Missense_Mutation	SNP	C	T	26	117	c.200C>T	c.(199-201)TCC>TTC	p.S67F
Pat_04	Pre-Treatment	EPB41L4B	54566	37	9	112020521	112020521	Missense_Mutation	SNP	G	A	9	30	c.688C>T	c.(688-690)CGG>TGG	p.R230W
Pat_04	Pre-Treatment	MUSK	4593	37	9	113563038	113563038	Missense_Mutation	SNP	G	A	4	26	c.2380G>A	c.(2380-2382)GAG>AAG	p.E794K
Pat_04	Pre-Treatment	C9orf84	158401	37	9	114510461	114510461	Missense_Mutation	SNP	C	T	12	53	c.689G>A	c.(688-690)GGA>GAA	p.G230E
Pat_04	Pre-Treatment	OR1N2	138882	37	9	125315890	125315890	Missense_Mutation	SNP	C	T	17	67	c.442C>T	c.(442-444)CAT>TAT	p.H148Y
Pat_04	Pre-Treatment	CIZ1	25792	37	9	130938729	130938729	Missense_Mutation	SNP	G	A	13	57	c.1844C>T	c.(1843-1845)CCT>CTT	p.P615L
Pat_04	Pre-Treatment	GPR107	57720	37	9	132839594	132839594	Missense_Mutation	SNP	A	G	7	45	c.323A>G	c.(322-324)TAC>TGC	p.Y108C
Pat_04	Pre-Treatment	ASS1	445	37	9	133355154	133355154	Missense_Mutation	SNP	C	T	21	69	c.740C>T	c.(739-741)TCC>TTC	p.S247F
Pat_04	Pre-Treatment	NUP214	8021	37	9	134025772	134025772	Missense_Mutation	SNP	C	T	5	73	c.2102C>T	c.(2101-2103)CCT>CTT	p.P701L
Pat_04	Pre-Treatment	ADAMTS13	11093	37	9	136319646	136319646	Missense_Mutation	SNP	G	A	5	44	c.3154G>A	c.(3154-3156)GAG>AAG	p.E1052K
Pat_04	Pre-Treatment	COL5A1	1289	37	9	137622248	137622248	Missense_Mutation	SNP	C	T	6	40	c.1091C>T	c.(1090-1092)CCC>CTC	p.P364L
Pat_04	Pre-Treatment	COL5A1	1289	37	9	137702140	137702140	Missense_Mutation	SNP	G	A	5	53	c.3514G>A	c.(3514-3516)GAC>AAC	p.D1172N
Pat_04	Pre-Treatment	CAMSAP1	157922	37	9	138714655	138714655	Missense_Mutation	SNP	C	T	5	38	c.1852G>A	c.(1852-1854)GGG>AGG	p.G618R
Pat_04	Pre-Treatment	NOTCH1	4851	37	9	139410495	139410495	Missense_Mutation	SNP	G	A	17	96	c.1607C>T	c.(1606-1608)CCC>CTC	p.P536L
Pat_04	Pre-Treatment	EDF1	8721	37	9	139757778	139757778	Missense_Mutation	SNP	G	A	12	69	c.253C>T	c.(253-255)CGG>TGG	p.R85W
Pat_04	Pre-Treatment	NDOR1	27158	37	9	140100762	140100762	Splice_Site	SNP	G	A	5	189	c.213_splice	c.e2+1	p.K71_splice
Pat_04	Pre-Treatment	MXRA5	25878	37	X	3248116	3248116	Missense_Mutation	SNP	G	A	3	10	c.652C>T	c.(652-654)CCG>TCG	p.P218S
Pat_04	Pre-Treatment	FRMPD4	9758	37	X	12735733	12735733	Missense_Mutation	SNP	G	A	30	70	c.2788G>A	c.(2788-2790)GAA>AAA	p.E930K
Pat_04	Pre-Treatment	ZRSR2	8233	37	X	15838410	15838410	Missense_Mutation	SNP	C	T	25	93	c.908C>T	c.(907-909)CCC>CTC	p.P303L
Pat_04	Pre-Treatment	BEND2	139105	37	X	18221675	18221675	Missense_Mutation	SNP	C	T	6	40	c.853G>A	c.(853-855)GAA>AAA	p.E285K
Pat_04	Pre-Treatment	SH3KBP1	30011	37	X	19764542	19764542	Missense_Mutation	SNP	C	T	11	29	c.180G>A	c.(178-180)ATG>ATA	p.M60I
Pat_04	Pre-Treatment	CNKSR2	22866	37	X	21450761	21450761	Missense_Mutation	SNP	C	A	6	51	c.260C>A	c.(259-261)ACC>AAC	p.T87N
Pat_04	Pre-Treatment	ZFX	7543	37	X	24229378	24229378	Missense_Mutation	SNP	C	T	31	57	c.2303C>T	c.(2302-2304)TCC>TTC	p.S768F
Pat_04	Pre-Treatment	PPP1R3F	89801	37	X	49142945	49142945	Missense_Mutation	SNP	C	T	6	14	c.1793C>T	c.(1792-1794)TCG>TTG	p.S598L
Pat_04	Pre-Treatment	MAGEE2	139599	37	X	75004584	75004584	Missense_Mutation	SNP	C	T	4	18	c.303G>A	c.(301-303)ATG>ATA	p.M101I
Pat_04	Pre-Treatment	PCDH11X	27328	37	X	91090729	91090729	Nonsense_Mutation	SNP	C	T	40	63	c.226C>T	c.(226-228)CGA>TGA	p.R76*
Pat_04	Pre-Treatment	BEX1	55859	37	X	102318005	102318005	Missense_Mutation	SNP	C	T	28	56	c.198G>A	c.(196-198)ATG>ATA	p.M66I
Pat_04	Pre-Treatment	NRK	203447	37	X	105168911	105168911	Missense_Mutation	SNP	G	A	14	23	c.3200G>A	c.(3199-3201)CGA>CAA	p.R1067Q
Pat_04	Pre-Treatment	TRPC5	7224	37	X	111155953	111155953	Missense_Mutation	SNP	C	T	19	53	c.466G>A	c.(466-468)GAA>AAA	p.E156K
Pat_04	Pre-Treatment	ZCCHC16	340595	37	X	111698539	111698539	Missense_Mutation	SNP	G	A	18	43	c.583G>A	c.(583-585)GAA>AAA	p.E195K
Pat_04	Pre-Treatment	SASH3	54440	37	X	128922438	128922438	Missense_Mutation	SNP	C	T	7	14	c.185C>T	c.(184-186)CCA>CTA	p.P62L
Pat_04	Pre-Treatment	IGSF1	3547	37	X	130415793	130415793	Missense_Mutation	SNP	C	T	9	15	c.1372G>A	c.(1372-1374)GAA>AAA	p.E458K
Pat_04	Pre-Treatment	SAGE1	55511	37	X	134988220	134988220	Missense_Mutation	SNP	G	A	13	29	c.492G>A	c.(490-492)ATG>ATA	p.M164I
Pat_04	Pre-Treatment	GPR112	139378	37	X	135427792	135427792	Missense_Mutation	SNP	G	A	16	29	c.1927G>A	c.(1927-1929)GAT>AAT	p.D643N
Pat_04	Pre-Treatment	CDR1	1038	37	X	139865876	139865876	Missense_Mutation	SNP	C	T	14	36	c.656G>A	c.(655-657)GGA>GAA	p.G219E
Pat_04	Pre-Treatment	GABRE	2564	37	X	151124290	151124290	Missense_Mutation	SNP	C	T	22	47	c.827G>A	c.(826-828)CGG>CAG	p.R276Q
Pat_04	Pre-Treatment	MAGEA10	4109	37	X	151303876	151303876	Missense_Mutation	SNP	C	T	23	37	c.217G>A	c.(217-219)GAG>AAG	p.E73K
Pat_04	Pre-Treatment	MAGEA6	4105	37	X	151870118	151870118	Missense_Mutation	SNP	G	A	28	69	c.808G>A	c.(808-810)GAG>AAG	p.E270K

Pat_04	Pre-Treatment	USP9Y	8287	37	Y	14872445	14872445	Missense_Mutation	SNP	C	T	8	10	c.1798C>T	c.(1798-1800)CGC>TGC	p.R600C
Pat_04	Post-Resistance	DNALI1	7802	37	1	38023207	38023207	Missense_Mutation	SNP	C	T	5	124	c.151C>T	c.(151-153)CGG>TGG	p.R51W
Pat_04	Post-Resistance	SLAMF9	89886	37	1	159923915	159923915	Missense_Mutation	SNP	G	A	3	57	c.13C>T	c.(13-15)CCT>TCT	p.P5S
Pat_04	Post-Resistance	SLAMF1	6504	37	1	160616672	160616672	Missense_Mutation	SNP	T	C	3	31	c.64A>G	c.(64-66)AGC>GGC	p.S22G
Pat_04	Post-Resistance	CAMSAP1L1	23271	37	1	200816379	200816379	Missense_Mutation	SNP	C	T	4	94	c.1184C>T	c.(1183-1185)CCT>CTT	p.P395L
Pat_04	Post-Resistance	CENPF	1063	37	1	214819239	214819239	Nonsense_Mutation	SNP	C	G	4	78	c.6326C>G	c.(6325-6327)TCA>TGA	p.S2109*
Pat_04	Post-Resistance	BICC1	80114	37	10	60566860	60566860	Missense_Mutation	SNP	A	C	6	130	c.2318A>C	c.(2317-2319)AAG>ACG	p.K773T
Pat_04	Post-Resistance	OR10A4	283297	37	11	6898467	6898467	Missense_Mutation	SNP	G	C	5	112	c.589G>C	c.(589-591)GAA>CAA	p.E197Q
Pat_04	Post-Resistance	OR4D11	219986	37	11	59271557	59271557	Missense_Mutation	SNP	G	A	7	235	c.509G>A	c.(508-510)GGA>GAA	p.G170E
Pat_04	Post-Resistance	CCDC15	80071	37	11	124857585	124857585	Missense_Mutation	SNP	C	A	4	118	c.1463C>A	c.(1462-1464)CCC>CAC	p.P488H
Pat_04	Post-Resistance	DCAF4	26094	37	14	73425449	73425449	Missense_Mutation	SNP	C	T	6	161	c.1424C>T	c.(1423-1425)TCC>TTC	p.S475F
Pat_04	Post-Resistance	TUBGCP4	27229	37	15	43668311	43668311	Missense_Mutation	SNP	C	T	7	215	c.94C>T	c.(94-96)CCT>TCT	p.P32S
Pat_04	Post-Resistance	ACSM2B	348158	37	16	20570625	20570625	Missense_Mutation	SNP	G	A	3	51	c.322C>T	c.(322-324)CGT>TGT	p.R108C
Pat_04	Post-Resistance	SENP3	26168	37	17	7473708	7473709	Missense_Mutation	DNP	CC	TT	4	100	.1376_1377CC>T	c.(1375-1377)CCC>CTT	p.P459L
Pat_04	Post-Resistance	HAP1	9001	37	17	39881183	39881183	Missense_Mutation	SNP	C	T	24	364	c.1786G>A	c.(1786-1788)GAA>AAA	p.E596K
Pat_04	Post-Resistance	MAPT	4137	37	17	44060753	44060753	Missense_Mutation	SNP	G	A	4	25	c.583G>A	c.(583-585)GAC>AAC	p.D195N
Pat_04	Post-Resistance	ITGB3	3690	37	17	45369775	45369775	Missense_Mutation	SNP	G	A	4	114	c.1531G>A	c.(1531-1533)GAA>AAA	p.E511K
Pat_04	Post-Resistance	HOXB5	3215	37	17	46669678	46669678	Missense_Mutation	SNP	C	T	6	203	c.703G>A	c.(703-705)GAG>AAG	p.E235K
Pat_04	Post-Resistance	MED13	9969	37	17	60088215	60088215	Missense_Mutation	SNP	G	A	4	89	c.1663C>T	c.(1663-1665)CCT>TCT	p.P555S
Pat_04	Post-Resistance	APOB	338	37	2	21232704	21232704	Missense_Mutation	SNP	C	T	3	59	c.7036G>A	c.(7036-7038)GAG>AAG	p.E2346K
Pat_04	Post-Resistance	SLC4A5	57835	37	2	74452032	74452032	Missense_Mutation	SNP	C	T	3	39	c.3229G>A	c.(3229-3231)GAA>AAA	p.E1077K
Pat_04	Post-Resistance	RBM44	375316	37	2	238725794	238725794	Missense_Mutation	SNP	G	A	8	81	c.235G>A	c.(235-237)GAG>AAG	p.E79K
Pat_04	Post-Resistance	KCNK15	60598	37	20	43378866	43378866	Missense_Mutation	SNP	G	T	6	15	c.380G>T	c.(379-381)AGC>ATC	p.S127I
Pat_04	Post-Resistance	ZSWIM3	140831	37	20	44506623	44506623	Missense_Mutation	SNP	G	A	3	57	c.1426G>A	c.(1426-1428)GCA>ACA	p.A476T
Pat_04	Post-Resistance	SLC13A3	64849	37	20	45188756	45188756	Nonsense_Mutation	SNP	G	A	9	275	c.1714C>T	c.(1714-1716)CAG>TAG	p.Q572*
Pat_04	Post-Resistance	SCN5A	6331	37	3	38645271	38645271	Missense_Mutation	SNP	C	T	4	67	c.1822G>A	c.(1822-1824)GAC>AAC	p.D608N
Pat_04	Post-Resistance	GOLGB1	2804	37	3	121413651	121413651	Nonsense_Mutation	SNP	G	A	5	172	c.5704C>T	c.(5704-5706)CAA>TAA	p.Q1902*
Pat_04	Post-Resistance	EBF1	1879	37	5	158223448	158223448	Missense_Mutation	SNP	C	T	4	70	c.814G>A	c.(814-816)GGA>AGA	p.G272R
Pat_04	Post-Resistance	HLA-DOA	3111	37	6	32975249	32975249	Missense_Mutation	SNP	C	T	9	245	c.452G>A	c.(451-453)GGC>GAC	p.G151D
Pat_04	Post-Resistance	MEP1A	4224	37	6	46777273	46777273	Missense_Mutation	SNP	G	A	7	172	c.379G>A	c.(379-381)GGG>AGG	p.G127R
Pat_04	Post-Resistance	PTPRK	5796	37	6	128306900	128306900	Missense_Mutation	SNP	G	A	4	85	c.3214C>T	c.(3214-3216)CCT>TCT	p.P1072S
Pat_04	Post-Resistance	NPC1L1	29881	37	7	44579280	44579280	Missense_Mutation	SNP	C	T	4	106	c.716G>A	c.(715-717)GGG>GAG	p.G239E
Pat_04	Post-Resistance	BAZ1B	9031	37	7	72865214	72865215	Missense_Mutation	DNP	GG	AA	6	139	.3542_3543CC>T	c.(3541-3543)TCC>TTT	p.S1181F
Pat_04	Post-Resistance	STAG3	10734	37	7	99787166	99787166	Missense_Mutation	SNP	C	T	8	113	c.814C>T	c.(814-816)CCA>TCA	p.P272S
Pat_04	Post-Resistance	TFEC	22797	37	7	115596807	115596807	Missense_Mutation	SNP	C	T	5	62	c.308G>A	c.(307-309)GGA>GAA	p.G103E
Pat_04	Post-Resistance	TAS2R39	259285	37	7	142881106	142881106	Missense_Mutation	SNP	A	G	4	59	c.595A>G	c.(595-597)ACA>GCA	p.T199A
Pat_04	Post-Resistance	ADAM7	8756	37	8	24350704	24350704	Missense_Mutation	SNP	G	A	3	36	c.1804G>A	c.(1804-1806)GGC>AGC	p.G602S
Pat_04	Post-Resistance	ANK1	286	37	8	41550683	41550683	Missense_Mutation	SNP	C	T	5	113	c.3569G>A	c.(3568-3570)GGA>GAA	p.G1190E
Pat_04	Post-Resistance	ZRSR2	8233	37	X	15838410	15838410	Missense_Mutation	SNP	C	T	4	103	c.908C>T	c.(907-909)CCC>CTC	p.P303L
Pat_04	Post-Resistance	NRK	203447	37	X	105168911	105168911	Missense_Mutation	SNP	G	A	4	48	c.3200G>A	c.(3199-3201)CGA>CAA	p.R1067Q
Pat_04	Post-Resistance	MAGEA6	4105	37	X	151870118	151870118	Missense_Mutation	SNP	G	A	5	102	c.808G>A	c.(808-810)GAG>AAG	p.E270K
Pat_07	Post-Resistance	CDK11B	984	37	1	1572288	1572288	Missense_Mutation	SNP	G	A	3	58	c.1771C>T	c.(1771-1773)CGC>TGC	p.R591C
Pat_07	Post-Resistance	SPATA21	374955	37	1	16730232	16730232	Missense_Mutation	SNP	C	T	70	189	c.991G>A	c.(991-993)GAA>AAA	p.E331K
Pat_07	Post-Resistance	C1orf172	126695	37	1	27278407	27278407	Missense_Mutation	SNP	C	T	19	40	c.465G>A	c.(463-465)ATG>ATA	p.M155I
Pat_07	Post-Resistance	SLC1A7	6512	37	1	53556345	53556345	Missense_Mutation	SNP	C	T	3	49	c.1165G>A	c.(1165-1167)GCC>ACC	p.A389T
Pat_07	Post-Resistance	MTMR11	10903	37	1	149903250	149903250	Nonsense_Mutation	SNP	G	A	6	234	c.1192C>T	c.(1192-1194)CGA>TGA	p.R398*
Pat_07	Post-Resistance	TCHH	7062	37	1	152084627	152084627	Missense_Mutation	SNP	C	G	4	120	c.1066G>C	c.(1066-1068)GAG>CAG	p.E356Q

Pat_07	Post-Resistance	RPTN	126638	37	1	152128617	152128617	Missense_Mutation	SNP	T	C	18	773	c.958A>G	c.(958-960)AGT>GGT	p.S320G
Pat_07	Post-Resistance	DENND4B	9909	37	1	153907256	153907256	Missense_Mutation	SNP	T	A	3	43	c.2753A>T	c.(2752-2754)GAG>GTG	p.E918V
Pat_07	Post-Resistance	C1orf156	92342	37	1	169761849	169761849	Missense_Mutation	SNP	C	T	4	118	c.988G>A	c.(988-990)GTA>ATA	p.V330I
Pat_07	Post-Resistance	USH2A	7399	37	1	216498769	216498769	Missense_Mutation	SNP	G	T	48	263	c.1021C>A	c.(1021-1023)CCT>ACT	p.P341T
Pat_07	Post-Resistance	OBSCN	84033	37	1	228473933	228473933	Missense_Mutation	SNP	C	G	3	55	c.9159C>G	c.(9157-9159)ATC>ATG	p.I3053M
Pat_07	Post-Resistance	CSTF2T	23283	37	10	53458337	53458337	Missense_Mutation	SNP	G	A	4	147	c.973C>T	c.(973-975)CCT>TCT	p.P325S
Pat_07	Post-Resistance	PTEN	5728	37	10	89685305	89685305	Missense_Mutation	SNP	T	G	34	44	c.200T>G	c.(199-201)ATA>AGA	p.I67R
Pat_07	Post-Resistance	LRP4	4038	37	11	46920467	46920467	Missense_Mutation	SNP	C	T	3	57	c.664G>A	c.(664-666)GAG>AAG	p.E222K
Pat_07	Post-Resistance	OR5I1	10798	37	11	55703585	55703585	Missense_Mutation	SNP	C	T	21	42	c.292G>A	c.(292-294)GGG>AGG	p.G98R
Pat_07	Post-Resistance	OR5M1	390168	37	11	56380362	56380362	Missense_Mutation	SNP	T	G	3	34	c.617A>C	c.(616-618)AAT>ACT	p.N206T
Pat_07	Post-Resistance	VWCE	220001	37	11	61040737	61040737	Nonsense_Mutation	SNP	G	A	3	42	c.1633C>T	c.(1633-1635)CGA>TGA	p.R545*
Pat_07	Post-Resistance	TRPC6	7225	37	11	101342884	101342884	Missense_Mutation	SNP	G	A	64	265	c.2189C>T	c.(2188-2190)TCA>TTA	p.S730L
Pat_07	Post-Resistance	PIH1D2	120379	37	11	111942424	111942424	Missense_Mutation	SNP	G	A	4	156	c.236C>T	c.(235-237)CCC>CTC	p.P79L
Pat_07	Post-Resistance	TROAP	10024	37	12	49724403	49724403	Missense_Mutation	SNP	A	G	5	71	c.1775A>G	c.(1774-1776)TAC>TGC	p.Y592C
Pat_07	Post-Resistance	HOXC6	3223	37	12	54422448	54422448	Missense_Mutation	SNP	G	A	4	103	c.143G>A	c.(142-144)CGG>CAG	p.R48Q
Pat_07	Post-Resistance	R3HDM2	22864	37	12	57660556	57660556	Missense_Mutation	SNP	G	A	13	50	c.2047C>T	c.(2047-2049)CCC>TCC	p.P683S
Pat_07	Post-Resistance	ANO4	121601	37	12	101514302	101514302	Missense_Mutation	SNP	C	T	4	81	c.2575C>T	c.(2575-2577)CGG>TGG	p.R859W
Pat_07	Post-Resistance	STAB2	55576	37	12	104031803	104031803	Missense_Mutation	SNP	C	T	110	227	c.719C>T	c.(718-720)CCA>CTA	p.P240L
Pat_07	Post-Resistance	FICD	11153	37	12	108910963	108910963	Missense_Mutation	SNP	G	A	4	69	c.214G>A	c.(214-216)GCC>ACC	p.A72T
Pat_07	Post-Resistance	GPC6	10082	37	13	94197599	94197599	Missense_Mutation	SNP	G	A	81	266	c.244G>A	c.(244-246)GAA>AAA	p.E82K
Pat_07	Post-Resistance	OR6S1	341799	37	14	21109390	21109390	Missense_Mutation	SNP	C	T	4	80	c.461G>A	c.(460-462)GGA>GAA	p.G154E
Pat_07	Post-Resistance	ABHD4	63874	37	14	23072420	23072420	Missense_Mutation	SNP	G	T	7	50	c.238G>T	c.(238-240)GGC>TGC	p.G80C
Pat_07	Post-Resistance	SLC35F4	341880	37	14	58030954	58030954	Missense_Mutation	SNP	C	T	11	51	c.1465G>A	c.(1465-1467)GAA>AAA	p.E489K
Pat_07	Post-Resistance	PACS2	23241	37	14	105849187	105849187	Missense_Mutation	SNP	G	T	4	63	c.1550G>T	c.(1549-1551)TGC>TTC	p.C517F
Pat_07	Post-Resistance	MAN2A2	4122	37	15	91455366	91455366	Missense_Mutation	SNP	C	T	4	112	c.2203C>T	c.(2203-2205)CGC>TGC	p.R735C
Pat_07	Post-Resistance	PARN	5073	37	16	14530588	14530588	Missense_Mutation	SNP	G	A	3	42	c.1906C>T	c.(1906-1908)CCT>TCT	p.P636S
Pat_07	Post-Resistance	KCTD19	146212	37	16	67323581	67323581	Missense_Mutation	SNP	G	A	4	67	c.2672C>T	c.(2671-2673)ACA>ATA	p.T891I
Pat_07	Post-Resistance	KCTD19	146212	37	16	67337074	67337074	Nonsense_Mutation	SNP	G	T	4	126	c.618C>A	c.(616-618)TGC>TGA	p.C206*
Pat_07	Post-Resistance	HYDIN	54768	37	16	71007806	71007806	Missense_Mutation	SNP	C	T	29	240	c.5152G>A	c.(5152-5154)GAA>AAA	p.E1718K
Pat_07	Post-Resistance	USP10	9100	37	16	84812668	84812668	Missense_Mutation	SNP	C	T	7	150	c.2377C>T	c.(2377-2379)CGC>TGC	p.R793C
Pat_07	Post-Resistance	ZCCHC14	23174	37	16	87445310	87445310	Missense_Mutation	SNP	G	A	3	52	c.2606C>T	c.(2605-2607)ACG>ATG	p.T869M
Pat_07	Post-Resistance	TP53	7157	37	17	7579313	7579313	Missense_Mutation	SNP	G	C	58	69	c.374C>G	c.(373-375)ACG>AGG	p.T125R
Pat_07	Post-Resistance	MYH13	8735	37	17	10216027	10216027	Missense_Mutation	SNP	G	A	4	15	c.4229C>T	c.(4228-4230)ACG>ATG	p.T1410M
Pat_07	Post-Resistance	MYH3	4621	37	17	10538859	10538859	Missense_Mutation	SNP	C	G	4	110	c.3997G>C	c.(3997-3999)GCC>CCC	p.A1333P
Pat_07	Post-Resistance	PSMB3	5691	37	17	36916709	36916709	Missense_Mutation	SNP	G	C	4	98	c.322G>C	c.(322-324)GTC>CTC	p.V108L
Pat_07	Post-Resistance	CCR10	2826	37	17	40831789	40831789	Missense_Mutation	SNP	C	T	3	49	c.871G>A	c.(871-873)GCA>ACA	p.A291T
Pat_07	Post-Resistance	FASN	2194	37	17	80045872	80045872	Missense_Mutation	SNP	G	T	13	21	c.2824C>A	c.(2824-2826)CGT>AGT	p.R942S
Pat_07	Post-Resistance	MC5R	4161	37	18	13826482	13826482	Missense_Mutation	SNP	G	A	3	58	c.718G>A	c.(718-720)GTC>ATC	p.V240I
Pat_07	Post-Resistance	CABYR	26256	37	18	21736742	21736742	Missense_Mutation	SNP	T	C	20	36	c.1277T>C	c.(1276-1278)ATA>ACA	p.I426T
Pat_07	Post-Resistance	C19orf26	255057	37	19	1231136	1231136	Missense_Mutation	SNP	C	T	4	63	c.1100G>A	c.(1099-1101)CGC>CAC	p.R367H
Pat_07	Post-Resistance	LRG1	116844	37	19	4538365	4538365	Missense_Mutation	SNP	G	A	106	150	c.631C>T	c.(631-633)CCG>TCG	p.P211S
Pat_07	Post-Resistance	CD209	30835	37	19	7810767	7810767	Missense_Mutation	SNP	G	A	5	155	c.385C>T	c.(385-387)CGG>TGG	p.R129W
Pat_07	Post-Resistance	BEST2	54831	37	19	12863491	12863491	Missense_Mutation	SNP	T	A	4	75	c.85T>A	c.(85-87)TAC>AAC	p.Y29N
Pat_07	Post-Resistance	CCDC105	126402	37	19	15124565	15124565	Missense_Mutation	SNP	G	A	9	14	c.652G>A	c.(652-654)GAA>AAA	p.E218K
Pat_07	Post-Resistance	ZNF708	7562	37	19	21476519	21476519	Missense_Mutation	SNP	T	C	4	143	c.1249A>G	c.(1249-1251)AAG>GAG	p.K417E
Pat_07	Post-Resistance	MLL4	9757	37	19	36223350	36223350	Missense_Mutation	SNP	C	G	4	54	c.5900C>G	c.(5899-5901)CCA>CGA	p.P1967R
Pat_07	Post-Resistance	MLL4	9757	37	19	36223454	36223454	Missense_Mutation	SNP	C	T	6	42	c.6004C>T	c.(6004-6006)CCC>TCC	p.P2002S

Pat_07	Post-Resistance	MLL4	9757	37	19	36223614	36223614	Missense_Mutation	SNP	C	T	4	14	c.6164C>T	c.(6163-6165)GCC>GTC	p.A2055V
Pat_07	Post-Resistance	RYR1	6261	37	19	39068576	39068576	Missense_Mutation	SNP	G	A	35	195	c.14191G>A	c.(14191-14193)GAC>AAC	p.D4731N
Pat_07	Post-Resistance	RYR1	6261	37	19	39070688	39070688	Missense_Mutation	SNP	G	A	32	148	c.14431G>A	c.(14431-14433)GCT>ACT	p.A4811T
Pat_07	Post-Resistance	DMPK	1760	37	19	46274654	46274654	Missense_Mutation	SNP	G	A	3	38	c.1631C>T	c.(1630-1632)GCT>GTT	p.A544V
Pat_07	Post-Resistance	NUCB1	4924	37	19	49407692	49407692	Missense_Mutation	SNP	C	T	4	78	c.224C>T	c.(223-225)GCC>GTC	p.A75V
Pat_07	Post-Resistance	PRR12	57479	37	19	50102575	50102575	Missense_Mutation	SNP	C	T	4	70	c.3725C>T	c.(3724-3726)TCG>TTG	p.S1242L
Pat_07	Post-Resistance	GALP	85569	37	19	56688491	56688491	Missense_Mutation	SNP	C	T	10	41	c.14C>T	c.(13-15)TCC>TTC	p.S5F
Pat_07	Post-Resistance	ZNF324B	388569	37	19	58966859	58966859	Missense_Mutation	SNP	G	A	3	65	c.548G>A	c.(547-549)CGG>CAG	p.R183Q
Pat_07	Post-Resistance	ZNF512	84450	37	2	27844283	27844283	Missense_Mutation	SNP	G	C	3	68	c.1659G>C	c.(1657-1659)CAG>CAC	p.Q553H
Pat_07	Post-Resistance	SLC8A1	6546	37	2	40656685	40656685	Missense_Mutation	SNP	C	A	4	76	c.736G>T	c.(736-738)GTT>TTT	p.V246F
Pat_07	Post-Resistance	XPO1	7514	37	2	61725837	61725837	Missense_Mutation	SNP	T	C	5	181	c.730A>G	c.(730-732)ACC>GCC	p.T244A
Pat_07	Post-Resistance	ACTR1B	10120	37	2	98274713	98274713	Missense_Mutation	SNP	T	C	18	70	c.724A>G	c.(724-726)ACG>GCG	p.T242A
Pat_07	Post-Resistance	ARHGAP15	55843	37	2	144008140	144008140	Missense_Mutation	SNP	G	A	27	190	c.445G>A	c.(445-447)GAA>AAA	p.E149K
Pat_07	Post-Resistance	TTN	7273	37	2	179418692	179418692	Nonsense_Mutation	SNP	G	A	9	39	c.81442C>T	c.(81442-81444)CAG>TAG	p.Q27148*
Pat_07	Post-Resistance	C20orf118	140711	37	20	35507585	35507585	Nonsense_Mutation	SNP	C	T	10	46	c.331C>T	c.(331-333)CAG>TAG	p.Q111*
Pat_07	Post-Resistance	AURKA	6790	37	20	54963222	54963222	Missense_Mutation	SNP	C	A	49	114	c.32G>T	c.(31-33)GGA>GTA	p.G11V
Pat_07	Post-Resistance	PIGP	51227	37	21	38444778	38444778	Missense_Mutation	SNP	G	T	129	284	c.110C>A	c.(109-111)GCG>GAG	p.A37E
Pat_07	Post-Resistance	PLAC4	191585	37	21	42551255	42551255	Missense_Mutation	SNP	G	A	3	30	c.301C>T	c.(301-303)CCC>TCC	p.P101S
Pat_07	Post-Resistance	SCN5A	6331	37	3	38591907	38591907	Missense_Mutation	SNP	C	T	37	79	c.5956G>A	c.(5956-5958)GAT>AAT	p.D1986N
Pat_07	Post-Resistance	SCN5A	6331	37	3	38601660	38601660	Missense_Mutation	SNP	C	T	3	21	c.4223G>A	c.(4222-4224)GGG>GAG	p.G1408E
Pat_07	Post-Resistance	GPX1	2876	37	3	49395482	49395482	Missense_Mutation	SNP	G	C	3	71	c.230C>G	c.(229-231)CCG>CGG	p.P77R
Pat_07	Post-Resistance	ITIH4	3700	37	3	52853421	52853421	Missense_Mutation	SNP	G	A	4	65	c.2065C>T	c.(2065-2067)CGT>TGT	p.R689C
Pat_07	Post-Resistance	CACNA2D3	55799	37	3	54905569	54905569	Missense_Mutation	SNP	G	A	19	55	c.1630G>A	c.(1630-1632)GAA>AAA	p.E544K
Pat_07	Post-Resistance	WDR52	55779	37	3	113138974	113138974	Missense_Mutation	SNP	C	T	4	149	c.460G>A	c.(460-462)GAC>AAC	p.D154N
Pat_07	Post-Resistance	PAQR3	152559	37	4	79845092	79845092	Missense_Mutation	SNP	G	A	4	104	c.712C>T	c.(712-714)CCC>TCC	p.P238S
Pat_07	Post-Resistance	SKP2	6502	37	5	36182097	36182097	Missense_Mutation	SNP	A	T	22	98	c.1239A>T	c.(1237-1239)AAA>AAT	p.K413N
Pat_07	Post-Resistance	SPZ1	84654	37	5	79616461	79616461	Missense_Mutation	SNP	G	C	6	226	c.427G>C	c.(427-429)GAG>CAG	p.E143Q
Pat_07	Post-Resistance	ZFYVE16	9765	37	5	79744086	79744086	Missense_Mutation	SNP	A	G	64	136	c.2966A>G	c.(2965-2967)AAT>AGT	p.N989S
Pat_07	Post-Resistance	GPR98	84059	37	5	89949385	89949385	Missense_Mutation	SNP	G	A	4	102	c.3994G>A	c.(3994-3996)GGA>AGA	p.G1332R
Pat_07	Post-Resistance	UNC5A	90249	37	5	176304697	176304697	Missense_Mutation	SNP	G	A	3	17	c.1628G>A	c.(1627-1629)AGC>AAC	p.S543N
Pat_07	Post-Resistance	HLA-J	3137	37	6	29977342	29977342	Missense_Mutation	SNP	A	T	6	168	c.361A>T	c.(361-363)AGG>TGG	p.R121W
Pat_07	Post-Resistance	ITPR3	3710	37	6	33661448	33661448	Missense_Mutation	SNP	C	T	4	102	c.7751C>T	c.(7750-7752)ACG>ATG	p.T2584M
Pat_07	Post-Resistance	CAPN11	11131	37	6	44145101	44145101	Missense_Mutation	SNP	C	T	4	117	c.1360C>T	c.(1360-1362)CGG>TGG	p.R454W
Pat_07	Post-Resistance	KLHL31	401265	37	6	53519236	53519236	Missense_Mutation	SNP	T	C	125	390	c.835A>G	c.(835-837)ATG>GTG	p.M279V
Pat_07	Post-Resistance	SNAP91	9892	37	6	84317520	84317520	Missense_Mutation	SNP	G	A	7	76	c.920C>T	c.(919-921)CCA>CTA	p.P307L
Pat_07	Post-Resistance	INTS1	26173	37	7	1542573	1542573	Missense_Mutation	SNP	G	A	60	160	c.313C>T	c.(313-315)CCG>TCG	p.P105S
Pat_07	Post-Resistance	BZW2	28969	37	7	16734531	16734531	Missense_Mutation	SNP	C	T	44	139	c.724C>T	c.(724-726)CTT>TTT	p.L242F
Pat_07	Post-Resistance	DNAH11	8701	37	7	21727099	21727099	Missense_Mutation	SNP	G	A	3	67	c.5899G>A	c.(5899-5901)GTA>ATA	p.V1967I
Pat_07	Post-Resistance	AEBP1	165	37	7	44148898	44148898	Missense_Mutation	SNP	G	A	3	44	c.1108G>A	c.(1108-1110)GGC>AGC	p.G370S
Pat_07	Post-Resistance	DYNC1I1	1780	37	7	95709792	95709792	Missense_Mutation	SNP	G	A	70	255	c.1819G>A	c.(1819-1821)GTT>ATT	p.V607I
Pat_07	Post-Resistance	CCDC136	64753	37	7	128457843	128457843	Missense_Mutation	SNP	C	T	86	235	c.3395C>T	c.(3394-3396)TCC>TTC	p.S1132F
Pat_07	Post-Resistance	BRAF	673	37	7	140453136	140453136	Missense_Mutation	SNP	A	T	60	220	c.1799T>A	c.(1798-1800)GTG>GAG	p.V600E
Pat_07	Post-Resistance	CNTNAP2	26047	37	7	146829338	146829338	Missense_Mutation	SNP	G	A	33	150	c.1085G>A	c.(1084-1086)GGA>GAA	p.G362E
Pat_07	Post-Resistance	HTR5A	3361	37	7	154875949	154875949	Missense_Mutation	SNP	C	T	4	46	c.826C>T	c.(826-828)CGG>TGG	p.R276W
Pat_07	Post-Resistance	ADAM2	2515	37	8	39624492	39624492	Missense_Mutation	SNP	G	A	61	306	c.1382C>T	c.(1381-1383)TCA>TTA	p.S461L
Pat_07	Post-Resistance	VDAC3	7419	37	8	42262973	42262973	Missense_Mutation	SNP	A	G	42	102	c.845A>G	c.(844-846)GAA>GGA	p.E282G
Pat_07	Post-Resistance	FLJ46321	389763	37	9	84609997	84609997	Missense_Mutation	SNP	G	A	3	41	c.4612G>A	c.(4612-4614)GTG>ATG	p.V1538M

Pat_07	Post-Resistance	FAM22F	54754	37	9	97082748	97082748	Missense_Mutation	SNP	G	C	3	59	c.1110C>G	c.(1108-1110)AAC>AAG	p.N370K
Pat_07	Post-Resistance	SVEP1	79987	37	9	113228255	113228255	Missense_Mutation	SNP	G	A	3	50	c.3212C>T	c.(3211-3213)TCG>TTG	p.S1071L
Pat_07	Post-Resistance	TEX11	56159	37	X	69811630	69811630	Missense_Mutation	SNP	T	A	26	103	c.2156A>T	c.(2155-2157)AAT>ATT	p.N719I
Pat_07	Pre-Treatment	SPATA21	374955	37	1	16730232	16730232	Missense_Mutation	SNP	C	T	18	50	c.991G>A	c.(991-993)GAA>AAA	p.E331K
Pat_07	Pre-Treatment	C1orf172	126695	37	1	27278407	27278407	Missense_Mutation	SNP	C	T	6	2	c.465G>A	c.(463-465)ATG>ATA	p.M155I
Pat_07	Pre-Treatment	CDC20	991	37	1	43826466	43826466	Missense_Mutation	SNP	C	T	3	28	c.911C>T	c.(910-912)ACA>ATA	p.T304I
Pat_07	Pre-Treatment	USH2A	7399	37	1	216498769	216498769	Missense_Mutation	SNP	G	T	12	39	c.1021C>A	c.(1021-1023)CCT>ACT	p.P341T
Pat_07	Pre-Treatment	PTEN	5728	37	10	89685305	89685305	Missense_Mutation	SNP	T	G	2	2	c.200T>G	c.(199-201)ATA>AGA	p.I67R
Pat_07	Pre-Treatment	TH	7054	37	11	2189789	2189789	Missense_Mutation	SNP	T	C	2	6	c.512A>G	c.(511-513)GAC>GGC	p.D171G
Pat_07	Pre-Treatment	OR5I1	10798	37	11	55703585	55703585	Missense_Mutation	SNP	C	T	6	3	c.292G>A	c.(292-294)GGG>AGG	p.G98R
Pat_07	Pre-Treatment	TRPC6	7225	37	11	101342884	101342884	Missense_Mutation	SNP	G	A	23	21	c.2189C>T	c.(2188-2190)TCA>TTA	p.S730L
Pat_07	Pre-Treatment	ESPL1	9700	37	12	53686437	53686437	Missense_Mutation	SNP	T	A	5	16	c.5992T>A	c.(5992-5994)TAT>AAT	p.Y1998N
Pat_07	Pre-Treatment	NUP37	79023	37	12	102470618	102470618	Missense_Mutation	SNP	G	C	2	4	c.730C>G	c.(730-732)CAA>GAA	p.Q244E
Pat_07	Pre-Treatment	STAB2	55576	37	12	104031803	104031803	Missense_Mutation	SNP	C	T	33	26	c.719C>T	c.(718-720)CCA>CTA	p.P240L
Pat_07	Pre-Treatment	GPC6	10082	37	13	94197599	94197599	Missense_Mutation	SNP	G	A	20	30	c.244G>A	c.(244-246)GAA>AAA	p.E82K
Pat_07	Pre-Treatment	AKAP6	9472	37	14	33014743	33014743	Missense_Mutation	SNP	C	G	3	26	c.884C>G	c.(883-885)TCT>TGT	p.S295C
Pat_07	Pre-Treatment	SLC35F4	341880	37	14	58030954	58030954	Missense_Mutation	SNP	C	T	4	7	c.1465G>A	c.(1465-1467)GAA>AAA	p.E489K
Pat_07	Pre-Treatment	NPIP	9284	37	16	15045731	15045731	Missense_Mutation	SNP	C	T	5	49	c.902C>T	c.(901-903)GCG>GTG	p.A301V
Pat_07	Pre-Treatment	ZNF768	79724	37	16	30536380	30536380	Missense_Mutation	SNP	G	T	3	22	c.1081C>A	c.(1081-1083)CTG>ATG	p.L361M
Pat_07	Pre-Treatment	HYDIN	54768	37	16	71007806	71007806	Missense_Mutation	SNP	C	T	11	56	c.5152G>A	c.(5152-5154)GAA>AAA	p.E1718K
Pat_07	Pre-Treatment	TP53	7157	37	17	7579313	7579313	Missense_Mutation	SNP	G	C	9	11	c.374C>G	c.(373-375)ACG>AGG	p.T125R
Pat_07	Pre-Treatment	PIK3R5	23533	37	17	8794225	8794225	Missense_Mutation	SNP	C	A	2	2	c.487G>T	c.(487-489)GTG>TTG	p.V163L
Pat_07	Pre-Treatment	KSR1	8844	37	17	25938606	25938606	Missense_Mutation	SNP	A	G	2	5	c.2099A>G	c.(2098-2100)GAA>GGA	p.E700G
Pat_07	Pre-Treatment	FASN	2194	37	17	80045872	80045872	Missense_Mutation	SNP	G	T	4	7	c.2824C>A	c.(2824-2826)CGT>AGT	p.R942S
Pat_07	Pre-Treatment	POTEC	388468	37	18	14542843	14542843	Nonsense_Mutation	SNP	C	T	5	87	c.303G>A	c.(301-303)TGG>TGA	p.W101*
Pat_07	Pre-Treatment	CABYR	26256	37	18	21736742	21736742	Missense_Mutation	SNP	T	C	9	0	c.1277T>C	c.(1276-1278)ATA>ACA	p.I426T
Pat_07	Pre-Treatment	MYO5B	4645	37	18	47364067	47364067	Missense_Mutation	SNP	C	T	3	36	c.4958G>A	c.(4957-4959)TGC>TAC	p.C1653Y
Pat_07	Pre-Treatment	LRG1	116844	37	19	4538365	4538365	Missense_Mutation	SNP	G	A	36	39	c.631C>T	c.(631-633)CCG>TCG	p.P211S
Pat_07	Pre-Treatment	PRAM1	84106	37	19	8555381	8555381	Missense_Mutation	SNP	G	A	2	3	c.1919C>T	c.(1918-1920)CCC>CTC	p.P640L
Pat_07	Pre-Treatment	CCDC105	126402	37	19	15124565	15124565	Missense_Mutation	SNP	G	A	4	2	c.652G>A	c.(652-654)GAA>AAA	p.E218K
Pat_07	Pre-Treatment	MLL4	9757	37	19	36223454	36223454	Missense_Mutation	SNP	C	T	5	10	c.6004C>T	c.(6004-6006)CCC>TCC	p.P2002S
Pat_07	Pre-Treatment	MLL4	9757	37	19	36223614	36223614	Missense_Mutation	SNP	C	T	2	1	c.6164C>T	c.(6163-6165)GCC>GTC	p.A2055V
Pat_07	Pre-Treatment	RYR1	6261	37	19	39068576	39068576	Missense_Mutation	SNP	G	A	13	28	c.14191G>A	c.(14191-14193)GAC>AAC	p.D4731N
Pat_07	Pre-Treatment	RYR1	6261	37	19	39070688	39070688	Missense_Mutation	SNP	G	A	9	26	c.14431G>A	c.(14431-14433)GCT>ACT	p.A4811T
Pat_07	Pre-Treatment	PSG8	440533	37	19	43258518	43258518	Missense_Mutation	SNP	C	T	5	82	c.1210G>A	c.(1210-1212)GAA>AAA	p.E404K
Pat_07	Pre-Treatment	ZNF880	400713	37	19	52877636	52877636	Missense_Mutation	SNP	C	T	3	8	c.224C>T	c.(223-225)GCA>GTA	p.A75V
Pat_07	Pre-Treatment	BRSK1	84446	37	19	55814773	55814773	Missense_Mutation	SNP	G	A	3	26	c.1123G>A	c.(1123-1125)GTT>ATT	p.V375I
Pat_07	Pre-Treatment	ZNF71	58491	37	19	57133922	57133922	Missense_Mutation	SNP	G	T	4	62	c.1267G>T	c.(1267-1269)GCC>TCC	p.A423S
Pat_07	Pre-Treatment	TLX2	3196	37	2	74743207	74743207	Missense_Mutation	SNP	C	G	3	13	c.746C>G	c.(745-747)CCG>CGG	p.P249R
Pat_07	Pre-Treatment	ACTR1B	10120	37	2	98274713	98274713	Missense_Mutation	SNP	T	C	4	22	c.724A>G	c.(724-726)ACG>GCG	p.T242A
Pat_07	Pre-Treatment	POTEF	728378	37	2	130877802	130877802	Missense_Mutation	SNP	T	C	5	112	c.287A>G	c.(286-288)AAC>AGC	p.N96S
Pat_07	Pre-Treatment	ARHGAP15	55843	37	2	144008140	144008140	Missense_Mutation	SNP	G	A	4	17	c.445G>A	c.(445-447)GAA>AAA	p.E149K
Pat_07	Pre-Treatment	SP3	6670	37	2	174820556	174820556	Missense_Mutation	SNP	T	C	17	54	c.684A>G	c.(682-684)ATA>ATG	p.I228M
Pat_07	Pre-Treatment	TTN	7273	37	2	179418692	179418692	Nonsense_Mutation	SNP	G	A	5	10	c.81442C>T	c.(81442-81444)CAG>TAG	p.Q27148*
Pat_07	Pre-Treatment	AURKA	6790	37	20	54963222	54963222	Missense_Mutation	SNP	C	A	12	19	c.32G>T	c.(31-33)GGA>GTA	p.G11V
Pat_07	Pre-Treatment	PIGP	51227	37	21	38444778	38444778	Missense_Mutation	SNP	G	T	21	42	c.110C>A	c.(109-111)GCG>GAG	p.A37E
Pat_07	Pre-Treatment	SCN5A	6331	37	3	38591907	38591907	Missense_Mutation	SNP	C	T	7	19	c.5956G>A	c.(5956-5958)GAT>AAT	p.D1986N

Pat_07	Pre-Treatment	CACNA2D3	55799	37	3	54905569	54905569	Missense_Mutation	SNP	G	A	4	19	c.1630G>A	c.(1630-1632)GAA>AAA	p.E544K
Pat_07	Pre-Treatment	PPP2R3A	5523	37	3	135825106	135825106	Missense_Mutation	SNP	G	A	3	17	c.3271G>A	c.(3271-3273)GCT>ACT	p.A1091T
Pat_07	Pre-Treatment	PHC3	80012	37	3	169866990	169866990	Missense_Mutation	SNP	G	A	2	5	c.421C>T	c.(421-423)CGT>TGT	p.R141C
Pat_07	Pre-Treatment	CRMP1	1400	37	4	5830394	5830394	Missense_Mutation	SNP	G	A	2	5	c.1283C>T	c.(1282-1284)GCG>GTG	p.A428V
Pat_07	Pre-Treatment	SKP2	6502	37	5	36182097	36182097	Missense_Mutation	SNP	A	T	3	16	c.1239A>T	c.(1237-1239)AAA>AAT	p.K413N
Pat_07	Pre-Treatment	ZFYVE16	9765	37	5	79744086	79744086	Missense_Mutation	SNP	A	G	8	10	c.2966A>G	c.(2965-2967)AAT>AGT	p.N989S
Pat_07	Pre-Treatment	FBLL1	345630	37	5	167957226	167957226	Missense_Mutation	SNP	C	G	2	8	c.432C>G	c.(430-432)ATC>ATG	p.I144M
Pat_07	Pre-Treatment	KLHL31	401265	37	6	53519236	53519236	Missense_Mutation	SNP	T	C	41	66	c.835A>G	c.(835-837)ATG>GTG	p.M279V
Pat_07	Pre-Treatment	INTS1	26173	37	7	1542573	1542573	Missense_Mutation	SNP	G	A	21	42	c.313C>T	c.(313-315)CCG>TCG	p.P105S
Pat_07	Pre-Treatment	BZW2	28969	37	7	16734531	16734531	Missense_Mutation	SNP	C	T	9	22	c.724C>T	c.(724-726)CTT>TTT	p.L242F
Pat_07	Pre-Treatment	STK31	56164	37	7	23821044	23821044	Missense_Mutation	SNP	G	C	3	10	c.1972G>C	c.(1972-1974)GAT>CAT	p.D658H
Pat_07	Pre-Treatment	CCDC146	57639	37	7	76908259	76908259	Missense_Mutation	SNP	G	C	2	10	c.1535G>C	c.(1534-1536)AGA>ACA	p.R512T
Pat_07	Pre-Treatment	DYNC1I1	1780	37	7	95709792	95709792	Missense_Mutation	SNP	G	A	17	32	c.1819G>A	c.(1819-1821)GTT>ATT	p.V607I
Pat_07	Pre-Treatment	CCDC136	64753	37	7	128457843	128457843	Missense_Mutation	SNP	C	T	18	75	c.3395C>T	c.(3394-3396)TCC>TTC	p.S1132F
Pat_07	Pre-Treatment	BRAF	673	37	7	140453136	140453136	Missense_Mutation	SNP	A	T	8	17	c.1799T>A	c.(1798-1800)GTG>GAG	p.V600E
Pat_07	Pre-Treatment	CNTNAP2	26047	37	7	146829338	146829338	Missense_Mutation	SNP	G	A	8	35	c.1085G>A	c.(1084-1086)GGA>GAA	p.G362E
Pat_07	Pre-Treatment	ADAM2	2515	37	8	39624492	39624492	Missense_Mutation	SNP	G	A	14	26	c.1382C>T	c.(1381-1383)TCA>TTA	p.S461L
Pat_07	Pre-Treatment	VDAC3	7419	37	8	42262973	42262973	Missense_Mutation	SNP	A	G	5	16	c.845A>G	c.(844-846)GAA>GGA	p.E282G
Pat_07	Pre-Treatment	GSDMC	56169	37	8	130760981	130760981	Missense_Mutation	SNP	C	A	5	24	c.1293G>T	c.(1291-1293)AGG>AGT	p.R431S
Pat_07	Pre-Treatment	BAI1	575	37	8	143559674	143559674	Missense_Mutation	SNP	A	G	2	3	c.1514A>G	c.(1513-1515)CAG>CGG	p.Q505R
Pat_07	Pre-Treatment	RGS3	5998	37	9	116346689	116346689	Missense_Mutation	SNP	C	G	2	5	c.2997C>G	c.(2995-2997)TTC>TTG	p.F999L
Pat_07	Pre-Treatment	PRICKLE3	4007	37	X	49034778	49034778	Missense_Mutation	SNP	C	T	2	4	c.611G>A	c.(610-612)CGT>CAT	p.R204H
Pat_07	Pre-Treatment	FOXP3	50943	37	X	49107805	49107805	Missense_Mutation	SNP	G	A	2	2	c.1286C>T	c.(1285-1287)CCT>CTT	p.P429L
Pat_07	Pre-Treatment	TEX11	56159	37	X	69811630	69811630	Missense_Mutation	SNP	T	A	9	16	c.2156A>T	c.(2155-2157)AAT>ATT	p.N719I
Pat_14	Pre-Treatment	CHD5	26038	37	1	6195368	6195368	Missense_Mutation	SNP	C	T	63	237	c.2792G>A	c.(2791-2793)CGG>CAG	p.R931Q
Pat_14	Pre-Treatment	CASZ1	54897	37	1	10720030	10720030	Missense_Mutation	SNP	G	A	79	184	c.1069C>T	c.(1069-1071)CCC>TCC	p.P357S
Pat_14	Pre-Treatment	FBLIM1	54751	37	1	16093915	16093915	Missense_Mutation	SNP	C	T	65	176	c.295C>T	c.(295-297)CCT>TCT	p.P99S
Pat_14	Pre-Treatment	HSPB7	27129	37	1	16342172	16342172	Missense_Mutation	SNP	G	A	76	199	c.416C>T	c.(415-417)TCG>TTG	p.S139L
Pat_14	Pre-Treatment	PLA2G2D	26279	37	1	20442962	20442962	Missense_Mutation	SNP	G	A	41	163	c.49C>T	c.(49-51)CCA>TCA	p.P17S
Pat_14	Pre-Treatment	EIF4G3	8672	37	1	21306872	21306872	Missense_Mutation	SNP	G	A	15	70	c.280C>T	c.(280-282)CCT>TCT	p.P94S
Pat_14	Pre-Treatment	ALPL	249	37	1	21887685	21887685	Missense_Mutation	SNP	C	T	20	90	c.277C>T	c.(277-279)CCC>TCC	p.P93S
Pat_14	Pre-Treatment	HSPG2	3339	37	1	22170789	22170789	Missense_Mutation	SNP	G	A	60	222	c.8468C>T	c.(8467-8469)CCA>CTA	p.P2823L
Pat_14	Pre-Treatment	GRHL3	57822	37	1	24663027	24663027	Missense_Mutation	SNP	C	A	5	421	c.337C>A	c.(337-339)CAC>AAC	p.H113N
Pat_14	Pre-Treatment	CCDC21	64793	37	1	26595111	26595111	Missense_Mutation	SNP	G	C	3	152	c.1479G>C	c.(1477-1479)CAG>CAC	p.Q493H
Pat_14	Pre-Treatment	FAM76A	199870	37	1	28081811	28081811	Missense_Mutation	SNP	G	T	6	360	c.705G>T	c.(703-705)AAG>AAT	p.K235N
Pat_14	Pre-Treatment	HIVEP3	59269	37	1	42047984	42047984	Missense_Mutation	SNP	G	A	93	363	c.2485C>T	c.(2485-2487)CCA>TCA	p.P829S
Pat_14	Pre-Treatment	HIVEP3	59269	37	1	42050203	42050203	Missense_Mutation	SNP	G	A	126	564	c.266C>T	c.(265-267)TCC>TTC	p.S89F
Pat_14	Pre-Treatment	ERMAP	114625	37	1	43308877	43308877	Nonsense_Mutation	SNP	C	T	30	93	c.1402C>T	c.(1402-1404)CAG>TAG	p.Q468*
Pat_14	Pre-Treatment	TIE1	7075	37	1	43779472	43779472	Missense_Mutation	SNP	C	A	4	50	c.2242C>A	c.(2242-2244)CAA>AAA	p.Q748K
Pat_14	Pre-Treatment	PTPRF	5792	37	1	44072115	44072115	Missense_Mutation	SNP	G	A	122	354	c.3688G>A	c.(3688-3690)GAA>AAA	p.E1230K
Pat_14	Pre-Treatment	ZCCHC11	23318	37	1	52896717	52896717	Missense_Mutation	SNP	G	A	76	329	c.4676C>T	c.(4675-4677)TCC>TTC	p.S1559F
Pat_14	Pre-Treatment	ZCCHC11	23318	37	1	52962816	52962816	Missense_Mutation	SNP	G	A	25	127	c.1039C>T	c.(1039-1041)CCT>TCT	p.P347S
Pat_14	Pre-Treatment	CDCP2	200008	37	1	54606902	54606902	Missense_Mutation	SNP	G	A	35	128	c.632C>T	c.(631-633)CCC>CTC	p.P211L
Pat_14	Pre-Treatment	DAB1	1600	37	1	57756681	57756681	Nonsense_Mutation	SNP	G	A	68	243	c.22C>T	c.(22-24)CAA>TAA	p.Q8*
Pat_14	Pre-Treatment	FGGY	55277	37	1	60019876	60019876	Nonsense_Mutation	SNP	G	T	42	182	c.880G>T	c.(880-882)GGA>TGA	p.G294*
Pat_14	Pre-Treatment	C1orf87	127795	37	1	60520908	60520908	Missense_Mutation	SNP	C	T	133	588	c.310G>A	c.(310-312)GGG>AGG	p.G104R
Pat_14	Pre-Treatment	ANGPTL3	27329	37	1	63070330	63070331	Nonsense_Mutation	DNP	GG	TA	41	201	.1225_1226GG>T	c.(1225-1227)GGA>TAA	p.G409*

Pat_14	Pre-Treatment	C1orf173	127254	37	1	75065504	75065504	Missense_Mutation	SNP	T	G	106	238	c.1601A>C	c.(1600-1602)AAA>ACA	p.K534T
Pat_14	Pre-Treatment	LPHN2	23266	37	1	82408790	82408790	Missense_Mutation	SNP	C	T	42	166	c.535C>T	c.(535-537)CGT>TGT	p.R179C
Pat_14	Pre-Treatment	LPHN2	23266	37	1	82433875	82433875	Missense_Mutation	SNP	G	A	104	341	c.2464G>A	c.(2464-2466)GAA>AAA	p.E822K
Pat_14	Pre-Treatment	LPHN2	23266	37	1	82437570	82437570	Missense_Mutation	SNP	A	T	27	111	c.2938A>T	c.(2938-2940)AGC>TGC	p.S980C
Pat_14	Pre-Treatment	AKNAD1	254268	37	1	109377579	109377579	Missense_Mutation	SNP	C	T	52	143	c.1636G>A	c.(1636-1638)GAG>AAG	p.E546K
Pat_14	Pre-Treatment	NOTCH2	4853	37	1	120506410	120506410	Nonsense_Mutation	SNP	C	A	6	278	c.1702G>T	c.(1702-1704)GAG>TAG	p.E568*
Pat_14	Pre-Treatment	SV2A	9900	37	1	149883419	149883419	Missense_Mutation	SNP	C	T	23	137	c.736G>A	c.(736-738)GCC>ACC	p.A246T
Pat_14	Pre-Treatment	OTUD7B	56957	37	1	149937753	149937753	Missense_Mutation	SNP	G	A	24	109	c.553C>T	c.(553-555)CCT>TCT	p.P185S
Pat_14	Pre-Treatment	HRNR	388697	37	1	152191730	152191730	Missense_Mutation	SNP	C	T	34	162	c.2375G>A	c.(2374-2376)GGC>GAC	p.G792D
Pat_14	Pre-Treatment	CRNN	49860	37	1	152382612	152382612	Missense_Mutation	SNP	G	T	9	816	c.946C>A	c.(946-948)CAG>AAG	p.Q316K
Pat_14	Pre-Treatment	FCRL4	83417	37	1	157559111	157559111	Missense_Mutation	SNP	C	T	45	203	c.190G>A	c.(190-192)GGA>AGA	p.G64R
Pat_14	Pre-Treatment	FCRL3	115352	37	1	157665275	157665275	Missense_Mutation	SNP	G	A	78	278	c.1255C>T	c.(1255-1257)CAT>TAT	p.H419Y
Pat_14	Pre-Treatment	OR10T2	128360	37	1	158368890	158368890	Missense_Mutation	SNP	G	A	94	390	c.367C>T	c.(367-369)CGC>TGC	p.R123C
Pat_14	Pre-Treatment	SPTA1	6708	37	1	158651382	158651382	Missense_Mutation	SNP	G	A	6	476	c.466C>T	c.(466-468)CGG>TGG	p.R156W
Pat_14	Pre-Treatment	OR6K2	81448	37	1	158669671	158669671	Missense_Mutation	SNP	G	A	38	110	c.772C>T	c.(772-774)CTC>TTC	p.L258F
Pat_14	Pre-Treatment	ARHGAP30	257106	37	1	161019028	161019028	Missense_Mutation	SNP	C	T	104	333	c.1783G>A	c.(1783-1785)GGC>AGC	p.G595S
Pat_14	Pre-Treatment	ARHGAP30	257106	37	1	161022509	161022509	Missense_Mutation	SNP	G	T	5	185	c.743C>A	c.(742-744)CCA>CAA	p.P248Q
Pat_14	Pre-Treatment	PVRL4	81607	37	1	161044155	161044155	Missense_Mutation	SNP	C	T	46	247	c.1009G>A	c.(1009-1011)GAA>AAA	p.E337K
Pat_14	Pre-Treatment	DEDD	9191	37	1	161094217	161094217	Missense_Mutation	SNP	C	A	6	414	c.36G>T	c.(34-36)TGG>TGT	p.W12C
Pat_14	Pre-Treatment	HSPA7	3311	37	1	161576424	161576424	Missense_Mutation	SNP	C	A	27	116	c.344C>A	c.(343-345)ACG>AAG	p.T115K
Pat_14	Pre-Treatment	NUF2	83540	37	1	163297332	163297332	Nonsense_Mutation	SNP	C	T	87	296	c.178C>T	c.(178-180)CGA>TGA	p.R60*
Pat_14	Pre-Treatment	ILDR2	387597	37	1	166927137	166927137	Missense_Mutation	SNP	C	T	108	364	c.248G>A	c.(247-249)AGA>AAA	p.R83K
Pat_14	Pre-Treatment	SLC9A11	284525	37	1	173506179	173506179	Splice_Site	SNP	C	T	68	260	c.1558_splice	c.e14-1	p.S520_splice
Pat_14	Pre-Treatment	SEC16B	89866	37	1	177913715	177913715	Missense_Mutation	SNP	G	A	139	441	c.1862C>T	c.(1861-1863)TCC>TTC	p.S621F
Pat_14	Pre-Treatment	C1orf49	84066	37	1	178483877	178483877	Missense_Mutation	SNP	A	G	44	167	c.133A>G	c.(133-135)AAA>GAA	p.K45E
Pat_14	Pre-Treatment	CRB1	23418	37	1	197390634	197390634	Missense_Mutation	SNP	C	T	139	492	c.1676C>T	c.(1675-1677)TCC>TTC	p.S559F
Pat_14	Pre-Treatment	PKP1	5317	37	1	201286742	201286742	Missense_Mutation	SNP	C	T	35	160	c.889C>T	c.(889-891)CGC>TGC	p.R297C
Pat_14	Pre-Treatment	CR2	1380	37	1	207648462	207648463	Missense_Mutation	DNP	GT	TC	22	537	.2440_2441GT>T	c.(2440-2442)GTT>TCT	p.V814S
Pat_14	Pre-Treatment	IRF6	3664	37	1	209961966	209961966	Missense_Mutation	SNP	C	T	40	99	c.1203G>A	c.(1201-1203)ATG>ATA	p.M401I
Pat_14	Pre-Treatment	C1orf107	27042	37	1	210012390	210012390	Missense_Mutation	SNP	C	T	58	228	c.1199C>T	c.(1198-1200)CCC>CTC	p.P400L
Pat_14	Pre-Treatment	KCNH1	3756	37	1	211256133	211256133	Missense_Mutation	SNP	G	T	7	504	c.547C>A	c.(547-549)CGC>AGC	p.R183S
Pat_14	Pre-Treatment	USH2A	7399	37	1	216348660	216348660	Missense_Mutation	SNP	G	A	35	143	c.4561C>T	c.(4561-4563)CGT>TGT	p.R1521C
Pat_14	Pre-Treatment	DEGS1	8560	37	1	224377361	224377361	Missense_Mutation	SNP	G	T	6	475	c.165G>T	c.(163-165)TTG>TTT	p.L55F
Pat_14	Pre-Treatment	OBSCN	84033	37	1	228466922	228466922	Missense_Mutation	SNP	G	A	4	122	c.7173G>A	c.(7171-7173)ATG>ATA	p.M2391I
Pat_14	Pre-Treatment	OBSCN	84033	37	1	228481282	228481282	Missense_Mutation	SNP	G	A	60	186	c.11096G>A	.(11095-11097)GGG>GA	p.G3699E
Pat_14	Pre-Treatment	SLC35F3	148641	37	1	234041310	234041310	Missense_Mutation	SNP	G	A	24	65	c.89G>A	c.(88-90)AGA>AAA	p.R30K
Pat_14	Pre-Treatment	TBCE	6905	37	1	235594040	235594040	Missense_Mutation	SNP	C	T	32	104	c.581C>T	c.(580-582)CCC>CTC	p.P194L
Pat_14	Pre-Treatment	MTR	4548	37	1	236979780	236979780	Missense_Mutation	SNP	G	T	7	646	c.701G>T	c.(700-702)CGG>CTG	p.R234L
Pat_14	Pre-Treatment	RYR2	6262	37	1	237791305	237791305	Missense_Mutation	SNP	C	A	42	167	c.6365C>A	c.(6364-6366)TCC>TAC	p.S2122Y
Pat_14	Pre-Treatment	GREM2	64388	37	1	240656286	240656286	Missense_Mutation	SNP	C	A	4	222	c.490G>T	c.(490-492)GAC>TAC	p.D164Y
Pat_14	Pre-Treatment	SDCCAG8	10806	37	1	243456460	243456460	Missense_Mutation	SNP	C	T	89	337	c.614C>T	c.(613-615)CCA>CTA	p.P205L
Pat_14	Pre-Treatment	KIF26B	55083	37	1	245847653	245847653	Nonsense_Mutation	SNP	C	T	27	86	c.2377C>T	c.(2377-2379)CAG>TAG	p.Q793*
Pat_14	Pre-Treatment	OR2G2	81470	37	1	247751937	247751937	Missense_Mutation	SNP	G	A	64	233	c.276G>A	c.(274-276)ATG>ATA	p.M92I
Pat_14	Pre-Treatment	OR2T4	127074	37	1	248524908	248524908	Missense_Mutation	SNP	G	A	6	222	c.26G>A	c.(25-27)AGC>AAC	p.S9N
Pat_14	Pre-Treatment	OR2T4	127074	37	1	248524937	248524937	Missense_Mutation	SNP	A	T	7	204	c.55A>T	c.(55-57)ATG>TTG	p.M19L
Pat_14	Pre-Treatment	PITRM1	10531	37	10	3197815	3197815	Missense_Mutation	SNP	G	A	74	331	c.1493C>T	c.(1492-1494)TCC>TTC	p.S498F
Pat_14	Pre-Treatment	AKR1C3	8644	37	10	5147829	5147829	Missense_Mutation	SNP	G	A	13	81	c.889G>A	c.(889-891)GAT>AAT	p.D297N

Pat_14	Pre-Treatment	BEND7	222389	37	10	13481404	13481404	Missense_Mutation	SNP	T	C	3	245	c.1175A>G	c.(1174-1176)AAG>AGG	p.K392R
Pat_14	Pre-Treatment	CDNF	441549	37	10	14867561	14867561	Missense_Mutation	SNP	C	A	6	597	c.302G>T	c.(301-303)CGC>CTC	p.R101L
Pat_14	Pre-Treatment	PLXDC2	84898	37	10	20335828	20335828	Nonsense_Mutation	SNP	C	T	94	319	c.355C>T	c.(355-357)CGA>TGA	p.R119*
Pat_14	Pre-Treatment	NEBL	10529	37	10	21074831	21074831	Missense_Mutation	SNP	C	T	48	258	c.2890G>A	c.(2890-2892)GAT>AAT	p.D964N
Pat_14	Pre-Treatment	KIAA1217	56243	37	10	24762896	24762896	Missense_Mutation	SNP	G	A	28	96	c.1586G>A	c.(1585-1587)GGA>GAA	p.G529E
Pat_14	Pre-Treatment	ARMC4	55130	37	10	28224135	28224135	Missense_Mutation	SNP	C	T	89	217	c.2299G>A	c.(2299-2301)GAT>AAT	p.D767N
Pat_14	Pre-Treatment	ZEB1	6935	37	10	31810788	31810788	Missense_Mutation	SNP	C	A	5	249	c.2525C>A	c.(2524-2526)GCA>GAA	p.A842E
Pat_14	Pre-Treatment	GDF10	2662	37	10	48438431	48438431	Missense_Mutation	SNP	C	T	8	63	c.280G>A	c.(280-282)GGA>AGA	p.G94R
Pat_14	Pre-Treatment	A1CF	29974	37	10	52603788	52603788	Missense_Mutation	SNP	C	T	54	217	c.194G>A	c.(193-195)CGA>CAA	p.R65Q
Pat_14	Pre-Treatment	PCDH15	65217	37	10	55698632	55698632	Nonsense_Mutation	SNP	G	A	66	328	c.3316C>T	c.(3316-3318)CGA>TGA	p.R1106*
Pat_14	Pre-Treatment	PCDH15	65217	37	10	55782797	55782797	Missense_Mutation	SNP	C	T	71	281	c.2381G>A	c.(2380-2382)GGA>GAA	p.G794E
Pat_14	Pre-Treatment	ANK3	288	37	10	61822910	61822910	Missense_Mutation	SNP	C	G	12	114	c.12554G>C	c.(12553-12555)AGT>ACT	p.S4185T
Pat_14	Pre-Treatment	ANK3	288	37	10	62149254	62149254	Missense_Mutation	SNP	C	T	19	176	c.43G>A	c.(43-45)GAA>AAA	p.E15K
Pat_14	Pre-Treatment	ARID5B	84159	37	10	63851834	63851834	Missense_Mutation	SNP	C	T	92	243	c.2612C>T	c.(2611-2613)CCT>CTT	p.P871L
Pat_14	Pre-Treatment	LRRTM3	347731	37	10	68687134	68687134	Missense_Mutation	SNP	C	T	77	459	c.460C>T	c.(460-462)CGG>TGG	p.R154W
Pat_14	Pre-Treatment	MYPN	84665	37	10	69908165	69908165	Missense_Mutation	SNP	C	T	137	418	c.1186C>T	c.(1186-1188)CCA>TCA	p.P396S
Pat_14	Pre-Treatment	NEUROG3	50674	37	10	71332702	71332702	Missense_Mutation	SNP	G	T	5	173	c.98C>A	c.(97-99)ACG>AAG	p.T33K
Pat_14	Pre-Treatment	SLC29A3	55315	37	10	73121911	73121911	Missense_Mutation	SNP	C	T	61	620	c.974C>T	c.(973-975)GCC>GTC	p.A325V
Pat_14	Pre-Treatment	NRG3	10718	37	10	84118593	84118593	Missense_Mutation	SNP	G	A	56	193	c.922G>A	c.(922-924)GAA>AAA	p.E308K
Pat_14	Pre-Treatment	OPN4	94233	37	10	88421097	88421097	Missense_Mutation	SNP	C	T	59	320	c.1025C>T	c.(1024-1026)TCT>TTT	p.S342F
Pat_14	Pre-Treatment	FAM35A	54537	37	10	88911122	88911122	Missense_Mutation	SNP	G	C	4	158	c.11G>C	c.(10-12)GGA>GCA	p.G4A
Pat_14	Pre-Treatment	PDE6C	5146	37	10	95422350	95422351	Missense_Mutation	DNP	CC	TT	21	161	.2317_2318CC>T	c.(2317-2319)CCT>TTT	p.P773F
Pat_14	Pre-Treatment	PDLIM1	9124	37	10	97023643	97023643	Missense_Mutation	SNP	C	T	74	211	c.511G>A	c.(511-513)GGG>AGG	p.G171R
Pat_14	Pre-Treatment	CRTAC1	55118	37	10	99655022	99655022	Missense_Mutation	SNP	G	A	58	190	c.1466C>T	c.(1465-1467)CCC>CTC	p.P489L
Pat_14	Pre-Treatment	SORCS3	22986	37	10	107022096	107022096	Missense_Mutation	SNP	C	T	49	280	c.3451C>T	c.(3451-3453)CCT>TCT	p.P1151S
Pat_14	Pre-Treatment	PNLIPRP2	5408	37	10	118386465	118386465	Missense_Mutation	SNP	C	T	18	84	c.424C>T	c.(424-426)CGG>TGG	p.R142W
Pat_14	Pre-Treatment	C10orf46	143384	37	10	120450911	120450911	Nonsense_Mutation	SNP	C	T	57	320	c.891G>A	c.(889-891)TGG>TGA	p.W297*
Pat_14	Pre-Treatment	INPP5F	22876	37	10	121563697	121563697	Missense_Mutation	SNP	T	A	71	206	c.1129T>A	c.(1129-1131)TTG>ATG	p.L377M
Pat_14	Pre-Treatment	GPR123	84435	37	10	134910478	134910478	Missense_Mutation	SNP	G	A	38	185	c.4G>A	c.(4-6)GAT>AAT	p.D2N
Pat_14	Pre-Treatment	TRPM5	29850	37	11	2434754	2434754	Missense_Mutation	SNP	C	T	33	104	c.1955G>A	c.(1954-1956)GGA>GAA	p.G652E
Pat_14	Pre-Treatment	MRGPRE	116534	37	11	3249972	3249972	Missense_Mutation	SNP	C	G	3	188	c.55G>C	c.(55-57)GAT>CAT	p.D19H
Pat_14	Pre-Treatment	UBQLNL	143630	37	11	5537092	5537092	Missense_Mutation	SNP	A	G	85	386	c.580T>C	c.(580-582)TTC>CTC	p.F194L
Pat_14	Pre-Treatment	OR52H1	390067	37	11	5565843	5565843	Missense_Mutation	SNP	G	C	4	367	c.911C>G	c.(910-912)ACC>AGC	p.T304S
Pat_14	Pre-Treatment	TRIM5	85363	37	11	5686554	5686554	Missense_Mutation	SNP	G	A	63	225	c.967C>T	c.(967-969)CCG>TCG	p.P323S
Pat_14	Pre-Treatment	OR52L1	338751	37	11	6007290	6007290	Missense_Mutation	SNP	G	A	15	64	c.871C>T	c.(871-873)CAT>TAT	p.H291Y
Pat_14	Pre-Treatment	DNHD1	144132	37	11	6532555	6532555	Missense_Mutation	SNP	T	A	55	225	c.1288T>A	c.(1288-1290)TGC>AGC	p.C430S
Pat_14	Pre-Treatment	PIK3C2A	5286	37	11	17151004	17151004	Missense_Mutation	SNP	G	A	52	202	c.2242C>T	c.(2242-2244)CCT>TCT	p.P748S
Pat_14	Pre-Treatment	MRGPRX1	259249	37	11	18956018	18956018	Missense_Mutation	SNP	G	A	82	308	c.314C>T	c.(313-315)TCC>TTC	p.S105F
Pat_14	Pre-Treatment	ANO5	203859	37	11	22248977	22248977	Missense_Mutation	SNP	C	T	112	319	c.493C>T	c.(493-495)CCT>TCT	p.P165S
Pat_14	Pre-Treatment	ANO5	203859	37	11	22291925	22291925	Missense_Mutation	SNP	G	A	97	263	c.1966G>A	c.(1966-1968)GAG>AAG	p.E656K
Pat_14	Pre-Treatment	APIP	51074	37	11	34904298	34904298	Missense_Mutation	SNP	G	A	63	238	c.695C>T	c.(694-696)TCA>TTA	p.S232L
Pat_14	Pre-Treatment	RAG2	5897	37	11	36615495	36615495	Missense_Mutation	SNP	G	A	70	294	c.224C>T	c.(223-225)CCA>CTA	p.P75L
Pat_14	Pre-Treatment	F2	2147	37	11	46747649	46747649	Missense_Mutation	SNP	G	A	109	398	c.800G>A	c.(799-801)GGG>GAG	p.G267E
Pat_14	Pre-Treatment	FOLH1	2346	37	11	49190795	49190795	Missense_Mutation	SNP	G	A	32	127	c.1324C>T	c.(1324-1326)CTT>TTT	p.L442F
Pat_14	Pre-Treatment	OR4C12	283093	37	11	50003139	50003139	Nonsense_Mutation	SNP	C	T	21	129	c.899G>A	c.(898-900)TGG>TAG	p.W300*
Pat_14	Pre-Treatment	OR4C16	219428	37	11	55339875	55339875	Missense_Mutation	SNP	C	T	117	594	c.272C>T	c.(271-273)TCC>TTC	p.S91F
Pat_14	Pre-Treatment	OR5D14	219436	37	11	55563888	55563888	Missense_Mutation	SNP	T	A	45	201	c.857T>A	c.(856-858)ATG>AAG	p.M286K

Pat_14	Pre-Treatment	OR8K5	219453	37	11	55927247	55927247	Missense_Mutation	SNP	G	A	49	248	c.547C>T	c.(547-549)CCT>TCT	p.P183S
Pat_14	Pre-Treatment	OR5T1	390155	37	11	56043488	56043489	Missense_Mutation	DNP	TT	AC	138	547	c.374_375TT>AC	c.(373-375)TTT>TAC	p.F125Y
Pat_14	Pre-Treatment	HRASLS5	117245	37	11	63231049	63231049	Missense_Mutation	SNP	C	T	89	298	c.766G>A	c.(766-768)GAA>AAA	p.E256K
Pat_14	Pre-Treatment	PRDX5	25824	37	11	64088247	64088247	Missense_Mutation	SNP	C	A	9	719	c.421C>A	c.(421-423)CAC>AAC	p.H141N
Pat_14	Pre-Treatment	EHD1	10938	37	11	64622143	64622143	Missense_Mutation	SNP	C	A	75	232	c.1267G>T	c.(1267-1269)GGG>TGG	p.G423W
Pat_14	Pre-Treatment	BATF2	116071	37	11	64756651	64756651	Missense_Mutation	SNP	G	A	29	159	c.775C>T	c.(775-777)CAC>TAC	p.H259Y
Pat_14	Pre-Treatment	SPDYC	387778	37	11	64939917	64939917	Missense_Mutation	SNP	C	A	7	676	c.357C>A	c.(355-357)AAC>AAA	p.N119K
Pat_14	Pre-Treatment	PCNXL3	399909	37	11	65391983	65391983	Missense_Mutation	SNP	C	A	4	104	c.2758C>A	c.(2758-2760)CTG>ATG	p.L920M
Pat_14	Pre-Treatment	NPAS4	266743	37	11	66190234	66190234	Missense_Mutation	SNP	C	T	78	337	c.520C>T	c.(520-522)CAT>TAT	p.H174Y
Pat_14	Pre-Treatment	ANKRD13D	338692	37	11	67067357	67067357	Missense_Mutation	SNP	G	A	5	366	c.679G>A	c.(679-681)GGG>AGG	p.G227R
Pat_14	Pre-Treatment	PITPNM1	9600	37	11	67267481	67267481	Splice_Site	SNP	C	T	31	87	c.968_splice	c.e6-1	p.G323_splice
Pat_14	Pre-Treatment	THRSP	7069	37	11	77775144	77775144	Missense_Mutation	SNP	G	A	50	188	c.217G>A	c.(217-219)GGG>AGG	p.G73R
Pat_14	Pre-Treatment	NARS2	79731	37	11	78270604	78270604	Missense_Mutation	SNP	C	T	110	357	c.575G>A	c.(574-576)GGA>GAA	p.G192E
Pat_14	Pre-Treatment	ODZ4	26011	37	11	78423527	78423527	Missense_Mutation	SNP	C	T	29	236	c.4054G>A	c.(4054-4056)GGC>AGC	p.G1352S
Pat_14	Pre-Treatment	CCDC81	60494	37	11	86123469	86123469	Missense_Mutation	SNP	T	C	124	496	c.1259T>C	c.(1258-1260)CTT>CCT	p.L420P
Pat_14	Pre-Treatment	PGR	5241	37	11	100999605	100999605	Missense_Mutation	SNP	C	T	47	123	c.197G>A	c.(196-198)GGA>GAA	p.G66E
Pat_14	Pre-Treatment	C11orf70	85016	37	11	101946634	101946634	Missense_Mutation	SNP	G	A	40	147	c.466G>A	c.(466-468)GAA>AAA	p.E156K
Pat_14	Pre-Treatment	MMP10	4319	37	11	102647343	102647343	Nonsense_Mutation	SNP	C	A	6	422	c.787G>T	c.(787-789)GGA>TGA	p.G263*
Pat_14	Pre-Treatment	MMP12	4321	37	11	102734918	102734918	Missense_Mutation	SNP	C	T	29	115	c.1271G>A	c.(1270-1272)GGA>GAA	p.G424E
Pat_14	Pre-Treatment	CASP4	837	37	11	104820317	104820317	Missense_Mutation	SNP	C	T	136	576	c.734G>A	c.(733-735)AGT>AAT	p.S245N
Pat_14	Pre-Treatment	GUCY1A2	2977	37	11	106681104	106681104	Missense_Mutation	SNP	C	T	51	199	c.1307G>A	c.(1306-1308)CGA>CAA	p.R436Q
Pat_14	Pre-Treatment	LAYN	143903	37	11	111414717	111414717	Missense_Mutation	SNP	G	A	44	185	c.179G>A	c.(178-180)CGA>CAA	p.R60Q
Pat_14	Pre-Treatment	NCAM1	4684	37	11	113104016	113104016	Missense_Mutation	SNP	C	T	30	77	c.1394C>T	c.(1393-1395)TCC>TTC	p.S465F
Pat_14	Pre-Treatment	NNMT	4837	37	11	114183057	114183057	Missense_Mutation	SNP	G	T	40	153	c.653G>T	c.(652-654)CGG>CTG	p.R218L
Pat_14	Pre-Treatment	TMPRSS4	56649	37	11	117969708	117969708	Missense_Mutation	SNP	C	T	62	273	c.52C>T	c.(52-54)CCC>TCC	p.P18S
Pat_14	Pre-Treatment	GRIK4	2900	37	11	120837994	120837994	Missense_Mutation	SNP	G	A	22	140	c.2357G>A	c.(2356-2358)GGA>GAA	p.G786E
Pat_14	Pre-Treatment	SORL1	6653	37	11	121492954	121492954	Missense_Mutation	SNP	G	A	24	101	c.6148G>A	c.(6148-6150)GAA>AAA	p.E2050K
Pat_14	Pre-Treatment	OR4D5	219875	37	11	123810920	123810920	Missense_Mutation	SNP	G	A	156	553	c.597G>A	c.(595-597)ATG>ATA	p.M199I
Pat_14	Pre-Treatment	OR10S1	219873	37	11	123848328	123848328	Missense_Mutation	SNP	T	C	88	334	c.71A>G	c.(70-72)CAC>CGC	p.H24R
Pat_14	Pre-Treatment	PANX3	116337	37	11	124482962	124482962	Missense_Mutation	SNP	C	T	41	232	c.268C>T	c.(268-270)CAC>TAC	p.H90Y
Pat_14	Pre-Treatment	KCNJ1	3758	37	11	128709089	128709089	Missense_Mutation	SNP	C	T	33	150	c.1107G>A	c.(1105-1107)ATG>ATA	p.M369I
Pat_14	Pre-Treatment	SLC6A12	6539	37	12	319047	319047	Missense_Mutation	SNP	G	A	111	356	c.106C>T	c.(106-108)CGG>TGG	p.R36W
Pat_14	Pre-Treatment	CACNA1C	775	37	12	2705123	2705123	Missense_Mutation	SNP	C	T	50	242	c.2747C>T	c.(2746-2748)TCC>TTC	p.S916F
Pat_14	Pre-Treatment	FGF6	2251	37	12	4554433	4554433	Missense_Mutation	SNP	G	A	14	64	c.304C>T	c.(304-306)CCC>TCC	p.P102S
Pat_14	Pre-Treatment	GALNT8	26290	37	12	4881716	4881716	Missense_Mutation	SNP	G	A	73	255	c.1867G>A	c.(1867-1869)GAA>AAA	p.E623K
Pat_14	Pre-Treatment	VWF	7450	37	12	6155903	6155903	Missense_Mutation	SNP	G	A	60	273	c.2267C>T	c.(2266-2268)CCC>CTC	p.P756L
Pat_14	Pre-Treatment	C1S	716	37	12	7169837	7169837	Missense_Mutation	SNP	G	A	93	234	c.64G>A	c.(64-66)GAG>AAG	p.E22K
Pat_14	Pre-Treatment	C1R	715	37	12	7188116	7188116	Missense_Mutation	SNP	G	A	23	72	c.1838C>T	c.(1837-1839)CCC>CTC	p.P613L
Pat_14	Pre-Treatment	CLEC6A	93978	37	12	8608733	8608733	Missense_Mutation	SNP	G	A	51	205	c.26G>A	c.(25-27)AGT>AAT	p.S9N
Pat_14	Pre-Treatment	KLRD1	3824	37	12	10460576	10460576	Splice_Site	SNP	G	A	5	34	c.-99_splice	c.e2-1	
Pat_14	Pre-Treatment	TAS2R7	50837	37	12	10954929	10954929	Missense_Mutation	SNP	C	T	61	190	c.241G>A	c.(241-243)GAA>AAA	p.E81K
Pat_14	Pre-Treatment	PRB3	5544	37	12	11420521	11420521	Missense_Mutation	SNP	C	T	6	314	c.662G>A	c.(661-663)CGT>CAT	p.R221H
Pat_14	Pre-Treatment	PRB2	653247	37	12	11545928	11545928	Missense_Mutation	SNP	G	A	128	564	c.1084C>T	c.(1084-1086)CCT>TCT	p.P362S
Pat_14	Pre-Treatment	PLBD1	79887	37	12	14659191	14659191	Missense_Mutation	SNP	C	T	37	133	c.1384G>A	c.(1384-1386)GAT>AAT	p.D462N
Pat_14	Pre-Treatment	RERGL	79785	37	12	18241861	18241861	Missense_Mutation	SNP	A	T	88	348	c.85T>A	c.(85-87)TTC>ATC	p.F29I
Pat_14	Pre-Treatment	RERGL	79785	37	12	18241863	18241863	Missense_Mutation	SNP	C	T	88	348	c.83G>A	c.(82-84)CGA>CAA	p.R28Q
Pat_14	Pre-Treatment	PIK3C2G	5288	37	12	18716344	18716344	Missense_Mutation	SNP	G	A	18	71	c.3691G>A	c.(3691-3693)GAA>AAA	p.E1231K

Pat_14	Pre-Treatment	PIK3C2G	5288	37	12	18747486	18747486	Missense_Mutation	SNP	C	T	39	205	c.3947C>T	c.(3946-3948)TCA>TTA	p.S1316L
Pat_14	Pre-Treatment	PPFIBP1	8496	37	12	27844758	27844758	Missense_Mutation	SNP	C	A	6	429	c.2780C>A	c.(2779-2781)CCA>CAA	p.P927Q
Pat_14	Pre-Treatment	CNTN1	1272	37	12	41337941	41337941	Missense_Mutation	SNP	A	T	28	159	c.1652A>T	c.(1651-1653)AAA>ATA	p.K551I
Pat_14	Pre-Treatment	ADAMTS20	80070	37	12	43822473	43822473	Missense_Mutation	SNP	G	T	16	56	c.3619C>A	c.(3619-3621)CCT>ACT	p.P1207T
Pat_14	Pre-Treatment	SLC38A1	81539	37	12	46598337	46598337	Missense_Mutation	SNP	C	A	5	428	c.683G>T	c.(682-684)TGT>TTT	p.C228F
Pat_14	Pre-Treatment	FAM113B	91523	37	12	47629943	47629943	Missense_Mutation	SNP	G	A	116	432	c.1097G>A	c.(1096-1098)GGT>GAT	p.G366D
Pat_14	Pre-Treatment	COL2A1	1280	37	12	48376302	48376302	Missense_Mutation	SNP	C	T	38	100	c.2284G>A	c.(2284-2286)GGG>AGG	p.G762R
Pat_14	Pre-Treatment	MLL2	8085	37	12	49445925	49445925	Missense_Mutation	SNP	G	A	16	83	c.1541C>T	c.(1540-1542)CCA>CTA	p.P514L
Pat_14	Pre-Treatment	SLC11A2	4891	37	12	51388361	51388361	Missense_Mutation	SNP	T	A	81	340	c.1043A>T	c.(1042-1044)GAT>GTT	p.D348V
Pat_14	Pre-Treatment	KRT72	140807	37	12	52985397	52985397	Nonsense_Mutation	SNP	G	A	71	333	c.814C>T	c.(814-816)CAG>TAG	p.Q272*
Pat_14	Pre-Treatment	KRT8	3856	37	12	53298675	53298675	Missense_Mutation	SNP	A	C	4	75	c.91T>G	c.(91-93)TCC>GCC	p.S31A
Pat_14	Pre-Treatment	EIF4B	1975	37	12	53421607	53421607	Missense_Mutation	SNP	T	C	3	331	c.709T>C	c.(709-711)TAT>CAT	p.Y237H
Pat_14	Pre-Treatment	HOXC9	3225	37	12	54396315	54396315	Missense_Mutation	SNP	A	G	52	186	c.640A>G	c.(640-642)AAT>GAT	p.N214D
Pat_14	Pre-Treatment	DGKA	1606	37	12	56333012	56333012	Missense_Mutation	SNP	G	T	6	368	c.517G>T	c.(517-519)GGC>TGC	p.G173C
Pat_14	Pre-Treatment	ANKRD52	283373	37	12	56647157	56647157	Missense_Mutation	SNP	C	A	102	428	c.1015G>T	c.(1015-1017)GGG>TGG	p.G339W
Pat_14	Pre-Treatment	MYO1A	4640	37	12	57430162	57430162	Nonsense_Mutation	SNP	G	A	13	436	c.2278C>T	c.(2278-2280)CGA>TGA	p.R760*
Pat_14	Pre-Treatment	MYO1A	4640	37	12	57437652	57437652	Missense_Mutation	SNP	G	A	49	145	c.880C>T	c.(880-882)CGT>TGT	p.R294C
Pat_14	Pre-Treatment	SLC26A10	65012	37	12	58016715	58016715	Missense_Mutation	SNP	C	A	5	175	c.937C>A	c.(937-939)CAG>AAG	p.Q313K
Pat_14	Pre-Treatment	BEST3	144453	37	12	70049336	70049336	Missense_Mutation	SNP	G	A	34	140	c.1358C>T	c.(1357-1359)TCC>TTC	p.S453F
Pat_14	Pre-Treatment	TRHDE	29953	37	12	72680600	72680600	Missense_Mutation	SNP	G	A	125	397	c.919G>A	c.(919-921)GAA>AAA	p.E307K
Pat_14	Pre-Treatment	C12orf50	160419	37	12	88420303	88420303	Missense_Mutation	SNP	G	A	49	142	c.95C>T	c.(94-96)CCT>CTT	p.P32L
Pat_14	Pre-Treatment	DUSP6	1848	37	12	89743104	89743104	Missense_Mutation	SNP	G	A	94	318	c.1073C>T	c.(1072-1074)CCA>CTA	p.P358L
Pat_14	Pre-Treatment	DCN	1634	37	12	91550900	91550900	Missense_Mutation	SNP	G	A	90	351	c.604C>T	c.(604-606)CTC>TTC	p.L202F
Pat_14	Pre-Treatment	EEA1	8411	37	12	93245024	93245024	Missense_Mutation	SNP	C	G	3	155	c.661G>C	c.(661-663)GAA>CAA	p.E221Q
Pat_14	Pre-Treatment	NTN4	59277	37	12	96181219	96181219	Missense_Mutation	SNP	G	A	51	221	c.83C>T	c.(82-84)TCC>TTC	p.S28F
Pat_14	Pre-Treatment	ANKS1B	56899	37	12	99640084	99640084	Missense_Mutation	SNP	C	T	14	63	c.2315G>A	c.(2314-2316)AGA>AAA	p.R772K
Pat_14	Pre-Treatment	SLC17A8	246213	37	12	100751255	100751255	Missense_Mutation	SNP	T	C	49	155	c.86T>C	c.(85-87)TTG>TCG	p.L29S
Pat_14	Pre-Treatment	GNPTAB	79158	37	12	102158687	102158687	Missense_Mutation	SNP	G	T	32	117	c.2008C>A	c.(2008-2010)CCC>ACC	p.P670T
Pat_14	Pre-Treatment	WSCD2	9671	37	12	108618518	108618518	Missense_Mutation	SNP	G	A	86	353	c.685G>A	c.(685-687)GGA>AGA	p.G229R
Pat_14	Pre-Treatment	DTX1	1840	37	12	113515335	113515335	Missense_Mutation	SNP	T	G	7	271	c.366T>G	c.(364-366)GAT>GAG	p.D122E
Pat_14	Pre-Treatment	LHX5	64211	37	12	113907044	113907044	Missense_Mutation	SNP	C	T	85	271	c.280G>A	c.(280-282)GTG>ATG	p.V94M
Pat_14	Pre-Treatment	TBX3	6926	37	12	115115433	115115433	Missense_Mutation	SNP	G	A	63	274	c.893C>T	c.(892-894)CCT>CTT	p.P298L
Pat_14	Pre-Treatment	TBX3	6926	37	12	115120950	115120950	Missense_Mutation	SNP	G	A	57	259	c.56C>T	c.(55-57)CCG>CTG	p.P19L
Pat_14	Pre-Treatment	PIWIL1	9271	37	12	130846145	130846145	Missense_Mutation	SNP	C	A	9	446	c.1969C>A	c.(1969-1971)CGC>AGC	p.R657S
Pat_14	Pre-Treatment	DDX51	317781	37	12	132627346	132627346	Missense_Mutation	SNP	G	C	4	465	c.597C>G	c.(595-597)ATC>ATG	p.I199M
Pat_14	Pre-Treatment	MIPEP	4285	37	13	24436442	24436442	Missense_Mutation	SNP	G	A	13	37	c.1052C>T	c.(1051-1053)TCC>TTC	p.S351F
Pat_14	Pre-Treatment	MTUS2	23281	37	13	29599623	29599623	Missense_Mutation	SNP	G	A	25	54	c.818G>A	c.(817-819)GGG>GAG	p.G273E
Pat_14	Pre-Treatment	MTUS2	23281	37	13	29600712	29600712	Missense_Mutation	SNP	G	A	33	73	c.1907G>A	c.(1906-1908)AGG>AAG	p.R636K
Pat_14	Pre-Treatment	FRY	10129	37	13	32691490	32691490	Missense_Mutation	SNP	C	T	50	107	c.344C>T	c.(343-345)TCC>TTC	p.S115F
Pat_14	Pre-Treatment	FRY	10129	37	13	32786506	32786506	Missense_Mutation	SNP	G	A	8	110	c.4669G>A	c.(4669-4671)GAA>AAA	p.E1557K
Pat_14	Pre-Treatment	PDS5B	23047	37	13	33258144	33258144	Missense_Mutation	SNP	G	A	80	491	c.1187G>A	c.(1186-1188)AGA>AAA	p.R396K
Pat_14	Pre-Treatment	C13orf23	80209	37	13	39588439	39588439	Missense_Mutation	SNP	G	A	4	207	c.950C>T	c.(949-951)CCA>CTA	p.P317L
Pat_14	Pre-Treatment	ELF1	1997	37	13	41507692	41507692	Missense_Mutation	SNP	G	A	99	502	c.1729C>T	c.(1729-1731)CAT>TAT	p.H577Y
Pat_14	Pre-Treatment	ATP7B	540	37	13	52534336	52534336	Missense_Mutation	SNP	G	A	130	188	c.2069C>T	c.(2068-2070)CCA>CTA	p.P690L
Pat_14	Pre-Treatment	SLITRK6	84189	37	13	86369430	86369430	Missense_Mutation	SNP	C	T	37	101	c.1214G>A	c.(1213-1215)GGA>GAA	p.G405E
Pat_14	Pre-Treatment	ABCC4	10257	37	13	95673860	95673860	Missense_Mutation	SNP	G	A	102	445	c.3947C>T	c.(3946-3948)TCG>TTG	p.S1316L
Pat_14	Pre-Treatment	DOCK9	23348	37	13	99554550	99554550	Missense_Mutation	SNP	G	A	28	192	c.1375C>T	c.(1375-1377)CCG>TCG	p.P459S

Pat_14	Pre-Treatment	CARS2	79587	37	13	111299538	111299538	Missense_Mutation	SNP	A	G	3	164	c.1103T>C	c.(1102-1104)CTG>CCG	p.L368P
Pat_14	Pre-Treatment	GRK1	6011	37	13	114321898	114321898	Missense_Mutation	SNP	C	G	3	190	c.197C>G	c.(196-198)CCC>CGC	p.P66R
Pat_14	Pre-Treatment	OR4N5	390437	37	14	20612317	20612317	Nonsense_Mutation	SNP	C	A	6	598	c.423C>A	c.(421-423)TGC>TGA	p.C141*
Pat_14	Pre-Treatment	SLC7A8	23428	37	14	23635719	23635719	Nonsense_Mutation	SNP	G	T	8	473	c.182C>A	c.(181-183)TCG>TAG	p.S61*
Pat_14	Pre-Treatment	DHRS4L1	728635	37	14	24506951	24506951	Splice_Site	SNP	G	A	23	99	c.129_splice	c.e2-1	p.W43_splice
Pat_14	Pre-Treatment	NYNRIN	57523	37	14	24885336	24885336	Missense_Mutation	SNP	G	A	28	89	c.4381G>A	c.(4381-4383)GAT>AAT	p.D1461N
Pat_14	Pre-Treatment	CTSG	1511	37	14	25043966	25043966	Missense_Mutation	SNP	G	A	95	189	c.254C>T	c.(253-255)ACC>ATC	p.T85I
Pat_14	Pre-Treatment	SRP54	6729	37	14	35483027	35483027	Missense_Mutation	SNP	C	T	43	143	c.805C>T	c.(805-807)CCG>TCG	p.P269S
Pat_14	Pre-Treatment	FANCM	57697	37	14	45633748	45633748	Missense_Mutation	SNP	T	G	21	33	c.1768T>G	c.(1768-1770)TCT>GCT	p.S590A
Pat_14	Pre-Treatment	PYGL	5836	37	14	51404530	51404530	Missense_Mutation	SNP	A	G	19	325	c.269T>C	c.(268-270)TTT>TCT	p.F90S
Pat_14	Pre-Treatment	TBPL2	387332	37	14	55890921	55890921	Missense_Mutation	SNP	C	T	93	256	c.1007G>A	c.(1006-1008)CGA>CAA	p.R336Q
Pat_14	Pre-Treatment	RAB15	376267	37	14	65417845	65417845	Missense_Mutation	SNP	T	C	3	311	c.271A>G	c.(271-273)AGC>GGC	p.S91G
Pat_14	Pre-Treatment	GALNTL1	57452	37	14	69805425	69805426	Missense_Mutation	DNP	GG	TT	5	290	.1025_1026GG>T	c.(1024-1026)CGG>CTT	p.R342L
Pat_14	Pre-Treatment	SIPA1L1	26037	37	14	72190563	72190563	Missense_Mutation	SNP	G	A	86	191	c.4471G>A	c.(4471-4473)GAA>AAA	p.E1491K
Pat_14	Pre-Treatment	ZFYVE1	53349	37	14	73441645	73441645	Missense_Mutation	SNP	G	A	72	215	c.1829C>T	c.(1828-1830)TCC>TTC	p.S610F
Pat_14	Pre-Treatment	C14orf179	112752	37	14	76548655	76548655	Missense_Mutation	SNP	G	A	214	506	c.313G>A	c.(313-315)GAT>AAT	p.D105N
Pat_14	Pre-Treatment	C14orf174	161394	37	14	77845247	77845247	Missense_Mutation	SNP	G	A	107	253	c.1486G>A	c.(1486-1488)GAT>AAT	p.D496N
Pat_14	Pre-Treatment	SEL1L	6400	37	14	81969220	81969220	Missense_Mutation	SNP	G	A	5	173	c.622C>T	c.(622-624)CGG>TGG	p.R208W
Pat_14	Pre-Treatment	CCDC88C	440193	37	14	91780236	91780236	Missense_Mutation	SNP	C	T	23	37	c.1924G>A	c.(1924-1926)GAG>AAG	p.E642K
Pat_14	Pre-Treatment	DICER1	23405	37	14	95556978	95556978	Missense_Mutation	SNP	C	A	6	582	c.5626G>T	c.(5626-5628)GGG>TGG	p.G1876W
Pat_14	Pre-Treatment	CCNK	8812	37	14	99968696	99968696	Missense_Mutation	SNP	C	T	32	75	c.728C>T	c.(727-729)CCG>CTG	p.P243L
Pat_14	Pre-Treatment	TDRD9	122402	37	14	104490968	104490968	Missense_Mutation	SNP	A	G	3	346	c.2669A>G	c.(2668-2670)GAC>GGC	p.D890G
Pat_14	Pre-Treatment	INF2	64423	37	14	105179249	105179249	Nonsense_Mutation	SNP	G	T	5	200	c.2695G>T	c.(2695-2697)GAG>TAG	p.E899*
Pat_14	Pre-Treatment	CYFIP1	23191	37	15	22990172	22990172	Missense_Mutation	SNP	A	G	3	331	c.2792A>G	c.(2791-2793)GAG>GGG	p.E931G
Pat_14	Pre-Treatment	HERC2	8924	37	15	28377302	28377302	Missense_Mutation	SNP	C	A	4	136	c.12514G>T	.(12514-12516)GGG>TG	p.G4172W
Pat_14	Pre-Treatment	KLF13	51621	37	15	31664395	31664395	Missense_Mutation	SNP	C	T	18	86	c.760C>T	c.(760-762)CCG>TCG	p.P254S
Pat_14	Pre-Treatment	RYR3	6263	37	15	33954667	33954667	Missense_Mutation	SNP	G	A	10	75	c.4936G>A	c.(4936-4938)GAG>AAG	p.E1646K
Pat_14	Pre-Treatment	SLC12A6	9990	37	15	34543111	34543111	Missense_Mutation	SNP	G	A	36	179	c.1481C>T	c.(1480-1482)CCC>CTC	p.P494L
Pat_14	Pre-Treatment	GJD2	57369	37	15	35045277	35045277	Missense_Mutation	SNP	G	A	56	344	c.368C>T	c.(367-369)TCC>TTC	p.S123F
Pat_14	Pre-Treatment	RASGRP1	10125	37	15	38818501	38818501	Missense_Mutation	SNP	G	T	5	270	c.325C>A	c.(325-327)CTC>ATC	p.L109I
Pat_14	Pre-Treatment	VPS18	57617	37	15	41193079	41193079	Missense_Mutation	SNP	C	T	64	336	c.2063C>T	c.(2062-2064)GCC>GTC	p.A688V
Pat_14	Pre-Treatment	JMJD7-PLA2G4B	8681	37	15	42127058	42127058	Missense_Mutation	SNP	C	A	23	217	c.185C>A	c.(184-186)CCG>CAG	p.P62Q
Pat_14	Pre-Treatment	TGM5	9333	37	15	43525409	43525409	Missense_Mutation	SNP	A	T	27	166	c.2143T>A	c.(2143-2145)TAT>AAT	p.Y715N
Pat_14	Pre-Treatment	MYEF2	50804	37	15	48444477	48444477	Missense_Mutation	SNP	C	A	7	541	c.1092G>T	c.(1090-1092)ATG>ATT	p.M364I
Pat_14	Pre-Treatment	TRPM7	54822	37	15	50926736	50926736	Missense_Mutation	SNP	G	A	17	78	c.850C>T	c.(850-852)CCT>TCT	p.P284S
Pat_14	Pre-Treatment	DMXL2	23312	37	15	51758498	51758498	Missense_Mutation	SNP	G	A	22	123	c.7400C>T	c.(7399-7401)CCT>CTT	p.P2467L
Pat_14	Pre-Treatment	UNC13C	440279	37	15	54305717	54305717	Missense_Mutation	SNP	C	T	42	255	c.617C>T	c.(616-618)TCC>TTC	p.S206F
Pat_14	Pre-Treatment	UNC13C	440279	37	15	54307600	54307600	Missense_Mutation	SNP	C	T	55	156	c.2500C>T	c.(2500-2502)CGG>TGG	p.R834W
Pat_14	Pre-Treatment	DENND4A	10260	37	15	65960342	65960342	Missense_Mutation	SNP	C	A	5	260	c.4775G>T	c.(4774-4776)GGC>GTC	p.G1592V
Pat_14	Pre-Treatment	NOX5	79400	37	15	69335023	69335023	Missense_Mutation	SNP	C	T	57	229	c.1525C>T	c.(1525-1527)CGG>TGG	p.R509W
Pat_14	Pre-Treatment	GRAMD2	196996	37	15	72454678	72454679	Missense_Mutation	DNP	GG	AA	21	215	c.996_997CC>TT	(994-999)TTCCGT>TTTT	p.R333C
Pat_14	Pre-Treatment	STRA6	64220	37	15	74476238	74476238	Nonsense_Mutation	SNP	C	T	112	374	c.1259G>A	c.(1258-1260)TGG>TAG	p.W420*
Pat_14	Pre-Treatment	MESDC2	23184	37	15	81271702	81271702	Missense_Mutation	SNP	T	C	4	323	c.563A>G	c.(562-564)CAG>CGG	p.Q188R
Pat_14	Pre-Treatment	FAM154B	283726	37	15	82575383	82575383	Missense_Mutation	SNP	C	T	42	226	c.1177C>T	c.(1177-1179)CCT>TCT	p.P393S
Pat_14	Pre-Treatment	ADAMTSL3	57188	37	15	84558978	84558978	Missense_Mutation	SNP	G	A	5	405	c.1190G>A	c.(1189-1191)AGC>AAC	p.S397N
Pat_14	Pre-Treatment	ADAMTSL3	57188	37	15	84568434	84568434	Missense_Mutation	SNP	A	G	25	110	c.1651A>G	c.(1651-1653)AAA>GAA	p.K551E
Pat_14	Pre-Treatment	SLC28A1	9154	37	15	85478657	85478657	Missense_Mutation	SNP	G	A	90	290	c.1489G>A	c.(1489-1491)GAG>AAG	p.E497K

Pat_14	Pre-Treatment	BLM	641	37	15	91358373	91358373	Missense_Mutation	SNP	C	T	72	321	c.4118C>T	c.(4117-4119)TCC>TTC	p.S1373F
Pat_14	Pre-Treatment	SV2B	9899	37	15	91809816	91809816	Missense_Mutation	SNP	C	T	66	182	c.1013C>T	c.(1012-1014)TCC>TTC	p.S338F
Pat_14	Pre-Treatment	IGF1R	3480	37	15	99251225	99251225	Missense_Mutation	SNP	G	A	64	294	c.529G>A	c.(529-531)GAA>AAA	p.E177K
Pat_14	Pre-Treatment	AMDHD2	51005	37	16	2578360	2578360	Missense_Mutation	SNP	G	A	5	275	c.841G>A	c.(841-843)GCC>ACC	p.A281T
Pat_14	Pre-Treatment	MEFV	4210	37	16	3304352	3304352	Missense_Mutation	SNP	C	T	60	196	c.716G>A	c.(715-717)CGA>CAA	p.R239Q
Pat_14	Pre-Treatment	ZNF597	146434	37	16	3486952	3486952	Missense_Mutation	SNP	A	T	73	207	c.747T>A	c.(745-747)TTT>TTA	p.F249L
Pat_14	Pre-Treatment	NAT15	79903	37	16	3526336	3526336	Missense_Mutation	SNP	G	A	4	131	c.109G>A	c.(109-111)GAG>AAG	p.E37K
Pat_14	Pre-Treatment	CREBBP	1387	37	16	3777898	3777898	Missense_Mutation	SNP	G	T	9	627	c.7150C>A	c.(7150-7152)CAC>AAC	p.H2384N
Pat_14	Pre-Treatment	TFAP4	7023	37	16	4308090	4308090	Missense_Mutation	SNP	C	A	9	88	c.983G>T	c.(982-984)CGG>CTG	p.R328L
Pat_14	Pre-Treatment	GRIN2A	2903	37	16	9857524	9857524	Missense_Mutation	SNP	C	T	77	281	c.3877G>A	c.(3877-3879)GAT>AAT	p.D1293N
Pat_14	Pre-Treatment	CPPED1	55313	37	16	12798754	12798754	Missense_Mutation	SNP	C	T	36	152	c.442G>A	c.(442-444)GAT>AAT	p.D148N
Pat_14	Pre-Treatment	TMC7	79905	37	16	19067890	19067890	Missense_Mutation	SNP	C	A	8	347	c.1898C>A	c.(1897-1899)CCG>CAG	p.P633Q
Pat_14	Pre-Treatment	DNAH3	55567	37	16	21011603	21011603	Nonsense_Mutation	SNP	G	A	68	278	c.6364C>T	c.(6364-6366)CGA>TGA	p.R2122*
Pat_14	Pre-Treatment	ZKSCAN2	342357	37	16	25258412	25258413	Nonsense_Mutation	DNP	GG	AA	55	314	.1104_1105CC>T	102-1107)CCCCGA>CCT	p.R369*
Pat_14	Pre-Treatment	JMJD5	79831	37	16	27224960	27224960	Missense_Mutation	SNP	C	T	74	260	c.553C>T	c.(553-555)CCC>TCC	p.P185S
Pat_14	Pre-Treatment	IL21R	50615	37	16	27445671	27445671	Nonsense_Mutation	SNP	G	A	44	221	c.53G>A	c.(52-54)TGG>TAG	p.W18*
Pat_14	Pre-Treatment	ATP2A1	487	37	16	28914229	28914229	Missense_Mutation	SNP	A	G	26	79	c.2741A>G	c.(2740-2742)AAC>AGC	p.N914S
Pat_14	Pre-Treatment	LAT	27040	37	16	28997920	28997920	Missense_Mutation	SNP	G	T	62	193	c.370G>T	c.(370-372)GGG>TGG	p.G124W
Pat_14	Pre-Treatment	ITGAL	3683	37	16	30506115	30506115	Missense_Mutation	SNP	C	T	85	327	c.1447C>T	c.(1447-1449)CCA>TCA	p.P483S
Pat_14	Pre-Treatment	PRSS36	146547	37	16	31153226	31153226	Missense_Mutation	SNP	C	T	62	274	c.1577G>A	c.(1576-1578)GGA>GAA	p.G526E
Pat_14	Pre-Treatment	ITGAD	3681	37	16	31414929	31414929	Missense_Mutation	SNP	G	A	87	271	c.667G>A	c.(667-669)GGC>AGC	p.G223S
Pat_14	Pre-Treatment	ITGAD	3681	37	16	31424409	31424409	Splice_Site	SNP	G	A	85	290	c.1839_splice	c.e16-1	p.R613_splice
Pat_14	Pre-Treatment	DNAJA2	10294	37	16	46991096	46991096	Missense_Mutation	SNP	G	A	116	456	c.1084C>T	c.(1084-1086)CCT>TCT	p.P362S
Pat_14	Pre-Treatment	NOD2	64127	37	16	50745620	50745620	Missense_Mutation	SNP	G	A	25	112	c.1798G>A	c.(1798-1800)GAA>AAA	p.E600K
Pat_14	Pre-Treatment	CHD9	80205	37	16	53260396	53260396	Missense_Mutation	SNP	C	T	57	229	c.2015C>T	c.(2014-2016)CCT>CTT	p.P672L
Pat_14	Pre-Treatment	GOT2	2806	37	16	58743443	58743443	Missense_Mutation	SNP	G	T	9	772	c.1048C>A	c.(1048-1050)CGC>AGC	p.R350S
Pat_14	Pre-Treatment	CDH8	1006	37	16	61859038	61859038	Missense_Mutation	SNP	T	G	63	236	c.713A>C	c.(712-714)GAG>GCG	p.E238A
Pat_14	Pre-Treatment	CDH5	1003	37	16	66434769	66434769	Missense_Mutation	SNP	C	T	85	303	c.1687C>T	c.(1687-1689)CCA>TCA	p.P563S
Pat_14	Pre-Treatment	ACD	65057	37	16	67694191	67694191	Missense_Mutation	SNP	C	T	18	32	c.191G>A	c.(190-192)AGG>AAG	p.R64K
Pat_14	Pre-Treatment	HYDIN	54768	37	16	70852271	70852271	Missense_Mutation	SNP	G	T	22	87	c.14629C>A	.(14629-14631)CAG>AA	p.Q4877K
Pat_14	Pre-Treatment	HYDIN	54768	37	16	70926314	70926314	Missense_Mutation	SNP	G	A	35	403	c.9364C>T	c.(9364-9366)CAT>TAT	p.H3122Y
Pat_14	Pre-Treatment	HYDIN	54768	37	16	71025252	71025252	Missense_Mutation	SNP	C	T	50	202	c.3833G>A	c.(3832-3834)AGA>AAA	p.R1278K
Pat_14	Pre-Treatment	ADAMTS18	170692	37	16	77331258	77331258	Missense_Mutation	SNP	G	A	112	420	c.2729C>T	c.(2728-2730)TCC>TTC	p.S910F
Pat_14	Pre-Treatment	BCMO1	53630	37	16	81279203	81279203	Missense_Mutation	SNP	G	A	35	171	c.188G>A	c.(187-189)AGA>AAA	p.R63K
Pat_14	Pre-Treatment	OSGIN1	29948	37	16	83999411	83999411	Missense_Mutation	SNP	C	G	23	142	c.1482C>G	c.(1480-1482)GAC>GAG	p.D494E
Pat_14	Pre-Treatment	LRRC50	123872	37	16	84189196	84189196	Missense_Mutation	SNP	C	T	126	512	c.583C>T	c.(583-585)CCA>TCA	p.P195S
Pat_14	Pre-Treatment	PELP1	27043	37	17	4576107	4576108	Missense_Mutation	DNP	GG	AA	18	50	.2178_2179CC>T	176-2181)GGCCCT>GGT	p.P727S
Pat_14	Pre-Treatment	PER1	5187	37	17	8052016	8052016	Missense_Mutation	SNP	G	A	163	221	c.994C>T	c.(994-996)CCT>TCT	p.P332S
Pat_14	Pre-Treatment	SPDYE4	388333	37	17	8656483	8656483	Nonsense_Mutation	SNP	C	T	73	113	c.687G>A	c.(685-687)TGG>TGA	p.W229*
Pat_14	Pre-Treatment	MYH4	4622	37	17	10348621	10348622	Missense_Mutation	DNP	CC	TT	214	308	.5227_5228GG>A	c.(5227-5229)GGA>AAA	p.G1743K
Pat_14	Pre-Treatment	MYH4	4622	37	17	10369870	10369870	Missense_Mutation	SNP	C	T	320	384	c.193G>A	c.(193-195)GAA>AAA	p.E65K
Pat_14	Pre-Treatment	DNAH9	1770	37	17	11772556	11772556	Missense_Mutation	SNP	C	T	136	196	c.10039C>T	c.(10039-10041)CTT>TTT	p.L3347F
Pat_14	Pre-Treatment	MAP2K4	6416	37	17	11998935	11998935	Missense_Mutation	SNP	T	C	189	217	c.437T>C	c.(436-438)CTT>CCT	p.L146P
Pat_14	Pre-Treatment	DRG2	1819	37	17	18010522	18010522	Missense_Mutation	SNP	C	T	87	146	c.1063C>T	c.(1063-1065)CAT>TAT	p.H355Y
Pat_14	Pre-Treatment	CCL11	6356	37	17	32612736	32612736	Translation_Start_Site	SNP	A	T	46	35	c.-91A>T	.(-93--89)AAAGG>AATGG	
Pat_14	Pre-Treatment	HNF1B	6928	37	17	36091704	36091704	Missense_Mutation	SNP	G	C	3	265	c.927C>G	c.(925-927)TTC>TTG	p.F309L
Pat_14	Pre-Treatment	WIPF2	147179	37	17	38421101	38421101	Missense_Mutation	SNP	C	T	169	267	c.673C>T	c.(673-675)CCT>TCT	p.P225S

Pat_14	Pre-Treatment	KRTAP4-11	653240	37	17	39274087	39274087	Missense_Mutation	SNP	G	C	3	19	c.481C>G	c.(481-483)CTG>GTG	p.L161V
Pat_14	Pre-Treatment	KRT13	3860	37	17	39659290	39659290	Missense_Mutation	SNP	G	T	8	846	c.796C>A	c.(796-798)CCA>ACA	p.P266T
Pat_14	Pre-Treatment	PRR15L	79170	37	17	46030561	46030561	Missense_Mutation	SNP	G	A	194	261	c.40C>T	c.(40-42)CGG>TGG	p.R14W
Pat_14	Pre-Treatment	CA10	56934	37	17	49713248	49713248	Missense_Mutation	SNP	T	A	105	152	c.757A>T	c.(757-759)ATG>TTG	p.M253L
Pat_14	Pre-Treatment	TMEM49	81671	37	17	57915754	57915754	Missense_Mutation	SNP	C	A	6	170	c.1073C>A	c.(1072-1074)CCA>CAA	p.P358Q
Pat_14	Pre-Treatment	ACE	1636	37	17	61566036	61566036	Missense_Mutation	SNP	G	A	5	363	c.2333G>A	c.(2332-2334)CGG>CAG	p.R778Q
Pat_14	Pre-Treatment	KCNH6	81033	37	17	61619707	61619707	Missense_Mutation	SNP	G	T	7	389	c.2060G>T	c.(2059-2061)CGG>CTG	p.R687L
Pat_14	Pre-Treatment	ABCA10	10349	37	17	67150435	67150435	Missense_Mutation	SNP	C	T	72	343	c.3727G>A	c.(3727-3729)GCT>ACT	p.A1243T
Pat_14	Pre-Treatment	CDC42EP4	23580	37	17	71282170	71282170	Missense_Mutation	SNP	G	A	5	174	c.470C>T	c.(469-471)GCG>GTG	p.A157V
Pat_14	Pre-Treatment	NAT9	26151	37	17	72769065	72769065	Missense_Mutation	SNP	T	G	3	231	c.304A>C	c.(304-306)ACC>CCC	p.T102P
Pat_14	Pre-Treatment	AZI1	22994	37	17	79180631	79180631	Missense_Mutation	SNP	C	T	5	294	c.428G>A	c.(427-429)CGG>CAG	p.R143Q
Pat_14	Pre-Treatment	TGIF1	7050	37	18	3457741	3457741	Missense_Mutation	SNP	T	C	98	231	c.1009T>C	c.(1009-1011)TTC>CTC	p.F337L
Pat_14	Pre-Treatment	APCDD1	147495	37	18	10471774	10471774	Missense_Mutation	SNP	G	A	4	184	c.490G>A	c.(490-492)GGC>AGC	p.G164S
Pat_14	Pre-Treatment	ZNF532	55205	37	18	56601744	56601744	Missense_Mutation	SNP	C	T	138	400	c.2426C>T	c.(2425-2427)TCT>TTT	p.S809F
Pat_14	Pre-Treatment	MC4R	4160	37	18	58039374	58039374	Missense_Mutation	SNP	G	A	75	135	c.209C>T	c.(208-210)GCC>GTC	p.A70V
Pat_14	Pre-Treatment	SERPINB2	5055	37	18	61570201	61570201	Missense_Mutation	SNP	G	A	49	93	c.910G>A	c.(910-912)GAA>AAA	p.E304K
Pat_14	Pre-Treatment	KCNG2	26251	37	18	77659043	77659043	Nonsense_Mutation	SNP	G	T	4	95	c.628G>T	c.(628-630)GAG>TAG	p.E210*
Pat_14	Pre-Treatment	WDR18	57418	37	19	990886	990886	Missense_Mutation	SNP	C	T	43	154	c.632C>T	c.(631-633)TCC>TTC	p.S211F
Pat_14	Pre-Treatment	MIDN	90007	37	19	1257216	1257216	Missense_Mutation	SNP	C	T	50	208	c.1352C>T	c.(1351-1353)TCC>TTC	p.S451F
Pat_14	Pre-Treatment	ADAT3	113179	37	19	1912950	1912950	Missense_Mutation	SNP	G	A	6	363	c.856G>A	c.(856-858)GTG>ATG	p.V286M
Pat_14	Pre-Treatment	MLLT1	4298	37	19	6213774	6213774	Missense_Mutation	SNP	T	C	81	384	c.1442A>G	c.(1441-1443)AAG>AGG	p.K481R
Pat_14	Pre-Treatment	SH2D3A	10045	37	19	6755140	6755140	Missense_Mutation	SNP	G	A	7	738	c.683C>T	c.(682-684)CCC>CTC	p.P228L
Pat_14	Pre-Treatment	CD320	51293	37	19	8367766	8367767	Missense_Mutation	DNP	GC	AA	45	126	c.600_601GC>TT	598-603)GGGCCC>GGTT	p.P201S
Pat_14	Pre-Treatment	MUC16	94025	37	19	9047354	9047354	Missense_Mutation	SNP	G	T	79	332	c.34277C>A	c.(34276-34278)TCT>TAT	p.S11426Y
Pat_14	Pre-Treatment	MUC16	94025	37	19	9061335	9061335	Missense_Mutation	SNP	G	A	37	136	c.26111C>T	c.(26110-26112)TCC>TTC	p.S8704F
Pat_14	Pre-Treatment	MUC16	94025	37	19	9062852	9062852	Missense_Mutation	SNP	C	A	40	168	c.24594G>T	c.(24592-24594)ATG>ATT	p.M8198I
Pat_14	Pre-Treatment	MUC16	94025	37	19	9063976	9063976	Missense_Mutation	SNP	C	T	66	226	c.23470G>A	c.(23470-23472)GAG>AAG	p.E7824K
Pat_14	Pre-Treatment	MUC16	94025	37	19	9083554	9083554	Missense_Mutation	SNP	C	T	94	291	c.8261G>A	c.(8260-8262)GGA>GAA	p.G2754E
Pat_14	Pre-Treatment	OR7D4	125958	37	19	9324939	9324939	Missense_Mutation	SNP	G	A	84	389	c.575C>T	c.(574-576)ACC>ATC	p.T192I
Pat_14	Pre-Treatment	TYK2	7297	37	19	10479071	10479071	Missense_Mutation	SNP	G	A	86	240	c.217C>T	c.(217-219)CTC>TTC	p.L73F
Pat_14	Pre-Treatment	CCDC151	115948	37	19	11537729	11537729	Missense_Mutation	SNP	C	T	64	169	c.576G>A	c.(574-576)ATG>ATA	p.M192I
Pat_14	Pre-Treatment	ZNF823	55552	37	19	11833661	11833661	Missense_Mutation	SNP	G	A	74	422	c.688C>T	c.(688-690)CCT>TCT	p.P230S
Pat_14	Pre-Treatment	CACNA1A	773	37	19	13397485	13397485	Missense_Mutation	SNP	C	T	34	102	c.3388G>A	c.(3388-3390)GGG>AGG	p.G1130R
Pat_14	Pre-Treatment	CACNA1A	773	37	19	13419021	13419021	Missense_Mutation	SNP	G	A	27	77	c.1829C>T	c.(1828-1830)TCC>TTC	p.S610F
Pat_14	Pre-Treatment	OR1I1	126370	37	19	15198581	15198581	Nonsense_Mutation	SNP	G	A	34	157	c.705G>A	c.(703-705)TGG>TGA	p.W235*
Pat_14	Pre-Treatment	CYP4F3	4051	37	19	15760899	15760899	Missense_Mutation	SNP	G	A	105	346	c.824G>A	c.(823-825)CGC>CAC	p.R275H
Pat_14	Pre-Treatment	OR10H3	26532	37	19	15852299	15852299	Missense_Mutation	SNP	C	T	152	624	c.97C>T	c.(97-99)CTC>TTC	p.L33F
Pat_14	Pre-Treatment	C19orf42	79086	37	19	16770257	16770257	Missense_Mutation	SNP	T	C	14	60	c.70A>G	c.(70-72)AAA>GAA	p.K24E
Pat_14	Pre-Treatment	CPAMD8	27151	37	19	17100494	17100494	Nonsense_Mutation	SNP	G	A	59	299	c.1495C>T	c.(1495-1497)CAG>TAG	p.Q499*
Pat_14	Pre-Treatment	USHBP1	83878	37	19	17373526	17373527	Missense_Mutation	DNP	GG	AA	63	199	c.476_477CC>TT	c.(475-477)TCC>TTT	p.S159F
Pat_14	Pre-Treatment	BST2	684	37	19	17516235	17516235	Missense_Mutation	SNP	G	T	5	222	c.150C>A	c.(148-150)AGC>AGA	p.S50R
Pat_14	Pre-Treatment	ZNF493	284443	37	19	21606030	21606030	Missense_Mutation	SNP	C	T	73	220	c.185C>T	c.(184-186)TCA>TTA	p.S62L
Pat_14	Pre-Treatment	ZNF493	284443	37	19	21606468	21606468	Missense_Mutation	SNP	C	T	4	198	c.623C>T	c.(622-624)CCT>CTT	p.P208L
Pat_14	Pre-Treatment	ZNF257	113835	37	19	22255698	22255698	Missense_Mutation	SNP	G	A	87	384	c.91G>A	c.(91-93)GAT>AAT	p.D31N
Pat_14	Pre-Treatment	ZNF676	163223	37	19	22363786	22363786	Missense_Mutation	SNP	T	C	4	263	c.733A>G	c.(733-735)ATA>GTA	p.I245V
Pat_14	Pre-Treatment	ZNF254	9534	37	19	24310427	24310427	Missense_Mutation	SNP	A	G	4	88	c.1625A>G	c.(1624-1626)GAA>GGA	p.E542G
Pat_14	Pre-Treatment	ZNF254	9534	37	19	24310450	24310450	Missense_Mutation	SNP	A	G	4	85	c.1648A>G	c.(1648-1650)AAA>GAA	p.K550E

Pat_14	Pre-Treatment	CCDC123	84902	37	19	33417101	33417101	Missense_Mutation	SNP	G	T	7	776	c.1159C>A	c.(1159-1161)CTC>ATC	p.L387I
Pat_14	Pre-Treatment	SBSN	374897	37	19	36018946	36018947	Missense_Mutation	DNP	CG	AT	6	661	c.237_238CG>AT	235-240)ACCGGC>ACAT	p.G80C
Pat_14	Pre-Treatment	MLL4	9757	37	19	36210698	36210698	Missense_Mutation	SNP	G	A	110	504	c.449G>A	c.(448-450)CGA>CAA	p.R150Q
Pat_14	Pre-Treatment	MLL4	9757	37	19	36211733	36211733	Missense_Mutation	SNP	C	T	3	27	c.1484C>T	c.(1483-1485)CCC>CTC	p.P495L
Pat_14	Pre-Treatment	ZNF790	388536	37	19	37310689	37310689	Missense_Mutation	SNP	G	C	37	178	c.557C>G	c.(556-558)ACT>AGT	p.T186S
Pat_14	Pre-Treatment	ZFP30	22835	37	19	38127104	38127104	Missense_Mutation	SNP	C	T	32	121	c.338G>A	c.(337-339)GGA>GAA	p.G113E
Pat_14	Pre-Treatment	RYR1	6261	37	19	38943640	38943640	Missense_Mutation	SNP	C	A	4	115	c.1426C>A	c.(1426-1428)CTC>ATC	p.L476I
Pat_14	Pre-Treatment	MAP4K1	11184	37	19	39100292	39100292	Missense_Mutation	SNP	C	T	33	99	c.950G>A	c.(949-951)CGG>CAG	p.R317Q
Pat_14	Pre-Treatment	CLC	1178	37	19	40222064	40222064	Missense_Mutation	SNP	C	T	187	611	c.385G>A	c.(385-387)GAT>AAT	p.D129N
Pat_14	Pre-Treatment	PRX	57716	37	19	40902350	40902350	Missense_Mutation	SNP	G	A	105	423	c.1909C>T	c.(1909-1911)CCT>TCT	p.P637S
Pat_14	Pre-Treatment	ADCK4	79934	37	19	41220022	41220022	Missense_Mutation	SNP	C	A	7	433	c.239G>T	c.(238-240)CGA>CTA	p.R80L
Pat_14	Pre-Treatment	CEACAM6	4680	37	19	42265289	42265289	Missense_Mutation	SNP	C	A	136	599	c.557C>A	c.(556-558)CCG>CAG	p.P186Q
Pat_14	Pre-Treatment	GRIK5	2901	37	19	42546734	42546734	Nonsense_Mutation	SNP	C	T	109	333	c.1443G>A	c.(1441-1443)TGG>TGA	p.W481*
Pat_14	Pre-Treatment	ZNF235	9310	37	19	44792651	44792651	Missense_Mutation	SNP	G	A	90	288	c.937C>T	c.(937-939)CGT>TGT	p.R313C
Pat_14	Pre-Treatment	GLTSCR2	29997	37	19	48253489	48253489	Missense_Mutation	SNP	C	T	35	182	c.344C>T	c.(343-345)CCC>CTC	p.P115L
Pat_14	Pre-Treatment	RPL18	6141	37	19	49120056	49120056	Missense_Mutation	SNP	C	A	6	431	c.224G>T	c.(223-225)CGG>CTG	p.R75L
Pat_14	Pre-Treatment	SIGLEC12	89858	37	19	52003546	52003546	Missense_Mutation	SNP	C	T	59	283	c.436G>A	c.(436-438)GAC>AAC	p.D146N
Pat_14	Pre-Treatment	ZNF845	91664	37	19	53856479	53856479	Missense_Mutation	SNP	G	A	24	157	c.2551G>A	c.(2551-2553)GCA>ACA	p.A851T
Pat_14	Pre-Treatment	ZNF845	91664	37	19	53856702	53856702	Missense_Mutation	SNP	G	A	5	113	c.2774G>A	c.(2773-2775)CGT>CAT	p.R925H
Pat_14	Pre-Treatment	LILRB3	11025	37	19	54722249	54722249	Missense_Mutation	SNP	C	A	10	484	c.1574G>T	c.(1573-1575)AGG>ATG	p.R525M
Pat_14	Pre-Treatment	LILRB4	11006	37	19	55175850	55175850	Missense_Mutation	SNP	G	A	91	318	c.569G>A	c.(568-570)GGG>GAG	p.G190E
Pat_14	Pre-Treatment	KIR3DL1	3811	37	19	55333028	55333028	Missense_Mutation	SNP	G	A	89	367	c.664G>A	c.(664-666)GAG>AAG	p.E222K
Pat_14	Pre-Treatment	NLRP9	338321	37	19	56243555	56243555	Missense_Mutation	SNP	C	T	38	168	c.1642G>A	c.(1642-1644)GGT>AGT	p.G548S
Pat_14	Pre-Treatment	PEG3	5178	37	19	57335765	57335765	Missense_Mutation	SNP	C	T	6	462	c.259G>A	c.(259-261)GAG>AAG	p.E87K
Pat_14	Pre-Treatment	ZIM3	114026	37	19	57646558	57646558	Missense_Mutation	SNP	T	C	70	276	c.1147A>G	c.(1147-1149)AAA>GAA	p.K383E
Pat_14	Pre-Treatment	ZNF776	284309	37	19	58264977	58264977	Nonsense_Mutation	SNP	C	A	6	297	c.479C>A	c.(478-480)TCA>TAA	p.S160*
Pat_14	Pre-Treatment	ZNF417	147687	37	19	58420829	58420829	Missense_Mutation	SNP	A	C	7	385	c.817T>G	c.(817-819)TGT>GGT	p.C273G
Pat_14	Pre-Treatment	ZNF418	147686	37	19	58437669	58437669	Missense_Mutation	SNP	G	T	91	320	c.1880C>A	c.(1879-1881)TCC>TAC	p.S627Y
Pat_14	Pre-Treatment	ZNF135	7694	37	19	58579005	58579005	Missense_Mutation	SNP	C	A	6	213	c.1189C>A	c.(1189-1191)CAT>AAT	p.H397N
Pat_14	Pre-Treatment	PXDN	7837	37	2	1653202	1653202	Missense_Mutation	SNP	G	A	70	306	c.2350C>T	c.(2350-2352)CAC>TAC	p.H784Y
Pat_14	Pre-Treatment	MYT1L	23040	37	2	1906950	1906950	Missense_Mutation	SNP	G	A	76	240	c.1934C>T	c.(1933-1935)TCG>TTG	p.S645L
Pat_14	Pre-Treatment	MYT1L	23040	37	2	1926607	1926608	Missense_Mutation	DNP	CC	TT	111	369	c.933_934GG>AA	(931-936)ATGGAA>ATAA	.311_312ME>I
Pat_14	Pre-Treatment	KLF11	8462	37	2	10188198	10188198	Missense_Mutation	SNP	A	G	3	307	c.734A>G	c.(733-735)GAC>GGC	p.D245G
Pat_14	Pre-Treatment	NBAS	51594	37	2	15319125	15319125	Missense_Mutation	SNP	G	A	57	259	c.6827C>T	c.(6826-6828)ACG>ATG	p.T2276M
Pat_14	Pre-Treatment	RHOQ	23433	37	2	46803262	46803262	Missense_Mutation	SNP	A	G	3	148	c.238A>G	c.(238-240)ATG>GTG	p.M80V
Pat_14	Pre-Treatment	PSME4	23198	37	2	54114545	54114545	Missense_Mutation	SNP	G	A	55	217	c.4580C>T	c.(4579-4581)TCG>TTG	p.S1527L
Pat_14	Pre-Treatment	PUS10	150962	37	2	61236080	61236080	Missense_Mutation	SNP	G	A	4	81	c.197C>T	c.(196-198)CCA>CTA	p.P66L
Pat_14	Pre-Treatment	GKN1	56287	37	2	69207165	69207165	Missense_Mutation	SNP	C	T	96	279	c.478C>T	c.(478-480)CCA>TCA	p.P160S
Pat_14	Pre-Treatment	CNGA3	1261	37	2	98994194	98994194	Missense_Mutation	SNP	G	A	18	117	c.146G>A	c.(145-147)GGG>GAG	p.G49E
Pat_14	Pre-Treatment	C2orf55	343990	37	2	99439615	99439615	Missense_Mutation	SNP	T	A	22	56	c.1121A>T	c.(1120-1122)GAG>GTG	p.E374V
Pat_14	Pre-Treatment	TBC1D8	11138	37	2	101650036	101650037	Missense_Mutation	DNP	GG	AA	69	252	.1742_1743CC>T	c.(1741-1743)GCC>GTT	p.A581V
Pat_14	Pre-Treatment	RGPD4	285190	37	2	108496501	108496501	Missense_Mutation	SNP	C	T	118	480	c.5002C>T	c.(5002-5004)CAC>TAC	p.H1668Y
Pat_14	Pre-Treatment	SLC5A7	60482	37	2	108627121	108627121	Missense_Mutation	SNP	C	T	35	157	c.1547C>T	c.(1546-1548)GCT>GTT	p.A516V
Pat_14	Pre-Treatment	PCDP1	200373	37	2	120409605	120409605	Missense_Mutation	SNP	G	A	56	234	c.1516G>A	c.(1516-1518)GAA>AAA	p.E506K
Pat_14	Pre-Treatment	CNTNAP5	129684	37	2	124979360	124979360	Missense_Mutation	SNP	G	A	17	81	c.161G>A	c.(160-162)AGC>AAC	p.S54N
Pat_14	Pre-Treatment	CNTNAP5	129684	37	2	125367477	125367477	Missense_Mutation	SNP	A	C	57	264	c.1853A>C	c.(1852-1854)CAG>CCG	p.Q618P
Pat_14	Pre-Treatment	HS6ST1	9394	37	2	129026421	129026421	Missense_Mutation	SNP	A	G	4	276	c.551T>C	c.(550-552)CTA>CCA	p.L184P

Pat_14	Pre-Treatment	IMP4	92856	37	2	131103457	131103457	Missense_Mutation	SNP	C	T	22	135	c.545C>T	c.(544-546)GCC>GTC	p.A182V
Pat_14	Pre-Treatment	LOC401010	401010	37	2	132201466	132201466	Missense_Mutation	SNP	G	A	63	196	c.536C>T	c.(535-537)CCC>CTC	p.P179L
Pat_14	Pre-Treatment	NCKAP5	344148	37	2	133541688	133541688	Missense_Mutation	SNP	G	A	46	308	c.2696C>T	c.(2695-2697)CCT>CTT	p.P899L
Pat_14	Pre-Treatment	THSD7B	80731	37	2	137814118	137814118	Missense_Mutation	SNP	G	A	17	85	c.175G>A	c.(175-177)GAA>AAA	p.E59K
Pat_14	Pre-Treatment	THSD7B	80731	37	2	137814551	137814551	Missense_Mutation	SNP	T	G	122	441	c.608T>G	c.(607-609)CTT>CGT	p.L203R
Pat_14	Pre-Treatment	THSD7B	80731	37	2	138420994	138420994	Missense_Mutation	SNP	G	A	6	29	c.4413G>A	c.(4411-4413)ATG>ATA	p.M1471I
Pat_14	Pre-Treatment	LRP1B	53353	37	2	141122229	141122229	Splice_Site	SNP	C	T	25	97	c.11131_splice	c.e72+1	p.V3711_splice
Pat_14	Pre-Treatment	LRP1B	53353	37	2	141259366	141259366	Missense_Mutation	SNP	C	T	37	161	c.8740G>A	c.(8740-8742)GAT>AAT	p.D2914N
Pat_14	Pre-Treatment	LRP1B	53353	37	2	141946145	141946145	Missense_Mutation	SNP	T	G	78	199	c.858A>C	c.(856-858)CAA>CAC	p.Q286H
Pat_14	Pre-Treatment	KYNU	8942	37	2	143743562	143743562	Missense_Mutation	SNP	G	A	61	208	c.874G>A	c.(874-876)GAA>AAA	p.E292K
Pat_14	Pre-Treatment	NEB	4703	37	2	152473940	152473940	Missense_Mutation	SNP	G	A	4	36	c.10390C>T	c.(10390-10392)CAT>TAT	p.H3464Y
Pat_14	Pre-Treatment	FMNL2	114793	37	2	153435429	153435429	Missense_Mutation	SNP	C	T	24	141	c.733C>T	c.(733-735)CCA>TCA	p.P245S
Pat_14	Pre-Treatment	KCNJ3	3760	37	2	155711613	155711613	Missense_Mutation	SNP	G	A	39	170	c.1294G>A	c.(1294-1296)GAC>AAC	p.D432N
Pat_14	Pre-Treatment	UPP2	151531	37	2	158974352	158974352	Missense_Mutation	SNP	C	T	82	314	c.356C>T	c.(355-357)CCC>CTC	p.P119L
Pat_14	Pre-Treatment	SLC4A10	57282	37	2	162738887	162738887	Missense_Mutation	SNP	G	A	15	56	c.1127G>A	c.(1126-1128)GGA>GAA	p.G376E
Pat_14	Pre-Treatment	KCNH7	90134	37	2	163291770	163291770	Missense_Mutation	SNP	C	T	57	251	c.1892G>A	c.(1891-1893)GGG>GAG	p.G631E
Pat_14	Pre-Treatment	COBLL1	22837	37	2	165542499	165542499	Missense_Mutation	SNP	C	T	58	227	c.3659G>A	c.(3658-3660)AGA>AAA	p.R1220K
Pat_14	Pre-Treatment	SCN3A	6328	37	2	165947616	165947616	Missense_Mutation	SNP	C	T	101	310	c.5047G>A	c.(5047-5049)GAA>AAA	p.E1683K
Pat_14	Pre-Treatment	SCN2A	6326	37	2	166167031	166167031	Missense_Mutation	SNP	C	T	50	200	c.896C>T	c.(895-897)TCA>TTA	p.S299L
Pat_14	Pre-Treatment	SCN9A	6335	37	2	167160796	167160796	Nonsense_Mutation	SNP	G	A	24	96	c.640C>T	c.(640-642)CGA>TGA	p.R214*
Pat_14	Pre-Treatment	LRP2	4036	37	2	170103911	170103911	Missense_Mutation	SNP	G	A	60	239	c.2885C>T	c.(2884-2886)TCG>TTG	p.S962L
Pat_14	Pre-Treatment	TTN	7273	37	2	179496982	179496982	Missense_Mutation	SNP	C	T	15	46	c.35935G>A	c.(35935-35937)GAA>AAA	p.E11979K
Pat_14	Pre-Treatment	TTN	7273	37	2	179594264	179594264	Missense_Mutation	SNP	G	A	53	214	c.14887C>T	c.(14887-14889)CCT>TCT	p.P4963S
Pat_14	Pre-Treatment	TTN	7273	37	2	179595259	179595259	Missense_Mutation	SNP	G	T	9	657	c.14269C>A	c.(14269-14271)CAA>AAA	p.Q4757K
Pat_14	Pre-Treatment	TTN	7273	37	2	179597833	179597833	Missense_Mutation	SNP	G	A	22	95	c.12338C>T	c.(12337-12339)CCA>CTA	p.P4113L
Pat_14	Pre-Treatment	TTN	7273	37	2	179612065	179612065	Missense_Mutation	SNP	C	T	40	206	c.15062G>A	c.(15061-15063)GGA>GAA	p.G5021E
Pat_14	Pre-Treatment	TTN	7273	37	2	179615447	179615447	Missense_Mutation	SNP	C	T	20	73	c.11680G>A	c.(11680-11682)GAA>AAA	p.E3894K
Pat_14	Pre-Treatment	TTN	7273	37	2	179616446	179616446	Missense_Mutation	SNP	G	A	76	218	c.10681C>T	c.(10681-10683)CAC>TAC	p.H3561Y
Pat_14	Pre-Treatment	TTN	7273	37	2	179641217	179641217	Missense_Mutation	SNP	G	A	73	295	c.5374C>T	c.(5374-5376)CTT>TTT	p.L1792F
Pat_14	Pre-Treatment	WDR75	84128	37	2	190329839	190329839	Missense_Mutation	SNP	A	T	4	153	c.1148A>T	c.(1147-1149)TAT>TTT	p.Y383F
Pat_14	Pre-Treatment	OBFC2A	64859	37	2	192550343	192550343	Missense_Mutation	SNP	G	A	6	38	c.464G>A	c.(463-465)GGC>GAC	p.G155D
Pat_14	Pre-Treatment	DNAH7	56171	37	2	196723344	196723344	Missense_Mutation	SNP	C	T	23	99	c.7921G>A	c.(7921-7923)GAA>AAA	p.E2641K
Pat_14	Pre-Treatment	DNAH7	56171	37	2	196884016	196884016	Missense_Mutation	SNP	C	T	40	153	c.747G>A	c.(745-747)ATG>ATA	p.M249I
Pat_14	Pre-Treatment	PGAP1	80055	37	2	197791194	197791194	Missense_Mutation	SNP	C	A	7	773	c.147G>T	c.(145-147)CAG>CAT	p.Q49H
Pat_14	Pre-Treatment	NBEAL1	65065	37	2	204045126	204045126	Missense_Mutation	SNP	G	T	85	373	c.6399G>T	c.(6397-6399)CAG>CAT	p.Q2133H
Pat_14	Pre-Treatment	ZDBF2	57683	37	2	207170939	207170939	Missense_Mutation	SNP	C	T	18	78	c.1687C>T	c.(1687-1689)CGG>TGG	p.R563W
Pat_14	Pre-Treatment	C2orf80	389073	37	2	209036721	209036721	Missense_Mutation	SNP	G	T	11	816	c.445C>A	c.(445-447)CGC>AGC	p.R149S
Pat_14	Pre-Treatment	ERBB4	2066	37	2	212295699	212295699	Missense_Mutation	SNP	C	T	92	333	c.2614G>A	c.(2614-2616)GAA>AAA	p.E872K
Pat_14	Pre-Treatment	TNS1	7145	37	2	218712377	218712377	Missense_Mutation	SNP	G	A	49	147	c.2488C>T	c.(2488-2490)CCA>TCA	p.P830S
Pat_14	Pre-Treatment	TNS1	7145	37	2	218745694	218745694	Nonsense_Mutation	SNP	A	C	59	200	c.981T>G	c.(979-981)TAT>TAG	p.Y327*
Pat_14	Pre-Treatment	GLB1L	79411	37	2	220102571	220102571	Missense_Mutation	SNP	C	T	53	275	c.1450G>A	c.(1450-1452)GGG>AGG	p.G484R
Pat_14	Pre-Treatment	GMPPA	29926	37	2	220366237	220366237	Missense_Mutation	SNP	C	A	7	667	c.178C>A	c.(178-180)CAA>AAA	p.Q60K
Pat_14	Pre-Treatment	ACCN4	55515	37	2	220400018	220400018	Nonsense_Mutation	SNP	A	T	10	70	c.1525A>T	c.(1525-1527)AAG>TAG	p.K509*
Pat_14	Pre-Treatment	SPHKAP	80309	37	2	228881246	228881246	Missense_Mutation	SNP	C	T	28	133	c.4324G>A	c.(4324-4326)GAA>AAA	p.E1442K
Pat_14	Pre-Treatment	GPR55	9290	37	2	231775425	231775425	Nonsense_Mutation	SNP	G	A	55	228	c.253C>T	c.(253-255)CAG>TAG	p.Q85*
Pat_14	Pre-Treatment	INPP5D	3635	37	2	233995276	233995276	Missense_Mutation	SNP	G	A	40	91	c.583G>A	c.(583-585)GAC>AAC	p.D195N
Pat_14	Pre-Treatment	DEFB125	245938	37	20	76774	76774	Missense_Mutation	SNP	G	A	135	646	c.187G>A	c.(187-189)GAA>AAA	p.E63K

Pat_14	Pre-Treatment	C20orf27	54976	37	20	3734734	3734734	Missense_Mutation	SNP	C	T	46	74	c.496G>A	c.(496-498)GAG>AAG	p.E166K
Pat_14	Pre-Treatment	SMOX	54498	37	20	4155742	4155742	Missense_Mutation	SNP	C	A	7	694	c.40C>A	c.(40-42)CCT>ACT	p.P14T
Pat_14	Pre-Treatment	PAK7	57144	37	20	9546769	9546769	Missense_Mutation	SNP	G	A	24	89	c.1253C>T	c.(1252-1254)TCC>TTC	p.S418F
Pat_14	Pre-Treatment	SSTR4	6754	37	20	23016400	23016400	Missense_Mutation	SNP	G	A	125	456	c.280G>A	c.(280-282)GAG>AAG	p.E94K
Pat_14	Pre-Treatment	FRG1B	284802	37	20	29625877	29625877	Missense_Mutation	SNP	G	A	7	274	c.31G>A	c.(31-33)GCC>ACC	p.A11T
Pat_14	Pre-Treatment	COMMD7	149951	37	20	31294383	31294383	Splice_Site	SNP	A	G	3	154	c.336_splice	c.e5+1	p.K112_splice
Pat_14	Pre-Treatment	MYH7B	57644	37	20	33586662	33586662	Nonsense_Mutation	SNP	G	A	21	157	c.4260G>A	c.(4258-4260)TGG>TGA	p.W1420*
Pat_14	Pre-Treatment	CHD6	84181	37	20	40054738	40054738	Missense_Mutation	SNP	C	A	9	772	c.4124G>T	c.(4123-4125)CGG>CTG	p.R1375L
Pat_14	Pre-Treatment	PTPRT	11122	37	20	40827982	40827982	Missense_Mutation	SNP	C	T	115	252	c.2389G>A	c.(2389-2391)GAG>AAG	p.E797K
Pat_14	Pre-Treatment	MYBL2	4605	37	20	42344630	42344630	Missense_Mutation	SNP	G	A	222	436	c.2006G>A	c.(2005-2007)GGG>GAG	p.G669E
Pat_14	Pre-Treatment	TOX2	84969	37	20	42635208	42635208	Missense_Mutation	SNP	A	T	180	295	c.214A>T	c.(214-216)AAC>TAC	p.N72Y
Pat_14	Pre-Treatment	SEMG1	6406	37	20	43836308	43836308	Missense_Mutation	SNP	C	T	57	357	c.370C>T	c.(370-372)CAC>TAC	p.H124Y
Pat_14	Pre-Treatment	SDC4	6385	37	20	43959102	43959102	Missense_Mutation	SNP	A	G	112	177	c.349T>C	c.(349-351)TCA>CCA	p.S117P
Pat_14	Pre-Treatment	SLC9A8	23315	37	20	48491319	48491319	Missense_Mutation	SNP	C	T	253	480	c.1036C>T	c.(1036-1038)CTC>TTC	p.L346F
Pat_14	Pre-Treatment	CASS4	57091	37	20	55028094	55028094	Missense_Mutation	SNP	C	T	40	160	c.1862C>T	c.(1861-1863)TCA>TTA	p.S621L
Pat_14	Pre-Treatment	TAF4	6874	37	20	60578276	60578276	Nonsense_Mutation	SNP	G	T	6	548	c.2426C>A	c.(2425-2427)TCG>TAG	p.S809*
Pat_14	Pre-Treatment	OSBPL2	9885	37	20	60866788	60866788	Nonsense_Mutation	SNP	G	T	81	454	c.1279G>T	c.(1279-1281)GAG>TAG	p.E427*
Pat_14	Pre-Treatment	EEF1A2	1917	37	20	62121835	62121836	Missense_Mutation	DNP	GG	AA	41	74	.1025_1026CC>T	c.(1024-1026)TCC>TTT	p.S342F
Pat_14	Pre-Treatment	SRMS	6725	37	20	62174747	62174747	Missense_Mutation	SNP	C	T	5	402	c.565G>A	c.(565-567)GGC>AGC	p.G189S
Pat_14	Pre-Treatment	TPTE	7179	37	21	10914373	10914373	Missense_Mutation	SNP	C	T	24	121	c.1346G>A	c.(1345-1347)GGA>GAA	p.G449E
Pat_14	Pre-Treatment	POTED	317754	37	21	14983006	14983006	Missense_Mutation	SNP	C	T	12	153	c.457C>T	c.(457-459)CCC>TCC	p.P153S
Pat_14	Pre-Treatment	USP25	29761	37	21	17236609	17236609	Missense_Mutation	SNP	G	A	4	283	c.2360G>A	c.(2359-2361)AGG>AAG	p.R787K
Pat_14	Pre-Treatment	CYYR1	116159	37	21	27840893	27840893	Missense_Mutation	SNP	G	A	70	243	c.392C>T	c.(391-393)CCA>CTA	p.P131L
Pat_14	Pre-Treatment	GRIK1	2897	37	21	30968846	30968846	Missense_Mutation	SNP	C	A	86	396	c.1251G>T	c.(1249-1251)AAG>AAT	p.K417N
Pat_14	Pre-Treatment	KCNE2	9992	37	21	35742905	35742905	Missense_Mutation	SNP	C	T	56	218	c.128C>T	c.(127-129)GCT>GTT	p.A43V
Pat_14	Pre-Treatment	CHAF1B	8208	37	21	37785564	37785564	Missense_Mutation	SNP	C	T	4	215	c.1444C>T	c.(1444-1446)CGG>TGG	p.R482W
Pat_14	Pre-Treatment	TFF1	7031	37	21	43783391	43783391	Missense_Mutation	SNP	G	A	51	134	c.211C>T	c.(211-213)CCT>TCT	p.P71S
Pat_14	Pre-Treatment	RSPH1	89765	37	21	43913099	43913099	Missense_Mutation	SNP	C	T	169	604	c.145G>A	c.(145-147)GAA>AAA	p.E49K
Pat_14	Pre-Treatment	KRTAP10-7	386675	37	21	46020592	46020592	Missense_Mutation	SNP	C	T	47	143	c.71C>T	c.(70-72)TCC>TTC	p.S24F
Pat_14	Pre-Treatment	KRTAP10-12	386685	37	21	46117718	46117718	Missense_Mutation	SNP	C	A	9	672	c.602C>A	c.(601-603)CCT>CAT	p.P201H
Pat_14	Pre-Treatment	PCNT	5116	37	21	47754654	47754654	Missense_Mutation	SNP	C	A	8	599	c.611C>A	c.(610-612)CCA>CAA	p.P204Q
Pat_14	Pre-Treatment	SLC25A1	6576	37	22	19164124	19164124	Missense_Mutation	SNP	G	T	4	251	c.714C>A	c.(712-714)AAC>AAA	p.N238K
Pat_14	Pre-Treatment	CCDC116	164592	37	22	21991067	21991067	Missense_Mutation	SNP	C	T	81	93	c.1550C>T	c.(1549-1551)TCC>TTC	p.S517F
Pat_14	Pre-Treatment	HPS4	89781	37	22	26864540	26864540	Missense_Mutation	SNP	G	A	105	120	c.646C>T	c.(646-648)CAC>TAC	p.H216Y
Pat_14	Pre-Treatment	NEFH	4744	37	22	29885739	29885739	Missense_Mutation	SNP	T	A	6	299	c.2110T>A	c.(2110-2112)TCC>ACC	p.S704T
Pat_14	Pre-Treatment	MYH9	4627	37	22	36697687	36697687	Missense_Mutation	SNP	G	A	74	91	c.2524C>T	c.(2524-2526)CGG>TGG	p.R842W
Pat_14	Pre-Treatment	TMPRSS6	164656	37	22	37482392	37482392	Missense_Mutation	SNP	C	T	32	43	c.931G>A	c.(931-933)GTC>ATC	p.V311I
Pat_14	Pre-Treatment	PICK1	9463	37	22	38461035	38461035	Missense_Mutation	SNP	G	T	8	551	c.180G>T	c.(178-180)TTG>TTT	p.L60F
Pat_14	Pre-Treatment	DDX17	10521	37	22	38882109	38882109	Missense_Mutation	SNP	C	A	5	313	c.2027G>T	c.(2026-2028)AGC>ATC	p.S676I
Pat_14	Pre-Treatment	GRAP2	9402	37	22	40356161	40356161	Missense_Mutation	SNP	C	A	238	272	c.273C>A	c.(271-273)GAC>GAA	p.D91E
Pat_14	Pre-Treatment	TTLL12	23170	37	22	43579143	43579143	Missense_Mutation	SNP	C	A	6	470	c.190G>T	c.(190-192)GGG>TGG	p.G64W
Pat_14	Pre-Treatment	PLXNB2	23654	37	22	50720285	50720285	Missense_Mutation	SNP	G	A	4	224	c.3343C>T	c.(3343-3345)CGG>TGG	p.R1115W
Pat_14	Pre-Treatment	CNTN6	27255	37	3	1424632	1424632	Missense_Mutation	SNP	C	T	64	229	c.2173C>T	c.(2173-2175)CCA>TCA	p.P725S
Pat_14	Pre-Treatment	CNTN4	152330	37	3	3097837	3097837	Missense_Mutation	SNP	C	T	69	300	c.3014C>T	c.(3013-3015)TCG>TTG	p.S1005L
Pat_14	Pre-Treatment	ITPR1	3708	37	3	4808220	4808220	Missense_Mutation	SNP	T	C	3	214	c.5407T>C	c.(5407-5409)TTT>CTT	p.F1803L
Pat_14	Pre-Treatment	GRIP2	80852	37	3	14552975	14552975	Missense_Mutation	SNP	T	A	36	72	c.2027A>T	c.(2026-2028)AAA>ATA	p.K676I
Pat_14	Pre-Treatment	THRB	7068	37	3	24169132	24169132	Missense_Mutation	SNP	C	T	133	496	c.1002G>A	c.(1000-1002)ATG>ATA	p.M334I

Pat_14	Pre-Treatment	TGFBR2	7048	37	3	30733067	30733067	Missense_Mutation	SNP	C	G	72	248	c.1680C>G	c.(1678-1680)GAC>GAG	p.D560E
Pat_14	Pre-Treatment	GADL1	339896	37	3	30769837	30769837	Missense_Mutation	SNP	C	T	40	162	c.1463G>A	c.(1462-1464)GGA>GAA	p.G488E
Pat_14	Pre-Treatment	ZNF860	344787	37	3	32031383	32031383	Missense_Mutation	SNP	G	A	85	284	c.812G>A	c.(811-813)CGA>CAA	p.R271Q
Pat_14	Pre-Treatment	ARPP21	10777	37	3	35729257	35729257	Missense_Mutation	SNP	T	A	43	214	c.288T>A	c.(286-288)AGT>AGA	p.S96R
Pat_14	Pre-Treatment	TRANK1	9881	37	3	36880179	36880179	Missense_Mutation	SNP	C	G	19	96	c.3527G>C	c.(3526-3528)GGT>GCT	p.G1176A
Pat_14	Pre-Treatment	GOLGA4	2803	37	3	37388719	37388719	Nonsense_Mutation	SNP	G	T	5	407	c.6508G>T	c.(6508-6510)GGA>TGA	p.G2170*
Pat_14	Pre-Treatment	TTC21A	199223	37	3	39151609	39151609	Missense_Mutation	SNP	C	T	49	160	c.247C>T	c.(247-249)CAC>TAC	p.H83Y
Pat_14	Pre-Treatment	TRAK1	22906	37	3	42229637	42229637	Missense_Mutation	SNP	C	A	6	379	c.581C>A	c.(580-582)CCG>CAG	p.P194Q
Pat_14	Pre-Treatment	ZNF167	55888	37	3	44612818	44612818	Missense_Mutation	SNP	G	A	75	213	c.2216G>A	c.(2215-2217)CGA>CAA	p.R739Q
Pat_14	Pre-Treatment	LIMD1	8994	37	3	45637266	45637266	Missense_Mutation	SNP	G	A	4	181	c.895G>A	c.(895-897)GCA>ACA	p.A299T
Pat_14	Pre-Treatment	CCRL2	9034	37	3	46450597	46450597	Missense_Mutation	SNP	G	A	100	296	c.1027G>A	c.(1027-1029)GAA>AAA	p.E343K
Pat_14	Pre-Treatment	ALS2CL	259173	37	3	46712485	46712485	Nonsense_Mutation	SNP	C	A	115	401	c.2851G>T	c.(2851-2853)GAG>TAG	p.E951*
Pat_14	Pre-Treatment	COL7A1	1294	37	3	48618019	48618019	Nonsense_Mutation	SNP	G	A	4	116	c.5047C>T	c.(5047-5049)CGA>TGA	p.R1683*
Pat_14	Pre-Treatment	IMPDH2	3615	37	3	49065338	49065338	Missense_Mutation	SNP	C	A	4	86	c.336G>T	c.(334-336)CAG>CAT	p.Q112H
Pat_14	Pre-Treatment	WNT5A	7474	37	3	55504548	55504548	Missense_Mutation	SNP	T	G	14	38	c.715A>C	c.(715-717)AAG>CAG	p.K239Q
Pat_14	Pre-Treatment	CADPS	8618	37	3	62518660	62518660	Missense_Mutation	SNP	C	T	85	303	c.2177G>A	c.(2176-2178)CGA>CAA	p.R726Q
Pat_14	Pre-Treatment	ADAMTS9	56999	37	3	64592701	64592701	Missense_Mutation	SNP	C	A	24	536	c.3409G>T	c.(3409-3411)GGG>TGG	p.G1137W
Pat_14	Pre-Treatment	TMF1	7110	37	3	69097491	69097491	Missense_Mutation	SNP	G	A	146	616	c.365C>T	c.(364-366)TCA>TTA	p.S122L
Pat_14	Pre-Treatment	LMOD3	56203	37	3	69168038	69168038	Missense_Mutation	SNP	G	C	13	86	c.1468C>G	c.(1468-1470)CTG>GTG	p.L490V
Pat_14	Pre-Treatment	VGLL3	389136	37	3	87017835	87017835	Missense_Mutation	SNP	T	A	21	93	c.842A>T	c.(841-843)AAG>ATG	p.K281M
Pat_14	Pre-Treatment	EPHA6	285220	37	3	96945187	96945187	Missense_Mutation	SNP	G	A	83	336	c.1194G>A	c.(1192-1194)ATG>ATA	p.M398I
Pat_14	Pre-Treatment	CD96	10225	37	3	111298054	111298054	Missense_Mutation	SNP	A	G	67	274	c.772A>G	c.(772-774)AGG>GGG	p.R258G
Pat_14	Pre-Treatment	TAGLN3	29114	37	3	111719719	111719719	Missense_Mutation	SNP	C	T	117	405	c.281C>T	c.(280-282)TCC>TTC	p.S94F
Pat_14	Pre-Treatment	C3orf15	89876	37	3	119449097	119449097	Missense_Mutation	SNP	A	T	83	320	c.891A>T	c.(889-891)AAA>AAT	p.K297N
Pat_14	Pre-Treatment	STXBP5L	9515	37	3	120924797	120924797	Missense_Mutation	SNP	C	T	30	151	c.905C>T	c.(904-906)TCT>TTT	p.S302F
Pat_14	Pre-Treatment	SLC15A2	6565	37	3	121613331	121613331	Missense_Mutation	SNP	C	T	82	260	c.8C>T	c.(7-9)CCT>CTT	p.P3L
Pat_14	Pre-Treatment	CCDC14	64770	37	3	123663780	123663780	Missense_Mutation	SNP	G	A	32	135	c.1403C>T	c.(1402-1404)CCA>CTA	p.P468L
Pat_14	Pre-Treatment	SLC12A8	84561	37	3	124839501	124839501	Missense_Mutation	SNP	C	T	20	87	c.766G>A	c.(766-768)GAC>AAC	p.D256N
Pat_14	Pre-Treatment	EEFSEC	60678	37	3	127983587	127983587	Missense_Mutation	SNP	T	C	3	197	c.749T>C	c.(748-750)ATC>ACC	p.I250T
Pat_14	Pre-Treatment	PLXND1	23129	37	3	129289909	129289910	Missense_Mutation	DNP	CG	AT	6	740	.3573_3574CG>A	571-3576)CCCGGG>CCA	p.G1192W
Pat_14	Pre-Treatment	TMEM108	66000	37	3	133099648	133099648	Missense_Mutation	SNP	G	A	47	185	c.1093G>A	c.(1093-1095)GAT>AAT	p.D365N
Pat_14	Pre-Treatment	RAB6B	51560	37	3	133558447	133558447	Nonsense_Mutation	SNP	G	A	92	317	c.304C>T	c.(304-306)CAA>TAA	p.Q102*
Pat_14	Pre-Treatment	DZIP1L	199221	37	3	137787171	137787171	Nonsense_Mutation	SNP	G	A	4	208	c.1654C>T	c.(1654-1656)CAG>TAG	p.Q552*
Pat_14	Pre-Treatment	SIAH2	6478	37	3	150460311	150460311	Missense_Mutation	SNP	G	T	6	443	c.592C>A	c.(592-594)CTT>ATT	p.L198I
Pat_14	Pre-Treatment	IGSF10	285313	37	3	151163294	151163294	Missense_Mutation	SNP	G	T	4	238	c.4475C>A	c.(4474-4476)ACT>AAT	p.T1492N
Pat_14	Pre-Treatment	SERPINI2	5276	37	3	167189388	167189388	Missense_Mutation	SNP	C	T	74	305	c.235G>A	c.(235-237)GAA>AAA	p.E79K
Pat_14	Pre-Treatment	NAALADL2	254827	37	3	175181255	175181255	Missense_Mutation	SNP	G	A	16	58	c.1301G>A	c.(1300-1302)GGA>GAA	p.G434E
Pat_14	Pre-Treatment	CCDC39	339829	37	3	180377266	180377266	Missense_Mutation	SNP	C	T	34	148	c.712G>A	c.(712-714)GAT>AAT	p.D238N
Pat_14	Pre-Treatment	EIF4G1	1981	37	3	184052572	184052572	Missense_Mutation	SNP	C	T	100	366	c.4676C>T	c.(4675-4677)GCC>GTC	p.A1559V
Pat_14	Pre-Treatment	C3orf70	285382	37	3	184800847	184800847	Missense_Mutation	SNP	G	A	93	455	c.701C>T	c.(700-702)TCC>TTC	p.S234F
Pat_14	Pre-Treatment	RTP1	132112	37	3	186915381	186915381	Nonsense_Mutation	SNP	G	A	85	301	c.78G>A	c.(76-78)TGG>TGA	p.W26*
Pat_14	Pre-Treatment	MASP1	5648	37	3	187003740	187003740	Missense_Mutation	SNP	G	A	69	246	c.110C>T	c.(109-111)CCA>CTA	p.P37L
Pat_14	Pre-Treatment	RTP2	344892	37	3	187416366	187416366	Missense_Mutation	SNP	G	A	49	185	c.598C>T	c.(598-600)CGC>TGC	p.R200C
Pat_14	Pre-Treatment	LEPREL1	55214	37	3	189711976	189711976	Missense_Mutation	SNP	C	T	44	205	c.730G>A	c.(730-732)GAT>AAT	p.D244N
Pat_14	Pre-Treatment	ATP13A5	344905	37	3	193031914	193031914	Missense_Mutation	SNP	T	A	40	465	c.2227A>T	c.(2227-2229)ATC>TTC	p.I743F
Pat_14	Pre-Treatment	MUC4	4585	37	3	195516473	195516473	Missense_Mutation	SNP	C	T	103	305	c.1978G>A	c.(1978-1980)GAC>AAC	p.D660N
Pat_14	Pre-Treatment	LMLN	89782	37	3	197717465	197717465	Missense_Mutation	SNP	G	A	84	275	c.965G>A	c.(964-966)CGA>CAA	p.R322Q

Pat_14	Pre-Treatment	ZNF595	152687	37	4	59969	59969	Missense_Mutation	SNP	C	T	10	280	c.149C>T	c.(148-150)CCA>CTA	p.P50L
Pat_14	Pre-Treatment	PDE6B	5158	37	4	628610	628610	Missense_Mutation	SNP	G	A	66	151	c.613G>A	c.(613-615)GAC>AAC	p.D205N
Pat_14	Pre-Treatment	FGFRL1	53834	37	4	1018918	1018918	Missense_Mutation	SNP	C	T	15	40	c.1298C>T	c.(1297-1299)CCC>CTC	p.P433L
Pat_14	Pre-Treatment	SLBP	7884	37	4	1695421	1695421	Missense_Mutation	SNP	G	T	6	246	c.716C>A	c.(715-717)CCC>CAC	p.P239H
Pat_14	Pre-Treatment	SH3TC1	54436	37	4	8226937	8226937	Missense_Mutation	SNP	G	A	31	46	c.1279G>A	c.(1279-1281)GAA>AAA	p.E427K
Pat_14	Pre-Treatment	STIM2	57620	37	4	27024457	27024457	Missense_Mutation	SNP	C	A	5	243	c.2365C>A	c.(2365-2367)CGC>AGC	p.R789S
Pat_14	Pre-Treatment	TLR10	81793	37	4	38777034	38777034	Missense_Mutation	SNP	G	T	47	106	c.178C>A	c.(178-180)CTT>ATT	p.L60I
Pat_14	Pre-Treatment	KIAA1211	57482	37	4	57182501	57182501	Missense_Mutation	SNP	G	A	32	63	c.2833G>A	c.(2833-2835)GCT>ACT	p.A945T
Pat_14	Pre-Treatment	TMPRSS11B	132724	37	4	69100328	69100328	Missense_Mutation	SNP	C	T	57	159	c.322G>A	c.(322-324)GGT>AGT	p.G108S
Pat_14	Pre-Treatment	CCDC158	339965	37	4	77292608	77292608	Missense_Mutation	SNP	C	T	47	75	c.1111G>A	c.(1111-1113)GAA>AAA	p.E371K
Pat_14	Pre-Treatment	CXCL13	10563	37	4	78528940	78528940	Nonsense_Mutation	SNP	C	T	71	154	c.148C>T	c.(148-150)CGA>TGA	p.R50*
Pat_14	Pre-Treatment	NKX6-1	4825	37	4	85416846	85416847	Missense_Mutation	DNP	CC	TT	83	281	c.821_822GG>AA	c.(820-822)GGG>GAA	p.G274E
Pat_14	Pre-Treatment	MEPE	56955	37	4	88767137	88767137	Missense_Mutation	SNP	C	T	23	52	c.1117C>T	c.(1117-1119)CAT>TAT	p.H373Y
Pat_14	Pre-Treatment	ABCG2	9429	37	4	89052255	89052255	Missense_Mutation	SNP	C	A	8	589	c.489G>T	c.(487-489)AGG>AGT	p.R163S
Pat_14	Pre-Treatment	FAM190A	401145	37	4	91234040	91234040	Missense_Mutation	SNP	C	T	7	14	c.1351C>T	c.(1351-1353)CGT>TGT	p.R451C
Pat_14	Pre-Treatment	FAM190A	401145	37	4	91549378	91549378	Nonsense_Mutation	SNP	C	T	22	52	c.1927C>T	c.(1927-1929)CAA>TAA	p.Q643*
Pat_14	Pre-Treatment	ADH4	127	37	4	100052663	100052663	Missense_Mutation	SNP	C	T	55	121	c.835G>A	c.(835-837)GAA>AAA	p.E279K
Pat_14	Pre-Treatment	ANK2	287	37	4	114254292	114254292	Missense_Mutation	SNP	G	A	5	297	c.3307G>A	c.(3307-3309)GAC>AAC	p.D1103N
Pat_14	Pre-Treatment	PDE5A	8654	37	4	120419851	120419851	Missense_Mutation	SNP	C	T	111	185	c.2533G>A	c.(2533-2535)GGC>AGC	p.G845S
Pat_14	Pre-Treatment	PRDM5	11107	37	4	121774608	121774608	Missense_Mutation	SNP	G	A	232	491	c.265C>T	c.(265-267)CCA>TCA	p.P89S
Pat_14	Pre-Treatment	FAT4	79633	37	4	126237672	126237672	Missense_Mutation	SNP	G	T	6	433	c.106G>T	c.(106-108)GGG>TGG	p.G36W
Pat_14	Pre-Treatment	HHIP	64399	37	4	145567955	145567955	Missense_Mutation	SNP	A	G	32	97	c.128A>G	c.(127-129)AAC>AGC	p.N43S
Pat_14	Pre-Treatment	DCHS2	54798	37	4	155219534	155219534	Missense_Mutation	SNP	C	A	7	321	c.4567G>T	c.(4567-4569)GGT>TGT	p.G1523C
Pat_14	Pre-Treatment	FGA	2243	37	4	155507677	155507677	Missense_Mutation	SNP	G	T	4	248	c.904C>A	c.(904-906)CCT>ACT	p.P302T
Pat_14	Pre-Treatment	GUCY1B3	2983	37	4	156723706	156723706	Missense_Mutation	SNP	C	T	17	42	c.1388C>T	c.(1387-1389)TCC>TTC	p.S463F
Pat_14	Pre-Treatment	CTSO	1519	37	4	156858553	156858553	Missense_Mutation	SNP	G	A	47	123	c.635C>T	c.(634-636)TCT>TTT	p.S212F
Pat_14	Pre-Treatment	NEIL3	55247	37	4	178274739	178274739	Missense_Mutation	SNP	T	G	7	268	c.1317T>G	c.(1315-1317)GAT>GAG	p.D439E
Pat_14	Pre-Treatment	PDLIM3	27295	37	4	186435488	186435488	Missense_Mutation	SNP	C	A	5	327	c.334G>T	c.(334-336)GGG>TGG	p.G112W
Pat_14	Pre-Treatment	SORBS2	8470	37	4	186544155	186544155	Missense_Mutation	SNP	C	A	8	230	c.2416G>T	c.(2416-2418)GGG>TGG	p.G806W
Pat_14	Pre-Treatment	CTNND2	1501	37	5	11565098	11565098	Missense_Mutation	SNP	C	T	46	151	c.245G>A	c.(244-246)CGA>CAA	p.R82Q
Pat_14	Pre-Treatment	DNAH5	1767	37	5	13781040	13781040	Missense_Mutation	SNP	C	T	50	140	c.8849G>A	c.(8848-8850)GGA>GAA	p.G2950E
Pat_14	Pre-Treatment	FAM105B	90268	37	5	14678841	14678841	Missense_Mutation	SNP	A	G	44	112	c.281A>G	c.(280-282)AAA>AGA	p.K94R
Pat_14	Pre-Treatment	PRDM9	56979	37	5	23523433	23523433	Missense_Mutation	SNP	G	A	51	210	c.916G>A	c.(916-918)GAT>AAT	p.D306N
Pat_14	Pre-Treatment	SPEF2	79925	37	5	35771819	35771819	Missense_Mutation	SNP	G	A	9	40	c.3910G>A	c.(3910-3912)GAG>AAG	p.E1304K
Pat_14	Pre-Treatment	FYB	2533	37	5	39202834	39202834	Missense_Mutation	SNP	C	T	17	37	c.229G>A	c.(229-231)GAA>AAA	p.E77K
Pat_14	Pre-Treatment	HEATR7B2	133558	37	5	41045898	41045898	Nonsense_Mutation	SNP	G	A	161	522	c.1786C>T	c.(1786-1788)CAG>TAG	p.Q596*
Pat_14	Pre-Treatment	OXCT1	5019	37	5	41853607	41853607	Missense_Mutation	SNP	G	A	4	169	c.328C>T	c.(328-330)CGC>TGC	p.R110C
Pat_14	Pre-Treatment	GHR	2690	37	5	42695140	42695140	Missense_Mutation	SNP	A	G	48	134	c.388A>G	c.(388-390)ACT>GCT	p.T130A
Pat_14	Pre-Treatment	IL31RA	133396	37	5	55202002	55202002	Missense_Mutation	SNP	T	A	114	293	c.1138T>A	c.(1138-1140)TCT>ACT	p.S380T
Pat_14	Pre-Treatment	HAPLN1	1404	37	5	82948521	82948521	Missense_Mutation	SNP	G	A	89	273	c.223C>T	c.(223-225)CAT>TAT	p.H75Y
Pat_14	Pre-Treatment	ARSK	153642	37	5	94918703	94918703	Missense_Mutation	SNP	G	A	6	396	c.500G>A	c.(499-501)AGG>AAG	p.R167K
Pat_14	Pre-Treatment	APC	324	37	5	112174268	112174268	Missense_Mutation	SNP	A	C	69	201	c.2977A>C	c.(2977-2979)AAG>CAG	p.K993Q
Pat_14	Pre-Treatment	CHSY3	337876	37	5	129520087	129520087	Missense_Mutation	SNP	C	T	38	114	c.1252C>T	c.(1252-1254)CGC>TGC	p.R418C
Pat_14	Pre-Treatment	FNIP1	96459	37	5	131066631	131066631	Missense_Mutation	SNP	G	A	61	132	c.320C>T	c.(319-321)TCT>TTT	p.S107F
Pat_14	Pre-Treatment	IL13	3596	37	5	131995518	131995518	Missense_Mutation	SNP	G	T	37	82	c.331G>T	c.(331-333)GGG>TGG	p.G111W
Pat_14	Pre-Treatment	DDX46	9879	37	5	134154607	134154607	Missense_Mutation	SNP	G	A	35	91	c.2887G>A	c.(2887-2889)GAA>AAA	p.E963K
Pat_14	Pre-Treatment	TRPC7	57113	37	5	135587487	135587487	Missense_Mutation	SNP	C	T	4	161	c.1426G>A	c.(1426-1428)GGG>AGG	p.G476R

Pat_14	Pre-Treatment	KLHL3	26249	37	5	137045463	137045463	Missense_Mutation	SNP	G	A	99	243	c.217C>T	c.(217-219)CCC>TCC	p.P73S
Pat_14	Pre-Treatment	PCDHA7	56141	37	5	140215352	140215352	Missense_Mutation	SNP	G	A	77	166	c.1384G>A	c.(1384-1386)GTG>ATG	p.V462M
Pat_14	Pre-Treatment	PCDHB7	56129	37	5	140553374	140553374	Missense_Mutation	SNP	C	G	4	321	c.958C>G	c.(958-960)CAG>GAG	p.Q320E
Pat_14	Pre-Treatment	GNPDA1	10007	37	5	141385873	141385873	Missense_Mutation	SNP	G	T	5	216	c.245C>A	c.(244-246)CCG>CAG	p.P82Q
Pat_14	Pre-Treatment	SPINK1	6690	37	5	147209175	147209175	Missense_Mutation	SNP	G	A	63	124	c.74C>T	c.(73-75)TCC>TTC	p.S25F
Pat_14	Pre-Treatment	CSF1R	1436	37	5	149460362	149460362	Missense_Mutation	SNP	C	T	15	44	c.275G>A	c.(274-276)GGA>GAA	p.G92E
Pat_14	Pre-Treatment	TIMD4	91937	37	5	156375486	156375486	Nonsense_Mutation	SNP	G	C	4	172	c.785C>G	c.(784-786)TCA>TGA	p.S262*
Pat_14	Pre-Treatment	ODZ2	57451	37	5	167671462	167671462	Missense_Mutation	SNP	G	A	26	58	c.5531G>A	c.(5530-5532)CGA>CAA	p.R1844Q
Pat_14	Pre-Treatment	FGF18	8817	37	5	170863238	170863238	Missense_Mutation	SNP	C	T	4	101	c.211C>T	c.(211-213)CGC>TGC	p.R71C
Pat_14	Pre-Treatment	C5orf41	153222	37	5	172518273	172518273	Missense_Mutation	SNP	T	C	14	47	c.1091T>C	c.(1090-1092)GTT>GCT	p.V364A
Pat_14	Pre-Treatment	HMP19	51617	37	5	173473792	173473792	Missense_Mutation	SNP	G	A	111	233	c.34G>A	c.(34-36)GGA>AGA	p.G12R
Pat_14	Pre-Treatment	UNC5A	90249	37	5	176305503	176305503	Missense_Mutation	SNP	G	A	67	150	c.2047G>A	c.(2047-2049)GGC>AGC	p.G683S
Pat_14	Pre-Treatment	MYLK4	340156	37	6	2689143	2689143	Missense_Mutation	SNP	C	A	7	753	c.283G>T	c.(283-285)GCC>TCC	p.A95S
Pat_14	Pre-Treatment	C6orf146	222826	37	6	4069088	4069088	Missense_Mutation	SNP	C	T	26	140	c.1369G>A	c.(1369-1371)GAA>AAA	p.E457K
Pat_14	Pre-Treatment	DSP	1832	37	6	7574391	7574391	Missense_Mutation	SNP	G	A	67	283	c.2203G>A	c.(2203-2205)GGT>AGT	p.G735S
Pat_14	Pre-Treatment	HIVEP1	3096	37	6	12164204	12164204	Missense_Mutation	SNP	C	T	44	159	c.7667C>T	c.(7666-7668)CCC>CTC	p.P2556L
Pat_14	Pre-Treatment	EDN1	1906	37	6	12294298	12294298	Missense_Mutation	SNP	T	G	81	334	c.358T>G	c.(358-360)TGG>GGG	p.W120G
Pat_14	Pre-Treatment	BTN3A1	11119	37	6	26406217	26406217	Missense_Mutation	SNP	C	T	98	434	c.166C>T	c.(166-168)CCG>TCG	p.P56S
Pat_14	Pre-Treatment	PRSS16	10279	37	6	27216651	27216651	Missense_Mutation	SNP	G	T	6	327	c.263G>T	c.(262-264)TGG>TTG	p.W88L
Pat_14	Pre-Treatment	SCAND3	114821	37	6	28542612	28542612	Missense_Mutation	SNP	G	A	35	124	c.1870C>T	c.(1870-1872)CAT>TAT	p.H624Y
Pat_14	Pre-Treatment	OR5V1	81696	37	6	29323149	29323149	Missense_Mutation	SNP	G	A	134	482	c.824C>T	c.(823-825)TCA>TTA	p.S275L
Pat_14	Pre-Treatment	TNF	7124	37	6	31545084	31545084	Missense_Mutation	SNP	C	T	82	257	c.472C>T	c.(472-474)CGC>TGC	p.R158C
Pat_14	Pre-Treatment	EHMT2	10919	37	6	31847961	31847961	Nonsense_Mutation	SNP	G	T	5	197	c.3533C>A	c.(3532-3534)TCA>TAA	p.S1178*
Pat_14	Pre-Treatment	TNXB	7148	37	6	32032724	32032724	Missense_Mutation	SNP	G	A	7	99	c.6715C>T	c.(6715-6717)CGG>TGG	p.R2239W
Pat_14	Pre-Treatment	SPDEF	25803	37	6	34507032	34507032	Missense_Mutation	SNP	T	A	154	517	c.824A>T	c.(823-825)GAG>GTG	p.E275V
Pat_14	Pre-Treatment	C6orf222	389384	37	6	36291138	36291138	Missense_Mutation	SNP	C	T	87	330	c.1403G>A	c.(1402-1404)CGA>CAA	p.R468Q
Pat_14	Pre-Treatment	DNAH8	1769	37	6	38790614	38790614	Missense_Mutation	SNP	G	A	15	67	c.2873G>A	c.(2872-2874)AGA>AAA	p.R958K
Pat_14	Pre-Treatment	DNAH8	1769	37	6	38793989	38793989	Missense_Mutation	SNP	G	A	43	133	c.3254G>A	c.(3253-3255)CGA>CAA	p.R1085Q
Pat_14	Pre-Treatment	DNAH8	1769	37	6	38863996	38863996	Missense_Mutation	SNP	G	A	26	144	c.8284G>A	c.(8284-8286)GAA>AAA	p.E2762K
Pat_14	Pre-Treatment	CUL9	23113	37	6	43188237	43188237	Missense_Mutation	SNP	A	C	9	775	c.6323A>C	c.(6322-6324)AAC>ACC	p.N2108T
Pat_14	Pre-Treatment	CLIC5	53405	37	6	45922948	45922948	Missense_Mutation	SNP	G	A	48	142	c.574C>T	c.(574-576)CCT>TCT	p.P192S
Pat_14	Pre-Treatment	TDRD6	221400	37	6	46659919	46659919	Missense_Mutation	SNP	C	T	143	594	c.4054C>T	c.(4054-4056)CCT>TCT	p.P1352S
Pat_14	Pre-Treatment	GPR115	221393	37	6	47681717	47681717	Missense_Mutation	SNP	C	T	52	209	c.736C>T	c.(736-738)CAC>TAC	p.H246Y
Pat_14	Pre-Treatment	PGK2	5232	37	6	49754605	49754605	Missense_Mutation	SNP	C	T	42	287	c.296G>A	c.(295-297)TGT>TAT	p.C99Y
Pat_14	Pre-Treatment	MCM3	4172	37	6	52147627	52147627	Missense_Mutation	SNP	G	A	18	108	c.224C>T	c.(223-225)GCC>GTC	p.A75V
Pat_14	Pre-Treatment	TINAG	27283	37	6	54245350	54245350	Missense_Mutation	SNP	G	T	22	164	c.1277G>T	c.(1276-1278)GGG>GTG	p.G426V
Pat_14	Pre-Treatment	FAM83B	222584	37	6	54804839	54804839	Missense_Mutation	SNP	G	A	37	249	c.1070G>A	c.(1069-1071)GGA>GAA	p.G357E
Pat_14	Pre-Treatment	GFRAL	389400	37	6	55223831	55223831	Missense_Mutation	SNP	C	T	94	375	c.847C>T	c.(847-849)CTT>TTT	p.L283F
Pat_14	Pre-Treatment	HMGCLL1	54511	37	6	55406860	55406860	Missense_Mutation	SNP	T	C	35	112	c.277A>G	c.(277-279)AAG>GAG	p.K93E
Pat_14	Pre-Treatment	BMP5	653	37	6	55620477	55620477	Missense_Mutation	SNP	G	A	51	182	c.1219C>T	c.(1219-1221)CAT>TAT	p.H407Y
Pat_14	Pre-Treatment	COL21A1	81578	37	6	55932118	55932118	Missense_Mutation	SNP	C	T	38	162	c.2102G>A	c.(2101-2103)GGA>GAA	p.G701E
Pat_14	Pre-Treatment	COL21A1	81578	37	6	56021744	56021744	Missense_Mutation	SNP	C	T	16	88	c.1375G>A	c.(1375-1377)GAC>AAC	p.D459N
Pat_14	Pre-Treatment	COL21A1	81578	37	6	56035908	56035908	Missense_Mutation	SNP	C	T	74	298	c.659G>A	c.(658-660)CGA>CAA	p.R220Q
Pat_14	Pre-Treatment	BAI3	577	37	6	69349189	69349189	Missense_Mutation	SNP	G	A	63	194	c.622G>A	c.(622-624)GAC>AAC	p.D208N
Pat_14	Pre-Treatment	COL19A1	1310	37	6	70639347	70639348	Missense_Mutation	DNP	GT	AA	26	165	c.421_422GT>AA	c.(421-423)GTG>AAG	p.V141K
Pat_14	Pre-Treatment	COL12A1	1303	37	6	75893077	75893077	Missense_Mutation	SNP	C	T	125	462	c.1580G>A	c.(1579-1581)AGA>AAA	p.R527K
Pat_14	Pre-Treatment	IMPG1	3617	37	6	76660536	76660536	Missense_Mutation	SNP	C	T	29	100	c.1567G>A	c.(1567-1569)GAT>AAT	p.D523N

Pat_14	Pre-Treatment	DOPEY1	23033	37	6	83840033	83840033	Missense_Mutation	SNP	C	A	6	220	c.2533C>A	c.(2533-2535)CAG>AAG	p.Q845K
Pat_14	Pre-Treatment	GJB7	375519	37	6	87994082	87994082	Missense_Mutation	SNP	C	A	6	418	c.549G>T	c.(547-549)TTG>TTT	p.L183F
Pat_14	Pre-Treatment	ANKRD6	22881	37	6	90340178	90340179	Missense_Mutation	DNP	GG	AA	40	189	.1639_1640GG>A	c.(1639-1641)GGT>AAT	p.G547N
Pat_14	Pre-Treatment	GPR63	81491	37	6	97246787	97246787	Missense_Mutation	SNP	A	C	74	264	c.821T>G	c.(820-822)TTG>TGG	p.L274W
Pat_14	Pre-Treatment	WISP3	8838	37	6	112389575	112389575	Missense_Mutation	SNP	G	A	29	85	c.757G>A	c.(757-759)GAC>AAC	p.D253N
Pat_14	Pre-Treatment	LAMA4	3910	37	6	112454670	112454670	Missense_Mutation	SNP	G	A	77	256	c.3577C>T	c.(3577-3579)CCC>TCC	p.P1193S
Pat_14	Pre-Treatment	C6orf191	253582	37	6	130164717	130164717	Missense_Mutation	SNP	C	T	85	374	c.151G>A	c.(151-153)GAT>AAT	p.D51N
Pat_14	Pre-Treatment	EPB41L2	2037	37	6	131216236	131216236	Missense_Mutation	SNP	C	A	82	566	c.1260G>T	c.(1258-1260)AAG>AAT	p.K420N
Pat_14	Pre-Treatment	TBPL1	9519	37	6	134308154	134308154	Missense_Mutation	SNP	T	G	4	200	c.537T>G	c.(535-537)TTT>TTG	p.F179L
Pat_14	Pre-Treatment	PDE7B	27115	37	6	136468578	136468578	Missense_Mutation	SNP	C	T	94	385	c.256C>T	c.(256-258)CGT>TGT	p.R86C
Pat_14	Pre-Treatment	TAB2	23118	37	6	149691140	149691140	Missense_Mutation	SNP	C	A	5	285	c.7C>A	c.(7-9)CAA>AAA	p.Q3K
Pat_14	Pre-Treatment	SYNE1	23345	37	6	152728184	152728184	Missense_Mutation	SNP	G	A	102	403	c.6688C>T	c.(6688-6690)CAC>TAC	p.H2230Y
Pat_14	Pre-Treatment	VIP	7432	37	6	153073313	153073313	Missense_Mutation	SNP	A	T	33	129	c.1A>T	c.(1-3)ATG>TTG	p.M1L
Pat_14	Pre-Treatment	C6orf35	729515	37	6	157739911	157739911	Missense_Mutation	SNP	G	A	63	193	c.230C>T	c.(229-231)TCC>TTC	p.S77F
Pat_14	Pre-Treatment	SYNJ2	8871	37	6	158485655	158485656	Missense_Mutation	DNP	CC	TT	133	395	.1232_1233CC>T	c.(1231-1233)ACC>ATT	p.T411I
Pat_14	Pre-Treatment	SLC22A1	6580	37	6	160575922	160575922	Missense_Mutation	SNP	C	T	51	205	c.1478C>T	c.(1477-1479)GCC>GTC	p.A493V
Pat_14	Pre-Treatment	LPA	4018	37	6	161027610	161027610	Missense_Mutation	SNP	C	A	9	627	c.2684G>T	c.(2683-2685)TGG>TTG	p.W895L
Pat_14	Pre-Treatment	TTYH3	80727	37	7	2686861	2686861	Missense_Mutation	SNP	C	T	8	48	c.379C>T	c.(379-381)CGC>TGC	p.R127C
Pat_14	Pre-Treatment	DGKB	1607	37	7	14622740	14622740	Missense_Mutation	SNP	G	A	38	118	c.1459C>T	c.(1459-1461)CCT>TCT	p.P487S
Pat_14	Pre-Treatment	DGKB	1607	37	7	14758224	14758224	Missense_Mutation	SNP	C	T	49	157	c.409G>A	c.(409-411)GAC>AAC	p.D137N
Pat_14	Pre-Treatment	ABCB5	340273	37	7	20721158	20721158	Missense_Mutation	SNP	G	A	5	265	c.403G>A	c.(403-405)GCA>ACA	p.A135T
Pat_14	Pre-Treatment	ABCB5	340273	37	7	20782689	20782689	Missense_Mutation	SNP	G	A	44	102	c.1879G>A	c.(1879-1881)GGA>AGA	p.G627R
Pat_14	Pre-Treatment	ABCB5	340273	37	7	20795245	20795245	Nonstop_Mutation	SNP	T	C	5	212	c.2437T>C	c.(2437-2439)TGA>CGA	p.*813R
Pat_14	Pre-Treatment	INMT	11185	37	7	30795335	30795335	Missense_Mutation	SNP	G	T	7	266	c.660G>T	c.(658-660)GAG>GAT	p.E220D
Pat_14	Pre-Treatment	AVL9	23080	37	7	32598232	32598232	Missense_Mutation	SNP	T	C	4	261	c.671T>C	c.(670-672)CTT>CCT	p.L224P
Pat_14	Pre-Treatment	FKBP9	11328	37	7	33035909	33035909	Missense_Mutation	SNP	C	A	5	190	c.1174C>A	c.(1174-1176)CTC>ATC	p.L392I
Pat_14	Pre-Treatment	BBS9	27241	37	7	33312753	33312753	Nonsense_Mutation	SNP	C	T	92	307	c.832C>T	c.(832-834)CGA>TGA	p.R278*
Pat_14	Pre-Treatment	HERPUD2	64224	37	7	35678059	35678059	Missense_Mutation	SNP	C	T	40	154	c.518G>A	c.(517-519)GGG>GAG	p.G173E
Pat_14	Pre-Treatment	WBSCR17	64409	37	7	71130513	71130513	Missense_Mutation	SNP	C	T	62	253	c.1198C>T	c.(1198-1200)CGC>TGC	p.R400C
Pat_14	Pre-Treatment	NCF1	653361	37	7	74203043	74203043	Missense_Mutation	SNP	C	G	20	11	c.1046C>G	c.(1045-1047)CCG>CGG	p.P349R
Pat_14	Pre-Treatment	PCLO	27445	37	7	82579285	82579285	Missense_Mutation	SNP	C	T	47	177	c.10619G>A	.(10618-10620)CGG>CA	p.R3540Q
Pat_14	Pre-Treatment	PCLO	27445	37	7	82582375	82582375	Missense_Mutation	SNP	G	A	57	233	c.7894C>T	c.(7894-7896)CCA>TCA	p.P2632S
Pat_14	Pre-Treatment	PCLO	27445	37	7	82764221	82764221	Missense_Mutation	SNP	C	T	149	644	c.2645G>A	c.(2644-2646)CGA>CAA	p.R882Q
Pat_14	Pre-Treatment	NPTX2	4885	37	7	98254422	98254422	Missense_Mutation	SNP	G	A	81	314	c.832G>A	c.(832-834)GAG>AAG	p.E278K
Pat_14	Pre-Treatment	TRRAP	8295	37	7	98509802	98509802	Missense_Mutation	SNP	C	T	82	376	c.2165C>T	c.(2164-2166)TCC>TTC	p.S722F
Pat_14	Pre-Treatment	TRRAP	8295	37	7	98569556	98569557	Nonsense_Mutation	DNP	CC	TT	77	227	.7806_7807CC>T	804-7809)CTCCGA>CTTT	p.R2603*
Pat_14	Pre-Treatment	TAF6	6878	37	7	99705102	99705102	Missense_Mutation	SNP	C	A	8	707	c.1801G>T	c.(1801-1803)GGG>TGG	p.G601W
Pat_14	Pre-Treatment	ZAN	7455	37	7	100350453	100350453	Missense_Mutation	SNP	T	C	5	278	c.2725T>C	c.(2725-2727)TCC>CCC	p.S909P
Pat_14	Pre-Treatment	ZAN	7455	37	7	100350456	100350456	Missense_Mutation	SNP	C	A	8	274	c.2728C>A	c.(2728-2730)CCA>ACA	p.P910T
Pat_14	Pre-Treatment	AP1S1	1174	37	7	100802423	100802423	Missense_Mutation	SNP	C	A	4	119	c.375C>A	c.(373-375)GAC>GAA	p.D125E
Pat_14	Pre-Treatment	LAMB4	22798	37	7	107756552	107756552	Missense_Mutation	SNP	G	A	84	345	c.89C>T	c.(88-90)CCC>CTC	p.P30L
Pat_14	Pre-Treatment	IFRD1	3475	37	7	112108165	112108165	Missense_Mutation	SNP	G	A	4	210	c.1036G>A	c.(1036-1038)GTG>ATG	p.V346M
Pat_14	Pre-Treatment	CTTNBP2	83992	37	7	117431611	117431611	Missense_Mutation	SNP	G	A	93	334	c.1639C>T	c.(1639-1641)CCA>TCA	p.P547S
Pat_14	Pre-Treatment	CTTNBP2	83992	37	7	117432130	117432130	Missense_Mutation	SNP	G	A	65	233	c.1120C>T	c.(1120-1122)CCA>TCA	p.P374S
Pat_14	Pre-Treatment	PTPRZ1	5803	37	7	121652066	121652066	Missense_Mutation	SNP	C	T	97	417	c.2966C>T	c.(2965-2967)GCC>GTC	p.A989V
Pat_14	Pre-Treatment	AASS	10157	37	7	121716632	121716632	Missense_Mutation	SNP	G	A	38	130	c.2692C>T	c.(2692-2694)CCC>TCC	p.P898S
Pat_14	Pre-Treatment	CADPS2	93664	37	7	122261678	122261678	Missense_Mutation	SNP	C	T	36	142	c.961G>A	c.(961-963)GAA>AAA	p.E321K

Pat_14	Pre-Treatment	BPGM	669	37	7	134346804	134346804	Missense_Mutation	SNP	C	T	34	231	c.545C>T	c.(544-546)ACC>ATC	p.T182I
Pat_14	Pre-Treatment	DENND2A	27147	37	7	140301680	140301680	Missense_Mutation	SNP	C	T	27	76	c.518G>A	c.(517-519)GGG>GAG	p.G173E
Pat_14	Pre-Treatment	BRAF	673	37	7	140453136	140453136	Missense_Mutation	SNP	A	T	63	267	c.1799T>A	c.(1798-1800)GTG>GAG	p.V600E
Pat_14	Pre-Treatment	OR9A4	130075	37	7	141619270	141619270	Missense_Mutation	SNP	C	T	79	340	c.595C>T	c.(595-597)CTC>TTC	p.L199F
Pat_14	Pre-Treatment	MGAM	8972	37	7	141732625	141732625	Missense_Mutation	SNP	G	A	9	74	c.1585G>A	c.(1585-1587)GAT>AAT	p.D529N
Pat_14	Pre-Treatment	KEL	3792	37	7	142640601	142640601	Missense_Mutation	SNP	G	A	6	307	c.1675C>T	c.(1675-1677)CCC>TCC	p.P559S
Pat_14	Pre-Treatment	OR9A2	135924	37	7	142723766	142723766	Missense_Mutation	SNP	C	T	82	242	c.454G>A	c.(454-456)GAA>AAA	p.E152K
Pat_14	Pre-Treatment	OR6V1	346517	37	7	142749456	142749456	Missense_Mutation	SNP	C	A	118	346	c.19C>A	c.(19-21)CCC>ACC	p.P7T
Pat_14	Pre-Treatment	ABCF2	10061	37	7	150921095	150921095	Missense_Mutation	SNP	G	A	103	275	c.473C>T	c.(472-474)CCC>CTC	p.P158L
Pat_14	Pre-Treatment	SMARCD3	6604	37	7	150936538	150936538	Nonsense_Mutation	SNP	C	A	6	180	c.1342G>T	c.(1342-1344)GAG>TAG	p.E448*
Pat_14	Pre-Treatment	RBM33	155435	37	7	155534718	155534718	Missense_Mutation	SNP	G	A	5	163	c.2255G>A	c.(2254-2256)AGC>AAC	p.S752N
Pat_14	Pre-Treatment	MYOM2	9172	37	8	2021482	2021483	Missense_Mutation	DNP	CC	TT	56	168	.1022_1023CC>T	c.(1021-1023)TCC>TTT	p.S341F
Pat_14	Pre-Treatment	MYOM2	9172	37	8	2071239	2071239	Splice_Site	SNP	G	A	45	130	c.3567_splice	c.e29+1	p.K1189_splice
Pat_14	Pre-Treatment	CSMD1	64478	37	8	2876014	2876014	Missense_Mutation	SNP	C	T	183	574	c.8017G>A	c.(8017-8019)GAA>AAA	p.E2673K
Pat_14	Pre-Treatment	CSMD1	64478	37	8	3165278	3165278	Missense_Mutation	SNP	G	A	67	391	c.3892C>T	c.(3892-3894)CCG>TCG	p.P1298S
Pat_14	Pre-Treatment	DEFA6	1671	37	8	6782377	6782377	Missense_Mutation	SNP	G	A	88	297	c.266C>T	c.(265-267)ACT>ATT	p.T89I
Pat_14	Pre-Treatment	ZDHHC2	51201	37	8	17055156	17055156	Missense_Mutation	SNP	G	A	90	330	c.439G>A	c.(439-441)GAT>AAT	p.D147N
Pat_14	Pre-Treatment	SLC18A1	6570	37	8	20008178	20008178	Missense_Mutation	SNP	G	A	146	552	c.1093C>T	c.(1093-1095)CGG>TGG	p.R365W
Pat_14	Pre-Treatment	SLC25A37	51312	37	8	23429298	23429298	Missense_Mutation	SNP	C	T	36	129	c.947C>T	c.(946-948)TCT>TTT	p.S316F
Pat_14	Pre-Treatment	ADAM28	10863	37	8	24199262	24199262	Missense_Mutation	SNP	G	A	59	337	c.1822G>A	c.(1822-1824)GAT>AAT	p.D608N
Pat_14	Pre-Treatment	ADAM7	8756	37	8	24339789	24339789	Missense_Mutation	SNP	A	C	63	326	c.840A>C	c.(838-840)AAA>AAC	p.K280N
Pat_14	Pre-Treatment	CLU	1191	37	8	27457371	27457371	Missense_Mutation	SNP	C	T	13	101	c.1090G>A	c.(1090-1092)GAG>AAG	p.E364K
Pat_14	Pre-Treatment	ELP3	55140	37	8	28017935	28017935	Missense_Mutation	SNP	C	T	37	134	c.1447C>T	c.(1447-1449)CCT>TCT	p.P483S
Pat_14	Pre-Treatment	POTEA	340441	37	8	43155707	43155707	Missense_Mutation	SNP	G	A	69	277	c.635G>A	c.(634-636)CGA>CAA	p.R212Q
Pat_14	Pre-Treatment	PCMTD1	115294	37	8	52733158	52733158	Missense_Mutation	SNP	C	T	30	556	c.827G>A	c.(826-828)AGG>AAG	p.R276K
Pat_14	Pre-Treatment	RB1CC1	9821	37	8	53570266	53570266	Missense_Mutation	SNP	G	T	8	393	c.2123C>A	c.(2122-2124)CCA>CAA	p.P708Q
Pat_14	Pre-Treatment	XKR4	114786	37	8	56015355	56015355	Missense_Mutation	SNP	G	A	30	92	c.307G>A	c.(307-309)GAG>AAG	p.E103K
Pat_14	Pre-Treatment	CLVS1	157807	37	8	62289312	62289312	Missense_Mutation	SNP	C	T	40	170	c.604C>T	c.(604-606)CTT>TTT	p.L202F
Pat_14	Pre-Treatment	CYP7B1	9420	37	8	65537058	65537058	Missense_Mutation	SNP	G	A	42	195	c.161C>T	c.(160-162)CCT>CTT	p.P54L
Pat_14	Pre-Treatment	KCNB2	9312	37	8	73480219	73480219	Missense_Mutation	SNP	G	A	36	177	c.250G>A	c.(250-252)GAG>AAG	p.E84K
Pat_14	Pre-Treatment	RUNX1T1	862	37	8	92982891	92982891	Missense_Mutation	SNP	T	C	49	182	c.1534A>G	c.(1534-1536)AGC>GGC	p.S512G
Pat_14	Pre-Treatment	RAD54B	25788	37	8	95416372	95416372	Missense_Mutation	SNP	C	A	4	177	c.877G>T	c.(877-879)GTA>TTA	p.V293L
Pat_14	Pre-Treatment	MATN2	4147	37	8	99040006	99040006	Missense_Mutation	SNP	G	C	3	186	c.2305G>C	c.(2305-2307)GGA>CGA	p.G769R
Pat_14	Pre-Treatment	ODF1	4956	37	8	103564256	103564256	Missense_Mutation	SNP	G	A	24	103	c.301G>A	c.(301-303)GAG>AAG	p.E101K
Pat_14	Pre-Treatment	TM7SF4	81501	37	8	105367211	105367211	Missense_Mutation	SNP	C	T	34	150	c.1136C>T	c.(1135-1137)CCT>CTT	p.P379L
Pat_14	Pre-Treatment	PKHD1L1	93035	37	8	110478926	110478926	Missense_Mutation	SNP	C	T	28	82	c.8533C>T	c.(8533-8535)CAC>TAC	p.H2845Y
Pat_14	Pre-Treatment	CSMD3	114788	37	8	113267629	113267629	Missense_Mutation	SNP	G	T	18	101	c.9890C>A	c.(9889-9891)CCT>CAT	p.P3297H
Pat_14	Pre-Treatment	PTK2	5747	37	8	141745399	141745399	Missense_Mutation	SNP	A	G	3	93	c.1981T>C	c.(1981-1983)TAT>CAT	p.Y661H
Pat_14	Pre-Treatment	RECQL4	9401	37	8	145740757	145740757	Missense_Mutation	SNP	G	A	32	112	c.1343C>T	c.(1342-1344)CCC>CTC	p.P448L
Pat_14	Pre-Treatment	DOCK8	81704	37	9	422104	422104	Missense_Mutation	SNP	C	T	72	173	c.4210C>T	c.(4210-4212)CAT>TAT	p.H1404Y
Pat_14	Pre-Treatment	PTPRD	5789	37	9	8375948	8375948	Missense_Mutation	SNP	A	G	52	117	c.4649T>C	c.(4648-4650)GTT>GCT	p.V1550A
Pat_14	Pre-Treatment	ARID3C	138715	37	9	34627758	34627758	Missense_Mutation	SNP	G	A	43	99	c.254C>T	c.(253-255)TCG>TTG	p.S85L
Pat_14	Pre-Treatment	CNTNAP3	79937	37	9	39109157	39109157	Nonsense_Mutation	SNP	G	A	29	91	c.2365C>T	c.(2365-2367)CAG>TAG	p.Q789*
Pat_14	Pre-Treatment	TRPM3	80036	37	9	73399102	73399102	Missense_Mutation	SNP	G	A	72	261	c.1067C>T	c.(1066-1068)CCC>CTC	p.P356L
Pat_14	Pre-Treatment	PRUNE2	158471	37	9	79320862	79320862	Missense_Mutation	SNP	C	T	99	420	c.6328G>A	c.(6328-6330)GAT>AAT	p.D2110N
Pat_14	Pre-Treatment	PRUNE2	158471	37	9	79323973	79323973	Missense_Mutation	SNP	C	T	110	383	c.3217G>A	c.(3217-3219)GAA>AAA	p.E1073K
Pat_14	Pre-Treatment	FOXB2	442425	37	9	79634773	79634773	Missense_Mutation	SNP	A	G	49	181	c.203A>G	c.(202-204)AAC>AGC	p.N68S

Pat_14	Pre-Treatment	SLC28A3	64078	37	9	86893162	86893162	Missense_Mutation	SNP	T	G	51	147	c.2047A>C	c.(2047-2049)AAC>CAC	p.N683H
Pat_14	Pre-Treatment	DIRAS2	54769	37	9	93375767	93375767	Missense_Mutation	SNP	G	T	7	357	c.343C>A	c.(343-345)CCC>ACC	p.P115T
Pat_14	Pre-Treatment	FAM120AOS	158293	37	9	96214912	96214912	Missense_Mutation	SNP	C	A	31	117	c.80G>T	c.(79-81)AGT>ATT	p.S27I
Pat_14	Pre-Treatment	FAM22F	54754	37	9	97082748	97082748	Missense_Mutation	SNP	G	C	3	161	c.1110C>G	c.(1108-1110)AAC>AAG	p.N370K
Pat_14	Pre-Treatment	GABBR2	9568	37	9	101235533	101235533	Missense_Mutation	SNP	G	T	5	253	c.894C>A	c.(892-894)AAC>AAA	p.N298K
Pat_14	Pre-Treatment	NR4A3	8013	37	9	102590490	102590490	Missense_Mutation	SNP	C	T	108	423	c.166C>T	c.(166-168)CCC>TCC	p.P56S
Pat_14	Pre-Treatment	STX17	55014	37	9	102722408	102722408	Missense_Mutation	SNP	C	A	88	404	c.553C>A	c.(553-555)CTG>ATG	p.L185M
Pat_14	Pre-Treatment	PPP3R2	5535	37	9	104356864	104356864	Nonsense_Mutation	SNP	G	A	77	286	c.349C>T	c.(349-351)CAG>TAG	p.Q117*
Pat_14	Pre-Treatment	PPP3R2	5535	37	9	104357094	104357094	Missense_Mutation	SNP	G	A	80	222	c.119C>T	c.(118-120)TCT>TTT	p.S40F
Pat_14	Pre-Treatment	OR13C8	138802	37	9	107332262	107332262	Missense_Mutation	SNP	A	C	22	206	c.814A>C	c.(814-816)AAT>CAT	p.N272H
Pat_14	Pre-Treatment	OR13C9	286362	37	9	107379777	107379777	Missense_Mutation	SNP	C	T	52	178	c.709G>A	c.(709-711)GCT>ACT	p.A237T
Pat_14	Pre-Treatment	SVEP1	79987	37	9	113265384	113265384	Missense_Mutation	SNP	C	T	83	292	c.1417G>A	c.(1417-1419)GAA>AAA	p.E473K
Pat_14	Pre-Treatment	SVEP1	79987	37	9	113265434	113265434	Missense_Mutation	SNP	A	G	121	379	c.1367T>C	c.(1366-1368)ATG>ACG	p.M456T
Pat_14	Pre-Treatment	ZNF483	158399	37	9	114304974	114304974	Missense_Mutation	SNP	G	C	55	193	c.1759G>C	c.(1759-1761)GCC>CCC	p.A587P
Pat_14	Pre-Treatment	PAPPA	5069	37	9	119028231	119028231	Missense_Mutation	SNP	G	A	47	148	c.2828G>A	c.(2827-2829)GGA>GAA	p.G943E
Pat_14	Pre-Treatment	MEGF9	1955	37	9	123367743	123367743	Nonsense_Mutation	SNP	G	A	31	113	c.1645C>T	c.(1645-1647)CAA>TAA	p.Q549*
Pat_14	Pre-Treatment	LRRC8A	56262	37	9	131669646	131669646	Missense_Mutation	SNP	C	T	82	226	c.203C>T	c.(202-204)TCG>TTG	p.S68L
Pat_14	Pre-Treatment	RAPGEF1	2889	37	9	134501482	134501482	Missense_Mutation	SNP	A	G	3	88	c.1478T>C	c.(1477-1479)CTG>CCG	p.L493P
Pat_14	Pre-Treatment	COL5A1	1289	37	9	137701116	137701116	Missense_Mutation	SNP	C	T	6	32	c.3454C>T	c.(3454-3456)CCT>TCT	p.P1152S
Pat_14	Pre-Treatment	GLT6D1	360203	37	9	138516147	138516147	Missense_Mutation	SNP	C	A	6	345	c.627G>T	c.(625-627)GAG>GAT	p.E209D
Pat_14	Pre-Treatment	PMPCA	23203	37	9	139307004	139307004	Missense_Mutation	SNP	G	A	34	150	c.337G>A	c.(337-339)GAA>AAA	p.E113K
Pat_14	Pre-Treatment	FUT7	2529	37	9	139925577	139925577	Missense_Mutation	SNP	G	A	6	326	c.614C>T	c.(613-615)GCC>GTC	p.A205V
Pat_14	Pre-Treatment	NDOR1	27158	37	9	140109367	140109367	Missense_Mutation	SNP	C	T	73	210	c.962C>T	c.(961-963)TCC>TTC	p.S321F
Pat_14	Pre-Treatment	SLC25A6	293	37	X	1508364	1508364	Missense_Mutation	SNP	G	A	104	433	c.368C>T	c.(367-369)GCC>GTC	p.A123V
Pat_14	Pre-Treatment	XG	7499	37	X	2712599	2712599	Missense_Mutation	SNP	G	A	28	159	c.277G>A	c.(277-279)GAT>AAT	p.D93N
Pat_14	Pre-Treatment	GYG2	8908	37	X	2777926	2777926	Missense_Mutation	SNP	G	A	31	124	c.750G>A	c.(748-750)ATG>ATA	p.M250I
Pat_14	Pre-Treatment	ARSH	347527	37	X	2933220	2933220	Missense_Mutation	SNP	C	T	17	66	c.550C>T	c.(550-552)CCC>TCC	p.P184S
Pat_14	Pre-Treatment	MXRA5	25878	37	X	3235375	3235375	Missense_Mutation	SNP	T	A	13	66	c.6347A>T	c.(6346-6348)GAC>GTC	p.D2116V
Pat_14	Pre-Treatment	MXRA5	25878	37	X	3239504	3239504	Missense_Mutation	SNP	G	T	30	111	c.4222C>A	c.(4222-4224)CCC>ACC	p.P1408T
Pat_14	Pre-Treatment	NLGN4X	57502	37	X	5811450	5811450	Missense_Mutation	SNP	G	A	26	201	c.1859C>T	c.(1858-1860)TCA>TTA	p.S620L
Pat_14	Pre-Treatment	NLGN4X	57502	37	X	5827142	5827142	Missense_Mutation	SNP	G	A	49	197	c.764C>T	c.(763-765)GCT>GTT	p.A255V
Pat_14	Pre-Treatment	NLGN4X	57502	37	X	5827172	5827172	Missense_Mutation	SNP	G	A	42	184	c.734C>T	c.(733-735)CCC>CTC	p.P245L
Pat_14	Pre-Treatment	VCX	26609	37	X	7811770	7811770	Missense_Mutation	SNP	G	A	57	639	c.334G>A	c.(334-336)GAA>AAA	p.E112K
Pat_14	Pre-Treatment	WWC3	55841	37	X	10102545	10102545	Missense_Mutation	SNP	G	A	7	444	c.2672G>A	c.(2671-2673)CGC>CAC	p.R891H
Pat_14	Pre-Treatment	HCCS	3052	37	X	11135447	11135447	Missense_Mutation	SNP	G	A	127	581	c.313G>A	c.(313-315)GAA>AAA	p.E105K
Pat_14	Pre-Treatment	HCCS	3052	37	X	11139100	11139100	Missense_Mutation	SNP	C	T	72	439	c.595C>T	c.(595-597)CGT>TGT	p.R199C
Pat_14	Pre-Treatment	GLRA2	2742	37	X	14550453	14550453	Missense_Mutation	SNP	G	A	58	345	c.161G>A	c.(160-162)AGG>AAG	p.R54K
Pat_14	Pre-Treatment	MOSPD2	158747	37	X	14929528	14929528	Missense_Mutation	SNP	T	C	19	66	c.872T>C	c.(871-873)CTT>CCT	p.L291P
Pat_14	Pre-Treatment	SCML1	6322	37	X	17768162	17768162	Missense_Mutation	SNP	C	A	8	568	c.452C>A	c.(451-453)CCG>CAG	p.P151Q
Pat_14	Pre-Treatment	GPR64	10149	37	X	19025376	19025376	Missense_Mutation	SNP	A	T	84	427	c.1666T>A	c.(1666-1668)TTA>ATA	p.L556I
Pat_14	Pre-Treatment	PDHA1	5160	37	X	19371203	19371203	Missense_Mutation	SNP	G	A	100	571	c.422G>A	c.(421-423)CGA>CAA	p.R141Q
Pat_14	Pre-Treatment	MAP3K15	389840	37	X	19416419	19416419	Missense_Mutation	SNP	C	T	137	685	c.416G>A	c.(415-417)GGG>GAG	p.G139E
Pat_14	Pre-Treatment	MAP7D2	256714	37	X	20028977	20028978	Missense_Mutation	DNP	GG	AA	67	397	.2142_2143CC>T	2140-2145)AACCTT>AATT	p.L715F
Pat_14	Pre-Treatment	ZNF645	158506	37	X	22291373	22291373	Nonsense_Mutation	SNP	G	T	6	520	c.265G>T	c.(265-267)GGA>TGA	p.G89*
Pat_14	Pre-Treatment	SAT1	6303	37	X	23801803	23801803	Missense_Mutation	SNP	A	G	37	129	c.95A>G	c.(94-96)GAA>GGA	p.E32G
Pat_14	Pre-Treatment	PDK3	5165	37	X	24521545	24521545	Missense_Mutation	SNP	C	A	72	216	c.422C>A	c.(421-423)CCT>CAT	p.P141H
Pat_14	Pre-Treatment	POLA1	5422	37	X	24735407	24735407	Missense_Mutation	SNP	G	A	64	207	c.689G>A	c.(688-690)GGC>GAC	p.G230D

Pat_14	Pre-Treatment	MAGEB18	286514	37	X	26157394	26157394	Missense_Mutation	SNP	G	A	21	58	c.292G>A	c.(292-294)GAA>AAA	p.E98K
Pat_14	Pre-Treatment	GPR34	2857	37	X	41555572	41555572	Missense_Mutation	SNP	T	C	4	119	c.686T>C	c.(685-687)CTA>CCA	p.L229P
Pat_14	Pre-Treatment	GPR34	2857	37	X	41555592	41555592	Missense_Mutation	SNP	C	T	18	69	c.706C>T	c.(706-708)CTT>TTT	p.L236F
Pat_14	Pre-Treatment	MAOB	4129	37	X	43656391	43656391	Missense_Mutation	SNP	G	A	71	343	c.599C>T	c.(598-600)TCG>TTG	p.S200L
Pat_14	Pre-Treatment	USP11	8237	37	X	47104279	47104279	Missense_Mutation	SNP	C	T	41	158	c.2171C>T	c.(2170-2172)TCC>TTC	p.S724F
Pat_14	Pre-Treatment	ZNF41	7592	37	X	47307289	47307289	Missense_Mutation	SNP	C	T	37	193	c.2006G>A	c.(2005-2007)AGA>AAA	p.R669K
Pat_14	Pre-Treatment	PPP1R3F	89801	37	X	49142678	49142679	Missense_Mutation	DNP	GG	AA	24	127	.1526_1527GG>A	c.(1525-1527)GGG>GAA	p.G509E
Pat_14	Pre-Treatment	DGKK	139189	37	X	50119065	50119065	Missense_Mutation	SNP	G	T	18	117	c.3372C>A	c.(3370-3372)GAC>GAA	p.D1124E
Pat_14	Pre-Treatment	SSX7	280658	37	X	52682006	52682006	Missense_Mutation	SNP	G	A	50	287	c.98C>T	c.(97-99)TCT>TTT	p.S33F
Pat_14	Pre-Treatment	TSPYL2	64061	37	X	53111883	53111883	Missense_Mutation	SNP	C	T	5	17	c.203C>T	c.(202-204)CCC>CTC	p.P68L
Pat_14	Pre-Treatment	ITIH5L	347365	37	X	54781500	54781500	Missense_Mutation	SNP	C	T	83	381	c.3152G>A	c.(3151-3153)GGA>GAA	p.G1051E
Pat_14	Pre-Treatment	TRO	7216	37	X	54949425	54949425	Missense_Mutation	SNP	C	A	5	180	c.460C>A	c.(460-462)CAA>AAA	p.Q154K
Pat_14	Pre-Treatment	HEPH	9843	37	X	65408222	65408222	Missense_Mutation	SNP	C	T	4	17	c.656C>T	c.(655-657)CCT>CTT	p.P219L
Pat_14	Pre-Treatment	PJA1	64219	37	X	68381389	68381389	Missense_Mutation	SNP	C	T	56	209	c.1693G>A	c.(1693-1695)GCC>ACC	p.A565T
Pat_14	Pre-Treatment	DGAT2L6	347516	37	X	69419665	69419665	Missense_Mutation	SNP	G	T	5	214	c.200G>T	c.(199-201)GGC>GTC	p.G67V
Pat_14	Pre-Treatment	TAF1	6872	37	X	70597592	70597592	Missense_Mutation	SNP	C	T	65	345	c.851C>T	c.(850-852)TCA>TTA	p.S284L
Pat_14	Pre-Treatment	NAP1L2	4674	37	X	72433494	72433494	Missense_Mutation	SNP	G	A	38	103	c.835C>T	c.(835-837)CCT>TCT	p.P279S
Pat_14	Pre-Treatment	TNMD	64102	37	X	99852643	99852643	Missense_Mutation	SNP	C	T	54	180	c.566C>T	c.(565-567)ACT>ATT	p.T189I
Pat_14	Pre-Treatment	DRP2	1821	37	X	100497387	100497387	Missense_Mutation	SNP	T	A	139	596	c.902T>A	c.(901-903)ATT>AAT	p.I301N
Pat_14	Pre-Treatment	ARMCX1	51309	37	X	100808511	100808511	Missense_Mutation	SNP	G	A	88	493	c.598G>A	c.(598-600)GAT>AAT	p.D200N
Pat_14	Pre-Treatment	ARMCX1	51309	37	X	100809053	100809053	Missense_Mutation	SNP	A	T	17	99	c.1140A>T	c.(1138-1140)GAA>GAT	p.E380D
Pat_14	Pre-Treatment	ARMCX3	51566	37	X	100881069	100881069	Missense_Mutation	SNP	C	A	7	616	c.1100C>A	c.(1099-1101)GCC>GAC	p.A367D
Pat_14	Pre-Treatment	ZMAT1	84460	37	X	101139146	101139146	Missense_Mutation	SNP	C	T	112	649	c.740G>A	c.(739-741)GGA>GAA	p.G247E
Pat_14	Pre-Treatment	GPRASP1	9737	37	X	101912133	101912133	Nonsense_Mutation	SNP	C	T	131	474	c.3292C>T	c.(3292-3294)CAG>TAG	p.Q1098*
Pat_14	Pre-Treatment	NRK	203447	37	X	105150462	105150462	Missense_Mutation	SNP	C	T	8	29	c.901C>T	c.(901-903)CGT>TGT	p.R301C
Pat_14	Pre-Treatment	SERPINA7	6906	37	X	105279352	105279352	Missense_Mutation	SNP	G	A	117	364	c.647C>T	c.(646-648)CCA>CTA	p.P216L
Pat_14	Pre-Treatment	SERPINA7	6906	37	X	105280502	105280502	Missense_Mutation	SNP	C	T	121	483	c.548G>A	c.(547-549)GGG>GAG	p.G183E
Pat_14	Pre-Treatment	MORC4	79710	37	X	106201686	106201686	Missense_Mutation	SNP	G	A	4	242	c.1265C>T	c.(1264-1266)CCT>CTT	p.P422L
Pat_14	Pre-Treatment	ATG4A	115201	37	X	107396209	107396209	Missense_Mutation	SNP	G	A	19	111	c.1018G>A	c.(1018-1020)GAA>AAA	p.E340K
Pat_14	Pre-Treatment	COL4A5	1287	37	X	107925011	107925011	Missense_Mutation	SNP	C	T	66	226	c.4109C>T	c.(4108-4110)CCT>CTT	p.P1370L
Pat_14	Pre-Treatment	COL4A5	1287	37	X	107938575	107938575	Missense_Mutation	SNP	C	T	76	412	c.4900C>T	c.(4900-4902)CCC>TCC	p.P1634S
Pat_14	Pre-Treatment	RGAG1	57529	37	X	109695288	109695288	Missense_Mutation	SNP	G	A	90	306	c.1443G>A	c.(1441-1443)ATG>ATA	p.M481I
Pat_14	Pre-Treatment	HTR2C	3358	37	X	113965791	113965791	Missense_Mutation	SNP	G	A	107	521	c.124G>A	c.(124-126)GAT>AAT	p.D42N
Pat_14	Pre-Treatment	SLC6A14	11254	37	X	115573945	115573945	Missense_Mutation	SNP	C	T	89	386	c.437C>T	c.(436-438)TCT>TTT	p.S146F
Pat_14	Pre-Treatment	THOC2	57187	37	X	122800960	122800960	Missense_Mutation	SNP	C	T	57	272	c.1187G>A	c.(1186-1188)CGA>CAA	p.R396Q
Pat_14	Pre-Treatment	MST4	51765	37	X	131188719	131188719	Missense_Mutation	SNP	T	A	56	324	c.103T>A	c.(103-105)TTT>ATT	p.F35I
Pat_14	Pre-Treatment	GPC3	2719	37	X	132887882	132887882	Missense_Mutation	SNP	G	A	61	316	c.659C>T	c.(658-660)TCC>TTC	p.S220F
Pat_14	Pre-Treatment	DDX26B	203522	37	X	134703264	134703264	Missense_Mutation	SNP	G	A	47	229	c.1195G>A	c.(1195-1197)GAC>AAC	p.D399N
Pat_14	Pre-Treatment	MAP7D3	79649	37	X	135313960	135313960	Missense_Mutation	SNP	G	A	56	331	c.1156C>T	c.(1156-1158)CCG>TCG	p.P386S
Pat_14	Pre-Treatment	SPANXE	171489	37	X	140785698	140785698	Missense_Mutation	SNP	C	T	146	591	c.218G>A	c.(217-219)CGA>CAA	p.R73Q
Pat_14	Pre-Treatment	FMR1	2332	37	X	147014282	147014282	Missense_Mutation	SNP	G	A	19	88	c.880G>A	c.(880-882)GGC>AGC	p.G294S
Pat_14	Pre-Treatment	FMR1	2332	37	X	147019004	147019004	Missense_Mutation	SNP	C	T	24	200	c.1010C>T	c.(1009-1011)TCC>TTC	p.S337F
Pat_14	Pre-Treatment	FMR1NB	158521	37	X	147088287	147088287	Missense_Mutation	SNP	G	A	90	533	c.463G>A	c.(463-465)GAA>AAA	p.E155K
Pat_14	Pre-Treatment	MTM1	4534	37	X	149831957	149831957	Missense_Mutation	SNP	G	A	23	139	c.1519G>A	c.(1519-1521)GAA>AAA	p.E507K
Pat_14	Pre-Treatment	MTM1	4534	37	X	149832076	149832076	Missense_Mutation	SNP	G	C	69	336	c.1638G>C	c.(1636-1638)AAG>AAC	p.K546N
Pat_14	Pre-Treatment	HMGB3	3149	37	X	150156314	150156314	Missense_Mutation	SNP	G	A	33	183	c.530G>A	c.(529-531)CGG>CAG	p.R177Q
Pat_14	Pre-Treatment	IDH3G	3421	37	X	153052370	153052370	Missense_Mutation	SNP	C	A	7	660	c.810G>T	c.(808-810)ATG>ATT	p.M270I

Pat_14	Pre-Treatment	FLNA	2316	37	X	153580606	153580606	Missense_Mutation	SNP	C	T	15	75	c.6712G>A	c.(6712-6714)GCC>ACC	p.A2238T
Pat_14	Pre-Treatment	FAM50A	9130	37	X	153673981	153673981	Missense_Mutation	SNP	G	A	69	220	c.112G>A	c.(112-114)GAG>AAG	p.E38K
Pat_14	Post-Resistance	MRPL20	55052	37	1	1337517	1337517	Missense_Mutation	SNP	C	A	6	631	c.396G>T	c.(394-396)TTG>TTT	p.L132F
Pat_14	Post-Resistance	SLC35E2	9906	37	1	1670392	1670392	Missense_Mutation	SNP	G	A	3	46	c.427C>T	c.(427-429)CTT>TTT	p.L143F
Pat_14	Post-Resistance	PRDM16	63976	37	1	3342201	3342201	Missense_Mutation	SNP	G	A	4	293	c.2996G>A	c.(2995-2997)CGG>CAG	p.R999Q
Pat_14	Post-Resistance	PIK3CD	5293	37	1	9780004	9780004	Missense_Mutation	SNP	T	G	22	690	c.1268T>G	c.(1267-1269)CTC>CGC	p.L423R
Pat_14	Post-Resistance	MTHFR	4524	37	1	11860307	11860307	Missense_Mutation	SNP	C	T	7	740	c.548G>A	c.(547-549)CGA>CAA	p.R183Q
Pat_14	Post-Resistance	VPS13D	55187	37	1	12387746	12387746	Missense_Mutation	SNP	G	A	8	625	c.8032G>A	c.(8032-8034)GAA>AAA	p.E2678K
Pat_14	Post-Resistance	TMEM82	388595	37	1	16073424	16073424	Missense_Mutation	SNP	G	A	3	69	c.820G>A	c.(820-822)GGC>AGC	p.G274S
Pat_14	Post-Resistance	ARHGEF19	128272	37	1	16528960	16528960	Missense_Mutation	SNP	G	A	4	132	c.2017C>T	c.(2017-2019)CTC>TTC	p.L673F
Pat_14	Post-Resistance	TAS1R2	80834	37	1	19175834	19175834	Splice_Site	SNP	C	T	4	134	c.1467_splice	c.e4+1	p.T489_splice
Pat_14	Post-Resistance	UBR4	23352	37	1	19500845	19500845	Missense_Mutation	SNP	T	C	10	135	c.2950A>G	c.(2950-2952)AGG>GGG	p.R984G
Pat_14	Post-Resistance	TMCO4	255104	37	1	20009544	20009544	Missense_Mutation	SNP	C	T	5	421	c.1894G>A	c.(1894-1896)GGG>AGG	p.G632R
Pat_14	Post-Resistance	ZNF683	257101	37	1	26688465	26688465	Missense_Mutation	SNP	G	A	4	249	c.1252C>T	c.(1252-1254)CGC>TGC	p.R418C
Pat_14	Post-Resistance	GPN2	54707	37	1	27216448	27216448	Missense_Mutation	SNP	G	A	3	64	c.140C>T	c.(139-141)CCG>CTG	p.P47L
Pat_14	Post-Resistance	EYA3	2140	37	1	28362145	28362146	Missense_Mutation	DNP	GG	AA	9	595	c.270_271CC>TT	(268-273)TACCCT>TATTC	p.P91S
Pat_14	Post-Resistance	MATN1	4146	37	1	31188972	31188972	Missense_Mutation	SNP	G	A	4	301	c.991C>T	c.(991-993)CGC>TGC	p.R331C
Pat_14	Post-Resistance	HCRTR1	3061	37	1	32089159	32089159	Nonsense_Mutation	SNP	G	A	5	137	c.774G>A	c.(772-774)TGG>TGA	p.W258*
Pat_14	Post-Resistance	NASP	4678	37	1	46068000	46068000	Missense_Mutation	SNP	G	A	6	536	c.181G>A	c.(181-183)GCA>ACA	p.A61T
Pat_14	Post-Resistance	LEPR	3953	37	1	66102393	66102393	Missense_Mutation	SNP	G	A	6	480	c.3193G>A	c.(3193-3195)GGA>AGA	p.G1065R
Pat_14	Post-Resistance	SGIP1	84251	37	1	67155937	67155937	Missense_Mutation	SNP	C	T	5	651	c.1508C>T	c.(1507-1509)GCT>GTT	p.A503V
Pat_14	Post-Resistance	ZZZ3	26009	37	1	78097637	78097637	Missense_Mutation	SNP	G	A	5	435	c.1403C>T	c.(1402-1404)TCT>TTT	p.S468F
Pat_14	Post-Resistance	SPATA1	64173	37	1	84988111	84988111	Missense_Mutation	SNP	G	A	6	468	c.248G>A	c.(247-249)CGT>CAT	p.R83H
Pat_14	Post-Resistance	MCOLN2	255231	37	1	85403726	85403726	Missense_Mutation	SNP	T	C	3	233	c.1150A>G	c.(1150-1152)ACC>GCC	p.T384A
Pat_14	Post-Resistance	GFI1	2672	37	1	92944274	92944274	Missense_Mutation	SNP	A	G	6	358	c.961T>C	c.(961-963)TTC>CTC	p.F321L
Pat_14	Post-Resistance	WDR77	79084	37	1	111985384	111985384	Splice_Site	SNP	C	T	3	101	c.692_splice	c.e8-1	p.G231_splice
Pat_14	Post-Resistance	VANGL1	81839	37	1	116225094	116225094	Missense_Mutation	SNP	G	A	6	335	c.922G>A	c.(922-924)GGG>AGG	p.G308R
Pat_14	Post-Resistance	REG4	83998	37	1	120345764	120345764	Missense_Mutation	SNP	G	A	4	198	c.92C>T	c.(91-93)GCT>GTT	p.A31V
Pat_14	Post-Resistance	POGZ	23126	37	1	151414670	151414670	Missense_Mutation	SNP	G	A	4	184	c.11C>T	c.(10-12)ACC>ATC	p.T4I
Pat_14	Post-Resistance	RPTN	126638	37	1	152127833	152127833	Missense_Mutation	SNP	G	A	13	846	c.1742C>T	c.(1741-1743)TCC>TTC	p.S581F
Pat_14	Post-Resistance	NUP210L	91181	37	1	154029322	154029322	Missense_Mutation	SNP	C	T	6	332	c.3209G>A	c.(3208-3210)AGA>AAA	p.R1070K
Pat_14	Post-Resistance	THBS3	7059	37	1	155172167	155172167	Missense_Mutation	SNP	G	A	5	371	c.983C>T	c.(982-984)CCG>CTG	p.P328L
Pat_14	Post-Resistance	CCT3	7203	37	1	156287302	156287302	Nonsense_Mutation	SNP	G	A	43	695	c.796C>T	c.(796-798)CGA>TGA	p.R266*
Pat_14	Post-Resistance	DCAF8	50717	37	1	160208525	160208525	Missense_Mutation	SNP	G	A	4	112	c.736C>T	c.(736-738)CCT>TCT	p.P246S
Pat_14	Post-Resistance	SLAMF6	114836	37	1	160460002	160460002	Missense_Mutation	SNP	C	T	29	498	c.782G>A	c.(781-783)CGA>CAA	p.R261Q
Pat_14	Post-Resistance	ADAMTS4	9507	37	1	161161952	161161952	Missense_Mutation	SNP	G	A	4	271	c.1990C>T	c.(1990-1992)CGC>TGC	p.R664C
Pat_14	Post-Resistance	TMCO1	54499	37	1	165697280	165697280	Missense_Mutation	SNP	G	A	7	331	c.547C>T	c.(547-549)CCT>TCT	p.P183S
Pat_14	Post-Resistance	GPR161	23432	37	1	168066390	168066390	Missense_Mutation	SNP	C	A	4	299	c.455G>T	c.(454-456)TGG>TTG	p.W152L
Pat_14	Post-Resistance	FMO1	2326	37	1	171254581	171254581	Missense_Mutation	SNP	C	G	3	181	c.1497C>G	c.(1495-1497)ATC>ATG	p.I499M
Pat_14	Post-Resistance	ANGPTL1	9068	37	1	178834461	178834461	Missense_Mutation	SNP	G	C	3	150	c.451C>G	c.(451-453)CTT>GTT	p.L151V
Pat_14	Post-Resistance	HMCN1	83872	37	1	186076094	186076094	Missense_Mutation	SNP	C	G	4	446	c.10849C>G	c.(10849-10851)CAT>GAT	p.H3617D
Pat_14	Post-Resistance	PRG4	10216	37	1	186276415	186276415	Missense_Mutation	SNP	C	G	3	282	c.1564C>G	c.(1564-1566)CCT>GCT	p.P522A
Pat_14	Post-Resistance	TPR	7175	37	1	186289534	186289534	Missense_Mutation	SNP	C	A	4	204	c.6478G>T	c.(6478-6480)GGT>TGT	p.G2160C
Pat_14	Post-Resistance	NEK7	140609	37	1	198231733	198231733	Missense_Mutation	SNP	G	A	5	601	c.227G>A	c.(226-228)CGT>CAT	p.R76H
Pat_14	Post-Resistance	PKP1	5317	37	1	201294905	201294905	Missense_Mutation	SNP	C	T	4	239	c.2108C>T	c.(2107-2109)GCT>GTT	p.A703V
Pat_14	Post-Resistance	NFASC	23114	37	1	204944482	204944482	Missense_Mutation	SNP	G	A	15	507	c.1642G>A	c.(1642-1644)GAC>AAC	p.D548N
Pat_14	Post-Resistance	RASSF5	83593	37	1	206757842	206757842	Missense_Mutation	SNP	G	A	6	704	c.814G>A	c.(814-816)GCT>ACT	p.A272T

Pat_14	Post-Resistance	CD55	1604	37	1	207499054	207499054	Missense_Mutation	SNP	C	T	6	455	c.566C>T	c.(565-567)TCA>TTA	p.S189L
Pat_14	Post-Resistance	ANGEL2	90806	37	1	213178649	213178649	Missense_Mutation	SNP	C	T	4	264	c.860G>A	c.(859-861)GGA>GAA	p.G287E
Pat_14	Post-Resistance	HHIPL2	79802	37	1	222705401	222705401	Missense_Mutation	SNP	C	T	4	112	c.1630G>A	c.(1630-1632)GAT>AAT	p.D544N
Pat_14	Post-Resistance	SCCPDH	51097	37	1	246930548	246930548	Missense_Mutation	SNP	C	A	4	277	c.1236C>A	c.(1234-1236)GAC>GAA	p.D412E
Pat_14	Post-Resistance	CAMK1D	57118	37	10	12833213	12833213	Missense_Mutation	SNP	G	A	4	438	c.622G>A	c.(622-624)GGA>AGA	p.G208R
Pat_14	Post-Resistance	LOC387646	387646	37	10	27538021	27538021	Missense_Mutation	SNP	G	A	7	585	c.1372C>T	c.(1372-1374)CCA>TCA	p.P458S
Pat_14	Post-Resistance	LOC387646	387646	37	10	27539257	27539257	Missense_Mutation	SNP	C	T	5	230	c.136G>A	c.(136-138)GAG>AAG	p.E46K
Pat_14	Post-Resistance	ANKRD30A	91074	37	10	37441009	37441009	Missense_Mutation	SNP	C	T	7	288	c.1499C>T	c.(1498-1500)TCC>TTC	p.S500F
Pat_14	Post-Resistance	PCDH15	65217	37	10	55719502	55719502	Missense_Mutation	SNP	C	T	4	174	c.3112G>A	c.(3112-3114)GAG>AAG	p.E1038K
Pat_14	Post-Resistance	LRRTM3	347731	37	10	68686937	68686937	Missense_Mutation	SNP	C	T	4	481	c.263C>T	c.(262-264)ACC>ATC	p.T88I
Pat_14	Post-Resistance	AGAP5	729092	37	10	75434521	75434521	Missense_Mutation	SNP	G	A	7	576	c.1897C>T	c.(1897-1899)CGC>TGC	p.R633C
Pat_14	Post-Resistance	KIAA0913	23053	37	10	75553993	75553993	Missense_Mutation	SNP	G	A	5	557	c.2714G>A	c.(2713-2715)CGG>CAG	p.R905Q
Pat_14	Post-Resistance	LGI1	9211	37	10	95556737	95556737	Missense_Mutation	SNP	T	C	4	311	c.851T>C	c.(850-852)GTA>GCA	p.V284A
Pat_14	Post-Resistance	PDLIM1	9124	37	10	97007004	97007004	Missense_Mutation	SNP	A	G	14	272	c.653T>C	c.(652-654)GTT>GCT	p.V218A
Pat_14	Post-Resistance	CWF19L1	55280	37	10	101997957	101997957	Missense_Mutation	SNP	G	A	4	492	c.1076C>T	c.(1075-1077)TCT>TTT	p.S359F
Pat_14	Post-Resistance	RPL13AP6	644511	37	10	112696573	112696573	Missense_Mutation	SNP	T	C	6	38	c.419A>G	c.(418-420)CAC>CGC	p.H140R
Pat_14	Post-Resistance	TECTB	6975	37	10	114046122	114046122	Missense_Mutation	SNP	G	C	4	303	c.456G>C	c.(454-456)GAG>GAC	p.E152D
Pat_14	Post-Resistance	PNLIP	5406	37	10	118315596	118315596	Missense_Mutation	SNP	G	A	30	610	c.896G>A	c.(895-897)GGA>GAA	p.G299E
Pat_14	Post-Resistance	VAX1	11023	37	10	118896051	118896051	Missense_Mutation	SNP	G	A	4	134	c.361C>T	c.(361-363)CGC>TGC	p.R121C
Pat_14	Post-Resistance	SIRT3	23410	37	11	224158	224158	Missense_Mutation	SNP	G	A	4	187	c.889C>T	c.(889-891)CCG>TCG	p.P297S
Pat_14	Post-Resistance	CDHR5	53841	37	11	617476	617476	Missense_Mutation	SNP	C	T	4	201	c.2413G>A	c.(2413-2415)GTT>ATT	p.V805I
Pat_14	Post-Resistance	CEND1	51286	37	11	788498	788498	Missense_Mutation	SNP	G	A	7	610	c.79C>T	c.(79-81)CCC>TCC	p.P27S
Pat_14	Post-Resistance	MUC5B	727897	37	11	1270916	1270916	Missense_Mutation	SNP	C	T	5	457	c.14225C>T	c.(14224-14226)CCG>CTG	p.P4742L
Pat_14	Post-Resistance	KRTAP5-1	387264	37	11	1606443	1606443	Missense_Mutation	SNP	T	C	5	490	c.37A>G	c.(37-39)AGC>GGC	p.S13G
Pat_14	Post-Resistance	NUP98	4928	37	11	3726490	3726490	Missense_Mutation	SNP	C	T	4	323	c.3022G>A	c.(3022-3024)GAA>AAA	p.E1008K
Pat_14	Post-Resistance	OR52I2	143502	37	11	4608538	4608538	Missense_Mutation	SNP	C	T	5	210	c.496C>T	c.(496-498)CTC>TTC	p.L166F
Pat_14	Post-Resistance	MUC15	143662	37	11	26582751	26582751	Missense_Mutation	SNP	G	A	5	175	c.866C>T	c.(865-867)CCG>CTG	p.P289L
Pat_14	Post-Resistance	PDHX	8050	37	11	35016537	35016537	Missense_Mutation	SNP	G	A	5	487	c.1324G>A	c.(1324-1326)GTT>ATT	p.V442I
Pat_14	Post-Resistance	PAMR1	25891	37	11	35456299	35456299	Missense_Mutation	SNP	G	A	7	491	c.1387C>T	c.(1387-1389)CCG>TCG	p.P463S
Pat_14	Post-Resistance	CD82	3732	37	11	44621717	44621717	Missense_Mutation	SNP	G	A	5	364	c.73G>A	c.(73-75)GCA>ACA	p.A25T
Pat_14	Post-Resistance	KIAA0652	9776	37	11	46690091	46690091	Missense_Mutation	SNP	C	A	7	503	c.1195C>A	c.(1195-1197)CCC>ACC	p.P399T
Pat_14	Post-Resistance	NR1H3	10062	37	11	47283236	47283236	Missense_Mutation	SNP	C	T	4	255	c.847C>T	c.(847-849)CGG>TGG	p.R283W
Pat_14	Post-Resistance	OR5L2	26338	37	11	55595079	55595079	Missense_Mutation	SNP	C	T	8	623	c.385C>T	c.(385-387)CCC>TCC	p.P129S
Pat_14	Post-Resistance	TMEM132A	54972	37	11	60703700	60703700	Missense_Mutation	SNP	C	T	4	227	c.2393C>T	c.(2392-2394)GCA>GTA	p.A798V
Pat_14	Post-Resistance	DAK	26007	37	11	61105443	61105444	Missense_Mutation	DNP	GG	AA	6	336	c.34_35GG>AA	c.(34-36)GGC>AAC	p.G12N
Pat_14	Post-Resistance	SLC22A9	114571	37	11	63137889	63137889	Missense_Mutation	SNP	G	A	22	354	c.361G>A	c.(361-363)GTG>ATG	p.V121M
Pat_14	Post-Resistance	PYGM	5837	37	11	64514193	64514193	Missense_Mutation	SNP	G	A	4	282	c.2467C>T	c.(2467-2469)CGG>TGG	p.R823W
Pat_14	Post-Resistance	KDM2A	22992	37	11	66983373	66983373	Missense_Mutation	SNP	G	A	7	813	c.640G>A	c.(640-642)GAC>AAC	p.D214N
Pat_14	Post-Resistance	LRP5	4041	37	11	68216515	68216515	Missense_Mutation	SNP	T	C	4	428	c.4825T>C	c.(4825-4827)TCC>CCC	p.S1609P
Pat_14	Post-Resistance	FOLR1	2348	37	11	71906493	71906493	Nonsense_Mutation	SNP	G	A	23	417	c.347G>A	c.(346-348)TGG>TAG	p.W116*
Pat_14	Post-Resistance	INPPL1	3636	37	11	71944716	71944716	Missense_Mutation	SNP	G	A	5	579	c.2140G>A	c.(2140-2142)GTC>ATC	p.V714I
Pat_14	Post-Resistance	FAM168A	23201	37	11	73120604	73120604	Missense_Mutation	SNP	G	A	35	419	c.550C>T	c.(550-552)CCT>TCT	p.P184S
Pat_14	Post-Resistance	RSF1	51773	37	11	77402217	77402217	Missense_Mutation	SNP	G	A	4	356	c.2887C>T	c.(2887-2889)CGT>TGT	p.R963C
Pat_14	Post-Resistance	USP35	57558	37	11	77921641	77921641	Missense_Mutation	SNP	C	T	7	458	c.2740C>T	c.(2740-2742)CCT>TCT	p.P914S
Pat_14	Post-Resistance	PRSS23	11098	37	11	86518693	86518693	Missense_Mutation	SNP	G	A	5	580	c.8G>A	c.(7-9)GGG>GAG	p.G3E
Pat_14	Post-Resistance	ENDOD1	23052	37	11	94862534	94862534	Missense_Mutation	SNP	C	T	6	484	c.1294C>T	c.(1294-1296)CGT>TGT	p.R432C
Pat_14	Post-Resistance	ELMOD1	55531	37	11	107535837	107535837	Missense_Mutation	SNP	C	T	9	542	c.919C>T	c.(919-921)CGC>TGC	p.R307C

Pat_14	Post-Resistance	RAB39	54734	37	11	107799505	107799505	Missense_Mutation	SNP	G	A	3	46	c.211G>A	c.(211-213)GGA>AGA	p.G71R
Pat_14	Post-Resistance	CUL5	8065	37	11	107940828	107940828	Missense_Mutation	SNP	G	A	6	503	c.786G>A	c.(784-786)ATG>ATA	p.M262I
Pat_14	Post-Resistance	SIDT2	51092	37	11	117063304	117063304	Missense_Mutation	SNP	C	T	4	387	c.1996C>T	c.(1996-1998)CGC>TGC	p.R666C
Pat_14	Post-Resistance	SLC37A4	2542	37	11	118896706	118896706	Missense_Mutation	SNP	G	A	3	73	c.955C>T	c.(955-957)CGG>TGG	p.R319W
Pat_14	Post-Resistance	NLRX1	79671	37	11	119045519	119045519	Missense_Mutation	SNP	C	T	4	186	c.1207C>T	c.(1207-1209)CGC>TGC	p.R403C
Pat_14	Post-Resistance	SORL1	6653	37	11	121448004	121448004	Missense_Mutation	SNP	C	T	4	371	c.3475C>T	c.(3475-3477)CGG>TGG	p.R1159W
Pat_14	Post-Resistance	OR8D4	338662	37	11	123777707	123777707	Missense_Mutation	SNP	C	T	35	655	c.569C>T	c.(568-570)TCC>TTC	p.S190F
Pat_14	Post-Resistance	C11orf45	219833	37	11	128774412	128774412	Missense_Mutation	SNP	G	A	4	367	c.50C>T	c.(49-51)CCG>CTG	p.P17L
Pat_14	Post-Resistance	LOC100288778	100288778	37	12	88651	88651	Missense_Mutation	SNP	A	G	5	36	c.160A>G	c.(160-162)AGC>GGC	p.S54G
Pat_14	Post-Resistance	CD4	920	37	12	6927640	6927640	Missense_Mutation	SNP	G	A	4	281	c.1210G>A	c.(1210-1212)GGC>AGC	p.G404S
Pat_14	Post-Resistance	CLEC4A	50856	37	12	8278202	8278202	Missense_Mutation	SNP	C	T	9	327	c.128C>T	c.(127-129)CCC>CTC	p.P43L
Pat_14	Post-Resistance	CLEC4E	26253	37	12	8692544	8692544	Splice_Site	SNP	C	T	4	364	c.38_splice	c.e2-1	p.E13_splice
Pat_14	Post-Resistance	A2ML1	144568	37	12	9007419	9007419	Missense_Mutation	SNP	G	A	4	301	c.2756G>A	c.(2755-2757)TGC>TAC	p.C919Y
Pat_14	Post-Resistance	A2M	2	37	12	9254219	9254219	Missense_Mutation	SNP	C	T	4	162	c.1318G>A	c.(1318-1320)GAA>AAA	p.E440K
Pat_14	Post-Resistance	PRB3	5544	37	12	11420521	11420521	Missense_Mutation	SNP	C	T	9	332	c.662G>A	c.(661-663)CGT>CAT	p.R221H
Pat_14	Post-Resistance	PRB4	5545	37	12	11461694	11461694	Missense_Mutation	SNP	G	A	8	704	c.223C>T	c.(223-225)CCA>TCA	p.P75S
Pat_14	Post-Resistance	SLCO1B1	10599	37	12	21331569	21331569	Missense_Mutation	SNP	C	T	8	361	c.541C>T	c.(541-543)CGT>TGT	p.R181C
Pat_14	Post-Resistance	C12orf35	55196	37	12	32134340	32134340	Missense_Mutation	SNP	G	A	5	185	c.451G>A	c.(451-453)GCA>ACA	p.A151T
Pat_14	Post-Resistance	KIF21A	55605	37	12	39726854	39726854	Missense_Mutation	SNP	A	G	4	397	c.2543T>C	c.(2542-2544)GTT>GCT	p.V848A
Pat_14	Post-Resistance	FAM113B	91523	37	12	47629250	47629251	Missense_Mutation	DNP	CC	TT	9	293	c.404_405CC>TT	c.(403-405)TCC>TTT	p.S135F
Pat_14	Post-Resistance	CCNT1	904	37	12	49087735	49087735	Missense_Mutation	SNP	G	A	4	463	c.1262C>T	c.(1261-1263)GCT>GTT	p.A421V
Pat_14	Post-Resistance	FMNL3	91010	37	12	50043290	50043290	Missense_Mutation	SNP	G	A	5	320	c.2267C>T	c.(2266-2268)TCC>TTC	p.S756F
Pat_14	Post-Resistance	KRT8	3856	37	12	53298675	53298675	Missense_Mutation	SNP	A	C	4	49	c.91T>G	c.(91-93)TCC>GCC	p.S31A
Pat_14	Post-Resistance	ATF7	11016	37	12	53925613	53925613	Missense_Mutation	SNP	G	A	4	94	c.875C>T	c.(874-876)ACT>ATT	p.T292I
Pat_14	Post-Resistance	ORMDL2	29095	37	12	56213210	56213210	Missense_Mutation	SNP	G	A	13	599	c.259G>A	c.(259-261)GAG>AAG	p.E87K
Pat_14	Post-Resistance	BAZ2A	11176	37	12	56993106	56993106	Missense_Mutation	SNP	G	A	4	114	c.5215C>T	c.(5215-5217)CCA>TCA	p.P1739S
Pat_14	Post-Resistance	ATP5B	506	37	12	57032915	57032915	Missense_Mutation	SNP	G	C	5	706	c.1464C>G	c.(1462-1464)ATC>ATG	p.I488M
Pat_14	Post-Resistance	ARHGAP9	64333	37	12	57872988	57872988	Missense_Mutation	SNP	C	T	4	332	c.415G>A	c.(415-417)GAA>AAA	p.E139K
Pat_14	Post-Resistance	LGR5	8549	37	12	71978321	71978321	Missense_Mutation	SNP	C	T	7	292	c.2531C>T	c.(2530-2532)TCA>TTA	p.S844L
Pat_14	Post-Resistance	TPH2	121278	37	12	72338465	72338465	Missense_Mutation	SNP	C	A	5	418	c.539C>A	c.(538-540)CCA>CAA	p.P180Q
Pat_14	Post-Resistance	C12orf50	160419	37	12	88381686	88381686	Missense_Mutation	SNP	G	A	4	336	c.758C>T	c.(757-759)ACG>ATG	p.T253M
Pat_14	Post-Resistance	STAB2	55576	37	12	104049270	104049270	Missense_Mutation	SNP	G	A	4	354	c.1645G>A	c.(1645-1647)GTT>ATT	p.V549I
Pat_14	Post-Resistance	RFX4	5992	37	12	107090148	107090148	Missense_Mutation	SNP	G	A	4	478	c.757G>A	c.(757-759)GGC>AGC	p.G253S
Pat_14	Post-Resistance	UBE3B	89910	37	12	109928880	109928880	Missense_Mutation	SNP	C	T	4	399	c.661C>T	c.(661-663)CGT>TGT	p.R221C
Pat_14	Post-Resistance	P2RX4	5025	37	12	121660807	121660807	Missense_Mutation	SNP	C	T	4	182	c.485C>T	c.(484-486)GCG>GTG	p.A162V
Pat_14	Post-Resistance	ANAPC5	51433	37	12	121766151	121766151	Missense_Mutation	SNP	C	G	9	203	c.1272G>C	c.(1270-1272)CAG>CAC	p.Q424H
Pat_14	Post-Resistance	CLIP1	6249	37	12	122862135	122862135	Missense_Mutation	SNP	G	A	5	561	c.458C>T	c.(457-459)ACG>ATG	p.T153M
Pat_14	Post-Resistance	SLC15A4	121260	37	12	129278838	129278838	Missense_Mutation	SNP	G	A	5	303	c.1637C>T	c.(1636-1638)ACC>ATC	p.T546I
Pat_14	Post-Resistance	TMEM132D	121256	37	12	129694154	129694154	Missense_Mutation	SNP	C	T	4	288	c.1354G>A	c.(1354-1356)GTG>ATG	p.V452M
Pat_14	Post-Resistance	TMEM132D	121256	37	12	130185201	130185201	Missense_Mutation	SNP	G	A	4	252	c.122C>T	c.(121-123)TCC>TTC	p.S41F
Pat_14	Post-Resistance	PIWIL1	9271	37	12	130847613	130847613	Missense_Mutation	SNP	G	A	4	327	c.2119G>A	c.(2119-2121)GGC>AGC	p.G707S
Pat_14	Post-Resistance	SFRS8	6433	37	12	132199411	132199411	Missense_Mutation	SNP	A	C	4	325	c.433A>C	c.(433-435)AGC>CGC	p.S145R
Pat_14	Post-Resistance	PARP4	143	37	13	25023942	25023942	Missense_Mutation	SNP	G	A	16	435	c.3028C>T	c.(3028-3030)CGT>TGT	p.R1010C
Pat_14	Post-Resistance	FRY	10129	37	13	32783778	32783778	Missense_Mutation	SNP	C	A	4	393	c.4332C>A	c.(4330-4332)AAC>AAA	p.N1444K
Pat_14	Post-Resistance	CSNK1A1L	122011	37	13	37679360	37679360	Missense_Mutation	SNP	C	T	5	433	c.34G>A	c.(34-36)GTT>ATT	p.V12I
Pat_14	Post-Resistance	ENOX1	55068	37	13	43788193	43788193	Missense_Mutation	SNP	G	A	4	314	c.1865C>T	c.(1864-1866)ACG>ATG	p.T622M
Pat_14	Post-Resistance	COL4A1	1282	37	13	110827023	110827023	Missense_Mutation	SNP	C	T	5	298	c.3272G>A	c.(3271-3273)GGA>GAA	p.G1091E

Pat_14	Post-Resistance	TUBGCP3	10426	37	13	113212517	113212517	Missense_Mutation	SNP	G	A	9	95	c.541C>T	c.(541-543)CTC>TTC	p.L181F
Pat_14	Post-Resistance	PARP2	10038	37	14	20822408	20822408	Splice_Site	SNP	T	C	3	167	c.802_splice	c.e8+2	p.G268_splice
Pat_14	Post-Resistance	TEP1	7011	37	14	20854275	20854275	Missense_Mutation	SNP	G	A	10	310	c.2941C>T	c.(2941-2943)CCC>TCC	p.P981S
Pat_14	Post-Resistance	CHD8	57680	37	14	21862547	21862547	Missense_Mutation	SNP	G	A	3	109	c.4651C>T	c.(4651-4653)CGC>TGC	p.R1551C
Pat_14	Post-Resistance	TOX4	9878	37	14	21957005	21957005	Missense_Mutation	SNP	G	A	5	451	c.575G>A	c.(574-576)CGG>CAG	p.R192Q
Pat_14	Post-Resistance	ACIN1	22985	37	14	23538765	23538765	Missense_Mutation	SNP	C	T	5	237	c.2359G>A	c.(2359-2361)GAA>AAA	p.E787K
Pat_14	Post-Resistance	IPO4	79711	37	14	24654449	24654449	Nonsense_Mutation	SNP	C	A	4	271	c.1348G>T	c.(1348-1350)GGA>TGA	p.G450*
Pat_14	Post-Resistance	NOVA1	4857	37	14	26917194	26917194	Missense_Mutation	SNP	G	A	10	404	c.1495C>T	c.(1495-1497)CGG>TGG	p.R499W
Pat_14	Post-Resistance	SEC23A	10484	37	14	39560787	39560787	Missense_Mutation	SNP	A	G	5	490	c.497T>C	c.(496-498)CTT>CCT	p.L166P
Pat_14	Post-Resistance	MIA2	117153	37	14	39716391	39716391	Missense_Mutation	SNP	G	A	5	361	c.613G>A	c.(613-615)GAA>AAA	p.E205K
Pat_14	Post-Resistance	FSCB	84075	37	14	44975634	44975634	Missense_Mutation	SNP	G	A	6	691	c.557C>T	c.(556-558)TCG>TTG	p.S186L
Pat_14	Post-Resistance	DLGAP5	9787	37	14	55637464	55637464	Missense_Mutation	SNP	C	G	17	486	c.1343G>C	c.(1342-1344)TGC>TCC	p.C448S
Pat_14	Post-Resistance	DACT1	51339	37	14	59112128	59112128	Missense_Mutation	SNP	G	A	4	400	c.787G>A	c.(787-789)GGG>AGG	p.G263R
Pat_14	Post-Resistance	TMEM30B	161291	37	14	61747099	61747099	Missense_Mutation	SNP	G	A	4	226	c.767C>T	c.(766-768)ACG>ATG	p.T256M
Pat_14	Post-Resistance	KCNH5	27133	37	14	63269251	63269251	Missense_Mutation	SNP	G	C	3	138	c.1618C>G	c.(1618-1620)CTA>GTA	p.L540V
Pat_14	Post-Resistance	SYNE2	23224	37	14	64564748	64564748	Missense_Mutation	SNP	G	A	5	227	c.12190G>A	c.(12190-12192)GTA>ATA	p.V4064I
Pat_14	Post-Resistance	ADAM20	8748	37	14	70990196	70990196	Missense_Mutation	SNP	G	A	5	696	c.1429C>T	c.(1429-1431)CGG>TGG	p.R477W
Pat_14	Post-Resistance	BTBD7	55727	37	14	93709199	93709199	Missense_Mutation	SNP	T	C	3	242	c.2819A>G	c.(2818-2820)CAG>CGG	p.Q940R
Pat_14	Post-Resistance	HHIPL1	84439	37	14	100123450	100123450	Missense_Mutation	SNP	C	T	7	828	c.1016C>T	c.(1015-1017)CCC>CTC	p.P339L
Pat_14	Post-Resistance	CXADRP2	646243	37	15	22016479	22016479	Missense_Mutation	SNP	C	G	3	226	c.238G>C	c.(238-240)GTA>CTA	p.V80L
Pat_14	Post-Resistance	VPS18	57617	37	15	41192067	41192067	Missense_Mutation	SNP	G	A	4	217	c.1051G>A	c.(1051-1053)GGG>AGG	p.G351R
Pat_14	Post-Resistance	DLL4	54567	37	15	41229632	41229632	Missense_Mutation	SNP	C	T	7	713	c.1960C>T	c.(1960-1962)CGG>TGG	p.R654W
Pat_14	Post-Resistance	RPAP1	26015	37	15	41819381	41819381	Missense_Mutation	SNP	A	G	3	289	c.1730T>C	c.(1729-1731)CTG>CCG	p.L577P
Pat_14	Post-Resistance	MAPKBP1	23005	37	15	42104784	42104784	Missense_Mutation	SNP	G	A	4	429	c.569G>A	c.(568-570)AGC>AAC	p.S190N
Pat_14	Post-Resistance	UBR1	197131	37	15	43330042	43330042	Missense_Mutation	SNP	G	A	4	233	c.1951C>T	c.(1951-1953)CGT>TGT	p.R651C
Pat_14	Post-Resistance	WDR76	79968	37	15	44158523	44158523	Missense_Mutation	SNP	G	A	4	372	c.1814G>A	c.(1813-1815)CGG>CAG	p.R605Q
Pat_14	Post-Resistance	GALK2	2585	37	15	49620159	49620159	Missense_Mutation	SNP	G	A	4	368	c.1180G>A	c.(1180-1182)GCT>ACT	p.A394T
Pat_14	Post-Resistance	SLC27A2	11001	37	15	50518269	50518269	Missense_Mutation	SNP	C	T	5	331	c.1252C>T	c.(1252-1254)CCC>TCC	p.P418S
Pat_14	Post-Resistance	CYP19A1	1588	37	15	51514680	51514680	Missense_Mutation	SNP	G	A	4	201	c.494C>T	c.(493-495)GCT>GTT	p.A165V
Pat_14	Post-Resistance	CILP	8483	37	15	65496902	65496902	Missense_Mutation	SNP	G	T	4	149	c.623C>A	c.(622-624)CCA>CAA	p.P208Q
Pat_14	Post-Resistance	HCN4	10021	37	15	73616107	73616107	Missense_Mutation	SNP	G	A	4	184	c.2327C>T	c.(2326-2328)CCG>CTG	p.P776L
Pat_14	Post-Resistance	CYP1A1	1543	37	15	75013595	75013595	Missense_Mutation	SNP	A	G	4	449	c.1111T>C	c.(1111-1113)TTC>CTC	p.F371L
Pat_14	Post-Resistance	C15orf17	57184	37	15	75195124	75195125	Missense_Mutation	DNP	CC	TT	4	242	c.432_433GG>AA	430-435)CAGGTG>CAAA	p.V145M
Pat_14	Post-Resistance	IL16	3603	37	15	81585370	81585370	Missense_Mutation	SNP	T	C	3	252	c.1894T>C	c.(1894-1896)TGT>CGT	p.C632R
Pat_14	Post-Resistance	MEX3B	84206	37	15	82336691	82336691	Missense_Mutation	SNP	G	T	7	269	c.520C>A	c.(520-522)CTC>ATC	p.L174I
Pat_14	Post-Resistance	EFTUD1	79631	37	15	82512090	82512090	Missense_Mutation	SNP	A	G	4	230	c.1514T>C	c.(1513-1515)TTT>TCT	p.F505S
Pat_14	Post-Resistance	AKAP13	11214	37	15	86124220	86124220	Missense_Mutation	SNP	A	G	6	586	c.2921A>G	c.(2920-2922)AAG>AGG	p.K974R
Pat_14	Post-Resistance	ACAN	176	37	15	89402396	89402396	Missense_Mutation	SNP	G	A	4	251	c.6580G>A	c.(6580-6582)GAC>AAC	p.D2194N
Pat_14	Post-Resistance	FURIN	5045	37	15	91423995	91423995	Missense_Mutation	SNP	C	T	3	103	c.1631C>T	c.(1630-1632)TCT>TTT	p.S544F
Pat_14	Post-Resistance	ADAMTS17	170691	37	15	100692818	100692818	Missense_Mutation	SNP	T	C	3	346	c.1472A>G	c.(1471-1473)GAG>GGG	p.E491G
Pat_14	Post-Resistance	IFT140	9742	37	16	1634306	1634306	Missense_Mutation	SNP	G	A	4	168	c.1271C>T	c.(1270-1272)CCG>CTG	p.P424L
Pat_14	Post-Resistance	A2BP1	54715	37	16	7568246	7568246	Missense_Mutation	SNP	C	T	6	608	c.125C>T	c.(124-126)ACG>ATG	p.T42M
Pat_14	Post-Resistance	GP2	2813	37	16	20327283	20327283	Missense_Mutation	SNP	C	T	4	406	c.1505G>A	c.(1504-1506)CGG>CAG	p.R502Q
Pat_14	Post-Resistance	ARHGAP17	55114	37	16	24942360	24942360	Missense_Mutation	SNP	G	A	6	697	c.2260C>T	c.(2260-2262)CCT>TCT	p.P754S
Pat_14	Post-Resistance	CLN3	1201	37	16	28499967	28499967	Missense_Mutation	SNP	G	A	5	652	c.239C>T	c.(238-240)ACG>ATG	p.T80M
Pat_14	Post-Resistance	SH2B1	25970	37	16	28878676	28878676	Missense_Mutation	SNP	C	T	18	749	c.964C>T	c.(964-966)CCC>TCC	p.P322S
Pat_14	Post-Resistance	FBXL19	54620	37	16	30938689	30938689	Missense_Mutation	SNP	G	A	3	44	c.298G>A	c.(298-300)GTG>ATG	p.V100M

Pat_14	Post-Resistance	HSD3B7	80270	37	16	30997438	30997438	Missense_Mutation	SNP	G	A	5	146	c.235G>A	c.(235-237)GGA>AGA	p.G79R
Pat_14	Post-Resistance	PDXDC2	283970	37	16	70016263	70016263	Missense_Mutation	SNP	C	T	5	156	c.439G>A	c.(439-441)GCC>ACC	p.A147T
Pat_14	Post-Resistance	CNTNAP4	85445	37	16	76528834	76528834	Missense_Mutation	SNP	G	A	14	514	c.2108G>A	c.(2107-2109)GGA>GAA	p.G703E
Pat_14	Post-Resistance	CDH13	1012	37	16	83636110	83636110	Missense_Mutation	SNP	G	A	5	761	c.1012G>A	c.(1012-1014)GGA>AGA	p.G338R
Pat_14	Post-Resistance	KIAA1609	57707	37	16	84516203	84516203	Missense_Mutation	SNP	C	T	27	318	c.1072G>A	c.(1072-1074)GGA>AGA	p.G358R
Pat_14	Post-Resistance	NLRP1	22861	37	17	5463015	5463015	Missense_Mutation	SNP	C	T	10	622	c.1001G>A	c.(1000-1002)GGG>GAG	p.G334E
Pat_14	Post-Resistance	AIPL1	23746	37	17	6328839	6328839	Missense_Mutation	SNP	G	A	4	196	c.1096C>T	c.(1096-1098)CCC>TCC	p.P366S
Pat_14	Post-Resistance	AIPL1	23746	37	17	6331798	6331798	Missense_Mutation	SNP	C	T	5	201	c.305G>A	c.(304-306)CGG>CAG	p.R102Q
Pat_14	Post-Resistance	NEURL4	84461	37	17	7220648	7220648	Missense_Mutation	SNP	G	A	9	240	c.4360C>T	c.(4360-4362)CCT>TCT	p.P1454S
Pat_14	Post-Resistance	C17orf74	201243	37	17	7329696	7329696	Missense_Mutation	SNP	G	A	5	209	c.386G>A	c.(385-387)CGC>CAC	p.R129H
Pat_14	Post-Resistance	DNAH2	146754	37	17	7727548	7727548	Missense_Mutation	SNP	G	A	4	138	c.11588G>A	c.(11587-11589)CGC>CAC	p.R3863H
Pat_14	Post-Resistance	CHD3	1107	37	17	7807866	7807866	Missense_Mutation	SNP	C	T	4	231	c.4001C>T	c.(4000-4002)GCC>GTC	p.A1334V
Pat_14	Post-Resistance	GUCY2D	3000	37	17	7919139	7919139	Missense_Mutation	SNP	G	A	4	137	c.3023G>A	c.(3022-3024)CGC>CAC	p.R1008H
Pat_14	Post-Resistance	FLII	2314	37	17	18151926	18151926	Missense_Mutation	SNP	G	A	5	183	c.2128C>T	c.(2128-2130)CCC>TCC	p.P710S
Pat_14	Post-Resistance	LGALS9C	654346	37	17	18387258	18387258	Missense_Mutation	SNP	G	A	4	266	c.109G>A	c.(109-111)GTT>ATT	p.V37I
Pat_14	Post-Resistance	LGALS9B	284194	37	17	20363690	20363690	Missense_Mutation	SNP	C	T	7	618	c.106G>A	c.(106-108)GCC>ACC	p.A36T
Pat_14	Post-Resistance	SEZ6	124925	37	17	27285151	27285151	Missense_Mutation	SNP	G	A	4	342	c.2116C>T	c.(2116-2118)CGC>TGC	p.R706C
Pat_14	Post-Resistance	TMEM132E	124842	37	17	32964715	32964715	Missense_Mutation	SNP	G	A	4	293	c.2419G>A	c.(2419-2421)GTC>ATC	p.V807I
Pat_14	Post-Resistance	KRTAP4-11	653240	37	17	39274087	39274087	Missense_Mutation	SNP	G	C	5	36	c.481C>G	c.(481-483)CTG>GTG	p.L161V
Pat_14	Post-Resistance	CNTNAP1	8506	37	17	40844667	40844667	Missense_Mutation	SNP	G	A	6	336	c.2681G>A	c.(2680-2682)CGG>CAG	p.R894Q
Pat_14	Post-Resistance	PLEKHM1	9842	37	17	43516901	43516901	Missense_Mutation	SNP	A	G	5	286	c.3001T>C	c.(3001-3003)TGC>CGC	p.C1001R
Pat_14	Post-Resistance	NPEPPS	9520	37	17	45662879	45662879	Missense_Mutation	SNP	G	A	5	302	c.662G>A	c.(661-663)CGG>CAG	p.R221Q
Pat_14	Post-Resistance	B4GALNT2	124872	37	17	47218694	47218694	Nonsense_Mutation	SNP	C	T	13	541	c.280C>T	c.(280-282)CAA>TAA	p.Q94*
Pat_14	Post-Resistance	TOB1	10140	37	17	48940765	48940765	Missense_Mutation	SNP	G	A	4	400	c.614C>T	c.(613-615)TCT>TTT	p.S205F
Pat_14	Post-Resistance	SPAG9	9043	37	17	49073942	49073942	Missense_Mutation	SNP	G	A	8	187	c.1952C>T	c.(1951-1953)CCT>CTT	p.P651L
Pat_14	Post-Resistance	PCTP	58488	37	17	53851097	53851097	Missense_Mutation	SNP	C	T	5	165	c.352C>T	c.(352-354)CGG>TGG	p.R118W
Pat_14	Post-Resistance	VEZF1	7716	37	17	56052085	56052085	Missense_Mutation	SNP	G	A	5	805	c.1315C>T	c.(1315-1317)CCA>TCA	p.P439S
Pat_14	Post-Resistance	BZRAP1	9256	37	17	56386642	56386642	Missense_Mutation	SNP	T	C	3	150	c.3991A>G	c.(3991-3993)AGC>GGC	p.S1331G
Pat_14	Post-Resistance	CSHL1	1444	37	17	61987841	61987841	Missense_Mutation	SNP	G	A	5	614	c.245C>T	c.(244-246)TCC>TTC	p.S82F
Pat_14	Post-Resistance	ABCA9	10350	37	17	67041360	67041360	Missense_Mutation	SNP	G	A	4	167	c.422C>T	c.(421-423)TCT>TTT	p.S141F
Pat_14	Post-Resistance	CASKIN2	57513	37	17	73498943	73498943	Missense_Mutation	SNP	G	A	4	194	c.2212C>T	c.(2212-2214)CGG>TGG	p.R738W
Pat_14	Post-Resistance	UNC13D	201294	37	17	73831985	73831985	Missense_Mutation	SNP	G	A	5	374	c.1547C>T	c.(1546-1548)ACC>ATC	p.T516I
Pat_14	Post-Resistance	SEC14L1	6397	37	17	75196737	75196737	Missense_Mutation	SNP	T	C	16	422	c.991T>C	c.(991-993)TGG>CGG	p.W331R
Pat_14	Post-Resistance	CCDC40	55036	37	17	78013907	78013907	Missense_Mutation	SNP	T	G	6	274	c.390T>G	c.(388-390)GAT>GAG	p.D130E
Pat_14	Post-Resistance	RNF213	57674	37	17	78326796	78326796	Missense_Mutation	SNP	G	A	5	285	c.4579G>A	c.(4579-4581)GAT>AAT	p.D1527N
Pat_14	Post-Resistance	FOXK2	3607	37	17	80559253	80559253	Missense_Mutation	SNP	G	A	4	314	c.1861G>A	c.(1861-1863)GGT>AGT	p.G621S
Pat_14	Post-Resistance	APCDD1	147495	37	18	10487662	10487662	Missense_Mutation	SNP	G	A	4	371	c.1172G>A	c.(1171-1173)GGG>GAG	p.G391E
Pat_14	Post-Resistance	SPIRE1	56907	37	18	12452287	12452287	Missense_Mutation	SNP	G	A	4	145	c.1979C>T	c.(1978-1980)ACT>ATT	p.T660I
Pat_14	Post-Resistance	FAM59A	64762	37	18	29850273	29850273	Missense_Mutation	SNP	G	A	4	174	c.1640C>T	c.(1639-1641)CCC>CTC	p.P547L
Pat_14	Post-Resistance	ASXL3	80816	37	18	31323920	31323920	Missense_Mutation	SNP	C	T	5	382	c.4108C>T	c.(4108-4110)CCT>TCT	p.P1370S
Pat_14	Post-Resistance	KIAA1328	57536	37	18	34647216	34647216	Missense_Mutation	SNP	C	T	13	306	c.940C>T	c.(940-942)CGT>TGT	p.R314C
Pat_14	Post-Resistance	ZNF555	148254	37	19	2853183	2853183	Missense_Mutation	SNP	G	A	3	103	c.1120G>A	c.(1120-1122)GGG>AGG	p.G374R
Pat_14	Post-Resistance	TLE6	79816	37	19	2987935	2987935	Missense_Mutation	SNP	G	A	3	72	c.296G>A	c.(295-297)GGT>GAT	p.G99D
Pat_14	Post-Resistance	TJP3	27134	37	19	3736227	3736227	Missense_Mutation	SNP	G	A	4	192	c.1291G>A	c.(1291-1293)GGG>AGG	p.G431R
Pat_14	Post-Resistance	UBXN6	80700	37	19	4453936	4453936	Nonsense_Mutation	SNP	G	A	5	365	c.238C>T	c.(238-240)CGA>TGA	p.R80*
Pat_14	Post-Resistance	PLIN4	729359	37	19	4512254	4512254	Missense_Mutation	SNP	G	A	6	667	c.1676C>T	c.(1675-1677)ACG>ATG	p.T559M
Pat_14	Post-Resistance	LASS4	79603	37	19	8320743	8320743	Missense_Mutation	SNP	G	A	4	305	c.448G>A	c.(448-450)GGC>AGC	p.G150S

Pat_14	Post-Resistance	ADAMTS10	81794	37	19	8651052	8651052	Missense_Mutation	SNP	G	T	13	112	c.2614C>A	c.(2614-2616)CTG>ATG	p.L872M
Pat_14	Post-Resistance	ZNF844	284391	37	19	12187475	12187475	Missense_Mutation	SNP	C	G	7	178	c.1540C>G	c.(1540-1542)CAT>GAT	p.H514D
Pat_14	Post-Resistance	ZNF563	147837	37	19	12429554	12429554	Missense_Mutation	SNP	C	T	6	663	c.1285G>A	c.(1285-1287)GCG>ACG	p.A429T
Pat_14	Post-Resistance	FBXW9	84261	37	19	12807325	12807325	Missense_Mutation	SNP	G	C	4	218	c.71C>G	c.(70-72)ACA>AGA	p.T24R
Pat_14	Post-Resistance	NOTCH3	4854	37	19	15289953	15289953	Missense_Mutation	SNP	G	A	4	144	c.3601C>T	c.(3601-3603)CGC>TGC	p.R1201C
Pat_14	Post-Resistance	CHERP	10523	37	19	16643452	16643452	Missense_Mutation	SNP	G	A	4	204	c.631C>T	c.(631-633)CGG>TGG	p.R211W
Pat_14	Post-Resistance	MYO9B	4650	37	19	17316119	17316119	Missense_Mutation	SNP	C	A	4	253	c.5038C>A	c.(5038-5040)CAC>AAC	p.H1680N
Pat_14	Post-Resistance	ZNF93	81931	37	19	20045359	20045359	Missense_Mutation	SNP	C	T	5	88	c.1595C>T	c.(1594-1596)ACT>ATT	p.T532I
Pat_14	Post-Resistance	ZNF493	284443	37	19	21606468	21606468	Missense_Mutation	SNP	C	T	5	200	c.623C>T	c.(622-624)CCT>CTT	p.P208L
Pat_14	Post-Resistance	ZNF208	7757	37	19	22154648	22154648	Missense_Mutation	SNP	C	T	8	489	c.2804G>A	c.(2803-2805)GGC>GAC	p.G935D
Pat_14	Post-Resistance	ZNF492	57615	37	19	22847710	22847710	Missense_Mutation	SNP	A	G	3	164	c.1239A>G	c.(1237-1239)ATA>ATG	p.I413M
Pat_14	Post-Resistance	ZNF254	9534	37	19	24310427	24310427	Missense_Mutation	SNP	A	G	4	121	c.1625A>G	c.(1624-1626)GAA>GGA	p.E542G
Pat_14	Post-Resistance	ZNF254	9534	37	19	24310450	24310450	Missense_Mutation	SNP	A	G	5	116	c.1648A>G	c.(1648-1650)AAA>GAA	p.K550E
Pat_14	Post-Resistance	ZNF599	148103	37	19	35250121	35250121	Missense_Mutation	SNP	G	A	4	327	c.1585C>T	c.(1585-1587)CAC>TAC	p.H529Y
Pat_14	Post-Resistance	FAM187B	148109	37	19	35719243	35719243	Missense_Mutation	SNP	G	A	35	435	c.341C>T	c.(340-342)ACC>ATC	p.T114I
Pat_14	Post-Resistance	RBM42	79171	37	19	36124129	36124129	Missense_Mutation	SNP	C	G	9	388	c.659C>G	c.(658-660)TCC>TGC	p.S220C
Pat_14	Post-Resistance	SIPA1L3	23094	37	19	38682888	38682888	Missense_Mutation	SNP	G	A	5	137	c.4534G>A	c.(4534-4536)GAT>AAT	p.D1512N
Pat_14	Post-Resistance	NCCRP1	342897	37	19	39691050	39691050	Missense_Mutation	SNP	C	T	5	605	c.613C>T	c.(613-615)CGC>TGC	p.R205C
Pat_14	Post-Resistance	AXL	558	37	19	41762394	41762394	Missense_Mutation	SNP	G	A	8	562	c.2074G>A	c.(2074-2076)GGG>AGG	p.G692R
Pat_14	Post-Resistance	PSG1	5669	37	19	43382115	43382115	Missense_Mutation	SNP	C	T	19	480	c.380G>A	c.(379-381)GGA>GAA	p.G127E
Pat_14	Post-Resistance	FOSB	2354	37	19	45973932	45973932	Missense_Mutation	SNP	G	A	9	684	c.172G>A	c.(172-174)GTC>ATC	p.V58I
Pat_14	Post-Resistance	STRN4	29888	37	19	47241447	47241447	Missense_Mutation	SNP	T	C	4	451	c.434A>G	c.(433-435)GAG>GGG	p.E145G
Pat_14	Post-Resistance	ZC3H4	23211	37	19	47585519	47585519	Missense_Mutation	SNP	G	A	4	368	c.1252C>T	c.(1252-1254)CTC>TTC	p.L418F
Pat_14	Post-Resistance	MYBPC2	4606	37	19	50939956	50939956	Missense_Mutation	SNP	C	T	21	420	c.428C>T	c.(427-429)ACC>ATC	p.T143I
Pat_14	Post-Resistance	ZNF845	91664	37	19	53855196	53855196	Missense_Mutation	SNP	T	C	4	479	c.1268T>C	c.(1267-1269)ATG>ACG	p.M423T
Pat_14	Post-Resistance	LILRB1	10859	37	19	55146187	55146187	Nonsense_Mutation	SNP	C	T	5	480	c.1456C>T	c.(1456-1458)CGA>TGA	p.R486*
Pat_14	Post-Resistance	SUV420H2	84787	37	19	55853392	55853392	Missense_Mutation	SNP	C	T	5	302	c.88C>T	c.(88-90)CGC>TGC	p.R30C
Pat_14	Post-Resistance	GREB1	9687	37	2	11758857	11758857	Missense_Mutation	SNP	T	C	3	104	c.3856T>C	c.(3856-3858)TCC>CCC	p.S1286P
Pat_14	Post-Resistance	DNAJC27	51277	37	2	25186339	25186339	Missense_Mutation	SNP	G	A	4	201	c.175C>T	c.(175-177)CAC>TAC	p.H59Y
Pat_14	Post-Resistance	IFT172	26160	37	2	27706202	27706202	Missense_Mutation	SNP	G	A	4	374	c.524C>T	c.(523-525)ACC>ATC	p.T175I
Pat_14	Post-Resistance	RHOQ	23433	37	2	46803262	46803262	Missense_Mutation	SNP	A	G	6	177	c.238A>G	c.(238-240)ATG>GTG	p.M80V
Pat_14	Post-Resistance	EHBP1	23301	37	2	63092007	63092007	Missense_Mutation	SNP	C	T	13	278	c.1004C>T	c.(1003-1005)TCT>TTT	p.S335F
Pat_14	Post-Resistance	DYSF	8291	37	2	71891405	71891405	Missense_Mutation	SNP	G	A	5	314	c.4894G>A	c.(4894-4896)GAG>AAG	p.E1632K
Pat_14	Post-Resistance	SPR	6697	37	2	73118620	73118620	Missense_Mutation	SNP	A	G	3	234	c.740A>G	c.(739-741)AAG>AGG	p.K247R
Pat_14	Post-Resistance	RAB11FIP5	26056	37	2	73316241	73316241	Missense_Mutation	SNP	G	A	4	267	c.634C>T	c.(634-636)CTC>TTC	p.L212F
Pat_14	Post-Resistance	DQX1	165545	37	2	74747144	74747144	Missense_Mutation	SNP	G	A	4	357	c.1513C>T	c.(1513-1515)CGT>TGT	p.R505C
Pat_14	Post-Resistance	CIAO1	9391	37	2	96934352	96934352	Missense_Mutation	SNP	G	A	4	275	c.647G>A	c.(646-648)CGT>CAT	p.R216H
Pat_14	Post-Resistance	RALB	5899	37	2	121043657	121043657	Missense_Mutation	SNP	A	G	3	197	c.322A>G	c.(322-324)AGG>GGG	p.R108G
Pat_14	Post-Resistance	CNTNAP5	129684	37	2	125204410	125204410	Missense_Mutation	SNP	G	A	4	326	c.814G>A	c.(814-816)GTC>ATC	p.V272I
Pat_14	Post-Resistance	MCM6	4175	37	2	136626254	136626254	Missense_Mutation	SNP	C	T	5	656	c.542G>A	c.(541-543)CGA>CAA	p.R181Q
Pat_14	Post-Resistance	THSD7B	80731	37	2	137814304	137814304	Missense_Mutation	SNP	A	G	5	367	c.361A>G	c.(361-363)ACT>GCT	p.T121A
Pat_14	Post-Resistance	LRP1B	53353	37	2	141208202	141208202	Missense_Mutation	SNP	G	A	8	354	c.9992C>T	c.(9991-9993)CCA>CTA	p.P3331L
Pat_14	Post-Resistance	GTDC1	79712	37	2	144714897	144714897	Missense_Mutation	SNP	G	A	7	117	c.995C>T	c.(994-996)TCA>TTA	p.S332L
Pat_14	Post-Resistance	NEB	4703	37	2	152372987	152372987	Missense_Mutation	SNP	G	T	4	121	c.17788C>A	c.(17788-17790)CAG>AAG	p.Q5930K
Pat_14	Post-Resistance	NEB	4703	37	2	152524349	152524349	Missense_Mutation	SNP	G	A	4	229	c.4688C>T	c.(4687-4689)GCT>GTT	p.A1563V
Pat_14	Post-Resistance	XIRP2	129446	37	2	168104942	168104942	Missense_Mutation	SNP	C	T	5	611	c.7040C>T	c.(7039-7041)CCT>CTT	p.P2347L
Pat_14	Post-Resistance	GAD1	2571	37	2	171686086	171686086	Missense_Mutation	SNP	G	A	6	493	c.247G>A	c.(247-249)GAC>AAC	p.D83N

Pat_14	Post-Resistance	TTN	7273	37	2	179414500	179414500	Missense_Mutation	SNP	G	A	4	239	c.84245C>T	c.(84244-84246)GCT>GTT	p.A28082V
Pat_14	Post-Resistance	TTN	7273	37	2	179648466	179648466	Missense_Mutation	SNP	G	A	4	424	c.2822C>T	c.(2821-2823)ACT>ATT	p.T941I
Pat_14	Post-Resistance	ZNF804A	91752	37	2	185802120	185802120	Missense_Mutation	SNP	C	T	4	260	c.1997C>T	c.(1996-1998)TCC>TTC	p.S666F
Pat_14	Post-Resistance	HIBCH	26275	37	2	191161649	191161649	Missense_Mutation	SNP	C	T	4	186	c.109G>A	c.(109-111)GAG>AAG	p.E37K
Pat_14	Post-Resistance	DNAH7	56171	37	2	196729009	196729009	Missense_Mutation	SNP	A	G	5	439	c.7370T>C	c.(7369-7371)CTT>CCT	p.L2457P
Pat_14	Post-Resistance	FAM126B	285172	37	2	201846171	201846171	Missense_Mutation	SNP	C	A	5	155	c.1415G>T	c.(1414-1416)GGC>GTC	p.G472V
Pat_14	Post-Resistance	GPR1	2825	37	2	207041771	207041771	Nonsense_Mutation	SNP	C	T	14	715	c.201G>A	c.(199-201)TGG>TGA	p.W67*
Pat_14	Post-Resistance	STK36	27148	37	2	219549917	219549917	Missense_Mutation	SNP	G	A	4	315	c.1346G>A	c.(1345-1347)CGC>CAC	p.R449H
Pat_14	Post-Resistance	GMPPA	29926	37	2	220366688	220366688	Missense_Mutation	SNP	G	A	8	723	c.358G>A	c.(358-360)GAC>AAC	p.D120N
Pat_14	Post-Resistance	CHPF	79586	37	2	220405271	220405271	Missense_Mutation	SNP	G	A	4	80	c.1162C>T	c.(1162-1164)CGC>TGC	p.R388C
Pat_14	Post-Resistance	GIGYF2	26058	37	2	233613724	233613724	Missense_Mutation	SNP	T	C	5	729	c.199T>C	c.(199-201)TTT>CTT	p.F67L
Pat_14	Post-Resistance	CAPN10	11132	37	2	241534672	241534672	Missense_Mutation	SNP	C	T	4	175	c.1229C>T	c.(1228-1230)GCG>GTG	p.A410V
Pat_14	Post-Resistance	UBOX5	22888	37	20	3102308	3102308	Missense_Mutation	SNP	G	A	3	76	c.977C>T	c.(976-978)GCC>GTC	p.A326V
Pat_14	Post-Resistance	KIF16B	55614	37	20	16488677	16488678	Missense_Mutation	DNP	GG	AA	8	788	c.624_625CC>TT	622-627)AACCGG>AATT	p.R209W
Pat_14	Post-Resistance	SLC24A3	57419	37	20	19261698	19261698	Missense_Mutation	SNP	G	A	5	269	c.238G>A	c.(238-240)GGA>AGA	p.G80R
Pat_14	Post-Resistance	GGTLC1	92086	37	20	23966333	23966333	Missense_Mutation	SNP	C	T	7	527	c.502G>A	c.(502-504)GTC>ATC	p.V168I
Pat_14	Post-Resistance	FRG1B	284802	37	20	29625877	29625877	Missense_Mutation	SNP	G	A	6	284	c.31G>A	c.(31-33)GCC>ACC	p.A11T
Pat_14	Post-Resistance	C20orf160	140706	37	20	30617510	30617510	Missense_Mutation	SNP	G	A	4	316	c.1207G>A	c.(1207-1209)GTA>ATA	p.V403I
Pat_14	Post-Resistance	ASXL1	171023	37	20	31022349	31022349	Missense_Mutation	SNP	A	G	3	147	c.1834A>G	c.(1834-1836)AGG>GGG	p.R612G
Pat_14	Post-Resistance	RALGAPB	57148	37	20	37153566	37153566	Missense_Mutation	SNP	C	T	11	702	c.1765C>T	c.(1765-1767)CTT>TTT	p.L589F
Pat_14	Post-Resistance	TOP1	7150	37	20	39742758	39742759	Missense_Mutation	DNP	CC	TT	6	484	.1601_1602CC>T	c.(1600-1602)TCC>TTT	p.S534F
Pat_14	Post-Resistance	TP53TG5	27296	37	20	44002605	44002605	Missense_Mutation	SNP	C	T	4	487	c.815G>A	c.(814-816)AGA>AAA	p.R272K
Pat_14	Post-Resistance	ATP9A	10079	37	20	50273517	50273517	Missense_Mutation	SNP	T	C	3	163	c.1466A>G	c.(1465-1467)GAA>GGA	p.E489G
Pat_14	Post-Resistance	RTEL1	51750	37	20	62319071	62319071	Missense_Mutation	SNP	C	T	3	36	c.1429C>T	c.(1429-1431)CTT>TTT	p.L477F
Pat_14	Post-Resistance	ZNF512B	57473	37	20	62593633	62593633	Missense_Mutation	SNP	G	A	4	323	c.2258C>T	c.(2257-2259)CCC>CTC	p.P753L
Pat_14	Post-Resistance	KRTAP19-3	337970	37	21	31864146	31864146	Missense_Mutation	SNP	A	T	13	706	c.130T>A	c.(130-132)TAC>AAC	p.Y44N
Pat_14	Post-Resistance	PPIL2	23759	37	22	22024860	22024860	Missense_Mutation	SNP	C	T	21	427	c.88C>T	c.(88-90)CCA>TCA	p.P30S
Pat_14	Post-Resistance	BCR	613	37	22	23654017	23654017	Missense_Mutation	SNP	G	A	4	284	c.3316G>A	c.(3316-3318)GAC>AAC	p.D1106N
Pat_14	Post-Resistance	SUSD2	56241	37	22	24580812	24580812	Missense_Mutation	SNP	C	T	9	163	c.686C>T	c.(685-687)TCT>TTT	p.S229F
Pat_14	Post-Resistance	AP1B1	162	37	22	29737502	29737502	Missense_Mutation	SNP	G	A	5	158	c.1784C>T	c.(1783-1785)CCT>CTT	p.P595L
Pat_14	Post-Resistance	NEFH	4744	37	22	29885739	29885739	Missense_Mutation	SNP	T	A	8	281	c.2110T>A	c.(2110-2112)TCC>ACC	p.S704T
Pat_14	Post-Resistance	ELFN2	114794	37	22	37771400	37771400	Missense_Mutation	SNP	C	T	4	226	c.175G>A	c.(175-177)GAC>AAC	p.D59N
Pat_14	Post-Resistance	TRIOBP	11078	37	22	38111837	38111837	Missense_Mutation	SNP	C	T	4	103	c.524C>T	c.(523-525)CCG>CTG	p.P175L
Pat_14	Post-Resistance	CSNK1E	1454	37	22	38699005	38699005	Missense_Mutation	SNP	G	A	4	234	c.197C>T	c.(196-198)CCG>CTG	p.P66L
Pat_14	Post-Resistance	L3MBTL2	83746	37	22	41609924	41609924	Missense_Mutation	SNP	G	A	4	413	c.290G>A	c.(289-291)GGT>GAT	p.G97D
Pat_14	Post-Resistance	ZC3H7B	23264	37	22	41742126	41742126	Missense_Mutation	SNP	G	C	4	432	c.1579G>C	c.(1579-1581)GAC>CAC	p.D527H
Pat_14	Post-Resistance	ZC3H7B	23264	37	22	41752721	41752721	Missense_Mutation	SNP	G	A	5	376	c.2590G>A	c.(2590-2592)GAG>AAG	p.E864K
Pat_14	Post-Resistance	ARPP21	10777	37	3	35758848	35758848	Missense_Mutation	SNP	C	T	5	262	c.994C>T	c.(994-996)CGG>TGG	p.R332W
Pat_14	Post-Resistance	ITGA9	3680	37	3	37555329	37555329	Missense_Mutation	SNP	G	A	4	218	c.973G>A	c.(973-975)GCC>ACC	p.A325T
Pat_14	Post-Resistance	SLC22A13	9390	37	3	38316485	38316485	Missense_Mutation	SNP	G	A	5	392	c.643G>A	c.(643-645)GAA>AAA	p.E215K
Pat_14	Post-Resistance	SCN5A	6331	37	3	38639332	38639332	Missense_Mutation	SNP	G	A	19	429	c.2150C>T	c.(2149-2151)CCG>CTG	p.P717L
Pat_14	Post-Resistance	CTNNB1	1499	37	3	41266655	41266655	Missense_Mutation	SNP	G	A	4	330	c.452G>A	c.(451-453)CGT>CAT	p.R151H
Pat_14	Post-Resistance	TRAK1	22906	37	3	42251330	42251330	Missense_Mutation	SNP	G	A	4	442	c.1816G>A	c.(1816-1818)GGT>AGT	p.G606S
Pat_14	Post-Resistance	TRAK1	22906	37	3	42251351	42251351	Missense_Mutation	SNP	C	T	4	473	c.1837C>T	c.(1837-1839)CGG>TGG	p.R613W
Pat_14	Post-Resistance	LARS2	23395	37	3	45517981	45517981	Missense_Mutation	SNP	G	A	6	567	c.880G>A	c.(880-882)GAA>AAA	p.E294K
Pat_14	Post-Resistance	CCR9	10803	37	3	45942572	45942572	Missense_Mutation	SNP	C	T	5	746	c.292C>T	c.(292-294)CTT>TTT	p.L98F
Pat_14	Post-Resistance	CXCR6	10663	37	3	45988712	45988712	Missense_Mutation	SNP	T	C	3	239	c.739T>C	c.(739-741)TTC>CTC	p.F247L

Pat_14	Post-Resistance	MYL3	4634	37	3	46901025	46901025	Missense_Mutation	SNP	C	T	5	351	c.421G>A	c.(421-423)GAC>AAC	p.D141N
Pat_14	Post-Resistance	CCDC51	79714	37	3	48475137	48475137	Missense_Mutation	SNP	G	A	6	585	c.457C>T	c.(457-459)CTC>TTC	p.L153F
Pat_14	Post-Resistance	CELSR3	1951	37	3	48694384	48694384	Missense_Mutation	SNP	C	A	3	33	c.4146G>T	c.(4144-4146)GAG>GAT	p.E1382D
Pat_14	Post-Resistance	MST1R	4486	37	3	49924924	49924924	Missense_Mutation	SNP	T	C	3	231	c.4019A>G	c.(4018-4020)GAG>GGG	p.E1340G
Pat_14	Post-Resistance	DOCK3	1795	37	3	51393845	51393845	Missense_Mutation	SNP	G	T	8	582	c.4424G>T	c.(4423-4425)TGG>TTG	p.W1475L
Pat_14	Post-Resistance	ABHD6	57406	37	3	58253031	58253031	Missense_Mutation	SNP	G	A	4	246	c.235G>A	c.(235-237)GGA>AGA	p.G79R
Pat_14	Post-Resistance	PRICKLE2	166336	37	3	64132635	64132635	Missense_Mutation	SNP	C	T	6	377	c.1531G>A	c.(1531-1533)GGG>AGG	p.G511R
Pat_14	Post-Resistance	LRIG1	26018	37	3	66444614	66444614	Missense_Mutation	SNP	C	T	5	125	c.1318G>A	c.(1318-1320)GAC>AAC	p.D440N
Pat_14	Post-Resistance	EPHA3	2042	37	3	89445067	89445067	Missense_Mutation	SNP	C	T	6	695	c.1387C>T	c.(1387-1389)CCT>TCT	p.P463S
Pat_14	Post-Resistance	EPHA6	285220	37	3	96945167	96945167	Missense_Mutation	SNP	C	T	16	355	c.1174C>T	c.(1174-1176)CCA>TCA	p.P392S
Pat_14	Post-Resistance	SIDT1	54847	37	3	113321944	113321944	Missense_Mutation	SNP	G	A	5	303	c.1210G>A	c.(1210-1212)GAC>AAC	p.D404N
Pat_14	Post-Resistance	DRD3	1814	37	3	113866406	113866406	Splice_Site	SNP	T	C	3	216	c.384_splice	c.e5-1	p.R128_splice
Pat_14	Post-Resistance	UPK1B	7348	37	3	118913151	118913152	Missense_Mutation	DNP	CC	TT	8	515	c.554_555CC>TT	c.(553-555)CCC>CTT	p.P185L
Pat_14	Post-Resistance	TMEM39A	55254	37	3	119180867	119180867	Missense_Mutation	SNP	G	C	3	271	c.55C>G	c.(55-57)CCT>GCT	p.P19A
Pat_14	Post-Resistance	HEG1	57493	37	3	124689597	124689598	Missense_Mutation	DNP	CC	TT	4	77	.4044_4045GG>A	042-4047)CCGGCC>CCA	p.A1349T
Pat_14	Post-Resistance	ACAD11	84129	37	3	132358402	132358402	Missense_Mutation	SNP	A	T	4	309	c.636T>A	c.(634-636)AAT>AAA	p.N212K
Pat_14	Post-Resistance	BFSP2	8419	37	3	133185671	133185671	Splice_Site	SNP	G	A	4	265	c.892_splice	c.e5-1	p.Q298_splice
Pat_14	Post-Resistance	FAM194A	131831	37	3	150377899	150377899	Missense_Mutation	SNP	C	T	6	479	c.1772G>A	c.(1771-1773)GGA>GAA	p.G591E
Pat_14	Post-Resistance	GFM1	85476	37	3	158408011	158408011	Missense_Mutation	SNP	C	T	7	663	c.1969C>T	c.(1969-1971)CCA>TCA	p.P657S
Pat_14	Post-Resistance	MECOM	2122	37	3	168810866	168810866	Missense_Mutation	SNP	G	A	5	413	c.2480C>T	c.(2479-2481)TCT>TTT	p.S827F
Pat_14	Post-Resistance	ABCC5	10057	37	3	183679394	183679394	Missense_Mutation	SNP	T	C	9	389	c.2284A>G	c.(2284-2286)ACG>GCG	p.T762A
Pat_14	Post-Resistance	ATP13A4	84239	37	3	193174929	193174929	Missense_Mutation	SNP	C	G	4	577	c.1775G>C	c.(1774-1776)GGA>GCA	p.G592A
Pat_14	Post-Resistance	ZNF595	152687	37	4	86680	86680	Missense_Mutation	SNP	G	T	3	88	c.1286G>T	c.(1285-1287)TGT>TTT	p.C429F
Pat_14	Post-Resistance	ZNF518B	85460	37	4	10446454	10446454	Missense_Mutation	SNP	G	A	5	502	c.1499C>T	c.(1498-1500)GCT>GTT	p.A500V
Pat_14	Post-Resistance	SLIT2	9353	37	4	20568984	20568984	Missense_Mutation	SNP	G	A	13	678	c.2825G>A	c.(2824-2826)CGA>CAA	p.R942Q
Pat_14	Post-Resistance	TEC	7006	37	4	48147510	48147510	Nonsense_Mutation	SNP	G	A	7	698	c.1168C>T	c.(1168-1170)CGA>TGA	p.R390*
Pat_14	Post-Resistance	SLAIN2	57606	37	4	48384798	48384798	Missense_Mutation	SNP	G	A	20	429	c.1076G>A	c.(1075-1077)AGA>AAA	p.R359K
Pat_14	Post-Resistance	CENPC1	1060	37	4	68374698	68374698	Missense_Mutation	SNP	T	C	3	259	c.1738A>G	c.(1738-1740)AGG>GGG	p.R580G
Pat_14	Post-Resistance	GK2	2712	37	4	80327898	80327898	Missense_Mutation	SNP	C	T	24	486	c.1457G>A	c.(1456-1458)CGA>CAA	p.R486Q
Pat_14	Post-Resistance	PTPN13	5783	37	4	87728980	87728980	Missense_Mutation	SNP	G	A	4	319	c.7013G>A	c.(7012-7014)CGA>CAA	p.R2338Q
Pat_14	Post-Resistance	HSPA4L	22824	37	4	128722393	128722393	Splice_Site	SNP	G	A	4	188	c.529_splice	c.e5+1	p.V177_splice
Pat_14	Post-Resistance	HSPA4L	22824	37	4	128726356	128726356	Missense_Mutation	SNP	G	A	6	251	c.1114G>A	c.(1114-1116)GTT>ATT	p.V372I
Pat_14	Post-Resistance	OTUD4	54726	37	4	146064530	146064530	Missense_Mutation	SNP	G	A	11	239	c.1475C>T	c.(1474-1476)TCT>TTT	p.S492F
Pat_14	Post-Resistance	SH3D19	152503	37	4	152095993	152095993	Nonsense_Mutation	SNP	G	A	7	810	c.523C>T	c.(523-525)CAA>TAA	p.Q175*
Pat_14	Post-Resistance	SH3D19	152503	37	4	152096238	152096238	Missense_Mutation	SNP	G	A	5	471	c.278C>T	c.(277-279)GCG>GTG	p.A93V
Pat_14	Post-Resistance	FGB	2244	37	4	155487659	155487660	Missense_Mutation	DNP	GG	AA	4	412	c.325_326GG>AA	c.(325-327)GGA>AAA	p.G109K
Pat_14	Post-Resistance	MFAP3L	9848	37	4	170912598	170912598	Nonsense_Mutation	SNP	G	T	8	333	c.1161C>A	c.(1159-1161)TAC>TAA	p.Y387*
Pat_14	Post-Resistance	ENPP6	133121	37	4	185038920	185038920	Missense_Mutation	SNP	A	T	8	566	c.667T>A	c.(667-669)TGG>AGG	p.W223R
Pat_14	Post-Resistance	C5orf22	55322	37	5	31535966	31535966	Missense_Mutation	SNP	T	G	23	445	c.343T>G	c.(343-345)TTA>GTA	p.L115V
Pat_14	Post-Resistance	ADAMTS12	81792	37	5	33561164	33561164	Missense_Mutation	SNP	A	G	6	524	c.4093T>C	c.(4093-4095)TGT>CGT	p.C1365R
Pat_14	Post-Resistance	LMBRD2	92255	37	5	36136535	36136535	Missense_Mutation	SNP	T	G	4	438	c.623A>C	c.(622-624)GAA>GCA	p.E208A
Pat_14	Post-Resistance	C6	729	37	5	41159266	41159266	Missense_Mutation	SNP	G	A	6	362	c.1774C>T	c.(1774-1776)CCT>TCT	p.P592S
Pat_14	Post-Resistance	C5orf39	389289	37	5	43039815	43039815	Missense_Mutation	SNP	C	T	5	476	c.334G>A	c.(334-336)GAA>AAA	p.E112K
Pat_14	Post-Resistance	NNT	23530	37	5	43702770	43702770	Missense_Mutation	SNP	G	A	4	286	c.3043G>A	c.(3043-3045)GCA>ACA	p.A1015T
Pat_14	Post-Resistance	MAP3K1	4214	37	5	56170995	56170995	Missense_Mutation	SNP	G	A	4	189	c.1823G>A	c.(1822-1824)GGC>GAC	p.G608D
Pat_14	Post-Resistance	POLK	51426	37	5	74892412	74892412	Missense_Mutation	SNP	G	A	8	709	c.1894G>A	c.(1894-1896)GGG>AGG	p.G632R
Pat_14	Post-Resistance	CMYA5	202333	37	5	79034663	79034663	Missense_Mutation	SNP	G	A	4	262	c.10075G>A	c.(10075-10077)GGT>AGT	p.G3359S

Pat_14	Post-Resistance	PCSK1	5122	37	5	95746650	95746650	Missense_Mutation	SNP	C	T	10	561	c.923G>A	c.(922-924)GGA>GAA	p.G308E
Pat_14	Post-Resistance	GDF9	2661	37	5	132197700	132197700	Missense_Mutation	SNP	G	A	4	161	c.946C>T	c.(946-948)CGT>TGT	p.R316C
Pat_14	Post-Resistance	TRPC7	57113	37	5	135651286	135651286	Missense_Mutation	SNP	T	C	3	160	c.959A>G	c.(958-960)AAG>AGG	p.K320R
Pat_14	Post-Resistance	KDM3B	51780	37	5	137763748	137763749	Missense_Mutation	DNP	CC	TT	10	781	.4726_4727CC>T	c.(4726-4728)CCC>TTC	p.P1576F
Pat_14	Post-Resistance	PCDHA12	56137	37	5	140256817	140256817	Missense_Mutation	SNP	C	T	5	377	c.1760C>T	c.(1759-1761)GCG>GTG	p.A587V
Pat_14	Post-Resistance	PCDHAC1	56135	37	5	140308149	140308149	Missense_Mutation	SNP	C	T	8	672	c.1672C>T	c.(1672-1674)CCC>TCC	p.P558S
Pat_14	Post-Resistance	PCDHB7	56129	37	5	140553044	140553044	Missense_Mutation	SNP	T	G	6	275	c.628T>G	c.(628-630)TTA>GTA	p.L210V
Pat_14	Post-Resistance	PCDHGA6	56109	37	5	140754614	140754614	Missense_Mutation	SNP	C	T	12	712	c.964C>T	c.(964-966)CGG>TGG	p.R322W
Pat_14	Post-Resistance	LARP1	23367	37	5	154181706	154181706	Missense_Mutation	SNP	G	A	5	507	c.1856G>A	c.(1855-1857)CGG>CAG	p.R619Q
Pat_14	Post-Resistance	FAM71B	153745	37	5	156590333	156590333	Missense_Mutation	SNP	C	T	4	456	c.943G>A	c.(943-945)GGA>AGA	p.G315R
Pat_14	Post-Resistance	CYFIP2	26999	37	5	156752647	156752647	Splice_Site	SNP	G	A	3	114	c.1982_splice	c.e19+1	p.E661_splice
Pat_14	Post-Resistance	GABRA6	2559	37	5	161113355	161113355	Splice_Site	SNP	G	A	5	482	c.157_splice	c.e2+1	p.G53_splice
Pat_14	Post-Resistance	GABRG2	2566	37	5	161576150	161576150	Missense_Mutation	SNP	C	A	5	465	c.959C>A	c.(958-960)ACC>AAC	p.T320N
Pat_14	Post-Resistance	ODZ2	57451	37	5	167545386	167545386	Missense_Mutation	SNP	G	A	6	697	c.1903G>A	c.(1903-1905)GTG>ATG	p.V635M
Pat_14	Post-Resistance	CCDC99	54908	37	5	169028328	169028328	Missense_Mutation	SNP	C	T	5	381	c.1369C>T	c.(1369-1371)CCT>TCT	p.P457S
Pat_14	Post-Resistance	BNIP1	662	37	5	172581385	172581385	Missense_Mutation	SNP	G	A	4	74	c.238G>A	c.(238-240)GAA>AAA	p.E80K
Pat_14	Post-Resistance	AGXT2L2	85007	37	5	177641822	177641822	Nonsense_Mutation	SNP	C	A	5	183	c.1147G>T	c.(1147-1149)GAA>TAA	p.E383*
Pat_14	Post-Resistance	GRM6	2916	37	5	178413942	178413942	Missense_Mutation	SNP	G	A	4	82	c.1397C>T	c.(1396-1398)GCG>GTG	p.A466V
Pat_14	Post-Resistance	DSP	1832	37	6	7542195	7542195	Missense_Mutation	SNP	G	A	3	63	c.47G>A	c.(46-48)CGC>CAC	p.R16H
Pat_14	Post-Resistance	KIF13A	63971	37	6	17796976	17796976	Missense_Mutation	SNP	G	A	4	376	c.2866C>T	c.(2866-2868)CAC>TAC	p.H956Y
Pat_14	Post-Resistance	TRIM38	10475	37	6	25973502	25973502	Missense_Mutation	SNP	G	A	4	204	c.863G>A	c.(862-864)AGG>AAG	p.R288K
Pat_14	Post-Resistance	HLA-F	3134	37	6	29694752	29694752	Missense_Mutation	SNP	C	T	5	402	c.1129C>T	c.(1129-1131)CGG>TGG	p.R377W
Pat_14	Post-Resistance	RNF39	80352	37	6	30039106	30039106	Missense_Mutation	SNP	C	T	5	24	c.1045G>A	c.(1045-1047)GCA>ACA	p.A349T
Pat_14	Post-Resistance	MDC1	9656	37	6	30670608	30670608	Missense_Mutation	SNP	G	A	4	344	c.5912C>T	c.(5911-5913)ACC>ATC	p.T1971I
Pat_14	Post-Resistance	MDC1	9656	37	6	30673197	30673197	Missense_Mutation	SNP	A	G	5	734	c.3763T>C	c.(3763-3765)TCC>CCC	p.S1255P
Pat_14	Post-Resistance	MICA	4276	37	6	31378439	31378439	Missense_Mutation	SNP	T	C	3	136	c.190T>C	c.(190-192)TGC>CGC	p.C64R
Pat_14	Post-Resistance	FKBPL	63943	37	6	32097007	32097007	Missense_Mutation	SNP	G	A	4	289	c.551C>T	c.(550-552)CCT>CTT	p.P184L
Pat_14	Post-Resistance	HLA-DQB1	3119	37	6	32629750	32629750	Missense_Mutation	SNP	C	T	9	332	c.655G>A	c.(655-657)GAG>AAG	p.E219K
Pat_14	Post-Resistance	IP6K3	117283	37	6	33703198	33703198	Missense_Mutation	SNP	T	C	3	190	c.56A>G	c.(55-57)GAG>GGG	p.E19G
Pat_14	Post-Resistance	ZNF318	24149	37	6	43306907	43306907	Nonsense_Mutation	SNP	G	C	4	374	c.4829C>G	c.(4828-4830)TCA>TGA	p.S1610*
Pat_14	Post-Resistance	MRPL14	64928	37	6	44081926	44081926	Missense_Mutation	SNP	G	A	6	635	c.92C>T	c.(91-93)GCG>GTG	p.A31V
Pat_14	Post-Resistance	GCLC	2729	37	6	53387279	53387279	Missense_Mutation	SNP	C	T	4	398	c.197G>A	c.(196-198)CGG>CAG	p.R66Q
Pat_14	Post-Resistance	GJA10	84694	37	6	90605005	90605005	Missense_Mutation	SNP	G	T	4	230	c.818G>T	c.(817-819)TGC>TTC	p.C273F
Pat_14	Post-Resistance	MCHR2	84539	37	6	100390897	100390897	Missense_Mutation	SNP	G	A	6	499	c.515C>T	c.(514-516)TCG>TTG	p.S172L
Pat_14	Post-Resistance	AKD1	221264	37	6	109863293	109863293	Missense_Mutation	SNP	G	A	5	74	c.3307C>T	c.(3307-3309)CTT>TTT	p.L1103F
Pat_14	Post-Resistance	TAAR9	134860	37	6	132859993	132859994	Missense_Mutation	DNP	GG	AA	5	315	c.565_566GG>AA	c.(565-567)GGC>AAC	p.G189N
Pat_14	Post-Resistance	TAAR2	9287	37	6	132939068	132939068	Missense_Mutation	SNP	C	T	4	469	c.277G>A	c.(277-279)GGA>AGA	p.G93R
Pat_14	Post-Resistance	MTHFD1L	25902	37	6	151258007	151258007	Missense_Mutation	SNP	G	A	5	456	c.1324G>A	c.(1324-1326)GCA>ACA	p.A442T
Pat_14	Post-Resistance	SYNE1	23345	37	6	152644827	152644827	Missense_Mutation	SNP	G	A	10	224	c.15703C>T	c.(15703-15705)CCT>TCT	p.P5235S
Pat_14	Post-Resistance	LPA	4018	37	6	160998262	160998262	Missense_Mutation	SNP	T	G	5	552	c.4537A>C	c.(4537-4539)ATA>CTA	p.I1513L
Pat_14	Post-Resistance	PLG	5340	37	6	161139864	161139864	Missense_Mutation	SNP	C	T	5	163	c.1090C>T	c.(1090-1092)CCC>TCC	p.P364S
Pat_14	Post-Resistance	MICALL2	79778	37	7	1488316	1488316	Missense_Mutation	SNP	G	A	4	425	c.274C>T	c.(274-276)CGG>TGG	p.R92W
Pat_14	Post-Resistance	MAD1L1	8379	37	7	2255527	2255527	Missense_Mutation	SNP	T	C	3	374	c.917A>G	c.(916-918)GAG>GGG	p.E306G
Pat_14	Post-Resistance	FOXK1	221937	37	7	4794206	4794206	Missense_Mutation	SNP	C	T	6	129	c.863C>T	c.(862-864)TCG>TTG	p.S288L
Pat_14	Post-Resistance	SLC29A4	222962	37	7	5336750	5336750	Missense_Mutation	SNP	G	A	4	170	c.803G>A	c.(802-804)AGC>AAC	p.S268N
Pat_14	Post-Resistance	TBX20	57057	37	7	35242077	35242077	Missense_Mutation	SNP	G	A	3	51	c.1309C>T	c.(1309-1311)CGC>TGC	p.R437C
Pat_14	Post-Resistance	ABCA13	154664	37	7	48528941	48528941	Missense_Mutation	SNP	G	A	3	91	c.13291G>A	.(13291-13293)GGA>AG	p.G4431R

Pat_14	Post-Resistance	NCF1	653361	37	7	74203043	74203043	Missense_Mutation	SNP	C	G	14	17	c.1046C>G	c.(1045-1047)CCG>CGG	p.P349R
Pat_14	Post-Resistance	SEMA3E	9723	37	7	83029517	83029517	Missense_Mutation	SNP	G	A	33	575	c.1193C>T	c.(1192-1194)CCT>CTT	p.P398L
Pat_14	Post-Resistance	SHFM1	7979	37	7	96303133	96303133	Missense_Mutation	SNP	G	A	6	284	c.209C>T	c.(208-210)CCG>CTG	p.P70L
Pat_14	Post-Resistance	MEPCE	56257	37	7	100028939	100028939	Missense_Mutation	SNP	G	A	5	179	c.1298G>A	c.(1297-1299)CGC>CAC	p.R433H
Pat_14	Post-Resistance	SERPINE1	5054	37	7	100775236	100775236	Missense_Mutation	SNP	G	A	6	666	c.586G>A	c.(586-588)GGC>AGC	p.G196S
Pat_14	Post-Resistance	MYL10	93408	37	7	101256984	101256984	Missense_Mutation	SNP	T	G	5	252	c.540A>C	c.(538-540)AAA>AAC	p.K180N
Pat_14	Post-Resistance	LAMB1	3912	37	7	107594047	107594047	Missense_Mutation	SNP	G	A	4	449	c.3007C>T	c.(3007-3009)CAC>TAC	p.H1003Y
Pat_14	Post-Resistance	SLC13A1	6561	37	7	122811882	122811882	Nonsense_Mutation	SNP	C	T	18	505	c.305G>A	c.(304-306)TGG>TAG	p.W102*
Pat_14	Post-Resistance	IQUB	154865	37	7	123097521	123097521	Missense_Mutation	SNP	T	C	22	778	c.2107A>G	c.(2107-2109)AAA>GAA	p.K703E
Pat_14	Post-Resistance	IMPDH1	3614	37	7	128040908	128040908	Missense_Mutation	SNP	G	A	5	474	c.287C>T	c.(286-288)ACC>ATC	p.T96I
Pat_14	Post-Resistance	ZYX	7791	37	7	143087029	143087029	Missense_Mutation	SNP	G	A	5	447	c.1573G>A	c.(1573-1575)GCC>ACC	p.A525T
Pat_14	Post-Resistance	SSPO	23145	37	7	149492654	149492654	Missense_Mutation	SNP	C	T	4	228	c.6434C>T	c.(6433-6435)TCC>TTC	p.S2145F
Pat_14	Post-Resistance	KCNH2	3757	37	7	150654525	150654525	Missense_Mutation	SNP	G	A	4	164	c.982C>T	c.(982-984)CGC>TGC	p.R328C
Pat_14	Post-Resistance	ARHGEF10	9639	37	8	1876747	1876747	Missense_Mutation	SNP	C	T	4	284	c.2852C>T	c.(2851-2853)CCG>CTG	p.P951L
Pat_14	Post-Resistance	USP17L2	377630	37	8	11996169	11996169	Missense_Mutation	SNP	C	T	5	246	c.101G>A	c.(100-102)CGG>CAG	p.R34Q
Pat_14	Post-Resistance	MYST3	7994	37	8	41790228	41790228	Missense_Mutation	SNP	A	G	5	271	c.5510T>C	c.(5509-5511)ATT>ACT	p.I1837T
Pat_14	Post-Resistance	VDAC3	7419	37	8	42260935	42260935	Missense_Mutation	SNP	G	T	5	414	c.658G>T	c.(658-660)GGC>TGC	p.G220C
Pat_14	Post-Resistance	CHRNB3	1142	37	8	42563922	42563922	Missense_Mutation	SNP	G	A	11	355	c.115G>A	c.(115-117)GGT>AGT	p.G39S
Pat_14	Post-Resistance	POTEA	340441	37	8	43152432	43152432	Missense_Mutation	SNP	G	A	5	487	c.418G>A	c.(418-420)GTA>ATA	p.V140I
Pat_14	Post-Resistance	SNTG1	54212	37	8	51314853	51314853	Missense_Mutation	SNP	G	A	45	453	c.111G>A	c.(109-111)ATG>ATA	p.M37I
Pat_14	Post-Resistance	SOX17	64321	37	8	55370914	55370914	Missense_Mutation	SNP	G	T	4	120	c.216G>T	c.(214-216)ATG>ATT	p.M72I
Pat_14	Post-Resistance	CSMD3	114788	37	8	113649069	113649069	Missense_Mutation	SNP	C	T	4	368	c.3692G>A	c.(3691-3693)AGT>AAT	p.S1231N
Pat_14	Post-Resistance	ZFAT	57623	37	8	135612684	135612684	Missense_Mutation	SNP	C	T	6	520	c.2470G>A	c.(2470-2472)GCA>ACA	p.A824T
Pat_14	Post-Resistance	ZFAT	57623	37	8	135622838	135622838	Missense_Mutation	SNP	G	A	4	299	c.509C>T	c.(508-510)TCG>TTG	p.S170L
Pat_14	Post-Resistance	CYP11B1	1584	37	8	143958489	143958489	Missense_Mutation	SNP	C	T	3	60	c.545G>A	c.(544-546)GGG>GAG	p.G182E
Pat_14	Post-Resistance	KIAA1432	57589	37	9	5763645	5763645	Missense_Mutation	SNP	C	T	4	390	c.2381C>T	c.(2380-2382)GCT>GTT	p.A794V
Pat_14	Post-Resistance	RANBP6	26953	37	9	6012658	6012658	Missense_Mutation	SNP	T	G	6	330	c.2950A>C	c.(2950-2952)ATA>CTA	p.I984L
Pat_14	Post-Resistance	KIAA1797	54914	37	9	20874719	20874719	Missense_Mutation	SNP	G	A	5	475	c.2230G>A	c.(2230-2232)GAT>AAT	p.D744N
Pat_14	Post-Resistance	LOC442421	442421	37	9	66499680	66499680	Missense_Mutation	SNP	C	T	13	110	c.490C>T	c.(490-492)CCC>TCC	p.P164S
Pat_14	Post-Resistance	TMC1	117531	37	9	75309467	75309467	Missense_Mutation	SNP	G	A	4	171	c.73G>A	c.(73-75)GAA>AAA	p.E25K
Pat_14	Post-Resistance	GNA14	9630	37	9	80043941	80043941	Missense_Mutation	SNP	A	G	9	749	c.605T>C	c.(604-606)GTT>GCT	p.V202A
Pat_14	Post-Resistance	NTRK2	4915	37	9	87359971	87359971	Missense_Mutation	SNP	G	A	6	348	c.1279G>A	c.(1279-1281)GGT>AGT	p.G427S
Pat_14	Post-Resistance	FAM22F	54754	37	9	97082748	97082748	Missense_Mutation	SNP	G	C	3	118	c.1110C>G	c.(1108-1110)AAC>AAG	p.N370K
Pat_14	Post-Resistance	ZNF462	58499	37	9	109746481	109746481	Missense_Mutation	SNP	C	T	7	460	c.6847C>T	c.(6847-6849)CCC>TCC	p.P2283S
Pat_14	Post-Resistance	SLC31A1	1317	37	9	116022686	116022686	Missense_Mutation	SNP	G	A	6	579	c.506G>A	c.(505-507)GGT>GAT	p.G169D
Pat_14	Post-Resistance	COL27A1	85301	37	9	116930718	116930718	Missense_Mutation	SNP	G	A	4	125	c.883G>A	c.(883-885)GCC>ACC	p.A295T
Pat_14	Post-Resistance	TNC	3371	37	9	117826314	117826314	Missense_Mutation	SNP	G	A	11	685	c.3521C>T	c.(3520-3522)GCC>GTC	p.A1174V
Pat_14	Post-Resistance	ASTN2	23245	37	9	120053778	120053778	Missense_Mutation	SNP	C	T	5	178	c.457G>A	c.(457-459)GCG>ACG	p.A153T
Pat_14	Post-Resistance	SETX	23064	37	9	135203113	135203113	Missense_Mutation	SNP	T	C	3	410	c.3872A>G	c.(3871-3873)AAG>AGG	p.K1291R
Pat_14	Post-Resistance	TMEM8C	389827	37	9	136389862	136389862	Missense_Mutation	SNP	C	A	4	185	c.105G>T	c.(103-105)ATG>ATT	p.M35I
Pat_14	Post-Resistance	NOTCH1	4851	37	9	139411819	139411819	Missense_Mutation	SNP	C	T	3	55	c.1460G>A	c.(1459-1461)TGC>TAC	p.C487Y
Pat_14	Post-Resistance	GRIN1	2902	37	9	140055804	140055804	Missense_Mutation	SNP	G	A	4	222	c.1403G>A	c.(1402-1404)CGG>CAG	p.R468Q
Pat_14	Post-Resistance	EHMT1	79813	37	9	140611486	140611486	Missense_Mutation	SNP	C	T	5	193	c.494C>T	c.(493-495)CCA>CTA	p.P165L
Pat_14	Post-Resistance	PIR	8544	37	X	15474002	15474002	Missense_Mutation	SNP	G	A	6	526	c.449C>T	c.(448-450)GCT>GTT	p.A150V
Pat_14	Post-Resistance	IL1RAPL1	11141	37	X	29414442	29414442	Missense_Mutation	SNP	T	C	3	278	c.430T>C	c.(430-432)TAT>CAT	p.Y144H
Pat_14	Post-Resistance	TAB3	257397	37	X	30872463	30872463	Missense_Mutation	SNP	G	A	4	415	c.1319C>T	c.(1318-1320)ACT>ATT	p.T440I
Pat_14	Post-Resistance	DMD	1756	37	X	32583858	32583858	Nonsense_Mutation	SNP	C	T	6	715	c.1953G>A	c.(1951-1953)TGG>TGA	p.W651*

Pat_14	Post-Resistance	FAM47C	442444	37	X	37028134	37028134	Missense_Mutation	SNP	C	T	9	408	c.1651C>T	c.(1651-1653)CCT>TCT	p.P551S
Pat_14	Post-Resistance	RBM10	8241	37	X	47030588	47030588	Missense_Mutation	SNP	G	T	3	82	c.363G>T	c.(361-363)GAG>GAT	p.E121D
Pat_14	Post-Resistance	WDR13	64743	37	X	48460495	48460495	Missense_Mutation	SNP	G	A	4	166	c.1055G>A	c.(1054-1056)AGC>AAC	p.S352N
Pat_14	Post-Resistance	TEX11	56159	37	X	69849510	69849510	Missense_Mutation	SNP	C	T	6	407	c.1604G>A	c.(1603-1605)AGA>AAA	p.R535K
Pat_14	Post-Resistance	KIAA2022	340533	37	X	73963437	73963438	Missense_Mutation	DNP	CC	TT	5	590	c.954_955GG>AA	952-957)CAGGAC>CAAA	p.D319N
Pat_14	Post-Resistance	ATP7A	538	37	X	77258680	77258680	Missense_Mutation	SNP	G	A	8	790	c.1654G>A	c.(1654-1656)GGA>AGA	p.G552R
Pat_14	Post-Resistance	ARL13A	392509	37	X	100240658	100240658	Missense_Mutation	SNP	C	T	4	339	c.133C>T	c.(133-135)CTT>TTT	p.L45F
Pat_14	Post-Resistance	DRP2	1821	37	X	100500047	100500047	Missense_Mutation	SNP	A	G	6	644	c.1096A>G	c.(1096-1098)AAA>GAA	p.K366E
Pat_14	Post-Resistance	MORC4	79710	37	X	106185282	106185282	Missense_Mutation	SNP	G	A	4	397	c.2546C>T	c.(2545-2547)ACC>ATC	p.T849I
Pat_14	Post-Resistance	IRS4	8471	37	X	107976582	107976582	Missense_Mutation	SNP	G	A	5	407	c.2993C>T	c.(2992-2994)CCT>CTT	p.P998L
Pat_14	Post-Resistance	DCX	1641	37	X	110576315	110576315	Missense_Mutation	SNP	G	A	5	203	c.1015C>T	c.(1015-1017)CGC>TGC	p.R339C
Pat_14	Post-Resistance	TRPC5	7224	37	X	111090573	111090573	Missense_Mutation	SNP	G	A	6	515	c.1469C>T	c.(1468-1470)TCG>TTG	p.S490L
Pat_14	Post-Resistance	RPL39	6170	37	X	118923908	118923908	Missense_Mutation	SNP	G	A	14	455	c.70C>T	c.(70-72)CCC>TCC	p.P24S
Pat_14	Post-Resistance	DDX26B	203522	37	X	134654864	134654864	Translation_Start_Site	SNP	G	A	4	378	c.-53G>A	c.(-55--51)CAGTG>CAATG	
Pat_14	Post-Resistance	MAP7D3	79649	37	X	135314011	135314011	Missense_Mutation	SNP	G	A	5	442	c.1105C>T	c.(1105-1107)CTC>TTC	p.L369F
Pat_14	Post-Resistance	MAGEA11	4110	37	X	148797987	148797987	Missense_Mutation	SNP	G	A	5	453	c.841G>A	c.(841-843)GAA>AAA	p.E281K
Pat_14	Post-Resistance	MTMR1	8776	37	X	149912863	149912863	Missense_Mutation	SNP	G	A	9	704	c.1480G>A	c.(1480-1482)GAT>AAT	p.D494N
Pat_14	Post-Resistance	TMEM187	8269	37	X	153248187	153248187	Missense_Mutation	SNP	G	A	5	255	c.674G>A	c.(673-675)GGC>GAC	p.G225D
Pat_14	Post-Resistance	MPP1	4354	37	X	154014640	154014640	Missense_Mutation	SNP	T	A	10	845	c.516A>T	c.(514-516)AAA>AAT	p.K172N
Pat_14	Post-Resistance	TMLHE	55217	37	X	154741371	154741371	Missense_Mutation	SNP	G	A	6	635	c.721C>T	c.(721-723)CGG>TGG	p.R241W
Pat_15	Pre-Treatment	PLEKHG5	57449	37	1	6528263	6528263	Missense_Mutation	SNP	G	A	18	14	c.2801C>T	c.(2800-2802)TCC>TTC	p.S934F
Pat_15	Pre-Treatment	PRAMEF4	400735	37	1	12943025	12943025	Missense_Mutation	SNP	C	T	25	30	c.191G>A	c.(190-192)CGC>CAC	p.R64H
Pat_15	Pre-Treatment	ATP13A2	23400	37	1	17332247	17332247	Missense_Mutation	SNP	G	A	10	11	c.37C>T	c.(37-39)CCC>TCC	p.P13S
Pat_15	Pre-Treatment	KLHDC7A	127707	37	1	18809751	18809751	Missense_Mutation	SNP	C	T	70	78	c.2276C>T	c.(2275-2277)ACC>ATC	p.T759I
Pat_15	Pre-Treatment	SYTL1	84958	37	1	27673988	27673988	Nonsense_Mutation	SNP	C	T	23	41	c.268C>T	c.(268-270)CAG>TAG	p.Q90*
Pat_15	Pre-Treatment	TESK2	10420	37	1	45813599	45813599	Missense_Mutation	SNP	G	A	49	57	c.614C>T	c.(613-615)CCC>CTC	p.P205L
Pat_15	Pre-Treatment	PODN	127435	37	1	53544264	53544264	Missense_Mutation	SNP	T	C	17	21	c.1226T>C	c.(1225-1227)TTG>TCG	p.L409S
Pat_15	Pre-Treatment	ELTD1	64123	37	1	79412055	79412055	Missense_Mutation	SNP	T	G	12	1	c.229A>C	c.(229-231)AAC>CAC	p.N77H
Pat_15	Pre-Treatment	CLCA4	22802	37	1	87031683	87031683	Missense_Mutation	SNP	G	A	36	1	c.934G>A	c.(934-936)GAT>AAT	p.D312N
Pat_15	Pre-Treatment	ACP6	51205	37	1	147131860	147131860	Missense_Mutation	SNP	G	A	14	20	c.250C>T	c.(250-252)CCA>TCA	p.P84S
Pat_15	Pre-Treatment	NBPF16	728936	37	1	148754841	148754841	Missense_Mutation	SNP	C	G	3	28	c.1497C>G	c.(1495-1497)AGC>AGG	p.S499R
Pat_15	Pre-Treatment	CD1E	913	37	1	158325309	158325309	Missense_Mutation	SNP	G	A	5	12	c.575G>A	c.(574-576)CGA>CAA	p.R192Q
Pat_15	Pre-Treatment	OR10Z1	128368	37	1	158576814	158576814	Missense_Mutation	SNP	G	A	41	41	c.586G>A	c.(586-588)GAG>AAG	p.E196K
Pat_15	Pre-Treatment	DNM3	26052	37	1	172017826	172017826	Missense_Mutation	SNP	C	T	31	42	c.1271C>T	c.(1270-1272)TCC>TTC	p.S424F
Pat_15	Pre-Treatment	SLC9A11	284525	37	1	173552668	173552668	Missense_Mutation	SNP	C	T	16	21	c.617G>A	c.(616-618)AGA>AAA	p.R206K
Pat_15	Pre-Treatment	ASTN1	460	37	1	176992682	176992683	Missense_Mutation	DNP	CC	TT	10	18	.1295_1296GG>A	c.(1294-1296)GGG>GAA	p.G432E
Pat_15	Pre-Treatment	CFHR3	10878	37	1	196748941	196748941	Missense_Mutation	SNP	C	T	2	2	c.268C>T	c.(268-270)CCT>TCT	p.P90S
Pat_15	Pre-Treatment	CFHR5	81494	37	1	196953100	196953100	Missense_Mutation	SNP	C	T	14	11	c.263C>T	c.(262-264)TCC>TTC	p.S88F
Pat_15	Pre-Treatment	F13B	2165	37	1	197026464	197026464	Missense_Mutation	SNP	C	T	27	50	c.937G>A	c.(937-939)GAA>AAA	p.E313K
Pat_15	Pre-Treatment	HEATR1	55127	37	1	236730082	236730082	Missense_Mutation	SNP	G	A	28	39	c.4172C>T	c.(4171-4173)CCG>CTG	p.P1391L
Pat_15	Pre-Treatment	FAM171A1	221061	37	10	15296773	15296773	Missense_Mutation	SNP	G	A	15	1	c.524C>T	c.(523-525)CCT>CTT	p.P175L
Pat_15	Pre-Treatment	C10orf72	196740	37	10	50227768	50227768	Missense_Mutation	SNP	G	A	11	0	c.890C>T	c.(889-891)CCC>CTC	p.P297L
Pat_15	Pre-Treatment	C10orf71	118461	37	10	50532304	50532304	Missense_Mutation	SNP	C	T	10	1	c.1714C>T	c.(1714-1716)CCC>TCC	p.P572S
Pat_15	Pre-Treatment	CPEB3	22849	37	10	93902788	93902788	Missense_Mutation	SNP	T	C	33	0	c.1451A>G	c.(1450-1452)AAA>AGA	p.K484R
Pat_15	Pre-Treatment	HELLS	3070	37	10	96361363	96361363	Missense_Mutation	SNP	C	T	4	2	c.2501C>T	c.(2500-2502)CCT>CTT	p.P834L
Pat_15	Pre-Treatment	CYP2C18	1562	37	10	96448031	96448031	Missense_Mutation	SNP	G	A	26	3	c.481G>A	c.(481-483)GCC>ACC	p.A161T
Pat_15	Pre-Treatment	CYP2C18	1562	37	10	96454828	96454828	Nonsense_Mutation	SNP	G	A	3	0	c.636G>A	c.(634-636)TGG>TGA	p.W212*

Pat_15	Pre-Treatment	CYP2C8	1558	37	10	96797060	96797060	Missense_Mutation	SNP	C	T	10	1	c.1298G>A	c.(1297-1299)CGA>CAA	p.R433Q
Pat_15	Pre-Treatment	C10orf62	414157	37	10	99349869	99349869	Missense_Mutation	SNP	C	T	34	2	c.215C>T	c.(214-216)ACG>ATG	p.T72M
Pat_15	Pre-Treatment	NRAP	4892	37	10	115388776	115388776	Missense_Mutation	SNP	T	C	39	0	c.2045A>G	c.(2044-2046)CAG>CGG	p.Q682R
Pat_15	Pre-Treatment	OR51G2	81282	37	11	4936406	4936406	Missense_Mutation	SNP	G	A	24	0	c.488C>T	c.(487-489)CCA>CTA	p.P163L
Pat_15	Pre-Treatment	ZNF215	7762	37	11	6976921	6976921	Missense_Mutation	SNP	A	G	2	17	c.713A>G	c.(712-714)GAC>GGC	p.D238G
Pat_15	Pre-Treatment	PTH	5741	37	11	13514049	13514049	Missense_Mutation	SNP	T	A	15	1	c.251A>T	c.(250-252)AAA>ATA	p.K84I
Pat_15	Pre-Treatment	AGBL2	79841	37	11	47698946	47698946	Missense_Mutation	SNP	T	G	13	0	c.2024A>C	c.(2023-2025)CAG>CCG	p.Q675P
Pat_15	Pre-Treatment	OR5L2	26338	37	11	55595616	55595616	Missense_Mutation	SNP	A	C	8	3	c.922A>C	c.(922-924)AAA>CAA	p.K308Q
Pat_15	Pre-Treatment	OR8H3	390152	37	11	55889999	55889999	Missense_Mutation	SNP	C	T	71	8	c.151C>T	c.(151-153)CGC>TGC	p.R51C
Pat_15	Pre-Treatment	OR5T3	390154	37	11	56019973	56019973	Missense_Mutation	SNP	G	A	20	0	c.298G>A	c.(298-300)GAT>AAT	p.D100N
Pat_15	Pre-Treatment	OR9G9	504191	37	11	56467892	56467892	Missense_Mutation	SNP	A	G	15	32	c.29A>G	c.(28-30)GAG>GGG	p.E10G
Pat_15	Pre-Treatment	DTX4	23220	37	11	58949848	58949848	Missense_Mutation	SNP	A	G	4	1	c.848A>G	c.(847-849)AAG>AGG	p.K283R
Pat_15	Pre-Treatment	ARAP1	116985	37	11	72421519	72421519	Missense_Mutation	SNP	G	A	26	43	c.1327C>T	c.(1327-1329)CGC>TGC	p.R443C
Pat_15	Pre-Treatment	TMEM126B	55863	37	11	85347238	85347238	Missense_Mutation	SNP	G	A	6	0	c.568G>A	c.(568-570)GAA>AAA	p.E190K
Pat_15	Pre-Treatment	KDM4DL	390245	37	11	94759611	94759611	Nonsense_Mutation	SNP	G	A	14	0	c.890G>A	c.(889-891)TGG>TAG	p.W297*
Pat_15	Pre-Treatment	CNTN5	53942	37	11	100095458	100095458	Missense_Mutation	SNP	T	G	21	0	c.1919T>G	c.(1918-1920)ATC>AGC	p.I640S
Pat_15	Pre-Treatment	PGR	5241	37	11	100962501	100962501	Missense_Mutation	SNP	C	T	20	0	c.1896G>A	c.(1894-1896)ATG>ATA	p.M632I
Pat_15	Pre-Treatment	GUCY1A2	2977	37	11	106810341	106810341	Nonsense_Mutation	SNP	G	A	14	0	c.1051C>T	c.(1051-1053)CGA>TGA	p.R351*
Pat_15	Pre-Treatment	AQP2	359	37	12	50344822	50344822	Missense_Mutation	SNP	C	T	29	2	c.209C>T	c.(208-210)GCC>GTC	p.A70V
Pat_15	Pre-Treatment	KRT75	9119	37	12	52825810	52825810	Missense_Mutation	SNP	C	T	32	26	c.754G>A	c.(754-756)GAA>AAA	p.E252K
Pat_15	Pre-Treatment	STAB2	55576	37	12	104063395	104063395	Missense_Mutation	SNP	G	A	23	21	c.2249G>A	c.(2248-2250)GGA>GAA	p.G750E
Pat_15	Pre-Treatment	UNC119B	84747	37	12	121157744	121157744	Missense_Mutation	SNP	C	T	41	35	c.665C>T	c.(664-666)CCT>CTT	p.P222L
Pat_15	Pre-Treatment	DNAH10	196385	37	12	124402294	124402295	Missense_Mutation	DNP	GG	AA	2	0	10812_10813GG>	10-10815)ACGGGG>AC	p.G3605R
Pat_15	Pre-Treatment	SLITRK1	114798	37	13	84453751	84453751	Missense_Mutation	SNP	G	A	24	0	c.1892C>T	c.(1891-1893)TCC>TTC	p.S631F
Pat_15	Pre-Treatment	DOCK9	23348	37	13	99478165	99478165	Missense_Mutation	SNP	G	A	7	1	c.4987C>T	c.(4987-4989)CCC>TCC	p.P1663S
Pat_15	Pre-Treatment	POTEG	404785	37	14	19553522	19553522	Missense_Mutation	SNP	A	G	11	112	c.106A>G	c.(106-108)AGG>GGG	p.R36G
Pat_15	Pre-Treatment	SEL1L	6400	37	14	82000079	82000079	Missense_Mutation	SNP	G	A	22	0	c.10C>T	c.(10-12)CGG>TGG	p.R4W
Pat_15	Pre-Treatment	SLC24A4	123041	37	14	92953088	92953088	Missense_Mutation	SNP	C	T	46	0	c.1450C>T	c.(1450-1452)CCA>TCA	p.P484S
Pat_15	Pre-Treatment	KIAA1409	57578	37	14	93994911	93994911	Missense_Mutation	SNP	T	G	28	3	c.440T>G	c.(439-441)ATA>AGA	p.I147R
Pat_15	Pre-Treatment	MAP2K1	5604	37	15	66729163	66729163	Missense_Mutation	SNP	C	T	60	42	c.371C>T	c.(370-372)CCG>CTG	p.P124L
Pat_15	Pre-Treatment	GRAMD2	196996	37	15	72456010	72456010	Missense_Mutation	SNP	G	A	21	11	c.689C>T	c.(688-690)CCA>CTA	p.P230L
Pat_15	Pre-Treatment	C15orf39	56905	37	15	75500784	75500784	Missense_Mutation	SNP	C	T	7	11	c.2395C>T	c.(2395-2397)CCC>TCC	p.P799S
Pat_15	Pre-Treatment	ACSBG1	23205	37	15	78466162	78466162	Missense_Mutation	SNP	G	T	33	19	c.1862C>A	c.(1861-1863)ACC>AAC	p.T621N
Pat_15	Pre-Treatment	SLCO3A1	28232	37	15	92397255	92397255	Missense_Mutation	SNP	C	G	2	24	c.117C>G	c.(115-117)ATC>ATG	p.I39M
Pat_15	Pre-Treatment	BTBD12	84464	37	16	3640521	3640521	Missense_Mutation	SNP	G	A	37	41	c.3118C>T	c.(3118-3120)CCC>TCC	p.P1040S
Pat_15	Pre-Treatment	MGRN1	23295	37	16	4731705	4731705	Missense_Mutation	SNP	C	T	26	36	c.1286C>T	c.(1285-1287)CCC>CTC	p.P429L
Pat_15	Pre-Treatment	COG7	91949	37	16	23409399	23409399	Missense_Mutation	SNP	A	C	21	41	c.1855T>G	c.(1855-1857)TTT>GTT	p.F619V
Pat_15	Pre-Treatment	HS3ST4	9951	37	16	26147561	26147561	Missense_Mutation	SNP	G	A	7	12	c.1363G>A	c.(1363-1365)GAT>AAT	p.D455N
Pat_15	Pre-Treatment	NOD2	64127	37	16	50733452	50733452	Missense_Mutation	SNP	G	A	88	97	c.127G>A	c.(127-129)GAG>AAG	p.E43K
Pat_15	Pre-Treatment	CES7	221223	37	16	55907781	55907781	Nonsense_Mutation	SNP	C	T	20	20	c.242G>A	c.(241-243)TGG>TAG	p.W81*
Pat_15	Pre-Treatment	TXNL4B	54957	37	16	72120568	72120568	Missense_Mutation	SNP	G	A	29	40	c.418C>T	c.(418-420)CCC>TCC	p.P140S
Pat_15	Pre-Treatment	CLEC18B	497190	37	16	74447009	74447009	Missense_Mutation	SNP	C	T	23	38	c.602G>A	c.(601-603)GGT>GAT	p.G201D
Pat_15	Pre-Treatment	TRAPPC2L	51693	37	16	88925060	88925060	Missense_Mutation	SNP	G	A	122	137	c.67G>A	c.(67-69)GAG>AAG	p.E23K
Pat_15	Pre-Treatment	ANKRD11	29123	37	16	89351925	89351925	Missense_Mutation	SNP	G	A	40	46	c.1025C>T	c.(1024-1026)CCC>CTC	p.P342L
Pat_15	Pre-Treatment	OR3A2	4995	37	17	3181572	3181572	Missense_Mutation	SNP	A	T	17	0	c.658T>A	c.(658-660)TTG>ATG	p.L220M
Pat_15	Pre-Treatment	TP53	7157	37	17	7574003	7574003	Nonsense_Mutation	SNP	G	A	28	0	c.1024C>T	c.(1024-1026)CGA>TGA	p.R342*
Pat_15	Pre-Treatment	NCOR1	9611	37	17	15938172	15938172	Missense_Mutation	SNP	C	T	32	1	c.7042G>A	c.(7042-7044)GAA>AAA	p.E2348K

Pat_15	Pre-Treatment	SLFN13	146857	37	17	33768288	33768288	Missense_Mutation	SNP	G	A	52	37	c.2020C>T	c.(2020-2022)CGT>TGT	p.R674C
Pat_15	Pre-Treatment	GAS2L2	246176	37	17	34072788	34072788	Nonsense_Mutation	SNP	C	T	30	12	c.1728G>A	c.(1726-1728)TGG>TGA	p.W576*
Pat_15	Pre-Treatment	KRT222	125113	37	17	38816377	38816378	Missense_Mutation	DNP	CC	TG	32	26	c.307_308GG>CA	c.(307-309)GGA>CAA	p.G103Q
Pat_15	Pre-Treatment	TTLL6	284076	37	17	46846574	46846574	Missense_Mutation	SNP	C	T	24	61	c.2453G>A	c.(2452-2454)AGC>AAC	p.S818N
Pat_15	Pre-Treatment	B4GALNT2	124872	37	17	47210448	47210448	Missense_Mutation	SNP	G	A	8	9	c.61G>A	c.(61-63)GAA>AAA	p.E21K
Pat_15	Pre-Treatment	ANKFN1	162282	37	17	54520276	54520276	Missense_Mutation	SNP	G	A	38	14	c.1090G>A	c.(1090-1092)GCA>ACA	p.A364T
Pat_15	Pre-Treatment	KCNH6	81033	37	17	61621705	61621705	Missense_Mutation	SNP	G	A	9	22	c.2437G>A	c.(2437-2439)GAA>AAA	p.E813K
Pat_15	Pre-Treatment	SCN4A	6329	37	17	62018276	62018276	Missense_Mutation	SNP	G	A	8	13	c.5366C>T	c.(5365-5367)TCG>TTG	p.S1789L
Pat_15	Pre-Treatment	KCNJ16	3773	37	17	68128770	68128770	Missense_Mutation	SNP	C	T	11	48	c.542C>T	c.(541-543)ACC>ATC	p.T181I
Pat_15	Pre-Treatment	CD300C	10871	37	17	72540900	72540900	Missense_Mutation	SNP	G	A	17	69	c.248C>T	c.(247-249)TCC>TTC	p.S83F
Pat_15	Pre-Treatment	MGAT5B	146664	37	17	74936524	74936524	Missense_Mutation	SNP	C	T	32	66	c.1652C>T	c.(1651-1653)CCC>CTC	p.P551L
Pat_15	Pre-Treatment	NPTX1	4884	37	17	78444806	78444806	Missense_Mutation	SNP	G	A	9	33	c.1106C>T	c.(1105-1107)ACC>ATC	p.T369I
Pat_15	Pre-Treatment	DSC1	1823	37	18	28720185	28720185	Missense_Mutation	SNP	C	G	32	33	c.1340G>C	c.(1339-1341)AGC>ACC	p.S447T
Pat_15	Pre-Treatment	DSG1	1828	37	18	28934588	28934588	Missense_Mutation	SNP	C	T	68	59	c.2429C>T	c.(2428-2430)TCT>TTT	p.S810F
Pat_15	Pre-Treatment	RNF165	494470	37	18	44036562	44036562	Missense_Mutation	SNP	G	A	40	53	c.1004G>A	c.(1003-1005)CGA>CAA	p.R335Q
Pat_15	Pre-Treatment	SERPINB11	89778	37	18	61377533	61377533	Missense_Mutation	SNP	C	T	10	13	c.106C>T	c.(106-108)CTT>TTT	p.L36F
Pat_15	Pre-Treatment	MIER2	54531	37	19	334444	334444	Missense_Mutation	SNP	G	A	31	54	c.199C>T	c.(199-201)CCA>TCA	p.P67S
Pat_15	Pre-Treatment	MADCAM1	8174	37	19	501699	501699	Missense_Mutation	SNP	C	T	31	18	c.698C>T	c.(697-699)CCC>CTC	p.P233L
Pat_15	Pre-Treatment	C3	718	37	19	6686166	6686166	Missense_Mutation	SNP	C	T	42	87	c.3779G>A	c.(3778-3780)AGA>AAA	p.R1260K
Pat_15	Pre-Treatment	VAV1	7409	37	19	6828459	6828459	Missense_Mutation	SNP	G	A	24	16	c.1053G>A	c.(1051-1053)ATG>ATA	p.M351I
Pat_15	Pre-Treatment	FBN3	84467	37	19	8155007	8155007	Missense_Mutation	SNP	C	T	11	11	c.6160G>A	c.(6160-6162)GAA>AAA	p.E2054K
Pat_15	Pre-Treatment	MUC16	94025	37	19	9068553	9068553	Missense_Mutation	SNP	G	A	16	85	c.18893C>T	c.(18892-18894)TCT>TTT	p.S6298F
Pat_15	Pre-Treatment	MUC16	94025	37	19	9085237	9085237	Missense_Mutation	SNP	G	A	9	8	c.6578C>T	c.(6577-6579)TCC>TTC	p.S2193F
Pat_15	Pre-Treatment	MUC16	94025	37	19	9089503	9089503	Missense_Mutation	SNP	G	A	51	26	c.2312C>T	c.(2311-2313)TCC>TTC	p.S771F
Pat_15	Pre-Treatment	ZNF560	147741	37	19	9578116	9578116	Missense_Mutation	SNP	G	A	6	18	c.1507C>T	c.(1507-1509)CTT>TTT	p.L503F
Pat_15	Pre-Treatment	ZNF302	55900	37	19	35175919	35175919	Missense_Mutation	SNP	C	T	7	12	c.1109C>T	c.(1108-1110)TCG>TTG	p.S370L
Pat_15	Pre-Treatment	LIG1	3978	37	19	48660312	48660312	Missense_Mutation	SNP	G	A	34	102	c.329C>T	c.(328-330)CCC>CTC	p.P110L
Pat_15	Pre-Treatment	MYH14	79784	37	19	50789874	50789874	Missense_Mutation	SNP	G	A	4	2	c.4552G>A	c.(4552-4554)GAG>AAG	p.E1518K
Pat_15	Pre-Treatment	KLK5	25818	37	19	51453324	51453324	Missense_Mutation	SNP	G	A	13	10	c.122C>T	c.(121-123)ACC>ATC	p.T41I
Pat_15	Pre-Treatment	ZNF761	388561	37	19	53959722	53959722	Missense_Mutation	SNP	G	A	10	41	c.1961G>A	c.(1960-1962)AGA>AAA	p.R654K
Pat_15	Pre-Treatment	ZNF470	388566	37	19	57089054	57089054	Missense_Mutation	SNP	T	A	20	15	c.1257T>A	c.(1255-1257)CAT>CAA	p.H419Q
Pat_15	Pre-Treatment	PEG3	5178	37	19	57335821	57335821	Missense_Mutation	SNP	C	T	36	24	c.203G>A	c.(202-204)CGA>CAA	p.R68Q
Pat_15	Pre-Treatment	ZNF749	388567	37	19	57956341	57956341	Nonsense_Mutation	SNP	G	T	11	27	c.1825G>T	c.(1825-1827)GAA>TAA	p.E609*
Pat_15	Pre-Treatment	ZNF549	256051	37	19	58050291	58050291	Missense_Mutation	SNP	C	T	18	34	c.1919C>T	c.(1918-1920)CCC>CTC	p.P640L
Pat_15	Pre-Treatment	MSGN1	343930	37	2	17998224	17998224	Missense_Mutation	SNP	C	T	16	314	c.439C>T	c.(439-441)CTC>TTC	p.L147F
Pat_15	Pre-Treatment	TMEM17	200728	37	2	62728427	62728427	Missense_Mutation	SNP	G	A	41	25	c.514C>T	c.(514-516)CGT>TGT	p.R172C
Pat_15	Pre-Treatment	LOXL3	84695	37	2	74761292	74761292	Missense_Mutation	SNP	G	A	3	53	c.2011C>T	c.(2011-2013)CGG>TGG	p.R671W
Pat_15	Pre-Treatment	IL1A	3552	37	2	113539322	113539322	Missense_Mutation	SNP	A	T	34	21	c.178T>A	c.(178-180)TCT>ACT	p.S60T
Pat_15	Pre-Treatment	THSD7B	80731	37	2	137814051	137814051	Nonsense_Mutation	SNP	G	A	15	34	c.108G>A	c.(106-108)TGG>TGA	p.W36*
Pat_15	Pre-Treatment	SCN1A	6323	37	2	166872167	166872167	Missense_Mutation	SNP	G	A	19	38	c.3467C>T	c.(3466-3468)CCC>CTC	p.P1156L
Pat_15	Pre-Treatment	LRP2	4036	37	2	170092425	170092425	Missense_Mutation	SNP	C	T	35	15	c.4845G>A	c.(4843-4845)ATG>ATA	p.M1615I
Pat_15	Pre-Treatment	SP3	6670	37	2	174819867	174819867	Missense_Mutation	SNP	G	A	19	20	c.1373C>T	c.(1372-1374)TCT>TTT	p.S458F
Pat_15	Pre-Treatment	OSBPL6	114880	37	2	179236922	179236922	Nonsense_Mutation	SNP	C	T	24	18	c.1357C>T	c.(1357-1359)CAG>TAG	p.Q453*
Pat_15	Pre-Treatment	TTN	7273	37	2	179472244	179472244	Missense_Mutation	SNP	C	T	60	146	c.45467G>A	c.(45466-45468)GGA>GA	p.G15156E
Pat_15	Pre-Treatment	TTN	7273	37	2	179611961	179611961	Missense_Mutation	SNP	C	T	4	21	c.15166G>A	c.(15166-15168)GGG>AG	p.G5056R
Pat_15	Pre-Treatment	DNAH7	56171	37	2	196834754	196834754	Missense_Mutation	SNP	G	A	17	18	c.2123C>T	c.(2122-2124)TCA>TTA	p.S708L
Pat_15	Pre-Treatment	ORC2L	4999	37	2	201785036	201785036	Missense_Mutation	SNP	A	C	18	11	c.1375T>G	c.(1375-1377)TCC>GCC	p.S459A

Pat_15	Pre-Treatment	PARD3B	117583	37	2	206165386	206165386	Missense_Mutation	SNP	G	A	15	49	c.2318G>A	c.(2317-2319)CGA>CAA	p.R773Q
Pat_15	Pre-Treatment	ABCB6	10058	37	2	220078321	220078322	Missense_Mutation	DNP	GT	AG	20	14	.1645_1646AC>C	c.(1645-1647)ACC>CTC	p.T549L
Pat_15	Pre-Treatment	UGT1A8	54576	37	2	234527050	234527050	Missense_Mutation	SNP	G	A	62	186	c.697G>A	c.(697-699)GAA>AAA	p.E233K
Pat_15	Pre-Treatment	ANGPT4	51378	37	20	896818	896818	Missense_Mutation	SNP	G	A	17	42	c.40C>T	c.(40-42)CTT>TTT	p.L14F
Pat_15	Pre-Treatment	PROKR2	128674	37	20	5294778	5294778	Missense_Mutation	SNP	G	A	44	33	c.238C>T	c.(238-240)CGC>TGC	p.R80C
Pat_15	Pre-Treatment	ISM1	140862	37	20	13273020	13273020	Splice_Site	SNP	G	A	8	10	c.788_splice	c.e5-1	p.G263_splice
Pat_15	Pre-Treatment	SEL1L2	80343	37	20	13867031	13867031	Missense_Mutation	SNP	T	A	14	29	c.803A>T	c.(802-804)GAA>GTA	p.E268V
Pat_15	Pre-Treatment	DEFB123	245936	37	20	30037844	30037844	Missense_Mutation	SNP	G	A	61	70	c.71G>A	c.(70-72)AGA>AAA	p.R24K
Pat_15	Pre-Treatment	EPB41L1	2036	37	20	34785884	34785884	Missense_Mutation	SNP	G	A	44	47	c.1589G>A	c.(1588-1590)CGA>CAA	p.R530Q
Pat_15	Pre-Treatment	SGK2	10110	37	20	42195107	42195107	Missense_Mutation	SNP	C	T	58	75	c.152C>T	c.(151-153)CCC>CTC	p.P51L
Pat_15	Pre-Treatment	NCAM2	4685	37	21	22664426	22664426	Missense_Mutation	SNP	C	T	19	21	c.484C>T	c.(484-486)CGG>TGG	p.R162W
Pat_15	Pre-Treatment	RCAN1	1827	37	21	35893880	35893880	Missense_Mutation	SNP	G	A	12	10	c.503C>T	c.(502-504)CCG>CTG	p.P168L
Pat_15	Pre-Treatment	CLDN14	23562	37	21	37833465	37833465	Missense_Mutation	SNP	C	T	23	30	c.529G>A	c.(529-531)GGT>AGT	p.G177S
Pat_15	Pre-Treatment	TMPRSS3	64699	37	21	43795974	43795974	Missense_Mutation	SNP	C	T	25	103	c.1198G>A	c.(1198-1200)GAC>AAC	p.D400N
Pat_15	Pre-Treatment	SEZ6L	23544	37	22	26761419	26761419	Missense_Mutation	SNP	G	A	14	17	c.2681G>A	c.(2680-2682)GGA>GAA	p.G894E
Pat_15	Pre-Treatment	TRIOBP	11078	37	22	38121864	38121864	Missense_Mutation	SNP	C	T	142	64	c.3301C>T	c.(3301-3303)CCC>TCC	p.P1101S
Pat_15	Pre-Treatment	MGAT3	4248	37	22	39884748	39884748	Missense_Mutation	SNP	G	A	9	17	c.1396G>A	c.(1396-1398)GAC>AAC	p.D466N
Pat_15	Pre-Treatment	MOV10L1	54456	37	22	50563983	50563983	Missense_Mutation	SNP	C	T	22	15	c.1732C>T	c.(1732-1734)CCT>TCT	p.P578S
Pat_15	Pre-Treatment	EOMES	8320	37	3	27761764	27761764	Missense_Mutation	SNP	G	A	62	108	c.934C>T	c.(934-936)CAC>TAC	p.H312Y
Pat_15	Pre-Treatment	SCN5A	6331	37	3	38651383	38651383	Missense_Mutation	SNP	A	G	20	41	c.776T>C	c.(775-777)TTC>TCC	p.F259S
Pat_15	Pre-Treatment	SCN10A	6336	37	3	38833541	38833541	Missense_Mutation	SNP	G	A	51	119	c.389C>T	c.(388-390)TCG>TTG	p.S130L
Pat_15	Pre-Treatment	SCN11A	11280	37	3	38938485	38938485	Missense_Mutation	SNP	C	T	27	22	c.2254G>A	c.(2254-2256)GGG>AGG	p.G752R
Pat_15	Pre-Treatment	NAT6	24142	37	3	50334112	50334113	Missense_Mutation	DNP	GG	AA	29	23	c.782_783CC>TT	c.(781-783)CCC>CTT	p.P261L
Pat_15	Pre-Treatment	DNAH1	25981	37	3	52396446	52396446	Missense_Mutation	SNP	C	T	18	14	c.5023C>T	c.(5023-5025)CCA>TCA	p.P1675S
Pat_15	Pre-Treatment	NSUN3	63899	37	3	93813923	93813923	Missense_Mutation	SNP	C	T	19	85	c.668C>T	c.(667-669)TCT>TTT	p.S223F
Pat_15	Pre-Treatment	OR5H15	403274	37	3	97888187	97888187	Missense_Mutation	SNP	T	C	5	2	c.644T>C	c.(643-645)CTT>CCT	p.L215P
Pat_15	Pre-Treatment	OR5K1	26339	37	3	98189268	98189268	Missense_Mutation	SNP	C	T	9	15	c.848C>T	c.(847-849)CCC>CTC	p.P283L
Pat_15	Pre-Treatment	ZBED2	79413	37	3	111312555	111312555	Missense_Mutation	SNP	C	T	66	66	c.494G>A	c.(493-495)AGG>AAG	p.R165K
Pat_15	Pre-Treatment	KIAA2018	205717	37	3	113388981	113388981	Missense_Mutation	SNP	G	A	28	29	c.146C>T	c.(145-147)CCT>CTT	p.P49L
Pat_15	Pre-Treatment	PARP14	54625	37	3	122411238	122411238	Missense_Mutation	SNP	C	T	20	11	c.446C>T	c.(445-447)TCT>TTT	p.S149F
Pat_15	Pre-Treatment	COL6A6	131873	37	3	130287019	130287019	Missense_Mutation	SNP	C	T	68	126	c.1972C>T	c.(1972-1974)CGG>TGG	p.R658W
Pat_15	Pre-Treatment	TMEM108	66000	37	3	133099154	133099154	Missense_Mutation	SNP	G	A	29	42	c.599G>A	c.(598-600)CGA>CAA	p.R200Q
Pat_15	Pre-Treatment	PRR23A	729627	37	3	138724642	138724642	Missense_Mutation	SNP	C	T	12	19	c.469G>A	c.(469-471)GAG>AAG	p.E157K
Pat_15	Pre-Treatment	GK5	256356	37	3	141905075	141905075	Missense_Mutation	SNP	G	A	55	30	c.716C>T	c.(715-717)TCG>TTG	p.S239L
Pat_15	Pre-Treatment	CP	1356	37	3	148930484	148930484	Missense_Mutation	SNP	C	T	9	9	c.148G>A	c.(148-150)GAA>AAA	p.E50K
Pat_15	Pre-Treatment	ZBBX	79740	37	3	167045887	167045887	Missense_Mutation	SNP	C	T	40	41	c.705G>A	c.(703-705)ATG>ATA	p.M235I
Pat_15	Pre-Treatment	MECOM	2122	37	3	168833285	168833285	Missense_Mutation	SNP	C	T	5	32	c.1811G>A	c.(1810-1812)CGA>CAA	p.R604Q
Pat_15	Pre-Treatment	TP63	8626	37	3	189608604	189608604	Missense_Mutation	SNP	C	T	55	47	c.1679C>T	c.(1678-1680)TCA>TTA	p.S560L
Pat_15	Pre-Treatment	DLG1	1739	37	3	197009603	197009603	Missense_Mutation	SNP	T	G	4	145	c.265A>C	c.(265-267)AGC>CGC	p.S89R
Pat_15	Pre-Treatment	SLC2A9	56606	37	4	10027572	10027572	Missense_Mutation	SNP	C	T	17	19	c.19G>A	c.(19-21)GAC>AAC	p.D7N
Pat_15	Pre-Treatment	ZNF518B	85460	37	4	10445035	10445035	Missense_Mutation	SNP	A	G	14	23	c.2918T>C	c.(2917-2919)GTT>GCT	p.V973A
Pat_15	Pre-Treatment	FAM114A1	92689	37	4	38937371	38937371	Missense_Mutation	SNP	C	T	19	9	c.1496C>T	c.(1495-1497)TCT>TTT	p.S499F
Pat_15	Pre-Treatment	YIPF7	285525	37	4	44624506	44624506	Missense_Mutation	SNP	C	T	6	6	c.768G>A	c.(766-768)ATG>ATA	p.M256I
Pat_15	Pre-Treatment	SPATA18	132671	37	4	52945993	52945994	Missense_Mutation	DNP	GG	AA	66	38	.1263_1264GG>A	261-1266)CAGGAG>CAA	p.E422K
Pat_15	Pre-Treatment	CCDC158	339965	37	4	77288596	77288596	Missense_Mutation	SNP	C	T	39	18	c.1681G>A	c.(1681-1683)GAC>AAC	p.D561N
Pat_15	Pre-Treatment	LEF1	51176	37	4	108985500	108985500	Missense_Mutation	SNP	G	A	28	19	c.1157C>T	c.(1156-1158)TCT>TTT	p.S386F
Pat_15	Pre-Treatment	ANK2	287	37	4	114279594	114279594	Missense_Mutation	SNP	C	T	36	40	c.9820C>T	c.(9820-9822)CCC>TCC	p.P3274S

Pat_15	Pre-Treatment	SYNPO2	171024	37	4	119947945	119947945	Missense_Mutation	SNP	C	T	28	9	c.421C>T	c.(421-423)CCC>TCC	p.P141S
Pat_15	Pre-Treatment	WDR17	116966	37	4	177046428	177046428	Missense_Mutation	SNP	T	C	25	43	c.784T>C	c.(784-786)TTT>CTT	p.F262L
Pat_15	Pre-Treatment	FAM173B	134145	37	5	10239375	10239376	Missense_Mutation	DNP	CC	TT	29	65	c.109_110GG>AA	c.(109-111)GGG>AAG	p.G37K
Pat_15	Pre-Treatment	DNAH5	1767	37	5	13901435	13901435	Missense_Mutation	SNP	T	G	11	16	c.1978A>C	c.(1978-1980)ATT>CTT	p.I660L
Pat_15	Pre-Treatment	TTC33	23548	37	5	40730441	40730441	Missense_Mutation	SNP	G	A	46	53	c.226C>T	c.(226-228)CGG>TGG	p.R76W
Pat_15	Pre-Treatment	HCN1	348980	37	5	45303881	45303881	Missense_Mutation	SNP	C	T	62	58	c.1438G>A	c.(1438-1440)GAT>AAT	p.D480N
Pat_15	Pre-Treatment	MARVELD2	153562	37	5	68728909	68728909	Missense_Mutation	SNP	G	A	80	92	c.1492G>A	c.(1492-1494)GAA>AAA	p.E498K
Pat_15	Pre-Treatment	BDP1	55814	37	5	70838063	70838063	Missense_Mutation	SNP	C	T	21	32	c.6383C>T	c.(6382-6384)ACC>ATC	p.T2128I
Pat_15	Pre-Treatment	CMYA5	202333	37	5	79025094	79025094	Missense_Mutation	SNP	C	T	6	4	c.506C>T	c.(505-507)CCT>CTT	p.P169L
Pat_15	Pre-Treatment	GPR98	84059	37	5	90086870	90086870	Missense_Mutation	SNP	G	A	11	9	c.14224G>A	c.(14224-14226)GAA>AAA	p.E4742K
Pat_15	Pre-Treatment	NRG2	9542	37	5	139232080	139232080	Missense_Mutation	SNP	G	A	47	45	c.1481C>T	c.(1480-1482)TCT>TTT	p.S494F
Pat_15	Pre-Treatment	PCDHB2	56133	37	5	140474559	140474559	Missense_Mutation	SNP	C	T	23	20	c.185C>T	c.(184-186)GCT>GTT	p.A62V
Pat_15	Pre-Treatment	PCDHB8	56128	37	5	140559872	140559872	Missense_Mutation	SNP	G	A	41	56	c.2257G>A	c.(2257-2259)GAG>AAG	p.E753K
Pat_15	Pre-Treatment	PCDHGB5	56101	37	5	140779112	140779112	Missense_Mutation	SNP	C	T	12	8	c.1418C>T	c.(1417-1419)TCG>TTG	p.S473L
Pat_15	Pre-Treatment	C5orf40	408263	37	5	156770294	156770294	Missense_Mutation	SNP	G	A	27	45	c.251C>T	c.(250-252)CCT>CTT	p.P84L
Pat_15	Pre-Treatment	TMED9	54732	37	5	177020742	177020742	Missense_Mutation	SNP	C	T	83	120	c.377C>T	c.(376-378)TCC>TTC	p.S126F
Pat_15	Pre-Treatment	NEDD9	4739	37	6	11185787	11185787	Missense_Mutation	SNP	G	A	51	56	c.2113C>T	c.(2113-2115)CGG>TGG	p.R705W
Pat_15	Pre-Treatment	C6orf105	84830	37	6	11766609	11766609	Splice_Site	SNP	C	T	30	20	c.289_splice	c.e3-1	p.F97_splice
Pat_15	Pre-Treatment	HIVEP1	3096	37	6	12122375	12122375	Missense_Mutation	SNP	C	T	14	16	c.2347C>T	c.(2347-2349)CCC>TCC	p.P783S
Pat_15	Pre-Treatment	ZNF193	7746	37	6	28200708	28200708	Missense_Mutation	SNP	A	C	3	43	c.937A>C	c.(937-939)AAG>CAG	p.K313Q
Pat_15	Pre-Treatment	OR12D3	81797	37	6	29343062	29343062	Missense_Mutation	SNP	C	T	7	1	c.3G>A	c.(1-3)ATG>ATA	p.M1I
Pat_15	Pre-Treatment	OR2H1	26716	37	6	29430333	29430333	Missense_Mutation	SNP	C	T	19	47	c.787C>T	c.(787-789)CCG>TCG	p.P263S
Pat_15	Pre-Treatment	UBD	10537	37	6	29524095	29524095	Missense_Mutation	SNP	C	T	20	9	c.60G>A	c.(58-60)ATG>ATA	p.M20I
Pat_15	Pre-Treatment	DNAH8	1769	37	6	38750805	38750805	Missense_Mutation	SNP	C	T	30	11	c.1634C>T	c.(1633-1635)CCG>CTG	p.P545L
Pat_15	Pre-Treatment	TTBK1	84630	37	6	43251530	43251530	Missense_Mutation	SNP	C	T	11	30	c.3052C>T	c.(3052-3054)CCG>TCG	p.P1018S
Pat_15	Pre-Treatment	GPR116	221395	37	6	46834662	46834662	Missense_Mutation	SNP	C	T	14	15	c.1834G>A	c.(1834-1836)GCA>ACA	p.A612T
Pat_15	Pre-Treatment	BMP5	653	37	6	55659083	55659083	Missense_Mutation	SNP	C	T	11	21	c.826G>A	c.(826-828)GGG>AGG	p.G276R
Pat_15	Pre-Treatment	MDN1	23195	37	6	90400405	90400406	Missense_Mutation	DNP	GG	AA	25	14	10735_10736CC>	c.(10735-10737)CCC>TTC	p.P3579F
Pat_15	Pre-Treatment	BACH2	60468	37	6	90642342	90642342	Missense_Mutation	SNP	C	T	15	5	c.2311G>A	c.(2311-2313)GAG>AAG	p.E771K
Pat_15	Pre-Treatment	EPHA7	2045	37	6	94066675	94066675	Missense_Mutation	SNP	C	T	24	55	c.1084G>A	c.(1084-1086)GAT>AAT	p.D362N
Pat_15	Pre-Treatment	RFX6	222546	37	6	117248274	117248274	Missense_Mutation	SNP	A	C	25	58	c.1970A>C	c.(1969-1971)AAC>ACC	p.N657T
Pat_15	Pre-Treatment	KIAA1244	57221	37	6	138584659	138584659	Missense_Mutation	SNP	T	G	14	22	c.2039T>G	c.(2038-2040)CTG>CGG	p.L680R
Pat_15	Pre-Treatment	HECA	51696	37	6	139488098	139488098	Missense_Mutation	SNP	T	A	13	53	c.949T>A	c.(949-951)TTC>ATC	p.F317I
Pat_15	Pre-Treatment	HIVEP2	3097	37	6	143081427	143081427	Missense_Mutation	SNP	T	C	4	199	c.5998A>G	c.(5998-6000)AGG>GGG	p.R2000G
Pat_15	Pre-Treatment	TIAM2	26230	37	6	155504535	155504535	Missense_Mutation	SNP	G	A	32	45	c.2965G>A	c.(2965-2967)GAC>AAC	p.D989N
Pat_15	Pre-Treatment	SLC22A3	6581	37	6	160831795	160831795	Missense_Mutation	SNP	C	T	17	35	c.892C>T	c.(892-894)CGG>TGG	p.R298W
Pat_15	Pre-Treatment	STK31	56164	37	7	23809328	23809328	Missense_Mutation	SNP	G	A	48	49	c.1666G>A	c.(1666-1668)GAG>AAG	p.E556K
Pat_15	Pre-Treatment	ADCYAP1R1	117	37	7	31117659	31117659	Missense_Mutation	SNP	G	A	38	56	c.211G>A	c.(211-213)GAG>AAG	p.E71K
Pat_15	Pre-Treatment	TXNDC3	51314	37	7	37924797	37924797	Nonsense_Mutation	SNP	G	A	11	13	c.1190G>A	c.(1189-1191)TGG>TAG	p.W397*
Pat_15	Pre-Treatment	ZNF479	90827	37	7	57187720	57187720	Missense_Mutation	SNP	C	T	29	30	c.1402G>A	c.(1402-1404)GAA>AAA	p.E468K
Pat_15	Pre-Treatment	MAGI2	9863	37	7	77973134	77973134	Missense_Mutation	SNP	G	A	25	35	c.1369C>T	c.(1369-1371)CCG>TCG	p.P457S
Pat_15	Pre-Treatment	ABCB4	5244	37	7	87083905	87083905	Missense_Mutation	SNP	T	G	4	11	c.290A>C	c.(289-291)AAC>ACC	p.N97T
Pat_15	Pre-Treatment	ZNF804B	219578	37	7	88963666	88963666	Nonsense_Mutation	SNP	G	A	27	31	c.1370G>A	c.(1369-1371)TGG>TAG	p.W457*
Pat_15	Pre-Treatment	ZNF804B	219578	37	7	88964142	88964142	Missense_Mutation	SNP	G	C	6	9	c.1846G>C	c.(1846-1848)GCA>CCA	p.A616P
Pat_15	Pre-Treatment	TRRAP	8295	37	7	98602945	98602945	Missense_Mutation	SNP	C	T	34	42	c.10685C>T	c.(10684-10686)ACC>ATC	p.T3562I
Pat_15	Pre-Treatment	RELN	5649	37	7	103155634	103155634	Missense_Mutation	SNP	G	A	14	30	c.8117C>T	c.(8116-8118)TCA>TTA	p.S2706L
Pat_15	Pre-Treatment	WNT2	7472	37	7	116955394	116955394	Missense_Mutation	SNP	C	T	6	11	c.319G>A	c.(319-321)GAA>AAA	p.E107K

Pat_15	Pre-Treatment	BRAF	673	37	7	140453136	140453136	Missense_Mutation	SNP	A	T	31	41	c.1799T>A	c.(1798-1800)GTG>GAG	p.V600E
Pat_15	Pre-Treatment	FAM115C	285966	37	7	143421630	143421630	Missense_Mutation	SNP	G	T	3	4	c.2345G>T	c.(2344-2346)TGG>TTG	p.W782L
Pat_15	Pre-Treatment	OR2F2	135948	37	7	143632858	143632858	Missense_Mutation	SNP	C	T	36	36	c.533C>T	c.(532-534)TCC>TTC	p.S178F
Pat_15	Pre-Treatment	CNTNAP2	26047	37	7	146805370	146805370	Missense_Mutation	SNP	G	A	19	17	c.682G>A	c.(682-684)GGA>AGA	p.G228R
Pat_15	Pre-Treatment	GIMAP8	155038	37	7	150171171	150171171	Missense_Mutation	SNP	C	T	59	47	c.754C>T	c.(754-756)CTT>TTT	p.L252F
Pat_15	Pre-Treatment	NOS3	4846	37	7	150698472	150698472	Missense_Mutation	SNP	G	A	36	33	c.1387G>A	c.(1387-1389)GAG>AAG	p.E463K
Pat_15	Pre-Treatment	PAXIP1	22976	37	7	154774994	154774994	Missense_Mutation	SNP	C	A	12	22	c.373G>T	c.(373-375)GGG>TGG	p.G125W
Pat_15	Pre-Treatment	SPAG11B	10407	37	8	7320378	7320378	Missense_Mutation	SNP	G	A	27	41	c.65C>T	c.(64-66)TCG>TTG	p.S22L
Pat_15	Pre-Treatment	STC1	6781	37	8	23708930	23708930	Missense_Mutation	SNP	C	T	69	47	c.376G>A	c.(376-378)GAA>AAA	p.E126K
Pat_15	Pre-Treatment	ADAMDEC1	27299	37	8	24251634	24251634	Missense_Mutation	SNP	G	A	7	18	c.337G>A	c.(337-339)GAA>AAA	p.E113K
Pat_15	Pre-Treatment	ADAM18	8749	37	8	39537690	39537690	Missense_Mutation	SNP	C	T	5	10	c.1766C>T	c.(1765-1767)TCA>TTA	p.S589L
Pat_15	Pre-Treatment	DCAF4L2	138009	37	8	88886025	88886025	Missense_Mutation	SNP	C	T	37	20	c.175G>A	c.(175-177)GTC>ATC	p.V59I
Pat_15	Pre-Treatment	HRSP12	10247	37	8	99116755	99116755	Missense_Mutation	SNP	G	A	39	26	c.313C>T	c.(313-315)CCT>TCT	p.P105S
Pat_15	Pre-Treatment	GRHL2	79977	37	8	102643916	102643916	Missense_Mutation	SNP	G	A	7	9	c.1309G>A	c.(1309-1311)GGG>AGG	p.G437R
Pat_15	Pre-Treatment	FAM135B	51059	37	8	139163688	139163688	Missense_Mutation	SNP	C	T	6	18	c.3030G>A	c.(3028-3030)ATG>ATA	p.M1010I
Pat_15	Pre-Treatment	APBA1	320	37	9	72131644	72131644	Missense_Mutation	SNP	C	T	5	12	c.483G>A	c.(481-483)ATG>ATA	p.M161I
Pat_15	Pre-Treatment	PCSK5	5125	37	9	78601135	78601136	Missense_Mutation	DNP	CC	TT	36	35	c.385_386CC>TT	c.(385-387)CCC>TTC	p.P129F
Pat_15	Pre-Treatment	OR1L4	254973	37	9	125487162	125487162	Missense_Mutation	SNP	G	A	5	19	c.894G>A	c.(892-894)ATG>ATA	p.M298I
Pat_15	Pre-Treatment	IER5L	389792	37	9	131939665	131939665	Missense_Mutation	SNP	G	A	3	3	c.667C>T	c.(667-669)CCG>TCG	p.P223S
Pat_15	Pre-Treatment	LAMC3	10319	37	9	133907487	133907487	Missense_Mutation	SNP	G	A	46	95	c.734G>A	c.(733-735)GGG>GAG	p.G245E
Pat_15	Pre-Treatment	IL3RA	3563	37	X	1497566	1497566	Missense_Mutation	SNP	G	A	6	27	c.889G>A	c.(889-891)GAG>AAG	p.E297K
Pat_15	Pre-Treatment	MXRA5	25878	37	X	3240542	3240542	Missense_Mutation	SNP	C	T	78	23	c.3184G>A	c.(3184-3186)GAG>AAG	p.E1062K
Pat_15	Pre-Treatment	FAM9B	171483	37	X	8995964	8995964	Missense_Mutation	SNP	C	T	16	51	c.437G>A	c.(436-438)AGT>AAT	p.S146N
Pat_15	Pre-Treatment	MAGEB1	4112	37	X	30269273	30269273	Nonsense_Mutation	SNP	G	A	5	10	c.663G>A	c.(661-663)TGG>TGA	p.W221*
Pat_15	Pre-Treatment	SSX5	6758	37	X	48051681	48051681	Missense_Mutation	SNP	C	T	110	35	c.317G>A	c.(316-318)GGA>GAA	p.G106E
Pat_15	Pre-Treatment	TBC1D25	4943	37	X	48417570	48417570	Nonsense_Mutation	SNP	C	T	7	22	c.541C>T	c.(541-543)CAA>TAA	p.Q181*
Pat_15	Pre-Treatment	DGKK	139189	37	X	50121099	50121099	Missense_Mutation	SNP	G	A	39	22	c.3109C>T	c.(3109-3111)CGG>TGG	p.R1037W
Pat_15	Pre-Treatment	BMP15	9210	37	X	50659560	50659560	Missense_Mutation	SNP	T	C	63	35	c.1132T>C	c.(1132-1134)TAC>CAC	p.Y378H
Pat_15	Pre-Treatment	SPANXN5	494197	37	X	52826389	52826389	Splice_Site	SNP	G	A	51	28	c.1_splice	c.e1-1	p.M1_splice
Pat_15	Pre-Treatment	NHSL2	340527	37	X	71359877	71359877	Missense_Mutation	SNP	G	A	5	18	c.2479G>A	c.(2479-2481)GAC>AAC	p.D827N
Pat_15	Pre-Treatment	RPS6KA6	27330	37	X	83319404	83319404	Missense_Mutation	SNP	T	C	7	9	c.2119A>G	c.(2119-2121)ATG>GTG	p.M707V
Pat_15	Pre-Treatment	WDR44	54521	37	X	117566799	117566799	Missense_Mutation	SNP	G	A	33	113	c.1793G>A	c.(1792-1794)CGG>CAG	p.R598Q
Pat_15	Pre-Treatment	UTP14A	10813	37	X	129041393	129041393	Missense_Mutation	SNP	A	G	18	61	c.77A>G	c.(76-78)TAC>TGC	p.Y26C
Pat_15	Pre-Treatment	RBMX2	51634	37	X	129546533	129546533	Missense_Mutation	SNP	C	T	12	26	c.680C>T	c.(679-681)TCC>TTC	p.S227F
Pat_15	Pre-Treatment	GPC3	2719	37	X	132670264	132670265	Nonsense_Mutation	DNP	GG	TA	50	31	.1630_1631CC>T	c.(1630-1632)CCG>TAG	p.P544*
Pat_15	Pre-Treatment	BRS3	680	37	X	135572476	135572476	Missense_Mutation	SNP	C	T	4	10	c.619C>T	c.(619-621)CCT>TCT	p.P207S
Pat_15	Pre-Treatment	FGF13	2258	37	X	137715099	137715099	Missense_Mutation	SNP	C	T	13	34	c.650G>A	c.(649-651)CGA>CAA	p.R217Q
Pat_15	Pre-Treatment	MAGEA3	4102	37	X	151935794	151935794	Nonsense_Mutation	SNP	G	A	121	52	c.373C>T	c.(373-375)CGA>TGA	p.R125*
Pat_15	Pre-Treatment	SPRY3	10251	37	X	155004072	155004072	Missense_Mutation	SNP	G	A	21	77	c.539G>A	c.(538-540)AGC>AAC	p.S180N
Pat_15	Pre-Treatment	SPRY3	10251	37	X	155004080	155004080	Missense_Mutation	SNP	G	C	21	75	c.547G>C	c.(547-549)GAT>CAT	p.D183H
Pat_15	Post-Resistance	GABRD	2563	37	1	1956458	1956458	Missense_Mutation	SNP	C	T	4	218	c.146C>T	c.(145-147)GCC>GTC	p.A49V
Pat_15	Post-Resistance	PLEKHG5	57449	37	1	6528263	6528263	Missense_Mutation	SNP	G	A	37	90	c.2801C>T	c.(2800-2802)TCC>TTC	p.S934F
Pat_15	Post-Resistance	PRAMEF4	400735	37	1	12943025	12943025	Missense_Mutation	SNP	C	T	72	246	c.191G>A	c.(190-192)CGC>CAC	p.R64H
Pat_15	Post-Resistance	TMEM51	55092	37	1	15541590	15541590	Missense_Mutation	SNP	G	C	3	345	c.7G>C	c.(7-9)GCC>CCC	p.A3P
Pat_15	Post-Resistance	EPHA2	1969	37	1	16461548	16461548	Missense_Mutation	SNP	T	C	49	664	c.1565A>G	c.(1564-1566)CAC>CGC	p.H522R
Pat_15	Post-Resistance	ATP13A2	23400	37	1	17332247	17332247	Missense_Mutation	SNP	G	A	25	64	c.37C>T	c.(37-39)CCC>TCC	p.P13S
Pat_15	Post-Resistance	KLHDC7A	127707	37	1	18809751	18809751	Missense_Mutation	SNP	C	T	153	477	c.2276C>T	c.(2275-2277)ACC>ATC	p.T759I

Pat_15	Post-Resistance	UBR4	23352	37	1	19431583	19431583	Missense_Mutation	SNP	C	T	5	288	c.12604G>A	c.(12604-12606)GCT>ACT	p.A4202T
Pat_15	Post-Resistance	NBPF3	84224	37	1	21807432	21807432	Missense_Mutation	SNP	A	G	5	671	c.1391A>G	c.(1390-1392)AAG>AGG	p.K464R
Pat_15	Post-Resistance	EPHA8	2046	37	1	22927891	22927891	Missense_Mutation	SNP	G	A	5	418	c.2828G>A	c.(2827-2829)CGC>CAC	p.R943H
Pat_15	Post-Resistance	CATSPER4	378807	37	1	26524479	26524479	Missense_Mutation	SNP	G	A	6	609	c.589G>A	c.(589-591)GTG>ATG	p.V197M
Pat_15	Post-Resistance	SYTL1	84958	37	1	27673988	27673988	Nonsense_Mutation	SNP	C	T	74	262	c.268C>T	c.(268-270)CAG>TAG	p.Q90*
Pat_15	Post-Resistance	EIF3I	8668	37	1	32692039	32692039	Missense_Mutation	SNP	G	T	8	843	c.436G>T	c.(436-438)GAC>TAC	p.D146Y
Pat_15	Post-Resistance	EIF2C4	192670	37	1	36307229	36307229	Missense_Mutation	SNP	G	A	4	406	c.2053G>A	c.(2053-2055)GAA>AAA	p.E685K
Pat_15	Post-Resistance	CDC20	991	37	1	43824999	43824999	Missense_Mutation	SNP	C	T	4	239	c.113C>T	c.(112-114)CCG>CTG	p.P38L
Pat_15	Post-Resistance	TESK2	10420	37	1	45813599	45813599	Missense_Mutation	SNP	G	A	75	316	c.614C>T	c.(613-615)CCC>CTC	p.P205L
Pat_15	Post-Resistance	RAD54L	8438	37	1	46739343	46739343	Missense_Mutation	SNP	A	G	3	159	c.1534A>G	c.(1534-1536)AGC>GGC	p.S512G
Pat_15	Post-Resistance	SPATA6	54558	37	1	48861020	48861020	Missense_Mutation	SNP	G	A	5	190	c.787C>T	c.(787-789)CCC>TCC	p.P263S
Pat_15	Post-Resistance	PODN	127435	37	1	53544264	53544264	Missense_Mutation	SNP	T	C	46	159	c.1226T>C	c.(1225-1227)TTG>TCG	p.L409S
Pat_15	Post-Resistance	PARS2	25973	37	1	55223505	55223505	Missense_Mutation	SNP	G	A	4	353	c.1330C>T	c.(1330-1332)CCT>TCT	p.P444S
Pat_15	Post-Resistance	HOOK1	51361	37	1	60330906	60330906	Missense_Mutation	SNP	T	A	4	196	c.1733T>A	c.(1732-1734)ATA>AAA	p.I578K
Pat_15	Post-Resistance	CACHD1	57685	37	1	65016314	65016314	Nonsense_Mutation	SNP	C	A	4	205	c.83C>A	c.(82-84)TCA>TAA	p.S28*
Pat_15	Post-Resistance	ELTD1	64123	37	1	79412055	79412055	Missense_Mutation	SNP	T	G	33	75	c.229A>C	c.(229-231)AAC>CAC	p.N77H
Pat_15	Post-Resistance	CLCA4	22802	37	1	87031683	87031683	Missense_Mutation	SNP	G	A	64	187	c.934G>A	c.(934-936)GAT>AAT	p.D312N
Pat_15	Post-Resistance	NOTCH2	4853	37	1	120612013	120612013	Missense_Mutation	SNP	G	A	6	85	c.8C>T	c.(7-9)GCC>GTC	p.A3V
Pat_15	Post-Resistance	ACP6	51205	37	1	147131860	147131860	Missense_Mutation	SNP	G	A	45	130	c.250C>T	c.(250-252)CCA>TCA	p.P84S
Pat_15	Post-Resistance	FLG2	388698	37	1	152326724	152326724	Nonsense_Mutation	SNP	C	A	5	372	c.3538G>T	c.(3538-3540)GGA>TGA	p.G1180*
Pat_15	Post-Resistance	CD1E	913	37	1	158325309	158325309	Missense_Mutation	SNP	G	A	34	131	c.575G>A	c.(574-576)CGA>CAA	p.R192Q
Pat_15	Post-Resistance	OR10Z1	128368	37	1	158576814	158576814	Missense_Mutation	SNP	G	A	99	331	c.586G>A	c.(586-588)GAG>AAG	p.E196K
Pat_15	Post-Resistance	OR6K6	128371	37	1	158725536	158725536	Missense_Mutation	SNP	T	C	5	433	c.931T>C	c.(931-933)TTT>CTT	p.F311L
Pat_15	Post-Resistance	FCRL6	343413	37	1	159778148	159778148	Missense_Mutation	SNP	G	A	4	157	c.233G>A	c.(232-234)CGT>CAT	p.R78H
Pat_15	Post-Resistance	ARHGAP30	257106	37	1	161021422	161021422	Missense_Mutation	SNP	C	T	4	222	c.1102G>A	c.(1102-1104)GCA>ACA	p.A368T
Pat_15	Post-Resistance	DNM3	26052	37	1	172017826	172017826	Missense_Mutation	SNP	C	T	69	199	c.1271C>T	c.(1270-1272)TCC>TTC	p.S424F
Pat_15	Post-Resistance	SLC9A11	284525	37	1	173552668	173552668	Missense_Mutation	SNP	C	T	46	171	c.617G>A	c.(616-618)AGA>AAA	p.R206K
Pat_15	Post-Resistance	ASTN1	460	37	1	176992682	176992683	Missense_Mutation	DNP	CC	TT	32	151	.1295_1296GG>A	c.(1294-1296)GGG>GAA	p.G432E
Pat_15	Post-Resistance	PRG4	10216	37	1	186276959	186276959	Missense_Mutation	SNP	A	G	3	396	c.2108A>G	c.(2107-2109)GAG>GGG	p.E703G
Pat_15	Post-Resistance	CFHR3	10878	37	1	196748941	196748941	Missense_Mutation	SNP	C	T	10	27	c.268C>T	c.(268-270)CCT>TCT	p.P90S
Pat_15	Post-Resistance	CFHR5	81494	37	1	196953100	196953100	Missense_Mutation	SNP	C	T	40	130	c.263C>T	c.(262-264)TCC>TTC	p.S88F
Pat_15	Post-Resistance	F13B	2165	37	1	197026464	197026464	Missense_Mutation	SNP	C	T	98	366	c.937G>A	c.(937-939)GAA>AAA	p.E313K
Pat_15	Post-Resistance	ASPM	259266	37	1	197115477	197115478	Missense_Mutation	DNP	CC	TT	22	51	c.90_91GG>AA	(88-93)GAGGAG>GAAAA	p.E31K
Pat_15	Post-Resistance	DYRK3	8444	37	1	206821132	206821132	Missense_Mutation	SNP	T	C	4	540	c.589T>C	c.(589-591)TAT>CAT	p.Y197H
Pat_15	Post-Resistance	PLXNA2	5362	37	1	208390847	208390847	Missense_Mutation	SNP	G	A	6	705	c.421C>T	c.(421-423)CGG>TGG	p.R141W
Pat_15	Post-Resistance	HHAT	55733	37	1	210761301	210761301	Missense_Mutation	SNP	C	T	6	314	c.1103C>T	c.(1102-1104)ACG>ATG	p.T368M
Pat_15	Post-Resistance	USH2A	7399	37	1	215990535	215990535	Missense_Mutation	SNP	G	A	4	248	c.9374C>T	c.(9373-9375)TCT>TTT	p.S3125F
Pat_15	Post-Resistance	EPRS	2058	37	1	220179511	220179511	Missense_Mutation	SNP	C	A	5	483	c.1887G>T	c.(1885-1887)TTG>TTT	p.L629F
Pat_15	Post-Resistance	HLX	3142	37	1	221057861	221057861	Missense_Mutation	SNP	G	A	3	65	c.1282G>A	c.(1282-1284)GGC>AGC	p.G428S
Pat_15	Post-Resistance	HEATR1	55127	37	1	236730082	236730082	Missense_Mutation	SNP	G	A	57	210	c.4172C>T	c.(4171-4173)CCG>CTG	p.P1391L
Pat_15	Post-Resistance	GTPBP4	23560	37	10	1046616	1046616	Splice_Site	SNP	G	A	3	67	c.655_splice	c.e7-1	p.V219_splice
Pat_15	Post-Resistance	UCMA	221044	37	10	13275586	13275586	Missense_Mutation	SNP	G	A	4	453	c.172C>T	c.(172-174)CTC>TTC	p.L58F
Pat_15	Post-Resistance	FAM171A1	221061	37	10	15296773	15296773	Missense_Mutation	SNP	G	A	27	99	c.524C>T	c.(523-525)CCT>CTT	p.P175L
Pat_15	Post-Resistance	HSD17B7P2	158160	37	10	38654432	38654432	Missense_Mutation	SNP	A	G	7	153	c.524A>G	c.(523-525)AAT>AGT	p.N175S
Pat_15	Post-Resistance	C10orf72	196740	37	10	50227768	50227768	Missense_Mutation	SNP	G	A	42	122	c.890C>T	c.(889-891)CCC>CTC	p.P297L
Pat_15	Post-Resistance	C10orf71	118461	37	10	50532304	50532304	Missense_Mutation	SNP	C	T	51	113	c.1714C>T	c.(1714-1716)CCC>TCC	p.P572S
Pat_15	Post-Resistance	CTNNA3	29119	37	10	68526077	68526077	Missense_Mutation	SNP	T	C	4	446	c.1226A>G	c.(1225-1227)AAG>AGG	p.K409R

Pat_15	Post-Resistance	CPEB3	22849	37	10	93902788	93902788	Missense_Mutation	SNP	T	C	65	196	c.1451A>G	c.(1450-1452)AAA>AGA	p.K484R
Pat_15	Post-Resistance	IDE	3416	37	10	94216180	94216180	Missense_Mutation	SNP	C	A	5	256	c.2832G>T	c.(2830-2832)TTG>TTT	p.L944F
Pat_15	Post-Resistance	PLCE1	51196	37	10	96033331	96033331	Missense_Mutation	SNP	G	A	3	106	c.4519G>A	c.(4519-4521)GAA>AAA	p.E1507K
Pat_15	Post-Resistance	HELLS	3070	37	10	96361363	96361363	Missense_Mutation	SNP	C	T	32	90	c.2501C>T	c.(2500-2502)CCT>CTT	p.P834L
Pat_15	Post-Resistance	CYP2C18	1562	37	10	96448031	96448031	Missense_Mutation	SNP	G	A	102	196	c.481G>A	c.(481-483)GCC>ACC	p.A161T
Pat_15	Post-Resistance	CYP2C18	1562	37	10	96454828	96454828	Nonsense_Mutation	SNP	G	A	21	34	c.636G>A	c.(634-636)TGG>TGA	p.W212*
Pat_15	Post-Resistance	CYP2C8	1558	37	10	96797060	96797060	Missense_Mutation	SNP	C	T	22	50	c.1298G>A	c.(1297-1299)CGA>CAA	p.R433Q
Pat_15	Post-Resistance	C10orf62	414157	37	10	99349869	99349869	Missense_Mutation	SNP	C	T	62	161	c.215C>T	c.(214-216)ACG>ATG	p.T72M
Pat_15	Post-Resistance	SH3PXD2A	9644	37	10	105362640	105362640	Missense_Mutation	SNP	G	A	6	758	c.2251C>T	c.(2251-2253)CGG>TGG	p.R751W
Pat_15	Post-Resistance	RPL13AP6	644511	37	10	112696673	112696673	Missense_Mutation	SNP	A	G	3	129	c.319T>C	c.(319-321)TGC>CGC	p.C107R
Pat_15	Post-Resistance	NRAP	4892	37	10	115388776	115388776	Missense_Mutation	SNP	T	C	61	132	c.2045A>G	c.(2044-2046)CAG>CGG	p.Q682R
Pat_15	Post-Resistance	NHLRC2	374354	37	10	115664694	115664694	Missense_Mutation	SNP	C	A	4	344	c.1823C>A	c.(1822-1824)GCG>GAG	p.A608E
Pat_15	Post-Resistance	LRRC56	115399	37	11	541577	541577	Missense_Mutation	SNP	C	T	5	287	c.218C>T	c.(217-219)ACG>ATG	p.T73M
Pat_15	Post-Resistance	OR51G2	81282	37	11	4936406	4936406	Missense_Mutation	SNP	G	A	40	135	c.488C>T	c.(487-489)CCA>CTA	p.P163L
Pat_15	Post-Resistance	UBQLN3	50613	37	11	5530256	5530256	Missense_Mutation	SNP	G	A	4	392	c.533C>T	c.(532-534)CCG>CTG	p.P178L
Pat_15	Post-Resistance	MRVI1	10335	37	11	10598004	10598004	Missense_Mutation	SNP	A	G	3	285	c.2614T>C	c.(2614-2616)TAC>CAC	p.Y872H
Pat_15	Post-Resistance	PTH	5741	37	11	13514049	13514049	Missense_Mutation	SNP	T	A	76	153	c.251A>T	c.(250-252)AAA>ATA	p.K84I
Pat_15	Post-Resistance	ARFGAP2	84364	37	11	47196645	47196645	Missense_Mutation	SNP	C	A	6	586	c.401G>T	c.(400-402)TGG>TTG	p.W134L
Pat_15	Post-Resistance	AGBL2	79841	37	11	47698946	47698946	Missense_Mutation	SNP	T	G	30	57	c.2024A>C	c.(2023-2025)CAG>CCG	p.Q675P
Pat_15	Post-Resistance	OR5L2	26338	37	11	55595616	55595616	Missense_Mutation	SNP	A	C	22	98	c.922A>C	c.(922-924)AAA>CAA	p.K308Q
Pat_15	Post-Resistance	OR8H3	390152	37	11	55889999	55889999	Missense_Mutation	SNP	C	T	202	503	c.151C>T	c.(151-153)CGC>TGC	p.R51C
Pat_15	Post-Resistance	OR5T3	390154	37	11	56019973	56019973	Missense_Mutation	SNP	G	A	71	169	c.298G>A	c.(298-300)GAT>AAT	p.D100N
Pat_15	Post-Resistance	OR9G9	504191	37	11	56467892	56467892	Missense_Mutation	SNP	A	G	25	256	c.29A>G	c.(28-30)GAG>GGG	p.E10G
Pat_15	Post-Resistance	DTX4	23220	37	11	58949848	58949848	Missense_Mutation	SNP	A	G	19	53	c.848A>G	c.(847-849)AAG>AGG	p.K283R
Pat_15	Post-Resistance	CYBASC3	220002	37	11	61118495	61118495	Missense_Mutation	SNP	G	A	4	189	c.673C>T	c.(673-675)CGC>TGC	p.R225C
Pat_15	Post-Resistance	KCNK7	10089	37	11	65360983	65360983	Missense_Mutation	SNP	G	A	4	225	c.682C>T	c.(682-684)CCC>TCC	p.P228S
Pat_15	Post-Resistance	ADRBK1	156	37	11	67049161	67049161	Missense_Mutation	SNP	C	T	4	311	c.788C>T	c.(787-789)ACG>ATG	p.T263M
Pat_15	Post-Resistance	LRP5	4041	37	11	68216515	68216515	Missense_Mutation	SNP	T	C	4	438	c.4825T>C	c.(4825-4827)TCC>CCC	p.S1609P
Pat_15	Post-Resistance	ARAP1	116985	37	11	72421519	72421519	Missense_Mutation	SNP	G	A	42	290	c.1327C>T	c.(1327-1329)CGC>TGC	p.R443C
Pat_15	Post-Resistance	ARHGEF17	9828	37	11	73021314	73021314	Missense_Mutation	SNP	C	A	6	154	c.1631C>A	c.(1630-1632)GCA>GAA	p.A544E
Pat_15	Post-Resistance	TMEM126B	55863	37	11	85347238	85347238	Missense_Mutation	SNP	G	A	21	49	c.568G>A	c.(568-570)GAA>AAA	p.E190K
Pat_15	Post-Resistance	GRM5	2915	37	11	88780558	88780558	Missense_Mutation	SNP	C	A	4	208	c.483G>T	c.(481-483)TTG>TTT	p.L161F
Pat_15	Post-Resistance	KDM4DL	390245	37	11	94759611	94759611	Nonsense_Mutation	SNP	G	A	26	52	c.890G>A	c.(889-891)TGG>TAG	p.W297*
Pat_15	Post-Resistance	CNTN5	53942	37	11	100095458	100095458	Missense_Mutation	SNP	T	G	66	170	c.1919T>G	c.(1918-1920)ATC>AGC	p.I640S
Pat_15	Post-Resistance	PGR	5241	37	11	100962501	100962501	Missense_Mutation	SNP	C	T	27	149	c.1896G>A	c.(1894-1896)ATG>ATA	p.M632I
Pat_15	Post-Resistance	GUCY1A2	2977	37	11	106810341	106810341	Nonsense_Mutation	SNP	G	A	42	64	c.1051C>T	c.(1051-1053)CGA>TGA	p.R351*
Pat_15	Post-Resistance	ARHGAP20	57569	37	11	110462808	110462808	Missense_Mutation	SNP	G	T	5	453	c.1036C>A	c.(1036-1038)CAC>AAC	p.H346N
Pat_15	Post-Resistance	TMEM25	84866	37	11	118403728	118403728	Missense_Mutation	SNP	C	A	4	151	c.479C>A	c.(478-480)CCG>CAG	p.P160Q
Pat_15	Post-Resistance	GRIK4	2900	37	11	120827502	120827502	Nonsense_Mutation	SNP	G	T	4	473	c.1714G>T	c.(1714-1716)GAG>TAG	p.E572*
Pat_15	Post-Resistance	CCDC15	80071	37	11	124857495	124857495	Missense_Mutation	SNP	A	C	7	253	c.1373A>C	c.(1372-1374)CAC>CCC	p.H458P
Pat_15	Post-Resistance	NINJ2	4815	37	12	772558	772558	Missense_Mutation	SNP	G	A	6	527	c.107C>T	c.(106-108)CCG>CTG	p.P36L
Pat_15	Post-Resistance	C1S	716	37	12	7172542	7172542	Missense_Mutation	SNP	G	A	4	390	c.656G>A	c.(655-657)CGG>CAG	p.R219Q
Pat_15	Post-Resistance	PRR4	11272	37	12	10999736	10999736	Missense_Mutation	SNP	T	C	5	786	c.331A>G	c.(331-333)AGC>GGC	p.S111G
Pat_15	Post-Resistance	CREBL2	1389	37	12	12765117	12765117	Missense_Mutation	SNP	G	A	4	420	c.11G>A	c.(10-12)AGT>AAT	p.S4N
Pat_15	Post-Resistance	LRMP	4033	37	12	25260902	25260902	Missense_Mutation	SNP	G	A	5	364	c.1408G>A	c.(1408-1410)GCT>ACT	p.A470T
Pat_15	Post-Resistance	SFRS2IP	9169	37	12	46320998	46320998	Missense_Mutation	SNP	T	C	4	200	c.2486A>G	c.(2485-2487)AAG>AGG	p.K829R
Pat_15	Post-Resistance	CCNT1	904	37	12	49087790	49087790	Missense_Mutation	SNP	G	T	6	686	c.1207C>A	c.(1207-1209)CAG>AAG	p.Q403K

Pat_15	Post-Resistance	AQP2	359	37	12	50344822	50344822	Missense_Mutation	SNP	C	T	33	99	c.209C>T	c.(208-210)GCC>GTC	p.A70V
Pat_15	Post-Resistance	SLC11A2	4891	37	12	51394183	51394183	Missense_Mutation	SNP	C	A	5	219	c.449G>T	c.(448-450)TGG>TTG	p.W150L
Pat_15	Post-Resistance	KRT75	9119	37	12	52825810	52825810	Missense_Mutation	SNP	C	T	52	212	c.754G>A	c.(754-756)GAA>AAA	p.E252K
Pat_15	Post-Resistance	NFE2	4778	37	12	54686462	54686462	Missense_Mutation	SNP	C	T	4	295	c.818G>A	c.(817-819)CGG>CAG	p.R273Q
Pat_15	Post-Resistance	RDH5	5959	37	12	56115517	56115517	Missense_Mutation	SNP	G	A	4	293	c.355G>A	c.(355-357)GGA>AGA	p.G119R
Pat_15	Post-Resistance	NACA	4666	37	12	57118247	57118247	Missense_Mutation	SNP	T	C	4	70	c.59A>G	c.(58-60)CAG>CGG	p.Q20R
Pat_15	Post-Resistance	SLC5A8	160728	37	12	101603571	101603571	Missense_Mutation	SNP	G	A	4	211	c.56C>T	c.(55-57)GCG>GTG	p.A19V
Pat_15	Post-Resistance	UTP20	27340	37	12	101711330	101711330	Missense_Mutation	SNP	C	A	5	298	c.2627C>A	c.(2626-2628)GCA>GAA	p.A876E
Pat_15	Post-Resistance	STAB2	55576	37	12	104063395	104063395	Missense_Mutation	SNP	G	A	67	234	c.2249G>A	c.(2248-2250)GGA>GAA	p.G750E
Pat_15	Post-Resistance	TPCN1	53373	37	12	113706592	113706592	Missense_Mutation	SNP	G	A	4	213	c.574G>A	c.(574-576)GTA>ATA	p.V192I
Pat_15	Post-Resistance	SDSL	113675	37	12	113873331	113873331	Missense_Mutation	SNP	G	A	6	699	c.641G>A	c.(640-642)GGC>GAC	p.G214D
Pat_15	Post-Resistance	UNC119B	84747	37	12	121157744	121157744	Missense_Mutation	SNP	C	T	73	186	c.665C>T	c.(664-666)CCT>CTT	p.P222L
Pat_15	Post-Resistance	VPS33A	65082	37	12	122748200	122748200	Missense_Mutation	SNP	G	A	4	152	c.215C>T	c.(214-216)CCG>CTG	p.P72L
Pat_15	Post-Resistance	RNF6	6049	37	13	26788595	26788595	Missense_Mutation	SNP	G	T	5	331	c.1424C>A	c.(1423-1425)CCA>CAA	p.P475Q
Pat_15	Post-Resistance	TSC22D1	8848	37	13	45149288	45149288	Missense_Mutation	SNP	G	A	4	382	c.923C>T	c.(922-924)ACT>ATT	p.T308I
Pat_15	Post-Resistance	UTP14C	9724	37	13	52604045	52604045	Missense_Mutation	SNP	G	A	4	287	c.1105G>A	c.(1105-1107)GGA>AGA	p.G369R
Pat_15	Post-Resistance	SLITRK1	114798	37	13	84453751	84453751	Missense_Mutation	SNP	G	A	86	88	c.1892C>T	c.(1891-1893)TCC>TTC	p.S631F
Pat_15	Post-Resistance	DOCK9	23348	37	13	99478165	99478165	Missense_Mutation	SNP	G	A	25	29	c.4987C>T	c.(4987-4989)CCC>TCC	p.P1663S
Pat_15	Post-Resistance	NOVA1	4857	37	14	26917974	26917974	Missense_Mutation	SNP	G	T	5	353	c.715C>A	c.(715-717)CAG>AAG	p.Q239K
Pat_15	Post-Resistance	DAAM1	23002	37	14	59834280	59834280	Missense_Mutation	SNP	A	G	3	145	c.2990A>G	c.(2989-2991)AAG>AGG	p.K997R
Pat_15	Post-Resistance	LTBP2	4053	37	14	74975535	74975535	Missense_Mutation	SNP	T	C	3	135	c.3524A>G	c.(3523-3525)GAG>GGG	p.E1175G
Pat_15	Post-Resistance	SEL1L	6400	37	14	82000079	82000079	Missense_Mutation	SNP	G	A	39	73	c.10C>T	c.(10-12)CGG>TGG	p.R4W
Pat_15	Post-Resistance	SLC24A4	123041	37	14	92953088	92953088	Missense_Mutation	SNP	C	T	77	143	c.1450C>T	c.(1450-1452)CCA>TCA	p.P484S
Pat_15	Post-Resistance	KIAA1409	57578	37	14	93994911	93994911	Missense_Mutation	SNP	T	G	98	196	c.440T>G	c.(439-441)ATA>AGA	p.I147R
Pat_15	Post-Resistance	SERPINA11	256394	37	14	94912800	94912800	Missense_Mutation	SNP	G	T	7	344	c.785C>A	c.(784-786)ACC>AAC	p.T262N
Pat_15	Post-Resistance	AHNAK2	113146	37	14	105422953	105422953	Missense_Mutation	SNP	C	T	4	400	c.287G>A	c.(286-288)CGG>CAG	p.R96Q
Pat_15	Post-Resistance	MAGEL2	54551	37	15	23889390	23889390	Missense_Mutation	SNP	A	C	3	123	c.1691T>G	c.(1690-1692)CTA>CGA	p.L564R
Pat_15	Post-Resistance	GABRB3	2562	37	15	26793230	26793230	Missense_Mutation	SNP	T	A	29	666	c.1132A>T	c.(1132-1134)ATG>TTG	p.M378L
Pat_15	Post-Resistance	GREM1	26585	37	15	33023142	33023142	Missense_Mutation	SNP	C	T	4	161	c.251C>T	c.(250-252)ACG>ATG	p.T84M
Pat_15	Post-Resistance	BMF	90427	37	15	40396398	40396398	Missense_Mutation	SNP	G	A	6	781	c.436C>T	c.(436-438)CGG>TGG	p.R146W
Pat_15	Post-Resistance	EHD4	30844	37	15	42193253	42193253	Missense_Mutation	SNP	T	C	3	121	c.1216A>G	c.(1216-1218)AGC>GGC	p.S406G
Pat_15	Post-Resistance	KIAA1370	56204	37	15	52877033	52877033	Missense_Mutation	SNP	C	A	4	96	c.2986G>T	c.(2986-2988)GTA>TTA	p.V996L
Pat_15	Post-Resistance	RFX7	64864	37	15	56386544	56386544	Nonsense_Mutation	SNP	G	A	5	465	c.3382C>T	c.(3382-3384)CAG>TAG	p.Q1128*
Pat_15	Post-Resistance	SLTM	79811	37	15	59175909	59175909	Missense_Mutation	SNP	G	A	5	458	c.2912C>T	c.(2911-2913)CCA>CTA	p.P971L
Pat_15	Post-Resistance	RNF111	54778	37	15	59359058	59359058	Missense_Mutation	SNP	G	A	4	398	c.1462G>A	c.(1462-1464)GGA>AGA	p.G488R
Pat_15	Post-Resistance	VPS13C	54832	37	15	62208095	62208095	Missense_Mutation	SNP	G	A	4	325	c.8182C>T	c.(8182-8184)CGC>TGC	p.R2728C
Pat_15	Post-Resistance	FBXL22	283807	37	15	63893617	63893617	Missense_Mutation	SNP	T	G	6	33	c.458T>G	c.(457-459)TTG>TGG	p.L153W
Pat_15	Post-Resistance	ZNF609	23060	37	15	64966288	64966288	Missense_Mutation	SNP	G	A	6	576	c.1235G>A	c.(1234-1236)GGC>GAC	p.G412D
Pat_15	Post-Resistance	MAP2K1	5604	37	15	66729163	66729163	Missense_Mutation	SNP	C	T	118	236	c.371C>T	c.(370-372)CCG>CTG	p.P124L
Pat_15	Post-Resistance	GRAMD2	196996	37	15	72456010	72456010	Missense_Mutation	SNP	G	A	52	136	c.689C>T	c.(688-690)CCA>CTA	p.P230L
Pat_15	Post-Resistance	CD276	80381	37	15	73996161	73996161	Missense_Mutation	SNP	G	A	4	250	c.895G>A	c.(895-897)GAA>AAA	p.E299K
Pat_15	Post-Resistance	UBL7	84993	37	15	74741588	74741588	Missense_Mutation	SNP	G	A	4	257	c.821C>T	c.(820-822)ACC>ATC	p.T274I
Pat_15	Post-Resistance	C15orf39	56905	37	15	75500784	75500784	Missense_Mutation	SNP	C	T	18	69	c.2395C>T	c.(2395-2397)CCC>TCC	p.P799S
Pat_15	Post-Resistance	HMG20A	10363	37	15	77750795	77750795	Missense_Mutation	SNP	G	C	3	363	c.46G>C	c.(46-48)GAT>CAT	p.D16H
Pat_15	Post-Resistance	ACSBG1	23205	37	15	78466162	78466162	Missense_Mutation	SNP	G	T	61	177	c.1862C>A	c.(1861-1863)ACC>AAC	p.T621N
Pat_15	Post-Resistance	KIAA1024	23251	37	15	79750210	79750210	Missense_Mutation	SNP	G	A	4	487	c.1721G>A	c.(1720-1722)AGC>AAC	p.S574N
Pat_15	Post-Resistance	LRRK1	79705	37	15	101569437	101569437	Missense_Mutation	SNP	G	A	4	241	c.2963G>A	c.(2962-2964)AGC>AAC	p.S988N

Pat_15	Post-Resistance	WDR90	197335	37	16	716594	716594	Missense_Mutation	SNP	C	T	4	154	c.4880C>T	c.(4879-4881)ACG>ATG	p.T1627M
Pat_15	Post-Resistance	BTBD12	84464	37	16	3634827	3634827	Missense_Mutation	SNP	G	A	6	717	c.4682C>T	c.(4681-4683)ACG>ATG	p.T1561M
Pat_15	Post-Resistance	BTBD12	84464	37	16	3640521	3640521	Missense_Mutation	SNP	G	A	65	225	c.3118C>T	c.(3118-3120)CCC>TCC	p.P1040S
Pat_15	Post-Resistance	MGRN1	23295	37	16	4731705	4731705	Missense_Mutation	SNP	C	T	58	148	c.1286C>T	c.(1285-1287)CCC>CTC	p.P429L
Pat_15	Post-Resistance	ABCC6	368	37	16	16251532	16251532	Missense_Mutation	SNP	G	C	3	196	c.3870C>G	c.(3868-3870)CAC>CAG	p.H1290Q
Pat_15	Post-Resistance	COG7	91949	37	16	23409399	23409399	Missense_Mutation	SNP	A	C	55	251	c.1855T>G	c.(1855-1857)TTT>GTT	p.F619V
Pat_15	Post-Resistance	HS3ST4	9951	37	16	26147561	26147561	Missense_Mutation	SNP	G	A	31	111	c.1363G>A	c.(1363-1365)GAT>AAT	p.D455N
Pat_15	Post-Resistance	ZNF629	23361	37	16	30795033	30795033	Missense_Mutation	SNP	A	G	3	196	c.616T>C	c.(616-618)TAC>CAC	p.Y206H
Pat_15	Post-Resistance	ABCC12	94160	37	16	48175173	48175173	Missense_Mutation	SNP	C	G	5	256	c.367G>C	c.(367-369)GTG>CTG	p.V123L
Pat_15	Post-Resistance	NOD2	64127	37	16	50733452	50733452	Missense_Mutation	SNP	G	A	201	420	c.127G>A	c.(127-129)GAG>AAG	p.E43K
Pat_15	Post-Resistance	CES7	221223	37	16	55907781	55907781	Nonsense_Mutation	SNP	C	T	28	125	c.242G>A	c.(241-243)TGG>TAG	p.W81*
Pat_15	Post-Resistance	KATNB1	10300	37	16	57789260	57789260	Missense_Mutation	SNP	G	A	4	187	c.1420G>A	c.(1420-1422)GTG>ATG	p.V474M
Pat_15	Post-Resistance	CES3	23491	37	16	66997147	66997147	Missense_Mutation	SNP	G	A	5	446	c.148G>A	c.(148-150)GTG>ATG	p.V50M
Pat_15	Post-Resistance	FHOD1	29109	37	16	67264550	67264550	Missense_Mutation	SNP	G	A	6	769	c.2812C>T	c.(2812-2814)CGC>TGC	p.R938C
Pat_15	Post-Resistance	SLC7A6OS	84138	37	16	68337993	68337993	Missense_Mutation	SNP	G	A	5	412	c.614C>T	c.(613-615)ACG>ATG	p.T205M
Pat_15	Post-Resistance	TXNL4B	54957	37	16	72120568	72120568	Missense_Mutation	SNP	G	A	54	287	c.418C>T	c.(418-420)CCC>TCC	p.P140S
Pat_15	Post-Resistance	CLEC18B	497190	37	16	74447009	74447009	Missense_Mutation	SNP	C	T	69	175	c.602G>A	c.(601-603)GGT>GAT	p.G201D
Pat_15	Post-Resistance	TRAPPC2L	51693	37	16	88925060	88925060	Missense_Mutation	SNP	G	A	168	518	c.67G>A	c.(67-69)GAG>AAG	p.E23K
Pat_15	Post-Resistance	ANKRD11	29123	37	16	89351925	89351925	Missense_Mutation	SNP	G	A	85	219	c.1025C>T	c.(1024-1026)CCC>CTC	p.P342L
Pat_15	Post-Resistance	CDK10	8558	37	16	89755676	89755676	Missense_Mutation	SNP	G	A	4	352	c.104G>A	c.(103-105)AGT>AAT	p.S35N
Pat_15	Post-Resistance	OR3A2	4995	37	17	3181572	3181572	Missense_Mutation	SNP	A	T	57	131	c.658T>A	c.(658-660)TTG>ATG	p.L220M
Pat_15	Post-Resistance	OR1E2	8388	37	17	3336519	3336519	Missense_Mutation	SNP	C	A	4	151	c.617G>T	c.(616-618)TGG>TTG	p.W206L
Pat_15	Post-Resistance	GLTPD2	388323	37	17	4692317	4692317	Missense_Mutation	SNP	C	T	4	94	c.11C>T	c.(10-12)GCG>GTG	p.A4V
Pat_15	Post-Resistance	KIF1C	10749	37	17	4926841	4926841	Missense_Mutation	SNP	G	A	4	195	c.2707G>A	c.(2707-2709)GCC>ACC	p.A903T
Pat_15	Post-Resistance	TP53	7157	37	17	7574003	7574003	Nonsense_Mutation	SNP	G	A	54	99	c.1024C>T	c.(1024-1026)CGA>TGA	p.R342*
Pat_15	Post-Resistance	ALOX12B	242	37	17	7984230	7984230	Missense_Mutation	SNP	G	A	5	351	c.499C>T	c.(499-501)CGG>TGG	p.R167W
Pat_15	Post-Resistance	MYH10	4628	37	17	8381736	8381736	Missense_Mutation	SNP	G	A	4	372	c.5533C>T	c.(5533-5535)CGT>TGT	p.R1845C
Pat_15	Post-Resistance	CCDC42	146849	37	17	8647476	8647476	Missense_Mutation	SNP	G	A	4	183	c.110C>T	c.(109-111)TCG>TTG	p.S37L
Pat_15	Post-Resistance	USP43	124739	37	17	9613321	9613321	Missense_Mutation	SNP	G	A	5	166	c.2060G>A	c.(2059-2061)AGC>AAC	p.S687N
Pat_15	Post-Resistance	MYH13	8735	37	17	10216600	10216600	Missense_Mutation	SNP	C	A	8	538	c.4056G>T	c.(4054-4056)GAG>GAT	p.E1352D
Pat_15	Post-Resistance	NCOR1	9611	37	17	15938172	15938172	Missense_Mutation	SNP	C	T	89	178	c.7042G>A	c.(7042-7044)GAA>AAA	p.E2348K
Pat_15	Post-Resistance	UBB	7314	37	17	16285453	16285453	Missense_Mutation	SNP	C	A	4	285	c.232C>A	c.(232-234)CAG>AAG	p.Q78K
Pat_15	Post-Resistance	FOXN1	8456	37	17	26861352	26861352	Missense_Mutation	SNP	G	A	4	427	c.931G>A	c.(931-933)GCA>ACA	p.A311T
Pat_15	Post-Resistance	LRRC37B2	147172	37	17	28961033	28961033	Missense_Mutation	SNP	T	G	3	95	c.496T>G	c.(496-498)TAT>GAT	p.Y166D
Pat_15	Post-Resistance	SLFN13	146857	37	17	33768288	33768288	Missense_Mutation	SNP	G	A	113	305	c.2020C>T	c.(2020-2022)CGT>TGT	p.R674C
Pat_15	Post-Resistance	GAS2L2	246176	37	17	34072788	34072788	Nonsense_Mutation	SNP	C	T	61	183	c.1728G>A	c.(1726-1728)TGG>TGA	p.W576*
Pat_15	Post-Resistance	ERBB2	2064	37	17	37864622	37864622	Missense_Mutation	SNP	A	G	3	359	c.274A>G	c.(274-276)AGG>GGG	p.R92G
Pat_15	Post-Resistance	IKZF3	22806	37	17	37947831	37947831	Missense_Mutation	SNP	G	A	4	303	c.430C>T	c.(430-432)CGC>TGC	p.R144C
Pat_15	Post-Resistance	KRT222	125113	37	17	38816377	38816378	Missense_Mutation	DNP	CC	TG	55	237	c.307_308GG>CA	c.(307-309)GGA>CAA	p.G103Q
Pat_15	Post-Resistance	KRTAP4-8	728224	37	17	39254021	39254021	Missense_Mutation	SNP	C	T	6	226	c.316G>A	c.(316-318)GTG>ATG	p.V106M
Pat_15	Post-Resistance	KLHL11	55175	37	17	40010117	40010117	Missense_Mutation	SNP	C	A	7	609	c.2002G>T	c.(2002-2004)GGC>TGC	p.G668C
Pat_15	Post-Resistance	BECN1	8678	37	17	40970804	40970804	Splice_Site	SNP	C	T	4	234	c.351_splice	c.e5+1	p.K117_splice
Pat_15	Post-Resistance	GPATCH8	23131	37	17	42512474	42512474	Missense_Mutation	SNP	C	T	19	172	c.307G>A	c.(307-309)GTA>ATA	p.V103I
Pat_15	Post-Resistance	TTLL6	284076	37	17	46846574	46846574	Missense_Mutation	SNP	C	T	42	298	c.2453G>A	c.(2452-2454)AGC>AAC	p.S818N
Pat_15	Post-Resistance	B4GALNT2	124872	37	17	47210448	47210448	Missense_Mutation	SNP	G	A	16	57	c.61G>A	c.(61-63)GAA>AAA	p.E21K
Pat_15	Post-Resistance	ANKFN1	162282	37	17	54520276	54520276	Missense_Mutation	SNP	G	A	77	239	c.1090G>A	c.(1090-1092)GCA>ACA	p.A364T
Pat_15	Post-Resistance	KCNH6	81033	37	17	61621705	61621705	Missense_Mutation	SNP	G	A	24	156	c.2437G>A	c.(2437-2439)GAA>AAA	p.E813K

Pat_15	Post-Resistance	ABCA6	23460	37	17	67096999	67096999	Missense_Mutation	SNP	C	A	5	228	c.2951G>T	c.(2950-2952)GGG>GTG	p.G984V
Pat_15	Post-Resistance	KCNJ16	3773	37	17	68128770	68128770	Missense_Mutation	SNP	C	T	54	376	c.542C>T	c.(541-543)ACC>ATC	p.T181I
Pat_15	Post-Resistance	CD300C	10871	37	17	72540900	72540900	Missense_Mutation	SNP	G	A	39	265	c.248C>T	c.(247-249)TCC>TTC	p.S83F
Pat_15	Post-Resistance	NUP85	79902	37	17	73208113	73208113	Missense_Mutation	SNP	G	T	4	166	c.317G>T	c.(316-318)CGA>CTA	p.R106L
Pat_15	Post-Resistance	MGAT5B	146664	37	17	74936524	74936524	Missense_Mutation	SNP	C	T	54	395	c.1652C>T	c.(1651-1653)CCC>CTC	p.P551L
Pat_15	Post-Resistance	USP36	57602	37	17	76810604	76810604	Missense_Mutation	SNP	G	A	4	201	c.1054C>T	c.(1054-1056)CGT>TGT	p.R352C
Pat_15	Post-Resistance	SLC26A11	284129	37	17	78201660	78201660	Missense_Mutation	SNP	C	G	6	416	c.637C>G	c.(637-639)CTG>GTG	p.L213V
Pat_15	Post-Resistance	NPTX1	4884	37	17	78444806	78444806	Missense_Mutation	SNP	G	A	23	147	c.1106C>T	c.(1105-1107)ACC>ATC	p.T369I
Pat_15	Post-Resistance	ACTG1	71	37	17	79478120	79478120	Missense_Mutation	SNP	C	T	4	381	c.817G>A	c.(817-819)GGC>AGC	p.G273S
Pat_15	Post-Resistance	SPIRE1	56907	37	18	12506574	12506574	Missense_Mutation	SNP	G	A	6	675	c.874C>T	c.(874-876)CGG>TGG	p.R292W
Pat_15	Post-Resistance	DSC1	1823	37	18	28720185	28720185	Missense_Mutation	SNP	C	G	84	290	c.1340G>C	c.(1339-1341)AGC>ACC	p.S447T
Pat_15	Post-Resistance	DSG1	1828	37	18	28934588	28934588	Missense_Mutation	SNP	C	T	113	433	c.2429C>T	c.(2428-2430)TCT>TTT	p.S810F
Pat_15	Post-Resistance	ASXL3	80816	37	18	31319233	31319233	Missense_Mutation	SNP	G	A	4	95	c.1865G>A	c.(1864-1866)TGT>TAT	p.C622Y
Pat_15	Post-Resistance	RNF165	494470	37	18	44036562	44036562	Missense_Mutation	SNP	G	A	123	393	c.1004G>A	c.(1003-1005)CGA>CAA	p.R335Q
Pat_15	Post-Resistance	LIPG	9388	37	18	47093924	47093924	Missense_Mutation	SNP	A	G	4	312	c.392A>G	c.(391-393)TAC>TGC	p.Y131C
Pat_15	Post-Resistance	SERPINB11	89778	37	18	61377533	61377533	Missense_Mutation	SNP	C	T	56	175	c.106C>T	c.(106-108)CTT>TTT	p.L36F
Pat_15	Post-Resistance	MIER2	54531	37	19	334444	334444	Missense_Mutation	SNP	G	A	63	369	c.199C>T	c.(199-201)CCA>TCA	p.P67S
Pat_15	Post-Resistance	MADCAM1	8174	37	19	501699	501699	Missense_Mutation	SNP	C	T	42	111	c.698C>T	c.(697-699)CCC>CTC	p.P233L
Pat_15	Post-Resistance	MED16	10025	37	19	889802	889802	Missense_Mutation	SNP	G	A	3	75	c.283C>T	c.(283-285)CGG>TGG	p.R95W
Pat_15	Post-Resistance	ZNF555	148254	37	19	2853202	2853202	Missense_Mutation	SNP	C	T	4	135	c.1139C>T	c.(1138-1140)CCC>CTC	p.P380L
Pat_15	Post-Resistance	ZNF57	126295	37	19	2917807	2917807	Missense_Mutation	SNP	A	C	5	291	c.1188A>C	c.(1186-1188)CAA>CAC	p.Q396H
Pat_15	Post-Resistance	ZNF57	126295	37	19	2917901	2917901	Missense_Mutation	SNP	A	G	3	261	c.1282A>G	c.(1282-1284)ACC>GCC	p.T428A
Pat_15	Post-Resistance	TNFSF9	8744	37	19	6531088	6531088	Missense_Mutation	SNP	C	T	4	350	c.41C>T	c.(40-42)CCG>CTG	p.P14L
Pat_15	Post-Resistance	C3	718	37	19	6686166	6686166	Missense_Mutation	SNP	C	T	77	614	c.3779G>A	c.(3778-3780)AGA>AAA	p.R1260K
Pat_15	Post-Resistance	VAV1	7409	37	19	6828459	6828459	Missense_Mutation	SNP	G	A	39	127	c.1053G>A	c.(1051-1053)ATG>ATA	p.M351I
Pat_15	Post-Resistance	FBN3	84467	37	19	8155007	8155007	Missense_Mutation	SNP	C	T	51	129	c.6160G>A	c.(6160-6162)GAA>AAA	p.E2054K
Pat_15	Post-Resistance	MYO1F	4542	37	19	8595411	8595411	Missense_Mutation	SNP	G	A	6	626	c.2090C>T	c.(2089-2091)GCC>GTC	p.A697V
Pat_15	Post-Resistance	MUC16	94025	37	19	9016993	9016993	Missense_Mutation	SNP	G	A	5	347	c.38002C>T	c.(38002-38004)CCC>TCC	p.P12668S
Pat_15	Post-Resistance	MUC16	94025	37	19	9068553	9068553	Missense_Mutation	SNP	G	A	66	431	c.18893C>T	c.(18892-18894)TCT>TTT	p.S6298F
Pat_15	Post-Resistance	MUC16	94025	37	19	9085237	9085237	Missense_Mutation	SNP	G	A	12	80	c.6578C>T	c.(6577-6579)TCC>TTC	p.S2193F
Pat_15	Post-Resistance	MUC16	94025	37	19	9089503	9089503	Missense_Mutation	SNP	G	A	125	455	c.2312C>T	c.(2311-2313)TCC>TTC	p.S771F
Pat_15	Post-Resistance	ZNF560	147741	37	19	9578116	9578116	Missense_Mutation	SNP	G	A	34	190	c.1507C>T	c.(1507-1509)CTT>TTT	p.L503F
Pat_15	Post-Resistance	DNMT1	1786	37	19	10305545	10305545	Missense_Mutation	SNP	G	A	4	171	c.31C>T	c.(31-33)CCC>TCC	p.P11S
Pat_15	Post-Resistance	ZNF844	284391	37	19	12187307	12187307	Missense_Mutation	SNP	G	C	5	349	c.1372G>C	c.(1372-1374)GAT>CAT	p.D458H
Pat_15	Post-Resistance	EMR2	30817	37	19	14875368	14875368	Missense_Mutation	SNP	G	T	4	154	c.961C>A	c.(961-963)CTG>ATG	p.L321M
Pat_15	Post-Resistance	ABHD8	79575	37	19	17412212	17412212	Missense_Mutation	SNP	G	A	4	200	c.214C>T	c.(214-216)CTC>TTC	p.L72F
Pat_15	Post-Resistance	ZNF493	284443	37	19	21606468	21606468	Missense_Mutation	SNP	C	T	6	199	c.623C>T	c.(622-624)CCT>CTT	p.P208L
Pat_15	Post-Resistance	ZNF208	7757	37	19	22156590	22156590	Missense_Mutation	SNP	C	T	5	279	c.1246G>A	c.(1246-1248)GAG>AAG	p.E416K
Pat_15	Post-Resistance	ZNF492	57615	37	19	22847739	22847739	Missense_Mutation	SNP	G	A	5	198	c.1268G>A	c.(1267-1269)TGT>TAT	p.C423Y
Pat_15	Post-Resistance	ZNF675	171392	37	19	23836350	23836350	Missense_Mutation	SNP	A	C	3	122	c.1385T>G	c.(1384-1386)ATC>AGC	p.I462S
Pat_15	Post-Resistance	ZNF302	55900	37	19	35175919	35175919	Missense_Mutation	SNP	C	T	8	106	c.1109C>T	c.(1108-1110)TCG>TTG	p.S370L
Pat_15	Post-Resistance	SUPT5H	6829	37	19	39964104	39964104	Missense_Mutation	SNP	G	A	5	317	c.2435G>A	c.(2434-2436)AGC>AAC	p.S812N
Pat_15	Post-Resistance	BLVRB	645	37	19	40957283	40957283	Missense_Mutation	SNP	G	A	3	61	c.451C>T	c.(451-453)CCG>TCG	p.P151S
Pat_15	Post-Resistance	CADM4	199731	37	19	44130387	44130387	Missense_Mutation	SNP	G	A	4	212	c.553C>T	c.(553-555)CGG>TGG	p.R185W
Pat_15	Post-Resistance	HIF3A	64344	37	19	46825161	46825161	Missense_Mutation	SNP	G	A	4	196	c.1273G>A	c.(1273-1275)GCT>ACT	p.A425T
Pat_15	Post-Resistance	ZC3H4	23211	37	19	47572412	47572412	Missense_Mutation	SNP	C	G	5	333	c.2335G>C	c.(2335-2337)GAG>CAG	p.E779Q
Pat_15	Post-Resistance	LIG1	3978	37	19	48660312	48660312	Missense_Mutation	SNP	G	A	90	651	c.329C>T	c.(328-330)CCC>CTC	p.P110L

Pat_15	Post-Resistance	PPP1R15A	23645	37	19	49377986	49377986	Nonsense_Mutation	SNP	G	A	4	323	c.1496G>A	c.(1495-1497)TGG>TAG	p.W499*
Pat_15	Post-Resistance	MYH14	79784	37	19	50789874	50789874	Missense_Mutation	SNP	G	A	13	33	c.4552G>A	c.(4552-4554)GAG>AAG	p.E1518K
Pat_15	Post-Resistance	KLK5	25818	37	19	51453324	51453324	Missense_Mutation	SNP	G	A	37	107	c.122C>T	c.(121-123)ACC>ATC	p.T41I
Pat_15	Post-Resistance	ZNF836	162962	37	19	52659224	52659224	Missense_Mutation	SNP	A	T	8	712	c.1712T>A	c.(1711-1713)ATT>AAT	p.I571N
Pat_15	Post-Resistance	ZNF836	162962	37	19	52659243	52659243	Missense_Mutation	SNP	A	C	5	651	c.1693T>G	c.(1693-1695)TAC>GAC	p.Y565D
Pat_15	Post-Resistance	ZNF845	91664	37	19	53855196	53855197	Missense_Mutation	DNP	TG	CA	7	463	.1268_1269TG>C	c.(1267-1269)ATG>ACA	p.M423T
Pat_15	Post-Resistance	ZNF761	388561	37	19	53959722	53959722	Missense_Mutation	SNP	G	A	39	303	c.1961G>A	c.(1960-1962)AGA>AAA	p.R654K
Pat_15	Post-Resistance	RPS9	6203	37	19	54710159	54710159	Missense_Mutation	SNP	G	A	4	214	c.236G>A	c.(235-237)CGG>CAG	p.R79Q
Pat_15	Post-Resistance	ZNF667	63934	37	19	56972086	56972086	Missense_Mutation	SNP	C	A	5	370	c.132G>T	c.(130-132)TTG>TTT	p.L44F
Pat_15	Post-Resistance	ZNF470	388566	37	19	57089054	57089054	Missense_Mutation	SNP	T	A	82	182	c.1257T>A	c.(1255-1257)CAT>CAA	p.H419Q
Pat_15	Post-Resistance	PEG3	5178	37	19	57335821	57335821	Missense_Mutation	SNP	C	T	122	265	c.203G>A	c.(202-204)CGA>CAA	p.R68Q
Pat_15	Post-Resistance	ZNF749	388567	37	19	57956341	57956341	Nonsense_Mutation	SNP	G	T	36	237	c.1825G>T	c.(1825-1827)GAA>TAA	p.E609*
Pat_15	Post-Resistance	ZNF419	79744	37	19	58005146	58005146	Missense_Mutation	SNP	C	G	3	458	c.1221C>G	c.(1219-1221)TTC>TTG	p.F407L
Pat_15	Post-Resistance	ZNF549	256051	37	19	58050291	58050291	Missense_Mutation	SNP	C	T	34	272	c.1919C>T	c.(1918-1920)CCC>CTC	p.P640L
Pat_15	Post-Resistance	ZNF132	7691	37	19	58945225	58945225	Missense_Mutation	SNP	C	A	4	228	c.1586G>T	c.(1585-1587)AGC>ATC	p.S529I
Pat_15	Post-Resistance	MSGN1	343930	37	2	17998224	17998224	Missense_Mutation	SNP	C	T	46	586	c.439C>T	c.(439-441)CTC>TTC	p.L147F
Pat_15	Post-Resistance	KCNS3	3790	37	2	18112936	18112936	Missense_Mutation	SNP	G	A	4	344	c.661G>A	c.(661-663)GTG>ATG	p.V221M
Pat_15	Post-Resistance	ADCY3	109	37	2	25062892	25062892	Missense_Mutation	SNP	C	A	4	406	c.1205G>T	c.(1204-1206)CGG>CTG	p.R402L
Pat_15	Post-Resistance	KIF3C	3797	37	2	26204389	26204389	Missense_Mutation	SNP	C	T	5	440	c.398G>A	c.(397-399)CGC>CAC	p.R133H
Pat_15	Post-Resistance	NRBP1	29959	37	2	27662739	27662739	Missense_Mutation	SNP	C	T	5	430	c.1010C>T	c.(1009-1011)GCG>GTG	p.A337V
Pat_15	Post-Resistance	C2orf16	84226	37	2	27804726	27804726	Nonsense_Mutation	SNP	G	T	8	779	c.5287G>T	c.(5287-5289)GAG>TAG	p.E1763*
Pat_15	Post-Resistance	SPTBN1	6711	37	2	54839304	54839304	Missense_Mutation	SNP	C	T	4	320	c.307C>T	c.(307-309)CCC>TCC	p.P103S
Pat_15	Post-Resistance	TMEM17	200728	37	2	62728427	62728427	Missense_Mutation	SNP	G	A	84	259	c.514C>T	c.(514-516)CGT>TGT	p.R172C
Pat_15	Post-Resistance	TGFBRAP1	9392	37	2	105915093	105915093	Missense_Mutation	SNP	G	A	5	214	c.758C>T	c.(757-759)GCG>GTG	p.A253V
Pat_15	Post-Resistance	IL1A	3552	37	2	113539322	113539322	Missense_Mutation	SNP	A	T	102	226	c.178T>A	c.(178-180)TCT>ACT	p.S60T
Pat_15	Post-Resistance	ERCC3	2071	37	2	128044304	128044304	Missense_Mutation	SNP	G	C	6	517	c.1317C>G	c.(1315-1317)ATC>ATG	p.I439M
Pat_15	Post-Resistance	THSD7B	80731	37	2	137814051	137814051	Nonsense_Mutation	SNP	G	A	43	275	c.108G>A	c.(106-108)TGG>TGA	p.W36*
Pat_15	Post-Resistance	SCN1A	6323	37	2	166872167	166872167	Missense_Mutation	SNP	G	A	60	348	c.3467C>T	c.(3466-3468)CCC>CTC	p.P1156L
Pat_15	Post-Resistance	XIRP2	129446	37	2	168107398	168107398	Missense_Mutation	SNP	C	A	5	477	c.9496C>A	c.(9496-9498)CAC>AAC	p.H3166N
Pat_15	Post-Resistance	LRP2	4036	37	2	170092425	170092425	Missense_Mutation	SNP	C	T	60	202	c.4845G>A	c.(4843-4845)ATG>ATA	p.M1615I
Pat_15	Post-Resistance	SP3	6670	37	2	174819867	174819867	Missense_Mutation	SNP	G	A	52	152	c.1373C>T	c.(1372-1374)TCT>TTT	p.S458F
Pat_15	Post-Resistance	SP3	6670	37	2	174820401	174820401	Missense_Mutation	SNP	G	A	4	412	c.839C>T	c.(838-840)TCG>TTG	p.S280L
Pat_15	Post-Resistance	OSBPL6	114880	37	2	179236922	179236922	Nonsense_Mutation	SNP	C	T	55	215	c.1357C>T	c.(1357-1359)CAG>TAG	p.Q453*
Pat_15	Post-Resistance	TTN	7273	37	2	179472244	179472244	Missense_Mutation	SNP	C	T	94	716	c.45467G>A	.(45466-45468)GGA>GA	p.G15156E
Pat_15	Post-Resistance	TTN	7273	37	2	179579099	179579099	Missense_Mutation	SNP	G	A	5	344	c.22670C>T	c.(22669-22671)CCA>CTA	p.P7557L
Pat_15	Post-Resistance	TTN	7273	37	2	179611961	179611961	Missense_Mutation	SNP	C	T	27	205	c.15166G>A	.(15166-15168)GGG>AG	p.G5056R
Pat_15	Post-Resistance	ASNSD1	54529	37	2	190532243	190532243	Missense_Mutation	SNP	G	A	6	780	c.1385G>A	c.(1384-1386)TGT>TAT	p.C462Y
Pat_15	Post-Resistance	DNAH7	56171	37	2	196834754	196834754	Missense_Mutation	SNP	G	A	51	163	c.2123C>T	c.(2122-2124)TCA>TTA	p.S708L
Pat_15	Post-Resistance	ORC2L	4999	37	2	201785036	201785036	Missense_Mutation	SNP	A	C	57	160	c.1375T>G	c.(1375-1377)TCC>GCC	p.S459A
Pat_15	Post-Resistance	PARD3B	117583	37	2	206165386	206165386	Missense_Mutation	SNP	G	A	43	403	c.2318G>A	c.(2317-2319)CGA>CAA	p.R773Q
Pat_15	Post-Resistance	C2orf24	27013	37	2	220039772	220039772	Missense_Mutation	SNP	G	A	4	352	c.319C>T	c.(319-321)CGG>TGG	p.R107W
Pat_15	Post-Resistance	ABCB6	10058	37	2	220078321	220078322	Missense_Mutation	DNP	GT	AG	58	163	.1645_1646AC>C	c.(1645-1647)ACC>CTC	p.T549L
Pat_15	Post-Resistance	UGT1A8	54576	37	2	234527050	234527050	Missense_Mutation	SNP	G	A	133	726	c.697G>A	c.(697-699)GAA>AAA	p.E233K
Pat_15	Post-Resistance	ANGPT4	51378	37	20	896818	896818	Missense_Mutation	SNP	G	A	55	157	c.40C>T	c.(40-42)CTT>TTT	p.L14F
Pat_15	Post-Resistance	PROKR2	128674	37	20	5294778	5294778	Missense_Mutation	SNP	G	A	97	262	c.238C>T	c.(238-240)CGC>TGC	p.R80C
Pat_15	Post-Resistance	GPCPD1	56261	37	20	5550886	5550886	Splice_Site	SNP	C	A	4	215	c.1057_splice	c.e12-1	p.G353_splice
Pat_15	Post-Resistance	BMP2	650	37	20	6759302	6759302	Missense_Mutation	SNP	G	A	4	86	c.757G>A	c.(757-759)GAT>AAT	p.D253N

Pat_15	Post-Resistance	ISM1	140862	37	20	13273020	13273020	Splice_Site	SNP	G	A	16	53	c.788_splice	c.e5-1	p.G263_splice
Pat_15	Post-Resistance	SEL1L2	80343	37	20	13867031	13867031	Missense_Mutation	SNP	T	A	44	142	c.803A>T	c.(802-804)GAA>GTA	p.E268V
Pat_15	Post-Resistance	DEFB123	245936	37	20	30037844	30037844	Missense_Mutation	SNP	G	A	131	343	c.71G>A	c.(70-72)AGA>AAA	p.R24K
Pat_15	Post-Resistance	EPB41L1	2036	37	20	34785884	34785884	Missense_Mutation	SNP	G	A	100	271	c.1589G>A	c.(1588-1590)CGA>CAA	p.R530Q
Pat_15	Post-Resistance	SGK2	10110	37	20	42195107	42195107	Missense_Mutation	SNP	C	T	117	470	c.152C>T	c.(151-153)CCC>CTC	p.P51L
Pat_15	Post-Resistance	NCOA3	8202	37	20	46264358	46264358	Missense_Mutation	SNP	G	T	6	333	c.1405G>T	c.(1405-1407)GGG>TGG	p.G469W
Pat_15	Post-Resistance	SLCO4A1	28231	37	20	61288117	61288117	Missense_Mutation	SNP	G	A	4	185	c.311G>A	c.(310-312)GGC>GAC	p.G104D
Pat_15	Post-Resistance	SRMS	6725	37	20	62173897	62173897	Missense_Mutation	SNP	G	T	4	236	c.683C>A	c.(682-684)TCC>TAC	p.S228Y
Pat_15	Post-Resistance	ARFRP1	10139	37	20	62338413	62338413	Missense_Mutation	SNP	A	G	3	130	c.31T>C	c.(31-33)TAC>CAC	p.Y11H
Pat_15	Post-Resistance	NCAM2	4685	37	21	22664426	22664426	Missense_Mutation	SNP	C	T	60	218	c.484C>T	c.(484-486)CGG>TGG	p.R162W
Pat_15	Post-Resistance	RCAN1	1827	37	21	35893880	35893880	Missense_Mutation	SNP	G	A	27	96	c.503C>T	c.(502-504)CCG>CTG	p.P168L
Pat_15	Post-Resistance	CLDN14	23562	37	21	37833465	37833465	Missense_Mutation	SNP	C	T	61	217	c.529G>A	c.(529-531)GGT>AGT	p.G177S
Pat_15	Post-Resistance	TMPRSS3	64699	37	21	43795974	43795974	Missense_Mutation	SNP	C	T	49	430	c.1198G>A	c.(1198-1200)GAC>AAC	p.D400N
Pat_15	Post-Resistance	WDR4	10785	37	21	44282413	44282413	Missense_Mutation	SNP	G	A	14	83	c.545C>T	c.(544-546)TCC>TTC	p.S182F
Pat_15	Post-Resistance	LSS	4047	37	21	47614504	47614504	Missense_Mutation	SNP	C	T	4	178	c.1889G>A	c.(1888-1890)GGG>GAG	p.G630E
Pat_15	Post-Resistance	SEZ6L	23544	37	22	26761419	26761419	Missense_Mutation	SNP	G	A	47	248	c.2681G>A	c.(2680-2682)GGA>GAA	p.G894E
Pat_15	Post-Resistance	TRIOBP	11078	37	22	38121864	38121864	Missense_Mutation	SNP	C	T	175	504	c.3301C>T	c.(3301-3303)CCC>TCC	p.P1101S
Pat_15	Post-Resistance	MGAT3	4248	37	22	39884748	39884748	Missense_Mutation	SNP	G	A	13	88	c.1396G>A	c.(1396-1398)GAC>AAC	p.D466N
Pat_15	Post-Resistance	POLDIP3	84271	37	22	42998840	42998840	Missense_Mutation	SNP	G	A	5	553	c.386C>T	c.(385-387)GCT>GTT	p.A129V
Pat_15	Post-Resistance	MOV10L1	54456	37	22	50563983	50563983	Missense_Mutation	SNP	C	T	38	206	c.1732C>T	c.(1732-1734)CCT>TCT	p.P578S
Pat_15	Post-Resistance	CAV3	859	37	3	8787386	8787386	Missense_Mutation	SNP	T	C	3	117	c.289T>C	c.(289-291)TTC>CTC	p.F97L
Pat_15	Post-Resistance	BRPF1	7862	37	3	9776336	9776336	Missense_Mutation	SNP	G	A	4	322	c.512G>A	c.(511-513)AGC>AAC	p.S171N
Pat_15	Post-Resistance	XPC	7508	37	3	14190192	14190192	Missense_Mutation	SNP	G	T	5	297	c.2290C>A	c.(2290-2292)CCC>ACC	p.P764T
Pat_15	Post-Resistance	EOMES	8320	37	3	27761764	27761764	Missense_Mutation	SNP	G	A	96	626	c.934C>T	c.(934-936)CAC>TAC	p.H312Y
Pat_15	Post-Resistance	SCN5A	6331	37	3	38651383	38651383	Missense_Mutation	SNP	A	G	45	319	c.776T>C	c.(775-777)TTC>TCC	p.F259S
Pat_15	Post-Resistance	SCN10A	6336	37	3	38833541	38833541	Missense_Mutation	SNP	G	A	71	624	c.389C>T	c.(388-390)TCG>TTG	p.S130L
Pat_15	Post-Resistance	SCN11A	11280	37	3	38938485	38938485	Missense_Mutation	SNP	C	T	59	230	c.2254G>A	c.(2254-2256)GGG>AGG	p.G752R
Pat_15	Post-Resistance	CCR9	10803	37	3	45942900	45942900	Missense_Mutation	SNP	G	A	5	365	c.620G>A	c.(619-621)AGC>AAC	p.S207N
Pat_15	Post-Resistance	SHISA5	51246	37	3	48510919	48510919	Missense_Mutation	SNP	G	A	6	303	c.484C>T	c.(484-486)CCT>TCT	p.P162S
Pat_15	Post-Resistance	UBA7	7318	37	3	49845261	49845261	Missense_Mutation	SNP	G	T	6	121	c.2623C>A	c.(2623-2625)CCA>ACA	p.P875T
Pat_15	Post-Resistance	NAT6	24142	37	3	50334112	50334113	Missense_Mutation	DNP	GG	AA	73	211	c.782_783CC>TT	c.(781-783)CCC>CTT	p.P261L
Pat_15	Post-Resistance	GRM2	2912	37	3	51751789	51751789	Missense_Mutation	SNP	G	A	4	244	c.2501G>A	c.(2500-2502)CGC>CAC	p.R834H
Pat_15	Post-Resistance	GLYCTK	132158	37	3	52325843	52325843	Missense_Mutation	SNP	G	A	4	333	c.610G>A	c.(610-612)GCC>ACC	p.A204T
Pat_15	Post-Resistance	DNAH1	25981	37	3	52366226	52366226	Missense_Mutation	SNP	C	T	3	47	c.1102C>T	c.(1102-1104)CCT>TCT	p.P368S
Pat_15	Post-Resistance	DNAH1	25981	37	3	52396446	52396446	Missense_Mutation	SNP	C	T	36	109	c.5023C>T	c.(5023-5025)CCA>TCA	p.P1675S
Pat_15	Post-Resistance	BAP1	8314	37	3	52437720	52437720	Missense_Mutation	SNP	G	A	4	121	c.1441C>T	c.(1441-1443)CAC>TAC	p.H481Y
Pat_15	Post-Resistance	STAB1	23166	37	3	52555956	52555956	Missense_Mutation	SNP	G	A	4	214	c.6260G>A	c.(6259-6261)CGT>CAT	p.R2087H
Pat_15	Post-Resistance	SPATA12	353324	37	3	57108230	57108230	Nonsense_Mutation	SNP	G	T	6	717	c.508G>T	c.(508-510)GAG>TAG	p.E170*
Pat_15	Post-Resistance	NSUN3	63899	37	3	93813923	93813923	Missense_Mutation	SNP	C	T	47	414	c.668C>T	c.(667-669)TCT>TTT	p.S223F
Pat_15	Post-Resistance	OR5H15	403274	37	3	97888187	97888187	Missense_Mutation	SNP	T	C	20	48	c.644T>C	c.(643-645)CTT>CCT	p.L215P
Pat_15	Post-Resistance	OR5K1	26339	37	3	98189268	98189268	Missense_Mutation	SNP	C	T	29	123	c.848C>T	c.(847-849)CCC>CTC	p.P283L
Pat_15	Post-Resistance	GPR128	84873	37	3	100374026	100374026	Splice_Site	SNP	G	A	4	247	c.1726_splice	c.e12+1	p.G576_splice
Pat_15	Post-Resistance	ZBED2	79413	37	3	111312555	111312555	Missense_Mutation	SNP	C	T	171	402	c.494G>A	c.(493-495)AGG>AAG	p.R165K
Pat_15	Post-Resistance	KIAA2018	205717	37	3	113388981	113388981	Missense_Mutation	SNP	G	A	82	196	c.146C>T	c.(145-147)CCT>CTT	p.P49L
Pat_15	Post-Resistance	STXBP5L	9515	37	3	120957925	120957925	Missense_Mutation	SNP	C	T	32	166	c.1292C>T	c.(1291-1293)TCT>TTT	p.S431F
Pat_15	Post-Resistance	PARP14	54625	37	3	122411238	122411238	Missense_Mutation	SNP	C	T	90	155	c.446C>T	c.(445-447)TCT>TTT	p.S149F
Pat_15	Post-Resistance	COL6A6	131873	37	3	130287019	130287019	Missense_Mutation	SNP	C	T	117	603	c.1972C>T	c.(1972-1974)CGG>TGG	p.R658W

Pat_15	Post-Resistance	TMEM108	66000	37	3	133099154	133099154	Missense_Mutation	SNP	G	A	57	193	c.599G>A	c.(598-600)CGA>CAA	p.R200Q
Pat_15	Post-Resistance	PPP2R3A	5523	37	3	135820941	135820941	Missense_Mutation	SNP	G	A	4	330	c.3020G>A	c.(3019-3021)CGG>CAG	p.R1007Q
Pat_15	Post-Resistance	PRR23A	729627	37	3	138724642	138724642	Missense_Mutation	SNP	C	T	35	119	c.469G>A	c.(469-471)GAG>AAG	p.E157K
Pat_15	Post-Resistance	GK5	256356	37	3	141905075	141905075	Missense_Mutation	SNP	G	A	134	249	c.716C>T	c.(715-717)TCG>TTG	p.S239L
Pat_15	Post-Resistance	CHST2	9435	37	3	142840380	142840380	Missense_Mutation	SNP	G	A	4	180	c.722G>A	c.(721-723)GGG>GAG	p.G241E
Pat_15	Post-Resistance	CP	1356	37	3	148930484	148930484	Missense_Mutation	SNP	C	T	48	108	c.148G>A	c.(148-150)GAA>AAA	p.E50K
Pat_15	Post-Resistance	ZBBX	79740	37	3	167045887	167045887	Missense_Mutation	SNP	C	T	104	222	c.705G>A	c.(703-705)ATG>ATA	p.M235I
Pat_15	Post-Resistance	MECOM	2122	37	3	168833285	168833285	Missense_Mutation	SNP	C	T	38	145	c.1811G>A	c.(1810-1812)CGA>CAA	p.R604Q
Pat_15	Post-Resistance	EIF4G1	1981	37	3	184045084	184045084	Missense_Mutation	SNP	G	A	6	490	c.3509G>A	c.(3508-3510)CGT>CAT	p.R1170H
Pat_15	Post-Resistance	CHRD	8646	37	3	184100315	184100315	Missense_Mutation	SNP	G	A	6	562	c.838G>A	c.(838-840)GCA>ACA	p.A280T
Pat_15	Post-Resistance	TP63	8626	37	3	189608604	189608604	Missense_Mutation	SNP	C	T	120	304	c.1679C>T	c.(1678-1680)TCA>TTA	p.S560L
Pat_15	Post-Resistance	MUC4	4585	37	3	195495909	195495909	Missense_Mutation	SNP	G	A	4	227	c.13129C>T	c.(13129-13131)CTC>TTC	p.L4377F
Pat_15	Post-Resistance	ZNF141	7700	37	4	367194	367194	Missense_Mutation	SNP	C	T	5	237	c.968C>T	c.(967-969)TCC>TTC	p.S323F
Pat_15	Post-Resistance	ZNF141	7700	37	4	367226	367226	Missense_Mutation	SNP	A	G	3	189	c.1000A>G	c.(1000-1002)ACT>GCT	p.T334A
Pat_15	Post-Resistance	OTOP1	133060	37	4	4199303	4199303	Missense_Mutation	SNP	G	A	4	358	c.1258C>T	c.(1258-1260)CGC>TGC	p.R420C
Pat_15	Post-Resistance	SLC2A9	56606	37	4	10027572	10027572	Missense_Mutation	SNP	C	T	29	137	c.19G>A	c.(19-21)GAC>AAC	p.D7N
Pat_15	Post-Resistance	ZNF518B	85460	37	4	10445035	10445035	Missense_Mutation	SNP	A	G	34	284	c.2918T>C	c.(2917-2919)GTT>GCT	p.V973A
Pat_15	Post-Resistance	SLIT2	9353	37	4	20569198	20569198	Missense_Mutation	SNP	G	A	4	300	c.2908G>A	c.(2908-2910)GGA>AGA	p.G970R
Pat_15	Post-Resistance	FAM114A1	92689	37	4	38937371	38937371	Missense_Mutation	SNP	C	T	38	138	c.1496C>T	c.(1495-1497)TCT>TTT	p.S499F
Pat_15	Post-Resistance	YIPF7	285525	37	4	44624506	44624506	Missense_Mutation	SNP	C	T	50	128	c.768G>A	c.(766-768)ATG>ATA	p.M256I
Pat_15	Post-Resistance	SPATA18	132671	37	4	52945993	52945994	Missense_Mutation	DNP	GG	AA	134	430	.1263_1264GG>A	261-1266)CAGGAG>CAA	p.E422K
Pat_15	Post-Resistance	KDR	3791	37	4	55964878	55964878	Missense_Mutation	SNP	G	A	5	348	c.2359C>T	c.(2359-2361)CGG>TGG	p.R787W
Pat_15	Post-Resistance	ENAM	10117	37	4	71510004	71510004	Missense_Mutation	SNP	G	A	4	324	c.2861G>A	c.(2860-2862)AGG>AAG	p.R954K
Pat_15	Post-Resistance	CCDC158	339965	37	4	77288596	77288596	Missense_Mutation	SNP	C	T	70	174	c.1681G>A	c.(1681-1683)GAC>AAC	p.D561N
Pat_15	Post-Resistance	BMP2K	55589	37	4	79792085	79792085	Missense_Mutation	SNP	G	C	3	159	c.1380G>C	c.(1378-1380)CAG>CAC	p.Q460H
Pat_15	Post-Resistance	DAPP1	27071	37	4	100774378	100774378	Missense_Mutation	SNP	C	T	10	73	c.362C>T	c.(361-363)ACT>ATT	p.T121I
Pat_15	Post-Resistance	LEF1	51176	37	4	108985500	108985500	Missense_Mutation	SNP	G	A	67	160	c.1157C>T	c.(1156-1158)TCT>TTT	p.S386F
Pat_15	Post-Resistance	ANK2	287	37	4	114279594	114279594	Missense_Mutation	SNP	C	T	126	296	c.9820C>T	c.(9820-9822)CCC>TCC	p.P3274S
Pat_15	Post-Resistance	SYNPO2	171024	37	4	119947945	119947945	Missense_Mutation	SNP	C	T	69	150	c.421C>T	c.(421-423)CCC>TCC	p.P141S
Pat_15	Post-Resistance	KIAA0922	23240	37	4	154553895	154553895	Nonsense_Mutation	SNP	G	A	4	219	c.4230G>A	c.(4228-4230)TGG>TGA	p.W1410*
Pat_15	Post-Resistance	GALNTL6	442117	37	4	173730599	173730599	Missense_Mutation	SNP	G	T	5	280	c.641G>T	c.(640-642)CGG>CTG	p.R214L
Pat_15	Post-Resistance	WDR17	116966	37	4	177046428	177046428	Missense_Mutation	SNP	T	C	61	348	c.784T>C	c.(784-786)TTT>CTT	p.F262L
Pat_15	Post-Resistance	TRIML1	339976	37	4	189061099	189061099	Missense_Mutation	SNP	C	A	4	244	c.387C>A	c.(385-387)AGC>AGA	p.S129R
Pat_15	Post-Resistance	FAM173B	134145	37	5	10239375	10239376	Missense_Mutation	DNP	CC	TT	62	426	c.109_110GG>AA	c.(109-111)GGG>AAG	p.G37K
Pat_15	Post-Resistance	DNAH5	1767	37	5	13901435	13901435	Missense_Mutation	SNP	T	G	50	151	c.1978A>C	c.(1978-1980)ATT>CTT	p.I660L
Pat_15	Post-Resistance	C5orf42	65250	37	5	37183163	37183163	Missense_Mutation	SNP	C	A	6	271	c.5120G>T	c.(5119-5121)TGG>TTG	p.W1707L
Pat_15	Post-Resistance	TTC33	23548	37	5	40730441	40730441	Missense_Mutation	SNP	G	A	60	277	c.226C>T	c.(226-228)CGG>TGG	p.R76W
Pat_15	Post-Resistance	HCN1	348980	37	5	45303881	45303881	Missense_Mutation	SNP	C	T	127	474	c.1438G>A	c.(1438-1440)GAT>AAT	p.D480N
Pat_15	Post-Resistance	MARVELD2	153562	37	5	68728909	68728909	Missense_Mutation	SNP	G	A	140	490	c.1492G>A	c.(1492-1494)GAA>AAA	p.E498K
Pat_15	Post-Resistance	BDP1	55814	37	5	70838063	70838063	Missense_Mutation	SNP	C	T	41	161	c.6383C>T	c.(6382-6384)ACC>ATC	p.T2128I
Pat_15	Post-Resistance	ENC1	8507	37	5	73931196	73931196	Missense_Mutation	SNP	G	A	4	237	c.1115C>T	c.(1114-1116)GCC>GTC	p.A372V
Pat_15	Post-Resistance	F2RL1	2150	37	5	76129526	76129526	Missense_Mutation	SNP	G	A	7	722	c.1094G>A	c.(1093-1095)CGC>CAC	p.R365H
Pat_15	Post-Resistance	CMYA5	202333	37	5	79025094	79025094	Missense_Mutation	SNP	C	T	13	79	c.506C>T	c.(505-507)CCT>CTT	p.P169L
Pat_15	Post-Resistance	SPZ1	84654	37	5	79616947	79616947	Missense_Mutation	SNP	G	A	6	351	c.913G>A	c.(913-915)GAA>AAA	p.E305K
Pat_15	Post-Resistance	GPR98	84059	37	5	90086870	90086870	Missense_Mutation	SNP	G	A	27	74	c.14224G>A	c.(14224-14226)GAA>AAA	p.E4742K
Pat_15	Post-Resistance	FAM174A	345757	37	5	99871538	99871538	Missense_Mutation	SNP	G	A	4	137	c.304G>A	c.(304-306)GAA>AAA	p.E102K
Pat_15	Post-Resistance	FSTL4	23105	37	5	132535139	132535139	Missense_Mutation	SNP	T	C	3	400	c.2177A>G	c.(2176-2178)TAT>TGT	p.Y726C

Pat_15	Post-Resistance	NRG2	9542	37	5	139232080	139232080	Missense_Mutation	SNP	G	A	106	243	c.1481C>T	c.(1480-1482)TCT>TTT	p.S494F
Pat_15	Post-Resistance	PCDHB2	56133	37	5	140474559	140474559	Missense_Mutation	SNP	C	T	54	193	c.185C>T	c.(184-186)GCT>GTT	p.A62V
Pat_15	Post-Resistance	PCDHB8	56128	37	5	140559872	140559872	Missense_Mutation	SNP	G	A	98	336	c.2257G>A	c.(2257-2259)GAG>AAG	p.E753K
Pat_15	Post-Resistance	PCDHGB5	56101	37	5	140779112	140779112	Missense_Mutation	SNP	C	T	23	80	c.1418C>T	c.(1417-1419)TCG>TTG	p.S473L
Pat_15	Post-Resistance	YIPF5	81555	37	5	143545158	143545158	Missense_Mutation	SNP	C	A	5	451	c.121G>T	c.(121-123)GGC>TGC	p.G41C
Pat_15	Post-Resistance	PCYOX1L	78991	37	5	148742211	148742211	Missense_Mutation	SNP	G	C	4	268	c.100G>C	c.(100-102)GCT>CCT	p.A34P
Pat_15	Post-Resistance	PDGFRB	5159	37	5	149498342	149498342	Missense_Mutation	SNP	G	A	5	607	c.2872C>T	c.(2872-2874)CTC>TTC	p.L958F
Pat_15	Post-Resistance	C5orf40	408263	37	5	156770294	156770294	Missense_Mutation	SNP	G	A	103	384	c.251C>T	c.(250-252)CCT>CTT	p.P84L
Pat_15	Post-Resistance	DOCK2	1794	37	5	169472901	169472901	Missense_Mutation	SNP	C	A	6	397	c.3958C>A	c.(3958-3960)CAG>AAG	p.Q1320K
Pat_15	Post-Resistance	TSPAN17	26262	37	5	176079915	176079915	Splice_Site	SNP	G	A	5	378	c.456_splice	c.e4+1	p.Y152_splice
Pat_15	Post-Resistance	TMED9	54732	37	5	177020742	177020742	Missense_Mutation	SNP	C	T	147	544	c.377C>T	c.(376-378)TCC>TTC	p.S126F
Pat_15	Post-Resistance	ZNF454	285676	37	5	178392900	178392900	Missense_Mutation	SNP	A	G	3	277	c.1495A>G	c.(1495-1497)AAT>GAT	p.N499D
Pat_15	Post-Resistance	MGAT1	4245	37	5	180219454	180219454	Missense_Mutation	SNP	G	A	4	413	c.518C>T	c.(517-519)CCG>CTG	p.P173L
Pat_15	Post-Resistance	TRIM41	90933	37	5	180660728	180660728	Missense_Mutation	SNP	G	A	5	331	c.1256G>A	c.(1255-1257)AGG>AAG	p.R419K
Pat_15	Post-Resistance	SYCP2L	221711	37	6	10894172	10894172	Nonsense_Mutation	SNP	G	T	7	56	c.151G>T	c.(151-153)GAG>TAG	p.E51*
Pat_15	Post-Resistance	NEDD9	4739	37	6	11185787	11185787	Missense_Mutation	SNP	G	A	80	280	c.2113C>T	c.(2113-2115)CGG>TGG	p.R705W
Pat_15	Post-Resistance	C6orf105	84830	37	6	11766609	11766609	Splice_Site	SNP	C	T	35	197	c.289_splice	c.e3-1	p.F97_splice
Pat_15	Post-Resistance	HIVEP1	3096	37	6	12122375	12122375	Missense_Mutation	SNP	C	T	30	174	c.2347C>T	c.(2347-2349)CCC>TCC	p.P783S
Pat_15	Post-Resistance	OR12D3	81797	37	6	29343062	29343062	Missense_Mutation	SNP	C	T	25	74	c.3G>A	c.(1-3)ATG>ATA	p.M1I
Pat_15	Post-Resistance	OR2H1	26716	37	6	29430333	29430333	Missense_Mutation	SNP	C	T	33	321	c.787C>T	c.(787-789)CCG>TCG	p.P263S
Pat_15	Post-Resistance	UBD	10537	37	6	29524095	29524095	Missense_Mutation	SNP	C	T	59	146	c.60G>A	c.(58-60)ATG>ATA	p.M20I
Pat_15	Post-Resistance	MDC1	9656	37	6	30673061	30673061	Missense_Mutation	SNP	G	A	6	757	c.3899C>T	c.(3898-3900)CCT>CTT	p.P1300L
Pat_15	Post-Resistance	CCHCR1	54535	37	6	31116267	31116267	Missense_Mutation	SNP	G	A	4	217	c.1228C>T	c.(1228-1230)CGT>TGT	p.R410C
Pat_15	Post-Resistance	WDR46	9277	37	6	33255136	33255136	Missense_Mutation	SNP	G	A	4	246	c.875C>T	c.(874-876)ACA>ATA	p.T292I
Pat_15	Post-Resistance	SCUBE3	222663	37	6	35195465	35195465	Missense_Mutation	SNP	G	A	4	206	c.194G>A	c.(193-195)GGC>GAC	p.G65D
Pat_15	Post-Resistance	RNF8	9025	37	6	37358522	37358522	Missense_Mutation	SNP	G	C	4	216	c.1446G>C	c.(1444-1446)AAG>AAC	p.K482N
Pat_15	Post-Resistance	DNAH8	1769	37	6	38750805	38750805	Missense_Mutation	SNP	C	T	36	143	c.1634C>T	c.(1633-1635)CCG>CTG	p.P545L
Pat_15	Post-Resistance	TTBK1	84630	37	6	43251530	43251530	Missense_Mutation	SNP	C	T	17	159	c.3052C>T	c.(3052-3054)CCG>TCG	p.P1018S
Pat_15	Post-Resistance	GPR116	221395	37	6	46834662	46834662	Missense_Mutation	SNP	C	T	43	134	c.1834G>A	c.(1834-1836)GCA>ACA	p.A612T
Pat_15	Post-Resistance	FBXO9	26268	37	6	52947334	52947334	Nonsense_Mutation	SNP	C	T	4	285	c.601C>T	c.(601-603)CGA>TGA	p.R201*
Pat_15	Post-Resistance	BMP5	653	37	6	55659083	55659083	Missense_Mutation	SNP	C	T	24	169	c.826G>A	c.(826-828)GGG>AGG	p.G276R
Pat_15	Post-Resistance	COL12A1	1303	37	6	75807004	75807004	Missense_Mutation	SNP	C	A	4	348	c.8542G>T	c.(8542-8544)GGT>TGT	p.G2848C
Pat_15	Post-Resistance	MDN1	23195	37	6	90400405	90400406	Missense_Mutation	DNP	GG	AA	60	182	10735_10736CC>	c.(10735-10737)CCC>TTC	p.P3579F
Pat_15	Post-Resistance	BACH2	60468	37	6	90642342	90642342	Missense_Mutation	SNP	C	T	22	89	c.2311G>A	c.(2311-2313)GAG>AAG	p.E771K
Pat_15	Post-Resistance	EPHA7	2045	37	6	94066675	94066675	Missense_Mutation	SNP	C	T	21	273	c.1084G>A	c.(1084-1086)GAT>AAT	p.D362N
Pat_15	Post-Resistance	ASCC3	10973	37	6	101215121	101215121	Missense_Mutation	SNP	G	A	5	442	c.1496C>T	c.(1495-1497)GCC>GTC	p.A499V
Pat_15	Post-Resistance	WASF1	8936	37	6	110423000	110423000	Missense_Mutation	SNP	C	T	8	562	c.1313G>A	c.(1312-1314)CGA>CAA	p.R438Q
Pat_15	Post-Resistance	RFX6	222546	37	6	117248274	117248274	Missense_Mutation	SNP	A	C	36	446	c.1970A>C	c.(1969-1971)AAC>ACC	p.N657T
Pat_15	Post-Resistance	KIAA1244	57221	37	6	138584659	138584659	Missense_Mutation	SNP	T	G	23	153	c.2039T>G	c.(2038-2040)CTG>CGG	p.L680R
Pat_15	Post-Resistance	HECA	51696	37	6	139488098	139488098	Missense_Mutation	SNP	T	A	37	257	c.949T>A	c.(949-951)TTC>ATC	p.F317I
Pat_15	Post-Resistance	TIAM2	26230	37	6	155504535	155504535	Missense_Mutation	SNP	G	A	91	228	c.2965G>A	c.(2965-2967)GAC>AAC	p.D989N
Pat_15	Post-Resistance	SLC22A3	6581	37	6	160831795	160831795	Missense_Mutation	SNP	C	T	40	253	c.892C>T	c.(892-894)CGG>TGG	p.R298W
Pat_15	Post-Resistance	STK31	56164	37	7	23809328	23809328	Missense_Mutation	SNP	G	A	90	416	c.1666G>A	c.(1666-1668)GAG>AAG	p.E556K
Pat_15	Post-Resistance	ADCYAP1R1	117	37	7	31117659	31117659	Missense_Mutation	SNP	G	A	69	404	c.211G>A	c.(211-213)GAG>AAG	p.E71K
Pat_15	Post-Resistance	TXNDC3	51314	37	7	37924797	37924797	Nonsense_Mutation	SNP	G	A	24	132	c.1190G>A	c.(1189-1191)TGG>TAG	p.W397*
Pat_15	Post-Resistance	POU6F2	11281	37	7	39379598	39379598	Missense_Mutation	SNP	C	A	7	464	c.869C>A	c.(868-870)CCA>CAA	p.P290Q
Pat_15	Post-Resistance	LANCL2	55915	37	7	55459549	55459549	Missense_Mutation	SNP	G	A	4	351	c.268G>A	c.(268-270)GAA>AAA	p.E90K

Pat_15	Post-Resistance	ZNF479	90827	37	7	57187720	57187720	Missense_Mutation	SNP	C	T	61	342	c.1402G>A	c.(1402-1404)GAA>AAA	p.E468K
Pat_15	Post-Resistance	ZNF727	442319	37	7	63538638	63538638	Missense_Mutation	SNP	G	C	4	80	c.1211G>C	c.(1210-1212)AGC>ACC	p.S404T
Pat_15	Post-Resistance	ZNF679	168417	37	7	63726725	63726725	Missense_Mutation	SNP	A	C	18	126	c.714A>C	c.(712-714)AAA>AAC	p.K238N
Pat_15	Post-Resistance	MAGI2	9863	37	7	77973134	77973134	Missense_Mutation	SNP	G	A	69	191	c.1369C>T	c.(1369-1371)CCG>TCG	p.P457S
Pat_15	Post-Resistance	ABCB4	5244	37	7	87083905	87083905	Missense_Mutation	SNP	T	G	31	77	c.290A>C	c.(289-291)AAC>ACC	p.N97T
Pat_15	Post-Resistance	ZNF804B	219578	37	7	88963666	88963666	Nonsense_Mutation	SNP	G	A	77	177	c.1370G>A	c.(1369-1371)TGG>TAG	p.W457*
Pat_15	Post-Resistance	ZNF804B	219578	37	7	88964142	88964142	Missense_Mutation	SNP	G	C	38	102	c.1846G>C	c.(1846-1848)GCA>CCA	p.A616P
Pat_15	Post-Resistance	TRRAP	8295	37	7	98602945	98602945	Missense_Mutation	SNP	C	T	40	231	c.10685C>T	c.(10684-10686)ACC>ATC	p.T3562I
Pat_15	Post-Resistance	ZAN	7455	37	7	100350361	100350361	Missense_Mutation	SNP	T	C	9	453	c.2633T>C	c.(2632-2634)CTC>CCC	p.L878P
Pat_15	Post-Resistance	MUC17	140453	37	7	100684677	100684677	Missense_Mutation	SNP	G	A	7	851	c.9980G>A	c.(9979-9981)GGT>GAT	p.G3327D
Pat_15	Post-Resistance	DPY19L2P2	349152	37	7	102825947	102825947	Missense_Mutation	SNP	A	G	5	320	c.1048T>C	c.(1048-1050)TGT>CGT	p.C350R
Pat_15	Post-Resistance	RELN	5649	37	7	103155634	103155634	Missense_Mutation	SNP	G	A	35	127	c.8117C>T	c.(8116-8118)TCA>TTA	p.S2706L
Pat_15	Post-Resistance	CADPS2	93664	37	7	121960292	121960292	Missense_Mutation	SNP	G	T	5	360	c.3818C>A	c.(3817-3819)ACA>AAA	p.T1273K
Pat_15	Post-Resistance	GPR37	2861	37	7	124386991	124386991	Missense_Mutation	SNP	G	A	5	469	c.1430C>T	c.(1429-1431)ACC>ATC	p.T477I
Pat_15	Post-Resistance	FLNC	2318	37	7	128494136	128494136	Missense_Mutation	SNP	G	A	4	132	c.6593G>A	c.(6592-6594)GGC>GAC	p.G2198D
Pat_15	Post-Resistance	BRAF	673	37	7	140453136	140453136	Missense_Mutation	SNP	A	T	740	148	c.1799T>A	c.(1798-1800)GTG>GAG	p.V600E
Pat_15	Post-Resistance	FAM115C	285966	37	7	143421630	143421630	Missense_Mutation	SNP	G	T	7	58	c.2345G>T	c.(2344-2346)TGG>TTG	p.W782L
Pat_15	Post-Resistance	OR2F2	135948	37	7	143632858	143632858	Missense_Mutation	SNP	C	T	45	259	c.533C>T	c.(532-534)TCC>TTC	p.S178F
Pat_15	Post-Resistance	CNTNAP2	26047	37	7	146805370	146805370	Missense_Mutation	SNP	G	A	44	138	c.682G>A	c.(682-684)GGA>AGA	p.G228R
Pat_15	Post-Resistance	GIMAP8	155038	37	7	150171171	150171171	Missense_Mutation	SNP	C	T	136	393	c.754C>T	c.(754-756)CTT>TTT	p.L252F
Pat_15	Post-Resistance	NOS3	4846	37	7	150698472	150698472	Missense_Mutation	SNP	G	A	44	184	c.1387G>A	c.(1387-1389)GAG>AAG	p.E463K
Pat_15	Post-Resistance	PAXIP1	22976	37	7	154774994	154774994	Missense_Mutation	SNP	C	A	24	87	c.373G>T	c.(373-375)GGG>TGG	p.G125W
Pat_15	Post-Resistance	SPAG11B	10407	37	8	7320378	7320378	Missense_Mutation	SNP	G	A	78	419	c.65C>T	c.(64-66)TCG>TTG	p.S22L
Pat_15	Post-Resistance	STC1	6781	37	8	23708930	23708930	Missense_Mutation	SNP	C	T	141	318	c.376G>A	c.(376-378)GAA>AAA	p.E126K
Pat_15	Post-Resistance	ADAMDEC1	27299	37	8	24251634	24251634	Missense_Mutation	SNP	G	A	24	220	c.337G>A	c.(337-339)GAA>AAA	p.E113K
Pat_15	Post-Resistance	ZNF703	80139	37	8	37556061	37556061	Missense_Mutation	SNP	T	C	3	129	c.1642T>C	c.(1642-1644)TAT>CAT	p.Y548H
Pat_15	Post-Resistance	ADAM18	8749	37	8	39537690	39537690	Missense_Mutation	SNP	C	T	13	139	c.1766C>T	c.(1765-1767)TCA>TTA	p.S589L
Pat_15	Post-Resistance	SGK196	84197	37	8	42958806	42958806	Missense_Mutation	SNP	G	T	5	624	c.115G>T	c.(115-117)GAC>TAC	p.D39Y
Pat_15	Post-Resistance	NSMAF	8439	37	8	59496726	59496726	Missense_Mutation	SNP	C	G	4	455	c.2693G>C	c.(2692-2694)TGT>TCT	p.C898S
Pat_15	Post-Resistance	DCAF4L2	138009	37	8	88886025	88886025	Missense_Mutation	SNP	C	T	71	198	c.175G>A	c.(175-177)GTC>ATC	p.V59I
Pat_15	Post-Resistance	NECAB1	64168	37	8	91893351	91893351	Missense_Mutation	SNP	C	A	3	39	c.350C>A	c.(349-351)ACA>AAA	p.T117K
Pat_15	Post-Resistance	HRSP12	10247	37	8	99116755	99116755	Missense_Mutation	SNP	G	A	69	243	c.313C>T	c.(313-315)CCT>TCT	p.P105S
Pat_15	Post-Resistance	GRHL2	79977	37	8	102643916	102643916	Missense_Mutation	SNP	G	A	31	121	c.1309G>A	c.(1309-1311)GGG>AGG	p.G437R
Pat_15	Post-Resistance	SNTB1	6641	37	8	121823920	121823920	Missense_Mutation	SNP	G	A	5	235	c.164C>T	c.(163-165)GCG>GTG	p.A55V
Pat_15	Post-Resistance	FAM135B	51059	37	8	139163688	139163688	Missense_Mutation	SNP	C	T	21	141	c.3030G>A	c.(3028-3030)ATG>ATA	p.M1010I
Pat_15	Post-Resistance	BAI1	575	37	8	143603440	143603440	Missense_Mutation	SNP	C	T	4	181	c.3139C>T	c.(3139-3141)CGC>TGC	p.R1047C
Pat_15	Post-Resistance	ZNF250	58500	37	8	146107447	146107447	Missense_Mutation	SNP	C	T	5	251	c.1136G>A	c.(1135-1137)CGC>CAC	p.R379H
Pat_15	Post-Resistance	FAM122A	116224	37	9	71395823	71395823	Missense_Mutation	SNP	G	A	5	775	c.743G>A	c.(742-744)AGC>AAC	p.S248N
Pat_15	Post-Resistance	APBA1	320	37	9	72131644	72131644	Missense_Mutation	SNP	C	T	15	71	c.483G>A	c.(481-483)ATG>ATA	p.M161I
Pat_15	Post-Resistance	PCSK5	5125	37	9	78601135	78601136	Missense_Mutation	DNP	CC	TT	87	313	c.385_386CC>TT	c.(385-387)CCC>TTC	p.P129F
Pat_15	Post-Resistance	SLC35D2	11046	37	9	99113404	99113404	Missense_Mutation	SNP	C	T	4	345	c.469G>A	c.(469-471)GGG>AGG	p.G157R
Pat_15	Post-Resistance	OR1L4	254973	37	9	125487162	125487162	Missense_Mutation	SNP	G	A	20	151	c.894G>A	c.(892-894)ATG>ATA	p.M298I
Pat_15	Post-Resistance	LRSAM1	90678	37	9	130241662	130241662	Nonsense_Mutation	SNP	G	T	5	303	c.781G>T	c.(781-783)GAA>TAA	p.E261*
Pat_15	Post-Resistance	IER5L	389792	37	9	131939665	131939665	Missense_Mutation	SNP	G	A	20	26	c.667C>T	c.(667-669)CCG>TCG	p.P223S
Pat_15	Post-Resistance	LAMC3	10319	37	9	133907487	133907487	Missense_Mutation	SNP	G	A	74	418	c.734G>A	c.(733-735)GGG>GAG	p.G245E
Pat_15	Post-Resistance	COL5A1	1289	37	9	137701066	137701066	Missense_Mutation	SNP	G	A	7	25	c.3404G>A	c.(3403-3405)GGT>GAT	p.G1135D
Pat_15	Post-Resistance	NELF	26012	37	9	140343925	140343925	Missense_Mutation	SNP	G	A	5	184	c.1514C>T	c.(1513-1515)ACG>ATG	p.T505M

Pat_15	Post-Resistance	IL3RA	3563	37	X	1497566	1497566	Missense_Mutation	SNP	G	A	12	112	c.889G>A	c.(889-891)GAG>AAG	p.E297K
Pat_15	Post-Resistance	MXRA5	25878	37	X	3240542	3240542	Missense_Mutation	SNP	C	T	109	272	c.3184G>A	c.(3184-3186)GAG>AAG	p.E1062K
Pat_15	Post-Resistance	FAM9B	171483	37	X	8995964	8995964	Missense_Mutation	SNP	C	T	43	310	c.437G>A	c.(436-438)AGT>AAT	p.S146N
Pat_15	Post-Resistance	MAGEB1	4112	37	X	30269273	30269273	Nonsense_Mutation	SNP	G	A	14	75	c.663G>A	c.(661-663)TGG>TGA	p.W221*
Pat_15	Post-Resistance	RPGR	6103	37	X	38146469	38146469	Missense_Mutation	SNP	C	T	14	74	c.1783G>A	c.(1783-1785)GAT>AAT	p.D595N
Pat_15	Post-Resistance	RBM10	8241	37	X	47032530	47032530	Missense_Mutation	SNP	C	T	4	295	c.436C>T	c.(436-438)CGT>TGT	p.R146C
Pat_15	Post-Resistance	SSX5	6758	37	X	48051681	48051681	Missense_Mutation	SNP	C	T	226	540	c.317G>A	c.(316-318)GGA>GAA	p.G106E
Pat_15	Post-Resistance	TBC1D25	4943	37	X	48417570	48417570	Nonsense_Mutation	SNP	C	T	28	159	c.541C>T	c.(541-543)CAA>TAA	p.Q181*
Pat_15	Post-Resistance	HDAC6	10013	37	X	48664806	48664806	Missense_Mutation	SNP	C	A	5	287	c.469C>A	c.(469-471)CAG>AAG	p.Q157K
Pat_15	Post-Resistance	FOXP3	50943	37	X	49113925	49113925	Missense_Mutation	SNP	G	A	20	151	c.413C>T	c.(412-414)ACT>ATT	p.T138I
Pat_15	Post-Resistance	DGKK	139189	37	X	50121099	50121099	Missense_Mutation	SNP	G	A	86	306	c.3109C>T	c.(3109-3111)CGG>TGG	p.R1037W
Pat_15	Post-Resistance	BMP15	9210	37	X	50659560	50659560	Missense_Mutation	SNP	T	C	120	394	c.1132T>C	c.(1132-1134)TAC>CAC	p.Y378H
Pat_15	Post-Resistance	SPANXN5	494197	37	X	52826389	52826389	Splice_Site	SNP	G	A	100	374	c.1_splice	c.e1-1	p.M1_splice
Pat_15	Post-Resistance	IQSEC2	23096	37	X	53279908	53279908	Missense_Mutation	SNP	C	T	5	126	c.1850G>A	c.(1849-1851)CGC>CAC	p.R617H
Pat_15	Post-Resistance	NHSL2	340527	37	X	71359877	71359877	Missense_Mutation	SNP	G	A	15	91	c.2479G>A	c.(2479-2481)GAC>AAC	p.D827N
Pat_15	Post-Resistance	RPS6KA6	27330	37	X	83319404	83319404	Missense_Mutation	SNP	T	C	18	99	c.2119A>G	c.(2119-2121)ATG>GTG	p.M707V
Pat_15	Post-Resistance	BTK	695	37	X	100617183	100617183	Missense_Mutation	SNP	G	A	5	436	c.566C>T	c.(565-567)CCC>CTC	p.P189L
Pat_15	Post-Resistance	MORF4L2	9643	37	X	102931453	102931453	Nonsense_Mutation	SNP	G	T	5	459	c.503C>A	c.(502-504)TCG>TAG	p.S168*
Pat_15	Post-Resistance	TEX13A	56157	37	X	104463861	104463861	Missense_Mutation	SNP	A	G	3	233	c.1015T>C	c.(1015-1017)TTT>CTT	p.F339L
Pat_15	Post-Resistance	NRK	203447	37	X	105150405	105150405	Splice_Site	SNP	A	G	2	32	c.846_splice	c.e11-2	p.W282_splice
Pat_15	Post-Resistance	CLDN2	9075	37	X	106171813	106171813	Missense_Mutation	SNP	G	A	5	375	c.355G>A	c.(355-357)GTA>ATA	p.V119I
Pat_15	Post-Resistance	WDR44	54521	37	X	117566799	117566799	Missense_Mutation	SNP	G	A	86	654	c.1793G>A	c.(1792-1794)CGG>CAG	p.R598Q
Pat_15	Post-Resistance	AKAP14	158798	37	X	119048663	119048663	Missense_Mutation	SNP	A	T	19	115	c.263A>T	c.(262-264)AAG>ATG	p.K88M
Pat_15	Post-Resistance	UTP14A	10813	37	X	129041393	129041393	Missense_Mutation	SNP	A	G	32	242	c.77A>G	c.(76-78)TAC>TGC	p.Y26C
Pat_15	Post-Resistance	RBMX2	51634	37	X	129546533	129546533	Missense_Mutation	SNP	C	T	34	214	c.680C>T	c.(679-681)TCC>TTC	p.S227F
Pat_15	Post-Resistance	MBNL3	55796	37	X	131526325	131526325	Missense_Mutation	SNP	G	A	4	226	c.380C>T	c.(379-381)CCT>CTT	p.P127L
Pat_15	Post-Resistance	GPC3	2719	37	X	132670264	132670265	Nonsense_Mutation	DNP	GG	TA	85	306	.1630_1631CC>T	c.(1630-1632)CCG>TAG	p.P544*
Pat_15	Post-Resistance	BRS3	680	37	X	135572476	135572476	Missense_Mutation	SNP	C	T	18	146	c.619C>T	c.(619-621)CCT>TCT	p.P207S
Pat_15	Post-Resistance	FGF13	2258	37	X	137715099	137715099	Missense_Mutation	SNP	C	T	64	349	c.650G>A	c.(649-651)CGA>CAA	p.R217Q
Pat_15	Post-Resistance	MAGEA3	4102	37	X	151935794	151935794	Nonsense_Mutation	SNP	G	A	203	447	c.373C>T	c.(373-375)CGA>TGA	p.R125*
Pat_15	Post-Resistance	SPRY3	10251	37	X	155004072	155004072	Missense_Mutation	SNP	G	A	67	495	c.539G>A	c.(538-540)AGC>AAC	p.S180N
Pat_15	Post-Resistance	SPRY3	10251	37	X	155004080	155004080	Missense_Mutation	SNP	G	C	62	486	c.547G>C	c.(547-549)GAT>CAT	p.D183H
Pat_26	Pre-Treatment	CCNL2	81669	37	1	1326156	1326156	Missense_Mutation	SNP	C	T	6	363	c.749G>A	c.(748-750)CGG>CAG	p.R250Q
Pat_26	Pre-Treatment	NADK	65220	37	1	1687996	1687996	Missense_Mutation	SNP	C	T	4	168	c.445G>A	c.(445-447)GCC>ACC	p.A149T
Pat_26	Pre-Treatment	CHD5	26038	37	1	6208967	6208967	Missense_Mutation	SNP	T	A	153	246	c.1330A>T	c.(1330-1332)AAC>TAC	p.N444Y
Pat_26	Pre-Treatment	RPL22	6146	37	1	6253023	6253023	Missense_Mutation	SNP	A	G	69	155	c.209T>C	c.(208-210)ATC>ACC	p.I70T
Pat_26	Pre-Treatment	CLSTN1	22883	37	1	9804587	9804587	Missense_Mutation	SNP	C	T	60	99	c.1100G>A	c.(1099-1101)GGC>GAC	p.G367D
Pat_26	Pre-Treatment	CLCN6	1185	37	1	11896071	11896071	Missense_Mutation	SNP	C	T	4	185	c.1841C>T	c.(1840-1842)CCG>CTG	p.P614L
Pat_26	Pre-Treatment	PRAMEF12	390999	37	1	12835134	12835134	Missense_Mutation	SNP	G	A	63	118	c.124G>A	c.(124-126)GAG>AAG	p.E42K
Pat_26	Pre-Treatment	RSC1A1	6248	37	1	15988098	15988098	Missense_Mutation	SNP	C	T	6	579	c.1735C>T	c.(1735-1737)CGC>TGC	p.R579C
Pat_26	Pre-Treatment	CLCNKB	1188	37	1	16372179	16372179	Missense_Mutation	SNP	G	A	4	173	c.227G>A	c.(226-228)CGA>CAA	p.R76Q
Pat_26	Pre-Treatment	CLCNKB	1188	37	1	16382951	16382951	Missense_Mutation	SNP	C	T	219	511	c.1964C>T	c.(1963-1965)TCC>TTC	p.S655F
Pat_26	Pre-Treatment	HTR6	3362	37	1	20005079	20005079	Missense_Mutation	SNP	C	T	69	127	c.734C>T	c.(733-735)CCA>CTA	p.P245L
Pat_26	Pre-Treatment	RAP1GAP	5909	37	1	21924548	21924548	Missense_Mutation	SNP	C	T	4	43	c.1889G>A	c.(1888-1890)CGA>CAA	p.R630Q
Pat_26	Pre-Treatment	HSPG2	3339	37	1	22166016	22166016	Missense_Mutation	SNP	G	A	68	87	c.9737C>T	c.(9736-9738)TCC>TTC	p.S3246F
Pat_26	Pre-Treatment	HSPG2	3339	37	1	22201165	22201165	Missense_Mutation	SNP	G	A	4	63	c.3472C>T	c.(3472-3474)CGC>TGC	p.R1158C
Pat_26	Pre-Treatment	HSPG2	3339	37	1	22207917	22207917	Missense_Mutation	SNP	T	C	243	424	c.1733A>G	c.(1732-1734)CAC>CGC	p.H578R

Pat_26	Pre-Treatment	WDTC1	23038	37	1	27627806	27627806	Missense_Mutation	SNP	G	A	5	276	c.1322G>A	c.(1321-1323)CGC>CAC	p.R441H
Pat_26	Pre-Treatment	MAP3K6	9064	37	1	27690481	27690481	Missense_Mutation	SNP	C	T	4	118	c.791G>A	c.(790-792)CGG>CAG	p.R264Q
Pat_26	Pre-Treatment	GMEB1	10691	37	1	29019522	29019522	Nonsense_Mutation	SNP	G	A	81	162	c.435G>A	c.(433-435)TGG>TGA	p.W145*
Pat_26	Pre-Treatment	GMEB1	10691	37	1	29029024	29029024	Missense_Mutation	SNP	G	A	4	165	c.703G>A	c.(703-705)GCT>ACT	p.A235T
Pat_26	Pre-Treatment	ZBTB8A	653121	37	1	33065841	33065841	Missense_Mutation	SNP	G	A	3	22	c.1147G>A	c.(1147-1149)GCT>ACT	p.A383T
Pat_26	Pre-Treatment	KIAA0754	643314	37	1	39879250	39879250	Missense_Mutation	SNP	A	G	4	59	c.3313A>G	c.(3313-3315)ACC>GCC	p.T1105A
Pat_26	Pre-Treatment	ZSWIM5	57643	37	1	45485767	45485767	Missense_Mutation	SNP	C	T	5	153	c.2666G>A	c.(2665-2667)CGA>CAA	p.R889Q
Pat_26	Pre-Treatment	ZSWIM5	57643	37	1	45500051	45500051	Nonsense_Mutation	SNP	C	T	158	295	c.2382G>A	c.(2380-2382)TGG>TGA	p.W794*
Pat_26	Pre-Treatment	CYP4A11	1579	37	1	47399864	47399864	Missense_Mutation	SNP	C	T	35	53	c.1072G>A	c.(1072-1074)GGA>AGA	p.G358R
Pat_26	Pre-Treatment	TAL1	6886	37	1	47691430	47691430	Missense_Mutation	SNP	G	A	3	24	c.131C>T	c.(130-132)GCG>GTG	p.A44V
Pat_26	Pre-Treatment	CYB5RL	606495	37	1	54653410	54653411	Missense_Mutation	DNP	CC	TT	24	101	c.349_350GG>AA	c.(349-351)GGG>AAG	p.G117K
Pat_26	Pre-Treatment	KANK4	163782	37	1	62739144	62739145	Missense_Mutation	DNP	CC	TT	29	78	.1631_1632GG>A	c.(1630-1632)GGG>GAA	p.G544E
Pat_26	Pre-Treatment	LEPR	3953	37	1	66075751	66075751	Nonsense_Mutation	SNP	G	A	117	190	c.1874G>A	c.(1873-1875)TGG>TAG	p.W625*
Pat_26	Pre-Treatment	C1orf173	127254	37	1	75055569	75055569	Missense_Mutation	SNP	T	G	57	91	c.1922A>C	c.(1921-1923)GAA>GCA	p.E641A
Pat_26	Pre-Treatment	CLCA4	22802	37	1	87025931	87025931	Missense_Mutation	SNP	G	A	126	183	c.338G>A	c.(337-339)AGA>AAA	p.R113K
Pat_26	Pre-Treatment	CCBL2	56267	37	1	89420900	89420900	Missense_Mutation	SNP	G	A	51	82	c.796C>T	c.(796-798)CCA>TCA	p.P266S
Pat_26	Pre-Treatment	DBT	1629	37	1	100715333	100715334	Missense_Mutation	DNP	CC	TT	130	262	c.43_44GG>AA	c.(43-45)GGG>AAG	p.G15K
Pat_26	Pre-Treatment	COL11A1	1301	37	1	103488309	103488309	Missense_Mutation	SNP	T	C	69	92	c.1234A>G	c.(1234-1236)ACA>GCA	p.T412A
Pat_26	Pre-Treatment	EPS8L3	79574	37	1	110301230	110301230	Missense_Mutation	SNP	C	T	31	72	c.517G>A	c.(517-519)GAA>AAA	p.E173K
Pat_26	Pre-Treatment	CHIA	27159	37	1	111862000	111862000	Missense_Mutation	SNP	G	A	24	82	c.1087G>A	c.(1087-1089)GAT>AAT	p.D363N
Pat_26	Pre-Treatment	NBPF7	343505	37	1	120381953	120381953	Missense_Mutation	SNP	T	C	7	420	c.692A>G	c.(691-693)TAT>TGT	p.Y231C
Pat_26	Pre-Treatment	C1orf51	148523	37	1	150255843	150255843	Missense_Mutation	SNP	C	T	7	541	c.166C>T	c.(166-168)CGG>TGG	p.R56W
Pat_26	Pre-Treatment	SETDB1	9869	37	1	150933578	150933578	Missense_Mutation	SNP	G	A	4	190	c.3040G>A	c.(3040-3042)GCT>ACT	p.A1014T
Pat_26	Pre-Treatment	TCHHL1	126637	37	1	152058977	152058977	Missense_Mutation	SNP	C	T	71	162	c.1181G>A	c.(1180-1182)AGG>AAG	p.R394K
Pat_26	Pre-Treatment	TCHH	7062	37	1	152084545	152084546	Missense_Mutation	DNP	AG	TC	4	68	.1147_1148CT>G	c.(1147-1149)CTG>GAG	p.L383E
Pat_26	Pre-Treatment	HRNR	388697	37	1	152188190	152188191	Missense_Mutation	DNP	CC	TT	46	789	.5914_5915GG>A	c.(5914-5916)GGG>AAG	p.G1972K
Pat_26	Pre-Treatment	IVL	3713	37	1	152882733	152882733	Missense_Mutation	SNP	G	A	15	31	c.460G>A	c.(460-462)GAG>AAG	p.E154K
Pat_26	Pre-Treatment	SHC1	6464	37	1	154941887	154941887	Missense_Mutation	SNP	G	A	4	160	c.533C>T	c.(532-534)GCC>GTC	p.A178V
Pat_26	Pre-Treatment	PKLR	5313	37	1	155264330	155264330	Missense_Mutation	SNP	G	A	4	167	c.908C>T	c.(907-909)CCG>CTG	p.P303L
Pat_26	Pre-Treatment	UBQLN4	56893	37	1	156023426	156023426	Missense_Mutation	SNP	T	C	44	58	c.67A>G	c.(67-69)AAG>GAG	p.K23E
Pat_26	Pre-Treatment	SLC25A44	9673	37	1	156177775	156177775	Missense_Mutation	SNP	C	T	61	141	c.724C>T	c.(724-726)CCC>TCC	p.P242S
Pat_26	Pre-Treatment	IQGAP3	128239	37	1	156526371	156526371	Missense_Mutation	SNP	G	A	35	100	c.1244C>T	c.(1243-1245)TCG>TTG	p.S415L
Pat_26	Pre-Treatment	OR10K1	391109	37	1	158435545	158435545	Missense_Mutation	SNP	T	C	124	203	c.194T>C	c.(193-195)ATC>ACC	p.I65T
Pat_26	Pre-Treatment	SPTA1	6708	37	1	158637692	158637692	Missense_Mutation	SNP	A	G	9	41	c.1994T>C	c.(1993-1995)GTT>GCT	p.V665A
Pat_26	Pre-Treatment	SLAMF9	89886	37	1	159922273	159922273	Missense_Mutation	SNP	C	T	155	338	c.443G>A	c.(442-444)GGT>GAT	p.G148D
Pat_26	Pre-Treatment	FAM5B	57795	37	1	177249624	177249624	Missense_Mutation	SNP	G	A	46	76	c.1312G>A	c.(1312-1314)GAA>AAA	p.E438K
Pat_26	Pre-Treatment	PLA2G4A	5321	37	1	186919851	186919851	Missense_Mutation	SNP	G	A	4	173	c.1327G>A	c.(1327-1329)GAA>AAA	p.E443K
Pat_26	Pre-Treatment	B3GALT2	8707	37	1	193149624	193149624	Missense_Mutation	SNP	G	A	4	151	c.1069C>T	c.(1069-1071)CCC>TCC	p.P357S
Pat_26	Pre-Treatment	ASPM	259266	37	1	197101477	197101477	Missense_Mutation	SNP	G	A	4	186	c.2425C>T	c.(2425-2427)CGT>TGT	p.R809C
Pat_26	Pre-Treatment	PLEKHA6	22874	37	1	204214787	204214787	Missense_Mutation	SNP	C	T	93	153	c.1988G>A	c.(1987-1989)AGG>AAG	p.R663K
Pat_26	Pre-Treatment	LRRN2	10446	37	1	204588452	204588452	Missense_Mutation	SNP	C	T	55	99	c.669G>A	c.(667-669)ATG>ATA	p.M223I
Pat_26	Pre-Treatment	LGTN	1939	37	1	206784591	206784591	Missense_Mutation	SNP	C	T	4	160	c.193G>A	c.(193-195)GTG>ATG	p.V65M
Pat_26	Pre-Treatment	CR2	1380	37	1	207642243	207642243	Missense_Mutation	SNP	G	A	28	42	c.733G>A	c.(733-735)GGG>AGG	p.G245R
Pat_26	Pre-Treatment	KCNH1	3756	37	1	210857201	210857201	Missense_Mutation	SNP	C	T	4	174	c.2392G>A	c.(2392-2394)GTA>ATA	p.V798I
Pat_26	Pre-Treatment	USH2A	7399	37	1	216373318	216373318	Missense_Mutation	SNP	T	G	82	114	c.3462A>C	c.(3460-3462)TTA>TTC	p.L1154F
Pat_26	Pre-Treatment	IARS2	55699	37	1	220287738	220287738	Missense_Mutation	SNP	G	T	139	234	c.1562G>T	c.(1561-1563)TGT>TTT	p.C521F
Pat_26	Pre-Treatment	TP53BP2	7159	37	1	223986100	223986100	Missense_Mutation	SNP	G	A	5	348	c.1765C>T	c.(1765-1767)CGG>TGG	p.R589W

Pat_26	Pre-Treatment	CDC42BPA	8476	37	1	227387267	227387267	Missense_Mutation	SNP	G	C	4	120	c.441C>G	c.(439-441)GAC>GAG	p.D147E
Pat_26	Pre-Treatment	GJC2	57165	37	1	228346181	228346181	Missense_Mutation	SNP	C	T	6	437	c.722C>T	c.(721-723)CCG>CTG	p.P241L
Pat_26	Pre-Treatment	OBSCN	84033	37	1	228556579	228556579	Missense_Mutation	SNP	G	A	5	316	c.19924G>A	c.(19924-19926)GAA>AAA	p.E6642K
Pat_26	Pre-Treatment	OBSCN	84033	37	1	228557898	228557898	Missense_Mutation	SNP	C	T	4	167	c.20125C>T	c.(20125-20127)CGG>TGG	p.R6709W
Pat_26	Pre-Treatment	ACTN2	88	37	1	236911034	236911034	Nonsense_Mutation	SNP	C	T	37	57	c.1474C>T	c.(1474-1476)CGA>TGA	p.R492*
Pat_26	Pre-Treatment	FMN2	56776	37	1	240370570	240370570	Missense_Mutation	SNP	G	A	5	186	c.2458G>A	c.(2458-2460)GCT>ACT	p.A820T
Pat_26	Pre-Treatment	CNST	163882	37	1	246810825	246810825	Missense_Mutation	SNP	G	A	9	635	c.1322G>A	c.(1321-1323)CGT>CAT	p.R441H
Pat_26	Pre-Treatment	TUBB8	347688	37	10	93674	93674	Missense_Mutation	SNP	G	C	3	91	c.658C>G	c.(658-660)CCC>GCC	p.P220A
Pat_26	Pre-Treatment	IL2RA	3559	37	10	6066213	6066213	Missense_Mutation	SNP	G	A	51	69	c.361C>T	c.(361-363)CTT>TTT	p.L121F
Pat_26	Pre-Treatment	RBM17	84991	37	10	6143307	6143307	Missense_Mutation	SNP	G	A	4	165	c.197G>A	c.(196-198)CGG>CAG	p.R66Q
Pat_26	Pre-Treatment	ITIH5	80760	37	10	7608059	7608059	Nonsense_Mutation	SNP	G	A	4	184	c.2461C>T	c.(2461-2463)CGA>TGA	p.R821*
Pat_26	Pre-Treatment	KIAA1217	56243	37	10	24762599	24762599	Missense_Mutation	SNP	G	A	4	185	c.1289G>A	c.(1288-1290)CGG>CAG	p.R430Q
Pat_26	Pre-Treatment	KIAA1217	56243	37	10	24822108	24822108	Missense_Mutation	SNP	C	T	48	113	c.3356C>T	c.(3355-3357)TCC>TTC	p.S1119F
Pat_26	Pre-Treatment	GPR158	57512	37	10	25701332	25701332	Missense_Mutation	SNP	C	T	163	407	c.1265C>T	c.(1264-1266)TCC>TTC	p.S422F
Pat_26	Pre-Treatment	KIAA1462	57608	37	10	30318160	30318160	Missense_Mutation	SNP	C	T	78	163	c.917G>A	c.(916-918)GGA>GAA	p.G306E
Pat_26	Pre-Treatment	PARD3	56288	37	10	34671581	34671581	Missense_Mutation	SNP	C	T	4	124	c.1286G>A	c.(1285-1287)GGA>GAA	p.G429E
Pat_26	Pre-Treatment	ANKRD30A	91074	37	10	37430688	37430688	Missense_Mutation	SNP	C	T	15	141	c.695C>T	c.(694-696)GCG>GTG	p.A232V
Pat_26	Pre-Treatment	ANKRD30A	91074	37	10	37430910	37430910	Missense_Mutation	SNP	C	T	5	163	c.917C>T	c.(916-918)ACG>ATG	p.T306M
Pat_26	Pre-Treatment	ZNF248	57209	37	10	38120643	38120643	Missense_Mutation	SNP	G	A	80	137	c.1640C>T	c.(1639-1641)CCG>CTG	p.P547L
Pat_26	Pre-Treatment	RBP3	5949	37	10	48388771	48388771	Missense_Mutation	SNP	G	A	51	90	c.2107C>T	c.(2107-2109)CAC>TAC	p.H703Y
Pat_26	Pre-Treatment	RBP3	5949	37	10	48389305	48389305	Missense_Mutation	SNP	C	T	21	59	c.1573G>A	c.(1573-1575)GAG>AAG	p.E525K
Pat_26	Pre-Treatment	RBP3	5949	37	10	48389757	48389757	Missense_Mutation	SNP	G	A	37	98	c.1121C>T	c.(1120-1122)GCC>GTC	p.A374V
Pat_26	Pre-Treatment	ANK3	288	37	10	61898789	61898789	Missense_Mutation	SNP	C	T	84	136	c.2671G>A	c.(2671-2673)GAA>AAA	p.E891K
Pat_26	Pre-Treatment	ANK3	288	37	10	61941146	61941146	Nonsense_Mutation	SNP	G	A	92	190	c.2125C>T	c.(2125-2127)CGA>TGA	p.R709*
Pat_26	Pre-Treatment	RHOBTB1	9886	37	10	62645968	62645968	Missense_Mutation	SNP	C	A	4	163	c.1477G>T	c.(1477-1479)GAT>TAT	p.D493Y
Pat_26	Pre-Treatment	LRRTM3	347731	37	10	68687639	68687640	Missense_Mutation	DNP	CC	TT	24	58	c.965_966CC>TT	c.(964-966)TCC>TTT	p.S322F
Pat_26	Pre-Treatment	STOX1	219736	37	10	70644422	70644422	Missense_Mutation	SNP	C	G	81	167	c.870C>G	c.(868-870)CAC>CAG	p.H290Q
Pat_26	Pre-Treatment	SEC24C	9632	37	10	75519901	75519901	Nonsense_Mutation	SNP	C	T	114	259	c.607C>T	c.(607-609)CAG>TAG	p.Q203*
Pat_26	Pre-Treatment	MMRN2	79812	37	10	88703034	88703034	Missense_Mutation	SNP	C	T	5	261	c.1507G>A	c.(1507-1509)GTC>ATC	p.V503I
Pat_26	Pre-Treatment	FAM35A	54537	37	10	88917886	88917886	Missense_Mutation	SNP	G	A	4	92	c.1607G>A	c.(1606-1608)AGT>AAT	p.S536N
Pat_26	Pre-Treatment	PIPSL	266971	37	10	95719536	95719536	Missense_Mutation	SNP	C	T	54	115	c.1618G>A	c.(1618-1620)GAT>AAT	p.D540N
Pat_26	Pre-Treatment	PLCE1	51196	37	10	96076413	96076413	Missense_Mutation	SNP	A	G	18	39	c.6242A>G	c.(6241-6243)CAG>CGG	p.Q2081R
Pat_26	Pre-Treatment	CYP2C19	1557	37	10	96609752	96609752	Missense_Mutation	SNP	C	T	101	180	c.1228C>T	c.(1228-1230)CGT>TGT	p.R410C
Pat_26	Pre-Treatment	LOXL4	84171	37	10	100016625	100016625	Missense_Mutation	SNP	C	T	5	252	c.1340G>A	c.(1339-1341)GGG>GAG	p.G447E
Pat_26	Pre-Treatment	GBF1	8729	37	10	104126216	104126216	Missense_Mutation	SNP	G	A	4	157	c.2383G>A	c.(2383-2385)GCA>ACA	p.A795T
Pat_26	Pre-Treatment	C10orf26	54838	37	10	104557799	104557799	Missense_Mutation	SNP	C	A	6	249	c.77C>A	c.(76-78)ACA>AAA	p.T26K
Pat_26	Pre-Treatment	C10orf79	80217	37	10	105890056	105890056	Missense_Mutation	SNP	T	G	55	120	c.4839A>C	c.(4837-4839)AAA>AAC	p.K1613N
Pat_26	Pre-Treatment	AFAP1L2	84632	37	10	116068248	116068248	Missense_Mutation	SNP	G	A	130	137	c.911C>T	c.(910-912)GCT>GTT	p.A304V
Pat_26	Pre-Treatment	KCNK18	338567	37	10	118957156	118957156	Missense_Mutation	SNP	G	A	4	140	c.157G>A	c.(157-159)GCA>ACA	p.A53T
Pat_26	Pre-Treatment	TACC2	10579	37	10	123988957	123988957	Missense_Mutation	SNP	G	A	243	593	c.7993G>A	c.(7993-7995)GAC>AAC	p.D2665N
Pat_26	Pre-Treatment	DMBT1	1755	37	10	124350190	124350190	Missense_Mutation	SNP	C	T	270	405	c.2117C>T	c.(2116-2118)TCC>TTC	p.S706F
Pat_26	Pre-Treatment	CUZD1	50624	37	10	124595694	124595694	Missense_Mutation	SNP	C	A	88	209	c.990G>T	c.(988-990)AAG>AAT	p.K330N
Pat_26	Pre-Treatment	C10orf90	118611	37	10	128193393	128193393	Nonsense_Mutation	SNP	C	A	45	140	c.376G>T	c.(376-378)GAG>TAG	p.E126*
Pat_26	Pre-Treatment	PWWP2B	170394	37	10	134218351	134218351	Missense_Mutation	SNP	C	T	4	114	c.347C>T	c.(346-348)CCG>CTG	p.P116L
Pat_26	Pre-Treatment	KNDC1	85442	37	10	135013019	135013019	Missense_Mutation	SNP	C	T	56	205	c.2816C>T	c.(2815-2817)TCC>TTC	p.S939F
Pat_26	Pre-Treatment	ADAM8	101	37	10	135085316	135085316	Missense_Mutation	SNP	C	T	4	178	c.983G>A	c.(982-984)AGC>AAC	p.S328N
Pat_26	Pre-Treatment	SYCE1	93426	37	10	135369530	135369530	Missense_Mutation	SNP	C	T	79	216	c.550G>A	c.(550-552)GAG>AAG	p.E184K

Pat_26	Pre-Treatment	OSBPL5	114879	37	11	3129158	3129158	Missense_Mutation	SNP	C	T	4	120	c.709G>A	c.(709-711)GCC>ACC	p.A237T
Pat_26	Pre-Treatment	OR51Q1	390061	37	11	5444196	5444196	Missense_Mutation	SNP	C	T	67	209	c.766C>T	c.(766-768)CCC>TCC	p.P256S
Pat_26	Pre-Treatment	OR56A5	390084	37	11	5988988	5988988	Missense_Mutation	SNP	G	A	7	8	c.737C>T	c.(736-738)TCC>TTC	p.S246F
Pat_26	Pre-Treatment	OR52L1	338751	37	11	6008061	6008061	Missense_Mutation	SNP	C	T	14	27	c.100G>A	c.(100-102)GGG>AGG	p.G34R
Pat_26	Pre-Treatment	ZNF214	7761	37	11	7021649	7021649	Missense_Mutation	SNP	C	T	54	81	c.1265G>A	c.(1264-1266)GGC>GAC	p.G422D
Pat_26	Pre-Treatment	RBMXL2	27288	37	11	7111168	7111168	Missense_Mutation	SNP	C	T	69	92	c.817C>T	c.(817-819)CAT>TAT	p.H273Y
Pat_26	Pre-Treatment	NRIP3	56675	37	11	9007284	9007284	Missense_Mutation	SNP	C	T	4	182	c.536G>A	c.(535-537)CGC>CAC	p.R179H
Pat_26	Pre-Treatment	SCUBE2	57758	37	11	9049060	9049060	Missense_Mutation	SNP	G	A	52	69	c.2465C>T	c.(2464-2466)TCC>TTC	p.S822F
Pat_26	Pre-Treatment	DENND5A	23258	37	11	9228225	9228225	Missense_Mutation	SNP	C	T	7	366	c.286G>A	c.(286-288)GGA>AGA	p.G96R
Pat_26	Pre-Treatment	CSNK2A1P	283106	37	11	11373631	11373631	Missense_Mutation	SNP	C	T	4	189	c.1036G>A	c.(1036-1038)GTC>ATC	p.V346I
Pat_26	Pre-Treatment	MICALCL	84953	37	11	12316354	12316354	Missense_Mutation	SNP	C	T	3	11	c.1376C>T	c.(1375-1377)CCT>CTT	p.P459L
Pat_26	Pre-Treatment	ARNTL	406	37	11	13397274	13397275	Missense_Mutation	DNP	AG	TA	27	59	.1290_1291AG>T	288-1293)GAAGTA>GAT	.430_431EV>
Pat_26	Pre-Treatment	LDHA	3939	37	11	18426998	18426998	Missense_Mutation	SNP	C	T	4	142	c.713C>T	c.(712-714)GCT>GTT	p.A238V
Pat_26	Pre-Treatment	PRMT3	10196	37	11	20529860	20529861	Nonsense_Mutation	DNP	GA	TT	30	49	.1497_1498GA>T	1495-1500)TTGAAA>TTTT	.499_500LK>
Pat_26	Pre-Treatment	SLC6A5	9152	37	11	20649627	20649627	Nonsense_Mutation	SNP	C	A	4	132	c.1497C>A	c.(1495-1497)TAC>TAA	p.Y499*
Pat_26	Pre-Treatment	CHST1	8534	37	11	45671392	45671392	Missense_Mutation	SNP	C	T	4	132	c.1082G>A	c.(1081-1083)CGC>CAC	p.R361H
Pat_26	Pre-Treatment	MAPK8IP1	9479	37	11	45925556	45925556	Missense_Mutation	SNP	G	A	155	372	c.1510G>A	c.(1510-1512)GAA>AAA	p.E504K
Pat_26	Pre-Treatment	GYLTL1B	120071	37	11	45949470	45949470	Splice_Site	SNP	G	A	56	72	c.1605_splice	c.e12-1	p.R535_splice
Pat_26	Pre-Treatment	FOLH1	2346	37	11	49175447	49175447	Missense_Mutation	SNP	C	T	42	82	c.1921G>A	c.(1921-1923)GAA>AAA	p.E641K
Pat_26	Pre-Treatment	OR4A15	81328	37	11	55136144	55136144	Missense_Mutation	SNP	G	A	31	51	c.785G>A	c.(784-786)CGA>CAA	p.R262Q
Pat_26	Pre-Treatment	P2RX3	5024	37	11	57137381	57137381	Missense_Mutation	SNP	G	A	5	190	c.1105G>A	c.(1105-1107)GCG>ACG	p.A369T
Pat_26	Pre-Treatment	CTNND1	1500	37	11	57572210	57572210	Missense_Mutation	SNP	C	A	4	139	c.1680C>A	c.(1678-1680)TTC>TTA	p.F560L
Pat_26	Pre-Treatment	OR5B3	441608	37	11	58170239	58170239	Missense_Mutation	SNP	G	A	19	18	c.644C>T	c.(643-645)TCC>TTC	p.S215F
Pat_26	Pre-Treatment	MS4A4A	51338	37	11	60064709	60064709	Missense_Mutation	SNP	G	A	60	114	c.241G>A	c.(241-243)GGA>AGA	p.G81R
Pat_26	Pre-Treatment	TMEM132A	54972	37	11	60702845	60702845	Missense_Mutation	SNP	G	A	5	76	c.1958G>A	c.(1957-1959)CGG>CAG	p.R653Q
Pat_26	Pre-Treatment	RPLP0P2	113157	37	11	61404326	61404326	Missense_Mutation	SNP	G	A	4	162	c.175G>A	c.(175-177)GCC>ACC	p.A59T
Pat_26	Pre-Treatment	FADS2	9415	37	11	61608002	61608002	Missense_Mutation	SNP	A	C	159	170	c.515A>C	c.(514-516)CAG>CCG	p.Q172P
Pat_26	Pre-Treatment	INCENP	3619	37	11	61897748	61897748	Missense_Mutation	SNP	C	T	5	171	c.749C>T	c.(748-750)ACG>ATG	p.T250M
Pat_26	Pre-Treatment	EML3	256364	37	11	62374475	62374475	Missense_Mutation	SNP	G	A	4	135	c.1459C>T	c.(1459-1461)CGG>TGG	p.R487W
Pat_26	Pre-Treatment	GPR137	56834	37	11	64054028	64054028	Missense_Mutation	SNP	C	T	5	250	c.32C>T	c.(31-33)GCT>GTT	p.A11V
Pat_26	Pre-Treatment	CDC42BPG	55561	37	11	64596984	64596984	Missense_Mutation	SNP	C	T	4	58	c.3926G>A	c.(3925-3927)CGT>CAT	p.R1309H
Pat_26	Pre-Treatment	SIPA1	6494	37	11	65413346	65413346	Missense_Mutation	SNP	C	G	64	234	c.1181C>G	c.(1180-1182)TCC>TGC	p.S394C
Pat_26	Pre-Treatment	KLC2	64837	37	11	66030347	66030347	Missense_Mutation	SNP	C	T	208	380	c.592C>T	c.(592-594)CTC>TTC	p.L198F
Pat_26	Pre-Treatment	CCS	9973	37	11	66373047	66373047	Missense_Mutation	SNP	G	A	30	63	c.655G>A	c.(655-657)GGG>AGG	p.G219R
Pat_26	Pre-Treatment	FGF19	9965	37	11	69518121	69518121	Missense_Mutation	SNP	T	C	27	30	c.244A>G	c.(244-246)ATC>GTC	p.I82V
Pat_26	Pre-Treatment	SHANK2	22941	37	11	70319273	70319273	Missense_Mutation	SNP	C	T	87	162	c.5251G>A	c.(5251-5253)GAT>AAT	p.D1751N
Pat_26	Pre-Treatment	INPPL1	3636	37	11	71946922	71946922	Missense_Mutation	SNP	C	T	114	143	c.2771C>T	c.(2770-2772)GCC>GTC	p.A924V
Pat_26	Pre-Treatment	ARAP1	116985	37	11	72424274	72424274	Missense_Mutation	SNP	C	T	4	148	c.694G>A	c.(694-696)GAT>AAT	p.D232N
Pat_26	Pre-Treatment	RELT	84957	37	11	73105710	73105710	Missense_Mutation	SNP	C	T	56	50	c.977C>T	c.(976-978)CCG>CTG	p.P326L
Pat_26	Pre-Treatment	C2CD3	26005	37	11	73803545	73803545	Missense_Mutation	SNP	G	A	4	180	c.3433C>T	c.(3433-3435)CGT>TGT	p.R1145C
Pat_26	Pre-Treatment	THRSP	7069	37	11	77775184	77775184	Missense_Mutation	SNP	G	A	4	126	c.257G>A	c.(256-258)GGC>GAC	p.G86D
Pat_26	Pre-Treatment	FAT3	120114	37	11	92615946	92615946	Missense_Mutation	SNP	G	C	10	25	c.12324G>C	.(12322-12324)GAG>GA	p.E4108D
Pat_26	Pre-Treatment	HEPHL1	341208	37	11	93797538	93797538	Nonsense_Mutation	SNP	C	T	30	41	c.670C>T	c.(670-672)CGA>TGA	p.R224*
Pat_26	Pre-Treatment	PDGFD	80310	37	11	103870789	103870789	Missense_Mutation	SNP	C	T	37	82	c.319G>A	c.(319-321)GAT>AAT	p.D107N
Pat_26	Pre-Treatment	GRIA4	2893	37	11	105483095	105483096	Missense_Mutation	DNP	CC	TT	51	111	c.181_182CC>TT	c.(181-183)CCT>TTT	p.P61F
Pat_26	Pre-Treatment	FAM55A	120400	37	11	114393075	114393075	Missense_Mutation	SNP	G	A	130	171	c.833C>T	c.(832-834)CCT>CTT	p.P278L
Pat_26	Pre-Treatment	PHLDB1	23187	37	11	118498590	118498590	Missense_Mutation	SNP	C	T	12	30	c.1051C>T	c.(1051-1053)CGG>TGG	p.R351W

Pat_26	Pre-Treatment	USP2	9099	37	11	119243422	119243422	Missense_Mutation	SNP	C	T	4	186	c.769G>A	c.(769-771)GGC>AGC	p.G257S
Pat_26	Pre-Treatment	CCDC15	80071	37	11	124857827	124857827	Missense_Mutation	SNP	G	T	10	451	c.1705G>T	c.(1705-1707)GTT>TTT	p.V569F
Pat_26	Pre-Treatment	KCNJ5	3762	37	11	128781257	128781257	Missense_Mutation	SNP	G	A	5	350	c.89G>A	c.(88-90)CGC>CAC	p.R30H
Pat_26	Pre-Treatment	VPS26B	112936	37	11	134113147	134113147	Missense_Mutation	SNP	C	T	4	156	c.680C>T	c.(679-681)ACG>ATG	p.T227M
Pat_26	Pre-Treatment	GLB1L2	89944	37	11	134241034	134241034	Missense_Mutation	SNP	C	T	6	192	c.1348C>T	c.(1348-1350)CGG>TGG	p.R450W
Pat_26	Pre-Treatment	MLF2	8079	37	12	6861105	6861105	Missense_Mutation	SNP	G	A	99	198	c.166C>T	c.(166-168)CGC>TGC	p.R56C
Pat_26	Pre-Treatment	PHB2	11331	37	12	7079605	7079605	Nonsense_Mutation	SNP	G	C	3	36	c.102C>G	c.(100-102)TAC>TAG	p.Y34*
Pat_26	Pre-Treatment	GDF3	9573	37	12	7848090	7848090	Missense_Mutation	SNP	G	A	8	140	c.235C>T	c.(235-237)CGC>TGC	p.R79C
Pat_26	Pre-Treatment	DPPA3	359787	37	12	7864169	7864169	Missense_Mutation	SNP	G	A	29	78	c.3G>A	c.(1-3)ATG>ATA	p.M1I
Pat_26	Pre-Treatment	CLEC4E	26253	37	12	8687260	8687260	Missense_Mutation	SNP	G	A	26	48	c.634C>T	c.(634-636)CCT>TCT	p.P212S
Pat_26	Pre-Treatment	A2M	2	37	12	9264799	9264799	Missense_Mutation	SNP	G	A	46	70	c.439C>T	c.(439-441)CGT>TGT	p.R147C
Pat_26	Pre-Treatment	PIK3C2G	5288	37	12	18552721	18552721	Missense_Mutation	SNP	C	T	21	32	c.2132C>T	c.(2131-2133)ACC>ATC	p.T711I
Pat_26	Pre-Treatment	SLCO1C1	53919	37	12	20874764	20874764	Missense_Mutation	SNP	C	T	36	85	c.802C>T	c.(802-804)CCC>TCC	p.P268S
Pat_26	Pre-Treatment	GYS2	2998	37	12	21712612	21712612	Missense_Mutation	SNP	C	T	23	56	c.1202G>A	c.(1201-1203)GGA>GAA	p.G401E
Pat_26	Pre-Treatment	LRRK2	120892	37	12	40677921	40677921	Nonsense_Mutation	SNP	T	G	22	19	c.2486T>G	c.(2485-2487)TTA>TGA	p.L829*
Pat_26	Pre-Treatment	ADAMTS20	80070	37	12	43945044	43945044	Missense_Mutation	SNP	C	T	17	45	c.121G>A	c.(121-123)GAA>AAA	p.E41K
Pat_26	Pre-Treatment	IRAK4	51135	37	12	44165165	44165165	Missense_Mutation	SNP	C	T	28	74	c.304C>T	c.(304-306)CCA>TCA	p.P102S
Pat_26	Pre-Treatment	SFRS2IP	9169	37	12	46321745	46321745	Missense_Mutation	SNP	T	A	46	91	c.1739A>T	c.(1738-1740)AAT>ATT	p.N580I
Pat_26	Pre-Treatment	ADCY6	112	37	12	49164660	49164660	Missense_Mutation	SNP	C	T	4	165	c.3145G>A	c.(3145-3147)GAT>AAT	p.D1049N
Pat_26	Pre-Treatment	TROAP	10024	37	12	49724357	49724357	Missense_Mutation	SNP	G	A	5	139	c.1729G>A	c.(1729-1731)GTA>ATA	p.V577I
Pat_26	Pre-Treatment	KRT7	3855	37	12	52629068	52629068	Missense_Mutation	SNP	C	G	3	109	c.454C>G	c.(454-456)CTT>GTT	p.L152V
Pat_26	Pre-Treatment	KRT75	9119	37	12	52825359	52825359	Missense_Mutation	SNP	C	T	77	159	c.838G>A	c.(838-840)GAG>AAG	p.E280K
Pat_26	Pre-Treatment	KRT5	3852	37	12	52913836	52913836	Missense_Mutation	SNP	C	T	5	339	c.245G>A	c.(244-246)AGC>AAC	p.S82N
Pat_26	Pre-Treatment	KRT74	121391	37	12	52960769	52960769	Missense_Mutation	SNP	C	T	182	251	c.1574G>A	c.(1573-1575)AGG>AAG	p.R525K
Pat_26	Pre-Treatment	ITGB7	3695	37	12	53587011	53587011	Missense_Mutation	SNP	G	A	6	169	c.1639C>T	c.(1639-1641)CGC>TGC	p.R547C
Pat_26	Pre-Treatment	NEUROD4	58158	37	12	55420303	55420303	Missense_Mutation	SNP	C	T	22	73	c.80C>T	c.(79-81)TCC>TTC	p.S27F
Pat_26	Pre-Treatment	TMEM194A	23306	37	12	57466641	57466641	Missense_Mutation	SNP	C	T	5	214	c.182G>A	c.(181-183)CGT>CAT	p.R61H
Pat_26	Pre-Treatment	NAV3	89795	37	12	78400838	78400838	Missense_Mutation	SNP	C	T	53	92	c.1520C>T	c.(1519-1521)CCT>CTT	p.P507L
Pat_26	Pre-Treatment	ACSS3	79611	37	12	81528778	81528778	Missense_Mutation	SNP	G	A	5	98	c.640G>A	c.(640-642)GTA>ATA	p.V214I
Pat_26	Pre-Treatment	CEP290	80184	37	12	88453692	88453692	Missense_Mutation	SNP	G	A	5	13	c.6628C>T	c.(6628-6630)CGT>TGT	p.R2210C
Pat_26	Pre-Treatment	SLC17A8	246213	37	12	100813848	100813848	Missense_Mutation	SNP	G	A	12	37	c.1681G>A	c.(1681-1683)GAA>AAA	p.E561K
Pat_26	Pre-Treatment	ACACB	32	37	12	109675040	109675040	Missense_Mutation	SNP	G	A	6	524	c.4517G>A	c.(4516-4518)CGT>CAT	p.R1506H
Pat_26	Pre-Treatment	ACACB	32	37	12	109677677	109677677	Missense_Mutation	SNP	C	T	4	132	c.4705C>T	c.(4705-4707)CTC>TTC	p.L1569F
Pat_26	Pre-Treatment	KCTD10	83892	37	12	109889456	109889456	Missense_Mutation	SNP	G	A	4	183	c.886C>T	c.(886-888)CGC>TGC	p.R296C
Pat_26	Pre-Treatment	C12orf51	283450	37	12	112622629	112622629	Missense_Mutation	SNP	C	T	4	161	c.8875G>A	c.(8875-8877)GCC>ACC	p.A2959T
Pat_26	Pre-Treatment	C12orf51	283450	37	12	112673400	112673400	Missense_Mutation	SNP	G	A	15	41	c.4367C>T	c.(4366-4368)CCC>CTC	p.P1456L
Pat_26	Pre-Treatment	NOS1	4842	37	12	117655918	117655918	Missense_Mutation	SNP	C	T	263	461	c.4222G>A	c.(4222-4224)GAA>AAA	p.E1408K
Pat_26	Pre-Treatment	SRRM4	84530	37	12	119592047	119592047	Splice_Site	SNP	G	A	3	22	c.1392_splice	c.e12-1	p.R464_splice
Pat_26	Pre-Treatment	DNAH10	196385	37	12	124416393	124416393	Missense_Mutation	SNP	G	A	79	161	c.12773G>A	c.(12772-12774)AGG>AAG	p.R4258K
Pat_26	Pre-Treatment	EP400	57634	37	12	132535158	132535158	Missense_Mutation	SNP	C	T	178	285	c.7352C>T	c.(7351-7353)CCC>CTC	p.P2451L
Pat_26	Pre-Treatment	TPTE2	93492	37	13	20010385	20010385	Missense_Mutation	SNP	C	T	16	30	c.1097G>A	c.(1096-1098)GGA>GAA	p.G366E
Pat_26	Pre-Treatment	SPG20	23111	37	13	36909531	36909531	Missense_Mutation	SNP	G	A	10	33	c.437C>T	c.(436-438)TCA>TTA	p.S146L
Pat_26	Pre-Treatment	C13orf23	80209	37	13	39587324	39587324	Missense_Mutation	SNP	G	A	4	159	c.2065C>T	c.(2065-2067)CCC>TCC	p.P689S
Pat_26	Pre-Treatment	C13orf23	80209	37	13	39588230	39588230	Missense_Mutation	SNP	G	A	4	160	c.1159C>T	c.(1159-1161)CGG>TGG	p.R387W
Pat_26	Pre-Treatment	RCBTB2	1102	37	13	49077000	49077000	Missense_Mutation	SNP	G	A	5	265	c.977C>T	c.(976-978)ACG>ATG	p.T326M
Pat_26	Pre-Treatment	COL4A2	1284	37	13	111080895	111080895	Missense_Mutation	SNP	G	A	54	81	c.442G>A	c.(442-444)GGG>AGG	p.G148R
Pat_26	Pre-Treatment	POTEG	404785	37	14	19563496	19563496	Missense_Mutation	SNP	C	G	6	394	c.1010C>G	c.(1009-1011)TCT>TGT	p.S337C

Pat_26	Pre-Treatment	CHD8	57680	37	14	21873900	21873901	Missense_Mutation	DNP	CC	TA	172	366	.2193_2194GG>T	191-2196)GGGGAT>GGT	p.D732N
Pat_26	Pre-Treatment	MYH6	4624	37	14	23865496	23865496	Missense_Mutation	SNP	C	T	6	489	c.2426G>A	c.(2425-2427)CGC>CAC	p.R809H
Pat_26	Pre-Treatment	NYNRIN	57523	37	14	24877187	24877187	Missense_Mutation	SNP	G	T	69	154	c.311G>T	c.(310-312)TGG>TTG	p.W104L
Pat_26	Pre-Treatment	FOXG1	2290	37	14	29236526	29236526	Missense_Mutation	SNP	C	T	4	72	c.41C>T	c.(40-42)CCC>CTC	p.P14L
Pat_26	Pre-Treatment	KCNH5	27133	37	14	63174459	63174459	Missense_Mutation	SNP	C	T	106	159	c.2734G>A	c.(2734-2736)GAA>AAA	p.E912K
Pat_26	Pre-Treatment	ESR2	2100	37	14	64746815	64746815	Missense_Mutation	SNP	G	A	213	429	c.419C>T	c.(418-420)CCA>CTA	p.P140L
Pat_26	Pre-Treatment	SPTB	6710	37	14	65260468	65260468	Missense_Mutation	SNP	C	A	4	149	c.1913G>T	c.(1912-1914)CGA>CTA	p.R638L
Pat_26	Pre-Treatment	RDH12	145226	37	14	68195937	68195938	Missense_Mutation	DNP	CC	TT	209	401	c.688_689CC>TT	c.(688-690)CCA>TTA	p.P230L
Pat_26	Pre-Treatment	PCNX	22990	37	14	71540340	71540340	Missense_Mutation	SNP	C	T	6	287	c.4931C>T	c.(4930-4932)CCT>CTT	p.P1644L
Pat_26	Pre-Treatment	BATF	10538	37	14	75991472	75991472	Missense_Mutation	SNP	C	T	22	47	c.109C>T	c.(109-111)CGT>TGT	p.R37C
Pat_26	Pre-Treatment	PTPN21	11099	37	14	88945940	88945940	Missense_Mutation	SNP	G	C	17	35	c.1835C>G	c.(1834-1836)CCC>CGC	p.P612R
Pat_26	Pre-Treatment	KIAA1409	57578	37	14	94121601	94121601	Missense_Mutation	SNP	T	G	72	87	c.5956T>G	c.(5956-5958)TTA>GTA	p.L1986V
Pat_26	Pre-Treatment	OTUB2	78990	37	14	94503808	94503808	Missense_Mutation	SNP	G	A	4	107	c.86G>A	c.(85-87)CGG>CAG	p.R29Q
Pat_26	Pre-Treatment	SERPINA11	256394	37	14	94912755	94912755	Missense_Mutation	SNP	A	G	69	148	c.830T>C	c.(829-831)GTC>GCC	p.V277A
Pat_26	Pre-Treatment	TNFAIP2	7127	37	14	103598032	103598032	Missense_Mutation	SNP	G	A	26	44	c.1355G>A	c.(1354-1356)GGC>GAC	p.G452D
Pat_26	Pre-Treatment	ZFYVE21	79038	37	14	104195467	104195467	Missense_Mutation	SNP	A	C	102	135	c.474A>C	c.(472-474)GAA>GAC	p.E158D
Pat_26	Pre-Treatment	C15orf2	23742	37	15	24921709	24921709	Missense_Mutation	SNP	C	T	38	67	c.695C>T	c.(694-696)TCC>TTC	p.S232F
Pat_26	Pre-Treatment	APBA2	321	37	15	29346439	29346439	Missense_Mutation	SNP	G	A	6	291	c.352G>A	c.(352-354)GGG>AGG	p.G118R
Pat_26	Pre-Treatment	TRPM1	4308	37	15	31294509	31294509	Missense_Mutation	SNP	G	A	76	149	c.4328C>T	c.(4327-4329)TCC>TTC	p.S1443F
Pat_26	Pre-Treatment	EIF2AK4	440275	37	15	40284383	40284383	Missense_Mutation	SNP	G	A	4	174	c.2639G>A	c.(2638-2640)AGC>AAC	p.S880N
Pat_26	Pre-Treatment	CASC5	57082	37	15	40951646	40951646	Missense_Mutation	SNP	G	A	5	279	c.6901G>A	c.(6901-6903)GTT>ATT	p.V2301I
Pat_26	Pre-Treatment	TYRO3	7301	37	15	41870343	41870343	Missense_Mutation	SNP	C	T	4	85	c.2542C>T	c.(2542-2544)CGG>TGG	p.R848W
Pat_26	Pre-Treatment	MGA	23269	37	15	42032237	42032237	Missense_Mutation	SNP	C	T	6	357	c.269C>T	c.(268-270)ACT>ATT	p.T90I
Pat_26	Pre-Treatment	PLA2G4E	123745	37	15	42280247	42280247	Missense_Mutation	SNP	C	T	4	92	c.1744G>A	c.(1744-1746)GAA>AAA	p.E582K
Pat_26	Pre-Treatment	CAPN3	825	37	15	42652253	42652253	Missense_Mutation	SNP	G	A	277	424	c.250G>A	c.(250-252)GAG>AAG	p.E84K
Pat_26	Pre-Treatment	TMOD3	29766	37	15	52188725	52188725	Splice_Site	SNP	T	C	5	235	c.735_splice	c.e7+2	p.T245_splice
Pat_26	Pre-Treatment	UNC13C	440279	37	15	54307264	54307264	Missense_Mutation	SNP	C	T	11	16	c.2164C>T	c.(2164-2166)CCA>TCA	p.P722S
Pat_26	Pre-Treatment	UNC13C	440279	37	15	54792293	54792293	Missense_Mutation	SNP	G	T	4	78	c.5077G>T	c.(5077-5079)GTC>TTC	p.V1693F
Pat_26	Pre-Treatment	RFX7	64864	37	15	56386019	56386019	Missense_Mutation	SNP	C	T	5	193	c.3907G>A	c.(3907-3909)GAT>AAT	p.D1303N
Pat_26	Pre-Treatment	NOX5	79400	37	15	69320658	69320658	Missense_Mutation	SNP	G	A	5	193	c.278G>A	c.(277-279)AGC>AAC	p.S93N
Pat_26	Pre-Treatment	MYO9A	4649	37	15	72244206	72244206	Missense_Mutation	SNP	C	A	5	182	c.2214G>T	c.(2212-2214)TTG>TTT	p.L738F
Pat_26	Pre-Treatment	ISLR2	57611	37	15	74425750	74425750	Missense_Mutation	SNP	G	C	77	130	c.655G>C	c.(655-657)GGG>CGG	p.G219R
Pat_26	Pre-Treatment	CCDC33	80125	37	15	74559027	74559027	Missense_Mutation	SNP	C	T	99	211	c.328C>T	c.(328-330)CTC>TTC	p.L110F
Pat_26	Pre-Treatment	ADAMTSL3	57188	37	15	84651796	84651796	Missense_Mutation	SNP	G	A	4	101	c.3416G>A	c.(3415-3417)CGG>CAG	p.R1139Q
Pat_26	Pre-Treatment	NTRK3	4916	37	15	88727501	88727501	Missense_Mutation	SNP	G	A	4	157	c.278C>T	c.(277-279)ACG>ATG	p.T93M
Pat_26	Pre-Treatment	PCSK6	5046	37	15	101933424	101933424	Missense_Mutation	SNP	C	T	13	29	c.1202G>A	c.(1201-1203)CGA>CAA	p.R401Q
Pat_26	Pre-Treatment	OR4F15	390649	37	15	102359169	102359169	Nonsense_Mutation	SNP	G	A	155	240	c.780G>A	c.(778-780)TGG>TGA	p.W260*
Pat_26	Pre-Treatment	MPG	4350	37	16	135516	135516	Missense_Mutation	SNP	G	A	6	161	c.637G>A	c.(637-639)GAG>AAG	p.E213K
Pat_26	Pre-Treatment	TMEM8A	58986	37	16	427097	427097	Missense_Mutation	SNP	G	A	132	331	c.575C>T	c.(574-576)TCC>TTC	p.S192F
Pat_26	Pre-Treatment	PIGQ	9091	37	16	624666	624666	Missense_Mutation	SNP	G	A	19	38	c.592G>A	c.(592-594)GCC>ACC	p.A198T
Pat_26	Pre-Treatment	CCNF	899	37	16	2499427	2499427	Missense_Mutation	SNP	G	A	5	227	c.1363G>A	c.(1363-1365)GCA>ACA	p.A455T
Pat_26	Pre-Treatment	SRRM2	23524	37	16	2820426	2820426	Missense_Mutation	SNP	C	T	4	105	c.8095C>T	c.(8095-8097)CGC>TGC	p.R2699C
Pat_26	Pre-Treatment	KREMEN2	79412	37	16	3016700	3016700	Missense_Mutation	SNP	C	T	4	182	c.544C>T	c.(544-546)CGG>TGG	p.R182W
Pat_26	Pre-Treatment	A2BP1	54715	37	16	7726824	7726824	Missense_Mutation	SNP	G	A	105	189	c.979G>A	c.(979-981)GCT>ACT	p.A327T
Pat_26	Pre-Treatment	USP7	7874	37	16	9004607	9004607	Missense_Mutation	SNP	A	C	82	135	c.1156T>G	c.(1156-1158)TTA>GTA	p.L386V
Pat_26	Pre-Treatment	GRIN2A	2903	37	16	9858471	9858471	Missense_Mutation	SNP	T	G	41	69	c.2930A>C	c.(2929-2931)AAC>ACC	p.N977T
Pat_26	Pre-Treatment	TMC7	79905	37	16	19049221	19049221	Missense_Mutation	SNP	G	A	30	95	c.1031G>A	c.(1030-1032)CGG>CAG	p.R344Q

Pat_26	Pre-Treatment	TMC7	79905	37	16	19051720	19051720	Missense_Mutation	SNP	G	A	5	284	c.1289G>A	c.(1288-1290)CGC>CAC	p.R430H
Pat_26	Pre-Treatment	C16orf88	400506	37	16	19718435	19718435	Missense_Mutation	SNP	G	A	4	82	c.1174C>T	c.(1174-1176)CGC>TGC	p.R392C
Pat_26	Pre-Treatment	ACSM2B	348158	37	16	20559454	20559454	Missense_Mutation	SNP	G	A	92	183	c.1028C>T	c.(1027-1029)CCA>CTA	p.P343L
Pat_26	Pre-Treatment	USP31	57478	37	16	23091371	23091371	Missense_Mutation	SNP	G	A	4	180	c.2072C>T	c.(2071-2073)CCG>CTG	p.P691L
Pat_26	Pre-Treatment	ERN2	10595	37	16	23702196	23702196	Missense_Mutation	SNP	C	T	24	60	c.2881G>A	c.(2881-2883)GAC>AAC	p.D961N
Pat_26	Pre-Treatment	PRKCB	5579	37	16	24196465	24196465	Missense_Mutation	SNP	G	A	89	155	c.1567G>A	c.(1567-1569)GAT>AAT	p.D523N
Pat_26	Pre-Treatment	GTF3C1	2975	37	16	27480794	27480794	Missense_Mutation	SNP	C	T	7	264	c.4892G>A	c.(4891-4893)CGG>CAG	p.R1631Q
Pat_26	Pre-Treatment	C16orf93	90835	37	16	30770779	30770779	Missense_Mutation	SNP	G	A	6	150	c.541C>T	c.(541-543)CGG>TGG	p.R181W
Pat_26	Pre-Treatment	ABCC11	85320	37	16	48209286	48209286	Missense_Mutation	SNP	G	A	42	93	c.3581C>T	c.(3580-3582)CCC>CTC	p.P1194L
Pat_26	Pre-Treatment	BRD7	29117	37	16	50354573	50354573	Splice_Site	SNP	C	T	6	381	c.1612_splice	c.e15+1	p.E538_splice
Pat_26	Pre-Treatment	IRX3	79191	37	16	54319429	54319430	Nonsense_Mutation	DNP	GG	AA	11	17	c.363_364CC>TT	361-366)GGCCAG>GGTT	p.Q122*
Pat_26	Pre-Treatment	C16orf80	29105	37	16	58148803	58148803	Nonsense_Mutation	SNP	G	A	5	264	c.487C>T	c.(487-489)CGA>TGA	p.R163*
Pat_26	Pre-Treatment	B3GNT9	84752	37	16	67183730	67183730	Missense_Mutation	SNP	G	A	4	61	c.659C>T	c.(658-660)CCC>CTC	p.P220L
Pat_26	Pre-Treatment	LOC283922	283922	37	16	74366443	74366443	Missense_Mutation	SNP	G	A	9	11	c.925C>T	c.(925-927)CCC>TCC	p.P309S
Pat_26	Pre-Treatment	ADAMTS18	170692	37	16	77359782	77359782	Missense_Mutation	SNP	T	A	99	117	c.2013A>T	c.(2011-2013)AAA>AAT	p.K671N
Pat_26	Pre-Treatment	VAT1L	57687	37	16	77850891	77850891	Missense_Mutation	SNP	G	A	147	228	c.307G>A	c.(307-309)GGA>AGA	p.G103R
Pat_26	Pre-Treatment	CRISPLD2	83716	37	16	84906599	84906599	Missense_Mutation	SNP	C	T	216	298	c.983C>T	c.(982-984)TCG>TTG	p.S328L
Pat_26	Pre-Treatment	FAM92B	339145	37	16	85143843	85143843	Missense_Mutation	SNP	G	A	4	187	c.244C>T	c.(244-246)CGG>TGG	p.R82W
Pat_26	Pre-Treatment	SLC7A5	8140	37	16	87871496	87871496	Missense_Mutation	SNP	C	A	4	92	c.1095G>T	c.(1093-1095)ATG>ATT	p.M365I
Pat_26	Pre-Treatment	ABR	29	37	17	953422	953422	Splice_Site	SNP	C	T	37	68	c.1660_splice	c.e16-1	p.E554_splice
Pat_26	Pre-Treatment	DPH1	1801	37	17	1940207	1940207	Missense_Mutation	SNP	G	A	4	126	c.652G>A	c.(652-654)GGC>AGC	p.G218S
Pat_26	Pre-Treatment	SMG6	23293	37	17	1972173	1972173	Missense_Mutation	SNP	G	A	43	129	c.3734C>T	c.(3733-3735)CCT>CTT	p.P1245L
Pat_26	Pre-Treatment	P2RX5	5026	37	17	3593794	3593794	Missense_Mutation	SNP	G	A	4	89	c.460C>T	c.(460-462)CGG>TGG	p.R154W
Pat_26	Pre-Treatment	ATP2A3	489	37	17	3840720	3840720	Missense_Mutation	SNP	C	T	4	121	c.2311G>A	c.(2311-2313)GAG>AAG	p.E771K
Pat_26	Pre-Treatment	MYBBP1A	10514	37	17	4448928	4448928	Missense_Mutation	SNP	G	A	6	184	c.2050C>T	c.(2050-2052)CGT>TGT	p.R684C
Pat_26	Pre-Treatment	PLD2	5338	37	17	4725974	4725974	Missense_Mutation	SNP	C	T	6	303	c.2617C>T	c.(2617-2619)CGG>TGG	p.R873W
Pat_26	Pre-Treatment	CAMTA2	23125	37	17	4885114	4885114	Missense_Mutation	SNP	C	T	4	42	c.424G>A	c.(424-426)GTC>ATC	p.V142I
Pat_26	Pre-Treatment	KIF1C	10749	37	17	4904079	4904079	Missense_Mutation	SNP	C	T	141	256	c.119C>T	c.(118-120)CCT>CTT	p.P40L
Pat_26	Pre-Treatment	ZBTB4	57659	37	17	7366704	7366704	Missense_Mutation	SNP	G	A	4	29	c.1597C>T	c.(1597-1599)CCC>TCC	p.P533S
Pat_26	Pre-Treatment	AMAC1L3	643664	37	17	7386000	7386000	Missense_Mutation	SNP	G	A	49	101	c.697G>A	c.(697-699)GGC>AGC	p.G233S
Pat_26	Pre-Treatment	ALOXE3	59344	37	17	8000085	8000085	Missense_Mutation	SNP	C	T	27	53	c.1996G>A	c.(1996-1998)GAG>AAG	p.E666K
Pat_26	Pre-Treatment	ARHGEF15	22899	37	17	8219159	8219159	Missense_Mutation	SNP	C	T	4	160	c.1508C>T	c.(1507-1509)CCT>CTT	p.P503L
Pat_26	Pre-Treatment	MYH8	4626	37	17	10315967	10315967	Missense_Mutation	SNP	A	G	174	465	c.1226T>C	c.(1225-1227)GTT>GCT	p.V409A
Pat_26	Pre-Treatment	MYH4	4622	37	17	10356968	10356968	Missense_Mutation	SNP	C	T	147	238	c.2926G>A	c.(2926-2928)GAG>AAG	p.E976K
Pat_26	Pre-Treatment	MYH1	4619	37	17	10406565	10406565	Missense_Mutation	SNP	C	T	45	96	c.2692G>A	c.(2692-2694)GAA>AAA	p.E898K
Pat_26	Pre-Treatment	DNAH9	1770	37	17	11593135	11593136	Missense_Mutation	DNP	GG	AA	11	12	.3996_3997GG>A	994-3999)ATGGAG>ATAA	332_1333ME
Pat_26	Pre-Treatment	MYOCD	93649	37	17	12647615	12647616	Missense_Mutation	DNP	CC	TT	33	111	c.833_834CC>TT	c.(832-834)TCC>TTT	p.S278F
Pat_26	Pre-Treatment	CDRT1	374286	37	17	15522784	15522784	Missense_Mutation	SNP	G	A	49	513	c.43C>T	c.(43-45)CGT>TGT	p.R15C
Pat_26	Pre-Treatment	ZNF286A	57335	37	17	15619675	15619676	Missense_Mutation	DNP	GG	AA	6	26	c.637_638GG>AA	c.(637-639)GGA>AAA	p.G213K
Pat_26	Pre-Treatment	MPRIP	23164	37	17	17046078	17046078	Missense_Mutation	SNP	G	A	4	149	c.1034G>A	c.(1033-1035)CGG>CAG	p.R345Q
Pat_26	Pre-Treatment	C17orf39	79018	37	17	17968502	17968502	Missense_Mutation	SNP	C	T	77	157	c.848C>T	c.(847-849)TCC>TTC	p.S283F
Pat_26	Pre-Treatment	FLII	2314	37	17	18151111	18151111	Missense_Mutation	SNP	C	T	4	174	c.2347G>A	c.(2347-2349)GAC>AAC	p.D783N
Pat_26	Pre-Treatment	TOP3A	7156	37	17	18208438	18208438	Missense_Mutation	SNP	C	T	5	233	c.487G>A	c.(487-489)GTG>ATG	p.V163M
Pat_26	Pre-Treatment	FBXW10	10517	37	17	18647600	18647600	Missense_Mutation	SNP	C	T	85	182	c.43C>T	c.(43-45)CGT>TGT	p.R15C
Pat_26	Pre-Treatment	MFAP4	4239	37	17	19288516	19288516	Missense_Mutation	SNP	G	A	7	260	c.416C>T	c.(415-417)ACG>ATG	p.T139M
Pat_26	Pre-Treatment	IFT20	90410	37	17	26657555	26657555	Splice_Site	SNP	C	T	59	110	c.128_splice	c.e3-1	p.K43_splice
Pat_26	Pre-Treatment	ACCN1	40	37	17	31355368	31355368	Missense_Mutation	SNP	C	T	61	99	c.877G>A	c.(877-879)GAG>AAG	p.E293K

Pat_26	Pre-Treatment	C17orf78	284099	37	17	35746197	35746197	Missense_Mutation	SNP	C	T	3	18	c.650C>T	c.(649-651)GCC>GTC	p.A217V
Pat_26	Pre-Treatment	SRCIN1	80725	37	17	36707439	36707439	Missense_Mutation	SNP	C	T	16	18	c.2914G>A	c.(2914-2916)GGC>AGC	p.G972S
Pat_26	Pre-Treatment	PIP4K2B	8396	37	17	36940540	36940540	Nonsense_Mutation	SNP	G	A	4	159	c.310C>T	c.(310-312)CGA>TGA	p.R104*
Pat_26	Pre-Treatment	STAC2	342667	37	17	37369806	37369806	Missense_Mutation	SNP	C	T	159	285	c.947G>A	c.(946-948)GGA>GAA	p.G316E
Pat_26	Pre-Treatment	KRT16	3868	37	17	39767374	39767374	Missense_Mutation	SNP	C	T	179	376	c.880G>A	c.(880-882)GAG>AAG	p.E294K
Pat_26	Pre-Treatment	KLHL10	317719	37	17	40001942	40001942	Missense_Mutation	SNP	G	A	4	187	c.1249G>A	c.(1249-1251)GCC>ACC	p.A417T
Pat_26	Pre-Treatment	TUBG2	27175	37	17	40818663	40818663	Missense_Mutation	SNP	C	T	6	284	c.1201C>T	c.(1201-1203)CGG>TGG	p.R401W
Pat_26	Pre-Treatment	CNTNAP1	8506	37	17	40838985	40838985	Missense_Mutation	SNP	G	A	4	132	c.965G>A	c.(964-966)GGC>GAC	p.G322D
Pat_26	Pre-Treatment	SLC4A1	6521	37	17	42335380	42335380	Missense_Mutation	SNP	G	A	4	185	c.1256C>T	c.(1255-1257)CCC>CTC	p.P419L
Pat_26	Pre-Treatment	KIF18B	146909	37	17	43011708	43011708	Missense_Mutation	SNP	G	A	4	48	c.778C>T	c.(778-780)CGG>TGG	p.R260W
Pat_26	Pre-Treatment	DCAKD	79877	37	17	43101938	43101938	Missense_Mutation	SNP	G	A	6	231	c.559C>T	c.(559-561)CGC>TGC	p.R187C
Pat_26	Pre-Treatment	ARHGAP27	201176	37	17	43481696	43481696	Missense_Mutation	SNP	G	A	4	105	c.395C>T	c.(394-396)CCA>CTA	p.P132L
Pat_26	Pre-Treatment	GOSR2	9570	37	17	45006917	45006917	Missense_Mutation	SNP	C	T	4	182	c.61C>T	c.(61-63)CGC>TGC	p.R21C
Pat_26	Pre-Treatment	COL1A1	1277	37	17	48278816	48278816	Missense_Mutation	SNP	G	A	4	150	c.59C>T	c.(58-60)ACG>ATG	p.T20M
Pat_26	Pre-Treatment	XYLT2	64132	37	17	48431912	48431912	Missense_Mutation	SNP	G	A	4	140	c.772G>A	c.(772-774)GAG>AAG	p.E258K
Pat_26	Pre-Treatment	CHAD	1101	37	17	48545571	48545571	Missense_Mutation	SNP	C	T	5	229	c.604G>A	c.(604-606)GTG>ATG	p.V202M
Pat_26	Pre-Treatment	STXBP4	252983	37	17	53076778	53076778	Missense_Mutation	SNP	G	A	4	165	c.253G>A	c.(253-255)GAA>AAA	p.E85K
Pat_26	Pre-Treatment	4-Sep	5414	37	17	56599121	56599122	Missense_Mutation	DNP	GG	AA	117	201	c.890_891CC>TT	c.(889-891)CCC>CTT	p.P297L
Pat_26	Pre-Treatment	CA4	762	37	17	58235695	58235695	Missense_Mutation	SNP	A	T	106	172	c.632A>T	c.(631-633)GAG>GTG	p.E211V
Pat_26	Pre-Treatment	MED13	9969	37	17	60033088	60033088	Missense_Mutation	SNP	G	A	4	169	c.5735C>T	c.(5734-5736)GCT>GTT	p.A1912V
Pat_26	Pre-Treatment	ACE	1636	37	17	61570849	61570849	Missense_Mutation	SNP	G	A	81	142	c.2965G>A	c.(2965-2967)GAA>AAA	p.E989K
Pat_26	Pre-Treatment	PSMC5	5705	37	17	61908260	61908260	Missense_Mutation	SNP	C	T	42	78	c.644C>T	c.(643-645)TCT>TTT	p.S215F
Pat_26	Pre-Treatment	SCN4A	6329	37	17	62025357	62025357	Missense_Mutation	SNP	C	T	4	143	c.3211G>A	c.(3211-3213)GTC>ATC	p.V1071I
Pat_26	Pre-Treatment	CCDC46	201134	37	17	63637111	63637111	Missense_Mutation	SNP	C	T	74	146	c.2770G>A	c.(2770-2772)GAA>AAA	p.E924K
Pat_26	Pre-Treatment	ABCA9	10350	37	17	66982452	66982452	Missense_Mutation	SNP	C	T	4	117	c.4061G>A	c.(4060-4062)GGG>GAG	p.G1354E
Pat_26	Pre-Treatment	OTOP3	347741	37	17	72938043	72938043	Nonsense_Mutation	SNP	C	T	5	136	c.538C>T	c.(538-540)CGA>TGA	p.R180*
Pat_26	Pre-Treatment	FBF1	85302	37	17	73911211	73911211	Missense_Mutation	SNP	G	A	4	58	c.2470C>T	c.(2470-2472)CGG>TGG	p.R824W
Pat_26	Pre-Treatment	CANT1	124583	37	17	76993085	76993085	Missense_Mutation	SNP	G	A	247	513	c.620C>T	c.(619-621)ACC>ATC	p.T207I
Pat_26	Pre-Treatment	C17orf70	80233	37	17	79514124	79514124	Missense_Mutation	SNP	G	A	4	134	c.1984C>T	c.(1984-1986)CAC>TAC	p.H662Y
Pat_26	Pre-Treatment	CSNK1D	1453	37	17	80210954	80210954	Missense_Mutation	SNP	C	T	5	215	c.503G>A	c.(502-504)CGT>CAT	p.R168H
Pat_26	Pre-Treatment	LAMA1	284217	37	18	6986168	6986168	Missense_Mutation	SNP	G	A	6	368	c.5347C>T	c.(5347-5349)CTC>TTC	p.L1783F
Pat_26	Pre-Treatment	LAMA3	3909	37	18	21526172	21526172	Missense_Mutation	SNP	G	A	63	28	c.9275G>A	c.(9274-9276)GGA>GAA	p.G3092E
Pat_26	Pre-Treatment	SETBP1	26040	37	18	42643613	42643613	Missense_Mutation	SNP	G	C	15	39	c.4741G>C	c.(4741-4743)GCC>CCC	p.A1581P
Pat_26	Pre-Treatment	RNF165	494470	37	18	44035938	44035938	Missense_Mutation	SNP	G	A	32	42	c.818G>A	c.(817-819)CGA>CAA	p.R273Q
Pat_26	Pre-Treatment	STARD6	147323	37	18	51863532	51863532	Missense_Mutation	SNP	G	A	74	125	c.230C>T	c.(229-231)TCA>TTA	p.S77L
Pat_26	Pre-Treatment	NEDD4L	23327	37	18	55833021	55833021	Missense_Mutation	SNP	G	A	6	19	c.50G>A	c.(49-51)GGA>GAA	p.G17E
Pat_26	Pre-Treatment	CCBE1	147372	37	18	57115221	57115221	Missense_Mutation	SNP	G	A	86	141	c.769C>T	c.(769-771)CCT>TCT	p.P257S
Pat_26	Pre-Treatment	SERPINB2	5055	37	18	61582740	61582740	Missense_Mutation	SNP	C	T	36	97	c.419C>T	c.(418-420)TCC>TTC	p.S140F
Pat_26	Pre-Treatment	ATP9B	374868	37	18	77132838	77132838	Missense_Mutation	SNP	C	T	37	60	c.3026C>T	c.(3025-3027)TCC>TTC	p.S1009F
Pat_26	Pre-Treatment	NFATC1	4772	37	18	77171045	77171045	Missense_Mutation	SNP	C	T	19	30	c.770C>T	c.(769-771)TCC>TTC	p.S257F
Pat_26	Pre-Treatment	PCSK4	54760	37	19	1483328	1483328	Missense_Mutation	SNP	G	A	4	33	c.1526C>T	c.(1525-1527)TCG>TTG	p.S509L
Pat_26	Pre-Treatment	PCSK4	54760	37	19	1486989	1486989	Missense_Mutation	SNP	C	T	6	449	c.931G>A	c.(931-933)GAC>AAC	p.D311N
Pat_26	Pre-Treatment	SPPL2B	56928	37	19	2345328	2345328	Missense_Mutation	SNP	G	A	4	160	c.1354G>A	c.(1354-1356)GCC>ACC	p.A452T
Pat_26	Pre-Treatment	ZNF555	148254	37	19	2853202	2853202	Missense_Mutation	SNP	C	T	6	103	c.1139C>T	c.(1138-1140)CCC>CTC	p.P380L
Pat_26	Pre-Treatment	TJP3	27134	37	19	3734334	3734334	Missense_Mutation	SNP	A	G	52	137	c.986A>G	c.(985-987)GAC>GGC	p.D329G
Pat_26	Pre-Treatment	UHRF1	29128	37	19	4954685	4954685	Missense_Mutation	SNP	C	T	12	15	c.1982C>T	c.(1981-1983)TCC>TTC	p.S661F
Pat_26	Pre-Treatment	RFX2	5990	37	19	6013085	6013085	Missense_Mutation	SNP	G	A	205	381	c.811C>T	c.(811-813)CGT>TGT	p.R271C

Pat_26	Pre-Treatment	C3	718	37	19	6712584	6712584	Missense_Mutation	SNP	G	A	216	347	c.1054C>T	c.(1054-1056)CCC>TCC	p.P352S
Pat_26	Pre-Treatment	PNPLA6	10908	37	19	7620564	7620564	Missense_Mutation	SNP	C	T	4	113	c.3038C>T	c.(3037-3039)ACG>ATG	p.T1013M
Pat_26	Pre-Treatment	NDUFA7	4701	37	19	8381449	8381449	Missense_Mutation	SNP	C	T	5	185	c.182G>A	c.(181-183)CGG>CAG	p.R61Q
Pat_26	Pre-Treatment	MUC16	94025	37	19	9009608	9009608	Missense_Mutation	SNP	C	T	189	351	c.39118G>A	c.(39118-39120)GAG>AA	p.E13040K
Pat_26	Pre-Treatment	MUC16	94025	37	19	9071925	9071925	Missense_Mutation	SNP	G	A	194	420	c.15521C>T	c.(15520-15522)TCC>TTC	p.S5174F
Pat_26	Pre-Treatment	ZNF699	374879	37	19	9406866	9406866	Missense_Mutation	SNP	G	A	57	101	c.1214C>T	c.(1213-1215)TCC>TTC	p.S405F
Pat_26	Pre-Treatment	KRI1	65095	37	19	10670123	10670123	Missense_Mutation	SNP	C	T	5	170	c.1124G>A	c.(1123-1125)CGG>CAG	p.R375Q
Pat_26	Pre-Treatment	SMARCA4	6597	37	19	11136975	11136975	Splice_Site	SNP	G	A	47	111	c.3169_splice	c.e23-1	p.E1057_splice
Pat_26	Pre-Treatment	ZNF625	90589	37	19	12257002	12257002	Missense_Mutation	SNP	C	T	41	72	c.31G>A	c.(31-33)GAT>AAT	p.D11N
Pat_26	Pre-Treatment	C19orf43	79002	37	19	12841792	12841792	Missense_Mutation	SNP	G	A	4	174	c.514C>T	c.(514-516)CGG>TGG	p.R172W
Pat_26	Pre-Treatment	TRMT1	55621	37	19	13216194	13216194	Missense_Mutation	SNP	C	T	201	277	c.1720G>A	c.(1720-1722)GAA>AAA	p.E574K
Pat_26	Pre-Treatment	LPHN1	22859	37	19	14273598	14273598	Missense_Mutation	SNP	C	T	4	133	c.1030G>A	c.(1030-1032)GTG>ATG	p.V344M
Pat_26	Pre-Treatment	NOTCH3	4854	37	19	15299917	15299917	Missense_Mutation	SNP	G	A	5	309	c.1261C>T	c.(1261-1263)CGT>TGT	p.R421C
Pat_26	Pre-Treatment	EPS15L1	58513	37	19	16515431	16515431	Missense_Mutation	SNP	C	T	4	189	c.1396G>A	c.(1396-1398)GTC>ATC	p.V466I
Pat_26	Pre-Treatment	NWD1	284434	37	19	16861221	16861221	Nonsense_Mutation	SNP	C	T	21	42	c.1768C>T	c.(1768-1770)CGA>TGA	p.R590*
Pat_26	Pre-Treatment	MAST3	23031	37	19	18239751	18239751	Missense_Mutation	SNP	G	A	4	160	c.1126G>A	c.(1126-1128)GGA>AGA	p.G376R
Pat_26	Pre-Treatment	MAST3	23031	37	19	18242814	18242814	Missense_Mutation	SNP	C	A	6	304	c.1441C>A	c.(1441-1443)CTG>ATG	p.L481M
Pat_26	Pre-Treatment	PGPEP1	54858	37	19	18453701	18453701	Missense_Mutation	SNP	G	A	5	308	c.67G>A	c.(67-69)GCC>ACC	p.A23T
Pat_26	Pre-Treatment	PBX4	80714	37	19	19681432	19681432	Missense_Mutation	SNP	C	T	50	105	c.404G>A	c.(403-405)CGA>CAA	p.R135Q
Pat_26	Pre-Treatment	ZNF682	91120	37	19	20117740	20117740	Missense_Mutation	SNP	G	A	7	15	c.571C>T	c.(571-573)CAT>TAT	p.H191Y
Pat_26	Pre-Treatment	ZNF676	163223	37	19	22363227	22363227	Missense_Mutation	SNP	C	G	5	221	c.1292G>C	c.(1291-1293)AGC>ACC	p.S431T
Pat_26	Pre-Treatment	ZNF98	148198	37	19	22574760	22574760	Missense_Mutation	SNP	C	A	4	94	c.1277G>T	c.(1276-1278)AGA>ATA	p.R426I
Pat_26	Pre-Treatment	ZNF536	9745	37	19	31039483	31039483	Missense_Mutation	SNP	C	T	67	132	c.2957C>T	c.(2956-2958)TCC>TTC	p.S986F
Pat_26	Pre-Treatment	TSHZ3	57616	37	19	31769341	31769341	Missense_Mutation	SNP	G	C	72	121	c.1358C>G	c.(1357-1359)ACG>AGG	p.T453R
Pat_26	Pre-Treatment	GPATCH1	55094	37	19	33603401	33603401	Missense_Mutation	SNP	G	A	6	385	c.1774G>A	c.(1774-1776)GGG>AGG	p.G592R
Pat_26	Pre-Treatment	ZNF567	163081	37	19	37210680	37210680	Missense_Mutation	SNP	C	T	4	155	c.1054C>T	c.(1054-1056)CTC>TTC	p.L352F
Pat_26	Pre-Treatment	SIPA1L3	23094	37	19	38621187	38621187	Missense_Mutation	SNP	G	A	82	180	c.2918G>A	c.(2917-2919)GGG>GAG	p.G973E
Pat_26	Pre-Treatment	C19orf33	64073	37	19	38795321	38795321	Missense_Mutation	SNP	G	C	4	146	c.196G>C	c.(196-198)GTG>CTG	p.V66L
Pat_26	Pre-Treatment	SIRT2	22933	37	19	39384056	39384056	Missense_Mutation	SNP	C	T	4	135	c.224G>A	c.(223-225)CGC>CAC	p.R75H
Pat_26	Pre-Treatment	TIMM50	92609	37	19	39976330	39976330	Missense_Mutation	SNP	G	A	108	214	c.684G>A	c.(682-684)ATG>ATA	p.M228I
Pat_26	Pre-Treatment	FCGBP	8857	37	19	40373993	40373993	Missense_Mutation	SNP	C	T	20	183	c.12085G>A	c.(12085-12087)GGG>AG	p.G4029R
Pat_26	Pre-Treatment	FCGBP	8857	37	19	40391996	40391996	Splice_Site	SNP	A	G	53	114	c.8388_splice	c.e17+1	p.E2796_splice
Pat_26	Pre-Treatment	ZNF574	64763	37	19	42584599	42584599	Missense_Mutation	SNP	G	A	5	333	c.1841G>A	c.(1840-1842)CGC>CAC	p.R614H
Pat_26	Pre-Treatment	ZNF526	116115	37	19	42729055	42729055	Missense_Mutation	SNP	C	T	6	342	c.500C>T	c.(499-501)ACG>ATG	p.T167M
Pat_26	Pre-Treatment	CIC	23152	37	19	42795519	42795519	Missense_Mutation	SNP	C	T	83	162	c.2599C>T	c.(2599-2601)CCA>TCA	p.P867S
Pat_26	Pre-Treatment	CADM4	199731	37	19	44130363	44130363	Missense_Mutation	SNP	C	T	5	190	c.577G>A	c.(577-579)GAC>AAC	p.D193N
Pat_26	Pre-Treatment	ZNF226	7769	37	19	44680470	44680470	Missense_Mutation	SNP	T	C	115	190	c.1055T>C	c.(1054-1056)GTT>GCT	p.V352A
Pat_26	Pre-Treatment	CBLC	23624	37	19	45296788	45296788	Missense_Mutation	SNP	G	A	4	130	c.1195G>A	c.(1195-1197)GTG>ATG	p.V399M
Pat_26	Pre-Treatment	PPM1N	147699	37	19	46003802	46003803	Missense_Mutation	DNP	GG	AA	26	50	.1146_1147GG>A	44-1149)GGGGGA>GGA	p.G383R
Pat_26	Pre-Treatment	QPCTL	54814	37	19	46205173	46205173	Splice_Site	SNP	G	A	6	131	c.1003_splice	c.e6+1	p.G335_splice
Pat_26	Pre-Treatment	CCDC8	83987	37	19	46914959	46914959	Missense_Mutation	SNP	T	C	10	474	c.1109A>G	c.(1108-1110)GAG>GGG	p.E370G
Pat_26	Pre-Treatment	CCDC155	147872	37	19	49900950	49900950	Missense_Mutation	SNP	G	A	123	291	c.443G>A	c.(442-444)GGA>GAA	p.G148E
Pat_26	Pre-Treatment	ALDH16A1	126133	37	19	49971731	49971731	Missense_Mutation	SNP	G	A	8	756	c.2032G>A	c.(2032-2034)GTG>ATG	p.V678M
Pat_26	Pre-Treatment	MYBPC2	4606	37	19	50964868	50964868	Missense_Mutation	SNP	G	A	54	91	c.3001G>A	c.(3001-3003)GAA>AAA	p.E1001K
Pat_26	Pre-Treatment	KLK1	3816	37	19	51323644	51323645	Missense_Mutation	DNP	GG	TA	149	356	c.261_262CC>TA	259-264)GCCCAG>GCTA	p.Q88K
Pat_26	Pre-Treatment	KLK8	11202	37	19	51499463	51499463	Missense_Mutation	SNP	G	A	47	113	c.635C>T	c.(634-636)TCT>TTT	p.S212F
Pat_26	Pre-Treatment	KLK9	284366	37	19	51512494	51512494	Missense_Mutation	SNP	C	T	17	36	c.145G>A	c.(145-147)GGG>AGG	p.G49R

Pat_26	Pre-Treatment	KLK12	43849	37	19	51532685	51532685	Missense_Mutation	SNP	C	A	4	165	c.620G>T	c.(619-621)GGG>GTG	p.G207V
Pat_26	Pre-Treatment	SIGLEC10	89790	37	19	51918507	51918507	Missense_Mutation	SNP	C	T	83	188	c.1258G>A	c.(1258-1260)GAA>AAA	p.E420K
Pat_26	Pre-Treatment	ZNF468	90333	37	19	53357599	53357599	Splice_Site	SNP	C	T	21	30	c.-72_splice	c.e2-1	
Pat_26	Pre-Treatment	DPRX	503834	37	19	54140195	54140195	Missense_Mutation	SNP	C	T	81	212	c.529C>T	c.(529-531)CAT>TAT	p.H177Y
Pat_26	Pre-Treatment	SYT5	6861	37	19	55686566	55686566	Missense_Mutation	SNP	C	T	12	13	c.682G>A	c.(682-684)GAG>AAG	p.E228K
Pat_26	Pre-Treatment	NLRP5	126206	37	19	56539255	56539255	Missense_Mutation	SNP	G	A	15	42	c.1656G>A	c.(1654-1656)ATG>ATA	p.M552I
Pat_26	Pre-Treatment	ZNF583	147949	37	19	56934818	56934818	Missense_Mutation	SNP	G	A	38	83	c.791G>A	c.(790-792)GGA>GAA	p.G264E
Pat_26	Pre-Treatment	ZSCAN4	201516	37	19	58187625	58187625	Missense_Mutation	SNP	G	A	38	91	c.112G>A	c.(112-114)GGG>AGG	p.G38R
Pat_26	Pre-Treatment	ZNF135	7694	37	19	58578529	58578529	Missense_Mutation	SNP	G	A	5	331	c.713G>A	c.(712-714)AGC>AAC	p.S238N
Pat_26	Pre-Treatment	MYT1L	23040	37	2	1983518	1983518	Missense_Mutation	SNP	C	T	4	118	c.32G>A	c.(31-33)CGC>CAC	p.R11H
Pat_26	Pre-Treatment	NBAS	51594	37	2	15696937	15696937	Nonsense_Mutation	SNP	A	T	51	88	c.179T>A	c.(178-180)TTA>TAA	p.L60*
Pat_26	Pre-Treatment	DDX1	1653	37	2	15769796	15769796	Missense_Mutation	SNP	G	A	4	104	c.1946G>A	c.(1945-1947)TGT>TAT	p.C649Y
Pat_26	Pre-Treatment	APOB	338	37	2	21236086	21236086	Missense_Mutation	SNP	G	A	172	274	c.4162C>T	c.(4162-4164)CGT>TGT	p.R1388C
Pat_26	Pre-Treatment	DPYSL5	56896	37	2	27164901	27164901	Missense_Mutation	SNP	G	T	126	229	c.1173G>T	c.(1171-1173)AAG>AAT	p.K391N
Pat_26	Pre-Treatment	DNAJC5G	285126	37	2	27503075	27503075	Missense_Mutation	SNP	G	A	109	183	c.562G>A	c.(562-564)GAT>AAT	p.D188N
Pat_26	Pre-Treatment	NLRC4	58484	37	2	32475886	32475886	Missense_Mutation	SNP	C	T	32	46	c.1047G>A	c.(1045-1047)ATG>ATA	p.M349I
Pat_26	Pre-Treatment	FAM98A	25940	37	2	33809982	33809982	Missense_Mutation	SNP	C	T	5	317	c.1418G>A	c.(1417-1419)CGT>CAT	p.R473H
Pat_26	Pre-Treatment	VIT	5212	37	2	37035774	37035774	Missense_Mutation	SNP	G	A	5	338	c.1549G>A	c.(1549-1551)GGC>AGC	p.G517S
Pat_26	Pre-Treatment	EIF2AK2	5610	37	2	37365691	37365691	Missense_Mutation	SNP	G	A	4	188	c.554C>T	c.(553-555)ACG>ATG	p.T185M
Pat_26	Pre-Treatment	LRPPRC	10128	37	2	44201383	44201383	Missense_Mutation	SNP	G	A	4	133	c.1061C>T	c.(1060-1062)GCG>GTG	p.A354V
Pat_26	Pre-Treatment	MSH6	2956	37	2	48033373	48033373	Missense_Mutation	SNP	C	A	4	144	c.3677C>A	c.(3676-3678)GCA>GAA	p.A1226E
Pat_26	Pre-Treatment	TSPYL6	388951	37	2	54483054	54483054	Missense_Mutation	SNP	G	A	5	181	c.235C>T	c.(235-237)CGC>TGC	p.R79C
Pat_26	Pre-Treatment	BCL11A	53335	37	2	60689281	60689281	Missense_Mutation	SNP	C	T	30	39	c.766G>A	c.(766-768)GAA>AAA	p.E256K
Pat_26	Pre-Treatment	USP34	9736	37	2	61605504	61605504	Missense_Mutation	SNP	G	C	55	113	c.1070C>G	c.(1069-1071)ACA>AGA	p.T357R
Pat_26	Pre-Treatment	DYSF	8291	37	2	71797734	71797734	Missense_Mutation	SNP	G	A	39	62	c.3037G>A	c.(3037-3039)GAG>AAG	p.E1013K
Pat_26	Pre-Treatment	DYSF	8291	37	2	71801437	71801437	Missense_Mutation	SNP	G	A	6	319	c.3284G>A	c.(3283-3285)CGC>CAC	p.R1095H
Pat_26	Pre-Treatment	SLC4A5	57835	37	2	74481792	74481792	Missense_Mutation	SNP	G	A	158	290	c.1067C>T	c.(1066-1068)TCC>TTC	p.S356F
Pat_26	Pre-Treatment	DCTN1	1639	37	2	74592757	74592757	Missense_Mutation	SNP	G	A	5	206	c.2914C>T	c.(2914-2916)CGG>TGG	p.R972W
Pat_26	Pre-Treatment	TLX2	3196	37	2	74742790	74742790	Missense_Mutation	SNP	G	A	7	495	c.431G>A	c.(430-432)CGC>CAC	p.R144H
Pat_26	Pre-Treatment	DQX1	165545	37	2	74751396	74751396	Missense_Mutation	SNP	G	A	6	368	c.470C>T	c.(469-471)TCG>TTG	p.S157L
Pat_26	Pre-Treatment	HK2	3099	37	2	75094769	75094769	Missense_Mutation	SNP	G	A	236	454	c.233G>A	c.(232-234)GGA>GAA	p.G78E
Pat_26	Pre-Treatment	LOC285033	285033	37	2	96906408	96906408	Missense_Mutation	SNP	C	T	60	72	c.347C>T	c.(346-348)TCC>TTC	p.S116F
Pat_26	Pre-Treatment	NCAPH	23397	37	2	97019928	97019928	Missense_Mutation	SNP	C	T	8	361	c.1010C>T	c.(1009-1011)TCG>TTG	p.S337L
Pat_26	Pre-Treatment	TSGA10	80705	37	2	99634699	99634699	Missense_Mutation	SNP	C	T	46	89	c.2036G>A	c.(2035-2037)CGA>CAA	p.R679Q
Pat_26	Pre-Treatment	REV1	51455	37	2	100052317	100052317	Nonsense_Mutation	SNP	G	A	5	316	c.1300C>T	c.(1300-1302)CGA>TGA	p.R434*
Pat_26	Pre-Treatment	ST6GAL2	84620	37	2	107459818	107459818	Missense_Mutation	SNP	G	A	25	48	c.616C>T	c.(616-618)CGG>TGG	p.R206W
Pat_26	Pre-Treatment	ST6GAL2	84620	37	2	107460402	107460402	Missense_Mutation	SNP	C	T	47	69	c.32G>A	c.(31-33)CGA>CAA	p.R11Q
Pat_26	Pre-Treatment	RGPD4	285190	37	2	108488208	108488208	Missense_Mutation	SNP	G	A	202	322	c.3748G>A	c.(3748-3750)GAT>AAT	p.D1250N
Pat_26	Pre-Treatment	SLC5A7	60482	37	2	108626702	108626702	Missense_Mutation	SNP	A	T	63	120	c.1128A>T	c.(1126-1128)GAA>GAT	p.E376D
Pat_26	Pre-Treatment	SULT1C2	6819	37	2	108921643	108921643	Nonsense_Mutation	SNP	G	A	100	197	c.518G>A	c.(517-519)TGG>TAG	p.W173*
Pat_26	Pre-Treatment	SULT1C4	27233	37	2	108999611	108999611	Missense_Mutation	SNP	G	T	34	57	c.456G>T	c.(454-456)ATG>ATT	p.M152I
Pat_26	Pre-Treatment	NCKAP5	344148	37	2	133540369	133540370	Missense_Mutation	DNP	CA	TT	6	19	.4014_4015TG>A	012-4017)GTTGGG>GTAA	p.G1339R
Pat_26	Pre-Treatment	LCT	3938	37	2	136566672	136566672	Missense_Mutation	SNP	C	T	19	24	c.3245G>A	c.(3244-3246)GGG>GAG	p.G1082E
Pat_26	Pre-Treatment	THSD7B	80731	37	2	137872755	137872755	Missense_Mutation	SNP	G	A	68	91	c.1168G>A	c.(1168-1170)GAT>AAT	p.D390N
Pat_26	Pre-Treatment	LRP1B	53353	37	2	141298592	141298592	Missense_Mutation	SNP	T	C	115	166	c.7463A>G	c.(7462-7464)AAT>AGT	p.N2488S
Pat_26	Pre-Treatment	NEB	4703	37	2	152466537	152466537	Missense_Mutation	SNP	C	T	27	60	c.11387G>A	c.(11386-11388)GGA>GAA	p.G3796E
Pat_26	Pre-Treatment	TANC1	85461	37	2	160076367	160076367	Missense_Mutation	SNP	G	A	5	137	c.3667G>A	c.(3667-3669)GAT>AAT	p.D1223N

Pat_26	Pre-Treatment	GRB14	2888	37	2	165365320	165365320	Missense_Mutation	SNP	C	T	59	131	c.859G>A	c.(859-861)GAT>AAT	p.D287N
Pat_26	Pre-Treatment	SCN3A	6328	37	2	166032843	166032843	Missense_Mutation	SNP	G	A	56	84	c.62C>T	c.(61-63)TCT>TTT	p.S21F
Pat_26	Pre-Treatment	LRP2	4036	37	2	170147469	170147469	Missense_Mutation	SNP	C	T	34	101	c.808G>A	c.(808-810)GAA>AAA	p.E270K
Pat_26	Pre-Treatment	TTN	7273	37	2	179416831	179416831	Missense_Mutation	SNP	C	T	102	175	c.83092G>A	c.(83092-83094)GAA>AAA	p.E27698K
Pat_26	Pre-Treatment	TTN	7273	37	2	179427038	179427038	Missense_Mutation	SNP	C	T	44	83	c.76117G>A	c.(76117-76119)GAA>AAA	p.E25373K
Pat_26	Pre-Treatment	TTN	7273	37	2	179430017	179430017	Missense_Mutation	SNP	C	T	37	121	c.73138G>A	c.(73138-73140)GGA>AGA	p.G24380R
Pat_26	Pre-Treatment	TTN	7273	37	2	179452410	179452410	Missense_Mutation	SNP	C	T	22	36	c.55922G>A	c.(55921-55923)CGA>CAA	p.R18641Q
Pat_26	Pre-Treatment	TTN	7273	37	2	179473588	179473588	Missense_Mutation	SNP	T	C	45	97	c.44446A>G	c.(44446-44448)ACC>GCC	p.T14816A
Pat_26	Pre-Treatment	TTN	7273	37	2	179569999	179569999	Missense_Mutation	SNP	C	T	8	18	c.25774G>A	c.(25774-25776)GAA>AAA	p.E8592K
Pat_26	Pre-Treatment	COL3A1	1281	37	2	189868772	189868772	Missense_Mutation	SNP	G	A	4	89	c.2726G>A	c.(2725-2727)GGT>GAT	p.G909D
Pat_26	Pre-Treatment	COL5A2	1290	37	2	189910528	189910528	Missense_Mutation	SNP	G	A	40	94	c.3307C>T	c.(3307-3309)CCG>TCG	p.P1103S
Pat_26	Pre-Treatment	COL5A2	1290	37	2	189936782	189936782	Missense_Mutation	SNP	C	A	3	12	c.1142G>T	c.(1141-1143)GGA>GTA	p.G381V
Pat_26	Pre-Treatment	SLC40A1	30061	37	2	190426638	190426638	Missense_Mutation	SNP	C	T	4	89	c.1682G>A	c.(1681-1683)AGG>AAG	p.R561K
Pat_26	Pre-Treatment	ANKAR	150709	37	2	190606067	190606067	Splice_Site	SNP	G	A	20	44	c.3488_splice	c.e19-1	p.G1163_splice
Pat_26	Pre-Treatment	NAB1	4664	37	2	191550329	191550329	Missense_Mutation	SNP	C	T	43	89	c.1223C>T	c.(1222-1224)CCT>CTT	p.P408L
Pat_26	Pre-Treatment	SDPR	8436	37	2	192701440	192701440	Missense_Mutation	SNP	C	T	7	22	c.487G>A	c.(487-489)GAA>AAA	p.E163K
Pat_26	Pre-Treatment	TMEFF2	23671	37	2	192818525	192818525	Missense_Mutation	SNP	T	C	5	166	c.908A>G	c.(907-909)AAG>AGG	p.K303R
Pat_26	Pre-Treatment	CCDC150	284992	37	2	197511152	197511152	Missense_Mutation	SNP	C	A	7	287	c.100C>A	c.(100-102)CAA>AAA	p.Q34K
Pat_26	Pre-Treatment	ANKRD44	91526	37	2	197987432	197987432	Missense_Mutation	SNP	G	A	6	180	c.635C>T	c.(634-636)GCT>GTT	p.A212V
Pat_26	Pre-Treatment	AOX1	316	37	2	201523919	201523919	Missense_Mutation	SNP	C	T	4	144	c.3203C>T	c.(3202-3204)TCG>TTG	p.S1068L
Pat_26	Pre-Treatment	ICA1L	130026	37	2	203684548	203684548	Missense_Mutation	SNP	G	A	50	84	c.434C>T	c.(433-435)ACC>ATC	p.T145I
Pat_26	Pre-Treatment	CPS1	1373	37	2	211444459	211444459	Missense_Mutation	SNP	G	A	52	127	c.493G>A	c.(493-495)GAC>AAC	p.D165N
Pat_26	Pre-Treatment	VWC2L	402117	37	2	215279114	215279114	Missense_Mutation	SNP	G	A	26	45	c.197G>A	c.(196-198)CGA>CAA	p.R66Q
Pat_26	Pre-Treatment	BARD1	580	37	2	215633994	215633994	Missense_Mutation	SNP	C	T	4	124	c.1357G>A	c.(1357-1359)GAT>AAT	p.D453N
Pat_26	Pre-Treatment	ATIC	471	37	2	216182921	216182921	Missense_Mutation	SNP	G	A	134	255	c.188G>A	c.(187-189)GGA>GAA	p.G63E
Pat_26	Pre-Treatment	VIL1	7429	37	2	219301222	219301222	Missense_Mutation	SNP	T	C	198	357	c.1844T>C	c.(1843-1845)CTG>CCG	p.L615P
Pat_26	Pre-Treatment	TTLL4	9654	37	2	219603034	219603034	Missense_Mutation	SNP	C	T	56	124	c.635C>T	c.(634-636)TCC>TTC	p.S212F
Pat_26	Pre-Treatment	KCNE4	23704	37	2	223917957	223917957	Missense_Mutation	SNP	A	G	4	169	c.409A>G	c.(409-411)ACC>GCC	p.T137A
Pat_26	Pre-Treatment	ALPPL2	251	37	2	233272555	233272555	Missense_Mutation	SNP	G	A	76	121	c.476G>A	c.(475-477)GGA>GAA	p.G159E
Pat_26	Pre-Treatment	DGKD	8527	37	2	234368933	234368933	Missense_Mutation	SNP	G	A	80	127	c.2923G>A	c.(2923-2925)GAG>AAG	p.E975K
Pat_26	Pre-Treatment	PER2	8864	37	2	239186525	239186525	Missense_Mutation	SNP	G	A	29	71	c.53C>T	c.(52-54)CCC>CTC	p.P18L
Pat_26	Pre-Treatment	ANO7	50636	37	2	242139610	242139610	Missense_Mutation	SNP	C	T	89	110	c.686C>T	c.(685-687)TCC>TTC	p.S229F
Pat_26	Pre-Treatment	ANO7	50636	37	2	242149925	242149925	Missense_Mutation	SNP	G	A	5	346	c.1663G>A	c.(1663-1665)GTC>ATC	p.V555I
Pat_26	Pre-Treatment	FARP2	9855	37	2	242380792	242380792	Missense_Mutation	SNP	C	T	118	163	c.1232C>T	c.(1231-1233)CCC>CTC	p.P411L
Pat_26	Pre-Treatment	TGM3	7053	37	20	2320592	2320592	Missense_Mutation	SNP	G	A	4	79	c.1893G>A	c.(1891-1893)ATG>ATA	p.M631I
Pat_26	Pre-Treatment	TMC2	117532	37	20	2572971	2572971	Missense_Mutation	SNP	C	T	117	154	c.850C>T	c.(850-852)CCC>TCC	p.P284S
Pat_26	Pre-Treatment	PRND	23627	37	20	4705663	4705663	Missense_Mutation	SNP	C	T	4	186	c.466C>T	c.(466-468)CGG>TGG	p.R156W
Pat_26	Pre-Treatment	RIN2	54453	37	20	19941428	19941428	Missense_Mutation	SNP	G	A	9	19	c.436G>A	c.(436-438)GAA>AAA	p.E146K
Pat_26	Pre-Treatment	REM1	28954	37	20	30070268	30070268	Missense_Mutation	SNP	G	A	6	161	c.602G>A	c.(601-603)CGC>CAC	p.R201H
Pat_26	Pre-Treatment	XKR7	343702	37	20	30585052	30585052	Missense_Mutation	SNP	C	T	71	157	c.1532C>T	c.(1531-1533)CCA>CTA	p.P511L
Pat_26	Pre-Treatment	HCK	3055	37	20	30671801	30671801	Missense_Mutation	SNP	C	G	64	133	c.637C>G	c.(637-639)CGA>GGA	p.R213G
Pat_26	Pre-Treatment	ITCH	83737	37	20	32981622	32981622	Missense_Mutation	SNP	C	T	131	240	c.5C>T	c.(4-6)TCT>TTT	p.S2F
Pat_26	Pre-Treatment	RBM12	10137	37	20	34242575	34242575	Missense_Mutation	SNP	G	A	4	156	c.670C>T	c.(670-672)CCC>TCC	p.P224S
Pat_26	Pre-Treatment	DLGAP4	22839	37	20	35127676	35127676	Missense_Mutation	SNP	C	T	5	352	c.2042C>T	c.(2041-2043)TCG>TTG	p.S681L
Pat_26	Pre-Treatment	NCOA5	57727	37	20	44699128	44699128	Missense_Mutation	SNP	G	A	151	284	c.86C>T	c.(85-87)TCC>TTC	p.S29F
Pat_26	Pre-Treatment	STAU1	6780	37	20	47739771	47739771	Missense_Mutation	SNP	G	A	81	173	c.824C>T	c.(823-825)CCA>CTA	p.P275L
Pat_26	Pre-Treatment	NFATC2	4773	37	20	50139963	50139963	Missense_Mutation	SNP	G	A	4	48	c.817C>T	c.(817-819)CGG>TGG	p.R273W

Pat_26	Pre-Treatment	LAMA5	3911	37	20	60885365	60885365	Missense_Mutation	SNP	G	A	4	151	c.10603C>T	c.(10603-10605)CTC>TTC	p.L3535F
Pat_26	Pre-Treatment	LAMA5	3911	37	20	60921968	60921968	Splice_Site	SNP	C	T	5	289	c.1072_splice	c.e7+1	p.S358_splice
Pat_26	Pre-Treatment	UCKL1	54963	37	20	62571742	62571742	Missense_Mutation	SNP	G	A	4	124	c.1399C>T	c.(1399-1401)CGC>TGC	p.R467C
Pat_26	Pre-Treatment	TCEA2	6919	37	20	62700845	62700845	Splice_Site	SNP	G	A	4	187	c.460_splice	c.e5+1	p.H154_splice
Pat_26	Pre-Treatment	SON	6651	37	21	34924871	34924871	Nonsense_Mutation	SNP	C	T	5	310	c.3334C>T	c.(3334-3336)CGA>TGA	p.R1112*
Pat_26	Pre-Treatment	MCM3AP	8888	37	21	47693423	47693423	Missense_Mutation	SNP	C	T	5	112	c.2075G>A	c.(2074-2076)CGG>CAG	p.R692Q
Pat_26	Pre-Treatment	HIRA	7290	37	22	19375245	19375245	Missense_Mutation	SNP	C	T	5	87	c.1102G>A	c.(1102-1104)GAG>AAG	p.E368K
Pat_26	Pre-Treatment	CDC45	8318	37	22	19471512	19471512	Missense_Mutation	SNP	G	A	4	192	c.470G>A	c.(469-471)CGC>CAC	p.R157H
Pat_26	Pre-Treatment	TRMT2A	27037	37	22	20103604	20103604	Missense_Mutation	SNP	G	A	5	389	c.556C>T	c.(556-558)CGG>TGG	p.R186W
Pat_26	Pre-Treatment	RIMBP3	85376	37	22	20457214	20457214	Missense_Mutation	SNP	G	A	22	47	c.4088C>T	c.(4087-4089)CCC>CTC	p.P1363L
Pat_26	Pre-Treatment	ADRBK2	157	37	22	26107059	26107059	Missense_Mutation	SNP	C	T	4	139	c.1420C>T	c.(1420-1422)CGG>TGG	p.R474W
Pat_26	Pre-Treatment	SRRD	402055	37	22	26884387	26884387	Missense_Mutation	SNP	C	T	155	271	c.542C>T	c.(541-543)CCT>CTT	p.P181L
Pat_26	Pre-Treatment	EMID1	129080	37	22	29627106	29627106	Missense_Mutation	SNP	G	A	4	188	c.557G>A	c.(556-558)AGC>AAC	p.S186N
Pat_26	Pre-Treatment	GAS2L1	10634	37	22	29708404	29708404	Missense_Mutation	SNP	G	A	4	136	c.1964G>A	c.(1963-1965)CGC>CAC	p.R655H
Pat_26	Pre-Treatment	GAL3ST1	9514	37	22	30951719	30951719	Missense_Mutation	SNP	C	T	124	248	c.493G>A	c.(493-495)GAC>AAC	p.D165N
Pat_26	Pre-Treatment	TCN2	6948	37	22	31008971	31008971	Missense_Mutation	SNP	G	T	48	131	c.369G>T	c.(367-369)AAG>AAT	p.K123N
Pat_26	Pre-Treatment	SMTN	6525	37	22	31487688	31487688	Missense_Mutation	SNP	C	T	86	206	c.1487C>T	c.(1486-1488)CCG>CTG	p.P496L
Pat_26	Pre-Treatment	SFI1	9814	37	22	32000931	32000931	Missense_Mutation	SNP	G	A	7	57	c.2054G>A	c.(2053-2055)CGC>CAC	p.R685H
Pat_26	Pre-Treatment	TRIOBP	11078	37	22	38119918	38119918	Missense_Mutation	SNP	C	G	9	293	c.1355C>G	c.(1354-1356)ACA>AGA	p.T452R
Pat_26	Pre-Treatment	TRIOBP	11078	37	22	38120437	38120437	Missense_Mutation	SNP	G	C	7	442	c.1874G>C	c.(1873-1875)AGA>ACA	p.R625T
Pat_26	Pre-Treatment	TRIOBP	11078	37	22	38151639	38151639	Missense_Mutation	SNP	G	A	6	311	c.5660G>A	c.(5659-5661)CGT>CAT	p.R1887H
Pat_26	Pre-Treatment	MKL1	57591	37	22	40816901	40816901	Missense_Mutation	SNP	C	G	6	240	c.831G>C	c.(829-831)CAG>CAC	p.Q277H
Pat_26	Pre-Treatment	EP300	2033	37	22	41531849	41531850	Missense_Mutation	DNP	GG	AA	47	130	.1561_1562GG>A	c.(1561-1563)GGA>AAA	p.G521K
Pat_26	Pre-Treatment	CYP2D6	1565	37	22	42523908	42523908	Missense_Mutation	SNP	C	T	115	280	c.921G>A	c.(919-921)ATG>ATA	p.M307I
Pat_26	Pre-Treatment	CYP2D7P1	1564	37	22	42537916	42537916	Nonsense_Mutation	SNP	G	A	3	40	c.535C>T	c.(535-537)CGA>TGA	p.R179*
Pat_26	Pre-Treatment	CERK	64781	37	22	47116880	47116880	Missense_Mutation	SNP	C	T	7	595	c.175G>A	c.(175-177)GCC>ACC	p.A59T
Pat_26	Pre-Treatment	PLXNB2	23654	37	22	50716022	50716022	Missense_Mutation	SNP	G	A	5	276	c.5194C>T	c.(5194-5196)CGC>TGC	p.R1732C
Pat_26	Pre-Treatment	SAPS2	9701	37	22	50873439	50873439	Missense_Mutation	SNP	G	A	4	181	c.1445G>A	c.(1444-1446)CGG>CAG	p.R482Q
Pat_26	Pre-Treatment	SAPS2	9701	37	22	50874861	50874861	Missense_Mutation	SNP	C	T	9	20	c.1582C>T	c.(1582-1584)CGC>TGC	p.R528C
Pat_26	Pre-Treatment	CHL1	10752	37	3	382573	382573	Missense_Mutation	SNP	C	T	19	82	c.482C>T	c.(481-483)CCT>CTT	p.P161L
Pat_26	Pre-Treatment	ITPR1	3708	37	3	4829776	4829776	Missense_Mutation	SNP	G	C	5	23	c.6617G>C	c.(6616-6618)CGG>CCG	p.R2206P
Pat_26	Pre-Treatment	C3orf32	51066	37	3	8669448	8669448	Missense_Mutation	SNP	C	T	4	168	c.544G>A	c.(544-546)GGA>AGA	p.G182R
Pat_26	Pre-Treatment	ATG7	10533	37	3	11402205	11402205	Missense_Mutation	SNP	C	T	236	442	c.1630C>T	c.(1630-1632)CCT>TCT	p.P544S
Pat_26	Pre-Treatment	IQSEC1	9922	37	3	12963729	12963729	Missense_Mutation	SNP	C	T	5	141	c.1786G>A	c.(1786-1788)GAG>AAG	p.E596K
Pat_26	Pre-Treatment	ZNF385D	79750	37	3	21552508	21552508	Missense_Mutation	SNP	G	A	37	48	c.284C>T	c.(283-285)GCT>GTT	p.A95V
Pat_26	Pre-Treatment	ARPP21	10777	37	3	35833903	35833903	Missense_Mutation	SNP	G	A	135	245	c.2062G>A	c.(2062-2064)GGA>AGA	p.G688R
Pat_26	Pre-Treatment	SLC22A13	9390	37	3	38307500	38307500	Missense_Mutation	SNP	G	A	5	215	c.149G>A	c.(148-150)TGT>TAT	p.C50Y
Pat_26	Pre-Treatment	XYLB	9942	37	3	38416711	38416711	Missense_Mutation	SNP	G	T	5	202	c.965G>T	c.(964-966)TGC>TTC	p.C322F
Pat_26	Pre-Treatment	SCN11A	11280	37	3	38946734	38946734	Nonsense_Mutation	SNP	G	A	103	151	c.1552C>T	c.(1552-1554)CAA>TAA	p.Q518*
Pat_26	Pre-Treatment	SCN11A	11280	37	3	38949450	38949450	Missense_Mutation	SNP	C	A	13	68	c.1463G>T	c.(1462-1464)TGC>TTC	p.C488F
Pat_26	Pre-Treatment	ZNF502	91392	37	3	44763369	44763369	Missense_Mutation	SNP	A	G	3	86	c.1060A>G	c.(1060-1062)AAA>GAA	p.K354E
Pat_26	Pre-Treatment	CDCP1	64866	37	3	45127257	45127257	Missense_Mutation	SNP	G	A	4	121	c.2384C>T	c.(2383-2385)CCT>CTT	p.P795L
Pat_26	Pre-Treatment	CDCP1	64866	37	3	45153823	45153823	Missense_Mutation	SNP	C	T	239	378	c.407G>A	c.(406-408)GGT>GAT	p.G136D
Pat_26	Pre-Treatment	CCRL2	9034	37	3	46450190	46450190	Missense_Mutation	SNP	C	T	4	178	c.620C>T	c.(619-621)TCG>TTG	p.S207L
Pat_26	Pre-Treatment	PRSS50	29122	37	3	46753818	46753818	Missense_Mutation	SNP	C	T	27	23	c.1076G>A	c.(1075-1077)GGG>GAG	p.G359E
Pat_26	Pre-Treatment	CELSR3	1951	37	3	48683635	48683635	Missense_Mutation	SNP	C	T	4	137	c.7351G>A	c.(7351-7353)GGA>AGA	p.G2451R
Pat_26	Pre-Treatment	BSN	8927	37	3	49694737	49694737	Missense_Mutation	SNP	G	A	4	123	c.7748G>A	c.(7747-7749)AGC>AAC	p.S2583N

Pat_26	Pre-Treatment	ABHD14B	84836	37	3	52005634	52005634	Missense_Mutation	SNP	G	A	41	53	c.53C>T	c.(52-54)GCC>GTC	p.A18V
Pat_26	Pre-Treatment	DUSP7	1849	37	3	52085136	52085136	Missense_Mutation	SNP	C	T	4	159	c.955G>A	c.(955-957)GAA>AAA	p.E319K
Pat_26	Pre-Treatment	GLYCTK	132158	37	3	52324365	52324365	Missense_Mutation	SNP	G	A	4	116	c.7G>A	c.(7-9)GCA>ACA	p.A3T
Pat_26	Pre-Treatment	BAP1	8314	37	3	52437677	52437677	Missense_Mutation	SNP	G	A	4	95	c.1484C>T	c.(1483-1485)ACG>ATG	p.T495M
Pat_26	Pre-Treatment	FAM107A	11170	37	3	58555481	58555481	Missense_Mutation	SNP	T	C	32	63	c.107A>G	c.(106-108)AAC>AGC	p.N36S
Pat_26	Pre-Treatment	SUCLG2	8801	37	3	67571047	67571048	Missense_Mutation	DNP	AG	TT	5	176	c.428_429CT>AA	c.(427-429)GCT>GAA	p.A143E
Pat_26	Pre-Treatment	ROBO2	6092	37	3	77637968	77637968	Missense_Mutation	SNP	T	G	49	94	c.2567T>G	c.(2566-2568)GTG>GGG	p.V856G
Pat_26	Pre-Treatment	CRYBG3	131544	37	3	97596417	97596417	Missense_Mutation	SNP	C	T	33	60	c.535C>T	c.(535-537)CTC>TTC	p.L179F
Pat_26	Pre-Treatment	CBLB	868	37	3	105464833	105464833	Missense_Mutation	SNP	G	A	93	148	c.773C>T	c.(772-774)CCA>CTA	p.P258L
Pat_26	Pre-Treatment	GUCA1C	9626	37	3	108672495	108672495	Missense_Mutation	SNP	C	T	89	178	c.115G>A	c.(115-117)GAA>AAA	p.E39K
Pat_26	Pre-Treatment	MORC1	27136	37	3	108751574	108751574	Missense_Mutation	SNP	C	T	12	29	c.1558G>A	c.(1558-1560)GAA>AAA	p.E520K
Pat_26	Pre-Treatment	WDR52	55779	37	3	113146126	113146126	Missense_Mutation	SNP	C	T	28	39	c.161G>A	c.(160-162)GGG>GAG	p.G54E
Pat_26	Pre-Treatment	POLQ	10721	37	3	121256023	121256023	Missense_Mutation	SNP	C	T	87	182	c.664G>A	c.(664-666)GGA>AGA	p.G222R
Pat_26	Pre-Treatment	SLC15A2	6565	37	3	121647395	121647395	Missense_Mutation	SNP	C	T	66	145	c.1334C>T	c.(1333-1335)TCC>TTC	p.S445F
Pat_26	Pre-Treatment	MYLK	4638	37	3	123457860	123457861	Missense_Mutation	DNP	CC	TT	20	60	c.471_472GG>AA	469-474)GGGGAG>GGAA	p.E158K
Pat_26	Pre-Treatment	KALRN	8997	37	3	123987869	123987869	Missense_Mutation	SNP	G	A	4	27	c.730G>A	c.(730-732)GAG>AAG	p.E244K
Pat_26	Pre-Treatment	UMPS	7372	37	3	124449427	124449427	Missense_Mutation	SNP	T	C	5	173	c.109T>C	c.(109-111)TAC>CAC	p.Y37H
Pat_26	Pre-Treatment	SEC61A1	29927	37	3	127786827	127786827	Missense_Mutation	SNP	T	C	176	362	c.1169T>C	c.(1168-1170)GTT>GCT	p.V390A
Pat_26	Pre-Treatment	COL6A6	131873	37	3	130311915	130311915	Missense_Mutation	SNP	G	A	184	325	c.4382G>A	c.(4381-4383)GGG>GAG	p.G1461E
Pat_26	Pre-Treatment	ATP2C1	27032	37	3	130698165	130698165	Missense_Mutation	SNP	C	T	93	134	c.1643C>T	c.(1642-1644)CCT>CTT	p.P548L
Pat_26	Pre-Treatment	DNAJC13	23317	37	3	132169656	132169656	Missense_Mutation	SNP	G	A	30	68	c.502G>A	c.(502-504)GGA>AGA	p.G168R
Pat_26	Pre-Treatment	AMOTL2	51421	37	3	134090038	134090038	Nonsense_Mutation	SNP	G	A	35	57	c.412C>T	c.(412-414)CAG>TAG	p.Q138*
Pat_26	Pre-Treatment	PCCB	5096	37	3	136012707	136012707	Splice_Site	SNP	G	A	5	225	c.763_splice	c.e7+1	p.G255_splice
Pat_26	Pre-Treatment	HPS3	84343	37	3	148876530	148876530	Missense_Mutation	SNP	G	A	5	380	c.1769G>A	c.(1768-1770)CGC>CAC	p.R590H
Pat_26	Pre-Treatment	WWTR1	25937	37	3	149238728	149238728	Missense_Mutation	SNP	C	T	5	337	c.1067G>A	c.(1066-1068)CGT>CAT	p.R356H
Pat_26	Pre-Treatment	B3GNT5	84002	37	3	182988256	182988256	Missense_Mutation	SNP	C	T	92	166	c.670C>T	c.(670-672)CAT>TAT	p.H224Y
Pat_26	Pre-Treatment	YEATS2	55689	37	3	183493736	183493736	Missense_Mutation	SNP	G	A	6	336	c.2402G>A	c.(2401-2403)AGT>AAT	p.S801N
Pat_26	Pre-Treatment	DVL3	1857	37	3	183885727	183885727	Missense_Mutation	SNP	T	C	72	186	c.1372T>C	c.(1372-1374)TTC>CTC	p.F458L
Pat_26	Pre-Treatment	FAM131A	131408	37	3	184062624	184062624	Missense_Mutation	SNP	G	A	4	139	c.874G>A	c.(874-876)GCC>ACC	p.A292T
Pat_26	Pre-Treatment	FAM43A	131583	37	3	194407998	194407998	Missense_Mutation	SNP	G	A	3	24	c.443G>A	c.(442-444)CGG>CAG	p.R148Q
Pat_26	Pre-Treatment	OSTalpha	200931	37	3	195955029	195955029	Missense_Mutation	SNP	G	A	207	392	c.406G>A	c.(406-408)GAA>AAA	p.E136K
Pat_26	Pre-Treatment	GAK	2580	37	4	843685	843685	Missense_Mutation	SNP	C	T	4	66	c.3829G>A	c.(3829-3831)GAC>AAC	p.D1277N
Pat_26	Pre-Treatment	MAEA	10296	37	4	1326630	1326630	Missense_Mutation	SNP	G	A	4	102	c.742G>A	c.(742-744)GAC>AAC	p.D248N
Pat_26	Pre-Treatment	ZFYVE28	57732	37	4	2307157	2307157	Missense_Mutation	SNP	C	T	4	144	c.910G>A	c.(910-912)GCT>ACT	p.A304T
Pat_26	Pre-Treatment	RGS12	6002	37	4	3418686	3418686	Missense_Mutation	SNP	C	T	118	231	c.2474C>T	c.(2473-2475)TCC>TTC	p.S825F
Pat_26	Pre-Treatment	JAKMIP1	152789	37	4	6087308	6087308	Missense_Mutation	SNP	C	T	136	266	c.673G>A	c.(673-675)GAA>AAA	p.E225K
Pat_26	Pre-Treatment	GBA3	57733	37	4	22748945	22748945	Missense_Mutation	SNP	G	A	66	146	c.313G>A	c.(313-315)GAT>AAT	p.D105N
Pat_26	Pre-Treatment	LIMCH1	22998	37	4	41682113	41682113	Missense_Mutation	SNP	G	A	13	18	c.2458G>A	c.(2458-2460)GAG>AAG	p.E820K
Pat_26	Pre-Treatment	GABRB1	2560	37	4	47408782	47408782	Missense_Mutation	SNP	G	A	51	124	c.919G>A	c.(919-921)GAT>AAT	p.D307N
Pat_26	Pre-Treatment	KDR	3791	37	4	55984966	55984966	Missense_Mutation	SNP	C	T	50	80	c.163G>A	c.(163-165)GGA>AGA	p.G55R
Pat_26	Pre-Treatment	PAICS	10606	37	4	57325591	57325591	Nonsense_Mutation	SNP	C	T	27	69	c.1165C>T	c.(1165-1167)CAG>TAG	p.Q389*
Pat_26	Pre-Treatment	EPHA5	2044	37	4	66230894	66230894	Missense_Mutation	SNP	G	A	4	120	c.2077C>T	c.(2077-2079)CGT>TGT	p.R693C
Pat_26	Pre-Treatment	GNRHR	2798	37	4	68619972	68619972	Missense_Mutation	SNP	G	A	5	353	c.82C>T	c.(82-84)CTC>TTC	p.L28F
Pat_26	Pre-Treatment	TMPRSS11B	132724	37	4	69097030	69097030	Missense_Mutation	SNP	C	T	40	59	c.577G>A	c.(577-579)GAG>AAG	p.E193K
Pat_26	Pre-Treatment	UGT2B28	54490	37	4	70146547	70146547	Missense_Mutation	SNP	C	T	39	103	c.329C>T	c.(328-330)TCA>TTA	p.S110L
Pat_26	Pre-Treatment	UGT2B28	54490	37	4	70148286	70148286	Missense_Mutation	SNP	G	A	68	125	c.776G>A	c.(775-777)CGA>CAA	p.R259Q
Pat_26	Pre-Treatment	AMBN	258	37	4	71471945	71471945	Missense_Mutation	SNP	G	A	34	74	c.842G>A	c.(841-843)GGA>GAA	p.G281E

Pat_26	Pre-Treatment	PTPN13	5783	37	4	87687584	87687584	Splice_Site	SNP	G	T	3	35	c.4244_splice	c.e27-1	.G1415_splice
Pat_26	Pre-Treatment	HERC3	8916	37	4	89571065	89571065	Missense_Mutation	SNP	G	A	4	158	c.301G>A	c.(301-303)GAC>AAC	p.D101N
Pat_26	Pre-Treatment	MTTP	4547	37	4	100515972	100515972	Missense_Mutation	SNP	G	A	7	249	c.841G>A	c.(841-843)GAT>AAT	p.D281N
Pat_26	Pre-Treatment	CENPE	1062	37	4	104057392	104057392	Missense_Mutation	SNP	G	A	35	93	c.6428C>T	c.(6427-6429)TCA>TTA	p.S2143L
Pat_26	Pre-Treatment	GSTCD	79807	37	4	106766720	106766721	Missense_Mutation	DNP	GG	AA	36	56	.1888_1889GG>A	c.(1888-1890)GGA>AAA	p.G630K
Pat_26	Pre-Treatment	ANK2	287	37	4	114163336	114163336	Nonsense_Mutation	SNP	C	T	4	164	c.862C>T	c.(862-864)CGA>TGA	p.R288*
Pat_26	Pre-Treatment	BBS12	166379	37	4	123664573	123664573	Missense_Mutation	SNP	C	T	4	137	c.1526C>T	c.(1525-1527)ACT>ATT	p.T509I
Pat_26	Pre-Treatment	FAT4	79633	37	4	126372621	126372621	Missense_Mutation	SNP	G	A	94	156	c.10450G>A	c.(10450-10452)GAT>AAT	p.D3484N
Pat_26	Pre-Treatment	FAT4	79633	37	4	126398438	126398438	Missense_Mutation	SNP	G	A	73	145	c.12422G>A	.(12421-12423)GGA>GA	p.G4141E
Pat_26	Pre-Treatment	ARFIP1	27236	37	4	153750801	153750802	Missense_Mutation	DNP	CC	TT	65	136	c.16_17CC>TT	c.(16-18)CCC>TTC	p.P6F
Pat_26	Pre-Treatment	GLRA3	8001	37	4	175598335	175598335	Missense_Mutation	SNP	G	A	44	83	c.821C>T	c.(820-822)TCA>TTA	p.S274L
Pat_26	Pre-Treatment	AGA	175	37	4	178361497	178361497	Missense_Mutation	SNP	C	T	6	420	c.211G>A	c.(211-213)GGC>AGC	p.G71S
Pat_26	Pre-Treatment	LPCAT1	79888	37	5	1481075	1481075	Missense_Mutation	SNP	G	A	7	517	c.743C>T	c.(742-744)ACG>ATG	p.T248M
Pat_26	Pre-Treatment	IRX4	50805	37	5	1879941	1879941	Missense_Mutation	SNP	C	T	28	34	c.413G>A	c.(412-414)GGA>GAA	p.G138E
Pat_26	Pre-Treatment	MED10	84246	37	5	6372626	6372626	Missense_Mutation	SNP	G	A	8	225	c.398C>T	c.(397-399)CCG>CTG	p.P133L
Pat_26	Pre-Treatment	CTNND2	1501	37	5	10992705	10992705	Missense_Mutation	SNP	G	A	61	133	c.3169C>T	c.(3169-3171)CCC>TCC	p.P1057S
Pat_26	Pre-Treatment	DNAH5	1767	37	5	13771050	13771050	Missense_Mutation	SNP	C	T	36	73	c.9413G>A	c.(9412-9414)AGT>AAT	p.S3138N
Pat_26	Pre-Treatment	11-Mar	441061	37	5	16091014	16091014	Missense_Mutation	SNP	C	T	24	67	c.870G>A	c.(868-870)ATG>ATA	p.M290I
Pat_26	Pre-Treatment	CDH18	1016	37	5	19721546	19721546	Missense_Mutation	SNP	C	T	50	148	c.553G>A	c.(553-555)GAT>AAT	p.D185N
Pat_26	Pre-Treatment	CDH18	1016	37	5	19839093	19839093	Missense_Mutation	SNP	C	T	25	78	c.3G>A	c.(1-3)ATG>ATA	p.M1I
Pat_26	Pre-Treatment	PRDM9	56979	37	5	23509648	23509648	Missense_Mutation	SNP	G	A	80	173	c.139G>A	c.(139-141)GAG>AAG	p.E47K
Pat_26	Pre-Treatment	CDH10	1008	37	5	24487995	24487995	Missense_Mutation	SNP	T	A	43	65	c.2144A>T	c.(2143-2145)AAT>ATT	p.N715I
Pat_26	Pre-Treatment	RNASEN	29102	37	5	31410922	31410922	Missense_Mutation	SNP	C	T	5	228	c.3598G>A	c.(3598-3600)GCC>ACC	p.A1200T
Pat_26	Pre-Treatment	PDZD2	23037	37	5	32052798	32052798	Missense_Mutation	SNP	G	A	5	327	c.1747G>A	c.(1747-1749)GTC>ATC	p.V583I
Pat_26	Pre-Treatment	PDZD2	23037	37	5	32087434	32087434	Missense_Mutation	SNP	G	A	91	90	c.3880G>A	c.(3880-3882)GAG>AAG	p.E1294K
Pat_26	Pre-Treatment	PDZD2	23037	37	5	32089159	32089159	Missense_Mutation	SNP	G	A	4	74	c.5605G>A	c.(5605-5607)GCA>ACA	p.A1869T
Pat_26	Pre-Treatment	C5orf42	65250	37	5	37169549	37169549	Missense_Mutation	SNP	C	T	4	89	c.6577G>A	c.(6577-6579)GGA>AGA	p.G2193R
Pat_26	Pre-Treatment	RICTOR	253260	37	5	38959295	38959295	Splice_Site	SNP	A	T	4	104	c.2178_splice	c.e22+1	p.D726_splice
Pat_26	Pre-Treatment	C6	729	37	5	41186251	41186251	Missense_Mutation	SNP	C	T	26	60	c.647G>A	c.(646-648)GGA>GAA	p.G216E
Pat_26	Pre-Treatment	IPO11	51194	37	5	61887486	61887486	Missense_Mutation	SNP	G	A	31	52	c.2665G>A	c.(2665-2667)GGA>AGA	p.G889R
Pat_26	Pre-Treatment	MARVELD2	153562	37	5	68728399	68728399	Missense_Mutation	SNP	A	G	26	57	c.1228A>G	c.(1228-1230)AAT>GAT	p.N410D
Pat_26	Pre-Treatment	ENC1	8507	37	5	73930869	73930869	Missense_Mutation	SNP	G	A	46	111	c.1442C>T	c.(1441-1443)CCC>CTC	p.P481L
Pat_26	Pre-Treatment	PDE8B	8622	37	5	76714055	76714055	Missense_Mutation	SNP	G	A	16	37	c.1913G>A	c.(1912-1914)GGA>GAA	p.G638E
Pat_26	Pre-Treatment	ANKRD34B	340120	37	5	79854638	79854638	Missense_Mutation	SNP	G	A	34	70	c.1201C>T	c.(1201-1203)CCT>TCT	p.P401S
Pat_26	Pre-Treatment	NBPF22P	285622	37	5	85578532	85578532	Missense_Mutation	SNP	G	T	6	191	c.9G>T	c.(7-9)TTG>TTT	p.L3F
Pat_26	Pre-Treatment	GPR98	84059	37	5	89933551	89933551	Missense_Mutation	SNP	C	T	4	19	c.2026C>T	c.(2026-2028)CCC>TCC	p.P676S
Pat_26	Pre-Treatment	GPR98	84059	37	5	90024556	90024556	Missense_Mutation	SNP	C	T	94	197	c.10232C>T	.(10231-10233)GCC>GT	p.A3411V
Pat_26	Pre-Treatment	GPR98	84059	37	5	90111487	90111487	Missense_Mutation	SNP	G	A	5	15	c.16130G>A	.(16129-16131)GGA>GA	p.G5377E
Pat_26	Pre-Treatment	PAM	5066	37	5	102345512	102345512	Missense_Mutation	SNP	G	A	30	60	c.2273G>A	c.(2272-2274)GGA>GAA	p.G758E
Pat_26	Pre-Treatment	ZNF474	133923	37	5	121488745	121488745	Missense_Mutation	SNP	G	A	4	117	c.1060G>A	c.(1060-1062)GCA>ACA	p.A354T
Pat_26	Pre-Treatment	SNCAIP	9627	37	5	121739548	121739548	Missense_Mutation	SNP	G	A	143	109	c.118G>A	c.(118-120)GAA>AAA	p.E40K
Pat_26	Pre-Treatment	PCDHA1	56147	37	5	140166416	140166416	Missense_Mutation	SNP	G	A	32	21	c.541G>A	c.(541-543)GAT>AAT	p.D181N
Pat_26	Pre-Treatment	PCDHA3	56145	37	5	140182635	140182635	Missense_Mutation	SNP	C	T	5	243	c.1853C>T	c.(1852-1854)GCG>GTG	p.A618V
Pat_26	Pre-Treatment	PCDHA4	56144	37	5	140188460	140188460	Missense_Mutation	SNP	C	A	4	112	c.1688C>A	c.(1687-1689)CCA>CAA	p.P563Q
Pat_26	Pre-Treatment	PCDHGB3	56102	37	5	140752101	140752101	Missense_Mutation	SNP	C	T	92	66	c.2140C>T	c.(2140-2142)CGC>TGC	p.R714C
Pat_26	Pre-Treatment	FAT2	2196	37	5	150885533	150885533	Missense_Mutation	SNP	C	T	6	280	c.12643G>A	c.(12643-12645)GTG>ATG	p.V4215M
Pat_26	Pre-Treatment	FAT2	2196	37	5	150917383	150917383	Missense_Mutation	SNP	G	A	6	212	c.9164C>T	c.(9163-9165)GCG>GTG	p.A3055V

Pat_26	Pre-Treatment	GLRA1	2741	37	5	151239530	151239530	Missense_Mutation	SNP	C	T	57	97	c.292G>A	c.(292-294)GAC>AAC	p.D98N
Pat_26	Pre-Treatment	MFAP3	4238	37	5	153432575	153432575	Missense_Mutation	SNP	C	T	117	205	c.391C>T	c.(391-393)CGT>TGT	p.R131C
Pat_26	Pre-Treatment	NIPAL4	348938	37	5	156899928	156899928	Missense_Mutation	SNP	C	T	51	106	c.1361C>T	c.(1360-1362)TCA>TTA	p.S454L
Pat_26	Pre-Treatment	GABRB2	2561	37	5	160753392	160753392	Missense_Mutation	SNP	C	T	90	164	c.1174G>A	c.(1174-1176)GAT>AAT	p.D392N
Pat_26	Pre-Treatment	DOCK2	1794	37	5	169461429	169461429	Missense_Mutation	SNP	C	A	5	186	c.3494C>A	c.(3493-3495)CCA>CAA	p.P1165Q
Pat_26	Pre-Treatment	MGAT4B	11282	37	5	179228422	179228422	Missense_Mutation	SNP	G	A	5	309	c.470C>T	c.(469-471)TCG>TTG	p.S157L
Pat_26	Pre-Treatment	FARS2	10667	37	6	5771562	5771562	Missense_Mutation	SNP	G	A	5	265	c.1256G>A	c.(1255-1257)CGC>CAC	p.R419H
Pat_26	Pre-Treatment	RREB1	6239	37	6	7231502	7231502	Missense_Mutation	SNP	C	T	191	359	c.3170C>T	c.(3169-3171)CCC>CTC	p.P1057L
Pat_26	Pre-Treatment	PHACTR1	221692	37	6	13053737	13053737	Missense_Mutation	SNP	G	A	4	101	c.391G>A	c.(391-393)GAA>AAA	p.E131K
Pat_26	Pre-Treatment	TBC1D7	51256	37	6	13327103	13327103	Missense_Mutation	SNP	G	A	4	122	c.28C>T	c.(28-30)CGT>TGT	p.R10C
Pat_26	Pre-Treatment	NKAPL	222698	37	6	28227372	28227372	Missense_Mutation	SNP	C	T	4	107	c.223C>T	c.(223-225)CTC>TTC	p.L75F
Pat_26	Pre-Treatment	SCAND3	114821	37	6	28540442	28540442	Missense_Mutation	SNP	C	T	73	110	c.3224G>A	c.(3223-3225)CGA>CAA	p.R1075Q
Pat_26	Pre-Treatment	DDR1	780	37	6	30857092	30857092	Missense_Mutation	SNP	G	A	5	139	c.302G>A	c.(301-303)GGC>GAC	p.G101D
Pat_26	Pre-Treatment	PSORS1C2	170680	37	6	31105837	31105837	Nonsense_Mutation	SNP	C	T	5	140	c.302G>A	c.(301-303)TGG>TAG	p.W101*
Pat_26	Pre-Treatment	BAT2	7916	37	6	31592996	31592996	Missense_Mutation	SNP	C	T	71	120	c.512C>T	c.(511-513)CCG>CTG	p.P171L
Pat_26	Pre-Treatment	BAT2	7916	37	6	31593808	31593808	Missense_Mutation	SNP	G	A	5	183	c.851G>A	c.(850-852)CGT>CAT	p.R284H
Pat_26	Pre-Treatment	BAT2	7916	37	6	31599185	31599185	Missense_Mutation	SNP	G	A	3	25	c.2735G>A	c.(2734-2736)GGC>GAC	p.G912D
Pat_26	Pre-Treatment	C4A	720	37	6	31963519	31963519	Missense_Mutation	SNP	C	T	74	300	c.3178C>T	c.(3178-3180)CGG>TGG	p.R1060W
Pat_26	Pre-Treatment	TNXB	7148	37	6	32037342	32037342	Missense_Mutation	SNP	C	T	4	188	c.5575G>A	c.(5575-5577)GTC>ATC	p.V1859I
Pat_26	Pre-Treatment	TAPBP	6892	37	6	33281045	33281045	Nonsense_Mutation	SNP	G	A	5	281	c.418C>T	c.(418-420)CGA>TGA	p.R140*
Pat_26	Pre-Treatment	ITPR3	3710	37	6	33647686	33647686	Missense_Mutation	SNP	G	A	4	114	c.4000G>A	c.(4000-4002)GTG>ATG	p.V1334M
Pat_26	Pre-Treatment	SPDEF	25803	37	6	34512223	34512223	Missense_Mutation	SNP	C	T	4	106	c.10G>A	c.(10-12)GCC>ACC	p.A4T
Pat_26	Pre-Treatment	DNAH8	1769	37	6	38875853	38875853	Missense_Mutation	SNP	C	T	22	31	c.8819C>T	c.(8818-8820)TCA>TTA	p.S2940L
Pat_26	Pre-Treatment	GLP1R	2740	37	6	39046935	39046935	Missense_Mutation	SNP	A	T	180	318	c.1002A>T	c.(1000-1002)AAA>AAT	p.K334N
Pat_26	Pre-Treatment	LRFN2	57497	37	6	40399991	40399991	Missense_Mutation	SNP	G	A	5	251	c.862C>T	c.(862-864)CCG>TCG	p.P288S
Pat_26	Pre-Treatment	FOXP4	116113	37	6	41555536	41555536	Missense_Mutation	SNP	C	T	12	26	c.878C>T	c.(877-879)TCC>TTC	p.S293F
Pat_26	Pre-Treatment	CUL9	23113	37	6	43166401	43166401	Missense_Mutation	SNP	G	A	7	495	c.2858G>A	c.(2857-2859)CGA>CAA	p.R953Q
Pat_26	Pre-Treatment	SLC22A7	10864	37	6	43266358	43266358	Missense_Mutation	SNP	G	A	14	19	c.262G>A	c.(262-264)GCT>ACT	p.A88T
Pat_26	Pre-Treatment	GTPBP2	54676	37	6	43592343	43592343	Missense_Mutation	SNP	C	T	59	89	c.1004G>A	c.(1003-1005)CGG>CAG	p.R335Q
Pat_26	Pre-Treatment	TMEM63B	55362	37	6	44117686	44117686	Missense_Mutation	SNP	G	A	44	74	c.1504G>A	c.(1504-1506)GAA>AAA	p.E502K
Pat_26	Pre-Treatment	RUNX2	860	37	6	45480097	45480097	Missense_Mutation	SNP	G	A	5	355	c.974G>A	c.(973-975)CGG>CAG	p.R325Q
Pat_26	Pre-Treatment	COL21A1	81578	37	6	55933885	55933885	Missense_Mutation	SNP	C	T	13	18	c.2050G>A	c.(2050-2052)GAA>AAA	p.E684K
Pat_26	Pre-Treatment	BAI3	577	37	6	70082297	70082297	Splice_Site	SNP	G	A	10	12	c.4240_splice	c.e30-1	p.R1414_splice
Pat_26	Pre-Treatment	COL9A1	1297	37	6	70990721	70990721	Missense_Mutation	SNP	G	A	3	46	c.898C>T	c.(898-900)CCC>TCC	p.P300S
Pat_26	Pre-Treatment	GPR63	81491	37	6	97247496	97247496	Missense_Mutation	SNP	G	A	37	69	c.112C>T	c.(112-114)CCT>TCT	p.P38S
Pat_26	Pre-Treatment	WISP3	8838	37	6	112390739	112390739	Nonsense_Mutation	SNP	G	A	48	75	c.981G>A	c.(979-981)TGG>TGA	p.W327*
Pat_26	Pre-Treatment	NT5DC1	221294	37	6	116544279	116544279	Missense_Mutation	SNP	C	T	95	58	c.787C>T	c.(787-789)CCT>TCT	p.P263S
Pat_26	Pre-Treatment	ROS1	6098	37	6	117650583	117650583	Missense_Mutation	SNP	G	A	26	31	c.5275C>T	c.(5275-5277)CCC>TCC	p.P1759S
Pat_26	Pre-Treatment	GJA1	2697	37	6	121768405	121768405	Missense_Mutation	SNP	G	A	4	195	c.412G>A	c.(412-414)GGT>AGT	p.G138S
Pat_26	Pre-Treatment	NCOA7	135112	37	6	126242132	126242132	Missense_Mutation	SNP	G	A	4	139	c.2288G>A	c.(2287-2289)AGC>AAC	p.S763N
Pat_26	Pre-Treatment	ARG1	383	37	6	131900341	131900341	Missense_Mutation	SNP	G	A	49	31	c.221G>A	c.(220-222)GGA>GAA	p.G74E
Pat_26	Pre-Treatment	CTAGE9	643854	37	6	132031227	132031227	Missense_Mutation	SNP	G	A	42	19	c.931C>T	c.(931-933)CCG>TCG	p.P311S
Pat_26	Pre-Treatment	IL20RA	53832	37	6	137338238	137338238	Missense_Mutation	SNP	G	A	19	13	c.91C>T	c.(91-93)CCC>TCC	p.P31S
Pat_26	Pre-Treatment	LATS1	9113	37	6	149997811	149997811	Nonsense_Mutation	SNP	G	A	31	17	c.2656C>T	c.(2656-2658)CGA>TGA	p.R886*
Pat_26	Pre-Treatment	PPP1R14C	81706	37	6	150535953	150535953	Nonsense_Mutation	SNP	C	A	4	120	c.380C>A	c.(379-381)TCA>TAA	p.S127*
Pat_26	Pre-Treatment	SYNE1	23345	37	6	152730807	152730807	Missense_Mutation	SNP	C	T	56	33	c.6268G>A	c.(6268-6270)GAA>AAA	p.E2090K
Pat_26	Pre-Treatment	RSPH3	83861	37	6	159403527	159403527	Missense_Mutation	SNP	C	T	4	85	c.1112G>A	c.(1111-1113)CGA>CAA	p.R371Q

Pat_26	Pre-Treatment	PHF10	55274	37	6	170115848	170115848	Missense_Mutation	SNP	C	T	44	37	c.649G>A	c.(649-651)GAA>AAA	p.E217K
Pat_26	Pre-Treatment	CHST12	55501	37	7	2472575	2472575	Missense_Mutation	SNP	G	A	4	159	c.301G>A	c.(301-303)GTG>ATG	p.V101M
Pat_26	Pre-Treatment	RADIL	55698	37	7	4874803	4874803	Missense_Mutation	SNP	G	A	22	51	c.851C>T	c.(850-852)CCC>CTC	p.P284L
Pat_26	Pre-Treatment	USP42	84132	37	7	6189601	6189601	Missense_Mutation	SNP	G	A	4	60	c.1774G>A	c.(1774-1776)GTG>ATG	p.V592M
Pat_26	Pre-Treatment	USP42	84132	37	7	6194300	6194300	Missense_Mutation	SNP	G	A	4	114	c.3115G>A	c.(3115-3117)GAG>AAG	p.E1039K
Pat_26	Pre-Treatment	RAC1	5879	37	7	6426892	6426892	Missense_Mutation	SNP	C	T	108	159	c.85C>T	c.(85-87)CCT>TCT	p.P29S
Pat_26	Pre-Treatment	THSD7A	221981	37	7	11521546	11521546	Missense_Mutation	SNP	G	A	4	152	c.1886C>T	c.(1885-1887)GCC>GTC	p.A629V
Pat_26	Pre-Treatment	KLHL7	55975	37	7	23164306	23164306	Splice_Site	SNP	G	C	3	91	c.224_splice	c.e3-1	p.T75_splice
Pat_26	Pre-Treatment	DFNA5	1687	37	7	24789342	24789342	Missense_Mutation	SNP	C	T	90	182	c.52G>A	c.(52-54)GAC>AAC	p.D18N
Pat_26	Pre-Treatment	EVX1	2128	37	7	27285964	27285964	Missense_Mutation	SNP	C	T	4	69	c.1144C>T	c.(1144-1146)CTC>TTC	p.L382F
Pat_26	Pre-Treatment	ADCYAP1R1	117	37	7	31146156	31146156	Missense_Mutation	SNP	G	A	6	314	c.1265G>A	c.(1264-1266)CGT>CAT	p.R422H
Pat_26	Pre-Treatment	OGDH	4967	37	7	44734078	44734078	Missense_Mutation	SNP	C	T	79	128	c.1571C>T	c.(1570-1572)CCG>CTG	p.P524L
Pat_26	Pre-Treatment	ADCY1	107	37	7	45743044	45743044	Missense_Mutation	SNP	C	T	5	149	c.2524C>T	c.(2524-2526)CCG>TCG	p.P842S
Pat_26	Pre-Treatment	TNS3	64759	37	7	47343138	47343138	Missense_Mutation	SNP	G	A	7	14	c.2867C>T	c.(2866-2868)CCC>CTC	p.P956L
Pat_26	Pre-Treatment	PKD1L1	168507	37	7	47867041	47867041	Missense_Mutation	SNP	C	T	4	82	c.6761G>A	c.(6760-6762)CGC>CAC	p.R2254H
Pat_26	Pre-Treatment	PKD1L1	168507	37	7	47904813	47904813	Splice_Site	SNP	C	T	12	23	c.4149_splice	c.e26+1	p.K1383_splice
Pat_26	Pre-Treatment	ABCA13	154664	37	7	48353922	48353922	Missense_Mutation	SNP	G	A	14	17	c.9775G>A	c.(9775-9777)GAT>AAT	p.D3259N
Pat_26	Pre-Treatment	NCF1	653361	37	7	74193632	74193632	Missense_Mutation	SNP	G	A	5	324	c.259G>A	c.(259-261)GCC>ACC	p.A87T
Pat_26	Pre-Treatment	DTX2	113878	37	7	76134733	76134733	Missense_Mutation	SNP	T	C	13	29	c.1684T>C	c.(1684-1686)TTC>CTC	p.F562L
Pat_26	Pre-Treatment	PCLO	27445	37	7	82764309	82764309	Missense_Mutation	SNP	C	T	66	148	c.2557G>A	c.(2557-2559)GAA>AAA	p.E853K
Pat_26	Pre-Treatment	SEMA3A	10371	37	7	83592633	83592633	Missense_Mutation	SNP	C	T	57	115	c.1748G>A	c.(1747-1749)AGA>AAA	p.R583K
Pat_26	Pre-Treatment	STEAP2	261729	37	7	89856645	89856645	Missense_Mutation	SNP	G	A	4	176	c.853G>A	c.(853-855)GGC>AGC	p.G285S
Pat_26	Pre-Treatment	SAMD9	54809	37	7	92732185	92732186	Missense_Mutation	DNP	GG	AA	35	44	.3225_3226CC>T	3223-3228)ATCCAT>ATTT	p.H1076Y
Pat_26	Pre-Treatment	COL1A2	1278	37	7	94055131	94055131	Missense_Mutation	SNP	G	A	8	15	c.2905G>A	c.(2905-2907)GTG>ATG	p.V969M
Pat_26	Pre-Treatment	ARPC1B	10095	37	7	98988637	98988637	Missense_Mutation	SNP	G	A	4	101	c.622G>A	c.(622-624)GTC>ATC	p.V208I
Pat_26	Pre-Treatment	ZKSCAN1	7586	37	7	99621904	99621904	Missense_Mutation	SNP	G	A	4	148	c.554G>A	c.(553-555)CGG>CAG	p.R185Q
Pat_26	Pre-Treatment	STAG3	10734	37	7	99796940	99796940	Missense_Mutation	SNP	G	A	6	293	c.1523G>A	c.(1522-1524)CGG>CAG	p.R508Q
Pat_26	Pre-Treatment	EPHB4	2050	37	7	100410379	100410379	Missense_Mutation	SNP	G	A	21	54	c.2108C>T	c.(2107-2109)TCC>TTC	p.S703F
Pat_26	Pre-Treatment	PMPCB	9512	37	7	102949522	102949522	Missense_Mutation	SNP	C	T	4	160	c.973C>T	c.(973-975)CGC>TGC	p.R325C
Pat_26	Pre-Treatment	MLL5	55904	37	7	104742439	104742439	Missense_Mutation	SNP	G	A	5	310	c.1994G>A	c.(1993-1995)CGT>CAT	p.R665H
Pat_26	Pre-Treatment	SRPK2	6733	37	7	104783638	104783638	Missense_Mutation	SNP	G	A	59	136	c.920C>T	c.(919-921)ACC>ATC	p.T307I
Pat_26	Pre-Treatment	PPP1R3A	5506	37	7	113519690	113519690	Missense_Mutation	SNP	C	T	31	53	c.1457G>A	c.(1456-1458)CGA>CAA	p.R486Q
Pat_26	Pre-Treatment	ASB15	142685	37	7	123269228	123269228	Missense_Mutation	SNP	G	A	21	59	c.1180G>A	c.(1180-1182)GAA>AAA	p.E394K
Pat_26	Pre-Treatment	PAX4	5078	37	7	127253881	127253881	Missense_Mutation	SNP	C	T	4	138	c.467G>A	c.(466-468)GGT>GAT	p.G156D
Pat_26	Pre-Treatment	OPN1SW	611	37	7	128413880	128413880	Missense_Mutation	SNP	C	T	6	155	c.750G>A	c.(748-750)ATG>ATA	p.M250I
Pat_26	Pre-Treatment	RAB19	401409	37	7	140107616	140107616	Missense_Mutation	SNP	G	A	4	185	c.170G>A	c.(169-171)CGT>CAT	p.R57H
Pat_26	Pre-Treatment	DENND2A	27147	37	7	140301735	140301735	Missense_Mutation	SNP	C	T	63	103	c.463G>A	c.(463-465)GAT>AAT	p.D155N
Pat_26	Pre-Treatment	BRAF	673	37	7	140453136	140453136	Missense_Mutation	SNP	A	T	47	120	c.1799T>A	c.(1798-1800)GTG>GAG	p.V600E
Pat_26	Pre-Treatment	MGAM	8972	37	7	141731520	141731520	Missense_Mutation	SNP	C	T	78	175	c.1511C>T	c.(1510-1512)CCC>CTC	p.P504L
Pat_26	Pre-Treatment	C7orf34	135927	37	7	142636842	142636842	Missense_Mutation	SNP	C	T	14	31	c.199C>T	c.(199-201)CCC>TCC	p.P67S
Pat_26	Pre-Treatment	OR2F2	135948	37	7	143633023	143633023	Missense_Mutation	SNP	G	A	50	94	c.698G>A	c.(697-699)GGA>GAA	p.G233E
Pat_26	Pre-Treatment	PDIA4	9601	37	7	148705250	148705250	Splice_Site	SNP	C	T	4	111	c.1131_splice	c.e7+1	p.Q377_splice
Pat_26	Pre-Treatment	SSPO	23145	37	7	149477388	149477388	Missense_Mutation	SNP	G	A	4	25	c.1459G>A	c.(1459-1461)GAG>AAG	p.E487K
Pat_26	Pre-Treatment	GIMAP5	55340	37	7	150439711	150439711	Missense_Mutation	SNP	G	C	126	256	c.484G>C	c.(484-486)GAT>CAT	p.D162H
Pat_26	Pre-Treatment	KCNH2	3757	37	7	150649680	150649680	Missense_Mutation	SNP	T	A	8	655	c.1390A>T	c.(1390-1392)ATT>TTT	p.I464F
Pat_26	Pre-Treatment	VIPR2	7434	37	7	158902542	158902542	Missense_Mutation	SNP	G	A	73	151	c.220C>T	c.(220-222)CCC>TCC	p.P74S
Pat_26	Pre-Treatment	CSMD1	64478	37	8	3059206	3059206	Missense_Mutation	SNP	C	T	19	37	c.5029G>A	c.(5029-5031)GAT>AAT	p.D1677N

Pat_26	Pre-Treatment	AGPAT5	55326	37	8	6588251	6588251	Missense_Mutation	SNP	C	G	8	273	c.309C>G	c.(307-309)GAC>GAG	p.D103E
Pat_26	Pre-Treatment	BLK	640	37	8	11405589	11405589	Missense_Mutation	SNP	G	A	5	346	c.224G>A	c.(223-225)CGG>CAG	p.R75Q
Pat_26	Pre-Treatment	PCM1	5108	37	8	17823629	17823629	Missense_Mutation	SNP	G	A	4	134	c.2977G>A	c.(2977-2979)GTA>ATA	p.V993I
Pat_26	Pre-Treatment	ASAH1	427	37	8	17924743	17924743	Missense_Mutation	SNP	G	A	4	119	c.368C>T	c.(367-369)ACT>ATT	p.T123I
Pat_26	Pre-Treatment	SLC18A1	6570	37	8	20007227	20007227	Missense_Mutation	SNP	G	A	43	67	c.1106C>T	c.(1105-1107)TCC>TTC	p.S369F
Pat_26	Pre-Treatment	XPO7	23039	37	8	21844746	21844746	Missense_Mutation	SNP	C	T	4	184	c.1672C>T	c.(1672-1674)CGT>TGT	p.R558C
Pat_26	Pre-Treatment	ADAMDEC1	27299	37	8	24251607	24251607	Missense_Mutation	SNP	G	A	43	97	c.310G>A	c.(310-312)GAA>AAA	p.E104K
Pat_26	Pre-Treatment	ADAM7	8756	37	8	24300055	24300055	Missense_Mutation	SNP	G	A	121	212	c.122G>A	c.(121-123)CGA>CAA	p.R41Q
Pat_26	Pre-Treatment	ADAM7	8756	37	8	24339742	24339742	Missense_Mutation	SNP	G	A	18	32	c.793G>A	c.(793-795)GAA>AAA	p.E265K
Pat_26	Pre-Treatment	BNIP3L	665	37	8	26252780	26252780	Missense_Mutation	SNP	G	A	40	98	c.319G>A	c.(319-321)GAT>AAT	p.D107N
Pat_26	Pre-Treatment	BNIP3L	665	37	8	26252782	26252782	Missense_Mutation	SNP	T	A	42	97	c.321T>A	c.(319-321)GAT>GAA	p.D107E
Pat_26	Pre-Treatment	SCARA3	51435	37	8	27516870	27516870	Missense_Mutation	SNP	G	A	31	57	c.1183G>A	c.(1183-1185)GAG>AAG	p.E395K
Pat_26	Pre-Treatment	FBXO16	157574	37	8	28340887	28340887	Missense_Mutation	SNP	T	G	162	245	c.77A>C	c.(76-78)AAC>ACC	p.N26T
Pat_26	Pre-Treatment	ADAM32	203102	37	8	39022685	39022685	Missense_Mutation	SNP	T	C	2	5	c.803T>C	c.(802-804)CTA>CCA	p.L268P
Pat_26	Pre-Treatment	MCM4	4173	37	8	48877195	48877195	Missense_Mutation	SNP	C	T	42	72	c.755C>T	c.(754-756)TCA>TTA	p.S252L
Pat_26	Pre-Treatment	MCM4	4173	37	8	48885469	48885469	Missense_Mutation	SNP	C	T	4	177	c.1981C>T	c.(1981-1983)CGT>TGT	p.R661C
Pat_26	Pre-Treatment	PXDNL	137902	37	8	52321593	52321593	Missense_Mutation	SNP	C	T	4	112	c.2591G>A	c.(2590-2592)CGC>CAC	p.R864H
Pat_26	Pre-Treatment	FAM110B	90362	37	8	59058956	59058956	Missense_Mutation	SNP	C	T	58	64	c.167C>T	c.(166-168)GCC>GTC	p.A56V
Pat_26	Pre-Treatment	NSMAF	8439	37	8	59508216	59508216	Missense_Mutation	SNP	C	T	31	64	c.1795G>A	c.(1795-1797)GAA>AAA	p.E599K
Pat_26	Pre-Treatment	YTHDF3	253943	37	8	64100034	64100034	Missense_Mutation	SNP	G	T	4	152	c.1465G>T	c.(1465-1467)GCT>TCT	p.A489S
Pat_26	Pre-Treatment	ARFGEF1	10565	37	8	68170417	68170417	Missense_Mutation	SNP	G	A	32	51	c.2344C>T	c.(2344-2346)CGT>TGT	p.R782C
Pat_26	Pre-Treatment	SLCO5A1	81796	37	8	70585280	70585280	Missense_Mutation	SNP	G	A	5	241	c.2371C>T	c.(2371-2373)CGG>TGG	p.R791W
Pat_26	Pre-Treatment	CA1	759	37	8	86253846	86253846	Missense_Mutation	SNP	C	T	29	106	c.19G>A	c.(19-21)GGA>AGA	p.G7R
Pat_26	Pre-Treatment	INTS8	55656	37	8	95840000	95840000	Missense_Mutation	SNP	C	T	151	250	c.497C>T	c.(496-498)CCC>CTC	p.P166L
Pat_26	Pre-Treatment	VPS13B	157680	37	8	100791192	100791192	Missense_Mutation	SNP	C	T	131	233	c.7787C>T	c.(7786-7788)TCT>TTT	p.S2596F
Pat_26	Pre-Treatment	UBR5	51366	37	8	103316274	103316274	Missense_Mutation	SNP	C	T	4	88	c.2951G>A	c.(2950-2952)CGA>CAA	p.R984Q
Pat_26	Pre-Treatment	TRHR	7201	37	8	110131570	110131570	Missense_Mutation	SNP	C	A	76	192	c.1083C>A	c.(1081-1083)GAC>GAA	p.D361E
Pat_26	Pre-Treatment	SLC30A8	169026	37	8	118147586	118147586	Missense_Mutation	SNP	C	T	6	382	c.20C>T	c.(19-21)ACG>ATG	p.T7M
Pat_26	Pre-Treatment	SAMD12	401474	37	8	119593082	119593082	Missense_Mutation	SNP	C	T	36	92	c.64G>A	c.(64-66)GAA>AAA	p.E22K
Pat_26	Pre-Treatment	COL14A1	7373	37	8	121210152	121210152	Missense_Mutation	SNP	G	A	20	32	c.695G>A	c.(694-696)GGA>GAA	p.G232E
Pat_26	Pre-Treatment	ADCY8	114	37	8	131880114	131880114	Missense_Mutation	SNP	G	T	33	92	c.2188C>A	c.(2188-2190)CAA>AAA	p.Q730K
Pat_26	Pre-Treatment	TG	7038	37	8	133900276	133900276	Missense_Mutation	SNP	G	A	9	139	c.2224G>A	c.(2224-2226)GTG>ATG	p.V742M
Pat_26	Pre-Treatment	COL22A1	169044	37	8	139815131	139815131	Missense_Mutation	SNP	C	T	69	112	c.1541G>A	c.(1540-1542)GGA>GAA	p.G514E
Pat_26	Pre-Treatment	COL22A1	169044	37	8	139839023	139839023	Missense_Mutation	SNP	C	T	16	35	c.847G>A	c.(847-849)GAT>AAT	p.D283N
Pat_26	Pre-Treatment	MAPK15	225689	37	8	144803950	144803950	Missense_Mutation	SNP	C	T	63	160	c.1358C>T	c.(1357-1359)CCC>CTC	p.P453L
Pat_26	Pre-Treatment	EPPK1	83481	37	8	144942527	144942527	Missense_Mutation	SNP	C	T	143	236	c.4895G>A	c.(4894-4896)GGA>GAA	p.G1632E
Pat_26	Pre-Treatment	GPAA1	8733	37	8	145139945	145139945	Splice_Site	SNP	C	T	4	181	c.1165_splice	c.e9-1	p.A389_splice
Pat_26	Pre-Treatment	SHARPIN	81858	37	8	145154311	145154311	Missense_Mutation	SNP	G	A	6	287	c.791C>T	c.(790-792)CCG>CTG	p.P264L
Pat_26	Pre-Treatment	CPSF1	29894	37	8	145621935	145621935	Missense_Mutation	SNP	G	A	126	220	c.2704C>T	c.(2704-2706)CGT>TGT	p.R902C
Pat_26	Pre-Treatment	KANK1	23189	37	9	738505	738505	Splice_Site	SNP	G	A	5	150	c.3553_splice	c.e12+1	p.D1185_splice
Pat_26	Pre-Treatment	VLDLR	7436	37	9	2639918	2639918	Nonsense_Mutation	SNP	C	T	5	340	c.262C>T	c.(262-264)CGA>TGA	p.R88*
Pat_26	Pre-Treatment	ADAMTSL1	92949	37	9	18905849	18905849	Missense_Mutation	SNP	G	A	4	68	c.4921G>A	c.(4921-4923)GGC>AGC	p.G1641S
Pat_26	Pre-Treatment	CDKN2A	1029	37	9	21971017	21971017	Missense_Mutation	SNP	G	A	92	39	c.341C>T	c.(340-342)CCC>CTC	p.P114L
Pat_26	Pre-Treatment	TAF1L	138474	37	9	32633981	32633981	Missense_Mutation	SNP	G	A	44	83	c.1597C>T	c.(1597-1599)CCT>TCT	p.P533S
Pat_26	Pre-Treatment	UNC13B	10497	37	9	35400332	35400332	Missense_Mutation	SNP	T	G	173	271	c.4129T>G	c.(4129-4131)TTC>GTC	p.F1377V
Pat_26	Pre-Treatment	TLN1	7094	37	9	35724203	35724203	Missense_Mutation	SNP	G	A	6	210	c.640C>T	c.(640-642)CTC>TTC	p.L214F
Pat_26	Pre-Treatment	HRCT1	646962	37	9	35906475	35906475	Missense_Mutation	SNP	G	A	7	338	c.191G>A	c.(190-192)CGG>CAG	p.R64Q

Pat_26	Pre-Treatment	MELK	9833	37	9	36677266	36677266	Missense_Mutation	SNP	C	T	4	137	c.1888C>T	c.(1888-1890)CGG>TGG	p.R630W
Pat_26	Pre-Treatment	SHB	6461	37	9	37974811	37974811	Missense_Mutation	SNP	G	A	11	151	c.862C>T	c.(862-864)CGG>TGG	p.R288W
Pat_26	Pre-Treatment	ALDH1B1	219	37	9	38395779	38395779	Missense_Mutation	SNP	C	T	90	155	c.34C>T	c.(34-36)CTC>TTC	p.L12F
Pat_26	Pre-Treatment	PRUNE2	158471	37	9	79323461	79323462	Missense_Mutation	DNP	TG	AA	3	23	.3728_3729CA>T	c.(3727-3729)TCA>TTT	p.S1243F
Pat_26	Pre-Treatment	SHC3	53358	37	9	91690061	91690061	Missense_Mutation	SNP	G	A	4	91	c.692C>T	c.(691-693)ACG>ATG	p.T231M
Pat_26	Pre-Treatment	PTCH1	5727	37	9	98209618	98209618	Missense_Mutation	SNP	G	A	38	36	c.3920C>T	c.(3919-3921)CCC>CTC	p.P1307L
Pat_26	Pre-Treatment	SVEP1	79987	37	9	113171099	113171099	Missense_Mutation	SNP	G	A	167	118	c.6781C>T	c.(6781-6783)CCT>TCT	p.P2261S
Pat_26	Pre-Treatment	ZNF883	169834	37	9	115760269	115760269	Missense_Mutation	SNP	G	A	21	20	c.271C>T	c.(271-273)CAT>TAT	p.H91Y
Pat_26	Pre-Treatment	ALAD	210	37	9	116152752	116152752	Missense_Mutation	SNP	G	A	4	100	c.503C>T	c.(502-504)TCG>TTG	p.S168L
Pat_26	Pre-Treatment	PAPPA	5069	37	9	119124940	119124940	Missense_Mutation	SNP	G	A	28	26	c.4417G>A	c.(4417-4419)GAG>AAG	p.E1473K
Pat_26	Pre-Treatment	C5	727	37	9	123752040	123752040	Missense_Mutation	SNP	A	G	3	77	c.2960T>C	c.(2959-2961)ATC>ACC	p.I987T
Pat_26	Pre-Treatment	MORN5	254956	37	9	124931981	124931981	Missense_Mutation	SNP	G	A	4	190	c.253G>A	c.(253-255)GAC>AAC	p.D85N
Pat_26	Pre-Treatment	MRRF	92399	37	9	125033246	125033246	Missense_Mutation	SNP	G	A	6	308	c.76G>A	c.(76-78)GTT>ATT	p.V26I
Pat_26	Pre-Treatment	CRB2	286204	37	9	126133014	126133014	Missense_Mutation	SNP	C	T	76	33	c.1682C>T	c.(1681-1683)CCG>CTG	p.P561L
Pat_26	Pre-Treatment	NEK6	10783	37	9	127088681	127088681	Missense_Mutation	SNP	G	A	4	190	c.478G>A	c.(478-480)GTG>ATG	p.V160M
Pat_26	Pre-Treatment	WDR38	401551	37	9	127619155	127619155	Missense_Mutation	SNP	C	T	5	292	c.763C>T	c.(763-765)CGC>TGC	p.R255C
Pat_26	Pre-Treatment	SH2D3C	10044	37	9	130511626	130511626	Missense_Mutation	SNP	C	T	4	160	c.1003G>A	c.(1003-1005)GGA>AGA	p.G335R
Pat_26	Pre-Treatment	DNM1	1759	37	9	130996357	130996357	Missense_Mutation	SNP	C	T	3	68	c.1393C>T	c.(1393-1395)CGG>TGG	p.R465W
Pat_26	Pre-Treatment	ASB6	140459	37	9	132400230	132400230	Missense_Mutation	SNP	C	T	32	47	c.1105G>A	c.(1105-1107)GAG>AAG	p.E369K
Pat_26	Pre-Treatment	NUP214	8021	37	9	134103565	134103565	Missense_Mutation	SNP	C	T	4	158	c.5921C>T	c.(5920-5922)CCA>CTA	p.P1974L
Pat_26	Pre-Treatment	TTF1	7270	37	9	135251433	135251433	Nonsense_Mutation	SNP	G	A	37	63	c.2587C>T	c.(2587-2589)CGA>TGA	p.R863*
Pat_26	Pre-Treatment	REXO4	57109	37	9	136277539	136277539	Missense_Mutation	SNP	G	T	234	431	c.790C>A	c.(790-792)CGT>AGT	p.R264S
Pat_26	Pre-Treatment	COL5A1	1289	37	9	137622245	137622245	Missense_Mutation	SNP	A	G	48	117	c.1088A>G	c.(1087-1089)AAC>AGC	p.N363S
Pat_26	Pre-Treatment	NOTCH1	4851	37	9	139405210	139405210	Missense_Mutation	SNP	G	A	4	186	c.2635C>T	c.(2635-2637)CGG>TGG	p.R879W
Pat_26	Pre-Treatment	ABCA2	20	37	9	139910568	139910568	Missense_Mutation	SNP	C	T	7	389	c.3160G>A	c.(3160-3162)GAC>AAC	p.D1054N
Pat_26	Pre-Treatment	EHMT1	79813	37	9	140646844	140646844	Missense_Mutation	SNP	G	A	38	60	c.1232G>A	c.(1231-1233)GGT>GAT	p.G411D
Pat_26	Pre-Treatment	P2RY8	286530	37	X	1584415	1584415	Missense_Mutation	SNP	C	T	73	149	c.1037G>A	c.(1036-1038)GGA>GAA	p.G346E
Pat_26	Pre-Treatment	SCML2	10389	37	X	18323215	18323215	Missense_Mutation	SNP	G	A	182	65	c.607C>T	c.(607-609)CAT>TAT	p.H203Y
Pat_26	Pre-Treatment	RS1	6247	37	X	18660260	18660260	Missense_Mutation	SNP	G	A	4	192	c.539C>T	c.(538-540)TCG>TTG	p.S180L
Pat_26	Pre-Treatment	DCAF8L1	139425	37	X	27999163	27999163	Missense_Mutation	SNP	C	T	91	38	c.289G>A	c.(289-291)GAG>AAG	p.E97K
Pat_26	Pre-Treatment	BCOR	54880	37	X	39934294	39934294	Missense_Mutation	SNP	C	T	4	99	c.305G>A	c.(304-306)CGG>CAG	p.R102Q
Pat_26	Pre-Treatment	EBP	10682	37	X	48386759	48386759	Missense_Mutation	SNP	C	T	13	8	c.607C>T	c.(607-609)CTT>TTT	p.L203F
Pat_26	Pre-Treatment	SHROOM4	57477	37	X	50351180	50351180	Missense_Mutation	SNP	T	C	3	51	c.2962A>G	c.(2962-2964)ATG>GTG	p.M988V
Pat_26	Pre-Treatment	MTMR8	55613	37	X	63548752	63548752	Missense_Mutation	SNP	G	A	13	3	c.1381C>T	c.(1381-1383)CCT>TCT	p.P461S
Pat_26	Pre-Treatment	GJB1	2705	37	X	70444122	70444122	Missense_Mutation	SNP	G	A	4	164	c.565G>A	c.(565-567)GTC>ATC	p.V189I
Pat_26	Pre-Treatment	ACRC	93953	37	X	70823920	70823920	Missense_Mutation	SNP	C	T	7	112	c.793C>T	c.(793-795)CCC>TCC	p.P265S
Pat_26	Pre-Treatment	PHKA1	5255	37	X	71802396	71802396	Missense_Mutation	SNP	C	T	4	59	c.3350G>A	c.(3349-3351)CGT>CAT	p.R1117H
Pat_26	Pre-Treatment	BRWD3	254065	37	X	79943625	79943625	Splice_Site	SNP	C	T	55	26	c.3808_splice	c.e34-1	p.D1270_splic
Pat_26	Pre-Treatment	BRWD3	254065	37	X	79978255	79978255	Missense_Mutation	SNP	T	A	4	79	c.1682A>T	c.(1681-1683)TAT>TTT	p.Y561F
Pat_26	Pre-Treatment	KLHL4	56062	37	X	86880764	86880764	Missense_Mutation	SNP	T	C	3	44	c.1292T>C	c.(1291-1293)CTT>CCT	p.L431P
Pat_26	Pre-Treatment	TAF7L	54457	37	X	100547925	100547925	Missense_Mutation	SNP	G	A	5	341	c.109C>T	c.(109-111)CGT>TGT	p.R37C
Pat_26	Pre-Treatment	BTK	695	37	X	100611788	100611788	Missense_Mutation	SNP	C	T	4	149	c.1333G>A	c.(1333-1335)GAA>AAA	p.E445K
Pat_26	Pre-Treatment	NRK	203447	37	X	105159770	105159770	Missense_Mutation	SNP	C	T	58	15	c.2398C>T	c.(2398-2400)CAT>TAT	p.H800Y
Pat_26	Pre-Treatment	VSIG1	340547	37	X	107320552	107320552	Nonsense_Mutation	SNP	G	T	127	45	c.1105G>T	c.(1105-1107)GAG>TAG	p.E369*
Pat_26	Pre-Treatment	COL4A5	1287	37	X	107858195	107858195	Missense_Mutation	SNP	G	A	46	23	c.2450G>A	c.(2449-2451)GGA>GAA	p.G817E
Pat_26	Pre-Treatment	COL4A5	1287	37	X	107923915	107923915	Missense_Mutation	SNP	C	T	41	18	c.3949C>T	c.(3949-3951)CCT>TCT	p.P1317S
Pat_26	Pre-Treatment	IRS4	8471	37	X	107977986	107977986	Missense_Mutation	SNP	C	T	6	348	c.1589G>A	c.(1588-1590)CGA>CAA	p.R530Q

Pat_26	Pre-Treatment	TMEM164	84187	37	X	109416580	109416580	Missense_Mutation	SNP	G	A	7	153	c.795G>A	c.(793-795)ATG>ATA	p.M265I
Pat_26	Pre-Treatment	SLC6A14	11254	37	X	115582616	115582616	Missense_Mutation	SNP	G	A	29	15	c.940G>A	c.(940-942)GAT>AAT	p.D314N
Pat_26	Pre-Treatment	NKRF	55922	37	X	118723625	118723625	Missense_Mutation	SNP	C	T	5	253	c.1763G>A	c.(1762-1764)CGG>CAG	p.R588Q
Pat_26	Pre-Treatment	OCRL	4952	37	X	128722937	128722937	Missense_Mutation	SNP	G	A	5	202	c.2416G>A	c.(2416-2418)GAG>AAG	p.E806K
Pat_26	Pre-Treatment	IGSF1	3547	37	X	130410004	130410004	Missense_Mutation	SNP	T	A	70	21	c.2827A>T	c.(2827-2829)ATC>TTC	p.I943F
Pat_26	Pre-Treatment	GPR112	139378	37	X	135427418	135427418	Missense_Mutation	SNP	C	T	4	115	c.1553C>T	c.(1552-1554)CCT>CTT	p.P518L
Pat_26	Pre-Treatment	BRS3	680	37	X	135574449	135574449	Missense_Mutation	SNP	C	T	5	184	c.1115C>T	c.(1114-1116)CCG>CTG	p.P372L
Pat_26	Pre-Treatment	MAGEC1	9947	37	X	140993780	140993780	Missense_Mutation	SNP	C	T	8	370	c.590C>T	c.(589-591)CCA>CTA	p.P197L
Pat_26	Pre-Treatment	MAGEC1	9947	37	X	140994583	140994583	Nonsense_Mutation	SNP	A	T	9	162	c.1393A>T	c.(1393-1395)AGA>TGA	p.R465*
Pat_26	Pre-Treatment	MAGEC1	9947	37	X	140994585	140994585	Missense_Mutation	SNP	A	T	9	165	c.1395A>T	c.(1393-1395)AGA>AGT	p.R465S
Pat_26	Pre-Treatment	MAGEC1	9947	37	X	140995273	140995273	Missense_Mutation	SNP	C	T	40	13	c.2083C>T	c.(2083-2085)CCT>TCT	p.P695S
Pat_26	Pre-Treatment	FLNA	2316	37	X	153593043	153593043	Missense_Mutation	SNP	C	T	4	120	c.1873G>A	c.(1873-1875)GAC>AAC	p.D625N
Pat_26	Post-Resistance	ATAD3B	83858	37	1	1431000	1431000	Missense_Mutation	SNP	C	T	3	60	c.1750C>T	c.(1750-1752)CCC>TCC	p.P584S
Pat_26	Post-Resistance	CHD5	26038	37	1	6208967	6208967	Missense_Mutation	SNP	T	A	15	272	c.1330A>T	c.(1330-1332)AAC>TAC	p.N444Y
Pat_26	Post-Resistance	RPL22	6146	37	1	6253023	6253023	Missense_Mutation	SNP	A	G	35	210	c.209T>C	c.(208-210)ATC>ACC	p.I70T
Pat_26	Post-Resistance	CLSTN1	22883	37	1	9804587	9804587	Missense_Mutation	SNP	C	T	12	112	c.1100G>A	c.(1099-1101)GGC>GAC	p.G367D
Pat_26	Post-Resistance	PRAMEF12	390999	37	1	12835134	12835134	Missense_Mutation	SNP	G	A	10	113	c.124G>A	c.(124-126)GAG>AAG	p.E42K
Pat_26	Post-Resistance	TMEM82	388595	37	1	16069534	16069534	Missense_Mutation	SNP	G	A	19	202	c.181G>A	c.(181-183)GAA>AAA	p.E61K
Pat_26	Post-Resistance	CLCNKB	1188	37	1	16382951	16382951	Missense_Mutation	SNP	C	T	38	654	c.1964C>T	c.(1963-1965)TCC>TTC	p.S655F
Pat_26	Post-Resistance	HSPG2	3339	37	1	22166016	22166016	Missense_Mutation	SNP	G	A	15	84	c.9737C>T	c.(9736-9738)TCC>TTC	p.S3246F
Pat_26	Post-Resistance	GMEB1	10691	37	1	29019522	29019522	Nonsense_Mutation	SNP	G	A	20	192	c.435G>A	c.(433-435)TGG>TGA	p.W145*
Pat_26	Post-Resistance	MTF1	4520	37	1	38281155	38281155	Missense_Mutation	SNP	G	A	6	151	c.1915C>T	c.(1915-1917)CGG>TGG	p.R639W
Pat_26	Post-Resistance	ZSWIM5	57643	37	1	45500051	45500051	Nonsense_Mutation	SNP	C	T	33	400	c.2382G>A	c.(2380-2382)TGG>TGA	p.W794*
Pat_26	Post-Resistance	CYB5RL	606495	37	1	54653410	54653411	Missense_Mutation	DNP	CC	TT	5	122	c.349_350GG>AA	c.(349-351)GGG>AAG	p.G117K
Pat_26	Post-Resistance	C1orf173	127254	37	1	75055569	75055569	Missense_Mutation	SNP	T	G	7	151	c.1922A>C	c.(1921-1923)GAA>GCA	p.E641A
Pat_26	Post-Resistance	CLCA4	22802	37	1	87025931	87025931	Missense_Mutation	SNP	G	A	24	332	c.338G>A	c.(337-339)AGA>AAA	p.R113K
Pat_26	Post-Resistance	CCBL2	56267	37	1	89420900	89420900	Missense_Mutation	SNP	G	A	4	128	c.796C>T	c.(796-798)CCA>TCA	p.P266S
Pat_26	Post-Resistance	DBT	1629	37	1	100715333	100715334	Missense_Mutation	DNP	CC	TT	14	408	c.43_44GG>AA	c.(43-45)GGG>AAG	p.G15K
Pat_26	Post-Resistance	COL11A1	1301	37	1	103488309	103488309	Missense_Mutation	SNP	T	C	23	212	c.1234A>G	c.(1234-1236)ACA>GCA	p.T412A
Pat_26	Post-Resistance	EPS8L3	79574	37	1	110301230	110301230	Missense_Mutation	SNP	C	T	4	104	c.517G>A	c.(517-519)GAA>AAA	p.E173K
Pat_26	Post-Resistance	NBPF10	100132406	37	1	145362111	145362111	Missense_Mutation	SNP	T	G	7	271	c.9644T>G	c.(9643-9645)CTG>CGG	p.L3215R
Pat_26	Post-Resistance	TCHHL1	126637	37	1	152058977	152058977	Missense_Mutation	SNP	C	T	37	237	c.1181G>A	c.(1180-1182)AGG>AAG	p.R394K
Pat_26	Post-Resistance	HRNR	388697	37	1	152188190	152188191	Missense_Mutation	DNP	CC	TT	37	813	.5914_5915GG>A	c.(5914-5916)GGG>AAG	p.G1972K
Pat_26	Post-Resistance	IVL	3713	37	1	152882733	152882733	Missense_Mutation	SNP	G	A	9	45	c.460G>A	c.(460-462)GAG>AAG	p.E154K
Pat_26	Post-Resistance	UBQLN4	56893	37	1	156023426	156023426	Missense_Mutation	SNP	T	C	21	83	c.67A>G	c.(67-69)AAG>GAG	p.K23E
Pat_26	Post-Resistance	IQGAP3	128239	37	1	156526371	156526371	Missense_Mutation	SNP	G	A	18	127	c.1244C>T	c.(1243-1245)TCG>TTG	p.S415L
Pat_26	Post-Resistance	OR10K1	391109	37	1	158435545	158435545	Missense_Mutation	SNP	T	C	20	404	c.194T>C	c.(193-195)ATC>ACC	p.I65T
Pat_26	Post-Resistance	SLAMF9	89886	37	1	159922273	159922273	Missense_Mutation	SNP	C	T	76	467	c.443G>A	c.(442-444)GGT>GAT	p.G148D
Pat_26	Post-Resistance	FAM5B	57795	37	1	177249624	177249624	Missense_Mutation	SNP	G	A	7	114	c.1312G>A	c.(1312-1314)GAA>AAA	p.E438K
Pat_26	Post-Resistance	KIF14	9928	37	1	200574423	200574423	Missense_Mutation	SNP	C	G	4	128	c.1734G>C	c.(1732-1734)ATG>ATC	p.M578I
Pat_26	Post-Resistance	PLEKHA6	22874	37	1	204214787	204214787	Missense_Mutation	SNP	C	T	19	201	c.1988G>A	c.(1987-1989)AGG>AAG	p.R663K
Pat_26	Post-Resistance	LRRN2	10446	37	1	204588452	204588452	Missense_Mutation	SNP	C	T	10	103	c.669G>A	c.(667-669)ATG>ATA	p.M223I
Pat_26	Post-Resistance	CR2	1380	37	1	207642243	207642243	Missense_Mutation	SNP	G	A	6	83	c.733G>A	c.(733-735)GGG>AGG	p.G245R
Pat_26	Post-Resistance	IARS2	55699	37	1	220287738	220287738	Missense_Mutation	SNP	G	T	61	462	c.1562G>T	c.(1561-1563)TGT>TTT	p.C521F
Pat_26	Post-Resistance	PCNXL2	80003	37	1	233231594	233231594	Missense_Mutation	SNP	G	A	5	49	c.3853C>T	c.(3853-3855)CAC>TAC	p.H1285Y
Pat_26	Post-Resistance	ACTN2	88	37	1	236911034	236911034	Nonsense_Mutation	SNP	C	T	13	103	c.1474C>T	c.(1474-1476)CGA>TGA	p.R492*
Pat_26	Post-Resistance	MTR	4548	37	1	236966868	236966868	Missense_Mutation	SNP	C	T	24	274	c.175C>T	c.(175-177)CAT>TAT	p.H59Y

Pat_26	Post-Resistance	IL2RA	3559	37	10	6066213	6066213	Missense_Mutation	SNP	G	A	9	125	c.361C>T	c.(361-363)CTT>TTT	p.L121F
Pat_26	Post-Resistance	KIAA1217	56243	37	10	24822108	24822108	Missense_Mutation	SNP	C	T	12	136	c.3356C>T	c.(3355-3357)TCC>TTC	p.S1119F
Pat_26	Post-Resistance	GPR158	57512	37	10	25701332	25701332	Missense_Mutation	SNP	C	T	44	644	c.1265C>T	c.(1264-1266)TCC>TTC	p.S422F
Pat_26	Post-Resistance	MYO3A	53904	37	10	26312962	26312962	Missense_Mutation	SNP	C	A	20	560	c.743C>A	c.(742-744)CCA>CAA	p.P248Q
Pat_26	Post-Resistance	KIAA1462	57608	37	10	30318160	30318160	Missense_Mutation	SNP	C	T	36	248	c.917G>A	c.(916-918)GGA>GAA	p.G306E
Pat_26	Post-Resistance	ZNF248	57209	37	10	38120643	38120643	Missense_Mutation	SNP	G	A	25	224	c.1640C>T	c.(1639-1641)CCG>CTG	p.P547L
Pat_26	Post-Resistance	RBP3	5949	37	10	48389305	48389305	Missense_Mutation	SNP	C	T	6	52	c.1573G>A	c.(1573-1575)GAG>AAG	p.E525K
Pat_26	Post-Resistance	RBP3	5949	37	10	48389757	48389757	Missense_Mutation	SNP	G	A	6	85	c.1121C>T	c.(1120-1122)GCC>GTC	p.A374V
Pat_26	Post-Resistance	ANK3	288	37	10	61898789	61898789	Missense_Mutation	SNP	C	T	27	257	c.2671G>A	c.(2671-2673)GAA>AAA	p.E891K
Pat_26	Post-Resistance	ANK3	288	37	10	61941146	61941146	Nonsense_Mutation	SNP	G	A	11	276	c.2125C>T	c.(2125-2127)CGA>TGA	p.R709*
Pat_26	Post-Resistance	LRRTM3	347731	37	10	68687639	68687640	Missense_Mutation	DNP	CC	TT	6	83	c.965_966CC>TT	c.(964-966)TCC>TTT	p.S322F
Pat_26	Post-Resistance	STOX1	219736	37	10	70644422	70644422	Missense_Mutation	SNP	C	G	24	197	c.870C>G	c.(868-870)CAC>CAG	p.H290Q
Pat_26	Post-Resistance	SEC24C	9632	37	10	75519901	75519901	Nonsense_Mutation	SNP	C	T	29	359	c.607C>T	c.(607-609)CAG>TAG	p.Q203*
Pat_26	Post-Resistance	PIPSL	266971	37	10	95719536	95719536	Missense_Mutation	SNP	C	T	12	156	c.1618G>A	c.(1618-1620)GAT>AAT	p.D540N
Pat_26	Post-Resistance	CYP2C19	1557	37	10	96609752	96609752	Missense_Mutation	SNP	C	T	21	309	c.1228C>T	c.(1228-1230)CGT>TGT	p.R410C
Pat_26	Post-Resistance	C10orf79	80217	37	10	105890056	105890056	Missense_Mutation	SNP	T	G	12	180	c.4839A>C	c.(4837-4839)AAA>AAC	p.K1613N
Pat_26	Post-Resistance	WDR11	55717	37	10	122626180	122626180	Missense_Mutation	SNP	C	T	56	399	c.1094C>T	c.(1093-1095)CCT>CTT	p.P365L
Pat_26	Post-Resistance	TACC2	10579	37	10	123988957	123988957	Missense_Mutation	SNP	G	A	35	798	c.7993G>A	c.(7993-7995)GAC>AAC	p.D2665N
Pat_26	Post-Resistance	DMBT1	1755	37	10	124350190	124350190	Missense_Mutation	SNP	C	T	30	379	c.2117C>T	c.(2116-2118)TCC>TTC	p.S706F
Pat_26	Post-Resistance	CUZD1	50624	37	10	124595694	124595694	Missense_Mutation	SNP	C	A	11	298	c.990G>T	c.(988-990)AAG>AAT	p.K330N
Pat_26	Post-Resistance	C10orf90	118611	37	10	128193393	128193393	Nonsense_Mutation	SNP	C	A	11	102	c.376G>T	c.(376-378)GAG>TAG	p.E126*
Pat_26	Post-Resistance	KNDC1	85442	37	10	135013019	135013019	Missense_Mutation	SNP	C	T	9	135	c.2816C>T	c.(2815-2817)TCC>TTC	p.S939F
Pat_26	Post-Resistance	SYCE1	93426	37	10	135369530	135369530	Missense_Mutation	SNP	C	T	8	191	c.550G>A	c.(550-552)GAG>AAG	p.E184K
Pat_26	Post-Resistance	OR51Q1	390061	37	11	5444196	5444196	Missense_Mutation	SNP	C	T	31	284	c.766C>T	c.(766-768)CCC>TCC	p.P256S
Pat_26	Post-Resistance	OR52N4	390072	37	11	5776203	5776203	Missense_Mutation	SNP	G	A	12	148	c.233G>A	c.(232-234)AGT>AAT	p.S78N
Pat_26	Post-Resistance	RBMXL2	27288	37	11	7111168	7111168	Missense_Mutation	SNP	C	T	6	92	c.817C>T	c.(817-819)CAT>TAT	p.H273Y
Pat_26	Post-Resistance	ARNTL	406	37	11	13397274	13397275	Missense_Mutation	DNP	AG	TA	7	77	.1290_1291AG>T	288-1293)GAAGTA>GAT	.430_431EV>
Pat_26	Post-Resistance	PRDM11	56981	37	11	45246185	45246185	Missense_Mutation	SNP	C	T	37	316	c.1262C>T	c.(1261-1263)TCA>TTA	p.S421L
Pat_26	Post-Resistance	GYLTL1B	120071	37	11	45949470	45949470	Splice_Site	SNP	G	A	14	123	c.1605_splice	c.e12-1	p.R535_splice
Pat_26	Post-Resistance	FOLH1	2346	37	11	49175447	49175447	Missense_Mutation	SNP	C	T	13	153	c.1921G>A	c.(1921-1923)GAA>AAA	p.E641K
Pat_26	Post-Resistance	OR4A15	81328	37	11	55136144	55136144	Missense_Mutation	SNP	G	A	9	107	c.785G>A	c.(784-786)CGA>CAA	p.R262Q
Pat_26	Post-Resistance	ZDHHC5	25921	37	11	57456099	57456099	Nonsense_Mutation	SNP	C	T	6	289	c.346C>T	c.(346-348)CGA>TGA	p.R116*
Pat_26	Post-Resistance	OR5B3	441608	37	11	58170239	58170239	Missense_Mutation	SNP	G	A	4	65	c.644C>T	c.(643-645)TCC>TTC	p.S215F
Pat_26	Post-Resistance	MS4A4A	51338	37	11	60064709	60064709	Missense_Mutation	SNP	G	A	31	234	c.241G>A	c.(241-243)GGA>AGA	p.G81R
Pat_26	Post-Resistance	FADS2	9415	37	11	61608002	61608002	Missense_Mutation	SNP	A	C	38	357	c.515A>C	c.(514-516)CAG>CCG	p.Q172P
Pat_26	Post-Resistance	SLC22A6	9356	37	11	62748482	62748483	Missense_Mutation	DNP	GG	AA	6	143	.1011_1012CC>T	009-1014)CACCTC>CATT	p.L338F
Pat_26	Post-Resistance	SIPA1	6494	37	11	65413346	65413346	Missense_Mutation	SNP	C	G	9	316	c.1181C>G	c.(1180-1182)TCC>TGC	p.S394C
Pat_26	Post-Resistance	KLC2	64837	37	11	66030347	66030347	Missense_Mutation	SNP	C	T	52	607	c.592C>T	c.(592-594)CTC>TTC	p.L198F
Pat_26	Post-Resistance	CCS	9973	37	11	66373047	66373047	Missense_Mutation	SNP	G	A	15	101	c.655G>A	c.(655-657)GGG>AGG	p.G219R
Pat_26	Post-Resistance	FGF19	9965	37	11	69518121	69518121	Missense_Mutation	SNP	T	C	8	43	c.244A>G	c.(244-246)ATC>GTC	p.I82V
Pat_26	Post-Resistance	INPPL1	3636	37	11	71946922	71946922	Missense_Mutation	SNP	C	T	33	192	c.2771C>T	c.(2770-2772)GCC>GTC	p.A924V
Pat_26	Post-Resistance	RELT	84957	37	11	73105710	73105710	Missense_Mutation	SNP	C	T	10	89	c.977C>T	c.(976-978)CCG>CTG	p.P326L
Pat_26	Post-Resistance	HEPHL1	341208	37	11	93797538	93797538	Nonsense_Mutation	SNP	C	T	7	99	c.670C>T	c.(670-672)CGA>TGA	p.R224*
Pat_26	Post-Resistance	GRIA4	2893	37	11	105483095	105483096	Missense_Mutation	DNP	CC	TT	11	148	c.181_182CC>TT	c.(181-183)CCT>TTT	p.P61F
Pat_26	Post-Resistance	SIK2	23235	37	11	111590703	111590703	Missense_Mutation	SNP	C	A	4	110	c.1471C>A	c.(1471-1473)CAA>AAA	p.Q491K
Pat_26	Post-Resistance	IGSF9B	22997	37	11	133802070	133802070	Missense_Mutation	SNP	C	T	3	20	c.1006G>A	c.(1006-1008)GTG>ATG	p.V336M
Pat_26	Post-Resistance	MLF2	8079	37	12	6861105	6861105	Missense_Mutation	SNP	G	A	32	366	c.166C>T	c.(166-168)CGC>TGC	p.R56C

Pat_26	Post-Resistance	CLEC4E	26253	37	12	8687260	8687260	Missense_Mutation	SNP	G	A	6	119	c.634C>T	c.(634-636)CCT>TCT	p.P212S
Pat_26	Post-Resistance	A2M	2	37	12	9264799	9264799	Missense_Mutation	SNP	G	A	20	147	c.439C>T	c.(439-441)CGT>TGT	p.R147C
Pat_26	Post-Resistance	PRB4	5545	37	12	11461775	11461775	Missense_Mutation	SNP	G	T	31	399	c.142C>A	c.(142-144)CAA>AAA	p.Q48K
Pat_26	Post-Resistance	PIK3C2G	5288	37	12	18552721	18552721	Missense_Mutation	SNP	C	T	5	68	c.2132C>T	c.(2131-2133)ACC>ATC	p.T711I
Pat_26	Post-Resistance	SLCO1C1	53919	37	12	20874764	20874764	Missense_Mutation	SNP	C	T	16	120	c.802C>T	c.(802-804)CCC>TCC	p.P268S
Pat_26	Post-Resistance	LRRK2	120892	37	12	40677921	40677921	Nonsense_Mutation	SNP	T	G	8	82	c.2486T>G	c.(2485-2487)TTA>TGA	p.L829*
Pat_26	Post-Resistance	IRAK4	51135	37	12	44165165	44165165	Missense_Mutation	SNP	C	T	5	145	c.304C>T	c.(304-306)CCA>TCA	p.P102S
Pat_26	Post-Resistance	KRT75	9119	37	12	52825359	52825359	Missense_Mutation	SNP	C	T	8	247	c.838G>A	c.(838-840)GAG>AAG	p.E280K
Pat_26	Post-Resistance	KRT74	121391	37	12	52960769	52960769	Missense_Mutation	SNP	C	T	20	370	c.1574G>A	c.(1573-1575)AGG>AAG	p.R525K
Pat_26	Post-Resistance	NAV3	89795	37	12	78400838	78400838	Missense_Mutation	SNP	C	T	10	138	c.1520C>T	c.(1519-1521)CCT>CTT	p.P507L
Pat_26	Post-Resistance	C12orf51	283450	37	12	112673400	112673400	Missense_Mutation	SNP	G	A	6	69	c.4367C>T	c.(4366-4368)CCC>CTC	p.P1456L
Pat_26	Post-Resistance	NOS1	4842	37	12	117655918	117655918	Missense_Mutation	SNP	C	T	24	740	c.4222G>A	c.(4222-4224)GAA>AAA	p.E1408K
Pat_26	Post-Resistance	SRRM4	84530	37	12	119592047	119592047	Splice_Site	SNP	G	A	3	12	c.1392_splice	c.e12-1	p.R464_splice
Pat_26	Post-Resistance	DNAH10	196385	37	12	124416393	124416393	Missense_Mutation	SNP	G	A	30	215	c.12773G>A	c.(12772-12774)AGG>AAG	p.R4258K
Pat_26	Post-Resistance	EP400	57634	37	12	132535158	132535158	Missense_Mutation	SNP	C	T	19	435	c.7352C>T	c.(7351-7353)CCC>CTC	p.P2451L
Pat_26	Post-Resistance	TPTE2	93492	37	13	20010385	20010385	Missense_Mutation	SNP	C	T	8	33	c.1097G>A	c.(1096-1098)GGA>GAA	p.G366E
Pat_26	Post-Resistance	CENPJ	55835	37	13	25479499	25479499	Nonsense_Mutation	SNP	G	A	26	281	c.2677C>T	c.(2677-2679)CAA>TAA	p.Q893*
Pat_26	Post-Resistance	SPG20	23111	37	13	36909531	36909531	Missense_Mutation	SNP	G	A	5	43	c.437C>T	c.(436-438)TCA>TTA	p.S146L
Pat_26	Post-Resistance	C13orf18	80183	37	13	47011869	47011869	Translation_Start_Site	SNP	C	T	6	38	c.-604G>A	(-606--602)GCGTG>GCATG	
Pat_26	Post-Resistance	CHD8	57680	37	14	21873900	21873901	Missense_Mutation	DNP	CC	TA	41	617	.2193_2194GG>T	191-2196)GGGGAT>GGT	p.D732N
Pat_26	Post-Resistance	SALL2	6297	37	14	21992852	21992852	Missense_Mutation	SNP	C	T	5	65	c.1010G>A	c.(1009-1011)CGA>CAA	p.R337Q
Pat_26	Post-Resistance	ADCY4	196883	37	14	24799117	24799117	Missense_Mutation	SNP	C	A	53	634	c.1166G>T	c.(1165-1167)TGG>TTG	p.W389L
Pat_26	Post-Resistance	NYNRIN	57523	37	14	24877187	24877187	Missense_Mutation	SNP	G	T	24	185	c.311G>T	c.(310-312)TGG>TTG	p.W104L
Pat_26	Post-Resistance	C14orf166	51637	37	14	52460480	52460480	Missense_Mutation	SNP	C	G	22	213	c.226C>G	c.(226-228)CGA>GGA	p.R76G
Pat_26	Post-Resistance	KCNH5	27133	37	14	63174459	63174459	Missense_Mutation	SNP	C	T	24	278	c.2734G>A	c.(2734-2736)GAA>AAA	p.E912K
Pat_26	Post-Resistance	ESR2	2100	37	14	64746815	64746815	Missense_Mutation	SNP	G	A	50	633	c.419C>T	c.(418-420)CCA>CTA	p.P140L
Pat_26	Post-Resistance	RDH12	145226	37	14	68195937	68195938	Missense_Mutation	DNP	CC	TT	42	437	c.688_689CC>TT	c.(688-690)CCA>TTA	p.P230L
Pat_26	Post-Resistance	BATF	10538	37	14	75991472	75991472	Missense_Mutation	SNP	C	T	7	108	c.109C>T	c.(109-111)CGT>TGT	p.R37C
Pat_26	Post-Resistance	PTPN21	11099	37	14	88945940	88945940	Missense_Mutation	SNP	G	C	5	31	c.1835C>G	c.(1834-1836)CCC>CGC	p.P612R
Pat_26	Post-Resistance	KIAA1409	57578	37	14	94121601	94121601	Missense_Mutation	SNP	T	G	27	157	c.5956T>G	c.(5956-5958)TTA>GTA	p.L1986V
Pat_26	Post-Resistance	SERPINA11	256394	37	14	94912755	94912755	Missense_Mutation	SNP	A	G	7	173	c.830T>C	c.(829-831)GTC>GCC	p.V277A
Pat_26	Post-Resistance	TNFAIP2	7127	37	14	103598032	103598032	Missense_Mutation	SNP	G	A	6	44	c.1355G>A	c.(1354-1356)GGC>GAC	p.G452D
Pat_26	Post-Resistance	ZFYVE21	79038	37	14	104195467	104195467	Missense_Mutation	SNP	A	C	23	205	c.474A>C	c.(472-474)GAA>GAC	p.E158D
Pat_26	Post-Resistance	KIF26A	26153	37	14	104641431	104641431	Missense_Mutation	SNP	C	T	3	30	c.2306C>T	c.(2305-2307)ACG>ATG	p.T769M
Pat_26	Post-Resistance	CASC5	57082	37	15	40915757	40915757	Missense_Mutation	SNP	G	A	4	100	c.3373G>A	c.(3373-3375)GAA>AAA	p.E1125K
Pat_26	Post-Resistance	CAPN3	825	37	15	42652253	42652253	Missense_Mutation	SNP	G	A	67	609	c.250G>A	c.(250-252)GAG>AAG	p.E84K
Pat_26	Post-Resistance	PCSK6	5046	37	15	101933424	101933424	Missense_Mutation	SNP	C	T	3	36	c.1202G>A	c.(1201-1203)CGA>CAA	p.R401Q
Pat_26	Post-Resistance	OR4F15	390649	37	15	102359169	102359169	Nonsense_Mutation	SNP	G	A	17	378	c.780G>A	c.(778-780)TGG>TGA	p.W260*
Pat_26	Post-Resistance	TMEM8A	58986	37	16	427097	427097	Missense_Mutation	SNP	G	A	25	385	c.575C>T	c.(574-576)TCC>TTC	p.S192F
Pat_26	Post-Resistance	PIGQ	9091	37	16	624666	624666	Missense_Mutation	SNP	G	A	4	26	c.592G>A	c.(592-594)GCC>ACC	p.A198T
Pat_26	Post-Resistance	TBC1D24	57465	37	16	2546985	2546985	Missense_Mutation	SNP	C	T	9	216	c.836C>T	c.(835-837)ACG>ATG	p.T279M
Pat_26	Post-Resistance	GRIN2A	2903	37	16	9858471	9858471	Missense_Mutation	SNP	T	G	11	108	c.2930A>C	c.(2929-2931)AAC>ACC	p.N977T
Pat_26	Post-Resistance	DEXI	28955	37	16	11035603	11035603	Missense_Mutation	SNP	A	G	17	243	c.260T>C	c.(259-261)CTC>CCC	p.L87P
Pat_26	Post-Resistance	TMC7	79905	37	16	19049221	19049221	Missense_Mutation	SNP	G	A	4	113	c.1031G>A	c.(1030-1032)CGG>CAG	p.R344Q
Pat_26	Post-Resistance	ACSM2B	348158	37	16	20559454	20559454	Missense_Mutation	SNP	G	A	21	280	c.1028C>T	c.(1027-1029)CCA>CTA	p.P343L
Pat_26	Post-Resistance	ZP2	7783	37	16	21213081	21213081	Missense_Mutation	SNP	G	A	37	284	c.1450C>T	c.(1450-1452)CCA>TCA	p.P484S
Pat_26	Post-Resistance	SCNN1B	6338	37	16	23360188	23360188	Missense_Mutation	SNP	A	T	5	154	c.268A>T	c.(268-270)ATG>TTG	p.M90L

Pat_26	Post-Resistance	PRKCB	5579	37	16	24196465	24196465	Missense_Mutation	SNP	G	A	9	249	c.1567G>A	c.(1567-1569)GAT>AAT	p.D523N
Pat_26	Post-Resistance	ABCC11	85320	37	16	48209286	48209286	Missense_Mutation	SNP	G	A	8	77	c.3581C>T	c.(3580-3582)CCC>CTC	p.P1194L
Pat_26	Post-Resistance	HEATR3	55027	37	16	50118111	50118111	Missense_Mutation	SNP	C	T	6	191	c.1199C>T	c.(1198-1200)TCC>TTC	p.S400F
Pat_26	Post-Resistance	CDH3	1001	37	16	68679319	68679319	Missense_Mutation	SNP	C	T	4	104	c.37C>T	c.(37-39)CTT>TTT	p.L13F
Pat_26	Post-Resistance	ADAMTS18	170692	37	16	77359782	77359782	Missense_Mutation	SNP	T	A	9	229	c.2013A>T	c.(2011-2013)AAA>AAT	p.K671N
Pat_26	Post-Resistance	VAT1L	57687	37	16	77850891	77850891	Missense_Mutation	SNP	G	A	16	290	c.307G>A	c.(307-309)GGA>AGA	p.G103R
Pat_26	Post-Resistance	KCNG4	93107	37	16	84270809	84270809	Missense_Mutation	SNP	C	T	5	183	c.283G>A	c.(283-285)GAG>AAG	p.E95K
Pat_26	Post-Resistance	CRISPLD2	83716	37	16	84906599	84906599	Missense_Mutation	SNP	C	T	22	367	c.983C>T	c.(982-984)TCG>TTG	p.S328L
Pat_26	Post-Resistance	ABR	29	37	17	953422	953422	Splice_Site	SNP	C	T	4	89	c.1660_splice	c.e16-1	p.E554_splice
Pat_26	Post-Resistance	SMG6	23293	37	17	1972173	1972173	Missense_Mutation	SNP	G	A	13	165	c.3734C>T	c.(3733-3735)CCT>CTT	p.P1245L
Pat_26	Post-Resistance	AMAC1L3	643664	37	17	7386000	7386000	Missense_Mutation	SNP	G	A	25	182	c.697G>A	c.(697-699)GGC>AGC	p.G233S
Pat_26	Post-Resistance	MYH8	4626	37	17	10315967	10315967	Missense_Mutation	SNP	A	G	50	649	c.1226T>C	c.(1225-1227)GTT>GCT	p.V409A
Pat_26	Post-Resistance	MYH4	4622	37	17	10356968	10356968	Missense_Mutation	SNP	C	T	47	488	c.2926G>A	c.(2926-2928)GAG>AAG	p.E976K
Pat_26	Post-Resistance	MYH1	4619	37	17	10406565	10406565	Missense_Mutation	SNP	C	T	12	160	c.2692G>A	c.(2692-2694)GAA>AAA	p.E898K
Pat_26	Post-Resistance	MYH2	4620	37	17	10428264	10428264	Missense_Mutation	SNP	C	T	25	310	c.4781G>A	c.(4780-4782)AGA>AAA	p.R1594K
Pat_26	Post-Resistance	CDRT1	374286	37	17	15522784	15522784	Missense_Mutation	SNP	G	A	9	672	c.43C>T	c.(43-45)CGT>TGT	p.R15C
Pat_26	Post-Resistance	C17orf39	79018	37	17	17968502	17968502	Missense_Mutation	SNP	C	T	30	176	c.848C>T	c.(847-849)TCC>TTC	p.S283F
Pat_26	Post-Resistance	FBXW10	10517	37	17	18647600	18647600	Missense_Mutation	SNP	C	T	30	267	c.43C>T	c.(43-45)CGT>TGT	p.R15C
Pat_26	Post-Resistance	IFT20	90410	37	17	26657555	26657555	Splice_Site	SNP	C	T	26	212	c.128_splice	c.e3-1	p.K43_splice
Pat_26	Post-Resistance	ACCN1	40	37	17	31355368	31355368	Missense_Mutation	SNP	C	T	9	122	c.877G>A	c.(877-879)GAG>AAG	p.E293K
Pat_26	Post-Resistance	SRCIN1	80725	37	17	36707439	36707439	Missense_Mutation	SNP	C	T	5	33	c.2914G>A	c.(2914-2916)GGC>AGC	p.G972S
Pat_26	Post-Resistance	STAC2	342667	37	17	37369806	37369806	Missense_Mutation	SNP	C	T	36	396	c.947G>A	c.(946-948)GGA>GAA	p.G316E
Pat_26	Post-Resistance	KRT16	3868	37	17	39767374	39767374	Missense_Mutation	SNP	C	T	48	426	c.880G>A	c.(880-882)GAG>AAG	p.E294K
Pat_26	Post-Resistance	4-Sep	5414	37	17	56599121	56599122	Missense_Mutation	DNP	GG	AA	31	294	c.890_891CC>TT	c.(889-891)CCC>CTT	p.P297L
Pat_26	Post-Resistance	CA4	762	37	17	58235695	58235695	Missense_Mutation	SNP	A	T	19	190	c.632A>T	c.(631-633)GAG>GTG	p.E211V
Pat_26	Post-Resistance	ACE	1636	37	17	61570849	61570849	Missense_Mutation	SNP	G	A	21	189	c.2965G>A	c.(2965-2967)GAA>AAA	p.E989K
Pat_26	Post-Resistance	PSMC5	5705	37	17	61908260	61908260	Missense_Mutation	SNP	C	T	18	193	c.644C>T	c.(643-645)TCT>TTT	p.S215F
Pat_26	Post-Resistance	TEX2	55852	37	17	62271078	62271078	Missense_Mutation	SNP	G	A	5	134	c.2017C>T	c.(2017-2019)CGC>TGC	p.R673C
Pat_26	Post-Resistance	CCDC46	201134	37	17	63637111	63637111	Missense_Mutation	SNP	C	T	23	269	c.2770G>A	c.(2770-2772)GAA>AAA	p.E924K
Pat_26	Post-Resistance	CANT1	124583	37	17	76993085	76993085	Missense_Mutation	SNP	G	A	61	621	c.620C>T	c.(619-621)ACC>ATC	p.T207I
Pat_26	Post-Resistance	TXNDC2	84203	37	18	9886894	9886894	Missense_Mutation	SNP	A	G	9	267	c.418A>G	c.(418-420)AAA>GAA	p.K140E
Pat_26	Post-Resistance	POTEC	388468	37	18	14542880	14542880	Missense_Mutation	SNP	G	A	21	656	c.266C>T	c.(265-267)TCC>TTC	p.S89F
Pat_26	Post-Resistance	ROCK1	6093	37	18	18586707	18586707	Nonsense_Mutation	SNP	G	A	20	359	c.1591C>T	c.(1591-1593)CAG>TAG	p.Q531*
Pat_26	Post-Resistance	LAMA3	3909	37	18	21526172	21526172	Missense_Mutation	SNP	G	A	7	189	c.9275G>A	c.(9274-9276)GGA>GAA	p.G3092E
Pat_26	Post-Resistance	SETBP1	26040	37	18	42643613	42643613	Missense_Mutation	SNP	G	C	10	30	c.4741G>C	c.(4741-4743)GCC>CCC	p.A1581P
Pat_26	Post-Resistance	RNF165	494470	37	18	44035938	44035938	Missense_Mutation	SNP	G	A	7	69	c.818G>A	c.(817-819)CGA>CAA	p.R273Q
Pat_26	Post-Resistance	STARD6	147323	37	18	51863532	51863532	Missense_Mutation	SNP	G	A	7	259	c.230C>T	c.(229-231)TCA>TTA	p.S77L
Pat_26	Post-Resistance	CCBE1	147372	37	18	57115221	57115221	Missense_Mutation	SNP	G	A	11	189	c.769C>T	c.(769-771)CCT>TCT	p.P257S
Pat_26	Post-Resistance	SERPINB2	5055	37	18	61582740	61582740	Missense_Mutation	SNP	C	T	12	197	c.419C>T	c.(418-420)TCC>TTC	p.S140F
Pat_26	Post-Resistance	ATP9B	374868	37	18	77132838	77132838	Missense_Mutation	SNP	C	T	10	120	c.3026C>T	c.(3025-3027)TCC>TTC	p.S1009F
Pat_26	Post-Resistance	NFATC1	4772	37	18	77171045	77171045	Missense_Mutation	SNP	C	T	11	41	c.770C>T	c.(769-771)TCC>TTC	p.S257F
Pat_26	Post-Resistance	TJP3	27134	37	19	3728653	3728653	Missense_Mutation	SNP	G	A	4	80	c.157G>A	c.(157-159)GGT>AGT	p.G53S
Pat_26	Post-Resistance	TJP3	27134	37	19	3734334	3734334	Missense_Mutation	SNP	A	G	7	182	c.986A>G	c.(985-987)GAC>GGC	p.D329G
Pat_26	Post-Resistance	ZFR2	23217	37	19	3831498	3831498	Missense_Mutation	SNP	G	A	3	14	c.655C>T	c.(655-657)CCT>TCT	p.P219S
Pat_26	Post-Resistance	RFX2	5990	37	19	6013085	6013085	Missense_Mutation	SNP	G	A	16	453	c.811C>T	c.(811-813)CGT>TGT	p.R271C
Pat_26	Post-Resistance	C3	718	37	19	6712584	6712584	Missense_Mutation	SNP	G	A	28	448	c.1054C>T	c.(1054-1056)CCC>TCC	p.P352S
Pat_26	Post-Resistance	MUC16	94025	37	19	9071925	9071925	Missense_Mutation	SNP	G	A	38	551	c.15521C>T	c.(15520-15522)TCC>TTC	p.S5174F

Pat_26	Post-Resistance	ZNF699	374879	37	19	9406866	9406866	Missense_Mutation	SNP	G	A	6	216	c.1214C>T	c.(1213-1215)TCC>TTC	p.S405F
Pat_26	Post-Resistance	SMARCA4	6597	37	19	11136975	11136975	Splice_Site	SNP	G	A	15	111	c.3169_splice	c.e23-1	p.E1057_splice
Pat_26	Post-Resistance	ACP5	54	37	19	11688119	11688119	Missense_Mutation	SNP	G	A	4	122	c.14C>T	c.(13-15)ACG>ATG	p.T5M
Pat_26	Post-Resistance	ZNF625	90589	37	19	12257002	12257002	Missense_Mutation	SNP	C	T	7	117	c.31G>A	c.(31-33)GAT>AAT	p.D11N
Pat_26	Post-Resistance	TRMT1	55621	37	19	13216194	13216194	Missense_Mutation	SNP	C	T	49	411	c.1720G>A	c.(1720-1722)GAA>AAA	p.E574K
Pat_26	Post-Resistance	LPHN1	22859	37	19	14273589	14273589	Missense_Mutation	SNP	C	G	4	95	c.1039G>C	c.(1039-1041)GCC>CCC	p.A347P
Pat_26	Post-Resistance	ELL	8178	37	19	18572645	18572645	Missense_Mutation	SNP	G	A	10	288	c.487C>T	c.(487-489)CGG>TGG	p.R163W
Pat_26	Post-Resistance	PBX4	80714	37	19	19681432	19681432	Missense_Mutation	SNP	C	T	5	128	c.404G>A	c.(403-405)CGA>CAA	p.R135Q
Pat_26	Post-Resistance	ZNF536	9745	37	19	31039483	31039483	Missense_Mutation	SNP	C	T	10	140	c.2957C>T	c.(2956-2958)TCC>TTC	p.S986F
Pat_26	Post-Resistance	TSHZ3	57616	37	19	31769341	31769341	Missense_Mutation	SNP	G	C	18	176	c.1358C>G	c.(1357-1359)ACG>AGG	p.T453R
Pat_26	Post-Resistance	SIPA1L3	23094	37	19	38621187	38621187	Missense_Mutation	SNP	G	A	25	188	c.2918G>A	c.(2917-2919)GGG>GAG	p.G973E
Pat_26	Post-Resistance	SIPA1L3	23094	37	19	38643532	38643532	Missense_Mutation	SNP	G	A	7	333	c.3586G>A	c.(3586-3588)GAT>AAT	p.D1196N
Pat_26	Post-Resistance	TIMM50	92609	37	19	39976330	39976330	Missense_Mutation	SNP	G	A	40	234	c.684G>A	c.(682-684)ATG>ATA	p.M228I
Pat_26	Post-Resistance	FCGBP	8857	37	19	40373993	40373993	Missense_Mutation	SNP	C	T	5	172	c.12085G>A	c.(12085-12087)GGG>AG	p.G4029R
Pat_26	Post-Resistance	CYP2A6	1548	37	19	41354650	41354650	Missense_Mutation	SNP	C	T	4	52	c.362G>A	c.(361-363)GGG>GAG	p.G121E
Pat_26	Post-Resistance	CIC	23152	37	19	42795519	42795519	Missense_Mutation	SNP	C	T	12	226	c.2599C>T	c.(2599-2601)CCA>TCA	p.P867S
Pat_26	Post-Resistance	PPM1N	147699	37	19	46003802	46003803	Missense_Mutation	DNP	GG	AA	5	87	.1146_1147GG>A	44-1149)GGGGGA>GGA	p.G383R
Pat_26	Post-Resistance	CCDC155	147872	37	19	49900950	49900950	Missense_Mutation	SNP	G	A	42	377	c.443G>A	c.(442-444)GGA>GAA	p.G148E
Pat_26	Post-Resistance	SCAF1	58506	37	19	50150084	50150085	Missense_Mutation	DNP	AC	TT	4	61	c.475_476AC>TT	c.(475-477)ACG>TTG	p.T159L
Pat_26	Post-Resistance	MYBPC2	4606	37	19	50964868	50964868	Missense_Mutation	SNP	G	A	7	92	c.3001G>A	c.(3001-3003)GAA>AAA	p.E1001K
Pat_26	Post-Resistance	KLK1	3816	37	19	51323644	51323645	Missense_Mutation	DNP	GG	TA	42	566	c.261_262CC>TA	259-264)GCCCAG>GCTA	p.Q88K
Pat_26	Post-Resistance	KLK8	11202	37	19	51499463	51499463	Missense_Mutation	SNP	G	A	6	147	c.635C>T	c.(634-636)TCT>TTT	p.S212F
Pat_26	Post-Resistance	SIGLEC10	89790	37	19	51918507	51918507	Missense_Mutation	SNP	C	T	28	236	c.1258G>A	c.(1258-1260)GAA>AAA	p.E420K
Pat_26	Post-Resistance	ZNF432	9668	37	19	52537586	52537586	Missense_Mutation	SNP	C	T	20	241	c.1346G>A	c.(1345-1347)CGA>CAA	p.R449Q
Pat_26	Post-Resistance	ZNF578	147660	37	19	53014626	53014626	Missense_Mutation	SNP	C	G	6	385	c.992C>G	c.(991-993)ACA>AGA	p.T331R
Pat_26	Post-Resistance	ZSCAN4	201516	37	19	58187625	58187625	Missense_Mutation	SNP	G	A	16	147	c.112G>A	c.(112-114)GGG>AGG	p.G38R
Pat_26	Post-Resistance	NBAS	51594	37	2	15696937	15696937	Nonsense_Mutation	SNP	A	T	29	242	c.179T>A	c.(178-180)TTA>TAA	p.L60*
Pat_26	Post-Resistance	APOB	338	37	2	21236086	21236086	Missense_Mutation	SNP	G	A	31	472	c.4162C>T	c.(4162-4164)CGT>TGT	p.R1388C
Pat_26	Post-Resistance	DPYSL5	56896	37	2	27164901	27164901	Missense_Mutation	SNP	G	T	12	290	c.1173G>T	c.(1171-1173)AAG>AAT	p.K391N
Pat_26	Post-Resistance	DNAJC5G	285126	37	2	27503075	27503075	Missense_Mutation	SNP	G	A	20	305	c.562G>A	c.(562-564)GAT>AAT	p.D188N
Pat_26	Post-Resistance	RBKS	64080	37	2	28050589	28050589	Missense_Mutation	SNP	C	T	3	70	c.640G>A	c.(640-642)GCT>ACT	p.A214T
Pat_26	Post-Resistance	XDH	7498	37	2	31605866	31605867	Splice_Site	DNP	CC	TT	4	127	c.1038_splice	c.e11+1	p.A346_splice
Pat_26	Post-Resistance	PRKCE	5581	37	2	46207491	46207491	Missense_Mutation	SNP	G	T	26	224	c.664G>T	c.(664-666)GGG>TGG	p.G222W
Pat_26	Post-Resistance	BCL11A	53335	37	2	60689281	60689281	Missense_Mutation	SNP	C	T	6	108	c.766G>A	c.(766-768)GAA>AAA	p.E256K
Pat_26	Post-Resistance	USP34	9736	37	2	61605504	61605504	Missense_Mutation	SNP	G	C	26	187	c.1070C>G	c.(1069-1071)ACA>AGA	p.T357R
Pat_26	Post-Resistance	DYSF	8291	37	2	71797734	71797734	Missense_Mutation	SNP	G	A	6	72	c.3037G>A	c.(3037-3039)GAG>AAG	p.E1013K
Pat_26	Post-Resistance	SLC4A5	57835	37	2	74481792	74481792	Missense_Mutation	SNP	G	A	36	418	c.1067C>T	c.(1066-1068)TCC>TTC	p.S356F
Pat_26	Post-Resistance	TRIM43	129868	37	2	96259896	96259896	Missense_Mutation	SNP	C	T	3	75	c.125C>T	c.(124-126)TCG>TTG	p.S42L
Pat_26	Post-Resistance	LOC285033	285033	37	2	96906408	96906408	Missense_Mutation	SNP	C	T	15	144	c.347C>T	c.(346-348)TCC>TTC	p.S116F
Pat_26	Post-Resistance	TSGA10	80705	37	2	99634699	99634699	Missense_Mutation	SNP	C	T	23	155	c.2036G>A	c.(2035-2037)CGA>CAA	p.R679Q
Pat_26	Post-Resistance	ST6GAL2	84620	37	2	107460402	107460402	Missense_Mutation	SNP	C	T	4	77	c.32G>A	c.(31-33)CGA>CAA	p.R11Q
Pat_26	Post-Resistance	RGPD4	285190	37	2	108488208	108488208	Missense_Mutation	SNP	G	A	60	654	c.3748G>A	c.(3748-3750)GAT>AAT	p.D1250N
Pat_26	Post-Resistance	SLC5A7	60482	37	2	108626702	108626702	Missense_Mutation	SNP	A	T	15	152	c.1128A>T	c.(1126-1128)GAA>GAT	p.E376D
Pat_26	Post-Resistance	SULT1C2	6819	37	2	108921643	108921643	Nonsense_Mutation	SNP	G	A	29	283	c.518G>A	c.(517-519)TGG>TAG	p.W173*
Pat_26	Post-Resistance	SULT1C4	27233	37	2	108999611	108999611	Missense_Mutation	SNP	G	T	12	105	c.456G>T	c.(454-456)ATG>ATT	p.M152I
Pat_26	Post-Resistance	PSD4	23550	37	2	113955328	113955328	Missense_Mutation	SNP	G	A	8	183	c.2462G>A	c.(2461-2463)GGA>GAA	p.G821E
Pat_26	Post-Resistance	RALB	5899	37	2	121047325	121047325	Missense_Mutation	SNP	G	A	3	74	c.493G>A	c.(493-495)GTG>ATG	p.V165M

Pat_26	Post-Resistance	LRP1B	53353	37	2	141298592	141298592	Missense_Mutation	SNP	T	C	54	352	c.7463A>G	c.(7462-7464)AAT>AGT	p.N2488S
Pat_26	Post-Resistance	LRP1B	53353	37	2	141359209	141359209	Splice_Site	SNP	C	T	5	41	c.6800_splice	c.e42-1	p.N2267_splice
Pat_26	Post-Resistance	NEB	4703	37	2	152466537	152466537	Missense_Mutation	SNP	C	T	6	80	c.11387G>A	c.(11386-11388)GGA>GAA	p.G3796E
Pat_26	Post-Resistance	GRB14	2888	37	2	165365320	165365320	Missense_Mutation	SNP	C	T	10	229	c.859G>A	c.(859-861)GAT>AAT	p.D287N
Pat_26	Post-Resistance	SCN3A	6328	37	2	166032843	166032843	Missense_Mutation	SNP	G	A	19	196	c.62C>T	c.(61-63)TCT>TTT	p.S21F
Pat_26	Post-Resistance	XIRP2	129446	37	2	167760216	167760216	Missense_Mutation	SNP	C	T	3	86	c.224C>T	c.(223-225)CCG>CTG	p.P75L
Pat_26	Post-Resistance	LRP2	4036	37	2	170147469	170147469	Missense_Mutation	SNP	C	T	12	136	c.808G>A	c.(808-810)GAA>AAA	p.E270K
Pat_26	Post-Resistance	TTN	7273	37	2	179416831	179416831	Missense_Mutation	SNP	C	T	32	346	c.83092G>A	c.(83092-83094)GAA>AAA	p.E27698K
Pat_26	Post-Resistance	TTN	7273	37	2	179427038	179427038	Missense_Mutation	SNP	C	T	8	110	c.76117G>A	c.(76117-76119)GAA>AAA	p.E25373K
Pat_26	Post-Resistance	TTN	7273	37	2	179430017	179430017	Missense_Mutation	SNP	C	T	7	222	c.73138G>A	c.(73138-73140)GGA>AGA	p.G24380R
Pat_26	Post-Resistance	TTN	7273	37	2	179569999	179569999	Missense_Mutation	SNP	C	T	5	71	c.25774G>A	c.(25774-25776)GAA>AAA	p.E8592K
Pat_26	Post-Resistance	FAM171B	165215	37	2	187615998	187615998	Missense_Mutation	SNP	C	T	11	102	c.862C>T	c.(862-864)CGC>TGC	p.R288C
Pat_26	Post-Resistance	COL5A2	1290	37	2	189910528	189910528	Missense_Mutation	SNP	G	A	8	134	c.3307C>T	c.(3307-3309)CCG>TCG	p.P1103S
Pat_26	Post-Resistance	ANKAR	150709	37	2	190606067	190606067	Splice_Site	SNP	G	A	11	132	c.3488_splice	c.e19-1	p.G1163_splice
Pat_26	Post-Resistance	NAB1	4664	37	2	191550329	191550329	Missense_Mutation	SNP	C	T	22	192	c.1223C>T	c.(1222-1224)CCT>CTT	p.P408L
Pat_26	Post-Resistance	ICA1L	130026	37	2	203684548	203684548	Missense_Mutation	SNP	G	A	19	119	c.434C>T	c.(433-435)ACC>ATC	p.T145I
Pat_26	Post-Resistance	CPS1	1373	37	2	211444459	211444459	Missense_Mutation	SNP	G	A	26	241	c.493G>A	c.(493-495)GAC>AAC	p.D165N
Pat_26	Post-Resistance	ATIC	471	37	2	216182921	216182921	Missense_Mutation	SNP	G	A	54	386	c.188G>A	c.(187-189)GGA>GAA	p.G63E
Pat_26	Post-Resistance	VIL1	7429	37	2	219301222	219301222	Missense_Mutation	SNP	T	C	41	483	c.1844T>C	c.(1843-1845)CTG>CCG	p.L615P
Pat_26	Post-Resistance	TTLL4	9654	37	2	219603034	219603034	Missense_Mutation	SNP	C	T	21	200	c.635C>T	c.(634-636)TCC>TTC	p.S212F
Pat_26	Post-Resistance	SGPP2	130367	37	2	223389667	223389667	Missense_Mutation	SNP	C	T	4	133	c.563C>T	c.(562-564)CCA>CTA	p.P188L
Pat_26	Post-Resistance	ALPPL2	251	37	2	233272555	233272555	Missense_Mutation	SNP	G	A	23	154	c.476G>A	c.(475-477)GGA>GAA	p.G159E
Pat_26	Post-Resistance	PER2	8864	37	2	239186525	239186525	Missense_Mutation	SNP	G	A	9	87	c.53C>T	c.(52-54)CCC>CTC	p.P18L
Pat_26	Post-Resistance	ANO7	50636	37	2	242139610	242139610	Missense_Mutation	SNP	C	T	16	127	c.686C>T	c.(685-687)TCC>TTC	p.S229F
Pat_26	Post-Resistance	FARP2	9855	37	2	242380792	242380792	Missense_Mutation	SNP	C	T	36	222	c.1232C>T	c.(1231-1233)CCC>CTC	p.P411L
Pat_26	Post-Resistance	D2HGDH	728294	37	2	242695408	242695408	Missense_Mutation	SNP	G	A	4	107	c.1285G>A	c.(1285-1287)GTG>ATG	p.V429M
Pat_26	Post-Resistance	TMC2	117532	37	20	2572971	2572971	Missense_Mutation	SNP	C	T	16	258	c.850C>T	c.(850-852)CCC>TCC	p.P284S
Pat_26	Post-Resistance	SEL1L2	80343	37	20	13846138	13846138	Missense_Mutation	SNP	A	C	8	91	c.1427T>G	c.(1426-1428)CTA>CGA	p.L476R
Pat_26	Post-Resistance	XKR7	343702	37	20	30585052	30585052	Missense_Mutation	SNP	C	T	6	193	c.1532C>T	c.(1531-1533)CCA>CTA	p.P511L
Pat_26	Post-Resistance	ITCH	83737	37	20	32981622	32981622	Missense_Mutation	SNP	C	T	11	425	c.5C>T	c.(4-6)TCT>TTT	p.S2F
Pat_26	Post-Resistance	STAU1	6780	37	20	47739771	47739771	Missense_Mutation	SNP	G	A	18	190	c.824C>T	c.(823-825)CCA>CTA	p.P275L
Pat_26	Post-Resistance	DDX27	55661	37	20	47858702	47858702	Missense_Mutation	SNP	G	A	4	114	c.2168G>A	c.(2167-2169)CGG>CAG	p.R723Q
Pat_26	Post-Resistance	SRRD	402055	37	22	26884387	26884387	Missense_Mutation	SNP	C	T	62	558	c.542C>T	c.(541-543)CCT>CTT	p.P181L
Pat_26	Post-Resistance	GAL3ST1	9514	37	22	30951719	30951719	Missense_Mutation	SNP	C	T	17	249	c.493G>A	c.(493-495)GAC>AAC	p.D165N
Pat_26	Post-Resistance	TCN2	6948	37	22	31008971	31008971	Missense_Mutation	SNP	G	T	6	155	c.369G>T	c.(367-369)AAG>AAT	p.K123N
Pat_26	Post-Resistance	SMTN	6525	37	22	31487688	31487688	Missense_Mutation	SNP	C	T	13	248	c.1487C>T	c.(1486-1488)CCG>CTG	p.P496L
Pat_26	Post-Resistance	SYNGR1	9145	37	22	39777743	39777743	Missense_Mutation	SNP	G	A	5	252	c.526G>A	c.(526-528)GCC>ACC	p.A176T
Pat_26	Post-Resistance	EP300	2033	37	22	41531849	41531850	Missense_Mutation	DNP	GG	AA	16	178	.1561_1562GG>AA	c.(1561-1563)GGA>AAA	p.G521K
Pat_26	Post-Resistance	CYP2D6	1565	37	22	42523908	42523908	Missense_Mutation	SNP	C	T	20	303	c.921G>A	c.(919-921)ATG>ATA	p.M307I
Pat_26	Post-Resistance	SAPS2	9701	37	22	50874861	50874861	Missense_Mutation	SNP	C	T	7	20	c.1582C>T	c.(1582-1584)CGC>TGC	p.R528C
Pat_26	Post-Resistance	SBF1	6305	37	22	50885576	50885576	Missense_Mutation	SNP	C	T	3	54	c.5677G>A	c.(5677-5679)GCC>ACC	p.A1893T
Pat_26	Post-Resistance	CHL1	10752	37	3	382573	382573	Missense_Mutation	SNP	C	T	18	146	c.482C>T	c.(481-483)CCT>CTT	p.P161L
Pat_26	Post-Resistance	ZNF385D	79750	37	3	21552508	21552508	Missense_Mutation	SNP	G	A	7	95	c.284C>T	c.(283-285)GCT>GTT	p.A95V
Pat_26	Post-Resistance	ARPP21	10777	37	3	35833903	35833903	Missense_Mutation	SNP	G	A	39	440	c.2062G>A	c.(2062-2064)GGA>AGA	p.G688R
Pat_26	Post-Resistance	SCN11A	11280	37	3	38946734	38946734	Nonsense_Mutation	SNP	G	A	30	257	c.1552C>T	c.(1552-1554)CAA>TAA	p.Q518*
Pat_26	Post-Resistance	SCN11A	11280	37	3	38949450	38949450	Missense_Mutation	SNP	C	A	11	91	c.1463G>T	c.(1462-1464)TGC>TTC	p.C488F
Pat_26	Post-Resistance	VIPR1	7433	37	3	42577630	42577630	Missense_Mutation	SNP	G	A	3	43	c.1231G>A	c.(1231-1233)GTC>ATC	p.V411I

Pat_26	Post-Resistance	CDCP1	64866	37	3	45153823	45153823	Missense_Mutation	SNP	C	T	95	669	c.407G>A	c.(406-408)GGT>GAT	p.G136D
Pat_26	Post-Resistance	CBLB	868	37	3	105464833	105464833	Missense_Mutation	SNP	G	A	37	366	c.773C>T	c.(772-774)CCA>CTA	p.P258L
Pat_26	Post-Resistance	GUCA1C	9626	37	3	108672495	108672495	Missense_Mutation	SNP	C	T	27	299	c.115G>A	c.(115-117)GAA>AAA	p.E39K
Pat_26	Post-Resistance	WDR52	55779	37	3	113146126	113146126	Missense_Mutation	SNP	C	T	6	110	c.161G>A	c.(160-162)GGG>GAG	p.G54E
Pat_26	Post-Resistance	POLQ	10721	37	3	121256023	121256023	Missense_Mutation	SNP	C	T	24	314	c.664G>A	c.(664-666)GGA>AGA	p.G222R
Pat_26	Post-Resistance	SLC15A2	6565	37	3	121647395	121647395	Missense_Mutation	SNP	C	T	26	281	c.1334C>T	c.(1333-1335)TCC>TTC	p.S445F
Pat_26	Post-Resistance	MYLK	4638	37	3	123457860	123457861	Missense_Mutation	DNP	CC	TT	4	80	c.471_472GG>AA	469-474)GGGGAG>GGAA	p.E158K
Pat_26	Post-Resistance	SEC61A1	29927	37	3	127786827	127786827	Missense_Mutation	SNP	T	C	53	495	c.1169T>C	c.(1168-1170)GTT>GCT	p.V390A
Pat_26	Post-Resistance	COL6A6	131873	37	3	130311915	130311915	Missense_Mutation	SNP	G	A	52	589	c.4382G>A	c.(4381-4383)GGG>GAG	p.G1461E
Pat_26	Post-Resistance	ATP2C1	27032	37	3	130698165	130698165	Missense_Mutation	SNP	C	T	41	290	c.1643C>T	c.(1642-1644)CCT>CTT	p.P548L
Pat_26	Post-Resistance	DNAJC13	23317	37	3	132169656	132169656	Missense_Mutation	SNP	G	A	18	142	c.502G>A	c.(502-504)GGA>AGA	p.G168R
Pat_26	Post-Resistance	AMOTL2	51421	37	3	134090038	134090038	Nonsense_Mutation	SNP	G	A	9	64	c.412C>T	c.(412-414)CAG>TAG	p.Q138*
Pat_26	Post-Resistance	B3GNT5	84002	37	3	182988256	182988256	Missense_Mutation	SNP	C	T	33	370	c.670C>T	c.(670-672)CAT>TAT	p.H224Y
Pat_26	Post-Resistance	DVL3	1857	37	3	183885727	183885727	Missense_Mutation	SNP	T	C	19	299	c.1372T>C	c.(1372-1374)TTC>CTC	p.F458L
Pat_26	Post-Resistance	OSTalpha	200931	37	3	195955029	195955029	Missense_Mutation	SNP	G	A	59	624	c.406G>A	c.(406-408)GAA>AAA	p.E136K
Pat_26	Post-Resistance	RGS12	6002	37	4	3418686	3418686	Missense_Mutation	SNP	C	T	32	294	c.2474C>T	c.(2473-2475)TCC>TTC	p.S825F
Pat_26	Post-Resistance	GBA3	57733	37	4	22748945	22748945	Missense_Mutation	SNP	G	A	11	282	c.313G>A	c.(313-315)GAT>AAT	p.D105N
Pat_26	Post-Resistance	GABRB1	2560	37	4	47408782	47408782	Missense_Mutation	SNP	G	A	17	163	c.919G>A	c.(919-921)GAT>AAT	p.D307N
Pat_26	Post-Resistance	KDR	3791	37	4	55984966	55984966	Missense_Mutation	SNP	C	T	4	96	c.163G>A	c.(163-165)GGA>AGA	p.G55R
Pat_26	Post-Resistance	UGT2B28	54490	37	4	70146547	70146547	Missense_Mutation	SNP	C	T	13	190	c.329C>T	c.(328-330)TCA>TTA	p.S110L
Pat_26	Post-Resistance	UGT2B28	54490	37	4	70148286	70148286	Missense_Mutation	SNP	G	A	28	251	c.776G>A	c.(775-777)CGA>CAA	p.R259Q
Pat_26	Post-Resistance	CENPE	1062	37	4	104057392	104057392	Missense_Mutation	SNP	G	A	14	152	c.6428C>T	c.(6427-6429)TCA>TTA	p.S2143L
Pat_26	Post-Resistance	GSTCD	79807	37	4	106766720	106766721	Missense_Mutation	DNP	GG	AA	6	97	.1888_1889GG>A	c.(1888-1890)GGA>AAA	p.G630K
Pat_26	Post-Resistance	FAT4	79633	37	4	126372621	126372621	Missense_Mutation	SNP	G	A	33	247	c.10450G>A	c.(10450-10452)GAT>AAT	p.D3484N
Pat_26	Post-Resistance	FAT4	79633	37	4	126398438	126398438	Missense_Mutation	SNP	G	A	38	342	c.12422G>A	c.(12421-12423)GGA>GA	p.G4141E
Pat_26	Post-Resistance	ARFIP1	27236	37	4	153750802	153750802	Missense_Mutation	SNP	C	T	5	251	c.17C>T	c.(16-18)CCC>CTC	p.P6L
Pat_26	Post-Resistance	GLRA3	8001	37	4	175598335	175598335	Missense_Mutation	SNP	G	A	12	133	c.821C>T	c.(820-822)TCA>TTA	p.S274L
Pat_26	Post-Resistance	CTNND2	1501	37	5	10992705	10992705	Missense_Mutation	SNP	G	A	8	155	c.3169C>T	c.(3169-3171)CCC>TCC	p.P1057S
Pat_26	Post-Resistance	FBXL7	23194	37	5	15928154	15928154	Missense_Mutation	SNP	C	T	3	80	c.283C>T	c.(283-285)CGC>TGC	p.R95C
Pat_26	Post-Resistance	CDH18	1016	37	5	19721546	19721546	Missense_Mutation	SNP	C	T	13	211	c.553G>A	c.(553-555)GAT>AAT	p.D185N
Pat_26	Post-Resistance	CDH18	1016	37	5	19839093	19839093	Missense_Mutation	SNP	C	T	13	118	c.3G>A	c.(1-3)ATG>ATA	p.M1I
Pat_26	Post-Resistance	PRDM9	56979	37	5	23509648	23509648	Missense_Mutation	SNP	G	A	23	239	c.139G>A	c.(139-141)GAG>AAG	p.E47K
Pat_26	Post-Resistance	CDH10	1008	37	5	24487995	24487995	Missense_Mutation	SNP	T	A	9	181	c.2144A>T	c.(2143-2145)AAT>ATT	p.N715I
Pat_26	Post-Resistance	PDZD2	23037	37	5	32087434	32087434	Missense_Mutation	SNP	G	A	18	117	c.3880G>A	c.(3880-3882)GAG>AAG	p.E1294K
Pat_26	Post-Resistance	LMBRD2	92255	37	5	36123060	36123060	Missense_Mutation	SNP	G	A	5	25	c.826C>T	c.(826-828)CCT>TCT	p.P276S
Pat_26	Post-Resistance	MARVELD2	153562	37	5	68728399	68728399	Missense_Mutation	SNP	A	G	10	88	c.1228A>G	c.(1228-1230)AAT>GAT	p.N410D
Pat_26	Post-Resistance	ENC1	8507	37	5	73930869	73930869	Missense_Mutation	SNP	G	A	15	177	c.1442C>T	c.(1441-1443)CCC>CTC	p.P481L
Pat_26	Post-Resistance	SPZ1	84654	37	5	79616605	79616605	Missense_Mutation	SNP	C	G	6	151	c.571C>G	c.(571-573)CAG>GAG	p.Q191E
Pat_26	Post-Resistance	ANKRD34B	340120	37	5	79854638	79854638	Missense_Mutation	SNP	G	A	14	106	c.1201C>T	c.(1201-1203)CCT>TCT	p.P401S
Pat_26	Post-Resistance	GPR98	84059	37	5	89988548	89988548	Missense_Mutation	SNP	C	T	6	28	c.7078C>T	c.(7078-7080)CGT>TGT	p.R2360C
Pat_26	Post-Resistance	GPR98	84059	37	5	90024556	90024556	Missense_Mutation	SNP	C	T	24	275	c.10232C>T	c.(10231-10233)GCC>GT	p.A3411V
Pat_26	Post-Resistance	GPR98	84059	37	5	90111487	90111487	Missense_Mutation	SNP	G	A	3	21	c.16130G>A	c.(16129-16131)GGA>GA	p.G5377E
Pat_26	Post-Resistance	PAM	5066	37	5	102345512	102345512	Missense_Mutation	SNP	G	A	15	145	c.2273G>A	c.(2272-2274)GGA>GAA	p.G758E
Pat_26	Post-Resistance	SNCAIP	9627	37	5	121739548	121739548	Missense_Mutation	SNP	G	A	16	344	c.118G>A	c.(118-120)GAA>AAA	p.E40K
Pat_26	Post-Resistance	KIF3A	11127	37	5	132051999	132051999	Missense_Mutation	SNP	G	A	4	153	c.892C>T	c.(892-894)CGT>TGT	p.R298C
Pat_26	Post-Resistance	PCDHA1	56147	37	5	140166416	140166416	Missense_Mutation	SNP	G	A	17	77	c.541G>A	c.(541-543)GAT>AAT	p.D181N
Pat_26	Post-Resistance	PCDHGB3	56102	37	5	140752101	140752101	Missense_Mutation	SNP	C	T	20	209	c.2140C>T	c.(2140-2142)CGC>TGC	p.R714C

Pat_26	Post-Resistance	PPARGC1B	133522	37	5	149212900	149212900	Missense_Mutation	SNP	C	T	4	73	c.1264C>T	c.(1264-1266)CGG>TGG	p.R422W
Pat_26	Post-Resistance	MFAP3	4238	37	5	153432575	153432575	Missense_Mutation	SNP	C	T	43	369	c.391C>T	c.(391-393)CGT>TGT	p.R131C
Pat_26	Post-Resistance	EBF1	1879	37	5	158523996	158523996	Missense_Mutation	SNP	C	T	3	64	c.277G>A	c.(277-279)GTG>ATG	p.V93M
Pat_26	Post-Resistance	GABRB2	2561	37	5	160753392	160753392	Missense_Mutation	SNP	C	T	12	204	c.1174G>A	c.(1174-1176)GAT>AAT	p.D392N
Pat_26	Post-Resistance	SCAND3	114821	37	6	28540442	28540442	Missense_Mutation	SNP	C	T	20	185	c.3224G>A	c.(3223-3225)CGA>CAA	p.R1075Q
Pat_26	Post-Resistance	TRIM26	7726	37	6	30166508	30166508	Missense_Mutation	SNP	G	A	3	56	c.373C>T	c.(373-375)CGG>TGG	p.R125W
Pat_26	Post-Resistance	C4A	720	37	6	31963519	31963519	Missense_Mutation	SNP	C	T	18	320	c.3178C>T	c.(3178-3180)CGG>TGG	p.R1060W
Pat_26	Post-Resistance	DNAH8	1769	37	6	38875853	38875853	Missense_Mutation	SNP	C	T	4	58	c.8819C>T	c.(8818-8820)TCA>TTA	p.S2940L
Pat_26	Post-Resistance	GLP1R	2740	37	6	39046935	39046935	Missense_Mutation	SNP	A	T	40	450	c.1002A>T	c.(1000-1002)AAA>AAT	p.K334N
Pat_26	Post-Resistance	SLC22A7	10864	37	6	43266358	43266358	Missense_Mutation	SNP	G	A	6	40	c.262G>A	c.(262-264)GCT>ACT	p.A88T
Pat_26	Post-Resistance	MEP1A	4224	37	6	46800961	46800961	Missense_Mutation	SNP	C	T	20	158	c.1295C>T	c.(1294-1296)CCC>CTC	p.P432L
Pat_26	Post-Resistance	GPR110	266977	37	6	46977301	46977301	Missense_Mutation	SNP	G	A	4	68	c.1870C>T	c.(1870-1872)CGT>TGT	p.R624C
Pat_26	Post-Resistance	COL21A1	81578	37	6	55933885	55933885	Missense_Mutation	SNP	C	T	5	44	c.2050G>A	c.(2050-2052)GAA>AAA	p.E684K
Pat_26	Post-Resistance	BAI3	577	37	6	70082297	70082297	Splice_Site	SNP	G	A	4	41	c.4240_splice	c.e30-1	p.R1414_splice
Pat_26	Post-Resistance	WISP3	8838	37	6	112390739	112390739	Nonsense_Mutation	SNP	G	A	12	154	c.981G>A	c.(979-981)TGG>TGA	p.W327*
Pat_26	Post-Resistance	NT5DC1	221294	37	6	116544279	116544279	Missense_Mutation	SNP	C	T	26	217	c.787C>T	c.(787-789)CCT>TCT	p.P263S
Pat_26	Post-Resistance	ARG1	383	37	6	131900341	131900341	Missense_Mutation	SNP	G	A	8	117	c.221G>A	c.(220-222)GGA>GAA	p.G74E
Pat_26	Post-Resistance	CTAGE9	643854	37	6	132031227	132031227	Missense_Mutation	SNP	G	A	19	73	c.931C>T	c.(931-933)CCG>TCG	p.P311S
Pat_26	Post-Resistance	LATS1	9113	37	6	149997811	149997811	Nonsense_Mutation	SNP	G	A	13	58	c.2656C>T	c.(2656-2658)CGA>TGA	p.R886*
Pat_26	Post-Resistance	SYNE1	23345	37	6	152730807	152730807	Missense_Mutation	SNP	C	T	17	156	c.6268G>A	c.(6268-6270)GAA>AAA	p.E2090K
Pat_26	Post-Resistance	PHF10	55274	37	6	170115848	170115848	Missense_Mutation	SNP	C	T	20	151	c.649G>A	c.(649-651)GAA>AAA	p.E217K
Pat_26	Post-Resistance	DLL1	28514	37	6	170592725	170592725	Missense_Mutation	SNP	C	T	3	28	c.1642G>A	c.(1642-1644)GTG>ATG	p.V548M
Pat_26	Post-Resistance	RADIL	55698	37	7	4874803	4874803	Missense_Mutation	SNP	G	A	4	56	c.851C>T	c.(850-852)CCC>CTC	p.P284L
Pat_26	Post-Resistance	RAC1	5879	37	7	6426892	6426892	Missense_Mutation	SNP	C	T	26	418	c.85C>T	c.(85-87)CCT>TCT	p.P29S
Pat_26	Post-Resistance	DFNA5	1687	37	7	24789342	24789342	Missense_Mutation	SNP	C	T	39	338	c.52G>A	c.(52-54)GAC>AAC	p.D18N
Pat_26	Post-Resistance	OGDH	4967	37	7	44734078	44734078	Missense_Mutation	SNP	C	T	14	149	c.1571C>T	c.(1570-1572)CCG>CTG	p.P524L
Pat_26	Post-Resistance	TNS3	64759	37	7	47343138	47343138	Missense_Mutation	SNP	G	A	7	19	c.2867C>T	c.(2866-2868)CCC>CTC	p.P956L
Pat_26	Post-Resistance	ABCA13	154664	37	7	48353922	48353922	Missense_Mutation	SNP	G	A	6	37	c.9775G>A	c.(9775-9777)GAT>AAT	p.D3259N
Pat_26	Post-Resistance	AUTS2	26053	37	7	70255866	70255866	Missense_Mutation	SNP	C	A	5	100	c.3664C>A	c.(3664-3666)CCG>ACG	p.P1222T
Pat_26	Post-Resistance	DTX2	113878	37	7	76134733	76134733	Missense_Mutation	SNP	T	C	4	42	c.1684T>C	c.(1684-1686)TTC>CTC	p.F562L
Pat_26	Post-Resistance	RSBN1L	222194	37	7	77408468	77408468	Missense_Mutation	SNP	G	A	3	72	c.2524G>A	c.(2524-2526)GAT>AAT	p.D842N
Pat_26	Post-Resistance	PCLO	27445	37	7	82764309	82764309	Missense_Mutation	SNP	C	T	24	271	c.2557G>A	c.(2557-2559)GAA>AAA	p.E853K
Pat_26	Post-Resistance	SEMA3A	10371	37	7	83592633	83592633	Missense_Mutation	SNP	C	T	22	241	c.1748G>A	c.(1747-1749)AGA>AAA	p.R583K
Pat_26	Post-Resistance	EPHB4	2050	37	7	100410379	100410379	Missense_Mutation	SNP	G	A	8	66	c.2108C>T	c.(2107-2109)TCC>TTC	p.S703F
Pat_26	Post-Resistance	SPDYE6	729597	37	7	101989089	101989089	Missense_Mutation	SNP	C	T	9	271	c.784G>A	c.(784-786)GAC>AAC	p.D262N
Pat_26	Post-Resistance	SRPK2	6733	37	7	104783638	104783638	Missense_Mutation	SNP	G	A	26	191	c.920C>T	c.(919-921)ACC>ATC	p.T307I
Pat_26	Post-Resistance	MGAM	8972	37	7	141731520	141731520	Missense_Mutation	SNP	C	T	32	298	c.1511C>T	c.(1510-1512)CCC>CTC	p.P504L
Pat_26	Post-Resistance	OR2F2	135948	37	7	143633023	143633023	Missense_Mutation	SNP	G	A	10	160	c.698G>A	c.(697-699)GGA>GAA	p.G233E
Pat_26	Post-Resistance	GIMAP5	55340	37	7	150439711	150439711	Missense_Mutation	SNP	G	C	33	476	c.484G>C	c.(484-486)GAT>CAT	p.D162H
Pat_26	Post-Resistance	VIPR2	7434	37	7	158902542	158902542	Missense_Mutation	SNP	G	A	20	220	c.220C>T	c.(220-222)CCC>TCC	p.P74S
Pat_26	Post-Resistance	CSMD1	64478	37	8	3059206	3059206	Missense_Mutation	SNP	C	T	3	42	c.5029G>A	c.(5029-5031)GAT>AAT	p.D1677N
Pat_26	Post-Resistance	SLC18A1	6570	37	8	20007227	20007227	Missense_Mutation	SNP	G	A	7	96	c.1106C>T	c.(1105-1107)TCC>TTC	p.S369F
Pat_26	Post-Resistance	HR	55806	37	8	21976539	21976540	Missense_Mutation	DNP	GG	AA	9	197	.3136_3137CC>T	c.(3136-3138)CCG>TTG	p.P1046L
Pat_26	Post-Resistance	ADAMDEC1	27299	37	8	24251607	24251607	Missense_Mutation	SNP	G	A	15	205	c.310G>A	c.(310-312)GAA>AAA	p.E104K
Pat_26	Post-Resistance	ADAM7	8756	37	8	24339742	24339742	Missense_Mutation	SNP	G	A	9	99	c.793G>A	c.(793-795)GAA>AAA	p.E265K
Pat_26	Post-Resistance	BNIP3L	665	37	8	26252780	26252780	Missense_Mutation	SNP	G	A	17	143	c.319G>A	c.(319-321)GAT>AAT	p.D107N
Pat_26	Post-Resistance	BNIP3L	665	37	8	26252782	26252782	Missense_Mutation	SNP	T	A	17	149	c.321T>A	c.(319-321)GAT>GAA	p.D107E

Pat_26	Post-Resistance	SCARA3	51435	37	8	27516870	27516870	Missense_Mutation	SNP	G	A	7	92	c.1183G>A	c.(1183-1185)GAG>AAG	p.E395K
Pat_26	Post-Resistance	FBXO16	157574	37	8	28340887	28340887	Missense_Mutation	SNP	T	G	27	342	c.77A>C	c.(76-78)AAC>ACC	p.N26T
Pat_26	Post-Resistance	MCM4	4173	37	8	48877195	48877195	Missense_Mutation	SNP	C	T	18	158	c.755C>T	c.(754-756)TCA>TTA	p.S252L
Pat_26	Post-Resistance	FAM110B	90362	37	8	59058956	59058956	Missense_Mutation	SNP	C	T	16	115	c.167C>T	c.(166-168)GCC>GTC	p.A56V
Pat_26	Post-Resistance	NSMAF	8439	37	8	59508216	59508216	Missense_Mutation	SNP	C	T	20	110	c.1795G>A	c.(1795-1797)GAA>AAA	p.E599K
Pat_26	Post-Resistance	ARFGEF1	10565	37	8	68170417	68170417	Missense_Mutation	SNP	G	A	10	109	c.2344C>T	c.(2344-2346)CGT>TGT	p.R782C
Pat_26	Post-Resistance	CA1	759	37	8	86253846	86253846	Missense_Mutation	SNP	C	T	11	177	c.19G>A	c.(19-21)GGA>AGA	p.G7R
Pat_26	Post-Resistance	INTS8	55656	37	8	95840000	95840000	Missense_Mutation	SNP	C	T	48	467	c.497C>T	c.(496-498)CCC>CTC	p.P166L
Pat_26	Post-Resistance	VPS13B	157680	37	8	100791192	100791192	Missense_Mutation	SNP	C	T	24	363	c.7787C>T	c.(7786-7788)TCT>TTT	p.S2596F
Pat_26	Post-Resistance	TRHR	7201	37	8	110131570	110131570	Missense_Mutation	SNP	C	A	23	304	c.1083C>A	c.(1081-1083)GAC>GAA	p.D361E
Pat_26	Post-Resistance	COL14A1	7373	37	8	121210152	121210152	Missense_Mutation	SNP	G	A	5	74	c.695G>A	c.(694-696)GGA>GAA	p.G232E
Pat_26	Post-Resistance	ADCY8	114	37	8	131880114	131880114	Missense_Mutation	SNP	G	T	17	144	c.2188C>A	c.(2188-2190)CAA>AAA	p.Q730K
Pat_26	Post-Resistance	COL22A1	169044	37	8	139727950	139727950	Missense_Mutation	SNP	C	T	21	191	c.2492G>A	c.(2491-2493)GGA>GAA	p.G831E
Pat_26	Post-Resistance	COL22A1	169044	37	8	139815131	139815131	Missense_Mutation	SNP	C	T	16	124	c.1541G>A	c.(1540-1542)GGA>GAA	p.G514E
Pat_26	Post-Resistance	MAPK15	225689	37	8	144803950	144803950	Missense_Mutation	SNP	C	T	20	125	c.1358C>T	c.(1357-1359)CCC>CTC	p.P453L
Pat_26	Post-Resistance	EPPK1	83481	37	8	144942527	144942527	Missense_Mutation	SNP	C	T	16	304	c.4895G>A	c.(4894-4896)GGA>GAA	p.G1632E
Pat_26	Post-Resistance	CPSF1	29894	37	8	145621935	145621935	Missense_Mutation	SNP	G	A	26	221	c.2704C>T	c.(2704-2706)CGT>TGT	p.R902C
Pat_26	Post-Resistance	RANBP6	26953	37	9	6012658	6012658	Missense_Mutation	SNP	T	G	5	237	c.2950A>C	c.(2950-2952)ATA>CTA	p.I984L
Pat_26	Post-Resistance	GLDC	2731	37	9	6534743	6534743	Missense_Mutation	SNP	G	A	4	159	c.2884C>T	c.(2884-2886)CGG>TGG	p.R962W
Pat_26	Post-Resistance	CDKN2A	1029	37	9	21971017	21971017	Missense_Mutation	SNP	G	A	20	97	c.341C>T	c.(340-342)CCC>CTC	p.P114L
Pat_26	Post-Resistance	UNC13B	10497	37	9	35400332	35400332	Missense_Mutation	SNP	T	G	44	370	c.4129T>G	c.(4129-4131)TTC>GTC	p.F1377V
Pat_26	Post-Resistance	ALDH1B1	219	37	9	38395779	38395779	Missense_Mutation	SNP	C	T	26	181	c.34C>T	c.(34-36)CTC>TTC	p.L12F
Pat_26	Post-Resistance	FAM22F	54754	37	9	97082748	97082748	Missense_Mutation	SNP	G	C	4	68	c.1110C>G	c.(1108-1110)AAC>AAG	p.N370K
Pat_26	Post-Resistance	COL15A1	1306	37	9	101797339	101797339	Missense_Mutation	SNP	A	G	3	102	c.2123A>G	c.(2122-2124)AAG>AGG	p.K708R
Pat_26	Post-Resistance	SVEP1	79987	37	9	113171099	113171099	Missense_Mutation	SNP	G	A	33	347	c.6781C>T	c.(6781-6783)CCT>TCT	p.P2261S
Pat_26	Post-Resistance	ZNF883	169834	37	9	115760269	115760269	Missense_Mutation	SNP	G	A	7	94	c.271C>T	c.(271-273)CAT>TAT	p.H91Y
Pat_26	Post-Resistance	CRB2	286204	37	9	126133014	126133014	Missense_Mutation	SNP	C	T	4	82	c.1682C>T	c.(1681-1683)CCG>CTG	p.P561L
Pat_26	Post-Resistance	PPP2R4	5524	37	9	131890300	131890300	Missense_Mutation	SNP	G	A	3	45	c.274G>A	c.(274-276)GAT>AAT	p.D92N
Pat_26	Post-Resistance	ASB6	140459	37	9	132400230	132400230	Missense_Mutation	SNP	C	T	7	77	c.1105G>A	c.(1105-1107)GAG>AAG	p.E369K
Pat_26	Post-Resistance	TTF1	7270	37	9	135251433	135251433	Nonsense_Mutation	SNP	G	A	6	144	c.2587C>T	c.(2587-2589)CGA>TGA	p.R863*
Pat_26	Post-Resistance	REXO4	57109	37	9	136277539	136277539	Missense_Mutation	SNP	G	T	72	571	c.790C>A	c.(790-792)CGT>AGT	p.R264S
Pat_26	Post-Resistance	C9orf172	389813	37	9	139740328	139740328	Missense_Mutation	SNP	C	T	3	24	c.1462C>T	c.(1462-1464)CGG>TGG	p.R488W
Pat_26	Post-Resistance	SCML2	10389	37	X	18323215	18323215	Missense_Mutation	SNP	G	A	49	279	c.607C>T	c.(607-609)CAT>TAT	p.H203Y
Pat_26	Post-Resistance	DCAF8L1	139425	37	X	27999163	27999163	Missense_Mutation	SNP	C	T	20	143	c.289G>A	c.(289-291)GAG>AAG	p.E97K
Pat_26	Post-Resistance	BRWD3	254065	37	X	79943625	79943625	Splice_Site	SNP	C	T	16	94	c.3808_splice	c.e34-1	p.D1270_splice
Pat_26	Post-Resistance	NRK	203447	37	X	105159770	105159770	Missense_Mutation	SNP	C	T	17	71	c.2398C>T	c.(2398-2400)CAT>TAT	p.H800Y
Pat_26	Post-Resistance	VSIG1	340547	37	X	107320552	107320552	Nonsense_Mutation	SNP	G	T	34	158	c.1105G>T	c.(1105-1107)GAG>TAG	p.E369*
Pat_26	Post-Resistance	COL4A5	1287	37	X	107858195	107858195	Missense_Mutation	SNP	G	A	19	68	c.2450G>A	c.(2449-2451)GGA>GAA	p.G817E
Pat_26	Post-Resistance	COL4A5	1287	37	X	107923915	107923915	Missense_Mutation	SNP	C	T	7	64	c.3949C>T	c.(3949-3951)CCT>TCT	p.P1317S
Pat_26	Post-Resistance	IGSF1	3547	37	X	130410004	130410004	Missense_Mutation	SNP	T	A	15	71	c.2827A>T	c.(2827-2829)ATC>TTC	p.I943F
Pat_26	Post-Resistance	MAGEC1	9947	37	X	140995273	140995273	Missense_Mutation	SNP	C	T	8	31	c.2083C>T	c.(2083-2085)CCT>TCT	p.P695S
Pat_29	Pre-Treatment	PTEN	5728	37	10	89653815	89653815	Missense_Mutation	SNP	C	A	19	114	c.113C>A	c.(112-114)CCT>CAT	p.P38H
Pat_29	Pre-Treatment	GOLGA8E	390535	37	15	23444064	23444064	Missense_Mutation	SNP	G	C	12	35	c.719G>C	c.(718-720)AGT>ACT	p.S240T
Pat_29	Pre-Treatment	MPP2	4355	37	17	41957260	41957260	Missense_Mutation	SNP	G	A	15	123	c.1378C>T	c.(1378-1380)CGC>TGC	p.R460C
Pat_29	Pre-Treatment	ZNF799	90576	37	19	12501446	12501446	Missense_Mutation	SNP	T	C	5	56	c.1766A>G	c.(1765-1767)GAA>GGA	p.E589G
Pat_29	Pre-Treatment	SCN9A	6335	37	2	167133552	167133552	Missense_Mutation	SNP	C	T	52	404	c.2782G>A	c.(2782-2784)GCT>ACT	p.A928T
Pat_29	Pre-Treatment	PTGIS	5740	37	20	48129665	48129665	Missense_Mutation	SNP	G	T	6	69	c.1158C>A	c.(1156-1158)TTC>TTA	p.F386L

Pat_29	Pre-Treatment	HDAC10	83933	37	22	50686538	50686538	Missense_Mutation	SNP	G	A	5	38	c.1118C>T	c.(1117-1119)TCC>TTC	p.S373F
Pat_29	Pre-Treatment	MAGI1	9223	37	3	66023938	66023938	Missense_Mutation	SNP	G	T	16	109	c.46C>A	c.(46-48)CAC>AAC	p.H16N
Pat_29	Pre-Treatment	PIK3R1	5295	37	5	67588090	67588090	Missense_Mutation	SNP	T	G	14	113	c.920T>G	c.(919-921)CTG>CGG	p.L307R
Pat_29	Post-Resistance	AMY2B	280	37	1	104120142	104120142	Missense_Mutation	SNP	A	G	6	142	c.1132A>G	c.(1132-1134)AAT>GAT	p.N378D
Pat_29	Post-Resistance	NBPF9	400818	37	1	144815953	144815953	Missense_Mutation	SNP	A	G	4	10	c.1324A>G	c.(1324-1326)AAT>GAT	p.N442D
Pat_29	Post-Resistance	PRG4	10216	37	1	186276052	186276052	Missense_Mutation	SNP	A	C	6	57	c.1201A>C	c.(1201-1203)ACC>CCC	p.T401P
Pat_29	Post-Resistance	PTEN	5728	37	10	89653815	89653815	Missense_Mutation	SNP	C	A	7	74	c.113C>A	c.(112-114)CCT>CAT	p.P38H
Pat_29	Post-Resistance	LOC220429	220429	37	13	50466624	50466624	Missense_Mutation	SNP	G	T	6	53	c.1898G>T	c.(1897-1899)CGC>CTC	p.R633L
Pat_29	Post-Resistance	GOLGA8E	390535	37	15	23444064	23444064	Missense_Mutation	SNP	G	C	3	40	c.719G>C	c.(718-720)AGT>ACT	p.S240T
Pat_29	Post-Resistance	SMG1	23049	37	16	18887642	18887642	Missense_Mutation	SNP	T	C	3	25	c.1694A>G	c.(1693-1695)TAT>TGT	p.Y565C
Pat_29	Post-Resistance	PRDM7	11105	37	16	90126823	90126823	Missense_Mutation	SNP	T	G	5	83	c.1159A>C	c.(1159-1161)ATG>CTG	p.M387L
Pat_29	Post-Resistance	MPP2	4355	37	17	41957260	41957260	Missense_Mutation	SNP	G	A	14	135	c.1378C>T	c.(1378-1380)CGC>TGC	p.R460C
Pat_29	Post-Resistance	RNF157	114804	37	17	74163736	74163736	Missense_Mutation	SNP	C	T	3	61	c.439G>A	c.(439-441)GCC>ACC	p.A147T
Pat_29	Post-Resistance	ZNF780A	284323	37	19	40580552	40580552	Missense_Mutation	SNP	T	G	9	165	c.1797A>C	c.(1795-1797)CAA>CAC	p.Q599H
Pat_29	Post-Resistance	ZNF649	65251	37	19	52394652	52394652	Missense_Mutation	SNP	C	T	5	81	c.737G>A	c.(736-738)AGG>AAG	p.R246K
Pat_29	Post-Resistance	ZNF578	147660	37	19	53014565	53014565	Missense_Mutation	SNP	G	A	5	117	c.931G>A	c.(931-933)GGT>AGT	p.G311S
Pat_29	Post-Resistance	SCN9A	6335	37	2	167133552	167133552	Missense_Mutation	SNP	C	T	35	353	c.2782G>A	c.(2782-2784)GCT>ACT	p.A928T
Pat_29	Post-Resistance	GGTLC1	92086	37	20	23966333	23966333	Missense_Mutation	SNP	C	T	5	128	c.502G>A	c.(502-504)GTC>ATC	p.V168I
Pat_29	Post-Resistance	FRG1B	284802	37	20	29625941	29625941	Missense_Mutation	SNP	A	T	3	63	c.95A>T	c.(94-96)GAT>GTT	p.D32V
Pat_29	Post-Resistance	PTGIS	5740	37	20	48129665	48129665	Missense_Mutation	SNP	G	T	11	69	c.1158C>A	c.(1156-1158)TTC>TTA	p.F386L
Pat_29	Post-Resistance	CCT8	10694	37	21	30440001	30440001	Missense_Mutation	SNP	A	G	4	84	c.257T>C	c.(256-258)ATT>ACT	p.I86T
Pat_29	Post-Resistance	PCNT	5116	37	21	47754527	47754527	Missense_Mutation	SNP	A	G	6	168	c.484A>G	c.(484-486)AGT>GGT	p.S162G
Pat_29	Post-Resistance	ZNF721	170960	37	4	435653	435653	Missense_Mutation	SNP	C	T	3	60	c.2603G>A	c.(2602-2604)GGA>GAA	p.G868E
Pat_29	Post-Resistance	PIK3R1	5295	37	5	67588090	67588090	Missense_Mutation	SNP	T	G	12	82	c.920T>G	c.(919-921)CTG>CGG	p.L307R
Pat_29	Post-Resistance	C6orf129	154467	37	6	37451045	37451045	Missense_Mutation	SNP	G	A	3	45	c.211C>T	c.(211-213)CGG>TGG	p.R71W
Pat_29	Post-Resistance	KIF25	3834	37	6	168430272	168430272	Missense_Mutation	SNP	T	A	3	47	c.7T>A	c.(7-9)TGG>AGG	p.W3R
Pat_29	Post-Resistance	SYBU	55638	37	8	110592227	110592227	Missense_Mutation	SNP	C	G	10	76	c.535G>C	c.(535-537)GGT>CGT	p.G179R
Pat_34	Pre-Treatment	CPSF3L	54973	37	1	1249257	1249257	Missense_Mutation	SNP	A	T	45	58	c.812T>A	c.(811-813)CTG>CAG	p.L271Q
Pat_34	Pre-Treatment	TAS1R3	83756	37	1	1267227	1267227	Missense_Mutation	SNP	A	G	14	26	c.401A>G	c.(400-402)TAC>TGC	p.Y134C
Pat_34	Pre-Treatment	TAS1R1	80835	37	1	6635049	6635049	Missense_Mutation	SNP	C	T	8	30	c.857C>T	c.(856-858)TCC>TTC	p.S286F
Pat_34	Pre-Treatment	KLHL21	9903	37	1	6653672	6653673	Missense_Mutation	DNP	AC	CT	11	45	.1546_1547GT>A	c.(1546-1548)GTC>AGC	p.V516S
Pat_34	Pre-Treatment	CAMTA1	23261	37	1	7806003	7806003	Missense_Mutation	SNP	C	T	67	104	c.4469C>T	c.(4468-4470)CCC>CTC	p.P1490L
Pat_34	Pre-Treatment	SLC2A7	155184	37	1	9063499	9063499	Missense_Mutation	SNP	G	A	22	55	c.1399C>T	c.(1399-1401)CCG>TCG	p.P467S
Pat_34	Pre-Treatment	PTCHD2	57540	37	1	11574470	11574470	Missense_Mutation	SNP	G	A	3	49	c.1340G>A	c.(1339-1341)GGG>GAG	p.G447E
Pat_34	Pre-Treatment	UQCRHL	440567	37	1	16133889	16133889	Missense_Mutation	SNP	G	A	73	181	c.256C>T	c.(256-258)CTC>TTC	p.L86F
Pat_34	Pre-Treatment	KLHDC7A	127707	37	1	18807959	18807959	Missense_Mutation	SNP	G	A	17	29	c.484G>A	c.(484-486)GGC>AGC	p.G162S
Pat_34	Pre-Treatment	PAX7	5081	37	1	19062357	19062357	Missense_Mutation	SNP	G	A	32	62	c.1387G>A	c.(1387-1389)GGC>AGC	p.G463S
Pat_34	Pre-Treatment	USP48	84196	37	1	22055189	22055189	Missense_Mutation	SNP	G	A	42	99	c.1324C>T	c.(1324-1326)CGG>TGG	p.R442W
Pat_34	Pre-Treatment	RHCE	6006	37	1	25718584	25718584	Missense_Mutation	SNP	A	T	52	112	c.535T>A	c.(535-537)TTT>ATT	p.F179I
Pat_34	Pre-Treatment	MAP3K6	9064	37	1	27683183	27683183	Missense_Mutation	SNP	G	A	11	31	c.3422C>T	c.(3421-3423)TCC>TTC	p.S1141F
Pat_34	Pre-Treatment	C1orf94	84970	37	1	34667756	34667756	Missense_Mutation	SNP	C	T	34	75	c.772C>T	c.(772-774)CCT>TCT	p.P258S
Pat_34	Pre-Treatment	YRDC	79693	37	1	38272853	38272853	Missense_Mutation	SNP	T	C	37	56	c.424A>G	c.(424-426)AAA>GAA	p.K142E
Pat_34	Pre-Treatment	HPCAL4	51440	37	1	40150247	40150247	Missense_Mutation	SNP	G	A	18	40	c.29C>T	c.(28-30)CCC>CTC	p.P10L
Pat_34	Pre-Treatment	BMP8B	656	37	1	40228808	40228809	Missense_Mutation	DNP	CC	TG	49	84	.1014_1015GG>C	012-1017)CTGGAC>CTC	p.D339N
Pat_34	Pre-Treatment	ERMAP	114625	37	1	43308649	43308649	Missense_Mutation	SNP	C	T	34	99	c.1174C>T	c.(1174-1176)CGC>TGC	p.R392C
Pat_34	Pre-Treatment	CYP4A11	1579	37	1	47399642	47399642	Missense_Mutation	SNP	G	A	16	23	c.1198C>T	c.(1198-1200)CCT>TCT	p.P400S
Pat_34	Pre-Treatment	CYP4A11	1579	37	1	47399647	47399647	Missense_Mutation	SNP	G	A	16	23	c.1193C>T	c.(1192-1194)ACC>ATC	p.T398I

Pat_34	Pre-Treatment	C1orf168	199920	37	1	57189346	57189346	Missense_Mutation	SNP	G	A	7	22	c.1889C>T	c.(1888-1890)CCT>CTT	p.P630L
Pat_34	Pre-Treatment	TM2D1	83941	37	1	62190753	62190754	Missense_Mutation	DNP	CC	TT	33	41	c.39_40GG>AA	(37-42)GAGGCC>GAAAC	p.A14T
Pat_34	Pre-Treatment	KANK4	163782	37	1	62739098	62739098	Missense_Mutation	SNP	T	A	16	18	c.1678A>T	c.(1678-1680)ATT>TTT	p.I560F
Pat_34	Pre-Treatment	GNG12	55970	37	1	68171168	68171168	Missense_Mutation	SNP	G	A	25	42	c.185C>T	c.(184-186)CCT>CTT	p.P62L
Pat_34	Pre-Treatment	GBP2	2634	37	1	89573974	89573974	Missense_Mutation	SNP	C	T	21	53	c.1660G>A	c.(1660-1662)GAA>AAA	p.E554K
Pat_34	Pre-Treatment	HFM1	164045	37	1	91841113	91841113	Missense_Mutation	SNP	T	G	51	74	c.1567A>C	c.(1567-1569)ATG>CTG	p.M523L
Pat_34	Pre-Treatment	ARHGAP29	9411	37	1	94650565	94650565	Missense_Mutation	SNP	C	T	22	65	c.1972G>A	c.(1972-1974)GGT>AGT	p.G658S
Pat_34	Pre-Treatment	DPYD	1806	37	1	98348842	98348842	Missense_Mutation	SNP	C	T	28	54	c.128G>A	c.(127-129)AGA>AAA	p.R43K
Pat_34	Pre-Treatment	COL11A1	1301	37	1	103427740	103427740	Missense_Mutation	SNP	C	T	27	48	c.3106G>A	c.(3106-3108)GGA>AGA	p.G1036R
Pat_34	Pre-Treatment	FNDC7	163479	37	1	109270504	109270504	Missense_Mutation	SNP	C	T	62	115	c.1186C>T	c.(1186-1188)CGT>TGT	p.R396C
Pat_34	Pre-Treatment	CD2	914	37	1	117297532	117297532	Missense_Mutation	SNP	G	A	18	55	c.341G>A	c.(340-342)GGA>GAA	p.G114E
Pat_34	Pre-Treatment	NBPF10	100132406	37	1	145360574	145360574	Missense_Mutation	SNP	G	C	9	110	c.9424G>C	c.(9424-9426)GAT>CAT	p.D3142H
Pat_34	Pre-Treatment	ANKRD35	148741	37	1	145561208	145561208	Missense_Mutation	SNP	G	A	14	15	c.896G>A	c.(895-897)AGG>AAG	p.R299K
Pat_34	Pre-Treatment	FLG2	388698	37	1	152325517	152325517	Missense_Mutation	SNP	C	T	92	152	c.4745G>A	c.(4744-4746)AGT>AAT	p.S1582N
Pat_34	Pre-Treatment	KPRP	448834	37	1	152733041	152733041	Missense_Mutation	SNP	G	A	10	24	c.977G>A	c.(976-978)CGA>CAA	p.R326Q
Pat_34	Pre-Treatment	BCAN	63827	37	1	156616754	156616754	Missense_Mutation	SNP	G	A	5	14	c.253G>A	c.(253-255)GGC>AGC	p.G85S
Pat_34	Pre-Treatment	OR6N2	81442	37	1	158746611	158746611	Missense_Mutation	SNP	C	T	26	72	c.815G>A	c.(814-816)CGA>CAA	p.R272Q
Pat_34	Pre-Treatment	ITLN1	55600	37	1	160849190	160849190	Missense_Mutation	SNP	C	T	55	92	c.700G>A	c.(700-702)GGA>AGA	p.G234R
Pat_34	Pre-Treatment	FMO4	2329	37	1	171310709	171310709	Nonsense_Mutation	SNP	C	T	28	67	c.1408C>T	c.(1408-1410)CAG>TAG	p.Q470*
Pat_34	Pre-Treatment	TNFSF18	8995	37	1	173010845	173010845	Missense_Mutation	SNP	G	A	48	115	c.262C>T	c.(262-264)CCC>TCC	p.P88S
Pat_34	Pre-Treatment	TNN	63923	37	1	175092658	175092658	Missense_Mutation	SNP	G	A	23	53	c.2773G>A	c.(2773-2775)GAG>AAG	p.E925K
Pat_34	Pre-Treatment	ABL2	27	37	1	179077623	179077623	Missense_Mutation	SNP	G	T	20	36	c.2779C>A	c.(2779-2781)CAC>AAC	p.H927N
Pat_34	Pre-Treatment	CEP350	9857	37	1	180063085	180063085	Missense_Mutation	SNP	A	T	19	23	c.7845A>T	c.(7843-7845)AAA>AAT	p.K2615N
Pat_34	Pre-Treatment	SMG7	9887	37	1	183486887	183486887	Missense_Mutation	SNP	C	T	85	222	c.244C>T	c.(244-246)CCG>TCG	p.P82S
Pat_34	Pre-Treatment	PRG4	10216	37	1	186275983	186275983	Missense_Mutation	SNP	C	A	7	125	c.1132C>A	c.(1132-1134)CCC>ACC	p.P378T
Pat_34	Pre-Treatment	PRG4	10216	37	1	186276169	186276169	Missense_Mutation	SNP	C	A	6	79	c.1318C>A	c.(1318-1320)CCC>ACC	p.P440T
Pat_34	Pre-Treatment	FAM5C	339479	37	1	190067918	190067918	Missense_Mutation	SNP	G	A	39	102	c.1531C>T	c.(1531-1533)CAT>TAT	p.H511Y
Pat_34	Pre-Treatment	CFHR4	10877	37	1	196887393	196887393	Missense_Mutation	SNP	G	A	22	39	c.853G>A	c.(853-855)GGA>AGA	p.G285R
Pat_34	Pre-Treatment	CFHR5	81494	37	1	196953220	196953220	Missense_Mutation	SNP	C	T	38	100	c.383C>T	c.(382-384)TCG>TTG	p.S128L
Pat_34	Pre-Treatment	KIF14	9928	37	1	200574433	200574433	Missense_Mutation	SNP	G	A	29	72	c.1724C>T	c.(1723-1725)ACC>ATC	p.T575I
Pat_34	Pre-Treatment	CACNA1S	779	37	1	201009767	201009767	Missense_Mutation	SNP	G	A	10	28	c.5209C>T	c.(5209-5211)CCT>TCT	p.P1737S
Pat_34	Pre-Treatment	TNNT2	7139	37	1	201342349	201342349	Missense_Mutation	SNP	C	T	56	88	c.34G>A	c.(34-36)GAG>AAG	p.E12K
Pat_34	Pre-Treatment	LAMB3	3914	37	1	209791821	209791821	Missense_Mutation	SNP	A	G	14	43	c.2885T>C	c.(2884-2886)TTG>TCG	p.L962S
Pat_34	Pre-Treatment	SUSD4	55061	37	1	223396599	223396599	Missense_Mutation	SNP	A	T	22	41	c.1436T>A	c.(1435-1437)ATT>AAT	p.I479N
Pat_34	Pre-Treatment	KIAA1383	54627	37	1	232940851	232940851	Missense_Mutation	SNP	C	T	59	78	c.82C>T	c.(82-84)CTC>TTC	p.L28F
Pat_34	Pre-Treatment	TOMM20	9804	37	1	235277223	235277223	Missense_Mutation	SNP	C	T	49	65	c.253G>A	c.(253-255)GAA>AAA	p.E85K
Pat_34	Pre-Treatment	RGS7	6000	37	1	241261981	241261981	Missense_Mutation	SNP	G	A	11	27	c.160C>T	c.(160-162)CCT>TCT	p.P54S
Pat_34	Pre-Treatment	OR2W5	441932	37	1	247655048	247655048	Missense_Mutation	SNP	C	T	38	86	c.619C>T	c.(619-621)CCT>TCT	p.P207S
Pat_34	Pre-Treatment	OR2M7	391196	37	1	248486965	248486965	Missense_Mutation	SNP	C	T	48	66	c.906G>A	c.(904-906)ATG>ATA	p.M302I
Pat_34	Pre-Treatment	BEND7	222389	37	10	13534798	13534798	Missense_Mutation	SNP	T	A	10	25	c.494A>T	c.(493-495)AAA>ATA	p.K165I
Pat_34	Pre-Treatment	NEBL	10529	37	10	21102872	21102872	Missense_Mutation	SNP	G	A	17	63	c.2342C>T	c.(2341-2343)TCA>TTA	p.S781L
Pat_34	Pre-Treatment	KIAA1217	56243	37	10	24820788	24820788	Missense_Mutation	SNP	G	A	14	41	c.3112G>A	c.(3112-3114)GAA>AAA	p.E1038K
Pat_34	Pre-Treatment	MYO3A	53904	37	10	26417388	26417388	Missense_Mutation	SNP	C	T	24	53	c.2183C>T	c.(2182-2184)TCC>TTC	p.S728F
Pat_34	Pre-Treatment	ACBD5	91452	37	10	27499931	27499931	Missense_Mutation	SNP	G	A	73	150	c.1016C>T	c.(1015-1017)TCT>TTT	p.S339F
Pat_34	Pre-Treatment	KIAA1462	57608	37	10	30316735	30316735	Missense_Mutation	SNP	C	T	15	31	c.2342G>A	c.(2341-2343)CGA>CAA	p.R781Q
Pat_34	Pre-Treatment	ZNF33A	7581	37	10	38344719	38344719	Missense_Mutation	SNP	C	T	78	161	c.1664C>T	c.(1663-1665)CCC>CTC	p.P555L
Pat_34	Pre-Treatment	HSD17B7P2	158160	37	10	38654432	38654432	Missense_Mutation	SNP	A	G	6	129	c.524A>G	c.(523-525)AAT>AGT	p.N175S

Pat_34	Pre-Treatment	RTKN2	219790	37	10	63957995	63957995	Missense_Mutation	SNP	T	G	83	133	c.1502A>C	c.(1501-1503)AAG>ACG	p.K501T
Pat_34	Pre-Treatment	CTNNA3	29119	37	10	68381479	68381479	Missense_Mutation	SNP	C	T	21	68	c.1345G>A	c.(1345-1347)GCC>ACC	p.A449T
Pat_34	Pre-Treatment	RRP12	23223	37	10	99126533	99126533	Missense_Mutation	SNP	C	T	38	93	c.3181G>A	c.(3181-3183)GAG>AAG	p.E1061K
Pat_34	Pre-Treatment	PSD	5662	37	10	104176662	104176662	Missense_Mutation	SNP	G	A	10	23	c.134C>T	c.(133-135)TCC>TTC	p.S45F
Pat_34	Pre-Treatment	COL17A1	1308	37	10	105810641	105810641	Missense_Mutation	SNP	C	T	12	51	c.2057G>A	c.(2056-2058)GGG>GAG	p.G686E
Pat_34	Pre-Treatment	CDHR5	53841	37	11	618833	618833	Missense_Mutation	SNP	G	C	4	98	c.1726C>G	c.(1726-1728)CCA>GCA	p.P576A
Pat_34	Pre-Treatment	OR52R1	119695	37	11	4824842	4824842	Missense_Mutation	SNP	G	A	24	61	c.1006C>T	c.(1006-1008)CCA>TCA	p.P336S
Pat_34	Pre-Treatment	MMP26	56547	37	11	5011900	5011900	Nonsense_Mutation	SNP	G	A	52	64	c.393G>A	c.(391-393)TGG>TGA	p.W131*
Pat_34	Pre-Treatment	OR52B6	340980	37	11	5602186	5602186	Missense_Mutation	SNP	C	G	5	33	c.80C>G	c.(79-81)ACT>AGT	p.T27S
Pat_34	Pre-Treatment	OR56A3	390083	37	11	5969466	5969466	Missense_Mutation	SNP	G	A	32	45	c.890G>A	c.(889-891)GGG>GAG	p.G297E
Pat_34	Pre-Treatment	OR56A1	120796	37	11	6048048	6048048	Missense_Mutation	SNP	G	A	34	55	c.887C>T	c.(886-888)CCT>CTT	p.P296L
Pat_34	Pre-Treatment	FAM160A2	84067	37	11	6244994	6244994	Missense_Mutation	SNP	G	A	39	74	c.623C>T	c.(622-624)CCC>CTC	p.P208L
Pat_34	Pre-Treatment	OR10A6	390093	37	11	7949948	7949948	Missense_Mutation	SNP	C	T	61	86	c.262G>A	c.(262-264)GAA>AAA	p.E88K
Pat_34	Pre-Treatment	STK33	65975	37	11	8496277	8496277	Missense_Mutation	SNP	C	T	19	40	c.176G>A	c.(175-177)AGA>AAA	p.R59K
Pat_34	Pre-Treatment	RNF141	50862	37	11	10555660	10555660	Missense_Mutation	SNP	A	C	127	249	c.46T>G	c.(46-48)TTA>GTA	p.L16V
Pat_34	Pre-Treatment	ANO3	63982	37	11	26621181	26621181	Missense_Mutation	SNP	T	A	51	83	c.1756T>A	c.(1756-1758)TTC>ATC	p.F586I
Pat_34	Pre-Treatment	MPPED2	744	37	11	30516918	30516918	Missense_Mutation	SNP	G	A	47	117	c.461C>T	c.(460-462)TCC>TTC	p.S154F
Pat_34	Pre-Treatment	LRP4	4038	37	11	46920574	46920574	Missense_Mutation	SNP	A	C	12	25	c.557T>G	c.(556-558)GTG>GGG	p.V186G
Pat_34	Pre-Treatment	OR4X2	119764	37	11	48266686	48266686	Missense_Mutation	SNP	C	T	51	102	c.31C>T	c.(31-33)CCC>TCC	p.P11S
Pat_34	Pre-Treatment	OR4S2	219431	37	11	55418495	55418495	Missense_Mutation	SNP	G	A	39	84	c.116G>A	c.(115-117)GGA>GAA	p.G39E
Pat_34	Pre-Treatment	OR5L1	219437	37	11	55579578	55579578	Missense_Mutation	SNP	G	A	87	162	c.636G>A	c.(634-636)ATG>ATA	p.M212I
Pat_34	Pre-Treatment	OR5D18	219438	37	11	55588003	55588003	Missense_Mutation	SNP	G	A	43	84	c.898G>A	c.(898-900)GAT>AAT	p.D300N
Pat_34	Pre-Treatment	OR5J2	282775	37	11	55944567	55944568	Missense_Mutation	DNP	CC	TT	52	122	c.474_475CC>TT	(472-477)ATCCAC>ATTTA	p.H159Y
Pat_34	Pre-Treatment	OR10Q1	219960	37	11	57995785	57995785	Missense_Mutation	SNP	G	A	17	32	c.563C>T	c.(562-564)CCC>CTC	p.P188L
Pat_34	Pre-Treatment	OR5A1	219982	37	11	59211441	59211441	Missense_Mutation	SNP	C	T	75	130	c.800C>T	c.(799-801)TCC>TTC	p.S267F
Pat_34	Pre-Treatment	OR4D6	219983	37	11	59224986	59224986	Missense_Mutation	SNP	G	A	36	73	c.553G>A	c.(553-555)GTA>ATA	p.V185I
Pat_34	Pre-Treatment	SLC22A11	55867	37	11	64323786	64323786	Nonsense_Mutation	SNP	G	A	4	7	c.315G>A	c.(313-315)TGG>TGA	p.W105*
Pat_34	Pre-Treatment	MEN1	4221	37	11	64575049	64575049	Missense_Mutation	SNP	G	A	33	24	c.773C>T	c.(772-774)TCG>TTG	p.S258L
Pat_34	Pre-Treatment	TSGA10IP	254187	37	11	65714942	65714942	Nonsense_Mutation	SNP	C	T	5	12	c.646C>T	c.(646-648)CAG>TAG	p.Q216*
Pat_34	Pre-Treatment	CPT1A	1374	37	11	68564371	68564371	Missense_Mutation	SNP	G	A	24	49	c.724C>T	c.(724-726)CTC>TTC	p.L242F
Pat_34	Pre-Treatment	USP35	57558	37	11	77920570	77920570	Missense_Mutation	SNP	G	A	19	24	c.1669G>A	c.(1669-1671)GAG>AAG	p.E557K
Pat_34	Pre-Treatment	CCDC83	220047	37	11	85593676	85593676	Missense_Mutation	SNP	G	A	22	66	c.301G>A	c.(301-303)GAA>AAA	p.E101K
Pat_34	Pre-Treatment	PGR	5241	37	11	100920777	100920777	Missense_Mutation	SNP	C	T	30	48	c.2371G>A	c.(2371-2373)GAA>AAA	p.E791K
Pat_34	Pre-Treatment	MMP3	4314	37	11	102713427	102713427	Nonsense_Mutation	SNP	C	T	14	45	c.326G>A	c.(325-327)TGG>TAG	p.W109*
Pat_34	Pre-Treatment	MMP13	4322	37	11	102815074	102815074	Missense_Mutation	SNP	C	T	111	172	c.1337G>A	c.(1336-1338)GGA>GAA	p.G446E
Pat_34	Pre-Treatment	MMP13	4322	37	11	102826171	102826171	Missense_Mutation	SNP	C	T	71	178	c.172G>A	c.(172-174)GAG>AAG	p.E58K
Pat_34	Pre-Treatment	MMP13	4322	37	11	102826209	102826209	Missense_Mutation	SNP	G	A	82	185	c.134C>T	c.(133-135)TCA>TTA	p.S45L
Pat_34	Pre-Treatment	CASP4	837	37	11	104819383	104819383	Missense_Mutation	SNP	C	A	42	99	c.802G>T	c.(802-804)GTC>TTC	p.V268F
Pat_34	Pre-Treatment	APOA5	116519	37	11	116661479	116661479	Missense_Mutation	SNP	C	T	35	68	c.466G>A	c.(466-468)GAA>AAA	p.E156K
Pat_34	Pre-Treatment	CCDC15	80071	37	11	124857585	124857585	Missense_Mutation	SNP	C	A	9	200	c.1463C>A	c.(1462-1464)CCC>CAC	p.P488H
Pat_34	Pre-Treatment	IGSF9B	22997	37	11	133801026	133801026	Missense_Mutation	SNP	C	T	16	29	c.1372G>A	c.(1372-1374)GGG>AGG	p.G458R
Pat_34	Pre-Treatment	SLC6A13	6540	37	12	344366	344366	Missense_Mutation	SNP	G	A	21	45	c.721C>T	c.(721-723)CCT>TCT	p.P241S
Pat_34	Pre-Treatment	B4GALNT3	283358	37	12	662585	662585	Missense_Mutation	SNP	T	G	11	29	c.1496T>G	c.(1495-1497)TTC>TGC	p.F499C
Pat_34	Pre-Treatment	DDX47	51202	37	12	12976886	12976886	Missense_Mutation	SNP	G	A	79	149	c.833G>A	c.(832-834)AGA>AAA	p.R278K
Pat_34	Pre-Treatment	COL2A1	1280	37	12	48393734	48393734	Missense_Mutation	SNP	G	A	38	69	c.260C>T	c.(259-261)CCC>CTC	p.P87L
Pat_34	Pre-Treatment	ASB8	140461	37	12	48545051	48545051	Missense_Mutation	SNP	G	A	38	79	c.167C>T	c.(166-168)CCC>CTC	p.P56L
Pat_34	Pre-Treatment	ZNF641	121274	37	12	48741114	48741114	Missense_Mutation	SNP	G	A	13	17	c.239C>T	c.(238-240)CCC>CTC	p.P80L

Pat_34	Pre-Treatment	KRT83	3889	37	12	52709803	52709803	Missense_Mutation	SNP	G	A	26	46	c.1136C>T	c.(1135-1137)GCC>GTC	p.A379V
Pat_34	Pre-Treatment	KRT71	112802	37	12	52940196	52940196	Missense_Mutation	SNP	G	A	15	46	c.1199C>T	c.(1198-1200)GCC>GTC	p.A400V
Pat_34	Pre-Treatment	SOAT2	8435	37	12	53512692	53512692	Nonsense_Mutation	SNP	G	A	36	84	c.882G>A	c.(880-882)TGG>TGA	p.W294*
Pat_34	Pre-Treatment	HOXC6	3223	37	12	54422402	54422402	Missense_Mutation	SNP	C	T	39	66	c.97C>T	c.(97-99)CCA>TCA	p.P33S
Pat_34	Pre-Treatment	GPR84	53831	37	12	54757263	54757263	Missense_Mutation	SNP	G	A	10	39	c.373C>T	c.(373-375)CCT>TCT	p.P125S
Pat_34	Pre-Treatment	OR6C1	390321	37	12	55714642	55714642	Missense_Mutation	SNP	G	A	19	49	c.259G>A	c.(259-261)GAT>AAT	p.D87N
Pat_34	Pre-Treatment	OR6C68	403284	37	12	55887086	55887086	Missense_Mutation	SNP	C	T	19	28	c.940C>T	c.(940-942)CGT>TGT	p.R314C
Pat_34	Pre-Treatment	ERBB3	2065	37	12	56489517	56489517	Missense_Mutation	SNP	G	A	61	78	c.1982G>A	c.(1981-1983)GGC>GAC	p.G661D
Pat_34	Pre-Treatment	MIP	4284	37	12	56848061	56848061	Nonsense_Mutation	SNP	G	A	32	77	c.337C>T	c.(337-339)CGA>TGA	p.R113*
Pat_34	Pre-Treatment	CAPS2	84698	37	12	75692690	75692690	Missense_Mutation	SNP	G	A	26	50	c.968C>T	c.(967-969)TCC>TTC	p.S323F
Pat_34	Pre-Treatment	ACSS3	79611	37	12	81627225	81627225	Missense_Mutation	SNP	G	A	82	126	c.1694G>A	c.(1693-1695)AGA>AAA	p.R565K
Pat_34	Pre-Treatment	C12orf12	196477	37	12	91347831	91347831	Missense_Mutation	SNP	G	A	39	26	c.689C>T	c.(688-690)TCC>TTC	p.S230F
Pat_34	Pre-Treatment	USP44	84101	37	12	95914958	95914958	Missense_Mutation	SNP	C	T	49	116	c.1754G>A	c.(1753-1755)CGA>CAA	p.R585Q
Pat_34	Pre-Treatment	SLC17A8	246213	37	12	100811903	100811903	Missense_Mutation	SNP	C	T	44	98	c.1394C>T	c.(1393-1395)CCC>CTC	p.P465L
Pat_34	Pre-Treatment	MYBPC1	4604	37	12	102025848	102025848	Missense_Mutation	SNP	G	A	58	117	c.413G>A	c.(412-414)GGA>GAA	p.G138E
Pat_34	Pre-Treatment	STAB2	55576	37	12	103984679	103984679	Missense_Mutation	SNP	G	A	44	54	c.86G>A	c.(85-87)AGA>AAA	p.R29K
Pat_34	Pre-Treatment	NUAK1	9891	37	12	106461061	106461061	Missense_Mutation	SNP	G	A	38	71	c.1505C>T	c.(1504-1506)CCC>CTC	p.P502L
Pat_34	Pre-Treatment	MED13L	23389	37	12	116420380	116420380	Missense_Mutation	SNP	G	A	9	45	c.4984C>T	c.(4984-4986)CCC>TCC	p.P1662S
Pat_34	Pre-Treatment	GCN1L1	10985	37	12	120594729	120594729	Missense_Mutation	SNP	G	A	42	101	c.3155C>T	c.(3154-3156)TCG>TTG	p.S1052L
Pat_34	Pre-Treatment	DNAH10	196385	37	12	124330625	124330625	Missense_Mutation	SNP	G	A	30	53	c.5384G>A	c.(5383-5385)GGC>GAC	p.G1795D
Pat_34	Pre-Treatment	TMEM132D	121256	37	12	129559037	129559037	Missense_Mutation	SNP	G	A	17	30	c.2683C>T	c.(2683-2685)CCC>TCC	p.P895S
Pat_34	Pre-Treatment	NBEA	26960	37	13	35756549	35756549	Missense_Mutation	SNP	C	T	56	97	c.4715C>T	c.(4714-4716)TCG>TTG	p.S1572L
Pat_34	Pre-Treatment	FREM2	341640	37	13	39263960	39263960	Missense_Mutation	SNP	A	T	21	59	c.2479A>T	c.(2479-2481)AAC>TAC	p.N827Y
Pat_34	Pre-Treatment	NALCN	259232	37	13	101755534	101755534	Missense_Mutation	SNP	C	T	64	131	c.3046G>A	c.(3046-3048)GAA>AAA	p.E1016K
Pat_34	Pre-Treatment	COL4A1	1282	37	13	110838732	110838732	Missense_Mutation	SNP	C	T	58	109	c.1897G>A	c.(1897-1899)GGT>AGT	p.G633S
Pat_34	Pre-Treatment	ADCY4	196883	37	14	24795044	24795044	Missense_Mutation	SNP	C	T	5	24	c.1705G>A	c.(1705-1707)GAG>AAG	p.E569K
Pat_34	Pre-Treatment	NFATC4	4776	37	14	24845785	24845785	Missense_Mutation	SNP	C	T	13	29	c.2342C>T	c.(2341-2343)TCC>TTC	p.S781F
Pat_34	Pre-Treatment	STRN3	29966	37	14	31420127	31420127	Missense_Mutation	SNP	G	A	36	80	c.484C>T	c.(484-486)CCC>TCC	p.P162S
Pat_34	Pre-Treatment	AKAP6	9472	37	14	33292765	33292765	Missense_Mutation	SNP	G	A	23	47	c.5746G>A	c.(5746-5748)GTA>ATA	p.V1916I
Pat_34	Pre-Treatment	NPAS3	64067	37	14	33684606	33684606	Missense_Mutation	SNP	G	A	25	36	c.359G>A	c.(358-360)GGC>GAC	p.G120D
Pat_34	Pre-Treatment	SPTB	6710	37	14	65260474	65260474	Missense_Mutation	SNP	G	A	28	45	c.1907C>T	c.(1906-1908)TCC>TTC	p.S636F
Pat_34	Pre-Treatment	SLC8A3	6547	37	14	70634304	70634304	Missense_Mutation	SNP	C	T	14	29	c.836G>A	c.(835-837)GGT>GAT	p.G279D
Pat_34	Pre-Treatment	TMEM90A	646658	37	14	74876101	74876101	Missense_Mutation	SNP	G	A	44	91	c.347C>T	c.(346-348)ACC>ATC	p.T116I
Pat_34	Pre-Treatment	GPR68	8111	37	14	91700776	91700776	Missense_Mutation	SNP	C	T	3	8	c.619G>A	c.(619-621)GGC>AGC	p.G207S
Pat_34	Pre-Treatment	CATSPERB	79820	37	14	92047331	92047331	Missense_Mutation	SNP	G	A	23	38	c.3253C>T	c.(3253-3255)CCG>TCG	p.P1085S
Pat_34	Pre-Treatment	SERPINA4	5267	37	14	95033402	95033402	Missense_Mutation	SNP	G	A	14	24	c.745G>A	c.(745-747)GAC>AAC	p.D249N
Pat_34	Pre-Treatment	DICER1	23405	37	14	95595923	95595923	Missense_Mutation	SNP	G	A	24	64	c.620C>T	c.(619-621)GCT>GTT	p.A207V
Pat_34	Pre-Treatment	GOLGA8E	390535	37	15	23444052	23444052	Missense_Mutation	SNP	G	A	4	28	c.707G>A	c.(706-708)CGG>CAG	p.R236Q
Pat_34	Pre-Treatment	APBA2	321	37	15	29398915	29398915	Missense_Mutation	SNP	G	C	23	63	c.1810G>C	c.(1810-1812)GGC>CGC	p.G604R
Pat_34	Pre-Treatment	TRPM1	4308	37	15	31294602	31294602	Missense_Mutation	SNP	G	A	73	130	c.4235C>T	c.(4234-4236)TCC>TTC	p.S1412F
Pat_34	Pre-Treatment	C15orf55	256646	37	15	34646835	34646835	Missense_Mutation	SNP	G	A	41	83	c.1180G>A	c.(1180-1182)GAA>AAA	p.E394K
Pat_34	Pre-Treatment	THBS1	7057	37	15	39881178	39881178	Missense_Mutation	SNP	C	T	154	320	c.1664C>T	c.(1663-1665)CCC>CTC	p.P555L
Pat_34	Pre-Treatment	GCOM1	145781	37	15	57967226	57967226	Missense_Mutation	SNP	G	A	16	44	c.1264G>A	c.(1264-1266)GAA>AAA	p.E422K
Pat_34	Pre-Treatment	LIPC	3990	37	15	58830612	58830612	Missense_Mutation	SNP	G	A	140	262	c.169G>A	c.(169-171)GAA>AAA	p.E57K
Pat_34	Pre-Treatment	IQCH	64799	37	15	67687881	67687881	Missense_Mutation	SNP	G	A	38	96	c.1885G>A	c.(1885-1887)GAT>AAT	p.D629N
Pat_34	Pre-Treatment	TBC1D2B	23102	37	15	78290635	78290635	Missense_Mutation	SNP	C	T	3	20	c.2759G>A	c.(2758-2760)CGA>CAA	p.R920Q
Pat_34	Pre-Treatment	KIAA1024	23251	37	15	79750195	79750195	Missense_Mutation	SNP	A	G	91	55	c.1706A>G	c.(1705-1707)AAT>AGT	p.N569S

Pat_34	Pre-Treatment	KIAA1199	57214	37	15	81199085	81199085	Missense_Mutation	SNP	T	C	33	75	c.1493T>C	c.(1492-1494)ATC>ACC	p.I498T
Pat_34	Pre-Treatment	BNC1	646	37	15	83926276	83926276	Missense_Mutation	SNP	G	A	31	108	c.2903C>T	c.(2902-2904)TCG>TTG	p.S968L
Pat_34	Pre-Treatment	LRRC28	123355	37	15	99892582	99892582	Nonsense_Mutation	SNP	C	T	149	133	c.601C>T	c.(601-603)CGA>TGA	p.R201*
Pat_34	Pre-Treatment	CACNA1H	8912	37	16	1262003	1262003	Missense_Mutation	SNP	G	T	59	131	c.4624G>T	c.(4624-4626)GTC>TTC	p.V1542F
Pat_34	Pre-Treatment	MEFV	4210	37	16	3306401	3306401	Nonsense_Mutation	SNP	C	A	16	87	c.187G>T	c.(187-189)GAA>TAA	p.E63*
Pat_34	Pre-Treatment	GRIN2A	2903	37	16	9858426	9858426	Missense_Mutation	SNP	T	C	17	40	c.2975A>G	c.(2974-2976)AAC>AGC	p.N992S
Pat_34	Pre-Treatment	GRIN2A	2903	37	16	9858531	9858531	Missense_Mutation	SNP	C	T	38	85	c.2870G>A	c.(2869-2871)GGA>GAA	p.G957E
Pat_34	Pre-Treatment	DNAH3	55567	37	16	20976195	20976195	Missense_Mutation	SNP	C	T	11	25	c.9011G>A	c.(9010-9012)GGA>GAA	p.G3004E
Pat_34	Pre-Treatment	CACNG3	10368	37	16	24268230	24268230	Missense_Mutation	SNP	G	A	20	43	c.155G>A	c.(154-156)AGG>AAG	p.R52K
Pat_34	Pre-Treatment	MYLPF	29895	37	16	30387514	30387514	Missense_Mutation	SNP	G	A	44	76	c.145G>A	c.(145-147)GAC>AAC	p.D49N
Pat_34	Pre-Treatment	SRCAP	10847	37	16	30750632	30750632	Nonsense_Mutation	SNP	C	T	21	46	c.9271C>T	c.(9271-9273)CAG>TAG	p.Q3091*
Pat_34	Pre-Treatment	TSNAXIP1	55815	37	16	67854818	67854818	Missense_Mutation	SNP	G	A	138	254	c.62G>A	c.(61-63)CGA>CAA	p.R21Q
Pat_34	Pre-Treatment	KIAA1609	57707	37	16	84520258	84520258	Missense_Mutation	SNP	C	T	31	48	c.937G>A	c.(937-939)GAG>AAG	p.E313K
Pat_34	Pre-Treatment	PRPF8	10594	37	17	1563786	1563786	Missense_Mutation	SNP	C	G	105	204	c.4725G>C	c.(4723-4725)CAG>CAC	p.Q1575H
Pat_34	Pre-Treatment	KIAA0664	23277	37	17	2601572	2601572	Missense_Mutation	SNP	G	A	4	9	c.1465C>T	c.(1465-1467)CCC>TCC	p.P489S
Pat_34	Pre-Treatment	ALOX12	239	37	17	6913569	6913569	Missense_Mutation	SNP	C	A	17	37	c.1819C>A	c.(1819-1821)CTG>ATG	p.L607M
Pat_34	Pre-Treatment	FXR2	9513	37	17	7498047	7498047	Missense_Mutation	SNP	C	A	43	106	c.860G>T	c.(859-861)AGC>ATC	p.S287I
Pat_34	Pre-Treatment	DNAH9	1770	37	17	11556287	11556287	Missense_Mutation	SNP	G	A	21	47	c.2563G>A	c.(2563-2565)GAA>AAA	p.E855K
Pat_34	Pre-Treatment	MEIS3P1	4213	37	17	15690494	15690494	Nonsense_Mutation	SNP	C	T	12	18	c.310C>T	c.(310-312)CGA>TGA	p.R104*
Pat_34	Pre-Treatment	MYO15A	51168	37	17	18040988	18040988	Missense_Mutation	SNP	G	A	8	20	c.4870G>A	c.(4870-4872)GAG>AAG	p.E1624K
Pat_34	Pre-Treatment	KIAA0100	9703	37	17	26960304	26960304	Missense_Mutation	SNP	G	A	53	122	c.3581C>T	c.(3580-3582)TCT>TTT	p.S1194F
Pat_34	Pre-Treatment	ERAL1	26284	37	17	27183350	27183350	Missense_Mutation	SNP	C	T	75	138	c.352C>T	c.(352-354)CTC>TTC	p.L118F
Pat_34	Pre-Treatment	PHF12	57649	37	17	27251145	27251145	Missense_Mutation	SNP	G	A	3	33	c.497C>T	c.(496-498)ACA>ATA	p.T166I
Pat_34	Pre-Treatment	GSDMB	55876	37	17	38073346	38073346	Missense_Mutation	SNP	G	T	22	46	c.224C>A	c.(223-225)TCT>TAT	p.S75Y
Pat_34	Pre-Treatment	KRTAP1-5	83895	37	17	39183145	39183145	Missense_Mutation	SNP	A	G	12	44	c.263T>C	c.(262-264)ATC>ACC	p.I88T
Pat_34	Pre-Treatment	KRTAP1-3	81850	37	17	39190779	39190779	Missense_Mutation	SNP	T	C	3	31	c.295A>G	c.(295-297)AGT>GGT	p.S99G
Pat_34	Pre-Treatment	KRT33B	3884	37	17	39525713	39525713	Missense_Mutation	SNP	G	A	19	48	c.290C>T	c.(289-291)CCC>CTC	p.P97L
Pat_34	Pre-Treatment	HSPB9	94086	37	17	40275328	40275328	Missense_Mutation	SNP	G	A	22	46	c.460G>A	c.(460-462)GCT>ACT	p.A154T
Pat_34	Pre-Treatment	TUBG2	27175	37	17	40818392	40818392	Missense_Mutation	SNP	C	T	7	60	c.1048C>T	c.(1048-1050)CCG>TCG	p.P350S
Pat_34	Pre-Treatment	FZD2	2535	37	17	42636130	42636130	Missense_Mutation	SNP	G	A	34	61	c.1074G>A	c.(1072-1074)ATG>ATA	p.M358I
Pat_34	Pre-Treatment	CLTC	1213	37	17	57742161	57742161	Missense_Mutation	SNP	C	T	20	85	c.1535C>T	c.(1534-1536)CCA>CTA	p.P512L
Pat_34	Pre-Treatment	KCNH6	81033	37	17	61622585	61622585	Missense_Mutation	SNP	C	T	7	27	c.2651C>T	c.(2650-2652)CCA>CTA	p.P884L
Pat_34	Pre-Treatment	USH1G	124590	37	17	72916405	72916406	Missense_Mutation	DNP	GG	AA	6	28	c.525_526CC>TT	(523-528)ACCCTC>ACTTT	p.L176F
Pat_34	Pre-Treatment	KIAA0802	23255	37	18	8718510	8718510	Missense_Mutation	SNP	G	A	23	48	c.62G>A	c.(61-63)CGA>CAA	p.R21Q
Pat_34	Pre-Treatment	POTEC	388468	37	18	14542791	14542791	Missense_Mutation	SNP	C	T	7	102	c.355G>A	c.(355-357)GCT>ACT	p.A119T
Pat_34	Pre-Treatment	DSG3	1830	37	18	29044209	29044209	Missense_Mutation	SNP	G	A	24	91	c.1135G>A	c.(1135-1137)GAA>AAA	p.E379K
Pat_34	Pre-Treatment	C18orf25	147339	37	18	43796140	43796141	Missense_Mutation	DNP	CT	TG	128	278	c.294_295CT>TG	(292-297)TCCTCT>TCTG	p.S99A
Pat_34	Pre-Treatment	DCC	1630	37	18	50589821	50589821	Nonsense_Mutation	SNP	C	T	22	82	c.1132C>T	c.(1132-1134)CAG>TAG	p.Q378*
Pat_34	Pre-Treatment	SERPINB13	5275	37	18	61264422	61264422	Missense_Mutation	SNP	C	T	13	27	c.1001C>T	c.(1000-1002)TCC>TTC	p.S334F
Pat_34	Pre-Treatment	MUC16	94025	37	19	9066695	9066695	Missense_Mutation	SNP	C	T	46	123	c.20751G>A	c.(20749-20751)ATG>ATA	p.M6917I
Pat_34	Pre-Treatment	MUC16	94025	37	19	9088391	9088391	Missense_Mutation	SNP	C	T	6	16	c.3424G>A	c.(3424-3426)GAT>AAT	p.D1142N
Pat_34	Pre-Treatment	ZNF491	126069	37	19	11916917	11916917	Nonsense_Mutation	SNP	C	A	30	77	c.149C>A	c.(148-150)TCA>TAA	p.S50*
Pat_34	Pre-Treatment	ZNF700	90592	37	19	12036029	12036029	Missense_Mutation	SNP	C	T	21	57	c.4C>T	c.(4-6)CCC>TCC	p.P2S
Pat_34	Pre-Treatment	ZNF799	90576	37	19	12502496	12502496	Missense_Mutation	SNP	G	A	20	52	c.716C>T	c.(715-717)TCC>TTC	p.S239F
Pat_34	Pre-Treatment	ZNF443	10224	37	19	12542270	12542270	Missense_Mutation	SNP	G	A	16	245	c.716C>T	c.(715-717)TCC>TTC	p.S239F
Pat_34	Pre-Treatment	IL27RA	9466	37	19	14157320	14157320	Missense_Mutation	SNP	G	A	44	90	c.1031G>A	c.(1030-1032)GGG>GAG	p.G344E
Pat_34	Pre-Treatment	CYP4F12	66002	37	19	15807869	15807869	Missense_Mutation	SNP	G	A	16	42	c.1549G>A	c.(1549-1551)GAG>AAG	p.E517K

Pat_34	Pre-Treatment	KIAA1683	80726	37	19	18377809	18377809	Missense_Mutation	SNP	G	A	11	21	c.541C>T	c.(541-543)CTT>TTT	p.L181F
Pat_34	Pre-Treatment	KIAA1683	80726	37	19	18377976	18377976	Missense_Mutation	SNP	G	A	10	29	c.374C>T	c.(373-375)TCC>TTC	p.S125F
Pat_34	Pre-Treatment	ZNF682	91120	37	19	20117152	20117152	Missense_Mutation	SNP	G	C	36	81	c.1159C>G	c.(1159-1161)CAC>GAC	p.H387D
Pat_34	Pre-Treatment	ZNF208	7757	37	19	22155698	22155698	Missense_Mutation	SNP	C	T	31	77	c.1838G>A	c.(1837-1839)AGA>AAA	p.R613K
Pat_34	Pre-Treatment	ANKRD27	84079	37	19	33135332	33135332	Missense_Mutation	SNP	T	C	131	229	c.424A>G	c.(424-426)AGA>GGA	p.R142G
Pat_34	Pre-Treatment	WDR62	284403	37	19	36590388	36590388	Nonsense_Mutation	SNP	C	T	29	39	c.2608C>T	c.(2608-2610)CAA>TAA	p.Q870*
Pat_34	Pre-Treatment	SHKBP1	92799	37	19	41094620	41094620	Missense_Mutation	SNP	C	T	41	71	c.1427C>T	c.(1426-1428)TCC>TTC	p.S476F
Pat_34	Pre-Treatment	BCAM	4059	37	19	45316847	45316847	Missense_Mutation	SNP	G	A	30	53	c.754G>A	c.(754-756)GAC>AAC	p.D252N
Pat_34	Pre-Treatment	KLK15	55554	37	19	51330167	51330167	Missense_Mutation	SNP	C	T	7	16	c.448G>A	c.(448-450)GAG>AAG	p.E150K
Pat_34	Pre-Treatment	SIGLEC10	89790	37	19	51918540	51918540	Missense_Mutation	SNP	C	T	13	43	c.1225G>A	c.(1225-1227)GTC>ATC	p.V409I
Pat_34	Pre-Treatment	ZNF614	80110	37	19	52519323	52519323	Missense_Mutation	SNP	G	A	50	111	c.1528C>T	c.(1528-1530)CCT>TCT	p.P510S
Pat_34	Pre-Treatment	ZNF578	147660	37	19	53014565	53014565	Missense_Mutation	SNP	G	A	6	174	c.931G>A	c.(931-933)GGT>AGT	p.G311S
Pat_34	Pre-Treatment	LILRA4	23547	37	19	54848372	54848372	Missense_Mutation	SNP	G	C	10	33	c.995C>G	c.(994-996)CCC>CGC	p.P332R
Pat_34	Pre-Treatment	NCR1	9437	37	19	55424071	55424071	Nonsense_Mutation	SNP	G	A	32	49	c.747G>A	c.(745-747)TGG>TGA	p.W249*
Pat_34	Pre-Treatment	NLRP7	199713	37	19	55450863	55450863	Missense_Mutation	SNP	C	T	9	29	c.1324G>A	c.(1324-1326)GAG>AAG	p.E442K
Pat_34	Pre-Treatment	BRSK1	84446	37	19	55816721	55816721	Missense_Mutation	SNP	C	T	23	43	c.1750C>T	c.(1750-1752)CCA>TCA	p.P584S
Pat_34	Pre-Treatment	NLRP8	126205	37	19	56473497	56473497	Missense_Mutation	SNP	G	A	31	84	c.2107G>A	c.(2107-2109)GAT>AAT	p.D703N
Pat_34	Pre-Treatment	ZNF583	147949	37	19	56934995	56934995	Missense_Mutation	SNP	C	T	55	59	c.968C>T	c.(967-969)CCT>CTT	p.P323L
Pat_34	Pre-Treatment	ZNF470	388566	37	19	57089330	57089330	Nonsense_Mutation	SNP	T	A	22	75	c.1533T>A	c.(1531-1533)TGT>TGA	p.C511*
Pat_34	Pre-Treatment	ZSCAN4	201516	37	19	58189890	58189890	Missense_Mutation	SNP	G	A	26	64	c.919G>A	c.(919-921)GGA>AGA	p.G307R
Pat_34	Pre-Treatment	TPO	7173	37	2	1437254	1437254	Missense_Mutation	SNP	C	T	8	40	c.224C>T	c.(223-225)TCT>TTT	p.S75F
Pat_34	Pre-Treatment	MYT1L	23040	37	2	1926615	1926615	Missense_Mutation	SNP	C	T	37	104	c.926G>A	c.(925-927)GGA>GAA	p.G309E
Pat_34	Pre-Treatment	GRHL1	29841	37	2	10101402	10101402	Missense_Mutation	SNP	G	T	45	127	c.506G>T	c.(505-507)GGA>GTA	p.G169V
Pat_34	Pre-Treatment	ASXL2	55252	37	2	25973219	25973219	Missense_Mutation	SNP	C	A	67	85	c.1206G>T	c.(1204-1206)AAG>AAT	p.K402N
Pat_34	Pre-Treatment	C2orf70	339778	37	2	26800463	26800463	Missense_Mutation	SNP	G	A	43	74	c.428G>A	c.(427-429)AGG>AAG	p.R143K
Pat_34	Pre-Treatment	C2orf71	388939	37	2	29295418	29295419	Missense_Mutation	DNP	CC	TT	28	43	.1709_1710GG>A	c.(1708-1710)GGG>GAA	p.G570E
Pat_34	Pre-Treatment	SLC8A1	6546	37	2	40342607	40342607	Missense_Mutation	SNP	G	A	19	31	c.2708C>T	c.(2707-2709)TCC>TTC	p.S903F
Pat_34	Pre-Treatment	STON1-GTF2A1L	286749	37	2	48808409	48808409	Missense_Mutation	SNP	G	A	8	36	c.637G>A	c.(637-639)GAG>AAG	p.E213K
Pat_34	Pre-Treatment	LHCGR	3973	37	2	48915903	48915903	Missense_Mutation	SNP	G	A	63	112	c.1033C>T	c.(1033-1035)CCT>TCT	p.P345S
Pat_34	Pre-Treatment	FSHR	2492	37	2	49191025	49191025	Missense_Mutation	SNP	G	A	81	163	c.935C>T	c.(934-936)TCC>TTC	p.S312F
Pat_34	Pre-Treatment	ALMS1	7840	37	2	73676976	73676976	Nonsense_Mutation	SNP	C	T	25	88	c.3325C>T	c.(3325-3327)CAA>TAA	p.Q1109*
Pat_34	Pre-Treatment	CNGA3	1261	37	2	99013639	99013639	Missense_Mutation	SNP	T	G	13	42	c.2006T>G	c.(2005-2007)GTG>GGG	p.V669G
Pat_34	Pre-Treatment	IL1RL1	9173	37	2	102958742	102958742	Missense_Mutation	SNP	G	A	14	38	c.670G>A	c.(670-672)GAA>AAA	p.E224K
Pat_34	Pre-Treatment	GCC2	9648	37	2	109088421	109088421	Missense_Mutation	SNP	T	C	26	29	c.2636T>C	c.(2635-2637)TTA>TCA	p.L879S
Pat_34	Pre-Treatment	CBWD2	150472	37	2	114195560	114195561	Missense_Mutation	DNP	GG	AA	115	214	c.115_116GG>AA	c.(115-117)GGC>AAC	p.G39N
Pat_34	Pre-Treatment	LCT	3938	37	2	136566093	136566093	Missense_Mutation	SNP	C	T	73	173	c.3824G>A	c.(3823-3825)GGA>GAA	p.G1275E
Pat_34	Pre-Treatment	ZEB2	9839	37	2	145156983	145156983	Missense_Mutation	SNP	G	A	67	97	c.1771C>T	c.(1771-1773)CCT>TCT	p.P591S
Pat_34	Pre-Treatment	XIRP2	129446	37	2	168107372	168107372	Missense_Mutation	SNP	G	A	31	53	c.9470G>A	c.(9469-9471)AGG>AAG	p.R3157K
Pat_34	Pre-Treatment	NEUROD1	4760	37	2	182543365	182543365	Missense_Mutation	SNP	C	T	6	11	c.223G>A	c.(223-225)GAG>AAG	p.E75K
Pat_34	Pre-Treatment	PDE1A	5136	37	2	183387049	183387049	Missense_Mutation	SNP	G	A	36	125	c.55C>T	c.(55-57)CTT>TTT	p.L19F
Pat_34	Pre-Treatment	ITGAV	3685	37	2	187490312	187490312	Missense_Mutation	SNP	C	T	19	35	c.521C>T	c.(520-522)TCA>TTA	p.S174L
Pat_34	Pre-Treatment	COL5A2	1290	37	2	189899755	189899755	Missense_Mutation	SNP	C	T	40	51	c.4240G>A	c.(4240-4242)GAT>AAT	p.D1414N
Pat_34	Pre-Treatment	DNAH7	56171	37	2	196699031	196699031	Nonsense_Mutation	SNP	C	T	13	34	c.8999G>A	c.(8998-9000)TGG>TAG	p.W3000*
Pat_34	Pre-Treatment	EEF1B2	1933	37	2	207025358	207025358	Missense_Mutation	SNP	A	G	7	272	c.127A>G	c.(127-129)AGC>GGC	p.S43G
Pat_34	Pre-Treatment	MYL1	4632	37	2	211179730	211179730	Missense_Mutation	SNP	C	T	31	83	c.37G>A	c.(37-39)GCG>ACG	p.A13T
Pat_34	Pre-Treatment	STK36	27148	37	2	219549881	219549881	Missense_Mutation	SNP	C	T	29	39	c.1310C>T	c.(1309-1311)CCT>CTT	p.P437L
Pat_34	Pre-Treatment	SPEG	10290	37	2	220309459	220309459	Missense_Mutation	SNP	C	T	6	7	c.473C>T	c.(472-474)CCC>CTC	p.P158L

Pat_34	Pre-Treatment	SPEG	10290	37	2	220354390	220354390	Missense_Mutation	SNP	C	T	56	166	c.8650C>T	c.(8650-8652)CCA>TCA	p.P2884S
Pat_34	Pre-Treatment	INHA	3623	37	2	220439748	220439748	Missense_Mutation	SNP	C	T	44	100	c.601C>T	c.(601-603)CCC>TCC	p.P201S
Pat_34	Pre-Treatment	EPHA4	2043	37	2	222429090	222429090	Missense_Mutation	SNP	C	T	73	158	c.184G>A	c.(184-186)GAA>AAA	p.E62K
Pat_34	Pre-Treatment	COL4A4	1286	37	2	227920783	227920783	Missense_Mutation	SNP	G	A	22	18	c.2594C>T	c.(2593-2595)CCA>CTA	p.P865L
Pat_34	Pre-Treatment	COL4A4	1286	37	2	227945173	227945173	Missense_Mutation	SNP	C	T	31	73	c.1789G>A	c.(1789-1791)GAT>AAT	p.D597N
Pat_34	Pre-Treatment	ITM2C	81618	37	2	231738206	231738206	Missense_Mutation	SNP	G	A	14	42	c.195G>A	c.(193-195)ATG>ATA	p.M65I
Pat_34	Pre-Treatment	NMUR1	10316	37	2	232390057	232390057	Nonsense_Mutation	SNP	C	T	26	45	c.978G>A	c.(976-978)TGG>TGA	p.W326*
Pat_34	Pre-Treatment	CRNKL1	51340	37	20	20032949	20032950	Missense_Mutation	DNP	GG	AA	24	59	c.520_521CC>TT	c.(520-522)CCC>TTC	p.P174F
Pat_34	Pre-Treatment	EPB41L1	2036	37	20	34763552	34763552	Missense_Mutation	SNP	C	T	21	43	c.257C>T	c.(256-258)TCG>TTG	p.S86L
Pat_34	Pre-Treatment	LBP	3929	37	20	36999956	36999956	Missense_Mutation	SNP	G	A	15	45	c.1250G>A	c.(1249-1251)GGA>GAA	p.G417E
Pat_34	Pre-Treatment	PPP1R16B	26051	37	20	37536813	37536813	Missense_Mutation	SNP	A	G	19	27	c.1171A>G	c.(1171-1173)ACA>GCA	p.T391A
Pat_34	Pre-Treatment	CTCFL	140690	37	20	56094410	56094410	Missense_Mutation	SNP	C	T	67	141	c.778G>A	c.(778-780)GAT>AAT	p.D260N
Pat_34	Pre-Treatment	GNAS	2778	37	20	57484421	57484421	Missense_Mutation	SNP	G	A	23	41	c.2531G>A	c.(2530-2532)CGT>CAT	p.R844H
Pat_34	Pre-Treatment	SYCP2	10388	37	20	58452447	58452447	Missense_Mutation	SNP	G	A	35	63	c.3143C>T	c.(3142-3144)CCA>CTA	p.P1048L
Pat_34	Pre-Treatment	PTK6	5753	37	20	62164008	62164008	Missense_Mutation	SNP	C	T	29	40	c.703G>A	c.(703-705)GAG>AAG	p.E235K
Pat_34	Pre-Treatment	IL17RA	23765	37	22	17583143	17583143	Missense_Mutation	SNP	C	T	44	110	c.713C>T	c.(712-714)CCG>CTG	p.P238L
Pat_34	Pre-Treatment	PES1	23481	37	22	30977000	30977000	Missense_Mutation	SNP	C	T	15	26	c.911G>A	c.(910-912)GGG>GAG	p.G304E
Pat_34	Pre-Treatment	SYN3	8224	37	22	33327460	33327461	Missense_Mutation	DNP	AT	TA	25	32	c.375_376AT>TA	(373-378)GAATTC>GATAT	.125_126EF>D
Pat_34	Pre-Treatment	APOL5	80831	37	22	36123223	36123223	Missense_Mutation	SNP	C	T	36	64	c.1108C>T	c.(1108-1110)CGT>TGT	p.R370C
Pat_34	Pre-Treatment	EFCAB6	64800	37	22	44068143	44068143	Missense_Mutation	SNP	G	A	16	43	c.1462C>T	c.(1462-1464)CTC>TTC	p.L488F
Pat_34	Pre-Treatment	CRELD2	79174	37	22	50320924	50320924	Missense_Mutation	SNP	C	T	44	136	c.1031C>T	c.(1030-1032)CCG>CTG	p.P344L
Pat_34	Pre-Treatment	PLXNB2	23654	37	22	50728418	50728418	Missense_Mutation	SNP	G	A	24	28	c.596C>T	c.(595-597)GCC>GTC	p.A199V
Pat_34	Pre-Treatment	CHL1	10752	37	3	443320	443320	Missense_Mutation	SNP	G	A	28	43	c.3349G>A	c.(3349-3351)GAA>AAA	p.E1117K
Pat_34	Pre-Treatment	SRGAP3	9901	37	3	9146424	9146424	Missense_Mutation	SNP	C	T	42	80	c.363G>A	c.(361-363)ATG>ATA	p.M121I
Pat_34	Pre-Treatment	ZFYVE20	64145	37	3	15123998	15123998	Missense_Mutation	SNP	G	A	44	105	c.716C>T	c.(715-717)TCG>TTG	p.S239L
Pat_34	Pre-Treatment	ZNF385D	79750	37	3	21467063	21467063	Missense_Mutation	SNP	C	T	22	56	c.773G>A	c.(772-774)GGA>GAA	p.G258E
Pat_34	Pre-Treatment	DLEC1	9940	37	3	38135198	38135198	Missense_Mutation	SNP	G	A	23	42	c.1859G>A	c.(1858-1860)CGA>CAA	p.R620Q
Pat_34	Pre-Treatment	DLEC1	9940	37	3	38138190	38138190	Missense_Mutation	SNP	G	A	65	107	c.2302G>A	c.(2302-2304)GAG>AAG	p.E768K
Pat_34	Pre-Treatment	SCN5A	6331	37	3	38592959	38592959	Missense_Mutation	SNP	C	T	44	85	c.4904G>A	c.(4903-4905)AGA>AAA	p.R1635K
Pat_34	Pre-Treatment	SCN11A	11280	37	3	38889129	38889129	Missense_Mutation	SNP	G	A	10	29	c.4432C>T	c.(4432-4434)CGG>TGG	p.R1478W
Pat_34	Pre-Treatment	ALS2CL	259173	37	3	46717781	46717781	Nonsense_Mutation	SNP	G	A	28	41	c.2140C>T	c.(2140-2142)CAG>TAG	p.Q714*
Pat_34	Pre-Treatment	NAT6	24142	37	3	50334738	50334738	Missense_Mutation	SNP	G	A	15	38	c.157C>T	c.(157-159)CCA>TCA	p.P53S
Pat_34	Pre-Treatment	RBM15B	29890	37	3	51430589	51430589	Missense_Mutation	SNP	C	T	23	46	c.1759C>T	c.(1759-1761)CCC>TCC	p.P587S
Pat_34	Pre-Treatment	DNAH1	25981	37	3	52430710	52430710	Missense_Mutation	SNP	C	T	28	36	c.11507C>T	c.(11506-11508)CCC>CTC	p.P3836L
Pat_34	Pre-Treatment	DNAH1	25981	37	3	52431891	52431891	Missense_Mutation	SNP	G	A	9	21	c.11956G>A	c.(11956-11958)GAG>AAG	p.E3986K
Pat_34	Pre-Treatment	BAP1	8314	37	3	52440379	52440379	Missense_Mutation	SNP	C	T	42	61	c.673G>A	c.(673-675)GAC>AAC	p.D225N
Pat_34	Pre-Treatment	PHF7	51533	37	3	52455718	52455718	Nonsense_Mutation	SNP	C	T	28	59	c.628C>T	c.(628-630)CGA>TGA	p.R210*
Pat_34	Pre-Treatment	STAB1	23166	37	3	52539103	52539103	Missense_Mutation	SNP	C	T	11	33	c.1462C>T	c.(1462-1464)CAC>TAC	p.H488Y
Pat_34	Pre-Treatment	ERC2	26059	37	3	56330247	56330247	Missense_Mutation	SNP	C	T	85	186	c.874G>A	c.(874-876)GAA>AAA	p.E292K
Pat_34	Pre-Treatment	ADAMTS9	56999	37	3	64672429	64672429	Missense_Mutation	SNP	A	T	15	38	c.331T>A	c.(331-333)TTT>ATT	p.F111I
Pat_34	Pre-Treatment	MAGI1	9223	37	3	65369230	65369230	Missense_Mutation	SNP	C	T	32	62	c.2485G>A	c.(2485-2487)GGT>AGT	p.G829S
Pat_34	Pre-Treatment	EPHA3	2042	37	3	89259565	89259565	Missense_Mutation	SNP	G	A	139	196	c.709G>A	c.(709-711)GAA>AAA	p.E237K
Pat_34	Pre-Treatment	OR5K2	402135	37	3	98216796	98216797	Missense_Mutation	DNP	GG	AA	58	125	c.272_273GG>AA	c.(271-273)AGG>AAA	p.R91K
Pat_34	Pre-Treatment	MYH15	22989	37	3	108204049	108204049	Missense_Mutation	SNP	G	A	45	130	c.1063C>T	c.(1063-1065)CCT>TCT	p.P355S
Pat_34	Pre-Treatment	TRAT1	50852	37	3	108568024	108568024	Missense_Mutation	SNP	G	A	22	58	c.226G>A	c.(226-228)GAA>AAA	p.E76K
Pat_34	Pre-Treatment	CASR	846	37	3	121980930	121980930	Missense_Mutation	SNP	G	A	15	19	c.1048G>A	c.(1048-1050)GAG>AAG	p.E350K
Pat_34	Pre-Treatment	PODXL2	50512	37	3	127379563	127379563	Missense_Mutation	SNP	C	T	32	54	c.692C>T	c.(691-693)TCA>TTA	p.S231L

Pat_34	Pre-Treatment	KBTBD12	166348	37	3	127702997	127702998	Nonsense_Mutation	DNP	GG	AA	33	93	.1748_1749GG>A	c.(1747-1749)TGG>TAA	p.W583*
Pat_34	Pre-Treatment	PIK3R4	30849	37	3	130409479	130409479	Nonsense_Mutation	SNP	G	A	19	42	c.3118C>T	c.(3118-3120)CGA>TGA	p.R1040*
Pat_34	Pre-Treatment	ANAPC13	25847	37	3	134197511	134197511	Missense_Mutation	SNP	G	A	68	87	c.146C>T	c.(145-147)TCT>TTT	p.S49F
Pat_34	Pre-Treatment	SI	6476	37	3	164725741	164725741	Nonsense_Mutation	SNP	G	A	69	162	c.4225C>T	c.(4225-4227)CAA>TAA	p.Q1409*
Pat_34	Pre-Treatment	SI	6476	37	3	164748501	164748501	Missense_Mutation	SNP	G	A	116	187	c.2891C>T	c.(2890-2892)ACG>ATG	p.T964M
Pat_34	Pre-Treatment	SERPINI2	5276	37	3	167170732	167170732	Missense_Mutation	SNP	C	T	10	37	c.956G>A	c.(955-957)GGA>GAA	p.G319E
Pat_34	Pre-Treatment	ATP11B	23200	37	3	182615093	182615093	Missense_Mutation	SNP	G	A	37	85	c.3051G>A	c.(3049-3051)ATG>ATA	p.M1017I
Pat_34	Pre-Treatment	ECE2	9718	37	3	184008359	184008359	Missense_Mutation	SNP	C	T	73	149	c.2024C>T	c.(2023-2025)CCC>CTC	p.P675L
Pat_34	Pre-Treatment	PDGFRA	5156	37	4	55144652	55144652	Missense_Mutation	SNP	G	A	30	61	c.2126G>A	c.(2125-2127)GGA>GAA	p.G709E
Pat_34	Pre-Treatment	AASDH	132949	37	4	57215455	57215455	Missense_Mutation	SNP	G	A	29	118	c.2462C>T	c.(2461-2463)TCT>TTT	p.S821F
Pat_34	Pre-Treatment	PPEF2	5470	37	4	76811162	76811162	Missense_Mutation	SNP	G	A	59	152	c.365C>T	c.(364-366)CCA>CTA	p.P122L
Pat_34	Pre-Treatment	FRAS1	80144	37	4	79400632	79400632	Missense_Mutation	SNP	G	A	26	42	c.8203G>A	c.(8203-8205)GGG>AGG	p.G2735R
Pat_34	Pre-Treatment	WDFY3	23001	37	4	85715869	85715869	Missense_Mutation	SNP	G	A	8	30	c.3290C>T	c.(3289-3291)CCC>CTC	p.P1097L
Pat_34	Pre-Treatment	ADH1A	124	37	4	100205934	100205934	Missense_Mutation	SNP	G	A	20	47	c.286C>T	c.(286-288)CCT>TCT	p.P96S
Pat_34	Pre-Treatment	SYNPO2	171024	37	4	119951711	119951711	Missense_Mutation	SNP	G	A	76	166	c.1781G>A	c.(1780-1782)GGG>GAG	p.G594E
Pat_34	Pre-Treatment	SCLT1	132320	37	4	129924980	129924981	Missense_Mutation	DNP	GG	AA	35	73	c.341_342CC>TT	c.(340-342)CCC>CTT	p.P114L
Pat_34	Pre-Treatment	DCHS2	54798	37	4	155241618	155241618	Missense_Mutation	SNP	C	T	66	116	c.3568G>A	c.(3568-3570)GAT>AAT	p.D1190N
Pat_34	Pre-Treatment	DCHS2	54798	37	4	155242155	155242155	Missense_Mutation	SNP	C	T	29	104	c.3031G>A	c.(3031-3033)GAA>AAA	p.E1011K
Pat_34	Pre-Treatment	GLRB	2743	37	4	158057999	158057999	Missense_Mutation	SNP	C	T	33	69	c.571C>T	c.(571-573)CCC>TCC	p.P191S
Pat_34	Pre-Treatment	RXFP1	59350	37	4	159533469	159533469	Missense_Mutation	SNP	G	A	11	34	c.635G>A	c.(634-636)CGA>CAA	p.R212Q
Pat_34	Pre-Treatment	KLHL2	11275	37	4	166220758	166220758	Missense_Mutation	SNP	T	A	40	77	c.871T>A	c.(871-873)TTA>ATA	p.L291I
Pat_34	Pre-Treatment	TLL1	7092	37	4	167022028	167022028	Nonstop_Mutation	SNP	A	C	7	13	c.3042A>C	c.(3040-3042)TAA>TAC	p.*1014Y
Pat_34	Pre-Treatment	SPOCK3	50859	37	4	167833862	167833862	Nonsense_Mutation	SNP	C	T	16	56	c.392G>A	c.(391-393)TGG>TAG	p.W131*
Pat_34	Pre-Treatment	VEGFC	7424	37	4	177650855	177650855	Missense_Mutation	SNP	T	A	50	81	c.193A>T	c.(193-195)AGT>TGT	p.S65C
Pat_34	Pre-Treatment	NSUN2	54888	37	5	6600050	6600050	Missense_Mutation	SNP	G	A	49	86	c.2293C>T	c.(2293-2295)CCA>TCA	p.P765S
Pat_34	Pre-Treatment	CDH18	1016	37	5	19747261	19747261	Missense_Mutation	SNP	C	T	48	99	c.313G>A	c.(313-315)GAT>AAT	p.D105N
Pat_34	Pre-Treatment	CAPSL	133690	37	5	35910616	35910616	Missense_Mutation	SNP	T	A	5	22	c.167A>T	c.(166-168)AAT>ATT	p.N56I
Pat_34	Pre-Treatment	FGF10	2255	37	5	44305174	44305174	Missense_Mutation	SNP	C	T	37	97	c.550G>A	c.(550-552)GGA>AGA	p.G184R
Pat_34	Pre-Treatment	RAB3C	115827	37	5	58120900	58120900	Missense_Mutation	SNP	C	T	53	70	c.407C>T	c.(406-408)GCC>GTC	p.A136V
Pat_34	Pre-Treatment	PIK3R1	5295	37	5	67589660	67589660	Nonsense_Mutation	SNP	C	T	26	64	c.1423C>T	c.(1423-1425)CAG>TAG	p.Q475*
Pat_34	Pre-Treatment	SLC30A5	64924	37	5	68409009	68409009	Missense_Mutation	SNP	T	G	24	44	c.490T>G	c.(490-492)TTG>GTG	p.L164V
Pat_34	Pre-Treatment	WDR41	55255	37	5	76728976	76728976	Missense_Mutation	SNP	A	G	63	100	c.1364T>C	c.(1363-1365)TTA>TCA	p.L455S
Pat_34	Pre-Treatment	VCAN	1462	37	5	82818080	82818080	Missense_Mutation	SNP	C	T	31	95	c.3955C>T	c.(3955-3957)CAC>TAC	p.H1319Y
Pat_34	Pre-Treatment	EDIL3	10085	37	5	83402499	83402499	Missense_Mutation	SNP	C	T	43	95	c.619G>A	c.(619-621)GCT>ACT	p.A207T
Pat_34	Pre-Treatment	PAM	5066	37	5	102360975	102360975	Missense_Mutation	SNP	C	T	40	103	c.2626C>T	c.(2626-2628)CCG>TCG	p.P876S
Pat_34	Pre-Treatment	MEGF10	84466	37	5	126771158	126771159	Nonsense_Mutation	DNP	GG	AA	51	72	.2081_2082GG>A	c.(2080-2082)TGG>TAA	p.W694*
Pat_34	Pre-Treatment	PRRC1	133619	37	5	126860501	126860501	Missense_Mutation	SNP	C	T	113	250	c.382C>T	c.(382-384)CCT>TCT	p.P128S
Pat_34	Pre-Treatment	PCDHA7	56141	37	5	140216016	140216016	Missense_Mutation	SNP	C	T	44	90	c.2048C>T	c.(2047-2049)TCG>TTG	p.S683L
Pat_34	Pre-Treatment	PCDHA11	56138	37	5	140249746	140249746	Missense_Mutation	SNP	C	T	24	48	c.1058C>T	c.(1057-1059)TCC>TTC	p.S353F
Pat_34	Pre-Treatment	PCDHB4	56131	37	5	140503385	140503385	Missense_Mutation	SNP	C	T	26	54	c.1805C>T	c.(1804-1806)TCG>TTG	p.S602L
Pat_34	Pre-Treatment	PCDHB8	56128	37	5	140558145	140558145	Missense_Mutation	SNP	C	T	21	114	c.530C>T	c.(529-531)TCC>TTC	p.S177F
Pat_34	Pre-Treatment	JAKMIP2	9832	37	5	147051353	147051353	Missense_Mutation	SNP	C	T	10	33	c.17G>A	c.(16-18)CGA>CAA	p.R6Q
Pat_34	Pre-Treatment	GRIA1	2890	37	5	152873499	152873499	Missense_Mutation	SNP	C	T	45	85	c.94C>T	c.(94-96)CCA>TCA	p.P32S
Pat_34	Pre-Treatment	FBXW11	23291	37	5	171326098	171326098	Nonsense_Mutation	SNP	C	T	34	37	c.561G>A	c.(559-561)TGG>TGA	p.W187*
Pat_34	Pre-Treatment	RNF44	22838	37	5	175956549	175956549	Missense_Mutation	SNP	C	T	22	94	c.1111G>A	c.(1111-1113)GAC>AAC	p.D371N
Pat_34	Pre-Treatment	UNC5A	90249	37	5	176306446	176306446	Missense_Mutation	SNP	G	A	33	62	c.2320G>A	c.(2320-2322)GGT>AGT	p.G774S
Pat_34	Pre-Treatment	HIVEP1	3096	37	6	12122235	12122235	Missense_Mutation	SNP	G	A	4	82	c.2207G>A	c.(2206-2208)CGC>CAC	p.R736H

Pat_34	Pre-Treatment	ZNF391	346157	37	6	27368259	27368259	Missense_Mutation	SNP	C	T	48	76	c.110C>T	c.(109-111)TCT>TTT	p.S37F
Pat_34	Pre-Treatment	OR2B6	26212	37	6	27925904	27925904	Missense_Mutation	SNP	G	A	16	60	c.886G>A	c.(886-888)GAG>AAG	p.E296K
Pat_34	Pre-Treatment	SCAND3	114821	37	6	28543374	28543374	Missense_Mutation	SNP	C	T	32	124	c.1108G>A	c.(1108-1110)GAA>AAA	p.E370K
Pat_34	Pre-Treatment	OR14J1	442191	37	6	29274969	29274969	Missense_Mutation	SNP	G	A	96	80	c.503G>A	c.(502-504)GGG>GAG	p.G168E
Pat_34	Pre-Treatment	CSNK2B	1460	37	6	31634628	31634628	Missense_Mutation	SNP	T	A	28	87	c.20T>A	c.(19-21)GTG>GAG	p.V7E
Pat_34	Pre-Treatment	MSH5	4439	37	6	31728479	31728480	Missense_Mutation	DNP	AC	TT	36	111	.1825_1826AC>T	c.(1825-1827)ACA>TTA	p.T609L
Pat_34	Pre-Treatment	EHMT2	10919	37	6	31854456	31854456	Missense_Mutation	SNP	C	T	12	39	c.2245G>A	c.(2245-2247)GAG>AAG	p.E749K
Pat_34	Pre-Treatment	HLA-DQB2	3120	37	6	32726774	32726774	Missense_Mutation	SNP	C	T	7	104	c.499G>A	c.(499-501)GCC>ACC	p.A167T
Pat_34	Pre-Treatment	TULP1	7287	37	6	35473947	35473948	Missense_Mutation	DNP	CC	TT	3	20	c.831_832GG>AA	829-834)AAGGAG>AAAA	p.E278K
Pat_34	Pre-Treatment	SLC26A8	116369	37	6	35967813	35967813	Missense_Mutation	SNP	G	A	53	197	c.401C>T	c.(400-402)TCG>TTG	p.S134L
Pat_34	Pre-Treatment	DNAH8	1769	37	6	38897346	38897347	Nonsense_Mutation	DNP	CC	TT	143	153	10527_10528CC>	525-10530)GGCCGA>GG	p.R3510*
Pat_34	Pre-Treatment	TTBK1	84630	37	6	43222346	43222346	Missense_Mutation	SNP	G	A	39	77	c.533G>A	c.(532-534)GGG>GAG	p.G178E
Pat_34	Pre-Treatment	ZNF318	24149	37	6	43305131	43305131	Missense_Mutation	SNP	G	A	11	33	c.6605C>T	c.(6604-6606)TCC>TTC	p.S2202F
Pat_34	Pre-Treatment	SPATS1	221409	37	6	44329579	44329579	Missense_Mutation	SNP	C	T	92	144	c.424C>T	c.(424-426)CGT>TGT	p.R142C
Pat_34	Pre-Treatment	TFAP2D	83741	37	6	50681806	50681806	Missense_Mutation	SNP	A	G	20	47	c.38A>G	c.(37-39)GAG>GGG	p.E13G
Pat_34	Pre-Treatment	GFRAL	389400	37	6	55266626	55266626	Missense_Mutation	SNP	C	T	29	75	c.1160C>T	c.(1159-1161)TCG>TTG	p.S387L
Pat_34	Pre-Treatment	BAI3	577	37	6	70042848	70042848	Missense_Mutation	SNP	A	C	58	71	c.3136A>C	c.(3136-3138)AAA>CAA	p.K1046Q
Pat_34	Pre-Treatment	BAI3	577	37	6	70071078	70071078	Missense_Mutation	SNP	G	A	6	26	c.3913G>A	c.(3913-3915)GAA>AAA	p.E1305K
Pat_34	Pre-Treatment	TTK	7272	37	6	80749438	80749438	Missense_Mutation	SNP	C	T	63	127	c.2156C>T	c.(2155-2157)TCC>TTC	p.S719F
Pat_34	Pre-Treatment	C6orf58	352999	37	6	127901476	127901476	Missense_Mutation	SNP	C	T	60	61	c.455C>T	c.(454-456)TCA>TTA	p.S152L
Pat_34	Pre-Treatment	EPB41L2	2037	37	6	131191209	131191209	Missense_Mutation	SNP	C	T	37	45	c.2101G>A	c.(2101-2103)GAC>AAC	p.D701N
Pat_34	Pre-Treatment	BCLAF1	9774	37	6	136599198	136599198	Missense_Mutation	SNP	G	A	7	58	c.821C>T	c.(820-822)TCT>TTT	p.S274F
Pat_34	Pre-Treatment	ECT2L	345930	37	6	139135637	139135637	Missense_Mutation	SNP	G	A	24	23	c.76G>A	c.(76-78)GAA>AAA	p.E26K
Pat_34	Pre-Treatment	RAC1	5879	37	7	6426892	6426892	Missense_Mutation	SNP	C	T	211	85	c.85C>T	c.(85-87)CCT>TCT	p.P29S
Pat_34	Pre-Treatment	AUTS2	26053	37	7	70240352	70240352	Missense_Mutation	SNP	C	T	108	34	c.1912C>T	c.(1912-1914)CCT>TCT	p.P638S
Pat_34	Pre-Treatment	TYW1B	441250	37	7	72081809	72081809	Missense_Mutation	SNP	T	C	6	140	c.1633A>G	c.(1633-1635)AGA>GGA	p.R545G
Pat_34	Pre-Treatment	NSUN5P2	260294	37	7	72420466	72420466	Missense_Mutation	SNP	C	T	7	57	c.122G>A	c.(121-123)CGC>CAC	p.R41H
Pat_34	Pre-Treatment	WBSCR28	135886	37	7	73279685	73279685	Missense_Mutation	SNP	G	T	16	15	c.435G>T	c.(433-435)TTG>TTT	p.L145F
Pat_34	Pre-Treatment	PION	54103	37	7	76958695	76958695	Missense_Mutation	SNP	C	T	45	29	c.1688G>A	c.(1687-1689)AGA>AAA	p.R563K
Pat_34	Pre-Treatment	SEMA3E	9723	37	7	82997177	82997177	Missense_Mutation	SNP	C	T	70	24	c.2053G>A	c.(2053-2055)GAC>AAC	p.D685N
Pat_34	Pre-Treatment	CROT	54677	37	7	87022093	87022093	Missense_Mutation	SNP	G	T	64	29	c.1552G>T	c.(1552-1554)GGT>TGT	p.G518C
Pat_34	Pre-Treatment	HEPACAM2	253012	37	7	92848544	92848544	Missense_Mutation	SNP	C	T	55	25	c.300G>A	c.(298-300)ATG>ATA	p.M100I
Pat_34	Pre-Treatment	ZAN	7455	37	7	100353009	100353009	Nonsense_Mutation	SNP	C	A	51	21	c.3285C>A	c.(3283-3285)TGC>TGA	p.C1095*
Pat_34	Pre-Treatment	LAMB4	22798	37	7	107717454	107717454	Missense_Mutation	SNP	C	T	62	35	c.2059G>A	c.(2059-2061)GAT>AAT	p.D687N
Pat_34	Pre-Treatment	CFTR	1080	37	7	117232010	117232010	Missense_Mutation	SNP	A	T	57	27	c.1789A>T	c.(1789-1791)AAC>TAC	p.N597Y
Pat_34	Pre-Treatment	SLC13A1	6561	37	7	122768932	122768932	Missense_Mutation	SNP	C	T	47	22	c.1100G>A	c.(1099-1101)GGA>GAA	p.G367E
Pat_34	Pre-Treatment	BRAF	673	37	7	140453136	140453137	Missense_Mutation	DNP	AC	TT	96	42	.1798_1799GT>A	c.(1798-1800)GTG>AAG	p.V600K
Pat_34	Pre-Treatment	PIP	5304	37	7	142836684	142836685	Missense_Mutation	DNP	CC	TT	86	76	c.390_391CC>TT	(388-393)ATCCCC>ATTT	p.P131S
Pat_34	Pre-Treatment	EPHA1	2041	37	7	143091909	143091909	Missense_Mutation	SNP	C	T	34	18	c.2344G>A	c.(2344-2346)GAA>AAA	p.E782K
Pat_34	Pre-Treatment	SSPO	23145	37	7	149481966	149481966	Missense_Mutation	SNP	C	T	28	14	c.2756C>T	c.(2755-2757)TCA>TTA	p.S919L
Pat_34	Pre-Treatment	CSMD1	64478	37	8	3265475	3265475	Missense_Mutation	SNP	C	T	13	20	c.2020G>A	c.(2020-2022)GAA>AAA	p.E674K
Pat_34	Pre-Treatment	NAT2	10	37	8	18257798	18257799	Missense_Mutation	DNP	CC	TT	30	64	c.285_286CC>TT	(283-288)ATCCCT>ATTT	p.P96S
Pat_34	Pre-Treatment	SH2D4A	63898	37	8	19214768	19214768	Missense_Mutation	SNP	C	T	69	143	c.568C>T	c.(568-570)CGT>TGT	p.R190C
Pat_34	Pre-Treatment	LOXL2	4017	37	8	23225606	23225606	Missense_Mutation	SNP	C	T	36	67	c.259G>A	c.(259-261)GAC>AAC	p.D87N
Pat_34	Pre-Treatment	SCARA5	286133	37	8	27764748	27764748	Missense_Mutation	SNP	C	T	26	49	c.1013G>A	c.(1012-1014)AGA>AAA	p.R338K
Pat_34	Pre-Treatment	TEX15	56154	37	8	30695023	30695023	Missense_Mutation	SNP	G	A	7	32	c.7628C>T	c.(7627-7629)TCA>TTA	p.S2543L
Pat_34	Pre-Treatment	ADAM2	2515	37	8	39604085	39604085	Missense_Mutation	SNP	G	A	11	49	c.2080C>T	c.(2080-2082)CCT>TCT	p.P694S

Pat_34	Pre-Treatment	CHRNA6	8973	37	8	42611759	42611759	Missense_Mutation	SNP	C	T	62	74	c.583G>A	c.(583-585)GTG>ATG	p.V195M
Pat_34	Pre-Treatment	CLVS1	157807	37	8	62212408	62212408	Missense_Mutation	SNP	C	T	14	33	c.22C>T	c.(22-24)CCA>TCA	p.P8S
Pat_34	Pre-Treatment	CLVS1	157807	37	8	62370966	62370966	Missense_Mutation	SNP	G	A	31	69	c.842G>A	c.(841-843)GGA>GAA	p.G281E
Pat_34	Pre-Treatment	TRPA1	8989	37	8	72963103	72963103	Nonsense_Mutation	SNP	C	T	24	53	c.1815G>A	c.(1813-1815)TGG>TGA	p.W605*
Pat_34	Pre-Treatment	EPPK1	83481	37	8	144942264	144942264	Missense_Mutation	SNP	C	T	15	56	c.5158G>A	c.(5158-5160)GAC>AAC	p.D1720N
Pat_34	Pre-Treatment	PTPRD	5789	37	9	8485920	8485920	Missense_Mutation	SNP	A	T	39	43	c.2897T>A	c.(2896-2898)CTC>CAC	p.L966H
Pat_34	Pre-Treatment	FREM1	158326	37	9	14842347	14842347	Missense_Mutation	SNP	C	T	30	29	c.1705G>A	c.(1705-1707)GAG>AAG	p.E569K
Pat_34	Pre-Treatment	TAF1L	138474	37	9	32633458	32633458	Missense_Mutation	SNP	C	T	32	30	c.2120G>A	c.(2119-2121)GGA>GAA	p.G707E
Pat_34	Pre-Treatment	RECK	8434	37	9	36083496	36083496	Missense_Mutation	SNP	C	T	27	17	c.574C>T	c.(574-576)CCA>TCA	p.P192S
Pat_34	Pre-Treatment	UBQLN1	29979	37	9	86294917	86294917	Missense_Mutation	SNP	C	T	33	17	c.484G>A	c.(484-486)GGT>AGT	p.G162S
Pat_34	Pre-Treatment	INVS	27130	37	9	102866838	102866838	Missense_Mutation	SNP	C	T	26	30	c.35C>T	c.(34-36)TCA>TTA	p.S12L
Pat_34	Pre-Treatment	ABCA1	19	37	9	107594964	107594964	Missense_Mutation	SNP	A	C	42	42	c.1400T>G	c.(1399-1401)TTG>TGG	p.L467W
Pat_34	Pre-Treatment	FCN2	2220	37	9	137772689	137772689	Missense_Mutation	SNP	G	A	8	9	c.22G>A	c.(22-24)GGG>AGG	p.G8R
Pat_34	Pre-Treatment	CACNA1B	774	37	9	140811767	140811767	Missense_Mutation	SNP	C	T	22	65	c.850C>T	c.(850-852)CGG>TGG	p.R284W
Pat_34	Pre-Treatment	ATXN3L	92552	37	X	13337593	13337593	Missense_Mutation	SNP	C	T	65	32	c.461G>A	c.(460-462)CGA>CAA	p.R154Q
Pat_34	Pre-Treatment	ACE2	59272	37	X	15599367	15599367	Nonsense_Mutation	SNP	C	T	142	38	c.1047G>A	c.(1045-1047)TGG>TGA	p.W349*
Pat_34	Pre-Treatment	CXorf22	170063	37	X	35966478	35966478	Missense_Mutation	SNP	C	T	59	22	c.565C>T	c.(565-567)CCA>TCA	p.P189S
Pat_34	Pre-Treatment	CXorf22	170063	37	X	35993371	35993371	Missense_Mutation	SNP	G	A	47	42	c.2362G>A	c.(2362-2364)GAT>AAT	p.D788N
Pat_34	Pre-Treatment	SLC9A7	84679	37	X	46466433	46466433	Missense_Mutation	SNP	G	A	32	19	c.2132C>T	c.(2131-2133)TCG>TTG	p.S711L
Pat_34	Pre-Treatment	OPHN1	4983	37	X	67421548	67421548	Missense_Mutation	SNP	G	A	42	14	c.938C>T	c.(937-939)CCC>CTC	p.P313L
Pat_34	Pre-Treatment	TRMT2B	79979	37	X	100274023	100274023	Missense_Mutation	SNP	G	A	49	21	c.1325C>T	c.(1324-1326)GCC>GTC	p.A442V
Pat_34	Pre-Treatment	HTR2C	3358	37	X	114141666	114141666	Nonsense_Mutation	SNP	G	A	53	16	c.1065G>A	c.(1063-1065)TGG>TGA	p.W355*
Pat_34	Pre-Treatment	MST4	51765	37	X	131202291	131202291	Missense_Mutation	SNP	G	A	60	34	c.379G>A	c.(379-381)GAA>AAA	p.E127K
Pat_34	Pre-Treatment	MAGEC2	51438	37	X	141291601	141291601	Missense_Mutation	SNP	G	A	23	7	c.173C>T	c.(172-174)TCC>TTC	p.S58F
Pat_34	Pre-Treatment	GABRA3	2556	37	X	151336938	151336938	Missense_Mutation	SNP	G	A	62	40	c.1241C>T	c.(1240-1242)TCC>TTC	p.S414F
Pat_46	Pre-Treatment	AGRN	375790	37	1	985282	985282	Splice_Site	SNP	G	A	8	18	c.4745_splice	c.e27-1	p.G1582_splice
Pat_46	Pre-Treatment	ACTRT2	140625	37	1	2938383	2938383	Nonsense_Mutation	SNP	C	T	5	15	c.133C>T	c.(133-135)CAG>TAG	p.Q45*
Pat_46	Pre-Treatment	CAMTA1	23261	37	1	7724780	7724780	Missense_Mutation	SNP	G	A	5	16	c.2173G>A	c.(2173-2175)GGG>AGG	p.G725R
Pat_46	Pre-Treatment	RERE	473	37	1	8557562	8557562	Missense_Mutation	SNP	G	A	32	79	c.907C>T	c.(907-909)CCT>TCT	p.P303S
Pat_46	Pre-Treatment	PRAMEF12	390999	37	1	12835119	12835119	Missense_Mutation	SNP	C	T	7	22	c.109C>T	c.(109-111)CCC>TCC	p.P37S
Pat_46	Pre-Treatment	PRAMEF11	440560	37	1	12884991	12884991	Missense_Mutation	SNP	G	A	52	76	c.1120C>T	c.(1120-1122)CCT>TCT	p.P374S
Pat_46	Pre-Treatment	PRAMEF8	391002	37	1	12979781	12979781	Missense_Mutation	SNP	G	A	13	36	c.973G>A	c.(973-975)GAC>AAC	p.D325N
Pat_46	Pre-Treatment	PRAMEF18	391003	37	1	13695812	13695812	Missense_Mutation	SNP	G	A	12	124	c.1153C>T	c.(1153-1155)CAC>TAC	p.H385Y
Pat_46	Pre-Treatment	TMCO4	255104	37	1	20009888	20009888	Missense_Mutation	SNP	G	A	9	17	c.1550C>T	c.(1549-1551)GCC>GTC	p.A517V
Pat_46	Pre-Treatment	KIF17	57576	37	1	20998491	20998491	Missense_Mutation	SNP	C	T	11	15	c.2662G>A	c.(2662-2664)GAA>AAA	p.E888K
Pat_46	Pre-Treatment	EIF4G3	8672	37	1	21180063	21180063	Missense_Mutation	SNP	T	G	6	14	c.3373A>C	c.(3373-3375)ACC>CCC	p.T1125P
Pat_46	Pre-Treatment	TMEM57	55219	37	1	25773296	25773296	Missense_Mutation	SNP	C	T	3	11	c.124C>T	c.(124-126)CTC>TTC	p.L42F
Pat_46	Pre-Treatment	C1orf172	126695	37	1	27278781	27278781	Missense_Mutation	SNP	C	T	10	23	c.91G>A	c.(91-93)GAT>AAT	p.D31N
Pat_46	Pre-Treatment	BAI2	576	37	1	32202278	32202278	Missense_Mutation	SNP	G	A	9	21	c.3026C>T	c.(3025-3027)TCC>TTC	p.S1009F
Pat_46	Pre-Treatment	COL9A2	1298	37	1	40767522	40767522	Missense_Mutation	SNP	C	T	5	15	c.1832G>A	c.(1831-1833)CGG>CAG	p.R611Q
Pat_46	Pre-Treatment	TIE1	7075	37	1	43777724	43777724	Missense_Mutation	SNP	C	T	21	52	c.1552C>T	c.(1552-1554)CGT>TGT	p.R518C
Pat_46	Pre-Treatment	PTCH2	8643	37	1	45293837	45293837	Missense_Mutation	SNP	A	T	15	32	c.1736T>A	c.(1735-1737)ATC>AAC	p.I579N
Pat_46	Pre-Treatment	PRKAA2	5563	37	1	57140179	57140179	Missense_Mutation	SNP	C	T	4	32	c.220C>T	c.(220-222)CCT>TCT	p.P74S
Pat_46	Pre-Treatment	C1orf168	199920	37	1	57254664	57254664	Missense_Mutation	SNP	G	A	19	50	c.901C>T	c.(901-903)CCC>TCC	p.P301S
Pat_46	Pre-Treatment	C8A	731	37	1	57341860	57341860	Missense_Mutation	SNP	G	A	14	35	c.442G>A	c.(442-444)GGA>AGA	p.G148R
Pat_46	Pre-Treatment	C8A	731	37	1	57349289	57349289	Missense_Mutation	SNP	G	A	10	35	c.790G>A	c.(790-792)GGT>AGT	p.G264S
Pat_46	Pre-Treatment	C8A	731	37	1	57378223	57378223	Missense_Mutation	SNP	C	T	22	60	c.1528C>T	c.(1528-1530)CTC>TTC	p.L510F

Pat_46	Pre-Treatment	C8B	732	37	1	57417816	57417816	Missense_Mutation	SNP	G	A	27	111	c.571C>T	c.(571-573)CTT>TTT	p.L191F
Pat_46	Pre-Treatment	NFIA	4774	37	1	61554084	61554085	Nonsense_Mutation	DNP	GA	AT	31	109	c.291_292GA>AT	289-294)GGGAAA>GGAT	p.K98*
Pat_46	Pre-Treatment	ANGPTL3	27329	37	1	63069640	63069640	Missense_Mutation	SNP	G	A	5	12	c.932G>A	c.(931-933)GGA>GAA	p.G311E
Pat_46	Pre-Treatment	JAK1	3716	37	1	65344731	65344732	Missense_Mutation	DNP	GG	AA	5	20	c.305_306CC>TT	c.(304-306)TCC>TTT	p.S102F
Pat_46	Pre-Treatment	C1orf173	127254	37	1	75102109	75102109	Missense_Mutation	SNP	G	A	65	164	c.458C>T	c.(457-459)CCA>CTA	p.P153L
Pat_46	Pre-Treatment	FRRS1	391059	37	1	100176461	100176461	Missense_Mutation	SNP	G	A	11	29	c.1525C>T	c.(1525-1527)CCT>TCT	p.P509S
Pat_46	Pre-Treatment	AGL	178	37	1	100327245	100327245	Missense_Mutation	SNP	C	T	16	65	c.269C>T	c.(268-270)TCA>TTA	p.S90L
Pat_46	Pre-Treatment	GSTM5	2949	37	1	110256309	110256309	Missense_Mutation	SNP	C	T	7	23	c.286C>T	c.(286-288)CGT>TGT	p.R96C
Pat_46	Pre-Treatment	OVGP1	5016	37	1	111964197	111964197	Missense_Mutation	SNP	G	A	10	23	c.707C>T	c.(706-708)CCC>CTC	p.P236L
Pat_46	Pre-Treatment	WDR77	79084	37	1	111991249	111991249	Missense_Mutation	SNP	G	A	43	87	c.293C>T	c.(292-294)TCC>TTC	p.S98F
Pat_46	Pre-Treatment	RSBN1	54665	37	1	114340403	114340403	Nonsense_Mutation	SNP	A	T	45	72	c.959T>A	c.(958-960)TTA>TAA	p.L320*
Pat_46	Pre-Treatment	VTCN1	79679	37	1	117695923	117695923	Nonsense_Mutation	SNP	G	A	16	37	c.514C>T	c.(514-516)CGA>TGA	p.R172*
Pat_46	Pre-Treatment	SPAG17	200162	37	1	118570912	118570912	Missense_Mutation	SNP	C	T	25	70	c.3715G>A	c.(3715-3717)GGA>AGA	p.G1239R
Pat_46	Pre-Treatment	WARS2	10352	37	1	119619088	119619088	Missense_Mutation	SNP	G	A	18	77	c.233C>T	c.(232-234)TCC>TTC	p.S78F
Pat_46	Pre-Treatment	ITGA10	8515	37	1	145533166	145533166	Missense_Mutation	SNP	C	T	3	62	c.1261C>T	c.(1261-1263)CCC>TCC	p.P421S
Pat_46	Pre-Treatment	ANKRD35	148741	37	1	145561391	145561391	Missense_Mutation	SNP	C	T	15	7	c.1079C>T	c.(1078-1080)TCT>TTT	p.S360F
Pat_46	Pre-Treatment	ECM1	1893	37	1	150483973	150483973	Missense_Mutation	SNP	C	T	23	130	c.749C>T	c.(748-750)TCG>TTG	p.S250L
Pat_46	Pre-Treatment	HRNR	388697	37	1	152192583	152192583	Missense_Mutation	SNP	C	T	72	362	c.1522G>A	c.(1522-1524)GGA>AGA	p.G508R
Pat_46	Pre-Treatment	HRNR	388697	37	1	152193753	152193753	Missense_Mutation	SNP	C	T	44	35	c.352G>A	c.(352-354)GAG>AAG	p.E118K
Pat_46	Pre-Treatment	FLG	2312	37	1	152280773	152280773	Missense_Mutation	SNP	C	T	49	240	c.6589G>A	c.(6589-6591)GAA>AAA	p.E2197K
Pat_46	Pre-Treatment	FLG	2312	37	1	152286716	152286716	Missense_Mutation	SNP	C	T	21	20	c.646G>A	c.(646-648)GAT>AAT	p.D216N
Pat_46	Pre-Treatment	CRNN	49860	37	1	152382906	152382906	Missense_Mutation	SNP	C	T	118	83	c.652G>A	c.(652-654)GAC>AAC	p.D218N
Pat_46	Pre-Treatment	LCE1E	353135	37	1	152760070	152760070	Missense_Mutation	SNP	C	T	45	16	c.295C>T	c.(295-297)CCC>TCC	p.P99S
Pat_46	Pre-Treatment	FAM189B	10712	37	1	155220484	155220484	Missense_Mutation	SNP	G	A	23	24	c.1093C>T	c.(1093-1095)CGC>TGC	p.R365C
Pat_46	Pre-Treatment	OR10K1	391109	37	1	158435659	158435659	Missense_Mutation	SNP	C	T	18	129	c.308C>T	c.(307-309)TCC>TTC	p.S103F
Pat_46	Pre-Treatment	SPTA1	6708	37	1	158646045	158646045	Missense_Mutation	SNP	G	A	47	285	c.998C>T	c.(997-999)TCC>TTC	p.S333F
Pat_46	Pre-Treatment	OR10J3	441911	37	1	159284365	159284365	Missense_Mutation	SNP	A	C	39	196	c.85T>G	c.(85-87)TTT>GTT	p.F29V
Pat_46	Pre-Treatment	PVRL4	81607	37	1	161049730	161049730	Missense_Mutation	SNP	G	A	62	50	c.89C>T	c.(88-90)CCC>CTC	p.P30L
Pat_46	Pre-Treatment	ADAMTS4	9507	37	1	161163432	161163432	Missense_Mutation	SNP	G	A	268	244	c.1733C>T	c.(1732-1734)TCA>TTA	p.S578L
Pat_46	Pre-Treatment	F5	2153	37	1	169512194	169512194	Missense_Mutation	SNP	G	A	228	151	c.2134C>T	c.(2134-2136)CGT>TGT	p.R712C
Pat_46	Pre-Treatment	SELE	6401	37	1	169698486	169698486	Nonsense_Mutation	SNP	G	A	7	46	c.931C>T	c.(931-933)CAG>TAG	p.Q311*
Pat_46	Pre-Treatment	PAPPA2	60676	37	1	176709263	176709263	Missense_Mutation	SNP	C	T	19	124	c.4082C>T	c.(4081-4083)TCC>TTC	p.S1361F
Pat_46	Pre-Treatment	ASTN1	460	37	1	176833520	176833520	Missense_Mutation	SNP	C	T	20	94	c.3785G>A	c.(3784-3786)GGA>GAA	p.G1262E
Pat_46	Pre-Treatment	CACNA1E	777	37	1	181745241	181745241	Missense_Mutation	SNP	T	C	35	253	c.5144T>C	c.(5143-5145)CTC>CCC	p.L1715P
Pat_46	Pre-Treatment	HMCN1	83872	37	1	186024803	186024803	Missense_Mutation	SNP	C	T	43	210	c.7141C>T	c.(7141-7143)CAT>TAT	p.H2381Y
Pat_46	Pre-Treatment	PRG4	10216	37	1	186275983	186275983	Missense_Mutation	SNP	C	A	4	108	c.1132C>A	c.(1132-1134)CCC>ACC	p.P378T
Pat_46	Pre-Treatment	RGS21	431704	37	1	192335238	192335238	Nonsense_Mutation	SNP	G	A	11	13	c.443G>A	c.(442-444)TGG>TAG	p.W148*
Pat_46	Pre-Treatment	CRB1	23418	37	1	197404528	197404528	Missense_Mutation	SNP	G	A	8	49	c.3535G>A	c.(3535-3537)GAT>AAT	p.D1179N
Pat_46	Pre-Treatment	KIF14	9928	37	1	200574423	200574423	Missense_Mutation	SNP	C	G	3	62	c.1734G>C	c.(1732-1734)ATG>ATC	p.M578I
Pat_46	Pre-Treatment	SNRPE	6635	37	1	203834217	203834217	Missense_Mutation	SNP	C	T	19	94	c.193C>T	c.(193-195)CAT>TAT	p.H65Y
Pat_46	Pre-Treatment	C4BPA	722	37	1	207297538	207297538	Missense_Mutation	SNP	C	T	86	69	c.533C>T	c.(532-534)CCT>CTT	p.P178L
Pat_46	Pre-Treatment	CR1	1378	37	1	207762056	207762056	Missense_Mutation	SNP	G	A	11	36	c.4397G>A	c.(4396-4398)GGA>GAA	p.G1466E
Pat_46	Pre-Treatment	USH2A	7399	37	1	215844436	215844436	Missense_Mutation	SNP	C	T	54	27	c.14011G>A	c.(14011-14013)GAA>AAA	p.E4671K
Pat_46	Pre-Treatment	OBSCN	84033	37	1	228468465	228468465	Missense_Mutation	SNP	C	T	12	4	c.8165C>T	c.(8164-8166)TCC>TTC	p.S2722F
Pat_46	Pre-Treatment	SLC35F3	148641	37	1	234367322	234367322	Missense_Mutation	SNP	C	T	32	126	c.236C>T	c.(235-237)TCG>TTG	p.S79L
Pat_46	Pre-Treatment	RYR2	6262	37	1	237777611	237777611	Missense_Mutation	SNP	C	T	25	19	c.5183C>T	c.(5182-5184)CCC>CTC	p.P1728L
Pat_46	Pre-Treatment	FMN2	56776	37	1	240255852	240255852	Missense_Mutation	SNP	G	A	4	1	c.443G>A	c.(442-444)GGG>GAG	p.G148E

Pat_46	Pre-Treatment	FMN2	56776	37	1	240371051	240371051	Missense_Mutation	SNP	C	T	17	140	c.2939C>T	c.(2938-2940)CCT>CTT	p.P980L
Pat_46	Pre-Treatment	OR2L13	284521	37	1	248263515	248263515	Missense_Mutation	SNP	C	T	55	54	c.838C>T	c.(838-840)CTT>TTT	p.L280F
Pat_46	Pre-Treatment	TUBAL3	79861	37	10	5436006	5436006	Missense_Mutation	SNP	A	T	19	81	c.815T>A	c.(814-816)ATA>AAA	p.I272K
Pat_46	Pre-Treatment	OLAH	55301	37	10	15107598	15107598	Missense_Mutation	SNP	C	T	6	19	c.418C>T	c.(418-420)CGC>TGC	p.R140C
Pat_46	Pre-Treatment	FAM171A1	221061	37	10	15255489	15255489	Missense_Mutation	SNP	T	G	17	31	c.2098A>C	c.(2098-2100)AAG>CAG	p.K700Q
Pat_46	Pre-Treatment	ITGA8	8516	37	10	15590507	15590507	Missense_Mutation	SNP	C	T	24	39	c.2827G>A	c.(2827-2829)GAA>AAA	p.E943K
Pat_46	Pre-Treatment	ITGA8	8516	37	10	15646281	15646281	Missense_Mutation	SNP	C	T	15	37	c.2044G>A	c.(2044-2046)GGA>AGA	p.G682R
Pat_46	Pre-Treatment	NEBL	10529	37	10	21120192	21120192	Missense_Mutation	SNP	C	T	18	50	c.1604G>A	c.(1603-1605)GGA>GAA	p.G535E
Pat_46	Pre-Treatment	PIP4K2A	5305	37	10	22898620	22898620	Missense_Mutation	SNP	G	C	45	111	c.171C>G	c.(169-171)ATC>ATG	p.I57M
Pat_46	Pre-Treatment	PTCHD3	374308	37	10	27702954	27702954	Missense_Mutation	SNP	G	A	14	39	c.226C>T	c.(226-228)CCC>TCC	p.P76S
Pat_46	Pre-Treatment	MPP7	143098	37	10	28408594	28408594	Missense_Mutation	SNP	G	A	23	61	c.938C>T	c.(937-939)TCC>TTC	p.S313F
Pat_46	Pre-Treatment	ANKRD30A	91074	37	10	37490242	37490242	Missense_Mutation	SNP	G	A	7	27	c.2690G>A	c.(2689-2691)GGA>GAA	p.G897E
Pat_46	Pre-Treatment	ZNF37A	7587	37	10	38407040	38407040	Missense_Mutation	SNP	C	T	9	33	c.961C>T	c.(961-963)CAT>TAT	p.H321Y
Pat_46	Pre-Treatment	ALOX5	240	37	10	45939214	45939214	Missense_Mutation	SNP	G	A	7	17	c.1612G>A	c.(1612-1614)GAG>AAG	p.E538K
Pat_46	Pre-Treatment	FRMPD2	143162	37	10	49430394	49430394	Missense_Mutation	SNP	G	A	23	69	c.1417C>T	c.(1417-1419)CTT>TTT	p.L473F
Pat_46	Pre-Treatment	OGDHL	55753	37	10	50953927	50953927	Missense_Mutation	SNP	C	T	17	47	c.1393G>A	c.(1393-1395)GAT>AAT	p.D465N
Pat_46	Pre-Treatment	NCOA4	8031	37	10	51579247	51579247	Missense_Mutation	SNP	C	T	31	114	c.106C>T	c.(106-108)CGG>TGG	p.R36W
Pat_46	Pre-Treatment	PCDH15	65217	37	10	55955628	55955628	Missense_Mutation	SNP	G	A	11	34	c.1120C>T	c.(1120-1122)CCT>TCT	p.P374S
Pat_46	Pre-Treatment	ANK3	288	37	10	61829433	61829433	Missense_Mutation	SNP	C	T	8	42	c.11206G>A	c.(11206-11208)GAA>AAA	p.E3736K
Pat_46	Pre-Treatment	CTNNA3	29119	37	10	67862998	67862998	Missense_Mutation	SNP	C	T	10	30	c.1894G>A	c.(1894-1896)GAA>AAA	p.E632K
Pat_46	Pre-Treatment	COL13A1	1305	37	10	71712675	71712675	Missense_Mutation	SNP	G	A	7	25	c.2063G>A	c.(2062-2064)GGG>GAG	p.G688E
Pat_46	Pre-Treatment	OIT3	170392	37	10	74658610	74658610	Missense_Mutation	SNP	G	A	5	19	c.250G>A	c.(250-252)GCA>ACA	p.A84T
Pat_46	Pre-Treatment	C10orf55	414236	37	10	75671974	75671974	Missense_Mutation	SNP	G	A	12	61	c.29C>T	c.(28-30)TCG>TTG	p.S10L
Pat_46	Pre-Treatment	SFTPA1	653509	37	10	81373492	81373492	Splice_Site	SNP	G	A	24	69	c.371_splice	c.e6-1	p.A124_splice
Pat_46	Pre-Treatment	IFIT1	3434	37	10	91162729	91162729	Missense_Mutation	SNP	G	A	48	108	c.697G>A	c.(697-699)GAA>AAA	p.E233K
Pat_46	Pre-Treatment	CYP2C18	1562	37	10	96447594	96447594	Missense_Mutation	SNP	G	A	32	92	c.236G>A	c.(235-237)GGA>GAA	p.G79E
Pat_46	Pre-Treatment	TACC2	10579	37	10	123970436	123970436	Missense_Mutation	SNP	G	A	12	45	c.6496G>A	c.(6496-6498)GGG>AGG	p.G2166R
Pat_46	Pre-Treatment	GPR26	2849	37	10	125434378	125434378	Missense_Mutation	SNP	G	A	11	22	c.713G>A	c.(712-714)CGA>CAA	p.R238Q
Pat_46	Pre-Treatment	CPXM2	119587	37	10	125528202	125528202	Missense_Mutation	SNP	C	T	38	109	c.1139G>A	c.(1138-1140)GGC>GAC	p.G380D
Pat_46	Pre-Treatment	C10orf137	26098	37	10	127424384	127424384	Missense_Mutation	SNP	C	T	33	78	c.1669C>T	c.(1669-1671)CCA>TCA	p.P557S
Pat_46	Pre-Treatment	ADAM12	8038	37	10	127760213	127760213	Missense_Mutation	SNP	G	A	18	42	c.1165C>T	c.(1165-1167)CCC>TCC	p.P389S
Pat_46	Pre-Treatment	C10orf90	118611	37	10	128192921	128192921	Missense_Mutation	SNP	G	C	40	81	c.848C>G	c.(847-849)CCC>CGC	p.P283R
Pat_46	Pre-Treatment	OR52E2	119678	37	11	5080110	5080110	Missense_Mutation	SNP	G	A	12	23	c.748C>T	c.(748-750)CTT>TTT	p.L250F
Pat_46	Pre-Treatment	OR52E8	390079	37	11	5878290	5878290	Missense_Mutation	SNP	C	T	12	23	c.643G>A	c.(643-645)GAT>AAT	p.D215N
Pat_46	Pre-Treatment	OR52L1	338751	37	11	6007836	6007836	Missense_Mutation	SNP	C	T	6	28	c.325G>A	c.(325-327)GAG>AAG	p.E109K
Pat_46	Pre-Treatment	CNGA4	1262	37	11	6261737	6261737	Missense_Mutation	SNP	C	T	11	27	c.713C>T	c.(712-714)CCA>CTA	p.P238L
Pat_46	Pre-Treatment	DCHS1	8642	37	11	6662520	6662520	Missense_Mutation	SNP	G	A	13	53	c.325C>T	c.(325-327)CGT>TGT	p.R109C
Pat_46	Pre-Treatment	OR2AG1	144125	37	11	6806965	6806966	Missense_Mutation	DNP	GG	AA	11	30	c.697_698GG>AA	c.(697-699)GGG>AAG	p.G233K
Pat_46	Pre-Treatment	ZNF215	7762	37	11	6964847	6964847	Missense_Mutation	SNP	A	C	31	70	c.687A>C	c.(685-687)AAA>AAC	p.K229N
Pat_46	Pre-Treatment	NLRP14	338323	37	11	7064044	7064044	Missense_Mutation	SNP	G	A	15	46	c.787G>A	c.(787-789)GAA>AAA	p.E263K
Pat_46	Pre-Treatment	NLRP14	338323	37	11	7064261	7064261	Missense_Mutation	SNP	G	A	26	52	c.1004G>A	c.(1003-1005)AGA>AAA	p.R335K
Pat_46	Pre-Treatment	NLRP14	338323	37	11	7091675	7091675	Missense_Mutation	SNP	T	C	17	23	c.3134T>C	c.(3133-3135)CTA>CCA	p.L1045P
Pat_46	Pre-Treatment	ST5	6764	37	11	8751675	8751675	Missense_Mutation	SNP	G	A	28	55	c.1162C>T	c.(1162-1164)CCC>TCC	p.P388S
Pat_46	Pre-Treatment	IGSF22	283284	37	11	18731120	18731120	Missense_Mutation	SNP	C	T	11	35	c.2812G>A	c.(2812-2814)GAG>AAG	p.E938K
Pat_46	Pre-Treatment	GAS2	2620	37	11	22707294	22707294	Missense_Mutation	SNP	G	A	10	25	c.226G>A	c.(226-228)GAG>AAG	p.E76K
Pat_46	Pre-Treatment	CSTF3	1479	37	11	33124691	33124691	Missense_Mutation	SNP	G	A	18	32	c.625C>T	c.(625-627)CGG>TGG	p.R209W
Pat_46	Pre-Treatment	RAG2	5897	37	11	36615100	36615100	Missense_Mutation	SNP	G	A	32	86	c.619C>T	c.(619-621)CAT>TAT	p.H207Y

Pat_46	Pre-Treatment	PHF21A	51317	37	11	45987010	45987011	Missense_Mutation	DNP	GG	AA	13	40	c.848_849CC>TT	c.(847-849)CCC>CTT	p.P283L
Pat_46	Pre-Treatment	PTPRJ	5795	37	11	48134313	48134313	Missense_Mutation	SNP	C	T	58	98	c.130C>T	c.(130-132)CCT>TCT	p.P44S
Pat_46	Pre-Treatment	OR4A47	403253	37	11	48510571	48510571	Missense_Mutation	SNP	C	T	20	31	c.227C>T	c.(226-228)TCC>TTC	p.S76F
Pat_46	Pre-Treatment	TRIM48	79097	37	11	55032647	55032647	Missense_Mutation	SNP	G	A	49	24	c.316G>A	c.(316-318)GAG>AAG	p.E106K
Pat_46	Pre-Treatment	OR4C6	219432	37	11	55432600	55432600	Splice_Site	SNP	G	A	17	15	c.-41_splice	c.e3-1	
Pat_46	Pre-Treatment	OR5L2	26338	37	11	55594915	55594915	Missense_Mutation	SNP	C	T	143	90	c.221C>T	c.(220-222)TCC>TTC	p.S74F
Pat_46	Pre-Treatment	OR5AS1	219447	37	11	55798826	55798826	Missense_Mutation	SNP	C	T	13	64	c.932C>T	c.(931-933)TCA>TTA	p.S311L
Pat_46	Pre-Treatment	OR8H2	390151	37	11	55873258	55873258	Missense_Mutation	SNP	G	A	5	27	c.740G>A	c.(739-741)GGA>GAA	p.G247E
Pat_46	Pre-Treatment	OR8J1	219477	37	11	56128414	56128414	Missense_Mutation	SNP	C	T	22	29	c.692C>T	c.(691-693)TCA>TTA	p.S231L
Pat_46	Pre-Treatment	APLNR	187	37	11	57004463	57004463	Missense_Mutation	SNP	C	T	9	58	c.16G>A	c.(16-18)GAT>AAT	p.D6N
Pat_46	Pre-Treatment	SSRP1	6749	37	11	57099948	57099948	Missense_Mutation	SNP	G	A	55	239	c.781C>T	c.(781-783)CCC>TCC	p.P261S
Pat_46	Pre-Treatment	FAM111A	63901	37	11	58919839	58919839	Missense_Mutation	SNP	C	T	13	108	c.698C>T	c.(697-699)TCC>TTC	p.S233F
Pat_46	Pre-Treatment	OR4D11	219986	37	11	59271374	59271374	Missense_Mutation	SNP	G	A	64	44	c.326G>A	c.(325-327)GGG>GAG	p.G109E
Pat_46	Pre-Treatment	OR4D9	390199	37	11	59283079	59283079	Missense_Mutation	SNP	G	A	47	253	c.694G>A	c.(694-696)GGC>AGC	p.G232S
Pat_46	Pre-Treatment	MS4A2	2206	37	11	59861474	59861474	Missense_Mutation	SNP	G	A	28	133	c.575G>A	c.(574-576)GGA>GAA	p.G192E
Pat_46	Pre-Treatment	DAK	26007	37	11	61105584	61105584	Missense_Mutation	SNP	C	T	33	24	c.175C>T	c.(175-177)CAT>TAT	p.H59Y
Pat_46	Pre-Treatment	MTA2	9219	37	11	62366028	62366028	Missense_Mutation	SNP	G	A	63	315	c.274C>T	c.(274-276)CGG>TGG	p.R92W
Pat_46	Pre-Treatment	SLC22A25	387601	37	11	62933592	62933592	Missense_Mutation	SNP	C	T	48	30	c.1209G>A	c.(1207-1209)ATG>ATA	p.M403I
Pat_46	Pre-Treatment	SLC22A10	387775	37	11	63057642	63057642	Missense_Mutation	SNP	C	T	25	14	c.5C>T	c.(4-6)GCC>GTC	p.A2V
Pat_46	Pre-Treatment	SLC22A10	387775	37	11	63072267	63072267	Missense_Mutation	SNP	G	A	18	90	c.1504G>A	c.(1504-1506)GGA>AGA	p.G502R
Pat_46	Pre-Treatment	SLC22A12	116085	37	11	64359368	64359368	Missense_Mutation	SNP	G	A	22	24	c.340G>A	c.(340-342)GAG>AAG	p.E114K
Pat_46	Pre-Treatment	CDC42BPG	55561	37	11	64606627	64606627	Missense_Mutation	SNP	G	A	61	55	c.754C>T	c.(754-756)CAC>TAC	p.H252Y
Pat_46	Pre-Treatment	TM7SF2	7108	37	11	64883503	64883503	Missense_Mutation	SNP	G	A	54	45	c.1235G>A	c.(1234-1236)CGC>CAC	p.R412H
Pat_46	Pre-Treatment	CABP2	51475	37	11	67286622	67286622	Missense_Mutation	SNP	C	T	27	19	c.651G>A	c.(649-651)ATG>ATA	p.M217I
Pat_46	Pre-Treatment	PPFIA1	8500	37	11	70194471	70194471	Missense_Mutation	SNP	G	A	52	65	c.2108G>A	c.(2107-2109)CGA>CAA	p.R703Q
Pat_46	Pre-Treatment	ODZ4	26011	37	11	78381419	78381419	Missense_Mutation	SNP	C	T	3	5	c.5971G>A	c.(5971-5973)GAC>AAC	p.D1991N
Pat_46	Pre-Treatment	PICALM	8301	37	11	85718599	85718599	Missense_Mutation	SNP	G	A	78	82	c.793C>T	c.(793-795)CCA>TCA	p.P265S
Pat_46	Pre-Treatment	MTNR1B	4544	37	11	92715261	92715261	Missense_Mutation	SNP	T	A	49	49	c.872T>A	c.(871-873)GTC>GAC	p.V291D
Pat_46	Pre-Treatment	HEPHL1	341208	37	11	93808340	93808340	Missense_Mutation	SNP	G	A	6	5	c.1505G>A	c.(1504-1506)GGA>GAA	p.G502E
Pat_46	Pre-Treatment	TRPC6	7225	37	11	101342086	101342086	Missense_Mutation	SNP	C	T	16	31	c.2237G>A	c.(2236-2238)AGG>AAG	p.R746K
Pat_46	Pre-Treatment	HTR3A	3359	37	11	113848499	113848499	Missense_Mutation	SNP	G	A	7	8	c.92G>A	c.(91-93)AGG>AAG	p.R31K
Pat_46	Pre-Treatment	APOA4	337	37	11	116692155	116692155	Missense_Mutation	SNP	C	T	28	55	c.619G>A	c.(619-621)GAA>AAA	p.E207K
Pat_46	Pre-Treatment	TECTA	7007	37	11	121036027	121036027	Missense_Mutation	SNP	G	A	9	8	c.5318G>A	c.(5317-5319)CGA>CAA	p.R1773Q
Pat_46	Pre-Treatment	SPA17	53340	37	11	124564280	124564280	Missense_Mutation	SNP	G	A	8	21	c.394G>A	c.(394-396)GAG>AAG	p.E132K
Pat_46	Pre-Treatment	DCP1B	196513	37	12	2062350	2062350	Missense_Mutation	SNP	C	G	2	20	c.756G>C	c.(754-756)CAG>CAC	p.Q252H
Pat_46	Pre-Treatment	A2M	2	37	12	9232385	9232385	Missense_Mutation	SNP	T	A	7	11	c.2881A>T	c.(2881-2883)AAC>TAC	p.N961Y
Pat_46	Pre-Treatment	PZP	5858	37	12	9305466	9305466	Missense_Mutation	SNP	C	T	19	49	c.4075G>A	c.(4075-4077)GAT>AAT	p.D1359N
Pat_46	Pre-Treatment	PRB2	653247	37	12	11546515	11546515	Missense_Mutation	SNP	C	T	35	77	c.497G>A	c.(496-498)GGA>GAA	p.G166E
Pat_46	Pre-Treatment	PIK3C2G	5288	37	12	18699323	18699323	Missense_Mutation	SNP	C	T	6	11	c.3424C>T	c.(3424-3426)CGT>TGT	p.R1142C
Pat_46	Pre-Treatment	PIK3C2G	5288	37	12	18747456	18747456	Missense_Mutation	SNP	C	T	20	48	c.3917C>T	c.(3916-3918)TCT>TTT	p.S1306F
Pat_46	Pre-Treatment	PLCZ1	89869	37	12	18837172	18837172	Missense_Mutation	SNP	G	A	19	47	c.1633C>T	c.(1633-1635)CAT>TAT	p.H545Y
Pat_46	Pre-Treatment	CAPZA3	93661	37	12	18891857	18891857	Missense_Mutation	SNP	G	A	4	15	c.655G>A	c.(655-657)GCT>ACT	p.A219T
Pat_46	Pre-Treatment	ABCC9	10060	37	12	21997810	21997810	Missense_Mutation	SNP	C	T	8	30	c.3136G>A	c.(3136-3138)GGC>AGC	p.G1046S
Pat_46	Pre-Treatment	OVCH1	341350	37	12	29598333	29598333	Missense_Mutation	SNP	C	T	5	12	c.2759G>A	c.(2758-2760)GGA>GAA	p.G920E
Pat_46	Pre-Treatment	C12orf72	254013	37	12	31814975	31814975	Missense_Mutation	SNP	C	T	10	21	c.88C>T	c.(88-90)CCC>TCC	p.P30S
Pat_46	Pre-Treatment	PKP2	5318	37	12	33003862	33003862	Missense_Mutation	SNP	C	T	13	40	c.1216G>A	c.(1216-1218)GTT>ATT	p.V406I
Pat_46	Pre-Treatment	C12orf40	283461	37	12	40114899	40114899	Missense_Mutation	SNP	C	T	23	68	c.1805C>T	c.(1804-1806)TCT>TTT	p.S602F

Pat_46	Pre-Treatment	CACNB3	784	37	12	49218065	49218065	Missense_Mutation	SNP	G	A	4	24	c.316G>A	c.(316-318)GGG>AGG	p.G106R
Pat_46	Pre-Treatment	GALNT6	11226	37	12	51773135	51773135	Missense_Mutation	SNP	G	A	4	24	c.431C>T	c.(430-432)GCC>GTC	p.A144V
Pat_46	Pre-Treatment	KRT6B	3854	37	12	52841737	52841737	Missense_Mutation	SNP	C	T	32	59	c.1249G>A	c.(1249-1251)GAG>AAG	p.E417K
Pat_46	Pre-Treatment	ESPL1	9700	37	12	53673634	53673634	Missense_Mutation	SNP	G	A	4	120	c.2483G>A	c.(2482-2484)TGT>TAT	p.C828Y
Pat_46	Pre-Treatment	ESPL1	9700	37	12	53677195	53677195	Missense_Mutation	SNP	C	T	23	46	c.2950C>T	c.(2950-2952)CTT>TTT	p.L984F
Pat_46	Pre-Treatment	OR6C76	390326	37	12	55820086	55820086	Missense_Mutation	SNP	G	A	22	95	c.49G>A	c.(49-51)GAT>AAT	p.D17N
Pat_46	Pre-Treatment	ERBB3	2065	37	12	56482351	56482351	Missense_Mutation	SNP	C	T	120	193	c.899C>T	c.(898-900)TCC>TTC	p.S300F
Pat_46	Pre-Treatment	ERBB3	2065	37	12	56493646	56493646	Missense_Mutation	SNP	C	T	20	42	c.2962C>T	c.(2962-2964)CCT>TCT	p.P988S
Pat_46	Pre-Treatment	TSFM	10102	37	12	58179958	58179958	Missense_Mutation	SNP	C	T	3	6	c.244C>T	c.(244-246)CTC>TTC	p.L82F
Pat_46	Pre-Treatment	MDM2	4193	37	12	69233409	69233409	Missense_Mutation	SNP	C	T	21	55	c.1274C>T	c.(1273-1275)ACC>ATC	p.T425I
Pat_46	Pre-Treatment	SYT1	6857	37	12	79693221	79693221	Missense_Mutation	SNP	C	T	28	64	c.700C>T	c.(700-702)CGT>TGT	p.R234C
Pat_46	Pre-Treatment	ACSS3	79611	37	12	81503391	81503391	Missense_Mutation	SNP	G	A	14	40	c.364G>A	c.(364-366)GAA>AAA	p.E122K
Pat_46	Pre-Treatment	PPFIA2	8499	37	12	81657060	81657060	Missense_Mutation	SNP	C	T	5	10	c.3665G>A	c.(3664-3666)GGA>GAA	p.G1222E
Pat_46	Pre-Treatment	SCYL2	55681	37	12	100691888	100691888	Missense_Mutation	SNP	C	T	9	17	c.415C>T	c.(415-417)CCT>TCT	p.P139S
Pat_46	Pre-Treatment	SLC5A8	160728	37	12	101551118	101551118	Missense_Mutation	SNP	G	A	12	24	c.1772C>T	c.(1771-1773)GCT>GTT	p.A591V
Pat_46	Pre-Treatment	OAS1	4938	37	12	113357332	113357332	Nonsense_Mutation	SNP	G	T	22	55	c.1177G>T	c.(1177-1179)GAG>TAG	p.E393*
Pat_46	Pre-Treatment	CCDC60	160777	37	12	119909929	119909929	Missense_Mutation	SNP	G	A	33	75	c.301G>A	c.(301-303)GAA>AAA	p.E101K
Pat_46	Pre-Treatment	OASL	8638	37	12	121458618	121458618	Missense_Mutation	SNP	G	A	22	36	c.1291C>T	c.(1291-1293)CCC>TCC	p.P431S
Pat_46	Pre-Treatment	DNAH10	196385	37	12	124281297	124281297	Missense_Mutation	SNP	G	A	23	42	c.1727G>A	c.(1726-1728)CGA>CAA	p.R576Q
Pat_46	Pre-Treatment	RIMBP2	23504	37	12	130926662	130926662	Missense_Mutation	SNP	G	A	4	8	c.1184C>T	c.(1183-1185)TCC>TTC	p.S395F
Pat_46	Pre-Treatment	GJB2	2706	37	13	20763467	20763467	Missense_Mutation	SNP	G	A	15	36	c.254C>T	c.(253-255)TCC>TTC	p.S85F
Pat_46	Pre-Treatment	PAN3	255967	37	13	28846200	28846200	Nonsense_Mutation	SNP	C	T	16	45	c.1603C>T	c.(1603-1605)CAG>TAG	p.Q535*
Pat_46	Pre-Treatment	RXFP2	122042	37	13	32355867	32355867	Missense_Mutation	SNP	C	T	21	32	c.845C>T	c.(844-846)TCG>TTG	p.S282L
Pat_46	Pre-Treatment	STARD13	90627	37	13	33704213	33704213	Missense_Mutation	SNP	C	T	11	17	c.601G>A	c.(601-603)GAA>AAA	p.E201K
Pat_46	Pre-Treatment	SPG20	23111	37	13	36905658	36905658	Missense_Mutation	SNP	G	A	20	72	c.886C>T	c.(886-888)CCT>TCT	p.P296S
Pat_46	Pre-Treatment	RB1	5925	37	13	48934240	48934240	Missense_Mutation	SNP	C	T	16	53	c.695C>T	c.(694-696)CCC>CTC	p.P232L
Pat_46	Pre-Treatment	LECT1	11061	37	13	53298197	53298197	Missense_Mutation	SNP	C	T	12	25	c.403G>A	c.(403-405)GCG>ACG	p.A135T
Pat_46	Pre-Treatment	SCEL	8796	37	13	78130735	78130735	Missense_Mutation	SNP	G	A	58	133	c.48G>A	c.(46-48)ATG>ATA	p.M16I
Pat_46	Pre-Treatment	DZIP1	22873	37	13	96241436	96241436	Missense_Mutation	SNP	G	A	10	32	c.1999C>T	c.(1999-2001)CCT>TCT	p.P667S
Pat_46	Pre-Treatment	ATP11A	23250	37	13	113508817	113508817	Missense_Mutation	SNP	G	A	3	51	c.2216G>A	c.(2215-2217)GGG>GAG	p.G739E
Pat_46	Pre-Treatment	OR4Q3	441669	37	14	20216488	20216488	Missense_Mutation	SNP	A	T	17	29	c.902A>T	c.(901-903)AAG>ATG	p.K301M
Pat_46	Pre-Treatment	OR11G2	390439	37	14	20665672	20665672	Missense_Mutation	SNP	G	A	4	20	c.178G>A	c.(178-180)GAG>AAG	p.E60K
Pat_46	Pre-Treatment	MYH6	4624	37	14	23876313	23876314	Missense_Mutation	DNP	GG	AA	41	113	c.119_120CC>TT	c.(118-120)CCC>CTT	p.P40L
Pat_46	Pre-Treatment	NPAS3	64067	37	14	33684488	33684488	Missense_Mutation	SNP	C	T	26	67	c.241C>T	c.(241-243)CCT>TCT	p.P81S
Pat_46	Pre-Treatment	MIPOL1	145282	37	14	37838774	37838774	Missense_Mutation	SNP	C	T	19	47	c.881C>T	c.(880-882)TCA>TTA	p.S294L
Pat_46	Pre-Treatment	RPL10L	140801	37	14	47120366	47120366	Missense_Mutation	SNP	G	A	15	54	c.574C>T	c.(574-576)CCT>TCT	p.P192S
Pat_46	Pre-Treatment	PTGDR	5729	37	14	52741476	52741476	Missense_Mutation	SNP	G	A	4	25	c.874G>A	c.(874-876)GAT>AAT	p.D292N
Pat_46	Pre-Treatment	C14orf101	54916	37	14	57070568	57070568	Missense_Mutation	SNP	C	T	3	42	c.380C>T	c.(379-381)GCG>GTG	p.A127V
Pat_46	Pre-Treatment	PPM1A	5494	37	14	60749713	60749713	Nonsense_Mutation	SNP	A	T	19	42	c.292A>T	c.(292-294)AAG>TAG	p.K98*
Pat_46	Pre-Treatment	PPM1A	5494	37	14	60752390	60752391	Missense_Mutation	DNP	CC	TT	24	83	c.883_884CC>TT	c.(883-885)CCC>TTC	p.P295F
Pat_46	Pre-Treatment	PTPN21	11099	37	14	88951470	88951470	Missense_Mutation	SNP	G	A	25	39	c.1028C>T	c.(1027-1029)CCG>CTG	p.P343L
Pat_46	Pre-Treatment	TDP1	55775	37	14	90446978	90446978	Splice_Site	SNP	T	C	9	22	c.884_splice	c.e8+2	p.G295_splice
Pat_46	Pre-Treatment	CATSPERB	79820	37	14	92136196	92136196	Missense_Mutation	SNP	G	A	9	25	c.1249C>T	c.(1249-1251)CAT>TAT	p.H417Y
Pat_46	Pre-Treatment	CATSPERB	79820	37	14	92159779	92159779	Missense_Mutation	SNP	C	T	13	43	c.661G>A	c.(661-663)GAT>AAT	p.D221N
Pat_46	Pre-Treatment	KIAA1409	57578	37	14	93944038	93944038	Missense_Mutation	SNP	G	A	36	112	c.52G>A	c.(52-54)GAA>AAA	p.E18K
Pat_46	Pre-Treatment	PRIMA1	145270	37	14	94245551	94245551	Missense_Mutation	SNP	G	A	7	10	c.200C>T	c.(199-201)CCG>CTG	p.P67L
Pat_46	Pre-Treatment	SERPINA4	5267	37	14	95029923	95029923	Missense_Mutation	SNP	C	T	15	37	c.104C>T	c.(103-105)TCC>TTC	p.S35F

Pat_46	Pre-Treatment	C14orf177	283598	37	14	99182719	99182719	Missense_Mutation	SNP	G	T	3	4	c.191G>T	c.(190-192)AGG>ATG	p.R64M
Pat_46	Pre-Treatment	TECPR2	9895	37	14	102900690	102900691	Missense_Mutation	DNP	GG	AA	22	51	.1536_1537GG>A	534-1539)CTGGGC>CTA	p.G513S
Pat_46	Pre-Treatment	TECPR2	9895	37	14	102901094	102901094	Missense_Mutation	SNP	C	T	9	22	c.1940C>T	c.(1939-1941)TCA>TTA	p.S647L
Pat_46	Pre-Treatment	CDC42BPB	9578	37	14	103434988	103434988	Missense_Mutation	SNP	T	A	24	55	c.2061A>T	c.(2059-2061)AAA>AAT	p.K687N
Pat_46	Pre-Treatment	AKT1	207	37	14	105240265	105240265	Missense_Mutation	SNP	T	C	9	9	c.686A>G	c.(685-687)TAC>TGC	p.Y229C
Pat_46	Pre-Treatment	TJP1	7082	37	15	30026556	30026556	Missense_Mutation	SNP	T	C	22	19	c.1438A>G	c.(1438-1440)AGA>GGA	p.R480G
Pat_46	Pre-Treatment	BUB1B	701	37	15	40457265	40457265	Missense_Mutation	SNP	C	T	65	81	c.47C>T	c.(46-48)TCC>TTC	p.S16F
Pat_46	Pre-Treatment	RPAP1	26015	37	15	41817292	41817293	Nonsense_Mutation	DNP	GG	AA	10	16	.1971_1972CC>T	969-1974)CCCCAA>CCT	p.Q658*
Pat_46	Pre-Treatment	TYRO3	7301	37	15	41860520	41860520	Missense_Mutation	SNP	G	A	4	59	c.1067G>A	c.(1066-1068)GGA>GAA	p.G356E
Pat_46	Pre-Treatment	GANC	2595	37	15	42632068	42632068	Missense_Mutation	SNP	C	T	22	21	c.2045C>T	c.(2044-2046)TCT>TTT	p.S682F
Pat_46	Pre-Treatment	ZFP106	64397	37	15	42734497	42734498	Missense_Mutation	DNP	GA	AT	17	47	.3467_3468TC>A	c.(3466-3468)TTC>TAT	p.F1156Y
Pat_46	Pre-Treatment	UNC13C	440279	37	15	54305661	54305661	Nonsense_Mutation	SNP	G	A	25	25	c.561G>A	c.(559-561)TGG>TGA	p.W187*
Pat_46	Pre-Treatment	RNF111	54778	37	15	59323443	59323443	Missense_Mutation	SNP	C	T	29	54	c.422C>T	c.(421-423)CCT>CTT	p.P141L
Pat_46	Pre-Treatment	FAM81A	145773	37	15	59752164	59752164	Missense_Mutation	SNP	C	T	3	20	c.53C>T	c.(52-54)TCC>TTC	p.S18F
Pat_46	Pre-Treatment	DENND4A	10260	37	15	66048767	66048767	Missense_Mutation	SNP	G	A	19	40	c.22C>T	c.(22-24)CGT>TGT	p.R8C
Pat_46	Pre-Treatment	LRRC49	54839	37	15	71329552	71329552	Missense_Mutation	SNP	G	A	12	26	c.1738G>A	c.(1738-1740)GGA>AGA	p.G580R
Pat_46	Pre-Treatment	PARP6	56965	37	15	72552884	72552884	Missense_Mutation	SNP	G	A	168	156	c.691C>T	c.(691-693)CCC>TCC	p.P231S
Pat_46	Pre-Treatment	HCN4	10021	37	15	73616108	73616108	Missense_Mutation	SNP	G	A	12	13	c.2326C>T	c.(2326-2328)CCG>TCG	p.P776S
Pat_46	Pre-Treatment	CYP11A1	1583	37	15	74630935	74630935	Missense_Mutation	SNP	C	T	50	62	c.1411G>A	c.(1411-1413)GAG>AAG	p.E471K
Pat_46	Pre-Treatment	MAN2C1	4123	37	15	75648366	75648366	Missense_Mutation	SNP	G	A	3	3	c.3004C>T	c.(3004-3006)CTC>TTC	p.L1002F
Pat_46	Pre-Treatment	RASGRF1	5923	37	15	79296299	79296299	Missense_Mutation	SNP	C	T	10	36	c.2342G>A	c.(2341-2343)GGC>GAC	p.G781D
Pat_46	Pre-Treatment	KIAA1199	57214	37	15	81201454	81201454	Missense_Mutation	SNP	A	G	21	34	c.1604A>G	c.(1603-1605)AAG>AGG	p.K535R
Pat_46	Pre-Treatment	TMC3	342125	37	15	81633741	81633741	Nonsense_Mutation	SNP	G	A	4	30	c.1834C>T	c.(1834-1836)CGA>TGA	p.R612*
Pat_46	Pre-Treatment	BNC1	646	37	15	83935634	83935634	Missense_Mutation	SNP	G	A	36	119	c.389C>T	c.(388-390)GCC>GTC	p.A130V
Pat_46	Pre-Treatment	ALPK3	57538	37	15	85400266	85400266	Missense_Mutation	SNP	C	T	5	40	c.2903C>T	c.(2902-2904)CCA>CTA	p.P968L
Pat_46	Pre-Treatment	SLCO3A1	28232	37	15	92671649	92671649	Missense_Mutation	SNP	C	T	48	162	c.1442C>T	c.(1441-1443)TCC>TTC	p.S481F
Pat_46	Pre-Treatment	RAB11FIP3	9727	37	16	553054	553054	Missense_Mutation	SNP	C	T	16	22	c.1352C>T	c.(1351-1353)TCC>TTC	p.S451F
Pat_46	Pre-Treatment	WDR90	197335	37	16	715701	715701	Missense_Mutation	SNP	C	T	39	69	c.4334C>T	c.(4333-4335)CCC>CTC	p.P1445L
Pat_46	Pre-Treatment	CLDN9	9080	37	16	3063829	3063829	Missense_Mutation	SNP	C	T	4	17	c.466C>T	c.(466-468)CTC>TTC	p.L156F
Pat_46	Pre-Treatment	ZSCAN10	84891	37	16	3140474	3140474	Missense_Mutation	SNP	C	T	22	67	c.796G>A	c.(796-798)GGG>AGG	p.G266R
Pat_46	Pre-Treatment	BTBD12	84464	37	16	3639345	3639345	Missense_Mutation	SNP	G	A	19	48	c.4294C>T	c.(4294-4296)CCC>TCC	p.P1432S
Pat_46	Pre-Treatment	TXNDC11	51061	37	16	11781756	11781756	Nonsense_Mutation	SNP	G	A	22	38	c.2191C>T	c.(2191-2193)CAG>TAG	p.Q731*
Pat_46	Pre-Treatment	MYH11	4629	37	16	15847317	15847317	Missense_Mutation	SNP	T	G	20	49	c.1798A>C	c.(1798-1800)AAT>CAT	p.N600H
Pat_46	Pre-Treatment	ABCC1	4363	37	16	16230351	16230351	Missense_Mutation	SNP	C	T	10	15	c.4142C>T	c.(4141-4143)TCG>TTG	p.S1381L
Pat_46	Pre-Treatment	SMG1	23049	37	16	18902236	18902236	Missense_Mutation	SNP	A	C	17	52	c.557T>G	c.(556-558)GTT>GGT	p.V186G
Pat_46	Pre-Treatment	COQ7	10229	37	16	19088679	19088679	Missense_Mutation	SNP	G	A	9	11	c.559G>A	c.(559-561)GAC>AAC	p.D187N
Pat_46	Pre-Treatment	ACSM5	54988	37	16	20451185	20451185	Missense_Mutation	SNP	C	T	7	36	c.1600C>T	c.(1600-1602)CGG>TGG	p.R534W
Pat_46	Pre-Treatment	SLC7A5P2	387254	37	16	21531296	21531297	Missense_Mutation	DNP	GG	AA	8	55	c.390_391CC>TT	(388-393)TTCCTC>TTTTT	p.L131F
Pat_46	Pre-Treatment	CACNG3	10368	37	16	24358111	24358111	Missense_Mutation	SNP	G	A	9	36	c.268G>A	c.(268-270)GAA>AAA	p.E90K
Pat_46	Pre-Treatment	GSG1L	146395	37	16	27802741	27802742	Missense_Mutation	DNP	CC	TT	11	21	c.945_946GG>AA	943-948)CAGGAA>CAAA	p.E316K
Pat_46	Pre-Treatment	NFATC2IP	84901	37	16	28975053	28975053	Missense_Mutation	SNP	C	T	21	44	c.1129C>T	c.(1129-1131)CAC>TAC	p.H377Y
Pat_46	Pre-Treatment	SEZ6L2	26470	37	16	29891358	29891359	Missense_Mutation	DNP	GG	AA	3	10	.1399_1400CC>T	c.(1399-1401)CCC>TTC	p.P467F
Pat_46	Pre-Treatment	SETD1A	9739	37	16	30975992	30975992	Missense_Mutation	SNP	C	T	41	80	c.929C>T	c.(928-930)TCC>TTC	p.S310F
Pat_46	Pre-Treatment	ADCY7	113	37	16	50339705	50339705	Missense_Mutation	SNP	C	T	22	28	c.1697C>T	c.(1696-1698)TCC>TTC	p.S566F
Pat_46	Pre-Treatment	SALL1	6299	37	16	51172844	51172844	Missense_Mutation	SNP	G	A	9	23	c.3289C>T	c.(3289-3291)CCT>TCT	p.P1097S
Pat_46	Pre-Treatment	NLRC5	84166	37	16	57063972	57063972	Missense_Mutation	SNP	C	T	26	53	c.2393C>T	c.(2392-2394)CCT>CTT	p.P798L
Pat_46	Pre-Treatment	CNOT1	23019	37	16	58589203	58589203	Missense_Mutation	SNP	G	A	19	41	c.2843C>T	c.(2842-2844)TCC>TTC	p.S948F

Pat_46	Pre-Treatment	FHOD1	29109	37	16	67281301	67281301	Nonsense_Mutation	SNP	C	A	17	17	c.13G>T	c.(13-15)GAA>TAA	p.E5*
Pat_46	Pre-Treatment	HYDIN	54768	37	16	70891632	70891632	Missense_Mutation	SNP	G	A	6	67	c.12268C>T	c.(12268-12270)CTC>TTC	p.L4090F
Pat_46	Pre-Treatment	TAT	6898	37	16	71610233	71610233	Missense_Mutation	SNP	G	A	17	24	c.86C>T	c.(85-87)TCT>TTT	p.S29F
Pat_46	Pre-Treatment	ADAT1	23536	37	16	75637046	75637046	Missense_Mutation	SNP	A	G	43	83	c.1313T>C	c.(1312-1314)CTC>CCC	p.L438P
Pat_46	Pre-Treatment	CDYL2	124359	37	16	80718827	80718827	Missense_Mutation	SNP	G	A	14	23	c.224C>T	c.(223-225)TCC>TTC	p.S75F
Pat_46	Pre-Treatment	CDH13	1012	37	16	83065713	83065713	Missense_Mutation	SNP	A	G	9	5	c.256A>G	c.(256-258)AAC>GAC	p.N86D
Pat_46	Pre-Treatment	PRDM7	11105	37	16	90126912	90126912	Missense_Mutation	SNP	G	T	4	79	c.1070C>A	c.(1069-1071)TCT>TAT	p.S357Y
Pat_46	Pre-Treatment	TRPV3	162514	37	17	3430168	3430168	Missense_Mutation	SNP	A	C	11	15	c.1557T>G	c.(1555-1557)GAT>GAG	p.D519E
Pat_46	Pre-Treatment	TEKT1	83659	37	17	6716194	6716194	Missense_Mutation	SNP	C	T	25	95	c.808G>A	c.(808-810)GAT>AAT	p.D270N
Pat_46	Pre-Treatment	WRAP53	55135	37	17	7604862	7604862	Missense_Mutation	SNP	C	T	21	55	c.817C>T	c.(817-819)CAC>TAC	p.H273Y
Pat_46	Pre-Treatment	ARHGEF15	22899	37	17	8216390	8216390	Missense_Mutation	SNP	C	T	21	58	c.752C>T	c.(751-753)CCC>CTC	p.P251L
Pat_46	Pre-Treatment	USP43	124739	37	17	9631397	9631397	Missense_Mutation	SNP	C	T	6	15	c.2462C>T	c.(2461-2463)TCC>TTC	p.S821F
Pat_46	Pre-Treatment	MYH1	4619	37	17	10399641	10399641	Missense_Mutation	SNP	C	T	28	52	c.4882G>A	c.(4882-4884)GAA>AAA	p.E1628K
Pat_46	Pre-Treatment	MYH2	4620	37	17	10432384	10432384	Missense_Mutation	SNP	C	T	10	25	c.3367G>A	c.(3367-3369)GAG>AAG	p.E1123K
Pat_46	Pre-Treatment	RICH2	9912	37	17	12847457	12847457	Missense_Mutation	SNP	G	A	14	24	c.805G>A	c.(805-807)GCC>ACC	p.A269T
Pat_46	Pre-Treatment	KIAA0100	9703	37	17	26961586	26961586	Missense_Mutation	SNP	G	A	17	46	c.3019C>T	c.(3019-3021)CTT>TTT	p.L1007F
Pat_46	Pre-Treatment	PHF12	57649	37	17	27248740	27248740	Missense_Mutation	SNP	G	A	13	53	c.802C>T	c.(802-804)CCC>TCC	p.P268S
Pat_46	Pre-Treatment	NF1	4763	37	17	29677227	29677227	Nonsense_Mutation	SNP	C	T	24	59	c.7348C>T	c.(7348-7350)CGA>TGA	p.R2450*
Pat_46	Pre-Treatment	ACCN1	40	37	17	31350879	31350879	Missense_Mutation	SNP	G	A	12	12	c.1196C>T	c.(1195-1197)TCA>TTA	p.S399L
Pat_46	Pre-Treatment	ACCN1	40	37	17	31438943	31438943	Missense_Mutation	SNP	C	T	32	74	c.698G>A	c.(697-699)GGA>GAA	p.G233E
Pat_46	Pre-Treatment	UNC45B	146862	37	17	33491151	33491151	Missense_Mutation	SNP	G	A	65	202	c.1117G>A	c.(1117-1119)GAT>AAT	p.D373N
Pat_46	Pre-Treatment	SLFN12L	342615	37	17	33802259	33802259	Missense_Mutation	SNP	C	T	10	19	c.1537G>A	c.(1537-1539)GAG>AAG	p.E513K
Pat_46	Pre-Treatment	KRT32	3882	37	17	39619092	39619092	Missense_Mutation	SNP	C	T	22	23	c.1207G>A	c.(1207-1209)GAG>AAG	p.E403K
Pat_46	Pre-Treatment	KRT9	3857	37	17	39727863	39727863	Missense_Mutation	SNP	C	T	4	8	c.382G>A	c.(382-384)GGG>AGG	p.G128R
Pat_46	Pre-Treatment	KRT14	3861	37	17	39742707	39742707	Missense_Mutation	SNP	G	A	17	38	c.380C>T	c.(379-381)GCC>GTC	p.A127V
Pat_46	Pre-Treatment	WNK4	65266	37	17	40932960	40932960	Missense_Mutation	SNP	G	A	55	31	c.244G>A	c.(244-246)GAC>AAC	p.D82N
Pat_46	Pre-Treatment	MEOX1	4222	37	17	41719375	41719375	Missense_Mutation	SNP	C	T	47	65	c.668G>A	c.(667-669)AGG>AAG	p.R223K
Pat_46	Pre-Treatment	TMEM101	84336	37	17	42092239	42092239	Missense_Mutation	SNP	A	G	3	67	c.82T>C	c.(82-84)TTT>CTT	p.F28L
Pat_46	Pre-Treatment	KIAA1267	284058	37	17	44249109	44249109	Missense_Mutation	SNP	G	A	33	55	c.401C>T	c.(400-402)TCC>TTC	p.S134F
Pat_46	Pre-Treatment	KPNA2	3838	37	17	66033562	66033562	Missense_Mutation	SNP	C	T	31	84	c.164C>T	c.(163-165)TCA>TTA	p.S55L
Pat_46	Pre-Treatment	C17orf28	283987	37	17	72959073	72959073	Missense_Mutation	SNP	C	T	15	47	c.491G>A	c.(490-492)CGG>CAG	p.R164Q
Pat_46	Pre-Treatment	FOXJ1	2302	37	17	74133889	74133889	Missense_Mutation	SNP	C	A	3	11	c.811G>T	c.(811-813)GGG>TGG	p.G271W
Pat_46	Pre-Treatment	9-Sep	10801	37	17	75398213	75398213	Missense_Mutation	SNP	C	T	18	42	c.149C>T	c.(148-150)CCC>CTC	p.P50L
Pat_46	Pre-Treatment	LGALS3BP	3959	37	17	76968668	76968668	Missense_Mutation	SNP	G	A	4	33	c.748C>T	c.(748-750)CTC>TTC	p.L250F
Pat_46	Pre-Treatment	SMCHD1	23347	37	18	2750443	2750443	Missense_Mutation	SNP	C	T	5	7	c.4103C>T	c.(4102-4104)CCC>CTC	p.P1368L
Pat_46	Pre-Treatment	TXNDC2	84203	37	18	9887184	9887184	Missense_Mutation	SNP	G	C	30	77	c.708G>C	c.(706-708)GAG>GAC	p.E236D
Pat_46	Pre-Treatment	ANKRD30B	374860	37	18	14799105	14799105	Missense_Mutation	SNP	C	T	11	33	c.2035C>T	c.(2035-2037)CCT>TCT	p.P679S
Pat_46	Pre-Treatment	NPC1	4864	37	18	21134821	21134821	Nonsense_Mutation	SNP	A	T	15	43	c.1454T>A	c.(1453-1455)TTA>TAA	p.L485*
Pat_46	Pre-Treatment	NPC1	4864	37	18	21134840	21134840	Missense_Mutation	SNP	A	T	20	46	c.1435T>A	c.(1435-1437)TGC>AGC	p.C479S
Pat_46	Pre-Treatment	LAMA3	3909	37	18	21487610	21487610	Missense_Mutation	SNP	G	A	51	131	c.6815G>A	c.(6814-6816)GGT>GAT	p.G2272D
Pat_46	Pre-Treatment	CDH2	1000	37	18	25570308	25570308	Missense_Mutation	SNP	C	T	14	34	c.1351G>A	c.(1351-1353)GAC>AAC	p.D451N
Pat_46	Pre-Treatment	DSC3	1825	37	18	28584314	28584314	Missense_Mutation	SNP	G	A	8	17	c.1907C>T	c.(1906-1908)TCA>TTA	p.S636L
Pat_46	Pre-Treatment	DSC2	1824	37	18	28672144	28672144	Nonsense_Mutation	SNP	T	A	16	30	c.274A>T	c.(274-276)AGA>TGA	p.R92*
Pat_46	Pre-Treatment	DSC1	1823	37	18	28714650	28714651	Missense_Mutation	DNP	AT	TA	11	18	.1760_1761AT>T	c.(1759-1761)AAT>ATA	p.N587I
Pat_46	Pre-Treatment	KIAA1012	22878	37	18	29470717	29470717	Missense_Mutation	SNP	C	T	22	80	c.1709G>A	c.(1708-1710)CGA>CAA	p.R570Q
Pat_46	Pre-Treatment	RIT2	6014	37	18	40695456	40695456	Missense_Mutation	SNP	G	A	32	61	c.29C>T	c.(28-30)TCC>TTC	p.S10F
Pat_46	Pre-Treatment	SLC14A1	6563	37	18	43319493	43319493	Missense_Mutation	SNP	G	A	19	39	c.812G>A	c.(811-813)GGA>GAA	p.G271E

Pat_46	Pre-Treatment	PSTPIP2	9050	37	18	43570702	43570702	Missense_Mutation	SNP	G	A	6	13	c.941C>T	c.(940-942)CCT>CTT	p.P314L
Pat_46	Pre-Treatment	TCEB3B	51224	37	18	44560363	44560363	Missense_Mutation	SNP	C	T	4	8	c.1273G>A	c.(1273-1275)GAT>AAT	p.D425N
Pat_46	Pre-Treatment	TCEB3B	51224	37	18	44561172	44561172	Missense_Mutation	SNP	C	T	6	18	c.464G>A	c.(463-465)AGA>AAA	p.R155K
Pat_46	Pre-Treatment	DCC	1630	37	18	50432428	50432428	Missense_Mutation	SNP	C	T	13	58	c.427C>T	c.(427-429)CTT>TTT	p.L143F
Pat_46	Pre-Treatment	DCC	1630	37	18	50741963	50741963	Missense_Mutation	SNP	C	T	33	88	c.1907C>T	c.(1906-1908)TCA>TTA	p.S636L
Pat_46	Pre-Treatment	ALPK2	115701	37	18	56246363	56246363	Missense_Mutation	SNP	G	A	24	54	c.1645C>T	c.(1645-1647)CCG>TCG	p.P549S
Pat_46	Pre-Treatment	SERPINB7	8710	37	18	61465919	61465919	Missense_Mutation	SNP	G	A	36	92	c.536G>A	c.(535-537)GGC>GAC	p.G179D
Pat_46	Pre-Treatment	CDH7	1005	37	18	63547837	63547837	Missense_Mutation	SNP	G	A	11	20	c.2065G>A	c.(2065-2067)GAA>AAA	p.E689K
Pat_46	Pre-Treatment	ZNF516	9658	37	18	74092154	74092154	Missense_Mutation	SNP	G	A	17	38	c.1916C>T	c.(1915-1917)ACC>ATC	p.T639I
Pat_46	Pre-Treatment	SALL3	27164	37	18	76753541	76753541	Missense_Mutation	SNP	C	T	3	14	c.1550C>T	c.(1549-1551)CCC>CTC	p.P517L
Pat_46	Pre-Treatment	HCN2	610	37	19	613987	613987	Missense_Mutation	SNP	C	T	3	70	c.1961C>T	c.(1960-1962)ACG>ATG	p.T654M
Pat_46	Pre-Treatment	CNN2	1265	37	19	1037859	1037859	Missense_Mutation	SNP	C	T	32	28	c.890C>T	c.(889-891)CCT>CTT	p.P297L
Pat_46	Pre-Treatment	ZNF556	80032	37	19	2877942	2877942	Missense_Mutation	SNP	C	T	16	6	c.986C>T	c.(985-987)TCC>TTC	p.S329F
Pat_46	Pre-Treatment	PIP5K1C	23396	37	19	3661061	3661061	Missense_Mutation	SNP	G	A	50	25	c.371C>T	c.(370-372)CCC>CTC	p.P124L
Pat_46	Pre-Treatment	ZNF557	79230	37	19	7083094	7083094	Missense_Mutation	SNP	A	G	3	63	c.611A>G	c.(610-612)AAT>AGT	p.N204S
Pat_46	Pre-Treatment	MUC16	94025	37	19	9045834	9045834	Missense_Mutation	SNP	C	T	20	16	c.35797G>A	c.(35797-35799)GAA>AAA	p.E11933K
Pat_46	Pre-Treatment	MUC16	94025	37	19	9045848	9045848	Missense_Mutation	SNP	G	A	22	14	c.35783C>T	c.(35782-35784)TCA>TTA	p.S11928L
Pat_46	Pre-Treatment	MUC16	94025	37	19	9068949	9068949	Missense_Mutation	SNP	G	A	22	18	c.18497C>T	c.(18496-18498)TCT>TTT	p.S6166F
Pat_46	Pre-Treatment	ZNF799	90576	37	19	12501446	12501446	Missense_Mutation	SNP	T	C	3	28	c.1766A>G	c.(1765-1767)GAA>GGA	p.E589G
Pat_46	Pre-Treatment	CYP4F22	126410	37	19	15651274	15651274	Missense_Mutation	SNP	T	C	41	39	c.685T>C	c.(685-687)TAT>CAT	p.Y229H
Pat_46	Pre-Treatment	OR10H2	26538	37	19	15839088	15839088	Missense_Mutation	SNP	C	T	13	14	c.235C>T	c.(235-237)CCG>TCG	p.P79S
Pat_46	Pre-Treatment	USHBP1	83878	37	19	17367350	17367350	Missense_Mutation	SNP	C	T	41	26	c.1400G>A	c.(1399-1401)GGG>GAG	p.G467E
Pat_46	Pre-Treatment	ZNF93	81931	37	19	20045182	20045182	Missense_Mutation	SNP	A	G	5	71	c.1418A>G	c.(1417-1419)AAA>AGA	p.K473R
Pat_46	Pre-Treatment	ZNF93	81931	37	19	20045266	20045266	Missense_Mutation	SNP	A	G	5	69	c.1502A>G	c.(1501-1503)AAA>AGA	p.K501R
Pat_46	Pre-Treatment	ZNF626	199777	37	19	20807643	20807643	Missense_Mutation	SNP	C	T	3	90	c.1040G>A	c.(1039-1041)GGC>GAC	p.G347D
Pat_46	Pre-Treatment	ZNF626	199777	37	19	20808006	20808006	Missense_Mutation	SNP	T	C	4	78	c.677A>G	c.(676-678)GAG>GGG	p.E226G
Pat_46	Pre-Treatment	ZNF626	199777	37	19	20808090	20808090	Missense_Mutation	SNP	C	T	5	61	c.593G>A	c.(592-594)GGG>GAG	p.G198E
Pat_46	Pre-Treatment	ZNF257	113835	37	19	22271507	22271507	Missense_Mutation	SNP	G	A	20	77	c.955G>A	c.(955-957)GAA>AAA	p.E319K
Pat_46	Pre-Treatment	ZNF676	163223	37	19	22363003	22363003	Missense_Mutation	SNP	T	C	24	73	c.1516A>G	c.(1516-1518)AAA>GAA	p.K506E
Pat_46	Pre-Treatment	ZNF676	163223	37	19	22363008	22363008	Missense_Mutation	SNP	C	G	3	91	c.1511G>C	c.(1510-1512)CGC>CCC	p.R504P
Pat_46	Pre-Treatment	ZNF98	148198	37	19	22574629	22574629	Missense_Mutation	SNP	C	T	21	60	c.1408G>A	c.(1408-1410)GCT>ACT	p.A470T
Pat_46	Pre-Treatment	ZNF99	7652	37	19	22939400	22939400	Missense_Mutation	SNP	G	C	3	81	c.2771C>G	c.(2770-2772)GCT>GGT	p.A924G
Pat_46	Pre-Treatment	ZNF99	7652	37	19	22942448	22942448	Missense_Mutation	SNP	T	A	3	5	c.326A>T	c.(325-327)GAT>GTT	p.D109V
Pat_46	Pre-Treatment	LRP3	4037	37	19	33695665	33695665	Missense_Mutation	SNP	T	C	10	22	c.382T>C	c.(382-384)TTC>CTC	p.F128L
Pat_46	Pre-Treatment	KIRREL2	84063	37	19	36357300	36357300	Missense_Mutation	SNP	C	T	44	120	c.2033C>T	c.(2032-2034)TCC>TTC	p.S678F
Pat_46	Pre-Treatment	ZNF565	147929	37	19	36673967	36673967	Missense_Mutation	SNP	G	A	11	47	c.901C>T	c.(901-903)CAC>TAC	p.H301Y
Pat_46	Pre-Treatment	ZNF383	163087	37	19	37734537	37734537	Missense_Mutation	SNP	C	T	10	31	c.1399C>T	c.(1399-1401)CGT>TGT	p.R467C
Pat_46	Pre-Treatment	DLL3	10683	37	19	39998559	39998559	Missense_Mutation	SNP	C	T	4	25	c.1763C>T	c.(1762-1764)GCG>GTG	p.A588V
Pat_46	Pre-Treatment	CLC	1178	37	19	40225069	40225070	Missense_Mutation	DNP	GG	AT	47	121	c.156_157CC>AT	.(154-159)TTCCAT>TTATA	p.52_53FH>LY
Pat_46	Pre-Treatment	SHKBP1	92799	37	19	41086687	41086687	Missense_Mutation	SNP	C	T	21	39	c.689C>T	c.(688-690)TCC>TTC	p.S230F
Pat_46	Pre-Treatment	CEACAM5	1048	37	19	42213788	42213788	Missense_Mutation	SNP	G	A	26	82	c.254G>A	c.(253-255)GGA>GAA	p.G85E
Pat_46	Pre-Treatment	GRIK5	2901	37	19	42525609	42525609	Nonsense_Mutation	SNP	C	T	5	9	c.1715G>A	c.(1714-1716)TGG>TAG	p.W572*
Pat_46	Pre-Treatment	PSG8	440533	37	19	43262211	43262211	Missense_Mutation	SNP	C	T	86	165	c.652G>A	c.(652-654)GAA>AAA	p.E218K
Pat_46	Pre-Treatment	PSG1	5669	37	19	43376195	43376195	Missense_Mutation	SNP	C	T	21	45	c.433G>A	c.(433-435)GAG>AAG	p.E145K
Pat_46	Pre-Treatment	PSG9	5678	37	19	43762435	43762435	Missense_Mutation	SNP	G	A	42	96	c.1162C>T	c.(1162-1164)CAT>TAT	p.H388Y
Pat_46	Pre-Treatment	ZNF233	353355	37	19	44777762	44777762	Missense_Mutation	SNP	G	A	5	15	c.949G>A	c.(949-951)GGT>AGT	p.G317S
Pat_46	Pre-Treatment	PPP5C	5536	37	19	46887130	46887130	Missense_Mutation	SNP	C	T	25	76	c.793C>T	c.(793-795)CCC>TCC	p.P265S

Pat_46	Pre-Treatment	EHD2	30846	37	19	48220035	48220035	Missense_Mutation	SNP	G	A	7	19	c.166G>A	c.(166-168)GAC>AAC	p.D56N
Pat_46	Pre-Treatment	ZNF175	7728	37	19	52091536	52091536	Missense_Mutation	SNP	C	T	11	25	c.1952C>T	c.(1951-1953)TCG>TTG	p.S651L
Pat_46	Pre-Treatment	SIGLEC5	8778	37	19	52131203	52131203	Missense_Mutation	SNP	G	A	11	32	c.881C>T	c.(880-882)TCC>TTC	p.S294F
Pat_46	Pre-Treatment	FPR2	2358	37	19	52272576	52272576	Missense_Mutation	SNP	G	A	16	30	c.665G>A	c.(664-666)GGG>GAG	p.G222E
Pat_46	Pre-Treatment	FPR3	2359	37	19	52327313	52327313	Missense_Mutation	SNP	G	A	17	62	c.312G>A	c.(310-312)ATG>ATA	p.M104I
Pat_46	Pre-Treatment	ZNF611	81856	37	19	53209661	53209661	Missense_Mutation	SNP	G	A	20	51	c.647C>T	c.(646-648)TCA>TTA	p.S216L
Pat_46	Pre-Treatment	ZNF415	55786	37	19	53612783	53612783	Missense_Mutation	SNP	C	T	12	34	c.659G>A	c.(658-660)GGT>GAT	p.G220D
Pat_46	Pre-Treatment	KIR2DS4	3809	37	19	55351067	55351067	Missense_Mutation	SNP	G	A	37	112	c.577G>A	c.(577-579)GGA>AGA	p.G193R
Pat_46	Pre-Treatment	NLRP8	126205	37	19	56490764	56490764	Missense_Mutation	SNP	G	A	18	53	c.2881G>A	c.(2881-2883)GAA>AAA	p.E961K
Pat_46	Pre-Treatment	ZFP28	140612	37	19	57066001	57066001	Missense_Mutation	SNP	C	T	17	51	c.1847C>T	c.(1846-1848)CCT>CTT	p.P616L
Pat_46	Pre-Treatment	ZNF329	79673	37	19	58640786	58640786	Missense_Mutation	SNP	G	A	42	122	c.85C>T	c.(85-87)CCC>TCC	p.P29S
Pat_46	Pre-Treatment	ZNF8	7554	37	19	58805844	58805844	Missense_Mutation	SNP	C	T	11	21	c.670C>T	c.(670-672)CCA>TCA	p.P224S
Pat_46	Pre-Treatment	PXDN	7837	37	2	1667507	1667507	Missense_Mutation	SNP	G	C	4	55	c.1437C>G	c.(1435-1437)CAC>CAG	p.H479Q
Pat_46	Pre-Treatment	APOB	338	37	2	21256261	21256261	Missense_Mutation	SNP	G	A	15	28	c.1034C>T	c.(1033-1035)GCT>GTT	p.A345V
Pat_46	Pre-Treatment	ATAD2B	54454	37	2	24046313	24046313	Missense_Mutation	SNP	C	T	20	28	c.1946G>A	c.(1945-1947)AGT>AAT	p.S649N
Pat_46	Pre-Treatment	KIF3C	3797	37	2	26204074	26204074	Missense_Mutation	SNP	C	T	4	81	c.713G>A	c.(712-714)CGA>CAA	p.R238Q
Pat_46	Pre-Treatment	SLC5A6	8884	37	2	27425706	27425706	Missense_Mutation	SNP	G	A	32	69	c.1250C>T	c.(1249-1251)TCC>TTC	p.S417F
Pat_46	Pre-Treatment	C2orf16	84226	37	2	27804700	27804700	Missense_Mutation	SNP	C	T	75	199	c.5261C>T	c.(5260-5262)TCT>TTT	p.S1754F
Pat_46	Pre-Treatment	FAM179A	165186	37	2	29225533	29225533	Missense_Mutation	SNP	G	A	3	18	c.559G>A	c.(559-561)GCC>ACC	p.A187T
Pat_46	Pre-Treatment	C2orf71	388939	37	2	29296101	29296101	Missense_Mutation	SNP	G	A	32	46	c.1027C>T	c.(1027-1029)CTC>TTC	p.L343F
Pat_46	Pre-Treatment	HEATR5B	54497	37	2	37227870	37227870	Missense_Mutation	SNP	G	A	18	50	c.5404C>T	c.(5404-5406)CCT>TCT	p.P1802S
Pat_46	Pre-Treatment	CEBPZ	10153	37	2	37455246	37455246	Nonsense_Mutation	SNP	G	A	8	27	c.1090C>T	c.(1090-1092)CGA>TGA	p.R364*
Pat_46	Pre-Treatment	LOC728819	728819	37	2	43902786	43902786	Missense_Mutation	SNP	A	T	8	20	c.676T>A	c.(676-678)TAT>AAT	p.Y226N
Pat_46	Pre-Treatment	FSHR	2492	37	2	49190018	49190018	Missense_Mutation	SNP	C	T	5	17	c.1942G>A	c.(1942-1944)GAA>AAA	p.E648K
Pat_46	Pre-Treatment	ETAA1	54465	37	2	67631235	67631235	Missense_Mutation	SNP	C	T	3	11	c.1421C>T	c.(1420-1422)TCC>TTC	p.S474F
Pat_46	Pre-Treatment	CCT7	10574	37	2	73474975	73474975	Missense_Mutation	SNP	C	T	16	31	c.704C>T	c.(703-705)CCC>CTC	p.P235L
Pat_46	Pre-Treatment	ALMS1	7840	37	2	73675797	73675797	Missense_Mutation	SNP	C	T	32	81	c.2146C>T	c.(2146-2148)CCC>TCC	p.P716S
Pat_46	Pre-Treatment	CTNNA2	1496	37	2	80874951	80874951	Missense_Mutation	SNP	C	T	29	52	c.2816C>T	c.(2815-2817)TCG>TTG	p.S939L
Pat_46	Pre-Treatment	SFTPB	6439	37	2	85893781	85893781	Missense_Mutation	SNP	C	T	3	111	c.352G>A	c.(352-354)GAC>AAC	p.D118N
Pat_46	Pre-Treatment	EIF2AK3	9451	37	2	88874860	88874860	Missense_Mutation	SNP	G	A	38	91	c.2141C>T	c.(2140-2142)CCT>CTT	p.P714L
Pat_46	Pre-Treatment	VWA3B	200403	37	2	98844782	98844782	Missense_Mutation	SNP	G	A	16	26	c.2137G>A	c.(2137-2139)GAT>AAT	p.D713N
Pat_46	Pre-Treatment	SLC9A4	389015	37	2	103142776	103142776	Missense_Mutation	SNP	G	A	28	66	c.2009G>A	c.(2008-2010)GGA>GAA	p.G670E
Pat_46	Pre-Treatment	RANBP2	5903	37	2	109384260	109384260	Missense_Mutation	SNP	G	A	5	244	c.7265G>A	c.(7264-7266)CGT>CAT	p.R2422H
Pat_46	Pre-Treatment	IL1A	3552	37	2	113532775	113532775	Missense_Mutation	SNP	C	T	25	71	c.685G>A	c.(685-687)GGC>AGC	p.G229S
Pat_46	Pre-Treatment	IL1B	3553	37	2	113587942	113587942	Missense_Mutation	SNP	G	A	16	32	c.806C>T	c.(805-807)TCC>TTC	p.S269F
Pat_46	Pre-Treatment	NCKAP5	344148	37	2	133489429	133489429	Missense_Mutation	SNP	G	A	13	25	c.5324C>T	c.(5323-5325)TCC>TTC	p.S1775F
Pat_46	Pre-Treatment	YSK4	80122	37	2	135763044	135763044	Missense_Mutation	SNP	G	A	18	34	c.196C>T	c.(196-198)CCC>TCC	p.P66S
Pat_46	Pre-Treatment	ARHGAP15	55843	37	2	143974010	143974010	Missense_Mutation	SNP	C	G	6	24	c.292C>G	c.(292-294)CTA>GTA	p.L98V
Pat_46	Pre-Treatment	NEB	4703	37	2	152370918	152370918	Missense_Mutation	SNP	C	T	39	106	c.17938G>A	c.(17938-17940)GAA>AAA	p.E5980K
Pat_46	Pre-Treatment	CCDC148	130940	37	2	159077171	159077171	Missense_Mutation	SNP	C	T	6	8	c.1306G>A	c.(1306-1308)GAT>AAT	p.D436N
Pat_46	Pre-Treatment	LY75	4065	37	2	160742933	160742933	Missense_Mutation	SNP	G	A	13	38	c.911C>T	c.(910-912)CCA>CTA	p.P304L
Pat_46	Pre-Treatment	ITGB6	3694	37	2	161052127	161052127	Splice_Site	SNP	C	T	15	34	c.347_splice	c.e4-1	p.G116_splice
Pat_46	Pre-Treatment	SCN3A	6328	37	2	165953782	165953782	Missense_Mutation	SNP	A	C	5	67	c.4219T>G	c.(4219-4221)TAT>GAT	p.Y1407D
Pat_46	Pre-Treatment	SCN1A	6323	37	2	166897895	166897895	Nonsense_Mutation	SNP	C	T	21	70	c.2228G>A	c.(2227-2229)TGG>TAG	p.W743*
Pat_46	Pre-Treatment	G6PC2	57818	37	2	169761055	169761055	Nonsense_Mutation	SNP	G	A	94	229	c.369G>A	c.(367-369)TGG>TGA	p.W123*
Pat_46	Pre-Treatment	ITGA6	3655	37	2	173339794	173339794	Missense_Mutation	SNP	C	T	10	38	c.1124C>T	c.(1123-1125)TCT>TTT	p.S375F
Pat_46	Pre-Treatment	PDE11A	50940	37	2	178879150	178879150	Missense_Mutation	SNP	C	T	12	27	c.950G>A	c.(949-951)GGA>GAA	p.G317E

Pat_46	Pre-Treatment	TTN	7273	37	2	179417758	179417758	Missense_Mutation	SNP	G	A	6	6	c.82165C>T	c.(82165-82167)CCT>TCT	p.P27389S
Pat_46	Pre-Treatment	TTN	7273	37	2	179426396	179426397	Missense_Mutation	DNP	GG	AA	8	21	76758_76759CC>	756-76761)CCCCCA>CCT	p.P25587S
Pat_46	Pre-Treatment	TTN	7273	37	2	179431936	179431936	Nonsense_Mutation	SNP	C	T	17	52	c.71219G>A	c.(71218-71220)TGG>TAG	p.W23740*
Pat_46	Pre-Treatment	TTN	7273	37	2	179435273	179435273	Missense_Mutation	SNP	T	C	5	10	c.67882A>G	c.(67882-67884)ACT>GCT	p.T22628A
Pat_46	Pre-Treatment	TTN	7273	37	2	179439473	179439473	Missense_Mutation	SNP	C	G	16	57	c.63682G>C	c.(63682-63684)GAG>CAG	p.E21228Q
Pat_46	Pre-Treatment	TTN	7273	37	2	179464532	179464532	Missense_Mutation	SNP	C	T	11	19	c.48392G>A	c.(48391-48393)GGA>GAA	p.G16131E
Pat_46	Pre-Treatment	TTN	7273	37	2	179475048	179475048	Missense_Mutation	SNP	C	T	14	34	c.43501G>A	c.(43501-43503)GAA>AAA	p.E14501K
Pat_46	Pre-Treatment	TTN	7273	37	2	179483347	179483347	Missense_Mutation	SNP	C	T	17	46	c.39226G>A	c.(39226-39228)GGA>AGA	p.G13076R
Pat_46	Pre-Treatment	TTN	7273	37	2	179542534	179542534	Missense_Mutation	SNP	C	T	19	52	c.30373G>A	c.(30373-30375)GAA>AAA	p.E10125K
Pat_46	Pre-Treatment	TTN	7273	37	2	179584152	179584152	Missense_Mutation	SNP	G	A	17	28	c.20233C>T	c.(20233-20235)CGC>TGC	p.R6745C
Pat_46	Pre-Treatment	ZNF804A	91752	37	2	185802432	185802432	Missense_Mutation	SNP	G	A	17	35	c.2309G>A	c.(2308-2310)CGA>CAA	p.R770Q
Pat_46	Pre-Treatment	CLK1	1195	37	2	201724923	201724923	Nonsense_Mutation	SNP	T	A	41	142	c.406A>T	c.(406-408)AAA>TAA	p.K136*
Pat_46	Pre-Treatment	ZDBF2	57683	37	2	207173096	207173096	Missense_Mutation	SNP	G	A	5	14	c.3844G>A	c.(3844-3846)GAT>AAT	p.D1282N
Pat_46	Pre-Treatment	CRYGC	1420	37	2	208994365	208994365	Missense_Mutation	SNP	C	T	53	123	c.52G>A	c.(52-54)GAA>AAA	p.E18K
Pat_46	Pre-Treatment	MAP2	4133	37	2	210570403	210570403	Missense_Mutation	SNP	T	A	56	130	c.4684T>A	c.(4684-4686)TCC>ACC	p.S1562T
Pat_46	Pre-Treatment	MYL1	4632	37	2	211163257	211163257	Missense_Mutation	SNP	C	T	11	21	c.191G>A	c.(190-192)AGA>AAA	p.R64K
Pat_46	Pre-Treatment	SLC4A3	6508	37	2	220496794	220496794	Missense_Mutation	SNP	C	T	7	10	c.916C>T	c.(916-918)CGC>TGC	p.R306C
Pat_46	Pre-Treatment	SLC4A3	6508	37	2	220498087	220498087	Missense_Mutation	SNP	C	T	14	30	c.1369C>T	c.(1369-1371)CCC>TCC	p.P457S
Pat_46	Pre-Treatment	PAX3	5077	37	2	223160307	223160307	Missense_Mutation	SNP	A	T	34	63	c.391T>A	c.(391-393)TGG>AGG	p.W131R
Pat_46	Pre-Treatment	SPHKAP	80309	37	2	228860378	228860378	Missense_Mutation	SNP	G	A	7	7	c.4481C>T	c.(4480-4482)GCT>GTT	p.A1494V
Pat_46	Pre-Treatment	PID1	55022	37	2	229890692	229890692	Missense_Mutation	SNP	C	T	13	33	c.409G>A	c.(409-411)GAA>AAA	p.E137K
Pat_46	Pre-Treatment	SP140	11262	37	2	231108493	231108493	Missense_Mutation	SNP	G	A	25	62	c.538G>A	c.(538-540)GAA>AAA	p.E180K
Pat_46	Pre-Treatment	ITM2C	81618	37	2	231742251	231742251	Missense_Mutation	SNP	G	A	3	59	c.698G>A	c.(697-699)CGG>CAG	p.R233Q
Pat_46	Pre-Treatment	NMUR1	10316	37	2	232393481	232393481	Missense_Mutation	SNP	A	G	11	56	c.251T>C	c.(250-252)GTC>GCC	p.V84A
Pat_46	Pre-Treatment	UGT1A1	54658	37	2	234669433	234669433	Missense_Mutation	SNP	C	T	26	74	c.500C>T	c.(499-501)CCC>CTC	p.P167L
Pat_46	Pre-Treatment	RSPO4	343637	37	20	947880	947880	Missense_Mutation	SNP	C	T	20	44	c.346G>A	c.(346-348)GGG>AGG	p.G116R
Pat_46	Pre-Treatment	FRG1B	284802	37	20	29628243	29628243	Missense_Mutation	SNP	T	C	4	133	c.155T>C	c.(154-156)TTG>TCG	p.L52S
Pat_46	Pre-Treatment	FRG1B	284802	37	20	29628245	29628245	Missense_Mutation	SNP	G	A	4	130	c.157G>A	c.(157-159)GCC>ACC	p.A53T
Pat_46	Pre-Treatment	DEFB115	245929	37	20	29847311	29847311	Missense_Mutation	SNP	C	T	7	23	c.143C>T	c.(142-144)TCA>TTA	p.S48L
Pat_46	Pre-Treatment	DEFB116	245930	37	20	29891208	29891208	Missense_Mutation	SNP	G	A	22	38	c.116C>T	c.(115-117)CCA>CTA	p.P39L
Pat_46	Pre-Treatment	C20orf185	359710	37	20	31644471	31644471	Missense_Mutation	SNP	G	A	9	17	c.248G>A	c.(247-249)GGA>GAA	p.G83E
Pat_46	Pre-Treatment	NECAB3	63941	37	20	32257228	32257228	Missense_Mutation	SNP	C	T	33	106	c.340G>A	c.(340-342)GAA>AAA	p.E114K
Pat_46	Pre-Treatment	ACSS2	55902	37	20	33502209	33502209	Missense_Mutation	SNP	C	T	12	25	c.803C>T	c.(802-804)CCC>CTC	p.P268L
Pat_46	Pre-Treatment	PTPRT	11122	37	20	40735493	40735493	Missense_Mutation	SNP	C	G	17	49	c.3323G>C	c.(3322-3324)GGG>GCG	p.G1108A
Pat_46	Pre-Treatment	PTPRT	11122	37	20	40743942	40743942	Missense_Mutation	SNP	C	T	25	45	c.2996G>A	c.(2995-2997)CGA>CAA	p.R999Q
Pat_46	Pre-Treatment	PTPRT	11122	37	20	40747054	40747054	Missense_Mutation	SNP	C	T	21	55	c.2971G>A	c.(2971-2973)GAA>AAA	p.E991K
Pat_46	Pre-Treatment	PTPRT	11122	37	20	41100912	41100912	Missense_Mutation	SNP	C	T	15	36	c.1444G>A	c.(1444-1446)GAA>AAA	p.E482K
Pat_46	Pre-Treatment	PTPRT	11122	37	20	41306689	41306689	Missense_Mutation	SNP	C	T	4	23	c.970G>A	c.(970-972)GAA>AAA	p.E324K
Pat_46	Pre-Treatment	MMP9	4318	37	20	44639672	44639672	Missense_Mutation	SNP	C	T	12	33	c.632C>T	c.(631-633)TCC>TTC	p.S211F
Pat_46	Pre-Treatment	CDH22	64405	37	20	44815559	44815559	Missense_Mutation	SNP	G	A	50	132	c.1451C>T	c.(1450-1452)TCC>TTC	p.S484F
Pat_46	Pre-Treatment	SLC13A3	64849	37	20	45224923	45224923	Missense_Mutation	SNP	C	T	34	93	c.667G>A	c.(667-669)GAG>AAG	p.E223K
Pat_46	Pre-Treatment	SULF2	55959	37	20	46295003	46295004	Splice_Site	DNP	CC	TT	16	63	c.1805_splice	c.e12+1	p.R602_splice
Pat_46	Pre-Treatment	KCNB1	3745	37	20	47990627	47990627	Nonsense_Mutation	SNP	C	T	14	50	c.1470G>A	c.(1468-1470)TGG>TGA	p.W490*
Pat_46	Pre-Treatment	CASS4	57091	37	20	55033513	55033513	Missense_Mutation	SNP	C	A	30	66	c.2071C>A	c.(2071-2073)CAC>AAC	p.H691N
Pat_46	Pre-Treatment	ZNF831	128611	37	20	57766991	57766991	Missense_Mutation	SNP	C	T	7	3	c.917C>T	c.(916-918)TCG>TTG	p.S306L
Pat_46	Pre-Treatment	ZNF831	128611	37	20	57770957	57770957	Nonsense_Mutation	SNP	C	T	36	102	c.3772C>T	c.(3772-3774)CAG>TAG	p.Q1258*
Pat_46	Pre-Treatment	ZNF831	128611	37	20	57829544	57829544	Missense_Mutation	SNP	G	A	13	40	c.4780G>A	c.(4780-4782)GGC>AGC	p.G1594S

Pat_46	Pre-Treatment	ADRM1	11047	37	20	60882672	60882672	Missense_Mutation	SNP	C	T	3	46	c.644C>T	c.(643-645)GCG>GTG	p.A215V
Pat_46	Pre-Treatment	ITSN1	6453	37	21	35140024	35140024	Nonsense_Mutation	SNP	C	T	7	37	c.934C>T	c.(934-936)CGA>TGA	p.R312*
Pat_46	Pre-Treatment	DSCAM	1826	37	21	41550881	41550881	Missense_Mutation	SNP	C	T	9	28	c.2920G>A	c.(2920-2922)GAG>AAG	p.E974K
Pat_46	Pre-Treatment	UBASH3A	53347	37	21	43826440	43826440	Missense_Mutation	SNP	G	A	10	47	c.137G>A	c.(136-138)GGG>GAG	p.G46E
Pat_46	Pre-Treatment	DGCR2	9993	37	22	19028601	19028601	Missense_Mutation	SNP	G	A	10	34	c.1366C>T	c.(1366-1368)CAC>TAC	p.H456Y
Pat_46	Pre-Treatment	ZNF74	7625	37	22	20760788	20760788	Missense_Mutation	SNP	G	A	4	126	c.1465G>A	c.(1465-1467)GTG>ATG	p.V489M
Pat_46	Pre-Treatment	MYO18B	84700	37	22	26286768	26286768	Missense_Mutation	SNP	G	A	18	36	c.4360G>A	c.(4360-4362)GAT>AAT	p.D1454N
Pat_46	Pre-Treatment	ASPHD2	57168	37	22	26829939	26829939	Missense_Mutation	SNP	G	A	12	33	c.358G>A	c.(358-360)GAG>AAG	p.E120K
Pat_46	Pre-Treatment	RBM9	23543	37	22	36155947	36155947	Missense_Mutation	SNP	G	A	28	41	c.1097C>T	c.(1096-1098)CCC>CTC	p.P366L
Pat_46	Pre-Treatment	CSF2RB	1439	37	22	37333540	37333540	Missense_Mutation	SNP	G	A	4	13	c.1690G>A	c.(1690-1692)GAG>AAG	p.E564K
Pat_46	Pre-Treatment	CSF2RB	1439	37	22	37334044	37334044	Missense_Mutation	SNP	C	T	4	32	c.2194C>T	c.(2194-2196)CCC>TCC	p.P732S
Pat_46	Pre-Treatment	RANGAP1	5905	37	22	41657514	41657514	Missense_Mutation	SNP	A	C	5	21	c.551T>G	c.(550-552)GTC>GGC	p.V184G
Pat_46	Pre-Treatment	PMM1	5372	37	22	41973333	41973333	Missense_Mutation	SNP	G	A	23	60	c.778C>T	c.(778-780)CAT>TAT	p.H260Y
Pat_46	Pre-Treatment	PMM1	5372	37	22	41973900	41973900	Missense_Mutation	SNP	G	A	20	54	c.578C>T	c.(577-579)CCC>CTC	p.P193L
Pat_46	Pre-Treatment	SREBF2	6721	37	22	42296417	42296417	Missense_Mutation	SNP	C	T	8	28	c.2822C>T	c.(2821-2823)TCC>TTC	p.S941F
Pat_46	Pre-Treatment	TNFRSF13C	115650	37	22	42321522	42321522	Missense_Mutation	SNP	G	A	7	33	c.404C>T	c.(403-405)CCG>CTG	p.P135L
Pat_46	Pre-Treatment	PHF21B	112885	37	22	45309869	45309869	Missense_Mutation	SNP	G	A	18	27	c.664C>T	c.(664-666)CCT>TCT	p.P222S
Pat_46	Pre-Treatment	GTSE1	51512	37	22	46704247	46704247	Missense_Mutation	SNP	C	T	22	58	c.169C>T	c.(169-171)CCC>TCC	p.P57S
Pat_46	Pre-Treatment	MOV10L1	54456	37	22	50537923	50537923	Missense_Mutation	SNP	C	T	5	13	c.334C>T	c.(334-336)CCC>TCC	p.P112S
Pat_46	Pre-Treatment	PANX2	56666	37	22	50617383	50617383	Missense_Mutation	SNP	G	A	5	15	c.1711G>A	c.(1711-1713)GAA>AAA	p.E571K
Pat_46	Pre-Treatment	KLHDC7B	113730	37	22	50988202	50988202	Missense_Mutation	SNP	C	T	4	10	c.1607C>T	c.(1606-1608)ACC>ATC	p.T536I
Pat_46	Pre-Treatment	ACR	49	37	22	51178379	51178379	Missense_Mutation	SNP	C	T	5	20	c.539C>T	c.(538-540)GCC>GTC	p.A180V
Pat_46	Pre-Treatment	IRAK2	3656	37	3	10268062	10268062	Missense_Mutation	SNP	C	T	10	22	c.1217C>T	c.(1216-1218)GCC>GTC	p.A406V
Pat_46	Pre-Treatment	IQSEC1	9922	37	3	12957209	12957209	Missense_Mutation	SNP	G	A	40	99	c.2087C>T	c.(2086-2088)CCC>CTC	p.P696L
Pat_46	Pre-Treatment	NR2C2	7182	37	3	15055225	15055226	Missense_Mutation	DNP	TC	GT	10	28	c.202_203TC>GT	c.(202-204)TCC>GTC	p.S68V
Pat_46	Pre-Treatment	SCN5A	6331	37	3	38646255	38646255	Missense_Mutation	SNP	G	A	13	14	c.1483C>T	c.(1483-1485)CCC>TCC	p.P495S
Pat_46	Pre-Treatment	SCN10A	6336	37	3	38739255	38739255	Missense_Mutation	SNP	T	C	8	21	c.5456A>G	c.(5455-5457)GAT>GGT	p.D1819G
Pat_46	Pre-Treatment	XIRP1	165904	37	3	39227066	39227066	Missense_Mutation	SNP	G	A	10	38	c.3871C>T	c.(3871-3873)CTT>TTT	p.L1291F
Pat_46	Pre-Treatment	MYRIP	25924	37	3	40211568	40211568	Missense_Mutation	SNP	C	T	3	87	c.857C>T	c.(856-858)GCT>GTT	p.A286V
Pat_46	Pre-Treatment	MYRIP	25924	37	3	40275539	40275539	Missense_Mutation	SNP	G	A	25	42	c.2095G>A	c.(2095-2097)GAA>AAA	p.E699K
Pat_46	Pre-Treatment	ULK4	54986	37	3	41860958	41860958	Missense_Mutation	SNP	G	A	15	29	c.1805C>T	c.(1804-1806)CCC>CTC	p.P602L
Pat_46	Pre-Treatment	CCBP2	1238	37	3	42906733	42906733	Missense_Mutation	SNP	C	T	16	42	c.739C>T	c.(739-741)CGG>TGG	p.R247W
Pat_46	Pre-Treatment	COL7A1	1294	37	3	48629552	48629552	Missense_Mutation	SNP	G	A	20	42	c.1223C>T	c.(1222-1224)TCC>TTC	p.S408F
Pat_46	Pre-Treatment	QARS	5859	37	3	49137892	49137892	Splice_Site	SNP	C	T	12	27	c.977_splice	c.e12-1	p.G326_splice
Pat_46	Pre-Treatment	DOCK3	1795	37	3	51101878	51101878	Splice_Site	SNP	G	A	27	58	c.316_splice	c.e6-1	p.K106_splice
Pat_46	Pre-Treatment	DOCK3	1795	37	3	51352520	51352520	Missense_Mutation	SNP	G	A	14	34	c.3363G>A	c.(3361-3363)ATG>ATA	p.M1121I
Pat_46	Pre-Treatment	CACNA1D	776	37	3	53835211	53835211	Missense_Mutation	SNP	G	A	18	54	c.5167G>A	c.(5167-5169)GAT>AAT	p.D1723N
Pat_46	Pre-Treatment	CACNA2D3	55799	37	3	55107857	55107857	Missense_Mutation	SNP	C	T	5	8	c.3154C>T	c.(3154-3156)CCA>TCA	p.P1052S
Pat_46	Pre-Treatment	ERC2	26059	37	3	55922538	55922538	Missense_Mutation	SNP	C	T	31	79	c.2443G>A	c.(2443-2445)GAA>AAA	p.E815K
Pat_46	Pre-Treatment	RPP14	11102	37	3	58303182	58303182	Missense_Mutation	SNP	C	T	7	13	c.334C>T	c.(334-336)CTT>TTT	p.L112F
Pat_46	Pre-Treatment	CADPS	8618	37	3	62522224	62522224	Missense_Mutation	SNP	C	T	26	89	c.1999G>A	c.(1999-2001)GAA>AAA	p.E667K
Pat_46	Pre-Treatment	ADAMTS9	56999	37	3	64640105	64640105	Missense_Mutation	SNP	G	A	26	89	c.1240C>T	c.(1240-1242)CCC>TCC	p.P414S
Pat_46	Pre-Treatment	KBTBD8	84541	37	3	67054118	67054118	Missense_Mutation	SNP	C	T	8	21	c.727C>T	c.(727-729)CCT>TCT	p.P243S
Pat_46	Pre-Treatment	FAM86D	692099	37	3	75472210	75472211	Missense_Mutation	DNP	GG	AA	19	46	c.639_640CC>TT	37-642)GGCCGG>GGTT	p.R214W
Pat_46	Pre-Treatment	EPHA3	2042	37	3	89528644	89528644	Missense_Mutation	SNP	C	T	6	17	c.2944C>T	c.(2944-2946)CCC>TCC	p.P982S
Pat_46	Pre-Treatment	EPHA6	285220	37	3	97124042	97124042	Missense_Mutation	SNP	G	A	7	6	c.1655G>A	c.(1654-1656)AGC>AAC	p.S552N
Pat_46	Pre-Treatment	EPHA6	285220	37	3	97167559	97167559	Missense_Mutation	SNP	G	A	28	22	c.1879G>A	c.(1879-1881)GAA>AAA	p.E627K

Pat_46	Pre-Treatment	MYH15	22989	37	3	108117645	108117645	Missense_Mutation	SNP	C	T	68	74	c.5032G>A	c.(5032-5034)GAT>AAT	p.D1678N
Pat_46	Pre-Treatment	CD86	942	37	3	121838341	121838341	Missense_Mutation	SNP	C	T	6	17	c.950C>T	c.(949-951)TCG>TTG	p.S317L
Pat_46	Pre-Treatment	FAM162A	26355	37	3	122126227	122126228	Missense_Mutation	DNP	GG	AA	13	23	c.363_364GG>AA	361-366)GAGGGC>GAAA	p.G122S
Pat_46	Pre-Treatment	EEFSEC	60678	37	3	127981041	127981041	Missense_Mutation	SNP	C	T	9	29	c.595C>T	c.(595-597)CCA>TCA	p.P199S
Pat_46	Pre-Treatment	C3orf36	80111	37	3	133647323	133647323	Missense_Mutation	SNP	C	G	4	7	c.325G>C	c.(325-327)GGG>CGG	p.G109R
Pat_46	Pre-Treatment	IL20RB	53833	37	3	136699340	136699340	Missense_Mutation	SNP	C	T	38	125	c.121C>T	c.(121-123)CTC>TTC	p.L41F
Pat_46	Pre-Treatment	CLSTN2	64084	37	3	140284946	140284946	Missense_Mutation	SNP	G	A	5	21	c.2719G>A	c.(2719-2721)GAA>AAA	p.E907K
Pat_46	Pre-Treatment	ATR	545	37	3	142188288	142188288	Missense_Mutation	SNP	C	T	26	68	c.6443G>A	c.(6442-6444)CGA>CAA	p.R2148Q
Pat_46	Pre-Treatment	MED12L	116931	37	3	150845664	150845664	Missense_Mutation	SNP	C	T	9	27	c.449C>T	c.(448-450)TCT>TTT	p.S150F
Pat_46	Pre-Treatment	TRIM59	286827	37	3	160156050	160156050	Missense_Mutation	SNP	A	C	13	34	c.922T>G	c.(922-924)TCT>GCT	p.S308A
Pat_46	Pre-Treatment	SI	6476	37	3	164735377	164735377	Missense_Mutation	SNP	G	A	17	59	c.3718C>T	c.(3718-3720)CGG>TGG	p.R1240W
Pat_46	Pre-Treatment	SLITRK3	22865	37	3	164906436	164906436	Missense_Mutation	SNP	G	A	13	17	c.2183C>T	c.(2182-2184)TCC>TTC	p.S728F
Pat_46	Pre-Treatment	SERPINI2	5276	37	3	167189541	167189541	Missense_Mutation	SNP	C	T	33	64	c.82G>A	c.(82-84)GAA>AAA	p.E28K
Pat_46	Pre-Treatment	WDR49	151790	37	3	167322110	167322110	Missense_Mutation	SNP	G	A	18	43	c.82C>T	c.(82-84)CAC>TAC	p.H28Y
Pat_46	Pre-Treatment	EIF2B5	8893	37	3	183861313	183861313	Missense_Mutation	SNP	C	T	22	45	c.1829C>T	c.(1828-1830)TCC>TTC	p.S610F
Pat_46	Pre-Treatment	C3orf65	646600	37	3	185434414	185434414	Missense_Mutation	SNP	G	A	8	6	c.247G>A	c.(247-249)GAA>AAA	p.E83K
Pat_46	Pre-Treatment	TPRG1	285386	37	3	188956652	188956652	Missense_Mutation	SNP	C	T	27	78	c.433C>T	c.(433-435)CGC>TGC	p.R145C
Pat_46	Pre-Treatment	C3orf21	152002	37	3	194790515	194790516	Missense_Mutation	DNP	CC	TT	6	24	.1110_1111GG>A	108-1113)GAGGCC>GAA	p.A371T
Pat_46	Pre-Treatment	PDE6B	5158	37	4	647869	647869	Missense_Mutation	SNP	G	A	9	40	c.853G>A	c.(853-855)GAA>AAA	p.E285K
Pat_46	Pre-Treatment	WHSC1	7468	37	4	1961339	1961339	Missense_Mutation	SNP	C	T	29	60	c.3127C>T	c.(3127-3129)CCG>TCG	p.P1043S
Pat_46	Pre-Treatment	SH3TC1	54436	37	4	8239332	8239332	Missense_Mutation	SNP	G	A	12	32	c.3688G>A	c.(3688-3690)GAG>AAG	p.E1230K
Pat_46	Pre-Treatment	CPZ	8532	37	4	8621304	8621304	Missense_Mutation	SNP	C	T	6	13	c.1919C>T	c.(1918-1920)TCG>TTG	p.S640L
Pat_46	Pre-Treatment	ZNF518B	85460	37	4	10446289	10446289	Missense_Mutation	SNP	G	A	14	28	c.1664C>T	c.(1663-1665)TCT>TTT	p.S555F
Pat_46	Pre-Treatment	DCAF16	54876	37	4	17805374	17805374	Missense_Mutation	SNP	G	A	33	84	c.391C>T	c.(391-393)CCC>TCC	p.P131S
Pat_46	Pre-Treatment	SLIT2	9353	37	4	20543159	20543159	Missense_Mutation	SNP	G	A	17	32	c.2060G>A	c.(2059-2061)GGA>GAA	p.G687E
Pat_46	Pre-Treatment	GBA3	57733	37	4	22820361	22820361	Missense_Mutation	SNP	G	A	2	5	c.1225G>A	c.(1225-1227)GTC>ATC	p.V409I
Pat_46	Pre-Treatment	DHX15	1665	37	4	24544625	24544625	Missense_Mutation	SNP	C	T	45	81	c.1273G>A	c.(1273-1275)GAG>AAG	p.E425K
Pat_46	Pre-Treatment	TMPRSS11D	9407	37	4	68698974	68698974	Missense_Mutation	SNP	C	T	23	58	c.640G>A	c.(640-642)GGC>AGC	p.G214S
Pat_46	Pre-Treatment	UGT2B4	7363	37	4	70350974	70350974	Missense_Mutation	SNP	G	A	79	167	c.1262C>T	c.(1261-1263)TCG>TTG	p.S421L
Pat_46	Pre-Treatment	CSN1S1	1446	37	4	70802196	70802196	Missense_Mutation	SNP	G	A	4	17	c.152G>A	c.(151-153)AGG>AAG	p.R51K
Pat_46	Pre-Treatment	PROL1	58503	37	4	71265005	71265005	Missense_Mutation	SNP	G	A	8	21	c.3G>A	c.(1-3)ATG>ATA	p.M1I
Pat_46	Pre-Treatment	SHROOM3	57619	37	4	77661164	77661164	Missense_Mutation	SNP	C	T	3	97	c.1838C>T	c.(1837-1839)GCG>GTG	p.A613V
Pat_46	Pre-Treatment	FRAS1	80144	37	4	79400818	79400818	Missense_Mutation	SNP	G	A	19	37	c.8389G>A	c.(8389-8391)GAT>AAT	p.D2797N
Pat_46	Pre-Treatment	NAA11	84779	37	4	80246788	80246788	Missense_Mutation	SNP	G	A	6	33	c.244C>T	c.(244-246)CGG>TGG	p.R82W
Pat_46	Pre-Treatment	ANTXR2	118429	37	4	80952816	80952816	Missense_Mutation	SNP	G	A	4	13	c.827C>T	c.(826-828)TCT>TTT	p.S276F
Pat_46	Pre-Treatment	RASGEF1B	153020	37	4	82369228	82369228	Missense_Mutation	SNP	C	T	11	43	c.649G>A	c.(649-651)GAG>AAG	p.E217K
Pat_46	Pre-Treatment	WDFY3	23001	37	4	85722863	85722863	Missense_Mutation	SNP	G	A	43	68	c.2762C>T	c.(2761-2763)CCG>CTG	p.P921L
Pat_46	Pre-Treatment	C4orf37	285555	37	4	98480246	98480246	Missense_Mutation	SNP	C	T	22	38	c.1343G>A	c.(1342-1344)GGA>GAA	p.G448E
Pat_46	Pre-Treatment	ENPEP	2028	37	4	111436534	111436534	Missense_Mutation	SNP	G	A	11	29	c.1445G>A	c.(1444-1446)GGA>GAA	p.G482E
Pat_46	Pre-Treatment	PITX2	5308	37	4	111542496	111542496	Missense_Mutation	SNP	C	T	14	21	c.214G>A	c.(214-216)GAG>AAG	p.E72K
Pat_46	Pre-Treatment	C4orf31	79625	37	4	121958606	121958606	Missense_Mutation	SNP	G	A	36	98	c.520C>T	c.(520-522)CCT>TCT	p.P174S
Pat_46	Pre-Treatment	ADAD1	132612	37	4	123317478	123317478	Missense_Mutation	SNP	C	T	12	22	c.670C>T	c.(670-672)CGT>TGT	p.R224C
Pat_46	Pre-Treatment	FAT4	79633	37	4	126367686	126367686	Missense_Mutation	SNP	C	T	32	94	c.7432C>T	c.(7432-7434)CCT>TCT	p.P2478S
Pat_46	Pre-Treatment	PCDH18	54510	37	4	138450896	138450896	Missense_Mutation	SNP	G	A	8	35	c.2347C>T	c.(2347-2349)CCT>TCT	p.P783S
Pat_46	Pre-Treatment	PCDH18	54510	37	4	138451292	138451292	Missense_Mutation	SNP	C	T	49	107	c.1951G>A	c.(1951-1953)GAA>AAA	p.E651K
Pat_46	Pre-Treatment	UCP1	7350	37	4	141483360	141483360	Missense_Mutation	SNP	C	T	43	98	c.796G>A	c.(796-798)GCT>ACT	p.A266T
Pat_46	Pre-Treatment	UCP1	7350	37	4	141484553	141484553	Missense_Mutation	SNP	C	T	28	82	c.445G>A	c.(445-447)GGA>AGA	p.G149R

Pat_46	Pre-Treatment	RNF150	57484	37	4	141832457	141832457	Missense_Mutation	SNP	C	T	20	37	c.1039G>A	c.(1039-1041)GGA>AGA	p.G347R
Pat_46	Pre-Treatment	GYPA	2993	37	4	145040883	145040883	Missense_Mutation	SNP	G	A	12	37	c.188C>T	c.(187-189)TCA>TTA	p.S63L
Pat_46	Pre-Treatment	HHIP	64399	37	4	145629453	145629453	Missense_Mutation	SNP	G	A	15	35	c.1291G>A	c.(1291-1293)GAT>AAT	p.D431N
Pat_46	Pre-Treatment	DDX60L	91351	37	4	169348425	169348425	Missense_Mutation	SNP	G	A	6	24	c.1726C>T	c.(1726-1728)CTC>TTC	p.L576F
Pat_46	Pre-Treatment	ADAM29	11086	37	4	175897562	175897562	Missense_Mutation	SNP	G	A	20	54	c.886G>A	c.(886-888)GGG>AGG	p.G296R
Pat_46	Pre-Treatment	VEGFC	7424	37	4	177608980	177608980	Missense_Mutation	SNP	C	T	23	51	c.806G>A	c.(805-807)GGA>GAA	p.G269E
Pat_46	Pre-Treatment	PDCD6	10016	37	5	306758	306758	Missense_Mutation	SNP	G	A	22	63	c.250G>A	c.(250-252)GAG>AAG	p.E84K
Pat_46	Pre-Treatment	SLC6A18	348932	37	5	1225747	1225747	Missense_Mutation	SNP	G	A	13	57	c.155G>A	c.(154-156)GGA>GAA	p.G52E
Pat_46	Pre-Treatment	TERT	7015	37	5	1272361	1272361	Missense_Mutation	SNP	C	T	8	18	c.2321G>A	c.(2320-2322)CGA>CAA	p.R774Q
Pat_46	Pre-Treatment	SLC6A3	6531	37	5	1443135	1443135	Missense_Mutation	SNP	G	A	10	27	c.178C>T	c.(178-180)CGG>TGG	p.R60W
Pat_46	Pre-Treatment	CDH18	1016	37	5	19483585	19483585	Missense_Mutation	SNP	C	T	16	30	c.1707G>A	c.(1705-1707)ATG>ATA	p.M569I
Pat_46	Pre-Treatment	AGXT2	64902	37	5	35035333	35035333	Missense_Mutation	SNP	G	A	20	44	c.575C>T	c.(574-576)TCT>TTT	p.S192F
Pat_46	Pre-Treatment	PRLR	5618	37	5	35065648	35065648	Missense_Mutation	SNP	C	T	12	31	c.1412G>A	c.(1411-1413)GGA>GAA	p.G471E
Pat_46	Pre-Treatment	EGFLAM	133584	37	5	38438503	38438503	Missense_Mutation	SNP	G	A	9	18	c.2410G>A	c.(2410-2412)GAG>AAG	p.E804K
Pat_46	Pre-Treatment	C7	730	37	5	40964918	40964918	Missense_Mutation	SNP	C	T	29	64	c.1825C>T	c.(1825-1827)CCA>TCA	p.P609S
Pat_46	Pre-Treatment	HEATR7B2	133558	37	5	41033154	41033154	Missense_Mutation	SNP	C	T	15	27	c.2350G>A	c.(2350-2352)GGT>AGT	p.G784S
Pat_46	Pre-Treatment	HTR1A	3350	37	5	63257543	63257543	Missense_Mutation	SNP	C	T	10	14	c.4G>A	c.(4-6)GAT>AAT	p.D2N
Pat_46	Pre-Treatment	MAP1B	4131	37	5	71493512	71493512	Missense_Mutation	SNP	C	T	5	8	c.4330C>T	c.(4330-4332)CCA>TCA	p.P1444S
Pat_46	Pre-Treatment	NSA2	10412	37	5	74064801	74064801	Missense_Mutation	SNP	C	T	5	15	c.49C>T	c.(49-51)CGT>TGT	p.R17C
Pat_46	Pre-Treatment	LOC644936	644936	37	5	79595930	79595930	Missense_Mutation	SNP	G	A	3	11	c.227C>T	c.(226-228)TCC>TTC	p.S76F
Pat_46	Pre-Treatment	GPR98	84059	37	5	89949088	89949089	Missense_Mutation	DNP	CC	TT	12	14	.3697_3698CC>T	c.(3697-3699)CCA>TTA	p.P1233L
Pat_46	Pre-Treatment	GPR98	84059	37	5	90000242	90000242	Missense_Mutation	SNP	G	A	3	12	c.8323G>A	c.(8323-8325)GAT>AAT	p.D2775N
Pat_46	Pre-Treatment	GPR98	84059	37	5	90002111	90002111	Missense_Mutation	SNP	G	A	5	17	c.8630G>A	c.(8629-8631)GGA>GAA	p.G2877E
Pat_46	Pre-Treatment	GPR98	84059	37	5	90016807	90016807	Nonsense_Mutation	SNP	C	T	19	69	c.9679C>T	c.(9679-9681)CGA>TGA	p.R3227*
Pat_46	Pre-Treatment	SNCAIP	9627	37	5	121761182	121761182	Missense_Mutation	SNP	G	A	14	68	c.1138G>A	c.(1138-1140)GAG>AAG	p.E380K
Pat_46	Pre-Treatment	MEGF10	84466	37	5	126732229	126732229	Missense_Mutation	SNP	G	A	67	114	c.418G>A	c.(418-420)GAT>AAT	p.D140N
Pat_46	Pre-Treatment	FSTL4	23105	37	5	132939572	132939572	Missense_Mutation	SNP	C	T	33	85	c.103G>A	c.(103-105)GGT>AGT	p.G35S
Pat_46	Pre-Treatment	PCDHA3	56145	37	5	140181752	140181752	Missense_Mutation	SNP	G	A	25	43	c.970G>A	c.(970-972)GAT>AAT	p.D324N
Pat_46	Pre-Treatment	PCDHA7	56141	37	5	140214185	140214185	Missense_Mutation	SNP	G	A	56	127	c.217G>A	c.(217-219)GAT>AAT	p.D73N
Pat_46	Pre-Treatment	PCDHA13	56136	37	5	140263676	140263676	Missense_Mutation	SNP	C	T	29	55	c.1823C>T	c.(1822-1824)TCG>TTG	p.S608L
Pat_46	Pre-Treatment	PCDHB1	29930	37	5	140432910	140432910	Nonsense_Mutation	SNP	C	T	4	18	c.1855C>T	c.(1855-1857)CAA>TAA	p.Q619*
Pat_46	Pre-Treatment	PCDHB5	26167	37	5	140516773	140516773	Missense_Mutation	SNP	C	T	5	59	c.1757C>T	c.(1756-1758)ACC>ATC	p.T586I
Pat_46	Pre-Treatment	PCDHB7	56129	37	5	140554176	140554176	Missense_Mutation	SNP	C	T	3	75	c.1760C>T	c.(1759-1761)ACC>ATC	p.T587I
Pat_46	Pre-Treatment	PCDHB11	56125	37	5	140581524	140581524	Missense_Mutation	SNP	C	T	40	70	c.2177C>T	c.(2176-2178)TCG>TTG	p.S726L
Pat_46	Pre-Treatment	PCDHB12	56124	37	5	140590287	140590287	Missense_Mutation	SNP	C	T	33	153	c.1808C>T	c.(1807-1809)TCG>TTG	p.S603L
Pat_46	Pre-Treatment	PCDHGC4	56098	37	5	140866751	140866751	Missense_Mutation	SNP	C	T	9	32	c.2011C>T	c.(2011-2013)CCA>TCA	p.P671S
Pat_46	Pre-Treatment	PCDH1	5097	37	5	141236930	141236930	Missense_Mutation	SNP	G	A	9	24	c.3206C>T	c.(3205-3207)CCG>CTG	p.P1069L
Pat_46	Pre-Treatment	PCDH12	51294	37	5	141335229	141335229	Missense_Mutation	SNP	C	T	7	50	c.2188G>A	c.(2188-2190)GGG>AGG	p.G730R
Pat_46	Pre-Treatment	ADRB2	154	37	5	148207458	148207458	Missense_Mutation	SNP	C	T	5	22	c.1064C>T	c.(1063-1065)TCC>TTC	p.S355F
Pat_46	Pre-Treatment	SLC26A2	1836	37	5	149357514	149357514	Missense_Mutation	SNP	C	T	25	54	c.299C>T	c.(298-300)CCA>CTA	p.P100L
Pat_46	Pre-Treatment	FAM71B	153745	37	5	156592693	156592693	Missense_Mutation	SNP	C	T	12	73	c.487G>A	c.(487-489)GAT>AAT	p.D163N
Pat_46	Pre-Treatment	ATP10B	23120	37	5	160018110	160018110	Missense_Mutation	SNP	C	T	11	30	c.3601G>A	c.(3601-3603)GAT>AAT	p.D1201N
Pat_46	Pre-Treatment	GABRA6	2559	37	5	161128618	161128618	Missense_Mutation	SNP	C	A	19	50	c.1201C>A	c.(1201-1203)CCT>ACT	p.P401T
Pat_46	Pre-Treatment	FAM153B	202134	37	5	175528070	175528070	Missense_Mutation	SNP	G	A	13	81	c.583G>A	c.(583-585)GAG>AAG	p.E195K
Pat_46	Pre-Treatment	UNC5A	90249	37	5	176306404	176306404	Missense_Mutation	SNP	C	T	17	43	c.2278C>T	c.(2278-2280)CGG>TGG	p.R760W
Pat_46	Pre-Treatment	FAM153C	653316	37	5	177473889	177473889	Missense_Mutation	SNP	C	T	15	33	c.290C>T	c.(289-291)TCC>TTC	p.S97F
Pat_46	Pre-Treatment	DSP	1832	37	6	7570741	7570742	Missense_Mutation	DNP	CC	TT	35	125	.1646_1647CC>T	c.(1645-1647)TCC>TTT	p.S549F

Pat_46	Pre-Treatment	BMP6	654	37	6	7845540	7845540	Nonsense_Mutation	SNP	C	T	7	28	c.832C>T	c.(832-834)CAA>TAA	p.Q278*
Pat_46	Pre-Treatment	HIVEP1	3096	37	6	12015883	12015883	Missense_Mutation	SNP	C	T	25	161	c.22C>T	c.(22-24)CAT>TAT	p.H8Y
Pat_46	Pre-Treatment	RANBP9	10048	37	6	13711709	13711709	Missense_Mutation	SNP	G	T	3	34	c.29C>A	c.(28-30)CCG>CAG	p.P10Q
Pat_46	Pre-Treatment	CAP2	10486	37	6	17507904	17507904	Missense_Mutation	SNP	G	A	14	126	c.477G>A	c.(475-477)ATG>ATA	p.M159I
Pat_46	Pre-Treatment	LRRC16A	55604	37	6	25516015	25516015	Missense_Mutation	SNP	G	A	17	24	c.1745G>A	c.(1744-1746)GGA>GAA	p.G582E
Pat_46	Pre-Treatment	HIST1H2BE	8344	37	6	26184054	26184054	Missense_Mutation	SNP	C	T	41	135	c.31C>T	c.(31-33)CCG>TCG	p.P11S
Pat_46	Pre-Treatment	BTN2A3	54718	37	6	26431314	26431314	Missense_Mutation	SNP	T	A	15	19	c.1232T>A	c.(1231-1233)CTG>CAG	p.L411Q
Pat_46	Pre-Treatment	BTN1A1	696	37	6	26508950	26508950	Missense_Mutation	SNP	G	A	79	111	c.1129G>A	c.(1129-1131)GAG>AAG	p.E377K
Pat_46	Pre-Treatment	PRSS16	10279	37	6	27222818	27222818	Missense_Mutation	SNP	G	A	42	89	c.1384G>A	c.(1384-1386)GAA>AAA	p.E462K
Pat_46	Pre-Treatment	GPX5	2880	37	6	28497304	28497304	Missense_Mutation	SNP	C	T	60	56	c.164C>T	c.(163-165)TCC>TTC	p.S55F
Pat_46	Pre-Treatment	PPP1R11	6992	37	6	30037019	30037019	Missense_Mutation	SNP	C	T	136	176	c.317C>T	c.(316-318)ACC>ATC	p.T106I
Pat_46	Pre-Treatment	MDC1	9656	37	6	30680836	30680836	Missense_Mutation	SNP	G	A	41	116	c.883C>T	c.(883-885)CCT>TCT	p.P295S
Pat_46	Pre-Treatment	DPCR1	135656	37	6	30919743	30919743	Missense_Mutation	SNP	G	A	4	28	c.3502G>A	c.(3502-3504)GAA>AAA	p.E1168K
Pat_46	Pre-Treatment	C6orf15	29113	37	6	31079628	31079628	Missense_Mutation	SNP	G	A	8	27	c.508C>T	c.(508-510)CAC>TAC	p.H170Y
Pat_46	Pre-Treatment	TNF	7124	37	6	31543429	31543429	Translation_Start_Site	SNP	C	T	8	44	c.-89C>T	.(-91--87)GACGC>GATGC	
Pat_46	Pre-Treatment	TNF	7124	37	6	31545117	31545117	Missense_Mutation	SNP	C	T	40	51	c.505C>T	c.(505-507)CTC>TTC	p.L169F
Pat_46	Pre-Treatment	AIF1	199	37	6	31584627	31584627	Missense_Mutation	SNP	G	A	5	63	c.394G>A	c.(394-396)GAA>AAA	p.E132K
Pat_46	Pre-Treatment	CYP21A2	1589	37	6	32008885	32008885	Missense_Mutation	SNP	G	A	5	32	c.1462G>A	c.(1462-1464)GCC>ACC	p.A488T
Pat_46	Pre-Treatment	COL11A2	1302	37	6	33138143	33138144	Missense_Mutation	DNP	GG	AA	7	26	.3541_3542CC>T	c.(3541-3543)CCC>TTC	p.P1181F
Pat_46	Pre-Treatment	SLC39A7	7922	37	6	33170381	33170381	Missense_Mutation	SNP	G	A	7	34	c.844G>A	c.(844-846)GAA>AAA	p.E282K
Pat_46	Pre-Treatment	DNAH8	1769	37	6	38867559	38867559	Missense_Mutation	SNP	G	A	19	87	c.8420G>A	c.(8419-8421)CGA>CAA	p.R2807Q
Pat_46	Pre-Treatment	DNAH8	1769	37	6	38980323	38980323	Missense_Mutation	SNP	G	A	23	187	c.12973G>A	c.(12973-12975)GAA>AA	p.E4325K
Pat_46	Pre-Treatment	XPO5	57510	37	6	43541245	43541245	Missense_Mutation	SNP	C	T	20	37	c.199G>A	c.(199-201)GGC>AGC	p.G67S
Pat_46	Pre-Treatment	CRISP2	7180	37	6	49660530	49660530	Missense_Mutation	SNP	C	T	19	23	c.688G>A	c.(688-690)GAA>AAA	p.E230K
Pat_46	Pre-Treatment	LRRC1	55227	37	6	53764608	53764608	Missense_Mutation	SNP	C	T	19	17	c.706C>T	c.(706-708)CCT>TCT	p.P236S
Pat_46	Pre-Treatment	FAM83B	222584	37	6	54805519	54805519	Missense_Mutation	SNP	C	T	5	21	c.1750C>T	c.(1750-1752)CCT>TCT	p.P584S
Pat_46	Pre-Treatment	FAM83B	222584	37	6	54806308	54806308	Missense_Mutation	SNP	G	A	9	10	c.2539G>A	c.(2539-2541)GAA>AAA	p.E847K
Pat_46	Pre-Treatment	BMP5	653	37	6	55739516	55739516	Missense_Mutation	SNP	C	T	19	28	c.148G>A	c.(148-150)GAA>AAA	p.E50K
Pat_46	Pre-Treatment	GUSBL2	375513	37	6	58250821	58250821	Missense_Mutation	SNP	G	A	9	30	c.431C>T	c.(430-432)TCG>TTG	p.S144L
Pat_46	Pre-Treatment	EYS	346007	37	6	66054034	66054034	Missense_Mutation	SNP	G	A	13	19	c.1496C>T	c.(1495-1497)GCC>GTC	p.A499V
Pat_46	Pre-Treatment	RIMS1	22999	37	6	72968786	72968786	Missense_Mutation	SNP	G	A	19	18	c.3025G>A	c.(3025-3027)GAT>AAT	p.D1009N
Pat_46	Pre-Treatment	UBE2CBP	90025	37	6	83667051	83667051	Missense_Mutation	SNP	G	A	24	32	c.1129C>T	c.(1129-1131)CGC>TGC	p.R377C
Pat_46	Pre-Treatment	EPHA7	2045	37	6	93964415	93964415	Missense_Mutation	SNP	C	T	24	45	c.2482G>A	c.(2482-2484)GAA>AAA	p.E828K
Pat_46	Pre-Treatment	DDO	8528	37	6	110726085	110726085	Missense_Mutation	SNP	C	T	10	15	c.434G>A	c.(433-435)CGA>CAA	p.R145Q
Pat_46	Pre-Treatment	DSE	29940	37	6	116752138	116752138	Nonsense_Mutation	SNP	T	A	25	25	c.692T>A	c.(691-693)TTA>TAA	p.L231*
Pat_46	Pre-Treatment	TMEM200A	114801	37	6	130762249	130762249	Missense_Mutation	SNP	G	A	6	8	c.682G>A	c.(682-684)GAG>AAG	p.E228K
Pat_46	Pre-Treatment	BCLAF1	9774	37	6	136599063	136599063	Missense_Mutation	SNP	G	A	8	93	c.956C>T	c.(955-957)TCC>TTC	p.S319F
Pat_46	Pre-Treatment	IL20RA	53832	37	6	137332467	137332467	Nonsense_Mutation	SNP	C	T	23	29	c.347G>A	c.(346-348)TGG>TAG	p.W116*
Pat_46	Pre-Treatment	KIAA1244	57221	37	6	138628471	138628471	Missense_Mutation	SNP	G	A	45	43	c.3910G>A	c.(3910-3912)GAA>AAA	p.E1304K
Pat_46	Pre-Treatment	SYNE1	23345	37	6	152454491	152454491	Missense_Mutation	SNP	G	A	31	47	c.25921C>T	.(25921-25923)CGG>TG	p.R8641W
Pat_46	Pre-Treatment	MLLT4	4301	37	6	168352148	168352149	Missense_Mutation	DNP	CC	TT	29	56	.4090_4091CC>T	c.(4090-4092)CCT>TTT	p.P1364F
Pat_46	Pre-Treatment	CARD11	84433	37	7	2968290	2968290	Missense_Mutation	SNP	C	T	35	47	c.1696G>A	c.(1696-1698)GAG>AAG	p.E566K
Pat_46	Pre-Treatment	LOC389458	389458	37	7	5112052	5112052	Missense_Mutation	SNP	C	T	4	6	c.359C>T	c.(358-360)CCG>CTG	p.P120L
Pat_46	Pre-Treatment	RSPH10B2	728194	37	7	5983103	5983103	Missense_Mutation	SNP	C	T	3	35	c.1610G>A	c.(1609-1611)GGC>GAC	p.G537D
Pat_46	Pre-Treatment	RAC1	5879	37	7	6426892	6426892	Missense_Mutation	SNP	C	T	39	132	c.85C>T	c.(85-87)CCT>TCT	p.P29S
Pat_46	Pre-Treatment	THSD7A	221981	37	7	11485877	11485877	Missense_Mutation	SNP	C	T	45	138	c.2875G>A	c.(2875-2877)GAC>AAC	p.D959N
Pat_46	Pre-Treatment	PRPS1L1	221823	37	7	18067003	18067003	Nonsense_Mutation	SNP	G	A	27	72	c.403C>T	c.(403-405)CAG>TAG	p.Q135*

Pat_46	Pre-Treatment	ITGB8	3696	37	7	20441600	20441600	Missense_Mutation	SNP	C	T	80	265	c.1538C>T	c.(1537-1539)TCA>TTA	p.S513L
Pat_46	Pre-Treatment	DNAH11	8701	37	7	21908587	21908587	Missense_Mutation	SNP	G	A	11	16	c.11966G>A	c.(11965-11967)GGA>GAA	p.G3989E
Pat_46	Pre-Treatment	RAPGEF5	9771	37	7	22259516	22259516	Missense_Mutation	SNP	G	A	23	26	c.506C>T	c.(505-507)ACG>ATG	p.T169M
Pat_46	Pre-Treatment	GGCT	79017	37	7	30538488	30538488	Missense_Mutation	SNP	T	G	16	43	c.354A>C	c.(352-354)AAA>AAC	p.K118N
Pat_46	Pre-Treatment	ADCYAP1R1	117	37	7	31146129	31146129	Missense_Mutation	SNP	G	A	26	35	c.1238G>A	c.(1237-1239)CGA>CAA	p.R413Q
Pat_46	Pre-Treatment	DPY19L2P1	554236	37	7	35130022	35130022	Missense_Mutation	SNP	C	T	24	126	c.1163G>A	c.(1162-1164)CGA>CAA	p.R388Q
Pat_46	Pre-Treatment	TBX20	57057	37	7	35242110	35242110	Nonsense_Mutation	SNP	G	A	8	17	c.1276C>T	c.(1276-1278)CAG>TAG	p.Q426*
Pat_46	Pre-Treatment	TXNDC3	51314	37	7	37907434	37907434	Missense_Mutation	SNP	G	A	35	29	c.752G>A	c.(751-753)CGA>CAA	p.R251Q
Pat_46	Pre-Treatment	TBRG4	9238	37	7	45143798	45143798	Missense_Mutation	SNP	G	A	12	56	c.965C>T	c.(964-966)TCC>TTC	p.S322F
Pat_46	Pre-Treatment	CDC14C	168448	37	7	48965358	48965358	Missense_Mutation	SNP	C	T	14	41	c.1090C>T	c.(1090-1092)CTC>TTC	p.L364F
Pat_46	Pre-Treatment	VSTM2A	222008	37	7	54610488	54610488	Missense_Mutation	SNP	G	A	23	27	c.65G>A	c.(64-66)GGG>GAG	p.G22E
Pat_46	Pre-Treatment	ZNF479	90827	37	7	57193770	57193770	Missense_Mutation	SNP	C	T	21	87	c.217G>A	c.(217-219)GAG>AAG	p.E73K
Pat_46	Pre-Treatment	ZNF716	441234	37	7	57528735	57528735	Missense_Mutation	SNP	G	A	11	24	c.568G>A	c.(568-570)GAT>AAT	p.D190N
Pat_46	Pre-Treatment	ZNF679	168417	37	7	63721281	63721281	Missense_Mutation	SNP	G	A	5	26	c.236G>A	c.(235-237)AGA>AAA	p.R79K
Pat_46	Pre-Treatment	WBSCR17	64409	37	7	71036340	71036340	Missense_Mutation	SNP	C	T	24	57	c.1033C>T	c.(1033-1035)CCT>TCT	p.P345S
Pat_46	Pre-Treatment	HGF	3082	37	7	81335690	81335690	Missense_Mutation	SNP	C	T	59	142	c.1670G>A	c.(1669-1671)GGA>GAA	p.G557E
Pat_46	Pre-Treatment	CALCR	799	37	7	93098063	93098063	Missense_Mutation	SNP	G	A	32	79	c.539C>T	c.(538-540)ACC>ATC	p.T180I
Pat_46	Pre-Treatment	LMTK2	22853	37	7	97833294	97833294	Missense_Mutation	SNP	C	T	10	35	c.4279C>T	c.(4279-4281)CCT>TCT	p.P1427S
Pat_46	Pre-Treatment	STAG3	10734	37	7	99802959	99802959	Missense_Mutation	SNP	G	A	14	35	c.3190G>A	c.(3190-3192)GAG>AAG	p.E1064K
Pat_46	Pre-Treatment	ZAN	7455	37	7	100365586	100365586	Missense_Mutation	SNP	G	A	5	21	c.4993G>A	c.(4993-4995)GAA>AAA	p.E1665K
Pat_46	Pre-Treatment	MUC17	140453	37	7	100682297	100682297	Missense_Mutation	SNP	A	G	104	233	c.7600A>G	c.(7600-7602)ACC>GCC	p.T2534A
Pat_46	Pre-Treatment	RABL5	64792	37	7	100958513	100958513	Missense_Mutation	SNP	G	A	12	19	c.460C>T	c.(460-462)CCT>TCT	p.P154S
Pat_46	Pre-Treatment	RELN	5649	37	7	103205974	103205974	Nonsense_Mutation	SNP	C	T	7	10	c.4961G>A	c.(4960-4962)TGG>TAG	p.W1654*
Pat_46	Pre-Treatment	RELN	5649	37	7	103214615	103214615	Missense_Mutation	SNP	C	T	49	70	c.4435G>A	c.(4435-4437)GAT>AAT	p.D1479N
Pat_46	Pre-Treatment	RELN	5649	37	7	103243912	103243912	Missense_Mutation	SNP	C	T	16	58	c.3172G>A	c.(3172-3174)GAA>AAA	p.E1058K
Pat_46	Pre-Treatment	PPP1R3A	5506	37	7	113517816	113517816	Missense_Mutation	SNP	C	T	21	65	c.3331G>A	c.(3331-3333)GAA>AAA	p.E1111K
Pat_46	Pre-Treatment	WNT2	7472	37	7	116937870	116937870	Missense_Mutation	SNP	G	A	59	108	c.649C>T	c.(649-651)CTC>TTC	p.L217F
Pat_46	Pre-Treatment	CFTR	1080	37	7	117174417	117174417	Missense_Mutation	SNP	G	A	13	41	c.577G>A	c.(577-579)GAA>AAA	p.E193K
Pat_46	Pre-Treatment	PTPRZ1	5803	37	7	121653193	121653193	Missense_Mutation	SNP	C	T	68	171	c.4093C>T	c.(4093-4095)CAT>TAT	p.H1365Y
Pat_46	Pre-Treatment	DGKI	9162	37	7	137271862	137271862	Missense_Mutation	SNP	C	T	166	84	c.1406G>A	c.(1405-1407)CGA>CAA	p.R469Q
Pat_46	Pre-Treatment	BRAF	673	37	7	140453136	140453137	Missense_Mutation	DNP	AC	TT	77	43	.1798_1799GT>A	c.(1798-1800)GTG>AAG	p.V600K
Pat_46	Pre-Treatment	BRAF	673	37	7	140494149	140494149	Missense_Mutation	SNP	G	A	110	63	c.1099C>T	c.(1099-1101)CCC>TCC	p.P367S
Pat_46	Pre-Treatment	CLEC5A	23601	37	7	141635652	141635652	Missense_Mutation	SNP	C	T	101	53	c.307G>A	c.(307-309)GGA>AGA	p.G103R
Pat_46	Pre-Treatment	TAS2R38	5726	37	7	141673425	141673425	Missense_Mutation	SNP	G	A	27	181	c.65C>T	c.(64-66)TCA>TTA	p.S22L
Pat_46	Pre-Treatment	PRSS1	5644	37	7	142460779	142460779	Missense_Mutation	SNP	G	A	76	31	c.652G>A	c.(652-654)GAT>AAT	p.D218N
Pat_46	Pre-Treatment	TRY6	154754	37	7	142479974	142479974	Missense_Mutation	SNP	C	T	27	247	c.106C>T	c.(106-108)CCC>TCC	p.P36S
Pat_46	Pre-Treatment	OR6V1	346517	37	7	142750081	142750081	Missense_Mutation	SNP	C	T	118	137	c.644C>T	c.(643-645)TCC>TTC	p.S215F
Pat_46	Pre-Treatment	FAM115C	285966	37	7	143417077	143417077	Missense_Mutation	SNP	G	A	13	7	c.925G>A	c.(925-927)GAT>AAT	p.D309N
Pat_46	Pre-Treatment	OR2A5	393046	37	7	143748144	143748144	Missense_Mutation	SNP	C	T	42	202	c.650C>T	c.(649-651)TCC>TTC	p.S217F
Pat_46	Pre-Treatment	SSPO	23145	37	7	149492370	149492370	Missense_Mutation	SNP	G	A	65	23	c.6259G>A	c.(6259-6261)GAA>AAA	p.E2087K
Pat_46	Pre-Treatment	GIMAP4	55303	37	7	150269283	150269283	Missense_Mutation	SNP	G	A	7	23	c.125G>A	c.(124-126)GGA>GAA	p.G42E
Pat_46	Pre-Treatment	KCNH2	3757	37	7	150648777	150648777	Nonsense_Mutation	SNP	C	T	12	35	c.1704G>A	c.(1702-1704)TGG>TGA	p.W568*
Pat_46	Pre-Treatment	CSMD1	64478	37	8	2876151	2876151	Missense_Mutation	SNP	G	A	3	28	c.7880C>T	c.(7879-7881)TCC>TTC	p.S2627F
Pat_46	Pre-Treatment	CSMD1	64478	37	8	3265610	3265610	Missense_Mutation	SNP	C	T	4	33	c.1885G>A	c.(1885-1887)GAT>AAT	p.D629N
Pat_46	Pre-Treatment	BLK	640	37	8	11412979	11412979	Missense_Mutation	SNP	G	A	19	43	c.758G>A	c.(757-759)GGC>GAC	p.G253D
Pat_46	Pre-Treatment	USP17L2	377630	37	8	11995806	11995806	Missense_Mutation	SNP	C	T	5	31	c.464G>A	c.(463-465)AGA>AAA	p.R155K
Pat_46	Pre-Treatment	TNFRSF10D	8793	37	8	23003424	23003424	Missense_Mutation	SNP	C	T	9	57	c.493G>A	c.(493-495)GGG>AGG	p.G165R

Pat_46	Pre-Treatment	ADAM7	8756	37	8	24346730	24346730	Missense_Mutation	SNP	G	A	13	57	c.1150G>A	c.(1150-1152)GAT>AAT	p.D384N
Pat_46	Pre-Treatment	EBF2	64641	37	8	25718726	25718726	Missense_Mutation	SNP	C	T	4	39	c.1181G>A	c.(1180-1182)CGA>CAA	p.R394Q
Pat_46	Pre-Treatment	EBF2	64641	37	8	25744298	25744298	Missense_Mutation	SNP	C	T	6	26	c.982G>A	c.(982-984)GGA>AGA	p.G328R
Pat_46	Pre-Treatment	PNMA2	10687	37	8	26365277	26365277	Missense_Mutation	SNP	C	T	12	15	c.995G>A	c.(994-996)CGG>CAG	p.R332Q
Pat_46	Pre-Treatment	ADAM32	203102	37	8	39008925	39008925	Missense_Mutation	SNP	A	G	2	12	c.383A>G	c.(382-384)TAT>TGT	p.Y128C
Pat_46	Pre-Treatment	IDO2	169355	37	8	39872871	39872871	Missense_Mutation	SNP	G	A	10	21	c.1013G>A	c.(1012-1014)GGA>GAA	p.G338E
Pat_46	Pre-Treatment	SLC20A2	6575	37	8	42302254	42302254	Missense_Mutation	SNP	C	T	4	13	c.640G>A	c.(640-642)GCC>ACC	p.A214T
Pat_46	Pre-Treatment	RP1	6101	37	8	55539065	55539065	Missense_Mutation	SNP	G	A	9	21	c.2623G>A	c.(2623-2625)GAT>AAT	p.D875N
Pat_46	Pre-Treatment	XKR4	114786	37	8	56436473	56436473	Missense_Mutation	SNP	G	A	30	44	c.1640G>A	c.(1639-1641)CGG>CAG	p.R547Q
Pat_46	Pre-Treatment	CA8	767	37	8	61178606	61178606	Missense_Mutation	SNP	G	A	3	19	c.295C>T	c.(295-297)CTT>TTT	p.L99F
Pat_46	Pre-Treatment	CYP7B1	9420	37	8	65528256	65528257	Missense_Mutation	DNP	TC	AT	38	72	c.841_842GA>AT	c.(841-843)GAA>ATA	p.E281I
Pat_46	Pre-Treatment	SGK3	23678	37	8	67759522	67759522	Missense_Mutation	SNP	C	T	14	29	c.1169C>T	c.(1168-1170)TCC>TTC	p.S390F
Pat_46	Pre-Treatment	SLCO5A1	81796	37	8	70594486	70594486	Missense_Mutation	SNP	G	A	34	90	c.1715C>T	c.(1714-1716)TCA>TTA	p.S572L
Pat_46	Pre-Treatment	NCOA2	10499	37	8	71069454	71069454	Missense_Mutation	SNP	C	G	14	44	c.1146G>C	c.(1144-1146)ATG>ATC	p.M382I
Pat_46	Pre-Treatment	CA1	759	37	8	86249277	86249277	Missense_Mutation	SNP	G	A	5	22	c.251C>T	c.(250-252)CCT>CTT	p.P84L
Pat_46	Pre-Treatment	CDH17	1015	37	8	95188867	95188867	Missense_Mutation	SNP	G	A	6	23	c.326C>T	c.(325-327)CCA>CTA	p.P109L
Pat_46	Pre-Treatment	RGS22	26166	37	8	101075915	101075915	Missense_Mutation	SNP	G	A	6	21	c.1081C>T	c.(1081-1083)CAT>TAT	p.H361Y
Pat_46	Pre-Treatment	RIMS2	9699	37	8	104898050	104898050	Missense_Mutation	SNP	G	A	8	18	c.557G>A	c.(556-558)CGA>CAA	p.R186Q
Pat_46	Pre-Treatment	PKHD1L1	93035	37	8	110394750	110394750	Missense_Mutation	SNP	G	A	32	112	c.367G>A	c.(367-369)GAA>AAA	p.E123K
Pat_46	Pre-Treatment	PKHD1L1	93035	37	8	110413769	110413769	Missense_Mutation	SNP	C	T	10	43	c.1325C>T	c.(1324-1326)TCC>TTC	p.S442F
Pat_46	Pre-Treatment	PKHD1L1	93035	37	8	110457449	110457449	Missense_Mutation	SNP	G	A	18	31	c.5351G>A	c.(5350-5352)GGA>GAA	p.G1784E
Pat_46	Pre-Treatment	FER1L6	654463	37	8	125076600	125076600	Missense_Mutation	SNP	C	T	26	57	c.3341C>T	c.(3340-3342)TCG>TTG	p.S1114L
Pat_46	Pre-Treatment	MGC70857	414919	37	8	145753440	145753440	Missense_Mutation	SNP	G	A	10	23	c.173C>T	c.(172-174)TCC>TTC	p.S58F
Pat_46	Pre-Treatment	ADAMTSL1	92949	37	9	18662013	18662013	Missense_Mutation	SNP	G	A	39	47	c.1027G>A	c.(1027-1029)GAG>AAG	p.E343K
Pat_46	Pre-Treatment	SLC24A2	25769	37	9	19786182	19786182	Missense_Mutation	SNP	C	T	17	22	c.683G>A	c.(682-684)AGA>AAA	p.R228K
Pat_46	Pre-Treatment	TAF1L	138474	37	9	32635478	32635478	Missense_Mutation	SNP	G	A	22	27	c.100C>T	c.(100-102)CCA>TCA	p.P34S
Pat_46	Pre-Treatment	ALDH1B1	219	37	9	38397279	38397279	Missense_Mutation	SNP	G	A	5	5	c.1534G>A	c.(1534-1536)GTT>ATT	p.V512I
Pat_46	Pre-Treatment	ANXA1	301	37	9	75775212	75775212	Missense_Mutation	SNP	G	A	38	68	c.304G>A	c.(304-306)GGT>AGT	p.G102S
Pat_46	Pre-Treatment	TRPM6	140803	37	9	77386635	77386635	Nonsense_Mutation	SNP	G	A	15	46	c.3520C>T	c.(3520-3522)CGA>TGA	p.R1174*
Pat_46	Pre-Treatment	TRPM6	140803	37	9	77400944	77400944	Nonsense_Mutation	SNP	G	C	22	51	c.2765C>G	c.(2764-2766)TCA>TGA	p.S922*
Pat_46	Pre-Treatment	NTRK2	4915	37	9	87563428	87563428	Missense_Mutation	SNP	G	A	12	22	c.1768G>A	c.(1768-1770)GAG>AAG	p.E590K
Pat_46	Pre-Treatment	C9orf79	286234	37	9	90503694	90503694	Missense_Mutation	SNP	C	T	10	24	c.4292C>T	c.(4291-4293)CCA>CTA	p.P1431L
Pat_46	Pre-Treatment	NFIL3	4783	37	9	94172686	94172686	Missense_Mutation	SNP	C	T	11	62	c.331G>A	c.(331-333)GAA>AAA	p.E111K
Pat_46	Pre-Treatment	ECM2	1842	37	9	95280064	95280064	Missense_Mutation	SNP	C	T	24	40	c.386G>A	c.(385-387)GGA>GAA	p.G129E
Pat_46	Pre-Treatment	FGD3	89846	37	9	95776206	95776206	Missense_Mutation	SNP	G	A	31	111	c.1108G>A	c.(1108-1110)GAA>AAA	p.E370K
Pat_46	Pre-Treatment	PPP3R2	5535	37	9	104357194	104357194	Missense_Mutation	SNP	C	T	22	46	c.19G>A	c.(19-21)GAG>AAG	p.E7K
Pat_46	Pre-Treatment	GRIN3A	116443	37	9	104432484	104432484	Missense_Mutation	SNP	G	A	17	25	c.2210C>T	c.(2209-2211)CCA>CTA	p.P737L
Pat_46	Pre-Treatment	GRIN3A	116443	37	9	104449092	104449092	Missense_Mutation	SNP	C	T	3	16	c.1090G>A	c.(1090-1092)GAA>AAA	p.E364K
Pat_46	Pre-Treatment	OR13C4	138804	37	9	107289213	107289213	Missense_Mutation	SNP	G	A	36	86	c.278C>T	c.(277-279)TCC>TTC	p.S93F
Pat_46	Pre-Treatment	C9orf5	23731	37	9	111795771	111795771	Missense_Mutation	SNP	G	A	19	39	c.2410C>T	c.(2410-2412)CCT>TCT	p.P804S
Pat_46	Pre-Treatment	SVEP1	79987	37	9	113169529	113169529	Missense_Mutation	SNP	C	T	35	68	c.8351G>A	c.(8350-8352)GGA>GAA	p.G2784E
Pat_46	Pre-Treatment	SVEP1	79987	37	9	113170760	113170760	Missense_Mutation	SNP	G	A	9	23	c.7120C>T	c.(7120-7122)CCT>TCT	p.P2374S
Pat_46	Pre-Treatment	SVEP1	79987	37	9	113276344	113276344	Missense_Mutation	SNP	C	T	6	14	c.1007G>A	c.(1006-1008)GGA>GAA	p.G336E
Pat_46	Pre-Treatment	SVEP1	79987	37	9	113312330	113312330	Missense_Mutation	SNP	C	T	29	76	c.586G>A	c.(586-588)GAT>AAT	p.D196N
Pat_46	Pre-Treatment	TNC	3371	37	9	117853113	117853113	Missense_Mutation	SNP	G	A	46	115	c.185C>T	c.(184-186)TCC>TTC	p.S62F
Pat_46	Pre-Treatment	DBC1	1620	37	9	122001016	122001016	Missense_Mutation	SNP	G	A	13	36	c.602C>T	c.(601-603)CCT>CTT	p.P201L
Pat_46	Pre-Treatment	TRAF1	7185	37	9	123673716	123673716	Missense_Mutation	SNP	C	T	9	23	c.781G>A	c.(781-783)GAG>AAG	p.E261K

Pat_46	Pre-Treatment	PTGS1	5742	37	9	125154609	125154609	Missense_Mutation	SNP	C	T	14	25	c.1586C>T	c.(1585-1587)TCC>TTC	p.S529F
Pat_46	Pre-Treatment	OR1L3	26735	37	9	125437757	125437757	Missense_Mutation	SNP	G	A	34	78	c.349G>A	c.(349-351)GCT>ACT	p.A117T
Pat_46	Pre-Treatment	GLE1	2733	37	9	131300352	131300352	Missense_Mutation	SNP	C	T	10	12	c.1864C>T	c.(1864-1866)CTC>TTC	p.L622F
Pat_46	Pre-Treatment	PKN3	29941	37	9	131469652	131469652	Missense_Mutation	SNP	C	T	15	23	c.803C>T	c.(802-804)TCA>TTA	p.S268L
Pat_46	Pre-Treatment	KCNT1	57582	37	9	138657003	138657003	Missense_Mutation	SNP	G	A	15	44	c.1162G>A	c.(1162-1164)GAC>AAC	p.D388N
Pat_46	Pre-Treatment	ARSF	416	37	X	3002685	3002685	Missense_Mutation	SNP	G	C	6	13	c.808G>C	c.(808-810)GAA>CAA	p.E270Q
Pat_46	Pre-Treatment	TBL1X	6907	37	X	9652089	9652089	Missense_Mutation	SNP	C	T	9	59	c.218C>T	c.(217-219)TCC>TTC	p.S73F
Pat_46	Pre-Treatment	ARHGAP6	395	37	X	11272704	11272704	Missense_Mutation	SNP	C	A	8	56	c.712G>T	c.(712-714)GAC>TAC	p.D238Y
Pat_46	Pre-Treatment	TLR7	51284	37	X	12904279	12904279	Missense_Mutation	SNP	G	A	11	33	c.652G>A	c.(652-654)GCC>ACC	p.A218T
Pat_46	Pre-Treatment	GEMIN8	54960	37	X	14027232	14027232	Missense_Mutation	SNP	C	T	5	62	c.529G>A	c.(529-531)GAC>AAC	p.D177N
Pat_46	Pre-Treatment	GLRA2	2742	37	X	14550395	14550395	Missense_Mutation	SNP	G	A	16	73	c.103G>A	c.(103-105)GGA>AGA	p.G35R
Pat_46	Pre-Treatment	GLRA2	2742	37	X	14550467	14550467	Missense_Mutation	SNP	G	A	38	57	c.175G>A	c.(175-177)GAT>AAT	p.D59N
Pat_46	Pre-Treatment	RAI2	10742	37	X	17818903	17818903	Missense_Mutation	SNP	C	T	6	42	c.1228G>A	c.(1228-1230)GAG>AAG	p.E410K
Pat_46	Pre-Treatment	PDHA1	5160	37	X	19368083	19368083	Missense_Mutation	SNP	G	A	8	41	c.146G>A	c.(145-147)GGC>GAC	p.G49D
Pat_46	Pre-Treatment	RPS6KA3	6197	37	X	20252902	20252902	Missense_Mutation	SNP	C	T	5	74	c.100G>A	c.(100-102)GGA>AGA	p.G34R
Pat_46	Pre-Treatment	APOO	79135	37	X	23898990	23898990	Missense_Mutation	SNP	G	A	12	14	c.89C>T	c.(88-90)CCT>CTT	p.P30L
Pat_46	Pre-Treatment	RPGR	6103	37	X	38147138	38147138	Missense_Mutation	SNP	C	T	16	76	c.1729G>A	c.(1729-1731)GAA>AAA	p.E577K
Pat_46	Pre-Treatment	USP9X	8239	37	X	41084022	41084022	Missense_Mutation	SNP	G	A	19	94	c.6779G>A	c.(6778-6780)GGT>GAT	p.G2260D
Pat_46	Pre-Treatment	CASK	8573	37	X	41393962	41393962	Missense_Mutation	SNP	G	A	23	51	c.2299C>T	c.(2299-2301)CCA>TCA	p.P767S
Pat_46	Pre-Treatment	CXorf36	79742	37	X	45059986	45059986	Missense_Mutation	SNP	G	A	5	6	c.86C>T	c.(85-87)TCT>TTT	p.S29F
Pat_46	Pre-Treatment	ZNF182	7569	37	X	47837038	47837038	Missense_Mutation	SNP	G	A	28	40	c.448C>T	c.(448-450)CTT>TTT	p.L150F
Pat_46	Pre-Treatment	WAS	7454	37	X	48549500	48549500	Missense_Mutation	SNP	G	A	5	52	c.1456G>A	c.(1456-1458)GAA>AAA	p.E486K
Pat_46	Pre-Treatment	RRAGB	10325	37	X	55779873	55779873	Missense_Mutation	SNP	G	A	5	23	c.745G>A	c.(745-747)GAA>AAA	p.E249K
Pat_46	Pre-Treatment	KIF4A	24137	37	X	69563831	69563831	Missense_Mutation	SNP	C	T	3	12	c.1430C>T	c.(1429-1431)TCG>TTG	p.S477L
Pat_46	Pre-Treatment	NAP1L2	4674	37	X	72433746	72433746	Missense_Mutation	SNP	C	T	16	17	c.583G>A	c.(583-585)GAA>AAA	p.E195K
Pat_46	Pre-Treatment	NAP1L2	4674	37	X	72434160	72434160	Missense_Mutation	SNP	C	T	8	10	c.169G>A	c.(169-171)GAA>AAA	p.E57K
Pat_46	Pre-Treatment	NXF3	56000	37	X	102338545	102338545	Missense_Mutation	SNP	G	A	50	49	c.427C>T	c.(427-429)CCA>TCA	p.P143S
Pat_46	Pre-Treatment	NRK	203447	37	X	105181449	105181449	Missense_Mutation	SNP	G	A	3	3	c.3674G>A	c.(3673-3675)GGA>GAA	p.G1225E
Pat_46	Pre-Treatment	COL4A5	1287	37	X	107834341	107834341	Nonsense_Mutation	SNP	C	T	12	7	c.1219C>T	c.(1219-1221)CAG>TAG	p.Q407*
Pat_46	Pre-Treatment	COL4A5	1287	37	X	107840679	107840679	Missense_Mutation	SNP	C	T	4	15	c.1660C>T	c.(1660-1662)CCA>TCA	p.P554S
Pat_46	Pre-Treatment	TRPC5	7224	37	X	111019987	111019987	Nonsense_Mutation	SNP	T	A	22	23	c.2476A>T	c.(2476-2478)AAG>TAG	p.K826*
Pat_46	Pre-Treatment	TFDP3	51270	37	X	132351393	132351393	Missense_Mutation	SNP	C	T	13	14	c.895G>A	c.(895-897)GGC>AGC	p.G299S
Pat_46	Pre-Treatment	SAGE1	55511	37	X	134994087	134994087	Missense_Mutation	SNP	G	A	9	15	c.2496G>A	c.(2494-2496)ATG>ATA	p.M832I
Pat_46	Pre-Treatment	MCF2	4168	37	X	138669924	138669924	Nonsense_Mutation	SNP	G	A	16	26	c.2473C>T	c.(2473-2475)CAA>TAA	p.Q825*
Pat_46	Pre-Treatment	PASD1	139135	37	X	150789990	150789990	Missense_Mutation	SNP	G	A	14	16	c.344G>A	c.(343-345)GGA>GAA	p.G115E
Pat_46	Pre-Treatment	MAGEA6	4105	37	X	151870202	151870202	Missense_Mutation	SNP	C	T	31	51	c.892C>T	c.(892-894)CGC>TGC	p.R298C
Pat_46	Pre-Treatment	MAGEA3	4102	37	X	151935227	151935227	Missense_Mutation	SNP	C	T	45	56	c.940G>A	c.(940-942)GAG>AAG	p.E314K
Pat_46	Post-Resistance	RERE	473	37	1	8557562	8557562	Missense_Mutation	SNP	G	A	7	77	c.907C>T	c.(907-909)CCT>TCT	p.P303S
Pat_46	Post-Resistance	PRAMEF12	390999	37	1	12835119	12835119	Missense_Mutation	SNP	C	T	4	16	c.109C>T	c.(109-111)CCC>TCC	p.P37S
Pat_46	Post-Resistance	PRAMEF11	440560	37	1	12884991	12884991	Missense_Mutation	SNP	G	A	9	81	c.1120C>T	c.(1120-1122)CCT>TCT	p.P374S
Pat_46	Post-Resistance	PRAMEF8	391002	37	1	12979781	12979781	Missense_Mutation	SNP	G	A	3	22	c.973G>A	c.(973-975)GAC>AAC	p.D325N
Pat_46	Post-Resistance	TMEM50A	23585	37	1	25679423	25679423	Missense_Mutation	SNP	A	G	8	79	c.325A>G	c.(325-327)ATT>GTT	p.I109V
Pat_46	Post-Resistance	TMEM57	55219	37	1	25773296	25773296	Missense_Mutation	SNP	C	T	3	17	c.124C>T	c.(124-126)CTC>TTC	p.L42F
Pat_46	Post-Resistance	CSMD2	114784	37	1	34008335	34008335	Missense_Mutation	SNP	C	T	5	12	c.8830G>A	c.(8830-8832)GAC>AAC	p.D2944N
Pat_46	Post-Resistance	PTCH2	8643	37	1	45293837	45293837	Missense_Mutation	SNP	A	T	5	16	c.1736T>A	c.(1735-1737)ATC>AAC	p.I579N
Pat_46	Post-Resistance	KIAA0494	9813	37	1	47155318	47155318	Missense_Mutation	SNP	G	A	15	92	c.736C>T	c.(736-738)CCG>TCG	p.P246S
Pat_46	Post-Resistance	PPAP2B	8613	37	1	56977670	56977670	Missense_Mutation	SNP	C	T	4	45	c.788G>A	c.(787-789)GGA>GAA	p.G263E

Pat_46	Post-Resistance	PRKAA2	5563	37	1	57140179	57140179	Missense_Mutation	SNP	C	T	11	53	c.220C>T	c.(220-222)CCT>TCT	p.P74S
Pat_46	Post-Resistance	C1orf168	199920	37	1	57219580	57219580	Missense_Mutation	SNP	C	T	6	46	c.1159G>A	c.(1159-1161)GAA>AAA	p.E387K
Pat_46	Post-Resistance	C1orf168	199920	37	1	57254664	57254664	Missense_Mutation	SNP	G	A	4	39	c.901C>T	c.(901-903)CCC>TCC	p.P301S
Pat_46	Post-Resistance	C8A	731	37	1	57341860	57341860	Missense_Mutation	SNP	G	A	4	38	c.442G>A	c.(442-444)GGA>AGA	p.G148R
Pat_46	Post-Resistance	C8A	731	37	1	57378223	57378223	Missense_Mutation	SNP	C	T	7	40	c.1528C>T	c.(1528-1530)CTC>TTC	p.L510F
Pat_46	Post-Resistance	C8B	732	37	1	57417816	57417816	Missense_Mutation	SNP	G	A	9	108	c.571C>T	c.(571-573)CTT>TTT	p.L191F
Pat_46	Post-Resistance	NFIA	4774	37	1	61554084	61554085	Nonsense_Mutation	DNP	GA	AT	10	130	c.291_292GA>AT	289-294)GGGAAA>GGAT	p.K98*
Pat_46	Post-Resistance	ANGPTL3	27329	37	1	63069640	63069640	Missense_Mutation	SNP	G	A	7	44	c.932G>A	c.(931-933)GGA>GAA	p.G311E
Pat_46	Post-Resistance	WDR78	79819	37	1	67337106	67337106	Missense_Mutation	SNP	C	T	3	22	c.887G>A	c.(886-888)GGA>GAA	p.G296E
Pat_46	Post-Resistance	LRRIQ3	127255	37	1	74507177	74507177	Nonsense_Mutation	SNP	G	A	8	87	c.1438C>T	c.(1438-1440)CAG>TAG	p.Q480*
Pat_46	Post-Resistance	LRRC8D	55144	37	1	90400752	90400752	Missense_Mutation	SNP	G	A	5	65	c.2125G>A	c.(2125-2127)GAG>AAG	p.E709K
Pat_46	Post-Resistance	FRRS1	391059	37	1	100176461	100176461	Missense_Mutation	SNP	G	A	3	19	c.1525C>T	c.(1525-1527)CCT>TCT	p.P509S
Pat_46	Post-Resistance	AGL	178	37	1	100327245	100327245	Missense_Mutation	SNP	C	T	8	78	c.269C>T	c.(268-270)TCA>TTA	p.S90L
Pat_46	Post-Resistance	OLFM3	118427	37	1	102296359	102296359	Missense_Mutation	SNP	C	T	10	72	c.301G>A	c.(301-303)GAA>AAA	p.E101K
Pat_46	Post-Resistance	C1orf103	55791	37	1	111490682	111490682	Missense_Mutation	SNP	C	T	12	99	c.2209G>A	c.(2209-2211)GAA>AAA	p.E737K
Pat_46	Post-Resistance	OVGP1	5016	37	1	111964197	111964197	Missense_Mutation	SNP	G	A	5	46	c.707C>T	c.(706-708)CCC>CTC	p.P236L
Pat_46	Post-Resistance	WDR77	79084	37	1	111991249	111991249	Missense_Mutation	SNP	G	A	4	43	c.293C>T	c.(292-294)TCC>TTC	p.S98F
Pat_46	Post-Resistance	RSBN1	54665	37	1	114340403	114340403	Nonsense_Mutation	SNP	A	T	11	88	c.959T>A	c.(958-960)TTA>TAA	p.L320*
Pat_46	Post-Resistance	VTCN1	79679	37	1	117699309	117699309	Missense_Mutation	SNP	C	T	6	41	c.332G>A	c.(331-333)GGC>GAC	p.G111D
Pat_46	Post-Resistance	SPAG17	200162	37	1	118570912	118570912	Missense_Mutation	SNP	C	T	11	55	c.3715G>A	c.(3715-3717)GGA>AGA	p.G1239R
Pat_46	Post-Resistance	WARS2	10352	37	1	119619088	119619088	Missense_Mutation	SNP	G	A	6	54	c.233C>T	c.(232-234)TCC>TTC	p.S78F
Pat_46	Post-Resistance	HIST2H2AB	317772	37	1	149859168	149859168	Missense_Mutation	SNP	C	T	15	136	c.299G>A	c.(298-300)GGT>GAT	p.G100D
Pat_46	Post-Resistance	ECM1	1893	37	1	150483973	150483973	Missense_Mutation	SNP	C	T	6	40	c.749C>T	c.(748-750)TCG>TTG	p.S250L
Pat_46	Post-Resistance	C1orf56	54964	37	1	151021165	151021165	Missense_Mutation	SNP	G	A	17	168	c.842G>A	c.(841-843)AGT>AAT	p.S281N
Pat_46	Post-Resistance	HRNR	388697	37	1	152192583	152192583	Missense_Mutation	SNP	C	T	17	220	c.1522G>A	c.(1522-1524)GGA>AGA	p.G508R
Pat_46	Post-Resistance	HRNR	388697	37	1	152193753	152193753	Missense_Mutation	SNP	C	T	18	53	c.352G>A	c.(352-354)GAG>AAG	p.E118K
Pat_46	Post-Resistance	FLG	2312	37	1	152286716	152286716	Missense_Mutation	SNP	C	T	13	46	c.646G>A	c.(646-648)GAT>AAT	p.D216N
Pat_46	Post-Resistance	CRNN	49860	37	1	152382906	152382906	Missense_Mutation	SNP	C	T	28	80	c.652G>A	c.(652-654)GAC>AAC	p.D218N
Pat_46	Post-Resistance	LCE1E	353135	37	1	152760070	152760070	Missense_Mutation	SNP	C	T	5	26	c.295C>T	c.(295-297)CCC>TCC	p.P99S
Pat_46	Post-Resistance	UBAP2L	9898	37	1	154221896	154221896	Missense_Mutation	SNP	C	T	10	91	c.1196C>T	c.(1195-1197)CCA>CTA	p.P399L
Pat_46	Post-Resistance	DCST1	149095	37	1	155015964	155015964	Missense_Mutation	SNP	C	T	5	24	c.1151C>T	c.(1150-1152)ACT>ATT	p.T384I
Pat_46	Post-Resistance	FAM189B	10712	37	1	155220484	155220484	Missense_Mutation	SNP	G	A	5	13	c.1093C>T	c.(1093-1095)CGC>TGC	p.R365C
Pat_46	Post-Resistance	OR10K1	391109	37	1	158435659	158435659	Missense_Mutation	SNP	C	T	7	58	c.308C>T	c.(307-309)TCC>TTC	p.S103F
Pat_46	Post-Resistance	SPTA1	6708	37	1	158646045	158646045	Missense_Mutation	SNP	G	A	16	141	c.998C>T	c.(997-999)TCC>TTC	p.S333F
Pat_46	Post-Resistance	OR10J3	441911	37	1	159284365	159284365	Missense_Mutation	SNP	A	C	12	198	c.85T>G	c.(85-87)TTT>GTT	p.F29V
Pat_46	Post-Resistance	PVRL4	81607	37	1	161049730	161049730	Missense_Mutation	SNP	G	A	10	42	c.89C>T	c.(88-90)CCC>CTC	p.P30L
Pat_46	Post-Resistance	ADAMTS4	9507	37	1	161163432	161163432	Missense_Mutation	SNP	G	A	41	141	c.1733C>T	c.(1732-1734)TCA>TTA	p.S578L
Pat_46	Post-Resistance	F5	2153	37	1	169512194	169512194	Missense_Mutation	SNP	G	A	67	118	c.2134C>T	c.(2134-2136)CGT>TGT	p.R712C
Pat_46	Post-Resistance	SELE	6401	37	1	169698486	169698486	Nonsense_Mutation	SNP	G	A	4	24	c.931C>T	c.(931-933)CAG>TAG	p.Q311*
Pat_46	Post-Resistance	BAT2L2	23215	37	1	171509906	171509906	Missense_Mutation	SNP	C	T	8	48	c.3295C>T	c.(3295-3297)CCA>TCA	p.P1099S
Pat_46	Post-Resistance	ASTN1	460	37	1	176833520	176833520	Missense_Mutation	SNP	C	T	6	55	c.3785G>A	c.(3784-3786)GGA>GAA	p.G1262E
Pat_46	Post-Resistance	CACNA1E	777	37	1	181745241	181745241	Missense_Mutation	SNP	T	C	12	156	c.5144T>C	c.(5143-5145)CTC>CCC	p.L1715P
Pat_46	Post-Resistance	HMCN1	83872	37	1	186024803	186024803	Missense_Mutation	SNP	C	T	13	112	c.7141C>T	c.(7141-7143)CAT>TAT	p.H2381Y
Pat_46	Post-Resistance	HMCN1	83872	37	1	186121957	186121957	Missense_Mutation	SNP	G	A	7	130	c.14972G>A	c.(14971-14973)AGT>AAT	p.S4991N
Pat_46	Post-Resistance	RGS21	431704	37	1	192335238	192335238	Nonsense_Mutation	SNP	G	A	15	34	c.443G>A	c.(442-444)TGG>TAG	p.W148*
Pat_46	Post-Resistance	CAMSAP1L1	23271	37	1	200818755	200818755	Missense_Mutation	SNP	C	T	6	102	c.2891C>T	c.(2890-2892)CCT>CTT	p.P964L
Pat_46	Post-Resistance	SNRPE	6635	37	1	203834217	203834217	Missense_Mutation	SNP	C	T	14	91	c.193C>T	c.(193-195)CAT>TAT	p.H65Y

Pat_46	Post-Resistance	C4BPA	722	37	1	207297538	207297538	Missense_Mutation	SNP	C	T	16	71	c.533C>T	c.(532-534)CCT>CTT	p.P178L
Pat_46	Post-Resistance	INTS7	25896	37	1	212151816	212151816	Missense_Mutation	SNP	C	T	6	33	c.1268G>A	c.(1267-1269)AGG>AAG	p.R423K
Pat_46	Post-Resistance	USH2A	7399	37	1	215844436	215844436	Missense_Mutation	SNP	C	T	18	39	c.14011G>A	c.(14011-14013)GAA>AAA	p.E4671K
Pat_46	Post-Resistance	USH2A	7399	37	1	215847707	215847707	Missense_Mutation	SNP	C	T	6	68	c.13546G>A	.(13546-13548)GGG>AG	p.G4516R
Pat_46	Post-Resistance	RAB3GAP2	25782	37	1	220369723	220369723	Missense_Mutation	SNP	G	A	6	47	c.829C>T	c.(829-831)CCC>TCC	p.P277S
Pat_46	Post-Resistance	MOSC2	54996	37	1	220955223	220955223	Missense_Mutation	SNP	C	T	11	125	c.988C>T	c.(988-990)CCT>TCT	p.P330S
Pat_46	Post-Resistance	OBSCN	84033	37	1	228468465	228468465	Missense_Mutation	SNP	C	T	3	2	c.8165C>T	c.(8164-8166)TCC>TTC	p.S2722F
Pat_46	Post-Resistance	SLC35F3	148641	37	1	234367322	234367322	Missense_Mutation	SNP	C	T	11	72	c.236C>T	c.(235-237)TCG>TTG	p.S79L
Pat_46	Post-Resistance	RYR2	6262	37	1	237777611	237777611	Missense_Mutation	SNP	C	T	4	12	c.5183C>T	c.(5182-5184)CCC>CTC	p.P1728L
Pat_46	Post-Resistance	OR2W5	441932	37	1	247655264	247655264	Missense_Mutation	SNP	C	T	5	61	c.835C>T	c.(835-837)CAC>TAC	p.H279Y
Pat_46	Post-Resistance	OR2L13	284521	37	1	248263515	248263515	Missense_Mutation	SNP	C	T	16	27	c.838C>T	c.(838-840)CTT>TTT	p.L280F
Pat_46	Post-Resistance	TUBAL3	79861	37	10	5436006	5436006	Missense_Mutation	SNP	A	T	9	52	c.815T>A	c.(814-816)ATA>AAA	p.I272K
Pat_46	Post-Resistance	OLAH	55301	37	10	15107598	15107598	Missense_Mutation	SNP	C	T	4	32	c.418C>T	c.(418-420)CGC>TGC	p.R140C
Pat_46	Post-Resistance	ITGA8	8516	37	10	15590507	15590507	Missense_Mutation	SNP	C	T	8	35	c.2827G>A	c.(2827-2829)GAA>AAA	p.E943K
Pat_46	Post-Resistance	ITGA8	8516	37	10	15646281	15646281	Missense_Mutation	SNP	C	T	5	37	c.2044G>A	c.(2044-2046)GGA>AGA	p.G682R
Pat_46	Post-Resistance	PIP4K2A	5305	37	10	22898620	22898620	Missense_Mutation	SNP	G	C	17	82	c.171C>G	c.(169-171)ATC>ATG	p.I57M
Pat_46	Post-Resistance	PTCHD3	374308	37	10	27702954	27702955	Missense_Mutation	DNP	GG	AA	4	23	c.225_226CC>TT	223-228)CCCCCC>CCTT	p.P76S
Pat_46	Post-Resistance	MPP7	143098	37	10	28408594	28408594	Missense_Mutation	SNP	G	A	13	100	c.938C>T	c.(937-939)TCC>TTC	p.S313F
Pat_46	Post-Resistance	ANKRD30A	91074	37	10	37490242	37490242	Missense_Mutation	SNP	G	A	4	44	c.2690G>A	c.(2689-2691)GGA>GAA	p.G897E
Pat_46	Post-Resistance	ZNF37A	7587	37	10	38407040	38407040	Missense_Mutation	SNP	C	T	6	50	c.961C>T	c.(961-963)CAT>TAT	p.H321Y
Pat_46	Post-Resistance	FRMPD2	143162	37	10	49430394	49430394	Missense_Mutation	SNP	G	A	8	52	c.1417C>T	c.(1417-1419)CTT>TTT	p.L473F
Pat_46	Post-Resistance	OGDHL	55753	37	10	50953927	50953927	Missense_Mutation	SNP	C	T	4	26	c.1393G>A	c.(1393-1395)GAT>AAT	p.D465N
Pat_46	Post-Resistance	NCOA4	8031	37	10	51579247	51579247	Missense_Mutation	SNP	C	T	19	95	c.106C>T	c.(106-108)CGG>TGG	p.R36W
Pat_46	Post-Resistance	PCDH15	65217	37	10	55955628	55955628	Missense_Mutation	SNP	G	A	4	46	c.1120C>T	c.(1120-1122)CCT>TCT	p.P374S
Pat_46	Post-Resistance	BICC1	80114	37	10	60558923	60558923	Missense_Mutation	SNP	C	T	5	9	c.1636C>T	c.(1636-1638)CCT>TCT	p.P546S
Pat_46	Post-Resistance	ANK3	288	37	10	61829433	61829433	Missense_Mutation	SNP	C	T	6	63	c.11206G>A	c.(11206-11208)GAA>AAA	p.E3736K
Pat_46	Post-Resistance	COL13A1	1305	37	10	71712675	71712675	Missense_Mutation	SNP	G	A	5	28	c.2063G>A	c.(2062-2064)GGG>GAG	p.G688E
Pat_46	Post-Resistance	C10orf55	414236	37	10	75671974	75671974	Missense_Mutation	SNP	G	A	4	40	c.29C>T	c.(28-30)TCG>TTG	p.S10L
Pat_46	Post-Resistance	SFTPA1	653509	37	10	81373492	81373492	Splice_Site	SNP	G	A	5	60	c.371_splice	c.e6-1	p.A124_splice
Pat_46	Post-Resistance	IFIT1	3434	37	10	91162729	91162729	Missense_Mutation	SNP	G	A	15	130	c.697G>A	c.(697-699)GAA>AAA	p.E233K
Pat_46	Post-Resistance	CYP2C18	1562	37	10	96447594	96447594	Missense_Mutation	SNP	G	A	10	81	c.236G>A	c.(235-237)GGA>GAA	p.G79E
Pat_46	Post-Resistance	FAM178A	55719	37	10	102684341	102684341	Missense_Mutation	SNP	C	T	7	99	c.1583C>T	c.(1582-1584)ACT>ATT	p.T528I
Pat_46	Post-Resistance	TACC2	10579	37	10	123970436	123970436	Missense_Mutation	SNP	G	A	15	81	c.6496G>A	c.(6496-6498)GGG>AGG	p.G2166R
Pat_46	Post-Resistance	C10orf137	26098	37	10	127424384	127424384	Missense_Mutation	SNP	C	T	9	71	c.1669C>T	c.(1669-1671)CCA>TCA	p.P557S
Pat_46	Post-Resistance	C10orf90	118611	37	10	128192921	128192921	Missense_Mutation	SNP	G	C	6	61	c.848C>G	c.(847-849)CCC>CGC	p.P283R
Pat_46	Post-Resistance	ZNF215	7762	37	11	6964847	6964847	Missense_Mutation	SNP	A	C	12	100	c.687A>C	c.(685-687)AAA>AAC	p.K229N
Pat_46	Post-Resistance	NLRP14	338323	37	11	7064044	7064044	Missense_Mutation	SNP	G	A	9	69	c.787G>A	c.(787-789)GAA>AAA	p.E263K
Pat_46	Post-Resistance	NLRP14	338323	37	11	7091675	7091675	Missense_Mutation	SNP	T	C	6	41	c.3134T>C	c.(3133-3135)CTA>CCA	p.L1045P
Pat_46	Post-Resistance	PPFIBP2	8495	37	11	7586787	7586787	Missense_Mutation	SNP	C	T	7	104	c.68C>T	c.(67-69)ACT>ATT	p.T23I
Pat_46	Post-Resistance	ST5	6764	37	11	8751675	8751675	Missense_Mutation	SNP	G	A	6	47	c.1162C>T	c.(1162-1164)CCC>TCC	p.P388S
Pat_46	Post-Resistance	TEAD1	7003	37	11	12901301	12901301	Missense_Mutation	SNP	C	T	5	36	c.332C>T	c.(331-333)TCC>TTC	p.S111F
Pat_46	Post-Resistance	BTBD10	84280	37	11	13424775	13424775	Missense_Mutation	SNP	C	T	21	126	c.1057G>A	c.(1057-1059)GAT>AAT	p.D353N
Pat_46	Post-Resistance	GAS2	2620	37	11	22707294	22707294	Missense_Mutation	SNP	G	A	7	40	c.226G>A	c.(226-228)GAG>AAG	p.E76K
Pat_46	Post-Resistance	CCDC73	493860	37	11	32720870	32720870	Missense_Mutation	SNP	C	T	4	31	c.317G>A	c.(316-318)GGA>GAA	p.G106E
Pat_46	Post-Resistance	CSTF3	1479	37	11	33124691	33124691	Missense_Mutation	SNP	G	A	9	37	c.625C>T	c.(625-627)CGG>TGG	p.R209W
Pat_46	Post-Resistance	RAG2	5897	37	11	36615100	36615100	Missense_Mutation	SNP	G	A	7	88	c.619C>T	c.(619-621)CAT>TAT	p.H207Y
Pat_46	Post-Resistance	PTPMT1	114971	37	11	47587227	47587227	Missense_Mutation	SNP	C	T	2	2	c.53C>T	c.(52-54)CCG>CTG	p.P18L

Pat_46	Post-Resistance	PTPRJ	5795	37	11	48134313	48134313	Missense_Mutation	SNP	C	T	15	80	c.130C>T	c.(130-132)CCT>TCT	p.P44S
Pat_46	Post-Resistance	TRIM48	79097	37	11	55032647	55032647	Missense_Mutation	SNP	G	A	15	37	c.316G>A	c.(316-318)GAG>AAG	p.E106K
Pat_46	Post-Resistance	OR4C6	219432	37	11	55432600	55432600	Splice_Site	SNP	G	A	7	18	c.-41_splice	c.e3-1	
Pat_46	Post-Resistance	OR5L2	26338	37	11	55594915	55594915	Missense_Mutation	SNP	C	T	48	81	c.221C>T	c.(220-222)TCC>TTC	p.S74F
Pat_46	Post-Resistance	OR5AS1	219447	37	11	55798826	55798826	Missense_Mutation	SNP	C	T	5	32	c.932C>T	c.(931-933)TCA>TTA	p.S311L
Pat_46	Post-Resistance	OR8H2	390151	37	11	55873258	55873258	Missense_Mutation	SNP	G	A	8	44	c.740G>A	c.(739-741)GGA>GAA	p.G247E
Pat_46	Post-Resistance	OR8J1	219477	37	11	56128414	56128414	Missense_Mutation	SNP	C	T	8	21	c.692C>T	c.(691-693)TCA>TTA	p.S231L
Pat_46	Post-Resistance	FAM111A	63901	37	11	58919839	58919839	Missense_Mutation	SNP	C	T	5	74	c.698C>T	c.(697-699)TCC>TTC	p.S233F
Pat_46	Post-Resistance	OR4D11	219986	37	11	59271374	59271374	Missense_Mutation	SNP	G	A	12	39	c.326G>A	c.(325-327)GGG>GAG	p.G109E
Pat_46	Post-Resistance	OR4D9	390199	37	11	59283079	59283079	Missense_Mutation	SNP	G	A	7	100	c.694G>A	c.(694-696)GGC>AGC	p.G232S
Pat_46	Post-Resistance	OSBP	5007	37	11	59344425	59344425	Missense_Mutation	SNP	G	A	21	222	c.2134C>T	c.(2134-2136)CCC>TCC	p.P712S
Pat_46	Post-Resistance	MS4A2	2206	37	11	59861474	59861474	Missense_Mutation	SNP	G	A	7	73	c.575G>A	c.(574-576)GGA>GAA	p.G192E
Pat_46	Post-Resistance	DAK	26007	37	11	61105584	61105584	Missense_Mutation	SNP	C	T	4	16	c.175C>T	c.(175-177)CAT>TAT	p.H59Y
Pat_46	Post-Resistance	AHNAK	79026	37	11	62292075	62292075	Missense_Mutation	SNP	G	A	5	45	c.9814C>T	c.(9814-9816)CCA>TCA	p.P3272S
Pat_46	Post-Resistance	MTA2	9219	37	11	62366028	62366028	Missense_Mutation	SNP	G	A	23	177	c.274C>T	c.(274-276)CGG>TGG	p.R92W
Pat_46	Post-Resistance	SLC22A25	387601	37	11	62933592	62933592	Missense_Mutation	SNP	C	T	18	21	c.1209G>A	c.(1207-1209)ATG>ATA	p.M403I
Pat_46	Post-Resistance	SLC22A10	387775	37	11	63057642	63057642	Missense_Mutation	SNP	C	T	7	11	c.5C>T	c.(4-6)GCC>GTC	p.A2V
Pat_46	Post-Resistance	SLC22A10	387775	37	11	63072267	63072267	Missense_Mutation	SNP	G	A	10	63	c.1504G>A	c.(1504-1506)GGA>AGA	p.G502R
Pat_46	Post-Resistance	SLC22A12	116085	37	11	64359368	64359368	Missense_Mutation	SNP	G	A	5	8	c.340G>A	c.(340-342)GAG>AAG	p.E114K
Pat_46	Post-Resistance	CDC42BPG	55561	37	11	64606627	64606627	Missense_Mutation	SNP	G	A	15	36	c.754C>T	c.(754-756)CAC>TAC	p.H252Y
Pat_46	Post-Resistance	TM7SF2	7108	37	11	64882284	64882284	Missense_Mutation	SNP	G	A	4	32	c.703G>A	c.(703-705)GGT>AGT	p.G235S
Pat_46	Post-Resistance	TM7SF2	7108	37	11	64883503	64883503	Missense_Mutation	SNP	G	A	9	24	c.1235G>A	c.(1234-1236)CGC>CAC	p.R412H
Pat_46	Post-Resistance	NPAS4	266743	37	11	66192378	66192378	Missense_Mutation	SNP	T	A	9	43	c.2017T>A	c.(2017-2019)TCC>ACC	p.S673T
Pat_46	Post-Resistance	CABP2	51475	37	11	67286622	67286622	Missense_Mutation	SNP	C	T	4	43	c.651G>A	c.(649-651)ATG>ATA	p.M217I
Pat_46	Post-Resistance	PPFIA1	8500	37	11	70194471	70194471	Missense_Mutation	SNP	G	A	7	56	c.2108G>A	c.(2107-2109)CGA>CAA	p.R703Q
Pat_46	Post-Resistance	SYTL2	54843	37	11	85425493	85425493	Missense_Mutation	SNP	C	T	5	62	c.1673G>A	c.(1672-1674)AGG>AAG	p.R558K
Pat_46	Post-Resistance	PICALM	8301	37	11	85718599	85718599	Missense_Mutation	SNP	G	A	14	106	c.793C>T	c.(793-795)CCA>TCA	p.P265S
Pat_46	Post-Resistance	TRPC6	7225	37	11	101342086	101342086	Missense_Mutation	SNP	C	T	5	44	c.2237G>A	c.(2236-2238)AGG>AAG	p.R746K
Pat_46	Post-Resistance	APOA4	337	37	11	116692155	116692155	Missense_Mutation	SNP	C	T	7	56	c.619G>A	c.(619-621)GAA>AAA	p.E207K
Pat_46	Post-Resistance	SPA17	53340	37	11	124564280	124564280	Missense_Mutation	SNP	G	A	8	61	c.394G>A	c.(394-396)GAG>AAG	p.E132K
Pat_46	Post-Resistance	NFRKB	4798	37	11	129740050	129740050	Missense_Mutation	SNP	G	A	4	51	c.2870C>T	c.(2869-2871)CCC>CTC	p.P957L
Pat_46	Post-Resistance	WNK1	65125	37	12	995120	995120	Missense_Mutation	SNP	C	T	9	167	c.5150C>T	c.(5149-5151)CCA>CTA	p.P1717L
Pat_46	Post-Resistance	PRB2	653247	37	12	11546515	11546515	Missense_Mutation	SNP	C	T	20	133	c.497G>A	c.(496-498)GGA>GAA	p.G166E
Pat_46	Post-Resistance	PIK3C2G	5288	37	12	18747456	18747456	Missense_Mutation	SNP	C	T	7	62	c.3917C>T	c.(3916-3918)TCT>TTT	p.S1306F
Pat_46	Post-Resistance	PLCZ1	89869	37	12	18837172	18837172	Missense_Mutation	SNP	G	A	6	54	c.1633C>T	c.(1633-1635)CAT>TAT	p.H545Y
Pat_46	Post-Resistance	ABCC9	10060	37	12	21997810	21997810	Missense_Mutation	SNP	C	T	6	30	c.3136G>A	c.(3136-3138)GGC>AGC	p.G1046S
Pat_46	Post-Resistance	OVCH1	341350	37	12	29598333	29598333	Missense_Mutation	SNP	C	T	3	13	c.2759G>A	c.(2758-2760)GGA>GAA	p.G920E
Pat_46	Post-Resistance	C12orf40	283461	37	12	40114899	40114899	Missense_Mutation	SNP	C	T	12	81	c.1805C>T	c.(1804-1806)TCT>TTT	p.S602F
Pat_46	Post-Resistance	ZNF641	121274	37	12	48737343	48737343	Nonsense_Mutation	SNP	G	A	4	19	c.730C>T	c.(730-732)CAG>TAG	p.Q244*
Pat_46	Post-Resistance	DIP2B	57609	37	12	51084862	51084862	Missense_Mutation	SNP	G	A	7	53	c.1582G>A	c.(1582-1584)GGA>AGA	p.G528R
Pat_46	Post-Resistance	GALNT6	11226	37	12	51773135	51773135	Missense_Mutation	SNP	G	A	3	19	c.431C>T	c.(430-432)GCC>GTC	p.A144V
Pat_46	Post-Resistance	KRT6B	3854	37	12	52841737	52841737	Missense_Mutation	SNP	C	T	4	48	c.1249G>A	c.(1249-1251)GAG>AAG	p.E417K
Pat_46	Post-Resistance	ESPL1	9700	37	12	53677195	53677195	Missense_Mutation	SNP	C	T	5	64	c.2950C>T	c.(2950-2952)CTT>TTT	p.L984F
Pat_46	Post-Resistance	OR6C76	390326	37	12	55820086	55820086	Missense_Mutation	SNP	G	A	16	93	c.49G>A	c.(49-51)GAT>AAT	p.D17N
Pat_46	Post-Resistance	ERBB3	2065	37	12	56482351	56482351	Missense_Mutation	SNP	C	T	21	123	c.899C>T	c.(898-900)TCC>TTC	p.S300F
Pat_46	Post-Resistance	ERBB3	2065	37	12	56493646	56493646	Missense_Mutation	SNP	C	T	7	35	c.2962C>T	c.(2962-2964)CCT>TCT	p.P988S
Pat_46	Post-Resistance	TAC3	6866	37	12	57406203	57406203	Missense_Mutation	SNP	G	A	4	31	c.326C>T	c.(325-327)CCC>CTC	p.P109L

Pat_46	Post-Resistance	MDM2	4193	37	12	69233409	69233409	Missense_Mutation	SNP	C	T	16	82	c.1274C>T	c.(1273-1275)ACC>ATC	p.T425I
Pat_46	Post-Resistance	ACSS3	79611	37	12	81503391	81503391	Missense_Mutation	SNP	G	A	8	43	c.364G>A	c.(364-366)GAA>AAA	p.E122K
Pat_46	Post-Resistance	SCYL2	55681	37	12	100676720	100676720	Splice_Site	SNP	G	A	3	20	c.-27_splice	c.e2-1	
Pat_46	Post-Resistance	SLC5A8	160728	37	12	101551118	101551118	Missense_Mutation	SNP	G	A	7	20	c.1772C>T	c.(1771-1773)GCT>GTT	p.A591V
Pat_46	Post-Resistance	CCDC63	160762	37	12	111342415	111342415	Missense_Mutation	SNP	G	A	4	39	c.1366G>A	c.(1366-1368)GAC>AAC	p.D456N
Pat_46	Post-Resistance	ATXN2	6311	37	12	111923086	111923086	Missense_Mutation	SNP	G	A	10	121	c.2987C>T	c.(2986-2988)ACA>ATA	p.T996I
Pat_46	Post-Resistance	CLIP1	6249	37	12	122862378	122862378	Missense_Mutation	SNP	C	T	13	134	c.215G>A	c.(214-216)GGA>GAA	p.G72E
Pat_46	Post-Resistance	DNAH10	196385	37	12	124281297	124281297	Missense_Mutation	SNP	G	A	8	42	c.1727G>A	c.(1726-1728)CGA>CAA	p.R576Q
Pat_46	Post-Resistance	GALNT9	50614	37	12	132681768	132681768	Missense_Mutation	SNP	G	A	3	16	c.1696C>T	c.(1696-1698)CGC>TGC	p.R566C
Pat_46	Post-Resistance	CHFR	55743	37	12	133438221	133438221	Splice_Site	SNP	C	T	3	9	c.620_splice	c.e7-1	p.G207_splice
Pat_46	Post-Resistance	CHFR	55743	37	12	133448918	133448918	Missense_Mutation	SNP	G	A	8	92	c.296C>T	c.(295-297)ACT>ATT	p.T99I
Pat_46	Post-Resistance	GJB2	2706	37	13	20763467	20763467	Missense_Mutation	SNP	G	A	4	23	c.254C>T	c.(253-255)TCC>TTC	p.S85F
Pat_46	Post-Resistance	PAN3	255967	37	13	28846200	28846200	Nonsense_Mutation	SNP	C	T	9	61	c.1603C>T	c.(1603-1605)CAG>TAG	p.Q535*
Pat_46	Post-Resistance	STARD13	90627	37	13	33704213	33704213	Missense_Mutation	SNP	C	T	2	5	c.601G>A	c.(601-603)GAA>AAA	p.E201K
Pat_46	Post-Resistance	SPG20	23111	37	13	36905658	36905658	Missense_Mutation	SNP	G	A	8	68	c.886C>T	c.(886-888)CCT>TCT	p.P296S
Pat_46	Post-Resistance	NUFIP1	26747	37	13	45517755	45517755	Missense_Mutation	SNP	C	T	7	110	c.1193G>A	c.(1192-1194)AGC>AAC	p.S398N
Pat_46	Post-Resistance	SCEL	8796	37	13	78130735	78130735	Missense_Mutation	SNP	G	A	20	137	c.48G>A	c.(46-48)ATG>ATA	p.M16I
Pat_46	Post-Resistance	COL4A1	1282	37	13	110864805	110864805	Missense_Mutation	SNP	G	A	8	120	c.346C>T	c.(346-348)CCG>TCG	p.P116S
Pat_46	Post-Resistance	TMEM55B	90809	37	14	20928435	20928435	Missense_Mutation	SNP	C	T	5	49	c.356G>A	c.(355-357)GGG>GAG	p.G119E
Pat_46	Post-Resistance	REM2	161253	37	14	23354141	23354141	Missense_Mutation	SNP	G	A	5	28	c.362G>A	c.(361-363)GGG>GAG	p.G121E
Pat_46	Post-Resistance	MYH6	4624	37	14	23876313	23876314	Missense_Mutation	DNP	GG	AA	12	109	c.119_120CC>TT	c.(118-120)CCC>CTT	p.P40L
Pat_46	Post-Resistance	NPAS3	64067	37	14	33684488	33684488	Missense_Mutation	SNP	C	T	7	59	c.241C>T	c.(241-243)CCT>TCT	p.P81S
Pat_46	Post-Resistance	MIPOL1	145282	37	14	37838774	37838774	Missense_Mutation	SNP	C	T	6	39	c.881C>T	c.(880-882)TCA>TTA	p.S294L
Pat_46	Post-Resistance	SOS2	6655	37	14	50611980	50611980	Missense_Mutation	SNP	C	T	7	78	c.2575G>A	c.(2575-2577)GTT>ATT	p.V859I
Pat_46	Post-Resistance	PTGDR	5729	37	14	52741476	52741476	Missense_Mutation	SNP	G	A	4	23	c.874G>A	c.(874-876)GAT>AAT	p.D292N
Pat_46	Post-Resistance	TOMM20L	387990	37	14	58869404	58869404	Missense_Mutation	SNP	G	A	11	72	c.187G>A	c.(187-189)GAT>AAT	p.D63N
Pat_46	Post-Resistance	PPM1A	5494	37	14	60749713	60749713	Nonsense_Mutation	SNP	A	T	4	42	c.292A>T	c.(292-294)AAG>TAG	p.K98*
Pat_46	Post-Resistance	PPM1A	5494	37	14	60752390	60752391	Missense_Mutation	DNP	CC	TT	12	97	c.883_884CC>TT	c.(883-885)CCC>TTC	p.P295F
Pat_46	Post-Resistance	NEK9	91754	37	14	75553828	75553828	Missense_Mutation	SNP	C	T	7	116	c.2710G>A	c.(2710-2712)GGT>AGT	p.G904S
Pat_46	Post-Resistance	KIAA1409	57578	37	14	93944038	93944038	Missense_Mutation	SNP	G	A	8	77	c.52G>A	c.(52-54)GAA>AAA	p.E18K
Pat_46	Post-Resistance	DICER1	23405	37	14	95571421	95571421	Missense_Mutation	SNP	G	A	7	85	c.3256C>T	c.(3256-3258)CCT>TCT	p.P1086S
Pat_46	Post-Resistance	TECPR2	9895	37	14	102901094	102901094	Missense_Mutation	SNP	C	T	3	23	c.1940C>T	c.(1939-1941)TCA>TTA	p.S647L
Pat_46	Post-Resistance	CDC42BPB	9578	37	14	103434988	103434988	Missense_Mutation	SNP	T	A	6	54	c.2061A>T	c.(2059-2061)AAA>AAT	p.K687N
Pat_46	Post-Resistance	MTA1	9112	37	14	105932778	105932778	Missense_Mutation	SNP	C	T	3	10	c.1640C>T	c.(1639-1641)CCC>CTC	p.P547L
Pat_46	Post-Resistance	TJP1	7082	37	15	30026556	30026556	Missense_Mutation	SNP	T	C	20	39	c.1438A>G	c.(1438-1440)AGA>GGA	p.R480G
Pat_46	Post-Resistance	BUB1B	701	37	15	40457265	40457265	Missense_Mutation	SNP	C	T	19	45	c.47C>T	c.(46-48)TCC>TTC	p.S16F
Pat_46	Post-Resistance	RPAP1	26015	37	15	41817292	41817293	Nonsense_Mutation	DNP	GG	AA	3	8	.1971_1972CC>T	969-1974)CCCCAA>CCT	p.Q658*
Pat_46	Post-Resistance	GANC	2595	37	15	42632068	42632068	Missense_Mutation	SNP	C	T	6	20	c.2045C>T	c.(2044-2046)TCT>TTT	p.S682F
Pat_46	Post-Resistance	CTDSPL2	51496	37	15	44751361	44751361	Missense_Mutation	SNP	C	T	12	95	c.149C>T	c.(148-150)TCT>TTT	p.S50F
Pat_46	Post-Resistance	GABPB1	2553	37	15	50593519	50593519	Missense_Mutation	SNP	G	A	8	145	c.518C>T	c.(517-519)ACT>ATT	p.T173I
Pat_46	Post-Resistance	WDR72	256764	37	15	54003587	54003587	Missense_Mutation	SNP	C	T	5	67	c.803G>A	c.(802-804)AGA>AAA	p.R268K
Pat_46	Post-Resistance	UNC13C	440279	37	15	54305661	54305661	Nonsense_Mutation	SNP	G	A	14	60	c.561G>A	c.(559-561)TGG>TGA	p.W187*
Pat_46	Post-Resistance	RNF111	54778	37	15	59323443	59323443	Missense_Mutation	SNP	C	T	12	49	c.422C>T	c.(421-423)CCT>CTT	p.P141L
Pat_46	Post-Resistance	HERC1	8925	37	15	63986325	63986325	Missense_Mutation	SNP	C	T	4	19	c.5512G>A	c.(5512-5514)GTT>ATT	p.V1838I
Pat_46	Post-Resistance	CSNK1G1	53944	37	15	64499716	64499716	Missense_Mutation	SNP	C	T	5	23	c.757G>A	c.(757-759)GGA>AGA	p.G253R
Pat_46	Post-Resistance	DENND4A	10260	37	15	66048767	66048767	Missense_Mutation	SNP	G	A	11	52	c.22C>T	c.(22-24)CGT>TGT	p.R8C
Pat_46	Post-Resistance	IQCH	64799	37	15	67793004	67793004	Missense_Mutation	SNP	G	A	5	35	c.3004G>A	c.(3004-3006)GTA>ATA	p.V1002I

Pat_46	Post-Resistance	LRRC49	54839	37	15	71329552	71329552	Missense_Mutation	SNP	G	A	14	103	c.1738G>A	c.(1738-1740)GGA>AGA	p.G580R
Pat_46	Post-Resistance	PARP6	56965	37	15	72552884	72552884	Missense_Mutation	SNP	G	A	26	146	c.691C>T	c.(691-693)CCC>TCC	p.P231S
Pat_46	Post-Resistance	CYP11A1	1583	37	15	74630935	74630935	Missense_Mutation	SNP	C	T	6	58	c.1411G>A	c.(1411-1413)GAG>AAG	p.E471K
Pat_46	Post-Resistance	KIAA1199	57214	37	15	81201454	81201454	Missense_Mutation	SNP	A	G	4	13	c.1604A>G	c.(1603-1605)AAG>AGG	p.K535R
Pat_46	Post-Resistance	ALPK3	57538	37	15	85400266	85400266	Missense_Mutation	SNP	C	T	9	60	c.2903C>T	c.(2902-2904)CCA>CTA	p.P968L
Pat_46	Post-Resistance	SLCO3A1	28232	37	15	92671649	92671649	Missense_Mutation	SNP	C	T	6	82	c.1442C>T	c.(1441-1443)TCC>TTC	p.S481F
Pat_46	Post-Resistance	IGF1R	3480	37	15	99478232	99478232	Missense_Mutation	SNP	G	A	4	47	c.3136G>A	c.(3136-3138)GAG>AAG	p.E1046K
Pat_46	Post-Resistance	PKD1	5310	37	16	2158389	2158389	Missense_Mutation	SNP	A	G	3	17	c.6779T>C	c.(6778-6780)ATT>ACT	p.I2260T
Pat_46	Post-Resistance	BTBD12	84464	37	16	3640514	3640514	Missense_Mutation	SNP	C	T	3	18	c.3125G>A	c.(3124-3126)GGC>GAC	p.G1042D
Pat_46	Post-Resistance	SMG1	23049	37	16	18902236	18902236	Missense_Mutation	SNP	A	C	6	50	c.557T>G	c.(556-558)GTT>GGT	p.V186G
Pat_46	Post-Resistance	CACNG3	10368	37	16	24358111	24358111	Missense_Mutation	SNP	G	A	5	39	c.268G>A	c.(268-270)GAA>AAA	p.E90K
Pat_46	Post-Resistance	SETD1A	9739	37	16	30975992	30975992	Missense_Mutation	SNP	C	T	8	50	c.929C>T	c.(928-930)TCC>TTC	p.S310F
Pat_46	Post-Resistance	GPT2	84706	37	16	46958446	46958446	Missense_Mutation	SNP	A	T	5	26	c.1358A>T	c.(1357-1359)GAG>GTG	p.E453V
Pat_46	Post-Resistance	CDH11	1009	37	16	65032695	65032695	Missense_Mutation	SNP	C	T	5	22	c.293G>A	c.(292-294)GGA>GAA	p.G98E
Pat_46	Post-Resistance	CMTM3	123920	37	16	66642333	66642333	Missense_Mutation	SNP	A	C	7	30	c.269A>C	c.(268-270)AAT>ACT	p.N90T
Pat_46	Post-Resistance	KIAA0895L	653319	37	16	67210754	67210754	Missense_Mutation	SNP	C	T	6	46	c.1376G>A	c.(1375-1377)CGG>CAG	p.R459Q
Pat_46	Post-Resistance	TAT	6898	37	16	71610233	71610233	Missense_Mutation	SNP	G	A	4	42	c.86C>T	c.(85-87)TCT>TTT	p.S29F
Pat_46	Post-Resistance	ADAT1	23536	37	16	75637046	75637046	Missense_Mutation	SNP	A	G	13	126	c.1313T>C	c.(1312-1314)CTC>CCC	p.L438P
Pat_46	Post-Resistance	GAN	8139	37	16	81411197	81411197	Missense_Mutation	SNP	C	T	6	78	c.1790C>T	c.(1789-1791)CCT>CTT	p.P597L
Pat_46	Post-Resistance	HSDL1	83693	37	16	84163799	84163800	Missense_Mutation	DNP	CC	TT	11	69	c.457_458GG>AA	c.(457-459)GGT>AAT	p.G153N
Pat_46	Post-Resistance	NLRP1	22861	37	17	5436241	5436241	Missense_Mutation	SNP	C	T	3	22	c.3197G>A	c.(3196-3198)GGG>GAG	p.G1066E
Pat_46	Post-Resistance	ADORA2B	136	37	17	15878556	15878556	Missense_Mutation	SNP	C	T	6	100	c.899C>T	c.(898-900)ACT>ATT	p.T300I
Pat_46	Post-Resistance	CCDC144NL	339184	37	17	20799030	20799030	Missense_Mutation	SNP	G	A	7	39	c.304C>T	c.(304-306)CCT>TCT	p.P102S
Pat_46	Post-Resistance	PHF12	57649	37	17	27248740	27248740	Missense_Mutation	SNP	G	A	11	78	c.802C>T	c.(802-804)CCC>TCC	p.P268S
Pat_46	Post-Resistance	NF1	4763	37	17	29677227	29677227	Nonsense_Mutation	SNP	C	T	19	114	c.7348C>T	c.(7348-7350)CGA>TGA	p.R2450*
Pat_46	Post-Resistance	UNC45B	146862	37	17	33491151	33491151	Missense_Mutation	SNP	G	A	10	117	c.1117G>A	c.(1117-1119)GAT>AAT	p.D373N
Pat_46	Post-Resistance	KRT32	3882	37	17	39619092	39619092	Missense_Mutation	SNP	C	T	3	12	c.1207G>A	c.(1207-1209)GAG>AAG	p.E403K
Pat_46	Post-Resistance	KRT14	3861	37	17	39742707	39742707	Missense_Mutation	SNP	G	A	6	31	c.380C>T	c.(379-381)GCC>GTC	p.A127V
Pat_46	Post-Resistance	WNK4	65266	37	17	40932960	40932960	Missense_Mutation	SNP	G	A	5	15	c.244G>A	c.(244-246)GAC>AAC	p.D82N
Pat_46	Post-Resistance	MEOX1	4222	37	17	41719375	41719375	Missense_Mutation	SNP	C	T	16	60	c.668G>A	c.(667-669)AGG>AAG	p.R223K
Pat_46	Post-Resistance	KIAA1267	284058	37	17	44249109	44249109	Missense_Mutation	SNP	G	A	27	89	c.401C>T	c.(400-402)TCC>TTC	p.S134F
Pat_46	Post-Resistance	HLF	3131	37	17	53345193	53345193	Missense_Mutation	SNP	G	A	6	58	c.197G>A	c.(196-198)GGG>GAG	p.G66E
Pat_46	Post-Resistance	KPNA2	3838	37	17	66033562	66033562	Missense_Mutation	SNP	C	T	10	64	c.164C>T	c.(163-165)TCA>TTA	p.S55L
Pat_46	Post-Resistance	ICT1	3396	37	17	73013191	73013191	Missense_Mutation	SNP	G	A	4	50	c.205G>A	c.(205-207)GAC>AAC	p.D69N
Pat_46	Post-Resistance	ATP5H	10476	37	17	73036233	73036233	Missense_Mutation	SNP	G	A	11	174	c.245C>T	c.(244-246)CCA>CTA	p.P82L
Pat_46	Post-Resistance	SMCHD1	23347	37	18	2750443	2750443	Missense_Mutation	SNP	C	T	3	8	c.4103C>T	c.(4102-4104)CCC>CTC	p.P1368L
Pat_46	Post-Resistance	TXNDC2	84203	37	18	9887184	9887184	Missense_Mutation	SNP	G	C	12	78	c.708G>C	c.(706-708)GAG>GAC	p.E236D
Pat_46	Post-Resistance	ANKRD30B	374860	37	18	14799105	14799105	Missense_Mutation	SNP	C	T	5	58	c.2035C>T	c.(2035-2037)CCT>TCT	p.P679S
Pat_46	Post-Resistance	NPC1	4864	37	18	21134821	21134821	Nonsense_Mutation	SNP	A	T	6	35	c.1454T>A	c.(1453-1455)TTA>TAA	p.L485*
Pat_46	Post-Resistance	NPC1	4864	37	18	21134840	21134840	Missense_Mutation	SNP	A	T	7	38	c.1435T>A	c.(1435-1437)TGC>AGC	p.C479S
Pat_46	Post-Resistance	LAMA3	3909	37	18	21419844	21419844	Missense_Mutation	SNP	C	T	9	70	c.3287C>T	c.(3286-3288)TCG>TTG	p.S1096L
Pat_46	Post-Resistance	LAMA3	3909	37	18	21487610	21487610	Missense_Mutation	SNP	G	A	17	115	c.6815G>A	c.(6814-6816)GGT>GAT	p.G2272D
Pat_46	Post-Resistance	DSC3	1825	37	18	28584314	28584314	Missense_Mutation	SNP	G	A	4	34	c.1907C>T	c.(1906-1908)TCA>TTA	p.S636L
Pat_46	Post-Resistance	DSC2	1824	37	18	28672144	28672144	Nonsense_Mutation	SNP	T	A	5	54	c.274A>T	c.(274-276)AGA>TGA	p.R92*
Pat_46	Post-Resistance	KIAA1012	22878	37	18	29470717	29470717	Missense_Mutation	SNP	C	T	6	74	c.1709G>A	c.(1708-1710)CGA>CAA	p.R570Q
Pat_46	Post-Resistance	PSTPIP2	9050	37	18	43570702	43570702	Missense_Mutation	SNP	G	A	5	34	c.941C>T	c.(940-942)CCT>CTT	p.P314L
Pat_46	Post-Resistance	TCEB3B	51224	37	18	44560363	44560363	Missense_Mutation	SNP	C	T	7	21	c.1273G>A	c.(1273-1275)GAT>AAT	p.D425N

Pat_46	Post-Resistance	TCEB3B	51224	37	18	44561172	44561172	Missense_Mutation	SNP	C	T	5	17	c.464G>A	c.(463-465)AGA>AAA	p.R155K
Pat_46	Post-Resistance	DCC	1630	37	18	50432428	50432428	Missense_Mutation	SNP	C	T	5	47	c.427C>T	c.(427-429)CTT>TTT	p.L143F
Pat_46	Post-Resistance	DCC	1630	37	18	50741963	50741963	Missense_Mutation	SNP	C	T	9	81	c.1907C>T	c.(1906-1908)TCA>TTA	p.S636L
Pat_46	Post-Resistance	ALPK2	115701	37	18	56246363	56246363	Missense_Mutation	SNP	G	A	8	48	c.1645C>T	c.(1645-1647)CCG>TCG	p.P549S
Pat_46	Post-Resistance	SERPINB7	8710	37	18	61465919	61465919	Missense_Mutation	SNP	G	A	11	78	c.536G>A	c.(535-537)GGC>GAC	p.G179D
Pat_46	Post-Resistance	CDH7	1005	37	18	63547837	63547837	Missense_Mutation	SNP	G	A	7	42	c.2065G>A	c.(2065-2067)GAA>AAA	p.E689K
Pat_46	Post-Resistance	CNN2	1265	37	19	1037859	1037859	Missense_Mutation	SNP	C	T	7	25	c.890C>T	c.(889-891)CCT>CTT	p.P297L
Pat_46	Post-Resistance	PIP5K1C	23396	37	19	3661061	3661061	Missense_Mutation	SNP	G	A	11	30	c.371C>T	c.(370-372)CCC>CTC	p.P124L
Pat_46	Post-Resistance	CREB3L3	84699	37	19	4157169	4157169	Missense_Mutation	SNP	G	A	5	26	c.334G>A	c.(334-336)GGC>AGC	p.G112S
Pat_46	Post-Resistance	ZNF557	79230	37	19	7076509	7076509	Missense_Mutation	SNP	G	A	5	58	c.217G>A	c.(217-219)GCC>ACC	p.A73T
Pat_46	Post-Resistance	MUC16	94025	37	19	9045834	9045834	Missense_Mutation	SNP	C	T	9	21	c.35797G>A	c.(35797-35799)GAA>AAA	p.E11933K
Pat_46	Post-Resistance	MUC16	94025	37	19	9045848	9045848	Missense_Mutation	SNP	G	A	9	17	c.35783C>T	c.(35782-35784)TCA>TTA	p.S11928L
Pat_46	Post-Resistance	MUC16	94025	37	19	9068949	9068949	Missense_Mutation	SNP	G	A	7	30	c.18497C>T	c.(18496-18498)TCT>TTT	p.S6166F
Pat_46	Post-Resistance	ZNF562	54811	37	19	9764053	9764053	Missense_Mutation	SNP	C	T	7	30	c.853G>A	c.(853-855)GAG>AAG	p.E285K
Pat_46	Post-Resistance	CYP4F22	126410	37	19	15651274	15651274	Missense_Mutation	SNP	T	C	8	31	c.685T>C	c.(685-687)TAT>CAT	p.Y229H
Pat_46	Post-Resistance	USHBP1	83878	37	19	17367350	17367350	Missense_Mutation	SNP	C	T	3	16	c.1400G>A	c.(1399-1401)GGG>GAG	p.G467E
Pat_46	Post-Resistance	ZNF676	163223	37	19	22363003	22363003	Missense_Mutation	SNP	T	C	10	89	c.1516A>G	c.(1516-1518)AAA>GAA	p.K506E
Pat_46	Post-Resistance	ZNF507	22847	37	19	32873430	32873430	Nonsense_Mutation	SNP	G	A	7	83	c.2418G>A	c.(2416-2418)TGG>TGA	p.W806*
Pat_46	Post-Resistance	KIRREL2	84063	37	19	36357300	36357300	Missense_Mutation	SNP	C	T	9	96	c.2033C>T	c.(2032-2034)TCC>TTC	p.S678F
Pat_46	Post-Resistance	ZNF565	147929	37	19	36673967	36673967	Missense_Mutation	SNP	G	A	6	33	c.901C>T	c.(901-903)CAC>TAC	p.H301Y
Pat_46	Post-Resistance	ZNF383	163087	37	19	37734537	37734537	Missense_Mutation	SNP	C	T	6	47	c.1399C>T	c.(1399-1401)CGT>TGT	p.R467C
Pat_46	Post-Resistance	CLC	1178	37	19	40225070	40225070	Missense_Mutation	SNP	G	T	7	96	c.156C>A	c.(154-156)TTC>TTA	p.F52L
Pat_46	Post-Resistance	SHKBP1	92799	37	19	41086687	41086687	Missense_Mutation	SNP	C	T	5	33	c.689C>T	c.(688-690)TCC>TTC	p.S230F
Pat_46	Post-Resistance	CEACAM5	1048	37	19	42213788	42213788	Missense_Mutation	SNP	G	A	5	63	c.254G>A	c.(253-255)GGA>GAA	p.G85E
Pat_46	Post-Resistance	PSG8	440533	37	19	43262211	43262211	Missense_Mutation	SNP	C	T	21	154	c.652G>A	c.(652-654)GAA>AAA	p.E218K
Pat_46	Post-Resistance	PSG1	5669	37	19	43376195	43376195	Missense_Mutation	SNP	C	T	12	46	c.433G>A	c.(433-435)GAG>AAG	p.E145K
Pat_46	Post-Resistance	PSG9	5678	37	19	43762435	43762435	Missense_Mutation	SNP	G	A	16	128	c.1162C>T	c.(1162-1164)CAT>TAT	p.H388Y
Pat_46	Post-Resistance	CCDC9	26093	37	19	47761596	47761596	Translation_Start_Site	SNP	G	A	3	24	c.-61G>A	c.(-63--59)CAGTG>CAATG	
Pat_46	Post-Resistance	ZNF175	7728	37	19	52091536	52091536	Missense_Mutation	SNP	C	T	4	32	c.1952C>T	c.(1951-1953)TCG>TTG	p.S651L
Pat_46	Post-Resistance	SIGLEC5	8778	37	19	52131203	52131203	Missense_Mutation	SNP	G	A	5	28	c.881C>T	c.(880-882)TCC>TTC	p.S294F
Pat_46	Post-Resistance	FPR2	2358	37	19	52272576	52272576	Missense_Mutation	SNP	G	A	3	18	c.665G>A	c.(664-666)GGG>GAG	p.G222E
Pat_46	Post-Resistance	FPR3	2359	37	19	52327313	52327313	Missense_Mutation	SNP	G	A	6	39	c.312G>A	c.(310-312)ATG>ATA	p.M104I
Pat_46	Post-Resistance	ZNF611	81856	37	19	53209661	53209661	Missense_Mutation	SNP	G	A	9	93	c.647C>T	c.(646-648)TCA>TTA	p.S216L
Pat_46	Post-Resistance	KIR2DS4	3809	37	19	55351067	55351067	Missense_Mutation	SNP	G	A	5	55	c.577G>A	c.(577-579)GGA>AGA	p.G193R
Pat_46	Post-Resistance	NLRP8	126205	37	19	56490764	56490764	Missense_Mutation	SNP	G	A	8	36	c.2881G>A	c.(2881-2883)GAA>AAA	p.E961K
Pat_46	Post-Resistance	ZFP28	140612	37	19	57066001	57066001	Missense_Mutation	SNP	C	T	5	66	c.1847C>T	c.(1846-1848)CCT>CTT	p.P616L
Pat_46	Post-Resistance	ZNF329	79673	37	19	58640786	58640786	Missense_Mutation	SNP	G	A	14	127	c.85C>T	c.(85-87)CCC>TCC	p.P29S
Pat_46	Post-Resistance	ATAD2B	54454	37	2	24046313	24046313	Missense_Mutation	SNP	C	T	4	23	c.1946G>A	c.(1945-1947)AGT>AAT	p.S649N
Pat_46	Post-Resistance	GPN1	11321	37	2	27864126	27864126	Missense_Mutation	SNP	G	A	8	65	c.862G>A	c.(862-864)GAA>AAA	p.E288K
Pat_46	Post-Resistance	C2orf71	388939	37	2	29296101	29296101	Missense_Mutation	SNP	G	A	6	24	c.1027C>T	c.(1027-1029)CTC>TTC	p.L343F
Pat_46	Post-Resistance	CCT7	10574	37	2	73474975	73474975	Missense_Mutation	SNP	C	T	6	40	c.704C>T	c.(703-705)CCC>CTC	p.P235L
Pat_46	Post-Resistance	ALMS1	7840	37	2	73651805	73651805	Missense_Mutation	SNP	C	T	4	27	c.1015C>T	c.(1015-1017)CGT>TGT	p.R339C
Pat_46	Post-Resistance	CTNNA2	1496	37	2	80874951	80874951	Missense_Mutation	SNP	C	T	13	100	c.2816C>T	c.(2815-2817)TCG>TTG	p.S939L
Pat_46	Post-Resistance	EIF2AK3	9451	37	2	88874860	88874860	Missense_Mutation	SNP	G	A	8	87	c.2141C>T	c.(2140-2142)CCT>CTT	p.P714L
Pat_46	Post-Resistance	SLC9A4	389015	37	2	103142776	103142776	Missense_Mutation	SNP	G	A	9	59	c.2009G>A	c.(2008-2010)GGA>GAA	p.G670E
Pat_46	Post-Resistance	IL1A	3552	37	2	113532775	113532775	Missense_Mutation	SNP	C	T	5	60	c.685G>A	c.(685-687)GGC>AGC	p.G229S
Pat_46	Post-Resistance	NCKAP5	344148	37	2	133489429	133489429	Missense_Mutation	SNP	G	A	4	35	c.5324C>T	c.(5323-5325)TCC>TTC	p.S1775F

Pat_46	Post-Resistance	ARHGAP15	55843	37	2	143974010	143974010	Missense_Mutation	SNP	C	G	5	41	c.292C>G	c.(292-294)CTA>GTA	p.L98V
Pat_46	Post-Resistance	CCDC148	130940	37	2	159077171	159077171	Missense_Mutation	SNP	C	T	9	26	c.1306G>A	c.(1306-1308)GAT>AAT	p.D436N
Pat_46	Post-Resistance	LY75	4065	37	2	160742933	160742933	Missense_Mutation	SNP	G	A	7	36	c.911C>T	c.(910-912)CCA>CTA	p.P304L
Pat_46	Post-Resistance	ITGB6	3694	37	2	161052127	161052127	Splice_Site	SNP	C	T	5	34	c.347_splice	c.e4-1	p.G116_splice
Pat_46	Post-Resistance	SCN1A	6323	37	2	166897895	166897895	Nonsense_Mutation	SNP	C	T	9	85	c.2228G>A	c.(2227-2229)TGG>TAG	p.W743*
Pat_46	Post-Resistance	G6PC2	57818	37	2	169761055	169761055	Nonsense_Mutation	SNP	G	A	22	164	c.369G>A	c.(367-369)TGG>TGA	p.W123*
Pat_46	Post-Resistance	UBR3	130507	37	2	170938268	170938268	Missense_Mutation	SNP	G	A	5	45	c.5582G>A	c.(5581-5583)AGA>AAA	p.R1861K
Pat_46	Post-Resistance	ITGA6	3655	37	2	173339794	173339794	Missense_Mutation	SNP	C	T	5	31	c.1124C>T	c.(1123-1125)TCT>TTT	p.S375F
Pat_46	Post-Resistance	TTN	7273	37	2	179401036	179401036	Missense_Mutation	SNP	C	T	3	23	c.92734G>A	c.(92734-92736)GAA>AAA	p.E30912K
Pat_46	Post-Resistance	TTN	7273	37	2	179431936	179431936	Nonsense_Mutation	SNP	C	T	8	67	c.71219G>A	c.(71218-71220)TGG>TAG	p.W23740*
Pat_46	Post-Resistance	TTN	7273	37	2	179435273	179435273	Missense_Mutation	SNP	T	C	3	21	c.67882A>G	c.(67882-67884)ACT>GCT	p.T22628A
Pat_46	Post-Resistance	TTN	7273	37	2	179439473	179439473	Missense_Mutation	SNP	C	G	4	40	c.63682G>C	c.(63682-63684)GAG>CAG	p.E21228Q
Pat_46	Post-Resistance	TTN	7273	37	2	179475048	179475048	Missense_Mutation	SNP	C	T	7	45	c.43501G>A	c.(43501-43503)GAA>AAA	p.E14501K
Pat_46	Post-Resistance	TTN	7273	37	2	179483347	179483347	Missense_Mutation	SNP	C	T	7	99	c.39226G>A	c.(39226-39228)GGA>AGA	p.G13076R
Pat_46	Post-Resistance	TTN	7273	37	2	179517063	179517063	Missense_Mutation	SNP	G	A	13	122	c.31837C>T	c.(31837-31839)CCC>TCC	p.P10613S
Pat_46	Post-Resistance	TTN	7273	37	2	179542534	179542534	Missense_Mutation	SNP	C	T	12	79	c.30373G>A	c.(30373-30375)GAA>AAA	p.E10125K
Pat_46	Post-Resistance	TTN	7273	37	2	179584152	179584152	Missense_Mutation	SNP	G	A	5	22	c.20233C>T	c.(20233-20235)CGC>TGC	p.R6745C
Pat_46	Post-Resistance	ZNF804A	91752	37	2	185802432	185802432	Missense_Mutation	SNP	G	A	10	37	c.2309G>A	c.(2308-2310)CGA>CAA	p.R770Q
Pat_46	Post-Resistance	CLK1	1195	37	2	201724923	201724923	Nonsense_Mutation	SNP	T	A	15	105	c.406A>T	c.(406-408)AAA>TAA	p.K136*
Pat_46	Post-Resistance	ZDBF2	57683	37	2	207173096	207173096	Missense_Mutation	SNP	G	A	4	21	c.3844G>A	c.(3844-3846)GAT>AAT	p.D1282N
Pat_46	Post-Resistance	CRYGC	1420	37	2	208994365	208994365	Missense_Mutation	SNP	C	T	7	74	c.52G>A	c.(52-54)GAA>AAA	p.E18K
Pat_46	Post-Resistance	MAP2	4133	37	2	210558852	210558852	Missense_Mutation	SNP	G	A	3	20	c.1958G>A	c.(1957-1959)AGT>AAT	p.S653N
Pat_46	Post-Resistance	MAP2	4133	37	2	210570403	210570403	Missense_Mutation	SNP	T	A	16	127	c.4684T>A	c.(4684-4686)TCC>ACC	p.S1562T
Pat_46	Post-Resistance	MYL1	4632	37	2	211163257	211163257	Missense_Mutation	SNP	C	T	9	25	c.191G>A	c.(190-192)AGA>AAA	p.R64K
Pat_46	Post-Resistance	SLC23A3	151295	37	2	220032706	220032706	Missense_Mutation	SNP	G	A	6	47	c.859C>T	c.(859-861)CCC>TCC	p.P287S
Pat_46	Post-Resistance	SLC4A3	6508	37	2	220496794	220496794	Missense_Mutation	SNP	C	T	3	24	c.916C>T	c.(916-918)CGC>TGC	p.R306C
Pat_46	Post-Resistance	SP140	11262	37	2	231108493	231108493	Missense_Mutation	SNP	G	A	9	36	c.538G>A	c.(538-540)GAA>AAA	p.E180K
Pat_46	Post-Resistance	NMUR1	10316	37	2	232393481	232393481	Missense_Mutation	SNP	A	G	3	19	c.251T>C	c.(250-252)GTC>GCC	p.V84A
Pat_46	Post-Resistance	SPTLC3	55304	37	20	13098356	13098356	Missense_Mutation	SNP	A	G	5	20	c.1136A>G	c.(1135-1137)TAC>TGC	p.Y379C
Pat_46	Post-Resistance	C20orf3	57136	37	20	24964594	24964594	Missense_Mutation	SNP	G	A	4	31	c.157C>T	c.(157-159)CCC>TCC	p.P53S
Pat_46	Post-Resistance	DEFB116	245930	37	20	29891208	29891208	Missense_Mutation	SNP	G	A	7	47	c.116C>T	c.(115-117)CCA>CTA	p.P39L
Pat_46	Post-Resistance	NECAB3	63941	37	20	32257228	32257228	Missense_Mutation	SNP	C	T	8	55	c.340G>A	c.(340-342)GAA>AAA	p.E114K
Pat_46	Post-Resistance	PTPRT	11122	37	20	40735493	40735493	Missense_Mutation	SNP	C	G	3	34	c.3323G>C	c.(3322-3324)GGG>GCG	p.G1108A
Pat_46	Post-Resistance	PTPRT	11122	37	20	40743942	40743942	Missense_Mutation	SNP	C	T	4	49	c.2996G>A	c.(2995-2997)CGA>CAA	p.R999Q
Pat_46	Post-Resistance	PTPRT	11122	37	20	40747054	40747054	Missense_Mutation	SNP	C	T	5	35	c.2971G>A	c.(2971-2973)GAA>AAA	p.E991K
Pat_46	Post-Resistance	MMP9	4318	37	20	44639672	44639672	Missense_Mutation	SNP	C	T	7	18	c.632C>T	c.(631-633)TCC>TTC	p.S211F
Pat_46	Post-Resistance	CDH22	64405	37	20	44815559	44815559	Missense_Mutation	SNP	G	A	8	78	c.1451C>T	c.(1450-1452)TCC>TTC	p.S484F
Pat_46	Post-Resistance	SLC13A3	64849	37	20	45224923	45224923	Missense_Mutation	SNP	C	T	7	73	c.667G>A	c.(667-669)GAG>AAG	p.E223K
Pat_46	Post-Resistance	KCNB1	3745	37	20	47990627	47990627	Nonsense_Mutation	SNP	C	T	10	72	c.1470G>A	c.(1468-1470)TGG>TGA	p.W490*
Pat_46	Post-Resistance	ZNF831	128611	37	20	57770957	57770957	Nonsense_Mutation	SNP	C	T	8	92	c.3772C>T	c.(3772-3774)CAG>TAG	p.Q1258*
Pat_46	Post-Resistance	ZNF831	128611	37	20	57829544	57829544	Missense_Mutation	SNP	G	A	5	37	c.4780G>A	c.(4780-4782)GGC>AGC	p.G1594S
Pat_46	Post-Resistance	ITSN1	6453	37	21	35140024	35140024	Nonsense_Mutation	SNP	C	T	8	40	c.934C>T	c.(934-936)CGA>TGA	p.R312*
Pat_46	Post-Resistance	DSCAM	1826	37	21	41550881	41550881	Missense_Mutation	SNP	C	T	4	20	c.2920G>A	c.(2920-2922)GAG>AAG	p.E974K
Pat_46	Post-Resistance	UBASH3A	53347	37	21	43826440	43826440	Missense_Mutation	SNP	G	A	4	41	c.137G>A	c.(136-138)GGG>GAG	p.G46E
Pat_46	Post-Resistance	MYO18B	84700	37	22	26286768	26286768	Missense_Mutation	SNP	G	A	5	23	c.4360G>A	c.(4360-4362)GAT>AAT	p.D1454N
Pat_46	Post-Resistance	ASPHD2	57168	37	22	26829939	26829939	Missense_Mutation	SNP	G	A	3	22	c.358G>A	c.(358-360)GAG>AAG	p.E120K
Pat_46	Post-Resistance	SOX10	6663	37	22	38370118	38370118	Missense_Mutation	SNP	G	A	8	147	c.785C>T	c.(784-786)TCC>TTC	p.S262F

Pat_46	Post-Resistance	RANGAP1	5905	37	22	41657514	41657514	Missense_Mutation	SNP	A	C	5	28	c.551T>G	c.(550-552)GTC>GGC	p.V184G
Pat_46	Post-Resistance	PMM1	5372	37	22	41973333	41973333	Missense_Mutation	SNP	G	A	7	44	c.778C>T	c.(778-780)CAT>TAT	p.H260Y
Pat_46	Post-Resistance	PMM1	5372	37	22	41973900	41973900	Missense_Mutation	SNP	G	A	4	25	c.578C>T	c.(577-579)CCC>CTC	p.P193L
Pat_46	Post-Resistance	PACSIN2	11252	37	22	43289619	43289619	Missense_Mutation	SNP	C	T	4	48	c.61G>A	c.(61-63)GTC>ATC	p.V21I
Pat_46	Post-Resistance	PHF21B	112885	37	22	45309869	45309869	Missense_Mutation	SNP	G	A	5	15	c.664C>T	c.(664-666)CCT>TCT	p.P222S
Pat_46	Post-Resistance	ACR	49	37	22	51178379	51178379	Missense_Mutation	SNP	C	T	3	9	c.539C>T	c.(538-540)GCC>GTC	p.A180V
Pat_46	Post-Resistance	IQSEC1	9922	37	3	12957209	12957209	Missense_Mutation	SNP	G	A	7	48	c.2087C>T	c.(2086-2088)CCC>CTC	p.P696L
Pat_46	Post-Resistance	MYRIP	25924	37	3	40275539	40275539	Missense_Mutation	SNP	G	A	7	36	c.2095G>A	c.(2095-2097)GAA>AAA	p.E699K
Pat_46	Post-Resistance	CCBP2	1238	37	3	42906733	42906733	Missense_Mutation	SNP	C	T	4	44	c.739C>T	c.(739-741)CGG>TGG	p.R247W
Pat_46	Post-Resistance	SEMA3B	7869	37	3	50307880	50307880	Missense_Mutation	SNP	C	T	6	45	c.284C>T	c.(283-285)CCT>CTT	p.P95L
Pat_46	Post-Resistance	DOCK3	1795	37	3	51101878	51101878	Splice_Site	SNP	G	A	11	83	c.316_splice	c.e6-1	p.K106_splice
Pat_46	Post-Resistance	DOCK3	1795	37	3	51352520	51352520	Missense_Mutation	SNP	G	A	4	35	c.3363G>A	c.(3361-3363)ATG>ATA	p.M1121I
Pat_46	Post-Resistance	CACNA1D	776	37	3	53835211	53835211	Missense_Mutation	SNP	G	A	6	43	c.5167G>A	c.(5167-5169)GAT>AAT	p.D1723N
Pat_46	Post-Resistance	ERC2	26059	37	3	55922538	55922538	Missense_Mutation	SNP	C	T	11	65	c.2443G>A	c.(2443-2445)GAA>AAA	p.E815K
Pat_46	Post-Resistance	CADPS	8618	37	3	62522224	62522224	Missense_Mutation	SNP	C	T	12	73	c.1999G>A	c.(1999-2001)GAA>AAA	p.E667K
Pat_46	Post-Resistance	ADAMTS9	56999	37	3	64640105	64640105	Missense_Mutation	SNP	G	A	5	72	c.1240C>T	c.(1240-1242)CCC>TCC	p.P414S
Pat_46	Post-Resistance	EPHA6	285220	37	3	97167559	97167559	Missense_Mutation	SNP	G	A	5	67	c.1879G>A	c.(1879-1881)GAA>AAA	p.E627K
Pat_46	Post-Resistance	DCBLD2	131566	37	3	98520477	98520477	Missense_Mutation	SNP	C	T	3	12	c.1687G>A	c.(1687-1689)GGC>AGC	p.G563S
Pat_46	Post-Resistance	MYH15	22989	37	3	108117645	108117645	Missense_Mutation	SNP	C	T	19	133	c.5032G>A	c.(5032-5034)GAT>AAT	p.D1678N
Pat_46	Post-Resistance	EAF2	55840	37	3	121575857	121575857	Splice_Site	SNP	G	A	7	54	c.339_splice	c.e4-1	p.R113_splice
Pat_46	Post-Resistance	CD86	942	37	3	121838341	121838341	Missense_Mutation	SNP	C	T	5	47	c.950C>T	c.(949-951)TCG>TTG	p.S317L
Pat_46	Post-Resistance	EEFSEC	60678	37	3	127981041	127981041	Missense_Mutation	SNP	C	T	6	39	c.595C>T	c.(595-597)CCA>TCA	p.P199S
Pat_46	Post-Resistance	IL20RB	53833	37	3	136699340	136699340	Missense_Mutation	SNP	C	T	15	110	c.121C>T	c.(121-123)CTC>TTC	p.L41F
Pat_46	Post-Resistance	ATR	545	37	3	142188288	142188288	Missense_Mutation	SNP	C	T	11	57	c.6443G>A	c.(6442-6444)CGA>CAA	p.R2148Q
Pat_46	Post-Resistance	MED12L	116931	37	3	150845664	150845664	Missense_Mutation	SNP	C	T	6	42	c.449C>T	c.(448-450)TCT>TTT	p.S150F
Pat_46	Post-Resistance	TRIM59	286827	37	3	160156050	160156050	Missense_Mutation	SNP	A	C	11	81	c.922T>G	c.(922-924)TCT>GCT	p.S308A
Pat_46	Post-Resistance	SERPINI2	5276	37	3	167189541	167189541	Missense_Mutation	SNP	C	T	14	113	c.82G>A	c.(82-84)GAA>AAA	p.E28K
Pat_46	Post-Resistance	WDR49	151790	37	3	167322110	167322110	Missense_Mutation	SNP	G	A	4	38	c.82C>T	c.(82-84)CAC>TAC	p.H28Y
Pat_46	Post-Resistance	EIF2B5	8893	37	3	183861313	183861313	Missense_Mutation	SNP	C	T	6	27	c.1829C>T	c.(1828-1830)TCC>TTC	p.S610F
Pat_46	Post-Resistance	TPRG1	285386	37	3	188956652	188956652	Missense_Mutation	SNP	C	T	4	50	c.433C>T	c.(433-435)CGC>TGC	p.R145C
Pat_46	Post-Resistance	WHSC1	7468	37	4	1961339	1961339	Missense_Mutation	SNP	C	T	8	47	c.3127C>T	c.(3127-3129)CCG>TCG	p.P1043S
Pat_46	Post-Resistance	ZFYVE28	57732	37	4	2306844	2306844	Missense_Mutation	SNP	C	T	4	18	c.1223G>A	c.(1222-1224)GGG>GAG	p.G408E
Pat_46	Post-Resistance	ZNF518B	85460	37	4	10446289	10446289	Missense_Mutation	SNP	G	A	10	47	c.1664C>T	c.(1663-1665)TCT>TTT	p.S555F
Pat_46	Post-Resistance	DCAF16	54876	37	4	17805374	17805374	Missense_Mutation	SNP	G	A	9	68	c.391C>T	c.(391-393)CCC>TCC	p.P131S
Pat_46	Post-Resistance	SLIT2	9353	37	4	20543159	20543159	Missense_Mutation	SNP	G	A	7	41	c.2060G>A	c.(2059-2061)GGA>GAA	p.G687E
Pat_46	Post-Resistance	DHX15	1665	37	4	24544625	24544625	Missense_Mutation	SNP	C	T	11	91	c.1273G>A	c.(1273-1275)GAG>AAG	p.E425K
Pat_46	Post-Resistance	TEC	7006	37	4	48147095	48147095	Splice_Site	SNP	C	T	6	63	c.1470_splice	c.e14+1	p.L490_splice
Pat_46	Post-Resistance	EPHA5	2044	37	4	66356268	66356268	Missense_Mutation	SNP	C	T	5	43	c.1229G>A	c.(1228-1230)GGT>GAT	p.G410D
Pat_46	Post-Resistance	TMPRSS11D	9407	37	4	68698974	68698974	Missense_Mutation	SNP	C	T	5	35	c.640G>A	c.(640-642)GGC>AGC	p.G214S
Pat_46	Post-Resistance	UGT2B4	7363	37	4	70350974	70350974	Missense_Mutation	SNP	G	A	17	173	c.1262C>T	c.(1261-1263)TCG>TTG	p.S421L
Pat_46	Post-Resistance	CSN1S1	1446	37	4	70802196	70802196	Missense_Mutation	SNP	G	A	3	15	c.152G>A	c.(151-153)AGG>AAG	p.R51K
Pat_46	Post-Resistance	PROL1	58503	37	4	71265005	71265005	Missense_Mutation	SNP	G	A	9	43	c.3G>A	c.(1-3)ATG>ATA	p.M1I
Pat_46	Post-Resistance	NAA11	84779	37	4	80246788	80246788	Missense_Mutation	SNP	G	A	4	22	c.244C>T	c.(244-246)CGG>TGG	p.R82W
Pat_46	Post-Resistance	ANTXR2	118429	37	4	80952816	80952816	Missense_Mutation	SNP	G	A	4	7	c.827C>T	c.(826-828)TCT>TTT	p.S276F
Pat_46	Post-Resistance	WDFY3	23001	37	4	85722863	85722863	Missense_Mutation	SNP	G	A	11	66	c.2762C>T	c.(2761-2763)CCG>CTG	p.P921L
Pat_46	Post-Resistance	C4orf37	285555	37	4	98480246	98480246	Missense_Mutation	SNP	C	T	9	91	c.1343G>A	c.(1342-1344)GGA>GAA	p.G448E
Pat_46	Post-Resistance	INTS12	57117	37	4	106604152	106604152	Missense_Mutation	SNP	G	A	9	111	c.1127C>T	c.(1126-1128)TCA>TTA	p.S376L

Pat_46	Post-Resistance	ENPEP	2028	37	4	111436534	111436534	Missense_Mutation	SNP	G	A	9	48	c.1445G>A	c.(1444-1446)GGA>GAA	p.G482E
Pat_46	Post-Resistance	PITX2	5308	37	4	111542496	111542496	Missense_Mutation	SNP	C	T	5	24	c.214G>A	c.(214-216)GAG>AAG	p.E72K
Pat_46	Post-Resistance	UGT8	7368	37	4	115544379	115544379	Missense_Mutation	SNP	G	A	6	54	c.343G>A	c.(343-345)GAC>AAC	p.D115N
Pat_46	Post-Resistance	KIAA1109	84162	37	4	123175410	123175410	Missense_Mutation	SNP	G	A	7	46	c.5983G>A	c.(5983-5985)GAT>AAT	p.D1995N
Pat_46	Post-Resistance	ANKRD50	57182	37	4	125593264	125593264	Missense_Mutation	SNP	C	T	14	118	c.1168G>A	c.(1168-1170)GAT>AAT	p.D390N
Pat_46	Post-Resistance	FAT4	79633	37	4	126240196	126240196	Missense_Mutation	SNP	C	T	3	23	c.2630C>T	c.(2629-2631)ACT>ATT	p.T877I
Pat_46	Post-Resistance	FAT4	79633	37	4	126367686	126367686	Missense_Mutation	SNP	C	T	7	74	c.7432C>T	c.(7432-7434)CCT>TCT	p.P2478S
Pat_46	Post-Resistance	PCDH18	54510	37	4	138451292	138451292	Missense_Mutation	SNP	C	T	14	99	c.1951G>A	c.(1951-1953)GAA>AAA	p.E651K
Pat_46	Post-Resistance	UCP1	7350	37	4	141483360	141483360	Missense_Mutation	SNP	C	T	10	107	c.796G>A	c.(796-798)GCT>ACT	p.A266T
Pat_46	Post-Resistance	UCP1	7350	37	4	141484553	141484553	Missense_Mutation	SNP	C	T	11	91	c.445G>A	c.(445-447)GGA>AGA	p.G149R
Pat_46	Post-Resistance	RNF150	57484	37	4	141832457	141832457	Missense_Mutation	SNP	C	T	4	33	c.1039G>A	c.(1039-1041)GGA>AGA	p.G347R
Pat_46	Post-Resistance	GYPA	2993	37	4	145040883	145040883	Missense_Mutation	SNP	G	A	5	60	c.188C>T	c.(187-189)TCA>TTA	p.S63L
Pat_46	Post-Resistance	HHIP	64399	37	4	145629453	145629453	Missense_Mutation	SNP	G	A	5	30	c.1291G>A	c.(1291-1293)GAT>AAT	p.D431N
Pat_46	Post-Resistance	DDX60L	91351	37	4	169348425	169348425	Missense_Mutation	SNP	G	A	6	29	c.1726C>T	c.(1726-1728)CTC>TTC	p.L576F
Pat_46	Post-Resistance	ADAM29	11086	37	4	175897562	175897562	Missense_Mutation	SNP	G	A	7	58	c.886G>A	c.(886-888)GGG>AGG	p.G296R
Pat_46	Post-Resistance	WDR17	116966	37	4	177041134	177041134	Missense_Mutation	SNP	C	T	8	91	c.496C>T	c.(496-498)CAC>TAC	p.H166Y
Pat_46	Post-Resistance	VEGFC	7424	37	4	177608980	177608980	Missense_Mutation	SNP	C	T	6	34	c.806G>A	c.(805-807)GGA>GAA	p.G269E
Pat_46	Post-Resistance	PDCD6	10016	37	5	306758	306758	Missense_Mutation	SNP	G	A	7	39	c.250G>A	c.(250-252)GAG>AAG	p.E84K
Pat_46	Post-Resistance	SLC6A18	348932	37	5	1225747	1225747	Missense_Mutation	SNP	G	A	3	22	c.155G>A	c.(154-156)GGA>GAA	p.G52E
Pat_46	Post-Resistance	TAS2R1	50834	37	5	9629784	9629784	Missense_Mutation	SNP	T	C	2	19	c.361A>G	c.(361-363)AGG>GGG	p.R121G
Pat_46	Post-Resistance	PRLR	5618	37	5	35065648	35065648	Missense_Mutation	SNP	C	T	6	35	c.1412G>A	c.(1411-1413)GGA>GAA	p.G471E
Pat_46	Post-Resistance	HEATR7B2	133558	37	5	41033154	41033154	Missense_Mutation	SNP	C	T	4	19	c.2350G>A	c.(2350-2352)GGT>AGT	p.G784S
Pat_46	Post-Resistance	DHX29	54505	37	5	54593223	54593223	Missense_Mutation	SNP	C	T	4	32	c.265G>A	c.(265-267)GTA>ATA	p.V89I
Pat_46	Post-Resistance	ERCC8	1161	37	5	60199531	60199531	Missense_Mutation	SNP	C	T	8	82	c.494G>A	c.(493-495)GGA>GAA	p.G165E
Pat_46	Post-Resistance	MAP1B	4131	37	5	71493512	71493512	Missense_Mutation	SNP	C	T	3	24	c.4330C>T	c.(4330-4332)CCA>TCA	p.P1444S
Pat_46	Post-Resistance	TMEM174	134288	37	5	72469955	72469955	Missense_Mutation	SNP	C	T	5	41	c.695C>T	c.(694-696)CCT>CTT	p.P232L
Pat_46	Post-Resistance	LOC644936	644936	37	5	79595930	79595930	Missense_Mutation	SNP	G	A	4	8	c.227C>T	c.(226-228)TCC>TTC	p.S76F
Pat_46	Post-Resistance	GPR98	84059	37	5	90016807	90016807	Nonsense_Mutation	SNP	C	T	8	79	c.9679C>T	c.(9679-9681)CGA>TGA	p.R3227*
Pat_46	Post-Resistance	LNPEP	4012	37	5	96329625	96329625	Missense_Mutation	SNP	G	A	6	56	c.1357G>A	c.(1357-1359)GCG>ACG	p.A453T
Pat_46	Post-Resistance	SRP19	6728	37	5	112203167	112203167	Missense_Mutation	SNP	G	A	5	50	c.368G>A	c.(367-369)GGA>GAA	p.G123E
Pat_46	Post-Resistance	CEP120	153241	37	5	122726902	122726902	Missense_Mutation	SNP	G	A	9	107	c.940C>T	c.(940-942)CCA>TCA	p.P314S
Pat_46	Post-Resistance	LMNB1	4001	37	5	126147552	126147552	Missense_Mutation	SNP	G	A	4	40	c.901G>A	c.(901-903)GAG>AAG	p.E301K
Pat_46	Post-Resistance	MEGF10	84466	37	5	126732229	126732229	Missense_Mutation	SNP	G	A	12	96	c.418G>A	c.(418-420)GAT>AAT	p.D140N
Pat_46	Post-Resistance	NKHD1-EIF4EBP	404734	37	5	139892499	139892499	Missense_Mutation	SNP	T	G	8	57	c.4191T>G	c.(4189-4191)ATT>ATG	p.I1397M
Pat_46	Post-Resistance	PCDHA3	56145	37	5	140181752	140181752	Missense_Mutation	SNP	G	A	6	66	c.970G>A	c.(970-972)GAT>AAT	p.D324N
Pat_46	Post-Resistance	PCDHA7	56141	37	5	140214185	140214185	Missense_Mutation	SNP	G	A	14	94	c.217G>A	c.(217-219)GAT>AAT	p.D73N
Pat_46	Post-Resistance	PCDHA13	56136	37	5	140263676	140263676	Missense_Mutation	SNP	C	T	8	54	c.1823C>T	c.(1822-1824)TCG>TTG	p.S608L
Pat_46	Post-Resistance	PCDHB11	56125	37	5	140581524	140581524	Missense_Mutation	SNP	C	T	8	75	c.2177C>T	c.(2176-2178)TCG>TTG	p.S726L
Pat_46	Post-Resistance	PCDHB12	56124	37	5	140590287	140590287	Missense_Mutation	SNP	C	T	6	98	c.1808C>T	c.(1807-1809)TCG>TTG	p.S603L
Pat_46	Post-Resistance	PCDH1	5097	37	5	141236930	141236930	Missense_Mutation	SNP	G	A	3	9	c.3206C>T	c.(3205-3207)CCG>CTG	p.P1069L
Pat_46	Post-Resistance	SLC26A2	1836	37	5	149357514	149357514	Missense_Mutation	SNP	C	T	7	70	c.299C>T	c.(298-300)CCA>CTA	p.P100L
Pat_46	Post-Resistance	ATP10B	23120	37	5	160018110	160018110	Missense_Mutation	SNP	C	T	3	22	c.3601G>A	c.(3601-3603)GAT>AAT	p.D1201N
Pat_46	Post-Resistance	GABRA6	2559	37	5	161128618	161128618	Missense_Mutation	SNP	C	A	7	45	c.1201C>A	c.(1201-1203)CCT>ACT	p.P401T
Pat_46	Post-Resistance	WWC1	23286	37	5	167836957	167836957	Missense_Mutation	SNP	G	A	13	65	c.898G>A	c.(898-900)GAG>AAG	p.E300K
Pat_46	Post-Resistance	SLIT3	6586	37	5	168098219	168098219	Missense_Mutation	SNP	G	A	4	19	c.4111C>T	c.(4111-4113)CCC>TCC	p.P1371S
Pat_46	Post-Resistance	FAM153C	653316	37	5	177473889	177473889	Missense_Mutation	SNP	C	T	7	27	c.290C>T	c.(289-291)TCC>TTC	p.S97F
Pat_46	Post-Resistance	DSP	1832	37	6	7570741	7570742	Missense_Mutation	DNP	CC	TT	5	59	.1646_1647CC>T	c.(1645-1647)TCC>TTT	p.S549F

Pat_46	Post-Resistance	HIVEP1	3096	37	6	12015883	12015883	Missense_Mutation	SNP	C	T	12	132	c.22C>T	c.(22-24)CAT>TAT	p.H8Y
Pat_46	Post-Resistance	CAP2	10486	37	6	17507904	17507904	Missense_Mutation	SNP	G	A	7	122	c.477G>A	c.(475-477)ATG>ATA	p.M159I
Pat_46	Post-Resistance	LRRC16A	55604	37	6	25516015	25516015	Missense_Mutation	SNP	G	A	8	14	c.1745G>A	c.(1744-1746)GGA>GAA	p.G582E
Pat_46	Post-Resistance	HIST1H2BE	8344	37	6	26184054	26184054	Missense_Mutation	SNP	C	T	11	61	c.31C>T	c.(31-33)CCG>TCG	p.P11S
Pat_46	Post-Resistance	BTN2A3	54718	37	6	26431314	26431314	Missense_Mutation	SNP	T	A	3	24	c.1232T>A	c.(1231-1233)CTG>CAG	p.L411Q
Pat_46	Post-Resistance	BTN1A1	696	37	6	26508950	26508950	Missense_Mutation	SNP	G	A	22	70	c.1129G>A	c.(1129-1131)GAG>AAG	p.E377K
Pat_46	Post-Resistance	PRSS16	10279	37	6	27222818	27222818	Missense_Mutation	SNP	G	A	9	68	c.1384G>A	c.(1384-1386)GAA>AAA	p.E462K
Pat_46	Post-Resistance	GPX5	2880	37	6	28497304	28497304	Missense_Mutation	SNP	C	T	12	49	c.164C>T	c.(163-165)TCC>TTC	p.S55F
Pat_46	Post-Resistance	PPP1R11	6992	37	6	30037019	30037019	Missense_Mutation	SNP	C	T	38	106	c.317C>T	c.(316-318)ACC>ATC	p.T106I
Pat_46	Post-Resistance	MDC1	9656	37	6	30680836	30680836	Missense_Mutation	SNP	G	A	4	50	c.883C>T	c.(883-885)CCT>TCT	p.P295S
Pat_46	Post-Resistance	C6orf15	29113	37	6	31079628	31079628	Missense_Mutation	SNP	G	A	4	29	c.508C>T	c.(508-510)CAC>TAC	p.H170Y
Pat_46	Post-Resistance	BAT1	7919	37	6	31498949	31498949	Missense_Mutation	SNP	C	T	8	86	c.1003G>A	c.(1003-1005)GAT>AAT	p.D335N
Pat_46	Post-Resistance	TNF	7124	37	6	31545117	31545117	Missense_Mutation	SNP	C	T	7	18	c.505C>T	c.(505-507)CTC>TTC	p.L169F
Pat_46	Post-Resistance	BAT3	7917	37	6	31615444	31615444	Missense_Mutation	SNP	G	A	6	40	c.730C>T	c.(730-732)CCA>TCA	p.P244S
Pat_46	Post-Resistance	SLC39A7	7922	37	6	33170381	33170381	Missense_Mutation	SNP	G	A	7	40	c.844G>A	c.(844-846)GAA>AAA	p.E282K
Pat_46	Post-Resistance	DNAH8	1769	37	6	38919096	38919096	Missense_Mutation	SNP	C	T	9	63	c.11600C>T	c.(11599-11601)TCT>TTT	p.S3867F
Pat_46	Post-Resistance	DNAH8	1769	37	6	38980323	38980323	Missense_Mutation	SNP	G	A	13	143	c.12973G>A	c.(12973-12975)GAA>AAA	p.E4325K
Pat_46	Post-Resistance	XPO5	57510	37	6	43541245	43541245	Missense_Mutation	SNP	C	T	5	50	c.199G>A	c.(199-201)GGC>AGC	p.G67S
Pat_46	Post-Resistance	CRISP2	7180	37	6	49660530	49660530	Missense_Mutation	SNP	C	T	8	45	c.688G>A	c.(688-690)GAA>AAA	p.E230K
Pat_46	Post-Resistance	LRRC1	55227	37	6	53764608	53764608	Missense_Mutation	SNP	C	T	6	34	c.706C>T	c.(706-708)CCT>TCT	p.P236S
Pat_46	Post-Resistance	FAM83B	222584	37	6	54805519	54805519	Missense_Mutation	SNP	C	T	4	31	c.1750C>T	c.(1750-1752)CCT>TCT	p.P584S
Pat_46	Post-Resistance	FAM83B	222584	37	6	54806308	54806308	Missense_Mutation	SNP	G	A	5	32	c.2539G>A	c.(2539-2541)GAA>AAA	p.E847K
Pat_46	Post-Resistance	BMP5	653	37	6	55739516	55739516	Missense_Mutation	SNP	C	T	15	75	c.148G>A	c.(148-150)GAA>AAA	p.E50K
Pat_46	Post-Resistance	GUSBL2	375513	37	6	58250821	58250821	Missense_Mutation	SNP	G	A	3	20	c.431C>T	c.(430-432)TCG>TTG	p.S144L
Pat_46	Post-Resistance	RIMS1	22999	37	6	72968786	72968786	Missense_Mutation	SNP	G	A	5	33	c.3025G>A	c.(3025-3027)GAT>AAT	p.D1009N
Pat_46	Post-Resistance	UBE2CBP	90025	37	6	83667051	83667051	Missense_Mutation	SNP	G	A	9	48	c.1129C>T	c.(1129-1131)CGC>TGC	p.R377C
Pat_46	Post-Resistance	EPHA7	2045	37	6	93964415	93964415	Missense_Mutation	SNP	C	T	7	35	c.2482G>A	c.(2482-2484)GAA>AAA	p.E828K
Pat_46	Post-Resistance	SIM1	6492	37	6	100838850	100838850	Missense_Mutation	SNP	T	G	11	57	c.1688A>C	c.(1687-1689)AAA>ACA	p.K563T
Pat_46	Post-Resistance	DDO	8528	37	6	110726085	110726085	Missense_Mutation	SNP	C	T	5	30	c.434G>A	c.(433-435)CGA>CAA	p.R145Q
Pat_46	Post-Resistance	DSE	29940	37	6	116752138	116752138	Nonsense_Mutation	SNP	T	A	5	34	c.692T>A	c.(691-693)TTA>TAA	p.L231*
Pat_46	Post-Resistance	ARHGAP18	93663	37	6	129901275	129901275	Missense_Mutation	SNP	C	T	4	44	c.1840G>A	c.(1840-1842)GGG>AGG	p.G614R
Pat_46	Post-Resistance	IL20RA	53832	37	6	137332467	137332467	Nonsense_Mutation	SNP	C	T	9	57	c.347G>A	c.(346-348)TGG>TAG	p.W116*
Pat_46	Post-Resistance	KIAA1244	57221	37	6	138628471	138628471	Missense_Mutation	SNP	G	A	15	64	c.3910G>A	c.(3910-3912)GAA>AAA	p.E1304K
Pat_46	Post-Resistance	SYNE1	23345	37	6	152454491	152454491	Missense_Mutation	SNP	G	A	9	80	c.25921C>T	c.(25921-25923)CGG>TGG	p.R8641W
Pat_46	Post-Resistance	MLLT4	4301	37	6	168352148	168352149	Missense_Mutation	DNP	CC	TT	8	69	.4090_4091CC>TT	c.(4090-4092)CCT>TTT	p.P1364F
Pat_46	Post-Resistance	THSD7A	221981	37	7	11441554	11441554	Nonsense_Mutation	SNP	G	A	9	109	c.4279C>T	c.(4279-4281)CAG>TAG	p.Q1427*
Pat_46	Post-Resistance	THSD7A	221981	37	7	11485877	11485877	Missense_Mutation	SNP	C	T	19	136	c.2875G>A	c.(2875-2877)GAC>AAC	p.D959N
Pat_46	Post-Resistance	PRPS1L1	221823	37	7	18067003	18067003	Nonsense_Mutation	SNP	G	A	9	62	c.403C>T	c.(403-405)CAG>TAG	p.Q135*
Pat_46	Post-Resistance	HDAC9	9734	37	7	18788643	18788643	Missense_Mutation	SNP	C	T	5	23	c.1916C>T	c.(1915-1917)CCC>CTC	p.P639L
Pat_46	Post-Resistance	ITGB8	3696	37	7	20441600	20441600	Missense_Mutation	SNP	C	T	33	222	c.1538C>T	c.(1537-1539)TCA>TTA	p.S513L
Pat_46	Post-Resistance	RAPGEF5	9771	37	7	22259516	22259516	Missense_Mutation	SNP	G	A	12	65	c.506C>T	c.(505-507)ACG>ATG	p.T169M
Pat_46	Post-Resistance	GGCT	79017	37	7	30538488	30538488	Missense_Mutation	SNP	T	G	15	87	c.354A>C	c.(352-354)AAA>AAC	p.K118N
Pat_46	Post-Resistance	ADCYAP1R1	117	37	7	31146129	31146129	Missense_Mutation	SNP	G	A	6	31	c.1238G>A	c.(1237-1239)CGA>CAA	p.R413Q
Pat_46	Post-Resistance	TXNDC3	51314	37	7	37907434	37907434	Missense_Mutation	SNP	G	A	7	45	c.752G>A	c.(751-753)CGA>CAA	p.R251Q
Pat_46	Post-Resistance	VSTM2A	222008	37	7	54610488	54610488	Missense_Mutation	SNP	G	A	10	68	c.65G>A	c.(64-66)GGG>GAG	p.G22E
Pat_46	Post-Resistance	ZNF716	441234	37	7	57528735	57528735	Missense_Mutation	SNP	G	A	7	28	c.568G>A	c.(568-570)GAT>AAT	p.D190N
Pat_46	Post-Resistance	ZNF679	168417	37	7	63721281	63721281	Missense_Mutation	SNP	G	A	5	40	c.236G>A	c.(235-237)AGA>AAA	p.R79K

Pat_46	Post-Resistance	ZNF107	51427	37	7	64126635	64126635	Translation_Start_Site	SNP	C	T	7	62	c.-661C>T	(-663--659)GACGC>GATGC	
Pat_46	Post-Resistance	HGF	3082	37	7	81335690	81335690	Missense_Mutation	SNP	C	T	19	116	c.1670G>A	c.(1669-1671)GGA>GAA	p.G557E
Pat_46	Post-Resistance	RUNDC3B	154661	37	7	87280226	87280226	Missense_Mutation	SNP	G	A	5	55	c.211G>A	c.(211-213)GAA>AAA	p.E71K
Pat_46	Post-Resistance	FZD1	8321	37	7	90895178	90895178	Missense_Mutation	SNP	T	C	5	41	c.983T>C	c.(982-984)GTG>GCG	p.V328A
Pat_46	Post-Resistance	CALCR	799	37	7	93098063	93098063	Missense_Mutation	SNP	G	A	11	82	c.539C>T	c.(538-540)ACC>ATC	p.T180I
Pat_46	Post-Resistance	SRRT	51593	37	7	100482042	100482042	Missense_Mutation	SNP	G	C	2	8	c.811G>C	c.(811-813)GAG>CAG	p.E271Q
Pat_46	Post-Resistance	MUC17	140453	37	7	100682297	100682297	Missense_Mutation	SNP	A	G	33	168	c.7600A>G	c.(7600-7602)ACC>GCC	p.T2534A
Pat_46	Post-Resistance	RABL5	64792	37	7	100958513	100958513	Missense_Mutation	SNP	G	A	4	25	c.460C>T	c.(460-462)CCT>TCT	p.P154S
Pat_46	Post-Resistance	RELN	5649	37	7	103214615	103214615	Missense_Mutation	SNP	C	T	21	98	c.4435G>A	c.(4435-4437)GAT>AAT	p.D1479N
Pat_46	Post-Resistance	RELN	5649	37	7	103243912	103243912	Missense_Mutation	SNP	C	T	4	38	c.3172G>A	c.(3172-3174)GAA>AAA	p.E1058K
Pat_46	Post-Resistance	PPP1R3A	5506	37	7	113517816	113517816	Missense_Mutation	SNP	C	T	8	78	c.3331G>A	c.(3331-3333)GAA>AAA	p.E1111K
Pat_46	Post-Resistance	WNT2	7472	37	7	116937870	116937870	Missense_Mutation	SNP	G	A	18	94	c.649C>T	c.(649-651)CTC>TTC	p.L217F
Pat_46	Post-Resistance	CFTR	1080	37	7	117174417	117174417	Missense_Mutation	SNP	G	A	6	65	c.577G>A	c.(577-579)GAA>AAA	p.E193K
Pat_46	Post-Resistance	PTPRZ1	5803	37	7	121653193	121653193	Missense_Mutation	SNP	C	T	20	122	c.4093C>T	c.(4093-4095)CAT>TAT	p.H1365Y
Pat_46	Post-Resistance	DGKI	9162	37	7	137271862	137271862	Missense_Mutation	SNP	C	T	34	46	c.1406G>A	c.(1405-1407)CGA>CAA	p.R469Q
Pat_46	Post-Resistance	BRAF	673	37	7	140453136	140453137	Missense_Mutation	DNP	AC	TT	34	64	.1798_1799GT>A	c.(1798-1800)GTG>AAG	p.V600K
Pat_46	Post-Resistance	BRAF	673	37	7	140494149	140494149	Missense_Mutation	SNP	G	A	55	54	c.1099C>T	c.(1099-1101)CCC>TCC	p.P367S
Pat_46	Post-Resistance	CLEC5A	23601	37	7	141635652	141635652	Missense_Mutation	SNP	C	T	24	55	c.307G>A	c.(307-309)GGA>AGA	p.G103R
Pat_46	Post-Resistance	TAS2R38	5726	37	7	141673425	141673425	Missense_Mutation	SNP	G	A	7	101	c.65C>T	c.(64-66)TCA>TTA	p.S22L
Pat_46	Post-Resistance	PRSS1	5644	37	7	142460779	142460779	Missense_Mutation	SNP	G	A	14	30	c.652G>A	c.(652-654)GAT>AAT	p.D218N
Pat_46	Post-Resistance	OR6V1	346517	37	7	142750081	142750081	Missense_Mutation	SNP	C	T	28	76	c.644C>T	c.(643-645)TCC>TTC	p.S215F
Pat_46	Post-Resistance	FAM115C	285966	37	7	143417077	143417077	Missense_Mutation	SNP	G	A	5	9	c.925G>A	c.(925-927)GAT>AAT	p.D309N
Pat_46	Post-Resistance	OR2A5	393046	37	7	143748144	143748144	Missense_Mutation	SNP	C	T	11	87	c.650C>T	c.(649-651)TCC>TTC	p.S217F
Pat_46	Post-Resistance	EZH2	2146	37	7	148506474	148506474	Missense_Mutation	SNP	C	T	10	135	c.2023G>A	c.(2023-2025)GTG>ATG	p.V675M
Pat_46	Post-Resistance	SSPO	23145	37	7	149492370	149492370	Missense_Mutation	SNP	G	A	11	22	c.6259G>A	c.(6259-6261)GAA>AAA	p.E2087K
Pat_46	Post-Resistance	AGAP3	116988	37	7	150817132	150817132	Missense_Mutation	SNP	C	T	3	18	c.1028C>T	c.(1027-1029)CCC>CTC	p.P343L
Pat_46	Post-Resistance	MYOM2	9172	37	8	2088749	2088749	Missense_Mutation	SNP	A	G	5	47	c.3904A>G	c.(3904-3906)ACT>GCT	p.T1302A
Pat_46	Post-Resistance	CSMD1	64478	37	8	2944658	2944658	Missense_Mutation	SNP	C	T	4	24	c.7438G>A	c.(7438-7440)GGC>AGC	p.G2480S
Pat_46	Post-Resistance	CSMD1	64478	37	8	3265610	3265610	Missense_Mutation	SNP	C	T	5	47	c.1885G>A	c.(1885-1887)GAT>AAT	p.D629N
Pat_46	Post-Resistance	FGF20	26281	37	8	16850627	16850627	Missense_Mutation	SNP	G	A	6	70	c.590C>T	c.(589-591)CCA>CTA	p.P197L
Pat_46	Post-Resistance	SH2D4A	63898	37	8	19250880	19250880	Missense_Mutation	SNP	C	T	9	61	c.1100C>T	c.(1099-1101)CCC>CTC	p.P367L
Pat_46	Post-Resistance	POLR3D	661	37	8	22107963	22107963	Missense_Mutation	SNP	G	A	7	37	c.1129G>A	c.(1129-1131)GGA>AGA	p.G377R
Pat_46	Post-Resistance	ADAM7	8756	37	8	24346730	24346730	Missense_Mutation	SNP	G	A	5	54	c.1150G>A	c.(1150-1152)GAT>AAT	p.D384N
Pat_46	Post-Resistance	EBF2	64641	37	8	25744298	25744298	Missense_Mutation	SNP	C	T	11	36	c.982G>A	c.(982-984)GGA>AGA	p.G328R
Pat_46	Post-Resistance	PNMA2	10687	37	8	26365277	26365277	Missense_Mutation	SNP	C	T	4	21	c.995G>A	c.(994-996)CGG>CAG	p.R332Q
Pat_46	Post-Resistance	IDO1	3620	37	8	39776418	39776418	Missense_Mutation	SNP	G	A	6	52	c.388G>A	c.(388-390)GTC>ATC	p.V130I
Pat_46	Post-Resistance	IDO2	169355	37	8	39872871	39872871	Missense_Mutation	SNP	G	A	4	15	c.1013G>A	c.(1012-1014)GGA>GAA	p.G338E
Pat_46	Post-Resistance	GINS4	84296	37	8	41393924	41393924	Missense_Mutation	SNP	C	T	4	23	c.142C>T	c.(142-144)CCT>TCT	p.P48S
Pat_46	Post-Resistance	SLC20A2	6575	37	8	42302254	42302254	Missense_Mutation	SNP	C	T	4	22	c.640G>A	c.(640-642)GCC>ACC	p.A214T
Pat_46	Post-Resistance	MCM4	4173	37	8	48875363	48875363	Missense_Mutation	SNP	G	A	16	137	c.541G>A	c.(541-543)GAA>AAA	p.E181K
Pat_46	Post-Resistance	EFCAB1	79645	37	8	49637324	49637324	Missense_Mutation	SNP	G	A	4	39	c.613C>T	c.(613-615)CCA>TCA	p.P205S
Pat_46	Post-Resistance	RP1	6101	37	8	55539065	55539065	Missense_Mutation	SNP	G	A	6	38	c.2623G>A	c.(2623-2625)GAT>AAT	p.D875N
Pat_46	Post-Resistance	CA8	767	37	8	61178606	61178606	Missense_Mutation	SNP	G	A	3	23	c.295C>T	c.(295-297)CTT>TTT	p.L99F
Pat_46	Post-Resistance	CYP7B1	9420	37	8	65528256	65528257	Missense_Mutation	DNP	TC	AT	8	96	c.841_842GA>AT	c.(841-843)GAA>ATA	p.E281I
Pat_46	Post-Resistance	SGK3	23678	37	8	67759522	67759522	Missense_Mutation	SNP	C	T	7	52	c.1169C>T	c.(1168-1170)TCC>TTC	p.S390F
Pat_46	Post-Resistance	CA1	759	37	8	86249277	86249277	Missense_Mutation	SNP	G	A	4	30	c.251C>T	c.(250-252)CCT>CTT	p.P84L
Pat_46	Post-Resistance	RGS22	26166	37	8	101075915	101075915	Missense_Mutation	SNP	G	A	9	26	c.1081C>T	c.(1081-1083)CAT>TAT	p.H361Y

Pat_46	Post-Resistance	RIMS2	9699	37	8	104898050	104898050	Missense_Mutation	SNP	G	A	4	10	c.557G>A	c.(556-558)CGA>CAA	p.R186Q
Pat_46	Post-Resistance	PKHD1L1	93035	37	8	110394750	110394750	Missense_Mutation	SNP	G	A	14	128	c.367G>A	c.(367-369)GAA>AAA	p.E123K
Pat_46	Post-Resistance	PKHD1L1	93035	37	8	110413769	110413769	Missense_Mutation	SNP	C	T	5	50	c.1325C>T	c.(1324-1326)TCC>TTC	p.S442F
Pat_46	Post-Resistance	PKHD1L1	93035	37	8	110457449	110457449	Missense_Mutation	SNP	G	A	5	32	c.5351G>A	c.(5350-5352)GGA>GAA	p.G1784E
Pat_46	Post-Resistance	FER1L6	654463	37	8	125076600	125076600	Missense_Mutation	SNP	C	T	5	75	c.3341C>T	c.(3340-3342)TCG>TTG	p.S1114L
Pat_46	Post-Resistance	KIFC2	90990	37	8	145697560	145697560	Nonsense_Mutation	SNP	C	T	4	13	c.1525C>T	c.(1525-1527)CAG>TAG	p.Q509*
Pat_46	Post-Resistance	MGC70857	414919	37	8	145753440	145753440	Missense_Mutation	SNP	G	A	3	17	c.173C>T	c.(172-174)TCC>TTC	p.S58F
Pat_46	Post-Resistance	ADAMTSL1	92949	37	9	18662013	18662013	Missense_Mutation	SNP	G	A	21	88	c.1027G>A	c.(1027-1029)GAG>AAG	p.E343K
Pat_46	Post-Resistance	SLC24A2	25769	37	9	19786182	19786182	Missense_Mutation	SNP	C	T	7	40	c.683G>A	c.(682-684)AGA>AAA	p.R228K
Pat_46	Post-Resistance	TAF1L	138474	37	9	32635478	32635478	Missense_Mutation	SNP	G	A	6	56	c.100C>T	c.(100-102)CCA>TCA	p.P34S
Pat_46	Post-Resistance	NUDT2	318	37	9	34339095	34339095	Missense_Mutation	SNP	G	T	5	33	c.58G>T	c.(58-60)GAC>TAC	p.D20Y
Pat_46	Post-Resistance	ANXA1	301	37	9	75775212	75775212	Missense_Mutation	SNP	G	A	18	78	c.304G>A	c.(304-306)GGT>AGT	p.G102S
Pat_46	Post-Resistance	TRPM6	140803	37	9	77386635	77386635	Nonsense_Mutation	SNP	G	A	6	56	c.3520C>T	c.(3520-3522)CGA>TGA	p.R1174*
Pat_46	Post-Resistance	TRPM6	140803	37	9	77400944	77400944	Nonsense_Mutation	SNP	G	C	15	62	c.2765C>G	c.(2764-2766)TCA>TGA	p.S922*
Pat_46	Post-Resistance	HNRNPK	3190	37	9	86587088	86587088	Missense_Mutation	SNP	C	T	5	68	c.662G>A	c.(661-663)CGT>CAT	p.R221H
Pat_46	Post-Resistance	RMI1	80010	37	9	86617448	86617448	Missense_Mutation	SNP	C	T	16	127	c.1547C>T	c.(1546-1548)ACC>ATC	p.T516I
Pat_46	Post-Resistance	C9orf79	286234	37	9	90503694	90503694	Missense_Mutation	SNP	C	T	3	21	c.4292C>T	c.(4291-4293)CCA>CTA	p.P1431L
Pat_46	Post-Resistance	NFIL3	4783	37	9	94172686	94172686	Missense_Mutation	SNP	C	T	11	118	c.331G>A	c.(331-333)GAA>AAA	p.E111K
Pat_46	Post-Resistance	ECM2	1842	37	9	95280064	95280064	Missense_Mutation	SNP	C	T	6	50	c.386G>A	c.(385-387)GGA>GAA	p.G129E
Pat_46	Post-Resistance	FGD3	89846	37	9	95776206	95776206	Missense_Mutation	SNP	G	A	13	81	c.1108G>A	c.(1108-1110)GAA>AAA	p.E370K
Pat_46	Post-Resistance	PTPDC1	138639	37	9	96860382	96860382	Nonsense_Mutation	SNP	C	T	4	19	c.1372C>T	c.(1372-1374)CAG>TAG	p.Q458*
Pat_46	Post-Resistance	PPP3R2	5535	37	9	104357194	104357194	Missense_Mutation	SNP	C	T	6	45	c.19G>A	c.(19-21)GAG>AAG	p.E7K
Pat_46	Post-Resistance	GRIN3A	116443	37	9	104432484	104432484	Missense_Mutation	SNP	G	A	8	40	c.2210C>T	c.(2209-2211)CCA>CTA	p.P737L
Pat_46	Post-Resistance	OR13C4	138804	37	9	107289213	107289213	Missense_Mutation	SNP	G	A	13	80	c.278C>T	c.(277-279)TCC>TTC	p.S93F
Pat_46	Post-Resistance	ABCA1	19	37	9	107574961	107574961	Missense_Mutation	SNP	C	T	5	59	c.3944G>A	c.(3943-3945)GGG>GAG	p.G1315E
Pat_46	Post-Resistance	IKBKAP	8518	37	9	111665890	111665890	Missense_Mutation	SNP	G	A	12	63	c.1703C>T	c.(1702-1704)TCA>TTA	p.S568L
Pat_46	Post-Resistance	C9orf5	23731	37	9	111795771	111795771	Missense_Mutation	SNP	G	A	4	31	c.2410C>T	c.(2410-2412)CCT>TCT	p.P804S
Pat_46	Post-Resistance	SVEP1	79987	37	9	113170760	113170760	Missense_Mutation	SNP	G	A	3	18	c.7120C>T	c.(7120-7122)CCT>TCT	p.P2374S
Pat_46	Post-Resistance	SVEP1	79987	37	9	113312330	113312330	Missense_Mutation	SNP	C	T	6	71	c.586G>A	c.(586-588)GAT>AAT	p.D196N
Pat_46	Post-Resistance	KIAA0368	23392	37	9	114184472	114184472	Missense_Mutation	SNP	G	A	8	57	c.1808C>T	c.(1807-1809)CCA>CTA	p.P603L
Pat_46	Post-Resistance	FKBP15	23307	37	9	115940928	115940928	Missense_Mutation	SNP	C	T	3	11	c.2068G>A	c.(2068-2070)GTG>ATG	p.V690M
Pat_46	Post-Resistance	TNC	3371	37	9	117853113	117853113	Missense_Mutation	SNP	G	A	13	66	c.185C>T	c.(184-186)TCC>TTC	p.S62F
Pat_46	Post-Resistance	DBC1	1620	37	9	122001016	122001016	Missense_Mutation	SNP	G	A	6	24	c.602C>T	c.(601-603)CCT>CTT	p.P201L
Pat_46	Post-Resistance	PSMD5	5711	37	9	123605142	123605142	Missense_Mutation	SNP	C	T	2	1	c.46G>A	c.(46-48)GAA>AAA	p.E16K
Pat_46	Post-Resistance	KCNT1	57582	37	9	138657003	138657003	Missense_Mutation	SNP	G	A	5	28	c.1162G>A	c.(1162-1164)GAC>AAC	p.D388N
Pat_46	Post-Resistance	TBL1X	6907	37	X	9652089	9652089	Missense_Mutation	SNP	C	T	5	48	c.218C>T	c.(217-219)TCC>TTC	p.S73F
Pat_46	Post-Resistance	ARHGAP6	395	37	X	11272704	11272704	Missense_Mutation	SNP	C	A	10	57	c.712G>T	c.(712-714)GAC>TAC	p.D238Y
Pat_46	Post-Resistance	GEMIN8	54960	37	X	14027232	14027232	Missense_Mutation	SNP	C	T	13	54	c.529G>A	c.(529-531)GAC>AAC	p.D177N
Pat_46	Post-Resistance	GLRA2	2742	37	X	14550395	14550395	Missense_Mutation	SNP	G	A	12	76	c.103G>A	c.(103-105)GGA>AGA	p.G35R
Pat_46	Post-Resistance	GLRA2	2742	37	X	14550467	14550467	Missense_Mutation	SNP	G	A	10	96	c.175G>A	c.(175-177)GAT>AAT	p.D59N
Pat_46	Post-Resistance	RAI2	10742	37	X	17818903	17818903	Missense_Mutation	SNP	C	T	4	39	c.1228G>A	c.(1228-1230)GAG>AAG	p.E410K
Pat_46	Post-Resistance	PDHA1	5160	37	X	19368083	19368083	Missense_Mutation	SNP	G	A	5	26	c.146G>A	c.(145-147)GGC>GAC	p.G49D
Pat_46	Post-Resistance	RPS6KA3	6197	37	X	20252902	20252902	Missense_Mutation	SNP	C	T	7	52	c.100G>A	c.(100-102)GGA>AGA	p.G34R
Pat_46	Post-Resistance	APOO	79135	37	X	23898990	23898990	Missense_Mutation	SNP	G	A	4	28	c.89C>T	c.(88-90)CCT>CTT	p.P30L
Pat_46	Post-Resistance	KLHL15	80311	37	X	24006750	24006750	Missense_Mutation	SNP	G	A	11	96	c.1103C>T	c.(1102-1104)CCA>CTA	p.P368L
Pat_46	Post-Resistance	FAM47C	442444	37	X	37026904	37026904	Missense_Mutation	SNP	A	G	3	21	c.421A>G	c.(421-423)ATG>GTG	p.M141V
Pat_46	Post-Resistance	USP9X	8239	37	X	41084022	41084022	Missense_Mutation	SNP	G	A	6	78	c.6779G>A	c.(6778-6780)GGT>GAT	p.G2260D

Pat_46	Post-Resistance	CASK	8573	37	X	41393962	41393962	Missense_Mutation	SNP	G	A	18	70	c.2299C>T	c.(2299-2301)CCA>TCA	p.P767S
Pat_46	Post-Resistance	ZNF182	7569	37	X	47837038	47837038	Missense_Mutation	SNP	G	A	9	56	c.448C>T	c.(448-450)CTT>TTT	p.L150F
Pat_46	Post-Resistance	MTMR8	55613	37	X	63444876	63444876	Missense_Mutation	SNP	G	A	3	13	c.1780C>T	c.(1780-1782)CGT>TGT	p.R594C
Pat_46	Post-Resistance	FOXO4	4303	37	X	70321554	70321554	Missense_Mutation	SNP	G	A	3	24	c.1474G>A	c.(1474-1476)GAT>AAT	p.D492N
Pat_46	Post-Resistance	ACRC	93953	37	X	70823916	70823916	Missense_Mutation	SNP	A	T	5	54	c.789A>T	c.(787-789)GAA>GAT	p.E263D
Pat_46	Post-Resistance	NAP1L2	4674	37	X	72433746	72433746	Missense_Mutation	SNP	C	T	4	18	c.583G>A	c.(583-585)GAA>AAA	p.E195K
Pat_46	Post-Resistance	NAP1L2	4674	37	X	72434160	72434160	Missense_Mutation	SNP	C	T	7	21	c.169G>A	c.(169-171)GAA>AAA	p.E57K
Pat_46	Post-Resistance	RLIM	51132	37	X	73814150	73814150	Missense_Mutation	SNP	C	T	7	52	c.244G>A	c.(244-246)GAA>AAA	p.E82K
Pat_46	Post-Resistance	KIAA2022	340533	37	X	73963274	73963274	Missense_Mutation	SNP	C	A	12	49	c.1118G>T	c.(1117-1119)TGG>TTG	p.W373L
Pat_46	Post-Resistance	DRP2	1821	37	X	100490897	100490897	Missense_Mutation	SNP	G	A	11	82	c.166G>A	c.(166-168)GTT>ATT	p.V56I
Pat_46	Post-Resistance	ARMCX3	51566	37	X	100880625	100880625	Missense_Mutation	SNP	C	T	5	53	c.656C>T	c.(655-657)TCT>TTT	p.S219F
Pat_46	Post-Resistance	NXF3	56000	37	X	102338545	102338545	Missense_Mutation	SNP	G	A	15	91	c.427C>T	c.(427-429)CCA>TCA	p.P143S
Pat_46	Post-Resistance	COL4A6	1288	37	X	107408689	107408689	Missense_Mutation	SNP	C	T	4	12	c.3722G>A	c.(3721-3723)GGT>GAT	p.G1241D
Pat_46	Post-Resistance	COL4A6	1288	37	X	107448668	107448668	Splice_Site	SNP	C	T	11	200	c.690_splice	c.e11+1	p.K230_splice
Pat_46	Post-Resistance	COL4A5	1287	37	X	107834341	107834341	Nonsense_Mutation	SNP	C	T	4	33	c.1219C>T	c.(1219-1221)CAG>TAG	p.Q407*
Pat_46	Post-Resistance	COL4A5	1287	37	X	107840679	107840679	Missense_Mutation	SNP	C	T	4	45	c.1660C>T	c.(1660-1662)CCA>TCA	p.P554S
Pat_46	Post-Resistance	GUCY2F	2986	37	X	108636233	108636233	Missense_Mutation	SNP	G	A	11	138	c.2476C>T	c.(2476-2478)CGG>TGG	p.R826W
Pat_46	Post-Resistance	TRPC5	7224	37	X	111019987	111019987	Nonsense_Mutation	SNP	T	A	5	44	c.2476A>T	c.(2476-2478)AAG>TAG	p.K826*
Pat_46	Post-Resistance	PLS3	5358	37	X	114877821	114877821	Splice_Site	SNP	G	A	5	35	c.1183_splice	c.e10+1	p.G395_splice
Pat_46	Post-Resistance	CUL4B	8450	37	X	119691888	119691888	Missense_Mutation	SNP	G	A	4	37	c.617C>T	c.(616-618)CCT>CTT	p.P206L
Pat_46	Post-Resistance	GRIA3	2892	37	X	122598729	122598729	Missense_Mutation	SNP	C	T	9	95	c.2090C>T	c.(2089-2091)GCT>GTT	p.A697V
Pat_46	Post-Resistance	SAGE1	55511	37	X	134994087	134994087	Missense_Mutation	SNP	G	A	4	39	c.2496G>A	c.(2494-2496)ATG>ATA	p.M832I
Pat_46	Post-Resistance	MAP7D3	79649	37	X	135309517	135309517	Missense_Mutation	SNP	C	T	6	87	c.1960G>A	c.(1960-1962)GAT>AAT	p.D654N
Pat_46	Post-Resistance	MCF2	4168	37	X	138678928	138678928	Missense_Mutation	SNP	C	T	6	49	c.2057G>A	c.(2056-2058)GGA>GAA	p.G686E
Pat_46	Post-Resistance	UBE2NL	389898	37	X	142967564	142967564	Missense_Mutation	SNP	C	T	13	77	c.362C>T	c.(361-363)CCA>CTA	p.P121L
Pat_46	Post-Resistance	AFF2	2334	37	X	148037446	148037446	Missense_Mutation	SNP	G	A	11	127	c.1871G>A	c.(1870-1872)AGG>AAG	p.R624K
Pat_46	Post-Resistance	MAGEA6	4105	37	X	151870202	151870202	Missense_Mutation	SNP	C	T	5	42	c.892C>T	c.(892-894)CGC>TGC	p.R298C
Pat_46	Post-Resistance	MAGEA3	4102	37	X	151935227	151935227	Missense_Mutation	SNP	C	T	10	60	c.940G>A	c.(940-942)GAG>AAG	p.E314K
Pat_46	Post-Resistance	F8	2157	37	X	154132706	154132706	Missense_Mutation	SNP	C	T	7	124	c.5680G>A	c.(5680-5682)GAA>AAA	p.E1894K
Pat_46	Post-Resistance	F8	2157	37	X	154159268	154159268	Missense_Mutation	SNP	C	T	6	42	c.2797G>A	c.(2797-2799)GAT>AAT	p.D933N
Pat_48	Pre-Treatment	GIPC2	54810	37	1	78585136	78585136	Missense_Mutation	SNP	G	A	9	27	c.667G>A	c.(667-669)GCA>ACA	p.A223T
Pat_48	Pre-Treatment	CLCA2	9635	37	1	86890069	86890069	Missense_Mutation	SNP	A	G	6	29	c.139A>G	c.(139-141)ATT>GTT	p.I47V
Pat_48	Pre-Treatment	DUSP27	92235	37	1	167097709	167097709	Missense_Mutation	SNP	C	T	5	4	c.3341C>T	c.(3340-3342)TCT>TTT	p.S1114F
Pat_48	Pre-Treatment	CACNA1E	777	37	1	181549815	181549815	Missense_Mutation	SNP	C	T	55	54	c.854C>T	c.(853-855)CCC>CTC	p.P285L
Pat_48	Pre-Treatment	OR14A16	284532	37	1	247978163	247978163	Missense_Mutation	SNP	C	T	7	26	c.869G>A	c.(868-870)AGA>AAA	p.R290K
Pat_48	Pre-Treatment	OR14A16	284532	37	1	247978557	247978557	Missense_Mutation	SNP	C	T	42	39	c.475G>A	c.(475-477)GCT>ACT	p.A159T
Pat_48	Pre-Treatment	ANKRD30A	91074	37	10	37431050	37431050	Missense_Mutation	SNP	G	C	3	23	c.1057G>C	c.(1057-1059)GCA>CCA	p.A353P
Pat_48	Pre-Treatment	ZNF239	8187	37	10	44052942	44052942	Missense_Mutation	SNP	G	A	8	21	c.586C>T	c.(586-588)CCA>TCA	p.P196S
Pat_48	Pre-Treatment	C10orf72	196740	37	10	50285269	50285269	Missense_Mutation	SNP	G	A	15	7	c.629C>T	c.(628-630)TCC>TTC	p.S210F
Pat_48	Pre-Treatment	OR52J3	119679	37	11	5068593	5068593	Missense_Mutation	SNP	C	T	12	53	c.838C>T	c.(838-840)CTC>TTC	p.L280F
Pat_48	Pre-Treatment	IGSF22	283284	37	11	18741637	18741637	Missense_Mutation	SNP	C	T	4	31	c.492G>A	c.(490-492)ATG>ATA	p.M164I
Pat_48	Pre-Treatment	OR4C46	119749	37	11	51515587	51515587	Missense_Mutation	SNP	A	T	12	40	c.306A>T	c.(304-306)GAA>GAT	p.E102D
Pat_48	Pre-Treatment	OR10W1	81341	37	11	58034652	58034652	Missense_Mutation	SNP	G	A	7	63	c.679C>T	c.(679-681)CGG>TGG	p.R227W
Pat_48	Pre-Treatment	SLC22A10	387775	37	11	63067056	63067056	Missense_Mutation	SNP	G	A	3	39	c.1025G>A	c.(1024-1026)CGC>CAC	p.R342H
Pat_48	Pre-Treatment	CLEC9A	283420	37	12	10215746	10215746	Nonsense_Mutation	SNP	C	T	28	81	c.412C>T	c.(412-414)CAA>TAA	p.Q138*
Pat_48	Pre-Treatment	PRB3	5544	37	12	11420152	11420152	Missense_Mutation	SNP	G	A	3	34	c.904C>T	c.(904-906)CCT>TCT	p.P302S
Pat_48	Pre-Treatment	PRB2	653247	37	12	11546795	11546795	Missense_Mutation	SNP	G	A	3	27	c.217C>T	c.(217-219)CCT>TCT	p.P73S

Pat_48	Pre-Treatment	OR4K1	79544	37	14	20404061	20404061	Missense_Mutation	SNP	C	T	13	11	c.236C>T	c.(235-237)CCC>CTC	p.P79L
Pat_48	Pre-Treatment	EFTUD1	79631	37	15	82512090	82512090	Missense_Mutation	SNP	A	G	2	20	c.1514T>C	c.(1513-1515)TTT>TCT	p.F505S
Pat_48	Pre-Treatment	GRIN2A	2903	37	16	9857895	9857895	Missense_Mutation	SNP	C	T	6	31	c.3506G>A	c.(3505-3507)CGG>CAG	p.R1169Q
Pat_48	Pre-Treatment	SPIRE2	84501	37	16	89895131	89895131	Missense_Mutation	SNP	G	A	2	3	c.173G>A	c.(172-174)CGC>CAC	p.R58H
Pat_48	Pre-Treatment	DNAH2	146754	37	17	7697572	7697572	Missense_Mutation	SNP	G	A	19	16	c.7570G>A	c.(7570-7572)GAA>AAA	p.E2524K
Pat_48	Pre-Treatment	EVPLL	645027	37	17	18286166	18286166	Missense_Mutation	SNP	C	T	8	10	c.499C>T	c.(499-501)CCG>TCG	p.P167S
Pat_48	Pre-Treatment	SGCA	6442	37	17	48245758	48245758	Missense_Mutation	SNP	G	A	2	5	c.409G>A	c.(409-411)GAG>AAG	p.E137K
Pat_48	Pre-Treatment	KIF2B	84643	37	17	51901215	51901215	Missense_Mutation	SNP	C	T	7	28	c.821C>T	c.(820-822)GCC>GTC	p.A274V
Pat_48	Pre-Treatment	CXXC1	30827	37	18	47812290	47812290	Missense_Mutation	SNP	C	G	4	42	c.468G>C	c.(466-468)CAG>CAC	p.Q156H
Pat_48	Pre-Treatment	ZNF563	147837	37	19	12430274	12430274	Missense_Mutation	SNP	C	G	19	48	c.565G>C	c.(565-567)GTA>CTA	p.V189L
Pat_48	Pre-Treatment	LILRA3	11026	37	19	54803582	54803582	Missense_Mutation	SNP	C	T	11	21	c.242G>A	c.(241-243)GGC>GAC	p.G81D
Pat_48	Pre-Treatment	SNTG2	54221	37	2	1094046	1094046	Missense_Mutation	SNP	C	T	15	13	c.275C>T	c.(274-276)TCT>TTT	p.S92F
Pat_48	Pre-Treatment	REG1B	5968	37	2	79313967	79313967	Missense_Mutation	SNP	C	T	14	55	c.154G>A	c.(154-156)GAA>AAA	p.E52K
Pat_48	Pre-Treatment	LRP2	4036	37	2	170094612	170094612	Missense_Mutation	SNP	C	T	6	21	c.4495G>A	c.(4495-4497)GAC>AAC	p.D1499N
Pat_48	Pre-Treatment	TTN	7273	37	2	179472587	179472587	Missense_Mutation	SNP	G	A	55	81	c.45223C>T	c.(45223-45225)CGG>TG	p.R15075W
Pat_48	Pre-Treatment	HECW2	57520	37	2	197297975	197297975	Missense_Mutation	SNP	C	T	12	35	c.173G>A	c.(172-174)CGC>CAC	p.R58H
Pat_48	Pre-Treatment	SNTA1	6640	37	20	32000563	32000563	Missense_Mutation	SNP	C	A	3	26	c.727G>T	c.(727-729)GGT>TGT	p.G243C
Pat_48	Pre-Treatment	CDH26	60437	37	20	58559801	58559801	Missense_Mutation	SNP	G	A	30	53	c.649G>A	c.(649-651)GGT>AGT	p.G217S
Pat_48	Pre-Treatment	SMTN	6525	37	22	31495070	31495070	Missense_Mutation	SNP	G	A	3	42	c.2356G>A	c.(2356-2358)GCC>ACC	p.A786T
Pat_48	Pre-Treatment	ATP2B2	491	37	3	10401759	10401759	Missense_Mutation	SNP	C	T	17	38	c.1708G>A	c.(1708-1710)GAG>AAG	p.E570K
Pat_48	Pre-Treatment	COL6A6	131873	37	3	130300841	130300841	Missense_Mutation	SNP	T	G	2	4	c.3899T>G	c.(3898-3900)CTT>CGT	p.L1300R
Pat_48	Pre-Treatment	PPARGC1A	10891	37	4	23815404	23815404	Missense_Mutation	SNP	G	A	4	22	c.1702C>T	c.(1702-1704)CGT>TGT	p.R568C
Pat_48	Pre-Treatment	DMXL1	1657	37	5	118482588	118482588	Nonsense_Mutation	SNP	C	T	38	65	c.2626C>T	c.(2626-2628)CAA>TAA	p.Q876*
Pat_48	Pre-Treatment	PCDHA12	56137	37	5	140255890	140255890	Missense_Mutation	SNP	C	T	21	21	c.833C>T	c.(832-834)TCC>TTC	p.S278F
Pat_48	Pre-Treatment	ITK	3702	37	5	156635937	156635937	Missense_Mutation	SNP	G	A	16	32	c.176G>A	c.(175-177)CGA>CAA	p.R59Q
Pat_48	Pre-Treatment	OR2B2	81697	37	6	27879370	27879370	Missense_Mutation	SNP	G	A	27	33	c.728C>T	c.(727-729)TCC>TTC	p.S243F
Pat_48	Pre-Treatment	ITPR3	3710	37	6	33663553	33663553	Missense_Mutation	SNP	G	A	3	37	c.8012G>A	c.(8011-8013)CGC>CAC	p.R2671H
Pat_48	Pre-Treatment	AKAP9	10142	37	7	91726492	91726492	Nonsense_Mutation	SNP	G	T	3	8	c.10219G>T	c.(10219-10221)GAG>TAG	p.E3407*
Pat_48	Pre-Treatment	BRAF	673	37	7	140453136	140453136	Missense_Mutation	SNP	A	T	70	69	c.1799T>A	c.(1798-1800)GTG>GAG	p.V600E
Pat_48	Pre-Treatment	CNPY1	285888	37	7	155301649	155301649	Missense_Mutation	SNP	T	C	8	16	c.84A>G	c.(82-84)ATA>ATG	p.I28M
Pat_48	Pre-Treatment	EBF2	64641	37	8	25718726	25718726	Missense_Mutation	SNP	C	T	12	44	c.1181G>A	c.(1180-1182)CGA>CAA	p.R394Q
Pat_48	Pre-Treatment	ST18	9705	37	8	53084412	53084412	Missense_Mutation	SNP	C	T	21	166	c.1009G>A	c.(1009-1011)GGG>AGG	p.G337R
Pat_48	Pre-Treatment	COL14A1	7373	37	8	121295981	121295981	Missense_Mutation	SNP	A	G	9	36	c.3931A>G	c.(3931-3933)AAA>GAA	p.K1311E
Pat_48	Pre-Treatment	SVEP1	79987	37	9	113169542	113169542	Missense_Mutation	SNP	G	A	30	19	c.8338C>T	c.(8338-8340)CCA>TCA	p.P2780S
Pat_48	Pre-Treatment	MXRA5	25878	37	X	3228326	3228326	Missense_Mutation	SNP	T	C	15	4	c.7918A>G	c.(7918-7920)AAC>GAC	p.N2640D
Pat_48	Post-Resistance	GIPC2	54810	37	1	78585136	78585136	Missense_Mutation	SNP	G	A	3	43	c.667G>A	c.(667-669)GCA>ACA	p.A223T
Pat_48	Post-Resistance	CLCA2	9635	37	1	86890069	86890069	Missense_Mutation	SNP	A	G	10	36	c.139A>G	c.(139-141)ATT>GTT	p.I47V
Pat_48	Post-Resistance	HORMAD1	84072	37	1	150680884	150680884	Splice_Site	SNP	C	T	13	22	c.396_splice	c.e9-1	p.S132_splice
Pat_48	Post-Resistance	DUSP27	92235	37	1	167097709	167097709	Missense_Mutation	SNP	C	T	9	16	c.3341C>T	c.(3340-3342)TCT>TTT	p.S1114F
Pat_48	Post-Resistance	CACNA1E	777	37	1	181549815	181549815	Missense_Mutation	SNP	C	T	53	136	c.854C>T	c.(853-855)CCC>CTC	p.P285L
Pat_48	Post-Resistance	OR14A16	284532	37	1	247978163	247978163	Missense_Mutation	SNP	C	T	12	55	c.869G>A	c.(868-870)AGA>AAA	p.R290K
Pat_48	Post-Resistance	OR14A16	284532	37	1	247978557	247978557	Missense_Mutation	SNP	C	T	30	100	c.475G>A	c.(475-477)GCT>ACT	p.A159T
Pat_48	Post-Resistance	ZNF239	8187	37	10	44052942	44052942	Missense_Mutation	SNP	G	A	24	39	c.586C>T	c.(586-588)CCA>TCA	p.P196S
Pat_48	Post-Resistance	C10orf72	196740	37	10	50285269	50285269	Missense_Mutation	SNP	G	A	14	23	c.629C>T	c.(628-630)TCC>TTC	p.S210F
Pat_48	Post-Resistance	BUB3	9184	37	10	124914464	124914464	Nonsense_Mutation	SNP	C	T	3	91	c.31C>T	c.(31-33)CAG>TAG	p.Q11*
Pat_48	Post-Resistance	OR52J3	119679	37	11	5068593	5068593	Missense_Mutation	SNP	C	T	19	82	c.838C>T	c.(838-840)CTC>TTC	p.L280F
Pat_48	Post-Resistance	IGSF22	283284	37	11	18741637	18741637	Missense_Mutation	SNP	C	T	18	57	c.492G>A	c.(490-492)ATG>ATA	p.M164I

Pat_48	Post-Resistance	OR4C46	119749	37	11	51515587	51515587	Missense_Mutation	SNP	A	T	11	72	c.306A>T	c.(304-306)GAA>GAT	p.E102D
Pat_48	Post-Resistance	OR10W1	81341	37	11	58034652	58034652	Missense_Mutation	SNP	G	A	13	71	c.679C>T	c.(679-681)CGG>TGG	p.R227W
Pat_48	Post-Resistance	CLEC9A	283420	37	12	10215746	10215746	Nonsense_Mutation	SNP	C	T	27	134	c.412C>T	c.(412-414)CAA>TAA	p.Q138*
Pat_48	Post-Resistance	TPCN1	53373	37	12	113729700	113729700	Missense_Mutation	SNP	G	A	3	61	c.2050G>A	c.(2050-2052)GCC>ACC	p.A684T
Pat_48	Post-Resistance	CIT	11113	37	12	120128123	120128123	Missense_Mutation	SNP	C	T	5	8	c.5893G>A	c.(5893-5895)GAG>AAG	p.E1965K
Pat_48	Post-Resistance	KNTC1	9735	37	12	123071263	123071263	Missense_Mutation	SNP	C	T	4	31	c.3689C>T	c.(3688-3690)CCC>CTC	p.P1230L
Pat_48	Post-Resistance	OR4K1	79544	37	14	20404061	20404061	Missense_Mutation	SNP	C	T	49	38	c.236C>T	c.(235-237)CCC>CTC	p.P79L
Pat_48	Post-Resistance	ADAM20	8748	37	14	70991270	70991270	Missense_Mutation	SNP	C	T	3	61	c.355G>A	c.(355-357)GGA>AGA	p.G119R
Pat_48	Post-Resistance	PKD1	5310	37	16	2154550	2154550	Missense_Mutation	SNP	C	T	3	6	c.8110G>A	c.(8110-8112)GCG>ACG	p.A2704T
Pat_48	Post-Resistance	GRIN2A	2903	37	16	9857895	9857895	Missense_Mutation	SNP	C	T	23	71	c.3506G>A	c.(3505-3507)CGG>CAG	p.R1169Q
Pat_48	Post-Resistance	DNAH2	146754	37	17	7697572	7697572	Missense_Mutation	SNP	G	A	7	32	c.7570G>A	c.(7570-7572)GAA>AAA	p.E2524K
Pat_48	Post-Resistance	EVPLL	645027	37	17	18286166	18286166	Missense_Mutation	SNP	C	T	7	13	c.499C>T	c.(499-501)CCG>TCG	p.P167S
Pat_48	Post-Resistance	SGCA	6442	37	17	48245758	48245758	Missense_Mutation	SNP	G	A	5	5	c.409G>A	c.(409-411)GAG>AAG	p.E137K
Pat_48	Post-Resistance	ZNF563	147837	37	19	12430274	12430274	Missense_Mutation	SNP	C	G	39	112	c.565G>C	c.(565-567)GTA>CTA	p.V189L
Pat_48	Post-Resistance	ZNF534	147658	37	19	52942028	52942028	Missense_Mutation	SNP	G	A	15	21	c.1354G>A	c.(1354-1356)GAA>AAA	p.E452K
Pat_48	Post-Resistance	LILRA3	11026	37	19	54803582	54803582	Missense_Mutation	SNP	C	T	17	27	c.242G>A	c.(241-243)GGC>GAC	p.G81D
Pat_48	Post-Resistance	SNTG2	54221	37	2	1094046	1094046	Missense_Mutation	SNP	C	T	42	23	c.275C>T	c.(274-276)TCT>TTT	p.S92F
Pat_48	Post-Resistance	TTN	7273	37	2	179472587	179472587	Missense_Mutation	SNP	G	A	161	58	c.45223C>T	c.(45223-45225)CGG>TGG	p.R15075W
Pat_48	Post-Resistance	CSNK2A1	1457	37	20	470440	470440	Missense_Mutation	SNP	T	C	3	83	c.707A>G	c.(706-708)CAT>CGT	p.H236R
Pat_48	Post-Resistance	FRG1B	284802	37	20	29625875	29625875	Missense_Mutation	SNP	T	C	4	50	c.29T>C	c.(28-30)ATC>ACC	p.I10T
Pat_48	Post-Resistance	CDH26	60437	37	20	58559801	58559801	Missense_Mutation	SNP	G	A	52	75	c.649G>A	c.(649-651)GGT>AGT	p.G217S
Pat_48	Post-Resistance	KRTAP12-3	386683	37	21	46078147	46078147	Missense_Mutation	SNP	T	C	5	40	c.251T>C	c.(250-252)CTC>CCC	p.L84P
Pat_48	Post-Resistance	ATP2B2	491	37	3	10401759	10401759	Missense_Mutation	SNP	C	T	18	41	c.1708G>A	c.(1708-1710)GAG>AAG	p.E570K
Pat_48	Post-Resistance	GHSR	2693	37	3	172165537	172165538	Missense_Mutation	DNP	GG	AA	7	19	c.666_667CC>TT	(664-669)TTCCTT>TTTTT	p.L223F
Pat_48	Post-Resistance	PIK3CA	5290	37	3	178952085	178952085	Missense_Mutation	SNP	A	G	23	96	c.3140A>G	c.(3139-3141)CAT>CGT	p.H1047R
Pat_48	Post-Resistance	ABCC5	10057	37	3	183679443	183679443	Splice_Site	SNP	C	T	24	85	c.2236_splice	c.e16-1	p.Y746_splice
Pat_48	Post-Resistance	PPARGC1A	10891	37	4	23815404	23815404	Missense_Mutation	SNP	G	A	13	49	c.1702C>T	c.(1702-1704)CGT>TGT	p.R568C
Pat_48	Post-Resistance	FSTL5	56884	37	4	162421220	162421220	Missense_Mutation	SNP	T	A	4	33	c.1406A>T	c.(1405-1407)GAA>GTA	p.E469V
Pat_48	Post-Resistance	PRDM9	56979	37	5	23527251	23527251	Missense_Mutation	SNP	C	T	5	140	c.2054C>T	c.(2053-2055)ACA>ATA	p.T685I
Pat_48	Post-Resistance	DMXL1	1657	37	5	118482588	118482588	Nonsense_Mutation	SNP	C	T	27	65	c.2626C>T	c.(2626-2628)CAA>TAA	p.Q876*
Pat_48	Post-Resistance	PCDHA12	56137	37	5	140255890	140255890	Missense_Mutation	SNP	C	T	29	90	c.833C>T	c.(832-834)TCC>TTC	p.S278F
Pat_48	Post-Resistance	ITK	3702	37	5	156635937	156635937	Missense_Mutation	SNP	G	A	17	59	c.176G>A	c.(175-177)CGA>CAA	p.R59Q
Pat_48	Post-Resistance	OR2B2	81697	37	6	27879370	27879370	Missense_Mutation	SNP	G	A	34	52	c.728C>T	c.(727-729)TCC>TTC	p.S243F
Pat_48	Post-Resistance	OR2W1	26692	37	6	29012935	29012935	Nonsense_Mutation	SNP	A	C	11	52	c.18T>G	c.(16-18)TAT>TAG	p.Y6*
Pat_48	Post-Resistance	SYNGAP1	8831	37	6	33400584	33400584	Splice_Site	SNP	G	A	3	71	c.509_splice	c.e5+1	p.R170_splice
Pat_48	Post-Resistance	AKAP9	10142	37	7	91726492	91726492	Nonsense_Mutation	SNP	G	T	9	16	c.10219G>T	c.(10219-10221)GAG>TAG	p.E3407*
Pat_48	Post-Resistance	BRAF	673	37	7	140453136	140453136	Missense_Mutation	SNP	A	T	56	94	c.1799T>A	c.(1798-1800)GTG>GAG	p.V600E
Pat_48	Post-Resistance	SSBP1	6742	37	7	141445300	141445300	Nonsense_Mutation	SNP	C	T	15	125	c.319C>T	c.(319-321)CGA>TGA	p.R107*
Pat_48	Post-Resistance	CNPY1	285888	37	7	155301649	155301649	Missense_Mutation	SNP	T	C	33	34	c.84A>G	c.(82-84)ATA>ATG	p.I28M
Pat_48	Post-Resistance	EBF2	64641	37	8	25718726	25718726	Missense_Mutation	SNP	C	T	26	63	c.1181G>A	c.(1180-1182)CGA>CAA	p.R394Q
Pat_48	Post-Resistance	GSR	2936	37	8	30539534	30539534	Missense_Mutation	SNP	A	G	26	142	c.1198T>C	c.(1198-1200)TAT>CAT	p.Y400H
Pat_48	Post-Resistance	ST18	9705	37	8	53084412	53084412	Missense_Mutation	SNP	C	T	34	362	c.1009G>A	c.(1009-1011)GGG>AGG	p.G337R
Pat_48	Post-Resistance	COL14A1	7373	37	8	121295981	121295981	Missense_Mutation	SNP	A	G	43	99	c.3931A>G	c.(3931-3933)AAA>GAA	p.K1311E
Pat_48	Post-Resistance	C8orf73	642475	37	8	144650052	144650052	Nonsense_Mutation	SNP	G	A	7	48	c.1771C>T	c.(1771-1773)CGA>TGA	p.R591*
Pat_48	Post-Resistance	SVEP1	79987	37	9	113169542	113169542	Missense_Mutation	SNP	G	A	58	38	c.8338C>T	c.(8338-8340)CCA>TCA	p.P2780S
Pat_48	Post-Resistance	TRUB2	26995	37	9	131083986	131083986	Missense_Mutation	SNP	C	T	3	6	c.133G>A	c.(133-135)GCT>ACT	p.A45T
Pat_48	Post-Resistance	MXRA5	25878	37	X	3228326	3228326	Missense_Mutation	SNP	T	C	10	10	c.7918A>G	c.(7918-7920)AAC>GAC	p.N2640D

Pat_48	Post-Resistance	FAM120C	54954	37	X	54209061	54209061	Missense_Mutation	SNP	G	A	2	6	c.571C>T	c.(571-573)CGG>TGG	p.R191W
Pat_49	Post-Resistance	COL16A1	1307	37	1	32148563	32148563	Missense_Mutation	SNP	G	A	3	46	c.2510C>T	c.(2509-2511)CCT>CTT	p.P837L
Pat_49	Post-Resistance	AK3L1	205	37	1	65656511	65656511	Missense_Mutation	SNP	T	A	6	16	c.264T>A	c.(262-264)GAT>GAA	p.D88E
Pat_49	Post-Resistance	IL12RB2	3595	37	1	67861606	67861606	Missense_Mutation	SNP	T	C	19	65	c.2423T>C	c.(2422-2424)CTC>CCC	p.L808P
Pat_49	Post-Resistance	AGL	178	37	1	100327118	100327118	Missense_Mutation	SNP	A	G	6	12	c.142A>G	c.(142-144)ACA>GCA	p.T48A
Pat_49	Post-Resistance	ANP32E	81611	37	1	150198989	150198989	Missense_Mutation	SNP	T	A	4	17	c.632A>T	c.(631-633)GAG>GTG	p.E211V
Pat_49	Post-Resistance	GBA	2629	37	1	155209424	155209424	Missense_Mutation	SNP	G	A	6	11	c.437C>T	c.(436-438)TCG>TTG	p.S146L
Pat_49	Post-Resistance	TPR	7175	37	1	186292909	186292909	Missense_Mutation	SNP	C	T	9	25	c.6206G>A	c.(6205-6207)CGA>CAA	p.R2069Q
Pat_49	Post-Resistance	FAM5C	339479	37	1	190423812	190423812	Missense_Mutation	SNP	C	T	6	9	c.209G>A	c.(208-210)GGA>GAA	p.G70E
Pat_49	Post-Resistance	CRB1	23418	37	1	197390934	197390934	Missense_Mutation	SNP	C	T	13	21	c.1976C>T	c.(1975-1977)TCG>TTG	p.S659L
Pat_49	Post-Resistance	PRKCQ	5588	37	10	6483994	6483994	Missense_Mutation	SNP	C	T	8	18	c.1697G>A	c.(1696-1698)GGG>GAG	p.G566E
Pat_49	Post-Resistance	UPF2	26019	37	10	12021112	12021112	Missense_Mutation	SNP	T	A	15	14	c.1897A>T	c.(1897-1899)ATG>TTG	p.M633L
Pat_49	Post-Resistance	ADAMTS14	140766	37	10	72513618	72513618	Missense_Mutation	SNP	G	A	3	6	c.2792G>A	c.(2791-2793)CGG>CAG	p.R931Q
Pat_49	Post-Resistance	ITPRIP	85450	37	10	106074705	106074705	Missense_Mutation	SNP	G	A	25	12	c.1105C>T	c.(1105-1107)CCC>TCC	p.P369S
Pat_49	Post-Resistance	BET1L	51272	37	11	205975	205975	Missense_Mutation	SNP	A	G	19	57	c.88T>C	c.(88-90)TCC>CCC	p.S30P
Pat_49	Post-Resistance	OR56A3	390083	37	11	5968605	5968605	Missense_Mutation	SNP	C	T	5	7	c.29C>T	c.(28-30)TCC>TTC	p.S10F
Pat_49	Post-Resistance	NAT10	55226	37	11	34163857	34163857	Missense_Mutation	SNP	G	T	6	19	c.2847G>T	c.(2845-2847)AAG>AAT	p.K949N
Pat_49	Post-Resistance	SLC1A2	6506	37	11	35308478	35308478	Missense_Mutation	SNP	G	A	29	58	c.1112C>T	c.(1111-1113)ACC>ATC	p.T371I
Pat_49	Post-Resistance	OR5D13	390142	37	11	55541256	55541256	Missense_Mutation	SNP	T	A	20	36	c.343T>A	c.(343-345)TTC>ATC	p.F115I
Pat_49	Post-Resistance	OR5AR1	219493	37	11	56431439	56431439	Missense_Mutation	SNP	C	T	22	50	c.278C>T	c.(277-279)TCC>TTC	p.S93F
Pat_49	Post-Resistance	TMEM132A	54972	37	11	60702238	60702238	Splice_Site	SNP	T	G	13	9	c.1836_splice	c.e9+2	p.E612_splice
Pat_49	Post-Resistance	AHNAK	79026	37	11	62294795	62294796	Missense_Mutation	DNP	GG	AT	25	57	.7093_7094CC>A	c.(7093-7095)CCA>ATA	p.P2365I
Pat_49	Post-Resistance	POLA2	23649	37	11	65047045	65047045	Missense_Mutation	SNP	T	C	8	47	c.692T>C	c.(691-693)CTC>CCC	p.L231P
Pat_49	Post-Resistance	FRMD8	83786	37	11	65161799	65161799	Missense_Mutation	SNP	C	T	3	5	c.484C>T	c.(484-486)CCG>TCG	p.P162S
Pat_49	Post-Resistance	KRTAP5-8	57830	37	11	71249558	71249558	Missense_Mutation	SNP	T	A	7	226	c.457T>A	c.(457-459)TGC>AGC	p.C153S
Pat_49	Post-Resistance	HEPHL1	341208	37	11	93834384	93834384	Missense_Mutation	SNP	G	A	11	30	c.2458G>A	c.(2458-2460)GGC>AGC	p.G820S
Pat_49	Post-Resistance	TTC12	54970	37	11	113196299	113196299	Missense_Mutation	SNP	A	G	2	21	c.376A>G	c.(376-378)ATC>GTC	p.I126V
Pat_49	Post-Resistance	OR8G2	26492	37	11	124096240	124096240	Missense_Mutation	SNP	G	A	3	9	c.843G>A	c.(841-843)ATG>ATA	p.M281I
Pat_49	Post-Resistance	SLC6A12	6539	37	12	305370	305370	Missense_Mutation	SNP	G	A	2	3	c.1246C>T	c.(1246-1248)CGG>TGG	p.R416W
Pat_49	Post-Resistance	B4GALNT3	283358	37	12	665952	665952	Missense_Mutation	SNP	C	T	4	6	c.2300C>T	c.(2299-2301)ACC>ATC	p.T767I
Pat_49	Post-Resistance	ITPR2	3709	37	12	26553126	26553126	Missense_Mutation	SNP	C	T	17	40	c.7465G>A	c.(7465-7467)GTG>ATG	p.V2489M
Pat_49	Post-Resistance	DIP2B	57609	37	12	51097957	51097957	Missense_Mutation	SNP	G	T	15	23	c.2360G>T	c.(2359-2361)GGG>GTG	p.G787V
Pat_49	Post-Resistance	NAV3	89795	37	12	78574780	78574780	Missense_Mutation	SNP	G	A	17	14	c.5647G>A	c.(5647-5649)GGA>AGA	p.G1883R
Pat_49	Post-Resistance	C12orf63	374467	37	12	97073462	97073462	Missense_Mutation	SNP	C	T	14	32	c.923C>T	c.(922-924)TCC>TTC	p.S308F
Pat_49	Post-Resistance	SLC17A8	246213	37	12	100813710	100813710	Missense_Mutation	SNP	C	T	3	8	c.1543C>T	c.(1543-1545)CTC>TTC	p.L515F
Pat_49	Post-Resistance	ALDH1L2	160428	37	12	105467639	105467639	Missense_Mutation	SNP	C	T	21	15	c.193G>A	c.(193-195)GCT>ACT	p.A65T
Pat_49	Post-Resistance	GTF2H3	2967	37	12	124118393	124118393	Translation_Start_Site	SNP	G	A	9	55	c.-13G>A	.(-15--11)AGGTG>AGATG	
Pat_49	Post-Resistance	EP400	57634	37	12	132516601	132516601	Missense_Mutation	SNP	T	C	11	49	c.5858T>C	c.(5857-5859)GTG>GCG	p.V1953A
Pat_49	Post-Resistance	LMO7	4008	37	13	76381683	76381683	Missense_Mutation	SNP	A	G	3	14	c.565A>G	c.(565-567)AAA>GAA	p.K189E
Pat_49	Post-Resistance	CDKL1	8814	37	14	50883181	50883181	Splice_Site	SNP	G	A	9	11	c.1_splice	c.e1-1	p.M1_splice
Pat_49	Post-Resistance	CLMN	79789	37	14	95663021	95663021	Missense_Mutation	SNP	G	A	10	20	c.2522C>T	c.(2521-2523)TCC>TTC	p.S841F
Pat_49	Post-Resistance	BCL11B	64919	37	14	99641426	99641426	Missense_Mutation	SNP	C	T	3	23	c.1747G>A	c.(1747-1749)GCG>ACG	p.A583T
Pat_49	Post-Resistance	GOLGA8G	283768	37	15	28769153	28769153	Missense_Mutation	SNP	T	C	3	19	c.701A>G	c.(700-702)GAG>GGG	p.E234G
Pat_49	Post-Resistance	TGM7	116179	37	15	43577124	43577124	Missense_Mutation	SNP	G	A	3	45	c.892C>T	c.(892-894)CGT>TGT	p.R298C
Pat_49	Post-Resistance	IQCH	64799	37	15	67713773	67713773	Missense_Mutation	SNP	C	T	8	14	c.2363C>T	c.(2362-2364)ACC>ATC	p.T788I
Pat_49	Post-Resistance	GOLGA6A	342096	37	15	74372995	74372995	Missense_Mutation	SNP	C	T	3	25	c.166G>A	c.(166-168)GAG>AAG	p.E56K
Pat_49	Post-Resistance	IREB2	3658	37	15	78755351	78755352	Missense_Mutation	DNP	AC	TT	14	54	c.194_195AC>TT	c.(193-195)AAC>ATT	p.N65I

Pat_49	Post-Resistance	RASGRF1	5923	37	15	79265755	79265755	Missense_Mutation	SNP	G	A	5	34	c.3550C>T	c.(3550-3552)CCA>TCA	p.P1184S
Pat_49	Post-Resistance	LRRK1	79705	37	15	101586260	101586260	Missense_Mutation	SNP	C	T	31	56	c.3038C>T	c.(3037-3039)ACC>ATC	p.T1013I
Pat_49	Post-Resistance	WFIKKN1	117166	37	16	683041	683041	Missense_Mutation	SNP	G	A	3	29	c.631G>A	c.(631-633)GGC>AGC	p.G211S
Pat_49	Post-Resistance	ZNF205	7755	37	16	3169496	3169496	Missense_Mutation	SNP	C	T	3	1	c.835C>T	c.(835-837)CCG>TCG	p.P279S
Pat_49	Post-Resistance	RSL1D1	26156	37	16	11941535	11941535	Missense_Mutation	SNP	G	A	5	38	c.374C>T	c.(373-375)ACC>ATC	p.T125I
Pat_49	Post-Resistance	XYLT1	64131	37	16	17202673	17202673	Missense_Mutation	SNP	C	T	4	24	c.2759G>A	c.(2758-2760)TGT>TAT	p.C920Y
Pat_49	Post-Resistance	DNAH3	55567	37	16	20986583	20986583	Missense_Mutation	SNP	A	C	7	52	c.8231T>G	c.(8230-8232)GTT>GGT	p.V2744G
Pat_49	Post-Resistance	HEATR3	55027	37	16	50102761	50102761	Missense_Mutation	SNP	G	C	10	49	c.382G>C	c.(382-384)GTT>CTT	p.V128L
Pat_49	Post-Resistance	SALL1	6299	37	16	51176030	51176030	Missense_Mutation	SNP	G	A	13	69	c.103C>T	c.(103-105)CGC>TGC	p.R35C
Pat_49	Post-Resistance	OGFOD1	55239	37	16	56504456	56504456	Missense_Mutation	SNP	G	C	14	13	c.1038G>C	c.(1036-1038)AAG>AAC	p.K346N
Pat_49	Post-Resistance	BBS2	583	37	16	56531693	56531693	Missense_Mutation	SNP	G	A	5	38	c.1759C>T	c.(1759-1761)CCT>TCT	p.P587S
Pat_49	Post-Resistance	CDYL2	124359	37	16	80646560	80646560	Missense_Mutation	SNP	G	A	15	25	c.1181C>T	c.(1180-1182)TCC>TTC	p.S394F
Pat_49	Post-Resistance	ANKRD11	29123	37	16	89352018	89352018	Missense_Mutation	SNP	G	A	10	27	c.932C>T	c.(931-933)TCC>TTC	p.S311F
Pat_49	Post-Resistance	C17orf97	400566	37	17	263584	263584	Missense_Mutation	SNP	C	T	3	35	c.980C>T	c.(979-981)ACT>ATT	p.T327I
Pat_49	Post-Resistance	P2RX1	5023	37	17	3819429	3819429	Missense_Mutation	SNP	C	T	11	60	c.91G>A	c.(91-93)GTT>ATT	p.V31I
Pat_49	Post-Resistance	TEKT3	64518	37	17	15234809	15234809	Missense_Mutation	SNP	T	G	5	17	c.94A>C	c.(94-96)AGC>CGC	p.S32R
Pat_49	Post-Resistance	LGALS9B	284194	37	17	20363690	20363690	Missense_Mutation	SNP	C	T	6	61	c.106G>A	c.(106-108)GCC>ACC	p.A36T
Pat_49	Post-Resistance	GHDC	84514	37	17	40342744	40342744	Missense_Mutation	SNP	C	T	7	24	c.1186G>A	c.(1186-1188)GAT>AAT	p.D396N
Pat_49	Post-Resistance	TBC1D3P2	440452	37	17	60349342	60349342	Missense_Mutation	SNP	C	T	6	165	c.206G>A	c.(205-207)CGG>CAG	p.R69Q
Pat_49	Post-Resistance	SOCS3	9021	37	17	76354699	76354699	Missense_Mutation	SNP	G	A	10	15	c.478C>T	c.(478-480)CCC>TCC	p.P160S
Pat_49	Post-Resistance	AFG3L2	10939	37	18	12351210	12351210	Splice_Site	SNP	C	A	5	19	c.1427_splice	c.e12-1	p.G476_splice
Pat_49	Post-Resistance	INO80C	125476	37	18	33048651	33048651	Missense_Mutation	SNP	G	A	25	37	c.503C>T	c.(502-504)TCC>TTC	p.S168F
Pat_49	Post-Resistance	DCC	1630	37	18	50918073	50918073	Missense_Mutation	SNP	C	A	11	30	c.2504C>A	c.(2503-2505)ACC>AAC	p.T835N
Pat_49	Post-Resistance	TNFRSF11A	8792	37	18	60036217	60036217	Missense_Mutation	SNP	C	T	3	24	c.1067C>T	c.(1066-1068)CCC>CTC	p.P356L
Pat_49	Post-Resistance	CSNK1G2	1455	37	19	1969835	1969835	Missense_Mutation	SNP	G	A	7	3	c.64G>A	c.(64-66)GGC>AGC	p.G22S
Pat_49	Post-Resistance	DPP9	91039	37	19	4702054	4702054	Missense_Mutation	SNP	G	A	17	59	c.997C>T	c.(997-999)CGG>TGG	p.R333W
Pat_49	Post-Resistance	OR7D4	125958	37	19	9325267	9325267	Missense_Mutation	SNP	C	T	12	25	c.247G>A	c.(247-249)GTG>ATG	p.V83M
Pat_49	Post-Resistance	ILVBL	10994	37	19	15233968	15233968	Missense_Mutation	SNP	G	A	20	32	c.424C>T	c.(424-426)CCA>TCA	p.P142S
Pat_49	Post-Resistance	ZNF99	7652	37	19	22939999	22939999	Missense_Mutation	SNP	C	T	7	13	c.2332G>A	c.(2332-2334)GAA>AAA	p.E778K
Pat_49	Post-Resistance	KCNK6	9424	37	19	38817514	38817514	Missense_Mutation	SNP	T	G	15	49	c.604T>G	c.(604-606)TTG>GTG	p.L202V
Pat_49	Post-Resistance	FCGBP	8857	37	19	40408560	40408560	Missense_Mutation	SNP	G	A	4	15	c.4279C>T	c.(4279-4281)CCC>TCC	p.P1427S
Pat_49	Post-Resistance	PSG8	440533	37	19	43262152	43262152	Splice_Site	SNP	A	C	24	104	c.709_splice	c.e3+1	p.P237_splice
Pat_49	Post-Resistance	IRGC	56269	37	19	44222774	44222774	Missense_Mutation	SNP	G	A	25	34	c.64G>A	c.(64-66)GAA>AAA	p.E22K
Pat_49	Post-Resistance	PNKP	11284	37	19	50368527	50368527	Missense_Mutation	SNP	G	A	15	27	c.355C>T	c.(355-357)CCG>TCG	p.P119S
Pat_49	Post-Resistance	KIR3DL2	3812	37	19	55363717	55363717	Missense_Mutation	SNP	C	T	16	40	c.335C>T	c.(334-336)CCC>CTC	p.P112L
Pat_49	Post-Resistance	NLRP13	126204	37	19	56419257	56419257	Missense_Mutation	SNP	T	C	26	43	c.2348A>G	c.(2347-2349)AAG>AGG	p.K783R
Pat_49	Post-Resistance	C2orf42	54980	37	2	70392719	70392719	Missense_Mutation	SNP	G	A	4	16	c.1193C>T	c.(1192-1194)GCC>GTC	p.A398V
Pat_49	Post-Resistance	ERCC3	2071	37	2	128018874	128018874	Missense_Mutation	SNP	T	A	6	19	c.1994A>T	c.(1993-1995)CAG>CTG	p.Q665L
Pat_49	Post-Resistance	LRP1B	53353	37	2	141609275	141609275	Missense_Mutation	SNP	C	T	6	34	c.4657G>A	c.(4657-4659)GCC>ACC	p.A1553T
Pat_49	Post-Resistance	CYTIP	9595	37	2	158272395	158272395	Missense_Mutation	SNP	C	T	8	31	c.874G>A	c.(874-876)GAT>AAT	p.D292N
Pat_49	Post-Resistance	ACVR1	90	37	2	158636932	158636932	Missense_Mutation	SNP	G	T	6	16	c.248C>A	c.(247-249)ACC>AAC	p.T83N
Pat_49	Post-Resistance	TTN	7273	37	2	179459164	179459164	Missense_Mutation	SNP	C	T	4	23	c.50353G>A	c.(50353-50355)GAT>AAT	p.D16785N
Pat_49	Post-Resistance	AOX1	316	37	2	201507424	201507424	Missense_Mutation	SNP	C	T	4	14	c.2747C>T	c.(2746-2748)TCC>TTC	p.S916F
Pat_49	Post-Resistance	COL6A3	1293	37	2	238283655	238283655	Missense_Mutation	SNP	C	T	5	24	c.3079G>A	c.(3079-3081)GAA>AAA	p.E1027K
Pat_49	Post-Resistance	C20orf26	26074	37	20	20208996	20208996	Missense_Mutation	SNP	C	T	29	65	c.2036C>T	c.(2035-2037)TCC>TTC	p.S679F
Pat_49	Post-Resistance	MYH7B	57644	37	20	33570285	33570285	Missense_Mutation	SNP	C	T	12	61	c.677C>T	c.(676-678)ACG>ATG	p.T226M
Pat_49	Post-Resistance	GNAS	2778	37	20	57415537	57415537	Missense_Mutation	SNP	G	A	34	144	c.376G>A	c.(376-378)GAG>AAG	p.E126K

Pat_49	Post-Resistance	SLCO4A1	28231	37	20	61290067	61290067	Missense_Mutation	SNP	G	A	15	20	c.835G>A	c.(835-837)GGC>AGC	p.G279S
Pat_49	Post-Resistance	ZBTB46	140685	37	20	62421827	62421827	Missense_Mutation	SNP	A	G	8	36	c.284T>C	c.(283-285)CTG>CCG	p.L95P
Pat_49	Post-Resistance	ETS2	2114	37	21	40191544	40191544	Missense_Mutation	SNP	C	T	8	13	c.929C>T	c.(928-930)TCC>TTC	p.S310F
Pat_49	Post-Resistance	KRTAP10-11	386678	37	21	46066427	46066427	Missense_Mutation	SNP	C	A	20	81	c.52C>A	c.(52-54)CAG>AAG	p.Q18K
Pat_49	Post-Resistance	NEFH	4744	37	22	29885781	29885781	Missense_Mutation	SNP	T	A	4	81	c.2152T>A	c.(2152-2154)TCC>ACC	p.S718T
Pat_49	Post-Resistance	NEFH	4744	37	22	29885998	29885998	Missense_Mutation	SNP	A	T	5	23	c.2369A>T	c.(2368-2370)AAG>ATG	p.K790M
Pat_49	Post-Resistance	TMEM184B	25829	37	22	38622865	38622865	Missense_Mutation	SNP	A	G	2	8	c.538T>C	c.(538-540)TTC>CTC	p.F180L
Pat_49	Post-Resistance	PNPLA3	80339	37	22	44328953	44328953	Missense_Mutation	SNP	C	T	24	50	c.682C>T	c.(682-684)CCC>TCC	p.P228S
Pat_49	Post-Resistance	CPT1B	1375	37	22	51009598	51009598	Missense_Mutation	SNP	C	A	17	41	c.1864G>T	c.(1864-1866)GGG>TGG	p.G622W
Pat_49	Post-Resistance	XIRP1	165904	37	3	39228610	39228610	Missense_Mutation	SNP	C	T	3	13	c.2327G>A	c.(2326-2328)CGG>CAG	p.R776Q
Pat_49	Post-Resistance	COL7A1	1294	37	3	48604437	48604437	Missense_Mutation	SNP	C	T	5	4	c.8129G>A	c.(8128-8130)GGC>GAC	p.G2710D
Pat_49	Post-Resistance	FAM3D	131177	37	3	58631315	58631315	Missense_Mutation	SNP	G	A	3	29	c.184C>T	c.(184-186)CCA>TCA	p.P62S
Pat_49	Post-Resistance	FAM86D	692099	37	3	75475622	75475622	Nonsense_Mutation	SNP	G	A	14	65	c.616C>T	c.(616-618)CAG>TAG	p.Q206*
Pat_49	Post-Resistance	OR5AC2	81050	37	3	97806176	97806176	Missense_Mutation	SNP	G	A	13	27	c.160G>A	c.(160-162)GAC>AAC	p.D54N
Pat_49	Post-Resistance	OR5H6	79295	37	3	97983342	97983342	Missense_Mutation	SNP	C	T	18	40	c.214C>T	c.(214-216)CAT>TAT	p.H72Y
Pat_49	Post-Resistance	POLQ	10721	37	3	121206296	121206296	Missense_Mutation	SNP	T	C	20	40	c.5482A>G	c.(5482-5484)ATT>GTT	p.I1828V
Pat_49	Post-Resistance	MYLK	4638	37	3	123452908	123452908	Missense_Mutation	SNP	C	T	3	12	c.935G>A	c.(934-936)AGC>AAC	p.S312N
Pat_49	Post-Resistance	PODXL2	50512	37	3	127379452	127379452	Missense_Mutation	SNP	G	A	9	30	c.581G>A	c.(580-582)GGA>GAA	p.G194E
Pat_49	Post-Resistance	ZNF721	170960	37	4	436628	436628	Missense_Mutation	SNP	A	T	5	53	c.1628T>A	c.(1627-1629)ATC>AAC	p.I543N
Pat_49	Post-Resistance	ZNF721	170960	37	4	436647	436647	Missense_Mutation	SNP	C	T	4	48	c.1609G>A	c.(1609-1611)GCC>ACC	p.A537T
Pat_49	Post-Resistance	OTOP1	133060	37	4	4190678	4190678	Missense_Mutation	SNP	C	T	8	39	c.1691G>A	c.(1690-1692)GGC>GAC	p.G564D
Pat_49	Post-Resistance	GABRG1	2565	37	4	46099335	46099335	Missense_Mutation	SNP	C	T	4	28	c.136G>A	c.(136-138)GAT>AAT	p.D46N
Pat_49	Post-Resistance	ADH1A	124	37	4	100201357	100201357	Missense_Mutation	SNP	G	A	16	49	c.908C>T	c.(907-909)TCA>TTA	p.S303L
Pat_49	Post-Resistance	MAP9	79884	37	4	156268946	156268946	Missense_Mutation	SNP	T	C	3	15	c.1933A>G	c.(1933-1935)AAA>GAA	p.K645E
Pat_49	Post-Resistance	SLC12A7	10723	37	5	1083982	1083982	Missense_Mutation	SNP	G	A	15	45	c.1007C>T	c.(1006-1008)TCC>TTC	p.S336F
Pat_49	Post-Resistance	CDH18	1016	37	5	19473613	19473613	Missense_Mutation	SNP	G	A	3	11	c.2095C>T	c.(2095-2097)CCC>TCC	p.P699S
Pat_49	Post-Resistance	CDH6	1004	37	5	31305531	31305531	Missense_Mutation	SNP	T	C	7	42	c.1250T>C	c.(1249-1251)GTC>GCC	p.V417A
Pat_49	Post-Resistance	C5orf42	65250	37	5	37108562	37108562	Missense_Mutation	SNP	G	A	10	26	c.9250C>T	c.(9250-9252)CCG>TCG	p.P3084S
Pat_49	Post-Resistance	PPAP2A	8611	37	5	54771240	54771240	Missense_Mutation	SNP	G	A	4	11	c.97C>T	c.(97-99)CCC>TCC	p.P33S
Pat_49	Post-Resistance	GPR98	84059	37	5	90124894	90124894	Missense_Mutation	SNP	C	T	28	51	c.16502C>T	c.(16501-16503)TCT>TTT	p.S5501F
Pat_49	Post-Resistance	ELL2	22936	37	5	95224676	95224676	Missense_Mutation	SNP	G	A	2	2	c.1822C>T	c.(1822-1824)CAT>TAT	p.H608Y
Pat_49	Post-Resistance	RIOK2	55781	37	5	96508946	96508946	Missense_Mutation	SNP	G	A	7	24	c.520C>T	c.(520-522)CCA>TCA	p.P174S
Pat_49	Post-Resistance	MCC	4163	37	5	112379327	112379327	Missense_Mutation	SNP	C	T	11	33	c.2086G>A	c.(2086-2088)GAG>AAG	p.E696K
Pat_49	Post-Resistance	CHSY3	337876	37	5	129520444	129520444	Missense_Mutation	SNP	T	C	7	16	c.1609T>C	c.(1609-1611)TAC>CAC	p.Y537H
Pat_49	Post-Resistance	RPP40	10799	37	6	4995482	4995482	Missense_Mutation	SNP	G	A	20	10	c.922C>T	c.(922-924)CCA>TCA	p.P308S
Pat_49	Post-Resistance	ETV7	51513	37	6	36339107	36339107	Missense_Mutation	SNP	C	T	8	3	c.664G>A	c.(664-666)GAC>AAC	p.D222N
Pat_49	Post-Resistance	UBR2	23304	37	6	42633184	42633184	Missense_Mutation	SNP	T	C	178	441	c.3736T>C	c.(3736-3738)TGG>CGG	p.W1246R
Pat_49	Post-Resistance	UBR2	23304	37	6	42633226	42633226	Missense_Mutation	SNP	C	A	94	248	c.3778C>A	c.(3778-3780)CTT>ATT	p.L1260I
Pat_49	Post-Resistance	MAP3K4	4216	37	6	161469799	161469799	Missense_Mutation	SNP	C	G	4	14	c.495C>G	c.(493-495)TTC>TTG	p.F165L
Pat_49	Post-Resistance	KIF25	3834	37	6	168430272	168430272	Missense_Mutation	SNP	T	A	3	40	c.7T>A	c.(7-9)TGG>AGG	p.W3R
Pat_49	Post-Resistance	SDK1	221935	37	7	4091391	4091391	Missense_Mutation	SNP	C	T	15	57	c.2840C>T	c.(2839-2841)TCC>TTC	p.S947F
Pat_49	Post-Resistance	MYO1G	64005	37	7	45005268	45005269	Missense_Mutation	DNP	GG	AA	5	35	.2348_2349CC>T	c.(2347-2349)CCC>CTT	p.P783L
Pat_49	Post-Resistance	ZNF479	90827	37	7	57187809	57187809	Missense_Mutation	SNP	T	G	4	24	c.1313A>C	c.(1312-1314)AAA>ACA	p.K438T
Pat_49	Post-Resistance	AUTS2	26053	37	7	70229874	70229874	Missense_Mutation	SNP	C	T	3	39	c.1351C>T	c.(1351-1353)CCC>TCC	p.P451S
Pat_49	Post-Resistance	KIAA1324L	222223	37	7	86521053	86521053	Missense_Mutation	SNP	G	A	15	25	c.3017C>T	c.(3016-3018)TCT>TTT	p.S1006F
Pat_49	Post-Resistance	KCND2	3751	37	7	119915065	119915065	Missense_Mutation	SNP	G	A	13	94	c.379G>A	c.(379-381)GAA>AAA	p.E127K
Pat_49	Post-Resistance	BRAF	673	37	7	140453136	140453136	Missense_Mutation	SNP	A	T	27	23	c.1799T>A	c.(1798-1800)GTG>GAG	p.V600E

Pat_49	Post-Resistance	OR9A4	130075	37	7	141619283	141619283	Missense_Mutation	SNP	C	T	18	15	c.608C>T	c.(607-609)GCT>GTT	p.A203V
Pat_49	Post-Resistance	MGAM	8972	37	7	141750570	141750570	Missense_Mutation	SNP	T	A	7	7	c.2711T>A	c.(2710-2712)ATT>AAT	p.I904N
Pat_49	Post-Resistance	TRY6	154754	37	7	142481775	142481775	Splice_Site	SNP	G	A	50	8	c.455_splice	c.e4-1	p.A152_splice
Pat_49	Post-Resistance	ZNF786	136051	37	7	148769113	148769114	Missense_Mutation	DNP	GG	AA	7	6	c.750_751CC>TT	748-753)CGCCGG>CGTT	p.R251W
Pat_49	Post-Resistance	ZFPM2	23414	37	8	106813457	106813457	Missense_Mutation	SNP	G	A	64	30	c.1147G>A	c.(1147-1149)GAG>AAG	p.E383K
Pat_49	Post-Resistance	DENND3	22898	37	8	142200513	142200513	Missense_Mutation	SNP	T	C	8	40	c.3136T>C	c.(3136-3138)TGC>CGC	p.C1046R
Pat_49	Post-Resistance	PTPRD	5789	37	9	8341914	8341914	Missense_Mutation	SNP	C	T	6	5	c.4726G>A	c.(4726-4728)GAA>AAA	p.E1576K
Pat_49	Post-Resistance	TEK	7010	37	9	27212859	27212859	Missense_Mutation	SNP	C	G	9	6	c.2841C>G	c.(2839-2841)GAC>GAG	p.D947E
Pat_49	Post-Resistance	FAM22G	441457	37	9	99697727	99697727	Missense_Mutation	SNP	G	C	77	41	c.831G>C	c.(829-831)GAG>GAC	p.E277D
Pat_49	Post-Resistance	OFD1	8481	37	X	13771510	13771510	Missense_Mutation	SNP	A	G	4	35	c.1079A>G	c.(1078-1080)GAC>GGC	p.D360G
Pat_49	Post-Resistance	FAM48B1	100130302	37	X	24381778	24381778	Missense_Mutation	SNP	G	A	14	38	c.901G>A	c.(901-903)GCC>ACC	p.A301T
Pat_49	Post-Resistance	USP51	158880	37	X	55513698	55513698	Missense_Mutation	SNP	G	A	4	14	c.1675C>T	c.(1675-1677)CCA>TCA	p.P559S
Pat_49	Post-Resistance	FGF16	8823	37	X	76711891	76711891	Missense_Mutation	SNP	G	A	8	36	c.229G>A	c.(229-231)GAT>AAT	p.D77N
Pat_49	Post-Resistance	ARL13A	392509	37	X	100241834	100241834	Missense_Mutation	SNP	A	G	6	6	c.430A>G	c.(430-432)ATT>GTT	p.I144V
Pat_49	Post-Resistance	NXF5	55998	37	X	101096684	101096684	Missense_Mutation	SNP	C	T	47	85	c.202G>A	c.(202-204)GAT>AAT	p.D68N
Pat_49	Post-Resistance	GPRASP2	114928	37	X	101970977	101970977	Missense_Mutation	SNP	G	A	14	15	c.1180G>A	c.(1180-1182)GAA>AAA	p.E394K
Pat_49	Post-Resistance	H2BFM	286436	37	X	103294880	103294880	Missense_Mutation	SNP	A	G	3	14	c.337A>G	c.(337-339)ACC>GCC	p.T113A
Pat_49	Post-Resistance	NRK	203447	37	X	105167141	105167141	Missense_Mutation	SNP	C	T	24	49	c.2642C>T	c.(2641-2643)TCA>TTA	p.S881L
Pat_49	Post-Resistance	LHFPL1	340596	37	X	111914593	111914593	Missense_Mutation	SNP	C	T	46	129	c.26G>A	c.(25-27)GGA>GAA	p.G9E
Pat_49	Post-Resistance	ODZ1	10178	37	X	123654454	123654454	Missense_Mutation	SNP	G	A	34	47	c.3214C>T	c.(3214-3216)CCC>TCC	p.P1072S
Pat_49	Post-Resistance	BRS3	680	37	X	135570618	135570618	Missense_Mutation	SNP	C	A	12	81	c.345C>A	c.(343-345)TTC>TTA	p.F115L
Pat_49	Post-Resistance	MAGEC3	139081	37	X	140984949	140984949	Missense_Mutation	SNP	C	T	10	17	c.1405C>T	c.(1405-1407)CTC>TTC	p.L469F
Pat_49	Post-Resistance	GABRA3	2556	37	X	151514055	151514055	Missense_Mutation	SNP	C	T	15	43	c.260G>A	c.(259-261)GGA>GAA	p.G87E
Pat_50	Pre-Treatment	DVL1	1855	37	1	1277436	1277436	Missense_Mutation	SNP	C	T	3	6	c.463G>A	c.(463-465)GAG>AAG	p.E155K
Pat_50	Pre-Treatment	KIAA1751	85452	37	1	1890560	1890560	Missense_Mutation	SNP	G	A	33	53	c.1850C>T	c.(1849-1851)TCG>TTG	p.S617L
Pat_50	Pre-Treatment	NPHP4	261734	37	1	6012873	6012873	Missense_Mutation	SNP	G	A	3	7	c.697C>T	c.(697-699)CTC>TTC	p.L233F
Pat_50	Pre-Treatment	PRAMEF1	65121	37	1	12853499	12853499	Missense_Mutation	SNP	G	A	39	73	c.123G>A	c.(121-123)ATG>ATA	p.M41I
Pat_50	Pre-Treatment	KIAA1522	57648	37	1	33235549	33235549	Missense_Mutation	SNP	C	T	10	4	c.592C>T	c.(592-594)CCC>TCC	p.P198S
Pat_50	Pre-Treatment	LRRIQ3	127255	37	1	74507479	74507479	Missense_Mutation	SNP	G	A	24	50	c.1136C>T	c.(1135-1137)CCT>CTT	p.P379L
Pat_50	Pre-Treatment	COL24A1	255631	37	1	86523621	86523621	Missense_Mutation	SNP	C	T	29	36	c.1844G>A	c.(1843-1845)GGT>GAT	p.G615D
Pat_50	Pre-Treatment	SYT6	148281	37	1	114680470	114680470	Missense_Mutation	SNP	C	T	46	69	c.463G>A	c.(463-465)GAT>AAT	p.D155N
Pat_50	Pre-Treatment	NGF	4803	37	1	115829314	115829314	Missense_Mutation	SNP	C	A	27	42	c.103G>T	c.(103-105)GCC>TCC	p.A35S
Pat_50	Pre-Treatment	WDR3	10885	37	1	118499713	118499713	Missense_Mutation	SNP	G	T	38	74	c.2476G>T	c.(2476-2478)GTG>TTG	p.V826L
Pat_50	Pre-Treatment	OTUD7B	56957	37	1	149939374	149939374	Missense_Mutation	SNP	G	A	53	70	c.347C>T	c.(346-348)TCC>TTC	p.S116F
Pat_50	Pre-Treatment	GABPB2	126626	37	1	151090674	151090674	Missense_Mutation	SNP	G	A	32	51	c.1289G>A	c.(1288-1290)GGG>GAG	p.G430E
Pat_50	Pre-Treatment	S100A7A	338324	37	1	153391748	153391748	Missense_Mutation	SNP	G	A	72	41	c.269G>A	c.(268-270)AGC>AAC	p.S90N
Pat_50	Pre-Treatment	SLC39A1	27173	37	1	153933163	153933163	Missense_Mutation	SNP	A	C	33	144	c.386T>G	c.(385-387)ATC>AGC	p.I129S
Pat_50	Pre-Treatment	YY1AP1	55249	37	1	155629899	155629900	Missense_Mutation	DNP	GG	AA	11	80	.1939_1940CC>T	c.(1939-1941)CCC>TTC	p.P647F
Pat_50	Pre-Treatment	FCRL1	115350	37	1	157772325	157772325	Missense_Mutation	SNP	C	T	109	56	c.449G>A	c.(448-450)GGG>GAG	p.G150E
Pat_50	Pre-Treatment	CD1A	909	37	1	158225110	158225110	Missense_Mutation	SNP	C	T	118	40	c.295C>T	c.(295-297)CGT>TGT	p.R99C
Pat_50	Pre-Treatment	OR10K1	391109	37	1	158436249	158436249	Missense_Mutation	SNP	G	A	207	97	c.898G>A	c.(898-900)GCC>ACC	p.A300T
Pat_50	Pre-Treatment	SPTA1	6708	37	1	158607893	158607893	Missense_Mutation	SNP	C	T	33	112	c.5119G>A	c.(5119-5121)GAA>AAA	p.E1707K
Pat_50	Pre-Treatment	F11R	50848	37	1	160970564	160970564	Missense_Mutation	SNP	G	A	91	51	c.245C>T	c.(244-246)TCC>TTC	p.S82F
Pat_50	Pre-Treatment	ATF6	22926	37	1	161789463	161789463	Missense_Mutation	SNP	G	A	27	20	c.950G>A	c.(949-951)CGA>CAA	p.R317Q
Pat_50	Pre-Treatment	EDEM3	80267	37	1	184688682	184688682	Missense_Mutation	SNP	C	G	144	58	c.972G>C	c.(970-972)AGG>AGC	p.R324S
Pat_50	Pre-Treatment	PTPRC	5788	37	1	198685892	198685892	Missense_Mutation	SNP	C	T	21	46	c.1367C>T	c.(1366-1368)TCA>TTA	p.S456L
Pat_50	Pre-Treatment	NFASC	23114	37	1	204948583	204948583	Missense_Mutation	SNP	G	A	100	234	c.2072G>A	c.(2071-2073)CGG>CAG	p.R691Q

Pat_50	Pre-Treatment	USH2A	7399	37	1	216371732	216371732	Missense_Mutation	SNP	C	T	68	47	c.4006G>A	c.(4006-4008)GAG>AAG	p.E1336K
Pat_50	Pre-Treatment	FH	2271	37	1	241669350	241669350	Missense_Mutation	SNP	C	T	42	24	c.857G>A	c.(856-858)AGA>AAA	p.R286K
Pat_50	Pre-Treatment	OR2M3	127062	37	1	248367019	248367019	Missense_Mutation	SNP	C	T	141	690	c.650C>T	c.(649-651)TCC>TTC	p.S217F
Pat_50	Pre-Treatment	MYO3A	53904	37	10	26490216	26490216	Missense_Mutation	SNP	G	A	6	3	c.4568G>A	c.(4567-4569)CGA>CAA	p.R1523Q
Pat_50	Pre-Treatment	ARMC4	55130	37	10	28272855	28272855	Missense_Mutation	SNP	C	T	31	15	c.736G>A	c.(736-738)GAA>AAA	p.E246K
Pat_50	Pre-Treatment	PCDH15	65217	37	10	55566459	55566459	Missense_Mutation	SNP	C	T	95	57	c.4929G>A	c.(4927-4929)ATG>ATA	p.M1643I
Pat_50	Pre-Treatment	EGR2	1959	37	10	64573485	64573485	Missense_Mutation	SNP	C	T	5	3	c.913G>A	c.(913-915)GCC>ACC	p.A305T
Pat_50	Pre-Treatment	POLR3A	11128	37	10	79741292	79741292	Missense_Mutation	SNP	G	A	267	129	c.3785C>T	c.(3784-3786)GCC>GTC	p.A1262V
Pat_50	Pre-Treatment	COL17A1	1308	37	10	105792721	105792721	Missense_Mutation	SNP	C	T	4	3	c.4300G>A	c.(4300-4302)GGA>AGA	p.G1434R
Pat_50	Pre-Treatment	SORCS3	22986	37	10	107005328	107005328	Missense_Mutation	SNP	C	T	71	42	c.2897C>T	c.(2896-2898)TCC>TTC	p.S966F
Pat_50	Pre-Treatment	DCLRE1A	9937	37	10	115596901	115596901	Missense_Mutation	SNP	G	A	85	38	c.2882C>T	c.(2881-2883)CCT>CTT	p.P961L
Pat_50	Pre-Treatment	INPP5F	22876	37	10	121571446	121571446	Missense_Mutation	SNP	C	T	24	14	c.1865C>T	c.(1864-1866)GCC>GTC	p.A622V
Pat_50	Pre-Treatment	MUC6	4588	37	11	1020098	1020098	Missense_Mutation	SNP	G	A	4	3	c.3800C>T	c.(3799-3801)TCC>TTC	p.S1267F
Pat_50	Pre-Treatment	KCNQ1	3784	37	11	2604711	2604711	Nonsense_Mutation	SNP	G	A	64	116	c.968G>A	c.(967-969)TGG>TAG	p.W323*
Pat_50	Pre-Treatment	OR51G2	81282	37	11	4936698	4936698	Missense_Mutation	SNP	G	A	13	19	c.196C>T	c.(196-198)CTC>TTC	p.L66F
Pat_50	Pre-Treatment	OR56A5	390084	37	11	5988824	5988824	Missense_Mutation	SNP	C	T	11	38	c.901G>A	c.(901-903)GAG>AAG	p.E301K
Pat_50	Pre-Treatment	ABCC8	6833	37	11	17449861	17449861	Missense_Mutation	SNP	C	T	48	70	c.2015G>A	c.(2014-2016)GGC>GAC	p.G672D
Pat_50	Pre-Treatment	USH1C	10083	37	11	17547952	17547952	Missense_Mutation	SNP	C	T	10	18	c.616G>A	c.(616-618)GAA>AAA	p.E206K
Pat_50	Pre-Treatment	SLC17A6	57084	37	11	22364792	22364792	Splice_Site	SNP	G	A	48	82	c.340_splice	c.e3-1	p.K114_splice
Pat_50	Pre-Treatment	OR4X2	119764	37	11	48266909	48266909	Missense_Mutation	SNP	C	T	52	69	c.254C>T	c.(253-255)TCT>TTT	p.S85F
Pat_50	Pre-Treatment	FOLH1	2346	37	11	49204734	49204734	Missense_Mutation	SNP	G	A	22	44	c.887C>T	c.(886-888)CCA>CTA	p.P296L
Pat_50	Pre-Treatment	OR10Q1	219960	37	11	57995785	57995785	Missense_Mutation	SNP	G	A	30	43	c.563C>T	c.(562-564)CCC>CTC	p.P188L
Pat_50	Pre-Treatment	CD5	921	37	11	60886756	60886757	Missense_Mutation	DNP	GG	AA	44	68	c.514_515GG>AA	c.(514-516)GGC>AAC	p.G172N
Pat_50	Pre-Treatment	SLC22A6	9356	37	11	62747211	62747211	Missense_Mutation	SNP	G	A	14	22	c.1247C>T	c.(1246-1248)CCC>CTC	p.P416L
Pat_50	Pre-Treatment	SLC22A10	387775	37	11	63064783	63064783	Missense_Mutation	SNP	G	A	36	94	c.515G>A	c.(514-516)CGA>CAA	p.R172Q
Pat_50	Pre-Treatment	CCDC87	55231	37	11	66358610	66358610	Missense_Mutation	SNP	G	A	25	47	c.1877C>T	c.(1876-1878)GCC>GTC	p.A626V
Pat_50	Pre-Treatment	FCHSD2	9873	37	11	72695210	72695210	Missense_Mutation	SNP	C	T	22	44	c.628G>A	c.(628-630)GAT>AAT	p.D210N
Pat_50	Pre-Treatment	DLG2	1740	37	11	84245620	84245620	Missense_Mutation	SNP	G	A	47	98	c.197C>T	c.(196-198)CCT>CTT	p.P66L
Pat_50	Pre-Treatment	GRM5	2915	37	11	88301106	88301106	Missense_Mutation	SNP	G	A	24	37	c.1745C>T	c.(1744-1746)GCA>GTA	p.A582V
Pat_50	Pre-Treatment	TECTA	7007	37	11	121030881	121030881	Missense_Mutation	SNP	G	A	48	30	c.4727G>A	c.(4726-4728)GGT>GAT	p.G1576D
Pat_50	Pre-Treatment	CACNA1C	775	37	12	2714279	2714279	Missense_Mutation	SNP	G	A	32	54	c.3053G>A	c.(3052-3054)CGA>CAA	p.R1018Q
Pat_50	Pre-Treatment	C1R	715	37	12	7188356	7188356	Missense_Mutation	SNP	C	T	63	118	c.1598G>A	c.(1597-1599)GGA>GAA	p.G533E
Pat_50	Pre-Treatment	CD163	9332	37	12	7637812	7637812	Missense_Mutation	SNP	G	A	26	42	c.2659C>T	c.(2659-2661)CCC>TCC	p.P887S
Pat_50	Pre-Treatment	PZP	5858	37	12	9356381	9356381	Missense_Mutation	SNP	G	A	31	57	c.250C>T	c.(250-252)CAC>TAC	p.H84Y
Pat_50	Pre-Treatment	PRB2	653247	37	12	11546389	11546389	Missense_Mutation	SNP	C	T	37	77	c.623G>A	c.(622-624)GGA>GAA	p.G208E
Pat_50	Pre-Treatment	MANSC1	54682	37	12	12483724	12483724	Missense_Mutation	SNP	G	A	16	31	c.533C>T	c.(532-534)TCC>TTC	p.S178F
Pat_50	Pre-Treatment	GUCY2C	2984	37	12	14769616	14769616	Missense_Mutation	SNP	C	T	62	103	c.2921G>A	c.(2920-2922)AGA>AAA	p.R974K
Pat_50	Pre-Treatment	GYS2	2998	37	12	21690022	21690022	Missense_Mutation	SNP	C	T	27	47	c.1978G>A	c.(1978-1980)GAA>AAA	p.E660K
Pat_50	Pre-Treatment	ARNTL2	56938	37	12	27543031	27543031	Missense_Mutation	SNP	G	A	89	125	c.778G>A	c.(778-780)GGT>AGT	p.G260S
Pat_50	Pre-Treatment	ALG10	84920	37	12	34179706	34179706	Missense_Mutation	SNP	G	T	60	164	c.1278G>T	c.(1276-1278)AGG>AGT	p.R426S
Pat_50	Pre-Treatment	MLL2	8085	37	12	49424716	49424716	Missense_Mutation	SNP	C	T	9	15	c.13631G>A	.(13630-13632)GGG>GA	p.G4544E
Pat_50	Pre-Treatment	ITGB7	3695	37	12	53589178	53589178	Missense_Mutation	SNP	G	A	39	82	c.1141C>T	c.(1141-1143)CTC>TTC	p.L381F
Pat_50	Pre-Treatment	HOXC11	3227	37	12	54367101	54367101	Missense_Mutation	SNP	G	T	22	38	c.76G>T	c.(76-78)GGG>TGG	p.G26W
Pat_50	Pre-Treatment	RASSF9	9182	37	12	86198653	86198653	Missense_Mutation	SNP	C	T	64	119	c.1135G>A	c.(1135-1137)GAA>AAA	p.E379K
Pat_50	Pre-Treatment	DCN	1634	37	12	91539975	91539975	Missense_Mutation	SNP	G	A	33	54	c.940C>T	c.(940-942)CCA>TCA	p.P314S
Pat_50	Pre-Treatment	UHRF1BP1L	23074	37	12	100453301	100453301	Missense_Mutation	SNP	G	A	20	30	c.1754C>T	c.(1753-1755)CCT>CTT	p.P585L
Pat_50	Pre-Treatment	C12orf48	55010	37	12	102559652	102559652	Missense_Mutation	SNP	C	T	25	44	c.812C>T	c.(811-813)CCA>CTA	p.P271L

Pat_50	Pre-Treatment	STAB2	55576	37	12	103984763	103984763	Missense_Mutation	SNP	G	A	60	72	c.170G>A	c.(169-171)GGT>GAT	p.G57D
Pat_50	Pre-Treatment	NT5DC3	51559	37	12	104171671	104171671	Missense_Mutation	SNP	G	A	24	42	c.1583C>T	c.(1582-1584)CCC>CTC	p.P528L
Pat_50	Pre-Treatment	SETD8	387893	37	12	123875282	123875282	Missense_Mutation	SNP	G	A	5	82	c.238G>A	c.(238-240)GAA>AAA	p.E80K
Pat_50	Pre-Treatment	POLE	5426	37	12	133201341	133201341	Missense_Mutation	SNP	G	A	28	58	c.6803C>T	c.(6802-6804)TCG>TTG	p.S2268L
Pat_50	Pre-Treatment	SGCG	6445	37	13	23869586	23869586	Missense_Mutation	SNP	G	A	46	79	c.538G>A	c.(538-540)GAG>AAG	p.E180K
Pat_50	Pre-Treatment	RNF17	56163	37	13	25338391	25338391	Missense_Mutation	SNP	G	A	10	17	c.50G>A	c.(49-51)CGA>CAA	p.R17Q
Pat_50	Pre-Treatment	RPL21	6144	37	13	27830643	27830643	Missense_Mutation	SNP	C	T	11	13	c.464C>T	c.(463-465)CCC>CTC	p.P155L
Pat_50	Pre-Treatment	P704P	641455	37	14	20020119	20020119	Missense_Mutation	SNP	C	G	5	132	c.102G>C	c.(100-102)TGG>TGC	p.W34C
Pat_50	Pre-Treatment	OR10G3	26533	37	14	22038227	22038227	Missense_Mutation	SNP	G	A	39	32	c.649C>T	c.(649-651)CTC>TTC	p.L217F
Pat_50	Pre-Treatment	GALNTL1	57452	37	14	69813821	69813821	Missense_Mutation	SNP	G	A	32	10	c.1336G>A	c.(1336-1338)GGC>AGC	p.G446S
Pat_50	Pre-Treatment	DIO2	1734	37	14	80669327	80669327	Missense_Mutation	SNP	G	A	28	16	c.527C>T	c.(526-528)TCC>TTC	p.S176F
Pat_50	Pre-Treatment	GALC	2581	37	14	88434719	88434719	Missense_Mutation	SNP	G	A	54	27	c.868C>T	c.(868-870)CGC>TGC	p.R290C
Pat_50	Pre-Treatment	SERPINA10	51156	37	14	94756345	94756345	Missense_Mutation	SNP	G	A	25	15	c.586C>T	c.(586-588)CGC>TGC	p.R196C
Pat_50	Pre-Treatment	BDKRB2	624	37	14	96707003	96707003	Nonsense_Mutation	SNP	G	A	110	43	c.338G>A	c.(337-339)TGG>TAG	p.W113*
Pat_50	Pre-Treatment	TP53BP1	7158	37	15	43712661	43712661	Missense_Mutation	SNP	G	A	144	64	c.4508C>T	c.(4507-4509)TCT>TTT	p.S1503F
Pat_50	Pre-Treatment	DUOX2	50506	37	15	45393022	45393022	Missense_Mutation	SNP	C	T	7	17	c.2936G>A	c.(2935-2937)GGA>GAA	p.G979E
Pat_50	Pre-Treatment	MYO5C	55930	37	15	52510745	52510745	Missense_Mutation	SNP	C	T	23	30	c.3925G>A	c.(3925-3927)GAA>AAA	p.E1309K
Pat_50	Pre-Treatment	UNC13C	440279	37	15	54306933	54306934	Missense_Mutation	DNP	GG	AA	8	95	.1833_1834GG>A	831-1836)CAGGGT>CAA	p.G612S
Pat_50	Pre-Treatment	SPESP1	246777	37	15	69223036	69223036	Missense_Mutation	SNP	C	T	58	78	c.44C>T	c.(43-45)TCG>TTG	p.S15L
Pat_50	Pre-Treatment	FAM154B	283726	37	15	82574540	82574540	Missense_Mutation	SNP	G	A	46	85	c.334G>A	c.(334-336)GGA>AGA	p.G112R
Pat_50	Pre-Treatment	SSTR5	6755	37	16	1129185	1129185	Missense_Mutation	SNP	C	T	20	34	c.317C>T	c.(316-318)CCC>CTC	p.P106L
Pat_50	Pre-Treatment	UNKL	64718	37	16	1417751	1417751	Missense_Mutation	SNP	G	A	16	7	c.815C>T	c.(814-816)CCA>CTA	p.P272L
Pat_50	Pre-Treatment	IGFALS	3483	37	16	1840633	1840633	Missense_Mutation	SNP	C	G	2	10	c.1786G>C	c.(1786-1788)GAC>CAC	p.D596H
Pat_50	Pre-Treatment	ADCY9	115	37	16	4042200	4042200	Missense_Mutation	SNP	C	A	79	34	c.2154G>T	c.(2152-2154)AAG>AAT	p.K718N
Pat_50	Pre-Treatment	USP7	7874	37	16	8989007	8989007	Missense_Mutation	SNP	C	T	232	169	c.2920G>A	c.(2920-2922)GAA>AAA	p.E974K
Pat_50	Pre-Treatment	GRIN2A	2903	37	16	9858007	9858007	Missense_Mutation	SNP	G	A	73	64	c.3394C>T	c.(3394-3396)CCA>TCA	p.P1132S
Pat_50	Pre-Treatment	ATF7IP2	80063	37	16	10524907	10524907	Missense_Mutation	SNP	G	A	86	60	c.430G>A	c.(430-432)GAT>AAT	p.D144N
Pat_50	Pre-Treatment	ACSM1	116285	37	16	20702348	20702348	Missense_Mutation	SNP	C	T	33	79	c.163G>A	c.(163-165)GTA>ATA	p.V55I
Pat_50	Pre-Treatment	ZNF646	9726	37	16	31090592	31090592	Missense_Mutation	SNP	G	A	92	90	c.2947G>A	c.(2947-2949)GGG>AGG	p.G983R
Pat_50	Pre-Treatment	GNAO1	2775	37	16	56309868	56309868	Missense_Mutation	SNP	G	A	3	24	c.187G>A	c.(187-189)GGA>AGA	p.G63R
Pat_50	Pre-Treatment	NLRC5	84166	37	16	57092967	57092967	Missense_Mutation	SNP	C	T	87	58	c.3914C>T	c.(3913-3915)TCA>TTA	p.S1305L
Pat_50	Pre-Treatment	SPG7	6687	37	16	89611170	89611170	Missense_Mutation	SNP	C	T	42	29	c.1439C>T	c.(1438-1440)CCC>CTC	p.P480L
Pat_50	Pre-Treatment	DPH1	1801	37	17	1936837	1936837	Missense_Mutation	SNP	C	T	4	55	c.115C>T	c.(115-117)CCT>TCT	p.P39S
Pat_50	Pre-Treatment	SLC2A4	6517	37	17	7186907	7186907	Missense_Mutation	SNP	C	T	39	23	c.266C>T	c.(265-267)TCC>TTC	p.S89F
Pat_50	Pre-Treatment	STX8	9482	37	17	9471692	9471692	Missense_Mutation	SNP	G	A	7	8	c.113C>T	c.(112-114)CCA>CTA	p.P38L
Pat_50	Pre-Treatment	TBC1D3	729873	37	17	36288203	36288203	Nonsense_Mutation	SNP	C	T	66	543	c.289C>T	c.(289-291)CGA>TGA	p.R97*
Pat_50	Pre-Treatment	KRT24	192666	37	17	38859487	38859487	Missense_Mutation	SNP	A	T	95	139	c.459T>A	c.(457-459)AAT>AAA	p.N153K
Pat_50	Pre-Treatment	KRT25	147183	37	17	38911541	38911541	Translation_Start_Site	SNP	G	A	21	15	c.-17C>T	c.(-19--15)AACGC>AATGC	
Pat_50	Pre-Treatment	PHB	5245	37	17	47489114	47489114	Missense_Mutation	SNP	G	A	25	39	c.176C>T	c.(175-177)CCG>CTG	p.P59L
Pat_50	Pre-Treatment	LRRC59	55379	37	17	48470215	48470215	Missense_Mutation	SNP	C	A	43	81	c.209G>T	c.(208-210)AGT>ATT	p.S70I
Pat_50	Pre-Treatment	ANKFN1	162282	37	17	54403587	54403587	Missense_Mutation	SNP	G	A	41	80	c.68G>A	c.(67-69)GGA>GAA	p.G23E
Pat_50	Pre-Treatment	MPO	4353	37	17	56355368	56355368	Missense_Mutation	SNP	C	T	39	102	c.1024G>A	c.(1024-1026)GTG>ATG	p.V342M
Pat_50	Pre-Treatment	SMARCD2	6603	37	17	61914292	61914292	Missense_Mutation	SNP	T	C	56	64	c.557A>G	c.(556-558)AAG>AGG	p.K186R
Pat_50	Pre-Treatment	MGAT5B	146664	37	17	74902134	74902134	Missense_Mutation	SNP	C	T	48	87	c.923C>T	c.(922-924)TCC>TTC	p.S308F
Pat_50	Pre-Treatment	NOL4	8715	37	18	31673540	31673540	Missense_Mutation	SNP	C	T	19	20	c.661G>A	c.(661-663)GAT>AAT	p.D221N
Pat_50	Pre-Treatment	FHOD3	80206	37	18	34298461	34298461	Nonsense_Mutation	SNP	T	A	31	45	c.2624T>A	c.(2623-2625)TTA>TAA	p.L875*
Pat_50	Pre-Treatment	SLC14A2	8170	37	18	43205738	43205738	Missense_Mutation	SNP	C	T	13	28	c.241C>T	c.(241-243)CGG>TGG	p.R81W

Pat_50	Pre-Treatment	MYO5B	4645	37	18	47563269	47563269	Missense_Mutation	SNP	C	T	16	29	c.406G>A	c.(406-408)GAC>AAC	p.D136N
Pat_50	Pre-Treatment	DCC	1630	37	18	50451618	50451618	Missense_Mutation	SNP	C	A	46	76	c.863C>A	c.(862-864)TCT>TAT	p.S288Y
Pat_50	Pre-Treatment	EMR1	2015	37	19	6901985	6901985	Missense_Mutation	SNP	C	T	90	123	c.614C>T	c.(613-615)TCC>TTC	p.S205F
Pat_50	Pre-Treatment	ZNF699	374879	37	19	9407410	9407410	Nonsense_Mutation	SNP	G	A	48	93	c.670C>T	c.(670-672)CAG>TAG	p.Q224*
Pat_50	Pre-Treatment	ABHD8	79575	37	19	17411692	17411692	Missense_Mutation	SNP	C	T	114	189	c.734G>A	c.(733-735)CGA>CAA	p.R245Q
Pat_50	Pre-Treatment	AXL	558	37	19	41758775	41758775	Missense_Mutation	SNP	G	A	13	35	c.1829G>A	c.(1828-1830)CGA>CAA	p.R610Q
Pat_50	Pre-Treatment	PSG1	5669	37	19	43383685	43383685	Missense_Mutation	SNP	C	T	58	93	c.49G>A	c.(49-51)GGG>AGG	p.G17R
Pat_50	Pre-Treatment	CEACAM20	125931	37	19	45016125	45016125	Missense_Mutation	SNP	G	A	8	20	c.1525C>T	c.(1525-1527)CCT>TCT	p.P509S
Pat_50	Pre-Treatment	CCDC8	83987	37	19	46915238	46915238	Missense_Mutation	SNP	C	T	54	47	c.830G>A	c.(829-831)CGC>CAC	p.R277H
Pat_50	Pre-Treatment	KCNC3	3748	37	19	50826610	50826610	Missense_Mutation	SNP	G	A	33	72	c.1600C>T	c.(1600-1602)CCT>TCT	p.P534S
Pat_50	Pre-Treatment	ZNF610	162963	37	19	52852406	52852406	Splice_Site	SNP	G	A	22	45	c.-18_splice	c.e3-1	
Pat_50	Pre-Treatment	ZNF331	55422	37	19	54080277	54080277	Missense_Mutation	SNP	G	A	43	94	c.463G>A	c.(463-465)GGT>AGT	p.G155S
Pat_50	Pre-Treatment	NLRP7	199713	37	19	55444994	55444994	Missense_Mutation	SNP	C	T	20	34	c.2585G>A	c.(2584-2586)GGG>GAG	p.G862E
Pat_50	Pre-Treatment	ALK	238	37	2	29455223	29455223	Missense_Mutation	SNP	C	T	35	58	c.2579G>A	c.(2578-2580)AGA>AAA	p.R860K
Pat_50	Pre-Treatment	FUNDC2P2	388965	37	2	84518171	84518171	Missense_Mutation	SNP	G	A	49	99	c.229G>A	c.(229-231)GGA>AGA	p.G77R
Pat_50	Pre-Treatment	IL1RL1	9173	37	2	102968248	102968248	Missense_Mutation	SNP	G	A	11	10	c.1538G>A	c.(1537-1539)AGG>AAG	p.R513K
Pat_50	Pre-Treatment	IL18RAP	8807	37	2	103061800	103061800	Missense_Mutation	SNP	G	A	19	44	c.1072G>A	c.(1072-1074)GTG>ATG	p.V358M
Pat_50	Pre-Treatment	MARCO	8685	37	2	119750806	119750806	Missense_Mutation	SNP	T	A	95	156	c.1359T>A	c.(1357-1359)AAT>AAA	p.N453K
Pat_50	Pre-Treatment	RAB6C	84084	37	2	130738023	130738023	Missense_Mutation	SNP	G	A	99	193	c.335G>A	c.(334-336)AGA>AAA	p.R112K
Pat_50	Pre-Treatment	YSK4	80122	37	2	135738574	135738574	Missense_Mutation	SNP	C	T	19	52	c.3737G>A	c.(3736-3738)CGG>CAG	p.R1246Q
Pat_50	Pre-Treatment	THSD7B	80731	37	2	138208505	138208505	Missense_Mutation	SNP	G	A	22	30	c.2957G>A	c.(2956-2958)GGA>GAA	p.G986E
Pat_50	Pre-Treatment	NEB	4703	37	2	152522870	152522870	Missense_Mutation	SNP	C	T	33	49	c.4765G>A	c.(4765-4767)GGA>AGA	p.G1589R
Pat_50	Pre-Treatment	SCN3A	6328	37	2	166011012	166011012	Missense_Mutation	SNP	C	T	27	71	c.1330G>A	c.(1330-1332)GAA>AAA	p.E444K
Pat_50	Pre-Treatment	SCN1A	6323	37	2	166900483	166900483	Missense_Mutation	SNP	C	T	48	70	c.1739G>A	c.(1738-1740)CGA>CAA	p.R580Q
Pat_50	Pre-Treatment	TTN	7273	37	2	179454177	179454177	Missense_Mutation	SNP	C	T	16	42	c.54571G>A	c.(54571-54573)GAA>AAA	p.E18191K
Pat_50	Pre-Treatment	TTN	7273	37	2	179472521	179472521	Missense_Mutation	SNP	C	T	33	61	c.45289G>A	c.(45289-45291)GAA>AAA	p.E15097K
Pat_50	Pre-Treatment	TTN	7273	37	2	179542377	179542377	Missense_Mutation	SNP	A	C	9	11	c.30530T>G	c.(30529-30531)GTT>GGT	p.V10177G
Pat_50	Pre-Treatment	TTN	7273	37	2	179603955	179603955	Missense_Mutation	SNP	C	T	12	11	c.13492G>A	c.(13492-13494)GAA>AAA	p.E4498K
Pat_50	Pre-Treatment	TTN	7273	37	2	179648811	179648811	Missense_Mutation	SNP	C	T	72	101	c.2761G>A	c.(2761-2763)GGA>AGA	p.G921R
Pat_50	Pre-Treatment	CCDC141	285025	37	2	179732779	179732779	Missense_Mutation	SNP	C	T	30	53	c.823G>A	c.(823-825)GAC>AAC	p.D275N
Pat_50	Pre-Treatment	CALCRL	10203	37	2	188216840	188216840	Splice_Site	SNP	C	T	38	76	c.1128_splice	c.e13+1	p.Q376_splice
Pat_50	Pre-Treatment	EEF1B2	1933	37	2	207025358	207025358	Missense_Mutation	SNP	A	G	8	217	c.127A>G	c.(127-129)AGC>GGC	p.S43G
Pat_50	Pre-Treatment	IKZF2	22807	37	2	213872485	213872485	Missense_Mutation	SNP	G	T	25	44	c.1180C>A	c.(1180-1182)CAG>AAG	p.Q394K
Pat_50	Pre-Treatment	SPAG16	79582	37	2	214794733	214794733	Missense_Mutation	SNP	G	A	34	94	c.1264G>A	c.(1264-1266)GAT>AAT	p.D422N
Pat_50	Pre-Treatment	SLC19A3	80704	37	2	228563559	228563559	Missense_Mutation	SNP	C	A	11	37	c.872G>T	c.(871-873)GGT>GTT	p.G291V
Pat_50	Pre-Treatment	INPP5D	3635	37	2	233990542	233990542	Missense_Mutation	SNP	C	T	12	25	c.437C>T	c.(436-438)TCA>TTA	p.S146L
Pat_50	Pre-Treatment	SIRPG	55423	37	20	1629761	1629761	Nonsense_Mutation	SNP	G	A	38	78	c.367C>T	c.(367-369)CGA>TGA	p.R123*
Pat_50	Pre-Treatment	CSTL1	128817	37	20	23421110	23421110	Missense_Mutation	SNP	G	A	89	111	c.206G>A	c.(205-207)CGA>CAA	p.R69Q
Pat_50	Pre-Treatment	FRG1B	284802	37	20	29614323	29614323	Translation_Start_Site	SNP	C	T	4	51	c.-10C>T	c.(-12--8)TACGT>TATGT	
Pat_50	Pre-Treatment	CDK5RAP1	51654	37	20	31984608	31984608	Missense_Mutation	SNP	G	A	70	133	c.263C>T	c.(262-264)CCC>CTC	p.P88L
Pat_50	Pre-Treatment	PHF20	51230	37	20	34459629	34459629	Missense_Mutation	SNP	C	T	96	172	c.1160C>T	c.(1159-1161)TCC>TTC	p.S387F
Pat_50	Pre-Treatment	USP25	29761	37	21	17172094	17172094	Missense_Mutation	SNP	G	A	16	24	c.574G>A	c.(574-576)GAA>AAA	p.E192K
Pat_50	Pre-Treatment	DSCAM	1826	37	21	41452132	41452133	Missense_Mutation	DNP	CC	TT	25	91	.4366_4367GG>A	c.(4366-4368)GGA>AAA	p.G1456K
Pat_50	Pre-Treatment	CRYAA	1409	37	21	44589354	44589354	Missense_Mutation	SNP	C	T	95	163	c.145C>T	c.(145-147)CGC>TGC	p.R49C
Pat_50	Pre-Treatment	KRTAP10-7	386675	37	21	46020555	46020555	Missense_Mutation	SNP	G	A	19	48	c.34G>A	c.(34-36)GAC>AAC	p.D12N
Pat_50	Pre-Treatment	DIP2A	23181	37	21	47975994	47975994	Missense_Mutation	SNP	C	T	62	111	c.3488C>T	c.(3487-3489)GCG>GTG	p.A1163V
Pat_50	Pre-Treatment	SGSM1	129049	37	22	25294443	25294443	Missense_Mutation	SNP	C	T	39	75	c.2692C>T	c.(2692-2694)CTC>TTC	p.L898F

Pat_50	Pre-Treatment	SAMM50	25813	37	22	44377322	44377323	Missense_Mutation	DNP	CC	TT	46	89	c.988_989CC>TT	c.(988-990)CCG>TTG	p.P330L
Pat_50	Pre-Treatment	TTC38	55020	37	22	46674503	46674503	Missense_Mutation	SNP	C	T	33	89	c.560C>T	c.(559-561)TCT>TTT	p.S187F
Pat_50	Pre-Treatment	HDAC10	83933	37	22	50687265	50687265	Missense_Mutation	SNP	G	A	10	27	c.811C>T	c.(811-813)CCT>TCT	p.P271S
Pat_50	Pre-Treatment	CHL1	10752	37	3	391049	391049	Missense_Mutation	SNP	C	T	7	6	c.808C>T	c.(808-810)CCA>TCA	p.P270S
Pat_50	Pre-Treatment	TMEM43	79188	37	3	14172412	14172412	Missense_Mutation	SNP	G	A	26	72	c.253G>A	c.(253-255)GAA>AAA	p.E85K
Pat_50	Pre-Treatment	TRIM71	131405	37	3	32932354	32932354	Missense_Mutation	SNP	G	A	35	52	c.1658G>A	c.(1657-1659)CGA>CAA	p.R553Q
Pat_50	Pre-Treatment	SCN10A	6336	37	3	38753837	38753837	Missense_Mutation	SNP	G	A	69	121	c.3904C>T	c.(3904-3906)CTC>TTC	p.L1302F
Pat_50	Pre-Treatment	SCN11A	11280	37	3	38950574	38950574	Missense_Mutation	SNP	C	T	57	132	c.1213G>A	c.(1213-1215)GAG>AAG	p.E405K
Pat_50	Pre-Treatment	ZDHHC3	51304	37	3	44968333	44968333	Missense_Mutation	SNP	C	T	38	48	c.832G>A	c.(832-834)GAA>AAA	p.E278K
Pat_50	Pre-Treatment	CELSR3	1951	37	3	48677875	48677875	Missense_Mutation	SNP	C	T	25	73	c.9143G>A	c.(9142-9144)GGT>GAT	p.G3048D
Pat_50	Pre-Treatment	STAB1	23166	37	3	52547899	52547899	Missense_Mutation	SNP	G	A	167	218	c.3349G>A	c.(3349-3351)GTC>ATC	p.V1117I
Pat_50	Pre-Treatment	CACNA2D3	55799	37	3	55021771	55021771	Missense_Mutation	SNP	C	T	8	16	c.2681C>T	c.(2680-2682)TCC>TTC	p.S894F
Pat_50	Pre-Treatment	DNASE1L3	1776	37	3	58178442	58178442	Missense_Mutation	SNP	C	T	20	22	c.890G>A	c.(889-891)AGG>AAG	p.R297K
Pat_50	Pre-Treatment	PLSCR4	57088	37	3	145913062	145913062	Missense_Mutation	SNP	G	A	86	58	c.794C>T	c.(793-795)TCC>TTC	p.S265F
Pat_50	Pre-Treatment	BCHE	590	37	3	165547930	165547930	Nonsense_Mutation	SNP	G	A	31	55	c.892C>T	c.(892-894)CAA>TAA	p.Q298*
Pat_50	Pre-Treatment	ZBBX	79740	37	3	167039963	167039963	Missense_Mutation	SNP	C	T	23	43	c.925G>A	c.(925-927)GAA>AAA	p.E309K
Pat_50	Pre-Treatment	ZBBX	79740	37	3	167051692	167051692	Missense_Mutation	SNP	C	T	20	39	c.610G>A	c.(610-612)GAG>AAG	p.E204K
Pat_50	Pre-Treatment	MUC4	4585	37	3	195505836	195505836	Missense_Mutation	SNP	G	C	4	8	c.12231C>G	c.(12229-12231)CAC>CAG	p.H4077Q
Pat_50	Pre-Treatment	ZNF718	255403	37	4	59997	59997	Missense_Mutation	SNP	A	C	21	330	c.177A>C	c.(175-177)AGA>AGC	p.R59S
Pat_50	Pre-Treatment	WHSC1	7468	37	4	1906028	1906028	Missense_Mutation	SNP	C	T	58	74	c.683C>T	c.(682-684)TCC>TTC	p.S228F
Pat_50	Pre-Treatment	DOK7	285489	37	4	3494893	3494893	Missense_Mutation	SNP	G	A	9	13	c.1180G>A	c.(1180-1182)GAG>AAG	p.E394K
Pat_50	Pre-Treatment	BEND4	389206	37	4	42119597	42119597	Missense_Mutation	SNP	C	T	5	9	c.1543G>A	c.(1543-1545)GAT>AAT	p.D515N
Pat_50	Pre-Treatment	CWH43	80157	37	4	48996789	48996789	Nonsense_Mutation	SNP	G	A	44	61	c.665G>A	c.(664-666)TGG>TAG	p.W222*
Pat_50	Pre-Treatment	KDR	3791	37	4	55962492	55962492	Missense_Mutation	SNP	C	G	29	57	c.2632G>C	c.(2632-2634)GAG>CAG	p.E878Q
Pat_50	Pre-Treatment	UGT2A3	79799	37	4	69798408	69798408	Nonsense_Mutation	SNP	G	A	99	148	c.934C>T	c.(934-936)CAA>TAA	p.Q312*
Pat_50	Pre-Treatment	ADH1B	125	37	4	100235028	100235028	Missense_Mutation	SNP	C	T	85	166	c.778G>A	c.(778-780)GAT>AAT	p.D260N
Pat_50	Pre-Treatment	ADH7	131	37	4	100341788	100341788	Missense_Mutation	SNP	G	A	40	54	c.763C>T	c.(763-765)CCC>TCC	p.P255S
Pat_50	Pre-Treatment	MTTP	4547	37	4	100504612	100504612	Missense_Mutation	SNP	A	T	41	47	c.331A>T	c.(331-333)ATG>TTG	p.M111L
Pat_50	Pre-Treatment	BANK1	55024	37	4	102776251	102776251	Missense_Mutation	SNP	G	A	12	18	c.529G>A	c.(529-531)GAA>AAA	p.E177K
Pat_50	Pre-Treatment	FAT4	79633	37	4	126370438	126370438	Missense_Mutation	SNP	C	T	34	72	c.8267C>T	c.(8266-8268)TCA>TTA	p.S2756L
Pat_50	Pre-Treatment	FAT4	79633	37	4	126371365	126371365	Missense_Mutation	SNP	G	A	20	38	c.9194G>A	c.(9193-9195)GGA>GAA	p.G3065E
Pat_50	Pre-Treatment	FAT4	79633	37	4	126372196	126372196	Missense_Mutation	SNP	G	A	24	47	c.10025G>A	c.(10024-10026)CGA>CAA	p.R3342Q
Pat_50	Pre-Treatment	FAT4	79633	37	4	126373455	126373455	Missense_Mutation	SNP	C	T	30	50	c.11284C>T	c.(11284-11286)CTT>TTT	p.L3762F
Pat_50	Pre-Treatment	PET112L	5188	37	4	152637172	152637172	Missense_Mutation	SNP	G	A	20	32	c.752C>T	c.(751-753)GCG>GTG	p.A251V
Pat_50	Pre-Treatment	ANP32C	23520	37	4	165118284	165118284	Missense_Mutation	SNP	C	T	9	16	c.580G>A	c.(580-582)GGT>AGT	p.G194S
Pat_50	Pre-Treatment	ODZ3	55714	37	4	183652198	183652198	Missense_Mutation	SNP	G	A	46	66	c.2873G>A	c.(2872-2874)GGA>GAA	p.G958E
Pat_50	Pre-Treatment	CDH18	1016	37	5	19473516	19473516	Missense_Mutation	SNP	G	A	24	41	c.2192C>T	c.(2191-2193)CCT>CTT	p.P731L
Pat_50	Pre-Treatment	HCN1	348980	37	5	45262124	45262124	Missense_Mutation	SNP	G	A	30	52	c.2572C>T	c.(2572-2574)CCA>TCA	p.P858S
Pat_50	Pre-Treatment	HCN1	348980	37	5	45262208	45262208	Missense_Mutation	SNP	C	T	7	16	c.2488G>A	c.(2488-2490)GGG>AGG	p.G830R
Pat_50	Pre-Treatment	DEPDC1B	55789	37	5	59941334	59941334	Missense_Mutation	SNP	G	A	27	50	c.563C>T	c.(562-564)TCT>TTT	p.S188F
Pat_50	Pre-Treatment	THBS4	7060	37	5	79357530	79357530	Missense_Mutation	SNP	C	T	53	77	c.1000C>T	c.(1000-1002)CCC>TCC	p.P334S
Pat_50	Pre-Treatment	VCAN	1462	37	5	82837487	82837487	Missense_Mutation	SNP	C	G	31	50	c.8665C>G	c.(8665-8667)CCT>GCT	p.P2889A
Pat_50	Pre-Treatment	EDIL3	10085	37	5	83360543	83360543	Missense_Mutation	SNP	C	T	27	36	c.928G>A	c.(928-930)GAA>AAA	p.E310K
Pat_50	Pre-Treatment	GPR98	84059	37	5	90052379	90052379	Missense_Mutation	SNP	G	A	25	51	c.11689G>A	c.(11689-11691)GAA>AAA	p.E3897K
Pat_50	Pre-Treatment	LMNB1	4001	37	5	126154785	126154785	Missense_Mutation	SNP	G	A	25	57	c.1111G>A	c.(1111-1113)GAC>AAC	p.D371N
Pat_50	Pre-Treatment	ADAMTS19	171019	37	5	128887601	128887601	Splice_Site	SNP	G	A	14	21	c.1354_splice	c.e7+1	p.G452_splice
Pat_50	Pre-Treatment	PCDHA4	56144	37	5	140188712	140188712	Missense_Mutation	SNP	T	C	98	149	c.1940T>C	c.(1939-1941)CTA>CCA	p.L647P

Pat_50	Pre-Treatment	PCDHB1	29930	37	5	140431179	140431179	Missense_Mutation	SNP	G	T	18	19	c.124G>T	c.(124-126)GGC>TGC	p.G42C
Pat_50	Pre-Treatment	PCDHB5	26167	37	5	140515473	140515473	Missense_Mutation	SNP	C	T	49	71	c.457C>T	c.(457-459)CCC>TCC	p.P153S
Pat_50	Pre-Treatment	PPARGC1B	133522	37	5	149212480	149212480	Missense_Mutation	SNP	G	A	66	33	c.844G>A	c.(844-846)GAA>AAA	p.E282K
Pat_50	Pre-Treatment	GEMIN5	25929	37	5	154304034	154304035	Missense_Mutation	DNP	GG	AA	128	69	.1373_1374CC>T	c.(1372-1374)TCC>TTT	p.S458F
Pat_50	Pre-Treatment	GABRB2	2561	37	5	160763764	160763764	Missense_Mutation	SNP	G	T	5	176	c.554C>A	c.(553-555)ACT>AAT	p.T185N
Pat_50	Pre-Treatment	SLIT3	6586	37	5	168216586	168216586	Missense_Mutation	SNP	C	T	21	23	c.1058G>A	c.(1057-1059)GGC>GAC	p.G353D
Pat_50	Pre-Treatment	N4BP3	23138	37	5	177547467	177547467	Missense_Mutation	SNP	C	T	30	61	c.619C>T	c.(619-621)CCC>TCC	p.P207S
Pat_50	Pre-Treatment	COL11A2	1302	37	6	33136336	33136336	Missense_Mutation	SNP	G	A	24	6	c.3920C>T	c.(3919-3921)CCC>CTC	p.P1307L
Pat_50	Pre-Treatment	BMP5	653	37	6	55638936	55638936	Missense_Mutation	SNP	C	T	112	40	c.938G>A	c.(937-939)CGA>CAA	p.R313Q
Pat_50	Pre-Treatment	PRIM2	5558	37	6	57512660	57512660	Missense_Mutation	SNP	G	A	39	452	c.1488G>A	c.(1486-1488)ATG>ATA	p.M496I
Pat_50	Pre-Treatment	BAI3	577	37	6	69772894	69772894	Missense_Mutation	SNP	C	T	149	34	c.2402C>T	c.(2401-2403)TCG>TTG	p.S801L
Pat_50	Pre-Treatment	TULP4	56995	37	6	158923787	158923787	Missense_Mutation	SNP	C	T	13	3	c.3092C>T	c.(3091-3093)CCA>CTA	p.P1031L
Pat_50	Pre-Treatment	MAP3K4	4216	37	6	161523006	161523006	Missense_Mutation	SNP	C	T	50	12	c.3757C>T	c.(3757-3759)CCC>TCC	p.P1253S
Pat_50	Pre-Treatment	FSCN1	6624	37	7	5644942	5644942	Missense_Mutation	SNP	C	T	44	96	c.1319C>T	c.(1318-1320)GCG>GTG	p.A440V
Pat_50	Pre-Treatment	TAX1BP1	8887	37	7	27825049	27825049	Missense_Mutation	SNP	G	A	52	165	c.793G>A	c.(793-795)GAA>AAA	p.E265K
Pat_50	Pre-Treatment	LOC168474	168474	37	7	64313602	64313602	Missense_Mutation	SNP	G	A	44	80	c.25C>T	c.(25-27)CTT>TTT	p.L9F
Pat_50	Pre-Treatment	TYW1B	441250	37	7	72209576	72209576	Missense_Mutation	SNP	C	G	5	135	c.967G>C	c.(967-969)GAT>CAT	p.D323H
Pat_50	Pre-Treatment	TRIM50	135892	37	7	72727081	72727081	Missense_Mutation	SNP	C	T	5	18	c.1300G>A	c.(1300-1302)GAT>AAT	p.D434N
Pat_50	Pre-Treatment	VPS37D	155382	37	7	73085570	73085570	Missense_Mutation	SNP	C	T	5	9	c.620C>T	c.(619-621)CCA>CTA	p.P207L
Pat_50	Pre-Treatment	RSBN1L	222194	37	7	77325812	77325812	Missense_Mutation	SNP	A	T	63	189	c.26A>T	c.(25-27)CAC>CTC	p.H9L
Pat_50	Pre-Treatment	ZNF804B	219578	37	7	88964065	88964065	Missense_Mutation	SNP	A	T	38	36	c.1769A>T	c.(1768-1770)GAT>GTT	p.D590V
Pat_50	Pre-Treatment	AKAP9	10142	37	7	91667802	91667802	Missense_Mutation	SNP	A	T	56	98	c.4408A>T	c.(4408-4410)AAT>TAT	p.N1470Y
Pat_50	Pre-Treatment	TECPR1	25851	37	7	97872900	97872900	Missense_Mutation	SNP	G	A	9	63	c.536C>T	c.(535-537)CCC>CTC	p.P179L
Pat_50	Pre-Treatment	TRRAP	8295	37	7	98522843	98522843	Missense_Mutation	SNP	G	A	67	273	c.2932G>A	c.(2932-2934)GAG>AAG	p.E978K
Pat_50	Pre-Treatment	CYP3A5	1577	37	7	99272200	99272200	Nonsense_Mutation	SNP	C	T	65	63	c.174G>A	c.(172-174)TGG>TGA	p.W58*
Pat_50	Pre-Treatment	TRIM56	81844	37	7	100732610	100732610	Missense_Mutation	SNP	G	A	46	178	c.2017G>A	c.(2017-2019)GGG>AGG	p.G673R
Pat_50	Pre-Treatment	CFTR	1080	37	7	117180254	117180254	Missense_Mutation	SNP	C	T	43	54	c.970C>T	c.(970-972)CCC>TCC	p.P324S
Pat_50	Pre-Treatment	FLNC	2318	37	7	128491610	128491610	Missense_Mutation	SNP	G	A	62	151	c.5770G>A	c.(5770-5772)GGA>AGA	p.G1924R
Pat_50	Pre-Treatment	AKR1D1	6718	37	7	137782687	137782687	Missense_Mutation	SNP	G	A	40	110	c.454G>A	c.(454-456)GAG>AAG	p.E152K
Pat_50	Pre-Treatment	BRAF	673	37	7	140453136	140453136	Missense_Mutation	SNP	A	T	38	116	c.1799T>A	c.(1798-1800)GTG>GAG	p.V600E
Pat_50	Pre-Treatment	KIAA1147	57189	37	7	141364711	141364711	Missense_Mutation	SNP	C	T	6	12	c.1096G>A	c.(1096-1098)GAG>AAG	p.E366K
Pat_50	Pre-Treatment	OR9A4	130075	37	7	141619129	141619129	Missense_Mutation	SNP	G	A	57	125	c.454G>A	c.(454-456)GGG>AGG	p.G152R
Pat_50	Pre-Treatment	MGAM	8972	37	7	141727431	141727431	Missense_Mutation	SNP	C	T	13	51	c.1117C>T	c.(1117-1119)CCC>TCC	p.P373S
Pat_50	Pre-Treatment	OR2A5	393046	37	7	143747845	143747845	Missense_Mutation	SNP	G	A	82	243	c.351G>A	c.(349-351)ATG>ATA	p.M117I
Pat_50	Pre-Treatment	ZNF425	155054	37	7	148801272	148801272	Missense_Mutation	SNP	G	A	19	37	c.1691C>T	c.(1690-1692)TCC>TTC	p.S564F
Pat_50	Pre-Treatment	ZNF425	155054	37	7	148801879	148801879	Missense_Mutation	SNP	C	T	27	74	c.1084G>A	c.(1084-1086)GAG>AAG	p.E362K
Pat_50	Pre-Treatment	PDGFRL	5157	37	8	17486262	17486262	Missense_Mutation	SNP	G	T	13	28	c.772G>T	c.(772-774)GTC>TTC	p.V258F
Pat_50	Pre-Treatment	SLC39A14	23516	37	8	22277162	22277162	Missense_Mutation	SNP	C	T	28	50	c.1430C>T	c.(1429-1431)ACC>ATC	p.T477I
Pat_50	Pre-Treatment	TACC1	6867	37	8	38677627	38677627	Missense_Mutation	SNP	C	T	14	24	c.865C>T	c.(865-867)CCT>TCT	p.P289S
Pat_50	Pre-Treatment	IDO2	169355	37	8	39840204	39840204	Missense_Mutation	SNP	G	A	8	18	c.388G>A	c.(388-390)GAA>AAA	p.E130K
Pat_50	Pre-Treatment	DKK4	27121	37	8	42232314	42232314	Missense_Mutation	SNP	C	T	67	286	c.380G>A	c.(379-381)AGG>AAG	p.R127K
Pat_50	Pre-Treatment	C8orf40	114926	37	8	42401673	42401673	Missense_Mutation	SNP	G	A	65	160	c.58G>A	c.(58-60)GAA>AAA	p.E20K
Pat_50	Pre-Treatment	C8orf22	492307	37	8	49985441	49985441	Nonsense_Mutation	SNP	C	T	103	87	c.52C>T	c.(52-54)CGA>TGA	p.R18*
Pat_50	Pre-Treatment	PXDNL	137902	37	8	52320998	52320999	Missense_Mutation	DNP	AG	TA	12	15	.3185_3186CT>T	c.(3184-3186)CCT>CTA	p.P1062L
Pat_50	Pre-Treatment	RP1	6101	37	8	55537472	55537472	Missense_Mutation	SNP	G	A	26	28	c.1030G>A	c.(1030-1032)GAA>AAA	p.E344K
Pat_50	Pre-Treatment	ARMC1	55156	37	8	66539551	66539551	Missense_Mutation	SNP	G	A	84	153	c.83C>T	c.(82-84)CCG>CTG	p.P28L
Pat_50	Pre-Treatment	VCPIP1	80124	37	8	67576520	67576520	Missense_Mutation	SNP	C	T	37	48	c.2674G>A	c.(2674-2676)GAA>AAA	p.E892K

Pat_50	Pre-Treatment	ZFHX4	79776	37	8	77690621	77690621	Missense_Mutation	SNP	G	A	87	205	c.3193G>A	c.(3193-3195)GAG>AAG	p.E1065K
Pat_50	Pre-Treatment	ANGPT1	284	37	8	108315583	108315583	Missense_Mutation	SNP	C	T	27	40	c.821G>A	c.(820-822)GGA>GAA	p.G274E
Pat_50	Pre-Treatment	PKHD1L1	93035	37	8	110477438	110477438	Missense_Mutation	SNP	G	A	34	80	c.8377G>A	c.(8377-8379)GAA>AAA	p.E2793K
Pat_50	Pre-Treatment	EPPK1	83481	37	8	144946434	144946434	Missense_Mutation	SNP	C	T	20	24	c.988G>A	c.(988-990)GAC>AAC	p.D330N
Pat_50	Pre-Treatment	SPATC1	375686	37	8	145095916	145095916	Missense_Mutation	SNP	C	T	47	108	c.1214C>T	c.(1213-1215)CCA>CTA	p.P405L
Pat_50	Pre-Treatment	DMRT3	58524	37	9	990295	990295	Missense_Mutation	SNP	G	A	35	15	c.709G>A	c.(709-711)GGG>AGG	p.G237R
Pat_50	Pre-Treatment	FREM1	158326	37	9	14737509	14737509	Missense_Mutation	SNP	G	A	4	7	c.6425C>T	c.(6424-6426)TCT>TTT	p.S2142F
Pat_50	Pre-Treatment	PTCH1	5727	37	9	98211496	98211496	Missense_Mutation	SNP	G	A	2	2	c.3659C>T	c.(3658-3660)TCC>TTC	p.S1220F
Pat_50	Pre-Treatment	TNFSF15	9966	37	9	117552881	117552881	Missense_Mutation	SNP	C	T	14	26	c.607G>A	c.(607-609)GAA>AAA	p.E203K
Pat_50	Pre-Treatment	ASTN2	23245	37	9	119739028	119739028	Missense_Mutation	SNP	G	T	35	61	c.1628C>A	c.(1627-1629)CCT>CAT	p.P543H
Pat_50	Pre-Treatment	FAM129B	64855	37	9	130270409	130270409	Missense_Mutation	SNP	G	A	21	54	c.1505C>T	c.(1504-1506)CCG>CTG	p.P502L
Pat_50	Pre-Treatment	LCN10	414332	37	9	139636390	139636390	Missense_Mutation	SNP	G	A	6	5	c.200C>T	c.(199-201)GCG>GTG	p.A67V
Pat_50	Pre-Treatment	ANAPC2	29882	37	9	140076151	140076151	Missense_Mutation	SNP	G	A	3	13	c.1450C>T	c.(1450-1452)CCT>TCT	p.P484S
Pat_50	Pre-Treatment	MXRA5	25878	37	X	3242018	3242018	Missense_Mutation	SNP	C	T	7	3	c.1708G>A	c.(1708-1710)GTA>ATA	p.V570I
Pat_50	Pre-Treatment	ACOT9	23597	37	X	23748990	23748990	Missense_Mutation	SNP	G	A	43	11	c.278C>T	c.(277-279)CCT>CTT	p.P93L
Pat_50	Pre-Treatment	USP11	8237	37	X	47100745	47100745	Missense_Mutation	SNP	C	A	47	13	c.1045C>A	c.(1045-1047)CGC>AGC	p.R349S
Pat_50	Pre-Treatment	DGKK	139189	37	X	50122653	50122653	Missense_Mutation	SNP	T	C	30	15	c.2834A>G	c.(2833-2835)AAC>AGC	p.N945S
Pat_50	Pre-Treatment	BMP15	9210	37	X	50659404	50659404	Nonsense_Mutation	SNP	C	T	91	24	c.976C>T	c.(976-978)CGA>TGA	p.R326*
Pat_50	Pre-Treatment	DACH2	117154	37	X	86069716	86069716	Missense_Mutation	SNP	G	T	18	8	c.1563G>T	c.(1561-1563)AAG>AAT	p.K521N
Pat_50	Pre-Treatment	TRPC5	7224	37	X	111097211	111097211	Missense_Mutation	SNP	G	A	21	5	c.1024C>T	c.(1024-1026)CCC>TCC	p.P342S
Pat_50	Pre-Treatment	AGTR2	186	37	X	115303706	115303706	Missense_Mutation	SNP	G	A	51	12	c.173G>A	c.(172-174)GGA>GAA	p.G58E
Pat_50	Pre-Treatment	UTY	7404	37	Y	15467220	15467220	Missense_Mutation	SNP	G	T	5	7	c.1433C>A	c.(1432-1434)ACT>AAT	p.T478N
Pat_54	Pre-Treatment	MIIP	60672	37	1	12081815	12081815	Missense_Mutation	SNP	G	A	3	26	c.32G>A	c.(31-33)CGG>CAG	p.R11Q
Pat_54	Pre-Treatment	MYOM3	127294	37	1	24426248	24426248	Missense_Mutation	SNP	C	T	42	70	c.578G>A	c.(577-579)CGG>CAG	p.R193Q
Pat_54	Pre-Treatment	UBXN11	91544	37	1	26628209	26628209	Nonsense_Mutation	SNP	G	A	3	42	c.76C>T	c.(76-78)CGA>TGA	p.R26*
Pat_54	Pre-Treatment	ZNF683	257101	37	1	26689618	26689618	Missense_Mutation	SNP	G	A	4	35	c.1042C>T	c.(1042-1044)CGT>TGT	p.R348C
Pat_54	Pre-Treatment	CCDC17	149483	37	1	46088654	46088654	Missense_Mutation	SNP	C	T	3	42	c.629G>A	c.(628-630)CGC>CAC	p.R210H
Pat_54	Pre-Treatment	DAB1	1600	37	1	57476832	57476832	Missense_Mutation	SNP	C	T	93	96	c.1558G>A	c.(1558-1560)GAA>AAA	p.E520K
Pat_54	Pre-Treatment	PALMD	54873	37	1	100155377	100155377	Missense_Mutation	SNP	C	T	62	79	c.1561C>T	c.(1561-1563)CCA>TCA	p.P521S
Pat_54	Pre-Treatment	C1orf103	55791	37	1	111506306	111506306	Nonsense_Mutation	SNP	G	T	4	21	c.5C>A	c.(4-6)TCA>TAA	p.S2*
Pat_54	Pre-Treatment	AMPD1	270	37	1	115217461	115217462	Missense_Mutation	DNP	GG	AA	34	51	c.1711_1712CC>TT	c.(1711-1713)CCT>TTT	p.P571F
Pat_54	Pre-Treatment	RORC	6097	37	1	151780010	151780010	Missense_Mutation	SNP	G	A	4	63	c.1495C>T	c.(1495-1497)CCT>TCT	p.P499S
Pat_54	Pre-Treatment	TCHHL1	126637	37	1	152060576	152060576	Missense_Mutation	SNP	A	G	59	56	c.44T>C	c.(43-45)TTC>TCC	p.F15S
Pat_54	Pre-Treatment	CD1C	911	37	1	158263018	158263018	Missense_Mutation	SNP	G	A	126	197	c.906G>A	c.(904-906)ATG>ATA	p.M302I
Pat_54	Pre-Treatment	PBX1	5087	37	1	164769081	164769081	Missense_Mutation	SNP	C	T	3	38	c.656C>T	c.(655-657)ACG>ATG	p.T219M
Pat_54	Pre-Treatment	HMCN1	83872	37	1	186077644	186077644	Missense_Mutation	SNP	G	A	75	94	c.10904G>A	c.(10903-10905)CGG>CAG	p.R3635Q
Pat_54	Pre-Treatment	OPTC	26254	37	1	203467929	203467929	Missense_Mutation	SNP	G	A	4	79	c.491G>A	c.(490-492)CGC>CAC	p.R164H
Pat_54	Pre-Treatment	SLC41A1	254428	37	1	205768949	205768949	Nonsense_Mutation	SNP	C	A	4	27	c.490G>T	c.(490-492)GGA>TGA	p.G164*
Pat_54	Pre-Treatment	TLR5	7100	37	1	223285778	223285778	Missense_Mutation	SNP	G	A	26	31	c.596C>T	c.(595-597)TCC>TTC	p.S199F
Pat_54	Pre-Treatment	PCNXL2	80003	37	1	233134884	233134884	Missense_Mutation	SNP	C	T	13	27	c.5570G>A	c.(5569-5571)AGA>AAA	p.R1857K
Pat_54	Pre-Treatment	CEP170	9859	37	1	243328992	243328992	Missense_Mutation	SNP	G	A	77	592	c.2270C>T	c.(2269-2271)GCT>GTT	p.A757V
Pat_54	Pre-Treatment	KIF26B	55083	37	1	245851056	245851056	Missense_Mutation	SNP	C	T	2	1	c.4771C>T	c.(4771-4773)CGG>TGG	p.R1591W
Pat_54	Pre-Treatment	OR2W3	343171	37	1	248059147	248059147	Missense_Mutation	SNP	G	A	32	78	c.259G>A	c.(259-261)GGA>AGA	p.G87R
Pat_54	Pre-Treatment	OR2L8	391190	37	1	248112588	248112588	Missense_Mutation	SNP	G	A	107	192	c.429G>A	c.(427-429)ATG>ATA	p.M143I
Pat_54	Pre-Treatment	MLLT10	8028	37	10	22016848	22016848	Missense_Mutation	SNP	T	A	41	69	c.2102T>A	c.(2101-2103)CTC>CAC	p.L701H
Pat_54	Pre-Treatment	HSD17B7P2	158160	37	10	38654432	38654432	Missense_Mutation	SNP	A	G	5	92	c.524A>G	c.(523-525)AAT>AGT	p.N175S
Pat_54	Pre-Treatment	TACR2	6865	37	10	71175934	71175934	Missense_Mutation	SNP	G	A	4	45	c.146C>T	c.(145-147)ACG>ATG	p.T49M

Pat_54	Pre-Treatment	CDH23	64072	37	10	73562965	73562965	Splice_Site	SNP	G	C	2	2	c.7661_splice	c.e53-1	p.E2554_splice
Pat_54	Pre-Treatment	MYOF	26509	37	10	95132803	95132803	Missense_Mutation	SNP	G	A	4	88	c.2341C>T	c.(2341-2343)CGG>TGG	p.R781W
Pat_54	Pre-Treatment	PLCE1	51196	37	10	95931110	95931110	Missense_Mutation	SNP	C	T	73	29	c.1666C>T	c.(1666-1668)CTT>TTT	p.L556F
Pat_54	Pre-Treatment	ENTPD1	953	37	10	97607282	97607282	Missense_Mutation	SNP	A	G	4	71	c.893A>G	c.(892-894)AAG>AGG	p.K298R
Pat_54	Pre-Treatment	PDZD7	79955	37	10	102780377	102780377	Missense_Mutation	SNP	C	T	3	25	c.926G>A	c.(925-927)CGA>CAA	p.R309Q
Pat_54	Pre-Treatment	HABP2	3026	37	10	115343993	115343993	Missense_Mutation	SNP	C	T	35	14	c.1324C>T	c.(1324-1326)CCC>TCC	p.P442S
Pat_54	Pre-Treatment	VWA2	340706	37	10	116038556	116038556	Nonsense_Mutation	SNP	G	A	4	34	c.779G>A	c.(778-780)TGG>TAG	p.W260*
Pat_54	Pre-Treatment	C10orf82	143379	37	10	118424324	118424324	Missense_Mutation	SNP	A	T	83	21	c.409T>A	c.(409-411)TTC>ATC	p.F137I
Pat_54	Pre-Treatment	SLC17A6	57084	37	11	22380960	22380960	Missense_Mutation	SNP	G	A	18	33	c.460G>A	c.(460-462)GTT>ATT	p.V154I
Pat_54	Pre-Treatment	FADS2	9415	37	11	61605353	61605353	Missense_Mutation	SNP	G	A	4	42	c.311G>A	c.(310-312)GGC>GAC	p.G104D
Pat_54	Pre-Treatment	WDR74	54663	37	11	62607032	62607032	Missense_Mutation	SNP	G	A	6	125	c.11C>T	c.(10-12)GCT>GTT	p.A4V
Pat_54	Pre-Treatment	C11orf2	738	37	11	64878928	64878928	Missense_Mutation	SNP	T	C	43	41	c.2218T>C	c.(2218-2220)TGG>CGG	p.W740R
Pat_54	Pre-Treatment	CATSPER1	117144	37	11	65792842	65792842	Missense_Mutation	SNP	C	T	35	16	c.1009G>A	c.(1009-1011)GAT>AAT	p.D337N
Pat_54	Pre-Treatment	KRTAP5-9	3846	37	11	71259984	71259984	Missense_Mutation	SNP	C	T	47	89	c.281C>T	c.(280-282)TCA>TTA	p.S94L
Pat_54	Pre-Treatment	PAAF1	80227	37	11	73610270	73610270	Missense_Mutation	SNP	C	T	4	83	c.362C>T	c.(361-363)GCT>GTT	p.A121V
Pat_54	Pre-Treatment	RNF169	254225	37	11	74547747	74547747	Missense_Mutation	SNP	G	A	4	91	c.2099G>A	c.(2098-2100)CGG>CAG	p.R700Q
Pat_54	Pre-Treatment	CREBZF	58487	37	11	85375769	85375769	Missense_Mutation	SNP	G	A	22	21	c.151C>T	c.(151-153)CCC>TCC	p.P51S
Pat_54	Pre-Treatment	FOLH1B	219595	37	11	89395322	89395322	Translation_Start_Site	SNP	C	T	7	64	c.-93C>T	c.(-95--91)TACGC>TATGC	
Pat_54	Pre-Treatment	AMOTL1	154810	37	11	94599225	94599225	Missense_Mutation	SNP	G	A	4	92	c.2380G>A	c.(2380-2382)GTT>ATT	p.V794I
Pat_54	Pre-Treatment	HINFP	25988	37	11	119002563	119002563	Missense_Mutation	SNP	C	T	4	48	c.547C>T	c.(547-549)CGC>TGC	p.R183C
Pat_54	Pre-Treatment	CACNA1C	775	37	12	2786272	2786272	Missense_Mutation	SNP	C	T	13	32	c.4985C>T	c.(4984-4986)ACC>ATC	p.T1662I
Pat_54	Pre-Treatment	NDUFA9	4704	37	12	4796218	4796218	Missense_Mutation	SNP	C	T	4	44	c.1078C>T	c.(1078-1080)CGC>TGC	p.R360C
Pat_54	Pre-Treatment	CD163	9332	37	12	7654044	7654044	Missense_Mutation	SNP	C	T	66	118	c.148G>A	c.(148-150)GAG>AAG	p.E50K
Pat_54	Pre-Treatment	STYK1	55359	37	12	10783893	10783893	Missense_Mutation	SNP	G	A	22	68	c.202C>T	c.(202-204)CCT>TCT	p.P68S
Pat_54	Pre-Treatment	GUCY2C	2984	37	12	14836145	14836145	Missense_Mutation	SNP	C	T	53	51	c.442G>A	c.(442-444)GGA>AGA	p.G148R
Pat_54	Pre-Treatment	GRASP	160622	37	12	52408555	52408555	Missense_Mutation	SNP	C	T	2	0	c.760C>T	c.(760-762)CCG>TCG	p.P254S
Pat_54	Pre-Treatment	KIAA0748	9840	37	12	55357630	55357630	Missense_Mutation	SNP	C	T	53	68	c.551G>A	c.(550-552)CGA>CAA	p.R184Q
Pat_54	Pre-Treatment	FAM119B	25895	37	12	58174134	58174134	Missense_Mutation	SNP	G	A	4	64	c.386G>A	c.(385-387)CGT>CAT	p.R129H
Pat_54	Pre-Treatment	SRGAP1	57522	37	12	64456734	64456734	Missense_Mutation	SNP	C	A	4	62	c.839C>A	c.(838-840)GCC>GAC	p.A280D
Pat_54	Pre-Treatment	LEMD3	23592	37	12	65639998	65639998	Nonsense_Mutation	SNP	C	T	113	92	c.2629C>T	c.(2629-2631)CAG>TAG	p.Q877*
Pat_54	Pre-Treatment	ANO4	121601	37	12	101510497	101510497	Nonsense_Mutation	SNP	C	T	91	17	c.2491C>T	c.(2491-2493)CGA>TGA	p.R831*
Pat_54	Pre-Treatment	ASCL1	429	37	12	103352363	103352363	Missense_Mutation	SNP	A	T	7	1	c.341A>T	c.(340-342)CAG>CTG	p.Q114L
Pat_54	Pre-Treatment	MYL2	4633	37	12	111348978	111348978	Missense_Mutation	SNP	A	G	66	114	c.404T>C	c.(403-405)GTT>GCT	p.V135A
Pat_54	Pre-Treatment	ALDH2	217	37	12	112241685	112241685	Nonsense_Mutation	SNP	G	T	4	43	c.1429G>T	c.(1429-1431)GGA>TGA	p.G477*
Pat_54	Pre-Treatment	C12orf51	283450	37	12	112703772	112703772	Missense_Mutation	SNP	C	A	4	47	c.1112G>T	c.(1111-1113)GGA>GTA	p.G371V
Pat_54	Pre-Treatment	OAS2	4939	37	12	113435446	113435446	Missense_Mutation	SNP	C	T	26	32	c.749C>T	c.(748-750)ACC>ATC	p.T250I
Pat_54	Pre-Treatment	DHX37	57647	37	12	125465142	125465142	Missense_Mutation	SNP	G	A	3	26	c.632C>T	c.(631-633)CCG>CTG	p.P211L
Pat_54	Pre-Treatment	CKAP2	26586	37	13	53035029	53035029	Splice_Site	SNP	A	T	5	71	c.156_splice	c.e3-2	p.S52_splice
Pat_54	Pre-Treatment	LOC647288	647288	37	13	75814354	75814354	Missense_Mutation	SNP	C	G	9	104	c.123G>C	c.(121-123)TGG>TGC	p.W41C
Pat_54	Pre-Treatment	OR4K5	79317	37	14	20389181	20389181	Missense_Mutation	SNP	G	A	70	250	c.416G>A	c.(415-417)AGG>AAG	p.R139K
Pat_54	Pre-Treatment	CLEC14A	161198	37	14	38724021	38724021	Missense_Mutation	SNP	C	A	4	32	c.1207G>T	c.(1207-1209)GTG>TTG	p.V403L
Pat_54	Pre-Treatment	ARID4A	5926	37	14	58831016	58831016	Missense_Mutation	SNP	C	T	56	150	c.2209C>T	c.(2209-2211)CCA>TCA	p.P737S
Pat_54	Pre-Treatment	AHNAK2	113146	37	14	105416167	105416167	Missense_Mutation	SNP	G	A	56	74	c.5621C>T	c.(5620-5622)CCG>CTG	p.P1874L
Pat_54	Pre-Treatment	MKRN3	7681	37	15	23810949	23810949	Missense_Mutation	SNP	C	T	9	2	c.20C>T	c.(19-21)CCC>CTC	p.P7L
Pat_54	Pre-Treatment	DUOXA1	90527	37	15	45412968	45412968	Missense_Mutation	SNP	A	G	79	114	c.376T>C	c.(376-378)TAC>CAC	p.Y126H
Pat_54	Pre-Treatment	SLC27A2	11001	37	15	50489714	50489714	Missense_Mutation	SNP	G	A	45	64	c.496G>A	c.(496-498)GAA>AAA	p.E166K
Pat_54	Pre-Treatment	DMXL2	23312	37	15	51763533	51763533	Missense_Mutation	SNP	G	A	117	197	c.7276C>T	c.(7276-7278)CCT>TCT	p.P2426S

Pat_54	Pre-Treatment	GRINL1A	81488	37	15	58001466	58001466	Missense_Mutation	SNP	G	A	4	77	c.668G>A	c.(667-669)AGT>AAT	p.S223N
Pat_54	Pre-Treatment	ALDH1A2	8854	37	15	58258016	58258016	Missense_Mutation	SNP	G	C	4	77	c.808C>G	c.(808-810)CTT>GTT	p.L270V
Pat_54	Pre-Treatment	MEGF11	84465	37	15	66249895	66249895	Missense_Mutation	SNP	G	A	4	25	c.1277C>T	c.(1276-1278)CCG>CTG	p.P426L
Pat_54	Pre-Treatment	IQCH	64799	37	15	67713708	67713708	Missense_Mutation	SNP	A	T	34	51	c.2298A>T	c.(2296-2298)AAA>AAT	p.K766N
Pat_54	Pre-Treatment	CD276	80381	37	15	73995154	73995154	Missense_Mutation	SNP	G	A	11	17	c.460G>A	c.(460-462)GAC>AAC	p.D154N
Pat_54	Pre-Treatment	CLK3	1198	37	15	74922126	74922126	Missense_Mutation	SNP	C	A	4	22	c.1819C>A	c.(1819-1821)CAG>AAG	p.Q607K
Pat_54	Pre-Treatment	DET1	55070	37	15	89056264	89056265	Missense_Mutation	DNP	GG	AA	17	56	.1570_1571CC>T	c.(1570-1572)CCT>TTT	p.P524F
Pat_54	Pre-Treatment	CRAMP1L	57585	37	16	1719001	1719001	Splice_Site	SNP	G	A	4	34	c.3335_splice	c.e18-1	p.G1112_splice
Pat_54	Pre-Treatment	GRIN2A	2903	37	16	9857692	9857692	Missense_Mutation	SNP	C	T	30	42	c.3709G>A	c.(3709-3711)GAT>AAT	p.D1237N
Pat_54	Pre-Treatment	SCNN1G	6340	37	16	23200768	23200768	Missense_Mutation	SNP	C	T	63	101	c.394C>T	c.(394-396)CCA>TCA	p.P132S
Pat_54	Pre-Treatment	ZNF319	57567	37	16	58031403	58031403	Missense_Mutation	SNP	C	T	4	83	c.767G>A	c.(766-768)CGG>CAG	p.R256Q
Pat_54	Pre-Treatment	FUK	197258	37	16	70508488	70508488	Missense_Mutation	SNP	C	G	2	3	c.2046C>G	c.(2044-2046)ATC>ATG	p.I682M
Pat_54	Pre-Treatment	CHST4	10164	37	16	71570893	71570893	Missense_Mutation	SNP	G	A	37	35	c.313G>A	c.(313-315)GAC>AAC	p.D105N
Pat_54	Pre-Treatment	LRRC50	123872	37	16	84203728	84203728	Missense_Mutation	SNP	G	A	28	37	c.1294G>A	c.(1294-1296)GAG>AAG	p.E432K
Pat_54	Pre-Treatment	TMEM88	92162	37	17	7758793	7758793	Missense_Mutation	SNP	G	A	4	93	c.241G>A	c.(241-243)GCG>ACG	p.A81T
Pat_54	Pre-Treatment	MYH13	8735	37	17	10215380	10215380	Nonsense_Mutation	SNP	C	T	26	23	c.4379G>A	c.(4378-4380)TGG>TAG	p.W1460*
Pat_54	Pre-Treatment	MYOCD	93649	37	17	12661487	12661487	Missense_Mutation	SNP	C	T	30	60	c.2144C>T	c.(2143-2145)TCA>TTA	p.S715L
Pat_54	Pre-Treatment	MYO15A	51168	37	17	18025416	18025417	Missense_Mutation	DNP	CC	TT	7	27	.3302_3303CC>T	c.(3301-3303)CCC>CTT	p.P1101L
Pat_54	Pre-Treatment	SLFN11	91607	37	17	33690140	33690141	Missense_Mutation	DNP	CC	TT	57	90	c.686_687GG>AA	c.(685-687)AGG>AAA	p.R229K
Pat_54	Pre-Treatment	TCAP	8557	37	17	37821998	37821998	Missense_Mutation	SNP	G	A	3	14	c.140G>A	c.(139-141)AGA>AAA	p.R47K
Pat_54	Pre-Treatment	WIPF2	147179	37	17	38416832	38416832	Nonsense_Mutation	SNP	C	T	82	107	c.109C>T	c.(109-111)CGA>TGA	p.R37*
Pat_54	Pre-Treatment	KPNB1	3837	37	17	45734389	45734389	Nonsense_Mutation	SNP	C	A	4	76	c.446C>A	c.(445-447)TCG>TAG	p.S149*
Pat_54	Pre-Treatment	CD300A	11314	37	17	72469768	72469768	Missense_Mutation	SNP	T	C	4	89	c.134T>C	c.(133-135)CTC>CCC	p.L45P
Pat_54	Pre-Treatment	ST6GALNAC1	55808	37	17	74621474	74621474	Missense_Mutation	SNP	C	T	19	35	c.1741G>A	c.(1741-1743)GAT>AAT	p.D581N
Pat_54	Pre-Treatment	ROCK1	6093	37	18	18564360	18564360	Missense_Mutation	SNP	A	G	62	85	c.2441T>C	c.(2440-2442)TTA>TCA	p.L814S
Pat_54	Pre-Treatment	LAMA3	3909	37	18	21501017	21501017	Missense_Mutation	SNP	C	T	31	52	c.8042C>T	c.(8041-8043)TCG>TTG	p.S2681L
Pat_54	Pre-Treatment	CXXC1	30827	37	18	47812290	47812290	Missense_Mutation	SNP	C	G	4	47	c.468G>C	c.(466-468)CAG>CAC	p.Q156H
Pat_54	Pre-Treatment	LMAN1	3998	37	18	57016392	57016393	Missense_Mutation	DNP	GG	AT	90	162	c.715_716CC>AT	c.(715-717)CCT>ATT	p.P239I
Pat_54	Pre-Treatment	ATP9B	374868	37	18	77134011	77134011	Missense_Mutation	SNP	G	A	4	88	c.3184G>A	c.(3184-3186)GTC>ATC	p.V1062I
Pat_54	Pre-Treatment	NFATC1	4772	37	18	77170984	77170984	Missense_Mutation	SNP	T	C	4	36	c.709T>C	c.(709-711)TCC>CCC	p.S237P
Pat_54	Pre-Treatment	KCNG2	26251	37	18	77659606	77659606	Missense_Mutation	SNP	G	T	4	73	c.1191G>T	c.(1189-1191)ATG>ATT	p.M397I
Pat_54	Pre-Treatment	CSNK1G2	1455	37	19	1980168	1980168	Missense_Mutation	SNP	G	A	29	50	c.1214G>A	c.(1213-1215)AGG>AAG	p.R405K
Pat_54	Pre-Treatment	DOT1L	84444	37	19	2216629	2216629	Missense_Mutation	SNP	C	T	4	71	c.2273C>T	c.(2272-2274)CCG>CTG	p.P758L
Pat_54	Pre-Treatment	NFIC	4782	37	19	3381956	3381956	Missense_Mutation	SNP	G	A	4	95	c.277G>A	c.(277-279)GTG>ATG	p.V93M
Pat_54	Pre-Treatment	INSR	3643	37	19	7168079	7168080	Missense_Mutation	DNP	AA	GG	34	49	.1509_1510TT>C	507-1512)TCTTAC>TCCC	p.Y504H
Pat_54	Pre-Treatment	FBN3	84467	37	19	8183894	8183894	Missense_Mutation	SNP	C	T	3	26	c.3224G>A	c.(3223-3225)TGT>TAT	p.C1075Y
Pat_54	Pre-Treatment	RAD23A	5886	37	19	13060127	13060127	Nonsense_Mutation	SNP	C	T	4	94	c.718C>T	c.(718-720)CAG>TAG	p.Q240*
Pat_54	Pre-Treatment	WIZ	58525	37	19	15537901	15537901	Missense_Mutation	SNP	G	A	4	25	c.1495C>T	c.(1495-1497)CGG>TGG	p.R499W
Pat_54	Pre-Treatment	OR10H5	284433	37	19	15905351	15905351	Missense_Mutation	SNP	C	T	25	42	c.493C>T	c.(493-495)CAC>TAC	p.H165Y
Pat_54	Pre-Treatment	CILP2	148113	37	19	19655285	19655285	Missense_Mutation	SNP	C	T	38	40	c.1931C>T	c.(1930-1932)TCC>TTC	p.S644F
Pat_54	Pre-Treatment	ZNF98	148198	37	19	22574496	22574496	Missense_Mutation	SNP	C	T	81	172	c.1541G>A	c.(1540-1542)GGA>GAA	p.G514E
Pat_54	Pre-Treatment	ZNF536	9745	37	19	31040061	31040061	Missense_Mutation	SNP	G	A	42	64	c.3535G>A	c.(3535-3537)GAT>AAT	p.D1179N
Pat_54	Pre-Treatment	CCDC123	84902	37	19	33450921	33450921	Missense_Mutation	SNP	G	A	3	39	c.190C>T	c.(190-192)CGG>TGG	p.R64W
Pat_54	Pre-Treatment	RASGRP4	115727	37	19	38910631	38910631	Missense_Mutation	SNP	G	A	6	47	c.532C>T	c.(532-534)CCC>TCC	p.P178S
Pat_54	Pre-Treatment	RYR1	6261	37	19	38951170	38951170	Missense_Mutation	SNP	T	C	31	66	c.2516T>C	c.(2515-2517)GTG>GCG	p.V839A
Pat_54	Pre-Treatment	LTBP4	8425	37	19	41115562	41115562	Missense_Mutation	SNP	G	T	3	23	c.1754G>T	c.(1753-1755)TGC>TTC	p.C585F
Pat_54	Pre-Treatment	TRAPPC6A	79090	37	19	45668433	45668433	Missense_Mutation	SNP	G	C	2	5	c.104C>G	c.(103-105)TCG>TGG	p.S35W

Pat_54	Pre-Treatment	NOSIP	51070	37	19	50060161	50060161	Missense_Mutation	SNP	C	T	4	11	c.508G>A	c.(508-510)GAA>AAA	p.E170K
Pat_54	Pre-Treatment	NR1H2	7376	37	19	50885834	50885834	Missense_Mutation	SNP	C	T	4	75	c.1361C>T	c.(1360-1362)TCG>TTG	p.S454L
Pat_54	Pre-Treatment	SYT3	84258	37	19	51140638	51140638	Missense_Mutation	SNP	G	A	3	31	c.31C>T	c.(31-33)CGG>TGG	p.R11W
Pat_54	Pre-Treatment	NLRP12	91662	37	19	54308587	54308587	Missense_Mutation	SNP	C	T	50	77	c.2361G>A	c.(2359-2361)ATG>ATA	p.M787I
Pat_54	Pre-Treatment	LILRA2	11027	37	19	55098691	55098691	Missense_Mutation	SNP	G	A	47	60	c.1330G>A	c.(1330-1332)GAT>AAT	p.D444N
Pat_54	Pre-Treatment	NLRP8	126205	37	19	56459510	56459510	Missense_Mutation	SNP	G	C	3	37	c.242G>C	c.(241-243)TGG>TCG	p.W81S
Pat_54	Pre-Treatment	C2orf43	60526	37	2	20939959	20939959	Missense_Mutation	SNP	G	A	59	55	c.475C>T	c.(475-477)CGT>TGT	p.R159C
Pat_54	Pre-Treatment	APOB	338	37	2	21245826	21245826	Missense_Mutation	SNP	C	T	41	62	c.2693G>A	c.(2692-2694)GGG>GAG	p.G898E
Pat_54	Pre-Treatment	SLC4A1AP	22950	37	2	27888056	27888056	Missense_Mutation	SNP	G	T	119	181	c.915G>T	c.(913-915)AAG>AAT	p.K305N
Pat_54	Pre-Treatment	SPR	6697	37	2	73118628	73118628	Missense_Mutation	SNP	T	C	33	55	c.748T>C	c.(748-750)TTC>CTC	p.F250L
Pat_54	Pre-Treatment	TET3	200424	37	2	74328434	74328434	Missense_Mutation	SNP	C	T	3	26	c.4114C>T	c.(4114-4116)CGG>TGG	p.R1372W
Pat_54	Pre-Treatment	KRCC1	51315	37	2	88327862	88327862	Missense_Mutation	SNP	G	A	37	37	c.221C>T	c.(220-222)TCA>TTA	p.S74L
Pat_54	Pre-Treatment	CNGA3	1261	37	2	98996705	98996705	Missense_Mutation	SNP	C	T	4	87	c.283C>T	c.(283-285)CCG>TCG	p.P95S
Pat_54	Pre-Treatment	TBC1D8	11138	37	2	101650113	101650113	Missense_Mutation	SNP	G	A	4	65	c.1666C>T	c.(1666-1668)CGC>TGC	p.R556C
Pat_54	Pre-Treatment	SH3RF3	344558	37	2	109964181	109964181	Missense_Mutation	SNP	G	A	4	35	c.625G>A	c.(625-627)GAA>AAA	p.E209K
Pat_54	Pre-Treatment	INHBB	3625	37	2	121104080	121104080	Missense_Mutation	SNP	G	C	2	6	c.316G>C	c.(316-318)GCC>CCC	p.A106P
Pat_54	Pre-Treatment	LRP1B	53353	37	2	141130635	141130635	Nonsense_Mutation	SNP	C	T	105	156	c.10710G>A	c.(10708-10710)TGG>TGA	p.W3570*
Pat_54	Pre-Treatment	LRP2	4036	37	2	170031891	170031891	Missense_Mutation	SNP	G	A	40	51	c.10580C>T	c.(10579-10581)CCT>CTT	p.P3527L
Pat_54	Pre-Treatment	TTN	7273	37	2	179433220	179433220	Missense_Mutation	SNP	G	T	4	71	c.69935C>A	c.(69934-69936)ACA>AAA	p.T23312K
Pat_54	Pre-Treatment	TTN	7273	37	2	179621344	179621344	Missense_Mutation	SNP	G	A	32	37	c.10346C>T	c.(10345-10347)TCC>TTC	p.S3449F
Pat_54	Pre-Treatment	SATB2	23314	37	2	200233369	200233369	Missense_Mutation	SNP	T	G	60	81	c.659A>C	c.(658-660)CAG>CCG	p.Q220P
Pat_54	Pre-Treatment	TRAK2	66008	37	2	202245723	202245723	Missense_Mutation	SNP	G	A	83	167	c.2288C>T	c.(2287-2289)CCC>CTC	p.P763L
Pat_54	Pre-Treatment	STK36	27148	37	2	219557366	219557366	Missense_Mutation	SNP	C	T	28	51	c.1976C>T	c.(1975-1977)TCC>TTC	p.S659F
Pat_54	Pre-Treatment	ABCB6	10058	37	2	220080797	220080797	Missense_Mutation	SNP	C	A	4	28	c.1076G>T	c.(1075-1077)CGC>CTC	p.R359L
Pat_54	Pre-Treatment	SPHKAP	80309	37	2	228882449	228882449	Missense_Mutation	SNP	C	T	43	54	c.3121G>A	c.(3121-3123)GAA>AAA	p.E1041K
Pat_54	Pre-Treatment	GPR35	2859	37	2	241569971	241569971	Missense_Mutation	SNP	G	A	13	13	c.602G>A	c.(601-603)AGG>AAG	p.R201K
Pat_54	Pre-Treatment	FRG1B	284802	37	20	29628236	29628236	Missense_Mutation	SNP	G	C	14	549	c.148G>C	c.(148-150)GCT>CCT	p.A50P
Pat_54	Pre-Treatment	DNMT3B	1789	37	20	31387093	31387093	Missense_Mutation	SNP	G	A	4	41	c.1718G>A	c.(1717-1719)CGG>CAG	p.R573Q
Pat_54	Pre-Treatment	EPB41L1	2036	37	20	34763552	34763552	Missense_Mutation	SNP	C	T	43	52	c.257C>T	c.(256-258)TCG>TTG	p.S86L
Pat_54	Pre-Treatment	C20orf132	140699	37	20	35749373	35749373	Missense_Mutation	SNP	C	T	17	37	c.2073G>A	c.(2071-2073)ATG>ATA	p.M691I
Pat_54	Pre-Treatment	NCOA3	8202	37	20	46256364	46256364	Missense_Mutation	SNP	C	T	100	140	c.592C>T	c.(592-594)CGT>TGT	p.R198C
Pat_54	Pre-Treatment	LAMA5	3911	37	20	60887493	60887493	Missense_Mutation	SNP	G	A	3	21	c.9323C>T	c.(9322-9324)ACG>ATG	p.T3108M
Pat_54	Pre-Treatment	TPTE	7179	37	21	10914373	10914373	Missense_Mutation	SNP	C	T	12	70	c.1346G>A	c.(1345-1347)GGA>GAA	p.G449E
Pat_54	Pre-Treatment	NRIP1	8204	37	21	16338494	16338494	Missense_Mutation	SNP	G	A	4	76	c.2020C>T	c.(2020-2022)CTC>TTC	p.L674F
Pat_54	Pre-Treatment	KRTAP24-1	643803	37	21	31654844	31654844	Missense_Mutation	SNP	C	A	6	137	c.407G>T	c.(406-408)CGA>CTA	p.R136L
Pat_54	Pre-Treatment	ERG	2078	37	21	39755465	39755465	Missense_Mutation	SNP	G	A	6	33	c.1321C>T	c.(1321-1323)CAC>TAC	p.H441Y
Pat_54	Pre-Treatment	UBASH3A	53347	37	21	43862610	43862610	Missense_Mutation	SNP	T	G	76	81	c.1535T>G	c.(1534-1536)TTT>TGT	p.F512C
Pat_54	Pre-Treatment	SLC25A18	83733	37	22	18072870	18072870	Nonsense_Mutation	SNP	G	A	21	52	c.816G>A	c.(814-816)TGG>TGA	p.W272*
Pat_54	Pre-Treatment	BCR	613	37	22	23524202	23524202	Missense_Mutation	SNP	G	T	4	47	c.1055G>T	c.(1054-1056)CGC>CTC	p.R352L
Pat_54	Pre-Treatment	MYO18B	84700	37	22	26423117	26423117	Missense_Mutation	SNP	G	A	26	31	c.7177G>A	c.(7177-7179)GAT>AAT	p.D2393N
Pat_54	Pre-Treatment	MYH9	4627	37	22	36708162	36708162	Missense_Mutation	SNP	G	A	48	77	c.1660C>T	c.(1660-1662)CCC>TCC	p.P554S
Pat_54	Pre-Treatment	CACNG2	10369	37	22	36962426	36962426	Missense_Mutation	SNP	C	T	31	69	c.410G>A	c.(409-411)AGT>AAT	p.S137N
Pat_54	Pre-Treatment	TRIOBP	11078	37	22	38120833	38120833	Missense_Mutation	SNP	C	T	66	85	c.2270C>T	c.(2269-2271)TCC>TTC	p.S757F
Pat_54	Pre-Treatment	KDELR3	11015	37	22	38878539	38878539	Nonstop_Mutation	SNP	T	C	59	85	c.643T>C	c.(643-645)TGA>CGA	p.*215R
Pat_54	Pre-Treatment	ACO2	50	37	22	41923423	41923423	Missense_Mutation	SNP	C	A	26	50	c.2085C>A	c.(2083-2085)CAC>CAA	p.H695Q
Pat_54	Pre-Treatment	TSPO	706	37	22	43558971	43558971	Missense_Mutation	SNP	C	T	2	2	c.203C>T	c.(202-204)GCG>GTG	p.A68V
Pat_54	Pre-Treatment	PNPLA5	150379	37	22	44277442	44277442	Missense_Mutation	SNP	T	A	3	10	c.1195A>T	c.(1195-1197)ATC>TTC	p.I399F

Pat_54	Pre-Treatment	ZNF385D	79750	37	3	21552450	21552450	Missense_Mutation	SNP	C	T	36	55	c.342G>A	c.(340-342)ATG>ATA	p.M114I
Pat_54	Pre-Treatment	XIRP1	165904	37	3	39230164	39230164	Missense_Mutation	SNP	C	T	4	84	c.773G>A	c.(772-774)CGG>CAG	p.R258Q
Pat_54	Pre-Treatment	AMT	275	37	3	49456545	49456545	Missense_Mutation	SNP	C	G	3	32	c.736G>C	c.(736-738)GCT>CCT	p.A246P
Pat_54	Pre-Treatment	GRM2	2912	37	3	51743354	51743354	Missense_Mutation	SNP	C	T	24	23	c.355C>T	c.(355-357)CAC>TAC	p.H119Y
Pat_54	Pre-Treatment	DNAH1	25981	37	3	52415658	52415658	Missense_Mutation	SNP	G	A	8	4	c.7611G>A	c.(7609-7611)ATG>ATA	p.M2537I
Pat_54	Pre-Treatment	IL17RD	54756	37	3	57143616	57143616	Missense_Mutation	SNP	G	A	50	86	c.499C>T	c.(499-501)CCT>TCT	p.P167S
Pat_54	Pre-Treatment	FLNB	2317	37	3	58109342	58109342	Missense_Mutation	SNP	C	T	53	67	c.3649C>T	c.(3649-3651)CCC>TCC	p.P1217S
Pat_54	Pre-Treatment	MAGI1	9223	37	3	65456160	65456160	Splice_Site	SNP	C	G	5	58	c.758_splice	c.e5-1	p.A253_splice
Pat_54	Pre-Treatment	CCDC80	151887	37	3	112358233	112358233	Missense_Mutation	SNP	C	T	4	53	c.520G>A	c.(520-522)GAT>AAT	p.D174N
Pat_54	Pre-Treatment	PLS1	5357	37	3	142389898	142389898	Missense_Mutation	SNP	G	A	120	166	c.298G>A	c.(298-300)GAA>AAA	p.E100K
Pat_54	Pre-Treatment	GK2	2712	37	4	80329072	80329072	Missense_Mutation	SNP	C	T	79	124	c.283G>A	c.(283-285)GAA>AAA	p.E95K
Pat_54	Pre-Treatment	HERC6	55008	37	4	89311882	89311882	Missense_Mutation	SNP	C	T	4	39	c.515C>T	c.(514-516)CCG>CTG	p.P172L
Pat_54	Pre-Treatment	MMRN1	22915	37	4	90816651	90816651	Nonsense_Mutation	SNP	C	T	44	45	c.529C>T	c.(529-531)CGA>TGA	p.R177*
Pat_54	Pre-Treatment	FABP2	2169	37	4	120241839	120241839	Missense_Mutation	SNP	C	T	48	89	c.226G>A	c.(226-228)GGA>AGA	p.G76R
Pat_54	Pre-Treatment	FAT4	79633	37	4	126237652	126237652	Missense_Mutation	SNP	G	T	6	130	c.86G>T	c.(85-87)TGG>TTG	p.W29L
Pat_54	Pre-Treatment	GRIA2	2891	37	4	158281253	158281253	Missense_Mutation	SNP	C	T	64	75	c.2249C>T	c.(2248-2250)TCC>TTC	p.S750F
Pat_54	Pre-Treatment	C4orf45	152940	37	4	159836407	159836407	Missense_Mutation	SNP	C	A	4	39	c.461G>T	c.(460-462)TGG>TTG	p.W154L
Pat_54	Pre-Treatment	MTNR1A	4543	37	4	187454897	187454897	Nonsense_Mutation	SNP	C	T	70	66	c.999G>A	c.(997-999)TGG>TGA	p.W333*
Pat_54	Pre-Treatment	FRG1	2483	37	4	190878596	190878596	Missense_Mutation	SNP	G	A	8	225	c.476G>A	c.(475-477)TGC>TAC	p.C159Y
Pat_54	Pre-Treatment	TUBB4Q	56604	37	4	190904535	190904535	Missense_Mutation	SNP	G	A	22	4	c.445C>T	c.(445-447)CTT>TTT	p.L149F
Pat_54	Pre-Treatment	DNAH5	1767	37	5	13883031	13883031	Missense_Mutation	SNP	G	T	4	63	c.3156C>A	c.(3154-3156)AGC>AGA	p.S1052R
Pat_54	Pre-Treatment	SLC45A2	51151	37	5	33984420	33984420	Missense_Mutation	SNP	G	A	3	14	c.269C>T	c.(268-270)TCG>TTG	p.S90L
Pat_54	Pre-Treatment	PARP8	79668	37	5	50092850	50092850	Missense_Mutation	SNP	G	A	4	68	c.1463G>A	c.(1462-1464)CGT>CAT	p.R488H
Pat_54	Pre-Treatment	SNX18	112574	37	5	53815031	53815031	Missense_Mutation	SNP	G	A	4	33	c.1249G>A	c.(1249-1251)GCT>ACT	p.A417T
Pat_54	Pre-Treatment	PCSK1	5122	37	5	95728961	95728961	Missense_Mutation	SNP	C	T	46	16	c.2006G>A	c.(2005-2007)CGA>CAA	p.R669Q
Pat_54	Pre-Treatment	SHROOM1	134549	37	5	132159156	132159156	Missense_Mutation	SNP	C	G	2	4	c.2012G>C	c.(2011-2013)CGG>CCG	p.R671P
Pat_54	Pre-Treatment	KLHL3	26249	37	5	136961519	136961519	Missense_Mutation	SNP	G	A	4	80	c.1658C>T	c.(1657-1659)TCG>TTG	p.S553L
Pat_54	Pre-Treatment	NRG2	9542	37	5	139228173	139228173	Missense_Mutation	SNP	C	T	2	0	c.1882G>A	c.(1882-1884)GCC>ACC	p.A628T
Pat_54	Pre-Treatment	JAKMIP2	9832	37	5	147051353	147051353	Missense_Mutation	SNP	C	T	19	9	c.17G>A	c.(16-18)CGA>CAA	p.R6Q
Pat_54	Pre-Treatment	C5orf40	408263	37	5	156769905	156769905	Missense_Mutation	SNP	C	A	4	32	c.640G>T	c.(640-642)GAC>TAC	p.D214Y
Pat_54	Pre-Treatment	STK10	6793	37	5	171520724	171520724	Missense_Mutation	SNP	C	T	3	26	c.1246G>A	c.(1246-1248)GTG>ATG	p.V416M
Pat_54	Pre-Treatment	UIMC1	51720	37	5	176334117	176334117	Missense_Mutation	SNP	G	A	25	17	c.1910C>T	c.(1909-1911)TCA>TTA	p.S637L
Pat_54	Pre-Treatment	SLC34A1	6569	37	5	176825036	176825036	Missense_Mutation	SNP	C	T	4	89	c.1669C>T	c.(1669-1671)CTC>TTC	p.L557F
Pat_54	Pre-Treatment	FARS2	10667	37	6	5771589	5771589	Missense_Mutation	SNP	G	A	25	64	c.1283G>A	c.(1282-1284)AGA>AAA	p.R428K
Pat_54	Pre-Treatment	TRIM15	89870	37	6	30139833	30139833	Missense_Mutation	SNP	G	A	2	3	c.1105G>A	c.(1105-1107)GGG>AGG	p.G369R
Pat_54	Pre-Treatment	MICB	4277	37	6	31473468	31473468	Missense_Mutation	SNP	G	A	29	38	c.145G>A	c.(145-147)GGA>AGA	p.G49R
Pat_54	Pre-Treatment	LYPLA2P1	653639	37	6	33333333	33333333	Missense_Mutation	SNP	G	A	6	17	c.673C>T	c.(673-675)CCT>TCT	p.P225S
Pat_54	Pre-Treatment	DNAH8	1769	37	6	38905839	38905839	Missense_Mutation	SNP	G	A	4	67	c.11002G>A	c.(11002-11004)GCA>ACA	p.A3668T
Pat_54	Pre-Treatment	GPR115	221393	37	6	47682606	47682606	Missense_Mutation	SNP	G	A	100	101	c.1625G>A	c.(1624-1626)GGC>GAC	p.G542D
Pat_54	Pre-Treatment	COL12A1	1303	37	6	75829185	75829185	Missense_Mutation	SNP	G	A	58	20	c.7091C>T	c.(7090-7092)TCA>TTA	p.S2364L
Pat_54	Pre-Treatment	FABP7	2173	37	6	123102265	123102265	Missense_Mutation	SNP	C	A	4	87	c.274C>A	c.(274-276)CTT>ATT	p.L92I
Pat_54	Pre-Treatment	MAP7	9053	37	6	136682273	136682273	Missense_Mutation	SNP	G	A	3	35	c.1571C>T	c.(1570-1572)ACG>ATG	p.T524M
Pat_54	Pre-Treatment	ADAT2	134637	37	6	143759801	143759801	Missense_Mutation	SNP	G	A	94	34	c.127C>T	c.(127-129)CCT>TCT	p.P43S
Pat_54	Pre-Treatment	GRM1	2911	37	6	146720715	146720715	Missense_Mutation	SNP	G	A	4	39	c.2540G>A	c.(2539-2541)CGC>CAC	p.R847H
Pat_54	Pre-Treatment	IGF2R	3482	37	6	160461747	160461747	Missense_Mutation	SNP	C	T	4	93	c.1471C>T	c.(1471-1473)CGC>TGC	p.R491C
Pat_54	Pre-Treatment	MLLT4	4301	37	6	168316019	168316019	Missense_Mutation	SNP	C	T	3	28	c.2447C>T	c.(2446-2448)GCG>GTG	p.A816V
Pat_54	Pre-Treatment	DGKB	1607	37	7	14647077	14647077	Missense_Mutation	SNP	C	T	69	62	c.1418G>A	c.(1417-1419)GGA>GAA	p.G473E

Pat_54	Pre-Treatment	UPP1	7378	37	7	48139293	48139293	Missense_Mutation	SNP	C	T	76	83	c.71C>T	c.(70-72)CCA>CTA	p.P24L
Pat_54	Pre-Treatment	ABCA13	154664	37	7	48314172	48314172	Missense_Mutation	SNP	G	A	99	82	c.4909G>A	c.(4909-4911)GAT>AAT	p.D1637N
Pat_54	Pre-Treatment	HGF	3082	37	7	81372774	81372774	Missense_Mutation	SNP	C	T	27	39	c.760G>A	c.(760-762)GGC>AGC	p.G254S
Pat_54	Pre-Treatment	CUX1	1523	37	7	101882615	101882615	Missense_Mutation	SNP	G	A	4	46	c.3638G>A	c.(3637-3639)CGG>CAG	p.R1213Q
Pat_54	Pre-Treatment	PPP1R3A	5506	37	7	113518778	113518778	Missense_Mutation	SNP	C	T	28	31	c.2369G>A	c.(2368-2370)CGA>CAA	p.R790Q
Pat_54	Pre-Treatment	KCND2	3751	37	7	119915104	119915104	Missense_Mutation	SNP	C	T	44	51	c.418C>T	c.(418-420)CGC>TGC	p.R140C
Pat_54	Pre-Treatment	C7orf58	79974	37	7	120911459	120911459	Missense_Mutation	SNP	G	A	93	127	c.2843G>A	c.(2842-2844)GGG>GAG	p.G948E
Pat_54	Pre-Treatment	BRAF	673	37	7	140453136	140453136	Missense_Mutation	SNP	A	T	79	97	c.1799T>A	c.(1798-1800)GTG>GAG	p.V600E
Pat_54	Pre-Treatment	PRSS37	136242	37	7	141536292	141536292	Missense_Mutation	SNP	C	T	39	43	c.611G>A	c.(610-612)GGA>GAA	p.G204E
Pat_54	Pre-Treatment	OR9A2	135924	37	7	142724121	142724121	Missense_Mutation	SNP	G	C	31	36	c.99C>G	c.(97-99)TTC>TTG	p.F33L
Pat_54	Pre-Treatment	OR2F2	135948	37	7	143633062	143633062	Missense_Mutation	SNP	C	T	4	93	c.737C>T	c.(736-738)ACG>ATG	p.T246M
Pat_54	Pre-Treatment	TNFRSF10D	8793	37	8	23012464	23012464	Missense_Mutation	SNP	C	T	10	23	c.179G>A	c.(178-180)CGG>CAG	p.R60Q
Pat_54	Pre-Treatment	LOXL2	4017	37	8	23191094	23191095	Missense_Mutation	DNP	GG	TA	27	22	c.785_786CC>TA	c.(784-786)TCC>TTA	p.S262L
Pat_54	Pre-Treatment	PURG	29942	37	8	30889547	30889547	Missense_Mutation	SNP	C	T	5	89	c.752G>A	c.(751-753)CGA>CAA	p.R251Q
Pat_54	Pre-Treatment	PMP2	5375	37	8	82357090	82357090	Missense_Mutation	SNP	C	T	184	91	c.208G>A	c.(208-210)GAA>AAA	p.E70K
Pat_54	Pre-Treatment	CA1	759	37	8	86240815	86240815	Missense_Mutation	SNP	C	T	310	131	c.760G>A	c.(760-762)GGC>AGC	p.G254S
Pat_54	Pre-Treatment	CDH17	1015	37	8	95164286	95164286	Missense_Mutation	SNP	G	A	37	151	c.1606C>T	c.(1606-1608)CCT>TCT	p.P536S
Pat_54	Pre-Treatment	MTERFD1	51001	37	8	97258585	97258585	Missense_Mutation	SNP	C	T	110	70	c.775G>A	c.(775-777)GAT>AAT	p.D259N
Pat_54	Pre-Treatment	TRPS1	7227	37	8	116632264	116632264	Missense_Mutation	SNP	G	A	53	125	c.22C>T	c.(22-24)CCT>TCT	p.P8S
Pat_54	Pre-Treatment	DEPDC6	64798	37	8	121019091	121019091	Missense_Mutation	SNP	C	T	133	61	c.973C>T	c.(973-975)CCG>TCG	p.P325S
Pat_54	Pre-Treatment	NFKBIL2	4796	37	8	145661076	145661076	Missense_Mutation	SNP	G	A	4	76	c.2740C>T	c.(2740-2742)CCC>TCC	p.P914S
Pat_54	Pre-Treatment	SLC1A1	6505	37	9	4572341	4572341	Missense_Mutation	SNP	C	G	329	46	c.720C>G	c.(718-720)TTC>TTG	p.F240L
Pat_54	Pre-Treatment	RANBP6	26953	37	9	6012658	6012658	Missense_Mutation	SNP	T	G	3	20	c.2950A>C	c.(2950-2952)ATA>CTA	p.I984L
Pat_54	Pre-Treatment	CER1	9350	37	9	14722348	14722348	Missense_Mutation	SNP	C	T	31	5	c.323G>A	c.(322-324)GGG>GAG	p.G108E
Pat_54	Pre-Treatment	TAF1L	138474	37	9	32631815	32631815	Missense_Mutation	SNP	G	A	3	39	c.3763C>T	c.(3763-3765)CGG>TGG	p.R1255W
Pat_54	Pre-Treatment	PIGO	84720	37	9	35090224	35090224	Missense_Mutation	SNP	G	A	4	82	c.2908C>T	c.(2908-2910)CGG>TGG	p.R970W
Pat_54	Pre-Treatment	LOC286238	286238	37	9	91262333	91262333	Missense_Mutation	SNP	C	T	14	13	c.310G>A	c.(310-312)GAA>AAA	p.E104K
Pat_54	Pre-Treatment	ROR2	4920	37	9	94486974	94486974	Missense_Mutation	SNP	G	A	3	29	c.1802C>T	c.(1801-1803)GCG>GTG	p.A601V
Pat_54	Pre-Treatment	OR13C3	138803	37	9	107298641	107298641	Missense_Mutation	SNP	G	A	119	160	c.454C>T	c.(454-456)CGT>TGT	p.R152C
Pat_54	Pre-Treatment	UCK1	83549	37	9	134404363	134404363	Missense_Mutation	SNP	C	T	4	77	c.571G>A	c.(571-573)GTG>ATG	p.V191M
Pat_54	Pre-Treatment	PNPLA7	375775	37	9	140356758	140356758	Missense_Mutation	SNP	G	A	5	128	c.3443C>T	c.(3442-3444)ACG>ATG	p.T1148M
Pat_54	Pre-Treatment	ARSF	416	37	X	3030250	3030250	Missense_Mutation	SNP	G	A	30	46	c.1426G>A	c.(1426-1428)GTA>ATA	p.V476I
Pat_54	Pre-Treatment	MXRA5	25878	37	X	3228497	3228497	Missense_Mutation	SNP	C	T	3	5	c.7747G>A	c.(7747-7749)GAT>AAT	p.D2583N
Pat_54	Pre-Treatment	DDX53	168400	37	X	23018769	23018769	Missense_Mutation	SNP	G	A	87	109	c.595G>A	c.(595-597)GAA>AAA	p.E199K
Pat_54	Pre-Treatment	MAGEB1	4112	37	X	30269335	30269335	Missense_Mutation	SNP	G	A	4	63	c.725G>A	c.(724-726)CGT>CAT	p.R242H
Pat_54	Pre-Treatment	HUWE1	10075	37	X	53577633	53577633	Missense_Mutation	SNP	T	C	39	70	c.9482A>G	c.(9481-9483)CAT>CGT	p.H3161R
Pat_54	Pre-Treatment	WNK3	65267	37	X	54275818	54275818	Missense_Mutation	SNP	G	A	4	96	c.2963C>T	c.(2962-2964)CCA>CTA	p.P988L
Pat_54	Pre-Treatment	ZDHHC15	158866	37	X	74648947	74648947	Missense_Mutation	SNP	G	A	64	58	c.569C>T	c.(568-570)ACG>ATG	p.T190M
Pat_54	Pre-Treatment	ESX1	80712	37	X	103495237	103495237	Missense_Mutation	SNP	G	A	9	6	c.893C>T	c.(892-894)CCG>CTG	p.P298L
Pat_54	Pre-Treatment	LRCH2	57631	37	X	114418999	114418999	Missense_Mutation	SNP	C	T	24	33	c.596G>A	c.(595-597)GGG>GAG	p.G199E
Pat_54	Pre-Treatment	DOCK11	139818	37	X	117758535	117758535	Missense_Mutation	SNP	C	T	226	452	c.3505C>T	c.(3505-3507)CCC>TCC	p.P1169S
Pat_54	Pre-Treatment	CT47B1	643311	37	X	120007788	120007788	Missense_Mutation	SNP	C	T	311	475	c.862G>A	c.(862-864)GAT>AAT	p.D288N
Pat_54	Pre-Treatment	STAG2	10735	37	X	123181208	123181208	Missense_Mutation	SNP	G	A	78	102	c.672G>A	c.(670-672)ATG>ATA	p.M224I
Pat_54	Pre-Treatment	CD99L2	83692	37	X	149983391	149983391	Missense_Mutation	SNP	G	A	165	299	c.221C>T	c.(220-222)GCT>GTT	p.A74V
Pat_54	Pre-Treatment	PLXNA3	55558	37	X	153694839	153694839	Missense_Mutation	SNP	G	A	21	27	c.2920G>A	c.(2920-2922)GAG>AAG	p.E974K
Pat_55	Pre-Treatment	TESK2	10420	37	1	45810777	45810777	Missense_Mutation	SNP	G	T	48	93	c.1451C>A	c.(1450-1452)CCA>CAA	p.P484Q
Pat_55	Pre-Treatment	LPHN2	23266	37	1	82408887	82408887	Missense_Mutation	SNP	G	A	30	39	c.632G>A	c.(631-633)GGA>GAA	p.G211E

Pat_55	Pre-Treatment	PKN2	5586	37	1	89298971	89298971	Missense_Mutation	SNP	C	A	24	31	c.2795C>A	c.(2794-2796)CCA>CAA	p.P932Q
Pat_55	Pre-Treatment	TBX15	6913	37	1	119427953	119427953	Missense_Mutation	SNP	C	T	22	12	c.893G>A	c.(892-894)CGA>CAA	p.R298Q
Pat_55	Pre-Treatment	ITGA10	8515	37	1	145533490	145533490	Missense_Mutation	SNP	G	A	10	22	c.1373G>A	c.(1372-1374)GGA>GAA	p.G458E
Pat_55	Pre-Treatment	TCHHL1	126637	37	1	152058489	152058489	Missense_Mutation	SNP	C	T	21	35	c.1669G>A	c.(1669-1671)GAA>AAA	p.E557K
Pat_55	Pre-Treatment	RGS16	6004	37	1	182571247	182571247	Missense_Mutation	SNP	C	G	26	186	c.241G>C	c.(241-243)GCT>CCT	p.A81P
Pat_55	Pre-Treatment	LAMC1	3915	37	1	183095388	183095389	Missense_Mutation	DNP	GG	AA	40	74	.2935_2936GG>A	c.(2935-2937)GGC>AAC	p.G979N
Pat_55	Pre-Treatment	AKT3	10000	37	1	243859016	243859016	Missense_Mutation	SNP	C	T	5	7	c.49G>A	c.(49-51)GAA>AAA	p.E17K
Pat_55	Pre-Treatment	ABCC2	1244	37	10	101591417	101591417	Missense_Mutation	SNP	C	T	30	66	c.2933C>T	c.(2932-2934)TCG>TTG	p.S978L
Pat_55	Pre-Treatment	MMP26	56547	37	11	5010966	5010967	Missense_Mutation	DNP	GG	AA	6	24	c.188_189GG>AA	c.(187-189)CGG>CAA	p.R63Q
Pat_55	Pre-Treatment	LPXN	9404	37	11	58295144	58295144	Missense_Mutation	SNP	G	A	11	17	c.944C>T	c.(943-945)CCA>CTA	p.P315L
Pat_55	Pre-Treatment	CCDC91	55297	37	12	28544279	28544279	Missense_Mutation	SNP	G	A	16	35	c.697G>A	c.(697-699)GAA>AAA	p.E233K
Pat_55	Pre-Treatment	SLC24A6	80024	37	12	113745599	113745600	Missense_Mutation	DNP	GG	AA	29	8	.1307_1308CC>T	c.(1306-1308)GCC>GTT	p.A436V
Pat_55	Pre-Treatment	ATP12A	479	37	13	25272803	25272803	Missense_Mutation	SNP	T	C	3	22	c.1520T>C	c.(1519-1521)ATC>ACC	p.I507T
Pat_55	Pre-Treatment	OR4K13	390433	37	14	20502407	20502407	Missense_Mutation	SNP	G	A	25	34	c.511C>T	c.(511-513)CCC>TCC	p.P171S
Pat_55	Pre-Treatment	SLC8A3	6547	37	14	70634811	70634811	Missense_Mutation	SNP	C	T	10	10	c.329G>A	c.(328-330)AGG>AAG	p.R110K
Pat_55	Pre-Treatment	SIPA1L1	26037	37	14	72200448	72200448	Missense_Mutation	SNP	G	A	20	40	c.4990G>A	c.(4990-4992)GAC>AAC	p.D1664N
Pat_55	Pre-Treatment	AQR	9716	37	15	35252991	35252991	Missense_Mutation	SNP	C	T	4	4	c.157G>A	c.(157-159)GAG>AAG	p.E53K
Pat_55	Pre-Treatment	CGNL1	84952	37	15	57820877	57820877	Missense_Mutation	SNP	G	A	53	75	c.3065G>A	c.(3064-3066)CGG>CAG	p.R1022Q
Pat_55	Pre-Treatment	ST8SIA2	8128	37	15	92977587	92977587	Missense_Mutation	SNP	C	T	14	42	c.272C>T	c.(271-273)ACG>ATG	p.T91M
Pat_55	Pre-Treatment	ADCY9	115	37	16	4016579	4016579	Missense_Mutation	SNP	C	T	38	77	c.3259G>A	c.(3259-3261)GAG>AAG	p.E1087K
Pat_55	Pre-Treatment	RRN3	54700	37	16	15179515	15179515	Missense_Mutation	SNP	A	T	6	10	c.513T>A	c.(511-513)GAT>GAA	p.D171E
Pat_55	Pre-Treatment	ADAMTS18	170692	37	16	77398138	77398138	Missense_Mutation	SNP	C	T	37	73	c.919G>A	c.(919-921)GAA>AAA	p.E307K
Pat_55	Pre-Treatment	LRRC50	123872	37	16	84203783	84203783	Missense_Mutation	SNP	C	T	18	28	c.1349C>T	c.(1348-1350)CCG>CTG	p.P450L
Pat_55	Pre-Treatment	CHD3	1107	37	17	7797762	7797762	Missense_Mutation	SNP	G	A	47	63	c.1105G>A	c.(1105-1107)GAG>AAG	p.E369K
Pat_55	Pre-Treatment	CCT6B	10693	37	17	33267624	33267624	Missense_Mutation	SNP	G	A	6	22	c.902C>T	c.(901-903)TCC>TTC	p.S301F
Pat_55	Pre-Treatment	ACACA	31	37	17	35479508	35479508	Missense_Mutation	SNP	C	T	51	105	c.5972G>A	c.(5971-5973)CGA>CAA	p.R1991Q
Pat_55	Pre-Treatment	CD300LG	146894	37	17	41930295	41930295	Missense_Mutation	SNP	C	T	32	90	c.395C>T	c.(394-396)CCC>CTC	p.P132L
Pat_55	Pre-Treatment	KIAA1328	57536	37	18	34802008	34802008	Nonsense_Mutation	SNP	C	T	4	17	c.1552C>T	c.(1552-1554)CAG>TAG	p.Q518*
Pat_55	Pre-Treatment	ZNF799	90576	37	19	12501446	12501446	Missense_Mutation	SNP	T	C	4	30	c.1766A>G	c.(1765-1767)GAA>GGA	p.E589G
Pat_55	Pre-Treatment	OR7A10	390892	37	19	14952652	14952652	Missense_Mutation	SNP	A	G	4	52	c.38T>C	c.(37-39)CTT>CCT	p.L13P
Pat_55	Pre-Treatment	ZNF626	199777	37	19	20808090	20808090	Missense_Mutation	SNP	C	T	4	48	c.593G>A	c.(592-594)GGG>GAG	p.G198E
Pat_55	Pre-Treatment	ZNF91	7644	37	19	23544867	23544867	Missense_Mutation	SNP	T	C	5	122	c.914A>G	c.(913-915)CAT>CGT	p.H305R
Pat_55	Pre-Treatment	RYR1	6261	37	19	39018357	39018357	Missense_Mutation	SNP	C	T	14	14	c.10757C>T	.(10756-10758)GCC>GT	p.A3586V
Pat_55	Pre-Treatment	ZNF534	147658	37	19	52942507	52942507	Missense_Mutation	SNP	A	T	3	16	c.1833A>T	c.(1831-1833)AAA>AAT	p.K611N
Pat_55	Pre-Treatment	ZNF845	91664	37	19	53856702	53856702	Missense_Mutation	SNP	G	A	9	127	c.2774G>A	c.(2773-2775)CGT>CAT	p.R925H
Pat_55	Pre-Treatment	ZNF761	388561	37	19	53958318	53958318	Missense_Mutation	SNP	C	T	35	60	c.557C>T	c.(556-558)ACC>ATC	p.T186I
Pat_55	Pre-Treatment	HEATR5B	54497	37	2	37283664	37283664	Missense_Mutation	SNP	G	A	21	116	c.2318C>T	c.(2317-2319)CCC>CTC	p.P773L
Pat_55	Pre-Treatment	ZNF638	27332	37	2	71577099	71577099	Missense_Mutation	SNP	T	C	15	119	c.1015T>C	c.(1015-1017)TCG>CCG	p.S339P
Pat_55	Pre-Treatment	ZEB2	9839	37	2	145157238	145157238	Missense_Mutation	SNP	G	A	28	66	c.1516C>T	c.(1516-1518)CCT>TCT	p.P506S
Pat_55	Pre-Treatment	RQCD1	9125	37	2	219449405	219449406	Missense_Mutation	DNP	CC	TT	82	51	c.391_392CC>TT	c.(391-393)CCC>TTC	p.P131F
Pat_55	Pre-Treatment	TGM3	7053	37	20	2308804	2308804	Nonsense_Mutation	SNP	C	T	26	77	c.1126C>T	c.(1126-1128)CGA>TGA	p.R376*
Pat_55	Pre-Treatment	LPIN3	64900	37	20	39978485	39978485	Missense_Mutation	SNP	C	T	4	22	c.710C>T	c.(709-711)CCC>CTC	p.P237L
Pat_55	Pre-Treatment	XKR3	150165	37	22	17265144	17265144	Missense_Mutation	SNP	G	A	7	19	c.745C>T	c.(745-747)CGT>TGT	p.R249C
Pat_55	Pre-Treatment	SCN10A	6336	37	3	38760146	38760146	Missense_Mutation	SNP	T	C	36	63	c.3679A>G	c.(3679-3681)AAT>GAT	p.N1227D
Pat_55	Pre-Treatment	RRP9	9136	37	3	51969478	51969478	Missense_Mutation	SNP	T	C	15	31	c.851A>G	c.(850-852)GAC>GGC	p.D284G
Pat_55	Pre-Treatment	NISCH	11188	37	3	52492810	52492810	Missense_Mutation	SNP	C	T	11	29	c.310C>T	c.(310-312)CCT>TCT	p.P104S
Pat_55	Pre-Treatment	SH3BP2	6452	37	4	2831570	2831570	Missense_Mutation	SNP	G	A	3	72	c.937G>A	c.(937-939)GGG>AGG	p.G313R

Pat_55	Pre-Treatment	LPHN3	23284	37	4	62363063	62363063	Missense_Mutation	SNP	C	T	4	15	c.52C>T	c.(52-54)CAT>TAT	p.H18Y
Pat_55	Pre-Treatment	MUC7	4589	37	4	71347138	71347138	Missense_Mutation	SNP	C	T	7	292	c.677C>T	c.(676-678)CCA>CTA	p.P226L
Pat_55	Pre-Treatment	MMRN1	22915	37	4	90874228	90874228	Missense_Mutation	SNP	C	T	17	35	c.3346C>T	c.(3346-3348)CCT>TCT	p.P1116S
Pat_55	Pre-Treatment	DCHS2	54798	37	4	155287505	155287505	Missense_Mutation	SNP	G	A	14	42	c.551C>T	c.(550-552)ACG>ATG	p.T184M
Pat_55	Pre-Treatment	TRIML2	205860	37	4	189022221	189022221	Missense_Mutation	SNP	C	T	4	17	c.319G>A	c.(319-321)GAA>AAA	p.E107K
Pat_55	Pre-Treatment	MYO10	4651	37	5	16763627	16763627	Nonsense_Mutation	SNP	C	T	16	139	c.1457G>A	c.(1456-1458)TGG>TAG	p.W486*
Pat_55	Pre-Treatment	DPYSL3	1809	37	5	146785236	146785236	Missense_Mutation	SNP	G	A	95	85	c.748C>T	c.(748-750)CTC>TTC	p.L250F
Pat_55	Pre-Treatment	KPNA5	3841	37	6	117043419	117043419	Missense_Mutation	SNP	C	T	16	6	c.887C>T	c.(886-888)TCT>TTT	p.S296F
Pat_55	Pre-Treatment	PLEKHG1	57480	37	6	151151742	151151742	Nonsense_Mutation	SNP	C	T	24	14	c.1495C>T	c.(1495-1497)CAG>TAG	p.Q499*
Pat_55	Pre-Treatment	ABCA13	154664	37	7	48314892	48314892	Missense_Mutation	SNP	A	G	6	36	c.5629A>G	c.(5629-5631)AGC>GGC	p.S1877G
Pat_55	Pre-Treatment	CCDC136	64753	37	7	128455933	128455933	Missense_Mutation	SNP	C	T	14	8	c.3311C>T	c.(3310-3312)TCC>TTC	p.S1104F
Pat_55	Pre-Treatment	BRAF	673	37	7	140453136	140453136	Missense_Mutation	SNP	A	T	34	40	c.1799T>A	c.(1798-1800)GTG>GAG	p.V600E
Pat_55	Pre-Treatment	CNTNAP2	26047	37	7	147844762	147844762	Missense_Mutation	SNP	G	A	9	45	c.2734G>A	c.(2734-2736)GGC>AGC	p.G912S
Pat_55	Pre-Treatment	ZNF425	155054	37	7	148800760	148800760	Missense_Mutation	SNP	C	T	5	13	c.2203G>A	c.(2203-2205)GGG>AGG	p.G735R
Pat_55	Pre-Treatment	KIF13B	23303	37	8	29006228	29006229	Missense_Mutation	DNP	GG	AA	10	34	.1678_1679CC>T	c.(1678-1680)CCC>TTC	p.P560F
Pat_55	Pre-Treatment	TOX	9760	37	8	59750713	59750713	Missense_Mutation	SNP	G	A	28	90	c.851C>T	c.(850-852)CCA>CTA	p.P284L
Pat_55	Pre-Treatment	MPDZ	8777	37	9	13223586	13223586	Missense_Mutation	SNP	C	T	18	8	c.517G>A	c.(517-519)GGC>AGC	p.G173S
Pat_55	Pre-Treatment	MAOB	4129	37	X	43637936	43637936	Missense_Mutation	SNP	G	A	6	5	c.1130C>T	c.(1129-1131)GCT>GTT	p.A377V
Pat_55	Pre-Treatment	ZNF81	347344	37	X	47775358	47775358	Missense_Mutation	SNP	G	A	13	22	c.1313G>A	c.(1312-1314)GGA>GAA	p.G438E
Pat_55	Pre-Treatment	HUWE1	10075	37	X	53610865	53610866	Missense_Mutation	DNP	CC	TT	27	45	.5172_5173GG>A	170-5175)TTGGCC>TTAA	p.A1725T
Pat_55	Pre-Treatment	HUWE1	10075	37	X	53652192	53652192	Missense_Mutation	SNP	G	C	15	90	c.1517C>G	c.(1516-1518)GCA>GGA	p.A506G
Pat_55	Pre-Treatment	KIAA2022	340533	37	X	73960365	73960365	Missense_Mutation	SNP	C	T	7	7	c.4027G>A	c.(4027-4029)GAA>AAA	p.E1343K
Pat_55	Pre-Treatment	POF1B	79983	37	X	84600936	84600936	Missense_Mutation	SNP	C	T	51	125	c.653G>A	c.(652-654)GGA>GAA	p.G218E
Pat_55	Pre-Treatment	COL4A5	1287	37	X	107923946	107923946	Missense_Mutation	SNP	G	A	17	19	c.3980G>A	c.(3979-3981)GGA>GAA	p.G1327E
Pat_55	Pre-Treatment	DOCK11	139818	37	X	117695382	117695382	Missense_Mutation	SNP	C	T	19	25	c.595C>T	c.(595-597)CCT>TCT	p.P199S
Pat_55	Pre-Treatment	MAGEC1	9947	37	X	140993455	140993455	Missense_Mutation	SNP	G	A	3	66	c.265G>A	c.(265-267)GGC>AGC	p.G89S
Pat_55	Pre-Treatment	MAGEA10	4109	37	X	151303080	151303080	Missense_Mutation	SNP	T	C	34	55	c.1013A>G	c.(1012-1014)GAA>GGA	p.E338G
Pat_60	Pre-Treatment	MIB2	142678	37	1	1560692	1560692	Missense_Mutation	SNP	G	A	2	0	c.922G>A	c.(922-924)GTG>ATG	p.V308M
Pat_60	Pre-Treatment	PLEKHG5	57449	37	1	6531685	6531685	Missense_Mutation	SNP	G	A	2	1	c.1312C>T	c.(1312-1314)CGC>TGC	p.R438C
Pat_60	Pre-Treatment	PRDM2	7799	37	1	14107382	14107382	Missense_Mutation	SNP	C	T	29	111	c.3092C>T	c.(3091-3093)CCC>CTC	p.P1031L
Pat_60	Pre-Treatment	AGMAT	79814	37	1	15904220	15904220	Missense_Mutation	SNP	C	T	10	35	c.860G>A	c.(859-861)GGG>GAG	p.G287E
Pat_60	Pre-Treatment	AGMAT	79814	37	1	15911204	15911204	Missense_Mutation	SNP	G	A	2	2	c.259C>T	c.(259-261)CGG>TGG	p.R87W
Pat_60	Pre-Treatment	UBR4	23352	37	1	19467910	19467910	Missense_Mutation	SNP	G	A	8	30	c.8419C>T	c.(8419-8421)CCA>TCA	p.P2807S
Pat_60	Pre-Treatment	LCK	3932	37	1	32740638	32740638	Missense_Mutation	SNP	G	A	4	82	c.232G>A	c.(232-234)GGA>AGA	p.G78R
Pat_60	Pre-Treatment	GRIK3	2899	37	1	37325557	37325557	Missense_Mutation	SNP	C	T	4	40	c.848G>A	c.(847-849)CGG>CAG	p.R283Q
Pat_60	Pre-Treatment	EIF2B3	8891	37	1	45363093	45363093	Missense_Mutation	SNP	G	A	4	40	c.590C>T	c.(589-591)ACG>ATG	p.T197M
Pat_60	Pre-Treatment	MAGOH	4116	37	1	53692748	53692748	Missense_Mutation	SNP	A	G	3	65	c.410T>C	c.(409-411)ATT>ACT	p.I137T
Pat_60	Pre-Treatment	INADL	10207	37	1	62582843	62582843	Nonsense_Mutation	SNP	C	T	21	97	c.4843C>T	c.(4843-4845)CGA>TGA	p.R1615*
Pat_60	Pre-Treatment	KANK4	163782	37	1	62740084	62740084	Missense_Mutation	SNP	C	T	3	11	c.692G>A	c.(691-693)GGA>GAA	p.G231E
Pat_60	Pre-Treatment	C1orf146	388649	37	1	92710383	92710383	Missense_Mutation	SNP	A	C	33	131	c.377A>C	c.(376-378)AAT>ACT	p.N126T
Pat_60	Pre-Treatment	COL11A1	1301	37	1	103470043	103470043	Missense_Mutation	SNP	C	T	14	64	c.1901G>A	c.(1900-1902)GGA>GAA	p.G634E
Pat_60	Pre-Treatment	PRMT6	55170	37	1	107599699	107599699	Missense_Mutation	SNP	G	A	3	29	c.362G>A	c.(361-363)CGG>CAG	p.R121Q
Pat_60	Pre-Treatment	C1orf194	127003	37	1	109649210	109649210	Missense_Mutation	SNP	C	T	39	140	c.386G>A	c.(385-387)AGA>AAA	p.R129K
Pat_60	Pre-Treatment	SYCP1	6847	37	1	115428861	115428861	Missense_Mutation	SNP	C	T	50	160	c.1121C>T	c.(1120-1122)TCG>TTG	p.S374L
Pat_60	Pre-Treatment	PHGDH	26227	37	1	120285616	120285616	Missense_Mutation	SNP	C	T	4	77	c.1396C>T	c.(1396-1398)CTC>TTC	p.L466F
Pat_60	Pre-Treatment	NOTCH2NL	388677	37	1	145290447	145290447	Missense_Mutation	SNP	C	T	21	546	c.653C>T	c.(652-654)CCT>CTT	p.P218L
Pat_60	Pre-Treatment	NBPF10	100132406	37	1	145304523	145304523	Missense_Mutation	SNP	C	T	70	433	c.1456C>T	c.(1456-1458)CAT>TAT	p.H486Y

Pat_60	Pre-Treatment	RPRD2	23248	37	1	150429902	150429902	Missense_Mutation	SNP	C	T	50	147	c.1009C>T	c.(1009-1011)CCT>TCT	p.P337S
Pat_60	Pre-Treatment	RFX5	5993	37	1	151315846	151315846	Missense_Mutation	SNP	G	A	16	41	c.830C>T	c.(829-831)GCC>GTC	p.A277V
Pat_60	Pre-Treatment	S100A7L2	645922	37	1	153410754	153410754	Missense_Mutation	SNP	G	A	15	73	c.85C>T	c.(85-87)CGC>TGC	p.R29C
Pat_60	Pre-Treatment	UBE2Q1	55585	37	1	154528003	154528003	Missense_Mutation	SNP	C	A	4	71	c.438G>T	c.(436-438)TTG>TTT	p.L146F
Pat_60	Pre-Treatment	OR10K1	391109	37	1	158435891	158435891	Missense_Mutation	SNP	C	A	31	176	c.540C>A	c.(538-540)GAC>GAA	p.D180E
Pat_60	Pre-Treatment	SLAMF7	57823	37	1	160722031	160722031	Missense_Mutation	SNP	C	T	3	67	c.929C>T	c.(928-930)CCG>CTG	p.P310L
Pat_60	Pre-Treatment	FMO2	2327	37	1	171173088	171173088	Missense_Mutation	SNP	C	T	3	63	c.712C>T	c.(712-714)CGG>TGG	p.R238W
Pat_60	Pre-Treatment	RABGAP1L	9910	37	1	174363191	174363191	Missense_Mutation	SNP	C	T	64	120	c.1618C>T	c.(1618-1620)CCT>TCT	p.P540S
Pat_60	Pre-Treatment	ZNF648	127665	37	1	182026271	182026271	Missense_Mutation	SNP	C	T	2	0	c.875G>A	c.(874-876)GGC>GAC	p.G292D
Pat_60	Pre-Treatment	RGS18	64407	37	1	192128444	192128444	Missense_Mutation	SNP	G	A	12	62	c.214G>A	c.(214-216)GAA>AAA	p.E72K
Pat_60	Pre-Treatment	DDX59	83479	37	1	200633067	200633067	Missense_Mutation	SNP	G	A	17	84	c.952C>T	c.(952-954)CGT>TGT	p.R318C
Pat_60	Pre-Treatment	CAMSAP1L1	23271	37	1	200819038	200819038	Missense_Mutation	SNP	A	T	4	61	c.3174A>T	c.(3172-3174)AAA>AAT	p.K1058N
Pat_60	Pre-Treatment	LGR6	59352	37	1	202270330	202270330	Missense_Mutation	SNP	C	T	6	36	c.896C>T	c.(895-897)TCG>TTG	p.S299L
Pat_60	Pre-Treatment	TMCC2	9911	37	1	205238112	205238112	Missense_Mutation	SNP	C	T	11	50	c.782C>T	c.(781-783)CCC>CTC	p.P261L
Pat_60	Pre-Treatment	HEATR1	55127	37	1	236729334	236729334	Missense_Mutation	SNP	T	A	4	39	c.4320A>T	c.(4318-4320)TTA>TTT	p.L1440F
Pat_60	Pre-Treatment	ACTN2	88	37	1	236924453	236924453	Missense_Mutation	SNP	C	T	4	45	c.2506C>T	c.(2506-2508)CGG>TGG	p.R836W
Pat_60	Pre-Treatment	SMYD3	64754	37	1	246498703	246498703	Missense_Mutation	SNP	G	A	54	147	c.302C>T	c.(301-303)TCC>TTC	p.S101F
Pat_60	Pre-Treatment	C1orf150	148823	37	1	247737445	247737445	Missense_Mutation	SNP	G	A	22	101	c.169G>A	c.(169-171)GAA>AAA	p.E57K
Pat_60	Pre-Treatment	C10orf18	54906	37	10	5788409	5788409	Missense_Mutation	SNP	G	A	3	52	c.3025G>A	c.(3025-3027)GCA>ACA	p.A1009T
Pat_60	Pre-Treatment	TAF3	83860	37	10	8006435	8006435	Missense_Mutation	SNP	C	T	7	16	c.962C>T	c.(961-963)CCC>CTC	p.P321L
Pat_60	Pre-Treatment	CAMK1D	57118	37	10	12803005	12803005	Missense_Mutation	SNP	G	A	7	47	c.358G>A	c.(358-360)GAT>AAT	p.D120N
Pat_60	Pre-Treatment	MYO3A	53904	37	10	26355954	26355954	Missense_Mutation	SNP	C	T	28	104	c.1004C>T	c.(1003-1005)TCC>TTC	p.S335F
Pat_60	Pre-Treatment	APBB1IP	54518	37	10	26849663	26849663	Missense_Mutation	SNP	G	A	7	35	c.1259G>A	c.(1258-1260)GGG>GAG	p.G420E
Pat_60	Pre-Treatment	ARMC4	55130	37	10	28225687	28225688	Nonsense_Mutation	DNP	CC	TT	49	162	.2219_2220GG>A	c.(2218-2220)TGG>TAA	p.W740*
Pat_60	Pre-Treatment	ANKRD30A	91074	37	10	37425564	37425564	Missense_Mutation	SNP	G	A	6	22	c.617G>A	c.(616-618)CGA>CAA	p.R206Q
Pat_60	Pre-Treatment	ARHGAP22	58504	37	10	49667836	49667836	Missense_Mutation	SNP	G	A	3	31	c.550C>T	c.(550-552)CGG>TGG	p.R184W
Pat_60	Pre-Treatment	OGDHL	55753	37	10	50948765	50948765	Missense_Mutation	SNP	C	T	2	2	c.2131G>A	c.(2131-2133)GGA>AGA	p.G711R
Pat_60	Pre-Treatment	MBL2	4153	37	10	54531224	54531224	Missense_Mutation	SNP	C	T	25	65	c.172G>A	c.(172-174)GAA>AAA	p.E58K
Pat_60	Pre-Treatment	PCDH15	65217	37	10	55570336	55570336	Missense_Mutation	SNP	C	T	29	137	c.4498G>A	c.(4498-4500)GAA>AAA	p.E1500K
Pat_60	Pre-Treatment	MYOF	26509	37	10	95157032	95157032	Missense_Mutation	SNP	C	T	4	70	c.1306G>A	c.(1306-1308)GAA>AAA	p.E436K
Pat_60	Pre-Treatment	CYP2C9	1559	37	10	96745844	96745844	Missense_Mutation	SNP	C	T	50	133	c.1204C>T	c.(1204-1206)CCC>TCC	p.P402S
Pat_60	Pre-Treatment	SCD	6319	37	10	102120518	102120518	Missense_Mutation	SNP	C	T	50	101	c.908C>T	c.(907-909)TCC>TTC	p.S303F
Pat_60	Pre-Treatment	PPRC1	23082	37	10	103904025	103904025	Missense_Mutation	SNP	C	T	3	48	c.3569C>T	c.(3568-3570)CCT>CTT	p.P1190L
Pat_60	Pre-Treatment	SORCS1	114815	37	10	108366965	108366965	Missense_Mutation	SNP	G	A	22	45	c.3124C>T	c.(3124-3126)CCA>TCA	p.P1042S
Pat_60	Pre-Treatment	KIAA1598	57698	37	10	118687348	118687348	Missense_Mutation	SNP	G	A	55	117	c.1067C>T	c.(1066-1068)CCT>CTT	p.P356L
Pat_60	Pre-Treatment	DMBT1	1755	37	10	124395670	124395670	Missense_Mutation	SNP	G	A	4	13	c.6325G>A	c.(6325-6327)GGG>AGG	p.G2109R
Pat_60	Pre-Treatment	DMBT1	1755	37	10	124399773	124399773	Missense_Mutation	SNP	C	A	20	80	c.6773C>A	c.(6772-6774)TCC>TAC	p.S2258Y
Pat_60	Pre-Treatment	JAKMIP3	282973	37	10	133954015	133954015	Missense_Mutation	SNP	T	C	2	6	c.1405T>C	c.(1405-1407)TCC>CCC	p.S469P
Pat_60	Pre-Treatment	KRTAP5-1	387264	37	11	1606166	1606166	Missense_Mutation	SNP	G	C	4	32	c.314C>G	c.(313-315)TCC>TGC	p.S105C
Pat_60	Pre-Treatment	OR51A4	401666	37	11	4967801	4967801	Missense_Mutation	SNP	G	A	15	34	c.530C>T	c.(529-531)TCC>TTC	p.S177F
Pat_60	Pre-Treatment	HBE1	3046	37	11	5290787	5290787	Missense_Mutation	SNP	G	A	13	41	c.212C>T	c.(211-213)TCC>TTC	p.S71F
Pat_60	Pre-Treatment	TRIM6-TRIM34	445372	37	11	5664622	5664622	Missense_Mutation	SNP	C	T	22	81	c.2212C>T	c.(2212-2214)CGT>TGT	p.R738C
Pat_60	Pre-Treatment	TRIM22	10346	37	11	5729503	5729503	Missense_Mutation	SNP	G	A	3	58	c.874G>A	c.(874-876)GAG>AAG	p.E292K
Pat_60	Pre-Treatment	TRIM3	10612	37	11	6477363	6477363	Missense_Mutation	SNP	C	T	3	57	c.1472G>A	c.(1471-1473)GGT>GAT	p.G491D
Pat_60	Pre-Treatment	SPON1	10418	37	11	14063077	14063077	Missense_Mutation	SNP	G	A	32	219	c.355G>A	c.(355-357)GAA>AAA	p.E119K
Pat_60	Pre-Treatment	KCNJ11	3767	37	11	17408942	17408942	Missense_Mutation	SNP	G	A	5	14	c.697C>T	c.(697-699)CTC>TTC	p.L233F
Pat_60	Pre-Treatment	SLC6A5	9152	37	11	20639381	20639381	Nonsense_Mutation	SNP	G	A	28	75	c.1211G>A	c.(1210-1212)TGG>TAG	p.W404*

Pat_60	Pre-Treatment	QSER1	79832	37	11	32956501	32956501	Missense_Mutation	SNP	C	T	52	186	c.3310C>T	c.(3310-3312)CCA>TCA	p.P1104S
Pat_60	Pre-Treatment	DAGLA	747	37	11	61498913	61498913	Missense_Mutation	SNP	C	T	5	92	c.974C>T	c.(973-975)TCG>TTG	p.S325L
Pat_60	Pre-Treatment	LRRN4CL	221091	37	11	62455559	62455559	Missense_Mutation	SNP	T	A	3	23	c.422A>T	c.(421-423)AAG>ATG	p.K141M
Pat_60	Pre-Treatment	ESRRA	2101	37	11	64083386	64083386	Missense_Mutation	SNP	A	G	3	26	c.1220A>G	c.(1219-1221)AAG>AGG	p.K407R
Pat_60	Pre-Treatment	RIN1	9610	37	11	66103142	66103142	Missense_Mutation	SNP	C	G	2	7	c.394G>C	c.(394-396)GAG>CAG	p.E132Q
Pat_60	Pre-Treatment	NPAS4	266743	37	11	66190601	66190601	Missense_Mutation	SNP	A	G	5	8	c.706A>G	c.(706-708)ATC>GTC	p.I236V
Pat_60	Pre-Treatment	PPP1CA	5499	37	11	67168288	67168288	Missense_Mutation	SNP	C	T	5	138	c.290G>A	c.(289-291)GGC>GAC	p.G97D
Pat_60	Pre-Treatment	IL18BP	10068	37	11	71712851	71712851	Missense_Mutation	SNP	C	T	4	56	c.529C>T	c.(529-531)CCC>TCC	p.P177S
Pat_60	Pre-Treatment	P2RY2	5029	37	11	72945673	72945673	Missense_Mutation	SNP	G	A	3	8	c.469G>A	c.(469-471)GTG>ATG	p.V157M
Pat_60	Pre-Treatment	MOGAT2	80168	37	11	75431138	75431138	Missense_Mutation	SNP	C	T	6	150	c.193C>T	c.(193-195)CGG>TGG	p.R65W
Pat_60	Pre-Treatment	DRD2	1813	37	11	113283314	113283314	Missense_Mutation	SNP	C	T	9	32	c.1102G>A	c.(1102-1104)GAG>AAG	p.E368K
Pat_60	Pre-Treatment	TMPRSS4	56649	37	11	117975469	117975469	Missense_Mutation	SNP	C	T	10	35	c.374C>T	c.(373-375)TCT>TTT	p.S125F
Pat_60	Pre-Treatment	TECTA	7007	37	11	121032866	121032866	Missense_Mutation	SNP	G	T	3	49	c.5059G>T	c.(5059-5061)GGT>TGT	p.G1687C
Pat_60	Pre-Treatment	CCDC15	80071	37	11	124857495	124857495	Missense_Mutation	SNP	A	C	10	248	c.1373A>C	c.(1372-1374)CAC>CCC	p.H458P
Pat_60	Pre-Treatment	SLC2A14	144195	37	12	7970507	7970507	Missense_Mutation	SNP	G	A	3	17	c.1264C>T	c.(1264-1266)CGC>TGC	p.R422C
Pat_60	Pre-Treatment	RECQL	5965	37	12	21624361	21624361	Splice_Site	SNP	C	T	4	51	c.1667_splice	c.e14+1	p.K556_splice
Pat_60	Pre-Treatment	GYS2	2998	37	12	21692230	21692230	Missense_Mutation	SNP	G	A	32	142	c.1852C>T	c.(1852-1854)CCA>TCA	p.P618S
Pat_60	Pre-Treatment	BCAT1	586	37	12	24982759	24982759	Missense_Mutation	SNP	G	T	3	43	c.1117C>A	c.(1117-1119)CAG>AAG	p.Q373K
Pat_60	Pre-Treatment	TMTC1	83857	37	12	29673644	29673644	Nonsense_Mutation	SNP	T	A	16	44	c.1471A>T	c.(1471-1473)AAA>TAA	p.K491*
Pat_60	Pre-Treatment	CACNB3	784	37	12	49219475	49219475	Missense_Mutation	SNP	C	T	20	88	c.665C>T	c.(664-666)TCC>TTC	p.S222F
Pat_60	Pre-Treatment	KRT74	121391	37	12	52966259	52966259	Missense_Mutation	SNP	G	T	4	63	c.664C>A	c.(664-666)CTG>ATG	p.L222M
Pat_60	Pre-Treatment	KRT79	338785	37	12	53225247	53225247	Missense_Mutation	SNP	C	T	29	91	c.641G>A	c.(640-642)GGG>GAG	p.G214E
Pat_60	Pre-Treatment	ESPL1	9700	37	12	53668692	53668692	Missense_Mutation	SNP	C	T	4	41	c.1598C>T	c.(1597-1599)GCC>GTC	p.A533V
Pat_60	Pre-Treatment	SLC26A10	65012	37	12	58015202	58015202	Missense_Mutation	SNP	C	G	2	4	c.547C>G	c.(547-549)CTC>GTC	p.L183V
Pat_60	Pre-Treatment	PTPRB	5787	37	12	70956819	70956819	Missense_Mutation	SNP	C	T	4	27	c.3319G>A	c.(3319-3321)GCC>ACC	p.A1107T
Pat_60	Pre-Treatment	ACSS3	79611	37	12	81610767	81610767	Missense_Mutation	SNP	G	A	19	39	c.1442G>A	c.(1441-1443)GGA>GAA	p.G481E
Pat_60	Pre-Treatment	RFX4	5992	37	12	107075789	107075789	Missense_Mutation	SNP	C	T	33	88	c.334C>T	c.(334-336)CCT>TCT	p.P112S
Pat_60	Pre-Treatment	RASAL1	8437	37	12	113539775	113539775	Missense_Mutation	SNP	C	T	33	66	c.2141G>A	c.(2140-2142)GGG>GAG	p.G714E
Pat_60	Pre-Treatment	HPD	3242	37	12	122277882	122277882	Missense_Mutation	SNP	G	A	4	111	c.1027C>T	c.(1027-1029)CGG>TGG	p.R343W
Pat_60	Pre-Treatment	TMEM132D	121256	37	12	129563125	129563125	Missense_Mutation	SNP	A	G	17	27	c.2069T>C	c.(2068-2070)ATC>ACC	p.I690T
Pat_60	Pre-Treatment	FARP1	10160	37	13	99083480	99083480	Missense_Mutation	SNP	G	A	2	0	c.2089G>A	c.(2089-2091)GAG>AAG	p.E697K
Pat_60	Pre-Treatment	FAM70B	348013	37	13	114514844	114514844	Missense_Mutation	SNP	C	T	23	46	c.949C>T	c.(949-951)CCG>TCG	p.P317S
Pat_60	Pre-Treatment	OR4N5	390437	37	14	20612733	20612733	Missense_Mutation	SNP	C	T	27	112	c.839C>T	c.(838-840)CCT>CTT	p.P280L
Pat_60	Pre-Treatment	TEP1	7011	37	14	20864835	20864835	Missense_Mutation	SNP	C	T	4	42	c.1604G>A	c.(1603-1605)CGG>CAG	p.R535Q
Pat_60	Pre-Treatment	ZNF219	51222	37	14	21559639	21559639	Missense_Mutation	SNP	C	T	4	67	c.1495G>A	c.(1495-1497)GAT>AAT	p.D499N
Pat_60	Pre-Treatment	CHD8	57680	37	14	21860068	21860068	Nonsense_Mutation	SNP	A	T	12	62	c.5972T>A	c.(5971-5973)TTG>TAG	p.L1991*
Pat_60	Pre-Treatment	FAM179B	23116	37	14	45431830	45431830	Missense_Mutation	SNP	C	T	3	18	c.206C>T	c.(205-207)TCG>TTG	p.S69L
Pat_60	Pre-Treatment	C14orf37	145407	37	14	58605719	58605719	Missense_Mutation	SNP	G	A	25	52	c.358C>T	c.(358-360)CCC>TCC	p.P120S
Pat_60	Pre-Treatment	PLEKHG3	26030	37	14	65208999	65208999	Missense_Mutation	SNP	G	A	18	32	c.2764G>A	c.(2764-2766)GTC>ATC	p.V922I
Pat_60	Pre-Treatment	GALNTL1	57452	37	14	69806275	69806275	Missense_Mutation	SNP	G	A	16	47	c.1126G>A	c.(1126-1128)GAT>AAT	p.D376N
Pat_60	Pre-Treatment	C14orf115	55237	37	14	74824993	74824993	Missense_Mutation	SNP	C	T	3	10	c.1507C>T	c.(1507-1509)CCC>TCC	p.P503S
Pat_60	Pre-Treatment	C14orf115	55237	37	14	74825503	74825503	Missense_Mutation	SNP	G	A	5	33	c.2017G>A	c.(2017-2019)GAG>AAG	p.E673K
Pat_60	Pre-Treatment	TTLL5	23093	37	14	76184295	76184295	Missense_Mutation	SNP	G	A	4	77	c.832G>A	c.(832-834)GAT>AAT	p.D278N
Pat_60	Pre-Treatment	CCDC88C	440193	37	14	91760643	91760643	Missense_Mutation	SNP	C	T	3	7	c.3986G>A	c.(3985-3987)GGG>GAG	p.G1329E
Pat_60	Pre-Treatment	ADSSL1	122622	37	14	105208199	105208199	Missense_Mutation	SNP	G	T	4	43	c.808G>T	c.(808-810)GTG>TTG	p.V270L
Pat_60	Pre-Treatment	OR4N3P	390539	37	15	22414263	22414263	Missense_Mutation	SNP	G	A	16	280	c.562G>A	c.(562-564)GAC>AAC	p.D188N
Pat_60	Pre-Treatment	SLC28A2	9153	37	15	45556117	45556117	Missense_Mutation	SNP	G	T	5	44	c.485G>T	c.(484-486)TGG>TTG	p.W162L

Pat_60	Pre-Treatment	UNC13C	440279	37	15	54685300	54685300	Missense_Mutation	SNP	G	A	19	75	c.4768G>A	c.(4768-4770)GAT>AAT	p.D1590N
Pat_60	Pre-Treatment	NPTN	27020	37	15	73862544	73862544	Missense_Mutation	SNP	A	C	17	113	c.1061T>G	c.(1060-1062)GTG>GGG	p.V354G
Pat_60	Pre-Treatment	SCAPER	49855	37	15	76696982	76696982	Missense_Mutation	SNP	G	A	4	65	c.3350C>T	c.(3349-3351)GCC>GTC	p.A1117V
Pat_60	Pre-Treatment	ADAMTSL3	57188	37	15	84324532	84324532	Missense_Mutation	SNP	C	T	4	24	c.19C>T	c.(19-21)CCC>TCC	p.P7S
Pat_60	Pre-Treatment	ZNF592	9640	37	15	85327009	85327009	Missense_Mutation	SNP	C	T	9	71	c.1103C>T	c.(1102-1104)TCC>TTC	p.S368F
Pat_60	Pre-Treatment	SLC28A1	9154	37	15	85476379	85476379	Missense_Mutation	SNP	G	A	87	150	c.1087G>A	c.(1087-1089)GAT>AAT	p.D363N
Pat_60	Pre-Treatment	ACAN	176	37	15	89386843	89386843	Missense_Mutation	SNP	G	A	4	66	c.1015G>A	c.(1015-1017)GAC>AAC	p.D339N
Pat_60	Pre-Treatment	CHD2	1106	37	15	93567784	93567784	Missense_Mutation	SNP	C	A	4	76	c.5336C>A	c.(5335-5337)CCA>CAA	p.P1779Q
Pat_60	Pre-Treatment	MEF2A	4205	37	15	100214629	100214629	Missense_Mutation	SNP	C	T	192	239	c.428C>T	c.(427-429)TCT>TTT	p.S143F
Pat_60	Pre-Treatment	PDIA2	64714	37	16	332826	332826	Translation_Start_Site	SNP	G	A	2	0	c.-343G>A	(-345--341)CCGTG>CCATG	
Pat_60	Pre-Treatment	TMEM8A	58986	37	16	427387	427387	Missense_Mutation	SNP	G	C	2	7	c.498C>G	c.(496-498)ATC>ATG	p.I166M
Pat_60	Pre-Treatment	ZNF598	90850	37	16	2052425	2052425	Splice_Site	SNP	C	T	4	65	c.678_splice	c.e7-1	p.S226_splice
Pat_60	Pre-Treatment	PRSS33	260429	37	16	2835914	2835914	Missense_Mutation	SNP	C	T	2	2	c.128G>A	c.(127-129)GGC>GAC	p.G43D
Pat_60	Pre-Treatment	GRIN2A	2903	37	16	9858006	9858006	Missense_Mutation	SNP	G	A	15	64	c.3395C>T	c.(3394-3396)CCA>CTA	p.P1132L
Pat_60	Pre-Treatment	PDILT	204474	37	16	20384233	20384233	Missense_Mutation	SNP	G	A	13	23	c.809C>T	c.(808-810)TCC>TTC	p.S270F
Pat_60	Pre-Treatment	USP31	57478	37	16	23083444	23083444	Missense_Mutation	SNP	C	A	5	45	c.2410G>T	c.(2410-2412)GCA>TCA	p.A804S
Pat_60	Pre-Treatment	UBFD1	56061	37	16	23569454	23569454	Missense_Mutation	SNP	C	T	4	59	c.209C>T	c.(208-210)TCG>TTG	p.S70L
Pat_60	Pre-Treatment	ZNF629	23361	37	16	30795131	30795131	Missense_Mutation	SNP	G	A	3	26	c.518C>T	c.(517-519)ACG>ATG	p.T173M
Pat_60	Pre-Treatment	ITGAD	3681	37	16	31429882	31429882	Missense_Mutation	SNP	G	A	4	68	c.2777G>A	c.(2776-2778)AGC>AAC	p.S926N
Pat_60	Pre-Treatment	BRD7	29117	37	16	50354288	50354288	Nonsense_Mutation	SNP	G	A	27	83	c.1627C>T	c.(1627-1629)CAG>TAG	p.Q543*
Pat_60	Pre-Treatment	NKD1	85407	37	16	50583455	50583455	Nonsense_Mutation	SNP	C	T	3	8	c.181C>T	c.(181-183)CGA>TGA	p.R61*
Pat_60	Pre-Treatment	TOX3	27324	37	16	52497934	52497934	Missense_Mutation	SNP	G	A	9	33	c.320C>T	c.(319-321)CCC>CTC	p.P107L
Pat_60	Pre-Treatment	KLHL36	79786	37	16	84695383	84695383	Missense_Mutation	SNP	G	A	4	25	c.1495G>A	c.(1495-1497)GGG>AGG	p.G499R
Pat_60	Pre-Treatment	PRDM7	11105	37	16	90126823	90126823	Missense_Mutation	SNP	T	G	5	66	c.1159A>C	c.(1159-1161)ATG>CTG	p.M387L
Pat_60	Pre-Treatment	PRDM7	11105	37	16	90126912	90126912	Missense_Mutation	SNP	G	T	4	54	c.1070C>A	c.(1069-1071)TCT>TAT	p.S357Y
Pat_60	Pre-Treatment	GEMIN4	50628	37	17	650856	650856	Missense_Mutation	SNP	G	A	3	30	c.427C>T	c.(427-429)CGC>TGC	p.R143C
Pat_60	Pre-Treatment	MYH2	4620	37	17	10435009	10435009	Missense_Mutation	SNP	C	T	20	43	c.2638G>A	c.(2638-2640)GAA>AAA	p.E880K
Pat_60	Pre-Treatment	MYH2	4620	37	17	10435020	10435020	Missense_Mutation	SNP	C	T	9	67	c.2627G>A	c.(2626-2628)AGG>AAG	p.R876K
Pat_60	Pre-Treatment	CCDC144A	9720	37	17	16635945	16635945	Missense_Mutation	SNP	G	A	5	11	c.2383G>A	c.(2383-2385)GAA>AAA	p.E795K
Pat_60	Pre-Treatment	LLGL1	3996	37	17	18139948	18139948	Nonsense_Mutation	SNP	G	A	3	34	c.1380G>A	c.(1378-1380)TGG>TGA	p.W460*
Pat_60	Pre-Treatment	SMCR7	125170	37	17	18167296	18167296	Missense_Mutation	SNP	C	T	2	0	c.583C>T	c.(583-585)CGT>TGT	p.R195C
Pat_60	Pre-Treatment	SPAG5	10615	37	17	26919042	26919042	Missense_Mutation	SNP	C	T	3	46	c.1220G>A	c.(1219-1221)GGC>GAC	p.G407D
Pat_60	Pre-Treatment	SRCIN1	80725	37	17	36700119	36700119	Missense_Mutation	SNP	G	A	4	10	c.3356C>T	c.(3355-3357)CCC>CTC	p.P1119L
Pat_60	Pre-Treatment	WIPF2	147179	37	17	38418845	38418845	Nonsense_Mutation	SNP	C	T	15	48	c.265C>T	c.(265-267)CAA>TAA	p.Q89*
Pat_60	Pre-Treatment	KLHL11	55175	37	17	40010222	40010222	Nonsense_Mutation	SNP	G	A	3	50	c.1897C>T	c.(1897-1899)CGA>TGA	p.R633*
Pat_60	Pre-Treatment	CNTD1	124817	37	17	40957867	40957867	Missense_Mutation	SNP	C	T	4	64	c.545C>T	c.(544-546)CCC>CTC	p.P182L
Pat_60	Pre-Treatment	OSBPL7	114881	37	17	45885688	45885688	Missense_Mutation	SNP	T	C	6	30	c.2498A>G	c.(2497-2499)TAT>TGT	p.Y833C
Pat_60	Pre-Treatment	KCNH6	81033	37	17	61611628	61611628	Missense_Mutation	SNP	G	A	3	30	c.1057G>A	c.(1057-1059)GCC>ACC	p.A353T
Pat_60	Pre-Treatment	ABCA6	23460	37	17	67079429	67079429	Missense_Mutation	SNP	G	A	19	68	c.4399C>T	c.(4399-4401)CTC>TTC	p.L1467F
Pat_60	Pre-Treatment	DNAI2	64446	37	17	72310300	72310300	Missense_Mutation	SNP	G	C	2	7	c.1763G>C	c.(1762-1764)GGA>GCA	p.G588A
Pat_60	Pre-Treatment	CD300C	10871	37	17	72539093	72539093	Missense_Mutation	SNP	G	A	7	23	c.434C>T	c.(433-435)TCC>TTC	p.S145F
Pat_60	Pre-Treatment	RNF213	57674	37	17	78319066	78319066	Missense_Mutation	SNP	G	A	5	95	c.1150G>A	c.(1150-1152)GAC>AAC	p.D384N
Pat_60	Pre-Treatment	LAMA1	284217	37	18	7015756	7015756	Missense_Mutation	SNP	C	T	4	71	c.3091G>A	c.(3091-3093)GGG>AGG	p.G1031R
Pat_60	Pre-Treatment	LAMA3	3909	37	18	21329415	21329415	Missense_Mutation	SNP	G	A	5	23	c.589G>A	c.(589-591)GAA>AAA	p.E197K
Pat_60	Pre-Treatment	PHLPP1	23239	37	18	60582241	60582241	Missense_Mutation	SNP	G	A	4	22	c.1268G>A	c.(1267-1269)CGC>CAC	p.R423H
Pat_60	Pre-Treatment	CDH7	1005	37	18	63547825	63547825	Missense_Mutation	SNP	G	A	22	66	c.2053G>A	c.(2053-2055)GAT>AAT	p.D685N
Pat_60	Pre-Treatment	NETO1	81832	37	18	70417450	70417450	Missense_Mutation	SNP	C	T	9	28	c.1388G>A	c.(1387-1389)GGA>GAA	p.G463E

Pat_60	Pre-Treatment	C19orf59	199675	37	19	7743386	7743386	Missense_Mutation	SNP	C	T	8	27	c.383C>T	c.(382-384)TCC>TTC	p.S128F
Pat_60	Pre-Treatment	TSPAN16	26526	37	19	11408863	11408863	Missense_Mutation	SNP	G	A	12	38	c.115G>A	c.(115-117)GGA>AGA	p.G39R
Pat_60	Pre-Treatment	ZNF563	147837	37	19	12429722	12429722	Missense_Mutation	SNP	T	C	10	225	c.1117A>G	c.(1117-1119)ACG>GCG	p.T373A
Pat_60	Pre-Treatment	RFX1	5989	37	19	14074714	14074714	Nonsense_Mutation	SNP	G	A	2	0	c.2317C>T	c.(2317-2319)CAG>TAG	p.Q773*
Pat_60	Pre-Treatment	CPAMD8	27151	37	19	17010338	17010338	Missense_Mutation	SNP	C	T	7	35	c.4937G>A	c.(4936-4938)GGG>GAG	p.G1646E
Pat_60	Pre-Treatment	ZNF93	81931	37	19	20045182	20045182	Missense_Mutation	SNP	A	G	6	198	c.1418A>G	c.(1417-1419)AAA>AGA	p.K473R
Pat_60	Pre-Treatment	LGI4	163175	37	19	35617799	35617799	Missense_Mutation	SNP	C	T	7	17	c.751G>A	c.(751-753)GAC>AAC	p.D251N
Pat_60	Pre-Treatment	FXYD1	5348	37	19	35631041	35631041	Missense_Mutation	SNP	G	A	20	52	c.58G>A	c.(58-60)GCA>ACA	p.A20T
Pat_60	Pre-Treatment	PSG11	5680	37	19	43522979	43522979	Missense_Mutation	SNP	C	T	41	190	c.652G>A	c.(652-654)GAA>AAA	p.E218K
Pat_60	Pre-Treatment	GPR77	27202	37	19	47844378	47844378	Missense_Mutation	SNP	C	T	14	40	c.322C>T	c.(322-324)CGG>TGG	p.R108W
Pat_60	Pre-Treatment	PRR12	57479	37	19	50100975	50100975	Missense_Mutation	SNP	G	C	2	6	c.3383G>C	c.(3382-3384)TGC>TCC	p.C1128S
Pat_60	Pre-Treatment	PRR12	57479	37	19	50104837	50104837	Nonsense_Mutation	SNP	C	T	2	1	c.4435C>T	c.(4435-4437)CAG>TAG	p.Q1479*
Pat_60	Pre-Treatment	SHANK1	50944	37	19	51207744	51207744	Nonsense_Mutation	SNP	G	A	21	47	c.1105C>T	c.(1105-1107)CGA>TGA	p.R369*
Pat_60	Pre-Treatment	ZNF616	90317	37	19	52619191	52619191	Missense_Mutation	SNP	C	T	7	185	c.1226G>A	c.(1225-1227)TGC>TAC	p.C409Y
Pat_60	Pre-Treatment	ZNF534	147658	37	19	52942507	52942507	Missense_Mutation	SNP	A	T	3	24	c.1833A>T	c.(1831-1833)AAA>AAT	p.K611N
Pat_60	Pre-Treatment	ZNF816A	125893	37	19	53454058	53454058	Missense_Mutation	SNP	C	G	9	423	c.970G>C	c.(970-972)GAG>CAG	p.E324Q
Pat_60	Pre-Treatment	VN1R2	317701	37	19	53762364	53762364	Missense_Mutation	SNP	T	A	15	62	c.736T>A	c.(736-738)TTG>ATG	p.L246M
Pat_60	Pre-Treatment	NLRP12	91662	37	19	54313084	54313084	Missense_Mutation	SNP	G	A	6	16	c.1829C>T	c.(1828-1830)TCC>TTC	p.S610F
Pat_60	Pre-Treatment	LILRA3	11026	37	19	54802025	54802025	Missense_Mutation	SNP	G	A	10	77	c.1163C>T	c.(1162-1164)ACC>ATC	p.T388I
Pat_60	Pre-Treatment	LILRB1	10859	37	19	55146569	55146569	Missense_Mutation	SNP	G	C	2	3	c.1498G>C	c.(1498-1500)GAT>CAT	p.D500H
Pat_60	Pre-Treatment	NLRP2	55655	37	19	55501464	55501464	Missense_Mutation	SNP	C	T	3	49	c.2441C>T	c.(2440-2442)ACG>ATG	p.T814M
Pat_60	Pre-Treatment	TNNT1	7138	37	19	55652634	55652634	Missense_Mutation	SNP	C	T	4	21	c.229G>A	c.(229-231)GAG>AAG	p.E77K
Pat_60	Pre-Treatment	PTPRH	5794	37	19	55710101	55710101	Missense_Mutation	SNP	C	T	8	24	c.1600G>A	c.(1600-1602)GAA>AAA	p.E534K
Pat_60	Pre-Treatment	SAPS1	22870	37	19	55741984	55741985	Missense_Mutation	DNP	GA	AC	7	6	.2638_2639TC>G	c.(2638-2640)TCC>GTC	p.S880V
Pat_60	Pre-Treatment	ZNF582	147948	37	19	56903117	56903117	Missense_Mutation	SNP	G	A	12	70	c.5C>T	c.(4-6)TCC>TTC	p.S2F
Pat_60	Pre-Treatment	ZNF324B	388569	37	19	58966837	58966837	Missense_Mutation	SNP	G	A	3	34	c.526G>A	c.(526-528)GAA>AAA	p.E176K
Pat_60	Pre-Treatment	ZNF512	84450	37	2	27844170	27844170	Missense_Mutation	SNP	G	A	5	61	c.1546G>A	c.(1546-1548)GAG>AAG	p.E516K
Pat_60	Pre-Treatment	CAPN13	92291	37	2	30974117	30974117	Missense_Mutation	SNP	C	T	5	38	c.1088G>A	c.(1087-1089)GGA>GAA	p.G363E
Pat_60	Pre-Treatment	PPM1B	5495	37	2	44428478	44428478	Missense_Mutation	SNP	C	T	107	328	c.140C>T	c.(139-141)CCT>CTT	p.P47L
Pat_60	Pre-Treatment	TSPYL6	388951	37	2	54483258	54483258	Missense_Mutation	SNP	C	T	4	50	c.31G>A	c.(31-33)GCT>ACT	p.A11T
Pat_60	Pre-Treatment	AFF3	3899	37	2	100182007	100182007	Missense_Mutation	SNP	C	T	41	79	c.3061G>A	c.(3061-3063)GGC>AGC	p.G1021S
Pat_60	Pre-Treatment	TBC1D8	11138	37	2	101654100	101654100	Missense_Mutation	SNP	G	A	15	68	c.1301C>T	c.(1300-1302)TCT>TTT	p.S434F
Pat_60	Pre-Treatment	RNF149	284996	37	2	101898386	101898386	Missense_Mutation	SNP	G	A	6	158	c.1094C>T	c.(1093-1095)GCT>GTT	p.A365V
Pat_60	Pre-Treatment	IL18R1	8809	37	2	103013120	103013120	Missense_Mutation	SNP	G	A	12	58	c.1400G>A	c.(1399-1401)AGA>AAA	p.R467K
Pat_60	Pre-Treatment	SULT1C2	6819	37	2	108921994	108921994	Missense_Mutation	SNP	C	T	17	37	c.721C>T	c.(721-723)CGT>TGT	p.R241C
Pat_60	Pre-Treatment	RABL2A	11159	37	2	114392676	114392676	Missense_Mutation	SNP	C	T	11	37	c.266C>T	c.(265-267)TCC>TTC	p.S89F
Pat_60	Pre-Treatment	MARCO	8685	37	2	119750742	119750742	Missense_Mutation	SNP	G	A	14	73	c.1295G>A	c.(1294-1296)CGA>CAA	p.R432Q
Pat_60	Pre-Treatment	TFCP2L1	29842	37	2	122004453	122004453	Missense_Mutation	SNP	C	T	24	68	c.598G>A	c.(598-600)GAG>AAG	p.E200K
Pat_60	Pre-Treatment	POTEF	728378	37	2	130877782	130877782	Missense_Mutation	SNP	A	G	5	103	c.307T>C	c.(307-309)TGC>CGC	p.C103R
Pat_60	Pre-Treatment	POTEF	728378	37	2	130877802	130877802	Missense_Mutation	SNP	T	C	5	124	c.287A>G	c.(286-288)AAC>AGC	p.N96S
Pat_60	Pre-Treatment	POTEF	728378	37	2	130877893	130877893	Missense_Mutation	SNP	G	A	5	130	c.196C>T	c.(196-198)CGC>TGC	p.R66C
Pat_60	Pre-Treatment	R3HDM1	23518	37	2	136409471	136409471	Missense_Mutation	SNP	C	T	4	53	c.1792C>T	c.(1792-1794)CCA>TCA	p.P598S
Pat_60	Pre-Treatment	THSD7B	80731	37	2	137814542	137814542	Missense_Mutation	SNP	C	T	27	131	c.599C>T	c.(598-600)TCC>TTC	p.S200F
Pat_60	Pre-Treatment	ZEB2	9839	37	2	145161680	145161680	Missense_Mutation	SNP	G	A	11	36	c.610C>T	c.(610-612)CCA>TCA	p.P204S
Pat_60	Pre-Treatment	NEB	4703	37	2	152548828	152548828	Missense_Mutation	SNP	A	T	19	60	c.1945T>A	c.(1945-1947)TAC>AAC	p.Y649N
Pat_60	Pre-Treatment	SCN1A	6323	37	2	166872150	166872150	Missense_Mutation	SNP	C	T	48	122	c.3484G>A	c.(3484-3486)GAA>AAA	p.E1162K
Pat_60	Pre-Treatment	PPIG	9360	37	2	170465247	170465247	Missense_Mutation	SNP	C	A	4	88	c.356C>A	c.(355-357)ACA>AAA	p.T119K

Pat_60	Pre-Treatment	COL3A1	1281	37	2	189854850	189854850	Missense_Mutation	SNP	G	A	16	75	c.719G>A	c.(718-720)GGA>GAA	p.G240E
Pat_60	Pre-Treatment	CCDC150	284992	37	2	197583288	197583288	Missense_Mutation	SNP	C	T	4	78	c.1928C>T	c.(1927-1929)GCG>GTG	p.A643V
Pat_60	Pre-Treatment	MARS2	92935	37	2	198570245	198570245	Missense_Mutation	SNP	A	G	13	31	c.116A>G	c.(115-117)GAT>GGT	p.D39G
Pat_60	Pre-Treatment	CDK15	65061	37	2	202672367	202672367	Splice_Site	SNP	G	A	4	72	c.273_splice	c.e2+1	p.W91_splice
Pat_60	Pre-Treatment	CXCR2	3579	37	2	218999955	218999955	Missense_Mutation	SNP	G	A	4	35	c.431G>A	c.(430-432)CGT>CAT	p.R144H
Pat_60	Pre-Treatment	RNF25	64320	37	2	219529257	219529257	Missense_Mutation	SNP	G	A	3	26	c.803C>T	c.(802-804)CCT>CTT	p.P268L
Pat_60	Pre-Treatment	EPHA4	2043	37	2	222428987	222428987	Missense_Mutation	SNP	C	T	19	111	c.287G>A	c.(286-288)AGG>AAG	p.R96K
Pat_60	Pre-Treatment	COL4A4	1286	37	2	227953434	227953434	Missense_Mutation	SNP	G	A	11	22	c.1558C>T	c.(1558-1560)CCT>TCT	p.P520S
Pat_60	Pre-Treatment	AGFG1	3267	37	2	228384716	228384716	Missense_Mutation	SNP	C	T	39	112	c.314C>T	c.(313-315)CCA>CTA	p.P105L
Pat_60	Pre-Treatment	INPP5D	3635	37	2	234079721	234079721	Missense_Mutation	SNP	A	T	3	27	c.1912A>T	c.(1912-1914)ATC>TTC	p.I638F
Pat_60	Pre-Treatment	SH3BP4	23677	37	2	235950285	235950285	Missense_Mutation	SNP	G	A	3	39	c.872G>A	c.(871-873)AGG>AAG	p.R291K
Pat_60	Pre-Treatment	HDLBP	3069	37	2	242176128	242176128	Missense_Mutation	SNP	C	T	3	34	c.2806G>A	c.(2806-2808)GAG>AAG	p.E936K
Pat_60	Pre-Treatment	HDLBP	3069	37	2	242186295	242186295	Missense_Mutation	SNP	G	A	7	159	c.1822C>T	c.(1822-1824)CGT>TGT	p.R608C
Pat_60	Pre-Treatment	CRNKL1	51340	37	20	20029140	20029140	Missense_Mutation	SNP	C	T	5	56	c.785G>A	c.(784-786)CGA>CAA	p.R262Q
Pat_60	Pre-Treatment	FRG1B	284802	37	20	29628243	29628243	Missense_Mutation	SNP	T	C	11	273	c.155T>C	c.(154-156)TTG>TCG	p.L52S
Pat_60	Pre-Treatment	FRG1B	284802	37	20	29628245	29628245	Missense_Mutation	SNP	G	A	10	270	c.157G>A	c.(157-159)GCC>ACC	p.A53T
Pat_60	Pre-Treatment	CBFA2T2	9139	37	20	32217691	32217691	Missense_Mutation	SNP	G	A	3	30	c.1226G>A	c.(1225-1227)AGC>AAC	p.S409N
Pat_60	Pre-Treatment	FAM83C	128876	37	20	33874856	33874856	Missense_Mutation	SNP	C	T	4	25	c.1726G>A	c.(1726-1728)GGT>AGT	p.G576S
Pat_60	Pre-Treatment	NCOA3	8202	37	20	46265037	46265038	Missense_Mutation	DNP	CC	TT	21	71	.1907_1908CC>T	c.(1906-1908)TCC>TTT	p.S636F
Pat_60	Pre-Treatment	ZNFX1	57169	37	20	47887292	47887292	Missense_Mutation	SNP	G	A	33	140	c.1057C>T	c.(1057-1059)CTT>TTT	p.L353F
Pat_60	Pre-Treatment	SLC9A8	23315	37	20	48503428	48503428	Missense_Mutation	SNP	C	T	12	45	c.1631C>T	c.(1630-1632)ACG>ATG	p.T544M
Pat_60	Pre-Treatment	TPTE	7179	37	21	10934997	10934997	Missense_Mutation	SNP	C	T	13	220	c.796G>A	c.(796-798)GAA>AAA	p.E266K
Pat_60	Pre-Treatment	BAGE2	85319	37	21	11058226	11058226	Missense_Mutation	SNP	G	C	27	87	c.214C>G	c.(214-216)CCT>GCT	p.P72A
Pat_60	Pre-Treatment	SAMSN1	64092	37	21	15884895	15884895	Splice_Site	SNP	C	T	12	79	c.280_splice	c.e4-1	p.D94_splice
Pat_60	Pre-Treatment	KRTAP24-1	643803	37	21	31655006	31655006	Missense_Mutation	SNP	C	A	4	61	c.245G>T	c.(244-246)AGT>ATT	p.S82I
Pat_60	Pre-Treatment	KRTAP13-2	337959	37	21	31744209	31744209	Missense_Mutation	SNP	C	T	4	61	c.323G>A	c.(322-324)CGC>CAC	p.R108H
Pat_60	Pre-Treatment	UBASH3A	53347	37	21	43846901	43846901	Missense_Mutation	SNP	G	A	3	54	c.1142G>A	c.(1141-1143)AGG>AAG	p.R381K
Pat_60	Pre-Treatment	KRTAP10-6	386674	37	21	46011562	46011562	Missense_Mutation	SNP	G	C	4	56	c.804C>G	c.(802-804)CAC>CAG	p.H268Q
Pat_60	Pre-Treatment	POTEH	23784	37	22	16287387	16287387	Missense_Mutation	SNP	C	T	3	52	c.499G>A	c.(499-501)GAG>AAG	p.E167K
Pat_60	Pre-Treatment	POTEH	23784	37	22	16287542	16287542	Missense_Mutation	SNP	C	T	6	170	c.344G>A	c.(343-345)AGC>AAC	p.S115N
Pat_60	Pre-Treatment	GGT1	2678	37	22	25024123	25024123	Missense_Mutation	SNP	C	T	4	66	c.1412C>T	c.(1411-1413)GCT>GTT	p.A471V
Pat_60	Pre-Treatment	IGLL3	91353	37	22	25715872	25715872	Missense_Mutation	SNP	C	T	4	58	c.494C>T	c.(493-495)ACC>ATC	p.T165I
Pat_60	Pre-Treatment	CCDC157	550631	37	22	30772519	30772519	Missense_Mutation	SNP	C	T	6	201	c.2044C>T	c.(2044-2046)CCT>TCT	p.P682S
Pat_60	Pre-Treatment	MORC2	22880	37	22	31328692	31328692	Missense_Mutation	SNP	C	T	3	33	c.2401G>A	c.(2401-2403)GAT>AAT	p.D801N
Pat_60	Pre-Treatment	PPARA	5465	37	22	46627789	46627789	Missense_Mutation	SNP	G	A	3	43	c.812G>A	c.(811-813)CGC>CAC	p.R271H
Pat_60	Pre-Treatment	CELSR1	9620	37	22	46930933	46930933	Missense_Mutation	SNP	C	T	4	37	c.2135G>A	c.(2134-2136)CGC>CAC	p.R712H
Pat_60	Pre-Treatment	SRGAP3	9901	37	3	9146424	9146424	Missense_Mutation	SNP	C	T	6	34	c.363G>A	c.(361-363)ATG>ATA	p.M121I
Pat_60	Pre-Treatment	FGD5	152273	37	3	14861314	14861314	Missense_Mutation	SNP	G	T	2	0	c.736G>T	c.(736-738)GCT>TCT	p.A246S
Pat_60	Pre-Treatment	LRRC3B	116135	37	3	26751407	26751407	Missense_Mutation	SNP	G	A	12	37	c.244G>A	c.(244-246)GAA>AAA	p.E82K
Pat_60	Pre-Treatment	C3orf35	339883	37	3	37458971	37458971	Missense_Mutation	SNP	C	T	10	20	c.214C>T	c.(214-216)CTT>TTT	p.L72F
Pat_60	Pre-Treatment	SCN11A	11280	37	3	38913199	38913199	Missense_Mutation	SNP	C	T	7	33	c.3496G>A	c.(3496-3498)GTG>ATG	p.V1166M
Pat_60	Pre-Treatment	KBTBD5	131377	37	3	42728002	42728002	Missense_Mutation	SNP	G	A	46	102	c.892G>A	c.(892-894)GCC>ACC	p.A298T
Pat_60	Pre-Treatment	CCR9	10803	37	3	45942741	45942741	Missense_Mutation	SNP	C	A	4	33	c.461C>A	c.(460-462)GCA>GAA	p.A154E
Pat_60	Pre-Treatment	COL7A1	1294	37	3	48602626	48602626	Missense_Mutation	SNP	G	A	3	12	c.8536C>T	c.(8536-8538)CCC>TCC	p.P2846S
Pat_60	Pre-Treatment	UBA7	7318	37	3	49850941	49850941	Missense_Mutation	SNP	G	A	11	47	c.196C>T	c.(196-198)CCC>TCC	p.P66S
Pat_60	Pre-Treatment	ADAMTS9	56999	37	3	64579933	64579933	Splice_Site	SNP	C	T	25	86	c.4356_splice	c.e28+1	p.S1452_splice
Pat_60	Pre-Treatment	EPHA3	2042	37	3	89499348	89499348	Missense_Mutation	SNP	G	A	11	38	c.2518G>A	c.(2518-2520)GGC>AGC	p.G840S

Pat_60	Pre-Treatment	ABI3BP	25890	37	3	100497211	100497211	Missense_Mutation	SNP	C	T	3	54	c.2117G>A	c.(2116-2118)CGC>CAC	p.R706H
Pat_60	Pre-Treatment	ALCAM	214	37	3	105268981	105268981	Missense_Mutation	SNP	C	T	54	210	c.1385C>T	c.(1384-1386)TCT>TTT	p.S462F
Pat_60	Pre-Treatment	CCDC54	84692	37	3	107096571	107096571	Missense_Mutation	SNP	C	T	54	179	c.137C>T	c.(136-138)CCC>CTC	p.P46L
Pat_60	Pre-Treatment	GUCA1C	9626	37	3	108626922	108626922	Missense_Mutation	SNP	C	T	3	38	c.577G>A	c.(577-579)GAC>AAC	p.D193N
Pat_60	Pre-Treatment	DPPA2	151871	37	3	109023481	109023481	Missense_Mutation	SNP	G	A	8	51	c.695C>T	c.(694-696)TCG>TTG	p.S232L
Pat_60	Pre-Treatment	CD96	10225	37	3	111263979	111263979	Missense_Mutation	SNP	G	A	29	145	c.148G>A	c.(148-150)GTA>ATA	p.V50I
Pat_60	Pre-Treatment	KIAA2018	205717	37	3	113379206	113379206	Missense_Mutation	SNP	G	T	3	56	c.1323C>A	c.(1321-1323)AAC>AAA	p.N441K
Pat_60	Pre-Treatment	ATP6V1A	523	37	3	113513976	113513976	Missense_Mutation	SNP	C	T	18	58	c.1151C>T	c.(1150-1152)TCG>TTG	p.S384L
Pat_60	Pre-Treatment	RHO	6010	37	3	129251606	129251606	Missense_Mutation	SNP	G	A	4	35	c.927G>A	c.(925-927)ATG>ATA	p.M309I
Pat_60	Pre-Treatment	COL6A6	131873	37	3	130282320	130282320	Missense_Mutation	SNP	G	A	9	27	c.473G>A	c.(472-474)GGA>GAA	p.G158E
Pat_60	Pre-Treatment	GRK7	131890	37	3	141526568	141526568	Missense_Mutation	SNP	G	A	24	71	c.1132G>A	c.(1132-1134)GGA>AGA	p.G378R
Pat_60	Pre-Treatment	GRK7	131890	37	3	141535584	141535584	Missense_Mutation	SNP	C	T	9	81	c.1354C>T	c.(1354-1356)CAT>TAT	p.H452Y
Pat_60	Pre-Treatment	PLSCR4	57088	37	3	145924423	145924423	Missense_Mutation	SNP	G	A	4	64	c.244C>T	c.(244-246)CGG>TGG	p.R82W
Pat_60	Pre-Treatment	PIK3CA	5290	37	3	178936076	178936076	Missense_Mutation	SNP	C	T	24	89	c.1618C>T	c.(1618-1620)CTC>TTC	p.L540F
Pat_60	Pre-Treatment	ABCF3	55324	37	3	183906159	183906159	Missense_Mutation	SNP	G	A	4	96	c.800G>A	c.(799-801)AGG>AAG	p.R267K
Pat_60	Pre-Treatment	MASP1	5648	37	3	187003811	187003812	Missense_Mutation	DNP	GG	AA	6	35	c.38_39CC>TT	c.(37-39)TCC>TTT	p.S13F
Pat_60	Pre-Treatment	BCL6	604	37	3	187451346	187451346	Missense_Mutation	SNP	G	A	55	169	c.136C>T	c.(136-138)CAT>TAT	p.H46Y
Pat_60	Pre-Treatment	ZNF595	152687	37	4	59971	59971	Missense_Mutation	SNP	G	A	22	482	c.151G>A	c.(151-153)GAC>AAC	p.D51N
Pat_60	Pre-Treatment	SORCS2	57537	37	4	7398082	7398082	Missense_Mutation	SNP	G	A	3	24	c.548G>A	c.(547-549)CGG>CAG	p.R183Q
Pat_60	Pre-Treatment	DHX15	1665	37	4	24556475	24556475	Missense_Mutation	SNP	G	A	63	221	c.953C>T	c.(952-954)CCT>CTT	p.P318L
Pat_60	Pre-Treatment	TBC1D19	55296	37	4	26616029	26616029	Splice_Site	SNP	G	A	15	75	c.173_splice	c.e3-1	p.G58_splice
Pat_60	Pre-Treatment	LRRC66	339977	37	4	52862055	52862055	Missense_Mutation	SNP	G	T	3	14	c.1133C>A	c.(1132-1134)GCG>GAG	p.A378E
Pat_60	Pre-Treatment	ARL9	132946	37	4	57384885	57384885	Missense_Mutation	SNP	C	A	5	112	c.58C>A	c.(58-60)CTA>ATA	p.L20I
Pat_60	Pre-Treatment	MUC7	4589	37	4	71347312	71347312	Missense_Mutation	SNP	C	T	79	225	c.851C>T	c.(850-852)CCA>CTA	p.P284L
Pat_60	Pre-Treatment	NPFFR2	10886	37	4	73013491	73013491	Missense_Mutation	SNP	G	A	14	52	c.1531G>A	c.(1531-1533)GAA>AAA	p.E511K
Pat_60	Pre-Treatment	GPRIN3	285513	37	4	90170888	90170888	Missense_Mutation	SNP	G	T	5	113	c.374C>A	c.(373-375)CCA>CAA	p.P125Q
Pat_60	Pre-Treatment	EMCN	51705	37	4	101331494	101331494	Missense_Mutation	SNP	C	T	44	116	c.770G>A	c.(769-771)GGA>GAA	p.G257E
Pat_60	Pre-Treatment	HSPA4L	22824	37	4	128732745	128732745	Missense_Mutation	SNP	C	A	4	59	c.1532C>A	c.(1531-1533)CCA>CAA	p.P511Q
Pat_60	Pre-Treatment	PCDH18	54510	37	4	138451711	138451711	Missense_Mutation	SNP	C	T	24	107	c.1532G>A	c.(1531-1533)GGA>GAA	p.G511E
Pat_60	Pre-Treatment	MAML3	55534	37	4	140641414	140641414	Missense_Mutation	SNP	C	T	3	39	c.2465G>A	c.(2464-2466)CGG>CAG	p.R822Q
Pat_60	Pre-Treatment	SORBS2	8470	37	4	186545415	186545415	Missense_Mutation	SNP	C	T	11	14	c.1156G>A	c.(1156-1158)GAT>AAT	p.D386N
Pat_60	Pre-Treatment	DNAH5	1767	37	5	13769246	13769246	Splice_Site	SNP	C	T	19	100	c.9721_splice	c.e58-1	p.V3241_splice
Pat_60	Pre-Treatment	DNAH5	1767	37	5	13865814	13865814	Missense_Mutation	SNP	C	T	12	37	c.4318G>A	c.(4318-4320)GAA>AAA	p.E1440K
Pat_60	Pre-Treatment	PDZD2	23037	37	5	31799647	31799647	Missense_Mutation	SNP	G	A	15	60	c.292G>A	c.(292-294)GAA>AAA	p.E98K
Pat_60	Pre-Treatment	ADAMTS12	81792	37	5	33648935	33648935	Missense_Mutation	SNP	C	T	15	52	c.1471G>A	c.(1471-1473)GAA>AAA	p.E491K
Pat_60	Pre-Treatment	EGFLAM	133584	37	5	38370509	38370509	Missense_Mutation	SNP	G	A	3	27	c.657G>A	c.(655-657)ATG>ATA	p.M219I
Pat_60	Pre-Treatment	OSMR	9180	37	5	38904103	38904103	Missense_Mutation	SNP	C	T	9	47	c.1111C>T	c.(1111-1113)CAT>TAT	p.H371Y
Pat_60	Pre-Treatment	FBXL21	26223	37	5	135277202	135277202	Missense_Mutation	SNP	A	C	6	29	c.1147A>C	c.(1147-1149)ATC>CTC	p.I383L
Pat_60	Pre-Treatment	PCDHA5	56143	37	5	140202306	140202306	Missense_Mutation	SNP	G	A	12	26	c.946G>A	c.(946-948)GAA>AAA	p.E316K
Pat_60	Pre-Treatment	PCDHA5	56143	37	5	140202678	140202678	Missense_Mutation	SNP	G	A	4	42	c.1318G>A	c.(1318-1320)GTG>ATG	p.V440M
Pat_60	Pre-Treatment	PCDHA13	56136	37	5	140263608	140263609	Missense_Mutation	DNP	GG	AA	4	19	.1755_1756GG>A	753-1758)GTGGGT>GTA	p.G586S
Pat_60	Pre-Treatment	PCDHB17	54661	37	5	140536776	140536776	Missense_Mutation	SNP	T	G	5	11	c.1197T>G	c.(1195-1197)AAT>AAG	p.N399K
Pat_60	Pre-Treatment	PPP2R2B	5521	37	5	146077647	146077647	Missense_Mutation	SNP	C	T	36	162	c.229G>A	c.(229-231)GAA>AAA	p.E77K
Pat_60	Pre-Treatment	SPINK5	11005	37	5	147503414	147503414	Nonsense_Mutation	SNP	C	T	17	52	c.2557C>T	c.(2557-2559)CGA>TGA	p.R853*
Pat_60	Pre-Treatment	FBXO38	81545	37	5	147807131	147807131	Missense_Mutation	SNP	G	T	4	31	c.2274G>T	c.(2272-2274)GAG>GAT	p.E758D
Pat_60	Pre-Treatment	FAT2	2196	37	5	150932903	150932903	Missense_Mutation	SNP	G	A	3	51	c.3991C>T	c.(3991-3993)CGG>TGG	p.R1331W
Pat_60	Pre-Treatment	ODZ2	57451	37	5	167517603	167517603	Missense_Mutation	SNP	G	A	16	46	c.1540G>A	c.(1540-1542)GGG>AGG	p.G514R

Pat_60	Pre-Treatment	DCDC2	51473	37	6	24278352	24278352	Missense_Mutation	SNP	C	T	4	51	c.847G>A	c.(847-849)GTG>ATG	p.V283M
Pat_60	Pre-Treatment	KIAA0319	9856	37	6	24556868	24556868	Nonsense_Mutation	SNP	G	A	4	35	c.2824C>T	c.(2824-2826)CAG>TAG	p.Q942*
Pat_60	Pre-Treatment	ZNF165	7718	37	6	28057020	28057020	Missense_Mutation	SNP	C	G	3	72	c.1230C>G	c.(1228-1230)AAC>AAG	p.N410K
Pat_60	Pre-Treatment	HLA-L	3139	37	6	30229388	30229388	Missense_Mutation	SNP	C	T	5	126	c.356C>T	c.(355-357)CCC>CTC	p.P119L
Pat_60	Pre-Treatment	BAT5	7920	37	6	31659379	31659379	Missense_Mutation	SNP	C	T	4	44	c.820G>A	c.(820-822)GCT>ACT	p.A274T
Pat_60	Pre-Treatment	FKBP5	2289	37	6	35558971	35558971	Missense_Mutation	SNP	G	A	20	96	c.692C>T	c.(691-693)CCT>CTT	p.P231L
Pat_60	Pre-Treatment	BRPF3	27154	37	6	36178152	36178152	Missense_Mutation	SNP	C	T	13	44	c.2026C>T	c.(2026-2028)CAC>TAC	p.H676Y
Pat_60	Pre-Treatment	C6orf222	389384	37	6	36298400	36298400	Missense_Mutation	SNP	T	A	7	28	c.68A>T	c.(67-69)CAG>CTG	p.Q23L
Pat_60	Pre-Treatment	MEP1A	4224	37	6	46797239	46797239	Missense_Mutation	SNP	G	A	41	162	c.1075G>A	c.(1075-1077)GTT>ATT	p.V359I
Pat_60	Pre-Treatment	FAM83B	222584	37	6	54804943	54804943	Missense_Mutation	SNP	G	A	16	66	c.1174G>A	c.(1174-1176)GAA>AAA	p.E392K
Pat_60	Pre-Treatment	BAI3	577	37	6	69728368	69728368	Missense_Mutation	SNP	C	T	36	80	c.2084C>T	c.(2083-2085)TCA>TTA	p.S695L
Pat_60	Pre-Treatment	COL9A1	1297	37	6	70990720	70990720	Missense_Mutation	SNP	G	A	5	16	c.899C>T	c.(898-900)CCC>CTC	p.P300L
Pat_60	Pre-Treatment	ROS1	6098	37	6	117700235	117700235	Missense_Mutation	SNP	G	A	19	69	c.2584C>T	c.(2584-2586)CTT>TTT	p.L862F
Pat_60	Pre-Treatment	DCBLD1	285761	37	6	117841060	117841061	Missense_Mutation	DNP	CC	TA	39	94	c.407_408CC>TA	c.(406-408)TCC>TTA	p.S136L
Pat_60	Pre-Treatment	SAMD3	154075	37	6	130465688	130465688	Missense_Mutation	SNP	C	T	8	56	c.1540G>A	c.(1540-1542)GGA>AGA	p.G514R
Pat_60	Pre-Treatment	TMEM200A	114801	37	6	130762526	130762526	Missense_Mutation	SNP	G	A	15	49	c.959G>A	c.(958-960)AGG>AAG	p.R320K
Pat_60	Pre-Treatment	TMEM200A	114801	37	6	130762853	130762853	Missense_Mutation	SNP	G	A	17	73	c.1286G>A	c.(1285-1287)GGA>GAA	p.G429E
Pat_60	Pre-Treatment	TXLNB	167838	37	6	139609804	139609804	Missense_Mutation	SNP	C	T	19	62	c.233G>A	c.(232-234)GGG>GAG	p.G78E
Pat_60	Pre-Treatment	NOX3	50508	37	6	155717999	155717999	Missense_Mutation	SNP	G	A	57	154	c.1678C>T	c.(1678-1680)CAT>TAT	p.H560Y
Pat_60	Pre-Treatment	TAGAP	117289	37	6	159465024	159465024	Missense_Mutation	SNP	C	T	46	284	c.67G>A	c.(67-69)GAA>AAA	p.E23K
Pat_60	Pre-Treatment	IGF2R	3482	37	6	160461636	160461636	Missense_Mutation	SNP	T	C	31	99	c.1360T>C	c.(1360-1362)TGC>CGC	p.C454R
Pat_60	Pre-Treatment	RPS6KA2	6196	37	6	166923789	166923789	Missense_Mutation	SNP	G	A	20	72	c.355C>T	c.(355-357)CCC>TCC	p.P119S
Pat_60	Pre-Treatment	THBS2	7058	37	6	169648945	169648945	Missense_Mutation	SNP	C	T	4	75	c.176G>A	c.(175-177)CGC>CAC	p.R59H
Pat_60	Pre-Treatment	DPY19L2P1	554236	37	7	35131480	35131480	Missense_Mutation	SNP	A	T	5	86	c.1106T>A	c.(1105-1107)CTT>CAT	p.L369H
Pat_60	Pre-Treatment	NPC1L1	29881	37	7	44578911	44578911	Missense_Mutation	SNP	G	A	4	36	c.1085C>T	c.(1084-1086)CCG>CTG	p.P362L
Pat_60	Pre-Treatment	TNS3	64759	37	7	47343018	47343018	Missense_Mutation	SNP	G	A	15	13	c.2987C>T	c.(2986-2988)CCT>CTT	p.P996L
Pat_60	Pre-Treatment	ZNF727	442319	37	7	63538806	63538806	Missense_Mutation	SNP	C	G	10	85	c.1379C>G	c.(1378-1380)ACC>AGC	p.T460S
Pat_60	Pre-Treatment	ZNF727	442319	37	7	63538818	63538818	Missense_Mutation	SNP	C	T	8	76	c.1391C>T	c.(1390-1392)TCC>TTC	p.S464F
Pat_60	Pre-Treatment	TPST1	8460	37	7	65706122	65706122	Missense_Mutation	SNP	T	A	46	63	c.710T>A	c.(709-711)GTT>GAT	p.V237D
Pat_60	Pre-Treatment	SPDYE5	442590	37	7	75130895	75130895	Missense_Mutation	SNP	C	T	14	313	c.770C>T	c.(769-771)CCG>CTG	p.P257L
Pat_60	Pre-Treatment	POR	5447	37	7	75609725	75609725	Missense_Mutation	SNP	G	T	4	58	c.435G>T	c.(433-435)GAG>GAT	p.E145D
Pat_60	Pre-Treatment	PCLO	27445	37	7	82583326	82583326	Missense_Mutation	SNP	C	T	75	172	c.6943G>A	c.(6943-6945)GAA>AAA	p.E2315K
Pat_60	Pre-Treatment	PCLO	27445	37	7	82764435	82764435	Missense_Mutation	SNP	C	T	31	119	c.2431G>A	c.(2431-2433)GAA>AAA	p.E811K
Pat_60	Pre-Treatment	C7orf63	79846	37	7	89912208	89912208	Missense_Mutation	SNP	C	T	65	115	c.1375C>T	c.(1375-1377)CCG>TCG	p.P459S
Pat_60	Pre-Treatment	COL1A2	1278	37	7	94054936	94054936	Missense_Mutation	SNP	C	A	21	89	c.2796C>A	c.(2794-2796)AAC>AAA	p.N932K
Pat_60	Pre-Treatment	TECPR1	25851	37	7	97851045	97851045	Missense_Mutation	SNP	G	A	13	24	c.3085C>T	c.(3085-3087)CCG>TCG	p.P1029S
Pat_60	Pre-Treatment	RINT1	60561	37	7	105182999	105183000	Missense_Mutation	DNP	CC	TT	58	102	c.418_419CC>TT	c.(418-420)CCT>TTT	p.P140F
Pat_60	Pre-Treatment	CHRM2	1129	37	7	136700538	136700538	Missense_Mutation	SNP	C	T	43	72	c.926C>T	c.(925-927)TCC>TTC	p.S309F
Pat_60	Pre-Treatment	BRAF	673	37	7	140453136	140453136	Missense_Mutation	SNP	A	T	60	154	c.1799T>A	c.(1798-1800)GTG>GAG	p.V600E
Pat_60	Pre-Treatment	MGAM	8972	37	7	141736669	141736669	Missense_Mutation	SNP	C	T	46	137	c.2123C>T	c.(2122-2124)TCC>TTC	p.S708F
Pat_60	Pre-Treatment	TRPV5	56302	37	7	142612674	142612674	Missense_Mutation	SNP	G	A	23	49	c.1187C>T	c.(1186-1188)GCT>GTT	p.A396V
Pat_60	Pre-Treatment	TMEM176A	55365	37	7	150501550	150501550	Missense_Mutation	SNP	C	A	4	63	c.656C>A	c.(655-657)CCA>CAA	p.P219Q
Pat_60	Pre-Treatment	SLC4A2	6522	37	7	150761646	150761646	Missense_Mutation	SNP	C	T	26	160	c.251C>T	c.(250-252)CCA>CTA	p.P84L
Pat_60	Pre-Treatment	OR4F21	441308	37	8	116882	116882	Missense_Mutation	SNP	G	A	7	160	c.143C>T	c.(142-144)TCT>TTT	p.S48F
Pat_60	Pre-Treatment	TEX15	56154	37	8	30701064	30701064	Missense_Mutation	SNP	C	T	8	52	c.5470G>A	c.(5470-5472)GAC>AAC	p.D1824N
Pat_60	Pre-Treatment	IDO2	169355	37	8	39871214	39871214	Missense_Mutation	SNP	C	T	6	11	c.889C>T	c.(889-891)CGT>TGT	p.R297C
Pat_60	Pre-Treatment	PXDNL	137902	37	8	52233411	52233411	Missense_Mutation	SNP	A	G	34	112	c.4193T>C	c.(4192-4194)GTT>GCT	p.V1398A

Pat_60	Pre-Treatment	RP1	6101	37	8	55539311	55539311	Missense_Mutation	SNP	C	T	7	27	c.2869C>T	c.(2869-2871)CCC>TCC	p.P957S
Pat_60	Pre-Treatment	RSPO2	340419	37	8	109001454	109001454	Missense_Mutation	SNP	G	A	16	45	c.113C>T	c.(112-114)CCC>CTC	p.P38L
Pat_60	Pre-Treatment	PKHD1L1	93035	37	8	110422157	110422157	Missense_Mutation	SNP	G	A	12	48	c.2035G>A	c.(2035-2037)GAA>AAA	p.E679K
Pat_60	Pre-Treatment	PHF20L1	51105	37	8	133854806	133854806	Nonsense_Mutation	SNP	C	T	4	86	c.2434C>T	c.(2434-2436)CGA>TGA	p.R812*
Pat_60	Pre-Treatment	NAPRT1	93100	37	8	144657647	144657647	Missense_Mutation	SNP	C	T	6	32	c.1237G>A	c.(1237-1239)GAG>AAG	p.E413K
Pat_60	Pre-Treatment	SCRIB	23513	37	8	144892711	144892711	Missense_Mutation	SNP	C	T	4	29	c.1468G>A	c.(1468-1470)GGG>AGG	p.G490R
Pat_60	Pre-Treatment	HEATR7A	727957	37	8	145235352	145235352	Missense_Mutation	SNP	C	T	3	28	c.488C>T	c.(487-489)CCA>CTA	p.P163L
Pat_60	Pre-Treatment	FOXH1	8928	37	8	145700055	145700055	Missense_Mutation	SNP	G	A	2	1	c.664C>T	c.(664-666)CTT>TTT	p.L222F
Pat_60	Pre-Treatment	C9orf66	157983	37	9	214571	214571	Missense_Mutation	SNP	C	G	3	48	c.826G>C	c.(826-828)GTA>CTA	p.V276L
Pat_60	Pre-Treatment	TAF1L	138474	37	9	32635567	32635567	Missense_Mutation	SNP	C	T	3	35	c.11G>A	c.(10-12)GGC>GAC	p.G4D
Pat_60	Pre-Treatment	ECM2	1842	37	9	95277148	95277148	Missense_Mutation	SNP	C	A	4	79	c.819G>T	c.(817-819)GAG>GAT	p.E273D
Pat_60	Pre-Treatment	FBP1	2203	37	9	97367767	97367767	Missense_Mutation	SNP	G	A	4	17	c.797C>T	c.(796-798)CCC>CTC	p.P266L
Pat_60	Pre-Treatment	TDRD7	23424	37	9	100227273	100227273	Missense_Mutation	SNP	G	A	4	41	c.1592G>A	c.(1591-1593)CGG>CAG	p.R531Q
Pat_60	Pre-Treatment	LPPR1	54886	37	9	104048494	104048494	Missense_Mutation	SNP	C	T	17	59	c.361C>T	c.(361-363)CTT>TTT	p.L121F
Pat_60	Pre-Treatment	DFNB31	25861	37	9	117228648	117228648	Missense_Mutation	SNP	G	A	4	70	c.862C>T	c.(862-864)CGG>TGG	p.R288W
Pat_60	Pre-Treatment	TNC	3371	37	9	117849526	117849526	Missense_Mutation	SNP	T	A	4	64	c.484A>T	c.(484-486)AGC>TGC	p.S162C
Pat_60	Pre-Treatment	C9orf86	55684	37	9	139726805	139726805	Missense_Mutation	SNP	C	T	8	17	c.688C>T	c.(688-690)CCA>TCA	p.P230S
Pat_60	Pre-Treatment	MAP3K15	389840	37	X	19389142	19389142	Missense_Mutation	SNP	C	A	3	20	c.1760G>T	c.(1759-1761)TGG>TTG	p.W587L
Pat_60	Pre-Treatment	ZNF645	158506	37	X	22292379	22292379	Missense_Mutation	SNP	G	A	3	41	c.1271G>A	c.(1270-1272)CGG>CAG	p.R424Q
Pat_60	Pre-Treatment	USP11	8237	37	X	47092338	47092338	Missense_Mutation	SNP	G	A	48	42	c.25G>A	c.(25-27)GGG>AGG	p.G9R
Pat_60	Pre-Treatment	MED12	9968	37	X	70343001	70343001	Nonsense_Mutation	SNP	C	A	4	56	c.1542C>A	c.(1540-1542)TGC>TGA	p.C514*
Pat_60	Pre-Treatment	NLGN3	54413	37	X	70389720	70389720	Missense_Mutation	SNP	G	A	2	0	c.2260G>A	c.(2260-2262)GAG>AAG	p.E754K
Pat_60	Pre-Treatment	RHOXF2B	727940	37	X	119211063	119211063	Nonsense_Mutation	SNP	C	T	7	7	c.270G>A	c.(268-270)TGG>TGA	p.W90*
Pat_60	Pre-Treatment	ACTRT1	139741	37	X	127185072	127185072	Nonsense_Mutation	SNP	G	A	37	57	c.1114C>T	c.(1114-1116)CAA>TAA	p.Q372*
Pat_60	Pre-Treatment	GABRQ	55879	37	X	151821199	151821199	Missense_Mutation	SNP	G	A	5	23	c.1354G>A	c.(1354-1356)GAT>AAT	p.D452N
Pat_60	Pre-Treatment	FAM58A	92002	37	X	152860138	152860138	Splice_Site	SNP	C	T	4	19	c.111_splice	c.e2-1	p.R37_splice
Pat_60	Post-Resistance	RER1	11079	37	1	2334544	2334544	Missense_Mutation	SNP	G	A	4	175	c.572G>A	c.(571-573)GGC>GAC	p.G191D
Pat_60	Post-Resistance	PLEKHG5	57449	37	1	6528590	6528590	Missense_Mutation	SNP	G	A	4	47	c.2474C>T	c.(2473-2475)ACG>ATG	p.T825M
Pat_60	Post-Resistance	PGD	5226	37	1	10477527	10477527	Missense_Mutation	SNP	G	A	4	112	c.1070G>A	c.(1069-1071)GGC>GAC	p.G357D
Pat_60	Post-Resistance	PRDM2	7799	37	1	14106586	14106586	Missense_Mutation	SNP	G	A	4	129	c.2296G>A	c.(2296-2298)GCC>ACC	p.A766T
Pat_60	Post-Resistance	PRDM2	7799	37	1	14107382	14107382	Missense_Mutation	SNP	C	T	38	146	c.3092C>T	c.(3091-3093)CCC>CTC	p.P1031L
Pat_60	Post-Resistance	AGMAT	79814	37	1	15904220	15904220	Missense_Mutation	SNP	C	T	18	84	c.860G>A	c.(859-861)GGG>GAG	p.G287E
Pat_60	Post-Resistance	SPEN	23013	37	1	16261229	16261229	Missense_Mutation	SNP	G	A	4	98	c.8494G>A	c.(8494-8496)GCC>ACC	p.A2832T
Pat_60	Post-Resistance	ZBTB17	7709	37	1	16268546	16268546	Missense_Mutation	SNP	C	T	4	54	c.2330G>A	c.(2329-2331)CGC>CAC	p.R777H
Pat_60	Post-Resistance	FBXO42	54455	37	1	16583189	16583189	Missense_Mutation	SNP	C	A	4	134	c.568G>T	c.(568-570)GGT>TGT	p.G190C
Pat_60	Post-Resistance	PAX7	5081	37	1	19062346	19062346	Missense_Mutation	SNP	G	A	4	91	c.1376G>A	c.(1375-1377)GGC>GAC	p.G459D
Pat_60	Post-Resistance	RAP1GAP	5909	37	1	21926018	21926018	Missense_Mutation	SNP	G	A	4	61	c.1745C>T	c.(1744-1746)ACG>ATG	p.T582M
Pat_60	Post-Resistance	RUNX3	864	37	1	25254076	25254076	Missense_Mutation	SNP	C	T	4	147	c.428G>A	c.(427-429)CGC>CAC	p.R143H
Pat_60	Post-Resistance	UBXN11	91544	37	1	26610879	26610879	Missense_Mutation	SNP	G	A	4	69	c.947C>T	c.(946-948)GCC>GTC	p.A316V
Pat_60	Post-Resistance	SF3A3	10946	37	1	38435058	38435058	Nonsense_Mutation	SNP	G	A	4	119	c.1249C>T	c.(1249-1251)CGA>TGA	p.R417*
Pat_60	Post-Resistance	MACF1	23499	37	1	39896494	39896494	Missense_Mutation	SNP	G	A	4	157	c.12571G>A	c.(12571-12573)GAT>AAT	p.D4191N
Pat_60	Post-Resistance	KDM4A	9682	37	1	44137341	44137341	Missense_Mutation	SNP	C	G	3	98	c.1529C>G	c.(1528-1530)TCT>TGT	p.S510C
Pat_60	Post-Resistance	OSBPL9	114883	37	1	52252264	52252264	Missense_Mutation	SNP	G	A	4	134	c.1975G>A	c.(1975-1977)GAT>AAT	p.D659N
Pat_60	Post-Resistance	CPT2	1376	37	1	53676382	53676382	Missense_Mutation	SNP	G	A	4	63	c.1036G>A	c.(1036-1038)GAT>AAT	p.D346N
Pat_60	Post-Resistance	INADL	10207	37	1	62582843	62582843	Nonsense_Mutation	SNP	C	T	44	182	c.4843C>T	c.(4843-4845)CGA>TGA	p.R1615*
Pat_60	Post-Resistance	KANK4	163782	37	1	62740084	62740084	Missense_Mutation	SNP	C	T	10	39	c.692G>A	c.(691-693)GGA>GAA	p.G231E
Pat_60	Post-Resistance	C1orf146	388649	37	1	92710383	92710383	Missense_Mutation	SNP	A	C	38	161	c.377A>C	c.(376-378)AAT>ACT	p.N126T

Pat_60	Post-Resistance	COL11A1	1301	37	1	103470043	103470043	Missense_Mutation	SNP	C	T	26	101	c.1901G>A	c.(1900-1902)GGA>GAA	p.G634E
Pat_60	Post-Resistance	CLCC1	23155	37	1	109479710	109479710	Missense_Mutation	SNP	C	T	4	175	c.1372G>A	c.(1372-1374)GTG>ATG	p.V458M
Pat_60	Post-Resistance	C1orf194	127003	37	1	109649210	109649210	Missense_Mutation	SNP	C	T	75	204	c.386G>A	c.(385-387)AGA>AAA	p.R129K
Pat_60	Post-Resistance	KIAA1324	57535	37	1	109707201	109707201	Missense_Mutation	SNP	G	A	4	182	c.355G>A	c.(355-357)GGC>AGC	p.G119S
Pat_60	Post-Resistance	KCNA10	3744	37	1	111061007	111061007	Missense_Mutation	SNP	G	A	4	129	c.403C>T	c.(403-405)CGG>TGG	p.R135W
Pat_60	Post-Resistance	SYCP1	6847	37	1	115428861	115428861	Missense_Mutation	SNP	C	T	85	283	c.1121C>T	c.(1120-1122)TCG>TTG	p.S374L
Pat_60	Post-Resistance	ATP1A1	476	37	1	116946598	116946598	Splice_Site	SNP	G	A	4	137	c.3043_splice	c.e22+1	.G1015_splice
Pat_60	Post-Resistance	PHGDH	26227	37	1	120277981	120277981	Missense_Mutation	SNP	G	A	4	128	c.707G>A	c.(706-708)CGT>CAT	p.R236H
Pat_60	Post-Resistance	NOTCH2NL	388677	37	1	145290447	145290447	Missense_Mutation	SNP	C	T	30	662	c.653C>T	c.(652-654)CCT>CTT	p.P218L
Pat_60	Post-Resistance	NBPF10	100132406	37	1	145304523	145304523	Missense_Mutation	SNP	C	T	75	609	c.1456C>T	c.(1456-1458)CAT>TAT	p.H486Y
Pat_60	Post-Resistance	ITGA10	8515	37	1	145527721	145527721	Missense_Mutation	SNP	G	A	4	115	c.161G>A	c.(160-162)CGA>CAA	p.R54Q
Pat_60	Post-Resistance	RPRD2	23248	37	1	150429902	150429902	Missense_Mutation	SNP	C	T	80	231	c.1009C>T	c.(1009-1011)CCT>TCT	p.P337S
Pat_60	Post-Resistance	PSMD4	5710	37	1	151237946	151237946	Missense_Mutation	SNP	C	T	4	70	c.515C>T	c.(514-516)ACA>ATA	p.T172I
Pat_60	Post-Resistance	RFX5	5993	37	1	151315846	151315846	Missense_Mutation	SNP	G	A	32	66	c.830C>T	c.(829-831)GCC>GTC	p.A277V
Pat_60	Post-Resistance	TCHH	7062	37	1	152083040	152083040	Missense_Mutation	SNP	G	A	4	172	c.2653C>T	c.(2653-2655)CGC>TGC	p.R885C
Pat_60	Post-Resistance	S100A7L2	645922	37	1	153410754	153410754	Missense_Mutation	SNP	G	A	27	87	c.85C>T	c.(85-87)CGC>TGC	p.R29C
Pat_60	Post-Resistance	ADAR	103	37	1	154558299	154558299	Missense_Mutation	SNP	C	A	4	45	c.3245G>T	c.(3244-3246)TGT>TTT	p.C1082F
Pat_60	Post-Resistance	RUSC1	23623	37	1	155292654	155292654	Missense_Mutation	SNP	C	T	3	37	c.1090C>T	c.(1090-1092)CCT>TCT	p.P364S
Pat_60	Post-Resistance	ASH1L	55870	37	1	155451975	155451975	Missense_Mutation	SNP	G	A	4	108	c.686C>T	c.(685-687)CCT>CTT	p.P229L
Pat_60	Post-Resistance	IQGAP3	128239	37	1	156526468	156526468	Missense_Mutation	SNP	G	A	3	60	c.1147C>T	c.(1147-1149)CGG>TGG	p.R383W
Pat_60	Post-Resistance	CD1A	909	37	1	158226022	158226022	Missense_Mutation	SNP	G	A	4	165	c.554G>A	c.(553-555)CGT>CAT	p.R185H
Pat_60	Post-Resistance	OR10K1	391109	37	1	158435891	158435891	Missense_Mutation	SNP	C	A	85	336	c.540C>A	c.(538-540)GAC>GAA	p.D180E
Pat_60	Post-Resistance	DUSP12	11266	37	1	161719662	161719662	Missense_Mutation	SNP	C	T	3	26	c.71C>T	c.(70-72)GCC>GTC	p.A24V
Pat_60	Post-Resistance	FMO2	2327	37	1	171174431	171174431	Missense_Mutation	SNP	G	A	4	67	c.841G>A	c.(841-843)GAA>AAA	p.E281K
Pat_60	Post-Resistance	RABGAP1L	9910	37	1	174363191	174363191	Missense_Mutation	SNP	C	T	48	205	c.1618C>T	c.(1618-1620)CCT>TCT	p.P540S
Pat_60	Post-Resistance	LAMC2	3918	37	1	183205739	183205739	Missense_Mutation	SNP	G	T	4	183	c.2601G>T	c.(2599-2601)CAG>CAT	p.Q867H
Pat_60	Post-Resistance	RGS18	64407	37	1	192128444	192128444	Missense_Mutation	SNP	G	A	24	82	c.214G>A	c.(214-216)GAA>AAA	p.E72K
Pat_60	Post-Resistance	KIF14	9928	37	1	200574423	200574423	Missense_Mutation	SNP	C	T	6	195	c.1734G>A	c.(1732-1734)ATG>ATA	p.M578I
Pat_60	Post-Resistance	KIF14	9928	37	1	200574445	200574445	Missense_Mutation	SNP	T	A	6	200	c.1712A>T	c.(1711-1713)CAT>CTT	p.H571L
Pat_60	Post-Resistance	DDX59	83479	37	1	200633067	200633067	Missense_Mutation	SNP	G	A	29	122	c.952C>T	c.(952-954)CGT>TGT	p.R318C
Pat_60	Post-Resistance	RNPEP	6051	37	1	201965280	201965280	Missense_Mutation	SNP	G	A	3	79	c.743G>A	c.(742-744)CGG>CAG	p.R248Q
Pat_60	Post-Resistance	LGR6	59352	37	1	202270330	202270330	Missense_Mutation	SNP	C	T	19	69	c.896C>T	c.(895-897)TCG>TTG	p.S299L
Pat_60	Post-Resistance	PPP1R15B	84919	37	1	204380470	204380470	Missense_Mutation	SNP	A	G	5	169	c.70T>C	c.(70-72)TTT>CTT	p.F24L
Pat_60	Post-Resistance	MDM4	4194	37	1	204513793	204513793	Missense_Mutation	SNP	G	A	4	150	c.803G>A	c.(802-804)GGG>GAG	p.G268E
Pat_60	Post-Resistance	TMCC2	9911	37	1	205238112	205238112	Missense_Mutation	SNP	C	T	46	110	c.782C>T	c.(781-783)CCC>CTC	p.P261L
Pat_60	Post-Resistance	PFKFB2	5208	37	1	207235391	207235391	Missense_Mutation	SNP	G	A	4	147	c.179G>A	c.(178-180)CGC>CAC	p.R60H
Pat_60	Post-Resistance	EPRS	2058	37	1	220146710	220146710	Missense_Mutation	SNP	G	A	5	242	c.4114C>T	c.(4114-4116)CGT>TGT	p.R1372C
Pat_60	Post-Resistance	C1orf57	84284	37	1	233092163	233092163	Missense_Mutation	SNP	C	A	4	91	c.268C>A	c.(268-270)CAG>AAG	p.Q90K
Pat_60	Post-Resistance	SMYD3	64754	37	1	246498703	246498703	Missense_Mutation	SNP	G	A	91	272	c.302C>T	c.(301-303)TCC>TTC	p.S101F
Pat_60	Post-Resistance	C1orf150	148823	37	1	247737445	247737445	Missense_Mutation	SNP	G	A	64	310	c.169G>A	c.(169-171)GAA>AAA	p.E57K
Pat_60	Post-Resistance	OR2T12	127064	37	1	248458256	248458256	Missense_Mutation	SNP	A	G	4	109	c.625T>C	c.(625-627)TTT>CTT	p.F209L
Pat_60	Post-Resistance	TAF3	83860	37	10	8006435	8006435	Missense_Mutation	SNP	C	T	13	25	c.962C>T	c.(961-963)CCC>CTC	p.P321L
Pat_60	Post-Resistance	CAMK1D	57118	37	10	12803005	12803005	Missense_Mutation	SNP	G	A	20	121	c.358G>A	c.(358-360)GAT>AAT	p.D120N
Pat_60	Post-Resistance	PIP4K2A	5305	37	10	22830768	22830768	Missense_Mutation	SNP	G	A	4	165	c.1001C>T	c.(1000-1002)CCG>CTG	p.P334L
Pat_60	Post-Resistance	MYO3A	53904	37	10	26355954	26355954	Missense_Mutation	SNP	C	T	35	169	c.1004C>T	c.(1003-1005)TCC>TTC	p.S335F
Pat_60	Post-Resistance	APBB1IP	54518	37	10	26849663	26849663	Missense_Mutation	SNP	G	A	17	67	c.1259G>A	c.(1258-1260)GGG>GAG	p.G420E
Pat_60	Post-Resistance	ARMC4	55130	37	10	28225687	28225688	Nonsense_Mutation	DNP	CC	TT	73	322	.2219_2220GG>A	c.(2218-2220)TGG>TAA	p.W740*

Pat_60	Post-Resistance	SVIL	6840	37	10	29784024	29784024	Missense_Mutation	SNP	C	T	6	48	c.3751G>A	c.(3751-3753)GAA>AAA	p.E1251K
Pat_60	Post-Resistance	C10orf68	79741	37	10	33135342	33135342	Missense_Mutation	SNP	G	T	4	194	c.1372G>T	c.(1372-1374)GAT>TAT	p.D458Y
Pat_60	Post-Resistance	ANKRD30A	91074	37	10	37425564	37425564	Missense_Mutation	SNP	G	A	13	46	c.617G>A	c.(616-618)CGA>CAA	p.R206Q
Pat_60	Post-Resistance	MBL2	4153	37	10	54531224	54531224	Missense_Mutation	SNP	C	T	27	118	c.172G>A	c.(172-174)GAA>AAA	p.E58K
Pat_60	Post-Resistance	PCDH15	65217	37	10	55570336	55570336	Missense_Mutation	SNP	C	T	58	157	c.4498G>A	c.(4498-4500)GAA>AAA	p.E1500K
Pat_60	Post-Resistance	DLG5	9231	37	10	79565517	79565518	Missense_Mutation	DNP	CC	TT	30	104	.5069_5070GG>A	c.(5068-5070)CGG>CAA	p.R1690Q
Pat_60	Post-Resistance	ACTA2	59	37	10	90697849	90697849	Missense_Mutation	SNP	G	A	4	147	c.959C>T	c.(958-960)ACG>ATG	p.T320M
Pat_60	Post-Resistance	CYP2C9	1559	37	10	96745844	96745844	Missense_Mutation	SNP	C	T	72	315	c.1204C>T	c.(1204-1206)CCC>TCC	p.P402S
Pat_60	Post-Resistance	DNTT	1791	37	10	98064324	98064324	Missense_Mutation	SNP	G	A	4	98	c.70G>A	c.(70-72)GCC>ACC	p.A24T
Pat_60	Post-Resistance	SLIT1	6585	37	10	98823964	98823964	Missense_Mutation	SNP	G	A	13	24	c.590C>T	c.(589-591)CCC>CTC	p.P197L
Pat_60	Post-Resistance	SCD	6319	37	10	102120518	102120518	Missense_Mutation	SNP	C	T	85	154	c.908C>T	c.(907-909)TCC>TTC	p.S303F
Pat_60	Post-Resistance	MRPL43	84545	37	10	102739080	102739080	Missense_Mutation	SNP	G	A	4	125	c.578C>T	c.(577-579)CCA>CTA	p.P193L
Pat_60	Post-Resistance	SORCS1	114815	37	10	108366965	108366965	Missense_Mutation	SNP	G	A	22	61	c.3124C>T	c.(3124-3126)CCA>TCA	p.P1042S
Pat_60	Post-Resistance	RPL13AP6	644511	37	10	112696573	112696573	Missense_Mutation	SNP	T	C	9	41	c.419A>G	c.(418-420)CAC>CGC	p.H140R
Pat_60	Post-Resistance	KIAA1598	57698	37	10	118687348	118687348	Missense_Mutation	SNP	G	A	59	223	c.1067C>T	c.(1066-1068)CCT>CTT	p.P356L
Pat_60	Post-Resistance	EIF3A	8661	37	10	120801755	120801755	Missense_Mutation	SNP	T	A	6	338	c.3277A>T	c.(3277-3279)ATG>TTG	p.M1093L
Pat_60	Post-Resistance	DMBT1	1755	37	10	124395670	124395670	Missense_Mutation	SNP	G	A	5	45	c.6325G>A	c.(6325-6327)GGG>AGG	p.G2109R
Pat_60	Post-Resistance	DMBT1	1755	37	10	124399773	124399773	Missense_Mutation	SNP	C	A	45	123	c.6773C>A	c.(6772-6774)TCC>TAC	p.S2258Y
Pat_60	Post-Resistance	FAM175B	23172	37	10	126523485	126523485	Missense_Mutation	SNP	G	A	5	172	c.1193G>A	c.(1192-1194)CGA>CAA	p.R398Q
Pat_60	Post-Resistance	ANO9	338440	37	11	433344	433344	Missense_Mutation	SNP	G	A	3	37	c.320C>T	c.(319-321)GCC>GTC	p.A107V
Pat_60	Post-Resistance	SYT8	90019	37	11	1858477	1858477	Missense_Mutation	SNP	C	T	7	11	c.1022C>T	c.(1021-1023)CCC>CTC	p.P341L
Pat_60	Post-Resistance	DNHD1	144132	37	11	6540836	6540836	Missense_Mutation	SNP	G	A	4	193	c.1399G>A	c.(1399-1401)GAG>AAG	p.E467K
Pat_60	Post-Resistance	CYP2R1	120227	37	11	14902017	14902017	Missense_Mutation	SNP	G	T	4	125	c.665C>A	c.(664-666)GCC>GAC	p.A222D
Pat_60	Post-Resistance	KCNJ11	3767	37	11	17408942	17408942	Missense_Mutation	SNP	G	A	7	17	c.697C>T	c.(697-699)CTC>TTC	p.L233F
Pat_60	Post-Resistance	SLC6A5	9152	37	11	20639381	20639381	Nonsense_Mutation	SNP	G	A	47	125	c.1211G>A	c.(1210-1212)TGG>TAG	p.W404*
Pat_60	Post-Resistance	QSER1	79832	37	11	32956501	32956501	Missense_Mutation	SNP	C	T	71	113	c.3310C>T	c.(3310-3312)CCA>TCA	p.P1104S
Pat_60	Post-Resistance	CDCA5	113130	37	11	64851021	64851021	Missense_Mutation	SNP	G	A	4	105	c.143C>T	c.(142-144)ACA>ATA	p.T48I
Pat_60	Post-Resistance	NPAS4	266743	37	11	66190601	66190601	Missense_Mutation	SNP	A	G	5	14	c.706A>G	c.(706-708)ATC>GTC	p.I236V
Pat_60	Post-Resistance	DRD2	1813	37	11	113283314	113283314	Missense_Mutation	SNP	C	T	20	35	c.1102G>A	c.(1102-1104)GAG>AAG	p.E368K
Pat_60	Post-Resistance	TMPRSS4	56649	37	11	117975469	117975469	Missense_Mutation	SNP	C	T	21	79	c.374C>T	c.(373-375)TCT>TTT	p.S125F
Pat_60	Post-Resistance	TREH	11181	37	11	118529412	118529412	Missense_Mutation	SNP	C	T	2	1	c.1576G>A	c.(1576-1578)GGG>AGG	p.G526R
Pat_60	Post-Resistance	CCDC15	80071	37	11	124857495	124857495	Missense_Mutation	SNP	A	C	11	387	c.1373A>C	c.(1372-1374)CAC>CCC	p.H458P
Pat_60	Post-Resistance	RPUSD4	84881	37	11	126075452	126075452	Missense_Mutation	SNP	C	T	4	146	c.707G>A	c.(706-708)CGC>CAC	p.R236H
Pat_60	Post-Resistance	FAM118B	79607	37	11	126132015	126132015	Missense_Mutation	SNP	G	A	4	177	c.1043G>A	c.(1042-1044)GGC>GAC	p.G348D
Pat_60	Post-Resistance	IGSF9B	22997	37	11	133792616	133792616	Missense_Mutation	SNP	G	A	2	2	c.2129C>T	c.(2128-2130)CCG>CTG	p.P710L
Pat_60	Post-Resistance	CACNA1C	775	37	12	2690883	2690883	Missense_Mutation	SNP	G	A	5	34	c.2023G>A	c.(2023-2025)GGA>AGA	p.G675R
Pat_60	Post-Resistance	C12orf32	83695	37	12	2997518	2997518	Missense_Mutation	SNP	G	A	4	163	c.610G>A	c.(610-612)GAG>AAG	p.E204K
Pat_60	Post-Resistance	VWF	7450	37	12	6138549	6138549	Missense_Mutation	SNP	G	A	5	201	c.2926C>T	c.(2926-2928)CGC>TGC	p.R976C
Pat_60	Post-Resistance	A2ML1	144568	37	12	9010693	9010693	Missense_Mutation	SNP	A	G	7	8	c.3259A>G	c.(3259-3261)ATG>GTG	p.M1087V
Pat_60	Post-Resistance	A2ML1	144568	37	12	9016423	9016423	Missense_Mutation	SNP	C	T	4	139	c.3536C>T	c.(3535-3537)CCA>CTA	p.P1179L
Pat_60	Post-Resistance	CD69	969	37	12	9907192	9907192	Missense_Mutation	SNP	A	C	95	317	c.482T>G	c.(481-483)TTT>TGT	p.F161C
Pat_60	Post-Resistance	PRB2	653247	37	12	11546771	11546771	Missense_Mutation	SNP	G	C	6	348	c.241C>G	c.(241-243)CCA>GCA	p.P81A
Pat_60	Post-Resistance	LRP6	4040	37	12	12274091	12274091	Missense_Mutation	SNP	G	A	3	46	c.4811C>T	c.(4810-4812)CCG>CTG	p.P1604L
Pat_60	Post-Resistance	GYS2	2998	37	12	21692230	21692230	Missense_Mutation	SNP	G	A	76	327	c.1852C>T	c.(1852-1854)CCA>TCA	p.P618S
Pat_60	Post-Resistance	TMTC1	83857	37	12	29673644	29673644	Nonsense_Mutation	SNP	T	A	26	89	c.1471A>T	c.(1471-1473)AAA>TAA	p.K491*
Pat_60	Post-Resistance	SLC2A13	114134	37	12	40441979	40441979	Missense_Mutation	SNP	G	A	5	322	c.590C>T	c.(589-591)GCG>GTG	p.A197V
Pat_60	Post-Resistance	PFKM	5213	37	12	48538907	48538907	Missense_Mutation	SNP	C	T	4	129	c.2086C>T	c.(2086-2088)CGT>TGT	p.R696C

Pat_60	Post-Resistance	CACNB3	784	37	12	49219475	49219475	Missense_Mutation	SNP	C	T	36	125	c.665C>T	c.(664-666)TCC>TTC	p.S222F
Pat_60	Post-Resistance	RACGAP1	29127	37	12	50390908	50390908	Missense_Mutation	SNP	C	T	4	149	c.959G>A	c.(958-960)CGT>CAT	p.R320H
Pat_60	Post-Resistance	KRT8	3856	37	12	53292473	53292473	Missense_Mutation	SNP	C	T	5	200	c.1192G>A	c.(1192-1194)GAG>AAG	p.E398K
Pat_60	Post-Resistance	ESPL1	9700	37	12	53680574	53680574	Missense_Mutation	SNP	C	T	3	85	c.4054C>T	c.(4054-4056)CGG>TGG	p.R1352W
Pat_60	Post-Resistance	KIF5A	3798	37	12	57957435	57957435	Missense_Mutation	SNP	G	T	4	185	c.250G>T	c.(250-252)GCT>TCT	p.A84S
Pat_60	Post-Resistance	RAP1B	5908	37	12	69050092	69050092	Missense_Mutation	SNP	A	G	4	236	c.331A>G	c.(331-333)ATG>GTG	p.M111V
Pat_60	Post-Resistance	PTPRB	5787	37	12	70956819	70956819	Missense_Mutation	SNP	C	T	11	31	c.3319G>A	c.(3319-3321)GCC>ACC	p.A1107T
Pat_60	Post-Resistance	PTPRB	5787	37	12	71029645	71029645	Missense_Mutation	SNP	C	T	4	37	c.257G>A	c.(256-258)CGC>CAC	p.R86H
Pat_60	Post-Resistance	PTPRR	5801	37	12	71155318	71155318	Missense_Mutation	SNP	C	T	6	345	c.560G>A	c.(559-561)CGT>CAT	p.R187H
Pat_60	Post-Resistance	TBC1D15	64786	37	12	72307707	72307707	Splice_Site	SNP	G	A	5	194	c.1518_splice	c.e13+1	p.M506_splice
Pat_60	Post-Resistance	ACSS3	79611	37	12	81610767	81610767	Missense_Mutation	SNP	G	A	27	92	c.1442G>A	c.(1441-1443)GGA>GAA	p.G481E
Pat_60	Post-Resistance	SLC41A2	84102	37	12	105321753	105321753	Missense_Mutation	SNP	G	T	4	123	c.553C>A	c.(553-555)CAG>AAG	p.Q185K
Pat_60	Post-Resistance	RFX4	5992	37	12	107075789	107075789	Missense_Mutation	SNP	C	T	65	200	c.334C>T	c.(334-336)CCT>TCT	p.P112S
Pat_60	Post-Resistance	RASAL1	8437	37	12	113539775	113539775	Missense_Mutation	SNP	C	T	41	120	c.2141G>A	c.(2140-2142)GGG>GAG	p.G714E
Pat_60	Post-Resistance	RNF10	9921	37	12	121002888	121002888	Missense_Mutation	SNP	G	A	5	386	c.1679G>A	c.(1678-1680)CGT>CAT	p.R560H
Pat_60	Post-Resistance	ANAPC5	51433	37	12	121773427	121773427	Missense_Mutation	SNP	C	T	5	311	c.859G>A	c.(859-861)GAA>AAA	p.E287K
Pat_60	Post-Resistance	TMEM132D	121256	37	12	129563125	129563125	Missense_Mutation	SNP	A	G	31	131	c.2069T>C	c.(2068-2070)ATC>ACC	p.I690T
Pat_60	Post-Resistance	NUPL1	9818	37	13	25894666	25894666	Splice_Site	SNP	A	T	4	117	c.711_splice	c.e8-2	p.E237_splice
Pat_60	Post-Resistance	RNF6	6049	37	13	26788695	26788695	Missense_Mutation	SNP	G	A	5	192	c.1324C>T	c.(1324-1326)CGC>TGC	p.R442C
Pat_60	Post-Resistance	FLT1	2321	37	13	29004251	29004251	Missense_Mutation	SNP	C	T	4	89	c.1042G>A	c.(1042-1044)GCT>ACT	p.A348T
Pat_60	Post-Resistance	DGKH	160851	37	13	42739570	42739570	Splice_Site	SNP	G	A	4	169	c.958_splice	c.e8+1	p.G320_splice
Pat_60	Post-Resistance	ATP7B	540	37	13	52511468	52511468	Missense_Mutation	SNP	C	T	4	57	c.3965G>A	c.(3964-3966)CGC>CAC	p.R1322H
Pat_60	Post-Resistance	DIAPH3	81624	37	13	60384961	60384961	Missense_Mutation	SNP	G	A	3	75	c.3124C>T	c.(3124-3126)CGC>TGC	p.R1042C
Pat_60	Post-Resistance	LMO7	4008	37	13	76397821	76397821	Missense_Mutation	SNP	C	A	4	170	c.2062C>A	c.(2062-2064)CAG>AAG	p.Q688K
Pat_60	Post-Resistance	TPP2	7174	37	13	103299599	103299599	Nonsense_Mutation	SNP	G	T	4	95	c.2533G>T	c.(2533-2535)GAA>TAA	p.E845*
Pat_60	Post-Resistance	COL4A2	1284	37	13	111147701	111147701	Missense_Mutation	SNP	A	C	30	90	c.3647A>C	c.(3646-3648)CAC>CCC	p.H1216P
Pat_60	Post-Resistance	FAM70B	348013	37	13	114514844	114514844	Missense_Mutation	SNP	C	T	44	85	c.949C>T	c.(949-951)CCG>TCG	p.P317S
Pat_60	Post-Resistance	OR4N5	390437	37	14	20612733	20612733	Missense_Mutation	SNP	C	T	86	260	c.839C>T	c.(838-840)CCT>CTT	p.P280L
Pat_60	Post-Resistance	CHD8	57680	37	14	21860068	21860068	Nonsense_Mutation	SNP	A	T	19	85	c.5972T>A	c.(5971-5973)TTG>TAG	p.L1991*
Pat_60	Post-Resistance	MRPL52	122704	37	14	23303432	23303432	Nonsense_Mutation	SNP	C	T	4	136	c.274C>T	c.(274-276)CAG>TAG	p.Q92*
Pat_60	Post-Resistance	LRP10	26020	37	14	23345043	23345043	Missense_Mutation	SNP	C	T	4	87	c.886C>T	c.(886-888)CGT>TGT	p.R296C
Pat_60	Post-Resistance	REM2	161253	37	14	23354093	23354093	Missense_Mutation	SNP	A	G	3	75	c.314A>G	c.(313-315)GAG>GGG	p.E105G
Pat_60	Post-Resistance	RBM23	55147	37	14	23375485	23375485	Missense_Mutation	SNP	C	T	5	155	c.320G>A	c.(319-321)CGT>CAT	p.R107H
Pat_60	Post-Resistance	PRMT5	10419	37	14	23392017	23392017	Missense_Mutation	SNP	G	A	3	69	c.1513C>T	c.(1513-1515)CGG>TGG	p.R505W
Pat_60	Post-Resistance	C14orf37	145407	37	14	58605719	58605719	Missense_Mutation	SNP	G	A	18	82	c.358C>T	c.(358-360)CCC>TCC	p.P120S
Pat_60	Post-Resistance	PLEKHG3	26030	37	14	65194686	65194686	Missense_Mutation	SNP	C	T	2	0	c.337C>T	c.(337-339)CGC>TGC	p.R113C
Pat_60	Post-Resistance	GALNTL1	57452	37	14	69806275	69806275	Missense_Mutation	SNP	G	A	36	104	c.1126G>A	c.(1126-1128)GAT>AAT	p.D376N
Pat_60	Post-Resistance	SFRS5	6430	37	14	70238000	70238000	Missense_Mutation	SNP	G	A	5	383	c.641G>A	c.(640-642)CGG>CAG	p.R214Q
Pat_60	Post-Resistance	ADAM20	8748	37	14	70990455	70990455	Missense_Mutation	SNP	C	A	4	124	c.1170G>T	c.(1168-1170)TTG>TTT	p.L390F
Pat_60	Post-Resistance	C14orf115	55237	37	14	74825503	74825503	Missense_Mutation	SNP	G	A	27	50	c.2017G>A	c.(2017-2019)GAG>AAG	p.E673K
Pat_60	Post-Resistance	ANGEL1	23357	37	14	77275950	77275950	Missense_Mutation	SNP	G	A	4	152	c.101C>T	c.(100-102)GCG>GTG	p.A34V
Pat_60	Post-Resistance	CCDC88C	440193	37	14	91760643	91760643	Missense_Mutation	SNP	C	T	5	26	c.3986G>A	c.(3985-3987)GGG>GAG	p.G1329E
Pat_60	Post-Resistance	DLK1	8788	37	14	101198450	101198450	Missense_Mutation	SNP	G	A	25	113	c.334G>A	c.(334-336)GAA>AAA	p.E112K
Pat_60	Post-Resistance	OR4N3P	390539	37	15	22414263	22414263	Missense_Mutation	SNP	G	A	41	671	c.562G>A	c.(562-564)GAC>AAC	p.D188N
Pat_60	Post-Resistance	DLL4	54567	37	15	41228860	41228860	Missense_Mutation	SNP	C	T	3	37	c.1675C>T	c.(1675-1677)CGG>TGG	p.R559W
Pat_60	Post-Resistance	UNC13C	440279	37	15	54685300	54685300	Missense_Mutation	SNP	G	A	44	106	c.4768G>A	c.(4768-4770)GAT>AAT	p.D1590N
Pat_60	Post-Resistance	HERC1	8925	37	15	63950785	63950785	Missense_Mutation	SNP	G	A	4	110	c.9557C>T	c.(9556-9558)GCC>GTC	p.A3186V

Pat_60	Post-Resistance	TIPIN	54962	37	15	66641409	66641409	Missense_Mutation	SNP	A	G	3	61	c.464T>C	c.(463-465)GTT>GCT	p.V155A
Pat_60	Post-Resistance	GRAMD2	196996	37	15	72462197	72462197	Missense_Mutation	SNP	G	C	4	176	c.125C>G	c.(124-126)CCG>CGG	p.P42R
Pat_60	Post-Resistance	PKM2	5315	37	15	72492040	72492040	Missense_Mutation	SNP	C	T	4	89	c.1547G>A	c.(1546-1548)CGC>CAC	p.R516H
Pat_60	Post-Resistance	NPTN	27020	37	15	73862544	73862544	Missense_Mutation	SNP	A	C	33	184	c.1061T>G	c.(1060-1062)GTG>GGG	p.V354G
Pat_60	Post-Resistance	ADAMTSL3	57188	37	15	84324532	84324532	Missense_Mutation	SNP	C	T	20	41	c.19C>T	c.(19-21)CCC>TCC	p.P7S
Pat_60	Post-Resistance	ZNF592	9640	37	15	85327009	85327009	Missense_Mutation	SNP	C	T	16	109	c.1103C>T	c.(1102-1104)TCC>TTC	p.S368F
Pat_60	Post-Resistance	ALPK3	57538	37	15	85407771	85407771	Missense_Mutation	SNP	G	A	4	135	c.5204G>A	c.(5203-5205)CGG>CAG	p.R1735Q
Pat_60	Post-Resistance	SLC28A1	9154	37	15	85476379	85476379	Missense_Mutation	SNP	G	A	188	272	c.1087G>A	c.(1087-1089)GAT>AAT	p.D363N
Pat_60	Post-Resistance	MAN2A2	4122	37	15	91448870	91448870	Missense_Mutation	SNP	G	A	4	91	c.452G>A	c.(451-453)GGC>GAC	p.G151D
Pat_60	Post-Resistance	IGF1R	3480	37	15	99465453	99465453	Missense_Mutation	SNP	G	A	5	133	c.2278G>A	c.(2278-2280)GCA>ACA	p.A760T
Pat_60	Post-Resistance	MEF2A	4205	37	15	100214629	100214629	Missense_Mutation	SNP	C	T	254	396	c.428C>T	c.(427-429)TCT>TTT	p.S143F
Pat_60	Post-Resistance	BAIAP3	8938	37	16	1394480	1394480	Missense_Mutation	SNP	G	A	4	83	c.1718G>A	c.(1717-1719)CGT>CAT	p.R573H
Pat_60	Post-Resistance	BTBD12	84464	37	16	3647932	3647932	Missense_Mutation	SNP	C	T	4	95	c.1232G>A	c.(1231-1233)CGG>CAG	p.R411Q
Pat_60	Post-Resistance	GRIN2A	2903	37	16	9858006	9858006	Missense_Mutation	SNP	G	A	37	152	c.3395C>T	c.(3394-3396)CCA>CTA	p.P1132L
Pat_60	Post-Resistance	SMG1	23049	37	16	18845658	18845658	Missense_Mutation	SNP	C	T	4	81	c.8433G>A	c.(8431-8433)ATG>ATA	p.M2811I
Pat_60	Post-Resistance	PDILT	204474	37	16	20384233	20384233	Missense_Mutation	SNP	G	A	25	86	c.809C>T	c.(808-810)TCC>TTC	p.S270F
Pat_60	Post-Resistance	ACSM2B	348158	37	16	20576125	20576125	Missense_Mutation	SNP	C	T	4	97	c.43G>A	c.(43-45)GGT>AGT	p.G15S
Pat_60	Post-Resistance	SCNN1G	6340	37	16	23226699	23226699	Missense_Mutation	SNP	C	T	4	141	c.1859C>T	c.(1858-1860)CCC>CTC	p.P620L
Pat_60	Post-Resistance	NSMCE1	197370	37	16	27268846	27268846	Missense_Mutation	SNP	G	A	5	186	c.46C>T	c.(46-48)CGG>TGG	p.R16W
Pat_60	Post-Resistance	KIAA0556	23247	37	16	27761489	27761489	Missense_Mutation	SNP	G	A	4	102	c.3208G>A	c.(3208-3210)GTT>ATT	p.V1070I
Pat_60	Post-Resistance	BRD7	29117	37	16	50354288	50354288	Nonsense_Mutation	SNP	G	A	53	128	c.1627C>T	c.(1627-1629)CAG>TAG	p.Q543*
Pat_60	Post-Resistance	TOX3	27324	37	16	52497934	52497934	Missense_Mutation	SNP	G	A	33	65	c.320C>T	c.(319-321)CCC>CTC	p.P107L
Pat_60	Post-Resistance	AKTIP	64400	37	16	53532384	53532384	Missense_Mutation	SNP	G	A	4	123	c.167C>T	c.(166-168)CCT>CTT	p.P56L
Pat_60	Post-Resistance	NFATC3	4775	37	16	68200795	68200795	Nonsense_Mutation	SNP	C	T	4	105	c.1651C>T	c.(1651-1653)CGA>TGA	p.R551*
Pat_60	Post-Resistance	ST3GAL2	6483	37	16	70415743	70415743	Missense_Mutation	SNP	G	A	5	139	c.902C>T	c.(901-903)GCC>GTC	p.A301V
Pat_60	Post-Resistance	HYDIN	54768	37	16	71004449	71004449	Missense_Mutation	SNP	C	T	17	43	c.5590G>A	c.(5590-5592)GAT>AAT	p.D1864N
Pat_60	Post-Resistance	CLEC18B	497190	37	16	74446957	74446957	Nonsense_Mutation	SNP	C	T	8	45	c.654G>A	c.(652-654)TGG>TGA	p.W218*
Pat_60	Post-Resistance	ATMIN	23300	37	16	81078113	81078113	Missense_Mutation	SNP	A	G	4	141	c.2010A>G	c.(2008-2010)ATA>ATG	p.I670M
Pat_60	Post-Resistance	KIAA1609	57707	37	16	84513551	84513551	Missense_Mutation	SNP	C	T	3	54	c.1339G>A	c.(1339-1341)GAA>AAA	p.E447K
Pat_60	Post-Resistance	ZDHHC7	55625	37	16	85010098	85010098	Missense_Mutation	SNP	G	T	3	32	c.778C>A	c.(778-780)CCC>ACC	p.P260T
Pat_60	Post-Resistance	JPH3	57338	37	16	87678403	87678403	Missense_Mutation	SNP	G	A	3	49	c.922G>A	c.(922-924)GGG>AGG	p.G308R
Pat_60	Post-Resistance	FANCA	2175	37	16	89836993	89836993	Missense_Mutation	SNP	G	A	4	11	c.2201C>T	c.(2200-2202)TCC>TTC	p.S734F
Pat_60	Post-Resistance	PRDM7	11105	37	16	90126823	90126823	Missense_Mutation	SNP	T	G	5	100	c.1159A>C	c.(1159-1161)ATG>CTG	p.M387L
Pat_60	Post-Resistance	C17orf97	400566	37	17	263346	263346	Missense_Mutation	SNP	G	A	5	93	c.742G>A	c.(742-744)GAC>AAC	p.D248N
Pat_60	Post-Resistance	SCARF1	8578	37	17	1538786	1538786	Missense_Mutation	SNP	G	A	4	133	c.1759C>T	c.(1759-1761)CGG>TGG	p.R587W
Pat_60	Post-Resistance	CTNS	1497	37	17	3560052	3560052	Missense_Mutation	SNP	T	A	6	150	c.644T>A	c.(643-645)CTC>CAC	p.L215H
Pat_60	Post-Resistance	USP6	9098	37	17	5040979	5040979	Missense_Mutation	SNP	G	A	7	533	c.859G>A	c.(859-861)GTG>ATG	p.V287M
Pat_60	Post-Resistance	NLRP1	22861	37	17	5461927	5461927	Missense_Mutation	SNP	C	T	15	78	c.2089G>A	c.(2089-2091)GGG>AGG	p.G697R
Pat_60	Post-Resistance	ALOXE3	59344	37	17	8018372	8018372	Nonsense_Mutation	SNP	C	T	33	115	c.438G>A	c.(436-438)TGG>TGA	p.W146*
Pat_60	Post-Resistance	SLC25A35	399512	37	17	8194183	8194183	Nonsense_Mutation	SNP	G	A	4	148	c.706C>T	c.(706-708)CAG>TAG	p.Q236*
Pat_60	Post-Resistance	MYH4	4622	37	17	10351355	10351355	Missense_Mutation	SNP	T	C	11	232	c.4745A>G	c.(4744-4746)GAA>GGA	p.E1582G
Pat_60	Post-Resistance	MYH2	4620	37	17	10435009	10435009	Missense_Mutation	SNP	C	T	48	144	c.2638G>A	c.(2638-2640)GAA>AAA	p.E880K
Pat_60	Post-Resistance	MYH2	4620	37	17	10435020	10435020	Missense_Mutation	SNP	C	T	44	161	c.2627G>A	c.(2626-2628)AGG>AAG	p.R876K
Pat_60	Post-Resistance	TRIM16	10626	37	17	15532480	15532480	Missense_Mutation	SNP	C	T	4	113	c.1144G>A	c.(1144-1146)GCA>ACA	p.A382T
Pat_60	Post-Resistance	CCDC144A	9720	37	17	16635945	16635945	Missense_Mutation	SNP	G	A	10	47	c.2383G>A	c.(2383-2385)GAA>AAA	p.E795K
Pat_60	Post-Resistance	LGALS9C	654346	37	17	18395795	18395795	Missense_Mutation	SNP	C	T	22	134	c.697C>T	c.(697-699)CCG>TCG	p.P233S
Pat_60	Post-Resistance	ACACA	31	37	17	35454791	35454791	Missense_Mutation	SNP	G	A	5	178	c.6583C>T	c.(6583-6585)CGG>TGG	p.R2195W

Pat_60	Post-Resistance	HNF1B	6928	37	17	36059083	36059083	Missense_Mutation	SNP	T	C	3	72	c.1652A>G	c.(1651-1653)CAG>CGG	p.Q551R
Pat_60	Post-Resistance	CSF3	1440	37	17	38172082	38172082	Missense_Mutation	SNP	C	T	3	18	c.179C>T	c.(178-180)GCG>GTG	p.A60V
Pat_60	Post-Resistance	WIPF2	147179	37	17	38418845	38418845	Nonsense_Mutation	SNP	C	T	31	64	c.265C>T	c.(265-267)CAA>TAA	p.Q89*
Pat_60	Post-Resistance	KRTAP1-1	81851	37	17	39197597	39197597	Missense_Mutation	SNP	C	T	29	43	c.53G>A	c.(52-54)GGG>GAG	p.G18E
Pat_60	Post-Resistance	KAT2A	2648	37	17	40269499	40269499	Missense_Mutation	SNP	C	T	3	54	c.1544G>A	c.(1543-1545)CGG>CAG	p.R515Q
Pat_60	Post-Resistance	CCDC103	388389	37	17	42979934	42979934	Missense_Mutation	SNP	C	T	4	118	c.478C>T	c.(478-480)CGG>TGG	p.R160W
Pat_60	Post-Resistance	KPNB1	3837	37	17	45757957	45757957	Missense_Mutation	SNP	G	A	4	173	c.2552G>A	c.(2551-2553)CGG>CAG	p.R851Q
Pat_60	Post-Resistance	OSBPL7	114881	37	17	45885688	45885688	Missense_Mutation	SNP	T	C	12	45	c.2498A>G	c.(2497-2499)TAT>TGT	p.Y833C
Pat_60	Post-Resistance	CDK5RAP3	80279	37	17	46058837	46058837	Missense_Mutation	SNP	G	A	4	191	c.1490G>A	c.(1489-1491)CGC>CAC	p.R497H
Pat_60	Post-Resistance	HSF5	124535	37	17	56557433	56557433	Missense_Mutation	SNP	G	A	5	179	c.746C>T	c.(745-747)TCA>TTA	p.S249L
Pat_60	Post-Resistance	PRR11	55771	37	17	57262915	57262915	Missense_Mutation	SNP	G	A	4	123	c.394G>A	c.(394-396)GCA>ACA	p.A132T
Pat_60	Post-Resistance	PLEKHM1P	440456	37	17	62796646	62796646	Missense_Mutation	SNP	G	A	8	32	c.394C>T	c.(394-396)CCC>TCC	p.P132S
Pat_60	Post-Resistance	BPTF	2186	37	17	65850238	65850238	Missense_Mutation	SNP	C	T	4	185	c.796C>T	c.(796-798)CGC>TGC	p.R266C
Pat_60	Post-Resistance	ABCA6	23460	37	17	67079429	67079429	Missense_Mutation	SNP	G	A	16	95	c.4399C>T	c.(4399-4401)CTC>TTC	p.L1467F
Pat_60	Post-Resistance	CD300C	10871	37	17	72539117	72539117	Missense_Mutation	SNP	G	A	15	59	c.410C>T	c.(409-411)ACC>ATC	p.T137I
Pat_60	Post-Resistance	KIAA0195	9772	37	17	73489599	73489599	Missense_Mutation	SNP	C	T	4	72	c.2114C>T	c.(2113-2115)ACC>ATC	p.T705I
Pat_60	Post-Resistance	NPLOC4	55666	37	17	79573769	79573769	Missense_Mutation	SNP	G	A	3	48	c.602C>T	c.(601-603)CCG>CTG	p.P201L
Pat_60	Post-Resistance	RBBP8	5932	37	18	20606151	20606151	Missense_Mutation	SNP	G	A	4	124	c.2642G>A	c.(2641-2643)CGT>CAT	p.R881H
Pat_60	Post-Resistance	LAMA3	3909	37	18	21329415	21329415	Missense_Mutation	SNP	G	A	7	30	c.589G>A	c.(589-591)GAA>AAA	p.E197K
Pat_60	Post-Resistance	DSC3	1825	37	18	28576947	28576947	Missense_Mutation	SNP	C	T	33	77	c.2303G>A	c.(2302-2304)GGA>GAA	p.G768E
Pat_60	Post-Resistance	TTR	7276	37	18	29178613	29178613	Missense_Mutation	SNP	C	T	4	103	c.419C>T	c.(418-420)GCT>GTT	p.A140V
Pat_60	Post-Resistance	CDH7	1005	37	18	63547825	63547825	Missense_Mutation	SNP	G	A	37	123	c.2053G>A	c.(2053-2055)GAT>AAT	p.D685N
Pat_60	Post-Resistance	NETO1	81832	37	18	70417450	70417450	Missense_Mutation	SNP	C	T	14	69	c.1388G>A	c.(1387-1389)GGA>GAA	p.G463E
Pat_60	Post-Resistance	HCN2	610	37	19	615927	615927	Missense_Mutation	SNP	G	A	4	35	c.2123G>A	c.(2122-2124)GGT>GAT	p.G708D
Pat_60	Post-Resistance	DPP9	91039	37	19	4714134	4714134	Missense_Mutation	SNP	G	A	3	54	c.272C>T	c.(271-273)ACG>ATG	p.T91M
Pat_60	Post-Resistance	TICAM1	148022	37	19	4816882	4816882	Missense_Mutation	SNP	G	A	3	52	c.1508C>T	c.(1507-1509)ACG>ATG	p.T503M
Pat_60	Post-Resistance	TICAM1	148022	37	19	4817390	4817390	Missense_Mutation	SNP	G	A	4	95	c.1000C>T	c.(1000-1002)CTC>TTC	p.L334F
Pat_60	Post-Resistance	SH2D3A	10045	37	19	6755143	6755143	Missense_Mutation	SNP	C	T	5	266	c.680G>A	c.(679-681)CGT>CAT	p.R227H
Pat_60	Post-Resistance	C19orf59	199675	37	19	7743386	7743386	Missense_Mutation	SNP	C	T	8	55	c.383C>T	c.(382-384)TCC>TTC	p.S128F
Pat_60	Post-Resistance	CD209	30835	37	19	7810835	7810835	Missense_Mutation	SNP	T	C	5	243	c.317A>G	c.(316-318)CAG>CGG	p.Q106R
Pat_60	Post-Resistance	MUC16	94025	37	19	9089200	9089200	Missense_Mutation	SNP	G	A	3	7	c.2615C>T	c.(2614-2616)CCA>CTA	p.P872L
Pat_60	Post-Resistance	TYK2	7297	37	19	10461832	10461832	Missense_Mutation	SNP	G	A	12	13	c.3325C>T	c.(3325-3327)CTT>TTT	p.L1109F
Pat_60	Post-Resistance	QTRT1	81890	37	19	10823303	10823303	Missense_Mutation	SNP	C	T	4	142	c.860C>T	c.(859-861)GCG>GTG	p.A287V
Pat_60	Post-Resistance	TSPAN16	26526	37	19	11408863	11408863	Missense_Mutation	SNP	G	A	24	60	c.115G>A	c.(115-117)GGA>AGA	p.G39R
Pat_60	Post-Resistance	ZNF700	90592	37	19	12060645	12060645	Missense_Mutation	SNP	T	A	8	337	c.1806T>A	c.(1804-1806)AGT>AGA	p.S602R
Pat_60	Post-Resistance	ZNF700	90592	37	19	12060647	12060647	Missense_Mutation	SNP	G	C	6	338	c.1808G>C	c.(1807-1809)TGT>TCT	p.C603S
Pat_60	Post-Resistance	ZNF878	729747	37	19	12155757	12155757	Missense_Mutation	SNP	C	A	10	292	c.600G>T	c.(598-600)AGG>AGT	p.R200S
Pat_60	Post-Resistance	ZNF799	90576	37	19	12501446	12501446	Missense_Mutation	SNP	T	C	6	147	c.1766A>G	c.(1765-1767)GAA>GGA	p.E589G
Pat_60	Post-Resistance	IL27RA	9466	37	19	14160009	14160009	Missense_Mutation	SNP	C	T	4	72	c.1285C>T	c.(1285-1287)CCT>TCT	p.P429S
Pat_60	Post-Resistance	FAM129C	199786	37	19	17653011	17653011	Missense_Mutation	SNP	C	T	4	151	c.1330C>T	c.(1330-1332)CGG>TGG	p.R444W
Pat_60	Post-Resistance	RFXANK	8625	37	19	19308410	19308410	Missense_Mutation	SNP	G	A	3	40	c.418G>A	c.(418-420)GTT>ATT	p.V140I
Pat_60	Post-Resistance	CILP2	148113	37	19	19656316	19656316	Missense_Mutation	SNP	G	A	3	14	c.2962G>A	c.(2962-2964)GCA>ACA	p.A988T
Pat_60	Post-Resistance	ZNF93	81931	37	19	20045182	20045182	Missense_Mutation	SNP	A	G	5	345	c.1418A>G	c.(1417-1419)AAA>AGA	p.K473R
Pat_60	Post-Resistance	ZNF93	81931	37	19	20045266	20045266	Missense_Mutation	SNP	A	G	7	378	c.1502A>G	c.(1501-1503)AAA>AGA	p.K501R
Pat_60	Post-Resistance	ZNF737	100129842	37	19	20728254	20728254	Missense_Mutation	SNP	C	G	4	142	c.755G>C	c.(754-756)AGT>ACT	p.S252T
Pat_60	Post-Resistance	ZNF626	199777	37	19	20808090	20808090	Missense_Mutation	SNP	C	T	6	196	c.593G>A	c.(592-594)GGG>GAG	p.G198E
Pat_60	Post-Resistance	ZNF708	7562	37	19	21476519	21476519	Missense_Mutation	SNP	T	C	7	173	c.1249A>G	c.(1249-1251)AAG>GAG	p.K417E

Pat_60	Post-Resistance	ZNF91	7644	37	19	23544783	23544783	Missense_Mutation	SNP	C	T	8	533	c.998G>A	c.(997-999)CGT>CAT	p.R333H
Pat_60	Post-Resistance	C19orf2	8725	37	19	30500088	30500088	Missense_Mutation	SNP	G	T	5	54	c.863G>T	c.(862-864)TGT>TTT	p.C288F
Pat_60	Post-Resistance	ANKRD27	84079	37	19	33089136	33089136	Missense_Mutation	SNP	G	A	5	202	c.3068C>T	c.(3067-3069)ACG>ATG	p.T1023M
Pat_60	Post-Resistance	SLC7A10	56301	37	19	33703799	33703799	Missense_Mutation	SNP	G	A	4	44	c.466C>T	c.(466-468)CCC>TCC	p.P156S
Pat_60	Post-Resistance	LGI4	163175	37	19	35617799	35617799	Missense_Mutation	SNP	C	T	14	27	c.751G>A	c.(751-753)GAC>AAC	p.D251N
Pat_60	Post-Resistance	FXYD1	5348	37	19	35631041	35631041	Missense_Mutation	SNP	G	A	20	85	c.58G>A	c.(58-60)GCA>ACA	p.A20T
Pat_60	Post-Resistance	PRODH2	58510	37	19	36297393	36297393	Missense_Mutation	SNP	C	T	4	165	c.1168G>A	c.(1168-1170)GTG>ATG	p.V390M
Pat_60	Post-Resistance	ZFP82	284406	37	19	36883767	36883767	Missense_Mutation	SNP	G	A	31	115	c.1475C>T	c.(1474-1476)TCC>TTC	p.S492F
Pat_60	Post-Resistance	HKR1	284459	37	19	37854172	37854172	Missense_Mutation	SNP	C	T	5	245	c.1475C>T	c.(1474-1476)ACG>ATG	p.T492M
Pat_60	Post-Resistance	PRX	57716	37	19	40902620	40902620	Missense_Mutation	SNP	G	C	7	290	c.1639C>G	c.(1639-1641)CAG>GAG	p.Q547E
Pat_60	Post-Resistance	CEACAM3	1084	37	19	42300616	42300616	Missense_Mutation	SNP	C	T	4	118	c.7C>T	c.(7-9)CCC>TCC	p.P3S
Pat_60	Post-Resistance	PSG11	5680	37	19	43522979	43522979	Missense_Mutation	SNP	C	T	117	423	c.652G>A	c.(652-654)GAA>AAA	p.E218K
Pat_60	Post-Resistance	QPCTL	54814	37	19	46198776	46198776	Missense_Mutation	SNP	C	A	5	231	c.433C>A	c.(433-435)CCA>ACA	p.P145T
Pat_60	Post-Resistance	TRPM4	54795	37	19	49703901	49703901	Missense_Mutation	SNP	G	A	4	88	c.2812G>A	c.(2812-2814)GGC>AGC	p.G938S
Pat_60	Post-Resistance	MED25	81857	37	19	50333849	50333849	Missense_Mutation	SNP	C	T	7	21	c.901C>T	c.(901-903)CCT>TCT	p.P301S
Pat_60	Post-Resistance	SHANK1	50944	37	19	51207744	51207744	Nonsense_Mutation	SNP	G	A	46	140	c.1105C>T	c.(1105-1107)CGA>TGA	p.R369*
Pat_60	Post-Resistance	VN1R2	317701	37	19	53762364	53762364	Missense_Mutation	SNP	T	A	37	123	c.736T>A	c.(736-738)TTG>ATG	p.L246M
Pat_60	Post-Resistance	NLRP12	91662	37	19	54313084	54313084	Missense_Mutation	SNP	G	A	27	100	c.1829C>T	c.(1828-1830)TCC>TTC	p.S610F
Pat_60	Post-Resistance	LILRA3	11026	37	19	54802025	54802025	Missense_Mutation	SNP	G	A	55	190	c.1163C>T	c.(1162-1164)ACC>ATC	p.T388I
Pat_60	Post-Resistance	TNNT1	7138	37	19	55652634	55652634	Missense_Mutation	SNP	C	T	13	41	c.229G>A	c.(229-231)GAG>AAG	p.E77K
Pat_60	Post-Resistance	PTPRH	5794	37	19	55710101	55710101	Missense_Mutation	SNP	C	T	22	55	c.1600G>A	c.(1600-1602)GAA>AAA	p.E534K
Pat_60	Post-Resistance	SAPS1	22870	37	19	55741984	55741985	Missense_Mutation	DNP	GA	AC	7	12	.2638_2639TC>G	c.(2638-2640)TCC>GTC	p.S880V
Pat_60	Post-Resistance	NLRP8	126205	37	19	56466334	56466334	Missense_Mutation	SNP	G	A	32	118	c.910G>A	c.(910-912)GAA>AAA	p.E304K
Pat_60	Post-Resistance	ZNF582	147948	37	19	56903117	56903117	Missense_Mutation	SNP	G	A	38	143	c.5C>T	c.(4-6)TCC>TTC	p.S2F
Pat_60	Post-Resistance	ZNF324B	388569	37	19	58965148	58965148	Missense_Mutation	SNP	G	A	4	159	c.80G>A	c.(79-81)CGC>CAC	p.R27H
Pat_60	Post-Resistance	CHMP2A	27243	37	19	59063796	59063796	Missense_Mutation	SNP	G	A	4	80	c.178C>T	c.(178-180)CGC>TGC	p.R60C
Pat_60	Post-Resistance	C2orf44	80304	37	2	24262277	24262277	Missense_Mutation	SNP	C	A	4	143	c.88G>T	c.(88-90)GAT>TAT	p.D30Y
Pat_60	Post-Resistance	DPYSL5	56896	37	2	27121449	27121449	Missense_Mutation	SNP	G	A	4	115	c.82G>A	c.(82-84)GTC>ATC	p.V28I
Pat_60	Post-Resistance	CAPN13	92291	37	2	30974117	30974117	Missense_Mutation	SNP	C	T	13	51	c.1088G>A	c.(1087-1089)GGA>GAA	p.G363E
Pat_60	Post-Resistance	PPM1B	5495	37	2	44428478	44428478	Missense_Mutation	SNP	C	T	140	405	c.140C>T	c.(139-141)CCT>CTT	p.P47L
Pat_60	Post-Resistance	BMP10	27302	37	2	69093407	69093407	Missense_Mutation	SNP	G	T	4	101	c.631C>A	c.(631-633)CAA>AAA	p.Q211K
Pat_60	Post-Resistance	GMCL1	64395	37	2	70068151	70068151	Missense_Mutation	SNP	G	A	4	135	c.559G>A	c.(559-561)GCA>ACA	p.A187T
Pat_60	Post-Resistance	ALMS1	7840	37	2	73830432	73830432	Splice_Site	SNP	G	A	4	147	c.12365_splice	c.e23+1	p.R4122_splice
Pat_60	Post-Resistance	CTNNA2	1496	37	2	79878741	79878741	Missense_Mutation	SNP	G	A	4	191	c.59G>A	c.(58-60)CGG>CAG	p.R20Q
Pat_60	Post-Resistance	TMEM127	55654	37	2	96919572	96919572	Nonsense_Mutation	SNP	G	A	4	64	c.691C>T	c.(691-693)CAG>TAG	p.Q231*
Pat_60	Post-Resistance	C2orf55	343990	37	2	99438325	99438325	Missense_Mutation	SNP	C	T	9	34	c.2411G>A	c.(2410-2412)GGA>GAA	p.G804E
Pat_60	Post-Resistance	AFF3	3899	37	2	100182007	100182007	Missense_Mutation	SNP	C	T	39	155	c.3061G>A	c.(3061-3063)GGC>AGC	p.G1021S
Pat_60	Post-Resistance	TBC1D8	11138	37	2	101654100	101654100	Missense_Mutation	SNP	G	A	24	127	c.1301C>T	c.(1300-1302)TCT>TTT	p.S434F
Pat_60	Post-Resistance	IL18R1	8809	37	2	103013120	103013120	Missense_Mutation	SNP	G	A	43	84	c.1400G>A	c.(1399-1401)AGA>AAA	p.R467K
Pat_60	Post-Resistance	C2orf40	84417	37	2	106688341	106688341	Nonsense_Mutation	SNP	C	T	31	100	c.121C>T	c.(121-123)CGA>TGA	p.R41*
Pat_60	Post-Resistance	SULT1C2	6819	37	2	108921994	108921994	Missense_Mutation	SNP	C	T	24	98	c.721C>T	c.(721-723)CGT>TGT	p.R241C
Pat_60	Post-Resistance	WASH2P	375260	37	2	114355129	114355129	Missense_Mutation	SNP	G	A	3	23	c.506G>A	c.(505-507)CGC>CAC	p.R169H
Pat_60	Post-Resistance	RABL2A	11159	37	2	114392676	114392676	Missense_Mutation	SNP	C	T	35	81	c.266C>T	c.(265-267)TCC>TTC	p.S89F
Pat_60	Post-Resistance	MARCO	8685	37	2	119750742	119750742	Missense_Mutation	SNP	G	A	48	143	c.1295G>A	c.(1294-1296)CGA>CAA	p.R432Q
Pat_60	Post-Resistance	TFCP2L1	29842	37	2	122004453	122004453	Missense_Mutation	SNP	C	T	27	125	c.598G>A	c.(598-600)GAG>AAG	p.E200K
Pat_60	Post-Resistance	THSD7B	80731	37	2	137814542	137814542	Missense_Mutation	SNP	C	T	67	235	c.599C>T	c.(598-600)TCC>TTC	p.S200F
Pat_60	Post-Resistance	ZEB2	9839	37	2	145161680	145161680	Missense_Mutation	SNP	G	A	36	89	c.610C>T	c.(610-612)CCA>TCA	p.P204S

Pat_60	Post-Resistance	NEB	4703	37	2	152548828	152548828	Missense_Mutation	SNP	A	T	17	95	c.1945T>A	c.(1945-1947)TAC>AAC	p.Y649N
Pat_60	Post-Resistance	RPRM	56475	37	2	154334953	154334953	Missense_Mutation	SNP	C	T	3	45	c.127G>A	c.(127-129)GAG>AAG	p.E43K
Pat_60	Post-Resistance	SCN1A	6323	37	2	166872150	166872150	Missense_Mutation	SNP	C	T	83	254	c.3484G>A	c.(3484-3486)GAA>AAA	p.E1162K
Pat_60	Post-Resistance	STK39	27347	37	2	169038500	169038500	Missense_Mutation	SNP	C	T	4	173	c.309G>A	c.(307-309)ATG>ATA	p.M103I
Pat_60	Post-Resistance	LRP2	4036	37	2	170048380	170048380	Missense_Mutation	SNP	G	T	4	186	c.8994C>A	c.(8992-8994)TTC>TTA	p.F2998L
Pat_60	Post-Resistance	METTL5	29081	37	2	170676111	170676111	Missense_Mutation	SNP	C	T	4	140	c.449G>A	c.(448-450)AGA>AAA	p.R150K
Pat_60	Post-Resistance	COL3A1	1281	37	2	189854850	189854850	Missense_Mutation	SNP	G	A	34	157	c.719G>A	c.(718-720)GGA>GAA	p.G240E
Pat_60	Post-Resistance	MARS2	92935	37	2	198570245	198570245	Missense_Mutation	SNP	A	G	20	53	c.116A>G	c.(115-117)GAT>GGT	p.D39G
Pat_60	Post-Resistance	CCNYL1	151195	37	2	208618390	208618390	Missense_Mutation	SNP	G	A	4	185	c.895G>A	c.(895-897)GGT>AGT	p.G299S
Pat_60	Post-Resistance	DES	1674	37	2	220283231	220283231	Missense_Mutation	SNP	G	A	3	23	c.47G>A	c.(46-48)CGC>CAC	p.R16H
Pat_60	Post-Resistance	EPHA4	2043	37	2	222428987	222428987	Missense_Mutation	SNP	C	T	48	209	c.287G>A	c.(286-288)AGG>AAG	p.R96K
Pat_60	Post-Resistance	COL4A4	1286	37	2	227953434	227953434	Missense_Mutation	SNP	G	A	19	82	c.1558C>T	c.(1558-1560)CCT>TCT	p.P520S
Pat_60	Post-Resistance	AGFG1	3267	37	2	228384716	228384716	Missense_Mutation	SNP	C	T	74	173	c.314C>T	c.(313-315)CCA>CTA	p.P105L
Pat_60	Post-Resistance	INPP5D	3635	37	2	234079721	234079721	Missense_Mutation	SNP	A	T	13	53	c.1912A>T	c.(1912-1914)ATC>TTC	p.I638F
Pat_60	Post-Resistance	LRRFIP1	9208	37	2	238668812	238668812	Missense_Mutation	SNP	T	A	4	141	c.853T>A	c.(853-855)TTA>ATA	p.L285I
Pat_60	Post-Resistance	CPXM1	56265	37	20	2777038	2777038	Missense_Mutation	SNP	C	T	29	89	c.1097G>A	c.(1096-1098)GGG>GAG	p.G366E
Pat_60	Post-Resistance	PANK2	80025	37	20	3869901	3869901	Missense_Mutation	SNP	G	A	3	37	c.154G>A	c.(154-156)GGA>AGA	p.G52R
Pat_60	Post-Resistance	ANKRD5	63926	37	20	10019194	10019194	Missense_Mutation	SNP	G	A	4	104	c.245G>A	c.(244-246)TGT>TAT	p.C82Y
Pat_60	Post-Resistance	ZNF341	84905	37	20	32379219	32379219	Missense_Mutation	SNP	G	A	3	32	c.2461G>A	c.(2461-2463)GCT>ACT	p.A821T
Pat_60	Post-Resistance	MMP24	10893	37	20	33862287	33862287	Missense_Mutation	SNP	G	A	4	102	c.1813G>A	c.(1813-1815)GTG>ATG	p.V605M
Pat_60	Post-Resistance	FAM83C	128876	37	20	33874856	33874856	Missense_Mutation	SNP	C	T	9	29	c.1726G>A	c.(1726-1728)GGT>AGT	p.G576S
Pat_60	Post-Resistance	PIGT	51604	37	20	44049037	44049037	Nonsense_Mutation	SNP	C	T	3	47	c.835C>T	c.(835-837)CGA>TGA	p.R279*
Pat_60	Post-Resistance	NCOA3	8202	37	20	46265037	46265038	Missense_Mutation	DNP	CC	TT	38	110	.1907_1908CC>T	c.(1906-1908)TCC>TTT	p.S636F
Pat_60	Post-Resistance	PREX1	57580	37	20	47266569	47266569	Missense_Mutation	SNP	C	T	4	70	c.2993G>A	c.(2992-2994)CGC>CAC	p.R998H
Pat_60	Post-Resistance	ZNFX1	57169	37	20	47887292	47887292	Missense_Mutation	SNP	G	A	76	238	c.1057C>T	c.(1057-1059)CTT>TTT	p.L353F
Pat_60	Post-Resistance	SLC9A8	23315	37	20	48503428	48503428	Missense_Mutation	SNP	C	T	16	84	c.1631C>T	c.(1630-1632)ACG>ATG	p.T544M
Pat_60	Post-Resistance	NFATC2	4773	37	20	50092091	50092091	Missense_Mutation	SNP	G	A	5	256	c.1439C>T	c.(1438-1440)ACG>ATG	p.T480M
Pat_60	Post-Resistance	ZFP64	55734	37	20	50701503	50701503	Missense_Mutation	SNP	G	A	4	86	c.1531C>T	c.(1531-1533)CGC>TGC	p.R511C
Pat_60	Post-Resistance	ZNF217	7764	37	20	52193618	52193618	Missense_Mutation	SNP	T	C	6	392	c.1685A>G	c.(1684-1686)GAT>GGT	p.D562G
Pat_60	Post-Resistance	CTSZ	1522	37	20	57576697	57576697	Missense_Mutation	SNP	G	A	4	78	c.310C>T	c.(310-312)CGG>TGG	p.R104W
Pat_60	Post-Resistance	OGFR	11054	37	20	61441864	61441864	Nonsense_Mutation	SNP	C	T	4	117	c.412C>T	c.(412-414)CGA>TGA	p.R138*
Pat_60	Post-Resistance	TPTE	7179	37	21	10934997	10934997	Missense_Mutation	SNP	C	T	41	436	c.796G>A	c.(796-798)GAA>AAA	p.E266K
Pat_60	Post-Resistance	SAMSN1	64092	37	21	15884895	15884895	Splice_Site	SNP	C	T	26	123	c.280_splice	c.e4-1	p.D94_splice
Pat_60	Post-Resistance	RNF160	26046	37	21	30353449	30353449	Missense_Mutation	SNP	C	T	4	96	c.940G>A	c.(940-942)GTA>ATA	p.V314I
Pat_60	Post-Resistance	CHAF1B	8208	37	21	37775128	37775128	Missense_Mutation	SNP	G	A	7	556	c.736G>A	c.(736-738)GGA>AGA	p.G246R
Pat_60	Post-Resistance	POTEH	23784	37	22	16287387	16287387	Missense_Mutation	SNP	C	T	20	140	c.499G>A	c.(499-501)GAG>AAG	p.E167K
Pat_60	Post-Resistance	PPIL2	23759	37	22	22043087	22043087	Missense_Mutation	SNP	G	A	4	187	c.1088G>A	c.(1087-1089)CGC>CAC	p.R363H
Pat_60	Post-Resistance	ADORA2A	135	37	22	24837399	24837399	Missense_Mutation	SNP	G	A	4	38	c.1181G>A	c.(1180-1182)TGC>TAC	p.C394Y
Pat_60	Post-Resistance	PIWIL3	440822	37	22	25130079	25130079	Missense_Mutation	SNP	C	T	4	152	c.1679G>A	c.(1678-1680)CGG>CAG	p.R560Q
Pat_60	Post-Resistance	PIWIL3	440822	37	22	25145722	25145722	Missense_Mutation	SNP	T	C	4	151	c.1154A>G	c.(1153-1155)AAG>AGG	p.K385R
Pat_60	Post-Resistance	HPS4	89781	37	22	26854486	26854486	Missense_Mutation	SNP	G	A	4	99	c.1771C>T	c.(1771-1773)CCC>TCC	p.P591S
Pat_60	Post-Resistance	OSM	5008	37	22	30659934	30659934	Missense_Mutation	SNP	G	A	4	181	c.697C>T	c.(697-699)CGC>TGC	p.R233C
Pat_60	Post-Resistance	TIMP3	7078	37	22	33253267	33253267	Missense_Mutation	SNP	T	G	30	130	c.236T>G	c.(235-237)GTG>GGG	p.V79G
Pat_60	Post-Resistance	LARGE	9215	37	22	33673126	33673126	Missense_Mutation	SNP	G	A	4	174	c.1993C>T	c.(1993-1995)CGT>TGT	p.R665C
Pat_60	Post-Resistance	MYH9	4627	37	22	36737462	36737462	Missense_Mutation	SNP	G	A	5	176	c.443C>T	c.(442-444)CCT>CTT	p.P148L
Pat_60	Post-Resistance	C22orf33	339669	37	22	37398038	37398038	Missense_Mutation	SNP	C	T	4	53	c.329G>A	c.(328-330)GGA>GAA	p.G110E
Pat_60	Post-Resistance	ENTHD1	150350	37	22	40140135	40140135	Missense_Mutation	SNP	G	A	32	131	c.1373C>T	c.(1372-1374)TCC>TTC	p.S458F

Pat_60	Post-Resistance	MKL1	57591	37	22	40814967	40814967	Missense_Mutation	SNP	G	A	4	60	c.1475C>T	c.(1474-1476)TCG>TTG	p.S492L
Pat_60	Post-Resistance	ZC3H7B	23264	37	22	41753416	41753416	Missense_Mutation	SNP	G	A	4	161	c.2917G>A	c.(2917-2919)GCC>ACC	p.A973T
Pat_60	Post-Resistance	CELSR1	9620	37	22	46930127	46930127	Missense_Mutation	SNP	C	T	4	137	c.2941G>A	c.(2941-2943)GCC>ACC	p.A981T
Pat_60	Post-Resistance	PLXNB2	23654	37	22	50721158	50721158	Missense_Mutation	SNP	G	A	4	20	c.2969C>T	c.(2968-2970)CCG>CTG	p.P990L
Pat_60	Post-Resistance	CNTN4	152330	37	3	2944618	2944618	Missense_Mutation	SNP	C	T	4	65	c.1136C>T	c.(1135-1137)GCT>GTT	p.A379V
Pat_60	Post-Resistance	SRGAP3	9901	37	3	9146424	9146424	Missense_Mutation	SNP	C	T	30	74	c.363G>A	c.(361-363)ATG>ATA	p.M121I
Pat_60	Post-Resistance	GRIP2	80852	37	3	14558673	14558673	Missense_Mutation	SNP	G	A	8	42	c.1499C>T	c.(1498-1500)TCC>TTC	p.S500F
Pat_60	Post-Resistance	C3orf20	84077	37	3	14725869	14725869	Missense_Mutation	SNP	G	A	4	123	c.605G>A	c.(604-606)AGC>AAC	p.S202N
Pat_60	Post-Resistance	TOP2B	7155	37	3	25665167	25665167	Missense_Mutation	SNP	G	A	4	98	c.2566C>T	c.(2566-2568)CGT>TGT	p.R856C
Pat_60	Post-Resistance	LRRC3B	116135	37	3	26751407	26751407	Missense_Mutation	SNP	G	A	13	90	c.244G>A	c.(244-246)GAA>AAA	p.E82K
Pat_60	Post-Resistance	SUSD5	26032	37	3	33195084	33195084	Missense_Mutation	SNP	G	A	4	66	c.1040C>T	c.(1039-1041)TCG>TTG	p.S347L
Pat_60	Post-Resistance	C3orf35	339883	37	3	37458971	37458971	Missense_Mutation	SNP	C	T	11	58	c.214C>T	c.(214-216)CTT>TTT	p.L72F
Pat_60	Post-Resistance	SCN11A	11280	37	3	38913199	38913199	Missense_Mutation	SNP	C	T	18	66	c.3496G>A	c.(3496-3498)GTG>ATG	p.V1166M
Pat_60	Post-Resistance	KBTBD5	131377	37	3	42728002	42728002	Missense_Mutation	SNP	G	A	63	258	c.892G>A	c.(892-894)GCC>ACC	p.A298T
Pat_60	Post-Resistance	SLC6A20	54716	37	3	45804477	45804477	Missense_Mutation	SNP	G	A	5	195	c.1391C>T	c.(1390-1392)GCG>GTG	p.A464V
Pat_60	Post-Resistance	C3orf71	646450	37	3	48955819	48955819	Missense_Mutation	SNP	G	A	5	175	c.764C>T	c.(763-765)ACG>ATG	p.T255M
Pat_60	Post-Resistance	UBA7	7318	37	3	49850941	49850941	Missense_Mutation	SNP	G	A	30	93	c.196C>T	c.(196-198)CCC>TCC	p.P66S
Pat_60	Post-Resistance	HYAL2	8692	37	3	50355847	50355847	Missense_Mutation	SNP	G	A	4	83	c.1135C>T	c.(1135-1137)CGC>TGC	p.R379C
Pat_60	Post-Resistance	DOCK3	1795	37	3	51378711	51378712	Nonsense_Mutation	DNP	GG	AA	10	36	.3810_3811GG>A	808-3813)TGGGAG>TGA	270_1271WE
Pat_60	Post-Resistance	EPHA3	2042	37	3	89499348	89499348	Missense_Mutation	SNP	G	A	28	80	c.2518G>A	c.(2518-2520)GGC>AGC	p.G840S
Pat_60	Post-Resistance	ALCAM	214	37	3	105268981	105268981	Missense_Mutation	SNP	C	T	97	482	c.1385C>T	c.(1384-1386)TCT>TTT	p.S462F
Pat_60	Post-Resistance	CCDC54	84692	37	3	107096571	107096571	Missense_Mutation	SNP	C	T	65	282	c.137C>T	c.(136-138)CCC>CTC	p.P46L
Pat_60	Post-Resistance	DPPA2	151871	37	3	109023481	109023481	Missense_Mutation	SNP	G	A	19	118	c.695C>T	c.(694-696)TCG>TTG	p.S232L
Pat_60	Post-Resistance	CD96	10225	37	3	111263979	111263979	Missense_Mutation	SNP	G	A	66	203	c.148G>A	c.(148-150)GTA>ATA	p.V50I
Pat_60	Post-Resistance	ATP6V1A	523	37	3	113513976	113513976	Missense_Mutation	SNP	C	T	35	113	c.1151C>T	c.(1150-1152)TCG>TTG	p.S384L
Pat_60	Post-Resistance	KALRN	8997	37	3	123946875	123946875	Missense_Mutation	SNP	C	T	70	207	c.106C>T	c.(106-108)CTT>TTT	p.L36F
Pat_60	Post-Resistance	RHO	6010	37	3	129251606	129251606	Missense_Mutation	SNP	G	A	20	61	c.927G>A	c.(925-927)ATG>ATA	p.M309I
Pat_60	Post-Resistance	COL6A6	131873	37	3	130282320	130282320	Missense_Mutation	SNP	G	A	16	60	c.473G>A	c.(472-474)GGA>GAA	p.G158E
Pat_60	Post-Resistance	CLDN18	51208	37	3	137717873	137717873	Nonsense_Mutation	SNP	C	T	4	170	c.163C>T	c.(163-165)CGA>TGA	p.R55*
Pat_60	Post-Resistance	GRK7	131890	37	3	141535584	141535584	Missense_Mutation	SNP	C	T	45	154	c.1354C>T	c.(1354-1356)CAT>TAT	p.H452Y
Pat_60	Post-Resistance	ZIC1	7545	37	3	147130368	147130368	Missense_Mutation	SNP	G	A	4	142	c.1046G>A	c.(1045-1047)CGC>CAC	p.R349H
Pat_60	Post-Resistance	IGSF10	285313	37	3	151156133	151156134	Nonsense_Mutation	DNP	CC	TT	57	197	.6215_6216GG>A	c.(6214-6216)TGG>TAA	p.W2072*
Pat_60	Post-Resistance	PIK3CA	5290	37	3	178936076	178936076	Missense_Mutation	SNP	C	T	48	125	c.1618C>T	c.(1618-1620)CTC>TTC	p.L540F
Pat_60	Post-Resistance	ATP11B	23200	37	3	182598736	182598736	Missense_Mutation	SNP	G	A	4	169	c.2476G>A	c.(2476-2478)GTA>ATA	p.V826I
Pat_60	Post-Resistance	VPS8	23355	37	3	184586815	184586815	Missense_Mutation	SNP	G	A	3	41	c.1582G>A	c.(1582-1584)GCA>ACA	p.A528T
Pat_60	Post-Resistance	MASP1	5648	37	3	187003811	187003812	Missense_Mutation	DNP	GG	AA	18	85	c.38_39CC>TT	c.(37-39)TCC>TTT	p.S13F
Pat_60	Post-Resistance	BCL6	604	37	3	187451346	187451346	Missense_Mutation	SNP	G	A	70	248	c.136C>T	c.(136-138)CAT>TAT	p.H46Y
Pat_60	Post-Resistance	LEPREL1	55214	37	3	189705374	189705374	Missense_Mutation	SNP	T	A	22	90	c.1040A>T	c.(1039-1041)GAT>GTT	p.D347V
Pat_60	Post-Resistance	ZNF595	152687	37	4	59971	59971	Missense_Mutation	SNP	G	A	40	845	c.151G>A	c.(151-153)GAC>AAC	p.D51N
Pat_60	Post-Resistance	RGS12	6002	37	4	3418818	3418818	Missense_Mutation	SNP	A	G	3	36	c.2606A>G	c.(2605-2607)AAG>AGG	p.K869R
Pat_60	Post-Resistance	ACOX3	8310	37	4	8418142	8418142	Missense_Mutation	SNP	G	A	4	162	c.107C>T	c.(106-108)GCG>GTG	p.A36V
Pat_60	Post-Resistance	DHX15	1665	37	4	24556475	24556475	Missense_Mutation	SNP	G	A	89	244	c.953C>T	c.(952-954)CCT>CTT	p.P318L
Pat_60	Post-Resistance	TBC1D19	55296	37	4	26616029	26616029	Splice_Site	SNP	G	A	28	133	c.173_splice	c.e3-1	p.G58_splice
Pat_60	Post-Resistance	KLHL5	51088	37	4	39098412	39098412	Missense_Mutation	SNP	G	A	4	186	c.1352G>A	c.(1351-1353)CGA>CAA	p.R451Q
Pat_60	Post-Resistance	UGDH	7358	37	4	39512092	39512092	Missense_Mutation	SNP	C	T	4	166	c.544G>A	c.(544-546)GGG>AGG	p.G182R
Pat_60	Post-Resistance	FRYL	285527	37	4	48551532	48551532	Missense_Mutation	SNP	T	C	3	72	c.4742A>G	c.(4741-4743)GAT>GGT	p.D1581G
Pat_60	Post-Resistance	ARL9	132946	37	4	57384853	57384853	Missense_Mutation	SNP	G	A	4	194	c.26G>A	c.(25-27)AGT>AAT	p.S9N

Pat_60	Post-Resistance	MUC7	4589	37	4	71347138	71347138	Missense_Mutation	SNP	C	T	9	504	c.677C>T	c.(676-678)CCA>CTA	p.P226L
Pat_60	Post-Resistance	MUC7	4589	37	4	71347312	71347312	Missense_Mutation	SNP	C	T	120	481	c.851C>T	c.(850-852)CCA>CTA	p.P284L
Pat_60	Post-Resistance	NPFFR2	10886	37	4	73013491	73013491	Missense_Mutation	SNP	G	A	35	105	c.1531G>A	c.(1531-1533)GAA>AAA	p.E511K
Pat_60	Post-Resistance	SHROOM3	57619	37	4	77661877	77661877	Missense_Mutation	SNP	G	A	4	129	c.2551G>A	c.(2551-2553)GGG>AGG	p.G851R
Pat_60	Post-Resistance	CNOT6L	246175	37	4	78663361	78663361	Missense_Mutation	SNP	G	A	3	78	c.806C>T	c.(805-807)GCC>GTC	p.A269V
Pat_60	Post-Resistance	EMCN	51705	37	4	101331494	101331494	Missense_Mutation	SNP	C	T	70	225	c.770G>A	c.(769-771)GGA>GAA	p.G257E
Pat_60	Post-Resistance	ELOVL6	79071	37	4	110972801	110972801	Missense_Mutation	SNP	C	T	4	101	c.491G>A	c.(490-492)GGT>GAT	p.G164D
Pat_60	Post-Resistance	PCDH18	54510	37	4	138451711	138451711	Missense_Mutation	SNP	C	T	52	209	c.1532G>A	c.(1531-1533)GGA>GAA	p.G511E
Pat_60	Post-Resistance	FGB	2244	37	4	155488947	155488947	Nonsense_Mutation	SNP	C	A	7	294	c.693C>A	c.(691-693)TGC>TGA	p.C231*
Pat_60	Post-Resistance	SORBS2	8470	37	4	186545415	186545415	Missense_Mutation	SNP	C	T	19	38	c.1156G>A	c.(1156-1158)GAT>AAT	p.D386N
Pat_60	Post-Resistance	SLC6A19	340024	37	5	1217046	1217046	Missense_Mutation	SNP	G	A	4	118	c.1159G>A	c.(1159-1161)GCC>ACC	p.A387T
Pat_60	Post-Resistance	IRX1	79192	37	5	3600291	3600291	Missense_Mutation	SNP	C	A	3	57	c.1229C>A	c.(1228-1230)CCA>CAA	p.P410Q
Pat_60	Post-Resistance	DNAH5	1767	37	5	13769246	13769246	Splice_Site	SNP	C	T	70	264	c.9721_splice	c.e58-1	p.V3241_splice
Pat_60	Post-Resistance	DNAH5	1767	37	5	13865814	13865814	Missense_Mutation	SNP	C	T	16	104	c.4318G>A	c.(4318-4320)GAA>AAA	p.E1440K
Pat_60	Post-Resistance	PRDM9	56979	37	5	23527083	23527083	Missense_Mutation	SNP	G	C	4	145	c.1886G>C	c.(1885-1887)AGA>ACA	p.R629T
Pat_60	Post-Resistance	CDH10	1008	37	5	24491748	24491748	Missense_Mutation	SNP	G	A	4	139	c.1813C>T	c.(1813-1815)CTC>TTC	p.L605F
Pat_60	Post-Resistance	ADAMTS12	81792	37	5	33648935	33648935	Missense_Mutation	SNP	C	T	22	81	c.1471G>A	c.(1471-1473)GAA>AAA	p.E491K
Pat_60	Post-Resistance	EGFLAM	133584	37	5	38370509	38370509	Missense_Mutation	SNP	G	A	14	55	c.657G>A	c.(655-657)ATG>ATA	p.M219I
Pat_60	Post-Resistance	OSMR	9180	37	5	38904103	38904103	Missense_Mutation	SNP	C	T	23	102	c.1111C>T	c.(1111-1113)CAT>TAT	p.H371Y
Pat_60	Post-Resistance	IL6ST	3572	37	5	55260069	55260069	Missense_Mutation	SNP	G	A	5	158	c.563C>T	c.(562-564)ACT>ATT	p.T188I
Pat_60	Post-Resistance	MAST4	375449	37	5	66459994	66459994	Missense_Mutation	SNP	G	A	5	10	c.4420G>A	c.(4420-4422)GGC>AGC	p.G1474S
Pat_60	Post-Resistance	FBN2	2201	37	5	127681049	127681049	Missense_Mutation	SNP	C	T	4	155	c.3217G>A	c.(3217-3219)GAC>AAC	p.D1073N
Pat_60	Post-Resistance	FBXL21	26223	37	5	135277202	135277202	Missense_Mutation	SNP	A	C	12	23	c.1147A>C	c.(1147-1149)ATC>CTC	p.I383L
Pat_60	Post-Resistance	UBE2D2	7322	37	5	139003042	139003042	Missense_Mutation	SNP	G	A	4	141	c.394G>A	c.(394-396)GAA>AAA	p.E132K
Pat_60	Post-Resistance	PCDHA13	56136	37	5	140263608	140263609	Missense_Mutation	DNP	GG	AA	22	34	.1755_1756GG>A	753-1758)GTGGGT>GTA	p.G586S
Pat_60	Post-Resistance	PCDHB1	29930	37	5	140432969	140432969	Missense_Mutation	SNP	G	T	4	144	c.1914G>T	c.(1912-1914)ATG>ATT	p.M638I
Pat_60	Post-Resistance	PCDHGA3	56112	37	5	140725042	140725042	Missense_Mutation	SNP	G	A	4	154	c.1442G>A	c.(1441-1443)AGC>AAC	p.S481N
Pat_60	Post-Resistance	PCDHGA3	56112	37	5	140725705	140725705	Missense_Mutation	SNP	G	A	4	100	c.2105G>A	c.(2104-2106)TGC>TAC	p.C702Y
Pat_60	Post-Resistance	PPP2R2B	5521	37	5	146077647	146077647	Missense_Mutation	SNP	C	T	85	165	c.229G>A	c.(229-231)GAA>AAA	p.E77K
Pat_60	Post-Resistance	G3BP1	10146	37	5	151179525	151179525	Nonsense_Mutation	SNP	C	T	4	89	c.919C>T	c.(919-921)CGA>TGA	p.R307*
Pat_60	Post-Resistance	RARS	5917	37	5	167944932	167944932	Missense_Mutation	SNP	C	T	4	145	c.1738C>T	c.(1738-1740)CGG>TGG	p.R580W
Pat_60	Post-Resistance	DSP	1832	37	6	7578114	7578114	Missense_Mutation	SNP	C	A	4	122	c.2980C>A	c.(2980-2982)CAA>AAA	p.Q994K
Pat_60	Post-Resistance	BTN3A3	10384	37	6	26448550	26448550	Missense_Mutation	SNP	G	A	4	156	c.790G>A	c.(790-792)GCA>ACA	p.A264T
Pat_60	Post-Resistance	MDC1	9656	37	6	30673208	30673208	Missense_Mutation	SNP	T	C	7	344	c.3752A>G	c.(3751-3753)CAG>CGG	p.Q1251R
Pat_60	Post-Resistance	TNXB	7148	37	6	32023823	32023823	Missense_Mutation	SNP	T	C	5	83	c.8272A>G	c.(8272-8274)ATC>GTC	p.I2758V
Pat_60	Post-Resistance	GRM4	2914	37	6	33995965	33995965	Missense_Mutation	SNP	G	A	4	40	c.2621C>T	c.(2620-2622)ACG>ATG	p.T874M
Pat_60	Post-Resistance	FKBP5	2289	37	6	35558971	35558971	Missense_Mutation	SNP	G	A	56	132	c.692C>T	c.(691-693)CCT>CTT	p.P231L
Pat_60	Post-Resistance	BRPF3	27154	37	6	36178152	36178152	Missense_Mutation	SNP	C	T	21	70	c.2026C>T	c.(2026-2028)CAC>TAC	p.H676Y
Pat_60	Post-Resistance	C6orf222	389384	37	6	36298400	36298400	Missense_Mutation	SNP	T	A	29	85	c.68A>T	c.(67-69)CAG>CTG	p.Q23L
Pat_60	Post-Resistance	SLC22A7	10864	37	6	43270428	43270428	Missense_Mutation	SNP	G	A	4	7	c.1312G>A	c.(1312-1314)GGG>AGG	p.G438R
Pat_60	Post-Resistance	TJAP1	93643	37	6	43473429	43473429	Missense_Mutation	SNP	A	T	4	21	c.1510A>T	c.(1510-1512)AGG>TGG	p.R504W
Pat_60	Post-Resistance	ENPP5	59084	37	6	46135935	46135935	Missense_Mutation	SNP	G	A	4	173	c.65C>T	c.(64-66)TCT>TTT	p.S22F
Pat_60	Post-Resistance	MEP1A	4224	37	6	46797239	46797239	Missense_Mutation	SNP	G	A	70	258	c.1075G>A	c.(1075-1077)GTT>ATT	p.V359I
Pat_60	Post-Resistance	GPR111	222611	37	6	47649532	47649532	Missense_Mutation	SNP	C	A	4	119	c.1237C>A	c.(1237-1239)CAA>AAA	p.Q413K
Pat_60	Post-Resistance	FAM83B	222584	37	6	54804943	54804943	Missense_Mutation	SNP	G	A	39	149	c.1174G>A	c.(1174-1176)GAA>AAA	p.E392K
Pat_60	Post-Resistance	BAI3	577	37	6	69728368	69728368	Missense_Mutation	SNP	C	T	66	185	c.2084C>T	c.(2083-2085)TCA>TTA	p.S695L
Pat_60	Post-Resistance	COL9A1	1297	37	6	70990720	70990720	Missense_Mutation	SNP	G	A	20	27	c.899C>T	c.(898-900)CCC>CTC	p.P300L

Pat_60	Post-Resistance	SNX14	57231	37	6	86235901	86235901	Missense_Mutation	SNP	A	G	3	54	c.2050T>C	c.(2050-2052)TCC>CCC	p.S684P
Pat_60	Post-Resistance	ANKRD6	22881	37	6	90340517	90340517	Missense_Mutation	SNP	G	A	3	43	c.1978G>A	c.(1978-1980)GAC>AAC	p.D660N
Pat_60	Post-Resistance	REV3L	5980	37	6	111689143	111689143	Missense_Mutation	SNP	G	A	4	124	c.5848C>T	c.(5848-5850)CGT>TGT	p.R1950C
Pat_60	Post-Resistance	ROS1	6098	37	6	117700235	117700235	Missense_Mutation	SNP	G	A	27	115	c.2584C>T	c.(2584-2586)CTT>TTT	p.L862F
Pat_60	Post-Resistance	DCBLD1	285761	37	6	117841060	117841061	Missense_Mutation	DNP	CC	TA	47	166	c.407_408CC>TA	c.(406-408)TCC>TTA	p.S136L
Pat_60	Post-Resistance	C6orf174	387104	37	6	127836060	127836060	Missense_Mutation	SNP	G	A	4	150	c.1234C>T	c.(1234-1236)CGC>TGC	p.R412C
Pat_60	Post-Resistance	SAMD3	154075	37	6	130465688	130465688	Missense_Mutation	SNP	C	T	14	90	c.1540G>A	c.(1540-1542)GGA>AGA	p.G514R
Pat_60	Post-Resistance	TMEM200A	114801	37	6	130762526	130762526	Missense_Mutation	SNP	G	A	27	69	c.959G>A	c.(958-960)AGG>AAG	p.R320K
Pat_60	Post-Resistance	TMEM200A	114801	37	6	130762853	130762853	Missense_Mutation	SNP	G	A	38	125	c.1286G>A	c.(1285-1287)GGA>GAA	p.G429E
Pat_60	Post-Resistance	TXLNB	167838	37	6	139609804	139609804	Missense_Mutation	SNP	C	T	33	110	c.233G>A	c.(232-234)GGG>GAG	p.G78E
Pat_60	Post-Resistance	SYNE1	23345	37	6	152651594	152651594	Missense_Mutation	SNP	G	T	4	170	c.14226C>A	c.(14224-14226)AGC>AGA	p.S4742R
Pat_60	Post-Resistance	NOX3	50508	37	6	155717999	155717999	Missense_Mutation	SNP	G	A	59	191	c.1678C>T	c.(1678-1680)CAT>TAT	p.H560Y
Pat_60	Post-Resistance	TAGAP	117289	37	6	159465024	159465024	Missense_Mutation	SNP	C	T	73	257	c.67G>A	c.(67-69)GAA>AAA	p.E23K
Pat_60	Post-Resistance	IGF2R	3482	37	6	160461636	160461636	Missense_Mutation	SNP	T	C	39	177	c.1360T>C	c.(1360-1362)TGC>CGC	p.C454R
Pat_60	Post-Resistance	RPS6KA2	6196	37	6	166923789	166923789	Missense_Mutation	SNP	G	A	36	82	c.355C>T	c.(355-357)CCC>TCC	p.P119S
Pat_60	Post-Resistance	THBS2	7058	37	6	169626274	169626274	Splice_Site	SNP	C	T	4	151	c.2538_splice	c.e17+1	p.Q846_splice
Pat_60	Post-Resistance	NOD1	10392	37	7	30491021	30491021	Missense_Mutation	SNP	G	A	4	55	c.2012C>T	c.(2011-2013)GCG>GTG	p.A671V
Pat_60	Post-Resistance	DPY19L2P1	554236	37	7	35121264	35121264	Missense_Mutation	SNP	C	G	4	163	c.1342G>C	c.(1342-1344)GCC>CCC	p.A448P
Pat_60	Post-Resistance	CDK13	8621	37	7	40132797	40132797	Nonsense_Mutation	SNP	C	T	4	166	c.3649C>T	c.(3649-3651)CAA>TAA	p.Q1217*
Pat_60	Post-Resistance	ZMIZ2	83637	37	7	44799025	44799025	Missense_Mutation	SNP	T	G	5	33	c.959T>G	c.(958-960)CTG>CGG	p.L320R
Pat_60	Post-Resistance	TNS3	64759	37	7	47343018	47343018	Missense_Mutation	SNP	G	A	13	61	c.2987C>T	c.(2986-2988)CCT>CTT	p.P996L
Pat_60	Post-Resistance	ZNF727	442319	37	7	63538818	63538818	Missense_Mutation	SNP	C	T	18	104	c.1391C>T	c.(1390-1392)TCC>TTC	p.S464F
Pat_60	Post-Resistance	TPST1	8460	37	7	65706122	65706122	Missense_Mutation	SNP	T	A	49	85	c.710T>A	c.(709-711)GTT>GAT	p.V237D
Pat_60	Post-Resistance	POM121	9883	37	7	72413479	72413479	Missense_Mutation	SNP	G	A	4	143	c.2947G>A	c.(2947-2949)GCC>ACC	p.A983T
Pat_60	Post-Resistance	NCF1B	654816	37	7	72639986	72639986	Missense_Mutation	SNP	G	A	4	112	c.217G>A	c.(217-219)GGC>AGC	p.G73S
Pat_60	Post-Resistance	TRIM50	135892	37	7	72738623	72738623	Missense_Mutation	SNP	C	T	3	48	c.163G>A	c.(163-165)GTG>ATG	p.V55M
Pat_60	Post-Resistance	PCLO	27445	37	7	82583326	82583326	Missense_Mutation	SNP	C	T	177	429	c.6943G>A	c.(6943-6945)GAA>AAA	p.E2315K
Pat_60	Post-Resistance	PCLO	27445	37	7	82764435	82764435	Missense_Mutation	SNP	C	T	58	353	c.2431G>A	c.(2431-2433)GAA>AAA	p.E811K
Pat_60	Post-Resistance	PCLO	27445	37	7	82784561	82784561	Missense_Mutation	SNP	G	T	4	121	c.1396C>A	c.(1396-1398)CCA>ACA	p.P466T
Pat_60	Post-Resistance	C7orf63	79846	37	7	89912208	89912208	Missense_Mutation	SNP	C	T	75	129	c.1375C>T	c.(1375-1377)CCG>TCG	p.P459S
Pat_60	Post-Resistance	COL1A2	1278	37	7	94054936	94054936	Missense_Mutation	SNP	C	A	79	196	c.2796C>A	c.(2794-2796)AAC>AAA	p.N932K
Pat_60	Post-Resistance	TECPR1	25851	37	7	97851045	97851045	Missense_Mutation	SNP	G	A	28	61	c.3085C>T	c.(3085-3087)CCG>TCG	p.P1029S
Pat_60	Post-Resistance	RINT1	60561	37	7	105182999	105183000	Missense_Mutation	DNP	CC	TT	85	194	c.418_419CC>TT	c.(418-420)CCT>TTT	p.P140F
Pat_60	Post-Resistance	CTTNBP2	83992	37	7	117432598	117432598	Nonsense_Mutation	SNP	G	A	8	122	c.652C>T	c.(652-654)CGA>TGA	p.R218*
Pat_60	Post-Resistance	RNF148	378925	37	7	122342636	122342636	Missense_Mutation	SNP	C	T	31	100	c.169G>A	c.(169-171)GGA>AGA	p.G57R
Pat_60	Post-Resistance	FLNC	2318	37	7	128478750	128478750	Missense_Mutation	SNP	C	T	5	256	c.1304C>T	c.(1303-1305)ACG>ATG	p.T435M
Pat_60	Post-Resistance	TMEM209	84928	37	7	129813718	129813718	Missense_Mutation	SNP	G	A	108	650	c.1406C>T	c.(1405-1407)CCC>CTC	p.P469L
Pat_60	Post-Resistance	CHRM2	1129	37	7	136700538	136700538	Missense_Mutation	SNP	C	T	67	161	c.926C>T	c.(925-927)TCC>TTC	p.S309F
Pat_60	Post-Resistance	BRAF	673	37	7	140453136	140453136	Missense_Mutation	SNP	A	T	121	235	c.1799T>A	c.(1798-1800)GTG>GAG	p.V600E
Pat_60	Post-Resistance	MGAM	8972	37	7	141736669	141736669	Missense_Mutation	SNP	C	T	142	396	c.2123C>T	c.(2122-2124)TCC>TTC	p.S708F
Pat_60	Post-Resistance	TRPV5	56302	37	7	142612674	142612674	Missense_Mutation	SNP	G	A	44	113	c.1187C>T	c.(1186-1188)GCT>GTT	p.A396V
Pat_60	Post-Resistance	SLC4A2	6522	37	7	150761646	150761646	Missense_Mutation	SNP	C	T	36	228	c.251C>T	c.(250-252)CCA>CTA	p.P84L
Pat_60	Post-Resistance	RBM33	155435	37	7	155537881	155537881	Missense_Mutation	SNP	G	A	4	61	c.2564G>A	c.(2563-2565)GGT>GAT	p.G855D
Pat_60	Post-Resistance	FAM167A	83648	37	8	11301715	11301715	Missense_Mutation	SNP	G	A	10	14	c.206C>T	c.(205-207)GCG>GTG	p.A69V
Pat_60	Post-Resistance	C8orf79	57604	37	8	12878820	12878820	Missense_Mutation	SNP	G	A	6	172	c.632G>A	c.(631-633)CGG>CAG	p.R211Q
Pat_60	Post-Resistance	LOXL2	4017	37	8	23186065	23186065	Missense_Mutation	SNP	C	T	4	148	c.980G>A	c.(979-981)CGA>CAA	p.R327Q
Pat_60	Post-Resistance	CHRNA2	1135	37	8	27320702	27320702	Missense_Mutation	SNP	C	T	19	46	c.1258G>A	c.(1258-1260)GAG>AAG	p.E420K

Pat_60	Post-Resistance	INTS9	55756	37	8	28638399	28638399	Missense_Mutation	SNP	T	C	4	190	c.1211A>G	c.(1210-1212)GAC>GGC	p.D404G
Pat_60	Post-Resistance	TEX15	56154	37	8	30701064	30701064	Missense_Mutation	SNP	C	T	18	99	c.5470G>A	c.(5470-5472)GAC>AAC	p.D1824N
Pat_60	Post-Resistance	ADAM2	2515	37	8	39678544	39678544	Missense_Mutation	SNP	A	G	7	229	c.490T>C	c.(490-492)TCC>CCC	p.S164P
Pat_60	Post-Resistance	IDO2	169355	37	8	39871214	39871214	Missense_Mutation	SNP	C	T	8	29	c.889C>T	c.(889-891)CGT>TGT	p.R297C
Pat_60	Post-Resistance	PXDNL	137902	37	8	52233411	52233411	Missense_Mutation	SNP	A	G	76	251	c.4193T>C	c.(4192-4194)GTT>GCT	p.V1398A
Pat_60	Post-Resistance	RP1	6101	37	8	55539311	55539311	Missense_Mutation	SNP	C	T	13	76	c.2869C>T	c.(2869-2871)CCC>TCC	p.P957S
Pat_60	Post-Resistance	CA13	377677	37	8	86171748	86171748	Missense_Mutation	SNP	G	A	4	159	c.334G>A	c.(334-336)GGA>AGA	p.G112R
Pat_60	Post-Resistance	CA1	759	37	8	86250519	86250519	Missense_Mutation	SNP	G	A	78	346	c.197C>T	c.(196-198)TCC>TTC	p.S66F
Pat_60	Post-Resistance	RPL30	6156	37	8	99054923	99054923	Missense_Mutation	SNP	G	A	4	192	c.248C>T	c.(247-249)ACA>ATA	p.T83I
Pat_60	Post-Resistance	VPS13B	157680	37	8	100654205	100654205	Missense_Mutation	SNP	G	A	5	299	c.5462G>A	c.(5461-5463)CGT>CAT	p.R1821H
Pat_60	Post-Resistance	RSPO2	340419	37	8	109001454	109001454	Missense_Mutation	SNP	G	A	28	122	c.113C>T	c.(112-114)CCC>CTC	p.P38L
Pat_60	Post-Resistance	PKHD1L1	93035	37	8	110422157	110422157	Missense_Mutation	SNP	G	A	16	50	c.2035G>A	c.(2035-2037)GAA>AAA	p.E679K
Pat_60	Post-Resistance	TAF2	6873	37	8	120744407	120744407	Missense_Mutation	SNP	C	A	5	169	c.3357G>T	c.(3355-3357)TTG>TTT	p.L1119F
Pat_60	Post-Resistance	WDR67	93594	37	8	124156984	124156984	Missense_Mutation	SNP	C	T	10	55	c.2863C>T	c.(2863-2865)CGT>TGT	p.R955C
Pat_60	Post-Resistance	FAM49B	51571	37	8	130866534	130866534	Missense_Mutation	SNP	C	T	5	315	c.494G>A	c.(493-495)CGT>CAT	p.R165H
Pat_60	Post-Resistance	SLA	6503	37	8	134060132	134060132	Nonsense_Mutation	SNP	G	A	4	94	c.295C>T	c.(295-297)CAG>TAG	p.Q99*
Pat_60	Post-Resistance	FREM1	158326	37	9	14859217	14859217	Missense_Mutation	SNP	G	A	3	62	c.595C>T	c.(595-597)CGT>TGT	p.R199C
Pat_60	Post-Resistance	RUSC2	9853	37	9	35556355	35556355	Missense_Mutation	SNP	T	C	3	84	c.2893T>C	c.(2893-2895)TTT>CTT	p.F965L
Pat_60	Post-Resistance	NPR2	4882	37	9	35799708	35799708	Missense_Mutation	SNP	G	A	4	118	c.967G>A	c.(967-969)GTG>ATG	p.V323M
Pat_60	Post-Resistance	PAX5	5079	37	9	36966665	36966665	Missense_Mutation	SNP	G	A	3	58	c.661C>T	c.(661-663)CGG>TGG	p.R221W
Pat_60	Post-Resistance	FOXD4L5	653427	37	9	70177752	70177752	Missense_Mutation	SNP	C	T	6	211	c.232G>A	c.(232-234)GGC>AGC	p.G78S
Pat_60	Post-Resistance	PIP5K1B	8395	37	9	71509553	71509553	Missense_Mutation	SNP	G	A	4	152	c.770G>A	c.(769-771)CGG>CAG	p.R257Q
Pat_60	Post-Resistance	WNK2	65268	37	9	96051292	96051292	Missense_Mutation	SNP	G	C	2	6	c.4367G>C	c.(4366-4368)GGT>GCT	p.G1456A
Pat_60	Post-Resistance	FBP1	2203	37	9	97367767	97367767	Missense_Mutation	SNP	G	A	14	29	c.797C>T	c.(796-798)CCC>CTC	p.P266L
Pat_60	Post-Resistance	HSD17B3	3293	37	9	99003072	99003072	Missense_Mutation	SNP	C	T	4	96	c.790G>A	c.(790-792)GAA>AAA	p.E264K
Pat_60	Post-Resistance	LPPR1	54886	37	9	104048494	104048494	Missense_Mutation	SNP	C	T	46	81	c.361C>T	c.(361-363)CTT>TTT	p.L121F
Pat_60	Post-Resistance	ZNF189	7743	37	9	104171614	104171614	Missense_Mutation	SNP	A	T	4	105	c.1564A>T	c.(1564-1566)AGT>TGT	p.S522C
Pat_60	Post-Resistance	PTGS1	5742	37	9	125154705	125154705	Missense_Mutation	SNP	C	T	4	89	c.1682C>T	c.(1681-1683)GCC>GTC	p.A561V
Pat_60	Post-Resistance	FPGS	2356	37	9	130571982	130571982	Nonsense_Mutation	SNP	G	A	3	27	c.1080G>A	c.(1078-1080)TGG>TGA	p.W360*
Pat_60	Post-Resistance	SPTAN1	6709	37	9	131344986	131344986	Missense_Mutation	SNP	G	A	4	176	c.1664G>A	c.(1663-1665)CGC>CAC	p.R555H
Pat_60	Post-Resistance	ZER1	10444	37	9	131516203	131516203	Missense_Mutation	SNP	T	C	2	5	c.194A>G	c.(193-195)GAG>GGG	p.E65G
Pat_60	Post-Resistance	SH3GLB2	56904	37	9	131772409	131772409	Missense_Mutation	SNP	C	A	4	60	c.728G>T	c.(727-729)AGT>ATT	p.S243I
Pat_60	Post-Resistance	MED27	9442	37	9	134814787	134814787	Missense_Mutation	SNP	C	G	3	73	c.554G>C	c.(553-555)GGA>GCA	p.G185A
Pat_60	Post-Resistance	C9orf86	55684	37	9	139726805	139726805	Missense_Mutation	SNP	C	T	13	37	c.688C>T	c.(688-690)CCA>TCA	p.P230S
Pat_60	Post-Resistance	ANAPC2	29882	37	9	140082098	140082098	Missense_Mutation	SNP	T	C	3	69	c.575A>G	c.(574-576)GAA>GGA	p.E192G
Pat_60	Post-Resistance	ASMTL	8623	37	X	1537003	1537003	Missense_Mutation	SNP	G	A	3	39	c.1385C>T	c.(1384-1386)ACG>ATG	p.T462M
Pat_60	Post-Resistance	PTCHD1	139411	37	X	23398090	23398090	Missense_Mutation	SNP	G	A	5	272	c.734G>A	c.(733-735)AGC>AAC	p.S245N
Pat_60	Post-Resistance	USP11	8237	37	X	47092338	47092338	Missense_Mutation	SNP	G	A	48	39	c.25G>A	c.(25-27)GGG>AGG	p.G9R
Pat_60	Post-Resistance	MAGED1	9500	37	X	51643393	51643393	Splice_Site	SNP	G	A	4	27	c.1959_splice	c.e11+1	p.E653_splice
Pat_60	Post-Resistance	PJA1	64219	37	X	68382694	68382694	Missense_Mutation	SNP	C	T	24	24	c.388G>A	c.(388-390)GGG>AGG	p.G130R
Pat_60	Post-Resistance	NLGN3	54413	37	X	70389720	70389720	Missense_Mutation	SNP	G	A	5	8	c.2260G>A	c.(2260-2262)GAG>AAG	p.E754K
Pat_60	Post-Resistance	ATRX	546	37	X	76855029	76855029	Missense_Mutation	SNP	T	C	6	509	c.5807A>G	c.(5806-5808)AAG>AGG	p.K1936R
Pat_60	Post-Resistance	PCDH19	57526	37	X	99662793	99662793	Missense_Mutation	SNP	C	T	4	121	c.803G>A	c.(802-804)GGC>GAC	p.G268D
Pat_60	Post-Resistance	NOX1	27035	37	X	100117659	100117659	Missense_Mutation	SNP	G	A	5	387	c.488C>T	c.(487-489)ACG>ATG	p.T163M
Pat_60	Post-Resistance	ARMCX5	64860	37	X	101857282	101857282	Missense_Mutation	SNP	G	T	4	68	c.213G>T	c.(211-213)ATG>ATT	p.M71I
Pat_60	Post-Resistance	RGAG1	57529	37	X	109697656	109697656	Missense_Mutation	SNP	C	T	4	109	c.3811C>T	c.(3811-3813)CGG>TGG	p.R1271W
Pat_60	Post-Resistance	RHOXF2B	727940	37	X	119211063	119211063	Nonsense_Mutation	SNP	C	T	21	31	c.270G>A	c.(268-270)TGG>TGA	p.W90*

Pat_60	Post-Resistance	ACTRT1	139741	37	X	127185072	127185072	Nonsense_Mutation	SNP	G	A	87	133	c.1114C>T	c.(1114-1116)CAA>TAA	p.Q372*
Pat_60	Post-Resistance	MAGEC1	9947	37	X	140993959	140993959	Nonsense_Mutation	SNP	C	T	14	212	c.769C>T	c.(769-771)CAG>TAG	p.Q257*
Pat_60	Post-Resistance	SLITRK4	139065	37	X	142717365	142717365	Missense_Mutation	SNP	C	A	4	190	c.1560G>T	c.(1558-1560)TTG>TTT	p.L520F
Pat_60	Post-Resistance	FMR1NB	158521	37	X	147090174	147090174	Missense_Mutation	SNP	C	T	3	67	c.575C>T	c.(574-576)GCG>GTG	p.A192V
Pat_60	Post-Resistance	MAMLD1	10046	37	X	149638078	149638078	Missense_Mutation	SNP	G	A	4	83	c.233G>A	c.(232-234)GGC>GAC	p.G78D
Pat_60	Post-Resistance	GABRQ	55879	37	X	151821199	151821199	Missense_Mutation	SNP	G	A	50	52	c.1354G>A	c.(1354-1356)GAT>AAT	p.D452N
Pat_60	Post-Resistance	FAM58A	92002	37	X	152860138	152860138	Splice_Site	SNP	C	T	23	21	c.111_splice	c.e2-1	p.R37_splice
Pat_60	Post-Resistance	NAA10	8260	37	X	153195459	153195459	Missense_Mutation	SNP	G	T	4	49	c.689C>A	c.(688-690)GCC>GAC	p.A230D
Pat_65	Pre-Treatment	MMEL1	79258	37	1	2528092	2528092	Missense_Mutation	SNP	G	A	4	204	c.1309C>T	c.(1309-1311)CGT>TGT	p.R437C
Pat_65	Pre-Treatment	PER3	8863	37	1	7890053	7890053	Missense_Mutation	SNP	G	A	8	242	c.3019G>A	c.(3019-3021)GCT>ACT	p.A1007T
Pat_65	Pre-Treatment	RERE	473	37	1	8418949	8418949	Missense_Mutation	SNP	G	A	5	250	c.3646C>T	c.(3646-3648)CGC>TGC	p.R1216C
Pat_65	Pre-Treatment	CLSTN1	22883	37	1	9791341	9791341	Missense_Mutation	SNP	G	A	6	489	c.2671C>T	c.(2671-2673)CGG>TGG	p.R891W
Pat_65	Pre-Treatment	PRDM2	7799	37	1	14075950	14075950	Missense_Mutation	SNP	G	A	4	58	c.479G>A	c.(478-480)CGG>CAG	p.R160Q
Pat_65	Pre-Treatment	ESPNP	284729	37	1	17034085	17034085	Nonsense_Mutation	SNP	C	T	3	33	c.405G>A	c.(403-405)TGG>TGA	p.W135*
Pat_65	Pre-Treatment	PADI6	353238	37	1	17708479	17708479	Missense_Mutation	SNP	C	A	5	220	c.571C>A	c.(571-573)CAG>AAG	p.Q191K
Pat_65	Pre-Treatment	PHACTR4	65979	37	1	28793081	28793081	Missense_Mutation	SNP	G	A	5	256	c.625G>A	c.(625-627)GCT>ACT	p.A209T
Pat_65	Pre-Treatment	RBBP4	5928	37	1	33134600	33134600	Missense_Mutation	SNP	G	A	4	234	c.628G>A	c.(628-630)GTT>ATT	p.V210I
Pat_65	Pre-Treatment	KIAA1522	57648	37	1	33236639	33236639	Missense_Mutation	SNP	G	A	5	242	c.1682G>A	c.(1681-1683)CGC>CAC	p.R561H
Pat_65	Pre-Treatment	CLSPN	63967	37	1	36226459	36226459	Missense_Mutation	SNP	C	G	5	220	c.1063G>C	c.(1063-1065)GAA>CAA	p.E355Q
Pat_65	Pre-Treatment	THRAP3	9967	37	1	36748255	36748255	Missense_Mutation	SNP	C	T	5	303	c.91C>T	c.(91-93)CGG>TGG	p.R31W
Pat_65	Pre-Treatment	MACF1	23499	37	1	39549961	39549961	Missense_Mutation	SNP	G	A	4	277	c.71G>A	c.(70-72)CGA>CAA	p.R24Q
Pat_65	Pre-Treatment	KIAA0494	9813	37	1	47181982	47181982	Missense_Mutation	SNP	C	T	4	148	c.319G>A	c.(319-321)GAA>AAA	p.E107K
Pat_65	Pre-Treatment	STIL	6491	37	1	47726112	47726112	Missense_Mutation	SNP	C	T	4	230	c.2926G>A	c.(2926-2928)GTT>ATT	p.V976I
Pat_65	Pre-Treatment	GLIS1	148979	37	1	54059801	54059801	Missense_Mutation	SNP	C	T	4	119	c.775G>A	c.(775-777)GAG>AAG	p.E259K
Pat_65	Pre-Treatment	CELSR2	1952	37	1	109794316	109794316	Missense_Mutation	SNP	C	T	4	178	c.1615C>T	c.(1615-1617)CGC>TGC	p.R539C
Pat_65	Pre-Treatment	CELSR2	1952	37	1	109807532	109807532	Missense_Mutation	SNP	C	T	172	340	c.5507C>T	c.(5506-5508)CCG>CTG	p.P1836L
Pat_65	Pre-Treatment	SLC6A17	388662	37	1	110734723	110734723	Missense_Mutation	SNP	G	A	6	298	c.994G>A	c.(994-996)GAT>AAT	p.D332N
Pat_65	Pre-Treatment	SLC6A17	388662	37	1	110737360	110737360	Missense_Mutation	SNP	G	A	6	328	c.1459G>A	c.(1459-1461)GAC>AAC	p.D487N
Pat_65	Pre-Treatment	MOV10	4343	37	1	113237483	113237483	Missense_Mutation	SNP	G	A	4	223	c.1585G>A	c.(1585-1587)GGC>AGC	p.G529S
Pat_65	Pre-Treatment	LRIG2	9860	37	1	113637047	113637047	Missense_Mutation	SNP	G	A	6	388	c.602G>A	c.(601-603)CGT>CAT	p.R201H
Pat_65	Pre-Treatment	CD2	914	37	1	117303224	117303224	Missense_Mutation	SNP	G	A	65	187	c.583G>A	c.(583-585)GAA>AAA	p.E195K
Pat_65	Pre-Treatment	NOTCH2	4853	37	1	120506320	120506320	Missense_Mutation	SNP	C	T	8	804	c.1792G>A	c.(1792-1794)GGG>AGG	p.G598R
Pat_65	Pre-Treatment	PDE4DIP	9659	37	1	144879284	144879284	Missense_Mutation	SNP	G	A	64	264	c.4166C>T	c.(4165-4167)TCG>TTG	p.S1389L
Pat_65	Pre-Treatment	LIX1L	128077	37	1	145477408	145477408	Missense_Mutation	SNP	G	A	3	42	c.250G>A	c.(250-252)GTG>ATG	p.V84M
Pat_65	Pre-Treatment	BCL9	607	37	1	147092225	147092225	Missense_Mutation	SNP	C	T	53	23	c.2264C>T	c.(2263-2265)TCA>TTA	p.S755L
Pat_65	Pre-Treatment	PI4KB	5298	37	1	151288450	151288450	Missense_Mutation	SNP	C	T	5	199	c.508G>A	c.(508-510)GAG>AAG	p.E170K
Pat_65	Pre-Treatment	INTS3	65123	37	1	153740181	153740181	Missense_Mutation	SNP	G	A	5	307	c.2122G>A	c.(2122-2124)GAG>AAG	p.E708K
Pat_65	Pre-Treatment	CHRNB2	1141	37	1	154543672	154543672	Missense_Mutation	SNP	G	A	5	416	c.373G>A	c.(373-375)GGC>AGC	p.G125S
Pat_65	Pre-Treatment	MRPL24	79590	37	1	156708166	156708166	Missense_Mutation	SNP	C	T	8	846	c.248G>A	c.(247-249)CGA>CAA	p.R83Q
Pat_65	Pre-Treatment	LY9	4063	37	1	160786536	160786536	Missense_Mutation	SNP	G	A	16	241	c.1225G>A	c.(1225-1227)GAA>AAA	p.E409K
Pat_65	Pre-Treatment	UCK2	7371	37	1	165860559	165860559	Missense_Mutation	SNP	G	A	4	301	c.356G>A	c.(355-357)CGG>CAG	p.R119Q
Pat_65	Pre-Treatment	TNN	63923	37	1	175046699	175046699	Missense_Mutation	SNP	G	A	4	83	c.145G>A	c.(145-147)GAT>AAT	p.D49N
Pat_65	Pre-Treatment	RASAL2	9462	37	1	178427390	178427390	Missense_Mutation	SNP	G	A	6	187	c.2540G>A	c.(2539-2541)CGG>CAG	p.R847Q
Pat_65	Pre-Treatment	PRG4	10216	37	1	186276274	186276274	Missense_Mutation	SNP	G	T	4	169	c.1423G>T	c.(1423-1425)GCA>TCA	p.A475S
Pat_65	Pre-Treatment	PTPRC	5788	37	1	198721496	198721496	Missense_Mutation	SNP	C	T	15	253	c.3320C>T	c.(3319-3321)TCC>TTC	p.S1107F
Pat_65	Pre-Treatment	GPR37L1	9283	37	1	202097164	202097164	Missense_Mutation	SNP	G	A	4	262	c.926G>A	c.(925-927)CGC>CAC	p.R309H
Pat_65	Pre-Treatment	PTPN7	5778	37	1	202126888	202126888	Missense_Mutation	SNP	G	C	210	110	c.370C>G	c.(370-372)CGA>GGA	p.R124G

Pat_65	Pre-Treatment	PTPN14	5784	37	1	214549623	214549623	Missense_Mutation	SNP	C	T	6	189	c.2846G>A	c.(2845-2847)CGA>CAA	p.R949Q
Pat_65	Pre-Treatment	OBSCN	84033	37	1	228402500	228402500	Missense_Mutation	SNP	A	G	3	56	c.1529A>G	c.(1528-1530)AAG>AGG	p.K510R
Pat_65	Pre-Treatment	ACTN2	88	37	1	236902617	236902617	Missense_Mutation	SNP	C	T	6	607	c.892C>T	c.(892-894)CGT>TGT	p.R298C
Pat_65	Pre-Treatment	CNST	163882	37	1	246755003	246755003	Missense_Mutation	SNP	G	A	7	435	c.139G>A	c.(139-141)GGG>AGG	p.G47R
Pat_65	Pre-Treatment	OR2T4	127074	37	1	248524937	248524937	Missense_Mutation	SNP	A	T	5	354	c.55A>T	c.(55-57)ATG>TTG	p.M19L
Pat_65	Pre-Treatment	PGBD2	267002	37	1	249212114	249212114	Missense_Mutation	SNP	G	A	4	150	c.1331G>A	c.(1330-1332)CGG>CAG	p.R444Q
Pat_65	Pre-Treatment	CACNB2	783	37	10	18795450	18795451	Missense_Mutation	DNP	CC	TT	38	63	c.644_645CC>TT	c.(643-645)TCC>TTT	p.S215F
Pat_65	Pre-Treatment	KIAA1462	57608	37	10	30318556	30318556	Missense_Mutation	SNP	C	T	6	449	c.521G>A	c.(520-522)CGA>CAA	p.R174Q
Pat_65	Pre-Treatment	ANKRD30A	91074	37	10	37430688	37430688	Missense_Mutation	SNP	C	T	5	134	c.695C>T	c.(694-696)GCG>GTG	p.A232V
Pat_65	Pre-Treatment	ANKRD30A	91074	37	10	37430948	37430948	Missense_Mutation	SNP	C	G	8	144	c.955C>G	c.(955-957)CCA>GCA	p.P319A
Pat_65	Pre-Treatment	ANKRD30A	91074	37	10	37431050	37431050	Missense_Mutation	SNP	G	C	10	114	c.1057G>C	c.(1057-1059)GCA>CCA	p.A353P
Pat_65	Pre-Treatment	PGBD3	267004	37	10	50723897	50723897	Missense_Mutation	SNP	C	A	5	287	c.1264G>T	c.(1264-1266)GCC>TCC	p.A422S
Pat_65	Pre-Treatment	OGDHL	55753	37	10	50953529	50953529	Missense_Mutation	SNP	C	T	4	173	c.1490G>A	c.(1489-1491)CGG>CAG	p.R497Q
Pat_65	Pre-Treatment	SGMS1	259230	37	10	52103520	52103520	Missense_Mutation	SNP	G	A	53	87	c.355C>T	c.(355-357)CCC>TCC	p.P119S
Pat_65	Pre-Treatment	JMJD1C	221037	37	10	64944404	64944404	Missense_Mutation	SNP	G	A	4	199	c.6925C>T	c.(6925-6927)CGT>TGT	p.R2309C
Pat_65	Pre-Treatment	PLA2G12B	84647	37	10	74701011	74701011	Missense_Mutation	SNP	G	A	6	644	c.382C>T	c.(382-384)CGC>TGC	p.R128C
Pat_65	Pre-Treatment	KIAA0913	23053	37	10	75557222	75557222	Missense_Mutation	SNP	C	T	4	100	c.3506C>T	c.(3505-3507)GCC>GTC	p.A1169V
Pat_65	Pre-Treatment	PANK1	53354	37	10	91353604	91353604	Nonsense_Mutation	SNP	G	A	6	536	c.1453C>T	c.(1453-1455)CGA>TGA	p.R485*
Pat_65	Pre-Treatment	HECTD2	143279	37	10	93242776	93242776	Missense_Mutation	SNP	G	A	4	184	c.764G>A	c.(763-765)CGA>CAA	p.R255Q
Pat_65	Pre-Treatment	UBTD1	80019	37	10	99327791	99327791	Missense_Mutation	SNP	G	A	6	326	c.191G>A	c.(190-192)CGC>CAC	p.R64H
Pat_65	Pre-Treatment	POLL	27343	37	10	103340109	103340109	Missense_Mutation	SNP	C	T	91	110	c.1259G>A	c.(1258-1260)CGG>CAG	p.R420Q
Pat_65	Pre-Treatment	ITPRIP	85450	37	10	106075233	106075233	Missense_Mutation	SNP	C	T	4	217	c.577G>A	c.(577-579)GTG>ATG	p.V193M
Pat_65	Pre-Treatment	RPL13AP6	644511	37	10	112696573	112696573	Missense_Mutation	SNP	T	C	6	27	c.419A>G	c.(418-420)CAC>CGC	p.H140R
Pat_65	Pre-Treatment	DPYSL4	10570	37	10	134010404	134010404	Missense_Mutation	SNP	G	A	4	202	c.518G>A	c.(517-519)CGG>CAG	p.R173Q
Pat_65	Pre-Treatment	DPYSL4	10570	37	10	134016193	134016193	Missense_Mutation	SNP	C	T	4	156	c.1325C>T	c.(1324-1326)GCG>GTG	p.A442V
Pat_65	Pre-Treatment	TALDO1	6888	37	11	764390	764390	Missense_Mutation	SNP	G	A	4	130	c.938G>A	c.(937-939)CGC>CAC	p.R313H
Pat_65	Pre-Treatment	TRIM21	6737	37	11	4411261	4411261	Missense_Mutation	SNP	G	A	34	73	c.379C>T	c.(379-381)CCT>TCT	p.P127S
Pat_65	Pre-Treatment	OR51F1	256892	37	11	4791114	4791114	Missense_Mutation	SNP	G	A	37	66	c.34C>T	c.(34-36)CCA>TCA	p.P12S
Pat_65	Pre-Treatment	HPX	3263	37	11	6458877	6458877	Missense_Mutation	SNP	G	A	4	170	c.496C>T	c.(496-498)CGC>TGC	p.R166C
Pat_65	Pre-Treatment	SBF2	81846	37	11	9871756	9871756	Missense_Mutation	SNP	G	A	45	98	c.2620C>T	c.(2620-2622)CTT>TTT	p.L874F
Pat_65	Pre-Treatment	PSMA1	5682	37	11	14532449	14532449	Missense_Mutation	SNP	G	A	4	231	c.593C>T	c.(592-594)ACG>ATG	p.T198M
Pat_65	Pre-Treatment	ABCC8	6833	37	11	17464321	17464321	Missense_Mutation	SNP	G	A	5	226	c.1576C>T	c.(1576-1578)CGC>TGC	p.R526C
Pat_65	Pre-Treatment	NELL1	4745	37	11	20699519	20699519	Missense_Mutation	SNP	G	A	4	275	c.97G>A	c.(97-99)GTC>ATC	p.V33I
Pat_65	Pre-Treatment	ANO3	63982	37	11	26681879	26681879	Missense_Mutation	SNP	G	A	6	489	c.2834G>A	c.(2833-2835)CGA>CAA	p.R945Q
Pat_65	Pre-Treatment	F2	2147	37	11	46747651	46747651	Missense_Mutation	SNP	G	A	5	399	c.802G>A	c.(802-804)GAT>AAT	p.D268N
Pat_65	Pre-Treatment	OR5AR1	219493	37	11	56431526	56431526	Missense_Mutation	SNP	G	A	6	378	c.365G>A	c.(364-366)CGT>CAT	p.R122H
Pat_65	Pre-Treatment	OR4D10	390197	37	11	59245348	59245348	Nonsense_Mutation	SNP	G	A	120	260	c.446G>A	c.(445-447)TGG>TAG	p.W149*
Pat_65	Pre-Treatment	DDB1	1642	37	11	61071414	61071414	Missense_Mutation	SNP	C	T	5	321	c.2755G>A	c.(2755-2757)GAC>AAC	p.D919N
Pat_65	Pre-Treatment	PLCB3	5331	37	11	64030025	64030025	Missense_Mutation	SNP	C	T	5	211	c.2185C>T	c.(2185-2187)CGG>TGG	p.R729W
Pat_65	Pre-Treatment	CD248	57124	37	11	66083598	66083598	Missense_Mutation	SNP	G	A	4	159	c.901C>T	c.(901-903)CGG>TGG	p.R301W
Pat_65	Pre-Treatment	RBM4B	83759	37	11	66436559	66436559	Missense_Mutation	SNP	C	T	4	264	c.616G>A	c.(616-618)GGG>AGG	p.G206R
Pat_65	Pre-Treatment	SPTBN2	6712	37	11	66472458	66472458	Missense_Mutation	SNP	C	A	4	146	c.2289G>T	c.(2287-2289)TTG>TTT	p.L763F
Pat_65	Pre-Treatment	TSKU	25987	37	11	76506727	76506727	Missense_Mutation	SNP	G	A	4	134	c.67G>A	c.(67-69)GGG>AGG	p.G23R
Pat_65	Pre-Treatment	MYO7A	4647	37	11	76867967	76867967	Missense_Mutation	SNP	G	A	5	279	c.652G>A	c.(652-654)GAC>AAC	p.D218N
Pat_65	Pre-Treatment	MMP8	4317	37	11	102592182	102592182	Missense_Mutation	SNP	C	T	69	145	c.572G>A	c.(571-573)GGA>GAA	p.G191E
Pat_65	Pre-Treatment	MMP12	4321	37	11	102734976	102734976	Missense_Mutation	SNP	C	T	18	61	c.1213G>A	c.(1213-1215)GAA>AAA	p.E405K
Pat_65	Pre-Treatment	FXYD2	486	37	11	117695380	117695380	Missense_Mutation	SNP	G	A	4	253	c.14C>T	c.(13-15)TCG>TTG	p.S5L

Pat_65	Pre-Treatment	TMEM25	84866	37	11	118403655	118403655	Missense_Mutation	SNP	G	A	5	249	c.406G>A	c.(406-408)GGC>AGC	p.G136S
Pat_65	Pre-Treatment	ZNF202	7753	37	11	123598937	123598937	Missense_Mutation	SNP	A	G	4	269	c.736T>C	c.(736-738)TTT>CTT	p.F246L
Pat_65	Pre-Treatment	OR10S1	219873	37	11	123848217	123848217	Missense_Mutation	SNP	G	A	32	42	c.182C>T	c.(181-183)ACT>ATT	p.T61I
Pat_65	Pre-Treatment	OR10G7	390265	37	11	123909343	123909343	Nonsense_Mutation	SNP	G	T	101	514	c.366C>A	c.(364-366)TAC>TAA	p.Y122*
Pat_65	Pre-Treatment	VAMP1	6843	37	12	6575461	6575461	Missense_Mutation	SNP	C	T	5	304	c.59G>A	c.(58-60)GGT>GAT	p.G20D
Pat_65	Pre-Treatment	ETV6	2120	37	12	12022670	12022670	Missense_Mutation	SNP	G	A	6	435	c.776G>A	c.(775-777)CGG>CAG	p.R259Q
Pat_65	Pre-Treatment	RPL13AP20	387841	37	12	13028751	13028751	Missense_Mutation	SNP	G	C	32	65	c.319G>C	c.(319-321)GGC>CGC	p.G107R
Pat_65	Pre-Treatment	SLCO1C1	53919	37	12	20874891	20874891	Missense_Mutation	SNP	C	T	28	37	c.929C>T	c.(928-930)TCT>TTT	p.S310F
Pat_65	Pre-Treatment	IFLTD1	160492	37	12	25672949	25672949	Missense_Mutation	SNP	C	T	6	146	c.796G>A	c.(796-798)GTT>ATT	p.V266I
Pat_65	Pre-Treatment	C12orf54	121273	37	12	48877092	48877092	Missense_Mutation	SNP	C	T	81	189	c.13C>T	c.(13-15)CCC>TCC	p.P5S
Pat_65	Pre-Treatment	TROAP	10024	37	12	49724304	49724304	Missense_Mutation	SNP	G	A	12	129	c.1676G>A	c.(1675-1677)TGC>TAC	p.C559Y
Pat_65	Pre-Treatment	LETMD1	25875	37	12	51449775	51449775	Missense_Mutation	SNP	C	T	4	234	c.631C>T	c.(631-633)CGG>TGG	p.R211W
Pat_65	Pre-Treatment	KRT86	3892	37	12	52699156	52699156	Missense_Mutation	SNP	C	T	7	689	c.868C>T	c.(868-870)CGG>TGG	p.R290W
Pat_65	Pre-Treatment	AMHR2	269	37	12	53823690	53823690	Nonsense_Mutation	SNP	C	T	4	160	c.1216C>T	c.(1216-1218)CGA>TGA	p.R406*
Pat_65	Pre-Treatment	NFE2	4778	37	12	54688973	54688974	Missense_Mutation	DNP	CT	TG	82	229	c.59_60AG>CA	c.(58-60)GAG>GCA	p.E20A
Pat_65	Pre-Treatment	ACAD10	80724	37	12	112130602	112130602	Missense_Mutation	SNP	G	A	6	488	c.89G>A	c.(88-90)GGG>GAG	p.G30E
Pat_65	Pre-Treatment	FBXW8	26259	37	12	117462033	117462034	Missense_Mutation	DNP	GG	AA	53	135	.1449_1450GG>A	1447-1452)ATGGAT>ATAA	.483_484MD>I
Pat_65	Pre-Treatment	CCDC60	160777	37	12	119926577	119926577	Missense_Mutation	SNP	C	T	76	163	c.463C>T	c.(463-465)CGC>TGC	p.R155C
Pat_65	Pre-Treatment	GOLGA3	2802	37	12	133385015	133385015	Missense_Mutation	SNP	G	A	5	472	c.640C>T	c.(640-642)CGC>TGC	p.R214C
Pat_65	Pre-Treatment	PARP4	143	37	13	25000674	25000674	Missense_Mutation	SNP	G	A	4	214	c.4909C>T	c.(4909-4911)CGC>TGC	p.R1637C
Pat_65	Pre-Treatment	PABPC3	5042	37	13	25670931	25670931	Nonsense_Mutation	SNP	G	T	5	174	c.595G>T	c.(595-597)GGA>TGA	p.G199*
Pat_65	Pre-Treatment	FREM2	341640	37	13	39264066	39264066	Missense_Mutation	SNP	C	T	4	181	c.2585C>T	c.(2584-2586)GCC>GTC	p.A862V
Pat_65	Pre-Treatment	FREM2	341640	37	13	39266018	39266018	Missense_Mutation	SNP	G	A	8	522	c.4537G>A	c.(4537-4539)GAT>AAT	p.D1513N
Pat_65	Pre-Treatment	RCBTB1	55213	37	13	50141334	50141334	Missense_Mutation	SNP	C	T	4	164	c.82G>A	c.(82-84)GGC>AGC	p.G28S
Pat_65	Pre-Treatment	LOC220429	220429	37	13	50466425	50466425	Missense_Mutation	SNP	C	T	52	90	c.1699C>T	c.(1699-1701)CAC>TAC	p.H567Y
Pat_65	Pre-Treatment	RNF113B	140432	37	13	98829120	98829120	Missense_Mutation	SNP	G	A	4	130	c.371C>T	c.(370-372)ACG>ATG	p.T124M
Pat_65	Pre-Treatment	PSMB11	122706	37	14	23512120	23512120	Missense_Mutation	SNP	G	A	5	131	c.686G>A	c.(685-687)CGG>CAG	p.R229Q
Pat_65	Pre-Treatment	IPO4	79711	37	14	24653268	24653268	Missense_Mutation	SNP	G	A	4	217	c.1805C>T	c.(1804-1806)GCG>GTG	p.A602V
Pat_65	Pre-Treatment	TM9SF1	10548	37	14	24659625	24659625	Missense_Mutation	SNP	G	A	4	204	c.1388C>T	c.(1387-1389)ACT>ATT	p.T463I
Pat_65	Pre-Treatment	HECTD1	25831	37	14	31585636	31585636	Missense_Mutation	SNP	T	G	70	150	c.5424A>C	c.(5422-5424)GAA>GAC	p.E1808D
Pat_65	Pre-Treatment	AKAP6	9472	37	14	33069982	33069982	Missense_Mutation	SNP	G	A	4	173	c.2714G>A	c.(2713-2715)GGG>GAG	p.G905E
Pat_65	Pre-Treatment	AKAP6	9472	37	14	33292951	33292951	Missense_Mutation	SNP	A	G	4	233	c.5932A>G	c.(5932-5934)ACT>GCT	p.T1978A
Pat_65	Pre-Treatment	OTX2	5015	37	14	57268637	57268637	Missense_Mutation	SNP	C	A	4	156	c.686G>T	c.(685-687)AGC>ATC	p.S229I
Pat_65	Pre-Treatment	RTN1	6252	37	14	60063471	60063471	Missense_Mutation	SNP	C	T	147	287	c.2323G>A	c.(2323-2325)GCT>ACT	p.A775T
Pat_65	Pre-Treatment	PAPLN	89932	37	14	73732131	73732131	Missense_Mutation	SNP	G	A	4	257	c.3179G>A	c.(3178-3180)CGG>CAG	p.R1060Q
Pat_65	Pre-Treatment	C14orf43	91748	37	14	74205340	74205340	Missense_Mutation	SNP	G	A	4	176	c.1372C>T	c.(1372-1374)CGC>TGC	p.R458C
Pat_65	Pre-Treatment	C14orf43	91748	37	14	74205754	74205754	Nonsense_Mutation	SNP	C	A	4	63	c.958G>T	c.(958-960)GAA>TAA	p.E320*
Pat_65	Pre-Treatment	TTLL5	23093	37	14	76165558	76165558	Nonsense_Mutation	SNP	G	A	37	103	c.530G>A	c.(529-531)TGG>TAG	p.W177*
Pat_65	Pre-Treatment	WARS	7453	37	14	100835507	100835507	Missense_Mutation	SNP	G	A	4	148	c.16C>T	c.(16-18)CCC>TCC	p.P6S
Pat_65	Pre-Treatment	KIAA0284	283638	37	14	105349558	105349558	Missense_Mutation	SNP	G	A	12	681	c.764G>A	c.(763-765)GGT>GAT	p.G255D
Pat_65	Pre-Treatment	ATP10A	57194	37	15	25958904	25958904	Missense_Mutation	SNP	C	T	6	251	c.2261G>A	c.(2260-2262)CGG>CAG	p.R754Q
Pat_65	Pre-Treatment	GABRG3	2567	37	15	27777804	27777804	Missense_Mutation	SNP	C	T	35	84	c.1181C>T	c.(1180-1182)TCC>TTC	p.S394F
Pat_65	Pre-Treatment	DLL4	54567	37	15	41228851	41228851	Missense_Mutation	SNP	C	T	4	63	c.1666C>T	c.(1666-1668)CGG>TGG	p.R556W
Pat_65	Pre-Treatment	TUBGCP4	27229	37	15	43677989	43677989	Missense_Mutation	SNP	C	T	4	208	c.724C>T	c.(724-726)CGC>TGC	p.R242C
Pat_65	Pre-Treatment	HERC1	8925	37	15	63970126	63970126	Missense_Mutation	SNP	G	A	7	633	c.6988C>T	c.(6988-6990)CGC>TGC	p.R2330C
Pat_65	Pre-Treatment	LBXCOR1	390598	37	15	68119364	68119365	Missense_Mutation	DNP	CC	TT	14	39	.1066_1067CC>T	c.(1066-1068)CCT>TTT	p.P356F
Pat_65	Pre-Treatment	PTPN9	5780	37	15	75819488	75819488	Missense_Mutation	SNP	G	A	5	312	c.178C>T	c.(178-180)CGT>TGT	p.R60C

Pat_65	Pre-Treatment	SNX33	257364	37	15	75941463	75941463	Missense_Mutation	SNP	C	T	153	327	c.20C>T	c.(19-21)GCC>GTC	p.A7V
Pat_65	Pre-Treatment	IREB2	3658	37	15	78790399	78790399	Missense_Mutation	SNP	G	A	6	446	c.2806G>A	c.(2806-2808)GTG>ATG	p.V936M
Pat_65	Pre-Treatment	STARD5	80765	37	15	81605689	81605689	Missense_Mutation	SNP	G	A	5	502	c.550C>T	c.(550-552)CTC>TTC	p.L184F
Pat_65	Pre-Treatment	PDIA2	64714	37	16	334584	334584	Missense_Mutation	SNP	G	A	17	35	c.397G>A	c.(397-399)GAG>AAG	p.E133K
Pat_65	Pre-Treatment	SOLH	6650	37	16	598100	598100	Missense_Mutation	SNP	G	A	3	17	c.1262G>A	c.(1261-1263)TGT>TAT	p.C421Y
Pat_65	Pre-Treatment	IFT140	9742	37	16	1570021	1570021	Missense_Mutation	SNP	C	T	4	127	c.3901G>A	c.(3901-3903)GAC>AAC	p.D1301N
Pat_65	Pre-Treatment	IFT140	9742	37	16	1575305	1575305	Missense_Mutation	SNP	G	A	19	341	c.2791C>T	c.(2791-2793)CGC>TGC	p.R931C
Pat_65	Pre-Treatment	TBC1D24	57465	37	16	2546352	2546352	Missense_Mutation	SNP	C	T	4	257	c.203C>T	c.(202-204)ACG>ATG	p.T68M
Pat_65	Pre-Treatment	TBC1D24	57465	37	16	2546873	2546873	Missense_Mutation	SNP	C	T	4	196	c.724C>T	c.(724-726)CGC>TGC	p.R242C
Pat_65	Pre-Treatment	SRRM2	23524	37	16	2817091	2817091	Missense_Mutation	SNP	A	G	85	189	c.6562A>G	c.(6562-6564)ATC>GTC	p.I2188V
Pat_65	Pre-Treatment	BTBD12	84464	37	16	3641121	3641121	Missense_Mutation	SNP	C	T	5	221	c.2518G>A	c.(2518-2520)GAA>AAA	p.E840K
Pat_65	Pre-Treatment	ATF7IP2	80063	37	16	10532009	10532009	Missense_Mutation	SNP	G	T	5	179	c.1012G>T	c.(1012-1014)GAT>TAT	p.D338Y
Pat_65	Pre-Treatment	NPIP	9284	37	16	15045791	15045791	Missense_Mutation	SNP	C	T	8	591	c.962C>T	c.(961-963)CCA>CTA	p.P321L
Pat_65	Pre-Treatment	DNAH3	55567	37	16	21051173	21051173	Splice_Site	SNP	C	T	103	230	c.4730_splice	c.e33+1	p.S1577_splice
Pat_65	Pre-Treatment	NDUFAB1	4706	37	16	23598564	23598564	Missense_Mutation	SNP	C	T	4	227	c.245G>A	c.(244-246)CGT>CAT	p.R82H
Pat_65	Pre-Treatment	TNRC6A	27327	37	16	24816962	24816962	Missense_Mutation	SNP	G	A	6	594	c.4159G>A	c.(4159-4161)GGT>AGT	p.G1387S
Pat_65	Pre-Treatment	HEATR3	55027	37	16	50112912	50112912	Missense_Mutation	SNP	G	A	4	123	c.1024G>A	c.(1024-1026)GTT>ATT	p.V342I
Pat_65	Pre-Treatment	ARL2BP	23568	37	16	57286171	57286171	Missense_Mutation	SNP	C	T	4	207	c.484C>T	c.(484-486)CGG>TGG	p.R162W
Pat_65	Pre-Treatment	CDH16	1014	37	16	66943281	66943281	Missense_Mutation	SNP	C	T	4	169	c.2281G>A	c.(2281-2283)GTG>ATG	p.V761M
Pat_65	Pre-Treatment	DDX28	55794	37	16	68055631	68055631	Missense_Mutation	SNP	C	T	4	182	c.1475G>A	c.(1474-1476)GGG>GAG	p.G492E
Pat_65	Pre-Treatment	VAC14	55697	37	16	70818015	70818015	Splice_Site	SNP	C	T	6	239	c.594_splice	c.e5+1	p.W198_splice
Pat_65	Pre-Treatment	CHST4	10164	37	16	71570876	71570876	Missense_Mutation	SNP	G	A	69	138	c.296G>A	c.(295-297)CGG>CAG	p.R99Q
Pat_65	Pre-Treatment	PHLPP2	23035	37	16	71710415	71710415	Missense_Mutation	SNP	C	T	4	217	c.1406G>A	c.(1405-1407)CGG>CAG	p.R469Q
Pat_65	Pre-Treatment	CLEC3A	10143	37	16	78062081	78062081	Nonsense_Mutation	SNP	C	T	4	100	c.193C>T	c.(193-195)CAG>TAG	p.Q65*
Pat_65	Pre-Treatment	MBTPS1	8720	37	16	84104299	84104299	Missense_Mutation	SNP	G	A	5	357	c.1676C>T	c.(1675-1677)TCG>TTG	p.S559L
Pat_65	Pre-Treatment	TAF1C	9013	37	16	84213175	84213175	Missense_Mutation	SNP	C	T	4	92	c.1982G>A	c.(1981-1983)CGC>CAC	p.R661H
Pat_65	Pre-Treatment	SERPINF2	5345	37	17	1650407	1650408	Missense_Mutation	DNP	CC	AT	22	45	c.462_463CC>AT	460-465)GACCTG>GAAT	p.D154E
Pat_65	Pre-Treatment	RPA1	6117	37	17	1780522	1780522	Missense_Mutation	SNP	C	T	4	260	c.604C>T	c.(604-606)CGT>TGT	p.R202C
Pat_65	Pre-Treatment	OR3A1	4994	37	17	3195650	3195650	Missense_Mutation	SNP	C	A	4	149	c.227G>T	c.(226-228)TGC>TTC	p.C76F
Pat_65	Pre-Treatment	ZMYND15	84225	37	17	4647542	4647542	Missense_Mutation	SNP	G	A	90	205	c.1436G>A	c.(1435-1437)GGG>GAG	p.G479E
Pat_65	Pre-Treatment	FAM64A	54478	37	17	6350844	6350844	Missense_Mutation	SNP	G	A	130	245	c.356G>A	c.(355-357)AGG>AAG	p.R119K
Pat_65	Pre-Treatment	DNAH2	146754	37	17	7640548	7640548	Missense_Mutation	SNP	G	A	4	278	c.1142G>A	c.(1141-1143)CGG>CAG	p.R381Q
Pat_65	Pre-Treatment	DNAH2	146754	37	17	7683487	7683487	Missense_Mutation	SNP	G	A	6	616	c.5735G>A	c.(5734-5736)CGC>CAC	p.R1912H
Pat_65	Pre-Treatment	MYH4	4622	37	17	10355278	10355278	Missense_Mutation	SNP	C	T	103	219	c.3718G>A	c.(3718-3720)GAG>AAG	p.E1240K
Pat_65	Pre-Treatment	DNAH9	1770	37	17	11540095	11540095	Missense_Mutation	SNP	G	A	125	280	c.1780G>A	c.(1780-1782)GAA>AAA	p.E594K
Pat_65	Pre-Treatment	C17orf76	388341	37	17	16365643	16365643	Missense_Mutation	SNP	G	A	4	158	c.304C>T	c.(304-306)CGG>TGG	p.R102W
Pat_65	Pre-Treatment	SREBF1	6720	37	17	17723595	17723595	Missense_Mutation	SNP	G	A	5	379	c.332C>T	c.(331-333)CCG>CTG	p.P111L
Pat_65	Pre-Treatment	EPN2	22905	37	17	19186863	19186863	Missense_Mutation	SNP	G	A	4	168	c.431G>A	c.(430-432)AGG>AAG	p.R144K
Pat_65	Pre-Treatment	GIT1	28964	37	17	27904247	27904247	Missense_Mutation	SNP	G	A	6	453	c.1000C>T	c.(1000-1002)CGC>TGC	p.R334C
Pat_65	Pre-Treatment	RNF135	84282	37	17	29324337	29324337	Missense_Mutation	SNP	C	T	4	187	c.757C>T	c.(757-759)CGG>TGG	p.R253W
Pat_65	Pre-Treatment	PIP4K2B	8396	37	17	36934618	36934618	Missense_Mutation	SNP	G	A	6	529	c.662C>T	c.(661-663)ACG>ATG	p.T221M
Pat_65	Pre-Treatment	ERBB2	2064	37	17	37871746	37871746	Missense_Mutation	SNP	G	A	4	237	c.1270G>A	c.(1270-1272)GTC>ATC	p.V424I
Pat_65	Pre-Treatment	KRT23	25984	37	17	39086344	39086344	Missense_Mutation	SNP	C	T	30	72	c.484G>A	c.(484-486)GAA>AAA	p.E162K
Pat_65	Pre-Treatment	CNTNAP1	8506	37	17	40839014	40839014	Missense_Mutation	SNP	G	A	5	269	c.994G>A	c.(994-996)GTC>ATC	p.V332I
Pat_65	Pre-Treatment	CCDC56	28958	37	17	40947839	40947839	Missense_Mutation	SNP	C	T	4	96	c.419G>A	c.(418-420)CGC>CAC	p.R140H
Pat_65	Pre-Treatment	CDC27	996	37	17	45234366	45234366	Missense_Mutation	SNP	G	A	5	309	c.755C>T	c.(754-756)TCC>TTC	p.S252F
Pat_65	Pre-Treatment	OSBPL7	114881	37	17	45890750	45890750	Missense_Mutation	SNP	G	A	4	116	c.1619C>T	c.(1618-1620)GCT>GTT	p.A540V

Pat_65	Pre-Treatment	PHB	5245	37	17	47489082	47489082	Missense_Mutation	SNP	G	A	4	192	c.208C>T	c.(208-210)CGT>TGT	p.R70C
Pat_65	Pre-Treatment	AKAP1	8165	37	17	55195774	55195774	Missense_Mutation	SNP	G	A	5	393	c.2533G>A	c.(2533-2535)GCC>ACC	p.A845T
Pat_65	Pre-Treatment	ABCA9	10350	37	17	67028403	67028403	Nonsense_Mutation	SNP	G	A	4	185	c.1291C>T	c.(1291-1293)CGA>TGA	p.R431*
Pat_65	Pre-Treatment	FBF1	85302	37	17	73922171	73922171	Missense_Mutation	SNP	G	A	3	69	c.766C>T	c.(766-768)CGC>TGC	p.R256C
Pat_65	Pre-Treatment	EMILIN2	84034	37	18	2909817	2909817	Missense_Mutation	SNP	G	A	5	237	c.2824G>A	c.(2824-2826)GGG>AGG	p.G942R
Pat_65	Pre-Treatment	LAMA1	284217	37	18	6948540	6948540	Missense_Mutation	SNP	G	A	91	161	c.8572C>T	c.(8572-8574)CCT>TCT	p.P2858S
Pat_65	Pre-Treatment	LAMA1	284217	37	18	6971871	6971871	Missense_Mutation	SNP	C	T	5	390	c.6884G>A	c.(6883-6885)CGT>CAT	p.R2295H
Pat_65	Pre-Treatment	RALBP1	10928	37	18	9530883	9530883	Missense_Mutation	SNP	G	A	5	142	c.1399G>A	c.(1399-1401)GTT>ATT	p.V467I
Pat_65	Pre-Treatment	TXNDC2	84203	37	18	9887437	9887437	Missense_Mutation	SNP	G	A	13	505	c.961G>A	c.(961-963)GCC>ACC	p.A321T
Pat_65	Pre-Treatment	TXNDC2	84203	37	18	9887452	9887452	Missense_Mutation	SNP	G	A	8	514	c.976G>A	c.(976-978)GAG>AAG	p.E326K
Pat_65	Pre-Treatment	KIAA1012	22878	37	18	29419285	29419285	Missense_Mutation	SNP	G	A	29	67	c.3973C>T	c.(3973-3975)CAT>TAT	p.H1325Y
Pat_65	Pre-Treatment	ACAA2	10449	37	18	47310261	47310261	Missense_Mutation	SNP	C	T	4	217	c.1150G>A	c.(1150-1152)GGA>AGA	p.G384R
Pat_65	Pre-Treatment	SERPINB2	5055	37	18	61569055	61569055	Missense_Mutation	SNP	G	A	56	112	c.617G>A	c.(616-618)GGA>GAA	p.G206E
Pat_65	Pre-Treatment	CDH19	28513	37	18	64176387	64176387	Missense_Mutation	SNP	G	A	5	536	c.1673C>T	c.(1672-1674)CCG>CTG	p.P558L
Pat_65	Pre-Treatment	MED16	10025	37	19	889781	889781	Missense_Mutation	SNP	C	T	26	42	c.304G>A	c.(304-306)GAC>AAC	p.D102N
Pat_65	Pre-Treatment	LMNB2	84823	37	19	2434378	2434378	Missense_Mutation	SNP	C	T	4	201	c.1057G>A	c.(1057-1059)GAG>AAG	p.E353K
Pat_65	Pre-Treatment	ZNF555	148254	37	19	2853202	2853202	Missense_Mutation	SNP	C	T	5	169	c.1139C>T	c.(1138-1140)CCC>CTC	p.P380L
Pat_65	Pre-Treatment	AES	166	37	19	3057730	3057730	Missense_Mutation	SNP	C	T	4	236	c.136G>A	c.(136-138)GAA>AAA	p.E46K
Pat_65	Pre-Treatment	EEF2	1938	37	19	3979865	3979865	Missense_Mutation	SNP	C	A	4	98	c.1546G>T	c.(1546-1548)GAC>TAC	p.D516Y
Pat_65	Pre-Treatment	PLIN4	729359	37	19	4510875	4510875	Missense_Mutation	SNP	C	A	27	124	c.3055G>T	c.(3055-3057)GGG>TGG	p.G1019W
Pat_65	Pre-Treatment	PLIN4	729359	37	19	4511345	4511345	Missense_Mutation	SNP	G	T	5	354	c.2585C>A	c.(2584-2586)GCC>GAC	p.A862D
Pat_65	Pre-Treatment	DPP9	91039	37	19	4704265	4704265	Missense_Mutation	SNP	G	A	5	293	c.478C>T	c.(478-480)CGG>TGG	p.R160W
Pat_65	Pre-Treatment	FUT5	2527	37	19	5867303	5867303	Nonsense_Mutation	SNP	C	T	63	125	c.434G>A	c.(433-435)TGG>TAG	p.W145*
Pat_65	Pre-Treatment	GTF2F1	2962	37	19	6383373	6383373	Missense_Mutation	SNP	C	T	5	204	c.631G>A	c.(631-633)GAG>AAG	p.E211K
Pat_65	Pre-Treatment	ZNF557	79230	37	19	7083094	7083094	Missense_Mutation	SNP	A	G	9	330	c.611A>G	c.(610-612)AAT>AGT	p.N204S
Pat_65	Pre-Treatment	CLEC4M	10332	37	19	7830867	7830868	Missense_Mutation	DNP	CC	GG	9	222	c.489_490CC>GG	87-492)ACCCGG>ACGG	p.R164G
Pat_65	Pre-Treatment	MAP2K7	5609	37	19	7968947	7968947	Missense_Mutation	SNP	A	T	5	76	c.118A>T	c.(118-120)AGG>TGG	p.R40W
Pat_65	Pre-Treatment	ELAVL1	1994	37	19	8032566	8032566	Missense_Mutation	SNP	G	T	5	164	c.539C>A	c.(538-540)ACA>AAA	p.T180K
Pat_65	Pre-Treatment	FBN3	84467	37	19	8196706	8196706	Missense_Mutation	SNP	G	C	22	42	c.1722C>G	c.(1720-1722)GAC>GAG	p.D574E
Pat_65	Pre-Treatment	MUC16	94025	37	19	9063807	9063807	Missense_Mutation	SNP	G	A	82	162	c.23639C>T	c.(23638-23640)TCA>TTA	p.S7880L
Pat_65	Pre-Treatment	MAST1	22983	37	19	12985295	12985295	Missense_Mutation	SNP	C	T	4	68	c.4324C>T	c.(4324-4326)CGG>TGG	p.R1442W
Pat_65	Pre-Treatment	WIZ	58525	37	19	15538201	15538201	Missense_Mutation	SNP	C	T	4	115	c.1195G>A	c.(1195-1197)GAC>AAC	p.D399N
Pat_65	Pre-Treatment	CYP4F3	4051	37	19	15763737	15763737	Missense_Mutation	SNP	G	A	74	143	c.1090G>A	c.(1090-1092)GAC>AAC	p.D364N
Pat_65	Pre-Treatment	ZNF90	7643	37	19	20230036	20230036	Missense_Mutation	SNP	G	T	7	298	c.1673G>T	c.(1672-1674)AGT>ATT	p.S558I
Pat_65	Pre-Treatment	ZNF430	80264	37	19	21240543	21240543	Missense_Mutation	SNP	G	A	8	347	c.1429G>A	c.(1429-1431)GTA>ATA	p.V477I
Pat_65	Pre-Treatment	ZNF708	7562	37	19	21476249	21476249	Missense_Mutation	SNP	T	C	10	332	c.1519A>G	c.(1519-1521)AAA>GAA	p.K507E
Pat_65	Pre-Treatment	ZNF708	7562	37	19	21476519	21476519	Missense_Mutation	SNP	T	C	4	188	c.1249A>G	c.(1249-1251)AAG>GAG	p.K417E
Pat_65	Pre-Treatment	ZNF708	7562	37	19	21476603	21476603	Missense_Mutation	SNP	C	T	5	426	c.1165G>A	c.(1165-1167)GAG>AAG	p.E389K
Pat_65	Pre-Treatment	ZNF493	284443	37	19	21607059	21607059	Missense_Mutation	SNP	C	G	5	220	c.1214C>G	c.(1213-1215)ACT>AGT	p.T405S
Pat_65	Pre-Treatment	ZNF98	148198	37	19	22574676	22574676	Missense_Mutation	SNP	A	C	6	272	c.1361T>G	c.(1360-1362)ATA>AGA	p.I454R
Pat_65	Pre-Treatment	ZNF254	9534	37	19	24310450	24310450	Missense_Mutation	SNP	A	G	12	210	c.1648A>G	c.(1648-1650)AAA>GAA	p.K550E
Pat_65	Pre-Treatment	NFKBID	84807	37	19	36380809	36380809	Missense_Mutation	SNP	C	T	6	352	c.871G>A	c.(871-873)GGG>AGG	p.G291R
Pat_65	Pre-Treatment	ERF	2077	37	19	42753854	42753854	Missense_Mutation	SNP	G	A	4	133	c.410C>T	c.(409-411)TCG>TTG	p.S137L
Pat_65	Pre-Treatment	CIC	23152	37	19	42791752	42791752	Missense_Mutation	SNP	G	A	5	310	c.638G>A	c.(637-639)CGG>CAG	p.R213Q
Pat_65	Pre-Treatment	CIC	23152	37	19	42793183	42793183	Missense_Mutation	SNP	G	A	5	499	c.1075G>A	c.(1075-1077)GGG>AGG	p.G359R
Pat_65	Pre-Treatment	LIPE	3991	37	19	42911936	42911936	Missense_Mutation	SNP	G	A	4	120	c.1664C>T	c.(1663-1665)GCC>GTC	p.A555V
Pat_65	Pre-Treatment	PSG6	5675	37	19	43585170	43585170	Missense_Mutation	SNP	C	T	160	342	c.293G>A	c.(292-294)CGA>CAA	p.R98Q

Pat_65	Pre-Treatment	CCDC8	83987	37	19	46914959	46914959	Missense_Mutation	SNP	T	C	10	411	c.1109A>G	c.(1108-1110)GAG>GGG	p.E370G
Pat_65	Pre-Treatment	GRLF1	2909	37	19	47423683	47423683	Missense_Mutation	SNP	G	A	4	255	c.1751G>A	c.(1750-1752)CGG>CAG	p.R584Q
Pat_65	Pre-Treatment	SPHK2	56848	37	19	49131527	49131527	Missense_Mutation	SNP	C	T	4	176	c.865C>T	c.(865-867)CAC>TAC	p.H289Y
Pat_65	Pre-Treatment	IRF3	3661	37	19	50165513	50165513	Missense_Mutation	SNP	C	T	5	219	c.674G>A	c.(673-675)GGC>GAC	p.G225D
Pat_65	Pre-Treatment	SIGLEC6	946	37	19	52034696	52034696	Missense_Mutation	SNP	C	T	4	286	c.145G>A	c.(145-147)GTA>ATA	p.V49I
Pat_65	Pre-Treatment	ZNF528	84436	37	19	52918874	52918874	Missense_Mutation	SNP	T	G	7	268	c.769T>G	c.(769-771)TCA>GCA	p.S257A
Pat_65	Pre-Treatment	ZNF816A	125893	37	19	53453583	53453583	Missense_Mutation	SNP	G	T	5	304	c.1445C>A	c.(1444-1446)ACA>AAA	p.T482K
Pat_65	Pre-Treatment	LILRB5	10990	37	19	54759278	54759278	Missense_Mutation	SNP	G	A	4	143	c.823C>T	c.(823-825)CTC>TTC	p.L275F
Pat_65	Pre-Treatment	CCDC106	29903	37	19	56163951	56163951	Missense_Mutation	SNP	G	A	4	165	c.682G>A	c.(682-684)GAG>AAG	p.E228K
Pat_65	Pre-Treatment	GALP	85569	37	19	56694582	56694582	Splice_Site	SNP	G	A	4	206	c.295_splice	c.e5+1	p.D99_splice
Pat_65	Pre-Treatment	ZSCAN4	201516	37	19	58189533	58189533	Splice_Site	SNP	G	A	77	145	c.563_splice	c.e5-1	p.G188_splice
Pat_65	Pre-Treatment	COLEC11	78989	37	2	3691583	3691583	Missense_Mutation	SNP	G	A	5	447	c.691G>A	c.(691-693)GGT>AGT	p.G231S
Pat_65	Pre-Treatment	GRHL1	29841	37	2	10133365	10133365	Missense_Mutation	SNP	G	A	4	169	c.1492G>A	c.(1492-1494)GGT>AGT	p.G498S
Pat_65	Pre-Treatment	APOB	338	37	2	21229136	21229136	Missense_Mutation	SNP	G	A	5	355	c.10604C>T	c.(10603-10605)ACT>ATT	p.T3535I
Pat_65	Pre-Treatment	ATAD2B	54454	37	2	24118737	24118737	Missense_Mutation	SNP	C	T	5	268	c.320G>A	c.(319-321)CGA>CAA	p.R107Q
Pat_65	Pre-Treatment	NCOA1	8648	37	2	24933956	24933956	Missense_Mutation	SNP	G	A	4	161	c.2575G>A	c.(2575-2577)GCC>ACC	p.A859T
Pat_65	Pre-Treatment	CAD	790	37	2	27464072	27464072	Missense_Mutation	SNP	G	A	6	565	c.5785G>A	c.(5785-5787)GTC>ATC	p.V1929I
Pat_65	Pre-Treatment	XDH	7498	37	2	31560538	31560538	Missense_Mutation	SNP	C	T	5	413	c.3920G>A	c.(3919-3921)CGC>CAC	p.R1307H
Pat_65	Pre-Treatment	BIRC6	57448	37	2	32703713	32703713	Missense_Mutation	SNP	G	A	4	174	c.7079G>A	c.(7078-7080)CGC>CAC	p.R2360H
Pat_65	Pre-Treatment	PSME4	23198	37	2	54150222	54150222	Missense_Mutation	SNP	G	A	5	356	c.1942C>T	c.(1942-1944)CCC>TCC	p.P648S
Pat_65	Pre-Treatment	PSME4	23198	37	2	54155364	54155364	Missense_Mutation	SNP	G	A	4	195	c.1393C>T	c.(1393-1395)CGC>TGC	p.R465C
Pat_65	Pre-Treatment	RPL23AP32	56969	37	2	54756736	54756737	Missense_Mutation	DNP	TT	CC	17	221	c.254_255TT>CC	c.(253-255)TTT>TCC	p.F85S
Pat_65	Pre-Treatment	GFPT1	2673	37	2	69590794	69590794	Missense_Mutation	SNP	C	T	27	62	c.232G>A	c.(232-234)GAT>AAT	p.D78N
Pat_65	Pre-Treatment	DQX1	165545	37	2	74749737	74749737	Missense_Mutation	SNP	C	T	7	359	c.1465G>A	c.(1465-1467)GAG>AAG	p.E489K
Pat_65	Pre-Treatment	FAM176A	84141	37	2	75745202	75745202	Missense_Mutation	SNP	G	A	4	234	c.65C>T	c.(64-66)GCG>GTG	p.A22V
Pat_65	Pre-Treatment	IMMT	10989	37	2	86393689	86393689	Missense_Mutation	SNP	G	A	4	177	c.734C>T	c.(733-735)GCG>GTG	p.A245V
Pat_65	Pre-Treatment	LMAN2L	81562	37	2	97377624	97377624	Missense_Mutation	SNP	G	A	5	430	c.646C>T	c.(646-648)CGC>TGC	p.R216C
Pat_65	Pre-Treatment	AFF3	3899	37	2	100210409	100210409	Missense_Mutation	SNP	C	T	3	38	c.1714G>A	c.(1714-1716)GCG>ACG	p.A572T
Pat_65	Pre-Treatment	CBWD2	150472	37	2	114218249	114218249	Splice_Site	SNP	G	A	12	177	c.529_splice	c.e7-1	p.H177_splice
Pat_65	Pre-Treatment	WASH2P	375260	37	2	114355998	114355998	Missense_Mutation	SNP	C	G	6	48	c.616C>G	c.(616-618)CAC>GAC	p.H206D
Pat_65	Pre-Treatment	POTEE	445582	37	2	131976198	131976198	Missense_Mutation	SNP	A	G	5	445	c.223A>G	c.(223-225)AGT>GGT	p.S75G
Pat_65	Pre-Treatment	ITGB6	3694	37	2	160980358	160980358	Missense_Mutation	SNP	C	T	5	433	c.1925G>A	c.(1924-1926)CGA>CAA	p.R642Q
Pat_65	Pre-Treatment	TTN	7273	37	2	179669338	179669338	Missense_Mutation	SNP	G	A	5	152	c.32C>T	c.(31-33)CCG>CTG	p.P11L
Pat_65	Pre-Treatment	ZSWIM2	151112	37	2	187693420	187693420	Missense_Mutation	SNP	G	A	43	84	c.1193C>T	c.(1192-1194)TCA>TTA	p.S398L
Pat_65	Pre-Treatment	NBEAL1	65065	37	2	204001498	204001498	Splice_Site	SNP	G	A	6	400	c.4478_splice	c.e28+1	p.T1493_splice
Pat_65	Pre-Treatment	CRYGA	1418	37	2	209025629	209025629	Missense_Mutation	SNP	G	A	6	525	c.424C>T	c.(424-426)CGG>TGG	p.R142W
Pat_65	Pre-Treatment	PTH2R	5746	37	2	209271775	209271775	Missense_Mutation	SNP	G	A	5	326	c.7G>A	c.(7-9)GGG>AGG	p.G3R
Pat_65	Pre-Treatment	SPEG	10290	37	2	220353355	220353355	Missense_Mutation	SNP	G	A	4	176	c.7994G>A	c.(7993-7995)AGC>AAC	p.S2665N
Pat_65	Pre-Treatment	KIAA1486	57624	37	2	226378287	226378287	Missense_Mutation	SNP	C	T	45	109	c.422C>T	c.(421-423)CCC>CTC	p.P141L
Pat_65	Pre-Treatment	IRS1	3667	37	2	227661578	227661578	Missense_Mutation	SNP	C	T	4	121	c.1877G>A	c.(1876-1878)CGA>CAA	p.R626Q
Pat_65	Pre-Treatment	COL4A3	1285	37	2	228172425	228172425	Splice_Site	SNP	G	A	4	182	c.4253_splice	c.e48-1	p.G1418_splice
Pat_65	Pre-Treatment	ARMC9	80210	37	2	232127058	232127058	Missense_Mutation	SNP	G	A	6	562	c.1066G>A	c.(1066-1068)GTT>ATT	p.V356I
Pat_65	Pre-Treatment	NMUR1	10316	37	2	232393418	232393418	Missense_Mutation	SNP	G	A	6	466	c.314C>T	c.(313-315)TCG>TTG	p.S105L
Pat_65	Pre-Treatment	NEU2	4759	37	2	233897427	233897427	Missense_Mutation	SNP	G	A	5	463	c.46G>A	c.(46-48)GGA>AGA	p.G16R
Pat_65	Pre-Treatment	PRNP	5621	37	20	4680318	4680318	Missense_Mutation	SNP	G	A	4	214	c.452G>A	c.(451-453)CGT>CAT	p.R151H
Pat_65	Pre-Treatment	RBL1	5933	37	20	35651207	35651207	Missense_Mutation	SNP	C	T	4	204	c.2405G>A	c.(2404-2406)CGC>CAC	p.R802H
Pat_65	Pre-Treatment	LPIN3	64900	37	20	39974612	39974612	Missense_Mutation	SNP	G	A	4	231	c.169G>A	c.(169-171)GTC>ATC	p.V57I

Pat_65	Pre-Treatment	WFDC8	90199	37	20	44180787	44180787	Missense_Mutation	SNP	G	C	44	103	c.604C>G	c.(604-606)CCA>GCA	p.P202A
Pat_65	Pre-Treatment	MMP9	4318	37	20	44641918	44641918	Missense_Mutation	SNP	G	A	6	643	c.1355G>A	c.(1354-1356)CGG>CAG	p.R452Q
Pat_65	Pre-Treatment	ATP9A	10079	37	20	50241846	50241846	Missense_Mutation	SNP	G	A	4	191	c.1901C>T	c.(1900-1902)ACG>ATG	p.T634M
Pat_65	Pre-Treatment	TSHZ2	128553	37	20	51871822	51871822	Missense_Mutation	SNP	G	A	88	169	c.1825G>A	c.(1825-1827)GAA>AAA	p.E609K
Pat_65	Pre-Treatment	EDN3	1908	37	20	57899500	57899500	Missense_Mutation	SNP	G	A	107	230	c.703G>A	c.(703-705)GAA>AAA	p.E235K
Pat_65	Pre-Treatment	ZNF512B	57473	37	20	62597990	62597990	Missense_Mutation	SNP	C	T	4	178	c.538G>A	c.(538-540)GTC>ATC	p.V180I
Pat_65	Pre-Treatment	UMODL1	89766	37	21	43547792	43547792	Missense_Mutation	SNP	C	T	4	91	c.3541C>T	c.(3541-3543)CCC>TCC	p.P1181S
Pat_65	Pre-Treatment	PCNT	5116	37	21	47831565	47831565	Missense_Mutation	SNP	G	A	4	150	c.5578G>A	c.(5578-5580)GAA>AAA	p.E1860K
Pat_65	Pre-Treatment	MICAL3	57553	37	22	18300668	18300668	Missense_Mutation	SNP	C	T	4	91	c.4759G>A	c.(4759-4761)GCG>ACG	p.A1587T
Pat_65	Pre-Treatment	C1QTNF6	114904	37	22	37578529	37578529	Missense_Mutation	SNP	G	A	4	225	c.479C>T	c.(478-480)GCG>GTG	p.A160V
Pat_65	Pre-Treatment	TRIOBP	11078	37	22	38120437	38120437	Missense_Mutation	SNP	G	C	7	535	c.1874G>C	c.(1873-1875)AGA>ACA	p.R625T
Pat_65	Pre-Treatment	TRIOBP	11078	37	22	38120668	38120668	Missense_Mutation	SNP	A	T	7	331	c.2105A>T	c.(2104-2106)CAA>CTA	p.Q702L
Pat_65	Pre-Treatment	MKL1	57591	37	22	40816901	40816901	Missense_Mutation	SNP	C	G	6	272	c.831G>C	c.(829-831)CAG>CAC	p.Q277H
Pat_65	Pre-Treatment	SMC1B	27127	37	22	45789558	45789558	Missense_Mutation	SNP	C	T	4	180	c.1501G>A	c.(1501-1503)GCA>ACA	p.A501T
Pat_65	Pre-Treatment	ARSA	410	37	22	51065300	51065300	Missense_Mutation	SNP	G	A	6	504	c.640C>T	c.(640-642)CGC>TGC	p.R214C
Pat_65	Pre-Treatment	GRM7	2917	37	3	7188164	7188164	Missense_Mutation	SNP	C	T	6	442	c.545C>T	c.(544-546)ACG>ATG	p.T182M
Pat_65	Pre-Treatment	GRM7	2917	37	3	7456728	7456728	Missense_Mutation	SNP	C	T	4	134	c.1052C>T	c.(1051-1053)ACG>ATG	p.T351M
Pat_65	Pre-Treatment	ATP2B2	491	37	3	10442706	10442706	Missense_Mutation	SNP	C	T	52	83	c.712G>A	c.(712-714)GAA>AAA	p.E238K
Pat_65	Pre-Treatment	ZNF860	344787	37	3	32031840	32031840	Missense_Mutation	SNP	G	C	4	90	c.1269G>C	c.(1267-1269)GAG>GAC	p.E423D
Pat_65	Pre-Treatment	ARPP21	10777	37	3	35763105	35763105	Missense_Mutation	SNP	G	A	20	62	c.1004G>A	c.(1003-1005)AGA>AAA	p.R335K
Pat_65	Pre-Treatment	TRANK1	9881	37	3	36898026	36898026	Missense_Mutation	SNP	C	T	6	468	c.1405G>A	c.(1405-1407)GAC>AAC	p.D469N
Pat_65	Pre-Treatment	ZNF621	285268	37	3	40571763	40571763	Missense_Mutation	SNP	G	A	4	244	c.215G>A	c.(214-216)GGC>GAC	p.G72D
Pat_65	Pre-Treatment	KBTBD5	131377	37	3	42730184	42730184	Missense_Mutation	SNP	G	A	4	230	c.1396G>A	c.(1396-1398)GTA>ATA	p.V466I
Pat_65	Pre-Treatment	LTF	4057	37	3	46495836	46495836	Missense_Mutation	SNP	C	T	127	327	c.662G>A	c.(661-663)GGG>GAG	p.G221E
Pat_65	Pre-Treatment	ALS2CL	259173	37	3	46716140	46716140	Missense_Mutation	SNP	C	T	4	202	c.2345G>A	c.(2344-2346)CGG>CAG	p.R782Q
Pat_65	Pre-Treatment	CELSR3	1951	37	3	48699362	48699362	Missense_Mutation	SNP	G	A	79	137	c.706C>T	c.(706-708)CCA>TCA	p.P236S
Pat_65	Pre-Treatment	GMPPB	29925	37	3	49760118	49760118	Missense_Mutation	SNP	G	A	4	184	c.472C>T	c.(472-474)CGG>TGG	p.R158W
Pat_65	Pre-Treatment	RAD54L2	23132	37	3	51697329	51697329	Missense_Mutation	SNP	C	T	4	116	c.4297C>T	c.(4297-4299)CGG>TGG	p.R1433W
Pat_65	Pre-Treatment	STAB1	23166	37	3	52554552	52554552	Missense_Mutation	SNP	G	C	60	116	c.5636G>C	c.(5635-5637)CGG>CCG	p.R1879P
Pat_65	Pre-Treatment	TMEM110	375346	37	3	52876888	52876888	Missense_Mutation	SNP	G	A	4	107	c.707C>T	c.(706-708)TCG>TTG	p.S236L
Pat_65	Pre-Treatment	GPR27	2850	37	3	71803846	71803846	Missense_Mutation	SNP	C	T	3	39	c.646C>T	c.(646-648)CCC>TCC	p.P216S
Pat_65	Pre-Treatment	FLJ10213	55096	37	3	73111864	73111864	Missense_Mutation	SNP	G	A	4	273	c.632G>A	c.(631-633)CGA>CAA	p.R211Q
Pat_65	Pre-Treatment	PDZRN3	23024	37	3	73433967	73433967	Missense_Mutation	SNP	A	G	15	41	c.1750T>C	c.(1750-1752)TCG>CCG	p.S584P
Pat_65	Pre-Treatment	OR5H15	403274	37	3	97887932	97887932	Missense_Mutation	SNP	T	C	145	259	c.389T>C	c.(388-390)TTA>TCA	p.L130S
Pat_65	Pre-Treatment	FAM55C	91775	37	3	101504465	101504465	Missense_Mutation	SNP	C	T	6	601	c.25C>T	c.(25-27)CGG>TGG	p.R9W
Pat_65	Pre-Treatment	FAM55C	91775	37	3	101535709	101535709	Nonsense_Mutation	SNP	G	A	66	99	c.993G>A	c.(991-993)TGG>TGA	p.W331*
Pat_65	Pre-Treatment	ATG3	64422	37	3	112277264	112277264	Missense_Mutation	SNP	C	T	54	129	c.73G>A	c.(73-75)GAA>AAA	p.E25K
Pat_65	Pre-Treatment	ARHGAP31	57514	37	3	119121119	119121119	Missense_Mutation	SNP	C	T	4	233	c.1520C>T	c.(1519-1521)ACG>ATG	p.T507M
Pat_65	Pre-Treatment	C3orf1	51300	37	3	119236128	119236128	Nonsense_Mutation	SNP	C	T	6	612	c.673C>T	c.(673-675)CGA>TGA	p.R225*
Pat_65	Pre-Treatment	DTX3L	151636	37	3	122289501	122289501	Missense_Mutation	SNP	G	A	4	245	c.2135G>A	c.(2134-2136)CGG>CAG	p.R712Q
Pat_65	Pre-Treatment	HSPBAP1	79663	37	3	122459659	122459659	Missense_Mutation	SNP	C	A	6	237	c.1000G>T	c.(1000-1002)GAT>TAT	p.D334Y
Pat_65	Pre-Treatment	B3GNT5	84002	37	3	182988272	182988272	Missense_Mutation	SNP	C	T	6	435	c.686C>T	c.(685-687)CCC>CTC	p.P229L
Pat_65	Pre-Treatment	IGF2BP2	10644	37	3	185364845	185364845	Missense_Mutation	SNP	C	T	6	430	c.1675G>A	c.(1675-1677)GTC>ATC	p.V559I
Pat_65	Pre-Treatment	IGF2BP2	10644	37	3	185416115	185416115	Missense_Mutation	SNP	C	T	4	233	c.260G>A	c.(259-261)CGA>CAA	p.R87Q
Pat_65	Pre-Treatment	MUC4	4585	37	3	195505772	195505772	Missense_Mutation	SNP	C	G	4	42	c.12295G>C	c.(12295-12297)GTC>CTC	p.V4099L
Pat_65	Pre-Treatment	MUC4	4585	37	3	195505829	195505829	Missense_Mutation	SNP	G	A	4	31	c.12238C>T	c.(12238-12240)CCT>TCT	p.P4080S
Pat_65	Pre-Treatment	KIAA0226	9711	37	3	197431550	197431550	Missense_Mutation	SNP	T	C	68	130	c.326A>G	c.(325-327)GAC>GGC	p.D109G

Pat_65	Pre-Treatment	ZNF141	7700	37	4	367161	367161	Missense_Mutation	SNP	A	C	4	291	c.935A>C	c.(934-936)AAA>ACA	p.K312T
Pat_65	Pre-Treatment	HTT	3064	37	4	3230426	3230426	Missense_Mutation	SNP	G	A	4	75	c.7939G>A	c.(7939-7941)GAC>AAC	p.D2647N
Pat_65	Pre-Treatment	FRYL	285527	37	4	48591761	48591761	Splice_Site	SNP	C	T	4	202	c.1640_splice	c.e18+1	p.T547_splice
Pat_65	Pre-Treatment	SGMS2	166929	37	4	108816945	108816945	Missense_Mutation	SNP	C	T	4	227	c.236C>T	c.(235-237)ACG>ATG	p.T79M
Pat_65	Pre-Treatment	TRPC3	7222	37	4	122854046	122854046	Missense_Mutation	SNP	C	T	5	290	c.367G>A	c.(367-369)GGC>AGC	p.G123S
Pat_65	Pre-Treatment	OTUD4	54726	37	4	146065495	146065495	Missense_Mutation	SNP	C	T	6	617	c.1319G>A	c.(1318-1320)CGG>CAG	p.R440Q
Pat_65	Pre-Treatment	ZNF827	152485	37	4	146824080	146824080	Missense_Mutation	SNP	C	T	4	187	c.331G>A	c.(331-333)GAT>AAT	p.D111N
Pat_65	Pre-Treatment	MAP9	79884	37	4	156294408	156294409	Missense_Mutation	DNP	AC	TT	42	150	c.360_361GT>AA	358-363)GGGTGT>GGAA	p.C121S
Pat_65	Pre-Treatment	TDO2	6999	37	4	156830052	156830052	Missense_Mutation	SNP	G	A	7	385	c.317G>A	c.(316-318)AGG>AAG	p.R106K
Pat_65	Pre-Treatment	TMEM192	201931	37	4	166009643	166009643	Missense_Mutation	SNP	A	G	4	117	c.551T>C	c.(550-552)CTG>CCG	p.L184P
Pat_65	Pre-Treatment	GALNTL6	442117	37	4	173269760	173269760	Missense_Mutation	SNP	G	A	6	562	c.473G>A	c.(472-474)CGG>CAG	p.R158Q
Pat_65	Pre-Treatment	PRDM9	56979	37	5	23510044	23510044	Missense_Mutation	SNP	G	A	69	120	c.209G>A	c.(208-210)CGA>CAA	p.R70Q
Pat_65	Pre-Treatment	UGT3A2	167127	37	5	36039579	36039579	Missense_Mutation	SNP	C	T	78	137	c.1075G>A	c.(1075-1077)GCT>ACT	p.A359T
Pat_65	Pre-Treatment	ADAMTS6	11174	37	5	64492856	64492856	Missense_Mutation	SNP	G	A	32	95	c.2698C>T	c.(2698-2700)CCA>TCA	p.P900S
Pat_65	Pre-Treatment	TAF9	6880	37	5	68661089	68661089	Missense_Mutation	SNP	G	A	6	521	c.476C>T	c.(475-477)ACT>ATT	p.T159I
Pat_65	Pre-Treatment	MEF2C	4208	37	5	88018554	88018554	Missense_Mutation	SNP	G	A	8	380	c.1289C>T	c.(1288-1290)TCG>TTG	p.S430L
Pat_65	Pre-Treatment	TTC37	9652	37	5	94814124	94814124	Missense_Mutation	SNP	G	A	78	167	c.4235C>T	c.(4234-4236)TCC>TTC	p.S1412F
Pat_65	Pre-Treatment	YTHDC2	64848	37	5	112889355	112889355	Missense_Mutation	SNP	G	A	6	516	c.1936G>A	c.(1936-1938)GAC>AAC	p.D646N
Pat_65	Pre-Treatment	BRD8	10902	37	5	137502305	137502305	Missense_Mutation	SNP	G	T	4	174	c.899C>A	c.(898-900)CCT>CAT	p.P300H
Pat_65	Pre-Treatment	PCDHA3	56145	37	5	140182959	140182959	Missense_Mutation	SNP	C	T	5	307	c.2177C>T	c.(2176-2178)CCG>CTG	p.P726L
Pat_65	Pre-Treatment	PCDHA8	56140	37	5	140223265	140223265	Missense_Mutation	SNP	G	A	45	12	c.2359G>A	c.(2359-2361)GAA>AAA	p.E787K
Pat_65	Pre-Treatment	PCDHA12	56137	37	5	140257294	140257294	Missense_Mutation	SNP	G	A	50	94	c.2237G>A	c.(2236-2238)GGG>GAG	p.G746E
Pat_65	Pre-Treatment	TNIP1	10318	37	5	150436398	150436398	Missense_Mutation	SNP	G	A	4	158	c.556C>T	c.(556-558)CGC>TGC	p.R186C
Pat_65	Pre-Treatment	ADAM19	8728	37	5	156936308	156936308	Splice_Site	SNP	C	T	4	194	c.905_splice	c.e9+1	p.T302_splice
Pat_65	Pre-Treatment	ODZ2	57451	37	5	167689477	167689477	Nonsense_Mutation	SNP	C	T	3	22	c.7960C>T	c.(7960-7962)CGA>TGA	p.R2654*
Pat_65	Pre-Treatment	HK3	3101	37	5	176314737	176314737	Missense_Mutation	SNP	C	T	4	170	c.1315G>A	c.(1315-1317)GTC>ATC	p.V439I
Pat_65	Pre-Treatment	FGFR4	2264	37	5	176524649	176524649	Missense_Mutation	SNP	T	C	4	156	c.2381T>C	c.(2380-2382)TTC>TCC	p.F794S
Pat_65	Pre-Treatment	GRM6	2916	37	5	178418522	178418522	Missense_Mutation	SNP	C	T	202	483	c.760G>A	c.(760-762)GAA>AAA	p.E254K
Pat_65	Pre-Treatment	FLT4	2324	37	5	180043408	180043408	Missense_Mutation	SNP	G	A	5	268	c.3178C>T	c.(3178-3180)CGG>TGG	p.R1060W
Pat_65	Pre-Treatment	OR2V2	285659	37	5	180582588	180582588	Missense_Mutation	SNP	G	A	6	632	c.646G>A	c.(646-648)GTG>ATG	p.V216M
Pat_65	Pre-Treatment	HUS1B	135458	37	6	656422	656422	Missense_Mutation	SNP	C	T	7	816	c.523G>A	c.(523-525)GTG>ATG	p.V175M
Pat_65	Pre-Treatment	TUBB2B	347733	37	6	3225029	3225029	Missense_Mutation	SNP	C	T	5	283	c.1294G>A	c.(1294-1296)GAA>AAA	p.E432K
Pat_65	Pre-Treatment	HLA-H	3136	37	6	29856489	29856489	Missense_Mutation	SNP	G	A	7	228	c.484G>A	c.(484-486)GAG>AAG	p.E162K
Pat_65	Pre-Treatment	PPP1R10	5514	37	6	30574582	30574582	Missense_Mutation	SNP	C	T	5	208	c.434G>A	c.(433-435)CGC>CAC	p.R145H
Pat_65	Pre-Treatment	DHX16	8449	37	6	30630755	30630755	Missense_Mutation	SNP	C	T	5	446	c.1361G>A	c.(1360-1362)CGG>CAG	p.R454Q
Pat_65	Pre-Treatment	NRM	11270	37	6	30656692	30656692	Missense_Mutation	SNP	C	T	4	141	c.535G>A	c.(535-537)GAG>AAG	p.E179K
Pat_65	Pre-Treatment	ZBTB12	221527	37	6	31868812	31868812	Missense_Mutation	SNP	C	T	125	200	c.271G>A	c.(271-273)GGC>AGC	p.G91S
Pat_65	Pre-Treatment	LYPLA2P1	653639	37	6	33333333	33333333	Missense_Mutation	SNP	G	A	4	60	c.673C>T	c.(673-675)CCT>TCT	p.P225S
Pat_65	Pre-Treatment	DNAH8	1769	37	6	38820545	38820545	Missense_Mutation	SNP	G	A	6	277	c.4891G>A	c.(4891-4893)GTC>ATC	p.V1631I
Pat_65	Pre-Treatment	TTBK1	84630	37	6	43226825	43226825	Missense_Mutation	SNP	G	A	5	258	c.1066G>A	c.(1066-1068)GAG>AAG	p.E356K
Pat_65	Pre-Treatment	AARS2	57505	37	6	44269817	44269817	Missense_Mutation	SNP	G	A	4	227	c.2578C>T	c.(2578-2580)CGT>TGT	p.R860C
Pat_65	Pre-Treatment	PHF3	23469	37	6	64421921	64421921	Missense_Mutation	SNP	A	C	70	113	c.4437A>C	c.(4435-4437)CAA>CAC	p.Q1479H
Pat_65	Pre-Treatment	TPBG	7162	37	6	83074893	83074893	Missense_Mutation	SNP	C	T	4	152	c.215C>T	c.(214-216)GCG>GTG	p.A72V
Pat_65	Pre-Treatment	SLC35A1	10559	37	6	88210957	88210957	Missense_Mutation	SNP	G	A	4	241	c.436G>A	c.(436-438)GTT>ATT	p.V146I
Pat_65	Pre-Treatment	ORC3L	23595	37	6	88304120	88304120	Missense_Mutation	SNP	C	A	4	132	c.74C>A	c.(73-75)CCA>CAA	p.P25Q
Pat_65	Pre-Treatment	GRIK2	2898	37	6	102124549	102124549	Missense_Mutation	SNP	G	A	4	112	c.593G>A	c.(592-594)CGA>CAA	p.R198Q
Pat_65	Pre-Treatment	REPS1	85021	37	6	139266381	139266381	Missense_Mutation	SNP	C	A	4	81	c.603G>T	c.(601-603)TGG>TGT	p.W201C

Pat_65	Pre-Treatment	NOX3	50508	37	6	155743916	155743916	Missense_Mutation	SNP	G	A	7	672	c.1220C>T	c.(1219-1221)GCG>GTG	p.A407V
Pat_65	Pre-Treatment	TULP4	56995	37	6	158882724	158882724	Missense_Mutation	SNP	G	A	5	275	c.989G>A	c.(988-990)CGT>CAT	p.R330H
Pat_65	Pre-Treatment	SDK1	221935	37	7	4189032	4189032	Missense_Mutation	SNP	G	A	3	44	c.4562G>A	c.(4561-4563)CGG>CAG	p.R1521Q
Pat_65	Pre-Treatment	OSBPL3	26031	37	7	24874289	24874289	Missense_Mutation	SNP	G	A	6	414	c.1562C>T	c.(1561-1563)CCG>CTG	p.P521L
Pat_65	Pre-Treatment	CPVL	54504	37	7	29152381	29152381	Missense_Mutation	SNP	C	T	72	121	c.227G>A	c.(226-228)GGC>GAC	p.G76D
Pat_65	Pre-Treatment	NEUROD6	63974	37	7	31378158	31378158	Missense_Mutation	SNP	G	A	49	89	c.725C>T	c.(724-726)TCC>TTC	p.S242F
Pat_65	Pre-Treatment	IGFBP3	3486	37	7	45954519	45954519	Missense_Mutation	SNP	C	T	4	173	c.776G>A	c.(775-777)CGG>CAG	p.R259Q
Pat_65	Pre-Treatment	ZNF716	441234	37	7	57529068	57529068	Missense_Mutation	SNP	T	C	5	329	c.901T>C	c.(901-903)TGT>CGT	p.C301R
Pat_65	Pre-Treatment	ZNF735	730291	37	7	63680397	63680397	Missense_Mutation	SNP	A	G	5	435	c.968A>G	c.(967-969)AAA>AGA	p.K323R
Pat_65	Pre-Treatment	ZNF735	730291	37	7	63680406	63680406	Missense_Mutation	SNP	C	A	7	427	c.977C>A	c.(976-978)ACA>AAA	p.T326K
Pat_65	Pre-Treatment	ZNF92	168374	37	7	64863839	64863840	Missense_Mutation	DNP	CC	AT	5	316	c.812_813CC>AT	c.(811-813)ACC>AAT	p.T271N
Pat_65	Pre-Treatment	GTPBP10	85865	37	7	89982259	89982259	Missense_Mutation	SNP	T	G	139	36	c.163T>G	c.(163-165)TTA>GTA	p.L55V
Pat_65	Pre-Treatment	TRRAP	8295	37	7	98563361	98563361	Missense_Mutation	SNP	C	T	5	303	c.6998C>T	c.(6997-6999)ACG>ATG	p.T2333M
Pat_65	Pre-Treatment	ACHE	43	37	7	100489992	100489992	Nonsense_Mutation	SNP	G	A	4	265	c.1516C>T	c.(1516-1518)CGA>TGA	p.R506*
Pat_65	Pre-Treatment	MUC17	140453	37	7	100684253	100684253	Missense_Mutation	SNP	G	A	8	876	c.9556G>A	c.(9556-9558)GCA>ACA	p.A3186T
Pat_65	Pre-Treatment	CFTR	1080	37	7	117175426	117175426	Missense_Mutation	SNP	T	C	4	138	c.704T>C	c.(703-705)CTT>CCT	p.L235P
Pat_65	Pre-Treatment	CTTNBP2	83992	37	7	117431380	117431380	Missense_Mutation	SNP	C	G	4	156	c.1870G>C	c.(1870-1872)GCA>CCA	p.A624P
Pat_65	Pre-Treatment	BRAF	673	37	7	140453136	140453136	Missense_Mutation	SNP	A	T	154	73	c.1799T>A	c.(1798-1800)GTG>GAG	p.V600E
Pat_65	Pre-Treatment	GALNTL5	168391	37	7	151699961	151699961	Missense_Mutation	SNP	G	A	150	50	c.821G>A	c.(820-822)GGA>GAA	p.G274E
Pat_65	Pre-Treatment	EN2	2020	37	7	155251298	155251298	Missense_Mutation	SNP	C	T	3	42	c.226C>T	c.(226-228)CGG>TGG	p.R76W
Pat_65	Pre-Treatment	UBE3C	9690	37	7	157041215	157041215	Missense_Mutation	SNP	G	A	6	597	c.2635G>A	c.(2635-2637)GAT>AAT	p.D879N
Pat_65	Pre-Treatment	DLGAP2	9228	37	8	1497601	1497601	Missense_Mutation	SNP	C	G	47	353	c.742C>G	c.(742-744)CCC>GCC	p.P248A
Pat_65	Pre-Treatment	ADAM2	2515	37	8	39682391	39682391	Missense_Mutation	SNP	C	T	14	56	c.214G>A	c.(214-216)GTT>ATT	p.V72I
Pat_65	Pre-Treatment	ZMAT4	79698	37	8	40554908	40554908	Missense_Mutation	SNP	C	T	63	61	c.205G>A	c.(205-207)GAC>AAC	p.D69N
Pat_65	Pre-Treatment	PLAT	5327	37	8	42033531	42033531	Missense_Mutation	SNP	G	A	5	186	c.1669C>T	c.(1669-1671)CGT>TGT	p.R557C
Pat_65	Pre-Treatment	HGSNAT	138050	37	8	43014188	43014188	Splice_Site	SNP	G	A	4	245	c.493_splice	c.e4+1	p.P165_splice
Pat_65	Pre-Treatment	KCNS2	3788	37	8	99440329	99440329	Missense_Mutation	SNP	C	T	7	180	c.122C>T	c.(121-123)ACG>ATG	p.T41M
Pat_65	Pre-Treatment	PKHD1L1	93035	37	8	110457287	110457287	Missense_Mutation	SNP	G	A	244	254	c.5189G>A	c.(5188-5190)GGA>GAA	p.G1730E
Pat_65	Pre-Treatment	GRINA	2907	37	8	145066663	145066663	Missense_Mutation	SNP	G	A	4	256	c.853G>A	c.(853-855)GTG>ATG	p.V285M
Pat_65	Pre-Treatment	DMRTA1	63951	37	9	22451762	22451762	Missense_Mutation	SNP	T	A	4	63	c.1367T>A	c.(1366-1368)CTA>CAA	p.L456Q
Pat_65	Pre-Treatment	ACO1	48	37	9	32436330	32436330	Missense_Mutation	SNP	C	T	5	343	c.2182C>T	c.(2182-2184)CGC>TGC	p.R728C
Pat_65	Pre-Treatment	LOC442421	442421	37	9	66499680	66499680	Missense_Mutation	SNP	C	A	7	52	c.490C>A	c.(490-492)CCC>ACC	p.P164T
Pat_65	Pre-Treatment	AGTPBP1	23287	37	9	88247645	88247646	Missense_Mutation	DNP	GG	AA	52	72	.1946_1947CC>T	c.(1945-1947)CCC>CTT	p.P649L
Pat_65	Pre-Treatment	KIAA1529	57653	37	9	100056345	100056345	Missense_Mutation	SNP	G	A	6	183	c.203G>A	c.(202-204)CGC>CAC	p.R68H
Pat_65	Pre-Treatment	ANKS6	203286	37	9	101552632	101552632	Missense_Mutation	SNP	C	T	4	144	c.616G>A	c.(616-618)GTG>ATG	p.V206M
Pat_65	Pre-Treatment	C9orf80	58493	37	9	115451893	115451893	Missense_Mutation	SNP	C	G	4	118	c.133G>C	c.(133-135)GCA>CCA	p.A45P
Pat_65	Pre-Treatment	OR1N2	138882	37	9	125315993	125315993	Missense_Mutation	SNP	G	A	4	140	c.545G>A	c.(544-546)CGC>CAC	p.R182H
Pat_65	Pre-Treatment	RXRA	6256	37	9	137328339	137328339	Missense_Mutation	SNP	C	T	101	197	c.1268C>T	c.(1267-1269)CCG>CTG	p.P423L
Pat_65	Pre-Treatment	NACC2	138151	37	9	138905119	138905120	Missense_Mutation	DNP	CC	TT	87	154	.1180_1181GG>A	c.(1180-1182)GGG>AAG	p.G394K
Pat_65	Pre-Treatment	NOTCH1	4851	37	9	139395158	139395158	Missense_Mutation	SNP	G	A	8	475	c.5780C>T	c.(5779-5781)ACG>ATG	p.T1927M
Pat_65	Pre-Treatment	MID1	4281	37	X	10463658	10463658	Missense_Mutation	SNP	C	T	4	248	c.830G>A	c.(829-831)CGA>CAA	p.R277Q
Pat_65	Pre-Treatment	TLR8	51311	37	X	12938514	12938514	Missense_Mutation	SNP	G	A	4	251	c.1355G>A	c.(1354-1356)CGG>CAG	p.R452Q
Pat_65	Pre-Treatment	PCYT1B	9468	37	X	24690709	24690709	Missense_Mutation	SNP	C	T	4	218	c.41G>A	c.(40-42)CGC>CAC	p.R14H
Pat_65	Pre-Treatment	POLA1	5422	37	X	24721465	24721465	Splice_Site	SNP	G	A	4	95	c.247_splice	c.e3+1	p.D83_splice
Pat_65	Pre-Treatment	DGKK	139189	37	X	50213347	50213347	Missense_Mutation	SNP	G	A	7	322	c.331C>T	c.(331-333)CCA>TCA	p.P111S
Pat_65	Pre-Treatment	ZMYM3	9203	37	X	70468943	70468943	Missense_Mutation	SNP	C	T	8	529	c.1547G>A	c.(1546-1548)CGT>CAT	p.R516H
Pat_65	Pre-Treatment	TAF1	6872	37	X	70626490	70626490	Missense_Mutation	SNP	C	T	4	88	c.3998C>T	c.(3997-3999)GCG>GTG	p.A1333V

Pat_65	Pre-Treatment	NAP1L2	4674	37	X	72433704	72433704	Missense_Mutation	SNP	C	T	10	39	c.625G>A	c.(625-627)GAT>AAT	p.D209N
Pat_65	Pre-Treatment	DOCK11	139818	37	X	117773430	117773430	Missense_Mutation	SNP	G	A	144	134	c.4034G>A	c.(4033-4035)GGA>GAA	p.G1345E
Pat_65	Pre-Treatment	ACTRT1	139741	37	X	127185115	127185115	Missense_Mutation	SNP	C	A	19	428	c.1071G>T	c.(1069-1071)TGG>TGT	p.W357C
Pat_65	Pre-Treatment	MAGEA8	4107	37	X	149013756	149013756	Missense_Mutation	SNP	G	A	4	278	c.710G>A	c.(709-711)AGG>AAG	p.R237K
Pat_65	Pre-Treatment	SLC10A3	8273	37	X	153715905	153715905	Missense_Mutation	SNP	C	T	4	97	c.1375G>A	c.(1375-1377)GAG>AAG	p.E459K
Pat_65	Pre-Treatment	CTAG2	30848	37	X	153880823	153880823	Nonsense_Mutation	SNP	G	A	4	186	c.352C>T	c.(352-354)CGA>TGA	p.R118*
Pat_65	Pre-Treatment	IL9R	3581	37	X	155232601	155232601	Missense_Mutation	SNP	G	A	4	220	c.59G>A	c.(58-60)CGA>CAA	p.R20Q
Pat_66	Pre-Treatment	MMEL1	79258	37	1	2524280	2524280	Missense_Mutation	SNP	C	T	24	18	c.1993G>A	c.(1993-1995)GAA>AAA	p.E665K
Pat_66	Pre-Treatment	RPL22	6146	37	1	6253010	6253011	Missense_Mutation	DNP	GG	AA	44	74	c.221_222CC>TT	c.(220-222)TCC>TTT	p.S74F
Pat_66	Pre-Treatment	TNFRSF8	943	37	1	12175771	12175771	Missense_Mutation	SNP	G	A	3	31	c.931G>A	c.(931-933)GTC>ATC	p.V311I
Pat_66	Pre-Treatment	TNFRSF1B	7133	37	1	12253087	12253087	Missense_Mutation	SNP	C	T	45	10	c.719C>T	c.(718-720)TCC>TTC	p.S240F
Pat_66	Pre-Treatment	DHRS3	9249	37	1	12632834	12632834	Missense_Mutation	SNP	C	T	14	0	c.746G>A	c.(745-747)AGG>AAG	p.R249K
Pat_66	Pre-Treatment	PRAMEF1	65121	37	1	12855948	12855948	Missense_Mutation	SNP	G	A	5	214	c.1228G>A	c.(1228-1230)GAG>AAG	p.E410K
Pat_66	Pre-Treatment	SPEN	23013	37	1	16254758	16254758	Missense_Mutation	SNP	G	A	5	168	c.2023G>A	c.(2023-2025)GAT>AAT	p.D675N
Pat_66	Pre-Treatment	CLCNKB	1188	37	1	16376354	16376354	Missense_Mutation	SNP	G	A	76	141	c.911G>A	c.(910-912)CGA>CAA	p.R304Q
Pat_66	Pre-Treatment	PADI3	51702	37	1	17606895	17606895	Missense_Mutation	SNP	G	A	51	20	c.1606G>A	c.(1606-1608)GAC>AAC	p.D536N
Pat_66	Pre-Treatment	AKR7L	246181	37	1	19595147	19595148	Missense_Mutation	DNP	GG	AA	29	47	c.752_753CC>TT	c.(751-753)GCC>GTT	p.A251V
Pat_66	Pre-Treatment	PLA2G2E	30814	37	1	20248809	20248809	Missense_Mutation	SNP	C	T	10	18	c.268G>A	c.(268-270)GAA>AAA	p.E90K
Pat_66	Pre-Treatment	EPHB2	2048	37	1	23233295	23233295	Missense_Mutation	SNP	G	A	16	36	c.1981G>A	c.(1981-1983)GAG>AAG	p.E661K
Pat_66	Pre-Treatment	MYOM3	127294	37	1	24413262	24413262	Missense_Mutation	SNP	G	A	41	49	c.1670C>T	c.(1669-1671)TCC>TTC	p.S557F
Pat_66	Pre-Treatment	RPS6KA1	6195	37	1	26883580	26883580	Missense_Mutation	SNP	G	A	4	91	c.1073G>A	c.(1072-1074)CGC>CAC	p.R358H
Pat_66	Pre-Treatment	KPNA6	23633	37	1	32632830	32632830	Missense_Mutation	SNP	C	T	101	173	c.1177C>T	c.(1177-1179)CGT>TGT	p.R393C
Pat_66	Pre-Treatment	PHC2	1912	37	1	33796967	33796967	Missense_Mutation	SNP	G	A	153	20	c.1985C>T	c.(1984-1986)TCC>TTC	p.S662F
Pat_66	Pre-Treatment	CSMD2	114784	37	1	34038256	34038256	Missense_Mutation	SNP	C	T	21	40	c.7618G>A	c.(7618-7620)GGA>AGA	p.G2540R
Pat_66	Pre-Treatment	C1orf94	84970	37	1	34677886	34677886	Missense_Mutation	SNP	C	T	29	41	c.1030C>T	c.(1030-1032)CCT>TCT	p.P344S
Pat_66	Pre-Treatment	NFYC	4802	37	1	41236234	41236234	Missense_Mutation	SNP	C	A	3	9	c.1111C>A	c.(1111-1113)CAG>AAG	p.Q371K
Pat_66	Pre-Treatment	CCDC30	728621	37	1	43110444	43110444	Missense_Mutation	SNP	G	A	35	54	c.1856G>A	c.(1855-1857)CGA>CAA	p.R619Q
Pat_66	Pre-Treatment	C1orf50	79078	37	1	43240523	43240523	Missense_Mutation	SNP	C	T	73	6	c.398C>T	c.(397-399)TCC>TTC	p.S133F
Pat_66	Pre-Treatment	WDR65	149465	37	1	43663258	43663258	Missense_Mutation	SNP	C	T	98	128	c.1157C>T	c.(1156-1158)CCA>CTA	p.P386L
Pat_66	Pre-Treatment	PDZK1IP1	10158	37	1	47655595	47655595	Missense_Mutation	SNP	G	A	10	16	c.10C>T	c.(10-12)CTC>TTC	p.L4F
Pat_66	Pre-Treatment	ELAVL4	1996	37	1	50661383	50661383	Missense_Mutation	SNP	C	T	148	19	c.659C>T	c.(658-660)GCC>GTC	p.A220V
Pat_66	Pre-Treatment	C1orf175	374977	37	1	55166993	55166993	Missense_Mutation	SNP	G	A	13	6	c.3283G>A	c.(3283-3285)GAC>AAC	p.D1095N
Pat_66	Pre-Treatment	PCSK9	255738	37	1	55512304	55512304	Missense_Mutation	SNP	G	A	28	31	c.508G>A	c.(508-510)GAA>AAA	p.E170K
Pat_66	Pre-Treatment	PPAP2B	8613	37	1	56989520	56989520	Missense_Mutation	SNP	G	A	21	47	c.608C>T	c.(607-609)TCC>TTC	p.S203F
Pat_66	Pre-Treatment	C1orf168	199920	37	1	57185864	57185864	Missense_Mutation	SNP	G	A	18	18	c.2113C>T	c.(2113-2115)CGT>TGT	p.R705C
Pat_66	Pre-Treatment	C8A	731	37	1	57351708	57351708	Missense_Mutation	SNP	C	T	37	2	c.964C>T	c.(964-966)CCA>TCA	p.P322S
Pat_66	Pre-Treatment	C1orf87	127795	37	1	60505761	60505761	Missense_Mutation	SNP	G	A	30	38	c.575C>T	c.(574-576)TCC>TTC	p.S192F
Pat_66	Pre-Treatment	ATG4C	84938	37	1	63307135	63307135	Nonsense_Mutation	SNP	C	T	36	65	c.1126C>T	c.(1126-1128)CGA>TGA	p.R376*
Pat_66	Pre-Treatment	ELTD1	64123	37	1	79392644	79392644	Missense_Mutation	SNP	G	A	31	4	c.1010C>T	c.(1009-1011)TCA>TTA	p.S337L
Pat_66	Pre-Treatment	ELTD1	64123	37	1	79402013	79402013	Missense_Mutation	SNP	A	T	59	100	c.844T>A	c.(844-846)TTT>ATT	p.F282I
Pat_66	Pre-Treatment	LPHN2	23266	37	1	82434986	82434986	Missense_Mutation	SNP	G	A	65	86	c.2597G>A	c.(2596-2598)CGA>CAA	p.R866Q
Pat_66	Pre-Treatment	BTBD8	284697	37	1	92568178	92568178	Missense_Mutation	SNP	G	A	36	44	c.496G>A	c.(496-498)GAA>AAA	p.E166K
Pat_66	Pre-Treatment	ABCA4	24	37	1	94544208	94544208	Missense_Mutation	SNP	C	T	339	49	c.1294G>A	c.(1294-1296)GAA>AAA	p.E432K
Pat_66	Pre-Treatment	PALMD	54873	37	1	100154655	100154655	Missense_Mutation	SNP	G	A	31	37	c.839G>A	c.(838-840)GGA>GAA	p.G280E
Pat_66	Pre-Treatment	CDC14A	8556	37	1	100949903	100949903	Nonsense_Mutation	SNP	C	T	12	3	c.1033C>T	c.(1033-1035)CGA>TGA	p.R345*
Pat_66	Pre-Treatment	COL11A1	1301	37	1	103354187	103354187	Splice_Site	SNP	C	T	42	6	c.4555_splice	c.e62-1	p.G1519_splice
Pat_66	Pre-Treatment	CLCC1	23155	37	1	109477342	109477342	Missense_Mutation	SNP	C	T	51	52	c.1606G>A	c.(1606-1608)GGT>AGT	p.G536S

Pat_66	Pre-Treatment	AMPD2	271	37	1	110169919	110169919	Missense_Mutation	SNP	C	T	4	176	c.1003C>T	c.(1003-1005)CGC>TGC	p.R335C
Pat_66	Pre-Treatment	DENND2C	163259	37	1	115142028	115142028	Missense_Mutation	SNP	G	A	42	63	c.2150C>T	c.(2149-2151)CCG>CTG	p.P717L
Pat_66	Pre-Treatment	AMPD1	270	37	1	115220959	115220959	Missense_Mutation	SNP	G	A	62	123	c.1087C>T	c.(1087-1089)CAT>TAT	p.H363Y
Pat_66	Pre-Treatment	SPAG17	200162	37	1	118548203	118548203	Missense_Mutation	SNP	G	A	14	26	c.4610C>T	c.(4609-4611)TCT>TTT	p.S1537F
Pat_66	Pre-Treatment	SPAG17	200162	37	1	118567995	118567996	Missense_Mutation	DNP	GG	AA	60	19	.3774_3775CC>T	772-3777)GTCCGT>GTTT	p.R1259C
Pat_66	Pre-Treatment	HSD3B1	3283	37	1	120050113	120050113	Missense_Mutation	SNP	G	A	56	547	c.14G>A	c.(13-15)AGC>AAC	p.S5N
Pat_66	Pre-Treatment	ADAM30	11085	37	1	120437687	120437687	Missense_Mutation	SNP	G	A	30	857	c.1273C>T	c.(1273-1275)CGG>TGG	p.R425W
Pat_66	Pre-Treatment	NBPF9	400818	37	1	144220816	144220816	Missense_Mutation	SNP	A	G	6	508	c.2189A>G	c.(2188-2190)GAG>GGG	p.E730G
Pat_66	Pre-Treatment	PDE4DIP	9659	37	1	144873949	144873949	Missense_Mutation	SNP	C	T	66	831	c.5008G>A	c.(5008-5010)GAA>AAA	p.E1670K
Pat_66	Pre-Treatment	PDE4DIP	9659	37	1	144911896	144911896	Missense_Mutation	SNP	G	A	203	669	c.2213C>T	c.(2212-2214)CCC>CTC	p.P738L
Pat_66	Pre-Treatment	PDE4DIP	9659	37	1	145021144	145021144	Missense_Mutation	SNP	C	T	20	733	c.44G>A	c.(43-45)GGG>GAG	p.G15E
Pat_66	Pre-Treatment	ITGA10	8515	37	1	145533143	145533143	Missense_Mutation	SNP	G	A	4	118	c.1238G>A	c.(1237-1239)CGA>CAA	p.R413Q
Pat_66	Pre-Treatment	FMO5	2330	37	1	146658634	146658634	Missense_Mutation	SNP	C	A	38	69	c.1447G>T	c.(1447-1449)GGG>TGG	p.G483W
Pat_66	Pre-Treatment	FMO5	2330	37	1	146658675	146658675	Missense_Mutation	SNP	G	A	4	134	c.1406C>T	c.(1405-1407)ACT>ATT	p.T469I
Pat_66	Pre-Treatment	GJA5	2702	37	1	147230556	147230556	Missense_Mutation	SNP	G	A	4	181	c.791C>T	c.(790-792)CCC>CTC	p.P264L
Pat_66	Pre-Treatment	RORC	6097	37	1	151787506	151787506	Missense_Mutation	SNP	G	A	32	150	c.694C>T	c.(694-696)CGT>TGT	p.R232C
Pat_66	Pre-Treatment	TCHHL1	126637	37	1	152059317	152059317	Missense_Mutation	SNP	C	T	42	252	c.841G>A	c.(841-843)GAA>AAA	p.E281K
Pat_66	Pre-Treatment	TCHH	7062	37	1	152085463	152085463	Missense_Mutation	SNP	A	G	12	66	c.230T>C	c.(229-231)TTT>TCT	p.F77S
Pat_66	Pre-Treatment	FLG	2312	37	1	152278795	152278795	Missense_Mutation	SNP	G	A	121	798	c.8567C>T	c.(8566-8568)TCG>TTG	p.S2856L
Pat_66	Pre-Treatment	CRNN	49860	37	1	152382770	152382770	Missense_Mutation	SNP	T	C	12	628	c.788A>G	c.(787-789)GAC>GGC	p.D263G
Pat_66	Pre-Treatment	SPRR1A	6698	37	1	152957867	152957867	Missense_Mutation	SNP	C	T	57	356	c.161C>T	c.(160-162)CCT>CTT	p.P54L
Pat_66	Pre-Treatment	PGLYRP4	57115	37	1	153317697	153317697	Missense_Mutation	SNP	C	T	48	61	c.301G>A	c.(301-303)GAA>AAA	p.E101K
Pat_66	Pre-Treatment	SHE	126669	37	1	154461646	154461646	Missense_Mutation	SNP	C	T	81	58	c.905G>A	c.(904-906)AGG>AAG	p.R302K
Pat_66	Pre-Treatment	GON4L	54856	37	1	155736404	155736404	Nonsense_Mutation	SNP	G	A	130	81	c.2860C>T	c.(2860-2862)CGA>TGA	p.R954*
Pat_66	Pre-Treatment	BCAN	63827	37	1	156616815	156616815	Missense_Mutation	SNP	G	A	3	40	c.314G>A	c.(313-315)CGG>CAG	p.R105Q
Pat_66	Pre-Treatment	PEAR1	375033	37	1	156876497	156876497	Missense_Mutation	SNP	G	A	47	203	c.469G>A	c.(469-471)GAT>AAT	p.D157N
Pat_66	Pre-Treatment	SPTA1	6708	37	1	158617387	158617387	Missense_Mutation	SNP	C	T	84	160	c.3838G>A	c.(3838-3840)GAT>AAT	p.D1280N
Pat_66	Pre-Treatment	SPTA1	6708	37	1	158623143	158623143	Missense_Mutation	SNP	C	A	4	192	c.3109G>T	c.(3109-3111)GAT>TAT	p.D1037Y
Pat_66	Pre-Treatment	SPTA1	6708	37	1	158648325	158648325	Splice_Site	SNP	C	T	15	72	c.679_splice	c.e6-1	p.E227_splice
Pat_66	Pre-Treatment	FCRL6	343413	37	1	159778010	159778010	Missense_Mutation	SNP	G	A	69	63	c.95G>A	c.(94-96)GGA>GAA	p.G32E
Pat_66	Pre-Treatment	CCDC19	25790	37	1	159847207	159847207	Missense_Mutation	SNP	C	T	143	381	c.1090G>A	c.(1090-1092)GAG>AAG	p.E364K
Pat_66	Pre-Treatment	KCNJ10	3766	37	1	160011806	160011806	Missense_Mutation	SNP	T	C	65	293	c.517A>G	c.(517-519)AAG>GAG	p.K173E
Pat_66	Pre-Treatment	CD84	8832	37	1	160518077	160518077	Missense_Mutation	SNP	G	A	43	101	c.1007C>T	c.(1006-1008)CCT>CTT	p.P336L
Pat_66	Pre-Treatment	CD244	51744	37	1	160811406	160811406	Missense_Mutation	SNP	A	G	31	59	c.347T>C	c.(346-348)GTT>GCT	p.V116A
Pat_66	Pre-Treatment	ITLN2	142683	37	1	160922485	160922485	Missense_Mutation	SNP	C	T	112	68	c.118G>A	c.(118-120)GAA>AAA	p.E40K
Pat_66	Pre-Treatment	POU2F1	5451	37	1	167370724	167370724	Missense_Mutation	SNP	G	A	4	148	c.1417G>A	c.(1417-1419)GCA>ACA	p.A473T
Pat_66	Pre-Treatment	ADCY10	55811	37	1	167839543	167839543	Missense_Mutation	SNP	C	T	24	94	c.1568G>A	c.(1567-1569)AGC>AAC	p.S523N
Pat_66	Pre-Treatment	DCAF6	55827	37	1	168044611	168044611	Missense_Mutation	SNP	C	T	4	106	c.2521C>T	c.(2521-2523)CGG>TGG	p.R841W
Pat_66	Pre-Treatment	F5	2153	37	1	169510846	169510846	Missense_Mutation	SNP	C	T	63	287	c.3482G>A	c.(3481-3483)CGA>CAA	p.R1161Q
Pat_66	Pre-Treatment	F5	2153	37	1	169512248	169512248	Missense_Mutation	SNP	C	T	57	316	c.2080G>A	c.(2080-2082)GAG>AAG	p.E694K
Pat_66	Pre-Treatment	C1orf9	51430	37	1	172544695	172544695	Missense_Mutation	SNP	C	T	30	132	c.1195C>T	c.(1195-1197)CAT>TAT	p.H399Y
Pat_66	Pre-Treatment	TNR	7143	37	1	175332955	175332955	Missense_Mutation	SNP	G	A	50	47	c.2596C>T	c.(2596-2598)CCC>TCC	p.P866S
Pat_66	Pre-Treatment	TNR	7143	37	1	175372582	175372582	Missense_Mutation	SNP	C	T	118	548	c.670G>A	c.(670-672)GAG>AAG	p.E224K
Pat_66	Pre-Treatment	PAPPA2	60676	37	1	176525780	176525780	Missense_Mutation	SNP	C	T	178	294	c.322C>T	c.(322-324)CCC>TCC	p.P108S
Pat_66	Pre-Treatment	PAPPA2	60676	37	1	176564722	176564722	Missense_Mutation	SNP	C	T	40	66	c.1982C>T	c.(1981-1983)TCA>TTA	p.S661L
Pat_66	Pre-Treatment	FAM5B	57795	37	1	177250146	177250146	Missense_Mutation	SNP	G	A	43	66	c.1834G>A	c.(1834-1836)GAC>AAC	p.D612N
Pat_66	Pre-Treatment	C1orf125	126859	37	1	179460799	179460799	Missense_Mutation	SNP	G	A	144	277	c.2218G>A	c.(2218-2220)GGA>AGA	p.G740R

Pat_66	Pre-Treatment	C1orf125	126859	37	1	179502990	179502990	Missense_Mutation	SNP	G	A	113	217	c.2776G>A	c.(2776-2778)GAA>AAA	p.E926K
Pat_66	Pre-Treatment	TDRD5	163589	37	1	179603683	179603683	Nonsense_Mutation	SNP	G	A	38	202	c.1218G>A	c.(1216-1218)TGG>TGA	p.W406*
Pat_66	Pre-Treatment	TDRD5	163589	37	1	179631290	179631290	Missense_Mutation	SNP	G	A	42	240	c.2212G>A	c.(2212-2214)GAT>AAT	p.D738N
Pat_66	Pre-Treatment	CEP350	9857	37	1	180063743	180063743	Missense_Mutation	SNP	C	T	12	61	c.8503C>T	c.(8503-8505)CCC>TCC	p.P2835S
Pat_66	Pre-Treatment	CACNA1E	777	37	1	181727969	181727969	Missense_Mutation	SNP	G	A	70	139	c.4570G>A	c.(4570-4572)GAA>AAA	p.E1524K
Pat_66	Pre-Treatment	CACNA1E	777	37	1	181754457	181754457	Missense_Mutation	SNP	C	T	31	54	c.5582C>T	c.(5581-5583)TCT>TTT	p.S1861F
Pat_66	Pre-Treatment	DHX9	1660	37	1	182845668	182845668	Missense_Mutation	SNP	G	A	4	159	c.2116G>A	c.(2116-2118)GTA>ATA	p.V706I
Pat_66	Pre-Treatment	DHX9	1660	37	1	182852412	182852412	Missense_Mutation	SNP	G	A	4	160	c.3053G>A	c.(3052-3054)CGT>CAT	p.R1018H
Pat_66	Pre-Treatment	FAM129A	116496	37	1	184764647	184764647	Missense_Mutation	SNP	C	T	201	167	c.2251G>A	c.(2251-2253)GAG>AAG	p.E751K
Pat_66	Pre-Treatment	HMCN1	83872	37	1	185951498	185951498	Missense_Mutation	SNP	C	T	4	229	c.2767C>T	c.(2767-2769)CGG>TGG	p.R923W
Pat_66	Pre-Treatment	TPR	7175	37	1	186305706	186305706	Nonsense_Mutation	SNP	G	A	5	262	c.4627C>T	c.(4627-4629)CGA>TGA	p.R1543*
Pat_66	Pre-Treatment	F13B	2165	37	1	197030191	197030191	Missense_Mutation	SNP	G	A	31	30	c.466C>T	c.(466-468)CCT>TCT	p.P156S
Pat_66	Pre-Treatment	ASPM	259266	37	1	197073189	197073189	Missense_Mutation	SNP	G	A	62	351	c.5192C>T	c.(5191-5193)TCT>TTT	p.S1731F
Pat_66	Pre-Treatment	CRB1	23418	37	1	197298046	197298046	Missense_Mutation	SNP	G	A	25	101	c.565G>A	c.(565-567)GAA>AAA	p.E189K
Pat_66	Pre-Treatment	CRB1	23418	37	1	197390166	197390166	Missense_Mutation	SNP	C	T	43	229	c.1208C>T	c.(1207-1209)TCA>TTA	p.S403L
Pat_66	Pre-Treatment	CRB1	23418	37	1	197396686	197396686	Missense_Mutation	SNP	G	A	51	39	c.2231G>A	c.(2230-2232)CGA>CAA	p.R744Q
Pat_66	Pre-Treatment	KIF14	9928	37	1	200574423	200574423	Missense_Mutation	SNP	C	G	5	184	c.1734G>C	c.(1732-1734)ATG>ATC	p.M578I
Pat_66	Pre-Treatment	CACNA1S	779	37	1	201031145	201031145	Missense_Mutation	SNP	C	T	26	79	c.2980G>A	c.(2980-2982)GAC>AAC	p.D994N
Pat_66	Pre-Treatment	ATP2B4	493	37	1	203669940	203669940	Missense_Mutation	SNP	G	A	33	156	c.790G>A	c.(790-792)GAA>AAA	p.E264K
Pat_66	Pre-Treatment	TMCC2	9911	37	1	205211090	205211090	Missense_Mutation	SNP	C	T	23	108	c.665C>T	c.(664-666)TCC>TTC	p.S222F
Pat_66	Pre-Treatment	SRGAP2	23380	37	1	206623810	206623810	Missense_Mutation	SNP	G	A	11	103	c.1918G>A	c.(1918-1920)GAA>AAA	p.E640K
Pat_66	Pre-Treatment	DYRK3	8444	37	1	206811054	206811054	Missense_Mutation	SNP	G	A	88	178	c.137G>A	c.(136-138)TGT>TAT	p.C46Y
Pat_66	Pre-Treatment	PIGR	5284	37	1	207106409	207106409	Missense_Mutation	SNP	C	T	28	135	c.1808G>A	c.(1807-1809)AGG>AAG	p.R603K
Pat_66	Pre-Treatment	CR2	1380	37	1	207642174	207642174	Missense_Mutation	SNP	C	T	66	66	c.664C>T	c.(664-666)CCC>TCC	p.P222S
Pat_66	Pre-Treatment	CR1	1378	37	1	207679317	207679317	Missense_Mutation	SNP	C	T	42	230	c.190C>T	c.(190-192)CCC>TCC	p.P64S
Pat_66	Pre-Treatment	G0S2	50486	37	1	209849265	209849265	Missense_Mutation	SNP	C	T	6	32	c.236C>T	c.(235-237)GCC>GTC	p.A79V
Pat_66	Pre-Treatment	KCNH1	3756	37	1	211192571	211192571	Missense_Mutation	SNP	G	A	45	105	c.586C>T	c.(586-588)CCC>TCC	p.P196S
Pat_66	Pre-Treatment	DTL	51514	37	1	212274211	212274211	Missense_Mutation	SNP	C	T	29	133	c.1879C>T	c.(1879-1881)CCG>TCG	p.P627S
Pat_66	Pre-Treatment	FAM71A	149647	37	1	212799828	212799828	Missense_Mutation	SNP	C	T	30	75	c.1609C>T	c.(1609-1611)CTT>TTT	p.L537F
Pat_66	Pre-Treatment	PROX1	5629	37	1	214170159	214170159	Missense_Mutation	SNP	C	T	19	123	c.281C>T	c.(280-282)TCC>TTC	p.S94F
Pat_66	Pre-Treatment	USH2A	7399	37	1	216040499	216040499	Missense_Mutation	SNP	C	T	23	81	c.8695G>A	c.(8695-8697)GAA>AAA	p.E2899K
Pat_66	Pre-Treatment	HHIPL2	79802	37	1	222713487	222713487	Missense_Mutation	SNP	G	A	91	77	c.1315C>T	c.(1315-1317)CGG>TGG	p.R439W
Pat_66	Pre-Treatment	TP53BP2	7159	37	1	223987704	223987704	Missense_Mutation	SNP	C	T	4	217	c.1382G>A	c.(1381-1383)CGT>CAT	p.R461H
Pat_66	Pre-Treatment	GUK1	2987	37	1	228334563	228334563	Nonsense_Mutation	SNP	G	T	128	157	c.175G>T	c.(175-177)GAG>TAG	p.E59*
Pat_66	Pre-Treatment	OBSCN	84033	37	1	228523512	228523512	Missense_Mutation	SNP	G	A	54	145	c.16426G>A	c.(16426-16428)GAG>AAG	p.E5476K
Pat_66	Pre-Treatment	TRIM67	440730	37	1	231299671	231299671	Missense_Mutation	SNP	G	A	18	15	c.956G>A	c.(955-957)CGA>CAA	p.R319Q
Pat_66	Pre-Treatment	SIPA1L2	57568	37	1	232574866	232574866	Missense_Mutation	SNP	G	A	25	71	c.4019C>T	c.(4018-4020)TCC>TTC	p.S1340F
Pat_66	Pre-Treatment	KIAA1804	84451	37	1	233515051	233515051	Missense_Mutation	SNP	G	C	122	161	c.2299G>C	c.(2299-2301)GCT>CCT	p.A767P
Pat_66	Pre-Treatment	LYST	1130	37	1	235972754	235972754	Missense_Mutation	SNP	A	G	68	79	c.1364T>C	c.(1363-1365)CTG>CCG	p.L455P
Pat_66	Pre-Treatment	RYR2	6262	37	1	237881784	237881784	Missense_Mutation	SNP	G	A	54	41	c.10517G>A	c.(10516-10518)CGA>CAA	p.R3506Q
Pat_66	Pre-Treatment	CHRM3	1131	37	1	240072495	240072495	Missense_Mutation	SNP	C	T	153	142	c.1744C>T	c.(1744-1746)CAC>TAC	p.H582Y
Pat_66	Pre-Treatment	FMN2	56776	37	1	240370261	240370261	Missense_Mutation	SNP	G	A	28	124	c.2149G>A	c.(2149-2151)GCC>ACC	p.A717T
Pat_66	Pre-Treatment	FMN2	56776	37	1	240371033	240371033	Missense_Mutation	SNP	G	A	166	470	c.2921G>A	c.(2920-2922)GGA>GAA	p.G974E
Pat_66	Pre-Treatment	FMN2	56776	37	1	240635749	240635749	Missense_Mutation	SNP	G	A	45	120	c.5138G>A	c.(5137-5139)GGA>GAA	p.G1713E
Pat_66	Pre-Treatment	OR2G3	81469	37	1	247768951	247768951	Missense_Mutation	SNP	C	T	32	135	c.64C>T	c.(64-66)CGT>TGT	p.R22C
Pat_66	Pre-Treatment	TRIM58	25893	37	1	248039747	248039747	Missense_Mutation	SNP	G	A	18	117	c.1417G>A	c.(1417-1419)GAT>AAT	p.D473N
Pat_66	Pre-Treatment	OR2M4	26245	37	1	248403078	248403078	Missense_Mutation	SNP	C	T	31	197	c.848C>T	c.(847-849)CCT>CTT	p.P283L

Pat_66	Pre-Treatment	OR2M7	391196	37	1	248487446	248487446	Missense_Mutation	SNP	C	T	268	486	c.425G>A	c.(424-426)GGA>GAA	p.G142E
Pat_66	Pre-Treatment	OR2T4	127074	37	1	248525495	248525495	Missense_Mutation	SNP	G	A	218	236	c.613G>A	c.(613-615)GAG>AAG	p.E205K
Pat_66	Pre-Treatment	OR2T3	343173	37	1	248636667	248636667	Nonsense_Mutation	SNP	C	T	22	103	c.16C>T	c.(16-18)CAG>TAG	p.Q6*
Pat_66	Pre-Treatment	FBXO18	84893	37	10	5963488	5963488	Missense_Mutation	SNP	C	T	4	84	c.2278C>T	c.(2278-2280)CGG>TGG	p.R760W
Pat_66	Pre-Treatment	ITIH5	80760	37	10	7618968	7618968	Missense_Mutation	SNP	C	T	22	25	c.1426G>A	c.(1426-1428)GAT>AAT	p.D476N
Pat_66	Pre-Treatment	KIAA1217	56243	37	10	24832481	24832481	Missense_Mutation	SNP	G	A	30	34	c.4282G>A	c.(4282-4284)GGG>AGG	p.G1428R
Pat_66	Pre-Treatment	GPR158	57512	37	10	25887388	25887388	Missense_Mutation	SNP	C	T	97	123	c.2833C>T	c.(2833-2835)CAC>TAC	p.H945Y
Pat_66	Pre-Treatment	MYO3A	53904	37	10	26285456	26285456	Missense_Mutation	SNP	G	A	34	50	c.341G>A	c.(340-342)GGA>GAA	p.G114E
Pat_66	Pre-Treatment	GAD2	2572	37	10	26558061	26558061	Missense_Mutation	SNP	C	T	20	40	c.934C>T	c.(934-936)CCA>TCA	p.P312S
Pat_66	Pre-Treatment	PTCHD3	374308	37	10	27687287	27687287	Missense_Mutation	SNP	G	A	15	21	c.2240C>T	c.(2239-2241)TCC>TTC	p.S747F
Pat_66	Pre-Treatment	PTCHD3	374308	37	10	27702468	27702468	Missense_Mutation	SNP	C	T	18	15	c.712G>A	c.(712-714)GAT>AAT	p.D238N
Pat_66	Pre-Treatment	NRP1	8829	37	10	33559629	33559629	Missense_Mutation	SNP	G	A	34	57	c.404C>T	c.(403-405)TCC>TTC	p.S135F
Pat_66	Pre-Treatment	ANKRD30A	91074	37	10	37431050	37431050	Missense_Mutation	SNP	G	C	7	146	c.1057G>C	c.(1057-1059)GCA>CCA	p.A353P
Pat_66	Pre-Treatment	ANKRD30A	91074	37	10	37508235	37508235	Missense_Mutation	SNP	C	T	26	44	c.3427C>T	c.(3427-3429)CAT>TAT	p.H1143Y
Pat_66	Pre-Treatment	RET	5979	37	10	43597970	43597970	Missense_Mutation	SNP	C	T	35	24	c.518C>T	c.(517-519)TCC>TTC	p.S173F
Pat_66	Pre-Treatment	HNRNPA3P1	10151	37	10	44285799	44285799	Missense_Mutation	SNP	C	T	4	17	c.37G>A	c.(37-39)GAC>AAC	p.D13N
Pat_66	Pre-Treatment	PPYR1	5540	37	10	47086856	47086856	Missense_Mutation	SNP	G	A	14	67	c.73G>A	c.(73-75)GGC>AGC	p.G25S
Pat_66	Pre-Treatment	LRRC18	474354	37	10	50122059	50122059	Missense_Mutation	SNP	G	A	16	35	c.142C>T	c.(142-144)CGC>TGC	p.R48C
Pat_66	Pre-Treatment	DRGX	644168	37	10	50594888	50594888	Missense_Mutation	SNP	C	T	75	119	c.266G>A	c.(265-267)AGA>AAA	p.R89K
Pat_66	Pre-Treatment	ASAH2	56624	37	10	51974546	51974546	Missense_Mutation	SNP	C	T	9	45	c.1097G>A	c.(1096-1098)GGA>GAA	p.G366E
Pat_66	Pre-Treatment	PCDH15	65217	37	10	55568568	55568568	Missense_Mutation	SNP	C	T	15	20	c.5257G>A	c.(5257-5259)GAA>AAA	p.E1753K
Pat_66	Pre-Treatment	PCDH15	65217	37	10	55996643	55996643	Nonsense_Mutation	SNP	G	A	61	108	c.925C>T	c.(925-927)CAG>TAG	p.Q309*
Pat_66	Pre-Treatment	ANK3	288	37	10	61830234	61830234	Missense_Mutation	SNP	C	T	18	56	c.10405G>A	.(10405-10407)GAG>AAG	p.E3469K
Pat_66	Pre-Treatment	AIFM2	84883	37	10	71877624	71877624	Missense_Mutation	SNP	G	A	26	31	c.560C>T	c.(559-561)TCC>TTC	p.S187F
Pat_66	Pre-Treatment	UNC5B	219699	37	10	73058927	73058927	Missense_Mutation	SNP	G	A	81	115	c.2731G>A	c.(2731-2733)GAA>AAA	p.E911K
Pat_66	Pre-Treatment	CDH23	64072	37	10	73270964	73270964	Missense_Mutation	SNP	C	T	46	62	c.424C>T	c.(424-426)CCT>TCT	p.P142S
Pat_66	Pre-Treatment	OIT3	170392	37	10	74666458	74666458	Missense_Mutation	SNP	G	A	143	250	c.649G>A	c.(649-651)GAT>AAT	p.D217N
Pat_66	Pre-Treatment	PLAU	5328	37	10	75671985	75671985	Missense_Mutation	SNP	G	A	4	73	c.98G>A	c.(97-99)TGT>TAT	p.C33Y
Pat_66	Pre-Treatment	RPS24	6229	37	10	79795158	79795158	Missense_Mutation	SNP	C	T	75	116	c.52C>T	c.(52-54)CTT>TTT	p.L18F
Pat_66	Pre-Treatment	OPN4	94233	37	10	88415938	88415938	Nonsense_Mutation	SNP	G	A	27	50	c.171G>A	c.(169-171)TGG>TGA	p.W57*
Pat_66	Pre-Treatment	ANKRD22	118932	37	10	90582747	90582747	Missense_Mutation	SNP	C	T	50	65	c.527G>A	c.(526-528)CGG>CAG	p.R176Q
Pat_66	Pre-Treatment	ACTA2	59	37	10	90699264	90699264	Missense_Mutation	SNP	C	T	4	148	c.808G>A	c.(808-810)GGG>AGG	p.G270R
Pat_66	Pre-Treatment	LIPA	3988	37	10	90984889	90984889	Missense_Mutation	SNP	G	A	131	177	c.635C>T	c.(634-636)CCT>CTT	p.P212L
Pat_66	Pre-Treatment	IFIT1B	439996	37	10	91143767	91143767	Missense_Mutation	SNP	G	A	104	147	c.697G>A	c.(697-699)GAA>AAA	p.E233K
Pat_66	Pre-Treatment	PDE6C	5146	37	10	95372651	95372651	Missense_Mutation	SNP	G	A	34	52	c.169G>A	c.(169-171)GAG>AAG	p.E57K
Pat_66	Pre-Treatment	PDE6C	5146	37	10	95380518	95380518	Missense_Mutation	SNP	G	A	46	54	c.610G>A	c.(610-612)GAA>AAA	p.E204K
Pat_66	Pre-Treatment	PLCE1	51196	37	10	96025599	96025599	Missense_Mutation	SNP	G	A	39	58	c.4165G>A	c.(4165-4167)GAG>AAG	p.E1389K
Pat_66	Pre-Treatment	COX15	1355	37	10	101486739	101486739	Missense_Mutation	SNP	G	A	4	67	c.568C>T	c.(568-570)CTC>TTC	p.L190F
Pat_66	Pre-Treatment	SEMA4G	57715	37	10	102733352	102733352	Missense_Mutation	SNP	G	A	4	52	c.322G>A	c.(322-324)GGG>AGG	p.G108R
Pat_66	Pre-Treatment	PPRC1	23082	37	10	103908203	103908203	Missense_Mutation	SNP	C	T	44	77	c.4475C>T	c.(4474-4476)TCC>TTC	p.S1492F
Pat_66	Pre-Treatment	CCDC147	159686	37	10	106130749	106130749	Nonsense_Mutation	SNP	C	T	24	33	c.1027C>T	c.(1027-1029)CAA>TAA	p.Q343*
Pat_66	Pre-Treatment	C10orf81	79949	37	10	115528596	115528596	Missense_Mutation	SNP	T	C	37	47	c.364T>C	c.(364-366)TCC>CCC	p.S122P
Pat_66	Pre-Treatment	C10orf81	79949	37	10	115536905	115536905	Missense_Mutation	SNP	C	T	17	24	c.1054C>T	c.(1054-1056)CCA>TCA	p.P352S
Pat_66	Pre-Treatment	VWA2	340706	37	10	116042283	116042283	Missense_Mutation	SNP	G	A	36	64	c.842G>A	c.(841-843)AGA>AAA	p.R281K
Pat_66	Pre-Treatment	ABLIM1	3983	37	10	116232858	116232859	Missense_Mutation	DNP	CC	TT	48	72	.1152_1153GG>A	150-1155)AAGGAT>AAA	p.D385N
Pat_66	Pre-Treatment	FAM160B1	57700	37	10	116606865	116606865	Missense_Mutation	SNP	C	T	28	39	c.1585C>T	c.(1585-1587)CCA>TCA	p.P529S
Pat_66	Pre-Treatment	ATRNL1	26033	37	10	117154214	117154214	Missense_Mutation	SNP	G	A	19	51	c.3221G>A	c.(3220-3222)GGA>GAA	p.G1074E

Pat_66	Pre-Treatment	ATRNL1	26033	37	10	117154237	117154237	Missense_Mutation	SNP	G	A	19	45	c.3244G>A	c.(3244-3246)GGA>AGA	p.G1082R
Pat_66	Pre-Treatment	C10orf96	374355	37	10	118084841	118084841	Missense_Mutation	SNP	G	A	10	28	c.106G>A	c.(106-108)GAA>AAA	p.E36K
Pat_66	Pre-Treatment	PDZD8	118987	37	10	119049715	119049715	Nonsense_Mutation	SNP	G	A	44	59	c.1243C>T	c.(1243-1245)CGA>TGA	p.R415*
Pat_66	Pre-Treatment	RAB11FIP2	22841	37	10	119799657	119799657	Missense_Mutation	SNP	G	A	59	94	c.773C>T	c.(772-774)TCC>TTC	p.S258F
Pat_66	Pre-Treatment	WDR11	55717	37	10	122650387	122650387	Missense_Mutation	SNP	C	A	5	110	c.2503C>A	c.(2503-2505)CAA>AAA	p.Q835K
Pat_66	Pre-Treatment	TACC2	10579	37	10	123970328	123970328	Missense_Mutation	SNP	C	T	103	100	c.6388C>T	c.(6388-6390)CCG>TCG	p.P2130S
Pat_66	Pre-Treatment	DMBT1	1755	37	10	124399739	124399739	Missense_Mutation	SNP	G	A	104	118	c.6739G>A	c.(6739-6741)GAA>AAA	p.E2247K
Pat_66	Pre-Treatment	C10orf90	118611	37	10	128193141	128193141	Missense_Mutation	SNP	G	A	29	54	c.628C>T	c.(628-630)CCC>TCC	p.P210S
Pat_66	Pre-Treatment	MGMT	4255	37	10	131557529	131557529	Missense_Mutation	SNP	C	T	37	65	c.431C>T	c.(430-432)TCT>TTT	p.S144F
Pat_66	Pre-Treatment	LOC653544	653544	37	10	135491123	135491123	Missense_Mutation	SNP	G	A	4	29	c.734G>A	c.(733-735)GGC>GAC	p.G245D
Pat_66	Pre-Treatment	B4GALNT4	338707	37	11	380161	380161	Missense_Mutation	SNP	G	A	23	9	c.2674G>A	c.(2674-2676)GAG>AAG	p.E892K
Pat_66	Pre-Treatment	MUC6	4588	37	11	1018596	1018596	Missense_Mutation	SNP	G	A	4	127	c.4205C>T	c.(4204-4206)ACC>ATC	p.T1402I
Pat_66	Pre-Treatment	MUC2	4583	37	11	1087928	1087928	Missense_Mutation	SNP	G	A	8	30	c.3403G>A	c.(3403-3405)GAG>AAG	p.E1135K
Pat_66	Pre-Treatment	KRTAP5-5	439915	37	11	1651483	1651483	Missense_Mutation	SNP	G	C	4	88	c.413G>C	c.(412-414)GGC>GCC	p.G138A
Pat_66	Pre-Treatment	OR52K2	119774	37	11	4470799	4470799	Missense_Mutation	SNP	C	T	42	123	c.230C>T	c.(229-231)TCC>TTC	p.S77F
Pat_66	Pre-Treatment	OR52K1	390036	37	11	4510449	4510449	Missense_Mutation	SNP	C	T	16	57	c.319C>T	c.(319-321)CAC>TAC	p.H107Y
Pat_66	Pre-Treatment	OR51E1	143503	37	11	4673818	4673818	Missense_Mutation	SNP	C	T	58	165	c.62C>T	c.(61-63)CCT>CTT	p.P21L
Pat_66	Pre-Treatment	OR52J3	119679	37	11	5068657	5068657	Missense_Mutation	SNP	G	A	20	51	c.902G>A	c.(901-903)CGA>CAA	p.R301Q
Pat_66	Pre-Treatment	OR52E2	119678	37	11	5080127	5080127	Missense_Mutation	SNP	G	A	25	68	c.731C>T	c.(730-732)TCA>TTA	p.S244L
Pat_66	Pre-Treatment	OR52A5	390054	37	11	5153503	5153503	Missense_Mutation	SNP	G	A	10	55	c.370C>T	c.(370-372)CGC>TGC	p.R124C
Pat_66	Pre-Treatment	HBG2	3048	37	11	5275587	5275587	Missense_Mutation	SNP	C	T	39	306	c.250G>A	c.(250-252)GGC>AGC	p.G84S
Pat_66	Pre-Treatment	HBE1	3046	37	11	5289767	5289767	Missense_Mutation	SNP	C	T	104	278	c.376G>A	c.(376-378)GAA>AAA	p.E126K
Pat_66	Pre-Treatment	OR51I1	390063	37	11	5462162	5462162	Missense_Mutation	SNP	G	A	7	26	c.583C>T	c.(583-585)CAT>TAT	p.H195Y
Pat_66	Pre-Treatment	OR51I1	390063	37	11	5462402	5462402	Missense_Mutation	SNP	C	T	23	52	c.343G>A	c.(343-345)GGC>AGC	p.G115S
Pat_66	Pre-Treatment	OR52N2	390077	37	11	5842451	5842451	Missense_Mutation	SNP	G	A	80	59	c.886G>A	c.(886-888)GGA>AGA	p.G296R
Pat_66	Pre-Treatment	ZNF215	7762	37	11	6962867	6962867	Nonsense_Mutation	SNP	C	T	36	66	c.466C>T	c.(466-468)CGA>TGA	p.R156*
Pat_66	Pre-Treatment	RBMXL2	27288	37	11	7110403	7110403	Missense_Mutation	SNP	G	A	30	70	c.52G>A	c.(52-54)GAA>AAA	p.E18K
Pat_66	Pre-Treatment	OR10A3	26496	37	11	7960946	7960946	Missense_Mutation	SNP	C	T	36	117	c.122G>A	c.(121-123)GGA>GAA	p.G41E
Pat_66	Pre-Treatment	STK33	65975	37	11	8414233	8414233	Missense_Mutation	SNP	G	A	22	45	c.1369C>T	c.(1369-1371)CCT>TCT	p.P457S
Pat_66	Pre-Treatment	STK33	65975	37	11	8496281	8496281	Missense_Mutation	SNP	C	T	19	52	c.172G>A	c.(172-174)GAG>AAG	p.E58K
Pat_66	Pre-Treatment	SCUBE2	57758	37	11	9100985	9100985	Missense_Mutation	SNP	G	A	143	107	c.328C>T	c.(328-330)CGT>TGT	p.R110C
Pat_66	Pre-Treatment	SPON1	10418	37	11	14280867	14280867	Missense_Mutation	SNP	C	T	14	48	c.1534C>T	c.(1534-1536)CCC>TCC	p.P512S
Pat_66	Pre-Treatment	PLEKHA7	144100	37	11	16848076	16848076	Missense_Mutation	SNP	C	T	114	74	c.934G>A	c.(934-936)GAA>AAA	p.E312K
Pat_66	Pre-Treatment	TPH1	7166	37	11	18042606	18042606	Missense_Mutation	SNP	C	T	112	285	c.1267G>A	c.(1267-1269)GAG>AAG	p.E423K
Pat_66	Pre-Treatment	IGSF22	283284	37	11	18731951	18731951	Missense_Mutation	SNP	C	T	71	72	c.2624G>A	c.(2623-2625)CGA>CAA	p.R875Q
Pat_66	Pre-Treatment	DCDC1	341019	37	11	31327239	31327239	Missense_Mutation	SNP	G	A	155	111	c.677C>T	c.(676-678)CCT>CTT	p.P226L
Pat_66	Pre-Treatment	WT1	7490	37	11	32417935	32417935	Missense_Mutation	SNP	C	T	19	67	c.1117G>A	c.(1117-1119)GGA>AGA	p.G373R
Pat_66	Pre-Treatment	CCDC73	493860	37	11	32663586	32663586	Missense_Mutation	SNP	C	T	16	56	c.982G>A	c.(982-984)GAA>AAA	p.E328K
Pat_66	Pre-Treatment	PAMR1	25891	37	11	35453921	35453921	Missense_Mutation	SNP	C	T	37	111	c.2146G>A	c.(2146-2148)GAA>AAA	p.E716K
Pat_66	Pre-Treatment	RAG2	5897	37	11	36615492	36615492	Missense_Mutation	SNP	G	T	4	165	c.227C>A	c.(226-228)GCC>GAC	p.A76D
Pat_66	Pre-Treatment	CHST1	8534	37	11	45671975	45671975	Missense_Mutation	SNP	C	T	47	25	c.499G>A	c.(499-501)GAC>AAC	p.D167N
Pat_66	Pre-Treatment	OR4A47	403253	37	11	48510399	48510399	Missense_Mutation	SNP	C	T	12	27	c.55C>T	c.(55-57)CCA>TCA	p.P19S
Pat_66	Pre-Treatment	LOC440040	440040	37	11	49598368	49598368	Missense_Mutation	SNP	G	A	31	52	c.481G>A	c.(481-483)GTT>ATT	p.V161I
Pat_66	Pre-Treatment	OR4A5	81318	37	11	51412108	51412108	Missense_Mutation	SNP	C	T	35	80	c.288G>A	c.(286-288)ATG>ATA	p.M96I
Pat_66	Pre-Treatment	OR4P4	81300	37	11	55405837	55405837	Missense_Mutation	SNP	G	A	48	148	c.4G>A	c.(4-6)GAA>AAA	p.E2K
Pat_66	Pre-Treatment	OR10AG1	282770	37	11	55735269	55735269	Missense_Mutation	SNP	C	T	16	38	c.671G>A	c.(670-672)GGA>GAA	p.G224E
Pat_66	Pre-Treatment	OR10AG1	282770	37	11	55735468	55735468	Missense_Mutation	SNP	G	A	27	48	c.472C>T	c.(472-474)CCC>TCC	p.P158S

Pat_66	Pre-Treatment	OR8H3	390152	37	11	55889867	55889867	Missense_Mutation	SNP	G	A	93	217	c.19G>A	c.(19-21)GAC>AAC	p.D7N
Pat_66	Pre-Treatment	LRRC55	219527	37	11	56949959	56949959	Missense_Mutation	SNP	C	T	28	58	c.592C>T	c.(592-594)CCC>TCC	p.P198S
Pat_66	Pre-Treatment	TCN1	6947	37	11	59623449	59623449	Missense_Mutation	SNP	G	A	44	117	c.830C>T	c.(829-831)TCT>TTT	p.S277F
Pat_66	Pre-Treatment	SLC22A25	387601	37	11	62997084	62997084	Missense_Mutation	SNP	C	T	10	55	c.41G>A	c.(40-42)GGG>GAG	p.G14E
Pat_66	Pre-Treatment	RTN3	10313	37	11	63488139	63488139	Missense_Mutation	SNP	C	T	21	97	c.2165C>T	c.(2164-2166)CCT>CTT	p.P722L
Pat_66	Pre-Treatment	C11orf84	144097	37	11	63585435	63585435	Missense_Mutation	SNP	G	A	5	65	c.286G>A	c.(286-288)GCT>ACT	p.A96T
Pat_66	Pre-Treatment	SLC22A11	55867	37	11	64323790	64323790	Missense_Mutation	SNP	G	A	25	62	c.319G>A	c.(319-321)GAA>AAA	p.E107K
Pat_66	Pre-Treatment	ATG2A	23130	37	11	64673934	64673934	Missense_Mutation	SNP	G	A	20	44	c.3055C>T	c.(3055-3057)CCA>TCA	p.P1019S
Pat_66	Pre-Treatment	SLC22A20	440044	37	11	64981843	64981843	Missense_Mutation	SNP	C	T	38	28	c.422C>T	c.(421-423)TCC>TTC	p.S141F
Pat_66	Pre-Treatment	CORO1B	57175	37	11	67209258	67209258	Nonsense_Mutation	SNP	G	A	4	127	c.400C>T	c.(400-402)CGA>TGA	p.R134*
Pat_66	Pre-Treatment	GSTP1	2950	37	11	67354022	67354022	Missense_Mutation	SNP	C	T	13	31	c.607C>T	c.(607-609)CCC>TCC	p.P203S
Pat_66	Pre-Treatment	CPT1A	1374	37	11	68542901	68542901	Splice_Site	SNP	C	T	40	103	c.1459_splice	c.e13-1	p.Y487_splice
Pat_66	Pre-Treatment	MRGPRD	116512	37	11	68747555	68747555	Missense_Mutation	SNP	G	A	16	40	c.901C>T	c.(901-903)CGC>TGC	p.R301C
Pat_66	Pre-Treatment	C2CD3	26005	37	11	73806308	73806308	Missense_Mutation	SNP	G	A	107	79	c.3125C>T	c.(3124-3126)TCC>TTC	p.S1042F
Pat_66	Pre-Treatment	WNT11	7481	37	11	75902646	75902646	Missense_Mutation	SNP	C	T	36	59	c.852G>A	c.(850-852)ATG>ATA	p.M284I
Pat_66	Pre-Treatment	MYO7A	4647	37	11	76900471	76900472	Missense_Mutation	DNP	TC	AT	23	92	.3586_3587TC>A	c.(3586-3588)TCT>ATT	p.S1196I
Pat_66	Pre-Treatment	GDPD4	220032	37	11	76944140	76944140	Missense_Mutation	SNP	G	A	28	79	c.1319C>T	c.(1318-1320)TCC>TTC	p.S440F
Pat_66	Pre-Treatment	THRSP	7069	37	11	77774983	77774983	Missense_Mutation	SNP	G	A	4	92	c.56G>A	c.(55-57)CGG>CAG	p.R19Q
Pat_66	Pre-Treatment	CCDC83	220047	37	11	85584267	85584267	Missense_Mutation	SNP	G	A	13	41	c.109G>A	c.(109-111)GAA>AAA	p.E37K
Pat_66	Pre-Treatment	CCDC81	60494	37	11	86098570	86098570	Missense_Mutation	SNP	C	T	84	56	c.154C>T	c.(154-156)CCA>TCA	p.P52S
Pat_66	Pre-Treatment	TRIM49	57093	37	11	89531599	89531599	Missense_Mutation	SNP	C	A	23	105	c.1058G>T	c.(1057-1059)TGG>TTG	p.W353L
Pat_66	Pre-Treatment	SLC36A4	120103	37	11	92916023	92916023	Missense_Mutation	SNP	G	A	45	139	c.308C>T	c.(307-309)TCT>TTT	p.S103F
Pat_66	Pre-Treatment	CCDC67	159989	37	11	93088694	93088694	Nonsense_Mutation	SNP	C	T	17	45	c.187C>T	c.(187-189)CAG>TAG	p.Q63*
Pat_66	Pre-Treatment	CNTN5	53942	37	11	100061937	100061937	Missense_Mutation	SNP	G	A	19	56	c.1660G>A	c.(1660-1662)GAA>AAA	p.E554K
Pat_66	Pre-Treatment	C11orf65	160140	37	11	108256687	108256687	Nonsense_Mutation	SNP	C	T	103	225	c.747G>A	c.(745-747)TGG>TGA	p.W249*
Pat_66	Pre-Treatment	POU2AF1	5450	37	11	111228415	111228415	Missense_Mutation	SNP	C	T	6	16	c.211G>A	c.(211-213)GAA>AAA	p.E71K
Pat_66	Pre-Treatment	TTC12	54970	37	11	113234613	113234613	Missense_Mutation	SNP	C	T	21	71	c.1780C>T	c.(1780-1782)CAT>TAT	p.H594Y
Pat_66	Pre-Treatment	FAM55A	120400	37	11	114400973	114400973	Missense_Mutation	SNP	C	T	26	67	c.331G>A	c.(331-333)GAG>AAG	p.E111K
Pat_66	Pre-Treatment	DSCAML1	57453	37	11	117299054	117299054	Missense_Mutation	SNP	G	A	33	96	c.6332C>T	c.(6331-6333)ACC>ATC	p.T2111I
Pat_66	Pre-Treatment	TMPRSS13	84000	37	11	117789469	117789469	Missense_Mutation	SNP	G	A	30	87	c.106C>T	c.(106-108)CCA>TCA	p.P36S
Pat_66	Pre-Treatment	TMPRSS13	84000	37	11	117789522	117789522	Missense_Mutation	SNP	C	T	34	75	c.53G>A	c.(52-54)GGA>GAA	p.G18E
Pat_66	Pre-Treatment	IL10RA	3587	37	11	117870019	117870019	Missense_Mutation	SNP	C	T	71	39	c.1400C>T	c.(1399-1401)TCG>TTG	p.S467L
Pat_66	Pre-Treatment	MLL	4297	37	11	118342464	118342464	Missense_Mutation	SNP	C	T	24	61	c.590C>T	c.(589-591)TCC>TTC	p.S197F
Pat_66	Pre-Treatment	BCL9L	283149	37	11	118773200	118773200	Nonsense_Mutation	SNP	C	A	4	45	c.1252G>T	c.(1252-1254)GAG>TAG	p.E418*
Pat_66	Pre-Treatment	TRIM29	23650	37	11	120008255	120008255	Missense_Mutation	SNP	G	A	16	79	c.485C>T	c.(484-486)TCA>TTA	p.S162L
Pat_66	Pre-Treatment	POU2F3	25833	37	11	120170352	120170352	Missense_Mutation	SNP	C	T	50	142	c.278C>T	c.(277-279)CCG>CTG	p.P93L
Pat_66	Pre-Treatment	TECTA	7007	37	11	120998545	120998545	Missense_Mutation	SNP	C	T	72	119	c.1859C>T	c.(1858-1860)TCG>TTG	p.S620L
Pat_66	Pre-Treatment	OR10S1	219873	37	11	123847618	123847618	Missense_Mutation	SNP	C	T	53	35	c.781G>A	c.(781-783)GGG>AGG	p.G261R
Pat_66	Pre-Treatment	CACNA1C	775	37	12	2714297	2714297	Missense_Mutation	SNP	G	A	30	106	c.3071G>A	c.(3070-3072)AGG>AAG	p.R1024K
Pat_66	Pre-Treatment	CACNA1C	775	37	12	2794921	2794921	Missense_Mutation	SNP	G	A	23	97	c.5842G>A	c.(5842-5844)GAA>AAA	p.E1948K
Pat_66	Pre-Treatment	NRIP2	83714	37	12	2939989	2939989	Missense_Mutation	SNP	C	T	31	153	c.380G>A	c.(379-381)GGA>GAA	p.G127E
Pat_66	Pre-Treatment	CHD4	1108	37	12	6702276	6702276	Missense_Mutation	SNP	A	C	84	80	c.2633T>G	c.(2632-2634)CTG>CGG	p.L878R
Pat_66	Pre-Treatment	ACRBP	84519	37	12	6753751	6753751	Nonsense_Mutation	SNP	G	A	30	93	c.496C>T	c.(496-498)CAG>TAG	p.Q166*
Pat_66	Pre-Treatment	ACSM4	341392	37	12	7457006	7457006	Missense_Mutation	SNP	C	T	97	356	c.79C>T	c.(79-81)CAC>TAC	p.H27Y
Pat_66	Pre-Treatment	CD163L1	283316	37	12	7585299	7585299	Missense_Mutation	SNP	C	T	38	144	c.479G>A	c.(478-480)GGA>GAA	p.G160E
Pat_66	Pre-Treatment	CD163	9332	37	12	7632593	7632593	Splice_Site	SNP	C	T	9	55	c.3344_splice	c.e16-1	p.E1115_splice
Pat_66	Pre-Treatment	CLEC4C	170482	37	12	7883403	7883403	Missense_Mutation	SNP	C	T	113	177	c.487G>A	c.(487-489)GAA>AAA	p.E163K

Pat_66	Pre-Treatment	PZP	5858	37	12	9360916	9360916	Missense_Mutation	SNP	G	A	37	134	c.22C>T	c.(22-24)CAT>TAT	p.H8Y
Pat_66	Pre-Treatment	GRIN2B	2904	37	12	13717329	13717329	Missense_Mutation	SNP	G	A	52	268	c.2843C>T	c.(2842-2844)TCC>TTC	p.S948F
Pat_66	Pre-Treatment	GUCY2C	2984	37	12	14805929	14805929	Missense_Mutation	SNP	C	T	65	263	c.1490G>A	c.(1489-1491)CGA>CAA	p.R497Q
Pat_66	Pre-Treatment	PTPRO	5800	37	12	15677760	15677760	Missense_Mutation	SNP	C	T	66	71	c.1904C>T	c.(1903-1905)CCG>CTG	p.P635L
Pat_66	Pre-Treatment	SLCO1B3	28234	37	12	21015405	21015405	Missense_Mutation	SNP	C	T	68	264	c.541C>T	c.(541-543)CGT>TGT	p.R181C
Pat_66	Pre-Treatment	PKP2	5318	37	12	32949074	32949074	Nonsense_Mutation	SNP	G	A	42	161	c.2458C>T	c.(2458-2460)CAG>TAG	p.Q820*
Pat_66	Pre-Treatment	PKP2	5318	37	12	32975517	32975517	Missense_Mutation	SNP	C	T	48	147	c.1855G>A	c.(1855-1857)GAG>AAG	p.E619K
Pat_66	Pre-Treatment	PDZRN4	29951	37	12	41966248	41966248	Missense_Mutation	SNP	G	A	36	61	c.1070G>A	c.(1069-1071)GGA>GAA	p.G357E
Pat_66	Pre-Treatment	ADAMTS20	80070	37	12	43821115	43821115	Missense_Mutation	SNP	C	T	17	46	c.4103G>A	c.(4102-4104)GGA>GAA	p.G1368E
Pat_66	Pre-Treatment	FAM113B	91523	37	12	47629420	47629420	Missense_Mutation	SNP	G	A	28	2	c.574G>A	c.(574-576)GAA>AAA	p.E192K
Pat_66	Pre-Treatment	COL2A1	1280	37	12	48381456	48381456	Missense_Mutation	SNP	C	T	21	2	c.1159G>A	c.(1159-1161)GGT>AGT	p.G387S
Pat_66	Pre-Treatment	COL2A1	1280	37	12	48391659	48391659	Missense_Mutation	SNP	C	T	157	23	c.424G>A	c.(424-426)GAA>AAA	p.E142K
Pat_66	Pre-Treatment	TROAP	10024	37	12	49724474	49724474	Missense_Mutation	SNP	C	T	28	43	c.1846C>T	c.(1846-1848)CCA>TCA	p.P616S
Pat_66	Pre-Treatment	NCKAP5L	57701	37	12	50196918	50196918	Missense_Mutation	SNP	C	T	4	127	c.154G>A	c.(154-156)GAA>AAA	p.E52K
Pat_66	Pre-Treatment	RACGAP1	29127	37	12	50390867	50390867	Missense_Mutation	SNP	G	A	76	13	c.1000C>T	c.(1000-1002)CCC>TCC	p.P334S
Pat_66	Pre-Treatment	BIN2	51411	37	12	51685722	51685722	Nonsense_Mutation	SNP	G	A	3	60	c.1168C>T	c.(1168-1170)CGA>TGA	p.R390*
Pat_66	Pre-Treatment	SLC4A8	9498	37	12	51856106	51856106	Missense_Mutation	SNP	G	A	4	135	c.1114G>A	c.(1114-1116)GTA>ATA	p.V372I
Pat_66	Pre-Treatment	KRT5	3852	37	12	52913609	52913609	Missense_Mutation	SNP	C	T	155	14	c.472G>A	c.(472-474)GAC>AAC	p.D158N
Pat_66	Pre-Treatment	KRT71	112802	37	12	52946833	52946833	Missense_Mutation	SNP	C	T	45	62	c.29G>A	c.(28-30)GGA>GAA	p.G10E
Pat_66	Pre-Treatment	KRT1	3848	37	12	53074098	53074098	Missense_Mutation	SNP	C	A	4	167	c.35G>T	c.(34-36)CGA>CTA	p.R12L
Pat_66	Pre-Treatment	KRT77	374454	37	12	53086344	53086344	Missense_Mutation	SNP	C	T	28	32	c.1288G>A	c.(1288-1290)GAC>AAC	p.D430N
Pat_66	Pre-Treatment	KRT79	338785	37	12	53225263	53225263	Missense_Mutation	SNP	G	A	74	96	c.625C>T	c.(625-627)CTT>TTT	p.L209F
Pat_66	Pre-Treatment	OR9K2	441639	37	12	55524113	55524113	Missense_Mutation	SNP	G	A	39	52	c.561G>A	c.(559-561)ATG>ATA	p.M187I
Pat_66	Pre-Treatment	PA2G4	5036	37	12	56500493	56500493	Missense_Mutation	SNP	G	A	95	14	c.210G>A	c.(208-210)ATG>ATA	p.M70I
Pat_66	Pre-Treatment	RBMS2	5939	37	12	56975929	56975929	Missense_Mutation	SNP	C	T	4	167	c.866C>T	c.(865-867)TCG>TTG	p.S289L
Pat_66	Pre-Treatment	INHBC	3626	37	12	57843650	57843650	Missense_Mutation	SNP	C	T	36	56	c.904C>T	c.(904-906)CTC>TTC	p.L302F
Pat_66	Pre-Treatment	FRS2	10818	37	12	69968724	69968724	Missense_Mutation	SNP	C	A	4	116	c.1516C>A	c.(1516-1518)CTG>ATG	p.L506M
Pat_66	Pre-Treatment	LRRC10	376132	37	12	70004495	70004495	Missense_Mutation	SNP	G	C	27	4	c.124C>G	c.(124-126)CGC>GGC	p.R42G
Pat_66	Pre-Treatment	BEST3	144453	37	12	70049336	70049336	Missense_Mutation	SNP	G	A	13	23	c.1358C>T	c.(1357-1359)TCC>TTC	p.S453F
Pat_66	Pre-Treatment	PTPRR	5801	37	12	71092066	71092066	Missense_Mutation	SNP	G	A	31	38	c.1258C>T	c.(1258-1260)CGC>TGC	p.R420C
Pat_66	Pre-Treatment	SLC41A2	84102	37	12	105199060	105199060	Missense_Mutation	SNP	C	T	268	58	c.1592G>A	c.(1591-1593)GGA>GAA	p.G531E
Pat_66	Pre-Treatment	CMKLR1	1240	37	12	108686279	108686279	Missense_Mutation	SNP	C	A	4	92	c.461G>T	c.(460-462)CGC>CTC	p.R154L
Pat_66	Pre-Treatment	ATXN2	6311	37	12	111891568	111891568	Missense_Mutation	SNP	C	T	3	47	c.3826G>A	c.(3826-3828)GGT>AGT	p.G1276S
Pat_66	Pre-Treatment	RPH3A	22895	37	12	113327831	113327831	Missense_Mutation	SNP	G	A	232	21	c.1566G>A	c.(1564-1566)ATG>ATA	p.M522I
Pat_66	Pre-Treatment	TBX5	6910	37	12	114793909	114793909	Missense_Mutation	SNP	C	T	66	11	c.985G>A	c.(985-987)GAA>AAA	p.E329K
Pat_66	Pre-Treatment	KSR2	283455	37	12	117907512	117907512	Missense_Mutation	SNP	C	T	11	5	c.2714G>A	c.(2713-2715)CGA>CAA	p.R905Q
Pat_66	Pre-Treatment	GCN1L1	10985	37	12	120602516	120602516	Missense_Mutation	SNP	G	A	4	95	c.1622C>T	c.(1621-1623)ACT>ATT	p.T541I
Pat_66	Pre-Treatment	CLIP1	6249	37	12	122839678	122839678	Missense_Mutation	SNP	C	T	4	182	c.1187G>A	c.(1186-1188)CGG>CAG	p.R396Q
Pat_66	Pre-Treatment	KNTC1	9735	37	12	123087161	123087161	Missense_Mutation	SNP	C	T	9	17	c.4699C>T	c.(4699-4701)CCT>TCT	p.P1567S
Pat_66	Pre-Treatment	GPR109A	338442	37	12	123187791	123187791	Missense_Mutation	SNP	C	T	19	134	c.40G>A	c.(40-42)GAC>AAC	p.D14N
Pat_66	Pre-Treatment	GPR109B	8843	37	12	123201245	123201245	Missense_Mutation	SNP	C	T	25	42	c.40G>A	c.(40-42)GAC>AAC	p.D14N
Pat_66	Pre-Treatment	ZNF664	144348	37	12	124496836	124496836	Missense_Mutation	SNP	C	T	16	120	c.145C>T	c.(145-147)CAT>TAT	p.H49Y
Pat_66	Pre-Treatment	TUBA3C	7278	37	13	19748014	19748014	Missense_Mutation	SNP	C	T	94	121	c.1342G>A	c.(1342-1344)GAA>AAA	p.E448K
Pat_66	Pre-Treatment	TPTE2	93492	37	13	20000591	20000591	Missense_Mutation	SNP	C	T	54	304	c.1369G>A	c.(1369-1371)GAT>AAT	p.D457N
Pat_66	Pre-Treatment	LATS2	26524	37	13	21563291	21563291	Missense_Mutation	SNP	G	A	16	25	c.628C>T	c.(628-630)CCG>TCG	p.P210S
Pat_66	Pre-Treatment	SACS	26278	37	13	23906683	23906683	Missense_Mutation	SNP	C	T	49	58	c.11332G>A	c.(11332-11334)GAA>AAA	p.E3778K
Pat_66	Pre-Treatment	SACS	26278	37	13	23911221	23911221	Missense_Mutation	SNP	G	A	43	50	c.6794C>T	c.(6793-6795)TCC>TTC	p.S2265F

Pat_66	Pre-Treatment	TNFRSF19	55504	37	13	24200917	24200917	Missense_Mutation	SNP	C	T	49	65	c.431C>T	c.(430-432)CCT>CTT	p.P144L
Pat_66	Pre-Treatment	ATP12A	479	37	13	25275001	25275001	Missense_Mutation	SNP	G	A	49	156	c.1822G>A	c.(1822-1824)GAT>AAT	p.D608N
Pat_66	Pre-Treatment	RNF17	56163	37	13	25367193	25367193	Missense_Mutation	SNP	G	A	18	74	c.949G>A	c.(949-951)GAA>AAA	p.E317K
Pat_66	Pre-Treatment	FAM123A	219287	37	13	25744067	25744067	Missense_Mutation	SNP	C	T	30	51	c.1691G>A	c.(1690-1692)GGA>GAA	p.G564E
Pat_66	Pre-Treatment	GPR12	2835	37	13	27333591	27333591	Missense_Mutation	SNP	G	A	27	159	c.374C>T	c.(373-375)TCT>TTT	p.S125F
Pat_66	Pre-Treatment	FLT3	2322	37	13	28597508	28597508	Missense_Mutation	SNP	C	T	18	66	c.2397G>A	c.(2395-2397)ATG>ATA	p.M799I
Pat_66	Pre-Treatment	MTUS2	23281	37	13	29898806	29898806	Missense_Mutation	SNP	C	T	12	17	c.2893C>T	c.(2893-2895)CCT>TCT	p.P965S
Pat_66	Pre-Treatment	SLC7A1	6541	37	13	30097424	30097424	Missense_Mutation	SNP	G	A	42	225	c.1028C>T	c.(1027-1029)TCC>TTC	p.S343F
Pat_66	Pre-Treatment	RXFP2	122042	37	13	32332428	32332428	Missense_Mutation	SNP	C	T	147	155	c.128C>T	c.(127-129)CCT>CTT	p.P43L
Pat_66	Pre-Treatment	RXFP2	122042	37	13	32367034	32367034	Missense_Mutation	SNP	G	A	40	67	c.1595G>A	c.(1594-1596)CGA>CAA	p.R532Q
Pat_66	Pre-Treatment	BRCA2	675	37	13	32953493	32953493	Missense_Mutation	SNP	C	T	48	53	c.8794C>T	c.(8794-8796)CAC>TAC	p.H2932Y
Pat_66	Pre-Treatment	KL	9365	37	13	33638147	33638147	Missense_Mutation	SNP	G	A	111	114	c.2863G>A	c.(2863-2865)GGC>AGC	p.G955S
Pat_66	Pre-Treatment	SMAD9	4093	37	13	37453501	37453501	Missense_Mutation	SNP	G	A	22	71	c.326C>T	c.(325-327)CCG>CTG	p.P109L
Pat_66	Pre-Treatment	POSTN	10631	37	13	38137477	38137477	Missense_Mutation	SNP	G	A	16	49	c.2504C>T	c.(2503-2505)TCT>TTT	p.S835F
Pat_66	Pre-Treatment	TRPC4	7223	37	13	38320108	38320108	Missense_Mutation	SNP	C	T	246	324	c.863G>A	c.(862-864)AGA>AAA	p.R288K
Pat_66	Pre-Treatment	FREM2	341640	37	13	39264248	39264248	Missense_Mutation	SNP	C	T	24	110	c.2767C>T	c.(2767-2769)CAT>TAT	p.H923Y
Pat_66	Pre-Treatment	HTR2A	3356	37	13	47409577	47409577	Missense_Mutation	SNP	C	T	48	53	c.811G>A	c.(811-813)GAT>AAT	p.D271N
Pat_66	Pre-Treatment	LOC220429	220429	37	13	50467032	50467032	Missense_Mutation	SNP	C	T	129	113	c.2306C>T	c.(2305-2307)TCC>TTC	p.S769F
Pat_66	Pre-Treatment	ATP7B	540	37	13	52524456	52524456	Missense_Mutation	SNP	C	T	38	46	c.2527G>A	c.(2527-2529)GGG>AGG	p.G843R
Pat_66	Pre-Treatment	CKAP2	26586	37	13	53035367	53035367	Missense_Mutation	SNP	C	T	51	62	c.409C>T	c.(409-411)CCC>TCC	p.P137S
Pat_66	Pre-Treatment	PCDH9	5101	37	13	67801017	67801017	Missense_Mutation	SNP	C	T	31	144	c.1556G>A	c.(1555-1557)CGA>CAA	p.R519Q
Pat_66	Pre-Treatment	DACH1	1602	37	13	72063191	72063191	Missense_Mutation	SNP	G	A	108	418	c.1660C>T	c.(1660-1662)CCA>TCA	p.P554S
Pat_66	Pre-Treatment	C13orf37	440145	37	13	73293130	73293130	Missense_Mutation	SNP	G	A	5	303	c.185C>T	c.(184-186)TCG>TTG	p.S62L
Pat_66	Pre-Treatment	SLITRK1	114798	37	13	84455341	84455341	Missense_Mutation	SNP	G	A	56	208	c.302C>T	c.(301-303)GCT>GTT	p.A101V
Pat_66	Pre-Treatment	CLDN10	9071	37	13	96229529	96229529	Missense_Mutation	SNP	C	T	32	55	c.509C>T	c.(508-510)TCA>TTA	p.S170L
Pat_66	Pre-Treatment	CLYBL	171425	37	13	100425206	100425206	Missense_Mutation	SNP	C	T	65	64	c.191C>T	c.(190-192)TCC>TTC	p.S64F
Pat_66	Pre-Treatment	TMTC4	84899	37	13	101287277	101287277	Splice_Site	SNP	C	A	4	140	c.1317_splice	c.e10+1	p.K439_splice
Pat_66	Pre-Treatment	TMTC4	84899	37	13	101315295	101315295	Missense_Mutation	SNP	G	A	76	81	c.418C>T	c.(418-420)CGG>TGG	p.R140W
Pat_66	Pre-Treatment	KDELC1	79070	37	13	103449193	103449193	Nonsense_Mutation	SNP	G	A	22	62	c.349C>T	c.(349-351)CAA>TAA	p.Q117*
Pat_66	Pre-Treatment	GRTP1	79774	37	13	114005181	114005181	Missense_Mutation	SNP	C	T	127	157	c.448G>A	c.(448-450)GGA>AGA	p.G150R
Pat_66	Pre-Treatment	ADPRHL1	113622	37	13	114098878	114098878	Missense_Mutation	SNP	G	A	5	231	c.241C>T	c.(241-243)CGG>TGG	p.R81W
Pat_66	Pre-Treatment	OR4K5	79317	37	14	20388989	20388989	Missense_Mutation	SNP	C	T	93	433	c.224C>T	c.(223-225)TCT>TTT	p.S75F
Pat_66	Pre-Treatment	OR4K1	79544	37	14	20404108	20404108	Missense_Mutation	SNP	G	A	46	158	c.283G>A	c.(283-285)GAG>AAG	p.E95K
Pat_66	Pre-Treatment	RPGRIP1	57096	37	14	21795853	21795853	Missense_Mutation	SNP	C	T	34	97	c.2782C>T	c.(2782-2784)CCC>TCC	p.P928S
Pat_66	Pre-Treatment	CDH24	64403	37	14	23518872	23518872	Missense_Mutation	SNP	C	T	18	66	c.1675G>A	c.(1675-1677)GGC>AGC	p.G559S
Pat_66	Pre-Treatment	MYH6	4624	37	14	23856757	23856757	Missense_Mutation	SNP	G	A	36	73	c.4631C>T	c.(4630-4632)TCA>TTA	p.S1544L
Pat_66	Pre-Treatment	DCAF11	80344	37	14	24587633	24587633	Missense_Mutation	SNP	G	A	6	228	c.614G>A	c.(613-615)CGT>CAT	p.R205H
Pat_66	Pre-Treatment	CTSG	1511	37	14	25043589	25043589	Missense_Mutation	SNP	C	T	69	135	c.456G>A	c.(454-456)ATG>ATA	p.M152I
Pat_66	Pre-Treatment	TBPL2	387332	37	14	55895616	55895616	Missense_Mutation	SNP	C	T	112	80	c.865G>A	c.(865-867)GAT>AAT	p.D289N
Pat_66	Pre-Treatment	DAAM1	23002	37	14	59835509	59835509	Missense_Mutation	SNP	C	T	39	114	c.3169C>T	c.(3169-3171)CGC>TGC	p.R1057C
Pat_66	Pre-Treatment	SYNE2	23224	37	14	64494362	64494362	Missense_Mutation	SNP	C	T	66	55	c.6565C>T	c.(6565-6567)CTC>TTC	p.L2189F
Pat_66	Pre-Treatment	SYNE2	23224	37	14	64656922	64656922	Missense_Mutation	SNP	G	A	4	124	c.18005G>A	c.(18004-18006)CGT>CAT	p.R6002H
Pat_66	Pre-Treatment	ADAM21	8747	37	14	70924496	70924496	Missense_Mutation	SNP	G	A	27	108	c.280G>A	c.(280-282)GAT>AAT	p.D94N
Pat_66	Pre-Treatment	ADAM20	8748	37	14	70990444	70990444	Missense_Mutation	SNP	A	G	49	119	c.1181T>C	c.(1180-1182)CTT>CCT	p.L394P
Pat_66	Pre-Treatment	RGS6	9628	37	14	72976951	72976951	Missense_Mutation	SNP	G	A	70	183	c.1055G>A	c.(1054-1056)CGA>CAA	p.R352Q
Pat_66	Pre-Treatment	RBM25	58517	37	14	73570131	73570131	Missense_Mutation	SNP	C	T	37	26	c.1099C>T	c.(1099-1101)CGT>TGT	p.R367C
Pat_66	Pre-Treatment	PAPLN	89932	37	14	73729141	73729141	Missense_Mutation	SNP	G	A	8	19	c.2329G>A	c.(2329-2331)GGC>AGC	p.G777S

Pat_66	Pre-Treatment	YLPM1	56252	37	14	75230767	75230767	Missense_Mutation	SNP	C	T	48	117	c.575C>T	c.(574-576)TCG>TTG	p.S192L
Pat_66	Pre-Treatment	NEK9	91754	37	14	75568371	75568371	Missense_Mutation	SNP	G	A	4	181	c.1829C>T	c.(1828-1830)GCT>GTT	p.A610V
Pat_66	Pre-Treatment	NRXN3	9369	37	14	79181123	79181123	Missense_Mutation	SNP	G	A	7	555	c.566G>A	c.(565-567)CGC>CAC	p.R189H
Pat_66	Pre-Treatment	FLRT2	23768	37	14	86088927	86088927	Missense_Mutation	SNP	C	T	93	179	c.1069C>T	c.(1069-1071)CTT>TTT	p.L357F
Pat_66	Pre-Treatment	KCNK10	54207	37	14	88651959	88651959	Missense_Mutation	SNP	C	T	34	91	c.1537G>A	c.(1537-1539)GAG>AAG	p.E513K
Pat_66	Pre-Treatment	EML5	161436	37	14	89082537	89082537	Missense_Mutation	SNP	C	T	5	368	c.5846G>A	c.(5845-5847)CGA>CAA	p.R1949Q
Pat_66	Pre-Treatment	DDX24	57062	37	14	94528802	94528802	Missense_Mutation	SNP	G	A	35	84	c.884C>T	c.(883-885)TCT>TTT	p.S295F
Pat_66	Pre-Treatment	PPP4R4	57718	37	14	94741717	94741717	Missense_Mutation	SNP	C	T	100	309	c.2456C>T	c.(2455-2457)TCA>TTA	p.S819L
Pat_66	Pre-Treatment	BDKRB2	624	37	14	96707554	96707554	Missense_Mutation	SNP	C	T	46	17	c.889C>T	c.(889-891)CGC>TGC	p.R297C
Pat_66	Pre-Treatment	EML1	2009	37	14	100331938	100331938	Missense_Mutation	SNP	C	T	16	57	c.338C>T	c.(337-339)TCC>TTC	p.S113F
Pat_66	Pre-Treatment	WDR25	79446	37	14	100934439	100934439	Missense_Mutation	SNP	C	T	79	160	c.904C>T	c.(904-906)CCC>TCC	p.P302S
Pat_66	Pre-Treatment	DYNC1H1	1778	37	14	102478718	102478718	Missense_Mutation	SNP	C	T	35	105	c.6925C>T	c.(6925-6927)CCA>TCA	p.P2309S
Pat_66	Pre-Treatment	RCOR1	23186	37	14	103188553	103188553	Missense_Mutation	SNP	G	A	84	58	c.1210G>A	c.(1210-1212)GCA>ACA	p.A404T
Pat_66	Pre-Treatment	MARK3	4140	37	14	103958212	103958212	Missense_Mutation	SNP	G	A	4	132	c.1685G>A	c.(1684-1686)CGT>CAT	p.R562H
Pat_66	Pre-Treatment	TDRD9	122402	37	14	104516010	104516010	Nonsense_Mutation	SNP	G	A	7	17	c.4040G>A	c.(4039-4041)TGG>TAG	p.W1347*
Pat_66	Pre-Treatment	KIF26A	26153	37	14	104642925	104642925	Missense_Mutation	SNP	C	T	9	37	c.3800C>T	c.(3799-3801)TCC>TTC	p.S1267F
Pat_66	Pre-Treatment	AHNAK2	113146	37	14	105416293	105416293	Missense_Mutation	SNP	G	A	267	192	c.5495C>T	c.(5494-5496)TCG>TTG	p.S1832L
Pat_66	Pre-Treatment	MKRN3	7681	37	15	23811414	23811414	Missense_Mutation	SNP	C	G	38	37	c.485C>G	c.(484-486)GCT>GGT	p.A162G
Pat_66	Pre-Treatment	NDN	4692	37	15	23931560	23931560	Missense_Mutation	SNP	C	T	16	41	c.805G>A	c.(805-807)GAA>AAA	p.E269K
Pat_66	Pre-Treatment	OCA2	4948	37	15	28273183	28273184	Missense_Mutation	DNP	GG	AA	81	94	c.348_349CC>TT	.(346-351)TACCAT>TATTA	p.H117Y
Pat_66	Pre-Treatment	RYR3	6263	37	15	33765692	33765692	Missense_Mutation	SNP	G	A	17	101	c.124G>A	c.(124-126)GGA>AGA	p.G42R
Pat_66	Pre-Treatment	RYR3	6263	37	15	33831613	33831613	Nonsense_Mutation	SNP	C	T	12	14	c.496C>T	c.(496-498)CGA>TGA	p.R166*
Pat_66	Pre-Treatment	RYR3	6263	37	15	34040343	34040343	Missense_Mutation	SNP	G	A	52	116	c.8018G>A	c.(8017-8019)CGA>CAA	p.R2673Q
Pat_66	Pre-Treatment	PLCB2	5330	37	15	40585831	40585831	Missense_Mutation	SNP	C	T	72	60	c.2156G>A	c.(2155-2157)CGA>CAA	p.R719Q
Pat_66	Pre-Treatment	ATP8B4	79895	37	15	50223388	50223388	Missense_Mutation	SNP	C	T	31	122	c.1570G>A	c.(1570-1572)GGA>AGA	p.G524R
Pat_66	Pre-Treatment	SCG3	29106	37	15	51984482	51984482	Missense_Mutation	SNP	G	A	57	86	c.817G>A	c.(817-819)GAA>AAA	p.E273K
Pat_66	Pre-Treatment	UNC13C	440279	37	15	54306599	54306599	Missense_Mutation	SNP	G	A	5	57	c.1499G>A	c.(1498-1500)AGA>AAA	p.R500K
Pat_66	Pre-Treatment	UNC13C	440279	37	15	54914563	54914563	Missense_Mutation	SNP	C	T	67	128	c.6145C>T	c.(6145-6147)CAT>TAT	p.H2049Y
Pat_66	Pre-Treatment	CGNL1	84952	37	15	57731680	57731680	Missense_Mutation	SNP	G	A	52	137	c.1483G>A	c.(1483-1485)GAG>AAG	p.E495K
Pat_66	Pre-Treatment	LACTB	114294	37	15	63419580	63419580	Missense_Mutation	SNP	C	T	86	70	c.644C>T	c.(643-645)TCC>TTC	p.S215F
Pat_66	Pre-Treatment	RBPMS2	348093	37	15	65040652	65040652	Missense_Mutation	SNP	G	A	4	111	c.533C>T	c.(532-534)ACT>ATT	p.T178I
Pat_66	Pre-Treatment	DPP8	54878	37	15	65739250	65739250	Missense_Mutation	SNP	G	A	139	135	c.2669C>T	c.(2668-2670)TCA>TTA	p.S890L
Pat_66	Pre-Treatment	SMAD6	4091	37	15	67073466	67073466	Nonsense_Mutation	SNP	C	T	15	27	c.1084C>T	c.(1084-1086)CAG>TAG	p.Q362*
Pat_66	Pre-Treatment	IQCH	64799	37	15	67664995	67664995	Missense_Mutation	SNP	G	A	29	256	c.1300G>A	c.(1300-1302)GCC>ACC	p.A434T
Pat_66	Pre-Treatment	IQCH	64799	37	15	67713830	67713830	Missense_Mutation	SNP	G	A	67	48	c.2420G>A	c.(2419-2421)GGA>GAA	p.G807E
Pat_66	Pre-Treatment	LBXCOR1	390598	37	15	68123158	68123158	Missense_Mutation	SNP	G	A	221	228	c.2386G>A	c.(2386-2388)GAA>AAA	p.E796K
Pat_66	Pre-Treatment	ITGA11	22801	37	15	68603395	68603395	Nonsense_Mutation	SNP	C	T	17	18	c.3111G>A	c.(3109-3111)TGG>TGA	p.W1037*
Pat_66	Pre-Treatment	LRRC49	54839	37	15	71300951	71300951	Missense_Mutation	SNP	C	T	12	32	c.1403C>T	c.(1402-1404)TCT>TTT	p.S468F
Pat_66	Pre-Treatment	CT62	196993	37	15	71403603	71403603	Missense_Mutation	SNP	C	T	34	62	c.298G>A	c.(298-300)GAA>AAA	p.E100K
Pat_66	Pre-Treatment	LMAN1L	79748	37	15	75114194	75114194	Missense_Mutation	SNP	C	T	43	115	c.1084C>T	c.(1084-1086)CCA>TCA	p.P362S
Pat_66	Pre-Treatment	LMAN1L	79748	37	15	75115013	75115013	Missense_Mutation	SNP	G	A	61	42	c.1162G>A	c.(1162-1164)GGA>AGA	p.G388R
Pat_66	Pre-Treatment	ADAMTS7	11173	37	15	79059783	79059783	Missense_Mutation	SNP	C	T	21	36	c.2797G>A	c.(2797-2799)GAA>AAA	p.E933K
Pat_66	Pre-Treatment	IL16	3603	37	15	81585092	81585092	Missense_Mutation	SNP	T	G	35	24	c.1616T>G	c.(1615-1617)ATC>AGC	p.I539S
Pat_66	Pre-Treatment	FSD2	123722	37	15	83431013	83431013	Missense_Mutation	SNP	C	T	13	71	c.1838G>A	c.(1837-1839)GGA>GAA	p.G613E
Pat_66	Pre-Treatment	BNC1	646	37	15	83926294	83926294	Missense_Mutation	SNP	C	T	39	114	c.2885G>A	c.(2884-2886)GGC>GAC	p.G962D
Pat_66	Pre-Treatment	BNC1	646	37	15	83933555	83933555	Nonsense_Mutation	SNP	T	A	29	88	c.448A>T	c.(448-450)AAG>TAG	p.K150*
Pat_66	Pre-Treatment	SH3GL3	6457	37	15	84241415	84241415	Nonsense_Mutation	SNP	C	T	5	57	c.430C>T	c.(430-432)CAG>TAG	p.Q144*

Pat_66	Pre-Treatment	NTRK3	4916	37	15	88420258	88420258	Missense_Mutation	SNP	C	T	52	99	c.2428G>A	c.(2428-2430)GAA>AAA	p.E810K
Pat_66	Pre-Treatment	MFGE8	4240	37	15	89453073	89453073	Missense_Mutation	SNP	G	A	115	110	c.155C>T	c.(154-156)TCG>TTG	p.S52L
Pat_66	Pre-Treatment	VPS33B	26276	37	15	91548939	91548939	Missense_Mutation	SNP	G	A	4	235	c.1015C>T	c.(1015-1017)CGC>TGC	p.R339C
Pat_66	Pre-Treatment	C16orf11	146325	37	16	615167	615167	Missense_Mutation	SNP	C	T	41	26	c.1576C>T	c.(1576-1578)CCA>TCA	p.P526S
Pat_66	Pre-Treatment	MSLNL	401827	37	16	830540	830540	Missense_Mutation	SNP	G	A	7	321	c.461C>T	c.(460-462)CCG>CTG	p.P154L
Pat_66	Pre-Treatment	CASKIN1	57524	37	16	2235338	2235339	Missense_Mutation	DNP	CC	TT	10	51	.1119_1120GG>A	117-1122)GAGGAG>GAA	p.E374K
Pat_66	Pre-Treatment	SRRM2	23524	37	16	2816986	2816986	Missense_Mutation	SNP	G	A	4	151	c.6457G>A	c.(6457-6459)GGC>AGC	p.G2153S
Pat_66	Pre-Treatment	CREBBP	1387	37	16	3860755	3860755	Missense_Mutation	SNP	G	A	53	18	c.824C>T	c.(823-825)CCA>CTA	p.P275L
Pat_66	Pre-Treatment	SEC14L5	9717	37	16	5040771	5040771	Missense_Mutation	SNP	C	T	25	56	c.349C>T	c.(349-351)CAC>TAC	p.H117Y
Pat_66	Pre-Treatment	GRIN2A	2903	37	16	9857682	9857682	Missense_Mutation	SNP	A	G	22	74	c.3719T>C	c.(3718-3720)CTG>CCG	p.L1240P
Pat_66	Pre-Treatment	GRIN2A	2903	37	16	9862737	9862737	Missense_Mutation	SNP	G	A	47	161	c.2566C>T	c.(2566-2568)CGG>TGG	p.R856W
Pat_66	Pre-Treatment	TEKT5	146279	37	16	10769907	10769907	Nonsense_Mutation	SNP	C	T	40	143	c.995G>A	c.(994-996)TGG>TAG	p.W332*
Pat_66	Pre-Treatment	FAM18A	780776	37	16	10867934	10867934	Missense_Mutation	SNP	C	T	14	23	c.286G>A	c.(286-288)GAA>AAA	p.E96K
Pat_66	Pre-Treatment	ABCC6P1	653190	37	16	18603920	18603920	Missense_Mutation	SNP	C	T	7	29	c.887C>T	c.(886-888)GCC>GTC	p.A296V
Pat_66	Pre-Treatment	SMG1	23049	37	16	18844335	18844335	Missense_Mutation	SNP	G	A	258	130	c.8719C>T	c.(8719-8721)CTT>TTT	p.L2907F
Pat_66	Pre-Treatment	TMC5	79838	37	16	19490792	19490792	Missense_Mutation	SNP	C	T	242	124	c.2209C>T	c.(2209-2211)CTT>TTT	p.L737F
Pat_66	Pre-Treatment	DNAH3	55567	37	16	20974776	20974776	Missense_Mutation	SNP	C	T	10	51	c.10430G>A	c.(10429-10431)CGA>CAA	p.R3477Q
Pat_66	Pre-Treatment	DNAH3	55567	37	16	20981309	20981309	Missense_Mutation	SNP	C	T	30	65	c.8263G>A	c.(8263-8265)GAA>AAA	p.E2755K
Pat_66	Pre-Treatment	DNAH3	55567	37	16	21042407	21042407	Nonsense_Mutation	SNP	C	T	21	64	c.5399G>A	c.(5398-5400)TGG>TAG	p.W1800*
Pat_66	Pre-Treatment	SLC5A11	115584	37	16	24902310	24902310	Missense_Mutation	SNP	G	A	81	192	c.785G>A	c.(784-786)CGA>CAA	p.R262Q
Pat_66	Pre-Treatment	HS3ST4	9951	37	16	26147561	26147561	Missense_Mutation	SNP	G	A	5	41	c.1363G>A	c.(1363-1365)GAT>AAT	p.D455N
Pat_66	Pre-Treatment	XPO6	23214	37	16	28187341	28187341	Missense_Mutation	SNP	G	A	18	67	c.283C>T	c.(283-285)CTT>TTT	p.L95F
Pat_66	Pre-Treatment	CLN3	1201	37	16	28493675	28493675	Missense_Mutation	SNP	G	A	17	27	c.935C>T	c.(934-936)TCC>TTC	p.S312F
Pat_66	Pre-Treatment	DOC2A	8448	37	16	30020384	30020384	Missense_Mutation	SNP	G	A	30	101	c.460C>T	c.(460-462)CCC>TCC	p.P154S
Pat_66	Pre-Treatment	ZNF764	92595	37	16	30567066	30567066	Missense_Mutation	SNP	G	A	3	19	c.676C>T	c.(676-678)CGT>TGT	p.R226C
Pat_66	Pre-Treatment	ZNF689	115509	37	16	30616361	30616361	Missense_Mutation	SNP	G	A	4	139	c.727C>T	c.(727-729)CGG>TGG	p.R243W
Pat_66	Pre-Treatment	SRCAP	10847	37	16	30736222	30736222	Missense_Mutation	SNP	C	T	95	49	c.5477C>T	c.(5476-5478)TCG>TTG	p.S1826L
Pat_66	Pre-Treatment	ZNF267	10308	37	16	31927522	31927522	Missense_Mutation	SNP	A	G	7	183	c.1952A>G	c.(1951-1953)CAG>CGG	p.Q651R
Pat_66	Pre-Treatment	ZNF267	10308	37	16	31927534	31927534	Missense_Mutation	SNP	C	G	8	202	c.1964C>G	c.(1963-1965)ACT>AGT	p.T655S
Pat_66	Pre-Treatment	ZNF267	10308	37	16	31927690	31927690	Missense_Mutation	SNP	G	A	6	154	c.2120G>A	c.(2119-2121)CGG>CAG	p.R707Q
Pat_66	Pre-Treatment	ZNF267	10308	37	16	31927702	31927702	Missense_Mutation	SNP	G	C	5	156	c.2132G>C	c.(2131-2133)AGT>ACT	p.S711T
Pat_66	Pre-Treatment	ABCC12	94160	37	16	48145507	48145507	Missense_Mutation	SNP	C	T	126	439	c.2191G>A	c.(2191-2193)GAA>AAA	p.E731K
Pat_66	Pre-Treatment	ABCC12	94160	37	16	48149436	48149436	Missense_Mutation	SNP	C	T	29	70	c.1879G>A	c.(1879-1881)GAC>AAC	p.D627N
Pat_66	Pre-Treatment	NOD2	64127	37	16	50750505	50750505	Missense_Mutation	SNP	G	A	11	39	c.2470G>A	c.(2470-2472)GAT>AAT	p.D824N
Pat_66	Pre-Treatment	MMP2	4313	37	16	55523700	55523700	Missense_Mutation	SNP	G	A	4	78	c.1144G>A	c.(1144-1146)GAT>AAT	p.D382N
Pat_66	Pre-Treatment	CES1	1066	37	16	55857517	55857517	Missense_Mutation	SNP	C	T	21	51	c.481G>A	c.(481-483)GAA>AAA	p.E161K
Pat_66	Pre-Treatment	NLRC5	84166	37	16	57113531	57113531	Missense_Mutation	SNP	G	A	64	131	c.5311G>A	c.(5311-5313)GAA>AAA	p.E1771K
Pat_66	Pre-Treatment	SLC9A5	6553	37	16	67292224	67292224	Nonsense_Mutation	SNP	G	A	13	37	c.1500G>A	c.(1498-1500)TGG>TGA	p.W500*
Pat_66	Pre-Treatment	WWP2	11060	37	16	69967937	69967937	Missense_Mutation	SNP	G	A	4	193	c.1747G>A	c.(1747-1749)GGA>AGA	p.G583R
Pat_66	Pre-Treatment	PDPR	55066	37	16	70163019	70163019	Missense_Mutation	SNP	C	A	5	234	c.601C>A	c.(601-603)CAA>AAA	p.Q201K
Pat_66	Pre-Treatment	ZFHX3	463	37	16	72833968	72833968	Nonsense_Mutation	SNP	G	A	28	106	c.3925C>T	c.(3925-3927)CGA>TGA	p.R1309*
Pat_66	Pre-Treatment	CLEC18B	497190	37	16	74446997	74446997	Missense_Mutation	SNP	G	A	34	25	c.614C>T	c.(613-615)TCG>TTG	p.S205L
Pat_66	Pre-Treatment	LDHD	197257	37	16	75148832	75148832	Missense_Mutation	SNP	C	T	25	97	c.362G>A	c.(361-363)CGA>CAA	p.R121Q
Pat_66	Pre-Treatment	ADAMTS18	170692	37	16	77327052	77327052	Missense_Mutation	SNP	G	A	31	114	c.3110C>T	c.(3109-3111)CCT>CTT	p.P1037L
Pat_66	Pre-Treatment	ADAMTS18	170692	37	16	77389970	77389970	Missense_Mutation	SNP	C	A	4	119	c.1327G>T	c.(1327-1329)GGT>TGT	p.G443C
Pat_66	Pre-Treatment	WWOX	51741	37	16	79245565	79245565	Missense_Mutation	SNP	G	A	74	40	c.1117G>A	c.(1117-1119)GGG>AGG	p.G373R
Pat_66	Pre-Treatment	CDYL2	124359	37	16	80638323	80638323	Missense_Mutation	SNP	G	T	72	49	c.1483C>A	c.(1483-1485)CTT>ATT	p.L495I

Pat_66	Pre-Treatment	JPH3	57338	37	16	87723781	87723782	Missense_Mutation	DNP	GG	AA	8	1	.1815_1816GG>A	313-1818)GAGGAG>GAA	p.E606K
Pat_66	Pre-Treatment	PITPNA	5306	37	17	1451670	1451670	Missense_Mutation	SNP	G	A	4	67	c.209C>T	c.(208-210)ACG>ATG	p.T70M
Pat_66	Pre-Treatment	USP6	9098	37	17	5041493	5041493	Missense_Mutation	SNP	G	A	78	98	c.1003G>A	c.(1003-1005)GAT>AAT	p.D335N
Pat_66	Pre-Treatment	USP6	9098	37	17	5073977	5073977	Missense_Mutation	SNP	G	A	42	12	c.3721G>A	c.(3721-3723)GAC>AAC	p.D1241N
Pat_66	Pre-Treatment	DLG4	1742	37	17	7095296	7095296	Missense_Mutation	SNP	G	A	51	8	c.2021C>T	c.(2020-2022)TCG>TTG	p.S674L
Pat_66	Pre-Treatment	DNAH2	146754	37	17	7690282	7690282	Missense_Mutation	SNP	G	A	42	60	c.6534G>A	c.(6532-6534)ATG>ATA	p.M2178I
Pat_66	Pre-Treatment	DNAH2	146754	37	17	7700533	7700533	Missense_Mutation	SNP	G	A	116	20	c.7903G>A	c.(7903-7905)GAT>AAT	p.D2635N
Pat_66	Pre-Treatment	KDM6B	23135	37	17	7749407	7749407	Missense_Mutation	SNP	C	T	31	2	c.248C>T	c.(247-249)CCA>CTA	p.P83L
Pat_66	Pre-Treatment	KDM6B	23135	37	17	7750454	7750454	Missense_Mutation	SNP	C	T	63	130	c.941C>T	c.(940-942)CCA>CTA	p.P314L
Pat_66	Pre-Treatment	CHD3	1107	37	17	7797155	7797155	Nonsense_Mutation	SNP	C	T	4	228	c.826C>T	c.(826-828)CGA>TGA	p.R276*
Pat_66	Pre-Treatment	ARHGEF15	22899	37	17	8215586	8215587	Missense_Mutation	DNP	CC	TT	111	120	c.229_230CC>TT	c.(229-231)CCC>TTC	p.P77F
Pat_66	Pre-Treatment	PIK3R6	146850	37	17	8726352	8726352	Missense_Mutation	SNP	C	T	89	18	c.1678G>A	c.(1678-1680)GAA>AAA	p.E560K
Pat_66	Pre-Treatment	MYH4	4622	37	17	10351274	10351274	Missense_Mutation	SNP	A	G	4	226	c.4826T>C	c.(4825-4827)ATC>ACC	p.I1609T
Pat_66	Pre-Treatment	MYH3	4621	37	17	10555756	10555756	Missense_Mutation	SNP	T	A	4	85	c.329A>T	c.(328-330)TAC>TTC	p.Y110F
Pat_66	Pre-Treatment	DNAH9	1770	37	17	11865266	11865266	Missense_Mutation	SNP	G	A	91	11	c.12926G>A	c.(12925-12927)CGA>CAA	p.R4309Q
Pat_66	Pre-Treatment	ZNF624	57547	37	17	16525645	16525645	Missense_Mutation	SNP	G	C	4	167	c.2555C>G	c.(2554-2556)ACT>AGT	p.T852S
Pat_66	Pre-Treatment	TNFRSF13B	23495	37	17	16852099	16852099	Missense_Mutation	SNP	G	A	4	172	c.398C>T	c.(397-399)TCG>TTG	p.S133L
Pat_66	Pre-Treatment	TMEM132E	124842	37	17	32953976	32953976	Missense_Mutation	SNP	G	A	77	8	c.628G>A	c.(628-630)GAC>AAC	p.D210N
Pat_66	Pre-Treatment	TMEM132E	124842	37	17	32956071	32956071	Missense_Mutation	SNP	G	A	108	21	c.916G>A	c.(916-918)GAA>AAA	p.E306K
Pat_66	Pre-Treatment	DDX52	11056	37	17	35990143	35990143	Missense_Mutation	SNP	G	A	37	51	c.664C>T	c.(664-666)CCT>TCT	p.P222S
Pat_66	Pre-Treatment	THRA	7067	37	17	38233835	38233835	Missense_Mutation	SNP	C	T	143	21	c.196C>T	c.(196-198)CGC>TGC	p.R66C
Pat_66	Pre-Treatment	KRT35	3886	37	17	39634732	39634732	Missense_Mutation	SNP	C	T	58	60	c.880G>A	c.(880-882)GAG>AAG	p.E294K
Pat_66	Pre-Treatment	KRT36	8689	37	17	39642662	39642662	Missense_Mutation	SNP	G	A	23	13	c.1370C>T	c.(1369-1371)TCC>TTC	p.S457F
Pat_66	Pre-Treatment	JUP	3728	37	17	39919495	39919495	Missense_Mutation	SNP	C	T	85	12	c.1237G>A	c.(1237-1239)GGC>AGC	p.G413S
Pat_66	Pre-Treatment	VAT1	10493	37	17	41168547	41168547	Missense_Mutation	SNP	G	A	3	36	c.875C>T	c.(874-876)ACG>ATG	p.T292M
Pat_66	Pre-Treatment	GPATCH8	23131	37	17	42478520	42478520	Missense_Mutation	SNP	G	A	119	145	c.925C>T	c.(925-927)CCT>TCT	p.P309S
Pat_66	Pre-Treatment	WNT9B	7484	37	17	44950091	44950091	Missense_Mutation	SNP	G	A	9	29	c.286G>A	c.(286-288)GAG>AAG	p.E96K
Pat_66	Pre-Treatment	ITGB3	3690	37	17	45377890	45377890	Missense_Mutation	SNP	G	A	19	38	c.1960G>A	c.(1960-1962)GAA>AAA	p.E654K
Pat_66	Pre-Treatment	SKAP1	8631	37	17	46248022	46248022	Splice_Site	SNP	C	T	60	95	c.827_splice	c.e10-1	p.D276_splice
Pat_66	Pre-Treatment	COL1A1	1277	37	17	48269226	48269226	Missense_Mutation	SNP	C	T	10	3	c.2050G>A	c.(2050-2052)GAG>AAG	p.E684K
Pat_66	Pre-Treatment	ABCC3	8714	37	17	48734461	48734462	Missense_Mutation	DNP	GG	AA	27	46	c.403_404GG>AA	c.(403-405)GGG>AAG	p.G135K
Pat_66	Pre-Treatment	ABCC3	8714	37	17	48753849	48753849	Missense_Mutation	SNP	C	T	79	99	c.3278C>T	c.(3277-3279)TCC>TTC	p.S1093F
Pat_66	Pre-Treatment	BPTF	2186	37	17	65940393	65940393	Missense_Mutation	SNP	C	A	5	150	c.6605C>A	c.(6604-6606)CCA>CAA	p.P2202Q
Pat_66	Pre-Treatment	ABCA9	10350	37	17	66980206	66980206	Missense_Mutation	SNP	C	T	55	63	c.4490G>A	c.(4489-4491)GGA>GAA	p.G1497E
Pat_66	Pre-Treatment	KIF19	124602	37	17	72338051	72338051	Missense_Mutation	SNP	G	A	136	20	c.157G>A	c.(157-159)GAC>AAC	p.D53N
Pat_66	Pre-Treatment	BTBD17	388419	37	17	72356148	72356148	Missense_Mutation	SNP	C	T	33	53	c.322G>A	c.(322-324)GAG>AAG	p.E108K
Pat_66	Pre-Treatment	BTBD17	388419	37	17	72356307	72356307	Missense_Mutation	SNP	C	T	10	10	c.163G>A	c.(163-165)GAG>AAG	p.E55K
Pat_66	Pre-Treatment	CD300LF	146722	37	17	72691330	72691330	Missense_Mutation	SNP	C	T	54	3	c.778G>A	c.(778-780)GAA>AAA	p.E260K
Pat_66	Pre-Treatment	C17orf28	283987	37	17	72959865	72959865	Nonsense_Mutation	SNP	C	T	5	3	c.357G>A	c.(355-357)TGG>TGA	p.W119*
Pat_66	Pre-Treatment	EVPL	2125	37	17	74006052	74006052	Missense_Mutation	SNP	C	G	152	22	c.3234G>C	c.(3232-3234)GAG>GAC	p.E1078D
Pat_66	Pre-Treatment	TNRC6C	57690	37	17	76045412	76045412	Missense_Mutation	SNP	C	T	34	26	c.269C>T	c.(268-270)TCC>TTC	p.S90F
Pat_66	Pre-Treatment	ENPP7	339221	37	17	77707317	77707317	Missense_Mutation	SNP	G	A	122	162	c.265G>A	c.(265-267)GAG>AAG	p.E89K
Pat_66	Pre-Treatment	ENPP7	339221	37	17	77709088	77709088	Missense_Mutation	SNP	G	A	17	20	c.646G>A	c.(646-648)GTG>ATG	p.V216M
Pat_66	Pre-Treatment	CCDC40	55036	37	17	78061471	78061471	Missense_Mutation	SNP	G	A	54	7	c.2515G>A	c.(2515-2517)GAC>AAC	p.D839N
Pat_66	Pre-Treatment	CARD14	79092	37	17	78162308	78162308	Missense_Mutation	SNP	G	A	58	6	c.808G>A	c.(808-810)GAG>AAG	p.E270K
Pat_66	Pre-Treatment	NPLOC4	55666	37	17	79536082	79536082	Missense_Mutation	SNP	G	A	72	7	c.1409C>T	c.(1408-1410)CCA>CTA	p.P470L
Pat_66	Pre-Treatment	CLUL1	27098	37	18	624944	624944	Missense_Mutation	SNP	C	T	20	58	c.335C>T	c.(334-336)TCC>TTC	p.S112F

Pat_66	Pre-Treatment	SMCHD1	23347	37	18	2688411	2688411	Missense_Mutation	SNP	C	T	33	112	c.658C>T	c.(658-660)CGT>TGT	p.R220C
Pat_66	Pre-Treatment	MYOM1	8736	37	18	3151719	3151719	Missense_Mutation	SNP	C	T	85	94	c.1816G>A	c.(1816-1818)GAT>AAT	p.D606N
Pat_66	Pre-Treatment	DLGAP1	9229	37	18	3879714	3879714	Missense_Mutation	SNP	G	A	41	95	c.355C>T	c.(355-357)CAC>TAC	p.H119Y
Pat_66	Pre-Treatment	LAMA1	284217	37	18	6956684	6956684	Missense_Mutation	SNP	G	A	64	34	c.8045C>T	c.(8044-8046)GCT>GTT	p.A2682V
Pat_66	Pre-Treatment	LRRC30	339291	37	18	7231617	7231617	Missense_Mutation	SNP	G	A	85	44	c.481G>A	c.(481-483)GAC>AAC	p.D161N
Pat_66	Pre-Treatment	POTEC	388468	37	18	14542991	14542991	Missense_Mutation	SNP	G	A	8	517	c.155C>T	c.(154-156)TCC>TTC	p.S52F
Pat_66	Pre-Treatment	LAMA3	3909	37	18	21438774	21438774	Missense_Mutation	SNP	C	T	94	201	c.4403C>T	c.(4402-4404)TCA>TTA	p.S1468L
Pat_66	Pre-Treatment	LAMA3	3909	37	18	21487860	21487860	Missense_Mutation	SNP	G	A	43	92	c.6976G>A	c.(6976-6978)GAA>AAA	p.E2326K
Pat_66	Pre-Treatment	LAMA3	3909	37	18	21519250	21519250	Missense_Mutation	SNP	C	T	103	285	c.8926C>T	c.(8926-8928)CCA>TCA	p.P2976S
Pat_66	Pre-Treatment	TTC39C	125488	37	18	21662896	21662896	Missense_Mutation	SNP	C	T	74	184	c.835C>T	c.(835-837)CAT>TAT	p.H279Y
Pat_66	Pre-Treatment	DSG1	1828	37	18	28908228	28908229	Missense_Mutation	DNP	GG	AA	40	94	c.293_294GG>AA	c.(292-294)GGG>GAA	p.G98E
Pat_66	Pre-Treatment	DSG1	1828	37	18	28914126	28914126	Missense_Mutation	SNP	G	A	28	87	c.966G>A	c.(964-966)ATG>ATA	p.M322I
Pat_66	Pre-Treatment	DSG4	147409	37	18	28968334	28968334	Missense_Mutation	SNP	G	A	30	57	c.221G>A	c.(220-222)CGA>CAA	p.R74Q
Pat_66	Pre-Treatment	DSG4	147409	37	18	28993511	28993511	Nonsense_Mutation	SNP	C	T	98	85	c.3076C>T	c.(3076-3078)CGA>TGA	p.R1026*
Pat_66	Pre-Treatment	MYO5B	4645	37	18	47432825	47432825	Missense_Mutation	SNP	G	A	76	56	c.2378C>T	c.(2377-2379)ACC>ATC	p.T793I
Pat_66	Pre-Treatment	DCC	1630	37	18	51013302	51013302	Missense_Mutation	SNP	G	A	56	173	c.3872G>A	c.(3871-3873)CGA>CAA	p.R1291Q
Pat_66	Pre-Treatment	TCF4	6925	37	18	52942936	52942936	Nonsense_Mutation	SNP	G	A	332	217	c.703C>T	c.(703-705)CAG>TAG	p.Q235*
Pat_66	Pre-Treatment	LMAN1	3998	37	18	57006123	57006123	Missense_Mutation	SNP	G	A	72	54	c.1018C>T	c.(1018-1020)CGT>TGT	p.R340C
Pat_66	Pre-Treatment	SERPINB3	6317	37	18	61322991	61322991	Missense_Mutation	SNP	G	A	57	120	c.1073C>T	c.(1072-1074)TCA>TTA	p.S358L
Pat_66	Pre-Treatment	SERPINB10	5273	37	18	61584708	61584708	Missense_Mutation	SNP	G	A	10	27	c.187G>A	c.(187-189)GAC>AAC	p.D63N
Pat_66	Pre-Treatment	SERPINB10	5273	37	18	61597359	61597359	Missense_Mutation	SNP	G	A	69	62	c.571G>A	c.(571-573)GGA>AGA	p.G191R
Pat_66	Pre-Treatment	DSEL	92126	37	18	65180770	65180770	Nonsense_Mutation	SNP	C	T	54	58	c.1106G>A	c.(1105-1107)TGG>TAG	p.W369*
Pat_66	Pre-Treatment	ELANE	1991	37	19	853306	853306	Missense_Mutation	SNP	C	T	12	25	c.269C>T	c.(268-270)TCG>TTG	p.S90L
Pat_66	Pre-Treatment	C19orf29	58509	37	19	3614531	3614531	Missense_Mutation	SNP	T	C	3	33	c.1219A>G	c.(1219-1221)AAG>GAG	p.K407E
Pat_66	Pre-Treatment	HDGFRP2	84717	37	19	4501303	4501303	Missense_Mutation	SNP	G	T	57	39	c.1890G>T	c.(1888-1890)AGG>AGT	p.R630S
Pat_66	Pre-Treatment	TMEM146	257062	37	19	5754206	5754206	Missense_Mutation	SNP	G	A	91	240	c.1228G>A	c.(1228-1230)GAA>AAA	p.E410K
Pat_66	Pre-Treatment	FUT5	2527	37	19	5867287	5867287	Missense_Mutation	SNP	C	T	22	43	c.450G>A	c.(448-450)ATG>ATA	p.M150I
Pat_66	Pre-Treatment	TUBB4	10382	37	19	6495665	6495665	Missense_Mutation	SNP	C	T	4	110	c.845G>A	c.(844-846)CGG>CAG	p.R282Q
Pat_66	Pre-Treatment	C3	718	37	19	6711077	6711077	Missense_Mutation	SNP	G	A	14	330	c.1400C>T	c.(1399-1401)CCC>CTC	p.P467L
Pat_66	Pre-Treatment	VAV1	7409	37	19	6853048	6853048	Missense_Mutation	SNP	C	T	27	93	c.2290C>T	c.(2290-2292)CCC>TCC	p.P764S
Pat_66	Pre-Treatment	MUC16	94025	37	19	9026235	9026235	Missense_Mutation	SNP	C	T	137	377	c.36751G>A	.(36751-36753)GGC>AG	p.G12251S
Pat_66	Pre-Treatment	MUC16	94025	37	19	9069882	9069882	Missense_Mutation	DNP	C	T	88	64	c.17564G>A	.(17563-17565)GGA>GA	p.G5855E
Pat_66	Pre-Treatment	MUC16	94025	37	19	9076395	9076395	Missense_Mutation	SNP	C	T	42	114	c.11051G>A	c.(11050-11052)AGC>AAC	p.S3684N
Pat_66	Pre-Treatment	MUC16	94025	37	19	9087904	9087904	Missense_Mutation	SNP	G	A	21	40	c.3911C>T	c.(3910-3912)TCA>TTA	p.S1304L
Pat_66	Pre-Treatment	OR7E24	26648	37	19	9362042	9362042	Missense_Mutation	SNP	G	A	24	67	c.323G>A	c.(322-324)AGA>AAA	p.R108K
Pat_66	Pre-Treatment	SMARCA4	6597	37	19	11135028	11135028	Missense_Mutation	SNP	G	A	4	121	c.2995G>A	c.(2995-2997)GAC>AAC	p.D999N
Pat_66	Pre-Treatment	PRKCSH	5589	37	19	11552081	11552081	Missense_Mutation	SNP	C	T	135	92	c.377C>T	c.(376-378)TCC>TTC	p.S126F
Pat_66	Pre-Treatment	ZNF440	126070	37	19	11942890	11942890	Missense_Mutation	SNP	G	A	5	173	c.899G>A	c.(898-900)CGT>CAT	p.R300H
Pat_66	Pre-Treatment	ZNF700	90592	37	19	12060746	12060747	Missense_Mutation	DNP	AG	GA	9	355	.1907_1908AG>G	c.(1906-1908)CAG>CGA	p.Q636R
Pat_66	Pre-Treatment	ZNF844	284391	37	19	12187307	12187307	Missense_Mutation	SNP	G	C	9	305	c.1372G>C	c.(1372-1374)GAT>CAT	p.D458H
Pat_66	Pre-Treatment	ZNF844	284391	37	19	12187334	12187334	Missense_Mutation	SNP	G	A	6	249	c.1399G>A	c.(1399-1401)GAA>AAA	p.E467K
Pat_66	Pre-Treatment	ZNF844	284391	37	19	12187394	12187394	Missense_Mutation	SNP	T	C	5	201	c.1459T>C	c.(1459-1461)TTT>CTT	p.F487L
Pat_66	Pre-Treatment	ZNF844	284391	37	19	12187502	12187502	Missense_Mutation	SNP	A	G	5	143	c.1567A>G	c.(1567-1569)AAA>GAA	p.K523E
Pat_66	Pre-Treatment	ZNF564	163050	37	19	12637723	12637723	Missense_Mutation	SNP	C	T	6	338	c.1199G>A	c.(1198-1200)AGA>AAA	p.R400K
Pat_66	Pre-Treatment	BEST2	54831	37	19	12866232	12866232	Missense_Mutation	SNP	C	T	34	85	c.676C>T	c.(676-678)CAC>TAC	p.H226Y
Pat_66	Pre-Treatment	MAST1	22983	37	19	12976158	12976158	Missense_Mutation	SNP	C	T	27	53	c.1667C>T	c.(1666-1668)CCC>CTC	p.P556L
Pat_66	Pre-Treatment	EMR3	84658	37	19	14774286	14774286	Missense_Mutation	SNP	C	T	33	110	c.143G>A	c.(142-144)GGA>GAA	p.G48E

Pat_66	Pre-Treatment	CYP4F22	126410	37	19	15648767	15648767	Nonsense_Mutation	SNP	C	T	40	103	c.634C>T	c.(634-636)CAG>TAG	p.Q212*
Pat_66	Pre-Treatment	OR10H4	126541	37	19	16060671	16060671	Missense_Mutation	SNP	C	T	88	202	c.854C>T	c.(853-855)CCC>CTC	p.P285L
Pat_66	Pre-Treatment	CALR3	125972	37	19	16593379	16593379	Missense_Mutation	SNP	G	A	29	84	c.800C>T	c.(799-801)CCA>CTA	p.P267L
Pat_66	Pre-Treatment	UNC13A	23025	37	19	17780476	17780476	Missense_Mutation	SNP	C	T	6	14	c.544G>A	c.(544-546)GGA>AGA	p.G182R
Pat_66	Pre-Treatment	PDE4C	5143	37	19	18330058	18330058	Missense_Mutation	SNP	C	T	22	54	c.952G>A	c.(952-954)GAG>AAG	p.E318K
Pat_66	Pre-Treatment	SFRS14	10147	37	19	19105258	19105258	Missense_Mutation	SNP	C	T	5	361	c.3166G>A	c.(3166-3168)GGG>AGG	p.G1056R
Pat_66	Pre-Treatment	SFRS14	10147	37	19	19115132	19115132	Missense_Mutation	SNP	G	A	7	8	c.2774C>T	c.(2773-2775)CCC>CTC	p.P925L
Pat_66	Pre-Treatment	GATAD2A	54815	37	19	19603483	19603483	Missense_Mutation	SNP	C	T	4	153	c.496C>T	c.(496-498)CGG>TGG	p.R166W
Pat_66	Pre-Treatment	ZNF93	81931	37	19	20045187	20045187	Missense_Mutation	SNP	C	T	67	231	c.1423C>T	c.(1423-1425)CAT>TAT	p.H475Y
Pat_66	Pre-Treatment	ZNF737	100129842	37	19	20727684	20727684	Missense_Mutation	SNP	G	C	4	193	c.1325C>G	c.(1324-1326)ACA>AGA	p.T442R
Pat_66	Pre-Treatment	ZNF208	7757	37	19	22154249	22154249	Missense_Mutation	SNP	A	G	7	194	c.3203T>C	c.(3202-3204)CTC>CCC	p.L1068P
Pat_66	Pre-Treatment	ZNF208	7757	37	19	22155282	22155282	Missense_Mutation	SNP	T	C	9	185	c.2254A>G	c.(2254-2256)AAG>GAG	p.K752E
Pat_66	Pre-Treatment	ZNF208	7757	37	19	22156484	22156484	Missense_Mutation	SNP	G	T	6	304	c.1352C>A	c.(1351-1353)ACA>AAA	p.T451K
Pat_66	Pre-Treatment	ZNF208	7757	37	19	22156652	22156652	Missense_Mutation	SNP	T	G	5	244	c.1184A>C	c.(1183-1185)AAA>ACA	p.K395T
Pat_66	Pre-Treatment	ZNF257	113835	37	19	22271685	22271685	Missense_Mutation	SNP	G	A	16	85	c.1133G>A	c.(1132-1134)GGA>GAA	p.G378E
Pat_66	Pre-Treatment	ZNF676	163223	37	19	22363812	22363812	Missense_Mutation	SNP	C	T	84	333	c.707G>A	c.(706-708)CGA>CAA	p.R236Q
Pat_66	Pre-Treatment	ZNF99	7652	37	19	22940128	22940128	Nonsense_Mutation	SNP	T	A	76	128	c.2203A>T	c.(2203-2205)AAA>TAA	p.K735*
Pat_66	Pre-Treatment	ZNF99	7652	37	19	22941833	22941833	Missense_Mutation	SNP	G	T	43	109	c.605C>A	c.(604-606)GCT>GAT	p.A202D
Pat_66	Pre-Treatment	ZNF91	7644	37	19	23545434	23545434	Missense_Mutation	SNP	C	A	4	152	c.347G>T	c.(346-348)GGA>GTA	p.G116V
Pat_66	Pre-Treatment	ZNF675	171392	37	19	23836350	23836350	Missense_Mutation	SNP	A	C	4	148	c.1385T>G	c.(1384-1386)ATC>AGC	p.I462S
Pat_66	Pre-Treatment	ZNF681	148213	37	19	23926859	23926859	Missense_Mutation	SNP	C	T	187	128	c.1493G>A	c.(1492-1494)AGA>AAA	p.R498K
Pat_66	Pre-Treatment	RPSAP58	388524	37	19	24010418	24010418	Missense_Mutation	SNP	C	T	36	56	c.455C>T	c.(454-456)TCT>TTT	p.S152F
Pat_66	Pre-Treatment	ZNF536	9745	37	19	30935574	30935574	Missense_Mutation	SNP	G	A	56	155	c.1105G>A	c.(1105-1107)GAC>AAC	p.D369N
Pat_66	Pre-Treatment	ZNF30	90075	37	19	35435302	35435302	Missense_Mutation	SNP	C	A	4	78	c.1432C>A	c.(1432-1434)CAT>AAT	p.H478N
Pat_66	Pre-Treatment	SCN1B	6324	37	19	35524553	35524553	Missense_Mutation	SNP	G	A	83	166	c.358G>A	c.(358-360)GAG>AAG	p.E120K
Pat_66	Pre-Treatment	ZNF570	148268	37	19	37966904	37966904	Missense_Mutation	SNP	C	T	20	50	c.155C>T	c.(154-156)TCA>TTA	p.S52L
Pat_66	Pre-Treatment	SIPA1L3	23094	37	19	38610020	38610020	Missense_Mutation	SNP	C	T	166	93	c.2366C>T	c.(2365-2367)TCC>TTC	p.S789F
Pat_66	Pre-Treatment	ACTN4	81	37	19	39217717	39217717	Missense_Mutation	SNP	C	T	68	56	c.2311C>T	c.(2311-2313)CGG>TGG	p.R771W
Pat_66	Pre-Treatment	RINL	126432	37	19	39360246	39360247	Missense_Mutation	DNP	CC	TT	42	50	.1098_1099GG>A	096-1101)ATGGAG>ATAA	.366_367ME>I
Pat_66	Pre-Treatment	PSMC4	5704	37	19	40485793	40485793	Missense_Mutation	SNP	G	A	5	220	c.743G>A	c.(742-744)CGG>CAG	p.R248Q
Pat_66	Pre-Treatment	ZNF780B	163131	37	19	40541904	40541904	Missense_Mutation	SNP	G	A	47	182	c.862C>T	c.(862-864)CGT>TGT	p.R288C
Pat_66	Pre-Treatment	SERTAD3	29946	37	19	40947752	40947753	Missense_Mutation	DNP	GG	AA	17	0	c.235_236CC>TT	c.(235-237)CCC>TTC	p.P79F
Pat_66	Pre-Treatment	LTBP4	8425	37	19	41114441	41114441	Missense_Mutation	SNP	C	T	11	1	c.1559C>T	c.(1558-1560)CCC>CTC	p.P520L
Pat_66	Pre-Treatment	AXL	558	37	19	41743919	41743919	Missense_Mutation	SNP	C	T	57	102	c.854C>T	c.(853-855)TCG>TTG	p.S285L
Pat_66	Pre-Treatment	CEACAM5	1048	37	19	42213826	42213826	Nonsense_Mutation	SNP	C	T	138	240	c.292C>T	c.(292-294)CGA>TGA	p.R98*
Pat_66	Pre-Treatment	ARHGEF1	9138	37	19	42410699	42410699	Missense_Mutation	SNP	C	T	25	4	c.2582C>T	c.(2581-2583)CCC>CTC	p.P861L
Pat_66	Pre-Treatment	PSG8	440533	37	19	43268118	43268118	Missense_Mutation	SNP	C	T	17	358	c.380G>A	c.(379-381)GGA>GAA	p.G127E
Pat_66	Pre-Treatment	PSG8	440533	37	19	43268263	43268264	Missense_Mutation	DNP	TG	CA	7	272	c.234_235CA>TG	(232-237)TACATT>TATGT	p.I79V
Pat_66	Pre-Treatment	ZNF221	7638	37	19	44470916	44470916	Missense_Mutation	SNP	C	T	38	64	c.1262C>T	c.(1261-1263)TCC>TTC	p.S421F
Pat_66	Pre-Treatment	CEACAM20	125931	37	19	45026779	45026779	Missense_Mutation	SNP	G	A	47	5	c.635C>T	c.(634-636)ACG>ATG	p.T212M
Pat_66	Pre-Treatment	CEACAM16	388551	37	19	45211412	45211412	Missense_Mutation	SNP	C	T	3	28	c.1220C>T	c.(1219-1221)ACA>ATA	p.T407I
Pat_66	Pre-Treatment	SFRS16	11129	37	19	45570779	45570779	Missense_Mutation	SNP	C	T	22	0	c.1594C>T	c.(1594-1596)CCC>TCC	p.P532S
Pat_66	Pre-Treatment	CKM	1158	37	19	45811702	45811702	Missense_Mutation	SNP	C	T	29	46	c.742G>A	c.(742-744)GAG>AAG	p.E248K
Pat_66	Pre-Treatment	FBXO46	23403	37	19	46216507	46216507	Nonsense_Mutation	SNP	G	A	31	37	c.247C>T	c.(247-249)CGA>TGA	p.R83*
Pat_66	Pre-Treatment	NOVA2	4858	37	19	46443167	46443167	Missense_Mutation	SNP	G	A	5	63	c.1433C>T	c.(1432-1434)ACC>ATC	p.T478I
Pat_66	Pre-Treatment	ZC3H4	23211	37	19	47570496	47570496	Missense_Mutation	SNP	G	A	21	19	c.3029C>T	c.(3028-3030)CCC>CTC	p.P1010L
Pat_66	Pre-Treatment	RUVBL2	10856	37	19	49518890	49518890	Missense_Mutation	SNP	G	A	4	139	c.1313G>A	c.(1312-1314)CGC>CAC	p.R438H

Pat_66	Pre-Treatment	TEAD2	8463	37	19	49862699	49862699	Missense_Mutation	SNP	C	T	6	341	c.290G>A	c.(289-291)CGA>CAA	p.R97Q
Pat_66	Pre-Treatment	SIGLEC9	27180	37	19	51628484	51628484	Missense_Mutation	SNP	G	A	63	125	c.253G>A	c.(253-255)GAG>AAG	p.E85K
Pat_66	Pre-Treatment	ZNF841	284371	37	19	52569533	52569533	Missense_Mutation	SNP	A	C	4	89	c.1254T>G	c.(1252-1254)ATT>ATG	p.I418M
Pat_66	Pre-Treatment	ZNF28	7576	37	19	53302984	53302985	Missense_Mutation	DNP	TT	GA	8	363	.2113_2114AA>T	c.(2113-2115)AAC>TCC	p.N705S
Pat_66	Pre-Treatment	ZNF816A	125893	37	19	53453890	53453890	Missense_Mutation	SNP	G	C	10	401	c.1138C>G	c.(1138-1140)CAG>GAG	p.Q380E
Pat_66	Pre-Treatment	ZNF845	91664	37	19	53855197	53855197	Missense_Mutation	SNP	G	A	10	283	c.1269G>A	c.(1267-1269)ATG>ATA	p.M423I
Pat_66	Pre-Treatment	ZNF845	91664	37	19	53855364	53855364	Missense_Mutation	SNP	C	T	12	265	c.1436C>T	c.(1435-1437)ACA>ATA	p.T479I
Pat_66	Pre-Treatment	ZNF761	388561	37	19	53958983	53958983	Missense_Mutation	SNP	A	C	5	342	c.1222A>C	c.(1222-1224)AAA>CAA	p.K408Q
Pat_66	Pre-Treatment	ZNF331	55422	37	19	54074897	54074897	Nonsense_Mutation	SNP	C	T	155	235	c.49C>T	c.(49-51)CAG>TAG	p.Q17*
Pat_66	Pre-Treatment	NLRP12	91662	37	19	54314371	54314371	Missense_Mutation	SNP	C	T	30	44	c.542G>A	c.(541-543)CGG>CAG	p.R181Q
Pat_66	Pre-Treatment	MYADM	91663	37	19	54376901	54376901	Missense_Mutation	SNP	C	T	13	11	c.118C>T	c.(118-120)CGC>TGC	p.R40C
Pat_66	Pre-Treatment	CNOT3	4849	37	19	54651962	54651962	Missense_Mutation	SNP	C	T	15	12	c.974C>T	c.(973-975)TCC>TTC	p.S325F
Pat_66	Pre-Treatment	LILRA2	11027	37	19	55086452	55086452	Missense_Mutation	SNP	C	T	55	103	c.607C>T	c.(607-609)CCC>TCC	p.P203S
Pat_66	Pre-Treatment	LILRA1	11024	37	19	55106402	55106402	Missense_Mutation	SNP	G	A	26	40	c.343G>A	c.(343-345)GAG>AAG	p.E115K
Pat_66	Pre-Treatment	NCR1	9437	37	19	55417580	55417580	Splice_Site	SNP	G	A	4	166	c.34_splice	c.e1+1	p.G12_splice
Pat_66	Pre-Treatment	NLRP13	126204	37	19	56423340	56423340	Missense_Mutation	SNP	C	T	17	23	c.1843G>A	c.(1843-1845)GAA>AAA	p.E615K
Pat_66	Pre-Treatment	ZNF582	147948	37	19	56896125	56896125	Missense_Mutation	SNP	G	A	25	46	c.661C>T	c.(661-663)CAT>TAT	p.H221Y
Pat_66	Pre-Treatment	PEG3	5178	37	19	57325629	57325629	Missense_Mutation	SNP	G	A	51	50	c.4181C>T	c.(4180-4182)GCT>GTT	p.A1394V
Pat_66	Pre-Treatment	USP29	57663	37	19	57642078	57642078	Missense_Mutation	SNP	G	A	12	35	c.2035G>A	c.(2035-2037)GAG>AAG	p.E679K
Pat_66	Pre-Treatment	ZNF419	79744	37	19	58005274	58005274	Missense_Mutation	SNP	T	C	4	184	c.1349T>C	c.(1348-1350)ATT>ACT	p.I450T
Pat_66	Pre-Treatment	ZNF419	79744	37	19	58005314	58005314	Missense_Mutation	SNP	G	C	4	212	c.1389G>C	c.(1387-1389)TTG>TTC	p.L463F
Pat_66	Pre-Treatment	ZNF671	79891	37	19	58231944	58231944	Missense_Mutation	SNP	C	T	4	209	c.1510G>A	c.(1510-1512)GAA>AAA	p.E504K
Pat_66	Pre-Treatment	ZNF552	79818	37	19	58319596	58319596	Missense_Mutation	SNP	G	A	130	18	c.1036C>T	c.(1036-1038)CAC>TAC	p.H346Y
Pat_66	Pre-Treatment	TPO	7173	37	2	1459902	1459902	Missense_Mutation	SNP	G	A	32	18	c.667G>A	c.(667-669)GAT>AAT	p.D223N
Pat_66	Pre-Treatment	ALLC	55821	37	2	3727551	3727551	Nonsense_Mutation	SNP	C	T	24	86	c.265C>T	c.(265-267)CGA>TGA	p.R89*
Pat_66	Pre-Treatment	ALLC	55821	37	2	3730661	3730661	Missense_Mutation	SNP	C	T	121	343	c.508C>T	c.(508-510)CCA>TCA	p.P170S
Pat_66	Pre-Treatment	HPCAL1	3241	37	2	10560110	10560110	Missense_Mutation	SNP	G	A	89	62	c.227G>A	c.(226-228)GGC>GAC	p.G76D
Pat_66	Pre-Treatment	NT5C1B	93034	37	2	18758038	18758038	Splice_Site	SNP	C	T	36	133	c.1324_splice	c.e8+1	p.G442_splice
Pat_66	Pre-Treatment	APOB	338	37	2	21233256	21233256	Missense_Mutation	SNP	C	T	11	40	c.6484G>A	c.(6484-6486)GAT>AAT	p.D2162N
Pat_66	Pre-Treatment	OTOF	9381	37	2	26703859	26703859	Missense_Mutation	SNP	C	T	11	52	c.1598G>A	c.(1597-1599)GGC>GAC	p.G533D
Pat_66	Pre-Treatment	SLC4A1AP	22950	37	2	27900650	27900650	Nonsense_Mutation	SNP	C	A	4	132	c.1622C>A	c.(1621-1623)TCA>TAA	p.S541*
Pat_66	Pre-Treatment	C2orf71	388939	37	2	29296383	29296383	Missense_Mutation	SNP	C	T	84	63	c.745G>A	c.(745-747)GAG>AAG	p.E249K
Pat_66	Pre-Treatment	CAPN13	92291	37	2	30961151	30961151	Missense_Mutation	SNP	C	T	11	43	c.1603G>A	c.(1603-1605)GGG>AGG	p.G535R
Pat_66	Pre-Treatment	XDH	7498	37	2	31589745	31589745	Missense_Mutation	SNP	C	T	68	182	c.2313G>A	c.(2311-2313)ATG>ATA	p.M771I
Pat_66	Pre-Treatment	XDH	7498	37	2	31625943	31625944	Missense_Mutation	DNP	GG	AA	79	251	c.167_168CC>TT	c.(166-168)TCC>TTT	p.S56F
Pat_66	Pre-Treatment	MEMO1	51072	37	2	32145948	32145948	Missense_Mutation	SNP	G	A	90	66	c.244C>T	c.(244-246)CAT>TAT	p.H82Y
Pat_66	Pre-Treatment	SLC30A6	55676	37	2	32445559	32445559	Missense_Mutation	SNP	C	T	100	91	c.1163C>T	c.(1162-1164)TCA>TTA	p.S388L
Pat_66	Pre-Treatment	NRXN1	9378	37	2	50779970	50779970	Missense_Mutation	SNP	G	A	21	38	c.1634C>T	c.(1633-1635)TCA>TTA	p.S545L
Pat_66	Pre-Treatment	BCL11A	53335	37	2	60688543	60688543	Missense_Mutation	SNP	C	T	19	8	c.1504G>A	c.(1504-1506)GAG>AAG	p.E502K
Pat_66	Pre-Treatment	SLC1A4	6509	37	2	65228592	65228592	Missense_Mutation	SNP	C	T	40	133	c.538C>T	c.(538-540)CCC>TCC	p.P180S
Pat_66	Pre-Treatment	ETAA1	54465	37	2	67630832	67630832	Missense_Mutation	SNP	C	T	31	83	c.1018C>T	c.(1018-1020)CCA>TCA	p.P340S
Pat_66	Pre-Treatment	GKN1	56287	37	2	69207927	69207927	Missense_Mutation	SNP	C	T	26	49	c.572C>T	c.(571-573)TCC>TTC	p.S191F
Pat_66	Pre-Treatment	ADD2	119	37	2	70906086	70906086	Missense_Mutation	SNP	C	T	53	79	c.1133G>A	c.(1132-1134)AGA>AAA	p.R378K
Pat_66	Pre-Treatment	ACTG2	72	37	2	74136218	74136218	Missense_Mutation	SNP	G	A	5	302	c.403G>A	c.(403-405)GTC>ATC	p.V135I
Pat_66	Pre-Treatment	DQX1	165545	37	2	74746263	74746263	Missense_Mutation	SNP	C	T	36	72	c.1901G>A	c.(1900-1902)AGA>AAA	p.R634K
Pat_66	Pre-Treatment	DQX1	165545	37	2	74746696	74746696	Missense_Mutation	SNP	C	T	74	185	c.1793G>A	c.(1792-1794)GGA>GAA	p.G598E
Pat_66	Pre-Treatment	CTNNA2	1496	37	2	80782922	80782922	Nonsense_Mutation	SNP	C	T	44	134	c.1645C>T	c.(1645-1647)CGA>TGA	p.R549*

Pat_66	Pre-Treatment	ST3GAL5	8869	37	2	86074997	86074997	Missense_Mutation	SNP	C	T	113	76	c.649G>A	c.(649-651)GAT>AAT	p.D217N
Pat_66	Pre-Treatment	KRCC1	51315	37	2	88327934	88327934	Missense_Mutation	SNP	A	G	21	44	c.149T>C	c.(148-150)GTT>GCT	p.V50A
Pat_66	Pre-Treatment	EIF2AK3	9451	37	2	88874650	88874650	Missense_Mutation	SNP	G	A	146	368	c.2351C>T	c.(2350-2352)TCC>TTC	p.S784F
Pat_66	Pre-Treatment	ZNF514	84874	37	2	95815412	95815412	Missense_Mutation	SNP	G	A	87	41	c.818C>T	c.(817-819)TCG>TTG	p.S273L
Pat_66	Pre-Treatment	NMS	129521	37	2	101086963	101086963	Missense_Mutation	SNP	C	T	76	199	c.13C>T	c.(13-15)CGT>TGT	p.R5C
Pat_66	Pre-Treatment	IL18R1	8809	37	2	102979152	102979152	Missense_Mutation	SNP	G	T	5	266	c.32G>T	c.(31-33)TGG>TTG	p.W11L
Pat_66	Pre-Treatment	IL18R1	8809	37	2	103003322	103003322	Missense_Mutation	SNP	A	T	22	59	c.811A>T	c.(811-813)ACT>TCT	p.T271S
Pat_66	Pre-Treatment	IL18R1	8809	37	2	103011009	103011009	Missense_Mutation	SNP	G	A	33	73	c.1192G>A	c.(1192-1194)GAG>AAG	p.E398K
Pat_66	Pre-Treatment	RGPD4	285190	37	2	108455395	108455395	Missense_Mutation	SNP	G	A	118	302	c.380G>A	c.(379-381)GGA>GAA	p.G127E
Pat_66	Pre-Treatment	RGPD4	285190	37	2	108475865	108475865	Missense_Mutation	SNP	C	T	31	209	c.1489C>T	c.(1489-1491)CAC>TAC	p.H497Y
Pat_66	Pre-Treatment	SULT1C2	6819	37	2	108910209	108910210	Nonsense_Mutation	DNP	GG	AA	55	44	c.86_87GG>AA	c.(85-87)TGG>TAA	p.W29*
Pat_66	Pre-Treatment	RANBP2	5903	37	2	109382649	109382649	Missense_Mutation	SNP	C	T	48	158	c.5654C>T	c.(5653-5655)ACC>ATC	p.T1885I
Pat_66	Pre-Treatment	IL1B	3553	37	2	113591100	113591100	Missense_Mutation	SNP	C	T	48	149	c.152G>A	c.(151-153)CGA>CAA	p.R51Q
Pat_66	Pre-Treatment	MARCO	8685	37	2	119732096	119732096	Splice_Site	SNP	G	A	17	29	c.569_splice	c.e6-1	p.G190_splice
Pat_66	Pre-Treatment	GLI2	2736	37	2	121740454	121740454	Missense_Mutation	SNP	G	A	61	149	c.1681G>A	c.(1681-1683)GAG>AAG	p.E561K
Pat_66	Pre-Treatment	GLI2	2736	37	2	121743896	121743896	Missense_Mutation	SNP	G	A	57	34	c.1999G>A	c.(1999-2001)GAG>AAG	p.E667K
Pat_66	Pre-Treatment	BIN1	274	37	2	127808489	127808489	Splice_Site	SNP	C	T	28	81	c.1462_splice	c.e17-1	p.S488_splice
Pat_66	Pre-Treatment	ERCC3	2071	37	2	128015227	128015227	Missense_Mutation	SNP	C	T	41	103	c.2294G>A	c.(2293-2295)CGG>CAG	p.R765Q
Pat_66	Pre-Treatment	POTEF	728378	37	2	130877816	130877816	Missense_Mutation	SNP	C	T	95	336	c.273G>A	c.(271-273)ATG>ATA	p.M91I
Pat_66	Pre-Treatment	LOC150786	150786	37	2	132120554	132120554	Missense_Mutation	SNP	G	A	32	117	c.740C>T	c.(739-741)TCA>TTA	p.S247L
Pat_66	Pre-Treatment	LCT	3938	37	2	136561509	136561509	Missense_Mutation	SNP	C	T	10	23	c.4654G>A	c.(4654-4656)GCA>ACA	p.A1552T
Pat_66	Pre-Treatment	THSD7B	80731	37	2	137814013	137814013	Missense_Mutation	SNP	G	A	17	62	c.70G>A	c.(70-72)GAC>AAC	p.D24N
Pat_66	Pre-Treatment	LRP1B	53353	37	2	140992454	140992454	Splice_Site	SNP	C	T	29	17	c.13561_splice	c.e90-1	p.A4521_splice
Pat_66	Pre-Treatment	ZEB2	9839	37	2	145157783	145157783	Missense_Mutation	SNP	G	A	49	34	c.971C>T	c.(970-972)TCC>TTC	p.S324F
Pat_66	Pre-Treatment	KIF5C	3800	37	2	149793849	149793849	Missense_Mutation	SNP	G	A	9	18	c.343G>A	c.(343-345)GAT>AAT	p.D115N
Pat_66	Pre-Treatment	NEB	4703	37	2	152404848	152404848	Missense_Mutation	SNP	G	A	4	163	c.15028C>T	c.(15028-15030)CGG>TGG	p.R5010W
Pat_66	Pre-Treatment	GALNT13	114805	37	2	155102466	155102466	Missense_Mutation	SNP	G	C	69	41	c.828G>C	c.(826-828)AGG>AGC	p.R276S
Pat_66	Pre-Treatment	GALNT5	11227	37	2	158114925	158114925	Missense_Mutation	SNP	G	A	89	70	c.331G>A	c.(331-333)GAA>AAA	p.E111K
Pat_66	Pre-Treatment	CYTIP	9595	37	2	158272265	158272265	Missense_Mutation	SNP	C	T	23	83	c.1004G>A	c.(1003-1005)GGA>GAA	p.G335E
Pat_66	Pre-Treatment	LY75	4065	37	2	160671981	160671981	Missense_Mutation	SNP	C	T	24	42	c.4484G>A	c.(4483-4485)GGA>GAA	p.G1495E
Pat_66	Pre-Treatment	LY75	4065	37	2	160732154	160732154	Missense_Mutation	SNP	G	A	118	83	c.1775C>T	c.(1774-1776)GCT>GTT	p.A592V
Pat_66	Pre-Treatment	FIGN	55137	37	2	164467030	164467030	Missense_Mutation	SNP	G	A	38	107	c.1312C>T	c.(1312-1314)CTC>TTC	p.L438F
Pat_66	Pre-Treatment	FIGN	55137	37	2	164467113	164467113	Missense_Mutation	SNP	G	A	35	73	c.1229C>T	c.(1228-1230)TCA>TTA	p.S410L
Pat_66	Pre-Treatment	SLC38A11	151258	37	2	165809258	165809258	Missense_Mutation	SNP	G	A	30	73	c.20C>T	c.(19-21)CCT>CTT	p.P7L
Pat_66	Pre-Treatment	SCN3A	6328	37	2	165997486	165997486	Missense_Mutation	SNP	G	A	21	60	c.1694C>T	c.(1693-1695)TCC>TTC	p.S565F
Pat_66	Pre-Treatment	SCN2A	6326	37	2	166243485	166243485	Nonsense_Mutation	SNP	G	A	94	58	c.4781G>A	c.(4780-4782)TGG>TAG	p.W1594*
Pat_66	Pre-Treatment	SCN1A	6323	37	2	166892893	166892893	Missense_Mutation	SNP	C	T	18	26	c.3061G>A	c.(3061-3063)GAA>AAA	p.E1021K
Pat_66	Pre-Treatment	SCN1A	6323	37	2	166900267	166900267	Missense_Mutation	SNP	G	A	43	138	c.1955C>T	c.(1954-1956)TCC>TTC	p.S652F
Pat_66	Pre-Treatment	XIRP2	129446	37	2	168103996	168103996	Missense_Mutation	SNP	C	T	24	61	c.6094C>T	c.(6094-6096)CGT>TGT	p.R2032C
Pat_66	Pre-Treatment	XIRP2	129446	37	2	168104704	168104704	Missense_Mutation	SNP	G	A	21	61	c.6802G>A	c.(6802-6804)GAA>AAA	p.E2268K
Pat_66	Pre-Treatment	LRP2	4036	37	2	170048385	170048385	Missense_Mutation	SNP	C	T	38	103	c.8989G>A	c.(8989-8991)GAA>AAA	p.E2997K
Pat_66	Pre-Treatment	LRP2	4036	37	2	170139487	170139487	Missense_Mutation	SNP	C	T	140	104	c.1067G>A	c.(1066-1068)GGA>GAA	p.G356E
Pat_66	Pre-Treatment	KLHL23	151230	37	2	170606024	170606024	Missense_Mutation	SNP	G	A	24	81	c.1459G>A	c.(1459-1461)GAA>AAA	p.E487K
Pat_66	Pre-Treatment	HOXD8	3234	37	2	176996223	176996223	Nonsense_Mutation	SNP	G	A	93	239	c.756G>A	c.(754-756)TGG>TGA	p.W252*
Pat_66	Pre-Treatment	PDE11A	50940	37	2	178682595	178682595	Missense_Mutation	SNP	C	T	22	56	c.1634G>A	c.(1633-1635)CGA>CAA	p.R545Q
Pat_66	Pre-Treatment	OSBPL6	114880	37	2	179255827	179255827	Missense_Mutation	SNP	G	A	44	116	c.2329G>A	c.(2329-2331)GAA>AAA	p.E777K
Pat_66	Pre-Treatment	TTN	7273	37	2	179406231	179406231	Missense_Mutation	SNP	C	T	13	28	c.89869G>A	c.(89869-89871)GAT>AAT	p.D29957N

Pat_66	Pre-Treatment	TTN	7273	37	2	179419273	179419273	Missense_Mutation	SNP	C	T	27	50	c.81097G>A	c.(81097-81099)GGA>AGA	p.G27033R
Pat_66	Pre-Treatment	TTN	7273	37	2	179425040	179425040	Missense_Mutation	SNP	C	T	52	31	c.78115G>A	c.(78115-78117)GAT>AAT	p.D26039N
Pat_66	Pre-Treatment	TTN	7273	37	2	179435849	179435849	Missense_Mutation	SNP	G	A	99	59	c.67306C>T	c.(67306-67308)CGT>TGT	p.R22436C
Pat_66	Pre-Treatment	TTN	7273	37	2	179439721	179439721	Missense_Mutation	SNP	C	T	14	45	c.63434G>A	c.(63433-63435)GGA>GAA	p.G21145E
Pat_66	Pre-Treatment	TTN	7273	37	2	179444905	179444905	Missense_Mutation	SNP	G	A	43	14	c.59405C>T	c.(59404-59406)TCT>TTT	p.S19802F
Pat_66	Pre-Treatment	TTN	7273	37	2	179446868	179446868	Nonsense_Mutation	SNP	C	T	37	97	c.58524G>A	c.(58522-58524)TGG>TGA	p.W19508*
Pat_66	Pre-Treatment	TTN	7273	37	2	179464532	179464532	Missense_Mutation	SNP	C	T	40	40	c.48392G>A	c.(48391-48393)GGA>GAA	p.G16131E
Pat_66	Pre-Treatment	TTN	7273	37	2	179470324	179470324	Missense_Mutation	SNP	C	T	57	177	c.45994G>A	c.(45994-45996)GAA>AAA	p.E15332K
Pat_66	Pre-Treatment	TTN	7273	37	2	179474864	179474864	Missense_Mutation	SNP	C	T	62	44	c.43685G>A	c.(43684-43686)GGA>GAA	p.G14562E
Pat_66	Pre-Treatment	TTN	7273	37	2	179489312	179489312	Missense_Mutation	SNP	C	T	59	35	c.36991G>A	c.(36991-36993)GAA>AAA	p.E12331K
Pat_66	Pre-Treatment	TTN	7273	37	2	179495061	179495061	Missense_Mutation	SNP	A	T	24	60	c.36484T>A	c.(36484-36486)TCC>ACC	p.S12162T
Pat_66	Pre-Treatment	TTN	7273	37	2	179499351	179499351	Missense_Mutation	SNP	C	T	136	98	c.34453G>A	c.(34453-34455)GAA>AAA	p.E11485K
Pat_66	Pre-Treatment	TTN	7273	37	2	179592936	179592936	Missense_Mutation	SNP	C	T	11	38	c.15883G>A	c.(15883-15885)GAA>AAA	p.E5295K
Pat_66	Pre-Treatment	TTN	7273	37	2	179593309	179593309	Missense_Mutation	SNP	C	T	9	38	c.15612G>A	c.(15610-15612)ATG>ATA	p.M5204I
Pat_66	Pre-Treatment	TTN	7273	37	2	179600403	179600403	Missense_Mutation	SNP	C	T	15	48	c.11038G>A	c.(11038-11040)GAT>AAT	p.D3680N
Pat_66	Pre-Treatment	TTN	7273	37	2	179613248	179613248	Missense_Mutation	SNP	C	T	40	112	c.13879G>A	c.(13879-13881)GAT>AAT	p.D4627N
Pat_66	Pre-Treatment	TTN	7273	37	2	179615363	179615363	Missense_Mutation	SNP	C	T	10	34	c.11764G>A	c.(11764-11766)GAA>AAA	p.E3922K
Pat_66	Pre-Treatment	TTN	7273	37	2	179650604	179650604	Missense_Mutation	SNP	C	T	32	42	c.2341G>A	c.(2341-2343)GAT>AAT	p.D781N
Pat_66	Pre-Treatment	CCDC141	285025	37	2	179718227	179718227	Missense_Mutation	SNP	G	A	46	109	c.1460C>T	c.(1459-1461)TCA>TTA	p.S487L
Pat_66	Pre-Treatment	SESTD1	91404	37	2	180014055	180014055	Missense_Mutation	SNP	T	C	3	62	c.550A>G	c.(550-552)AGT>GGT	p.S184G
Pat_66	Pre-Treatment	ZNF385B	151126	37	2	180383269	180383269	Missense_Mutation	SNP	G	A	43	96	c.493C>T	c.(493-495)CGC>TGC	p.R165C
Pat_66	Pre-Treatment	PDE1A	5136	37	2	183129074	183129074	Missense_Mutation	SNP	C	T	19	85	c.169G>A	c.(169-171)GAA>AAA	p.E57K
Pat_66	Pre-Treatment	ZNF804A	91752	37	2	185803418	185803418	Missense_Mutation	SNP	C	T	44	98	c.3295C>T	c.(3295-3297)CAT>TAT	p.H1099Y
Pat_66	Pre-Treatment	ZSWIM2	151112	37	2	187697937	187697937	Missense_Mutation	SNP	G	A	15	21	c.851C>T	c.(850-852)TCA>TTA	p.S284L
Pat_66	Pre-Treatment	COL3A1	1281	37	2	189873887	189873887	Missense_Mutation	SNP	C	T	41	108	c.3763C>T	c.(3763-3765)CGT>TGT	p.R1255C
Pat_66	Pre-Treatment	COL5A2	1290	37	2	189898855	189898855	Missense_Mutation	SNP	C	T	31	56	c.4441G>A	c.(4441-4443)GAT>AAT	p.D1481N
Pat_66	Pre-Treatment	STAT1	6772	37	2	191841637	191841637	Missense_Mutation	SNP	G	A	31	85	c.1988C>T	c.(1987-1989)CCC>CTC	p.P663L
Pat_66	Pre-Treatment	DNAH7	56171	37	2	196726661	196726661	Missense_Mutation	SNP	C	T	21	30	c.7516G>A	c.(7516-7518)GAA>AAA	p.E2506K
Pat_66	Pre-Treatment	DNAH7	56171	37	2	196728926	196728926	Missense_Mutation	SNP	G	A	32	77	c.7453C>T	c.(7453-7455)CGT>TGT	p.R2485C
Pat_66	Pre-Treatment	DNAH7	56171	37	2	196729451	196729451	Missense_Mutation	SNP	G	A	49	168	c.6928C>T	c.(6928-6930)CCC>TCC	p.P2310S
Pat_66	Pre-Treatment	DNAH7	56171	37	2	196746518	196746518	Splice_Site	SNP	C	T	35	86	c.5961_splice	c.e36+1	p.T1987_splice
Pat_66	Pre-Treatment	BMPR2	659	37	2	203378445	203378445	Missense_Mutation	SNP	C	T	31	86	c.422C>T	c.(421-423)CCA>CTA	p.P141L
Pat_66	Pre-Treatment	PARD3B	117583	37	2	205983712	205983712	Missense_Mutation	SNP	G	A	42	101	c.748G>A	c.(748-750)GAA>AAA	p.E250K
Pat_66	Pre-Treatment	ZDBF2	57683	37	2	207174227	207174227	Missense_Mutation	SNP	G	A	41	46	c.4975G>A	c.(4975-4977)GGA>AGA	p.G1659R
Pat_66	Pre-Treatment	C2orf80	389073	37	2	209036796	209036796	Missense_Mutation	SNP	G	A	182	137	c.370C>T	c.(370-372)CCC>TCC	p.P124S
Pat_66	Pre-Treatment	MYL1	4632	37	2	211163161	211163161	Missense_Mutation	SNP	C	T	76	73	c.287G>A	c.(286-288)GGA>GAA	p.G96E
Pat_66	Pre-Treatment	ERBB4	2066	37	2	212288972	212288973	Missense_Mutation	DNP	GG	AA	27	62	.2773_2774CC>T	c.(2773-2775)CCA>TTA	p.P925L
Pat_66	Pre-Treatment	ERBB4	2066	37	2	212530121	212530122	Missense_Mutation	DNP	CC	TT	81	61	.1797_1798GG>A	795-1800)GGGGCA>GGA	p.A600T
Pat_66	Pre-Treatment	SPEG	10290	37	2	220332022	220332022	Missense_Mutation	SNP	G	T	4	86	c.3008G>T	c.(3007-3009)TGC>TTC	p.C1003F
Pat_66	Pre-Treatment	SPEG	10290	37	2	220355178	220355178	Missense_Mutation	SNP	G	A	4	78	c.8969G>A	c.(8968-8970)CGA>CAA	p.R2990Q
Pat_66	Pre-Treatment	COL4A4	1286	37	2	227886850	227886850	Missense_Mutation	SNP	C	T	89	259	c.4130G>A	c.(4129-4131)CGA>CAA	p.R1377Q
Pat_66	Pre-Treatment	WDR69	164781	37	2	228769705	228769705	Missense_Mutation	SNP	G	A	53	148	c.709G>A	c.(709-711)GGG>AGG	p.G237R
Pat_66	Pre-Treatment	SPHKAP	80309	37	2	228884799	228884799	Nonsense_Mutation	SNP	C	T	108	153	c.771G>A	c.(769-771)TGG>TGA	p.W257*
Pat_66	Pre-Treatment	SP140	11262	37	2	231112645	231112646	Missense_Mutation	DNP	GG	AA	67	216	c.757_758GG>AA	c.(757-759)GGG>AAG	p.G253K
Pat_66	Pre-Treatment	UGT1A7	54577	37	2	234591418	234591418	Nonsense_Mutation	SNP	C	T	122	324	c.835C>T	c.(835-837)CAG>TAG	p.Q279*
Pat_66	Pre-Treatment	RBM44	375316	37	2	238726382	238726382	Missense_Mutation	SNP	C	T	20	29	c.823C>T	c.(823-825)CAT>TAT	p.H275Y
Pat_66	Pre-Treatment	KIF1A	547	37	2	241715283	241715283	Missense_Mutation	SNP	G	A	15	60	c.943C>T	c.(943-945)CTC>TTC	p.L315F

Pat_66	Pre-Treatment	MCM8	84515	37	20	5965602	5965602	Missense_Mutation	SNP	G	A	4	114	c.1909G>A	c.(1909-1911)GTA>ATA	p.V637I
Pat_66	Pre-Treatment	LRRN4	164312	37	20	6022054	6022054	Missense_Mutation	SNP	G	A	4	158	c.1837C>T	c.(1837-1839)CGC>TGC	p.R613C
Pat_66	Pre-Treatment	PLCB1	23236	37	20	8709777	8709777	Nonsense_Mutation	SNP	G	A	41	87	c.1844G>A	c.(1843-1845)TGG>TAG	p.W615*
Pat_66	Pre-Treatment	PLCB4	5332	37	20	9424891	9424891	Splice_Site	SNP	G	A	13	100	c.2844_splice	c.e30+1	p.K948_splice
Pat_66	Pre-Treatment	FLRT3	23767	37	20	14306937	14306937	Missense_Mutation	SNP	G	A	102	256	c.1216C>T	c.(1216-1218)CCC>TCC	p.P406S
Pat_66	Pre-Treatment	KIF16B	55614	37	20	16488739	16488739	Missense_Mutation	SNP	G	A	85	179	c.563C>T	c.(562-564)TCC>TTC	p.S188F
Pat_66	Pre-Treatment	CSRP2BP	57325	37	20	18142722	18142723	Missense_Mutation	DNP	CC	GT	74	168	c.941_942CC>GT	c.(940-942)TCC>TGT	p.S314C
Pat_66	Pre-Treatment	PAX1	5075	37	20	21687513	21687513	Missense_Mutation	SNP	T	A	27	40	c.724T>A	c.(724-726)TCG>ACG	p.S242T
Pat_66	Pre-Treatment	NINL	22981	37	20	25462646	25462646	Missense_Mutation	SNP	G	A	32	98	c.1768C>T	c.(1768-1770)CCG>TCG	p.P590S
Pat_66	Pre-Treatment	FRG1B	284802	37	20	29614323	29614323	Translation_Start_Site	SNP	C	T	5	120	c.-10C>T	c.(-12--8)TACGT>TATGT	
Pat_66	Pre-Treatment	FRG1B	284802	37	20	29628278	29628278	Missense_Mutation	SNP	G	A	5	254	c.190G>A	c.(190-192)GCA>ACA	p.A64T
Pat_66	Pre-Treatment	XKR7	343702	37	20	30584944	30584944	Missense_Mutation	SNP	C	T	11	36	c.1424C>T	c.(1423-1425)TCC>TTC	p.S475F
Pat_66	Pre-Treatment	MYH7B	57644	37	20	33578870	33578870	Missense_Mutation	SNP	G	A	4	148	c.2255G>A	c.(2254-2256)CGG>CAG	p.R752Q
Pat_66	Pre-Treatment	GDF5	8200	37	20	34021854	34021854	Missense_Mutation	SNP	C	T	20	52	c.1359G>A	c.(1357-1359)ATG>ATA	p.M453I
Pat_66	Pre-Treatment	DHX35	60625	37	20	37650573	37650573	Missense_Mutation	SNP	C	T	47	202	c.1588C>T	c.(1588-1590)CAC>TAC	p.H530Y
Pat_66	Pre-Treatment	PTPRT	11122	37	20	40827958	40827958	Missense_Mutation	SNP	C	T	120	413	c.2413G>A	c.(2413-2415)GAC>AAC	p.D805N
Pat_66	Pre-Treatment	L3MBTL	26013	37	20	42157324	42157324	Missense_Mutation	SNP	C	T	31	126	c.824C>T	c.(823-825)TCG>TTG	p.S275L
Pat_66	Pre-Treatment	SEMG1	6406	37	20	43837052	43837052	Missense_Mutation	SNP	C	A	4	136	c.1114C>A	c.(1114-1116)CGC>AGC	p.R372S
Pat_66	Pre-Treatment	SEMG2	6407	37	20	43851414	43851414	Missense_Mutation	SNP	C	A	7	226	c.1141C>A	c.(1141-1143)CAA>AAA	p.Q381K
Pat_66	Pre-Treatment	SLC13A3	64849	37	20	45221058	45221058	Missense_Mutation	SNP	C	T	49	116	c.905G>A	c.(904-906)GGG>GAG	p.G302E
Pat_66	Pre-Treatment	SPATA2	9825	37	20	48523251	48523252	Missense_Mutation	DNP	GG	AT	11	67	c.467_468CC>AT	c.(466-468)ACC>AAT	p.T156N
Pat_66	Pre-Treatment	ATP9A	10079	37	20	50287677	50287677	Missense_Mutation	SNP	G	A	90	80	c.1157C>T	c.(1156-1158)TCG>TTG	p.S386L
Pat_66	Pre-Treatment	TSHZ2	128553	37	20	51870557	51870557	Missense_Mutation	SNP	C	T	22	97	c.560C>T	c.(559-561)TCG>TTG	p.S187L
Pat_66	Pre-Treatment	BMP7	655	37	20	55777567	55777567	Missense_Mutation	SNP	T	G	31	45	c.724A>C	c.(724-726)AAC>CAC	p.N242H
Pat_66	Pre-Treatment	RAB22A	57403	37	20	56928498	56928498	Missense_Mutation	SNP	C	T	8	68	c.281C>T	c.(280-282)TCA>TTA	p.S94L
Pat_66	Pre-Treatment	OSBPL2	9885	37	20	60854366	60854367	Nonsense_Mutation	DNP	CC	TT	22	34	c.645_646CC>TT	643-648)CCCCGA>CCTT	p.R216*
Pat_66	Pre-Treatment	NTSR1	4923	37	20	61340978	61340978	Missense_Mutation	SNP	G	A	22	85	c.419G>A	c.(418-420)GGC>GAC	p.G140D
Pat_66	Pre-Treatment	DIDO1	11083	37	20	61513394	61513394	Missense_Mutation	SNP	G	A	59	273	c.3914C>T	c.(3913-3915)TCG>TTG	p.S1305L
Pat_66	Pre-Treatment	BIRC7	79444	37	20	61869930	61869930	Missense_Mutation	SNP	G	A	80	129	c.541G>A	c.(541-543)GAA>AAA	p.E181K
Pat_66	Pre-Treatment	PRIC285	85441	37	20	62198657	62198657	Missense_Mutation	SNP	G	A	5	36	c.2054C>T	c.(2053-2055)TCG>TTG	p.S685L
Pat_66	Pre-Treatment	TPTE	7179	37	21	10959769	10959769	Missense_Mutation	SNP	C	T	32	233	c.205G>A	c.(205-207)GAA>AAA	p.E69K
Pat_66	Pre-Treatment	NCAM2	4685	37	21	22849621	22849621	Missense_Mutation	SNP	G	A	38	23	c.1906G>A	c.(1906-1908)GAA>AAA	p.E636K
Pat_66	Pre-Treatment	CLDN17	26285	37	21	31538923	31538923	Missense_Mutation	SNP	G	A	28	53	c.13C>T	c.(13-15)CCC>TCC	p.P5S
Pat_66	Pre-Treatment	MRAP	56246	37	21	33684248	33684248	Missense_Mutation	SNP	G	A	4	97	c.460G>A	c.(460-462)GTC>ATC	p.V154I
Pat_66	Pre-Treatment	C21orf59	56683	37	21	33984471	33984471	Missense_Mutation	SNP	G	A	3	12	c.83C>T	c.(82-84)ACG>ATG	p.T28M
Pat_66	Pre-Treatment	SON	6651	37	21	34922916	34922916	Missense_Mutation	SNP	C	T	8	27	c.1379C>T	c.(1378-1380)TCC>TTC	p.S460F
Pat_66	Pre-Treatment	ITSN1	6453	37	21	35257793	35257793	Missense_Mutation	SNP	G	A	65	161	c.4810G>A	c.(4810-4812)GAA>AAA	p.E1604K
Pat_66	Pre-Treatment	DOPEY2	9980	37	21	37583858	37583858	Missense_Mutation	SNP	C	T	55	147	c.689C>T	c.(688-690)TCT>TTT	p.S230F
Pat_66	Pre-Treatment	KCNJ15	3772	37	21	39672104	39672104	Nonsense_Mutation	SNP	G	A	32	97	c.921G>A	c.(919-921)TGG>TGA	p.W307*
Pat_66	Pre-Treatment	DSCAM	1826	37	21	41465792	41465792	Missense_Mutation	SNP	C	T	26	57	c.3706G>A	c.(3706-3708)GAG>AAG	p.E1236K
Pat_66	Pre-Treatment	DSCAM	1826	37	21	41496210	41496210	Missense_Mutation	SNP	G	A	51	94	c.3608C>T	c.(3607-3609)TCC>TTC	p.S1203F
Pat_66	Pre-Treatment	DSCAM	1826	37	21	41684260	41684260	Missense_Mutation	SNP	A	T	20	40	c.1810T>A	c.(1810-1812)TTT>ATT	p.F604I
Pat_66	Pre-Treatment	AIRE	326	37	21	45709666	45709666	Missense_Mutation	SNP	G	A	23	40	c.779G>A	c.(778-780)GGA>GAA	p.G260E
Pat_66	Pre-Treatment	KRTAP12-1	353332	37	21	46101837	46101837	Missense_Mutation	SNP	G	A	48	114	c.202C>T	c.(202-204)CCC>TCC	p.P68S
Pat_66	Pre-Treatment	SLC19A1	6573	37	21	46951971	46951971	Missense_Mutation	SNP	G	A	4	104	c.281C>T	c.(280-282)CCG>CTG	p.P94L
Pat_66	Pre-Treatment	COL6A2	1292	37	21	47542801	47542801	Missense_Mutation	SNP	G	A	49	37	c.1621G>A	c.(1621-1623)GAC>AAC	p.D541N
Pat_66	Pre-Treatment	PCNT	5116	37	21	47754536	47754536	Missense_Mutation	SNP	C	A	5	211	c.493C>A	c.(493-495)CCA>ACA	p.P165T

Pat_66	Pre-Treatment	CCT8L2	150160	37	22	17072623	17072623	Missense_Mutation	SNP	C	T	46	163	c.818G>A	c.(817-819)GGA>GAA	p.G273E
Pat_66	Pre-Treatment	GNB1L	54584	37	22	19794277	19794277	Nonsense_Mutation	SNP	G	A	10	25	c.421C>T	c.(421-423)CAG>TAG	p.Q141*
Pat_66	Pre-Treatment	ARVCF	421	37	22	19965012	19965012	Missense_Mutation	SNP	G	A	29	86	c.1796C>T	c.(1795-1797)CCC>CTC	p.P599L
Pat_66	Pre-Treatment	RTN4R	65078	37	22	20229382	20229382	Missense_Mutation	SNP	G	A	16	3	c.1274C>T	c.(1273-1275)ACC>ATC	p.T425I
Pat_66	Pre-Treatment	CABIN1	23523	37	22	24437594	24437594	Missense_Mutation	SNP	C	T	111	118	c.218C>T	c.(217-219)TCA>TTA	p.S73L
Pat_66	Pre-Treatment	MYO18B	84700	37	22	26423114	26423114	Missense_Mutation	SNP	G	A	64	58	c.7174G>A	c.(7174-7176)GAC>AAC	p.D2392N
Pat_66	Pre-Treatment	MYO18B	84700	37	22	26423139	26423139	Missense_Mutation	SNP	G	A	70	34	c.7199G>A	c.(7198-7200)GGA>GAA	p.G2400E
Pat_66	Pre-Treatment	LARGE	9215	37	22	33673104	33673104	Missense_Mutation	SNP	C	T	55	81	c.2015G>A	c.(2014-2016)CGG>CAG	p.R672Q
Pat_66	Pre-Treatment	C22orf33	339669	37	22	37396016	37396016	Missense_Mutation	SNP	C	T	20	64	c.499G>A	c.(499-501)GCT>ACT	p.A167T
Pat_66	Pre-Treatment	TMPRSS6	164656	37	22	37499391	37499391	Missense_Mutation	SNP	C	T	44	167	c.94G>A	c.(94-96)GAG>AAG	p.E32K
Pat_66	Pre-Treatment	PLA2G6	8398	37	22	38565377	38565378	Missense_Mutation	DNP	AG	TA	30	84	c.56_57CT>TA	c.(55-57)TCT>TTA	p.S19L
Pat_66	Pre-Treatment	MEI1	150365	37	22	42191808	42191808	Missense_Mutation	SNP	C	T	16	37	c.3736C>T	c.(3736-3738)CCC>TCC	p.P1246S
Pat_66	Pre-Treatment	SCUBE1	80274	37	22	43610249	43610249	Missense_Mutation	SNP	C	T	15	104	c.1900G>A	c.(1900-1902)GGG>AGG	p.G634R
Pat_66	Pre-Treatment	EFCAB6	64800	37	22	44004441	44004441	Nonsense_Mutation	SNP	G	A	28	105	c.2602C>T	c.(2602-2604)CGA>TGA	p.R868*
Pat_66	Pre-Treatment	C22orf9	23313	37	22	45607874	45607874	Missense_Mutation	SNP	G	A	4	119	c.179C>T	c.(178-180)GCG>GTG	p.A60V
Pat_66	Pre-Treatment	WNT7B	7477	37	22	46327115	46327115	Missense_Mutation	SNP	C	T	35	128	c.433G>A	c.(433-435)GAG>AAG	p.E145K
Pat_66	Pre-Treatment	TTLL8	164714	37	22	50488570	50488570	Missense_Mutation	SNP	G	A	42	19	c.158C>T	c.(157-159)CCG>CTG	p.P53L
Pat_66	Pre-Treatment	CNTN6	27255	37	3	1415682	1415682	Missense_Mutation	SNP	C	T	50	68	c.2020C>T	c.(2020-2022)CGT>TGT	p.R674C
Pat_66	Pre-Treatment	GRM7	2917	37	3	7620373	7620373	Missense_Mutation	SNP	C	T	71	11	c.1780C>T	c.(1780-1782)CCT>TCT	p.P594S
Pat_66	Pre-Treatment	C3orf24	115795	37	3	10146416	10146416	Missense_Mutation	SNP	C	T	58	14	c.43G>A	c.(43-45)GAG>AAG	p.E15K
Pat_66	Pre-Treatment	HRH1	3269	37	3	11301183	11301183	Missense_Mutation	SNP	C	T	29	32	c.460C>T	c.(460-462)CTC>TTC	p.L154F
Pat_66	Pre-Treatment	CAND2	23066	37	3	12858407	12858407	Missense_Mutation	SNP	C	T	54	74	c.1976C>T	c.(1975-1977)TCA>TTA	p.S659L
Pat_66	Pre-Treatment	CAND2	23066	37	3	12867118	12867118	Missense_Mutation	SNP	C	T	16	4	c.3190C>T	c.(3190-3192)CGG>TGG	p.R1064W
Pat_66	Pre-Treatment	NUP210	23225	37	3	13363156	13363156	Missense_Mutation	SNP	G	A	62	64	c.5095C>T	c.(5095-5097)CTT>TTT	p.L1699F
Pat_66	Pre-Treatment	NUP210	23225	37	3	13381425	13381425	Missense_Mutation	SNP	C	T	4	224	c.3400G>A	c.(3400-3402)GGG>AGG	p.G1134R
Pat_66	Pre-Treatment	SLC6A6	6533	37	3	14489157	14489157	Nonsense_Mutation	SNP	G	A	240	300	c.432G>A	c.(430-432)TGG>TGA	p.W144*
Pat_66	Pre-Treatment	LRRC3B	116135	37	3	26751500	26751500	Missense_Mutation	SNP	G	A	36	24	c.337G>A	c.(337-339)GAA>AAA	p.E113K
Pat_66	Pre-Treatment	NEK10	152110	37	3	27173423	27173423	Missense_Mutation	SNP	G	A	14	25	c.1136C>T	c.(1135-1137)TCC>TTC	p.S379F
Pat_66	Pre-Treatment	ZNF860	344787	37	3	32031985	32031985	Missense_Mutation	SNP	C	T	88	190	c.1414C>T	c.(1414-1416)CAT>TAT	p.H472Y
Pat_66	Pre-Treatment	STAC	6769	37	3	36484943	36484943	Missense_Mutation	SNP	G	A	33	41	c.199G>A	c.(199-201)GAA>AAA	p.E67K
Pat_66	Pre-Treatment	TRANK1	9881	37	3	36874872	36874872	Missense_Mutation	SNP	C	T	16	21	c.4420G>A	c.(4420-4422)GAA>AAA	p.E1474K
Pat_66	Pre-Treatment	SCN5A	6331	37	3	38629009	38629009	Missense_Mutation	SNP	G	A	19	30	c.2318C>T	c.(2317-2319)CCC>CTC	p.P773L
Pat_66	Pre-Treatment	SCN10A	6336	37	3	38739346	38739346	Missense_Mutation	SNP	C	T	17	25	c.5365G>A	c.(5365-5367)GAC>AAC	p.D1789N
Pat_66	Pre-Treatment	SCN11A	11280	37	3	38908826	38908826	Nonsense_Mutation	SNP	G	A	36	41	c.3937C>T	c.(3937-3939)CAA>TAA	p.Q1313*
Pat_66	Pre-Treatment	SCN11A	11280	37	3	38991597	38991597	Missense_Mutation	SNP	C	T	23	21	c.257G>A	c.(256-258)CGA>CAA	p.R86Q
Pat_66	Pre-Treatment	XIRP1	165904	37	3	39229645	39229645	Missense_Mutation	SNP	C	T	246	30	c.1292G>A	c.(1291-1293)AGG>AAG	p.R431K
Pat_66	Pre-Treatment	TGM4	7047	37	3	44952874	44952874	Missense_Mutation	SNP	C	T	99	13	c.1889C>T	c.(1888-1890)TCC>TTC	p.S630F
Pat_66	Pre-Treatment	CCR2	729230	37	3	46401245	46401245	Missense_Mutation	SNP	G	A	85	11	c.1019G>A	c.(1018-1020)GGA>GAA	p.G340E
Pat_66	Pre-Treatment	LTF	4057	37	3	46490487	46490487	Missense_Mutation	SNP	C	T	3	52	c.1079G>A	c.(1078-1080)CGG>CAG	p.R360Q
Pat_66	Pre-Treatment	BSN	8927	37	3	49695133	49695133	Missense_Mutation	SNP	G	A	101	16	c.8144G>A	c.(8143-8145)AGC>AAC	p.S2715N
Pat_66	Pre-Treatment	RNF123	63891	37	3	49753895	49753895	Missense_Mutation	SNP	G	A	4	232	c.3485G>A	c.(3484-3486)CGT>CAT	p.R1162H
Pat_66	Pre-Treatment	GRM2	2912	37	3	51752121	51752121	Missense_Mutation	SNP	C	T	113	151	c.2612C>T	c.(2611-2613)TCG>TTG	p.S871L
Pat_66	Pre-Treatment	CACNA2D3	55799	37	3	55108183	55108183	Nonsense_Mutation	SNP	C	T	74	27	c.3226C>T	c.(3226-3228)CAG>TAG	p.Q1076*
Pat_66	Pre-Treatment	ERC2	26059	37	3	56026131	56026131	Missense_Mutation	SNP	C	T	167	24	c.2209G>A	c.(2209-2211)GAG>AAG	p.E737K
Pat_66	Pre-Treatment	ERC2	26059	37	3	56114925	56114925	Missense_Mutation	SNP	C	T	32	5	c.1561G>A	c.(1561-1563)GGG>AGG	p.G521R
Pat_66	Pre-Treatment	DNAH12	201625	37	3	57494895	57494895	Missense_Mutation	SNP	C	T	44	80	c.514G>A	c.(514-516)GAA>AAA	p.E172K
Pat_66	Pre-Treatment	LRIG1	26018	37	3	66501990	66501990	Missense_Mutation	SNP	G	A	61	158	c.358C>T	c.(358-360)CTC>TTC	p.L120F

Pat_66	Pre-Treatment	CNTN3	5067	37	3	74350636	74350636	Missense_Mutation	SNP	C	T	88	14	c.2008G>A	c.(2008-2010)GAA>AAA	p.E670K
Pat_66	Pre-Treatment	FAM86D	692099	37	3	75475607	75475607	Missense_Mutation	SNP	C	T	5	11	c.631G>A	c.(631-633)GAG>AAG	p.E211K
Pat_66	Pre-Treatment	OR5H15	403274	37	3	97888247	97888247	Missense_Mutation	SNP	G	A	26	31	c.704G>A	c.(703-705)AGG>AAG	p.R235K
Pat_66	Pre-Treatment	OR5K4	403278	37	3	98073129	98073129	Missense_Mutation	SNP	G	A	40	66	c.432G>A	c.(430-432)ATG>ATA	p.M144I
Pat_66	Pre-Treatment	FILIP1L	11259	37	3	99567215	99567215	Missense_Mutation	SNP	T	A	205	16	c.3305A>T	c.(3304-3306)AAA>ATA	p.K1102I
Pat_66	Pre-Treatment	ATP6V1A	523	37	3	113524359	113524359	Missense_Mutation	SNP	C	T	60	6	c.1748C>T	c.(1747-1749)TCC>TTC	p.S583F
Pat_66	Pre-Treatment	DRD3	1814	37	3	113850076	113850076	Nonsense_Mutation	SNP	G	A	75	110	c.895C>T	c.(895-897)CGA>TGA	p.R299*
Pat_66	Pre-Treatment	FBXO40	51725	37	3	121341658	121341658	Missense_Mutation	SNP	G	A	16	28	c.1382G>A	c.(1381-1383)AGC>AAC	p.S461N
Pat_66	Pre-Treatment	PDIA5	10954	37	3	122849328	122849328	Missense_Mutation	SNP	C	T	22	12	c.775C>T	c.(775-777)CCG>TCG	p.P259S
Pat_66	Pre-Treatment	SLCO2A1	6578	37	3	133667539	133667539	Missense_Mutation	SNP	G	A	34	63	c.946C>T	c.(946-948)CCA>TCA	p.P316S
Pat_66	Pre-Treatment	KY	339855	37	3	134348520	134348520	Missense_Mutation	SNP	C	T	10	11	c.280G>A	c.(280-282)GAA>AAA	p.E94K
Pat_66	Pre-Treatment	ESYT3	83850	37	3	138183346	138183346	Missense_Mutation	SNP	G	A	49	7	c.1075G>A	c.(1075-1077)GAA>AAA	p.E359K
Pat_66	Pre-Treatment	TRIM42	287015	37	3	140397349	140397349	Missense_Mutation	SNP	G	A	41	3	c.278G>A	c.(277-279)AGC>AAC	p.S93N
Pat_66	Pre-Treatment	ATR	545	37	3	142188296	142188296	Missense_Mutation	SNP	C	A	5	98	c.6435G>T	c.(6433-6435)TTG>TTT	p.L2145F
Pat_66	Pre-Treatment	PLSCR2	57047	37	3	146159589	146159589	Missense_Mutation	SNP	C	T	26	8	c.665G>A	c.(664-666)AGA>AAA	p.R222K
Pat_66	Pre-Treatment	IGSF10	285313	37	3	151155772	151155772	Missense_Mutation	SNP	G	A	54	63	c.6577C>T	c.(6577-6579)CAT>TAT	p.H2193Y
Pat_66	Pre-Treatment	IGSF10	285313	37	3	151166374	151166374	Missense_Mutation	SNP	C	T	51	88	c.1395G>A	c.(1393-1395)ATG>ATA	p.M465I
Pat_66	Pre-Treatment	SLC33A1	9197	37	3	155551767	155551767	Missense_Mutation	SNP	C	T	27	31	c.1027G>A	c.(1027-1029)GAA>AAA	p.E343K
Pat_66	Pre-Treatment	ZBBX	79740	37	3	167090658	167090658	Nonsense_Mutation	SNP	C	T	23	47	c.32G>A	c.(31-33)TGG>TAG	p.W11*
Pat_66	Pre-Treatment	SERPINI2	5276	37	3	167170732	167170732	Missense_Mutation	SNP	C	T	49	5	c.956G>A	c.(955-957)GGA>GAA	p.G319E
Pat_66	Pre-Treatment	MECOM	2122	37	3	169099121	169099121	Missense_Mutation	SNP	G	A	107	10	c.229C>T	c.(229-231)CCT>TCT	p.P77S
Pat_66	Pre-Treatment	LRRC31	79782	37	3	169579573	169579573	Nonsense_Mutation	SNP	C	T	39	62	c.204G>A	c.(202-204)TGG>TGA	p.W68*
Pat_66	Pre-Treatment	CCDC39	339829	37	3	180377491	180377491	Missense_Mutation	SNP	C	T	21	35	c.583G>A	c.(583-585)GAA>AAA	p.E195K
Pat_66	Pre-Treatment	ATP11B	23200	37	3	182591616	182591616	Nonsense_Mutation	SNP	C	T	66	6	c.2065C>T	c.(2065-2067)CGA>TGA	p.R689*
Pat_66	Pre-Treatment	SDHAP2	727956	37	3	195410687	195410687	Missense_Mutation	SNP	T	A	5	34	c.584T>A	c.(583-585)GTG>GAG	p.V195E
Pat_66	Pre-Treatment	SDHAP2	727956	37	3	195410689	195410689	Missense_Mutation	SNP	C	T	5	34	c.586C>T	c.(586-588)CAC>TAC	p.H196Y
Pat_66	Pre-Treatment	MUC4	4585	37	3	195511945	195511945	Missense_Mutation	SNP	G	A	3	3	c.6506C>T	c.(6505-6507)GCA>GTA	p.A2169V
Pat_66	Pre-Treatment	OSTalpha	200931	37	3	195944720	195944720	Missense_Mutation	SNP	G	A	18	30	c.46G>A	c.(46-48)GCA>ACA	p.A16T
Pat_66	Pre-Treatment	ZNF732	654254	37	4	266054	266054	Missense_Mutation	SNP	C	T	41	75	c.589G>A	c.(589-591)GAA>AAA	p.E197K
Pat_66	Pre-Treatment	ZNF141	7700	37	4	367245	367245	Missense_Mutation	SNP	C	A	6	407	c.1019C>A	c.(1018-1020)ACA>AAA	p.T340K
Pat_66	Pre-Treatment	CRIPAK	285464	37	4	1388382	1388382	Missense_Mutation	SNP	C	T	8	765	c.83C>T	c.(82-84)GCC>GTC	p.A28V
Pat_66	Pre-Treatment	HAUS3	79441	37	4	2240511	2240511	Missense_Mutation	SNP	G	A	16	79	c.1169C>T	c.(1168-1170)TCA>TTA	p.S390L
Pat_66	Pre-Treatment	SH3BP2	6452	37	4	2831384	2831384	Missense_Mutation	SNP	G	T	4	132	c.751G>T	c.(751-753)GCT>TCT	p.A251S
Pat_66	Pre-Treatment	RGS12	6002	37	4	3318993	3318993	Missense_Mutation	SNP	G	A	5	219	c.1096G>A	c.(1096-1098)GAC>AAC	p.D366N
Pat_66	Pre-Treatment	JAKMIP1	152789	37	4	6064113	6064113	Nonsense_Mutation	SNP	G	A	29	126	c.1486C>T	c.(1486-1488)CAG>TAG	p.Q496*
Pat_66	Pre-Treatment	WFS1	7466	37	4	6303507	6303507	Missense_Mutation	SNP	C	T	92	293	c.1985C>T	c.(1984-1986)TCC>TTC	p.S662F
Pat_66	Pre-Treatment	CCDC96	257236	37	4	7043324	7043324	Missense_Mutation	SNP	C	T	309	391	c.1342G>A	c.(1342-1344)GAA>AAA	p.E448K
Pat_66	Pre-Treatment	SORCS2	57537	37	4	7705016	7705016	Missense_Mutation	SNP	G	A	30	18	c.1678G>A	c.(1678-1680)GAA>AAA	p.E560K
Pat_66	Pre-Treatment	CPZ	8532	37	4	8608525	8608525	Missense_Mutation	SNP	G	A	34	55	c.968G>A	c.(967-969)CGA>CAA	p.R323Q
Pat_66	Pre-Treatment	DRD5	1816	37	4	9784827	9784827	Missense_Mutation	SNP	G	A	21	52	c.1174G>A	c.(1174-1176)GAG>AAG	p.E392K
Pat_66	Pre-Treatment	C1QTNF7	114905	37	4	15437411	15437411	Missense_Mutation	SNP	G	A	27	127	c.44G>A	c.(43-45)AGT>AAT	p.S15N
Pat_66	Pre-Treatment	ARAP2	116984	37	4	36230679	36230679	Missense_Mutation	SNP	C	T	16	99	c.430G>A	c.(430-432)GAT>AAT	p.D144N
Pat_66	Pre-Treatment	BEND4	389206	37	4	42145862	42145862	Missense_Mutation	SNP	C	T	25	21	c.637G>A	c.(637-639)GAG>AAG	p.E213K
Pat_66	Pre-Treatment	GABRG1	2565	37	4	46125923	46125923	Missense_Mutation	SNP	G	A	9	73	c.8C>T	c.(7-9)CCT>CTT	p.P3L
Pat_66	Pre-Treatment	GABRA2	2555	37	4	46252411	46252411	Missense_Mutation	SNP	C	T	70	161	c.1270G>A	c.(1270-1272)GTT>ATT	p.V424I
Pat_66	Pre-Treatment	GABRB1	2560	37	4	47427775	47427775	Missense_Mutation	SNP	G	A	71	86	c.1165G>A	c.(1165-1167)GAC>AAC	p.D389N
Pat_66	Pre-Treatment	SLAIN2	57606	37	4	48384617	48384617	Missense_Mutation	SNP	C	T	4	117	c.895C>T	c.(895-897)CGG>TGG	p.R299W

Pat_66	Pre-Treatment	SLAIN2	57606	37	4	48384768	48384768	Missense_Mutation	SNP	C	T	47	249	c.1046C>T	c.(1045-1047)TCA>TTA	p.S349L
Pat_66	Pre-Treatment	CWH43	80157	37	4	49052739	49052739	Missense_Mutation	SNP	G	A	38	140	c.1894G>A	c.(1894-1896)GAA>AAA	p.E632K
Pat_66	Pre-Treatment	GSX2	170825	37	4	54967865	54967865	Missense_Mutation	SNP	C	T	106	292	c.691C>T	c.(691-693)CGG>TGG	p.R231W
Pat_66	Pre-Treatment	CEP135	9662	37	4	56878072	56878072	Missense_Mutation	SNP	G	A	5	173	c.2723G>A	c.(2722-2724)CGA>CAA	p.R908Q
Pat_66	Pre-Treatment	LPHN3	23284	37	4	62845425	62845425	Missense_Mutation	SNP	C	T	216	264	c.2746C>T	c.(2746-2748)CTC>TTC	p.L916F
Pat_66	Pre-Treatment	UBA6	55236	37	4	68534319	68534319	Missense_Mutation	SNP	C	T	23	90	c.743G>A	c.(742-744)CGA>CAA	p.R248Q
Pat_66	Pre-Treatment	TMPRSS11A	339967	37	4	68784890	68784890	Missense_Mutation	SNP	C	T	30	168	c.762G>A	c.(760-762)ATG>ATA	p.M254I
Pat_66	Pre-Treatment	UGT2B7	7364	37	4	69962813	69962813	Missense_Mutation	SNP	C	T	94	133	c.575C>T	c.(574-576)TCC>TTC	p.S192F
Pat_66	Pre-Treatment	UGT2B11	10720	37	4	70078301	70078301	Missense_Mutation	SNP	G	A	207	352	c.860C>T	c.(859-861)CCC>CTC	p.P287L
Pat_66	Pre-Treatment	AFP	174	37	4	74319573	74319573	Missense_Mutation	SNP	T	C	78	64	c.1744T>C	c.(1744-1746)TGC>CGC	p.C582R
Pat_66	Pre-Treatment	CCDC158	339965	37	4	77274293	77274293	Missense_Mutation	SNP	C	T	46	70	c.2428G>A	c.(2428-2430)GAA>AAA	p.E810K
Pat_66	Pre-Treatment	CXCL13	10563	37	4	78526977	78526977	Splice_Site	SNP	G	A	17	56	c.-41_splice	c.e2-1	
Pat_66	Pre-Treatment	HNRPDL	9987	37	4	83349262	83349262	Missense_Mutation	SNP	C	T	4	107	c.683G>A	c.(682-684)GGG>GAG	p.G228E
Pat_66	Pre-Treatment	HERC5	51191	37	4	89381275	89381275	Missense_Mutation	SNP	T	A	4	79	c.419T>A	c.(418-420)ATA>AAA	p.I140K
Pat_66	Pre-Treatment	HERC5	51191	37	4	89383393	89383394	Missense_Mutation	DNP	CC	AT	33	62	c.574_575CC>AT	c.(574-576)CCC>ATC	p.P192I
Pat_66	Pre-Treatment	FAM13A	10144	37	4	89950665	89950665	Missense_Mutation	SNP	C	T	157	205	c.163G>A	c.(163-165)GAG>AAG	p.E55K
Pat_66	Pre-Treatment	GPRIN3	285513	37	4	90168956	90168956	Missense_Mutation	SNP	G	A	33	211	c.2306C>T	c.(2305-2307)CCT>CTT	p.P769L
Pat_66	Pre-Treatment	MMRN1	22915	37	4	90872783	90872783	Missense_Mutation	SNP	C	T	4	99	c.3146C>T	c.(3145-3147)CCG>CTG	p.P1049L
Pat_66	Pre-Treatment	RAP1GDS1	5910	37	4	99337994	99337994	Nonsense_Mutation	SNP	G	T	5	195	c.862G>T	c.(862-864)GAG>TAG	p.E288*
Pat_66	Pre-Treatment	CENPE	1062	37	4	104068791	104068791	Missense_Mutation	SNP	G	A	31	81	c.3856C>T	c.(3856-3858)CAT>TAT	p.H1286Y
Pat_66	Pre-Treatment	TACR3	6870	37	4	104640330	104640330	Missense_Mutation	SNP	G	A	62	76	c.503C>T	c.(502-504)GCT>GTT	p.A168V
Pat_66	Pre-Treatment	CFI	3426	37	4	110670438	110670438	Missense_Mutation	SNP	C	T	364	390	c.1084G>A	c.(1084-1086)GGA>AGA	p.G362R
Pat_66	Pre-Treatment	ENPEP	2028	37	4	111397844	111397844	Nonsense_Mutation	SNP	C	T	32	151	c.274C>T	c.(274-276)CGA>TGA	p.R92*
Pat_66	Pre-Treatment	METTL14	57721	37	4	119618418	119618419	Nonsense_Mutation	DNP	AG	TT	4	110	c.585_586AG>TT	(583-588)TTAGAA>TTTTA	.195_196LE>F
Pat_66	Pre-Treatment	SYNPO2	171024	37	4	119951254	119951254	Missense_Mutation	SNP	G	A	28	133	c.1324G>A	c.(1324-1326)GAA>AAA	p.E442K
Pat_66	Pre-Treatment	FAT4	79633	37	4	126370225	126370225	Missense_Mutation	SNP	G	A	98	318	c.8054G>A	c.(8053-8055)CGA>CAA	p.R2685Q
Pat_66	Pre-Treatment	OTUD4	54726	37	4	146063437	146063437	Missense_Mutation	SNP	G	A	127	239	c.1538C>T	c.(1537-1539)TCT>TTT	p.S513F
Pat_66	Pre-Treatment	ZNF827	152485	37	4	146824058	146824058	Missense_Mutation	SNP	G	A	19	87	c.353C>T	c.(352-354)CCC>CTC	p.P118L
Pat_66	Pre-Treatment	EDNRA	1909	37	4	148406954	148406954	Missense_Mutation	SNP	C	T	31	79	c.121C>T	c.(121-123)CGT>TGT	p.R41C
Pat_66	Pre-Treatment	DCLK2	166614	37	4	151177262	151177262	Missense_Mutation	SNP	C	T	22	58	c.2164C>T	c.(2164-2166)CCT>TCT	p.P722S
Pat_66	Pre-Treatment	LRBA	987	37	4	151765281	151765281	Missense_Mutation	SNP	G	A	175	244	c.4540C>T	c.(4540-4542)CGG>TGG	p.R1514W
Pat_66	Pre-Treatment	TIGD4	201798	37	4	153690796	153690796	Missense_Mutation	SNP	G	A	29	105	c.1361C>T	c.(1360-1362)TCT>TTT	p.S454F
Pat_66	Pre-Treatment	TLR2	7097	37	4	154624199	154624199	Missense_Mutation	SNP	C	T	26	29	c.140C>T	c.(139-141)CCC>CTC	p.P47L
Pat_66	Pre-Treatment	NPY2R	4887	37	4	156135417	156135417	Missense_Mutation	SNP	C	T	38	45	c.326C>T	c.(325-327)ACC>ATC	p.T109I
Pat_66	Pre-Treatment	NPY5R	4889	37	4	164272282	164272282	Missense_Mutation	SNP	G	A	32	106	c.857G>A	c.(856-858)AGA>AAA	p.R286K
Pat_66	Pre-Treatment	TRIM61	391712	37	4	165891019	165891019	Missense_Mutation	SNP	C	T	30	99	c.136G>A	c.(136-138)GAT>AAT	p.D46N
Pat_66	Pre-Treatment	TRIM60	166655	37	4	165962177	165962177	Missense_Mutation	SNP	G	A	61	65	c.953G>A	c.(952-954)CGA>CAA	p.R318Q
Pat_66	Pre-Treatment	TLL1	7092	37	4	166999147	166999147	Missense_Mutation	SNP	G	A	68	51	c.2407G>A	c.(2407-2409)GAA>AAA	p.E803K
Pat_66	Pre-Treatment	TLL1	7092	37	4	166999157	166999157	Missense_Mutation	SNP	C	T	55	70	c.2417C>T	c.(2416-2418)GCC>GTC	p.A806V
Pat_66	Pre-Treatment	DDX60	55601	37	4	169194513	169194513	Missense_Mutation	SNP	G	A	22	114	c.2491C>T	c.(2491-2493)CGT>TGT	p.R831C
Pat_66	Pre-Treatment	DDX60L	91351	37	4	169296578	169296578	Missense_Mutation	SNP	G	A	7	45	c.4583C>T	c.(4582-4584)TCC>TTC	p.S1528F
Pat_66	Pre-Treatment	DDX60L	91351	37	4	169340497	169340497	Missense_Mutation	SNP	G	A	22	27	c.2566C>T	c.(2566-2568)CGC>TGC	p.R856C
Pat_66	Pre-Treatment	DDX60L	91351	37	4	169344911	169344911	Missense_Mutation	SNP	C	T	15	31	c.1945G>A	c.(1945-1947)GAT>AAT	p.D649N
Pat_66	Pre-Treatment	PALLD	23022	37	4	169606664	169606664	Missense_Mutation	SNP	G	A	85	280	c.1289G>A	c.(1288-1290)CGA>CAA	p.R430Q
Pat_66	Pre-Treatment	PALLD	23022	37	4	169835133	169835133	Missense_Mutation	SNP	G	A	66	214	c.2678G>A	c.(2677-2679)CGA>CAA	p.R893Q
Pat_66	Pre-Treatment	ADAM29	11086	37	4	175898063	175898063	Missense_Mutation	SNP	G	A	21	111	c.1387G>A	c.(1387-1389)GAT>AAT	p.D463N
Pat_66	Pre-Treatment	VEGFC	7424	37	4	177649057	177649058	Missense_Mutation	DNP	CC	TT	92	121	c.426_427GG>AA	424-429)AAGGAG>AAAA	p.E143K

Pat_66	Pre-Treatment	ODZ3	55714	37	4	183601824	183601824	Missense_Mutation	SNP	C	T	29	47	c.1768C>T	c.(1768-1770)CGT>TGT	p.R590C
Pat_66	Pre-Treatment	STOX2	56977	37	4	184930479	184930479	Missense_Mutation	SNP	G	A	39	131	c.488G>A	c.(487-489)AGG>AAG	p.R163K
Pat_66	Pre-Treatment	TLR3	7098	37	4	187003918	187003918	Missense_Mutation	SNP	C	T	37	37	c.1078C>T	c.(1078-1080)CTT>TTT	p.L360F
Pat_66	Pre-Treatment	KLKB1	3818	37	4	187155158	187155158	Nonsense_Mutation	SNP	C	T	106	141	c.274C>T	c.(274-276)CGA>TGA	p.R92*
Pat_66	Pre-Treatment	KLKB1	3818	37	4	187178430	187178430	Missense_Mutation	SNP	G	A	80	112	c.1636G>A	c.(1636-1638)GAA>AAA	p.E546K
Pat_66	Pre-Treatment	PAPD7	11044	37	5	6753031	6753031	Missense_Mutation	SNP	C	T	63	39	c.1315C>T	c.(1315-1317)CCT>TCT	p.P439S
Pat_66	Pre-Treatment	6-Mar	10299	37	5	10417496	10417496	Missense_Mutation	SNP	C	T	34	126	c.2263C>T	c.(2263-2265)CCT>TCT	p.P755S
Pat_66	Pre-Treatment	DNAH5	1767	37	5	13811899	13811899	Missense_Mutation	SNP	C	T	62	51	c.7264G>A	c.(7264-7266)GAA>AAA	p.E2422K
Pat_66	Pre-Treatment	DNAH5	1767	37	5	13811905	13811905	Missense_Mutation	SNP	C	T	26	81	c.7258G>A	c.(7258-7260)GAA>AAA	p.E2420K
Pat_66	Pre-Treatment	DNAH5	1767	37	5	13829780	13829780	Missense_Mutation	SNP	C	T	24	79	c.6283G>A	c.(6283-6285)GAA>AAA	p.E2095K
Pat_66	Pre-Treatment	DNAH5	1767	37	5	13830747	13830747	Missense_Mutation	SNP	G	A	34	98	c.6020C>T	c.(6019-6021)TCA>TTA	p.S2007L
Pat_66	Pre-Treatment	DNAH5	1767	37	5	13914025	13914025	Missense_Mutation	SNP	G	C	13	44	c.1363C>G	c.(1363-1365)CAA>GAA	p.Q455E
Pat_66	Pre-Treatment	TRIO	7204	37	5	14304621	14304621	Missense_Mutation	SNP	C	T	67	132	c.1420C>T	c.(1420-1422)CCC>TCC	p.P474S
Pat_66	Pre-Treatment	PRDM9	56979	37	5	23510065	23510065	Missense_Mutation	SNP	G	A	28	78	c.230G>A	c.(229-231)CGA>CAA	p.R77Q
Pat_66	Pre-Treatment	PDZD2	23037	37	5	31799771	31799771	Missense_Mutation	SNP	G	A	72	56	c.416G>A	c.(415-417)CGG>CAG	p.R139Q
Pat_66	Pre-Treatment	EGFLAM	133584	37	5	38406275	38406275	Missense_Mutation	SNP	G	A	20	59	c.760G>A	c.(760-762)GAC>AAC	p.D254N
Pat_66	Pre-Treatment	LIFR	3977	37	5	38504188	38504188	Missense_Mutation	SNP	C	T	41	85	c.1327G>A	c.(1327-1329)GAT>AAT	p.D443N
Pat_66	Pre-Treatment	C9	735	37	5	39311419	39311419	Missense_Mutation	SNP	G	A	54	42	c.931C>T	c.(931-933)CGC>TGC	p.R311C
Pat_66	Pre-Treatment	DAB2	1601	37	5	39383265	39383265	Missense_Mutation	SNP	G	A	75	162	c.796C>T	c.(796-798)CCT>TCT	p.P266S
Pat_66	Pre-Treatment	HEATR7B2	133558	37	5	41000423	41000423	Missense_Mutation	SNP	G	A	13	46	c.4381C>T	c.(4381-4383)CCC>TCC	p.P1461S
Pat_66	Pre-Treatment	C6	729	37	5	41150076	41150076	Missense_Mutation	SNP	C	T	29	68	c.2342G>A	c.(2341-2343)GGA>GAA	p.G781E
Pat_66	Pre-Treatment	GHR	2690	37	5	42718182	42718182	Missense_Mutation	SNP	C	T	25	84	c.904C>T	c.(904-906)CCA>TCA	p.P302S
Pat_66	Pre-Treatment	HSPB3	8988	37	5	53751825	53751825	Missense_Mutation	SNP	C	T	63	36	c.206C>T	c.(205-207)TCC>TTC	p.S69F
Pat_66	Pre-Treatment	ZNF366	167465	37	5	71756663	71756663	Missense_Mutation	SNP	C	T	37	61	c.661G>A	c.(661-663)GAG>AAG	p.E221K
Pat_66	Pre-Treatment	RGNEF	64283	37	5	73163733	73163733	Missense_Mutation	SNP	C	T	27	36	c.2185C>T	c.(2185-2187)CTC>TTC	p.L729F
Pat_66	Pre-Treatment	CMYA5	202333	37	5	79026699	79026699	Missense_Mutation	SNP	C	T	12	18	c.2111C>T	c.(2110-2112)TCA>TTA	p.S704L
Pat_66	Pre-Treatment	CMYA5	202333	37	5	79030700	79030700	Missense_Mutation	SNP	G	A	18	30	c.6112G>A	c.(6112-6114)GAA>AAA	p.E2038K
Pat_66	Pre-Treatment	CMYA5	202333	37	5	79030895	79030895	Missense_Mutation	SNP	G	A	14	20	c.6307G>A	c.(6307-6309)GAA>AAA	p.E2103K
Pat_66	Pre-Treatment	SPZ1	84654	37	5	79616461	79616461	Missense_Mutation	SNP	G	C	4	109	c.427G>C	c.(427-429)GAG>CAG	p.E143Q
Pat_66	Pre-Treatment	GPR98	84059	37	5	89923367	89923367	Missense_Mutation	SNP	C	T	56	90	c.1012C>T	c.(1012-1014)CAT>TAT	p.H338Y
Pat_66	Pre-Treatment	GPR98	84059	37	5	90052422	90052422	Missense_Mutation	SNP	G	A	15	9	c.11732G>A	c.(11731-11733)GGA>GAA	p.G3911E
Pat_66	Pre-Treatment	GPR98	84059	37	5	90136435	90136435	Missense_Mutation	SNP	C	T	29	39	c.16652C>T	c.(16651-16653)TCT>TTT	p.S5551F
Pat_66	Pre-Treatment	C5orf13	9315	37	5	111066734	111066734	Missense_Mutation	SNP	G	A	9	14	c.91C>T	c.(91-93)CCT>TCT	p.P31S
Pat_66	Pre-Treatment	DMXL1	1657	37	5	118482639	118482639	Missense_Mutation	SNP	C	T	17	42	c.2677C>T	c.(2677-2679)CCT>TCT	p.P893S
Pat_66	Pre-Treatment	TRPC7	57113	37	5	135692498	135692498	Missense_Mutation	SNP	G	A	34	51	c.575C>T	c.(574-576)CCC>CTC	p.P192L
Pat_66	Pre-Treatment	PCDHA2	56146	37	5	140174976	140174976	Missense_Mutation	SNP	C	T	37	46	c.427C>T	c.(427-429)CCC>TCC	p.P143S
Pat_66	Pre-Treatment	PCDHA5	56143	37	5	140201464	140201464	Missense_Mutation	SNP	C	T	4	88	c.104C>T	c.(103-105)CCG>CTG	p.P35L
Pat_66	Pre-Treatment	PCDHA11	56138	37	5	140249730	140249730	Missense_Mutation	SNP	G	A	41	53	c.1042G>A	c.(1042-1044)GAA>AAA	p.E348K
Pat_66	Pre-Treatment	PCDHB1	29930	37	5	140431504	140431504	Missense_Mutation	SNP	C	T	21	23	c.449C>T	c.(448-450)TCA>TTA	p.S150L
Pat_66	Pre-Treatment	PCDHB3	56132	37	5	140481257	140481257	Missense_Mutation	SNP	G	A	25	28	c.1024G>A	c.(1024-1026)GAC>AAC	p.D342N
Pat_66	Pre-Treatment	PCDHB6	56130	37	5	140529986	140529986	Missense_Mutation	SNP	G	A	40	53	c.148G>A	c.(148-150)GAC>AAC	p.D50N
Pat_66	Pre-Treatment	PCDHB7	56129	37	5	140554416	140554416	Missense_Mutation	SNP	C	T	29	337	c.2000C>T	c.(1999-2001)TCC>TTC	p.S667F
Pat_66	Pre-Treatment	PCDHB8	56128	37	5	140558516	140558516	Missense_Mutation	SNP	G	A	53	334	c.901G>A	c.(901-903)GAA>AAA	p.E301K
Pat_66	Pre-Treatment	PCDHB13	56123	37	5	140595079	140595079	Missense_Mutation	SNP	G	A	139	241	c.1384G>A	c.(1384-1386)GAG>AAG	p.E462K
Pat_66	Pre-Treatment	PCDHGA6	56109	37	5	140753757	140753757	Missense_Mutation	SNP	C	T	3	18	c.107C>T	c.(106-108)CCC>CTC	p.P36L
Pat_66	Pre-Treatment	PCDH1	5097	37	5	141243755	141243755	Missense_Mutation	SNP	T	A	31	31	c.2141A>T	c.(2140-2142)TAT>TTT	p.Y714F
Pat_66	Pre-Treatment	PPP2R2B	5521	37	5	145979853	145979853	Splice_Site	SNP	C	T	27	58	c.960_splice	c.e7+1	p.Q320_splice

Pat_66	Pre-Treatment	PPP2R2B	5521	37	5	146077647	146077647	Missense_Mutation	SNP	C	T	65	97	c.229G>A	c.(229-231)GAA>AAA	p.E77K
Pat_66	Pre-Treatment	HTR4	3360	37	5	147889397	147889397	Missense_Mutation	SNP	C	T	16	25	c.698G>A	c.(697-699)GGA>GAA	p.G233E
Pat_66	Pre-Treatment	KIF4B	285643	37	5	154395697	154395697	Missense_Mutation	SNP	G	A	21	21	c.2278G>A	c.(2278-2280)GCC>ACC	p.A760T
Pat_66	Pre-Treatment	KIF4B	285643	37	5	154395718	154395718	Missense_Mutation	SNP	C	T	18	30	c.2299C>T	c.(2299-2301)CTC>TTC	p.L767F
Pat_66	Pre-Treatment	MED7	9443	37	5	156566174	156566174	Missense_Mutation	SNP	A	G	18	23	c.269T>C	c.(268-270)TTG>TCG	p.L90S
Pat_66	Pre-Treatment	ODZ2	57451	37	5	167517676	167517676	Missense_Mutation	SNP	C	T	62	99	c.1613C>T	c.(1612-1614)GCC>GTC	p.A538V
Pat_66	Pre-Treatment	KCNIP1	30820	37	5	170162777	170162777	Missense_Mutation	SNP	G	A	34	64	c.651G>A	c.(649-651)ATG>ATA	p.M217I
Pat_66	Pre-Treatment	GFPT2	9945	37	5	179734231	179734231	Missense_Mutation	SNP	G	A	8	15	c.1619C>T	c.(1618-1620)TCG>TTG	p.S540L
Pat_66	Pre-Treatment	CNOT6	57472	37	5	179976951	179976951	Missense_Mutation	SNP	G	T	4	190	c.133G>T	c.(133-135)GCA>TCA	p.A45S
Pat_66	Pre-Treatment	HUS1B	135458	37	6	656730	656730	Missense_Mutation	SNP	G	A	8	23	c.215C>T	c.(214-216)TCG>TTG	p.S72L
Pat_66	Pre-Treatment	SYCP2L	221711	37	6	10891779	10891779	Missense_Mutation	SNP	G	A	32	147	c.43G>A	c.(43-45)GAT>AAT	p.D15N
Pat_66	Pre-Treatment	FAM65B	9750	37	6	24843752	24843752	Missense_Mutation	SNP	C	T	30	28	c.1258G>A	c.(1258-1260)GGA>AGA	p.G420R
Pat_66	Pre-Treatment	HIST1H2BA	255626	37	6	25727393	25727393	Missense_Mutation	SNP	G	A	31	135	c.257G>A	c.(256-258)AGC>AAC	p.S86N
Pat_66	Pre-Treatment	BTN3A3	10384	37	6	26452145	26452145	Missense_Mutation	SNP	G	A	33	80	c.1261G>A	c.(1261-1263)GGT>AGT	p.G421S
Pat_66	Pre-Treatment	HIST1H4J	8363	37	6	27791925	27791925	Missense_Mutation	SNP	G	A	4	149	c.23G>A	c.(22-24)GGG>GAG	p.G8E
Pat_66	Pre-Treatment	ZFP57	346171	37	6	29640902	29640902	Missense_Mutation	SNP	G	A	16	135	c.986C>T	c.(985-987)TCC>TTC	p.S329F
Pat_66	Pre-Treatment	RNF39	80352	37	6	30041250	30041250	Missense_Mutation	SNP	C	T	26	146	c.573G>A	c.(571-573)ATG>ATA	p.M191I
Pat_66	Pre-Treatment	TRIM10	10107	37	6	30128599	30128599	Missense_Mutation	SNP	C	T	24	42	c.37G>A	c.(37-39)GAA>AAA	p.E13K
Pat_66	Pre-Treatment	TCF19	6941	37	6	31129329	31129329	Missense_Mutation	SNP	C	T	195	151	c.344C>T	c.(343-345)TCG>TTG	p.S115L
Pat_66	Pre-Treatment	MICB	4277	37	6	31474038	31474039	Missense_Mutation	DNP	AG	TA	55	157	c.444_445AG>TA	(442-447)CAAGAA>CATA	148_149QE>H
Pat_66	Pre-Treatment	CYP21A2	1589	37	6	32008268	32008268	Missense_Mutation	SNP	G	A	15	106	c.1025G>A	c.(1024-1026)CGG>CAG	p.R342Q
Pat_66	Pre-Treatment	TNXB	7148	37	6	32037621	32037621	Missense_Mutation	SNP	C	T	36	45	c.5296G>A	c.(5296-5298)GAT>AAT	p.D1766N
Pat_66	Pre-Treatment	C6orf10	10665	37	6	32333953	32333953	Missense_Mutation	SNP	C	T	59	24	c.208G>A	c.(208-210)GAT>AAT	p.D70N
Pat_66	Pre-Treatment	RGL2	5863	37	6	33262929	33262929	Missense_Mutation	SNP	G	A	5	27	c.1184C>T	c.(1183-1185)TCC>TTC	p.S395F
Pat_66	Pre-Treatment	ITPR3	3710	37	6	33645396	33645396	Missense_Mutation	SNP	C	T	82	50	c.3638C>T	c.(3637-3639)CCC>CTC	p.P1213L
Pat_66	Pre-Treatment	SCUBE3	222663	37	6	35211766	35211766	Missense_Mutation	SNP	G	A	4	149	c.2098G>A	c.(2098-2100)GTA>ATA	p.V700I
Pat_66	Pre-Treatment	C6orf81	221481	37	6	35715395	35715395	Missense_Mutation	SNP	G	A	121	283	c.742G>A	c.(742-744)GAC>AAC	p.D248N
Pat_66	Pre-Treatment	FGD2	221472	37	6	36976617	36976617	Missense_Mutation	SNP	G	A	65	71	c.76G>A	c.(76-78)GAA>AAA	p.E26K
Pat_66	Pre-Treatment	DNAH8	1769	37	6	38905953	38905953	Nonsense_Mutation	SNP	C	T	75	138	c.11116C>T	c.(11116-11118)CAG>TAG	p.Q3706*
Pat_66	Pre-Treatment	TSPO2	222642	37	6	41011781	41011781	Missense_Mutation	SNP	G	T	4	170	c.418G>T	c.(418-420)GCC>TCC	p.A140S
Pat_66	Pre-Treatment	TRERF1	55809	37	6	42236737	42236737	Missense_Mutation	SNP	G	A	41	59	c.592C>T	c.(592-594)CCT>TCT	p.P198S
Pat_66	Pre-Treatment	CUL7	9820	37	6	43020187	43020187	Missense_Mutation	SNP	C	T	4	150	c.340G>A	c.(340-342)GTG>ATG	p.V114M
Pat_66	Pre-Treatment	TDRD6	221400	37	6	46660726	46660726	Missense_Mutation	SNP	C	T	6	207	c.4861C>T	c.(4861-4863)CCT>TCT	p.P1621S
Pat_66	Pre-Treatment	GPR115	221393	37	6	47682058	47682058	Nonsense_Mutation	SNP	G	A	40	106	c.1077G>A	c.(1075-1077)TGG>TGA	p.W359*
Pat_66	Pre-Treatment	HCRTR2	3062	37	6	55142185	55142185	Missense_Mutation	SNP	G	A	18	61	c.770G>A	c.(769-771)GGA>GAA	p.G257E
Pat_66	Pre-Treatment	GFRAL	389400	37	6	55264208	55264208	Missense_Mutation	SNP	G	A	33	173	c.1090G>A	c.(1090-1092)GGA>AGA	p.G364R
Pat_66	Pre-Treatment	HMGCLL1	54511	37	6	55406625	55406625	Missense_Mutation	SNP	G	A	71	80	c.289C>T	c.(289-291)CCT>TCT	p.P97S
Pat_66	Pre-Treatment	BMP5	653	37	6	55739342	55739342	Missense_Mutation	SNP	C	T	49	157	c.322G>A	c.(322-324)GAG>AAG	p.E108K
Pat_66	Pre-Treatment	DST	667	37	6	56516016	56516016	Missense_Mutation	SNP	A	G	16	37	c.1142T>C	c.(1141-1143)GTT>GCT	p.V381A
Pat_66	Pre-Treatment	BEND6	221336	37	6	56857314	56857314	Missense_Mutation	SNP	G	A	247	334	c.259G>A	c.(259-261)GAA>AAA	p.E87K
Pat_66	Pre-Treatment	ZNF451	26036	37	6	57013017	57013017	Missense_Mutation	SNP	C	T	14	34	c.2134C>T	c.(2134-2136)CCA>TCA	p.P712S
Pat_66	Pre-Treatment	KCNQ5	56479	37	6	73879550	73879550	Missense_Mutation	SNP	C	T	31	100	c.1550C>T	c.(1549-1551)CCA>CTA	p.P517L
Pat_66	Pre-Treatment	CD109	135228	37	6	74446167	74446167	Missense_Mutation	SNP	C	T	134	90	c.569C>T	c.(568-570)TCC>TTC	p.S190F
Pat_66	Pre-Treatment	COL12A1	1303	37	6	75887486	75887486	Missense_Mutation	SNP	C	T	182	483	c.2330G>A	c.(2329-2331)AGA>AAA	p.R777K
Pat_66	Pre-Treatment	COL12A1	1303	37	6	75892963	75892963	Missense_Mutation	SNP	C	T	49	137	c.1694G>A	c.(1693-1695)AGG>AAG	p.R565K
Pat_66	Pre-Treatment	FILIP1	27145	37	6	76022929	76022929	Missense_Mutation	SNP	C	T	15	53	c.2619G>A	c.(2617-2619)ATG>ATA	p.M873I
Pat_66	Pre-Treatment	LCA5	167691	37	6	80203380	80203380	Missense_Mutation	SNP	C	T	22	41	c.808G>A	c.(808-810)GAA>AAA	p.E270K

Pat_66	Pre-Treatment	IBTK	25998	37	6	82933317	82933317	Nonsense_Mutation	SNP	C	A	4	63	c.964G>T	c.(964-966)GGA>TGA	p.G322*
Pat_66	Pre-Treatment	DOPEY1	23033	37	6	83840052	83840052	Missense_Mutation	SNP	T	G	35	76	c.2552T>G	c.(2551-2553)GTT>GGT	p.V851G
Pat_66	Pre-Treatment	ME1	4199	37	6	83933615	83933615	Missense_Mutation	SNP	G	A	28	70	c.1313C>T	c.(1312-1314)CCA>CTA	p.P438L
Pat_66	Pre-Treatment	RARS2	57038	37	6	88224171	88224171	Missense_Mutation	SNP	C	A	31	67	c.1697G>T	c.(1696-1698)GGA>GTA	p.G566V
Pat_66	Pre-Treatment	UBE2J1	51465	37	6	90047951	90047951	Missense_Mutation	SNP	G	A	78	56	c.401C>T	c.(400-402)CCT>CTT	p.P134L
Pat_66	Pre-Treatment	KLHL32	114792	37	6	97587066	97587066	Missense_Mutation	SNP	G	A	55	152	c.1771G>A	c.(1771-1773)GGA>AGA	p.G591R
Pat_66	Pre-Treatment	SIM1	6492	37	6	100838394	100838394	Missense_Mutation	SNP	C	T	116	80	c.2144G>A	c.(2143-2145)GGA>GAA	p.G715E
Pat_66	Pre-Treatment	GRIK2	2898	37	6	102134176	102134176	Missense_Mutation	SNP	G	A	78	69	c.899G>A	c.(898-900)CGA>CAA	p.R300Q
Pat_66	Pre-Treatment	TUBE1	51175	37	6	112395985	112395985	Missense_Mutation	SNP	G	A	24	69	c.881C>T	c.(880-882)CCT>CTT	p.P294L
Pat_66	Pre-Treatment	FRK	2444	37	6	116265408	116265408	Missense_Mutation	SNP	T	C	36	58	c.1139A>G	c.(1138-1140)AAG>AGG	p.K380R
Pat_66	Pre-Treatment	DSE	29940	37	6	116757465	116757465	Missense_Mutation	SNP	G	A	32	80	c.1834G>A	c.(1834-1836)GGT>AGT	p.G612S
Pat_66	Pre-Treatment	GPRC6A	222545	37	6	117150200	117150200	Splice_Site	SNP	C	T	16	26	c.-21_splice	c.e1-1	
Pat_66	Pre-Treatment	RFX6	222546	37	6	117237412	117237412	Missense_Mutation	SNP	C	T	77	208	c.907C>T	c.(907-909)CTT>TTT	p.L303F
Pat_66	Pre-Treatment	MAN1A1	4121	37	6	119509588	119509589	Nonsense_Mutation	DNP	CC	TT	39	129	.1700_1701GG>A	c.(1699-1701)TGG>TAA	p.W567*
Pat_66	Pre-Treatment	PKIB	5570	37	6	123039097	123039097	Missense_Mutation	SNP	C	T	92	45	c.158C>T	c.(157-159)TCC>TTC	p.S53F
Pat_66	Pre-Treatment	CLVS2	134829	37	6	123332185	123332185	Missense_Mutation	SNP	G	A	53	129	c.445G>A	c.(445-447)GAA>AAA	p.E149K
Pat_66	Pre-Treatment	CLVS2	134829	37	6	123377000	123377000	Missense_Mutation	SNP	C	T	65	131	c.725C>T	c.(724-726)CCT>CTT	p.P242L
Pat_66	Pre-Treatment	C6orf174	387104	37	6	127796599	127796599	Missense_Mutation	SNP	C	T	109	98	c.2572G>A	c.(2572-2574)GAG>AAG	p.E858K
Pat_66	Pre-Treatment	THEMIS	387357	37	6	128150822	128150822	Missense_Mutation	SNP	C	T	34	108	c.508G>A	c.(508-510)GAA>AAA	p.E170K
Pat_66	Pre-Treatment	ENPP1	5167	37	6	132176145	132176145	Missense_Mutation	SNP	C	T	26	61	c.697C>T	c.(697-699)CCT>TCT	p.P233S
Pat_66	Pre-Treatment	IL22RA2	116379	37	6	137477948	137477948	Missense_Mutation	SNP	C	T	55	99	c.241G>A	c.(241-243)GGA>AGA	p.G81R
Pat_66	Pre-Treatment	TXLNB	167838	37	6	139563953	139563953	Missense_Mutation	SNP	G	T	4	125	c.1765C>A	c.(1765-1767)CAA>AAA	p.Q589K
Pat_66	Pre-Treatment	ULBP2	80328	37	6	150267721	150267721	Missense_Mutation	SNP	G	A	53	188	c.563G>A	c.(562-564)GGA>GAA	p.G188E
Pat_66	Pre-Treatment	TULP4	56995	37	6	158900787	158900787	Missense_Mutation	SNP	C	T	23	59	c.1031C>T	c.(1030-1032)CCC>CTC	p.P344L
Pat_66	Pre-Treatment	FNDC1	84624	37	6	159644649	159644649	Missense_Mutation	SNP	G	A	16	41	c.856G>A	c.(856-858)GAA>AAA	p.E286K
Pat_66	Pre-Treatment	FNDC1	84624	37	6	159646676	159646676	Missense_Mutation	SNP	G	A	168	124	c.994G>A	c.(994-996)GAA>AAA	p.E332K
Pat_66	Pre-Treatment	PNLDC1	154197	37	6	160232741	160232741	Missense_Mutation	SNP	G	A	47	135	c.829G>A	c.(829-831)GAT>AAT	p.D277N
Pat_66	Pre-Treatment	MLLT4	4301	37	6	168352389	168352389	Missense_Mutation	SNP	G	A	5	283	c.4331G>A	c.(4330-4332)CGC>CAC	p.R1444H
Pat_66	Pre-Treatment	GPER	2852	37	7	1131968	1131968	Missense_Mutation	SNP	G	C	3	16	c.604G>C	c.(604-606)GAC>CAC	p.D202H
Pat_66	Pre-Treatment	SDK1	221935	37	7	4153678	4153678	Missense_Mutation	SNP	G	A	20	80	c.3595G>A	c.(3595-3597)GAT>AAT	p.D1199N
Pat_66	Pre-Treatment	SDK1	221935	37	7	4277281	4277281	Nonsense_Mutation	SNP	C	T	34	117	c.5995C>T	c.(5995-5997)CAA>TAA	p.Q1999*
Pat_66	Pre-Treatment	COL28A1	340267	37	7	7570984	7570984	Missense_Mutation	SNP	G	A	40	58	c.676C>T	c.(676-678)CGT>TGT	p.R226C
Pat_66	Pre-Treatment	HDAC9	9734	37	7	18688097	18688097	Missense_Mutation	SNP	C	T	72	75	c.1249C>T	c.(1249-1251)CCC>TCC	p.P417S
Pat_66	Pre-Treatment	RAPGEF5	9771	37	7	22194161	22194161	Missense_Mutation	SNP	A	T	67	106	c.1239T>A	c.(1237-1239)AGT>AGA	p.S413R
Pat_66	Pre-Treatment	IGF2BP3	10643	37	7	23401193	23401193	Missense_Mutation	SNP	C	T	48	197	c.361G>A	c.(361-363)GTT>ATT	p.V121I
Pat_66	Pre-Treatment	TRA2A	29896	37	7	23545756	23545756	Splice_Site	SNP	C	T	62	202	c.770_splice	c.e6+1	p.R257_splice
Pat_66	Pre-Treatment	TRA2A	29896	37	7	23552556	23552556	Missense_Mutation	SNP	C	T	37	124	c.482G>A	c.(481-483)GGA>GAA	p.G161E
Pat_66	Pre-Treatment	C7orf46	340277	37	7	23740429	23740429	Missense_Mutation	SNP	C	T	54	245	c.770C>T	c.(769-771)TCA>TTA	p.S257L
Pat_66	Pre-Treatment	HOXA3	3200	37	7	27149851	27149851	Missense_Mutation	SNP	G	A	58	57	c.409C>T	c.(409-411)CCT>TCT	p.P137S
Pat_66	Pre-Treatment	ADCYAP1R1	117	37	7	31146231	31146231	Missense_Mutation	SNP	C	T	41	43	c.1340C>T	c.(1339-1341)TCC>TTC	p.S447F
Pat_66	Pre-Treatment	CCDC129	223075	37	7	31683329	31683329	Missense_Mutation	SNP	C	T	15	87	c.2345C>T	c.(2344-2346)TCC>TTC	p.S782F
Pat_66	Pre-Treatment	PDE1C	5137	37	7	31887625	31887625	Missense_Mutation	SNP	C	T	35	131	c.937G>A	c.(937-939)GAG>AAG	p.E313K
Pat_66	Pre-Treatment	PDE1C	5137	37	7	31912990	31912990	Missense_Mutation	SNP	G	A	32	69	c.524C>T	c.(523-525)TCC>TTC	p.S175F
Pat_66	Pre-Treatment	NPSR1	387129	37	7	34818083	34818083	Missense_Mutation	SNP	C	T	4	86	c.290C>T	c.(289-291)ACA>ATA	p.T97I
Pat_66	Pre-Treatment	DPY19L1	23333	37	7	35009080	35009080	Missense_Mutation	SNP	G	A	18	113	c.760C>T	c.(760-762)CCT>TCT	p.P254S
Pat_66	Pre-Treatment	DPY19L2P1	554236	37	7	35161208	35161208	Missense_Mutation	SNP	C	T	20	82	c.499G>A	c.(499-501)GAT>AAT	p.D167N
Pat_66	Pre-Treatment	CDK13	8621	37	7	40134171	40134171	Missense_Mutation	SNP	G	T	6	343	c.4131G>T	c.(4129-4131)TTG>TTT	p.L1377F

Pat_66	Pre-Treatment	PKD1L1	168507	37	7	47869170	47869170	Nonsense_Mutation	SNP	C	T	217	264	c.6588G>A	c.(6586-6588)TGG>TGA	p.W2196*
Pat_66	Pre-Treatment	IKZF1	10320	37	7	50468209	50468209	Missense_Mutation	SNP	G	A	26	134	c.1444G>A	c.(1444-1446)GGC>AGC	p.G482S
Pat_66	Pre-Treatment	COBL	23242	37	7	51152896	51152896	Nonsense_Mutation	SNP	C	A	4	173	c.1063G>T	c.(1063-1065)GAG>TAG	p.E355*
Pat_66	Pre-Treatment	ZNF727	442319	37	7	63538806	63538806	Missense_Mutation	SNP	C	G	10	136	c.1379C>G	c.(1378-1380)ACC>AGC	p.T460S
Pat_66	Pre-Treatment	CLDN3	1365	37	7	73183904	73183904	Missense_Mutation	SNP	A	G	9	12	c.476T>C	c.(475-477)ATG>ACG	p.M159T
Pat_66	Pre-Treatment	ELN	2006	37	7	73474260	73474260	Missense_Mutation	SNP	C	T	117	334	c.1477C>T	c.(1477-1479)CCT>TCT	p.P493S
Pat_66	Pre-Treatment	EIF4H	7458	37	7	73609166	73609166	Missense_Mutation	SNP	C	T	42	61	c.565C>T	c.(565-567)CCC>TCC	p.P189S
Pat_66	Pre-Treatment	POM121C	100101267	37	7	75051130	75051130	Missense_Mutation	SNP	G	A	53	103	c.2405C>T	c.(2404-2406)TCC>TTC	p.S802F
Pat_66	Pre-Treatment	ZP3	7784	37	7	76062838	76062838	Missense_Mutation	SNP	C	T	5	317	c.587C>T	c.(586-588)GCC>GTC	p.A196V
Pat_66	Pre-Treatment	PCLO	27445	37	7	82581211	82581211	Missense_Mutation	SNP	C	T	15	105	c.9058G>A	c.(9058-9060)GAC>AAC	p.D3020N
Pat_66	Pre-Treatment	PCLO	27445	37	7	82581886	82581886	Missense_Mutation	SNP	C	T	39	156	c.8383G>A	c.(8383-8385)GTG>ATG	p.V2795M
Pat_66	Pre-Treatment	PCLO	27445	37	7	82764398	82764398	Missense_Mutation	SNP	C	T	73	231	c.2468G>A	c.(2467-2469)CGA>CAA	p.R823Q
Pat_66	Pre-Treatment	PCLO	27445	37	7	82784411	82784411	Missense_Mutation	SNP	G	A	6	413	c.1546C>T	c.(1546-1548)CCA>TCA	p.P516S
Pat_66	Pre-Treatment	SEMA3E	9723	37	7	82996952	82996952	Missense_Mutation	SNP	G	A	182	218	c.2278C>T	c.(2278-2280)CGT>TGT	p.R760C
Pat_66	Pre-Treatment	ABCB1	5243	37	7	87179226	87179226	Missense_Mutation	SNP	C	T	93	341	c.1495G>A	c.(1495-1497)GAG>AAG	p.E499K
Pat_66	Pre-Treatment	CYP51A1	1595	37	7	91758208	91758208	Missense_Mutation	SNP	C	T	105	421	c.454G>A	c.(454-456)GAT>AAT	p.D152N
Pat_66	Pre-Treatment	SAMD9	54809	37	7	92733373	92733373	Missense_Mutation	SNP	C	T	100	173	c.2038G>A	c.(2038-2040)GAG>AAG	p.E680K
Pat_66	Pre-Treatment	SAMD9L	219285	37	7	92762385	92762385	Missense_Mutation	SNP	T	A	22	88	c.2900A>T	c.(2899-2901)TAT>TTT	p.Y967F
Pat_66	Pre-Treatment	HEPACAM2	253012	37	7	92848689	92848689	Missense_Mutation	SNP	G	A	43	153	c.155C>T	c.(154-156)CCC>CTC	p.P52L
Pat_66	Pre-Treatment	CALCR	799	37	7	93108698	93108698	Missense_Mutation	SNP	C	T	123	443	c.227G>A	c.(226-228)CGA>CAA	p.R76Q
Pat_66	Pre-Treatment	ZKSCAN1	7586	37	7	99631659	99631659	Missense_Mutation	SNP	C	T	26	108	c.1531C>T	c.(1531-1533)CAC>TAC	p.H511Y
Pat_66	Pre-Treatment	ZNF3	7551	37	7	99669002	99669002	Missense_Mutation	SNP	C	T	169	246	c.1105G>A	c.(1105-1107)GAA>AAA	p.E369K
Pat_66	Pre-Treatment	ZAN	7455	37	7	100349878	100349878	Missense_Mutation	SNP	C	T	8	410	c.2150C>T	c.(2149-2151)CCC>CTC	p.P717L
Pat_66	Pre-Treatment	ACHE	43	37	7	100490217	100490217	Missense_Mutation	SNP	C	T	25	28	c.1291G>A	c.(1291-1293)GAT>AAT	p.D431N
Pat_66	Pre-Treatment	MUC17	140453	37	7	100682094	100682094	Missense_Mutation	SNP	C	T	9	850	c.7397C>T	c.(7396-7398)ACG>ATG	p.T2466M
Pat_66	Pre-Treatment	MUC17	140453	37	7	100682156	100682156	Missense_Mutation	SNP	A	G	9	861	c.7459A>G	c.(7459-7461)ATG>GTG	p.M2487V
Pat_66	Pre-Treatment	MUC17	140453	37	7	100682158	100682158	Missense_Mutation	SNP	G	C	8	859	c.7461G>C	c.(7459-7461)ATG>ATC	p.M2487I
Pat_66	Pre-Treatment	MUC17	140453	37	7	100686392	100686392	Missense_Mutation	SNP	C	T	80	251	c.11695C>T	c.(11695-11697)CCT>TCT	p.P3899S
Pat_66	Pre-Treatment	LRRC17	10234	37	7	102585050	102585050	Missense_Mutation	SNP	G	A	20	73	c.1322G>A	c.(1321-1323)GGA>GAA	p.G441E
Pat_66	Pre-Treatment	FBXL13	222235	37	7	102604109	102604109	Missense_Mutation	SNP	C	T	17	80	c.595G>A	c.(595-597)GAT>AAT	p.D199N
Pat_66	Pre-Treatment	ARMC10	83787	37	7	102733020	102733020	Missense_Mutation	SNP	A	G	6	171	c.625A>G	c.(625-627)ACC>GCC	p.T209A
Pat_66	Pre-Treatment	DNAJC2	27000	37	7	102968109	102968109	Missense_Mutation	SNP	T	C	39	62	c.424A>G	c.(424-426)ACT>GCT	p.T142A
Pat_66	Pre-Treatment	RELN	5649	37	7	103130197	103130197	Missense_Mutation	SNP	C	T	12	33	c.9755G>A	c.(9754-9756)AGC>AAC	p.S3252N
Pat_66	Pre-Treatment	RELN	5649	37	7	103230142	103230142	Missense_Mutation	SNP	C	T	122	141	c.4046G>A	c.(4045-4047)GGA>GAA	p.G1349E
Pat_66	Pre-Treatment	PUS7	54517	37	7	105121497	105121497	Splice_Site	SNP	A	G	39	48	c.1175_splice	c.e9+1	p.R392_splice
Pat_66	Pre-Treatment	LAMB1	3912	37	7	107580783	107580784	Missense_Mutation	DNP	CC	TT	17	80	.3411_3412GG>A	409-3414)AGGGGC>AGA	p.G1138S
Pat_66	Pre-Treatment	LAMB1	3912	37	7	107626771	107626771	Missense_Mutation	SNP	G	A	36	183	c.461C>T	c.(460-462)TCC>TTC	p.S154F
Pat_66	Pre-Treatment	LAMB4	22798	37	7	107677900	107677900	Missense_Mutation	SNP	C	T	82	317	c.4612G>A	c.(4612-4614)GAT>AAT	p.D1538N
Pat_66	Pre-Treatment	CADPS2	93664	37	7	122001003	122001003	Missense_Mutation	SNP	G	A	10	63	c.3452C>T	c.(3451-3453)TCA>TTA	p.S1151L
Pat_66	Pre-Treatment	FLNC	2318	37	7	128492959	128492959	Missense_Mutation	SNP	C	T	55	51	c.6082C>T	c.(6082-6084)CCC>TCC	p.P2028S
Pat_66	Pre-Treatment	TSPAN33	340348	37	7	128807650	128807650	Nonsense_Mutation	SNP	C	T	48	50	c.787C>T	c.(787-789)CAG>TAG	p.Q263*
Pat_66	Pre-Treatment	KIAA1549	57670	37	7	138579122	138579122	Missense_Mutation	SNP	G	A	129	227	c.3998C>T	c.(3997-3999)CCT>CTT	p.P1333L
Pat_66	Pre-Treatment	KIAA1549	57670	37	7	138601892	138601892	Missense_Mutation	SNP	G	A	21	90	c.2480C>T	c.(2479-2481)TCT>TTT	p.S827F
Pat_66	Pre-Treatment	TBXAS1	6916	37	7	139655370	139655370	Missense_Mutation	SNP	G	A	86	95	c.793G>A	c.(793-795)GAA>AAA	p.E265K
Pat_66	Pre-Treatment	BRAF	673	37	7	140453136	140453136	Missense_Mutation	SNP	A	T	72	118	c.1799T>A	c.(1798-1800)GTG>GAG	p.V600E
Pat_66	Pre-Treatment	TAS2R4	50832	37	7	141478757	141478757	Missense_Mutation	SNP	C	T	198	260	c.469C>T	c.(469-471)CCT>TCT	p.P157S
Pat_66	Pre-Treatment	TRY6	154754	37	7	142479959	142479959	Missense_Mutation	SNP	G	A	52	347	c.91G>A	c.(91-93)GAG>AAG	p.E31K

Pat_66	Pre-Treatment	KEL	3792	37	7	142641771	142641771	Missense_Mutation	SNP	G	A	17	41	c.1372C>T	c.(1372-1374)CCC>TCC	p.P458S
Pat_66	Pre-Treatment	KEL	3792	37	7	142651429	142651429	Nonsense_Mutation	SNP	G	A	29	93	c.766C>T	c.(766-768)CAG>TAG	p.Q256*
Pat_66	Pre-Treatment	CLCN1	1180	37	7	143047677	143047677	Missense_Mutation	SNP	C	T	191	245	c.2525C>T	c.(2524-2526)TCA>TTA	p.S842L
Pat_66	Pre-Treatment	OR2F1	26211	37	7	143657212	143657212	Missense_Mutation	SNP	G	A	257	313	c.149G>A	c.(148-150)AGA>AAA	p.R50K
Pat_66	Pre-Treatment	ARHGEF5	7984	37	7	144062335	144062336	Missense_Mutation	DNP	CC	TT	21	150	.2573_2574CC>T	c.(2572-2574)TCC>TTT	p.S858F
Pat_66	Pre-Treatment	NOBOX	135935	37	7	144101747	144101747	Missense_Mutation	SNP	G	A	50	244	c.112C>T	c.(112-114)CCT>TCT	p.P38S
Pat_66	Pre-Treatment	TPK1	27010	37	7	144380069	144380069	Missense_Mutation	SNP	G	A	66	212	c.118C>T	c.(118-120)CTT>TTT	p.L40F
Pat_66	Pre-Treatment	CNTNAP2	26047	37	7	147259245	147259245	Missense_Mutation	SNP	C	T	32	95	c.1793C>T	c.(1792-1794)TCC>TTC	p.S598F
Pat_66	Pre-Treatment	ZNF425	155054	37	7	148802286	148802286	Missense_Mutation	SNP	G	A	22	83	c.677C>T	c.(676-678)TCG>TTG	p.S226L
Pat_66	Pre-Treatment	ZNF777	27153	37	7	149129231	149129231	Missense_Mutation	SNP	C	A	4	183	c.2132G>T	c.(2131-2133)CGC>CTC	p.R711L
Pat_66	Pre-Treatment	ZNF777	27153	37	7	149133705	149133705	Missense_Mutation	SNP	C	T	4	127	c.1300G>A	c.(1300-1302)GAA>AAA	p.E434K
Pat_66	Pre-Treatment	SSPO	23145	37	7	149509113	149509113	Missense_Mutation	SNP	C	T	24	67	c.9659C>T	c.(9658-9660)ACC>ATC	p.T3220I
Pat_66	Pre-Treatment	GIMAP8	155038	37	7	150164120	150164120	Missense_Mutation	SNP	G	A	20	94	c.334G>A	c.(334-336)GAA>AAA	p.E112K
Pat_66	Pre-Treatment	GIMAP8	155038	37	7	150171298	150171298	Missense_Mutation	SNP	G	A	22	55	c.881G>A	c.(880-882)AGA>AAA	p.R294K
Pat_66	Pre-Treatment	GIMAP7	168537	37	7	150217158	150217158	Missense_Mutation	SNP	A	C	24	86	c.96A>C	c.(94-96)GAA>GAC	p.E32D
Pat_66	Pre-Treatment	GIMAP6	474344	37	7	150325516	150325516	Missense_Mutation	SNP	C	T	178	529	c.170G>A	c.(169-171)GGA>GAA	p.G57E
Pat_66	Pre-Treatment	UBE3C	9690	37	7	156974272	156974272	Missense_Mutation	SNP	C	T	19	110	c.677C>T	c.(676-678)TCT>TTT	p.S226F
Pat_66	Pre-Treatment	MYOM2	9172	37	8	2005529	2005530	Missense_Mutation	DNP	CC	TT	11	30	c.327_328CC>TT	325-330)GCCCAC>GCTT	p.H110Y
Pat_66	Pre-Treatment	CSMD1	64478	37	8	2855550	2855550	Missense_Mutation	SNP	G	A	16	51	c.8363C>T	c.(8362-8364)CCT>CTT	p.P2788L
Pat_66	Pre-Treatment	CSMD1	64478	37	8	2876022	2876022	Missense_Mutation	SNP	C	T	373	271	c.8009G>A	c.(8008-8010)AGC>AAC	p.S2670N
Pat_66	Pre-Treatment	CSMD1	64478	37	8	3474275	3474275	Missense_Mutation	SNP	G	A	18	46	c.1054C>T	c.(1054-1056)CCT>TCT	p.P352S
Pat_66	Pre-Treatment	XKR5	389610	37	8	6682776	6682776	Missense_Mutation	SNP	C	T	22	24	c.338G>A	c.(337-339)CGA>CAA	p.R113Q
Pat_66	Pre-Treatment	RP1L1	94137	37	8	10464908	10464908	Missense_Mutation	SNP	C	T	45	140	c.6700G>A	c.(6700-6702)GAA>AAA	p.E2234K
Pat_66	Pre-Treatment	RP1L1	94137	37	8	10468055	10468055	Missense_Mutation	SNP	C	A	12	27	c.3553G>T	c.(3553-3555)GGG>TGG	p.G1185W
Pat_66	Pre-Treatment	HR	55806	37	8	21979204	21979204	Missense_Mutation	SNP	C	T	48	28	c.2125G>A	c.(2125-2127)GAA>AAA	p.E709K
Pat_66	Pre-Treatment	POLR3D	661	37	8	22108026	22108026	Missense_Mutation	SNP	C	T	7	352	c.1192C>T	c.(1192-1194)CGG>TGG	p.R398W
Pat_66	Pre-Treatment	LOXL2	4017	37	8	23217643	23217643	Missense_Mutation	SNP	G	A	43	83	c.491C>T	c.(490-492)CCT>CTT	p.P164L
Pat_66	Pre-Treatment	ADAM28	10863	37	8	24187516	24187516	Missense_Mutation	SNP	C	T	42	120	c.991C>T	c.(991-993)CTT>TTT	p.L331F
Pat_66	Pre-Treatment	ADAM7	8756	37	8	24350557	24350557	Missense_Mutation	SNP	G	A	29	22	c.1657G>A	c.(1657-1659)GAT>AAT	p.D553N
Pat_66	Pre-Treatment	NEFL	4747	37	8	24811034	24811034	Missense_Mutation	SNP	C	T	11	16	c.1444G>A	c.(1444-1446)GAC>AAC	p.D482N
Pat_66	Pre-Treatment	PNMA2	10687	37	8	26365883	26365883	Missense_Mutation	SNP	G	A	55	44	c.389C>T	c.(388-390)TCT>TTT	p.S130F
Pat_66	Pre-Treatment	BRF2	55290	37	8	37702440	37702440	Missense_Mutation	SNP	C	A	4	96	c.828G>T	c.(826-828)ATG>ATT	p.M276I
Pat_66	Pre-Treatment	ASH2L	9070	37	8	37972516	37972516	Nonsense_Mutation	SNP	C	T	34	24	c.775C>T	c.(775-777)CAG>TAG	p.Q259*
Pat_66	Pre-Treatment	ANK1	286	37	8	41530173	41530173	Missense_Mutation	SNP	C	T	108	82	c.4795G>A	c.(4795-4797)GAG>AAG	p.E1599K
Pat_66	Pre-Treatment	EFCAB1	79645	37	8	49642299	49642299	Missense_Mutation	SNP	C	T	22	59	c.451G>A	c.(451-453)GAA>AAA	p.E151K
Pat_66	Pre-Treatment	RB1CC1	9821	37	8	53554996	53554996	Missense_Mutation	SNP	G	T	44	90	c.4252C>A	c.(4252-4254)CCA>ACA	p.P1418T
Pat_66	Pre-Treatment	RP1	6101	37	8	55534017	55534017	Missense_Mutation	SNP	C	T	36	134	c.491C>T	c.(490-492)CCG>CTG	p.P164L
Pat_66	Pre-Treatment	RP1	6101	37	8	55539216	55539216	Missense_Mutation	SNP	C	T	15	40	c.2774C>T	c.(2773-2775)CCA>CTA	p.P925L
Pat_66	Pre-Treatment	XKR4	114786	37	8	56436133	56436133	Missense_Mutation	SNP	G	A	207	133	c.1300G>A	c.(1300-1302)GAC>AAC	p.D434N
Pat_66	Pre-Treatment	XKR4	114786	37	8	56436373	56436373	Missense_Mutation	SNP	C	T	41	108	c.1540C>T	c.(1540-1542)CAT>TAT	p.H514Y
Pat_66	Pre-Treatment	CHD7	55636	37	8	61655535	61655535	Missense_Mutation	SNP	C	T	4	80	c.1544C>T	c.(1543-1545)CCT>CTT	p.P515L
Pat_66	Pre-Treatment	CHD7	55636	37	8	61769426	61769426	Missense_Mutation	SNP	C	A	4	109	c.7587C>A	c.(7585-7587)CAC>CAA	p.H2529Q
Pat_66	Pre-Treatment	SULF1	23213	37	8	70514018	70514018	Missense_Mutation	SNP	C	T	89	303	c.1015C>T	c.(1015-1017)CGT>TGT	p.R339C
Pat_66	Pre-Treatment	SULF1	23213	37	8	70517147	70517147	Missense_Mutation	SNP	G	A	49	142	c.1357G>A	c.(1357-1359)GCC>ACC	p.A453T
Pat_66	Pre-Treatment	C8orf84	157869	37	8	73979655	73979655	Missense_Mutation	SNP	C	T	44	121	c.716G>A	c.(715-717)CGG>CAG	p.R239Q
Pat_66	Pre-Treatment	HNF4G	3174	37	8	76456156	76456156	Missense_Mutation	SNP	G	A	47	151	c.88G>A	c.(88-90)GAT>AAT	p.D30N
Pat_66	Pre-Treatment	ZFHX4	79776	37	8	77763577	77763577	Missense_Mutation	SNP	G	A	15	39	c.4285G>A	c.(4285-4287)GAA>AAA	p.E1429K

Pat_66	Pre-Treatment	ZFHX4	79776	37	8	77763842	77763842	Missense_Mutation	SNP	C	T	23	23	c.4550C>T	c.(4549-4551)TCA>TTA	p.S1517L
Pat_66	Pre-Treatment	ZFHX4	79776	37	8	77766736	77766736	Missense_Mutation	SNP	C	T	173	121	c.7444C>T	c.(7444-7446)CCG>TCG	p.P2482S
Pat_66	Pre-Treatment	FABP12	646486	37	8	82441830	82441830	Missense_Mutation	SNP	C	T	18	38	c.89G>A	c.(88-90)AGC>AAC	p.S30N
Pat_66	Pre-Treatment	CA1	759	37	8	86240796	86240796	Missense_Mutation	SNP	G	A	52	136	c.779C>T	c.(778-780)TCA>TTA	p.S260L
Pat_66	Pre-Treatment	CA1	759	37	8	86250541	86250541	Missense_Mutation	SNP	C	T	83	227	c.175G>A	c.(175-177)GAA>AAA	p.E59K
Pat_66	Pre-Treatment	CNGB3	54714	37	8	87755783	87755783	Missense_Mutation	SNP	G	A	71	45	c.73C>T	c.(73-75)CGT>TGT	p.R25C
Pat_66	Pre-Treatment	DCAF4L2	138009	37	8	88885877	88885877	Missense_Mutation	SNP	G	A	4	174	c.323C>T	c.(322-324)ACG>ATG	p.T108M
Pat_66	Pre-Treatment	SLC26A7	115111	37	8	92330577	92330577	Missense_Mutation	SNP	C	T	34	136	c.611C>T	c.(610-612)CCA>CTA	p.P204L
Pat_66	Pre-Treatment	VPS13B	157680	37	8	100711962	100711962	Missense_Mutation	SNP	C	T	27	79	c.6331C>T	c.(6331-6333)CAT>TAT	p.H2111Y
Pat_66	Pre-Treatment	VPS13B	157680	37	8	100833705	100833705	Nonsense_Mutation	SNP	C	T	60	136	c.9253C>T	c.(9253-9255)CAG>TAG	p.Q3085*
Pat_66	Pre-Treatment	LRP12	29967	37	8	105507435	105507435	Missense_Mutation	SNP	G	A	61	42	c.1583C>T	c.(1582-1584)TCA>TTA	p.S528L
Pat_66	Pre-Treatment	ZFPM2	23414	37	8	106813433	106813433	Nonsense_Mutation	SNP	C	T	78	236	c.1123C>T	c.(1123-1125)CAG>TAG	p.Q375*
Pat_66	Pre-Treatment	ABRA	137735	37	8	107773437	107773437	Missense_Mutation	SNP	C	T	40	75	c.974G>A	c.(973-975)CGA>CAA	p.R325Q
Pat_66	Pre-Treatment	PKHD1L1	93035	37	8	110416854	110416854	Missense_Mutation	SNP	G	A	15	40	c.1445G>A	c.(1444-1446)CGA>CAA	p.R482Q
Pat_66	Pre-Treatment	PKHD1L1	93035	37	8	110516633	110516633	Missense_Mutation	SNP	G	A	15	38	c.10906G>A	c.(10906-10908)GAT>AAT	p.D3636N
Pat_66	Pre-Treatment	CSMD3	114788	37	8	113323251	113323251	Missense_Mutation	SNP	G	A	122	72	c.7841C>T	c.(7840-7842)TCC>TTC	p.S2614F
Pat_66	Pre-Treatment	SLC30A8	169026	37	8	118184870	118184870	Missense_Mutation	SNP	C	T	56	161	c.1060C>T	c.(1060-1062)CCA>TCA	p.P354S
Pat_66	Pre-Treatment	COL14A1	7373	37	8	121357721	121357721	Missense_Mutation	SNP	G	A	22	39	c.4996G>A	c.(4996-4998)GGA>AGA	p.G1666R
Pat_66	Pre-Treatment	ANXA13	312	37	8	124749565	124749565	Missense_Mutation	SNP	G	A	39	90	c.10C>T	c.(10-12)CGT>TGT	p.R4C
Pat_66	Pre-Treatment	COL22A1	169044	37	8	139675952	139675952	Missense_Mutation	SNP	G	A	24	77	c.3182C>T	c.(3181-3183)TCC>TTC	p.S1061F
Pat_66	Pre-Treatment	BAI1	575	37	8	143602191	143602191	Missense_Mutation	SNP	C	T	22	75	c.2929C>T	c.(2929-2931)CGC>TGC	p.R977C
Pat_66	Pre-Treatment	PTPRD	5789	37	9	8499838	8499838	Missense_Mutation	SNP	G	A	31	25	c.2131C>T	c.(2131-2133)CCT>TCT	p.P711S
Pat_66	Pre-Treatment	FREM1	158326	37	9	14842587	14842587	Missense_Mutation	SNP	C	T	42	68	c.1465G>A	c.(1465-1467)GAC>AAC	p.D489N
Pat_66	Pre-Treatment	ADAMTSL1	92949	37	9	18504842	18504842	Missense_Mutation	SNP	C	T	4	140	c.79C>T	c.(79-81)CGC>TGC	p.R27C
Pat_66	Pre-Treatment	TAF1L	138474	37	9	32632096	32632096	Missense_Mutation	SNP	C	T	27	39	c.3482G>A	c.(3481-3483)GGA>GAA	p.G1161E
Pat_66	Pre-Treatment	SIT1	27240	37	9	35650036	35650036	Missense_Mutation	SNP	G	A	7	5	c.400C>T	c.(400-402)CCT>TCT	p.P134S
Pat_66	Pre-Treatment	C9orf128	392307	37	9	35826156	35826156	Missense_Mutation	SNP	C	T	41	2	c.3G>A	c.(1-3)ATG>ATA	p.M1I
Pat_66	Pre-Treatment	FAM75A5	727905	37	9	65506476	65506476	Missense_Mutation	SNP	A	C	4	27	c.1084T>G	c.(1084-1086)TAT>GAT	p.Y362D
Pat_66	Pre-Treatment	VPS13A	23230	37	9	79936480	79936480	Missense_Mutation	SNP	C	T	67	6	c.5648C>T	c.(5647-5649)TCC>TTC	p.S1883F
Pat_66	Pre-Treatment	DIRAS2	54769	37	9	93375722	93375722	Missense_Mutation	SNP	C	T	68	15	c.388G>A	c.(388-390)GAG>AAG	p.E130K
Pat_66	Pre-Treatment	ROR2	4920	37	9	94486933	94486933	Missense_Mutation	SNP	C	T	38	65	c.1843G>A	c.(1843-1845)GAC>AAC	p.D615N
Pat_66	Pre-Treatment	GRIN3A	116443	37	9	104432595	104432595	Missense_Mutation	SNP	G	A	79	145	c.2099C>T	c.(2098-2100)CCA>CTA	p.P700L
Pat_66	Pre-Treatment	GRIN3A	116443	37	9	104449113	104449113	Missense_Mutation	SNP	C	T	13	24	c.1069G>A	c.(1069-1071)GGA>AGA	p.G357R
Pat_66	Pre-Treatment	OR13C8	138802	37	9	107331728	107331728	Missense_Mutation	SNP	T	G	105	12	c.280T>G	c.(280-282)TTC>GTC	p.F94V
Pat_66	Pre-Treatment	KIAA1958	158405	37	9	115421766	115421766	Missense_Mutation	SNP	C	T	7	13	c.1568C>T	c.(1567-1569)TCG>TTG	p.S523L
Pat_66	Pre-Treatment	BSPRY	54836	37	9	116132216	116132216	Missense_Mutation	SNP	C	T	41	3	c.1003C>T	c.(1003-1005)CGT>TGT	p.R335C
Pat_66	Pre-Treatment	DBC1	1620	37	9	121929550	121929550	Missense_Mutation	SNP	G	A	86	14	c.2098C>T	c.(2098-2100)CGG>TGG	p.R700W
Pat_66	Pre-Treatment	OR1J1	347168	37	9	125239548	125239548	Missense_Mutation	SNP	G	A	31	41	c.658C>T	c.(658-660)CAC>TAC	p.H220Y
Pat_66	Pre-Treatment	OR1L8	138881	37	9	125329864	125329864	Missense_Mutation	SNP	T	A	43	79	c.893A>T	c.(892-894)AAA>ATA	p.K298I
Pat_66	Pre-Treatment	GAPVD1	26130	37	9	128116965	128116965	Missense_Mutation	SNP	G	A	5	181	c.3656G>A	c.(3655-3657)CGT>CAT	p.R1219H
Pat_66	Pre-Treatment	ST6GALNAC4	27090	37	9	130674947	130674947	Missense_Mutation	SNP	C	T	17	17	c.211G>A	c.(211-213)GAG>AAG	p.E71K
Pat_66	Pre-Treatment	NUP188	23511	37	9	131715114	131715114	Nonsense_Mutation	SNP	C	A	4	92	c.150C>A	c.(148-150)TAC>TAA	p.Y50*
Pat_66	Pre-Treatment	C9orf78	51759	37	9	132595784	132595784	Nonsense_Mutation	SNP	G	A	88	15	c.208C>T	c.(208-210)CAG>TAG	p.Q70*
Pat_66	Pre-Treatment	COL5A1	1289	37	9	137676892	137676892	Missense_Mutation	SNP	C	T	23	28	c.2542C>T	c.(2542-2544)CGC>TGC	p.R848C
Pat_66	Pre-Treatment	GLT6D1	360203	37	9	138516281	138516281	Missense_Mutation	SNP	C	T	17	33	c.493G>A	c.(493-495)GAG>AAG	p.E165K
Pat_66	Pre-Treatment	SOHLH1	402381	37	9	138586301	138586301	Missense_Mutation	SNP	G	A	21	23	c.878C>T	c.(877-879)TCT>TTT	p.S293F
Pat_66	Pre-Treatment	NOTCH1	4851	37	9	139410115	139410115	Missense_Mutation	SNP	A	G	2	3	c.1723T>C	c.(1723-1725)TGC>CGC	p.C575R

Pat_66	Pre-Treatment	CACNA1B	774	37	9	141012408	141012408	Missense_Mutation	SNP	G	A	18	2	c.5788G>A	c.(5788-5790)GAG>AAG	p.E1930K
Pat_66	Pre-Treatment	CSF2RA	1438	37	X	1409342	1409342	Missense_Mutation	SNP	G	A	249	481	c.586G>A	c.(586-588)GGA>AGA	p.G196R
Pat_66	Pre-Treatment	ARSF	416	37	X	3002631	3002631	Missense_Mutation	SNP	G	A	81	8	c.754G>A	c.(754-756)GAG>AAG	p.E252K
Pat_66	Pre-Treatment	OFD1	8481	37	X	13786855	13786855	Nonsense_Mutation	SNP	C	T	265	13	c.2947C>T	c.(2947-2949)CAA>TAA	p.Q983*
Pat_66	Pre-Treatment	ASB11	140456	37	X	15301686	15301686	Nonsense_Mutation	SNP	G	A	260	21	c.913C>T	c.(913-915)CAA>TAA	p.Q305*
Pat_66	Pre-Treatment	CA5B	11238	37	X	15794864	15794864	Missense_Mutation	SNP	G	T	4	115	c.646G>T	c.(646-648)GAC>TAC	p.D216Y
Pat_66	Pre-Treatment	MAP7D2	256714	37	X	20074807	20074807	Missense_Mutation	SNP	C	T	67	4	c.475G>A	c.(475-477)GGA>AGA	p.G159R
Pat_66	Pre-Treatment	PHEX	5251	37	X	22151661	22151661	Missense_Mutation	SNP	G	A	4	81	c.1324G>A	c.(1324-1326)GTT>ATT	p.V442I
Pat_66	Pre-Treatment	DDX53	168400	37	X	23019721	23019721	Missense_Mutation	SNP	G	A	79	4	c.1547G>A	c.(1546-1548)GGA>GAA	p.G516E
Pat_66	Pre-Treatment	ACOT9	23597	37	X	23723123	23723123	Missense_Mutation	SNP	A	G	4	116	c.1067T>C	c.(1066-1068)TTT>TCT	p.F356S
Pat_66	Pre-Treatment	KLHL15	80311	37	X	24006306	24006306	Missense_Mutation	SNP	T	C	199	17	c.1547A>G	c.(1546-1548)AAC>AGC	p.N516S
Pat_66	Pre-Treatment	MAGEB18	286514	37	X	26157979	26157979	Missense_Mutation	SNP	G	A	26	26	c.877G>A	c.(877-879)GAT>AAT	p.D293N
Pat_66	Pre-Treatment	MAGEB6	158809	37	X	26212462	26212462	Missense_Mutation	SNP	G	A	45	8	c.499G>A	c.(499-501)GAT>AAT	p.D167N
Pat_66	Pre-Treatment	MAGEB16	139604	37	X	35820977	35820977	Missense_Mutation	SNP	G	A	55	5	c.664G>A	c.(664-666)GAA>AAA	p.E222K
Pat_66	Pre-Treatment	FAM47C	442444	37	X	37028425	37028425	Missense_Mutation	SNP	A	G	6	242	c.1942A>G	c.(1942-1944)AAT>GAT	p.N648D
Pat_66	Pre-Treatment	CASK	8573	37	X	41646435	41646435	Missense_Mutation	SNP	C	T	4	107	c.274G>A	c.(274-276)GAA>AAA	p.E92K
Pat_66	Pre-Treatment	SLC38A5	92745	37	X	48320437	48320437	Missense_Mutation	SNP	G	A	25	4	c.727C>T	c.(727-729)CTC>TTC	p.L243F
Pat_66	Pre-Treatment	CCNB3	85417	37	X	50052469	50052469	Missense_Mutation	SNP	G	A	28	39	c.1300G>A	c.(1300-1302)GAA>AAA	p.E434K
Pat_66	Pre-Treatment	DGKK	139189	37	X	50122725	50122725	Missense_Mutation	SNP	C	T	35	30	c.2762G>A	c.(2761-2763)GGA>GAA	p.G921E
Pat_66	Pre-Treatment	IQSEC2	23096	37	X	53280121	53280121	Nonsense_Mutation	SNP	C	T	4	31	c.1637G>A	c.(1636-1638)TGG>TAG	p.W546*
Pat_66	Pre-Treatment	HUWE1	10075	37	X	53619395	53619395	Missense_Mutation	SNP	C	T	4	222	c.3935G>A	c.(3934-3936)CGC>CAC	p.R1312H
Pat_66	Pre-Treatment	FAM155B	27112	37	X	68725643	68725643	Missense_Mutation	SNP	C	T	40	33	c.518C>T	c.(517-519)TCC>TTC	p.S173F
Pat_66	Pre-Treatment	KIAA2022	340533	37	X	73961708	73961708	Missense_Mutation	SNP	G	A	19	2	c.2684C>T	c.(2683-2685)TCT>TTT	p.S895F
Pat_66	Pre-Treatment	ATRX	546	37	X	76855029	76855029	Missense_Mutation	SNP	T	C	7	459	c.5807A>G	c.(5806-5808)AAG>AGG	p.K1936R
Pat_66	Pre-Treatment	ATP7A	538	37	X	77267085	77267085	Missense_Mutation	SNP	C	T	134	144	c.2086C>T	c.(2086-2088)CAT>TAT	p.H696Y
Pat_66	Pre-Treatment	CPXCR1	53336	37	X	88009059	88009059	Missense_Mutation	SNP	G	A	29	1	c.644G>A	c.(643-645)GGA>GAA	p.G215E
Pat_66	Pre-Treatment	PCDH19	57526	37	X	99662470	99662470	Missense_Mutation	SNP	G	A	96	5	c.1126C>T	c.(1126-1128)CGC>TGC	p.R376C
Pat_66	Pre-Treatment	NOX1	27035	37	X	100105165	100105165	Missense_Mutation	SNP	C	T	54	5	c.1108G>A	c.(1108-1110)GAA>AAA	p.E370K
Pat_66	Pre-Treatment	DRP2	1821	37	X	100505510	100505510	Missense_Mutation	SNP	G	A	69	3	c.1639G>A	c.(1639-1641)GAA>AAA	p.E547K
Pat_66	Pre-Treatment	ALG13	79868	37	X	110951623	110951623	Splice_Site	SNP	T	A	5	241	c.750_splice	c.e4+2	p.Q250_splice
Pat_66	Pre-Treatment	C1GALT1C1	29071	37	X	119760088	119760088	Missense_Mutation	SNP	G	A	105	9	c.934C>T	c.(934-936)CCA>TCA	p.P312S
Pat_66	Pre-Treatment	ACTRT1	139741	37	X	127185392	127185392	Missense_Mutation	SNP	G	A	157	25	c.794C>T	c.(793-795)CCT>CTT	p.P265L
Pat_66	Pre-Treatment	XPNPEP2	7512	37	X	128880301	128880301	Missense_Mutation	SNP	G	A	13	42	c.388G>A	c.(388-390)GAG>AAG	p.E130K
Pat_66	Pre-Treatment	XPNPEP2	7512	37	X	128886312	128886312	Missense_Mutation	SNP	G	A	38	62	c.1008G>A	c.(1006-1008)ATG>ATA	p.M336I
Pat_66	Pre-Treatment	IGSF1	3547	37	X	130408659	130408659	Missense_Mutation	SNP	C	T	255	23	c.3665G>A	c.(3664-3666)GGA>GAA	p.G1222E
Pat_66	Pre-Treatment	USP26	83844	37	X	132160643	132160643	Missense_Mutation	SNP	C	T	131	7	c.1606G>A	c.(1606-1608)GAC>AAC	p.D536N
Pat_66	Pre-Treatment	GPR112	139378	37	X	135482020	135482020	Missense_Mutation	SNP	G	A	79	5	c.8320G>A	c.(8320-8322)GAT>AAT	p.D2774N
Pat_66	Pre-Treatment	ARHGEF6	9459	37	X	135760110	135760110	Missense_Mutation	SNP	C	A	4	125	c.1836G>T	c.(1834-1836)ATG>ATT	p.M612I
Pat_66	Pre-Treatment	MCF2	4168	37	X	138680593	138680593	Missense_Mutation	SNP	C	T	65	5	c.1901G>A	c.(1900-1902)CGA>CAA	p.R634Q
Pat_66	Pre-Treatment	SPANXC	64663	37	X	140335729	140335729	Missense_Mutation	SNP	G	A	171	15	c.215C>T	c.(214-216)GCC>GTC	p.A72V
Pat_66	Pre-Treatment	MAGEC1	9947	37	X	140993455	140993455	Missense_Mutation	SNP	G	A	4	158	c.265G>A	c.(265-267)GGC>AGC	p.G89S
Pat_66	Pre-Treatment	MAGEC2	51438	37	X	141291215	141291215	Missense_Mutation	SNP	C	T	190	16	c.559G>A	c.(559-561)GAG>AAG	p.E187K
Pat_66	Pre-Treatment	SLITRK4	139065	37	X	142716788	142716788	Missense_Mutation	SNP	C	T	56	61	c.2137G>A	c.(2137-2139)GAT>AAT	p.D713N
Pat_66	Pre-Treatment	SLITRK4	139065	37	X	142717159	142717159	Missense_Mutation	SNP	G	A	4	155	c.1766C>T	c.(1765-1767)GCA>GTA	p.A589V
Pat_66	Pre-Treatment	SLITRK4	139065	37	X	142718881	142718881	Missense_Mutation	SNP	G	A	78	4	c.44C>T	c.(43-45)TCG>TTG	p.S15L
Pat_66	Pre-Treatment	MAGEA10	4109	37	X	151303640	151303640	Missense_Mutation	SNP	C	T	54	51	c.453G>A	c.(451-453)ATG>ATA	p.M151I
Pat_66	Pre-Treatment	GABRQ	55879	37	X	151820055	151820055	Missense_Mutation	SNP	C	T	146	10	c.968C>T	c.(967-969)TCC>TTC	p.S323F

Pat_66	Pre-Treatment	GABRQ	55879	37	X	151821038	151821038	Missense_Mutation	SNP	C	T	48	43	c.1193C>T	c.(1192-1194)TCT>TTT	p.S398F
Pat_66	Pre-Treatment	MAGEA12	4111	37	X	151900077	151900077	Missense_Mutation	SNP	G	T	102	117	c.724C>A	c.(724-726)CCC>ACC	p.P242T
Pat_66	Pre-Treatment	MAGEA3	4102	37	X	151935410	151935410	Missense_Mutation	SNP	C	T	105	90	c.757G>A	c.(757-759)GAA>AAA	p.E253K
Pat_66	Pre-Treatment	OPN1LW	5956	37	X	153421817	153421817	Missense_Mutation	SNP	G	A	64	311	c.793G>A	c.(793-795)GAA>AAA	p.E265K
Pat_66	Pre-Treatment	PLXNA3	55558	37	X	153692563	153692563	Missense_Mutation	SNP	G	A	3	17	c.1735G>A	c.(1735-1737)GCG>ACG	p.A579T
Pat_04	Pre-Treatment	ZBTB40	9923	37	1	22838561	22838563	In_Frame_Del	DEL	AAG	-	7	79	.2395_2397delAA	c.(2395-2397)AAGdel	p.K803del
Pat_04	Pre-Treatment	SFRS11	9295	37	1	70705169	70705171	In_Frame_Del	DEL	AGG	-	7	151	c.766_768delAGG	c.(766-768)AGGdel	p.R259del
Pat_04	Pre-Treatment	ZC3H11A	9877	37	1	203786224	203786225	Frame_Shift_Ins	INS	-	T	7	63	c.26_27insT	c.(25-27)TATfs	p.Y9fs
Pat_04	Pre-Treatment	SCN3B	55800	37	11	123516308	123516308	Frame_Shift_Del	DEL	C	-	12	155	c.206delG	c.(205-207)GGTfs	p.G69fs
Pat_04	Pre-Treatment	EMG1	10436	37	12	7080212	7080213	Splice_Site	INS	-	C	7	22	c.129_splice	c.e2+1	p.L43_splice
Pat_04	Pre-Treatment	CTNNB1	1499	37	3	41266115	41266120	In_Frame_Del	DEL	GGTGCC	-	9	55	112_117delGGTG	c.(112-117)GGTGCCdel	p.GA38del
Pat_04	Pre-Treatment	UGT2B10	7365	37	4	69696370	69696370	Frame_Shift_Del	DEL	A	-	21	148	c.1360delA	c.(1360-1362)AAGfs	p.K454fs
Pat_04	Pre-Treatment	POM121	9883	37	7	72412603	72412604	Frame_Shift_Ins	INS	-	A	7	188	c.2071_2072insA	c.(2071-2073)CAAfs	p.Q691fs
Pat_04	Pre-Treatment	SMARCA2	6595	37	9	2039777	2039779	In_Frame_Del	DEL	CAG	-	6	7	c.667_669delCAG	c.(667-669)CAGdel	p.Q238del
Pat_04	Pre-Treatment	GRIN1	2902	37	9	140056884	140056886	In_Frame_Del	DEL	GAG	-	8	68	.1780_1782delGA	c.(1780-1782)GAGdel	p.E598del
Pat_04	Post-Resistance	ZBTB40	9923	37	1	22838561	22838563	In_Frame_Del	DEL	AAG	-	7	88	.2395_2397delAA	c.(2395-2397)AAGdel	p.K803del
Pat_04	Post-Resistance	CHGA	1113	37	14	93397924	93397926	In_Frame_Del	DEL	GAG	-	7	24	c.685_687delGAG	c.(685-687)GAGdel	p.E236del
Pat_04	Post-Resistance	GLG1	2734	37	16	74640754	74640756	In_Frame_Del	DEL	TGC	-	2	4	c.237_239delGCA	c.(235-240)CAGCAA>CAA	p.79_80QQ>Q
Pat_04	Post-Resistance	STRN4	29888	37	19	47226405	47226407	In_Frame_Del	DEL	GCT	-	2	4	.1729_1731delAG	c.(1729-1731)AGCdel	p.S577del
Pat_04	Post-Resistance	TCF20	6942	37	22	42610573	42610575	In_Frame_Del	DEL	AGG	-	7	133	c.737_739delCCT	c.(736-741)TCCTTC>TTC	p.S246del
Pat_04	Post-Resistance	TBC1D22A	25771	37	22	47189675	47189675	Frame_Shift_Del	DEL	C	-	2	4	c.397delC	c.(397-399)CCCfs	p.P133fs
Pat_04	Post-Resistance	MAP3K15	389840	37	X	19389184	19389185	Splice_Site	INS	-	A	2	4	c.1720_splice	c.e25-1	p.V574_splice
Pat_07	Post-Resistance	CAMTA1	23261	37	1	7811329	7811329	Frame_Shift_Del	DEL	A	-	7	510	c.4760delA	c.(4759-4761)CAAfs	p.Q1587fs
Pat_07	Post-Resistance	PIK3R3	8503	37	1	46546324	46546324	Frame_Shift_Del	DEL	C	-	8	760	c.205delG	c.(205-207)GATfs	p.D69fs
Pat_07	Post-Resistance	CTBS	1486	37	1	85039999	85040007	In_Frame_Del	DEL	GCAGCGCC	-	4	9	_100delTGGCGC	-102)CTGGCGCTGCGG>	p.LAL31del
Pat_07	Post-Resistance	ISG20L2	81875	37	1	156694023	156694023	Frame_Shift_Del	DEL	G	-	7	285	c.865delC	c.(865-867)CTCfs	p.L289fs
Pat_07	Post-Resistance	BAT2L2	23215	37	1	171511149	171511149	Frame_Shift_Del	DEL	A	-	11	162	c.4538delA	c.(4537-4539)GAAfs	p.E1513fs
Pat_07	Post-Resistance	PRG4	10216	37	1	186276284	186276286	In_Frame_Del	DEL	CTC	-	29	128	.1433_1435delCT	(1432-1437)ACTCCC>AC	p.P479del
Pat_07	Post-Resistance	KLHL12	59349	37	1	202862508	202862508	Frame_Shift_Del	DEL	C	-	7	721	c.1439delG	c.(1438-1440)GGAfs	p.G480fs
Pat_07	Post-Resistance	C10orf62	414157	37	10	99350236	99350237	Frame_Shift_Ins	INS	-	CA	7	196	c.582_583insCA	c.(580-585)AATCACfs	p.N194fs
Pat_07	Post-Resistance	OR10A5	144124	37	11	6867223	6867225	In_Frame_Del	DEL	TTC	-	7	156	c.310_312delTTC	c.(310-312)TTCdel	p.F108del
Pat_07	Post-Resistance	PIK3C2A	5286	37	11	17191097	17191097	Frame_Shift_Del	DEL	T	-	7	465	c.192delA	c.(190-192)AAAfs	p.K64fs
Pat_07	Post-Resistance	FOXJ2	55810	37	12	8200558	8200560	In_Frame_Del	DEL	CAG	-	14	97	c.898_900delCAG	c.(898-900)CAGdel	p.Q306del
Pat_07	Post-Resistance	PRB2	653247	37	12	11546732	11546733	In_Frame_Ins	INS	-	AGA	7	350	c.279_280insTCT	c.(277-282)insTCT	p.93_94insS
Pat_07	Post-Resistance	GPR19	2842	37	12	12814274	12814274	Frame_Shift_Del	DEL	T	-	11	499	c.1109delA	c.(1108-1110)AACfs	p.N370fs
Pat_07	Post-Resistance	FAR2	55711	37	12	29450110	29450110	Frame_Shift_Del	DEL	A	-	8	318	c.522delA	c.(520-522)CCAfs	p.P174fs
Pat_07	Post-Resistance	GSX1	219409	37	13	28367927	28367929	In_Frame_Del	DEL	GGC	-	8	136	c.637_639delGGC	c.(637-639)GGCdel	p.G218del
Pat_07	Post-Resistance	LRCH1	23143	37	13	47243183	47243186	Frame_Shift_Del	DEL	CCTG	-	7	818	.471_474delCCT	c.(469-474)GCCCTGfs	p.A157fs
Pat_07	Post-Resistance	DZIP1	22873	37	13	96293930	96293930	Frame_Shift_Del	DEL	C	-	7	324	c.216delG	c.(214-216)CTGfs	p.L72fs
Pat_07	Post-Resistance	FAM155A	728215	37	13	108518687	108518689	In_Frame_Del	DEL	CTG	-	7	70	c.256_258delCAG	c.(256-258)CAGdel	p.Q86del
Pat_07	Post-Resistance	ZFHX3	463	37	16	72821594	72821596	In_Frame_Del	DEL	GCC	-	7	139	0579_10581delG	c.(10579-10581)GGCdel	p.G3527del
Pat_07	Post-Resistance	FTSJ3	117246	37	17	61899155	61899157	In_Frame_Del	DEL	CTC	-	7	273	.1522_1524delGA	c.(1522-1524)GAGdel	p.E508del
Pat_07	Post-Resistance	CBX4	8535	37	17	77808241	77808243	In_Frame_Del	DEL	GTG	-	7	38	.1198_1200delCA	c.(1198-1200)CACdel	p.H400del
Pat_07	Post-Resistance	C19orf55	148137	37	19	36255947	36255949	In_Frame_Del	DEL	CTC	-	15	470	c.639_641delCTC	c.(637-642)ATCTCC>ATC	p.S218del
Pat_07	Post-Resistance	AXL	558	37	19	41743933	41743933	Frame_Shift_Del	DEL	C	-	8	232	c.868delC	c.(868-870)CCCfs	p.P290fs
Pat_07	Post-Resistance	HNRNPUL1	11100	37	19	41811694	41811695	Frame_Shift_Ins	INS	-	A	9	294	c.2376_2377insA	c.(2374-2379)TACAACfs	p.Y792fs
Pat_07	Post-Resistance	AFTPH	54812	37	2	64778672	64778674	In_Frame_Del	DEL	GAT	-	7	518	c.64_66delGAT	c.(64-66)GATdel	p.D26del

Pat_07	Post-Resistance	INPP5D	3635	37	2	234113090	234113090	Frame_Shift_Del	DEL	C	-	4	7	c.3294delC	c.(3292-3294)GGCfs	p.G1098fs
Pat_07	Post-Resistance	RASSF2	9770	37	20	4776492	4776494	In_Frame_Del	DEL	AGG	-	7	322	c.254_256delCCT	c.(253-258)TCCTGG>TGG	p.S85del
Pat_07	Post-Resistance	MED15	51586	37	22	20918817	20918819	In_Frame_Del	DEL	CAG	-	8	52	c.532_534delCAG	c.(532-534)CAGdel	p.Q188del
Pat_07	Post-Resistance	MYH9	4627	37	22	36689419	36689421	In_Frame_Del	DEL	CCT	-	8	177	.4049_4051delAG	(4048-4053)GAGGCC>GC	p.E1350del
Pat_07	Post-Resistance	XPC	7508	37	3	14219966	14219968	In_Frame_Del	DEL	CCT	-	8	139	c.101_103delAGG	c.(100-105)GAGGAT>GAT	p.E34del
Pat_07	Post-Resistance	SATB1	6304	37	3	18391133	18391135	In_Frame_Del	DEL	CTG	-	13	103	.1819_1821delCA	c.(1819-1821)CAGdel	p.Q607del
Pat_07	Post-Resistance	TMCC1	23023	37	3	129370576	129370578	In_Frame_Del	DEL	CTG	-	14	294	.1708_1710delCA	c.(1708-1710)CAGdel	p.Q570del
Pat_07	Post-Resistance	DBR1	51163	37	3	137880741	137880743	In_Frame_Del	DEL	TCG	-	7	227	.1623_1625delCG	.(1621-1626)GATGAT>GA	.541_542DD>
Pat_07	Post-Resistance	MED12L	116931	37	3	151148114	151148116	In_Frame_Del	DEL	CAG	-	18	290	.6331_6333delCA	c.(6331-6333)CAGdel	p.Q2115del
Pat_07	Post-Resistance	CRIPAK	285464	37	4	1389175	1389176	Frame_Shift_Del	DEL	CA	-	13	501	c.876_877delCA	c.(874-879)CTCACAfs	p.L292fs
Pat_07	Post-Resistance	CRIPAK	285464	37	4	1389206	1389207	Frame_Shift_Del	DEL	CA	-	7	525	c.907_908delCA	c.(907-909)CACfs	p.H303fs
Pat_07	Post-Resistance	CRIPAK	285464	37	4	1389297	1389298	Frame_Shift_Del	DEL	CA	-	8	473	c.998_999delCA	c.(997-999)TCAfs	p.S333fs
Pat_07	Post-Resistance	GABRG1	2565	37	4	46060358	46060358	Frame_Shift_Del	DEL	A	-	8	270	c.792delT	c.(790-792)TTTfs	p.F264fs
Pat_07	Post-Resistance	CDKL2	8999	37	4	76539579	76539580	Frame_Shift_Ins	INS	-	T	8	149	c.222_223insA	c.(220-225)AAACGAfs	p.K74fs
Pat_07	Post-Resistance	MCC	4163	37	5	112824048	112824049	In_Frame_Ins	INS	-	GCC	6	9	c.63_64insGGC	c.(61-66)insGGC	p.21_22insG
Pat_07	Post-Resistance	MRPS18B	28973	37	6	30587716	30587717	Frame_Shift_Ins	INS	-	T	7	746	c.304_305insT	c.(304-306)GGGfs	p.G102fs
Pat_07	Post-Resistance	KIAA1949	170954	37	6	30653494	30653496	In_Frame_Del	DEL	TGC	-	7	152	c.300_302delGCA	c.(298-303)CAGCAA>CAA	.100_101QQ>
Pat_07	Post-Resistance	SYNGAP1	8831	37	6	33410682	33410683	Frame_Shift_Del	DEL	CG	-	7	272	.2353_2354delCG	c.(2353-2355)CGCfs	p.R785fs
Pat_07	Post-Resistance	TFEB	7942	37	6	41658830	41658832	In_Frame_Del	DEL	TGC	-	7	51	c.120_122delGCA	c.(118-123)CAGCAA>CAA	p.40_41QQ>Q
Pat_07	Post-Resistance	SENP6	26054	37	6	76376441	76376443	In_Frame_Del	DEL	TGA	-	9	280	.1008_1010delTG	.(1006-1011)AGTGAT>AG	p.D341del
Pat_07	Post-Resistance	C7orf59	389541	37	7	99751029	99751029	Frame_Shift_Del	DEL	G	-	7	671	c.91delG	c.(91-93)GGGfs	p.G31fs
Pat_07	Post-Resistance	LUC7L2	51631	37	7	139094365	139094366	Frame_Shift_Del	DEL	AG	-	12	106	c.744_745delAG	c.(742-747)GAAGAGfs	p.E248fs
Pat_07	Post-Resistance	ESCO2	157570	37	8	27634576	27634577	Frame_Shift_Ins	INS	-	A	7	212	c.751_752insA	c.(751-753)GAAfs	p.E251fs
Pat_07	Post-Resistance	WDR67	93594	37	8	124140520	124140521	Splice_Site	INS	-	T	7	161	c.1885_splice	c.e14-1	p.F629_splice
Pat_07	Post-Resistance	SMARCA2	6595	37	9	2039777	2039779	In_Frame_Del	DEL	CAG	-	7	67	c.667_669delCAG	c.(667-669)CAGdel	p.Q238del
Pat_07	Post-Resistance	HRCT1	646962	37	9	35906348	35906350	In_Frame_Del	DEL	CTG	-	15	65	c.64_66delCTG	c.(64-66)CTGdel	p.L28del
Pat_07	Post-Resistance	NR4A3	8013	37	9	102590616	102590618	In_Frame_Del	DEL	CAC	-	7	113	c.292_294delCAC	c.(292-294)CACdel	p.H108del
Pat_07	Post-Resistance	GUCY2F	2986	37	X	108619355	108619355	Frame_Shift_Del	DEL	T	-	8	318	c.3192delA	c.(3190-3192)AAAfs	p.K1064fs
Pat_07	Pre-Treatment	IQCC	55721	37	1	32671285	32671285	Frame_Shift_Del	DEL	G	-	2	4	c.3delG	c.(1-3)ATGfs	p.M1fs
Pat_07	Pre-Treatment	PRG4	10216	37	1	186276284	186276286	In_Frame_Del	DEL	CTC	-	11	48	.1433_1435delCT	.(1432-1437)ACTCCC>AC	p.P479del
Pat_07	Pre-Treatment	FAM84A	151354	37	2	14774313	14774315	In_Frame_Del	DEL	CCA	-	3	5	c.210_212delCCA	.(208-213)CGCCAC>CGC	p.H71del
Pat_07	Pre-Treatment	MCC	4163	37	5	112824048	112824049	In_Frame_Ins	INS	-	GCC	2	4	c.63_64insGGC	c.(61-66)insGGC	p.21_22insG
Pat_07	Pre-Treatment	ZC3H3	23144	37	8	144522387	144522389	In_Frame_Del	DEL	GAG	-	3	4	.2637_2639delCT	.(2635-2640)TCCTCA>TC	.879_880SS>
Pat_14	Pre-Treatment	MFN2	9927	37	1	12052736	12052736	Frame_Shift_Del	DEL	T	-	11	816	c.300delT	c.(298-300)GCTfs	p.A100fs
Pat_14	Pre-Treatment	PRDM2	7799	37	1	14108728	14108728	Frame_Shift_Del	DEL	A	-	7	934	c.4438delA	c.(4438-4440)AAAfs	p.K1480fs
Pat_14	Pre-Treatment	ARHGEF10L	55160	37	1	17914103	17914103	Frame_Shift_Del	DEL	C	-	8	1123	c.186delC	c.(184-186)GACfs	p.D62fs
Pat_14	Pre-Treatment	HIVEP3	59269	37	1	42046910	42046910	Frame_Shift_Del	DEL	G	-	8	641	c.3559delC	c.(3559-3561)CAAfs	p.Q1187fs
Pat_14	Pre-Treatment	RIMKLA	284716	37	1	42875776	42875778	In_Frame_Del	DEL	GGT	-	9	674	c.603_605delGGT	.(601-606)CGGGTG>CGC	p.V205del
Pat_14	Pre-Treatment	B4GALT2	8704	37	1	44447007	44447009	In_Frame_Del	DEL	AGC	-	10	321	c.175_177delAGC	c.(175-177)AGCdel	p.S65del
Pat_14	Pre-Treatment	ZNF326	284695	37	1	90470782	90470784	In_Frame_Del	DEL	GTG	-	7	529	c.188_190delGTG	c.(187-192)AGTGGT>AGT	p.G68del
Pat_14	Pre-Treatment	SLC16A4	9122	37	1	110906427	110906427	Frame_Shift_Del	DEL	A	-	7	180	c.1425delT	c.(1423-1425)TTTfs	p.F475fs
Pat_14	Pre-Treatment	NOTCH2	4853	37	1	120612003	120612004	Frame_Shift_Del	DEL	GG	-	14	96	c.17_18delCC	c.(16-18)CCCfs	p.P6fs
Pat_14	Pre-Treatment	NOTCH2NL	388677	37	1	145281424	145281424	Frame_Shift_Del	DEL	T	-	8	4298	c.354delT	c.(352-354)AGTfs	p.S118fs
Pat_14	Pre-Treatment	ADAMTSL4	54507	37	1	150530506	150530506	Frame_Shift_Del	DEL	G	-	15	543	c.2263delG	c.(2263-2265)GGGfs	p.G755fs
Pat_14	Pre-Treatment	MCL1	4170	37	1	150551492	150551494	In_Frame_Del	DEL	TCC	-	7	370	c.513_515delGGA	.(511-516)GAGGAC>GAC	p.E171del
Pat_14	Pre-Treatment	TCHH	7062	37	1	152082957	152082959	In_Frame_Del	DEL	CTC	-	14	851	.2734_2736delGA	c.(2734-2736)GAGdel	p.E912del
Pat_14	Pre-Treatment	NES	10763	37	1	156642738	156642739	Frame_Shift_Ins	INS	-	AG	8	510	c.1241_1242insCT	c.(1240-1242)CTGfs	p.L414fs

Pat_14	Pre-Treatment	LMX1A	4009	37	1	165177332	165177334	In_Frame_Del	DEL	TGC	-	13	280	c.783_785delGCA	c.(781-786)CAGCAA>CAA	.261_262QQ>
Pat_14	Pre-Treatment	NMNAT2	23057	37	1	183221843	183221853	Frame_Shift_Del	DEL	CCACAACAT	-	49	432	_857delCATGTTG	847-858)CATGTTGTGGAT	p.H283fs
Pat_14	Pre-Treatment	CR1L	1379	37	1	207867814	207867814	Frame_Shift_Del	DEL	A	-	7	1085	c.580delA	c.(580-582)AAAfs	p.K194fs
Pat_14	Pre-Treatment	AGT	183	37	1	230839055	230839055	Frame_Shift_Del	DEL	A	-	8	321	c.1290delT	c.(1288-1290)TTTfs	p.F430fs
Pat_14	Pre-Treatment	SFMBT2	57713	37	10	7212995	7212997	In_Frame_Del	DEL	CTC	-	13	1170	.2437_2439delGA	c.(2437-2439)GAGdel	p.E813del
Pat_14	Pre-Treatment	KIAA1217	56243	37	10	24822125	24822127	In_Frame_Del	DEL	GAA	-	9	264	.3373_3375delGA	c.(3373-3375)GAAdel	p.E1129del
Pat_14	Pre-Treatment	MPP7	143098	37	10	28413012	28413013	Frame_Shift_Ins	INS	-	CTTC	62	626	c.562_563insGAA	c.(562-564)GTCfs	p.V188fs
Pat_14	Pre-Treatment	KIAA1462	57608	37	10	30316501	30316503	In_Frame_Del	DEL	CTG	-	15	232	.2574_2576delCA	(2572-2577)AGCAGT>AG	.858_859SS>
Pat_14	Pre-Treatment	FRMPD2	143162	37	10	49409420	49409420	Frame_Shift_Del	DEL	T	-	10	1255	c.1805delA	c.(1804-1806)AAGfs	p.K602fs
Pat_14	Pre-Treatment	AGAP6	414189	37	10	51769413	51769413	Frame_Shift_Del	DEL	G	-	7	1569	c.1528delG	c.(1528-1530)GGCfs	p.G510fs
Pat_14	Pre-Treatment	ZMIZ1	57178	37	10	81072446	81072446	Frame_Shift_Del	DEL	C	-	9	1495	c.3144delC	c.(3142-3144)GACfs	p.D1048fs
Pat_14	Pre-Treatment	TBC1D12	23232	37	10	96281817	96281817	Frame_Shift_Del	DEL	T	-	8	825	c.1867delT	c.(1867-1869)TTTfs	p.F623fs
Pat_14	Pre-Treatment	APBB1	322	37	11	6432437	6432438	Frame_Shift_Del	DEL	GG	-	7	716	c.140_141delCC	c.(139-141)CCCfs	p.P47fs
Pat_14	Pre-Treatment	PAMR1	25891	37	11	35513670	35513670	Frame_Shift_Del	DEL	C	-	8	1465	c.302delG	c.(301-303)GGTfs	p.G101fs
Pat_14	Pre-Treatment	MYBPC3	4607	37	11	47359101	47359103	In_Frame_Del	DEL	TCT	-	10	391	.2441_2443delAG	(2440-2445)AAGAGC>AG	p.K814del
Pat_14	Pre-Treatment	DAGLA	747	37	11	61507992	61507993	Frame_Shift_Del	DEL	CA	-	7	1325	c.1911_1912delCA	c.(1909-1914)TTCAATfs	p.F637fs
Pat_14	Pre-Treatment	FADS2	9415	37	11	61607885	61607887	In_Frame_Del	DEL	TCC	-	8	1259	c.398_400delTCC	c.(397-402)TTCCTC>TTC	p.L137del
Pat_14	Pre-Treatment	SF3B2	10992	37	11	65836145	65836146	Frame_Shift_Ins	INS	-	A	8	285	c.2617_2618insA	c.(2617-2619)CAAfs	p.Q873fs
Pat_14	Pre-Treatment	LRFN4	78999	37	11	66625231	66625233	In_Frame_Del	DEL	CTG	-	8	150	c.16_18delCTG	c.(16-18)CTGdel	p.L10del
Pat_14	Pre-Treatment	ATG16L2	89849	37	11	72528863	72528865	In_Frame_Del	DEL	AGG	-	9	354	c.281_283delAGG	.(280-285)CAGGAG>CA	p.E98del
Pat_14	Pre-Treatment	TMPRSS13	84000	37	11	117789346	117789360	In_Frame_Del	DEL	GAGATGCCC	-	8	271	9delGCCGGGCAT	)GGCCGGGCATCTCCA	p.GRASP72de
Pat_14	Pre-Treatment	DDX23	9416	37	12	49224409	49224409	Frame_Shift_Del	DEL	G	-	8	750	c.2306delC	c.(2305-2307)ACAfs	p.T769fs
Pat_14	Pre-Treatment	LRP1	4035	37	12	57605740	57605742	In_Frame_Del	DEL	TGC	-	19	1174	13289_13291delT	13288-13293)TTGCTG>T	4430_4431LL>
Pat_14	Pre-Treatment	UTP20	27340	37	12	101767538	101767539	Frame_Shift_Ins	INS	-	A	7	679	c.7124_7125insA	c.(7123-7125)GCAfs	p.A2375fs
Pat_14	Pre-Treatment	TCHP	84260	37	12	110344434	110344435	Frame_Shift_Ins	INS	-	A	10	274	c.514_515insA	c.(514-516)GAAfs	p.E172fs
Pat_14	Pre-Treatment	IFT81	28981	37	12	110573200	110573202	In_Frame_Del	DEL	AGA	-	89	362	c.654_656delAGA	c.(652-657)AGAGAA>AGA	p.E220del
Pat_14	Pre-Treatment	SFRS8	6433	37	12	132281734	132281736	In_Frame_Del	DEL	AGA	-	13	811	.2546_2548delAG	(2545-2550)GAGAAG>GA	p.K853del
Pat_14	Pre-Treatment	ATP12A	479	37	13	25262564	25262564	Frame_Shift_Del	DEL	G	-	7	1675	c.336delG	c.(334-336)GTGfs	p.V112fs
Pat_14	Pre-Treatment	RNF6	6049	37	13	26788241	26788241	Frame_Shift_Del	DEL	A	-	11	792	c.1778delT	c.(1777-1779)TTAfs	p.L593fs
Pat_14	Pre-Treatment	SPG20	23111	37	13	36903501	36903501	Frame_Shift_Del	DEL	T	-	9	1168	c.1162delA	c.(1162-1164)AGGfs	p.R388fs
Pat_14	Pre-Treatment	ZC3H13	23091	37	13	46553948	46553949	Frame_Shift_Del	DEL	CT	-	8	983	c.1911_1912delAG	c.(1909-1914)AGAGATfs	p.R637fs
Pat_14	Pre-Treatment	SLITRK1	114798	37	13	84455509	84455509	Frame_Shift_Del	DEL	T	-	7	555	c.134delA	c.(133-135)AAGfs	p.K45fs
Pat_14	Pre-Treatment	SLC10A2	6555	37	13	103705043	103705043	Frame_Shift_Del	DEL	G	-	7	467	c.512delC	c.(511-513)GCTfs	p.A171fs
Pat_14	Pre-Treatment	MGA	23269	37	15	42003383	42003385	In_Frame_Del	DEL	CAG	-	10	344	.2920_2922delCA	c.(2920-2922)CAGdel	p.Q981del
Pat_14	Pre-Treatment	MYO1E	4643	37	15	59464100	59464101	Frame_Shift_Del	DEL	GG	-	8	497	c.2475_2476delCC	c.(2473-2478)TCCCTCfs	p.S825fs
Pat_14	Pre-Treatment	RHBDF1	64285	37	16	109811	109811	Frame_Shift_Del	DEL	T	-	7	394	c.1736delA	c.(1735-1737)AACfs	p.N579fs
Pat_14	Pre-Treatment	ABCA3	21	37	16	2369649	2369651	In_Frame_Del	DEL	AGC	-	7	707	c.804_806delGCT	c.(802-807)CTGCTC>CTC	.268_269LL>L
Pat_14	Pre-Treatment	NTAN1	123803	37	16	15131931	15131931	Frame_Shift_Del	DEL	T	-	8	412	c.890delA	c.(889-891)AATfs	p.N297fs
Pat_14	Pre-Treatment	LOC100132247	100132247	37	16	22545744	22545755	In_Frame_Del	DEL	CACCCTCA	-	8	49	1451delTCCACCC	1452)CTTCCACCCTCAG	p.PPSA485del
Pat_14	Pre-Treatment	SLC5A11	115584	37	16	24921737	24921739	In_Frame_Del	DEL	CAG	-	10	415	.1761_1763delCA	(1759-1764)GCCAGC>GC	p.S592del
Pat_14	Pre-Treatment	ATP2A1	487	37	16	28913640	28913640	Frame_Shift_Del	DEL	C	-	11	787	c.2457delC	c.(2455-2457)CGCfs	p.R819fs
Pat_14	Pre-Treatment	CD2BP2	10421	37	16	30365550	30365552	In_Frame_Del	DEL	CAT	-	17	1610	c.170_172delATG	.(169-174)GATGGG>GG	p.D57del
Pat_14	Pre-Treatment	SETD1A	9739	37	16	30982809	30982811	In_Frame_Del	DEL	TCC	-	8	252	.3127_3129delTC	c.(3127-3129)TCCdel	p.S1058del
Pat_14	Pre-Treatment	IRX6	79190	37	16	55362674	55362676	In_Frame_Del	DEL	GAG	-	13	202	c.784_786delGAG	c.(784-786)GAGdel	p.E268del
Pat_14	Pre-Treatment	COQ9	57017	37	16	57486732	57486734	In_Frame_Del	DEL	GAG	-	11	802	c.262_264delGAG	c.(262-264)GAGdel	p.E91del
Pat_14	Pre-Treatment	NFAT5	10725	37	16	69726420	69726422	In_Frame_Del	DEL	CAG	-	8	179	.2638_2640delCA	c.(2638-2640)CAGdel	p.Q888del
Pat_14	Pre-Treatment	TSR1	55720	37	17	2232706	2232707	Frame_Shift_Del	DEL	CC	-	8	291	c.1833_1834delGG	c.(1831-1836)AAGGAAfs	p.K611fs

Pat_14	Pre-Treatment	C17orf74	201243	37	17	7329686	7329688	In_Frame_Del	DEL	CGC	-	9	462	c.376_378delCGC	c.(376-378)CGCdel	p.R130del
Pat_14	Pre-Treatment	CHRNB1	1140	37	17	7357666	7357668	In_Frame_Del	DEL	CTG	-	14	1091	c.871_873delCTG	c.(871-873)CTGdel	p.L294del
Pat_14	Pre-Treatment	FXR2	9513	37	17	7495872	7495874	In_Frame_Del	DEL	CGG	-	16	1647	.1773_1775delCC	(1771-1776)CGCCGT>CG	.591_592RR>
Pat_14	Pre-Treatment	KRBA2	124751	37	17	8272612	8272613	Frame_Shift_Del	DEL	TC	-	7	632	c.1318_1319delG	c.(1318-1320)GAAfs	p.E440fs
Pat_14	Pre-Treatment	NEK8	284086	37	17	27064478	27064480	In_Frame_Del	DEL	GCA	-	7	482	c.773_775delGCA	c.(772-777)TGCATC>TTC	.258_259CI>
Pat_14	Pre-Treatment	TIAF1	9220	37	17	27401055	27401056	Frame_Shift_Del	DEL	CA	-	10	640	c.162_163delTG	c.(160-165)TGTGGAfs	p.C54fs
Pat_14	Pre-Treatment	ZNF207	7756	37	17	30677314	30677316	In_Frame_Del	DEL	AAG	-	12	886	c.10_12delAAG	c.(10-12)AAGdel	p.K7del
Pat_14	Pre-Treatment	CDC27	996	37	17	45234336	45234336	Frame_Shift_Del	DEL	G	-	16	475	c.785delC	c.(784-786)CCAfs	p.P262fs
Pat_14	Pre-Treatment	COIL	8161	37	17	55028117	55028118	Frame_Shift_Ins	INS	-	T	9	321	c.485_486insA	c.(484-486)AACfs	p.N162fs
Pat_14	Pre-Treatment	TEX2	55852	37	17	62291438	62291440	In_Frame_Del	DEL	TCC	-	8	223	c.138_140delGGA	.(136-141)GAGGAA>GA	p.46_47EE>E
Pat_14	Pre-Treatment	FECH	2235	37	18	55226435	55226435	Frame_Shift_Del	DEL	G	-	8	701	c.746delC	c.(745-747)CCAfs	p.P249fs
Pat_14	Pre-Treatment	DENND1C	79958	37	19	6477251	6477251	Frame_Shift_Del	DEL	G	-	11	253	c.491delC	c.(490-492)CCTfs	p.P164fs
Pat_14	Pre-Treatment	DNMT1	1786	37	19	10262139	10262139	Frame_Shift_Del	DEL	T	-	7	806	c.2152delA	c.(2152-2154)ATGfs	p.M718fs
Pat_14	Pre-Treatment	TYK2	7297	37	19	10463112	10463113	Frame_Shift_Ins	INS	-	G	7	856	c.3315_3316insC	c.(3313-3318)CCCACGfs	p.P1105fs
Pat_14	Pre-Treatment	OR7C2	26658	37	19	15052829	15052829	Frame_Shift_Del	DEL	T	-	7	857	c.529delT	c.(529-531)TTTfs	p.F177fs
Pat_14	Pre-Treatment	HAUS8	93323	37	19	17160706	17160707	Frame_Shift_Del	DEL	GA	-	17	1234	c.1209_1210delT	c.(1207-1212)TCTCGTfs	p.S403fs
Pat_14	Pre-Treatment	PLVAP	83483	37	19	17476920	17476921	Frame_Shift_Del	DEL	TG	-	8	1313	c.453_454delCA	c.(451-456)AACAAGfs	p.N151fs
Pat_14	Pre-Treatment	SFRS14	10147	37	19	19136394	19136394	Frame_Shift_Del	DEL	T	-	15	761	c.763delA	c.(763-765)ATAfs	p.I255fs
Pat_14	Pre-Treatment	CILP2	148113	37	19	19654512	19654512	Frame_Shift_Del	DEL	C	-	10	1981	c.1158delC	c.(1156-1158)GACfs	p.D386fs
Pat_14	Pre-Treatment	PRODH2	58510	37	19	36293092	36293092	Splice_Site	DEL	C	-	7	1218	c.1426_splice	c.e10+1	p.G476_splice
Pat_14	Pre-Treatment	B3GNT8	374907	37	19	41931997	41931999	In_Frame_Del	DEL	CAG	-	8	548	c.685_687delCTG	c.(685-687)CTGdel	p.L229del
Pat_14	Pre-Treatment	ZNF574	64763	37	19	42584303	42584304	Frame_Shift_Del	DEL	CA	-	8	2054	c.1545_1546delC	c.(1543-1548)CGCACAfs	p.R515fs
Pat_14	Pre-Treatment	DHX34	9704	37	19	47883158	47883160	In_Frame_Del	DEL	GGA	-	9	212	.2898_2900delGG	(2896-2901)CTGGAG>CT	p.E971del
Pat_14	Pre-Treatment	KLK1	3816	37	19	51326962	51326963	Frame_Shift_Ins	INS	-	C	9	363	c.42_43insG	c.(40-45)GGGACTfs	p.G14fs
Pat_14	Pre-Treatment	LIM2	3982	37	19	51883791	51883791	Frame_Shift_Del	DEL	C	-	8	1249	c.428delG	c.(427-429)GGCfs	p.G143fs
Pat_14	Pre-Treatment	KIR2DL4	3805	37	19	55324675	55324675	Splice_Site	DEL	A	-	8	201	c.801_splice	c.e6+1	p.S267_splice
Pat_14	Pre-Treatment	PUM2	23369	37	2	20482977	20482979	In_Frame_Del	DEL	GCT	-	7	436	.1449_1451delAG	(1447-1452)GCAGCT>GC	.483_484AA>
Pat_14	Pre-Treatment	GPR113	165082	37	2	26534413	26534413	Frame_Shift_Del	DEL	C	-	7	728	c.2183delG	c.(2182-2184)GGTfs	p.G728fs
Pat_14	Pre-Treatment	HEATR5B	54497	37	2	37234330	37234330	Frame_Shift_Del	DEL	G	-	8	751	c.4640delC	c.(4639-4641)TCAfs	p.S1547fs
Pat_14	Pre-Treatment	DHX57	90957	37	2	39095411	39095413	In_Frame_Del	DEL	CCA	-	12	279	c.135_137delTGG	.(133-138)GGTGGA>GG	p.45_46GG>G
Pat_14	Pre-Treatment	MAP4K3	8491	37	2	39552702	39552702	Frame_Shift_Del	DEL	G	-	9	679	c.875delC	c.(874-876)CCAfs	p.P292fs
Pat_14	Pre-Treatment	VPS24	51652	37	2	86732976	86732978	In_Frame_Del	DEL	TCC	-	8	242	c.618_620delGGA	.(616-621)GAGGAA>GA	.206_207EE>
Pat_14	Pre-Treatment	LY75	4065	37	2	160738814	160738814	Frame_Shift_Del	DEL	T	-	7	891	c.1067delA	c.(1066-1068)TACfs	p.Y356fs
Pat_14	Pre-Treatment	KBTBD10	10324	37	2	170366496	170366496	Frame_Shift_Del	DEL	A	-	11	752	c.208delA	c.(208-210)AAAfs	p.K70fs
Pat_14	Pre-Treatment	GTF3C3	9330	37	2	197649613	197649614	Frame_Shift_Ins	INS	-	T	8	166	c.1081_1082insA	c.(1081-1083)ACTfs	p.T361fs
Pat_14	Pre-Treatment	ABCA12	26154	37	2	215876785	215876786	Frame_Shift_Del	DEL	GA	-	8	798	c.2030_2031delT	c.(2029-2031)CTCfs	p.L677fs
Pat_14	Pre-Treatment	TRPM8	79054	37	2	234879010	234879010	Frame_Shift_Del	DEL	C	-	9	2217	c.2295delC	c.(2293-2295)CACfs	p.H765fs
Pat_14	Pre-Treatment	PANK2	80025	37	20	3893120	3893120	Frame_Shift_Del	DEL	T	-	11	1258	c.1251delT	c.(1249-1251)ACTfs	p.T417fs
Pat_14	Pre-Treatment	CHGB	1114	37	20	5903283	5903285	In_Frame_Del	DEL	GAG	-	8	235	c.493_495delGAG	c.(493-495)GAGdel	p.E169del
Pat_14	Pre-Treatment	GZF1	64412	37	20	23345921	23345923	In_Frame_Del	DEL	GAG	-	9	146	c.901_903delGAG	c.(901-903)GAGdel	p.E306del
Pat_14	Pre-Treatment	FRG1B	284802	37	20	29628310	29628312	In_Frame_Del	DEL	AGG	-	7	348	c.222_224delAGG	.(220-225)GCAGGA>GC	p.G75del
Pat_14	Pre-Treatment	SGK2	10110	37	20	42195105	42195105	Frame_Shift_Del	DEL	C	-	7	1033	c.150delC	c.(148-150)GTCfs	p.V50fs
Pat_14	Pre-Treatment	SNX21	90203	37	20	44469908	44469908	Frame_Shift_Del	DEL	C	-	7	1326	c.1078delC	c.(1078-1080)CCCfs	p.P360fs
Pat_14	Pre-Treatment	YTHDF1	54915	37	20	61833650	61833652	In_Frame_Del	DEL	CCT	-	10	938	.1640_1642delAG	(1639-1644)GAGGTG>GT	p.E547del
Pat_14	Pre-Treatment	TCP10L	140290	37	21	33949091	33949091	Frame_Shift_Del	DEL	C	-	7	788	c.641delG	c.(640-642)GGTfs	p.G214fs
Pat_14	Pre-Treatment	DYRK1A	1859	37	21	38884370	38884372	In_Frame_Del	DEL	CAC	-	7	182	.1828_1830delCA	c.(1828-1830)CACdel	p.H619del
Pat_14	Pre-Treatment	TRIOBP	11078	37	22	38120323	38120325	In_Frame_Del	DEL	CCT	-	7	1227	.1760_1762delCC	(1759-1764)GCCTCC>GC	p.S589del

Pat_14	Pre-Treatment	PICK1	9463	37	22	38471034	38471036	In_Frame_Del	DEL	GGA	-	9	183	.1143_1145delGG	(1141-1146)GGGGAG>GG	p.E388del
Pat_14	Pre-Treatment	BIK	638	37	22	43525245	43525247	In_Frame_Del	DEL	GCT	-	13	328	c.417_419delGCT	.(415-420)GCGCTG>GCC	p.L144del
Pat_14	Pre-Treatment	PNPLA5	150379	37	22	44285319	44285319	Frame_Shift_Del	DEL	G	-	8	1396	c.592delC	c.(592-594)CAGfs	p.Q198fs
Pat_14	Pre-Treatment	TATDN2	9797	37	3	10291121	10291123	In_Frame_Del	DEL	CTC	-	8	959	c.237_239delCTC	c.(235-240)AACTCC>AAC	p.S83del
Pat_14	Pre-Treatment	XPC	7508	37	3	14219966	14219968	In_Frame_Del	DEL	CCT	-	9	168	c.101_103delAGG	c.(100-105)GAGGAT>GAT	p.E34del
Pat_14	Pre-Treatment	ZNF621	285268	37	3	40573864	40573864	Frame_Shift_Del	DEL	C	-	61	279	c.603delC	c.(601-603)CACfs	p.H201fs
Pat_14	Pre-Treatment	KIF15	56992	37	3	44872462	44872462	Frame_Shift_Del	DEL	G	-	7	927	c.3123delG	c.(3121-3123)CTGfs	p.L1041fs
Pat_14	Pre-Treatment	CDC25A	993	37	3	48200922	48200923	Frame_Shift_Del	DEL	TC	-	10	538	c.1345_1346delGA	c.(1345-1347)GATfs	p.D449fs
Pat_14	Pre-Treatment	ATRIP	84126	37	3	48505451	48505453	In_Frame_Del	DEL	CTG	-	7	1100	.1894_1896delCT	c.(1894-1896)CTGdel	p.L635del
Pat_14	Pre-Treatment	MED12L	116931	37	3	150877786	150877786	Frame_Shift_Del	DEL	C	-	8	530	c.1005delC	c.(1003-1005)GGCfs	p.G335fs
Pat_14	Pre-Treatment	PDE6B	5158	37	4	661763	661765	In_Frame_Del	DEL	AGG	-	8	550	.2471_2473delAG	(2470-2475)AAGGAG>AA	p.E828del
Pat_14	Pre-Treatment	OTOP1	133060	37	4	4228274	4228282	In_Frame_Del	DEL	CCACAGCAC	-	9	147	0_318delCTGCTG	.(310-318)CTGCTGTGGde	p.LLW104del
Pat_14	Pre-Treatment	EVC	2121	37	4	5809995	5809997	In_Frame_Del	DEL	CAG	-	9	347	.2629_2631delCA	c.(2629-2631)CAGdel	p.Q880del
Pat_14	Pre-Treatment	ADAD1	132612	37	4	123302211	123302211	Frame_Shift_Del	DEL	A	-	7	224	c.237delA	c.(235-237)CCAfs	p.P79fs
Pat_14	Pre-Treatment	INTU	27152	37	4	128564917	128564917	Frame_Shift_Del	DEL	A	-	7	149	c.388delA	c.(388-390)AAAfs	p.K130fs
Pat_14	Pre-Treatment	PDZD2	23037	37	5	32089576	32089576	Frame_Shift_Del	DEL	G	-	7	867	c.6022delG	c.(6022-6024)GAAfs	p.E2008fs
Pat_14	Pre-Treatment	SLC45A2	51151	37	5	33951732	33951732	Frame_Shift_Del	DEL	G	-	8	586	c.1083delC	c.(1081-1083)CTCfs	p.L361fs
Pat_14	Pre-Treatment	IK	3550	37	5	140032593	140032594	Frame_Shift_Del	DEL	GA	-	11	156	c.268_269delGA	c.(268-270)GAGfs	p.E90fs
Pat_14	Pre-Treatment	KCTD16	57528	37	5	143853531	143853531	Frame_Shift_Del	DEL	A	-	8	161	c.1141delA	c.(1141-1143)AAAfs	p.K381fs
Pat_14	Pre-Treatment	UIMC1	51720	37	5	176397741	176397741	Splice_Site	DEL	A	-	7	1013	c.357_splice	c.e4+1	p.N119_splice
Pat_14	Pre-Treatment	ZNF184	7738	37	6	27420810	27420810	Frame_Shift_Del	DEL	T	-	8	944	c.528delA	c.(526-528)AAAfs	p.K176fs
Pat_14	Pre-Treatment	OR2J2	26707	37	6	29141422	29141422	Frame_Shift_Del	DEL	A	-	7	323	c.10delA	c.(10-12)AAAfs	p.K4fs
Pat_14	Pre-Treatment	CDSN	1041	37	6	31084620	31084622	In_Frame_Del	DEL	CCA	-	7	120	c.770_772delTGG	.(769-774)GTGGAC>GAC	p.V257del
Pat_14	Pre-Treatment	BAT2	7916	37	6	31597456	31597457	Frame_Shift_Ins	INS	-	C	7	117	c.2088_2089insC	c.(2086-2091)CCACCCfs	p.P696fs
Pat_14	Pre-Treatment	TULP1	7287	37	6	35478775	35478777	In_Frame_Del	DEL	TCC	-	7	399	c.360_362delGGA	.(358-363)GAGGAA>GAA	.120_121EE>
Pat_14	Pre-Treatment	ICK	22858	37	6	52883129	52883129	Frame_Shift_Del	DEL	T	-	7	1142	c.662delA	c.(661-663)AAGfs	p.K221fs
Pat_14	Pre-Treatment	GRM1	2911	37	6	146755219	146755221	In_Frame_Del	DEL	GAG	-	7	732	.2872_2874delGA	c.(2872-2874)GAGdel	p.E961del
Pat_14	Pre-Treatment	NOX3	50508	37	6	155743925	155743926	Frame_Shift_Del	DEL	CA	-	7	1175	c.1210_1211delTG	c.(1210-1212)TGCfs	p.C404fs
Pat_14	Pre-Treatment	AGPAT4	56895	37	6	161560589	161560589	Frame_Shift_Del	DEL	G	-	8	742	c.907delC	c.(907-909)CGGfs	p.R303fs
Pat_14	Pre-Treatment	SKAP2	8935	37	7	26729949	26729949	Frame_Shift_Del	DEL	C	-	7	745	c.829delG	c.(829-831)GAAfs	p.E277fs
Pat_14	Pre-Treatment	GARS	2617	37	7	30634583	30634585	In_Frame_Del	DEL	CTG	-	8	154	c.46_48delCTG	c.(46-48)CTGdel	p.L20del
Pat_14	Pre-Treatment	POU6F2	11281	37	7	39379288	39379290	In_Frame_Del	DEL	CAG	-	9	171	c.559_561delCAG	c.(559-561)CAGdel	p.Q196del
Pat_14	Pre-Treatment	DDC	1644	37	7	50531075	50531075	Frame_Shift_Del	DEL	T	-	9	481	c.1297delA	c.(1297-1299)ATCfs	p.I433fs
Pat_14	Pre-Treatment	STX1A	6804	37	7	73123425	73123427	In_Frame_Del	DEL	CAT	-	9	975	c.56_58delATG	c.(55-60)GATGTC>GTC	p.D19del
Pat_14	Pre-Treatment	COL1A2	1278	37	7	94050333	94050333	Frame_Shift_Del	DEL	C	-	7	511	c.2308delC	c.(2308-2310)CCCfs	p.P770fs
Pat_14	Pre-Treatment	TRRAP	8295	37	7	98554101	98554101	Frame_Shift_Del	DEL	T	-	87	423	c.6155delT	c.(6154-6156)GTGfs	p.V2052fs
Pat_14	Pre-Treatment	SRRT	51593	37	7	100479332	100479332	Frame_Shift_Del	DEL	G	-	8	223	c.304delG	c.(304-306)GGGfs	p.G102fs
Pat_14	Pre-Treatment	ARHGEF5	7984	37	7	144076999	144077000	Frame_Shift_Del	DEL	GG	-	7	1275	c.4644_4645delGG	c.(4642-4647)CTGGAGfs	p.L1548fs
Pat_14	Pre-Treatment	TOX	9760	37	8	59750796	59750798	In_Frame_Del	DEL	CTT	-	9	366	c.766_768delAAG	c.(766-768)AAGdel	p.K256del
Pat_14	Pre-Treatment	PUF60	22827	37	8	144906520	144906522	In_Frame_Del	DEL	GCC	-	7	256	c.72_74delGGC	c.(70-75)GCGGCA>GCA	p.24_25AA>A
Pat_14	Pre-Treatment	PLEC	5339	37	8	145000951	145000953	Splice_Site	DEL	CCT	-	7	815	c.4455_splice	c.e30+1	p.E1485_splice
Pat_14	Pre-Treatment	RLN2	6019	37	9	5304560	5304561	Frame_Shift_Ins	INS	-	A	7	426	c.20_21insT	c.(19-21)TTCfs	p.F7fs
Pat_14	Pre-Treatment	C9orf131	138724	37	9	35045129	35045129	Frame_Shift_Del	DEL	C	-	7	2294	c.2503delC	c.(2503-2505)CCCfs	p.P835fs
Pat_14	Pre-Treatment	HRCT1	646962	37	9	35906605	35906607	In_Frame_Del	DEL	CCG	-	9	45	c.321_323delCCG	.(319-324)CACCGC>CAC	p.R108del
Pat_14	Pre-Treatment	ROR2	4920	37	9	94486026	94486028	In_Frame_Del	DEL	TCC	-	7	590	.2748_2750delGG	(2746-2751)GAGGAA>GA	.916_917EE>
Pat_14	Pre-Treatment	FKBP15	23307	37	9	115933927	115933928	Frame_Shift_Ins	INS	-	AGAAA	10	63	2591_2592insTTT	c.(2590-2592)AAGfs	p.K864fs
Pat_14	Pre-Treatment	FKBP15	23307	37	9	115969556	115969556	Frame_Shift_Del	DEL	T	-	8	1780	c.190delA	c.(190-192)ACAfs	p.T64fs

Pat_14	Pre-Treatment	GOLGA2	2801	37	9	131019390	131019390	Frame_Shift_Del	DEL	A	-	8	837	c.2965delT	c.(2965-2967)TACfs	p.Y989fs
Pat_14	Pre-Treatment	ABL1	25	37	9	133759490	133759492	In_Frame_Del	DEL	AAG	-	30	476	.1813_1815delAA	c.(1813-1815)AAGdel	p.K609del
Pat_14	Pre-Treatment	TTF1	7270	37	9	135277388	135277388	Frame_Shift_Del	DEL	T	-	9	223	c.821delA	c.(820-822)AAGfs	p.K274fs
Pat_14	Pre-Treatment	ADAMTS13	11093	37	9	136302969	136302969	Frame_Shift_Del	DEL	C	-	8	1002	c.1536delC	c.(1534-1536)GGCfs	p.G512fs
Pat_14	Pre-Treatment	NOTCH1	4851	37	9	139393375	139393376	Frame_Shift_Del	DEL	AG	-	7	1403	c.6155_6156delCT	c.(6154-6156)GCTfs	p.A2052fs
Pat_14	Pre-Treatment	GRIN1	2902	37	9	140056884	140056886	In_Frame_Del	DEL	GAG	-	9	282	.1780_1782delGA	c.(1780-1782)GAGdel	p.E598del
Pat_14	Pre-Treatment	ZBED1	9189	37	X	2408742	2408742	Frame_Shift_Del	DEL	C	-	7	1201	c.19delG	c.(19-21)GAGfs	p.E7fs
Pat_14	Pre-Treatment	RBM10	8241	37	X	47030467	47030469	In_Frame_Del	DEL	GGC	-	9	250	c.242_244delGGC	.(241-246)AGGCGG>AG	p.81_82RR>R
Pat_14	Pre-Treatment	SHROOM4	57477	37	X	50350672	50350674	In_Frame_Del	DEL	TCT	-	7	34	.3468_3470delAG	(3466-3471)GAAGAG>GA	1156_1157EE
Pat_14	Pre-Treatment	NUDT11	55190	37	X	51239296	51239309	Translation_Start_Site	DEL	TCGAGGCA	-	11	60			
Pat_14	Pre-Treatment	XAGE3	170626	37	X	52893878	52893878	Frame_Shift_Del	DEL	C	-	8	469	c.239delG	c.(238-240)GGTfs	p.G80fs
Pat_14	Pre-Treatment	CD99L2	83692	37	X	149984524	149984526	In_Frame_Del	DEL	GTG	-	10	1236	c.156_158delCAC	c.(154-159)ACCACA>ACA	p.52_53TT>T
Pat_14	Pre-Treatment	MAGEA10	4109	37	X	151303906	151303908	In_Frame_Del	DEL	AGG	-	13	315	c.185_187delCCT	c.(184-189)TCCTGC>TGC	p.S62del
Pat_14	Post-Resistance	PHF13	148479	37	1	6680069	6680071	In_Frame_Del	DEL	GAA	-	8	226	c.348_350delGAA	c.(346-351)CTGAAG>CTG	p.K121del
Pat_14	Post-Resistance	EXTL1	2134	37	1	26349533	26349535	In_Frame_Del	DEL	CCT	-	8	232	c.396_398delCCT	c.(394-399)TGCCTC>TGC	p.L137del
Pat_14	Post-Resistance	ARID1A	8289	37	1	27105931	27105931	Frame_Shift_Del	DEL	G	-	7	760	c.5542delG	c.(5542-5544)GGGfs	p.G1848fs
Pat_14	Post-Resistance	GPR3	2827	37	1	27721235	27721237	In_Frame_Del	DEL	CTG	-	7	1311	c.933_935delCTG	c.(931-936)GTCTGC>GTC	p.C315del
Pat_14	Post-Resistance	USP1	7398	37	1	62916272	62916272	Frame_Shift_Del	DEL	A	-	8	270	c.1978delA	c.(1978-1980)AAAfs	p.K660fs
Pat_14	Post-Resistance	ROR1	4919	37	1	64608186	64608187	Frame_Shift_Del	DEL	CA	-	11	800	.1027_1028delC	c.(1027-1029)CACfs	p.H343fs
Pat_14	Post-Resistance	EVI5	7813	37	1	93159366	93159366	Frame_Shift_Del	DEL	T	-	8	435	c.1222delA	c.(1222-1224)ATGfs	p.M408fs
Pat_14	Post-Resistance	AGL	178	37	1	100378028	100378028	Frame_Shift_Del	DEL	A	-	7	397	c.3904delA	c.(3904-3906)AAAfs	p.K1302fs
Pat_14	Post-Resistance	FNDC7	163479	37	1	109276138	109276138	Frame_Shift_Del	DEL	A	-	8	414	c.2124delA	c.(2122-2124)CCAfs	p.P708fs
Pat_14	Post-Resistance	ADAM30	11085	37	1	120436591	120436591	Frame_Shift_Del	DEL	T	-	7	846	c.2369delA	c.(2368-2370)AAGfs	p.K790fs
Pat_14	Post-Resistance	NOTCH2	4853	37	1	120612003	120612004	Frame_Shift_Del	DEL	GG	-	27	126	c.17_18delCC	c.(16-18)CCCfs	p.P6fs
Pat_14	Post-Resistance	PDE4DIP	9659	37	1	144917828	144917828	Frame_Shift_Del	DEL	A	-	7	1899	c.1458delT	c.(1456-1458)GTTfs	p.V486fs
Pat_14	Post-Resistance	ADAMTSL4	54507	37	1	150530506	150530506	Frame_Shift_Del	DEL	G	-	10	615	c.2263delG	c.(2263-2265)GGGfs	p.G755fs
Pat_14	Post-Resistance	PSMB4	5692	37	1	151374040	151374040	Frame_Shift_Del	DEL	A	-	10	1444	c.716delA	c.(715-717)GAAfs	p.E239fs
Pat_14	Post-Resistance	TCHH	7062	37	1	152082957	152082959	In_Frame_Del	DEL	CTC	-	15	608	.2734_2736delGA	c.(2734-2736)GAGdel	p.E912del
Pat_14	Post-Resistance	FLG2	388698	37	1	152328808	152328809	Frame_Shift_Del	DEL	CC	-	8	1568	.1453_1454delG	c.(1453-1455)GGCfs	p.G485fs
Pat_14	Post-Resistance	CD84	8832	37	1	160549189	160549189	Frame_Shift_Del	DEL	C	-	7	621	c.39delG	c.(37-39)CTGfs	p.L13fs
Pat_14	Post-Resistance	PCP4L1	654790	37	1	161254154	161254156	In_Frame_Del	DEL	GGA	-	12	618	c.90_92delGGA	c.(88-93)GCGGAG>GCG	p.E35del
Pat_14	Post-Resistance	LMX1A	4009	37	1	165177332	165177334	In_Frame_Del	DEL	TGC	-	9	193	c.783_785delGCA	c.(781-786)CAGCAA>CAA	.261_262QQ>
Pat_14	Post-Resistance	EPHX1	2052	37	1	226026384	226026384	Frame_Shift_Del	DEL	C	-	10	1212	c.394delC	c.(394-396)CCCfs	p.P132fs
Pat_14	Post-Resistance	ACBD3	64746	37	1	226352490	226352491	Frame_Shift_Ins	INS	-	T	10	383	c.568_569insA	c.(568-570)AGGfs	p.R190fs
Pat_14	Post-Resistance	SFMBT2	57713	37	10	7212995	7212997	In_Frame_Del	DEL	CTC	-	7	1071	.2437_2439delGA	c.(2437-2439)GAGdel	p.E813del
Pat_14	Post-Resistance	C10orf140	387640	37	10	21805466	21805467	In_Frame_Ins	INS	-	CCTCCT	7	8	285_1286insAGGA	85-1287)GGG>GAGGAG	.428_429insE
Pat_14	Post-Resistance	KIAA1462	57608	37	10	30316501	30316503	In_Frame_Del	DEL	CTG	-	10	251	.2574_2576delCA	(2572-2577)AGCAGT>AG	.858_859SS>
Pat_14	Post-Resistance	HELLS	3070	37	10	96331163	96331163	Frame_Shift_Del	DEL	A	-	7	195	c.454delA	c.(454-456)AAAfs	p.K152fs
Pat_14	Post-Resistance	C10orf62	414157	37	10	99350237	99350238	Frame_Shift_Del	DEL	CA	-	7	501	c.583_584delCA	c.(583-585)CACfs	p.H195fs
Pat_14	Post-Resistance	TACC2	10579	37	10	123970380	123970380	Frame_Shift_Del	DEL	C	-	8	614	c.6440delC	c.(6439-6441)ACCfs	p.T2147fs
Pat_14	Post-Resistance	PTPRE	5791	37	10	129876002	129876004	In_Frame_Del	DEL	AGC	-	7	456	.1847_1849delAG	(1846-1851)AAGCAG>AA	p.Q620del
Pat_14	Post-Resistance	F2	2147	37	11	46760648	46760648	Frame_Shift_Del	DEL	G	-	8	615	c.1705delG	c.(1705-1707)GGGfs	p.G569fs
Pat_14	Post-Resistance	FADS2	9415	37	11	61607885	61607887	In_Frame_Del	DEL	TCC	-	14	1109	c.398_400delTCC	c.(397-402)TTCCTC>TTC	p.L137del
Pat_14	Post-Resistance	FADS2	9415	37	11	61615748	61615748	Frame_Shift_Del	DEL	C	-	7	1213	c.736delC	c.(736-738)CCCfs	p.P246fs
Pat_14	Post-Resistance	CBL	867	37	11	119170435	119170435	Frame_Shift_Del	DEL	A	-	8	2347	c.2665delA	c.(2665-2667)AAAfs	p.K889fs
Pat_14	Post-Resistance	PRDM10	56980	37	11	129772249	129772251	In_Frame_Del	DEL	TGG	-	8	1405	.3440_3442delCC	.(3439-3444)ACCAAC>AA	p.T1147del
Pat_14	Post-Resistance	SLC39A5	283375	37	12	56628997	56628999	In_Frame_Del	DEL	CTG	-	8	828	c.691_693delCTG	c.(691-693)CTGdel	p.L234del

Pat_14	Post-Resistance	LRP1	4035	37	12	57605740	57605742	In_Frame_Del	DEL	TGC	-	16	849	13289_13291delT	(13288-13293)TTGCTG>T	4430_4431LL>
Pat_14	Post-Resistance	TMEM19	55266	37	12	72094757	72094757	Frame_Shift_Del	DEL	T	-	7	1353	c.993delT	c.(991-993)GGTfs	p.G331fs
Pat_14	Post-Resistance	KSR2	283455	37	12	118198939	118198939	Frame_Shift_Del	DEL	G	-	11	1581	c.776delC	c.(775-777)CCGfs	p.P259fs
Pat_14	Post-Resistance	SFRS8	6433	37	12	132281734	132281736	In_Frame_Del	DEL	AGA	-	17	696	.2546_2548delAG	.(2545-2550)GAGAAG>GA	p.K853del
Pat_14	Post-Resistance	FRY	10129	37	13	32653102	32653102	Frame_Shift_Del	DEL	A	-	9	1574	c.202delA	c.(202-204)AAAfs	p.K68fs
Pat_14	Post-Resistance	SLAIN1	122060	37	13	78320722	78320722	Frame_Shift_Del	DEL	A	-	8	620	c.498delA	c.(496-498)GGAfs	p.G166fs
Pat_14	Post-Resistance	SIPA1L1	26037	37	14	72190482	72190484	In_Frame_Del	DEL	TCC	-	7	539	.4390_4392delTC	c.(4390-4392)TCCdel	p.S1468del
Pat_14	Post-Resistance	CCNK	8812	37	14	99969244	99969246	In_Frame_Del	DEL	CAG	-	7	582	c.934_936delCAG	c.(934-936)CAGdel	p.Q315del
Pat_14	Post-Resistance	YY1	7528	37	14	100705708	100705710	In_Frame_Del	DEL	GAG	-	10	49	c.127_129delGAG	c.(127-129)GAGdel	p.E47del
Pat_14	Post-Resistance	DYNC1H1	1778	37	14	102445788	102445788	Frame_Shift_Del	DEL	T	-	11	574	c.477delT	c.(475-477)CCTfs	p.P159fs
Pat_14	Post-Resistance	ADAL	161823	37	15	43641115	43641115	Frame_Shift_Del	DEL	A	-	7	367	c.563delA	c.(562-564)CAAfs	p.Q188fs
Pat_14	Post-Resistance	ABCA3	21	37	16	2369649	2369651	In_Frame_Del	DEL	AGC	-	7	518	c.804_806delGCT	c.(802-807)CTGCTC>CTC	.268_269LL>L
Pat_14	Post-Resistance	GSPT1	2935	37	16	12009530	12009531	In_Frame_Ins	INS	-	CCG	6	10	c.47_48insCGG	c.(46-48)GGG>GGCGGG	p.16_16G>GG
Pat_14	Post-Resistance	KIAA0430	9665	37	16	15729982	15729984	In_Frame_Del	DEL	CCA	-	8	606	c.360_362delTGG	.(358-363)GGTGGC>GG	.120_121GG>
Pat_14	Post-Resistance	CD2BP2	10421	37	16	30365550	30365552	In_Frame_Del	DEL	CAT	-	12	1568	c.170_172delATG	.(169-174)GATGGG>GG	p.D57del
Pat_14	Post-Resistance	SETD1A	9739	37	16	30977317	30977317	Frame_Shift_Del	DEL	C	-	7	396	c.2115delC	c.(2113-2115)GGCfs	p.G705fs
Pat_14	Post-Resistance	FTO	79068	37	16	54145739	54145739	Frame_Shift_Del	DEL	A	-	10	1484	c.1430delA	c.(1429-1431)GAAfs	p.E477fs
Pat_14	Post-Resistance	IRX6	79190	37	16	55362674	55362676	In_Frame_Del	DEL	GAG	-	11	181	c.784_786delGAG	c.(784-786)GAGdel	p.E268del
Pat_14	Post-Resistance	COQ9	57017	37	16	57486732	57486734	In_Frame_Del	DEL	GAG	-	8	749	c.262_264delGAG	c.(262-264)GAGdel	p.E91del
Pat_14	Post-Resistance	CSNK2A2	1459	37	16	58198019	58198020	Frame_Shift_Del	DEL	CA	-	8	617	c.1008_1009delTG	c.(1006-1011)TGTGCAfs	p.C336fs
Pat_14	Post-Resistance	C16orf3	750	37	16	90095685	90095685	Frame_Shift_Del	DEL	C	-	7	641	c.66delG	c.(64-66)TGGfs	p.W22fs
Pat_14	Post-Resistance	FXR2	9513	37	17	7495872	7495874	In_Frame_Del	DEL	CGG	-	29	1465	.1773_1775delCC	(1771-1776)CGCCGT>CG	.591_592RR>
Pat_14	Post-Resistance	MYH10	4628	37	17	8397095	8397097	In_Frame_Del	DEL	CCT	-	9	209	.4070_4072delAG	(4069-4074)GAGGCC>GC	p.E1357del
Pat_14	Post-Resistance	EPN2	22905	37	17	19232950	19232950	Frame_Shift_Del	DEL	A	-	9	308	c.1401delA	c.(1399-1401)TCAfs	p.S467fs
Pat_14	Post-Resistance	ZNF207	7756	37	17	30677314	30677316	In_Frame_Del	DEL	AAG	-	9	885	c.10_12delAAG	c.(10-12)AAGdel	p.K7del
Pat_14	Post-Resistance	FKBP10	60681	37	17	39975559	39975559	Frame_Shift_Del	DEL	C	-	7	333	c.825delC	c.(823-825)CTCfs	p.L275fs
Pat_14	Post-Resistance	BRCA1	672	37	17	41246532	41246532	Frame_Shift_Del	DEL	T	-	7	891	c.1016delA	c.(1015-1017)AAGfs	p.K339fs
Pat_14	Post-Resistance	CDC27	996	37	17	45234336	45234336	Frame_Shift_Del	DEL	G	-	15	455	c.785delC	c.(784-786)CCAfs	p.P262fs
Pat_14	Post-Resistance	COIL	8161	37	17	55028117	55028118	Frame_Shift_Ins	INS	-	T	10	332	c.485_486insA	c.(484-486)AACfs	p.N162fs
Pat_14	Post-Resistance	MRC2	9902	37	17	60757562	60757564	In_Frame_Del	DEL	ACG	-	10	278	.2330_2332delAC	(2329-2334)CACGAC>CA	p.D781del
Pat_14	Post-Resistance	CDC42EP4	23580	37	17	71281585	71281587	In_Frame_Del	DEL	TCC	-	11	634	.1053_1055delGG	.(1051-1056)GAGGAT>GA	p.E351del
Pat_14	Post-Resistance	ITGB4	3691	37	17	73726384	73726384	Frame_Shift_Del	DEL	C	-	8	345	c.801delC	c.(799-801)TTCfs	p.F267fs
Pat_14	Post-Resistance	OSBPL1A	114876	37	18	21750331	21750331	Frame_Shift_Del	DEL	T	-	7	357	c.2378delA	c.(2377-2379)AATfs	p.N793fs
Pat_14	Post-Resistance	SH2D3A	10045	37	19	6755180	6755180	Frame_Shift_Del	DEL	G	-	7	925	c.643delC	c.(643-645)CGGfs	p.R215fs
Pat_14	Post-Resistance	HAUS8	93323	37	19	17160706	17160707	Frame_Shift_Del	DEL	GA	-	8	998	c.1209_1210delTC	c.(1207-1212)TCTCGTfs	p.S403fs
Pat_14	Post-Resistance	NCAN	1463	37	19	19360601	19360603	In_Frame_Del	DEL	CAC	-	7	264	.3847_3849delCA	c.(3847-3849)CACdel	p.H1287del
Pat_14	Post-Resistance	ZFP14	57677	37	19	36832330	36832330	Frame_Shift_Del	DEL	T	-	7	769	c.398delA	c.(397-399)AAGfs	p.K133fs
Pat_14	Post-Resistance	ZFP36	7538	37	19	39898948	39898950	In_Frame_Del	DEL	CAC	-	8	1083	c.590_592delCAC	c.(589-594)TCACCA>TCA	p.P201del
Pat_14	Post-Resistance	C19orf47	126526	37	19	40834399	40834399	Frame_Shift_Del	DEL	G	-	10	1226	c.471delC	c.(469-471)CCCfs	p.P157fs
Pat_14	Post-Resistance	NUCB1	4924	37	19	49425109	49425111	In_Frame_Del	DEL	AGC	-	7	259	.1199_1201delAG	.(1198-1203)AAGCAG>AA	p.Q407del
Pat_14	Post-Resistance	SIGLEC8	27181	37	19	51961617	51961619	In_Frame_Del	DEL	GCA	-	10	379	c.23_25delTGC	c.(22-27)CTGCCC>CCC	p.L8del
Pat_14	Post-Resistance	U2AF2	11338	37	19	56171899	56171901	In_Frame_Del	DEL	AGA	-	8	237	c.248_250delAGA	.(247-252)GAGAAG>GA	p.K87del
Pat_14	Post-Resistance	PUM2	23369	37	2	20482977	20482979	In_Frame_Del	DEL	GCT	-	8	471	.1449_1451delAG	.(1447-1452)GCAGCT>GC	.483_484AA>
Pat_14	Post-Resistance	DHX57	90957	37	2	39095411	39095413	In_Frame_Del	DEL	CCA	-	9	349	c.135_137delTGG	.(133-138)GGTGGA>GG	p.45_46GG>G
Pat_14	Post-Resistance	KBTBD10	10324	37	2	170366496	170366496	Frame_Shift_Del	DEL	A	-	11	820	c.208delA	c.(208-210)AAAfs	p.K70fs
Pat_14	Post-Resistance	DCAF17	80067	37	2	172309687	172309687	Frame_Shift_Del	DEL	T	-	8	410	c.591delT	c.(589-591)CCTfs	p.P197fs
Pat_14	Post-Resistance	GZF1	64412	37	20	23345921	23345923	In_Frame_Del	DEL	GAG	-	8	166	c.901_903delGAG	c.(901-903)GAGdel	p.E306del

Pat_14	Post-Resistance	E2F1	1869	37	20	32267581	32267582	Frame_Shift_Del	DEL	GG	-	7	546	c.551_552delCC	c.(550-552)TCCfs	p.S184fs
Pat_14	Post-Resistance	RTEL1	51750	37	20	62292822	62292824	In_Frame_Del	DEL	GCT	-	8	165	c.274_276delGCT	c.(274-276)GCTdel	p.A96del
Pat_14	Post-Resistance	TCP10L	140290	37	21	33949091	33949091	Frame_Shift_Del	DEL	C	-	10	747	c.641delG	c.(640-642)GGTfs	p.G214fs
Pat_14	Post-Resistance	DRG1	4733	37	22	31796702	31796704	In_Frame_Del	DEL	GGT	-	8	469	c.139_141delGGT	c.(139-141)GGTdel	p.G52del
Pat_14	Post-Resistance	FBXO7	25793	37	22	32894235	32894235	Frame_Shift_Del	DEL	G	-	7	1077	c.1287delG	c.(1285-1287)TTGfs	p.L429fs
Pat_14	Post-Resistance	SAPS2	9701	37	22	50876653	50876655	In_Frame_Del	DEL	TGA	-	7	741	.1890_1892delTG	c.(1888-1893)TTTGAT>TT	p.D633del
Pat_14	Post-Resistance	ITPR1	3708	37	3	4774895	4774895	Frame_Shift_Del	DEL	G	-	7	433	c.5200delG	c.(5200-5202)GGGfs	p.G1734fs
Pat_14	Post-Resistance	EDEM1	9695	37	3	5248941	5248941	Frame_Shift_Del	DEL	T	-	11	678	c.1321delT	c.(1321-1323)TTTfs	p.F441fs
Pat_14	Post-Resistance	XPC	7508	37	3	14219966	14219968	In_Frame_Del	DEL	CCT	-	12	199	c.101_103delAGG	c.(100-105)GAGGAT>GAT	p.E34del
Pat_14	Post-Resistance	ACVR2B	93	37	3	38524693	38524693	Frame_Shift_Del	DEL	C	-	8	710	c.1409delC	c.(1408-1410)TCCfs	p.S470fs
Pat_14	Post-Resistance	PLXNB1	5364	37	3	48465002	48465003	Frame_Shift_Ins	INS	-	A	9	503	c.1018_1019insT	c.(1018-1020)TGCfs	p.C340fs
Pat_14	Post-Resistance	MYLK	4638	37	3	123368043	123368044	Splice_Site	INS	-	G	9	476	c.4289_splice	c.e25-1	p.E1430_splice
Pat_14	Post-Resistance	TMCC1	23023	37	3	129546680	129546682	In_Frame_Del	DEL	GCA	-	8	332	c.540_542delTGC	c.(538-543)GCTGCA>GCA	.180_181AA>
Pat_14	Post-Resistance	DBR1	51163	37	3	137880741	137880743	In_Frame_Del	DEL	TCG	-	7	490	.1623_1625delCG	.(1621-1626)GATGAT>GA	.541_542DD>
Pat_14	Post-Resistance	PDE6B	5158	37	4	661763	661765	In_Frame_Del	DEL	AGG	-	8	557	.2471_2473delAG	(2470-2475)AAGGAG>AA	p.E828del
Pat_14	Post-Resistance	OTOP1	133060	37	4	4228274	4228282	In_Frame_Del	DEL	CACAGCA	-	7	134	_318delCTGCTG	.(310-318)CTGCTGTGGd	p.LLW104del
Pat_14	Post-Resistance	C1QTNF7	114905	37	4	15444120	15444120	Frame_Shift_Del	DEL	C	-	7	893	c.567delC	c.(565-567)TTCfs	p.F189fs
Pat_14	Post-Resistance	YTHDC1	91746	37	4	69202891	69202893	In_Frame_Del	DEL	TCC	-	7	207	c.735_737delGGA	c.(733-738)GAGGAA>GAA	.245_246EE>
Pat_14	Post-Resistance	PKD2	5311	37	4	88986559	88986559	Frame_Shift_Del	DEL	A	-	7	498	c.2152delA	c.(2152-2154)AAAfs	p.K718fs
Pat_14	Post-Resistance	NAP1L5	266812	37	4	89618484	89618486	In_Frame_Del	DEL	TCC	-	10	223	c.420_422delGGA	c.(418-423)GAGGAA>GAA	.140_141EE>
Pat_14	Post-Resistance	NPNT	255743	37	4	106863682	106863684	In_Frame_Del	DEL	CCA	-	7	391	c.982_984delCCA	c.(982-984)CCAdel	p.P333del
Pat_14	Post-Resistance	ANK2	287	37	4	114214679	114214681	In_Frame_Del	DEL	CAC	-	10	338	.2460_2462delCA	(2458-2463)GTCACC>GT	p.T826del
Pat_14	Post-Resistance	EXOSC9	5393	37	4	122728764	122728764	Frame_Shift_Del	DEL	T	-	7	765	c.592delT	c.(592-594)TTTfs	p.F198fs
Pat_14	Post-Resistance	CDH10	1008	37	5	24492973	24492973	Frame_Shift_Del	DEL	A	-	8	1131	c.1577delT	c.(1576-1578)TTCfs	p.F526fs
Pat_14	Post-Resistance	AFF4	27125	37	5	132270259	132270259	Frame_Shift_Del	DEL	T	-	8	1055	c.498delA	c.(496-498)AAAfs	p.K166fs
Pat_14	Post-Resistance	NKHD1-EIF4EBP	404734	37	5	139905676	139905676	Frame_Shift_Del	DEL	A	-	8	677	c.4588delA	c.(4588-4590)AAAfs	p.K1530fs
Pat_14	Post-Resistance	IK	3550	37	5	140032593	140032594	Frame_Shift_Del	DEL	GA	-	11	197	c.268_269delGA	c.(268-270)GAGfs	p.E90fs
Pat_14	Post-Resistance	HNRNPH1	3187	37	5	179043184	179043187	Frame_Shift_Del	DEL	GCTG	-	7	1314	1240_1243delCA	c.(1240-1245)CAGCAGfs	p.Q414fs
Pat_14	Post-Resistance	TUBB2B	347733	37	6	3225002	3225004	In_Frame_Del	DEL	CCT	-	7	409	.1319_1321delAG	(1318-1323)GAGGGC>GG	p.E440del
Pat_14	Post-Resistance	BAT2	7916	37	6	31597456	31597457	Frame_Shift_Ins	INS	-	C	10	117	c.2088_2089insC	c.(2086-2091)CCACCCfs	p.P696fs
Pat_14	Post-Resistance	TULP1	7287	37	6	35478775	35478777	In_Frame_Del	DEL	TCC	-	8	319	c.360_362delGGA	c.(358-363)GAGGAA>GAA	.120_121EE>
Pat_14	Post-Resistance	REPS1	85021	37	6	139266690	139266690	Frame_Shift_Del	DEL	T	-	8	1421	c.422delA	c.(421-423)AAGfs	p.K141fs
Pat_14	Post-Resistance	GRM1	2911	37	6	146350671	146350672	Frame_Shift_Ins	INS	-	T	7	622	c.18_19insT	c.(16-21)TTGTTTfs	p.L6fs
Pat_14	Post-Resistance	NOX3	50508	37	6	155743925	155743926	Frame_Shift_Del	DEL	CA	-	8	1330	c.1210_1211delT	c.(1210-1212)TGCfs	p.C404fs
Pat_14	Post-Resistance	PURB	5814	37	7	44924044	44924046	In_Frame_Del	DEL	CGC	-	8	906	c.902_904delGCG	c.(901-906)GGCGAA>GA	p.G301del
Pat_14	Post-Resistance	PTCD1	26024	37	7	99032605	99032607	In_Frame_Del	DEL	CTC	-	10	496	c.259_261delGAG	c.(259-261)GAGdel	p.E87del
Pat_14	Post-Resistance	SRRT	51593	37	7	100479332	100479332	Frame_Shift_Del	DEL	G	-	7	230	c.304delG	c.(304-306)GGGfs	p.G102fs
Pat_14	Post-Resistance	NAPEPLD	222236	37	7	102760122	102760123	Frame_Shift_Ins	INS	-	A	7	426	c.842_843insT	c.(841-843)TTCfs	p.F281fs
Pat_14	Post-Resistance	RINT1	60561	37	7	105190759	105190759	Frame_Shift_Del	DEL	G	-	8	973	c.1159delG	c.(1159-1161)GATfs	p.D387fs
Pat_14	Post-Resistance	CBLL1	79872	37	7	107395909	107395909	Frame_Shift_Del	DEL	A	-	8	1050	c.413delA	c.(412-414)GAAfs	p.E138fs
Pat_14	Post-Resistance	LUC7L2	51631	37	7	139094365	139094366	Frame_Shift_Del	DEL	AG	-	8	94	c.744_745delAG	c.(742-747)GAAGAGfs	p.E248fs
Pat_14	Post-Resistance	OR9A4	130075	37	7	141619203	141619203	Frame_Shift_Del	DEL	T	-	8	802	c.528delT	c.(526-528)AATfs	p.N176fs
Pat_14	Post-Resistance	XRCC2	7516	37	7	152346220	152346220	Frame_Shift_Del	DEL	A	-	9	478	c.350delT	c.(349-351)TTGfs	p.L117fs
Pat_14	Post-Resistance	SGK223	157285	37	8	8176387	8176388	In_Frame_Ins	INS	-	GGGGCG	16	49	97_3498insCGCC	96-3498)CCG>CCCGCC	166_1166P>P
Pat_14	Post-Resistance	NBN	4683	37	8	90967512	90967512	Frame_Shift_Del	DEL	T	-	9	605	c.1396delA	c.(1396-1398)AGGfs	p.R466fs
Pat_14	Post-Resistance	UBR5	51366	37	8	103289348	103289349	Frame_Shift_Ins	INS	-	T	7	493	c.6360_6361insA	c.(6358-6363)AAAGAAfs	p.K2120fs
Pat_14	Post-Resistance	MYC	4609	37	8	128750605	128750607	In_Frame_Del	DEL	CAG	-	7	297	c.97_99delCAG	c.(97-99)CAGdel	p.Q37del

Pat_14	Post-Resistance	PLEC	5339	37	8	145000951	145000953	Splice_Site	DEL	CCT	-	10	591	c.4455_splice	c.e30+1	p.E1485_splice
Pat_14	Post-Resistance	TAF1L	138474	37	9	32633584	32633584	Frame_Shift_Del	DEL	T	-	10	489	c.1994delA	c.(1993-1995)AAGfs	p.K665fs
Pat_14	Post-Resistance	HRCT1	646962	37	9	35906605	35906607	In_Frame_Del	DEL	CCG	-	8	62	c.321_323delCCG	.(319-324)CACCGC>CAC	p.R108del
Pat_14	Post-Resistance	ROR2	4920	37	9	94486026	94486028	In_Frame_Del	DEL	TCC	-	10	566	.2748_2750delGG	(2746-2751)GAGGAA>GA	.916_917EE>
Pat_14	Post-Resistance	ECM2	1842	37	9	95277146	95277148	In_Frame_Del	DEL	TCC	-	7	476	c.819_821delGGA	c.(817-822)GAGGAT>GAT	p.E273del
Pat_14	Post-Resistance	IPPK	64768	37	9	95418781	95418781	Frame_Shift_Del	DEL	T	-	8	730	c.182delA	c.(181-183)AATfs	p.N61fs
Pat_14	Post-Resistance	TNC	3371	37	9	117797539	117797539	Frame_Shift_Del	DEL	G	-	11	945	c.5731delC	c.(5731-5733)CGGfs	p.R1911fs
Pat_14	Post-Resistance	ABL1	25	37	9	133759490	133759492	In_Frame_Del	DEL	AAG	-	20	403	.1813_1815delAA	c.(1813-1815)AAGdel	p.K609del
Pat_14	Post-Resistance	SNAPC4	6621	37	9	139286460	139286462	In_Frame_Del	DEL	CTC	-	7	644	c.907_909delGAG	c.(907-909)GAGdel	p.E303del
Pat_14	Post-Resistance	DMD	1756	37	X	32361293	32361293	Frame_Shift_Del	DEL	T	-	8	648	c.5697delA	c.(5695-5697)AAAfs	p.K1899fs
Pat_14	Post-Resistance	NUDT11	55190	37	X	51239296	51239309	Translation_Start_Site	DEL	TCGAGGCA	-	14	68			
Pat_14	Post-Resistance	FAM199X	139231	37	X	103432837	103432839	In_Frame_Del	DEL	CAG	-	9	690	c.846_848delCAG	.(844-849)GCCAGC>GC	p.S286del
Pat_14	Post-Resistance	PAK3	5063	37	X	110406206	110406208	In_Frame_Del	DEL	GAA	-	7	432	c.577_579delGAA	c.(577-579)GAAdel	p.E197del
Pat_14	Post-Resistance	NKAP	79576	37	X	119072752	119072753	Frame_Shift_Del	DEL	TC	-	10	777	c.407_408delGA	c.(406-408)AGAfs	p.R136fs
Pat_14	Post-Resistance	CD99L2	83692	37	X	149984524	149984526	In_Frame_Del	DEL	GTG	-	13	1371	c.156_158delCAC	c.(154-159)ACCACA>ACA	p.52_53TT>T
Pat_14	Post-Resistance	MAGEA10	4109	37	X	151303906	151303908	In_Frame_Del	DEL	AGG	-	8	273	c.185_187delCCT	c.(184-189)TCCTGC>TGC	p.S62del
Pat_15	Pre-Treatment	DHX37	57647	37	12	125465270	125465272	In_Frame_Del	DEL	CTC	-	2	4	c.502_504delGAG	c.(502-504)GAGdel	p.E168del
Pat_15	Pre-Treatment	ZIC5	85416	37	13	100622668	100622670	In_Frame_Del	DEL	GGC	-	3	5	.1260_1262delGC	(1258-1263)CCGCCA>CC	.420_421PP>
Pat_15	Pre-Treatment	BAHCC1	57597	37	17	79424588	79424590	In_Frame_Del	DEL	AAG	-	3	5	.5011_5013delAA	c.(5011-5013)AAGdel	p.K1674del
Pat_15	Pre-Treatment	GTF2F1	2962	37	19	6381410	6381412	In_Frame_Del	DEL	CTC	-	2	4	c.976_978delGAG	c.(976-978)GAGdel	p.E326del
Pat_15	Pre-Treatment	MYCN	4613	37	2	16082314	16082314	Frame_Shift_Del	DEL	C	-	9	553	c.128delC	c.(127-129)ACCfs	p.T43fs
Pat_15	Pre-Treatment	THNSL2	55258	37	2	88482314	88482315	Frame_Shift_Del	DEL	TC	-	7	977	c.899_900delTC	c.(898-900)TTCfs	p.F300fs
Pat_15	Pre-Treatment	COX5B	1329	37	2	98263824	98263842	Frame_Shift_Del	DEL	CAAAGGGA	-	12	74	lGGCCCCAAAGG	3)CTGGCCCCAAAGGGA	p.L65fs
Pat_15	Pre-Treatment	CLTCL1	8218	37	22	19213154	19213154	Frame_Shift_Del	DEL	C	-	2	4	c.1950delG	c.(1948-1950)TGGfs	p.W650fs
Pat_15	Pre-Treatment	ARHGAP39	80728	37	8	145773342	145773344	In_Frame_Del	DEL	CTG	-	10	4	.1126_1128delCA	c.(1126-1128)CAGdel	p.Q376del
Pat_15	Post-Resistance	MEGF6	1953	37	1	3418424	3418424	Frame_Shift_Del	DEL	G	-	7	266	c.2250delC	c.(2248-2250)CCCfs	p.P750fs
Pat_15	Post-Resistance	PHF13	148479	37	1	6680069	6680071	In_Frame_Del	DEL	GAA	-	16	323	c.348_350delGAA	c.(346-351)CTGAAG>CTG	p.K121del
Pat_15	Post-Resistance	ZDHHC18	84243	37	1	27180318	27180318	Frame_Shift_Del	DEL	T	-	7	1027	c.1151delT	c.(1150-1152)GTAfs	p.V384fs
Pat_15	Post-Resistance	DLGAP3	58512	37	1	35370281	35370283	In_Frame_Del	DEL	TGG	-	7	674	c.702_704delCCA	.(700-705)CACCAG>CAG	p.H234del
Pat_15	Post-Resistance	TRIT1	54802	37	1	40313257	40313257	Frame_Shift_Del	DEL	T	-	7	1189	c.891delA	c.(889-891)AAAfs	p.K297fs
Pat_15	Post-Resistance	PTPRF	5792	37	1	44071946	44071948	In_Frame_Del	DEL	GCG	-	13	582	.3519_3521delGC	(3517-3522)CAGCGG>CA	p.R1178del
Pat_15	Post-Resistance	ANKRD13C	81573	37	1	70819873	70819873	Frame_Shift_Del	DEL	G	-	7	1245	c.219delC	c.(217-219)CCCfs	p.P73fs
Pat_15	Post-Resistance	ST6GALNAC5	81849	37	1	77334277	77334279	In_Frame_Del	DEL	GCA	-	9	187	c.111_113delGCA	.(109-114)CCGCAG>CC	p.Q49del
Pat_15	Post-Resistance	GSTM3	2947	37	1	110282062	110282062	Frame_Shift_Del	DEL	C	-	8	1780	c.178delG	c.(178-180)GACfs	p.D60fs
Pat_15	Post-Resistance	VANGL1	81839	37	1	116206586	116206586	Frame_Shift_Del	DEL	T	-	8	542	c.509delT	c.(508-510)CTTfs	p.L170fs
Pat_15	Post-Resistance	LINGO4	339398	37	1	151773603	151773603	Frame_Shift_Del	DEL	A	-	9	842	c.1578delT	c.(1576-1578)TTTfs	p.F526fs
Pat_15	Post-Resistance	NPR1	4881	37	1	153659175	153659175	Frame_Shift_Del	DEL	C	-	7	962	c.1812delC	c.(1810-1812)GACfs	p.D604fs
Pat_15	Post-Resistance	CR2	1380	37	1	207642044	207642044	Frame_Shift_Del	DEL	C	-	8	1132	c.618delC	c.(616-618)GTCfs	p.V206fs
Pat_15	Post-Resistance	LOC642587	642587	37	1	209605637	209605648	In_Frame_Del	DEL	CAGCAGCA	-	22	65	263delAGCAGCA	264)GTAGCAGCAGCAGC	p.AAAA93del
Pat_15	Post-Resistance	INTS7	25896	37	1	212115191	212115193	In_Frame_Del	DEL	TGC	-	9	1366	.2862_2864delGC	(2860-2865)CAGCAA>CA	.954_955QQ>
Pat_15	Post-Resistance	AGT	183	37	1	230839055	230839055	Frame_Shift_Del	DEL	A	-	7	334	c.1290delT	c.(1288-1290)TTTfs	p.F430fs
Pat_15	Post-Resistance	STAM	8027	37	10	17756616	17756618	In_Frame_Del	DEL	CTG	-	8	412	.1460_1462delCT	.(1459-1464)ACTGCT>AC	p.A491del
Pat_15	Post-Resistance	ERCC6	2074	37	10	50732139	50732141	In_Frame_Del	DEL	CCT	-	7	582	.1335_1337delAG	(1333-1338)GGAGGT>GG	.445_446GG>
Pat_15	Post-Resistance	PLAU	5328	37	10	75673298	75673298	Frame_Shift_Del	DEL	A	-	8	1353	c.462delA	c.(460-462)GGAfs	p.G154fs
Pat_15	Post-Resistance	CCNJ	54619	37	10	97816696	97816697	Frame_Shift_Del	DEL	GG	-	7	429	c.519_520delGG	c.(517-522)TTGGAAfs	p.L173fs
Pat_15	Post-Resistance	UBQLN3	50613	37	11	5529918	5529920	In_Frame_Del	DEL	TGG	-	8	868	c.869_871delCCA	.(868-873)ACCAGC>AGC	p.T290del
Pat_15	Post-Resistance	SMPD1	6609	37	11	6412853	6412854	Frame_Shift_Ins	INS	-	C	7	40	c.558_559insC	c.(556-561)CCGCCCfs	p.P186fs

Pat_15	Post-Resistance	KCNA4	3739	37	11	30034029	30034031	In_Frame_Del	DEL	TGG	-	9	269	c.195_197delCCA	.(193-198)CACCAG>CAG	p.H65del
Pat_15	Post-Resistance	C11orf46	120534	37	11	30352754	30352754	Frame_Shift_Del	DEL	A	-	11	433	c.259delA	c.(259-261)AAAfs	p.K87fs
Pat_15	Post-Resistance	CCDC73	493860	37	11	32635951	32635951	Frame_Shift_Del	DEL	T	-	10	111	c.1913delA	c.(1912-1914)AATfs	p.N638fs
Pat_15	Post-Resistance	ARHGAP1	392	37	11	46702224	46702224	Frame_Shift_Del	DEL	G	-	8	577	c.709delC	c.(709-711)CTGfs	p.L237fs
Pat_15	Post-Resistance	MTA2	9219	37	11	62361728	62361729	Splice_Site	INS	-	A	14	680	c.1841_splice	c.e17+1	p.R614_splice
Pat_15	Post-Resistance	KLC2	64837	37	11	66033664	66033664	Frame_Shift_Del	DEL	C	-	7	152	c.1703delC	c.(1702-1704)ACCfs	p.T568fs
Pat_15	Post-Resistance	CASP1	834	37	11	104901070	104901070	Frame_Shift_Del	DEL	T	-	8	597	c.614delA	c.(613-615)AATfs	p.N205fs
Pat_15	Post-Resistance	TMPRSS13	84000	37	11	117789346	117789360	In_Frame_Del	DEL	GAGATGCCC	-	9	248	9delGCCGGGCAT	)GGCCGGGCATCTCCAC	p.GRASP72de
Pat_15	Post-Resistance	IFFO1	25900	37	12	6649704	6649706	In_Frame_Del	DEL	GGC	-	8	484	.1623_1625delGC	(1621-1626)CCGCCA>CC	.541_542PP>
Pat_15	Post-Resistance	CLEC4A	50856	37	12	8281936	8281937	Frame_Shift_Ins	INS	-	A	9	175	c.276_277insA	c.(274-279)GTGAAAfs	p.V92fs
Pat_15	Post-Resistance	LRP1	4035	37	12	57605740	57605742	In_Frame_Del	DEL	TGC	-	16	865	13289_13291delT	13288-13293)TTGCTG>T	4430_4431LL>
Pat_15	Post-Resistance	TMBIM4	51643	37	12	66531936	66531937	Frame_Shift_Ins	INS	-	A	7	82	c.520_521insT	c.(520-522)TATfs	p.Y174fs
Pat_15	Post-Resistance	C12orf42	374470	37	12	103695960	103695960	Frame_Shift_Del	DEL	G	-	8	824	c.1009delC	c.(1009-1011)CGCfs	p.R337fs
Pat_15	Post-Resistance	ANKRD13A	88455	37	12	110471746	110471750	Frame_Shift_Del	DEL	AGTCC	-	9	117	493_1497delAGT	c.(1492-1497)GAGTCCfs	p.E498fs
Pat_15	Post-Resistance	SRRM4	84530	37	12	119594378	119594380	In_Frame_Del	DEL	CAG	-	8	270	.1611_1613delCA	.(1609-1614)TACAGC>TA	p.S542del
Pat_15	Post-Resistance	VPS33A	65082	37	12	122748169	122748169	Frame_Shift_Del	DEL	A	-	7	211	c.246delT	c.(244-246)TTTfs	p.F82fs
Pat_15	Post-Resistance	EP400	57634	37	12	132547138	132547139	In_Frame_Ins	INS	-	CAA	10	281	.8226_8227insCA	c.(8224-8229)insCAA	.2748_2749ins
Pat_15	Post-Resistance	B3GALTL	145173	37	13	31803392	31803392	Frame_Shift_Del	DEL	A	-	11	434	c.231delA	c.(229-231)TTAfs	p.L77fs
Pat_15	Post-Resistance	LMO7	4008	37	13	76415307	76415308	Frame_Shift_Del	DEL	AG	-	9	645	c.2946_2947delAG	c.(2944-2949)GCAGAGfs	p.A982fs
Pat_15	Post-Resistance	GAS6	2621	37	13	114542717	114542718	Frame_Shift_Ins	INS	-	C	8	884	c.449_450insG	c.(448-450)GGCfs	p.G150fs
Pat_15	Post-Resistance	PSMA6	5687	37	14	35782216	35782216	Frame_Shift_Del	DEL	A	-	8	720	c.539delA	c.(538-540)GAAfs	p.E180fs
Pat_15	Post-Resistance	KTN1	3895	37	14	56137475	56137475	Frame_Shift_Del	DEL	A	-	7	348	c.3296delA	c.(3295-3297)GAAfs	p.E1099fs
Pat_15	Post-Resistance	SYNE2	23224	37	14	64488704	64488704	Frame_Shift_Del	DEL	A	-	8	337	c.5482delA	c.(5482-5484)AAAfs	p.K1828fs
Pat_15	Post-Resistance	ZBTB1	22890	37	14	64989787	64989787	Frame_Shift_Del	DEL	A	-	8	709	c.1565delA	c.(1564-1566)CAAfs	p.Q522fs
Pat_15	Post-Resistance	HERC2	8924	37	15	28474843	28474843	Frame_Shift_Del	DEL	T	-	8	1202	c.4960delA	c.(4960-4962)ATGfs	p.M1654fs
Pat_15	Post-Resistance	SPINT1	6692	37	15	41149075	41149077	In_Frame_Del	DEL	CAC	-	10	1318	.1492_1494delCA	c.(1492-1494)CACdel	p.H501del
Pat_15	Post-Resistance	MAP1A	4130	37	15	43820164	43820164	Frame_Shift_Del	DEL	G	-	7	942	c.6493delG	c.(6493-6495)GCTfs	p.A2165fs
Pat_15	Post-Resistance	SIN3A	25942	37	15	75702506	75702507	Frame_Shift_Del	DEL	CC	-	7	874	c.1129_1130delGG	c.(1129-1131)GGAfs	p.G377fs
Pat_15	Post-Resistance	WDR90	197335	37	16	709106	709106	Frame_Shift_Del	DEL	C	-	9	544	c.3032delC	c.(3031-3033)GCCfs	p.A1011fs
Pat_15	Post-Resistance	UBN1	29855	37	16	4910691	4910693	In_Frame_Del	DEL	AGA	-	19	1076	c.698_700delAGA	.(697-702)GAGAAG>GAG	p.K238del
Pat_15	Post-Resistance	NOMO1	23420	37	16	14980695	14980695	Frame_Shift_Del	DEL	C	-	7	1517	c.3300delC	c.(3298-3300)TTCfs	p.F1100fs
Pat_15	Post-Resistance	TMC7	79905	37	16	19058506	19058506	Frame_Shift_Del	DEL	T	-	7	2074	c.1675delT	c.(1675-1677)TTTfs	p.F559fs
Pat_15	Post-Resistance	POLR3E	55718	37	16	22339834	22339834	Frame_Shift_Del	DEL	C	-	15	820	c.1870delC	c.(1870-1872)CCCfs	p.P624fs
Pat_15	Post-Resistance	RABEP2	79874	37	16	28931200	28931202	In_Frame_Del	DEL	CTG	-	14	296	c.337_339delCAG	c.(337-339)CAGdel	p.Q113del
Pat_15	Post-Resistance	PRRT2	112476	37	16	29825016	29825016	Frame_Shift_Del	DEL	C	-	10	89	c.641delC	c.(640-642)GCCfs	p.A214fs
Pat_15	Post-Resistance	EDC4	23644	37	16	67913786	67913788	In_Frame_Del	DEL	AGC	-	11	213	.1855_1857delAG	c.(1855-1857)AGCdel	p.S629del
Pat_15	Post-Resistance	ENO3	2027	37	17	4859894	4859894	Frame_Shift_Del	DEL	G	-	7	1010	c.1094delG	c.(1093-1095)TGGfs	p.W365fs
Pat_15	Post-Resistance	CHD3	1107	37	17	7801857	7801859	In_Frame_Del	DEL	AAG	-	9	292	.2095_2097delAA	c.(2095-2097)AAGdel	p.K703del
Pat_15	Post-Resistance	TIAF1	9220	37	17	27401055	27401056	Frame_Shift_Del	DEL	CA	-	7	492	c.162_163delTG	c.(160-165)TGTGGAfs	p.C54fs
Pat_15	Post-Resistance	GAS2L2	246176	37	17	34074257	34074257	Frame_Shift_Del	DEL	G	-	9	1466	c.863delC	c.(862-864)CCGfs	p.P288fs
Pat_15	Post-Resistance	ACACA	31	37	17	35600371	35600371	Frame_Shift_Del	DEL	G	-	11	1395	c.2736delC	c.(2734-2736)CCCfs	p.P912fs
Pat_15	Post-Resistance	CCDC103	388389	37	17	42980014	42980015	Frame_Shift_Del	DEL	AG	-	7	259	c.558_559delAG	c.(556-561)GCAGAGfs	p.A186fs
Pat_15	Post-Resistance	VEZF1	7716	37	17	56056605	56056607	In_Frame_Del	DEL	TGC	-	7	839	.1044_1046delGC	.(1042-1047)CAGCAA>CA	.348_349QQ>
Pat_15	Post-Resistance	USP32	84669	37	17	58257949	58257949	Frame_Shift_Del	DEL	T	-	10	834	c.4598delA	c.(4597-4599)AACfs	p.N1533fs
Pat_15	Post-Resistance	TNRC6C	57690	37	17	76046786	76046788	In_Frame_Del	DEL	CTG	-	7	835	.1643_1645delCT	.(1642-1647)ACTGCT>AC	p.A552del
Pat_15	Post-Resistance	SLC26A11	284129	37	17	78201649	78201651	In_Frame_Del	DEL	TGC	-	8	839	c.626_628delTGC	c.(625-630)ATGCTG>ATG	p.L213del
Pat_15	Post-Resistance	CEP192	55125	37	18	13052949	13052951	In_Frame_Del	DEL	CAG	-	10	1139	.3049_3051delCA	c.(3049-3051)CAGdel	p.Q1020del

Pat_15	Post-Resistance	GALNT1	2589	37	18	33234733	33234733	Frame_Shift_Del	DEL	A	-	9	501	c.107delA	c.(106-108)GAAfs	p.E36fs
Pat_15	Post-Resistance	CXXC1	30827	37	18	47812275	47812277	In_Frame_Del	DEL	CTG	-	8	244	c.481_483delCAG	c.(481-483)CAGdel	p.Q161del
Pat_15	Post-Resistance	C3	718	37	19	6707846	6707847	Frame_Shift_Del	DEL	GT	-	7	566	c.1939_1940delAC	c.(1939-1941)ACGfs	p.T647fs
Pat_15	Post-Resistance	SLC44A2	57153	37	19	10741961	10741961	Frame_Shift_Del	DEL	A	-	9	1255	c.341delA	c.(340-342)GAAfs	p.E114fs
Pat_15	Post-Resistance	NFIX	4784	37	19	13192587	13192589	In_Frame_Del	DEL	ACC	-	16	435	.1196_1198delAC	.(1195-1200)TACCAC>TA	p.H403del
Pat_15	Post-Resistance	CIB3	117286	37	19	16275653	16275654	Frame_Shift_Ins	INS	-	C	8	911	c.417_418insG	c.(415-420)GGGCTGfs	p.G139fs
Pat_15	Post-Resistance	CHERP	10523	37	19	16633994	16633994	Frame_Shift_Del	DEL	G	-	7	555	c.1849delC	c.(1849-1851)CATfs	p.H617fs
Pat_15	Post-Resistance	HAUS8	93323	37	19	17160706	17160707	Frame_Shift_Del	DEL	GA	-	9	1228	c.1209_1210delTC	c.(1207-1212)TCTCGTfs	p.S403fs
Pat_15	Post-Resistance	BCKDHA	593	37	19	41916544	41916544	Frame_Shift_Del	DEL	C	-	7	505	c.111delC	c.(109-111)CACfs	p.H37fs
Pat_15	Post-Resistance	SFRS16	11129	37	19	45556129	45556129	Frame_Shift_Del	DEL	C	-	8	701	c.278delC	c.(277-279)ACCfs	p.T93fs
Pat_15	Post-Resistance	KLC3	147700	37	19	45850756	45850758	In_Frame_Del	DEL	GAG	-	7	441	c.541_543delGAG	c.(541-543)GAGdel	p.E184del
Pat_15	Post-Resistance	PNMAL1	55228	37	19	46973195	46973197	In_Frame_Del	DEL	CTT	-	12	842	.1096_1098delAA	c.(1096-1098)AAGdel	p.K366del
Pat_15	Post-Resistance	SIGLEC8	27181	37	19	51961617	51961619	In_Frame_Del	DEL	GCA	-	9	409	c.23_25delTGC	c.(22-27)CTGCCC>CCC	p.L8del
Pat_15	Post-Resistance	LILRB1	10859	37	19	55146148	55146150	In_Frame_Del	DEL	CTC	-	7	158	.1417_1419delCT	c.(1417-1419)CTCdel	p.L479del
Pat_15	Post-Resistance	ADCY3	109	37	2	25141215	25141217	In_Frame_Del	DEL	CTG	-	9	246	c.640_642delCAG	c.(640-642)CAGdel	p.Q214del
Pat_15	Post-Resistance	SULT6B1	391365	37	2	37414553	37414553	Frame_Shift_Del	DEL	T	-	7	161	c.143delA	c.(142-144)AAGfs	p.K48fs
Pat_15	Post-Resistance	DHX57	90957	37	2	39095411	39095413	In_Frame_Del	DEL	CCA	-	12	289	c.135_137delTGG	.(133-138)GGTGGA>GG	p.45_46GG>G
Pat_15	Post-Resistance	RAB11FIP5	26056	37	2	73315337	73315339	In_Frame_Del	DEL	TGG	-	9	805	.1407_1409delCC	.(1405-1410)CACCAA>CA	p.H469del
Pat_15	Post-Resistance	KRCC1	51315	37	2	88327599	88327599	Frame_Shift_Del	DEL	T	-	7	358	c.484delA	c.(484-486)AGGfs	p.R162fs
Pat_15	Post-Resistance	THNSL2	55258	37	2	88482314	88482315	Frame_Shift_Del	DEL	TC	-	9	1827	c.899_900delTC	c.(898-900)TTCfs	p.F300fs
Pat_15	Post-Resistance	TMEM127	55654	37	2	96919781	96919783	In_Frame_Del	DEL	TGC	-	10	420	c.480_482delGCA	c.(478-483)CAGCAT>CAT	p.Q160del
Pat_15	Post-Resistance	COX5B	1329	37	2	98263824	98263842	Frame_Shift_Del	DEL	CAAAGGGA	-	25	466	lGGCCCCAAAGG	3)CTGGCCCCAAAGGGA	p.L65fs
Pat_15	Post-Resistance	NEB	4703	37	2	152550847	152550847	Frame_Shift_Del	DEL	T	-	9	1003	c.1886delA	c.(1885-1887)AACfs	p.N629fs
Pat_15	Post-Resistance	C2orf67	151050	37	2	210887680	210887680	Frame_Shift_Del	DEL	T	-	8	125	c.2957delA	c.(2956-2958)AATfs	p.N986fs
Pat_15	Post-Resistance	SLC11A1	6556	37	2	219252307	219252307	Frame_Shift_Del	DEL	T	-	9	1339	c.591delT	c.(589-591)GCTfs	p.A197fs
Pat_15	Post-Resistance	FAM134A	79137	37	2	220046969	220046970	Frame_Shift_Del	DEL	CC	-	8	977	c.1250_1251delCC	c.(1249-1251)TCCfs	p.S417fs
Pat_15	Post-Resistance	BCL2L1	598	37	20	30309591	30309591	Frame_Shift_Del	DEL	A	-	7	2171	c.431delT	c.(430-432)TTCfs	p.F144fs
Pat_15	Post-Resistance	EIF2S2	8894	37	20	32693175	32693175	Frame_Shift_Del	DEL	T	-	7	765	c.192delA	c.(190-192)AAAfs	p.K64fs
Pat_15	Post-Resistance	RTEL1	51750	37	20	62292822	62292824	In_Frame_Del	DEL	GCT	-	13	182	c.274_276delGCT	c.(274-276)GCTdel	p.A96del
Pat_15	Post-Resistance	RNF160	26046	37	21	30339206	30339206	Frame_Shift_Del	DEL	T	-	10	46	c.1745delA	c.(1744-1746)AATfs	p.N582fs
Pat_15	Post-Resistance	COL18A1	80781	37	21	46911183	46911183	Frame_Shift_Del	DEL	C	-	7	287	c.3357delC	c.(3355-3357)GGCfs	p.G1119fs
Pat_15	Post-Resistance	TBC1D10A	83874	37	22	30691732	30691732	Frame_Shift_Del	DEL	C	-	7	342	c.518delG	c.(517-519)GGCfs	p.G173fs
Pat_15	Post-Resistance	HMGXB4	10042	37	22	35661544	35661544	Frame_Shift_Del	DEL	A	-	12	176	c.1163delA	c.(1162-1164)GAAfs	p.E388fs
Pat_15	Post-Resistance	SGSM3	27352	37	22	40803318	40803318	Frame_Shift_Del	DEL	A	-	7	706	c.1354delA	c.(1354-1356)AAAfs	p.K452fs
Pat_15	Post-Resistance	EP300	2033	37	22	41574379	41574381	In_Frame_Del	DEL	CAG	-	7	271	.6664_6666delCA	c.(6664-6666)CAGdel	p.Q2225del
Pat_15	Post-Resistance	DYNC1LI1	51143	37	3	32571050	32571050	Frame_Shift_Del	DEL	T	-	7	136	c.1288delA	c.(1288-1290)ATTfs	p.I430fs
Pat_15	Post-Resistance	NKTR	4820	37	3	42679486	42679486	Frame_Shift_Del	DEL	A	-	7	332	c.2290delA	c.(2290-2292)AAAfs	p.K764fs
Pat_15	Post-Resistance	CCR3	1232	37	3	46306948	46306948	Frame_Shift_Del	DEL	T	-	7	1514	c.299delT	c.(298-300)GTTfs	p.V100fs
Pat_15	Post-Resistance	QARS	5859	37	3	49137217	49137220	Frame_Shift_Del	DEL	GAGT	-	7	800	1362_1365delACT	c.(1360-1365)TCACTCfs	p.S454fs
Pat_15	Post-Resistance	EPHA3	2042	37	3	89498505	89498506	Frame_Shift_Del	DEL	GG	-	8	938	c.2477_2478delGG	c.(2476-2478)TGGfs	p.W826fs
Pat_15	Post-Resistance	ZPLD1	131368	37	3	102181181	102181182	Frame_Shift_Ins	INS	-	A	12	437	c.639_640insA	c.(637-642)ACCAAAfs	p.T213fs
Pat_15	Post-Resistance	CDV3	55573	37	3	133292940	133292942	In_Frame_Del	DEL	AAG	-	7	68	c.52_54delAAG	c.(52-54)AAGdel	p.K22del
Pat_15	Post-Resistance	TXNDC6	347736	37	3	138023752	138023752	Frame_Shift_Del	DEL	G	-	8	1042	c.754delC	c.(754-756)CGTfs	p.R252fs
Pat_15	Post-Resistance	GOLIM4	27333	37	3	167747642	167747644	In_Frame_Del	DEL	CTG	-	8	249	.1357_1359delCA	c.(1357-1359)CAGdel	p.Q453del
Pat_15	Post-Resistance	ATP13A3	79572	37	3	194147849	194147850	Frame_Shift_Ins	INS	-	A	7	337	c.3079_3080insT	c.(3079-3081)TGGfs	p.W1027fs
Pat_15	Post-Resistance	PDE6B	5158	37	4	661763	661765	In_Frame_Del	DEL	AGG	-	9	544	.2471_2473delAG	(2470-2475)AAGGAG>AA	p.E828del
Pat_15	Post-Resistance	UGDH	7358	37	4	39515752	39515753	Frame_Shift_Ins	INS	-	A	7	357	c.214_215insT	c.(214-216)TCTfs	p.S72fs

Pat_15	Post-Resistance	OCIAD2	132299	37	4	48894833	48894833	Frame_Shift_Del	DEL	A	-	14	1544	c.339delT	c.(337-339)TTTfs	p.F113fs
Pat_15	Post-Resistance	NUP54	53371	37	4	77065307	77065309	In_Frame_Del	DEL	TGC	-	7	990	c.288_290delGCA	c.(286-291)CAGCAA>CAA	p.96_97QQ>Q
Pat_15	Post-Resistance	PCDH10	57575	37	4	134073569	134073571	In_Frame_Del	DEL	CTG	-	10	227	.2274_2276delCT	.(2272-2277)CTCTGC>CT	p.C763del
Pat_15	Post-Resistance	ZNF827	152485	37	4	146823381	146823383	In_Frame_Del	DEL	GTG	-	7	168	.1028_1030delCA	.(1027-1032)CCACAA>CA	p.P343del
Pat_15	Post-Resistance	FAT1	2195	37	4	187540708	187540708	Frame_Shift_Del	DEL	T	-	7	1432	c.7032delA	c.(7030-7032)CTAfs	p.L2344fs
Pat_15	Post-Resistance	DNAH5	1767	37	5	13919383	13919383	Frame_Shift_Del	DEL	T	-	8	1229	c.877delA	c.(877-879)AGAfs	p.R293fs
Pat_15	Post-Resistance	ZFR	51663	37	5	32419951	32419953	In_Frame_Del	DEL	GGT	-	13	1307	c.393_395delACC	.(391-396)CCACCC>CCC	.131_132PP>
Pat_15	Post-Resistance	MCC	4163	37	5	112824048	112824049	In_Frame_Ins	INS	-	GCC	12	50	c.63_64insGGC	c.(61-66)insGGC	p.21_22insG
Pat_15	Post-Resistance	ZNF608	57507	37	5	124079813	124079815	In_Frame_Del	DEL	CTC	-	11	829	c.868_870delGAG	c.(868-870)GAGdel	p.E290del
Pat_15	Post-Resistance	KDM3B	51780	37	5	137713477	137713477	Frame_Shift_Del	DEL	G	-	8	642	c.543delG	c.(541-543)TTGfs	p.L181fs
Pat_15	Post-Resistance	TIMD4	91937	37	5	156378745	156378747	In_Frame_Del	DEL	TTG	-	16	2239	c.455_457delCAA	.(454-459)ACAAGC>AGC	p.T152del
Pat_15	Post-Resistance	C5orf40	408263	37	5	156769910	156769910	Frame_Shift_Del	DEL	C	-	8	435	c.635delG	c.(634-636)GGTfs	p.G212fs
Pat_15	Post-Resistance	GABBR1	2550	37	6	29577144	29577144	Frame_Shift_Del	DEL	G	-	8	335	c.1721delC	c.(1720-1722)CCAfs	p.P574fs
Pat_15	Post-Resistance	FUCA2	2519	37	6	143832707	143832708	In_Frame_Ins	INS	-	GCAGCA	7	11	.64_65insTGCTG	(64-66)CCG>CTGCTGCC	p.21_22insLL
Pat_15	Post-Resistance	GRM1	2911	37	6	146755630	146755632	In_Frame_Del	DEL	GAC	-	10	830	.3283_3285delGA	c.(3283-3285)GACdel	p.D1099del
Pat_15	Post-Resistance	GRM1	2911	37	6	146755723	146755725	In_Frame_Del	DEL	GAG	-	8	465	.3376_3378delGA	c.(3376-3378)GAGdel	p.E1129del
Pat_15	Post-Resistance	EIF3B	8662	37	7	2404086	2404086	Frame_Shift_Del	DEL	G	-	8	571	c.1079delG	c.(1078-1080)TGGfs	p.W360fs
Pat_15	Post-Resistance	TRIL	9865	37	7	28996482	28996482	Frame_Shift_Del	DEL	G	-	7	624	c.1181delC	c.(1180-1182)CCGfs	p.P394fs
Pat_15	Post-Resistance	GARS	2617	37	7	30634583	30634585	In_Frame_Del	DEL	CTG	-	9	203	c.46_48delCTG	c.(46-48)CTGdel	p.L20del
Pat_15	Post-Resistance	HECW1	23072	37	7	43601485	43601486	Frame_Shift_Del	DEL	TA	-	7	358	c.4781_4782delTA	c.(4780-4782)TTAfs	p.L1594fs
Pat_15	Post-Resistance	C7orf57	136288	37	7	48092369	48092371	In_Frame_Del	DEL	GCA	-	7	488	c.678_680delGCA	c.(676-681)TTGCAG>TTG	p.Q230del
Pat_15	Post-Resistance	STYXL1	51657	37	7	75651194	75651196	In_Frame_Del	DEL	ATC	-	9	1717	c.280_282delGAT	c.(280-282)GATdel	p.D94del
Pat_15	Post-Resistance	ABCB4	5244	37	7	87074281	87074282	Frame_Shift_Ins	INS	-	A	9	152	c.1015_1016insT	c.(1015-1017)TCAfs	p.S339fs
Pat_15	Post-Resistance	CYP51A1	1595	37	7	91752494	91752494	Frame_Shift_Del	DEL	T	-	7	629	c.1026delA	c.(1024-1026)AAAfs	p.K342fs
Pat_15	Post-Resistance	ERI1	90459	37	8	8875845	8875845	Frame_Shift_Del	DEL	A	-	8	283	c.621delA	c.(619-621)CTAfs	p.L207fs
Pat_15	Post-Resistance	CHD7	55636	37	8	61735158	61735158	Frame_Shift_Del	DEL	T	-	7	975	c.3054delT	c.(3052-3054)CCTfs	p.P1018fs
Pat_15	Post-Resistance	SLC26A7	115111	37	8	92261932	92261932	Frame_Shift_Del	DEL	C	-	8	407	c.53delC	c.(52-54)ACCfs	p.T18fs
Pat_15	Post-Resistance	RGS22	26166	37	8	100990177	100990178	Frame_Shift_Ins	INS	-	T	10	194	c.3486_3487insA	c.(3484-3489)AAATTGfs	p.K1162fs
Pat_15	Post-Resistance	UBR5	51366	37	8	103289348	103289349	Frame_Shift_Ins	INS	-	T	10	492	c.6360_6361insA	c.(6358-6363)AAAGAAfs	p.K2120fs
Pat_15	Post-Resistance	ZC3H3	23144	37	8	144522387	144522389	In_Frame_Del	DEL	GAG	-	8	50	.2637_2639delCT	.(2635-2640)TCCTCA>TC	.879_880SS>
Pat_15	Post-Resistance	ZC3H3	23144	37	8	144621235	144621235	Frame_Shift_Del	DEL	C	-	7	391	c.302delG	c.(301-303)GGCfs	p.G101fs
Pat_15	Post-Resistance	ARHGAP39	80728	37	8	145773342	145773344	In_Frame_Del	DEL	CTG	-	22	33	.1126_1128delCA	c.(1126-1128)CAGdel	p.Q376del
Pat_15	Post-Resistance	PIGO	84720	37	9	35091693	35091693	Frame_Shift_Del	DEL	G	-	7	285	c.2191delC	c.(2191-2193)CGTfs	p.R731fs
Pat_15	Post-Resistance	NR4A3	8013	37	9	102590616	102590618	In_Frame_Del	DEL	CAC	-	13	160	c.292_294delCAC	c.(292-294)CACdel	p.H108del
Pat_15	Post-Resistance	C9orf43	257169	37	9	116187646	116187648	In_Frame_Del	DEL	GCA	-	10	245	c.888_890delGCA	.(886-891)CGGCAG>CG	p.Q304del
Pat_15	Post-Resistance	TNC	3371	37	9	117797539	117797539	Frame_Shift_Del	DEL	G	-	7	1035	c.5731delC	c.(5731-5733)CGGfs	p.R1911fs
Pat_15	Post-Resistance	C9orf114	51490	37	9	131591119	131591120	Frame_Shift_Ins	INS	-	T	12	357	c.102_103insA	c.(100-105)AAATGGfs	p.K34fs
Pat_15	Post-Resistance	NUP188	23511	37	9	131768602	131768602	Frame_Shift_Del	DEL	C	-	7	1361	c.5028delC	c.(5026-5028)CACfs	p.H1676fs
Pat_15	Post-Resistance	C9orf86	55684	37	9	139734633	139734635	In_Frame_Del	DEL	AGA	-	8	323	.1958_1960delAG	(1957-1962)GAGAAG>GA	p.K660del
Pat_15	Post-Resistance	GRIN1	2902	37	9	140056884	140056886	In_Frame_Del	DEL	GAG	-	10	196	.1780_1782delGA	c.(1780-1782)GAGdel	p.E598del
Pat_15	Post-Resistance	SSX1	6756	37	X	48125727	48125727	Frame_Shift_Del	DEL	A	-	7	1659	c.472delA	c.(472-474)AAAfs	p.K158fs
Pat_15	Post-Resistance	NAP1L3	4675	37	X	92928153	92928155	In_Frame_Del	DEL	TGC	-	8	99	c.149_151delGCA	c.(148-153)AGCACT>ACT	p.S50del
Pat_15	Post-Resistance	ARHGAP36	158763	37	X	130215725	130215725	Frame_Shift_Del	DEL	T	-	7	1051	c.86delT	c.(85-87)ATTfs	p.I29fs
Pat_15	Post-Resistance	IGSF1	3547	37	X	130411036	130411036	Frame_Shift_Del	DEL	C	-	11	2828	c.2485delG	c.(2485-2487)GCCfs	p.A829fs
Pat_15	Post-Resistance	AFF2	2334	37	X	147733548	147733548	Frame_Shift_Del	DEL	A	-	11	1185	c.76delA	c.(76-78)AAAfs	p.K26fs
Pat_15	Post-Resistance	PNMA3	29944	37	X	152225444	152225444	Frame_Shift_Del	DEL	G	-	9	881	c.32delG	c.(31-33)CGGfs	p.R11fs
Pat_26	Pre-Treatment	DFFA	1676	37	1	10532411	10532411	Frame_Shift_Del	DEL	G	-	178	360	c.105delC	c.(103-105)GCCfs	p.A35fs

Pat_26	Pre-Treatment	VPS13D	55187	37	1	12520281	12520282	Frame_Shift_Del	DEL	TA	-	8	512	.12492_12493delT	c.(12490-12495)GTTATAfs	p.V4164fs
Pat_26	Pre-Treatment	NBPF1	55672	37	1	16895577	16895577	Frame_Shift_Del	DEL	C	-	12	5547	c.2605delG	c.(2605-2607)GACfs	p.D869fs
Pat_26	Pre-Treatment	ZBTB40	9923	37	1	22838561	22838563	In_Frame_Del	DEL	AAG	-	13	184	.2395_2397delAA	c.(2395-2397)AAGdel	p.K803del
Pat_26	Pre-Treatment	EXTL1	2134	37	1	26349533	26349535	In_Frame_Del	DEL	CCT	-	8	277	c.396_398delCCT	c.(394-399)TGCCTC>TGC	p.L137del
Pat_26	Pre-Treatment	KIAA0467	23334	37	1	43890849	43890849	Frame_Shift_Del	DEL	C	-	8	634	c.90delC	c.(88-90)TTCfs	p.F30fs
Pat_26	Pre-Treatment	ZCCHC11	23318	37	1	52991351	52991351	Frame_Shift_Del	DEL	C	-	7	813	c.602delG	c.(601-603)GGAfs	p.G201fs
Pat_26	Pre-Treatment	C1orf173	127254	37	1	75102057	75102057	Frame_Shift_Del	DEL	G	-	10	1087	c.510delC	c.(508-510)CCCfs	p.P170fs
Pat_26	Pre-Treatment	C1orf183	55924	37	1	112270274	112270274	Frame_Shift_Del	DEL	G	-	7	497	c.210delC	c.(208-210)CCCfs	p.P70fs
Pat_26	Pre-Treatment	OTUD7B	56957	37	1	149916736	149916737	Frame_Shift_Del	DEL	TG	-	7	995	c.1551_1552delC	c.(1549-1554)CTCAAGfs	p.L517fs
Pat_26	Pre-Treatment	TCHH	7062	37	1	152082254	152082254	Frame_Shift_Del	DEL	G	-	7	432	c.3439delC	c.(3439-3441)CAGfs	p.Q1147fs
Pat_26	Pre-Treatment	PVRL4	81607	37	1	161044057	161044059	In_Frame_Del	DEL	CAC	-	9	587	.1105_1107delGT	c.(1105-1107)GTGdel	p.V369del
Pat_26	Pre-Treatment	RC3H1	149041	37	1	173930212	173930213	Splice_Site	DEL	TA	-	8	288	c.2370_splice	c.e12+1	p.E790_splice
Pat_26	Pre-Treatment	PRG4	10216	37	1	186276256	186276257	In_Frame_Ins	INS	-	CCA	12	361	.1405_1406insCC	(1405-1407)CCC>CCCAC	p.471_472insT
Pat_26	Pre-Treatment	PRG4	10216	37	1	186276433	186276434	In_Frame_Ins	INS	-	AGG	8	860	.1582_1583insAG	(1582-1584)AAG>AAGGA	p.528_529insE
Pat_26	Pre-Treatment	ASPM	259266	37	1	197065191	197065192	Frame_Shift_Del	DEL	AG	-	8	421	c.8923_8924delCT	c.(8923-8925)CTAfs	p.L2975fs
Pat_26	Pre-Treatment	TMEM9	252839	37	1	201115871	201115871	Frame_Shift_Del	DEL	G	-	7	878	c.264delC	c.(262-264)ATCfs	p.I88fs
Pat_26	Pre-Treatment	PLXNA2	5362	37	1	208315787	208315787	Frame_Shift_Del	DEL	G	-	10	793	c.1393delC	c.(1393-1395)CATfs	p.H465fs
Pat_26	Pre-Treatment	FBXO28	23219	37	1	224345250	224345250	Frame_Shift_Del	DEL	G	-	8	1361	c.909delG	c.(907-909)CTGfs	p.L303fs
Pat_26	Pre-Treatment	DIP2C	22982	37	10	412274	412275	Frame_Shift_Del	DEL	CA	-	7	160	c.2208_2209delTG	c.(2206-2211)TGTGCAfs	p.C736fs
Pat_26	Pre-Treatment	LARP4B	23185	37	10	863709	863709	Frame_Shift_Del	DEL	C	-	8	960	c.1651delG	c.(1651-1653)GAAfs	p.E551fs
Pat_26	Pre-Treatment	GDI2	2665	37	10	5808206	5808206	Frame_Shift_Del	DEL	G	-	7	321	c.1189delC	c.(1189-1191)CAGfs	p.Q397fs
Pat_26	Pre-Treatment	OPTN	10133	37	10	13151192	13151192	Frame_Shift_Del	DEL	C	-	7	877	c.70delC	c.(70-72)CCCfs	p.P24fs
Pat_26	Pre-Treatment	UNC5B	219699	37	10	73046457	73046457	Frame_Shift_Del	DEL	C	-	8	990	c.564delC	c.(562-564)CTCfs	p.L188fs
Pat_26	Pre-Treatment	ARHGAP19	84986	37	10	99019160	99019160	Frame_Shift_Del	DEL	T	-	7	478	c.839delA	c.(838-840)AATfs	p.N280fs
Pat_26	Pre-Treatment	CRTAC1	55118	37	10	99771034	99771034	Frame_Shift_Del	DEL	G	-	7	1048	c.85delC	c.(85-87)CAGfs	p.Q29fs
Pat_26	Pre-Treatment	CHST15	51363	37	10	125801815	125801816	Splice_Site	DEL	AC	-	8	589	c.1033_splice	c.e3+1	p.G345_splice
Pat_26	Pre-Treatment	OR51B6	390058	37	11	5373493	5373493	Frame_Shift_Del	DEL	T	-	14	442	c.756delT	c.(754-756)ACTfs	p.T252fs
Pat_26	Pre-Treatment	DNHD1	144132	37	11	6578614	6578616	In_Frame_Del	DEL	GAG	-	8	40	.8089_8091delGA	c.(8089-8091)GAGdel	p.E2703del
Pat_26	Pre-Treatment	DCHS1	8642	37	11	6662746	6662748	In_Frame_Del	DEL	CAG	-	9	72	c.97_99delCTG	c.(97-99)CTGdel	p.L33del
Pat_26	Pre-Treatment	EIF4G2	1982	37	11	10827460	10827460	Frame_Shift_Del	DEL	A	-	7	1349	c.242delT	c.(241-243)GTAfs	p.V81fs
Pat_26	Pre-Treatment	TCP11L1	55346	37	11	33083158	33083158	Frame_Shift_Del	DEL	G	-	7	169	c.858delG	c.(856-858)GTGfs	p.V286fs
Pat_26	Pre-Treatment	DGKZ	8525	37	11	46400752	46400753	Splice_Site	INS	-	C	9	677	c.3104_splice	c.e30-1	p.A1035_splice
Pat_26	Pre-Treatment	OR8H2	390151	37	11	55873096	55873097	Frame_Shift_Del	DEL	AC	-	8	746	c.578_579delAC	c.(577-579)TACfs	p.Y193fs
Pat_26	Pre-Treatment	OSBP	5007	37	11	59345731	59345731	Frame_Shift_Del	DEL	C	-	7	596	c.1951delG	c.(1951-1953)GAAfs	p.E651fs
Pat_26	Pre-Treatment	UBXN1	51035	37	11	62445420	62445420	Frame_Shift_Del	DEL	T	-	7	320	c.461delA	c.(460-462)AAGfs	p.K154fs
Pat_26	Pre-Treatment	C11orf95	65998	37	11	63533335	63533337	In_Frame_Del	DEL	TCC	-	13	54	c.579_581delGGA	.(577-582)GAGGAA>GAA	.193_194EE>I
Pat_26	Pre-Treatment	SLC22A12	116085	37	11	64368393	64368393	Frame_Shift_Del	DEL	C	-	8	777	c.1581delC	c.(1579-1581)ATCfs	p.I527fs
Pat_26	Pre-Treatment	DRAP1	10589	37	11	65688844	65688844	Frame_Shift_Del	DEL	C	-	7	1049	c.556delC	c.(556-558)CCCfs	p.P186fs
Pat_26	Pre-Treatment	CTTN	2017	37	11	70279751	70279752	Splice_Site	DEL	AG	-	7	493	c.1445_splice	c.e17-1	p.E482_splice
Pat_26	Pre-Treatment	ARAP1	116985	37	11	72412796	72412796	Frame_Shift_Del	DEL	C	-	8	1547	c.2200delG	c.(2200-2202)GAAfs	p.E734fs
Pat_26	Pre-Treatment	MOGAT2	80168	37	11	75431068	75431068	Frame_Shift_Del	DEL	C	-	7	817	c.123delC	c.(121-123)CTCfs	p.L41fs
Pat_26	Pre-Treatment	GAB2	9846	37	11	77991651	77991651	Frame_Shift_Del	DEL	G	-	7	858	c.372delC	c.(370-372)AGCfs	p.S124fs
Pat_26	Pre-Treatment	ODZ4	26011	37	11	78399200	78399200	Frame_Shift_Del	DEL	G	-	7	889	c.5159delC	c.(5158-5160)ACAfs	p.T1720fs
Pat_26	Pre-Treatment	ATM	472	37	11	108173585	108173586	Frame_Shift_Del	DEL	AG	-	7	172	c.5325_5326delA	c.(5323-5328)TTAGAAfs	p.L1775fs
Pat_26	Pre-Treatment	MLL	4297	37	11	118344186	118344186	Frame_Shift_Del	DEL	C	-	7	845	c.2312delC	c.(2311-2313)ACCfs	p.T771fs
Pat_26	Pre-Treatment	ARCN1	372	37	11	118463514	118463515	Frame_Shift_Del	DEL	GT	-	8	1429	c.1075_1076delGT	c.(1075-1077)GTAfs	p.V359fs
Pat_26	Pre-Treatment	PVRL1	5818	37	11	119535678	119535680	In_Frame_Del	DEL	CCT	-	7	92	.1331_1333delAG	(1330-1335)GAGGGC>GG	p.E444del

Pat_26	Pre-Treatment	SRPR	6734	37	11	126136150	126136150	Frame_Shift_Del	DEL	C	-	9	648	c.864delG	c.(862-864)GGGfs	p.G288fs
Pat_26	Pre-Treatment	KDM5A	5927	37	12	465621	465639	Frame_Shift_Del	DEL	GCCCACAA	-	11	92	lCCAAGGTTGTG	)CCCAAGGTTGTGGGCT	p.P246fs
Pat_26	Pre-Treatment	IFFO1	25900	37	12	6649704	6649706	In_Frame_Del	DEL	GGC	-	10	465	.1623_1625delGC	(1621-1626)CCGCCA>CC	.541_542PP>
Pat_26	Pre-Treatment	PRB1	5542	37	12	11506327	11506329	In_Frame_Del	DEL	GGA	-	12	180	c.708_710delTCC	c.(706-711)CCTCCA>CCA	.236_237PP>
Pat_26	Pre-Treatment	LRP6	4040	37	12	12339897	12339897	Frame_Shift_Del	DEL	G	-	9	1035	c.804delC	c.(802-804)CCCfs	p.P268fs
Pat_26	Pre-Treatment	TMTC1	83857	37	12	29671459	29671460	Frame_Shift_Del	DEL	CC	-	7	1113	c.1645_1646delG	c.(1645-1647)GGAfs	p.G549fs
Pat_26	Pre-Treatment	MLL2	8085	37	12	49445526	49445526	Frame_Shift_Del	DEL	G	-	7	301	c.1940delC	c.(1939-1941)CCAfs	p.P647fs
Pat_26	Pre-Treatment	SMARCC2	6601	37	12	56558379	56558381	In_Frame_Del	DEL	AGG	-	7	184	.3274_3276delCC	c.(3274-3276)CCTdel	p.P1092del
Pat_26	Pre-Treatment	MDM2	4193	37	12	69233316	69233317	Frame_Shift_Del	DEL	CA	-	8	219	c.1181_1182delCA	c.(1180-1182)TCAfs	p.S394fs
Pat_26	Pre-Treatment	CPSF6	11052	37	12	69652761	69652763	In_Frame_Del	DEL	TCC	-	8	850	.1086_1088delTC	.(1084-1089)TTTCCT>TT	p.P365del
Pat_26	Pre-Treatment	NAP1L1	4673	37	12	76444310	76444312	Splice_Site	DEL	CAT	-	7	364	c.1059_splice	c.e12+1	p.D353_splice
Pat_26	Pre-Treatment	E2F7	144455	37	12	77458337	77458337	Frame_Shift_Del	DEL	C	-	7	606	c.79delG	c.(79-81)GAAfs	p.E27fs
Pat_26	Pre-Treatment	MYO1H	283446	37	12	109826602	109826602	Frame_Shift_Del	DEL	G	-	7	1356	c.79delG	c.(79-81)GCCfs	p.A27fs
Pat_26	Pre-Treatment	MVK	4598	37	12	110034312	110034312	Frame_Shift_Del	DEL	C	-	8	677	c.1121delC	c.(1120-1122)GCCfs	p.A374fs
Pat_26	Pre-Treatment	TCTN1	79600	37	12	111078894	111078894	Frame_Shift_Del	DEL	G	-	8	588	c.1044delG	c.(1042-1044)CTGfs	p.L348fs
Pat_26	Pre-Treatment	TBX5	6910	37	12	114832616	114832616	Frame_Shift_Del	DEL	T	-	8	1003	c.593delA	c.(592-594)AATfs	p.N198fs
Pat_26	Pre-Treatment	CIT	11113	37	12	120260622	120260622	Splice_Site	DEL	A	-	7	410	c.1111_splice	c.e9+1	p.S371_splice
Pat_26	Pre-Treatment	CCDC92	80212	37	12	124421800	124421800	Frame_Shift_Del	DEL	G	-	7	190	c.801delC	c.(799-801)CCCfs	p.P267fs
Pat_26	Pre-Treatment	ZNF664	144348	37	12	124497356	124497357	Frame_Shift_Ins	INS	-	AA	8	722	c.665_666insAA	c.(664-666)ACAfs	p.T222fs
Pat_26	Pre-Treatment	SALL2	6297	37	14	21993077	21993079	In_Frame_Del	DEL	GAG	-	12	194	c.783_785delCTC	c.(781-786)TCCTCT>TCT	.261_262SS>
Pat_26	Pre-Treatment	CDH24	64403	37	14	23522825	23522825	Frame_Shift_Del	DEL	G	-	7	450	c.1106delC	c.(1105-1107)CCAfs	p.P369fs
Pat_26	Pre-Treatment	ACIN1	22985	37	14	23528677	23528678	Frame_Shift_Del	DEL	GA	-	7	575	c.3705_3706delTC	c.(3703-3708)GTTCAGfs	p.V1235fs
Pat_26	Pre-Treatment	EIF2S1	1965	37	14	67831574	67831574	Frame_Shift_Del	DEL	G	-	7	845	c.90delG	c.(88-90)ATGfs	p.M30fs
Pat_26	Pre-Treatment	YY1	7528	37	14	100705708	100705710	In_Frame_Del	DEL	GAG	-	10	120	c.127_129delGAG	c.(127-129)GAGdel	p.E47del
Pat_26	Pre-Treatment	TTBK2	146057	37	15	43075682	43075683	Frame_Shift_Del	DEL	GG	-	10	1523	c.1131_1132delCC	c.(1129-1134)CCCCAGfs	p.P377fs
Pat_26	Pre-Treatment	MYO5C	55930	37	15	52537588	52537588	Frame_Shift_Del	DEL	T	-	8	790	c.2141delA	c.(2140-2142)AAGfs	p.K714fs
Pat_26	Pre-Treatment	CLN6	54982	37	15	68504027	68504028	Frame_Shift_Del	DEL	TG	-	8	926	c.471_472delCA	c.(469-474)CTCAAGfs	p.L157fs
Pat_26	Pre-Treatment	FANCI	55215	37	15	89804908	89804908	Frame_Shift_Del	DEL	G	-	8	545	c.381delG	c.(379-381)TTGfs	p.L127fs
Pat_26	Pre-Treatment	UNC45A	55898	37	15	91485796	91485796	Frame_Shift_Del	DEL	A	-	7	222	c.817delA	c.(817-819)AAAfs	p.K273fs
Pat_26	Pre-Treatment	ALDH1A3	220	37	15	101438350	101438350	Frame_Shift_Del	DEL	G	-	9	292	c.843delG	c.(841-843)CTGfs	p.L281fs
Pat_26	Pre-Treatment	TMC5	79838	37	16	19451676	19451676	Frame_Shift_Del	DEL	C	-	8	806	c.316delC	c.(316-318)CCAfs	p.P106fs
Pat_26	Pre-Treatment	SLC5A11	115584	37	16	24921737	24921739	In_Frame_Del	DEL	CAG	-	7	330	.1761_1763delCA	(1759-1764)GCCAGC>GC	p.S592del
Pat_26	Pre-Treatment	SRCAP	10847	37	16	30736314	30736314	Frame_Shift_Del	DEL	C	-	8	1617	c.5569delC	c.(5569-5571)CCCfs	p.P1857fs
Pat_26	Pre-Treatment	ZNF423	23090	37	16	49660108	49660108	Frame_Shift_Del	DEL	G	-	7	959	c.3550delC	c.(3550-3552)CAAfs	p.Q1184fs
Pat_26	Pre-Treatment	SALL1	6299	37	16	51175656	51175658	In_Frame_Del	DEL	GCT	-	7	81	c.475_477delAGC	c.(475-477)AGCdel	p.S159del
Pat_26	Pre-Treatment	IRX6	79190	37	16	55362674	55362676	In_Frame_Del	DEL	GAG	-	16	248	c.784_786delGAG	c.(784-786)GAGdel	p.E268del
Pat_26	Pre-Treatment	CNGB1	1258	37	16	57983275	57983277	In_Frame_Del	DEL	TCC	-	9	135	.1101_1103delGG	(1099-1104)GAGGAA>GA	.367_368EE>
Pat_26	Pre-Treatment	EDC4	23644	37	16	67913767	67913769	In_Frame_Del	DEL	CAG	-	10	240	.1836_1838delCA	(1834-1839)CCCAGC>CC	p.S617del
Pat_26	Pre-Treatment	MLKL	197259	37	16	74709645	74709645	Frame_Shift_Del	DEL	C	-	8	443	c.1056delG	c.(1054-1056)TTGfs	p.L352fs
Pat_26	Pre-Treatment	CHD3	1107	37	17	7788212	7788214	In_Frame_Del	DEL	GAG	-	12	124	c.88_90delGAG	c.(88-90)GAGdel	p.E35del
Pat_26	Pre-Treatment	CHD3	1107	37	17	7801857	7801859	In_Frame_Del	DEL	AAG	-	7	192	.2095_2097delAA	c.(2095-2097)AAGdel	p.K703del
Pat_26	Pre-Treatment	RANGRF	29098	37	17	8192137	8192137	Frame_Shift_Del	DEL	G	-	7	683	c.31delG	c.(31-33)GGGfs	p.G11fs
Pat_26	Pre-Treatment	MYH10	4628	37	17	8397095	8397097	In_Frame_Del	DEL	CCT	-	11	153	.4070_4072delAG	(4069-4074)GAGGCC>GC	p.E1357del
Pat_26	Pre-Treatment	SMCR7	125170	37	17	18167778	18167780	In_Frame_Del	DEL	GCT	-	8	236	.1065_1067delGC	(1063-1068)CGGCTG>CG	p.L360del
Pat_26	Pre-Treatment	MAP2K3	5606	37	17	21208366	21208367	Frame_Shift_Del	DEL	GA	-	8	1244	c.700_701delGA	c.(700-702)GAGfs	p.E234fs
Pat_26	Pre-Treatment	CCT6B	10693	37	17	33255998	33255998	Frame_Shift_Del	DEL	T	-	7	216	c.1506delA	c.(1504-1506)AAAfs	p.K502fs
Pat_26	Pre-Treatment	RARA	5914	37	17	38508619	38508619	Frame_Shift_Del	DEL	G	-	8	897	c.667delG	c.(667-669)GACfs	p.D223fs

Pat_26	Pre-Treatment	STAT5B	6777	37	17	40370236	40370236	Frame_Shift_Del	DEL	G	-	8	272	c.1102delC	c.(1102-1104)CAGfs	p.Q368fs
Pat_26	Pre-Treatment	MAP3K14	9020	37	17	43348580	43348581	Frame_Shift_Del	DEL	TG	-	8	407	c.1665_1666delCA	c.(1663-1668)TACATCfs	p.Y555fs
Pat_26	Pre-Treatment	HOXB6	3216	37	17	46673842	46673842	Frame_Shift_Del	DEL	T	-	10	1019	c.608delA	c.(607-609)AAGfs	p.K203fs
Pat_26	Pre-Treatment	KIAA0195	9772	37	17	73491063	73491063	Frame_Shift_Del	DEL	C	-	7	747	c.2676delC	c.(2674-2676)ATCfs	p.I892fs
Pat_26	Pre-Treatment	ACOX1	51	37	17	73944473	73944473	Frame_Shift_Del	DEL	C	-	7	814	c.1794delG	c.(1792-1794)CTGfs	p.L598fs
Pat_26	Pre-Treatment	PTPRM	5797	37	18	8379261	8379261	Frame_Shift_Del	DEL	C	-	7	751	c.3670delC	c.(3670-3672)CCCfs	p.P1224fs
Pat_26	Pre-Treatment	LMAN1	3998	37	18	57013285	57013285	Splice_Site	DEL	T	-	7	194	c.823_splice	c.e8-1	p.P275_splice
Pat_26	Pre-Treatment	ADNP2	22850	37	18	77894260	77894261	Frame_Shift_Ins	INS	-	C	11	411	c.964_965insC	c.(964-966)TCCfs	p.S322fs
Pat_26	Pre-Treatment	HMHA1	23526	37	19	1080256	1080256	Frame_Shift_Del	DEL	C	-	7	1769	c.1706delC	c.(1705-1707)TCCfs	p.S569fs
Pat_26	Pre-Treatment	SMARCA4	6597	37	19	11101874	11101875	Frame_Shift_Ins	INS	-	CAGC	35	159	1294_1295insCAG	c.(1294-1296)ACAfs	p.T432fs
Pat_26	Pre-Treatment	CACNA1A	773	37	19	13445279	13445280	Frame_Shift_Del	DEL	CC	-	8	366	c.1110_1111delGG	c.(1108-1113)GTGGAGfs	p.V370fs
Pat_26	Pre-Treatment	KIAA0892	23383	37	19	19454650	19454651	Frame_Shift_Del	DEL	GG	-	9	1366	c.978_979delGG	c.(976-981)CTGGACfs	p.L326fs
Pat_26	Pre-Treatment	GATAD2A	54815	37	19	19613207	19613208	Frame_Shift_Del	DEL	CA	-	8	962	c.1643_1644delCA	c.(1642-1644)TCAfs	p.S548fs
Pat_26	Pre-Treatment	ATP4A	495	37	19	36054349	36054351	In_Frame_Del	DEL	CTT	-	9	1659	c.91_93delAAG	c.(91-93)AAGdel	p.K31del
Pat_26	Pre-Treatment	CEACAM5	1048	37	19	42224866	42224866	Frame_Shift_Del	DEL	C	-	13	1034	c.1796delC	c.(1795-1797)TCCfs	p.S599fs
Pat_26	Pre-Treatment	DMWD	1762	37	19	46289148	46289148	Frame_Shift_Del	DEL	C	-	7	1070	c.1606delG	c.(1606-1608)GCAfs	p.A536fs
Pat_26	Pre-Treatment	PPP1R15A	23645	37	19	49376824	49376826	In_Frame_Del	DEL	GAT	-	8	767	c.334_336delGAT	c.(334-336)GATdel	p.D115del
Pat_26	Pre-Treatment	PTH2	113091	37	19	49926531	49926533	In_Frame_Del	DEL	CAG	-	9	190	c.64_66delCTG	c.(64-66)CTGdel	p.L22del
Pat_26	Pre-Treatment	SLC27A5	10998	37	19	59009902	59009903	Frame_Shift_Del	DEL	CA	-	7	196	c.2052_2053delTG	c.(2050-2055)TGTGAGfs	p.C684fs
Pat_26	Pre-Treatment	LPIN1	23175	37	2	11919735	11919736	Frame_Shift_Ins	INS	-	CT	10	263	c.813_814insCT	c.(811-816)ATGCTTfs	p.M271fs
Pat_26	Pre-Treatment	AGBL5	60509	37	2	27278901	27278901	Frame_Shift_Del	DEL	C	-	12	1512	c.1260delC	c.(1258-1260)ATCfs	p.I420fs
Pat_26	Pre-Treatment	LTBP1	4052	37	2	33413655	33413655	Frame_Shift_Del	DEL	C	-	7	415	c.1438delC	c.(1438-1440)CCTfs	p.P480fs
Pat_26	Pre-Treatment	VRK2	7444	37	2	58313511	58313511	Frame_Shift_Del	DEL	A	-	7	573	c.294delA	c.(292-294)TTAfs	p.L98fs
Pat_26	Pre-Treatment	TIA1	7072	37	2	70451722	70451723	Frame_Shift_Del	DEL	AG	-	8	404	c.437_438delCT	c.(436-438)TCTfs	p.S146fs
Pat_26	Pre-Treatment	DYSF	8291	37	2	71909688	71909688	Frame_Shift_Del	DEL	A	-	7	637	c.6085delA	c.(6085-6087)ACCfs	p.T2029fs
Pat_26	Pre-Treatment	ALMS1	7840	37	2	73613032	73613037	In_Frame_Del	DEL	GGAGGA	-	8	47	.36_41delGGAGG	(34-42)CTGGAGGAG>CT	p.EE27del
Pat_26	Pre-Treatment	SEMA4C	54910	37	2	97533514	97533514	Splice_Site	DEL	C	-	7	2093	c.109_splice	c.e2+1	p.E37_splice
Pat_26	Pre-Treatment	EIF5B	9669	37	2	100013270	100013271	Frame_Shift_Del	DEL	TT	-	7	530	c.3302_3303delTT	c.(3301-3303)ATTfs	p.I1101fs
Pat_26	Pre-Treatment	TMEM182	130827	37	2	103378742	103378742	Frame_Shift_Del	DEL	G	-	9	268	c.66delG	c.(64-66)TTGfs	p.L22fs
Pat_26	Pre-Treatment	IWS1	55677	37	2	128262634	128262634	Frame_Shift_Del	DEL	G	-	8	581	c.845delC	c.(844-846)CCAfs	p.P282fs
Pat_26	Pre-Treatment	ACVR2A	92	37	2	148683686	148683686	Frame_Shift_Del	DEL	A	-	8	230	c.1303delA	c.(1303-1305)AAAfs	p.K435fs
Pat_26	Pre-Treatment	COBLL1	22837	37	2	165552062	165552062	Frame_Shift_Del	DEL	C	-	7	860	c.2155delG	c.(2155-2157)GATfs	p.D719fs
Pat_26	Pre-Treatment	TMBIM1	64114	37	2	219144792	219144792	Frame_Shift_Del	DEL	C	-	10	929	c.260delG	c.(259-261)GGAfs	p.G87fs
Pat_26	Pre-Treatment	RQCD1	9125	37	2	219449364	219449364	Frame_Shift_Del	DEL	T	-	13	1031	c.350delT	c.(349-351)CTTfs	p.L117fs
Pat_26	Pre-Treatment	FARSB	10056	37	2	223464670	223464670	Frame_Shift_Del	DEL	C	-	7	1141	c.1595delG	c.(1594-1596)GGAfs	p.G532fs
Pat_26	Pre-Treatment	PSMD1	5707	37	2	232026183	232026183	Frame_Shift_Del	DEL	A	-	8	1308	c.2348delA	c.(2347-2349)TATfs	p.Y783fs
Pat_26	Pre-Treatment	DGKD	8527	37	2	234371306	234371306	Frame_Shift_Del	DEL	C	-	8	1277	c.3111delC	c.(3109-3111)TTCfs	p.F1037fs
Pat_26	Pre-Treatment	C20orf96	140680	37	20	257983	257984	Frame_Shift_Del	DEL	TC	-	8	1116	c.606_607delGA	c.(604-609)GAGAAGfs	p.E202fs
Pat_26	Pre-Treatment	ATRN	8455	37	20	3540068	3540068	Frame_Shift_Del	DEL	C	-	7	585	c.1141delC	c.(1141-1143)CCAfs	p.P381fs
Pat_26	Pre-Treatment	BTBD3	22903	37	20	11899028	11899030	In_Frame_Del	DEL	CAG	-	7	592	c.105_107delCAG	c.(103-108)ACCAGC>ACC	p.S40del
Pat_26	Pre-Treatment	ISM1	140862	37	20	13202444	13202446	In_Frame_Del	DEL	GCT	-	4	9	c.21_23delGCT	c.(19-24)GAGCTG>GAG	p.L12del
Pat_26	Pre-Treatment	BCL2L1	598	37	20	30309941	30309942	Frame_Shift_Del	DEL	AA	-	8	574	c.80_81delTT	c.(79-81)TTTfs	p.F27fs
Pat_26	Pre-Treatment	TM9SF4	9777	37	20	30729643	30729643	Frame_Shift_Del	DEL	A	-	8	1001	c.473delA	c.(472-474)GAAfs	p.E158fs
Pat_26	Pre-Treatment	CHMP4B	128866	37	20	32439998	32439999	Frame_Shift_Ins	INS	-	A	8	977	c.599_600insA	c.(598-600)CCAfs	p.P200fs
Pat_26	Pre-Treatment	RALGAPB	57148	37	20	37146233	37146233	Frame_Shift_Del	DEL	C	-	8	735	c.1136delC	c.(1135-1137)ACCfs	p.T379fs
Pat_26	Pre-Treatment	SYS1-DBNDD2	767557	37	20	44038638	44038640	In_Frame_Del	DEL	CCT	-	8	30	c.344_346delCCT	c.(343-348)ACCTCC>ACC	p.S121del
Pat_26	Pre-Treatment	LSM14B	149986	37	20	60706554	60706554	Frame_Shift_Del	DEL	C	-	8	260	c.978delC	c.(976-978)CTCfs	p.L326fs

Pat_26	Pre-Treatment	SH3BGR	6450	37	21	40823995	40823995	Frame_Shift_Del	DEL	G	-	7	1071	c.162delG	c.(160-162)TTGfs	p.L54fs
Pat_26	Pre-Treatment	PCNT	5116	37	21	47851962	47851963	Frame_Shift_Del	DEL	GA	-	9	288	.8584_8585delG	c.(8584-8586)GAGfs	p.E2862fs
Pat_26	Pre-Treatment	UFD1L	7353	37	22	19443251	19443253	In_Frame_Del	DEL	TTC	-	8	1148	c.717_719delGAA	c.(715-720)AAGAAA>AAA	.239_240KK>
Pat_26	Pre-Treatment	MED15	51586	37	22	20918817	20918819	In_Frame_Del	DEL	CAG	-	8	104	c.532_534delCAG	c.(532-534)CAGdel	p.Q188del
Pat_26	Pre-Treatment	C22orf45	646023	37	22	24827042	24827042	Frame_Shift_Del	DEL	C	-	5	4	c.479delG	c.(478-480)TGAfs	p.*160fs
Pat_26	Pre-Treatment	TRIOBP	11078	37	22	38121934	38121934	Frame_Shift_Del	DEL	C	-	7	846	c.3371delC	c.(3370-3372)TCCfs	p.S1124fs
Pat_26	Pre-Treatment	FAM109B	150368	37	22	42473377	42473377	Frame_Shift_Del	DEL	G	-	13	481	c.80delG	c.(79-81)TGGfs	p.W27fs
Pat_26	Pre-Treatment	C22orf32	91689	37	22	42478046	42478048	In_Frame_Del	DEL	GAT	-	9	600	c.304_306delGAT	c.(304-306)GATdel	p.D107del
Pat_26	Pre-Treatment	TCF20	6942	37	22	42605990	42605992	In_Frame_Del	DEL	CTG	-	10	311	.5320_5322delCA	c.(5320-5322)CAGdel	p.Q1774del
Pat_26	Pre-Treatment	CNTN4	152330	37	3	3078967	3078967	Frame_Shift_Del	DEL	G	-	7	1499	c.2047delG	c.(2047-2049)GGGfs	p.G683fs
Pat_26	Pre-Treatment	CIDEC	63924	37	3	9908869	9908869	Frame_Shift_Del	DEL	G	-	11	832	c.666delC	c.(664-666)CCCfs	p.P222fs
Pat_26	Pre-Treatment	FANCD2	2177	37	3	10136049	10136049	Splice_Site	DEL	T	-	7	441	c.3963_splice	c.e40+2	.R1321_splic
Pat_26	Pre-Treatment	SH3BP5	9467	37	3	15373833	15373835	In_Frame_Del	DEL	TCC	-	7	57	c.81_83delGGA	c.(79-84)GAGGAA>GAA	p.27_28EE>E
Pat_26	Pre-Treatment	NCKIPSD	51517	37	3	48717021	48717023	In_Frame_Del	DEL	CTG	-	11	897	.1474_1476delCA	c.(1474-1476)CAGdel	p.Q492del
Pat_26	Pre-Treatment	IMPDH2	3615	37	3	49062664	49062665	Frame_Shift_Del	DEL	TG	-	7	1220	.1044_1045delC	c.(1042-1047)TACAAGfs	p.Y348fs
Pat_26	Pre-Treatment	QARS	5859	37	3	49140808	49140808	Frame_Shift_Del	DEL	G	-	8	1061	c.486delC	c.(484-486)GGCfs	p.G162fs
Pat_26	Pre-Treatment	PRKCD	5580	37	3	53220653	53220653	Frame_Shift_Del	DEL	G	-	13	1972	c.1294delG	c.(1294-1296)GGGfs	p.G432fs
Pat_26	Pre-Treatment	C3orf63	23272	37	3	56667404	56667404	Frame_Shift_Del	DEL	T	-	8	477	c.3232delA	c.(3232-3234)AGTfs	p.S1078fs
Pat_26	Pre-Treatment	GPR128	84873	37	3	100362146	100362146	Frame_Shift_Del	DEL	G	-	7	1273	c.735delG	c.(733-735)TTGfs	p.L245fs
Pat_26	Pre-Treatment	STAG1	10274	37	3	136096582	136096582	Frame_Shift_Del	DEL	C	-	8	363	c.2290delG	c.(2290-2292)GTAfs	p.V764fs
Pat_26	Pre-Treatment	FAM194A	131831	37	3	150421591	150421593	In_Frame_Del	DEL	TCC	-	9	94	c.93_95delGGA	c.(91-96)GAGGAA>GAA	p.31_32EE>E
Pat_26	Pre-Treatment	MBNL1	4154	37	3	152165430	152165430	Frame_Shift_Del	DEL	C	-	7	465	c.883delC	c.(883-885)CCCfs	p.P295fs
Pat_26	Pre-Treatment	IQCJ	654502	37	3	158983047	158983048	Frame_Shift_Del	DEL	GG	-	8	488	c.335_336delGG	c.(334-336)TGGfs	p.W112fs
Pat_26	Pre-Treatment	SI	6476	37	3	164741382	164741384	In_Frame_Del	DEL	GTG	-	8	312	.3073_3075delCA	c.(3073-3075)CACdel	p.H1025del
Pat_26	Pre-Treatment	FAM157A	728262	37	3	197880131	197880133	In_Frame_Del	DEL	GCA	-	7	55	c.210_212delGCA	.(208-213)TGGCAG>TG	p.Q84del
Pat_26	Pre-Treatment	CRIPAK	285464	37	4	1389360	1389361	Frame_Shift_Ins	INS	-	CA	7	1947	.1061_1062insC	c.(1060-1062)CTCfs	p.L354fs
Pat_26	Pre-Treatment	POLN	353497	37	4	2073875	2073875	Frame_Shift_Del	DEL	G	-	8	685	c.2669delC	c.(2668-2670)CCAfs	p.P890fs
Pat_26	Pre-Treatment	ADD1	118	37	4	2909553	2909554	Frame_Shift_Del	DEL	CC	-	7	679	.1497_1498delC	c.(1495-1500)GTCCAGfs	p.V499fs
Pat_26	Pre-Treatment	WFS1	7466	37	4	6303433	6303433	Frame_Shift_Del	DEL	G	-	8	1645	c.1911delG	c.(1909-1911)CTGfs	p.L637fs
Pat_26	Pre-Treatment	SHISA3	152573	37	4	42403363	42403363	Frame_Shift_Del	DEL	G	-	7	312	c.612delG	c.(610-612)CTGfs	p.L204fs
Pat_26	Pre-Treatment	REST	5978	37	4	57797637	57797638	Frame_Shift_Del	DEL	TT	-	8	543	c.2613_2614delTT	c.(2611-2616)AATTTAfs	p.N871fs
Pat_26	Pre-Treatment	MUC7	4589	37	4	71347351	71347351	Frame_Shift_Del	DEL	C	-	7	1380	c.890delC	c.(889-891)TCCfs	p.S297fs
Pat_26	Pre-Treatment	UTP3	57050	37	4	71555274	71555274	Frame_Shift_Del	DEL	G	-	8	1051	c.880delG	c.(880-882)GGAfs	p.G294fs
Pat_26	Pre-Treatment	RAB33B	83452	37	4	140375515	140375515	Frame_Shift_Del	DEL	G	-	7	273	c.166delG	c.(166-168)GGCfs	p.G56fs
Pat_26	Pre-Treatment	POU4F2	5458	37	4	147560457	147560458	In_Frame_Ins	INS	-	GGC	10	32	c.165_166insGGC	c.(163-168)insGGC	p.68_69insG
Pat_26	Pre-Treatment	FBXW7	55294	37	4	153244156	153244156	Frame_Shift_Del	DEL	C	-	8	1107	c.2001delG	c.(1999-2001)GGGfs	p.G667fs
Pat_26	Pre-Treatment	ADAMTS12	81792	37	5	33549462	33549462	Frame_Shift_Del	DEL	G	-	8	786	c.4152delC	c.(4150-4152)TTCfs	p.F1384fs
Pat_26	Pre-Treatment	ADAMTS12	81792	37	5	33616067	33616067	Frame_Shift_Del	DEL	A	-	8	320	c.2254delT	c.(2254-2256)TACfs	p.Y752fs
Pat_26	Pre-Treatment	PPAP2A	8611	37	5	54721111	54721128	In_Frame_Del	DEL	TCTTTAAA	-	17	77	delCTTCTTTTAAA	)ACTTCTTTTAAAGAAAG	.TSFKER254d
Pat_26	Pre-Treatment	SFRS12	140890	37	5	65457960	65457960	Frame_Shift_Del	DEL	G	-	8	463	c.87delG	c.(85-87)TTGfs	p.L29fs
Pat_26	Pre-Treatment	BDP1	55814	37	5	70766233	70766233	Frame_Shift_Del	DEL	T	-	8	160	c.931delT	c.(931-933)TTTfs	p.F311fs
Pat_26	Pre-Treatment	AP3S1	1176	37	5	115202418	115202421	Frame_Shift_Del	DEL	AAGA	-	10	105	.121_124delAAG	c.(121-126)AAGAGAfs	p.K41fs
Pat_26	Pre-Treatment	PPARGC1B	133522	37	5	149216510	149216510	Frame_Shift_Del	DEL	G	-	8	379	c.2492delG	c.(2491-2493)TGCfs	p.C831fs
Pat_26	Pre-Treatment	GPX3	2878	37	5	150406548	150406549	Frame_Shift_Del	DEL	GA	-	7	541	c.329_330delGA	c.(328-330)GGAfs	p.G110fs
Pat_26	Pre-Treatment	ADRA1B	147	37	5	159344829	159344832	Frame_Shift_Del	DEL	GCTG	-	14	851	.917_920delGCT	c.(916-921)TGCTGGfs	p.C306fs
Pat_26	Pre-Treatment	SLU7	10569	37	5	159841420	159841421	Frame_Shift_Del	DEL	GA	-	8	584	c.229_230delTC	c.(229-231)TCAfs	p.S77fs
Pat_26	Pre-Treatment	NOP16	51491	37	5	175815281	175815281	Frame_Shift_Del	DEL	C	-	8	639	c.171delG	c.(169-171)GGGfs	p.G57fs

Pat_26	Pre-Treatment	UIMC1	51720	37	5	176395609	176395609	Frame_Shift_Del	DEL	T	-	108	148	c.1147delA	c.(1147-1149)AGCfs	p.S383fs
Pat_26	Pre-Treatment	NSD1	64324	37	5	176721165	176721165	Frame_Shift_Del	DEL	A	-	8	588	c.6796delA	c.(6796-6798)AAAfs	p.K2266fs
Pat_26	Pre-Treatment	FOXC1	2296	37	6	1611802	1611803	In_Frame_Ins	INS	-	GGC	7	18	.1122_1123insGG	c.(1120-1125)insGGC	p.380_381insG
Pat_26	Pre-Treatment	ZNF192	7745	37	6	28121376	28121376	Frame_Shift_Del	DEL	G	-	7	351	c.1318delG	c.(1318-1320)GGGfs	p.G440fs
Pat_26	Pre-Treatment	TRIM10	10107	37	6	30126250	30126250	Frame_Shift_Del	DEL	C	-	8	1368	c.682delG	c.(682-684)GAGfs	p.E228fs
Pat_26	Pre-Treatment	DDR1	780	37	6	30863251	30863251	Frame_Shift_Del	DEL	C	-	8	1179	c.1584delC	c.(1582-1584)GGCfs	p.G528fs
Pat_26	Pre-Treatment	EHMT2	10919	37	6	31857330	31857332	In_Frame_Del	DEL	TCC	-	7	417	c.912_914delGGA	.(910-915)GAGGAA>GAA	.304_305EE>
Pat_26	Pre-Treatment	PHF1	5252	37	6	33380050	33380050	Frame_Shift_Del	DEL	C	-	7	332	c.10delC	c.(10-12)CCCfs	p.P4fs
Pat_26	Pre-Treatment	ZBTB9	221504	37	6	33423088	33423088	Frame_Shift_Del	DEL	C	-	7	1723	c.211delC	c.(211-213)CCTfs	p.P71fs
Pat_26	Pre-Treatment	FOXP4	116113	37	6	41555186	41555186	Frame_Shift_Del	DEL	C	-	7	1022	c.808delC	c.(808-810)CCCfs	p.P270fs
Pat_26	Pre-Treatment	DST	667	37	6	56382036	56382037	Frame_Shift_Ins	INS	-	T	8	959	.11959_11960ins	c.(11959-11961)ATCfs	p.I3987fs
Pat_26	Pre-Treatment	FBXL4	26235	37	6	99322265	99322266	Frame_Shift_Del	DEL	TT	-	7	341	.1754_1755delA	c.(1753-1755)AAAfs	p.K585fs
Pat_26	Pre-Treatment	ARID1B	57492	37	6	157100024	157100026	In_Frame_Del	DEL	GGA	-	9	80	c.787_789delGGA	c.(787-789)GGAdel	p.G270del
Pat_26	Pre-Treatment	DAGLB	221955	37	7	6474591	6474591	Frame_Shift_Del	DEL	C	-	7	229	c.480delG	c.(478-480)GGGfs	p.G160fs
Pat_26	Pre-Treatment	THSD7A	221981	37	7	11468637	11468637	Frame_Shift_Del	DEL	T	-	8	1379	c.3180delA	c.(3178-3180)AAAfs	p.K1060fs
Pat_26	Pre-Treatment	MACC1	346389	37	7	20199520	20199520	Frame_Shift_Del	DEL	T	-	8	335	c.464delA	c.(463-465)CAGfs	p.Q155fs
Pat_26	Pre-Treatment	AUTS2	26053	37	7	70229781	70229782	Frame_Shift_Ins	INS	-	A	9	29	c.1258_1259insA	c.(1258-1260)CCTfs	p.P420fs
Pat_26	Pre-Treatment	DTX2	113878	37	7	76112242	76112243	Frame_Shift_Ins	INS	-	C	7	2349	c.686_687insC	c.(685-687)CACfs	p.H229fs
Pat_26	Pre-Treatment	FGL2	10875	37	7	76826170	76826170	Frame_Shift_Del	DEL	C	-	8	478	c.746delG	c.(745-747)GGAfs	p.G249fs
Pat_26	Pre-Treatment	ZNF277	11179	37	7	111980965	111980965	Frame_Shift_Del	DEL	A	-	7	663	c.1048delA	c.(1048-1050)ATTfs	p.I350fs
Pat_26	Pre-Treatment	LUC7L2	51631	37	7	139094365	139094366	Frame_Shift_Del	DEL	AG	-	8	75	c.744_745delAG	c.(742-747)GAAGAGfs	p.E248fs
Pat_26	Pre-Treatment	PSD3	23362	37	8	18490121	18490121	Splice_Site	DEL	A	-	7	240	c.2410_splice	c.e11+1	p.T804_splice
Pat_26	Pre-Treatment	HNF4G	3174	37	8	76463653	76463653	Frame_Shift_Del	DEL	C	-	8	335	c.272delC	c.(271-273)ACCfs	p.T91fs
Pat_26	Pre-Treatment	CCNE2	9134	37	8	95902737	95902737	Frame_Shift_Del	DEL	T	-	8	1066	c.359delA	c.(358-360)AAGfs	p.K120fs
Pat_26	Pre-Treatment	RNF19A	25897	37	8	101276956	101276957	Frame_Shift_Del	DEL	CT	-	23	1219	.1248_1249delA	c.(1246-1251)ATAGCAfs	p.I416fs
Pat_26	Pre-Treatment	LRP12	29967	37	8	105503672	105503672	Frame_Shift_Del	DEL	C	-	9	297	c.1809delG	c.(1807-1809)TGGfs	p.W603fs
Pat_26	Pre-Treatment	ZFPM2	23414	37	8	106813426	106813426	Frame_Shift_Del	DEL	C	-	8	794	c.1116delC	c.(1114-1116)TTCfs	p.F372fs
Pat_26	Pre-Treatment	EIF2C2	27161	37	8	141554345	141554345	Frame_Shift_Del	DEL	G	-	7	1062	c.1806delC	c.(1804-1806)CCCfs	p.P602fs
Pat_26	Pre-Treatment	FAM83H	286077	37	8	144811169	144811170	Frame_Shift_Ins	INS	-	GT	7	833	c.704_705insAC	c.(703-705)GTGfs	p.V235fs
Pat_26	Pre-Treatment	LRRC24	441381	37	8	145749495	145749496	Frame_Shift_Del	DEL	TG	-	8	1415	c.605_606delCA	c.(604-606)ACAfs	p.T202fs
Pat_26	Pre-Treatment	KCNV2	169522	37	9	2718093	2718094	Frame_Shift_Del	DEL	CC	-	4	3	c.354_355delCC	c.(352-357)TTCCCCfs	p.F118fs
Pat_26	Pre-Treatment	NPR2	4882	37	9	35805643	35805643	Frame_Shift_Del	DEL	G	-	8	639	c.2023delG	c.(2023-2025)GATfs	p.D675fs
Pat_26	Pre-Treatment	PRRG1	5638	37	X	37312611	37312611	Frame_Shift_Del	DEL	C	-	8	407	c.394delC	c.(394-396)CCCfs	p.P132fs
Pat_26	Pre-Treatment	SHROOM4	57477	37	X	50556964	50556964	Frame_Shift_Del	DEL	C	-	43	19	c.55delG	c.(55-57)GCAfs	p.A19fs
Pat_26	Pre-Treatment	TRMT2B	79979	37	X	100278466	100278467	Frame_Shift_Del	DEL	AA	-	8	356	c.748_749delTT	c.(748-750)TTAfs	p.L250fs
Pat_26	Pre-Treatment	MAMLD1	10046	37	X	149639325	149639327	In_Frame_Del	DEL	CAG	-	8	156	.1480_1482delCA	c.(1480-1482)CAGdel	p.Q502del
Pat_26	Post-Resistance	DFFA	1676	37	1	10532411	10532411	Frame_Shift_Del	DEL	G	-	9	541	c.105delC	c.(103-105)GCCfs	p.A35fs
Pat_26	Post-Resistance	ZBTB40	9923	37	1	22838561	22838563	In_Frame_Del	DEL	AAG	-	10	162	.2395_2397delAA	c.(2395-2397)AAGdel	p.K803del
Pat_26	Post-Resistance	EXTL1	2134	37	1	26349533	26349535	In_Frame_Del	DEL	CCT	-	8	187	c.396_398delCCT	c.(394-399)TGCCTC>TGC	p.L137del
Pat_26	Post-Resistance	PDE4DIP	9659	37	1	144873913	144873913	Frame_Shift_Del	DEL	G	-	11	1806	c.5044delC	c.(5044-5046)CAGfs	p.Q1682fs
Pat_26	Post-Resistance	ECM1	1893	37	1	150483467	150483467	Frame_Shift_Del	DEL	C	-	9	1129	c.501delC	c.(499-501)TTCfs	p.F167fs
Pat_26	Post-Resistance	ARNT	405	37	1	150789283	150789283	Frame_Shift_Del	DEL	G	-	7	433	c.1783delC	c.(1783-1785)CGGfs	p.R595fs
Pat_26	Post-Resistance	RFX5	5993	37	1	151315123	151315123	Frame_Shift_Del	DEL	T	-	7	2538	c.1390delA	c.(1390-1392)AGGfs	p.R464fs
Pat_26	Post-Resistance	GPATCH4	54865	37	1	156568057	156568058	Frame_Shift_Del	DEL	TG	-	8	1878	c.222_223delCA	c.(220-225)TTCAACfs	p.F74fs
Pat_26	Post-Resistance	PVRL4	81607	37	1	161044057	161044059	In_Frame_Del	DEL	CAC	-	8	628	.1105_1107delGT	c.(1105-1107)GTGdel	p.V369del
Pat_26	Post-Resistance	PAPPA2	60676	37	1	176762724	176762724	Frame_Shift_Del	DEL	C	-	12	508	c.5049delC	c.(5047-5049)ATCfs	p.I1683fs
Pat_26	Post-Resistance	MTR	4548	37	1	237024474	237024474	Frame_Shift_Del	DEL	A	-	7	83	c.2093delA	c.(2092-2094)CAAfs	p.Q698fs

Pat_26	Post-Resistance	ABI1	10006	37	10	27040624	27040626	In_Frame_Del	DEL	TGG	-	8	367	.1252_1254delCC	c.(1252-1254)CCAdel	p.P418del
Pat_26	Post-Resistance	PARD3	56288	37	10	34671501	34671501	Frame_Shift_Del	DEL	T	-	7	422	c.1366delA	c.(1366-1368)ATAfs	p.I456fs
Pat_26	Post-Resistance	PCDH15	65217	37	10	56077158	56077160	In_Frame_Del	DEL	GTG	-	7	607	c.747_749delCAC	c.(745-750)ACCACT>ACT	.249_250TT>
Pat_26	Post-Resistance	STAMBPL1	57559	37	10	90682146	90682146	Frame_Shift_Del	DEL	A	-	11	230	c.1207delA	c.(1207-1209)AAAfs	p.K403fs
Pat_26	Post-Resistance	C10orf76	79591	37	10	103769184	103769184	Frame_Shift_Del	DEL	C	-	8	1092	c.901delG	c.(901-903)GCAfs	p.A301fs
Pat_26	Post-Resistance	C10orf118	55088	37	10	115891080	115891081	Frame_Shift_Del	DEL	TC	-	8	710	c.1926_1927delG	c.(1924-1929)TTGAAAfs	p.L642fs
Pat_26	Post-Resistance	SBF2	81846	37	11	9864178	9864180	In_Frame_Del	DEL	CAT	-	17	347	.3248_3250delAT	.(3247-3252)GATGTA>GT	p.D1083del
Pat_26	Post-Resistance	AHNAK	79026	37	11	62294917	62294917	Frame_Shift_Del	DEL	G	-	7	708	c.6972delC	c.(6970-6972)CCCfs	p.P2324fs
Pat_26	Post-Resistance	KAT5	10524	37	11	65480517	65480518	Frame_Shift_Del	DEL	AG	-	8	494	c.273_274delAG	c.(271-276)CCAGAGfs	p.P91fs
Pat_26	Post-Resistance	NDUFV1	4723	37	11	67379630	67379630	Frame_Shift_Del	DEL	G	-	8	1354	c.1202delG	c.(1201-1203)AGGfs	p.R401fs
Pat_26	Post-Resistance	PVRL1	5818	37	11	119535678	119535680	In_Frame_Del	DEL	CCT	-	12	74	.1331_1333delAG	(1330-1335)GAGGGC>GG	p.E444del
Pat_26	Post-Resistance	CDON	50937	37	11	125889533	125889533	Frame_Shift_Del	DEL	T	-	8	1082	c.477delA	c.(475-477)AAAfs	p.K159fs
Pat_26	Post-Resistance	PRB2	653247	37	12	11546605	11546607	In_Frame_Del	DEL	GGA	-	7	849	c.405_407delTCC	c.(403-408)CCTCCA>CCA	.135_136PP>
Pat_26	Post-Resistance	C12orf35	55196	37	12	32134718	32134720	In_Frame_Del	DEL	CCT	-	7	554	c.829_831delCCT	c.(829-831)CCTdel	p.P281del
Pat_26	Post-Resistance	TENC1	23371	37	12	53452903	53452903	Frame_Shift_Del	DEL	C	-	8	541	c.1478delC	c.(1477-1479)ACCfs	p.T493fs
Pat_26	Post-Resistance	ESPL1	9700	37	12	53683876	53683877	Frame_Shift_Del	DEL	TG	-	7	383	c.5121_5122delT	c.(5119-5124)ACTGTGfs	p.T1707fs
Pat_26	Post-Resistance	OR6C75	390323	37	12	55759486	55759486	Frame_Shift_Del	DEL	T	-	7	174	c.592delT	c.(592-594)TTTfs	p.F198fs
Pat_26	Post-Resistance	SMARCC2	6601	37	12	56558379	56558381	In_Frame_Del	DEL	AGG	-	9	146	.3274_3276delCC	c.(3274-3276)CCTdel	p.P1092del
Pat_26	Post-Resistance	TMEM194A	23306	37	12	57456936	57456936	Frame_Shift_Del	DEL	C	-	8	2456	c.946delG	c.(946-948)GAAfs	p.E316fs
Pat_26	Post-Resistance	APEX1	328	37	14	20923820	20923820	Frame_Shift_Del	DEL	A	-	7	772	c.16delA	c.(16-18)AAAfs	p.K6fs
Pat_26	Post-Resistance	PSMA6	5687	37	14	35782216	35782216	Frame_Shift_Del	DEL	A	-	13	707	c.539delA	c.(538-540)GAAfs	p.E180fs
Pat_26	Post-Resistance	ZFP36L1	677	37	14	69256523	69256524	Frame_Shift_Ins	INS	-	T	10	1241	c.743_744insA	c.(742-744)AATfs	p.N248fs
Pat_26	Post-Resistance	CCNK	8812	37	14	99969244	99969246	In_Frame_Del	DEL	CAG	-	9	638	c.934_936delCAG	c.(934-936)CAGdel	p.Q315del
Pat_26	Post-Resistance	SPINT1	6692	37	15	41149075	41149077	In_Frame_Del	DEL	CAC	-	10	1368	.1492_1494delCA	c.(1492-1494)CACdel	p.H501del
Pat_26	Post-Resistance	C15orf58	390637	37	15	90784232	90784232	Frame_Shift_Del	DEL	A	-	9	1739	c.92delA	c.(91-93)TATfs	p.Y31fs
Pat_26	Post-Resistance	SLC5A11	115584	37	16	24921737	24921739	In_Frame_Del	DEL	CAG	-	7	244	.1761_1763delCA	(1759-1764)GCCAGC>GC	p.S592del
Pat_26	Post-Resistance	KIAA0556	23247	37	16	27692779	27692779	Frame_Shift_Del	DEL	C	-	9	843	c.868delC	c.(868-870)CCCfs	p.P290fs
Pat_26	Post-Resistance	SRCAP	10847	37	16	30736314	30736314	Frame_Shift_Del	DEL	C	-	7	1305	c.5569delC	c.(5569-5571)CCCfs	p.P1857fs
Pat_26	Post-Resistance	CHRNB1	1140	37	17	7357666	7357668	In_Frame_Del	DEL	CTG	-	10	944	c.871_873delCTG	c.(871-873)CTGdel	p.L294del
Pat_26	Post-Resistance	CHD3	1107	37	17	7788212	7788214	In_Frame_Del	DEL	GAG	-	14	117	c.88_90delGAG	c.(88-90)GAGdel	p.E35del
Pat_26	Post-Resistance	CNTROB	116840	37	17	7843518	7843519	Frame_Shift_Del	DEL	GA	-	9	472	c.1269_1270delG	c.(1267-1272)CGGAGAfs	p.R423fs
Pat_26	Post-Resistance	NEK8	284086	37	17	27068996	27068996	Frame_Shift_Del	DEL	C	-	7	1151	c.2070delC	c.(2068-2070)GTCfs	p.V690fs
Pat_26	Post-Resistance	CASC3	22794	37	17	38324506	38324506	Frame_Shift_Del	DEL	C	-	7	851	c.1801delC	c.(1801-1803)CCCfs	p.P601fs
Pat_26	Post-Resistance	STAT5B	6777	37	17	40370236	40370236	Frame_Shift_Del	DEL	G	-	8	234	c.1102delC	c.(1102-1104)CAGfs	p.Q368fs
Pat_26	Post-Resistance	UBTF	7343	37	17	42290240	42290240	Frame_Shift_Del	DEL	G	-	7	1510	c.607delC	c.(607-609)CAGfs	p.Q203fs
Pat_26	Post-Resistance	UBTF	7343	37	17	42294029	42294029	Frame_Shift_Del	DEL	C	-	7	1063	c.102delG	c.(100-102)ATGfs	p.M34fs
Pat_26	Post-Resistance	PLCD3	113026	37	17	43192760	43192762	In_Frame_Del	DEL	TCC	-	7	153	.1509_1511delGG	.(1507-1512)GAGGAT>GA	p.E503del
Pat_26	Post-Resistance	CTDP1	9150	37	18	77477959	77477959	Frame_Shift_Del	DEL	G	-	7	182	c.2360delG	c.(2359-2361)CGGfs	p.R787fs
Pat_26	Post-Resistance	ACSBG2	81616	37	19	6147614	6147614	Frame_Shift_Del	DEL	C	-	7	1117	c.225delC	c.(223-225)GGCfs	p.G75fs
Pat_26	Post-Resistance	LGI4	163175	37	19	35625552	35625554	In_Frame_Del	DEL	CAG	-	7	105	c.31_33delCTG	c.(31-33)CTGdel	p.L11del
Pat_26	Post-Resistance	RYR1	6261	37	19	38964047	38964047	Frame_Shift_Del	DEL	C	-	7	348	c.3796delC	c.(3796-3798)CCCfs	p.P1266fs
Pat_26	Post-Resistance	LENG8	114823	37	19	54963859	54963861	In_Frame_Del	DEL	GCA	-	7	772	c.243_245delGCA	c.(241-246)TTGCAG>TTG	p.Q85del
Pat_26	Post-Resistance	ZEB2	9839	37	2	145274887	145274887	Frame_Shift_Del	DEL	G	-	9	888	c.31delC	c.(31-33)CGGfs	p.R11fs
Pat_26	Post-Resistance	ANKRD44	91526	37	2	197943383	197943384	Frame_Shift_Del	DEL	TG	-	7	16	c.1693_1694delC	c.(1693-1695)CATfs	p.H565fs
Pat_26	Post-Resistance	CYP20A1	57404	37	2	204150380	204150380	Frame_Shift_Del	DEL	A	-	8	204	c.896delA	c.(895-897)CAAfs	p.Q299fs
Pat_26	Post-Resistance	CTLA4	1493	37	2	204736166	204736166	Frame_Shift_Del	DEL	T	-	7	748	c.523delT	c.(523-525)TTTfs	p.F175fs
Pat_26	Post-Resistance	TNS1	7145	37	2	218712887	218712889	In_Frame_Del	DEL	GCT	-	8	47	.1976_1978delAG	(1975-1980)CAGCCT>CC	p.Q659del

Pat_26	Post-Resistance	INPP5D	3635	37	2	234072358	234072359	Frame_Shift_Ins	INS	-	C	7	653	c.1246_1247insC	c.(1246-1248)GCCfs	p.A416fs
Pat_26	Post-Resistance	DSN1	79980	37	20	35399448	35399448	Frame_Shift_Del	DEL	T	-	9	539	c.183delA	c.(181-183)AAAfs	p.K61fs
Pat_26	Post-Resistance	PSMA7	5688	37	20	60714134	60714134	Frame_Shift_Del	DEL	C	-	7	883	c.468delG	c.(466-468)TGGfs	p.W156fs
Pat_26	Post-Resistance	TCFL5	10732	37	20	61490718	61490719	Frame_Shift_Del	DEL	CC	-	8	1696	c.991_992delGG	c.(991-993)GGAfs	p.G331fs
Pat_26	Post-Resistance	SLC5A4	6527	37	22	32614619	32614621	In_Frame_Del	DEL	TCC	-	17	285	.1860_1862delGG	(1858-1863)GAGGAA>GA	.620_621EE>
Pat_26	Post-Resistance	C22orf32	91689	37	22	42478046	42478048	In_Frame_Del	DEL	GAT	-	14	953	c.304_306delGAT	c.(304-306)GATdel	p.D107del
Pat_26	Post-Resistance	C22orf9	23313	37	22	45598978	45598978	Frame_Shift_Del	DEL	G	-	7	952	c.745delC	c.(745-747)CAGfs	p.Q249fs
Pat_26	Post-Resistance	SRGAP3	9901	37	3	9034600	9034600	Frame_Shift_Del	DEL	C	-	7	671	c.2548delG	c.(2548-2550)GTGfs	p.V850fs
Pat_26	Post-Resistance	RAD54L2	23132	37	3	51624506	51624508	In_Frame_Del	DEL	GAG	-	7	68	c.70_72delGAG	c.(70-72)GAGdel	p.E30del
Pat_26	Post-Resistance	PRKCD	5580	37	3	53220653	53220653	Frame_Shift_Del	DEL	G	-	7	2146	c.1294delG	c.(1294-1296)GGGfs	p.G432fs
Pat_26	Post-Resistance	ZNF721	170960	37	4	436417	436417	Frame_Shift_Del	DEL	G	-	8	843	c.1839delC	c.(1837-1839)TACfs	p.Y613fs
Pat_26	Post-Resistance	CRIPAK	285464	37	4	1389360	1389361	Frame_Shift_Ins	INS	-	CA	8	1627	c.1061_1062insCA	c.(1060-1062)CTCfs	p.L354fs
Pat_26	Post-Resistance	NUDT9	53343	37	4	88344097	88344098	Frame_Shift_Del	DEL	TC	-	7	241	c.40_41delTC	c.(40-42)TCTfs	p.S14fs
Pat_26	Post-Resistance	KIAA0922	23240	37	4	154523492	154523492	Splice_Site	DEL	T	-	7	1008	c.2450_splice	c.e22+2	p.V817_splice
Pat_26	Post-Resistance	SH3RF1	57630	37	4	170043324	170043326	In_Frame_Del	DEL	CAG	-	12	169	.1271_1273delCT	(1270-1275)GCTGGA>GG	p.A424del
Pat_26	Post-Resistance	PPAP2A	8611	37	5	54721111	54721128	In_Frame_Del	DEL	TCTTTAAAA	-	8	181	delCTTCTTTTAAA	)ACTTCTTTTAAAGAAAG	.TSFKER254d
Pat_26	Post-Resistance	CENPH	64946	37	5	68492902	68492902	Frame_Shift_Del	DEL	A	-	7	204	c.337delA	c.(337-339)AAAfs	p.K113fs
Pat_26	Post-Resistance	NUDT12	83594	37	5	102894977	102894978	Frame_Shift_Del	DEL	TC	-	13	216	c.398_399delGA	c.(397-399)AGAfs	p.R133fs
Pat_26	Post-Resistance	APC	324	37	5	112173349	112173350	Frame_Shift_Del	DEL	TC	-	28	211	c.2058_2059delTC	c.(2056-2061)AATCTCfs	p.N686fs
Pat_26	Post-Resistance	AP3S1	1176	37	5	115202418	115202421	Frame_Shift_Del	DEL	AAGA	-	20	328	.121_124delAAGA	c.(121-126)AAGAGAfs	p.K41fs
Pat_26	Post-Resistance	PPIC	5480	37	5	122365013	122365014	Frame_Shift_Del	DEL	AG	-	8	303	c.217_218delCT	c.(217-219)CTAfs	p.L73fs
Pat_26	Post-Resistance	TCF7	6932	37	5	133473765	133473765	Frame_Shift_Del	DEL	C	-	7	1136	c.457delC	c.(457-459)CCCfs	p.P153fs
Pat_26	Post-Resistance	FAT2	2196	37	5	150886794	150886794	Frame_Shift_Del	DEL	G	-	8	484	c.12438delC	c.(12436-12438)CCCfs	p.P4146fs
Pat_26	Post-Resistance	HAVCR2	84868	37	5	156535948	156535950	In_Frame_Del	DEL	AGC	-	14	561	c.45_47delGCT	c.(43-48)CTGCTA>CTA	p.15_16LL>L
Pat_26	Post-Resistance	UIMC1	51720	37	5	176395609	176395609	Frame_Shift_Del	DEL	T	-	29	201	c.1147delA	c.(1147-1149)AGCfs	p.S383fs
Pat_26	Post-Resistance	NOL7	51406	37	6	13615667	13615668	In_Frame_Ins	INS	-	GGA	4	7	c.77_78insGGA	c.(76-78)TCG>TCGGAG	p.30_31insE
Pat_26	Post-Resistance	SYNGAP1	8831	37	6	33411201	33411203	In_Frame_Del	DEL	CAC	-	9	270	.2872_2874delCA	c.(2872-2874)CACdel	p.H966del
Pat_26	Post-Resistance	FAM162B	221303	37	6	117073772	117073772	Frame_Shift_Del	DEL	A	-	7	669	c.477delT	c.(475-477)GCTfs	p.A159fs
Pat_26	Post-Resistance	ARID1B	57492	37	6	157100024	157100026	In_Frame_Del	DEL	GGA	-	10	56	c.787_789delGGA	c.(787-789)GGAdel	p.G270del
Pat_26	Post-Resistance	EIF3B	8662	37	7	2405996	2405997	Frame_Shift_Del	DEL	CT	-	8	289	.1202_1203delCT	c.(1201-1203)CCTfs	p.P401fs
Pat_26	Post-Resistance	TWISTNB	221830	37	7	19738111	19738113	In_Frame_Del	DEL	TTC	-	8	931	c.843_845delGAA	c.(841-846)AAGAAA>AAA	.281_282KK>
Pat_26	Post-Resistance	GARS	2617	37	7	30634583	30634585	In_Frame_Del	DEL	CTG	-	13	185	c.46_48delCTG	c.(46-48)CTGdel	p.L20del
Pat_26	Post-Resistance	INHBA	3624	37	7	41739928	41739928	Frame_Shift_Del	DEL	C	-	7	750	c.45delG	c.(43-45)TGGfs	p.W15fs
Pat_26	Post-Resistance	TRRAP	8295	37	7	98569547	98569548	Frame_Shift_Del	DEL	GG	-	7	446	.7797_7798delG	c.(7795-7800)CTGGACfs	p.L2599fs
Pat_26	Post-Resistance	C8orf44	56260	37	8	67589968	67589968	Frame_Shift_Del	DEL	A	-	8	487	c.25delA	c.(25-27)AACfs	p.N9fs
Pat_26	Post-Resistance	ATAD2	29028	37	8	124368685	124368685	Frame_Shift_Del	DEL	A	-	11	208	c.1590delT	c.(1588-1590)TTTfs	p.F530fs
Pat_26	Post-Resistance	BAG1	573	37	9	33255870	33255870	Frame_Shift_Del	DEL	T	-	8	405	c.941delA	c.(940-942)AAGfs	p.K314fs
Pat_26	Post-Resistance	CIZ1	25792	37	9	130950208	130950209	Frame_Shift_Del	DEL	CC	-	8	792	c.291_292delGG	c.(289-294)CTGGACfs	p.L97fs
Pat_26	Post-Resistance	PRRG1	5638	37	X	37312611	37312611	Frame_Shift_Del	DEL	C	-	9	431	c.394delC	c.(394-396)CCCfs	p.P132fs
Pat_26	Post-Resistance	LAS1L	81887	37	X	64732694	64732694	Frame_Shift_Del	DEL	C	-	4	2	c.2166delG	c.(2164-2166)GGGfs	p.G722fs
Pat_26	Post-Resistance	NKAP	79576	37	X	119072752	119072753	Frame_Shift_Del	DEL	TC	-	7	234	c.407_408delGA	c.(406-408)AGAfs	p.R136fs
Pat_29	Pre-Treatment	MST1P9	11223	37	1	17086085	17086086	Frame_Shift_Ins	INS	-	C	7	92	c.811_812insG	c.(811-813)GCGfs	p.A271fs
Pat_29	Pre-Treatment	RBMXL1	494115	37	1	89448604	89448605	Frame_Shift_Ins	INS	-	GG	7	425	c.905_906insCC	c.(904-906)CCAfs	p.P302fs
Pat_29	Pre-Treatment	RPTN	126638	37	1	152127881	152127884	Frame_Shift_Del	DEL	TGTC	-	10	1524	1691_1694delGA	c.(1690-1695)AGACAAfs	p.R564fs
Pat_29	Pre-Treatment	LOR	4014	37	1	153233508	153233510	In_Frame_Del	DEL	GCA	-	4	5	c.83_85delGCA	c.(82-87)GGCAGC>GGC	p.S29del
Pat_29	Pre-Treatment	ANK3	288	37	10	61828745	61828747	In_Frame_Del	DEL	GTG	-	7	110	11892_11894delCA	11890-11895)ACCACT>A	3964_3965TT
Pat_29	Pre-Treatment	CPXM2	119587	37	10	125528165	125528167	In_Frame_Del	DEL	CAG	-	7	282	.1174_1176delCT	c.(1174-1176)CTGdel	p.L392del

Pat_29	Pre-Treatment	NFRKB	4798	37	11	129752495	129752496	Frame_Shift_Ins	INS	-	T	7	95	c.932_933insA	c.(931-933)AAGfs	p.K311fs
Pat_29	Pre-Treatment	PABPC3	5042	37	13	25671273	25671273	Frame_Shift_Del	DEL	G	-	28	478	c.937delG	c.(937-939)GCGfs	p.A313fs
Pat_29	Pre-Treatment	ZNF609	23060	37	15	64972995	64972997	In_Frame_Del	DEL	CAC	-	8	290	.4096_4098delCA	c.(4096-4098)CACdel	p.H1371del
Pat_29	Pre-Treatment	KDM6B	23135	37	17	7751859	7751861	In_Frame_Del	DEL	CAC	-	7	72	.2253_2255delCA	.(2251-2256)GTCACC>GT	p.T762del
Pat_29	Pre-Treatment	HAMP	57817	37	19	35773520	35773522	In_Frame_Del	DEL	CTC	-	10	243	c.40_42delCTC	c.(40-42)CTCdel	p.L18del
Pat_29	Pre-Treatment	ATP6V1C2	245973	37	2	10917819	10917820	Frame_Shift_Del	DEL	AG	-	12	112	c.934_935delAG	c.(934-936)AGAfs	p.R312fs
Pat_29	Pre-Treatment	FRG1B	284802	37	20	29628229	29628230	Frame_Shift_Ins	INS	-	A	9	277	c.141_142insA	c.(139-144)GGGAAAfs	p.G47fs
Pat_29	Pre-Treatment	MED15	51586	37	22	20918916	20918918	In_Frame_Del	DEL	CAG	-	8	26	c.631_633delCAG	c.(631-633)CAGdel	p.Q218del
Pat_29	Pre-Treatment	TFIP11	24144	37	22	26906183	26906185	In_Frame_Del	DEL	TCA	-	7	182	c.54_56delTGA	c.(52-57)GATGAC>GAC	p.18_19DD>D
Pat_29	Pre-Treatment	EDEM1	9695	37	3	5248941	5248941	Frame_Shift_Del	DEL	T	-	8	95	c.1321delT	c.(1321-1323)TTTfs	p.F441fs
Pat_29	Pre-Treatment	FIP1L1	81608	37	4	54319248	54319249	Frame_Shift_Del	DEL	AG	-	15	90	c.1447_1448delA	c.(1447-1449)AGAfs	p.R483fs
Pat_29	Pre-Treatment	SASH1	23328	37	6	148664242	148664243	In_Frame_Ins	INS	-	GAGCCC	4	6	.39_40insGAGCC	c.(37-42)insGAGCCC	p.23_24insEP
Pat_29	Pre-Treatment	STAU2	27067	37	8	74507471	74507471	Frame_Shift_Del	DEL	T	-	8	97	c.1091delA	c.(1090-1092)AATfs	p.N364fs
Pat_29	Pre-Treatment	VCP	7415	37	9	35059647	35059647	Frame_Shift_Del	DEL	T	-	10	145	c.1847delA	c.(1846-1848)AATfs	p.N616fs
Pat_29	Pre-Treatment	PHF8	23133	37	X	54011405	54011407	In_Frame_Del	DEL	CTC	-	7	182	.2491_2493delGA	c.(2491-2493)GAGdel	p.E831del
Pat_29	Pre-Treatment	IRS4	8471	37	X	107977802	107977803	Frame_Shift_Ins	INS	-	C	13	361	c.1772_1773insG	c.(1771-1773)GGCfs	p.G591fs
Pat_29	Pre-Treatment	CD99L2	83692	37	X	149984524	149984526	In_Frame_Del	DEL	GTG	-	8	261	c.156_158delCAC	c.(154-159)ACCACA>ACA	p.52_53TT>T
Pat_29	Post-Resistance	ARID1A	8289	37	1	27100182	27100184	In_Frame_Del	DEL	GCA	-	8	110	.3978_3980delGC	.(3976-3981)CCGCAG>CC	p.Q1334del
Pat_29	Post-Resistance	CPXM2	119587	37	10	125528165	125528167	In_Frame_Del	DEL	CAG	-	12	372	.1174_1176delCT	c.(1174-1176)CTGdel	p.L392del
Pat_29	Post-Resistance	KRTAP5-8	57830	37	11	71249125	71249126	In_Frame_Ins	INS	-	GCTCCGG	12	184	GCTGTGGCTCCG	nsGGCTGTGGCTCCGGC	_23insGCGS
Pat_29	Post-Resistance	PABPC3	5042	37	13	25671273	25671273	Frame_Shift_Del	DEL	G	-	13	535	c.937delG	c.(937-939)GCGfs	p.A313fs
Pat_29	Post-Resistance	SLC24A1	9187	37	15	65918177	65918179	In_Frame_Del	DEL	CTG	-	8	114	.1759_1761delCT	c.(1759-1761)CTGdel	p.L591del
Pat_29	Post-Resistance	SRCAP	10847	37	16	30736370	30736371	Frame_Shift_Ins	INS	-	C	10	211	c.5625_5626insC	c.(5623-5628)CAGCCCfs	p.Q1875fs
Pat_29	Post-Resistance	FXR2	9513	37	17	7495872	7495874	In_Frame_Del	DEL	CGG	-	11	456	.1773_1775delCC	(1771-1776)CGCCGT>CG	.591_592RR>
Pat_29	Post-Resistance	PFAS	5198	37	17	8167575	8167576	Frame_Shift_Ins	INS	-	A	9	88	c.1837_1838insA	c.(1837-1839)CAGfs	p.Q613fs
Pat_29	Post-Resistance	HAMP	57817	37	19	35773520	35773522	In_Frame_Del	DEL	CTC	-	11	296	c.40_42delCTC	c.(40-42)CTCdel	p.L18del
Pat_29	Post-Resistance	CNOT3	4849	37	19	54649671	54649671	Frame_Shift_Del	DEL	T	-	7	189	c.729delT	c.(727-729)CCCfs	p.P243fs
Pat_29	Post-Resistance	ATP6V1C2	245973	37	2	10917819	10917820	Frame_Shift_Del	DEL	AG	-	11	124	c.934_935delAG	c.(934-936)AGAfs	p.R312fs
Pat_29	Post-Resistance	FRG1B	284802	37	20	29628226	29628226	Splice_Site	DEL	G	-	11	209	c.139_splice	c.e3-1	p.G47_splice
Pat_29	Post-Resistance	FRG1B	284802	37	20	29628229	29628230	Frame_Shift_Ins	INS	-	A	14	206	c.141_142insA	c.(139-144)GGGAAAfs	p.G47fs
Pat_29	Post-Resistance	MED12L	116931	37	3	151148114	151148116	In_Frame_Del	DEL	CAG	-	8	123	.6331_6333delCA	c.(6331-6333)CAGdel	p.Q2115del
Pat_29	Post-Resistance	CRIPAK	285464	37	4	1389462	1389463	Frame_Shift_Del	DEL	CG	-	8	557	c.1163_1164delC	c.(1162-1164)ACGfs	p.T388fs
Pat_29	Post-Resistance	FIP1L1	81608	37	4	54319248	54319249	Frame_Shift_Del	DEL	AG	-	13	86	c.1447_1448delA	c.(1447-1449)AGAfs	p.R483fs
Pat_29	Post-Resistance	THBS4	7060	37	5	79372774	79372776	In_Frame_Del	DEL	TGA	-	8	504	.1989_1991delTG	.(1987-1992)TGTGAT>TG	p.D668del
Pat_29	Post-Resistance	PCDHB3	56132	37	5	140481964	140481976	Frame_Shift_Del	DEL	GGCGGCT	-	12	77	743delCCGGGCG	-1743)CCCCGGGCGGCT	p.P577fs
Pat_29	Post-Resistance	TREML2	79865	37	6	41168714	41168716	In_Frame_Del	DEL	CAG	-	8	69	c.31_33delCTG	c.(31-33)CTGdel	p.L11del
Pat_29	Post-Resistance	PHF8	23133	37	X	54011405	54011407	In_Frame_Del	DEL	CTC	-	13	208	.2491_2493delGA	c.(2491-2493)GAGdel	p.E831del
Pat_34	Pre-Treatment	PHACTR4	65979	37	1	28785729	28785730	Frame_Shift_Ins	INS	-	A	8	104	c.150_151insA	c.(148-153)AGGAAAfs	p.R50fs
Pat_34	Pre-Treatment	LRRIQ3	127255	37	1	74575212	74575213	Frame_Shift_Ins	INS	-	T	8	164	c.732_733insA	c.(730-735)AAACAGfs	p.K244fs
Pat_34	Pre-Treatment	FNDC7	163479	37	1	109276138	109276138	Frame_Shift_Del	DEL	A	-	7	149	c.2124delA	c.(2122-2124)CCAfs	p.P708fs
Pat_34	Pre-Treatment	MCL1	4170	37	1	150551492	150551494	In_Frame_Del	DEL	TCC	-	10	308	c.513_515delGGA	.(511-516)GAGGAC>GAC	p.E171del
Pat_34	Pre-Treatment	TM9SF3	56889	37	10	98336475	98336475	Frame_Shift_Del	DEL	T	-	7	380	c.214delA	c.(214-216)AGTfs	p.S72fs
Pat_34	Pre-Treatment	FNBP4	23360	37	11	47744589	47744591	In_Frame_Del	DEL	GGA	-	4	7	.2742_2744delTC	(2740-2745)CCTCCA>CC	.914_915PP>
Pat_34	Pre-Treatment	CASP5	838	37	11	104879687	104879687	Frame_Shift_Del	DEL	T	-	15	148	c.28delA	c.(28-30)AGGfs	p.R10fs
Pat_34	Pre-Treatment	DDX6	1656	37	11	118629613	118629614	Splice_Site	INS	-	G	7	420	c.865_splice	c.e9-1	p.N289_splice
Pat_34	Pre-Treatment	PRB2	653247	37	12	11546732	11546733	In_Frame_Ins	INS	-	AGA	8	252	c.279_280insTCT	c.(277-282)insTCT	p.93_94insS
Pat_34	Pre-Treatment	HOXC13	3229	37	12	54332774	54332776	In_Frame_Del	DEL	CGG	-	3	4	c.84_86delCGG	c.(82-87)ATCGGC>ATC	p.G38del

Pat_34	Pre-Treatment	OR6C75	390323	37	12	55759486	55759486	Frame_Shift_Del	DEL	T	-	8	215	c.592delT	c.(592-594)TTTfs	p.F198fs
Pat_34	Pre-Treatment	TPCN1	53373	37	12	113704096	113704098	In_Frame_Del	DEL	CTG	-	14	720	c.349_351delCTG	c.(349-351)CTGdel	p.L122del
Pat_34	Pre-Treatment	SBNO1	55206	37	12	123794283	123794283	Frame_Shift_Del	DEL	T	-	9	224	c.3416delA	c.(3415-3417)AATfs	p.N1139fs
Pat_34	Pre-Treatment	HECTD1	25831	37	14	31597933	31597933	Frame_Shift_Del	DEL	A	-	17	49	c.4644delT	c.(4642-4644)TTTfs	p.F1548fs
Pat_34	Pre-Treatment	NIPA1	123606	37	15	23086365	23086367	In_Frame_Del	DEL	GCC	-	2	4	c.45_47delGGC	c.(43-48)GCGGCC>GCC	p.15_16AA>A
Pat_34	Pre-Treatment	SLTM	79811	37	15	59182525	59182526	Frame_Shift_Del	DEL	TC	-	12	475	c.2033_2034delGA	c.(2032-2034)AGAfs	p.R678fs
Pat_34	Pre-Treatment	EIF3CL	728689	37	16	28734579	28734581	In_Frame_Del	DEL	GAG	-	8	906	c.871_873delGAG	c.(871-873)GAGdel	p.E295del
Pat_34	Pre-Treatment	RABEP2	79874	37	16	28931200	28931202	In_Frame_Del	DEL	CTG	-	8	64	c.337_339delCAG	c.(337-339)CAGdel	p.Q113del
Pat_34	Pre-Treatment	COQ9	57017	37	16	57486732	57486734	In_Frame_Del	DEL	GAG	-	8	318	c.262_264delGAG	c.(262-264)GAGdel	p.E91del
Pat_34	Pre-Treatment	SLC9A5	6553	37	16	67300017	67300019	In_Frame_Del	DEL	GAG	-	8	134	.2107_2109delGA	c.(2107-2109)GAGdel	p.E708del
Pat_34	Pre-Treatment	NFAT5	10725	37	16	69726420	69726422	In_Frame_Del	DEL	CAG	-	7	102	.2638_2640delCA	c.(2638-2640)CAGdel	p.Q888del
Pat_34	Pre-Treatment	KIAA0182	23199	37	16	85682290	85682290	Frame_Shift_Del	DEL	C	-	7	110	c.359delC	c.(358-360)ACCfs	p.T120fs
Pat_34	Pre-Treatment	CCDC144B	284047	37	17	18498059	18498060	Splice_Site	INS	-	A	2	4	c.1867_splice	c.e9-1	p.E623_splice
Pat_34	Pre-Treatment	SLC8A2	6543	37	19	47935681	47935683	In_Frame_Del	DEL	TCC	-	14	264	.2130_2132delGG	(2128-2133)GAGGAC>GA	p.E710del
Pat_34	Pre-Treatment	LRIG1	26018	37	3	66436625	66436627	In_Frame_Del	DEL	GCT	-	7	522	.1567_1569delAG	c.(1567-1569)AGCdel	p.S524del
Pat_34	Pre-Treatment	PDZD2	23037	37	5	32090174	32090175	Frame_Shift_Ins	INS	-	GG	94	163	c.6620_6621insGG	c.(6619-6621)TCGfs	p.S2207fs
Pat_34	Pre-Treatment	OSMR	9180	37	5	38886195	38886195	Frame_Shift_Del	DEL	A	-	36	39	c.894delA	c.(892-894)ATAfs	p.I298fs
Pat_34	Pre-Treatment	APC	324	37	5	112173823	112173823	Frame_Shift_Del	DEL	T	-	10	28	c.2532delT	c.(2530-2532)TCTfs	p.S844fs
Pat_34	Pre-Treatment	TIMD4	91937	37	5	156378745	156378747	In_Frame_Del	DEL	TTG	-	7	329	c.455_457delCAA	c.(454-459)ACAAGC>AGC	p.T152del
Pat_34	Pre-Treatment	SLC17A2	10246	37	6	25921520	25921520	Frame_Shift_Del	DEL	T	-	7	258	c.361delA	c.(361-363)ATGfs	p.M121fs
Pat_34	Pre-Treatment	MAS1L	116511	37	6	29455156	29455157	Frame_Shift_Del	DEL	AC	-	7	199	c.523_524delGT	c.(523-525)GTCfs	p.V175fs
Pat_34	Pre-Treatment	HLA-F	3134	37	6	29694802	29694803	Frame_Shift_Ins	INS	-	T	10	671	c.1179_1180insT	c.(1177-1182)TTGTTTfs	p.L393fs
Pat_34	Pre-Treatment	TREML2	79865	37	6	41168714	41168716	In_Frame_Del	DEL	CAG	-	7	97	c.31_33delCTG	c.(31-33)CTGdel	p.L11del
Pat_34	Pre-Treatment	MTHFD1L	25902	37	6	151358163	151358164	Frame_Shift_Ins	INS	-	A	7	133	c.2757_2758insA	c.(2755-2760)GACAAAfs	p.D919fs
Pat_34	Pre-Treatment	PHF14	9678	37	7	11075380	11075381	Frame_Shift_Del	DEL	AG	-	7	644	c.1569_1570delAG	c.(1567-1572)CAAGAGfs	p.Q523fs
Pat_34	Pre-Treatment	OGDH	4967	37	7	44684936	44684936	Frame_Shift_Del	DEL	T	-	8	399	c.233delT	c.(232-234)ATTfs	p.I78fs
Pat_34	Pre-Treatment	PEX1	5189	37	7	92146721	92146721	Frame_Shift_Del	DEL	T	-	8	171	c.1108delA	c.(1108-1110)ATTfs	p.I370fs
Pat_34	Pre-Treatment	FOXP2	93986	37	7	114270016	114270018	In_Frame_Del	DEL	CAG	-	7	188	c.553_555delCAG	c.(553-555)CAGdel	p.Q191del
Pat_34	Pre-Treatment	ZNF395	55893	37	8	28209226	28209228	In_Frame_Del	DEL	GCA	-	8	159	.1017_1019delTG	(1015-1020)GCTGCC>GC	.339_340AA>
Pat_34	Pre-Treatment	ZFHX4	79776	37	8	77765299	77765301	In_Frame_Del	DEL	CCT	-	9	7	.6007_6009delCC	c.(6007-6009)CCTdel	p.P2016del
Pat_34	Pre-Treatment	KCNQ3	3786	37	8	133150233	133150233	Frame_Shift_Del	DEL	T	-	8	200	c.1599delA	c.(1597-1599)AAAfs	p.K533fs
Pat_34	Pre-Treatment	PRRG1	5638	37	X	37312611	37312611	Frame_Shift_Del	DEL	C	-	8	226	c.394delC	c.(394-396)CCCfs	p.P132fs
Pat_34	Pre-Treatment	MAGEC1	9947	37	X	140994844	140994846	In_Frame_Del	DEL	CCT	-	7	153	.1654_1656delCC	c.(1654-1656)CCTdel	p.P553del
Pat_46	Pre-Treatment	SPRR3	6707	37	1	152975806	152975829	In_Frame_Del	DEL	CACCAAGG	-	13	93	AGGCTACACCA	CAGGCTACACCAAGGT	GYTKVPE104
Pat_46	Pre-Treatment	TCF7L2	6934	37	10	114925316	114925317	Frame_Shift_Ins	INS	-	A	7	97	c.1394_1395insA	c.(1393-1395)AGAfs	p.R465fs
Pat_46	Pre-Treatment	GPR19	2842	37	12	12814274	12814274	Frame_Shift_Del	DEL	T	-	7	169	c.1109delA	c.(1108-1110)AACfs	p.N370fs
Pat_46	Pre-Treatment	ANXA2	302	37	15	60646357	60646358	Frame_Shift_Ins	INS	-	C	20	60	c.583_584insG	c.(583-585)GCTfs	p.A195fs
Pat_46	Pre-Treatment	NPIP	9284	37	16	15045758	15045759	Frame_Shift_Ins	INS	-	GT	8	183	c.929_930insGT	c.(928-930)GAGfs	p.E310fs
Pat_46	Pre-Treatment	SRCAP	10847	37	16	30736370	30736371	Frame_Shift_Ins	INS	-	C	9	184	c.5625_5626insC	c.(5623-5628)CAGCCCfs	p.Q1875fs
Pat_46	Pre-Treatment	FAM83G	644815	37	17	18891619	18891620	Frame_Shift_Ins	INS	-	AC	22	57	c.630_631insGT	c.(628-633)AGTAACfs	p.S210fs
Pat_46	Pre-Treatment	PLCD3	113026	37	17	43192760	43192762	In_Frame_Del	DEL	TCC	-	7	64	.1509_1511delGG	.(1507-1512)GAGGAT>GA	p.E503del
Pat_46	Pre-Treatment	UNC13A	23025	37	19	17766924	17766926	In_Frame_Del	DEL	CCT	-	2	4	.1313_1315delAG	(1312-1317)GAGGTG>GT	p.E438del
Pat_46	Pre-Treatment	LILRB1	10859	37	19	55143029	55143030	Frame_Shift_Ins	INS	-	G	15	53	c.149_150insG	c.(148-150)CAGfs	p.Q50fs
Pat_46	Pre-Treatment	SLC9A4	389015	37	2	103149137	103149137	Frame_Shift_Del	DEL	A	-	10	67	c.2387delA	c.(2386-2388)CAAfs	p.Q796fs
Pat_46	Pre-Treatment	TP53TG5	27296	37	20	44004170	44004170	Frame_Shift_Del	DEL	T	-	12	54	c.277delA	c.(277-279)ACAfs	p.T93fs
Pat_46	Pre-Treatment	ARFGAP3	26286	37	22	43213780	43213780	Frame_Shift_Del	DEL	T	-	9	234	c.896delA	c.(895-897)AATfs	p.N299fs
Pat_46	Pre-Treatment	SLAIN2	57606	37	4	48344125	48344127	In_Frame_Del	DEL	GGA	-	2	4	c.369_371delGGA	.(367-372)TGGGAG>TG	p.E128del

Pat_46	Pre-Treatment	EYA4	2070	37	6	133802671	133802671	Frame_Shift_Del	DEL	T	-	55	84	c.1041delT	c.(1039-1041)TCTfs	p.S347fs
Pat_46	Pre-Treatment	BMP1	649	37	8	22054260	22054260	Frame_Shift_Del	DEL	C	-	8	41	c.1833delC	c.(1831-1833)TACfs	p.Y611fs
Pat_46	Pre-Treatment	CDKN2A	1029	37	9	21970915	21970915	Frame_Shift_Del	DEL	G	-	50	30	c.443delC	c.(442-444)GCGfs	p.A148fs
Pat_46	Pre-Treatment	PHF2	5253	37	9	96422612	96422612	Frame_Shift_Del	DEL	A	-	4	4	c.1468delA	c.(1468-1470)AAAfs	p.K490fs
Pat_46	Pre-Treatment	MXRA5	25878	37	X	3228759	3228759	Frame_Shift_Del	DEL	G	-	2	4	c.7485delC	c.(7483-7485)ATCfs	p.I2495fs
Pat_46	Pre-Treatment	CXorf23	256643	37	X	19983706	19983706	Frame_Shift_Del	DEL	G	-	24	45	c.730delC	c.(730-732)CTCfs	p.L244fs
Pat_46	Post-Resistance	PTPN6	5777	37	12	7070069	7070070	Frame_Shift_Del	DEL	CT	-	2	4	c.1774_1775delCT	c.(1774-1776)CTCfs	p.L592fs
Pat_46	Post-Resistance	CKB	1152	37	14	103988211	103988211	Frame_Shift_Del	DEL	A	-	2	4	c.425delT	c.(424-426)CTCfs	p.L142fs
Pat_46	Post-Resistance	SECTM1	6398	37	17	80285091	80285091	Frame_Shift_Del	DEL	G	-	2	4	c.26delC	c.(25-27)CCTfs	p.P9fs
Pat_46	Post-Resistance	KIAA0240	23506	37	6	42823616	42823616	Frame_Shift_Del	DEL	A	-	7	178	c.2069delA	c.(2068-2070)CAAfs	p.Q690fs
Pat_46	Post-Resistance	EYA4	2070	37	6	133802671	133802671	Frame_Shift_Del	DEL	T	-	17	128	c.1041delT	c.(1039-1041)TCTfs	p.S347fs
Pat_46	Post-Resistance	MLLT4	4301	37	6	168366692	168366694	In_Frame_Del	DEL	GAG	-	2	4	.5233_5235delGA	c.(5233-5235)GAGdel	p.E1750del
Pat_46	Post-Resistance	CXorf23	256643	37	X	19983706	19983706	Frame_Shift_Del	DEL	G	-	9	44	c.730delC	c.(730-732)CTCfs	p.L244fs
Pat_48	Pre-Treatment	PTEN	5728	37	10	89685308	89685309	Frame_Shift_Ins	INS	-	CAAT	13	5	c.203_204insCAA	c.(202-204)TACfs	p.Y68fs
Pat_48	Pre-Treatment	ADCY4	196883	37	14	24803757	24803759	In_Frame_Del	DEL	CAG	-	3	5	c.100_102delCTG	c.(100-102)CTGdel	p.L34del
Pat_48	Pre-Treatment	EIF2AK4	440275	37	15	40282508	40282508	Frame_Shift_Del	DEL	T	-	8	242	c.2561delT	c.(2560-2562)ATTfs	p.I854fs
Pat_48	Pre-Treatment	LOC342346	342346	37	16	4650184	4650186	In_Frame_Del	DEL	CTG	-	2	4	.3292_3294delCT	c.(3292-3294)CTGdel	p.L1101del
Pat_48	Pre-Treatment	USP43	124739	37	17	9631801	9631801	Frame_Shift_Del	DEL	A	-	2	4	c.2866delA	c.(2866-2868)AAGfs	p.K956fs
Pat_48	Pre-Treatment	C18orf34	374864	37	18	30913143	30913143	Frame_Shift_Del	DEL	T	-	3	4	c.874delA	c.(874-876)ATGfs	p.M292fs
Pat_48	Pre-Treatment	TTN	7273	37	2	179502131	179502131	Frame_Shift_Del	DEL	T	-	2	4	c.33188delA	c.(33187-33189)AAGfs	p.K11063fs
Pat_48	Pre-Treatment	CLASP2	23122	37	3	33602361	33602361	Frame_Shift_Del	DEL	T	-	7	187	c.2869delA	c.(2869-2871)ATGfs	p.M957fs
Pat_48	Pre-Treatment	CCDC96	257236	37	4	7044507	7044509	In_Frame_Del	DEL	CTC	-	4	7	c.157_159delGAG	c.(157-159)GAGdel	p.E53del
Pat_48	Pre-Treatment	LIAS	11019	37	4	39478697	39478697	Frame_Shift_Del	DEL	A	-	2	4	c.1081delA	c.(1081-1083)AAAfs	p.K361fs
Pat_48	Pre-Treatment	RGNEF	64283	37	5	73183484	73183484	Frame_Shift_Del	DEL	A	-	2	4	c.3367delA	c.(3367-3369)AAAfs	p.K1123fs
Pat_48	Pre-Treatment	GARS	2617	37	7	30634583	30634585	In_Frame_Del	DEL	CTG	-	14	106	c.46_48delCTG	c.(46-48)CTGdel	p.L20del
Pat_48	Pre-Treatment	TP53INP1	94241	37	8	95952409	95952411	In_Frame_Del	DEL	TCT	-	8	86	c.150_152delAGA	.(148-153)GAAGAG>GA	p.50_51EE>E
Pat_48	Post-Resistance	ACBD3	64746	37	1	226352490	226352491	Frame_Shift_Ins	INS	-	T	7	111	c.568_569insA	c.(568-570)AGGfs	p.R190fs
Pat_48	Post-Resistance	PTEN	5728	37	10	89685308	89685309	Frame_Shift_Ins	INS	-	CAAT	8	28	c.203_204insCAA	c.(202-204)TACfs	p.Y68fs
Pat_48	Post-Resistance	ZIC2	7546	37	13	100634833	100634834	Frame_Shift_Del	DEL	AG	-	2	4	c.515_516delAG	c.(514-516)CAGfs	p.Q172fs
Pat_48	Post-Resistance	BEGAIN	57596	37	14	101005271	101005273	In_Frame_Del	DEL	CCT	-	3	6	c.815_817delAGG	.(814-819)GAGGCC>GC	p.E272del
Pat_48	Post-Resistance	NME3	4832	37	16	1820705	1820705	Frame_Shift_Del	DEL	C	-	2	4	c.455delG	c.(454-456)CGCfs	p.R152fs
Pat_48	Post-Resistance	PABPN1L	390748	37	16	88931435	88931436	Frame_Shift_Del	DEL	GG	-	2	4	c.560_561delCC	c.(559-561)CCCfs	p.P187fs
Pat_48	Post-Resistance	C19orf20	91978	37	19	519175	519177	In_Frame_Del	DEL	GCC	-	2	4	c.625_627delGCC	c.(625-627)GCCdel	p.A211del
Pat_48	Post-Resistance	HIST1H1A	3024	37	6	26017448	26017448	Frame_Shift_Del	DEL	T	-	7	230	c.513delA	c.(511-513)AAAfs	p.K171fs
Pat_48	Post-Resistance	HOXA11	3207	37	7	27222462	27222462	Frame_Shift_Del	DEL	T	-	7	261	c.895delA	c.(895-897)ATTfs	p.I299fs
Pat_48	Post-Resistance	TP53INP1	94241	37	8	95952409	95952411	In_Frame_Del	DEL	TCT	-	9	221	c.150_152delAGA	.(148-153)GAAGAG>GA	p.50_51EE>E
Pat_48	Post-Resistance	FAM83H	286077	37	8	144807177	144807179	Splice_Site	DEL	CCT	-	3	6	c.4444_splice	c.e7-1	
Pat_49	Post-Resistance	COL8A2	1296	37	1	36564899	36564900	Frame_Shift_Del	DEL	GG	-	3	6	c.382_383delCC	c.(382-384)CCAfs	p.P128fs
Pat_49	Post-Resistance	APBB1	322	37	11	6432078	6432080	In_Frame_Del	DEL	TCA	-	3	3	c.498_500delTGA	c.(496-501)GATGAA>GAA	p.D166del
Pat_49	Post-Resistance	ZDHHC13	54503	37	11	19174128	19174129	Frame_Shift_Del	DEL	CT	-	3	4	c.770_771delCT	c.(769-771)GCTfs	p.A257fs
Pat_49	Post-Resistance	ARHGAP1	392	37	11	46702224	46702224	Frame_Shift_Del	DEL	G	-	7	141	c.709delC	c.(709-711)CTGfs	p.L237fs
Pat_49	Post-Resistance	C11orf95	65998	37	11	63533335	63533337	In_Frame_Del	DEL	TCC	-	6	11	c.579_581delGGA	.(577-582)GAGGAA>GA	.193_194EE>
Pat_49	Post-Resistance	C14orf45	80127	37	14	74489766	74489766	Frame_Shift_Del	DEL	G	-	2	4	c.204delG	c.(202-204)AAGfs	p.K68fs
Pat_49	Post-Resistance	PALM	5064	37	19	727620	727620	Frame_Shift_Del	DEL	G	-	2	4	c.195delG	c.(193-195)GAGfs	p.E65fs
Pat_49	Post-Resistance	COL5A3	50509	37	19	10079363	10079364	Frame_Shift_Del	DEL	GG	-	2	4	c.4193_4194delC	c.(4192-4194)CCCfs	p.P1398fs
Pat_49	Post-Resistance	TRIOBP	11078	37	22	38120245	38120253	In_Frame_Del	DEL	CTCCAGA	-	9	172	2_1690delCCTCC	1-1692)GCCTCCAGAACC	p.SRT562del
Pat_49	Post-Resistance	C22orf26	55267	37	22	46449890	46449890	Frame_Shift_Del	DEL	G	-	2	4	c.84delC	c.(82-84)CCCfs	p.P28fs

Pat_49	Post-Resistance	RPL9	6133	37	4	39459817	39459818	Frame_Shift_Ins	INS	-	T	2	4	c.158_159insA	c.(157-159)AAGfs	p.K53fs
Pat_49	Post-Resistance	NOL7	51406	37	6	13615698	13615698	Frame_Shift_Del	DEL	G	-	2	4	c.108delG	c.(106-108)TTGfs	p.L36fs
Pat_49	Post-Resistance	SLC17A2	10246	37	6	25921520	25921520	Frame_Shift_Del	DEL	T	-	8	63	c.361delA	c.(361-363)ATGfs	p.M121fs
Pat_49	Post-Resistance	BTN2A2	10385	37	6	26384091	26384093	In_Frame_Del	DEL	CCT	-	7	117	c.42_44delCCT	c.(40-45)TCCCTC>TCC	p.L24del
Pat_49	Post-Resistance	RBM33	155435	37	7	155531073	155531074	Frame_Shift_Del	DEL	CA	-	7	129	.1713_1714delCA	c.(1711-1716)CCCACAfs	p.P571fs
Pat_49	Post-Resistance	FAM83H	286077	37	8	144807177	144807179	Splice_Site	DEL	CCT	-	4	9	c.4444_splice	c.e7-1	
Pat_49	Post-Resistance	FAM83H	286077	37	8	144811169	144811170	Frame_Shift_Ins	INS	-	GT	7	367	c.704_705insAC	c.(703-705)GTGfs	p.V235fs
Pat_50	Pre-Treatment	PVRL4	81607	37	1	161044057	161044059	In_Frame_Del	DEL	CAC	-	7	439	.1105_1107delGT	c.(1105-1107)GTGdel	p.V369del
Pat_50	Pre-Treatment	KCNMA1	3778	37	10	79397371	79397373	In_Frame_Del	DEL	GCC	-	2	4	c.28_30delGGC	c.(28-30)GGCdel	p.G10del
Pat_50	Pre-Treatment	KIF21A	55605	37	12	39735366	39735368	In_Frame_Del	DEL	TCC	-	8	118	.1860_1862delGG	(1858-1863)GAGGAA>GA	.620_621EE>
Pat_50	Pre-Treatment	LRP1	4035	37	12	57605740	57605742	In_Frame_Del	DEL	TGC	-	8	255	13289_13291delT	13288-13293)TTGCTG>T	4430_4431LL
Pat_50	Pre-Treatment	CEP290	80184	37	12	88443088	88443090	In_Frame_Del	DEL	TTC	-	9	44	.7311_7313delGA	.(7309-7314)AAGAAT>AA	p.K2437del
Pat_50	Pre-Treatment	LOC100132247	100132247	37	16	22545744	22545755	In_Frame_Del	DEL	CACCCTCA	-	8	48	1451delTCCACC	1452)CTTCCACCCTCAG	p.PPSA485del
Pat_50	Pre-Treatment	ZNF207	7756	37	17	30685576	30685577	Frame_Shift_Del	DEL	AT	-	54	89	c.223_224delAT	c.(223-225)ATAfs	p.I75fs
Pat_50	Pre-Treatment	CYP4F3	4051	37	19	15769322	15769322	Frame_Shift_Del	DEL	T	-	7	579	c.1271delT	c.(1270-1272)GTTfs	p.V424fs
Pat_50	Pre-Treatment	ZNF471	57573	37	19	57022958	57022959	Frame_Shift_Del	DEL	AA	-	54	76	c.18_19delAA	c.(16-21)GTAAAAfs	p.V6fs
Pat_50	Pre-Treatment	PWP2	5822	37	21	45535692	45535694	In_Frame_Del	DEL	GAG	-	7	90	c.727_729delGAG	c.(727-729)GAGdel	p.E247del
Pat_50	Pre-Treatment	ARFGAP3	26286	37	22	43213780	43213780	Frame_Shift_Del	DEL	T	-	8	375	c.896delA	c.(895-897)AATfs	p.N299fs
Pat_50	Pre-Treatment	PKD2	5311	37	4	88929174	88929176	In_Frame_Del	DEL	GAG	-	5	11	c.289_291delGAG	c.(289-291)GAGdel	p.E102del
Pat_50	Pre-Treatment	HMGCR	3156	37	5	74646970	74646973	Frame_Shift_Del	DEL	AACA	-	41	69	1019_1022delAAC	c.(1018-1023)GAACAAfs	p.E340fs
Pat_50	Pre-Treatment	CSNK1A1	1452	37	5	148891411	148891413	In_Frame_Del	DEL	TAA	-	65	51	c.619_621delTTA	c.(619-621)TTAdel	p.L207del
Pat_50	Pre-Treatment	BHLHE22	27319	37	8	65494020	65494021	In_Frame_Ins	INS	-	GCA	9	8	c.673_674insGCA	.(673-675)GGC>GGCAG	p.234_235insS
Pat_54	Pre-Treatment	PHF13	148479	37	1	6680069	6680071	In_Frame_Del	DEL	GAA	-	8	109	c.348_350delGAA	c.(346-351)CTGAAG>CTG	p.K121del
Pat_54	Pre-Treatment	NBPF1	55672	37	1	16892196	16892196	Frame_Shift_Del	DEL	C	-	7	3466	c.3221delG	c.(3220-3222)TGCfs	p.C1074fs
Pat_54	Pre-Treatment	TMCO2	127391	37	1	40713708	40713709	Frame_Shift_Del	DEL	TC	-	11	461	c.43_44delTC	c.(43-45)TCTfs	p.S15fs
Pat_54	Pre-Treatment	NRD1	4898	37	1	52305911	52305912	Frame_Shift_Ins	INS	-	T	7	272	c.616_617insA	c.(616-618)ACTfs	p.T206fs
Pat_54	Pre-Treatment	TTC22	55001	37	1	55252709	55252709	Frame_Shift_Del	DEL	T	-	2	4	c.779delA	c.(778-780)AAGfs	p.K260fs
Pat_54	Pre-Treatment	CTH	1491	37	1	70877106	70877106	Frame_Shift_Del	DEL	A	-	7	632	c.8delA	c.(7-9)GAAfs	p.E3fs
Pat_54	Pre-Treatment	FNDC7	163479	37	1	109276138	109276138	Frame_Shift_Del	DEL	A	-	7	193	c.2124delA	c.(2122-2124)CCAfs	p.P708fs
Pat_54	Pre-Treatment	DARC	2532	37	1	159176226	159176227	Frame_Shift_Del	DEL	GG	-	8	557	c.997_998delGG	c.(997-999)GGAfs	p.G333fs
Pat_54	Pre-Treatment	SDHC	6391	37	1	161310394	161310395	Frame_Shift_Del	DEL	CC	-	9	791	c.190_191delCC	c.(190-192)CCCfs	p.P64fs
Pat_54	Pre-Treatment	CACNA1E	777	37	1	181680102	181680103	Frame_Shift_Del	DEL	AG	-	19	144	.1068_1069delA	c.(1066-1071)AAAGAGfs	p.K356fs
Pat_54	Pre-Treatment	APOBEC4	403314	37	1	183616826	183616828	In_Frame_Del	DEL	TTC	-	7	511	.1089_1091delGA	.(1087-1092)AAGAAA>AA	.363_364KK>
Pat_54	Pre-Treatment	PRG4	10216	37	1	186276127	186276128	In_Frame_Ins	INS	-	AGG	7	337	.1276_1277insAG	(1276-1278)AAG>AAGGA	p.426_427insE
Pat_54	Pre-Treatment	PLA2G4A	5321	37	1	186916018	186916018	Frame_Shift_Del	DEL	T	-	7	412	c.1189delT	c.(1189-1191)TTTfs	p.F397fs
Pat_54	Pre-Treatment	DNAJC1	64215	37	10	22208818	22208818	Frame_Shift_Del	DEL	T	-	8	675	c.578delA	c.(577-579)AAGfs	p.K193fs
Pat_54	Pre-Treatment	ZEB1	6935	37	10	31810582	31810582	Frame_Shift_Del	DEL	A	-	7	214	c.2319delA	c.(2317-2319)GCAfs	p.A773fs
Pat_54	Pre-Treatment	RUFY2	55680	37	10	70156583	70156583	Frame_Shift_Del	DEL	T	-	10	100	c.457delA	c.(457-459)ATGfs	p.M153fs
Pat_54	Pre-Treatment	ZMIZ1	57178	37	10	81072446	81072446	Frame_Shift_Del	DEL	C	-	7	420	c.3144delC	c.(3142-3144)GACfs	p.D1048fs
Pat_54	Pre-Treatment	POLL	27343	37	10	103345131	103345133	In_Frame_Del	DEL	GGA	-	9	88	c.513_515delTCC	c.(511-516)CCTCCC>CCC	.171_172PP>
Pat_54	Pre-Treatment	OR52N5	390075	37	11	5799652	5799652	Frame_Shift_Del	DEL	A	-	18	71	c.213delT	c.(211-213)TTTfs	p.F71fs
Pat_54	Pre-Treatment	OR8I2	120586	37	11	55861308	55861308	Frame_Shift_Del	DEL	T	-	9	448	c.525delT	c.(523-525)CATfs	p.H175fs
Pat_54	Pre-Treatment	NOX4	50507	37	11	89106662	89106663	Splice_Site	INS	-	A	12	486	c.1075_splice	c.e12-1	p.C359_splice
Pat_54	Pre-Treatment	PVRL1	5818	37	11	119535678	119535680	In_Frame_Del	DEL	CCT	-	7	25	.1331_1333delAG	(1330-1335)GAGGGC>GG	p.E444del
Pat_54	Pre-Treatment	NFRKB	4798	37	11	129752495	129752496	Frame_Shift_Ins	INS	-	T	8	212	c.932_933insA	c.(931-933)AAGfs	p.K311fs
Pat_54	Pre-Treatment	PRB2	653247	37	12	11546788	11546790	In_Frame_Del	DEL	GGA	-	8	271	c.222_224delTCC	c.(220-225)CCTCCA>CCA	p.74_75PP>P
Pat_54	Pre-Treatment	FAR2	55711	37	12	29450110	29450110	Frame_Shift_Del	DEL	A	-	11	422	c.522delA	c.(520-522)CCAfs	p.P174fs

Pat_54	Pre-Treatment	SFRS2IP	9169	37	12	46318575	46318577	In_Frame_Del	DEL	GGT	-	9	321	.3840_3842delAC	(3838-3843)CCACCC>CC	1280_1281PP>
Pat_54	Pre-Treatment	LIMA1	51474	37	12	50594574	50594574	Frame_Shift_Del	DEL	G	-	8	1343	c.958delC	c.(958-960)CAGfs	p.Q320fs
Pat_54	Pre-Treatment	SMARCC2	6601	37	12	56559113	56559113	Frame_Shift_Del	DEL	G	-	8	262	c.3128delC	c.(3127-3129)CCTfs	p.P1043fs
Pat_54	Pre-Treatment	FBXO21	23014	37	12	117624320	117624320	Frame_Shift_Del	DEL	A	-	7	227	c.432delT	c.(430-432)TTTfs	p.F144fs
Pat_54	Pre-Treatment	EP400	57634	37	12	132466907	132466907	Frame_Shift_Del	DEL	G	-	7	294	c.1813delG	c.(1813-1815)GCAfs	p.A605fs
Pat_54	Pre-Treatment	XPO4	64328	37	13	21436858	21436858	Frame_Shift_Del	DEL	G	-	7	473	c.315delC	c.(313-315)CCCfs	p.P105fs
Pat_54	Pre-Treatment	SACS	26278	37	13	23914687	23914687	Frame_Shift_Del	DEL	T	-	22	961	c.3328delA	c.(3328-3330)ATTfs	p.I1110fs
Pat_54	Pre-Treatment	TSC22D1	8848	37	13	45148706	45148708	In_Frame_Del	DEL	TGC	-	10	149	.1503_1505delGC	.(1501-1506)CAGCAA>CA	.501_502QQ>
Pat_54	Pre-Treatment	LMO7	4008	37	13	76415307	76415308	Frame_Shift_Del	DEL	AG	-	11	283	c.2946_2947delAC	c.(2944-2949)GCAGAGfs	p.A982fs
Pat_54	Pre-Treatment	MBNL2	10150	37	13	97928604	97928604	Frame_Shift_Del	DEL	C	-	8	788	c.115delC	c.(115-117)CCCfs	p.P39fs
Pat_54	Pre-Treatment	FERMT2	10979	37	14	53339633	53339633	Frame_Shift_Del	DEL	T	-	9	309	c.1157delA	c.(1156-1158)AAGfs	p.K386fs
Pat_54	Pre-Treatment	SIPA1L1	26037	37	14	72190482	72190484	In_Frame_Del	DEL	TCC	-	8	226	.4390_4392delTC	c.(4390-4392)TCCdel	p.S1468del
Pat_54	Pre-Treatment	RBM25	58517	37	14	73572607	73572608	Frame_Shift_Del	DEL	AG	-	10	91	c.1195_1196delAG	c.(1195-1197)AGAfs	p.R399fs
Pat_54	Pre-Treatment	DDX24	57062	37	14	94545821	94545823	In_Frame_Del	DEL	CCT	-	8	247	c.266_268delAGG	.(265-270)GAGGGA>GG	p.E89del
Pat_54	Pre-Treatment	C14orf49	161176	37	14	95916348	95916348	Frame_Shift_Del	DEL	C	-	2	4	c.1369delG	c.(1369-1371)GCCfs	p.A457fs
Pat_54	Pre-Treatment	KIF26A	26153	37	14	104642401	104642401	Frame_Shift_Del	DEL	G	-	2	4	c.3276delG	c.(3274-3276)GAGfs	p.E1092fs
Pat_54	Pre-Treatment	THBS1	7057	37	15	39885641	39885641	Frame_Shift_Del	DEL	C	-	8	493	c.3039delC	c.(3037-3039)TTCfs	p.F1013fs
Pat_54	Pre-Treatment	CASC4	113201	37	15	44624241	44624241	Frame_Shift_Del	DEL	A	-	125	186	c.541delA	c.(541-543)AAAfs	p.K181fs
Pat_54	Pre-Treatment	SPG11	80208	37	15	44905698	44905698	Frame_Shift_Del	DEL	T	-	8	267	c.3075delA	c.(3073-3075)AAAfs	p.K1025fs
Pat_54	Pre-Treatment	ARID3B	10620	37	15	74836290	74836292	In_Frame_Del	DEL	CAG	-	9	57	c.13_15delCAG	c.(13-15)CAGdel	p.Q15del
Pat_54	Pre-Treatment	CHD2	1106	37	15	93540315	93540316	Frame_Shift_Ins	INS	-	A	10	181	c.3724_3725insA	c.(3724-3726)GAAfs	p.E1242fs
Pat_54	Pre-Treatment	C16orf88	400506	37	16	19725706	19725706	Frame_Shift_Del	DEL	T	-	15	129	c.652delA	c.(652-654)ATCfs	p.I218fs
Pat_54	Pre-Treatment	RABEP2	79874	37	16	28931200	28931202	In_Frame_Del	DEL	CTG	-	8	77	c.337_339delCAG	c.(337-339)CAGdel	p.Q113del
Pat_54	Pre-Treatment	MYLPF	29895	37	16	30389140	30389140	Frame_Shift_Del	DEL	C	-	10	136	c.429delC	c.(427-429)TTCfs	p.F143fs
Pat_54	Pre-Treatment	COQ9	57017	37	16	57486732	57486734	In_Frame_Del	DEL	GAG	-	10	236	c.262_264delGAG	c.(262-264)GAGdel	p.E91del
Pat_54	Pre-Treatment	ZFP90	146198	37	16	68598462	68598463	Frame_Shift_Ins	INS	-	A	15	502	c.1772_1773insA	c.(1771-1773)CGAfs	p.R591fs
Pat_54	Pre-Treatment	CTNS	1497	37	17	3543532	3543532	Frame_Shift_Del	DEL	T	-	7	672	c.32delT	c.(31-33)CTTfs	p.L11fs
Pat_54	Pre-Treatment	C17orf85	55421	37	17	3721809	3721811	In_Frame_Del	DEL	TCC	-	7	228	.1056_1058delGG	(1054-1059)GAGGAA>GA	.352_353EE>
Pat_54	Pre-Treatment	PHF23	79142	37	17	7139558	7139558	Frame_Shift_Del	DEL	C	-	8	715	c.688delG	c.(688-690)GATfs	p.D230fs
Pat_54	Pre-Treatment	MYO15A	51168	37	17	18025395	18025396	Frame_Shift_Ins	INS	-	CAGGGCC	8	35	1_3282insCAGGG	c.(3280-3282)ATCfs	p.I1094fs
Pat_54	Pre-Treatment	MBTD1	54799	37	17	49281228	49281228	Frame_Shift_Del	DEL	C	-	7	712	c.663delG	c.(661-663)TGGfs	p.W221fs
Pat_54	Pre-Treatment	FTSJ3	117246	37	17	61901516	61901518	In_Frame_Del	DEL	TCC	-	7	343	.1080_1082delGG	(1078-1083)GAGGAA>GA	.360_361EE>
Pat_54	Pre-Treatment	RBBP8	5932	37	18	20572852	20572853	Frame_Shift_Ins	INS	-	A	12	235	c.1062_1063insA	c.(1060-1065)GGGAAAfs	p.G354fs
Pat_54	Pre-Treatment	CNDP1	84735	37	18	72245406	72245407	Frame_Shift_Del	DEL	TC	-	7	112	c.1011_1012delTC	c.(1009-1014)ATTCTAfs	p.I337fs
Pat_54	Pre-Treatment	TCF3	6929	37	19	1620979	1620979	Frame_Shift_Del	DEL	G	-	2	4	c.1081delC	c.(1081-1083)CAGfs	p.Q361fs
Pat_54	Pre-Treatment	GATAD2A	54815	37	19	19616235	19616235	Frame_Shift_Del	DEL	G	-	8	248	c.1854delG	c.(1852-1854)CTGfs	p.L618fs
Pat_54	Pre-Treatment	ASXL2	55252	37	2	26022304	26022306	In_Frame_Del	DEL	CTG	-	10	448	c.351_353delCAG	c.(349-354)AGCAGT>AGT	.117_118SS>
Pat_54	Pre-Treatment	SOS1	6654	37	2	39224072	39224073	Frame_Shift_Del	DEL	GA	-	8	603	c.3071_3072delTC	c.(3070-3072)CTCfs	p.L1024fs
Pat_54	Pre-Treatment	EHBP1	23301	37	2	63206352	63206353	Frame_Shift_Del	DEL	GA	-	7	398	c.2595_2596delGA	c.(2593-2598)CTGAGAfs	p.L865fs
Pat_54	Pre-Treatment	TGOLN2	10618	37	2	85554537	85554537	Frame_Shift_Del	DEL	T	-	7	2502	c.318delA	c.(316-318)AAAfs	p.K106fs
Pat_54	Pre-Treatment	GPR148	344561	37	2	131487754	131487755	Frame_Shift_Del	DEL	TT	-	4	9	c.1030_1031delTT	c.(1030-1032)TTTfs	p.F344fs
Pat_54	Pre-Treatment	NEB	4703	37	2	152550852	152550853	Frame_Shift_Del	DEL	GG	-	7	522	c.1880_1881delCC	c.(1879-1881)GCCfs	p.A627fs
Pat_54	Pre-Treatment	7-Mar	64844	37	2	160605268	160605268	Frame_Shift_Del	DEL	T	-	9	1163	c.1467delT	c.(1465-1467)CCTfs	p.P489fs
Pat_54	Pre-Treatment	PLA2R1	22925	37	2	160918876	160918878	In_Frame_Del	DEL	CAG	-	4	6	c.37_39delCTG	c.(37-39)CTGdel	p.L13del
Pat_54	Pre-Treatment	TTN	7273	37	2	179613763	179613763	Frame_Shift_Del	DEL	T	-	8	124	c.13364delA	c.(13363-13365)AAGfs	p.K4455fs
Pat_54	Pre-Treatment	GIGYF2	26058	37	2	233620985	233620987	In_Frame_Del	DEL	GAG	-	8	195	c.320_322delGAG	.(319-324)CGAGGA>CG	p.G111del
Pat_54	Pre-Treatment	MTERFD2	130916	37	2	242038902	242038903	Frame_Shift_Del	DEL	CA	-	8	471	c.515_516delTG	c.(514-516)GTGfs	p.V172fs

Pat_54	Pre-Treatment	PANK2	80025	37	20	3893120	3893120	Frame_Shift_Del	DEL	T	-	10	648	c.1251delT	c.(1249-1251)ACTfs	p.T417fs
Pat_54	Pre-Treatment	MCM8	84515	37	20	5935274	5935277	Frame_Shift_Del	DEL	TTGA	-	77	154	c.274_277delTTGA	c.(274-279)TTGATTfs	p.L92fs
Pat_54	Pre-Treatment	C20orf7	79133	37	20	13797838	13797838	Frame_Shift_Del	DEL	G	-	9	800	c.1020delG	c.(1018-1020)CCGfs	p.P340fs
Pat_54	Pre-Treatment	FRG1B	284802	37	20	29625899	29625900	Frame_Shift_Ins	INS	-	AT	11	314	c.53_54insAT	c.(52-54)AAAfs	p.K18fs
Pat_54	Pre-Treatment	SNX21	90203	37	20	44469908	44469908	Frame_Shift_Del	DEL	C	-	8	534	c.1078delC	c.(1078-1080)CCCfs	p.P360fs
Pat_54	Pre-Treatment	STAU1	6780	37	20	47740939	47740939	Frame_Shift_Del	DEL	G	-	10	999	c.795delC	c.(793-795)ATCfs	p.I265fs
Pat_54	Pre-Treatment	ZNF295	49854	37	21	43412088	43412088	Frame_Shift_Del	DEL	G	-	7	775	c.2117delC	c.(2116-2118)CCAfs	p.P706fs
Pat_54	Pre-Treatment	MN1	4330	37	22	28193063	28193064	Frame_Shift_Del	DEL	GA	-	4	6	c.3468_3469delTC	c.(3466-3471)CTTCAGfs	p.L1156fs
Pat_54	Pre-Treatment	EDEM1	9695	37	3	5244752	5244752	Frame_Shift_Del	DEL	G	-	7	582	c.960delG	c.(958-960)CTGfs	p.L320fs
Pat_54	Pre-Treatment	TRAK1	22906	37	3	42235351	42235351	Frame_Shift_Del	DEL	G	-	7	472	c.936delG	c.(934-936)CTGfs	p.L312fs
Pat_54	Pre-Treatment	DNAH12	201625	37	3	57509312	57509313	Frame_Shift_Ins	INS	-	T	7	220	c.276_277insA	c.(274-279)AAAGGAfs	p.K92fs
Pat_54	Pre-Treatment	FGFBP1	9982	37	4	15938177	15938178	Frame_Shift_Ins	INS	-	T	7	317	c.78_79insA	c.(76-81)AAAGTGfs	p.K26fs
Pat_54	Pre-Treatment	TLR1	7096	37	4	38798502	38798503	Frame_Shift_Del	DEL	CC	-	7	307	c.1950_1951delGG	c.(1948-1953)TGGGTGfs	p.W650fs
Pat_54	Pre-Treatment	CDKL2	8999	37	4	76539579	76539580	Frame_Shift_Ins	INS	-	T	10	200	c.222_223insA	c.(220-225)AAACGAfs	p.K74fs
Pat_54	Pre-Treatment	CDS1	1040	37	4	85556475	85556475	Frame_Shift_Del	DEL	T	-	13	219	c.781delT	c.(781-783)TTTfs	p.F261fs
Pat_54	Pre-Treatment	MMRN1	22915	37	4	90844391	90844393	In_Frame_Del	DEL	AGC	-	11	924	c.923_925delAGC	c.(922-927)GAGCAG>GAG	p.Q313del
Pat_54	Pre-Treatment	EMCN	51705	37	4	101338299	101338300	Splice_Site	DEL	CT	-	8	420	c.665_splice	c.e9-1	p.G222_splice
Pat_54	Pre-Treatment	ZNF330	27309	37	4	142143532	142143532	Frame_Shift_Del	DEL	A	-	7	142	c.7delA	c.(7-9)AAAfs	p.K3fs
Pat_54	Pre-Treatment	OTUD4	54726	37	4	146059009	146059010	Frame_Shift_Del	DEL	TC	-	9	488	c.2722_2723delGA	c.(2722-2724)GAAfs	p.E908fs
Pat_54	Pre-Treatment	LRBA	987	37	4	151829814	151829814	Frame_Shift_Del	DEL	G	-	7	240	c.1357delC	c.(1357-1359)CAGfs	p.Q453fs
Pat_54	Pre-Treatment	CDH10	1008	37	5	24492973	24492973	Frame_Shift_Del	DEL	A	-	8	486	c.1577delT	c.(1576-1578)TTCfs	p.F526fs
Pat_54	Pre-Treatment	MSH3	4437	37	5	79970915	79970915	Frame_Shift_Del	DEL	A	-	7	501	c.1141delA	c.(1141-1143)AAAfs	p.K381fs
Pat_54	Pre-Treatment	ANKHD1-EIF4EBP	404734	37	5	139905676	139905676	Frame_Shift_Del	DEL	A	-	9	358	c.4588delA	c.(4588-4590)AAAfs	p.K1530fs
Pat_54	Pre-Treatment	C5orf25	375484	37	5	175717107	175717109	In_Frame_Del	DEL	AGC	-	4	5	c.523_525delAGC	c.(523-525)AGCdel	p.S180del
Pat_54	Pre-Treatment	PHACTR1	221692	37	6	13228080	13228080	Frame_Shift_Del	DEL	A	-	7	337	c.1019delA	c.(1018-1020)TACfs	p.Y340fs
Pat_54	Pre-Treatment	DEK	7913	37	6	18237737	18237737	Frame_Shift_Del	DEL	T	-	7	234	c.773delA	c.(772-774)AAGfs	p.K258fs
Pat_54	Pre-Treatment	GABBR1	2550	37	6	29577144	29577144	Frame_Shift_Del	DEL	G	-	8	125	c.1721delC	c.(1720-1722)CCAfs	p.P574fs
Pat_54	Pre-Treatment	ARHGAP18	93663	37	6	129959602	129959603	Frame_Shift_Ins	INS	-	T	7	437	c.488_489insA	c.(487-489)AACfs	p.N163fs
Pat_54	Pre-Treatment	HGC6.3	100128124	37	6	168376971	168376972	Frame_Shift_Ins	INS	-	A	2	4	c.361_362insT	c.(361-363)TCCfs	p.S121fs
Pat_54	Pre-Treatment	GLCCI1	113263	37	7	8126097	8126099	In_Frame_Del	DEL	CAG	-	7	526	.1573_1575delCAG	c.(1573-1575)CAGdel	p.Q528del
Pat_54	Pre-Treatment	POU6F2	11281	37	7	39503812	39503812	Frame_Shift_Del	DEL	C	-	7	506	c.1603delC	c.(1603-1605)CCAfs	p.P535fs
Pat_54	Pre-Treatment	OGDH	4967	37	7	44684936	44684936	Frame_Shift_Del	DEL	T	-	12	509	c.233delT	c.(232-234)ATTfs	p.I78fs
Pat_54	Pre-Treatment	CYP51A1	1595	37	7	91752493	91752494	Frame_Shift_Ins	INS	-	T	9	413	c.1026_1027insA	c.(1024-1029)AAATGTfs	p.K342fs
Pat_54	Pre-Treatment	DYNC1I1	1780	37	7	95614249	95614249	Frame_Shift_Del	DEL	T	-	9	492	c.754delT	c.(754-756)TTTfs	p.F252fs
Pat_54	Pre-Treatment	CNOT4	4850	37	7	135098272	135098272	Frame_Shift_Del	DEL	C	-	7	457	c.652delG	c.(652-654)GATfs	p.D218fs
Pat_54	Pre-Treatment	PTPRN2	5799	37	7	158380330	158380332	In_Frame_Del	DEL	AGC	-	2	4	c.30_32delGCT	c.(28-33)CTGCTA>CTA	p.10_11LL>L
Pat_54	Pre-Treatment	RP1L1	94137	37	8	10465264	10465270	Frame_Shift_Del	DEL	CCTTCTG	-	8	465	38_6344delCAGA	(6337-6345)GCAGAAGGT	p.A2113fs
Pat_54	Pre-Treatment	CCDC25	55246	37	8	27606054	27606055	Frame_Shift_Del	DEL	AG	-	8	617	c.305_306delCT	c.(304-306)GCTfs	p.A102fs
Pat_54	Pre-Treatment	SULF1	23213	37	8	70514026	70514026	Frame_Shift_Del	DEL	T	-	8	1084	c.1023delT	c.(1021-1023)CCTfs	p.P341fs
Pat_54	Pre-Treatment	KCNB2	9312	37	8	73848175	73848175	Frame_Shift_Del	DEL	G	-	7	1240	c.585delG	c.(583-585)CTGfs	p.L195fs
Pat_54	Pre-Treatment	LRRCC1	85444	37	8	86038947	86038948	Frame_Shift_Del	DEL	AG	-	10	462	c.1296_1297delAG	c.(1294-1299)CAAGAGfs	p.Q432fs
Pat_54	Pre-Treatment	SLC26A7	115111	37	8	92406218	92406218	Frame_Shift_Del	DEL	T	-	12	431	c.1886delT	c.(1885-1887)ATTfs	p.I629fs
Pat_54	Pre-Treatment	TP53INP1	94241	37	8	95952409	95952411	In_Frame_Del	DEL	TCT	-	13	209	c.150_152delAGA	c.(148-153)GAAGAG>GAG	p.50_51EE>E
Pat_54	Pre-Treatment	RGS22	26166	37	8	101076229	101076229	Frame_Shift_Del	DEL	T	-	7	1438	c.767delA	c.(766-768)AAGfs	p.K256fs
Pat_54	Pre-Treatment	ENY2	56943	37	8	110351560	110351562	In_Frame_Del	DEL	TGC	-	8	659	c.95_97delTGC	c.(94-99)TTGCTG>TTG	p.32_33LL>L
Pat_54	Pre-Treatment	TRPS1	7227	37	8	116632272	116632272	Frame_Shift_Del	DEL	T	-	8	266	c.14delA	c.(13-15)AAGfs	p.K5fs
Pat_54	Pre-Treatment	ANXA13	312	37	8	124707762	124707762	Frame_Shift_Del	DEL	T	-	12	1413	c.451delA	c.(451-453)ATCfs	p.I151fs

Pat_54	Pre-Treatment	GLIS3	169792	37	9	4118450	4118450	Frame_Shift_Del	DEL	G	-	2	4	c.563delC	c.(562-564)CCGfs	p.P188fs
Pat_54	Pre-Treatment	TLN1	7094	37	9	35716473	35716473	Frame_Shift_Del	DEL	C	-	8	491	c.2539delG	c.(2539-2541)GAAfs	p.E847fs
Pat_54	Pre-Treatment	TXLNG	55787	37	X	16850849	16850850	Frame_Shift_Del	DEL	AG	-	13	149	c.968_969delAG	c.(967-969)CAGfs	p.Q323fs
Pat_54	Pre-Treatment	MAP7D2	256714	37	X	20031209	20031210	Frame_Shift_Del	DEL	CA	-	11	1122	c.1724_1725delTG	c.(1723-1725)GTGfs	p.V575fs
Pat_54	Pre-Treatment	SHROOM4	57477	37	X	50345634	50345634	Frame_Shift_Del	DEL	T	-	7	398	c.3941delA	c.(3940-3942)AAGfs	p.K1314fs
Pat_54	Pre-Treatment	MAGT1	84061	37	X	77131002	77131003	Frame_Shift_Del	DEL	CA	-	8	653	c.290_291delTG	c.(289-291)GTGfs	p.V97fs
Pat_54	Pre-Treatment	RBM41	55285	37	X	106312552	106312552	Frame_Shift_Del	DEL	T	-	8	492	c.1008delA	c.(1006-1008)AAAfs	p.K336fs
Pat_54	Pre-Treatment	GDI1	2664	37	X	153667141	153667141	Frame_Shift_Del	DEL	C	-	10	861	c.184delC	c.(184-186)CCCfs	p.P62fs
Pat_55	Pre-Treatment	PLEKHG5	57449	37	1	6536011	6536013	In_Frame_Del	DEL	CTC	-	13	232	c.295_297delGAG	c.(295-297)GAGdel	p.E99del
Pat_55	Pre-Treatment	ISG20L2	81875	37	1	156694023	156694023	Frame_Shift_Del	DEL	G	-	12	173	c.865delC	c.(865-867)CTCfs	p.L289fs
Pat_55	Pre-Treatment	CORO1B	57175	37	11	67208955	67208955	Frame_Shift_Del	DEL	A	-	16	15	c.485delT	c.(484-486)GTGfs	p.V162fs
Pat_55	Pre-Treatment	GSPT1	2935	37	16	12009530	12009531	In_Frame_Ins	INS	-	CCG	5	10	c.47_48insCGG	c.(46-48)GGG>GGCGGG	p.16_16G>GG
Pat_55	Pre-Treatment	NCOA6	23054	37	20	33330968	33330970	In_Frame_Del	DEL	TGC	-	9	127	.3090_3092delGC	.(3088-3093)CAGCAA>CA	030_1031QQ
Pat_55	Pre-Treatment	YTHDF1	54915	37	20	61833650	61833652	In_Frame_Del	DEL	CCT	-	9	193	.1640_1642delAG	(1639-1644)GAGGTG>GT	p.E547del
Pat_55	Pre-Treatment	TFIP11	24144	37	22	26906183	26906185	In_Frame_Del	DEL	TCA	-	7	153	c.54_56delTGA	c.(52-57)GATGAC>GAC	p.18_19DD>D
Pat_55	Pre-Treatment	TPRXL	348825	37	3	14105964	14105965	In_Frame_Ins	INS	-	AGC	4	4	c.288_289insAGC	c.(286-291)insAGC	p.102_103insS
Pat_55	Pre-Treatment	PAPD7	11044	37	5	6755013	6755014	Frame_Shift_Del	DEL	AC	-	7	100	c.1584_1585delAC	c.(1582-1587)AAACACfs	p.K528fs
Pat_55	Pre-Treatment	KCNN2	3781	37	5	113698631	113698632	In_Frame_Ins	INS	-	GCC	6	1	c.159_160insGCC	c.(157-162)insGCC	p.58_59insA
Pat_60	Pre-Treatment	TNFRSF25	8718	37	1	6522977	6522978	Frame_Shift_Del	DEL	CC	-	4	2	c.651_652delGG	c.(649-654)GGGGCCfs	p.G217fs
Pat_60	Pre-Treatment	FDPS	2224	37	1	155279648	155279648	Frame_Shift_Del	DEL	G	-	4	8	c.68delG	c.(67-69)CGGfs	p.R23fs
Pat_60	Pre-Treatment	8-Mar	220972	37	10	45953876	45953878	In_Frame_Del	DEL	GAG	-	22	163	c.685_687delCTC	c.(685-687)CTCdel	p.L229del
Pat_60	Pre-Treatment	C10orf58	84293	37	10	82182206	82182206	Frame_Shift_Del	DEL	A	-	7	159	c.212delA	c.(211-213)GAAfs	p.E71fs
Pat_60	Pre-Treatment	OR51M1	390059	37	11	5410982	5410982	Frame_Shift_Del	DEL	T	-	9	300	c.354delT	c.(352-354)TCTfs	p.S118fs
Pat_60	Pre-Treatment	PAMR1	25891	37	11	35513670	35513670	Frame_Shift_Del	DEL	C	-	7	467	c.302delG	c.(301-303)GGTfs	p.G101fs
Pat_60	Pre-Treatment	CBX5	23468	37	12	54645832	54645832	Frame_Shift_Del	DEL	T	-	7	317	c.317delA	c.(316-318)AAGfs	p.K106fs
Pat_60	Pre-Treatment	KIAA1704	55425	37	13	45580365	45580367	In_Frame_Del	DEL	GAT	-	8	441	c.250_252delGAT	c.(250-252)GATdel	p.D88del
Pat_60	Pre-Treatment	C14orf106	55320	37	14	45693722	45693722	Frame_Shift_Del	DEL	T	-	9	161	c.2068delA	c.(2068-2070)AGTfs	p.S690fs
Pat_60	Pre-Treatment	ZBTB1	22890	37	14	64989787	64989787	Frame_Shift_Del	DEL	A	-	8	474	c.1565delA	c.(1564-1566)CAAfs	p.Q522fs
Pat_60	Pre-Treatment	NPIP	9284	37	16	15045758	15045759	Frame_Shift_Ins	INS	-	GT	14	101	c.929_930insGT	c.(928-930)GAGfs	p.E310fs
Pat_60	Pre-Treatment	TAOK2	9344	37	16	29994531	29994533	In_Frame_Del	DEL	GAG	-	10	51	.1138_1140delGA	c.(1138-1140)GAGdel	p.E392del
Pat_60	Pre-Treatment	TERF2	7014	37	16	69419367	69419367	Frame_Shift_Del	DEL	C	-	8	286	c.276delG	c.(274-276)GGGfs	p.G92fs
Pat_60	Pre-Treatment	STRN	6801	37	2	37113870	37113870	Frame_Shift_Del	DEL	T	-	10	368	c.1031delA	c.(1030-1032)AAGfs	p.K344fs
Pat_60	Pre-Treatment	SPEG	10290	37	2	220327081	220327082	Frame_Shift_Ins	INS	-	G	2	4	c.2678_2679insG	c.(2677-2679)CAGfs	p.Q893fs
Pat_60	Pre-Treatment	DSTN	11034	37	20	17581488	17581489	Frame_Shift_Ins	INS	-	T	13	175	c.109_110insT	c.(109-111)ATTfs	p.I37fs
Pat_60	Pre-Treatment	GGT7	2686	37	20	33447805	33447805	Frame_Shift_Del	DEL	C	-	4	7	c.784delG	c.(784-786)GCCfs	p.A262fs
Pat_60	Pre-Treatment	KRTAP19-1	337882	37	21	31852433	31852433	Frame_Shift_Del	DEL	A	-	9	1443	c.204delT	c.(202-204)TTTfs	p.F68fs
Pat_60	Pre-Treatment	GABRG1	2565	37	4	46060358	46060358	Frame_Shift_Del	DEL	A	-	7	128	c.792delT	c.(790-792)TTTfs	p.F264fs
Pat_60	Pre-Treatment	SEC31A	22872	37	4	83745800	83745800	Frame_Shift_Del	DEL	T	-	8	118	c.3319delA	c.(3319-3321)ATTfs	p.I1107fs
Pat_60	Pre-Treatment	MAST4	375449	37	5	66459466	66459466	Frame_Shift_Del	DEL	C	-	5	3	c.3892delC	c.(3892-3894)CAGfs	p.Q1298fs
Pat_60	Pre-Treatment	RHOBTB3	22836	37	5	95124535	95124535	Frame_Shift_Del	DEL	C	-	7	151	c.1693delC	c.(1693-1695)CAAfs	p.Q565fs
Pat_60	Pre-Treatment	RIOK2	55781	37	5	96503489	96503490	Frame_Shift_Del	DEL	TC	-	7	354	c.1078_1079delGA	c.(1078-1080)GAAfs	p.E360fs
Pat_60	Pre-Treatment	RAPGEF6	51735	37	5	130815369	130815369	Frame_Shift_Del	DEL	T	-	12	245	c.1918delA	c.(1918-1920)AGTfs	p.S640fs
Pat_60	Pre-Treatment	CYP51A1	1595	37	7	91752494	91752494	Frame_Shift_Del	DEL	T	-	10	522	c.1026delA	c.(1024-1026)AAAfs	p.K342fs
Pat_60	Pre-Treatment	TTC16	158248	37	9	130493470	130493471	Frame_Shift_Del	DEL	CC	-	4	6	c.2408_2409delCC	c.(2407-2409)ACCfs	p.T803fs
Pat_60	Pre-Treatment	CACNA1B	774	37	9	140865845	140865846	Frame_Shift_Del	DEL	CG	-	4	2	c.1344_1345delCG	c.(1342-1347)TTCGCCfs	p.F448fs
Pat_60	Pre-Treatment	MED12	9968	37	X	70360680	70360682	In_Frame_Del	DEL	GCA	-	5	7	.6240_6242delGC	(6238-6243)CGGCAG>CG	p.Q2086del
Pat_60	Pre-Treatment	ABCD1	215	37	X	152991116	152991116	Frame_Shift_Del	DEL	G	-	2	4	c.395delG	c.(394-396)TGGfs	p.W132fs

Pat_60	Post-Resistance	RPL22	6146	37	1	6257785	6257785	Frame_Shift_Del	DEL	T	-	8	151	c.44delA	c.(43-45)AAGfs	p.K15fs
Pat_60	Post-Resistance	ARID1A	8289	37	1	27105931	27105931	Frame_Shift_Del	DEL	G	-	7	275	c.5542delG	c.(5542-5544)GGGfs	p.G1848fs
Pat_60	Post-Resistance	PHACTR4	65979	37	1	28800272	28800273	Frame_Shift_Ins	INS	-	C	7	481	c.1030_1031insC	c.(1030-1032)TCCfs	p.S344fs
Pat_60	Post-Resistance	GBP7	388646	37	1	89613322	89613322	Frame_Shift_Del	DEL	C	-	9	365	c.1293delG	c.(1291-1293)GGGfs	p.G431fs
Pat_60	Post-Resistance	SLC16A4	9122	37	1	110906426	110906427	Frame_Shift_Ins	INS	-	A	8	225	c.1425_1426insT	c.(1423-1428)TTTGTAfs	p.F475fs
Pat_60	Post-Resistance	APOBEC4	403314	37	1	183616826	183616828	In_Frame_Del	DEL	TTC	-	9	562	.1089_1091delGA	.(1087-1092)AAGAAA>AA	.363_364KK>
Pat_60	Post-Resistance	IPO9	55705	37	1	201843998	201844000	In_Frame_Del	DEL	GAG	-	7	225	.2872_2874delGA	c.(2872-2874)GAGdel	p.E962del
Pat_60	Post-Resistance	ZNF33A	7581	37	10	38345019	38345020	Frame_Shift_Del	DEL	AG	-	7	303	.1964_1965delA	c.(1963-1965)CAGfs	p.Q655fs
Pat_60	Post-Resistance	8-Mar	220972	37	10	45953876	45953878	In_Frame_Del	DEL	GAG	-	98	293	c.685_687delCTC	c.(685-687)CTCdel	p.L229del
Pat_60	Post-Resistance	TACC2	10579	37	10	123970380	123970380	Frame_Shift_Del	DEL	C	-	10	673	c.6440delC	c.(6439-6441)ACCfs	p.T2147fs
Pat_60	Post-Resistance	OR8D4	338662	37	11	123777441	123777442	Frame_Shift_Ins	INS	-	T	13	760	c.303_304insT	c.(301-306)CTGTTTfs	p.L101fs
Pat_60	Post-Resistance	GLB1L3	112937	37	11	134181005	134181005	Frame_Shift_Del	DEL	C	-	8	942	c.1228delC	c.(1228-1230)CCCfs	p.P410fs
Pat_60	Post-Resistance	PRB2	653247	37	12	11546732	11546733	In_Frame_Ins	INS	-	AGA	7	785	c.279_280insTCT	c.(277-282)insTCT	p.93_94insS
Pat_60	Post-Resistance	PRB2	653247	37	12	11546856	11546858	In_Frame_Del	DEL	AGA	-	8	503	c.154_156delTCT	c.(154-156)TCTdel	p.S52del
Pat_60	Post-Resistance	FAR2	55711	37	12	29450110	29450110	Frame_Shift_Del	DEL	A	-	9	364	c.522delA	c.(520-522)CCAfs	p.P174fs
Pat_60	Post-Resistance	KRT1	3848	37	12	53069236	53069256	In_Frame_Del	DEL	TACCTCCG	-	4	7	ITGGCTCCGGAG	ATGGCTCCGGAGGTAG	_559YGSGGS
Pat_60	Post-Resistance	CBX5	23468	37	12	54645832	54645832	Frame_Shift_Del	DEL	T	-	14	600	c.317delA	c.(316-318)AAGfs	p.K106fs
Pat_60	Post-Resistance	OR10A7	121364	37	12	55615114	55615116	In_Frame_Del	DEL	CTT	-	11	542	c.306_308delCTT	c.(304-309)TACTTC>TAC	p.F107del
Pat_60	Post-Resistance	MARS	4141	37	12	57883053	57883053	Frame_Shift_Del	DEL	T	-	12	136	c.204delT	c.(202-204)TATfs	p.Y68fs
Pat_60	Post-Resistance	IRAK3	11213	37	12	66610954	66610954	Frame_Shift_Del	DEL	A	-	9	1711	c.592delA	c.(592-594)AAAfs	p.K198fs
Pat_60	Post-Resistance	TMTC3	160418	37	12	88566417	88566417	Frame_Shift_Del	DEL	T	-	10	512	c.1094delT	c.(1093-1095)CTTfs	p.L365fs
Pat_60	Post-Resistance	PWP1	11137	37	12	108105958	108105958	Frame_Shift_Del	DEL	T	-	7	473	c.1467delT	c.(1465-1467)CCTfs	p.P489fs
Pat_60	Post-Resistance	TPTE2	93492	37	13	20041394	20041394	Frame_Shift_Del	DEL	A	-	9	203	c.483delT	c.(481-483)TTTfs	p.F161fs
Pat_60	Post-Resistance	SACS	26278	37	13	23914687	23914687	Frame_Shift_Del	DEL	T	-	20	889	c.3328delA	c.(3328-3330)ATTfs	p.I1110fs
Pat_60	Post-Resistance	SPG20	23111	37	13	36903501	36903501	Frame_Shift_Del	DEL	T	-	8	688	c.1162delA	c.(1162-1164)AGGfs	p.R388fs
Pat_60	Post-Resistance	KIAA1704	55425	37	13	45580365	45580367	In_Frame_Del	DEL	GAT	-	7	660	c.250_252delGAT	c.(250-252)GATdel	p.D88del
Pat_60	Post-Resistance	DIAPH3	81624	37	13	60582733	60582734	Frame_Shift_Ins	INS	-	T	13	453	c.958_959insA	c.(958-960)ATTfs	p.I320fs
Pat_60	Post-Resistance	TOX4	9878	37	14	21961060	21961062	In_Frame_Del	DEL	GCT	-	10	327	.1285_1287delGC	c.(1285-1287)GCTdel	p.A434del
Pat_60	Post-Resistance	C14orf106	55320	37	14	45693722	45693722	Frame_Shift_Del	DEL	T	-	16	311	c.2068delA	c.(2068-2070)AGTfs	p.S690fs
Pat_60	Post-Resistance	MLH3	27030	37	14	75514603	75514604	Frame_Shift_Ins	INS	-	T	8	287	c.1755_1756insA	c.(1753-1758)AAAGAAfs	p.K585fs
Pat_60	Post-Resistance	FOXN3	1112	37	14	89629149	89629151	In_Frame_Del	DEL	GAG	-	7	40	.1080_1082delCT	.(1078-1083)TCCTCA>TC	.360_361SS>
Pat_60	Post-Resistance	DDX24	57062	37	14	94545821	94545823	In_Frame_Del	DEL	CCT	-	7	250	c.266_268delAGG	.(265-270)GAGGGA>GG	p.E89del
Pat_60	Post-Resistance	RAGE	5891	37	14	102718302	102718303	Frame_Shift_Ins	INS	-	T	8	252	c.313_314insA	c.(313-315)ATTfs	p.I105fs
Pat_60	Post-Resistance	GABRG3	2567	37	15	27765237	27765237	Frame_Shift_Del	DEL	A	-	8	88	c.832delA	c.(832-834)AAAfs	p.K278fs
Pat_60	Post-Resistance	DMXL2	23312	37	15	51828841	51828857	Frame_Shift_Del	DEL	TTACTGTG	-	32	388	6delCTCCCACAG	1836)GCTCCCACAGTAA	p.A607fs
Pat_60	Post-Resistance	SLC24A1	9187	37	15	65943128	65943130	In_Frame_Del	DEL	GAG	-	10	51	.2641_2643delGA	c.(2641-2643)GAGdel	p.E890del
Pat_60	Post-Resistance	BLM	641	37	15	91310208	91310208	Frame_Shift_Del	DEL	A	-	8	518	c.2262delA	c.(2260-2262)TCAfs	p.S754fs
Pat_60	Post-Resistance	CHD2	1106	37	15	93545433	93545434	Frame_Shift_Ins	INS	-	A	11	264	c.4164_4165insA	c.(4162-4167)ATGAAAfs	p.M1388fs
Pat_60	Post-Resistance	ITGAL	3683	37	16	30531249	30531251	In_Frame_Del	DEL	GCT	-	7	322	.3300_3302delGC	(3298-3303)GGGCTG>GG	p.L1106del
Pat_60	Post-Resistance	CCL17	6361	37	16	57447886	57447886	Frame_Shift_Del	DEL	G	-	4	9	c.42delG	c.(40-42)CTGfs	p.L14fs
Pat_60	Post-Resistance	MED9	55090	37	17	17394705	17394707	In_Frame_Del	DEL	CAG	-	12	278	c.337_339delCAG	c.(337-339)CAGdel	p.Q117del
Pat_60	Post-Resistance	CDC42EP4	23580	37	17	71281585	71281587	In_Frame_Del	DEL	TCC	-	7	172	.1053_1055delGG	.(1051-1056)GAGGAT>GA	p.E351del
Pat_60	Post-Resistance	SIRT6	51548	37	19	4180893	4180893	Frame_Shift_Del	DEL	G	-	7	82	c.80delC	c.(79-81)CCGfs	p.P27fs
Pat_60	Post-Resistance	CD3EAP	10849	37	19	45911859	45911861	In_Frame_Del	DEL	GAA	-	7	311	c.633_635delGAA	.(631-636)CGGAAG>CG	p.K217del
Pat_60	Post-Resistance	ODC1	4953	37	2	10583625	10583625	Frame_Shift_Del	DEL	A	-	8	701	c.657delT	c.(655-657)TTTfs	p.F219fs
Pat_60	Post-Resistance	BRE	9577	37	2	28521301	28521301	Frame_Shift_Del	DEL	A	-	8	564	c.1031delA	c.(1030-1032)CAAfs	p.Q344fs
Pat_60	Post-Resistance	FAM98A	25940	37	2	33813402	33813402	Frame_Shift_Del	DEL	T	-	11	585	c.522delA	c.(520-522)AAAfs	p.K174fs

Pat_60	Post-Resistance	EPAS1	2034	37	2	46607704	46607704	Frame_Shift_Del	DEL	G	-	7	226	c.1893delG	c.(1891-1893)ATGfs	p.M631fs
Pat_60	Post-Resistance	AFTPH	54812	37	2	64778672	64778674	In_Frame_Del	DEL	GAT	-	14	415	c.64_66delGAT	c.(64-66)GATdel	p.D26del
Pat_60	Post-Resistance	RGPD1	400966	37	2	87211874	87211875	Splice_Site	INS	-	C	12	201	c.2582_splice	c.e19-2	p.V861_splice
Pat_60	Post-Resistance	REV1	51455	37	2	100055102	100055102	Frame_Shift_Del	DEL	T	-	15	429	c.1174delA	c.(1174-1176)ATGfs	p.M392fs
Pat_60	Post-Resistance	AAMP	14	37	2	219134766	219134766	Frame_Shift_Del	DEL	G	-	9	1020	c.44delC	c.(43-45)CCAfs	p.P15fs
Pat_60	Post-Resistance	RQCD1	9125	37	2	219449364	219449364	Frame_Shift_Del	DEL	T	-	9	1065	c.350delT	c.(349-351)CTTfs	p.L117fs
Pat_60	Post-Resistance	USP40	55230	37	2	234394236	234394237	Frame_Shift_Ins	INS	-	T	7	130	c.3477_3478insA	c.(3475-3480)AAACAAfs	p.K1159fs
Pat_60	Post-Resistance	PANK2	80025	37	20	3893120	3893120	Frame_Shift_Del	DEL	T	-	10	728	c.1251delT	c.(1249-1251)ACTfs	p.T417fs
Pat_60	Post-Resistance	ZMYND8	23613	37	20	45875071	45875072	Frame_Shift_Ins	INS	-	T	8	422	c.1904_1905insA	c.(1903-1905)AAGfs	p.K635fs
Pat_60	Post-Resistance	SYCP2	10388	37	20	58467047	58467047	Frame_Shift_Del	DEL	T	-	14	207	c.2362delA	c.(2362-2364)ATGfs	p.M788fs
Pat_60	Post-Resistance	C22orf43	51233	37	22	23959767	23959769	In_Frame_Del	DEL	CAT	-	8	282	c.512_514delATG	c.(511-516)GATGCC>GCC	p.D171del
Pat_60	Post-Resistance	SH3BP1	23616	37	22	38039752	38039754	In_Frame_Del	DEL	AGG	-	7	173	c.575_577delAGG	c.(574-579)AAGGAG>AAG	p.E197del
Pat_60	Post-Resistance	TNRC6B	23112	37	22	40681767	40681767	Frame_Shift_Del	DEL	C	-	7	1077	c.3701delC	c.(3700-3702)TCCfs	p.S1234fs
Pat_60	Post-Resistance	FILIP1L	11259	37	3	99568272	99568273	Frame_Shift_Ins	INS	-	T	8	354	c.2247_2248insA	c.(2245-2250)AAACTAfs	p.K749fs
Pat_60	Post-Resistance	PCOLCE2	26577	37	3	142548586	142548586	Frame_Shift_Del	DEL	T	-	7	610	c.813delA	c.(811-813)AAAfs	p.K271fs
Pat_60	Post-Resistance	RNF168	165918	37	3	196214338	196214338	Frame_Shift_Del	DEL	T	-	8	1046	c.490delA	c.(490-492)AGGfs	p.R164fs
Pat_60	Post-Resistance	GRK4	2868	37	4	3015470	3015470	Frame_Shift_Del	DEL	A	-	8	327	c.656delA	c.(655-657)CAAfs	p.Q219fs
Pat_60	Post-Resistance	RFC1	5981	37	4	39290395	39290395	Frame_Shift_Del	DEL	T	-	7	241	c.3433delA	c.(3433-3435)AGTfs	p.S1145fs
Pat_60	Post-Resistance	SEC24B	10427	37	4	110402913	110402915	In_Frame_Del	DEL	GAG	-	8	464	.1141_1143delGA	c.(1141-1143)GAGdel	p.E384del
Pat_60	Post-Resistance	OTUD4	54726	37	4	146077123	146077125	In_Frame_Del	DEL	CAG	-	10	355	c.458_460delCTG	c.(457-462)GCTGAT>GAT	p.A153del
Pat_60	Post-Resistance	TMEM192	201931	37	4	166033911	166033912	Frame_Shift_Ins	INS	-	C	8	108	c.14_15insG	c.(13-15)GGCfs	p.G5fs
Pat_60	Post-Resistance	ZFR	51663	37	5	32404161	32404161	Frame_Shift_Del	DEL	T	-	11	379	c.1074delA	c.(1072-1074)AAAfs	p.K358fs
Pat_60	Post-Resistance	LMNB1	4001	37	5	126168434	126168436	In_Frame_Del	DEL	GAG	-	7	382	.1660_1662delGA	c.(1660-1662)GAGdel	p.E559del
Pat_60	Post-Resistance	SLC22A4	6583	37	5	131676327	131676327	Frame_Shift_Del	DEL	T	-	9	333	c.1514delT	c.(1513-1515)CTTfs	p.L505fs
Pat_60	Post-Resistance	NRG2	9542	37	5	139422532	139422534	In_Frame_Del	DEL	GCT	-	2	4	c.121_123delAGC	c.(121-123)AGCdel	p.S41del
Pat_60	Post-Resistance	RBM27	54439	37	5	145647319	145647320	Frame_Shift_Ins	INS	-	A	8	179	c.2439_2440insA	c.(2437-2442)CTTAAAfs	p.L813fs
Pat_60	Post-Resistance	KIAA1949	170954	37	6	30653494	30653496	In_Frame_Del	DEL	TGC	-	8	109	c.300_302delGCA	c.(298-303)CAGCAA>CAA	.100_101QQ>
Pat_60	Post-Resistance	TREML2	79865	37	6	41168714	41168716	In_Frame_Del	DEL	CAG	-	7	65	c.31_33delCTG	c.(31-33)CTGdel	p.L11del
Pat_60	Post-Resistance	FOXP4	116113	37	6	41555186	41555186	Frame_Shift_Del	DEL	C	-	7	196	c.808delC	c.(808-810)CCCfs	p.P270fs
Pat_60	Post-Resistance	GRIK2	2898	37	6	102503432	102503432	Frame_Shift_Del	DEL	A	-	12	472	c.2539delA	c.(2539-2541)AAAfs	p.K847fs
Pat_60	Post-Resistance	FYN	2534	37	6	111983042	111983042	Frame_Shift_Del	DEL	T	-	7	527	c.1514delA	c.(1513-1515)AAGfs	p.K505fs
Pat_60	Post-Resistance	WISP3	8838	37	6	112389434	112389434	Frame_Shift_Del	DEL	A	-	12	142	c.616delA	c.(616-618)AAAfs	p.K206fs
Pat_60	Post-Resistance	C6orf174	387104	37	6	127804080	127804080	Frame_Shift_Del	DEL	T	-	8	616	c.1535delA	c.(1534-1536)AAGfs	p.K512fs
Pat_60	Post-Resistance	IFNGR1	3459	37	6	137519505	137519506	Frame_Shift_Del	DEL	CT	-	8	453	c.1132_1133delAG	c.(1132-1134)AGTfs	p.S378fs
Pat_60	Post-Resistance	MTHFD1L	25902	37	6	151358163	151358164	Frame_Shift_Ins	INS	-	A	7	276	c.2757_2758insA	c.(2755-2760)GACAAAfs	p.D919fs
Pat_60	Post-Resistance	ZDHHC4	55146	37	7	6621848	6621849	Frame_Shift_Ins	INS	-	T	9	777	c.336_337insT	c.(334-339)CTGTTTfs	p.L112fs
Pat_60	Post-Resistance	RSPH10B2	728194	37	7	6797480	6797480	Frame_Shift_Del	DEL	A	-	7	554	c.172delA	c.(172-174)AAAfs	p.K58fs
Pat_60	Post-Resistance	OSBPL3	26031	37	7	24910452	24910453	Frame_Shift_Del	DEL	TC	-	7	192	c.279_280delGA	c.(277-282)GAGAAGfs	p.E93fs
Pat_60	Post-Resistance	AEBP1	165	37	7	44153765	44153767	In_Frame_Del	DEL	GAG	-	7	159	.3382_3384delGA	c.(3382-3384)GAGdel	p.E1132del
Pat_60	Post-Resistance	TMEM60	85025	37	7	77423460	77423460	Frame_Shift_Del	DEL	T	-	19	568	c.231delA	c.(229-231)AAAfs	p.K77fs
Pat_60	Post-Resistance	ABCB4	5244	37	7	87032544	87032544	Frame_Shift_Del	DEL	T	-	7	831	c.3561delA	c.(3559-3561)AAAfs	p.K1187fs
Pat_60	Post-Resistance	ABCB4	5244	37	7	87074281	87074282	Frame_Shift_Ins	INS	-	A	9	134	c.1015_1016insT	c.(1015-1017)TCAfs	p.S339fs
Pat_60	Post-Resistance	CYP51A1	1595	37	7	91752494	91752494	Frame_Shift_Del	DEL	T	-	12	737	c.1026delA	c.(1024-1026)AAAfs	p.K342fs
Pat_60	Post-Resistance	CCDC132	55610	37	7	92923947	92923948	Frame_Shift_Ins	INS	-	G	10	630	c.1166_1167insG	c.(1165-1167)CAGfs	p.Q389fs
Pat_60	Post-Resistance	LMTK2	22853	37	7	97820131	97820132	Frame_Shift_Del	DEL	AG	-	9	1324	c.1090_1091delAG	c.(1090-1092)AGAfs	p.R364fs
Pat_60	Post-Resistance	STAG3	10734	37	7	99802723	99802723	Frame_Shift_Del	DEL	C	-	10	907	c.3047delC	c.(3046-3048)TCCfs	p.S1016fs
Pat_60	Post-Resistance	OR9A4	130075	37	7	141619203	141619203	Frame_Shift_Del	DEL	T	-	12	635	c.528delT	c.(526-528)AATfs	p.N176fs

Pat_60	Post-Resistance	XRCC2	7516	37	7	152346220	152346220	Frame_Shift_Del	DEL	A	-	9	377	c.350delT	c.(349-351)TTGfs	p.L117fs
Pat_60	Post-Resistance	RBM33	155435	37	7	155531073	155531074	Frame_Shift_Del	DEL	CA	-	14	347	.1713_1714delC	c.(1711-1716)CCCACAfs	p.P571fs
Pat_60	Post-Resistance	C8orf80	389643	37	8	27888776	27888776	Frame_Shift_Del	DEL	T	-	8	428	c.1892delA	c.(1891-1893)AATfs	p.N631fs
Pat_60	Post-Resistance	MYST3	7994	37	8	41836184	41836184	Frame_Shift_Del	DEL	T	-	9	1560	c.1019delA	c.(1018-1020)AACfs	p.N340fs
Pat_60	Post-Resistance	PCMTD1	115294	37	8	52733063	52733063	Frame_Shift_Del	DEL	T	-	14	191	c.922delA	c.(922-924)ATGfs	p.M308fs
Pat_60	Post-Resistance	PTPLAD2	401494	37	9	21007045	21007046	Frame_Shift_Ins	INS	-	T	9	235	c.689_690insA	c.(688-690)AAGfs	p.K230fs
Pat_60	Post-Resistance	NDOR1	27158	37	9	140100743	140100743	Frame_Shift_Del	DEL	C	-	7	807	c.195delC	c.(193-195)GACfs	p.D65fs
Pat_60	Post-Resistance	PASD1	139135	37	X	150817142	150817144	In_Frame_Del	DEL	GCT	-	7	273	c.685_687delGCT	c.(685-687)GCTdel	p.A236del
Pat_60	Post-Resistance	F8	2157	37	X	154157686	154157686	Frame_Shift_Del	DEL	T	-	9	170	c.4379delA	c.(4378-4380)AATfs	p.N1460fs
Pat_65	Pre-Treatment	ESPNP	284729	37	1	17034125	17034126	Frame_Shift_Ins	INS	-	AGCT	11	54	.364_365insAGC	c.(364-366)TGGfs	p.W122fs
Pat_65	Pre-Treatment	FAM43B	163933	37	1	20880268	20880270	In_Frame_Del	DEL	GAG	-	11	63	c.802_804delGAG	c.(802-804)GAGdel	p.E272del
Pat_65	Pre-Treatment	DLGAP3	58512	37	1	35370281	35370283	In_Frame_Del	DEL	TGG	-	9	518	c.702_704delCCA	.(700-705)CACCAG>CA	p.H234del
Pat_65	Pre-Treatment	TRIM33	51592	37	1	114968116	114968118	In_Frame_Del	DEL	TGT	-	10	1315	.1648_1650delAC	c.(1648-1650)ACAdel	p.T550del
Pat_65	Pre-Treatment	PIAS3	10401	37	1	145579285	145579285	Frame_Shift_Del	DEL	C	-	7	1032	c.622delC	c.(622-624)CCCfs	p.P208fs
Pat_65	Pre-Treatment	LOC200030	200030	37	1	148016436	148016436	Frame_Shift_Del	DEL	T	-	8	1057	c.1826delA	c.(1825-1827)AAGfs	p.K609fs
Pat_65	Pre-Treatment	LCE4A	199834	37	1	152681693	152681698	In_Frame_Del	DEL	TGTGGT	-	7	244	142_147delTGTG	c.(142-147)TGTGGTdel	p.CG48del
Pat_65	Pre-Treatment	PBXIP1	57326	37	1	154917508	154917510	In_Frame_Del	DEL	GGT	-	10	354	.2186_2188delAC	(2185-2190)CACCGG>CG	p.H729del
Pat_65	Pre-Treatment	LMX1A	4009	37	1	165177332	165177334	In_Frame_Del	DEL	TGC	-	7	113	c.783_785delGCA	c.(781-786)CAGCAA>CA	.261_262QQ>
Pat_65	Pre-Treatment	BAT2L2	23215	37	1	171511149	171511149	Frame_Shift_Del	DEL	A	-	8	159	c.4538delA	c.(4537-4539)GAAfs	p.E1513fs
Pat_65	Pre-Treatment	PRG4	10216	37	1	186276256	186276257	In_Frame_Ins	INS	-	CCA	7	274	.1405_1406insCC	(1405-1407)CCC>CCCAC	p.471_472insT
Pat_65	Pre-Treatment	PRG4	10216	37	1	186276374	186276376	In_Frame_Del	DEL	CCA	-	15	492	.1523_1525delCC	(1522-1527)CCCACC>CC	p.T511del
Pat_65	Pre-Treatment	GPATCH2	55105	37	1	217793189	217793189	Frame_Shift_Del	DEL	G	-	7	251	c.709delC	c.(709-711)CAGfs	p.Q237fs
Pat_65	Pre-Treatment	OBSCN	84033	37	1	228475979	228475980	Frame_Shift_Del	DEL	GT	-	9	358	10029_10030delG	.(10027-10032)TCGTGTf	p.S3343fs
Pat_65	Pre-Treatment	SFMBT2	57713	37	10	7212995	7212997	In_Frame_Del	DEL	CTC	-	8	830	.2437_2439delGA	c.(2437-2439)GAGdel	p.E813del
Pat_65	Pre-Treatment	PCDH15	65217	37	10	55698620	55698620	Frame_Shift_Del	DEL	C	-	7	365	c.3328delG	c.(3328-3330)GATfs	p.D1110fs
Pat_65	Pre-Treatment	ZMIZ1	57178	37	10	81072446	81072446	Frame_Shift_Del	DEL	C	-	7	1007	c.3144delC	c.(3142-3144)GACfs	p.D1048fs
Pat_65	Pre-Treatment	C10orf26	54838	37	10	104569669	104569671	In_Frame_Del	DEL	CAT	-	8	675	c.150_152delCAT	c.(148-153)ACCATC>ACC	p.I54del
Pat_65	Pre-Treatment	MUC6	4588	37	11	1031058	1031059	Splice_Site	INS	-	G	6	12	c.575_splice	c.e6-1	p.G192_splice
Pat_65	Pre-Treatment	DNHD1	144132	37	11	6578614	6578616	In_Frame_Del	DEL	GAG	-	7	52	.8089_8091delGA	c.(8089-8091)GAGdel	p.E2703del
Pat_65	Pre-Treatment	PRMT3	10196	37	11	20424503	20424503	Frame_Shift_Del	DEL	C	-	7	591	c.744delC	c.(742-744)TACfs	p.Y248fs
Pat_65	Pre-Treatment	MYBPC3	4607	37	11	47359101	47359103	In_Frame_Del	DEL	TCT	-	8	230	.2441_2443delAG	(2440-2445)AAGAGC>AG	p.K814del
Pat_65	Pre-Treatment	FADS2	9415	37	11	61615748	61615748	Frame_Shift_Del	DEL	C	-	11	1343	c.736delC	c.(736-738)CCCfs	p.P246fs
Pat_65	Pre-Treatment	C11orf95	65998	37	11	63531514	63531516	In_Frame_Del	DEL	CTC	-	9	86	.1579_1581delGA	c.(1579-1581)GAGdel	p.E527del
Pat_65	Pre-Treatment	C11orf95	65998	37	11	63533335	63533337	In_Frame_Del	DEL	TCC	-	11	66	c.579_581delGGA	.(577-582)GAGGAA>GA	.193_194EE>
Pat_65	Pre-Treatment	AIP	9049	37	11	67250670	67250670	Frame_Shift_Del	DEL	A	-	8	617	c.41delA	c.(40-42)CAAfs	p.Q14fs
Pat_65	Pre-Treatment	CD3G	917	37	11	118220583	118220583	Frame_Shift_Del	DEL	A	-	7	144	c.205delA	c.(205-207)AAAfs	p.K69fs
Pat_65	Pre-Treatment	CBL	867	37	11	119149356	119149358	In_Frame_Del	DEL	ATG	-	7	292	.1364_1366delAT	.(1363-1368)TATGAT>TA	p.D460del
Pat_65	Pre-Treatment	IFFO1	25900	37	12	6649704	6649706	In_Frame_Del	DEL	GGC	-	8	376	.1623_1625delGC	(1621-1626)CCGCCA>CC	.541_542PP>
Pat_65	Pre-Treatment	C1R	715	37	12	7187850	7187851	Frame_Shift_Ins	INS	-	T	7	469	c.2103_2104insA	c.(2101-2106)ATGGAGfs	p.M701fs
Pat_65	Pre-Treatment	PRB1	5542	37	12	11506632	11506633	In_Frame_Ins	INS	-	GGA	29	1425	c.404_405insTCC	c.(403-405)CCA>CCTCC	.135_135P>P
Pat_65	Pre-Treatment	PRB2	653247	37	12	11546233	11546235	In_Frame_Del	DEL	GGA	-	7	444	c.777_779delTCC	c.(775-780)CCTCCA>CC	.259_260PP>
Pat_65	Pre-Treatment	PRB2	653247	37	12	11546544	11546545	In_Frame_Ins	INS	-	GGA	8	1129	c.467_468insTCC	c.(466-468)CCA>CCTCC	.156_156P>P
Pat_65	Pre-Treatment	PRB2	653247	37	12	11546727	11546728	In_Frame_Ins	INS	-	GGA	26	1664	c.284_285insTCC	c.(283-285)CCA>CCTCCA	p.95_95P>PP
Pat_65	Pre-Treatment	PRB2	653247	37	12	11546732	11546733	In_Frame_Ins	INS	-	AGA	24	1527	c.279_280insTCT	c.(277-282)insTCT	p.93_94insS
Pat_65	Pre-Treatment	PRB2	653247	37	12	11546788	11546790	In_Frame_Del	DEL	GGA	-	28	577	c.222_224delTCC	c.(220-225)CCTCCA>CCA	p.74_75PP>P
Pat_65	Pre-Treatment	IFLTD1	160492	37	12	25679737	25679738	Frame_Shift_Del	DEL	GG	-	7	1096	c.580_581delCC	c.(580-582)CCAfs	p.P194fs
Pat_65	Pre-Treatment	FAR2	55711	37	12	29450110	29450110	Frame_Shift_Del	DEL	A	-	7	618	c.522delA	c.(520-522)CCAfs	p.P174fs

Pat_65	Pre-Treatment	CACNB3	784	37	12	49220567	49220567	Frame_Shift_Del	DEL	G	-	8	2265	c.920delG	c.(919-921)CGGfs	p.R307fs
Pat_65	Pre-Treatment	WNT1	7471	37	12	49373295	49373295	Frame_Shift_Del	DEL	C	-	9	437	c.149delC	c.(148-150)TCCfs	p.S50fs
Pat_65	Pre-Treatment	PRPF40B	25766	37	12	50025258	50025258	Frame_Shift_Del	DEL	C	-	12	704	c.93delC	c.(91-93)ATCfs	p.I31fs
Pat_65	Pre-Treatment	LRP1	4035	37	12	57572242	57572242	Frame_Shift_Del	DEL	G	-	8	610	c.4462delG	c.(4462-4464)GGGfs	p.G1488fs
Pat_65	Pre-Treatment	NAP1L1	4673	37	12	76454023	76454024	Frame_Shift_Del	DEL	GA	-	8	674	c.242_243delTC	c.(241-243)CTCfs	p.L81fs
Pat_65	Pre-Treatment	C12orf42	374470	37	12	103695960	103695960	Frame_Shift_Del	DEL	G	-	11	647	c.1009delC	c.(1009-1011)CGCfs	p.R337fs
Pat_65	Pre-Treatment	NT5DC3	51559	37	12	104187016	104187016	Frame_Shift_Del	DEL	C	-	7	1453	c.945delG	c.(943-945)GGGfs	p.G315fs
Pat_65	Pre-Treatment	KNTC1	9735	37	12	123068869	123068870	Frame_Shift_Del	DEL	TA	-	18	900	c.3308_3309delTA	c.(3307-3309)CTAfs	p.L1103fs
Pat_65	Pre-Treatment	SBNO1	55206	37	12	123794283	123794283	Frame_Shift_Del	DEL	T	-	12	464	c.3416delA	c.(3415-3417)AATfs	p.N1139fs
Pat_65	Pre-Treatment	PABPC3	5042	37	13	25671273	25671273	Frame_Shift_Del	DEL	G	-	20	1616	c.937delG	c.(937-939)GCGfs	p.A313fs
Pat_65	Pre-Treatment	PABPC3	5042	37	13	25671333	25671333	Frame_Shift_Del	DEL	A	-	8	777	c.997delA	c.(997-999)AAAfs	p.K333fs
Pat_65	Pre-Treatment	RNF6	6049	37	13	26788241	26788241	Frame_Shift_Del	DEL	A	-	10	602	c.1778delT	c.(1777-1779)TTAfs	p.L593fs
Pat_65	Pre-Treatment	WASF3	10810	37	13	27255386	27255387	Frame_Shift_Ins	INS	-	C	7	245	c.912_913insC	c.(910-915)CCGCCCfs	p.P304fs
Pat_65	Pre-Treatment	LRCH1	23143	37	13	47243183	47243186	Frame_Shift_Del	DEL	CCTG	-	8	1210	.471_474delCCT	c.(469-474)GCCCTGfs	p.A157fs
Pat_65	Pre-Treatment	LMO7	4008	37	13	76415307	76415308	Frame_Shift_Del	DEL	AG	-	7	370	.2946_2947delA	c.(2944-2949)GCAGAGfs	p.A982fs
Pat_65	Pre-Treatment	TRPM1	4308	37	15	31362391	31362391	Frame_Shift_Del	DEL	G	-	8	1453	c.56delC	c.(55-57)CCTfs	p.P19fs
Pat_65	Pre-Treatment	NOX5	79400	37	15	69328208	69328210	In_Frame_Del	DEL	CTG	-	8	1108	.1120_1122delCT	c.(1120-1122)CTGdel	p.L380del
Pat_65	Pre-Treatment	POLG	5428	37	15	89876828	89876830	In_Frame_Del	DEL	TGC	-	10	116	c.156_158delGCA	c.(154-159)CAGCAA>CAA	p.52_53QQ>Q
Pat_65	Pre-Treatment	CD2BP2	10421	37	16	30365550	30365552	In_Frame_Del	DEL	CAT	-	9	1732	c.170_172delATG	.(169-174)GATGGG>GG	p.D57del
Pat_65	Pre-Treatment	SALL1	6299	37	16	51175655	51175656	In_Frame_Ins	INS	-	GCT	18	45	c.477_478insAGC	c.(475-480)insAGC	p.159_160insS
Pat_65	Pre-Treatment	PLD2	5338	37	17	4713029	4713029	Frame_Shift_Del	DEL	G	-	8	906	c.658delG	c.(658-660)GGCfs	p.G220fs
Pat_65	Pre-Treatment	DHX33	56919	37	17	5372037	5372039	In_Frame_Del	DEL	CCT	-	8	123	c.141_143delAGG	.(139-144)GGAGGC>GG	p.47_48GG>G
Pat_65	Pre-Treatment	CHRNB1	1140	37	17	7357666	7357668	In_Frame_Del	DEL	CTG	-	9	905	c.871_873delCTG	c.(871-873)CTGdel	p.L294del
Pat_65	Pre-Treatment	CHD3	1107	37	17	7788212	7788214	In_Frame_Del	DEL	GAG	-	16	124	c.88_90delGAG	c.(88-90)GAGdel	p.E35del
Pat_65	Pre-Treatment	CHD3	1107	37	17	7801857	7801859	In_Frame_Del	DEL	AAG	-	9	225	.2095_2097delAA	c.(2095-2097)AAGdel	p.K703del
Pat_65	Pre-Treatment	SMCR7	125170	37	17	18167778	18167780	In_Frame_Del	DEL	GCT	-	12	187	.1065_1067delGC	(1063-1068)CGGCTG>CG	p.L360del
Pat_65	Pre-Treatment	WSB1	26118	37	17	25636240	25636241	Frame_Shift_Del	DEL	TA	-	7	1062	c.826_827delTA	c.(826-828)TATfs	p.Y276fs
Pat_65	Pre-Treatment	SUPT6H	6830	37	17	27001303	27001305	In_Frame_Del	DEL	GAG	-	9	248	c.112_114delGAG	c.(112-114)GAGdel	p.E43del
Pat_65	Pre-Treatment	ZNF207	7756	37	17	30677314	30677316	In_Frame_Del	DEL	AAG	-	14	1112	c.10_12delAAG	c.(10-12)AAGdel	p.K7del
Pat_65	Pre-Treatment	CDC6	990	37	17	38457159	38457159	Frame_Shift_Del	DEL	T	-	9	861	c.1329delT	c.(1327-1329)GGTfs	p.G443fs
Pat_65	Pre-Treatment	KRT10	3858	37	17	38978766	38978768	In_Frame_Del	DEL	TCC	-	23	162	c.70_72delGGA	c.(70-72)GGAdel	p.G24del
Pat_65	Pre-Treatment	KCNH4	23415	37	17	40328258	40328259	Frame_Shift_Ins	INS	-	C	8	560	c.642_643insG	c.(640-645)GGGTCTfs	p.G214fs
Pat_65	Pre-Treatment	XYLT2	64132	37	17	48433967	48433967	Frame_Shift_Del	DEL	C	-	8	357	c.1578delC	c.(1576-1578)TACfs	p.Y526fs
Pat_65	Pre-Treatment	BPTF	2186	37	17	65822267	65822269	In_Frame_Del	DEL	GAG	-	11	65	c.427_429delGAG	c.(427-429)GAGdel	p.E148del
Pat_65	Pre-Treatment	ITGB4	3691	37	17	73732157	73732158	Frame_Shift_Del	DEL	GT	-	9	1282	.1683_1684delG	c.(1681-1686)CAGTGTfs	p.Q561fs
Pat_65	Pre-Treatment	SS18	6760	37	18	23619289	23619289	Frame_Shift_Del	DEL	G	-	7	1142	c.739delC	c.(739-741)CAGfs	p.Q247fs
Pat_65	Pre-Treatment	WDR7	23335	37	18	54358513	54358513	Frame_Shift_Del	DEL	G	-	7	429	c.784delG	c.(784-786)GGGfs	p.G262fs
Pat_65	Pre-Treatment	ALPK2	115701	37	18	56246440	56246440	Frame_Shift_Del	DEL	T	-	8	1390	c.1568delA	c.(1567-1569)AAGfs	p.K523fs
Pat_65	Pre-Treatment	CCDC159	126075	37	19	11459665	11459666	Frame_Shift_Ins	INS	-	A	12	7	c.64_65insA	c.(64-66)GAGfs	p.E22fs
Pat_65	Pre-Treatment	ECSIT	51295	37	19	11618820	11618821	Frame_Shift_Ins	INS	-	G	7	787	c.781_782insC	c.(781-783)CAGfs	p.Q261fs
Pat_65	Pre-Treatment	KIAA1683	80726	37	19	18378236	18378236	Frame_Shift_Del	DEL	G	-	7	746	c.114delC	c.(112-114)CCCfs	p.P38fs
Pat_65	Pre-Treatment	SBSN	374897	37	19	36019046	36019047	Frame_Shift_Del	DEL	CT	-	7	983	c.137_138delAG	c.(136-138)GAGfs	p.E46fs
Pat_65	Pre-Treatment	ZFP36	7538	37	19	39898948	39898950	In_Frame_Del	DEL	CAC	-	9	1036	c.590_592delCAC	c.(589-594)TCACCA>TCA	p.P201del
Pat_65	Pre-Treatment	SFRS16	11129	37	19	45567607	45567609	In_Frame_Del	DEL	CTC	-	7	73	.1128_1130delCT	(1126-1131)CGCTCC>CG	p.S385del
Pat_65	Pre-Treatment	KLC3	147700	37	19	45850756	45850758	In_Frame_Del	DEL	GAG	-	12	460	c.541_543delGAG	c.(541-543)GAGdel	p.E184del
Pat_65	Pre-Treatment	GLTSCR1	29998	37	19	48197891	48197891	Frame_Shift_Del	DEL	C	-	7	202	c.2803delC	c.(2803-2805)CCCfs	p.P935fs
Pat_65	Pre-Treatment	ZNF175	7728	37	19	52091415	52091416	Frame_Shift_Del	DEL	AG	-	7	697	.1831_1832delA	c.(1831-1833)AGAfs	p.R611fs

Pat_65	Pre-Treatment	CNOT3	4849	37	19	54656613	54656613	Frame_Shift_Del	DEL	C	-	7	891	c.1914delC	c.(1912-1914)CTCfs	p.L638fs
Pat_65	Pre-Treatment	NTSR2	23620	37	2	11810004	11810006	In_Frame_Del	DEL	CAG	-	10	111	c.250_252delCTG	c.(250-252)CTGdel	p.L84del
Pat_65	Pre-Treatment	KIF3C	3797	37	2	26203464	26203466	In_Frame_Del	DEL	GTT	-	12	609	.1321_1323delAA	c.(1321-1323)AACdel	p.N441del
Pat_65	Pre-Treatment	FAM98A	25940	37	2	33813402	33813402	Frame_Shift_Del	DEL	T	-	7	499	c.522delA	c.(520-522)AAAfs	p.K174fs
Pat_65	Pre-Treatment	RIF1	55183	37	2	152293790	152293790	Frame_Shift_Del	DEL	T	-	9	673	c.1408delT	c.(1408-1410)TTTfs	p.F470fs
Pat_65	Pre-Treatment	FN1	2335	37	2	216285432	216285433	Frame_Shift_Del	DEL	CG	-	8	684	.1638_1639delC	c.(1636-1641)TTCGGTfs	p.F546fs
Pat_65	Pre-Treatment	SLC11A1	6556	37	2	219252307	219252307	Frame_Shift_Del	DEL	T	-	10	1106	c.591delT	c.(589-591)GCTfs	p.A197fs
Pat_65	Pre-Treatment	CCDC108	255101	37	2	219868691	219868692	Frame_Shift_Ins	INS	-	T	7	1402	c.5537_5538insA	c.(5536-5538)GAGfs	p.E1846fs
Pat_65	Pre-Treatment	TMEM90B	79953	37	20	24524183	24524185	In_Frame_Del	DEL	GGA	-	10	798	c.450_452delGGA	.(448-453)GTGGAG>GT	p.E155del
Pat_65	Pre-Treatment	EMILIN3	90187	37	20	39990829	39990829	Frame_Shift_Del	DEL	C	-	9	694	c.1380delG	c.(1378-1380)GGGfs	p.G460fs
Pat_65	Pre-Treatment	WFDC3	140686	37	20	44417572	44417572	Frame_Shift_Del	DEL	T	-	7	1524	c.209delA	c.(208-210)AAGfs	p.K70fs
Pat_65	Pre-Treatment	SALL4	57167	37	20	50408526	50408526	Frame_Shift_Del	DEL	G	-	8	1030	c.496delC	c.(496-498)CAGfs	p.Q166fs
Pat_65	Pre-Treatment	KRTAP21-1	337977	37	21	32127578	32127578	Frame_Shift_Del	DEL	C	-	15	1971	c.119delG	c.(118-120)TGTfs	p.C40fs
Pat_65	Pre-Treatment	TXN2	25828	37	22	36872888	36872888	Frame_Shift_Del	DEL	G	-	133	360	c.279delC	c.(277-279)TGCfs	p.C93fs
Pat_65	Pre-Treatment	TRIOBP	11078	37	22	38120392	38120400	In_Frame_Del	DEL	CTCCAGA	-	9	1028	_1837delCCTCC	8-1839)GCCTCCAGAACC	p.SRT611del
Pat_65	Pre-Treatment	POLR2F	5435	37	22	38363691	38363691	Frame_Shift_Del	DEL	G	-	8	824	c.353delG	c.(352-354)TGGfs	p.W118fs
Pat_65	Pre-Treatment	DDX17	10521	37	22	38881965	38881967	In_Frame_Del	DEL	GGA	-	8	474	.2169_2171delTC	(2167-2172)CCTCCC>CC	.723_724PP>
Pat_65	Pre-Treatment	MGAT3	4248	37	22	39884335	39884335	Frame_Shift_Del	DEL	T	-	8	567	c.983delT	c.(982-984)CTTfs	p.L328fs
Pat_65	Pre-Treatment	MAPK8IP2	23542	37	22	51041769	51041771	In_Frame_Del	DEL	GAG	-	10	65	c.289_291delGAG	c.(289-291)GAGdel	p.E103del
Pat_65	Pre-Treatment	XPC	7508	37	3	14219966	14219968	In_Frame_Del	DEL	CCT	-	7	216	c.101_103delAGG	c.(100-105)GAGGAT>GAT	p.E34del
Pat_65	Pre-Treatment	CLASP2	23122	37	3	33602361	33602361	Frame_Shift_Del	DEL	T	-	9	658	c.2869delA	c.(2869-2871)ATGfs	p.M957fs
Pat_65	Pre-Treatment	CDCP1	64866	37	3	45127479	45127479	Frame_Shift_Del	DEL	T	-	9	1588	c.2162delA	c.(2161-2163)AAGfs	p.K721fs
Pat_65	Pre-Treatment	MAP4	4134	37	3	47913510	47913510	Frame_Shift_Del	DEL	G	-	10	832	c.2403delC	c.(2401-2403)TCCfs	p.S801fs
Pat_65	Pre-Treatment	USP4	7375	37	3	49321969	49321971	In_Frame_Del	DEL	TCT	-	7	403	.2318_2320delAG	.(2317-2322)AAGACC>AC	p.K773del
Pat_65	Pre-Treatment	RAD54L2	23132	37	3	51624506	51624508	In_Frame_Del	DEL	GAG	-	7	85	c.70_72delGAG	c.(70-72)GAGdel	p.E30del
Pat_65	Pre-Treatment	ITIH4	3700	37	3	52847474	52847474	Frame_Shift_Del	DEL	G	-	7	664	c.2756delC	c.(2755-2757)CCGfs	p.P919fs
Pat_65	Pre-Treatment	VGLL3	389136	37	3	87027857	87027859	In_Frame_Del	DEL	CTC	-	16	203	c.220_222delGAG	c.(220-222)GAGdel	p.E74del
Pat_65	Pre-Treatment	OR5H14	403273	37	3	97868506	97868507	Frame_Shift_Del	DEL	TC	-	8	1163	c.277_278delTC	c.(277-279)TCTfs	p.S93fs
Pat_65	Pre-Treatment	ALCAM	214	37	3	105258856	105258856	Frame_Shift_Del	DEL	A	-	8	368	c.768delA	c.(766-768)CCAfs	p.P256fs
Pat_65	Pre-Treatment	EAF2	55840	37	3	121573658	121573659	Frame_Shift_Ins	INS	-	A	8	502	c.326_327insA	c.(325-327)GTAfs	p.V109fs
Pat_65	Pre-Treatment	P2RY1	5028	37	3	152554176	152554176	Frame_Shift_Del	DEL	G	-	12	804	c.605delG	c.(604-606)TGTfs	p.C202fs
Pat_65	Pre-Treatment	UGDH	7358	37	4	39515752	39515753	Frame_Shift_Ins	INS	-	A	7	205	c.214_215insT	c.(214-216)TCTfs	p.S72fs
Pat_65	Pre-Treatment	OCIAD2	132299	37	4	48894833	48894833	Frame_Shift_Del	DEL	A	-	8	1459	c.339delT	c.(337-339)TTTfs	p.F113fs
Pat_65	Pre-Treatment	RRH	10692	37	4	110756541	110756541	Frame_Shift_Del	DEL	T	-	9	366	c.317delT	c.(316-318)ATTfs	p.I106fs
Pat_65	Pre-Treatment	SCLT1	132320	37	4	129864163	129864163	Frame_Shift_Del	DEL	T	-	9	293	c.1620delA	c.(1618-1620)AAAfs	p.K540fs
Pat_65	Pre-Treatment	OTUD4	54726	37	4	146077123	146077125	In_Frame_Del	DEL	CAG	-	13	418	c.458_460delCTG	c.(457-462)GCTGAT>GAT	p.A153del
Pat_65	Pre-Treatment	C4orf41	60684	37	4	184614176	184614178	In_Frame_Del	DEL	GGA	-	7	479	.2113_2115delGG	c.(2113-2115)GGAdel	p.G708del
Pat_65	Pre-Treatment	PDZD2	23037	37	5	32090059	32090061	In_Frame_Del	DEL	TCC	-	8	662	.6505_6507delTC	c.(6505-6507)TCCdel	p.S2173del
Pat_65	Pre-Treatment	MSH3	4437	37	5	79970915	79970915	Frame_Shift_Del	DEL	A	-	21	965	c.1141delA	c.(1141-1143)AAAfs	p.K381fs
Pat_65	Pre-Treatment	AP3S1	1176	37	5	115202418	115202421	Frame_Shift_Del	DEL	AAGA	-	7	346	.121_124delAAG	c.(121-126)AAGAGAfs	p.K41fs
Pat_65	Pre-Treatment	FBXL21	26223	37	5	135273191	135273191	Frame_Shift_Del	DEL	G	-	7	495	c.444delG	c.(442-444)TTGfs	p.L148fs
Pat_65	Pre-Treatment	BRD8	10902	37	5	137495246	137495247	Frame_Shift_Del	DEL	AG	-	9	435	.2574_2575delCT	c.(2572-2577)CTCTTTfs	p.L858fs
Pat_65	Pre-Treatment	NUDCD2	134492	37	5	162884088	162884089	Splice_Site	INS	-	A	9	72	c.239_splice	c.e3-1	p.E80_splice
Pat_65	Pre-Treatment	CPLX2	10814	37	5	175306965	175306967	In_Frame_Del	DEL	GAG	-	8	166	c.322_324delGAG	c.(322-324)GAGdel	p.E114del
Pat_65	Pre-Treatment	C5orf25	375484	37	5	175740719	175740719	Frame_Shift_Del	DEL	T	-	8	1497	c.1703delT	c.(1702-1704)CTTfs	p.L568fs
Pat_65	Pre-Treatment	EXOC2	55770	37	6	637794	637794	Frame_Shift_Del	DEL	G	-	9	1175	c.25delC	c.(25-27)CTTfs	p.L9fs
Pat_65	Pre-Treatment	NKAPL	222698	37	6	28227519	28227520	Frame_Shift_Del	DEL	GA	-	9	865	c.370_371delGA	c.(370-372)GAGfs	p.E124fs

Pat_65	Pre-Treatment	PGBD1	84547	37	6	28254890	28254890	Frame_Shift_Del	DEL	A	-	7	580	c.587delA	c.(586-588)GAAfs	p.E196fs
Pat_65	Pre-Treatment	ZFP57	346171	37	6	29643729	29643730	Frame_Shift_Del	DEL	AA	-	7	1124	c.230_231delTT	c.(229-231)TTTfs	p.F77fs
Pat_65	Pre-Treatment	HLA-G	3135	37	6	29797196	29797196	Frame_Shift_Del	DEL	C	-	8	1459	c.621delC	c.(619-621)GACfs	p.D207fs
Pat_65	Pre-Treatment	DAXX	1616	37	6	33287898	33287900	In_Frame_Del	DEL	TCC	-	14	195	.1353_1355delGG	(1351-1356)GAGGAA>GA	.451_452EE>
Pat_65	Pre-Treatment	CNPY3	10695	37	6	42897358	42897360	In_Frame_Del	DEL	TGC	-	7	101	c.50_52delTGC	c.(49-54)TTGCTG>TTG	p.17_18LL>L
Pat_65	Pre-Treatment	ICK	22858	37	6	52883129	52883129	Frame_Shift_Del	DEL	T	-	10	1284	c.662delA	c.(661-663)AAGfs	p.K221fs
Pat_65	Pre-Treatment	DDX43	55510	37	6	74117732	74117732	Frame_Shift_Del	DEL	A	-	9	238	c.1087delA	c.(1087-1089)AAAfs	p.K363fs
Pat_65	Pre-Treatment	SLC17A5	26503	37	6	74351590	74351590	Frame_Shift_Del	DEL	A	-	7	671	c.349delT	c.(349-351)TATfs	p.Y117fs
Pat_65	Pre-Treatment	TTK	7272	37	6	80751896	80751897	Frame_Shift_Ins	INS	-	A	10	300	c.2551_2552insA	c.(2551-2553)GAAfs	p.E851fs
Pat_65	Pre-Treatment	C6orf165	154313	37	6	88144700	88144700	Frame_Shift_Del	DEL	A	-	8	271	c.1423delA	c.(1423-1425)AAAfs	p.K475fs
Pat_65	Pre-Treatment	MAP3K7	6885	37	6	91296568	91296570	In_Frame_Del	DEL	GAG	-	14	199	c.33_35delCTC	c.(31-36)TCCTCG>TCG	p.11_12SS>S
Pat_65	Pre-Treatment	IFNGR1	3459	37	6	137519505	137519506	Frame_Shift_Del	DEL	CT	-	8	620	c.1132_1133delAG	c.(1132-1134)AGTfs	p.S378fs
Pat_65	Pre-Treatment	OLIG3	167826	37	6	137815223	137815225	In_Frame_Del	DEL	GGC	-	8	356	c.83_85delGCC	c.(82-87)CGCCAC>CAC	p.R28del
Pat_65	Pre-Treatment	CCDC28A	25901	37	6	139097330	139097330	Frame_Shift_Del	DEL	A	-	8	430	c.343delA	c.(343-345)AAAfs	p.K115fs
Pat_65	Pre-Treatment	GRM1	2911	37	6	146755630	146755632	In_Frame_Del	DEL	GAC	-	8	484	.3283_3285delGA	c.(3283-3285)GACdel	p.D1099del
Pat_65	Pre-Treatment	MTHFD1L	25902	37	6	151358163	151358164	Frame_Shift_Ins	INS	-	A	13	244	c.2757_2758insA	c.(2755-2760)GACAAAfs	p.D919fs
Pat_65	Pre-Treatment	ZDHHC4	55146	37	7	6621848	6621849	Frame_Shift_Ins	INS	-	T	9	877	c.336_337insT	c.(334-339)CTGTTTfs	p.L112fs
Pat_65	Pre-Treatment	ZNF716	441234	37	7	57529089	57529091	In_Frame_Del	DEL	TCT	-	8	488	c.922_924delTCT	c.(922-924)TCTdel	p.S309del
Pat_65	Pre-Treatment	GPC2	221914	37	7	99771554	99771554	Frame_Shift_Del	DEL	C	-	7	667	c.796delG	c.(796-798)GTCfs	p.V266fs
Pat_65	Pre-Treatment	GIGYF1	64599	37	7	100283635	100283637	In_Frame_Del	DEL	TCC	-	11	221	.1014_1016delGG	(1012-1017)GAGGAA>GA	.338_339EE>
Pat_65	Pre-Treatment	FOXP2	93986	37	7	114270016	114270018	In_Frame_Del	DEL	CAG	-	12	333	c.553_555delCAG	c.(553-555)CAGdel	p.Q191del
Pat_65	Pre-Treatment	PAXIP1	22976	37	7	154760267	154760269	In_Frame_Del	DEL	CTG	-	8	47	.1642_1644delCA	c.(1642-1644)CAGdel	p.Q548del
Pat_65	Pre-Treatment	RBM33	155435	37	7	155531073	155531074	Frame_Shift_Del	DEL	CA	-	16	492	c.1713_1714delCA	c.(1711-1716)CCCACAfs	p.P571fs
Pat_65	Pre-Treatment	MCPH1	79648	37	8	6289099	6289099	Frame_Shift_Del	DEL	A	-	9	289	c.313delA	c.(313-315)AAAfs	p.K105fs
Pat_65	Pre-Treatment	RP1L1	94137	37	8	10467706	10467707	In_Frame_Ins	INS	-	CCC	14	654	.3901_3902insGG	(3901-3903)GTG>GGGGT	.1300_1301ins
Pat_65	Pre-Treatment	SGCZ	137868	37	8	13959894	13959895	Frame_Shift_Del	DEL	TG	-	7	534	c.734_735delCA	c.(733-735)ACAfs	p.T245fs
Pat_65	Pre-Treatment	ERLIN2	11160	37	8	37597949	37597950	Frame_Shift_Del	DEL	AT	-	8	1220	c.174_175delAT	c.(172-177)TCATATfs	p.S58fs
Pat_65	Pre-Treatment	RAB11FIP1	80223	37	8	37728933	37728933	Frame_Shift_Del	DEL	T	-	8	538	c.3387delA	c.(3385-3387)AAAfs	p.K1129fs
Pat_65	Pre-Treatment	MYST3	7994	37	8	41792323	41792323	Frame_Shift_Del	DEL	C	-	7	1714	c.3415delG	c.(3415-3417)GAGfs	p.E1139fs
Pat_65	Pre-Treatment	ARFGEF1	10565	37	8	68152482	68152483	Frame_Shift_Del	DEL	TG	-	9	721	c.2893_2894delCA	c.(2893-2895)CAAfs	p.Q965fs
Pat_65	Pre-Treatment	SLC26A7	115111	37	8	92401631	92401631	Frame_Shift_Del	DEL	T	-	9	1265	c.1741delT	c.(1741-1743)TTTfs	p.F581fs
Pat_65	Pre-Treatment	TM7SF4	81501	37	8	105361700	105361700	Frame_Shift_Del	DEL	G	-	7	1606	c.920delG	c.(919-921)TGGfs	p.W307fs
Pat_65	Pre-Treatment	ATAD2	29028	37	8	124368685	124368685	Frame_Shift_Del	DEL	A	-	9	266	c.1590delT	c.(1588-1590)TTTfs	p.F530fs
Pat_65	Pre-Treatment	FER1L6	654463	37	8	125080031	125080031	Frame_Shift_Del	DEL	A	-	7	256	c.3702delA	c.(3700-3702)GGAfs	p.G1234fs
Pat_65	Pre-Treatment	COL22A1	169044	37	8	139809072	139809072	Frame_Shift_Del	DEL	T	-	7	1586	c.1586delA	c.(1585-1587)AAGfs	p.K529fs
Pat_65	Pre-Treatment	PLEC	5339	37	8	145000951	145000953	Splice_Site	DEL	CCT	-	25	1223	c.4455_splice	c.e30+1	p.E1485_splice
Pat_65	Pre-Treatment	GRINA	2907	37	8	145065717	145065718	Frame_Shift_Ins	INS	-	C	7	222	c.326_327insC	c.(325-327)TTCfs	p.F109fs
Pat_65	Pre-Treatment	ADAMTSL1	92949	37	9	18680349	18680350	Frame_Shift_Ins	INS	-	G	11	187	c.1176_1177insG	c.(1174-1179)TGTGGGfs	p.C392fs
Pat_65	Pre-Treatment	VCP	7415	37	9	35062983	35062985	In_Frame_Del	DEL	AAG	-	9	470	c.801_803delCTT	c.(799-804)TTCTTG>TTG	p.F267del
Pat_65	Pre-Treatment	RALGDS	5900	37	9	135975698	135975700	In_Frame_Del	DEL	CTC	-	7	1627	.2524_2526delGA	c.(2524-2526)GAGdel	p.E842del
Pat_65	Pre-Treatment	GRIN1	2902	37	9	140056884	140056886	In_Frame_Del	DEL	GAG	-	23	265	.1780_1782delGA	c.(1780-1782)GAGdel	p.E598del
Pat_65	Pre-Treatment	ZMYND19	116225	37	9	140481541	140481542	Frame_Shift_Ins	INS	-	C	8	572	c.236_237insG	c.(235-237)GGCfs	p.G79fs
Pat_65	Pre-Treatment	PPP2R3B	28227	37	X	302052	302052	Frame_Shift_Del	DEL	T	-	7	652	c.1165delA	c.(1165-1167)ACAfs	p.T389fs
Pat_65	Pre-Treatment	NAP1L2	4674	37	X	72434104	72434104	Frame_Shift_Del	DEL	T	-	7	541	c.225delA	c.(223-225)AAAfs	p.K75fs
Pat_65	Pre-Treatment	IRS4	8471	37	X	107977802	107977803	Frame_Shift_Ins	INS	-	C	22	1427	c.1772_1773insG	c.(1771-1773)GGCfs	p.G591fs
Pat_65	Pre-Treatment	ATP2B3	492	37	X	152845611	152845611	Frame_Shift_Del	DEL	C	-	11	534	c.3518delC	c.(3517-3519)GCCfs	p.A1173fs
Pat_66	Pre-Treatment	LRRIQ3	127255	37	1	74575212	74575213	Frame_Shift_Ins	INS	-	T	19	138	c.732_733insA	c.(730-735)AAACAGfs	p.K244fs

Pat_66	Pre-Treatment	ST6GALNAC5	81849	37	1	77334277	77334279	In_Frame_Del	DEL	GCA	-	9	59	c.111_113delGCA	.(109-114)CCGCAG>CCG	p.Q49del
Pat_66	Pre-Treatment	ABCA4	24	37	1	94548992	94548992	Frame_Shift_Del	DEL	G	-	7	362	c.774delC	c.(772-774)CCCfs	p.P258fs
Pat_66	Pre-Treatment	PIAS3	10401	37	1	145579285	145579285	Frame_Shift_Del	DEL	C	-	9	879	c.622delC	c.(622-624)CCCfs	p.P208fs
Pat_66	Pre-Treatment	LOC200030	200030	37	1	148016436	148016436	Frame_Shift_Del	DEL	T	-	7	753	c.1826delA	c.(1825-1827)AAGfs	p.K609fs
Pat_66	Pre-Treatment	TCHH	7062	37	1	152082301	152082303	In_Frame_Del	DEL	CTC	-	7	499	.3390_3392delGA	.(3388-3393)AAGAGA>AA	p.R1133del
Pat_66	Pre-Treatment	LMNA	4000	37	1	156106980	156106981	Frame_Shift_Del	DEL	GC	-	18	15	.1565_1566delGC	c.(1564-1566)TGCfs	p.C522fs
Pat_66	Pre-Treatment	PVRL4	81607	37	1	161059028	161059030	In_Frame_Del	DEL	AGC	-	8	577	c.57_59delGCT	c.(55-60)CTGCTA>CTA	p.19_20LL>L
Pat_66	Pre-Treatment	PRG4	10216	37	1	186276010	186276011	In_Frame_Ins	INS	-	AGG	7	721	.1159_1160insAG	.(1159-1161)AAG>AAGGA	p.387_388insE
Pat_66	Pre-Treatment	PARP1	142	37	1	226570820	226570820	Frame_Shift_Del	DEL	G	-	7	923	c.1076delC	c.(1075-1077)CCAfs	p.P359fs
Pat_66	Pre-Treatment	OR2W5	441932	37	1	247654684	247654684	Frame_Shift_Del	DEL	G	-	7	270	c.255delG	c.(253-255)CTGfs	p.L85fs
Pat_66	Pre-Treatment	PGR	5241	37	11	100998255	100998255	Frame_Shift_Del	DEL	C	-	4	9	c.1547delG	c.(1546-1548)GGCfs	p.G516fs
Pat_66	Pre-Treatment	KDM5A	5927	37	12	416953	416953	Frame_Shift_Del	DEL	T	-	8	184	c.3597delA	c.(3595-3597)AAAfs	p.K1199fs
Pat_66	Pre-Treatment	PRB2	653247	37	12	11546506	11546508	In_Frame_Del	DEL	TTG	-	18	828	c.504_506delCAA	c.(502-507)AACAAG>AAG	p.N168del
Pat_66	Pre-Treatment	GPR19	2842	37	12	12814274	12814274	Frame_Shift_Del	DEL	T	-	13	417	c.1109delA	c.(1108-1110)AACfs	p.N370fs
Pat_66	Pre-Treatment	ARNTL2	56938	37	12	27543043	27543044	Frame_Shift_Del	DEL	CA	-	7	689	c.790_791delCA	c.(790-792)CACfs	p.H264fs
Pat_66	Pre-Treatment	INTS6	26512	37	13	51948408	51948408	Frame_Shift_Del	DEL	T	-	7	663	c.2040delA	c.(2038-2040)AAAfs	p.K680fs
Pat_66	Pre-Treatment	LAMP1	3916	37	13	113964033	113964034	Frame_Shift_Ins	INS	-	A	9	245	c.259_260insA	c.(259-261)GACfs	p.D87fs
Pat_66	Pre-Treatment	ZNF828	283489	37	13	115090966	115090966	Frame_Shift_Del	DEL	T	-	7	1340	c.1649delT	c.(1648-1650)CTTfs	p.L550fs
Pat_66	Pre-Treatment	EIF3CL	728689	37	16	28734579	28734581	In_Frame_Del	DEL	GAG	-	13	1750	c.871_873delGAG	c.(871-873)GAGdel	p.E295del
Pat_66	Pre-Treatment	PRRT2	112476	37	16	29825016	29825016	Frame_Shift_Del	DEL	C	-	7	28	c.641delC	c.(640-642)GCCfs	p.A214fs
Pat_66	Pre-Treatment	TBC1D3B	414059	37	17	34493617	34493617	Frame_Shift_Del	DEL	G	-	2	4	c.1408delC	c.(1408-1410)CGCfs	p.R470fs
Pat_66	Pre-Treatment	FBXO17	115290	37	19	39440619	39440619	Frame_Shift_Del	DEL	C	-	2	4	c.341delG	c.(340-342)TGCfs	p.C114fs
Pat_66	Pre-Treatment	HS1BP3	64342	37	2	20840864	20840864	Frame_Shift_Del	DEL	G	-	8	719	c.275delC	c.(274-276)CCAfs	p.P92fs
Pat_66	Pre-Treatment	DYSF	8291	37	2	71801420	71801422	In_Frame_Del	DEL	CCG	-	7	339	.3267_3269delCC	.(3265-3270)TTCCGC>TT	p.R1093del
Pat_66	Pre-Treatment	FAM117B	150864	37	2	203621969	203621969	Frame_Shift_Del	DEL	C	-	8	118	c.1138delC	c.(1138-1140)CCCfs	p.P380fs
Pat_66	Pre-Treatment	ALPP	250	37	2	233243529	233243531	In_Frame_Del	DEL	TGC	-	8	98	c.17_19delTGC	c.(16-21)ATGCTG>ATG	p.L13del
Pat_66	Pre-Treatment	ATRN	8455	37	20	3451934	3451936	In_Frame_Del	DEL	GCT	-	2	4	c.180_182delGCT	.(178-183)CGGCTG>CGG	p.L68del
Pat_66	Pre-Treatment	SYCP2	10388	37	20	58452518	58452519	Frame_Shift_Ins	INS	-	T	7	122	c.3071_3072insA	c.(3070-3072)AACfs	p.N1024fs
Pat_66	Pre-Treatment	GART	2618	37	21	34904722	34904739	In_Frame_Del	DEL	.CCACTGGC	-	109	479	elTGAAGGCCAG	GTGAAGGCCAGTGGTCT	.VKASGL147d
Pat_66	Pre-Treatment	PFKL	5211	37	21	45736153	45736155	In_Frame_Del	DEL	CAT	-	7	275	c.774_776delCAT	c.(772-777)AACATC>AAC	p.I262del
Pat_66	Pre-Treatment	PTTG1IP	754	37	21	46276194	46276196	In_Frame_Del	DEL	GCA	-	13	144	c.361_363delTGC	c.(361-363)TGCdel	p.C121del
Pat_66	Pre-Treatment	TOP3B	8940	37	22	22314097	22314097	Frame_Shift_Del	DEL	C	-	7	568	c.1666delG	c.(1666-1668)GTGfs	p.V556fs
Pat_66	Pre-Treatment	DDX17	10521	37	22	38895455	38895455	Frame_Shift_Del	DEL	C	-	8	513	c.488delG	c.(487-489)GGAfs	p.G163fs
Pat_66	Pre-Treatment	TAB1	10454	37	22	39772049	39772049	Frame_Shift_Del	DEL	C	-	9	605	c.108delC	c.(106-108)GACfs	p.D36fs
Pat_66	Pre-Treatment	LNP1	348801	37	3	100148586	100148588	In_Frame_Del	DEL	GAT	-	8	610	c.13_15delGAT	c.(13-15)GATdel	p.D10del
Pat_66	Pre-Treatment	EIF4G1	1981	37	3	184039744	184039746	In_Frame_Del	DEL	GAA	-	8	82	.1372_1374delGA	c.(1372-1374)GAAdel	p.E465del
Pat_66	Pre-Treatment	GP5	2814	37	3	194117710	194117710	Frame_Shift_Del	DEL	C	-	4	3	c.1302delG	c.(1300-1302)GGGfs	p.G434fs
Pat_66	Pre-Treatment	TMEM175	84286	37	4	946206	946207	Frame_Shift_Del	DEL	TG	-	7	487	c.430_431delTG	c.(430-432)TGTfs	p.C144fs
Pat_66	Pre-Treatment	CRIPAK	285464	37	4	1388441	1388442	Frame_Shift_Ins	INS	-	CG	8	2214	c.142_143insCG	c.(142-144)ATGfs	p.M48fs
Pat_66	Pre-Treatment	CRIPAK	285464	37	4	1388900	1388901	Frame_Shift_Del	DEL	CA	-	14	808	c.601_602delCA	c.(601-603)CACfs	p.H201fs
Pat_66	Pre-Treatment	NOP14	8602	37	4	2951689	2951689	Frame_Shift_Del	DEL	G	-	7	558	c.1254delC	c.(1252-1254)ACCfs	p.T418fs
Pat_66	Pre-Treatment	RGS12	6002	37	4	3430398	3430399	Frame_Shift_Ins	INS	-	A	7	153	c.3525_3526insA	c.(3523-3528)GGGAAAfs	p.G1175fs
Pat_66	Pre-Treatment	PROL1	58503	37	4	71275209	71275210	Frame_Shift_Del	DEL	CA	-	7	487	c.164_165delCA	c.(163-165)TCAfs	p.S55fs
Pat_66	Pre-Treatment	SEC31A	22872	37	4	83785675	83785677	In_Frame_Del	DEL	TGC	-	7	216	.1272_1274delGC	.(1270-1275)CAGCAC>CA	p.Q424del
Pat_66	Pre-Treatment	DMXL1	1657	37	5	118525523	118525524	Frame_Shift_Ins	INS	-	G	7	256	c.7256_7257insG	c.(7255-7257)GCGfs	p.A2419fs
Pat_66	Pre-Treatment	FOXC1	2296	37	6	1612018	1612020	In_Frame_Del	DEL	CGG	-	5	10	.1338_1340delCG	(1336-1341)CACGGC>CA	p.G456del
Pat_66	Pre-Treatment	TUBB2A	7280	37	6	3154114	3154116	In_Frame_Del	DEL	CCT	-	7	438	.1319_1321delAG	(1318-1323)GAGGGC>GG	p.E440del

Pat_66	Pre-Treatment	TUBB2B	347733	37	6	3225002	3225004	In_Frame_Del	DEL	CCT	-	9	351	.1319_1321delAG	(1318-1323)GAGGGC>GG	p.E440del
Pat_66	Pre-Treatment	HLA-J	3137	37	6	29977389	29977393	Frame_Shift_Del	DEL	CTTCT	-	17	109	.408_412delCTTC	c.(406-414)GACTTCTCTfs	p.D136fs
Pat_66	Pre-Treatment	GSTA2	2939	37	6	52617657	52617657	Frame_Shift_Del	DEL	C	-	12	2573	c.409delG	c.(409-411)GAAfs	p.E137fs
Pat_66	Pre-Treatment	GSTA1	2938	37	6	52658948	52658948	Frame_Shift_Del	DEL	T	-	8	1987	c.389delA	c.(388-390)AATfs	p.N130fs
Pat_66	Pre-Treatment	ICK	22858	37	6	52883129	52883129	Frame_Shift_Del	DEL	T	-	8	983	c.662delA	c.(661-663)AAGfs	p.K221fs
Pat_66	Pre-Treatment	PRDM1	639	37	6	106552831	106552832	Frame_Shift_Del	DEL	CT	-	8	954	c.796_797delCT	c.(796-798)CTCfs	p.L266fs
Pat_66	Pre-Treatment	MTHFD1L	25902	37	6	151358163	151358164	Frame_Shift_Ins	INS	-	A	10	225	c.2757_2758insA	c.(2755-2760)GACAAAfs	p.D919fs
Pat_66	Pre-Treatment	ZDHHC4	55146	37	7	6621849	6621849	Frame_Shift_Del	DEL	T	-	7	520	c.337delT	c.(337-339)TTTfs	p.F113fs
Pat_66	Pre-Treatment	SULF1	23213	37	8	70514026	70514026	Frame_Shift_Del	DEL	T	-	9	568	c.1023delT	c.(1021-1023)CCTfs	p.P341fs
Pat_66	Pre-Treatment	INTS8	55656	37	8	95877882	95877882	Frame_Shift_Del	DEL	T	-	9	592	c.2225delT	c.(2224-2226)ATAfs	p.I742fs
Pat_66	Pre-Treatment	ZC3H3	23144	37	8	144522387	144522389	In_Frame_Del	DEL	GAG	-	8	36	.2637_2639delCT	.(2635-2640)TCCTCA>TC	.879_880SS>
Pat_66	Pre-Treatment	OFD1	8481	37	X	13764946	13764946	Frame_Shift_Del	DEL	A	-	7	60	c.702delA	c.(700-702)GCAfs	p.A234fs
Pat_66	Pre-Treatment	CNKSR2	22866	37	X	21627678	21627680	In_Frame_Del	DEL	GAG	-	7	83	.2635_2637delGA	c.(2635-2637)GAGdel	p.E886del
Pat_66	Pre-Treatment	F8	2157	37	X	154157686	154157686	Frame_Shift_Del	DEL	T	-	11	139	c.4379delA	c.(4378-4380)AATfs	p.N1460fs
Pat_01	Pre-Treatment	PUSL1	126789	37	1	1245090	1245090	Missense_Mutation	SNP	C	T	26	40	c.503C>T	c.(502-504)GCC>GTC	p.A168V
Pat_01	Pre-Treatment	RER1	11079	37	1	2328642	2328642	Nonsense_Mutation	SNP	C	T	186	268	c.169C>T	c.(169-171)CGA>TGA	p.R57*
Pat_01	Pre-Treatment	MTOR	2475	37	1	11181367	11181367	Missense_Mutation	SNP	G	A	4	241	c.6869C>T	c.(6868-6870)GCC>GTC	p.A2290V
Pat_01	Pre-Treatment	PTCHD2	57540	37	1	11584007	11584007	Nonsense_Mutation	SNP	C	T	57	78	c.2371C>T	c.(2371-2373)CAG>TAG	p.Q791*
Pat_01	Pre-Treatment	FBXO44	93611	37	1	11718444	11718444	Missense_Mutation	SNP	C	T	139	191	c.386C>T	c.(385-387)TCA>TTA	p.S129L
Pat_01	Pre-Treatment	AADACL3	126767	37	1	12785574	12785574	Missense_Mutation	SNP	G	A	116	122	c.664G>A	c.(664-666)GAA>AAA	p.E222K
Pat_01	Pre-Treatment	LOC649330	649330	37	1	12907868	12907868	Missense_Mutation	SNP	C	T	62	323	c.275G>A	c.(274-276)CGA>CAA	p.R92Q
Pat_01	Pre-Treatment	LOC440563	440563	37	1	13183695	13183695	Missense_Mutation	SNP	C	T	64	94	c.178G>A	c.(178-180)GAG>AAG	p.E60K
Pat_01	Pre-Treatment	NBPF1	55672	37	1	16914254	16914254	Missense_Mutation	SNP	C	T	60	466	c.532G>A	c.(532-534)GAG>AAG	p.E178K
Pat_01	Pre-Treatment	MRTO4	51154	37	1	19584386	19584386	Missense_Mutation	SNP	C	T	141	160	c.401C>T	c.(400-402)ACT>ATT	p.T134I
Pat_01	Pre-Treatment	RAP1GAP	5909	37	1	21940528	21940529	Missense_Mutation	DNP	GT	AA	31	62	c.345_346AC>TT	(343-348)TCACTC>TCTT	p.L116F
Pat_01	Pre-Treatment	NIPAL3	57185	37	1	24790583	24790583	Missense_Mutation	SNP	C	T	23	65	c.994C>T	c.(994-996)CCC>TCC	p.P332S
Pat_01	Pre-Treatment	PAFAH2	5051	37	1	26301009	26301009	Missense_Mutation	SNP	T	C	3	203	c.891A>G	c.(889-891)ATA>ATG	p.I297M
Pat_01	Pre-Treatment	ZNF683	257101	37	1	26691195	26691195	Missense_Mutation	SNP	G	A	62	78	c.842C>T	c.(841-843)ACC>ATC	p.T281I
Pat_01	Pre-Treatment	KPNA6	23633	37	1	32627987	32627987	Missense_Mutation	SNP	C	T	319	366	c.773C>T	c.(772-774)TCT>TTT	p.S258F
Pat_01	Pre-Treatment	GJA4	2701	37	1	35260770	35260770	Missense_Mutation	SNP	C	T	65	100	c.956C>T	c.(955-957)CCC>CTC	p.P319L
Pat_01	Pre-Treatment	CSF3R	1441	37	1	36941122	36941122	Missense_Mutation	SNP	C	T	48	80	c.217G>A	c.(217-219)GGC>AGC	p.G73S
Pat_01	Pre-Treatment	KIAA0467	23334	37	1	43893276	43893276	Missense_Mutation	SNP	C	T	155	201	c.977C>T	c.(976-978)TCC>TTC	p.S326F
Pat_01	Pre-Treatment	FAAH	2166	37	1	46872027	46872027	Missense_Mutation	SNP	C	T	69	104	c.938C>T	c.(937-939)CCC>CTC	p.P313L
Pat_01	Pre-Treatment	TMEM61	199964	37	1	55457633	55457633	Missense_Mutation	SNP	G	A	4	142	c.490G>A	c.(490-492)GCC>ACC	p.A164T
Pat_01	Pre-Treatment	C8A	731	37	1	57383305	57383305	Missense_Mutation	SNP	A	C	65	16	c.1671A>C	c.(1669-1671)GAA>GAC	p.E557D
Pat_01	Pre-Treatment	COL11A1	1301	37	1	103404641	103404641	Missense_Mutation	SNP	C	T	218	51	c.3388G>A	c.(3388-3390)GAA>AAA	p.E1130K
Pat_01	Pre-Treatment	CSF1	1435	37	1	110467429	110467429	Missense_Mutation	SNP	C	T	21	26	c.1601C>T	c.(1600-1602)CCC>CTC	p.P534L
Pat_01	Pre-Treatment	OVGP1	5016	37	1	111957310	111957310	Missense_Mutation	SNP	G	A	128	159	c.1813C>T	c.(1813-1815)CCC>TCC	p.P605S
Pat_01	Pre-Treatment	MAGI3	260425	37	1	114157228	114157228	Missense_Mutation	SNP	C	T	110	147	c.1024C>T	c.(1024-1026)CCT>TCT	p.P342S
Pat_01	Pre-Treatment	SYT6	148281	37	1	114640492	114640492	Missense_Mutation	SNP	G	A	4	321	c.1117C>T	c.(1117-1119)CAC>TAC	p.H373Y
Pat_01	Pre-Treatment	SYCP1	6847	37	1	115419372	115419372	Missense_Mutation	SNP	G	A	11	15	c.742G>A	c.(742-744)GAA>AAA	p.E248K
Pat_01	Pre-Treatment	SPAG17	200162	37	1	118558629	118558629	Missense_Mutation	SNP	G	A	97	127	c.4246C>T	c.(4246-4248)CCA>TCA	p.P1416S
Pat_01	Pre-Treatment	NOTCH2	4853	37	1	120465049	120465049	Missense_Mutation	SNP	G	A	3	42	c.5023C>T	c.(5023-5025)CGC>TGC	p.R1675C
Pat_01	Pre-Treatment	NBPF9	400818	37	1	144828599	144828599	Missense_Mutation	SNP	G	A	6	370	c.2644G>A	c.(2644-2646)GGA>AGA	p.G882R
Pat_01	Pre-Treatment	C1orf56	54964	37	1	151020540	151020540	Missense_Mutation	SNP	G	A	4	108	c.217G>A	c.(217-219)GAC>AAC	p.D73N
Pat_01	Pre-Treatment	POGZ	23126	37	1	151380907	151380907	Missense_Mutation	SNP	G	C	4	179	c.2212C>G	c.(2212-2214)CAG>GAG	p.Q738E
Pat_01	Pre-Treatment	RORC	6097	37	1	151785723	151785723	Missense_Mutation	SNP	C	T	380	424	c.1166G>A	c.(1165-1167)CGA>CAA	p.R389Q

Pat_01	Pre-Treatment	TCHH	7062	37	1	152082320	152082320	Missense_Mutation	SNP	T	C	6	355	c.3373A>G	c.(3373-3375)AGA>GGA	p.R1125G
Pat_01	Pre-Treatment	RPTN	126638	37	1	152128886	152128886	Missense_Mutation	SNP	C	T	273	435	c.689G>A	c.(688-690)CGG>CAG	p.R230Q
Pat_01	Pre-Treatment	FLG	2312	37	1	152277449	152277449	Missense_Mutation	SNP	G	T	7	898	c.9913C>A	c.(9913-9915)CGC>AGC	p.R3305S
Pat_01	Pre-Treatment	FLG2	388698	37	1	152329769	152329769	Nonsense_Mutation	SNP	G	A	267	335	c.493C>T	c.(493-495)CAA>TAA	p.Q165*
Pat_01	Pre-Treatment	LCE1F	353137	37	1	152748887	152748887	Missense_Mutation	SNP	C	T	132	156	c.40C>T	c.(40-42)CCC>TCC	p.P14S
Pat_01	Pre-Treatment	PEAR1	375033	37	1	156874590	156874590	Missense_Mutation	SNP	C	T	163	173	c.152C>T	c.(151-153)CCC>CTC	p.P51L
Pat_01	Pre-Treatment	CD1C	911	37	1	158261934	158261934	Missense_Mutation	SNP	G	C	118	156	c.389G>C	c.(388-390)GGC>GCC	p.G130A
Pat_01	Pre-Treatment	OR10K2	391107	37	1	158389793	158389793	Missense_Mutation	SNP	C	T	88	127	c.864G>A	c.(862-864)ATG>ATA	p.M288I
Pat_01	Pre-Treatment	OR10J3	441911	37	1	159283990	159283990	Missense_Mutation	SNP	G	A	67	108	c.460C>T	c.(460-462)CTT>TTT	p.L154F
Pat_01	Pre-Treatment	PAPPA2	60676	37	1	176734857	176734857	Missense_Mutation	SNP	C	T	265	400	c.4207C>T	c.(4207-4209)CAT>TAT	p.H1403Y
Pat_01	Pre-Treatment	ASTN1	460	37	1	177001897	177001897	Missense_Mutation	SNP	G	A	78	116	c.560C>T	c.(559-561)CCG>CTG	p.P187L
Pat_01	Pre-Treatment	CEP350	9857	37	1	180062348	180062348	Missense_Mutation	SNP	C	T	5	19	c.7108C>T	c.(7108-7110)CCT>TCT	p.P2370S
Pat_01	Pre-Treatment	LAMC1	3915	37	1	182993000	182993000	Missense_Mutation	SNP	G	A	5	142	c.149G>A	c.(148-150)TGC>TAC	p.C50Y
Pat_01	Pre-Treatment	LAMC2	3918	37	1	183209476	183209476	Missense_Mutation	SNP	T	C	117	131	c.3278T>C	c.(3277-3279)GTT>GCT	p.V1093A
Pat_01	Pre-Treatment	NAV1	89796	37	1	201757704	201757704	Missense_Mutation	SNP	C	T	183	205	c.3104C>T	c.(3103-3105)TCC>TTC	p.S1035F
Pat_01	Pre-Treatment	LAX1	54900	37	1	203743384	203743385	Nonsense_Mutation	DNP	GG	TA	23	38	c.772_773GG>TA	c.(772-774)GGA>TAA	p.G258*
Pat_01	Pre-Treatment	NUAK2	81788	37	1	205273092	205273092	Missense_Mutation	SNP	C	T	36	32	c.1373G>A	c.(1372-1374)GGC>GAC	p.G458D
Pat_01	Pre-Treatment	LGTN	1939	37	1	206765163	206765163	Missense_Mutation	SNP	G	A	190	227	c.1699C>T	c.(1699-1701)CCT>TCT	p.P567S
Pat_01	Pre-Treatment	ATF3	467	37	1	212791476	212791476	Missense_Mutation	SNP	C	T	24	45	c.248C>T	c.(247-249)CCT>CTT	p.P83L
Pat_01	Pre-Treatment	CAPN9	10753	37	1	230916452	230916453	Missense_Mutation	DNP	CC	TT	101	118	.1479_1480CC>T	477-1482)ACCCGG>ACTT	p.R494W
Pat_01	Pre-Treatment	IRF2BP2	359948	37	1	234745204	234745204	Missense_Mutation	SNP	G	A	4	29	c.37C>T	c.(37-39)CGG>TGG	p.R13W
Pat_01	Pre-Treatment	FMN2	56776	37	1	240371107	240371107	Missense_Mutation	SNP	C	T	100	446	c.2995C>T	c.(2995-2997)CCT>TCT	p.P999S
Pat_01	Pre-Treatment	FMN2	56776	37	1	240371239	240371239	Missense_Mutation	SNP	C	T	14	266	c.3127C>T	c.(3127-3129)CCT>TCT	p.P1043S
Pat_01	Pre-Treatment	PLD5	200150	37	1	242277217	242277217	Missense_Mutation	SNP	G	C	4	251	c.1045C>G	c.(1045-1047)CCT>GCT	p.P349A
Pat_01	Pre-Treatment	OR14I1	401994	37	1	248845214	248845214	Missense_Mutation	SNP	C	T	75	99	c.392G>A	c.(391-393)AGA>AAA	p.R131K
Pat_01	Pre-Treatment	PFKP	5214	37	10	3155375	3155375	Missense_Mutation	SNP	C	T	23	23	c.1219C>T	c.(1219-1221)CCA>TCA	p.P407S
Pat_01	Pre-Treatment	FBXO18	84893	37	10	5948525	5948525	Missense_Mutation	SNP	C	T	148	160	c.683C>T	c.(682-684)CCG>CTG	p.P228L
Pat_01	Pre-Treatment	MCM10	55388	37	10	13213185	13213186	Missense_Mutation	DNP	CC	TT	33	50	c.271_272CC>TT	c.(271-273)CCC>TTC	p.P91F
Pat_01	Pre-Treatment	NEBL	10529	37	10	21102879	21102879	Missense_Mutation	SNP	G	A	98	133	c.2335C>T	c.(2335-2337)CAT>TAT	p.H779Y
Pat_01	Pre-Treatment	PTCHD3	374308	37	10	27703073	27703073	Missense_Mutation	SNP	G	A	292	379	c.107C>T	c.(106-108)TCG>TTG	p.S36L
Pat_01	Pre-Treatment	KIAA1462	57608	37	10	30317681	30317681	Missense_Mutation	SNP	C	T	191	225	c.1396G>A	c.(1396-1398)GGA>AGA	p.G466R
Pat_01	Pre-Treatment	LOC100129055	100129055	37	10	38466905	38466905	Splice_Site	SNP	T	G	33	38	c.365_splice	c.e2+2	
Pat_01	Pre-Treatment	ZNF33B	7582	37	10	43088920	43088920	Missense_Mutation	SNP	C	A	110	145	c.1478G>T	c.(1477-1479)GGA>GTA	p.G493V
Pat_01	Pre-Treatment	RASSF4	83937	37	10	45486500	45486500	Missense_Mutation	SNP	G	A	132	78	c.790G>A	c.(790-792)GTG>ATG	p.V264M
Pat_01	Pre-Treatment	GPRIN2	9721	37	10	46999934	46999934	Missense_Mutation	SNP	C	T	65	219	c.1054C>T	c.(1054-1056)CCG>TCG	p.P352S
Pat_01	Pre-Treatment	CHAT	1103	37	10	50863218	50863218	Missense_Mutation	SNP	G	A	475	156	c.1712G>A	c.(1711-1713)AGA>AAA	p.R571K
Pat_01	Pre-Treatment	CTNNA3	29119	37	10	68381509	68381509	Missense_Mutation	SNP	C	T	70	17	c.1315G>A	c.(1315-1317)GAA>AAA	p.E439K
Pat_01	Pre-Treatment	CDH23	64072	37	10	73537639	73537639	Missense_Mutation	SNP	T	C	3	101	c.5048T>C	c.(5047-5049)TTC>TCC	p.F1683S
Pat_01	Pre-Treatment	KCNMA1	3778	37	10	78708959	78708959	Missense_Mutation	SNP	C	T	192	45	c.2650G>A	c.(2650-2652)GAG>AAG	p.E884K
Pat_01	Pre-Treatment	PTEN	5728	37	10	89692793	89692793	Missense_Mutation	SNP	C	G	106	26	c.277C>G	c.(277-279)CAT>GAT	p.H93D
Pat_01	Pre-Treatment	NOC3L	64318	37	10	96099543	96099543	Missense_Mutation	SNP	G	A	59	7	c.1915C>T	c.(1915-1917)CCA>TCA	p.P639S
Pat_01	Pre-Treatment	NOC3L	64318	37	10	96110005	96110006	Missense_Mutation	DNP	GG	AA	169	39	c.992_993CC>TT	c.(991-993)TCC>TTT	p.S331F
Pat_01	Pre-Treatment	CYP2C8	1558	37	10	96829152	96829152	Missense_Mutation	SNP	G	A	73	12	c.8C>T	c.(7-9)CCT>CTT	p.P3L
Pat_01	Pre-Treatment	DNMBP	23268	37	10	101715970	101715970	Missense_Mutation	SNP	G	A	174	32	c.1261C>T	c.(1261-1263)CAT>TAT	p.H421Y
Pat_01	Pre-Treatment	CPN1	1369	37	10	101835766	101835766	Missense_Mutation	SNP	G	A	144	13	c.322C>T	c.(322-324)CGG>TGG	p.R108W
Pat_01	Pre-Treatment	CYP17A1	1586	37	10	104593858	104593858	Missense_Mutation	SNP	C	T	21	7	c.688G>A	c.(688-690)GAA>AAA	p.E230K
Pat_01	Pre-Treatment	SORCS3	22986	37	10	106970954	106970954	Missense_Mutation	SNP	C	T	83	16	c.2321C>T	c.(2320-2322)CCA>CTA	p.P774L

Pat_01	Pre-Treatment	RPL13AP6	644511	37	10	112696573	112696573	Missense_Mutation	SNP	T	C	4	26	c.419A>G	c.(418-420)CAC>CGC	p.H140R
Pat_01	Pre-Treatment	HABP2	3026	37	10	115335703	115335703	Missense_Mutation	SNP	C	T	254	50	c.271C>T	c.(271-273)CAT>TAT	p.H91Y
Pat_01	Pre-Treatment	DMBT1	1755	37	10	124358346	124358346	Nonsense_Mutation	SNP	C	T	505	107	c.3013C>T	c.(3013-3015)CGA>TGA	p.R1005*
Pat_01	Pre-Treatment	LRDD	55367	37	11	801458	801458	Missense_Mutation	SNP	C	T	16	19	c.1469G>A	c.(1468-1470)CGA>CAA	p.R490Q
Pat_01	Pre-Treatment	TH	7054	37	11	2186514	2186514	Nonsense_Mutation	SNP	G	A	181	235	c.1375C>T	c.(1375-1377)CAG>TAG	p.Q459*
Pat_01	Pre-Treatment	OR52E2	119678	37	11	5080830	5080830	Missense_Mutation	SNP	G	A	112	161	c.28C>T	c.(28-30)CAC>TAC	p.H10Y
Pat_01	Pre-Treatment	MRVI1	10335	37	11	10647848	10647848	Missense_Mutation	SNP	G	A	29	33	c.1033C>T	c.(1033-1035)CCG>TCG	p.P345S
Pat_01	Pre-Treatment	CYP2R1	120227	37	11	14901879	14901879	Missense_Mutation	SNP	C	T	48	83	c.803G>A	c.(802-804)AGA>AAA	p.R268K
Pat_01	Pre-Treatment	NAV2	89797	37	11	20065564	20065564	Missense_Mutation	SNP	C	T	135	164	c.3014C>T	c.(3013-3015)TCC>TTC	p.S1005F
Pat_01	Pre-Treatment	KCNA4	3739	37	11	30033313	30033313	Missense_Mutation	SNP	G	A	108	155	c.913C>T	c.(913-915)CCT>TCT	p.P305S
Pat_01	Pre-Treatment	DGKZ	8525	37	11	46397063	46397063	Missense_Mutation	SNP	G	A	20	18	c.2356G>A	c.(2356-2358)GTG>ATG	p.V786M
Pat_01	Pre-Treatment	OR4A15	81328	37	11	55135721	55135721	Missense_Mutation	SNP	C	T	224	43	c.362C>T	c.(361-363)TCC>TTC	p.S121F
Pat_01	Pre-Treatment	OR5D13	390142	37	11	55541751	55541751	Missense_Mutation	SNP	T	C	63	78	c.838T>C	c.(838-840)TAC>CAC	p.Y280H
Pat_01	Pre-Treatment	OR8K5	219453	37	11	55927516	55927516	Missense_Mutation	SNP	G	A	189	257	c.278C>T	c.(277-279)TCC>TTC	p.S93F
Pat_01	Pre-Treatment	MS4A2	2206	37	11	59863103	59863103	Missense_Mutation	SNP	G	A	98	17	c.709G>A	c.(709-711)GAA>AAA	p.E237K
Pat_01	Pre-Treatment	MS4A12	54860	37	11	60271189	60271189	Missense_Mutation	SNP	G	A	108	26	c.487G>A	c.(487-489)GGA>AGA	p.G163R
Pat_01	Pre-Treatment	INTS5	80789	37	11	62415054	62415054	Missense_Mutation	SNP	G	A	192	44	c.2498C>T	c.(2497-2499)CCC>CTC	p.P833L
Pat_01	Pre-Treatment	TSGA10IP	254187	37	11	65715236	65715236	Missense_Mutation	SNP	G	A	5	15	c.940G>A	c.(940-942)GAG>AAG	p.E314K
Pat_01	Pre-Treatment	MYEOV	26579	37	11	69063224	69063224	Missense_Mutation	SNP	G	A	128	173	c.307G>A	c.(307-309)GCT>ACT	p.A103T
Pat_01	Pre-Treatment	NEU3	10825	37	11	74717320	74717320	Missense_Mutation	SNP	G	T	201	412	c.1169G>T	c.(1168-1170)TGG>TTG	p.W390L
Pat_01	Pre-Treatment	DGAT2	84649	37	11	75501768	75501768	Missense_Mutation	SNP	C	T	156	475	c.421C>T	c.(421-423)CCC>TCC	p.P141S
Pat_01	Pre-Treatment	MYO7A	4647	37	11	76905558	76905558	Missense_Mutation	SNP	G	A	16	36	c.4312G>A	c.(4312-4314)GCC>ACC	p.A1438T
Pat_01	Pre-Treatment	MYO7A	4647	37	11	76924018	76924018	Missense_Mutation	SNP	C	T	9	58	c.6376C>T	c.(6376-6378)CCT>TCT	p.P2126S
Pat_01	Pre-Treatment	HEPHL1	341208	37	11	93779011	93779011	Missense_Mutation	SNP	C	T	41	17	c.343C>T	c.(343-345)CAT>TAT	p.H115Y
Pat_01	Pre-Treatment	C11orf65	160140	37	11	108277567	108277567	Missense_Mutation	SNP	C	T	78	17	c.352G>A	c.(352-354)GAT>AAT	p.D118N
Pat_01	Pre-Treatment	LAYN	143903	37	11	111430932	111430932	Missense_Mutation	SNP	G	A	90	18	c.898G>A	c.(898-900)GAA>AAA	p.E300K
Pat_01	Pre-Treatment	FAM55D	54827	37	11	114451040	114451040	Missense_Mutation	SNP	C	G	126	20	c.913G>C	c.(913-915)GAG>CAG	p.E305Q
Pat_01	Pre-Treatment	PRMT8	56341	37	12	3649787	3649787	Missense_Mutation	SNP	T	C	20	260	c.91T>C	c.(91-93)TCC>CCC	p.S31P
Pat_01	Pre-Treatment	EFCAB4B	84766	37	12	3789410	3789410	Missense_Mutation	SNP	C	T	85	121	c.334G>A	c.(334-336)GGA>AGA	p.G112R
Pat_01	Pre-Treatment	LAG3	3902	37	12	6887073	6887073	Missense_Mutation	SNP	C	T	92	111	c.1417C>T	c.(1417-1419)CTT>TTT	p.L473F
Pat_01	Pre-Treatment	A2M	2	37	12	9231867	9231867	Missense_Mutation	SNP	C	T	115	125	c.3092G>A	c.(3091-3093)CGA>CAA	p.R1031Q
Pat_01	Pre-Treatment	TAS2R14	50840	37	12	11091472	11091472	Missense_Mutation	SNP	G	A	48	63	c.335C>T	c.(334-336)GCC>GTC	p.A112V
Pat_01	Pre-Treatment	KIAA1467	57613	37	12	13219625	13219625	Nonsense_Mutation	SNP	C	T	170	204	c.904C>T	c.(904-906)CGA>TGA	p.R302*
Pat_01	Pre-Treatment	C12orf36	283422	37	12	13526349	13526349	Missense_Mutation	SNP	G	A	44	82	c.206C>T	c.(205-207)TCG>TTG	p.S69L
Pat_01	Pre-Treatment	PIK3C2G	5288	37	12	18650562	18650562	Missense_Mutation	SNP	G	A	64	78	c.2773G>A	c.(2773-2775)GAT>AAT	p.D925N
Pat_01	Pre-Treatment	PIK3C2G	5288	37	12	18650568	18650568	Missense_Mutation	SNP	C	T	66	80	c.2779C>T	c.(2779-2781)CGT>TGT	p.R927C
Pat_01	Pre-Treatment	CAPZA3	93661	37	12	18891723	18891723	Nonsense_Mutation	SNP	G	A	114	143	c.521G>A	c.(520-522)TGG>TAG	p.W174*
Pat_01	Pre-Treatment	GYS2	2998	37	12	21693487	21693487	Missense_Mutation	SNP	G	A	4	249	c.1666C>T	c.(1666-1668)CGG>TGG	p.R556W
Pat_01	Pre-Treatment	DDX11	1663	37	12	31237922	31237922	Missense_Mutation	SNP	G	C	5	76	c.500G>C	c.(499-501)AGA>ACA	p.R167T
Pat_01	Pre-Treatment	YARS2	51067	37	12	32908550	32908550	Missense_Mutation	SNP	G	A	112	137	c.259C>T	c.(259-261)CTT>TTT	p.L87F
Pat_01	Pre-Treatment	CNTN1	1272	37	12	41330675	41330675	Missense_Mutation	SNP	C	T	262	380	c.1078C>T	c.(1078-1080)CCT>TCT	p.P360S
Pat_01	Pre-Treatment	GALNT6	11226	37	12	51773172	51773172	Missense_Mutation	SNP	C	T	80	104	c.394G>A	c.(394-396)GAA>AAA	p.E132K
Pat_01	Pre-Treatment	KRT86	3892	37	12	52699481	52699481	Missense_Mutation	SNP	G	A	94	131	c.935G>A	c.(934-936)GGG>GAG	p.G312E
Pat_01	Pre-Treatment	KRT72	140807	37	12	52992823	52992823	Missense_Mutation	SNP	T	C	112	187	c.500A>G	c.(499-501)AAC>AGC	p.N167S
Pat_01	Pre-Treatment	NCKAP1L	3071	37	12	54914488	54914488	Missense_Mutation	SNP	C	T	352	403	c.1636C>T	c.(1636-1638)CGT>TGT	p.R546C
Pat_01	Pre-Treatment	LRP1	4035	37	12	57569758	57569758	Missense_Mutation	SNP	G	A	149	145	c.3860G>A	c.(3859-3861)GGA>GAA	p.G1287E
Pat_01	Pre-Treatment	DCTN2	10540	37	12	57929629	57929629	Splice_Site	SNP	C	T	27	46	c.106_splice	c.e3-1	p.E36_splice

Pat_01	Pre-Treatment	B4GALNT1	2583	37	12	58024260	58024260	Splice_Site	SNP	C	G	3	156	c.531_splice	c.e5+1	p.Q177_splice
Pat_01	Pre-Treatment	MGAT4C	25834	37	12	86373354	86373354	Missense_Mutation	SNP	C	T	9	18	c.1150G>A	c.(1150-1152)GAA>AAA	p.E384K
Pat_01	Pre-Treatment	SLC5A8	160728	37	12	101584309	101584309	Missense_Mutation	SNP	T	C	36	328	c.770A>G	c.(769-771)TAC>TGC	p.Y257C
Pat_01	Pre-Treatment	MYBPC1	4604	37	12	102071915	102071915	Missense_Mutation	SNP	G	C	115	155	c.3124G>C	c.(3124-3126)GAT>CAT	p.D1042H
Pat_01	Pre-Treatment	STAB2	55576	37	12	103988190	103988190	Missense_Mutation	SNP	G	A	281	370	c.233G>A	c.(232-234)AGA>AAA	p.R78K
Pat_01	Pre-Treatment	MYO1H	283446	37	12	109835549	109835549	Missense_Mutation	SNP	G	A	4	101	c.454G>A	c.(454-456)GCC>ACC	p.A152T
Pat_01	Pre-Treatment	IQCD	115811	37	12	113645584	113645584	Missense_Mutation	SNP	G	A	105	127	c.388C>T	c.(388-390)CGC>TGC	p.R130C
Pat_01	Pre-Treatment	RBM19	9904	37	12	114377919	114377919	Missense_Mutation	SNP	G	T	5	568	c.1784C>A	c.(1783-1785)CCG>CAG	p.P595Q
Pat_01	Pre-Treatment	RNF10	9921	37	12	121004694	121004694	Missense_Mutation	SNP	C	T	105	188	c.1952C>T	c.(1951-1953)TCC>TTC	p.S651F
Pat_01	Pre-Treatment	SETD8	387893	37	12	123868746	123868746	Missense_Mutation	SNP	A	G	43	47	c.1A>G	c.(1-3)ATG>GTG	p.M1V
Pat_01	Pre-Treatment	TMEM132D	121256	37	12	129559240	129559240	Missense_Mutation	SNP	G	A	120	154	c.2480C>T	c.(2479-2481)CCC>CTC	p.P827L
Pat_01	Pre-Treatment	LATS2	26524	37	13	21562822	21562822	Missense_Mutation	SNP	G	A	98	95	c.1097C>T	c.(1096-1098)TCC>TTC	p.S366F
Pat_01	Pre-Treatment	FLT3	2322	37	13	28636067	28636067	Missense_Mutation	SNP	G	A	80	120	c.305C>T	c.(304-306)TCC>TTC	p.S102F
Pat_01	Pre-Treatment	BRCA2	675	37	13	32905117	32905117	Missense_Mutation	SNP	C	T	46	66	c.743C>T	c.(742-744)GCT>GTT	p.A248V
Pat_01	Pre-Treatment	SPERT	220082	37	13	46287918	46287918	Missense_Mutation	SNP	A	T	15	19	c.758A>T	c.(757-759)GAG>GTG	p.E253V
Pat_01	Pre-Treatment	NEK3	4752	37	13	52718870	52718870	Nonsense_Mutation	SNP	G	A	47	58	c.760C>T	c.(760-762)CGA>TGA	p.R254*
Pat_01	Pre-Treatment	THSD1	55901	37	13	52972272	52972272	Missense_Mutation	SNP	T	C	222	257	c.116A>G	c.(115-117)AAC>AGC	p.N39S
Pat_01	Pre-Treatment	C13orf34	79866	37	13	73303124	73303124	Missense_Mutation	SNP	C	T	161	176	c.46C>T	c.(46-48)CCA>TCA	p.P16S
Pat_01	Pre-Treatment	ERCC5	2073	37	13	103528102	103528103	Missense_Mutation	DNP	CC	TT	51	82	.3410_3411CC>T	c.(3409-3411)CCC>CTT	p.P1137L
Pat_01	Pre-Treatment	COL4A1	1282	37	13	110813633	110813633	Nonsense_Mutation	SNP	G	A	4	179	c.4546C>T	c.(4546-4548)CGA>TGA	p.R1516*
Pat_01	Pre-Treatment	ING1	3621	37	13	111371747	111371747	Missense_Mutation	SNP	C	T	4	228	c.737C>T	c.(736-738)ACG>ATG	p.T246M
Pat_01	Pre-Treatment	POTEG	404785	37	14	19574211	19574211	Missense_Mutation	SNP	G	A	22	174	c.1268G>A	c.(1267-1269)GGA>GAA	p.G423E
Pat_01	Pre-Treatment	OR4N2	390429	37	14	20295951	20295951	Missense_Mutation	SNP	T	G	198	580	c.344T>G	c.(343-345)CTT>CGT	p.L115R
Pat_01	Pre-Treatment	EDDM3B	64184	37	14	21238594	21238594	Nonsense_Mutation	SNP	G	A	111	172	c.285G>A	c.(283-285)TGG>TGA	p.W95*
Pat_01	Pre-Treatment	SUPT16H	11198	37	14	21820896	21820896	Missense_Mutation	SNP	G	A	145	177	c.3080C>T	c.(3079-3081)TCG>TTG	p.S1027L
Pat_01	Pre-Treatment	NYNRIN	57523	37	14	24886179	24886179	Missense_Mutation	SNP	C	T	34	34	c.5224C>T	c.(5224-5226)CCT>TCT	p.P1742S
Pat_01	Pre-Treatment	NOVA1	4857	37	14	26949277	26949277	Missense_Mutation	SNP	T	C	173	189	c.353A>G	c.(352-354)GAA>GGA	p.E118G
Pat_01	Pre-Treatment	ARHGAP5	394	37	14	32560909	32560909	Missense_Mutation	SNP	C	T	74	108	c.1034C>T	c.(1033-1035)GCT>GTT	p.A345V
Pat_01	Pre-Treatment	MIA2	117153	37	14	39716382	39716382	Missense_Mutation	SNP	G	A	122	137	c.604G>A	c.(604-606)GAA>AAA	p.E202K
Pat_01	Pre-Treatment	SYT16	83851	37	14	62463164	62463164	Missense_Mutation	SNP	G	A	167	223	c.427G>A	c.(427-429)GAA>AAA	p.E143K
Pat_01	Pre-Treatment	ZFYVE26	23503	37	14	68233053	68233053	Missense_Mutation	SNP	G	A	152	246	c.5902C>T	c.(5902-5904)CCA>TCA	p.P1968S
Pat_01	Pre-Treatment	SIPA1L1	26037	37	14	72176267	72176267	Missense_Mutation	SNP	G	A	4	132	c.4157G>A	c.(4156-4158)CGG>CAG	p.R1386Q
Pat_01	Pre-Treatment	SIPA1L1	26037	37	14	72176309	72176309	Missense_Mutation	SNP	G	A	50	115	c.4199G>A	c.(4198-4200)AGC>AAC	p.S1400N
Pat_01	Pre-Treatment	NUMB	8650	37	14	73750939	73750939	Missense_Mutation	SNP	G	A	127	190	c.799C>T	c.(799-801)CCA>TCA	p.P267S
Pat_01	Pre-Treatment	STON2	85439	37	14	81744649	81744649	Nonsense_Mutation	SNP	C	A	5	297	c.1006G>T	c.(1006-1008)GAG>TAG	p.E336*
Pat_01	Pre-Treatment	KCNK10	54207	37	14	88693861	88693861	Missense_Mutation	SNP	G	A	149	223	c.524C>T	c.(523-525)CCG>CTG	p.P175L
Pat_01	Pre-Treatment	TTC7B	145567	37	14	91247111	91247111	Missense_Mutation	SNP	C	A	4	267	c.416G>T	c.(415-417)CGG>CTG	p.R139L
Pat_01	Pre-Treatment	FBLN5	10516	37	14	92353657	92353657	Splice_Site	SNP	C	T	189	257	c.620_splice	c.e7-1	p.D207_splice
Pat_01	Pre-Treatment	TCL1B	9623	37	14	96152937	96152937	Missense_Mutation	SNP	G	A	39	34	c.133G>A	c.(133-135)GAA>AAA	p.E45K
Pat_01	Pre-Treatment	TCL1A	8115	37	14	96178108	96178108	Missense_Mutation	SNP	A	C	40	73	c.329T>G	c.(328-330)CTG>CGG	p.L110R
Pat_01	Pre-Treatment	TECPR2	9895	37	14	102916167	102916167	Missense_Mutation	SNP	G	T	4	213	c.3277G>T	c.(3277-3279)GGC>TGC	p.G1093C
Pat_01	Pre-Treatment	C14orf180	400258	37	14	105054646	105054646	Missense_Mutation	SNP	G	A	180	312	c.277G>A	c.(277-279)GTG>ATG	p.V93M
Pat_01	Pre-Treatment	AHNAK2	113146	37	14	105407164	105407164	Missense_Mutation	SNP	G	A	4	105	c.14624C>T	c.(14623-14625)CCC>CTC	p.P4875L
Pat_01	Pre-Treatment	NUDT14	256281	37	14	105642910	105642910	Missense_Mutation	SNP	T	A	112	140	c.389A>T	c.(388-390)CAC>CTC	p.H130L
Pat_01	Pre-Treatment	C15orf2	23742	37	15	24923518	24923518	Missense_Mutation	SNP	T	C	130	233	c.2504T>C	c.(2503-2505)ATC>ACC	p.I835T
Pat_01	Pre-Treatment	ARHGAP11A	9824	37	15	32917400	32917400	Missense_Mutation	SNP	A	G	4	189	c.671A>G	c.(670-672)CAG>CGG	p.Q224R
Pat_01	Pre-Treatment	RYR3	6263	37	15	33954496	33954496	Missense_Mutation	SNP	C	T	21	36	c.4765C>T	c.(4765-4767)CTC>TTC	p.L1589F

Pat_01	Pre-Treatment	EIF2AK4	440275	37	15	40241377	40241377	Missense_Mutation	SNP	C	T	206	505	c.421C>T	c.(421-423)CCT>TCT	p.P141S
Pat_01	Pre-Treatment	PLA2G4F	255189	37	15	42442639	42442639	Missense_Mutation	SNP	C	T	56	113	c.817G>A	c.(817-819)GAG>AAG	p.E273K
Pat_01	Pre-Treatment	CGNL1	84952	37	15	57730330	57730330	Missense_Mutation	SNP	C	T	105	259	c.133C>T	c.(133-135)CGG>TGG	p.R45W
Pat_01	Pre-Treatment	CGNL1	84952	37	15	57731143	57731143	Missense_Mutation	SNP	G	A	76	163	c.946G>A	c.(946-948)GAT>AAT	p.D316N
Pat_01	Pre-Treatment	NARG2	79664	37	15	60741638	60741638	Missense_Mutation	SNP	T	C	126	312	c.1528A>G	c.(1528-1530)ACA>GCA	p.T510A
Pat_01	Pre-Treatment	IQCH	64799	37	15	67681327	67681327	Missense_Mutation	SNP	G	A	144	296	c.1615G>A	c.(1615-1617)GCT>ACT	p.A539T
Pat_01	Pre-Treatment	C15orf17	57184	37	15	75198620	75198620	Missense_Mutation	SNP	T	C	3	92	c.301A>G	c.(301-303)AGG>GGG	p.R101G
Pat_01	Pre-Treatment	IL16	3603	37	15	81552144	81552144	Missense_Mutation	SNP	C	T	158	107	c.344C>T	c.(343-345)CCT>CTT	p.P115L
Pat_01	Pre-Treatment	RCCD1	91433	37	15	91504926	91504926	Missense_Mutation	SNP	A	G	281	218	c.1058A>G	c.(1057-1059)CAA>CGA	p.Q353R
Pat_01	Pre-Treatment	MCTP2	55784	37	15	94913329	94913329	Missense_Mutation	SNP	C	T	74	120	c.1502C>T	c.(1501-1503)TCC>TTC	p.S501F
Pat_01	Pre-Treatment	SOLH	6650	37	16	603470	603470	Missense_Mutation	SNP	C	A	5	217	c.3215C>A	c.(3214-3216)CCA>CAA	p.P1072Q
Pat_01	Pre-Treatment	CCDC78	124093	37	16	775481	775481	Missense_Mutation	SNP	G	A	4	234	c.367C>T	c.(367-369)CGG>TGG	p.R123W
Pat_01	Pre-Treatment	CACNA1H	8912	37	16	1270224	1270224	Missense_Mutation	SNP	G	A	38	82	c.6292G>A	c.(6292-6294)GAC>AAC	p.D2098N
Pat_01	Pre-Treatment	TELO2	9894	37	16	1556291	1556292	Missense_Mutation	DNP	CC	TT	240	510	.2087_2088CC>T	c.(2086-2088)GCC>GTT	p.A696V
Pat_01	Pre-Treatment	C16orf90	646174	37	16	3544626	3544626	Missense_Mutation	SNP	C	T	58	94	c.298G>A	c.(298-300)GCC>ACC	p.A100T
Pat_01	Pre-Treatment	GRIN2A	2903	37	16	9916133	9916133	Missense_Mutation	SNP	C	T	92	379	c.2156G>A	c.(2155-2157)AGC>AAC	p.S719N
Pat_01	Pre-Treatment	SRCAP	10847	37	16	30734010	30734010	Missense_Mutation	SNP	C	T	504	75	c.3833C>T	c.(3832-3834)TCG>TTG	p.S1278L
Pat_01	Pre-Treatment	PHKB	5257	37	16	47683017	47683017	Missense_Mutation	SNP	C	T	126	44	c.1699C>T	c.(1699-1701)CGC>TGC	p.R567C
Pat_01	Pre-Treatment	CES3	23491	37	16	66997147	66997147	Missense_Mutation	SNP	G	A	6	461	c.148G>A	c.(148-150)GTG>ATG	p.V50M
Pat_01	Pre-Treatment	HSD17B2	3294	37	16	82069273	82069273	Nonsense_Mutation	SNP	C	T	225	321	c.244C>T	c.(244-246)CAG>TAG	p.Q82*
Pat_01	Pre-Treatment	GGT6	124975	37	17	4462049	4462049	Missense_Mutation	SNP	C	T	6	8	c.743G>A	c.(742-744)CGA>CAA	p.R248Q
Pat_01	Pre-Treatment	SHBG	6462	37	17	7536230	7536230	Missense_Mutation	SNP	A	T	37	49	c.1013A>T	c.(1012-1014)AAC>ATC	p.N338I
Pat_01	Pre-Treatment	DNAH2	146754	37	17	7727448	7727448	Missense_Mutation	SNP	G	A	136	210	c.11488G>A	c.(11488-11490)GAT>AAT	p.D3830N
Pat_01	Pre-Treatment	MYH4	4622	37	17	10357171	10357171	Missense_Mutation	SNP	C	T	199	315	c.2723G>A	c.(2722-2724)AGA>AAA	p.R908K
Pat_01	Pre-Treatment	MYH4	4622	37	17	10359819	10359819	Missense_Mutation	SNP	C	A	4	202	c.1951G>T	c.(1951-1953)GTG>TTG	p.V651L
Pat_01	Pre-Treatment	MYH4	4622	37	17	10363572	10363572	Missense_Mutation	SNP	G	A	210	235	c.1214C>T	c.(1213-1215)CCC>CTC	p.P405L
Pat_01	Pre-Treatment	KCNJ12	3768	37	17	21319835	21319835	Missense_Mutation	SNP	G	A	28	192	c.1181G>A	c.(1180-1182)GGA>GAA	p.G394E
Pat_01	Pre-Treatment	MYO18A	399687	37	17	27493378	27493378	Missense_Mutation	SNP	G	A	133	174	c.581C>T	c.(580-582)CCT>CTT	p.P194L
Pat_01	Pre-Treatment	SLFN11	91607	37	17	33679659	33679659	Missense_Mutation	SNP	C	T	36	56	c.2422G>A	c.(2422-2424)GAT>AAT	p.D808N
Pat_01	Pre-Treatment	PEX12	5193	37	17	33904992	33904992	Nonsense_Mutation	SNP	G	A	5	316	c.49C>T	c.(49-51)CAG>TAG	p.Q17*
Pat_01	Pre-Treatment	KRT20	54474	37	17	39036935	39036935	Missense_Mutation	SNP	T	A	145	160	c.561A>T	c.(559-561)AAA>AAT	p.K187N
Pat_01	Pre-Treatment	TTC25	83538	37	17	40101446	40101446	Missense_Mutation	SNP	G	A	30	53	c.1115G>A	c.(1114-1116)AGA>AAA	p.R372K
Pat_01	Pre-Treatment	ATP6V0A1	535	37	17	40642652	40642652	Missense_Mutation	SNP	C	T	61	100	c.1171C>T	c.(1171-1173)CCA>TCA	p.P391S
Pat_01	Pre-Treatment	RAMP2	10266	37	17	40914839	40914839	Nonsense_Mutation	SNP	G	A	114	138	c.497G>A	c.(496-498)TGG>TAG	p.W166*
Pat_01	Pre-Treatment	NSF	4905	37	17	44788422	44788422	Missense_Mutation	SNP	G	A	4	240	c.1564G>A	c.(1564-1566)GAG>AAG	p.E522K
Pat_01	Pre-Treatment	TTLL6	284076	37	17	46862461	46862461	Missense_Mutation	SNP	G	A	119	148	c.1864C>T	c.(1864-1866)CCC>TCC	p.P622S
Pat_01	Pre-Treatment	UBE2Z	65264	37	17	46993463	46993463	Missense_Mutation	SNP	C	T	43	75	c.604C>T	c.(604-606)CCA>TCA	p.P202S
Pat_01	Pre-Treatment	WFIKKN2	124857	37	17	48918261	48918261	Missense_Mutation	SNP	G	A	68	100	c.1612G>A	c.(1612-1614)GCC>ACC	p.A538T
Pat_01	Pre-Treatment	PPM1E	22843	37	17	57046948	57046948	Missense_Mutation	SNP	G	A	141	200	c.832G>A	c.(832-834)GTA>ATA	p.V278I
Pat_01	Pre-Treatment	MRC2	9902	37	17	60766309	60766309	Nonsense_Mutation	SNP	C	T	43	56	c.3322C>T	c.(3322-3324)CAG>TAG	p.Q1108*
Pat_01	Pre-Treatment	CD300E	342510	37	17	72613523	72613523	Missense_Mutation	SNP	A	G	70	110	c.122T>C	c.(121-123)ATG>ACG	p.M41T
Pat_01	Pre-Treatment	DSC1	1823	37	18	28711805	28711805	Missense_Mutation	SNP	C	T	52	78	c.2239G>A	c.(2239-2241)GAA>AAA	p.E747K
Pat_01	Pre-Treatment	DSG2	1829	37	18	29104411	29104411	Missense_Mutation	SNP	G	A	122	142	c.691G>A	c.(691-693)GAA>AAA	p.E231K
Pat_01	Pre-Treatment	TCEB3B	51224	37	18	44560359	44560359	Missense_Mutation	SNP	G	A	79	98	c.1277C>T	c.(1276-1278)TCG>TTG	p.S426L
Pat_01	Pre-Treatment	DCC	1630	37	18	50432696	50432696	Missense_Mutation	SNP	C	T	100	157	c.695C>T	c.(694-696)TCA>TTA	p.S232L
Pat_01	Pre-Treatment	ALPK2	115701	37	18	56246968	56246968	Missense_Mutation	SNP	T	C	140	233	c.1040A>G	c.(1039-1041)AAC>AGC	p.N347S
Pat_01	Pre-Treatment	ZNF407	55628	37	18	72589239	72589239	Missense_Mutation	SNP	C	T	126	132	c.4964C>T	c.(4963-4965)CCG>CTG	p.P1655L

Pat_01	Pre-Treatment	MED16	10025	37	19	875420	875420	Missense_Mutation	SNP	G	A	34	52	c.1595C>T	c.(1594-1596)TCG>TTG	p.S532L
Pat_01	Pre-Treatment	WDR18	57418	37	19	984364	984365	Missense_Mutation	DNP	CC	TT	28	29	c.11_12CC>TT	c.(10-12)CCC>CTT	p.P4L
Pat_01	Pre-Treatment	ZNF556	80032	37	19	2878101	2878101	Missense_Mutation	SNP	C	T	65	89	c.1145C>T	c.(1144-1146)TCC>TTC	p.S382F
Pat_01	Pre-Treatment	ZNF57	126295	37	19	2917857	2917857	Missense_Mutation	SNP	C	T	10	224	c.1238C>T	c.(1237-1239)ACG>ATG	p.T413M
Pat_01	Pre-Treatment	PTPRS	5802	37	19	5212427	5212427	Missense_Mutation	SNP	G	A	26	28	c.4690C>T	c.(4690-4692)CCA>TCA	p.P1564S
Pat_01	Pre-Treatment	RFX2	5990	37	19	6002814	6002814	Missense_Mutation	SNP	G	A	4	69	c.1568C>T	c.(1567-1569)GCG>GTG	p.A523V
Pat_01	Pre-Treatment	EMR1	2015	37	19	6908704	6908704	Missense_Mutation	SNP	C	T	26	53	c.1043C>T	c.(1042-1044)TCC>TTC	p.S348F
Pat_01	Pre-Treatment	FBN3	84467	37	19	8145902	8145902	Missense_Mutation	SNP	G	A	63	73	c.7438C>T	c.(7438-7440)CAC>TAC	p.H2480Y
Pat_01	Pre-Treatment	MUC16	94025	37	19	8959682	8959682	Missense_Mutation	SNP	C	T	48	58	c.43450G>A	c.(43450-43452)GAA>AAA	p.E14484K
Pat_01	Pre-Treatment	MUC16	94025	37	19	9013868	9013868	Missense_Mutation	SNP	G	A	38	71	c.38522C>T	c.(38521-38523)CCA>CTA	p.P12841L
Pat_01	Pre-Treatment	MUC16	94025	37	19	9016716	9016716	Missense_Mutation	SNP	C	T	50	52	c.38021G>A	.(38020-38022)GGG>GA	p.G12674E
Pat_01	Pre-Treatment	ZNF561	93134	37	19	9724705	9724705	Missense_Mutation	SNP	T	A	130	171	c.316A>T	c.(316-318)ATA>TTA	p.I106L
Pat_01	Pre-Treatment	ZNF844	284391	37	19	12187307	12187307	Missense_Mutation	SNP	G	C	7	249	c.1372G>C	c.(1372-1374)GAT>CAT	p.D458H
Pat_01	Pre-Treatment	ZNF844	284391	37	19	12187502	12187502	Missense_Mutation	SNP	A	G	8	90	c.1567A>G	c.(1567-1569)AAA>GAA	p.K523E
Pat_01	Pre-Treatment	IL27RA	9466	37	19	14157377	14157377	Missense_Mutation	SNP	A	G	157	214	c.1088A>G	c.(1087-1089)GAG>GGG	p.E363G
Pat_01	Pre-Treatment	NWD1	284434	37	19	16908555	16908555	Missense_Mutation	SNP	C	T	139	368	c.3317C>T	c.(3316-3318)TCG>TTG	p.S1106L
Pat_01	Pre-Treatment	UNC13A	23025	37	19	17743703	17743703	Missense_Mutation	SNP	G	A	63	157	c.3580C>T	c.(3580-3582)CGT>TGT	p.R1194C
Pat_01	Pre-Treatment	UNC13A	23025	37	19	17750670	17750671	Missense_Mutation	DNP	CC	TT	79	268	.3098_3099GG>A	c.(3097-3099)CGG>CAA	p.R1033Q
Pat_01	Pre-Treatment	UPF1	5976	37	19	18961603	18961603	Missense_Mutation	SNP	C	T	21	60	c.736C>T	c.(736-738)CCC>TCC	p.P246S
Pat_01	Pre-Treatment	ZNF99	7652	37	19	22939472	22939472	Missense_Mutation	SNP	A	G	5	93	c.2699T>C	c.(2698-2700)TTC>TCC	p.F900S
Pat_01	Pre-Treatment	ZNF99	7652	37	19	22939868	22939868	Missense_Mutation	SNP	C	G	69	86	c.2463G>C	c.(2461-2463)AAG>AAC	p.K821N
Pat_01	Pre-Treatment	UQCRFS1	7386	37	19	29698570	29698570	Missense_Mutation	SNP	G	A	74	129	c.710C>T	c.(709-711)CCT>CTT	p.P237L
Pat_01	Pre-Treatment	SLC7A9	11136	37	19	33355618	33355618	Missense_Mutation	SNP	G	A	148	255	c.152C>T	c.(151-153)TCC>TTC	p.S51F
Pat_01	Pre-Treatment	HPN	3249	37	19	35551596	35551596	Missense_Mutation	SNP	G	A	153	179	c.686G>A	c.(685-687)GGT>GAT	p.G229D
Pat_01	Pre-Treatment	NPHS1	4868	37	19	36322215	36322215	Missense_Mutation	SNP	C	T	108	158	c.3370G>A	c.(3370-3372)GAC>AAC	p.D1124N
Pat_01	Pre-Treatment	NPHS1	4868	37	19	36333452	36333452	Missense_Mutation	SNP	C	T	73	99	c.2335G>A	c.(2335-2337)GGA>AGA	p.G779R
Pat_01	Pre-Treatment	ZNF585B	92285	37	19	37677499	37677499	Nonsense_Mutation	SNP	G	A	202	308	c.940C>T	c.(940-942)CAG>TAG	p.Q314*
Pat_01	Pre-Treatment	CATSPERG	57828	37	19	38850110	38850110	Missense_Mutation	SNP	C	A	4	217	c.1497C>A	c.(1495-1497)AGC>AGA	p.S499R
Pat_01	Pre-Treatment	ZNF283	284349	37	19	44351759	44351759	Missense_Mutation	SNP	A	C	4	111	c.1006A>C	c.(1006-1008)AAA>CAA	p.K336Q
Pat_01	Pre-Treatment	ZNF229	7772	37	19	44933887	44933888	Missense_Mutation	DNP	CC	TT	141	239	.1068_1069GG>A	66-1071)AAGGGG>AAA	p.G357R
Pat_01	Pre-Treatment	KLC3	147700	37	19	45852115	45852115	Missense_Mutation	SNP	G	A	6	20	c.905G>A	c.(904-906)GGG>GAG	p.G302E
Pat_01	Pre-Treatment	IRF2BP1	26145	37	19	46388908	46388908	Missense_Mutation	SNP	G	T	3	47	c.125C>A	c.(124-126)GCG>GAG	p.A42E
Pat_01	Pre-Treatment	FAM83E	54854	37	19	49104526	49104526	Missense_Mutation	SNP	G	A	17	32	c.1277C>T	c.(1276-1278)CCG>CTG	p.P426L
Pat_01	Pre-Treatment	GYS1	2997	37	19	49472621	49472621	Missense_Mutation	SNP	G	A	3	33	c.2138C>T	c.(2137-2139)ACG>ATG	p.T713M
Pat_01	Pre-Treatment	MED25	81857	37	19	50335400	50335400	Missense_Mutation	SNP	C	T	54	79	c.1360C>T	c.(1360-1362)CCC>TCC	p.P454S
Pat_01	Pre-Treatment	SPIB	6689	37	19	50926223	50926223	Missense_Mutation	SNP	G	A	171	187	c.268G>A	c.(268-270)GAA>AAA	p.E90K
Pat_01	Pre-Treatment	SHANK1	50944	37	19	51191261	51191261	Missense_Mutation	SNP	G	A	143	178	c.2227C>T	c.(2227-2229)CGC>TGC	p.R743C
Pat_01	Pre-Treatment	GPR32	2854	37	19	51274491	51274491	Missense_Mutation	SNP	G	A	52	92	c.634G>A	c.(634-636)GGA>AGA	p.G212R
Pat_01	Pre-Treatment	KLK5	25818	37	19	51451976	51451976	Missense_Mutation	SNP	T	C	4	212	c.646A>G	c.(646-648)AGG>GGG	p.R216G
Pat_01	Pre-Treatment	ZNF845	91664	37	19	53856702	53856702	Missense_Mutation	SNP	G	A	4	83	c.2774G>A	c.(2773-2775)CGT>CAT	p.R925H
Pat_01	Pre-Treatment	LILRB5	10990	37	19	54759200	54759200	Missense_Mutation	SNP	G	A	83	146	c.901C>T	c.(901-903)CTC>TTC	p.L301F
Pat_01	Pre-Treatment	NLRP2	55655	37	19	55494049	55494049	Missense_Mutation	SNP	C	T	42	38	c.983C>T	c.(982-984)CCC>CTC	p.P328L
Pat_01	Pre-Treatment	USP29	57663	37	19	57642039	57642039	Missense_Mutation	SNP	G	A	43	66	c.1996G>A	c.(1996-1998)GGA>AGA	p.G666R
Pat_01	Pre-Treatment	C2orf39	92749	37	2	26663249	26663249	Missense_Mutation	SNP	C	T	29	62	c.892C>T	c.(892-894)CTT>TTT	p.L298F
Pat_01	Pre-Treatment	SRD5A2	6716	37	2	31756517	31756517	Missense_Mutation	SNP	C	T	10	13	c.471G>A	c.(469-471)ATG>ATA	p.M157I
Pat_01	Pre-Treatment	SOS1	6654	37	2	39213333	39213333	Missense_Mutation	SNP	G	A	199	370	c.3634C>T	c.(3634-3636)CCC>TCC	p.P1212S
Pat_01	Pre-Treatment	EFEMP1	2202	37	2	56108861	56108861	Missense_Mutation	SNP	C	T	252	343	c.526G>A	c.(526-528)GAG>AAG	p.E176K

Pat_01	Pre-Treatment	FAM161A	84140	37	2	62081080	62081080	Missense_Mutation	SNP	C	T	63	75	c.97G>A	c.(97-99)GAA>AAA	p.E33K
Pat_01	Pre-Treatment	REV1	51455	37	2	100020202	100020203	Missense_Mutation	DNP	CT	TC	167	258	.3121_3122AG>G	c.(3121-3123)AGG>GAG	p.R1041E
Pat_01	Pre-Treatment	DBI	1622	37	2	120128380	120128380	Splice_Site	SNP	T	C	3	118	c.190_splice	c.e3+2	p.G64_splice
Pat_01	Pre-Treatment	ARHGAP15	55843	37	2	144276883	144276883	Missense_Mutation	SNP	C	T	155	231	c.875C>T	c.(874-876)TCC>TTC	p.S292F
Pat_01	Pre-Treatment	NEB	4703	37	2	152518729	152518729	Missense_Mutation	SNP	G	A	82	86	c.5890C>T	c.(5890-5892)CCA>TCA	p.P1964S
Pat_01	Pre-Treatment	CACNB4	785	37	2	152727103	152727103	Missense_Mutation	SNP	T	G	42	69	c.641A>C	c.(640-642)GAT>GCT	p.D214A
Pat_01	Pre-Treatment	TANC1	85461	37	2	160087464	160087464	Missense_Mutation	SNP	C	A	4	194	c.5527C>A	c.(5527-5529)CAC>AAC	p.H1843N
Pat_01	Pre-Treatment	BAZ2B	29994	37	2	160242971	160242971	Nonsense_Mutation	SNP	G	A	242	302	c.3364C>T	c.(3364-3366)CAA>TAA	p.Q1122*
Pat_01	Pre-Treatment	KCNH7	90134	37	2	163693083	163693083	Missense_Mutation	SNP	C	T	71	122	c.271G>A	c.(271-273)GAG>AAG	p.E91K
Pat_01	Pre-Treatment	SCN3A	6328	37	2	165946757	165946757	Missense_Mutation	SNP	G	A	16	29	c.5906C>T	c.(5905-5907)TCC>TTC	p.S1969F
Pat_01	Pre-Treatment	LRP2	4036	37	2	170042104	170042104	Missense_Mutation	SNP	C	G	23	375	c.9754G>C	c.(9754-9756)GAG>CAG	p.E3252Q
Pat_01	Pre-Treatment	PPIG	9360	37	2	170463619	170463619	Missense_Mutation	SNP	G	A	214	364	c.250G>A	c.(250-252)GGA>AGA	p.G84R
Pat_01	Pre-Treatment	OSBPL6	114880	37	2	179213981	179213981	Missense_Mutation	SNP	C	T	359	441	c.1018C>T	c.(1018-1020)CGC>TGC	p.R340C
Pat_01	Pre-Treatment	TTN	7273	37	2	179426716	179426716	Missense_Mutation	SNP	A	T	29	43	c.76439T>A	c.(76438-76440)ATT>AAT	p.I25480N
Pat_01	Pre-Treatment	TTN	7273	37	2	179612027	179612027	Missense_Mutation	SNP	C	T	91	136	c.15100G>A	c.(15100-15102)GAA>AAA	p.E5034K
Pat_01	Pre-Treatment	TTN	7273	37	2	179613066	179613066	Missense_Mutation	SNP	C	T	111	166	c.14061G>A	c.(14059-14061)ATG>ATA	p.M4687I
Pat_01	Pre-Treatment	WDR12	55759	37	2	203757384	203757384	Nonsense_Mutation	SNP	G	A	99	147	c.697C>T	c.(697-699)CGA>TGA	p.R233*
Pat_01	Pre-Treatment	WDR12	55759	37	2	203760919	203760919	Missense_Mutation	SNP	T	C	46	62	c.478A>G	c.(478-480)AGT>GGT	p.S160G
Pat_01	Pre-Treatment	ABCA12	26154	37	2	215866284	215866284	Missense_Mutation	SNP	C	T	191	252	c.2861G>A	c.(2860-2862)GGA>GAA	p.G954E
Pat_01	Pre-Treatment	ALPI	248	37	2	233323569	233323569	Splice_Site	SNP	G	A	23	18	c.1301_splice	c.e11-1	p.G434_splice
Pat_01	Pre-Treatment	DNAJB3	414061	37	2	234652346	234652346	Missense_Mutation	SNP	C	T	201	208	c.217G>A	c.(217-219)GCG>ACG	p.A73T
Pat_01	Pre-Treatment	COL6A3	1293	37	2	238267865	238267865	Missense_Mutation	SNP	C	T	143	255	c.6338G>A	c.(6337-6339)GGT>GAT	p.G2113D
Pat_01	Pre-Treatment	DEFB125	245938	37	20	76798	76798	Missense_Mutation	SNP	C	T	292	385	c.211C>T	c.(211-213)CCT>TCT	p.P71S
Pat_01	Pre-Treatment	PLCB4	5332	37	20	9404512	9404512	Missense_Mutation	SNP	C	T	115	92	c.2401C>T	c.(2401-2403)CTT>TTT	p.L801F
Pat_01	Pre-Treatment	PAK7	57144	37	20	9561331	9561331	Missense_Mutation	SNP	G	A	288	379	c.451C>T	c.(451-453)CTC>TTC	p.L151F
Pat_01	Pre-Treatment	CBFA2T2	9139	37	20	32194875	32194875	Missense_Mutation	SNP	C	T	124	148	c.175C>T	c.(175-177)CCG>TCG	p.P59S
Pat_01	Pre-Treatment	C20orf111	51526	37	20	42825898	42825898	Missense_Mutation	SNP	G	A	85	116	c.673C>T	c.(673-675)CCC>TCC	p.P225S
Pat_01	Pre-Treatment	TSHZ2	128553	37	20	51872939	51872939	Missense_Mutation	SNP	C	T	59	98	c.2942C>T	c.(2941-2943)CCA>CTA	p.P981L
Pat_01	Pre-Treatment	KCNQ2	3785	37	20	62039819	62039819	Missense_Mutation	SNP	C	T	22	30	c.1834G>A	c.(1834-1836)GAG>AAG	p.E612K
Pat_01	Pre-Treatment	TPTE	7179	37	21	10942755	10942755	Missense_Mutation	SNP	C	T	197	614	c.686G>A	c.(685-687)CGA>CAA	p.R229Q
Pat_01	Pre-Treatment	KRTAP10-8	386681	37	21	46032171	46032171	Missense_Mutation	SNP	G	A	122	279	c.154G>A	c.(154-156)GAG>AAG	p.E52K
Pat_01	Pre-Treatment	PCNT	5116	37	21	47836365	47836365	Missense_Mutation	SNP	C	T	187	417	c.6533C>T	c.(6532-6534)CCC>CTC	p.P2178L
Pat_01	Pre-Treatment	POTEH	23784	37	22	16267070	16267070	Missense_Mutation	SNP	C	T	76	669	c.1379G>A	c.(1378-1380)GGA>GAA	p.G460E
Pat_01	Pre-Treatment	CCT8L2	150160	37	22	17072146	17072147	Missense_Mutation	DNP	CC	TT	41	89	.1294_1295GG>A	c.(1294-1296)GGG>AAG	p.G432K
Pat_01	Pre-Treatment	RTN4R	65078	37	22	20229672	20229672	Missense_Mutation	SNP	C	G	33	42	c.984G>C	c.(982-984)GAG>GAC	p.E328D
Pat_01	Pre-Treatment	EMID1	129080	37	22	29630293	29630293	Splice_Site	SNP	G	A	47	63	c.1024_splice	c.e12-1	p.G342_splice
Pat_01	Pre-Treatment	MTMR3	8897	37	22	30415933	30415933	Missense_Mutation	SNP	C	T	183	195	c.2285C>T	c.(2284-2286)TCA>TTA	p.S762L
Pat_01	Pre-Treatment	DEPDC5	9681	37	22	32200858	32200858	Missense_Mutation	SNP	C	T	309	347	c.1174C>T	c.(1174-1176)CGT>TGT	p.R392C
Pat_01	Pre-Treatment	RASD2	23551	37	22	35947904	35947904	Missense_Mutation	SNP	G	A	81	89	c.626G>A	c.(625-627)GGT>GAT	p.G209D
Pat_01	Pre-Treatment	TUBGCP6	85378	37	22	50659166	50659166	Missense_Mutation	SNP	T	C	5	286	c.3622A>G	c.(3622-3624)ACC>GCC	p.T1208A
Pat_01	Pre-Treatment	ITPR1	3708	37	3	4725218	4725218	Missense_Mutation	SNP	C	T	91	87	c.3283C>T	c.(3283-3285)CTC>TTC	p.L1095F
Pat_01	Pre-Treatment	IL17RC	84818	37	3	9970171	9970171	Splice_Site	SNP	G	A	5	424	c.1272_splice	c.e11+1	p.D424_splice
Pat_01	Pre-Treatment	FGD5	152273	37	3	14974174	14974174	Missense_Mutation	SNP	C	T	131	209	c.4288C>T	c.(4288-4290)CAC>TAC	p.H1430Y
Pat_01	Pre-Treatment	ZNF385D	79750	37	3	21478603	21478603	Missense_Mutation	SNP	C	T	114	163	c.532G>A	c.(532-534)GAA>AAA	p.E178K
Pat_01	Pre-Treatment	TRANK1	9881	37	3	36893807	36893807	Missense_Mutation	SNP	C	T	13	15	c.2797G>A	c.(2797-2799)GAT>AAT	p.D933N
Pat_01	Pre-Treatment	VILL	50853	37	3	38043308	38043308	Missense_Mutation	SNP	C	A	74	136	c.1436C>A	c.(1435-1437)CCC>CAC	p.P479H
Pat_01	Pre-Treatment	DLEC1	9940	37	3	38134291	38134292	Missense_Mutation	DNP	CC	TT	94	190	.1676_1677CC>T	c.(1675-1677)TCC>TTT	p.S559F

Pat_01	Pre-Treatment	SCN10A	6336	37	3	38740026	38740026	Missense_Mutation	SNP	G	A	100	135	c.4685C>T	c.(4684-4686)TCA>TTA	p.S1562L
Pat_01	Pre-Treatment	MYRIP	25924	37	3	40251444	40251444	Missense_Mutation	SNP	G	A	85	105	c.1765G>A	c.(1765-1767)GAG>AAG	p.E589K
Pat_01	Pre-Treatment	TRAK1	22906	37	3	42243999	42243999	Missense_Mutation	SNP	G	A	52	49	c.1499G>A	c.(1498-1500)AGG>AAG	p.R500K
Pat_01	Pre-Treatment	CCR1	1230	37	3	46244880	46244880	Missense_Mutation	SNP	G	A	80	87	c.925C>T	c.(925-927)CGG>TGG	p.R309W
Pat_01	Pre-Treatment	KLHL18	23276	37	3	47324519	47324519	Missense_Mutation	SNP	A	T	32	33	c.64A>T	c.(64-66)AGT>TGT	p.S22C
Pat_01	Pre-Treatment	BSN	8927	37	3	49689975	49689975	Missense_Mutation	SNP	C	T	47	87	c.2986C>T	c.(2986-2988)CCC>TCC	p.P996S
Pat_01	Pre-Treatment	OR5H15	403274	37	3	97887907	97887907	Missense_Mutation	SNP	C	T	227	300	c.364C>T	c.(364-366)CGC>TGC	p.R122C
Pat_01	Pre-Treatment	COL8A1	1295	37	3	99514930	99514930	Missense_Mutation	SNP	G	A	86	95	c.2185G>A	c.(2185-2187)GGG>AGG	p.G729R
Pat_01	Pre-Treatment	HHLA2	11148	37	3	108072466	108072466	Missense_Mutation	SNP	C	T	88	125	c.257C>T	c.(256-258)CCC>CTC	p.P86L
Pat_01	Pre-Treatment	C3orf30	152405	37	3	118865259	118865259	Missense_Mutation	SNP	G	A	83	114	c.223G>A	c.(223-225)GTA>ATA	p.V75I
Pat_01	Pre-Treatment	PARP9	83666	37	3	122278457	122278457	Missense_Mutation	SNP	G	A	185	311	c.11C>T	c.(10-12)TCC>TTC	p.S4F
Pat_01	Pre-Treatment	FAIM	55179	37	3	138340328	138340328	Missense_Mutation	SNP	G	A	118	132	c.58G>A	c.(58-60)GAA>AAA	p.E20K
Pat_01	Pre-Treatment	PLSCR4	57088	37	3	145912973	145912973	Missense_Mutation	SNP	G	A	157	148	c.883C>T	c.(883-885)CAC>TAC	p.H295Y
Pat_01	Pre-Treatment	SLC2A2	6514	37	3	170716922	170716922	Missense_Mutation	SNP	G	A	132	161	c.1102C>T	c.(1102-1104)CTC>TTC	p.L368F
Pat_01	Pre-Treatment	TNFSF10	8743	37	3	172227075	172227075	Missense_Mutation	SNP	C	T	77	108	c.350G>A	c.(349-351)AGA>AAA	p.R117K
Pat_01	Pre-Treatment	KCNMB2	10242	37	3	178545976	178545976	Missense_Mutation	SNP	G	A	177	220	c.238G>A	c.(238-240)GAA>AAA	p.E80K
Pat_01	Pre-Treatment	EPHB3	2049	37	3	184290328	184290328	Missense_Mutation	SNP	C	T	105	149	c.220C>T	c.(220-222)CCC>TCC	p.P74S
Pat_01	Pre-Treatment	TP63	8626	37	3	189586470	189586470	Missense_Mutation	SNP	C	T	156	212	c.1094C>T	c.(1093-1095)TCG>TTG	p.S365L
Pat_01	Pre-Treatment	PPARGC1A	10891	37	4	23815370	23815370	Missense_Mutation	SNP	G	A	69	101	c.1736C>T	c.(1735-1737)TCC>TTC	p.S579F
Pat_01	Pre-Treatment	CCKAR	886	37	4	26483678	26483678	Missense_Mutation	SNP	C	T	127	199	c.869G>A	c.(868-870)AGC>AAC	p.S290N
Pat_01	Pre-Treatment	TLR10	81793	37	4	38777051	38777051	Missense_Mutation	SNP	T	G	79	111	c.161A>C	c.(160-162)GAT>GCT	p.D54A
Pat_01	Pre-Treatment	SHISA3	152573	37	4	42403461	42403461	Missense_Mutation	SNP	C	T	136	141	c.710C>T	c.(709-711)TCC>TTC	p.S237F
Pat_01	Pre-Treatment	GABRA2	2555	37	4	46307695	46307695	Nonsense_Mutation	SNP	C	T	67	82	c.593G>A	c.(592-594)TGG>TAG	p.W198*
Pat_01	Pre-Treatment	CORIN	10699	37	4	47647188	47647188	Missense_Mutation	SNP	C	T	135	248	c.1867G>A	c.(1867-1869)GAA>AAA	p.E623K
Pat_01	Pre-Treatment	OCIAD2	132299	37	4	48901867	48901867	Missense_Mutation	SNP	C	T	102	176	c.142G>A	c.(142-144)GAA>AAA	p.E48K
Pat_01	Pre-Treatment	LNX1	84708	37	4	54364972	54364972	Missense_Mutation	SNP	T	A	102	161	c.814A>T	c.(814-816)ATT>TTT	p.I272F
Pat_01	Pre-Treatment	LPHN3	23284	37	4	62903453	62903453	Missense_Mutation	SNP	G	A	120	180	c.3392G>A	c.(3391-3393)CGA>CAA	p.R1131Q
Pat_01	Pre-Treatment	UGT2B10	7365	37	4	69693259	69693259	Missense_Mutation	SNP	G	A	201	331	c.1300G>A	c.(1300-1302)GAT>AAT	p.D434N
Pat_01	Pre-Treatment	UGT2B7	7364	37	4	69962580	69962580	Missense_Mutation	SNP	A	T	34	29	c.342A>T	c.(340-342)GAA>GAT	p.E114D
Pat_01	Pre-Treatment	ANKRD17	26057	37	4	73984530	73984530	Missense_Mutation	SNP	T	C	246	361	c.4063A>G	c.(4063-4065)ACT>GCT	p.T1355A
Pat_01	Pre-Treatment	GK2	2712	37	4	80327902	80327902	Missense_Mutation	SNP	C	T	156	214	c.1453G>A	c.(1453-1455)GAA>AAA	p.E485K
Pat_01	Pre-Treatment	HERC5	51191	37	4	89425504	89425504	Missense_Mutation	SNP	C	T	71	146	c.2704C>T	c.(2704-2706)CCC>TCC	p.P902S
Pat_01	Pre-Treatment	UNC5C	8633	37	4	96104089	96104089	Missense_Mutation	SNP	C	T	168	234	c.2410G>A	c.(2410-2412)GGA>AGA	p.G804R
Pat_01	Pre-Treatment	EGF	1950	37	4	110921002	110921002	Missense_Mutation	SNP	G	A	196	237	c.3173G>A	c.(3172-3174)AGG>AAG	p.R1058K
Pat_01	Pre-Treatment	PITX2	5308	37	4	111542415	111542415	Missense_Mutation	SNP	C	T	64	99	c.295G>A	c.(295-297)GAG>AAG	p.E99K
Pat_01	Pre-Treatment	DCHS2	54798	37	4	155157358	155157358	Missense_Mutation	SNP	G	A	212	287	c.7081C>T	c.(7081-7083)CAT>TAT	p.H2361Y
Pat_01	Pre-Treatment	DCHS2	54798	37	4	155298407	155298407	Missense_Mutation	SNP	C	T	102	173	c.424G>A	c.(424-426)GGG>AGG	p.G142R
Pat_01	Pre-Treatment	CLCN3	1182	37	4	170613292	170613292	Missense_Mutation	SNP	A	T	144	186	c.757A>T	c.(757-759)ATC>TTC	p.I253F
Pat_01	Pre-Treatment	ASB5	140458	37	4	177190238	177190238	Missense_Mutation	SNP	G	A	93	162	c.22C>T	c.(22-24)CGG>TGG	p.R8W
Pat_01	Pre-Treatment	ODZ3	55714	37	4	183652119	183652119	Missense_Mutation	SNP	C	T	64	116	c.2794C>T	c.(2794-2796)CCA>TCA	p.P932S
Pat_01	Pre-Treatment	CAPSL	133690	37	5	35904702	35904702	Missense_Mutation	SNP	G	A	179	261	c.572C>T	c.(571-573)TCC>TTC	p.S191F
Pat_01	Pre-Treatment	HEATR7B2	133558	37	5	41042300	41042300	Nonsense_Mutation	SNP	C	T	5	15	c.1847G>A	c.(1846-1848)TGG>TAG	p.W616*
Pat_01	Pre-Treatment	C5orf34	375444	37	5	43509374	43509374	Missense_Mutation	SNP	G	A	105	145	c.68C>T	c.(67-69)TCC>TTC	p.S23F
Pat_01	Pre-Treatment	NNT	23530	37	5	43704409	43704409	Missense_Mutation	SNP	C	A	6	535	c.3164C>A	c.(3163-3165)CCA>CAA	p.P1055Q
Pat_01	Pre-Treatment	SKIV2L2	23517	37	5	54662656	54662656	Missense_Mutation	SNP	C	T	212	282	c.1763C>T	c.(1762-1764)TCC>TTC	p.S588F
Pat_01	Pre-Treatment	MAST4	375449	37	5	66460811	66460812	Missense_Mutation	DNP	CC	AT	20	29	.5237_5238CC>A	c.(5236-5238)CCC>CAT	p.P1746H
Pat_01	Pre-Treatment	SPZ1	84654	37	5	79616461	79616461	Missense_Mutation	SNP	G	C	6	263	c.427G>C	c.(427-429)GAG>CAG	p.E143Q

Pat_01	Pre-Treatment	C5orf13	9315	37	5	111066622	111066622	Missense_Mutation	SNP	A	G	197	260	c.203T>C	c.(202-204)TTT>TCT	p.F68S
Pat_01	Pre-Treatment	SLC27A6	28965	37	5	128364084	128364084	Missense_Mutation	SNP	G	A	118	130	c.1501G>A	c.(1501-1503)GGA>AGA	p.G501R
Pat_01	Pre-Treatment	ACSL6	23305	37	5	131308419	131308419	Nonsense_Mutation	SNP	G	A	116	218	c.1261C>T	c.(1261-1263)CAG>TAG	p.Q421*
Pat_01	Pre-Treatment	PCDHB10	56126	37	5	140574481	140574481	Missense_Mutation	SNP	G	A	54	88	c.2356G>A	c.(2356-2358)GAA>AAA	p.E786K
Pat_01	Pre-Treatment	PCDHGA2	56113	37	5	140718983	140718983	Missense_Mutation	SNP	G	A	160	184	c.445G>A	c.(445-447)GGA>AGA	p.G149R
Pat_01	Pre-Treatment	PCDHGA2	56113	37	5	140720289	140720289	Missense_Mutation	SNP	C	T	238	298	c.1751C>T	c.(1750-1752)CCC>CTC	p.P584L
Pat_01	Pre-Treatment	PCDHGA8	9708	37	5	140772898	140772898	Missense_Mutation	SNP	G	A	138	167	c.518G>A	c.(517-519)AGC>AAC	p.S173N
Pat_01	Pre-Treatment	GRIA1	2890	37	5	153144170	153144170	Missense_Mutation	SNP	G	A	45	66	c.2000G>A	c.(1999-2001)GGA>GAA	p.G667E
Pat_01	Pre-Treatment	HAVCR2	84868	37	5	156514235	156514235	Missense_Mutation	SNP	C	T	72	120	c.784G>A	c.(784-786)GAA>AAA	p.E262K
Pat_01	Pre-Treatment	LSM11	134353	37	5	157182040	157182040	Missense_Mutation	SNP	C	T	92	101	c.851C>T	c.(850-852)TCC>TTC	p.S284F
Pat_01	Pre-Treatment	GABRP	2568	37	5	170239094	170239094	Missense_Mutation	SNP	G	A	168	153	c.1155G>A	c.(1153-1155)ATG>ATA	p.M385I
Pat_01	Pre-Treatment	COL23A1	91522	37	5	177689243	177689244	Missense_Mutation	DNP	CC	TT	11	16	c.649_650GG>AA	c.(649-651)GGA>AAA	p.G217K
Pat_01	Pre-Treatment	PECI	10455	37	6	4133937	4133937	Missense_Mutation	SNP	T	C	4	312	c.59A>G	c.(58-60)CAG>CGG	p.Q20R
Pat_01	Pre-Treatment	ATXN1	6310	37	6	16327485	16327485	Missense_Mutation	SNP	G	A	138	304	c.1057C>T	c.(1057-1059)CCT>TCT	p.P353S
Pat_01	Pre-Treatment	ZNF184	7738	37	6	27419417	27419417	Missense_Mutation	SNP	G	A	108	195	c.1921C>T	c.(1921-1923)CCC>TCC	p.P641S
Pat_01	Pre-Treatment	MDC1	9656	37	6	30672158	30672158	Missense_Mutation	SNP	G	A	464	297	c.4802C>T	c.(4801-4803)ACA>ATA	p.T1601I
Pat_01	Pre-Treatment	BAT2	7916	37	6	31595857	31595857	Missense_Mutation	SNP	C	T	219	396	c.1606C>T	c.(1606-1608)CCA>TCA	p.P536S
Pat_01	Pre-Treatment	BAT3	7917	37	6	31612903	31612903	Missense_Mutation	SNP	G	A	182	428	c.1207C>T	c.(1207-1209)CCT>TCT	p.P403S
Pat_01	Pre-Treatment	LY6G6F	259215	37	6	31685384	31685384	Missense_Mutation	SNP	C	T	240	603	c.952C>T	c.(952-954)CCA>TCA	p.P318S
Pat_01	Pre-Treatment	C2	717	37	6	31903781	31903781	Missense_Mutation	SNP	G	A	100	239	c.931G>A	c.(931-933)GAC>AAC	p.D311N
Pat_01	Pre-Treatment	TNXB	7148	37	6	32029318	32029318	Missense_Mutation	SNP	C	T	89	209	c.7348G>A	c.(7348-7350)GGG>AGG	p.G2450R
Pat_01	Pre-Treatment	TNXB	7148	37	6	32038093	32038093	Missense_Mutation	SNP	G	A	23	64	c.5089C>T	c.(5089-5091)CCT>TCT	p.P1697S
Pat_01	Pre-Treatment	HLA-DMB	3109	37	6	32903140	32903140	Missense_Mutation	SNP	G	A	335	269	c.754C>T	c.(754-756)CCT>TCT	p.P252S
Pat_01	Pre-Treatment	FKBP5	2289	37	6	35545009	35545009	Missense_Mutation	SNP	G	T	6	616	c.1028C>A	c.(1027-1029)GCC>GAC	p.A343D
Pat_01	Pre-Treatment	FGD2	221472	37	6	36988331	36988331	Missense_Mutation	SNP	G	A	16	70	c.1137G>A	c.(1135-1137)ATG>ATA	p.M379I
Pat_01	Pre-Treatment	AARS2	57505	37	6	44275040	44275040	Missense_Mutation	SNP	C	T	4	151	c.986G>A	c.(985-987)CGC>CAC	p.R329H
Pat_01	Pre-Treatment	PGK2	5232	37	6	49753750	49753750	Missense_Mutation	SNP	T	A	7	603	c.1151A>T	c.(1150-1152)AAC>ATC	p.N384I
Pat_01	Pre-Treatment	IL17F	112744	37	6	52103546	52103546	Missense_Mutation	SNP	G	A	69	68	c.236C>T	c.(235-237)ACC>ATC	p.T79I
Pat_01	Pre-Treatment	FAM83B	222584	37	6	54804808	54804808	Missense_Mutation	SNP	G	A	68	126	c.1039G>A	c.(1039-1041)GAA>AAA	p.E347K
Pat_01	Pre-Treatment	COL21A1	81578	37	6	55935569	55935569	Missense_Mutation	SNP	C	T	29	42	c.1993G>A	c.(1993-1995)GGG>AGG	p.G665R
Pat_01	Pre-Treatment	SMAP1	60682	37	6	71570002	71570002	Missense_Mutation	SNP	T	G	195	171	c.1369T>G	c.(1369-1371)TCA>GCA	p.S457A
Pat_01	Pre-Treatment	FILIP1	27145	37	6	76063340	76063340	Missense_Mutation	SNP	C	T	174	208	c.544G>A	c.(544-546)GAG>AAG	p.E182K
Pat_01	Pre-Treatment	CASP8AP2	9994	37	6	90577172	90577172	Missense_Mutation	SNP	C	T	86	16	c.4163C>T	c.(4162-4164)CCA>CTA	p.P1388L
Pat_01	Pre-Treatment	GJA10	84694	37	6	90604719	90604719	Missense_Mutation	SNP	C	T	256	42	c.532C>T	c.(532-534)CTC>TTC	p.L178F
Pat_01	Pre-Treatment	AIM1	202	37	6	107016361	107016361	Missense_Mutation	SNP	G	A	161	39	c.5092G>A	c.(5092-5094)GAT>AAT	p.D1698N
Pat_01	Pre-Treatment	RFX6	222546	37	6	117248438	117248438	Missense_Mutation	SNP	C	T	147	31	c.2134C>T	c.(2134-2136)CAC>TAC	p.H712Y
Pat_01	Pre-Treatment	ROS1	6098	37	6	117730754	117730754	Missense_Mutation	SNP	C	T	65	23	c.280G>A	c.(280-282)GAA>AAA	p.E94K
Pat_01	Pre-Treatment	CLDN20	49861	37	6	155596924	155596924	Missense_Mutation	SNP	C	A	4	236	c.71C>A	c.(70-72)GCC>GAC	p.A24D
Pat_01	Pre-Treatment	RADIL	55698	37	7	4841376	4841376	Missense_Mutation	SNP	G	A	24	35	c.2750C>T	c.(2749-2751)CCC>CTC	p.P917L
Pat_01	Pre-Treatment	PRPS1L1	221823	37	7	18066867	18066867	Missense_Mutation	SNP	G	A	106	142	c.539C>T	c.(538-540)TCC>TTC	p.S180F
Pat_01	Pre-Treatment	CREB5	9586	37	7	28547317	28547317	Missense_Mutation	SNP	G	A	167	243	c.253G>A	c.(253-255)GAG>AAG	p.E85K
Pat_01	Pre-Treatment	C7orf10	79783	37	7	40900016	40900016	Missense_Mutation	SNP	G	A	192	191	c.1255G>A	c.(1255-1257)GAT>AAT	p.D419N
Pat_01	Pre-Treatment	HECW1	23072	37	7	43400569	43400569	Missense_Mutation	SNP	C	T	84	132	c.545C>T	c.(544-546)TCG>TTG	p.S182L
Pat_01	Pre-Treatment	TBRG4	9238	37	7	45144223	45144223	Missense_Mutation	SNP	G	A	51	76	c.821C>T	c.(820-822)CCC>CTC	p.P274L
Pat_01	Pre-Treatment	TNS3	64759	37	7	47451336	47451337	Missense_Mutation	DNP	CC	TT	28	37	c.711_712GG>AA	709-714)AAGGGA>AAAA	p.G238R
Pat_01	Pre-Treatment	EGFR	1956	37	7	55266497	55266497	Missense_Mutation	SNP	G	A	119	147	c.2789G>A	c.(2788-2790)GGA>GAA	p.G930E
Pat_01	Pre-Treatment	ABCB4	5244	37	7	87060829	87060829	Missense_Mutation	SNP	C	T	241	295	c.1784G>A	c.(1783-1785)CGA>CAA	p.R595Q

Pat_01	Pre-Treatment	SAMD9	54809	37	7	92735311	92735311	Missense_Mutation	SNP	C	T	139	200	c.100G>A	c.(100-102)GAA>AAA	p.E34K
Pat_01	Pre-Treatment	TRRAP	8295	37	7	98509757	98509757	Missense_Mutation	SNP	C	T	159	231	c.2120C>T	c.(2119-2121)TCC>TTC	p.S707F
Pat_01	Pre-Treatment	OR2AE1	81392	37	7	99473956	99473956	Missense_Mutation	SNP	C	T	64	75	c.701G>A	c.(700-702)AGA>AAA	p.R234K
Pat_01	Pre-Treatment	ZAN	7455	37	7	100371434	100371434	Missense_Mutation	SNP	A	G	25	27	c.5725A>G	c.(5725-5727)AAA>GAA	p.K1909E
Pat_01	Pre-Treatment	MUC17	140453	37	7	100686354	100686354	Missense_Mutation	SNP	C	T	191	271	c.11657C>T	c.(11656-11658)CCA>CTA	p.P3886L
Pat_01	Pre-Treatment	MOGAT3	346606	37	7	100839568	100839568	Missense_Mutation	SNP	C	A	19	20	c.771G>T	c.(769-771)AAG>AAT	p.K257N
Pat_01	Pre-Treatment	RELN	5649	37	7	103137012	103137012	Missense_Mutation	SNP	C	T	167	222	c.9154G>A	c.(9154-9156)GAA>AAA	p.E3052K
Pat_01	Pre-Treatment	PIK3CG	5294	37	7	106519963	106519963	Splice_Site	SNP	G	A	98	156	c.2392_splice	c.e6-1	p.I798_splice
Pat_01	Pre-Treatment	SLC26A3	1811	37	7	107418680	107418680	Missense_Mutation	SNP	C	T	68	107	c.1454G>A	c.(1453-1455)GGG>GAG	p.G485E
Pat_01	Pre-Treatment	PTPRZ1	5803	37	7	121608040	121608040	Missense_Mutation	SNP	C	T	108	131	c.160C>T	c.(160-162)CCA>TCA	p.P54S
Pat_01	Pre-Treatment	SLC13A4	26266	37	7	135392875	135392875	Missense_Mutation	SNP	C	T	217	252	c.352G>A	c.(352-354)GCC>ACC	p.A118T
Pat_01	Pre-Treatment	KIAA1549	57670	37	7	138522701	138522701	Missense_Mutation	SNP	G	A	57	105	c.5803C>T	c.(5803-5805)CTC>TTC	p.L1935F
Pat_01	Pre-Treatment	BRAF	673	37	7	140453136	140453136	Missense_Mutation	SNP	A	T	225	175	c.1799T>A	c.(1798-1800)GTG>GAG	p.V600E
Pat_01	Pre-Treatment	KIAA1147	57189	37	7	141364740	141364740	Missense_Mutation	SNP	G	A	4	96	c.1067C>T	c.(1066-1068)GCT>GTT	p.A356V
Pat_01	Pre-Treatment	C7orf34	135927	37	7	142637618	142637618	Missense_Mutation	SNP	G	A	212	426	c.388G>A	c.(388-390)GGG>AGG	p.G130R
Pat_01	Pre-Treatment	CLCN1	1180	37	7	143036696	143036696	Missense_Mutation	SNP	G	T	84	232	c.1564G>T	c.(1564-1566)GGG>TGG	p.G522W
Pat_01	Pre-Treatment	SLC39A14	23516	37	8	22265980	22265980	Missense_Mutation	SNP	C	A	3	60	c.428C>A	c.(427-429)ACG>AAG	p.T143K
Pat_01	Pre-Treatment	DOCK5	80005	37	8	25253110	25253110	Nonsense_Mutation	SNP	G	T	157	30	c.4579G>T	c.(4579-4581)GAG>TAG	p.E1527*
Pat_01	Pre-Treatment	RP1	6101	37	8	55538849	55538849	Missense_Mutation	SNP	C	T	45	59	c.2407C>T	c.(2407-2409)CCT>TCT	p.P803S
Pat_01	Pre-Treatment	PREX2	80243	37	8	69000012	69000012	Missense_Mutation	SNP	T	C	276	405	c.2081T>C	c.(2080-2082)TTT>TCT	p.F694S
Pat_01	Pre-Treatment	ZFHX4	79776	37	8	77763772	77763772	Missense_Mutation	SNP	C	T	46	54	c.4480C>T	c.(4480-4482)CGT>TGT	p.R1494C
Pat_01	Pre-Treatment	SLC7A13	157724	37	8	87229869	87229869	Missense_Mutation	SNP	A	G	185	221	c.1009T>C	c.(1009-1011)TTT>CTT	p.F337L
Pat_01	Pre-Treatment	RGS22	26166	37	8	101020740	101020740	Missense_Mutation	SNP	C	T	42	51	c.2224G>A	c.(2224-2226)GAA>AAA	p.E742K
Pat_01	Pre-Treatment	TMEM74	157753	37	8	109796543	109796543	Missense_Mutation	SNP	C	T	96	125	c.785G>A	c.(784-786)CGA>CAA	p.R262Q
Pat_01	Pre-Treatment	FER1L6	654463	37	8	124998329	124998329	Missense_Mutation	SNP	G	A	55	115	c.1432G>A	c.(1432-1434)GAA>AAA	p.E478K
Pat_01	Pre-Treatment	FAM135B	51059	37	8	139255192	139255192	Missense_Mutation	SNP	G	A	102	140	c.662C>T	c.(661-663)TCC>TTC	p.S221F
Pat_01	Pre-Treatment	PYCRL	65263	37	8	144689142	144689142	Missense_Mutation	SNP	G	A	112	161	c.353C>T	c.(352-354)TCT>TTT	p.S118F
Pat_01	Pre-Treatment	ZNF707	286075	37	8	144776319	144776320	Missense_Mutation	DNP	CC	TT	10	12	c.735_736CC>TT	733-738)GACCGC>GATT	p.R246C
Pat_01	Pre-Treatment	IL33	90865	37	9	6251250	6251250	Missense_Mutation	SNP	G	A	230	38	c.328G>A	c.(328-330)GAT>AAT	p.D110N
Pat_01	Pre-Treatment	TAF1L	138474	37	9	32630610	32630610	Missense_Mutation	SNP	C	T	235	36	c.4968G>A	c.(4966-4968)ATG>ATA	p.M1656I
Pat_01	Pre-Treatment	GBA2	57704	37	9	35748472	35748472	Missense_Mutation	SNP	A	G	181	27	c.230T>C	c.(229-231)ATG>ACG	p.M77T
Pat_01	Pre-Treatment	PRUNE2	158471	37	9	79326061	79326061	Missense_Mutation	SNP	G	A	28	52	c.1129C>T	c.(1129-1131)CCC>TCC	p.P377S
Pat_01	Pre-Treatment	PHF2	5253	37	9	96422487	96422487	Missense_Mutation	SNP	C	T	32	36	c.1343C>T	c.(1342-1344)GCC>GTC	p.A448V
Pat_01	Pre-Treatment	HIATL1	84641	37	9	97207294	97207294	Missense_Mutation	SNP	G	A	222	347	c.559G>A	c.(559-561)GCA>ACA	p.A187T
Pat_01	Pre-Treatment	BAAT	570	37	9	104124894	104124894	Missense_Mutation	SNP	G	A	96	91	c.1073C>T	c.(1072-1074)CCT>CTT	p.P358L
Pat_01	Pre-Treatment	OR13C4	138804	37	9	107288802	107288802	Nonsense_Mutation	SNP	G	T	11	595	c.689C>A	c.(688-690)TCG>TAG	p.S230*
Pat_01	Pre-Treatment	COL27A1	85301	37	9	117068933	117068934	Missense_Mutation	DNP	GG	AA	45	108	.5072_5073GG>A	c.(5071-5073)AGG>AAA	p.R1691K
Pat_01	Pre-Treatment	TLR4	7099	37	9	120475271	120475271	Nonsense_Mutation	SNP	C	T	91	194	c.865C>T	c.(865-867)CGA>TGA	p.R289*
Pat_01	Pre-Treatment	OR1J2	26740	37	9	125273462	125273462	Missense_Mutation	SNP	C	T	96	117	c.382C>T	c.(382-384)CAC>TAC	p.H128Y
Pat_01	Pre-Treatment	OR1N2	138882	37	9	125316037	125316037	Missense_Mutation	SNP	G	A	230	299	c.589G>A	c.(589-591)GAT>AAT	p.D197N
Pat_01	Pre-Treatment	ABL1	25	37	9	133760646	133760646	Missense_Mutation	SNP	C	T	185	191	c.2969C>T	c.(2968-2970)TCG>TTG	p.S990L
Pat_01	Pre-Treatment	LAMC3	10319	37	9	133946908	133946908	Missense_Mutation	SNP	G	A	43	175	c.3107G>A	c.(3106-3108)GGG>GAG	p.G1036E
Pat_01	Pre-Treatment	ARHGAP6	395	37	X	11196354	11196354	Nonsense_Mutation	SNP	C	A	25	1	c.1495G>T	c.(1495-1497)GAA>TAA	p.E499*
Pat_01	Pre-Treatment	GSPT2	23708	37	X	51488398	51488398	Missense_Mutation	SNP	C	T	156	10	c.1676C>T	c.(1675-1677)TCC>TTC	p.S559F
Pat_01	Pre-Treatment	TCEAL6	158931	37	X	101395871	101395871	Missense_Mutation	SNP	C	T	142	11	c.433G>A	c.(433-435)GAT>AAT	p.D145N
Pat_01	Pre-Treatment	MUM1L1	139221	37	X	105450125	105450125	Missense_Mutation	SNP	G	A	50	3	c.700G>A	c.(700-702)GAA>AAA	p.E234K
Pat_01	Pre-Treatment	CAPN6	827	37	X	110491174	110491174	Missense_Mutation	SNP	G	A	430	47	c.1531C>T	c.(1531-1533)CGT>TGT	p.R511C

Pat_01	Pre-Treatment	GRIA3	2892	37	X	122459990	122459990	Missense_Mutation	SNP	G	A	209	16	c.622G>A	c.(622-624)GAA>AAA	p.E208K
Pat_01	Pre-Treatment	CXorf66	347487	37	X	139038701	139038701	Missense_Mutation	SNP	G	A	332	41	c.440C>T	c.(439-441)TCC>TTC	p.S147F
Pat_01	Post-Resistance	PUSL1	126789	37	1	1245090	1245090	Missense_Mutation	SNP	C	T	4	19	c.503C>T	c.(502-504)GCC>GTC	p.A168V
Pat_01	Post-Resistance	RER1	11079	37	1	2328642	2328642	Nonsense_Mutation	SNP	C	T	102	269	c.169C>T	c.(169-171)CGA>TGA	p.R57*
Pat_01	Post-Resistance	EXOSC10	5394	37	1	11129748	11129748	Missense_Mutation	SNP	C	T	7	757	c.2356G>A	c.(2356-2358)GAC>AAC	p.D786N
Pat_01	Post-Resistance	MTOR	2475	37	1	11259457	11259457	Missense_Mutation	SNP	G	A	4	248	c.4111C>T	c.(4111-4113)CCC>TCC	p.P1371S
Pat_01	Post-Resistance	PTCHD2	57540	37	1	11584007	11584007	Nonsense_Mutation	SNP	C	T	25	50	c.2371C>T	c.(2371-2373)CAG>TAG	p.Q791*
Pat_01	Post-Resistance	FBXO44	93611	37	1	11718444	11718444	Missense_Mutation	SNP	C	T	59	201	c.386C>T	c.(385-387)TCA>TTA	p.S129L
Pat_01	Post-Resistance	AADACL3	126767	37	1	12785574	12785574	Missense_Mutation	SNP	G	A	39	121	c.664G>A	c.(664-666)GAA>AAA	p.E222K
Pat_01	Post-Resistance	LOC649330	649330	37	1	12907868	12907868	Missense_Mutation	SNP	C	T	47	325	c.275G>A	c.(274-276)CGA>CAA	p.R92Q
Pat_01	Post-Resistance	LOC440563	440563	37	1	13183695	13183695	Missense_Mutation	SNP	C	T	33	86	c.178G>A	c.(178-180)GAG>AAG	p.E60K
Pat_01	Post-Resistance	NBPF1	55672	37	1	16914254	16914254	Missense_Mutation	SNP	C	T	36	464	c.532G>A	c.(532-534)GAG>AAG	p.E178K
Pat_01	Post-Resistance	PADI3	51702	37	1	17593271	17593271	Missense_Mutation	SNP	C	T	5	338	c.466C>T	c.(466-468)CGT>TGT	p.R156C
Pat_01	Post-Resistance	PADI3	51702	37	1	17607200	17607200	Missense_Mutation	SNP	G	A	4	309	c.1670G>A	c.(1669-1671)CGG>CAG	p.R557Q
Pat_01	Post-Resistance	UBR4	23352	37	1	19449373	19449373	Missense_Mutation	SNP	G	A	5	398	c.9770C>T	c.(9769-9771)ACA>ATA	p.T3257I
Pat_01	Post-Resistance	MRTO4	51154	37	1	19584386	19584386	Missense_Mutation	SNP	C	T	87	250	c.401C>T	c.(400-402)ACT>ATT	p.T134I
Pat_01	Post-Resistance	NBPF3	84224	37	1	21798107	21798107	Missense_Mutation	SNP	G	C	7	659	c.492G>C	c.(490-492)CAG>CAC	p.Q164H
Pat_01	Post-Resistance	RAP1GAP	5909	37	1	21940528	21940529	Missense_Mutation	DNP	GT	AA	13	61	c.345_346AC>TT	(343-348)TCACTC>TCTTT	p.L116F
Pat_01	Post-Resistance	NIPAL3	57185	37	1	24790583	24790583	Missense_Mutation	SNP	C	T	12	93	c.994C>T	c.(994-996)CCC>TCC	p.P332S
Pat_01	Post-Resistance	ZNF683	257101	37	1	26691195	26691195	Missense_Mutation	SNP	G	A	36	62	c.842C>T	c.(841-843)ACC>ATC	p.T281I
Pat_01	Post-Resistance	KPNA6	23633	37	1	32627987	32627987	Missense_Mutation	SNP	C	T	166	506	c.773C>T	c.(772-774)TCT>TTT	p.S258F
Pat_01	Post-Resistance	TRIM62	55223	37	1	33625433	33625433	Missense_Mutation	SNP	C	T	6	417	c.617G>A	c.(616-618)CGC>CAC	p.R206H
Pat_01	Post-Resistance	GJA4	2701	37	1	35260770	35260770	Missense_Mutation	SNP	C	T	21	80	c.956C>T	c.(955-957)CCC>CTC	p.P319L
Pat_01	Post-Resistance	CSF3R	1441	37	1	36941122	36941122	Missense_Mutation	SNP	C	T	20	72	c.217G>A	c.(217-219)GGC>AGC	p.G73S
Pat_01	Post-Resistance	GRIK3	2899	37	1	37356679	37356679	Missense_Mutation	SNP	G	A	7	616	c.134C>T	c.(133-135)GCG>GTG	p.A45V
Pat_01	Post-Resistance	RSPO1	284654	37	1	38095330	38095330	Missense_Mutation	SNP	G	A	4	92	c.4C>T	c.(4-6)CGG>TGG	p.R2W
Pat_01	Post-Resistance	EPHA10	284656	37	1	38186225	38186225	Missense_Mutation	SNP	C	T	3	31	c.2210G>A	c.(2209-2211)CGG>CAG	p.R737Q
Pat_01	Post-Resistance	KIAA0754	643314	37	1	39879016	39879016	Missense_Mutation	SNP	A	G	4	43	c.3079A>G	c.(3079-3081)ACC>GCC	p.T1027A
Pat_01	Post-Resistance	CLDN19	149461	37	1	43203975	43203975	Missense_Mutation	SNP	G	A	4	137	c.398C>T	c.(397-399)ACT>ATT	p.T133I
Pat_01	Post-Resistance	MPL	4352	37	1	43804223	43804223	Missense_Mutation	SNP	C	T	4	251	c.223C>T	c.(223-225)CGT>TGT	p.R75C
Pat_01	Post-Resistance	KIAA0467	23334	37	1	43893276	43893276	Missense_Mutation	SNP	C	T	66	189	c.977C>T	c.(976-978)TCC>TTC	p.S326F
Pat_01	Post-Resistance	MAST2	23139	37	1	46463409	46463409	Missense_Mutation	SNP	G	T	9	616	c.606G>T	c.(604-606)TTG>TTT	p.L202F
Pat_01	Post-Resistance	FAAH	2166	37	1	46872027	46872027	Missense_Mutation	SNP	C	T	24	103	c.938C>T	c.(937-939)CCC>CTC	p.P313L
Pat_01	Post-Resistance	FAAH	2166	37	1	46876526	46876526	Missense_Mutation	SNP	G	A	4	196	c.1316G>A	c.(1315-1317)CGT>CAT	p.R439H
Pat_01	Post-Resistance	C8A	731	37	1	57383305	57383305	Missense_Mutation	SNP	A	C	35	98	c.1671A>C	c.(1669-1671)GAA>GAC	p.E557D
Pat_01	Post-Resistance	DAB1	1600	37	1	57480703	57480703	Nonsense_Mutation	SNP	G	A	4	208	c.1297C>T	c.(1297-1299)CAG>TAG	p.Q433*
Pat_01	Post-Resistance	MIER1	57708	37	1	67436559	67436559	Missense_Mutation	SNP	C	T	89	222	c.841C>T	c.(841-843)CTT>TTT	p.L281F
Pat_01	Post-Resistance	PALMD	54873	37	1	100152323	100152323	Missense_Mutation	SNP	C	T	5	380	c.343C>T	c.(343-345)CGG>TGG	p.R115W
Pat_01	Post-Resistance	COL11A1	1301	37	1	103404641	103404641	Missense_Mutation	SNP	C	T	148	455	c.3388G>A	c.(3388-3390)GAA>AAA	p.E1130K
Pat_01	Post-Resistance	SLC25A24	29957	37	1	108697685	108697685	Missense_Mutation	SNP	G	A	5	381	c.742C>T	c.(742-744)CGC>TGC	p.R248C
Pat_01	Post-Resistance	CSF1	1435	37	1	110467429	110467429	Missense_Mutation	SNP	C	T	11	20	c.1601C>T	c.(1600-1602)CCC>CTC	p.P534L
Pat_01	Post-Resistance	OVGP1	5016	37	1	111957310	111957310	Missense_Mutation	SNP	G	A	65	128	c.1813C>T	c.(1813-1815)CCC>TCC	p.P605S
Pat_01	Post-Resistance	KCND3	3752	37	1	112525240	112525240	Missense_Mutation	SNP	G	A	4	175	c.109C>T	c.(109-111)CGG>TGG	p.R37W
Pat_01	Post-Resistance	MAGI3	260425	37	1	114157228	114157228	Missense_Mutation	SNP	C	T	86	241	c.1024C>T	c.(1024-1026)CCT>TCT	p.P342S
Pat_01	Post-Resistance	AMPD1	270	37	1	115217374	115217374	Missense_Mutation	SNP	T	C	4	215	c.1799A>G	c.(1798-1800)AAG>AGG	p.K600R
Pat_01	Post-Resistance	SYCP1	6847	37	1	115419372	115419372	Missense_Mutation	SNP	G	A	3	14	c.742G>A	c.(742-744)GAA>AAA	p.E248K
Pat_01	Post-Resistance	SPAG17	200162	37	1	118558629	118558629	Missense_Mutation	SNP	G	A	70	192	c.4246C>T	c.(4246-4248)CCA>TCA	p.P1416S

Pat_01	Post-Resistance	TXNIP	10628	37	1	145439827	145439827	Missense_Mutation	SNP	G	T	43	405	c.373G>T	c.(373-375)GTG>TTG	p.V125L
Pat_01	Post-Resistance	RORC	6097	37	1	151785723	151785723	Missense_Mutation	SNP	C	T	166	655	c.1166G>A	c.(1165-1167)CGA>CAA	p.R389Q
Pat_01	Post-Resistance	RPTN	126638	37	1	152128886	152128886	Missense_Mutation	SNP	C	T	285	425	c.689G>A	c.(688-690)CGG>CAG	p.R230Q
Pat_01	Post-Resistance	FLG2	388698	37	1	152329769	152329769	Nonsense_Mutation	SNP	G	A	120	467	c.493C>T	c.(493-495)CAA>TAA	p.Q165*
Pat_01	Post-Resistance	LCE1F	353137	37	1	152748887	152748887	Missense_Mutation	SNP	C	T	79	229	c.40C>T	c.(40-42)CCC>TCC	p.P14S
Pat_01	Post-Resistance	GATAD2B	57459	37	1	153788749	153788749	Missense_Mutation	SNP	C	A	5	374	c.1216G>T	c.(1216-1218)GGC>TGC	p.G406C
Pat_01	Post-Resistance	SLC39A1	27173	37	1	153935074	153935074	Missense_Mutation	SNP	G	A	4	119	c.118C>T	c.(118-120)CTC>TTC	p.L40F
Pat_01	Post-Resistance	RUSC1	23623	37	1	155292114	155292114	Missense_Mutation	SNP	G	A	4	275	c.550G>A	c.(550-552)GCC>ACC	p.A184T
Pat_01	Post-Resistance	PEAR1	375033	37	1	156874590	156874590	Missense_Mutation	SNP	C	T	47	242	c.152C>T	c.(151-153)CCC>CTC	p.P51L
Pat_01	Post-Resistance	PEAR1	375033	37	1	156880536	156880536	Splice_Site	SNP	G	A	5	260	c.1951_splice	c.e15+1	p.P651_splice
Pat_01	Post-Resistance	CD1C	911	37	1	158261934	158261934	Missense_Mutation	SNP	G	C	127	211	c.389G>C	c.(388-390)GGC>GCC	p.G130A
Pat_01	Post-Resistance	OR10K2	391107	37	1	158389793	158389793	Missense_Mutation	SNP	C	T	44	234	c.864G>A	c.(862-864)ATG>ATA	p.M288I
Pat_01	Post-Resistance	OR6K6	128371	37	1	158725536	158725536	Missense_Mutation	SNP	T	C	5	437	c.931T>C	c.(931-933)TTT>CTT	p.F311L
Pat_01	Post-Resistance	OR10J3	441911	37	1	159283990	159283990	Missense_Mutation	SNP	G	A	85	99	c.460C>T	c.(460-462)CTT>TTT	p.L154F
Pat_01	Post-Resistance	COPA	1314	37	1	160302304	160302304	Missense_Mutation	SNP	G	A	7	587	c.430C>T	c.(430-432)CAC>TAC	p.H144Y
Pat_01	Post-Resistance	PAPPA2	60676	37	1	176734857	176734857	Missense_Mutation	SNP	C	T	119	535	c.4207C>T	c.(4207-4209)CAT>TAT	p.H1403Y
Pat_01	Post-Resistance	ASTN1	460	37	1	177001897	177001897	Missense_Mutation	SNP	G	A	85	127	c.560C>T	c.(559-561)CCG>CTG	p.P187L
Pat_01	Post-Resistance	CEP350	9857	37	1	180062348	180062348	Missense_Mutation	SNP	C	T	6	23	c.7108C>T	c.(7108-7110)CCT>TCT	p.P2370S
Pat_01	Post-Resistance	KIAA1614	57710	37	1	180886095	180886095	Missense_Mutation	SNP	G	A	5	282	c.856G>A	c.(856-858)GCT>ACT	p.A286T
Pat_01	Post-Resistance	KIAA1614	57710	37	1	180904393	180904393	Missense_Mutation	SNP	G	A	3	36	c.1348G>A	c.(1348-1350)GTG>ATG	p.V450M
Pat_01	Post-Resistance	LAMC2	3918	37	1	183209476	183209476	Missense_Mutation	SNP	T	C	68	273	c.3278T>C	c.(3277-3279)GTT>GCT	p.V1093A
Pat_01	Post-Resistance	KIF14	9928	37	1	200574423	200574423	Missense_Mutation	SNP	C	G	7	344	c.1734G>C	c.(1732-1734)ATG>ATC	p.M578I
Pat_01	Post-Resistance	NAV1	89796	37	1	201757704	201757704	Missense_Mutation	SNP	C	T	166	256	c.3104C>T	c.(3103-3105)TCC>TTC	p.S1035F
Pat_01	Post-Resistance	ATP2B4	493	37	1	203668653	203668653	Missense_Mutation	SNP	G	A	6	382	c.457G>A	c.(457-459)GCA>ACA	p.A153T
Pat_01	Post-Resistance	LAX1	54900	37	1	203743384	203743385	Nonsense_Mutation	DNP	GG	TA	55	71	c.772_773GG>TA	c.(772-774)GGA>TAA	p.G258*
Pat_01	Post-Resistance	ZC3H11A	9877	37	1	203821508	203821508	Nonsense_Mutation	SNP	C	G	6	266	c.2414C>G	c.(2413-2415)TCA>TGA	p.S805*
Pat_01	Post-Resistance	NUAK2	81788	37	1	205273092	205273092	Missense_Mutation	SNP	C	T	24	40	c.1373G>A	c.(1372-1374)GGC>GAC	p.G458D
Pat_01	Post-Resistance	CTSE	1510	37	1	206318358	206318358	Missense_Mutation	SNP	G	A	4	180	c.116G>A	c.(115-117)CGG>CAG	p.R39Q
Pat_01	Post-Resistance	LGTN	1939	37	1	206765163	206765163	Missense_Mutation	SNP	G	A	219	325	c.1699C>T	c.(1699-1701)CCT>TCT	p.P567S
Pat_01	Post-Resistance	ATF3	467	37	1	212791476	212791476	Missense_Mutation	SNP	C	T	29	46	c.248C>T	c.(247-249)CCT>CTT	p.P83L
Pat_01	Post-Resistance	FAM71A	149647	37	1	212799737	212799737	Missense_Mutation	SNP	C	A	4	308	c.1518C>A	c.(1516-1518)CAC>CAA	p.H506Q
Pat_01	Post-Resistance	OBSCN	84033	37	1	228456389	228456389	Missense_Mutation	SNP	G	A	4	206	c.5020G>A	c.(5020-5022)GTG>ATG	p.V1674M
Pat_01	Post-Resistance	FMN2	56776	37	1	240371107	240371107	Missense_Mutation	SNP	C	T	76	470	c.2995C>T	c.(2995-2997)CCT>TCT	p.P999S
Pat_01	Post-Resistance	FMN2	56776	37	1	240371239	240371239	Missense_Mutation	SNP	C	T	9	307	c.3127C>T	c.(3127-3129)CCT>TCT	p.P1043S
Pat_01	Post-Resistance	ZNF695	57116	37	1	247150500	247150500	Missense_Mutation	SNP	A	T	4	112	c.1317T>A	c.(1315-1317)GAT>GAA	p.D439E
Pat_01	Post-Resistance	OR2T4	127074	37	1	248524908	248524908	Missense_Mutation	SNP	G	A	9	355	c.26G>A	c.(25-27)AGC>AAC	p.S9N
Pat_01	Post-Resistance	OR14I1	401994	37	1	248845214	248845214	Missense_Mutation	SNP	C	T	62	225	c.392G>A	c.(391-393)AGA>AAA	p.R131K
Pat_01	Post-Resistance	FBXO18	84893	37	10	5948525	5948525	Missense_Mutation	SNP	C	T	86	130	c.683C>T	c.(682-684)CCG>CTG	p.P228L
Pat_01	Post-Resistance	PFKFB3	5209	37	10	6257204	6257204	Missense_Mutation	SNP	C	A	4	165	c.223C>A	c.(223-225)CGC>AGC	p.R75S
Pat_01	Post-Resistance	SEPHS1	22929	37	10	13361156	13361156	Missense_Mutation	SNP	C	T	5	211	c.1165G>A	c.(1165-1167)GGG>AGG	p.G389R
Pat_01	Post-Resistance	ACBD5	91452	37	10	27499796	27499796	Missense_Mutation	SNP	C	A	5	398	c.1151G>T	c.(1150-1152)CGG>CTG	p.R384L
Pat_01	Post-Resistance	KIAA1462	57608	37	10	30317681	30317681	Missense_Mutation	SNP	C	T	66	168	c.1396G>A	c.(1396-1398)GGA>AGA	p.G466R
Pat_01	Post-Resistance	NRP1	8829	37	10	33515181	33515181	Missense_Mutation	SNP	C	T	4	152	c.1018G>A	c.(1018-1020)GGG>AGG	p.G340R
Pat_01	Post-Resistance	ANKRD30A	91074	37	10	37430688	37430688	Missense_Mutation	SNP	C	T	6	179	c.695C>T	c.(694-696)GCG>GTG	p.A232V
Pat_01	Post-Resistance	LOC100129055	100129055	37	10	38466905	38466905	Splice_Site	SNP	T	G	24	36	c.365_splice	c.e2+2	
Pat_01	Post-Resistance	CTNNA3	29119	37	10	68381509	68381509	Missense_Mutation	SNP	C	T	60	113	c.1315G>A	c.(1315-1317)GAA>AAA	p.E439K
Pat_01	Post-Resistance	SGPL1	8879	37	10	72637040	72637040	Missense_Mutation	SNP	C	T	4	232	c.1655C>T	c.(1654-1656)ACC>ATC	p.T552I

Pat_01	Post-Resistance	DNAJB12	54788	37	10	74103148	74103148	Missense_Mutation	SNP	G	T	3	31	c.535C>A	c.(535-537)CCT>ACT	p.P179T
Pat_01	Post-Resistance	KCNMA1	3778	37	10	78708959	78708959	Missense_Mutation	SNP	C	T	119	204	c.2650G>A	c.(2650-2652)GAG>AAG	p.E884K
Pat_01	Post-Resistance	ZMIZ1	57178	37	10	81065994	81065994	Missense_Mutation	SNP	T	C	3	112	c.2561T>C	c.(2560-2562)ATC>ACC	p.I854T
Pat_01	Post-Resistance	NOC3L	64318	37	10	96099543	96099543	Missense_Mutation	SNP	G	A	68	117	c.1915C>T	c.(1915-1917)CCA>TCA	p.P639S
Pat_01	Post-Resistance	NOC3L	64318	37	10	96110005	96110006	Missense_Mutation	DNP	GG	AA	118	289	c.992_993CC>TT	c.(991-993)TCC>TTT	p.S331F
Pat_01	Post-Resistance	CYP2C8	1558	37	10	96829152	96829152	Missense_Mutation	SNP	G	A	57	83	c.8C>T	c.(7-9)CCT>CTT	p.P3L
Pat_01	Post-Resistance	DNMBP	23268	37	10	101715970	101715970	Missense_Mutation	SNP	G	A	95	196	c.1261C>T	c.(1261-1263)CAT>TAT	p.H421Y
Pat_01	Post-Resistance	CPN1	1369	37	10	101835766	101835766	Missense_Mutation	SNP	G	A	98	129	c.322C>T	c.(322-324)CGG>TGG	p.R108W
Pat_01	Post-Resistance	CYP17A1	1586	37	10	104593858	104593858	Missense_Mutation	SNP	C	T	16	32	c.688G>A	c.(688-690)GAA>AAA	p.E230K
Pat_01	Post-Resistance	SORCS3	22986	37	10	106970954	106970954	Missense_Mutation	SNP	C	T	92	120	c.2321C>T	c.(2320-2322)CCA>CTA	p.P774L
Pat_01	Post-Resistance	HABP2	3026	37	10	115335703	115335703	Missense_Mutation	SNP	C	T	128	294	c.271C>T	c.(271-273)CAT>TAT	p.H91Y
Pat_01	Post-Resistance	WDR11	55717	37	10	122649430	122649430	Missense_Mutation	SNP	G	T	4	154	c.2252G>T	c.(2251-2253)TGG>TTG	p.W751L
Pat_01	Post-Resistance	DMBT1	1755	37	10	124358346	124358346	Nonsense_Mutation	SNP	C	T	219	410	c.3013C>T	c.(3013-3015)CGA>TGA	p.R1005*
Pat_01	Post-Resistance	C11orf35	256329	37	11	558623	558623	Missense_Mutation	SNP	G	A	3	30	c.302C>T	c.(301-303)CCG>CTG	p.P101L
Pat_01	Post-Resistance	PHRF1	57661	37	11	607432	607432	Missense_Mutation	SNP	G	C	4	219	c.1976G>C	c.(1975-1977)CGC>CCC	p.R659P
Pat_01	Post-Resistance	LRDD	55367	37	11	801458	801458	Missense_Mutation	SNP	C	T	3	25	c.1469G>A	c.(1468-1470)CGA>CAA	p.R490Q
Pat_01	Post-Resistance	DUSP8	1850	37	11	1580220	1580220	Missense_Mutation	SNP	G	A	3	43	c.436C>T	c.(436-438)CCC>TCC	p.P146S
Pat_01	Post-Resistance	TH	7054	37	11	2186514	2186514	Nonsense_Mutation	SNP	G	A	57	183	c.1375C>T	c.(1375-1377)CAG>TAG	p.Q459*
Pat_01	Post-Resistance	TRPM5	29850	37	11	2428999	2428999	Missense_Mutation	SNP	C	T	4	236	c.2926G>A	c.(2926-2928)GCC>ACC	p.A976T
Pat_01	Post-Resistance	OR51G2	81282	37	11	4936318	4936318	Missense_Mutation	SNP	C	A	22	142	c.576G>T	c.(574-576)TTG>TTT	p.L192F
Pat_01	Post-Resistance	OR52E2	119678	37	11	5080830	5080830	Missense_Mutation	SNP	G	A	83	281	c.28C>T	c.(28-30)CAC>TAC	p.H10Y
Pat_01	Post-Resistance	TRIM3	10612	37	11	6472620	6472620	Missense_Mutation	SNP	G	A	5	326	c.1582C>T	c.(1582-1584)CGC>TGC	p.R528C
Pat_01	Post-Resistance	MRVI1	10335	37	11	10647848	10647848	Missense_Mutation	SNP	G	A	21	24	c.1033C>T	c.(1033-1035)CCG>TCG	p.P345S
Pat_01	Post-Resistance	CYP2R1	120227	37	11	14901879	14901879	Missense_Mutation	SNP	C	T	46	109	c.803G>A	c.(802-804)AGA>AAA	p.R268K
Pat_01	Post-Resistance	ABCC8	6833	37	11	17419957	17419957	Missense_Mutation	SNP	C	T	4	180	c.3682G>A	c.(3682-3684)GAA>AAA	p.E1228K
Pat_01	Post-Resistance	TSG101	7251	37	11	18524059	18524059	Missense_Mutation	SNP	G	T	4	169	c.614C>A	c.(613-615)CCT>CAT	p.P205H
Pat_01	Post-Resistance	NAV2	89797	37	11	20065564	20065564	Missense_Mutation	SNP	C	T	85	239	c.3014C>T	c.(3013-3015)TCC>TTC	p.S1005F
Pat_01	Post-Resistance	KCNA4	3739	37	11	30033313	30033313	Missense_Mutation	SNP	G	A	49	177	c.913C>T	c.(913-915)CCT>TCT	p.P305S
Pat_01	Post-Resistance	LMO2	4005	37	11	33881054	33881054	Missense_Mutation	SNP	G	A	5	303	c.325C>T	c.(325-327)CGG>TGG	p.R109W
Pat_01	Post-Resistance	MAPK8IP1	9479	37	11	45925551	45925551	Missense_Mutation	SNP	G	A	4	259	c.1505G>A	c.(1504-1506)CGA>CAA	p.R502Q
Pat_01	Post-Resistance	OR4A15	81328	37	11	55135721	55135721	Missense_Mutation	SNP	C	T	111	237	c.362C>T	c.(361-363)TCC>TTC	p.S121F
Pat_01	Post-Resistance	OR5D13	390142	37	11	55541751	55541751	Missense_Mutation	SNP	T	C	35	97	c.838T>C	c.(838-840)TAC>CAC	p.Y280H
Pat_01	Post-Resistance	OR8K5	219453	37	11	55927516	55927516	Missense_Mutation	SNP	G	A	140	422	c.278C>T	c.(277-279)TCC>TTC	p.S93F
Pat_01	Post-Resistance	OR8J1	219477	37	11	56128479	56128479	Missense_Mutation	SNP	G	T	7	511	c.757G>T	c.(757-759)GGG>TGG	p.G253W
Pat_01	Post-Resistance	MS4A2	2206	37	11	59863103	59863103	Missense_Mutation	SNP	G	A	70	121	c.709G>A	c.(709-711)GAA>AAA	p.E237K
Pat_01	Post-Resistance	MS4A12	54860	37	11	60271189	60271189	Missense_Mutation	SNP	G	A	65	161	c.487G>A	c.(487-489)GGA>AGA	p.G163R
Pat_01	Post-Resistance	FADS2	9415	37	11	61615706	61615706	Missense_Mutation	SNP	G	T	5	359	c.694G>T	c.(694-696)GAT>TAT	p.D232Y
Pat_01	Post-Resistance	INTS5	80789	37	11	62415054	62415054	Missense_Mutation	SNP	G	A	119	187	c.2498C>T	c.(2497-2499)CCC>CTC	p.P833L
Pat_01	Post-Resistance	SART1	9092	37	11	65731545	65731545	Missense_Mutation	SNP	C	T	4	186	c.314C>T	c.(313-315)GCT>GTT	p.A105V
Pat_01	Post-Resistance	MYEOV	26579	37	11	69063224	69063224	Missense_Mutation	SNP	G	A	71	202	c.307G>A	c.(307-309)GCT>ACT	p.A103T
Pat_01	Post-Resistance	NEU3	10825	37	11	74717320	74717320	Missense_Mutation	SNP	G	T	79	338	c.1169G>T	c.(1168-1170)TGG>TTG	p.W390L
Pat_01	Post-Resistance	MAP6	4135	37	11	75298246	75298246	Missense_Mutation	SNP	G	T	6	275	c.2300C>A	c.(2299-2301)CCA>CAA	p.P767Q
Pat_01	Post-Resistance	DGAT2	84649	37	11	75501768	75501768	Missense_Mutation	SNP	C	T	79	335	c.421C>T	c.(421-423)CCC>TCC	p.P141S
Pat_01	Post-Resistance	MYO7A	4647	37	11	76924018	76924018	Missense_Mutation	SNP	C	T	7	29	c.6376C>T	c.(6376-6378)CCT>TCT	p.P2126S
Pat_01	Post-Resistance	ODZ4	26011	37	11	78380693	78380693	Missense_Mutation	SNP	G	A	6	472	c.6697C>T	c.(6697-6699)CGG>TGG	p.R2233W
Pat_01	Post-Resistance	PRSS23	11098	37	11	86518819	86518819	Missense_Mutation	SNP	C	T	5	298	c.134C>T	c.(133-135)ACC>ATC	p.T45I
Pat_01	Post-Resistance	TYR	7299	37	11	88924446	88924446	Missense_Mutation	SNP	G	A	5	338	c.896G>A	c.(895-897)CGT>CAT	p.R299H

Pat_01	Post-Resistance	HEPHL1	341208	37	11	93779011	93779011	Missense_Mutation	SNP	C	T	40	65	c.343C>T	c.(343-345)CAT>TAT	p.H115Y
Pat_01	Post-Resistance	C11orf65	160140	37	11	108277567	108277567	Missense_Mutation	SNP	C	T	81	116	c.352G>A	c.(352-354)GAT>AAT	p.D118N
Pat_01	Post-Resistance	C11orf53	341032	37	11	111156543	111156543	Missense_Mutation	SNP	G	A	4	237	c.475G>A	c.(475-477)GCT>ACT	p.A159T
Pat_01	Post-Resistance	LAYN	143903	37	11	111430932	111430932	Missense_Mutation	SNP	G	A	62	92	c.898G>A	c.(898-900)GAA>AAA	p.E300K
Pat_01	Post-Resistance	FAM55D	54827	37	11	114451040	114451040	Missense_Mutation	SNP	C	G	70	137	c.913G>C	c.(913-915)GAG>CAG	p.E305Q
Pat_01	Post-Resistance	OR10S1	219873	37	11	123847813	123847813	Missense_Mutation	SNP	G	A	4	190	c.586C>T	c.(586-588)CCC>TCC	p.P196S
Pat_01	Post-Resistance	LAG3	3902	37	12	6887073	6887073	Missense_Mutation	SNP	C	T	50	183	c.1417C>T	c.(1417-1419)CTT>TTT	p.L473F
Pat_01	Post-Resistance	A2M	2	37	12	9231867	9231867	Missense_Mutation	SNP	C	T	70	239	c.3092G>A	c.(3091-3093)CGA>CAA	p.R1031Q
Pat_01	Post-Resistance	TAS2R14	50840	37	12	11091472	11091472	Missense_Mutation	SNP	G	A	25	93	c.335C>T	c.(334-336)GCC>GTC	p.A112V
Pat_01	Post-Resistance	KIAA1467	57613	37	12	13219625	13219625	Nonsense_Mutation	SNP	C	T	94	293	c.904C>T	c.(904-906)CGA>TGA	p.R302*
Pat_01	Post-Resistance	C12orf36	283422	37	12	13526349	13526349	Missense_Mutation	SNP	G	A	15	77	c.206C>T	c.(205-207)TCG>TTG	p.S69L
Pat_01	Post-Resistance	PIK3C2G	5288	37	12	18650562	18650562	Missense_Mutation	SNP	G	A	46	152	c.2773G>A	c.(2773-2775)GAT>AAT	p.D925N
Pat_01	Post-Resistance	PIK3C2G	5288	37	12	18650568	18650568	Missense_Mutation	SNP	C	T	49	154	c.2779C>T	c.(2779-2781)CGT>TGT	p.R927C
Pat_01	Post-Resistance	CAPZA3	93661	37	12	18891723	18891723	Nonsense_Mutation	SNP	G	A	66	200	c.521G>A	c.(520-522)TGG>TAG	p.W174*
Pat_01	Post-Resistance	YARS2	51067	37	12	32908550	32908550	Missense_Mutation	SNP	G	A	52	170	c.259C>T	c.(259-261)CTT>TTT	p.L87F
Pat_01	Post-Resistance	CNTN1	1272	37	12	41330675	41330675	Missense_Mutation	SNP	C	T	163	481	c.1078C>T	c.(1078-1080)CCT>TCT	p.P360S
Pat_01	Post-Resistance	C1QL4	338761	37	12	49726992	49726992	Missense_Mutation	SNP	C	T	25	88	c.562G>A	c.(562-564)GAC>AAC	p.D188N
Pat_01	Post-Resistance	KCNH3	23416	37	12	49951176	49951176	Missense_Mutation	SNP	G	A	3	66	c.2692G>A	c.(2692-2694)GGA>AGA	p.G898R
Pat_01	Post-Resistance	DIP2B	57609	37	12	51133321	51133321	Missense_Mutation	SNP	G	A	5	142	c.4306G>A	c.(4306-4308)GGA>AGA	p.G1436R
Pat_01	Post-Resistance	SLC11A2	4891	37	12	51384723	51384723	Missense_Mutation	SNP	C	T	4	416	c.1430G>A	c.(1429-1431)CGG>CAG	p.R477Q
Pat_01	Post-Resistance	GALNT6	11226	37	12	51752996	51752996	Missense_Mutation	SNP	G	A	6	719	c.1288C>T	c.(1288-1290)CGC>TGC	p.R430C
Pat_01	Post-Resistance	GALNT6	11226	37	12	51773172	51773172	Missense_Mutation	SNP	C	T	45	123	c.394G>A	c.(394-396)GAA>AAA	p.E132K
Pat_01	Post-Resistance	KRT86	3892	37	12	52699481	52699481	Missense_Mutation	SNP	G	A	43	111	c.935G>A	c.(934-936)GGG>GAG	p.G312E
Pat_01	Post-Resistance	KRT72	140807	37	12	52992823	52992823	Missense_Mutation	SNP	T	C	47	159	c.500A>G	c.(499-501)AAC>AGC	p.N167S
Pat_01	Post-Resistance	NCKAP1L	3071	37	12	54914488	54914488	Missense_Mutation	SNP	C	T	165	537	c.1636C>T	c.(1636-1638)CGT>TGT	p.R546C
Pat_01	Post-Resistance	ERBB3	2065	37	12	56477573	56477573	Missense_Mutation	SNP	G	A	6	750	c.121G>A	c.(121-123)GAT>AAT	p.D41N
Pat_01	Post-Resistance	ZC3H10	84872	37	12	56514428	56514428	Missense_Mutation	SNP	G	A	3	61	c.82G>A	c.(82-84)GGG>AGG	p.G28R
Pat_01	Post-Resistance	LRP1	4035	37	12	57569758	57569758	Missense_Mutation	SNP	G	A	47	125	c.3860G>A	c.(3859-3861)GGA>GAA	p.G1287E
Pat_01	Post-Resistance	DCTN2	10540	37	12	57929629	57929629	Splice_Site	SNP	C	T	11	34	c.106_splice	c.e3-1	p.E36_splice
Pat_01	Post-Resistance	TMTC2	160335	37	12	83290051	83290051	Missense_Mutation	SNP	C	A	5	477	c.1109C>A	c.(1108-1110)GCA>GAA	p.A370E
Pat_01	Post-Resistance	MGAT4C	25834	37	12	86373354	86373354	Missense_Mutation	SNP	C	T	9	13	c.1150G>A	c.(1150-1152)GAA>AAA	p.E384K
Pat_01	Post-Resistance	SLC5A8	160728	37	12	101584307	101584307	Missense_Mutation	SNP	C	T	6	456	c.772G>A	c.(772-774)GGT>AGT	p.G258S
Pat_01	Post-Resistance	MYBPC1	4604	37	12	102071915	102071915	Missense_Mutation	SNP	G	C	95	245	c.3124G>C	c.(3124-3126)GAT>CAT	p.D1042H
Pat_01	Post-Resistance	PAH	5053	37	12	103234285	103234285	Missense_Mutation	SNP	G	A	5	369	c.1208C>T	c.(1207-1209)GCT>GTT	p.A403V
Pat_01	Post-Resistance	STAB2	55576	37	12	103988190	103988190	Missense_Mutation	SNP	G	A	195	505	c.233G>A	c.(232-234)AGA>AAA	p.R78K
Pat_01	Post-Resistance	IQCD	115811	37	12	113645584	113645584	Missense_Mutation	SNP	G	A	62	205	c.388C>T	c.(388-390)CGC>TGC	p.R130C
Pat_01	Post-Resistance	RNF10	9921	37	12	121004694	121004694	Missense_Mutation	SNP	C	T	85	215	c.1952C>T	c.(1951-1953)TCC>TTC	p.S651F
Pat_01	Post-Resistance	P2RX7	5027	37	12	121622268	121622268	Missense_Mutation	SNP	C	A	4	81	c.1451C>A	c.(1450-1452)CCA>CAA	p.P484Q
Pat_01	Post-Resistance	SETD8	387893	37	12	123868746	123868746	Missense_Mutation	SNP	A	G	25	79	c.1A>G	c.(1-3)ATG>GTG	p.M1V
Pat_01	Post-Resistance	TMEM132D	121256	37	12	129559240	129559240	Missense_Mutation	SNP	G	A	76	177	c.2480C>T	c.(2479-2481)CCC>CTC	p.P827L
Pat_01	Post-Resistance	EP400	57634	37	12	132514687	132514687	Missense_Mutation	SNP	G	A	5	407	c.5738G>A	c.(5737-5739)AGC>AAC	p.S1913N
Pat_01	Post-Resistance	LATS2	26524	37	13	21562822	21562822	Missense_Mutation	SNP	G	A	34	121	c.1097C>T	c.(1096-1098)TCC>TTC	p.S366F
Pat_01	Post-Resistance	FLT3	2322	37	13	28636067	28636067	Missense_Mutation	SNP	G	A	42	171	c.305C>T	c.(304-306)TCC>TTC	p.S102F
Pat_01	Post-Resistance	FRY	10129	37	13	32810251	32810251	Missense_Mutation	SNP	G	A	6	321	c.5752G>A	c.(5752-5754)GCT>ACT	p.A1918T
Pat_01	Post-Resistance	BRCA2	675	37	13	32905117	32905117	Missense_Mutation	SNP	C	T	36	97	c.743C>T	c.(742-744)GCT>GTT	p.A248V
Pat_01	Post-Resistance	ELF1	1997	37	13	41508063	41508063	Missense_Mutation	SNP	G	C	9	764	c.1358C>G	c.(1357-1359)GCC>GGC	p.A453G
Pat_01	Post-Resistance	SPERT	220082	37	13	46287918	46287918	Missense_Mutation	SNP	A	T	8	10	c.758A>T	c.(757-759)GAG>GTG	p.E253V

Pat_01	Post-Resistance	NEK3	4752	37	13	52718870	52718870	Nonsense_Mutation	SNP	G	A	39	138	c.760C>T	c.(760-762)CGA>TGA	p.R254*
Pat_01	Post-Resistance	THSD1	55901	37	13	52972272	52972272	Missense_Mutation	SNP	T	C	116	347	c.116A>G	c.(115-117)AAC>AGC	p.N39S
Pat_01	Post-Resistance	C13orf34	79866	37	13	73303124	73303124	Missense_Mutation	SNP	C	T	111	305	c.46C>T	c.(46-48)CCA>TCA	p.P16S
Pat_01	Post-Resistance	TMTC4	84899	37	13	101315255	101315255	Missense_Mutation	SNP	G	A	5	327	c.458C>T	c.(457-459)GCG>GTG	p.A153V
Pat_01	Post-Resistance	ERCC5	2073	37	13	103528102	103528103	Missense_Mutation	DNP	CC	TT	28	75	.3410_3411CC>T	c.(3409-3411)CCC>CTT	p.P1137L
Pat_01	Post-Resistance	GAS6	2621	37	13	114537621	114537621	Missense_Mutation	SNP	C	T	4	130	c.737G>A	c.(736-738)CGC>CAC	p.R246H
Pat_01	Post-Resistance	POTEG	404785	37	14	19574211	19574211	Missense_Mutation	SNP	G	A	14	154	c.1268G>A	c.(1267-1269)GGA>GAA	p.G423E
Pat_01	Post-Resistance	OR4N2	390429	37	14	20295951	20295951	Missense_Mutation	SNP	T	G	98	605	c.344T>G	c.(343-345)CTT>CGT	p.L115R
Pat_01	Post-Resistance	EDDM3B	64184	37	14	21238594	21238594	Nonsense_Mutation	SNP	G	A	73	214	c.285G>A	c.(283-285)TGG>TGA	p.W95*
Pat_01	Post-Resistance	SUPT16H	11198	37	14	21820896	21820896	Missense_Mutation	SNP	G	A	99	284	c.3080C>T	c.(3079-3081)TCG>TTG	p.S1027L
Pat_01	Post-Resistance	MYH7	4625	37	14	23885002	23885002	Missense_Mutation	SNP	C	T	4	181	c.4993G>A	c.(4993-4995)GAC>AAC	p.D1665N
Pat_01	Post-Resistance	TGM1	7051	37	14	24727800	24727800	Missense_Mutation	SNP	C	A	4	166	c.1239G>T	c.(1237-1239)ATG>ATT	p.M413I
Pat_01	Post-Resistance	NYNRIN	57523	37	14	24886179	24886179	Missense_Mutation	SNP	C	T	15	36	c.5224C>T	c.(5224-5226)CCT>TCT	p.P1742S
Pat_01	Post-Resistance	NOVA1	4857	37	14	26949277	26949277	Missense_Mutation	SNP	T	C	149	334	c.353A>G	c.(352-354)GAA>GGA	p.E118G
Pat_01	Post-Resistance	ARHGAP5	394	37	14	32560909	32560909	Missense_Mutation	SNP	C	T	61	170	c.1034C>T	c.(1033-1035)GCT>GTT	p.A345V
Pat_01	Post-Resistance	MIA2	117153	37	14	39716382	39716382	Missense_Mutation	SNP	G	A	77	270	c.604G>A	c.(604-606)GAA>AAA	p.E202K
Pat_01	Post-Resistance	SYT16	83851	37	14	62463164	62463164	Missense_Mutation	SNP	G	A	88	258	c.427G>A	c.(427-429)GAA>AAA	p.E143K
Pat_01	Post-Resistance	ZFYVE26	23503	37	14	68233053	68233053	Missense_Mutation	SNP	G	A	77	259	c.5902C>T	c.(5902-5904)CCA>TCA	p.P1968S
Pat_01	Post-Resistance	SIPA1L1	26037	37	14	72176309	72176309	Missense_Mutation	SNP	G	A	39	155	c.4199G>A	c.(4198-4200)AGC>AAC	p.S1400N
Pat_01	Post-Resistance	DCAF4	26094	37	14	73404717	73404717	Nonsense_Mutation	SNP	C	T	5	196	c.31C>T	c.(31-33)CGA>TGA	p.R11*
Pat_01	Post-Resistance	NUMB	8650	37	14	73750939	73750939	Missense_Mutation	SNP	G	A	97	218	c.799C>T	c.(799-801)CCA>TCA	p.P267S
Pat_01	Post-Resistance	KCNK10	54207	37	14	88693861	88693861	Missense_Mutation	SNP	G	A	212	163	c.524C>T	c.(523-525)CCG>CTG	p.P175L
Pat_01	Post-Resistance	ZC3H14	79882	37	14	89078090	89078090	Missense_Mutation	SNP	G	A	5	465	c.2206G>A	c.(2206-2208)GAA>AAA	p.E736K
Pat_01	Post-Resistance	CCDC88C	440193	37	14	91744472	91744472	Missense_Mutation	SNP	G	A	4	50	c.4852C>T	c.(4852-4854)CGG>TGG	p.R1618W
Pat_01	Post-Resistance	FBLN5	10516	37	14	92353657	92353657	Splice_Site	SNP	C	T	212	193	c.620_splice	c.e7-1	p.D207_splice
Pat_01	Post-Resistance	C15orf2	23742	37	15	24923518	24923518	Missense_Mutation	SNP	T	C	95	195	c.2504T>C	c.(2503-2505)ATC>ACC	p.I835T
Pat_01	Post-Resistance	RYR3	6263	37	15	33954496	33954496	Missense_Mutation	SNP	C	T	12	36	c.4765C>T	c.(4765-4767)CTC>TTC	p.L1589F
Pat_01	Post-Resistance	EIF2AK4	440275	37	15	40241377	40241377	Missense_Mutation	SNP	C	T	179	577	c.421C>T	c.(421-423)CCT>TCT	p.P141S
Pat_01	Post-Resistance	PLA2G4F	255189	37	15	42442639	42442639	Missense_Mutation	SNP	C	T	21	113	c.817G>A	c.(817-819)GAG>AAG	p.E273K
Pat_01	Post-Resistance	CGNL1	84952	37	15	57730330	57730330	Missense_Mutation	SNP	C	T	75	245	c.133C>T	c.(133-135)CGG>TGG	p.R45W
Pat_01	Post-Resistance	CGNL1	84952	37	15	57731143	57731143	Missense_Mutation	SNP	G	A	63	219	c.946G>A	c.(946-948)GAT>AAT	p.D316N
Pat_01	Post-Resistance	RNF111	54778	37	15	59376341	59376341	Missense_Mutation	SNP	C	T	5	268	c.2311C>T	c.(2311-2313)CGC>TGC	p.R771C
Pat_01	Post-Resistance	ZNF609	23060	37	15	64966162	64966162	Missense_Mutation	SNP	G	A	6	464	c.1109G>A	c.(1108-1110)GGT>GAT	p.G370D
Pat_01	Post-Resistance	IQCH	64799	37	15	67681327	67681327	Missense_Mutation	SNP	G	A	87	370	c.1615G>A	c.(1615-1617)GCT>ACT	p.A539T
Pat_01	Post-Resistance	TLE3	7090	37	15	70347482	70347482	Missense_Mutation	SNP	G	A	4	263	c.1493C>T	c.(1492-1494)ACG>ATG	p.T498M
Pat_01	Post-Resistance	IL16	3603	37	15	81552144	81552144	Missense_Mutation	SNP	C	T	108	198	c.344C>T	c.(343-345)CCT>CTT	p.P115L
Pat_01	Post-Resistance	IL16	3603	37	15	81584930	81584930	Missense_Mutation	SNP	G	A	4	210	c.1454G>A	c.(1453-1455)CGG>CAG	p.R485Q
Pat_01	Post-Resistance	AP3B2	8120	37	15	83334325	83334325	Missense_Mutation	SNP	G	A	4	258	c.1855C>T	c.(1855-1857)CGG>TGG	p.R619W
Pat_01	Post-Resistance	BNC1	646	37	15	83932525	83932525	Missense_Mutation	SNP	C	T	4	219	c.1478G>A	c.(1477-1479)CGC>CAC	p.R493H
Pat_01	Post-Resistance	BLM	641	37	15	91312750	91312750	Missense_Mutation	SNP	C	T	5	193	c.2489C>T	c.(2488-2490)ACG>ATG	p.T830M
Pat_01	Post-Resistance	MAN2A2	4122	37	15	91450665	91450665	Missense_Mutation	SNP	G	A	5	281	c.1136G>A	c.(1135-1137)CGC>CAC	p.R379H
Pat_01	Post-Resistance	RCCD1	91433	37	15	91504926	91504926	Missense_Mutation	SNP	A	G	142	264	c.1058A>G	c.(1057-1059)CAA>CGA	p.Q353R
Pat_01	Post-Resistance	MCTP2	55784	37	15	94913329	94913329	Missense_Mutation	SNP	C	T	77	200	c.1502C>T	c.(1501-1503)TCC>TTC	p.S501F
Pat_01	Post-Resistance	CACNA1H	8912	37	16	1270224	1270224	Missense_Mutation	SNP	G	A	10	42	c.6292G>A	c.(6292-6294)GAC>AAC	p.D2098N
Pat_01	Post-Resistance	TELO2	9894	37	16	1556291	1556292	Missense_Mutation	DNP	CC	TT	99	337	.2087_2088CC>T	c.(2086-2088)GCC>GTT	p.A696V
Pat_01	Post-Resistance	C16orf90	646174	37	16	3544626	3544626	Missense_Mutation	SNP	C	T	14	70	c.298G>A	c.(298-300)GCC>ACC	p.A100T
Pat_01	Post-Resistance	ABAT	18	37	16	8870303	8870303	Missense_Mutation	SNP	G	A	4	167	c.1225G>A	c.(1225-1227)GCC>ACC	p.A409T

Pat_01	Post-Resistance	GRIN2A	2903	37	16	9916133	9916133	Missense_Mutation	SNP	C	T	49	381	c.2156G>A	c.(2155-2157)AGC>AAC	p.S719N
Pat_01	Post-Resistance	NUBP1	4682	37	16	10855287	10855287	Missense_Mutation	SNP	G	A	5	431	c.673G>A	c.(673-675)GGG>AGG	p.G225R
Pat_01	Post-Resistance	ERN2	10595	37	16	23703591	23703591	Missense_Mutation	SNP	C	T	4	118	c.2306G>A	c.(2305-2307)AGC>AAC	p.S769N
Pat_01	Post-Resistance	SRCAP	10847	37	16	30734010	30734010	Missense_Mutation	SNP	C	T	244	407	c.3833C>T	c.(3832-3834)TCG>TTG	p.S1278L
Pat_01	Post-Resistance	PHKB	5257	37	16	47683017	47683017	Missense_Mutation	SNP	C	T	87	163	c.1699C>T	c.(1699-1701)CGC>TGC	p.R567C
Pat_01	Post-Resistance	CES2	8824	37	16	66974428	66974428	Nonsense_Mutation	SNP	G	T	6	360	c.838G>T	c.(838-840)GGA>TGA	p.G280*
Pat_01	Post-Resistance	ACD	65057	37	16	67694117	67694117	Missense_Mutation	SNP	C	T	5	184	c.265G>A	c.(265-267)GGT>AGT	p.G89S
Pat_01	Post-Resistance	HSD17B2	3294	37	16	82069273	82069273	Nonsense_Mutation	SNP	C	T	134	444	c.244C>T	c.(244-246)CAG>TAG	p.Q82*
Pat_01	Post-Resistance	SPG7	6687	37	16	89592858	89592858	Missense_Mutation	SNP	G	A	5	408	c.740G>A	c.(739-741)CGA>CAA	p.R247Q
Pat_01	Post-Resistance	PAFAH1B1	5048	37	17	2583545	2583545	Missense_Mutation	SNP	G	A	6	659	c.1090G>A	c.(1090-1092)GTA>ATA	p.V364I
Pat_01	Post-Resistance	SHBG	6462	37	17	7536230	7536230	Missense_Mutation	SNP	A	T	17	48	c.1013A>T	c.(1012-1014)AAC>ATC	p.N338I
Pat_01	Post-Resistance	DNAH2	146754	37	17	7727448	7727448	Missense_Mutation	SNP	G	A	87	241	c.11488G>A	c.(11488-11490)GAT>AAT	p.D3830N
Pat_01	Post-Resistance	DNAH2	146754	37	17	7735904	7735904	Missense_Mutation	SNP	C	A	7	680	c.12734C>A	c.(12733-12735)CCC>CAC	p.P4245H
Pat_01	Post-Resistance	MYH4	4622	37	17	10357171	10357171	Missense_Mutation	SNP	C	T	114	349	c.2723G>A	c.(2722-2724)AGA>AAA	p.R908K
Pat_01	Post-Resistance	MYH4	4622	37	17	10363572	10363572	Missense_Mutation	SNP	G	A	120	339	c.1214C>T	c.(1213-1215)CCC>CTC	p.P405L
Pat_01	Post-Resistance	MAP2K4	6416	37	17	11998959	11998959	Missense_Mutation	SNP	G	T	6	711	c.461G>T	c.(460-462)CGG>CTG	p.R154L
Pat_01	Post-Resistance	NCOR1	9611	37	17	15973659	15973659	Missense_Mutation	SNP	G	A	5	291	c.4333C>T	c.(4333-4335)CGT>TGT	p.R1445C
Pat_01	Post-Resistance	FLII	2314	37	17	18151015	18151015	Missense_Mutation	SNP	G	A	3	42	c.2443C>T	c.(2443-2445)CGC>TGC	p.R815C
Pat_01	Post-Resistance	KCNJ12	3768	37	17	21319835	21319835	Missense_Mutation	SNP	G	A	13	119	c.1181G>A	c.(1180-1182)GGA>GAA	p.G394E
Pat_01	Post-Resistance	MYO18A	399687	37	17	27493378	27493378	Missense_Mutation	SNP	G	A	73	205	c.581C>T	c.(580-582)CCT>CTT	p.P194L
Pat_01	Post-Resistance	EVI2B	2124	37	17	29632188	29632188	Missense_Mutation	SNP	G	A	7	861	c.440C>T	c.(439-441)ACT>ATT	p.T147I
Pat_01	Post-Resistance	SLFN11	91607	37	17	33679659	33679659	Missense_Mutation	SNP	C	T	25	55	c.2422G>A	c.(2422-2424)GAT>AAT	p.D808N
Pat_01	Post-Resistance	KRT20	54474	37	17	39036935	39036935	Missense_Mutation	SNP	T	A	67	176	c.561A>T	c.(559-561)AAA>AAT	p.K187N
Pat_01	Post-Resistance	TTC25	83538	37	17	40101446	40101446	Missense_Mutation	SNP	G	A	26	58	c.1115G>A	c.(1114-1116)AGA>AAA	p.R372K
Pat_01	Post-Resistance	NKIRAS2	28511	37	17	40175718	40175718	Missense_Mutation	SNP	G	A	4	270	c.383G>A	c.(382-384)CGG>CAG	p.R128Q
Pat_01	Post-Resistance	ATP6V0A1	535	37	17	40642652	40642652	Missense_Mutation	SNP	C	T	37	122	c.1171C>T	c.(1171-1173)CCA>TCA	p.P391S
Pat_01	Post-Resistance	RAMP2	10266	37	17	40914839	40914839	Nonsense_Mutation	SNP	G	A	54	168	c.497G>A	c.(496-498)TGG>TAG	p.W166*
Pat_01	Post-Resistance	MPP2	4355	37	17	41960323	41960323	Missense_Mutation	SNP	G	A	5	359	c.536C>T	c.(535-537)CCT>CTT	p.P179L
Pat_01	Post-Resistance	TTLL6	284076	37	17	46862461	46862461	Missense_Mutation	SNP	G	A	49	146	c.1864C>T	c.(1864-1866)CCC>TCC	p.P622S
Pat_01	Post-Resistance	WFIKKN2	124857	37	17	48918261	48918261	Missense_Mutation	SNP	G	A	54	89	c.1612G>A	c.(1612-1614)GCC>ACC	p.A538T
Pat_01	Post-Resistance	UTP18	51096	37	17	49337947	49337947	Missense_Mutation	SNP	T	C	3	56	c.2T>C	c.(1-3)ATG>ACG	p.M1T
Pat_01	Post-Resistance	TMEM100	55273	37	17	53798217	53798217	Missense_Mutation	SNP	G	A	5	204	c.215C>T	c.(214-216)ACC>ATC	p.T72I
Pat_01	Post-Resistance	PPM1E	22843	37	17	57046948	57046948	Missense_Mutation	SNP	G	A	122	288	c.832G>A	c.(832-834)GTA>ATA	p.V278I
Pat_01	Post-Resistance	MRC2	9902	37	17	60766309	60766309	Nonsense_Mutation	SNP	C	T	21	53	c.3322C>T	c.(3322-3324)CAG>TAG	p.Q1108*
Pat_01	Post-Resistance	ABCA9	10350	37	17	67045529	67045529	Missense_Mutation	SNP	G	A	5	421	c.199C>T	c.(199-201)CGT>TGT	p.R67C
Pat_01	Post-Resistance	CD300E	342510	37	17	72613523	72613523	Missense_Mutation	SNP	A	G	26	99	c.122T>C	c.(121-123)ATG>ACG	p.M41T
Pat_01	Post-Resistance	ACOX1	51	37	17	73953636	73953636	Nonsense_Mutation	SNP	G	A	4	186	c.442C>T	c.(442-444)CGA>TGA	p.R148*
Pat_01	Post-Resistance	BAHCC1	57597	37	17	79425454	79425454	Missense_Mutation	SNP	G	A	3	31	c.5305G>A	c.(5305-5307)GCC>ACC	p.A1769T
Pat_01	Post-Resistance	PYCR1	5831	37	17	79892944	79892944	Missense_Mutation	SNP	G	A	4	81	c.398C>T	c.(397-399)ACC>ATC	p.T133I
Pat_01	Post-Resistance	UTS2R	2837	37	17	80332543	80332543	Missense_Mutation	SNP	G	C	3	92	c.343G>C	c.(343-345)GAG>CAG	p.E115Q
Pat_01	Post-Resistance	DSG2	1829	37	18	29104411	29104411	Missense_Mutation	SNP	G	A	76	288	c.691G>A	c.(691-693)GAA>AAA	p.E231K
Pat_01	Post-Resistance	TCEB3B	51224	37	18	44560359	44560359	Missense_Mutation	SNP	G	A	40	98	c.1277C>T	c.(1276-1278)TCG>TTG	p.S426L
Pat_01	Post-Resistance	DCC	1630	37	18	50432696	50432696	Missense_Mutation	SNP	C	T	75	257	c.695C>T	c.(694-696)TCA>TTA	p.S232L
Pat_01	Post-Resistance	ALPK2	115701	37	18	56246968	56246968	Missense_Mutation	SNP	T	C	104	322	c.1040A>G	c.(1039-1041)AAC>AGC	p.N347S
Pat_01	Post-Resistance	ZNF407	55628	37	18	72589239	72589239	Missense_Mutation	SNP	C	T	56	174	c.4964C>T	c.(4963-4965)CCG>CTG	p.P1655L
Pat_01	Post-Resistance	SALL3	27164	37	18	76757027	76757027	Missense_Mutation	SNP	G	A	4	231	c.3608G>A	c.(3607-3609)CGG>CAG	p.R1203Q
Pat_01	Post-Resistance	WDR18	57418	37	19	984364	984365	Missense_Mutation	DNP	CC	TT	16	19	c.11_12CC>TT	c.(10-12)CCC>CTT	p.P4L

Pat_01	Post-Resistance	GPX4	2879	37	19	1105450	1105450	Nonsense_Mutation	SNP	C	T	4	219	c.265C>T	c.(265-267)CGA>TGA	p.R89*
Pat_01	Post-Resistance	ZNF556	80032	37	19	2878101	2878101	Missense_Mutation	SNP	C	T	37	56	c.1145C>T	c.(1144-1146)TCC>TTC	p.S382F
Pat_01	Post-Resistance	ADAMTS10	81794	37	19	8670136	8670136	Missense_Mutation	SNP	G	A	3	29	c.196C>T	c.(196-198)CGC>TGC	p.R66C
Pat_01	Post-Resistance	MUC16	94025	37	19	8959682	8959682	Missense_Mutation	SNP	C	T	22	38	c.43450G>A	c.(43450-43452)GAA>AAA	p.E14484K
Pat_01	Post-Resistance	MUC16	94025	37	19	9016716	9016716	Missense_Mutation	SNP	C	T	22	52	c.38021G>A	.(38020-38022)GGG>GA	p.G12674E
Pat_01	Post-Resistance	MUC16	94025	37	19	9066120	9066120	Missense_Mutation	SNP	G	A	3	92	c.21326C>T	c.(21325-21327)CCT>CTT	p.P7109L
Pat_01	Post-Resistance	MUC16	94025	37	19	9068104	9068104	Missense_Mutation	SNP	G	T	5	342	c.19342C>A	c.(19342-19344)CAA>AAA	p.Q6448K
Pat_01	Post-Resistance	ZNF559	84527	37	19	9452752	9452752	Missense_Mutation	SNP	G	A	4	185	c.625G>A	c.(625-627)GGA>AGA	p.G209R
Pat_01	Post-Resistance	ECSIT	51295	37	19	11624916	11624916	Nonsense_Mutation	SNP	C	A	4	58	c.217G>T	c.(217-219)GAG>TAG	p.E73*
Pat_01	Post-Resistance	KLF1	10661	37	19	12997929	12997929	Missense_Mutation	SNP	G	A	5	329	c.26C>T	c.(25-27)CCC>CTC	p.P9L
Pat_01	Post-Resistance	RAD23A	5886	37	19	13059604	13059604	Nonsense_Mutation	SNP	C	T	5	383	c.577C>T	c.(577-579)CGA>TGA	p.R193*
Pat_01	Post-Resistance	TPM4	7171	37	19	16178496	16178496	Missense_Mutation	SNP	G	A	9	224	c.62G>A	c.(61-63)CGC>CAC	p.R21H
Pat_01	Post-Resistance	UNC13A	23025	37	19	17743703	17743703	Missense_Mutation	SNP	G	A	35	87	c.3580C>T	c.(3580-3582)CGT>TGT	p.R1194C
Pat_01	Post-Resistance	UNC13A	23025	37	19	17750670	17750671	Missense_Mutation	DNP	CC	TT	33	160	.3098_3099GG>A	c.(3097-3099)CGG>CAA	p.R1033Q
Pat_01	Post-Resistance	ZNF737	100129842	37	19	20728113	20728113	Missense_Mutation	SNP	A	T	4	54	c.896T>A	c.(895-897)ATC>AAC	p.I299N
Pat_01	Post-Resistance	ZNF737	100129842	37	19	20728170	20728170	Missense_Mutation	SNP	G	C	3	63	c.839C>G	c.(838-840)ACT>AGT	p.T280S
Pat_01	Post-Resistance	ZNF430	80264	37	19	21240468	21240468	Missense_Mutation	SNP	A	T	4	108	c.1354A>T	c.(1354-1356)ACT>TCT	p.T452S
Pat_01	Post-Resistance	ZNF492	57615	37	19	22846958	22846958	Missense_Mutation	SNP	C	T	5	16	c.487C>T	c.(487-489)CAT>TAT	p.H163Y
Pat_01	Post-Resistance	ZNF99	7652	37	19	22939868	22939868	Missense_Mutation	SNP	C	G	57	93	c.2463G>C	c.(2461-2463)AAG>AAC	p.K821N
Pat_01	Post-Resistance	UQCRFS1	7386	37	19	29698570	29698570	Missense_Mutation	SNP	G	A	49	165	c.710C>T	c.(709-711)CCT>CTT	p.P237L
Pat_01	Post-Resistance	SLC7A9	11136	37	19	33355618	33355618	Missense_Mutation	SNP	G	A	70	240	c.152C>T	c.(151-153)TCC>TTC	p.S51F
Pat_01	Post-Resistance	HPN	3249	37	19	35551379	35551379	Missense_Mutation	SNP	G	C	4	348	c.583G>C	c.(583-585)GGG>CGG	p.G195R
Pat_01	Post-Resistance	HPN	3249	37	19	35551596	35551596	Missense_Mutation	SNP	G	A	65	173	c.686G>A	c.(685-687)GGT>GAT	p.G229D
Pat_01	Post-Resistance	USF2	7392	37	19	35769642	35769642	Missense_Mutation	SNP	C	A	7	600	c.769C>A	c.(769-771)CAG>AAG	p.Q257K
Pat_01	Post-Resistance	RBM42	79171	37	19	36122254	36122254	Missense_Mutation	SNP	G	A	4	346	c.389G>A	c.(388-390)CGG>CAG	p.R130Q
Pat_01	Post-Resistance	RBM42	79171	37	19	36125267	36125267	Nonsense_Mutation	SNP	G	A	3	51	c.1127G>A	c.(1126-1128)TGG>TAG	p.W376*
Pat_01	Post-Resistance	NPHS1	4868	37	19	36322215	36322215	Missense_Mutation	SNP	C	T	42	163	c.3370G>A	c.(3370-3372)GAC>AAC	p.D1124N
Pat_01	Post-Resistance	NPHS1	4868	37	19	36333452	36333452	Missense_Mutation	SNP	C	T	30	99	c.2335G>A	c.(2335-2337)GGA>AGA	p.G779R
Pat_01	Post-Resistance	ZNF585B	92285	37	19	37677499	37677499	Nonsense_Mutation	SNP	G	A	100	371	c.940C>T	c.(940-942)CAG>TAG	p.Q314*
Pat_01	Post-Resistance	ZNF283	284349	37	19	44351864	44351864	Missense_Mutation	SNP	G	T	5	272	c.1111G>T	c.(1111-1113)GGT>TGT	p.G371C
Pat_01	Post-Resistance	ZNF229	7772	37	19	44933887	44933888	Missense_Mutation	DNP	CC	TT	57	190	.1068_1069GG>A	066-1071)AAGGGG>AAA	p.G357R
Pat_01	Post-Resistance	KLC3	147700	37	19	45852115	45852115	Missense_Mutation	SNP	G	A	5	11	c.905G>A	c.(904-906)GGG>GAG	p.G302E
Pat_01	Post-Resistance	SYMPK	8189	37	19	46326698	46326698	Missense_Mutation	SNP	G	A	4	198	c.2632C>T	c.(2632-2634)CGG>TGG	p.R878W
Pat_01	Post-Resistance	EHD2	30846	37	19	48220167	48220167	Missense_Mutation	SNP	G	A	4	142	c.298G>A	c.(298-300)GTC>ATC	p.V100I
Pat_01	Post-Resistance	FAM83E	54854	37	19	49104526	49104526	Missense_Mutation	SNP	G	A	8	22	c.1277C>T	c.(1276-1278)CCG>CTG	p.P426L
Pat_01	Post-Resistance	PTH2	113091	37	19	49926533	49926533	Missense_Mutation	SNP	G	C	3	82	c.64C>G	c.(64-66)CTG>GTG	p.L22V
Pat_01	Post-Resistance	MED25	81857	37	19	50335400	50335400	Missense_Mutation	SNP	C	T	22	51	c.1360C>T	c.(1360-1362)CCC>TCC	p.P454S
Pat_01	Post-Resistance	SPIB	6689	37	19	50926223	50926223	Missense_Mutation	SNP	G	A	83	231	c.268G>A	c.(268-270)GAA>AAA	p.E90K
Pat_01	Post-Resistance	MYBPC2	4606	37	19	50939283	50939283	Missense_Mutation	SNP	G	A	3	23	c.211G>A	c.(211-213)GTC>ATC	p.V71I
Pat_01	Post-Resistance	SHANK1	50944	37	19	51191261	51191261	Missense_Mutation	SNP	G	A	60	189	c.2227C>T	c.(2227-2229)CGC>TGC	p.R743C
Pat_01	Post-Resistance	GPR32	2854	37	19	51274491	51274491	Missense_Mutation	SNP	G	A	21	91	c.634G>A	c.(634-636)GGA>AGA	p.G212R
Pat_01	Post-Resistance	ZNF614	80110	37	19	52519785	52519785	Missense_Mutation	SNP	G	A	5	333	c.1066C>T	c.(1066-1068)CGC>TGC	p.R356C
Pat_01	Post-Resistance	ZNF578	147660	37	19	53014565	53014565	Missense_Mutation	SNP	G	A	5	252	c.931G>A	c.(931-933)GGT>AGT	p.G311S
Pat_01	Post-Resistance	ZNF845	91664	37	19	53856702	53856702	Missense_Mutation	SNP	G	A	12	96	c.2774G>A	c.(2773-2775)CGT>CAT	p.R925H
Pat_01	Post-Resistance	LILRB5	10990	37	19	54759200	54759200	Missense_Mutation	SNP	G	A	41	143	c.901C>T	c.(901-903)CTC>TTC	p.L301F
Pat_01	Post-Resistance	NLRP2	55655	37	19	55494049	55494049	Missense_Mutation	SNP	C	T	6	36	c.983C>T	c.(982-984)CCC>CTC	p.P328L
Pat_01	Post-Resistance	SUV420H2	84787	37	19	55854192	55854192	Missense_Mutation	SNP	G	A	4	296	c.359G>A	c.(358-360)GGG>GAG	p.G120E

Pat_01	Post-Resistance	ZNF581	51545	37	19	56156401	56156401	Missense_Mutation	SNP	G	A	4	413	c.464G>A	c.(463-465)CGG>CAG	p.R155Q
Pat_01	Post-Resistance	USP29	57663	37	19	57642039	57642039	Missense_Mutation	SNP	G	A	27	60	c.1996G>A	c.(1996-1998)GGA>AGA	p.G666R
Pat_01	Post-Resistance	RSAD2	91543	37	2	7030435	7030435	Missense_Mutation	SNP	G	T	5	232	c.867G>T	c.(865-867)TTG>TTT	p.L289F
Pat_01	Post-Resistance	NBAS	51594	37	2	15601422	15601422	Missense_Mutation	SNP	G	T	5	392	c.2242C>A	c.(2242-2244)CAT>AAT	p.H748N
Pat_01	Post-Resistance	FAM179A	165186	37	2	29222211	29222211	Nonsense_Mutation	SNP	C	T	3	42	c.304C>T	c.(304-306)CAG>TAG	p.Q102*
Pat_01	Post-Resistance	SRD5A2	6716	37	2	31756517	31756517	Missense_Mutation	SNP	C	T	6	12	c.471G>A	c.(469-471)ATG>ATA	p.M157I
Pat_01	Post-Resistance	SOS1	6654	37	2	39213333	39213333	Missense_Mutation	SNP	G	A	140	521	c.3634C>T	c.(3634-3636)CCC>TCC	p.P1212S
Pat_01	Post-Resistance	EFEMP1	2202	37	2	56108861	56108861	Missense_Mutation	SNP	C	T	200	492	c.526G>A	c.(526-528)GAG>AAG	p.E176K
Pat_01	Post-Resistance	FAM161A	84140	37	2	62081080	62081080	Missense_Mutation	SNP	C	T	44	123	c.97G>A	c.(97-99)GAA>AAA	p.E33K
Pat_01	Post-Resistance	SEMA4F	10505	37	2	74906728	74906728	Missense_Mutation	SNP	C	T	6	817	c.1705C>T	c.(1705-1707)CGT>TGT	p.R569C
Pat_01	Post-Resistance	C2orf3	6936	37	2	75916281	75916281	Missense_Mutation	SNP	A	C	90	232	c.1410T>G	c.(1408-1410)ATT>ATG	p.I470M
Pat_01	Post-Resistance	REV1	51455	37	2	100020202	100020203	Missense_Mutation	DNP	CT	TC	114	397	.3121_3122AG>G	c.(3121-3123)AGG>GAG	p.R1041E
Pat_01	Post-Resistance	PSD4	23550	37	2	113940340	113940340	Missense_Mutation	SNP	G	A	5	76	c.307G>A	c.(307-309)GAT>AAT	p.D103N
Pat_01	Post-Resistance	PSD4	23550	37	2	113940344	113940344	Missense_Mutation	SNP	C	T	5	73	c.311C>T	c.(310-312)GCT>GTT	p.A104V
Pat_01	Post-Resistance	ARHGAP15	55843	37	2	144276883	144276883	Missense_Mutation	SNP	C	T	137	455	c.875C>T	c.(874-876)TCC>TTC	p.S292F
Pat_01	Post-Resistance	NEB	4703	37	2	152518729	152518729	Missense_Mutation	SNP	G	A	54	123	c.5890C>T	c.(5890-5892)CCA>TCA	p.P1964S
Pat_01	Post-Resistance	CACNB4	785	37	2	152727103	152727103	Missense_Mutation	SNP	T	G	36	131	c.641A>C	c.(640-642)GAT>GCT	p.D214A
Pat_01	Post-Resistance	BAZ2B	29994	37	2	160242971	160242971	Nonsense_Mutation	SNP	G	A	146	501	c.3364C>T	c.(3364-3366)CAA>TAA	p.Q1122*
Pat_01	Post-Resistance	KCNH7	90134	37	2	163693083	163693083	Missense_Mutation	SNP	C	T	40	132	c.271G>A	c.(271-273)GAG>AAG	p.E91K
Pat_01	Post-Resistance	SCN3A	6328	37	2	165946757	165946757	Missense_Mutation	SNP	G	A	10	37	c.5906C>T	c.(5905-5907)TCC>TTC	p.S1969F
Pat_01	Post-Resistance	LRP2	4036	37	2	170044739	170044739	Missense_Mutation	SNP	G	T	5	421	c.9069C>A	c.(9067-9069)GAC>GAA	p.D3023E
Pat_01	Post-Resistance	PPIG	9360	37	2	170463619	170463619	Missense_Mutation	SNP	G	A	158	507	c.250G>A	c.(250-252)GGA>AGA	p.G84R
Pat_01	Post-Resistance	DCAF17	80067	37	2	172306454	172306454	Missense_Mutation	SNP	C	A	5	313	c.524C>A	c.(523-525)GCA>GAA	p.A175E
Pat_01	Post-Resistance	OSBPL6	114880	37	2	179213981	179213981	Missense_Mutation	SNP	C	T	239	568	c.1018C>T	c.(1018-1020)CGC>TGC	p.R340C
Pat_01	Post-Resistance	TTN	7273	37	2	179400097	179400097	Missense_Mutation	SNP	C	T	96	240	c.93541G>A	c.(93541-93543)GTG>ATG	p.V31181M
Pat_01	Post-Resistance	TTN	7273	37	2	179413669	179413669	Missense_Mutation	SNP	C	T	5	336	c.84980G>A	c.(84979-84981)CGA>CAA	p.R28327Q
Pat_01	Post-Resistance	TTN	7273	37	2	179426716	179426716	Missense_Mutation	SNP	A	T	26	69	c.76439T>A	c.(76438-76440)ATT>AAT	p.I25480N
Pat_01	Post-Resistance	TTN	7273	37	2	179612027	179612027	Missense_Mutation	SNP	C	T	46	152	c.15100G>A	c.(15100-15102)GAA>AAA	p.E5034K
Pat_01	Post-Resistance	TTN	7273	37	2	179613066	179613066	Missense_Mutation	SNP	C	T	79	216	c.14061G>A	c.(14059-14061)ATG>ATA	p.M4687I
Pat_01	Post-Resistance	CCDC141	285025	37	2	179736940	179736940	Missense_Mutation	SNP	G	A	4	212	c.274C>T	c.(274-276)CGG>TGG	p.R92W
Pat_01	Post-Resistance	WDR12	55759	37	2	203757384	203757384	Nonsense_Mutation	SNP	G	A	105	285	c.697C>T	c.(697-699)CGA>TGA	p.R233*
Pat_01	Post-Resistance	ABI2	10152	37	2	204260420	204260420	Missense_Mutation	SNP	G	A	5	425	c.767G>A	c.(766-768)AGC>AAC	p.S256N
Pat_01	Post-Resistance	ABCA12	26154	37	2	215866284	215866284	Missense_Mutation	SNP	C	T	139	425	c.2861G>A	c.(2860-2862)GGA>GAA	p.G954E
Pat_01	Post-Resistance	GLB1L	79411	37	2	220101964	220101964	Missense_Mutation	SNP	G	A	4	283	c.1795C>T	c.(1795-1797)CTC>TTC	p.L599F
Pat_01	Post-Resistance	GLB1L	79411	37	2	220104504	220104504	Missense_Mutation	SNP	C	A	4	238	c.773G>T	c.(772-774)GGG>GTG	p.G258V
Pat_01	Post-Resistance	PTPRN	5798	37	2	220162747	220162747	Missense_Mutation	SNP	C	A	4	259	c.1747G>T	c.(1747-1749)GCC>TCC	p.A583S
Pat_01	Post-Resistance	ALPI	248	37	2	233323569	233323569	Splice_Site	SNP	G	A	11	24	c.1301_splice	c.e11-1	p.G434_splice
Pat_01	Post-Resistance	DNAJB3	414061	37	2	234652346	234652346	Missense_Mutation	SNP	C	T	72	243	c.217G>A	c.(217-219)GCG>ACG	p.A73T
Pat_01	Post-Resistance	COL6A3	1293	37	2	238267865	238267865	Missense_Mutation	SNP	C	T	75	279	c.6338G>A	c.(6337-6339)GGT>GAT	p.G2113D
Pat_01	Post-Resistance	RAMP1	10267	37	2	238785940	238785940	Missense_Mutation	SNP	C	A	5	330	c.127C>A	c.(127-129)CAG>AAG	p.Q43K
Pat_01	Post-Resistance	RNPEPL1	57140	37	2	241515022	241515022	Missense_Mutation	SNP	G	A	4	112	c.812G>A	c.(811-813)CGG>CAG	p.R271Q
Pat_01	Post-Resistance	BOK	666	37	2	242501783	242501783	Missense_Mutation	SNP	C	T	4	179	c.241C>T	c.(241-243)CGG>TGG	p.R81W
Pat_01	Post-Resistance	DEFB125	245938	37	20	76798	76798	Missense_Mutation	SNP	C	T	190	466	c.211C>T	c.(211-213)CCT>TCT	p.P71S
Pat_01	Post-Resistance	TGM3	7053	37	20	2291716	2291716	Missense_Mutation	SNP	G	A	5	411	c.481G>A	c.(481-483)GGC>AGC	p.G161S
Pat_01	Post-Resistance	FASTKD5	60493	37	20	3128950	3128950	Missense_Mutation	SNP	C	T	14	34	c.767G>A	c.(766-768)CGC>CAC	p.R256H
Pat_01	Post-Resistance	ATRN	8455	37	20	3543099	3543099	Missense_Mutation	SNP	C	A	5	326	c.1624C>A	c.(1624-1626)CAG>AAG	p.Q542K
Pat_01	Post-Resistance	PLCB4	5332	37	20	9404512	9404512	Missense_Mutation	SNP	C	T	48	127	c.2401C>T	c.(2401-2403)CTT>TTT	p.L801F

Pat_01	Post-Resistance	PAK7	57144	37	20	9561331	9561331	Missense_Mutation	SNP	G	A	164	504	c.451C>T	c.(451-453)CTC>TTC	p.L151F
Pat_01	Post-Resistance	PYGB	5834	37	20	25255312	25255312	Missense_Mutation	SNP	G	A	5	518	c.613G>A	c.(613-615)GGA>AGA	p.G205R
Pat_01	Post-Resistance	FRG1B	284802	37	20	29625885	29625885	Missense_Mutation	SNP	A	T	5	249	c.39A>T	c.(37-39)AAA>AAT	p.K13N
Pat_01	Post-Resistance	ASXL1	171023	37	20	31023766	31023766	Missense_Mutation	SNP	G	A	4	208	c.3251G>A	c.(3250-3252)AGT>AAT	p.S1084N
Pat_01	Post-Resistance	DNMT3B	1789	37	20	31385087	31385087	Missense_Mutation	SNP	G	A	6	230	c.1472G>A	c.(1471-1473)AGC>AAC	p.S491N
Pat_01	Post-Resistance	CBFA2T2	9139	37	20	32194875	32194875	Missense_Mutation	SNP	C	T	77	226	c.175C>T	c.(175-177)CCG>TCG	p.P59S
Pat_01	Post-Resistance	PLCG1	5335	37	20	39793679	39793679	Missense_Mutation	SNP	G	A	4	103	c.1324G>A	c.(1324-1326)GTG>ATG	p.V442M
Pat_01	Post-Resistance	PTPRT	11122	37	20	40735458	40735458	Missense_Mutation	SNP	G	A	5	307	c.3358C>T	c.(3358-3360)CGG>TGG	p.R1120W
Pat_01	Post-Resistance	C20orf111	51526	37	20	42825898	42825898	Missense_Mutation	SNP	G	A	46	147	c.673C>T	c.(673-675)CCC>TCC	p.P225S
Pat_01	Post-Resistance	ZMYND8	23613	37	20	45905157	45905157	Missense_Mutation	SNP	G	A	4	171	c.1321C>T	c.(1321-1323)CAC>TAC	p.H441Y
Pat_01	Post-Resistance	TSHZ2	128553	37	20	51872939	51872939	Missense_Mutation	SNP	C	T	24	66	c.2942C>T	c.(2941-2943)CCA>CTA	p.P981L
Pat_01	Post-Resistance	RAE1	8480	37	20	55948597	55948597	Missense_Mutation	SNP	G	A	6	305	c.709G>A	c.(709-711)GAG>AAG	p.E237K
Pat_01	Post-Resistance	CDH26	60437	37	20	58567473	58567473	Missense_Mutation	SNP	G	A	4	163	c.1324G>A	c.(1324-1326)GAC>AAC	p.D442N
Pat_01	Post-Resistance	TPTE	7179	37	21	10942755	10942755	Missense_Mutation	SNP	C	T	97	694	c.686G>A	c.(685-687)CGA>CAA	p.R229Q
Pat_01	Post-Resistance	DSCAM	1826	37	21	42080568	42080568	Missense_Mutation	SNP	C	A	111	490	c.173G>T	c.(172-174)TGG>TTG	p.W58L
Pat_01	Post-Resistance	PWP2	5822	37	21	45545973	45545973	Missense_Mutation	SNP	G	A	4	208	c.2047G>A	c.(2047-2049)GCG>ACG	p.A683T
Pat_01	Post-Resistance	KRTAP10-8	386681	37	21	46032171	46032171	Missense_Mutation	SNP	G	A	44	150	c.154G>A	c.(154-156)GAG>AAG	p.E52K
Pat_01	Post-Resistance	PCNT	5116	37	21	47836365	47836365	Missense_Mutation	SNP	C	T	66	312	c.6533C>T	c.(6532-6534)CCC>CTC	p.P2178L
Pat_01	Post-Resistance	POTEH	23784	37	22	16267070	16267070	Missense_Mutation	SNP	C	T	44	716	c.1379G>A	c.(1378-1380)GGA>GAA	p.G460E
Pat_01	Post-Resistance	CCT8L2	150160	37	22	17072146	17072147	Missense_Mutation	DNP	CC	TT	20	67	.1294_1295GG>A	c.(1294-1296)GGG>AAG	p.G432K
Pat_01	Post-Resistance	EMID1	129080	37	22	29630293	29630293	Splice_Site	SNP	G	A	24	66	c.1024_splice	c.e12-1	p.G342_splice
Pat_01	Post-Resistance	MTMR3	8897	37	22	30415933	30415933	Missense_Mutation	SNP	C	T	95	174	c.2285C>T	c.(2284-2286)TCA>TTA	p.S762L
Pat_01	Post-Resistance	CCDC157	550631	37	22	30772519	30772519	Missense_Mutation	SNP	C	T	9	651	c.2044C>T	c.(2044-2046)CCT>TCT	p.P682S
Pat_01	Post-Resistance	DEPDC5	9681	37	22	32200858	32200858	Missense_Mutation	SNP	C	T	222	471	c.1174C>T	c.(1174-1176)CGT>TGT	p.R392C
Pat_01	Post-Resistance	TOM1	10043	37	22	35719804	35719804	Missense_Mutation	SNP	G	A	6	335	c.545G>A	c.(544-546)GGC>GAC	p.G182D
Pat_01	Post-Resistance	RASD2	23551	37	22	35947904	35947904	Missense_Mutation	SNP	G	A	35	102	c.626G>A	c.(625-627)GGT>GAT	p.G209D
Pat_01	Post-Resistance	MYH9	4627	37	22	36680543	36680543	Missense_Mutation	SNP	G	A	4	171	c.5498C>T	c.(5497-5499)GCC>GTC	p.A1833V
Pat_01	Post-Resistance	TRIOBP	11078	37	22	38119860	38119860	Missense_Mutation	SNP	G	A	4	236	c.1297G>A	c.(1297-1299)GCC>ACC	p.A433T
Pat_01	Post-Resistance	ADSL	158	37	22	40757531	40757531	Nonsense_Mutation	SNP	C	A	6	516	c.902C>A	c.(901-903)TCA>TAA	p.S301*
Pat_01	Post-Resistance	XRCC6	2547	37	22	42032630	42032630	Missense_Mutation	SNP	G	A	5	355	c.445G>A	c.(445-447)GTC>ATC	p.V149I
Pat_01	Post-Resistance	SERHL2	253190	37	22	42956229	42956229	Missense_Mutation	SNP	G	A	4	260	c.571G>A	c.(571-573)GGG>AGG	p.G191R
Pat_01	Post-Resistance	SETMAR	6419	37	3	4354792	4354792	Nonsense_Mutation	SNP	C	T	4	138	c.367C>T	c.(367-369)CGA>TGA	p.R123*
Pat_01	Post-Resistance	ITPR1	3708	37	3	4725218	4725218	Missense_Mutation	SNP	C	T	47	100	c.3283C>T	c.(3283-3285)CTC>TTC	p.L1095F
Pat_01	Post-Resistance	OXTR	5021	37	3	8809536	8809536	Missense_Mutation	SNP	C	T	4	116	c.338G>A	c.(337-339)CGC>CAC	p.R113H
Pat_01	Post-Resistance	ATG7	10533	37	3	11399971	11399971	Missense_Mutation	SNP	G	A	5	350	c.1364G>A	c.(1363-1365)CGC>CAC	p.R455H
Pat_01	Post-Resistance	CAND2	23066	37	3	12869077	12869077	Missense_Mutation	SNP	G	A	5	361	c.3349G>A	c.(3349-3351)GGG>AGG	p.G1117R
Pat_01	Post-Resistance	FGD5	152273	37	3	14974174	14974174	Missense_Mutation	SNP	C	T	60	270	c.4288C>T	c.(4288-4290)CAC>TAC	p.H1430Y
Pat_01	Post-Resistance	KAT2B	8850	37	3	20167436	20167436	Missense_Mutation	SNP	G	A	6	635	c.1453G>A	c.(1453-1455)GCA>ACA	p.A485T
Pat_01	Post-Resistance	FBXL2	25827	37	3	33427035	33427035	Missense_Mutation	SNP	G	A	6	701	c.1207G>A	c.(1207-1209)GTC>ATC	p.V403I
Pat_01	Post-Resistance	CLASP2	23122	37	3	33704961	33704961	Missense_Mutation	SNP	C	T	4	350	c.691G>A	c.(691-693)GGT>AGT	p.G231S
Pat_01	Post-Resistance	TRANK1	9881	37	3	36873315	36873315	Missense_Mutation	SNP	G	A	4	257	c.5977C>T	c.(5977-5979)CGC>TGC	p.R1993C
Pat_01	Post-Resistance	TRANK1	9881	37	3	36893807	36893807	Missense_Mutation	SNP	C	T	6	29	c.2797G>A	c.(2797-2799)GAT>AAT	p.D933N
Pat_01	Post-Resistance	VILL	50853	37	3	38043308	38043308	Missense_Mutation	SNP	C	A	58	208	c.1436C>A	c.(1435-1437)CCC>CAC	p.P479H
Pat_01	Post-Resistance	DLEC1	9940	37	3	38134291	38134292	Missense_Mutation	DNP	CC	TT	43	232	.1676_1677CC>T	c.(1675-1677)TCC>TTT	p.S559F
Pat_01	Post-Resistance	SCN10A	6336	37	3	38740026	38740026	Missense_Mutation	SNP	G	A	45	148	c.4685C>T	c.(4684-4686)TCA>TTA	p.S1562L
Pat_01	Post-Resistance	MYRIP	25924	37	3	40251444	40251444	Missense_Mutation	SNP	G	A	53	149	c.1765G>A	c.(1765-1767)GAG>AAG	p.E589K
Pat_01	Post-Resistance	TRAK1	22906	37	3	42243999	42243999	Missense_Mutation	SNP	G	A	22	57	c.1499G>A	c.(1498-1500)AGG>AAG	p.R500K

Pat_01	Post-Resistance	ANO10	55129	37	3	43642014	43642014	Nonsense_Mutation	SNP	G	A	6	262	c.199C>T	c.(199-201)CAG>TAG	p.Q67*
Pat_01	Post-Resistance	CCR1	1230	37	3	46244880	46244880	Missense_Mutation	SNP	G	A	37	119	c.925C>T	c.(925-927)CGG>TGG	p.R309W
Pat_01	Post-Resistance	KLHL18	23276	37	3	47324519	47324519	Missense_Mutation	SNP	A	T	27	32	c.64A>T	c.(64-66)AGT>TGT	p.S22C
Pat_01	Post-Resistance	COL7A1	1294	37	3	48606836	48606836	Missense_Mutation	SNP	C	A	5	383	c.7658G>T	c.(7657-7659)CGG>CTG	p.R2553L
Pat_01	Post-Resistance	BSN	8927	37	3	49689975	49689975	Missense_Mutation	SNP	C	T	20	69	c.2986C>T	c.(2986-2988)CCC>TCC	p.P996S
Pat_01	Post-Resistance	DNAH1	25981	37	3	52387600	52387600	Missense_Mutation	SNP	G	A	3	37	c.3431G>A	c.(3430-3432)AGC>AAC	p.S1144N
Pat_01	Post-Resistance	DNAH1	25981	37	3	52428596	52428596	Missense_Mutation	SNP	C	T	4	161	c.10742C>T	c.(10741-10743)CCA>CTA	p.P3581L
Pat_01	Post-Resistance	PHF7	51533	37	3	52456871	52456871	Missense_Mutation	SNP	A	G	4	460	c.893A>G	c.(892-894)GAG>GGG	p.E298G
Pat_01	Post-Resistance	ROBO1	6091	37	3	78696802	78696802	Missense_Mutation	SNP	G	A	6	776	c.2816C>T	c.(2815-2817)CCG>CTG	p.P939L
Pat_01	Post-Resistance	OR5H15	403274	37	3	97887907	97887907	Missense_Mutation	SNP	C	T	123	398	c.364C>T	c.(364-366)CGC>TGC	p.R122C
Pat_01	Post-Resistance	COL8A1	1295	37	3	99514930	99514930	Missense_Mutation	SNP	G	A	47	131	c.2185G>A	c.(2185-2187)GGG>AGG	p.G729R
Pat_01	Post-Resistance	HHLA2	11148	37	3	108072466	108072466	Missense_Mutation	SNP	C	T	37	155	c.257C>T	c.(256-258)CCC>CTC	p.P86L
Pat_01	Post-Resistance	C3orf30	152405	37	3	118865259	118865259	Missense_Mutation	SNP	G	A	49	127	c.223G>A	c.(223-225)GTA>ATA	p.V75I
Pat_01	Post-Resistance	PARP9	83666	37	3	122278457	122278457	Missense_Mutation	SNP	G	A	120	469	c.11C>T	c.(10-12)TCC>TTC	p.S4F
Pat_01	Post-Resistance	PLXND1	23129	37	3	129280710	129280710	Missense_Mutation	SNP	C	T	4	399	c.4862G>A	c.(4861-4863)CGG>CAG	p.R1621Q
Pat_01	Post-Resistance	FAIM	55179	37	3	138340328	138340328	Missense_Mutation	SNP	G	A	105	219	c.58G>A	c.(58-60)GAA>AAA	p.E20K
Pat_01	Post-Resistance	SLC9A9	285195	37	3	143292992	143292992	Missense_Mutation	SNP	G	A	4	241	c.938C>T	c.(937-939)ACC>ATC	p.T313I
Pat_01	Post-Resistance	PLSCR4	57088	37	3	145912973	145912973	Missense_Mutation	SNP	G	A	98	300	c.883C>T	c.(883-885)CAC>TAC	p.H295Y
Pat_01	Post-Resistance	MED12L	116931	37	3	151129198	151129198	Missense_Mutation	SNP	G	A	5	468	c.5938G>A	c.(5938-5940)GTG>ATG	p.V1980M
Pat_01	Post-Resistance	IGSF10	285313	37	3	151165431	151165431	Missense_Mutation	SNP	G	A	5	215	c.2338C>T	c.(2338-2340)CCC>TCC	p.P780S
Pat_01	Post-Resistance	SLC2A2	6514	37	3	170716922	170716922	Missense_Mutation	SNP	G	A	113	264	c.1102C>T	c.(1102-1104)CTC>TTC	p.L368F
Pat_01	Post-Resistance	TNFSF10	8743	37	3	172227075	172227075	Missense_Mutation	SNP	C	T	51	214	c.350G>A	c.(349-351)AGA>AAA	p.R117K
Pat_01	Post-Resistance	NCEH1	57552	37	3	172351338	172351338	Missense_Mutation	SNP	C	G	4	331	c.1274G>C	c.(1273-1275)AGC>ACC	p.S425T
Pat_01	Post-Resistance	KCNMB2	10242	37	3	178545976	178545976	Missense_Mutation	SNP	G	A	129	355	c.238G>A	c.(238-240)GAA>AAA	p.E80K
Pat_01	Post-Resistance	FAM131A	131408	37	3	184060025	184060025	Missense_Mutation	SNP	G	T	4	229	c.404G>T	c.(403-405)CGC>CTC	p.R135L
Pat_01	Post-Resistance	EPHB3	2049	37	3	184290328	184290328	Missense_Mutation	SNP	C	T	50	135	c.220C>T	c.(220-222)CCC>TCC	p.P74S
Pat_01	Post-Resistance	TP63	8626	37	3	189586470	189586470	Missense_Mutation	SNP	C	T	127	340	c.1094C>T	c.(1093-1095)TCG>TTG	p.S365L
Pat_01	Post-Resistance	IL1RAP	3556	37	3	190338217	190338217	Missense_Mutation	SNP	G	A	6	662	c.691G>A	c.(691-693)GTA>ATA	p.V231I
Pat_01	Post-Resistance	MUC4	4585	37	3	195479245	195479245	Missense_Mutation	SNP	G	A	5	174	c.15197C>T	c.(15196-15198)TCG>TTG	p.S5066L
Pat_01	Post-Resistance	ZNF721	170960	37	4	436628	436628	Missense_Mutation	SNP	A	T	5	345	c.1628T>A	c.(1627-1629)ATC>AAC	p.I543N
Pat_01	Post-Resistance	ZNF721	170960	37	4	436647	436647	Missense_Mutation	SNP	C	T	9	347	c.1609G>A	c.(1609-1611)GCC>ACC	p.A537T
Pat_01	Post-Resistance	PIGG	54872	37	4	509834	509834	Missense_Mutation	SNP	C	T	4	345	c.974C>T	c.(973-975)CCG>CTG	p.P325L
Pat_01	Post-Resistance	DGKQ	1609	37	4	962665	962665	Missense_Mutation	SNP	G	A	3	46	c.385C>T	c.(385-387)CTC>TTC	p.L129F
Pat_01	Post-Resistance	ZFYVE28	57732	37	4	2341259	2341259	Missense_Mutation	SNP	G	A	3	45	c.442C>T	c.(442-444)CGG>TGG	p.R148W
Pat_01	Post-Resistance	PPARGC1A	10891	37	4	23815370	23815370	Missense_Mutation	SNP	G	A	54	145	c.1736C>T	c.(1735-1737)TCC>TTC	p.S579F
Pat_01	Post-Resistance	TLR10	81793	37	4	38777051	38777051	Missense_Mutation	SNP	T	G	47	175	c.161A>C	c.(160-162)GAT>GCT	p.D54A
Pat_01	Post-Resistance	SHISA3	152573	37	4	42403461	42403461	Missense_Mutation	SNP	C	T	62	193	c.710C>T	c.(709-711)TCC>TTC	p.S237F
Pat_01	Post-Resistance	GABRA2	2555	37	4	46307695	46307695	Nonsense_Mutation	SNP	C	T	37	116	c.593G>A	c.(592-594)TGG>TAG	p.W198*
Pat_01	Post-Resistance	CORIN	10699	37	4	47647188	47647188	Missense_Mutation	SNP	C	T	97	297	c.1867G>A	c.(1867-1869)GAA>AAA	p.E623K
Pat_01	Post-Resistance	OCIAD2	132299	37	4	48901867	48901867	Missense_Mutation	SNP	C	T	97	293	c.142G>A	c.(142-144)GAA>AAA	p.E48K
Pat_01	Post-Resistance	LNX1	84708	37	4	54364972	54364972	Missense_Mutation	SNP	T	A	75	178	c.814A>T	c.(814-816)ATT>TTT	p.I272F
Pat_01	Post-Resistance	LPHN3	23284	37	4	62903453	62903453	Missense_Mutation	SNP	G	A	107	328	c.3392G>A	c.(3391-3393)CGA>CAA	p.R1131Q
Pat_01	Post-Resistance	UGT2B10	7365	37	4	69693259	69693259	Missense_Mutation	SNP	G	A	103	383	c.1300G>A	c.(1300-1302)GAT>AAT	p.D434N
Pat_01	Post-Resistance	UGT2B7	7364	37	4	69962580	69962580	Missense_Mutation	SNP	A	T	19	48	c.342A>T	c.(340-342)GAA>GAT	p.E114D
Pat_01	Post-Resistance	MUC7	4589	37	4	71347138	71347138	Missense_Mutation	SNP	C	T	14	677	c.677C>T	c.(676-678)CCA>CTA	p.P226L
Pat_01	Post-Resistance	GC	2638	37	4	72631267	72631267	Nonsense_Mutation	SNP	G	A	6	394	c.355C>T	c.(355-357)CGA>TGA	p.R119*
Pat_01	Post-Resistance	ANKRD17	26057	37	4	73984530	73984530	Missense_Mutation	SNP	T	C	179	518	c.4063A>G	c.(4063-4065)ACT>GCT	p.T1355A

Pat_01	Post-Resistance	PPEF2	5470	37	4	76787390	76787390	Missense_Mutation	SNP	C	A	5	478	c.1872G>T	c.(1870-1872)GAG>GAT	p.E624D
Pat_01	Post-Resistance	GK2	2712	37	4	80327902	80327902	Missense_Mutation	SNP	C	T	103	261	c.1453G>A	c.(1453-1455)GAA>AAA	p.E485K
Pat_01	Post-Resistance	HERC5	51191	37	4	89425504	89425504	Missense_Mutation	SNP	C	T	50	224	c.2704C>T	c.(2704-2706)CCC>TCC	p.P902S
Pat_01	Post-Resistance	UNC5C	8633	37	4	96104089	96104089	Missense_Mutation	SNP	C	T	122	260	c.2410G>A	c.(2410-2412)GGA>AGA	p.G804R
Pat_01	Post-Resistance	EGF	1950	37	4	110921002	110921002	Missense_Mutation	SNP	G	A	110	292	c.3173G>A	c.(3172-3174)AGG>AAG	p.R1058K
Pat_01	Post-Resistance	ENPEP	2028	37	4	111441369	111441369	Splice_Site	SNP	A	T	4	229	c.1576_splice	c.e10-2	p.A526_splice
Pat_01	Post-Resistance	PITX2	5308	37	4	111542415	111542415	Missense_Mutation	SNP	C	T	42	123	c.295G>A	c.(295-297)GAG>AAG	p.E99K
Pat_01	Post-Resistance	FAT4	79633	37	4	126370224	126370224	Nonsense_Mutation	SNP	C	T	8	685	c.8053C>T	c.(8053-8055)CGA>TGA	p.R2685*
Pat_01	Post-Resistance	ELMOD2	255520	37	4	141461344	141461344	Missense_Mutation	SNP	C	T	4	136	c.422C>T	c.(421-423)ACG>ATG	p.T141M
Pat_01	Post-Resistance	DCHS2	54798	37	4	155157358	155157358	Missense_Mutation	SNP	G	A	128	337	c.7081C>T	c.(7081-7083)CAT>TAT	p.H2361Y
Pat_01	Post-Resistance	DCHS2	54798	37	4	155298407	155298407	Missense_Mutation	SNP	C	T	73	245	c.424G>A	c.(424-426)GGG>AGG	p.G142R
Pat_01	Post-Resistance	CLCN3	1182	37	4	170613292	170613292	Missense_Mutation	SNP	A	T	67	310	c.757A>T	c.(757-759)ATC>TTC	p.I253F
Pat_01	Post-Resistance	ASB5	140458	37	4	177138062	177138062	Missense_Mutation	SNP	C	T	5	451	c.769G>A	c.(769-771)GCA>ACA	p.A257T
Pat_01	Post-Resistance	ASB5	140458	37	4	177190238	177190238	Missense_Mutation	SNP	G	A	91	272	c.22C>T	c.(22-24)CGG>TGG	p.R8W
Pat_01	Post-Resistance	ODZ3	55714	37	4	183652119	183652119	Missense_Mutation	SNP	C	T	56	130	c.2794C>T	c.(2794-2796)CCA>TCA	p.P932S
Pat_01	Post-Resistance	STOX2	56977	37	4	184930961	184930961	Missense_Mutation	SNP	G	A	3	36	c.970G>A	c.(970-972)GTG>ATG	p.V324M
Pat_01	Post-Resistance	FAM149A	25854	37	4	187086560	187086560	Missense_Mutation	SNP	C	T	6	246	c.1106C>T	c.(1105-1107)CCG>CTG	p.P369L
Pat_01	Post-Resistance	C5orf23	79614	37	5	32789844	32789844	Missense_Mutation	SNP	G	A	5	364	c.337G>A	c.(337-339)GTC>ATC	p.V113I
Pat_01	Post-Resistance	CAPSL	133690	37	5	35904702	35904702	Missense_Mutation	SNP	G	A	149	412	c.572C>T	c.(571-573)TCC>TTC	p.S191F
Pat_01	Post-Resistance	EGFLAM	133584	37	5	38431379	38431379	Missense_Mutation	SNP	G	A	4	219	c.2155G>A	c.(2155-2157)GGA>AGA	p.G719R
Pat_01	Post-Resistance	HEATR7B2	133558	37	5	41042300	41042300	Nonsense_Mutation	SNP	C	T	10	11	c.1847G>A	c.(1846-1848)TGG>TAG	p.W616*
Pat_01	Post-Resistance	C5orf34	375444	37	5	43509374	43509374	Missense_Mutation	SNP	G	A	82	195	c.68C>T	c.(67-69)TCC>TTC	p.S23F
Pat_01	Post-Resistance	SKIV2L2	23517	37	5	54662656	54662656	Missense_Mutation	SNP	C	T	103	393	c.1763C>T	c.(1762-1764)TCC>TTC	p.S588F
Pat_01	Post-Resistance	MAST4	375449	37	5	66460811	66460812	Missense_Mutation	DNP	CC	AT	12	46	.5237_5238CC>A	c.(5236-5238)CCC>CAT	p.P1746H
Pat_01	Post-Resistance	ZFYVE16	9765	37	5	79770564	79770564	Missense_Mutation	SNP	G	A	4	206	c.4376G>A	c.(4375-4377)AGT>AAT	p.S1459N
Pat_01	Post-Resistance	RASA1	5921	37	5	86685291	86685291	Missense_Mutation	SNP	G	A	9	653	c.3007G>A	c.(3007-3009)GTG>ATG	p.V1003M
Pat_01	Post-Resistance	TTC37	9652	37	5	94833154	94833154	Missense_Mutation	SNP	C	T	4	207	c.3602G>A	c.(3601-3603)CGA>CAA	p.R1201Q
Pat_01	Post-Resistance	CAST	831	37	5	96086361	96086361	Nonsense_Mutation	SNP	C	A	6	254	c.1250C>A	c.(1249-1251)TCA>TAA	p.S417*
Pat_01	Post-Resistance	C5orf13	9315	37	5	111066622	111066622	Missense_Mutation	SNP	A	G	121	331	c.203T>C	c.(202-204)TTT>TCT	p.F68S
Pat_01	Post-Resistance	LOX	4015	37	5	121412595	121412595	Missense_Mutation	SNP	G	T	6	313	c.733C>A	c.(733-735)CTG>ATG	p.L245M
Pat_01	Post-Resistance	SLC27A6	28965	37	5	128364084	128364084	Missense_Mutation	SNP	G	A	76	256	c.1501G>A	c.(1501-1503)GGA>AGA	p.G501R
Pat_01	Post-Resistance	CHSY3	337876	37	5	129520415	129520415	Missense_Mutation	SNP	G	A	4	244	c.1580G>A	c.(1579-1581)CGC>CAC	p.R527H
Pat_01	Post-Resistance	ACSL6	23305	37	5	131308419	131308419	Nonsense_Mutation	SNP	G	A	65	237	c.1261C>T	c.(1261-1263)CAG>TAG	p.Q421*
Pat_01	Post-Resistance	HSPA9	3313	37	5	137892158	137892158	Missense_Mutation	SNP	C	T	6	760	c.1945G>A	c.(1945-1947)GAA>AAA	p.E649K
Pat_01	Post-Resistance	PCDHB10	56126	37	5	140574481	140574481	Missense_Mutation	SNP	G	A	40	89	c.2356G>A	c.(2356-2358)GAA>AAA	p.E786K
Pat_01	Post-Resistance	PCDHGA2	56113	37	5	140718983	140718983	Missense_Mutation	SNP	G	A	60	191	c.445G>A	c.(445-447)GGA>AGA	p.G149R
Pat_01	Post-Resistance	PCDHGA2	56113	37	5	140720289	140720289	Missense_Mutation	SNP	C	T	148	314	c.1751C>T	c.(1750-1752)CCC>CTC	p.P584L
Pat_01	Post-Resistance	PCDHGA8	9708	37	5	140772898	140772898	Missense_Mutation	SNP	G	A	56	160	c.518G>A	c.(517-519)AGC>AAC	p.S173N
Pat_01	Post-Resistance	PCDH12	51294	37	5	141335609	141335609	Missense_Mutation	SNP	G	A	5	210	c.1808C>T	c.(1807-1809)ACT>ATT	p.T603I
Pat_01	Post-Resistance	GM2A	2760	37	5	150646936	150646936	Missense_Mutation	SNP	G	A	4	182	c.506G>A	c.(505-507)CGC>CAC	p.R169H
Pat_01	Post-Resistance	GRIA1	2890	37	5	153144170	153144170	Missense_Mutation	SNP	G	A	36	101	c.2000G>A	c.(1999-2001)GGA>GAA	p.G667E
Pat_01	Post-Resistance	HAVCR2	84868	37	5	156514235	156514235	Missense_Mutation	SNP	C	T	37	163	c.784G>A	c.(784-786)GAA>AAA	p.E262K
Pat_01	Post-Resistance	LSM11	134353	37	5	157182040	157182040	Missense_Mutation	SNP	C	T	64	122	c.851C>T	c.(850-852)TCC>TTC	p.S284F
Pat_01	Post-Resistance	GABRP	2568	37	5	170239094	170239094	Missense_Mutation	SNP	G	A	80	265	c.1155G>A	c.(1153-1155)ATG>ATA	p.M385I
Pat_01	Post-Resistance	STC2	8614	37	5	172755184	172755184	Missense_Mutation	SNP	G	A	5	332	c.13C>T	c.(13-15)CGG>TGG	p.R5W
Pat_01	Post-Resistance	GFPT2	9945	37	5	179762866	179762866	Missense_Mutation	SNP	G	A	4	175	c.302C>T	c.(301-303)GCT>GTT	p.A101V
Pat_01	Post-Resistance	GNB2L1	10399	37	5	180665127	180665127	Missense_Mutation	SNP	G	A	5	432	c.749C>T	c.(748-750)GCT>GTT	p.A250V

Pat_01	Post-Resistance	ATXN1	6310	37	6	16327485	16327485	Missense_Mutation	SNP	G	A	78	245	c.1057C>T	c.(1057-1059)CCT>TCT	p.P353S
Pat_01	Post-Resistance	KDM1B	221656	37	6	18207708	18207708	Missense_Mutation	SNP	C	T	5	410	c.1130C>T	c.(1129-1131)TCG>TTG	p.S377L
Pat_01	Post-Resistance	ZNF184	7738	37	6	27419417	27419417	Missense_Mutation	SNP	G	A	46	232	c.1921C>T	c.(1921-1923)CCC>TCC	p.P641S
Pat_01	Post-Resistance	HLA-A	3105	37	6	29912859	29912859	Missense_Mutation	SNP	C	A	6	291	c.1036C>A	c.(1036-1038)CAG>AAG	p.Q346K
Pat_01	Post-Resistance	MDC1	9656	37	6	30672158	30672158	Missense_Mutation	SNP	G	A	299	391	c.4802C>T	c.(4801-4803)ACA>ATA	p.T1601I
Pat_01	Post-Resistance	MICB	4277	37	6	31473433	31473433	Missense_Mutation	SNP	A	G	5	425	c.110A>G	c.(109-111)CAG>CGG	p.Q37R
Pat_01	Post-Resistance	BAT2	7916	37	6	31595857	31595857	Missense_Mutation	SNP	C	T	87	343	c.1606C>T	c.(1606-1608)CCA>TCA	p.P536S
Pat_01	Post-Resistance	BAT3	7917	37	6	31612903	31612903	Missense_Mutation	SNP	G	A	93	343	c.1207C>T	c.(1207-1209)CCT>TCT	p.P403S
Pat_01	Post-Resistance	LY6G6F	259215	37	6	31685384	31685384	Missense_Mutation	SNP	C	T	134	632	c.952C>T	c.(952-954)CCA>TCA	p.P318S
Pat_01	Post-Resistance	C2	717	37	6	31903781	31903781	Missense_Mutation	SNP	G	A	50	187	c.931G>A	c.(931-933)GAC>AAC	p.D311N
Pat_01	Post-Resistance	TNXB	7148	37	6	32029318	32029318	Missense_Mutation	SNP	C	T	51	177	c.7348G>A	c.(7348-7350)GGG>AGG	p.G2450R
Pat_01	Post-Resistance	TNXB	7148	37	6	32038093	32038093	Missense_Mutation	SNP	G	A	19	30	c.5089C>T	c.(5089-5091)CCT>TCT	p.P1697S
Pat_01	Post-Resistance	HLA-DMB	3109	37	6	32903140	32903140	Missense_Mutation	SNP	G	A	213	362	c.754C>T	c.(754-756)CCT>TCT	p.P252S
Pat_01	Post-Resistance	FGD2	221472	37	6	36988331	36988331	Missense_Mutation	SNP	G	A	9	64	c.1137G>A	c.(1135-1137)ATG>ATA	p.M379I
Pat_01	Post-Resistance	TMEM63B	55362	37	6	44104121	44104121	Missense_Mutation	SNP	G	A	5	324	c.314G>A	c.(313-315)CGG>CAG	p.R105Q
Pat_01	Post-Resistance	CAPN11	11131	37	6	44144382	44144382	Missense_Mutation	SNP	G	A	5	325	c.1066G>A	c.(1066-1068)GGG>AGG	p.G356R
Pat_01	Post-Resistance	MEP1A	4224	37	6	46801249	46801249	Missense_Mutation	SNP	C	T	5	455	c.1583C>T	c.(1582-1584)ACT>ATT	p.T528I
Pat_01	Post-Resistance	IL17F	112744	37	6	52103546	52103546	Missense_Mutation	SNP	G	A	46	131	c.236C>T	c.(235-237)ACC>ATC	p.T79I
Pat_01	Post-Resistance	MCM3	4172	37	6	52148092	52148092	Missense_Mutation	SNP	C	T	5	424	c.191G>A	c.(190-192)CGG>CAG	p.R64Q
Pat_01	Post-Resistance	KLHL31	401265	37	6	53519577	53519577	Missense_Mutation	SNP	C	T	4	318	c.494G>A	c.(493-495)CGG>CAG	p.R165Q
Pat_01	Post-Resistance	FAM83B	222584	37	6	54804808	54804808	Missense_Mutation	SNP	G	A	59	137	c.1039G>A	c.(1039-1041)GAA>AAA	p.E347K
Pat_01	Post-Resistance	COL21A1	81578	37	6	55935569	55935569	Missense_Mutation	SNP	C	T	20	91	c.1993G>A	c.(1993-1995)GGG>AGG	p.G665R
Pat_01	Post-Resistance	SMAP1	60682	37	6	71570002	71570002	Missense_Mutation	SNP	T	G	160	342	c.1369T>G	c.(1369-1371)TCA>GCA	p.S457A
Pat_01	Post-Resistance	FILIP1	27145	37	6	76063340	76063340	Missense_Mutation	SNP	C	T	106	307	c.544G>A	c.(544-546)GAG>AAG	p.E182K
Pat_01	Post-Resistance	CASP8AP2	9994	37	6	90577172	90577172	Missense_Mutation	SNP	C	T	48	110	c.4163C>T	c.(4162-4164)CCA>CTA	p.P1388L
Pat_01	Post-Resistance	GJA10	84694	37	6	90604719	90604719	Missense_Mutation	SNP	C	T	115	255	c.532C>T	c.(532-534)CTC>TTC	p.L178F
Pat_01	Post-Resistance	AIM1	202	37	6	107016361	107016361	Missense_Mutation	SNP	G	A	127	262	c.5092G>A	c.(5092-5094)GAT>AAT	p.D1698N
Pat_01	Post-Resistance	FOXO3	2309	37	6	108985003	108985003	Missense_Mutation	SNP	C	T	4	107	c.967C>T	c.(967-969)CGC>TGC	p.R323C
Pat_01	Post-Resistance	LAMA4	3910	37	6	112437179	112437179	Nonsense_Mutation	SNP	C	A	5	255	c.4999G>T	c.(4999-5001)GGA>TGA	p.G1667*
Pat_01	Post-Resistance	RFX6	222546	37	6	117248438	117248438	Missense_Mutation	SNP	C	T	116	179	c.2134C>T	c.(2134-2136)CAC>TAC	p.H712Y
Pat_01	Post-Resistance	ROS1	6098	37	6	117730754	117730754	Missense_Mutation	SNP	C	T	50	129	c.280G>A	c.(280-282)GAA>AAA	p.E94K
Pat_01	Post-Resistance	GJA1	2697	37	6	121768295	121768295	Missense_Mutation	SNP	G	A	4	136	c.302G>A	c.(301-303)CGA>CAA	p.R101Q
Pat_01	Post-Resistance	SYNJ2	8871	37	6	158487565	158487565	Missense_Mutation	SNP	G	A	4	194	c.1615G>A	c.(1615-1617)GTG>ATG	p.V539M
Pat_01	Post-Resistance	KIF25	3834	37	6	168430266	168430266	Missense_Mutation	SNP	A	C	4	278	c.1A>C	c.(1-3)ATG>CTG	p.M1L
Pat_01	Post-Resistance	GPR146	115330	37	7	1097176	1097176	Missense_Mutation	SNP	G	A	4	62	c.25G>A	c.(25-27)GGC>AGC	p.G9S
Pat_01	Post-Resistance	RADIL	55698	37	7	4841376	4841376	Missense_Mutation	SNP	G	A	7	29	c.2750C>T	c.(2749-2751)CCC>CTC	p.P917L
Pat_01	Post-Resistance	WIPI2	26100	37	7	5232787	5232787	Missense_Mutation	SNP	G	A	6	481	c.113G>A	c.(112-114)CGT>CAT	p.R38H
Pat_01	Post-Resistance	PRPS1L1	221823	37	7	18066867	18066867	Missense_Mutation	SNP	G	A	69	188	c.539C>T	c.(538-540)TCC>TTC	p.S180F
Pat_01	Post-Resistance	CREB5	9586	37	7	28547317	28547317	Missense_Mutation	SNP	G	A	116	359	c.253G>A	c.(253-255)GAG>AAG	p.E85K
Pat_01	Post-Resistance	C7orf10	79783	37	7	40900016	40900016	Missense_Mutation	SNP	G	A	76	211	c.1255G>A	c.(1255-1257)GAT>AAT	p.D419N
Pat_01	Post-Resistance	HECW1	23072	37	7	43400569	43400569	Missense_Mutation	SNP	C	T	60	176	c.545C>T	c.(544-546)TCG>TTG	p.S182L
Pat_01	Post-Resistance	TBRG4	9238	37	7	45144223	45144223	Missense_Mutation	SNP	G	A	16	87	c.821C>T	c.(820-822)CCC>CTC	p.P274L
Pat_01	Post-Resistance	TNS3	64759	37	7	47451336	47451337	Missense_Mutation	DNP	CC	TT	22	51	c.711_712GG>AA	709-714)AAGGGA>AAAA	p.G238R
Pat_01	Post-Resistance	EGFR	1956	37	7	55266497	55266497	Missense_Mutation	SNP	G	A	76	198	c.2789G>A	c.(2788-2790)GGA>GAA	p.G930E
Pat_01	Post-Resistance	CLDN4	1364	37	7	73246133	73246133	Missense_Mutation	SNP	G	A	6	426	c.602G>A	c.(601-603)CGC>CAC	p.R201H
Pat_01	Post-Resistance	MAGI2	9863	37	7	77885454	77885454	Missense_Mutation	SNP	G	T	10	94	c.1853C>A	c.(1852-1854)ACT>AAT	p.T618N
Pat_01	Post-Resistance	ABCB4	5244	37	7	87060829	87060829	Missense_Mutation	SNP	C	T	173	449	c.1784G>A	c.(1783-1785)CGA>CAA	p.R595Q

Pat_01	Post-Resistance	SAMD9	54809	37	7	92735311	92735311	Missense_Mutation	SNP	C	T	95	313	c.100G>A	c.(100-102)GAA>AAA	p.E34K
Pat_01	Post-Resistance	TRRAP	8295	37	7	98509757	98509757	Missense_Mutation	SNP	C	T	88	288	c.2120C>T	c.(2119-2121)TCC>TTC	p.S707F
Pat_01	Post-Resistance	OR2AE1	81392	37	7	99473956	99473956	Missense_Mutation	SNP	C	T	32	78	c.701G>A	c.(700-702)AGA>AAA	p.R234K
Pat_01	Post-Resistance	ZAN	7455	37	7	100349941	100349941	Missense_Mutation	SNP	C	T	7	106	c.2213C>T	c.(2212-2214)CCC>CTC	p.P738L
Pat_01	Post-Resistance	ZAN	7455	37	7	100350361	100350361	Missense_Mutation	SNP	T	C	4	82	c.2633T>C	c.(2632-2634)CTC>CCC	p.L878P
Pat_01	Post-Resistance	ZAN	7455	37	7	100371434	100371434	Missense_Mutation	SNP	A	G	6	29	c.5725A>G	c.(5725-5727)AAA>GAA	p.K1909E
Pat_01	Post-Resistance	SLC12A9	56996	37	7	100453367	100453367	Missense_Mutation	SNP	G	A	5	457	c.356G>A	c.(355-357)AGC>AAC	p.S119N
Pat_01	Post-Resistance	MUC17	140453	37	7	100686354	100686354	Missense_Mutation	SNP	C	T	73	274	c.11657C>T	c.(11656-11658)CCA>CTA	p.P3886L
Pat_01	Post-Resistance	MOGAT3	346606	37	7	100839568	100839568	Missense_Mutation	SNP	C	A	10	19	c.771G>T	c.(769-771)AAG>AAT	p.K257N
Pat_01	Post-Resistance	RELN	5649	37	7	103137012	103137012	Missense_Mutation	SNP	C	T	114	328	c.9154G>A	c.(9154-9156)GAA>AAA	p.E3052K
Pat_01	Post-Resistance	PIK3CG	5294	37	7	106519963	106519963	Splice_Site	SNP	G	A	66	247	c.2392_splice	c.e6-1	p.I798_splice
Pat_01	Post-Resistance	SLC26A3	1811	37	7	107418680	107418680	Missense_Mutation	SNP	C	T	43	165	c.1454G>A	c.(1453-1455)GGG>GAG	p.G485E
Pat_01	Post-Resistance	SLC26A3	1811	37	7	107420160	107420160	Missense_Mutation	SNP	G	T	5	417	c.1360C>A	c.(1360-1362)CAG>AAG	p.Q454K
Pat_01	Post-Resistance	PTPRZ1	5803	37	7	121608040	121608040	Missense_Mutation	SNP	C	T	51	198	c.160C>T	c.(160-162)CCA>TCA	p.P54S
Pat_01	Post-Resistance	SLC13A4	26266	37	7	135392875	135392875	Missense_Mutation	SNP	C	T	110	302	c.352G>A	c.(352-354)GCC>ACC	p.A118T
Pat_01	Post-Resistance	KIAA1549	57670	37	7	138522701	138522701	Missense_Mutation	SNP	G	A	35	126	c.5803C>T	c.(5803-5805)CTC>TTC	p.L1935F
Pat_01	Post-Resistance	BRAF	673	37	7	140453136	140453136	Missense_Mutation	SNP	A	T	185	285	c.1799T>A	c.(1798-1800)GTG>GAG	p.V600E
Pat_01	Post-Resistance	C7orf34	135927	37	7	142637618	142637618	Missense_Mutation	SNP	G	A	135	393	c.388G>A	c.(388-390)GGG>AGG	p.G130R
Pat_01	Post-Resistance	OR6V1	346517	37	7	142749903	142749903	Missense_Mutation	SNP	C	T	5	391	c.466C>T	c.(466-468)CCC>TCC	p.P156S
Pat_01	Post-Resistance	CLCN1	1180	37	7	143029958	143029958	Missense_Mutation	SNP	G	A	6	625	c.1393G>A	c.(1393-1395)GTC>ATC	p.V465I
Pat_01	Post-Resistance	CLCN1	1180	37	7	143036696	143036696	Missense_Mutation	SNP	G	T	85	296	c.1564G>T	c.(1564-1566)GGG>TGG	p.G522W
Pat_01	Post-Resistance	KCNH2	3757	37	7	150654507	150654507	Missense_Mutation	SNP	G	A	4	167	c.1000C>T	c.(1000-1002)CCC>TCC	p.P334S
Pat_01	Post-Resistance	ENTPD4	9583	37	8	23305381	23305381	Missense_Mutation	SNP	G	A	6	361	c.224C>T	c.(223-225)ACC>ATC	p.T75I
Pat_01	Post-Resistance	DOCK5	80005	37	8	25253110	25253110	Nonsense_Mutation	SNP	G	T	88	180	c.4579G>T	c.(4579-4581)GAG>TAG	p.E1527*
Pat_01	Post-Resistance	WHSC1L1	54904	37	8	38173456	38173456	Missense_Mutation	SNP	C	T	5	507	c.1960G>A	c.(1960-1962)GAT>AAT	p.D654N
Pat_01	Post-Resistance	ADAM2	2515	37	8	39606935	39606935	Missense_Mutation	SNP	G	T	157	517	c.1910C>A	c.(1909-1911)GCT>GAT	p.A637D
Pat_01	Post-Resistance	RP1	6101	37	8	55538849	55538849	Missense_Mutation	SNP	C	T	21	94	c.2407C>T	c.(2407-2409)CCT>TCT	p.P803S
Pat_01	Post-Resistance	PREX2	80243	37	8	69000012	69000012	Missense_Mutation	SNP	T	C	161	551	c.2081T>C	c.(2080-2082)TTT>TCT	p.F694S
Pat_01	Post-Resistance	ZFHX4	79776	37	8	77763772	77763772	Missense_Mutation	SNP	C	T	37	75	c.4480C>T	c.(4480-4482)CGT>TGT	p.R1494C
Pat_01	Post-Resistance	SLC7A13	157724	37	8	87229869	87229869	Missense_Mutation	SNP	A	G	138	354	c.1009T>C	c.(1009-1011)TTT>CTT	p.F337L
Pat_01	Post-Resistance	RGS22	26166	37	8	101020740	101020740	Missense_Mutation	SNP	C	T	21	91	c.2224G>A	c.(2224-2226)GAA>AAA	p.E742K
Pat_01	Post-Resistance	TMEM74	157753	37	8	109796543	109796543	Missense_Mutation	SNP	C	T	54	126	c.785G>A	c.(784-786)CGA>CAA	p.R262Q
Pat_01	Post-Resistance	FAM135B	51059	37	8	139255192	139255192	Missense_Mutation	SNP	G	A	68	176	c.662C>T	c.(661-663)TCC>TTC	p.S221F
Pat_01	Post-Resistance	SLC45A4	57210	37	8	142228976	142228976	Missense_Mutation	SNP	C	T	4	154	c.610G>A	c.(610-612)GAG>AAG	p.E204K
Pat_01	Post-Resistance	PYCRL	65263	37	8	144689142	144689142	Missense_Mutation	SNP	G	A	45	162	c.353C>T	c.(352-354)TCT>TTT	p.S118F
Pat_01	Post-Resistance	ZNF707	286075	37	8	144776319	144776320	Missense_Mutation	DNP	CC	TT	9	11	c.735_736CC>TT	733-738)GACCGC>GATT	p.R246C
Pat_01	Post-Resistance	SCRIB	23513	37	8	144886826	144886826	Missense_Mutation	SNP	A	T	5	68	c.2921T>A	c.(2920-2922)ATA>AAA	p.I974K
Pat_01	Post-Resistance	NRBP2	340371	37	8	144918164	144918164	Missense_Mutation	SNP	G	A	3	60	c.1354C>T	c.(1354-1356)CGG>TGG	p.R452W
Pat_01	Post-Resistance	IL33	90865	37	9	6251250	6251250	Missense_Mutation	SNP	G	A	166	222	c.328G>A	c.(328-330)GAT>AAT	p.D110N
Pat_01	Post-Resistance	ADAMTSL1	92949	37	9	18657704	18657704	Nonsense_Mutation	SNP	G	A	4	301	c.902G>A	c.(901-903)TGG>TAG	p.W301*
Pat_01	Post-Resistance	TAF1L	138474	37	9	32630610	32630610	Missense_Mutation	SNP	C	T	121	197	c.4968G>A	c.(4966-4968)ATG>ATA	p.M1656I
Pat_01	Post-Resistance	GBA2	57704	37	9	35748472	35748472	Missense_Mutation	SNP	A	G	91	127	c.230T>C	c.(229-231)ATG>ACG	p.M77T
Pat_01	Post-Resistance	PRUNE2	158471	37	9	79326061	79326061	Missense_Mutation	SNP	G	A	20	49	c.1129C>T	c.(1129-1131)CCC>TCC	p.P377S
Pat_01	Post-Resistance	PHF2	5253	37	9	96422487	96422487	Missense_Mutation	SNP	C	T	7	26	c.1343C>T	c.(1342-1344)GCC>GTC	p.A448V
Pat_01	Post-Resistance	HIATL1	84641	37	9	97207294	97207294	Missense_Mutation	SNP	G	A	175	528	c.559G>A	c.(559-561)GCA>ACA	p.A187T
Pat_01	Post-Resistance	BAAT	570	37	9	104124894	104124894	Missense_Mutation	SNP	G	A	36	146	c.1073C>T	c.(1072-1074)CCT>CTT	p.P358L
Pat_01	Post-Resistance	RNF20	56254	37	9	104302911	104302911	Missense_Mutation	SNP	G	A	7	320	c.437G>A	c.(436-438)CGA>CAA	p.R146Q

Pat_01	Post-Resistance	ACTL7B	10880	37	9	111617721	111617721	Missense_Mutation	SNP	C	T	4	125	c.490G>A	c.(490-492)GCG>ACG	p.A164T
Pat_01	Post-Resistance	C9orf152	401546	37	9	112963727	112963727	Missense_Mutation	SNP	G	A	4	158	c.221C>T	c.(220-222)TCG>TTG	p.S74L
Pat_01	Post-Resistance	FKBP15	23307	37	9	115959229	115959229	Missense_Mutation	SNP	C	T	4	211	c.847G>A	c.(847-849)GAG>AAG	p.E283K
Pat_01	Post-Resistance	COL27A1	85301	37	9	117068933	117068934	Missense_Mutation	DNP	GG	AA	37	77	.5072_5073GG>A	c.(5071-5073)AGG>AAA	p.R1691K
Pat_01	Post-Resistance	TLR4	7099	37	9	120475271	120475271	Nonsense_Mutation	SNP	C	T	63	267	c.865C>T	c.(865-867)CGA>TGA	p.R289*
Pat_01	Post-Resistance	OR1J2	26740	37	9	125273462	125273462	Missense_Mutation	SNP	C	T	42	150	c.382C>T	c.(382-384)CAC>TAC	p.H128Y
Pat_01	Post-Resistance	OR1N2	138882	37	9	125316037	125316037	Missense_Mutation	SNP	G	A	125	353	c.589G>A	c.(589-591)GAT>AAT	p.D197N
Pat_01	Post-Resistance	FAM125B	89853	37	9	129184183	129184183	Missense_Mutation	SNP	G	A	5	501	c.713G>A	c.(712-714)CGG>CAG	p.R238Q
Pat_01	Post-Resistance	ABL1	25	37	9	133760646	133760646	Missense_Mutation	SNP	C	T	62	196	c.2969C>T	c.(2968-2970)TCG>TTG	p.S990L
Pat_01	Post-Resistance	LAMC3	10319	37	9	133946908	133946908	Missense_Mutation	SNP	G	A	11	163	c.3107G>A	c.(3106-3108)GGG>GAG	p.G1036E
Pat_01	Post-Resistance	RXRA	6256	37	9	137321028	137321028	Missense_Mutation	SNP	G	A	5	245	c.985G>A	c.(985-987)GGG>AGG	p.G329R
Pat_01	Post-Resistance	SLC34A3	142680	37	9	140126529	140126529	Missense_Mutation	SNP	T	C	4	409	c.91T>C	c.(91-93)TCC>CCC	p.S31P
Pat_01	Post-Resistance	SCML2	10389	37	X	18342090	18342090	Nonsense_Mutation	SNP	G	A	6	188	c.286C>T	c.(286-288)CGA>TGA	p.R96*
Pat_01	Post-Resistance	CNKSR2	22866	37	X	21550159	21550159	Missense_Mutation	SNP	G	A	4	115	c.1277G>A	c.(1276-1278)GGA>GAA	p.G426E
Pat_01	Post-Resistance	GSPT2	23708	37	X	51488398	51488398	Missense_Mutation	SNP	C	T	89	67	c.1676C>T	c.(1675-1677)TCC>TTC	p.S559F
Pat_01	Post-Resistance	FAM123B	139285	37	X	63413019	63413019	Missense_Mutation	SNP	C	T	4	188	c.148G>A	c.(148-150)GGT>AGT	p.G50S
Pat_01	Post-Resistance	TAF1	6872	37	X	70680617	70680617	Missense_Mutation	SNP	G	A	9	10	c.5360G>A	c.(5359-5361)GGG>GAG	p.G1787E
Pat_01	Post-Resistance	FAM46D	169966	37	X	79698739	79698739	Missense_Mutation	SNP	G	A	4	81	c.701G>A	c.(700-702)GGT>GAT	p.G234D
Pat_01	Post-Resistance	TCEAL6	158931	37	X	101395871	101395871	Missense_Mutation	SNP	C	T	54	69	c.433G>A	c.(433-435)GAT>AAT	p.D145N
Pat_01	Post-Resistance	MUM1L1	139221	37	X	105450125	105450125	Missense_Mutation	SNP	G	A	18	25	c.700G>A	c.(700-702)GAA>AAA	p.E234K
Pat_01	Post-Resistance	CAPN6	827	37	X	110491174	110491174	Missense_Mutation	SNP	G	A	252	241	c.1531C>T	c.(1531-1533)CGT>TGT	p.R511C
Pat_01	Post-Resistance	GRIA3	2892	37	X	122459990	122459990	Missense_Mutation	SNP	G	A	166	128	c.622G>A	c.(622-624)GAA>AAA	p.E208K
Pat_01	Post-Resistance	CXorf66	347487	37	X	139038701	139038701	Missense_Mutation	SNP	G	A	288	203	c.440C>T	c.(439-441)TCC>TTC	p.S147F
Pat_01	Post-Resistance	PLXNA3	55558	37	X	153700967	153700967	Missense_Mutation	SNP	G	A	4	259	c.5555G>A	c.(5554-5556)CGG>CAG	p.R1852Q
Pat_02	Post-Resistance	PANK4	55229	37	1	2447075	2447075	Missense_Mutation	SNP	C	T	4	104	c.1300G>A	c.(1300-1302)GAC>AAC	p.D434N
Pat_02	Post-Resistance	H6PD	9563	37	1	9323666	9323666	Missense_Mutation	SNP	T	G	46	68	c.1114T>G	c.(1114-1116)TTG>GTG	p.L372V
Pat_02	Post-Resistance	UBE4B	10277	37	1	10166338	10166338	Missense_Mutation	SNP	G	A	7	153	c.893G>A	c.(892-894)CGT>CAT	p.R298H
Pat_02	Post-Resistance	MIIP	60672	37	1	12091778	12091778	Splice_Site	SNP	G	A	4	207	c.1081_splice	c.e10-1	p.A361_splice
Pat_02	Post-Resistance	IGSF21	84966	37	1	18691963	18691963	Missense_Mutation	SNP	G	A	163	50	c.787G>A	c.(787-789)GAG>AAG	p.E263K
Pat_02	Post-Resistance	ARID1A	8289	37	1	27101115	27101115	Missense_Mutation	SNP	C	T	5	125	c.4397C>T	c.(4396-4398)GCA>GTA	p.A1466V
Pat_02	Post-Resistance	SDC3	9672	37	1	31349506	31349506	Missense_Mutation	SNP	G	A	3	44	c.763C>T	c.(763-765)CGG>TGG	p.R255W
Pat_02	Post-Resistance	GJB5	2709	37	1	35222956	35222956	Missense_Mutation	SNP	C	T	4	79	c.25C>T	c.(25-27)CTC>TTC	p.L9F
Pat_02	Post-Resistance	TFAP2E	339488	37	1	36054150	36054150	Missense_Mutation	SNP	G	A	6	71	c.782G>A	c.(781-783)CGC>CAC	p.R261H
Pat_02	Post-Resistance	SLC6A9	6536	37	1	44463225	44463225	Missense_Mutation	SNP	G	A	4	144	c.2113C>T	c.(2113-2115)CGG>TGG	p.R705W
Pat_02	Post-Resistance	DHCR24	1718	37	1	55319179	55319179	Missense_Mutation	SNP	T	C	3	57	c.1325A>G	c.(1324-1326)GAG>GGG	p.E442G
Pat_02	Post-Resistance	JUN	3725	37	1	59248082	59248082	Missense_Mutation	SNP	G	A	4	101	c.661C>T	c.(661-663)CGG>TGG	p.R221W
Pat_02	Post-Resistance	LPAR3	23566	37	1	85331140	85331140	Missense_Mutation	SNP	G	T	24	42	c.664C>A	c.(664-666)CCG>ACG	p.P222T
Pat_02	Post-Resistance	GBP3	2635	37	1	89477642	89477642	Missense_Mutation	SNP	C	T	4	103	c.937G>A	c.(937-939)GCA>ACA	p.A313T
Pat_02	Post-Resistance	LRRC8D	55144	37	1	90398877	90398877	Missense_Mutation	SNP	G	A	4	61	c.250G>A	c.(250-252)GCA>ACA	p.A84T
Pat_02	Post-Resistance	ALX3	257	37	1	110607256	110607257	Missense_Mutation	DNP	GG	AA	49	29	c.546_547CC>TT	544-549)GCCCGG>GCTT	p.R183W
Pat_02	Post-Resistance	NBPF16	728936	37	1	148753314	148753314	Missense_Mutation	SNP	A	G	10	69	c.1331A>G	c.(1330-1332)TAT>TGT	p.Y444C
Pat_02	Post-Resistance	SCNM1	79005	37	1	151141482	151141482	Missense_Mutation	SNP	G	A	113	30	c.614G>A	c.(613-615)GGA>GAA	p.G205E
Pat_02	Post-Resistance	RPTN	126638	37	1	152128617	152128617	Missense_Mutation	SNP	T	C	9	876	c.958A>G	c.(958-960)AGT>GGT	p.S320G
Pat_02	Post-Resistance	FLG	2312	37	1	152280647	152280647	Missense_Mutation	SNP	G	A	215	64	c.6715C>T	c.(6715-6717)CGG>TGG	p.R2239W
Pat_02	Post-Resistance	FLG	2312	37	1	152282909	152282909	Missense_Mutation	SNP	C	T	7	584	c.4453G>A	c.(4453-4455)GGT>AGT	p.G1485S
Pat_02	Post-Resistance	ADAR	103	37	1	154569345	154569345	Missense_Mutation	SNP	G	A	4	138	c.2206C>T	c.(2206-2208)CGC>TGC	p.R736C
Pat_02	Post-Resistance	ADAR	103	37	1	154574475	154574475	Missense_Mutation	SNP	C	T	5	119	c.643G>A	c.(643-645)GGT>AGT	p.G215S

Pat_02	Post-Resistance	HCN3	57657	37	1	155254346	155254346	Missense_Mutation	SNP	G	A	4	86	c.887G>A	c.(886-888)CGC>CAC	p.R296H
Pat_02	Post-Resistance	MEX3A	92312	37	1	156047240	156047240	Missense_Mutation	SNP	C	T	4	33	c.688G>A	c.(688-690)GTG>ATG	p.V230M
Pat_02	Post-Resistance	IQGAP3	128239	37	1	156535853	156535853	Missense_Mutation	SNP	C	A	6	262	c.326G>T	c.(325-327)TGG>TTG	p.W109L
Pat_02	Post-Resistance	FCRL5	83416	37	1	157516746	157516746	Missense_Mutation	SNP	C	A	4	134	c.294G>T	c.(292-294)TTG>TTT	p.L98F
Pat_02	Post-Resistance	FCGR2C	9103	37	1	161565349	161565349	Missense_Mutation	SNP	C	G	4	300	c.767C>G	c.(766-768)TCC>TGC	p.S256C
Pat_02	Post-Resistance	F5	2153	37	1	169510354	169510354	Missense_Mutation	SNP	A	G	8	760	c.3974T>C	c.(3973-3975)CTC>CCC	p.L1325P
Pat_02	Post-Resistance	C1orf105	92346	37	1	172434464	172434464	Nonsense_Mutation	SNP	C	T	64	32	c.367C>T	c.(367-369)CAG>TAG	p.Q123*
Pat_02	Post-Resistance	TNR	7143	37	1	175372465	175372465	Missense_Mutation	SNP	C	T	70	11	c.787G>A	c.(787-789)GAA>AAA	p.E263K
Pat_02	Post-Resistance	PAPPA2	60676	37	1	176564299	176564299	Missense_Mutation	SNP	G	T	21	37	c.1559G>T	c.(1558-1560)CGG>CTG	p.R520L
Pat_02	Post-Resistance	LAMC1	3915	37	1	183072636	183072636	Missense_Mutation	SNP	G	A	7	81	c.592G>A	c.(592-594)GGG>AGG	p.G198R
Pat_02	Post-Resistance	DSTYK	25778	37	1	205138570	205138570	Nonsense_Mutation	SNP	G	A	6	185	c.1045C>T	c.(1045-1047)CAG>TAG	p.Q349*
Pat_02	Post-Resistance	SMYD2	56950	37	1	214498026	214498026	Missense_Mutation	SNP	C	T	72	43	c.577C>T	c.(577-579)CAT>TAT	p.H193Y
Pat_02	Post-Resistance	ZNF669	79862	37	1	247263846	247263846	Missense_Mutation	SNP	C	T	4	207	c.1225G>A	c.(1225-1227)GAA>AAA	p.E409K
Pat_02	Post-Resistance	DIP2C	22982	37	10	410435	410435	Missense_Mutation	SNP	G	A	4	187	c.2356C>T	c.(2356-2358)CTC>TTC	p.L786F
Pat_02	Post-Resistance	ADARB2	105	37	10	1279761	1279761	Missense_Mutation	SNP	G	A	77	44	c.1388C>T	c.(1387-1389)TCG>TTG	p.S463L
Pat_02	Post-Resistance	SFMBT2	57713	37	10	7262417	7262417	Missense_Mutation	SNP	G	A	234	223	c.1286C>T	c.(1285-1287)TCC>TTC	p.S429F
Pat_02	Post-Resistance	C10orf140	387640	37	10	21804291	21804291	Missense_Mutation	SNP	C	A	44	156	c.2461G>T	c.(2461-2463)GAT>TAT	p.D821Y
Pat_02	Post-Resistance	EPC1	80314	37	10	32560521	32560521	Missense_Mutation	SNP	G	A	98	261	c.2399C>T	c.(2398-2400)TCC>TTC	p.S800F
Pat_02	Post-Resistance	ANKRD30A	91074	37	10	37508119	37508119	Missense_Mutation	SNP	G	A	163	220	c.3311G>A	c.(3310-3312)AGG>AAG	p.R1104K
Pat_02	Post-Resistance	HNRNPF	3185	37	10	43882221	43882221	Missense_Mutation	SNP	G	A	4	178	c.1112C>T	c.(1111-1113)GCG>GTG	p.A371V
Pat_02	Post-Resistance	ANK3	288	37	10	61829763	61829763	Missense_Mutation	SNP	C	T	27	82	c.10876G>A	c.(10876-10878)GAA>AAA	p.E3626K
Pat_02	Post-Resistance	LDB3	11155	37	10	88476299	88476299	Missense_Mutation	SNP	G	A	231	158	c.1447G>A	c.(1447-1449)GAG>AAG	p.E483K
Pat_02	Post-Resistance	MMRN2	79812	37	10	88702692	88702692	Missense_Mutation	SNP	C	T	25	18	c.1849G>A	c.(1849-1851)GAG>AAG	p.E617K
Pat_02	Post-Resistance	LIPJ	142910	37	10	90362398	90362398	Nonsense_Mutation	SNP	G	A	33	73	c.789G>A	c.(787-789)TGG>TGA	p.W263*
Pat_02	Post-Resistance	PIPSL	266971	37	10	95719963	95719963	Missense_Mutation	SNP	A	T	47	96	c.1191T>A	c.(1189-1191)TTT>TTA	p.F397L
Pat_02	Post-Resistance	DNTT	1791	37	10	98080472	98080472	Missense_Mutation	SNP	C	A	6	219	c.605C>A	c.(604-606)CCA>CAA	p.P202Q
Pat_02	Post-Resistance	CYP17A1	1586	37	10	104592293	104592293	Missense_Mutation	SNP	G	A	4	156	c.1114C>T	c.(1114-1116)CCC>TCC	p.P372S
Pat_02	Post-Resistance	SORCS3	22986	37	10	106924131	106924131	Nonsense_Mutation	SNP	G	A	28	57	c.1803G>A	c.(1801-1803)TGG>TGA	p.W601*
Pat_02	Post-Resistance	GRK5	2869	37	10	121203251	121203251	Missense_Mutation	SNP	C	T	10	16	c.1253C>T	c.(1252-1254)TCC>TTC	p.S418F
Pat_02	Post-Resistance	WDR11	55717	37	10	122626197	122626197	Missense_Mutation	SNP	G	A	5	228	c.1111G>A	c.(1111-1113)GCC>ACC	p.A371T
Pat_02	Post-Resistance	TACC2	10579	37	10	123844357	123844357	Missense_Mutation	SNP	C	T	33	70	c.2342C>T	c.(2341-2343)CCC>CTC	p.P781L
Pat_02	Post-Resistance	DMBT1	1755	37	10	124361487	124361487	Missense_Mutation	SNP	G	A	135	46	c.3518G>A	c.(3517-3519)GGA>GAA	p.G1173E
Pat_02	Post-Resistance	KRTAP5-3	387266	37	11	1629039	1629039	Missense_Mutation	SNP	A	T	6	304	c.577T>A	c.(577-579)TGC>AGC	p.C193S
Pat_02	Post-Resistance	OR51D1	390038	37	11	4661948	4661948	Missense_Mutation	SNP	G	A	37	62	c.928G>A	c.(928-930)GAG>AAG	p.E310K
Pat_02	Post-Resistance	OR52H1	390067	37	11	5565961	5565961	Missense_Mutation	SNP	A	T	58	113	c.793T>A	c.(793-795)TTC>ATC	p.F265I
Pat_02	Post-Resistance	APBB1	322	37	11	6425007	6425007	Missense_Mutation	SNP	G	A	4	131	c.767C>T	c.(766-768)CCG>CTG	p.P256L
Pat_02	Post-Resistance	PPFIBP2	8495	37	11	7672156	7672156	Missense_Mutation	SNP	C	T	4	152	c.2207C>T	c.(2206-2208)GCA>GTA	p.A736V
Pat_02	Post-Resistance	ST5	6764	37	11	8720827	8720827	Missense_Mutation	SNP	G	A	4	185	c.2831C>T	c.(2830-2832)CCC>CTC	p.P944L
Pat_02	Post-Resistance	DENND5A	23258	37	11	9165725	9165725	Missense_Mutation	SNP	T	C	4	145	c.3223A>G	c.(3223-3225)AGG>GGG	p.R1075G
Pat_02	Post-Resistance	CTR9	9646	37	11	10795560	10795560	Missense_Mutation	SNP	G	A	4	129	c.2729G>A	c.(2728-2730)CGT>CAT	p.R910H
Pat_02	Post-Resistance	ABCC8	6833	37	11	17452420	17452420	Missense_Mutation	SNP	C	A	7	258	c.1758G>T	c.(1756-1758)TTG>TTT	p.L586F
Pat_02	Post-Resistance	DEPDC7	91614	37	11	33052941	33052941	Missense_Mutation	SNP	C	T	4	92	c.800C>T	c.(799-801)TCG>TTG	p.S267L
Pat_02	Post-Resistance	CAT	847	37	11	34478338	34478338	Missense_Mutation	SNP	G	A	47	53	c.1030G>A	c.(1030-1032)GAG>AAG	p.E344K
Pat_02	Post-Resistance	DGKZ	8525	37	11	46388933	46388933	Missense_Mutation	SNP	G	A	4	73	c.821G>A	c.(820-822)AGT>AAT	p.S274N
Pat_02	Post-Resistance	MTCH2	23788	37	11	47644265	47644265	Missense_Mutation	SNP	C	A	4	72	c.813G>T	c.(811-813)ATG>ATT	p.M271I
Pat_02	Post-Resistance	OR8H2	390151	37	11	55872537	55872537	Missense_Mutation	SNP	A	G	5	363	c.19A>G	c.(19-21)AAC>GAC	p.N7D
Pat_02	Post-Resistance	SSRP1	6749	37	11	57094314	57094314	Missense_Mutation	SNP	A	T	7	27	c.1921T>A	c.(1921-1923)TCC>ACC	p.S641T

Pat_02	Post-Resistance	FADS1	3992	37	11	61579965	61579965	Missense_Mutation	SNP	G	A	4	127	c.662C>T	c.(661-663)GCG>GTG	p.A221V
Pat_02	Post-Resistance	PYGM	5837	37	11	64522942	64522942	Missense_Mutation	SNP	G	A	4	137	c.749C>T	c.(748-750)CCC>CTC	p.P250L
Pat_02	Post-Resistance	CDC42BPG	55561	37	11	64601265	64601265	Missense_Mutation	SNP	C	T	47	37	c.2510G>A	c.(2509-2511)AGG>AAG	p.R837K
Pat_02	Post-Resistance	ATG2A	23130	37	11	64684568	64684568	Nonsense_Mutation	SNP	C	A	6	242	c.40G>T	c.(40-42)GAG>TAG	p.E14*
Pat_02	Post-Resistance	EHBP1L1	254102	37	11	65349588	65349588	Missense_Mutation	SNP	C	T	9	31	c.1445C>T	c.(1444-1446)CCA>CTA	p.P482L
Pat_02	Post-Resistance	BBS1	582	37	11	66293622	66293622	Missense_Mutation	SNP	G	A	4	165	c.1139G>A	c.(1138-1140)CGG>CAG	p.R380Q
Pat_02	Post-Resistance	SSH3	54961	37	11	67075057	67075057	Missense_Mutation	SNP	G	A	4	168	c.640G>A	c.(640-642)GCT>ACT	p.A214T
Pat_02	Post-Resistance	PITPNM1	9600	37	11	67265710	67265710	Missense_Mutation	SNP	G	A	4	88	c.1568C>T	c.(1567-1569)ACC>ATC	p.T523I
Pat_02	Post-Resistance	KRTAP5-10	387273	37	11	71276959	71276959	Missense_Mutation	SNP	G	A	5	202	c.326G>A	c.(325-327)GGC>GAC	p.G109D
Pat_02	Post-Resistance	OR2AT4	341152	37	11	74799858	74799858	Missense_Mutation	SNP	C	T	103	121	c.901G>A	c.(901-903)GAT>AAT	p.D301N
Pat_02	Post-Resistance	TSKU	25987	37	11	76507090	76507090	Missense_Mutation	SNP	C	T	4	168	c.430C>T	c.(430-432)CGG>TGG	p.R144W
Pat_02	Post-Resistance	SYTL2	54843	37	11	85445603	85445603	Missense_Mutation	SNP	G	A	53	138	c.766C>T	c.(766-768)CCT>TCT	p.P256S
Pat_02	Post-Resistance	FAT3	120114	37	11	92085960	92085960	Missense_Mutation	SNP	G	C	35	253	c.682G>C	c.(682-684)GAT>CAT	p.D228H
Pat_02	Post-Resistance	CASP5	838	37	11	104871092	104871092	Missense_Mutation	SNP	G	A	6	285	c.848C>T	c.(847-849)CCG>CTG	p.P283L
Pat_02	Post-Resistance	GLB1L2	89944	37	11	134244085	134244085	Missense_Mutation	SNP	C	T	4	109	c.1642C>T	c.(1642-1644)CCT>TCT	p.P548S
Pat_02	Post-Resistance	ANO2	57101	37	12	5915230	5915230	Missense_Mutation	SNP	C	T	31	34	c.966G>A	c.(964-966)ATG>ATA	p.M322I
Pat_02	Post-Resistance	COPS7A	50813	37	12	6838528	6838528	Missense_Mutation	SNP	G	A	4	166	c.443G>A	c.(442-444)CGC>CAC	p.R148H
Pat_02	Post-Resistance	ACSM4	341392	37	12	7457031	7457031	Missense_Mutation	SNP	T	C	90	107	c.104T>C	c.(103-105)CTT>CCT	p.L35P
Pat_02	Post-Resistance	PRB2	653247	37	12	11546771	11546771	Missense_Mutation	SNP	G	C	6	322	c.241C>G	c.(241-243)CCA>GCA	p.P81A
Pat_02	Post-Resistance	CAPZA3	93661	37	12	18891609	18891609	Missense_Mutation	SNP	G	A	37	69	c.407G>A	c.(406-408)GGA>GAA	p.G136E
Pat_02	Post-Resistance	COL2A1	1280	37	12	48376705	48376705	Missense_Mutation	SNP	G	A	4	142	c.2119C>T	c.(2119-2121)CGT>TGT	p.R707C
Pat_02	Post-Resistance	CCNT1	904	37	12	49087949	49087949	Missense_Mutation	SNP	G	A	36	71	c.1048C>T	c.(1048-1050)CGG>TGG	p.R350W
Pat_02	Post-Resistance	TROAP	10024	37	12	49724304	49724304	Missense_Mutation	SNP	G	A	4	89	c.1676G>A	c.(1675-1677)TGC>TAC	p.C559Y
Pat_02	Post-Resistance	BIN2	51411	37	12	51685575	51685575	Missense_Mutation	SNP	C	T	17	50	c.1315G>A	c.(1315-1317)GCC>ACC	p.A439T
Pat_02	Post-Resistance	ESPL1	9700	37	12	53684700	53684700	Missense_Mutation	SNP	G	A	3	10	c.5440G>A	c.(5440-5442)GGC>AGC	p.G1814S
Pat_02	Post-Resistance	SMARCC2	6601	37	12	56583164	56583164	Missense_Mutation	SNP	G	A	4	139	c.82C>T	c.(82-84)CGG>TGG	p.R28W
Pat_02	Post-Resistance	SLC39A5	283375	37	12	56631072	56631072	Nonsense_Mutation	SNP	G	A	4	75	c.1427G>A	c.(1426-1428)TGG>TAG	p.W476*
Pat_02	Post-Resistance	B4GALNT1	2583	37	12	58021527	58021527	Missense_Mutation	SNP	G	A	11	20	c.1258C>T	c.(1258-1260)CAC>TAC	p.H420Y
Pat_02	Post-Resistance	OS9	10956	37	12	58109684	58109684	Missense_Mutation	SNP	C	T	6	360	c.721C>T	c.(721-723)CCG>TCG	p.P241S
Pat_02	Post-Resistance	APAF1	317	37	12	99061402	99061402	Missense_Mutation	SNP	G	A	4	145	c.1474G>A	c.(1474-1476)GCC>ACC	p.A492T
Pat_02	Post-Resistance	GAS2L3	283431	37	12	101012343	101012343	Missense_Mutation	SNP	G	A	4	132	c.626G>A	c.(625-627)CGG>CAG	p.R209Q
Pat_02	Post-Resistance	CRY1	1407	37	12	107391819	107391819	Missense_Mutation	SNP	G	C	4	188	c.1163C>G	c.(1162-1164)GCA>GGA	p.A388G
Pat_02	Post-Resistance	TCHP	84260	37	12	110346484	110346484	Missense_Mutation	SNP	C	T	4	12	c.793C>T	c.(793-795)CGG>TGG	p.R265W
Pat_02	Post-Resistance	ACAD10	80724	37	12	112194136	112194136	Splice_Site	SNP	G	A	13	18	c.3040_splice	c.e21-1	p.A1014_splice
Pat_02	Post-Resistance	KSR2	283455	37	12	117977577	117977577	Missense_Mutation	SNP	G	T	4	105	c.1547C>A	c.(1546-1548)CCC>CAC	p.P516H
Pat_02	Post-Resistance	NOC4L	79050	37	12	132631868	132631868	Missense_Mutation	SNP	G	A	4	14	c.388G>A	c.(388-390)GGA>AGA	p.G130R
Pat_02	Post-Resistance	POLE	5426	37	12	133237686	133237686	Missense_Mutation	SNP	C	A	5	288	c.2929G>T	c.(2929-2931)GGG>TGG	p.G977W
Pat_02	Post-Resistance	GJA3	2700	37	13	20716802	20716802	Missense_Mutation	SNP	G	A	4	80	c.626C>T	c.(625-627)GCG>GTG	p.A209V
Pat_02	Post-Resistance	FLT1	2321	37	13	28913433	28913433	Missense_Mutation	SNP	G	A	22	26	c.2360C>T	c.(2359-2361)TCT>TTT	p.S787F
Pat_02	Post-Resistance	NBEA	26960	37	13	35756497	35756497	Missense_Mutation	SNP	G	A	47	70	c.4663G>A	c.(4663-4665)GAT>AAT	p.D1555N
Pat_02	Post-Resistance	COG3	83548	37	13	46039319	46039319	Missense_Mutation	SNP	G	A	4	147	c.148G>A	c.(148-150)GCA>ACA	p.A50T
Pat_02	Post-Resistance	LOC220429	220429	37	13	50466381	50466381	Missense_Mutation	SNP	G	A	47	46	c.1655G>A	c.(1654-1656)GGG>GAG	p.G552E
Pat_02	Post-Resistance	C13orf1	57213	37	13	50495655	50495655	Missense_Mutation	SNP	G	A	4	215	c.452C>T	c.(451-453)CCA>CTA	p.P151L
Pat_02	Post-Resistance	TDRD3	81550	37	13	61102941	61102941	Missense_Mutation	SNP	T	C	29	36	c.1303T>C	c.(1303-1305)TAT>CAT	p.Y435H
Pat_02	Post-Resistance	DACH1	1602	37	13	72131228	72131228	Missense_Mutation	SNP	G	A	50	176	c.1498C>T	c.(1498-1500)CCT>TCT	p.P500S
Pat_02	Post-Resistance	C13orf39	196541	37	13	103346827	103346827	Missense_Mutation	SNP	C	T	8	22	c.22G>A	c.(22-24)GCG>ACG	p.A8T
Pat_02	Post-Resistance	METTL3	56339	37	14	21966454	21966454	Missense_Mutation	SNP	C	T	4	132	c.1691G>A	c.(1690-1692)CGG>CAG	p.R564Q

Pat_02	Post-Resistance	THTPA	79178	37	14	24026349	24026349	Nonsense_Mutation	SNP	G	A	4	86	c.383G>A	c.(382-384)TGG>TAG	p.W128*
Pat_02	Post-Resistance	PYGL	5836	37	14	51382590	51382591	Missense_Mutation	DNP	GG	AA	32	54	.1191_1192CC>T	189-1194)CTCCCT>CTTT	p.P398S
Pat_02	Post-Resistance	KCNH5	27133	37	14	63417027	63417027	Missense_Mutation	SNP	G	A	4	164	c.1193C>T	c.(1192-1194)ACT>ATT	p.T398I
Pat_02	Post-Resistance	FNTB	2342	37	14	65390803	65390803	Missense_Mutation	SNP	C	T	43	81	c.134C>T	c.(133-135)TCC>TTC	p.S45F
Pat_02	Post-Resistance	PLEKHH1	57475	37	14	68043130	68043130	Missense_Mutation	SNP	C	T	4	97	c.2371C>T	c.(2371-2373)CTC>TTC	p.L791F
Pat_02	Post-Resistance	PCNX	22990	37	14	71575507	71575507	Missense_Mutation	SNP	C	T	33	58	c.6488C>T	c.(6487-6489)TCA>TTA	p.S2163L
Pat_02	Post-Resistance	SIPA1L1	26037	37	14	72176188	72176188	Missense_Mutation	SNP	G	A	4	87	c.4078G>A	c.(4078-4080)GCA>ACA	p.A1360T
Pat_02	Post-Resistance	ACOT6	641372	37	14	74086109	74086109	Missense_Mutation	SNP	G	A	36	50	c.190G>A	c.(190-192)GAT>AAT	p.D64N
Pat_02	Post-Resistance	AHSA1	10598	37	14	77926131	77926131	Missense_Mutation	SNP	G	A	4	212	c.253G>A	c.(253-255)GTC>ATC	p.V85I
Pat_02	Post-Resistance	C14orf145	145508	37	14	81251316	81251316	Missense_Mutation	SNP	C	T	6	145	c.2134G>A	c.(2134-2136)GAA>AAA	p.E712K
Pat_02	Post-Resistance	BTBD7	55727	37	14	93730273	93730273	Missense_Mutation	SNP	G	A	51	92	c.1229C>T	c.(1228-1230)TCT>TTT	p.S410F
Pat_02	Post-Resistance	KIAA1409	57578	37	14	94071278	94071278	Missense_Mutation	SNP	C	T	9	21	c.3260C>T	c.(3259-3261)GCT>GTT	p.A1087V
Pat_02	Post-Resistance	PACS2	23241	37	14	105859672	105859672	Missense_Mutation	SNP	G	A	19	29	c.2551G>A	c.(2551-2553)GTC>ATC	p.V851I
Pat_02	Post-Resistance	OCA2	4948	37	15	28202788	28202788	Missense_Mutation	SNP	C	A	28	25	c.1730G>T	c.(1729-1731)GGG>GTG	p.G577V
Pat_02	Post-Resistance	PLCB2	5330	37	15	40582260	40582260	Missense_Mutation	SNP	G	A	58	44	c.3233C>T	c.(3232-3234)TCC>TTC	p.S1078F
Pat_02	Post-Resistance	MAP1A	4130	37	15	43813975	43813975	Missense_Mutation	SNP	C	G	4	89	c.304C>G	c.(304-306)CTG>GTG	p.L102V
Pat_02	Post-Resistance	HERC1	8925	37	15	63916019	63916019	Missense_Mutation	SNP	G	A	6	284	c.13516C>T	.(13516-13518)CGC>TGC	p.R4506C
Pat_02	Post-Resistance	HCN4	10021	37	15	73615699	73615699	Missense_Mutation	SNP	T	A	4	4	c.2735A>T	c.(2734-2736)AAG>ATG	p.K912M
Pat_02	Post-Resistance	BCL2A1	597	37	15	80263245	80263245	Missense_Mutation	SNP	G	T	371	251	c.217C>A	c.(217-219)CAA>AAA	p.Q73K
Pat_02	Post-Resistance	MEX3B	84206	37	15	82336750	82336750	Missense_Mutation	SNP	G	A	4	123	c.461C>T	c.(460-462)CCG>CTG	p.P154L
Pat_02	Post-Resistance	AGBL1	123624	37	15	86791075	86791075	Missense_Mutation	SNP	G	A	5	270	c.562G>A	c.(562-564)GCA>ACA	p.A188T
Pat_02	Post-Resistance	FANCI	55215	37	15	89804943	89804943	Missense_Mutation	SNP	C	T	7	385	c.416C>T	c.(415-417)ACG>ATG	p.T139M
Pat_02	Post-Resistance	MESP2	145873	37	15	90321375	90321375	Missense_Mutation	SNP	A	T	52	41	c.1004A>T	c.(1003-1005)CAG>CTG	p.Q335L
Pat_02	Post-Resistance	HS3ST6	64711	37	16	1961974	1961974	Missense_Mutation	SNP	C	T	4	38	c.553G>A	c.(553-555)GTG>ATG	p.V185M
Pat_02	Post-Resistance	CASKIN1	57524	37	16	2236767	2236767	Missense_Mutation	SNP	C	T	4	129	c.989G>A	c.(988-990)GGC>GAC	p.G330D
Pat_02	Post-Resistance	PRSS22	64063	37	16	2905646	2905646	Missense_Mutation	SNP	G	A	64	165	c.488C>T	c.(487-489)CCT>CTT	p.P163L
Pat_02	Post-Resistance	PKMYT1	9088	37	16	3024313	3024313	Missense_Mutation	SNP	G	A	3	25	c.1085C>T	c.(1084-1086)CCG>CTG	p.P362L
Pat_02	Post-Resistance	IL32	9235	37	16	3117607	3117607	Missense_Mutation	SNP	G	T	59	178	c.245G>T	c.(244-246)CGT>CTT	p.R82L
Pat_02	Post-Resistance	C16orf71	146562	37	16	4790598	4790598	Missense_Mutation	SNP	G	A	4	104	c.721G>A	c.(721-723)GCT>ACT	p.A241T
Pat_02	Post-Resistance	CIITA	4261	37	16	11000747	11000747	Missense_Mutation	SNP	G	T	5	171	c.1398G>T	c.(1396-1398)CAG>CAT	p.Q466H
Pat_02	Post-Resistance	TXNDC11	51061	37	16	11778031	11778031	Missense_Mutation	SNP	G	A	41	55	c.2305C>T	c.(2305-2307)CCC>TCC	p.P769S
Pat_02	Post-Resistance	GSPT1	2935	37	16	11971296	11971296	Missense_Mutation	SNP	G	C	17	37	c.1156C>G	c.(1156-1158)CTT>GTT	p.L386V
Pat_02	Post-Resistance	ABCC1	4363	37	16	16138351	16138351	Missense_Mutation	SNP	C	T	17	57	c.854C>T	c.(853-855)CCG>CTG	p.P285L
Pat_02	Post-Resistance	SYT17	51760	37	16	19236121	19236121	Missense_Mutation	SNP	C	T	77	89	c.1189C>T	c.(1189-1191)CCC>TCC	p.P397S
Pat_02	Post-Resistance	GPR139	124274	37	16	20043605	20043605	Missense_Mutation	SNP	C	T	79	71	c.514G>A	c.(514-516)GAA>AAA	p.E172K
Pat_02	Post-Resistance	ARHGAP17	55114	37	16	24942614	24942614	Missense_Mutation	SNP	T	C	4	301	c.2006A>G	c.(2005-2007)AAG>AGG	p.K669R
Pat_02	Post-Resistance	IL21R	50615	37	16	27457411	27457411	Splice_Site	SNP	T	A	3	33	c.867_splice	c.e8+2	p.K289_splice
Pat_02	Post-Resistance	GTF3C1	2975	37	16	27506194	27506194	Missense_Mutation	SNP	G	A	5	129	c.2668C>T	c.(2668-2670)CCC>TCC	p.P890S
Pat_02	Post-Resistance	SULT1A2	6799	37	16	28606997	28606997	Splice_Site	SNP	C	T	4	192	c.149_splice	c.e3-1	p.G50_splice
Pat_02	Post-Resistance	TBC1D10B	26000	37	16	30370102	30370102	Missense_Mutation	SNP	A	G	3	60	c.1679T>C	c.(1678-1680)CTG>CCG	p.L560P
Pat_02	Post-Resistance	PRSS36	146547	37	16	31152904	31152904	Missense_Mutation	SNP	G	A	37	101	c.1787C>T	c.(1786-1788)CCA>CTA	p.P596L
Pat_02	Post-Resistance	N4BP1	9683	37	16	48580158	48580158	Missense_Mutation	SNP	G	C	39	149	c.2233C>G	c.(2233-2235)CAG>GAG	p.Q745E
Pat_02	Post-Resistance	BRD7	29117	37	16	50373952	50373952	Missense_Mutation	SNP	G	A	48	191	c.637C>T	c.(637-639)CCA>TCA	p.P213S
Pat_02	Post-Resistance	TOX3	27324	37	16	52473606	52473606	Missense_Mutation	SNP	G	A	4	161	c.1262C>T	c.(1261-1263)ACG>ATG	p.T421M
Pat_02	Post-Resistance	CDH8	1006	37	16	62055094	62055094	Missense_Mutation	SNP	C	T	28	81	c.214G>A	c.(214-216)GAA>AAA	p.E72K
Pat_02	Post-Resistance	B3GNT9	84752	37	16	67183209	67183209	Missense_Mutation	SNP	C	T	3	30	c.1180G>A	c.(1180-1182)GCT>ACT	p.A394T
Pat_02	Post-Resistance	ADAMTS18	170692	37	16	77329007	77329007	Missense_Mutation	SNP	C	A	41	102	c.2819G>T	c.(2818-2820)TGG>TTG	p.W940L

Pat_02	Post-Resistance	LRRC50	123872	37	16	84203797	84203797	Missense_Mutation	SNP	G	A	4	163	c.1363G>A	c.(1363-1365)GTT>ATT	p.V455I
Pat_02	Post-Resistance	TRPV3	162514	37	17	3419802	3419802	Missense_Mutation	SNP	C	T	4	193	c.2147G>A	c.(2146-2148)CGG>CAG	p.R716Q
Pat_02	Post-Resistance	TRPV3	162514	37	17	3436091	3436092	Missense_Mutation	DNP	CC	TT	19	66	c.924_925GG>AA	922-927)GAGGAC>GAAA	p.D309N
Pat_02	Post-Resistance	GSG2	83903	37	17	3629315	3629315	Missense_Mutation	SNP	G	A	86	138	c.2086G>A	c.(2086-2088)GAT>AAT	p.D696N
Pat_02	Post-Resistance	ZNF594	84622	37	17	5086549	5086549	Missense_Mutation	SNP	G	A	6	200	c.1003C>T	c.(1003-1005)CGC>TGC	p.R335C
Pat_02	Post-Resistance	FBXO39	162517	37	17	6683191	6683191	Missense_Mutation	SNP	G	A	37	52	c.4G>A	c.(4-6)GAC>AAC	p.D2N
Pat_02	Post-Resistance	HES7	84667	37	17	8025134	8025134	Missense_Mutation	SNP	G	A	15	23	c.433C>T	c.(433-435)CCA>TCA	p.P145S
Pat_02	Post-Resistance	C17orf63	55731	37	17	27086148	27086148	Missense_Mutation	SNP	G	T	4	54	c.829C>A	c.(829-831)CAG>AAG	p.Q277K
Pat_02	Post-Resistance	RHOT1	55288	37	17	30528069	30528069	Missense_Mutation	SNP	G	A	4	100	c.1195G>A	c.(1195-1197)GTT>ATT	p.V399I
Pat_02	Post-Resistance	RHBDL3	162494	37	17	30625211	30625211	Missense_Mutation	SNP	G	A	5	98	c.769G>A	c.(769-771)GGT>AGT	p.G257S
Pat_02	Post-Resistance	DDX52	11056	37	17	36002256	36002256	Missense_Mutation	SNP	C	A	4	36	c.169G>T	c.(169-171)GGT>TGT	p.G57C
Pat_02	Post-Resistance	ZPBP2	124626	37	17	38031517	38031517	Missense_Mutation	SNP	G	A	12	33	c.719G>A	c.(718-720)CGA>CAA	p.R240Q
Pat_02	Post-Resistance	MED24	9862	37	17	38185157	38185157	Missense_Mutation	SNP	G	A	56	101	c.1331C>T	c.(1330-1332)TCC>TTC	p.S444F
Pat_02	Post-Resistance	KRT25	147183	37	17	38905539	38905539	Missense_Mutation	SNP	C	T	43	115	c.1214G>A	c.(1213-1215)GGA>GAA	p.G405E
Pat_02	Post-Resistance	KRT33A	3883	37	17	39506953	39506953	Missense_Mutation	SNP	G	A	4	83	c.67C>T	c.(67-69)CCC>TCC	p.P23S
Pat_02	Post-Resistance	WNK4	65266	37	17	40947840	40947840	Missense_Mutation	SNP	G	A	4	79	c.3220G>A	c.(3220-3222)GAC>AAC	p.D1074N
Pat_02	Post-Resistance	HDAC5	10014	37	17	42165927	42165927	Missense_Mutation	SNP	C	T	4	87	c.1427G>A	c.(1426-1428)CGT>CAT	p.R476H
Pat_02	Post-Resistance	ITGA2B	3674	37	17	42452064	42452064	Missense_Mutation	SNP	G	A	4	115	c.2906C>T	c.(2905-2907)GCG>GTG	p.A969V
Pat_02	Post-Resistance	FZD2	2535	37	17	42635928	42635928	Missense_Mutation	SNP	C	T	6	57	c.872C>T	c.(871-873)TCG>TTG	p.S291L
Pat_02	Post-Resistance	EFTUD2	9343	37	17	42942324	42942324	Missense_Mutation	SNP	C	G	4	275	c.1259G>C	c.(1258-1260)TGC>TCC	p.C420S
Pat_02	Post-Resistance	ABCC3	8714	37	17	48741383	48741383	Missense_Mutation	SNP	G	C	4	131	c.1249G>C	c.(1249-1251)GCC>CCC	p.A417P
Pat_02	Post-Resistance	NME1-NME2	654364	37	17	49233058	49233058	Missense_Mutation	SNP	G	A	4	153	c.118G>A	c.(118-120)GGG>AGG	p.G40R
Pat_02	Post-Resistance	ANKFN1	162282	37	17	54428221	54428221	Missense_Mutation	SNP	C	T	81	52	c.292C>T	c.(292-294)CGC>TGC	p.R98C
Pat_02	Post-Resistance	EPX	8288	37	17	56280605	56280605	Missense_Mutation	SNP	G	T	5	126	c.1872G>T	c.(1870-1872)TTG>TTT	p.L624F
Pat_02	Post-Resistance	SCN4A	6329	37	17	62049821	62049821	Missense_Mutation	SNP	C	T	4	78	c.283G>A	c.(283-285)GTA>ATA	p.V95I
Pat_02	Post-Resistance	RGS9	8787	37	17	63173858	63173858	Missense_Mutation	SNP	G	A	62	215	c.591G>A	c.(589-591)ATG>ATA	p.M197I
Pat_02	Post-Resistance	SLC9A3R1	9368	37	17	72758269	72758269	Missense_Mutation	SNP	C	G	4	183	c.560C>G	c.(559-561)CCG>CGG	p.P187R
Pat_02	Post-Resistance	RECQL5	9400	37	17	73623540	73623540	Missense_Mutation	SNP	C	T	70	189	c.2938G>A	c.(2938-2940)GAA>AAA	p.E980K
Pat_02	Post-Resistance	UBE2O	63893	37	17	74387583	74387583	Missense_Mutation	SNP	C	T	5	277	c.3320G>A	c.(3319-3321)CGC>CAC	p.R1107H
Pat_02	Post-Resistance	USP36	57602	37	17	76799510	76799510	Missense_Mutation	SNP	G	A	87	94	c.2767C>T	c.(2767-2769)CTT>TTT	p.L923F
Pat_02	Post-Resistance	CANT1	124583	37	17	76993313	76993313	Missense_Mutation	SNP	T	C	6	595	c.392A>G	c.(391-393)AAG>AGG	p.K131R
Pat_02	Post-Resistance	TBCD	6904	37	17	80882868	80882868	Missense_Mutation	SNP	C	T	4	11	c.2314C>T	c.(2314-2316)CGC>TGC	p.R772C
Pat_02	Post-Resistance	PPP4R1	9989	37	18	9583215	9583215	Missense_Mutation	SNP	G	A	4	111	c.818C>T	c.(817-819)GCT>GTT	p.A273V
Pat_02	Post-Resistance	TXNDC2	84203	37	18	9886894	9886894	Missense_Mutation	SNP	A	G	4	279	c.418A>G	c.(418-420)AAA>GAA	p.K140E
Pat_02	Post-Resistance	ASXL3	80816	37	18	31323203	31323203	Missense_Mutation	SNP	C	T	25	11	c.3391C>T	c.(3391-3393)CCT>TCT	p.P1131S
Pat_02	Post-Resistance	ASXL3	80816	37	18	31325379	31325379	Missense_Mutation	SNP	G	A	165	459	c.5567G>A	c.(5566-5568)GGG>GAG	p.G1856E
Pat_02	Post-Resistance	TCF4	6925	37	18	52901848	52901848	Missense_Mutation	SNP	G	A	151	126	c.1417C>T	c.(1417-1419)CCG>TCG	p.P473S
Pat_02	Post-Resistance	SERPINB4	6318	37	18	61328342	61328342	Missense_Mutation	SNP	C	T	167	134	c.109G>A	c.(109-111)GCA>ACA	p.A37T
Pat_02	Post-Resistance	SERPINB2	5055	37	18	61570220	61570220	Missense_Mutation	SNP	C	T	4	185	c.929C>T	c.(928-930)CCC>CTC	p.P310L
Pat_02	Post-Resistance	SALL3	27164	37	18	76754432	76754432	Missense_Mutation	SNP	C	T	6	56	c.2441C>T	c.(2440-2442)GCG>GTG	p.A814V
Pat_02	Post-Resistance	TMPRSS9	360200	37	19	2415763	2415763	Missense_Mutation	SNP	G	A	63	60	c.1567G>A	c.(1567-1569)GAA>AAA	p.E523K
Pat_02	Post-Resistance	ZNF57	126295	37	19	2917842	2917842	Missense_Mutation	SNP	G	A	9	143	c.1223G>A	c.(1222-1224)CGA>CAA	p.R408Q
Pat_02	Post-Resistance	C19orf28	126321	37	19	3548013	3548013	Missense_Mutation	SNP	C	A	35	76	c.670G>T	c.(670-672)GTG>TTG	p.V224L
Pat_02	Post-Resistance	MAP2K2	5605	37	19	4117584	4117584	Missense_Mutation	SNP	G	A	42	122	c.136C>T	c.(136-138)CTT>TTT	p.L46F
Pat_02	Post-Resistance	SHD	56961	37	19	4290446	4290446	Missense_Mutation	SNP	G	A	4	172	c.839G>A	c.(838-840)AGC>AAC	p.S280N
Pat_02	Post-Resistance	ARRDC5	645432	37	19	4902842	4902842	Missense_Mutation	SNP	G	A	67	84	c.38C>T	c.(37-39)CCC>CTC	p.P13L
Pat_02	Post-Resistance	PTPRS	5802	37	19	5244224	5244224	Missense_Mutation	SNP	G	A	4	97	c.1258C>T	c.(1258-1260)CGC>TGC	p.R420C

Pat_02	Post-Resistance	MCOLN1	57192	37	19	7589984	7589984	Nonsense_Mutation	SNP	C	T	23	89	c.169C>T	c.(169-171)CGA>TGA	p.R57*
Pat_02	Post-Resistance	MUC16	94025	37	19	9069874	9069874	Missense_Mutation	SNP	C	T	117	98	c.17572G>A	c.(17572-17574)GAA>AAA	p.E5858K
Pat_02	Post-Resistance	OR7E24	26648	37	19	9361936	9361936	Missense_Mutation	SNP	C	T	4	208	c.217C>T	c.(217-219)CTC>TTC	p.L73F
Pat_02	Post-Resistance	ZNF700	90592	37	19	12060061	12060061	Missense_Mutation	SNP	C	T	29	76	c.1222C>T	c.(1222-1224)CAT>TAT	p.H408Y
Pat_02	Post-Resistance	ZNF878	729747	37	19	12155673	12155673	Missense_Mutation	SNP	A	C	7	400	c.684T>G	c.(682-684)AGT>AGG	p.S228R
Pat_02	Post-Resistance	ZNF844	284391	37	19	12187307	12187307	Missense_Mutation	SNP	G	C	4	151	c.1372G>C	c.(1372-1374)GAT>CAT	p.D458H
Pat_02	Post-Resistance	ZNF564	163050	37	19	12637555	12637555	Missense_Mutation	SNP	T	C	6	260	c.1367A>G	c.(1366-1368)AAA>AGA	p.K456R
Pat_02	Post-Resistance	TRMT1	55621	37	19	13223529	13223529	Missense_Mutation	SNP	C	T	5	226	c.860G>A	c.(859-861)TGC>TAC	p.C287Y
Pat_02	Post-Resistance	CACNA1A	773	37	19	13443692	13443692	Missense_Mutation	SNP	G	A	20	74	c.1246C>T	c.(1246-1248)CCC>TCC	p.P416S
Pat_02	Post-Resistance	USHBP1	83878	37	19	17366283	17366283	Missense_Mutation	SNP	G	A	5	228	c.1603C>T	c.(1603-1605)CGG>TGG	p.R535W
Pat_02	Post-Resistance	ANO8	57719	37	19	17435723	17435723	Missense_Mutation	SNP	G	A	5	297	c.3134C>T	c.(3133-3135)CCG>CTG	p.P1045L
Pat_02	Post-Resistance	COMP	1311	37	19	18898299	18898299	Splice_Site	SNP	C	T	4	166	c.1135_splice	c.e10+1	p.R379_splice
Pat_02	Post-Resistance	TSSK6	83983	37	19	19626088	19626089	Missense_Mutation	DNP	GG	AA	47	41	c.148_149CC>TT	c.(148-150)CCG>TTG	p.P50L
Pat_02	Post-Resistance	ZNF626	199777	37	19	20808006	20808006	Missense_Mutation	SNP	T	C	4	143	c.677A>G	c.(676-678)GAG>GGG	p.E226G
Pat_02	Post-Resistance	ATP4A	495	37	19	36044045	36044045	Missense_Mutation	SNP	G	A	5	239	c.2645C>T	c.(2644-2646)ACG>ATG	p.T882M
Pat_02	Post-Resistance	THAP8	199745	37	19	36530878	36530878	Missense_Mutation	SNP	G	A	5	133	c.244C>T	c.(244-246)CCC>TCC	p.P82S
Pat_02	Post-Resistance	ZNF585B	92285	37	19	37676149	37676149	Missense_Mutation	SNP	G	A	74	206	c.2290C>T	c.(2290-2292)CAT>TAT	p.H764Y
Pat_02	Post-Resistance	SIPA1L3	23094	37	19	38600987	38600987	Nonsense_Mutation	SNP	C	T	20	71	c.2254C>T	c.(2254-2256)CGA>TGA	p.R752*
Pat_02	Post-Resistance	SYCN	342898	37	19	39694677	39694677	Missense_Mutation	SNP	C	A	6	22	c.218G>T	c.(217-219)TGG>TTG	p.W73L
Pat_02	Post-Resistance	MED29	55588	37	19	39888248	39888248	Missense_Mutation	SNP	C	T	4	145	c.575C>T	c.(574-576)GCC>GTC	p.A192V
Pat_02	Post-Resistance	ZNF780A	284323	37	19	40580552	40580552	Missense_Mutation	SNP	T	G	5	289	c.1797A>C	c.(1795-1797)CAA>CAC	p.Q599H
Pat_02	Post-Resistance	SPTBN4	57731	37	19	41066113	41066113	Missense_Mutation	SNP	G	A	4	109	c.5719G>A	c.(5719-5721)GGT>AGT	p.G1907S
Pat_02	Post-Resistance	CYP2B6	1555	37	19	41518343	41518343	Missense_Mutation	SNP	C	T	5	132	c.1105C>T	c.(1105-1107)CAC>TAC	p.H369Y
Pat_02	Post-Resistance	CYP2S1	29785	37	19	41709378	41709378	Missense_Mutation	SNP	C	T	17	26	c.1000C>T	c.(1000-1002)CGG>TGG	p.R334W
Pat_02	Post-Resistance	CEACAM6	4680	37	19	42265903	42265903	Missense_Mutation	SNP	C	T	28	106	c.730C>T	c.(730-732)CCC>TCC	p.P244S
Pat_02	Post-Resistance	ZC3H4	23211	37	19	47575940	47575940	Missense_Mutation	SNP	C	T	15	54	c.1471G>A	c.(1471-1473)GAG>AAG	p.E491K
Pat_02	Post-Resistance	LIG1	3978	37	19	48636318	48636318	Missense_Mutation	SNP	C	A	7	487	c.1646G>T	c.(1645-1647)CGG>CTG	p.R549L
Pat_02	Post-Resistance	FAM83E	54854	37	19	49113164	49113164	Missense_Mutation	SNP	C	G	3	138	c.727G>C	c.(727-729)GAC>CAC	p.D243H
Pat_02	Post-Resistance	FUZ	80199	37	19	50310433	50310433	Missense_Mutation	SNP	A	G	5	191	c.1232T>C	c.(1231-1233)CTG>CCG	p.L411P
Pat_02	Post-Resistance	ZNF845	91664	37	19	53855196	53855196	Missense_Mutation	SNP	T	C	4	242	c.1268T>C	c.(1267-1269)ATG>ACG	p.M423T
Pat_02	Post-Resistance	LILRB1	10859	37	19	55144109	55144109	Missense_Mutation	SNP	C	T	4	139	c.856C>T	c.(856-858)CCT>TCT	p.P286S
Pat_02	Post-Resistance	LILRB4	11006	37	19	55175463	55175463	Missense_Mutation	SNP	C	G	5	177	c.322C>G	c.(322-324)CAG>GAG	p.Q108E
Pat_02	Post-Resistance	PPP1R12C	54776	37	19	55607264	55607264	Missense_Mutation	SNP	G	A	128	79	c.1198C>T	c.(1198-1200)CCG>TCG	p.P400S
Pat_02	Post-Resistance	ZNF583	147949	37	19	56934293	56934293	Missense_Mutation	SNP	C	T	15	123	c.266C>T	c.(265-267)TCA>TTA	p.S89L
Pat_02	Post-Resistance	ZNF274	10782	37	19	58721354	58721354	Missense_Mutation	SNP	G	A	4	163	c.767G>A	c.(766-768)GGC>GAC	p.G256D
Pat_02	Post-Resistance	ROCK2	9475	37	2	11337309	11337309	Missense_Mutation	SNP	G	A	97	114	c.3445C>T	c.(3445-3447)CCA>TCA	p.P1149S
Pat_02	Post-Resistance	KRTCAP3	200634	37	2	27666038	27666038	Missense_Mutation	SNP	G	A	62	215	c.371G>A	c.(370-372)GGT>GAT	p.G124D
Pat_02	Post-Resistance	SIX3	6496	37	2	45169790	45169790	Missense_Mutation	SNP	C	T	3	24	c.547C>T	c.(547-549)CGC>TGC	p.R183C
Pat_02	Post-Resistance	EPAS1	2034	37	2	46597051	46597051	Missense_Mutation	SNP	A	G	3	71	c.865A>G	c.(865-867)ATG>GTG	p.M289V
Pat_02	Post-Resistance	WDR54	84058	37	2	74650623	74650623	Missense_Mutation	SNP	G	A	4	257	c.371G>A	c.(370-372)CGG>CAG	p.R124Q
Pat_02	Post-Resistance	PROM2	150696	37	2	95952320	95952320	Splice_Site	SNP	G	C	7	44	c.2040_splice	c.e17+1	p.V680_splice
Pat_02	Post-Resistance	IL18RAP	8807	37	2	103040432	103040432	Missense_Mutation	SNP	G	A	42	51	c.232G>A	c.(232-234)GAC>AAC	p.D78N
Pat_02	Post-Resistance	UXS1	80146	37	2	106729173	106729173	Missense_Mutation	SNP	G	A	4	97	c.793C>T	c.(793-795)CGC>TGC	p.R265C
Pat_02	Post-Resistance	INSIG2	51141	37	2	118860893	118860893	Missense_Mutation	SNP	G	A	5	233	c.365G>A	c.(364-366)AGT>AAT	p.S122N
Pat_02	Post-Resistance	EPB41L5	57669	37	2	120918494	120918494	Nonsense_Mutation	SNP	G	T	5	321	c.1831G>T	c.(1831-1833)GAG>TAG	p.E611*
Pat_02	Post-Resistance	GLI2	2736	37	2	121747862	121747862	Nonsense_Mutation	SNP	G	T	5	173	c.4372G>T	c.(4372-4374)GGA>TGA	p.G1458*
Pat_02	Post-Resistance	SCN9A	6335	37	2	167151136	167151136	Missense_Mutation	SNP	A	T	16	37	c.938T>A	c.(937-939)CTC>CAC	p.L313H

Pat_02	Post-Resistance	PDK1	5163	37	2	173435524	173435524	Missense_Mutation	SNP	C	T	4	143	c.917C>T	c.(916-918)ACG>ATG	p.T306M
Pat_02	Post-Resistance	HOXD10	3236	37	2	176983724	176983724	Missense_Mutation	SNP	C	A	4	138	c.788C>A	c.(787-789)GCA>GAA	p.A263E
Pat_02	Post-Resistance	TTN	7273	37	2	179584164	179584164	Missense_Mutation	SNP	G	A	26	100	c.20221C>T	c.(20221-20223)CCT>TCT	p.P6741S
Pat_02	Post-Resistance	TTN	7273	37	2	179605802	179605802	Missense_Mutation	SNP	G	A	79	305	c.11645C>T	c.(11644-11646)CCA>CTA	p.P3882L
Pat_02	Post-Resistance	TTN	7273	37	2	179632760	179632760	Missense_Mutation	SNP	C	T	41	151	c.9286G>A	c.(9286-9288)GAA>AAA	p.E3096K
Pat_02	Post-Resistance	CALCRL	10203	37	2	188216932	188216932	Missense_Mutation	SNP	C	T	21	99	c.1037G>A	c.(1036-1038)GGC>GAC	p.G346D
Pat_02	Post-Resistance	MYO1B	4430	37	2	192225446	192225446	Missense_Mutation	SNP	G	A	94	226	c.652G>A	c.(652-654)GAG>AAG	p.E218K
Pat_02	Post-Resistance	DNAH7	56171	37	2	196825573	196825573	Missense_Mutation	SNP	G	A	96	93	c.2302C>T	c.(2302-2304)CGT>TGT	p.R768C
Pat_02	Post-Resistance	CPS1	1373	37	2	211518789	211518789	Missense_Mutation	SNP	G	A	101	94	c.3521G>A	c.(3520-3522)CGA>CAA	p.R1174Q
Pat_02	Post-Resistance	VIL1	7429	37	2	219297613	219297613	Missense_Mutation	SNP	C	T	4	111	c.1439C>T	c.(1438-1440)CCA>CTA	p.P480L
Pat_02	Post-Resistance	AGAP1	116987	37	2	236659084	236659084	Missense_Mutation	SNP	G	A	87	258	c.625G>A	c.(625-627)GAG>AAG	p.E209K
Pat_02	Post-Resistance	IQCA1	79781	37	2	237300651	237300651	Missense_Mutation	SNP	G	A	5	204	c.1381C>T	c.(1381-1383)CGC>TGC	p.R461C
Pat_02	Post-Resistance	HDAC4	9759	37	2	240056075	240056075	Missense_Mutation	SNP	A	G	3	50	c.1160T>C	c.(1159-1161)CTT>CCT	p.L387P
Pat_02	Post-Resistance	ANO7	50636	37	2	242154310	242154310	Missense_Mutation	SNP	C	T	4	101	c.1981C>T	c.(1981-1983)CTC>TTC	p.L661F
Pat_02	Post-Resistance	GPCPD1	56261	37	20	5564948	5564948	Missense_Mutation	SNP	C	T	4	195	c.328G>A	c.(328-330)GAT>AAT	p.D110N
Pat_02	Post-Resistance	CSRP2BP	57325	37	20	18139799	18139799	Nonsense_Mutation	SNP	C	A	13	126	c.572C>A	c.(571-573)TCA>TAA	p.S191*
Pat_02	Post-Resistance	CST4	1472	37	20	23669492	23669492	Missense_Mutation	SNP	G	A	4	158	c.115C>T	c.(115-117)CTC>TTC	p.L39F
Pat_02	Post-Resistance	ITCH	83737	37	20	33049960	33049960	Missense_Mutation	SNP	C	T	61	80	c.1481C>T	c.(1480-1482)CCA>CTA	p.P494L
Pat_02	Post-Resistance	CEP250	11190	37	20	34097836	34097836	Missense_Mutation	SNP	G	A	4	169	c.7018G>A	c.(7018-7020)GGA>AGA	p.G2340R
Pat_02	Post-Resistance	PLCG1	5335	37	20	39795117	39795117	Missense_Mutation	SNP	T	G	3	97	c.2002T>G	c.(2002-2004)TGG>GGG	p.W668G
Pat_02	Post-Resistance	PTPRT	11122	37	20	41306578	41306578	Missense_Mutation	SNP	G	A	4	240	c.1081C>T	c.(1081-1083)CTC>TTC	p.L361F
Pat_02	Post-Resistance	WFDC10A	140832	37	20	44258532	44258532	Missense_Mutation	SNP	A	T	4	164	c.80A>T	c.(79-81)AAG>ATG	p.K27M
Pat_02	Post-Resistance	KCNB1	3745	37	20	47989852	47989852	Nonsense_Mutation	SNP	C	A	5	225	c.2245G>T	c.(2245-2247)GAG>TAG	p.E749*
Pat_02	Post-Resistance	ZGPAT	84619	37	20	62365029	62365029	Missense_Mutation	SNP	G	A	5	306	c.809G>A	c.(808-810)CGC>CAC	p.R270H
Pat_02	Post-Resistance	TPTE	7179	37	21	10921987	10921987	Missense_Mutation	SNP	C	T	22	119	c.1036G>A	c.(1036-1038)GGA>AGA	p.G346R
Pat_02	Post-Resistance	KRTAP24-1	643803	37	21	31655039	31655039	Missense_Mutation	SNP	C	A	105	90	c.212G>T	c.(211-213)TGC>TTC	p.C71F
Pat_02	Post-Resistance	GART	2618	37	21	34889834	34889834	Missense_Mutation	SNP	C	A	6	485	c.1784G>T	c.(1783-1785)CGA>CTA	p.R595L
Pat_02	Post-Resistance	DOPEY2	9980	37	21	37572684	37572684	Missense_Mutation	SNP	C	T	4	229	c.376C>T	c.(376-378)CTC>TTC	p.L126F
Pat_02	Post-Resistance	C21orf33	8209	37	21	45563173	45563173	Missense_Mutation	SNP	A	G	51	50	c.608A>G	c.(607-609)AAG>AGG	p.K203R
Pat_02	Post-Resistance	KRTAP10-11	386678	37	21	46066487	46066487	Missense_Mutation	SNP	G	A	51	134	c.112G>A	c.(112-114)GCC>ACC	p.A38T
Pat_02	Post-Resistance	KRTAP12-3	386683	37	21	46078068	46078068	Missense_Mutation	SNP	G	A	6	376	c.172G>A	c.(172-174)GTG>ATG	p.V58M
Pat_02	Post-Resistance	FTCD	10841	37	21	47571497	47571497	Missense_Mutation	SNP	C	A	4	138	c.611G>T	c.(610-612)CGG>CTG	p.R204L
Pat_02	Post-Resistance	PCNT	5116	37	21	47817317	47817317	Missense_Mutation	SNP	G	A	5	170	c.4355G>A	c.(4354-4356)GGG>GAG	p.G1452E
Pat_02	Post-Resistance	VPREB3	29802	37	22	24095185	24095185	Missense_Mutation	SNP	G	A	4	134	c.250C>T	c.(250-252)CCC>TCC	p.P84S
Pat_02	Post-Resistance	SUSD2	56241	37	22	24584196	24584196	Missense_Mutation	SNP	G	A	4	138	c.2345G>A	c.(2344-2346)CGC>CAC	p.R782H
Pat_02	Post-Resistance	RNF185	91445	37	22	31600480	31600480	Missense_Mutation	SNP	C	T	110	95	c.487C>T	c.(487-489)CCT>TCT	p.P163S
Pat_02	Post-Resistance	MGAT3	4248	37	22	39884185	39884185	Missense_Mutation	SNP	C	T	4	233	c.833C>T	c.(832-834)CCG>CTG	p.P278L
Pat_02	Post-Resistance	SGSM3	27352	37	22	40804428	40804428	Missense_Mutation	SNP	G	A	4	114	c.1777G>A	c.(1777-1779)GAG>AAG	p.E593K
Pat_02	Post-Resistance	EP300	2033	37	22	41564581	41564581	Missense_Mutation	SNP	G	A	4	178	c.4003G>A	c.(4003-4005)GTA>ATA	p.V1335I
Pat_02	Post-Resistance	TCF20	6942	37	22	42610675	42610675	Missense_Mutation	SNP	G	A	5	185	c.637C>T	c.(637-639)CGG>TGG	p.R213W
Pat_02	Post-Resistance	TUBGCP6	85378	37	22	50659166	50659166	Missense_Mutation	SNP	T	C	5	177	c.3622A>G	c.(3622-3624)ACC>GCC	p.T1208A
Pat_02	Post-Resistance	PLXNB2	23654	37	22	50718981	50718981	Missense_Mutation	SNP	G	A	6	190	c.4112C>T	c.(4111-4113)ACG>ATG	p.T1371M
Pat_02	Post-Resistance	NCAPH2	29781	37	22	50960618	50960618	Missense_Mutation	SNP	G	A	4	156	c.1171G>A	c.(1171-1173)GTC>ATC	p.V391I
Pat_02	Post-Resistance	SRGAP3	9901	37	3	9034696	9034696	Missense_Mutation	SNP	C	T	68	13	c.2452G>A	c.(2452-2454)GAG>AAG	p.E818K
Pat_02	Post-Resistance	SLC4A7	9497	37	3	27439823	27439823	Missense_Mutation	SNP	C	A	4	166	c.2422G>T	c.(2422-2424)GTA>TTA	p.V808L
Pat_02	Post-Resistance	CTNNB1	1499	37	3	41266136	41266136	Missense_Mutation	SNP	T	C	41	93	c.133T>C	c.(133-135)TCT>CCT	p.S45P
Pat_02	Post-Resistance	CCBP2	1238	37	3	42906595	42906595	Missense_Mutation	SNP	G	A	4	160	c.601G>A	c.(601-603)GGG>AGG	p.G201R

Pat_02	Post-Resistance	CDCP1	64866	37	3	45153928	45153928	Missense_Mutation	SNP	G	A	469	116	c.302C>T	c.(301-303)TCA>TTA	p.S101L
Pat_02	Post-Resistance	KIF9	64147	37	3	47277934	47277934	Missense_Mutation	SNP	C	T	4	102	c.2100G>A	c.(2098-2100)ATG>ATA	p.M700I
Pat_02	Post-Resistance	GPX1	2876	37	3	49395482	49395482	Missense_Mutation	SNP	G	C	4	43	c.230C>G	c.(229-231)CCG>CGG	p.P77R
Pat_02	Post-Resistance	BSN	8927	37	3	49699728	49699728	Missense_Mutation	SNP	T	C	3	45	c.10450T>C	c.(10450-10452)TCA>CCA	p.S3484P
Pat_02	Post-Resistance	CDHR4	389118	37	3	49836771	49836771	Missense_Mutation	SNP	G	A	4	45	c.149C>T	c.(148-150)ACA>ATA	p.T50I
Pat_02	Post-Resistance	DOCK3	1795	37	3	51263088	51263088	Missense_Mutation	SNP	C	T	143	66	c.1261C>T	c.(1261-1263)CGC>TGC	p.R421C
Pat_02	Post-Resistance	RBM15B	29890	37	3	51431274	51431274	Missense_Mutation	SNP	G	A	4	36	c.2444G>A	c.(2443-2445)GGT>GAT	p.G815D
Pat_02	Post-Resistance	NISCH	11188	37	3	52522296	52522296	Missense_Mutation	SNP	C	T	4	161	c.2788C>T	c.(2788-2790)CGT>TGT	p.R930C
Pat_02	Post-Resistance	ERC2	26059	37	3	55922487	55922487	Missense_Mutation	SNP	C	T	177	50	c.2494G>A	c.(2494-2496)GAA>AAA	p.E832K
Pat_02	Post-Resistance	NSUN3	63899	37	3	93845251	93845251	Missense_Mutation	SNP	T	G	3	87	c.940T>G	c.(940-942)TTA>GTA	p.L314V
Pat_02	Post-Resistance	ZPLD1	131368	37	3	102171787	102171787	Missense_Mutation	SNP	G	T	4	100	c.131G>T	c.(130-132)TGT>TTT	p.C44F
Pat_02	Post-Resistance	CD200R1	131450	37	3	112642585	112642585	Missense_Mutation	SNP	T	C	62	25	c.917A>G	c.(916-918)AAC>AGC	p.N306S
Pat_02	Post-Resistance	ADPRH	141	37	3	119301188	119301188	Missense_Mutation	SNP	G	A	4	124	c.172G>A	c.(172-174)GTG>ATG	p.V58M
Pat_02	Post-Resistance	MYLK	4638	37	3	123356964	123356964	Missense_Mutation	SNP	C	T	4	97	c.4915G>A	c.(4915-4917)GGC>AGC	p.G1639S
Pat_02	Post-Resistance	CCDC48	79825	37	3	128755927	128755927	Missense_Mutation	SNP	C	A	3	18	c.1557C>A	c.(1555-1557)GAC>GAA	p.D519E
Pat_02	Post-Resistance	NUDT16	131870	37	3	131101010	131101010	Missense_Mutation	SNP	G	A	5	72	c.160G>A	c.(160-162)GCT>ACT	p.A54T
Pat_02	Post-Resistance	LRRC31	79782	37	3	169569529	169569529	Missense_Mutation	SNP	G	A	43	34	c.1037C>T	c.(1036-1038)TCA>TTA	p.S346L
Pat_02	Post-Resistance	NAALADL2	254827	37	3	175184905	175184905	Missense_Mutation	SNP	G	A	4	104	c.1466G>A	c.(1465-1467)CGA>CAA	p.R489Q
Pat_02	Post-Resistance	FXR1	8087	37	3	180685998	180685998	Missense_Mutation	SNP	G	A	4	147	c.1358G>A	c.(1357-1359)CGA>CAA	p.R453Q
Pat_02	Post-Resistance	EIF2B5	8893	37	3	183855532	183855532	Missense_Mutation	SNP	C	T	89	31	c.445C>T	c.(445-447)CTT>TTT	p.L149F
Pat_02	Post-Resistance	ZNF721	170960	37	4	435639	435639	Missense_Mutation	SNP	T	C	3	84	c.2617A>G	c.(2617-2619)ACC>GCC	p.T873A
Pat_02	Post-Resistance	TACC3	10460	37	4	1730378	1730378	Missense_Mutation	SNP	C	T	115	70	c.1249C>T	c.(1249-1251)CCG>TCG	p.P417S
Pat_02	Post-Resistance	GPR78	27201	37	4	8584263	8584263	Missense_Mutation	SNP	G	A	4	69	c.674G>A	c.(673-675)CGG>CAG	p.R225Q
Pat_02	Post-Resistance	BOD1L	259282	37	4	13603683	13603683	Missense_Mutation	SNP	T	C	3	118	c.4841A>G	c.(4840-4842)GAA>GGA	p.E1614G
Pat_02	Post-Resistance	LOC344967	344967	37	4	40045496	40045496	Missense_Mutation	SNP	A	T	4	52	c.160T>A	c.(160-162)TCC>ACC	p.S54T
Pat_02	Post-Resistance	UGT2A1	10941	37	4	70455304	70455304	Missense_Mutation	SNP	C	T	166	71	c.1370G>A	c.(1369-1371)CGA>CAA	p.R457Q
Pat_02	Post-Resistance	PRSS12	8492	37	4	119204150	119204150	Missense_Mutation	SNP	C	T	5	293	c.2156G>A	c.(2155-2157)CGA>CAA	p.R719Q
Pat_02	Post-Resistance	FAT4	79633	37	4	126336563	126336563	Missense_Mutation	SNP	G	A	71	217	c.6445G>A	c.(6445-6447)GAT>AAT	p.D2149N
Pat_02	Post-Resistance	PLK4	10733	37	4	128814897	128814897	Missense_Mutation	SNP	G	A	80	462	c.2423G>A	c.(2422-2424)GGT>GAT	p.G808D
Pat_02	Post-Resistance	TBC1D9	23158	37	4	141583078	141583078	Missense_Mutation	SNP	G	A	5	66	c.1772C>T	c.(1771-1773)GCT>GTT	p.A591V
Pat_02	Post-Resistance	USP38	84640	37	4	144124642	144124642	Missense_Mutation	SNP	A	C	134	86	c.1132A>C	c.(1132-1134)ACA>CCA	p.T378P
Pat_02	Post-Resistance	DCHS2	54798	37	4	155157832	155157832	Missense_Mutation	SNP	C	A	4	245	c.6607G>T	c.(6607-6609)GTC>TTC	p.V2203F
Pat_02	Post-Resistance	FNIP2	57600	37	4	159790387	159790387	Missense_Mutation	SNP	G	A	4	165	c.2599G>A	c.(2599-2601)GGT>AGT	p.G867S
Pat_02	Post-Resistance	ODZ3	55714	37	4	183710474	183710474	Missense_Mutation	SNP	G	A	37	85	c.5533G>A	c.(5533-5535)GGA>AGA	p.G1845R
Pat_02	Post-Resistance	FAT1	2195	37	4	187557367	187557367	Missense_Mutation	SNP	C	T	5	173	c.3995G>A	c.(3994-3996)CGC>CAC	p.R1332H
Pat_02	Post-Resistance	ZFP42	132625	37	4	188924340	188924340	Missense_Mutation	SNP	G	A	37	194	c.379G>A	c.(379-381)GTA>ATA	p.V127I
Pat_02	Post-Resistance	DAB2	1601	37	5	39381588	39381588	Missense_Mutation	SNP	G	A	4	237	c.1472C>T	c.(1471-1473)GCT>GTT	p.A491V
Pat_02	Post-Resistance	CCL28	56477	37	5	43382119	43382119	Missense_Mutation	SNP	G	A	4	111	c.227C>T	c.(226-228)CCG>CTG	p.P76L
Pat_02	Post-Resistance	MAP3K1	4214	37	5	56161183	56161183	Missense_Mutation	SNP	G	A	28	74	c.1052G>A	c.(1051-1053)CGT>CAT	p.R351H
Pat_02	Post-Resistance	JMY	133746	37	5	78611961	78611961	Missense_Mutation	SNP	T	A	5	75	c.2798T>A	c.(2797-2799)GTA>GAA	p.V933E
Pat_02	Post-Resistance	CMYA5	202333	37	5	79027271	79027271	Missense_Mutation	SNP	C	T	63	17	c.2683C>T	c.(2683-2685)CCC>TCC	p.P895S
Pat_02	Post-Resistance	GPR98	84059	37	5	89986740	89986740	Missense_Mutation	SNP	G	A	18	35	c.6833G>A	c.(6832-6834)GGA>GAA	p.G2278E
Pat_02	Post-Resistance	ERAP2	64167	37	5	96224902	96224902	Missense_Mutation	SNP	C	T	4	114	c.863C>T	c.(862-864)GCA>GTA	p.A288V
Pat_02	Post-Resistance	DMXL1	1657	37	5	118469331	118469331	Missense_Mutation	SNP	G	A	4	113	c.1712G>A	c.(1711-1713)CGT>CAT	p.R571H
Pat_02	Post-Resistance	FBN2	2201	37	5	127645674	127645674	Splice_Site	SNP	C	T	4	206	c.5200_splice	c.e40+1	p.D1734_splice
Pat_02	Post-Resistance	KIF20A	10112	37	5	137519758	137519758	Missense_Mutation	SNP	G	A	4	135	c.1316G>A	c.(1315-1317)CGC>CAC	p.R439H
Pat_02	Post-Resistance	PCDHA6	56142	37	5	140208464	140208464	Missense_Mutation	SNP	G	A	31	76	c.788G>A	c.(787-789)AGA>AAA	p.R263K

Pat_02	Post-Resistance	PCDHA8	56140	37	5	140221712	140221712	Missense_Mutation	SNP	C	G	9	85	c.806C>G	c.(805-807)CCG>CGG	p.P269R
Pat_02	Post-Resistance	PCDHA12	56137	37	5	140255196	140255196	Missense_Mutation	SNP	C	T	104	26	c.139C>T	c.(139-141)CGC>TGC	p.R47C
Pat_02	Post-Resistance	PCDHGA11	56105	37	5	140802136	140802136	Missense_Mutation	SNP	G	A	5	263	c.1342G>A	c.(1342-1344)GAT>AAT	p.D448N
Pat_02	Post-Resistance	PDGFRB	5159	37	5	149497218	149497218	Missense_Mutation	SNP	C	A	5	144	c.3100G>T	c.(3100-3102)GAC>TAC	p.D1034Y
Pat_02	Post-Resistance	TNIP1	10318	37	5	150413198	150413198	Missense_Mutation	SNP	G	A	4	113	c.1750C>T	c.(1750-1752)CCA>TCA	p.P584S
Pat_02	Post-Resistance	GABRA6	2559	37	5	161113333	161113333	Missense_Mutation	SNP	C	T	67	118	c.136C>T	c.(136-138)CGG>TGG	p.R46W
Pat_02	Post-Resistance	ODZ2	57451	37	5	167689471	167689471	Missense_Mutation	SNP	A	G	2	5	c.7954A>G	c.(7954-7956)AGG>GGG	p.R2652G
Pat_02	Post-Resistance	STK10	6793	37	5	171471996	171471996	Missense_Mutation	SNP	G	A	4	131	c.2797C>T	c.(2797-2799)CGG>TGG	p.R933W
Pat_02	Post-Resistance	PDLIM7	9260	37	5	176911119	176911119	Missense_Mutation	SNP	G	A	4	144	c.1123C>T	c.(1123-1125)CGG>TGG	p.R375W
Pat_02	Post-Resistance	DOK3	79930	37	5	176936820	176936820	Missense_Mutation	SNP	G	A	5	99	c.34C>T	c.(34-36)CGT>TGT	p.R12C
Pat_02	Post-Resistance	RASGEF1C	255426	37	5	179554673	179554673	Missense_Mutation	SNP	C	A	37	12	c.650G>T	c.(649-651)CGG>CTG	p.R217L
Pat_02	Post-Resistance	PRSS16	10279	37	6	27215684	27215684	Nonsense_Mutation	SNP	G	T	42	91	c.94G>T	c.(94-96)GAG>TAG	p.E32*
Pat_02	Post-Resistance	ZNF323	64288	37	6	28294491	28294491	Missense_Mutation	SNP	T	C	93	154	c.673A>G	c.(673-675)AAG>GAG	p.K225E
Pat_02	Post-Resistance	GPX6	257202	37	6	28472193	28472193	Nonsense_Mutation	SNP	C	T	67	74	c.542G>A	c.(541-543)TGG>TAG	p.W181*
Pat_02	Post-Resistance	TREM1	54210	37	6	41250190	41250190	Nonsense_Mutation	SNP	G	A	40	56	c.349C>T	c.(349-351)CAG>TAG	p.Q117*
Pat_02	Post-Resistance	TRERF1	55809	37	6	42236589	42236589	Missense_Mutation	SNP	C	T	80	123	c.740G>A	c.(739-741)GGA>GAA	p.G247E
Pat_02	Post-Resistance	TTBK1	84630	37	6	43226814	43226814	Missense_Mutation	SNP	G	A	4	99	c.1055G>A	c.(1054-1056)CGG>CAG	p.R352Q
Pat_02	Post-Resistance	SLC22A7	10864	37	6	43271969	43271969	Missense_Mutation	SNP	G	A	4	140	c.1579G>A	c.(1579-1581)GTG>ATG	p.V527M
Pat_02	Post-Resistance	XPO5	57510	37	6	43535029	43535029	Nonsense_Mutation	SNP	C	T	41	45	c.711G>A	c.(709-711)TGG>TGA	p.W237*
Pat_02	Post-Resistance	RIMS1	22999	37	6	73000460	73000460	Missense_Mutation	SNP	T	A	65	156	c.3633T>A	c.(3631-3633)CAT>CAA	p.H1211Q
Pat_02	Post-Resistance	COL12A1	1303	37	6	75843624	75843624	Missense_Mutation	SNP	G	A	59	267	c.5614C>T	c.(5614-5616)CGT>TGT	p.R1872C
Pat_02	Post-Resistance	PPIL6	285755	37	6	109748299	109748299	Missense_Mutation	SNP	C	T	16	20	c.481G>A	c.(481-483)GAG>AAG	p.E161K
Pat_02	Post-Resistance	MAD1L1	8379	37	7	2188797	2188797	Missense_Mutation	SNP	C	T	4	90	c.1063G>A	c.(1063-1065)GTC>ATC	p.V355I
Pat_02	Post-Resistance	CARD11	84433	37	7	2977639	2977639	Missense_Mutation	SNP	G	A	5	306	c.1045C>T	c.(1045-1047)CTC>TTC	p.L349F
Pat_02	Post-Resistance	MEOX2	4223	37	7	15652223	15652223	Missense_Mutation	SNP	A	C	84	99	c.704T>G	c.(703-705)TTC>TGC	p.F235C
Pat_02	Post-Resistance	INMT	11185	37	7	30795310	30795310	Missense_Mutation	SNP	C	T	64	92	c.635C>T	c.(634-636)TCC>TTC	p.S212F
Pat_02	Post-Resistance	BBS9	27241	37	7	33312736	33312736	Missense_Mutation	SNP	A	G	119	163	c.815A>G	c.(814-816)AAG>AGG	p.K272R
Pat_02	Post-Resistance	BMPER	168667	37	7	34192733	34192733	Missense_Mutation	SNP	G	A	192	281	c.1906G>A	c.(1906-1908)GAT>AAT	p.D636N
Pat_02	Post-Resistance	SAMD9L	219285	37	7	92762896	92762896	Missense_Mutation	SNP	G	A	103	214	c.2389C>T	c.(2389-2391)CCT>TCT	p.P797S
Pat_02	Post-Resistance	CCDC132	55610	37	7	92938190	92938190	Missense_Mutation	SNP	G	T	5	264	c.1684G>T	c.(1684-1686)GAT>TAT	p.D562Y
Pat_02	Post-Resistance	TRRAP	8295	37	7	98581022	98581022	Missense_Mutation	SNP	G	A	5	300	c.8941G>A	c.(8941-8943)GTG>ATG	p.V2981M
Pat_02	Post-Resistance	CYP3A7	1551	37	7	99306869	99306869	Missense_Mutation	SNP	C	T	68	50	c.1042G>A	c.(1042-1044)GAT>AAT	p.D348N
Pat_02	Post-Resistance	MUC17	140453	37	7	100678524	100678524	Missense_Mutation	SNP	G	A	259	527	c.3827G>A	c.(3826-3828)GGA>GAA	p.G1276E
Pat_02	Post-Resistance	PLOD3	8985	37	7	100854914	100854914	Missense_Mutation	SNP	G	A	7	51	c.1316C>T	c.(1315-1317)GCC>GTC	p.A439V
Pat_02	Post-Resistance	LRWD1	222229	37	7	102113015	102113015	Missense_Mutation	SNP	C	T	4	55	c.1649C>T	c.(1648-1650)TCG>TTG	p.S550L
Pat_02	Post-Resistance	RELN	5649	37	7	103293071	103293071	Missense_Mutation	SNP	G	A	152	139	c.1690C>T	c.(1690-1692)CTC>TTC	p.L564F
Pat_02	Post-Resistance	PIK3CG	5294	37	7	106509799	106509799	Nonsense_Mutation	SNP	G	A	105	280	c.1793G>A	c.(1792-1794)TGG>TAG	p.W598*
Pat_02	Post-Resistance	MET	4233	37	7	116409720	116409720	Missense_Mutation	SNP	G	A	4	163	c.2605G>A	c.(2605-2607)GCA>ACA	p.A869T
Pat_02	Post-Resistance	WNT2	7472	37	7	116955208	116955208	Missense_Mutation	SNP	G	A	6	306	c.505C>T	c.(505-507)CGC>TGC	p.R169C
Pat_02	Post-Resistance	CADPS2	93664	37	7	122001057	122001057	Missense_Mutation	SNP	A	C	29	83	c.3398T>G	c.(3397-3399)GTG>GGG	p.V1133G
Pat_02	Post-Resistance	DENND2A	27147	37	7	140221853	140221853	Missense_Mutation	SNP	G	A	5	215	c.2713C>T	c.(2713-2715)CGC>TGC	p.R905C
Pat_02	Post-Resistance	BRAF	673	37	7	140453136	140453136	Missense_Mutation	SNP	A	T	673	123	c.1799T>A	c.(1798-1800)GTG>GAG	p.V600E
Pat_02	Post-Resistance	TRY6	154754	37	7	142482242	142482242	Missense_Mutation	SNP	G	A	10	122	c.622G>A	c.(622-624)GGA>AGA	p.G208R
Pat_02	Post-Resistance	ABP1	26	37	7	150554789	150554789	Missense_Mutation	SNP	C	T	101	108	c.1231C>T	c.(1231-1233)CAT>TAT	p.H411Y
Pat_02	Post-Resistance	RP1L1	94137	37	8	10466247	10466247	Missense_Mutation	SNP	C	A	87	137	c.5361G>T	c.(5359-5361)TTG>TTT	p.L1787F
Pat_02	Post-Resistance	FAM86B1	85002	37	8	12042891	12042891	Missense_Mutation	SNP	C	T	6	131	c.784G>A	c.(784-786)GAG>AAG	p.E262K
Pat_02	Post-Resistance	ADAM28	10863	37	8	24187552	24187552	Missense_Mutation	SNP	C	A	6	141	c.1027C>A	c.(1027-1029)CAC>AAC	p.H343N

Pat_02	Post-Resistance	TRIM35	23087	37	8	27145096	27145096	Missense_Mutation	SNP	T	G	7	7	c.1453A>C	c.(1453-1455)ATC>CTC	p.I485L
Pat_02	Post-Resistance	RP1	6101	37	8	55540842	55540842	Missense_Mutation	SNP	C	T	33	71	c.4400C>T	c.(4399-4401)TCT>TTT	p.S1467F
Pat_02	Post-Resistance	UBXN2B	137886	37	8	59345791	59345791	Missense_Mutation	SNP	C	A	6	401	c.412C>A	c.(412-414)CAG>AAG	p.Q138K
Pat_02	Post-Resistance	HNF4G	3174	37	8	76476288	76476288	Missense_Mutation	SNP	C	T	135	193	c.1184C>T	c.(1183-1185)TCA>TTA	p.S395L
Pat_02	Post-Resistance	ZFHX4	79776	37	8	77767909	77767909	Missense_Mutation	SNP	C	T	24	48	c.8617C>T	c.(8617-8619)CCC>TCC	p.P2873S
Pat_02	Post-Resistance	RIMS2	9699	37	8	105001576	105001576	Missense_Mutation	SNP	G	A	6	457	c.2305G>A	c.(2305-2307)GGA>AGA	p.G769R
Pat_02	Post-Resistance	ZFPM2	23414	37	8	106813502	106813502	Missense_Mutation	SNP	G	A	115	175	c.1192G>A	c.(1192-1194)GAA>AAA	p.E398K
Pat_02	Post-Resistance	KLHL38	340359	37	8	124664485	124664485	Missense_Mutation	SNP	G	A	5	302	c.682C>T	c.(682-684)CAC>TAC	p.H228Y
Pat_02	Post-Resistance	KCNQ3	3786	37	8	133492560	133492560	Missense_Mutation	SNP	G	A	3	27	c.220C>T	c.(220-222)CGC>TGC	p.R74C
Pat_02	Post-Resistance	FAM135B	51059	37	8	139164008	139164008	Missense_Mutation	SNP	G	A	4	246	c.2710C>T	c.(2710-2712)CCA>TCA	p.P904S
Pat_02	Post-Resistance	EPPK1	83481	37	8	144943163	144943163	Missense_Mutation	SNP	C	T	4	132	c.4259G>A	c.(4258-4260)CGC>CAC	p.R1420H
Pat_02	Post-Resistance	OPLAH	26873	37	8	145112821	145112821	Missense_Mutation	SNP	C	G	3	50	c.1094G>C	c.(1093-1095)GGC>GCC	p.G365A
Pat_02	Post-Resistance	NFKBIL2	4796	37	8	145659473	145659473	Missense_Mutation	SNP	G	A	4	73	c.3275C>T	c.(3274-3276)GCT>GTT	p.A1092V
Pat_02	Post-Resistance	GPT	2875	37	8	145729775	145729775	Missense_Mutation	SNP	G	A	4	106	c.88G>A	c.(88-90)GTG>ATG	p.V30M
Pat_02	Post-Resistance	PTPRD	5789	37	9	8518175	8518175	Missense_Mutation	SNP	C	T	331	54	c.1216G>A	c.(1216-1218)GAA>AAA	p.E406K
Pat_02	Post-Resistance	KIAA1797	54914	37	9	20881874	20881874	Missense_Mutation	SNP	G	T	4	200	c.2322G>T	c.(2320-2322)TTG>TTT	p.L774F
Pat_02	Post-Resistance	PTENP1	11191	37	9	33676158	33676158	Missense_Mutation	SNP	C	A	38	36	c.390G>T	c.(388-390)AAG>AAT	p.K130N
Pat_02	Post-Resistance	SEMA4D	10507	37	9	92002306	92002306	Missense_Mutation	SNP	C	T	4	146	c.1325G>A	c.(1324-1326)AGC>AAC	p.S442N
Pat_02	Post-Resistance	TEX10	54881	37	9	103066078	103066078	Nonsense_Mutation	SNP	G	A	4	230	c.2512C>T	c.(2512-2514)CGA>TGA	p.R838*
Pat_02	Post-Resistance	ST6GALNAC4	27090	37	9	130677018	130677018	Missense_Mutation	SNP	C	T	54	6	c.115G>A	c.(115-117)GAC>AAC	p.D39N
Pat_02	Post-Resistance	LAMC3	10319	37	9	133911584	133911584	Missense_Mutation	SNP	G	A	4	165	c.841G>A	c.(841-843)GGC>AGC	p.G281S
Pat_02	Post-Resistance	COL5A1	1289	37	9	137688743	137688744	Missense_Mutation	DNP	CC	GT	38	16	.2894_2895CC>G	c.(2893-2895)CCC>CGT	p.P965R
Pat_02	Post-Resistance	CACNA1B	774	37	9	140851279	140851279	Missense_Mutation	SNP	G	A	4	119	c.1243G>A	c.(1243-1245)GTG>ATG	p.V415M
Pat_02	Post-Resistance	CACNA1B	774	37	9	141014668	141014668	Missense_Mutation	SNP	C	T	3	13	c.6082C>T	c.(6082-6084)CGG>TGG	p.R2028W
Pat_02	Post-Resistance	FRMPD4	9758	37	X	12693004	12693004	Missense_Mutation	SNP	C	T	4	174	c.445C>T	c.(445-447)CTC>TTC	p.L149F
Pat_02	Post-Resistance	MAGEB4	4115	37	X	30261045	30261045	Missense_Mutation	SNP	C	T	67	13	c.793C>T	c.(793-795)CCC>TCC	p.P265S
Pat_02	Post-Resistance	CXorf22	170063	37	X	35993821	35993821	Missense_Mutation	SNP	G	A	113	23	c.2504G>A	c.(2503-2505)AGT>AAT	p.S835N
Pat_02	Post-Resistance	CXorf36	79742	37	X	45051207	45051207	Missense_Mutation	SNP	G	A	37	5	c.287C>T	c.(286-288)TCT>TTT	p.S96F
Pat_02	Post-Resistance	SUV39H1	6839	37	X	48558860	48558860	Nonsense_Mutation	SNP	G	T	4	117	c.544G>T	c.(544-546)GAG>TAG	p.E182*
Pat_02	Post-Resistance	PQBP1	10084	37	X	48760219	48760219	Missense_Mutation	SNP	C	T	3	21	c.656C>T	c.(655-657)ACA>ATA	p.T219I
Pat_02	Post-Resistance	CCNB3	85417	37	X	50089666	50089666	Missense_Mutation	SNP	C	T	136	21	c.3670C>T	c.(3670-3672)CGT>TGT	p.R1224C
Pat_02	Post-Resistance	HUWE1	10075	37	X	53571556	53571556	Missense_Mutation	SNP	C	T	3	44	c.11216G>A	c.(11215-11217)CGG>CAG	p.R3739Q
Pat_02	Post-Resistance	EDA2R	60401	37	X	65835823	65835823	Missense_Mutation	SNP	G	A	39	34	c.40C>T	c.(40-42)CGG>TGG	p.R14W
Pat_02	Post-Resistance	ERCC6L	54821	37	X	71427913	71427913	Missense_Mutation	SNP	G	A	4	113	c.704C>T	c.(703-705)ACC>ATC	p.T235I
Pat_02	Post-Resistance	MCART6	401612	37	X	103349781	103349781	Missense_Mutation	SNP	G	A	4	96	c.160C>T	c.(160-162)CGG>TGG	p.R54W
Pat_02	Post-Resistance	AKAP14	158798	37	X	119048672	119048672	Missense_Mutation	SNP	C	T	4	56	c.272C>T	c.(271-273)TCT>TTT	p.S91F
Pat_02	Post-Resistance	DCAF12L2	340578	37	X	125299771	125299771	Missense_Mutation	SNP	G	A	4	32	c.137C>T	c.(136-138)GCG>GTG	p.A46V
Pat_02	Post-Resistance	PASD1	139135	37	X	150844497	150844497	Missense_Mutation	SNP	G	A	133	34	c.2204G>A	c.(2203-2205)GGA>GAA	p.G735E
Pat_02	Post-Resistance	ATP2B3	492	37	X	152845623	152845623	Missense_Mutation	SNP	C	T	151	19	c.3530C>T	c.(3529-3531)CCG>CTG	p.P1177L
Pat_02	Post-Resistance	TAZ	6901	37	X	153649015	153649015	Missense_Mutation	SNP	G	A	4	170	c.718G>A	c.(718-720)GGG>AGG	p.G240R
Pat_02	Post-Resistance	PLXNA3	55558	37	X	153690600	153690600	Missense_Mutation	SNP	C	A	5	121	c.1267C>A	c.(1267-1269)CGC>AGC	p.R423S
Pat_05	Pre-Treatment	SCNN1D	6339	37	1	1226943	1226943	Missense_Mutation	SNP	G	A	9	11	c.1870G>A	c.(1870-1872)GAA>AAA	p.E624K
Pat_05	Pre-Treatment	LRRC47	57470	37	1	3703694	3703694	Missense_Mutation	SNP	C	T	4	157	c.796G>A	c.(796-798)GGG>AGG	p.G266R
Pat_05	Pre-Treatment	DFFB	1677	37	1	3786321	3786321	Missense_Mutation	SNP	A	C	10	37	c.663A>C	c.(661-663)GAA>GAC	p.E221D
Pat_05	Pre-Treatment	PIK3CD	5293	37	1	9783205	9783205	Missense_Mutation	SNP	C	T	277	330	c.2449C>T	c.(2449-2451)CCC>TCC	p.P817S
Pat_05	Pre-Treatment	LOC649330	649330	37	1	12907865	12907865	Missense_Mutation	SNP	C	T	42	256	c.278G>A	c.(277-279)GGA>GAA	p.G93E
Pat_05	Pre-Treatment	CLCNKA	1187	37	1	16351384	16351384	Missense_Mutation	SNP	G	A	66	55	c.356G>A	c.(355-357)GGA>GAA	p.G119E

Pat_05	Pre-Treatment	EIF4G3	8672	37	1	21299593	21299593	Splice_Site	SNP	C	T	36	149	c.326_splice	c.e6-1	p.G109_splice
Pat_05	Pre-Treatment	NBPF3	84224	37	1	21798156	21798156	Missense_Mutation	SNP	C	G	4	287	c.541C>G	c.(541-543)CAG>GAG	p.Q181E
Pat_05	Pre-Treatment	HSPG2	3339	37	1	22172603	22172603	Missense_Mutation	SNP	G	A	5	205	c.8462C>T	c.(8461-8463)CCC>CTC	p.P2821L
Pat_05	Pre-Treatment	PDIK1L	149420	37	1	26448998	26448998	Missense_Mutation	SNP	G	A	6	245	c.956G>A	c.(955-957)CGT>CAT	p.R319H
Pat_05	Pre-Treatment	SFN	2810	37	1	27189752	27189752	Missense_Mutation	SNP	G	A	5	168	c.49G>A	c.(49-51)GAA>AAA	p.E17K
Pat_05	Pre-Treatment	FAM46B	115572	37	1	27333219	27333219	Missense_Mutation	SNP	G	A	6	560	c.494C>T	c.(493-495)ACG>ATG	p.T165M
Pat_05	Pre-Treatment	ZBTB8A	653121	37	1	33058747	33058747	Missense_Mutation	SNP	C	T	71	229	c.215C>T	c.(214-216)TCC>TTC	p.S72F
Pat_05	Pre-Treatment	EIF2C4	192670	37	1	36288575	36288575	Missense_Mutation	SNP	C	T	5	337	c.298C>T	c.(298-300)CGG>TGG	p.R100W
Pat_05	Pre-Treatment	EPHA10	284656	37	1	38227610	38227611	Missense_Mutation	DNP	TG	CT	119	143	c.316_317CA>AG	c.(316-318)CAG>AGG	p.Q106R
Pat_05	Pre-Treatment	MACF1	23499	37	1	39765970	39765970	Missense_Mutation	SNP	G	A	5	274	c.2585G>A	c.(2584-2586)AGT>AAT	p.S862N
Pat_05	Pre-Treatment	TMCO2	127391	37	1	40713883	40713883	Missense_Mutation	SNP	G	A	79	87	c.218G>A	c.(217-219)CGA>CAA	p.R73Q
Pat_05	Pre-Treatment	EBNA1BP2	10969	37	1	43630421	43630421	Nonsense_Mutation	SNP	T	A	82	74	c.763A>T	c.(763-765)AAA>TAA	p.K255*
Pat_05	Pre-Treatment	PTPRF	5792	37	1	44069738	44069738	Missense_Mutation	SNP	G	A	4	123	c.2915G>A	c.(2914-2916)CGC>CAC	p.R972H
Pat_05	Pre-Treatment	CYP4Z1	199974	37	1	47571867	47571867	Missense_Mutation	SNP	G	A	116	109	c.1135G>A	c.(1135-1137)GTA>ATA	p.V379I
Pat_05	Pre-Treatment	TAL1	6886	37	1	47689711	47689711	Missense_Mutation	SNP	C	T	4	299	c.506G>A	c.(505-507)AGG>AAG	p.R169K
Pat_05	Pre-Treatment	INADL	10207	37	1	62614022	62614022	Missense_Mutation	SNP	C	T	150	194	c.5338C>T	c.(5338-5340)CTT>TTT	p.L1780F
Pat_05	Pre-Treatment	ROR1	4919	37	1	64608246	64608246	Missense_Mutation	SNP	C	T	4	236	c.1087C>T	c.(1087-1089)CGC>TGC	p.R363C
Pat_05	Pre-Treatment	RPE65	6121	37	1	68912507	68912507	Missense_Mutation	SNP	C	T	31	191	c.131G>A	c.(130-132)CGA>CAA	p.R44Q
Pat_05	Pre-Treatment	SLC44A5	204962	37	1	75708697	75708697	Splice_Site	SNP	C	T	57	67	c.346_splice	c.e8-1	p.I116_splice
Pat_05	Pre-Treatment	AMPD2	271	37	1	110172946	110172946	Missense_Mutation	SNP	G	A	6	571	c.2237G>A	c.(2236-2238)CGG>CAG	p.R746Q
Pat_05	Pre-Treatment	KCND3	3752	37	1	112525062	112525062	Missense_Mutation	SNP	T	C	47	57	c.287A>G	c.(286-288)AAC>AGC	p.N96S
Pat_05	Pre-Treatment	SYT6	148281	37	1	114680572	114680572	Missense_Mutation	SNP	G	A	4	136	c.361C>T	c.(361-363)CGC>TGC	p.R121C
Pat_05	Pre-Treatment	CD2	914	37	1	117297532	117297532	Missense_Mutation	SNP	G	A	22	66	c.341G>A	c.(340-342)GGA>GAA	p.G114E
Pat_05	Pre-Treatment	HMGCS2	3158	37	1	120302578	120302579	Missense_Mutation	DNP	GG	AA	25	45	c.593_594CC>TT	c.(592-594)GCC>GTT	p.A198V
Pat_05	Pre-Treatment	NOTCH2	4853	37	1	120458306	120458306	Missense_Mutation	SNP	G	A	6	420	c.7039C>T	c.(7039-7041)CGT>TGT	p.R2347C
Pat_05	Pre-Treatment	NOTCH2	4853	37	1	120461053	120461053	Missense_Mutation	SNP	C	T	74	273	c.5905G>A	c.(5905-5907)GAT>AAT	p.D1969N
Pat_05	Pre-Treatment	CA14	23632	37	1	150236277	150236277	Missense_Mutation	SNP	G	A	5	411	c.947G>A	c.(946-948)CGG>CAG	p.R316Q
Pat_05	Pre-Treatment	ECM1	1893	37	1	150482217	150482217	Missense_Mutation	SNP	C	T	143	272	c.202C>T	c.(202-204)CCC>TCC	p.P68S
Pat_05	Pre-Treatment	TCHHL1	126637	37	1	152058383	152058383	Missense_Mutation	SNP	G	T	47	342	c.1775C>A	c.(1774-1776)CCA>CAA	p.P592Q
Pat_05	Pre-Treatment	RPTN	126638	37	1	152129112	152129112	Missense_Mutation	SNP	C	T	353	480	c.463G>A	c.(463-465)GAT>AAT	p.D155N
Pat_05	Pre-Treatment	NES	10763	37	1	156642586	156642586	Missense_Mutation	SNP	G	A	110	199	c.1394C>T	c.(1393-1395)TCC>TTC	p.S465F
Pat_05	Pre-Treatment	ARHGEF11	9826	37	1	156909613	156909613	Missense_Mutation	SNP	T	C	34	80	c.3703A>G	c.(3703-3705)ACA>GCA	p.T1235A
Pat_05	Pre-Treatment	FCRL5	83416	37	1	157508968	157508968	Missense_Mutation	SNP	G	A	32	55	c.1310C>T	c.(1309-1311)TCT>TTT	p.S437F
Pat_05	Pre-Treatment	FCRL4	83417	37	1	157559113	157559113	Missense_Mutation	SNP	C	A	5	169	c.188G>T	c.(187-189)TGG>TTG	p.W63L
Pat_05	Pre-Treatment	FCRL1	115350	37	1	157771292	157771292	Missense_Mutation	SNP	G	A	4	167	c.962C>T	c.(961-963)ACC>ATC	p.T321I
Pat_05	Pre-Treatment	CD1C	911	37	1	158261967	158261967	Nonsense_Mutation	SNP	T	A	170	180	c.422T>A	c.(421-423)TTA>TAA	p.L141*
Pat_05	Pre-Treatment	FCRL6	343413	37	1	159779435	159779435	Missense_Mutation	SNP	C	T	73	105	c.848C>T	c.(847-849)TCC>TTC	p.S283F
Pat_05	Pre-Treatment	IGSF8	93185	37	1	160062228	160062228	Missense_Mutation	SNP	G	A	4	129	c.1570C>T	c.(1570-1572)CCC>TCC	p.P524S
Pat_05	Pre-Treatment	NR1I3	9970	37	1	161200970	161200970	Nonsense_Mutation	SNP	G	A	27	64	c.760C>T	c.(760-762)CGA>TGA	p.R254*
Pat_05	Pre-Treatment	DUSP12	11266	37	1	161722242	161722242	Missense_Mutation	SNP	G	A	271	363	c.662G>A	c.(661-663)TGT>TAT	p.C221Y
Pat_05	Pre-Treatment	TNR	7143	37	1	175331865	175331865	Missense_Mutation	SNP	C	T	87	208	c.2788G>A	c.(2788-2790)GAA>AAA	p.E930K
Pat_05	Pre-Treatment	TNR	7143	37	1	175334197	175334197	Missense_Mutation	SNP	C	A	4	163	c.2536G>T	c.(2536-2538)GCT>TCT	p.A846S
Pat_05	Pre-Treatment	IVNS1ABP	10625	37	1	185274667	185274667	Splice_Site	SNP	C	T	6	465	c.765_splice	c.e8+1	p.Q255_splice
Pat_05	Pre-Treatment	PRG4	10216	37	1	186275983	186275983	Missense_Mutation	SNP	C	A	7	291	c.1132C>A	c.(1132-1134)CCC>ACC	p.P378T
Pat_05	Pre-Treatment	PRG4	10216	37	1	186276169	186276169	Missense_Mutation	SNP	C	A	7	154	c.1318C>A	c.(1318-1320)CCC>ACC	p.P440T
Pat_05	Pre-Treatment	CR1	1378	37	1	207741267	207741267	Missense_Mutation	SNP	G	A	6	654	c.2701G>A	c.(2701-2703)GAC>AAC	p.D901N
Pat_05	Pre-Treatment	GPATCH2	55105	37	1	217622647	217622647	Missense_Mutation	SNP	G	A	6	425	c.1310C>T	c.(1309-1311)ACG>ATG	p.T437M

Pat_05	Pre-Treatment	DISP1	84976	37	1	223178708	223178709	Missense_Mutation	DNP	GG	AA	68	168	.3969_3970GG>A	67-3972)GAGGGC>GAA	p.G1324S
Pat_05	Pre-Treatment	OBSCN	84033	37	1	228557681	228557681	Missense_Mutation	SNP	G	A	5	304	c.20006G>A	c.(20005-20007)CGT>CAT	p.R6669H
Pat_05	Pre-Treatment	MTR	4548	37	1	236979830	236979831	Missense_Mutation	DNP	GG	AA	167	212	c.751_752GG>AA	c.(751-753)GGA>AAA	p.G251K
Pat_05	Pre-Treatment	MTR	4548	37	1	237044081	237044081	Missense_Mutation	SNP	C	T	4	305	c.2621C>T	c.(2620-2622)CCG>CTG	p.P874L
Pat_05	Pre-Treatment	TRIM58	25893	37	1	248039457	248039457	Missense_Mutation	SNP	C	T	84	184	c.1127C>T	c.(1126-1128)TCT>TTT	p.S376F
Pat_05	Pre-Treatment	PTER	9317	37	10	16553071	16553071	Missense_Mutation	SNP	G	A	3	41	c.866G>A	c.(865-867)TGT>TAT	p.C289Y
Pat_05	Pre-Treatment	PTCHD3	374308	37	10	27688070	27688070	Missense_Mutation	SNP	G	A	4	200	c.1457C>T	c.(1456-1458)GCG>GTG	p.A486V
Pat_05	Pre-Treatment	ZNF438	220929	37	10	31139194	31139194	Missense_Mutation	SNP	G	A	4	293	c.140C>T	c.(139-141)ACG>ATG	p.T47M
Pat_05	Pre-Treatment	ITGB1	3688	37	10	33200994	33200994	Missense_Mutation	SNP	C	T	4	186	c.1528G>A	c.(1528-1530)GAA>AAA	p.E510K
Pat_05	Pre-Treatment	ANKRD30A	91074	37	10	37430948	37430948	Missense_Mutation	SNP	C	G	5	116	c.955C>G	c.(955-957)CCA>GCA	p.P319A
Pat_05	Pre-Treatment	RASSF4	83937	37	10	45465703	45465703	Missense_Mutation	SNP	C	T	157	114	c.53C>T	c.(52-54)TCC>TTC	p.S18F
Pat_05	Pre-Treatment	GPRIN2	9721	37	10	46999128	46999128	Missense_Mutation	SNP	G	A	4	29	c.248G>A	c.(247-249)CGA>CAA	p.R83Q
Pat_05	Pre-Treatment	HNRNPH3	3189	37	10	70098394	70098394	Missense_Mutation	SNP	G	A	5	479	c.386G>A	c.(385-387)CGT>CAT	p.R129H
Pat_05	Pre-Treatment	CCAR1	55749	37	10	70551009	70551009	Missense_Mutation	SNP	G	T	4	205	c.3439G>T	c.(3439-3441)GGT>TGT	p.G1147C
Pat_05	Pre-Treatment	HK1	3098	37	10	71129293	71129293	Missense_Mutation	SNP	C	T	98	34	c.788C>T	c.(787-789)GCC>GTC	p.A263V
Pat_05	Pre-Treatment	NPFFR1	64106	37	10	72020400	72020400	Missense_Mutation	SNP	C	T	13	9	c.412G>A	c.(412-414)GAA>AAA	p.E138K
Pat_05	Pre-Treatment	UNC5B	219699	37	10	73050752	73050752	Missense_Mutation	SNP	G	A	6	384	c.1180G>A	c.(1180-1182)GTG>ATG	p.V394M
Pat_05	Pre-Treatment	CDH23	64072	37	10	73537617	73537617	Missense_Mutation	SNP	G	A	4	80	c.5026G>A	c.(5026-5028)GCA>ACA	p.A1676T
Pat_05	Pre-Treatment	SH2D4B	387694	37	10	82363523	82363523	Missense_Mutation	SNP	C	G	4	33	c.832C>G	c.(832-834)CTG>GTG	p.L278V
Pat_05	Pre-Treatment	GPAM	57678	37	10	113926167	113926167	Missense_Mutation	SNP	G	A	79	61	c.1214C>T	c.(1213-1215)TCC>TTC	p.S405F
Pat_05	Pre-Treatment	TCF7L2	6934	37	10	114901057	114901057	Missense_Mutation	SNP	G	A	32	96	c.667G>A	c.(667-669)GAC>AAC	p.D223N
Pat_05	Pre-Treatment	PNLIPRP1	5407	37	10	118352022	118352022	Missense_Mutation	SNP	G	A	78	44	c.299G>A	c.(298-300)GGA>GAA	p.G100E
Pat_05	Pre-Treatment	C10orf84	63877	37	10	120070744	120070744	Nonsense_Mutation	SNP	G	A	4	144	c.625C>T	c.(625-627)CGA>TGA	p.R209*
Pat_05	Pre-Treatment	EIF3A	8661	37	10	120801755	120801755	Missense_Mutation	SNP	T	A	7	465	c.3277A>T	c.(3277-3279)ATG>TTG	p.M1093L
Pat_05	Pre-Treatment	TACC2	10579	37	10	123842215	123842215	Missense_Mutation	SNP	G	C	3	77	c.200G>C	c.(199-201)AGC>ACC	p.S67T
Pat_05	Pre-Treatment	CPXM2	119587	37	10	125516869	125516869	Splice_Site	SNP	C	T	5	263	c.1778_splice	c.e12-1	p.S593_splice
Pat_05	Pre-Treatment	RIC8A	60626	37	11	212899	212899	Missense_Mutation	SNP	C	T	4	76	c.1273C>T	c.(1273-1275)CTC>TTC	p.L425F
Pat_05	Pre-Treatment	ATHL1	80162	37	11	293177	293177	Missense_Mutation	SNP	G	A	5	475	c.1285G>A	c.(1285-1287)GAC>AAC	p.D429N
Pat_05	Pre-Treatment	KRTAP5-4	387267	37	11	1642992	1642992	Missense_Mutation	SNP	C	T	4	130	c.470G>A	c.(469-471)TGT>TAT	p.C157Y
Pat_05	Pre-Treatment	HBBP1	3044	37	11	5264439	5264439	Missense_Mutation	SNP	G	A	33	10	c.47C>T	c.(46-48)TCC>TTC	p.S16F
Pat_05	Pre-Treatment	CNGA4	1262	37	11	6261640	6261640	Missense_Mutation	SNP	C	T	5	149	c.616C>T	c.(616-618)CCC>TCC	p.P206S
Pat_05	Pre-Treatment	SPON1	10418	37	11	14287201	14287201	Missense_Mutation	SNP	G	A	25	10	c.2392G>A	c.(2392-2394)GAG>AAG	p.E798K
Pat_05	Pre-Treatment	TRAF6	7189	37	11	36518686	36518686	Missense_Mutation	SNP	G	A	5	189	c.578C>T	c.(577-579)GCT>GTT	p.A193V
Pat_05	Pre-Treatment	OR4C13	283092	37	11	49974799	49974799	Missense_Mutation	SNP	G	A	97	64	c.825G>A	c.(823-825)ATG>ATA	p.M275I
Pat_05	Pre-Treatment	DDB1	1642	37	11	61068382	61068382	Missense_Mutation	SNP	G	A	4	152	c.3238C>T	c.(3238-3240)CGG>TGG	p.R1080W
Pat_05	Pre-Treatment	DAK	26007	37	11	61106607	61106607	Missense_Mutation	SNP	G	A	5	110	c.263G>A	c.(262-264)AGC>AAC	p.S88N
Pat_05	Pre-Treatment	FADS3	3995	37	11	61646018	61646018	Missense_Mutation	SNP	G	A	4	137	c.713C>T	c.(712-714)GCG>GTG	p.A238V
Pat_05	Pre-Treatment	CDC42BPG	55561	37	11	64599058	64599058	Missense_Mutation	SNP	G	A	4	75	c.3223C>T	c.(3223-3225)CCC>TCC	p.P1075S
Pat_05	Pre-Treatment	MUS81	80198	37	11	65632028	65632028	Missense_Mutation	SNP	G	A	4	166	c.1120G>A	c.(1120-1122)GTC>ATC	p.V374I
Pat_05	Pre-Treatment	SPTBN2	6712	37	11	66468356	66468356	Missense_Mutation	SNP	G	A	3	41	c.3214C>T	c.(3214-3216)CGC>TGC	p.R1072C
Pat_05	Pre-Treatment	PITPNM1	9600	37	11	67262337	67262337	Missense_Mutation	SNP	G	A	6	382	c.2722C>T	c.(2722-2724)CGC>TGC	p.R908C
Pat_05	Pre-Treatment	LRP5	4041	37	11	68191091	68191091	Missense_Mutation	SNP	C	G	4	155	c.3162C>G	c.(3160-3162)AGC>AGG	p.S1054R
Pat_05	Pre-Treatment	LRP5	4041	37	11	68205968	68205968	Missense_Mutation	SNP	C	T	72	39	c.4166C>T	c.(4165-4167)CCC>CTC	p.P1389L
Pat_05	Pre-Treatment	CPT1A	1374	37	11	68562334	68562334	Missense_Mutation	SNP	C	T	4	228	c.817G>A	c.(817-819)GGC>AGC	p.G273S
Pat_05	Pre-Treatment	SHANK2	22941	37	11	70331942	70331942	Missense_Mutation	SNP	C	T	3	39	c.4456G>A	c.(4456-4458)GTC>ATC	p.V1486I
Pat_05	Pre-Treatment	PDE2A	5138	37	11	72299879	72299879	Missense_Mutation	SNP	G	A	5	116	c.1019C>T	c.(1018-1020)ACT>ATT	p.T340I
Pat_05	Pre-Treatment	ARAP1	116985	37	11	72397100	72397100	Missense_Mutation	SNP	G	A	4	118	c.4322C>T	c.(4321-4323)GCG>GTG	p.A1441V

Pat_05	Pre-Treatment	RSF1	51773	37	11	77378399	77378399	Missense_Mutation	SNP	G	A	4	177	c.3889C>T	c.(3889-3891)CGC>TGC	p.R1297C
Pat_05	Pre-Treatment	GAB2	9846	37	11	77937876	77937876	Missense_Mutation	SNP	C	T	4	180	c.842G>A	c.(841-843)AGC>AAC	p.S281N
Pat_05	Pre-Treatment	HEPHL1	341208	37	11	93826703	93826703	Nonsense_Mutation	SNP	G	A	167	119	c.2331G>A	c.(2329-2331)TGG>TGA	p.W777*
Pat_05	Pre-Treatment	CNTN5	53942	37	11	100061987	100061987	Splice_Site	SNP	T	C	32	23	c.1708_splice	c.e14+2	p.E570_splice
Pat_05	Pre-Treatment	YAP1	10413	37	11	102033218	102033218	Missense_Mutation	SNP	C	T	304	208	c.604C>T	c.(604-606)CCC>TCC	p.P202S
Pat_05	Pre-Treatment	SIK2	23235	37	11	111574103	111574103	Nonsense_Mutation	SNP	C	T	4	221	c.904C>T	c.(904-906)CGA>TGA	p.R302*
Pat_05	Pre-Treatment	ALG9	79796	37	11	111728344	111728344	Missense_Mutation	SNP	G	A	4	174	c.682C>T	c.(682-684)CCA>TCA	p.P228S
Pat_05	Pre-Treatment	REXO2	25996	37	11	114314636	114314636	Missense_Mutation	SNP	G	A	4	59	c.290G>A	c.(289-291)TGT>TAT	p.C97Y
Pat_05	Pre-Treatment	FAM55D	54827	37	11	114451024	114451024	Missense_Mutation	SNP	C	A	4	176	c.929G>T	c.(928-930)GGA>GTA	p.G310V
Pat_05	Pre-Treatment	UBE4A	9354	37	11	118244386	118244386	Missense_Mutation	SNP	G	A	4	89	c.1102G>A	c.(1102-1104)GCC>ACC	p.A368T
Pat_05	Pre-Treatment	GRIK4	2900	37	11	120732828	120732828	Missense_Mutation	SNP	C	T	4	173	c.905C>T	c.(904-906)GCG>GTG	p.A302V
Pat_05	Pre-Treatment	NCAPD3	23310	37	11	134038828	134038828	Missense_Mutation	SNP	A	G	45	63	c.3223T>C	c.(3223-3225)TTC>CTC	p.F1075L
Pat_05	Pre-Treatment	WNK1	65125	37	12	988911	988911	Missense_Mutation	SNP	C	T	6	595	c.2546C>T	c.(2545-2547)CCT>CTT	p.P849L
Pat_05	Pre-Treatment	MLF2	8079	37	12	6861201	6861201	Missense_Mutation	SNP	G	A	4	237	c.70C>T	c.(70-72)CGT>TGT	p.R24C
Pat_05	Pre-Treatment	GDF3	9573	37	12	7842689	7842689	Missense_Mutation	SNP	G	A	42	93	c.880C>T	c.(880-882)CAT>TAT	p.H294Y
Pat_05	Pre-Treatment	A2M	2	37	12	9254150	9254150	Missense_Mutation	SNP	G	A	4	145	c.1387C>T	c.(1387-1389)CCC>TCC	p.P463S
Pat_05	Pre-Treatment	BCL2L14	79370	37	12	12232613	12232613	Missense_Mutation	SNP	C	T	5	331	c.374C>T	c.(373-375)TCG>TTG	p.S125L
Pat_05	Pre-Treatment	RPL13AP20	387841	37	12	13028826	13028826	Missense_Mutation	SNP	G	A	5	32	c.394G>A	c.(394-396)GCA>ACA	p.A132T
Pat_05	Pre-Treatment	KIAA1467	57613	37	12	13215874	13215874	Nonsense_Mutation	SNP	C	T	134	552	c.817C>T	c.(817-819)CGA>TGA	p.R273*
Pat_05	Pre-Treatment	ARHGDIB	397	37	12	15095590	15095590	Missense_Mutation	SNP	G	A	83	120	c.472C>T	c.(472-474)CCA>TCA	p.P158S
Pat_05	Pre-Treatment	KIAA0528	9847	37	12	22627777	22627777	Missense_Mutation	SNP	G	A	5	275	c.1951C>T	c.(1951-1953)CGC>TGC	p.R651C
Pat_05	Pre-Treatment	C12orf71	728858	37	12	27234382	27234382	Missense_Mutation	SNP	C	T	5	235	c.535G>A	c.(535-537)GCC>ACC	p.A179T
Pat_05	Pre-Treatment	COL2A1	1280	37	12	48367925	48367925	Missense_Mutation	SNP	G	A	4	159	c.4264C>T	c.(4264-4266)CGG>TGG	p.R1422W
Pat_05	Pre-Treatment	ANP32D	23519	37	12	48866508	48866508	Missense_Mutation	SNP	G	A	42	235	c.61G>A	c.(61-63)GAA>AAA	p.E21K
Pat_05	Pre-Treatment	METTL7A	25840	37	12	51319096	51319096	Missense_Mutation	SNP	G	A	4	83	c.275G>A	c.(274-276)TGC>TAC	p.C92Y
Pat_05	Pre-Treatment	ITGA5	3678	37	12	54798495	54798495	Missense_Mutation	SNP	C	T	29	133	c.1409G>A	c.(1408-1410)GGA>GAA	p.G470E
Pat_05	Pre-Treatment	PDE1B	5153	37	12	54943765	54943765	Missense_Mutation	SNP	T	G	9	38	c.109T>G	c.(109-111)TCT>GCT	p.S37A
Pat_05	Pre-Treatment	OR6C2	341416	37	12	55846399	55846399	Missense_Mutation	SNP	G	A	91	120	c.402G>A	c.(400-402)ATG>ATA	p.M134I
Pat_05	Pre-Treatment	SPRYD4	283377	37	12	56863096	56863096	Missense_Mutation	SNP	G	A	6	589	c.359G>A	c.(358-360)CGT>CAT	p.R120H
Pat_05	Pre-Treatment	NXPH4	11247	37	12	57619184	57619184	Missense_Mutation	SNP	G	A	20	68	c.581G>A	c.(580-582)GGG>GAG	p.G194E
Pat_05	Pre-Treatment	OS9	10956	37	12	58089596	58089596	Missense_Mutation	SNP	G	A	163	202	c.373G>A	c.(373-375)GGA>AGA	p.G125R
Pat_05	Pre-Treatment	FAM19A2	338811	37	12	62147474	62147474	Missense_Mutation	SNP	C	T	48	202	c.313G>A	c.(313-315)GAA>AAA	p.E105K
Pat_05	Pre-Treatment	TRHDE	29953	37	12	72866886	72866886	Missense_Mutation	SNP	G	A	6	601	c.1375G>A	c.(1375-1377)GTG>ATG	p.V459M
Pat_05	Pre-Treatment	SYT1	6857	37	12	79842697	79842697	Splice_Site	SNP	G	A	88	127	c.1063_splice	c.e12-1	p.K355_splice
Pat_05	Pre-Treatment	CEP290	80184	37	12	88452799	88452799	Splice_Site	SNP	T	C	3	53	c.6646_splice	c.e49-1	p.E2216_splice
Pat_05	Pre-Treatment	C12orf12	196477	37	12	91347894	91347894	Missense_Mutation	SNP	C	T	4	140	c.626G>A	c.(625-627)CGT>CAT	p.R209H
Pat_05	Pre-Treatment	UTP20	27340	37	12	101736806	101736806	Missense_Mutation	SNP	G	A	80	112	c.4384G>A	c.(4384-4386)GAA>AAA	p.E1462K
Pat_05	Pre-Treatment	C12orf51	283450	37	12	112654950	112654950	Missense_Mutation	SNP	G	A	3	52	c.5858C>T	c.(5857-5859)GCC>GTC	p.A1953V
Pat_05	Pre-Treatment	C12orf51	283450	37	12	112696965	112696965	Missense_Mutation	SNP	G	A	5	344	c.1682C>T	c.(1681-1683)GCG>GTG	p.A561V
Pat_05	Pre-Treatment	RNFT2	84900	37	12	117188100	117188100	Nonsense_Mutation	SNP	C	T	27	18	c.538C>T	c.(538-540)CAG>TAG	p.Q180*
Pat_05	Pre-Treatment	CCDC60	160777	37	12	119866487	119866487	Splice_Site	SNP	G	A	6	14	c.91_splice	c.e2-1	p.V31_splice
Pat_05	Pre-Treatment	COX6A1	1337	37	12	120875979	120875979	Missense_Mutation	SNP	G	A	4	89	c.50G>A	c.(49-51)CGC>CAC	p.R17H
Pat_05	Pre-Treatment	ACADS	35	37	12	121176677	121176677	Missense_Mutation	SNP	C	T	4	198	c.988C>T	c.(988-990)CGC>TGC	p.R330C
Pat_05	Pre-Treatment	PITPNM2	57605	37	12	123482049	123482049	Missense_Mutation	SNP	C	T	4	154	c.1295G>A	c.(1294-1296)GGC>GAC	p.G432D
Pat_05	Pre-Treatment	DNAH10	196385	37	12	124408932	124408932	Missense_Mutation	SNP	G	A	16	38	c.11365G>A	c.(11365-11367)GGG>AGG	p.G3789R
Pat_05	Pre-Treatment	SFRS8	6433	37	12	132195896	132195896	Missense_Mutation	SNP	C	T	5	203	c.122C>T	c.(121-123)GCC>GTC	p.A41V
Pat_05	Pre-Treatment	POLE	5426	37	12	133210876	133210876	Missense_Mutation	SNP	G	A	4	55	c.5900C>T	c.(5899-5901)GCG>GTG	p.A1967V

Pat_05	Pre-Treatment	SPATA13	221178	37	13	24863146	24863146	Nonsense_Mutation	SNP	C	T	4	162	c.802C>T	c.(802-804)CGA>TGA	p.R268*
Pat_05	Pre-Treatment	TRPC4	7223	37	13	38211066	38211066	Missense_Mutation	SNP	C	T	80	86	c.2908G>A	c.(2908-2910)GAA>AAA	p.E970K
Pat_05	Pre-Treatment	LHFP	10186	37	13	40175295	40175295	Missense_Mutation	SNP	G	A	4	107	c.59C>T	c.(58-60)GCT>GTT	p.A20V
Pat_05	Pre-Treatment	ELF1	1997	37	13	41515372	41515372	Missense_Mutation	SNP	G	A	6	392	c.941C>T	c.(940-942)TCG>TTG	p.S314L
Pat_05	Pre-Treatment	KIAA0564	23078	37	13	42164868	42164868	Missense_Mutation	SNP	G	C	4	288	c.5020C>G	c.(5020-5022)CAA>GAA	p.Q1674E
Pat_05	Pre-Treatment	COG3	83548	37	13	46070347	46070347	Missense_Mutation	SNP	G	A	4	272	c.1388G>A	c.(1387-1389)CGG>CAG	p.R463Q
Pat_05	Pre-Treatment	ATP7B	540	37	13	52518298	52518298	Missense_Mutation	SNP	C	T	49	40	c.3190G>A	c.(3190-3192)GAG>AAG	p.E1064K
Pat_05	Pre-Treatment	SCEL	8796	37	13	78173856	78173856	Missense_Mutation	SNP	G	A	3	69	c.890G>A	c.(889-891)AGT>AAT	p.S297N
Pat_05	Pre-Treatment	POTEG	404785	37	14	19566058	19566058	Missense_Mutation	SNP	G	A	4	234	c.1102G>A	c.(1102-1104)GTC>ATC	p.V368I
Pat_05	Pre-Treatment	MYH6	4624	37	14	23873585	23873586	Missense_Mutation	DNP	CC	TT	65	47	c.654_655GG>AA	652-657)GAGGAC>GAAA	p.D219N
Pat_05	Pre-Treatment	FAM158A	51016	37	14	24608377	24608377	Missense_Mutation	SNP	G	A	6	541	c.469C>T	c.(469-471)CGG>TGG	p.R157W
Pat_05	Pre-Treatment	RIPK3	11035	37	14	24807650	24807650	Missense_Mutation	SNP	A	G	39	172	c.595T>C	c.(595-597)TCC>CCC	p.S199P
Pat_05	Pre-Treatment	NFATC4	4776	37	14	24843005	24843005	Missense_Mutation	SNP	G	A	5	96	c.1664G>A	c.(1663-1665)CGG>CAG	p.R555Q
Pat_05	Pre-Treatment	RALGAPA1	253959	37	14	36211615	36211615	Missense_Mutation	SNP	C	T	7	7	c.1408G>A	c.(1408-1410)GAC>AAC	p.D470N
Pat_05	Pre-Treatment	MIA2	117153	37	14	39717268	39717268	Missense_Mutation	SNP	C	T	96	73	c.1490C>T	c.(1489-1491)ACT>ATT	p.T497I
Pat_05	Pre-Treatment	MIA2	117153	37	14	39722048	39722048	Nonsense_Mutation	SNP	C	G	55	112	c.1664C>G	c.(1663-1665)TCA>TGA	p.S555*
Pat_05	Pre-Treatment	SDCCAG1	9147	37	14	50269427	50269427	Missense_Mutation	SNP	G	A	25	54	c.1934C>T	c.(1933-1935)CCT>CTT	p.P645L
Pat_05	Pre-Treatment	SIX1	6495	37	14	61113294	61113294	Missense_Mutation	SNP	C	T	45	22	c.562G>A	c.(562-564)GAG>AAG	p.E188K
Pat_05	Pre-Treatment	SPTB	6710	37	14	65220427	65220427	Missense_Mutation	SNP	C	T	4	141	c.6430G>A	c.(6430-6432)GAT>AAT	p.D2144N
Pat_05	Pre-Treatment	ZFYVE26	23503	37	14	68260920	68260920	Missense_Mutation	SNP	C	T	320	175	c.2369G>A	c.(2368-2370)AGT>AAT	p.S790N
Pat_05	Pre-Treatment	PCNX	22990	37	14	71462618	71462618	Missense_Mutation	SNP	G	A	4	245	c.2605G>A	c.(2605-2607)GGT>AGT	p.G869S
Pat_05	Pre-Treatment	CRIP1	1396	37	14	105954671	105954671	Missense_Mutation	SNP	G	A	4	155	c.139G>A	c.(139-141)GAA>AAA	p.E47K
Pat_05	Pre-Treatment	THBS1	7057	37	15	39885837	39885837	Missense_Mutation	SNP	G	A	6	230	c.3235G>A	c.(3235-3237)GCC>ACC	p.A1079T
Pat_05	Pre-Treatment	EIF2AK4	440275	37	15	40284403	40284403	Missense_Mutation	SNP	G	A	45	150	c.2659G>A	c.(2659-2661)GGA>AGA	p.G887R
Pat_05	Pre-Treatment	CDAN1	146059	37	15	43026214	43026214	Missense_Mutation	SNP	G	A	36	130	c.1289C>T	c.(1288-1290)GCT>GTT	p.A430V
Pat_05	Pre-Treatment	TP53BP1	7158	37	15	43714147	43714147	Missense_Mutation	SNP	C	T	74	97	c.3991G>A	c.(3991-3993)GGG>AGG	p.G1331R
Pat_05	Pre-Treatment	SLC12A1	6557	37	15	48521475	48521475	Missense_Mutation	SNP	G	A	3	29	c.814G>A	c.(814-816)GTT>ATT	p.V272I
Pat_05	Pre-Treatment	FBN1	2200	37	15	48766757	48766757	Missense_Mutation	SNP	G	A	5	349	c.4055C>T	c.(4054-4056)CCC>CTC	p.P1352L
Pat_05	Pre-Treatment	MAP2K1	5604	37	15	66777460	66777460	Missense_Mutation	SNP	G	T	4	108	c.826G>T	c.(826-828)GGG>TGG	p.G276W
Pat_05	Pre-Treatment	TLE3	7090	37	15	70344778	70344778	Missense_Mutation	SNP	T	C	3	116	c.2069A>G	c.(2068-2070)AAG>AGG	p.K690R
Pat_05	Pre-Treatment	MYO9A	4649	37	15	72338507	72338507	Missense_Mutation	SNP	C	T	4	318	c.398G>A	c.(397-399)AGG>AAG	p.R133K
Pat_05	Pre-Treatment	TMEM202	338949	37	15	72700185	72700185	Missense_Mutation	SNP	C	T	81	46	c.773C>T	c.(772-774)TCT>TTT	p.S258F
Pat_05	Pre-Treatment	CYP1A2	1544	37	15	75042776	75042776	Missense_Mutation	SNP	G	A	4	252	c.697G>A	c.(697-699)GGG>AGG	p.G233R
Pat_05	Pre-Treatment	PSTPIP1	9051	37	15	77329473	77329473	Missense_Mutation	SNP	G	A	3	56	c.1207G>A	c.(1207-1209)GGG>AGG	p.G403R
Pat_05	Pre-Treatment	AKAP13	11214	37	15	86124402	86124402	Missense_Mutation	SNP	G	A	4	170	c.3103G>A	c.(3103-3105)GCA>ACA	p.A1035T
Pat_05	Pre-Treatment	ZNF710	374655	37	15	90622960	90622960	Nonsense_Mutation	SNP	G	T	34	211	c.1894G>T	c.(1894-1896)GAG>TAG	p.E632*
Pat_05	Pre-Treatment	LRRK1	79705	37	15	101523854	101523854	Missense_Mutation	SNP	C	T	4	154	c.383C>T	c.(382-384)GCG>GTG	p.A128V
Pat_05	Pre-Treatment	LRRK1	79705	37	15	101586289	101586289	Missense_Mutation	SNP	G	A	4	159	c.3067G>A	c.(3067-3069)GTT>ATT	p.V1023I
Pat_05	Pre-Treatment	TELO2	9894	37	16	1555588	1555588	Missense_Mutation	SNP	C	A	4	54	c.2020C>A	c.(2020-2022)CAG>AAG	p.Q674K
Pat_05	Pre-Treatment	MAPK8IP3	23162	37	16	1810460	1810460	Missense_Mutation	SNP	G	A	4	202	c.1381G>A	c.(1381-1383)GAG>AAG	p.E461K
Pat_05	Pre-Treatment	SPSB3	90864	37	16	1828154	1828154	Missense_Mutation	SNP	G	A	16	60	c.473C>T	c.(472-474)CCC>CTC	p.P158L
Pat_05	Pre-Treatment	RPL3L	6123	37	16	2002897	2002897	Missense_Mutation	SNP	G	A	4	259	c.343C>T	c.(343-345)CGG>TGG	p.R115W
Pat_05	Pre-Treatment	CASKIN1	57524	37	16	2237368	2237368	Missense_Mutation	SNP	G	A	4	159	c.712C>T	c.(712-714)CGG>TGG	p.R238W
Pat_05	Pre-Treatment	PRSS22	64063	37	16	2903228	2903228	Missense_Mutation	SNP	C	T	4	92	c.820G>A	c.(820-822)GTC>ATC	p.V274I
Pat_05	Pre-Treatment	PRSS22	64063	37	16	2903246	2903246	Missense_Mutation	SNP	C	T	26	46	c.802G>A	c.(802-804)GAG>AAG	p.E268K
Pat_05	Pre-Treatment	MMP25	64386	37	16	3107383	3107383	Missense_Mutation	SNP	C	T	5	178	c.911C>T	c.(910-912)TCG>TTG	p.S304L
Pat_05	Pre-Treatment	TIGD7	91151	37	16	3350332	3350332	Missense_Mutation	SNP	C	T	5	239	c.283G>A	c.(283-285)GGT>AGT	p.G95S

Pat_05	Pre-Treatment	CREBBP	1387	37	16	3819211	3819212	Missense_Mutation	DNP	GG	AA	88	99	.3023_3024CC>T	c.(3022-3024)CCC>CTT	p.P1008L
Pat_05	Pre-Treatment	GRIN2A	2903	37	16	9857613	9857613	Missense_Mutation	SNP	C	T	17	23	c.3788G>A	c.(3787-3789)GGG>GAG	p.G1263E
Pat_05	Pre-Treatment	GRIN2A	2903	37	16	9934962	9934962	Splice_Site	SNP	C	A	21	99	c.1329_splice	c.e6-1	p.N443_splice
Pat_05	Pre-Treatment	ATF7IP2	80063	37	16	10524659	10524659	Missense_Mutation	SNP	C	T	4	127	c.182C>T	c.(181-183)ACG>ATG	p.T61M
Pat_05	Pre-Treatment	KIAA0430	9665	37	16	15716945	15716945	Missense_Mutation	SNP	G	A	4	281	c.2306C>T	c.(2305-2307)CCG>CTG	p.P769L
Pat_05	Pre-Treatment	TMC7	79905	37	16	19027793	19027793	Missense_Mutation	SNP	G	A	5	155	c.333G>A	c.(331-333)ATG>ATA	p.M111I
Pat_05	Pre-Treatment	TMC5	79838	37	16	19451823	19451823	Missense_Mutation	SNP	C	T	89	135	c.463C>T	c.(463-465)CAT>TAT	p.H155Y
Pat_05	Pre-Treatment	DCUN1D3	123879	37	16	20871519	20871519	Missense_Mutation	SNP	G	A	6	497	c.604C>T	c.(604-606)CGG>TGG	p.R202W
Pat_05	Pre-Treatment	POLR3E	55718	37	16	22320292	22320292	Missense_Mutation	SNP	G	A	4	202	c.212G>A	c.(211-213)CGC>CAC	p.R71H
Pat_05	Pre-Treatment	PRKCB	5579	37	16	24104192	24104192	Missense_Mutation	SNP	C	T	44	168	c.610C>T	c.(610-612)CCC>TCC	p.P204S
Pat_05	Pre-Treatment	SRCAP	10847	37	16	30748905	30748905	Missense_Mutation	SNP	C	T	4	309	c.7544C>T	c.(7543-7545)CCA>CTA	p.P2515L
Pat_05	Pre-Treatment	ZNF646	9726	37	16	31088970	31088970	Missense_Mutation	SNP	C	T	28	29	c.1325C>T	c.(1324-1326)CCC>CTC	p.P442L
Pat_05	Pre-Treatment	CHD9	80205	37	16	53348813	53348813	Missense_Mutation	SNP	C	T	140	143	c.7441C>T	c.(7441-7443)CCT>TCT	p.P2481S
Pat_05	Pre-Treatment	RBL2	5934	37	16	53513130	53513130	Missense_Mutation	SNP	G	A	4	192	c.2768G>A	c.(2767-2769)CGG>CAG	p.R923Q
Pat_05	Pre-Treatment	RFWD3	55159	37	16	74683038	74683038	Missense_Mutation	SNP	G	A	163	164	c.784C>T	c.(784-786)CCC>TCC	p.P262S
Pat_05	Pre-Treatment	PKD1L2	114780	37	16	81167302	81167302	Missense_Mutation	SNP	G	A	21	32	c.5723C>T	c.(5722-5724)CCC>CTC	p.P1908L
Pat_05	Pre-Treatment	PLCG2	5336	37	16	81888165	81888165	Missense_Mutation	SNP	T	A	65	288	c.310T>A	c.(310-312)TTC>ATC	p.F104I
Pat_05	Pre-Treatment	ZCCHC14	23174	37	16	87445340	87445340	Missense_Mutation	SNP	G	A	3	49	c.2576C>T	c.(2575-2577)ACC>ATC	p.T859I
Pat_05	Pre-Treatment	CAMKK1	84254	37	17	3773120	3773120	Missense_Mutation	SNP	G	A	48	170	c.1187C>T	c.(1186-1188)ACG>ATG	p.T396M
Pat_05	Pre-Treatment	MYBBP1A	10514	37	17	4452718	4452718	Missense_Mutation	SNP	G	A	4	156	c.1339C>T	c.(1339-1341)CGG>TGG	p.R447W
Pat_05	Pre-Treatment	CAMTA2	23125	37	17	4883851	4883851	Missense_Mutation	SNP	G	A	6	410	c.766C>T	c.(766-768)CCC>TCC	p.P256S
Pat_05	Pre-Treatment	FBXO39	162517	37	17	6684059	6684059	Missense_Mutation	SNP	G	A	19	19	c.872G>A	c.(871-873)CGG>CAG	p.R291Q
Pat_05	Pre-Treatment	ACAP1	9744	37	17	7246739	7246739	Missense_Mutation	SNP	G	A	4	169	c.386G>A	c.(385-387)CGG>CAG	p.R129Q
Pat_05	Pre-Treatment	SUPT6H	6830	37	17	27023987	27023987	Missense_Mutation	SNP	C	T	177	291	c.4096C>T	c.(4096-4098)CAC>TAC	p.H1366Y
Pat_05	Pre-Treatment	LRRC37B	114659	37	17	30349585	30349585	Missense_Mutation	SNP	C	T	70	129	c.1420C>T	c.(1420-1422)CAT>TAT	p.H474Y
Pat_05	Pre-Treatment	LRRC37B	114659	37	17	30361940	30361940	Missense_Mutation	SNP	G	A	4	161	c.1988G>A	c.(1987-1989)CGC>CAC	p.R663H
Pat_05	Pre-Treatment	SRCIN1	80725	37	17	36717729	36717729	Missense_Mutation	SNP	G	A	4	80	c.1670C>T	c.(1669-1671)CCG>CTG	p.P557L
Pat_05	Pre-Treatment	KRT27	342574	37	17	38933948	38933948	Missense_Mutation	SNP	T	G	207	382	c.1009A>C	c.(1009-1011)AGT>CGT	p.S337R
Pat_05	Pre-Treatment	STAT5B	6777	37	17	40376882	40376882	Missense_Mutation	SNP	G	A	4	188	c.290C>T	c.(289-291)ACG>ATG	p.T97M
Pat_05	Pre-Treatment	BRCA1	672	37	17	41244316	41244316	Missense_Mutation	SNP	G	A	144	270	c.3232C>T	c.(3232-3234)CCA>TCA	p.P1078S
Pat_05	Pre-Treatment	RUNDC3A	10900	37	17	42390577	42390577	Missense_Mutation	SNP	G	A	4	169	c.329G>A	c.(328-330)AGC>AAC	p.S110N
Pat_05	Pre-Treatment	FMNL1	752	37	17	43320500	43320500	Missense_Mutation	SNP	G	A	117	219	c.2026G>A	c.(2026-2028)GAT>AAT	p.D676N
Pat_05	Pre-Treatment	WNT9B	7484	37	17	44953705	44953705	Missense_Mutation	SNP	G	A	4	95	c.695G>A	c.(694-696)CGT>CAT	p.R232H
Pat_05	Pre-Treatment	ITGB3	3690	37	17	45376743	45376743	Missense_Mutation	SNP	C	T	6	656	c.1760C>T	c.(1759-1761)ACC>ATC	p.T587I
Pat_05	Pre-Treatment	TBX21	30009	37	17	45822470	45822470	Missense_Mutation	SNP	G	A	3	51	c.1346G>A	c.(1345-1347)CGC>CAC	p.R449H
Pat_05	Pre-Treatment	OSBPL7	114881	37	17	45895918	45895918	Missense_Mutation	SNP	C	T	4	180	c.434G>A	c.(433-435)CGC>CAC	p.R145H
Pat_05	Pre-Treatment	CACNA1G	8913	37	17	48650037	48650037	Missense_Mutation	SNP	G	A	8	13	c.869G>A	c.(868-870)GGG>GAG	p.G290E
Pat_05	Pre-Treatment	SPAG9	9043	37	17	49079164	49079164	Missense_Mutation	SNP	C	T	167	263	c.1519G>A	c.(1519-1521)GAA>AAA	p.E507K
Pat_05	Pre-Treatment	OR4D1	26689	37	17	56232773	56232773	Missense_Mutation	SNP	C	T	69	142	c.259C>T	c.(259-261)CAT>TAT	p.H87Y
Pat_05	Pre-Treatment	TEX14	56155	37	17	56663170	56663170	Missense_Mutation	SNP	C	T	6	484	c.3080G>A	c.(3079-3081)AGC>AAC	p.S1027N
Pat_05	Pre-Treatment	TBC1D3P2	440452	37	17	60351236	60351236	Nonsense_Mutation	SNP	G	A	72	229	c.79C>T	c.(79-81)CGA>TGA	p.R27*
Pat_05	Pre-Treatment	ERN1	2081	37	17	62131707	62131707	Missense_Mutation	SNP	G	A	4	68	c.1856C>T	c.(1855-1857)TCG>TTG	p.S619L
Pat_05	Pre-Treatment	TEX2	55852	37	17	62291312	62291312	Missense_Mutation	SNP	G	A	8	754	c.266C>T	c.(265-267)GCT>GTT	p.A89V
Pat_05	Pre-Treatment	MRPL38	64978	37	17	73897876	73897877	Nonsense_Mutation	DNP	GG	AA	61	145	c.507_508CC>TT	505-510)CCCCGA>CCTT	p.R170*
Pat_05	Pre-Treatment	QRICH2	84074	37	17	74288788	74288788	Missense_Mutation	SNP	C	A	6	216	c.1522G>T	c.(1522-1524)GGC>TGC	p.G508C
Pat_05	Pre-Treatment	SYNGR2	9144	37	17	76166913	76166913	Missense_Mutation	SNP	G	A	6	605	c.115G>A	c.(115-117)GTG>ATG	p.V39M
Pat_05	Pre-Treatment	PGS1	9489	37	17	76399780	76399780	Missense_Mutation	SNP	G	A	4	235	c.1012G>A	c.(1012-1014)GCA>ACA	p.A338T

Pat_05	Pre-Treatment	BAHCC1	57597	37	17	79430706	79430706	Missense_Mutation	SNP	G	A	5	163	c.7690G>A	c.(7690-7692)GTG>ATG	p.V2564M
Pat_05	Pre-Treatment	KIAA0802	23255	37	18	8783903	8783903	Missense_Mutation	SNP	G	A	4	213	c.793G>A	c.(793-795)GGT>AGT	p.G265S
Pat_05	Pre-Treatment	MC5R	4161	37	18	13826417	13826417	Missense_Mutation	SNP	G	A	4	287	c.653G>A	c.(652-654)CGG>CAG	p.R218Q
Pat_05	Pre-Treatment	HAUS1	115106	37	18	43704860	43704860	Splice_Site	SNP	G	A	4	149	c.738_splice	c.e7+1	p.P246_splice
Pat_05	Pre-Treatment	C18orf25	147339	37	18	43796277	43796277	Missense_Mutation	SNP	G	A	4	141	c.431G>A	c.(430-432)CGA>CAA	p.R144Q
Pat_05	Pre-Treatment	ME2	4200	37	18	48442612	48442612	Missense_Mutation	SNP	A	C	84	169	c.467A>C	c.(466-468)AAG>ACG	p.K156T
Pat_05	Pre-Treatment	MBD2	8932	37	18	51731459	51731459	Missense_Mutation	SNP	C	T	38	130	c.611G>A	c.(610-612)AGC>AAC	p.S204N
Pat_05	Pre-Treatment	KIAA1468	57614	37	18	59949653	59949653	Missense_Mutation	SNP	G	A	6	422	c.3229G>A	c.(3229-3231)GCA>ACA	p.A1077T
Pat_05	Pre-Treatment	NETO1	81832	37	18	70423314	70423314	Missense_Mutation	SNP	C	T	111	104	c.937G>A	c.(937-939)GGA>AGA	p.G313R
Pat_05	Pre-Treatment	DAPK3	1613	37	19	3960100	3960100	Missense_Mutation	SNP	C	T	8	531	c.785G>A	c.(784-786)CGG>CAG	p.R262Q
Pat_05	Pre-Treatment	FSD1	79187	37	19	4306225	4306225	Missense_Mutation	SNP	G	A	5	238	c.142G>A	c.(142-144)GAA>AAA	p.E48K
Pat_05	Pre-Treatment	PLIN4	729359	37	19	4513325	4513325	Missense_Mutation	SNP	G	T	59	223	c.605C>A	c.(604-606)GCC>GAC	p.A202D
Pat_05	Pre-Treatment	PNPLA6	10908	37	19	7605827	7605827	Missense_Mutation	SNP	C	T	4	81	c.841C>T	c.(841-843)CGG>TGG	p.R281W
Pat_05	Pre-Treatment	XAB2	56949	37	19	7684735	7684735	Missense_Mutation	SNP	C	T	4	166	c.2404G>A	c.(2404-2406)GCC>ACC	p.A802T
Pat_05	Pre-Treatment	CLEC4M	10332	37	19	7833780	7833780	Missense_Mutation	SNP	C	T	36	187	c.1037C>T	c.(1036-1038)GCG>GTG	p.A346V
Pat_05	Pre-Treatment	ADAMTS10	81794	37	19	8670190	8670190	Missense_Mutation	SNP	C	T	6	9	c.142G>A	c.(142-144)GAC>AAC	p.D48N
Pat_05	Pre-Treatment	MUC16	94025	37	19	9061896	9061896	Missense_Mutation	SNP	G	C	58	59	c.25550C>G	c.(25549-25551)ACA>AGA	p.T8517R
Pat_05	Pre-Treatment	CARM1	10498	37	19	11018769	11018769	Missense_Mutation	SNP	G	A	6	353	c.401G>A	c.(400-402)CGG>CAG	p.R134Q
Pat_05	Pre-Treatment	ZNF844	284391	37	19	12187307	12187307	Missense_Mutation	SNP	G	C	4	145	c.1372G>C	c.(1372-1374)GAT>CAT	p.D458H
Pat_05	Pre-Treatment	ZNF443	10224	37	19	12542199	12542199	Missense_Mutation	SNP	G	A	14	354	c.787C>T	c.(787-789)CCT>TCT	p.P263S
Pat_05	Pre-Treatment	ZNF709	163051	37	19	12577561	12577561	Missense_Mutation	SNP	G	A	53	62	c.107C>T	c.(106-108)ACC>ATC	p.T36I
Pat_05	Pre-Treatment	ZNF490	57474	37	19	12692177	12692177	Nonsense_Mutation	SNP	G	A	17	73	c.712C>T	c.(712-714)CGA>TGA	p.R238*
Pat_05	Pre-Treatment	SYDE1	85360	37	19	15221541	15221541	Missense_Mutation	SNP	C	G	2	9	c.1285C>G	c.(1285-1287)CTG>GTG	p.L429V
Pat_05	Pre-Treatment	TMEM38A	79041	37	19	16799109	16799109	Missense_Mutation	SNP	C	T	4	73	c.827C>T	c.(826-828)TCG>TTG	p.S276L
Pat_05	Pre-Treatment	NWD1	284434	37	19	16875863	16875863	Missense_Mutation	SNP	C	T	29	104	c.2270C>T	c.(2269-2271)TCC>TTC	p.S757F
Pat_05	Pre-Treatment	ARRDC2	27106	37	19	18120628	18120628	Missense_Mutation	SNP	G	A	4	277	c.629G>A	c.(628-630)GGC>GAC	p.G210D
Pat_05	Pre-Treatment	ZNF431	170959	37	19	21366278	21366278	Missense_Mutation	SNP	A	C	26	19	c.1172A>C	c.(1171-1173)AAA>ACA	p.K391T
Pat_05	Pre-Treatment	ZNF676	163223	37	19	22362924	22362924	Missense_Mutation	SNP	G	C	3	122	c.1595C>G	c.(1594-1596)CCC>CGC	p.P532R
Pat_05	Pre-Treatment	ZNF99	7652	37	19	22939472	22939472	Missense_Mutation	SNP	A	G	3	61	c.2699T>C	c.(2698-2700)TTC>TCC	p.F900S
Pat_05	Pre-Treatment	LGI4	163175	37	19	35625512	35625512	Missense_Mutation	SNP	C	T	11	21	c.73G>A	c.(73-75)GGA>AGA	p.G25R
Pat_05	Pre-Treatment	ARHGAP33	115703	37	19	36268739	36268739	Nonsense_Mutation	SNP	C	T	4	226	c.118C>T	c.(118-120)CGA>TGA	p.R40*
Pat_05	Pre-Treatment	LRFN3	79414	37	19	36431189	36431189	Missense_Mutation	SNP	G	A	3	27	c.862G>A	c.(862-864)GAG>AAG	p.E288K
Pat_05	Pre-Treatment	COX7A1	1346	37	19	36642432	36642432	Missense_Mutation	SNP	G	A	4	264	c.119C>T	c.(118-120)CCG>CTG	p.P40L
Pat_05	Pre-Treatment	ZNF569	148266	37	19	37903561	37903561	Missense_Mutation	SNP	A	G	47	219	c.1999T>C	c.(1999-2001)TGT>CGT	p.C667R
Pat_05	Pre-Treatment	ZNF793	390927	37	19	38023312	38023312	Missense_Mutation	SNP	C	T	4	55	c.70C>T	c.(70-72)CGG>TGG	p.R24W
Pat_05	Pre-Treatment	ZNF571	51276	37	19	38055543	38055543	Missense_Mutation	SNP	C	G	20	22	c.1787G>C	c.(1786-1788)AGA>ACA	p.R596T
Pat_05	Pre-Treatment	RYR1	6261	37	19	38993310	38993310	Missense_Mutation	SNP	G	A	5	151	c.7778G>A	c.(7777-7779)CGT>CAT	p.R2593H
Pat_05	Pre-Treatment	ATP1A3	478	37	19	42474393	42474393	Missense_Mutation	SNP	G	A	4	104	c.2486C>T	c.(2485-2487)CCG>CTG	p.P829L
Pat_05	Pre-Treatment	ATP1A3	478	37	19	42482889	42482889	Missense_Mutation	SNP	G	A	4	190	c.1499C>T	c.(1498-1500)GCC>GTC	p.A500V
Pat_05	Pre-Treatment	ATP1A3	478	37	19	42486240	42486240	Missense_Mutation	SNP	C	T	4	117	c.1012G>A	c.(1012-1014)GCC>ACC	p.A338T
Pat_05	Pre-Treatment	XRCC1	7515	37	19	44048333	44048333	Missense_Mutation	SNP	G	A	3	41	c.1675C>T	c.(1675-1677)CGG>TGG	p.R559W
Pat_05	Pre-Treatment	IRGC	56269	37	19	44223896	44223896	Missense_Mutation	SNP	G	A	3	35	c.1186G>A	c.(1186-1188)GCC>ACC	p.A396T
Pat_05	Pre-Treatment	ZNF45	7596	37	19	44418575	44418575	Missense_Mutation	SNP	C	T	4	83	c.1013G>A	c.(1012-1014)GGC>GAC	p.G338D
Pat_05	Pre-Treatment	EXOC3L2	90332	37	19	45731020	45731020	Missense_Mutation	SNP	G	A	3	43	c.304C>T	c.(304-306)CGT>TGT	p.R102C
Pat_05	Pre-Treatment	SLC8A2	6543	37	19	47944435	47944435	Missense_Mutation	SNP	G	A	4	246	c.1876C>T	c.(1876-1878)CTC>TTC	p.L626F
Pat_05	Pre-Treatment	EHD2	30846	37	19	48229081	48229081	Missense_Mutation	SNP	C	T	4	172	c.515C>T	c.(514-516)CCG>CTG	p.P172L
Pat_05	Pre-Treatment	TRPM4	54795	37	19	49669383	49669383	Missense_Mutation	SNP	G	A	3	25	c.178G>A	c.(178-180)GTG>ATG	p.V60M

Pat_05	Pre-Treatment	TSKS	60385	37	19	50265367	50265367	Missense_Mutation	SNP	G	C	4	214	c.293C>G	c.(292-294)ACA>AGA	p.T98R
Pat_05	Pre-Treatment	MED25	81857	37	19	50333404	50333404	Missense_Mutation	SNP	G	A	4	135	c.748G>A	c.(748-750)GCC>ACC	p.A250T
Pat_05	Pre-Treatment	ZNF766	90321	37	19	52793753	52793753	Missense_Mutation	SNP	C	T	5	67	c.709C>T	c.(709-711)CGT>TGT	p.R237C
Pat_05	Pre-Treatment	NLRP12	91662	37	19	54313859	54313859	Missense_Mutation	SNP	G	A	4	143	c.1054C>T	c.(1054-1056)CGT>TGT	p.R352C
Pat_05	Pre-Treatment	LILRA1	11024	37	19	55106787	55106787	Missense_Mutation	SNP	C	T	82	118	c.581C>T	c.(580-582)TCG>TTG	p.S194L
Pat_05	Pre-Treatment	FCAR	2204	37	19	55396680	55396680	Missense_Mutation	SNP	C	T	21	20	c.104C>T	c.(103-105)TCG>TTG	p.S35L
Pat_05	Pre-Treatment	NLRP2	55655	37	19	55493593	55493593	Missense_Mutation	SNP	C	T	108	130	c.527C>T	c.(526-528)CCT>CTT	p.P176L
Pat_05	Pre-Treatment	BRSK1	84446	37	19	55817693	55817694	Missense_Mutation	DNP	CC	TT	45	60	.1964_1965CC>T	c.(1963-1965)TCC>TTT	p.S655F
Pat_05	Pre-Treatment	ZNF579	163033	37	19	56090054	56090054	Missense_Mutation	SNP	G	A	4	103	c.952C>T	c.(952-954)CGC>TGC	p.R318C
Pat_05	Pre-Treatment	NLRP8	126205	37	19	56499245	56499245	Missense_Mutation	SNP	G	A	75	88	c.3113G>A	c.(3112-3114)GGA>GAA	p.G1038E
Pat_05	Pre-Treatment	ZNF749	388567	37	19	57956264	57956264	Missense_Mutation	SNP	G	A	4	86	c.1748G>A	c.(1747-1749)CGT>CAT	p.R583H
Pat_05	Pre-Treatment	ZNF211	10520	37	19	58153436	58153436	Missense_Mutation	SNP	C	T	4	228	c.1582C>T	c.(1582-1584)CGC>TGC	p.R528C
Pat_05	Pre-Treatment	ZNF776	284309	37	19	58265885	58265885	Missense_Mutation	SNP	G	A	5	212	c.1387G>A	c.(1387-1389)GGA>AGA	p.G463R
Pat_05	Pre-Treatment	ZNF274	10782	37	19	58722998	58722998	Missense_Mutation	SNP	A	G	3	147	c.925A>G	c.(925-927)AGG>GGG	p.R309G
Pat_05	Pre-Treatment	ZNF446	55663	37	19	58988812	58988812	Missense_Mutation	SNP	G	C	3	150	c.227G>C	c.(226-228)GGC>GCC	p.G76A
Pat_05	Pre-Treatment	CGREF1	10669	37	2	27327236	27327236	Translation_Start_Site	SNP	C	A	4	76	c.-1G>T	c.(-3-1)AAGGA>AATGA	
Pat_05	Pre-Treatment	TRIM54	57159	37	2	27529154	27529154	Missense_Mutation	SNP	G	A	4	120	c.940G>A	c.(940-942)GTA>ATA	p.V314I
Pat_05	Pre-Treatment	GCKR	2646	37	2	27729725	27729725	Missense_Mutation	SNP	G	A	5	266	c.1039G>A	c.(1039-1041)GTA>ATA	p.V347I
Pat_05	Pre-Treatment	DPY30	84661	37	2	32254736	32254736	Missense_Mutation	SNP	G	A	5	180	c.154C>T	c.(154-156)CCA>TCA	p.P52S
Pat_05	Pre-Treatment	LTBP1	4052	37	2	33173962	33173962	Missense_Mutation	SNP	G	A	4	202	c.515G>A	c.(514-516)CGG>CAG	p.R172Q
Pat_05	Pre-Treatment	ANTXR1	84168	37	2	69472492	69472492	Missense_Mutation	SNP	C	T	6	0	c.1570C>T	c.(1570-1572)CCG>TCG	p.P524S
Pat_05	Pre-Treatment	ZNF638	27332	37	2	71595579	71595579	Missense_Mutation	SNP	G	A	5	317	c.2063G>A	c.(2062-2064)TGT>TAT	p.C688Y
Pat_05	Pre-Treatment	DUSP11	8446	37	2	73989939	73989939	Missense_Mutation	SNP	G	A	4	231	c.983C>T	c.(982-984)CCT>CTT	p.P328L
Pat_05	Pre-Treatment	CNNM4	26504	37	2	97464940	97464940	Missense_Mutation	SNP	G	A	4	173	c.1828G>A	c.(1828-1830)GAC>AAC	p.D610N
Pat_05	Pre-Treatment	ST6GAL2	84620	37	2	107423220	107423220	Missense_Mutation	SNP	C	T	38	110	c.1504G>A	c.(1504-1506)GAT>AAT	p.D502N
Pat_05	Pre-Treatment	PSD4	23550	37	2	113958879	113958879	Missense_Mutation	SNP	A	T	51	80	c.3058A>T	c.(3058-3060)AGC>TGC	p.S1020C
Pat_05	Pre-Treatment	PCDP1	200373	37	2	120383201	120383201	Missense_Mutation	SNP	C	T	4	217	c.595C>T	c.(595-597)CGT>TGT	p.R199C
Pat_05	Pre-Treatment	CNTNAP5	129684	37	2	124999956	124999956	Missense_Mutation	SNP	G	A	12	29	c.367G>A	c.(367-369)GAA>AAA	p.E123K
Pat_05	Pre-Treatment	POTEF	728378	37	2	130832668	130832668	Missense_Mutation	SNP	C	T	62	78	c.2377G>A	c.(2377-2379)GAG>AAG	p.E793K
Pat_05	Pre-Treatment	THSD7B	80731	37	2	138030231	138030231	Missense_Mutation	SNP	C	T	21	29	c.2302C>T	c.(2302-2304)CGG>TGG	p.R768W
Pat_05	Pre-Treatment	MBD5	55777	37	2	149247322	149247322	Missense_Mutation	SNP	G	A	4	198	c.3422G>A	c.(3421-3423)AGT>AAT	p.S1141N
Pat_05	Pre-Treatment	MMADHC	27249	37	2	150427616	150427616	Missense_Mutation	SNP	G	T	6	557	c.679C>A	c.(679-681)CCA>ACA	p.P227T
Pat_05	Pre-Treatment	NEB	4703	37	2	152506691	152506691	Missense_Mutation	SNP	T	G	35	56	c.7430A>C	c.(7429-7431)GAT>GCT	p.D2477A
Pat_05	Pre-Treatment	LRP2	4036	37	2	170175284	170175284	Missense_Mutation	SNP	G	A	5	410	c.298C>T	c.(298-300)CGT>TGT	p.R100C
Pat_05	Pre-Treatment	DYNC1I2	1781	37	2	172583344	172583344	Missense_Mutation	SNP	C	T	63	80	c.914C>T	c.(913-915)GCC>GTC	p.A305V
Pat_05	Pre-Treatment	DYNC1I2	1781	37	2	172583346	172583346	Missense_Mutation	SNP	C	T	62	81	c.916C>T	c.(916-918)CCT>TCT	p.P306S
Pat_05	Pre-Treatment	CIR1	9541	37	2	175213415	175213415	Missense_Mutation	SNP	C	T	4	241	c.1163G>A	c.(1162-1164)CGG>CAG	p.R388Q
Pat_05	Pre-Treatment	DFNB59	494513	37	2	179320879	179320879	Splice_Site	SNP	G	A	6	124	c.549_splice	c.e4+1	p.R183_splice
Pat_05	Pre-Treatment	TTN	7273	37	2	179404396	179404396	Missense_Mutation	SNP	G	A	85	115	c.90692C>T	c.(90691-90693)CCA>CTA	p.P30231L
Pat_05	Pre-Treatment	TTN	7273	37	2	179629358	179629358	Missense_Mutation	SNP	G	A	54	158	c.9884C>T	c.(9883-9885)ACG>ATG	p.T3295M
Pat_05	Pre-Treatment	TTN	7273	37	2	179664293	179664293	Missense_Mutation	SNP	G	A	43	139	c.835C>T	c.(835-837)CGG>TGG	p.R279W
Pat_05	Pre-Treatment	DNAH7	56171	37	2	196620918	196620918	Missense_Mutation	SNP	G	A	81	92	c.11525C>T	c.(11524-11526)CCA>CTA	p.P3842L
Pat_05	Pre-Treatment	DNAH7	56171	37	2	196749415	196749415	Missense_Mutation	SNP	C	T	27	165	c.5657G>A	c.(5656-5658)CGA>CAA	p.R1886Q
Pat_05	Pre-Treatment	AOX1	316	37	2	201477335	201477335	Missense_Mutation	SNP	G	A	61	246	c.1267G>A	c.(1267-1269)GAA>AAA	p.E423K
Pat_05	Pre-Treatment	NBEAL1	65065	37	2	204009383	204009383	Nonsense_Mutation	SNP	C	T	61	255	c.4822C>T	c.(4822-4824)CAG>TAG	p.Q1608*
Pat_05	Pre-Treatment	CRYGD	1421	37	2	208986579	208986579	Missense_Mutation	SNP	G	A	4	254	c.343C>T	c.(343-345)CGC>TGC	p.R115C
Pat_05	Pre-Treatment	IKZF2	22807	37	2	213872562	213872562	Missense_Mutation	SNP	A	T	18	28	c.1103T>A	c.(1102-1104)ATT>AAT	p.I368N

Pat_05	Pre-Treatment	COL4A4	1286	37	2	227876983	227876983	Missense_Mutation	SNP	C	T	4	97	c.4247G>A	c.(4246-4248)AGG>AAG	p.R1416K
Pat_05	Pre-Treatment	C2orf57	165100	37	2	232458669	232458669	Missense_Mutation	SNP	G	A	60	82	c.1007G>A	c.(1006-1008)GGA>GAA	p.G336E
Pat_05	Pre-Treatment	COL6A3	1293	37	2	238280543	238280543	Missense_Mutation	SNP	C	T	31	62	c.4117G>A	c.(4117-4119)GCA>ACA	p.A1373T
Pat_05	Pre-Treatment	SNRPB	6628	37	20	2443314	2443314	Missense_Mutation	SNP	G	A	4	265	c.653C>T	c.(652-654)CCG>CTG	p.P218L
Pat_05	Pre-Treatment	TMC2	117532	37	20	2573005	2573005	Missense_Mutation	SNP	G	A	5	413	c.884G>A	c.(883-885)CGG>CAG	p.R295Q
Pat_05	Pre-Treatment	BTBD3	22903	37	20	11903598	11903598	Missense_Mutation	SNP	G	T	51	125	c.853G>T	c.(853-855)GTT>TTT	p.V285F
Pat_05	Pre-Treatment	MACROD2	140733	37	20	15913932	15913932	Missense_Mutation	SNP	C	T	40	53	c.787C>T	c.(787-789)CCA>TCA	p.P263S
Pat_05	Pre-Treatment	ZNF133	7692	37	20	18297438	18297438	Missense_Mutation	SNP	C	T	4	155	c.1943C>T	c.(1942-1944)TCG>TTG	p.S648L
Pat_05	Pre-Treatment	CST2	1470	37	20	23807156	23807156	Missense_Mutation	SNP	G	A	23	59	c.142C>T	c.(142-144)CTT>TTT	p.L48F
Pat_05	Pre-Treatment	ZNF341	84905	37	20	32341156	32341156	Missense_Mutation	SNP	C	T	3	25	c.668C>T	c.(667-669)GCT>GTT	p.A223V
Pat_05	Pre-Treatment	ITCH	83737	37	20	33045246	33045246	Missense_Mutation	SNP	G	A	4	226	c.1385G>A	c.(1384-1386)CGA>CAA	p.R462Q
Pat_05	Pre-Treatment	CTNNBL1	56259	37	20	36361375	36361375	Missense_Mutation	SNP	G	T	4	119	c.125G>T	c.(124-126)CGG>CTG	p.R42L
Pat_05	Pre-Treatment	PLCG1	5335	37	20	39795470	39795470	Missense_Mutation	SNP	G	A	5	376	c.2272G>A	c.(2272-2274)GAG>AAG	p.E758K
Pat_05	Pre-Treatment	PTPRT	11122	37	20	41514545	41514545	Missense_Mutation	SNP	C	T	4	193	c.116G>A	c.(115-117)AGC>AAC	p.S39N
Pat_05	Pre-Treatment	GDAP1L1	78997	37	20	42887229	42887229	Missense_Mutation	SNP	G	A	3	27	c.529G>A	c.(529-531)GCC>ACC	p.A177T
Pat_05	Pre-Treatment	FITM2	128486	37	20	42935818	42935818	Missense_Mutation	SNP	G	A	71	50	c.236C>T	c.(235-237)ACC>ATC	p.T79I
Pat_05	Pre-Treatment	SEMG1	6406	37	20	43836440	43836440	Missense_Mutation	SNP	G	A	4	229	c.502G>A	c.(502-504)GTT>ATT	p.V168I
Pat_05	Pre-Treatment	ARFGEF2	10564	37	20	47614885	47614885	Missense_Mutation	SNP	G	A	5	501	c.3275G>A	c.(3274-3276)CGC>CAC	p.R1092H
Pat_05	Pre-Treatment	CSTF1	1477	37	20	54974209	54974209	Missense_Mutation	SNP	G	A	8	657	c.832G>A	c.(832-834)GTA>ATA	p.V278I
Pat_05	Pre-Treatment	TMPRSS15	5651	37	21	19737500	19737500	Missense_Mutation	SNP	G	A	79	291	c.730C>T	c.(730-732)CCA>TCA	p.P244S
Pat_05	Pre-Treatment	BACH1	571	37	21	30698389	30698389	Missense_Mutation	SNP	A	C	81	70	c.244A>C	c.(244-246)AAA>CAA	p.K82Q
Pat_05	Pre-Treatment	KRTAP24-1	643803	37	21	31654667	31654667	Missense_Mutation	SNP	G	A	38	162	c.584C>T	c.(583-585)TCC>TTC	p.S195F
Pat_05	Pre-Treatment	DSCAM	1826	37	21	41465753	41465753	Missense_Mutation	SNP	G	A	19	71	c.3745C>T	c.(3745-3747)CCC>TCC	p.P1249S
Pat_05	Pre-Treatment	C2CD2	25966	37	21	43319356	43319356	Missense_Mutation	SNP	G	A	3	47	c.1676C>T	c.(1675-1677)CCG>CTG	p.P559L
Pat_05	Pre-Treatment	PWP2	5822	37	21	45550523	45550523	Missense_Mutation	SNP	C	T	34	57	c.2630C>T	c.(2629-2631)TCC>TTC	p.S877F
Pat_05	Pre-Treatment	ICOSLG	23308	37	21	45655347	45655347	Missense_Mutation	SNP	C	T	4	113	c.505G>A	c.(505-507)GTG>ATG	p.V169M
Pat_05	Pre-Treatment	TRPM2	7226	37	21	45819208	45819208	Missense_Mutation	SNP	G	A	57	46	c.2092G>A	c.(2092-2094)GAA>AAA	p.E698K
Pat_05	Pre-Treatment	PRMT2	3275	37	21	48064360	48064360	Missense_Mutation	SNP	C	T	6	466	c.287C>T	c.(286-288)ACG>ATG	p.T96M
Pat_05	Pre-Treatment	CCT8L2	150160	37	22	17072668	17072668	Missense_Mutation	SNP	G	A	4	170	c.773C>T	c.(772-774)ACG>ATG	p.T258M
Pat_05	Pre-Treatment	GAB4	128954	37	22	17447197	17447197	Missense_Mutation	SNP	G	A	3	44	c.1081C>T	c.(1081-1083)CCC>TCC	p.P361S
Pat_05	Pre-Treatment	C22orf29	79680	37	22	19839682	19839682	Missense_Mutation	SNP	G	A	94	195	c.103C>T	c.(103-105)CCT>TCT	p.P35S
Pat_05	Pre-Treatment	DGCR8	54487	37	22	20073637	20073637	Missense_Mutation	SNP	G	A	4	194	c.151G>A	c.(151-153)GTT>ATT	p.V51I
Pat_05	Pre-Treatment	GNAZ	2781	37	22	23438492	23438492	Missense_Mutation	SNP	G	A	4	201	c.610G>A	c.(610-612)GGG>AGG	p.G204R
Pat_05	Pre-Treatment	SLC2A11	66035	37	22	24224998	24224998	Missense_Mutation	SNP	A	G	3	69	c.926A>G	c.(925-927)AAG>AGG	p.K309R
Pat_05	Pre-Treatment	CYTSA	23384	37	22	24730421	24730421	Missense_Mutation	SNP	G	A	5	388	c.2440G>A	c.(2440-2442)GTT>ATT	p.V814I
Pat_05	Pre-Treatment	TFIP11	24144	37	22	26890130	26890130	Missense_Mutation	SNP	C	T	101	188	c.2133G>A	c.(2131-2133)ATG>ATA	p.M711I
Pat_05	Pre-Treatment	CHEK2	11200	37	22	29091840	29091841	Missense_Mutation	DNP	TG	CA	6	173	.1116_1117CA>T	114-1119)TCCAAG>TCTG	p.K373E
Pat_05	Pre-Treatment	SMTN	6525	37	22	31492782	31492782	Missense_Mutation	SNP	G	A	4	182	c.1925G>A	c.(1924-1926)CGC>CAC	p.R642H
Pat_05	Pre-Treatment	PLA2G3	50487	37	22	31533809	31533809	Missense_Mutation	SNP	G	A	85	148	c.953C>T	c.(952-954)TCC>TTC	p.S318F
Pat_05	Pre-Treatment	BPIL2	254240	37	22	32831798	32831798	Missense_Mutation	SNP	G	A	4	194	c.817C>T	c.(817-819)CGC>TGC	p.R273C
Pat_05	Pre-Treatment	FAM83F	113828	37	22	40417674	40417674	Missense_Mutation	SNP	C	T	28	67	c.1160C>T	c.(1159-1161)CCC>CTC	p.P387L
Pat_05	Pre-Treatment	ZC3H7B	23264	37	22	41716718	41716718	Splice_Site	SNP	G	A	5	283	c.53_splice	c.e2+1	p.Q18_splice
Pat_05	Pre-Treatment	PLXNB2	23654	37	22	50716039	50716039	Missense_Mutation	SNP	G	A	4	189	c.5177C>T	c.(5176-5178)ACG>ATG	p.T1726M
Pat_05	Pre-Treatment	SHANK3	85358	37	22	51160550	51160550	Missense_Mutation	SNP	G	A	10	10	c.4337G>A	c.(4336-4338)AGG>AAG	p.R1446K
Pat_05	Pre-Treatment	CNTN4	152330	37	3	3067852	3067852	Missense_Mutation	SNP	C	T	6	171	c.1553C>T	c.(1552-1554)CCG>CTG	p.P518L
Pat_05	Pre-Treatment	LHFPL4	375323	37	3	9594264	9594264	Missense_Mutation	SNP	C	T	4	74	c.100G>A	c.(100-102)GCC>ACC	p.A34T
Pat_05	Pre-Treatment	BTD	686	37	3	15685958	15685958	Missense_Mutation	SNP	G	A	6	538	c.595G>A	c.(595-597)GTG>ATG	p.V199M

Pat_05	Pre-Treatment	SATB1	6304	37	3	18391108	18391108	Nonsense_Mutation	SNP	G	A	4	61	c.1846C>T	c.(1846-1848)CAG>TAG	p.Q616*
Pat_05	Pre-Treatment	STT3B	201595	37	3	31667620	31667620	Splice_Site	SNP	G	A	4	194	c.2073_splice	c.e13+1	p.R691_splice
Pat_05	Pre-Treatment	ZNF860	344787	37	3	32032046	32032046	Missense_Mutation	SNP	G	A	12	198	c.1475G>A	c.(1474-1476)CGT>CAT	p.R492H
Pat_05	Pre-Treatment	CNOT10	25904	37	3	32774919	32774919	Missense_Mutation	SNP	C	T	61	46	c.1220C>T	c.(1219-1221)TCT>TTT	p.S407F
Pat_05	Pre-Treatment	CCR9	10803	37	3	45942970	45942970	Missense_Mutation	SNP	G	A	52	37	c.690G>A	c.(688-690)ATG>ATA	p.M230I
Pat_05	Pre-Treatment	ATRIP	84126	37	3	48506434	48506434	Missense_Mutation	SNP	G	A	4	218	c.2260G>A	c.(2260-2262)GGG>AGG	p.G754R
Pat_05	Pre-Treatment	PFKFB4	5210	37	3	48573700	48573700	Missense_Mutation	SNP	G	A	5	203	c.829C>T	c.(829-831)CGG>TGG	p.R277W
Pat_05	Pre-Treatment	USP19	10869	37	3	49151487	49151487	Missense_Mutation	SNP	C	T	6	168	c.2134G>A	c.(2134-2136)GAA>AAA	p.E712K
Pat_05	Pre-Treatment	AMT	275	37	3	49455331	49455331	Missense_Mutation	SNP	C	T	4	86	c.953G>A	c.(952-954)CGG>CAG	p.R318Q
Pat_05	Pre-Treatment	BSN	8927	37	3	49699702	49699702	Missense_Mutation	SNP	G	A	3	40	c.10424G>A	c.(10423-10425)CGA>CAA	p.R3475Q
Pat_05	Pre-Treatment	UBA7	7318	37	3	49847481	49847481	Missense_Mutation	SNP	G	A	4	138	c.1769C>T	c.(1768-1770)GCT>GTT	p.A590V
Pat_05	Pre-Treatment	DOCK3	1795	37	3	51418535	51418535	Missense_Mutation	SNP	G	A	4	225	c.5638G>A	c.(5638-5640)GGC>AGC	p.G1880S
Pat_05	Pre-Treatment	IQCF2	389123	37	3	51897231	51897231	Missense_Mutation	SNP	C	T	28	88	c.340C>T	c.(340-342)CGT>TGT	p.R114C
Pat_05	Pre-Treatment	PCBP4	57060	37	3	51992100	51992100	Missense_Mutation	SNP	G	A	5	276	c.1189C>T	c.(1189-1191)CGG>TGG	p.R397W
Pat_05	Pre-Treatment	PBRM1	55193	37	3	52643768	52643768	Nonsense_Mutation	SNP	G	A	128	72	c.2128C>T	c.(2128-2130)CGA>TGA	p.R710*
Pat_05	Pre-Treatment	PRKCD	5580	37	3	53212443	53212443	Missense_Mutation	SNP	C	T	58	18	c.5C>T	c.(4-6)GCG>GTG	p.A2V
Pat_05	Pre-Treatment	C3orf67	200844	37	3	58849358	58849358	Missense_Mutation	SNP	T	C	68	94	c.1144A>G	c.(1144-1146)AAA>GAA	p.K382E
Pat_05	Pre-Treatment	ROBO2	6092	37	3	77542449	77542449	Missense_Mutation	SNP	C	T	95	176	c.722C>T	c.(721-723)GCT>GTT	p.A241V
Pat_05	Pre-Treatment	VGLL3	389136	37	3	87017908	87017908	Missense_Mutation	SNP	G	A	17	54	c.769C>T	c.(769-771)CCA>TCA	p.P257S
Pat_05	Pre-Treatment	RPL24	6152	37	3	101400004	101400004	Missense_Mutation	SNP	G	A	282	416	c.449C>T	c.(448-450)GCT>GTT	p.A150V
Pat_05	Pre-Treatment	IFT57	55081	37	3	107910402	107910402	Missense_Mutation	SNP	G	A	4	279	c.743C>T	c.(742-744)CCG>CTG	p.P248L
Pat_05	Pre-Treatment	PHLDB2	90102	37	3	111693337	111693337	Missense_Mutation	SNP	C	T	218	316	c.3689C>T	c.(3688-3690)TCG>TTG	p.S1230L
Pat_05	Pre-Treatment	ZBTB20	26137	37	3	114069979	114069979	Missense_Mutation	SNP	G	A	7	537	c.946C>T	c.(946-948)CGG>TGG	p.R316W
Pat_05	Pre-Treatment	CASR	846	37	3	122003250	122003250	Missense_Mutation	SNP	G	A	4	182	c.2449G>A	c.(2449-2451)GTC>ATC	p.V817I
Pat_05	Pre-Treatment	KALRN	8997	37	3	124438217	124438217	Missense_Mutation	SNP	G	A	4	240	c.8861G>A	c.(8860-8862)CGC>CAC	p.R2954H
Pat_05	Pre-Treatment	ROPN1B	152015	37	3	125691013	125691013	Missense_Mutation	SNP	A	G	4	123	c.116A>G	c.(115-117)GAT>GGT	p.D39G
Pat_05	Pre-Treatment	PLXNA1	5361	37	3	126749143	126749143	Missense_Mutation	SNP	C	T	5	264	c.5050C>T	c.(5050-5052)CGG>TGG	p.R1684W
Pat_05	Pre-Treatment	TF	7018	37	3	133478099	133478099	Missense_Mutation	SNP	T	C	114	197	c.1129T>C	c.(1129-1131)TGG>CGG	p.W377R
Pat_05	Pre-Treatment	SLCO2A1	6578	37	3	133654663	133654663	Missense_Mutation	SNP	C	T	16	31	c.1769G>A	c.(1768-1770)AGG>AAG	p.R590K
Pat_05	Pre-Treatment	TSC22D2	9819	37	3	150127751	150127751	Missense_Mutation	SNP	G	A	7	607	c.614G>A	c.(613-615)AGC>AAC	p.S205N
Pat_05	Pre-Treatment	IGSF10	285313	37	3	151165878	151165878	Missense_Mutation	SNP	T	C	101	181	c.1891A>G	c.(1891-1893)AGA>GGA	p.R631G
Pat_05	Pre-Treatment	DHX36	170506	37	3	154006677	154006677	Missense_Mutation	SNP	G	A	86	145	c.2009C>T	c.(2008-2010)TCC>TTC	p.S670F
Pat_05	Pre-Treatment	PLCH1	23007	37	3	155286035	155286035	Missense_Mutation	SNP	C	G	15	47	c.814G>C	c.(814-816)GTT>CTT	p.V272L
Pat_05	Pre-Treatment	WDR49	151790	37	3	167217991	167217991	Missense_Mutation	SNP	T	G	82	301	c.1925A>C	c.(1924-1926)GAA>GCA	p.E642A
Pat_05	Pre-Treatment	SLC7A14	57709	37	3	170216467	170216467	Missense_Mutation	SNP	C	T	4	206	c.748G>A	c.(748-750)GGC>AGC	p.G250S
Pat_05	Pre-Treatment	CCDC39	339829	37	3	180372597	180372597	Missense_Mutation	SNP	T	C	52	102	c.883A>G	c.(883-885)ACG>GCG	p.T295A
Pat_05	Pre-Treatment	MAP3K13	9175	37	3	185155242	185155243	Nonsense_Mutation	DNP	GG	AA	81	221	c.483_484GG>AA	481-486)TGGGAA>TGAA	161_162WE>*
Pat_05	Pre-Treatment	ATP13A4	84239	37	3	193156375	193156375	Splice_Site	SNP	T	C	3	95	c.2563_splice	c.e23-1	p.A855_splice
Pat_05	Pre-Treatment	FAM193A	8603	37	4	2733531	2733531	Missense_Mutation	SNP	G	A	4	219	c.3734G>A	c.(3733-3735)CGA>CAA	p.R1245Q
Pat_05	Pre-Treatment	BOD1L	259282	37	4	13603609	13603609	Missense_Mutation	SNP	C	T	6	464	c.4915G>A	c.(4915-4917)GAA>AAA	p.E1639K
Pat_05	Pre-Treatment	FGFBP1	9982	37	4	15938093	15938093	Missense_Mutation	SNP	C	A	5	242	c.163G>T	c.(163-165)GGG>TGG	p.G55W
Pat_05	Pre-Treatment	PI4K2B	55300	37	4	25278666	25278666	Missense_Mutation	SNP	G	A	4	206	c.1303G>A	c.(1303-1305)GGG>AGG	p.G435R
Pat_05	Pre-Treatment	ZCCHC4	29063	37	4	25353242	25353242	Nonsense_Mutation	SNP	G	A	130	139	c.942G>A	c.(940-942)TGG>TGA	p.W314*
Pat_05	Pre-Treatment	KLHL5	51088	37	4	39088270	39088270	Missense_Mutation	SNP	C	T	5	224	c.1174C>T	c.(1174-1176)CGT>TGT	p.R392C
Pat_05	Pre-Treatment	ATP8A1	10396	37	4	42448649	42448649	Missense_Mutation	SNP	C	T	35	97	c.2909G>A	c.(2908-2910)GGA>GAA	p.G970E
Pat_05	Pre-Treatment	GRXCR1	389207	37	4	43032429	43032429	Missense_Mutation	SNP	C	T	57	206	c.745C>T	c.(745-747)CCA>TCA	p.P249S
Pat_05	Pre-Treatment	USP46	64854	37	4	53464829	53464829	Missense_Mutation	SNP	C	T	28	24	c.964G>A	c.(964-966)GGC>AGC	p.G322S

Pat_05	Pre-Treatment	LNX1	84708	37	4	54374296	54374296	Missense_Mutation	SNP	G	A	15	35	c.479C>T	c.(478-480)CCC>CTC	p.P160L
Pat_05	Pre-Treatment	SRP72	6731	37	4	57333815	57333815	Missense_Mutation	SNP	G	A	5	101	c.14G>A	c.(13-15)GGC>GAC	p.G5D
Pat_05	Pre-Treatment	EPHA5	2044	37	4	66217147	66217147	Missense_Mutation	SNP	C	T	5	255	c.2468G>A	c.(2467-2469)CGG>CAG	p.R823Q
Pat_05	Pre-Treatment	UGT2A3	79799	37	4	69817162	69817162	Missense_Mutation	SNP	G	A	28	41	c.317C>T	c.(316-318)TCA>TTA	p.S106L
Pat_05	Pre-Treatment	UGT2B4	7363	37	4	70359495	70359495	Nonsense_Mutation	SNP	C	T	50	182	c.786G>A	c.(784-786)TGG>TGA	p.W262*
Pat_05	Pre-Treatment	GC	2638	37	4	72631312	72631312	Missense_Mutation	SNP	C	T	4	252	c.310G>A	c.(310-312)GTT>ATT	p.V104I
Pat_05	Pre-Treatment	ANKRD17	26057	37	4	73962892	73962892	Missense_Mutation	SNP	C	T	163	582	c.5119G>A	c.(5119-5121)GTA>ATA	p.V1707I
Pat_05	Pre-Treatment	PARM1	25849	37	4	75937682	75937682	Missense_Mutation	SNP	C	T	22	79	c.91C>T	c.(91-93)CTT>TTT	p.L31F
Pat_05	Pre-Treatment	RASGEF1B	153020	37	4	82362046	82362046	Missense_Mutation	SNP	C	T	5	471	c.1046G>A	c.(1045-1047)CGA>CAA	p.R349Q
Pat_05	Pre-Treatment	MTTP	4547	37	4	100530020	100530020	Missense_Mutation	SNP	C	T	81	234	c.1655C>T	c.(1654-1656)CCA>CTA	p.P552L
Pat_05	Pre-Treatment	UCP1	7350	37	4	141488965	141488965	Missense_Mutation	SNP	G	A	4	141	c.293C>T	c.(292-294)ACG>ATG	p.T98M
Pat_05	Pre-Treatment	IL15	3600	37	4	142651081	142651081	Missense_Mutation	SNP	C	T	64	234	c.322C>T	c.(322-324)CAT>TAT	p.H108Y
Pat_05	Pre-Treatment	TRIM2	23321	37	4	154217177	154217177	Missense_Mutation	SNP	T	G	40	108	c.1418T>G	c.(1417-1419)ATC>AGC	p.I473S
Pat_05	Pre-Treatment	NAF1	92345	37	4	164050291	164050291	Missense_Mutation	SNP	T	C	15	49	c.1243A>G	c.(1243-1245)AAT>GAT	p.N415D
Pat_05	Pre-Treatment	DDX60L	91351	37	4	169377245	169377245	Missense_Mutation	SNP	C	T	4	115	c.782G>A	c.(781-783)CGT>CAT	p.R261H
Pat_05	Pre-Treatment	ADAM29	11086	37	4	175897365	175897365	Missense_Mutation	SNP	A	C	59	151	c.689A>C	c.(688-690)AAT>ACT	p.N230T
Pat_05	Pre-Treatment	TRIML2	205860	37	4	189012598	189012598	Missense_Mutation	SNP	C	T	99	112	c.1093G>A	c.(1093-1095)GGA>AGA	p.G365R
Pat_05	Pre-Treatment	TRIO	7204	37	5	14280541	14280541	Missense_Mutation	SNP	C	T	60	62	c.343C>T	c.(343-345)CCC>TCC	p.P115S
Pat_05	Pre-Treatment	CDH6	1004	37	5	31267705	31267705	Missense_Mutation	SNP	G	A	30	99	c.125G>A	c.(124-126)GGA>GAA	p.G42E
Pat_05	Pre-Treatment	PDZD2	23037	37	5	32088467	32088467	Missense_Mutation	SNP	C	T	5	246	c.4913C>T	c.(4912-4914)CCG>CTG	p.P1638L
Pat_05	Pre-Treatment	SKP2	6502	37	5	36184070	36184070	Missense_Mutation	SNP	T	G	14	105	c.1190T>G	c.(1189-1191)TTT>TGT	p.F397C
Pat_05	Pre-Treatment	NIPBL	25836	37	5	37027515	37027515	Splice_Site	SNP	G	A	6	470	c.5862_splice	c.e32+1	p.N1954_splice
Pat_05	Pre-Treatment	EMB	133418	37	5	49707083	49707083	Missense_Mutation	SNP	C	T	74	162	c.331G>A	c.(331-333)GAG>AAG	p.E111K
Pat_05	Pre-Treatment	BDP1	55814	37	5	70806049	70806049	Missense_Mutation	SNP	G	A	7	141	c.3130G>A	c.(3130-3132)GTA>ATA	p.V1044I
Pat_05	Pre-Treatment	FAM169A	26049	37	5	74137411	74137411	Missense_Mutation	SNP	C	A	50	167	c.91G>T	c.(91-93)GAC>TAC	p.D31Y
Pat_05	Pre-Treatment	POC5	134359	37	5	74981222	74981222	Missense_Mutation	SNP	G	A	4	278	c.1217C>T	c.(1216-1218)CCT>CTT	p.P406L
Pat_05	Pre-Treatment	VCAN	1462	37	5	82786240	82786240	Missense_Mutation	SNP	G	A	5	457	c.394G>A	c.(394-396)GTC>ATC	p.V132I
Pat_05	Pre-Treatment	C5orf36	285600	37	5	93872768	93872768	Missense_Mutation	SNP	G	A	26	96	c.64C>T	c.(64-66)CCT>TCT	p.P22S
Pat_05	Pre-Treatment	ANKRD32	84250	37	5	94027853	94027853	Missense_Mutation	SNP	C	T	5	294	c.2587C>T	c.(2587-2589)CGT>TGT	p.R863C
Pat_05	Pre-Treatment	FAM81B	153643	37	5	94749692	94749692	Missense_Mutation	SNP	G	A	54	174	c.335G>A	c.(334-336)GGT>GAT	p.G112D
Pat_05	Pre-Treatment	EPB41L4A	64097	37	5	111540171	111540171	Missense_Mutation	SNP	G	A	5	252	c.1277C>T	c.(1276-1278)TCT>TTT	p.S426F
Pat_05	Pre-Treatment	SEMA6A	57556	37	5	115783196	115783196	Missense_Mutation	SNP	C	T	7	712	c.2206G>A	c.(2206-2208)GGC>AGC	p.G736S
Pat_05	Pre-Treatment	FBN2	2201	37	5	127624885	127624885	Missense_Mutation	SNP	C	T	61	211	c.6571G>A	c.(6571-6573)GAC>AAC	p.D2191N
Pat_05	Pre-Treatment	SLC27A6	28965	37	5	128363006	128363006	Missense_Mutation	SNP	G	A	5	292	c.1436G>A	c.(1435-1437)CGT>CAT	p.R479H
Pat_05	Pre-Treatment	WNT8A	7478	37	5	137426715	137426715	Missense_Mutation	SNP	G	A	4	200	c.1009G>A	c.(1009-1011)GCA>ACA	p.A337T
Pat_05	Pre-Treatment	KIF20A	10112	37	5	137520005	137520005	Missense_Mutation	SNP	G	A	6	505	c.1430G>A	c.(1429-1431)CGT>CAT	p.R477H
Pat_05	Pre-Treatment	PCDHA13	56136	37	5	140263298	140263298	Missense_Mutation	SNP	C	T	35	139	c.1445C>T	c.(1444-1446)GCG>GTG	p.A482V
Pat_05	Pre-Treatment	PCDHB7	56129	37	5	140554401	140554401	Missense_Mutation	SNP	T	A	30	80	c.1985T>A	c.(1984-1986)CTG>CAG	p.L662Q
Pat_05	Pre-Treatment	PCDHGA12	26025	37	5	140810870	140810870	Missense_Mutation	SNP	G	A	5	302	c.544G>A	c.(544-546)GTG>ATG	p.V182M
Pat_05	Pre-Treatment	RELL2	285613	37	5	141019543	141019543	Missense_Mutation	SNP	C	T	55	194	c.560C>T	c.(559-561)TCC>TTC	p.S187F
Pat_05	Pre-Treatment	SH3TC2	79628	37	5	148406153	148406153	Missense_Mutation	SNP	C	T	5	242	c.3035G>A	c.(3034-3036)CGG>CAG	p.R1012Q
Pat_05	Pre-Treatment	GRPEL2	134266	37	5	148730807	148730807	Nonsense_Mutation	SNP	C	T	4	196	c.640C>T	c.(640-642)CGA>TGA	p.R214*
Pat_05	Pre-Treatment	PPARGC1B	133522	37	5	149212436	149212436	Missense_Mutation	SNP	C	T	64	83	c.800C>T	c.(799-801)TCC>TTC	p.S267F
Pat_05	Pre-Treatment	PDE6A	5145	37	5	149242693	149242693	Missense_Mutation	SNP	G	A	7	676	c.2495C>T	c.(2494-2496)TCG>TTG	p.S832L
Pat_05	Pre-Treatment	CSF1R	1436	37	5	149433887	149433887	Missense_Mutation	SNP	G	A	4	239	c.2761C>T	c.(2761-2763)CGG>TGG	p.R921W
Pat_05	Pre-Treatment	GALNT10	55568	37	5	153755941	153755941	Missense_Mutation	SNP	G	A	4	85	c.673G>A	c.(673-675)GCC>ACC	p.A225T
Pat_05	Pre-Treatment	HAVCR2	84868	37	5	156525886	156525886	Missense_Mutation	SNP	G	A	14	95	c.505C>T	c.(505-507)CCT>TCT	p.P169S

Pat_05	Pre-Treatment	GABRA1	2554	37	5	161302610	161302610	Missense_Mutation	SNP	C	T	82	306	c.521C>T	c.(520-522)CCT>CTT	p.P174L
Pat_05	Pre-Treatment	SLIT3	6586	37	5	168093534	168093534	Missense_Mutation	SNP	G	T	13	30	c.4497C>A	c.(4495-4497)TTC>TTA	p.F1499L
Pat_05	Pre-Treatment	UNC5A	90249	37	5	176305636	176305637	Missense_Mutation	DNP	CC	TT	17	73	.2180_2181CC>T	c.(2179-2181)ACC>ATT	p.T727I
Pat_05	Pre-Treatment	DDX41	51428	37	5	176939374	176939374	Missense_Mutation	SNP	C	T	5	212	c.1570G>A	c.(1570-1572)GGG>AGG	p.G524R
Pat_05	Pre-Treatment	RNF130	55819	37	5	179440179	179440179	Missense_Mutation	SNP	C	T	6	366	c.575G>A	c.(574-576)CGT>CAT	p.R192H
Pat_05	Pre-Treatment	GCM2	9247	37	6	10875166	10875166	Missense_Mutation	SNP	C	T	39	101	c.583G>A	c.(583-585)GCA>ACA	p.A195T
Pat_05	Pre-Treatment	SLC17A4	10050	37	6	25769267	25769267	Missense_Mutation	SNP	C	T	52	132	c.146C>T	c.(145-147)TCA>TTA	p.S49L
Pat_05	Pre-Treatment	BTN1A1	696	37	6	26501521	26501521	Missense_Mutation	SNP	G	A	4	227	c.7G>A	c.(7-9)GTT>ATT	p.V3I
Pat_05	Pre-Treatment	ABCF1	23	37	6	30553992	30553992	Missense_Mutation	SNP	C	T	56	109	c.1795C>T	c.(1795-1797)CCT>TCT	p.P599S
Pat_05	Pre-Treatment	LY6G5B	58496	37	6	31639713	31639713	Missense_Mutation	SNP	C	T	145	332	c.260C>T	c.(259-261)ACC>ATC	p.T87I
Pat_05	Pre-Treatment	C6orf27	80737	37	6	31741166	31741166	Missense_Mutation	SNP	G	A	3	58	c.770C>T	c.(769-771)CCG>CTG	p.P257L
Pat_05	Pre-Treatment	C2	717	37	6	31903727	31903727	Missense_Mutation	SNP	G	A	4	311	c.877G>A	c.(877-879)GTT>ATT	p.V293I
Pat_05	Pre-Treatment	FKBPL	63943	37	6	32096828	32096828	Missense_Mutation	SNP	G	A	5	240	c.730C>T	c.(730-732)CCC>TCC	p.P244S
Pat_05	Pre-Treatment	EGFL8	80864	37	6	32135197	32135198	Missense_Mutation	DNP	GC	TG	84	99	c.672_673GC>TG	670-675)CGGCTG>CGTG	p.L225V
Pat_05	Pre-Treatment	PFDN6	10471	37	6	33258515	33258515	Missense_Mutation	SNP	C	T	4	233	c.283C>T	c.(283-285)CGG>TGG	p.R95W
Pat_05	Pre-Treatment	ITPR3	3710	37	6	33663491	33663491	Missense_Mutation	SNP	G	A	127	224	c.7950G>A	c.(7948-7950)ATG>ATA	p.M2650I
Pat_05	Pre-Treatment	FGD2	221472	37	6	36982714	36982714	Missense_Mutation	SNP	A	G	36	77	c.929A>G	c.(928-930)GAG>GGG	p.E310G
Pat_05	Pre-Treatment	FRS3	10817	37	6	41740560	41740561	Missense_Mutation	DNP	GG	AT	49	160	c.390_391CC>AT	(388-393)CTCCCT>CTAT	p.P131S
Pat_05	Pre-Treatment	TAF8	129685	37	6	42044898	42044898	Missense_Mutation	SNP	G	A	4	168	c.841G>A	c.(841-843)GGT>AGT	p.G281S
Pat_05	Pre-Treatment	DLK2	65989	37	6	43418776	43418776	Missense_Mutation	SNP	C	T	4	178	c.653G>A	c.(652-654)AGC>AAC	p.S218N
Pat_05	Pre-Treatment	RSPH9	221421	37	6	43618212	43618212	Missense_Mutation	SNP	G	A	76	147	c.328G>A	c.(328-330)GAA>AAA	p.E110K
Pat_05	Pre-Treatment	BMP5	653	37	6	55620369	55620369	Missense_Mutation	SNP	A	T	17	127	c.1327T>A	c.(1327-1329)TAT>AAT	p.Y443N
Pat_05	Pre-Treatment	BCKDHB	594	37	6	80878662	80878662	Missense_Mutation	SNP	G	A	4	131	c.548G>A	c.(547-549)CGG>CAG	p.R183Q
Pat_05	Pre-Treatment	GPR63	81491	37	6	97247429	97247429	Missense_Mutation	SNP	G	A	57	41	c.179C>T	c.(178-180)ACC>ATC	p.T60I
Pat_05	Pre-Treatment	PRDM13	59336	37	6	100056673	100056673	Nonsense_Mutation	SNP	G	A	35	22	c.201G>A	c.(199-201)TGG>TGA	p.W67*
Pat_05	Pre-Treatment	LAMA4	3910	37	6	112537649	112537649	Missense_Mutation	SNP	G	A	5	220	c.217C>T	c.(217-219)CAC>TAC	p.H73Y
Pat_05	Pre-Treatment	FAM26D	221301	37	6	116879223	116879223	Missense_Mutation	SNP	G	A	5	376	c.365G>A	c.(364-366)CGC>CAC	p.R122H
Pat_05	Pre-Treatment	KPNA5	3841	37	6	117043355	117043355	Missense_Mutation	SNP	G	A	5	283	c.823G>A	c.(823-825)GTG>ATG	p.V275M
Pat_05	Pre-Treatment	TAAR9	134860	37	6	132859898	132859898	Missense_Mutation	SNP	G	T	4	201	c.470G>T	c.(469-471)TGG>TTG	p.W157L
Pat_05	Pre-Treatment	KIAA1244	57221	37	6	138584535	138584535	Missense_Mutation	SNP	G	A	4	155	c.1915G>A	c.(1915-1917)GAT>AAT	p.D639N
Pat_05	Pre-Treatment	TAB2	23118	37	6	149700178	149700178	Missense_Mutation	SNP	C	T	4	161	c.1127C>T	c.(1126-1128)ACG>ATG	p.T376M
Pat_05	Pre-Treatment	SERAC1	84947	37	6	158567889	158567889	Missense_Mutation	SNP	G	A	5	367	c.412C>T	c.(412-414)CGG>TGG	p.R138W
Pat_05	Pre-Treatment	SLC22A1	6580	37	6	160557636	160557636	Missense_Mutation	SNP	C	T	4	258	c.1015C>T	c.(1015-1017)CGC>TGC	p.R339C
Pat_05	Pre-Treatment	HEATR2	54919	37	7	803533	803533	Missense_Mutation	SNP	C	T	6	566	c.1705C>T	c.(1705-1707)CGG>TGG	p.R569W
Pat_05	Pre-Treatment	GPER	2852	37	7	1132266	1132266	Missense_Mutation	SNP	C	T	6	244	c.902C>T	c.(901-903)GCC>GTC	p.A301V
Pat_05	Pre-Treatment	C7orf27	221927	37	7	2581453	2581453	Missense_Mutation	SNP	C	T	4	112	c.1033G>A	c.(1033-1035)GCA>ACA	p.A345T
Pat_05	Pre-Treatment	CARD11	84433	37	7	2946323	2946323	Missense_Mutation	SNP	C	G	4	219	c.3414G>C	c.(3412-3414)AAG>AAC	p.K1138N
Pat_05	Pre-Treatment	PAPOLB	56903	37	7	4899659	4899659	Missense_Mutation	SNP	G	A	51	54	c.1783C>T	c.(1783-1785)CCT>TCT	p.P595S
Pat_05	Pre-Treatment	FBXL18	80028	37	7	5545111	5545111	Missense_Mutation	SNP	G	A	5	255	c.169C>T	c.(169-171)CGG>TGG	p.R57W
Pat_05	Pre-Treatment	GLCCI1	113263	37	7	8110650	8110650	Missense_Mutation	SNP	C	T	7	430	c.1066C>T	c.(1066-1068)CGC>TGC	p.R356C
Pat_05	Pre-Treatment	THSD7A	221981	37	7	11450924	11450924	Missense_Mutation	SNP	C	A	106	119	c.3708G>T	c.(3706-3708)GAG>GAT	p.E1236D
Pat_05	Pre-Treatment	ABCB5	340273	37	7	20766661	20766661	Splice_Site	SNP	A	G	115	112	c.1291_splice	c.e13-2	p.I431_splice
Pat_05	Pre-Treatment	HOXA13	3209	37	7	27237911	27237911	Missense_Mutation	SNP	G	A	7	751	c.1073C>T	c.(1072-1074)ACG>ATG	p.T358M
Pat_05	Pre-Treatment	TXNDC3	51314	37	7	37907463	37907463	Missense_Mutation	SNP	C	A	21	105	c.781C>A	c.(781-783)CAG>AAG	p.Q261K
Pat_05	Pre-Treatment	MRPS24	64951	37	7	43906339	43906339	Missense_Mutation	SNP	G	A	5	430	c.463C>T	c.(463-465)CTC>TTC	p.L155F
Pat_05	Pre-Treatment	POLM	27434	37	7	44116204	44116204	Missense_Mutation	SNP	C	T	5	394	c.739G>A	c.(739-741)GGT>AGT	p.G247S
Pat_05	Pre-Treatment	MYO1G	64005	37	7	45005386	45005386	Missense_Mutation	SNP	C	T	74	123	c.2231G>A	c.(2230-2232)CGG>CAG	p.R744Q

Pat_05	Pre-Treatment	MYO1G	64005	37	7	45010555	45010555	Missense_Mutation	SNP	G	A	4	74	c.950C>T	c.(949-951)ACA>ATA	p.T317I
Pat_05	Pre-Treatment	ADCY1	107	37	7	45719384	45719384	Missense_Mutation	SNP	C	T	4	304	c.1975C>T	c.(1975-1977)CGG>TGG	p.R659W
Pat_05	Pre-Treatment	COBL	23242	37	7	51111341	51111342	Missense_Mutation	DNP	GG	AA	68	78	.1144_1145CC>T	c.(1144-1146)CCG>TTG	p.P382L
Pat_05	Pre-Treatment	FZD9	8326	37	7	72849988	72849988	Missense_Mutation	SNP	C	T	50	109	c.1651C>T	c.(1651-1653)CGG>TGG	p.R551W
Pat_05	Pre-Treatment	ELN	2006	37	7	73470634	73470634	Missense_Mutation	SNP	C	T	160	186	c.1184C>T	c.(1183-1185)CCT>CTT	p.P395L
Pat_05	Pre-Treatment	SPDYE5	442590	37	7	75130868	75130868	Splice_Site	SNP	G	A	7	533	c.744_splice	c.e6-1	p.W248_splice
Pat_05	Pre-Treatment	HIP1	3092	37	7	75211413	75211413	Missense_Mutation	SNP	C	T	3	75	c.520G>A	c.(520-522)GGA>AGA	p.G174R
Pat_05	Pre-Treatment	GRM3	2913	37	7	86394825	86394825	Missense_Mutation	SNP	G	A	6	517	c.364G>A	c.(364-366)GAA>AAA	p.E122K
Pat_05	Pre-Treatment	ABCB4	5244	37	7	87060845	87060845	Nonsense_Mutation	SNP	G	A	8	604	c.1768C>T	c.(1768-1770)CGA>TGA	p.R590*
Pat_05	Pre-Treatment	ANKIB1	54467	37	7	91948770	91948770	Missense_Mutation	SNP	C	T	6	400	c.613C>T	c.(613-615)CGG>TGG	p.R205W
Pat_05	Pre-Treatment	COL1A2	1278	37	7	94038912	94038912	Missense_Mutation	SNP	G	A	117	272	c.928G>A	c.(928-930)GGT>AGT	p.G310S
Pat_05	Pre-Treatment	SLC25A13	10165	37	7	95820559	95820559	Missense_Mutation	SNP	C	A	26	153	c.616G>T	c.(616-618)GCT>TCT	p.A206S
Pat_05	Pre-Treatment	ZNF3	7551	37	7	99669283	99669283	Missense_Mutation	SNP	C	T	5	279	c.824G>A	c.(823-825)CGG>CAG	p.R275Q
Pat_05	Pre-Treatment	PVRIG	79037	37	7	99817740	99817740	Missense_Mutation	SNP	C	T	3	28	c.122C>T	c.(121-123)ACC>ATC	p.T41I
Pat_05	Pre-Treatment	ZAN	7455	37	7	100355916	100355916	Missense_Mutation	SNP	C	T	4	145	c.3401C>T	c.(3400-3402)ACA>ATA	p.T1134I
Pat_05	Pre-Treatment	MUC17	140453	37	7	100679376	100679376	Missense_Mutation	SNP	G	A	7	709	c.4679G>A	c.(4678-4680)GGT>GAT	p.G1560D
Pat_05	Pre-Treatment	MUC17	140453	37	7	100687017	100687017	Missense_Mutation	SNP	C	T	77	160	c.12320C>T	c.(12319-12321)ACG>ATG	p.T4107M
Pat_05	Pre-Treatment	FBXL13	222235	37	7	102566739	102566739	Missense_Mutation	SNP	G	A	4	190	c.860C>T	c.(859-861)ACG>ATG	p.T287M
Pat_05	Pre-Treatment	RELN	5649	37	7	103138275	103138275	Missense_Mutation	SNP	G	A	5	279	c.8942C>T	c.(8941-8943)ACC>ATC	p.T2981I
Pat_05	Pre-Treatment	DOCK4	9732	37	7	111368532	111368532	Missense_Mutation	SNP	G	A	4	153	c.5699C>T	c.(5698-5700)CCG>CTG	p.P1900L
Pat_05	Pre-Treatment	PPP1R3A	5506	37	7	113558921	113558921	Missense_Mutation	SNP	C	T	174	183	c.131G>A	c.(130-132)CGA>CAA	p.R44Q
Pat_05	Pre-Treatment	CFTR	1080	37	7	117175335	117175335	Missense_Mutation	SNP	C	T	316	339	c.613C>T	c.(613-615)CCT>TCT	p.P205S
Pat_05	Pre-Treatment	GPR37	2861	37	7	124386989	124386989	Nonsense_Mutation	SNP	G	A	5	455	c.1432C>T	c.(1432-1434)CGA>TGA	p.R478*
Pat_05	Pre-Treatment	RBM28	55131	37	7	127965930	127965930	Nonsense_Mutation	SNP	G	A	5	288	c.1144C>T	c.(1144-1146)CAG>TAG	p.Q382*
Pat_05	Pre-Treatment	PLXNA4	91584	37	7	131817905	131817905	Missense_Mutation	SNP	G	T	125	175	c.5492C>A	c.(5491-5493)GCA>GAA	p.A1831E
Pat_05	Pre-Treatment	PLXNA4	91584	37	7	131872367	131872367	Splice_Site	SNP	C	T	96	250	c.2857_splice	c.e15-1	p.T953_splice
Pat_05	Pre-Treatment	BRAF	673	37	7	140453136	140453136	Missense_Mutation	SNP	A	T	170	228	c.1799T>A	c.(1798-1800)GTG>GAG	p.V600E
Pat_05	Pre-Treatment	TRYX3	136541	37	7	141954881	141954881	Missense_Mutation	SNP	C	T	279	376	c.430G>A	c.(430-432)GAT>AAT	p.D144N
Pat_05	Pre-Treatment	CLCN1	1180	37	7	143049018	143049018	Missense_Mutation	SNP	G	A	121	162	c.2927G>A	c.(2926-2928)CGA>CAA	p.R976Q
Pat_05	Pre-Treatment	OR2F2	135948	37	7	143633121	143633121	Missense_Mutation	SNP	C	G	103	234	c.796C>G	c.(796-798)CCC>GCC	p.P266A
Pat_05	Pre-Treatment	ABCB8	11194	37	7	150737671	150737672	Missense_Mutation	DNP	CC	TT	89	282	.1389_1390CC>T	387-1392)GTCCCC>GTTT	p.P464S
Pat_05	Pre-Treatment	ARHGEF10	9639	37	8	1851525	1851525	Missense_Mutation	SNP	G	A	4	141	c.1729G>A	c.(1729-1731)GCA>ACA	p.A577T
Pat_05	Pre-Treatment	ZDHHC2	51201	37	8	17067922	17067922	Missense_Mutation	SNP	A	G	58	50	c.883A>G	c.(883-885)ACT>GCT	p.T295A
Pat_05	Pre-Treatment	HR	55806	37	8	21984772	21984772	Missense_Mutation	SNP	G	A	5	265	c.1183C>T	c.(1183-1185)CGC>TGC	p.R395C
Pat_05	Pre-Treatment	BIN3	55909	37	8	22481830	22481830	Missense_Mutation	SNP	C	T	4	85	c.385G>A	c.(385-387)GAA>AAA	p.E129K
Pat_05	Pre-Treatment	TNFRSF10A	8797	37	8	23054654	23054654	Missense_Mutation	SNP	G	A	101	111	c.1078C>T	c.(1078-1080)CCC>TCC	p.P360S
Pat_05	Pre-Treatment	ADRA1A	148	37	8	26722089	26722089	Missense_Mutation	SNP	C	A	3	69	c.398G>T	c.(397-399)CGC>CTC	p.R133L
Pat_05	Pre-Treatment	HMBOX1	79618	37	8	28827691	28827691	Missense_Mutation	SNP	G	A	4	261	c.155G>A	c.(154-156)CGT>CAT	p.R52H
Pat_05	Pre-Treatment	RAB11FIP1	80223	37	8	37720621	37720621	Missense_Mutation	SNP	G	A	70	49	c.3644C>T	c.(3643-3645)CCC>CTC	p.P1215L
Pat_05	Pre-Treatment	ASH2L	9070	37	8	37963921	37963921	Missense_Mutation	SNP	G	A	4	231	c.214G>A	c.(214-216)GGT>AGT	p.G72S
Pat_05	Pre-Treatment	RB1CC1	9821	37	8	53586653	53586653	Missense_Mutation	SNP	C	T	7	819	c.754G>A	c.(754-756)GAA>AAA	p.E252K
Pat_05	Pre-Treatment	RP1	6101	37	8	55533983	55533983	Missense_Mutation	SNP	C	T	257	67	c.457C>T	c.(457-459)CCA>TCA	p.P153S
Pat_05	Pre-Treatment	CPA6	57094	37	8	68334828	68334828	Missense_Mutation	SNP	G	A	7	512	c.1225C>T	c.(1225-1227)CTC>TTC	p.L409F
Pat_05	Pre-Treatment	PREX2	80243	37	8	69136830	69136830	Missense_Mutation	SNP	G	A	5	250	c.4744G>A	c.(4744-4746)GTC>ATC	p.V1582I
Pat_05	Pre-Treatment	CALB1	793	37	8	91090621	91090621	Missense_Mutation	SNP	C	T	52	553	c.211G>A	c.(211-213)GGA>AGA	p.G71R
Pat_05	Pre-Treatment	VPS13B	157680	37	8	100861005	100861005	Missense_Mutation	SNP	T	C	591	139	c.10019T>C	c.(10018-10020)GTT>GCT	p.V3340A
Pat_05	Pre-Treatment	OXR1	55074	37	8	107763045	107763045	Missense_Mutation	SNP	C	T	4	252	c.2501C>T	c.(2500-2502)GCG>GTG	p.A834V

Pat_05	Pre-Treatment	ABRA	137735	37	8	107773354	107773354	Missense_Mutation	SNP	G	A	7	671	c.1057C>T	c.(1057-1059)CGT>TGT	p.R353C
Pat_05	Pre-Treatment	FAM83A	84985	37	8	124219632	124219632	Missense_Mutation	SNP	G	A	3	66	c.1009G>A	c.(1009-1011)GGC>AGC	p.G337S
Pat_05	Pre-Treatment	FER1L6	654463	37	8	124988301	124988301	Missense_Mutation	SNP	G	A	210	64	c.847G>A	c.(847-849)GAG>AAG	p.E283K
Pat_05	Pre-Treatment	SPATC1	375686	37	8	145095874	145095874	Missense_Mutation	SNP	G	A	5	335	c.1172G>A	c.(1171-1173)CGT>CAT	p.R391H
Pat_05	Pre-Treatment	ADCK5	203054	37	8	145603079	145603079	Nonsense_Mutation	SNP	C	T	4	55	c.16C>T	c.(16-18)CAG>TAG	p.Q6*
Pat_05	Pre-Treatment	C9orf82	79886	37	9	26887429	26887429	Missense_Mutation	SNP	A	G	3	89	c.386T>C	c.(385-387)CTG>CCG	p.L129P
Pat_05	Pre-Treatment	TAF1L	138474	37	9	32632706	32632706	Missense_Mutation	SNP	T	C	37	162	c.2872A>G	c.(2872-2874)ATT>GTT	p.I958V
Pat_05	Pre-Treatment	CNTNAP3	79937	37	9	39177472	39177472	Missense_Mutation	SNP	G	A	4	119	c.770C>T	c.(769-771)GCT>GTT	p.A257V
Pat_05	Pre-Treatment	TMC1	117531	37	9	75387387	75387387	Missense_Mutation	SNP	G	A	111	416	c.800G>A	c.(799-801)GGA>GAA	p.G267E
Pat_05	Pre-Treatment	PRUNE2	158471	37	9	79324445	79324445	Missense_Mutation	SNP	C	A	56	214	c.2745G>T	c.(2743-2745)AAG>AAT	p.K915N
Pat_05	Pre-Treatment	SHC3	53358	37	9	91793326	91793326	Missense_Mutation	SNP	G	A	4	150	c.50C>T	c.(49-51)TCG>TTG	p.S17L
Pat_05	Pre-Treatment	WNK2	65268	37	9	96009925	96009925	Missense_Mutation	SNP	C	T	13	6	c.1643C>T	c.(1642-1644)CCC>CTC	p.P548L
Pat_05	Pre-Treatment	TMOD1	7111	37	9	100286484	100286484	Missense_Mutation	SNP	G	A	4	225	c.14G>A	c.(13-15)CGA>CAA	p.R5Q
Pat_05	Pre-Treatment	KIAA0368	23392	37	9	114190363	114190363	Missense_Mutation	SNP	G	A	108	90	c.1543C>T	c.(1543-1545)CGC>TGC	p.R515C
Pat_05	Pre-Treatment	TNFSF15	9966	37	9	117554687	117554687	Missense_Mutation	SNP	C	T	34	96	c.301G>A	c.(301-303)GTT>ATT	p.V101I
Pat_05	Pre-Treatment	SPTAN1	6709	37	9	131394948	131394948	Missense_Mutation	SNP	G	A	4	165	c.7096G>A	c.(7096-7098)GAA>AAA	p.E2366K
Pat_05	Pre-Treatment	FAM73B	84895	37	9	131825860	131825860	Missense_Mutation	SNP	G	A	4	190	c.1120G>A	c.(1120-1122)GGG>AGG	p.G374R
Pat_05	Pre-Treatment	LAMC3	10319	37	9	133914341	133914341	Missense_Mutation	SNP	G	A	4	73	c.1067G>A	c.(1066-1068)CGT>CAT	p.R356H
Pat_05	Pre-Treatment	POMT1	10585	37	9	134396829	134396829	Missense_Mutation	SNP	C	T	4	167	c.1861C>T	c.(1861-1863)CGG>TGG	p.R621W
Pat_05	Pre-Treatment	ENTPD2	954	37	9	139945566	139945566	Missense_Mutation	SNP	G	A	4	169	c.562C>T	c.(562-564)CGG>TGG	p.R188W
Pat_05	Pre-Treatment	UAP1L1	91373	37	9	139974488	139974488	Missense_Mutation	SNP	G	A	5	185	c.1072G>A	c.(1072-1074)GTG>ATG	p.V358M
Pat_05	Pre-Treatment	ASMTL	8623	37	X	1546781	1546781	Missense_Mutation	SNP	G	A	42	114	c.743C>T	c.(742-744)CCC>CTC	p.P248L
Pat_05	Pre-Treatment	ZBED1	9189	37	X	2406806	2406806	Missense_Mutation	SNP	C	T	4	266	c.1955G>A	c.(1954-1956)CGG>CAG	p.R652Q
Pat_05	Pre-Treatment	CLCN4	1183	37	X	10188809	10188809	Missense_Mutation	SNP	G	A	5	268	c.2084G>A	c.(2083-2085)CGC>CAC	p.R695H
Pat_05	Pre-Treatment	TLR7	51284	37	X	12904646	12904646	Missense_Mutation	SNP	C	T	4	90	c.1019C>T	c.(1018-1020)CCC>CTC	p.P340L
Pat_05	Pre-Treatment	PIGA	5277	37	X	15339849	15339849	Nonsense_Mutation	SNP	G	A	6	498	c.1234C>T	c.(1234-1236)CGA>TGA	p.R412*
Pat_05	Pre-Treatment	MAP3K15	389840	37	X	19379645	19379645	Missense_Mutation	SNP	C	T	5	273	c.2171G>A	c.(2170-2172)CGG>CAG	p.R724Q
Pat_05	Pre-Treatment	MAGEB4	4115	37	X	30260287	30260287	Missense_Mutation	SNP	G	A	4	71	c.35G>A	c.(34-36)CGT>CAT	p.R12H
Pat_05	Pre-Treatment	SRPX	8406	37	X	38024076	38024076	Missense_Mutation	SNP	C	T	3	89	c.599G>A	c.(598-600)CGG>CAG	p.R200Q
Pat_05	Pre-Treatment	MED14	9282	37	X	40556385	40556385	Missense_Mutation	SNP	G	A	5	178	c.1541C>T	c.(1540-1542)ACG>ATG	p.T514M
Pat_05	Pre-Treatment	DDX3X	1654	37	X	41205843	41205843	Missense_Mutation	SNP	G	A	6	423	c.1583G>A	c.(1582-1584)CGT>CAT	p.R528H
Pat_05	Pre-Treatment	SSX3	10214	37	X	48213515	48213515	Missense_Mutation	SNP	G	A	4	139	c.199C>T	c.(199-201)CTC>TTC	p.L67F
Pat_05	Pre-Treatment	MAGIX	79917	37	X	49021378	49021378	Missense_Mutation	SNP	G	A	4	128	c.457G>A	c.(457-459)GTG>ATG	p.V153M
Pat_05	Pre-Treatment	CACNA1F	778	37	X	49065778	49065778	Missense_Mutation	SNP	C	T	3	20	c.4930G>A	c.(4930-4932)GAA>AAA	p.E1644K
Pat_05	Pre-Treatment	CACNA1F	778	37	X	49071632	49071632	Missense_Mutation	SNP	G	A	52	19	c.3544C>T	c.(3544-3546)CGT>TGT	p.R1182C
Pat_05	Pre-Treatment	DGAT2L6	347516	37	X	69397467	69397467	Missense_Mutation	SNP	G	A	128	32	c.35G>A	c.(34-36)GGC>GAC	p.G12D
Pat_05	Pre-Treatment	RGAG4	340526	37	X	71349790	71349790	Missense_Mutation	SNP	C	T	3	59	c.1601G>A	c.(1600-1602)CGC>CAC	p.R534H
Pat_05	Pre-Treatment	ODZ1	10178	37	X	123517994	123517994	Missense_Mutation	SNP	G	A	5	242	c.6766C>T	c.(6766-6768)CGT>TGT	p.R2256C
Pat_05	Pre-Treatment	MST4	51765	37	X	131202261	131202261	Missense_Mutation	SNP	G	A	93	36	c.349G>A	c.(349-351)GAT>AAT	p.D117N
Pat_05	Pre-Treatment	SLITRK2	84631	37	X	144905883	144905883	Missense_Mutation	SNP	G	A	4	208	c.1940G>A	c.(1939-1941)CGA>CAA	p.R647Q
Pat_05	Pre-Treatment	MAGEA8	4107	37	X	149013954	149013954	Missense_Mutation	SNP	C	T	132	36	c.908C>T	c.(907-909)TCC>TTC	p.S303F
Pat_05	Pre-Treatment	ZNF185	7739	37	X	152083292	152083292	Missense_Mutation	SNP	G	T	4	7	c.73G>T	c.(73-75)GTT>TTT	p.V25F
Pat_05	Pre-Treatment	PDZD4	57595	37	X	153069188	153069188	Missense_Mutation	SNP	G	A	4	122	c.1930C>T	c.(1930-1932)CGG>TGG	p.R644W
Pat_05	Pre-Treatment	PLXNA3	55558	37	X	153694180	153694180	Missense_Mutation	SNP	G	A	5	31	c.2522G>A	c.(2521-2523)CGC>CAC	p.R841H
Pat_05	Pre-Treatment	PLXNA3	55558	37	X	153696502	153696502	Missense_Mutation	SNP	C	T	4	133	c.3898C>T	c.(3898-3900)CGG>TGG	p.R1300W
Pat_05	Post-Resistance	SCNN1D	6339	37	1	1226943	1226943	Missense_Mutation	SNP	G	A	35	31	c.1870G>A	c.(1870-1872)GAA>AAA	p.E624K
Pat_05	Post-Resistance	DFFB	1677	37	1	3786321	3786321	Missense_Mutation	SNP	A	C	17	37	c.663A>C	c.(661-663)GAA>GAC	p.E221D

Pat_05	Post-Resistance	PIK3CD	5293	37	1	9783205	9783205	Missense_Mutation	SNP	C	T	334	360	c.2449C>T	c.(2449-2451)CCC>TCC	p.P817S
Pat_05	Post-Resistance	C1orf127	148345	37	1	11015213	11015213	Missense_Mutation	SNP	A	G	47	170	c.362T>C	c.(361-363)GTT>GCT	p.V121A
Pat_05	Post-Resistance	LOC649330	649330	37	1	12907865	12907865	Missense_Mutation	SNP	C	T	72	360	c.278G>A	c.(277-279)GGA>GAA	p.G93E
Pat_05	Post-Resistance	CLCNKA	1187	37	1	16351384	16351384	Missense_Mutation	SNP	G	A	89	69	c.356G>A	c.(355-357)GGA>GAA	p.G119E
Pat_05	Post-Resistance	PAX7	5081	37	1	19029699	19029699	Missense_Mutation	SNP	G	A	31	60	c.1064G>A	c.(1063-1065)CGC>CAC	p.R355H
Pat_05	Post-Resistance	EIF4G3	8672	37	1	21299593	21299593	Splice_Site	SNP	C	T	40	102	c.326_splice	c.e6-1	p.G109_splice
Pat_05	Post-Resistance	SFN	2810	37	1	27190112	27190112	Missense_Mutation	SNP	G	A	4	153	c.409G>A	c.(409-411)GGT>AGT	p.G137S
Pat_05	Post-Resistance	ZBTB8A	653121	37	1	33058747	33058747	Missense_Mutation	SNP	C	T	67	193	c.215C>T	c.(214-216)TCC>TTC	p.S72F
Pat_05	Post-Resistance	EPHA10	284656	37	1	38227610	38227611	Missense_Mutation	DNP	TG	CT	308	237	c.316_317CA>AG	c.(316-318)CAG>AGG	p.Q106R
Pat_05	Post-Resistance	TMCO2	127391	37	1	40713883	40713883	Missense_Mutation	SNP	G	A	67	71	c.218G>A	c.(217-219)CGA>CAA	p.R73Q
Pat_05	Post-Resistance	EBNA1BP2	10969	37	1	43630421	43630421	Nonsense_Mutation	SNP	T	A	74	58	c.763A>T	c.(763-765)AAA>TAA	p.K255*
Pat_05	Post-Resistance	CDC20	991	37	1	43824974	43824974	Missense_Mutation	SNP	C	A	4	191	c.88C>A	c.(88-90)CGC>AGC	p.R30S
Pat_05	Post-Resistance	CYP4Z1	199974	37	1	47571867	47571867	Missense_Mutation	SNP	G	A	182	97	c.1135G>A	c.(1135-1137)GTA>ATA	p.V379I
Pat_05	Post-Resistance	USP24	23358	37	1	55599790	55599790	Missense_Mutation	SNP	G	A	33	61	c.2854C>T	c.(2854-2856)CCA>TCA	p.P952S
Pat_05	Post-Resistance	INADL	10207	37	1	62614022	62614022	Missense_Mutation	SNP	C	T	180	169	c.5338C>T	c.(5338-5340)CTT>TTT	p.L1780F
Pat_05	Post-Resistance	EFCAB7	84455	37	1	63999792	63999792	Missense_Mutation	SNP	G	A	4	305	c.709G>A	c.(709-711)GCA>ACA	p.A237T
Pat_05	Post-Resistance	RPE65	6121	37	1	68912507	68912507	Missense_Mutation	SNP	C	T	51	184	c.131G>A	c.(130-132)CGA>CAA	p.R44Q
Pat_05	Post-Resistance	SLC44A5	204962	37	1	75708697	75708697	Splice_Site	SNP	C	T	53	47	c.346_splice	c.e8-1	p.I116_splice
Pat_05	Post-Resistance	KCND3	3752	37	1	112525062	112525062	Missense_Mutation	SNP	T	C	97	102	c.287A>G	c.(286-288)AAC>AGC	p.N96S
Pat_05	Post-Resistance	NRAS	4893	37	1	115256530	115256530	Missense_Mutation	SNP	G	T	92	415	c.181C>A	c.(181-183)CAA>AAA	p.Q61K
Pat_05	Post-Resistance	CD2	914	37	1	117297532	117297532	Missense_Mutation	SNP	G	A	29	27	c.341G>A	c.(340-342)GGA>GAA	p.G114E
Pat_05	Post-Resistance	HMGCS2	3158	37	1	120302578	120302579	Missense_Mutation	DNP	GG	AA	62	60	c.593_594CC>TT	c.(592-594)GCC>GTT	p.A198V
Pat_05	Post-Resistance	NOTCH2	4853	37	1	120461053	120461053	Missense_Mutation	SNP	C	T	130	334	c.5905G>A	c.(5905-5907)GAT>AAT	p.D1969N
Pat_05	Post-Resistance	LOC728989	728989	37	1	146493327	146493327	Missense_Mutation	SNP	G	A	35	113	c.586C>T	c.(586-588)CAT>TAT	p.H196Y
Pat_05	Post-Resistance	ECM1	1893	37	1	150482217	150482217	Missense_Mutation	SNP	C	T	158	300	c.202C>T	c.(202-204)CCC>TCC	p.P68S
Pat_05	Post-Resistance	TCHH	7062	37	1	152082220	152082220	Missense_Mutation	SNP	G	T	4	183	c.3473C>A	c.(3472-3474)CCG>CAG	p.P1158Q
Pat_05	Post-Resistance	RPTN	126638	37	1	152129112	152129112	Missense_Mutation	SNP	C	T	441	464	c.463G>A	c.(463-465)GAT>AAT	p.D155N
Pat_05	Post-Resistance	NES	10763	37	1	156642586	156642586	Missense_Mutation	SNP	G	A	100	189	c.1394C>T	c.(1393-1395)TCC>TTC	p.S465F
Pat_05	Post-Resistance	NTRK1	4914	37	1	156845875	156845875	Missense_Mutation	SNP	T	C	14	522	c.1505T>C	c.(1504-1506)GTT>GCT	p.V502A
Pat_05	Post-Resistance	ARHGEF11	9826	37	1	156909613	156909613	Missense_Mutation	SNP	T	C	46	122	c.3703A>G	c.(3703-3705)ACA>GCA	p.T1235A
Pat_05	Post-Resistance	FCRL5	83416	37	1	157508968	157508968	Missense_Mutation	SNP	G	A	60	81	c.1310C>T	c.(1309-1311)TCT>TTT	p.S437F
Pat_05	Post-Resistance	CD1C	911	37	1	158261967	158261967	Nonsense_Mutation	SNP	T	A	188	190	c.422T>A	c.(421-423)TTA>TAA	p.L141*
Pat_05	Post-Resistance	CD1E	913	37	1	158326534	158326534	Missense_Mutation	SNP	C	T	44	330	c.1015C>T	c.(1015-1017)CTT>TTT	p.L339F
Pat_05	Post-Resistance	FCRL6	343413	37	1	159779435	159779435	Missense_Mutation	SNP	C	T	124	118	c.848C>T	c.(847-849)TCC>TTC	p.S283F
Pat_05	Post-Resistance	NR1I3	9970	37	1	161200970	161200970	Nonsense_Mutation	SNP	G	A	19	51	c.760C>T	c.(760-762)CGA>TGA	p.R254*
Pat_05	Post-Resistance	DUSP12	11266	37	1	161722242	161722242	Missense_Mutation	SNP	G	A	222	226	c.662G>A	c.(661-663)TGT>TAT	p.C221Y
Pat_05	Post-Resistance	TNR	7143	37	1	175331865	175331865	Missense_Mutation	SNP	C	T	154	292	c.2788G>A	c.(2788-2790)GAA>AAA	p.E930K
Pat_05	Post-Resistance	PRG4	10216	37	1	186276544	186276544	Missense_Mutation	SNP	C	A	4	168	c.1693C>A	c.(1693-1695)CCC>ACC	p.P565T
Pat_05	Post-Resistance	DISP1	84976	37	1	223178708	223178709	Missense_Mutation	DNP	GG	AA	111	242	.3969_3970GG>A	67-3972)GAGGGC>GAA	p.G1324S
Pat_05	Post-Resistance	DISC1	27185	37	1	231829992	231829992	Missense_Mutation	SNP	C	G	40	180	c.488C>G	c.(487-489)GCC>GGC	p.A163G
Pat_05	Post-Resistance	MTR	4548	37	1	236979830	236979831	Missense_Mutation	DNP	GG	AA	158	206	c.751_752GG>AA	c.(751-753)GGA>AAA	p.G251K
Pat_05	Post-Resistance	TRIM58	25893	37	1	248039457	248039457	Missense_Mutation	SNP	C	T	104	254	c.1127C>T	c.(1126-1128)TCT>TTT	p.S376F
Pat_05	Post-Resistance	OR2L13	284521	37	1	248262696	248262696	Missense_Mutation	SNP	A	G	51	352	c.19A>G	c.(19-21)ACT>GCT	p.T7A
Pat_05	Post-Resistance	ANKRD30A	91074	37	10	37430948	37430948	Missense_Mutation	SNP	C	G	3	69	c.955C>G	c.(955-957)CCA>GCA	p.P319A
Pat_05	Post-Resistance	RASSF4	83937	37	10	45465703	45465703	Missense_Mutation	SNP	C	T	145	78	c.53C>T	c.(52-54)TCC>TTC	p.S18F
Pat_05	Post-Resistance	GPRIN2	9721	37	10	46999128	46999128	Missense_Mutation	SNP	G	A	19	53	c.248G>A	c.(247-249)CGA>CAA	p.R83Q
Pat_05	Post-Resistance	HK1	3098	37	10	71129293	71129293	Missense_Mutation	SNP	C	T	122	41	c.788C>T	c.(787-789)GCC>GTC	p.A263V

Pat_05	Post-Resistance	NPFFR1	64106	37	10	72020400	72020400	Missense_Mutation	SNP	C	T	9	7	c.412G>A	c.(412-414)GAA>AAA	p.E138K
Pat_05	Post-Resistance	GPAM	57678	37	10	113926167	113926167	Missense_Mutation	SNP	G	A	58	34	c.1214C>T	c.(1213-1215)TCC>TTC	p.S405F
Pat_05	Post-Resistance	PNLIPRP1	5407	37	10	118352022	118352022	Missense_Mutation	SNP	G	A	88	21	c.299G>A	c.(298-300)GGA>GAA	p.G100E
Pat_05	Post-Resistance	KRTAP5-5	439915	37	11	1651459	1651459	Missense_Mutation	SNP	G	T	4	60	c.389G>T	c.(388-390)GGC>GTC	p.G130V
Pat_05	Post-Resistance	HBBP1	3044	37	11	5264439	5264439	Missense_Mutation	SNP	G	A	44	9	c.47C>T	c.(46-48)TCC>TTC	p.S16F
Pat_05	Post-Resistance	OLFML1	283298	37	11	7509550	7509550	Missense_Mutation	SNP	G	A	4	149	c.322G>A	c.(322-324)GCT>ACT	p.A108T
Pat_05	Post-Resistance	SPON1	10418	37	11	14287201	14287201	Missense_Mutation	SNP	G	A	24	9	c.2392G>A	c.(2392-2394)GAG>AAG	p.E798K
Pat_05	Post-Resistance	CRY2	1408	37	11	45892471	45892471	Missense_Mutation	SNP	G	A	3	56	c.1691G>A	c.(1690-1692)AGC>AAC	p.S564N
Pat_05	Post-Resistance	OR4C13	283092	37	11	49974799	49974799	Missense_Mutation	SNP	G	A	96	33	c.825G>A	c.(823-825)ATG>ATA	p.M275I
Pat_05	Post-Resistance	OR4A5	81318	37	11	51412302	51412302	Missense_Mutation	SNP	T	C	27	49	c.94A>G	c.(94-96)ACA>GCA	p.T32A
Pat_05	Post-Resistance	FEN1	2237	37	11	61563828	61563828	Missense_Mutation	SNP	G	A	3	50	c.995G>A	c.(994-996)CGC>CAC	p.R332H
Pat_05	Post-Resistance	LRP5	4041	37	11	68205968	68205968	Missense_Mutation	SNP	C	T	108	49	c.4166C>T	c.(4165-4167)CCC>CTC	p.P1389L
Pat_05	Post-Resistance	HEPHL1	341208	37	11	93826703	93826703	Nonsense_Mutation	SNP	G	A	227	101	c.2331G>A	c.(2329-2331)TGG>TGA	p.W777*
Pat_05	Post-Resistance	CNTN5	53942	37	11	100061987	100061987	Splice_Site	SNP	T	C	25	8	c.1708_splice	c.e14+2	p.E570_splice
Pat_05	Post-Resistance	YAP1	10413	37	11	102033218	102033218	Missense_Mutation	SNP	C	T	238	128	c.604C>T	c.(604-606)CCC>TCC	p.P202S
Pat_05	Post-Resistance	NCAPD3	23310	37	11	134038828	134038828	Missense_Mutation	SNP	A	G	104	42	c.3223T>C	c.(3223-3225)TTC>CTC	p.F1075L
Pat_05	Post-Resistance	GDF3	9573	37	12	7842689	7842689	Missense_Mutation	SNP	G	A	129	113	c.880C>T	c.(880-882)CAT>TAT	p.H294Y
Pat_05	Post-Resistance	KIAA1467	57613	37	12	13215874	13215874	Nonsense_Mutation	SNP	C	T	178	519	c.817C>T	c.(817-819)CGA>TGA	p.R273*
Pat_05	Post-Resistance	ARHGDIB	397	37	12	15095590	15095590	Missense_Mutation	SNP	G	A	101	109	c.472C>T	c.(472-474)CCA>TCA	p.P158S
Pat_05	Post-Resistance	ANP32D	23519	37	12	48866508	48866508	Missense_Mutation	SNP	G	A	76	244	c.61G>A	c.(61-63)GAA>AAA	p.E21K
Pat_05	Post-Resistance	KRT8	3856	37	12	53298675	53298675	Missense_Mutation	SNP	A	C	3	38	c.91T>G	c.(91-93)TCC>GCC	p.S31A
Pat_05	Post-Resistance	ITGA5	3678	37	12	54798495	54798495	Missense_Mutation	SNP	C	T	38	120	c.1409G>A	c.(1408-1410)GGA>GAA	p.G470E
Pat_05	Post-Resistance	PDE1B	5153	37	12	54943765	54943765	Missense_Mutation	SNP	T	G	17	61	c.109T>G	c.(109-111)TCT>GCT	p.S37A
Pat_05	Post-Resistance	OR6C2	341416	37	12	55846399	55846399	Missense_Mutation	SNP	G	A	92	91	c.402G>A	c.(400-402)ATG>ATA	p.M134I
Pat_05	Post-Resistance	NXPH4	11247	37	12	57619184	57619184	Missense_Mutation	SNP	G	A	39	78	c.581G>A	c.(580-582)GGG>GAG	p.G194E
Pat_05	Post-Resistance	OS9	10956	37	12	58089596	58089596	Missense_Mutation	SNP	G	A	139	130	c.373G>A	c.(373-375)GGA>AGA	p.G125R
Pat_05	Post-Resistance	FAM19A2	338811	37	12	62147474	62147474	Missense_Mutation	SNP	C	T	55	177	c.313G>A	c.(313-315)GAA>AAA	p.E105K
Pat_05	Post-Resistance	SYT1	6857	37	12	79842697	79842697	Splice_Site	SNP	G	A	101	91	c.1063_splice	c.e12-1	p.K355_splice
Pat_05	Post-Resistance	UTP20	27340	37	12	101736806	101736806	Missense_Mutation	SNP	G	A	56	61	c.4384G>A	c.(4384-4386)GAA>AAA	p.E1462K
Pat_05	Post-Resistance	TRPV4	59341	37	12	110232243	110232243	Missense_Mutation	SNP	T	C	55	293	c.1382A>G	c.(1381-1383)GAC>GGC	p.D461G
Pat_05	Post-Resistance	RNFT2	84900	37	12	117188100	117188100	Nonsense_Mutation	SNP	C	T	27	36	c.538C>T	c.(538-540)CAG>TAG	p.Q180*
Pat_05	Post-Resistance	CCDC60	160777	37	12	119866487	119866487	Splice_Site	SNP	G	A	11	22	c.91_splice	c.e2-1	p.V31_splice
Pat_05	Post-Resistance	OGFOD2	79676	37	12	123463861	123463861	Missense_Mutation	SNP	C	A	4	142	c.1021C>A	c.(1021-1023)CCC>ACC	p.P341T
Pat_05	Post-Resistance	DNAH10	196385	37	12	124408932	124408932	Missense_Mutation	SNP	G	A	28	29	c.11365G>A	.(11365-11367)GGG>AG	p.G3789R
Pat_05	Post-Resistance	WASF3	10810	37	13	27250713	27250713	Missense_Mutation	SNP	C	T	7	109	c.568C>T	c.(568-570)CGT>TGT	p.R190C
Pat_05	Post-Resistance	TRPC4	7223	37	13	38211066	38211066	Missense_Mutation	SNP	C	T	82	93	c.2908G>A	c.(2908-2910)GAA>AAA	p.E970K
Pat_05	Post-Resistance	ATP7B	540	37	13	52518298	52518298	Missense_Mutation	SNP	C	T	89	106	c.3190G>A	c.(3190-3192)GAG>AAG	p.E1064K
Pat_05	Post-Resistance	OR4K13	390433	37	14	20502121	20502121	Missense_Mutation	SNP	G	A	19	34	c.797C>T	c.(796-798)TCG>TTG	p.S266L
Pat_05	Post-Resistance	MYH6	4624	37	14	23873585	23873586	Missense_Mutation	DNP	CC	TT	142	64	c.654_655GG>AA	652-657)GAGGAC>GAAA	p.D219N
Pat_05	Post-Resistance	RALGAPA1	253959	37	14	36211615	36211615	Missense_Mutation	SNP	C	T	3	0	c.1408G>A	c.(1408-1410)GAC>AAC	p.D470N
Pat_05	Post-Resistance	MIA2	117153	37	14	39717268	39717268	Missense_Mutation	SNP	C	T	101	29	c.1490C>T	c.(1489-1491)ACT>ATT	p.T497I
Pat_05	Post-Resistance	MUDENG	55745	37	14	57748805	57748805	Splice_Site	SNP	A	G	15	21	c.949_splice	c.e4-2	p.V317_splice
Pat_05	Post-Resistance	SIX1	6495	37	14	61113294	61113294	Missense_Mutation	SNP	C	T	53	9	c.562G>A	c.(562-564)GAG>AAG	p.E188K
Pat_05	Post-Resistance	ZFYVE26	23503	37	14	68260920	68260920	Missense_Mutation	SNP	C	T	349	163	c.2369G>A	c.(2368-2370)AGT>AAT	p.S790N
Pat_05	Post-Resistance	TMEM63C	57156	37	14	77686405	77686405	Missense_Mutation	SNP	C	T	8	3	c.287C>T	c.(286-288)TCC>TTC	p.S96F
Pat_05	Post-Resistance	HERC2	8924	37	15	28358816	28358816	Missense_Mutation	SNP	T	C	6	92	c.13922A>G	.(13921-13923)GAA>GG	p.E4641G
Pat_05	Post-Resistance	EIF2AK4	440275	37	15	40284403	40284403	Missense_Mutation	SNP	G	A	33	120	c.2659G>A	c.(2659-2661)GGA>AGA	p.G887R

Pat_05	Post-Resistance	CDAN1	146059	37	15	43026214	43026214	Missense_Mutation	SNP	G	A	40	106	c.1289C>T	c.(1288-1290)GCT>GTT	p.A430V
Pat_05	Post-Resistance	TP53BP1	7158	37	15	43714147	43714147	Missense_Mutation	SNP	C	T	90	84	c.3991G>A	c.(3991-3993)GGG>AGG	p.G1331R
Pat_05	Post-Resistance	TMEM202	338949	37	15	72700185	72700185	Missense_Mutation	SNP	C	T	56	55	c.773C>T	c.(772-774)TCT>TTT	p.S258F
Pat_05	Post-Resistance	NEO1	4756	37	15	73541473	73541473	Missense_Mutation	SNP	A	G	22	284	c.1679A>G	c.(1678-1680)GAA>GGA	p.E560G
Pat_05	Post-Resistance	LOC645752	645752	37	15	78207888	78207888	Missense_Mutation	SNP	A	C	3	75	c.1110T>G	c.(1108-1110)AAT>AAG	p.N370K
Pat_05	Post-Resistance	ZNF710	374655	37	15	90622960	90622960	Nonsense_Mutation	SNP	G	T	58	187	c.1894G>T	c.(1894-1896)GAG>TAG	p.E632*
Pat_05	Post-Resistance	WASH3P	374666	37	15	102515344	102515344	Missense_Mutation	SNP	A	C	4	56	c.568A>C	c.(568-570)AAG>CAG	p.K190Q
Pat_05	Post-Resistance	SPSB3	90864	37	16	1828154	1828154	Missense_Mutation	SNP	G	A	37	33	c.473C>T	c.(472-474)CCC>CTC	p.P158L
Pat_05	Post-Resistance	PRSS22	64063	37	16	2903246	2903246	Missense_Mutation	SNP	C	T	47	103	c.802G>A	c.(802-804)GAG>AAG	p.E268K
Pat_05	Post-Resistance	CREBBP	1387	37	16	3819211	3819212	Missense_Mutation	DNP	GG	AA	68	154	.3023_3024CC>T	c.(3022-3024)CCC>CTT	p.P1008L
Pat_05	Post-Resistance	GRIN2A	2903	37	16	9857613	9857613	Missense_Mutation	SNP	C	T	16	81	c.3788G>A	c.(3787-3789)GGG>GAG	p.G1263E
Pat_05	Post-Resistance	TMC5	79838	37	16	19451823	19451823	Missense_Mutation	SNP	C	T	103	299	c.463C>T	c.(463-465)CAT>TAT	p.H155Y
Pat_05	Post-Resistance	PRKCB	5579	37	16	24104192	24104192	Missense_Mutation	SNP	C	T	127	104	c.610C>T	c.(610-612)CCC>TCC	p.P204S
Pat_05	Post-Resistance	ZNF646	9726	37	16	31088970	31088970	Missense_Mutation	SNP	C	T	13	58	c.1325C>T	c.(1324-1326)CCC>CTC	p.P442L
Pat_05	Post-Resistance	CHD9	80205	37	16	53348813	53348813	Missense_Mutation	SNP	C	T	42	168	c.7441C>T	c.(7441-7443)CCT>TCT	p.P2481S
Pat_05	Post-Resistance	CDH16	1014	37	16	66945995	66945995	Nonsense_Mutation	SNP	G	A	4	118	c.1597C>T	c.(1597-1599)CAG>TAG	p.Q533*
Pat_05	Post-Resistance	PLEKHG4	25894	37	16	67314032	67314032	Missense_Mutation	SNP	A	G	4	171	c.85A>G	c.(85-87)AGG>GGG	p.R29G
Pat_05	Post-Resistance	RFWD3	55159	37	16	74683038	74683038	Missense_Mutation	SNP	G	A	73	171	c.784C>T	c.(784-786)CCC>TCC	p.P262S
Pat_05	Post-Resistance	PKD1L2	114780	37	16	81167302	81167302	Missense_Mutation	SNP	G	A	29	46	c.5723C>T	c.(5722-5724)CCC>CTC	p.P1908L
Pat_05	Post-Resistance	PLCG2	5336	37	16	81888165	81888165	Missense_Mutation	SNP	T	A	220	202	c.310T>A	c.(310-312)TTC>ATC	p.F104I
Pat_05	Post-Resistance	CAMKK1	84254	37	17	3773120	3773120	Missense_Mutation	SNP	G	A	74	269	c.1187C>T	c.(1186-1188)ACG>ATG	p.T396M
Pat_05	Post-Resistance	FBXO39	162517	37	17	6684059	6684059	Missense_Mutation	SNP	G	A	53	23	c.872G>A	c.(871-873)CGG>CAG	p.R291Q
Pat_05	Post-Resistance	TEKT3	64518	37	17	15234473	15234473	Nonsense_Mutation	SNP	G	A	42	103	c.430C>T	c.(430-432)CAA>TAA	p.Q144*
Pat_05	Post-Resistance	MAP2K3	5606	37	17	21205486	21205486	Missense_Mutation	SNP	A	G	16	220	c.431A>G	c.(430-432)GAC>GGC	p.D144G
Pat_05	Post-Resistance	SUPT6H	6830	37	17	27023987	27023987	Missense_Mutation	SNP	C	T	184	289	c.4096C>T	c.(4096-4098)CAC>TAC	p.H1366Y
Pat_05	Post-Resistance	LRRC37B	114659	37	17	30349585	30349585	Missense_Mutation	SNP	C	T	101	136	c.1420C>T	c.(1420-1422)CAT>TAT	p.H474Y
Pat_05	Post-Resistance	STARD3	10948	37	17	37817338	37817338	Missense_Mutation	SNP	G	A	4	154	c.1139G>A	c.(1138-1140)CGG>CAG	p.R380Q
Pat_05	Post-Resistance	KRT27	342574	37	17	38933948	38933948	Missense_Mutation	SNP	T	G	206	344	c.1009A>C	c.(1009-1011)AGT>CGT	p.S337R
Pat_05	Post-Resistance	BRCA1	672	37	17	41244316	41244316	Missense_Mutation	SNP	G	A	81	153	c.3232C>T	c.(3232-3234)CCA>TCA	p.P1078S
Pat_05	Post-Resistance	DHX8	1659	37	17	41598239	41598239	Missense_Mutation	SNP	A	G	3	313	c.3058A>G	c.(3058-3060)AGG>GGG	p.R1020G
Pat_05	Post-Resistance	FMNL1	752	37	17	43320500	43320500	Missense_Mutation	SNP	G	A	121	234	c.2026G>A	c.(2026-2028)GAT>AAT	p.D676N
Pat_05	Post-Resistance	CACNA1G	8913	37	17	48650037	48650037	Missense_Mutation	SNP	G	A	14	16	c.869G>A	c.(868-870)GGG>GAG	p.G290E
Pat_05	Post-Resistance	SPAG9	9043	37	17	49079164	49079164	Missense_Mutation	SNP	C	T	63	155	c.1519G>A	c.(1519-1521)GAA>AAA	p.E507K
Pat_05	Post-Resistance	SPAG9	9043	37	17	49157025	49157025	Missense_Mutation	SNP	T	C	3	123	c.344A>G	c.(343-345)AAG>AGG	p.K115R
Pat_05	Post-Resistance	OR4D1	26689	37	17	56232773	56232773	Missense_Mutation	SNP	C	T	137	204	c.259C>T	c.(259-261)CAT>TAT	p.H87Y
Pat_05	Post-Resistance	MRPL38	64978	37	17	73897876	73897877	Nonsense_Mutation	DNP	GG	AA	79	125	c.507_508CC>TT	505-510)CCCCGA>CCTT	p.R170*
Pat_05	Post-Resistance	TMC8	147138	37	17	76128447	76128447	Missense_Mutation	SNP	C	A	14	97	c.306C>A	c.(304-306)TTC>TTA	p.F102L
Pat_05	Post-Resistance	CDH2	1000	37	18	25572789	25572789	Missense_Mutation	SNP	G	A	53	106	c.1174C>T	c.(1174-1176)CCT>TCT	p.P392S
Pat_05	Post-Resistance	CCDC68	80323	37	18	52605289	52605289	Missense_Mutation	SNP	C	T	35	46	c.244G>A	c.(244-246)GAT>AAT	p.D82N
Pat_05	Post-Resistance	NETO1	81832	37	18	70423314	70423314	Missense_Mutation	SNP	C	T	53	104	c.937G>A	c.(937-939)GGA>AGA	p.G313R
Pat_05	Post-Resistance	SLC25A41	284427	37	19	6433587	6433587	Missense_Mutation	SNP	G	C	80	191	c.118C>G	c.(118-120)CCA>GCA	p.P40A
Pat_05	Post-Resistance	CLEC4M	10332	37	19	7833780	7833780	Missense_Mutation	SNP	C	T	67	249	c.1037C>T	c.(1036-1038)GCG>GTG	p.A346V
Pat_05	Post-Resistance	ADAMTS10	81794	37	19	8670190	8670190	Missense_Mutation	SNP	C	T	14	40	c.142G>A	c.(142-144)GAC>AAC	p.D48N
Pat_05	Post-Resistance	MUC16	94025	37	19	9061896	9061896	Missense_Mutation	SNP	G	C	61	193	c.25550C>G	c.(25549-25551)ACA>AGA	p.T8517R
Pat_05	Post-Resistance	DNMT1	1786	37	19	10260302	10260302	Missense_Mutation	SNP	C	A	6	572	c.2365G>T	c.(2365-2367)GGG>TGG	p.G789W
Pat_05	Post-Resistance	ZNF844	284391	37	19	12187307	12187307	Missense_Mutation	SNP	G	C	6	175	c.1372G>C	c.(1372-1374)GAT>CAT	p.D458H
Pat_05	Post-Resistance	ZNF844	284391	37	19	12187394	12187394	Missense_Mutation	SNP	T	C	3	62	c.1459T>C	c.(1459-1461)TTT>CTT	p.F487L

Pat_05	Post-Resistance	ZNF709	163051	37	19	12577561	12577561	Missense_Mutation	SNP	G	A	35	122	c.107C>T	c.(106-108)ACC>ATC	p.T36I
Pat_05	Post-Resistance	ZNF490	57474	37	19	12692177	12692177	Nonsense_Mutation	SNP	G	A	30	50	c.712C>T	c.(712-714)CGA>TGA	p.R238*
Pat_05	Post-Resistance	NOTCH3	4854	37	19	15290970	15290970	Missense_Mutation	SNP	G	C	19	334	c.3240C>G	c.(3238-3240)CAC>CAG	p.H1080Q
Pat_05	Post-Resistance	NWD1	284434	37	19	16875863	16875863	Missense_Mutation	SNP	C	T	113	121	c.2270C>T	c.(2269-2271)TCC>TTC	p.S757F
Pat_05	Post-Resistance	ZNF431	170959	37	19	21366278	21366278	Missense_Mutation	SNP	A	C	11	34	c.1172A>C	c.(1171-1173)AAA>ACA	p.K391T
Pat_05	Post-Resistance	LGI4	163175	37	19	35625512	35625512	Missense_Mutation	SNP	C	T	12	22	c.73G>A	c.(73-75)GGA>AGA	p.G25R
Pat_05	Post-Resistance	ZNF569	148266	37	19	37903561	37903561	Missense_Mutation	SNP	A	G	112	108	c.1999T>C	c.(1999-2001)TGT>CGT	p.C667R
Pat_05	Post-Resistance	ZNF571	51276	37	19	38055543	38055543	Missense_Mutation	SNP	C	G	16	36	c.1787G>C	c.(1786-1788)AGA>ACA	p.R596T
Pat_05	Post-Resistance	SHKBP1	92799	37	19	41094587	41094587	Missense_Mutation	SNP	T	C	19	426	c.1394T>C	c.(1393-1395)ATT>ACT	p.I465T
Pat_05	Post-Resistance	CARD8	22900	37	19	48724999	48724999	Missense_Mutation	SNP	T	A	5	130	c.831A>T	c.(829-831)AAA>AAT	p.K277N
Pat_05	Post-Resistance	PTH2	113091	37	19	49926533	49926533	Missense_Mutation	SNP	G	C	5	55	c.64C>G	c.(64-66)CTG>GTG	p.L22V
Pat_05	Post-Resistance	ZNF578	147660	37	19	53014551	53014551	Missense_Mutation	SNP	G	A	6	207	c.917G>A	c.(916-918)CGT>CAT	p.R306H
Pat_05	Post-Resistance	ZNF845	91664	37	19	53855197	53855197	Missense_Mutation	SNP	G	A	9	265	c.1269G>A	c.(1267-1269)ATG>ATA	p.M423I
Pat_05	Post-Resistance	LILRA1	11024	37	19	55106787	55106787	Missense_Mutation	SNP	C	T	96	322	c.581C>T	c.(580-582)TCG>TTG	p.S194L
Pat_05	Post-Resistance	LILRB1	10859	37	19	55146098	55146098	Missense_Mutation	SNP	G	A	7	13	c.1367G>A	c.(1366-1368)GGA>GAA	p.G456E
Pat_05	Post-Resistance	FCAR	2204	37	19	55396680	55396680	Missense_Mutation	SNP	C	T	16	57	c.104C>T	c.(103-105)TCG>TTG	p.S35L
Pat_05	Post-Resistance	NLRP2	55655	37	19	55493593	55493593	Missense_Mutation	SNP	C	T	113	321	c.527C>T	c.(526-528)CCT>CTT	p.P176L
Pat_05	Post-Resistance	BRSK1	84446	37	19	55817693	55817694	Missense_Mutation	DNP	CC	TT	41	118	.1964_1965CC>T	c.(1963-1965)TCC>TTT	p.S655F
Pat_05	Post-Resistance	NLRP8	126205	37	19	56499245	56499245	Missense_Mutation	SNP	G	A	65	198	c.3113G>A	c.(3112-3114)GGA>GAA	p.G1038E
Pat_05	Post-Resistance	CRIM1	51232	37	2	36726470	36726470	Missense_Mutation	SNP	G	A	4	313	c.1481G>A	c.(1480-1482)CGG>CAG	p.R494Q
Pat_05	Post-Resistance	LRPPRC	10128	37	2	44132911	44132911	Missense_Mutation	SNP	G	T	37	70	c.3284C>A	c.(3283-3285)ACC>AAC	p.T1095N
Pat_05	Post-Resistance	ANTXR1	84168	37	2	69472492	69472492	Missense_Mutation	SNP	C	T	15	5	c.1570C>T	c.(1570-1572)CCG>TCG	p.P524S
Pat_05	Post-Resistance	ARID5A	10865	37	2	97217971	97217971	Missense_Mutation	SNP	C	A	4	312	c.1706C>A	c.(1705-1707)CCG>CAG	p.P569Q
Pat_05	Post-Resistance	ST6GAL2	84620	37	2	107423220	107423220	Missense_Mutation	SNP	C	T	35	155	c.1504G>A	c.(1504-1506)GAT>AAT	p.D502N
Pat_05	Post-Resistance	FBLN7	129804	37	2	112922604	112922604	Missense_Mutation	SNP	G	A	4	145	c.262G>A	c.(262-264)GCA>ACA	p.A88T
Pat_05	Post-Resistance	PSD4	23550	37	2	113958879	113958879	Missense_Mutation	SNP	A	T	71	91	c.3058A>T	c.(3058-3060)AGC>TGC	p.S1020C
Pat_05	Post-Resistance	CNTNAP5	129684	37	2	124999956	124999956	Missense_Mutation	SNP	G	A	14	23	c.367G>A	c.(367-369)GAA>AAA	p.E123K
Pat_05	Post-Resistance	POTEF	728378	37	2	130832668	130832668	Missense_Mutation	SNP	C	T	173	106	c.2377G>A	c.(2377-2379)GAG>AAG	p.E793K
Pat_05	Post-Resistance	THSD7B	80731	37	2	138030231	138030231	Missense_Mutation	SNP	C	T	24	31	c.2302C>T	c.(2302-2304)CGG>TGG	p.R768W
Pat_05	Post-Resistance	NMI	9111	37	2	152127343	152127343	Missense_Mutation	SNP	T	G	16	87	c.788A>C	c.(787-789)GAA>GCA	p.E263A
Pat_05	Post-Resistance	NEB	4703	37	2	152506691	152506691	Missense_Mutation	SNP	T	G	48	43	c.7430A>C	c.(7429-7431)GAT>GCT	p.D2477A
Pat_05	Post-Resistance	DYNC1I2	1781	37	2	172583344	172583344	Missense_Mutation	SNP	C	T	62	38	c.914C>T	c.(913-915)GCC>GTC	p.A305V
Pat_05	Post-Resistance	DYNC1I2	1781	37	2	172583346	172583346	Missense_Mutation	SNP	C	T	62	37	c.916C>T	c.(916-918)CCT>TCT	p.P306S
Pat_05	Post-Resistance	TTN	7273	37	2	179404396	179404396	Missense_Mutation	SNP	G	A	133	111	c.90692C>T	c.(90691-90693)CCA>CTA	p.P30231L
Pat_05	Post-Resistance	TTN	7273	37	2	179629358	179629358	Missense_Mutation	SNP	G	A	66	146	c.9884C>T	c.(9883-9885)ACG>ATG	p.T3295M
Pat_05	Post-Resistance	TTN	7273	37	2	179664293	179664293	Missense_Mutation	SNP	G	A	39	129	c.835C>T	c.(835-837)CGG>TGG	p.R279W
Pat_05	Post-Resistance	DNAH7	56171	37	2	196620918	196620918	Missense_Mutation	SNP	G	A	96	72	c.11525C>T	c.(11524-11526)CCA>CTA	p.P3842L
Pat_05	Post-Resistance	DNAH7	56171	37	2	196749415	196749415	Missense_Mutation	SNP	C	T	42	147	c.5657G>A	c.(5656-5658)CGA>CAA	p.R1886Q
Pat_05	Post-Resistance	AOX1	316	37	2	201477335	201477335	Missense_Mutation	SNP	G	A	73	226	c.1267G>A	c.(1267-1269)GAA>AAA	p.E423K
Pat_05	Post-Resistance	NBEAL1	65065	37	2	204009383	204009383	Nonsense_Mutation	SNP	C	T	48	216	c.4822C>T	c.(4822-4824)CAG>TAG	p.Q1608*
Pat_05	Post-Resistance	NBEAL1	65065	37	2	204082051	204082051	Missense_Mutation	SNP	G	A	17	55	c.8059G>A	c.(8059-8061)GAA>AAA	p.E2687K
Pat_05	Post-Resistance	IKZF2	22807	37	2	213872562	213872562	Missense_Mutation	SNP	A	T	34	22	c.1103T>A	c.(1102-1104)ATT>AAT	p.I368N
Pat_05	Post-Resistance	CHPF	79586	37	2	220405190	220405190	Missense_Mutation	SNP	G	A	4	148	c.1243C>T	c.(1243-1245)CGT>TGT	p.R415C
Pat_05	Post-Resistance	C2orf57	165100	37	2	232458669	232458669	Missense_Mutation	SNP	G	A	113	82	c.1007G>A	c.(1006-1008)GGA>GAA	p.G336E
Pat_05	Post-Resistance	COL6A3	1293	37	2	238280543	238280543	Missense_Mutation	SNP	C	T	38	109	c.4117G>A	c.(4117-4119)GCA>ACA	p.A1373T
Pat_05	Post-Resistance	SIRPB2	284759	37	20	1471971	1471971	Missense_Mutation	SNP	G	A	13	53	c.35C>T	c.(34-36)GCC>GTC	p.A12V
Pat_05	Post-Resistance	MACROD2	140733	37	20	15913932	15913932	Missense_Mutation	SNP	C	T	44	31	c.787C>T	c.(787-789)CCA>TCA	p.P263S

Pat_05	Post-Resistance	CST2	1470	37	20	23807156	23807156	Missense_Mutation	SNP	G	A	36	84	c.142C>T	c.(142-144)CTT>TTT	p.L48F
Pat_05	Post-Resistance	FITM2	128486	37	20	42935818	42935818	Missense_Mutation	SNP	G	A	121	69	c.236C>T	c.(235-237)ACC>ATC	p.T79I
Pat_05	Post-Resistance	TMPRSS15	5651	37	21	19737500	19737500	Missense_Mutation	SNP	G	A	64	190	c.730C>T	c.(730-732)CCA>TCA	p.P244S
Pat_05	Post-Resistance	BACH1	571	37	21	30698389	30698389	Missense_Mutation	SNP	A	C	17	51	c.244A>C	c.(244-246)AAA>CAA	p.K82Q
Pat_05	Post-Resistance	KRTAP24-1	643803	37	21	31654667	31654667	Missense_Mutation	SNP	G	A	44	78	c.584C>T	c.(583-585)TCC>TTC	p.S195F
Pat_05	Post-Resistance	DSCAM	1826	37	21	41465753	41465753	Missense_Mutation	SNP	G	A	38	56	c.3745C>T	c.(3745-3747)CCC>TCC	p.P1249S
Pat_05	Post-Resistance	PWP2	5822	37	21	45550523	45550523	Missense_Mutation	SNP	C	T	33	69	c.2630C>T	c.(2629-2631)TCC>TTC	p.S877F
Pat_05	Post-Resistance	TRPM2	7226	37	21	45819208	45819208	Missense_Mutation	SNP	G	A	44	99	c.2092G>A	c.(2092-2094)GAA>AAA	p.E698K
Pat_05	Post-Resistance	SLC25A18	83733	37	22	18070764	18070764	Missense_Mutation	SNP	G	A	4	309	c.649G>A	c.(649-651)GGT>AGT	p.G217S
Pat_05	Post-Resistance	C22orf29	79680	37	22	19839682	19839682	Missense_Mutation	SNP	G	A	147	214	c.103C>T	c.(103-105)CCT>TCT	p.P35S
Pat_05	Post-Resistance	ZNF280B	140883	37	22	22843674	22843674	Missense_Mutation	SNP	A	G	4	158	c.50T>C	c.(49-51)ATA>ACA	p.I17T
Pat_05	Post-Resistance	TFIP11	24144	37	22	26890130	26890130	Missense_Mutation	SNP	C	T	83	131	c.2133G>A	c.(2131-2133)ATG>ATA	p.M711I
Pat_05	Post-Resistance	CHEK2	11200	37	22	29091840	29091841	Missense_Mutation	DNP	TG	CA	6	155	.1116_1117CA>T	114-1119)TCCAAG>TCTG	p.K373E
Pat_05	Post-Resistance	PLA2G3	50487	37	22	31533809	31533809	Missense_Mutation	SNP	G	A	190	263	c.953C>T	c.(952-954)TCC>TTC	p.S318F
Pat_05	Post-Resistance	PLA2G6	8398	37	22	38522451	38522451	Nonsense_Mutation	SNP	G	A	43	194	c.1354C>T	c.(1354-1356)CAG>TAG	p.Q452*
Pat_05	Post-Resistance	FAM83F	113828	37	22	40417674	40417674	Missense_Mutation	SNP	C	T	50	78	c.1160C>T	c.(1159-1161)CCC>CTC	p.P387L
Pat_05	Post-Resistance	ITPR1	3708	37	3	4776973	4776973	Nonsense_Mutation	SNP	C	T	4	224	c.5335C>T	c.(5335-5337)CGA>TGA	p.R1779*
Pat_05	Post-Resistance	CNOT10	25904	37	3	32774919	32774919	Missense_Mutation	SNP	C	T	55	15	c.1220C>T	c.(1219-1221)TCT>TTT	p.S407F
Pat_05	Post-Resistance	CCR9	10803	37	3	45942970	45942970	Missense_Mutation	SNP	G	A	157	32	c.690G>A	c.(688-690)ATG>ATA	p.M230I
Pat_05	Post-Resistance	CDC25A	993	37	3	48200932	48200932	Nonsense_Mutation	SNP	T	A	5	185	c.1336A>T	c.(1336-1338)AGA>TGA	p.R446*
Pat_05	Post-Resistance	PBRM1	55193	37	3	52643768	52643768	Nonsense_Mutation	SNP	G	A	130	32	c.2128C>T	c.(2128-2130)CGA>TGA	p.R710*
Pat_05	Post-Resistance	PRKCD	5580	37	3	53212443	53212443	Missense_Mutation	SNP	C	T	103	18	c.5C>T	c.(4-6)GCG>GTG	p.A2V
Pat_05	Post-Resistance	ACTR8	93973	37	3	53910077	53910077	Missense_Mutation	SNP	G	A	37	96	c.809C>T	c.(808-810)GCC>GTC	p.A270V
Pat_05	Post-Resistance	C3orf63	23272	37	3	56657550	56657550	Missense_Mutation	SNP	C	T	7	203	c.4345G>A	c.(4345-4347)GAT>AAT	p.D1449N
Pat_05	Post-Resistance	C3orf67	200844	37	3	58849358	58849358	Missense_Mutation	SNP	T	C	60	125	c.1144A>G	c.(1144-1146)AAA>GAA	p.K382E
Pat_05	Post-Resistance	ROBO2	6092	37	3	77542449	77542449	Missense_Mutation	SNP	C	T	144	140	c.722C>T	c.(721-723)GCT>GTT	p.A241V
Pat_05	Post-Resistance	VGLL3	389136	37	3	87017908	87017908	Missense_Mutation	SNP	G	A	39	48	c.769C>T	c.(769-771)CCA>TCA	p.P257S
Pat_05	Post-Resistance	RPL24	6152	37	3	101400004	101400004	Missense_Mutation	SNP	G	A	157	212	c.449C>T	c.(448-450)GCT>GTT	p.A150V
Pat_05	Post-Resistance	PHLDB2	90102	37	3	111664169	111664169	Nonsense_Mutation	SNP	A	T	4	136	c.2452A>T	c.(2452-2454)AAA>TAA	p.K818*
Pat_05	Post-Resistance	PHLDB2	90102	37	3	111693337	111693337	Missense_Mutation	SNP	C	T	169	215	c.3689C>T	c.(3688-3690)TCG>TTG	p.S1230L
Pat_05	Post-Resistance	BOC	91653	37	3	112998766	112998766	Missense_Mutation	SNP	G	A	69	218	c.2116G>A	c.(2116-2118)GGT>AGT	p.G706S
Pat_05	Post-Resistance	TF	7018	37	3	133478099	133478099	Missense_Mutation	SNP	T	C	49	179	c.1129T>C	c.(1129-1131)TGG>CGG	p.W377R
Pat_05	Post-Resistance	SLCO2A1	6578	37	3	133654663	133654663	Missense_Mutation	SNP	C	T	31	31	c.1769G>A	c.(1768-1770)AGG>AAG	p.R590K
Pat_05	Post-Resistance	IGSF10	285313	37	3	151165878	151165878	Missense_Mutation	SNP	T	C	56	144	c.1891A>G	c.(1891-1893)AGA>GGA	p.R631G
Pat_05	Post-Resistance	DHX36	170506	37	3	154006677	154006677	Missense_Mutation	SNP	G	A	19	82	c.2009C>T	c.(2008-2010)TCC>TTC	p.S670F
Pat_05	Post-Resistance	PLCH1	23007	37	3	155286035	155286035	Missense_Mutation	SNP	C	G	19	28	c.814G>C	c.(814-816)GTT>CTT	p.V272L
Pat_05	Post-Resistance	WDR49	151790	37	3	167217991	167217991	Missense_Mutation	SNP	T	G	30	202	c.1925A>C	c.(1924-1926)GAA>GCA	p.E642A
Pat_05	Post-Resistance	CCDC39	339829	37	3	180372597	180372597	Missense_Mutation	SNP	T	C	36	38	c.883A>G	c.(883-885)ACG>GCG	p.T295A
Pat_05	Post-Resistance	MAP3K13	9175	37	3	185155242	185155243	Nonsense_Mutation	DNP	GG	AA	112	113	c.483_484GG>AA	481-486)TGGGAA>TGAA	.161_162WE>*
Pat_05	Post-Resistance	ZCCHC4	29063	37	4	25353242	25353242	Nonsense_Mutation	SNP	G	A	84	89	c.942G>A	c.(940-942)TGG>TGA	p.W314*
Pat_05	Post-Resistance	ATP8A1	10396	37	4	42448649	42448649	Missense_Mutation	SNP	C	T	22	105	c.2909G>A	c.(2908-2910)GGA>GAA	p.G970E
Pat_05	Post-Resistance	GRXCR1	389207	37	4	43032429	43032429	Missense_Mutation	SNP	C	T	59	185	c.745C>T	c.(745-747)CCA>TCA	p.P249S
Pat_05	Post-Resistance	USP46	64854	37	4	53464829	53464829	Missense_Mutation	SNP	C	T	21	13	c.964G>A	c.(964-966)GGC>AGC	p.G322S
Pat_05	Post-Resistance	LNX1	84708	37	4	54374296	54374296	Missense_Mutation	SNP	G	A	13	48	c.479C>T	c.(478-480)CCC>CTC	p.P160L
Pat_05	Post-Resistance	UGT2A3	79799	37	4	69817162	69817162	Missense_Mutation	SNP	G	A	37	24	c.317C>T	c.(316-318)TCA>TTA	p.S106L
Pat_05	Post-Resistance	UGT2B4	7363	37	4	70359495	70359495	Nonsense_Mutation	SNP	C	T	60	196	c.786G>A	c.(784-786)TGG>TGA	p.W262*
Pat_05	Post-Resistance	PARM1	25849	37	4	75937682	75937682	Missense_Mutation	SNP	C	T	30	103	c.91C>T	c.(91-93)CTT>TTT	p.L31F

Pat_05	Post-Resistance	MTTP	4547	37	4	100530020	100530020	Missense_Mutation	SNP	C	T	63	185	c.1655C>T	c.(1654-1656)CCA>CTA	p.P552L
Pat_05	Post-Resistance	PCDH10	57575	37	4	134073761	134073761	Missense_Mutation	SNP	G	T	5	165	c.2466G>T	c.(2464-2466)CAG>CAT	p.Q822H
Pat_05	Post-Resistance	IL15	3600	37	4	142651081	142651081	Missense_Mutation	SNP	C	T	61	197	c.322C>T	c.(322-324)CAT>TAT	p.H108Y
Pat_05	Post-Resistance	EDNRA	1909	37	4	148407174	148407174	Missense_Mutation	SNP	G	A	66	358	c.341G>A	c.(340-342)GGC>GAC	p.G114D
Pat_05	Post-Resistance	TRIM2	23321	37	4	154217177	154217177	Missense_Mutation	SNP	T	G	22	97	c.1418T>G	c.(1417-1419)ATC>AGC	p.I473S
Pat_05	Post-Resistance	ADAM29	11086	37	4	175897365	175897365	Missense_Mutation	SNP	A	C	39	120	c.689A>C	c.(688-690)AAT>ACT	p.N230T
Pat_05	Post-Resistance	TRIML2	205860	37	4	189012598	189012598	Missense_Mutation	SNP	C	T	113	128	c.1093G>A	c.(1093-1095)GGA>AGA	p.G365R
Pat_05	Post-Resistance	AHRR	57491	37	5	376820	376820	Missense_Mutation	SNP	C	A	3	44	c.352C>A	c.(352-354)CTG>ATG	p.L118M
Pat_05	Post-Resistance	TRIO	7204	37	5	14280541	14280541	Missense_Mutation	SNP	C	T	68	66	c.343C>T	c.(343-345)CCC>TCC	p.P115S
Pat_05	Post-Resistance	CDH6	1004	37	5	31267705	31267705	Missense_Mutation	SNP	G	A	30	109	c.125G>A	c.(124-126)GGA>GAA	p.G42E
Pat_05	Post-Resistance	SKP2	6502	37	5	36184070	36184070	Missense_Mutation	SNP	T	G	15	74	c.1190T>G	c.(1189-1191)TTT>TGT	p.F397C
Pat_05	Post-Resistance	C6	729	37	5	41161914	41161914	Nonsense_Mutation	SNP	C	A	5	175	c.1339G>T	c.(1339-1341)GGA>TGA	p.G447*
Pat_05	Post-Resistance	EMB	133418	37	5	49707083	49707083	Missense_Mutation	SNP	C	T	78	96	c.331G>A	c.(331-333)GAG>AAG	p.E111K
Pat_05	Post-Resistance	BDP1	55814	37	5	70806049	70806049	Missense_Mutation	SNP	G	A	6	120	c.3130G>A	c.(3130-3132)GTA>ATA	p.V1044I
Pat_05	Post-Resistance	C5orf36	285600	37	5	93872768	93872768	Missense_Mutation	SNP	G	A	32	85	c.64C>T	c.(64-66)CCT>TCT	p.P22S
Pat_05	Post-Resistance	FAM81B	153643	37	5	94749692	94749692	Missense_Mutation	SNP	G	A	39	107	c.335G>A	c.(334-336)GGT>GAT	p.G112D
Pat_05	Post-Resistance	PHF15	23338	37	5	133914985	133914985	Missense_Mutation	SNP	G	A	4	94	c.2351G>A	c.(2350-2352)CGC>CAC	p.R784H
Pat_05	Post-Resistance	PCDHA13	56136	37	5	140263298	140263298	Missense_Mutation	SNP	C	T	103	218	c.1445C>T	c.(1444-1446)GCG>GTG	p.A482V
Pat_05	Post-Resistance	RELL2	285613	37	5	141019543	141019543	Missense_Mutation	SNP	C	T	84	229	c.560C>T	c.(559-561)TCC>TTC	p.S187F
Pat_05	Post-Resistance	PPARGC1B	133522	37	5	149212436	149212436	Missense_Mutation	SNP	C	T	111	110	c.800C>T	c.(799-801)TCC>TTC	p.S267F
Pat_05	Post-Resistance	HAVCR2	84868	37	5	156525886	156525886	Missense_Mutation	SNP	G	A	21	66	c.505C>T	c.(505-507)CCT>TCT	p.P169S
Pat_05	Post-Resistance	GABRA1	2554	37	5	161302610	161302610	Missense_Mutation	SNP	C	T	77	249	c.521C>T	c.(520-522)CCT>CTT	p.P174L
Pat_05	Post-Resistance	UNC5A	90249	37	5	176305636	176305637	Missense_Mutation	DNP	CC	TT	40	173	.2180_2181CC>T	c.(2179-2181)ACC>ATT	p.T727I
Pat_05	Post-Resistance	HK3	3101	37	5	176314556	176314556	Missense_Mutation	SNP	G	A	9	120	c.1496C>T	c.(1495-1497)GCG>GTG	p.A499V
Pat_05	Post-Resistance	TMED9	54732	37	5	177019253	177019253	Missense_Mutation	SNP	G	A	6	59	c.38G>A	c.(37-39)CGG>CAG	p.R13Q
Pat_05	Post-Resistance	F13A1	2162	37	6	6197494	6197494	Nonsense_Mutation	SNP	C	T	33	289	c.1178G>A	c.(1177-1179)TGG>TAG	p.W393*
Pat_05	Post-Resistance	GCM2	9247	37	6	10875166	10875166	Missense_Mutation	SNP	C	T	72	132	c.583G>A	c.(583-585)GCA>ACA	p.A195T
Pat_05	Post-Resistance	SLC17A4	10050	37	6	25769267	25769267	Missense_Mutation	SNP	C	T	121	113	c.146C>T	c.(145-147)TCA>TTA	p.S49L
Pat_05	Post-Resistance	ABCF1	23	37	6	30553992	30553992	Missense_Mutation	SNP	C	T	52	122	c.1795C>T	c.(1795-1797)CCT>TCT	p.P599S
Pat_05	Post-Resistance	VARS2	57176	37	6	30892318	30892318	Missense_Mutation	SNP	A	G	29	92	c.2654A>G	c.(2653-2655)TAC>TGC	p.Y885C
Pat_05	Post-Resistance	LY6G5B	58496	37	6	31639713	31639713	Missense_Mutation	SNP	C	T	185	353	c.260C>T	c.(259-261)ACC>ATC	p.T87I
Pat_05	Post-Resistance	EGFL8	80864	37	6	32135197	32135198	Missense_Mutation	DNP	GC	TG	118	107	c.672_673GC>TG	670-675)CGGCTG>CGTG	p.L225V
Pat_05	Post-Resistance	LYPLA2P1	653639	37	6	33333333	33333333	Missense_Mutation	SNP	G	A	8	72	c.673C>T	c.(673-675)CCT>TCT	p.P225S
Pat_05	Post-Resistance	ITPR3	3710	37	6	33663491	33663491	Missense_Mutation	SNP	G	A	221	228	c.7950G>A	c.(7948-7950)ATG>ATA	p.M2650I
Pat_05	Post-Resistance	FGD2	221472	37	6	36982714	36982714	Missense_Mutation	SNP	A	G	89	110	c.929A>G	c.(928-930)GAG>GGG	p.E310G
Pat_05	Post-Resistance	FRS3	10817	37	6	41740560	41740561	Missense_Mutation	DNP	GG	AT	182	169	c.390_391CC>AT	(388-393)CTCCCT>CTAT	p.P131S
Pat_05	Post-Resistance	RSPH9	221421	37	6	43618212	43618212	Missense_Mutation	SNP	G	A	68	167	c.328G>A	c.(328-330)GAA>AAA	p.E110K
Pat_05	Post-Resistance	PGK2	5232	37	6	49754405	49754405	Missense_Mutation	SNP	A	G	22	175	c.496T>C	c.(496-498)TTT>CTT	p.F166L
Pat_05	Post-Resistance	MDN1	23195	37	6	90504465	90504465	Nonsense_Mutation	SNP	C	A	4	120	c.385G>T	c.(385-387)GAG>TAG	p.E129*
Pat_05	Post-Resistance	GPR63	81491	37	6	97247429	97247429	Missense_Mutation	SNP	G	A	81	34	c.179C>T	c.(178-180)ACC>ATC	p.T60I
Pat_05	Post-Resistance	PRDM13	59336	37	6	100056673	100056673	Nonsense_Mutation	SNP	G	A	57	22	c.201G>A	c.(199-201)TGG>TGA	p.W67*
Pat_05	Post-Resistance	KIF25	3834	37	6	168430272	168430272	Missense_Mutation	SNP	T	A	8	161	c.7T>A	c.(7-9)TGG>AGG	p.W3R
Pat_05	Post-Resistance	PAPOLB	56903	37	7	4899659	4899659	Missense_Mutation	SNP	G	A	70	63	c.1783C>T	c.(1783-1785)CCT>TCT	p.P595S
Pat_05	Post-Resistance	THSD7A	221981	37	7	11450924	11450924	Missense_Mutation	SNP	C	A	87	75	c.3708G>T	c.(3706-3708)GAG>GAT	p.E1236D
Pat_05	Post-Resistance	ABCB5	340273	37	7	20766661	20766661	Splice_Site	SNP	A	G	70	83	c.1291_splice	c.e13-2	p.I431_splice
Pat_05	Post-Resistance	TRIL	9865	37	7	28996219	28996219	Missense_Mutation	SNP	G	C	7	51	c.1444C>G	c.(1444-1446)CTA>GTA	p.L482V
Pat_05	Post-Resistance	MYO1G	64005	37	7	45005386	45005386	Missense_Mutation	SNP	C	T	151	142	c.2231G>A	c.(2230-2232)CGG>CAG	p.R744Q

Pat_05	Post-Resistance	COBL	23242	37	7	51111341	51111342	Missense_Mutation	DNP	GG	AA	115	97	.1144_1145CC>T	c.(1144-1146)CCG>TTG	p.P382L
Pat_05	Post-Resistance	PHKG1	5260	37	7	56151072	56151072	Missense_Mutation	SNP	C	T	4	290	c.446G>A	c.(445-447)CGG>CAG	p.R149Q
Pat_05	Post-Resistance	FZD9	8326	37	7	72849988	72849988	Missense_Mutation	SNP	C	T	56	131	c.1651C>T	c.(1651-1653)CGG>TGG	p.R551W
Pat_05	Post-Resistance	ELN	2006	37	7	73470634	73470634	Missense_Mutation	SNP	C	T	295	312	c.1184C>T	c.(1183-1185)CCT>CTT	p.P395L
Pat_05	Post-Resistance	MTERF	7978	37	7	91503306	91503306	Missense_Mutation	SNP	C	T	4	147	c.802G>A	c.(802-804)GAG>AAG	p.E268K
Pat_05	Post-Resistance	COL1A2	1278	37	7	94038912	94038912	Missense_Mutation	SNP	G	A	117	219	c.928G>A	c.(928-930)GGT>AGT	p.G310S
Pat_05	Post-Resistance	LRCH4	4034	37	7	100173514	100173515	Missense_Mutation	DNP	GG	AT	10	19	.1755_1756CC>A	1753-1758)ATCCAT>ATAT	p.H586Y
Pat_05	Post-Resistance	FBXL13	222235	37	7	102473358	102473358	Missense_Mutation	SNP	C	G	18	416	c.1783G>C	c.(1783-1785)GAT>CAT	p.D595H
Pat_05	Post-Resistance	PPP1R3A	5506	37	7	113558921	113558921	Missense_Mutation	SNP	C	T	120	129	c.131G>A	c.(130-132)CGA>CAA	p.R44Q
Pat_05	Post-Resistance	CFTR	1080	37	7	117175335	117175335	Missense_Mutation	SNP	C	T	285	341	c.613C>T	c.(613-615)CCT>TCT	p.P205S
Pat_05	Post-Resistance	PLXNA4	91584	37	7	131817905	131817905	Missense_Mutation	SNP	G	T	313	299	c.5492C>A	c.(5491-5493)GCA>GAA	p.A1831E
Pat_05	Post-Resistance	PLXNA4	91584	37	7	131872367	131872367	Splice_Site	SNP	C	T	217	437	c.2857_splice	c.e15-1	p.T953_splice
Pat_05	Post-Resistance	BRAF	673	37	7	140453136	140453136	Missense_Mutation	SNP	A	T	144	174	c.1799T>A	c.(1798-1800)GTG>GAG	p.V600E
Pat_05	Post-Resistance	TRYX3	136541	37	7	141954881	141954881	Missense_Mutation	SNP	C	T	335	362	c.430G>A	c.(430-432)GAT>AAT	p.D144N
Pat_05	Post-Resistance	CLCN1	1180	37	7	143049018	143049018	Missense_Mutation	SNP	G	A	251	283	c.2927G>A	c.(2926-2928)CGA>CAA	p.R976Q
Pat_05	Post-Resistance	OR2F2	135948	37	7	143633121	143633121	Missense_Mutation	SNP	C	G	116	242	c.796C>G	c.(796-798)CCC>GCC	p.P266A
Pat_05	Post-Resistance	ABCB8	11194	37	7	150737671	150737672	Missense_Mutation	DNP	CC	TT	113	317	.1389_1390CC>T	387-1392)GTCCCC>GTT	p.P464S
Pat_05	Post-Resistance	ZDHHC2	51201	37	8	17067922	17067922	Missense_Mutation	SNP	A	G	37	17	c.883A>G	c.(883-885)ACT>GCT	p.T295A
Pat_05	Post-Resistance	FAM160B2	64760	37	8	21955042	21955042	Missense_Mutation	SNP	C	T	3	31	c.313C>T	c.(313-315)CGG>TGG	p.R105W
Pat_05	Post-Resistance	TNFRSF10A	8797	37	8	23054654	23054654	Missense_Mutation	SNP	G	A	134	78	c.1078C>T	c.(1078-1080)CCC>TCC	p.P360S
Pat_05	Post-Resistance	RAB11FIP1	80223	37	8	37720621	37720621	Missense_Mutation	SNP	G	A	115	29	c.3644C>T	c.(3643-3645)CCC>CTC	p.P1215L
Pat_05	Post-Resistance	ADAM18	8749	37	8	39505896	39505896	Nonsense_Mutation	SNP	C	A	3	48	c.1080C>A	c.(1078-1080)TGC>TGA	p.C360*
Pat_05	Post-Resistance	RP1	6101	37	8	55533983	55533983	Missense_Mutation	SNP	C	T	410	41	c.457C>T	c.(457-459)CCA>TCA	p.P153S
Pat_05	Post-Resistance	VPS13B	157680	37	8	100861005	100861005	Missense_Mutation	SNP	T	C	667	88	c.10019T>C	c.(10018-10020)GTT>GCT	p.V3340A
Pat_05	Post-Resistance	EXT1	2131	37	8	118831989	118831989	Missense_Mutation	SNP	T	C	18	478	c.1462A>G	c.(1462-1464)ACC>GCC	p.T488A
Pat_05	Post-Resistance	FER1L6	654463	37	8	124988301	124988301	Missense_Mutation	SNP	G	A	379	37	c.847G>A	c.(847-849)GAG>AAG	p.E283K
Pat_05	Post-Resistance	TAF1L	138474	37	9	32632706	32632706	Missense_Mutation	SNP	T	C	57	237	c.2872A>G	c.(2872-2874)ATT>GTT	p.I958V
Pat_05	Post-Resistance	TMC1	117531	37	9	75387387	75387387	Missense_Mutation	SNP	G	A	145	371	c.800G>A	c.(799-801)GGA>GAA	p.G267E
Pat_05	Post-Resistance	PRUNE2	158471	37	9	79324445	79324445	Missense_Mutation	SNP	C	A	65	227	c.2745G>T	c.(2743-2745)AAG>AAT	p.K915N
Pat_05	Post-Resistance	WNK2	65268	37	9	96009925	96009925	Missense_Mutation	SNP	C	T	13	8	c.1643C>T	c.(1642-1644)CCC>CTC	p.P548L
Pat_05	Post-Resistance	SMC2	10592	37	9	106894344	106894344	Missense_Mutation	SNP	C	G	7	37	c.3046C>G	c.(3046-3048)CTT>GTT	p.L1016V
Pat_05	Post-Resistance	ABCA1	19	37	9	107593369	107593369	Missense_Mutation	SNP	C	A	4	85	c.1729G>T	c.(1729-1731)GGT>TGT	p.G577C
Pat_05	Post-Resistance	C9orf4	23732	37	9	111909331	111909331	Missense_Mutation	SNP	C	T	6	345	c.615G>A	c.(613-615)ATG>ATA	p.M205I
Pat_05	Post-Resistance	KIAA0368	23392	37	9	114190363	114190363	Missense_Mutation	SNP	G	A	71	66	c.1543C>T	c.(1543-1545)CGC>TGC	p.R515C
Pat_05	Post-Resistance	SNAPC4	6621	37	9	139286993	139286993	Missense_Mutation	SNP	T	C	130	455	c.791A>G	c.(790-792)GAG>GGG	p.E264G
Pat_05	Post-Resistance	TUBB2C	10383	37	9	140136962	140136962	Missense_Mutation	SNP	G	T	4	158	c.292G>T	c.(292-294)GGG>TGG	p.G98W
Pat_05	Post-Resistance	ASMTL	8623	37	X	1546781	1546781	Missense_Mutation	SNP	G	A	105	158	c.743C>T	c.(742-744)CCC>CTC	p.P248L
Pat_05	Post-Resistance	CXorf59	286464	37	X	36091411	36091411	Missense_Mutation	SNP	C	A	63	122	c.346C>A	c.(346-348)CAG>AAG	p.Q116K
Pat_05	Post-Resistance	CACNA1F	778	37	X	49071632	49071632	Missense_Mutation	SNP	G	A	93	14	c.3544C>T	c.(3544-3546)CGT>TGT	p.R1182C
Pat_05	Post-Resistance	DGAT2L6	347516	37	X	69397467	69397467	Missense_Mutation	SNP	G	A	107	12	c.35G>A	c.(34-36)GGC>GAC	p.G12D
Pat_05	Post-Resistance	BEX5	340542	37	X	101409030	101409030	Missense_Mutation	SNP	G	A	4	95	c.208C>T	c.(208-210)CGG>TGG	p.R70W
Pat_05	Post-Resistance	MST4	51765	37	X	131202261	131202261	Missense_Mutation	SNP	G	A	80	16	c.349G>A	c.(349-351)GAT>AAT	p.D117N
Pat_05	Post-Resistance	MAGEA8	4107	37	X	149013954	149013954	Missense_Mutation	SNP	C	T	225	31	c.908C>T	c.(907-909)TCC>TTC	p.S303F
Pat_05	Post-Resistance	L1CAM	3897	37	X	153136388	153136388	Missense_Mutation	SNP	C	A	4	312	c.551G>T	c.(550-552)CGG>CTG	p.R184L
Pat_06	Pre-Treatment	AGRN	375790	37	1	979032	979032	Missense_Mutation	SNP	C	T	5	489	c.1718C>T	c.(1717-1719)ACG>ATG	p.T573M
Pat_06	Pre-Treatment	GLTPD1	80772	37	1	1262682	1262682	Missense_Mutation	SNP	C	T	4	197	c.184C>T	c.(184-186)CGG>TGG	p.R62W
Pat_06	Pre-Treatment	SSU72	29101	37	1	1509919	1509919	Missense_Mutation	SNP	G	C	3	139	c.19C>G	c.(19-21)CGG>GGG	p.R7G

Pat_06	Pre-Treatment	CDK11B	984	37	1	1571740	1571740	Missense_Mutation	SNP	C	T	3	39	c.2021G>A	c.(2020-2022)CGC>CAC	p.R674H
Pat_06	Pre-Treatment	RER1	11079	37	1	2332341	2332341	Missense_Mutation	SNP	C	A	6	565	c.332C>A	c.(331-333)CCC>CAC	p.P111H
Pat_06	Pre-Treatment	PANK4	55229	37	1	2445896	2445896	Missense_Mutation	SNP	G	A	5	268	c.1384C>T	c.(1384-1386)CGC>TGC	p.R462C
Pat_06	Pre-Treatment	ENO1	2023	37	1	8931965	8931965	Missense_Mutation	SNP	G	A	6	758	c.166C>T	c.(166-168)CGC>TGC	p.R56C
Pat_06	Pre-Treatment	PTCHD2	57540	37	1	11562754	11562754	Missense_Mutation	SNP	G	C	3	157	c.1116G>C	c.(1114-1116)ATG>ATC	p.M372I
Pat_06	Pre-Treatment	MFN2	9927	37	1	12057406	12057406	Missense_Mutation	SNP	G	A	5	430	c.527G>A	c.(526-528)GGC>GAC	p.G176D
Pat_06	Pre-Treatment	MIIP	60672	37	1	12081868	12081868	Missense_Mutation	SNP	C	G	3	210	c.85C>G	c.(85-87)CGG>GGG	p.R29G
Pat_06	Pre-Treatment	VPS13D	55187	37	1	12364562	12364562	Splice_Site	SNP	G	C	3	70	c.6217_splice	c.e26-1	p.E2073_splice
Pat_06	Pre-Treatment	PLEKHM2	23207	37	1	16054618	16054618	Missense_Mutation	SNP	G	A	3	75	c.1805G>A	c.(1804-1806)CGA>CAA	p.R602Q
Pat_06	Pre-Treatment	SPEN	23013	37	1	16263839	16263839	Missense_Mutation	SNP	G	A	6	173	c.10208G>A	c.(10207-10209)CGC>CAC	p.R3403H
Pat_06	Pre-Treatment	ZBTB17	7709	37	1	16271225	16271225	Missense_Mutation	SNP	G	A	4	277	c.1037C>T	c.(1036-1038)CCG>CTG	p.P346L
Pat_06	Pre-Treatment	ARHGEF10L	55160	37	1	17934459	17934459	Missense_Mutation	SNP	C	G	3	38	c.596C>G	c.(595-597)TCC>TGC	p.S199C
Pat_06	Pre-Treatment	TAS1R2	80834	37	1	19181045	19181045	Missense_Mutation	SNP	C	T	5	204	c.919G>A	c.(919-921)GAC>AAC	p.D307N
Pat_06	Pre-Treatment	CAMK2N1	55450	37	1	20811727	20811727	Missense_Mutation	SNP	T	C	3	55	c.146A>G	c.(145-147)CAG>CGG	p.Q49R
Pat_06	Pre-Treatment	SRRM1	10250	37	1	24979023	24979023	Missense_Mutation	SNP	G	C	3	139	c.824G>C	c.(823-825)CGA>CCA	p.R275P
Pat_06	Pre-Treatment	RHCE	6006	37	1	25735272	25735272	Missense_Mutation	SNP	G	C	3	108	c.237C>G	c.(235-237)TTC>TTG	p.F79L
Pat_06	Pre-Treatment	SNRNP40	9410	37	1	31766192	31766192	Missense_Mutation	SNP	G	A	4	169	c.145C>T	c.(145-147)CCT>TCT	p.P49S
Pat_06	Pre-Treatment	S100PBP	64766	37	1	33318727	33318727	Missense_Mutation	SNP	C	A	6	669	c.1072C>A	c.(1072-1074)CAG>AAG	p.Q358K
Pat_06	Pre-Treatment	DLGAP3	58512	37	1	35351777	35351777	Missense_Mutation	SNP	C	T	3	67	c.1496G>A	c.(1495-1497)CGG>CAG	p.R499Q
Pat_06	Pre-Treatment	SFPQ	6421	37	1	35653674	35653674	Missense_Mutation	SNP	C	T	6	746	c.1715G>A	c.(1714-1716)CGT>CAT	p.R572H
Pat_06	Pre-Treatment	EIF2C1	26523	37	1	36367850	36367850	Missense_Mutation	SNP	G	A	5	530	c.1309G>A	c.(1309-1311)GGG>AGG	p.G437R
Pat_06	Pre-Treatment	COL8A2	1296	37	1	36563511	36563511	Missense_Mutation	SNP	G	A	3	71	c.1771C>T	c.(1771-1773)CCC>TCC	p.P591S
Pat_06	Pre-Treatment	EPHA10	284656	37	1	38185243	38185243	Missense_Mutation	SNP	G	A	5	365	c.2599C>T	c.(2599-2601)CCC>TCC	p.P867S
Pat_06	Pre-Treatment	ZMYND12	84217	37	1	42921593	42921593	Missense_Mutation	SNP	G	A	5	287	c.76C>T	c.(76-78)CGG>TGG	p.R26W
Pat_06	Pre-Treatment	DMAP1	55929	37	1	44684119	44684119	Missense_Mutation	SNP	G	A	6	703	c.530G>A	c.(529-531)CGG>CAG	p.R177Q
Pat_06	Pre-Treatment	PTCH2	8643	37	1	45293555	45293555	Missense_Mutation	SNP	C	T	5	460	c.2018G>A	c.(2017-2019)CGC>CAC	p.R673H
Pat_06	Pre-Treatment	PTCH2	8643	37	1	45298004	45298004	Missense_Mutation	SNP	C	A	6	596	c.275G>T	c.(274-276)CGG>CTG	p.R92L
Pat_06	Pre-Treatment	HECTD3	79654	37	1	45471752	45471752	Missense_Mutation	SNP	G	A	6	579	c.1762C>T	c.(1762-1764)CCC>TCC	p.P588S
Pat_06	Pre-Treatment	FAAH	2166	37	1	46871294	46871294	Missense_Mutation	SNP	G	A	6	690	c.613G>A	c.(613-615)GTG>ATG	p.V205M
Pat_06	Pre-Treatment	ZYG11B	79699	37	1	53236827	53236827	Missense_Mutation	SNP	A	G	4	523	c.332A>G	c.(331-333)GAT>GGT	p.D111G
Pat_06	Pre-Treatment	MAGOH	4116	37	1	53692748	53692748	Missense_Mutation	SNP	A	G	5	223	c.410T>C	c.(409-411)ATT>ACT	p.I137T
Pat_06	Pre-Treatment	PRKAA2	5563	37	1	57170116	57170116	Nonsense_Mutation	SNP	C	T	6	730	c.1261C>T	c.(1261-1263)CGA>TGA	p.R421*
Pat_06	Pre-Treatment	CLCA1	1179	37	1	86960032	86960032	Missense_Mutation	SNP	C	T	78	104	c.1843C>T	c.(1843-1845)CGC>TGC	p.R615C
Pat_06	Pre-Treatment	CCDC18	343099	37	1	93646136	93646136	Missense_Mutation	SNP	A	G	4	276	c.49A>G	c.(49-51)AGT>GGT	p.S17G
Pat_06	Pre-Treatment	EXTL2	2135	37	1	101339811	101339811	Missense_Mutation	SNP	T	C	3	151	c.680A>G	c.(679-681)CAG>CGG	p.Q227R
Pat_06	Pre-Treatment	COL11A1	1301	37	1	103491773	103491773	Missense_Mutation	SNP	T	C	6	688	c.896A>G	c.(895-897)GAG>GGG	p.E299G
Pat_06	Pre-Treatment	SLC6A17	388662	37	1	110740738	110740738	Missense_Mutation	SNP	C	A	5	138	c.1856C>A	c.(1855-1857)GCA>GAA	p.A619E
Pat_06	Pre-Treatment	RBM15	64783	37	1	110884345	110884345	Missense_Mutation	SNP	G	A	6	558	c.2318G>A	c.(2317-2319)GGG>GAG	p.G773E
Pat_06	Pre-Treatment	KCNA2	3737	37	1	111146215	111146215	Missense_Mutation	SNP	G	T	5	396	c.1190C>A	c.(1189-1191)GCA>GAA	p.A397E
Pat_06	Pre-Treatment	ADAM30	11085	37	1	120438642	120438642	Missense_Mutation	SNP	T	C	3	274	c.318A>G	c.(316-318)ATA>ATG	p.I106M
Pat_06	Pre-Treatment	NBPF10	100132406	37	1	145325971	145325971	Missense_Mutation	SNP	G	C	12	375	c.4069G>C	c.(4069-4071)GAT>CAT	p.D1357H
Pat_06	Pre-Treatment	SV2A	9900	37	1	149883534	149883534	Splice_Site	SNP	T	C	3	98	c.623_splice	c.e3-1	p.G208_splice
Pat_06	Pre-Treatment	OTUD7B	56957	37	1	149949378	149949378	Missense_Mutation	SNP	G	A	6	751	c.68C>T	c.(67-69)GCG>GTG	p.A23V
Pat_06	Pre-Treatment	CTSK	1513	37	1	150779272	150779272	Missense_Mutation	SNP	G	A	4	394	c.10C>T	c.(10-12)CTC>TTC	p.L4F
Pat_06	Pre-Treatment	CGN	57530	37	1	151491709	151491709	Missense_Mutation	SNP	C	A	5	574	c.714C>A	c.(712-714)AGC>AGA	p.S238R
Pat_06	Pre-Treatment	CRNN	49860	37	1	152382571	152382571	Missense_Mutation	SNP	C	A	6	878	c.987G>T	c.(985-987)GAG>GAT	p.E329D
Pat_06	Pre-Treatment	SNAPIN	23557	37	1	153631271	153631271	Missense_Mutation	SNP	G	A	4	86	c.52G>A	c.(52-54)GGG>AGG	p.G18R

Pat_06	Pre-Treatment	ADAM15	8751	37	1	155028269	155028269	Missense_Mutation	SNP	C	T	8	664	c.616C>T	c.(616-618)CGG>TGG	p.R206W
Pat_06	Pre-Treatment	SYT11	23208	37	1	155838499	155838499	Missense_Mutation	SNP	G	A	5	326	c.778G>A	c.(778-780)GAG>AAG	p.E260K
Pat_06	Pre-Treatment	CD1C	911	37	1	158259891	158259891	Missense_Mutation	SNP	C	T	5	703	c.37C>T	c.(37-39)CTC>TTC	p.L13F
Pat_06	Pre-Treatment	OR6K6	128371	37	1	158724691	158724691	Missense_Mutation	SNP	C	T	7	572	c.86C>T	c.(85-87)ACG>ATG	p.T29M
Pat_06	Pre-Treatment	KCNJ10	3766	37	1	160012006	160012006	Missense_Mutation	SNP	G	A	5	461	c.317C>T	c.(316-318)ACC>ATC	p.T106I
Pat_06	Pre-Treatment	IGSF8	93185	37	1	160064979	160064979	Missense_Mutation	SNP	G	A	4	227	c.122C>T	c.(121-123)GCT>GTT	p.A41V
Pat_06	Pre-Treatment	ATP1A2	477	37	1	160098563	160098563	Missense_Mutation	SNP	C	T	6	520	c.1139C>T	c.(1138-1140)ACC>ATC	p.T380I
Pat_06	Pre-Treatment	CD84	8832	37	1	160523255	160523255	Missense_Mutation	SNP	C	A	5	654	c.673G>T	c.(673-675)GGG>TGG	p.G225W
Pat_06	Pre-Treatment	USF1	7391	37	1	161012372	161012372	Nonsense_Mutation	SNP	G	T	4	352	c.147C>A	c.(145-147)TAC>TAA	p.Y49*
Pat_06	Pre-Treatment	PVRL4	81607	37	1	161042507	161042507	Missense_Mutation	SNP	G	A	5	575	c.1477C>T	c.(1477-1479)CGG>TGG	p.R493W
Pat_06	Pre-Treatment	PVRL4	81607	37	1	161042585	161042585	Missense_Mutation	SNP	G	A	4	323	c.1399C>T	c.(1399-1401)CGG>TGG	p.R467W
Pat_06	Pre-Treatment	FCRLB	127943	37	1	161693372	161693372	Missense_Mutation	SNP	G	A	4	346	c.268G>A	c.(268-270)GCA>ACA	p.A90T
Pat_06	Pre-Treatment	ATF6	22926	37	1	161771859	161771859	Missense_Mutation	SNP	T	C	4	714	c.706T>C	c.(706-708)TCT>CCT	p.S236P
Pat_06	Pre-Treatment	NOS1AP	9722	37	1	162325042	162325042	Missense_Mutation	SNP	G	A	6	493	c.661G>A	c.(661-663)GTG>ATG	p.V221M
Pat_06	Pre-Treatment	GPA33	10223	37	1	167023600	167023600	Missense_Mutation	SNP	G	A	6	614	c.931C>T	c.(931-933)CGT>TGT	p.R311C
Pat_06	Pre-Treatment	SELE	6401	37	1	169699756	169699756	Missense_Mutation	SNP	C	G	5	204	c.532G>C	c.(532-534)GTG>CTG	p.V178L
Pat_06	Pre-Treatment	C1orf129	80133	37	1	170961471	170961471	Splice_Site	SNP	G	A	5	485	c.1194_splice	c.e12+1	p.A398_splice
Pat_06	Pre-Treatment	METTL13	51603	37	1	171753525	171753525	Missense_Mutation	SNP	A	G	3	188	c.799A>G	c.(799-801)AGT>GGT	p.S267G
Pat_06	Pre-Treatment	TNR	7143	37	1	175299353	175299353	Missense_Mutation	SNP	C	T	4	306	c.3650G>A	c.(3649-3651)AGG>AAG	p.R1217K
Pat_06	Pre-Treatment	TOR3A	64222	37	1	179054988	179054988	Missense_Mutation	SNP	C	T	6	334	c.599C>T	c.(598-600)ACG>ATG	p.T200M
Pat_06	Pre-Treatment	TOR1AIP1	26092	37	1	179886632	179886632	Missense_Mutation	SNP	G	A	5	833	c.1010G>A	c.(1009-1011)CGG>CAG	p.R337Q
Pat_06	Pre-Treatment	ACBD6	84320	37	1	180366741	180366741	Splice_Site	SNP	C	A	5	538	c.574_splice	c.e6-1	p.G192_splice
Pat_06	Pre-Treatment	XPR1	9213	37	1	180805753	180805753	Nonsense_Mutation	SNP	C	T	6	672	c.1402C>T	c.(1402-1404)CGA>TGA	p.R468*
Pat_06	Pre-Treatment	ASPM	259266	37	1	197115590	197115590	Translation_Start_Site	SNP	G	C	3	113	c.-22C>G	c.(-24--20)ATCCA>ATGCA	
Pat_06	Pre-Treatment	IPO9	55705	37	1	201832695	201832695	Missense_Mutation	SNP	C	T	5	587	c.1588C>T	c.(1588-1590)CCC>TCC	p.P530S
Pat_06	Pre-Treatment	PLXNA2	5362	37	1	208266148	208266148	Missense_Mutation	SNP	G	A	5	297	c.2080C>T	c.(2080-2082)CGG>TGG	p.R694W
Pat_06	Pre-Treatment	KCNH1	3756	37	1	210977413	210977413	Missense_Mutation	SNP	G	A	6	290	c.1558C>T	c.(1558-1560)CGG>TGG	p.R520W
Pat_06	Pre-Treatment	PROX1	5629	37	1	214170314	214170314	Missense_Mutation	SNP	A	G	4	702	c.436A>G	c.(436-438)AGG>GGG	p.R146G
Pat_06	Pre-Treatment	KCTD3	51133	37	1	215749250	215749250	Missense_Mutation	SNP	A	T	4	156	c.190A>T	c.(190-192)ATT>TTT	p.I64F
Pat_06	Pre-Treatment	DUSP10	11221	37	1	221879470	221879470	Missense_Mutation	SNP	G	A	6	807	c.1150C>T	c.(1150-1152)CGG>TGG	p.R384W
Pat_06	Pre-Treatment	ITPKB	3707	37	1	226924741	226924741	Missense_Mutation	SNP	T	C	4	587	c.419A>G	c.(418-420)AAC>AGC	p.N140S
Pat_06	Pre-Treatment	C1orf69	200205	37	1	228362629	228362629	Missense_Mutation	SNP	G	A	4	185	c.578G>A	c.(577-579)CGC>CAC	p.R193H
Pat_06	Pre-Treatment	TBCE	6905	37	1	235597525	235597525	Missense_Mutation	SNP	C	T	6	769	c.667C>T	c.(667-669)CGG>TGG	p.R223W
Pat_06	Pre-Treatment	ZNF238	10472	37	1	244218521	244218521	Missense_Mutation	SNP	G	A	5	392	c.1418G>A	c.(1417-1419)CGC>CAC	p.R473H
Pat_06	Pre-Treatment	CNST	163882	37	1	246754935	246754935	Missense_Mutation	SNP	G	A	5	741	c.71G>A	c.(70-72)AGC>AAC	p.S24N
Pat_06	Pre-Treatment	CNST	163882	37	1	246805294	246805294	Missense_Mutation	SNP	G	C	3	162	c.892G>C	c.(892-894)GTG>CTG	p.V298L
Pat_06	Pre-Treatment	OR2W5	441932	37	1	247654941	247654941	Missense_Mutation	SNP	G	A	8	488	c.512G>A	c.(511-513)CGT>CAT	p.R171H
Pat_06	Pre-Treatment	ASB13	79754	37	10	5693320	5693320	Missense_Mutation	SNP	C	T	3	38	c.238G>A	c.(238-240)GCT>ACT	p.A80T
Pat_06	Pre-Treatment	CAMK1D	57118	37	10	12867639	12867639	Missense_Mutation	SNP	G	A	6	725	c.989G>A	c.(988-990)AGT>AAT	p.S330N
Pat_06	Pre-Treatment	SUV39H2	79723	37	10	14939434	14939434	Missense_Mutation	SNP	G	A	9	790	c.587G>A	c.(586-588)CGA>CAA	p.R196Q
Pat_06	Pre-Treatment	PLXDC2	84898	37	10	20465997	20465997	Missense_Mutation	SNP	C	T	5	733	c.953C>T	c.(952-954)TCG>TTG	p.S318L
Pat_06	Pre-Treatment	ARMC3	219681	37	10	23290947	23290947	Missense_Mutation	SNP	G	A	4	342	c.1525G>A	c.(1525-1527)GGT>AGT	p.G509S
Pat_06	Pre-Treatment	ABI1	10006	37	10	27066118	27066118	Missense_Mutation	SNP	G	C	3	212	c.338C>G	c.(337-339)ACA>AGA	p.T113R
Pat_06	Pre-Treatment	ZNF438	220929	37	10	31137631	31137631	Missense_Mutation	SNP	C	T	6	541	c.1703G>A	c.(1702-1704)TGT>TAT	p.C568Y
Pat_06	Pre-Treatment	ANKRD30A	91074	37	10	37430688	37430688	Missense_Mutation	SNP	C	T	8	269	c.695C>T	c.(694-696)GCG>GTG	p.A232V
Pat_06	Pre-Treatment	ANKRD30A	91074	37	10	37431012	37431012	Missense_Mutation	SNP	T	C	7	448	c.1019T>C	c.(1018-1020)ATG>ACG	p.M340T
Pat_06	Pre-Treatment	ZNF33A	7581	37	10	38299713	38299713	Splice_Site	SNP	T	C	4	300	c.-44_splice	c.e1+2	

Pat_06	Pre-Treatment	HSD17B7P2	158160	37	10	38654432	38654432	Missense_Mutation	SNP	A	G	9	380	c.524A>G	c.(523-525)AAT>AGT	p.N175S
Pat_06	Pre-Treatment	HNRNPF	3185	37	10	43882717	43882717	Missense_Mutation	SNP	G	A	7	469	c.616C>T	c.(616-618)CGG>TGG	p.R206W
Pat_06	Pre-Treatment	TMEM72	643236	37	10	45427508	45427508	Missense_Mutation	SNP	T	C	3	85	c.200T>C	c.(199-201)ATC>ACC	p.I67T
Pat_06	Pre-Treatment	SYT15	83849	37	10	46967629	46967629	Missense_Mutation	SNP	G	A	9	696	c.448C>T	c.(448-450)CGG>TGG	p.R150W
Pat_06	Pre-Treatment	RBP3	5949	37	10	48389098	48389098	Missense_Mutation	SNP	G	A	5	562	c.1780C>T	c.(1780-1782)CCG>TCG	p.P594S
Pat_06	Pre-Treatment	ERCC6	2074	37	10	50678344	50678344	Missense_Mutation	SNP	C	T	7	890	c.3662G>A	c.(3661-3663)CGA>CAA	p.R1221Q
Pat_06	Pre-Treatment	ERCC6	2074	37	10	50740610	50740610	Missense_Mutation	SNP	C	T	4	439	c.401G>A	c.(400-402)CGG>CAG	p.R134Q
Pat_06	Pre-Treatment	TMEM26	219623	37	10	63212688	63212688	Missense_Mutation	SNP	G	A	5	655	c.152C>T	c.(151-153)GCG>GTG	p.A51V
Pat_06	Pre-Treatment	HERC4	26091	37	10	69785304	69785304	Missense_Mutation	SNP	G	A	5	795	c.907C>T	c.(907-909)CGG>TGG	p.R303W
Pat_06	Pre-Treatment	USP54	159195	37	10	75258736	75258736	Missense_Mutation	SNP	G	A	6	821	c.4706C>T	c.(4705-4707)ACT>ATT	p.T1569I
Pat_06	Pre-Treatment	SEC24C	9632	37	10	75530531	75530531	Missense_Mutation	SNP	G	A	5	576	c.3119G>A	c.(3118-3120)CGG>CAG	p.R1040Q
Pat_06	Pre-Treatment	PLCE1	51196	37	10	95995712	95995712	Missense_Mutation	SNP	G	T	6	515	c.2255G>T	c.(2254-2256)CGA>CTA	p.R752L
Pat_06	Pre-Treatment	CYP2C19	1557	37	10	96580323	96580323	Missense_Mutation	SNP	C	T	5	793	c.890C>T	c.(889-891)GCT>GTT	p.A297V
Pat_06	Pre-Treatment	ABCC2	1244	37	10	101591759	101591759	Missense_Mutation	SNP	C	G	4	756	c.3129C>G	c.(3127-3129)TTC>TTG	p.F1043L
Pat_06	Pre-Treatment	DNMBP	23268	37	10	101657981	101657981	Missense_Mutation	SNP	G	A	8	513	c.2782C>T	c.(2782-2784)CGT>TGT	p.R928C
Pat_06	Pre-Treatment	CHUK	1147	37	10	101969453	101969453	Missense_Mutation	SNP	G	A	5	236	c.1027C>T	c.(1027-1029)CGT>TGT	p.R343C
Pat_06	Pre-Treatment	PKD2L1	9033	37	10	102057356	102057356	Missense_Mutation	SNP	A	G	3	186	c.739T>C	c.(739-741)TAC>CAC	p.Y247H
Pat_06	Pre-Treatment	TLX1NB	100038246	37	10	102849583	102849583	Missense_Mutation	SNP	G	C	4	77	c.80C>G	c.(79-81)GCC>GGC	p.A27G
Pat_06	Pre-Treatment	NOLC1	9221	37	10	103920824	103920824	Missense_Mutation	SNP	A	G	4	211	c.1715A>G	c.(1714-1716)AAG>AGG	p.K572R
Pat_06	Pre-Treatment	PSD	5662	37	10	104162968	104162968	Missense_Mutation	SNP	G	A	3	60	c.3064C>T	c.(3064-3066)CGG>TGG	p.R1022W
Pat_06	Pre-Treatment	ACTR1A	10121	37	10	104244119	104244119	Missense_Mutation	SNP	C	G	3	165	c.455G>C	c.(454-456)AGG>ACG	p.R152T
Pat_06	Pre-Treatment	C10orf26	54838	37	10	104569725	104569725	Missense_Mutation	SNP	G	A	6	653	c.206G>A	c.(205-207)CGC>CAC	p.R69H
Pat_06	Pre-Treatment	C10orf79	80217	37	10	105944874	105944874	Missense_Mutation	SNP	G	T	5	602	c.2041C>A	c.(2041-2043)CAC>AAC	p.H681N
Pat_06	Pre-Treatment	MXI1	4601	37	10	112044696	112044696	Missense_Mutation	SNP	G	A	6	597	c.638G>A	c.(637-639)AGT>AAT	p.S213N
Pat_06	Pre-Treatment	TCF7L2	6934	37	10	114905837	114905837	Missense_Mutation	SNP	G	A	5	642	c.856G>A	c.(856-858)GTC>ATC	p.V286I
Pat_06	Pre-Treatment	NHLRC2	374354	37	10	115636654	115636654	Missense_Mutation	SNP	G	T	6	745	c.706G>T	c.(706-708)GAT>TAT	p.D236Y
Pat_06	Pre-Treatment	BAG3	9531	37	10	121429423	121429423	Missense_Mutation	SNP	G	A	5	650	c.241G>A	c.(241-243)GAA>AAA	p.E81K
Pat_06	Pre-Treatment	TACC2	10579	37	10	123842617	123842617	Nonsense_Mutation	SNP	C	A	4	174	c.602C>A	c.(601-603)TCG>TAG	p.S201*
Pat_06	Pre-Treatment	TACC2	10579	37	10	123847176	123847176	Missense_Mutation	SNP	T	C	3	109	c.5161T>C	c.(5161-5163)TCC>CCC	p.S1721P
Pat_06	Pre-Treatment	BCCIP	56647	37	10	127541703	127541703	Missense_Mutation	SNP	G	A	6	726	c.860G>A	c.(859-861)CGG>CAG	p.R287Q
Pat_06	Pre-Treatment	ECHS1	1892	37	10	135180462	135180462	Missense_Mutation	SNP	C	A	6	268	c.550G>T	c.(550-552)GGG>TGG	p.G184W
Pat_06	Pre-Treatment	SYCE1	93426	37	10	135372449	135372449	Missense_Mutation	SNP	T	C	3	154	c.203A>G	c.(202-204)AAG>AGG	p.K68R
Pat_06	Pre-Treatment	PHRF1	57661	37	11	597017	597017	Missense_Mutation	SNP	G	A	5	226	c.715G>A	c.(715-717)GCT>ACT	p.A239T
Pat_06	Pre-Treatment	CDHR5	53841	37	11	618647	618647	Missense_Mutation	SNP	G	C	4	611	c.1912C>G	c.(1912-1914)CCA>GCA	p.P638A
Pat_06	Pre-Treatment	CDHR5	53841	37	11	618767	618767	Missense_Mutation	SNP	C	T	8	735	c.1792G>A	c.(1792-1794)GGT>AGT	p.G598S
Pat_06	Pre-Treatment	AP2A2	161	37	11	993914	993914	Missense_Mutation	SNP	G	A	5	66	c.1711G>A	c.(1711-1713)GCA>ACA	p.A571T
Pat_06	Pre-Treatment	MUC6	4588	37	11	1016037	1016037	Missense_Mutation	SNP	G	A	5	795	c.6764C>T	c.(6763-6765)ACG>ATG	p.T2255M
Pat_06	Pre-Treatment	CTSD	1509	37	11	1782667	1782667	Missense_Mutation	SNP	G	A	4	307	c.100C>T	c.(100-102)CGG>TGG	p.R34W
Pat_06	Pre-Treatment	OR52B6	340980	37	11	5602528	5602528	Missense_Mutation	SNP	G	A	6	706	c.422G>A	c.(421-423)CGC>CAC	p.R141H
Pat_06	Pre-Treatment	OR52E8	390079	37	11	5878182	5878182	Missense_Mutation	SNP	C	A	5	409	c.751G>T	c.(751-753)GGT>TGT	p.G251C
Pat_06	Pre-Treatment	OR56A5	390084	37	11	5988961	5988961	Missense_Mutation	SNP	G	C	3	118	c.764C>G	c.(763-765)ACC>AGC	p.T255S
Pat_06	Pre-Treatment	ZNF143	7702	37	11	9546919	9546919	Missense_Mutation	SNP	C	A	6	643	c.1819C>A	c.(1819-1821)CAG>AAG	p.Q607K
Pat_06	Pre-Treatment	COPB1	1315	37	11	14508051	14508051	Splice_Site	SNP	C	A	5	681	c.700_splice	c.e7-1	p.V234_splice
Pat_06	Pre-Treatment	SOX6	55553	37	11	16007783	16007783	Missense_Mutation	SNP	C	T	6	820	c.2189G>A	c.(2188-2190)CGG>CAG	p.R730Q
Pat_06	Pre-Treatment	NAV2	89797	37	11	20122603	20122603	Missense_Mutation	SNP	G	A	7	688	c.6311G>A	c.(6310-6312)GGC>GAC	p.G2104D
Pat_06	Pre-Treatment	FANCF	2188	37	11	22647140	22647140	Missense_Mutation	SNP	C	A	6	215	c.217G>T	c.(217-219)GGG>TGG	p.G73W
Pat_06	Pre-Treatment	MUC15	143662	37	11	26582619	26582619	Missense_Mutation	SNP	G	A	5	708	c.998C>T	c.(997-999)TCT>TTT	p.S333F

Pat_06	Pre-Treatment	BDNF	627	37	11	27679711	27679711	Missense_Mutation	SNP	C	T	5	557	c.401G>A	c.(400-402)CGC>CAC	p.R134H
Pat_06	Pre-Treatment	DGKZ	8525	37	11	46388099	46388099	Missense_Mutation	SNP	C	T	3	59	c.293C>T	c.(292-294)ACC>ATC	p.T98I
Pat_06	Pre-Treatment	F2	2147	37	11	46741256	46741256	Missense_Mutation	SNP	C	A	3	60	c.84C>A	c.(82-84)TTC>TTA	p.F28L
Pat_06	Pre-Treatment	DDB2	1643	37	11	47256216	47256216	Missense_Mutation	SNP	G	A	5	396	c.695G>A	c.(694-696)GGC>GAC	p.G232D
Pat_06	Pre-Treatment	OR5D16	390144	37	11	55607088	55607088	Missense_Mutation	SNP	G	T	7	448	c.861G>T	c.(859-861)TTG>TTT	p.L287F
Pat_06	Pre-Treatment	OR5T2	219464	37	11	56000379	56000379	Missense_Mutation	SNP	G	A	4	347	c.283C>T	c.(283-285)CAC>TAC	p.H95Y
Pat_06	Pre-Treatment	GIF	2694	37	11	59608632	59608632	Missense_Mutation	SNP	G	A	5	755	c.677C>T	c.(676-678)ACT>ATT	p.T226I
Pat_06	Pre-Treatment	PRPF19	27339	37	11	60670218	60670218	Nonsense_Mutation	SNP	G	A	6	235	c.382C>T	c.(382-384)CGA>TGA	p.R128*
Pat_06	Pre-Treatment	C11orf84	144097	37	11	63585579	63585579	Missense_Mutation	SNP	G	A	4	300	c.430G>A	c.(430-432)GCT>ACT	p.A144T
Pat_06	Pre-Treatment	KCNK4	50801	37	11	64065695	64065695	Missense_Mutation	SNP	G	A	4	282	c.775G>A	c.(775-777)GTA>ATA	p.V259I
Pat_06	Pre-Treatment	SAC3D1	29901	37	11	64812129	64812129	Missense_Mutation	SNP	G	A	5	296	c.1007G>A	c.(1006-1008)CGT>CAT	p.R336H
Pat_06	Pre-Treatment	POLA2	23649	37	11	65063399	65063399	Missense_Mutation	SNP	G	A	8	800	c.1585G>A	c.(1585-1587)GCA>ACA	p.A529T
Pat_06	Pre-Treatment	SART1	9092	37	11	65733209	65733209	Missense_Mutation	SNP	G	T	6	286	c.697G>T	c.(697-699)GTC>TTC	p.V233F
Pat_06	Pre-Treatment	RIN1	9610	37	11	66103348	66103348	Splice_Site	SNP	C	G	3	75	c.268_splice	c.e3-1	p.T90_splice
Pat_06	Pre-Treatment	ACTN3	89	37	11	66325185	66325185	Missense_Mutation	SNP	C	T	3	69	c.913C>T	c.(913-915)CGC>TGC	p.R305C
Pat_06	Pre-Treatment	SPTBN2	6712	37	11	66467033	66467033	Missense_Mutation	SNP	G	A	6	662	c.3620C>T	c.(3619-3621)GCT>GTT	p.A1207V
Pat_06	Pre-Treatment	TBC1D10C	374403	37	11	67174358	67174358	Missense_Mutation	SNP	G	A	6	596	c.709G>A	c.(709-711)GTG>ATG	p.V237M
Pat_06	Pre-Treatment	CARNS1	57571	37	11	67187096	67187096	Missense_Mutation	SNP	G	A	3	48	c.622G>A	c.(622-624)GAG>AAG	p.E208K
Pat_06	Pre-Treatment	NDUFS8	4728	37	11	67800450	67800450	Missense_Mutation	SNP	G	A	5	587	c.170G>A	c.(169-171)CGC>CAC	p.R57H
Pat_06	Pre-Treatment	SUV420H1	51111	37	11	67925651	67925651	Missense_Mutation	SNP	C	T	6	858	c.2162G>A	c.(2161-2163)CGT>CAT	p.R721H
Pat_06	Pre-Treatment	CPT1A	1374	37	11	68560797	68560797	Missense_Mutation	SNP	G	C	3	97	c.953C>G	c.(952-954)CCA>CGA	p.P318R
Pat_06	Pre-Treatment	MRGPRF	116535	37	11	68772894	68772894	Missense_Mutation	SNP	C	A	3	32	c.884G>T	c.(883-885)GGG>GTG	p.G295V
Pat_06	Pre-Treatment	C11orf30	56946	37	11	76248884	76248884	Missense_Mutation	SNP	T	C	4	487	c.2405T>C	c.(2404-2406)CTG>CCG	p.L802P
Pat_06	Pre-Treatment	MYO7A	4647	37	11	76922326	76922326	Missense_Mutation	SNP	C	T	3	43	c.6181C>T	c.(6181-6183)CGG>TGG	p.R2061W
Pat_06	Pre-Treatment	FOLH1B	219595	37	11	89395322	89395322	Translation_Start_Site	SNP	C	T	6	237	c.-93C>T	c.(-95--91)TACGC>TATGC	
Pat_06	Pre-Treatment	FOLH1B	219595	37	11	89405075	89405075	Missense_Mutation	SNP	G	A	5	461	c.202G>A	c.(202-204)GGT>AGT	p.G68S
Pat_06	Pre-Treatment	NAALAD2	10003	37	11	89882229	89882229	Missense_Mutation	SNP	A	G	8	641	c.437A>G	c.(436-438)AAT>AGT	p.N146S
Pat_06	Pre-Treatment	FAT3	120114	37	11	92577545	92577545	Missense_Mutation	SNP	G	A	4	170	c.11012G>A	c.(11011-11013)CGC>CAC	p.R3671H
Pat_06	Pre-Treatment	AMOTL1	154810	37	11	94599195	94599195	Missense_Mutation	SNP	G	C	3	212	c.2350G>C	c.(2350-2352)GAC>CAC	p.D784H
Pat_06	Pre-Treatment	AMOTL1	154810	37	11	94602501	94602501	Missense_Mutation	SNP	G	A	4	121	c.2627G>A	c.(2626-2628)AGC>AAC	p.S876N
Pat_06	Pre-Treatment	CNTN5	53942	37	11	99872777	99872777	Missense_Mutation	SNP	G	A	3	120	c.889G>A	c.(889-891)GAA>AAA	p.E297K
Pat_06	Pre-Treatment	YAP1	10413	37	11	101984971	101984971	Missense_Mutation	SNP	G	T	7	581	c.418G>T	c.(418-420)GGG>TGG	p.G140W
Pat_06	Pre-Treatment	MMP7	4316	37	11	102401409	102401409	Missense_Mutation	SNP	G	A	5	529	c.23C>T	c.(22-24)GCT>GTT	p.A8V
Pat_06	Pre-Treatment	ARHGAP20	57569	37	11	110450900	110450900	Missense_Mutation	SNP	G	A	5	823	c.2770C>T	c.(2770-2772)CCC>TCC	p.P924S
Pat_06	Pre-Treatment	BTG4	54766	37	11	111365906	111365906	Missense_Mutation	SNP	G	C	5	531	c.644C>G	c.(643-645)GCT>GGT	p.A215G
Pat_06	Pre-Treatment	HTR3B	9177	37	11	113816851	113816851	Missense_Mutation	SNP	G	A	4	343	c.1318G>A	c.(1318-1320)GGC>AGC	p.G440S
Pat_06	Pre-Treatment	PAFAH1B2	5049	37	11	117023192	117023192	Missense_Mutation	SNP	C	T	5	338	c.29C>T	c.(28-30)GCT>GTT	p.A10V
Pat_06	Pre-Treatment	SIDT2	51092	37	11	117053466	117053466	Missense_Mutation	SNP	G	A	4	139	c.646G>A	c.(646-648)GTA>ATA	p.V216I
Pat_06	Pre-Treatment	PCSK7	9159	37	11	117094004	117094004	Missense_Mutation	SNP	G	A	4	306	c.1075C>T	c.(1075-1077)CGC>TGC	p.R359C
Pat_06	Pre-Treatment	DSCAML1	57453	37	11	117352718	117352718	Missense_Mutation	SNP	G	C	4	237	c.2699C>G	c.(2698-2700)GCC>GGC	p.A900G
Pat_06	Pre-Treatment	TRIM29	23650	37	11	119988981	119988981	Missense_Mutation	SNP	G	T	5	170	c.1577C>A	c.(1576-1578)TCT>TAT	p.S526Y
Pat_06	Pre-Treatment	GRIK4	2900	37	11	120776054	120776054	Missense_Mutation	SNP	G	A	6	652	c.1328G>A	c.(1327-1329)CGC>CAC	p.R443H
Pat_06	Pre-Treatment	HSPA8	3312	37	11	122928494	122928494	Missense_Mutation	SNP	G	A	5	459	c.1889C>T	c.(1888-1890)GCT>GTT	p.A630V
Pat_06	Pre-Treatment	VWA5A	4013	37	11	123989321	123989321	Missense_Mutation	SNP	C	G	3	206	c.551C>G	c.(550-552)GCC>GGC	p.A184G
Pat_06	Pre-Treatment	SPA17	53340	37	11	124545192	124545192	Missense_Mutation	SNP	G	A	5	548	c.32G>A	c.(31-33)CGA>CAA	p.R11Q
Pat_06	Pre-Treatment	ROBO3	64221	37	11	124742845	124742845	Missense_Mutation	SNP	T	C	3	119	c.1396T>C	c.(1396-1398)TCC>CCC	p.S466P
Pat_06	Pre-Treatment	HEPN1	641654	37	11	124789836	124789836	Missense_Mutation	SNP	G	A	5	291	c.190G>A	c.(190-192)GAA>AAA	p.E64K

Pat_06	Pre-Treatment	PKNOX2	63876	37	11	125221241	125221241	Missense_Mutation	SNP	A	G	3	73	c.40A>G	c.(40-42)ATG>GTG	p.M14V
Pat_06	Pre-Treatment	ACRV1	56	37	11	125548001	125548001	Missense_Mutation	SNP	C	T	4	243	c.244G>A	c.(244-246)GAG>AAG	p.E82K
Pat_06	Pre-Treatment	KIRREL3	84623	37	11	126343313	126343313	Missense_Mutation	SNP	C	T	3	47	c.482G>A	c.(481-483)CGT>CAT	p.R161H
Pat_06	Pre-Treatment	LOC100288778	100288778	37	12	90615	90615	Missense_Mutation	SNP	G	T	3	45	c.621G>T	c.(619-621)TTG>TTT	p.L207F
Pat_06	Pre-Treatment	CACNA2D4	93589	37	12	1969324	1969324	Missense_Mutation	SNP	C	G	3	176	c.1927G>C	c.(1927-1929)GAC>CAC	p.D643H
Pat_06	Pre-Treatment	KCNA6	3742	37	12	4919422	4919422	Missense_Mutation	SNP	G	A	5	458	c.215G>A	c.(214-216)CGG>CAG	p.R72Q
Pat_06	Pre-Treatment	CD9	928	37	12	6309672	6309672	Missense_Mutation	SNP	G	A	5	326	c.7G>A	c.(7-9)GTC>ATC	p.V3I
Pat_06	Pre-Treatment	PLEKHG6	55200	37	12	6428010	6428010	Missense_Mutation	SNP	G	C	3	284	c.1375G>C	c.(1375-1377)GAG>CAG	p.E459Q
Pat_06	Pre-Treatment	ZNF384	171017	37	12	6776926	6776926	Missense_Mutation	SNP	G	A	7	850	c.1688C>T	c.(1687-1689)ACT>ATT	p.T563I
Pat_06	Pre-Treatment	C12orf53	196500	37	12	6806933	6806933	Missense_Mutation	SNP	G	A	3	71	c.43C>T	c.(43-45)CTC>TTC	p.L15F
Pat_06	Pre-Treatment	CD163L1	283316	37	12	7527092	7527092	Missense_Mutation	SNP	C	T	5	451	c.3355G>A	c.(3355-3357)GGC>AGC	p.G1119S
Pat_06	Pre-Treatment	GPR19	2842	37	12	12815291	12815291	Missense_Mutation	SNP	G	A	8	782	c.92C>T	c.(91-93)ACA>ATA	p.T31I
Pat_06	Pre-Treatment	C12orf36	283422	37	12	13526349	13526349	Missense_Mutation	SNP	G	A	4	234	c.206C>T	c.(205-207)TCG>TTG	p.S69L
Pat_06	Pre-Treatment	C12orf72	254013	37	12	31815090	31815090	Missense_Mutation	SNP	A	G	4	510	c.203A>G	c.(202-204)CAG>CGG	p.Q68R
Pat_06	Pre-Treatment	FGD4	121512	37	12	32735075	32735075	Missense_Mutation	SNP	G	A	8	566	c.274G>A	c.(274-276)GGT>AGT	p.G92S
Pat_06	Pre-Treatment	DDX23	9416	37	12	49227133	49227133	Missense_Mutation	SNP	G	A	259	420	c.1730C>T	c.(1729-1731)CCA>CTA	p.P577L
Pat_06	Pre-Treatment	LMBR1L	55716	37	12	49495258	49495258	Missense_Mutation	SNP	C	T	4	141	c.1005G>A	c.(1003-1005)ATG>ATA	p.M335I
Pat_06	Pre-Treatment	FMNL3	91010	37	12	50043288	50043288	Missense_Mutation	SNP	C	T	5	455	c.2269G>A	c.(2269-2271)GTC>ATC	p.V757I
Pat_06	Pre-Treatment	SLC4A8	9498	37	12	51888762	51888762	Missense_Mutation	SNP	G	A	7	465	c.2803G>A	c.(2803-2805)GCA>ACA	p.A935T
Pat_06	Pre-Treatment	KRT86	3892	37	12	52702316	52702316	Missense_Mutation	SNP	T	C	3	176	c.1408T>C	c.(1408-1410)TGC>CGC	p.C470R
Pat_06	Pre-Treatment	KRT75	9119	37	12	52818456	52818456	Missense_Mutation	SNP	C	T	4	433	c.1501G>A	c.(1501-1503)GGC>AGC	p.G501S
Pat_06	Pre-Treatment	KRT8	3856	37	12	53292500	53292500	Missense_Mutation	SNP	C	T	6	627	c.1165G>A	c.(1165-1167)GCC>ACC	p.A389T
Pat_06	Pre-Treatment	AAAS	8086	37	12	53702942	53702942	Nonsense_Mutation	SNP	G	A	6	794	c.934C>T	c.(934-936)CGA>TGA	p.R312*
Pat_06	Pre-Treatment	AMHR2	269	37	12	53825045	53825045	Missense_Mutation	SNP	C	T	5	459	c.1510C>T	c.(1510-1512)CGC>TGC	p.R504C
Pat_06	Pre-Treatment	MMP19	4327	37	12	56231419	56231419	Missense_Mutation	SNP	G	A	5	331	c.1108C>T	c.(1108-1110)CCC>TCC	p.P370S
Pat_06	Pre-Treatment	DGKA	1606	37	12	56334462	56334462	Missense_Mutation	SNP	C	T	5	636	c.973C>T	c.(973-975)CGG>TGG	p.R325W
Pat_06	Pre-Treatment	CS	1431	37	12	56667537	56667537	Missense_Mutation	SNP	G	A	5	654	c.1064C>T	c.(1063-1065)CCG>CTG	p.P355L
Pat_06	Pre-Treatment	TIMELESS	8914	37	12	56817194	56817194	Missense_Mutation	SNP	G	A	6	511	c.2156C>T	c.(2155-2157)GCC>GTC	p.A719V
Pat_06	Pre-Treatment	TAC3	6866	37	12	57406612	57406612	Nonsense_Mutation	SNP	G	A	4	528	c.286C>T	c.(286-288)CAG>TAG	p.Q96*
Pat_06	Pre-Treatment	LRP1	4035	37	12	57603830	57603830	Missense_Mutation	SNP	G	A	5	464	c.12458G>A	c.(12457-12459)CGC>CAC	p.R4153H
Pat_06	Pre-Treatment	IFNG	3458	37	12	68549234	68549234	Missense_Mutation	SNP	G	T	6	579	c.400C>A	c.(400-402)CAT>AAT	p.H134N
Pat_06	Pre-Treatment	CPSF6	11052	37	12	69656305	69656305	Missense_Mutation	SNP	A	G	3	170	c.1622A>G	c.(1621-1623)GAG>GGG	p.E541G
Pat_06	Pre-Treatment	TMTC2	160335	37	12	83251250	83251250	Missense_Mutation	SNP	G	A	4	396	c.545G>A	c.(544-546)AGC>AAC	p.S182N
Pat_06	Pre-Treatment	C12orf12	196477	37	12	91347305	91347305	Missense_Mutation	SNP	G	C	4	212	c.1215C>G	c.(1213-1215)AAC>AAG	p.N405K
Pat_06	Pre-Treatment	SART3	9733	37	12	108930528	108930528	Missense_Mutation	SNP	G	C	3	221	c.1343C>G	c.(1342-1344)GCC>GGC	p.A448G
Pat_06	Pre-Treatment	ACACB	32	37	12	109704069	109704069	Missense_Mutation	SNP	G	A	4	293	c.7279G>A	c.(7279-7281)GTG>ATG	p.V2427M
Pat_06	Pre-Treatment	C12orf51	283450	37	12	112600845	112600845	Splice_Site	SNP	C	T	5	566	c.11854_splice	c.e68+1	p.G3952_splice
Pat_06	Pre-Treatment	C12orf51	283450	37	12	112674828	112674828	Missense_Mutation	SNP	C	G	3	103	c.4099G>C	c.(4099-4101)GCC>CCC	p.A1367P
Pat_06	Pre-Treatment	SLC24A6	80024	37	12	113753209	113753209	Missense_Mutation	SNP	G	A	3	46	c.1066C>T	c.(1066-1068)CGG>TGG	p.R356W
Pat_06	Pre-Treatment	MED13L	23389	37	12	116452921	116452921	Missense_Mutation	SNP	G	T	6	658	c.1168C>A	c.(1168-1170)CAG>AAG	p.Q390K
Pat_06	Pre-Treatment	MED13L	23389	37	12	116457208	116457208	Missense_Mutation	SNP	C	T	4	458	c.830G>A	c.(829-831)CGG>CAG	p.R277Q
Pat_06	Pre-Treatment	VSIG10	54621	37	12	118517169	118517169	Missense_Mutation	SNP	T	C	3	219	c.907A>G	c.(907-909)AGC>GGC	p.S303G
Pat_06	Pre-Treatment	CIT	11113	37	12	120135563	120135563	Missense_Mutation	SNP	G	A	7	502	c.5657C>T	c.(5656-5658)GCG>GTG	p.A1886V
Pat_06	Pre-Treatment	RPLP0	6175	37	12	120636757	120636757	Missense_Mutation	SNP	G	C	3	150	c.365C>G	c.(364-366)ACT>AGT	p.T122S
Pat_06	Pre-Treatment	CABP1	9478	37	12	121098115	121098115	Missense_Mutation	SNP	G	A	4	161	c.802G>A	c.(802-804)GAA>AAA	p.E268K
Pat_06	Pre-Treatment	CLIP1	6249	37	12	122862048	122862048	Missense_Mutation	SNP	G	A	5	726	c.545C>T	c.(544-546)ACG>ATG	p.T182M
Pat_06	Pre-Treatment	MPHOSPH9	10198	37	12	123705991	123705991	Missense_Mutation	SNP	G	A	52	147	c.344C>T	c.(343-345)TCT>TTT	p.S115F

Pat_06	Pre-Treatment	ATP6V0A2	23545	37	12	124242547	124242547	Missense_Mutation	SNP	T	C	4	323	c.2539T>C	c.(2539-2541)TCA>CCA	p.S847P
Pat_06	Pre-Treatment	TMEM132D	121256	37	12	130015713	130015713	Nonsense_Mutation	SNP	G	A	5	406	c.1006C>T	c.(1006-1008)CGA>TGA	p.R336*
Pat_06	Pre-Treatment	PUS1	80324	37	12	132416789	132416789	Missense_Mutation	SNP	T	C	3	262	c.373T>C	c.(373-375)TGT>CGT	p.C125R
Pat_06	Pre-Treatment	PUS1	80324	37	12	132426187	132426187	Missense_Mutation	SNP	G	A	5	724	c.895G>A	c.(895-897)GGC>AGC	p.G299S
Pat_06	Pre-Treatment	POLE	5426	37	12	133218233	133218233	Missense_Mutation	SNP	C	T	4	188	c.5378G>A	c.(5377-5379)AGG>AAG	p.R1793K
Pat_06	Pre-Treatment	ZNF10	7556	37	12	133732999	133732999	Missense_Mutation	SNP	C	A	6	821	c.1167C>A	c.(1165-1167)AGC>AGA	p.S389R
Pat_06	Pre-Treatment	GJB2	2706	37	13	20763513	20763513	Missense_Mutation	SNP	G	A	4	354	c.208C>T	c.(208-210)CCC>TCC	p.P70S
Pat_06	Pre-Treatment	IFT88	8100	37	13	21205209	21205209	Missense_Mutation	SNP	G	A	5	468	c.1381G>A	c.(1381-1383)GCT>ACT	p.A461T
Pat_06	Pre-Treatment	SACS	26278	37	13	23914963	23914963	Missense_Mutation	SNP	C	G	4	746	c.3052G>C	c.(3052-3054)GAG>CAG	p.E1018Q
Pat_06	Pre-Treatment	FREM2	341640	37	13	39265331	39265331	Missense_Mutation	SNP	G	T	6	822	c.3850G>T	c.(3850-3852)GGG>TGG	p.G1284W
Pat_06	Pre-Treatment	STOML3	161003	37	13	39550707	39550707	Missense_Mutation	SNP	G	A	5	277	c.199C>T	c.(199-201)CGC>TGC	p.R67C
Pat_06	Pre-Treatment	SIAH3	283514	37	13	46425647	46425647	Missense_Mutation	SNP	G	A	4	497	c.118C>T	c.(118-120)CCC>TCC	p.P40S
Pat_06	Pre-Treatment	C13orf18	80183	37	13	46919644	46919644	Missense_Mutation	SNP	G	T	3	53	c.1723C>A	c.(1723-1725)CTG>ATG	p.L575M
Pat_06	Pre-Treatment	C13orf18	80183	37	13	46924411	46924411	Missense_Mutation	SNP	G	A	3	53	c.1406C>T	c.(1405-1407)TCG>TTG	p.S469L
Pat_06	Pre-Treatment	RNF113B	140432	37	13	98829159	98829159	Missense_Mutation	SNP	G	A	4	260	c.332C>T	c.(331-333)ACC>ATC	p.T111I
Pat_06	Pre-Treatment	COL4A2	1284	37	13	111114691	111114691	Missense_Mutation	SNP	G	A	5	442	c.1736G>A	c.(1735-1737)CGC>CAC	p.R579H
Pat_06	Pre-Treatment	COL4A2	1284	37	13	111125465	111125465	Missense_Mutation	SNP	T	A	3	39	c.2393T>A	c.(2392-2394)CTT>CAT	p.L798H
Pat_06	Pre-Treatment	ING1	3621	37	13	111371695	111371695	Missense_Mutation	SNP	G	A	5	491	c.685G>A	c.(685-687)GAC>AAC	p.D229N
Pat_06	Pre-Treatment	ATP11A	23250	37	13	113508817	113508817	Missense_Mutation	SNP	G	A	5	464	c.2216G>A	c.(2215-2217)GGG>GAG	p.G739E
Pat_06	Pre-Treatment	PROZ	8858	37	13	113813020	113813020	Missense_Mutation	SNP	G	C	3	80	c.46G>C	c.(46-48)GCC>CCC	p.A16P
Pat_06	Pre-Treatment	PROZ	8858	37	13	113817386	113817386	Missense_Mutation	SNP	G	A	3	34	c.323G>A	c.(322-324)GGC>GAC	p.G108D
Pat_06	Pre-Treatment	CUL4A	8451	37	13	113889431	113889431	Missense_Mutation	SNP	G	A	7	445	c.820G>A	c.(820-822)GTA>ATA	p.V274I
Pat_06	Pre-Treatment	TTC5	91875	37	14	20763525	20763525	Missense_Mutation	SNP	G	A	5	460	c.1004C>T	c.(1003-1005)GCC>GTC	p.A335V
Pat_06	Pre-Treatment	RNASE2	6036	37	14	21424318	21424318	Missense_Mutation	SNP	G	A	5	617	c.388G>A	c.(388-390)GCA>ACA	p.A130T
Pat_06	Pre-Treatment	FLJ10357	55701	37	14	21552174	21552174	Missense_Mutation	SNP	G	A	4	80	c.3754G>A	c.(3754-3756)GAC>AAC	p.D1252N
Pat_06	Pre-Treatment	RPGRIP1	57096	37	14	21770737	21770737	Missense_Mutation	SNP	G	A	3	52	c.581G>A	c.(580-582)AGT>AAT	p.S194N
Pat_06	Pre-Treatment	DAD1	1603	37	14	23044076	23044076	Missense_Mutation	SNP	G	T	6	506	c.269C>A	c.(268-270)CCA>CAA	p.P90Q
Pat_06	Pre-Treatment	RBM23	55147	37	14	23371498	23371498	Nonsense_Mutation	SNP	G	A	6	423	c.1024C>T	c.(1024-1026)CGA>TGA	p.R342*
Pat_06	Pre-Treatment	DHRS2	10202	37	14	24108425	24108425	Missense_Mutation	SNP	G	A	5	672	c.178G>A	c.(178-180)GGG>AGG	p.G60R
Pat_06	Pre-Treatment	DCAF11	80344	37	14	24589061	24589061	Missense_Mutation	SNP	G	A	4	190	c.1048G>A	c.(1048-1050)GCA>ACA	p.A350T
Pat_06	Pre-Treatment	IRF9	10379	37	14	24631376	24631376	Missense_Mutation	SNP	G	A	6	769	c.23G>A	c.(22-24)TGC>TAC	p.C8Y
Pat_06	Pre-Treatment	RIPK3	11035	37	14	24808715	24808715	Missense_Mutation	SNP	G	A	6	796	c.109C>T	c.(109-111)CGG>TGG	p.R37W
Pat_06	Pre-Treatment	AKAP6	9472	37	14	33147587	33147587	Missense_Mutation	SNP	G	A	5	556	c.2801G>A	c.(2800-2802)AGC>AAC	p.S934N
Pat_06	Pre-Treatment	FBXO33	254170	37	14	39868790	39868790	Nonsense_Mutation	SNP	G	T	5	165	c.1598C>A	c.(1597-1599)TCA>TAA	p.S533*
Pat_06	Pre-Treatment	C14orf104	55172	37	14	50101657	50101657	Missense_Mutation	SNP	G	A	3	9	c.211C>T	c.(211-213)CAC>TAC	p.H71Y
Pat_06	Pre-Treatment	PSMC6	5706	37	14	53184828	53184828	Missense_Mutation	SNP	G	A	6	673	c.601G>A	c.(601-603)GTT>ATT	p.V201I
Pat_06	Pre-Treatment	C14orf39	317761	37	14	60908831	60908831	Missense_Mutation	SNP	C	A	6	511	c.1522G>T	c.(1522-1524)GCA>TCA	p.A508S
Pat_06	Pre-Treatment	SPTB	6710	37	14	65239449	65239449	Missense_Mutation	SNP	C	T	4	343	c.5402G>A	c.(5401-5403)CGC>CAC	p.R1801H
Pat_06	Pre-Treatment	FUT8	2530	37	14	66096305	66096305	Missense_Mutation	SNP	G	A	6	534	c.578G>A	c.(577-579)CGG>CAG	p.R193Q
Pat_06	Pre-Treatment	KIAA0247	9766	37	14	70125355	70125355	Missense_Mutation	SNP	G	A	5	588	c.46G>A	c.(46-48)GTG>ATG	p.V16M
Pat_06	Pre-Treatment	ZFYVE1	53349	37	14	73444864	73444864	Missense_Mutation	SNP	C	T	6	652	c.1498G>A	c.(1498-1500)GCA>ACA	p.A500T
Pat_06	Pre-Treatment	RBM25	58517	37	14	73544119	73544119	Missense_Mutation	SNP	G	A	5	388	c.199G>A	c.(199-201)GCA>ACA	p.A67T
Pat_06	Pre-Treatment	COQ6	51004	37	14	74425701	74425701	Missense_Mutation	SNP	G	A	4	328	c.640G>A	c.(640-642)GTA>ATA	p.V214I
Pat_06	Pre-Treatment	YLPM1	56252	37	14	75230568	75230568	Missense_Mutation	SNP	C	A	5	635	c.376C>A	c.(376-378)CAG>AAG	p.Q126K
Pat_06	Pre-Treatment	PROX2	283571	37	14	75329681	75329681	Missense_Mutation	SNP	G	A	4	375	c.857C>T	c.(856-858)GCT>GTT	p.A286V
Pat_06	Pre-Treatment	MLH3	27030	37	14	75513336	75513336	Missense_Mutation	SNP	G	A	6	737	c.3023C>T	c.(3022-3024)CCG>CTG	p.P1008L
Pat_06	Pre-Treatment	KIAA1737	85457	37	14	77579861	77579861	Missense_Mutation	SNP	G	T	5	602	c.400G>T	c.(400-402)GTA>TTA	p.V134L

Pat_06	Pre-Treatment	KIAA1737	85457	37	14	77580273	77580273	Missense_Mutation	SNP	G	A	5	512	c.812G>A	c.(811-813)AGC>AAC	p.S271N
Pat_06	Pre-Treatment	DIO2	1734	37	14	80669258	80669258	Missense_Mutation	SNP	A	G	4	417	c.596T>C	c.(595-597)CTG>CCG	p.L199P
Pat_06	Pre-Treatment	C14orf102	55051	37	14	90767615	90767615	Missense_Mutation	SNP	C	T	6	541	c.1513G>A	c.(1513-1515)GAC>AAC	p.D505N
Pat_06	Pre-Treatment	CALM1	801	37	14	90870735	90870735	Missense_Mutation	SNP	T	C	4	694	c.298T>C	c.(298-300)TAT>CAT	p.Y100H
Pat_06	Pre-Treatment	RIN3	79890	37	14	93119143	93119143	Missense_Mutation	SNP	C	A	5	490	c.1749C>A	c.(1747-1749)AGC>AGA	p.S583R
Pat_06	Pre-Treatment	BEGAIN	57596	37	14	101005646	101005646	Missense_Mutation	SNP	A	G	3	212	c.442T>C	c.(442-444)TCG>CCG	p.S148P
Pat_06	Pre-Treatment	KIF26A	26153	37	14	104639782	104639782	Missense_Mutation	SNP	G	A	3	38	c.1799G>A	c.(1798-1800)CGC>CAC	p.R600H
Pat_06	Pre-Treatment	CRIP1	1396	37	14	105954667	105954667	Splice_Site	SNP	G	A	5	431	c.136_splice	c.e4-1	p.H46_splice
Pat_06	Pre-Treatment	HERC2P2	400322	37	15	23312230	23312230	Missense_Mutation	SNP	T	C	3	136	c.2692A>G	c.(2692-2694)ATG>GTG	p.M898V
Pat_06	Pre-Treatment	C15orf53	400359	37	15	38990504	38990504	Missense_Mutation	SNP	G	A	6	303	c.298G>A	c.(298-300)GTC>ATC	p.V100I
Pat_06	Pre-Treatment	BAHD1	22893	37	15	40754275	40754275	Missense_Mutation	SNP	C	T	4	214	c.1597C>T	c.(1597-1599)CGT>TGT	p.R533C
Pat_06	Pre-Treatment	RAD51	5888	37	15	41022087	41022087	Missense_Mutation	SNP	G	A	5	376	c.811G>A	c.(811-813)GCT>ACT	p.A271T
Pat_06	Pre-Treatment	INO80	54617	37	15	41346195	41346195	Missense_Mutation	SNP	G	A	4	210	c.2206C>T	c.(2206-2208)CAC>TAC	p.H736Y
Pat_06	Pre-Treatment	JMJD7-PLA2G4B	8681	37	15	42137219	42137219	Missense_Mutation	SNP	G	A	3	38	c.1190G>A	c.(1189-1191)TGC>TAC	p.C397Y
Pat_06	Pre-Treatment	JMJD7-PLA2G4B	8681	37	15	42138219	42138219	Missense_Mutation	SNP	G	A	4	215	c.1574G>A	c.(1573-1575)CGC>CAC	p.R525H
Pat_06	Pre-Treatment	TUBGCP4	27229	37	15	43678142	43678142	Missense_Mutation	SNP	C	A	4	128	c.877C>A	c.(877-879)CTG>ATG	p.L293M
Pat_06	Pre-Treatment	DUOX1	53905	37	15	45428774	45428774	Missense_Mutation	SNP	G	A	6	600	c.973G>A	c.(973-975)GCC>ACC	p.A325T
Pat_06	Pre-Treatment	FBN1	2200	37	15	48725143	48725143	Missense_Mutation	SNP	C	T	6	641	c.6659G>A	c.(6658-6660)CGA>CAA	p.R2220Q
Pat_06	Pre-Treatment	C15orf33	196951	37	15	49833994	49833994	Missense_Mutation	SNP	C	A	6	723	c.757G>T	c.(757-759)GAT>TAT	p.D253Y
Pat_06	Pre-Treatment	ATP8B4	79895	37	15	50264941	50264941	Missense_Mutation	SNP	G	A	6	219	c.1081C>T	c.(1081-1083)CGG>TGG	p.R361W
Pat_06	Pre-Treatment	AQP9	366	37	15	58471493	58471493	Missense_Mutation	SNP	T	C	3	117	c.662T>C	c.(661-663)CTG>CCG	p.L221P
Pat_06	Pre-Treatment	LIPC	3990	37	15	58830669	58830669	Missense_Mutation	SNP	G	A	6	822	c.226G>A	c.(226-228)GGC>AGC	p.G76S
Pat_06	Pre-Treatment	LACTB	114294	37	15	63433955	63433955	Missense_Mutation	SNP	G	A	4	495	c.1595G>A	c.(1594-1596)AGC>AAC	p.S532N
Pat_06	Pre-Treatment	RAB8B	51762	37	15	63555808	63555808	Missense_Mutation	SNP	C	T	4	185	c.614C>T	c.(613-615)TCG>TTG	p.S205L
Pat_06	Pre-Treatment	FAM96A	84191	37	15	64365201	64365201	Nonsense_Mutation	SNP	G	A	7	697	c.412C>T	c.(412-414)CGA>TGA	p.R138*
Pat_06	Pre-Treatment	NOX5	79400	37	15	69223047	69223047	Missense_Mutation	SNP	G	A	5	537	c.20G>A	c.(19-21)GGC>GAC	p.G7D
Pat_06	Pre-Treatment	TLE3	7090	37	15	70344856	70344856	Missense_Mutation	SNP	G	A	6	157	c.1991C>T	c.(1990-1992)TCG>TTG	p.S664L
Pat_06	Pre-Treatment	TLE3	7090	37	15	70346798	70346798	Missense_Mutation	SNP	A	G	4	373	c.1814T>C	c.(1813-1815)CTG>CCG	p.L605P
Pat_06	Pre-Treatment	STOML1	9399	37	15	74276372	74276372	Missense_Mutation	SNP	C	T	5	209	c.1103G>A	c.(1102-1104)CGG>CAG	p.R368Q
Pat_06	Pre-Treatment	LINGO1	84894	37	15	77907197	77907197	Missense_Mutation	SNP	T	C	3	137	c.1052A>G	c.(1051-1053)GAG>GGG	p.E351G
Pat_06	Pre-Treatment	ADAMTS7	11173	37	15	79059759	79059759	Missense_Mutation	SNP	G	A	4	273	c.2821C>T	c.(2821-2823)CCC>TCC	p.P941S
Pat_06	Pre-Treatment	KIAA1024	23251	37	15	79748562	79748562	Missense_Mutation	SNP	G	A	6	490	c.73G>A	c.(73-75)GTT>ATT	p.V25I
Pat_06	Pre-Treatment	FAH	2184	37	15	80460423	80460423	Missense_Mutation	SNP	G	A	5	287	c.485G>A	c.(484-486)CGT>CAT	p.R162H
Pat_06	Pre-Treatment	BNC1	646	37	15	83932358	83932358	Missense_Mutation	SNP	C	T	5	416	c.1645G>A	c.(1645-1647)GAA>AAA	p.E549K
Pat_06	Pre-Treatment	WDR73	84942	37	15	85188797	85188797	Missense_Mutation	SNP	C	A	3	66	c.788G>T	c.(787-789)AGC>ATC	p.S263I
Pat_06	Pre-Treatment	AKAP13	11214	37	15	86124402	86124402	Missense_Mutation	SNP	G	A	5	345	c.3103G>A	c.(3103-3105)GCA>ACA	p.A1035T
Pat_06	Pre-Treatment	ANPEP	290	37	15	90344738	90344738	Missense_Mutation	SNP	C	T	5	361	c.1670G>A	c.(1669-1671)AGC>AAC	p.S557N
Pat_06	Pre-Treatment	TTLL13	440307	37	15	90800930	90800930	Missense_Mutation	SNP	G	A	5	626	c.911G>A	c.(910-912)CGG>CAG	p.R304Q
Pat_06	Pre-Treatment	PRC1	9055	37	15	91513716	91513716	Missense_Mutation	SNP	G	A	8	626	c.1490C>T	c.(1489-1491)ACG>ATG	p.T497M
Pat_06	Pre-Treatment	CHD2	1106	37	15	93540535	93540535	Missense_Mutation	SNP	G	A	5	657	c.3787G>A	c.(3787-3789)GTG>ATG	p.V1263M
Pat_06	Pre-Treatment	ADAMTS17	170691	37	15	100692893	100692893	Missense_Mutation	SNP	G	A	5	561	c.1397C>T	c.(1396-1398)CCG>CTG	p.P466L
Pat_06	Pre-Treatment	TM2D3	80213	37	15	102185305	102185305	Missense_Mutation	SNP	G	A	4	212	c.563C>T	c.(562-564)ACG>ATG	p.T188M
Pat_06	Pre-Treatment	TM2D3	80213	37	15	102186954	102186954	Missense_Mutation	SNP	G	A	6	653	c.476C>T	c.(475-477)ACG>ATG	p.T159M
Pat_06	Pre-Treatment	WASH3P	374666	37	15	102514187	102514187	Missense_Mutation	SNP	C	T	3	101	c.158C>T	c.(157-159)CCC>CTC	p.P53L
Pat_06	Pre-Treatment	WFIKKN1	117166	37	16	683596	683596	Missense_Mutation	SNP	G	A	3	51	c.1186G>A	c.(1186-1188)GGC>AGC	p.G396S
Pat_06	Pre-Treatment	RHOT2	89941	37	16	723559	723559	Missense_Mutation	SNP	G	A	7	527	c.1810G>A	c.(1810-1812)GCA>ACA	p.A604T
Pat_06	Pre-Treatment	METRN	79006	37	16	767370	767370	Missense_Mutation	SNP	G	A	3	32	c.865G>A	c.(865-867)GAG>AAG	p.E289K

Pat_06	Pre-Treatment	MSLNL	401827	37	16	825086	825086	Splice_Site	SNP	C	T	3	29	c.1487_splice	c.e7-1	p.G496_splice
Pat_06	Pre-Treatment	TSC2	7249	37	16	2124250	2124250	Missense_Mutation	SNP	G	C	3	246	c.2405G>C	c.(2404-2406)AGC>ACC	p.S802T
Pat_06	Pre-Treatment	PKD1	5310	37	16	2160688	2160688	Missense_Mutation	SNP	G	A	4	121	c.4480C>T	c.(4480-4482)CGC>TGC	p.R1494C
Pat_06	Pre-Treatment	CLDN9	9080	37	16	3063490	3063490	Missense_Mutation	SNP	G	A	5	676	c.127G>A	c.(127-129)GCC>ACC	p.A43T
Pat_06	Pre-Treatment	OR1F2P	26184	37	16	3265972	3265972	Missense_Mutation	SNP	G	A	6	431	c.263G>A	c.(262-264)CGC>CAC	p.R88H
Pat_06	Pre-Treatment	CREBBP	1387	37	16	3795351	3795351	Missense_Mutation	SNP	C	T	4	215	c.3841G>A	c.(3841-3843)GTT>ATT	p.V1281I
Pat_06	Pre-Treatment	ADCY9	115	37	16	4163951	4163951	Missense_Mutation	SNP	C	T	5	755	c.1493G>A	c.(1492-1494)GGC>GAC	p.G498D
Pat_06	Pre-Treatment	ADCY9	115	37	16	4164821	4164821	Missense_Mutation	SNP	G	A	5	345	c.623C>T	c.(622-624)ACG>ATG	p.T208M
Pat_06	Pre-Treatment	CORO7	79585	37	16	4410468	4410468	Missense_Mutation	SNP	G	A	3	88	c.1999C>T	c.(1999-2001)CGG>TGG	p.R667W
Pat_06	Pre-Treatment	HMOX2	3163	37	16	4557769	4557769	Missense_Mutation	SNP	G	A	4	279	c.260G>A	c.(259-261)CGC>CAC	p.R87H
Pat_06	Pre-Treatment	CIITA	4261	37	16	11001044	11001044	Missense_Mutation	SNP	G	C	3	116	c.1695G>C	c.(1693-1695)GAG>GAC	p.E565D
Pat_06	Pre-Treatment	KIAA0430	9665	37	16	15711209	15711209	Missense_Mutation	SNP	C	G	5	418	c.2904G>C	c.(2902-2904)GAG>GAC	p.E968D
Pat_06	Pre-Treatment	MYH11	4629	37	16	15850338	15850338	Missense_Mutation	SNP	C	G	4	432	c.1609G>C	c.(1609-1611)GAG>CAG	p.E537Q
Pat_06	Pre-Treatment	ABCC1	4363	37	16	16173267	16173267	Missense_Mutation	SNP	G	A	5	381	c.2047G>A	c.(2047-2049)GGA>AGA	p.G683R
Pat_06	Pre-Treatment	GPRC5B	51704	37	16	19883402	19883402	Missense_Mutation	SNP	A	G	3	133	c.766T>C	c.(766-768)TTC>CTC	p.F256L
Pat_06	Pre-Treatment	PALB2	79728	37	16	23614890	23614890	Missense_Mutation	SNP	G	A	5	462	c.3451C>T	c.(3451-3453)CTC>TTC	p.L1151F
Pat_06	Pre-Treatment	ERN2	10595	37	16	23724538	23724538	Missense_Mutation	SNP	G	A	3	26	c.115C>T	c.(115-117)CCT>TCT	p.P39S
Pat_06	Pre-Treatment	SH2B1	25970	37	16	28878028	28878028	Missense_Mutation	SNP	G	A	4	321	c.613G>A	c.(613-615)GGG>AGG	p.G205R
Pat_06	Pre-Treatment	KIF22	3835	37	16	29809938	29809938	Missense_Mutation	SNP	G	A	5	661	c.419G>A	c.(418-420)AGC>AAC	p.S140N
Pat_06	Pre-Treatment	MVP	9961	37	16	29848185	29848185	Missense_Mutation	SNP	C	G	3	153	c.815C>G	c.(814-816)CCC>CGC	p.P272R
Pat_06	Pre-Treatment	TAOK2	9344	37	16	29990581	29990581	Missense_Mutation	SNP	C	T	5	657	c.515C>T	c.(514-516)TCT>TTT	p.S172F
Pat_06	Pre-Treatment	ZNF646	9726	37	16	31090124	31090124	Missense_Mutation	SNP	G	T	6	804	c.2479G>T	c.(2479-2481)GGG>TGG	p.G827W
Pat_06	Pre-Treatment	PRSS36	146547	37	16	31150725	31150725	Missense_Mutation	SNP	G	A	5	490	c.2302C>T	c.(2302-2304)CCG>TCG	p.P768S
Pat_06	Pre-Treatment	C16orf58	64755	37	16	31508206	31508206	Missense_Mutation	SNP	G	C	3	119	c.666C>G	c.(664-666)AAC>AAG	p.N222K
Pat_06	Pre-Treatment	NETO2	81831	37	16	47163191	47163191	Missense_Mutation	SNP	G	A	6	797	c.176C>T	c.(175-177)TCG>TTG	p.S59L
Pat_06	Pre-Treatment	LONP2	83752	37	16	48337150	48337150	Missense_Mutation	SNP	G	A	8	810	c.1729G>A	c.(1729-1731)GTG>ATG	p.V577M
Pat_06	Pre-Treatment	SIAH1	6477	37	16	48395912	48395912	Missense_Mutation	SNP	G	A	4	228	c.428C>T	c.(427-429)GCT>GTT	p.A143V
Pat_06	Pre-Treatment	CBLN1	869	37	16	49315218	49315218	Missense_Mutation	SNP	G	C	3	194	c.159C>G	c.(157-159)ATC>ATG	p.I53M
Pat_06	Pre-Treatment	ZNF423	23090	37	16	49672212	49672212	Missense_Mutation	SNP	G	C	3	196	c.851C>G	c.(850-852)ACC>AGC	p.T284S
Pat_06	Pre-Treatment	TOX3	27324	37	16	52497917	52497917	Missense_Mutation	SNP	G	A	6	483	c.337C>T	c.(337-339)CTC>TTC	p.L113F
Pat_06	Pre-Treatment	CAPNS2	84290	37	16	55601312	55601312	Missense_Mutation	SNP	G	A	6	850	c.644G>A	c.(643-645)CGC>CAC	p.R215H
Pat_06	Pre-Treatment	NLRC5	84166	37	16	57113186	57113186	Missense_Mutation	SNP	C	A	5	341	c.5219C>A	c.(5218-5220)CCG>CAG	p.P1740Q
Pat_06	Pre-Treatment	ZNF319	57567	37	16	58031472	58031472	Missense_Mutation	SNP	G	A	5	445	c.698C>T	c.(697-699)ACG>ATG	p.T233M
Pat_06	Pre-Treatment	SETD6	79918	37	16	58549945	58549945	Missense_Mutation	SNP	C	T	3	56	c.278C>T	c.(277-279)CCG>CTG	p.P93L
Pat_06	Pre-Treatment	GOT2	2806	37	16	58768141	58768141	Translation_Start_Site	SNP	G	A	5	95	c.-8C>T	c.(-10--6)TACGG>TATGG	
Pat_06	Pre-Treatment	CES3	23491	37	16	66998260	66998260	Missense_Mutation	SNP	C	G	3	235	c.561C>G	c.(559-561)AGC>AGG	p.S187R
Pat_06	Pre-Treatment	KIAA0895L	653319	37	16	67213728	67213728	Missense_Mutation	SNP	C	T	5	442	c.704G>A	c.(703-705)TGC>TAC	p.C235Y
Pat_06	Pre-Treatment	PLEKHG4	25894	37	16	67318652	67318652	Missense_Mutation	SNP	G	A	4	199	c.1729G>A	c.(1729-1731)GCA>ACA	p.A577T
Pat_06	Pre-Treatment	ZDHHC1	29800	37	16	67432126	67432126	Missense_Mutation	SNP	G	A	8	721	c.916C>T	c.(916-918)CGG>TGG	p.R306W
Pat_06	Pre-Treatment	PMFBP1	83449	37	16	72170712	72170712	Missense_Mutation	SNP	T	C	5	293	c.925A>G	c.(925-927)AAG>GAG	p.K309E
Pat_06	Pre-Treatment	PKD1L2	114780	37	16	81199543	81199543	Missense_Mutation	SNP	C	T	8	43	c.3119G>A	c.(3118-3120)CGA>CAA	p.R1040Q
Pat_06	Pre-Treatment	PLCG2	5336	37	16	81929460	81929460	Nonsense_Mutation	SNP	G	A	5	610	c.1121G>A	c.(1120-1122)TGG>TAG	p.W374*
Pat_06	Pre-Treatment	PLCG2	5336	37	16	81929466	81929466	Missense_Mutation	SNP	G	A	5	639	c.1127G>A	c.(1126-1128)CGG>CAG	p.R376Q
Pat_06	Pre-Treatment	ZDHHC7	55625	37	16	85010044	85010044	Missense_Mutation	SNP	G	A	4	207	c.832C>T	c.(832-834)CCC>TCC	p.P278S
Pat_06	Pre-Treatment	ANKRD11	29123	37	16	89347191	89347191	Missense_Mutation	SNP	G	A	5	186	c.5759C>T	c.(5758-5760)ACG>ATG	p.T1920M
Pat_06	Pre-Treatment	RAP1GAP2	23108	37	17	2921464	2921464	Missense_Mutation	SNP	G	A	3	40	c.1604G>A	c.(1603-1605)AGC>AAC	p.S535N
Pat_06	Pre-Treatment	TRPV1	7442	37	17	3489127	3489127	Missense_Mutation	SNP	G	C	3	148	c.1318C>G	c.(1318-1320)CTG>GTG	p.L440V

Pat_06	Pre-Treatment	ATP2A3	489	37	17	3839752	3839752	Missense_Mutation	SNP	G	A	5	341	c.2333C>T	c.(2332-2334)ACG>ATG	p.T778M
Pat_06	Pre-Treatment	ANKFY1	51479	37	17	4082253	4082253	Nonsense_Mutation	SNP	G	A	5	640	c.2497C>T	c.(2497-2499)CGA>TGA	p.R833*
Pat_06	Pre-Treatment	PFN1	5216	37	17	4849266	4849266	Missense_Mutation	SNP	C	A	6	439	c.352G>T	c.(352-354)GGT>TGT	p.G118C
Pat_06	Pre-Treatment	CAMTA2	23125	37	17	4875559	4875559	Missense_Mutation	SNP	C	T	6	568	c.2776G>A	c.(2776-2778)GCT>ACT	p.A926T
Pat_06	Pre-Treatment	DERL2	51009	37	17	5384615	5384615	Splice_Site	SNP	C	T	5	349	c.327_splice	c.e4+1	p.T109_splice
Pat_06	Pre-Treatment	C17orf81	23587	37	17	7160182	7160182	Missense_Mutation	SNP	G	A	4	454	c.464G>A	c.(463-465)AGC>AAC	p.S155N
Pat_06	Pre-Treatment	TNK1	8711	37	17	7287867	7287867	Missense_Mutation	SNP	G	A	4	83	c.931G>A	c.(931-933)GTG>ATG	p.V311M
Pat_06	Pre-Treatment	C17orf74	201243	37	17	7329660	7329660	Missense_Mutation	SNP	G	A	5	532	c.350G>A	c.(349-351)AGT>AAT	p.S117N
Pat_06	Pre-Treatment	ZBTB4	57659	37	17	7366712	7366712	Missense_Mutation	SNP	G	A	4	95	c.1589C>T	c.(1588-1590)GCA>GTA	p.A530V
Pat_06	Pre-Treatment	DNAH2	146754	37	17	7697644	7697644	Missense_Mutation	SNP	C	T	5	353	c.7642C>T	c.(7642-7644)CGC>TGC	p.R2548C
Pat_06	Pre-Treatment	USP43	124739	37	17	9604461	9604461	Nonsense_Mutation	SNP	C	T	3	27	c.1561C>T	c.(1561-1563)CGA>TGA	p.R521*
Pat_06	Pre-Treatment	MYH2	4620	37	17	10430055	10430055	Missense_Mutation	SNP	G	A	6	606	c.4048C>T	c.(4048-4050)CGG>TGG	p.R1350W
Pat_06	Pre-Treatment	MAP2K4	6416	37	17	12028632	12028632	Missense_Mutation	SNP	G	A	5	726	c.835G>A	c.(835-837)GCA>ACA	p.A279T
Pat_06	Pre-Treatment	ELAC2	60528	37	17	12920211	12920211	Missense_Mutation	SNP	C	T	5	643	c.335G>A	c.(334-336)CGA>CAA	p.R112Q
Pat_06	Pre-Treatment	TRIM16	10626	37	17	15554529	15554529	Missense_Mutation	SNP	G	A	4	374	c.395C>T	c.(394-396)CCT>CTT	p.P132L
Pat_06	Pre-Treatment	UNC119	9094	37	17	26874365	26874365	Missense_Mutation	SNP	G	A	5	435	c.673C>T	c.(673-675)CGG>TGG	p.R225W
Pat_06	Pre-Treatment	SUPT6H	6830	37	17	27003267	27003267	Missense_Mutation	SNP	A	G	4	588	c.716A>G	c.(715-717)GAG>GGG	p.E239G
Pat_06	Pre-Treatment	RFFL	117584	37	17	33348494	33348494	Missense_Mutation	SNP	T	C	3	166	c.487A>G	c.(487-489)ACC>GCC	p.T163A
Pat_06	Pre-Treatment	GAS2L2	246176	37	17	34074192	34074192	Missense_Mutation	SNP	T	C	4	775	c.928A>G	c.(928-930)ACC>GCC	p.T310A
Pat_06	Pre-Treatment	TAF15	8148	37	17	34151144	34151144	Missense_Mutation	SNP	G	A	5	522	c.547G>A	c.(547-549)GGA>AGA	p.G183R
Pat_06	Pre-Treatment	MLLT6	4302	37	17	36873805	36873805	Missense_Mutation	SNP	T	C	3	208	c.1772T>C	c.(1771-1773)CTC>CCC	p.L591P
Pat_06	Pre-Treatment	ERBB2	2064	37	17	37866359	37866359	Missense_Mutation	SNP	G	A	5	678	c.664G>A	c.(664-666)GGT>AGT	p.G222S
Pat_06	Pre-Treatment	GRB7	2886	37	17	37899492	37899492	Missense_Mutation	SNP	G	A	6	319	c.523G>A	c.(523-525)GGA>AGA	p.G175R
Pat_06	Pre-Treatment	IGFBP4	3487	37	17	38610289	38610289	Missense_Mutation	SNP	G	A	7	736	c.617G>A	c.(616-618)CGC>CAC	p.R206H
Pat_06	Pre-Treatment	KRTAP4-11	653240	37	17	39274087	39274087	Missense_Mutation	SNP	G	C	3	53	c.481C>G	c.(481-483)CTG>GTG	p.L161V
Pat_06	Pre-Treatment	KRTAP4-5	85289	37	17	39305839	39305839	Missense_Mutation	SNP	A	T	4	194	c.181T>A	c.(181-183)TGC>AGC	p.C61S
Pat_06	Pre-Treatment	KRTAP4-4	84616	37	17	39316769	39316769	Missense_Mutation	SNP	T	A	7	582	c.175A>T	c.(175-177)ACC>TCC	p.T59S
Pat_06	Pre-Treatment	KRT17	3872	37	17	39775940	39775940	Missense_Mutation	SNP	G	A	7	415	c.1205C>T	c.(1204-1206)CCG>CTG	p.P402L
Pat_06	Pre-Treatment	GRN	2896	37	17	42426831	42426831	Missense_Mutation	SNP	G	T	5	418	c.176G>T	c.(175-177)GGC>GTC	p.G59V
Pat_06	Pre-Treatment	ITGA2B	3674	37	17	42461287	42461287	Missense_Mutation	SNP	C	G	3	151	c.973G>C	c.(973-975)GCT>CCT	p.A325P
Pat_06	Pre-Treatment	NMT1	4836	37	17	43182301	43182301	Missense_Mutation	SNP	A	G	3	256	c.1407A>G	c.(1405-1407)ATA>ATG	p.I469M
Pat_06	Pre-Treatment	KPNB1	3837	37	17	45754426	45754426	Missense_Mutation	SNP	G	A	5	680	c.2036G>A	c.(2035-2037)CGT>CAT	p.R679H
Pat_06	Pre-Treatment	COL1A1	1277	37	17	48265326	48265326	Missense_Mutation	SNP	C	A	6	612	c.3280G>T	c.(3280-3282)GGT>TGT	p.G1094C
Pat_06	Pre-Treatment	MYCBPAP	84073	37	17	48605535	48605535	Missense_Mutation	SNP	G	C	3	213	c.2440G>C	c.(2440-2442)GTG>CTG	p.V814L
Pat_06	Pre-Treatment	CACNA1G	8913	37	17	48655687	48655687	Nonsense_Mutation	SNP	C	A	5	282	c.2063C>A	c.(2062-2064)TCA>TAA	p.S688*
Pat_06	Pre-Treatment	MPO	4353	37	17	56350963	56350963	Missense_Mutation	SNP	G	A	281	493	c.1433C>T	c.(1432-1434)ACG>ATG	p.T478M
Pat_06	Pre-Treatment	HSF5	124535	37	17	56565325	56565325	Missense_Mutation	SNP	C	G	4	243	c.311G>C	c.(310-312)GGC>GCC	p.G104A
Pat_06	Pre-Treatment	C17orf47	284083	37	17	56620550	56620550	Missense_Mutation	SNP	C	T	4	259	c.998G>A	c.(997-999)CGC>CAC	p.R333H
Pat_06	Pre-Treatment	HEATR6	63897	37	17	58120947	58120947	Missense_Mutation	SNP	G	A	5	610	c.3523C>T	c.(3523-3525)CTC>TTC	p.L1175F
Pat_06	Pre-Treatment	TANC2	26115	37	17	61497713	61497713	Missense_Mutation	SNP	G	T	7	330	c.4370G>T	c.(4369-4371)AGC>ATC	p.S1457I
Pat_06	Pre-Treatment	ERN1	2081	37	17	62144291	62144291	Missense_Mutation	SNP	C	G	3	185	c.582G>C	c.(580-582)AAG>AAC	p.K194N
Pat_06	Pre-Treatment	SMURF2	64750	37	17	62543799	62543799	Missense_Mutation	SNP	C	A	7	617	c.1990G>T	c.(1990-1992)GAT>TAT	p.D664Y
Pat_06	Pre-Treatment	LRRC37A3	374819	37	17	62891134	62891134	Missense_Mutation	SNP	G	T	8	808	c.2242C>A	c.(2242-2244)CTT>ATT	p.L748I
Pat_06	Pre-Treatment	PSMD12	5718	37	17	65362605	65362605	Missense_Mutation	SNP	C	A	5	149	c.31G>T	c.(31-33)GGG>TGG	p.G11W
Pat_06	Pre-Treatment	BPTF	2186	37	17	65955937	65955937	Missense_Mutation	SNP	C	G	3	252	c.8207C>G	c.(8206-8208)ACT>AGT	p.T2736S
Pat_06	Pre-Treatment	ARSG	22901	37	17	66339924	66339924	Missense_Mutation	SNP	G	A	39	124	c.398G>A	c.(397-399)GGG>GAG	p.G133E
Pat_06	Pre-Treatment	ABCA10	10349	37	17	67153007	67153007	Missense_Mutation	SNP	C	T	4	136	c.3421G>A	c.(3421-3423)GGA>AGA	p.G1141R

Pat_06	Pre-Treatment	OTOP3	347741	37	17	72943400	72943400	Missense_Mutation	SNP	G	A	3	58	c.1450G>A	c.(1450-1452)GGC>AGC	p.G484S
Pat_06	Pre-Treatment	KIAA0195	9772	37	17	73487517	73487517	Missense_Mutation	SNP	G	A	5	473	c.1367G>A	c.(1366-1368)CGC>CAC	p.R456H
Pat_06	Pre-Treatment	CASKIN2	57513	37	17	73500322	73500322	Missense_Mutation	SNP	G	A	4	77	c.1441C>T	c.(1441-1443)CGG>TGG	p.R481W
Pat_06	Pre-Treatment	RNF157	114804	37	17	74163736	74163736	Missense_Mutation	SNP	C	T	8	514	c.439G>A	c.(439-441)GCC>ACC	p.A147T
Pat_06	Pre-Treatment	UBE2O	63893	37	17	74395668	74395668	Missense_Mutation	SNP	G	A	5	576	c.1490C>T	c.(1489-1491)TCT>TTT	p.S497F
Pat_06	Pre-Treatment	ST6GALNAC1	55808	37	17	74621927	74621927	Missense_Mutation	SNP	G	A	3	91	c.1579C>T	c.(1579-1581)CTC>TTC	p.L527F
Pat_06	Pre-Treatment	CBX4	8535	37	17	77807880	77807880	Missense_Mutation	SNP	C	T	5	391	c.1561G>A	c.(1561-1563)GAG>AAG	p.E521K
Pat_06	Pre-Treatment	TBC1D16	125058	37	17	77987204	77987204	Missense_Mutation	SNP	G	A	3	85	c.143C>T	c.(142-144)CCG>CTG	p.P48L
Pat_06	Pre-Treatment	FASN	2194	37	17	80040889	80040889	Missense_Mutation	SNP	C	G	4	248	c.5668G>C	c.(5668-5670)GCT>CCT	p.A1890P
Pat_06	Pre-Treatment	TBCD	6904	37	17	80885162	80885162	Missense_Mutation	SNP	G	A	4	144	c.2572G>A	c.(2572-2574)GAC>AAC	p.D858N
Pat_06	Pre-Treatment	MYOM1	8736	37	18	3129428	3129428	Missense_Mutation	SNP	G	A	6	589	c.2596C>T	c.(2596-2598)CCG>TCG	p.P866S
Pat_06	Pre-Treatment	EPB41L3	23136	37	18	5478412	5478412	Missense_Mutation	SNP	G	A	6	597	c.209C>T	c.(208-210)GCT>GTT	p.A70V
Pat_06	Pre-Treatment	KIAA1632	57724	37	18	43456258	43456258	Missense_Mutation	SNP	A	G	4	690	c.5992T>C	c.(5992-5994)TCA>CCA	p.S1998P
Pat_06	Pre-Treatment	KIAA1632	57724	37	18	43529482	43529482	Missense_Mutation	SNP	C	A	5	537	c.1465G>T	c.(1465-1467)GGT>TGT	p.G489C
Pat_06	Pre-Treatment	ST8SIA5	29906	37	18	44260450	44260450	Missense_Mutation	SNP	C	T	3	67	c.686G>A	c.(685-687)CGG>CAG	p.R229Q
Pat_06	Pre-Treatment	CCDC11	220136	37	18	47788477	47788477	Missense_Mutation	SNP	C	T	6	790	c.182G>A	c.(181-183)CGC>CAC	p.R61H
Pat_06	Pre-Treatment	ALPK2	115701	37	18	56202703	56202703	Missense_Mutation	SNP	T	C	4	590	c.4716A>G	c.(4714-4716)ATA>ATG	p.I1572M
Pat_06	Pre-Treatment	CDH19	28513	37	18	64235831	64235831	Missense_Mutation	SNP	C	A	6	634	c.312G>T	c.(310-312)AAG>AAT	p.K104N
Pat_06	Pre-Treatment	DSEL	92126	37	18	65179336	65179336	Missense_Mutation	SNP	T	C	4	745	c.2540A>G	c.(2539-2541)GAG>GGG	p.E847G
Pat_06	Pre-Treatment	FAM69C	125704	37	18	72109213	72109213	Missense_Mutation	SNP	C	T	5	598	c.1015G>A	c.(1015-1017)GCG>ACG	p.A339T
Pat_06	Pre-Treatment	REXO1	57455	37	19	1826936	1826936	Missense_Mutation	SNP	G	A	3	52	c.1852C>T	c.(1852-1854)CGG>TGG	p.R618W
Pat_06	Pre-Treatment	REXO1	57455	37	19	1828061	1828061	Missense_Mutation	SNP	G	A	3	105	c.727C>T	c.(727-729)CGG>TGG	p.R243W
Pat_06	Pre-Treatment	HMG20B	10362	37	19	3576268	3576268	Missense_Mutation	SNP	G	A	4	395	c.482G>A	c.(481-483)AGC>AAC	p.S161N
Pat_06	Pre-Treatment	DAPK3	1613	37	19	3964864	3964864	Missense_Mutation	SNP	C	A	6	510	c.188G>T	c.(187-189)CGG>CTG	p.R63L
Pat_06	Pre-Treatment	PLIN4	729359	37	19	4512545	4512545	Missense_Mutation	SNP	G	A	8	667	c.1385C>T	c.(1384-1386)GCT>GTT	p.A462V
Pat_06	Pre-Treatment	PTPRS	5802	37	19	5214699	5214699	Missense_Mutation	SNP	C	T	3	90	c.4367G>A	c.(4366-4368)CGG>CAG	p.R1456Q
Pat_06	Pre-Treatment	PTPRS	5802	37	19	5245864	5245864	Missense_Mutation	SNP	T	G	3	136	c.911A>C	c.(910-912)AAG>ACG	p.K304T
Pat_06	Pre-Treatment	RANBP3	8498	37	19	5918626	5918626	Nonsense_Mutation	SNP	G	A	6	689	c.1354C>T	c.(1354-1356)CGA>TGA	p.R452*
Pat_06	Pre-Treatment	DENND1C	79958	37	19	6480024	6480024	Missense_Mutation	SNP	G	A	3	83	c.56C>T	c.(55-57)GCG>GTG	p.A19V
Pat_06	Pre-Treatment	TNFSF9	8744	37	19	6532819	6532819	Missense_Mutation	SNP	C	A	6	635	c.290C>A	c.(289-291)GCC>GAC	p.A97D
Pat_06	Pre-Treatment	C3	718	37	19	6677992	6677992	Missense_Mutation	SNP	C	A	12	572	c.4893G>T	c.(4891-4893)TGG>TGT	p.W1631C
Pat_06	Pre-Treatment	TRIP10	9322	37	19	6750307	6750307	Missense_Mutation	SNP	G	T	5	593	c.1400G>T	c.(1399-1401)TGG>TTG	p.W467L
Pat_06	Pre-Treatment	ZNF557	79230	37	19	7076391	7076391	Splice_Site	SNP	G	T	6	585	c.100_splice	c.e5-1	p.G34_splice
Pat_06	Pre-Treatment	XAB2	56949	37	19	7688136	7688136	Missense_Mutation	SNP	G	A	4	437	c.1159C>T	c.(1159-1161)CCC>TCC	p.P387S
Pat_06	Pre-Treatment	CD209	30835	37	19	7810766	7810766	Missense_Mutation	SNP	C	T	11	735	c.386G>A	c.(385-387)CGG>CAG	p.R129Q
Pat_06	Pre-Treatment	MUC16	94025	37	19	9061705	9061705	Missense_Mutation	SNP	C	T	20	180	c.25741G>A	c.(25741-25743)GAG>AAG	p.E8581K
Pat_06	Pre-Treatment	AP1M2	10053	37	19	10685123	10685123	Missense_Mutation	SNP	G	A	3	29	c.1219C>T	c.(1219-1221)CCC>TCC	p.P407S
Pat_06	Pre-Treatment	SLC44A2	57153	37	19	10742169	10742169	Nonsense_Mutation	SNP	C	T	4	317	c.460C>T	c.(460-462)CAA>TAA	p.Q154*
Pat_06	Pre-Treatment	DOCK6	57572	37	19	11333418	11333418	Missense_Mutation	SNP	G	A	3	53	c.3233C>T	c.(3232-3234)ACC>ATC	p.T1078I
Pat_06	Pre-Treatment	ZNF844	284391	37	19	12187394	12187394	Missense_Mutation	SNP	T	C	6	166	c.1459T>C	c.(1459-1461)TTT>CTT	p.F487L
Pat_06	Pre-Treatment	MAST1	22983	37	19	12969451	12969451	Missense_Mutation	SNP	G	A	4	214	c.1264G>A	c.(1264-1266)GAG>AAG	p.E422K
Pat_06	Pre-Treatment	CACNA1A	773	37	19	13397728	13397728	Missense_Mutation	SNP	G	A	5	229	c.3145C>T	c.(3145-3147)CGG>TGG	p.R1049W
Pat_06	Pre-Treatment	DCAF15	90379	37	19	14071323	14071323	Missense_Mutation	SNP	A	G	3	47	c.1678A>G	c.(1678-1680)ATG>GTG	p.M560V
Pat_06	Pre-Treatment	LPHN1	22859	37	19	14273754	14273754	Missense_Mutation	SNP	C	A	3	57	c.874G>T	c.(874-876)GTG>TTG	p.V292L
Pat_06	Pre-Treatment	DDX39	10212	37	19	14521140	14521140	Missense_Mutation	SNP	C	T	5	398	c.620G>A	c.(619-621)CGG>CAG	p.R207Q
Pat_06	Pre-Treatment	EMR3	84658	37	19	14748977	14748977	Missense_Mutation	SNP	G	A	5	673	c.1424C>T	c.(1423-1425)CCC>CTC	p.P475L
Pat_06	Pre-Treatment	RASAL3	64926	37	19	15565012	15565012	Missense_Mutation	SNP	G	A	3	56	c.2227C>T	c.(2227-2229)CTT>TTT	p.L743F

Pat_06	Pre-Treatment	OR10H5	284433	37	19	15904883	15904883	Missense_Mutation	SNP	G	A	6	816	c.25G>A	c.(25-27)GTG>ATG	p.V9M
Pat_06	Pre-Treatment	KLF2	10365	37	19	16437754	16437754	Missense_Mutation	SNP	C	T	4	206	c.980C>T	c.(979-981)ACG>ATG	p.T327M
Pat_06	Pre-Treatment	NWD1	284434	37	19	16884020	16884020	Missense_Mutation	SNP	C	A	6	347	c.2494C>A	c.(2494-2496)CAA>AAA	p.Q832K
Pat_06	Pre-Treatment	IL12RB1	3594	37	19	18197608	18197608	Missense_Mutation	SNP	A	G	3	123	c.26T>C	c.(25-27)GTC>GCC	p.V9A
Pat_06	Pre-Treatment	GDF1	2657	37	19	18995067	18995067	Missense_Mutation	SNP	G	A	3	76	c.419C>T	c.(418-420)CCG>CTG	p.P140L
Pat_06	Pre-Treatment	KIAA0892	23383	37	19	19455713	19455713	Missense_Mutation	SNP	C	T	4	258	c.1133C>T	c.(1132-1134)GCA>GTA	p.A378V
Pat_06	Pre-Treatment	ZNF737	100129842	37	19	20727870	20727870	Missense_Mutation	SNP	C	G	4	219	c.1139G>C	c.(1138-1140)TGG>TCG	p.W380S
Pat_06	Pre-Treatment	ZNF626	199777	37	19	20808090	20808090	Missense_Mutation	SNP	C	T	6	172	c.593G>A	c.(592-594)GGG>GAG	p.G198E
Pat_06	Pre-Treatment	ZNF493	284443	37	19	21606468	21606468	Missense_Mutation	SNP	C	T	5	284	c.623C>T	c.(622-624)CCT>CTT	p.P208L
Pat_06	Pre-Treatment	ZNF493	284443	37	19	21606614	21606614	Missense_Mutation	SNP	G	A	6	209	c.769G>A	c.(769-771)GCC>ACC	p.A257T
Pat_06	Pre-Treatment	ZNF208	7757	37	19	22155878	22155878	Missense_Mutation	SNP	G	A	5	321	c.1658C>T	c.(1657-1659)ACT>ATT	p.T553I
Pat_06	Pre-Treatment	ZNF681	148213	37	19	23927372	23927372	Missense_Mutation	SNP	C	G	4	264	c.980G>C	c.(979-981)AGA>ACA	p.R327T
Pat_06	Pre-Treatment	CCNE1	898	37	19	30308147	30308147	Missense_Mutation	SNP	G	A	4	330	c.284G>A	c.(283-285)CGG>CAG	p.R95Q
Pat_06	Pre-Treatment	TSHZ3	57616	37	19	31767905	31767905	Missense_Mutation	SNP	G	A	6	256	c.2794C>T	c.(2794-2796)CGG>TGG	p.R932W
Pat_06	Pre-Treatment	GPI	2821	37	19	34856194	34856194	Missense_Mutation	SNP	C	T	4	195	c.23C>T	c.(22-24)CCC>CTC	p.P8L
Pat_06	Pre-Treatment	GPI	2821	37	19	34890476	34890476	Missense_Mutation	SNP	C	T	6	750	c.1414C>T	c.(1414-1416)CGC>TGC	p.R472C
Pat_06	Pre-Treatment	ZNF30	90075	37	19	35434144	35434144	Missense_Mutation	SNP	G	A	10	16	c.274G>A	c.(274-276)GAT>AAT	p.D92N
Pat_06	Pre-Treatment	ZNF420	147923	37	19	37619123	37619123	Missense_Mutation	SNP	G	C	3	284	c.1230G>C	c.(1228-1230)CAG>CAC	p.Q410H
Pat_06	Pre-Treatment	RYR1	6261	37	19	39062761	39062761	Missense_Mutation	SNP	G	A	4	528	c.13849G>A	c.(13849-13851)GGA>AGA	p.G4617R
Pat_06	Pre-Treatment	HNRNPL	3191	37	19	39336518	39336518	Missense_Mutation	SNP	A	G	4	670	c.599T>C	c.(598-600)CTG>CCG	p.L200P
Pat_06	Pre-Treatment	PLEKHG2	64857	37	19	39915153	39915153	Missense_Mutation	SNP	C	T	4	225	c.3380C>T	c.(3379-3381)GCC>GTC	p.A1127V
Pat_06	Pre-Treatment	FCGBP	8857	37	19	40420050	40420050	Missense_Mutation	SNP	C	T	85	258	c.2944G>A	c.(2944-2946)GAC>AAC	p.D982N
Pat_06	Pre-Treatment	CYP2B6	1555	37	19	41522550	41522550	Splice_Site	SNP	G	T	4	262	c.1295_splice	c.e9-1	p.G432_splice
Pat_06	Pre-Treatment	AXL	558	37	19	41725308	41725308	Missense_Mutation	SNP	G	A	3	78	c.11G>A	c.(10-12)CGG>CAG	p.R4Q
Pat_06	Pre-Treatment	EXOSC5	56915	37	19	41893466	41893466	Missense_Mutation	SNP	G	C	3	62	c.568C>G	c.(568-570)CGG>GGG	p.R190G
Pat_06	Pre-Treatment	ZNF155	7711	37	19	44501058	44501058	Missense_Mutation	SNP	G	A	6	596	c.1049G>A	c.(1048-1050)GGA>GAA	p.G350E
Pat_06	Pre-Treatment	ZNF284	342909	37	19	44590236	44590236	Missense_Mutation	SNP	G	A	5	292	c.605G>A	c.(604-606)CGC>CAC	p.R202H
Pat_06	Pre-Treatment	MARK4	57787	37	19	45801061	45801061	Missense_Mutation	SNP	G	A	3	34	c.1726G>A	c.(1726-1728)GAC>AAC	p.D576N
Pat_06	Pre-Treatment	PTGIR	5739	37	19	47127113	47127113	Missense_Mutation	SNP	G	A	3	83	c.370C>T	c.(370-372)CCC>TCC	p.P124S
Pat_06	Pre-Treatment	GRLF1	2909	37	19	47425372	47425372	Missense_Mutation	SNP	G	A	5	292	c.3440G>A	c.(3439-3441)CGC>CAC	p.R1147H
Pat_06	Pre-Treatment	NAPA	8775	37	19	47995315	47995315	Missense_Mutation	SNP	T	C	4	571	c.623A>G	c.(622-624)AAG>AGG	p.K208R
Pat_06	Pre-Treatment	EHD2	30846	37	19	48244171	48244171	Missense_Mutation	SNP	C	T	65	111	c.1114C>T	c.(1114-1116)CAC>TAC	p.H372Y
Pat_06	Pre-Treatment	LIG1	3978	37	19	48640915	48640915	Missense_Mutation	SNP	G	T	4	204	c.1118C>A	c.(1117-1119)GCA>GAA	p.A373E
Pat_06	Pre-Treatment	GRIN2D	2906	37	19	48908576	48908576	Nonsense_Mutation	SNP	C	T	3	103	c.1051C>T	c.(1051-1053)CAG>TAG	p.Q351*
Pat_06	Pre-Treatment	CA11	770	37	19	49143533	49143533	Missense_Mutation	SNP	C	A	6	425	c.290G>T	c.(289-291)CGG>CTG	p.R97L
Pat_06	Pre-Treatment	FUT2	2524	37	19	49207114	49207114	Missense_Mutation	SNP	G	A	6	578	c.901G>A	c.(901-903)GGA>AGA	p.G301R
Pat_06	Pre-Treatment	BCAT2	587	37	19	49309887	49309887	Missense_Mutation	SNP	C	T	5	700	c.187G>A	c.(187-189)GAC>AAC	p.D63N
Pat_06	Pre-Treatment	PLEKHA4	57664	37	19	49341337	49341337	Missense_Mutation	SNP	G	A	5	495	c.2014C>T	c.(2014-2016)CGG>TGG	p.R672W
Pat_06	Pre-Treatment	CCDC155	147872	37	19	49897837	49897837	Missense_Mutation	SNP	G	A	5	409	c.148G>A	c.(148-150)GGC>AGC	p.G50S
Pat_06	Pre-Treatment	ALDH16A1	126133	37	19	49965932	49965932	Missense_Mutation	SNP	G	A	4	161	c.1018G>A	c.(1018-1020)GTG>ATG	p.V340M
Pat_06	Pre-Treatment	MED25	81857	37	19	50339086	50339086	Missense_Mutation	SNP	G	C	3	71	c.1849G>C	c.(1849-1851)GCC>CCC	p.A617P
Pat_06	Pre-Treatment	POLD1	5424	37	19	50909518	50909518	Missense_Mutation	SNP	C	T	6	538	c.1322C>T	c.(1321-1323)ACG>ATG	p.T441M
Pat_06	Pre-Treatment	LRRC4B	94030	37	19	51052058	51052058	Missense_Mutation	SNP	G	A	3	35	c.38C>T	c.(37-39)CCG>CTG	p.P13L
Pat_06	Pre-Treatment	ZNF578	147660	37	19	53014626	53014626	Missense_Mutation	SNP	C	G	6	445	c.992C>G	c.(991-993)ACA>AGA	p.T331R
Pat_06	Pre-Treatment	ZNF578	147660	37	19	53014710	53014710	Missense_Mutation	SNP	G	C	8	434	c.1076G>C	c.(1075-1077)AGA>ACA	p.R359T
Pat_06	Pre-Treatment	ZNF761	388561	37	19	53957922	53957922	Missense_Mutation	SNP	C	T	6	453	c.161C>T	c.(160-162)ACG>ATG	p.T54M
Pat_06	Pre-Treatment	TSEN34	79042	37	19	54696087	54696087	Missense_Mutation	SNP	G	A	5	318	c.608G>A	c.(607-609)CGT>CAT	p.R203H

Pat_06	Pre-Treatment	LILRA4	23547	37	19	54849290	54849290	Missense_Mutation	SNP	C	G	3	218	c.572G>C	c.(571-573)GGT>GCT	p.G191A
Pat_06	Pre-Treatment	SYT5	6861	37	19	55686662	55686662	Missense_Mutation	SNP	A	G	4	114	c.586T>C	c.(586-588)TAC>CAC	p.Y196H
Pat_06	Pre-Treatment	SAPS1	22870	37	19	55743297	55743297	Missense_Mutation	SNP	G	A	3	72	c.2179C>T	c.(2179-2181)CCC>TCC	p.P727S
Pat_06	Pre-Treatment	SAPS1	22870	37	19	55756504	55756504	Missense_Mutation	SNP	G	A	4	150	c.602C>T	c.(601-603)CCG>CTG	p.P201L
Pat_06	Pre-Treatment	U2AF2	11338	37	19	56180135	56180135	Missense_Mutation	SNP	G	A	5	423	c.922G>A	c.(922-924)GTG>ATG	p.V308M
Pat_06	Pre-Treatment	NLRP11	204801	37	19	56320822	56320822	Missense_Mutation	SNP	G	A	6	618	c.1154C>T	c.(1153-1155)ACT>ATT	p.T385I
Pat_06	Pre-Treatment	ZNF71	58491	37	19	57133523	57133523	Missense_Mutation	SNP	C	T	5	428	c.868C>T	c.(868-870)CGC>TGC	p.R290C
Pat_06	Pre-Treatment	SLC27A5	10998	37	19	59009938	59009938	Missense_Mutation	SNP	G	A	4	171	c.2017C>T	c.(2017-2019)CGG>TGG	p.R673W
Pat_06	Pre-Treatment	MYT1L	23040	37	2	1796174	1796174	Missense_Mutation	SNP	C	G	3	148	c.3339G>C	c.(3337-3339)CAG>CAC	p.Q1113H
Pat_06	Pre-Treatment	KCNF1	3754	37	2	11053168	11053168	Missense_Mutation	SNP	G	A	4	183	c.616G>A	c.(616-618)GAG>AAG	p.E206K
Pat_06	Pre-Treatment	DPYSL5	56896	37	2	27165503	27165503	Missense_Mutation	SNP	G	A	4	303	c.1325G>A	c.(1324-1326)CGG>CAG	p.R442Q
Pat_06	Pre-Treatment	ZNF513	130557	37	2	27601720	27601720	Missense_Mutation	SNP	G	A	3	54	c.413C>T	c.(412-414)CCG>CTG	p.P138L
Pat_06	Pre-Treatment	C2orf16	84226	37	2	27804774	27804774	Nonsense_Mutation	SNP	G	T	8	827	c.5335G>T	c.(5335-5337)GAG>TAG	p.E1779*
Pat_06	Pre-Treatment	FAM179A	165186	37	2	29222223	29222223	Missense_Mutation	SNP	C	T	3	53	c.316C>T	c.(316-318)CTC>TTC	p.L106F
Pat_06	Pre-Treatment	ALK	238	37	2	29519754	29519754	Missense_Mutation	SNP	C	T	6	175	c.1817G>A	c.(1816-1818)AGG>AAG	p.R606K
Pat_06	Pre-Treatment	HEATR5B	54497	37	2	37302641	37302641	Missense_Mutation	SNP	C	A	6	794	c.584G>T	c.(583-585)TGT>TTT	p.C195F
Pat_06	Pre-Treatment	PRKCE	5581	37	2	46234724	46234724	Missense_Mutation	SNP	G	A	4	234	c.1187G>A	c.(1186-1188)CGG>CAG	p.R396Q
Pat_06	Pre-Treatment	MSH2	4436	37	2	47739544	47739544	Missense_Mutation	SNP	C	A	3	68	c.2737C>A	c.(2737-2739)CAG>AAG	p.Q913K
Pat_06	Pre-Treatment	SPTBN1	6711	37	2	54858212	54858212	Missense_Mutation	SNP	G	A	5	490	c.3028G>A	c.(3028-3030)GCA>ACA	p.A1010T
Pat_06	Pre-Treatment	PAPOLG	64895	37	2	61014687	61014687	Missense_Mutation	SNP	G	T	6	363	c.1328G>T	c.(1327-1329)CGG>CTG	p.R443L
Pat_06	Pre-Treatment	MDH1	4190	37	2	63833082	63833082	Missense_Mutation	SNP	G	C	4	794	c.799G>C	c.(799-801)GTG>CTG	p.V267L
Pat_06	Pre-Treatment	HSPC159	29094	37	2	64683497	64683497	Missense_Mutation	SNP	C	A	7	831	c.273C>A	c.(271-273)TTC>TTA	p.F91L
Pat_06	Pre-Treatment	SFXN5	94097	37	2	73188358	73188358	Missense_Mutation	SNP	G	A	5	190	c.847C>T	c.(847-849)CGC>TGC	p.R283C
Pat_06	Pre-Treatment	CCT7	10574	37	2	73477522	73477522	Missense_Mutation	SNP	C	T	5	545	c.1159C>T	c.(1159-1161)CGG>TGG	p.R387W
Pat_06	Pre-Treatment	ACTG2	72	37	2	74135861	74135861	Missense_Mutation	SNP	T	C	4	224	c.317T>C	c.(316-318)CTC>CCC	p.L106P
Pat_06	Pre-Treatment	TTC31	64427	37	2	74710251	74710251	Missense_Mutation	SNP	G	A	5	639	c.29G>A	c.(28-30)CGG>CAG	p.R10Q
Pat_06	Pre-Treatment	ZNF2	7549	37	2	95843243	95843243	Missense_Mutation	SNP	G	A	5	730	c.49G>A	c.(49-51)GAA>AAA	p.E17K
Pat_06	Pre-Treatment	VWA3B	200403	37	2	98779371	98779371	Missense_Mutation	SNP	G	A	4	237	c.1046G>A	c.(1045-1047)AGC>AAC	p.S349N
Pat_06	Pre-Treatment	TBC1D8	11138	37	2	101654946	101654946	Missense_Mutation	SNP	C	T	8	781	c.1207G>A	c.(1207-1209)GAC>AAC	p.D403N
Pat_06	Pre-Treatment	IL1RL2	8808	37	2	102849561	102849561	Missense_Mutation	SNP	G	A	6	341	c.1274G>A	c.(1273-1275)GGC>GAC	p.G425D
Pat_06	Pre-Treatment	SULT1C2	6819	37	2	108910735	108910735	Missense_Mutation	SNP	G	A	6	710	c.202G>A	c.(202-204)GTG>ATG	p.V68M
Pat_06	Pre-Treatment	BCL2L11	10018	37	2	111881718	111881718	Splice_Site	SNP	T	C	4	563	c.394_splice	c.e2+2	p.A132_splice
Pat_06	Pre-Treatment	LOC401010	401010	37	2	132200809	132200809	Missense_Mutation	SNP	A	G	3	112	c.1193T>C	c.(1192-1194)CTG>CCG	p.L398P
Pat_06	Pre-Treatment	GPR39	2863	37	2	133175192	133175192	Missense_Mutation	SNP	C	T	6	549	c.577C>T	c.(577-579)CGC>TGC	p.R193C
Pat_06	Pre-Treatment	THSD7B	80731	37	2	138169350	138169350	Missense_Mutation	SNP	G	A	5	525	c.2774G>A	c.(2773-2775)AGC>AAC	p.S925N
Pat_06	Pre-Treatment	THSD7B	80731	37	2	138208489	138208489	Missense_Mutation	SNP	T	C	4	282	c.2941T>C	c.(2941-2943)TGC>CGC	p.C981R
Pat_06	Pre-Treatment	MBD5	55777	37	2	149247153	149247153	Missense_Mutation	SNP	G	A	7	598	c.3253G>A	c.(3253-3255)GTA>ATA	p.V1085I
Pat_06	Pre-Treatment	LYPD6	130574	37	2	150305643	150305643	Missense_Mutation	SNP	G	C	3	219	c.199G>C	c.(199-201)GAC>CAC	p.D67H
Pat_06	Pre-Treatment	NEB	4703	37	2	152584266	152584266	Missense_Mutation	SNP	G	A	4	355	c.233C>T	c.(232-234)CCT>CTT	p.P78L
Pat_06	Pre-Treatment	CACNB4	785	37	2	152954896	152954896	Missense_Mutation	SNP	C	A	6	647	c.95G>T	c.(94-96)AGG>ATG	p.R32M
Pat_06	Pre-Treatment	ACVR1C	130399	37	2	158412733	158412733	Missense_Mutation	SNP	C	G	3	143	c.416G>C	c.(415-417)CGA>CCA	p.R139P
Pat_06	Pre-Treatment	SCN2A	6326	37	2	166245255	166245255	Missense_Mutation	SNP	C	T	5	511	c.4939C>T	c.(4939-4941)CGC>TGC	p.R1647C
Pat_06	Pre-Treatment	G6PC2	57818	37	2	169764282	169764282	Missense_Mutation	SNP	C	T	5	356	c.761C>T	c.(760-762)ACG>ATG	p.T254M
Pat_06	Pre-Treatment	MYO3B	140469	37	2	171376005	171376005	Missense_Mutation	SNP	G	A	5	414	c.3530G>A	c.(3529-3531)CGT>CAT	p.R1177H
Pat_06	Pre-Treatment	HAT1	8520	37	2	172822973	172822973	Missense_Mutation	SNP	G	A	6	667	c.655G>A	c.(655-657)GTA>ATA	p.V219I
Pat_06	Pre-Treatment	ITGA6	3655	37	2	173332254	173332254	Missense_Mutation	SNP	C	T	5	503	c.353C>T	c.(352-354)ACC>ATC	p.T118I
Pat_06	Pre-Treatment	CDCA7	83879	37	2	174223439	174223439	Splice_Site	SNP	G	A	4	187	c.22_splice	c.e2-1	p.Q8_splice

Pat_06	Pre-Treatment	ATF2	1386	37	2	175979479	175979479	Missense_Mutation	SNP	C	T	5	904	c.565G>A	c.(565-567)GTA>ATA	p.V189I
Pat_06	Pre-Treatment	RBM45	129831	37	2	178977533	178977533	Missense_Mutation	SNP	A	G	4	391	c.260A>G	c.(259-261)CAT>CGT	p.H87R
Pat_06	Pre-Treatment	TTN	7273	37	2	179469616	179469616	Missense_Mutation	SNP	G	A	4	271	c.46496C>T	c.(46495-46497)TCC>TTC	p.S15499F
Pat_06	Pre-Treatment	TTN	7273	37	2	179472553	179472553	Missense_Mutation	SNP	G	A	5	693	c.45257C>T	c.(45256-45258)CCG>CTG	p.P15086L
Pat_06	Pre-Treatment	TTN	7273	37	2	179605181	179605181	Missense_Mutation	SNP	G	A	4	167	c.12266C>T	c.(12265-12267)GCG>GTG	p.A4089V
Pat_06	Pre-Treatment	TTN	7273	37	2	179610475	179610475	Missense_Mutation	SNP	C	T	195	417	c.16652G>A	c.(16651-16653)GGA>GAA	p.G5551E
Pat_06	Pre-Treatment	TTN	7273	37	2	179648873	179648873	Missense_Mutation	SNP	T	C	5	625	c.2699A>G	c.(2698-2700)AAG>AGG	p.K900R
Pat_06	Pre-Treatment	CWC22	57703	37	2	180809888	180809888	Nonsense_Mutation	SNP	G	A	4	221	c.2695C>T	c.(2695-2697)CGA>TGA	p.R899*
Pat_06	Pre-Treatment	SSFA2	6744	37	2	182780684	182780684	Missense_Mutation	SNP	T	C	4	507	c.2317T>C	c.(2317-2319)TAT>CAT	p.Y773H
Pat_06	Pre-Treatment	MSTN	2660	37	2	190926979	190926979	Missense_Mutation	SNP	G	A	6	701	c.344C>T	c.(343-345)ACG>ATG	p.T115M
Pat_06	Pre-Treatment	KCTD18	130535	37	2	201369598	201369598	Missense_Mutation	SNP	T	C	5	362	c.245A>G	c.(244-246)GAG>GGG	p.E82G
Pat_06	Pre-Treatment	CD28	940	37	2	204594418	204594418	Missense_Mutation	SNP	T	C	6	808	c.457T>C	c.(457-459)TTT>CTT	p.F153L
Pat_06	Pre-Treatment	PARD3B	117583	37	2	206305378	206305378	Missense_Mutation	SNP	C	A	5	279	c.3026C>A	c.(3025-3027)CCA>CAA	p.P1009Q
Pat_06	Pre-Treatment	EEF1B2	1933	37	2	207026761	207026761	Splice_Site	SNP	G	T	5	499	c.331_splice	c.e5-1	p.E111_splice
Pat_06	Pre-Treatment	ZDBF2	57683	37	2	207173934	207173934	Missense_Mutation	SNP	G	A	3	47	c.4682G>A	c.(4681-4683)AGC>AAC	p.S1561N
Pat_06	Pre-Treatment	C2orf67	151050	37	2	210889861	210889861	Missense_Mutation	SNP	C	A	7	758	c.2531G>T	c.(2530-2532)TGG>TTG	p.W844L
Pat_06	Pre-Treatment	USP37	57695	37	2	219374792	219374792	Missense_Mutation	SNP	G	A	5	583	c.935C>T	c.(934-936)TCT>TTT	p.S312F
Pat_06	Pre-Treatment	RQCD1	9125	37	2	219457378	219457378	Missense_Mutation	SNP	C	A	6	729	c.679C>A	c.(679-681)CGT>AGT	p.R227S
Pat_06	Pre-Treatment	ZNF142	7701	37	2	219507245	219507245	Missense_Mutation	SNP	G	A	4	267	c.3994C>T	c.(3994-3996)CGC>TGC	p.R1332C
Pat_06	Pre-Treatment	TTLL4	9654	37	2	219602485	219602485	Missense_Mutation	SNP	C	T	5	352	c.86C>T	c.(85-87)CCT>CTT	p.P29L
Pat_06	Pre-Treatment	OBSL1	23363	37	2	220423961	220423961	Missense_Mutation	SNP	G	A	5	738	c.3212C>T	c.(3211-3213)ACT>ATT	p.T1071I
Pat_06	Pre-Treatment	SLC4A3	6508	37	2	220494381	220494381	Missense_Mutation	SNP	G	A	4	128	c.575G>A	c.(574-576)GGC>GAC	p.G192D
Pat_06	Pre-Treatment	COL4A4	1286	37	2	227896697	227896697	Missense_Mutation	SNP	C	G	3	81	c.3781G>C	c.(3781-3783)GGA>CGA	p.G1261R
Pat_06	Pre-Treatment	COL4A4	1286	37	2	227924297	227924297	Missense_Mutation	SNP	T	C	5	492	c.2207A>G	c.(2206-2208)AAG>AGG	p.K736R
Pat_06	Pre-Treatment	SPHKAP	80309	37	2	228858295	228858295	Missense_Mutation	SNP	T	C	3	107	c.4676A>G	c.(4675-4677)GAT>GGT	p.D1559G
Pat_06	Pre-Treatment	UGT1A7	54577	37	2	234590752	234590752	Missense_Mutation	SNP	G	A	8	823	c.169G>A	c.(169-171)GTA>ATA	p.V57I
Pat_06	Pre-Treatment	COL6A3	1293	37	2	238271946	238271946	Missense_Mutation	SNP	G	A	5	403	c.6013C>T	c.(6013-6015)CCC>TCC	p.P2005S
Pat_06	Pre-Treatment	ANKMY1	51281	37	2	241465678	241465678	Missense_Mutation	SNP	C	T	5	465	c.871G>A	c.(871-873)GCA>ACA	p.A291T
Pat_06	Pre-Treatment	KIF1A	547	37	2	241702471	241702471	Missense_Mutation	SNP	C	T	3	51	c.1960G>A	c.(1960-1962)GAG>AAG	p.E654K
Pat_06	Pre-Treatment	TRIB3	57761	37	20	372045	372045	Missense_Mutation	SNP	T	C	3	139	c.406T>C	c.(406-408)TTT>CTT	p.F136L
Pat_06	Pre-Treatment	TGM6	343641	37	20	2411570	2411570	Missense_Mutation	SNP	G	A	5	637	c.1864G>A	c.(1864-1866)GTT>ATT	p.V622I
Pat_06	Pre-Treatment	VPS16	64601	37	20	2844692	2844692	Missense_Mutation	SNP	G	A	5	578	c.1574G>A	c.(1573-1575)CGA>CAA	p.R525Q
Pat_06	Pre-Treatment	C20orf27	54976	37	20	3734797	3734797	Missense_Mutation	SNP	G	A	3	60	c.433C>T	c.(433-435)CAC>TAC	p.H145Y
Pat_06	Pre-Treatment	PYGB	5834	37	20	25263863	25263863	Missense_Mutation	SNP	C	T	4	290	c.1570C>T	c.(1570-1572)CCG>TCG	p.P524S
Pat_06	Pre-Treatment	NINL	22981	37	20	25493625	25493625	Missense_Mutation	SNP	G	T	5	464	c.295C>A	c.(295-297)CCT>ACT	p.P99T
Pat_06	Pre-Treatment	BCL2L1	598	37	20	30309595	30309595	Missense_Mutation	SNP	A	G	7	844	c.427T>C	c.(427-429)TTT>CTT	p.F143L
Pat_06	Pre-Treatment	ASXL1	171023	37	20	31022862	31022862	Missense_Mutation	SNP	C	T	9	284	c.2347C>T	c.(2347-2349)CCG>TCG	p.P783S
Pat_06	Pre-Treatment	C20orf112	140688	37	20	31041111	31041111	Missense_Mutation	SNP	T	C	3	161	c.761A>G	c.(760-762)GAG>GGG	p.E254G
Pat_06	Pre-Treatment	DLGAP4	22839	37	20	35060143	35060143	Missense_Mutation	SNP	G	A	4	264	c.23G>A	c.(22-24)CGC>CAC	p.R8H
Pat_06	Pre-Treatment	KIAA0406	9675	37	20	36640866	36640866	Missense_Mutation	SNP	C	A	5	298	c.1353G>T	c.(1351-1353)TGG>TGT	p.W451C
Pat_06	Pre-Treatment	DHX35	60625	37	20	37634964	37634964	Missense_Mutation	SNP	G	A	6	694	c.1187G>A	c.(1186-1188)CGT>CAT	p.R396H
Pat_06	Pre-Treatment	CDH22	64405	37	20	44828101	44828101	Missense_Mutation	SNP	C	T	5	130	c.1384G>A	c.(1384-1386)GCC>ACC	p.A462T
Pat_06	Pre-Treatment	ARFGEF2	10564	37	20	47630450	47630450	Missense_Mutation	SNP	G	A	6	531	c.4132G>A	c.(4132-4134)GTG>ATG	p.V1378M
Pat_06	Pre-Treatment	SLC9A8	23315	37	20	48491287	48491287	Missense_Mutation	SNP	C	T	6	658	c.1004C>T	c.(1003-1005)ACG>ATG	p.T335M
Pat_06	Pre-Treatment	KCNG1	3755	37	20	49620679	49620679	Missense_Mutation	SNP	C	T	4	241	c.1439G>A	c.(1438-1440)CGG>CAG	p.R480Q
Pat_06	Pre-Treatment	PCK1	5105	37	20	56136544	56136544	Missense_Mutation	SNP	C	A	5	468	c.77C>A	c.(76-78)GCA>GAA	p.A26E
Pat_06	Pre-Treatment	APCDD1L	164284	37	20	57042680	57042680	Missense_Mutation	SNP	G	C	3	127	c.223C>G	c.(223-225)CGC>GGC	p.R75G

Pat_06	Pre-Treatment	EDN3	1908	37	20	57896188	57896188	Missense_Mutation	SNP	G	T	6	690	c.482G>T	c.(481-483)TGT>TTT	p.C161F
Pat_06	Pre-Treatment	OSBPL2	9885	37	20	60847197	60847197	Missense_Mutation	SNP	C	T	4	329	c.275C>T	c.(274-276)ACG>ATG	p.T92M
Pat_06	Pre-Treatment	OSBPL2	9885	37	20	60866810	60866810	Missense_Mutation	SNP	G	A	7	611	c.1301G>A	c.(1300-1302)CGG>CAG	p.R434Q
Pat_06	Pre-Treatment	ADRM1	11047	37	20	60881352	60881352	Missense_Mutation	SNP	G	T	5	570	c.430G>T	c.(430-432)GGC>TGC	p.G144C
Pat_06	Pre-Treatment	LAMA5	3911	37	20	60921230	60921230	Missense_Mutation	SNP	C	A	5	101	c.1324G>T	c.(1324-1326)GAC>TAC	p.D442Y
Pat_06	Pre-Treatment	COL20A1	57642	37	20	61959682	61959682	Splice_Site	SNP	G	A	3	81	c.3614_splice	c.e34-1	p.S1205_splice
Pat_06	Pre-Treatment	PRIC285	85441	37	20	62197362	62197362	Missense_Mutation	SNP	C	T	3	53	c.2813G>A	c.(2812-2814)CGG>CAG	p.R938Q
Pat_06	Pre-Treatment	ZNF512B	57473	37	20	62598032	62598032	Nonsense_Mutation	SNP	G	A	5	213	c.496C>T	c.(496-498)CGA>TGA	p.R166*
Pat_06	Pre-Treatment	NCAM2	4685	37	21	22696706	22696706	Missense_Mutation	SNP	C	T	6	681	c.623C>T	c.(622-624)CCG>CTG	p.P208L
Pat_06	Pre-Treatment	USP16	10600	37	21	30414421	30414421	Missense_Mutation	SNP	G	A	5	294	c.1118G>A	c.(1117-1119)AGA>AAA	p.R373K
Pat_06	Pre-Treatment	CHAF1B	8208	37	21	37766943	37766943	Missense_Mutation	SNP	G	A	5	383	c.476G>A	c.(475-477)AGC>AAC	p.S159N
Pat_06	Pre-Treatment	UBE2G2	7327	37	21	46193549	46193549	Missense_Mutation	SNP	G	T	5	371	c.298C>A	c.(298-300)CCC>ACC	p.P100T
Pat_06	Pre-Treatment	MICAL3	57553	37	22	18370161	18370161	Missense_Mutation	SNP	T	C	3	219	c.1932A>G	c.(1930-1932)ATA>ATG	p.I644M
Pat_06	Pre-Treatment	GSTT2	2953	37	22	24300614	24300614	Missense_Mutation	SNP	G	A	4	152	c.383C>T	c.(382-384)CCC>CTC	p.P128L
Pat_06	Pre-Treatment	SUSD2	56241	37	22	24583962	24583962	Nonsense_Mutation	SNP	G	T	8	626	c.2200G>T	c.(2200-2202)GGA>TGA	p.G734*
Pat_06	Pre-Treatment	SGSM1	129049	37	22	25291235	25291235	Missense_Mutation	SNP	A	G	3	155	c.2164A>G	c.(2164-2166)AGC>GGC	p.S722G
Pat_06	Pre-Treatment	MN1	4330	37	22	28195963	28195963	Missense_Mutation	SNP	C	T	4	50	c.569G>A	c.(568-570)TGC>TAC	p.C190Y
Pat_06	Pre-Treatment	NEFH	4744	37	22	29885739	29885739	Missense_Mutation	SNP	T	A	6	324	c.2110T>A	c.(2110-2112)TCC>ACC	p.S704T
Pat_06	Pre-Treatment	PES1	23481	37	22	30977004	30977004	Missense_Mutation	SNP	C	T	5	210	c.907G>A	c.(907-909)GAT>AAT	p.D303N
Pat_06	Pre-Treatment	RNF185	91445	37	22	31588673	31588673	Nonsense_Mutation	SNP	G	A	5	602	c.180G>A	c.(178-180)TGG>TGA	p.W60*
Pat_06	Pre-Treatment	MYH9	4627	37	22	36705381	36705381	Missense_Mutation	SNP	C	A	4	346	c.1789G>T	c.(1789-1791)GCC>TCC	p.A597S
Pat_06	Pre-Treatment	MAFF	23764	37	22	38610560	38610560	Missense_Mutation	SNP	G	A	4	46	c.170G>A	c.(169-171)CGC>CAC	p.R57H
Pat_06	Pre-Treatment	DDX17	10521	37	22	38882269	38882269	Missense_Mutation	SNP	T	C	44	330	c.1867A>G	c.(1867-1869)AGT>GGT	p.S623G
Pat_06	Pre-Treatment	L3MBTL2	83746	37	22	41616870	41616870	Missense_Mutation	SNP	G	A	4	301	c.851G>A	c.(850-852)CGG>CAG	p.R284Q
Pat_06	Pre-Treatment	ZC3H7B	23264	37	22	41752674	41752674	Missense_Mutation	SNP	G	A	5	508	c.2543G>A	c.(2542-2544)GGC>GAC	p.G848D
Pat_06	Pre-Treatment	XRCC6	2547	37	22	42049589	42049589	Missense_Mutation	SNP	G	A	5	675	c.1186G>A	c.(1186-1188)GCA>ACA	p.A396T
Pat_06	Pre-Treatment	WBP2NL	164684	37	22	42415422	42415422	Missense_Mutation	SNP	G	A	4	191	c.170G>A	c.(169-171)CGG>CAG	p.R57Q
Pat_06	Pre-Treatment	CYP2D7P1	1564	37	22	42537318	42537318	Missense_Mutation	SNP	T	C	3	111	c.747A>G	c.(745-747)ATA>ATG	p.I249M
Pat_06	Pre-Treatment	SCUBE1	80274	37	22	43606234	43606234	Missense_Mutation	SNP	C	G	3	134	c.2396G>C	c.(2395-2397)GGC>GCC	p.G799A
Pat_06	Pre-Treatment	SCUBE1	80274	37	22	43610116	43610116	Missense_Mutation	SNP	C	T	5	304	c.2033G>A	c.(2032-2034)CGC>CAC	p.R678H
Pat_06	Pre-Treatment	NUP50	10762	37	22	45574769	45574769	Missense_Mutation	SNP	G	T	4	331	c.991G>T	c.(991-993)GGT>TGT	p.G331C
Pat_06	Pre-Treatment	UPK3A	7380	37	22	45691499	45691499	Missense_Mutation	SNP	G	A	7	353	c.763G>A	c.(763-765)GTT>ATT	p.V255I
Pat_06	Pre-Treatment	FAM19A5	25817	37	22	48885418	48885418	Missense_Mutation	SNP	C	T	3	19	c.14C>T	c.(13-15)CCC>CTC	p.P5L
Pat_06	Pre-Treatment	HDAC10	83933	37	22	50687828	50687828	Nonsense_Mutation	SNP	G	A	4	200	c.619C>T	c.(619-621)CGA>TGA	p.R207*
Pat_06	Pre-Treatment	MAPK11	5600	37	22	50703839	50703839	Missense_Mutation	SNP	C	G	4	347	c.926G>C	c.(925-927)AGC>ACC	p.S309T
Pat_06	Pre-Treatment	PLXNB2	23654	37	22	50719060	50719060	Missense_Mutation	SNP	G	A	4	187	c.4033C>T	c.(4033-4035)CGC>TGC	p.R1345C
Pat_06	Pre-Treatment	PLXNB2	23654	37	22	50720723	50720723	Missense_Mutation	SNP	C	T	4	296	c.3007G>A	c.(3007-3009)GTC>ATC	p.V1003I
Pat_06	Pre-Treatment	CPT1B	1375	37	22	51014749	51014749	Missense_Mutation	SNP	G	A	5	752	c.577C>T	c.(577-579)CGC>TGC	p.R193C
Pat_06	Pre-Treatment	SHANK3	85358	37	22	51142344	51142344	Missense_Mutation	SNP	G	A	3	63	c.1717G>A	c.(1717-1719)GAC>AAC	p.D573N
Pat_06	Pre-Treatment	SHANK3	85358	37	22	51142363	51142363	Missense_Mutation	SNP	G	A	3	55	c.1736G>A	c.(1735-1737)AGC>AAC	p.S579N
Pat_06	Pre-Treatment	LRRN1	57633	37	3	3887416	3887416	Missense_Mutation	SNP	G	A	6	614	c.1091G>A	c.(1090-1092)CGT>CAT	p.R364H
Pat_06	Pre-Treatment	OXTR	5021	37	3	8809414	8809414	Missense_Mutation	SNP	G	A	3	39	c.460C>T	c.(460-462)CGC>TGC	p.R154C
Pat_06	Pre-Treatment	SLC6A11	6538	37	3	10858143	10858143	Missense_Mutation	SNP	G	A	4	212	c.193G>A	c.(193-195)GGG>AGG	p.G65R
Pat_06	Pre-Treatment	MKRN2	23609	37	3	12611568	12611568	Splice_Site	SNP	A	T	5	592	c.156_splice	c.e3-2	p.R52_splice
Pat_06	Pre-Treatment	RAF1	5894	37	3	12641301	12641301	Missense_Mutation	SNP	G	A	7	542	c.997C>T	c.(997-999)CGT>TGT	p.R333C
Pat_06	Pre-Treatment	CAND2	23066	37	3	12856781	12856781	Missense_Mutation	SNP	G	A	5	369	c.1148G>A	c.(1147-1149)CGC>CAC	p.R383H
Pat_06	Pre-Treatment	KCNH8	131096	37	3	19575002	19575002	Missense_Mutation	SNP	G	A	5	567	c.2735G>A	c.(2734-2736)AGC>AAC	p.S912N

Pat_06	Pre-Treatment	ZCWPW2	152098	37	3	28454732	28454732	Nonsense_Mutation	SNP	G	A	5	750	c.173G>A	c.(172-174)TGG>TAG	p.W58*
Pat_06	Pre-Treatment	DCLK3	85443	37	3	36763056	36763056	Missense_Mutation	SNP	G	A	6	531	c.1547C>T	c.(1546-1548)ACC>ATC	p.T516I
Pat_06	Pre-Treatment	C3orf23	285343	37	3	44408953	44408953	Nonsense_Mutation	SNP	C	T	5	629	c.325C>T	c.(325-327)CGA>TGA	p.R109*
Pat_06	Pre-Treatment	TMEM42	131616	37	3	44905831	44905831	Missense_Mutation	SNP	G	A	6	327	c.335G>A	c.(334-336)AGC>AAC	p.S112N
Pat_06	Pre-Treatment	TGM4	7047	37	3	44945455	44945455	Missense_Mutation	SNP	G	A	6	563	c.1051G>A	c.(1051-1053)GCA>ACA	p.A351T
Pat_06	Pre-Treatment	PRSS45	377047	37	3	46784443	46784443	Missense_Mutation	SNP	T	C	3	122	c.413A>G	c.(412-414)GAC>GGC	p.D138G
Pat_06	Pre-Treatment	NBEAL2	23218	37	3	47042490	47042490	Splice_Site	SNP	G	A	4	103	c.4306_splice	c.e28-1	p.Q1436_splice
Pat_06	Pre-Treatment	NBEAL2	23218	37	3	47046741	47046741	Missense_Mutation	SNP	G	A	4	194	c.6490G>A	c.(6490-6492)GCA>ACA	p.A2164T
Pat_06	Pre-Treatment	TREX1	11277	37	3	48508332	48508332	Missense_Mutation	SNP	C	A	5	373	c.443C>A	c.(442-444)GCA>GAA	p.A148E
Pat_06	Pre-Treatment	COL7A1	1294	37	3	48624646	48624646	Missense_Mutation	SNP	T	C	3	192	c.3116A>G	c.(3115-3117)GAG>GGG	p.E1039G
Pat_06	Pre-Treatment	UQCRC1	7384	37	3	48637503	48637503	Missense_Mutation	SNP	C	T	5	415	c.1295G>A	c.(1294-1296)CGG>CAG	p.R432Q
Pat_06	Pre-Treatment	DALRD3	55152	37	3	49054762	49054762	Missense_Mutation	SNP	C	A	5	675	c.826G>T	c.(826-828)GGC>TGC	p.G276C
Pat_06	Pre-Treatment	C3orf54	389119	37	3	49842313	49842313	Missense_Mutation	SNP	C	A	6	668	c.757C>A	c.(757-759)CCA>ACA	p.P253T
Pat_06	Pre-Treatment	ZMYND10	51364	37	3	50382587	50382587	Missense_Mutation	SNP	G	C	3	249	c.169C>G	c.(169-171)CCC>GCC	p.P57A
Pat_06	Pre-Treatment	CACNA2D2	9254	37	3	50416528	50416528	Missense_Mutation	SNP	G	A	4	262	c.1255C>T	c.(1255-1257)CGG>TGG	p.R419W
Pat_06	Pre-Treatment	GPR62	118442	37	3	51989751	51989751	Missense_Mutation	SNP	C	G	3	72	c.83C>G	c.(82-84)GCA>GGA	p.A28G
Pat_06	Pre-Treatment	DNAH1	25981	37	3	52422617	52422617	Missense_Mutation	SNP	G	A	3	97	c.9355G>A	c.(9355-9357)GCT>ACT	p.A3119T
Pat_06	Pre-Treatment	STAB1	23166	37	3	52553979	52553979	Missense_Mutation	SNP	T	C	3	123	c.5255T>C	c.(5254-5256)CTG>CCG	p.L1752P
Pat_06	Pre-Treatment	STAB1	23166	37	3	52555459	52555459	Nonsense_Mutation	SNP	C	A	5	485	c.5991C>A	c.(5989-5991)TGC>TGA	p.C1997*
Pat_06	Pre-Treatment	ARHGEF3	50650	37	3	56763515	56763515	Missense_Mutation	SNP	G	A	5	697	c.1364C>T	c.(1363-1365)GCC>GTC	p.A455V
Pat_06	Pre-Treatment	PDE12	201626	37	3	57542450	57542450	Missense_Mutation	SNP	C	T	4	227	c.344C>T	c.(343-345)CCG>CTG	p.P115L
Pat_06	Pre-Treatment	SLMAP	7871	37	3	57743413	57743413	Missense_Mutation	SNP	C	T	5	274	c.35C>T	c.(34-36)CCG>CTG	p.P12L
Pat_06	Pre-Treatment	FLNB	2317	37	3	58134499	58134499	Missense_Mutation	SNP	G	A	5	362	c.6011G>A	c.(6010-6012)CGA>CAA	p.R2004Q
Pat_06	Pre-Treatment	FLNB	2317	37	3	58149042	58149042	Missense_Mutation	SNP	G	C	3	285	c.7183G>C	c.(7183-7185)GAA>CAA	p.E2395Q
Pat_06	Pre-Treatment	CPOX	1371	37	3	98307633	98307633	Missense_Mutation	SNP	C	T	5	355	c.877G>A	c.(877-879)GCT>ACT	p.A293T
Pat_06	Pre-Treatment	MYH15	22989	37	3	108107854	108107854	Missense_Mutation	SNP	C	T	5	718	c.5558G>A	c.(5557-5559)CGC>CAC	p.R1853H
Pat_06	Pre-Treatment	DRD3	1814	37	3	113866361	113866361	Missense_Mutation	SNP	C	T	4	433	c.427G>A	c.(427-429)GGA>AGA	p.G143R
Pat_06	Pre-Treatment	GSK3B	2932	37	3	119582436	119582436	Missense_Mutation	SNP	G	A	4	153	c.926C>T	c.(925-927)ACT>ATT	p.T309I
Pat_06	Pre-Treatment	POLQ	10721	37	3	121200622	121200622	Missense_Mutation	SNP	G	A	5	517	c.6008C>T	c.(6007-6009)CCG>CTG	p.P2003L
Pat_06	Pre-Treatment	PARP15	165631	37	3	122354745	122354745	Missense_Mutation	SNP	G	A	6	433	c.1835G>A	c.(1834-1836)AGA>AAA	p.R612K
Pat_06	Pre-Treatment	KALRN	8997	37	3	124438241	124438241	Missense_Mutation	SNP	G	A	6	456	c.8885G>A	c.(8884-8886)CGC>CAC	p.R2962H
Pat_06	Pre-Treatment	ITGB5	3693	37	3	124578098	124578098	Missense_Mutation	SNP	G	A	5	623	c.352C>T	c.(352-354)CTC>TTC	p.L118F
Pat_06	Pre-Treatment	MGLL	11343	37	3	127540645	127540645	Missense_Mutation	SNP	G	A	7	687	c.17C>T	c.(16-18)TCC>TTC	p.S6F
Pat_06	Pre-Treatment	EEFSEC	60678	37	3	128126978	128126978	Missense_Mutation	SNP	G	A	5	164	c.1667G>A	c.(1666-1668)CGT>CAT	p.R556H
Pat_06	Pre-Treatment	COPG	22820	37	3	128984621	128984621	Missense_Mutation	SNP	A	G	3	132	c.1454A>G	c.(1453-1455)GAG>GGG	p.E485G
Pat_06	Pre-Treatment	C3orf37	56941	37	3	129020824	129020824	Missense_Mutation	SNP	G	A	4	453	c.667G>A	c.(667-669)GTT>ATT	p.V223I
Pat_06	Pre-Treatment	RHO	6010	37	3	129251434	129251434	Missense_Mutation	SNP	G	A	4	232	c.755G>A	c.(754-756)CGC>CAC	p.R252H
Pat_06	Pre-Treatment	TMCC1	23023	37	3	129390101	129390101	Missense_Mutation	SNP	G	A	4	182	c.583C>T	c.(583-585)CGG>TGG	p.R195W
Pat_06	Pre-Treatment	COL6A6	131873	37	3	130381086	130381086	Nonsense_Mutation	SNP	C	T	6	831	c.6436C>T	c.(6436-6438)CGA>TGA	p.R2146*
Pat_06	Pre-Treatment	ACAD11	84129	37	3	132378514	132378514	Missense_Mutation	SNP	A	G	4	399	c.82T>C	c.(82-84)TAC>CAC	p.Y28H
Pat_06	Pre-Treatment	TF	7018	37	3	133494370	133494370	Missense_Mutation	SNP	C	T	6	790	c.1781C>T	c.(1780-1782)GCG>GTG	p.A594V
Pat_06	Pre-Treatment	RAB6B	51560	37	3	133614290	133614290	Missense_Mutation	SNP	A	C	4	451	c.21T>G	c.(19-21)TTT>TTG	p.F7L
Pat_06	Pre-Treatment	C3orf72	401089	37	3	138669327	138669327	Missense_Mutation	SNP	G	T	6	303	c.441G>T	c.(439-441)GAG>GAT	p.E147D
Pat_06	Pre-Treatment	ZBTB38	253461	37	3	141163446	141163446	Missense_Mutation	SNP	G	A	5	664	c.2216G>A	c.(2215-2217)AGC>AAC	p.S739N
Pat_06	Pre-Treatment	RASA2	5922	37	3	141289848	141289848	Missense_Mutation	SNP	G	A	4	231	c.958G>A	c.(958-960)GTG>ATG	p.V320M
Pat_06	Pre-Treatment	WWTR1	25937	37	3	149290707	149290707	Missense_Mutation	SNP	G	A	6	500	c.512C>T	c.(511-513)GCC>GTC	p.A171V
Pat_06	Pre-Treatment	LEKR1	389170	37	3	156710912	156710912	Missense_Mutation	SNP	C	A	4	277	c.43C>A	c.(43-45)CAG>AAG	p.Q15K

Pat_06	Pre-Treatment	RARRES1	5918	37	3	158415738	158415738	Missense_Mutation	SNP	C	G	3	99	c.694G>C	c.(694-696)GAT>CAT	p.D232H
Pat_06	Pre-Treatment	ABCC5	10057	37	3	183732084	183732084	Missense_Mutation	SNP	G	A	5	545	c.97C>T	c.(97-99)CGT>TGT	p.R33C
Pat_06	Pre-Treatment	PSMD2	5708	37	3	184020502	184020502	Missense_Mutation	SNP	G	A	5	729	c.899G>A	c.(898-900)CGG>CAG	p.R300Q
Pat_06	Pre-Treatment	CHRD	8646	37	3	184101422	184101422	Missense_Mutation	SNP	G	A	4	269	c.1432G>A	c.(1432-1434)GGA>AGA	p.G478R
Pat_06	Pre-Treatment	EIF4A2	1974	37	3	186501404	186501404	Missense_Mutation	SNP	C	G	215	497	c.5C>G	c.(4-6)TCT>TGT	p.S2C
Pat_06	Pre-Treatment	IL1RAP	3556	37	3	190338161	190338161	Missense_Mutation	SNP	G	C	5	605	c.635G>C	c.(634-636)TGT>TCT	p.C212S
Pat_06	Pre-Treatment	CCDC50	152137	37	3	191087826	191087826	Splice_Site	SNP	G	A	5	646	c.448_splice	c.e5+1	p.G150_splice
Pat_06	Pre-Treatment	TFRC	7037	37	3	195802104	195802104	Missense_Mutation	SNP	T	C	4	669	c.164A>G	c.(163-165)AAT>AGT	p.N55S
Pat_06	Pre-Treatment	PCYT1A	5130	37	3	195974321	195974321	Missense_Mutation	SNP	C	T	6	646	c.403G>A	c.(403-405)GCA>ACA	p.A135T
Pat_06	Pre-Treatment	BDH1	622	37	3	197238896	197238896	Missense_Mutation	SNP	G	A	8	767	c.902C>T	c.(901-903)GCT>GTT	p.A301V
Pat_06	Pre-Treatment	CRIPAK	285464	37	4	1388561	1388561	Missense_Mutation	SNP	A	T	6	896	c.262A>T	c.(262-264)ACA>TCA	p.T88S
Pat_06	Pre-Treatment	CRIPAK	285464	37	4	1389002	1389002	Nonsense_Mutation	SNP	C	T	5	848	c.703C>T	c.(703-705)CGA>TGA	p.R235*
Pat_06	Pre-Treatment	POLN	353497	37	4	2159586	2159586	Missense_Mutation	SNP	T	C	4	343	c.1664A>G	c.(1663-1665)AAG>AGG	p.K555R
Pat_06	Pre-Treatment	HTT	3064	37	4	3184132	3184132	Missense_Mutation	SNP	G	A	4	382	c.4807G>A	c.(4807-4809)GAC>AAC	p.D1603N
Pat_06	Pre-Treatment	RGS12	6002	37	4	3424654	3424654	Missense_Mutation	SNP	G	A	5	331	c.3056G>A	c.(3055-3057)AGT>AAT	p.S1019N
Pat_06	Pre-Treatment	PPP2R2C	5522	37	4	6325271	6325271	Missense_Mutation	SNP	T	C	3	132	c.1102A>G	c.(1102-1104)AAC>GAC	p.N368D
Pat_06	Pre-Treatment	CCDC96	257236	37	4	7043747	7043747	Missense_Mutation	SNP	G	T	6	587	c.919C>A	c.(919-921)CAG>AAG	p.Q307K
Pat_06	Pre-Treatment	SH3TC1	54436	37	4	8237223	8237223	Missense_Mutation	SNP	G	A	5	624	c.3346G>A	c.(3346-3348)GCT>ACT	p.A1116T
Pat_06	Pre-Treatment	LDB2	9079	37	4	16504318	16504318	Missense_Mutation	SNP	G	A	5	723	c.1070C>T	c.(1069-1071)CCC>CTC	p.P357L
Pat_06	Pre-Treatment	LAP3	51056	37	4	17609084	17609084	Missense_Mutation	SNP	G	A	6	618	c.1432G>A	c.(1432-1434)GCA>ACA	p.A478T
Pat_06	Pre-Treatment	GPR125	166647	37	4	22444334	22444334	Missense_Mutation	SNP	C	A	4	450	c.859G>T	c.(859-861)GAT>TAT	p.D287Y
Pat_06	Pre-Treatment	GPR125	166647	37	4	22456493	22456493	Missense_Mutation	SNP	G	A	5	551	c.469C>T	c.(469-471)CGG>TGG	p.R157W
Pat_06	Pre-Treatment	PPARGC1A	10891	37	4	23814645	23814645	Missense_Mutation	SNP	T	C	4	764	c.1897A>G	c.(1897-1899)AGG>GGG	p.R633G
Pat_06	Pre-Treatment	RBPJ	3516	37	4	26432059	26432059	Missense_Mutation	SNP	G	A	5	775	c.1102G>A	c.(1102-1104)GTA>ATA	p.V368I
Pat_06	Pre-Treatment	EPHA5	2044	37	4	66356248	66356248	Missense_Mutation	SNP	G	A	4	481	c.1249C>T	c.(1249-1251)CGG>TGG	p.R417W
Pat_06	Pre-Treatment	SLC4A4	8671	37	4	72215676	72215676	Missense_Mutation	SNP	G	A	5	530	c.437G>A	c.(436-438)AGC>AAC	p.S146N
Pat_06	Pre-Treatment	COX18	285521	37	4	73927540	73927540	Missense_Mutation	SNP	G	A	4	278	c.818C>T	c.(817-819)ACG>ATG	p.T273M
Pat_06	Pre-Treatment	ANKRD17	26057	37	4	73963913	73963913	Missense_Mutation	SNP	C	T	6	850	c.4898G>A	c.(4897-4899)CGT>CAT	p.R1633H
Pat_06	Pre-Treatment	KLHL8	57563	37	4	88106470	88106470	Missense_Mutation	SNP	G	A	5	734	c.698C>T	c.(697-699)GCT>GTT	p.A233V
Pat_06	Pre-Treatment	SPP1	6696	37	4	88901581	88901581	Missense_Mutation	SNP	C	G	3	215	c.211C>G	c.(211-213)CAA>GAA	p.Q71E
Pat_06	Pre-Treatment	HERC3	8916	37	4	89627981	89627981	Missense_Mutation	SNP	G	A	4	453	c.3023G>A	c.(3022-3024)GGG>GAG	p.G1008E
Pat_06	Pre-Treatment	ATOH1	474	37	4	94750976	94750976	Missense_Mutation	SNP	G	A	5	546	c.899G>A	c.(898-900)AGC>AAC	p.S300N
Pat_06	Pre-Treatment	UNC5C	8633	37	4	96141281	96141281	Missense_Mutation	SNP	T	C	3	184	c.1155A>G	c.(1153-1155)ATA>ATG	p.I385M
Pat_06	Pre-Treatment	MANBA	4126	37	4	103556001	103556001	Missense_Mutation	SNP	A	G	4	406	c.2359T>C	c.(2359-2361)TAC>CAC	p.Y787H
Pat_06	Pre-Treatment	ANK2	287	37	4	114203906	114203906	Missense_Mutation	SNP	G	A	4	207	c.1957G>A	c.(1957-1959)GCA>ACA	p.A653T
Pat_06	Pre-Treatment	SPATA5	166378	37	4	123868451	123868451	Missense_Mutation	SNP	G	A	5	191	c.1522G>A	c.(1522-1524)GCT>ACT	p.A508T
Pat_06	Pre-Treatment	PCDH10	57575	37	4	134072409	134072409	Missense_Mutation	SNP	G	A	4	288	c.1114G>A	c.(1114-1116)GCG>ACG	p.A372T
Pat_06	Pre-Treatment	USP38	84640	37	4	144130737	144130737	Missense_Mutation	SNP	C	G	3	222	c.1424C>G	c.(1423-1425)TCT>TGT	p.S475C
Pat_06	Pre-Treatment	ABCE1	6059	37	4	146029186	146029186	Missense_Mutation	SNP	T	C	4	386	c.209T>C	c.(208-210)TTA>TCA	p.L70S
Pat_06	Pre-Treatment	FHDC1	85462	37	4	153884196	153884196	Missense_Mutation	SNP	G	A	6	767	c.943G>A	c.(943-945)GTA>ATA	p.V315I
Pat_06	Pre-Treatment	RAPGEF2	9693	37	4	160266376	160266376	Missense_Mutation	SNP	C	A	6	806	c.2914C>A	c.(2914-2916)CAA>AAA	p.Q972K
Pat_06	Pre-Treatment	GK3P	2713	37	4	166200361	166200361	Missense_Mutation	SNP	C	T	7	508	c.437G>A	c.(436-438)AGC>AAC	p.S146N
Pat_06	Pre-Treatment	CLCN3	1182	37	4	170634391	170634391	Missense_Mutation	SNP	G	A	5	700	c.2311G>A	c.(2311-2313)GTG>ATG	p.V771M
Pat_06	Pre-Treatment	STOX2	56977	37	4	184930345	184930345	Missense_Mutation	SNP	C	A	3	98	c.354C>A	c.(352-354)CAC>CAA	p.H118Q
Pat_06	Pre-Treatment	STOX2	56977	37	4	184932540	184932540	Missense_Mutation	SNP	G	A	5	495	c.2549G>A	c.(2548-2550)AGC>AAC	p.S850N
Pat_06	Pre-Treatment	TUBB4Q	56604	37	4	190903752	190903752	Missense_Mutation	SNP	C	T	6	783	c.1228G>A	c.(1228-1230)GAG>AAG	p.E410K
Pat_06	Pre-Treatment	RICTOR	253260	37	5	38942984	38942984	Missense_Mutation	SNP	G	A	5	375	c.5003C>T	c.(5002-5004)CCG>CTG	p.P1668L

Pat_06	Pre-Treatment	HEATR7B2	133558	37	5	41015484	41015484	Missense_Mutation	SNP	T	C	3	223	c.2981A>G	c.(2980-2982)AAG>AGG	p.K994R
Pat_06	Pre-Treatment	ISL1	3670	37	5	50679521	50679521	Missense_Mutation	SNP	G	A	4	297	c.16G>A	c.(16-18)GAT>AAT	p.D6N
Pat_06	Pre-Treatment	PELO	53918	37	5	52096401	52096401	Missense_Mutation	SNP	G	A	4	323	c.173G>A	c.(172-174)AGC>AAC	p.S58N
Pat_06	Pre-Treatment	DDX4	54514	37	5	55110932	55110932	Missense_Mutation	SNP	C	A	9	768	c.1919C>A	c.(1918-1920)GCA>GAA	p.A640E
Pat_06	Pre-Treatment	RGS7BP	401190	37	5	63803671	63803671	Missense_Mutation	SNP	G	A	4	259	c.299G>A	c.(298-300)CGT>CAT	p.R100H
Pat_06	Pre-Treatment	RGS7BP	401190	37	5	63871612	63871612	Missense_Mutation	SNP	G	T	28	335	c.344G>T	c.(343-345)GGT>GTT	p.G115V
Pat_06	Pre-Treatment	ADAMTS6	11174	37	5	64492900	64492900	Missense_Mutation	SNP	C	T	5	575	c.2654G>A	c.(2653-2655)AGT>AAT	p.S885N
Pat_06	Pre-Treatment	ADAMTS6	11174	37	5	64756033	64756033	Nonsense_Mutation	SNP	G	A	5	741	c.595C>T	c.(595-597)CGA>TGA	p.R199*
Pat_06	Pre-Treatment	BDP1	55814	37	5	70806049	70806049	Missense_Mutation	SNP	G	A	8	339	c.3130G>A	c.(3130-3132)GTA>ATA	p.V1044I
Pat_06	Pre-Treatment	WDR41	55255	37	5	76736818	76736818	Missense_Mutation	SNP	C	A	7	220	c.702G>T	c.(700-702)TTG>TTT	p.L234F
Pat_06	Pre-Treatment	CMYA5	202333	37	5	79031109	79031109	Missense_Mutation	SNP	G	A	61	117	c.6521G>A	c.(6520-6522)GGA>GAA	p.G2174E
Pat_06	Pre-Treatment	HAPLN1	1404	37	5	82937463	82937463	Missense_Mutation	SNP	G	A	6	812	c.917C>T	c.(916-918)GCG>GTG	p.A306V
Pat_06	Pre-Treatment	LNPEP	4012	37	5	96315312	96315312	Missense_Mutation	SNP	G	A	6	564	c.490G>A	c.(490-492)GCA>ACA	p.A164T
Pat_06	Pre-Treatment	DTWD2	285605	37	5	118183873	118183873	Missense_Mutation	SNP	C	T	5	418	c.638G>A	c.(637-639)CGG>CAG	p.R213Q
Pat_06	Pre-Treatment	DMXL1	1657	37	5	118513729	118513729	Missense_Mutation	SNP	G	A	5	537	c.6925G>A	c.(6925-6927)GAG>AAG	p.E2309K
Pat_06	Pre-Treatment	SNCAIP	9627	37	5	121767682	121767682	Missense_Mutation	SNP	G	A	6	365	c.1201G>A	c.(1201-1203)GTA>ATA	p.V401I
Pat_06	Pre-Treatment	GRAMD3	65983	37	5	125816379	125816379	Missense_Mutation	SNP	C	T	5	655	c.715C>T	c.(715-717)CGC>TGC	p.R239C
Pat_06	Pre-Treatment	BRD8	10902	37	5	137503719	137503719	Missense_Mutation	SNP	C	T	6	793	c.691G>A	c.(691-693)GGT>AGT	p.G231S
Pat_06	Pre-Treatment	FAM53C	51307	37	5	137680844	137680844	Missense_Mutation	SNP	C	T	6	395	c.467C>T	c.(466-468)CCG>CTG	p.P156L
Pat_06	Pre-Treatment	CTNNA1	1495	37	5	138145828	138145828	Missense_Mutation	SNP	G	A	5	615	c.403G>A	c.(403-405)GTT>ATT	p.V135I
Pat_06	Pre-Treatment	PCDHA4	56144	37	5	140186912	140186912	Missense_Mutation	SNP	G	A	6	542	c.140G>A	c.(139-141)CGC>CAC	p.R47H
Pat_06	Pre-Treatment	PCDHA4	56144	37	5	140188628	140188628	Missense_Mutation	SNP	G	A	7	667	c.1856G>A	c.(1855-1857)CGC>CAC	p.R619H
Pat_06	Pre-Treatment	PCDHB8	56128	37	5	140558184	140558184	Missense_Mutation	SNP	G	A	4	135	c.569G>A	c.(568-570)AGG>AAG	p.R190K
Pat_06	Pre-Treatment	PCDHGA7	56108	37	5	140764210	140764210	Missense_Mutation	SNP	G	A	6	793	c.1744G>A	c.(1744-1746)GCA>ACA	p.A582T
Pat_06	Pre-Treatment	PCDHGB7	56099	37	5	140799101	140799101	Missense_Mutation	SNP	G	A	4	165	c.1675G>A	c.(1675-1677)GCA>ACA	p.A559T
Pat_06	Pre-Treatment	PCDHGA12	26025	37	5	140811950	140811950	Missense_Mutation	SNP	C	T	5	802	c.1624C>T	c.(1624-1626)CTC>TTC	p.L542F
Pat_06	Pre-Treatment	ARHGAP26	23092	37	5	142281595	142281595	Missense_Mutation	SNP	C	A	6	443	c.693C>A	c.(691-693)AGC>AGA	p.S231R
Pat_06	Pre-Treatment	TCERG1	10915	37	5	145838472	145838472	Missense_Mutation	SNP	G	A	5	802	c.464G>A	c.(463-465)CGT>CAT	p.R155H
Pat_06	Pre-Treatment	ARSI	340075	37	5	149676821	149676821	Missense_Mutation	SNP	A	G	5	687	c.1666T>C	c.(1666-1668)TTT>CTT	p.F556L
Pat_06	Pre-Treatment	SPARC	6678	37	5	151043744	151043744	Nonsense_Mutation	SNP	C	A	6	319	c.787G>T	c.(787-789)GAG>TAG	p.E263*
Pat_06	Pre-Treatment	FBLL1	345630	37	5	167957138	167957138	Missense_Mutation	SNP	G	A	3	61	c.344G>A	c.(343-345)CGC>CAC	p.R115H
Pat_06	Pre-Treatment	SH3PXD2B	285590	37	5	171766461	171766461	Missense_Mutation	SNP	G	A	6	377	c.1648C>T	c.(1648-1650)CGG>TGG	p.R550W
Pat_06	Pre-Treatment	UNC5A	90249	37	5	176301022	176301022	Missense_Mutation	SNP	G	A	5	225	c.940G>A	c.(940-942)GTC>ATC	p.V314I
Pat_06	Pre-Treatment	FGFR4	2264	37	5	176522545	176522545	Missense_Mutation	SNP	G	A	3	34	c.1642G>A	c.(1642-1644)GTG>ATG	p.V548M
Pat_06	Pre-Treatment	DDX41	51428	37	5	176941759	176941759	Missense_Mutation	SNP	C	T	6	633	c.878G>A	c.(877-879)CGC>CAC	p.R293H
Pat_06	Pre-Treatment	ADAMTS2	9509	37	5	178553062	178553062	Missense_Mutation	SNP	G	A	6	632	c.2687C>T	c.(2686-2688)GCC>GTC	p.A896V
Pat_06	Pre-Treatment	MAML1	9794	37	5	179193270	179193270	Missense_Mutation	SNP	C	T	6	754	c.1259C>T	c.(1258-1260)CCG>CTG	p.P420L
Pat_06	Pre-Treatment	PECI	10455	37	6	4130748	4130748	Missense_Mutation	SNP	G	A	5	587	c.359C>T	c.(358-360)CCT>CTT	p.P120L
Pat_06	Pre-Treatment	PECI	10455	37	6	4133832	4133832	Missense_Mutation	SNP	T	C	4	620	c.164A>G	c.(163-165)AAG>AGG	p.K55R
Pat_06	Pre-Treatment	TBC1D7	51256	37	6	13316811	13316811	Missense_Mutation	SNP	G	A	5	660	c.511C>T	c.(511-513)CCC>TCC	p.P171S
Pat_06	Pre-Treatment	CAP2	10486	37	6	17507511	17507511	Missense_Mutation	SNP	G	A	6	741	c.412G>A	c.(412-414)GAA>AAA	p.E138K
Pat_06	Pre-Treatment	CDKAL1	54901	37	6	20846368	20846368	Missense_Mutation	SNP	C	A	7	614	c.701C>A	c.(700-702)CCA>CAA	p.P234Q
Pat_06	Pre-Treatment	PRL	5617	37	6	22294729	22294729	Missense_Mutation	SNP	C	T	84	253	c.113G>A	c.(112-114)CGA>CAA	p.R38Q
Pat_06	Pre-Treatment	BTN3A1	11119	37	6	26408075	26408075	Missense_Mutation	SNP	G	A	5	881	c.610G>A	c.(610-612)GTA>ATA	p.V204I
Pat_06	Pre-Treatment	HLA-E	3133	37	6	30459102	30459102	Missense_Mutation	SNP	G	A	5	555	c.799G>A	c.(799-801)GCT>ACT	p.A267T
Pat_06	Pre-Treatment	GNL1	2794	37	6	30515027	30515027	Missense_Mutation	SNP	C	T	7	837	c.1303G>A	c.(1303-1305)GCC>ACC	p.A435T
Pat_06	Pre-Treatment	LSM2	57819	37	6	31765619	31765619	Missense_Mutation	SNP	C	T	6	854	c.203G>A	c.(202-204)CGA>CAA	p.R68Q

Pat_06	Pre-Treatment	CFB	629	37	6	31901429	31901429	Missense_Mutation	SNP	G	A	5	518	c.299G>A	c.(298-300)CGG>CAG	p.R100Q
Pat_06	Pre-Treatment	ITPR3	3710	37	6	33654231	33654231	Missense_Mutation	SNP	G	A	5	787	c.5914G>A	c.(5914-5916)GCA>ACA	p.A1972T
Pat_06	Pre-Treatment	DEF6	50619	37	6	35285693	35285693	Missense_Mutation	SNP	G	A	4	213	c.833G>A	c.(832-834)CGC>CAC	p.R278H
Pat_06	Pre-Treatment	PPARD	5467	37	6	35393740	35393740	Missense_Mutation	SNP	G	A	6	367	c.1210G>A	c.(1210-1212)GCT>ACT	p.A404T
Pat_06	Pre-Treatment	TULP1	7287	37	6	35477014	35477014	Missense_Mutation	SNP	T	C	4	872	c.794A>G	c.(793-795)AAG>AGG	p.K265R
Pat_06	Pre-Treatment	TRERF1	55809	37	6	42237177	42237177	Missense_Mutation	SNP	G	A	6	359	c.152C>T	c.(151-153)TCG>TTG	p.S51L
Pat_06	Pre-Treatment	C6orf223	221416	37	6	43970473	43970473	Missense_Mutation	SNP	G	A	3	48	c.339G>A	c.(337-339)ATG>ATA	p.M113I
Pat_06	Pre-Treatment	TMEM63B	55362	37	6	44119605	44119605	Missense_Mutation	SNP	G	A	6	458	c.1696G>A	c.(1696-1698)GGC>AGC	p.G566S
Pat_06	Pre-Treatment	TCTE1	202500	37	6	44250134	44250134	Missense_Mutation	SNP	G	A	5	372	c.1009C>T	c.(1009-1011)CGT>TGT	p.R337C
Pat_06	Pre-Treatment	ENPP4	22875	37	6	46107679	46107679	Missense_Mutation	SNP	G	T	7	715	c.359G>T	c.(358-360)TGG>TTG	p.W120L
Pat_06	Pre-Treatment	ELOVL5	60481	37	6	53139987	53139987	Missense_Mutation	SNP	G	A	6	495	c.397C>T	c.(397-399)CGC>TGC	p.R133C
Pat_06	Pre-Treatment	BAI3	577	37	6	69646414	69646414	Missense_Mutation	SNP	A	G	3	224	c.872A>G	c.(871-873)GAA>GGA	p.E291G
Pat_06	Pre-Treatment	COL9A1	1297	37	6	70993524	70993524	Splice_Site	SNP	C	G	24	32	c.697_splice	c.e6-1	p.F233_splice
Pat_06	Pre-Treatment	SMPD2	6610	37	6	109764797	109764797	Missense_Mutation	SNP	C	T	4	133	c.961C>T	c.(961-963)CGC>TGC	p.R321C
Pat_06	Pre-Treatment	C6orf186	728464	37	6	110636546	110636546	Missense_Mutation	SNP	C	A	6	477	c.556G>T	c.(556-558)GGG>TGG	p.G186W
Pat_06	Pre-Treatment	LAMA4	3910	37	6	112466034	112466034	Nonsense_Mutation	SNP	G	A	5	433	c.2455C>T	c.(2455-2457)CGA>TGA	p.R819*
Pat_06	Pre-Treatment	SLC35F1	222553	37	6	118556698	118556698	Nonsense_Mutation	SNP	C	T	4	239	c.376C>T	c.(376-378)CGA>TGA	p.R126*
Pat_06	Pre-Treatment	RNF146	81847	37	6	127608243	127608243	Missense_Mutation	SNP	G	A	4	207	c.485G>A	c.(484-486)CGT>CAT	p.R162H
Pat_06	Pre-Treatment	EYA4	2070	37	6	133849911	133849911	Missense_Mutation	SNP	C	T	5	765	c.1888C>T	c.(1888-1890)CTC>TTC	p.L630F
Pat_06	Pre-Treatment	IL20RA	53832	37	6	137323125	137323125	Missense_Mutation	SNP	C	G	3	163	c.1232G>C	c.(1231-1233)TGT>TCT	p.C411S
Pat_06	Pre-Treatment	ADAT2	134637	37	6	143771767	143771767	Missense_Mutation	SNP	G	A	5	476	c.29C>T	c.(28-30)GCT>GTT	p.A10V
Pat_06	Pre-Treatment	SHPRH	257218	37	6	146264619	146264619	Missense_Mutation	SNP	G	A	5	616	c.1898C>T	c.(1897-1899)GCT>GTT	p.A633V
Pat_06	Pre-Treatment	RBM16	22828	37	6	155116190	155116190	Missense_Mutation	SNP	C	T	6	582	c.523C>T	c.(523-525)CCT>TCT	p.P175S
Pat_06	Pre-Treatment	RSPH3	83861	37	6	159420638	159420638	Missense_Mutation	SNP	G	A	5	412	c.371C>T	c.(370-372)GCG>GTG	p.A124V
Pat_06	Pre-Treatment	MAP3K4	4216	37	6	161519315	161519315	Missense_Mutation	SNP	G	A	6	807	c.3530G>A	c.(3529-3531)CGG>CAG	p.R1177Q
Pat_06	Pre-Treatment	SMOC2	64094	37	6	168910632	168910632	Missense_Mutation	SNP	G	A	4	294	c.122G>A	c.(121-123)AGC>AAC	p.S41N
Pat_06	Pre-Treatment	CYP2W1	54905	37	7	1027080	1027080	Missense_Mutation	SNP	C	A	3	47	c.1056C>A	c.(1054-1056)CAC>CAA	p.H352Q
Pat_06	Pre-Treatment	TTYH3	80727	37	7	2696038	2696038	Missense_Mutation	SNP	G	A	6	372	c.1120G>A	c.(1120-1122)GTG>ATG	p.V374M
Pat_06	Pre-Treatment	TTYH3	80727	37	7	2698609	2698609	Missense_Mutation	SNP	A	G	4	759	c.1460A>G	c.(1459-1461)GAG>GGG	p.E487G
Pat_06	Pre-Treatment	CARD11	84433	37	7	2949714	2949714	Missense_Mutation	SNP	C	A	5	698	c.3230G>T	c.(3229-3231)CGG>CTG	p.R1077L
Pat_06	Pre-Treatment	TNRC18	84629	37	7	5352438	5352438	Missense_Mutation	SNP	G	A	3	49	c.8084C>T	c.(8083-8085)GCG>GTG	p.A2695V
Pat_06	Pre-Treatment	FBXL18	80028	37	7	5540665	5540665	Missense_Mutation	SNP	A	G	3	110	c.1235T>C	c.(1234-1236)CTG>CCG	p.L412P
Pat_06	Pre-Treatment	USP42	84132	37	7	6178755	6178755	Missense_Mutation	SNP	G	C	3	104	c.586G>C	c.(586-588)GAA>CAA	p.E196Q
Pat_06	Pre-Treatment	C7orf70	84792	37	7	6370424	6370424	Missense_Mutation	SNP	C	A	4	314	c.362G>T	c.(361-363)GGT>GTT	p.G121V
Pat_06	Pre-Treatment	DGKB	1607	37	7	14722395	14722395	Missense_Mutation	SNP	A	G	3	64	c.901T>C	c.(901-903)TCC>CCC	p.S301P
Pat_06	Pre-Treatment	AHR	196	37	7	17373614	17373614	Missense_Mutation	SNP	C	A	5	469	c.784C>A	c.(784-786)CAG>AAG	p.Q262K
Pat_06	Pre-Treatment	FAM126A	84668	37	7	22985627	22985627	Missense_Mutation	SNP	G	A	5	759	c.1147C>T	c.(1147-1149)CGG>TGG	p.R383W
Pat_06	Pre-Treatment	MPP6	51678	37	7	24720065	24720065	Missense_Mutation	SNP	G	A	7	707	c.1372G>A	c.(1372-1374)GCT>ACT	p.A458T
Pat_06	Pre-Treatment	POLM	27434	37	7	44113810	44113810	Missense_Mutation	SNP	C	T	3	39	c.991G>A	c.(991-993)GTG>ATG	p.V331M
Pat_06	Pre-Treatment	CDC14C	168448	37	7	48965490	48965490	Missense_Mutation	SNP	A	G	3	70	c.1222A>G	c.(1222-1224)AGA>GGA	p.R408G
Pat_06	Pre-Treatment	ZNF713	349075	37	7	56007015	56007015	Missense_Mutation	SNP	C	G	3	372	c.609C>G	c.(607-609)ATC>ATG	p.I203M
Pat_06	Pre-Treatment	GBAS	2631	37	7	56049244	56049245	Missense_Mutation	DNP	CG	TA	7	507	c.357_358CG>TA	355-360)GGCGAG>GGTA	p.E120K
Pat_06	Pre-Treatment	ZNF716	441234	37	7	57529068	57529068	Missense_Mutation	SNP	T	C	5	148	c.901T>C	c.(901-903)TGT>CGT	p.C301R
Pat_06	Pre-Treatment	ZNF735	730291	37	7	63680424	63680424	Missense_Mutation	SNP	A	G	3	182	c.995A>G	c.(994-996)AAA>AGA	p.K332R
Pat_06	Pre-Treatment	ABHD11	83451	37	7	73151601	73151601	Missense_Mutation	SNP	G	A	5	605	c.583C>T	c.(583-585)CGC>TGC	p.R195C
Pat_06	Pre-Treatment	POM121C	100101267	37	7	75070845	75070845	Missense_Mutation	SNP	G	A	25	48	c.656C>T	c.(655-657)CCG>CTG	p.P219L
Pat_06	Pre-Treatment	POM121C	100101267	37	7	75113598	75113598	Splice_Site	SNP	T	A	3	56	c.1_splice	c.e1-1	

Pat_06	Pre-Treatment	FGL2	10875	37	7	76826077	76826077	Missense_Mutation	SNP	C	G	4	606	c.839G>C	c.(838-840)AGG>ACG	p.R280T
Pat_06	Pre-Treatment	SEMA3D	223117	37	7	84628872	84628872	Missense_Mutation	SNP	G	A	5	666	c.2218C>T	c.(2218-2220)CGG>TGG	p.R740W
Pat_06	Pre-Treatment	MTERF	7978	37	7	91503708	91503708	Missense_Mutation	SNP	G	A	6	775	c.400C>T	c.(400-402)CGT>TGT	p.R134C
Pat_06	Pre-Treatment	AKAP9	10142	37	7	91732059	91732059	Missense_Mutation	SNP	C	T	6	833	c.11249C>T	c.(11248-11250)ACG>ATG	p.T3750M
Pat_06	Pre-Treatment	TRRAP	8295	37	7	98495427	98495427	Missense_Mutation	SNP	G	T	6	764	c.571G>T	c.(571-573)GGT>TGT	p.G191C
Pat_06	Pre-Treatment	CNPY4	245812	37	7	99720426	99720426	Missense_Mutation	SNP	C	A	4	204	c.362C>A	c.(361-363)GCA>GAA	p.A121E
Pat_06	Pre-Treatment	MEPCE	56257	37	7	100028081	100028081	Missense_Mutation	SNP	G	A	4	164	c.440G>A	c.(439-441)GGC>GAC	p.G147D
Pat_06	Pre-Treatment	MEPCE	56257	37	7	100028454	100028454	Missense_Mutation	SNP	G	C	4	687	c.813G>C	c.(811-813)CAG>CAC	p.Q271H
Pat_06	Pre-Treatment	LRCH4	4034	37	7	100175810	100175810	Missense_Mutation	SNP	C	G	3	213	c.920G>C	c.(919-921)AGT>ACT	p.S307T
Pat_06	Pre-Treatment	ZAN	7455	37	7	100377273	100377273	Missense_Mutation	SNP	G	A	3	19	c.6523G>A	c.(6523-6525)GGT>AGT	p.G2175S
Pat_06	Pre-Treatment	ZAN	7455	37	7	100391814	100391814	Nonsense_Mutation	SNP	G	T	6	383	c.8059G>T	c.(8059-8061)GAG>TAG	p.E2687*
Pat_06	Pre-Treatment	ACHE	43	37	7	100490114	100490114	Missense_Mutation	SNP	G	A	5	228	c.1394C>T	c.(1393-1395)GCT>GTT	p.A465V
Pat_06	Pre-Treatment	MUC17	140453	37	7	100681244	100681244	Missense_Mutation	SNP	A	G	7	877	c.6547A>G	c.(6547-6549)ACA>GCA	p.T2183A
Pat_06	Pre-Treatment	MUC17	140453	37	7	100681421	100681421	Missense_Mutation	SNP	G	A	10	813	c.6724G>A	c.(6724-6726)GCA>ACA	p.A2242T
Pat_06	Pre-Treatment	C7orf52	375607	37	7	100815749	100815749	Missense_Mutation	SNP	T	C	3	97	c.721A>G	c.(721-723)ACC>GCC	p.T241A
Pat_06	Pre-Treatment	RNF133	168433	37	7	122337948	122337948	Missense_Mutation	SNP	G	T	6	710	c.1025C>A	c.(1024-1026)CCT>CAT	p.P342H
Pat_06	Pre-Treatment	RBM28	55131	37	7	127964611	127964611	Splice_Site	SNP	C	T	6	789	c.1339_splice	c.e12+1	p.L447_splice
Pat_06	Pre-Treatment	CPA1	1357	37	7	130023248	130023248	Missense_Mutation	SNP	G	A	5	185	c.500G>A	c.(499-501)AGT>AAT	p.S167N
Pat_06	Pre-Treatment	PLXNA4	91584	37	7	132192500	132192500	Missense_Mutation	SNP	G	A	6	335	c.953C>T	c.(952-954)GCG>GTG	p.A318V
Pat_06	Pre-Treatment	AKR1B1	231	37	7	134135558	134135558	Missense_Mutation	SNP	G	C	3	218	c.331C>G	c.(331-333)CAC>GAC	p.H111D
Pat_06	Pre-Treatment	BRAF	673	37	7	140453136	140453136	Missense_Mutation	SNP	A	T	200	393	c.1799T>A	c.(1798-1800)GTG>GAG	p.V600E
Pat_06	Pre-Treatment	MGAM	8972	37	7	141759717	141759717	Missense_Mutation	SNP	A	G	3	146	c.4010A>G	c.(4009-4011)GAT>GGT	p.D1337G
Pat_06	Pre-Treatment	EPHB6	2051	37	7	142566372	142566372	Missense_Mutation	SNP	G	A	3	68	c.2161G>A	c.(2161-2163)GCA>ACA	p.A721T
Pat_06	Pre-Treatment	CASP2	835	37	7	142991775	142991775	Missense_Mutation	SNP	G	A	5	470	c.656G>A	c.(655-657)CGC>CAC	p.R219H
Pat_06	Pre-Treatment	OR2A14	135941	37	7	143826560	143826560	Missense_Mutation	SNP	T	C	4	654	c.355T>C	c.(355-357)TAT>CAT	p.Y119H
Pat_06	Pre-Treatment	ZNF786	136051	37	7	148768900	148768900	Missense_Mutation	SNP	C	T	3	81	c.964G>A	c.(964-966)GGG>AGG	p.G322R
Pat_06	Pre-Treatment	KRBA1	84626	37	7	149418621	149418621	Missense_Mutation	SNP	C	T	5	120	c.461C>T	c.(460-462)CCC>CTC	p.P154L
Pat_06	Pre-Treatment	SSPO	23145	37	7	149492356	149492356	Missense_Mutation	SNP	C	T	5	440	c.6245C>T	c.(6244-6246)TCG>TTG	p.S2082L
Pat_06	Pre-Treatment	SSPO	23145	37	7	149500048	149500048	Nonsense_Mutation	SNP	G	A	3	56	c.7674G>A	c.(7672-7674)TGG>TGA	p.W2558*
Pat_06	Pre-Treatment	REPIN1	29803	37	7	150068614	150068614	Missense_Mutation	SNP	G	C	3	148	c.284G>C	c.(283-285)CGC>CCC	p.R95P
Pat_06	Pre-Treatment	ABCF2	10061	37	7	150915205	150915205	Missense_Mutation	SNP	C	T	5	668	c.1300G>A	c.(1300-1302)GCA>ACA	p.A434T
Pat_06	Pre-Treatment	HTR5A	3361	37	7	154862859	154862859	Missense_Mutation	SNP	G	A	4	234	c.250G>A	c.(250-252)GTC>ATC	p.V84I
Pat_06	Pre-Treatment	RBM33	155435	37	7	155473430	155473430	Missense_Mutation	SNP	C	G	3	136	c.395C>G	c.(394-396)TCT>TGT	p.S132C
Pat_06	Pre-Treatment	RBM33	155435	37	7	155556600	155556600	Missense_Mutation	SNP	C	T	3	67	c.3074C>T	c.(3073-3075)ACG>ATG	p.T1025M
Pat_06	Pre-Treatment	CSMD1	64478	37	8	2944633	2944633	Missense_Mutation	SNP	G	A	4	299	c.7463C>T	c.(7462-7464)ACG>ATG	p.T2488M
Pat_06	Pre-Treatment	RP1L1	94137	37	8	10480360	10480360	Missense_Mutation	SNP	G	A	3	58	c.352C>T	c.(352-354)CGG>TGG	p.R118W
Pat_06	Pre-Treatment	EGR3	1960	37	8	22548122	22548122	Missense_Mutation	SNP	G	A	5	391	c.1028C>T	c.(1027-1029)GCG>GTG	p.A343V
Pat_06	Pre-Treatment	TNFRSF10C	8794	37	8	22974315	22974315	Missense_Mutation	SNP	A	T	6	568	c.551A>T	c.(550-552)AAC>ATC	p.N184I
Pat_06	Pre-Treatment	ADAM7	8756	37	8	24300000	24300000	Nonsense_Mutation	SNP	G	T	8	823	c.67G>T	c.(67-69)GGA>TGA	p.G23*
Pat_06	Pre-Treatment	PTK2B	2185	37	8	27297910	27297910	Missense_Mutation	SNP	A	G	4	573	c.1991A>G	c.(1990-1992)TAC>TGC	p.Y664C
Pat_06	Pre-Treatment	PLEKHA2	59339	37	8	38808387	38808387	Missense_Mutation	SNP	T	C	3	167	c.365T>C	c.(364-366)CTA>CCA	p.L122P
Pat_06	Pre-Treatment	PLAT	5327	37	8	42048920	42048920	Nonsense_Mutation	SNP	G	A	4	421	c.85C>T	c.(85-87)CGA>TGA	p.R29*
Pat_06	Pre-Treatment	PRKDC	5591	37	8	48690333	48690333	Missense_Mutation	SNP	G	A	8	684	c.11956C>T	c.(11956-11958)CAC>TAC	p.H3986Y
Pat_06	Pre-Treatment	SNTG1	54212	37	8	51465674	51465674	Missense_Mutation	SNP	G	C	4	449	c.745G>C	c.(745-747)GCT>CCT	p.A249P
Pat_06	Pre-Treatment	PXDNL	137902	37	8	52321132	52321132	Missense_Mutation	SNP	G	C	3	98	c.3052C>G	c.(3052-3054)CTG>GTG	p.L1018V
Pat_06	Pre-Treatment	TGS1	96764	37	8	56698341	56698341	Missense_Mutation	SNP	G	A	6	317	c.230G>A	c.(229-231)AGC>AAC	p.S77N
Pat_06	Pre-Treatment	KCNB2	9312	37	8	73849007	73849007	Missense_Mutation	SNP	G	A	5	579	c.1417G>A	c.(1417-1419)GGA>AGA	p.G473R

Pat_06	Pre-Treatment	ZFHX4	79776	37	8	77766927	77766927	Missense_Mutation	SNP	C	G	3	124	c.7635C>G	c.(7633-7635)TGC>TGG	p.C2545W
Pat_06	Pre-Treatment	ZFHX4	79776	37	8	77767580	77767580	Missense_Mutation	SNP	C	T	4	149	c.8288C>T	c.(8287-8289)ACG>ATG	p.T2763M
Pat_06	Pre-Treatment	CA13	377677	37	8	86193498	86193498	Missense_Mutation	SNP	G	A	6	826	c.709G>A	c.(709-711)GAA>AAA	p.E237K
Pat_06	Pre-Treatment	SLC26A7	115111	37	8	92364117	92364117	Splice_Site	SNP	T	C	71	476	c.1218_splice	c.e11+2	p.M406_splice
Pat_06	Pre-Treatment	INTS8	55656	37	8	95844352	95844352	Missense_Mutation	SNP	G	C	4	383	c.703G>C	c.(703-705)GAG>CAG	p.E235Q
Pat_06	Pre-Treatment	KCNS2	3788	37	8	99441018	99441018	Missense_Mutation	SNP	T	C	4	522	c.811T>C	c.(811-813)TTT>CTT	p.F271L
Pat_06	Pre-Treatment	CSMD3	114788	37	8	113697695	113697695	Nonsense_Mutation	SNP	G	A	5	713	c.2422C>T	c.(2422-2424)CGA>TGA	p.R808*
Pat_06	Pre-Treatment	FAM91A1	157769	37	8	124810390	124810390	Missense_Mutation	SNP	G	A	6	687	c.1472G>A	c.(1471-1473)AGC>AAC	p.S491N
Pat_06	Pre-Treatment	RNF139	11236	37	8	125487504	125487504	Missense_Mutation	SNP	G	A	5	686	c.154G>A	c.(154-156)GTG>ATG	p.V52M
Pat_06	Pre-Treatment	MYC	4609	37	8	128750830	128750830	Missense_Mutation	SNP	G	A	4	286	c.322G>A	c.(322-324)GGA>AGA	p.G108R
Pat_06	Pre-Treatment	COL22A1	169044	37	8	139890167	139890167	Missense_Mutation	SNP	C	T	3	45	c.484G>A	c.(484-486)GCG>ACG	p.A162T
Pat_06	Pre-Treatment	TRAPPC9	83696	37	8	141370260	141370260	Missense_Mutation	SNP	G	A	5	280	c.1384C>T	c.(1384-1386)CGT>TGT	p.R462C
Pat_06	Pre-Treatment	TRAPPC9	83696	37	8	141461321	141461321	Missense_Mutation	SNP	C	G	3	293	c.152G>C	c.(151-153)CGA>CCA	p.R51P
Pat_06	Pre-Treatment	PLEC	5339	37	8	145009217	145009217	Missense_Mutation	SNP	G	A	5	669	c.1198C>T	c.(1198-1200)CCC>TCC	p.P400S
Pat_06	Pre-Treatment	GPR172A	79581	37	8	145583616	145583616	Missense_Mutation	SNP	C	A	6	697	c.464C>A	c.(463-465)GCC>GAC	p.A155D
Pat_06	Pre-Treatment	NFKBIL2	4796	37	8	145660443	145660443	Missense_Mutation	SNP	G	A	3	51	c.2963C>T	c.(2962-2964)GCC>GTC	p.A988V
Pat_06	Pre-Treatment	ZNF34	80778	37	8	145998713	145998713	Missense_Mutation	SNP	G	A	4	409	c.1621C>T	c.(1621-1623)CGG>TGG	p.R541W
Pat_06	Pre-Treatment	ZNF16	7564	37	8	146157752	146157752	Missense_Mutation	SNP	T	C	88	181	c.421A>G	c.(421-423)ATG>GTG	p.M141V
Pat_06	Pre-Treatment	DMRT1	1761	37	9	841892	841892	Missense_Mutation	SNP	C	G	3	86	c.54C>G	c.(52-54)CAC>CAG	p.H18Q
Pat_06	Pre-Treatment	TMEM215	401498	37	9	32784414	32784414	Missense_Mutation	SNP	G	A	5	449	c.233G>A	c.(232-234)CGC>CAC	p.R78H
Pat_06	Pre-Treatment	DNAI1	27019	37	9	34485483	34485483	Missense_Mutation	SNP	G	A	4	278	c.229G>A	c.(229-231)GCA>ACA	p.A77T
Pat_06	Pre-Treatment	KIAA1045	23349	37	9	34971302	34971302	Missense_Mutation	SNP	G	A	5	694	c.7G>A	c.(7-9)GTG>ATG	p.V3M
Pat_06	Pre-Treatment	PIGO	84720	37	9	35093420	35093420	Missense_Mutation	SNP	C	G	3	230	c.937G>C	c.(937-939)GAG>CAG	p.E313Q
Pat_06	Pre-Treatment	UNC13B	10497	37	9	35375125	35375125	Nonsense_Mutation	SNP	C	A	6	810	c.1295C>A	c.(1294-1296)TCA>TAA	p.S432*
Pat_06	Pre-Treatment	UNC13B	10497	37	9	35381166	35381166	Missense_Mutation	SNP	A	G	4	300	c.2198A>G	c.(2197-2199)GAG>GGG	p.E733G
Pat_06	Pre-Treatment	TLN1	7094	37	9	35698170	35698170	Splice_Site	SNP	C	A	4	218	c.7372_splice	c.e56-1	p.A2458_splice
Pat_06	Pre-Treatment	GNE	10020	37	9	36246441	36246441	Missense_Mutation	SNP	A	G	4	519	c.203T>C	c.(202-204)ATT>ACT	p.I68T
Pat_06	Pre-Treatment	RORB	6096	37	9	77257530	77257530	Missense_Mutation	SNP	G	A	5	347	c.469G>A	c.(469-471)GTC>ATC	p.V157I
Pat_06	Pre-Treatment	TLE4	7091	37	9	82242364	82242364	Splice_Site	SNP	G	A	5	527	c.369_splice	c.e6+1	p.G123_splice
Pat_06	Pre-Treatment	ZCCHC6	79670	37	9	88940263	88940263	Missense_Mutation	SNP	C	T	5	646	c.1775G>A	c.(1774-1776)CGC>CAC	p.R592H
Pat_06	Pre-Treatment	ECM2	1842	37	9	95277041	95277041	Missense_Mutation	SNP	G	A	4	344	c.926C>T	c.(925-927)CCT>CTT	p.P309L
Pat_06	Pre-Treatment	HABP4	22927	37	9	99227656	99227656	Missense_Mutation	SNP	G	A	5	693	c.550G>A	c.(550-552)GGA>AGA	p.G184R
Pat_06	Pre-Treatment	NR4A3	8013	37	9	102590767	102590767	Missense_Mutation	SNP	T	C	5	433	c.443T>C	c.(442-444)TTC>TCC	p.F148S
Pat_06	Pre-Treatment	ACTL7A	10881	37	9	111625278	111625278	Missense_Mutation	SNP	G	T	4	375	c.676G>T	c.(676-678)GTG>TTG	p.V226L
Pat_06	Pre-Treatment	KIAA0368	23392	37	9	114204596	114204596	Missense_Mutation	SNP	G	T	4	113	c.913C>A	c.(913-915)CAG>AAG	p.Q305K
Pat_06	Pre-Treatment	KIAA1958	158405	37	9	115336949	115336949	Missense_Mutation	SNP	G	T	6	551	c.589G>T	c.(589-591)GAT>TAT	p.D197Y
Pat_06	Pre-Treatment	GSN	2934	37	9	124073053	124073053	Missense_Mutation	SNP	G	A	4	238	c.596G>A	c.(595-597)CGT>CAT	p.R199H
Pat_06	Pre-Treatment	DENND1A	57706	37	9	126202749	126202749	Missense_Mutation	SNP	C	T	6	366	c.1378G>A	c.(1378-1380)GCC>ACC	p.A460T
Pat_06	Pre-Treatment	MAPKAP1	79109	37	9	128419995	128419995	Missense_Mutation	SNP	G	A	5	478	c.433C>T	c.(433-435)CGC>TGC	p.R145C
Pat_06	Pre-Treatment	FAM129B	64855	37	9	130286119	130286119	Missense_Mutation	SNP	G	A	5	520	c.428C>T	c.(427-429)ACG>ATG	p.T143M
Pat_06	Pre-Treatment	DNM1	1759	37	9	130982527	130982527	Missense_Mutation	SNP	G	T	7	716	c.756G>T	c.(754-756)TTG>TTT	p.L252F
Pat_06	Pre-Treatment	PRDM12	59335	37	9	133540159	133540159	Missense_Mutation	SNP	G	A	3	49	c.119G>A	c.(118-120)CGC>CAC	p.R40H
Pat_06	Pre-Treatment	LAMC3	10319	37	9	133920958	133920958	Missense_Mutation	SNP	G	A	5	282	c.1430G>A	c.(1429-1431)TGC>TAC	p.C477Y
Pat_06	Pre-Treatment	MED27	9442	37	9	134769315	134769315	Missense_Mutation	SNP	A	T	4	425	c.638T>A	c.(637-639)ATA>AAA	p.I213K
Pat_06	Pre-Treatment	MED22	6837	37	9	136208477	136208477	Missense_Mutation	SNP	C	T	4	101	c.481G>A	c.(481-483)GAC>AAC	p.D161N
Pat_06	Pre-Treatment	NACC2	138151	37	9	138908200	138908200	Missense_Mutation	SNP	G	A	6	535	c.962C>T	c.(961-963)CCT>CTT	p.P321L
Pat_06	Pre-Treatment	QSOX2	169714	37	9	139115638	139115638	Missense_Mutation	SNP	C	G	3	176	c.646G>C	c.(646-648)GAA>CAA	p.E216Q

Pat_06	Pre-Treatment	PMPCA	23203	37	9	139313544	139313544	Missense_Mutation	SNP	G	A	5	512	c.1249G>A	c.(1249-1251)GGA>AGA	p.G417R
Pat_06	Pre-Treatment	PHPT1	29085	37	9	139745228	139745228	Missense_Mutation	SNP	G	A	5	337	c.307G>A	c.(307-309)GCC>ACC	p.A103T
Pat_06	Pre-Treatment	EXD3	54932	37	9	140201553	140201553	Missense_Mutation	SNP	C	A	3	71	c.2480G>T	c.(2479-2481)CGG>CTG	p.R827L
Pat_06	Pre-Treatment	EHMT1	79813	37	9	140712582	140712582	Missense_Mutation	SNP	G	A	5	407	c.3532G>A	c.(3532-3534)GAC>AAC	p.D1178N
Pat_06	Pre-Treatment	CACNA1B	774	37	9	140953156	140953156	Missense_Mutation	SNP	G	A	3	62	c.4444G>A	c.(4444-4446)GCC>ACC	p.A1482T
Pat_06	Pre-Treatment	PPP2R3B	28227	37	X	306382	306382	Missense_Mutation	SNP	G	A	5	529	c.905C>T	c.(904-906)GCG>GTG	p.A302V
Pat_06	Pre-Treatment	ARSD	414	37	X	2827952	2827952	Missense_Mutation	SNP	G	A	5	252	c.1204C>T	c.(1204-1206)CTC>TTC	p.L402F
Pat_06	Pre-Treatment	ARSH	347527	37	X	2928111	2928111	Missense_Mutation	SNP	C	A	5	538	c.133C>A	c.(133-135)CTT>ATT	p.L45I
Pat_06	Pre-Treatment	HDHD1A	8226	37	X	6995345	6995345	Missense_Mutation	SNP	G	C	3	133	c.426C>G	c.(424-426)GAC>GAG	p.D142E
Pat_06	Pre-Treatment	SCML1	6322	37	X	17768311	17768311	Missense_Mutation	SNP	G	A	6	682	c.601G>A	c.(601-603)GCA>ACA	p.A201T
Pat_06	Pre-Treatment	CDKL5	6792	37	X	18622375	18622375	Missense_Mutation	SNP	G	A	6	648	c.1331G>A	c.(1330-1332)CGC>CAC	p.R444H
Pat_06	Pre-Treatment	MAP3K15	389840	37	X	19413274	19413274	Missense_Mutation	SNP	G	A	6	710	c.544C>T	c.(544-546)CGC>TGC	p.R182C
Pat_06	Pre-Treatment	KLHL34	257240	37	X	21675236	21675236	Missense_Mutation	SNP	C	T	4	107	c.671G>A	c.(670-672)CGC>CAC	p.R224H
Pat_06	Pre-Treatment	CHST7	56548	37	X	46433733	46433733	Nonsense_Mutation	SNP	C	T	4	269	c.367C>T	c.(367-369)CAG>TAG	p.Q123*
Pat_06	Pre-Treatment	ZNF182	7569	37	X	47842367	47842367	Missense_Mutation	SNP	G	C	4	528	c.271C>G	c.(271-273)CCA>GCA	p.P91A
Pat_06	Pre-Treatment	HDAC6	10013	37	X	48673420	48673420	Missense_Mutation	SNP	A	G	3	103	c.1111A>G	c.(1111-1113)ATG>GTG	p.M371V
Pat_06	Pre-Treatment	ERAS	3266	37	X	48688086	48688086	Missense_Mutation	SNP	C	T	3	55	c.553C>T	c.(553-555)CGG>TGG	p.R185W
Pat_06	Pre-Treatment	TIMM17B	10245	37	X	48751207	48751207	Missense_Mutation	SNP	A	G	3	154	c.406T>C	c.(406-408)TAC>CAC	p.Y136H
Pat_06	Pre-Treatment	PQBP1	10084	37	X	48760267	48760267	Missense_Mutation	SNP	C	G	3	57	c.704C>G	c.(703-705)GCA>GGA	p.A235G
Pat_06	Pre-Treatment	KCND1	3750	37	X	48822652	48822652	Missense_Mutation	SNP	C	A	3	43	c.1528G>T	c.(1528-1530)GGC>TGC	p.G510C
Pat_06	Pre-Treatment	GRIPAP1	56850	37	X	48831634	48831634	Missense_Mutation	SNP	C	T	3	108	c.2366G>A	c.(2365-2367)CGG>CAG	p.R789Q
Pat_06	Pre-Treatment	WDR45	11152	37	X	48935361	48935361	Missense_Mutation	SNP	C	T	3	62	c.176G>A	c.(175-177)CGC>CAC	p.R59H
Pat_06	Pre-Treatment	GPKOW	27238	37	X	48979909	48979909	Missense_Mutation	SNP	C	T	4	136	c.164G>A	c.(163-165)AGG>AAG	p.R55K
Pat_06	Pre-Treatment	NUDT10	170685	37	X	51075840	51075840	Missense_Mutation	SNP	C	T	6	257	c.23C>T	c.(22-24)ACA>ATA	p.T8I
Pat_06	Pre-Treatment	GNL3L	54552	37	X	54578727	54578727	Missense_Mutation	SNP	G	A	5	776	c.1184G>A	c.(1183-1185)GGG>GAG	p.G395E
Pat_06	Pre-Treatment	ZXDB	158586	37	X	57620786	57620786	Nonsense_Mutation	SNP	G	T	7	720	c.2305G>T	c.(2305-2307)GGA>TGA	p.G769*
Pat_06	Pre-Treatment	FAM123B	139285	37	X	63412575	63412575	Missense_Mutation	SNP	C	G	3	129	c.592G>C	c.(592-594)GAG>CAG	p.E198Q
Pat_06	Pre-Treatment	OPHN1	4983	37	X	67412767	67412767	Missense_Mutation	SNP	A	G	5	501	c.1270T>C	c.(1270-1272)TTT>CTT	p.F424L
Pat_06	Pre-Treatment	MED12	9968	37	X	70338611	70338611	Missense_Mutation	SNP	G	A	4	69	c.7G>A	c.(7-9)GCC>ACC	p.A3T
Pat_06	Pre-Treatment	ACRC	93953	37	X	70823916	70823916	Missense_Mutation	SNP	A	T	6	354	c.789A>T	c.(787-789)GAA>GAT	p.E263D
Pat_06	Pre-Treatment	ACRC	93953	37	X	70823918	70823918	Missense_Mutation	SNP	C	T	7	359	c.791C>T	c.(790-792)GCT>GTT	p.A264V
Pat_06	Pre-Treatment	CXCR3	2833	37	X	70837057	70837057	Missense_Mutation	SNP	C	G	3	66	c.265G>C	c.(265-267)GAC>CAC	p.D89H
Pat_06	Pre-Treatment	SATL1	340562	37	X	84362573	84362573	Missense_Mutation	SNP	G	T	5	599	c.1402C>A	c.(1402-1404)CAA>AAA	p.Q468K
Pat_06	Pre-Treatment	DACH2	117154	37	X	85969692	85969692	Missense_Mutation	SNP	C	A	7	761	c.1073C>A	c.(1072-1074)CCA>CAA	p.P358Q
Pat_06	Pre-Treatment	GUCY2F	2986	37	X	108673592	108673592	Nonsense_Mutation	SNP	C	A	6	812	c.1735G>T	c.(1735-1737)GGA>TGA	p.G579*
Pat_06	Pre-Treatment	ACTRT1	139741	37	X	127185080	127185080	Missense_Mutation	SNP	G	C	6	836	c.1106C>G	c.(1105-1107)TCT>TGT	p.S369C
Pat_06	Pre-Treatment	ZNF280C	55609	37	X	129362974	129362974	Missense_Mutation	SNP	G	A	6	855	c.1124C>T	c.(1123-1125)ACA>ATA	p.T375I
Pat_06	Pre-Treatment	RBMX2	51634	37	X	129543337	129543337	Missense_Mutation	SNP	G	A	6	804	c.280G>A	c.(280-282)GTC>ATC	p.V94I
Pat_06	Pre-Treatment	IGSF1	3547	37	X	130419204	130419204	Missense_Mutation	SNP	G	A	5	633	c.616C>T	c.(616-618)CTC>TTC	p.L206F
Pat_06	Pre-Treatment	SPANXN2	494119	37	X	142795388	142795388	Missense_Mutation	SNP	T	C	5	872	c.290A>G	c.(289-291)CAG>CGG	p.Q97R
Pat_06	Pre-Treatment	PDZD4	57595	37	X	153069787	153069787	Missense_Mutation	SNP	G	A	4	226	c.1331C>T	c.(1330-1332)GCG>GTG	p.A444V
Pat_06	Pre-Treatment	FLNA	2316	37	X	153588658	153588658	Missense_Mutation	SNP	C	T	80	127	c.3505G>A	c.(3505-3507)GGG>AGG	p.G1169R
Pat_06	Pre-Treatment	FLNA	2316	37	X	153590869	153590869	Missense_Mutation	SNP	G	A	6	767	c.2482C>T	c.(2482-2484)CGC>TGC	p.R828C
Pat_06	Pre-Treatment	BRCC3	79184	37	X	154344379	154344379	Missense_Mutation	SNP	T	A	6	222	c.671T>A	c.(670-672)ATC>AAC	p.I224N
Pat_06	Post-Resistance	CHD5	26038	37	1	6188230	6188230	Missense_Mutation	SNP	G	A	4	351	c.3779C>T	c.(3778-3780)GCG>GTG	p.A1260V
Pat_06	Post-Resistance	PER3	8863	37	1	7880659	7880659	Missense_Mutation	SNP	G	A	4	281	c.1892G>A	c.(1891-1893)GGT>GAT	p.G631D
Pat_06	Post-Resistance	PER3	8863	37	1	7887738	7887738	Missense_Mutation	SNP	G	A	5	443	c.2725G>A	c.(2725-2727)GCA>ACA	p.A909T

Pat_06	Post-Resistance	SLC25A33	84275	37	1	9642420	9642420	Missense_Mutation	SNP	G	C	38	176	c.827G>C	c.(826-828)CGC>CCC	p.R276P
Pat_06	Post-Resistance	RBP7	116362	37	1	10067748	10067748	Missense_Mutation	SNP	T	G	3	167	c.194T>G	c.(193-195)TTT>TGT	p.F65C
Pat_06	Post-Resistance	PLOD1	5351	37	1	12023666	12023666	Missense_Mutation	SNP	G	A	3	50	c.1175G>A	c.(1174-1176)AGC>AAC	p.S392N
Pat_06	Post-Resistance	VPS13D	55187	37	1	12331126	12331126	Missense_Mutation	SNP	A	G	5	380	c.2048A>G	c.(2047-2049)CAG>CGG	p.Q683R
Pat_06	Post-Resistance	MST1P9	11223	37	1	17086103	17086103	Missense_Mutation	SNP	G	C	3	238	c.794C>G	c.(793-795)GCC>GGC	p.A265G
Pat_06	Post-Resistance	HP1BP3	50809	37	1	21071493	21071493	Nonsense_Mutation	SNP	G	A	4	254	c.1459C>T	c.(1459-1461)CAG>TAG	p.Q487*
Pat_06	Post-Resistance	E2F2	1870	37	1	23836582	23836582	Missense_Mutation	SNP	C	G	3	62	c.1104G>C	c.(1102-1104)TTG>TTC	p.L368F
Pat_06	Post-Resistance	RHCE	6006	37	1	25747287	25747287	Translation_Start_Site	SNP	G	A	5	138	c.-9C>T	c.(-11--7)GACGG>GATGG	
Pat_06	Post-Resistance	SEPN1	57190	37	1	26140653	26140653	Missense_Mutation	SNP	T	C	3	182	c.1586T>C	c.(1585-1587)CTG>CCG	p.L529P
Pat_06	Post-Resistance	PDIK1L	149420	37	1	26440781	26440781	Splice_Site	SNP	A	G	3	76	c.-16_splice	c.e2-2	
Pat_06	Post-Resistance	AHDC1	27245	37	1	27877945	27877945	Missense_Mutation	SNP	C	G	3	196	c.682G>C	c.(682-684)GAG>CAG	p.E228Q
Pat_06	Post-Resistance	BAI2	576	37	1	32193197	32193197	Missense_Mutation	SNP	T	C	3	81	c.4582A>G	c.(4582-4584)AGC>GGC	p.S1528G
Pat_06	Post-Resistance	EIF2C4	192670	37	1	36297718	36297718	Missense_Mutation	SNP	G	A	171	536	c.1177G>A	c.(1177-1179)GTC>ATC	p.V393I
Pat_06	Post-Resistance	ADPRHL2	54936	37	1	36557679	36557679	Missense_Mutation	SNP	G	A	5	396	c.685G>A	c.(685-687)GTC>ATC	p.V229I
Pat_06	Post-Resistance	ZC3H12A	80149	37	1	37948734	37948734	Missense_Mutation	SNP	G	C	3	119	c.1322G>C	c.(1321-1323)GGC>GCC	p.G441A
Pat_06	Post-Resistance	MACF1	23499	37	1	39782885	39782885	Splice_Site	SNP	G	A	3	115	c.3604_splice	c.e30-1	p.H1202_splice
Pat_06	Post-Resistance	MACF1	23499	37	1	39934318	39934318	Missense_Mutation	SNP	G	A	5	350	c.17132G>A	c.(17131-17133)CGT>CAT	p.R5711H
Pat_06	Post-Resistance	FOXJ3	22887	37	1	42647587	42647587	Splice_Site	SNP	C	T	4	279	c.1753_splice	c.e14+1	p.G585_splice
Pat_06	Post-Resistance	RIMKLA	284716	37	1	42880406	42880406	Missense_Mutation	SNP	G	A	5	298	c.937G>A	c.(937-939)GTC>ATC	p.V313I
Pat_06	Post-Resistance	WDR65	149465	37	1	43663269	43663269	Missense_Mutation	SNP	G	A	5	769	c.1168G>A	c.(1168-1170)GCA>ACA	p.A390T
Pat_06	Post-Resistance	KIAA0467	23334	37	1	43893032	43893032	Missense_Mutation	SNP	G	A	4	344	c.817G>A	c.(817-819)GCT>ACT	p.A273T
Pat_06	Post-Resistance	KIAA0467	23334	37	1	43897463	43897463	Missense_Mutation	SNP	G	A	7	720	c.2468G>A	c.(2467-2469)CGC>CAC	p.R823H
Pat_06	Post-Resistance	KIF2C	11004	37	1	45225987	45225987	Missense_Mutation	SNP	C	A	5	316	c.1403C>A	c.(1402-1404)TCC>TAC	p.S468Y
Pat_06	Post-Resistance	CYP4X1	260293	37	1	47501500	47501500	Missense_Mutation	SNP	G	A	4	414	c.515G>A	c.(514-516)AGC>AAC	p.S172N
Pat_06	Post-Resistance	PRKAA2	5563	37	1	57159461	57159461	Missense_Mutation	SNP	G	T	6	634	c.499G>T	c.(499-501)GGT>TGT	p.G167C
Pat_06	Post-Resistance	FGGY	55277	37	1	59787270	59787270	Missense_Mutation	SNP	G	A	4	244	c.49G>A	c.(49-51)GTT>ATT	p.V17I
Pat_06	Post-Resistance	LRRC40	55631	37	1	70671183	70671183	Missense_Mutation	SNP	G	C	3	204	c.41C>G	c.(40-42)GCT>GGT	p.A14G
Pat_06	Post-Resistance	CLCA1	1179	37	1	86960032	86960032	Missense_Mutation	SNP	C	T	43	128	c.1843C>T	c.(1843-1845)CGC>TGC	p.R615C
Pat_06	Post-Resistance	ZNF326	284695	37	1	90472996	90472996	Missense_Mutation	SNP	G	C	5	829	c.302G>C	c.(301-303)AGC>ACC	p.S101T
Pat_06	Post-Resistance	HSD3B2	3284	37	1	119985587	119985587	Missense_Mutation	SNP	G	A	7	412	c.394G>A	c.(394-396)GTC>ATC	p.V132I
Pat_06	Post-Resistance	HFE2	148738	37	1	145416929	145416929	Missense_Mutation	SNP	T	C	4	450	c.1274T>C	c.(1273-1275)ATT>ACT	p.I425T
Pat_06	Post-Resistance	ITGA10	8515	37	1	145539681	145539681	Splice_Site	SNP	A	G	3	159	c.3115_splice	c.e27-2	p.N1039_splice
Pat_06	Post-Resistance	FLG	2312	37	1	152283940	152283940	Missense_Mutation	SNP	C	G	9	696	c.3422G>C	c.(3421-3423)AGA>ACA	p.R1141T
Pat_06	Post-Resistance	THBS3	7059	37	1	155168388	155168388	Missense_Mutation	SNP	C	A	7	527	c.1886G>T	c.(1885-1887)GGG>GTG	p.G629V
Pat_06	Post-Resistance	FCRL5	83416	37	1	157516756	157516756	Missense_Mutation	SNP	G	T	142	360	c.284C>A	c.(283-285)CCT>CAT	p.P95H
Pat_06	Post-Resistance	CD5L	922	37	1	157805934	157805934	Nonsense_Mutation	SNP	C	A	6	325	c.67G>T	c.(67-69)GGA>TGA	p.G23*
Pat_06	Post-Resistance	KCNJ9	3765	37	1	160054329	160054329	Missense_Mutation	SNP	C	T	4	116	c.509C>T	c.(508-510)ACG>ATG	p.T170M
Pat_06	Post-Resistance	CASQ1	844	37	1	160160635	160160635	Missense_Mutation	SNP	G	A	5	510	c.94G>A	c.(94-96)GTA>ATA	p.V32I
Pat_06	Post-Resistance	COPA	1314	37	1	160265619	160265619	Missense_Mutation	SNP	G	A	6	570	c.2383C>T	c.(2383-2385)CTC>TTC	p.L795F
Pat_06	Post-Resistance	F5	2153	37	1	169529941	169529941	Missense_Mutation	SNP	C	A	6	784	c.437G>T	c.(436-438)CGA>CTA	p.R146L
Pat_06	Post-Resistance	BAT2L2	23215	37	1	171548518	171548518	Missense_Mutation	SNP	C	A	5	270	c.7179C>A	c.(7177-7179)GAC>GAA	p.D2393E
Pat_06	Post-Resistance	KLHL20	27252	37	1	173722401	173722401	Missense_Mutation	SNP	G	A	6	320	c.806G>A	c.(805-807)GGC>GAC	p.G269D
Pat_06	Post-Resistance	CEP350	9857	37	1	180080277	180080277	Missense_Mutation	SNP	G	A	4	266	c.9335G>A	c.(9334-9336)GGG>GAG	p.G3112E
Pat_06	Post-Resistance	CACNA1S	779	37	1	201058518	201058518	Missense_Mutation	SNP	G	C	3	219	c.768C>G	c.(766-768)ATC>ATG	p.I256M
Pat_06	Post-Resistance	MYOG	4656	37	1	203053852	203053852	Missense_Mutation	SNP	G	A	3	120	c.476C>T	c.(475-477)CCC>CTC	p.P159L
Pat_06	Post-Resistance	SERTAD4	56256	37	1	210415389	210415389	Missense_Mutation	SNP	A	G	3	224	c.778A>G	c.(778-780)ATA>GTA	p.I260V
Pat_06	Post-Resistance	TMEM206	55248	37	1	212558701	212558701	Missense_Mutation	SNP	G	A	6	547	c.410C>T	c.(409-411)CCT>CTT	p.P137L

Pat_06	Post-Resistance	ITPKB	3707	37	1	226923287	226923287	Missense_Mutation	SNP	G	A	6	771	c.1873C>T	c.(1873-1875)CGC>TGC	p.R625C
Pat_06	Post-Resistance	ZNF678	339500	37	1	227842427	227842427	Missense_Mutation	SNP	G	A	7	455	c.476G>A	c.(475-477)GGC>GAC	p.G159D
Pat_06	Post-Resistance	OBSCN	84033	37	1	228466587	228466587	Missense_Mutation	SNP	G	A	5	348	c.7057G>A	c.(7057-7059)GCA>ACA	p.A2353T
Pat_06	Post-Resistance	TARBP1	6894	37	1	234569236	234569236	Missense_Mutation	SNP	T	C	5	429	c.2314A>G	c.(2314-2316)AGG>GGG	p.R772G
Pat_06	Post-Resistance	TBCE	6905	37	1	235582831	235582831	Missense_Mutation	SNP	G	A	4	416	c.415G>A	c.(415-417)GTA>ATA	p.V139I
Pat_06	Post-Resistance	KIF26B	55083	37	1	245861488	245861488	Missense_Mutation	SNP	G	A	4	209	c.5905G>A	c.(5905-5907)GTC>ATC	p.V1969I
Pat_06	Post-Resistance	OR2L8	391190	37	1	248112794	248112794	Missense_Mutation	SNP	G	C	4	237	c.635G>C	c.(634-636)GGT>GCT	p.G212A
Pat_06	Post-Resistance	OR2G6	391211	37	1	248685330	248685330	Missense_Mutation	SNP	G	A	4	309	c.383G>A	c.(382-384)CGG>CAG	p.R128Q
Pat_06	Post-Resistance	SEPHS1	22929	37	10	13371732	13371732	Missense_Mutation	SNP	T	C	3	95	c.617A>G	c.(616-618)CAG>CGG	p.Q206R
Pat_06	Post-Resistance	FRMD4A	55691	37	10	13699067	13699067	Missense_Mutation	SNP	A	G	3	156	c.2522T>C	c.(2521-2523)ATC>ACC	p.I841T
Pat_06	Post-Resistance	ANKRD30A	91074	37	10	37430688	37430688	Missense_Mutation	SNP	C	T	6	343	c.695C>T	c.(694-696)GCG>GTG	p.A232V
Pat_06	Post-Resistance	ANKRD30A	91074	37	10	37431050	37431050	Missense_Mutation	SNP	G	C	7	272	c.1057G>C	c.(1057-1059)GCA>CCA	p.A353P
Pat_06	Post-Resistance	HSD17B7P2	158160	37	10	38654432	38654432	Missense_Mutation	SNP	A	G	4	345	c.524A>G	c.(523-525)AAT>AGT	p.N175S
Pat_06	Post-Resistance	ALOX5	240	37	10	45877943	45877943	Missense_Mutation	SNP	G	A	5	624	c.163G>A	c.(163-165)GAC>AAC	p.D55N
Pat_06	Post-Resistance	PARG	8505	37	10	51130381	51130381	Splice_Site	SNP	C	T	3	46	c.1662_splice	c.e6+1	p.K554_splice
Pat_06	Post-Resistance	HK1	3098	37	10	71146161	71146161	Missense_Mutation	SNP	T	C	3	188	c.1922T>C	c.(1921-1923)ATA>ACA	p.I641T
Pat_06	Post-Resistance	COL13A1	1305	37	10	71678072	71678072	Missense_Mutation	SNP	A	G	4	322	c.1028A>G	c.(1027-1029)AAG>AGG	p.K343R
Pat_06	Post-Resistance	ADAMTS14	140766	37	10	72498728	72498728	Missense_Mutation	SNP	G	A	4	261	c.1730G>A	c.(1729-1731)CGG>CAG	p.R577Q
Pat_06	Post-Resistance	SEC24C	9632	37	10	75529694	75529694	Missense_Mutation	SNP	G	A	7	839	c.2783G>A	c.(2782-2784)CGT>CAT	p.R928H
Pat_06	Post-Resistance	RPS24	6229	37	10	79795129	79795129	Missense_Mutation	SNP	G	A	5	527	c.23G>A	c.(22-24)CGC>CAC	p.R8H
Pat_06	Post-Resistance	IDE	3416	37	10	94228662	94228662	Missense_Mutation	SNP	C	T	4	268	c.2294G>A	c.(2293-2295)CGG>CAG	p.R765Q
Pat_06	Post-Resistance	EXOSC1	51013	37	10	99205520	99205520	Missense_Mutation	SNP	C	T	4	329	c.116G>A	c.(115-117)GGC>GAC	p.G39D
Pat_06	Post-Resistance	PNLIPRP1	5407	37	10	118350691	118350691	Splice_Site	SNP	G	C	3	221	c.49_splice	c.e2+1	p.G17_splice
Pat_06	Post-Resistance	TACC2	10579	37	10	123844309	123844309	Missense_Mutation	SNP	C	T	6	571	c.2294C>T	c.(2293-2295)CCG>CTG	p.P765L
Pat_06	Post-Resistance	PTPRE	5791	37	10	129868640	129868640	Missense_Mutation	SNP	C	A	7	460	c.1219C>A	c.(1219-1221)CTG>ATG	p.L407M
Pat_06	Post-Resistance	ADAM8	101	37	10	135080882	135080882	Missense_Mutation	SNP	C	A	3	105	c.2098G>T	c.(2098-2100)GTC>TTC	p.V700F
Pat_06	Post-Resistance	CDHR5	53841	37	11	618767	618767	Missense_Mutation	SNP	C	T	7	745	c.1792G>A	c.(1792-1794)GGT>AGT	p.G598S
Pat_06	Post-Resistance	LRDD	55367	37	11	802256	802256	Missense_Mutation	SNP	G	A	4	135	c.1115C>T	c.(1114-1116)CCT>CTT	p.P372L
Pat_06	Post-Resistance	MUC5B	727897	37	11	1266026	1266026	Missense_Mutation	SNP	C	A	137	517	c.9830C>A	c.(9829-9831)ACA>AAA	p.T3277K
Pat_06	Post-Resistance	TRIM68	55128	37	11	4621595	4621595	Missense_Mutation	SNP	G	A	4	266	c.1369C>T	c.(1369-1371)CGC>TGC	p.R457C
Pat_06	Post-Resistance	FAM160A2	84067	37	11	6239988	6239988	Missense_Mutation	SNP	A	G	4	462	c.1277T>C	c.(1276-1278)CTT>CCT	p.L426P
Pat_06	Post-Resistance	OR6A2	8590	37	11	6816547	6816547	Missense_Mutation	SNP	G	C	3	207	c.393C>G	c.(391-393)ATC>ATG	p.I131M
Pat_06	Post-Resistance	ASCL3	56676	37	11	8959228	8959228	Nonsense_Mutation	SNP	C	A	7	610	c.481G>T	c.(481-483)GGA>TGA	p.G161*
Pat_06	Post-Resistance	MRVI1	10335	37	11	10631309	10631309	Missense_Mutation	SNP	G	A	4	169	c.1537C>T	c.(1537-1539)CGC>TGC	p.R513C
Pat_06	Post-Resistance	MRVI1	10335	37	11	10649551	10649551	Missense_Mutation	SNP	G	A	4	285	c.674C>T	c.(673-675)CCG>CTG	p.P225L
Pat_06	Post-Resistance	CTR9	9646	37	11	10785879	10785879	Missense_Mutation	SNP	G	A	6	521	c.1309G>A	c.(1309-1311)GCA>ACA	p.A437T
Pat_06	Post-Resistance	LGR4	55366	37	11	27389521	27389521	Missense_Mutation	SNP	A	G	4	461	c.2749T>C	c.(2749-2751)TCA>CCA	p.S917P
Pat_06	Post-Resistance	NR1H3	10062	37	11	47281984	47281984	Missense_Mutation	SNP	A	G	6	352	c.257A>G	c.(256-258)AAG>AGG	p.K86R
Pat_06	Post-Resistance	CELF1	10658	37	11	47496908	47496908	Missense_Mutation	SNP	G	A	4	368	c.1169C>T	c.(1168-1170)GCT>GTT	p.A390V
Pat_06	Post-Resistance	OR4C16	219428	37	11	55340006	55340006	Missense_Mutation	SNP	A	C	22	770	c.403A>C	c.(403-405)AGC>CGC	p.S135R
Pat_06	Post-Resistance	APLNR	187	37	11	57004082	57004082	Missense_Mutation	SNP	T	C	3	62	c.397A>G	c.(397-399)AGG>GGG	p.R133G
Pat_06	Post-Resistance	PRG3	10394	37	11	57145305	57145305	Missense_Mutation	SNP	A	G	3	149	c.512T>C	c.(511-513)CTG>CCG	p.L171P
Pat_06	Post-Resistance	PRG3	10394	37	11	57147026	57147026	Missense_Mutation	SNP	T	A	6	481	c.316A>T	c.(316-318)AGG>TGG	p.R106W
Pat_06	Post-Resistance	SF1	7536	37	11	64535238	64535238	Missense_Mutation	SNP	G	A	5	298	c.1147C>T	c.(1147-1149)CAT>TAT	p.H383Y
Pat_06	Post-Resistance	BATF2	116071	37	11	64764355	64764355	Missense_Mutation	SNP	G	A	5	352	c.32C>T	c.(31-33)ACC>ATC	p.T11I
Pat_06	Post-Resistance	CDC42EP2	10435	37	11	65088503	65088503	Missense_Mutation	SNP	G	A	4	447	c.134G>A	c.(133-135)AGT>AAT	p.S45N
Pat_06	Post-Resistance	OVOL1	5017	37	11	65562658	65562658	Missense_Mutation	SNP	A	G	4	362	c.650A>G	c.(649-651)GAG>GGG	p.E217G

Pat_06	Post-Resistance	GAL3ST3	89792	37	11	65810814	65810814	Missense_Mutation	SNP	G	A	3	61	c.460C>T	c.(460-462)CCG>TCG	p.P154S
Pat_06	Post-Resistance	RBM14	10432	37	11	66394038	66394038	Missense_Mutation	SNP	C	A	7	200	c.1909C>A	c.(1909-1911)CGC>AGC	p.R637S
Pat_06	Post-Resistance	ANO1	55107	37	11	69950240	69950240	Missense_Mutation	SNP	C	T	4	148	c.676C>T	c.(676-678)CGG>TGG	p.R226W
Pat_06	Post-Resistance	CTTN	2017	37	11	70271450	70271450	Missense_Mutation	SNP	T	C	3	139	c.970T>C	c.(970-972)TTT>CTT	p.F324L
Pat_06	Post-Resistance	LRTOMT	220074	37	11	71806493	71806493	Missense_Mutation	SNP	G	A	5	288	c.506G>A	c.(505-507)CGC>CAC	p.R169H
Pat_06	Post-Resistance	ARAP1	116985	37	11	72409088	72409088	Missense_Mutation	SNP	G	A	3	51	c.2605C>T	c.(2605-2607)CCC>TCC	p.P869S
Pat_06	Post-Resistance	DNAJB13	374407	37	11	73670659	73670659	Missense_Mutation	SNP	A	G	4	386	c.293A>G	c.(292-294)AAG>AGG	p.K98R
Pat_06	Post-Resistance	C2CD3	26005	37	11	73765718	73765718	Splice_Site	SNP	T	C	3	331	c.5091_splice	c.e26-1	p.R1697_splice
Pat_06	Post-Resistance	XRRA1	143570	37	11	74554475	74554475	Missense_Mutation	SNP	C	T	3	118	c.2149G>A	c.(2149-2151)GAA>AAA	p.E717K
Pat_06	Post-Resistance	SLCO2B1	11309	37	11	74904599	74904599	Missense_Mutation	SNP	C	T	5	232	c.1412C>T	c.(1411-1413)GCG>GTG	p.A471V
Pat_06	Post-Resistance	MYO7A	4647	37	11	76871252	76871252	Missense_Mutation	SNP	T	G	3	47	c.1124T>G	c.(1123-1125)CTC>CGC	p.L375R
Pat_06	Post-Resistance	AQP11	282679	37	11	77301105	77301105	Nonsense_Mutation	SNP	C	A	5	163	c.68C>A	c.(67-69)TCG>TAG	p.S23*
Pat_06	Post-Resistance	FOLH1B	219595	37	11	89395322	89395322	Translation_Start_Site	SNP	C	T	7	185	c.-93C>T	c.(-95--91)TACGC>TATGC	
Pat_06	Post-Resistance	RAB39	54734	37	11	107799505	107799505	Missense_Mutation	SNP	G	A	3	55	c.211G>A	c.(211-213)GGA>AGA	p.G71R
Pat_06	Post-Resistance	BCO2	83875	37	11	112046410	112046410	Missense_Mutation	SNP	C	A	6	389	c.86C>A	c.(85-87)CCA>CAA	p.P29Q
Pat_06	Post-Resistance	SIDT2	51092	37	11	117053495	117053495	Missense_Mutation	SNP	G	A	4	136	c.675G>A	c.(673-675)ATG>ATA	p.M225I
Pat_06	Post-Resistance	CBL	867	37	11	119169068	119169068	Missense_Mutation	SNP	G	A	5	308	c.2252G>A	c.(2251-2253)GGT>GAT	p.G751D
Pat_06	Post-Resistance	NFRKB	4798	37	11	129739513	129739513	Missense_Mutation	SNP	G	A	4	261	c.3407C>T	c.(3406-3408)GCT>GTT	p.A1136V
Pat_06	Post-Resistance	ACAD8	27034	37	11	134131232	134131232	Missense_Mutation	SNP	G	A	5	523	c.905G>A	c.(904-906)CGG>CAG	p.R302Q
Pat_06	Post-Resistance	LRTM2	654429	37	12	1943849	1943849	Missense_Mutation	SNP	G	A	6	243	c.1075G>A	c.(1075-1077)GAG>AAG	p.E359K
Pat_06	Post-Resistance	DCP1B	196513	37	12	2062260	2062260	Missense_Mutation	SNP	G	C	3	237	c.846C>G	c.(844-846)CAC>CAG	p.H282Q
Pat_06	Post-Resistance	CHD4	1108	37	12	6703741	6703741	Missense_Mutation	SNP	C	T	4	451	c.2197G>A	c.(2197-2199)GGC>AGC	p.G733S
Pat_06	Post-Resistance	PHB2	11331	37	12	7077713	7077713	Missense_Mutation	SNP	T	C	3	180	c.338A>G	c.(337-339)AAT>AGT	p.N113S
Pat_06	Post-Resistance	ACSM4	341392	37	12	7463210	7463210	Missense_Mutation	SNP	A	G	3	157	c.488A>G	c.(487-489)AAG>AGG	p.K163R
Pat_06	Post-Resistance	MANSC1	54682	37	12	12483448	12483448	Missense_Mutation	SNP	G	A	4	342	c.809C>T	c.(808-810)CCT>CTT	p.P270L
Pat_06	Post-Resistance	ABCC9	10060	37	12	21968788	21968788	Missense_Mutation	SNP	T	C	6	759	c.3932A>G	c.(3931-3933)GAG>GGG	p.E1311G
Pat_06	Post-Resistance	DDX23	9416	37	12	49227133	49227133	Missense_Mutation	SNP	G	A	163	485	c.1730C>T	c.(1729-1731)CCA>CTA	p.P577L
Pat_06	Post-Resistance	C12orf44	60673	37	12	52467658	52467658	Missense_Mutation	SNP	C	A	4	416	c.224C>A	c.(223-225)GCC>GAC	p.A75D
Pat_06	Post-Resistance	KRT74	121391	37	12	52964517	52964517	Missense_Mutation	SNP	C	T	5	424	c.944G>A	c.(943-945)CGC>CAC	p.R315H
Pat_06	Post-Resistance	NFE2	4778	37	12	54687147	54687147	Nonsense_Mutation	SNP	C	A	6	378	c.133G>T	c.(133-135)GAG>TAG	p.E45*
Pat_06	Post-Resistance	ITGA7	3679	37	12	56096948	56096948	Missense_Mutation	SNP	G	A	4	198	c.221C>T	c.(220-222)GCT>GTT	p.A74V
Pat_06	Post-Resistance	LRP1	4035	37	12	57579344	57579344	Missense_Mutation	SNP	G	A	4	263	c.6494G>A	c.(6493-6495)GGG>GAG	p.G2165E
Pat_06	Post-Resistance	INHBE	83729	37	12	57850029	57850029	Missense_Mutation	SNP	C	T	6	778	c.451C>T	c.(451-453)CGC>TGC	p.R151C
Pat_06	Post-Resistance	SYT1	6857	37	12	79689885	79689885	Missense_Mutation	SNP	G	A	6	653	c.511G>A	c.(511-513)GCC>ACC	p.A171T
Pat_06	Post-Resistance	C12orf29	91298	37	12	88429460	88429460	Missense_Mutation	SNP	C	G	3	89	c.35C>G	c.(34-36)CCG>CGG	p.P12R
Pat_06	Post-Resistance	CHPT1	56994	37	12	102113926	102113926	Missense_Mutation	SNP	A	G	3	132	c.674A>G	c.(673-675)AAG>AGG	p.K225R
Pat_06	Post-Resistance	FOXN4	121643	37	12	109719400	109719400	Missense_Mutation	SNP	G	C	3	90	c.1106C>G	c.(1105-1107)GCA>GGA	p.A369G
Pat_06	Post-Resistance	UBE3B	89910	37	12	109939300	109939300	Missense_Mutation	SNP	G	A	5	455	c.1243G>A	c.(1243-1245)GCA>ACA	p.A415T
Pat_06	Post-Resistance	C12orf76	400073	37	12	110495075	110495075	Missense_Mutation	SNP	G	C	3	220	c.218C>G	c.(217-219)GCT>GGT	p.A73G
Pat_06	Post-Resistance	IFT81	28981	37	12	110573141	110573141	Missense_Mutation	SNP	G	A	4	302	c.595G>A	c.(595-597)GCT>ACT	p.A199T
Pat_06	Post-Resistance	C12orf51	283450	37	12	112646308	112646308	Missense_Mutation	SNP	T	G	3	191	c.6728A>C	c.(6727-6729)GAC>GCC	p.D2243A
Pat_06	Post-Resistance	C12orf51	283450	37	12	112670855	112670855	Missense_Mutation	SNP	C	T	3	91	c.4684G>A	c.(4684-4686)GGC>AGC	p.G1562S
Pat_06	Post-Resistance	DTX1	1840	37	12	113532899	113532899	Missense_Mutation	SNP	G	A	4	240	c.1439G>A	c.(1438-1440)GGT>GAT	p.G480D
Pat_06	Post-Resistance	SIRT4	23409	37	12	120750395	120750395	Missense_Mutation	SNP	G	A	3	81	c.634G>A	c.(634-636)GTC>ATC	p.V212I
Pat_06	Post-Resistance	KDM2B	84678	37	12	121880585	121880585	Missense_Mutation	SNP	G	A	3	63	c.2659C>T	c.(2659-2661)CGG>TGG	p.R887W
Pat_06	Post-Resistance	PITPNM2	57605	37	12	123474421	123474421	Missense_Mutation	SNP	T	G	12	74	c.2644A>C	c.(2644-2646)ACC>CCC	p.T882P
Pat_06	Post-Resistance	MPHOSPH9	10198	37	12	123705991	123705991	Missense_Mutation	SNP	G	A	20	103	c.344C>T	c.(343-345)TCT>TTT	p.S115F

Pat_06	Post-Resistance	SCARB1	949	37	12	125298879	125298879	Missense_Mutation	SNP	C	T	5	404	c.499G>A	c.(499-501)GGC>AGC	p.G167S
Pat_06	Post-Resistance	POLE	5426	37	12	133244194	133244194	Missense_Mutation	SNP	C	A	8	835	c.2214G>T	c.(2212-2214)AAG>AAT	p.K738N
Pat_06	Post-Resistance	PXMP2	5827	37	12	133277860	133277860	Missense_Mutation	SNP	G	A	5	466	c.424G>A	c.(424-426)GCC>ACC	p.A142T
Pat_06	Post-Resistance	EFHA1	221154	37	13	22070202	22070202	Missense_Mutation	SNP	G	A	4	375	c.1031C>T	c.(1030-1032)CCT>CTT	p.P344L
Pat_06	Post-Resistance	HTR2A	3356	37	13	47470011	47470011	Missense_Mutation	SNP	A	T	5	416	c.31T>A	c.(31-33)TTG>ATG	p.L11M
Pat_06	Post-Resistance	MLNR	2862	37	13	49794771	49794771	Missense_Mutation	SNP	C	G	3	140	c.298C>G	c.(298-300)CGC>GGC	p.R100G
Pat_06	Post-Resistance	SETDB2	83852	37	13	50050973	50050973	Missense_Mutation	SNP	C	A	143	503	c.703C>A	c.(703-705)CCA>ACA	p.P235T
Pat_06	Post-Resistance	UGGT2	55757	37	13	96675903	96675903	Missense_Mutation	SNP	C	T	4	398	c.352G>A	c.(352-354)GCT>ACT	p.A118T
Pat_06	Post-Resistance	FAM155A	728215	37	13	108518718	108518718	Missense_Mutation	SNP	T	C	4	264	c.227A>G	c.(226-228)CAG>CGG	p.Q76R
Pat_06	Post-Resistance	COL4A1	1282	37	13	110823044	110823044	Missense_Mutation	SNP	C	T	4	271	c.3592G>A	c.(3592-3594)GGG>AGG	p.G1198R
Pat_06	Post-Resistance	RAB20	55647	37	13	111213811	111213811	Missense_Mutation	SNP	G	A	4	327	c.56C>T	c.(55-57)ACG>ATG	p.T19M
Pat_06	Post-Resistance	TMCO3	55002	37	13	114203816	114203816	Missense_Mutation	SNP	G	A	4	406	c.1997G>A	c.(1996-1998)AGG>AAG	p.R666K
Pat_06	Post-Resistance	LRRC16B	90668	37	14	24534879	24534879	Missense_Mutation	SNP	G	A	6	597	c.3445G>A	c.(3445-3447)GCA>ACA	p.A1149T
Pat_06	Post-Resistance	C14orf21	161424	37	14	24771294	24771294	Missense_Mutation	SNP	G	A	5	415	c.932G>A	c.(931-933)GGT>GAT	p.G311D
Pat_06	Post-Resistance	FANCM	57697	37	14	45642373	45642373	Missense_Mutation	SNP	T	C	4	647	c.2276T>C	c.(2275-2277)ATA>ACA	p.I759T
Pat_06	Post-Resistance	RPL10L	140801	37	14	47120617	47120617	Missense_Mutation	SNP	G	A	4	472	c.323C>T	c.(322-324)GCT>GTT	p.A108V
Pat_06	Post-Resistance	TRIM9	114088	37	14	51467475	51467475	Nonsense_Mutation	SNP	G	A	6	438	c.1390C>T	c.(1390-1392)CAG>TAG	p.Q464*
Pat_06	Post-Resistance	DDHD1	80821	37	14	53540470	53540470	Missense_Mutation	SNP	G	C	11	393	c.1385C>G	c.(1384-1386)ACT>AGT	p.T462S
Pat_06	Post-Resistance	PRKCH	5583	37	14	61789174	61789174	Missense_Mutation	SNP	G	C	3	315	c.355G>C	c.(355-357)GAG>CAG	p.E119Q
Pat_06	Post-Resistance	MPP5	64398	37	14	67745960	67745960	Missense_Mutation	SNP	T	C	3	277	c.73T>C	c.(73-75)TCA>CCA	p.S25P
Pat_06	Post-Resistance	PAPLN	89932	37	14	73731013	73731013	Missense_Mutation	SNP	G	A	6	440	c.2956G>A	c.(2956-2958)GAC>AAC	p.D986N
Pat_06	Post-Resistance	FLVCR2	55640	37	14	76045862	76045862	Missense_Mutation	SNP	G	A	4	371	c.547G>A	c.(547-549)GGC>AGC	p.G183S
Pat_06	Post-Resistance	TGFB3	7043	37	14	76438059	76438059	Nonsense_Mutation	SNP	C	A	4	185	c.355G>T	c.(355-357)GAA>TAA	p.E119*
Pat_06	Post-Resistance	SPTLC2	9517	37	14	78043193	78043193	Missense_Mutation	SNP	C	A	6	802	c.548G>T	c.(547-549)CGG>CTG	p.R183L
Pat_06	Post-Resistance	CCDC88C	440193	37	14	91763725	91763725	Missense_Mutation	SNP	T	C	3	174	c.3890A>G	c.(3889-3891)CAG>CGG	p.Q1297R
Pat_06	Post-Resistance	EVL	51466	37	14	100551122	100551122	Missense_Mutation	SNP	G	A	5	494	c.104G>A	c.(103-105)CGG>CAG	p.R35Q
Pat_06	Post-Resistance	PPP2R5C	5527	37	14	102349868	102349868	Missense_Mutation	SNP	A	G	5	355	c.598A>G	c.(598-600)ATC>GTC	p.I200V
Pat_06	Post-Resistance	KIF26A	26153	37	14	104641515	104641515	Missense_Mutation	SNP	G	T	6	92	c.2390G>T	c.(2389-2391)GGG>GTG	p.G797V
Pat_06	Post-Resistance	TMEM179	388021	37	14	105070985	105070985	Missense_Mutation	SNP	C	T	3	94	c.94G>A	c.(94-96)GGC>AGC	p.G32S
Pat_06	Post-Resistance	MKRN3	7681	37	15	23811035	23811035	Nonsense_Mutation	SNP	G	T	6	440	c.106G>T	c.(106-108)GAG>TAG	p.E36*
Pat_06	Post-Resistance	SRP14	6727	37	15	40331084	40331084	Missense_Mutation	SNP	C	G	3	173	c.90G>C	c.(88-90)TTG>TTC	p.L30F
Pat_06	Post-Resistance	MGA	23269	37	15	41961367	41961367	Missense_Mutation	SNP	G	A	4	432	c.275G>A	c.(274-276)AGC>AAC	p.S92N
Pat_06	Post-Resistance	MGA	23269	37	15	42035149	42035149	Missense_Mutation	SNP	C	T	4	148	c.4991C>T	c.(4990-4992)ACT>ATT	p.T1664I
Pat_06	Post-Resistance	CDAN1	146059	37	15	43028876	43028876	Missense_Mutation	SNP	G	A	3	74	c.193C>T	c.(193-195)CTC>TTC	p.L65F
Pat_06	Post-Resistance	DUOX2	50506	37	15	45399164	45399164	Missense_Mutation	SNP	G	A	3	43	c.1697C>T	c.(1696-1698)GCA>GTA	p.A566V
Pat_06	Post-Resistance	GATM	2628	37	15	45658258	45658258	Nonsense_Mutation	SNP	G	A	5	566	c.964C>T	c.(964-966)CGA>TGA	p.R322*
Pat_06	Post-Resistance	SLC12A1	6557	37	15	48559860	48559860	Missense_Mutation	SNP	G	A	6	738	c.2257G>A	c.(2257-2259)GCA>ACA	p.A753T
Pat_06	Post-Resistance	ATP8B4	79895	37	15	50223403	50223403	Missense_Mutation	SNP	T	G	6	385	c.1555A>C	c.(1555-1557)ACA>CCA	p.T519P
Pat_06	Post-Resistance	C2CD4B	388125	37	15	62457078	62457078	Missense_Mutation	SNP	G	A	3	48	c.106C>T	c.(106-108)CCG>TCG	p.P36S
Pat_06	Post-Resistance	CCDC33	80125	37	15	74565112	74565112	Missense_Mutation	SNP	G	T	6	194	c.639G>T	c.(637-639)AAG>AAT	p.K213N
Pat_06	Post-Resistance	C15orf39	56905	37	15	75500955	75500955	Missense_Mutation	SNP	C	T	3	49	c.2566C>T	c.(2566-2568)CGG>TGG	p.R856W
Pat_06	Post-Resistance	SH2D7	646892	37	15	78390760	78390760	Missense_Mutation	SNP	G	C	4	387	c.467G>C	c.(466-468)CGG>CCG	p.R156P
Pat_06	Post-Resistance	IDH3A	3419	37	15	78454591	78454591	Missense_Mutation	SNP	G	A	7	709	c.493G>A	c.(493-495)GTG>ATG	p.V165M
Pat_06	Post-Resistance	HOMER2	9455	37	15	83532942	83532942	Missense_Mutation	SNP	C	T	4	269	c.364G>A	c.(364-366)GAG>AAG	p.E122K
Pat_06	Post-Resistance	LRRC28	123355	37	15	99892580	99892580	Missense_Mutation	SNP	G	T	6	730	c.599G>T	c.(598-600)GGT>GTT	p.G200V
Pat_06	Post-Resistance	PDIA2	64714	37	16	334792	334792	Missense_Mutation	SNP	G	C	3	68	c.540G>C	c.(538-540)CAG>CAC	p.Q180H
Pat_06	Post-Resistance	RAB11FIP3	9727	37	16	555582	555582	Missense_Mutation	SNP	A	G	3	118	c.1454A>G	c.(1453-1455)GAG>GGG	p.E485G

Pat_06	Post-Resistance	LMF1	64788	37	16	904562	904562	Missense_Mutation	SNP	G	T	3	46	c.1674C>A	c.(1672-1674)GAC>GAA	p.D558E
Pat_06	Post-Resistance	NUBP2	10101	37	16	1838600	1838600	Missense_Mutation	SNP	G	A	3	68	c.701G>A	c.(700-702)AGG>AAG	p.R234K
Pat_06	Post-Resistance	CASKIN1	57524	37	16	2229990	2229990	Missense_Mutation	SNP	G	A	3	60	c.3379C>T	c.(3379-3381)CGC>TGC	p.R1127C
Pat_06	Post-Resistance	DNASE1L2	1775	37	16	2287814	2287814	Missense_Mutation	SNP	G	T	3	81	c.638G>T	c.(637-639)CGG>CTG	p.R213L
Pat_06	Post-Resistance	GLIS2	84662	37	16	4385140	4385140	Missense_Mutation	SNP	G	A	5	453	c.602G>A	c.(601-603)GGG>GAG	p.G201E
Pat_06	Post-Resistance	C16orf72	29035	37	16	9210599	9210599	Missense_Mutation	SNP	T	C	7	560	c.658T>C	c.(658-660)TCG>CCG	p.S220P
Pat_06	Post-Resistance	ABCC6P1	653190	37	16	18586170	18586170	Missense_Mutation	SNP	G	A	3	21	c.136G>A	c.(136-138)GAA>AAA	p.E46K
Pat_06	Post-Resistance	GP2	2813	37	16	20334257	20334257	Nonsense_Mutation	SNP	C	A	6	436	c.589G>T	c.(589-591)GAG>TAG	p.E197*
Pat_06	Post-Resistance	DNAH3	55567	37	16	20975620	20975620	Missense_Mutation	SNP	T	C	3	220	c.9586A>G	c.(9586-9588)ATC>GTC	p.I3196V
Pat_06	Post-Resistance	LAT	27040	37	16	28997926	28997926	Missense_Mutation	SNP	G	A	5	270	c.376G>A	c.(376-378)GGA>AGA	p.G126R
Pat_06	Post-Resistance	ZNF764	92595	37	16	30569473	30569473	Missense_Mutation	SNP	G	A	3	80	c.31C>T	c.(31-33)CGG>TGG	p.R11W
Pat_06	Post-Resistance	ITGAM	3684	37	16	31289423	31289423	Missense_Mutation	SNP	G	A	3	53	c.1349G>A	c.(1348-1350)GGC>GAC	p.G450D
Pat_06	Post-Resistance	ITGAD	3681	37	16	31408747	31408747	Missense_Mutation	SNP	G	A	3	67	c.205G>A	c.(205-207)GCT>ACT	p.A69T
Pat_06	Post-Resistance	C16orf87	388272	37	16	46843668	46843668	Missense_Mutation	SNP	T	C	3	283	c.193A>G	c.(193-195)ACA>GCA	p.T65A
Pat_06	Post-Resistance	SALL1	6299	37	16	51173912	51173912	Missense_Mutation	SNP	G	A	5	267	c.2221C>T	c.(2221-2223)CGG>TGG	p.R741W
Pat_06	Post-Resistance	SALL1	6299	37	16	51175720	51175720	Missense_Mutation	SNP	C	T	4	137	c.413G>A	c.(412-414)GGC>GAC	p.G138D
Pat_06	Post-Resistance	ZNF319	57567	37	16	58031086	58031086	Missense_Mutation	SNP	G	A	5	297	c.1084C>T	c.(1084-1086)CGG>TGG	p.R362W
Pat_06	Post-Resistance	CDH5	1003	37	16	66434682	66434682	Missense_Mutation	SNP	G	A	6	761	c.1600G>A	c.(1600-1602)GCC>ACC	p.A534T
Pat_06	Post-Resistance	CMTM2	146225	37	16	66613713	66613713	Missense_Mutation	SNP	G	A	7	275	c.203G>A	c.(202-204)TGT>TAT	p.C68Y
Pat_06	Post-Resistance	ACD	65057	37	16	67694333	67694333	Missense_Mutation	SNP	C	T	4	113	c.49G>A	c.(49-51)GCA>ACA	p.A17T
Pat_06	Post-Resistance	PLA2G15	23659	37	16	68293315	68293315	Missense_Mutation	SNP	T	C	3	301	c.994T>C	c.(994-996)TAT>CAT	p.Y332H
Pat_06	Post-Resistance	CIRH1A	84916	37	16	69199414	69199414	Missense_Mutation	SNP	C	G	3	215	c.1818C>G	c.(1816-1818)ATC>ATG	p.I606M
Pat_06	Post-Resistance	NFAT5	10725	37	16	69727269	69727269	Missense_Mutation	SNP	G	A	5	705	c.3487G>A	c.(3487-3489)GCA>ACA	p.A1163T
Pat_06	Post-Resistance	RFWD3	55159	37	16	74666547	74666547	Missense_Mutation	SNP	G	A	4	209	c.1451C>T	c.(1450-1452)ACT>ATT	p.T484I
Pat_06	Post-Resistance	MON1B	22879	37	16	77227620	77227620	Missense_Mutation	SNP	G	A	6	497	c.421G>A	c.(421-423)GCC>ACC	p.A141T
Pat_06	Post-Resistance	RAP1GAP2	23108	37	17	2921371	2921371	Missense_Mutation	SNP	G	C	3	84	c.1511G>C	c.(1510-1512)CGC>CCC	p.R504P
Pat_06	Post-Resistance	P2RX5	5026	37	17	3582885	3582885	Missense_Mutation	SNP	T	C	3	164	c.1258A>G	c.(1258-1260)AGG>GGG	p.R420G
Pat_06	Post-Resistance	C17orf85	55421	37	17	3716504	3716504	Missense_Mutation	SNP	C	A	4	277	c.1697G>T	c.(1696-1698)AGG>ATG	p.R566M
Pat_06	Post-Resistance	KIAA0753	9851	37	17	6510532	6510532	Missense_Mutation	SNP	C	A	5	607	c.1888G>T	c.(1888-1890)GCC>TCC	p.A630S
Pat_06	Post-Resistance	C17orf74	201243	37	17	7330508	7330508	Missense_Mutation	SNP	A	G	4	323	c.1198A>G	c.(1198-1200)ACC>GCC	p.T400A
Pat_06	Post-Resistance	PER1	5187	37	17	8052785	8052785	Nonsense_Mutation	SNP	G	T	5	232	c.848C>A	c.(847-849)TCA>TAA	p.S283*
Pat_06	Post-Resistance	NTN1	9423	37	17	8926555	8926555	Missense_Mutation	SNP	G	A	3	47	c.865G>A	c.(865-867)GGC>AGC	p.G289S
Pat_06	Post-Resistance	MYH2	4620	37	17	10442604	10442604	Missense_Mutation	SNP	C	T	7	828	c.1334G>A	c.(1333-1335)CGC>CAC	p.R445H
Pat_06	Post-Resistance	DNAH9	1770	37	17	11642312	11642312	Missense_Mutation	SNP	C	T	6	347	c.5930C>T	c.(5929-5931)GCT>GTT	p.A1977V
Pat_06	Post-Resistance	TBC1D26	353149	37	17	15644445	15644445	Missense_Mutation	SNP	T	C	4	351	c.556T>C	c.(556-558)TAC>CAC	p.Y186H
Pat_06	Post-Resistance	ZNF624	57547	37	17	16526963	16526963	Missense_Mutation	SNP	C	G	3	239	c.1237G>C	c.(1237-1239)GAG>CAG	p.E413Q
Pat_06	Post-Resistance	MPRIP	23164	37	17	17062123	17062123	Missense_Mutation	SNP	G	A	5	401	c.1853G>A	c.(1852-1854)CGG>CAG	p.R618Q
Pat_06	Post-Resistance	TRIM16L	147166	37	17	18638618	18638618	Missense_Mutation	SNP	G	C	3	290	c.892G>C	c.(892-894)GAT>CAT	p.D298H
Pat_06	Post-Resistance	RNF112	7732	37	17	19316950	19316950	Missense_Mutation	SNP	A	G	3	217	c.781A>G	c.(781-783)AGG>GGG	p.R261G
Pat_06	Post-Resistance	MYO18A	399687	37	17	27421041	27421041	Missense_Mutation	SNP	C	T	4	191	c.4778G>A	c.(4777-4779)CGG>CAG	p.R1593Q
Pat_06	Post-Resistance	ACACA	31	37	17	35601610	35601610	Missense_Mutation	SNP	G	A	6	565	c.2525C>T	c.(2524-2526)ACG>ATG	p.T842M
Pat_06	Post-Resistance	MED24	9862	37	17	38189634	38189634	Missense_Mutation	SNP	C	T	3	110	c.635G>A	c.(634-636)CGG>CAG	p.R212Q
Pat_06	Post-Resistance	KRTAP1-3	81850	37	17	39190656	39190656	Missense_Mutation	SNP	C	G	4	408	c.418G>C	c.(418-420)GAG>CAG	p.E140Q
Pat_06	Post-Resistance	KRTAP4-11	653240	37	17	39274087	39274087	Missense_Mutation	SNP	G	C	4	97	c.481C>G	c.(481-483)CTG>GTG	p.L161V
Pat_06	Post-Resistance	KRT13	3860	37	17	39661436	39661436	Missense_Mutation	SNP	G	A	8	737	c.367C>T	c.(367-369)CGC>TGC	p.R123C
Pat_06	Post-Resistance	WNK4	65266	37	17	40933231	40933231	Missense_Mutation	SNP	G	A	6	368	c.515G>A	c.(514-516)CGA>CAA	p.R172Q
Pat_06	Post-Resistance	TMEM101	84336	37	17	42090407	42090407	Missense_Mutation	SNP	C	A	4	264	c.435G>T	c.(433-435)CAG>CAT	p.Q145H

Pat_06	Post-Resistance	PLCD3	113026	37	17	43195495	43195495	Missense_Mutation	SNP	G	T	6	273	c.1126C>A	c.(1126-1128)CAG>AAG	p.Q376K
Pat_06	Post-Resistance	CBX1	10951	37	17	46154339	46154339	Missense_Mutation	SNP	C	G	4	461	c.28G>C	c.(28-30)GTG>CTG	p.V10L
Pat_06	Post-Resistance	HOXB1	3211	37	17	46606940	46606940	Missense_Mutation	SNP	G	C	4	308	c.875C>G	c.(874-876)CCG>CGG	p.P292R
Pat_06	Post-Resistance	MSI2	124540	37	17	55729492	55729492	Missense_Mutation	SNP	G	A	7	657	c.760G>A	c.(760-762)GCA>ACA	p.A254T
Pat_06	Post-Resistance	MPO	4353	37	17	56350963	56350963	Missense_Mutation	SNP	G	A	384	476	c.1433C>T	c.(1432-1434)ACG>ATG	p.T478M
Pat_06	Post-Resistance	BCAS3	54828	37	17	59067378	59067378	Missense_Mutation	SNP	G	A	6	684	c.1268G>A	c.(1267-1269)AGT>AAT	p.S423N
Pat_06	Post-Resistance	MRC2	9902	37	17	60757617	60757617	Nonsense_Mutation	SNP	G	A	4	247	c.2385G>A	c.(2383-2385)TGG>TGA	p.W795*
Pat_06	Post-Resistance	TANC2	26115	37	17	61432228	61432228	Missense_Mutation	SNP	T	C	5	816	c.1837T>C	c.(1837-1839)TAC>CAC	p.Y613H
Pat_06	Post-Resistance	TANC2	26115	37	17	61483573	61483573	Missense_Mutation	SNP	G	A	6	765	c.3302G>A	c.(3301-3303)CGC>CAC	p.R1101H
Pat_06	Post-Resistance	TEX2	55852	37	17	62265647	62265647	Missense_Mutation	SNP	G	A	6	614	c.2305C>T	c.(2305-2307)CGG>TGG	p.R769W
Pat_06	Post-Resistance	BPTF	2186	37	17	65822438	65822438	Missense_Mutation	SNP	T	C	3	300	c.598T>C	c.(598-600)TAC>CAC	p.Y200H
Pat_06	Post-Resistance	ARSG	22901	37	17	66339924	66339924	Missense_Mutation	SNP	G	A	31	191	c.398G>A	c.(397-399)GGG>GAG	p.G133E
Pat_06	Post-Resistance	ABCA6	23460	37	17	67119437	67119437	Missense_Mutation	SNP	G	A	4	342	c.1379C>T	c.(1378-1380)CCC>CTC	p.P460L
Pat_06	Post-Resistance	TNRC6C	57690	37	17	76047105	76047105	Missense_Mutation	SNP	C	A	4	165	c.1962C>A	c.(1960-1962)AAC>AAA	p.N654K
Pat_06	Post-Resistance	NOTUM	147111	37	17	79913328	79913328	Missense_Mutation	SNP	G	A	4	114	c.1081C>T	c.(1081-1083)CGG>TGG	p.R361W
Pat_06	Post-Resistance	PSMG2	56984	37	18	12706720	12706720	Missense_Mutation	SNP	G	A	4	284	c.229G>A	c.(229-231)GTG>ATG	p.V77M
Pat_06	Post-Resistance	DSC3	1825	37	18	28576918	28576918	Missense_Mutation	SNP	T	C	5	194	c.2332A>G	c.(2332-2334)ACC>GCC	p.T778A
Pat_06	Post-Resistance	ELP2	55250	37	18	33709903	33709903	Missense_Mutation	SNP	G	A	5	436	c.7G>A	c.(7-9)GCA>ACA	p.A3T
Pat_06	Post-Resistance	KIAA1632	57724	37	18	43496522	43496522	Missense_Mutation	SNP	G	C	3	189	c.3265C>G	c.(3265-3267)CTA>GTA	p.L1089V
Pat_06	Post-Resistance	POLI	11201	37	18	51804162	51804162	Nonsense_Mutation	SNP	C	T	4	155	c.496C>T	c.(496-498)CAG>TAG	p.Q166*
Pat_06	Post-Resistance	ZNF236	7776	37	18	74631810	74631810	Missense_Mutation	SNP	C	G	4	455	c.3347C>G	c.(3346-3348)ACG>AGG	p.T1116R
Pat_06	Post-Resistance	MED16	10025	37	19	877161	877161	Nonsense_Mutation	SNP	G	C	3	65	c.1373C>G	c.(1372-1374)TCA>TGA	p.S458*
Pat_06	Post-Resistance	TCF3	6929	37	19	1622318	1622318	Missense_Mutation	SNP	C	T	3	64	c.646G>A	c.(646-648)GTG>ATG	p.V216M
Pat_06	Post-Resistance	ATP8B3	148229	37	19	1783118	1783118	Missense_Mutation	SNP	C	T	3	123	c.3812G>A	c.(3811-3813)CGG>CAG	p.R1271Q
Pat_06	Post-Resistance	LINGO3	645191	37	19	2290979	2290979	Missense_Mutation	SNP	A	G	3	87	c.797T>C	c.(796-798)CTG>CCG	p.L266P
Pat_06	Post-Resistance	LMNB2	84823	37	19	2456715	2456715	Missense_Mutation	SNP	G	A	3	74	c.157C>T	c.(157-159)CGG>TGG	p.R53W
Pat_06	Post-Resistance	ZNF57	126295	37	19	2918025	2918025	Missense_Mutation	SNP	T	C	4	277	c.1406T>C	c.(1405-1407)ATG>ACG	p.M469T
Pat_06	Post-Resistance	TLE6	79816	37	19	2987064	2987064	Translation_Start_Site	SNP	C	G	3	184	c.0C>G	c.(-2-2)ATCAT>ATGAT	
Pat_06	Post-Resistance	MPND	84954	37	19	4345742	4345742	Missense_Mutation	SNP	G	C	3	125	c.295G>C	c.(295-297)GGG>CGG	p.G99R
Pat_06	Post-Resistance	KDM4B	23030	37	19	5144155	5144155	Missense_Mutation	SNP	G	A	4	405	c.2728G>A	c.(2728-2730)GGT>AGT	p.G910S
Pat_06	Post-Resistance	SAFB2	9667	37	19	5592789	5592789	Missense_Mutation	SNP	G	A	4	175	c.2317C>T	c.(2317-2319)CGG>TGG	p.R773W
Pat_06	Post-Resistance	FUT3	2525	37	19	5844502	5844502	Missense_Mutation	SNP	G	T	7	595	c.349C>A	c.(349-351)CCT>ACT	p.P117T
Pat_06	Post-Resistance	PNPLA6	10908	37	19	7607465	7607465	Missense_Mutation	SNP	G	A	4	196	c.1298G>A	c.(1297-1299)CGC>CAC	p.R433H
Pat_06	Post-Resistance	ZNF560	147741	37	19	9578478	9578478	Missense_Mutation	SNP	C	T	6	553	c.1145G>A	c.(1144-1146)GGC>GAC	p.G382D
Pat_06	Post-Resistance	MRPL4	51073	37	19	10370467	10370467	Missense_Mutation	SNP	C	T	4	260	c.914C>T	c.(913-915)GCG>GTG	p.A305V
Pat_06	Post-Resistance	TYK2	7297	37	19	10476414	10476414	Missense_Mutation	SNP	C	G	3	95	c.790G>C	c.(790-792)GAG>CAG	p.E264Q
Pat_06	Post-Resistance	RTBDN	83546	37	19	12940673	12940673	Missense_Mutation	SNP	G	A	4	238	c.121C>T	c.(121-123)CAC>TAC	p.H41Y
Pat_06	Post-Resistance	PKN1	5585	37	19	14580274	14580274	Missense_Mutation	SNP	G	A	6	735	c.2098G>A	c.(2098-2100)GGT>AGT	p.G700S
Pat_06	Post-Resistance	SIN3B	23309	37	19	16986980	16986980	Missense_Mutation	SNP	A	G	3	166	c.2803A>G	c.(2803-2805)AGG>GGG	p.R935G
Pat_06	Post-Resistance	KIAA1683	80726	37	19	18376614	18376614	Missense_Mutation	SNP	T	C	3	140	c.1736A>G	c.(1735-1737)AAG>AGG	p.K579R
Pat_06	Post-Resistance	ZNF93	81931	37	19	20045200	20045200	Missense_Mutation	SNP	A	C	6	199	c.1436A>C	c.(1435-1437)AAA>ACA	p.K479T
Pat_06	Post-Resistance	ZNF93	81931	37	19	20045284	20045284	Missense_Mutation	SNP	A	C	6	171	c.1520A>C	c.(1519-1521)AAA>ACA	p.K507T
Pat_06	Post-Resistance	ZNF85	7639	37	19	21132642	21132642	Missense_Mutation	SNP	T	G	8	50	c.1322T>G	c.(1321-1323)CTT>CGT	p.L441R
Pat_06	Post-Resistance	ZNF493	284443	37	19	21606468	21606468	Missense_Mutation	SNP	C	T	4	201	c.623C>T	c.(622-624)CCT>CTT	p.P208L
Pat_06	Post-Resistance	ZNF208	7757	37	19	22155282	22155282	Missense_Mutation	SNP	T	C	6	181	c.2254A>G	c.(2254-2256)AAG>GAG	p.K752E
Pat_06	Post-Resistance	ZNF257	113835	37	19	22271961	22271961	Missense_Mutation	SNP	A	G	8	201	c.1409A>G	c.(1408-1410)CAG>CGG	p.Q470R
Pat_06	Post-Resistance	ZNF681	148213	37	19	23927139	23927139	Missense_Mutation	SNP	T	G	7	135	c.1213A>C	c.(1213-1215)AAG>CAG	p.K405Q

Pat_06	Post-Resistance	TSHZ3	57616	37	19	31768255	31768255	Missense_Mutation	SNP	G	A	4	312	c.2444C>T	c.(2443-2445)CCG>CTG	p.P815L
Pat_06	Post-Resistance	ZNF507	22847	37	19	32847588	32847588	Missense_Mutation	SNP	A	G	3	367	c.2194A>G	c.(2194-2196)AAT>GAT	p.N732D
Pat_06	Post-Resistance	ZNF30	90075	37	19	35434144	35434144	Missense_Mutation	SNP	G	A	6	16	c.274G>A	c.(274-276)GAT>AAT	p.D92N
Pat_06	Post-Resistance	FFAR2	2867	37	19	35940879	35940879	Missense_Mutation	SNP	G	C	3	134	c.263G>C	c.(262-264)GGC>GCC	p.G88A
Pat_06	Post-Resistance	RINL	126432	37	19	39360618	39360618	Missense_Mutation	SNP	T	C	3	53	c.965A>G	c.(964-966)GAT>GGT	p.D322G
Pat_06	Post-Resistance	PAF1	54623	37	19	39876648	39876648	Missense_Mutation	SNP	C	G	3	295	c.1579G>C	c.(1579-1581)GAT>CAT	p.D527H
Pat_06	Post-Resistance	PAF1	54623	37	19	39881474	39881474	Missense_Mutation	SNP	G	A	3	53	c.31C>T	c.(31-33)CGG>TGG	p.R11W
Pat_06	Post-Resistance	FCGBP	8857	37	19	40420050	40420050	Missense_Mutation	SNP	C	T	78	271	c.2944G>A	c.(2944-2946)GAC>AAC	p.D982N
Pat_06	Post-Resistance	HIPK4	147746	37	19	40886952	40886952	Missense_Mutation	SNP	C	G	3	202	c.946G>C	c.(946-948)GAC>CAC	p.D316H
Pat_06	Post-Resistance	CYP2A6	1548	37	19	41352877	41352877	Missense_Mutation	SNP	T	C	4	367	c.734A>G	c.(733-735)GAG>GGG	p.E245G
Pat_06	Post-Resistance	CYP2F1	1572	37	19	41628800	41628800	Missense_Mutation	SNP	G	A	6	250	c.896G>A	c.(895-897)GGC>GAC	p.G299D
Pat_06	Post-Resistance	CEACAM20	125931	37	19	45026903	45026903	Missense_Mutation	SNP	C	A	3	69	c.511G>T	c.(511-513)GTT>TTT	p.V171F
Pat_06	Post-Resistance	EHD2	30846	37	19	48244171	48244171	Missense_Mutation	SNP	C	T	45	96	c.1114C>T	c.(1114-1116)CAC>TAC	p.H372Y
Pat_06	Post-Resistance	PRRG2	5639	37	19	50086551	50086551	Missense_Mutation	SNP	G	C	3	193	c.75G>C	c.(73-75)GAG>GAC	p.E25D
Pat_06	Post-Resistance	AP2A1	160	37	19	50270424	50270424	Missense_Mutation	SNP	G	A	4	475	c.34G>A	c.(34-36)GGG>AGG	p.G12R
Pat_06	Post-Resistance	MED25	81857	37	19	50339574	50339574	Missense_Mutation	SNP	T	C	3	108	c.2057T>C	c.(2056-2058)CTG>CCG	p.L686P
Pat_06	Post-Resistance	MYH14	79784	37	19	50764812	50764812	Missense_Mutation	SNP	G	T	13	170	c.2382G>T	c.(2380-2382)CAG>CAT	p.Q794H
Pat_06	Post-Resistance	NAPSA	9476	37	19	50865325	50865325	Missense_Mutation	SNP	G	C	3	102	c.250C>G	c.(250-252)CTG>GTG	p.L84V
Pat_06	Post-Resistance	NR1H2	7376	37	19	50882003	50882003	Missense_Mutation	SNP	G	A	5	370	c.700G>A	c.(700-702)GCC>ACC	p.A234T
Pat_06	Post-Resistance	ZNF649	65251	37	19	52394769	52394769	Missense_Mutation	SNP	A	C	4	325	c.620T>G	c.(619-621)GTG>GGG	p.V207G
Pat_06	Post-Resistance	ZNF841	284371	37	19	52568410	52568410	Missense_Mutation	SNP	T	C	3	87	c.2377A>G	c.(2377-2379)AAT>GAT	p.N793D
Pat_06	Post-Resistance	ZNF600	162966	37	19	53269487	53269487	Missense_Mutation	SNP	G	T	7	764	c.1522C>A	c.(1522-1524)CGT>AGT	p.R508S
Pat_06	Post-Resistance	PRPF31	26121	37	19	54625963	54625963	Missense_Mutation	SNP	G	A	6	581	c.410G>A	c.(409-411)CGC>CAC	p.R137H
Pat_06	Post-Resistance	ZNF304	57343	37	19	57869118	57869118	Missense_Mutation	SNP	C	A	5	412	c.1881C>A	c.(1879-1881)AGC>AGA	p.S627R
Pat_06	Post-Resistance	CYS1	192668	37	2	10199005	10199005	Missense_Mutation	SNP	C	T	3	66	c.452G>A	c.(451-453)AGC>AAC	p.S151N
Pat_06	Post-Resistance	NTSR2	23620	37	2	11802254	11802254	Missense_Mutation	SNP	G	T	7	816	c.737C>A	c.(736-738)CCG>CAG	p.P246Q
Pat_06	Post-Resistance	MATN3	4148	37	2	20205877	20205877	Missense_Mutation	SNP	A	G	3	294	c.418T>C	c.(418-420)TAC>CAC	p.Y140H
Pat_06	Post-Resistance	CAD	790	37	2	27449125	27449125	Missense_Mutation	SNP	C	A	7	569	c.1969C>A	c.(1969-1971)CAG>AAG	p.Q657K
Pat_06	Post-Resistance	ZNF513	130557	37	2	27601381	27601381	Missense_Mutation	SNP	G	A	6	572	c.752C>T	c.(751-753)CCT>CTT	p.P251L
Pat_06	Post-Resistance	ZNF512	84450	37	2	27823636	27823636	Missense_Mutation	SNP	G	A	4	306	c.536G>A	c.(535-537)AGG>AAG	p.R179K
Pat_06	Post-Resistance	VIT	5212	37	2	36982146	36982146	Missense_Mutation	SNP	G	A	4	434	c.358G>A	c.(358-360)GGT>AGT	p.G120S
Pat_06	Post-Resistance	TMEM178	130733	37	2	39893503	39893503	Missense_Mutation	SNP	T	C	3	68	c.389T>C	c.(388-390)CTC>CCC	p.L130P
Pat_06	Post-Resistance	LRPPRC	10128	37	2	44132881	44132881	Missense_Mutation	SNP	G	A	5	506	c.3314C>T	c.(3313-3315)GCT>GTT	p.A1105V
Pat_06	Post-Resistance	MDH1	4190	37	2	63834072	63834072	Missense_Mutation	SNP	A	C	4	305	c.956A>C	c.(955-957)GAA>GCA	p.E319A
Pat_06	Post-Resistance	ADRA2B	151	37	2	96781851	96781851	Missense_Mutation	SNP	G	C	3	105	c.38C>G	c.(37-39)GCG>GGG	p.A13G
Pat_06	Post-Resistance	KIAA1310	55683	37	2	97270073	97270073	Nonsense_Mutation	SNP	G	C	3	266	c.2063C>G	c.(2062-2064)TCA>TGA	p.S688*
Pat_06	Post-Resistance	SLC9A2	6549	37	2	103321076	103321076	Missense_Mutation	SNP	G	A	5	461	c.1919G>A	c.(1918-1920)CGG>CAG	p.R640Q
Pat_06	Post-Resistance	FBLN7	129804	37	2	112917344	112917344	Missense_Mutation	SNP	G	A	3	46	c.167G>A	c.(166-168)CGC>CAC	p.R56H
Pat_06	Post-Resistance	ZC3H6	376940	37	2	113067600	113067600	Missense_Mutation	SNP	T	C	3	138	c.475T>C	c.(475-477)TAC>CAC	p.Y159H
Pat_06	Post-Resistance	UGGT1	56886	37	2	128900767	128900767	Missense_Mutation	SNP	G	T	5	611	c.1819G>T	c.(1819-1821)GGG>TGG	p.G607W
Pat_06	Post-Resistance	NCKAP5	344148	37	2	133541535	133541535	Missense_Mutation	SNP	G	C	3	142	c.2849C>G	c.(2848-2850)GCA>GGA	p.A950G
Pat_06	Post-Resistance	LCT	3938	37	2	136558358	136558358	Missense_Mutation	SNP	G	A	4	285	c.4685C>T	c.(4684-4686)ACT>ATT	p.T1562I
Pat_06	Post-Resistance	LCT	3938	37	2	136570402	136570402	Missense_Mutation	SNP	G	C	3	233	c.1832C>G	c.(1831-1833)CCA>CGA	p.P611R
Pat_06	Post-Resistance	KYNU	8942	37	2	143712436	143712436	Missense_Mutation	SNP	T	G	3	276	c.431T>G	c.(430-432)CTA>CGA	p.L144R
Pat_06	Post-Resistance	GALNT13	114805	37	2	155115620	155115620	Missense_Mutation	SNP	G	T	10	700	c.944G>T	c.(943-945)TGG>TTG	p.W315L
Pat_06	Post-Resistance	TTC30A	92104	37	2	178482916	178482916	Missense_Mutation	SNP	C	A	6	779	c.514G>T	c.(514-516)GCT>TCT	p.A172S
Pat_06	Post-Resistance	TTN	7273	37	2	179610475	179610475	Missense_Mutation	SNP	C	T	139	497	c.16652G>A	c.(16651-16653)GGA>GA	p.G5551E

Pat_06	Post-Resistance	STAT1	6772	37	2	191841571	191841571	Missense_Mutation	SNP	T	C	4	447	c.2054A>G	c.(2053-2055)AAG>AGG	p.K685R
Pat_06	Post-Resistance	SDPR	8436	37	2	192711366	192711366	Missense_Mutation	SNP	C	G	3	294	c.286G>C	c.(286-288)GAC>CAC	p.D96H
Pat_06	Post-Resistance	RAPH1	65059	37	2	204305505	204305505	Missense_Mutation	SNP	G	A	4	485	c.2408C>T	c.(2407-2409)CCA>CTA	p.P803L
Pat_06	Post-Resistance	PARD3B	117583	37	2	206037092	206037092	Missense_Mutation	SNP	A	G	3	199	c.1778A>G	c.(1777-1779)GAG>GGG	p.E593G
Pat_06	Post-Resistance	ZDBF2	57683	37	2	207176040	207176040	Missense_Mutation	SNP	A	G	3	36	c.6788A>G	c.(6787-6789)AAG>AGG	p.K2263R
Pat_06	Post-Resistance	TNS1	7145	37	2	218696222	218696222	Missense_Mutation	SNP	A	G	4	207	c.2954T>C	c.(2953-2955)CTG>CCG	p.L985P
Pat_06	Post-Resistance	DOCK10	55619	37	2	225659740	225659740	Missense_Mutation	SNP	C	A	6	748	c.5010G>T	c.(5008-5010)CAG>CAT	p.Q1670H
Pat_06	Post-Resistance	DOCK10	55619	37	2	225710253	225710253	Missense_Mutation	SNP	T	C	3	123	c.2342A>G	c.(2341-2343)GAG>GGG	p.E781G
Pat_06	Post-Resistance	ATG16L1	55054	37	2	234171821	234171821	Missense_Mutation	SNP	G	A	4	301	c.255G>A	c.(253-255)ATG>ATA	p.M85I
Pat_06	Post-Resistance	USP40	55230	37	2	234431912	234431912	Missense_Mutation	SNP	G	A	6	838	c.2138C>T	c.(2137-2139)ACG>ATG	p.T713M
Pat_06	Post-Resistance	GBX2	2637	37	2	237076365	237076365	Missense_Mutation	SNP	G	A	3	112	c.250C>T	c.(250-252)CCC>TCC	p.P84S
Pat_06	Post-Resistance	IQCA1	79781	37	2	237300984	237300984	Missense_Mutation	SNP	A	G	3	33	c.1220T>C	c.(1219-1221)ATG>ACG	p.M407T
Pat_06	Post-Resistance	PER2	8864	37	2	239171652	239171652	Missense_Mutation	SNP	G	C	3	256	c.1094C>G	c.(1093-1095)CCA>CGA	p.P365R
Pat_06	Post-Resistance	ASB1	51665	37	2	239342236	239342236	Missense_Mutation	SNP	C	G	3	180	c.91C>G	c.(91-93)CAT>GAT	p.H31D
Pat_06	Post-Resistance	GPC1	2817	37	2	241404077	241404077	Missense_Mutation	SNP	G	A	5	241	c.928G>A	c.(928-930)GTG>ATG	p.V310M
Pat_06	Post-Resistance	ANO7	50636	37	2	242152003	242152003	Missense_Mutation	SNP	G	A	3	153	c.1852G>A	c.(1852-1854)GGC>AGC	p.G618S
Pat_06	Post-Resistance	C2orf85	285093	37	2	242813889	242813889	Missense_Mutation	SNP	G	A	3	88	c.182G>A	c.(181-183)GGG>GAG	p.G61E
Pat_06	Post-Resistance	ATRN	8455	37	20	3528125	3528125	Nonsense_Mutation	SNP	C	A	4	239	c.932C>A	c.(931-933)TCA>TAA	p.S311*
Pat_06	Post-Resistance	PANK2	80025	37	20	3870051	3870051	Missense_Mutation	SNP	G	A	3	27	c.304G>A	c.(304-306)GCG>ACG	p.A102T
Pat_06	Post-Resistance	NKX2-4	644524	37	20	21377956	21377956	Missense_Mutation	SNP	T	C	3	93	c.82A>G	c.(82-84)AGC>GGC	p.S28G
Pat_06	Post-Resistance	SSTR4	6754	37	20	23016853	23016853	Missense_Mutation	SNP	G	A	5	309	c.733G>A	c.(733-735)GCT>ACT	p.A245T
Pat_06	Post-Resistance	SUN5	140732	37	20	31573702	31573702	Missense_Mutation	SNP	A	G	3	280	c.737T>C	c.(736-738)GTG>GCG	p.V246A
Pat_06	Post-Resistance	PROCR	10544	37	20	33762727	33762727	Missense_Mutation	SNP	G	A	3	38	c.293G>A	c.(292-294)CGC>CAC	p.R98H
Pat_06	Post-Resistance	SCAND1	51282	37	20	34542183	34542183	Missense_Mutation	SNP	C	G	3	209	c.24G>C	c.(22-24)TTG>TTC	p.L8F
Pat_06	Post-Resistance	SAMHD1	25939	37	20	35563541	35563541	Nonsense_Mutation	SNP	G	A	4	418	c.400C>T	c.(400-402)CGA>TGA	p.R134*
Pat_06	Post-Resistance	MYBL2	4605	37	20	42340156	42340156	Missense_Mutation	SNP	T	C	3	139	c.1634T>C	c.(1633-1635)TTG>TCG	p.L545S
Pat_06	Post-Resistance	ADA	100	37	20	43254215	43254215	Missense_Mutation	SNP	T	C	3	69	c.473A>G	c.(472-474)CAG>CGG	p.Q158R
Pat_06	Post-Resistance	TP53TG5	27296	37	20	44004010	44004010	Missense_Mutation	SNP	G	A	6	732	c.437C>T	c.(436-438)GCG>GTG	p.A146V
Pat_06	Post-Resistance	NEURL2	140825	37	20	44518913	44518913	Missense_Mutation	SNP	G	A	5	290	c.718C>T	c.(718-720)CGC>TGC	p.R240C
Pat_06	Post-Resistance	DDX27	55661	37	20	47853049	47853049	Splice_Site	SNP	T	C	3	173	c.1780_splice	c.e14+2	p.D594_splice
Pat_06	Post-Resistance	B4GALT5	9334	37	20	48256244	48256244	Nonsense_Mutation	SNP	C	T	6	711	c.888G>A	c.(886-888)TGG>TGA	p.W296*
Pat_06	Post-Resistance	SLC9A8	23315	37	20	48431630	48431630	Missense_Mutation	SNP	C	A	7	471	c.112C>A	c.(112-114)CCT>ACT	p.P38T
Pat_06	Post-Resistance	SPATA2	9825	37	20	48522326	48522326	Missense_Mutation	SNP	G	A	5	475	c.1393C>T	c.(1393-1395)CGC>TGC	p.R465C
Pat_06	Post-Resistance	TMEM189-UBE2V	387522	37	20	48746152	48746152	Missense_Mutation	SNP	C	T	4	465	c.409G>A	c.(409-411)GGG>AGG	p.G137R
Pat_06	Post-Resistance	CASS4	57091	37	20	55033771	55033771	Missense_Mutation	SNP	C	G	3	99	c.2329C>G	c.(2329-2331)CAC>GAC	p.H777D
Pat_06	Post-Resistance	ZBP1	81030	37	20	56191510	56191510	Missense_Mutation	SNP	T	C	4	441	c.49A>G	c.(49-51)AGA>GGA	p.R17G
Pat_06	Post-Resistance	SS18L1	26039	37	20	60747785	60747785	Missense_Mutation	SNP	G	A	5	472	c.964G>A	c.(964-966)GCG>ACG	p.A322T
Pat_06	Post-Resistance	COL20A1	57642	37	20	61929285	61929285	Missense_Mutation	SNP	G	A	5	383	c.106G>A	c.(106-108)GTG>ATG	p.V36M
Pat_06	Post-Resistance	NRIP1	8204	37	21	16339298	16339298	Missense_Mutation	SNP	C	G	6	808	c.1216G>C	c.(1216-1218)GAG>CAG	p.E406Q
Pat_06	Post-Resistance	SYNJ1	8867	37	21	34067386	34067386	Missense_Mutation	SNP	T	C	12	800	c.803A>G	c.(802-804)AAT>AGT	p.N268S
Pat_06	Post-Resistance	MX2	4600	37	21	42754364	42754364	Missense_Mutation	SNP	G	A	4	229	c.605G>A	c.(604-606)CGG>CAG	p.R202Q
Pat_06	Post-Resistance	ICOSLG	23308	37	21	45655431	45655431	Missense_Mutation	SNP	G	A	6	693	c.421C>T	c.(421-423)CCC>TCC	p.P141S
Pat_06	Post-Resistance	COL6A2	1292	37	21	47542067	47542067	Missense_Mutation	SNP	G	A	4	260	c.1567G>A	c.(1567-1569)GCA>ACA	p.A523T
Pat_06	Post-Resistance	GAB4	128954	37	22	17489052	17489052	Translation_Start_Site	SNP	G	A	3	42	c.-47C>T	c.(-49--45)AACGC>AATGC	
Pat_06	Post-Resistance	MICAL3	57553	37	22	18300139	18300139	Missense_Mutation	SNP	G	A	4	68	c.5288C>T	c.(5287-5289)ACC>ATC	p.T1763I
Pat_06	Post-Resistance	MICAL3	57553	37	22	18300679	18300679	Missense_Mutation	SNP	G	C	4	244	c.4748C>G	c.(4747-4749)CCC>CGC	p.P1583R
Pat_06	Post-Resistance	ZDHHC8	29801	37	22	20127660	20127660	Missense_Mutation	SNP	G	A	7	693	c.580G>A	c.(580-582)GGC>AGC	p.G194S

Pat_06	Post-Resistance	KLHL22	84861	37	22	20800753	20800753	Missense_Mutation	SNP	C	T	5	253	c.1516G>A	c.(1516-1518)GGA>AGA	p.G506R
Pat_06	Post-Resistance	LOC391322	391322	37	22	24373625	24373625	Missense_Mutation	SNP	G	A	3	71	c.124G>A	c.(124-126)GTA>ATA	p.V42I
Pat_06	Post-Resistance	CABIN1	23523	37	22	24560506	24560506	Missense_Mutation	SNP	C	A	5	301	c.4885C>A	c.(4885-4887)CTT>ATT	p.L1629I
Pat_06	Post-Resistance	GGT5	2687	37	22	24628048	24628048	Missense_Mutation	SNP	T	C	3	189	c.725A>G	c.(724-726)CAG>CGG	p.Q242R
Pat_06	Post-Resistance	EWSR1	2130	37	22	29678453	29678453	Missense_Mutation	SNP	T	C	3	268	c.488T>C	c.(487-489)CTA>CCA	p.L163P
Pat_06	Post-Resistance	GAS2L1	10634	37	22	29704568	29704568	Missense_Mutation	SNP	T	C	3	70	c.473T>C	c.(472-474)GTG>GCG	p.V158A
Pat_06	Post-Resistance	CABP7	164633	37	22	30125524	30125524	Missense_Mutation	SNP	C	T	6	443	c.614C>T	c.(613-615)GCG>GTG	p.A205V
Pat_06	Post-Resistance	TOM1	10043	37	22	35730374	35730374	Missense_Mutation	SNP	C	G	3	243	c.1081C>G	c.(1081-1083)CGA>GGA	p.R361G
Pat_06	Post-Resistance	LGALS1	3956	37	22	38074611	38074611	Missense_Mutation	SNP	A	G	3	107	c.211A>G	c.(211-213)ACC>GCC	p.T71A
Pat_06	Post-Resistance	NFAM1	150372	37	22	42807425	42807425	Missense_Mutation	SNP	T	C	3	80	c.439A>G	c.(439-441)ATC>GTC	p.I147V
Pat_06	Post-Resistance	PANX2	56666	37	22	50609350	50609350	Missense_Mutation	SNP	T	C	3	84	c.191T>C	c.(190-192)CTG>CCG	p.L64P
Pat_06	Post-Resistance	CPT1B	1375	37	22	51012066	51012066	Missense_Mutation	SNP	T	C	3	152	c.1049A>G	c.(1048-1050)GAG>GGG	p.E350G
Pat_06	Post-Resistance	SETMAR	6419	37	3	4354858	4354858	Missense_Mutation	SNP	A	G	4	240	c.433A>G	c.(433-435)AAG>GAG	p.K145E
Pat_06	Post-Resistance	RAF1	5894	37	3	12626736	12626736	Missense_Mutation	SNP	C	G	3	264	c.1553G>C	c.(1552-1554)CGA>CCA	p.R518P
Pat_06	Post-Resistance	GPD1L	23171	37	3	32200561	32200561	Missense_Mutation	SNP	G	A	4	468	c.812G>A	c.(811-813)CGG>CAG	p.R271Q
Pat_06	Post-Resistance	DCLK3	85443	37	3	36763141	36763141	Missense_Mutation	SNP	T	G	6	421	c.1462A>C	c.(1462-1464)AAT>CAT	p.N488H
Pat_06	Post-Resistance	SETD2	29072	37	3	47162297	47162297	Missense_Mutation	SNP	T	C	3	285	c.3829A>G	c.(3829-3831)AGC>GGC	p.S1277G
Pat_06	Post-Resistance	TREX1	11277	37	3	48506398	48506398	Translation_Start_Site	SNP	G	A	6	391	c.-1088G>A	1090--1086)GCGTG>GCATG	
Pat_06	Post-Resistance	BSN	8927	37	3	49690213	49690213	Missense_Mutation	SNP	G	A	3	115	c.3224G>A	c.(3223-3225)CGG>CAG	p.R1075Q
Pat_06	Post-Resistance	DOCK3	1795	37	3	51376408	51376408	Missense_Mutation	SNP	C	T	3	102	c.3715C>T	c.(3715-3717)CGC>TGC	p.R1239C
Pat_06	Post-Resistance	ATXN7	6314	37	3	63981284	63981284	Missense_Mutation	SNP	G	A	5	852	c.1786G>A	c.(1786-1788)GCA>ACA	p.A596T
Pat_06	Post-Resistance	ADAMTS9	56999	37	3	64673345	64673345	Translation_Start_Site	SNP	C	T	3	55	c.-11G>A	c.(-13--9)GGGTG>GGATG	
Pat_06	Post-Resistance	IMPG2	50939	37	3	101023117	101023117	Missense_Mutation	SNP	C	A	4	325	c.374G>T	c.(373-375)TGG>TTG	p.W125L
Pat_06	Post-Resistance	ADPRH	141	37	3	119306540	119306540	Missense_Mutation	SNP	T	C	4	338	c.889T>C	c.(889-891)TTT>CTT	p.F297L
Pat_06	Post-Resistance	CASR	846	37	3	121981026	121981026	Missense_Mutation	SNP	G	A	92	275	c.1144G>A	c.(1144-1146)GAC>AAC	p.D382N
Pat_06	Post-Resistance	CCDC14	64770	37	3	123633735	123633735	Nonsense_Mutation	SNP	G	C	3	207	c.2753C>G	c.(2752-2754)TCA>TGA	p.S918*
Pat_06	Post-Resistance	PLXNA1	5361	37	3	126708286	126708286	Missense_Mutation	SNP	C	T	7	851	c.781C>T	c.(781-783)CGG>TGG	p.R261W
Pat_06	Post-Resistance	MCM2	4171	37	3	127335840	127335840	Missense_Mutation	SNP	C	T	6	688	c.1652C>T	c.(1651-1653)GCG>GTG	p.A551V
Pat_06	Post-Resistance	KY	339855	37	3	134323197	134323197	Missense_Mutation	SNP	C	T	4	465	c.1210G>A	c.(1210-1212)GTG>ATG	p.V404M
Pat_06	Post-Resistance	DZIP1L	199221	37	3	137822486	137822486	Nonsense_Mutation	SNP	G	A	3	89	c.328C>T	c.(328-330)CAG>TAG	p.Q110*
Pat_06	Post-Resistance	CLSTN2	64084	37	3	140178544	140178544	Missense_Mutation	SNP	G	A	5	452	c.1155G>A	c.(1153-1155)ATG>ATA	p.M385I
Pat_06	Post-Resistance	GMPS	8833	37	3	155654264	155654264	Missense_Mutation	SNP	A	G	8	619	c.1945A>G	c.(1945-1947)ATA>GTA	p.I649V
Pat_06	Post-Resistance	SLC7A14	57709	37	3	170218966	170218966	Missense_Mutation	SNP	A	C	72	267	c.473T>G	c.(472-474)TTT>TGT	p.F158C
Pat_06	Post-Resistance	EIF4A2	1974	37	3	186501404	186501404	Missense_Mutation	SNP	C	G	176	491	c.5C>G	c.(4-6)TCT>TGT	p.S2C
Pat_06	Post-Resistance	ZNF732	654254	37	4	265139	265139	Missense_Mutation	SNP	C	T	4	52	c.1504G>A	c.(1504-1506)GAA>AAA	p.E502K
Pat_06	Post-Resistance	TBC1D14	57533	37	4	7016285	7016285	Splice_Site	SNP	G	A	4	166	c.1757_splice	c.e12+1	p.W586_splice
Pat_06	Post-Resistance	SH3TC1	54436	37	4	8230002	8230002	Nonsense_Mutation	SNP	C	T	4	311	c.2581C>T	c.(2581-2583)CAG>TAG	p.Q861*
Pat_06	Post-Resistance	BOD1L	259282	37	4	13601655	13601655	Missense_Mutation	SNP	G	A	3	79	c.6869C>T	c.(6868-6870)ACC>ATC	p.T2290I
Pat_06	Post-Resistance	PCDH7	5099	37	4	30724350	30724350	Missense_Mutation	SNP	G	A	4	231	c.1306G>A	c.(1306-1308)GTT>ATT	p.V436I
Pat_06	Post-Resistance	LRRC66	339977	37	4	52860732	52860732	Missense_Mutation	SNP	G	A	4	285	c.2456C>T	c.(2455-2457)CCG>CTG	p.P819L
Pat_06	Post-Resistance	PPBP	5473	37	4	74853048	74853048	Missense_Mutation	SNP	C	A	5	648	c.328G>T	c.(328-330)GCT>TCT	p.A110S
Pat_06	Post-Resistance	FRAS1	80144	37	4	79238664	79238664	Splice_Site	SNP	T	C	3	132	c.1960_splice	c.e17+2	p.A654_splice
Pat_06	Post-Resistance	FRAS1	80144	37	4	79295316	79295316	Missense_Mutation	SNP	G	A	6	679	c.3062G>A	c.(3061-3063)TGC>TAC	p.C1021Y
Pat_06	Post-Resistance	BBS12	166379	37	4	123664066	123664066	Missense_Mutation	SNP	T	C	3	265	c.1019T>C	c.(1018-1020)GTA>GCA	p.V340A
Pat_06	Post-Resistance	MAML3	55534	37	4	140811349	140811349	Missense_Mutation	SNP	G	A	5	649	c.1241C>T	c.(1240-1242)GCT>GTT	p.A414V
Pat_06	Post-Resistance	CMYA5	202333	37	5	79031109	79031109	Missense_Mutation	SNP	G	A	21	150	c.6521G>A	c.(6520-6522)GGA>GAA	p.G2174E
Pat_06	Post-Resistance	FAM170A	340069	37	5	118969733	118969733	Missense_Mutation	SNP	C	A	6	417	c.290C>A	c.(289-291)CCC>CAC	p.P97H

Pat_06	Post-Resistance	ISOC1	51015	37	5	128430619	128430619	Missense_Mutation	SNP	T	G	4	235	c.160T>G	c.(160-162)TTC>GTC	p.F54V
Pat_06	Post-Resistance	PSD2	84249	37	5	139193889	139193889	Missense_Mutation	SNP	G	T	6	258	c.956G>T	c.(955-957)CGC>CTC	p.R319L
Pat_06	Post-Resistance	SLC4A9	83697	37	5	139747047	139747047	Missense_Mutation	SNP	G	C	3	141	c.2128G>C	c.(2128-2130)GCC>CCC	p.A710P
Pat_06	Post-Resistance	SLC35A4	113829	37	5	139947539	139947539	Missense_Mutation	SNP	T	C	3	306	c.785T>C	c.(784-786)CTA>CCA	p.L262P
Pat_06	Post-Resistance	PCDHA2	56146	37	5	140175828	140175828	Missense_Mutation	SNP	G	A	6	739	c.1279G>A	c.(1279-1281)GCA>ACA	p.A427T
Pat_06	Post-Resistance	PCDHA13	56136	37	5	140263132	140263132	Missense_Mutation	SNP	G	A	6	858	c.1279G>A	c.(1279-1281)GCG>ACG	p.A427T
Pat_06	Post-Resistance	PCDHGC4	56098	37	5	140864841	140864841	Missense_Mutation	SNP	C	T	5	433	c.101C>T	c.(100-102)CCG>CTG	p.P34L
Pat_06	Post-Resistance	DIAPH1	1729	37	5	140953306	140953306	Missense_Mutation	SNP	G	A	3	89	c.2111C>T	c.(2110-2112)CCT>CTT	p.P704L
Pat_06	Post-Resistance	CSNK1A1	1452	37	5	148886617	148886617	Missense_Mutation	SNP	A	G	3	187	c.830T>C	c.(829-831)CTG>CCG	p.L277P
Pat_06	Post-Resistance	GALNT10	55568	37	5	153792462	153792462	Missense_Mutation	SNP	G	A	5	574	c.1400G>A	c.(1399-1401)GGC>GAC	p.G467D
Pat_06	Post-Resistance	SAP30L	79685	37	5	153830726	153830726	Missense_Mutation	SNP	A	G	3	233	c.277A>G	c.(277-279)AGT>GGT	p.S93G
Pat_06	Post-Resistance	KCNMB1	3779	37	5	169805934	169805934	Missense_Mutation	SNP	C	T	4	382	c.350G>A	c.(349-351)CGG>CAG	p.R117Q
Pat_06	Post-Resistance	GFPT2	9945	37	5	179740862	179740862	Missense_Mutation	SNP	G	A	4	94	c.1376C>T	c.(1375-1377)ACC>ATC	p.T459I
Pat_06	Post-Resistance	SLC22A23	63027	37	6	3273527	3273527	Missense_Mutation	SNP	G	A	6	757	c.1823C>T	c.(1822-1824)ACG>ATG	p.T608M
Pat_06	Post-Resistance	PRL	5617	37	6	22294729	22294729	Missense_Mutation	SNP	C	T	69	330	c.113G>A	c.(112-114)CGA>CAA	p.R38Q
Pat_06	Post-Resistance	ZSCAN23	222696	37	6	28403718	28403718	Missense_Mutation	SNP	C	A	5	385	c.326G>T	c.(325-327)AGA>ATA	p.R109I
Pat_06	Post-Resistance	CFB	629	37	6	31914934	31914934	Missense_Mutation	SNP	G	A	5	596	c.449G>A	c.(448-450)CGA>CAA	p.R150Q
Pat_06	Post-Resistance	SLC39A7	7922	37	6	33171342	33171342	Missense_Mutation	SNP	G	A	4	371	c.1162G>A	c.(1162-1164)GCA>ACA	p.A388T
Pat_06	Post-Resistance	ITPR3	3710	37	6	33635663	33635663	Missense_Mutation	SNP	G	A	6	527	c.1808G>A	c.(1807-1809)CGC>CAC	p.R603H
Pat_06	Post-Resistance	LEMD2	221496	37	6	33756788	33756788	Missense_Mutation	SNP	G	A	4	233	c.106C>T	c.(106-108)CGC>TGC	p.R36C
Pat_06	Post-Resistance	FGD2	221472	37	6	36995854	36995854	Missense_Mutation	SNP	T	C	3	175	c.1883T>C	c.(1882-1884)CTG>CCG	p.L628P
Pat_06	Post-Resistance	DAAM2	23500	37	6	39859198	39859198	Missense_Mutation	SNP	G	C	3	104	c.2227G>C	c.(2227-2229)GAC>CAC	p.D743H
Pat_06	Post-Resistance	ZNF318	24149	37	6	43322656	43322656	Missense_Mutation	SNP	G	A	4	263	c.2416C>T	c.(2416-2418)CCC>TCC	p.P806S
Pat_06	Post-Resistance	C6orf154	221424	37	6	43475355	43475355	Missense_Mutation	SNP	T	C	3	255	c.719A>G	c.(718-720)AAC>AGC	p.N240S
Pat_06	Post-Resistance	XPO5	57510	37	6	43523648	43523648	Missense_Mutation	SNP	T	G	3	292	c.1366A>C	c.(1366-1368)AAA>CAA	p.K456Q
Pat_06	Post-Resistance	SPATS1	221409	37	6	44320517	44320517	Missense_Mutation	SNP	C	G	3	205	c.194C>G	c.(193-195)CCC>CGC	p.P65R
Pat_06	Post-Resistance	TDRD6	221400	37	6	46657207	46657207	Missense_Mutation	SNP	C	G	3	255	c.1342C>G	c.(1342-1344)CAG>GAG	p.Q448E
Pat_06	Post-Resistance	PKHD1	5314	37	6	51875171	51875171	Missense_Mutation	SNP	G	A	6	480	c.5687C>T	c.(5686-5688)ACG>ATG	p.T1896M
Pat_06	Post-Resistance	COL9A1	1297	37	6	70993524	70993524	Splice_Site	SNP	C	G	24	34	c.697_splice	c.e6-1	p.F233_splice
Pat_06	Post-Resistance	PHIP	55023	37	6	79695070	79695070	Missense_Mutation	SNP	T	C	5	792	c.2536A>G	c.(2536-2538)AGT>GGT	p.S846G
Pat_06	Post-Resistance	ME1	4199	37	6	84025099	84025099	Missense_Mutation	SNP	G	A	5	364	c.634C>T	c.(634-636)CGG>TGG	p.R212W
Pat_06	Post-Resistance	ANKRD6	22881	37	6	90322066	90322066	Missense_Mutation	SNP	T	C	3	56	c.493T>C	c.(493-495)TCC>CCC	p.S165P
Pat_06	Post-Resistance	USP45	85015	37	6	99887732	99887732	Splice_Site	SNP	C	A	5	200	c.2074_splice	c.e16-1	p.A692_splice
Pat_06	Post-Resistance	LAMA4	3910	37	6	112512904	112512904	Missense_Mutation	SNP	C	T	4	280	c.652G>A	c.(652-654)GGA>AGA	p.G218R
Pat_06	Post-Resistance	LAMA2	3908	37	6	129775409	129775409	Missense_Mutation	SNP	A	G	3	199	c.6683A>G	c.(6682-6684)TAT>TGT	p.Y2228C
Pat_06	Post-Resistance	TMEM200A	114801	37	6	130762856	130762856	Missense_Mutation	SNP	A	G	3	274	c.1289A>G	c.(1288-1290)TAT>TGT	p.Y430C
Pat_06	Post-Resistance	HECA	51696	37	6	139495612	139495612	Missense_Mutation	SNP	G	A	6	799	c.1403G>A	c.(1402-1404)GGC>GAC	p.G468D
Pat_06	Post-Resistance	TXLNB	167838	37	6	139564000	139564000	Missense_Mutation	SNP	G	A	4	302	c.1718C>T	c.(1717-1719)CCT>CTT	p.P573L
Pat_06	Post-Resistance	GPR126	57211	37	6	142688774	142688774	Missense_Mutation	SNP	C	A	4	191	c.172C>A	c.(172-174)CCT>ACT	p.P58T
Pat_06	Post-Resistance	C6orf72	116254	37	6	149893643	149893643	Missense_Mutation	SNP	G	C	3	210	c.181G>C	c.(181-183)GTT>CTT	p.V61L
Pat_06	Post-Resistance	KATNA1	11104	37	6	149924440	149924440	Missense_Mutation	SNP	C	G	48	100	c.693G>C	c.(691-693)ATG>ATC	p.M231I
Pat_06	Post-Resistance	RSPH3	83861	37	6	159420638	159420638	Missense_Mutation	SNP	G	A	5	428	c.371C>T	c.(370-372)GCG>GTG	p.A124V
Pat_06	Post-Resistance	SLC22A2	6582	37	6	160645834	160645834	Missense_Mutation	SNP	C	T	4	245	c.1504G>A	c.(1504-1506)GTG>ATG	p.V502M
Pat_06	Post-Resistance	SFT2D1	113402	37	6	166755912	166755912	Missense_Mutation	SNP	C	T	3	30	c.58G>A	c.(58-60)GCG>ACG	p.A20T
Pat_06	Post-Resistance	INTS1	26173	37	7	1515926	1515926	Missense_Mutation	SNP	C	A	3	79	c.5317G>T	c.(5317-5319)GAT>TAT	p.D1773Y
Pat_06	Post-Resistance	SDK1	221935	37	7	4153892	4153892	Missense_Mutation	SNP	G	A	3	54	c.3809G>A	c.(3808-3810)CGG>CAG	p.R1270Q
Pat_06	Post-Resistance	FOXK1	221937	37	7	4794193	4794193	Missense_Mutation	SNP	G	A	5	318	c.850G>A	c.(850-852)GCA>ACA	p.A284T

Pat_06	Post-Resistance	DAGLB	221955	37	7	6464417	6464417	Missense_Mutation	SNP	A	G	5	451	c.1106T>C	c.(1105-1107)GTT>GCT	p.V369A
Pat_06	Post-Resistance	MIOS	54468	37	7	7612113	7612113	Missense_Mutation	SNP	G	A	4	349	c.7G>A	c.(7-9)GGT>AGT	p.G3S
Pat_06	Post-Resistance	SPDYE1	285955	37	7	44047000	44047000	Missense_Mutation	SNP	C	T	7	828	c.766C>T	c.(766-768)CCG>TCG	p.P256S
Pat_06	Post-Resistance	MYO1G	64005	37	7	45004684	45004684	Missense_Mutation	SNP	G	A	6	635	c.2386C>T	c.(2386-2388)CGG>TGG	p.R796W
Pat_06	Post-Resistance	IKZF1	10320	37	7	50468123	50468123	Missense_Mutation	SNP	G	A	4	245	c.1358G>A	c.(1357-1359)AGC>AAC	p.S453N
Pat_06	Post-Resistance	GRB10	2887	37	7	50672987	50672987	Missense_Mutation	SNP	C	A	5	312	c.1389G>T	c.(1387-1389)AGG>AGT	p.R463S
Pat_06	Post-Resistance	TYW1B	441250	37	7	72209564	72209564	Missense_Mutation	SNP	C	T	5	386	c.979G>A	c.(979-981)GAG>AAG	p.E327K
Pat_06	Post-Resistance	POM121C	100101267	37	7	75070845	75070845	Missense_Mutation	SNP	G	A	41	59	c.656C>T	c.(655-657)CCG>CTG	p.P219L
Pat_06	Post-Resistance	TMEM120A	83862	37	7	75617790	75617790	Missense_Mutation	SNP	G	A	6	786	c.422C>T	c.(421-423)ACC>ATC	p.T141I
Pat_06	Post-Resistance	CDK14	5218	37	7	90233532	90233532	Missense_Mutation	SNP	C	A	3	55	c.92C>A	c.(91-93)GCT>GAT	p.A31D
Pat_06	Post-Resistance	PEG10	23089	37	7	94293611	94293611	Missense_Mutation	SNP	G	C	3	156	c.971G>C	c.(970-972)CGC>CCC	p.R324P
Pat_06	Post-Resistance	AZGP1	563	37	7	99565784	99565784	Missense_Mutation	SNP	G	A	4	395	c.607C>T	c.(607-609)CGG>TGG	p.R203W
Pat_06	Post-Resistance	C7orf51	222950	37	7	100084595	100084595	Missense_Mutation	SNP	T	C	3	98	c.220T>C	c.(220-222)TGC>CGC	p.C74R
Pat_06	Post-Resistance	FBXO24	26261	37	7	100197706	100197706	Missense_Mutation	SNP	T	C	3	129	c.1259T>C	c.(1258-1260)CTG>CCG	p.L420P
Pat_06	Post-Resistance	GIGYF1	64599	37	7	100279543	100279543	Missense_Mutation	SNP	T	C	3	219	c.2999A>G	c.(2998-3000)GAG>GGG	p.E1000G
Pat_06	Post-Resistance	MUC17	140453	37	7	100683150	100683150	Missense_Mutation	SNP	A	T	171	732	c.8453A>T	c.(8452-8454)AAC>ATC	p.N2818I
Pat_06	Post-Resistance	VGF	7425	37	7	100807448	100807448	Missense_Mutation	SNP	G	A	3	80	c.677C>T	c.(676-678)CCG>CTG	p.P226L
Pat_06	Post-Resistance	C7orf52	375607	37	7	100815850	100815850	Missense_Mutation	SNP	G	A	3	47	c.620C>T	c.(619-621)ACC>ATC	p.T207I
Pat_06	Post-Resistance	PLOD3	8985	37	7	100855148	100855148	Missense_Mutation	SNP	C	G	3	118	c.1211G>C	c.(1210-1212)CGT>CCT	p.R404P
Pat_06	Post-Resistance	MYL10	93408	37	7	101267540	101267540	Missense_Mutation	SNP	G	A	4	241	c.83C>T	c.(82-84)CCG>CTG	p.P28L
Pat_06	Post-Resistance	DPY19L2P2	349152	37	7	102825947	102825947	Missense_Mutation	SNP	A	G	6	609	c.1048T>C	c.(1048-1050)TGT>CGT	p.C350R
Pat_06	Post-Resistance	COG5	10466	37	7	107204271	107204271	Missense_Mutation	SNP	G	C	3	405	c.164C>G	c.(163-165)ACA>AGA	p.T55R
Pat_06	Post-Resistance	CFTR	1080	37	7	117232572	117232572	Missense_Mutation	SNP	A	G	3	243	c.2351A>G	c.(2350-2352)CAC>CGC	p.H784R
Pat_06	Post-Resistance	GRM8	2918	37	7	126746570	126746570	Missense_Mutation	SNP	G	A	5	452	c.707C>T	c.(706-708)ACC>ATC	p.T236I
Pat_06	Post-Resistance	AKR1B1	231	37	7	134136435	134136435	Missense_Mutation	SNP	G	A	6	530	c.137C>T	c.(136-138)GCC>GTC	p.A46V
Pat_06	Post-Resistance	HIPK2	28996	37	7	139257680	139257680	Missense_Mutation	SNP	T	G	3	177	c.3590A>C	c.(3589-3591)TAC>TCC	p.Y1197S
Pat_06	Post-Resistance	BRAF	673	37	7	140453136	140453136	Missense_Mutation	SNP	A	T	210	324	c.1799T>A	c.(1798-1800)GTG>GAG	p.V600E
Pat_06	Post-Resistance	EZH2	2146	37	7	148511118	148511118	Missense_Mutation	SNP	G	A	8	796	c.1769C>T	c.(1768-1770)GCC>GTC	p.A590V
Pat_06	Post-Resistance	SSPO	23145	37	7	149489010	149489010	Missense_Mutation	SNP	G	A	4	220	c.5351G>A	c.(5350-5352)CGC>CAC	p.R1784H
Pat_06	Post-Resistance	MCPH1	79648	37	8	6296572	6296572	Missense_Mutation	SNP	A	G	3	123	c.535A>G	c.(535-537)AGA>GGA	p.R179G
Pat_06	Post-Resistance	USP17L2	377630	37	8	11994912	11994912	Missense_Mutation	SNP	C	T	6	370	c.1358G>A	c.(1357-1359)AGA>AAA	p.R453K
Pat_06	Post-Resistance	SLC39A14	23516	37	8	22273697	22273697	Missense_Mutation	SNP	G	A	6	353	c.1051G>A	c.(1051-1053)GAT>AAT	p.D351N
Pat_06	Post-Resistance	PTK2B	2185	37	8	27308269	27308269	Missense_Mutation	SNP	G	C	3	250	c.2344G>C	c.(2344-2346)GAG>CAG	p.E782Q
Pat_06	Post-Resistance	SCARA3	51435	37	8	27516933	27516933	Missense_Mutation	SNP	C	T	3	66	c.1246C>T	c.(1246-1248)CGC>TGC	p.R416C
Pat_06	Post-Resistance	RNF5P1	286140	37	8	38458594	38458594	Missense_Mutation	SNP	C	T	5	337	c.125G>A	c.(124-126)TGT>TAT	p.C42Y
Pat_06	Post-Resistance	FAM110B	90362	37	8	59059268	59059268	Missense_Mutation	SNP	C	G	4	60	c.479C>G	c.(478-480)GCG>GGG	p.A160G
Pat_06	Post-Resistance	ZFHX4	79776	37	8	77616835	77616835	Missense_Mutation	SNP	C	G	3	241	c.512C>G	c.(511-513)GCA>GGA	p.A171G
Pat_06	Post-Resistance	VPS13B	157680	37	8	100821631	100821631	Missense_Mutation	SNP	G	A	5	355	c.8045G>A	c.(8044-8046)GGC>GAC	p.G2682D
Pat_06	Post-Resistance	VPS13B	157680	37	8	100874058	100874058	Missense_Mutation	SNP	G	A	3	69	c.11174G>A	c.(11173-11175)CGG>CAG	p.R3725Q
Pat_06	Post-Resistance	PKHD1L1	93035	37	8	110504128	110504128	Nonsense_Mutation	SNP	C	T	3	120	c.10141C>T	c.(10141-10143)CGA>TGA	p.R3381*
Pat_06	Post-Resistance	DSCC1	79075	37	8	120867980	120867980	Missense_Mutation	SNP	G	A	4	56	c.56C>T	c.(55-57)GCG>GTG	p.A19V
Pat_06	Post-Resistance	COL14A1	7373	37	8	121292236	121292236	Missense_Mutation	SNP	A	G	4	360	c.3544A>G	c.(3544-3546)AGT>GGT	p.S1182G
Pat_06	Post-Resistance	ZHX2	22882	37	8	123965964	123965964	Nonsense_Mutation	SNP	C	A	5	425	c.2214C>A	c.(2212-2214)TGC>TGA	p.C738*
Pat_06	Post-Resistance	NDRG1	10397	37	8	134276788	134276788	Splice_Site	SNP	A	G	4	455	c.205_splice	c.e4+1	p.H69_splice
Pat_06	Post-Resistance	DENND3	22898	37	8	142185524	142185524	Missense_Mutation	SNP	G	T	7	374	c.2261G>T	c.(2260-2262)GGC>GTC	p.G754V
Pat_06	Post-Resistance	GPR20	2843	37	8	142367263	142367263	Missense_Mutation	SNP	A	G	3	62	c.761T>C	c.(760-762)TTC>TCC	p.F254S
Pat_06	Post-Resistance	BAI1	575	37	8	143607961	143607961	Missense_Mutation	SNP	C	T	4	226	c.3371C>T	c.(3370-3372)ACG>ATG	p.T1124M

Pat_06	Post-Resistance	ZNF16	7564	37	8	146157752	146157752	Missense_Mutation	SNP	T	C	63	199	c.421A>G	c.(421-423)ATG>GTG	p.M141V
Pat_06	Post-Resistance	TYRP1	7306	37	9	12707996	12707996	Splice_Site	SNP	G	C	3	91	c.1262_splice	c.e7-1	p.D421_splice
Pat_06	Post-Resistance	KLHL9	55958	37	9	21334255	21334255	Missense_Mutation	SNP	G	A	4	288	c.604C>T	c.(604-606)CTT>TTT	p.L202F
Pat_06	Post-Resistance	FBXO10	26267	37	9	37537229	37537229	Missense_Mutation	SNP	G	A	4	156	c.1297C>T	c.(1297-1299)CGC>TGC	p.R433C
Pat_06	Post-Resistance	TRPM3	80036	37	9	73233830	73233830	Missense_Mutation	SNP	C	T	5	445	c.2275G>A	c.(2275-2277)GAC>AAC	p.D759N
Pat_06	Post-Resistance	ZNF169	169841	37	9	97063314	97063314	Missense_Mutation	SNP	G	T	5	302	c.1474G>T	c.(1474-1476)GGG>TGG	p.G492W
Pat_06	Post-Resistance	ZNF462	58499	37	9	109691319	109691319	Missense_Mutation	SNP	G	A	6	459	c.5126G>A	c.(5125-5127)CGC>CAC	p.R1709H
Pat_06	Post-Resistance	KIAA0368	23392	37	9	114131392	114131392	Missense_Mutation	SNP	T	C	3	180	c.5570A>G	c.(5569-5571)AAG>AGG	p.K1857R
Pat_06	Post-Resistance	AKNA	80709	37	9	117099578	117099578	Missense_Mutation	SNP	G	A	5	401	c.4076C>T	c.(4075-4077)GCG>GTG	p.A1359V
Pat_06	Post-Resistance	FBXW2	26190	37	9	123550186	123550186	Missense_Mutation	SNP	C	A	130	439	c.351G>T	c.(349-351)TTG>TTT	p.L117F
Pat_06	Post-Resistance	ST6GALNAC4	27090	37	9	130676967	130676967	Missense_Mutation	SNP	A	G	3	247	c.166T>C	c.(166-168)TTC>CTC	p.F56L
Pat_06	Post-Resistance	ZER1	10444	37	9	131515603	131515603	Missense_Mutation	SNP	G	A	3	63	c.586C>T	c.(586-588)CGG>TGG	p.R196W
Pat_06	Post-Resistance	USP20	10868	37	9	132637886	132637886	Missense_Mutation	SNP	C	A	5	424	c.2266C>A	c.(2266-2268)CTG>ATG	p.L756M
Pat_06	Post-Resistance	FUBP3	8939	37	9	133506164	133506164	Missense_Mutation	SNP	G	C	3	188	c.1267G>C	c.(1267-1269)GAG>CAG	p.E423Q
Pat_06	Post-Resistance	BAT2L1	84726	37	9	134334694	134334694	Missense_Mutation	SNP	A	G	3	117	c.1355A>G	c.(1354-1356)CAG>CGG	p.Q452R
Pat_06	Post-Resistance	TTF1	7270	37	9	135266041	135266041	Missense_Mutation	SNP	C	A	6	712	c.2165G>T	c.(2164-2166)TGG>TTG	p.W722L
Pat_06	Post-Resistance	ADAMTS13	11093	37	9	136310144	136310144	Missense_Mutation	SNP	G	A	3	101	c.2581G>A	c.(2581-2583)GGG>AGG	p.G861R
Pat_06	Post-Resistance	DBH	1621	37	9	136505098	136505098	Missense_Mutation	SNP	A	G	3	235	c.470A>G	c.(469-471)AAG>AGG	p.K157R
Pat_06	Post-Resistance	FBXW5	54461	37	9	139837958	139837958	Missense_Mutation	SNP	G	A	4	111	c.194C>T	c.(193-195)GCG>GTG	p.A65V
Pat_06	Post-Resistance	GRIN1	2902	37	9	140057746	140057746	Missense_Mutation	SNP	G	A	5	554	c.2297G>A	c.(2296-2298)AGC>AAC	p.S766N
Pat_06	Post-Resistance	COBRA1	25920	37	9	140166616	140166616	Missense_Mutation	SNP	G	A	6	403	c.1429G>A	c.(1429-1431)GCC>ACC	p.A477T
Pat_06	Post-Resistance	TUBBP5	643224	37	9	141070695	141070695	Missense_Mutation	SNP	G	A	4	26	c.98G>A	c.(97-99)CGC>CAC	p.R33H
Pat_06	Post-Resistance	GPR64	10149	37	X	19031908	19031908	Missense_Mutation	SNP	G	A	6	811	c.995C>T	c.(994-996)ACC>ATC	p.T332I
Pat_06	Post-Resistance	PHEX	5251	37	X	22239812	22239812	Nonsense_Mutation	SNP	C	A	6	560	c.1851C>A	c.(1849-1851)TGC>TGA	p.C617*
Pat_06	Post-Resistance	DCAF8L1	139425	37	X	27998773	27998773	Missense_Mutation	SNP	G	A	5	421	c.679C>T	c.(679-681)CGG>TGG	p.R227W
Pat_06	Post-Resistance	DMD	1756	37	X	31366745	31366745	Missense_Mutation	SNP	C	T	5	199	c.9091G>A	c.(9091-9093)GTC>ATC	p.V3031I
Pat_06	Post-Resistance	FAM47C	442444	37	X	37027190	37027190	Missense_Mutation	SNP	T	C	8	539	c.707T>C	c.(706-708)CTG>CCG	p.L236P
Pat_06	Post-Resistance	SLC9A7	84679	37	X	46618310	46618310	Missense_Mutation	SNP	C	T	3	86	c.155G>A	c.(154-156)AGC>AAC	p.S52N
Pat_06	Post-Resistance	FTSJ1	24140	37	X	48340865	48340865	Missense_Mutation	SNP	T	C	3	209	c.730T>C	c.(730-732)TAT>CAT	p.Y244H
Pat_06	Post-Resistance	FTSJ1	24140	37	X	48341160	48341160	Missense_Mutation	SNP	G	C	3	151	c.935G>C	c.(934-936)TGC>TCC	p.C312S
Pat_06	Post-Resistance	CACNA1F	778	37	X	49081415	49081415	Missense_Mutation	SNP	G	A	4	168	c.1718C>T	c.(1717-1719)ACG>ATG	p.T573M
Pat_06	Post-Resistance	GNL3L	54552	37	X	54565532	54565532	Nonsense_Mutation	SNP	C	T	3	44	c.79C>T	c.(79-81)CAG>TAG	p.Q27*
Pat_06	Post-Resistance	GNL3L	54552	37	X	54569649	54569649	Missense_Mutation	SNP	T	C	3	195	c.400T>C	c.(400-402)TAC>CAC	p.Y134H
Pat_06	Post-Resistance	TRO	7216	37	X	54955605	54955605	Missense_Mutation	SNP	G	T	9	427	c.2448G>T	c.(2446-2448)ATG>ATT	p.M816I
Pat_06	Post-Resistance	RRAGB	10325	37	X	55757870	55757870	Missense_Mutation	SNP	T	C	3	215	c.451T>C	c.(451-453)TAT>CAT	p.Y151H
Pat_06	Post-Resistance	SYTL4	94121	37	X	99942091	99942091	Missense_Mutation	SNP	G	A	5	565	c.1157C>T	c.(1156-1158)GCT>GTT	p.A386V
Pat_06	Post-Resistance	RAB40AL	282808	37	X	102192775	102192775	Missense_Mutation	SNP	C	T	5	192	c.529C>T	c.(529-531)CGG>TGG	p.R177W
Pat_06	Post-Resistance	IL1RAPL2	26280	37	X	104478654	104478654	Missense_Mutation	SNP	A	G	4	379	c.509A>G	c.(508-510)AAG>AGG	p.K170R
Pat_06	Post-Resistance	BCORL1	63035	37	X	129149296	129149296	Missense_Mutation	SNP	G	A	4	467	c.2548G>A	c.(2548-2550)GGG>AGG	p.G850R
Pat_06	Post-Resistance	AFF2	2334	37	X	148037917	148037917	Missense_Mutation	SNP	T	C	8	684	c.2342T>C	c.(2341-2343)ATT>ACT	p.I781T
Pat_06	Post-Resistance	PLXNB3	5365	37	X	153033099	153033099	Missense_Mutation	SNP	C	A	6	68	c.817C>A	c.(817-819)CTG>ATG	p.L273M
Pat_06	Post-Resistance	PLXNB3	5365	37	X	153042342	153042342	Missense_Mutation	SNP	G	A	4	127	c.4834G>A	c.(4834-4836)GTC>ATC	p.V1612I
Pat_06	Post-Resistance	L1CAM	3897	37	X	153130579	153130579	Missense_Mutation	SNP	C	T	4	153	c.2836G>A	c.(2836-2838)GGC>AGC	p.G946S
Pat_06	Post-Resistance	GAB3	139716	37	X	153925486	153925486	Missense_Mutation	SNP	G	A	6	563	c.1345C>T	c.(1345-1347)CGG>TGG	p.R449W
Pat_08	Pre-Treatment	ACAP3	116983	37	1	1230911	1230911	Missense_Mutation	SNP	G	A	16	36	c.1729C>T	c.(1729-1731)CGC>TGC	p.R577C
Pat_08	Pre-Treatment	PANK4	55229	37	1	2452281	2452281	Missense_Mutation	SNP	G	A	28	39	c.487C>T	c.(487-489)CCC>TCC	p.P163S
Pat_08	Pre-Treatment	UBE4B	10277	37	1	10211599	10211599	Missense_Mutation	SNP	C	T	36	86	c.2906C>T	c.(2905-2907)TCC>TTC	p.S969F

Pat_08	Pre-Treatment	PRAMEF8	391002	37	1	12979691	12979691	Missense_Mutation	SNP	G	A	61	237	c.883G>A	c.(883-885)GAG>AAG	p.E295K
Pat_08	Pre-Treatment	FBLIM1	54751	37	1	16093982	16093982	Missense_Mutation	SNP	C	T	7	11	c.362C>T	c.(361-363)GCT>GTT	p.A121V
Pat_08	Pre-Treatment	KDM4A	9682	37	1	44132167	44132167	Missense_Mutation	SNP	C	T	79	120	c.718C>T	c.(718-720)CAC>TAC	p.H240Y
Pat_08	Pre-Treatment	C1orf168	199920	37	1	57216843	57216843	Nonsense_Mutation	SNP	G	A	15	28	c.1261C>T	c.(1261-1263)CAG>TAG	p.Q421*
Pat_08	Pre-Treatment	C8B	732	37	1	57422471	57422471	Missense_Mutation	SNP	C	T	183	382	c.362G>A	c.(361-363)CGA>CAA	p.R121Q
Pat_08	Pre-Treatment	C1orf173	127254	37	1	75072512	75072512	Missense_Mutation	SNP	C	T	57	93	c.1262G>A	c.(1261-1263)GGA>GAA	p.G421E
Pat_08	Pre-Treatment	LPHN2	23266	37	1	82409213	82409213	Missense_Mutation	SNP	G	A	45	84	c.958G>A	c.(958-960)GTC>ATC	p.V320I
Pat_08	Pre-Treatment	TGFBR3	7049	37	1	92184982	92184982	Missense_Mutation	SNP	G	A	73	146	c.1453C>T	c.(1453-1455)CCT>TCT	p.P485S
Pat_08	Pre-Treatment	COL11A1	1301	37	1	103440405	103440405	Missense_Mutation	SNP	G	A	16	31	c.2789C>T	c.(2788-2790)CCT>CTT	p.P930L
Pat_08	Pre-Treatment	MAGI3	260425	37	1	114225824	114225824	Missense_Mutation	SNP	G	A	24	54	c.3634G>A	c.(3634-3636)GAA>AAA	p.E1212K
Pat_08	Pre-Treatment	TBX15	6913	37	1	119469191	119469191	Missense_Mutation	SNP	G	A	26	54	c.145C>T	c.(145-147)CCA>TCA	p.P49S
Pat_08	Pre-Treatment	C1orf43	25912	37	1	154180066	154180066	Missense_Mutation	SNP	T	C	74	133	c.625A>G	c.(625-627)ACT>GCT	p.T209A
Pat_08	Pre-Treatment	RUSC1	23623	37	1	155295412	155295412	Missense_Mutation	SNP	C	T	32	91	c.1763C>T	c.(1762-1764)CCG>CTG	p.P588L
Pat_08	Pre-Treatment	CASQ1	844	37	1	160160558	160160558	Missense_Mutation	SNP	G	A	21	47	c.17G>A	c.(16-18)AGG>AAG	p.R6K
Pat_08	Pre-Treatment	C1orf192	257177	37	1	161335356	161335356	Missense_Mutation	SNP	A	T	141	196	c.308T>A	c.(307-309)CTC>CAC	p.L103H
Pat_08	Pre-Treatment	DARS2	55157	37	1	173802529	173802529	Missense_Mutation	SNP	C	T	8	6	c.508C>T	c.(508-510)CGG>TGG	p.R170W
Pat_08	Pre-Treatment	KIAA1614	57710	37	1	180885295	180885295	Missense_Mutation	SNP	C	T	25	53	c.56C>T	c.(55-57)CCC>CTC	p.P19L
Pat_08	Pre-Treatment	CACNA1E	777	37	1	181765951	181765951	Missense_Mutation	SNP	C	T	11	14	c.6227C>T	c.(6226-6228)TCC>TTC	p.S2076F
Pat_08	Pre-Treatment	KIF21B	23046	37	1	200945966	200945966	Missense_Mutation	SNP	C	T	10	25	c.4381G>A	c.(4381-4383)GTC>ATC	p.V1461I
Pat_08	Pre-Treatment	LGR6	59352	37	1	202276021	202276021	Missense_Mutation	SNP	G	A	23	43	c.1162G>A	c.(1162-1164)GAA>AAA	p.E388K
Pat_08	Pre-Treatment	PIGR	5284	37	1	207110830	207110830	Missense_Mutation	SNP	G	A	36	81	c.655C>T	c.(655-657)CTC>TTC	p.L219F
Pat_08	Pre-Treatment	GPATCH2	55105	37	1	217604543	217604543	Missense_Mutation	SNP	G	A	96	180	c.1531C>T	c.(1531-1533)CCT>TCT	p.P511S
Pat_08	Pre-Treatment	TLR5	7100	37	1	223286024	223286024	Missense_Mutation	SNP	C	T	61	87	c.350G>A	c.(349-351)GGA>GAA	p.G117E
Pat_08	Pre-Treatment	TTC13	79573	37	1	231060707	231060707	Missense_Mutation	SNP	G	A	60	119	c.1601C>T	c.(1600-1602)GCC>GTC	p.A534V
Pat_08	Pre-Treatment	SLC35F3	148641	37	1	234454596	234454596	Missense_Mutation	SNP	C	T	59	117	c.847C>T	c.(847-849)CCT>TCT	p.P283S
Pat_08	Pre-Treatment	NID1	4811	37	1	236187487	236187487	Missense_Mutation	SNP	G	A	39	70	c.2011C>T	c.(2011-2013)CCC>TCC	p.P671S
Pat_08	Pre-Treatment	RYR2	6262	37	1	237774224	237774224	Missense_Mutation	SNP	G	A	17	36	c.4846G>A	c.(4846-4848)GGC>AGC	p.G1616S
Pat_08	Pre-Treatment	NLRP3	114548	37	1	247582193	247582193	Missense_Mutation	SNP	C	T	18	19	c.97C>T	c.(97-99)CCT>TCT	p.P33S
Pat_08	Pre-Treatment	OR2G3	81469	37	1	247769368	247769368	Missense_Mutation	SNP	A	G	54	81	c.481A>G	c.(481-483)ACT>GCT	p.T161A
Pat_08	Pre-Treatment	CUBN	8029	37	10	17142048	17142048	Missense_Mutation	SNP	C	T	179	69	c.1721G>A	c.(1720-1722)AGA>AAA	p.R574K
Pat_08	Pre-Treatment	ASAH2	56624	37	10	52003017	52003017	Missense_Mutation	SNP	C	T	136	88	c.455G>A	c.(454-456)CGA>CAA	p.R152Q
Pat_08	Pre-Treatment	ARID5B	84159	37	10	63851366	63851366	Missense_Mutation	SNP	C	T	47	26	c.2144C>T	c.(2143-2145)CCT>CTT	p.P715L
Pat_08	Pre-Treatment	LRRTM3	347731	37	10	68687605	68687605	Missense_Mutation	SNP	G	A	41	26	c.931G>A	c.(931-933)GGG>AGG	p.G311R
Pat_08	Pre-Treatment	CYP2C18	1562	37	10	96466634	96466634	Missense_Mutation	SNP	G	A	24	14	c.736G>A	c.(736-738)GAG>AAG	p.E246K
Pat_08	Pre-Treatment	C10orf137	26098	37	10	127409788	127409788	Missense_Mutation	SNP	C	T	83	39	c.124C>T	c.(124-126)CTT>TTT	p.L42F
Pat_08	Pre-Treatment	ATHL1	80162	37	11	294703	294703	Missense_Mutation	SNP	C	T	144	273	c.2168C>T	c.(2167-2169)TCC>TTC	p.S723F
Pat_08	Pre-Treatment	MUC5B	727897	37	11	1262686	1262686	Missense_Mutation	SNP	G	A	17	27	c.6655G>A	c.(6655-6657)GAC>AAC	p.D2219N
Pat_08	Pre-Treatment	KRTAP5-5	439915	37	11	1651402	1651402	Missense_Mutation	SNP	C	T	31	66	c.332C>T	c.(331-333)TCC>TTC	p.S111F
Pat_08	Pre-Treatment	KCNQ1	3784	37	11	2606487	2606487	Missense_Mutation	SNP	A	G	37	88	c.1078A>G	c.(1078-1080)AGG>GGG	p.R360G
Pat_08	Pre-Treatment	SLC22A18	5002	37	11	2924603	2924603	Nonsense_Mutation	SNP	C	T	38	85	c.28C>T	c.(28-30)CAG>TAG	p.Q10*
Pat_08	Pre-Treatment	OR51S1	119692	37	11	4869568	4869568	Missense_Mutation	SNP	G	A	69	123	c.871C>T	c.(871-873)CCT>TCT	p.P291S
Pat_08	Pre-Treatment	OR51A4	401666	37	11	4967847	4967848	Missense_Mutation	DNP	GG	AA	61	110	c.483_484CC>TT	(481-486)TTCCCT>TTTTC	p.P162S
Pat_08	Pre-Treatment	OR51I1	390063	37	11	5462416	5462416	Missense_Mutation	SNP	G	A	28	47	c.329C>T	c.(328-330)TCC>TTC	p.S110F
Pat_08	Pre-Treatment	UBQLNL	143630	37	11	5536653	5536653	Missense_Mutation	SNP	G	A	80	119	c.1019C>T	c.(1018-1020)TCT>TTT	p.S340F
Pat_08	Pre-Treatment	OR52N5	390075	37	11	5799521	5799521	Missense_Mutation	SNP	C	T	25	56	c.344G>A	c.(343-345)GGG>GAG	p.G115E
Pat_08	Pre-Treatment	GTF2H1	2965	37	11	18379556	18379556	Missense_Mutation	SNP	C	T	23	62	c.1318C>T	c.(1318-1320)CTT>TTT	p.L440F
Pat_08	Pre-Treatment	CCDC34	91057	37	11	27379017	27379017	Missense_Mutation	SNP	G	A	70	81	c.431C>T	c.(430-432)CCA>CTA	p.P144L

Pat_08	Pre-Treatment	C11orf74	119710	37	11	36631726	36631726	Missense_Mutation	SNP	C	T	33	50	c.73C>T	c.(73-75)CTT>TTT	p.L25F
Pat_08	Pre-Treatment	CHST1	8534	37	11	45672110	45672110	Missense_Mutation	SNP	C	T	34	51	c.364G>A	c.(364-366)GAC>AAC	p.D122N
Pat_08	Pre-Treatment	RAPSN	5913	37	11	47463243	47463243	Missense_Mutation	SNP	C	T	20	40	c.832G>A	c.(832-834)GAG>AAG	p.E278K
Pat_08	Pre-Treatment	OR4D6	219983	37	11	59225019	59225019	Missense_Mutation	SNP	G	A	63	87	c.586G>A	c.(586-588)GAG>AAG	p.E196K
Pat_08	Pre-Treatment	AHNAK	79026	37	11	62286730	62286731	Missense_Mutation	DNP	GG	AA	149	223	15158_15159CC>	c.(15157-15159)GCC>GTT	p.A5053V
Pat_08	Pre-Treatment	TSGA10IP	254187	37	11	65714616	65714616	Missense_Mutation	SNP	C	T	7	12	c.320C>T	c.(319-321)CCC>CTC	p.P107L
Pat_08	Pre-Treatment	P4HA3	283208	37	11	74013458	74013458	Missense_Mutation	SNP	G	A	84	146	c.523C>T	c.(523-525)CGG>TGG	p.R175W
Pat_08	Pre-Treatment	C11orf67	28971	37	11	77553557	77553557	Missense_Mutation	SNP	A	T	9	28	c.15A>T	c.(13-15)GAA>GAT	p.E5D
Pat_08	Pre-Treatment	ODZ4	26011	37	11	78440676	78440676	Missense_Mutation	SNP	C	T	51	99	c.3151G>A	c.(3151-3153)GAA>AAA	p.E1051K
Pat_08	Pre-Treatment	TRPC6	7225	37	11	101375120	101375120	Missense_Mutation	SNP	T	C	39	65	c.580A>G	c.(580-582)ACC>GCC	p.T194A
Pat_08	Pre-Treatment	EXPH5	23086	37	11	108381210	108381210	Missense_Mutation	SNP	A	G	138	188	c.5024T>C	c.(5023-5025)ATT>ACT	p.I1675T
Pat_08	Pre-Treatment	USP28	57646	37	11	113701595	113701595	Missense_Mutation	SNP	G	A	67	125	c.904C>T	c.(904-906)CGT>TGT	p.R302C
Pat_08	Pre-Treatment	FAM55B	120406	37	11	114569092	114569092	Missense_Mutation	SNP	G	A	9	20	c.458G>A	c.(457-459)AGG>AAG	p.R153K
Pat_08	Pre-Treatment	DSCAML1	57453	37	11	117389456	117389456	Missense_Mutation	SNP	G	A	14	36	c.1415C>T	c.(1414-1416)TCG>TTG	p.S472L
Pat_08	Pre-Treatment	OR4D5	219875	37	11	123810973	123810973	Missense_Mutation	SNP	C	T	102	221	c.650C>T	c.(649-651)TCG>TTG	p.S217L
Pat_08	Pre-Treatment	VWA5A	4013	37	11	123994449	123994449	Missense_Mutation	SNP	G	A	32	43	c.1102G>A	c.(1102-1104)GAA>AAA	p.E368K
Pat_08	Pre-Treatment	OR8B8	26493	37	11	124310824	124310824	Missense_Mutation	SNP	G	A	34	58	c.158C>T	c.(157-159)TCT>TTT	p.S53F
Pat_08	Pre-Treatment	NTM	50863	37	11	132016408	132016408	Missense_Mutation	SNP	G	A	17	24	c.400G>A	c.(400-402)GTA>ATA	p.V134I
Pat_08	Pre-Treatment	DCP1B	196513	37	12	2061949	2061949	Missense_Mutation	SNP	C	T	20	41	c.1157G>A	c.(1156-1158)AGA>AAA	p.R386K
Pat_08	Pre-Treatment	CD163L1	283316	37	12	7596704	7596704	Missense_Mutation	SNP	G	A	42	90	c.20C>T	c.(19-21)TCG>TTG	p.S7L
Pat_08	Pre-Treatment	NANOG	79923	37	12	7947082	7947082	Missense_Mutation	SNP	G	A	7	15	c.444G>A	c.(442-444)ATG>ATA	p.M148I
Pat_08	Pre-Treatment	KLRC3	3823	37	12	10572989	10572989	Missense_Mutation	SNP	C	T	60	161	c.161G>A	c.(160-162)GGG>GAG	p.G54E
Pat_08	Pre-Treatment	ABCC9	10060	37	12	22065982	22065982	Missense_Mutation	SNP	G	A	37	56	c.835C>T	c.(835-837)CCA>TCA	p.P279S
Pat_08	Pre-Treatment	SYT10	341359	37	12	33579224	33579224	Missense_Mutation	SNP	C	T	45	78	c.358G>A	c.(358-360)GAA>AAA	p.E120K
Pat_08	Pre-Treatment	ADAMTS20	80070	37	12	43769952	43769952	Splice_Site	SNP	C	T	4	6	c.5221_splice	c.e35-1	p.I1741_splice
Pat_08	Pre-Treatment	ADAMTS20	80070	37	12	43945643	43945643	Missense_Mutation	SNP	G	A	32	47	c.82C>T	c.(82-84)CCC>TCC	p.P28S
Pat_08	Pre-Treatment	PUS7L	83448	37	12	44148157	44148157	Missense_Mutation	SNP	C	T	60	120	c.892G>A	c.(892-894)GGA>AGA	p.G298R
Pat_08	Pre-Treatment	COL2A1	1280	37	12	48389088	48389088	Missense_Mutation	SNP	G	A	66	108	c.712C>T	c.(712-714)CCC>TCC	p.P238S
Pat_08	Pre-Treatment	RND1	27289	37	12	49251927	49251927	Missense_Mutation	SNP	G	A	40	47	c.551C>T	c.(550-552)TCC>TTC	p.S184F
Pat_08	Pre-Treatment	KRT84	3890	37	12	52774929	52774929	Missense_Mutation	SNP	C	T	71	170	c.1138G>A	c.(1138-1140)GAG>AAG	p.E380K
Pat_08	Pre-Treatment	KRT6B	3854	37	12	52844377	52844377	Missense_Mutation	SNP	C	G	13	50	c.568G>C	c.(568-570)GTT>CTT	p.V190L
Pat_08	Pre-Treatment	KRT6A	3853	37	12	52885322	52885322	Missense_Mutation	SNP	C	T	28	90	c.739G>A	c.(739-741)GAG>AAG	p.E247K
Pat_08	Pre-Treatment	OR6C75	390323	37	12	55759372	55759372	Missense_Mutation	SNP	C	T	34	46	c.478C>T	c.(478-480)CTT>TTT	p.L160F
Pat_08	Pre-Treatment	GLI1	2735	37	12	57860059	57860059	Missense_Mutation	SNP	G	A	164	258	c.799G>A	c.(799-801)GAG>AAG	p.E267K
Pat_08	Pre-Treatment	MSRB3	253827	37	12	65722374	65722374	Missense_Mutation	SNP	C	T	45	64	c.275C>T	c.(274-276)CCA>CTA	p.P92L
Pat_08	Pre-Treatment	PTPRB	5787	37	12	71002869	71002869	Missense_Mutation	SNP	C	T	36	160	c.305G>A	c.(304-306)AGA>AAA	p.R102K
Pat_08	Pre-Treatment	C12orf12	196477	37	12	91348220	91348220	Nonsense_Mutation	SNP	C	T	13	18	c.300G>A	c.(298-300)TGG>TGA	p.W100*
Pat_08	Pre-Treatment	AMDHD1	144193	37	12	96356148	96356148	Missense_Mutation	SNP	G	A	23	46	c.829G>A	c.(829-831)GGA>AGA	p.G277R
Pat_08	Pre-Treatment	MMAB	326625	37	12	110006647	110006647	Missense_Mutation	SNP	C	T	49	75	c.218G>A	c.(217-219)GGA>GAA	p.G73E
Pat_08	Pre-Treatment	HPD	3242	37	12	122286921	122286921	Missense_Mutation	SNP	C	T	70	129	c.580G>A	c.(580-582)GTG>ATG	p.V194M
Pat_08	Pre-Treatment	ZCCHC8	55596	37	12	122958814	122958814	Missense_Mutation	SNP	C	T	42	95	c.1354G>A	c.(1354-1356)GTA>ATA	p.V452I
Pat_08	Pre-Treatment	GTF2H3	2967	37	12	124144370	124144370	Missense_Mutation	SNP	G	A	66	103	c.713G>A	c.(712-714)AGA>AAA	p.R238K
Pat_08	Pre-Treatment	RIMBP2	23504	37	12	130926738	130926738	Missense_Mutation	SNP	A	C	19	36	c.1108T>G	c.(1108-1110)TGC>GGC	p.C370G
Pat_08	Pre-Treatment	TUBA3C	7278	37	13	19752472	19752472	Missense_Mutation	SNP	C	T	45	72	c.289G>A	c.(289-291)GAA>AAA	p.E97K
Pat_08	Pre-Treatment	WASF3	10810	37	13	27259911	27259911	Missense_Mutation	SNP	C	T	24	37	c.1438C>T	c.(1438-1440)CGG>TGG	p.R480W
Pat_08	Pre-Treatment	GPR12	2835	37	13	27333521	27333521	Nonsense_Mutation	SNP	G	C	15	38	c.444C>G	c.(442-444)TAC>TAG	p.Y148*
Pat_08	Pre-Treatment	NBEA	26960	37	13	36124729	36124729	Missense_Mutation	SNP	G	A	13	30	c.6701G>A	c.(6700-6702)CGA>CAA	p.R2234Q

Pat_08	Pre-Treatment	NALCN	259232	37	13	101936361	101936361	Missense_Mutation	SNP	C	T	20	40	c.1057G>A	c.(1057-1059)GAA>AAA	p.E353K
Pat_08	Pre-Treatment	NOVA1	4857	37	14	26917922	26917922	Missense_Mutation	SNP	G	A	83	132	c.767C>T	c.(766-768)GCC>GTC	p.A256V
Pat_08	Pre-Treatment	NPAS3	64067	37	14	34204525	34204525	Missense_Mutation	SNP	C	T	49	97	c.839C>T	c.(838-840)TCA>TTA	p.S280L
Pat_08	Pre-Treatment	RALGAPA1	253959	37	14	36191052	36191052	Missense_Mutation	SNP	A	G	40	71	c.2108T>C	c.(2107-2109)GTT>GCT	p.V703A
Pat_08	Pre-Treatment	PNN	5411	37	14	39649841	39649842	Missense_Mutation	DNP	GG	AA	8	9	c.928_929GG>AA	c.(928-930)GGT>AAT	p.G310N
Pat_08	Pre-Treatment	CDKL1	8814	37	14	50844945	50844945	Missense_Mutation	SNP	G	A	21	25	c.1304C>T	c.(1303-1305)CCC>CTC	p.P435L
Pat_08	Pre-Treatment	KCNH5	27133	37	14	63174583	63174583	Missense_Mutation	SNP	T	A	47	76	c.2610A>T	c.(2608-2610)AAA>AAT	p.K870N
Pat_08	Pre-Treatment	ZFYVE26	23503	37	14	68274583	68274583	Missense_Mutation	SNP	G	A	68	122	c.418C>T	c.(418-420)CCA>TCA	p.P140S
Pat_08	Pre-Treatment	DPF3	8110	37	14	73141047	73141047	Missense_Mutation	SNP	G	A	10	14	c.772C>T	c.(772-774)CCC>TCC	p.P258S
Pat_08	Pre-Treatment	DPF3	8110	37	14	73190363	73190363	Missense_Mutation	SNP	C	T	115	213	c.503G>A	c.(502-504)CGA>CAA	p.R168Q
Pat_08	Pre-Treatment	NRXN3	9369	37	14	79181364	79181364	Missense_Mutation	SNP	G	A	25	53	c.807G>A	c.(805-807)ATG>ATA	p.M269I
Pat_08	Pre-Treatment	SERPINA10	51156	37	14	94754734	94754734	Missense_Mutation	SNP	C	T	21	30	c.881G>A	c.(880-882)GGA>GAA	p.G294E
Pat_08	Pre-Treatment	SERPINA1	5265	37	14	94847406	94847406	Missense_Mutation	SNP	A	C	19	23	c.719T>G	c.(718-720)GTG>GGG	p.V240G
Pat_08	Pre-Treatment	SERPINA9	327657	37	14	94935565	94935565	Missense_Mutation	SNP	G	A	38	32	c.667C>T	c.(667-669)CAC>TAC	p.H223Y
Pat_08	Pre-Treatment	THBS1	7057	37	15	39874759	39874759	Missense_Mutation	SNP	G	A	20	45	c.433G>A	c.(433-435)GAA>AAA	p.E145K
Pat_08	Pre-Treatment	DLL4	54567	37	15	41228744	41228744	Missense_Mutation	SNP	C	T	11	17	c.1559C>T	c.(1558-1560)CCC>CTC	p.P520L
Pat_08	Pre-Treatment	UNC13C	440279	37	15	54305875	54305875	Missense_Mutation	SNP	G	A	24	58	c.775G>A	c.(775-777)GAA>AAA	p.E259K
Pat_08	Pre-Treatment	UNC13C	440279	37	15	54557657	54557657	Missense_Mutation	SNP	G	A	3	2	c.3781G>A	c.(3781-3783)GGA>AGA	p.G1261R
Pat_08	Pre-Treatment	UNC13C	440279	37	15	54825218	54825218	Missense_Mutation	SNP	G	A	9	13	c.5650G>A	c.(5650-5652)GAT>AAT	p.D1884N
Pat_08	Pre-Treatment	FEM1B	10116	37	15	68582681	68582681	Missense_Mutation	SNP	C	T	46	81	c.985C>T	c.(985-987)CTT>TTT	p.L329F
Pat_08	Pre-Treatment	CSPG4	1464	37	15	75982510	75982510	Missense_Mutation	SNP	G	A	36	46	c.896C>T	c.(895-897)TCC>TTC	p.S299F
Pat_08	Pre-Treatment	IREB2	3658	37	15	78789516	78789516	Missense_Mutation	SNP	C	T	53	133	c.2644C>T	c.(2644-2646)CAT>TAT	p.H882Y
Pat_08	Pre-Treatment	ITFG3	83986	37	16	314061	314061	Missense_Mutation	SNP	C	T	21	56	c.1235C>T	c.(1234-1236)GCC>GTC	p.A412V
Pat_08	Pre-Treatment	PTX4	390667	37	16	1537629	1537629	Missense_Mutation	SNP	G	A	12	27	c.469C>T	c.(469-471)CAC>TAC	p.H157Y
Pat_08	Pre-Treatment	ABCC1	4363	37	16	16108367	16108367	Missense_Mutation	SNP	T	C	44	32	c.371T>C	c.(370-372)ATT>ACT	p.I124T
Pat_08	Pre-Treatment	DNAH3	55567	37	16	21098326	21098326	Nonsense_Mutation	SNP	C	T	54	118	c.2721G>A	c.(2719-2721)TGG>TGA	p.W907*
Pat_08	Pre-Treatment	RBBP6	5930	37	16	24580595	24580595	Missense_Mutation	SNP	C	T	29	66	c.2584C>T	c.(2584-2586)CCA>TCA	p.P862S
Pat_08	Pre-Treatment	C16orf78	123970	37	16	49407878	49407878	Missense_Mutation	SNP	G	A	33	70	c.28G>A	c.(28-30)GAT>AAT	p.D10N
Pat_08	Pre-Treatment	GALNS	2588	37	16	88902160	88902160	Missense_Mutation	SNP	G	A	22	52	c.731C>T	c.(730-732)CCC>CTC	p.P244L
Pat_08	Pre-Treatment	GALNS	2588	37	16	88904145	88904145	Missense_Mutation	SNP	G	A	48	97	c.451C>T	c.(451-453)CCC>TCC	p.P151S
Pat_08	Pre-Treatment	TRPV1	7442	37	17	3494574	3494574	Missense_Mutation	SNP	C	T	17	18	c.358G>A	c.(358-360)GAA>AAA	p.E120K
Pat_08	Pre-Treatment	ZZEF1	23140	37	17	4013068	4013068	Missense_Mutation	SNP	T	C	20	48	c.1156A>G	c.(1156-1158)AAG>GAG	p.K386E
Pat_08	Pre-Treatment	DHX33	56919	37	17	5352203	5352203	Missense_Mutation	SNP	C	T	35	34	c.1741G>A	c.(1741-1743)GAG>AAG	p.E581K
Pat_08	Pre-Treatment	PLSCR3	57048	37	17	7296213	7296213	Missense_Mutation	SNP	G	A	206	407	c.566C>T	c.(565-567)CCC>CTC	p.P189L
Pat_08	Pre-Treatment	GLP2R	9340	37	17	9729447	9729447	Missense_Mutation	SNP	G	A	9	6	c.67G>A	c.(67-69)GAG>AAG	p.E23K
Pat_08	Pre-Treatment	FOXN1	8456	37	17	26864216	26864216	Missense_Mutation	SNP	C	T	28	96	c.1709C>T	c.(1708-1710)TCG>TTG	p.S570L
Pat_08	Pre-Treatment	SLC6A4	6532	37	17	28548904	28548904	Missense_Mutation	SNP	C	T	45	103	c.73G>A	c.(73-75)GGA>AGA	p.G25R
Pat_08	Pre-Treatment	C17orf66	256957	37	17	34192286	34192286	Missense_Mutation	SNP	C	T	49	73	c.253G>A	c.(253-255)GAC>AAC	p.D85N
Pat_08	Pre-Treatment	KRT17	3872	37	17	39775880	39775880	Missense_Mutation	SNP	G	A	67	176	c.1265C>T	c.(1264-1266)TCC>TTC	p.S422F
Pat_08	Pre-Treatment	MPP2	4355	37	17	41956666	41956666	Missense_Mutation	SNP	C	T	53	119	c.1594G>A	c.(1594-1596)GGA>AGA	p.G532R
Pat_08	Pre-Treatment	FMNL1	752	37	17	43323883	43323883	Missense_Mutation	SNP	G	A	49	82	c.3223G>A	c.(3223-3225)GTG>ATG	p.V1075M
Pat_08	Pre-Treatment	KIAA1267	284058	37	17	44144090	44144090	Missense_Mutation	SNP	G	C	25	19	c.1661C>G	c.(1660-1662)CCT>CGT	p.P554R
Pat_08	Pre-Treatment	TEX14	56155	37	17	56671001	56671001	Missense_Mutation	SNP	C	T	46	74	c.2509G>A	c.(2509-2511)GGA>AGA	p.G837R
Pat_08	Pre-Treatment	RPTOR	57521	37	17	78919517	78919518	Missense_Mutation	DNP	CC	TT	25	86	.3076_3077CC>T	c.(3076-3078)CCC>TTC	p.P1026F
Pat_08	Pre-Treatment	CHMP1B	57132	37	18	11851859	11851859	Missense_Mutation	SNP	A	C	178	225	c.349A>C	c.(349-351)AAA>CAA	p.K117Q
Pat_08	Pre-Treatment	MC5R	4161	37	18	13825823	13825823	Missense_Mutation	SNP	A	G	32	75	c.59A>G	c.(58-60)AAC>AGC	p.N20S
Pat_08	Pre-Treatment	MEP1B	4225	37	18	29797780	29797780	Missense_Mutation	SNP	C	T	23	40	c.1943C>T	c.(1942-1944)TCC>TTC	p.S648F

Pat_08	Pre-Treatment	RIT2	6014	37	18	40323589	40323589	Missense_Mutation	SNP	G	A	36	45	c.523C>T	c.(523-525)CAT>TAT	p.H175Y
Pat_08	Pre-Treatment	DCC	1630	37	18	50937005	50937005	Missense_Mutation	SNP	G	A	32	51	c.3119G>A	c.(3118-3120)AGG>AAG	p.R1040K
Pat_08	Pre-Treatment	SERPINB4	6318	37	18	61305069	61305069	Missense_Mutation	SNP	C	T	38	59	c.1057G>A	c.(1057-1059)GAA>AAA	p.E353K
Pat_08	Pre-Treatment	SERPINB7	8710	37	18	61465976	61465976	Missense_Mutation	SNP	C	T	50	115	c.593C>T	c.(592-594)CCC>CTC	p.P198L
Pat_08	Pre-Treatment	NETO1	81832	37	18	70461455	70461455	Missense_Mutation	SNP	G	A	16	24	c.536C>T	c.(535-537)TCC>TTC	p.S179F
Pat_08	Pre-Treatment	C19orf21	126353	37	19	757983	757983	Missense_Mutation	SNP	G	A	14	14	c.1037G>A	c.(1036-1038)CGC>CAC	p.R346H
Pat_08	Pre-Treatment	FSD1	79187	37	19	4323535	4323535	Nonsense_Mutation	SNP	G	A	9	19	c.1386G>A	c.(1384-1386)TGG>TGA	p.W462*
Pat_08	Pre-Treatment	SEMA6B	10501	37	19	4550261	4550261	Missense_Mutation	SNP	C	T	42	57	c.1145G>A	c.(1144-1146)GGG>GAG	p.G382E
Pat_08	Pre-Treatment	KIAA0355	9710	37	19	34791443	34791443	Missense_Mutation	SNP	C	T	24	32	c.65C>T	c.(64-66)TCC>TTC	p.S22F
Pat_08	Pre-Treatment	ZNF568	374900	37	19	37488299	37488299	Missense_Mutation	SNP	A	G	4	6	c.1664A>G	c.(1663-1665)GAA>GGA	p.E555G
Pat_08	Pre-Treatment	ZNF585B	92285	37	19	37677976	37677976	Missense_Mutation	SNP	C	T	33	41	c.463G>A	c.(463-465)GAA>AAA	p.E155K
Pat_08	Pre-Treatment	LRFN1	57622	37	19	39805289	39805289	Missense_Mutation	SNP	G	A	11	9	c.688C>T	c.(688-690)CTC>TTC	p.L230F
Pat_08	Pre-Treatment	LTBP4	8425	37	19	41128389	41128390	Missense_Mutation	DNP	CC	TA	21	36	c.3502_3503CC>T	c.(3502-3504)CCC>TAC	p.P1168Y
Pat_08	Pre-Treatment	PSG4	5672	37	19	43702386	43702386	Missense_Mutation	SNP	G	A	171	272	c.472C>T	c.(472-474)CCC>TCC	p.P158S
Pat_08	Pre-Treatment	GEMIN7	79760	37	19	45593532	45593532	Nonsense_Mutation	SNP	C	T	21	49	c.160C>T	c.(160-162)CAG>TAG	p.Q54*
Pat_08	Pre-Treatment	GPR77	27202	37	19	47844070	47844070	Missense_Mutation	SNP	C	T	23	63	c.14C>T	c.(13-15)TCT>TTT	p.S5F
Pat_08	Pre-Treatment	CCDC155	147872	37	19	49898419	49898419	Missense_Mutation	SNP	C	T	9	25	c.205C>T	c.(205-207)CCC>TCC	p.P69S
Pat_08	Pre-Treatment	LILRB1	10859	37	19	55147034	55147034	Missense_Mutation	SNP	G	A	43	129	c.1624G>A	c.(1624-1626)GAG>AAG	p.E542K
Pat_08	Pre-Treatment	ZNF667	63934	37	19	56953336	56953336	Missense_Mutation	SNP	G	A	35	60	c.1028C>T	c.(1027-1029)TCA>TTA	p.S343L
Pat_08	Pre-Treatment	ZIM2	23619	37	19	57286247	57286247	Missense_Mutation	SNP	C	T	12	33	c.1393G>A	c.(1393-1395)GCC>ACC	p.A465T
Pat_08	Pre-Treatment	C2orf48	348738	37	2	10282381	10282382	Splice_Site	DNP	GG	AA	64	163	c.73_splice	c.e3-1	p.G25_splice
Pat_08	Pre-Treatment	HS1BP3	64342	37	2	20838401	20838401	Missense_Mutation	SNP	G	A	21	28	c.418C>T	c.(418-420)CCA>TCA	p.P140S
Pat_08	Pre-Treatment	APOB	338	37	2	21232695	21232695	Missense_Mutation	SNP	C	T	26	54	c.7045G>A	c.(7045-7047)GAA>AAA	p.E2349K
Pat_08	Pre-Treatment	ATAD2B	54454	37	2	24046220	24046220	Missense_Mutation	SNP	C	T	16	33	c.2039G>A	c.(2038-2040)AGA>AAA	p.R680K
Pat_08	Pre-Treatment	SLC4A1AP	22950	37	2	27886668	27886668	Missense_Mutation	SNP	C	T	102	159	c.49C>T	c.(49-51)CCA>TCA	p.P17S
Pat_08	Pre-Treatment	THADA	63892	37	2	43458330	43458331	Missense_Mutation	DNP	CC	TT	17	32	.5618_5619GG>A	c.(5617-5619)AGG>AAA	p.R1873K
Pat_08	Pre-Treatment	FSHR	2492	37	2	49190238	49190238	Missense_Mutation	SNP	C	T	10	23	c.1722G>A	c.(1720-1722)ATG>ATA	p.M574I
Pat_08	Pre-Treatment	ALMS1	7840	37	2	73681006	73681006	Missense_Mutation	SNP	C	T	24	46	c.7355C>T	c.(7354-7356)TCA>TTA	p.S2452L
Pat_08	Pre-Treatment	EPB41L5	57669	37	2	120848052	120848052	Nonsense_Mutation	SNP	C	T	92	119	c.1003C>T	c.(1003-1005)CGA>TGA	p.R335*
Pat_08	Pre-Treatment	CNTNAP5	129684	37	2	125204485	125204485	Missense_Mutation	SNP	G	A	75	122	c.889G>A	c.(889-891)GAG>AAG	p.E297K
Pat_08	Pre-Treatment	POTEF	728378	37	2	130832812	130832812	Missense_Mutation	SNP	C	T	19	58	c.2233G>A	c.(2233-2235)GGG>AGG	p.G745R
Pat_08	Pre-Treatment	LOC401010	401010	37	2	132200831	132200831	Missense_Mutation	SNP	C	T	5	6	c.1171G>A	c.(1171-1173)GAG>AAG	p.E391K
Pat_08	Pre-Treatment	LRP1B	53353	37	2	141116476	141116476	Missense_Mutation	SNP	C	T	39	95	c.11171G>A	c.(11170-11172)AGA>AAA	p.R3724K
Pat_08	Pre-Treatment	MBD5	55777	37	2	149226284	149226284	Missense_Mutation	SNP	C	T	41	80	c.772C>T	c.(772-774)CAT>TAT	p.H258Y
Pat_08	Pre-Treatment	NEB	4703	37	2	152381753	152381753	Missense_Mutation	SNP	C	T	36	58	c.17093G>A	c.(17092-17094)GGA>GA	p.G5698E
Pat_08	Pre-Treatment	KCNJ3	3760	37	2	155711304	155711304	Missense_Mutation	SNP	C	T	18	45	c.985C>T	c.(985-987)CCT>TCT	p.P329S
Pat_08	Pre-Treatment	SCN9A	6335	37	2	167085452	167085452	Missense_Mutation	SNP	G	A	34	74	c.3922C>T	c.(3922-3924)CCT>TCT	p.P1308S
Pat_08	Pre-Treatment	TTN	7273	37	2	179393620	179393620	Missense_Mutation	SNP	C	T	35	47	c.99154G>A	c.(99154-99156)GAA>AA	p.E33052K
Pat_08	Pre-Treatment	TTN	7273	37	2	179410756	179410756	Missense_Mutation	SNP	C	T	15	37	c.87503G>A	c.(87502-87504)GGA>GA	p.G29168E
Pat_08	Pre-Treatment	TTN	7273	37	2	179428394	179428394	Missense_Mutation	SNP	T	C	82	103	c.74761A>G	c.(74761-74763)ACA>GC	p.T24921A
Pat_08	Pre-Treatment	TTN	7273	37	2	179498194	179498194	Missense_Mutation	SNP	C	T	32	40	c.35188G>A	c.(35188-35190)GAA>AA	p.E11730K
Pat_08	Pre-Treatment	TTN	7273	37	2	179629430	179629430	Missense_Mutation	SNP	G	A	57	90	c.9812C>T	c.(9811-9813)TCC>TTC	p.S3271F
Pat_08	Pre-Treatment	TTN	7273	37	2	179654118	179654118	Missense_Mutation	SNP	C	T	41	63	c.2045G>A	c.(2044-2046)AGA>AAA	p.R682K
Pat_08	Pre-Treatment	SGOL2	151246	37	2	201437870	201437870	Missense_Mutation	SNP	A	T	25	46	c.2801A>T	c.(2800-2802)CAA>CTA	p.Q934L
Pat_08	Pre-Treatment	CD28	940	37	2	204594385	204594385	Missense_Mutation	SNP	C	T	68	128	c.424C>T	c.(424-426)CCA>TCA	p.P142S
Pat_08	Pre-Treatment	CRYGD	1421	37	2	208988904	208988904	Missense_Mutation	SNP	C	T	13	19	c.184G>A	c.(184-186)GAC>AAC	p.D62N
Pat_08	Pre-Treatment	CPS1	1373	37	2	211460248	211460248	Missense_Mutation	SNP	C	T	47	123	c.1301C>T	c.(1300-1302)TCC>TTC	p.S434F

Pat_08	Pre-Treatment	VIL1	7429	37	2	219296642	219296642	Missense_Mutation	SNP	C	A	11	32	c.1165C>A	c.(1165-1167)CAG>AAG	p.Q389K
Pat_08	Pre-Treatment	SPHKAP	80309	37	2	228855801	228855801	Missense_Mutation	SNP	C	T	30	44	c.4874G>A	c.(4873-4875)CGA>CAA	p.R1625Q
Pat_08	Pre-Treatment	CHRND	1144	37	2	233399978	233399978	Missense_Mutation	SNP	G	A	44	80	c.1510G>A	c.(1510-1512)GGG>AGG	p.G504R
Pat_08	Pre-Treatment	CHRNG	1146	37	2	233408401	233408401	Missense_Mutation	SNP	G	A	16	33	c.1027G>A	c.(1027-1029)GTC>ATC	p.V343I
Pat_08	Pre-Treatment	C2orf85	285093	37	2	242813940	242813940	Missense_Mutation	SNP	G	A	6	5	c.233G>A	c.(232-234)AGG>AAG	p.R78K
Pat_08	Pre-Treatment	PTPRT	11122	37	20	41306649	41306649	Missense_Mutation	SNP	G	A	70	120	c.1010C>T	c.(1009-1011)ACC>ATC	p.T337I
Pat_08	Pre-Treatment	CDH22	64405	37	20	44869692	44869692	Missense_Mutation	SNP	A	G	30	81	c.460T>C	c.(460-462)TTC>CTC	p.F154L
Pat_08	Pre-Treatment	TPTE	7179	37	21	11012916	11012916	Splice_Site	SNP	C	A	12	18	c.1704_splice	c.e9+1	
Pat_08	Pre-Treatment	SH3BGR	6450	37	21	40883698	40883698	Missense_Mutation	SNP	C	T	13	24	c.716C>T	c.(715-717)TCC>TTC	p.S239F
Pat_08	Pre-Treatment	DSCAM	1826	37	21	41452217	41452217	Missense_Mutation	SNP	G	A	40	55	c.4282C>T	c.(4282-4284)CCA>TCA	p.P1428S
Pat_08	Pre-Treatment	SLC37A1	54020	37	21	43963662	43963662	Missense_Mutation	SNP	G	A	53	77	c.680G>A	c.(679-681)GGA>GAA	p.G227E
Pat_08	Pre-Treatment	KRTAP10-6	386674	37	21	46011918	46011918	Missense_Mutation	SNP	G	A	57	278	c.448C>T	c.(448-450)CCC>TCC	p.P150S
Pat_08	Pre-Treatment	RTN4R	65078	37	22	20230526	20230526	Missense_Mutation	SNP	G	A	14	32	c.130C>T	c.(130-132)CCC>TCC	p.P44S
Pat_08	Pre-Treatment	AP1B1	162	37	22	29727834	29727834	Missense_Mutation	SNP	G	A	23	65	c.2381C>T	c.(2380-2382)TCC>TTC	p.S794F
Pat_08	Pre-Treatment	LARGE	9215	37	22	34046453	34046453	Missense_Mutation	SNP	G	A	74	72	c.308C>T	c.(307-309)TCC>TTC	p.S103F
Pat_08	Pre-Treatment	CYP2D7P1	1564	37	22	42537597	42537597	Missense_Mutation	SNP	A	G	15	48	c.662T>C	c.(661-663)TTG>TCG	p.L221S
Pat_08	Pre-Treatment	NUP210	23225	37	3	13370433	13370433	Missense_Mutation	SNP	G	A	11	27	c.4124C>T	c.(4123-4125)TCC>TTC	p.S1375F
Pat_08	Pre-Treatment	FGD5	152273	37	3	14862578	14862578	Missense_Mutation	SNP	A	G	17	46	c.2000A>G	c.(1999-2001)AAC>AGC	p.N667S
Pat_08	Pre-Treatment	UBP1	7342	37	3	33453119	33453119	Missense_Mutation	SNP	A	G	97	180	c.509T>C	c.(508-510)GTT>GCT	p.V170A
Pat_08	Pre-Treatment	TRANK1	9881	37	3	36874752	36874752	Missense_Mutation	SNP	C	T	28	49	c.4540G>A	c.(4540-4542)GAA>AAA	p.E1514K
Pat_08	Pre-Treatment	LRRFIP2	9209	37	3	37150142	37150142	Missense_Mutation	SNP	A	G	97	137	c.643T>C	c.(643-645)TAT>CAT	p.Y215H
Pat_08	Pre-Treatment	HHATL	57467	37	3	42735116	42735116	Missense_Mutation	SNP	C	T	15	29	c.1241G>A	c.(1240-1242)CGA>CAA	p.R414Q
Pat_08	Pre-Treatment	RHOA	387	37	3	49405936	49405936	Missense_Mutation	SNP	G	A	56	68	c.202C>T	c.(202-204)CGC>TGC	p.R68C
Pat_08	Pre-Treatment	CACNA1D	776	37	3	53766925	53766925	Missense_Mutation	SNP	A	T	27	52	c.2557A>T	c.(2557-2559)ATG>TTG	p.M853L
Pat_08	Pre-Treatment	C3orf26	84319	37	3	99536869	99536869	Missense_Mutation	SNP	G	A	38	50	c.46G>A	c.(46-48)GGA>AGA	p.G16R
Pat_08	Pre-Treatment	FBXO40	51725	37	3	121345753	121345753	Missense_Mutation	SNP	C	T	20	22	c.2126C>T	c.(2125-2127)TCC>TTC	p.S709F
Pat_08	Pre-Treatment	SLC15A2	6565	37	3	121613396	121613396	Nonsense_Mutation	SNP	C	T	154	276	c.73C>T	c.(73-75)CGA>TGA	p.R25*
Pat_08	Pre-Treatment	MECOM	2122	37	3	168838897	168838897	Missense_Mutation	SNP	G	A	37	49	c.515C>T	c.(514-516)TCG>TTG	p.S172L
Pat_08	Pre-Treatment	TP63	8626	37	3	189455588	189455588	Missense_Mutation	SNP	C	T	48	89	c.122C>T	c.(121-123)TCC>TTC	p.S41F
Pat_08	Pre-Treatment	TACC3	10460	37	4	1730226	1730226	Missense_Mutation	SNP	C	T	13	29	c.1097C>T	c.(1096-1098)CCC>CTC	p.P366L
Pat_08	Pre-Treatment	UGT2A3	79799	37	4	69817123	69817123	Missense_Mutation	SNP	C	T	18	17	c.356G>A	c.(355-357)GGA>GAA	p.G119E
Pat_08	Pre-Treatment	PARM1	25849	37	4	75938040	75938040	Missense_Mutation	SNP	C	T	99	195	c.449C>T	c.(448-450)TCC>TTC	p.S150F
Pat_08	Pre-Treatment	NAA11	84779	37	4	80246759	80246759	Missense_Mutation	SNP	C	T	15	18	c.273G>A	c.(271-273)ATG>ATA	p.M91I
Pat_08	Pre-Treatment	ARHGAP24	83478	37	4	86863344	86863344	Missense_Mutation	SNP	C	T	36	55	c.517C>T	c.(517-519)CTC>TTC	p.L173F
Pat_08	Pre-Treatment	IBSP	3381	37	4	88732988	88732988	Missense_Mutation	SNP	G	A	42	77	c.880G>A	c.(880-882)GAA>AAA	p.E294K
Pat_08	Pre-Treatment	FAM190A	401145	37	4	91229782	91229782	Missense_Mutation	SNP	C	T	11	27	c.347C>T	c.(346-348)TCT>TTT	p.S116F
Pat_08	Pre-Treatment	ADH1A	124	37	4	100208729	100208729	Missense_Mutation	SNP	G	A	14	41	c.112C>T	c.(112-114)CGT>TGT	p.R38C
Pat_08	Pre-Treatment	ADH1C	126	37	4	100266089	100266089	Missense_Mutation	SNP	G	A	77	154	c.497C>T	c.(496-498)CCC>CTC	p.P166L
Pat_08	Pre-Treatment	FAT4	79633	37	4	126372799	126372799	Missense_Mutation	SNP	C	T	48	96	c.10628C>T	c.(10627-10629)CCC>CTC	p.P3543L
Pat_08	Pre-Treatment	PCDH18	54510	37	4	138451129	138451129	Missense_Mutation	SNP	G	A	63	127	c.2114C>T	c.(2113-2115)TCC>TTC	p.S705F
Pat_08	Pre-Treatment	LRBA	987	37	4	151837674	151837674	Missense_Mutation	SNP	C	T	19	32	c.773G>A	c.(772-774)AGA>AAA	p.R258K
Pat_08	Pre-Treatment	FSTL5	56884	37	4	162376261	162376261	Missense_Mutation	SNP	C	A	38	57	c.1736G>T	c.(1735-1737)GGG>GTG	p.G579V
Pat_08	Pre-Treatment	1-Mar	55016	37	4	164507014	164507014	Missense_Mutation	SNP	G	A	35	48	c.310C>T	c.(310-312)CGC>TGC	p.R104C
Pat_08	Pre-Treatment	ANXA10	11199	37	4	169099049	169099049	Nonsense_Mutation	SNP	G	A	66	137	c.543G>A	c.(541-543)TGG>TGA	p.W181*
Pat_08	Pre-Treatment	GALNT7	51809	37	4	174242826	174242826	Missense_Mutation	SNP	A	T	27	40	c.1932A>T	c.(1930-1932)AAA>AAT	p.K644N
Pat_08	Pre-Treatment	SNX25	83891	37	4	186263251	186263251	Missense_Mutation	SNP	T	C	84	112	c.1676T>C	c.(1675-1677)TTA>TCA	p.L559S
Pat_08	Pre-Treatment	SEMA5A	9037	37	5	9197374	9197374	Missense_Mutation	SNP	C	T	116	140	c.974G>A	c.(973-975)AGC>AAC	p.S325N

Pat_08	Pre-Treatment	CTNND2	1501	37	5	11732369	11732369	Missense_Mutation	SNP	G	A	36	67	c.53C>T	c.(52-54)CCA>CTA	p.P18L
Pat_08	Pre-Treatment	DNAH5	1767	37	5	13754366	13754366	Missense_Mutation	SNP	C	T	62	96	c.10501G>A	c.(10501-10503)GAA>AAA	p.E3501K
Pat_08	Pre-Treatment	DNAH5	1767	37	5	13823476	13823476	Missense_Mutation	SNP	C	T	15	20	c.6583G>A	c.(6583-6585)GAT>AAT	p.D2195N
Pat_08	Pre-Treatment	CDH18	1016	37	5	19571761	19571761	Missense_Mutation	SNP	C	T	65	90	c.1180G>A	c.(1180-1182)GAA>AAA	p.E394K
Pat_08	Pre-Treatment	RAI14	26064	37	5	34814746	34814746	Missense_Mutation	SNP	C	T	63	90	c.911C>T	c.(910-912)TCG>TTG	p.S304L
Pat_08	Pre-Treatment	UGT3A1	133688	37	5	35965946	35965946	Missense_Mutation	SNP	C	T	28	32	c.385G>A	c.(385-387)GAT>AAT	p.D129N
Pat_08	Pre-Treatment	SLC1A3	6507	37	5	36686171	36686171	Missense_Mutation	SNP	C	T	21	56	c.1429C>T	c.(1429-1431)CGC>TGC	p.R477C
Pat_08	Pre-Treatment	RAB3C	115827	37	5	57913641	57913641	Missense_Mutation	SNP	G	A	15	20	c.196G>A	c.(196-198)GAT>AAT	p.D66N
Pat_08	Pre-Treatment	ADAMTS6	11174	37	5	64483859	64483859	Missense_Mutation	SNP	G	A	61	86	c.2894C>T	c.(2893-2895)GCT>GTT	p.A965V
Pat_08	Pre-Treatment	GPR98	84059	37	5	89949415	89949415	Missense_Mutation	SNP	C	T	11	21	c.4024C>T	c.(4024-4026)CCA>TCA	p.P1342S
Pat_08	Pre-Treatment	TSSK1B	83942	37	5	112770218	112770218	Missense_Mutation	SNP	C	T	21	24	c.319G>A	c.(319-321)GCC>ACC	p.A107T
Pat_08	Pre-Treatment	ADAMTS19	171019	37	5	128863489	128863489	Missense_Mutation	SNP	C	T	74	26	c.1117C>T	c.(1117-1119)CGT>TGT	p.R373C
Pat_08	Pre-Treatment	FSTL4	23105	37	5	132652260	132652260	Missense_Mutation	SNP	C	T	24	12	c.494G>A	c.(493-495)GGA>GAA	p.G165E
Pat_08	Pre-Treatment	PPP2R2B	5521	37	5	146017937	146017937	Missense_Mutation	SNP	C	T	24	63	c.667G>A	c.(667-669)GAG>AAG	p.E223K
Pat_08	Pre-Treatment	DPYSL3	1809	37	5	146781130	146781130	Missense_Mutation	SNP	G	A	13	25	c.941C>T	c.(940-942)CCG>CTG	p.P314L
Pat_08	Pre-Treatment	GABRA6	2559	37	5	161115979	161115979	Missense_Mutation	SNP	C	T	80	37	c.250C>T	c.(250-252)CGC>TGC	p.R84C
Pat_08	Pre-Treatment	ODZ2	57451	37	5	167622180	167622180	Splice_Site	SNP	G	A	6	19	c.2754_splice	c.e15-1	p.S918_splice
Pat_08	Pre-Treatment	ARL10	285598	37	5	175793384	175793384	Missense_Mutation	SNP	C	T	8	18	c.185C>T	c.(184-186)CCC>CTC	p.P62L
Pat_08	Pre-Treatment	RASGEF1C	255426	37	5	179529070	179529070	Splice_Site	SNP	C	T	14	18	c.1376_splice	c.e12+1	p.R459_splice
Pat_08	Pre-Treatment	MAK	4117	37	6	10802187	10802187	Missense_Mutation	SNP	C	T	45	215	c.769G>A	c.(769-771)GCT>ACT	p.A257T
Pat_08	Pre-Treatment	SCAND3	114821	37	6	28539827	28539828	Missense_Mutation	DNP	CC	TT	26	91	.3838_3839GG>A	c.(3838-3840)GGA>AAA	p.G1280K
Pat_08	Pre-Treatment	SCAND3	114821	37	6	28540785	28540785	Missense_Mutation	SNP	C	T	14	35	c.2881G>A	c.(2881-2883)GAA>AAA	p.E961K
Pat_08	Pre-Treatment	OR2J2	26707	37	6	29141910	29141910	Nonsense_Mutation	SNP	G	A	76	219	c.498G>A	c.(496-498)TGG>TGA	p.W166*
Pat_08	Pre-Treatment	DDR1	780	37	6	30860230	30860230	Missense_Mutation	SNP	C	T	28	71	c.1010C>T	c.(1009-1011)CCC>CTC	p.P337L
Pat_08	Pre-Treatment	TNXB	7148	37	6	32026008	32026008	Missense_Mutation	SNP	G	A	35	92	c.7652C>T	c.(7651-7653)TCC>TTC	p.S2551F
Pat_08	Pre-Treatment	HLA-DRA	3122	37	6	32410472	32410472	Splice_Site	SNP	T	C	79	201	c.328_splice	c.e2+2	p.V110_splice
Pat_08	Pre-Treatment	COL11A2	1302	37	6	33136737	33136737	Missense_Mutation	SNP	G	A	95	291	c.3847C>T	c.(3847-3849)CCT>TCT	p.P1283S
Pat_08	Pre-Treatment	IP6K3	117283	37	6	33690517	33690517	Missense_Mutation	SNP	C	T	50	161	c.1213G>A	c.(1213-1215)GAT>AAT	p.D405N
Pat_08	Pre-Treatment	GLP1R	2740	37	6	39047471	39047471	Missense_Mutation	SNP	C	T	25	90	c.1175C>T	c.(1174-1176)TCC>TTC	p.S392F
Pat_08	Pre-Treatment	TREML4	285852	37	6	41196525	41196525	Missense_Mutation	SNP	G	A	38	143	c.137G>A	c.(136-138)AGA>AAA	p.R46K
Pat_08	Pre-Treatment	TDRD6	221400	37	6	46659190	46659190	Nonsense_Mutation	SNP	G	T	77	203	c.3325G>T	c.(3325-3327)GAA>TAA	p.E1109*
Pat_08	Pre-Treatment	GPR115	221393	37	6	47681873	47681873	Missense_Mutation	SNP	T	G	36	39	c.892T>G	c.(892-894)TTG>GTG	p.L298V
Pat_08	Pre-Treatment	FAM83B	222584	37	6	54735196	54735196	Missense_Mutation	SNP	G	A	62	159	c.152G>A	c.(151-153)CGA>CAA	p.R51Q
Pat_08	Pre-Treatment	GFRAL	389400	37	6	55196641	55196641	Missense_Mutation	SNP	G	A	32	71	c.151G>A	c.(151-153)GAT>AAT	p.D51N
Pat_08	Pre-Treatment	KIAA1586	57691	37	6	56919090	56919090	Missense_Mutation	SNP	T	G	26	46	c.1793T>G	c.(1792-1794)TTT>TGT	p.F598C
Pat_08	Pre-Treatment	COL9A1	1297	37	6	70961981	70961981	Missense_Mutation	SNP	C	T	47	53	c.1802G>A	c.(1801-1803)GGA>GAA	p.G601E
Pat_08	Pre-Treatment	COL9A1	1297	37	6	70984435	70984435	Missense_Mutation	SNP	G	A	30	39	c.1016C>T	c.(1015-1017)TCA>TTA	p.S339L
Pat_08	Pre-Treatment	RIMS1	22999	37	6	73110352	73110352	Missense_Mutation	SNP	T	C	63	120	c.5015T>C	c.(5014-5016)CTC>CCC	p.L1672P
Pat_08	Pre-Treatment	EEF1A1	1915	37	6	74229701	74229701	Missense_Mutation	SNP	C	T	46	53	c.49G>A	c.(49-51)GAT>AAT	p.D17N
Pat_08	Pre-Treatment	CNR1	1268	37	6	88854819	88854819	Nonsense_Mutation	SNP	G	A	13	18	c.175C>T	c.(175-177)CAA>TAA	p.Q59*
Pat_08	Pre-Treatment	MCHR2	84539	37	6	100382356	100382356	Missense_Mutation	SNP	G	A	24	41	c.625C>T	c.(625-627)CCT>TCT	p.P209S
Pat_08	Pre-Treatment	RFX6	222546	37	6	117249966	117249966	Missense_Mutation	SNP	G	A	76	124	c.2443G>A	c.(2443-2445)GGA>AGA	p.G815R
Pat_08	Pre-Treatment	C6orf204	387119	37	6	118801656	118801656	Missense_Mutation	SNP	C	T	34	52	c.1766G>A	c.(1765-1767)AGA>AAA	p.R589K
Pat_08	Pre-Treatment	RSPO3	84870	37	6	127476496	127476496	Missense_Mutation	SNP	C	T	39	58	c.547C>T	c.(547-549)CCT>TCT	p.P183S
Pat_08	Pre-Treatment	PTPRK	5796	37	6	128388791	128388791	Missense_Mutation	SNP	C	T	63	115	c.2030G>A	c.(2029-2031)GGA>GAA	p.G677E
Pat_08	Pre-Treatment	L3MBTL3	84456	37	6	130425708	130425708	Missense_Mutation	SNP	C	T	58	91	c.1874C>T	c.(1873-1875)TCC>TTC	p.S625F
Pat_08	Pre-Treatment	SAMD3	154075	37	6	130465798	130465798	Missense_Mutation	SNP	C	T	38	59	c.1430G>A	c.(1429-1431)AGG>AAG	p.R477K

Pat_08	Pre-Treatment	ALDH8A1	64577	37	6	135239986	135239986	Missense_Mutation	SNP	C	T	84	123	c.1031G>A	c.(1030-1032)AGA>AAA	p.R344K
Pat_08	Pre-Treatment	TIAM2	26230	37	6	155450436	155450436	Missense_Mutation	SNP	C	T	33	62	c.79C>T	c.(79-81)CCT>TCT	p.P27S
Pat_08	Pre-Treatment	ARID1B	57492	37	6	157522541	157522541	Missense_Mutation	SNP	G	A	119	168	c.4759G>A	c.(4759-4761)GAG>AAG	p.E1587K
Pat_08	Pre-Treatment	MLLT4	4301	37	6	168370511	168370511	Missense_Mutation	SNP	T	A	16	15	c.5401T>A	c.(5401-5403)TTC>ATC	p.F1801I
Pat_08	Pre-Treatment	INTS1	26173	37	7	1513911	1513911	Missense_Mutation	SNP	A	G	17	79	c.5722T>C	c.(5722-5724)TTC>CTC	p.F1908L
Pat_08	Pre-Treatment	SDK1	221935	37	7	4107511	4107511	Missense_Mutation	SNP	G	A	12	34	c.2953G>A	c.(2953-2955)GAC>AAC	p.D985N
Pat_08	Pre-Treatment	STK31	56164	37	7	23776524	23776524	Missense_Mutation	SNP	G	A	13	52	c.844G>A	c.(844-846)GAA>AAA	p.E282K
Pat_08	Pre-Treatment	HOXA4	3201	37	7	27168950	27168950	Missense_Mutation	SNP	G	A	42	188	c.857C>T	c.(856-858)TCG>TTG	p.S286L
Pat_08	Pre-Treatment	HECW1	23072	37	7	43351600	43351600	Missense_Mutation	SNP	C	T	27	92	c.266C>T	c.(265-267)TCC>TTC	p.S89F
Pat_08	Pre-Treatment	VOPP1	81552	37	7	55540681	55540681	Missense_Mutation	SNP	G	A	11	44	c.386C>T	c.(385-387)CCT>CTT	p.P129L
Pat_08	Pre-Treatment	ZNF679	168417	37	7	63726958	63726958	Missense_Mutation	SNP	G	A	18	68	c.947G>A	c.(946-948)AGA>AAA	p.R316K
Pat_08	Pre-Treatment	WBSCR17	64409	37	7	71177084	71177084	Missense_Mutation	SNP	C	T	35	95	c.1750C>T	c.(1750-1752)CGC>TGC	p.R584C
Pat_08	Pre-Treatment	PCLO	27445	37	7	82544688	82544688	Missense_Mutation	SNP	G	A	7	16	c.12614C>T	c.(12613-12615)CCT>CTT	p.P4205L
Pat_08	Pre-Treatment	GRM3	2913	37	7	86394514	86394514	Missense_Mutation	SNP	G	A	52	137	c.53G>A	c.(52-54)GGA>GAA	p.G18E
Pat_08	Pre-Treatment	STEAP4	79689	37	7	87911999	87911999	Missense_Mutation	SNP	C	T	22	100	c.941G>A	c.(940-942)CGA>CAA	p.R314Q
Pat_08	Pre-Treatment	DYNC1I1	1780	37	7	95662058	95662058	Missense_Mutation	SNP	G	A	68	206	c.1247G>A	c.(1246-1248)TGT>TAT	p.C416Y
Pat_08	Pre-Treatment	BAIAP2L1	55971	37	7	97991713	97991713	Missense_Mutation	SNP	C	T	34	108	c.83G>A	c.(82-84)CGA>CAA	p.R28Q
Pat_08	Pre-Treatment	ACHE	43	37	7	100491517	100491517	Missense_Mutation	SNP	C	T	96	255	c.337G>A	c.(337-339)GGC>AGC	p.G113S
Pat_08	Pre-Treatment	CFTR	1080	37	7	117175443	117175443	Missense_Mutation	SNP	G	A	27	76	c.721G>A	c.(721-723)GGG>AGG	p.G241R
Pat_08	Pre-Treatment	KCND2	3751	37	7	119914743	119914743	Nonsense_Mutation	SNP	G	A	58	174	c.57G>A	c.(55-57)TGG>TGA	p.W19*
Pat_08	Pre-Treatment	RNF148	378925	37	7	122342384	122342384	Missense_Mutation	SNP	G	A	357	365	c.421C>T	c.(421-423)CCC>TCC	p.P141S
Pat_08	Pre-Treatment	TSGA14	95681	37	7	130041725	130041725	Missense_Mutation	SNP	T	A	44	99	c.639A>T	c.(637-639)GAA>GAT	p.E213D
Pat_08	Pre-Treatment	TRIM24	8805	37	7	138266508	138266508	Missense_Mutation	SNP	C	T	32	97	c.2785C>T	c.(2785-2787)CCT>TCT	p.P929S
Pat_08	Pre-Treatment	BRAF	673	37	7	140453136	140453136	Missense_Mutation	SNP	A	T	115	92	c.1799T>A	c.(1798-1800)GTG>GAG	p.V600E
Pat_08	Pre-Treatment	TAS2R38	5726	37	7	141672855	141672855	Missense_Mutation	SNP	G	A	31	32	c.635C>T	c.(634-636)TCT>TTT	p.S212F
Pat_08	Pre-Treatment	TRPV6	55503	37	7	142574981	142574981	Missense_Mutation	SNP	C	T	53	162	c.401G>A	c.(400-402)CGA>CAA	p.R134Q
Pat_08	Pre-Treatment	TRPV5	56302	37	7	142625242	142625242	Missense_Mutation	SNP	C	T	33	95	c.850G>A	c.(850-852)GAC>AAC	p.D284N
Pat_08	Pre-Treatment	CLCN1	1180	37	7	143018840	143018840	Missense_Mutation	SNP	C	T	53	107	c.595C>T	c.(595-597)CGT>TGT	p.R199C
Pat_08	Pre-Treatment	OR2F1	26211	37	7	143657859	143657859	Missense_Mutation	SNP	C	A	26	85	c.796C>A	c.(796-798)CCC>ACC	p.P266T
Pat_08	Pre-Treatment	ABP1	26	37	7	150554027	150554027	Missense_Mutation	SNP	G	A	38	103	c.469G>A	c.(469-471)GAA>AAA	p.E157K
Pat_08	Pre-Treatment	SCARA5	286133	37	8	27779754	27779754	Missense_Mutation	SNP	G	A	7	13	c.250C>T	c.(250-252)CCG>TCG	p.P84S
Pat_08	Pre-Treatment	GSR	2936	37	8	30553929	30553929	Missense_Mutation	SNP	A	G	66	129	c.763T>C	c.(763-765)TCT>CCT	p.S255P
Pat_08	Pre-Treatment	IDO2	169355	37	8	39845421	39845421	Missense_Mutation	SNP	G	A	9	28	c.520G>A	c.(520-522)GGA>AGA	p.G174R
Pat_08	Pre-Treatment	PXDNL	137902	37	8	52321700	52321700	Missense_Mutation	SNP	A	T	7	11	c.2484T>A	c.(2482-2484)GAT>GAA	p.D828E
Pat_08	Pre-Treatment	PXDNL	137902	37	8	52412271	52412271	Missense_Mutation	SNP	C	T	78	140	c.440G>A	c.(439-441)AGA>AAA	p.R147K
Pat_08	Pre-Treatment	RP1	6101	37	8	55537568	55537568	Nonsense_Mutation	SNP	C	T	14	29	c.1126C>T	c.(1126-1128)CGA>TGA	p.R376*
Pat_08	Pre-Treatment	RP1	6101	37	8	55538973	55538973	Missense_Mutation	SNP	C	T	23	34	c.2531C>T	c.(2530-2532)TCT>TTT	p.S844F
Pat_08	Pre-Treatment	TRIM55	84675	37	8	67086730	67086730	Nonsense_Mutation	SNP	C	T	49	75	c.1549C>T	c.(1549-1551)CAG>TAG	p.Q517*
Pat_08	Pre-Treatment	CPA6	57094	37	8	68423876	68423876	Missense_Mutation	SNP	T	G	67	85	c.332A>C	c.(331-333)GAT>GCT	p.D111A
Pat_08	Pre-Treatment	KCNB2	9312	37	8	73480001	73480001	Missense_Mutation	SNP	G	A	59	96	c.32G>A	c.(31-33)AGG>AAG	p.R11K
Pat_08	Pre-Treatment	TRHR	7201	37	8	110100064	110100064	Missense_Mutation	SNP	G	A	44	155	c.323G>A	c.(322-324)GGA>GAA	p.G108E
Pat_08	Pre-Treatment	PKHD1L1	93035	37	8	110468517	110468517	Missense_Mutation	SNP	C	T	25	50	c.6901C>T	c.(6901-6903)CGC>TGC	p.R2301C
Pat_08	Pre-Treatment	CSMD3	114788	37	8	113326683	113326683	Missense_Mutation	SNP	T	G	40	114	c.7524A>C	c.(7522-7524)GAA>GAC	p.E2508D
Pat_08	Pre-Treatment	CSMD3	114788	37	8	113392596	113392596	Missense_Mutation	SNP	G	A	63	192	c.6121C>T	c.(6121-6123)CAT>TAT	p.H2041Y
Pat_08	Pre-Treatment	FER1L6	654463	37	8	125061918	125061918	Missense_Mutation	SNP	C	T	39	86	c.2795C>T	c.(2794-2796)CCC>CTC	p.P932L
Pat_08	Pre-Treatment	COL22A1	169044	37	8	139611032	139611032	Missense_Mutation	SNP	C	T	41	98	c.4295G>A	c.(4294-4296)GGA>GAA	p.G1432E
Pat_08	Pre-Treatment	PTPRD	5789	37	9	8341129	8341129	Missense_Mutation	SNP	C	T	72	50	c.5087G>A	c.(5086-5088)GGA>GAA	p.G1696E

Pat_08	Pre-Treatment	CDKN2A	1029	37	9	21971186	21971186	Nonsense_Mutation	SNP	G	A	9	5	c.172C>T	c.(172-174)CGA>TGA	p.R58*
Pat_08	Pre-Treatment	TAF1L	138474	37	9	32633029	32633029	Missense_Mutation	SNP	T	G	45	45	c.2549A>C	c.(2548-2550)AAA>ACA	p.K850T
Pat_08	Pre-Treatment	OR2S2	56656	37	9	35957515	35957515	Missense_Mutation	SNP	G	A	74	116	c.581C>T	c.(580-582)TCC>TTC	p.S194F
Pat_08	Pre-Treatment	FRMPD1	22844	37	9	37692715	37692716	Missense_Mutation	DNP	GG	AA	36	67	c.77_78GG>AA	c.(76-78)CGG>CAA	p.R26Q
Pat_08	Pre-Treatment	FAM75A6	389730	37	9	43626820	43626820	Missense_Mutation	SNP	G	C	9	22	c.1867C>G	c.(1867-1869)CGG>GGG	p.R623G
Pat_08	Pre-Treatment	VPS13A	23230	37	9	79865130	79865130	Missense_Mutation	SNP	C	T	48	101	c.2155C>T	c.(2155-2157)CTT>TTT	p.L719F
Pat_08	Pre-Treatment	ZNF510	22869	37	9	99522622	99522622	Missense_Mutation	SNP	C	A	31	71	c.490G>T	c.(490-492)GTA>TTA	p.V164L
Pat_08	Pre-Treatment	OR13C9	286362	37	9	107380278	107380278	Missense_Mutation	SNP	C	T	30	57	c.208G>A	c.(208-210)GAC>AAC	p.D70N
Pat_08	Pre-Treatment	PTGS1	5742	37	9	125133515	125133515	Missense_Mutation	SNP	C	T	28	56	c.58C>T	c.(58-60)CCC>TCC	p.P20S
Pat_08	Pre-Treatment	NUP188	23511	37	9	131755873	131755873	Nonsense_Mutation	SNP	C	T	62	134	c.2917C>T	c.(2917-2919)CGA>TGA	p.R973*
Pat_08	Pre-Treatment	BAT2L1	84726	37	9	134350643	134350643	Missense_Mutation	SNP	C	T	9	28	c.3127C>T	c.(3127-3129)CCC>TCC	p.P1043S
Pat_08	Pre-Treatment	SURF6	6838	37	9	136200589	136200589	Nonsense_Mutation	SNP	G	A	31	44	c.358C>T	c.(358-360)CGA>TGA	p.R120*
Pat_08	Pre-Treatment	LCN10	414332	37	9	139636409	139636409	Missense_Mutation	SNP	C	T	13	19	c.181G>A	c.(181-183)GAC>AAC	p.D61N
Pat_08	Pre-Treatment	MXRA5	25878	37	X	3240874	3240874	Missense_Mutation	SNP	G	A	17	33	c.2852C>T	c.(2851-2853)TCG>TTG	p.S951L
Pat_08	Pre-Treatment	AMELX	265	37	X	11312955	11312955	Missense_Mutation	SNP	C	T	85	173	c.47C>T	c.(46-48)GCC>GTC	p.A16V
Pat_08	Pre-Treatment	PIGA	5277	37	X	15342966	15342966	Missense_Mutation	SNP	G	A	17	56	c.1009C>T	c.(1009-1011)CCT>TCT	p.P337S
Pat_08	Pre-Treatment	YY2	404281	37	X	21871579	21871579	Missense_Mutation	SNP	C	A	117	283	c.628C>A	c.(628-630)CAA>AAA	p.Q210K
Pat_08	Pre-Treatment	MAGEB18	286514	37	X	26157607	26157607	Missense_Mutation	SNP	C	T	9	14	c.505C>T	c.(505-507)CCC>TCC	p.P169S
Pat_08	Pre-Treatment	OTC	5009	37	X	38212012	38212012	Missense_Mutation	SNP	G	A	44	75	c.63G>A	c.(61-63)ATG>ATA	p.M21I
Pat_08	Pre-Treatment	CXorf38	159013	37	X	40496317	40496317	Missense_Mutation	SNP	A	T	48	85	c.563T>A	c.(562-564)TTT>TAT	p.F188Y
Pat_08	Pre-Treatment	MTMR8	55613	37	X	63555965	63555965	Missense_Mutation	SNP	G	A	38	66	c.1145C>T	c.(1144-1146)TCC>TTC	p.S382F
Pat_08	Pre-Treatment	EDA	1896	37	X	69247866	69247866	Missense_Mutation	SNP	C	A	8	8	c.686C>A	c.(685-687)CCT>CAT	p.P229H
Pat_08	Pre-Treatment	KIAA2022	340533	37	X	73960184	73960184	Missense_Mutation	SNP	C	T	94	176	c.4208G>A	c.(4207-4209)GGG>GAG	p.G1403E
Pat_08	Pre-Treatment	LPAR4	2846	37	X	78010473	78010473	Missense_Mutation	SNP	C	T	119	222	c.107C>T	c.(106-108)TCC>TTC	p.S36F
Pat_08	Pre-Treatment	APOOL	139322	37	X	84310875	84310875	Missense_Mutation	SNP	C	T	13	19	c.338C>T	c.(337-339)CCG>CTG	p.P113L
Pat_08	Pre-Treatment	KLHL4	56062	37	X	86880629	86880629	Missense_Mutation	SNP	C	T	28	78	c.1157C>T	c.(1156-1158)ACC>ATC	p.T386I
Pat_08	Pre-Treatment	CXorf57	55086	37	X	105912404	105912404	Missense_Mutation	SNP	G	A	155	349	c.2281G>A	c.(2281-2283)GAG>AAG	p.E761K
Pat_08	Pre-Treatment	TEX13B	56156	37	X	107225012	107225012	Missense_Mutation	SNP	C	T	104	220	c.346G>A	c.(346-348)GAA>AAA	p.E116K
Pat_08	Pre-Treatment	KIAA1210	57481	37	X	118222570	118222570	Missense_Mutation	SNP	G	A	13	25	c.2623C>T	c.(2623-2625)CTC>TTC	p.L875F
Pat_08	Pre-Treatment	ELF4	2000	37	X	129215252	129215252	Missense_Mutation	SNP	C	T	121	251	c.53G>A	c.(52-54)GGG>GAG	p.G18E
Pat_08	Pre-Treatment	IGSF1	3547	37	X	130419321	130419321	Missense_Mutation	SNP	C	T	61	129	c.499G>A	c.(499-501)GGA>AGA	p.G167R
Pat_08	Pre-Treatment	MAGEC1	9947	37	X	140994505	140994505	Missense_Mutation	SNP	C	T	34	91	c.1315C>T	c.(1315-1317)CCC>TCC	p.P439S
Pat_08	Pre-Treatment	FMR1	2332	37	X	147026391	147026391	Missense_Mutation	SNP	A	G	11	22	c.1474A>G	c.(1474-1476)ACT>GCT	p.T492A
Pat_08	Pre-Treatment	MAGEA4	4103	37	X	151092719	151092719	Nonsense_Mutation	SNP	C	T	53	66	c.583C>T	c.(583-585)CAG>TAG	p.Q195*
Pat_08	Pre-Treatment	MAGEA3	4102	37	X	151935383	151935383	Missense_Mutation	SNP	G	A	57	137	c.784C>T	c.(784-786)CCC>TCC	p.P262S
Pat_08	Pre-Treatment	PLXNA3	55558	37	X	153697535	153697535	Missense_Mutation	SNP	C	T	27	97	c.4571C>T	c.(4570-4572)CCC>CTC	p.P1524L
Pat_08	Pre-Treatment	F8	2157	37	X	154132258	154132258	Missense_Mutation	SNP	G	A	93	128	c.5921C>T	c.(5920-5922)TCT>TTT	p.S1974F
Pat_08	Pre-Treatment	TMLHE	55217	37	X	154736697	154736697	Missense_Mutation	SNP	G	A	94	138	c.857C>T	c.(856-858)CCT>CTT	p.P286L
Pat_08	Post-Resistance	ACAP3	116983	37	1	1230911	1230911	Missense_Mutation	SNP	G	A	26	44	c.1729C>T	c.(1729-1731)CGC>TGC	p.R577C
Pat_08	Post-Resistance	PANK4	55229	37	1	2452281	2452281	Missense_Mutation	SNP	G	A	46	81	c.487C>T	c.(487-489)CCC>TCC	p.P163S
Pat_08	Post-Resistance	PIK3CD	5293	37	1	9778878	9778878	Missense_Mutation	SNP	G	A	5	214	c.1147G>A	c.(1147-1149)GAC>AAC	p.D383N
Pat_08	Post-Resistance	UBE4B	10277	37	1	10211599	10211599	Missense_Mutation	SNP	C	T	68	136	c.2906C>T	c.(2905-2907)TCC>TTC	p.S969F
Pat_08	Post-Resistance	PRAMEF11	440560	37	1	12885059	12885059	Missense_Mutation	SNP	C	G	6	334	c.1052G>C	c.(1051-1053)TGC>TCC	p.C351S
Pat_08	Post-Resistance	PRAMEF8	391002	37	1	12979691	12979691	Missense_Mutation	SNP	G	A	132	489	c.883G>A	c.(883-885)GAG>AAG	p.E295K
Pat_08	Post-Resistance	FBLIM1	54751	37	1	16093982	16093982	Missense_Mutation	SNP	C	T	14	26	c.362C>T	c.(361-363)GCT>GTT	p.A121V
Pat_08	Post-Resistance	MST1P9	11223	37	1	17085872	17085872	Missense_Mutation	SNP	A	G	5	38	c.949T>C	c.(949-951)TGG>CGG	p.W317R
Pat_08	Post-Resistance	PIGV	55650	37	1	27120713	27120713	Missense_Mutation	SNP	T	C	4	215	c.188T>C	c.(187-189)CTG>CCG	p.L63P

Pat_08	Post-Resistance	SYTL1	84958	37	1	27675626	27675626	Missense_Mutation	SNP	C	T	4	134	c.515C>T	c.(514-516)GCG>GTG	p.A172V
Pat_08	Post-Resistance	KIAA0754	643314	37	1	39879250	39879250	Missense_Mutation	SNP	A	G	6	40	c.3313A>G	c.(3313-3315)ACC>GCC	p.T1105A
Pat_08	Post-Resistance	BMP8B	656	37	1	40226129	40226129	Missense_Mutation	SNP	G	T	5	490	c.1171C>A	c.(1171-1173)CAC>AAC	p.H391N
Pat_08	Post-Resistance	KDM4A	9682	37	1	44132167	44132167	Missense_Mutation	SNP	C	T	115	208	c.718C>T	c.(718-720)CAC>TAC	p.H240Y
Pat_08	Post-Resistance	BSND	7809	37	1	55472919	55472919	Missense_Mutation	SNP	A	C	38	135	c.522A>C	c.(520-522)GAA>GAC	p.E174D
Pat_08	Post-Resistance	C1orf168	199920	37	1	57216843	57216843	Nonsense_Mutation	SNP	G	A	31	52	c.1261C>T	c.(1261-1263)CAG>TAG	p.Q421*
Pat_08	Post-Resistance	C8B	732	37	1	57422471	57422471	Missense_Mutation	SNP	C	T	304	554	c.362G>A	c.(361-363)CGA>CAA	p.R121Q
Pat_08	Post-Resistance	C1orf173	127254	37	1	75072512	75072512	Missense_Mutation	SNP	C	T	101	184	c.1262G>A	c.(1261-1263)GGA>GAA	p.G421E
Pat_08	Post-Resistance	LPHN2	23266	37	1	82409213	82409213	Missense_Mutation	SNP	G	A	109	181	c.958G>A	c.(958-960)GTC>ATC	p.V320I
Pat_08	Post-Resistance	TGFBR3	7049	37	1	92184982	92184982	Missense_Mutation	SNP	G	A	188	318	c.1453C>T	c.(1453-1455)CCT>TCT	p.P485S
Pat_08	Post-Resistance	CCDC76	54482	37	1	100605978	100605978	Missense_Mutation	SNP	C	T	29	243	c.409C>T	c.(409-411)CTT>TTT	p.L137F
Pat_08	Post-Resistance	COL11A1	1301	37	1	103440405	103440405	Missense_Mutation	SNP	G	A	37	58	c.2789C>T	c.(2788-2790)CCT>CTT	p.P930L
Pat_08	Post-Resistance	CELSR2	1952	37	1	109806965	109806965	Missense_Mutation	SNP	G	A	5	341	c.5267G>A	c.(5266-5268)CGT>CAT	p.R1756H
Pat_08	Post-Resistance	MAGI3	260425	37	1	114225824	114225824	Missense_Mutation	SNP	G	A	65	99	c.3634G>A	c.(3634-3636)GAA>AAA	p.E1212K
Pat_08	Post-Resistance	NRAS	4893	37	1	115256530	115256530	Missense_Mutation	SNP	G	T	61	567	c.181C>A	c.(181-183)CAA>AAA	p.Q61K
Pat_08	Post-Resistance	TBX15	6913	37	1	119469191	119469191	Missense_Mutation	SNP	G	A	68	134	c.145C>T	c.(145-147)CCA>TCA	p.P49S
Pat_08	Post-Resistance	NBPF7	343505	37	1	120381953	120381953	Missense_Mutation	SNP	T	C	7	646	c.692A>G	c.(691-693)TAT>TGT	p.Y231C
Pat_08	Post-Resistance	HIST2H2BE	8349	37	1	149858153	149858153	Missense_Mutation	SNP	T	C	4	212	c.38A>G	c.(37-39)AAG>AGG	p.K13R
Pat_08	Post-Resistance	CRNN	49860	37	1	152382749	152382749	Missense_Mutation	SNP	G	A	6	644	c.809C>T	c.(808-810)ACC>ATC	p.T270I
Pat_08	Post-Resistance	CRNN	49860	37	1	152382770	152382770	Missense_Mutation	SNP	T	C	6	730	c.788A>G	c.(787-789)GAC>GGC	p.D263G
Pat_08	Post-Resistance	C1orf43	25912	37	1	154180066	154180066	Missense_Mutation	SNP	T	C	93	136	c.625A>G	c.(625-627)ACT>GCT	p.T209A
Pat_08	Post-Resistance	CLK2	1196	37	1	155236548	155236548	Missense_Mutation	SNP	C	T	4	180	c.810G>A	c.(808-810)ATG>ATA	p.M270I
Pat_08	Post-Resistance	RUSC1	23623	37	1	155295412	155295412	Missense_Mutation	SNP	C	T	38	70	c.1763C>T	c.(1762-1764)CCG>CTG	p.P588L
Pat_08	Post-Resistance	CASQ1	844	37	1	160160558	160160558	Missense_Mutation	SNP	G	A	47	79	c.17G>A	c.(16-18)AGG>AAG	p.R6K
Pat_08	Post-Resistance	C1orf192	257177	37	1	161335356	161335356	Missense_Mutation	SNP	A	T	156	291	c.308T>A	c.(307-309)CTC>CAC	p.L103H
Pat_08	Post-Resistance	DUSP27	92235	37	1	167096296	167096296	Missense_Mutation	SNP	T	A	3	39	c.1928T>A	c.(1927-1929)ATG>AAG	p.M643K
Pat_08	Post-Resistance	DARS2	55157	37	1	173802529	173802529	Missense_Mutation	SNP	C	T	13	16	c.508C>T	c.(508-510)CGG>TGG	p.R170W
Pat_08	Post-Resistance	KIAA1614	57710	37	1	180885295	180885295	Missense_Mutation	SNP	C	T	32	66	c.56C>T	c.(55-57)CCC>CTC	p.P19L
Pat_08	Post-Resistance	CACNA1E	777	37	1	181765951	181765951	Missense_Mutation	SNP	C	T	15	24	c.6227C>T	c.(6226-6228)TCC>TTC	p.S2076F
Pat_08	Post-Resistance	KIF21B	23046	37	1	200945966	200945966	Missense_Mutation	SNP	C	T	27	42	c.4381G>A	c.(4381-4383)GTC>ATC	p.V1461I
Pat_08	Post-Resistance	LGR6	59352	37	1	202276021	202276021	Missense_Mutation	SNP	G	A	48	108	c.1162G>A	c.(1162-1164)GAA>AAA	p.E388K
Pat_08	Post-Resistance	PIGR	5284	37	1	207110830	207110830	Missense_Mutation	SNP	G	A	80	126	c.655C>T	c.(655-657)CTC>TTC	p.L219F
Pat_08	Post-Resistance	GPATCH2	55105	37	1	217604543	217604543	Missense_Mutation	SNP	G	A	195	304	c.1531C>T	c.(1531-1533)CCT>TCT	p.P511S
Pat_08	Post-Resistance	TLR5	7100	37	1	223286024	223286024	Missense_Mutation	SNP	C	T	110	195	c.350G>A	c.(349-351)GGA>GAA	p.G117E
Pat_08	Post-Resistance	PARP1	142	37	1	226555964	226555964	Missense_Mutation	SNP	G	A	6	170	c.2213C>T	c.(2212-2214)ACC>ATC	p.T738I
Pat_08	Post-Resistance	TTC13	79573	37	1	231060707	231060707	Missense_Mutation	SNP	G	A	209	326	c.1601C>T	c.(1600-1602)GCC>GTC	p.A534V
Pat_08	Post-Resistance	SLC35F3	148641	37	1	234454596	234454596	Missense_Mutation	SNP	C	T	99	205	c.847C>T	c.(847-849)CCT>TCT	p.P283S
Pat_08	Post-Resistance	NID1	4811	37	1	236187487	236187487	Missense_Mutation	SNP	G	A	60	112	c.2011C>T	c.(2011-2013)CCC>TCC	p.P671S
Pat_08	Post-Resistance	RYR2	6262	37	1	237774224	237774224	Missense_Mutation	SNP	G	A	39	61	c.4846G>A	c.(4846-4848)GGC>AGC	p.G1616S
Pat_08	Post-Resistance	NLRP3	114548	37	1	247582193	247582193	Missense_Mutation	SNP	C	T	28	51	c.97C>T	c.(97-99)CCT>TCT	p.P33S
Pat_08	Post-Resistance	OR2G3	81469	37	1	247769368	247769368	Missense_Mutation	SNP	A	G	90	165	c.481A>G	c.(481-483)ACT>GCT	p.T161A
Pat_08	Post-Resistance	OR2T3	343173	37	1	248637439	248637439	Missense_Mutation	SNP	C	T	61	683	c.788C>T	c.(787-789)ACC>ATC	p.T263I
Pat_08	Post-Resistance	ADARB2	105	37	10	1262945	1262945	Missense_Mutation	SNP	C	T	12	47	c.1628G>A	c.(1627-1629)GGC>GAC	p.G543D
Pat_08	Post-Resistance	AKR1C1	1645	37	10	5014844	5014844	Missense_Mutation	SNP	G	A	96	184	c.749G>A	c.(748-750)CGA>CAA	p.R250Q
Pat_08	Post-Resistance	DHTKD1	55526	37	10	12143176	12143176	Missense_Mutation	SNP	T	C	13	26	c.1892T>C	c.(1891-1893)CTA>CCA	p.L631P
Pat_08	Post-Resistance	CUBN	8029	37	10	17142048	17142048	Missense_Mutation	SNP	C	T	182	266	c.1721G>A	c.(1720-1722)AGA>AAA	p.R574K
Pat_08	Post-Resistance	CACNB2	783	37	10	18828535	18828535	Missense_Mutation	SNP	A	G	90	125	c.1865A>G	c.(1864-1866)AAC>AGC	p.N622S

Pat_08	Post-Resistance	PLXDC2	84898	37	10	20506391	20506391	Missense_Mutation	SNP	G	A	58	73	c.1159G>A	c.(1159-1161)GAA>AAA	p.E387K
Pat_08	Post-Resistance	ANKRD30A	91074	37	10	37430688	37430688	Missense_Mutation	SNP	C	T	8	197	c.695C>T	c.(694-696)GCG>GTG	p.A232V
Pat_08	Post-Resistance	C10orf71	118461	37	10	50531430	50531430	Nonsense_Mutation	SNP	G	A	22	9	c.840G>A	c.(838-840)TGG>TGA	p.W280*
Pat_08	Post-Resistance	ASAH2	56624	37	10	52003017	52003017	Missense_Mutation	SNP	C	T	277	146	c.455G>A	c.(454-456)CGA>CAA	p.R152Q
Pat_08	Post-Resistance	ARID5B	84159	37	10	63851366	63851366	Missense_Mutation	SNP	C	T	128	60	c.2144C>T	c.(2143-2145)CCT>CTT	p.P715L
Pat_08	Post-Resistance	LRRTM3	347731	37	10	68687605	68687605	Missense_Mutation	SNP	G	A	138	50	c.931G>A	c.(931-933)GGG>AGG	p.G311R
Pat_08	Post-Resistance	PTEN	5728	37	10	89692886	89692886	Missense_Mutation	SNP	T	C	201	228	c.370T>C	c.(370-372)TGT>CGT	p.C124R
Pat_08	Post-Resistance	CYP2C18	1562	37	10	96466634	96466634	Missense_Mutation	SNP	G	A	61	29	c.736G>A	c.(736-738)GAG>AAG	p.E246K
Pat_08	Post-Resistance	ADRB1	153	37	10	115805027	115805027	Missense_Mutation	SNP	G	A	3	71	c.1136G>A	c.(1135-1137)CGC>CAC	p.R379H
Pat_08	Post-Resistance	C10orf137	26098	37	10	127409788	127409788	Missense_Mutation	SNP	C	T	87	58	c.124C>T	c.(124-126)CTT>TTT	p.L42F
Pat_08	Post-Resistance	ATHL1	80162	37	11	294703	294703	Missense_Mutation	SNP	C	T	213	326	c.2168C>T	c.(2167-2169)TCC>TTC	p.S723F
Pat_08	Post-Resistance	MUC5B	727897	37	11	1262686	1262686	Missense_Mutation	SNP	G	A	35	42	c.6655G>A	c.(6655-6657)GAC>AAC	p.D2219N
Pat_08	Post-Resistance	KRTAP5-3	387266	37	11	1629152	1629152	Missense_Mutation	SNP	C	A	9	829	c.464G>T	c.(463-465)TGC>TTC	p.C155F
Pat_08	Post-Resistance	KRTAP5-5	439915	37	11	1651402	1651402	Missense_Mutation	SNP	C	T	72	106	c.332C>T	c.(331-333)TCC>TTC	p.S111F
Pat_08	Post-Resistance	KCNQ1	3784	37	11	2606487	2606487	Missense_Mutation	SNP	A	G	40	117	c.1078A>G	c.(1078-1080)AGG>GGG	p.R360G
Pat_08	Post-Resistance	SLC22A18	5002	37	11	2924603	2924603	Nonsense_Mutation	SNP	C	T	46	73	c.28C>T	c.(28-30)CAG>TAG	p.Q10*
Pat_08	Post-Resistance	OR51S1	119692	37	11	4869568	4869568	Missense_Mutation	SNP	G	A	148	249	c.871C>T	c.(871-873)CCT>TCT	p.P291S
Pat_08	Post-Resistance	OR51A4	401666	37	11	4967847	4967848	Missense_Mutation	DNP	GG	AA	123	248	c.483_484CC>TT	(481-486)TTCCCT>TTTTC	p.P162S
Pat_08	Post-Resistance	OR51I1	390063	37	11	5462416	5462416	Missense_Mutation	SNP	G	A	73	141	c.329C>T	c.(328-330)TCC>TTC	p.S110F
Pat_08	Post-Resistance	UBQLNL	143630	37	11	5536653	5536653	Missense_Mutation	SNP	G	A	93	191	c.1019C>T	c.(1018-1020)TCT>TTT	p.S340F
Pat_08	Post-Resistance	OR52N5	390075	37	11	5799521	5799521	Missense_Mutation	SNP	C	T	103	157	c.344G>A	c.(343-345)GGG>GAG	p.G115E
Pat_08	Post-Resistance	GTF2H1	2965	37	11	18379556	18379556	Missense_Mutation	SNP	C	T	70	97	c.1318C>T	c.(1318-1320)CTT>TTT	p.L440F
Pat_08	Post-Resistance	CCDC34	91057	37	11	27379017	27379017	Missense_Mutation	SNP	G	A	88	116	c.431C>T	c.(430-432)CCA>CTA	p.P144L
Pat_08	Post-Resistance	C11orf74	119710	37	11	36631726	36631726	Missense_Mutation	SNP	C	T	48	99	c.73C>T	c.(73-75)CTT>TTT	p.L25F
Pat_08	Post-Resistance	CHST1	8534	37	11	45672110	45672110	Missense_Mutation	SNP	C	T	44	93	c.364G>A	c.(364-366)GAC>AAC	p.D122N
Pat_08	Post-Resistance	DGKZ	8525	37	11	46396591	46396591	Missense_Mutation	SNP	C	T	3	19	c.2270C>T	c.(2269-2271)TCG>TTG	p.S757L
Pat_08	Post-Resistance	RAPSN	5913	37	11	47463243	47463243	Missense_Mutation	SNP	C	T	57	64	c.832G>A	c.(832-834)GAG>AAG	p.E278K
Pat_08	Post-Resistance	OR4C3	256144	37	11	48347478	48347478	Nonsense_Mutation	SNP	G	A	4	54	c.986G>A	c.(985-987)TGG>TAG	p.W329*
Pat_08	Post-Resistance	APLNR	187	37	11	57003806	57003806	Missense_Mutation	SNP	C	T	4	220	c.673G>A	c.(673-675)GCC>ACC	p.A225T
Pat_08	Post-Resistance	OR4D6	219983	37	11	59225019	59225019	Missense_Mutation	SNP	G	A	108	128	c.586G>A	c.(586-588)GAG>AAG	p.E196K
Pat_08	Post-Resistance	AHNAK	79026	37	11	62286730	62286731	Missense_Mutation	DNP	GG	AA	196	394	15158_15159CC>	c.(15157-15159)GCC>GTT	p.A5053V
Pat_08	Post-Resistance	TSGA10IP	254187	37	11	65714616	65714616	Missense_Mutation	SNP	C	T	10	35	c.320C>T	c.(319-321)CCC>CTC	p.P107L
Pat_08	Post-Resistance	CD248	57124	37	11	66082377	66082377	Missense_Mutation	SNP	C	T	24	35	c.2122G>A	c.(2122-2124)GTG>ATG	p.V708M
Pat_08	Post-Resistance	P4HA3	283208	37	11	74013458	74013458	Missense_Mutation	SNP	G	A	197	273	c.523C>T	c.(523-525)CGG>TGG	p.R175W
Pat_08	Post-Resistance	ACER3	55331	37	11	76726095	76726095	Nonsense_Mutation	SNP	C	A	4	146	c.533C>A	c.(532-534)TCA>TAA	p.S178*
Pat_08	Post-Resistance	C11orf67	28971	37	11	77553557	77553557	Missense_Mutation	SNP	A	T	38	59	c.15A>T	c.(13-15)GAA>GAT	p.E5D
Pat_08	Post-Resistance	INTS4	92105	37	11	77614629	77614629	Missense_Mutation	SNP	A	G	5	93	c.2054T>C	c.(2053-2055)TTG>TCG	p.L685S
Pat_08	Post-Resistance	ODZ4	26011	37	11	78440676	78440676	Missense_Mutation	SNP	C	T	112	169	c.3151G>A	c.(3151-3153)GAA>AAA	p.E1051K
Pat_08	Post-Resistance	TRPC6	7225	37	11	101375120	101375120	Missense_Mutation	SNP	T	C	67	125	c.580A>G	c.(580-582)ACC>GCC	p.T194A
Pat_08	Post-Resistance	EXPH5	23086	37	11	108381210	108381210	Missense_Mutation	SNP	A	G	268	371	c.5024T>C	c.(5023-5025)ATT>ACT	p.I1675T
Pat_08	Post-Resistance	USP28	57646	37	11	113701595	113701595	Missense_Mutation	SNP	G	A	133	232	c.904C>T	c.(904-906)CGT>TGT	p.R302C
Pat_08	Post-Resistance	FAM55B	120406	37	11	114569092	114569092	Missense_Mutation	SNP	G	A	28	41	c.458G>A	c.(457-459)AGG>AAG	p.R153K
Pat_08	Post-Resistance	DSCAML1	57453	37	11	117389456	117389456	Missense_Mutation	SNP	G	A	30	46	c.1415C>T	c.(1414-1416)TCG>TTG	p.S472L
Pat_08	Post-Resistance	TMPRSS13	84000	37	11	117789462	117789462	Missense_Mutation	SNP	T	C	5	145	c.113A>G	c.(112-114)CAG>CGG	p.Q38R
Pat_08	Post-Resistance	TMPRSS13	84000	37	11	117789465	117789465	Missense_Mutation	SNP	G	C	5	146	c.110C>G	c.(109-111)GCC>GGC	p.A37G
Pat_08	Post-Resistance	OR4D5	219875	37	11	123810973	123810973	Missense_Mutation	SNP	C	T	238	422	c.650C>T	c.(649-651)TCG>TTG	p.S217L
Pat_08	Post-Resistance	VWA5A	4013	37	11	123994449	123994449	Missense_Mutation	SNP	G	A	50	97	c.1102G>A	c.(1102-1104)GAA>AAA	p.E368K

Pat_08	Post-Resistance	OR8B8	26493	37	11	124310824	124310824	Missense_Mutation	SNP	G	A	97	184	c.158C>T	c.(157-159)TCT>TTT	p.S53F
Pat_08	Post-Resistance	NTM	50863	37	11	132016408	132016408	Missense_Mutation	SNP	G	A	41	43	c.400G>A	c.(400-402)GTA>ATA	p.V134I
Pat_08	Post-Resistance	DCP1B	196513	37	12	2061949	2061949	Missense_Mutation	SNP	C	T	74	70	c.1157G>A	c.(1156-1158)AGA>AAA	p.R386K
Pat_08	Post-Resistance	CD163L1	283316	37	12	7596704	7596704	Missense_Mutation	SNP	G	A	67	145	c.20C>T	c.(19-21)TCG>TTG	p.S7L
Pat_08	Post-Resistance	NANOG	79923	37	12	7947082	7947082	Missense_Mutation	SNP	G	A	27	49	c.444G>A	c.(442-444)ATG>ATA	p.M148I
Pat_08	Post-Resistance	KLRC3	3823	37	12	10572989	10572989	Missense_Mutation	SNP	C	T	127	330	c.161G>A	c.(160-162)GGG>GAG	p.G54E
Pat_08	Post-Resistance	PRB2	653247	37	12	11546417	11546417	Missense_Mutation	SNP	C	T	136	194	c.595G>A	c.(595-597)GGA>AGA	p.G199R
Pat_08	Post-Resistance	ABCC9	10060	37	12	22065982	22065982	Missense_Mutation	SNP	G	A	68	118	c.835C>T	c.(835-837)CCA>TCA	p.P279S
Pat_08	Post-Resistance	SYT10	341359	37	12	33579224	33579224	Missense_Mutation	SNP	C	T	49	119	c.358G>A	c.(358-360)GAA>AAA	p.E120K
Pat_08	Post-Resistance	ADAMTS20	80070	37	12	43769952	43769952	Splice_Site	SNP	C	T	4	9	c.5221_splice	c.e35-1	p.I1741_splice
Pat_08	Post-Resistance	ADAMTS20	80070	37	12	43945643	43945643	Missense_Mutation	SNP	G	A	101	179	c.82C>T	c.(82-84)CCC>TCC	p.P28S
Pat_08	Post-Resistance	PUS7L	83448	37	12	44148157	44148157	Missense_Mutation	SNP	C	T	63	150	c.892G>A	c.(892-894)GGA>AGA	p.G298R
Pat_08	Post-Resistance	COL2A1	1280	37	12	48389088	48389088	Missense_Mutation	SNP	G	A	90	100	c.712C>T	c.(712-714)CCC>TCC	p.P238S
Pat_08	Post-Resistance	RND1	27289	37	12	49251927	49251927	Missense_Mutation	SNP	G	A	41	76	c.551C>T	c.(550-552)TCC>TTC	p.S184F
Pat_08	Post-Resistance	KRT84	3890	37	12	52774929	52774929	Missense_Mutation	SNP	C	T	168	283	c.1138G>A	c.(1138-1140)GAG>AAG	p.E380K
Pat_08	Post-Resistance	KRT6B	3854	37	12	52844377	52844377	Missense_Mutation	SNP	C	G	79	199	c.568G>C	c.(568-570)GTT>CTT	p.V190L
Pat_08	Post-Resistance	KRT6A	3853	37	12	52885322	52885322	Missense_Mutation	SNP	C	T	127	281	c.739G>A	c.(739-741)GAG>AAG	p.E247K
Pat_08	Post-Resistance	OR6C75	390323	37	12	55759372	55759372	Missense_Mutation	SNP	C	T	44	96	c.478C>T	c.(478-480)CTT>TTT	p.L160F
Pat_08	Post-Resistance	GLI1	2735	37	12	57860059	57860059	Missense_Mutation	SNP	G	A	214	359	c.799G>A	c.(799-801)GAG>AAG	p.E267K
Pat_08	Post-Resistance	MSRB3	253827	37	12	65722374	65722374	Missense_Mutation	SNP	C	T	60	119	c.275C>T	c.(274-276)CCA>CTA	p.P92L
Pat_08	Post-Resistance	PTPRB	5787	37	12	71002869	71002869	Missense_Mutation	SNP	C	T	51	265	c.305G>A	c.(304-306)AGA>AAA	p.R102K
Pat_08	Post-Resistance	C12orf12	196477	37	12	91348220	91348220	Nonsense_Mutation	SNP	C	T	25	41	c.300G>A	c.(298-300)TGG>TGA	p.W100*
Pat_08	Post-Resistance	AMDHD1	144193	37	12	96356148	96356148	Missense_Mutation	SNP	G	A	57	140	c.829G>A	c.(829-831)GGA>AGA	p.G277R
Pat_08	Post-Resistance	STAB2	55576	37	12	104046397	104046397	Missense_Mutation	SNP	G	A	4	160	c.1321G>A	c.(1321-1323)GGT>AGT	p.G441S
Pat_08	Post-Resistance	MMAB	326625	37	12	110006647	110006647	Missense_Mutation	SNP	C	T	49	113	c.218G>A	c.(217-219)GGA>GAA	p.G73E
Pat_08	Post-Resistance	ANAPC7	51434	37	12	110813898	110813898	Missense_Mutation	SNP	G	T	4	220	c.1583C>A	c.(1582-1584)GCA>GAA	p.A528E
Pat_08	Post-Resistance	OAS3	4940	37	12	113398950	113398950	Missense_Mutation	SNP	G	A	3	87	c.1732G>A	c.(1732-1734)GAG>AAG	p.E578K
Pat_08	Post-Resistance	HPD	3242	37	12	122286921	122286921	Missense_Mutation	SNP	C	T	100	170	c.580G>A	c.(580-582)GTG>ATG	p.V194M
Pat_08	Post-Resistance	ZCCHC8	55596	37	12	122958814	122958814	Missense_Mutation	SNP	C	T	83	111	c.1354G>A	c.(1354-1356)GTA>ATA	p.V452I
Pat_08	Post-Resistance	CDK2AP1	8099	37	12	123751793	123751793	Missense_Mutation	SNP	G	A	4	334	c.92C>T	c.(91-93)ACG>ATG	p.T31M
Pat_08	Post-Resistance	GTF2H3	2967	37	12	124144370	124144370	Missense_Mutation	SNP	G	A	83	137	c.713G>A	c.(712-714)AGA>AAA	p.R238K
Pat_08	Post-Resistance	RIMBP2	23504	37	12	130926738	130926738	Missense_Mutation	SNP	A	C	44	79	c.1108T>G	c.(1108-1110)TGC>GGC	p.C370G
Pat_08	Post-Resistance	TUBA3C	7278	37	13	19752472	19752472	Missense_Mutation	SNP	C	T	108	170	c.289G>A	c.(289-291)GAA>AAA	p.E97K
Pat_08	Post-Resistance	WASF3	10810	37	13	27259911	27259911	Missense_Mutation	SNP	C	T	55	61	c.1438C>T	c.(1438-1440)CGG>TGG	p.R480W
Pat_08	Post-Resistance	GPR12	2835	37	13	27333521	27333521	Nonsense_Mutation	SNP	G	C	55	132	c.444C>G	c.(442-444)TAC>TAG	p.Y148*
Pat_08	Post-Resistance	NBEA	26960	37	13	36124729	36124729	Missense_Mutation	SNP	G	A	29	48	c.6701G>A	c.(6700-6702)CGA>CAA	p.R2234Q
Pat_08	Post-Resistance	EDNRB	1910	37	13	78477736	78477736	Missense_Mutation	SNP	C	A	4	252	c.490G>T	c.(490-492)GCA>TCA	p.A164S
Pat_08	Post-Resistance	NALCN	259232	37	13	101936361	101936361	Missense_Mutation	SNP	C	T	40	74	c.1057G>A	c.(1057-1059)GAA>AAA	p.E353K
Pat_08	Post-Resistance	NOVA1	4857	37	14	26917922	26917922	Missense_Mutation	SNP	G	A	165	274	c.767C>T	c.(766-768)GCC>GTC	p.A256V
Pat_08	Post-Resistance	NPAS3	64067	37	14	34204525	34204525	Missense_Mutation	SNP	C	T	116	231	c.839C>T	c.(838-840)TCA>TTA	p.S280L
Pat_08	Post-Resistance	RALGAPA1	253959	37	14	36191052	36191052	Missense_Mutation	SNP	A	G	50	123	c.2108T>C	c.(2107-2109)GTT>GCT	p.V703A
Pat_08	Post-Resistance	PNN	5411	37	14	39649841	39649842	Missense_Mutation	DNP	GG	AA	27	47	c.928_929GG>AA	c.(928-930)GGT>AAT	p.G310N
Pat_08	Post-Resistance	CDKL1	8814	37	14	50844945	50844945	Missense_Mutation	SNP	G	A	32	46	c.1304C>T	c.(1303-1305)CCC>CTC	p.P435L
Pat_08	Post-Resistance	KCNH5	27133	37	14	63174583	63174583	Missense_Mutation	SNP	T	A	108	146	c.2610A>T	c.(2608-2610)AAA>AAT	p.K870N
Pat_08	Post-Resistance	ZFYVE26	23503	37	14	68274583	68274583	Missense_Mutation	SNP	G	A	134	212	c.418C>T	c.(418-420)CCA>TCA	p.P140S
Pat_08	Post-Resistance	DPF3	8110	37	14	73141047	73141047	Missense_Mutation	SNP	G	A	23	49	c.772C>T	c.(772-774)CCC>TCC	p.P258S
Pat_08	Post-Resistance	DPF3	8110	37	14	73190363	73190363	Missense_Mutation	SNP	C	T	174	322	c.503G>A	c.(502-504)CGA>CAA	p.R168Q

Pat_08	Post-Resistance	NRXN3	9369	37	14	79181364	79181364	Missense_Mutation	SNP	G	A	95	135	c.807G>A	c.(805-807)ATG>ATA	p.M269I
Pat_08	Post-Resistance	SERPINA10	51156	37	14	94754734	94754734	Missense_Mutation	SNP	C	T	40	69	c.881G>A	c.(880-882)GGA>GAA	p.G294E
Pat_08	Post-Resistance	SERPINA1	5265	37	14	94847406	94847406	Missense_Mutation	SNP	A	C	20	42	c.719T>G	c.(718-720)GTG>GGG	p.V240G
Pat_08	Post-Resistance	SERPINA9	327657	37	14	94935565	94935565	Missense_Mutation	SNP	G	A	84	93	c.667C>T	c.(667-669)CAC>TAC	p.H223Y
Pat_08	Post-Resistance	BRF1	2972	37	14	105752644	105752644	Missense_Mutation	SNP	G	A	23	43	c.254C>T	c.(253-255)ACC>ATC	p.T85I
Pat_08	Post-Resistance	NDN	4692	37	15	23932347	23932347	Missense_Mutation	SNP	C	A	8	47	c.18G>T	c.(16-18)AAG>AAT	p.K6N
Pat_08	Post-Resistance	THBS1	7057	37	15	39874759	39874759	Missense_Mutation	SNP	G	A	34	64	c.433G>A	c.(433-435)GAA>AAA	p.E145K
Pat_08	Post-Resistance	DLL4	54567	37	15	41228744	41228744	Missense_Mutation	SNP	C	T	13	21	c.1559C>T	c.(1558-1560)CCC>CTC	p.P520L
Pat_08	Post-Resistance	UNC13C	440279	37	15	54305875	54305875	Missense_Mutation	SNP	G	A	58	144	c.775G>A	c.(775-777)GAA>AAA	p.E259K
Pat_08	Post-Resistance	UNC13C	440279	37	15	54557657	54557657	Missense_Mutation	SNP	G	A	6	7	c.3781G>A	c.(3781-3783)GGA>AGA	p.G1261R
Pat_08	Post-Resistance	UNC13C	440279	37	15	54825218	54825218	Missense_Mutation	SNP	G	A	6	31	c.5650G>A	c.(5650-5652)GAT>AAT	p.D1884N
Pat_08	Post-Resistance	FEM1B	10116	37	15	68582681	68582681	Missense_Mutation	SNP	C	T	105	145	c.985C>T	c.(985-987)CTT>TTT	p.L329F
Pat_08	Post-Resistance	CSPG4	1464	37	15	75982510	75982510	Missense_Mutation	SNP	G	A	41	97	c.896C>T	c.(895-897)TCC>TTC	p.S299F
Pat_08	Post-Resistance	IREB2	3658	37	15	78789516	78789516	Missense_Mutation	SNP	C	T	91	208	c.2644C>T	c.(2644-2646)CAT>TAT	p.H882Y
Pat_08	Post-Resistance	KIAA1199	57214	37	15	81225737	81225737	Missense_Mutation	SNP	G	A	4	422	c.2945G>A	c.(2944-2946)CGG>CAG	p.R982Q
Pat_08	Post-Resistance	ITFG3	83986	37	16	314061	314061	Missense_Mutation	SNP	C	T	36	94	c.1235C>T	c.(1234-1236)GCC>GTC	p.A412V
Pat_08	Post-Resistance	PTX4	390667	37	16	1537629	1537629	Missense_Mutation	SNP	G	A	18	19	c.469C>T	c.(469-471)CAC>TAC	p.H157Y
Pat_08	Post-Resistance	ABCC1	4363	37	16	16108367	16108367	Missense_Mutation	SNP	T	C	50	73	c.371T>C	c.(370-372)ATT>ACT	p.I124T
Pat_08	Post-Resistance	DNAH3	55567	37	16	21098326	21098326	Nonsense_Mutation	SNP	C	T	115	287	c.2721G>A	c.(2719-2721)TGG>TGA	p.W907*
Pat_08	Post-Resistance	RBBP6	5930	37	16	24580595	24580595	Missense_Mutation	SNP	C	T	71	123	c.2584C>T	c.(2584-2586)CCA>TCA	p.P862S
Pat_08	Post-Resistance	ATP2A1	487	37	16	28890099	28890099	Missense_Mutation	SNP	A	G	3	100	c.107A>G	c.(106-108)TAC>TGC	p.Y36C
Pat_08	Post-Resistance	C16orf78	123970	37	16	49407878	49407878	Missense_Mutation	SNP	G	A	137	213	c.28G>A	c.(28-30)GAT>AAT	p.D10N
Pat_08	Post-Resistance	IRX5	10265	37	16	54965121	54965121	Missense_Mutation	SNP	C	T	7	56	c.11C>T	c.(10-12)CCG>CTG	p.P4L
Pat_08	Post-Resistance	CNOT1	23019	37	16	58621149	58621150	Missense_Mutation	DNP	CC	AA	4	177	c.388_389GG>TT	c.(388-390)GGC>TTC	p.G130F
Pat_08	Post-Resistance	GALNS	2588	37	16	88902160	88902160	Missense_Mutation	SNP	G	A	53	81	c.731C>T	c.(730-732)CCC>CTC	p.P244L
Pat_08	Post-Resistance	GALNS	2588	37	16	88904145	88904145	Missense_Mutation	SNP	G	A	81	153	c.451C>T	c.(451-453)CCC>TCC	p.P151S
Pat_08	Post-Resistance	SPG7	6687	37	16	89614503	89614503	Missense_Mutation	SNP	G	A	5	246	c.1645G>A	c.(1645-1647)GTG>ATG	p.V549M
Pat_08	Post-Resistance	TRPV1	7442	37	17	3494574	3494574	Missense_Mutation	SNP	C	T	35	29	c.358G>A	c.(358-360)GAA>AAA	p.E120K
Pat_08	Post-Resistance	ZZEF1	23140	37	17	4013068	4013068	Missense_Mutation	SNP	T	C	83	102	c.1156A>G	c.(1156-1158)AAG>GAG	p.K386E
Pat_08	Post-Resistance	DHX33	56919	37	17	5352203	5352203	Missense_Mutation	SNP	C	T	44	92	c.1741G>A	c.(1741-1743)GAG>AAG	p.E581K
Pat_08	Post-Resistance	PLSCR3	57048	37	17	7296213	7296213	Missense_Mutation	SNP	G	A	306	491	c.566C>T	c.(565-567)CCC>CTC	p.P189L
Pat_08	Post-Resistance	CHD3	1107	37	17	7807808	7807808	Missense_Mutation	SNP	C	T	45	304	c.3943C>T	c.(3943-3945)CCT>TCT	p.P1315S
Pat_08	Post-Resistance	GLP2R	9340	37	17	9729447	9729447	Missense_Mutation	SNP	G	A	11	19	c.67G>A	c.(67-69)GAG>AAG	p.E23K
Pat_08	Post-Resistance	MYO15A	51168	37	17	18022962	18022962	Missense_Mutation	SNP	C	T	31	160	c.848C>T	c.(847-849)CCC>CTC	p.P283L
Pat_08	Post-Resistance	FOXN1	8456	37	17	26864216	26864216	Missense_Mutation	SNP	C	T	116	179	c.1709C>T	c.(1708-1710)TCG>TTG	p.S570L
Pat_08	Post-Resistance	SLC6A4	6532	37	17	28548904	28548904	Missense_Mutation	SNP	C	T	78	166	c.73G>A	c.(73-75)GGA>AGA	p.G25R
Pat_08	Post-Resistance	C17orf66	256957	37	17	34192286	34192286	Missense_Mutation	SNP	C	T	81	143	c.253G>A	c.(253-255)GAC>AAC	p.D85N
Pat_08	Post-Resistance	WIPF2	147179	37	17	38420847	38420847	Missense_Mutation	SNP	G	A	244	394	c.419G>A	c.(418-420)AGC>AAC	p.S140N
Pat_08	Post-Resistance	KRT17	3872	37	17	39775880	39775880	Missense_Mutation	SNP	G	A	145	266	c.1265C>T	c.(1264-1266)TCC>TTC	p.S422F
Pat_08	Post-Resistance	MPP2	4355	37	17	41956666	41956666	Missense_Mutation	SNP	C	T	167	283	c.1594G>A	c.(1594-1596)GGA>AGA	p.G532R
Pat_08	Post-Resistance	FMNL1	752	37	17	43323883	43323883	Missense_Mutation	SNP	G	A	75	144	c.3223G>A	c.(3223-3225)GTG>ATG	p.V1075M
Pat_08	Post-Resistance	MAPT	4137	37	17	44061152	44061152	Missense_Mutation	SNP	C	T	10	25	c.982C>T	c.(982-984)CCA>TCA	p.P328S
Pat_08	Post-Resistance	KIAA1267	284058	37	17	44144090	44144090	Missense_Mutation	SNP	G	C	34	46	c.1661C>G	c.(1660-1662)CCT>CGT	p.P554R
Pat_08	Post-Resistance	TEX14	56155	37	17	56671001	56671001	Missense_Mutation	SNP	C	T	74	125	c.2509G>A	c.(2509-2511)GGA>AGA	p.G837R
Pat_08	Post-Resistance	CANT1	124583	37	17	76993313	76993313	Missense_Mutation	SNP	T	C	6	699	c.392A>G	c.(391-393)AAG>AGG	p.K131R
Pat_08	Post-Resistance	RPTOR	57521	37	17	78919517	78919518	Missense_Mutation	DNP	CC	TT	66	114	.3076_3077CC>T	c.(3076-3078)CCC>TTC	p.P1026F
Pat_08	Post-Resistance	CHMP1B	57132	37	18	11851859	11851859	Missense_Mutation	SNP	A	C	200	339	c.349A>C	c.(349-351)AAA>CAA	p.K117Q

Pat_08	Post-Resistance	MC5R	4161	37	18	13825823	13825823	Missense_Mutation	SNP	A	G	81	127	c.59A>G	c.(58-60)AAC>AGC	p.N20S
Pat_08	Post-Resistance	MEP1B	4225	37	18	29797780	29797780	Missense_Mutation	SNP	C	T	32	85	c.1943C>T	c.(1942-1944)TCC>TTC	p.S648F
Pat_08	Post-Resistance	RIT2	6014	37	18	40323589	40323589	Missense_Mutation	SNP	G	A	64	103	c.523C>T	c.(523-525)CAT>TAT	p.H175Y
Pat_08	Post-Resistance	DCC	1630	37	18	50937005	50937005	Missense_Mutation	SNP	G	A	66	105	c.3119G>A	c.(3118-3120)AGG>AAG	p.R1040K
Pat_08	Post-Resistance	SERPINB4	6318	37	18	61305069	61305069	Missense_Mutation	SNP	C	T	96	130	c.1057G>A	c.(1057-1059)GAA>AAA	p.E353K
Pat_08	Post-Resistance	SERPINB7	8710	37	18	61465976	61465976	Missense_Mutation	SNP	C	T	130	207	c.593C>T	c.(592-594)CCC>CTC	p.P198L
Pat_08	Post-Resistance	NETO1	81832	37	18	70461455	70461455	Missense_Mutation	SNP	G	A	50	79	c.536C>T	c.(535-537)TCC>TTC	p.S179F
Pat_08	Post-Resistance	ZNF57	126295	37	19	2917733	2917733	Missense_Mutation	SNP	G	A	7	238	c.1114G>A	c.(1114-1116)GCC>ACC	p.A372T
Pat_08	Post-Resistance	FSD1	79187	37	19	4323535	4323535	Nonsense_Mutation	SNP	G	A	12	26	c.1386G>A	c.(1384-1386)TGG>TGA	p.W462*
Pat_08	Post-Resistance	SEMA6B	10501	37	19	4550261	4550261	Missense_Mutation	SNP	C	T	71	95	c.1145G>A	c.(1144-1146)GGG>GAG	p.G382E
Pat_08	Post-Resistance	ZNF844	284391	37	19	12187502	12187502	Missense_Mutation	SNP	A	G	10	263	c.1567A>G	c.(1567-1569)AAA>GAA	p.K523E
Pat_08	Post-Resistance	ZNF333	84449	37	19	14815865	14815865	Splice_Site	SNP	G	A	4	104	c.307_splice	c.e6-1	p.G103_splice
Pat_08	Post-Resistance	UNC13A	23025	37	19	17766939	17766939	Missense_Mutation	SNP	C	T	8	8	c.1300G>A	c.(1300-1302)GAG>AAG	p.E434K
Pat_08	Post-Resistance	ZNF431	170959	37	19	21350459	21350459	Missense_Mutation	SNP	T	A	5	437	c.309T>A	c.(307-309)GAT>GAA	p.D103E
Pat_08	Post-Resistance	ZNF681	148213	37	19	23927372	23927372	Missense_Mutation	SNP	C	G	12	516	c.980G>C	c.(979-981)AGA>ACA	p.R327T
Pat_08	Post-Resistance	ZNF681	148213	37	19	23938352	23938352	Missense_Mutation	SNP	T	C	5	359	c.5A>G	c.(4-6)GAA>GGA	p.E2G
Pat_08	Post-Resistance	KIAA0355	9710	37	19	34791443	34791443	Missense_Mutation	SNP	C	T	41	61	c.65C>T	c.(64-66)TCC>TTC	p.S22F
Pat_08	Post-Resistance	CAPNS1	826	37	19	36633203	36633203	Missense_Mutation	SNP	G	A	4	333	c.211G>A	c.(211-213)GAG>AAG	p.E71K
Pat_08	Post-Resistance	ZNF585B	92285	37	19	37677976	37677976	Missense_Mutation	SNP	C	T	64	123	c.463G>A	c.(463-465)GAA>AAA	p.E155K
Pat_08	Post-Resistance	LRFN1	57622	37	19	39805289	39805289	Missense_Mutation	SNP	G	A	19	21	c.688C>T	c.(688-690)CTC>TTC	p.L230F
Pat_08	Post-Resistance	LTBP4	8425	37	19	41128389	41128390	Missense_Mutation	DNP	CC	TA	17	42	.3502_3503CC>T	c.(3502-3504)CCC>TAC	p.P1168Y
Pat_08	Post-Resistance	GEMIN7	79760	37	19	45593532	45593532	Nonsense_Mutation	SNP	C	T	55	53	c.160C>T	c.(160-162)CAG>TAG	p.Q54*
Pat_08	Post-Resistance	GPR77	27202	37	19	47844070	47844070	Missense_Mutation	SNP	C	T	78	143	c.14C>T	c.(13-15)TCT>TTT	p.S5F
Pat_08	Post-Resistance	CCDC155	147872	37	19	49898419	49898419	Missense_Mutation	SNP	C	T	27	32	c.205C>T	c.(205-207)CCC>TCC	p.P69S
Pat_08	Post-Resistance	ALDH16A1	126133	37	19	49962997	49962997	Missense_Mutation	SNP	G	A	4	192	c.391G>A	c.(391-393)GTT>ATT	p.V131I
Pat_08	Post-Resistance	ATF5	22809	37	19	50435876	50435876	Missense_Mutation	SNP	T	C	7	25	c.376T>C	c.(376-378)TCC>CCC	p.S126P
Pat_08	Post-Resistance	LILRA2	11027	37	19	55086932	55086932	Missense_Mutation	SNP	C	T	4	200	c.865C>T	c.(865-867)CAC>TAC	p.H289Y
Pat_08	Post-Resistance	LILRB1	10859	37	19	55147034	55147034	Missense_Mutation	SNP	G	A	191	306	c.1624G>A	c.(1624-1626)GAG>AAG	p.E542K
Pat_08	Post-Resistance	ZNF667	63934	37	19	56953336	56953336	Missense_Mutation	SNP	G	A	79	123	c.1028C>T	c.(1027-1029)TCA>TTA	p.S343L
Pat_08	Post-Resistance	ZIM2	23619	37	19	57286247	57286247	Missense_Mutation	SNP	C	T	58	94	c.1393G>A	c.(1393-1395)GCC>ACC	p.A465T
Pat_08	Post-Resistance	USP29	57663	37	19	57640433	57640433	Missense_Mutation	SNP	C	A	6	172	c.390C>A	c.(388-390)GAC>GAA	p.D130E
Pat_08	Post-Resistance	ASAP2	8853	37	2	9543385	9543385	Missense_Mutation	SNP	G	T	4	130	c.2950G>T	c.(2950-2952)GGC>TGC	p.G984C
Pat_08	Post-Resistance	C2orf48	348738	37	2	10282381	10282382	Splice_Site	DNP	GG	AA	99	235	c.73_splice	c.e3-1	p.G25_splice
Pat_08	Post-Resistance	HS1BP3	64342	37	2	20838401	20838401	Missense_Mutation	SNP	G	A	38	62	c.418C>T	c.(418-420)CCA>TCA	p.P140S
Pat_08	Post-Resistance	APOB	338	37	2	21232695	21232695	Missense_Mutation	SNP	C	T	62	103	c.7045G>A	c.(7045-7047)GAA>AAA	p.E2349K
Pat_08	Post-Resistance	ATAD2B	54454	37	2	24046220	24046220	Missense_Mutation	SNP	C	T	39	72	c.2039G>A	c.(2038-2040)AGA>AAA	p.R680K
Pat_08	Post-Resistance	SLC4A1AP	22950	37	2	27886668	27886668	Missense_Mutation	SNP	C	T	174	316	c.49C>T	c.(49-51)CCA>TCA	p.P17S
Pat_08	Post-Resistance	CRIM1	51232	37	2	36740798	36740798	Missense_Mutation	SNP	G	A	4	189	c.1880G>A	c.(1879-1881)CGG>CAG	p.R627Q
Pat_08	Post-Resistance	THADA	63892	37	2	43458330	43458331	Missense_Mutation	DNP	CC	TT	18	34	.5618_5619GG>A	c.(5617-5619)AGG>AAA	p.R1873K
Pat_08	Post-Resistance	FSHR	2492	37	2	49190238	49190238	Missense_Mutation	SNP	C	T	49	63	c.1722G>A	c.(1720-1722)ATG>ATA	p.M574I
Pat_08	Post-Resistance	ALMS1	7840	37	2	73681006	73681006	Missense_Mutation	SNP	C	T	55	120	c.7355C>T	c.(7354-7356)TCA>TTA	p.S2452L
Pat_08	Post-Resistance	EPB41L5	57669	37	2	120848052	120848052	Nonsense_Mutation	SNP	C	T	114	160	c.1003C>T	c.(1003-1005)CGA>TGA	p.R335*
Pat_08	Post-Resistance	CNTNAP5	129684	37	2	125204485	125204485	Missense_Mutation	SNP	G	A	215	269	c.889G>A	c.(889-891)GAG>AAG	p.E297K
Pat_08	Post-Resistance	POTEF	728378	37	2	130832812	130832812	Missense_Mutation	SNP	C	T	53	111	c.2233G>A	c.(2233-2235)GGG>AGG	p.G745R
Pat_08	Post-Resistance	LOC401010	401010	37	2	132200831	132200831	Missense_Mutation	SNP	C	T	19	24	c.1171G>A	c.(1171-1173)GAG>AAG	p.E391K
Pat_08	Post-Resistance	LRP1B	53353	37	2	141116476	141116476	Missense_Mutation	SNP	C	T	143	210	c.11171G>A	c.(11170-11172)AGA>AAA	p.R3724K
Pat_08	Post-Resistance	MBD5	55777	37	2	149226284	149226284	Missense_Mutation	SNP	C	T	90	176	c.772C>T	c.(772-774)CAT>TAT	p.H258Y

Pat_08	Post-Resistance	NEB	4703	37	2	152381753	152381753	Missense_Mutation	SNP	C	T	42	83	c.17093G>A	c.(17092-17094)GGA>GAA	p.G5698E
Pat_08	Post-Resistance	KCNJ3	3760	37	2	155711304	155711304	Missense_Mutation	SNP	C	T	48	88	c.985C>T	c.(985-987)CCT>TCT	p.P329S
Pat_08	Post-Resistance	SCN9A	6335	37	2	167085452	167085452	Missense_Mutation	SNP	G	A	104	191	c.3922C>T	c.(3922-3924)CCT>TCT	p.P1308S
Pat_08	Post-Resistance	DLX1	1745	37	2	172950632	172950632	Missense_Mutation	SNP	G	A	5	401	c.227G>A	c.(226-228)AGC>AAC	p.S76N
Pat_08	Post-Resistance	TTN	7273	37	2	179393620	179393620	Missense_Mutation	SNP	C	T	55	86	c.99154G>A	c.(99154-99156)GAA>AAA	p.E33052K
Pat_08	Post-Resistance	TTN	7273	37	2	179410756	179410756	Missense_Mutation	SNP	C	T	37	37	c.87503G>A	c.(87502-87504)GGA>GAA	p.G29168E
Pat_08	Post-Resistance	TTN	7273	37	2	179428394	179428394	Missense_Mutation	SNP	T	C	160	209	c.74761A>G	c.(74761-74763)ACA>GCA	p.T24921A
Pat_08	Post-Resistance	TTN	7273	37	2	179498194	179498194	Missense_Mutation	SNP	C	T	63	94	c.35188G>A	c.(35188-35190)GAA>AAA	p.E11730K
Pat_08	Post-Resistance	TTN	7273	37	2	179629430	179629430	Missense_Mutation	SNP	G	A	99	199	c.9812C>T	c.(9811-9813)TCC>TTC	p.S3271F
Pat_08	Post-Resistance	TTN	7273	37	2	179640313	179640313	Missense_Mutation	SNP	G	A	52	96	c.6278C>T	c.(6277-6279)TCT>TTT	p.S2093F
Pat_08	Post-Resistance	TTN	7273	37	2	179654118	179654118	Missense_Mutation	SNP	C	T	99	174	c.2045G>A	c.(2044-2046)AGA>AAA	p.R682K
Pat_08	Post-Resistance	SGOL2	151246	37	2	201437870	201437870	Missense_Mutation	SNP	A	T	117	150	c.2801A>T	c.(2800-2802)CAA>CTA	p.Q934L
Pat_08	Post-Resistance	CD28	940	37	2	204594385	204594385	Missense_Mutation	SNP	C	T	79	138	c.424C>T	c.(424-426)CCA>TCA	p.P142S
Pat_08	Post-Resistance	CRYGD	1421	37	2	208988904	208988904	Missense_Mutation	SNP	C	T	37	64	c.184G>A	c.(184-186)GAC>AAC	p.D62N
Pat_08	Post-Resistance	CPS1	1373	37	2	211460248	211460248	Missense_Mutation	SNP	C	T	131	199	c.1301C>T	c.(1300-1302)TCC>TTC	p.S434F
Pat_08	Post-Resistance	VIL1	7429	37	2	219296642	219296642	Missense_Mutation	SNP	C	A	38	76	c.1165C>A	c.(1165-1167)CAG>AAG	p.Q389K
Pat_08	Post-Resistance	SPHKAP	80309	37	2	228855801	228855801	Missense_Mutation	SNP	C	T	67	107	c.4874G>A	c.(4873-4875)CGA>CAA	p.R1625Q
Pat_08	Post-Resistance	CHRND	1144	37	2	233399978	233399978	Missense_Mutation	SNP	G	A	98	124	c.1510G>A	c.(1510-1512)GGG>AGG	p.G504R
Pat_08	Post-Resistance	CHRNG	1146	37	2	233408401	233408401	Missense_Mutation	SNP	G	A	62	99	c.1027G>A	c.(1027-1029)GTC>ATC	p.V343I
Pat_08	Post-Resistance	GPR35	2859	37	2	241569629	241569629	Missense_Mutation	SNP	C	T	76	145	c.260C>T	c.(259-261)CCG>CTG	p.P87L
Pat_08	Post-Resistance	GGTLC1	92086	37	20	23966333	23966333	Missense_Mutation	SNP	C	T	7	400	c.502G>A	c.(502-504)GTC>ATC	p.V168I
Pat_08	Post-Resistance	NCOA6	23054	37	20	33337594	33337594	Missense_Mutation	SNP	C	A	4	314	c.2404G>T	c.(2404-2406)GGT>TGT	p.G802C
Pat_08	Post-Resistance	PTPRT	11122	37	20	41306649	41306649	Missense_Mutation	SNP	G	A	89	142	c.1010C>T	c.(1009-1011)ACC>ATC	p.T337I
Pat_08	Post-Resistance	CDH22	64405	37	20	44869692	44869692	Missense_Mutation	SNP	A	G	58	165	c.460T>C	c.(460-462)TTC>CTC	p.F154L
Pat_08	Post-Resistance	BAGE2	85319	37	21	11058168	11058168	Missense_Mutation	SNP	A	T	4	258	c.272T>A	c.(271-273)CTG>CAG	p.L91Q
Pat_08	Post-Resistance	SH3BGR	6450	37	21	40883698	40883698	Missense_Mutation	SNP	C	T	48	66	c.716C>T	c.(715-717)TCC>TTC	p.S239F
Pat_08	Post-Resistance	DSCAM	1826	37	21	41452217	41452217	Missense_Mutation	SNP	G	A	75	136	c.4282C>T	c.(4282-4284)CCA>TCA	p.P1428S
Pat_08	Post-Resistance	SLC37A1	54020	37	21	43963662	43963662	Missense_Mutation	SNP	G	A	95	166	c.680G>A	c.(679-681)GGA>GAA	p.G227E
Pat_08	Post-Resistance	KRTAP10-6	386674	37	21	46011918	46011918	Missense_Mutation	SNP	G	A	183	567	c.448C>T	c.(448-450)CCC>TCC	p.P150S
Pat_08	Post-Resistance	RTN4R	65078	37	22	20230526	20230526	Missense_Mutation	SNP	G	A	25	45	c.130C>T	c.(130-132)CCC>TCC	p.P44S
Pat_08	Post-Resistance	AP1B1	162	37	22	29727834	29727834	Missense_Mutation	SNP	G	A	85	103	c.2381C>T	c.(2380-2382)TCC>TTC	p.S794F
Pat_08	Post-Resistance	LARGE	9215	37	22	34046453	34046453	Missense_Mutation	SNP	G	A	128	147	c.308C>T	c.(307-309)TCC>TTC	p.S103F
Pat_08	Post-Resistance	SBF1	6305	37	22	50902808	50902808	Missense_Mutation	SNP	G	A	4	267	c.1699C>T	c.(1699-1701)CGC>TGC	p.R567C
Pat_08	Post-Resistance	NUP210	23225	37	3	13370433	13370433	Missense_Mutation	SNP	G	A	31	68	c.4124C>T	c.(4123-4125)TCC>TTC	p.S1375F
Pat_08	Post-Resistance	FGD5	152273	37	3	14862578	14862578	Missense_Mutation	SNP	A	G	66	93	c.2000A>G	c.(1999-2001)AAC>AGC	p.N667S
Pat_08	Post-Resistance	UBP1	7342	37	3	33453119	33453119	Missense_Mutation	SNP	A	G	147	239	c.509T>C	c.(508-510)GTT>GCT	p.V170A
Pat_08	Post-Resistance	TRANK1	9881	37	3	36874752	36874752	Missense_Mutation	SNP	C	T	42	83	c.4540G>A	c.(4540-4542)GAA>AAA	p.E1514K
Pat_08	Post-Resistance	LRRFIP2	9209	37	3	37150142	37150142	Missense_Mutation	SNP	A	G	127	194	c.643T>C	c.(643-645)TAT>CAT	p.Y215H
Pat_08	Post-Resistance	HHATL	57467	37	3	42735116	42735116	Missense_Mutation	SNP	C	T	22	49	c.1241G>A	c.(1240-1242)CGA>CAA	p.R414Q
Pat_08	Post-Resistance	SETD2	29072	37	3	47125298	47125298	Missense_Mutation	SNP	T	C	4	405	c.5972A>G	c.(5971-5973)GAG>GGG	p.E1991G
Pat_08	Post-Resistance	RHOA	387	37	3	49405936	49405936	Missense_Mutation	SNP	G	A	117	138	c.202C>T	c.(202-204)CGC>TGC	p.R68C
Pat_08	Post-Resistance	DNAH1	25981	37	3	52392656	52392656	Missense_Mutation	SNP	C	T	18	87	c.4169C>T	c.(4168-4170)CCC>CTC	p.P1390L
Pat_08	Post-Resistance	CACNA1D	776	37	3	53766925	53766925	Missense_Mutation	SNP	A	T	53	78	c.2557A>T	c.(2557-2559)ATG>TTG	p.M853L
Pat_08	Post-Resistance	CNTN3	5067	37	3	74385793	74385793	Missense_Mutation	SNP	C	T	44	57	c.1381G>A	c.(1381-1383)GAT>AAT	p.D461N
Pat_08	Post-Resistance	C3orf26	84319	37	3	99536869	99536869	Missense_Mutation	SNP	G	A	80	81	c.46G>A	c.(46-48)GGA>AGA	p.G16R
Pat_08	Post-Resistance	FBXO40	51725	37	3	121345753	121345753	Missense_Mutation	SNP	C	T	39	65	c.2126C>T	c.(2125-2127)TCC>TTC	p.S709F
Pat_08	Post-Resistance	SLC15A2	6565	37	3	121613396	121613396	Nonsense_Mutation	SNP	C	T	324	477	c.73C>T	c.(73-75)CGA>TGA	p.R25*

Pat_08	Post-Resistance	OTOL1	131149	37	3	161221408	161221408	Missense_Mutation	SNP	G	A	23	48	c.1112G>A	c.(1111-1113)GGG>GAG	p.G371E
Pat_08	Post-Resistance	MECOM	2122	37	3	168838897	168838897	Missense_Mutation	SNP	G	A	56	96	c.515C>T	c.(514-516)TCG>TTG	p.S172L
Pat_08	Post-Resistance	TP63	8626	37	3	189455588	189455588	Missense_Mutation	SNP	C	T	84	130	c.122C>T	c.(121-123)TCC>TTC	p.S41F
Pat_08	Post-Resistance	MUC4	4585	37	3	195508133	195508133	Missense_Mutation	SNP	G	A	3	22	c.9934C>T	c.(9934-9936)CCT>TCT	p.P3312S
Pat_08	Post-Resistance	MUC4	4585	37	3	195511925	195511925	Missense_Mutation	SNP	A	G	6	25	c.6526T>C	c.(6526-6528)TCT>CCT	p.S2176P
Pat_08	Post-Resistance	SLC26A1	10861	37	4	984951	984951	Missense_Mutation	SNP	C	T	4	93	c.541G>A	c.(541-543)GCC>ACC	p.A181T
Pat_08	Post-Resistance	TACC3	10460	37	4	1730226	1730226	Missense_Mutation	SNP	C	T	35	78	c.1097C>T	c.(1096-1098)CCC>CTC	p.P366L
Pat_08	Post-Resistance	DEFB131	644414	37	4	9452106	9452106	Missense_Mutation	SNP	G	A	14	50	c.79G>A	c.(79-81)GAT>AAT	p.D27N
Pat_08	Post-Resistance	UGT2A3	79799	37	4	69817123	69817123	Missense_Mutation	SNP	C	T	29	55	c.356G>A	c.(355-357)GGA>GAA	p.G119E
Pat_08	Post-Resistance	PARM1	25849	37	4	75938040	75938040	Missense_Mutation	SNP	C	T	304	419	c.449C>T	c.(448-450)TCC>TTC	p.S150F
Pat_08	Post-Resistance	NAA11	84779	37	4	80246759	80246759	Missense_Mutation	SNP	C	T	44	51	c.273G>A	c.(271-273)ATG>ATA	p.M91I
Pat_08	Post-Resistance	ARHGAP24	83478	37	4	86863344	86863344	Missense_Mutation	SNP	C	T	64	101	c.517C>T	c.(517-519)CTC>TTC	p.L173F
Pat_08	Post-Resistance	DSPP	1834	37	4	88535148	88535148	Missense_Mutation	SNP	G	A	4	328	c.1334G>A	c.(1333-1335)AGC>AAC	p.S445N
Pat_08	Post-Resistance	IBSP	3381	37	4	88732988	88732988	Missense_Mutation	SNP	G	A	104	218	c.880G>A	c.(880-882)GAA>AAA	p.E294K
Pat_08	Post-Resistance	FAM190A	401145	37	4	91229782	91229782	Missense_Mutation	SNP	C	T	48	43	c.347C>T	c.(346-348)TCT>TTT	p.S116F
Pat_08	Post-Resistance	ADH1C	126	37	4	100266089	100266089	Missense_Mutation	SNP	G	A	201	339	c.497C>T	c.(496-498)CCC>CTC	p.P166L
Pat_08	Post-Resistance	FAT4	79633	37	4	126372799	126372799	Missense_Mutation	SNP	C	T	149	240	c.10628C>T	c.(10627-10629)CCC>CTC	p.P3543L
Pat_08	Post-Resistance	PCDH18	54510	37	4	138451129	138451129	Missense_Mutation	SNP	G	A	149	260	c.2114C>T	c.(2113-2115)TCC>TTC	p.S705F
Pat_08	Post-Resistance	LRBA	987	37	4	151837674	151837674	Missense_Mutation	SNP	C	T	27	60	c.773G>A	c.(772-774)AGA>AAA	p.R258K
Pat_08	Post-Resistance	FSTL5	56884	37	4	162376261	162376261	Missense_Mutation	SNP	C	A	78	113	c.1736G>T	c.(1735-1737)GGG>GTG	p.G579V
Pat_08	Post-Resistance	1-Mar	55016	37	4	164507014	164507014	Missense_Mutation	SNP	G	A	66	95	c.310C>T	c.(310-312)CGC>TGC	p.R104C
Pat_08	Post-Resistance	ANXA10	11199	37	4	169099049	169099049	Nonsense_Mutation	SNP	G	A	133	271	c.543G>A	c.(541-543)TGG>TGA	p.W181*
Pat_08	Post-Resistance	GALNT7	51809	37	4	174242826	174242826	Missense_Mutation	SNP	A	T	41	62	c.1932A>T	c.(1930-1932)AAA>AAT	p.K644N
Pat_08	Post-Resistance	SNX25	83891	37	4	186263251	186263251	Missense_Mutation	SNP	T	C	155	211	c.1676T>C	c.(1675-1677)TTA>TCA	p.L559S
Pat_08	Post-Resistance	SEMA5A	9037	37	5	9197374	9197374	Missense_Mutation	SNP	C	T	101	184	c.974G>A	c.(973-975)AGC>AAC	p.S325N
Pat_08	Post-Resistance	CTNND2	1501	37	5	11732369	11732369	Missense_Mutation	SNP	G	A	85	178	c.53C>T	c.(52-54)CCA>CTA	p.P18L
Pat_08	Post-Resistance	DNAH5	1767	37	5	13714578	13714578	Missense_Mutation	SNP	G	C	4	372	c.13061C>G	c.(13060-13062)GCG>GGC	p.A4354G
Pat_08	Post-Resistance	DNAH5	1767	37	5	13823476	13823476	Missense_Mutation	SNP	C	T	55	67	c.6583G>A	c.(6583-6585)GAT>AAT	p.D2195N
Pat_08	Post-Resistance	CDH18	1016	37	5	19571761	19571761	Missense_Mutation	SNP	C	T	114	152	c.1180G>A	c.(1180-1182)GAA>AAA	p.E394K
Pat_08	Post-Resistance	RAI14	26064	37	5	34814746	34814746	Missense_Mutation	SNP	C	T	66	139	c.911C>T	c.(910-912)TCG>TTG	p.S304L
Pat_08	Post-Resistance	UGT3A1	133688	37	5	35965946	35965946	Missense_Mutation	SNP	C	T	45	78	c.385G>A	c.(385-387)GAT>AAT	p.D129N
Pat_08	Post-Resistance	SLC1A3	6507	37	5	36686171	36686171	Missense_Mutation	SNP	C	T	78	126	c.1429C>T	c.(1429-1431)CGC>TGC	p.R477C
Pat_08	Post-Resistance	PLK2	10769	37	5	57752362	57752362	Missense_Mutation	SNP	T	C	4	390	c.1211A>G	c.(1210-1212)AAG>AGG	p.K404R
Pat_08	Post-Resistance	RAB3C	115827	37	5	57913641	57913641	Missense_Mutation	SNP	G	A	23	49	c.196G>A	c.(196-198)GAT>AAT	p.D66N
Pat_08	Post-Resistance	ADAMTS6	11174	37	5	64483859	64483859	Missense_Mutation	SNP	G	A	96	154	c.2894C>T	c.(2893-2895)GCT>GTT	p.A965V
Pat_08	Post-Resistance	FAM169A	26049	37	5	74077829	74077829	Missense_Mutation	SNP	G	A	15	136	c.1469C>T	c.(1468-1470)CCA>CTA	p.P490L
Pat_08	Post-Resistance	SPZ1	84654	37	5	79616605	79616605	Missense_Mutation	SNP	C	G	15	198	c.571C>G	c.(571-573)CAG>GAG	p.Q191E
Pat_08	Post-Resistance	GPR98	84059	37	5	89949415	89949415	Missense_Mutation	SNP	C	T	38	57	c.4024C>T	c.(4024-4026)CCA>TCA	p.P1342S
Pat_08	Post-Resistance	TSSK1B	83942	37	5	112770218	112770218	Missense_Mutation	SNP	C	T	39	63	c.319G>A	c.(319-321)GCC>ACC	p.A107T
Pat_08	Post-Resistance	ADAMTS19	171019	37	5	128863489	128863489	Missense_Mutation	SNP	C	T	125	66	c.1117C>T	c.(1117-1119)CGT>TGT	p.R373C
Pat_08	Post-Resistance	FSTL4	23105	37	5	132652260	132652260	Missense_Mutation	SNP	C	T	46	17	c.494G>A	c.(493-495)GGA>GAA	p.G165E
Pat_08	Post-Resistance	CTNNA1	1495	37	5	138265031	138265031	Missense_Mutation	SNP	G	A	3	87	c.1996G>A	c.(1996-1998)GGC>AGC	p.G666S
Pat_08	Post-Resistance	PCDHB17	54661	37	5	140536771	140536771	Missense_Mutation	SNP	G	A	23	28	c.1192G>A	c.(1192-1194)GAA>AAA	p.E398K
Pat_08	Post-Resistance	PPP2R2B	5521	37	5	146017937	146017937	Missense_Mutation	SNP	C	T	75	179	c.667G>A	c.(667-669)GAG>AAG	p.E223K
Pat_08	Post-Resistance	DPYSL3	1809	37	5	146781130	146781130	Missense_Mutation	SNP	G	A	36	42	c.941C>T	c.(940-942)CCG>CTG	p.P314L
Pat_08	Post-Resistance	PDGFRB	5159	37	5	149510138	149510138	Missense_Mutation	SNP	G	A	4	419	c.1331C>T	c.(1330-1332)CCG>CTG	p.P444L
Pat_08	Post-Resistance	GABRA6	2559	37	5	161115979	161115979	Missense_Mutation	SNP	C	T	100	67	c.250C>T	c.(250-252)CGC>TGC	p.R84C

Pat_08	Post-Resistance	ODZ2	57451	37	5	167622180	167622180	Splice_Site	SNP	G	A	15	27	c.2754_splice	c.e15-1	p.S918_splice
Pat_08	Post-Resistance	ARL10	285598	37	5	175793384	175793384	Missense_Mutation	SNP	C	T	6	18	c.185C>T	c.(184-186)CCC>CTC	p.P62L
Pat_08	Post-Resistance	RASGEF1C	255426	37	5	179529070	179529070	Splice_Site	SNP	C	T	25	80	c.1376_splice	c.e12+1	p.R459_splice
Pat_08	Post-Resistance	FOXC1	2296	37	6	1611150	1611150	Missense_Mutation	SNP	A	G	30	376	c.470A>G	c.(469-471)GAC>GGC	p.D157G
Pat_08	Post-Resistance	DSP	1832	37	6	7580784	7580784	Missense_Mutation	SNP	T	G	110	445	c.4361T>G	c.(4360-4362)GTC>GGC	p.V1454G
Pat_08	Post-Resistance	MAK	4117	37	6	10802187	10802187	Missense_Mutation	SNP	C	T	68	292	c.769G>A	c.(769-771)GCT>ACT	p.A257T
Pat_08	Post-Resistance	HIVEP1	3096	37	6	12123018	12123018	Missense_Mutation	SNP	C	T	140	587	c.2990C>T	c.(2989-2991)CCT>CTT	p.P997L
Pat_08	Post-Resistance	SCAND3	114821	37	6	28539827	28539828	Missense_Mutation	DNP	CC	TT	31	128	.3838_3839GG>A	c.(3838-3840)GGA>AAA	p.G1280K
Pat_08	Post-Resistance	SCAND3	114821	37	6	28540785	28540785	Missense_Mutation	SNP	C	T	52	129	c.2881G>A	c.(2881-2883)GAA>AAA	p.E961K
Pat_08	Post-Resistance	OR2J2	26707	37	6	29141910	29141910	Nonsense_Mutation	SNP	G	A	200	499	c.498G>A	c.(496-498)TGG>TGA	p.W166*
Pat_08	Post-Resistance	MDC1	9656	37	6	30672288	30672288	Missense_Mutation	SNP	C	A	10	664	c.4672G>T	c.(4672-4674)GGC>TGC	p.G1558C
Pat_08	Post-Resistance	DDR1	780	37	6	30860230	30860230	Missense_Mutation	SNP	C	T	35	69	c.1010C>T	c.(1009-1011)CCC>CTC	p.P337L
Pat_08	Post-Resistance	TNXB	7148	37	6	32026008	32026008	Missense_Mutation	SNP	G	A	43	144	c.7652C>T	c.(7651-7653)TCC>TTC	p.S2551F
Pat_08	Post-Resistance	HLA-DRA	3122	37	6	32410472	32410472	Splice_Site	SNP	T	C	192	436	c.328_splice	c.e2+2	p.V110_splice
Pat_08	Post-Resistance	COL11A2	1302	37	6	33136737	33136737	Missense_Mutation	SNP	G	A	95	274	c.3847C>T	c.(3847-3849)CCT>TCT	p.P1283S
Pat_08	Post-Resistance	LYPLA2P1	653639	37	6	33333333	33333333	Missense_Mutation	SNP	G	A	5	53	c.673C>T	c.(673-675)CCT>TCT	p.P225S
Pat_08	Post-Resistance	IP6K3	117283	37	6	33690517	33690517	Missense_Mutation	SNP	C	T	101	249	c.1213G>A	c.(1213-1215)GAT>AAT	p.D405N
Pat_08	Post-Resistance	GLP1R	2740	37	6	39047471	39047471	Missense_Mutation	SNP	C	T	50	160	c.1175C>T	c.(1174-1176)TCC>TTC	p.S392F
Pat_08	Post-Resistance	TREML4	285852	37	6	41196525	41196525	Missense_Mutation	SNP	G	A	112	352	c.137G>A	c.(136-138)AGA>AAA	p.R46K
Pat_08	Post-Resistance	ZNF318	24149	37	6	43324886	43324886	Missense_Mutation	SNP	T	C	18	365	c.1166A>G	c.(1165-1167)GAC>GGC	p.D389G
Pat_08	Post-Resistance	POLH	5429	37	6	43582164	43582164	Missense_Mutation	SNP	C	T	46	742	c.2012C>T	c.(2011-2013)CCC>CTC	p.P671L
Pat_08	Post-Resistance	TDRD6	221400	37	6	46659190	46659190	Nonsense_Mutation	SNP	G	T	141	338	c.3325G>T	c.(3325-3327)GAA>TAA	p.E1109*
Pat_08	Post-Resistance	GPR115	221393	37	6	47681873	47681873	Missense_Mutation	SNP	T	G	128	101	c.892T>G	c.(892-894)TTG>GTG	p.L298V
Pat_08	Post-Resistance	FAM83B	222584	37	6	54735196	54735196	Missense_Mutation	SNP	G	A	103	313	c.152G>A	c.(151-153)CGA>CAA	p.R51Q
Pat_08	Post-Resistance	GFRAL	389400	37	6	55196641	55196641	Missense_Mutation	SNP	G	A	52	123	c.151G>A	c.(151-153)GAT>AAT	p.D51N
Pat_08	Post-Resistance	KIAA1586	57691	37	6	56919090	56919090	Missense_Mutation	SNP	T	G	42	98	c.1793T>G	c.(1792-1794)TTT>TGT	p.F598C
Pat_08	Post-Resistance	COL9A1	1297	37	6	70961981	70961981	Missense_Mutation	SNP	C	T	71	137	c.1802G>A	c.(1801-1803)GGA>GAA	p.G601E
Pat_08	Post-Resistance	COL9A1	1297	37	6	70984435	70984435	Missense_Mutation	SNP	G	A	49	78	c.1016C>T	c.(1015-1017)TCA>TTA	p.S339L
Pat_08	Post-Resistance	RIMS1	22999	37	6	73110352	73110352	Missense_Mutation	SNP	T	C	135	240	c.5015T>C	c.(5014-5016)CTC>CCC	p.L1672P
Pat_08	Post-Resistance	EEF1A1	1915	37	6	74229701	74229701	Missense_Mutation	SNP	C	T	62	87	c.49G>A	c.(49-51)GAT>AAT	p.D17N
Pat_08	Post-Resistance	CNR1	1268	37	6	88854819	88854819	Nonsense_Mutation	SNP	G	A	16	54	c.175C>T	c.(175-177)CAA>TAA	p.Q59*
Pat_08	Post-Resistance	RFX6	222546	37	6	117249966	117249966	Missense_Mutation	SNP	G	A	195	344	c.2443G>A	c.(2443-2445)GGA>AGA	p.G815R
Pat_08	Post-Resistance	C6orf204	387119	37	6	118801656	118801656	Missense_Mutation	SNP	C	T	55	106	c.1766G>A	c.(1765-1767)AGA>AAA	p.R589K
Pat_08	Post-Resistance	FAM184A	79632	37	6	119345282	119345282	Missense_Mutation	SNP	C	T	48	95	c.856G>A	c.(856-858)GAT>AAT	p.D286N
Pat_08	Post-Resistance	RSPO3	84870	37	6	127476496	127476496	Missense_Mutation	SNP	C	T	75	121	c.547C>T	c.(547-549)CCT>TCT	p.P183S
Pat_08	Post-Resistance	PTPRK	5796	37	6	128388791	128388791	Missense_Mutation	SNP	C	T	119	228	c.2030G>A	c.(2029-2031)GGA>GAA	p.G677E
Pat_08	Post-Resistance	L3MBTL3	84456	37	6	130425708	130425708	Missense_Mutation	SNP	C	T	118	166	c.1874C>T	c.(1873-1875)TCC>TTC	p.S625F
Pat_08	Post-Resistance	SAMD3	154075	37	6	130465798	130465798	Missense_Mutation	SNP	C	T	92	147	c.1430G>A	c.(1429-1431)AGG>AAG	p.R477K
Pat_08	Post-Resistance	ALDH8A1	64577	37	6	135239986	135239986	Missense_Mutation	SNP	C	T	155	211	c.1031G>A	c.(1030-1032)AGA>AAA	p.R344K
Pat_08	Post-Resistance	FBXO30	84085	37	6	146126961	146126961	Missense_Mutation	SNP	G	A	54	432	c.581C>T	c.(580-582)GCT>GTT	p.A194V
Pat_08	Post-Resistance	TIAM2	26230	37	6	155450436	155450436	Missense_Mutation	SNP	C	T	75	172	c.79C>T	c.(79-81)CCT>TCT	p.P27S
Pat_08	Post-Resistance	ARID1B	57492	37	6	157522541	157522541	Missense_Mutation	SNP	G	A	235	421	c.4759G>A	c.(4759-4761)GAG>AAG	p.E1587K
Pat_08	Post-Resistance	MLLT4	4301	37	6	168370511	168370511	Missense_Mutation	SNP	T	A	32	34	c.5401T>A	c.(5401-5403)TTC>ATC	p.F1801I
Pat_08	Post-Resistance	INTS1	26173	37	7	1513911	1513911	Missense_Mutation	SNP	A	G	26	76	c.5722T>C	c.(5722-5724)TTC>CTC	p.F1908L
Pat_08	Post-Resistance	SDK1	221935	37	7	4107511	4107511	Missense_Mutation	SNP	G	A	12	43	c.2953G>A	c.(2953-2955)GAC>AAC	p.D985N
Pat_08	Post-Resistance	KIAA0415	9907	37	7	4824003	4824003	Splice_Site	SNP	G	A	3	48	c.790_splice	c.e6+1	p.D264_splice
Pat_08	Post-Resistance	STK31	56164	37	7	23776524	23776524	Missense_Mutation	SNP	G	A	13	79	c.844G>A	c.(844-846)GAA>AAA	p.E282K

Pat_08	Post-Resistance	HOXA4	3201	37	7	27168950	27168950	Missense_Mutation	SNP	G	A	96	220	c.857C>T	c.(856-858)TCG>TTG	p.S286L
Pat_08	Post-Resistance	HECW1	23072	37	7	43351600	43351600	Missense_Mutation	SNP	C	T	87	268	c.266C>T	c.(265-267)TCC>TTC	p.S89F
Pat_08	Post-Resistance	VOPP1	81552	37	7	55540681	55540681	Missense_Mutation	SNP	G	A	41	90	c.386C>T	c.(385-387)CCT>CTT	p.P129L
Pat_08	Post-Resistance	ZNF679	168417	37	7	63726958	63726958	Missense_Mutation	SNP	G	A	135	429	c.947G>A	c.(946-948)AGA>AAA	p.R316K
Pat_08	Post-Resistance	WBSCR17	64409	37	7	71177084	71177084	Missense_Mutation	SNP	C	T	89	227	c.1750C>T	c.(1750-1752)CGC>TGC	p.R584C
Pat_08	Post-Resistance	PCLO	27445	37	7	82544688	82544688	Missense_Mutation	SNP	G	A	30	70	c.12614C>T	c.(12613-12615)CCT>CTT	p.P4205L
Pat_08	Post-Resistance	GRM3	2913	37	7	86394514	86394514	Missense_Mutation	SNP	G	A	87	332	c.53G>A	c.(52-54)GGA>GAA	p.G18E
Pat_08	Post-Resistance	STEAP4	79689	37	7	87911999	87911999	Missense_Mutation	SNP	C	T	64	190	c.941G>A	c.(940-942)CGA>CAA	p.R314Q
Pat_08	Post-Resistance	DYNC1I1	1780	37	7	95662058	95662058	Missense_Mutation	SNP	G	A	159	417	c.1247G>A	c.(1246-1248)TGT>TAT	p.C416Y
Pat_08	Post-Resistance	BAIAP2L1	55971	37	7	97991713	97991713	Missense_Mutation	SNP	C	T	63	213	c.83G>A	c.(82-84)CGA>CAA	p.R28Q
Pat_08	Post-Resistance	ACHE	43	37	7	100491517	100491517	Missense_Mutation	SNP	C	T	115	275	c.337G>A	c.(337-339)GGC>AGC	p.G113S
Pat_08	Post-Resistance	NRCAM	4897	37	7	107880409	107880409	Missense_Mutation	SNP	G	A	73	258	c.100C>T	c.(100-102)CTT>TTT	p.L34F
Pat_08	Post-Resistance	CFTR	1080	37	7	117175443	117175443	Missense_Mutation	SNP	G	A	54	152	c.721G>A	c.(721-723)GGG>AGG	p.G241R
Pat_08	Post-Resistance	KCND2	3751	37	7	119914743	119914743	Nonsense_Mutation	SNP	G	A	128	326	c.57G>A	c.(55-57)TGG>TGA	p.W19*
Pat_08	Post-Resistance	RNF148	378925	37	7	122342384	122342384	Missense_Mutation	SNP	G	A	463	402	c.421C>T	c.(421-423)CCC>TCC	p.P141S
Pat_08	Post-Resistance	TSGA14	95681	37	7	130041725	130041725	Missense_Mutation	SNP	T	A	83	191	c.639A>T	c.(637-639)GAA>GAT	p.E213D
Pat_08	Post-Resistance	TRIM24	8805	37	7	138266508	138266508	Missense_Mutation	SNP	C	T	32	98	c.2785C>T	c.(2785-2787)CCT>TCT	p.P929S
Pat_08	Post-Resistance	BRAF	673	37	7	140453136	140453136	Missense_Mutation	SNP	A	T	826	75	c.1799T>A	c.(1798-1800)GTG>GAG	p.V600E
Pat_08	Post-Resistance	TAS2R38	5726	37	7	141672855	141672855	Missense_Mutation	SNP	G	A	483	146	c.635C>T	c.(634-636)TCT>TTT	p.S212F
Pat_08	Post-Resistance	TRPV6	55503	37	7	142574981	142574981	Missense_Mutation	SNP	C	T	24	341	c.401G>A	c.(400-402)CGA>CAA	p.R134Q
Pat_08	Post-Resistance	TRPV5	56302	37	7	142625242	142625242	Missense_Mutation	SNP	C	T	57	137	c.850G>A	c.(850-852)GAC>AAC	p.D284N
Pat_08	Post-Resistance	OR6V1	346517	37	7	142750371	142750371	Missense_Mutation	SNP	G	A	15	29	c.934G>A	c.(934-936)GCA>ACA	p.A312T
Pat_08	Post-Resistance	CLCN1	1180	37	7	143018840	143018840	Missense_Mutation	SNP	C	T	74	130	c.595C>T	c.(595-597)CGT>TGT	p.R199C
Pat_08	Post-Resistance	OR2F1	26211	37	7	143657859	143657859	Missense_Mutation	SNP	C	A	36	245	c.796C>A	c.(796-798)CCC>ACC	p.P266T
Pat_08	Post-Resistance	ABP1	26	37	7	150554027	150554027	Missense_Mutation	SNP	G	A	93	231	c.469G>A	c.(469-471)GAA>AAA	p.E157K
Pat_08	Post-Resistance	TNFRSF10C	8794	37	8	22974270	22974270	Missense_Mutation	SNP	A	C	4	345	c.506A>C	c.(505-507)AAC>ACC	p.N169T
Pat_08	Post-Resistance	SCARA5	286133	37	8	27779754	27779754	Missense_Mutation	SNP	G	A	17	29	c.250C>T	c.(250-252)CCG>TCG	p.P84S
Pat_08	Post-Resistance	GSR	2936	37	8	30553929	30553929	Missense_Mutation	SNP	A	G	134	255	c.763T>C	c.(763-765)TCT>CCT	p.S255P
Pat_08	Post-Resistance	IDO2	169355	37	8	39845421	39845421	Missense_Mutation	SNP	G	A	21	22	c.520G>A	c.(520-522)GGA>AGA	p.G174R
Pat_08	Post-Resistance	PXDNL	137902	37	8	52321700	52321700	Missense_Mutation	SNP	A	T	13	31	c.2484T>A	c.(2482-2484)GAT>GAA	p.D828E
Pat_08	Post-Resistance	PXDNL	137902	37	8	52412271	52412271	Missense_Mutation	SNP	C	T	118	245	c.440G>A	c.(439-441)AGA>AAA	p.R147K
Pat_08	Post-Resistance	RP1	6101	37	8	55537568	55537568	Nonsense_Mutation	SNP	C	T	48	81	c.1126C>T	c.(1126-1128)CGA>TGA	p.R376*
Pat_08	Post-Resistance	RP1	6101	37	8	55538973	55538973	Missense_Mutation	SNP	C	T	64	97	c.2531C>T	c.(2530-2532)TCT>TTT	p.S844F
Pat_08	Post-Resistance	TRIM55	84675	37	8	67086730	67086730	Nonsense_Mutation	SNP	C	T	131	197	c.1549C>T	c.(1549-1551)CAG>TAG	p.Q517*
Pat_08	Post-Resistance	CPA6	57094	37	8	68423876	68423876	Missense_Mutation	SNP	T	G	118	189	c.332A>C	c.(331-333)GAT>GCT	p.D111A
Pat_08	Post-Resistance	KCNB2	9312	37	8	73480001	73480001	Missense_Mutation	SNP	G	A	96	261	c.32G>A	c.(31-33)AGG>AAG	p.R11K
Pat_08	Post-Resistance	UBR5	51366	37	8	103354847	103354847	Missense_Mutation	SNP	G	A	4	318	c.952C>T	c.(952-954)CGT>TGT	p.R318C
Pat_08	Post-Resistance	TRHR	7201	37	8	110100064	110100064	Missense_Mutation	SNP	G	A	88	303	c.323G>A	c.(322-324)GGA>GAA	p.G108E
Pat_08	Post-Resistance	PKHD1L1	93035	37	8	110468517	110468517	Missense_Mutation	SNP	C	T	34	109	c.6901C>T	c.(6901-6903)CGC>TGC	p.R2301C
Pat_08	Post-Resistance	CSMD3	114788	37	8	113326683	113326683	Missense_Mutation	SNP	T	G	77	254	c.7524A>C	c.(7522-7524)GAA>GAC	p.E2508D
Pat_08	Post-Resistance	CSMD3	114788	37	8	113392596	113392596	Missense_Mutation	SNP	G	A	127	391	c.6121C>T	c.(6121-6123)CAT>TAT	p.H2041Y
Pat_08	Post-Resistance	FER1L6	654463	37	8	125061918	125061918	Missense_Mutation	SNP	C	T	90	175	c.2795C>T	c.(2794-2796)CCC>CTC	p.P932L
Pat_08	Post-Resistance	COL22A1	169044	37	8	139611032	139611032	Missense_Mutation	SNP	C	T	50	136	c.4295G>A	c.(4294-4296)GGA>GAA	p.G1432E
Pat_08	Post-Resistance	TRAPPC9	83696	37	8	141460925	141460925	Missense_Mutation	SNP	T	C	5	51	c.548A>G	c.(547-549)GAG>GGG	p.E183G
Pat_08	Post-Resistance	EIF2C2	27161	37	8	141545667	141545667	Missense_Mutation	SNP	A	G	75	202	c.2171T>C	c.(2170-2172)GTT>GCT	p.V724A
Pat_08	Post-Resistance	PTPRD	5789	37	9	8341129	8341129	Missense_Mutation	SNP	C	T	181	88	c.5087G>A	c.(5086-5088)GGA>GAA	p.G1696E
Pat_08	Post-Resistance	CNTLN	54875	37	9	17466725	17466725	Missense_Mutation	SNP	G	A	3	35	c.3688G>A	c.(3688-3690)GTA>ATA	p.V1230I

Pat_08	Post-Resistance	CDKN2A	1029	37	9	21971186	21971186	Nonsense_Mutation	SNP	G	A	18	8	c.172C>T	c.(172-174)CGA>TGA	p.R58*
Pat_08	Post-Resistance	TAF1L	138474	37	9	32633029	32633029	Missense_Mutation	SNP	T	G	121	125	c.2549A>C	c.(2548-2550)AAA>ACA	p.K850T
Pat_08	Post-Resistance	OR2S2	56656	37	9	35957515	35957515	Missense_Mutation	SNP	G	A	186	301	c.581C>T	c.(580-582)TCC>TTC	p.S194F
Pat_08	Post-Resistance	FRMPD1	22844	37	9	37692715	37692716	Missense_Mutation	DNP	GG	AA	98	200	c.77_78GG>AA	c.(76-78)CGG>CAA	p.R26Q
Pat_08	Post-Resistance	VPS13A	23230	37	9	79865130	79865130	Missense_Mutation	SNP	C	T	124	226	c.2155C>T	c.(2155-2157)CTT>TTT	p.L719F
Pat_08	Post-Resistance	FAM22F	54754	37	9	97082793	97082793	Missense_Mutation	SNP	C	G	4	83	c.1065G>C	c.(1063-1065)AAG>AAC	p.K355N
Pat_08	Post-Resistance	ZNF510	22869	37	9	99522622	99522622	Missense_Mutation	SNP	C	A	83	124	c.490G>T	c.(490-492)GTA>TTA	p.V164L
Pat_08	Post-Resistance	OR13C9	286362	37	9	107380278	107380278	Missense_Mutation	SNP	C	T	103	170	c.208G>A	c.(208-210)GAC>AAC	p.D70N
Pat_08	Post-Resistance	PTGS1	5742	37	9	125133515	125133515	Missense_Mutation	SNP	C	T	36	78	c.58C>T	c.(58-60)CCC>TCC	p.P20S
Pat_08	Post-Resistance	NUP188	23511	37	9	131755873	131755873	Nonsense_Mutation	SNP	C	T	144	214	c.2917C>T	c.(2917-2919)CGA>TGA	p.R973*
Pat_08	Post-Resistance	BAT2L1	84726	37	9	134350643	134350643	Missense_Mutation	SNP	C	T	26	51	c.3127C>T	c.(3127-3129)CCC>TCC	p.P1043S
Pat_08	Post-Resistance	SURF6	6838	37	9	136200589	136200589	Nonsense_Mutation	SNP	G	A	49	65	c.358C>T	c.(358-360)CGA>TGA	p.R120*
Pat_08	Post-Resistance	MRPS2	51116	37	9	138395713	138395713	Missense_Mutation	SNP	G	A	4	215	c.625G>A	c.(625-627)GTG>ATG	p.V209M
Pat_08	Post-Resistance	LCN10	414332	37	9	139636409	139636409	Missense_Mutation	SNP	C	T	12	18	c.181G>A	c.(181-183)GAC>AAC	p.D61N
Pat_08	Post-Resistance	MXRA5	25878	37	X	3240874	3240874	Missense_Mutation	SNP	G	A	61	90	c.2852C>T	c.(2851-2853)TCG>TTG	p.S951L
Pat_08	Post-Resistance	AMELX	265	37	X	11312955	11312955	Missense_Mutation	SNP	C	T	142	262	c.47C>T	c.(46-48)GCC>GTC	p.A16V
Pat_08	Post-Resistance	PIGA	5277	37	X	15342966	15342966	Missense_Mutation	SNP	G	A	33	56	c.1009C>T	c.(1009-1011)CCT>TCT	p.P337S
Pat_08	Post-Resistance	YY2	404281	37	X	21871579	21871579	Missense_Mutation	SNP	C	A	192	371	c.628C>A	c.(628-630)CAA>AAA	p.Q210K
Pat_08	Post-Resistance	EIF2S3	1968	37	X	24089743	24089743	Missense_Mutation	SNP	G	A	51	356	c.1081G>A	c.(1081-1083)GTC>ATC	p.V361I
Pat_08	Post-Resistance	MAGEB18	286514	37	X	26157607	26157607	Missense_Mutation	SNP	C	T	14	33	c.505C>T	c.(505-507)CCC>TCC	p.P169S
Pat_08	Post-Resistance	FAM47C	442444	37	X	37028026	37028026	Missense_Mutation	SNP	T	C	9	684	c.1543T>C	c.(1543-1545)TCT>CCT	p.S515P
Pat_08	Post-Resistance	OTC	5009	37	X	38212012	38212012	Missense_Mutation	SNP	G	A	81	139	c.63G>A	c.(61-63)ATG>ATA	p.M21I
Pat_08	Post-Resistance	CXorf38	159013	37	X	40496317	40496317	Missense_Mutation	SNP	A	T	78	102	c.563T>A	c.(562-564)TTT>TAT	p.F188Y
Pat_08	Post-Resistance	RBM3	5935	37	X	48433978	48433978	Missense_Mutation	SNP	C	T	3	78	c.133C>T	c.(133-135)CGG>TGG	p.R45W
Pat_08	Post-Resistance	MTMR8	55613	37	X	63555965	63555965	Missense_Mutation	SNP	G	A	46	107	c.1145C>T	c.(1144-1146)TCC>TTC	p.S382F
Pat_08	Post-Resistance	EDA	1896	37	X	69247866	69247866	Missense_Mutation	SNP	C	A	13	26	c.686C>A	c.(685-687)CCT>CAT	p.P229H
Pat_08	Post-Resistance	DLG3	1741	37	X	69712000	69712000	Missense_Mutation	SNP	A	G	7	20	c.1564A>G	c.(1564-1566)AGC>GGC	p.S522G
Pat_08	Post-Resistance	KIAA2022	340533	37	X	73960184	73960184	Missense_Mutation	SNP	C	T	212	394	c.4208G>A	c.(4207-4209)GGG>GAG	p.G1403E
Pat_08	Post-Resistance	LPAR4	2846	37	X	78010473	78010473	Missense_Mutation	SNP	C	T	274	499	c.107C>T	c.(106-108)TCC>TTC	p.S36F
Pat_08	Post-Resistance	APOOL	139322	37	X	84310875	84310875	Missense_Mutation	SNP	C	T	19	52	c.338C>T	c.(337-339)CCG>CTG	p.P113L
Pat_08	Post-Resistance	KLHL4	56062	37	X	86880629	86880629	Missense_Mutation	SNP	C	T	72	148	c.1157C>T	c.(1156-1158)ACC>ATC	p.T386I
Pat_08	Post-Resistance	CXorf57	55086	37	X	105912404	105912404	Missense_Mutation	SNP	G	A	308	532	c.2281G>A	c.(2281-2283)GAG>AAG	p.E761K
Pat_08	Post-Resistance	TEX13B	56156	37	X	107225012	107225012	Missense_Mutation	SNP	C	T	268	454	c.346G>A	c.(346-348)GAA>AAA	p.E116K
Pat_08	Post-Resistance	KIAA1210	57481	37	X	118222570	118222570	Missense_Mutation	SNP	G	A	28	54	c.2623C>T	c.(2623-2625)CTC>TTC	p.L875F
Pat_08	Post-Resistance	ELF4	2000	37	X	129215252	129215252	Missense_Mutation	SNP	C	T	247	459	c.53G>A	c.(52-54)GGG>GAG	p.G18E
Pat_08	Post-Resistance	IGSF1	3547	37	X	130419321	130419321	Missense_Mutation	SNP	C	T	153	286	c.499G>A	c.(499-501)GGA>AGA	p.G167R
Pat_08	Post-Resistance	MAGEC1	9947	37	X	140994505	140994505	Missense_Mutation	SNP	C	T	137	307	c.1315C>T	c.(1315-1317)CCC>TCC	p.P439S
Pat_08	Post-Resistance	FMR1	2332	37	X	147026391	147026391	Missense_Mutation	SNP	A	G	36	50	c.1474A>G	c.(1474-1476)ACT>GCT	p.T492A
Pat_08	Post-Resistance	MAGEA4	4103	37	X	151092719	151092719	Nonsense_Mutation	SNP	C	T	130	242	c.583C>T	c.(583-585)CAG>TAG	p.Q195*
Pat_08	Post-Resistance	MAGEA3	4102	37	X	151935383	151935383	Missense_Mutation	SNP	G	A	192	397	c.784C>T	c.(784-786)CCC>TCC	p.P262S
Pat_08	Post-Resistance	PLXNA3	55558	37	X	153697535	153697535	Missense_Mutation	SNP	C	T	61	164	c.4571C>T	c.(4570-4572)CCC>CTC	p.P1524L
Pat_08	Post-Resistance	F8	2157	37	X	154132258	154132258	Missense_Mutation	SNP	G	A	171	306	c.5921C>T	c.(5920-5922)TCT>TTT	p.S1974F
Pat_08	Post-Resistance	TMLHE	55217	37	X	154736697	154736697	Missense_Mutation	SNP	G	A	229	280	c.857C>T	c.(856-858)CCT>CTT	p.P286L
Pat_11	Pre-Treatment	KLHL17	339451	37	1	900402	900402	Missense_Mutation	SNP	G	A	4	82	c.1760G>A	c.(1759-1761)GGT>GAT	p.G587D
Pat_11	Pre-Treatment	PRDM16	63976	37	1	3319415	3319415	Missense_Mutation	SNP	G	A	4	151	c.737G>A	c.(736-738)CGG>CAG	p.R246Q
Pat_11	Pre-Treatment	SPSB1	80176	37	1	9416131	9416131	Nonsense_Mutation	SNP	C	T	6	272	c.181C>T	c.(181-183)CGA>TGA	p.R61*
Pat_11	Pre-Treatment	PEX14	5195	37	1	10689972	10689972	Missense_Mutation	SNP	T	G	51	108	c.1062T>G	c.(1060-1062)GAT>GAG	p.D354E

Pat_11	Pre-Treatment	OTUD3	23252	37	1	20234196	20234196	Missense_Mutation	SNP	C	T	4	167	c.1154C>T	c.(1153-1155)ACG>ATG	p.T385M
Pat_11	Pre-Treatment	ECE1	1889	37	1	21548295	21548295	Missense_Mutation	SNP	G	A	6	601	c.2081C>T	c.(2080-2082)TCG>TTG	p.S694L
Pat_11	Pre-Treatment	HSPG2	3339	37	1	22174273	22174273	Missense_Mutation	SNP	T	G	30	36	c.7934A>C	c.(7933-7935)CAG>CCG	p.Q2645P
Pat_11	Pre-Treatment	CELA3B	23436	37	1	22313162	22313162	Missense_Mutation	SNP	G	A	4	109	c.781G>A	c.(781-783)GAC>AAC	p.D261N
Pat_11	Pre-Treatment	EPHA8	2046	37	1	22927440	22927441	Missense_Mutation	DNP	GC	AT	5	217	.2588_2589GC>A	c.(2587-2589)TGC>TAT	p.C863Y
Pat_11	Pre-Treatment	MAN1C1	57134	37	1	26075788	26075788	Missense_Mutation	SNP	G	A	4	82	c.796G>A	c.(796-798)GGG>AGG	p.G266R
Pat_11	Pre-Treatment	AHDC1	27245	37	1	27876631	27876631	Missense_Mutation	SNP	G	A	4	164	c.1996C>T	c.(1996-1998)CGG>TGG	p.R666W
Pat_11	Pre-Treatment	EIF3I	8668	37	1	32691835	32691835	Missense_Mutation	SNP	G	A	5	248	c.314G>A	c.(313-315)GGC>GAC	p.G105D
Pat_11	Pre-Treatment	LCK	3932	37	1	32740659	32740659	Missense_Mutation	SNP	G	A	35	159	c.253G>A	c.(253-255)GGG>AGG	p.G85R
Pat_11	Pre-Treatment	KIAA0319L	79932	37	1	35900511	35900511	Missense_Mutation	SNP	C	T	4	126	c.3134G>A	c.(3133-3135)CGG>CAG	p.R1045Q
Pat_11	Pre-Treatment	NFYC	4802	37	1	41218859	41218859	Nonsense_Mutation	SNP	C	T	16	70	c.328C>T	c.(328-330)CAG>TAG	p.Q110*
Pat_11	Pre-Treatment	HIVEP3	59269	37	1	42046388	42046388	Missense_Mutation	SNP	G	A	4	167	c.4081C>T	c.(4081-4083)CCC>TCC	p.P1361S
Pat_11	Pre-Treatment	PTPRF	5792	37	1	44075097	44075097	Missense_Mutation	SNP	G	A	4	123	c.3901G>A	c.(3901-3903)GGA>AGA	p.G1301R
Pat_11	Pre-Treatment	PRDX1	5052	37	1	45980605	45980605	Missense_Mutation	SNP	G	A	4	216	c.323C>T	c.(322-324)CCG>CTG	p.P108L
Pat_11	Pre-Treatment	PCSK9	255738	37	1	55509558	55509558	Missense_Mutation	SNP	G	A	50	108	c.250G>A	c.(250-252)GAG>AAG	p.E84K
Pat_11	Pre-Treatment	ROR1	4919	37	1	64515506	64515506	Missense_Mutation	SNP	C	T	4	234	c.307C>T	c.(307-309)CGG>TGG	p.R103W
Pat_11	Pre-Treatment	COL24A1	255631	37	1	86557972	86557972	Missense_Mutation	SNP	C	T	4	95	c.1631G>A	c.(1630-1632)GGT>GAT	p.G544D
Pat_11	Pre-Treatment	HFM1	164045	37	1	91781722	91781723	Missense_Mutation	DNP	GG	AA	6	28	.2917_2918CC>T	c.(2917-2919)CCC>TTC	p.P973F
Pat_11	Pre-Treatment	TGFBR3	7049	37	1	92195405	92195405	Missense_Mutation	SNP	C	T	5	353	c.694G>A	c.(694-696)GTA>ATA	p.V232I
Pat_11	Pre-Treatment	ALG14	199857	37	1	95448657	95448657	Missense_Mutation	SNP	G	A	4	230	c.626C>T	c.(625-627)TCG>TTG	p.S209L
Pat_11	Pre-Treatment	DPYD	1806	37	1	98058782	98058782	Missense_Mutation	SNP	G	A	35	107	c.1120C>T	c.(1120-1122)CCT>TCT	p.P374S
Pat_11	Pre-Treatment	AMIGO1	57463	37	1	110050820	110050820	Missense_Mutation	SNP	G	A	4	126	c.715C>T	c.(715-717)CGG>TGG	p.R239W
Pat_11	Pre-Treatment	EPS8L3	79574	37	1	110294814	110294814	Missense_Mutation	SNP	G	A	5	197	c.1237C>T	c.(1237-1239)CGG>TGG	p.R413W
Pat_11	Pre-Treatment	RBM15	64783	37	1	110884345	110884345	Missense_Mutation	SNP	G	A	5	257	c.2318G>A	c.(2317-2319)GGG>GAG	p.G773E
Pat_11	Pre-Treatment	ATP5F1	515	37	1	111996918	111996918	Missense_Mutation	SNP	C	T	52	125	c.163C>T	c.(163-165)CGT>TGT	p.R55C
Pat_11	Pre-Treatment	RAP1A	5906	37	1	112247011	112247011	Missense_Mutation	SNP	G	A	4	118	c.371G>A	c.(370-372)CGA>CAA	p.R124Q
Pat_11	Pre-Treatment	DCLRE1B	64858	37	1	114449702	114449702	Missense_Mutation	SNP	G	A	5	214	c.274G>A	c.(274-276)GTA>ATA	p.V92I
Pat_11	Pre-Treatment	SYCP1	6847	37	1	115455721	115455721	Missense_Mutation	SNP	G	A	42	87	c.1597G>A	c.(1597-1599)GAA>AAA	p.E533K
Pat_11	Pre-Treatment	C1orf161	126868	37	1	116666738	116666738	Missense_Mutation	SNP	G	A	4	177	c.241G>A	c.(241-243)GGG>AGG	p.G81R
Pat_11	Pre-Treatment	TTF2	8458	37	1	117635516	117635516	Missense_Mutation	SNP	G	A	5	159	c.2969G>A	c.(2968-2970)AGC>AAC	p.S990N
Pat_11	Pre-Treatment	SPAG17	200162	37	1	118598455	118598455	Missense_Mutation	SNP	C	T	8	20	c.2623G>A	c.(2623-2625)GAG>AAG	p.E875K
Pat_11	Pre-Treatment	HSD3B2	3284	37	1	119985517	119985517	Missense_Mutation	SNP	C	G	12	35	c.324C>G	c.(322-324)ATC>ATG	p.I108M
Pat_11	Pre-Treatment	NBPF10	100132406	37	1	145360580	145360580	Missense_Mutation	SNP	A	G	7	91	c.9430A>G	c.(9430-9432)AAA>GAA	p.K3144E
Pat_11	Pre-Treatment	HIST2H2BE	8349	37	1	149858090	149858090	Missense_Mutation	SNP	C	T	5	350	c.101G>A	c.(100-102)CGC>CAC	p.R34H
Pat_11	Pre-Treatment	RPTN	126638	37	1	152128479	152128479	Missense_Mutation	SNP	G	A	370	446	c.1096C>T	c.(1096-1098)CAC>TAC	p.H366Y
Pat_11	Pre-Treatment	NUP210L	91181	37	1	153991444	153991444	Missense_Mutation	SNP	G	A	39	131	c.4618C>T	c.(4618-4620)CAT>TAT	p.H1540Y
Pat_11	Pre-Treatment	ADAR	103	37	1	154562404	154562404	Missense_Mutation	SNP	G	A	4	151	c.2497C>T	c.(2497-2499)CTC>TTC	p.L833F
Pat_11	Pre-Treatment	FCRL2	79368	37	1	157740438	157740438	Missense_Mutation	SNP	G	A	4	55	c.71C>T	c.(70-72)GCG>GTG	p.A24V
Pat_11	Pre-Treatment	TNN	63923	37	1	175067731	175067731	Missense_Mutation	SNP	G	A	56	137	c.2119G>A	c.(2119-2121)GAC>AAC	p.D707N
Pat_11	Pre-Treatment	ASTN1	460	37	1	176983946	176983946	Missense_Mutation	SNP	C	T	215	435	c.1504G>A	c.(1504-1506)GAA>AAA	p.E502K
Pat_11	Pre-Treatment	IER5	51278	37	1	181058769	181058769	Missense_Mutation	SNP	G	A	4	59	c.731G>A	c.(730-732)CGG>CAG	p.R244Q
Pat_11	Pre-Treatment	KCNT2	343450	37	1	196197409	196197409	Missense_Mutation	SNP	C	T	4	110	c.3353G>A	c.(3352-3354)AGA>AAA	p.R1118K
Pat_11	Pre-Treatment	GPR37L1	9283	37	1	202097367	202097367	Missense_Mutation	SNP	G	A	6	419	c.1129G>A	c.(1129-1131)GTC>ATC	p.V377I
Pat_11	Pre-Treatment	PLXNA2	5362	37	1	208391105	208391105	Missense_Mutation	SNP	C	T	5	376	c.163G>A	c.(163-165)GTC>ATC	p.V55I
Pat_11	Pre-Treatment	NEK2	4751	37	1	211843711	211843711	Missense_Mutation	SNP	C	T	4	284	c.677G>A	c.(676-678)GGG>GAG	p.G226E
Pat_11	Pre-Treatment	JMJD4	65094	37	1	227921686	227921686	Missense_Mutation	SNP	G	A	41	103	c.614C>T	c.(613-615)TCC>TTC	p.S205F
Pat_11	Pre-Treatment	TRIM17	51127	37	1	228596305	228596305	Missense_Mutation	SNP	G	A	4	206	c.1031C>T	c.(1030-1032)ACG>ATG	p.T344M

Pat_11	Pre-Treatment	TRIM67	440730	37	1	231299608	231299608	Missense_Mutation	SNP	G	A	3	26	c.893G>A	c.(892-894)CGC>CAC	p.R298H
Pat_11	Pre-Treatment	LYST	1130	37	1	235872531	235872531	Missense_Mutation	SNP	G	A	4	89	c.10003C>T	c.(10003-10005)CGT>TGT	p.R3335C
Pat_11	Pre-Treatment	OR2M5	127059	37	1	248309108	248309108	Missense_Mutation	SNP	G	A	109	339	c.659G>A	c.(658-660)CGA>CAA	p.R220Q
Pat_11	Pre-Treatment	PFKP	5214	37	10	3162234	3162234	Missense_Mutation	SNP	G	A	4	155	c.1681G>A	c.(1681-1683)GAC>AAC	p.D561N
Pat_11	Pre-Treatment	FAM107B	83641	37	10	14572407	14572407	Missense_Mutation	SNP	G	T	4	97	c.52C>A	c.(52-54)CAG>AAG	p.Q18K
Pat_11	Pre-Treatment	CUBN	8029	37	10	16932424	16932424	Missense_Mutation	SNP	C	T	4	111	c.8701G>A	c.(8701-8703)GTC>ATC	p.V2901I
Pat_11	Pre-Treatment	PDSS1	23590	37	10	27035313	27035313	Missense_Mutation	SNP	G	A	4	114	c.1159G>A	c.(1159-1161)GCA>ACA	p.A387T
Pat_11	Pre-Treatment	ARHGAP12	94134	37	10	32150388	32150388	Missense_Mutation	SNP	G	A	4	80	c.883C>T	c.(883-885)CCT>TCT	p.P295S
Pat_11	Pre-Treatment	ALOX5	240	37	10	45938974	45938974	Missense_Mutation	SNP	G	A	3	39	c.1562G>A	c.(1561-1563)CGC>CAC	p.R521H
Pat_11	Pre-Treatment	SIRT1	23411	37	10	69651214	69651214	Missense_Mutation	SNP	C	T	4	131	c.844C>T	c.(844-846)CGC>TGC	p.R282C
Pat_11	Pre-Treatment	MYPN	84665	37	10	69970102	69970102	Missense_Mutation	SNP	G	A	4	153	c.3853G>A	c.(3853-3855)GGA>AGA	p.G1285R
Pat_11	Pre-Treatment	CDHR1	92211	37	10	85974039	85974039	Missense_Mutation	SNP	C	T	4	68	c.2242C>T	c.(2242-2244)CCC>TCC	p.P748S
Pat_11	Pre-Treatment	CDHR1	92211	37	10	85974293	85974293	Missense_Mutation	SNP	G	T	4	133	c.2496G>T	c.(2494-2496)ATG>ATT	p.M832I
Pat_11	Pre-Treatment	BMPR1A	657	37	10	88659648	88659648	Splice_Site	SNP	G	A	4	102	c.430_splice	c.e6+1	p.G144_splice
Pat_11	Pre-Treatment	PTEN	5728	37	10	89692902	89692902	Missense_Mutation	SNP	G	A	94	112	c.386G>A	c.(385-387)GGA>GAA	p.G129E
Pat_11	Pre-Treatment	BLNK	29760	37	10	97969643	97969643	Missense_Mutation	SNP	C	T	120	161	c.697G>A	c.(697-699)GAA>AAA	p.E233K
Pat_11	Pre-Treatment	TM9SF3	56889	37	10	98287230	98287230	Missense_Mutation	SNP	G	A	4	76	c.1565C>T	c.(1564-1566)GCT>GTT	p.A522V
Pat_11	Pre-Treatment	SLIT1	6585	37	10	98924646	98924647	Missense_Mutation	DNP	CC	TT	43	55	c.198_199GG>AA	196-201)CTGGAA>CTAA	p.E67K
Pat_11	Pre-Treatment	PPRC1	23082	37	10	103901161	103901161	Missense_Mutation	SNP	C	T	50	51	c.2896C>T	c.(2896-2898)CCT>TCT	p.P966S
Pat_11	Pre-Treatment	SUFU	51684	37	10	104375134	104375134	Missense_Mutation	SNP	G	A	8	215	c.1132G>A	c.(1132-1134)GGA>AGA	p.G378R
Pat_11	Pre-Treatment	ABLIM1	3983	37	10	116213233	116213233	Missense_Mutation	SNP	G	A	5	79	c.1451C>T	c.(1450-1452)CCG>CTG	p.P484L
Pat_11	Pre-Treatment	ATRNL1	26033	37	10	117226706	117226706	Missense_Mutation	SNP	C	T	9	20	c.3440C>T	c.(3439-3441)TCA>TTA	p.S1147L
Pat_11	Pre-Treatment	DMBT1	1755	37	10	124348552	124348552	Missense_Mutation	SNP	G	A	6	582	c.1876G>A	c.(1876-1878)GTG>ATG	p.V626M
Pat_11	Pre-Treatment	UTF1	8433	37	10	135044752	135044752	Missense_Mutation	SNP	G	A	3	14	c.832G>A	c.(832-834)GCC>ACC	p.A278T
Pat_11	Pre-Treatment	PTDSS2	81490	37	11	487014	487014	Missense_Mutation	SNP	G	A	4	215	c.511G>A	c.(511-513)GGG>AGG	p.G171R
Pat_11	Pre-Treatment	OR52B4	143496	37	11	4388924	4388924	Missense_Mutation	SNP	C	A	13	34	c.602G>T	c.(601-603)GGG>GTG	p.G201V
Pat_11	Pre-Treatment	OR51M1	390059	37	11	5411079	5411079	Missense_Mutation	SNP	C	A	6	414	c.451C>A	c.(451-453)CAG>AAG	p.Q151K
Pat_11	Pre-Treatment	OR52N5	390075	37	11	5799538	5799538	Missense_Mutation	SNP	C	G	3	120	c.327G>C	c.(325-327)CAG>CAC	p.Q109H
Pat_11	Pre-Treatment	C11orf16	56673	37	11	8942909	8942909	Missense_Mutation	SNP	C	T	4	201	c.1358G>A	c.(1357-1359)CGG>CAG	p.R453Q
Pat_11	Pre-Treatment	TEAD1	7003	37	11	12951761	12951761	Missense_Mutation	SNP	G	A	4	241	c.1010G>A	c.(1009-1011)CGA>CAA	p.R337Q
Pat_11	Pre-Treatment	PDE3B	5140	37	11	14666034	14666034	Missense_Mutation	SNP	G	A	3	45	c.413G>A	c.(412-414)CGG>CAG	p.R138Q
Pat_11	Pre-Treatment	CCDC34	91057	37	11	27384420	27384420	Missense_Mutation	SNP	C	T	4	169	c.322G>A	c.(322-324)GCG>ACG	p.A108T
Pat_11	Pre-Treatment	PAMR1	25891	37	11	35456088	35456088	Missense_Mutation	SNP	C	T	4	298	c.1598G>A	c.(1597-1599)CGG>CAG	p.R533Q
Pat_11	Pre-Treatment	OR4C6	219432	37	11	55432767	55432767	Missense_Mutation	SNP	T	C	50	118	c.125T>C	c.(124-126)CTT>CCT	p.L42P
Pat_11	Pre-Treatment	SSRP1	6749	37	11	57100260	57100260	Missense_Mutation	SNP	G	A	4	107	c.607C>T	c.(607-609)CGG>TGG	p.R203W
Pat_11	Pre-Treatment	ZDHHC5	25921	37	11	57457663	57457663	Missense_Mutation	SNP	G	A	4	211	c.545G>A	c.(544-546)CGC>CAC	p.R182H
Pat_11	Pre-Treatment	MS4A5	64232	37	11	60201352	60201352	Missense_Mutation	SNP	C	A	5	210	c.454C>A	c.(454-456)CAA>AAA	p.Q152K
Pat_11	Pre-Treatment	DAGLA	747	37	11	61511654	61511654	Missense_Mutation	SNP	G	A	4	155	c.2822G>A	c.(2821-2823)AGC>AAC	p.S941N
Pat_11	Pre-Treatment	FERMT3	83706	37	11	63990542	63990542	Missense_Mutation	SNP	G	A	4	219	c.1705G>A	c.(1705-1707)GAG>AAG	p.E569K
Pat_11	Pre-Treatment	PYGM	5837	37	11	64514214	64514214	Missense_Mutation	SNP	G	A	4	186	c.2446C>T	c.(2446-2448)CGC>TGC	p.R816C
Pat_11	Pre-Treatment	SF1	7536	37	11	64535600	64535600	Missense_Mutation	SNP	G	A	4	184	c.1046C>T	c.(1045-1047)CCC>CTC	p.P349L
Pat_11	Pre-Treatment	CDC42BPG	55561	37	11	64599130	64599130	Missense_Mutation	SNP	C	T	3	42	c.3151G>A	c.(3151-3153)GAG>AAG	p.E1051K
Pat_11	Pre-Treatment	CAPN1	823	37	11	64974021	64974021	Nonsense_Mutation	SNP	C	T	6	339	c.1441C>T	c.(1441-1443)CGA>TGA	p.R481*
Pat_11	Pre-Treatment	BBS1	582	37	11	66294257	66294257	Nonsense_Mutation	SNP	C	T	6	365	c.1318C>T	c.(1318-1320)CGA>TGA	p.R440*
Pat_11	Pre-Treatment	SHANK2	22941	37	11	70332923	70332923	Missense_Mutation	SNP	C	T	29	146	c.3475G>A	c.(3475-3477)GGT>AGT	p.G1159S
Pat_11	Pre-Treatment	ME3	10873	37	11	86267649	86267649	Missense_Mutation	SNP	G	A	4	120	c.413C>T	c.(412-414)ACG>ATG	p.T138M
Pat_11	Pre-Treatment	CNTN5	53942	37	11	100141922	100141922	Missense_Mutation	SNP	G	T	4	62	c.2263G>T	c.(2263-2265)GGG>TGG	p.G755W

Pat_11	Pre-Treatment	MMP12	4321	37	11	102738092	102738092	Missense_Mutation	SNP	G	A	8	24	c.820C>T	c.(820-822)CCT>TCT	p.P274S
Pat_11	Pre-Treatment	MPZL3	196264	37	11	118107921	118107921	Missense_Mutation	SNP	G	A	5	241	c.295C>T	c.(295-297)CGG>TGG	p.R99W
Pat_11	Pre-Treatment	PVRL1	5818	37	11	119547812	119547812	Missense_Mutation	SNP	G	A	4	177	c.851C>T	c.(850-852)ACG>ATG	p.T284M
Pat_11	Pre-Treatment	ARHGEF12	23365	37	11	120298811	120298811	Missense_Mutation	SNP	G	A	7	438	c.440G>A	c.(439-441)CGC>CAC	p.R147H
Pat_11	Pre-Treatment	PATE2	399967	37	11	125647312	125647312	Missense_Mutation	SNP	G	A	28	77	c.307C>T	c.(307-309)CAT>TAT	p.H103Y
Pat_11	Pre-Treatment	NFRKB	4798	37	11	129739745	129739745	Missense_Mutation	SNP	G	A	28	39	c.3175C>T	c.(3175-3177)CGC>TGC	p.R1059C
Pat_11	Pre-Treatment	WNK1	65125	37	12	993904	993904	Missense_Mutation	SNP	C	T	4	187	c.3934C>T	c.(3934-3936)CGT>TGT	p.R1312C
Pat_11	Pre-Treatment	CACNA1C	775	37	12	2659138	2659138	Missense_Mutation	SNP	G	A	3	60	c.1420G>A	c.(1420-1422)GTC>ATC	p.V474I
Pat_11	Pre-Treatment	TEAD4	7004	37	12	3129886	3129886	Missense_Mutation	SNP	C	G	4	135	c.667C>G	c.(667-669)CTC>GTC	p.L223V
Pat_11	Pre-Treatment	KCNA6	3742	37	12	4919314	4919314	Missense_Mutation	SNP	G	A	5	283	c.107G>A	c.(106-108)GGC>GAC	p.G36D
Pat_11	Pre-Treatment	VWF	7450	37	12	6128346	6128346	Missense_Mutation	SNP	G	A	4	180	c.4238C>T	c.(4237-4239)CCG>CTG	p.P1413L
Pat_11	Pre-Treatment	A2M	2	37	12	9225445	9225445	Missense_Mutation	SNP	G	A	3	22	c.3779C>T	c.(3778-3780)GCT>GTT	p.A1260V
Pat_11	Pre-Treatment	GSG1	83445	37	12	13240841	13240841	Missense_Mutation	SNP	C	T	22	31	c.634G>A	c.(634-636)GGT>AGT	p.G212S
Pat_11	Pre-Treatment	PTPRO	5800	37	12	15673223	15673223	Missense_Mutation	SNP	G	A	4	232	c.1868G>A	c.(1867-1869)AGC>AAC	p.S623N
Pat_11	Pre-Treatment	ADAMTS20	80070	37	12	43826148	43826148	Missense_Mutation	SNP	C	T	37	70	c.3055G>A	c.(3055-3057)GAA>AAA	p.E1019K
Pat_11	Pre-Treatment	ADAMTS20	80070	37	12	43944932	43944932	Missense_Mutation	SNP	G	A	5	279	c.233C>T	c.(232-234)ACC>ATC	p.T78I
Pat_11	Pre-Treatment	ANO6	196527	37	12	45795629	45795629	Missense_Mutation	SNP	G	A	30	68	c.1438G>A	c.(1438-1440)GTG>ATG	p.V480M
Pat_11	Pre-Treatment	ARID2	196528	37	12	46231461	46231461	Missense_Mutation	SNP	C	A	4	179	c.1301C>A	c.(1300-1302)ACA>AAA	p.T434K
Pat_11	Pre-Treatment	CACNB3	784	37	12	49220596	49220596	Missense_Mutation	SNP	G	A	6	515	c.949G>A	c.(949-951)GTA>ATA	p.V317I
Pat_11	Pre-Treatment	MLL2	8085	37	12	49435269	49435269	Missense_Mutation	SNP	C	T	6	204	c.6284G>A	c.(6283-6285)CGT>CAT	p.R2095H
Pat_11	Pre-Treatment	LMBR1L	55716	37	12	49498254	49498254	Missense_Mutation	SNP	C	G	4	327	c.412G>C	c.(412-414)GAG>CAG	p.E138Q
Pat_11	Pre-Treatment	ITGB7	3695	37	12	53594156	53594156	Missense_Mutation	SNP	C	A	28	90	c.72G>T	c.(70-72)AAG>AAT	p.K24N
Pat_11	Pre-Treatment	RARG	5916	37	12	53607478	53607478	Missense_Mutation	SNP	G	A	4	197	c.820C>T	c.(820-822)CGT>TGT	p.R274C
Pat_11	Pre-Treatment	ESPL1	9700	37	12	53684141	53684141	Missense_Mutation	SNP	G	A	4	169	c.5252G>A	c.(5251-5253)CGT>CAT	p.R1751H
Pat_11	Pre-Treatment	NEUROD4	58158	37	12	55420311	55420311	Missense_Mutation	SNP	G	A	16	77	c.88G>A	c.(88-90)GAG>AAG	p.E30K
Pat_11	Pre-Treatment	OR9K2	441639	37	12	55524145	55524145	Missense_Mutation	SNP	C	T	42	107	c.593C>T	c.(592-594)GCT>GTT	p.A198V
Pat_11	Pre-Treatment	OR6C65	403282	37	12	55794361	55794361	Missense_Mutation	SNP	G	A	5	24	c.49G>A	c.(49-51)GAT>AAT	p.D17N
Pat_11	Pre-Treatment	MMP19	4327	37	12	56233343	56233343	Missense_Mutation	SNP	C	T	3	36	c.703G>A	c.(703-705)GAG>AAG	p.E235K
Pat_11	Pre-Treatment	RAB5B	5869	37	12	56380860	56380860	Missense_Mutation	SNP	G	A	4	166	c.116G>A	c.(115-117)CGT>CAT	p.R39H
Pat_11	Pre-Treatment	SLC39A5	283375	37	12	56630374	56630374	Missense_Mutation	SNP	G	A	5	210	c.1051G>A	c.(1051-1053)GCT>ACT	p.A351T
Pat_11	Pre-Treatment	PAN2	9924	37	12	56716911	56716911	Missense_Mutation	SNP	G	A	5	228	c.2440C>T	c.(2440-2442)CGC>TGC	p.R814C
Pat_11	Pre-Treatment	CAPS2	84698	37	12	75676125	75676126	Missense_Mutation	DNP	GG	AA	20	81	:.1574_1575CC>TT	c.(1573-1575)GCC>GTT	p.A525V
Pat_11	Pre-Treatment	USP44	84101	37	12	95922687	95922687	Missense_Mutation	SNP	C	T	26	41	c.1520G>A	c.(1519-1521)GGA>GAA	p.G507E
Pat_11	Pre-Treatment	STAB2	55576	37	12	104049352	104049352	Missense_Mutation	SNP	C	T	32	85	c.1727C>T	c.(1726-1728)TCT>TTT	p.S576F
Pat_11	Pre-Treatment	POLR3B	55703	37	12	106763422	106763422	Missense_Mutation	SNP	G	A	4	133	c.365G>A	c.(364-366)GGC>GAC	p.G122D
Pat_11	Pre-Treatment	BTBD11	121551	37	12	107937863	107937863	Missense_Mutation	SNP	G	A	19	70	c.1437G>A	c.(1435-1437)ATG>ATA	p.M479I
Pat_11	Pre-Treatment	BRAP	8315	37	12	112119534	112119534	Missense_Mutation	SNP	G	A	4	154	c.350C>T	c.(349-351)TCT>TTT	p.S117F
Pat_11	Pre-Treatment	SBNO1	55206	37	12	123810824	123810824	Nonsense_Mutation	SNP	G	A	5	376	c.1750C>T	c.(1750-1752)CGA>TGA	p.R584*
Pat_11	Pre-Treatment	SCARB1	949	37	12	125270907	125270907	Missense_Mutation	SNP	C	T	6	427	c.1397G>A	c.(1396-1398)AGC>AAC	p.S466N
Pat_11	Pre-Treatment	STARD13	90627	37	13	33692262	33692263	Missense_Mutation	DNP	CC	TT	15	60	.2220_2221GG>A	218-2223)CGGGAC>CGA	p.D741N
Pat_11	Pre-Treatment	TRPC4	7223	37	13	38211429	38211429	Missense_Mutation	SNP	G	A	16	55	c.2545C>T	c.(2545-2547)CAT>TAT	p.H849Y
Pat_11	Pre-Treatment	FREM2	341640	37	13	39338481	39338481	Nonsense_Mutation	SNP	G	A	20	62	c.5304G>A	c.(5302-5304)TGG>TGA	p.W1768*
Pat_11	Pre-Treatment	FNDC3A	22862	37	13	49781232	49781232	Missense_Mutation	SNP	G	A	4	196	c.3298G>A	c.(3298-3300)GAC>AAC	p.D1100N
Pat_11	Pre-Treatment	DACH1	1602	37	13	72440865	72440865	Missense_Mutation	SNP	G	A	4	92	c.43C>T	c.(43-45)CCC>TCC	p.P15S
Pat_11	Pre-Treatment	MYCBP2	23077	37	13	77754420	77754420	Missense_Mutation	SNP	G	A	4	295	c.4861C>T	c.(4861-4863)CGT>TGT	p.R1621C
Pat_11	Pre-Treatment	TGM1	7051	37	14	24724025	24724025	Missense_Mutation	SNP	G	A	4	106	c.1933C>T	c.(1933-1935)CGT>TGT	p.R645C
Pat_11	Pre-Treatment	ADCY4	196883	37	14	24799486	24799486	Missense_Mutation	SNP	G	A	4	188	c.946C>T	c.(946-948)CGG>TGG	p.R316W

Pat_11	Pre-Treatment	AKAP6	9472	37	14	33015522	33015522	Nonsense_Mutation	SNP	G	T	5	181	c.1663G>T	c.(1663-1665)GAG>TAG	p.E555*
Pat_11	Pre-Treatment	C14orf182	283551	37	14	50472409	50472409	Missense_Mutation	SNP	C	T	6	631	c.109G>A	c.(109-111)GAA>AAA	p.E37K
Pat_11	Pre-Treatment	SAV1	60485	37	14	51101951	51101951	Nonsense_Mutation	SNP	G	A	4	217	c.1102C>T	c.(1102-1104)CGA>TGA	p.R368*
Pat_11	Pre-Treatment	FERMT2	10979	37	14	53386014	53386014	Missense_Mutation	SNP	A	G	57	128	c.218T>C	c.(217-219)CTG>CCG	p.L73P
Pat_11	Pre-Treatment	ZFYVE1	53349	37	14	73464872	73464872	Missense_Mutation	SNP	G	A	4	136	c.635C>T	c.(634-636)CCG>CTG	p.P212L
Pat_11	Pre-Treatment	FOS	2353	37	14	75746817	75746817	Missense_Mutation	SNP	G	A	4	217	c.379G>A	c.(379-381)GGC>AGC	p.G127S
Pat_11	Pre-Treatment	STON2	85439	37	14	81737088	81737088	Missense_Mutation	SNP	C	T	6	345	c.2539G>A	c.(2539-2541)GTG>ATG	p.V847M
Pat_11	Pre-Treatment	SERPINA13	388007	37	14	95108015	95108015	Missense_Mutation	SNP	G	A	23	72	c.532G>A	c.(532-534)GAT>AAT	p.D178N
Pat_11	Pre-Treatment	TRAF3	7187	37	14	103369758	103369758	Missense_Mutation	SNP	G	A	5	171	c.1127G>A	c.(1126-1128)CGG>CAG	p.R376Q
Pat_11	Pre-Treatment	TNFAIP2	7127	37	14	103600073	103600073	Missense_Mutation	SNP	C	T	4	44	c.1756C>T	c.(1756-1758)CGC>TGC	p.R586C
Pat_11	Pre-Treatment	AHNAK2	113146	37	14	105416378	105416378	Missense_Mutation	SNP	G	A	7	574	c.5410C>T	c.(5410-5412)CGG>TGG	p.R1804W
Pat_11	Pre-Treatment	HERC2	8924	37	15	28361855	28361855	Missense_Mutation	SNP	G	A	6	490	c.13565C>T	c.(13564-13566)CCG>CTG	p.P4522L
Pat_11	Pre-Treatment	HERC2	8924	37	15	28446690	28446690	Missense_Mutation	SNP	G	A	4	141	c.7628C>T	c.(7627-7629)GCT>GTT	p.A2543V
Pat_11	Pre-Treatment	DISP2	85455	37	15	40659296	40659296	Missense_Mutation	SNP	G	A	6	189	c.983G>A	c.(982-984)CGG>CAG	p.R328Q
Pat_11	Pre-Treatment	JMJD7-PLA2G4B	8681	37	15	42140051	42140051	Missense_Mutation	SNP	C	T	14	43	c.2339C>T	c.(2338-2340)CCC>CTC	p.P780L
Pat_11	Pre-Treatment	PYGO1	26108	37	15	55839224	55839224	Missense_Mutation	SNP	G	A	5	153	c.257C>T	c.(256-258)TCG>TTG	p.S86L
Pat_11	Pre-Treatment	HERC1	8925	37	15	64045209	64045209	Missense_Mutation	SNP	C	T	5	189	c.1850G>A	c.(1849-1851)CGC>CAC	p.R617H
Pat_11	Pre-Treatment	DENND4A	10260	37	15	66021549	66021549	Missense_Mutation	SNP	G	A	4	24	c.1348C>T	c.(1348-1350)CCT>TCT	p.P450S
Pat_11	Pre-Treatment	LRRC49	54839	37	15	71305234	71305234	Missense_Mutation	SNP	C	T	46	88	c.1685C>T	c.(1684-1686)TCC>TTC	p.S562F
Pat_11	Pre-Treatment	ISLR	3671	37	15	74467617	74467617	Missense_Mutation	SNP	G	A	65	161	c.418G>A	c.(418-420)GAC>AAC	p.D140N
Pat_11	Pre-Treatment	ZFAND6	54469	37	15	80429857	80429857	Missense_Mutation	SNP	G	A	4	108	c.514G>A	c.(514-516)GTA>ATA	p.V172I
Pat_11	Pre-Treatment	SH3GL3	6457	37	15	84257417	84257417	Missense_Mutation	SNP	A	G	25	52	c.732A>G	c.(730-732)ATA>ATG	p.I244M
Pat_11	Pre-Treatment	ACAN	176	37	15	89382124	89382124	Nonsense_Mutation	SNP	C	T	113	302	c.301C>T	c.(301-303)CAG>TAG	p.Q101*
Pat_11	Pre-Treatment	RHCG	51458	37	15	90021162	90021162	Missense_Mutation	SNP	C	T	4	175	c.881G>A	c.(880-882)GGT>GAT	p.G294D
Pat_11	Pre-Treatment	ANPEP	290	37	15	90335729	90335729	Missense_Mutation	SNP	C	T	4	208	c.2314G>A	c.(2314-2316)GTC>ATC	p.V772I
Pat_11	Pre-Treatment	IDH2	3418	37	15	90628327	90628327	Missense_Mutation	SNP	G	A	4	186	c.1084C>T	c.(1084-1086)CGG>TGG	p.R362W
Pat_11	Pre-Treatment	CACNA1H	8912	37	16	1254407	1254407	Missense_Mutation	SNP	G	A	61	110	c.2400G>A	c.(2398-2400)ATG>ATA	p.M800I
Pat_11	Pre-Treatment	CACNA1H	8912	37	16	1270521	1270521	Missense_Mutation	SNP	C	T	15	86	c.6589C>T	c.(6589-6591)CCT>TCT	p.P2197S
Pat_11	Pre-Treatment	RPS2	6187	37	16	2012789	2012789	Missense_Mutation	SNP	C	T	5	13	c.497G>A	c.(496-498)CGC>CAC	p.R166H
Pat_11	Pre-Treatment	TBL3	10607	37	16	2024990	2024990	Missense_Mutation	SNP	G	A	5	288	c.526G>A	c.(526-528)GCC>ACC	p.A176T
Pat_11	Pre-Treatment	PKD1	5310	37	16	2153369	2153369	Missense_Mutation	SNP	C	T	7	542	c.8689G>A	c.(8689-8691)GTT>ATT	p.V2897I
Pat_11	Pre-Treatment	PKD1	5310	37	16	2153595	2153595	Missense_Mutation	SNP	G	T	49	130	c.8463C>A	c.(8461-8463)GAC>GAA	p.D2821E
Pat_11	Pre-Treatment	E4F1	1877	37	16	2283065	2283065	Missense_Mutation	SNP	G	A	4	186	c.937G>A	c.(937-939)GAG>AAG	p.E313K
Pat_11	Pre-Treatment	PRSS22	64063	37	16	2903258	2903258	Missense_Mutation	SNP	C	T	4	129	c.790G>A	c.(790-792)GAG>AAG	p.E264K
Pat_11	Pre-Treatment	TRAP1	10131	37	16	3713518	3713518	Missense_Mutation	SNP	G	A	4	208	c.1615C>T	c.(1615-1617)CTT>TTT	p.L539F
Pat_11	Pre-Treatment	CORO7	79585	37	16	4408068	4408068	Missense_Mutation	SNP	C	T	44	106	c.2494G>A	c.(2494-2496)GCT>ACT	p.A832T
Pat_11	Pre-Treatment	SEC14L5	9717	37	16	5041869	5041869	Nonsense_Mutation	SNP	G	T	4	45	c.505G>T	c.(505-507)GAG>TAG	p.E169*
Pat_11	Pre-Treatment	ABAT	18	37	16	8839938	8839938	Missense_Mutation	SNP	C	T	29	48	c.151C>T	c.(151-153)CCA>TCA	p.P51S
Pat_11	Pre-Treatment	CPPED1	55313	37	16	12798586	12798586	Nonsense_Mutation	SNP	G	A	4	205	c.610C>T	c.(610-612)CAG>TAG	p.Q204*
Pat_11	Pre-Treatment	SMG1	23049	37	16	18849753	18849753	Nonsense_Mutation	SNP	G	A	4	126	c.7120C>T	c.(7120-7122)CGA>TGA	p.R2374*
Pat_11	Pre-Treatment	UMOD	7369	37	16	20360480	20360480	Missense_Mutation	SNP	G	A	4	153	c.143C>T	c.(142-144)ACG>ATG	p.T48M
Pat_11	Pre-Treatment	CRYM	1428	37	16	21281121	21281121	Missense_Mutation	SNP	G	A	77	187	c.479C>T	c.(478-480)TCC>TTC	p.S160F
Pat_11	Pre-Treatment	SCNN1B	6338	37	16	23387165	23387165	Missense_Mutation	SNP	T	C	4	167	c.1259T>C	c.(1258-1260)TTC>TCC	p.F420S
Pat_11	Pre-Treatment	TNRC6A	27327	37	16	24802545	24802545	Missense_Mutation	SNP	C	T	30	78	c.2582C>T	c.(2581-2583)TCA>TTA	p.S861L
Pat_11	Pre-Treatment	HS3ST4	9951	37	16	26147376	26147376	Missense_Mutation	SNP	G	A	11	15	c.1178G>A	c.(1177-1179)GGG>GAG	p.G393E
Pat_11	Pre-Treatment	SPNS1	83985	37	16	28995158	28995158	Missense_Mutation	SNP	C	T	5	313	c.1372C>T	c.(1372-1374)CGG>TGG	p.R458W
Pat_11	Pre-Treatment	ARMC5	79798	37	16	31473898	31473898	Missense_Mutation	SNP	T	C	4	149	c.1030T>C	c.(1030-1032)TCC>CCC	p.S344P

Pat_11	Pre-Treatment	SLC5A2	6524	37	16	31494546	31494546	Missense_Mutation	SNP	C	T	5	224	c.89C>T	c.(88-90)GCT>GTT	p.A30V
Pat_11	Pre-Treatment	C16orf78	123970	37	16	49430391	49430391	Missense_Mutation	SNP	G	A	4	174	c.452G>A	c.(451-453)CGT>CAT	p.R151H
Pat_11	Pre-Treatment	RBL2	5934	37	16	53493466	53493466	Missense_Mutation	SNP	G	A	4	193	c.1283G>A	c.(1282-1284)CGT>CAT	p.R428H
Pat_11	Pre-Treatment	RSPRY1	89970	37	16	57238904	57238904	Missense_Mutation	SNP	C	T	3	36	c.334C>T	c.(334-336)CGG>TGG	p.R112W
Pat_11	Pre-Treatment	PARD6A	50855	37	16	67695840	67695840	Nonsense_Mutation	SNP	C	T	5	321	c.331C>T	c.(331-333)CAG>TAG	p.Q111*
Pat_11	Pre-Treatment	RANBP10	57610	37	16	67762380	67762380	Missense_Mutation	SNP	G	A	4	253	c.1387C>T	c.(1387-1389)CCC>TCC	p.P463S
Pat_11	Pre-Treatment	TSNAXIP1	55815	37	16	67854842	67854842	Missense_Mutation	SNP	G	A	5	368	c.86G>A	c.(85-87)CGG>CAG	p.R29Q
Pat_11	Pre-Treatment	ZFP90	146198	37	16	68598329	68598329	Missense_Mutation	SNP	C	T	43	51	c.1639C>T	c.(1639-1641)CAC>TAC	p.H547Y
Pat_11	Pre-Treatment	TERF2	7014	37	16	69390830	69390830	Missense_Mutation	SNP	G	A	4	262	c.1474C>T	c.(1474-1476)CGG>TGG	p.R492W
Pat_11	Pre-Treatment	FUK	197258	37	16	70503208	70503208	Missense_Mutation	SNP	G	A	6	291	c.937G>A	c.(937-939)GAT>AAT	p.D313N
Pat_11	Pre-Treatment	FUK	197258	37	16	70513230	70513230	Missense_Mutation	SNP	G	A	4	95	c.3077G>A	c.(3076-3078)GGT>GAT	p.G1026D
Pat_11	Pre-Treatment	NUDT7	283927	37	16	77769734	77769734	Missense_Mutation	SNP	G	A	96	277	c.199G>A	c.(199-201)GCC>ACC	p.A67T
Pat_11	Pre-Treatment	KIAA1609	57707	37	16	84520585	84520585	Missense_Mutation	SNP	G	A	4	197	c.610C>T	c.(610-612)CCC>TCC	p.P204S
Pat_11	Pre-Treatment	KLHL36	79786	37	16	84693409	84693409	Missense_Mutation	SNP	C	T	84	101	c.1181C>T	c.(1180-1182)TCC>TTC	p.S394F
Pat_11	Pre-Treatment	ANKFY1	51479	37	17	4080447	4080447	Missense_Mutation	SNP	C	T	74	156	c.2749G>A	c.(2749-2751)GGC>AGC	p.G917S
Pat_11	Pre-Treatment	ARRB2	409	37	17	4621942	4621942	Missense_Mutation	SNP	G	A	6	587	c.742G>A	c.(742-744)GCC>ACC	p.A248T
Pat_11	Pre-Treatment	DNAH2	146754	37	17	7674673	7674673	Missense_Mutation	SNP	G	A	5	262	c.4388G>A	c.(4387-4389)CGC>CAC	p.R1463H
Pat_11	Pre-Treatment	PER1	5187	37	17	8050861	8050861	Missense_Mutation	SNP	G	A	4	87	c.1424C>T	c.(1423-1425)GCC>GTC	p.A475V
Pat_11	Pre-Treatment	MYOCD	93649	37	17	12666896	12666896	Missense_Mutation	SNP	G	A	58	91	c.2752G>A	c.(2752-2754)GAT>AAT	p.D918N
Pat_11	Pre-Treatment	ALDH3A2	224	37	17	19575219	19575219	Missense_Mutation	SNP	G	A	4	303	c.1393G>A	c.(1393-1395)GGT>AGT	p.G465S
Pat_11	Pre-Treatment	SLC47A2	146802	37	17	19609972	19609972	Missense_Mutation	SNP	C	T	4	180	c.938G>A	c.(937-939)AGC>AAC	p.S313N
Pat_11	Pre-Treatment	CORO6	84940	37	17	27948318	27948318	Missense_Mutation	SNP	G	A	4	193	c.122C>T	c.(121-123)GCC>GTC	p.A41V
Pat_11	Pre-Treatment	RHBDL3	162494	37	17	30648000	30648000	Missense_Mutation	SNP	G	A	4	205	c.967G>A	c.(967-969)GTG>ATG	p.V323M
Pat_11	Pre-Treatment	NLE1	54475	37	17	33460253	33460253	Missense_Mutation	SNP	G	A	5	237	c.1382C>T	c.(1381-1383)GCT>GTT	p.A461V
Pat_11	Pre-Treatment	KRTAP4-8	728224	37	17	39253949	39253949	Missense_Mutation	SNP	T	A	3	23	c.388A>T	c.(388-390)AGC>TGC	p.S130C
Pat_11	Pre-Treatment	DHX8	1659	37	17	41598212	41598212	Missense_Mutation	SNP	A	T	4	168	c.3031A>T	c.(3031-3033)ATG>TTG	p.M1011L
Pat_11	Pre-Treatment	HDAC5	10014	37	17	42157535	42157535	Missense_Mutation	SNP	C	T	4	219	c.2884G>A	c.(2884-2886)GGG>AGG	p.G962R
Pat_11	Pre-Treatment	GFAP	2670	37	17	42989041	42989041	Missense_Mutation	SNP	G	A	4	157	c.905C>T	c.(904-906)ACG>ATG	p.T302M
Pat_11	Pre-Treatment	TTLL6	284076	37	17	46863599	46863599	Missense_Mutation	SNP	C	T	205	519	c.1688G>A	c.(1687-1689)AGA>AAA	p.R563K
Pat_11	Pre-Treatment	LPO	4025	37	17	56320353	56320353	Missense_Mutation	SNP	C	T	6	343	c.13C>T	c.(13-15)CTC>TTC	p.L5F
Pat_11	Pre-Treatment	LPO	4025	37	17	56329765	56329765	Missense_Mutation	SNP	G	A	31	55	c.1003G>A	c.(1003-1005)GAG>AAG	p.E335K
Pat_11	Pre-Treatment	RNF43	54894	37	17	56435851	56435851	Missense_Mutation	SNP	G	A	4	157	c.1286C>T	c.(1285-1287)GCT>GTT	p.A429V
Pat_11	Pre-Treatment	4-Sep	5414	37	17	56602494	56602494	Missense_Mutation	SNP	G	A	5	300	c.607C>T	c.(607-609)CGG>TGG	p.R203W
Pat_11	Pre-Treatment	USP32	84669	37	17	58303400	58303400	Missense_Mutation	SNP	C	T	4	185	c.1432G>A	c.(1432-1434)GGC>AGC	p.G478S
Pat_11	Pre-Treatment	CYB561	1534	37	17	61513430	61513430	Missense_Mutation	SNP	C	T	5	289	c.286G>A	c.(286-288)GTC>ATC	p.V96I
Pat_11	Pre-Treatment	GPR142	350383	37	17	72368438	72368438	Missense_Mutation	SNP	C	T	51	138	c.1088C>T	c.(1087-1089)ACC>ATC	p.T363I
Pat_11	Pre-Treatment	CASKIN2	57513	37	17	73498070	73498070	Missense_Mutation	SNP	C	T	4	177	c.3085G>A	c.(3085-3087)GAG>AAG	p.E1029K
Pat_11	Pre-Treatment	DNAH17	8632	37	17	76423087	76423087	Missense_Mutation	SNP	C	T	4	34	c.3691G>A	c.(3691-3693)GCC>ACC	p.A1231T
Pat_11	Pre-Treatment	EIF4A3	9775	37	17	78115177	78115177	Missense_Mutation	SNP	G	A	4	137	c.313C>T	c.(313-315)CGT>TGT	p.R105C
Pat_11	Pre-Treatment	AZI1	22994	37	17	79164742	79164742	Missense_Mutation	SNP	G	A	5	165	c.2917C>T	c.(2917-2919)CGG>TGG	p.R973W
Pat_11	Pre-Treatment	DCXR	51181	37	17	79994441	79994441	Missense_Mutation	SNP	C	T	5	259	c.427G>A	c.(427-429)GTA>ATA	p.V143I
Pat_11	Pre-Treatment	PTPRM	5797	37	18	8394603	8394603	Missense_Mutation	SNP	C	A	22	177	c.4299C>A	c.(4297-4299)GAC>GAA	p.D1433E
Pat_11	Pre-Treatment	PPP4R1	9989	37	18	9583194	9583194	Missense_Mutation	SNP	G	A	28	48	c.839C>T	c.(838-840)TCA>TTA	p.S280L
Pat_11	Pre-Treatment	CEP192	55125	37	18	13099507	13099507	Missense_Mutation	SNP	C	T	51	127	c.6590C>T	c.(6589-6591)TCC>TTC	p.S2197F
Pat_11	Pre-Treatment	ESCO1	114799	37	18	19154035	19154035	Missense_Mutation	SNP	G	A	6	489	c.770C>T	c.(769-771)CCG>CTG	p.P257L
Pat_11	Pre-Treatment	FHOD3	80206	37	18	34298520	34298520	Missense_Mutation	SNP	C	T	4	146	c.2683C>T	c.(2683-2685)CGT>TGT	p.R895C
Pat_11	Pre-Treatment	KIAA0427	9811	37	18	46284699	46284699	Missense_Mutation	SNP	G	A	7	701	c.994G>A	c.(994-996)GAG>AAG	p.E332K

Pat_11	Pre-Treatment	ST8SIA3	51046	37	18	55027323	55027323	Missense_Mutation	SNP	G	A	19	64	c.958G>A	c.(958-960)GGA>AGA	p.G320R
Pat_11	Pre-Treatment	SERPINB2	5055	37	18	61569770	61569770	Missense_Mutation	SNP	G	A	57	138	c.811G>A	c.(811-813)GAA>AAA	p.E271K
Pat_11	Pre-Treatment	CDH7	1005	37	18	63477055	63477055	Missense_Mutation	SNP	G	A	19	51	c.326G>A	c.(325-327)AGA>AAA	p.R109K
Pat_11	Pre-Treatment	RTTN	25914	37	18	67795690	67795690	Missense_Mutation	SNP	G	A	4	126	c.3047C>T	c.(3046-3048)CCG>CTG	p.P1016L
Pat_11	Pre-Treatment	TCF3	6929	37	19	1632048	1632048	Missense_Mutation	SNP	G	A	4	90	c.287C>T	c.(286-288)CCG>CTG	p.P96L
Pat_11	Pre-Treatment	C19orf36	113177	37	19	2097949	2097949	Missense_Mutation	SNP	G	A	4	121	c.392G>A	c.(391-393)CGC>CAC	p.R131H
Pat_11	Pre-Treatment	CLEC4G	339390	37	19	7794294	7794294	Missense_Mutation	SNP	G	T	5	141	c.840C>A	c.(838-840)AGC>AGA	p.S280R
Pat_11	Pre-Treatment	LASS4	79603	37	19	8322862	8322862	Missense_Mutation	SNP	C	T	57	178	c.841C>T	c.(841-843)CCC>TCC	p.P281S
Pat_11	Pre-Treatment	MUC16	94025	37	19	9045986	9045986	Missense_Mutation	SNP	G	A	114	217	c.35645C>T	c.(35644-35646)TCT>TTT	p.S11882F
Pat_11	Pre-Treatment	MUC16	94025	37	19	9065407	9065407	Missense_Mutation	SNP	T	G	3	70	c.22039A>C	c.(22039-22041)ACC>CCC	p.T7347P
Pat_11	Pre-Treatment	MUC16	94025	37	19	9066660	9066660	Missense_Mutation	SNP	G	A	133	246	c.20786C>T	c.(20785-20787)TCC>TTC	p.S6929F
Pat_11	Pre-Treatment	MUC16	94025	37	19	9082547	9082547	Missense_Mutation	SNP	C	T	107	216	c.9268G>A	c.(9268-9270)GAG>AAG	p.E3090K
Pat_11	Pre-Treatment	MUC16	94025	37	19	9084835	9084835	Missense_Mutation	SNP	G	A	23	50	c.6980C>T	c.(6979-6981)TCC>TTC	p.S2327F
Pat_11	Pre-Treatment	TYK2	7297	37	19	10465279	10465279	Missense_Mutation	SNP	G	A	4	164	c.2624C>T	c.(2623-2625)GCT>GTT	p.A875V
Pat_11	Pre-Treatment	ZNF700	90592	37	19	12060647	12060647	Missense_Mutation	SNP	G	C	7	199	c.1808G>C	c.(1807-1809)TGT>TCT	p.C603S
Pat_11	Pre-Treatment	SYCE2	256126	37	19	13029115	13029115	Missense_Mutation	SNP	G	A	4	219	c.52C>T	c.(52-54)CCG>TCG	p.P18S
Pat_11	Pre-Treatment	CACNA1A	773	37	19	13563820	13563820	Missense_Mutation	SNP	C	T	31	90	c.409G>A	c.(409-411)GAA>AAA	p.E137K
Pat_11	Pre-Treatment	ZSWIM4	65249	37	19	13939511	13939511	Missense_Mutation	SNP	G	A	6	422	c.2081G>A	c.(2080-2082)CGC>CAC	p.R694H
Pat_11	Pre-Treatment	CASP14	23581	37	19	15164421	15164421	Missense_Mutation	SNP	G	A	37	101	c.156G>A	c.(154-156)ATG>ATA	p.M52I
Pat_11	Pre-Treatment	OR1I1	126370	37	19	15197997	15197997	Nonsense_Mutation	SNP	G	T	4	82	c.121G>T	c.(121-123)GGA>TGA	p.G41*
Pat_11	Pre-Treatment	SLC35E1	79939	37	19	16666010	16666010	Missense_Mutation	SNP	C	T	6	231	c.955G>A	c.(955-957)GTC>ATC	p.V319I
Pat_11	Pre-Treatment	NWD1	284434	37	19	16860349	16860349	Missense_Mutation	SNP	G	A	4	129	c.896G>A	c.(895-897)CGC>CAC	p.R299H
Pat_11	Pre-Treatment	NR2F6	2063	37	19	17351518	17351518	Missense_Mutation	SNP	C	T	7	526	c.335G>A	c.(334-336)CGT>CAT	p.R112H
Pat_11	Pre-Treatment	NCAN	1463	37	19	19338690	19338690	Missense_Mutation	SNP	C	T	73	182	c.2261C>T	c.(2260-2262)CCG>CTG	p.P754L
Pat_11	Pre-Treatment	ZNF93	81931	37	19	20045355	20045355	Missense_Mutation	SNP	C	T	6	21	c.1591C>T	c.(1591-1593)CAT>TAT	p.H531Y
Pat_11	Pre-Treatment	ZNF737	100129842	37	19	20728254	20728254	Missense_Mutation	SNP	C	G	8	24	c.755G>C	c.(754-756)AGT>ACT	p.S252T
Pat_11	Pre-Treatment	ZNF708	7562	37	19	21476519	21476519	Missense_Mutation	SNP	T	C	3	36	c.1249A>G	c.(1249-1251)AAG>GAG	p.K417E
Pat_11	Pre-Treatment	ZNF208	7757	37	19	22156875	22156875	Missense_Mutation	SNP	C	T	33	68	c.961G>A	c.(961-963)GCC>ACC	p.A321T
Pat_11	Pre-Treatment	ZNF492	57615	37	19	22847625	22847625	Missense_Mutation	SNP	G	T	6	32	c.1154G>T	c.(1153-1155)AGA>ATA	p.R385I
Pat_11	Pre-Treatment	ZNF507	22847	37	19	32845727	32845727	Missense_Mutation	SNP	G	A	6	168	c.1991G>A	c.(1990-1992)CGA>CAA	p.R664Q
Pat_11	Pre-Treatment	KCTD15	79047	37	19	34302452	34302452	Missense_Mutation	SNP	G	A	4	108	c.688G>A	c.(688-690)GTA>ATA	p.V230I
Pat_11	Pre-Treatment	ZNF420	147923	37	19	37619781	37619781	Missense_Mutation	SNP	C	T	8	33	c.1888C>T	c.(1888-1890)CTT>TTT	p.L630F
Pat_11	Pre-Treatment	SIPA1L3	23094	37	19	38631876	38631876	Missense_Mutation	SNP	G	A	53	137	c.3196G>A	c.(3196-3198)GAA>AAA	p.E1066K
Pat_11	Pre-Treatment	RYR1	6261	37	19	39008205	39008205	Missense_Mutation	SNP	G	A	46	70	c.9892G>A	c.(9892-9894)GCC>ACC	p.A3298T
Pat_11	Pre-Treatment	ZFP36	7538	37	19	39899302	39899302	Missense_Mutation	SNP	G	A	4	122	c.944G>A	c.(943-945)CGA>CAA	p.R315Q
Pat_11	Pre-Treatment	CYP2S1	29785	37	19	41704744	41704744	Missense_Mutation	SNP	C	T	4	168	c.785C>T	c.(784-786)TCG>TTG	p.S262L
Pat_11	Pre-Treatment	TMEM145	284339	37	19	42827873	42827873	Missense_Mutation	SNP	G	A	5	323	c.1333G>A	c.(1333-1335)GTG>ATG	p.V445M
Pat_11	Pre-Treatment	RTN2	6253	37	19	45997954	45997954	Missense_Mutation	SNP	G	A	4	194	c.389C>T	c.(388-390)GCG>GTG	p.A130V
Pat_11	Pre-Treatment	SYMPK	8189	37	19	46319222	46319222	Missense_Mutation	SNP	G	A	3	34	c.3574C>T	c.(3574-3576)CGG>TGG	p.R1192W
Pat_11	Pre-Treatment	CCDC9	26093	37	19	47767873	47767873	Missense_Mutation	SNP	G	T	3	31	c.476G>T	c.(475-477)CGG>CTG	p.R159L
Pat_11	Pre-Treatment	NLRP4	147945	37	19	56382227	56382227	Missense_Mutation	SNP	G	A	46	122	c.2389G>A	c.(2389-2391)GAA>AAA	p.E797K
Pat_11	Pre-Treatment	ASAP2	8853	37	2	9475268	9475268	Missense_Mutation	SNP	G	A	4	163	c.809G>A	c.(808-810)CGA>CAA	p.R270Q
Pat_11	Pre-Treatment	GREB1	9687	37	2	11777890	11777890	Missense_Mutation	SNP	C	T	77	197	c.5395C>T	c.(5395-5397)CCG>TCG	p.P1799S
Pat_11	Pre-Treatment	KCNS3	3790	37	2	18112978	18112978	Missense_Mutation	SNP	G	A	5	297	c.703G>A	c.(703-705)GGG>AGG	p.G235R
Pat_11	Pre-Treatment	PUM2	23369	37	2	20453619	20453619	Missense_Mutation	SNP	C	A	4	247	c.3027G>T	c.(3025-3027)ATG>ATT	p.M1009I
Pat_11	Pre-Treatment	HS1BP3	64342	37	2	20840820	20840820	Missense_Mutation	SNP	C	T	131	297	c.319G>A	c.(319-321)GAG>AAG	p.E107K
Pat_11	Pre-Treatment	APOB	338	37	2	21232284	21232284	Missense_Mutation	SNP	C	T	35	76	c.7456G>A	c.(7456-7458)GAC>AAC	p.D2486N

Pat_11	Pre-Treatment	POMC	5443	37	2	25384581	25384581	Missense_Mutation	SNP	G	A	3	33	c.173C>T	c.(172-174)ACT>ATT	p.T58I
Pat_11	Pre-Treatment	NRBP1	29959	37	2	27658073	27658073	Missense_Mutation	SNP	G	A	5	274	c.640G>A	c.(640-642)GGA>AGA	p.G214R
Pat_11	Pre-Treatment	CCDC121	79635	37	2	27850624	27850624	Missense_Mutation	SNP	G	A	5	316	c.43C>T	c.(43-45)CGG>TGG	p.R15W
Pat_11	Pre-Treatment	LBH	81606	37	2	30480434	30480434	Nonsense_Mutation	SNP	G	T	31	63	c.265G>T	c.(265-267)GAG>TAG	p.E89*
Pat_11	Pre-Treatment	NLRC4	58484	37	2	32477568	32477568	Missense_Mutation	SNP	T	C	4	174	c.182A>G	c.(181-183)AAG>AGG	p.K61R
Pat_11	Pre-Treatment	LTBP1	4052	37	2	33468797	33468797	Nonsense_Mutation	SNP	C	T	54	137	c.1945C>T	c.(1945-1947)CGA>TGA	p.R649*
Pat_11	Pre-Treatment	RASGRP3	25780	37	2	33745717	33745717	Missense_Mutation	SNP	G	A	44	146	c.334G>A	c.(334-336)GAA>AAA	p.E112K
Pat_11	Pre-Treatment	SFRS7	6432	37	2	38972328	38972328	Missense_Mutation	SNP	G	A	4	180	c.664C>T	c.(664-666)CGT>TGT	p.R222C
Pat_11	Pre-Treatment	DHX57	90957	37	2	39088696	39088696	Missense_Mutation	SNP	G	A	14	72	c.856C>T	c.(856-858)CGC>TGC	p.R286C
Pat_11	Pre-Treatment	RAB11FIP5	26056	37	2	73315325	73315325	Missense_Mutation	SNP	C	T	4	259	c.1421G>A	c.(1420-1422)CGG>CAG	p.R474Q
Pat_11	Pre-Treatment	REG3G	130120	37	2	79254993	79254993	Missense_Mutation	SNP	G	T	5	188	c.394G>T	c.(394-396)GCA>TCA	p.A132S
Pat_11	Pre-Treatment	STARD7	56910	37	2	96858130	96858130	Missense_Mutation	SNP	G	A	4	273	c.820C>T	c.(820-822)CGT>TGT	p.R274C
Pat_11	Pre-Treatment	SNRNP200	23020	37	2	96948966	96948966	Missense_Mutation	SNP	G	A	4	229	c.4888C>T	c.(4888-4890)CGC>TGC	p.R1630C
Pat_11	Pre-Treatment	SEMA4C	54910	37	2	97526382	97526382	Missense_Mutation	SNP	G	A	43	141	c.2483C>T	c.(2482-2484)CCC>CTC	p.P828L
Pat_11	Pre-Treatment	ZAP70	7535	37	2	98349771	98349771	Missense_Mutation	SNP	C	T	22	66	c.802C>T	c.(802-804)CCC>TCC	p.P268S
Pat_11	Pre-Treatment	CHST10	9486	37	2	101014417	101014417	Missense_Mutation	SNP	G	A	57	138	c.380C>T	c.(379-381)CCC>CTC	p.P127L
Pat_11	Pre-Treatment	CKAP2L	150468	37	2	113514118	113514118	Missense_Mutation	SNP	G	A	4	176	c.830C>T	c.(829-831)ACG>ATG	p.T277M
Pat_11	Pre-Treatment	SLC35F5	80255	37	2	114500394	114500394	Missense_Mutation	SNP	G	C	42	90	c.625C>G	c.(625-627)CAT>GAT	p.H209D
Pat_11	Pre-Treatment	GLI2	2736	37	2	121747302	121747302	Missense_Mutation	SNP	G	A	4	160	c.3812G>A	c.(3811-3813)AGC>AAC	p.S1271N
Pat_11	Pre-Treatment	KIF5C	3800	37	2	149853804	149853804	Missense_Mutation	SNP	G	A	32	66	c.2050G>A	c.(2050-2052)GAT>AAT	p.D684N
Pat_11	Pre-Treatment	NEB	4703	37	2	152388337	152388337	Missense_Mutation	SNP	C	T	4	53	c.16388G>A	c.(16387-16389)CGT>CAT	p.R5463H
Pat_11	Pre-Treatment	GALNT13	114805	37	2	155099313	155099313	Missense_Mutation	SNP	G	A	15	59	c.581G>A	c.(580-582)CGA>CAA	p.R194Q
Pat_11	Pre-Treatment	DPP4	1803	37	2	162890087	162890087	Missense_Mutation	SNP	G	A	44	116	c.851C>T	c.(850-852)TCC>TTC	p.S284F
Pat_11	Pre-Treatment	MYO3B	140469	37	2	171070963	171070963	Missense_Mutation	SNP	G	A	56	155	c.396G>A	c.(394-396)ATG>ATA	p.M132I
Pat_11	Pre-Treatment	TLK1	9874	37	2	171974268	171974268	Missense_Mutation	SNP	C	T	4	311	c.239G>A	c.(238-240)AGT>AAT	p.S80N
Pat_11	Pre-Treatment	HOXD12	3238	37	2	176964663	176964663	Missense_Mutation	SNP	C	T	16	47	c.134C>T	c.(133-135)CCG>CTG	p.P45L
Pat_11	Pre-Treatment	ANKRD44	91526	37	2	197990134	197990134	Missense_Mutation	SNP	C	T	4	185	c.521G>A	c.(520-522)CGG>CAG	p.R174Q
Pat_11	Pre-Treatment	PLCL1	5334	37	2	198949130	198949130	Missense_Mutation	SNP	C	T	4	227	c.889C>T	c.(889-891)CGC>TGC	p.R297C
Pat_11	Pre-Treatment	GPBAR1	151306	37	2	219127739	219127739	Missense_Mutation	SNP	T	C	3	112	c.292T>C	c.(292-294)TCC>CCC	p.S98P
Pat_11	Pre-Treatment	PLCD4	84812	37	2	219499237	219499237	Missense_Mutation	SNP	C	T	4	170	c.1780C>T	c.(1780-1782)CGC>TGC	p.R594C
Pat_11	Pre-Treatment	PTPRN	5798	37	2	220161969	220161970	Missense_Mutation	DNP	CC	TT	37	109	.2073_2074GG>A	071-2076)ACGGGA>ACA	p.G692R
Pat_11	Pre-Treatment	SLC4A3	6508	37	2	220502499	220502499	Missense_Mutation	SNP	G	A	4	202	c.2732G>A	c.(2731-2733)CGC>CAC	p.R911H
Pat_11	Pre-Treatment	SPHKAP	80309	37	2	228882842	228882842	Missense_Mutation	SNP	G	A	5	290	c.2728C>T	c.(2728-2730)CTT>TTT	p.L910F
Pat_11	Pre-Treatment	TRIP12	9320	37	2	230664071	230664071	Nonsense_Mutation	SNP	G	A	4	175	c.3010C>T	c.(3010-3012)CGA>TGA	p.R1004*
Pat_11	Pre-Treatment	C2orf57	165100	37	2	232457897	232457897	Nonsense_Mutation	SNP	C	T	64	155	c.235C>T	c.(235-237)CAG>TAG	p.Q79*
Pat_11	Pre-Treatment	FARP2	9855	37	2	242380731	242380731	Missense_Mutation	SNP	C	T	56	154	c.1171C>T	c.(1171-1173)CCC>TCC	p.P391S
Pat_11	Pre-Treatment	TGM3	7053	37	20	2308864	2308864	Missense_Mutation	SNP	G	A	4	266	c.1186G>A	c.(1186-1188)GAC>AAC	p.D396N
Pat_11	Pre-Treatment	TGM6	343641	37	20	2381057	2381057	Missense_Mutation	SNP	G	A	4	248	c.956G>A	c.(955-957)CGG>CAG	p.R319Q
Pat_11	Pre-Treatment	VSX1	30813	37	20	25056997	25056997	Missense_Mutation	SNP	C	T	4	108	c.998G>A	c.(997-999)CGG>CAG	p.R333Q
Pat_11	Pre-Treatment	NINL	22981	37	20	25434259	25434259	Missense_Mutation	SNP	G	A	57	126	c.3977C>T	c.(3976-3978)TCC>TTC	p.S1326F
Pat_11	Pre-Treatment	FRG1B	284802	37	20	29625905	29625905	Missense_Mutation	SNP	T	C	3	105	c.59T>C	c.(58-60)CTT>CCT	p.L20P
Pat_11	Pre-Treatment	FRG1B	284802	37	20	29628243	29628243	Missense_Mutation	SNP	T	C	10	291	c.155T>C	c.(154-156)TTG>TCG	p.L52S
Pat_11	Pre-Treatment	FRG1B	284802	37	20	29628245	29628245	Missense_Mutation	SNP	G	A	10	292	c.157G>A	c.(157-159)GCC>ACC	p.A53T
Pat_11	Pre-Treatment	DEFB123	245936	37	20	30028545	30028545	Missense_Mutation	SNP	C	T	134	312	c.44C>T	c.(43-45)TCC>TTC	p.S15F
Pat_11	Pre-Treatment	DNMT3B	1789	37	20	31386388	31386388	Missense_Mutation	SNP	G	A	4	95	c.1613G>A	c.(1612-1614)CGC>CAC	p.R538H
Pat_11	Pre-Treatment	EDEM2	55741	37	20	33722668	33722668	Missense_Mutation	SNP	G	A	4	177	c.575C>T	c.(574-576)ACG>ATG	p.T192M
Pat_11	Pre-Treatment	TOP1	7150	37	20	39741459	39741459	Missense_Mutation	SNP	G	A	4	115	c.1346G>A	c.(1345-1347)CGG>CAG	p.R449Q

Pat_11	Pre-Treatment	C20orf111	51526	37	20	42826062	42826062	Missense_Mutation	SNP	G	A	4	204	c.509C>T	c.(508-510)ACC>ATC	p.T170I
Pat_11	Pre-Treatment	PABPC1L	80336	37	20	43559150	43559150	Missense_Mutation	SNP	C	T	215	423	c.1022C>T	c.(1021-1023)TCC>TTC	p.S341F
Pat_11	Pre-Treatment	SPATA2	9825	37	20	48524979	48524979	Missense_Mutation	SNP	G	A	4	134	c.49C>T	c.(49-51)CGG>TGG	p.R17W
Pat_11	Pre-Treatment	ZFP64	55734	37	20	50769739	50769739	Missense_Mutation	SNP	C	T	5	218	c.992G>A	c.(991-993)CGG>CAG	p.R331Q
Pat_11	Pre-Treatment	ZBTB46	140685	37	20	62422079	62422079	Missense_Mutation	SNP	G	A	4	120	c.32C>T	c.(31-33)ACG>ATG	p.T11M
Pat_11	Pre-Treatment	LIPI	149998	37	21	15535788	15535788	Missense_Mutation	SNP	G	A	25	65	c.1021C>T	c.(1021-1023)CTT>TTT	p.L341F
Pat_11	Pre-Treatment	BACH1	571	37	21	30693752	30693752	Missense_Mutation	SNP	G	A	5	324	c.151G>A	c.(151-153)GTG>ATG	p.V51M
Pat_11	Pre-Treatment	GRIK1	2897	37	21	30953811	30953811	Missense_Mutation	SNP	C	T	4	190	c.1846G>A	c.(1846-1848)GTG>ATG	p.V616M
Pat_11	Pre-Treatment	PDE9A	5152	37	21	44181005	44181005	Missense_Mutation	SNP	G	A	4	124	c.1073G>A	c.(1072-1074)GGC>GAC	p.G358D
Pat_11	Pre-Treatment	CBS	875	37	21	44492171	44492171	Missense_Mutation	SNP	G	A	4	193	c.133C>T	c.(133-135)CGG>TGG	p.R45W
Pat_11	Pre-Treatment	C21orf56	84221	37	21	47588239	47588239	Missense_Mutation	SNP	C	T	4	104	c.527G>A	c.(526-528)AGG>AAG	p.R176K
Pat_11	Pre-Treatment	POTEH	23784	37	22	16287488	16287488	Missense_Mutation	SNP	C	T	7	350	c.398G>A	c.(397-399)AGC>AAC	p.S133N
Pat_11	Pre-Treatment	TSSK2	23617	37	22	19119966	19119966	Nonsense_Mutation	SNP	G	T	6	205	c.1054G>T	c.(1054-1056)GAG>TAG	p.E352*
Pat_11	Pre-Treatment	RTN4R	65078	37	22	20229989	20229989	Missense_Mutation	SNP	G	A	4	214	c.667C>T	c.(667-669)CGT>TGT	p.R223C
Pat_11	Pre-Treatment	SLC7A4	6545	37	22	21386095	21386095	Missense_Mutation	SNP	G	A	4	116	c.7C>T	c.(7-9)CGG>TGG	p.R3W
Pat_11	Pre-Treatment	NF2	4771	37	22	30074207	30074207	Missense_Mutation	SNP	C	T	4	230	c.1469C>T	c.(1468-1470)CCG>CTG	p.P490L
Pat_11	Pre-Treatment	OSBP2	23762	37	22	31285598	31285599	Missense_Mutation	DNP	GG	AA	61	179	.1598_1599GG>A	c.(1597-1599)CGG>CAA	p.R533Q
Pat_11	Pre-Treatment	PIK3IP1	113791	37	22	31686951	31686951	Missense_Mutation	SNP	C	T	19	46	c.307G>A	c.(307-309)GAG>AAG	p.E103K
Pat_11	Pre-Treatment	C22orf33	339669	37	22	37398027	37398027	Nonsense_Mutation	SNP	G	A	18	39	c.340C>T	c.(340-342)CAG>TAG	p.Q114*
Pat_11	Pre-Treatment	GGA1	26088	37	22	38028092	38028092	Missense_Mutation	SNP	G	A	4	157	c.1618G>A	c.(1618-1620)GTG>ATG	p.V540M
Pat_11	Pre-Treatment	GTPBP1	9567	37	22	39104928	39104928	Missense_Mutation	SNP	G	A	4	247	c.271G>A	c.(271-273)GGA>AGA	p.G91R
Pat_11	Pre-Treatment	CBX7	23492	37	22	39534694	39534694	Nonsense_Mutation	SNP	G	A	4	210	c.193C>T	c.(193-195)CGA>TGA	p.R65*
Pat_11	Pre-Treatment	TNRC6B	23112	37	22	40708530	40708530	Nonsense_Mutation	SNP	G	A	18	61	c.4457G>A	c.(4456-4458)TGG>TAG	p.W1486*
Pat_11	Pre-Treatment	MKL1	57591	37	22	40827438	40827438	Missense_Mutation	SNP	G	A	198	475	c.110C>T	c.(109-111)TCG>TTG	p.S37L
Pat_11	Pre-Treatment	POLDIP3	84271	37	22	42999126	42999126	Missense_Mutation	SNP	C	A	91	267	c.100G>T	c.(100-102)GTT>TTT	p.V34F
Pat_11	Pre-Treatment	SCUBE1	80274	37	22	43614435	43614435	Nonsense_Mutation	SNP	G	A	5	193	c.1717C>T	c.(1717-1719)CGA>TGA	p.R573*
Pat_11	Pre-Treatment	C22orf26	55267	37	22	46449739	46449739	Missense_Mutation	SNP	G	A	3	15	c.235C>T	c.(235-237)CTC>TTC	p.L79F
Pat_11	Pre-Treatment	TTLL8	164714	37	22	50469033	50469033	Missense_Mutation	SNP	G	A	3	42	c.2029C>T	c.(2029-2031)CTC>TTC	p.L677F
Pat_11	Pre-Treatment	IL5RA	3568	37	3	3146593	3146593	Missense_Mutation	SNP	C	T	20	84	c.76G>A	c.(76-78)GAA>AAA	p.E26K
Pat_11	Pre-Treatment	SETD5	55209	37	3	9476073	9476073	Missense_Mutation	SNP	G	A	4	92	c.233G>A	c.(232-234)TGT>TAT	p.C78Y
Pat_11	Pre-Treatment	ATP2B2	491	37	3	10391870	10391870	Missense_Mutation	SNP	C	T	66	135	c.2330G>A	c.(2329-2331)CGA>CAA	p.R777Q
Pat_11	Pre-Treatment	NUP210	23225	37	3	13364899	13364899	Missense_Mutation	SNP	G	A	4	226	c.4678C>T	c.(4678-4680)CGT>TGT	p.R1560C
Pat_11	Pre-Treatment	XPC	7508	37	3	14190138	14190138	Missense_Mutation	SNP	C	T	4	202	c.2344G>A	c.(2344-2346)GTG>ATG	p.V782M
Pat_11	Pre-Treatment	FGD5	152273	37	3	14949183	14949183	Missense_Mutation	SNP	G	A	4	204	c.3301G>A	c.(3301-3303)GTC>ATC	p.V1101I
Pat_11	Pre-Treatment	GADL1	339896	37	3	30880557	30880557	Missense_Mutation	SNP	C	T	59	116	c.835G>A	c.(835-837)GGA>AGA	p.G279R
Pat_11	Pre-Treatment	MYD88	4615	37	3	38181482	38181483	Missense_Mutation	DNP	CC	TT	13	28	c.495_496CC>TT	493-498)GACCCC>GATT	p.P166S
Pat_11	Pre-Treatment	TRAK1	22906	37	3	42242402	42242402	Missense_Mutation	SNP	C	T	180	350	c.1283C>T	c.(1282-1284)TCC>TTC	p.S428F
Pat_11	Pre-Treatment	CCDC13	152206	37	3	42794147	42794147	Missense_Mutation	SNP	G	A	5	150	c.433C>T	c.(433-435)CGG>TGG	p.R145W
Pat_11	Pre-Treatment	XCR1	2829	37	3	46063010	46063010	Missense_Mutation	SNP	G	A	3	29	c.430C>T	c.(430-432)CGC>TGC	p.R144C
Pat_11	Pre-Treatment	PTPN23	25930	37	3	47446526	47446526	Missense_Mutation	SNP	C	A	4	213	c.319C>A	c.(319-321)CAT>AAT	p.H107N
Pat_11	Pre-Treatment	CSPG5	10675	37	3	47610605	47610605	Missense_Mutation	SNP	G	A	14	23	c.1495C>T	c.(1495-1497)CCC>TCC	p.P499S
Pat_11	Pre-Treatment	BSN	8927	37	3	49695090	49695090	Missense_Mutation	SNP	G	A	4	209	c.8101G>A	c.(8101-8103)GTC>ATC	p.V2701I
Pat_11	Pre-Treatment	DNAH1	25981	37	3	52406387	52406387	Missense_Mutation	SNP	A	G	4	161	c.6811A>G	c.(6811-6813)AGC>GGC	p.S2271G
Pat_11	Pre-Treatment	DNAH1	25981	37	3	52417438	52417438	Missense_Mutation	SNP	G	A	4	91	c.7978G>A	c.(7978-7980)GTC>ATC	p.V2660I
Pat_11	Pre-Treatment	NEK4	6787	37	3	52745882	52745882	Missense_Mutation	SNP	G	A	4	142	c.2437C>T	c.(2437-2439)CGT>TGT	p.R813C
Pat_11	Pre-Treatment	PRKCD	5580	37	3	53213714	53213714	Missense_Mutation	SNP	G	T	3	22	c.237G>T	c.(235-237)GAG>GAT	p.E79D
Pat_11	Pre-Treatment	ROBO2	6092	37	3	77089988	77089988	Missense_Mutation	SNP	C	G	42	104	c.52C>G	c.(52-54)CGG>GGG	p.R18G

Pat_11	Pre-Treatment	C3orf38	285237	37	3	88205268	88205268	Missense_Mutation	SNP	C	T	20	48	c.473C>T	c.(472-474)CCT>CTT	p.P158L
Pat_11	Pre-Treatment	EPHA6	285220	37	3	96706810	96706810	Missense_Mutation	SNP	T	G	28	44	c.1087T>G	c.(1087-1089)TAT>GAT	p.Y363D
Pat_11	Pre-Treatment	MORC1	27136	37	3	108813812	108813812	Missense_Mutation	SNP	G	A	9	11	c.527C>T	c.(526-528)CCA>CTA	p.P176L
Pat_11	Pre-Treatment	BOC	91653	37	3	113002341	113002341	Missense_Mutation	SNP	C	T	5	189	c.2515C>T	c.(2515-2517)CGG>TGG	p.R839W
Pat_11	Pre-Treatment	ZBTB20	26137	37	3	114070639	114070639	Missense_Mutation	SNP	C	T	4	165	c.286G>A	c.(286-288)GAG>AAG	p.E96K
Pat_11	Pre-Treatment	C3orf1	51300	37	3	119222428	119222428	Missense_Mutation	SNP	G	A	4	68	c.410G>A	c.(409-411)CGC>CAC	p.R137H
Pat_11	Pre-Treatment	ESYT3	83850	37	3	138183346	138183346	Missense_Mutation	SNP	G	A	70	115	c.1075G>A	c.(1075-1077)GAA>AAA	p.E359K
Pat_11	Pre-Treatment	PLOD2	5352	37	3	145789204	145789204	Missense_Mutation	SNP	G	A	4	138	c.1792C>T	c.(1792-1794)CGT>TGT	p.R598C
Pat_11	Pre-Treatment	AGTR1	185	37	3	148458956	148458956	Missense_Mutation	SNP	G	A	27	76	c.134G>A	c.(133-135)GGA>GAA	p.G45E
Pat_11	Pre-Treatment	CP	1356	37	3	148919931	148919931	Nonsense_Mutation	SNP	G	A	4	96	c.1306C>T	c.(1306-1308)CGA>TGA	p.R436*
Pat_11	Pre-Treatment	CP	1356	37	3	148939500	148939500	Missense_Mutation	SNP	C	T	28	34	c.80G>A	c.(79-81)GGA>GAA	p.G27E
Pat_11	Pre-Treatment	ZBBX	79740	37	3	167000053	167000053	Missense_Mutation	SNP	C	T	5	19	c.2110G>A	c.(2110-2112)GAA>AAA	p.E704K
Pat_11	Pre-Treatment	PHC3	80012	37	3	169820640	169820640	Missense_Mutation	SNP	G	A	4	88	c.2515C>T	c.(2515-2517)CGT>TGT	p.R839C
Pat_11	Pre-Treatment	SLC2A2	6514	37	3	170723136	170723136	Nonsense_Mutation	SNP	G	A	5	210	c.901C>T	c.(901-903)CGA>TGA	p.R301*
Pat_11	Pre-Treatment	EIF2B5	8893	37	3	183861316	183861316	Missense_Mutation	SNP	C	T	4	196	c.1832C>T	c.(1831-1833)CCG>CTG	p.P611L
Pat_11	Pre-Treatment	ABCF3	55324	37	3	183906156	183906156	Missense_Mutation	SNP	G	A	5	488	c.797G>A	c.(796-798)CGG>CAG	p.R266Q
Pat_11	Pre-Treatment	TP63	8626	37	3	189455576	189455576	Missense_Mutation	SNP	G	A	4	106	c.110G>A	c.(109-111)CGA>CAA	p.R37Q
Pat_11	Pre-Treatment	ATP13A5	344905	37	3	193081090	193081090	Missense_Mutation	SNP	C	T	21	65	c.319G>A	c.(319-321)GAA>AAA	p.E107K
Pat_11	Pre-Treatment	LSG1	55341	37	3	194365433	194365433	Missense_Mutation	SNP	C	T	4	45	c.1666G>A	c.(1666-1668)GTA>ATA	p.V556I
Pat_11	Pre-Treatment	MUC4	4585	37	3	195509171	195509171	Missense_Mutation	SNP	G	A	4	5	c.8896C>T	c.(8896-8898)CTT>TTT	p.L2966F
Pat_11	Pre-Treatment	ZNF721	170960	37	4	435649	435649	Missense_Mutation	SNP	T	G	7	55	c.2607A>C	c.(2605-2607)GAA>GAC	p.E869D
Pat_11	Pre-Treatment	ZNF721	170960	37	4	436992	436992	Missense_Mutation	SNP	G	C	28	53	c.1264C>G	c.(1264-1266)CGT>GGT	p.R422G
Pat_11	Pre-Treatment	ZBTB49	166793	37	4	4314795	4314795	Missense_Mutation	SNP	C	T	4	175	c.1330C>T	c.(1330-1332)CGG>TGG	p.R444W
Pat_11	Pre-Treatment	CC2D2A	57545	37	4	15552594	15552594	Missense_Mutation	SNP	G	A	4	155	c.2329G>A	c.(2329-2331)GTT>ATT	p.V777I
Pat_11	Pre-Treatment	SLIT2	9353	37	4	20530703	20530703	Missense_Mutation	SNP	C	T	44	113	c.1594C>T	c.(1594-1596)CCC>TCC	p.P532S
Pat_11	Pre-Treatment	GPR125	166647	37	4	22425818	22425818	Missense_Mutation	SNP	G	A	11	27	c.1601C>T	c.(1600-1602)TCA>TTA	p.S534L
Pat_11	Pre-Treatment	NSUN7	79730	37	4	40810375	40810375	Missense_Mutation	SNP	G	A	62	156	c.1576G>A	c.(1576-1578)GCC>ACC	p.A526T
Pat_11	Pre-Treatment	NMU	10874	37	4	56496606	56496606	Missense_Mutation	SNP	C	T	42	77	c.134G>A	c.(133-135)GGA>GAA	p.G45E
Pat_11	Pre-Treatment	UGT2B15	7366	37	4	69513083	69513083	Missense_Mutation	SNP	C	T	22	65	c.1332G>A	c.(1330-1332)ATG>ATA	p.M444I
Pat_11	Pre-Treatment	UGT2B10	7365	37	4	69693137	69693137	Missense_Mutation	SNP	C	T	31	110	c.1178C>T	c.(1177-1179)CCA>CTA	p.P393L
Pat_11	Pre-Treatment	RUFY3	22902	37	4	71629283	71629283	Missense_Mutation	SNP	C	T	11	28	c.367C>T	c.(367-369)CTC>TTC	p.L123F
Pat_11	Pre-Treatment	ALB	213	37	4	74275124	74275124	Missense_Mutation	SNP	C	T	27	59	c.535C>T	c.(535-537)CTT>TTT	p.L179F
Pat_11	Pre-Treatment	CCDC158	339965	37	4	77278541	77278541	Missense_Mutation	SNP	C	T	14	26	c.2159G>A	c.(2158-2160)GGA>GAA	p.G720E
Pat_11	Pre-Treatment	BMP2K	55589	37	4	79832429	79832429	Missense_Mutation	SNP	C	A	4	57	c.2728C>A	c.(2728-2730)CAA>AAA	p.Q910K
Pat_11	Pre-Treatment	AGXT2L1	64850	37	4	109670491	109670491	Missense_Mutation	SNP	C	T	47	105	c.830G>A	c.(829-831)GGA>GAA	p.G277E
Pat_11	Pre-Treatment	EGF	1950	37	4	110890251	110890251	Missense_Mutation	SNP	G	A	5	241	c.1700G>A	c.(1699-1701)CGT>CAT	p.R567H
Pat_11	Pre-Treatment	NDST4	64579	37	4	115769417	115769417	Missense_Mutation	SNP	C	T	22	51	c.1894G>A	c.(1894-1896)GAA>AAA	p.E632K
Pat_11	Pre-Treatment	FAT4	79633	37	4	126241411	126241411	Missense_Mutation	SNP	C	T	46	110	c.3845C>T	c.(3844-3846)TCC>TTC	p.S1282F
Pat_11	Pre-Treatment	FAT4	79633	37	4	126367659	126367659	Missense_Mutation	SNP	C	T	55	135	c.7405C>T	c.(7405-7407)CAC>TAC	p.H2469Y
Pat_11	Pre-Treatment	FAT4	79633	37	4	126411926	126411926	Missense_Mutation	SNP	C	T	15	59	c.13949C>T	c.(13948-13950)TCA>TTA	p.S4650L
Pat_11	Pre-Treatment	PET112L	5188	37	4	152637172	152637172	Missense_Mutation	SNP	G	A	4	151	c.752C>T	c.(751-753)GCG>GTG	p.A251V
Pat_11	Pre-Treatment	FHDC1	85462	37	4	153896764	153896764	Missense_Mutation	SNP	C	T	5	274	c.2321C>T	c.(2320-2322)TCG>TTG	p.S774L
Pat_11	Pre-Treatment	CLCN3	1182	37	4	170610226	170610226	Missense_Mutation	SNP	G	A	4	275	c.451G>A	c.(451-453)GAT>AAT	p.D151N
Pat_11	Pre-Treatment	ODZ3	55714	37	4	183609435	183609435	Missense_Mutation	SNP	G	A	4	119	c.2152G>A	c.(2152-2154)GAG>AAG	p.E718K
Pat_11	Pre-Treatment	CYP4V2	285440	37	4	187115720	187115720	Missense_Mutation	SNP	T	C	66	203	c.281T>C	c.(280-282)GTC>GCC	p.V94A
Pat_11	Pre-Treatment	NSUN2	54888	37	5	6616948	6616948	Missense_Mutation	SNP	G	T	4	206	c.913C>A	c.(913-915)CGC>AGC	p.R305S
Pat_11	Pre-Treatment	FASTKD3	79072	37	5	7867769	7867769	Missense_Mutation	SNP	T	C	3	50	c.428A>G	c.(427-429)AAG>AGG	p.K143R

Pat_11	Pre-Treatment	PRDM9	56979	37	5	23527220	23527220	Missense_Mutation	SNP	T	C	6	41	c.2023T>C	c.(2023-2025)TGG>CGG	p.W675R
Pat_11	Pre-Treatment	PRDM9	56979	37	5	23527251	23527251	Missense_Mutation	SNP	C	G	6	45	c.2054C>G	c.(2053-2055)ACA>AGA	p.T685R
Pat_11	Pre-Treatment	SLC1A3	6507	37	5	36608694	36608694	Missense_Mutation	SNP	G	A	4	226	c.169G>A	c.(169-171)GCT>ACT	p.A57T
Pat_11	Pre-Treatment	PELO	53918	37	5	52097642	52097642	Missense_Mutation	SNP	C	A	4	66	c.1126C>A	c.(1126-1128)CAA>AAA	p.Q376K
Pat_11	Pre-Treatment	CMYA5	202333	37	5	79030152	79030152	Missense_Mutation	SNP	C	T	17	25	c.5564C>T	c.(5563-5565)TCA>TTA	p.S1855L
Pat_11	Pre-Treatment	RASGRF2	5924	37	5	80369205	80369205	Missense_Mutation	SNP	G	A	4	89	c.821G>A	c.(820-822)CGT>CAT	p.R274H
Pat_11	Pre-Treatment	KIF20A	10112	37	5	137517403	137517403	Missense_Mutation	SNP	T	C	3	111	c.361T>C	c.(361-363)TTC>CTC	p.F121L
Pat_11	Pre-Treatment	PCDHA4	56144	37	5	140188055	140188055	Missense_Mutation	SNP	G	A	194	169	c.1283G>A	c.(1282-1284)CGA>CAA	p.R428Q
Pat_11	Pre-Treatment	PCDHA13	56136	37	5	140264174	140264174	Missense_Mutation	SNP	C	T	32	30	c.2321C>T	c.(2320-2322)CCC>CTC	p.P774L
Pat_11	Pre-Treatment	ARHGAP26	23092	37	5	142513638	142513638	Missense_Mutation	SNP	C	T	4	215	c.1805C>T	c.(1804-1806)ACG>ATG	p.T602M
Pat_11	Pre-Treatment	TCOF1	6949	37	5	149749166	149749166	Splice_Site	SNP	G	A	4	104	c.639_splice	c.e6+1	p.E213_splice
Pat_11	Pre-Treatment	CCDC69	26112	37	5	150581166	150581166	Missense_Mutation	SNP	C	T	31	60	c.208G>A	c.(208-210)GAA>AAA	p.E70K
Pat_11	Pre-Treatment	NIPAL4	348938	37	5	156899891	156899891	Missense_Mutation	SNP	G	A	4	78	c.1324G>A	c.(1324-1326)GTC>ATC	p.V442I
Pat_11	Pre-Treatment	DOCK2	1794	37	5	169506124	169506124	Missense_Mutation	SNP	G	A	3	31	c.5140G>A	c.(5140-5142)GCA>ACA	p.A1714T
Pat_11	Pre-Treatment	RIPK1	8737	37	6	3106280	3106280	Missense_Mutation	SNP	C	A	4	144	c.1571C>A	c.(1570-1572)CCA>CAA	p.P524Q
Pat_11	Pre-Treatment	RREB1	6239	37	6	7231562	7231562	Missense_Mutation	SNP	C	T	50	170	c.3230C>T	c.(3229-3231)TCG>TTG	p.S1077L
Pat_11	Pre-Treatment	OR2J2	26707	37	6	29142121	29142122	Nonsense_Mutation	DNP	AA	TG	84	101	c.709_710AA>TG	c.(709-711)AAA>TGA	p.K237*
Pat_11	Pre-Treatment	GTF2H4	2968	37	6	30877741	30877741	Missense_Mutation	SNP	G	A	5	317	c.275G>A	c.(274-276)GGC>GAC	p.G92D
Pat_11	Pre-Treatment	BAT5	7920	37	6	31658381	31658381	Splice_Site	SNP	T	A	5	182	c.844_splice	c.e10-1	p.V282_splice
Pat_11	Pre-Treatment	VARS	7407	37	6	31753059	31753060	Missense_Mutation	DNP	GG	AA	50	114	.1310_1311CC>T	c.(1309-1311)TCC>TTT	p.S437F
Pat_11	Pre-Treatment	TNXB	7148	37	6	32029197	32029197	Missense_Mutation	SNP	G	A	7	506	c.7469C>T	c.(7468-7470)CCG>CTG	p.P2490L
Pat_11	Pre-Treatment	CYP39A1	51302	37	6	46609950	46609950	Missense_Mutation	SNP	G	A	9	37	c.263C>T	c.(262-264)TCC>TTC	p.S88F
Pat_11	Pre-Treatment	GPR111	222611	37	6	47649202	47649202	Missense_Mutation	SNP	G	A	27	55	c.907G>A	c.(907-909)GGA>AGA	p.G303R
Pat_11	Pre-Treatment	KHDRBS2	202559	37	6	62604676	62604676	Missense_Mutation	SNP	C	T	16	56	c.674G>A	c.(673-675)GGA>GAA	p.G225E
Pat_11	Pre-Treatment	FAM135A	57579	37	6	71235250	71235250	Missense_Mutation	SNP	T	G	9	31	c.2463T>G	c.(2461-2463)AAT>AAG	p.N821K
Pat_11	Pre-Treatment	COL12A1	1303	37	6	75812336	75812336	Missense_Mutation	SNP	C	T	21	52	c.8392G>A	c.(8392-8394)GGA>AGA	p.G2798R
Pat_11	Pre-Treatment	DOPEY1	23033	37	6	83823141	83823141	Splice_Site	SNP	G	A	4	100	c.780_splice	c.e7+1	p.Q260_splice
Pat_11	Pre-Treatment	PRDM13	59336	37	6	100054917	100054917	Missense_Mutation	SNP	G	A	3	36	c.7G>A	c.(7-9)GGA>AGA	p.G3R
Pat_11	Pre-Treatment	ROS1	6098	37	6	117746814	117746814	Missense_Mutation	SNP	C	A	28	130	c.6G>T	c.(4-6)AAG>AAT	p.K2N
Pat_11	Pre-Treatment	THEMIS	387357	37	6	128134491	128134491	Missense_Mutation	SNP	C	T	48	72	c.1295G>A	c.(1294-1296)GGA>GAA	p.G432E
Pat_11	Pre-Treatment	GPR126	57211	37	6	142718806	142718806	Missense_Mutation	SNP	G	A	14	29	c.1481G>A	c.(1480-1482)GGA>GAA	p.G494E
Pat_11	Pre-Treatment	ULBP1	80329	37	6	150290274	150290274	Missense_Mutation	SNP	G	A	4	232	c.403G>A	c.(403-405)GGC>AGC	p.G135S
Pat_11	Pre-Treatment	OPRM1	4988	37	6	154412237	154412237	Missense_Mutation	SNP	G	A	4	179	c.794G>A	c.(793-795)CGC>CAC	p.R265H
Pat_11	Pre-Treatment	TIAM2	26230	37	6	155577870	155577870	Missense_Mutation	SNP	A	G	4	238	c.4721A>G	c.(4720-4722)GAC>GGC	p.D1574G
Pat_11	Pre-Treatment	EZR	7430	37	6	159187971	159187971	Missense_Mutation	SNP	C	T	6	459	c.1736G>A	c.(1735-1737)CGC>CAC	p.R579H
Pat_11	Pre-Treatment	TCP1	6950	37	6	160202027	160202027	Missense_Mutation	SNP	C	A	5	180	c.913G>T	c.(913-915)GCT>TCT	p.A305S
Pat_11	Pre-Treatment	TTLL2	83887	37	6	167754638	167754638	Nonsense_Mutation	SNP	T	A	4	76	c.1250T>A	c.(1249-1251)TTA>TAA	p.L417*
Pat_11	Pre-Treatment	MLLT4	4301	37	6	168303044	168303044	Missense_Mutation	SNP	G	A	44	138	c.1625G>A	c.(1624-1626)GGG>GAG	p.G542E
Pat_11	Pre-Treatment	SUN1	23353	37	7	897553	897553	Missense_Mutation	SNP	G	A	6	508	c.1483G>A	c.(1483-1485)GTG>ATG	p.V495M
Pat_11	Pre-Treatment	MICALL2	79778	37	7	1482008	1482008	Missense_Mutation	SNP	G	A	102	366	c.1531C>T	c.(1531-1533)CCT>TCT	p.P511S
Pat_11	Pre-Treatment	FOXK1	221937	37	7	4798977	4798977	Missense_Mutation	SNP	G	A	4	142	c.1447G>A	c.(1447-1449)GTG>ATG	p.V483M
Pat_11	Pre-Treatment	USP42	84132	37	7	6194258	6194258	Missense_Mutation	SNP	C	T	4	84	c.3073C>T	c.(3073-3075)CGG>TGG	p.R1025W
Pat_11	Pre-Treatment	PDE1C	5137	37	7	31876841	31876841	Missense_Mutation	SNP	G	A	4	173	c.1156C>T	c.(1156-1158)CTC>TTC	p.L386F
Pat_11	Pre-Treatment	ZMIZ2	83637	37	7	44805829	44805829	Missense_Mutation	SNP	C	T	143	128	c.2309C>T	c.(2308-2310)ACC>ATC	p.T770I
Pat_11	Pre-Treatment	ABCA13	154664	37	7	48563857	48563858	Missense_Mutation	DNP	CT	TC	5	33	14065_14066CT>	c.(14065-14067)CTC>TCC	p.L4689S
Pat_11	Pre-Treatment	PHKG1	5260	37	7	56151087	56151087	Missense_Mutation	SNP	A	G	124	143	c.431T>C	c.(430-432)CTC>CCC	p.L144P
Pat_11	Pre-Treatment	RHBDD2	57414	37	7	75511410	75511410	Missense_Mutation	SNP	G	C	4	165	c.442G>C	c.(442-444)GTC>CTC	p.V148L

Pat_11	Pre-Treatment	PCLO	27445	37	7	82508726	82508726	Missense_Mutation	SNP	A	C	7	26	c.13581T>G	c.(13579-13581)AGT>AGG	p.S4527R
Pat_11	Pre-Treatment	PTCD1	26024	37	7	99032496	99032496	Missense_Mutation	SNP	G	A	8	592	c.370C>T	c.(370-372)CCG>TCG	p.P124S
Pat_11	Pre-Treatment	GAL3ST4	79690	37	7	99764196	99764196	Missense_Mutation	SNP	G	A	5	308	c.358C>T	c.(358-360)CGC>TGC	p.R120C
Pat_11	Pre-Treatment	C7orf51	222950	37	7	100086437	100086437	Missense_Mutation	SNP	G	A	57	65	c.1093G>A	c.(1093-1095)GAG>AAG	p.E365K
Pat_11	Pre-Treatment	PRKRIP1	79706	37	7	102038134	102038134	Missense_Mutation	SNP	G	A	7	479	c.194G>A	c.(193-195)CGA>CAA	p.R65Q
Pat_11	Pre-Treatment	SLC26A4	5172	37	7	107336394	107336394	Missense_Mutation	SNP	C	T	6	441	c.1454C>T	c.(1453-1455)ACG>ATG	p.T485M
Pat_11	Pre-Treatment	LAMB4	22798	37	7	107671373	107671373	Nonsense_Mutation	SNP	G	A	4	237	c.4870C>T	c.(4870-4872)CGA>TGA	p.R1624*
Pat_11	Pre-Treatment	MET	4233	37	7	116435940	116435940	Splice_Site	SNP	G	A	49	77	c.3936_splice	c.e21-1	p.L1312_splice
Pat_11	Pre-Treatment	GRM8	2918	37	7	126173209	126173209	Missense_Mutation	SNP	C	T	13	59	c.2227G>A	c.(2227-2229)GAC>AAC	p.D743N
Pat_11	Pre-Treatment	NRF1	4899	37	7	129330250	129330250	Missense_Mutation	SNP	G	A	6	455	c.470G>A	c.(469-471)CGT>CAT	p.R157H
Pat_11	Pre-Treatment	PLXNA4	91584	37	7	131910920	131910920	Missense_Mutation	SNP	G	A	6	634	c.1982C>T	c.(1981-1983)TCG>TTG	p.S661L
Pat_11	Pre-Treatment	AKR1B10	57016	37	7	134216768	134216768	Missense_Mutation	SNP	G	A	65	407	c.343G>A	c.(343-345)GGA>AGA	p.G115R
Pat_11	Pre-Treatment	CNOT4	4850	37	7	135078712	135078712	Missense_Mutation	SNP	G	A	4	239	c.1585C>T	c.(1585-1587)CCG>TCG	p.P529S
Pat_11	Pre-Treatment	ARHGEF5	7984	37	7	144077039	144077039	Missense_Mutation	SNP	C	T	106	535	c.4684C>T	c.(4684-4686)CCT>TCT	p.P1562S
Pat_11	Pre-Treatment	KRBA1	84626	37	7	149418501	149418501	Missense_Mutation	SNP	G	A	4	296	c.341G>A	c.(340-342)CGA>CAA	p.R114Q
Pat_11	Pre-Treatment	SSPO	23145	37	7	149475923	149475923	Missense_Mutation	SNP	G	A	5	235	c.889G>A	c.(889-891)GTC>ATC	p.V297I
Pat_11	Pre-Treatment	GIMAP6	474344	37	7	150325195	150325195	Missense_Mutation	SNP	C	T	276	229	c.491G>A	c.(490-492)CGG>CAG	p.R164Q
Pat_11	Pre-Treatment	ACCN3	9311	37	7	150749528	150749528	Missense_Mutation	SNP	G	A	5	303	c.1484G>A	c.(1483-1485)CGA>CAA	p.R495Q
Pat_11	Pre-Treatment	C8orf58	541565	37	8	22459276	22459276	Missense_Mutation	SNP	C	T	14	171	c.568C>T	c.(568-570)CGC>TGC	p.R190C
Pat_11	Pre-Treatment	C8orf80	389643	37	8	27884505	27884505	Missense_Mutation	SNP	C	T	102	237	c.2219G>A	c.(2218-2220)GGG>GAG	p.G740E
Pat_11	Pre-Treatment	ADAM18	8749	37	8	39468096	39468096	Missense_Mutation	SNP	A	C	3	33	c.393A>C	c.(391-393)GAA>GAC	p.E131D
Pat_11	Pre-Treatment	RP1	6101	37	8	55540286	55540286	Missense_Mutation	SNP	C	T	66	140	c.3844C>T	c.(3844-3846)CCT>TCT	p.P1282S
Pat_11	Pre-Treatment	CYP7A1	1581	37	8	59405037	59405037	Missense_Mutation	SNP	G	A	4	137	c.1090C>T	c.(1090-1092)CGG>TGG	p.R364W
Pat_11	Pre-Treatment	C8orf34	116328	37	8	69358598	69358598	Nonsense_Mutation	SNP	T	A	3	25	c.252T>A	c.(250-252)TAT>TAA	p.Y84*
Pat_11	Pre-Treatment	PTDSS1	9791	37	8	97321795	97321795	Missense_Mutation	SNP	G	A	4	178	c.1018G>A	c.(1018-1020)GCT>ACT	p.A340T
Pat_11	Pre-Treatment	TRHR	7201	37	8	110100070	110100070	Missense_Mutation	SNP	A	T	31	59	c.329A>T	c.(328-330)AAT>ATT	p.N110I
Pat_11	Pre-Treatment	MTBP	27085	37	8	121518998	121518998	Missense_Mutation	SNP	C	T	31	65	c.1780C>T	c.(1780-1782)CCT>TCT	p.P594S
Pat_11	Pre-Treatment	PHF20L1	51105	37	8	133858100	133858100	Missense_Mutation	SNP	C	T	4	65	c.2986C>T	c.(2986-2988)CGC>TGC	p.R996C
Pat_11	Pre-Treatment	GPR172A	79581	37	8	145583036	145583036	Missense_Mutation	SNP	A	G	4	45	c.83A>G	c.(82-84)AAT>AGT	p.N28S
Pat_11	Pre-Treatment	RECQL4	9401	37	8	145738862	145738862	Missense_Mutation	SNP	G	A	4	128	c.2203C>T	c.(2203-2205)CGT>TGT	p.R735C
Pat_11	Pre-Treatment	IFNA8	3445	37	9	21409416	21409416	Missense_Mutation	SNP	C	T	57	62	c.241C>T	c.(241-243)CAT>TAT	p.H81Y
Pat_11	Pre-Treatment	C9orf71	169693	37	9	71152338	71152338	Missense_Mutation	SNP	T	C	3	62	c.350A>G	c.(349-351)GAG>GGG	p.E117G
Pat_11	Pre-Treatment	GNA14	9630	37	9	80043926	80043926	Missense_Mutation	SNP	G	A	5	309	c.620C>T	c.(619-621)TCG>TTG	p.S207L
Pat_11	Pre-Treatment	PHF2	5253	37	9	96436019	96436019	Missense_Mutation	SNP	G	A	4	106	c.2501G>A	c.(2500-2502)GGG>GAG	p.G834E
Pat_11	Pre-Treatment	TBC1D2	55357	37	9	100971098	100971098	Missense_Mutation	SNP	G	A	4	145	c.2002C>T	c.(2002-2004)CGC>TGC	p.R668C
Pat_11	Pre-Treatment	HSDL2	84263	37	9	115216443	115216443	Splice_Site	SNP	G	A	4	108	c.1015_splice	c.e9+1	p.G339_splice
Pat_11	Pre-Treatment	COL27A1	85301	37	9	116930263	116930263	Missense_Mutation	SNP	G	A	4	101	c.428G>A	c.(427-429)CGC>CAC	p.R143H
Pat_11	Pre-Treatment	C5	727	37	9	123779710	123779710	Nonsense_Mutation	SNP	C	T	3	55	c.1796G>A	c.(1795-1797)TGG>TAG	p.W599*
Pat_11	Pre-Treatment	GOLGA2	2801	37	9	131022758	131022758	Missense_Mutation	SNP	C	T	4	83	c.1663G>A	c.(1663-1665)GGA>AGA	p.G555R
Pat_11	Pre-Treatment	SEC16A	9919	37	9	139372043	139372043	Missense_Mutation	SNP	G	A	3	27	c.25C>T	c.(25-27)CCG>TCG	p.P9S
Pat_11	Pre-Treatment	RNF208	727800	37	9	140115264	140115264	Missense_Mutation	SNP	G	A	3	29	c.401C>T	c.(400-402)TCG>TTG	p.S134L
Pat_11	Pre-Treatment	ZNF645	158506	37	X	22291533	22291533	Missense_Mutation	SNP	G	A	29	13	c.425G>A	c.(424-426)CGA>CAA	p.R142Q
Pat_11	Pre-Treatment	KLHL15	80311	37	X	24006340	24006340	Missense_Mutation	SNP	C	T	4	82	c.1513G>A	c.(1513-1515)GAA>AAA	p.E505K
Pat_11	Pre-Treatment	MAGEB6	158809	37	X	26212382	26212382	Missense_Mutation	SNP	A	G	5	71	c.419A>G	c.(418-420)CAT>CGT	p.H140R
Pat_11	Pre-Treatment	MAGEB6	158809	37	X	26212388	26212388	Missense_Mutation	SNP	T	C	5	73	c.425T>C	c.(424-426)GTC>GCC	p.V142A
Pat_11	Pre-Treatment	RBM10	8241	37	X	47035968	47035968	Missense_Mutation	SNP	G	A	4	110	c.646G>A	c.(646-648)GAC>AAC	p.D216N
Pat_11	Pre-Treatment	CLCN5	1184	37	X	49853407	49853407	Missense_Mutation	SNP	G	A	4	191	c.1400G>A	c.(1399-1401)CGA>CAA	p.R467Q

Pat_11	Pre-Treatment	SMC1A	8243	37	X	53409199	53409199	Missense_Mutation	SNP	C	T	4	101	c.3391G>A	c.(3391-3393)GGG>AGG	p.G1131R
Pat_11	Pre-Treatment	NLGN3	54413	37	X	70375180	70375180	Missense_Mutation	SNP	G	A	4	145	c.694G>A	c.(694-696)GTC>ATC	p.V232I
Pat_11	Pre-Treatment	KIAA2022	340533	37	X	73960071	73960071	Missense_Mutation	SNP	C	T	44	30	c.4321G>A	c.(4321-4323)GGA>AGA	p.G1441R
Pat_11	Pre-Treatment	BEX4	56271	37	X	102471145	102471145	Missense_Mutation	SNP	G	A	3	26	c.64G>A	c.(64-66)GAA>AAA	p.E22K
Pat_11	Pre-Treatment	ALG13	79868	37	X	110951568	110951568	Nonsense_Mutation	SNP	C	T	6	168	c.697C>T	c.(697-699)CGA>TGA	p.R233*
Pat_11	Pre-Treatment	KLHL13	90293	37	X	117043419	117043419	Missense_Mutation	SNP	C	T	19	16	c.1211G>A	c.(1210-1212)GGA>GAA	p.G404E
Pat_11	Pre-Treatment	ODZ1	10178	37	X	123695521	123695521	Missense_Mutation	SNP	C	T	4	145	c.2434G>A	c.(2434-2436)GAT>AAT	p.D812N
Pat_11	Pre-Treatment	OCRL	4952	37	X	128691316	128691316	Missense_Mutation	SNP	C	T	50	34	c.253C>T	c.(253-255)CGG>TGG	p.R85W
Pat_11	Pre-Treatment	FMR1	2332	37	X	147024735	147024735	Missense_Mutation	SNP	C	A	4	174	c.1360C>A	c.(1360-1362)CGT>AGT	p.R454S
Pat_11	Pre-Treatment	MAGEA12	4111	37	X	151900637	151900637	Missense_Mutation	SNP	G	A	4	123	c.164C>T	c.(163-165)GCT>GTT	p.A55V
Pat_11	Pre-Treatment	PCDH11Y	83259	37	Y	4925057	4925057	Missense_Mutation	SNP	G	A	19	19	c.193G>A	c.(193-195)GAA>AAA	p.E65K
Pat_11	Pre-Treatment	PRKY	5616	37	Y	7172061	7172061	Missense_Mutation	SNP	G	A	4	114	c.250G>A	c.(250-252)GAC>AAC	p.D84N
Pat_11	Post-Resistance	TNFRSF4	7293	37	1	1148443	1148443	Missense_Mutation	SNP	G	A	4	139	c.299C>T	c.(298-300)ACG>ATG	p.T100M
Pat_11	Post-Resistance	PEX14	5195	37	1	10689972	10689972	Missense_Mutation	SNP	T	G	72	104	c.1062T>G	c.(1060-1062)GAT>GAG	p.D354E
Pat_11	Post-Resistance	HSPG2	3339	37	1	22160328	22160328	Missense_Mutation	SNP	G	A	3	44	c.10811C>T	c.(10810-10812)CCT>CTT	p.P3604L
Pat_11	Post-Resistance	HSPG2	3339	37	1	22174273	22174273	Missense_Mutation	SNP	T	G	39	52	c.7934A>C	c.(7933-7935)CAG>CCG	p.Q2645P
Pat_11	Post-Resistance	LCK	3932	37	1	32740659	32740659	Missense_Mutation	SNP	G	A	96	225	c.253G>A	c.(253-255)GGG>AGG	p.G85R
Pat_11	Post-Resistance	EPHA10	284656	37	1	38185610	38185610	Missense_Mutation	SNP	G	A	4	199	c.2533C>T	c.(2533-2535)CGG>TGG	p.R845W
Pat_11	Post-Resistance	NFYC	4802	37	1	41218859	41218859	Nonsense_Mutation	SNP	C	T	68	160	c.328C>T	c.(328-330)CAG>TAG	p.Q110*
Pat_11	Post-Resistance	PCSK9	255738	37	1	55509558	55509558	Missense_Mutation	SNP	G	A	44	116	c.250G>A	c.(250-252)GAG>AAG	p.E84K
Pat_11	Post-Resistance	HFM1	164045	37	1	91781722	91781723	Missense_Mutation	DNP	GG	AA	47	131	.2917_2918CC>T	c.(2917-2919)CCC>TTC	p.P973F
Pat_11	Post-Resistance	DPYD	1806	37	1	98058782	98058782	Missense_Mutation	SNP	G	A	119	238	c.1120C>T	c.(1120-1122)CCT>TCT	p.P374S
Pat_11	Post-Resistance	ATP5F1	515	37	1	111996918	111996918	Missense_Mutation	SNP	C	T	169	282	c.163C>T	c.(163-165)CGT>TGT	p.R55C
Pat_11	Post-Resistance	SYCP1	6847	37	1	115455721	115455721	Missense_Mutation	SNP	G	A	132	205	c.1597G>A	c.(1597-1599)GAA>AAA	p.E533K
Pat_11	Post-Resistance	SPAG17	200162	37	1	118598455	118598455	Missense_Mutation	SNP	C	T	71	118	c.2623G>A	c.(2623-2625)GAG>AAG	p.E875K
Pat_11	Post-Resistance	HSD3B2	3284	37	1	119985517	119985517	Missense_Mutation	SNP	C	G	71	93	c.324C>G	c.(322-324)ATC>ATG	p.I108M
Pat_11	Post-Resistance	NBPF10	100132406	37	1	145360574	145360574	Missense_Mutation	SNP	G	C	4	52	c.9424G>C	c.(9424-9426)GAT>CAT	p.D3142H
Pat_11	Post-Resistance	NBPF10	100132406	37	1	146398425	146398425	Missense_Mutation	SNP	C	A	7	455	c.1224C>A	c.(1222-1224)GAC>GAA	p.D408E
Pat_11	Post-Resistance	RPTN	126638	37	1	152128479	152128479	Missense_Mutation	SNP	G	A	512	456	c.1096C>T	c.(1096-1098)CAC>TAC	p.H366Y
Pat_11	Post-Resistance	NUP210L	91181	37	1	153991444	153991444	Missense_Mutation	SNP	G	A	123	414	c.4618C>T	c.(4618-4620)CAT>TAT	p.H1540Y
Pat_11	Post-Resistance	TNN	63923	37	1	175067731	175067731	Missense_Mutation	SNP	G	A	81	143	c.2119G>A	c.(2119-2121)GAC>AAC	p.D707N
Pat_11	Post-Resistance	ASTN1	460	37	1	176983946	176983946	Missense_Mutation	SNP	C	T	375	536	c.1504G>A	c.(1504-1506)GAA>AAA	p.E502K
Pat_11	Post-Resistance	CAPN2	824	37	1	223958170	223958170	Missense_Mutation	SNP	G	A	4	223	c.1846G>A	c.(1846-1848)GTT>ATT	p.V616I
Pat_11	Post-Resistance	JMJD4	65094	37	1	227921686	227921686	Missense_Mutation	SNP	G	A	78	133	c.614C>T	c.(613-615)TCC>TTC	p.S205F
Pat_11	Post-Resistance	OR2G3	81469	37	1	247769014	247769014	Missense_Mutation	SNP	T	G	34	744	c.127T>G	c.(127-129)TTC>GTC	p.F43V
Pat_11	Post-Resistance	OR2M5	127059	37	1	248309108	248309108	Missense_Mutation	SNP	G	A	294	549	c.659G>A	c.(658-660)CGA>CAA	p.R220Q
Pat_11	Post-Resistance	ITIH2	3698	37	10	7791188	7791188	Missense_Mutation	SNP	G	A	9	463	c.2732G>A	c.(2731-2733)GGA>GAA	p.G911E
Pat_11	Post-Resistance	PTEN	5728	37	10	89692902	89692902	Missense_Mutation	SNP	G	A	275	149	c.386G>A	c.(385-387)GGA>GAA	p.G129E
Pat_11	Post-Resistance	PIPSL	266971	37	10	95718629	95718629	Missense_Mutation	SNP	C	T	4	135	c.2525G>A	c.(2524-2526)GGC>GAC	p.G842D
Pat_11	Post-Resistance	BLNK	29760	37	10	97969643	97969643	Missense_Mutation	SNP	C	T	298	164	c.697G>A	c.(697-699)GAA>AAA	p.E233K
Pat_11	Post-Resistance	C10orf12	26148	37	10	98744038	98744038	Missense_Mutation	SNP	G	A	4	278	c.2891G>A	c.(2890-2892)AGT>AAT	p.S964N
Pat_11	Post-Resistance	SLIT1	6585	37	10	98924646	98924647	Missense_Mutation	DNP	CC	TT	172	87	c.198_199GG>AA	196-201)CTGGAA>CTAA	p.E67K
Pat_11	Post-Resistance	PPRC1	23082	37	10	103901161	103901161	Missense_Mutation	SNP	C	T	82	71	c.2896C>T	c.(2896-2898)CCT>TCT	p.P966S
Pat_11	Post-Resistance	RPL13AP6	644511	37	10	112696673	112696673	Missense_Mutation	SNP	A	G	4	64	c.319T>C	c.(319-321)TGC>CGC	p.C107R
Pat_11	Post-Resistance	ATRNL1	26033	37	10	117226706	117226706	Missense_Mutation	SNP	C	T	71	41	c.3440C>T	c.(3439-3441)TCA>TTA	p.S1147L
Pat_11	Post-Resistance	ANO9	338440	37	11	431763	431763	Missense_Mutation	SNP	T	C	4	159	c.470A>G	c.(469-471)GAG>GGG	p.E157G
Pat_11	Post-Resistance	OR52B4	143496	37	11	4388924	4388924	Missense_Mutation	SNP	C	A	73	148	c.602G>T	c.(601-603)GGG>GTG	p.G201V

Pat_11	Post-Resistance	OR10A3	26496	37	11	7960409	7960409	Missense_Mutation	SNP	C	G	5	268	c.659G>C	c.(658-660)CGA>CCA	p.R220P
Pat_11	Post-Resistance	BDNF	627	37	11	27679663	27679663	Missense_Mutation	SNP	G	A	276	380	c.449C>T	c.(448-450)GCG>GTG	p.A150V
Pat_11	Post-Resistance	MADD	8567	37	11	47303960	47303960	Missense_Mutation	SNP	G	A	4	295	c.1498G>A	c.(1498-1500)GCC>ACC	p.A500T
Pat_11	Post-Resistance	OR4C6	219432	37	11	55432767	55432767	Missense_Mutation	SNP	T	C	249	401	c.125T>C	c.(124-126)CTT>CCT	p.L42P
Pat_11	Post-Resistance	AHNAK	79026	37	11	62296070	62296070	Missense_Mutation	SNP	A	G	15	843	c.5819T>C	c.(5818-5820)GTG>GCG	p.V1940A
Pat_11	Post-Resistance	TMEM179B	374395	37	11	62557149	62557149	Missense_Mutation	SNP	G	A	6	412	c.496G>A	c.(496-498)GAA>AAA	p.E166K
Pat_11	Post-Resistance	SHANK2	22941	37	11	70332923	70332923	Missense_Mutation	SNP	C	T	82	207	c.3475G>A	c.(3475-3477)GGT>AGT	p.G1159S
Pat_11	Post-Resistance	MMP12	4321	37	11	102738092	102738092	Missense_Mutation	SNP	G	A	29	39	c.820C>T	c.(820-822)CCT>TCT	p.P274S
Pat_11	Post-Resistance	DSCAML1	57453	37	11	117309688	117309688	Nonsense_Mutation	SNP	G	A	4	108	c.4336C>T	c.(4336-4338)CAG>TAG	p.Q1446*
Pat_11	Post-Resistance	CXCR5	643	37	11	118764833	118764833	Missense_Mutation	SNP	C	T	4	220	c.580C>T	c.(580-582)CAT>TAT	p.H194Y
Pat_11	Post-Resistance	BCL9L	283149	37	11	118773151	118773151	Missense_Mutation	SNP	G	A	26	53	c.1301C>T	c.(1300-1302)CCC>CTC	p.P434L
Pat_11	Post-Resistance	PATE2	399967	37	11	125647312	125647312	Missense_Mutation	SNP	G	A	95	169	c.307C>T	c.(307-309)CAT>TAT	p.H103Y
Pat_11	Post-Resistance	NFRKB	4798	37	11	129739745	129739745	Missense_Mutation	SNP	G	A	52	81	c.3175C>T	c.(3175-3177)CGC>TGC	p.R1059C
Pat_11	Post-Resistance	CCDC77	84318	37	12	518560	518560	Missense_Mutation	SNP	C	T	4	300	c.11C>T	c.(10-12)ACC>ATC	p.T4I
Pat_11	Post-Resistance	GSG1	83445	37	12	13240841	13240841	Missense_Mutation	SNP	C	T	48	79	c.634G>A	c.(634-636)GGT>AGT	p.G212S
Pat_11	Post-Resistance	ADAMTS20	80070	37	12	43824179	43824179	Missense_Mutation	SNP	T	A	14	194	c.3357A>T	c.(3355-3357)GAA>GAT	p.E1119D
Pat_11	Post-Resistance	ADAMTS20	80070	37	12	43826148	43826148	Missense_Mutation	SNP	C	T	79	160	c.3055G>A	c.(3055-3057)GAA>AAA	p.E1019K
Pat_11	Post-Resistance	ANO6	196527	37	12	45795629	45795629	Missense_Mutation	SNP	G	A	122	228	c.1438G>A	c.(1438-1440)GTG>ATG	p.V480M
Pat_11	Post-Resistance	ITGB7	3695	37	12	53594156	53594156	Missense_Mutation	SNP	C	A	93	136	c.72G>T	c.(70-72)AAG>AAT	p.K24N
Pat_11	Post-Resistance	NEUROD4	58158	37	12	55420311	55420311	Missense_Mutation	SNP	G	A	63	108	c.88G>A	c.(88-90)GAG>AAG	p.E30K
Pat_11	Post-Resistance	OR9K2	441639	37	12	55524145	55524145	Missense_Mutation	SNP	C	T	123	176	c.593C>T	c.(592-594)GCT>GTT	p.A198V
Pat_11	Post-Resistance	OR6C65	403282	37	12	55794361	55794361	Missense_Mutation	SNP	G	A	43	81	c.49G>A	c.(49-51)GAT>AAT	p.D17N
Pat_11	Post-Resistance	CAPS2	84698	37	12	75676125	75676126	Missense_Mutation	DNP	GG	AA	157	362	.1574_1575CC>T	c.(1573-1575)GCC>GTT	p.A525V
Pat_11	Post-Resistance	USP44	84101	37	12	95922687	95922687	Missense_Mutation	SNP	C	T	61	91	c.1520G>A	c.(1519-1521)GGA>GAA	p.G507E
Pat_11	Post-Resistance	C12orf63	374467	37	12	97057618	97057618	Missense_Mutation	SNP	G	A	84	171	c.746G>A	c.(745-747)CGA>CAA	p.R249Q
Pat_11	Post-Resistance	SLC17A8	246213	37	12	100813881	100813881	Nonsense_Mutation	SNP	G	T	31	82	c.1714G>T	c.(1714-1716)GAG>TAG	p.E572*
Pat_11	Post-Resistance	STAB2	55576	37	12	104049352	104049352	Missense_Mutation	SNP	C	T	120	198	c.1727C>T	c.(1726-1728)TCT>TTT	p.S576F
Pat_11	Post-Resistance	BTBD11	121551	37	12	107937863	107937863	Missense_Mutation	SNP	G	A	58	142	c.1437G>A	c.(1435-1437)ATG>ATA	p.M479I
Pat_11	Post-Resistance	MED13L	23389	37	12	116440889	116440889	Missense_Mutation	SNP	G	A	4	295	c.2488C>T	c.(2488-2490)CGC>TGC	p.R830C
Pat_11	Post-Resistance	DNAH10	196385	37	12	124265681	124265681	Missense_Mutation	SNP	G	A	5	449	c.493G>A	c.(493-495)GTC>ATC	p.V165I
Pat_11	Post-Resistance	STARD13	90627	37	13	33692262	33692263	Missense_Mutation	DNP	CC	TT	202	144	.2220_2221GG>A	218-2223)CGGGAC>CGA	p.D741N
Pat_11	Post-Resistance	TRPC4	7223	37	13	38211429	38211429	Missense_Mutation	SNP	G	A	160	133	c.2545C>T	c.(2545-2547)CAT>TAT	p.H849Y
Pat_11	Post-Resistance	FREM2	341640	37	13	39338481	39338481	Nonsense_Mutation	SNP	G	A	72	257	c.5304G>A	c.(5302-5304)TGG>TGA	p.W1768*
Pat_11	Post-Resistance	NUFIP1	26747	37	13	45523884	45523884	Missense_Mutation	SNP	G	A	5	594	c.1111C>T	c.(1111-1113)CTT>TTT	p.L371F
Pat_11	Post-Resistance	FAM155A	728215	37	13	108518718	108518718	Missense_Mutation	SNP	T	C	4	240	c.227A>G	c.(226-228)CAG>CGG	p.Q76R
Pat_11	Post-Resistance	ATP11A	23250	37	13	113470511	113470511	Missense_Mutation	SNP	G	A	5	252	c.556G>A	c.(556-558)GAA>AAA	p.E186K
Pat_11	Post-Resistance	C14orf126	112487	37	14	31926599	31926599	Missense_Mutation	SNP	T	C	6	21	c.1A>G	c.(1-3)ATG>GTG	p.M1V
Pat_11	Post-Resistance	FERMT2	10979	37	14	53386014	53386014	Missense_Mutation	SNP	A	G	195	309	c.218T>C	c.(217-219)CTG>CCG	p.L73P
Pat_11	Post-Resistance	SIPA1L1	26037	37	14	72055973	72055973	Missense_Mutation	SNP	G	A	4	256	c.1384G>A	c.(1384-1386)GTA>ATA	p.V462I
Pat_11	Post-Resistance	SERPINA13	388007	37	14	95108015	95108015	Missense_Mutation	SNP	G	A	75	86	c.532G>A	c.(532-534)GAT>AAT	p.D178N
Pat_11	Post-Resistance	INF2	64423	37	14	105181082	105181082	Missense_Mutation	SNP	G	A	14	25	c.3583G>A	c.(3583-3585)GAG>AAG	p.E1195K
Pat_11	Post-Resistance	TRPM1	4308	37	15	31354879	31354879	Missense_Mutation	SNP	T	C	5	217	c.926A>G	c.(925-927)CAG>CGG	p.Q309R
Pat_11	Post-Resistance	JMJD7-PLA2G4B	8681	37	15	42140051	42140051	Missense_Mutation	SNP	C	T	25	42	c.2339C>T	c.(2338-2340)CCC>CTC	p.P780L
Pat_11	Post-Resistance	TTBK2	146057	37	15	43038408	43038408	Missense_Mutation	SNP	A	G	3	123	c.3320T>C	c.(3319-3321)CTT>CCT	p.L1107P
Pat_11	Post-Resistance	DENND4A	10260	37	15	66021549	66021549	Missense_Mutation	SNP	G	A	13	19	c.1348C>T	c.(1348-1350)CCT>TCT	p.P450S
Pat_11	Post-Resistance	LRRC49	54839	37	15	71305234	71305234	Missense_Mutation	SNP	C	T	144	284	c.1685C>T	c.(1684-1686)TCC>TTC	p.S562F
Pat_11	Post-Resistance	MYO9A	4649	37	15	72193624	72193624	Missense_Mutation	SNP	G	A	4	170	c.3058C>T	c.(3058-3060)CTC>TTC	p.L1020F

Pat_11	Post-Resistance	ISLR	3671	37	15	74467617	74467617	Missense_Mutation	SNP	G	A	99	169	c.418G>A	c.(418-420)GAC>AAC	p.D140N
Pat_11	Post-Resistance	SH3GL3	6457	37	15	84257417	84257417	Missense_Mutation	SNP	A	G	65	94	c.732A>G	c.(730-732)ATA>ATG	p.I244M
Pat_11	Post-Resistance	ACAN	176	37	15	89382124	89382124	Nonsense_Mutation	SNP	C	T	234	337	c.301C>T	c.(301-303)CAG>TAG	p.Q101*
Pat_11	Post-Resistance	CACNA1H	8912	37	16	1254407	1254407	Missense_Mutation	SNP	G	A	71	143	c.2400G>A	c.(2398-2400)ATG>ATA	p.M800I
Pat_11	Post-Resistance	CACNA1H	8912	37	16	1270521	1270521	Missense_Mutation	SNP	C	T	24	72	c.6589C>T	c.(6589-6591)CCT>TCT	p.P2197S
Pat_11	Post-Resistance	PKD1	5310	37	16	2153595	2153595	Missense_Mutation	SNP	G	T	76	169	c.8463C>A	c.(8461-8463)GAC>GAA	p.D2821E
Pat_11	Post-Resistance	SRRM2	23524	37	16	2816762	2816762	Missense_Mutation	SNP	G	A	5	383	c.6233G>A	c.(6232-6234)CGT>CAT	p.R2078H
Pat_11	Post-Resistance	CORO7	79585	37	16	4408068	4408068	Missense_Mutation	SNP	C	T	73	119	c.2494G>A	c.(2494-2496)GCT>ACT	p.A832T
Pat_11	Post-Resistance	ABAT	18	37	16	8839938	8839938	Missense_Mutation	SNP	C	T	56	115	c.151C>T	c.(151-153)CCA>TCA	p.P51S
Pat_11	Post-Resistance	ABAT	18	37	16	8844395	8844395	Missense_Mutation	SNP	A	G	5	598	c.315A>G	c.(313-315)ATA>ATG	p.I105M
Pat_11	Post-Resistance	SMG1	23049	37	16	18937330	18937330	Missense_Mutation	SNP	T	C	3	67	c.34A>G	c.(34-36)AGC>GGC	p.S12G
Pat_11	Post-Resistance	CRYM	1428	37	16	21281121	21281121	Missense_Mutation	SNP	G	A	164	295	c.479C>T	c.(478-480)TCC>TTC	p.S160F
Pat_11	Post-Resistance	TNRC6A	27327	37	16	24802545	24802545	Missense_Mutation	SNP	C	T	82	127	c.2582C>T	c.(2581-2583)TCA>TTA	p.S861L
Pat_11	Post-Resistance	HS3ST4	9951	37	16	26147376	26147376	Missense_Mutation	SNP	G	A	20	49	c.1178G>A	c.(1177-1179)GGG>GAG	p.G393E
Pat_11	Post-Resistance	TUFM	7284	37	16	28854424	28854424	Missense_Mutation	SNP	G	A	4	283	c.1240C>T	c.(1240-1242)CGG>TGG	p.R414W
Pat_11	Post-Resistance	BCL7C	9274	37	16	30905235	30905235	Missense_Mutation	SNP	G	A	5	249	c.31C>T	c.(31-33)CGG>TGG	p.R11W
Pat_11	Post-Resistance	SLC5A2	6524	37	16	31498937	31498937	Missense_Mutation	SNP	G	A	5	337	c.742G>A	c.(742-744)GTG>ATG	p.V248M
Pat_11	Post-Resistance	SLC9A5	6553	37	16	67293737	67293737	Missense_Mutation	SNP	G	A	6	288	c.1730G>A	c.(1729-1731)AGT>AAT	p.S577N
Pat_11	Post-Resistance	TSNAXIP1	55815	37	16	67860079	67860079	Missense_Mutation	SNP	G	A	5	191	c.1007G>A	c.(1006-1008)CGC>CAC	p.R336H
Pat_11	Post-Resistance	PSKH1	5681	37	16	67943268	67943268	Missense_Mutation	SNP	G	A	4	197	c.616G>A	c.(616-618)GTC>ATC	p.V206I
Pat_11	Post-Resistance	CTRL	1506	37	16	67964841	67964841	Missense_Mutation	SNP	G	A	5	289	c.218C>T	c.(217-219)GCT>GTT	p.A73V
Pat_11	Post-Resistance	ZFP90	146198	37	16	68598329	68598329	Missense_Mutation	SNP	C	T	131	132	c.1639C>T	c.(1639-1641)CAC>TAC	p.H547Y
Pat_11	Post-Resistance	NUDT7	283927	37	16	77769734	77769734	Missense_Mutation	SNP	G	A	237	532	c.199G>A	c.(199-201)GCC>ACC	p.A67T
Pat_11	Post-Resistance	KLHL36	79786	37	16	84693409	84693409	Missense_Mutation	SNP	C	T	203	182	c.1181C>T	c.(1180-1182)TCC>TTC	p.S394F
Pat_11	Post-Resistance	ANKFY1	51479	37	17	4080447	4080447	Missense_Mutation	SNP	C	T	139	208	c.2749G>A	c.(2749-2751)GGC>AGC	p.G917S
Pat_11	Post-Resistance	ALOX12	239	37	17	6902081	6902081	Missense_Mutation	SNP	G	A	4	200	c.467G>A	c.(466-468)CGT>CAT	p.R156H
Pat_11	Post-Resistance	MYOCD	93649	37	17	12666896	12666896	Missense_Mutation	SNP	G	A	116	163	c.2752G>A	c.(2752-2754)GAT>AAT	p.D918N
Pat_11	Post-Resistance	KRTAP4-8	728224	37	17	39254021	39254021	Missense_Mutation	SNP	C	T	5	203	c.316G>A	c.(316-318)GTG>ATG	p.V106M
Pat_11	Post-Resistance	KRTAP4-11	653240	37	17	39274150	39274150	Missense_Mutation	SNP	T	A	11	92	c.418A>T	c.(418-420)AGC>TGC	p.S140C
Pat_11	Post-Resistance	TTLL6	284076	37	17	46863599	46863599	Missense_Mutation	SNP	C	T	331	590	c.1688G>A	c.(1687-1689)AGA>AAA	p.R563K
Pat_11	Post-Resistance	LPO	4025	37	17	56329765	56329765	Missense_Mutation	SNP	G	A	59	87	c.1003G>A	c.(1003-1005)GAG>AAG	p.E335K
Pat_11	Post-Resistance	BPTF	2186	37	17	65822287	65822287	Missense_Mutation	SNP	C	G	3	40	c.447C>G	c.(445-447)GAC>GAG	p.D149E
Pat_11	Post-Resistance	GPR142	350383	37	17	72368438	72368438	Missense_Mutation	SNP	C	T	122	196	c.1088C>T	c.(1087-1089)ACC>ATC	p.T363I
Pat_11	Post-Resistance	PPP4R1	9989	37	18	9583194	9583194	Missense_Mutation	SNP	G	A	102	153	c.839C>T	c.(838-840)TCA>TTA	p.S280L
Pat_11	Post-Resistance	CEP192	55125	37	18	13099507	13099507	Missense_Mutation	SNP	C	T	142	331	c.6590C>T	c.(6589-6591)TCC>TTC	p.S2197F
Pat_11	Post-Resistance	ST8SIA3	51046	37	18	55027323	55027323	Missense_Mutation	SNP	G	A	83	131	c.958G>A	c.(958-960)GGA>AGA	p.G320R
Pat_11	Post-Resistance	SERPINB2	5055	37	18	61569770	61569770	Missense_Mutation	SNP	G	A	154	289	c.811G>A	c.(811-813)GAA>AAA	p.E271K
Pat_11	Post-Resistance	CDH7	1005	37	18	63477055	63477055	Missense_Mutation	SNP	G	A	85	114	c.326G>A	c.(325-327)AGA>AAA	p.R109K
Pat_11	Post-Resistance	RTTN	25914	37	18	67781759	67781759	Missense_Mutation	SNP	G	A	5	466	c.3605C>T	c.(3604-3606)GCT>GTT	p.A1202V
Pat_11	Post-Resistance	PNPLA6	10908	37	19	7619494	7619494	Missense_Mutation	SNP	G	A	5	343	c.2549G>A	c.(2548-2550)CGT>CAT	p.R850H
Pat_11	Post-Resistance	LASS4	79603	37	19	8322862	8322862	Missense_Mutation	SNP	C	T	129	304	c.841C>T	c.(841-843)CCC>TCC	p.P281S
Pat_11	Post-Resistance	MUC16	94025	37	19	9045986	9045986	Missense_Mutation	SNP	G	A	175	317	c.35645C>T	c.(35644-35646)TCT>TTT	p.S11882F
Pat_11	Post-Resistance	MUC16	94025	37	19	9066660	9066660	Missense_Mutation	SNP	G	A	284	503	c.20786C>T	c.(20785-20787)TCC>TTC	p.S6929F
Pat_11	Post-Resistance	MUC16	94025	37	19	9082547	9082547	Missense_Mutation	SNP	C	T	254	371	c.9268G>A	c.(9268-9270)GAG>AAG	p.E3090K
Pat_11	Post-Resistance	MUC16	94025	37	19	9084835	9084835	Missense_Mutation	SNP	G	A	37	91	c.6980C>T	c.(6979-6981)TCC>TTC	p.S2327F
Pat_11	Post-Resistance	COL5A3	50509	37	19	10112244	10112244	Missense_Mutation	SNP	G	A	4	286	c.1066C>T	c.(1066-1068)CGG>TGG	p.R356W
Pat_11	Post-Resistance	CACNA1A	773	37	19	13563820	13563820	Missense_Mutation	SNP	C	T	80	157	c.409G>A	c.(409-411)GAA>AAA	p.E137K

Pat_11	Post-Resistance	CASP14	23581	37	19	15164421	15164421	Missense_Mutation	SNP	G	A	95	216	c.156G>A	c.(154-156)ATG>ATA	p.M52I
Pat_11	Post-Resistance	ILVBL	10994	37	19	15234224	15234224	Missense_Mutation	SNP	G	A	4	236	c.299C>T	c.(298-300)ACG>ATG	p.T100M
Pat_11	Post-Resistance	NCAN	1463	37	19	19338690	19338690	Missense_Mutation	SNP	C	T	106	172	c.2261C>T	c.(2260-2262)CCG>CTG	p.P754L
Pat_11	Post-Resistance	ZNF93	81931	37	19	20045355	20045355	Missense_Mutation	SNP	C	T	37	105	c.1591C>T	c.(1591-1593)CAT>TAT	p.H531Y
Pat_11	Post-Resistance	ZNF43	7594	37	19	21991505	21991505	Missense_Mutation	SNP	T	A	5	314	c.1334A>T	c.(1333-1335)AAC>ATC	p.N445I
Pat_11	Post-Resistance	ZNF208	7757	37	19	22156875	22156875	Missense_Mutation	SNP	C	T	132	182	c.961G>A	c.(961-963)GCC>ACC	p.A321T
Pat_11	Post-Resistance	ZNF420	147923	37	19	37619781	37619781	Missense_Mutation	SNP	C	T	57	99	c.1888C>T	c.(1888-1890)CTT>TTT	p.L630F
Pat_11	Post-Resistance	SIPA1L3	23094	37	19	38631876	38631876	Missense_Mutation	SNP	G	A	129	222	c.3196G>A	c.(3196-3198)GAA>AAA	p.E1066K
Pat_11	Post-Resistance	RYR1	6261	37	19	39008205	39008205	Missense_Mutation	SNP	G	A	70	119	c.9892G>A	c.(9892-9894)GCC>ACC	p.A3298T
Pat_11	Post-Resistance	LGALS7B	653499	37	19	39281435	39281435	Missense_Mutation	SNP	G	A	27	71	c.202G>A	c.(202-204)GGC>AGC	p.G68S
Pat_11	Post-Resistance	CD3EAP	10849	37	19	45912107	45912107	Missense_Mutation	SNP	A	G	5	289	c.881A>G	c.(880-882)AAG>AGG	p.K294R
Pat_11	Post-Resistance	ZNF836	162962	37	19	52659224	52659224	Missense_Mutation	SNP	A	T	7	765	c.1712T>A	c.(1711-1713)ATT>AAT	p.I571N
Pat_11	Post-Resistance	NLRP4	147945	37	19	56382227	56382227	Missense_Mutation	SNP	G	A	99	186	c.2389G>A	c.(2389-2391)GAA>AAA	p.E797K
Pat_11	Post-Resistance	GREB1	9687	37	2	11777890	11777890	Missense_Mutation	SNP	C	T	124	212	c.5395C>T	c.(5395-5397)CCG>TCG	p.P1799S
Pat_11	Post-Resistance	HS1BP3	64342	37	2	20840820	20840820	Missense_Mutation	SNP	C	T	249	482	c.319G>A	c.(319-321)GAG>AAG	p.E107K
Pat_11	Post-Resistance	APOB	338	37	2	21232284	21232284	Missense_Mutation	SNP	C	T	119	214	c.7456G>A	c.(7456-7458)GAC>AAC	p.D2486N
Pat_11	Post-Resistance	LBH	81606	37	2	30480434	30480434	Nonsense_Mutation	SNP	G	T	59	106	c.265G>T	c.(265-267)GAG>TAG	p.E89*
Pat_11	Post-Resistance	LTBP1	4052	37	2	33468797	33468797	Nonsense_Mutation	SNP	C	T	173	298	c.1945C>T	c.(1945-1947)CGA>TGA	p.R649*
Pat_11	Post-Resistance	RASGRP3	25780	37	2	33745717	33745717	Missense_Mutation	SNP	G	A	198	316	c.334G>A	c.(334-336)GAA>AAA	p.E112K
Pat_11	Post-Resistance	DHX57	90957	37	2	39088696	39088696	Missense_Mutation	SNP	G	A	93	139	c.856C>T	c.(856-858)CGC>TGC	p.R286C
Pat_11	Post-Resistance	ALMS1P	200420	37	2	73900940	73900940	Missense_Mutation	SNP	G	A	6	11	c.217G>A	c.(217-219)GAA>AAA	p.E73K
Pat_11	Post-Resistance	LRRTM1	347730	37	2	80530256	80530256	Missense_Mutation	SNP	G	T	6	604	c.689C>A	c.(688-690)CCG>CAG	p.P230Q
Pat_11	Post-Resistance	SEMA4C	54910	37	2	97526382	97526382	Missense_Mutation	SNP	G	A	119	160	c.2483C>T	c.(2482-2484)CCC>CTC	p.P828L
Pat_11	Post-Resistance	ZAP70	7535	37	2	98349771	98349771	Missense_Mutation	SNP	C	T	27	70	c.802C>T	c.(802-804)CCC>TCC	p.P268S
Pat_11	Post-Resistance	CHST10	9486	37	2	101014417	101014417	Missense_Mutation	SNP	G	A	115	187	c.380C>T	c.(379-381)CCC>CTC	p.P127L
Pat_11	Post-Resistance	SLC35F5	80255	37	2	114500394	114500394	Missense_Mutation	SNP	G	C	110	199	c.625C>G	c.(625-627)CAT>GAT	p.H209D
Pat_11	Post-Resistance	LRP1B	53353	37	2	141625828	141625828	Missense_Mutation	SNP	G	A	9	116	c.4174C>T	c.(4174-4176)CTT>TTT	p.L1392F
Pat_11	Post-Resistance	KIF5C	3800	37	2	149853804	149853804	Missense_Mutation	SNP	G	A	44	106	c.2050G>A	c.(2050-2052)GAT>AAT	p.D684N
Pat_11	Post-Resistance	GALNT13	114805	37	2	155099313	155099313	Missense_Mutation	SNP	G	A	69	115	c.581G>A	c.(580-582)CGA>CAA	p.R194Q
Pat_11	Post-Resistance	ERMN	57471	37	2	158181947	158181947	Missense_Mutation	SNP	G	A	5	274	c.208C>T	c.(208-210)CTC>TTC	p.L70F
Pat_11	Post-Resistance	DPP4	1803	37	2	162890087	162890087	Missense_Mutation	SNP	G	A	112	226	c.851C>T	c.(850-852)TCC>TTC	p.S284F
Pat_11	Post-Resistance	MYO3B	140469	37	2	171070963	171070963	Missense_Mutation	SNP	G	A	123	260	c.396G>A	c.(394-396)ATG>ATA	p.M132I
Pat_11	Post-Resistance	HOXD12	3238	37	2	176964663	176964663	Missense_Mutation	SNP	C	T	58	94	c.134C>T	c.(133-135)CCG>CTG	p.P45L
Pat_11	Post-Resistance	TTN	7273	37	2	179604014	179604014	Missense_Mutation	SNP	T	G	5	87	c.13433A>C	c.(13432-13434)AAG>ACG	p.K4478T
Pat_11	Post-Resistance	SSFA2	6744	37	2	182780118	182780118	Missense_Mutation	SNP	C	T	4	137	c.1751C>T	c.(1750-1752)GCA>GTA	p.A584V
Pat_11	Post-Resistance	ZNF804A	91752	37	2	185801798	185801798	Missense_Mutation	SNP	G	A	27	72	c.1675G>A	c.(1675-1677)GAA>AAA	p.E559K
Pat_11	Post-Resistance	DNAH7	56171	37	2	196636434	196636434	Missense_Mutation	SNP	A	C	12	719	c.11383T>G	c.(11383-11385)TTA>GTA	p.L3795V
Pat_11	Post-Resistance	MAP2	4133	37	2	210574868	210574868	Missense_Mutation	SNP	G	A	4	155	c.4963G>A	c.(4963-4965)GCG>ACG	p.A1655T
Pat_11	Post-Resistance	SLC23A3	151295	37	2	220028969	220028969	Missense_Mutation	SNP	G	T	4	64	c.1259C>A	c.(1258-1260)CCA>CAA	p.P420Q
Pat_11	Post-Resistance	PTPRN	5798	37	2	220161969	220161970	Missense_Mutation	DNP	CC	TT	57	143	.2073_2074GG>A	071-2076)ACGGGA>ACA	p.G692R
Pat_11	Post-Resistance	PTPRN	5798	37	2	220172208	220172208	Missense_Mutation	SNP	G	A	5	336	c.238C>T	c.(238-240)CTC>TTC	p.L80F
Pat_11	Post-Resistance	C2orf57	165100	37	2	232457897	232457897	Nonsense_Mutation	SNP	C	T	171	270	c.235C>T	c.(235-237)CAG>TAG	p.Q79*
Pat_11	Post-Resistance	GIGYF2	26058	37	2	233681650	233681650	Missense_Mutation	SNP	G	A	4	276	c.2278G>A	c.(2278-2280)GAA>AAA	p.E760K
Pat_11	Post-Resistance	ESPNL	339768	37	2	239016478	239016478	Missense_Mutation	SNP	C	T	3	33	c.719C>T	c.(718-720)GCC>GTC	p.A240V
Pat_11	Post-Resistance	HDLBP	3069	37	2	242182015	242182015	Missense_Mutation	SNP	G	A	4	132	c.2029C>T	c.(2029-2031)CGC>TGC	p.R677C
Pat_11	Post-Resistance	FARP2	9855	37	2	242380731	242380731	Missense_Mutation	SNP	C	T	139	238	c.1171C>T	c.(1171-1173)CCC>TCC	p.P391S
Pat_11	Post-Resistance	NINL	22981	37	20	25434259	25434259	Missense_Mutation	SNP	G	A	75	157	c.3977C>T	c.(3976-3978)TCC>TTC	p.S1326F

Pat_11	Post-Resistance	FRG1B	284802	37	20	29625905	29625905	Missense_Mutation	SNP	T	C	5	438	c.59T>C	c.(58-60)CTT>CCT	p.L20P
Pat_11	Post-Resistance	DEFB123	245936	37	20	30028545	30028545	Missense_Mutation	SNP	C	T	275	478	c.44C>T	c.(43-45)TCC>TTC	p.S15F
Pat_11	Post-Resistance	PABPC1L	80336	37	20	43559150	43559150	Missense_Mutation	SNP	C	T	273	502	c.1022C>T	c.(1021-1023)TCC>TTC	p.S341F
Pat_11	Post-Resistance	SEMG2	6407	37	20	43851414	43851414	Missense_Mutation	SNP	C	A	5	350	c.1141C>A	c.(1141-1143)CAA>AAA	p.Q381K
Pat_11	Post-Resistance	ZNF831	128611	37	20	57767060	57767060	Missense_Mutation	SNP	C	T	35	43	c.986C>T	c.(985-987)GCC>GTC	p.A329V
Pat_11	Post-Resistance	BAGE2	85319	37	21	11098839	11098839	Translation_Start_Site	SNP	C	T	8	215	c.-121G>A	(-123--119)CCGTG>CCATG	
Pat_11	Post-Resistance	LIPI	149998	37	21	15535788	15535788	Missense_Mutation	SNP	G	A	139	262	c.1021C>T	c.(1021-1023)CTT>TTT	p.L341F
Pat_11	Post-Resistance	KRTAP21-2	337978	37	21	32119310	32119310	Nonsense_Mutation	SNP	G	A	5	558	c.211C>T	c.(211-213)CGA>TGA	p.R71*
Pat_11	Post-Resistance	PPIL2	23759	37	22	22049690	22049690	Missense_Mutation	SNP	G	A	19	32	c.1474G>A	c.(1474-1476)GCA>ACA	p.A492T
Pat_11	Post-Resistance	OSBP2	23762	37	22	31285598	31285599	Missense_Mutation	DNP	GG	AA	172	104	.1598_1599GG>A	c.(1597-1599)CGG>CAA	p.R533Q
Pat_11	Post-Resistance	PIK3IP1	113791	37	22	31686951	31686951	Missense_Mutation	SNP	C	T	27	15	c.307G>A	c.(307-309)GAG>AAG	p.E103K
Pat_11	Post-Resistance	C22orf33	339669	37	22	37398027	37398027	Nonsense_Mutation	SNP	G	A	28	61	c.340C>T	c.(340-342)CAG>TAG	p.Q114*
Pat_11	Post-Resistance	TNRC6B	23112	37	22	40708530	40708530	Nonsense_Mutation	SNP	G	A	105	249	c.4457G>A	c.(4456-4458)TGG>TAG	p.W1486*
Pat_11	Post-Resistance	MKL1	57591	37	22	40827438	40827438	Missense_Mutation	SNP	G	A	244	633	c.110C>T	c.(109-111)TCG>TTG	p.S37L
Pat_11	Post-Resistance	CELSR1	9620	37	22	46795724	46795724	Missense_Mutation	SNP	G	A	4	212	c.5302C>T	c.(5302-5304)CGG>TGG	p.R1768W
Pat_11	Post-Resistance	IL5RA	3568	37	3	3146593	3146593	Missense_Mutation	SNP	C	T	126	179	c.76G>A	c.(76-78)GAA>AAA	p.E26K
Pat_11	Post-Resistance	ATP2B2	491	37	3	10391870	10391870	Missense_Mutation	SNP	C	T	84	151	c.2330G>A	c.(2329-2331)CGA>CAA	p.R777Q
Pat_11	Post-Resistance	GADL1	339896	37	3	30880557	30880557	Missense_Mutation	SNP	C	T	102	194	c.835G>A	c.(835-837)GGA>AGA	p.G279R
Pat_11	Post-Resistance	MYD88	4615	37	3	38181482	38181483	Missense_Mutation	DNP	CC	TT	28	58	c.495_496CC>TT	493-498)GACCCC>GATT	p.P166S
Pat_11	Post-Resistance	TRAK1	22906	37	3	42242402	42242402	Missense_Mutation	SNP	C	T	260	497	c.1283C>T	c.(1282-1284)TCC>TTC	p.S428F
Pat_11	Post-Resistance	FYCO1	79443	37	3	45996861	45996861	Missense_Mutation	SNP	G	A	7	709	c.3824C>T	c.(3823-3825)CCG>CTG	p.P1275L
Pat_11	Post-Resistance	CSPG5	10675	37	3	47610605	47610605	Missense_Mutation	SNP	G	A	24	49	c.1495C>T	c.(1495-1497)CCC>TCC	p.P499S
Pat_11	Post-Resistance	RYBP	23429	37	3	72428255	72428255	Missense_Mutation	SNP	C	G	4	330	c.340G>C	c.(340-342)GAA>CAA	p.E114Q
Pat_11	Post-Resistance	ROBO2	6092	37	3	77089988	77089988	Missense_Mutation	SNP	C	G	144	354	c.52C>G	c.(52-54)CGG>GGG	p.R18G
Pat_11	Post-Resistance	C3orf38	285237	37	3	88205268	88205268	Missense_Mutation	SNP	C	T	73	87	c.473C>T	c.(472-474)CCT>CTT	p.P158L
Pat_11	Post-Resistance	EPHA6	285220	37	3	96706810	96706810	Missense_Mutation	SNP	T	G	63	92	c.1087T>G	c.(1087-1089)TAT>GAT	p.Y363D
Pat_11	Post-Resistance	MORC1	27136	37	3	108813812	108813812	Missense_Mutation	SNP	G	A	58	88	c.527C>T	c.(526-528)CCA>CTA	p.P176L
Pat_11	Post-Resistance	ESYT3	83850	37	3	138183346	138183346	Missense_Mutation	SNP	G	A	71	168	c.1075G>A	c.(1075-1077)GAA>AAA	p.E359K
Pat_11	Post-Resistance	AGTR1	185	37	3	148458956	148458956	Missense_Mutation	SNP	G	A	119	254	c.134G>A	c.(133-135)GGA>GAA	p.G45E
Pat_11	Post-Resistance	CP	1356	37	3	148924061	148924061	Missense_Mutation	SNP	C	A	5	462	c.1102G>T	c.(1102-1104)GGG>TGG	p.G368W
Pat_11	Post-Resistance	CP	1356	37	3	148939500	148939500	Missense_Mutation	SNP	C	T	85	146	c.80G>A	c.(79-81)GGA>GAA	p.G27E
Pat_11	Post-Resistance	ZBBX	79740	37	3	167000053	167000053	Missense_Mutation	SNP	C	T	47	108	c.2110G>A	c.(2110-2112)GAA>AAA	p.E704K
Pat_11	Post-Resistance	ATP13A5	344905	37	3	193081090	193081090	Missense_Mutation	SNP	C	T	91	167	c.319G>A	c.(319-321)GAA>AAA	p.E107K
Pat_11	Post-Resistance	ATP13A3	79572	37	3	194175075	194175075	Missense_Mutation	SNP	C	A	5	225	c.677G>T	c.(676-678)TGG>TTG	p.W226L
Pat_11	Post-Resistance	MUC4	4585	37	3	195505772	195505772	Missense_Mutation	SNP	C	G	3	39	c.12295G>C	c.(12295-12297)GTC>CTC	p.V4099L
Pat_11	Post-Resistance	ZNF732	654254	37	4	265307	265307	Missense_Mutation	SNP	T	C	4	86	c.1336A>G	c.(1336-1338)AAA>GAA	p.K446E
Pat_11	Post-Resistance	ZNF721	170960	37	4	436992	436992	Missense_Mutation	SNP	G	C	48	116	c.1264C>G	c.(1264-1266)CGT>GGT	p.R422G
Pat_11	Post-Resistance	FAM193A	8603	37	4	2673929	2673929	Missense_Mutation	SNP	G	A	5	238	c.1288G>A	c.(1288-1290)GGA>AGA	p.G430R
Pat_11	Post-Resistance	SLIT2	9353	37	4	20530703	20530703	Missense_Mutation	SNP	C	T	124	199	c.1594C>T	c.(1594-1596)CCC>TCC	p.P532S
Pat_11	Post-Resistance	GPR125	166647	37	4	22425818	22425818	Missense_Mutation	SNP	G	A	31	67	c.1601C>T	c.(1600-1602)TCA>TTA	p.S534L
Pat_11	Post-Resistance	NSUN7	79730	37	4	40810375	40810375	Missense_Mutation	SNP	G	A	103	229	c.1576G>A	c.(1576-1578)GCC>ACC	p.A526T
Pat_11	Post-Resistance	NMU	10874	37	4	56496606	56496606	Missense_Mutation	SNP	C	T	113	168	c.134G>A	c.(133-135)GGA>GAA	p.G45E
Pat_11	Post-Resistance	UGT2B15	7366	37	4	69513083	69513083	Missense_Mutation	SNP	C	T	110	238	c.1332G>A	c.(1330-1332)ATG>ATA	p.M444I
Pat_11	Post-Resistance	UGT2B10	7365	37	4	69693137	69693137	Missense_Mutation	SNP	C	T	222	404	c.1178C>T	c.(1177-1179)CCA>CTA	p.P393L
Pat_11	Post-Resistance	RUFY3	22902	37	4	71629283	71629283	Missense_Mutation	SNP	C	T	51	105	c.367C>T	c.(367-369)CTC>TTC	p.L123F
Pat_11	Post-Resistance	ALB	213	37	4	74275124	74275124	Missense_Mutation	SNP	C	T	107	194	c.535C>T	c.(535-537)CTT>TTT	p.L179F
Pat_11	Post-Resistance	USO1	8615	37	4	76714871	76714871	Missense_Mutation	SNP	G	C	3	51	c.1269G>C	c.(1267-1269)CAG>CAC	p.Q423H

Pat_11	Post-Resistance	CCDC158	339965	37	4	77278541	77278541	Missense_Mutation	SNP	C	T	41	113	c.2159G>A	c.(2158-2160)GGA>GAA	p.G720E
Pat_11	Post-Resistance	C4orf37	285555	37	4	99027141	99027141	Missense_Mutation	SNP	C	T	22	61	c.575G>A	c.(574-576)CGA>CAA	p.R192Q
Pat_11	Post-Resistance	AGXT2L1	64850	37	4	109670491	109670491	Missense_Mutation	SNP	C	T	114	236	c.830G>A	c.(829-831)GGA>GAA	p.G277E
Pat_11	Post-Resistance	NDST4	64579	37	4	115769417	115769417	Missense_Mutation	SNP	C	T	95	139	c.1894G>A	c.(1894-1896)GAA>AAA	p.E632K
Pat_11	Post-Resistance	FAT4	79633	37	4	126241411	126241411	Missense_Mutation	SNP	C	T	137	266	c.3845C>T	c.(3844-3846)TCC>TTC	p.S1282F
Pat_11	Post-Resistance	FAT4	79633	37	4	126367659	126367659	Missense_Mutation	SNP	C	T	198	344	c.7405C>T	c.(7405-7407)CAC>TAC	p.H2469Y
Pat_11	Post-Resistance	FAT4	79633	37	4	126411926	126411926	Missense_Mutation	SNP	C	T	60	121	c.13949C>T	c.(13948-13950)TCA>TTA	p.S4650L
Pat_11	Post-Resistance	TLL1	7092	37	4	167012495	167012495	Splice_Site	SNP	T	C	24	82	c.2656_splice	c.e19+2	p.E886_splice
Pat_11	Post-Resistance	ODZ3	55714	37	4	183635341	183635341	Missense_Mutation	SNP	G	A	4	153	c.2323G>A	c.(2323-2325)GTA>ATA	p.V775I
Pat_11	Post-Resistance	CYP4V2	285440	37	4	187115720	187115720	Missense_Mutation	SNP	T	C	155	293	c.281T>C	c.(280-282)GTC>GCC	p.V94A
Pat_11	Post-Resistance	FAT1	2195	37	4	187539729	187539729	Missense_Mutation	SNP	A	T	69	97	c.8011T>A	c.(8011-8013)TTC>ATC	p.F2671I
Pat_11	Post-Resistance	CMYA5	202333	37	5	79030152	79030152	Missense_Mutation	SNP	C	T	91	57	c.5564C>T	c.(5563-5565)TCA>TTA	p.S1855L
Pat_11	Post-Resistance	SLC22A4	6583	37	5	131630533	131630533	Missense_Mutation	SNP	G	A	3	32	c.224G>A	c.(223-225)CGC>CAC	p.R75H
Pat_11	Post-Resistance	PCDHA4	56144	37	5	140188055	140188055	Missense_Mutation	SNP	G	A	308	170	c.1283G>A	c.(1282-1284)CGA>CAA	p.R428Q
Pat_11	Post-Resistance	PCDHA13	56136	37	5	140264174	140264174	Missense_Mutation	SNP	C	T	53	27	c.2321C>T	c.(2320-2322)CCC>CTC	p.P774L
Pat_11	Post-Resistance	PCDHB10	56126	37	5	140573462	140573462	Missense_Mutation	SNP	A	C	195	139	c.1337A>C	c.(1336-1338)GAC>GCC	p.D446A
Pat_11	Post-Resistance	ARAP3	64411	37	5	141053295	141053295	Missense_Mutation	SNP	G	A	4	274	c.779C>T	c.(778-780)TCG>TTG	p.S260L
Pat_11	Post-Resistance	CCDC69	26112	37	5	150581166	150581166	Missense_Mutation	SNP	C	T	84	64	c.208G>A	c.(208-210)GAA>AAA	p.E70K
Pat_11	Post-Resistance	C5orf25	375484	37	5	175740719	175740719	Missense_Mutation	SNP	T	C	5	583	c.1703T>C	c.(1702-1704)CTT>CCT	p.L568P
Pat_11	Post-Resistance	RREB1	6239	37	6	7231562	7231562	Missense_Mutation	SNP	C	T	131	237	c.3230C>T	c.(3229-3231)TCG>TTG	p.S1077L
Pat_11	Post-Resistance	OR2J2	26707	37	6	29142121	29142122	Nonsense_Mutation	DNP	AA	TG	174	249	c.709_710AA>TG	c.(709-711)AAA>TGA	p.K237*
Pat_11	Post-Resistance	VARS	7407	37	6	31753059	31753060	Missense_Mutation	DNP	GG	AA	75	139	.1310_1311CC>T	c.(1309-1311)TCC>TTT	p.S437F
Pat_11	Post-Resistance	CYP39A1	51302	37	6	46609950	46609950	Missense_Mutation	SNP	G	A	70	118	c.263C>T	c.(262-264)TCC>TTC	p.S88F
Pat_11	Post-Resistance	GPR111	222611	37	6	47649202	47649202	Missense_Mutation	SNP	G	A	166	252	c.907G>A	c.(907-909)GGA>AGA	p.G303R
Pat_11	Post-Resistance	TFAP2B	7021	37	6	50796357	50796357	Missense_Mutation	SNP	G	A	5	490	c.566G>A	c.(565-567)GGC>GAC	p.G189D
Pat_11	Post-Resistance	KHDRBS2	202559	37	6	62604676	62604676	Missense_Mutation	SNP	C	T	41	53	c.674G>A	c.(673-675)GGA>GAA	p.G225E
Pat_11	Post-Resistance	FAM135A	57579	37	6	71235250	71235250	Missense_Mutation	SNP	T	G	67	125	c.2463T>G	c.(2461-2463)AAT>AAG	p.N821K
Pat_11	Post-Resistance	COL12A1	1303	37	6	75812336	75812336	Missense_Mutation	SNP	C	T	78	112	c.8392G>A	c.(8392-8394)GGA>AGA	p.G2798R
Pat_11	Post-Resistance	ROS1	6098	37	6	117746814	117746814	Missense_Mutation	SNP	C	A	165	314	c.6G>T	c.(4-6)AAG>AAT	p.K2N
Pat_11	Post-Resistance	THEMIS	387357	37	6	128134491	128134491	Missense_Mutation	SNP	C	T	107	191	c.1295G>A	c.(1294-1296)GGA>GAA	p.G432E
Pat_11	Post-Resistance	GPR126	57211	37	6	142718806	142718806	Missense_Mutation	SNP	G	A	50	98	c.1481G>A	c.(1480-1482)GGA>GAA	p.G494E
Pat_11	Post-Resistance	TIAM2	26230	37	6	155577851	155577851	Missense_Mutation	SNP	C	A	4	286	c.4702C>A	c.(4702-4704)CTG>ATG	p.L1568M
Pat_11	Post-Resistance	MLLT4	4301	37	6	168303044	168303044	Missense_Mutation	SNP	G	A	157	312	c.1625G>A	c.(1624-1626)GGG>GAG	p.G542E
Pat_11	Post-Resistance	MICALL2	79778	37	7	1482008	1482008	Missense_Mutation	SNP	G	A	160	510	c.1531C>T	c.(1531-1533)CCT>TCT	p.P511S
Pat_11	Post-Resistance	ZMIZ2	83637	37	7	44805829	44805829	Missense_Mutation	SNP	C	T	202	157	c.2309C>T	c.(2308-2310)ACC>ATC	p.T770I
Pat_11	Post-Resistance	PURB	5814	37	7	44924053	44924053	Missense_Mutation	SNP	C	T	7	759	c.895G>A	c.(895-897)GGC>AGC	p.G299S
Pat_11	Post-Resistance	ABCA13	154664	37	7	48563857	48563858	Missense_Mutation	DNP	CT	TC	29	79	14065_14066CT>	c.(14065-14067)CTC>TCC	p.L4689S
Pat_11	Post-Resistance	PHKG1	5260	37	7	56151087	56151087	Missense_Mutation	SNP	A	G	187	152	c.431T>C	c.(430-432)CTC>CCC	p.L144P
Pat_11	Post-Resistance	CLIP2	7461	37	7	73770864	73770864	Missense_Mutation	SNP	G	A	4	312	c.928G>A	c.(928-930)GCA>ACA	p.A310T
Pat_11	Post-Resistance	PCLO	27445	37	7	82508726	82508726	Missense_Mutation	SNP	A	C	31	115	c.13581T>G	.(13579-13581)AGT>AGG	p.S4527R
Pat_11	Post-Resistance	CROT	54677	37	7	87005238	87005238	Missense_Mutation	SNP	G	A	5	390	c.845G>A	c.(844-846)AGT>AAT	p.S282N
Pat_11	Post-Resistance	C7orf51	222950	37	7	100086437	100086437	Missense_Mutation	SNP	G	A	146	114	c.1093G>A	c.(1093-1095)GAG>AAG	p.E365K
Pat_11	Post-Resistance	MUC17	140453	37	7	100681244	100681244	Missense_Mutation	SNP	A	G	9	936	c.6547A>G	c.(6547-6549)ACA>GCA	p.T2183A
Pat_11	Post-Resistance	MET	4233	37	7	116435940	116435940	Splice_Site	SNP	G	A	222	205	c.3936_splice	c.e21-1	p.L1312_splice
Pat_11	Post-Resistance	GRM8	2918	37	7	126173209	126173209	Missense_Mutation	SNP	C	T	62	211	c.2227G>A	c.(2227-2229)GAC>AAC	p.D743N
Pat_11	Post-Resistance	AKR1B10	57016	37	7	134216768	134216768	Missense_Mutation	SNP	G	A	127	673	c.343G>A	c.(343-345)GGA>AGA	p.G115R
Pat_11	Post-Resistance	ARHGEF5	7984	37	7	144077039	144077039	Missense_Mutation	SNP	C	T	148	744	c.4684C>T	c.(4684-4686)CCT>TCT	p.P1562S

Pat_11	Post-Resistance	GIMAP6	474344	37	7	150325195	150325195	Missense_Mutation	SNP	C	T	463	262	c.491G>A	c.(490-492)CGG>CAG	p.R164Q
Pat_11	Post-Resistance	C8orf80	389643	37	8	27884505	27884505	Missense_Mutation	SNP	C	T	222	401	c.2219G>A	c.(2218-2220)GGG>GAG	p.G740E
Pat_11	Post-Resistance	RP1	6101	37	8	55540286	55540286	Missense_Mutation	SNP	C	T	228	369	c.3844C>T	c.(3844-3846)CCT>TCT	p.P1282S
Pat_11	Post-Resistance	GRHL2	79977	37	8	102555585	102555585	Missense_Mutation	SNP	C	T	5	424	c.137C>T	c.(136-138)GCA>GTA	p.A46V
Pat_11	Post-Resistance	ODF1	4956	37	8	103564056	103564056	Missense_Mutation	SNP	G	T	7	817	c.101G>T	c.(100-102)CGG>CTG	p.R34L
Pat_11	Post-Resistance	TRHR	7201	37	8	110100070	110100070	Missense_Mutation	SNP	A	T	156	217	c.329A>T	c.(328-330)AAT>ATT	p.N110I
Pat_11	Post-Resistance	MTBP	27085	37	8	121518998	121518998	Missense_Mutation	SNP	C	T	104	167	c.1780C>T	c.(1780-1782)CCT>TCT	p.P594S
Pat_11	Post-Resistance	SQLE	6713	37	8	126033112	126033112	Missense_Mutation	SNP	G	A	31	80	c.1531G>A	c.(1531-1533)GTA>ATA	p.V511I
Pat_11	Post-Resistance	IFNA8	3445	37	9	21409416	21409416	Missense_Mutation	SNP	C	T	146	104	c.241C>T	c.(241-243)CAT>TAT	p.H81Y
Pat_11	Post-Resistance	GNE	10020	37	9	36229078	36229078	Missense_Mutation	SNP	G	A	4	313	c.1010C>T	c.(1009-1011)GCT>GTT	p.A337V
Pat_11	Post-Resistance	ZNF645	158506	37	X	22291533	22291533	Missense_Mutation	SNP	G	A	96	28	c.425G>A	c.(424-426)CGA>CAA	p.R142Q
Pat_11	Post-Resistance	KIAA2022	340533	37	X	73960071	73960071	Missense_Mutation	SNP	C	T	117	52	c.4321G>A	c.(4321-4323)GGA>AGA	p.G1441R
Pat_11	Post-Resistance	KLHL13	90293	37	X	117043419	117043419	Missense_Mutation	SNP	C	T	88	30	c.1211G>A	c.(1210-1212)GGA>GAA	p.G404E
Pat_11	Post-Resistance	OCRL	4952	37	X	128691316	128691316	Missense_Mutation	SNP	C	T	87	38	c.253C>T	c.(253-255)CGG>TGG	p.R85W
Pat_11	Post-Resistance	PCDH11Y	83259	37	Y	4925057	4925057	Missense_Mutation	SNP	G	A	78	26	c.193G>A	c.(193-195)GAA>AAA	p.E65K
Pat_16	Post-Resistance	KIAA1751	85452	37	1	1920014	1920014	Missense_Mutation	SNP	C	A	37	87	c.233G>T	c.(232-234)CGG>CTG	p.R78L
Pat_16	Post-Resistance	GPR157	80045	37	1	9164611	9164611	Missense_Mutation	SNP	G	A	13	31	c.875C>T	c.(874-876)TCT>TTT	p.S292F
Pat_16	Post-Resistance	CLCNKA	1187	37	1	16358320	16358320	Missense_Mutation	SNP	C	T	109	74	c.1738C>T	c.(1738-1740)CCC>TCC	p.P580S
Pat_16	Post-Resistance	EIF4G3	8672	37	1	21183973	21183973	Missense_Mutation	SNP	C	T	6	534	c.3094G>A	c.(3094-3096)GAA>AAA	p.E1032K
Pat_16	Post-Resistance	NBPF3	84224	37	1	21797199	21797199	Missense_Mutation	SNP	G	A	74	84	c.418G>A	c.(418-420)GAG>AAG	p.E140K
Pat_16	Post-Resistance	RHD	6007	37	1	25611201	25611201	Missense_Mutation	SNP	G	A	4	180	c.286G>A	c.(286-288)GGC>AGC	p.G96S
Pat_16	Post-Resistance	UBXN11	91544	37	1	26612001	26612001	Missense_Mutation	SNP	A	T	5	22	c.806T>A	c.(805-807)TTT>TAT	p.F269Y
Pat_16	Post-Resistance	ARID1A	8289	37	1	27107000	27107000	Missense_Mutation	SNP	C	T	45	132	c.6611C>T	c.(6610-6612)GCC>GTC	p.A2204V
Pat_16	Post-Resistance	HCRTR1	3061	37	1	32090687	32090687	Missense_Mutation	SNP	C	T	3	33	c.1055C>T	c.(1054-1056)GCT>GTT	p.A352V
Pat_16	Post-Resistance	ZSCAN20	7579	37	1	33945010	33945010	Missense_Mutation	SNP	C	T	51	37	c.121C>T	c.(121-123)CGT>TGT	p.R41C
Pat_16	Post-Resistance	CSMD2	114784	37	1	33992823	33992823	Missense_Mutation	SNP	G	A	4	243	c.9775C>T	c.(9775-9777)CGG>TGG	p.R3259W
Pat_16	Post-Resistance	CSMD2	114784	37	1	34015872	34015872	Missense_Mutation	SNP	C	T	4	220	c.8390G>A	c.(8389-8391)CGG>CAG	p.R2797Q
Pat_16	Post-Resistance	CSMD2	114784	37	1	34285316	34285316	Missense_Mutation	SNP	C	T	8	57	c.1202G>A	c.(1201-1203)CGA>CAA	p.R401Q
Pat_16	Post-Resistance	C1orf216	127703	37	1	36181844	36181844	Missense_Mutation	SNP	G	A	4	124	c.79C>T	c.(79-81)CTC>TTC	p.L27F
Pat_16	Post-Resistance	PABPC4	8761	37	1	40034556	40034556	Missense_Mutation	SNP	C	T	4	276	c.794G>A	c.(793-795)CGT>CAT	p.R265H
Pat_16	Post-Resistance	ZNF642	339559	37	1	40954845	40954845	Missense_Mutation	SNP	G	A	184	132	c.305G>A	c.(304-306)CGA>CAA	p.R102Q
Pat_16	Post-Resistance	MUTYH	4595	37	1	45798966	45798966	Missense_Mutation	SNP	C	T	4	102	c.370G>A	c.(370-372)GCA>ACA	p.A124T
Pat_16	Post-Resistance	TOE1	114034	37	1	45808107	45808107	Nonsense_Mutation	SNP	C	T	4	220	c.544C>T	c.(544-546)CGA>TGA	p.R182*
Pat_16	Post-Resistance	ZFYVE9	9372	37	1	52798527	52798527	Missense_Mutation	SNP	G	A	4	157	c.3526G>A	c.(3526-3528)GTA>ATA	p.V1176I
Pat_16	Post-Resistance	C1orf163	65260	37	1	53153690	53153690	Missense_Mutation	SNP	T	C	4	301	c.398A>G	c.(397-399)AAG>AGG	p.K133R
Pat_16	Post-Resistance	GLIS1	148979	37	1	54060157	54060157	Missense_Mutation	SNP	C	T	3	87	c.419G>A	c.(418-420)CGG>CAG	p.R140Q
Pat_16	Post-Resistance	C8B	732	37	1	57422517	57422517	Missense_Mutation	SNP	C	T	212	161	c.316G>A	c.(316-318)GAA>AAA	p.E106K
Pat_16	Post-Resistance	DNAJC6	9829	37	1	65858497	65858497	Missense_Mutation	SNP	C	T	4	218	c.1681C>T	c.(1681-1683)CGC>TGC	p.R561C
Pat_16	Post-Resistance	LRRC7	57554	37	1	70493918	70493918	Missense_Mutation	SNP	C	T	82	78	c.1745C>T	c.(1744-1746)TCT>TTT	p.S582F
Pat_16	Post-Resistance	C1orf173	127254	37	1	75065480	75065480	Missense_Mutation	SNP	T	G	127	68	c.1625A>C	c.(1624-1626)AAA>ACA	p.K542T
Pat_16	Post-Resistance	CLCA1	1179	37	1	86951080	86951080	Missense_Mutation	SNP	A	T	47	79	c.790A>T	c.(790-792)AAT>TAT	p.N264Y
Pat_16	Post-Resistance	SH3GLB1	51100	37	1	87208874	87208874	Nonsense_Mutation	SNP	C	T	172	118	c.1054C>T	c.(1054-1056)CAG>TAG	p.Q352*
Pat_16	Post-Resistance	ARHGAP29	9411	37	1	94654489	94654489	Missense_Mutation	SNP	A	T	41	108	c.1585T>A	c.(1585-1587)TTT>ATT	p.F529I
Pat_16	Post-Resistance	CD53	963	37	1	111434995	111434995	Missense_Mutation	SNP	G	A	29	87	c.92G>A	c.(91-93)GGG>GAG	p.G31E
Pat_16	Post-Resistance	SYCP1	6847	37	1	115469144	115469144	Missense_Mutation	SNP	G	A	8	30	c.1886G>A	c.(1885-1887)GGT>GAT	p.G629D
Pat_16	Post-Resistance	CASQ2	845	37	1	116244011	116244011	Missense_Mutation	SNP	C	T	112	98	c.1051G>A	c.(1051-1053)GAT>AAT	p.D351N
Pat_16	Post-Resistance	PDE4DIP	9659	37	1	144881505	144881505	Nonsense_Mutation	SNP	G	A	137	323	c.3691C>T	c.(3691-3693)CAG>TAG	p.Q1231*

Pat_16	Post-Resistance	PDE4DIP	9659	37	1	145015949	145015949	Missense_Mutation	SNP	C	T	53	629	c.139G>A	c.(139-141)GAA>AAA	p.E47K
Pat_16	Post-Resistance	NBPF10	100132406	37	1	145323695	145323695	Missense_Mutation	SNP	C	T	10	666	c.3757C>T	c.(3757-3759)CCA>TCA	p.P1253S
Pat_16	Post-Resistance	NBPF10	100132406	37	1	145360560	145360560	Missense_Mutation	SNP	G	A	5	244	c.9410G>A	c.(9409-9411)AGC>AAC	p.S3137N
Pat_16	Post-Resistance	LASS2	29956	37	1	150939253	150939253	Missense_Mutation	SNP	C	T	4	175	c.827G>A	c.(826-828)CGA>CAA	p.R276Q
Pat_16	Post-Resistance	KPRP	448834	37	1	152733052	152733052	Missense_Mutation	SNP	T	A	42	96	c.988T>A	c.(988-990)TCC>ACC	p.S330T
Pat_16	Post-Resistance	S100A5	6276	37	1	153509861	153509861	Missense_Mutation	SNP	C	T	4	252	c.244G>A	c.(244-246)GAC>AAC	p.D82N
Pat_16	Post-Resistance	HCN3	57657	37	1	155254477	155254477	Missense_Mutation	SNP	G	A	4	269	c.1018G>A	c.(1018-1020)GCC>ACC	p.A340T
Pat_16	Post-Resistance	FCRL3	115352	37	1	157666963	157666963	Missense_Mutation	SNP	T	G	59	16	c.811A>C	c.(811-813)AAA>CAA	p.K271Q
Pat_16	Post-Resistance	ATP1A4	480	37	1	160141383	160141383	Missense_Mutation	SNP	T	A	171	113	c.1690T>A	c.(1690-1692)TTC>ATC	p.F564I
Pat_16	Post-Resistance	CD244	51744	37	1	160806026	160806026	Missense_Mutation	SNP	G	A	16	81	c.868C>T	c.(868-870)CCT>TCT	p.P290S
Pat_16	Post-Resistance	ARHGAP30	257106	37	1	161018907	161018907	Missense_Mutation	SNP	C	T	220	208	c.1904G>A	c.(1903-1905)GGA>GAA	p.G635E
Pat_16	Post-Resistance	NIT1	4817	37	1	161090340	161090340	Missense_Mutation	SNP	G	A	4	215	c.769G>A	c.(769-771)GCA>ACA	p.A257T
Pat_16	Post-Resistance	C1orf110	339512	37	1	162829392	162829392	Missense_Mutation	SNP	A	T	17	53	c.45T>A	c.(43-45)GAT>GAA	p.D15E
Pat_16	Post-Resistance	UCK2	7371	37	1	165865440	165865440	Missense_Mutation	SNP	G	A	7	551	c.370G>A	c.(370-372)GTT>ATT	p.V124I
Pat_16	Post-Resistance	MPZL1	9019	37	1	167757123	167757123	Missense_Mutation	SNP	G	A	175	131	c.775G>A	c.(775-777)GAG>AAG	p.E259K
Pat_16	Post-Resistance	SELL	6402	37	1	169670801	169670801	Missense_Mutation	SNP	C	A	4	12	c.981G>T	c.(979-981)AAG>AAT	p.K327N
Pat_16	Post-Resistance	SCYL3	57147	37	1	169823860	169823860	Missense_Mutation	SNP	C	T	4	260	c.1720G>A	c.(1720-1722)GAG>AAG	p.E574K
Pat_16	Post-Resistance	FMO1	2326	37	1	171254520	171254520	Missense_Mutation	SNP	G	A	46	39	c.1436G>A	c.(1435-1437)GGA>GAA	p.G479E
Pat_16	Post-Resistance	SLC9A11	284525	37	1	173490472	173490472	Missense_Mutation	SNP	C	T	25	93	c.2707G>A	c.(2707-2709)GGA>AGA	p.G903R
Pat_16	Post-Resistance	FAM5B	57795	37	1	177249565	177249565	Nonsense_Mutation	SNP	G	A	44	164	c.1253G>A	c.(1252-1254)TGG>TAG	p.W418*
Pat_16	Post-Resistance	C1orf49	84066	37	1	178489831	178489831	Missense_Mutation	SNP	A	T	36	20	c.365A>T	c.(364-366)GAG>GTG	p.E122V
Pat_16	Post-Resistance	C1orf125	126859	37	1	179414126	179414126	Missense_Mutation	SNP	G	A	30	38	c.1585G>A	c.(1585-1587)GAG>AAG	p.E529K
Pat_16	Post-Resistance	RGS16	6004	37	1	182572373	182572373	Missense_Mutation	SNP	C	T	6	635	c.146G>A	c.(145-147)AGC>AAC	p.S49N
Pat_16	Post-Resistance	HMCN1	83872	37	1	186077692	186077692	Missense_Mutation	SNP	C	T	63	62	c.10952C>T	c.(10951-10953)CCT>CTT	p.P3651L
Pat_16	Post-Resistance	CFH	3075	37	1	196684756	196684756	Missense_Mutation	SNP	G	A	152	110	c.1553G>A	c.(1552-1554)AGA>AAA	p.R518K
Pat_16	Post-Resistance	CFHR2	3080	37	1	196918654	196918654	Missense_Mutation	SNP	C	T	9	40	c.128C>T	c.(127-129)TCC>TTC	p.S43F
Pat_16	Post-Resistance	CFHR5	81494	37	1	196971612	196971612	Missense_Mutation	SNP	A	G	20	59	c.1148A>G	c.(1147-1149)GAA>GGA	p.E383G
Pat_16	Post-Resistance	CRB1	23418	37	1	197446813	197446813	Missense_Mutation	SNP	C	T	27	119	c.4025C>T	c.(4024-4026)TCC>TTC	p.S1342F
Pat_16	Post-Resistance	PIK3C2B	5287	37	1	204400899	204400899	Missense_Mutation	SNP	C	T	7	613	c.4178G>A	c.(4177-4179)CGA>CAA	p.R1393Q
Pat_16	Post-Resistance	SLC41A1	254428	37	1	205779410	205779410	Missense_Mutation	SNP	G	A	4	232	c.160C>T	c.(160-162)CGG>TGG	p.R54W
Pat_16	Post-Resistance	LAMB3	3914	37	1	209801395	209801395	Missense_Mutation	SNP	G	A	3	58	c.1273C>T	c.(1273-1275)CCG>TCG	p.P425S
Pat_16	Post-Resistance	TMEM206	55248	37	1	212550929	212550929	Missense_Mutation	SNP	C	T	5	290	c.758G>A	c.(757-759)CGG>CAG	p.R253Q
Pat_16	Post-Resistance	SPATA17	128153	37	1	217947824	217947824	Missense_Mutation	SNP	C	T	18	58	c.668C>T	c.(667-669)GCC>GTC	p.A223V
Pat_16	Post-Resistance	NVL	4931	37	1	224495956	224495956	Missense_Mutation	SNP	G	A	28	86	c.352C>T	c.(352-354)CAC>TAC	p.H118Y
Pat_16	Post-Resistance	ZP4	57829	37	1	238048472	238048472	Missense_Mutation	SNP	C	T	44	49	c.1304G>A	c.(1303-1305)AGG>AAG	p.R435K
Pat_16	Post-Resistance	KIF26B	55083	37	1	245848720	245848720	Missense_Mutation	SNP	C	T	3	59	c.2435C>T	c.(2434-2436)TCG>TTG	p.S812L
Pat_16	Post-Resistance	CNST	163882	37	1	246784866	246784866	Missense_Mutation	SNP	C	T	177	154	c.515C>T	c.(514-516)TCT>TTT	p.S172F
Pat_16	Post-Resistance	AHCTF1	25909	37	1	247012951	247012951	Missense_Mutation	SNP	A	C	37	90	c.6357T>G	c.(6355-6357)TTT>TTG	p.F2119L
Pat_16	Post-Resistance	PFKP	5214	37	10	3162204	3162204	Missense_Mutation	SNP	G	A	4	290	c.1651G>A	c.(1651-1653)GGG>AGG	p.G551R
Pat_16	Post-Resistance	ITIH2	3698	37	10	7773808	7773808	Missense_Mutation	SNP	G	A	4	257	c.1496G>A	c.(1495-1497)CGG>CAG	p.R499Q
Pat_16	Post-Resistance	FAM171A1	221061	37	10	15255386	15255386	Missense_Mutation	SNP	C	T	76	109	c.2201G>A	c.(2200-2202)GGA>GAA	p.G734E
Pat_16	Post-Resistance	CUBN	8029	37	10	16932454	16932454	Missense_Mutation	SNP	C	T	4	137	c.8671G>A	c.(8671-8673)GTT>ATT	p.V2891I
Pat_16	Post-Resistance	CUBN	8029	37	10	16967398	16967398	Missense_Mutation	SNP	G	A	4	90	c.6488C>T	c.(6487-6489)TCT>TTT	p.S2163F
Pat_16	Post-Resistance	PTCHD3	374308	37	10	27702480	27702480	Missense_Mutation	SNP	C	T	3	50	c.700G>A	c.(700-702)GGC>AGC	p.G234S
Pat_16	Post-Resistance	ANKRD30A	91074	37	10	37430661	37430661	Missense_Mutation	SNP	G	A	49	15	c.668G>A	c.(667-669)GGA>GAA	p.G223E
Pat_16	Post-Resistance	ANKRD30A	91074	37	10	37430754	37430754	Missense_Mutation	SNP	T	C	5	85	c.761T>C	c.(760-762)GTG>GCG	p.V254A
Pat_16	Post-Resistance	PRKG1	5592	37	10	54048576	54048576	Missense_Mutation	SNP	A	C	24	6	c.1755A>C	c.(1753-1755)AAA>AAC	p.K585N

Pat_16	Post-Resistance	BICC1	80114	37	10	60573673	60573673	Missense_Mutation	SNP	T	G	143	34	c.2460T>G	c.(2458-2460)AAT>AAG	p.N820K
Pat_16	Post-Resistance	MYPN	84665	37	10	69881782	69881782	Missense_Mutation	SNP	G	A	41	12	c.587G>A	c.(586-588)AGC>AAC	p.S196N
Pat_16	Post-Resistance	DDX21	9188	37	10	70728771	70728771	Missense_Mutation	SNP	C	T	4	150	c.1130C>T	c.(1129-1131)ACT>ATT	p.T377I
Pat_16	Post-Resistance	CDH23	64072	37	10	73466770	73466770	Missense_Mutation	SNP	G	A	3	26	c.3070G>A	c.(3070-3072)GTG>ATG	p.V1024M
Pat_16	Post-Resistance	STAMBPL1	57559	37	10	90672958	90672958	Missense_Mutation	SNP	C	T	4	121	c.521C>T	c.(520-522)TCG>TTG	p.S174L
Pat_16	Post-Resistance	CYP2C8	1558	37	10	96824645	96824645	Missense_Mutation	SNP	T	G	183	24	c.554A>C	c.(553-555)AAA>ACA	p.K185T
Pat_16	Post-Resistance	PIK3AP1	118788	37	10	98416562	98416562	Missense_Mutation	SNP	C	T	4	323	c.560G>A	c.(559-561)CGC>CAC	p.R187H
Pat_16	Post-Resistance	SLIT1	6585	37	10	98778837	98778837	Missense_Mutation	SNP	T	G	120	23	c.2774A>C	c.(2773-2775)AAG>ACG	p.K925T
Pat_16	Post-Resistance	SEMA4G	57715	37	10	102743232	102743232	Missense_Mutation	SNP	G	A	32	32	c.1876G>A	c.(1876-1878)GAT>AAT	p.D626N
Pat_16	Post-Resistance	POLL	27343	37	10	103342563	103342563	Missense_Mutation	SNP	A	C	292	29	c.1151T>G	c.(1150-1152)CTG>CGG	p.L384R
Pat_16	Post-Resistance	PDCD11	22984	37	10	105194638	105194638	Missense_Mutation	SNP	C	T	17	29	c.3751C>T	c.(3751-3753)CCC>TCC	p.P1251S
Pat_16	Post-Resistance	OBFC1	79991	37	10	105659885	105659885	Missense_Mutation	SNP	G	A	5	198	c.392C>T	c.(391-393)ACG>ATG	p.T131M
Pat_16	Post-Resistance	TACC2	10579	37	10	123845785	123845785	Missense_Mutation	SNP	C	T	178	20	c.3770C>T	c.(3769-3771)TCC>TTC	p.S1257F
Pat_16	Post-Resistance	CHST15	51363	37	10	125801958	125801958	Missense_Mutation	SNP	C	T	3	64	c.892G>A	c.(892-894)GTC>ATC	p.V298I
Pat_16	Post-Resistance	LRRC56	115399	37	11	554058	554058	Missense_Mutation	SNP	G	A	154	20	c.1411G>A	c.(1411-1413)GAC>AAC	p.D471N
Pat_16	Post-Resistance	EPS8L2	64787	37	11	726677	726677	Missense_Mutation	SNP	G	A	4	5	c.1993G>A	c.(1993-1995)GAG>AAG	p.E665K
Pat_16	Post-Resistance	MUC2	4583	37	11	1101129	1101129	Missense_Mutation	SNP	G	A	114	115	c.14614G>A	c.(14614-14616)GAG>AAG	p.E4872K
Pat_16	Post-Resistance	MUC5B	727897	37	11	1256566	1256566	Missense_Mutation	SNP	T	G	52	53	c.4780T>G	c.(4780-4782)TTC>GTC	p.F1594V
Pat_16	Post-Resistance	SLC22A18	5002	37	11	2929526	2929526	Missense_Mutation	SNP	G	A	4	114	c.208G>A	c.(208-210)GTG>ATG	p.V70M
Pat_16	Post-Resistance	OR51B2	79345	37	11	5345040	5345040	Missense_Mutation	SNP	G	A	47	4	c.488C>T	c.(487-489)TCA>TTA	p.S163L
Pat_16	Post-Resistance	OR5P2	120065	37	11	7817971	7817971	Missense_Mutation	SNP	A	C	54	38	c.519T>G	c.(517-519)TTT>TTG	p.F173L
Pat_16	Post-Resistance	PARVA	55742	37	11	12525959	12525959	Nonsense_Mutation	SNP	C	T	39	61	c.640C>T	c.(640-642)CAA>TAA	p.Q214*
Pat_16	Post-Resistance	PTPN5	84867	37	11	18764019	18764019	Missense_Mutation	SNP	G	A	4	98	c.515C>T	c.(514-516)CCA>CTA	p.P172L
Pat_16	Post-Resistance	KIF18A	81930	37	11	28045369	28045369	Missense_Mutation	SNP	C	G	3	122	c.2533G>C	c.(2533-2535)GAC>CAC	p.D845H
Pat_16	Post-Resistance	EXT2	2132	37	11	44228348	44228348	Missense_Mutation	SNP	C	T	41	5	c.1501C>T	c.(1501-1503)CTC>TTC	p.L501F
Pat_16	Post-Resistance	AMBRA1	55626	37	11	46567211	46567211	Nonsense_Mutation	SNP	C	T	231	37	c.494G>A	c.(493-495)TGG>TAG	p.W165*
Pat_16	Post-Resistance	ARHGAP1	392	37	11	46702064	46702065	Nonsense_Mutation	DNP	CC	AA	92	5	c.792_793GG>TT	790-795)AGGGAG>AGTT	.264_265RE>
Pat_16	Post-Resistance	F2	2147	37	11	46747480	46747480	Missense_Mutation	SNP	G	A	131	114	c.631G>A	c.(631-633)GAG>AAG	p.E211K
Pat_16	Post-Resistance	LRP4	4038	37	11	46894655	46894655	Missense_Mutation	SNP	G	A	4	258	c.4579C>T	c.(4579-4581)CGC>TGC	p.R1527C
Pat_16	Post-Resistance	DDB2	1643	37	11	47256351	47256351	Missense_Mutation	SNP	C	T	67	19	c.746C>T	c.(745-747)GCC>GTC	p.A249V
Pat_16	Post-Resistance	OR5M9	390162	37	11	56230826	56230826	Missense_Mutation	SNP	G	A	28	6	c.52C>T	c.(52-54)CGT>TGT	p.R18C
Pat_16	Post-Resistance	OR5B17	219965	37	11	58126355	58126355	Missense_Mutation	SNP	T	C	69	7	c.188A>G	c.(187-189)AAC>AGC	p.N63S
Pat_16	Post-Resistance	ZFP91	80829	37	11	58380251	58380251	Nonsense_Mutation	SNP	C	T	85	21	c.925C>T	c.(925-927)CAG>TAG	p.Q309*
Pat_16	Post-Resistance	TCN1	6947	37	11	59620691	59620691	Missense_Mutation	SNP	C	T	5	509	c.1225G>A	c.(1225-1227)GAA>AAA	p.E409K
Pat_16	Post-Resistance	OTUB1	55611	37	11	63764691	63764691	Missense_Mutation	SNP	G	A	4	275	c.593G>A	c.(592-594)CGG>CAG	p.R198Q
Pat_16	Post-Resistance	PLCB3	5331	37	11	64023930	64023930	Missense_Mutation	SNP	G	A	5	434	c.781G>A	c.(781-783)GAA>AAA	p.E261K
Pat_16	Post-Resistance	SPTBN2	6712	37	11	66466905	66466905	Missense_Mutation	SNP	G	A	53	73	c.3748C>T	c.(3748-3750)CGG>TGG	p.R1250W
Pat_16	Post-Resistance	LRP5	4041	37	11	68171099	68171099	Missense_Mutation	SNP	G	A	4	191	c.1733G>A	c.(1732-1734)CGG>CAG	p.R578Q
Pat_16	Post-Resistance	ARHGEF17	9828	37	11	73073492	73073492	Missense_Mutation	SNP	C	T	17	4	c.4709C>T	c.(4708-4710)TCG>TTG	p.S1570L
Pat_16	Post-Resistance	DNAJB13	374407	37	11	73677211	73677211	Missense_Mutation	SNP	C	T	52	4	c.521C>T	c.(520-522)ACC>ATC	p.T174I
Pat_16	Post-Resistance	DLG2	1740	37	11	83252744	83252744	Missense_Mutation	SNP	C	T	4	175	c.1783G>A	c.(1783-1785)GTC>ATC	p.V595I
Pat_16	Post-Resistance	HEPHL1	341208	37	11	93754593	93754593	Missense_Mutation	SNP	G	A	79	129	c.59G>A	c.(58-60)GGG>GAG	p.G20E
Pat_16	Post-Resistance	GRIA4	2893	37	11	105850461	105850461	Missense_Mutation	SNP	C	T	34	6	c.2704C>T	c.(2704-2706)CCA>TCA	p.P902S
Pat_16	Post-Resistance	DSCAML1	57453	37	11	117352818	117352819	Missense_Mutation	DNP	CC	TT	57	9	.2598_2599GG>A	596-2601)AAGGAG>AAA	p.E867K
Pat_16	Post-Resistance	FOXRED1	55572	37	11	126142921	126142921	Missense_Mutation	SNP	C	T	4	212	c.364C>T	c.(364-366)CCT>TCT	p.P122S
Pat_16	Post-Resistance	FOXRED1	55572	37	11	126145996	126145996	Missense_Mutation	SNP	G	A	4	102	c.853G>A	c.(853-855)GCC>ACC	p.A285T
Pat_16	Post-Resistance	LTBR	4055	37	12	6495261	6495261	Missense_Mutation	SNP	G	A	6	629	c.502G>A	c.(502-504)GTC>ATC	p.V168I

Pat_16	Post-Resistance	AICDA	57379	37	12	8759595	8759595	Missense_Mutation	SNP	G	A	3	49	c.22C>T	c.(22-24)CGG>TGG	p.R8W
Pat_16	Post-Resistance	A2ML1	144568	37	12	8975263	8975263	Missense_Mutation	SNP	C	T	67	134	c.16C>T	c.(16-18)CTT>TTT	p.L6F
Pat_16	Post-Resistance	PRB3	5544	37	12	11420711	11420711	Missense_Mutation	SNP	G	A	5	164	c.472C>T	c.(472-474)CGT>TGT	p.R158C
Pat_16	Post-Resistance	GRIN2B	2904	37	12	13716732	13716732	Missense_Mutation	SNP	T	A	31	32	c.3440A>T	c.(3439-3441)GAG>GTG	p.E1147V
Pat_16	Post-Resistance	LRMP	4033	37	12	25260897	25260898	Missense_Mutation	DNP	AT	TA	45	145	.1403_1404AT>T	c.(1402-1404)GAT>GTA	p.D468V
Pat_16	Post-Resistance	PRKAG1	5571	37	12	49396783	49396784	Nonsense_Mutation	DNP	GG	AA	50	132	c.894_895CC>TT	892-897)CACCGA>CATT	p.R299*
Pat_16	Post-Resistance	KRT4	3851	37	12	53202523	53202523	Missense_Mutation	SNP	C	T	77	239	c.1168G>A	c.(1168-1170)GAG>AAG	p.E390K
Pat_16	Post-Resistance	KRT18	3875	37	12	53345602	53345602	Nonsense_Mutation	SNP	C	T	33	78	c.910C>T	c.(910-912)CAG>TAG	p.Q304*
Pat_16	Post-Resistance	TENC1	23371	37	12	53454201	53454201	Missense_Mutation	SNP	C	T	4	100	c.2630C>T	c.(2629-2631)CCG>CTG	p.P877L
Pat_16	Post-Resistance	AMHR2	269	37	12	53823344	53823344	Missense_Mutation	SNP	C	T	85	56	c.1075C>T	c.(1075-1077)CCT>TCT	p.P359S
Pat_16	Post-Resistance	GPR84	53831	37	12	54756926	54756926	Missense_Mutation	SNP	C	T	5	646	c.710G>A	c.(709-711)CGT>CAT	p.R237H
Pat_16	Post-Resistance	KIAA0748	9840	37	12	55368225	55368225	Missense_Mutation	SNP	G	T	10	8	c.122C>A	c.(121-123)CCA>CAA	p.P41Q
Pat_16	Post-Resistance	OR6C3	254786	37	12	55726023	55726023	Missense_Mutation	SNP	C	T	125	435	c.539C>T	c.(538-540)CCC>CTC	p.P180L
Pat_16	Post-Resistance	IKZF4	64375	37	12	56427051	56427051	Missense_Mutation	SNP	C	T	109	240	c.943C>T	c.(943-945)CGT>TGT	p.R315C
Pat_16	Post-Resistance	ZC3H10	84872	37	12	56514623	56514623	Missense_Mutation	SNP	C	T	4	309	c.277C>T	c.(277-279)CGT>TGT	p.R93C
Pat_16	Post-Resistance	PAN2	9924	37	12	56720105	56720105	Missense_Mutation	SNP	G	A	3	52	c.1351C>T	c.(1351-1353)CGC>TGC	p.R451C
Pat_16	Post-Resistance	HSD17B6	8630	37	12	57167787	57167787	Missense_Mutation	SNP	G	A	4	110	c.151G>A	c.(151-153)GCA>ACA	p.A51T
Pat_16	Post-Resistance	SLC16A7	9194	37	12	60173255	60173256	Missense_Mutation	DNP	GG	AA	27	97	.1232_1233GG>A	c.(1231-1233)GGG>GAA	p.G411E
Pat_16	Post-Resistance	C12orf56	115749	37	12	64746799	64746799	Missense_Mutation	SNP	C	T	109	82	c.290G>A	c.(289-291)AGA>AAA	p.R97K
Pat_16	Post-Resistance	SLC6A15	55117	37	12	85255686	85255686	Missense_Mutation	SNP	G	A	5	203	c.1918C>T	c.(1918-1920)CGT>TGT	p.R640C
Pat_16	Post-Resistance	RASSF9	9182	37	12	86198724	86198724	Missense_Mutation	SNP	T	A	187	110	c.1064A>T	c.(1063-1065)AAA>ATA	p.K355I
Pat_16	Post-Resistance	LUM	4060	37	12	91497952	91497952	Missense_Mutation	SNP	G	A	33	127	c.1007C>T	c.(1006-1008)ACT>ATT	p.T336I
Pat_16	Post-Resistance	HAL	3034	37	12	96370437	96370437	Missense_Mutation	SNP	G	A	4	149	c.1702C>T	c.(1702-1704)CGT>TGT	p.R568C
Pat_16	Post-Resistance	UTP20	27340	37	12	101760395	101760395	Missense_Mutation	SNP	C	T	6	434	c.6185C>T	c.(6184-6186)CCC>CTC	p.P2062L
Pat_16	Post-Resistance	TDG	6996	37	12	104378525	104378525	Splice_Site	SNP	A	C	3	65	c.793_splice	c.e8-2	p.L265_splice
Pat_16	Post-Resistance	FICD	11153	37	12	108912995	108912995	Missense_Mutation	SNP	C	T	4	224	c.1120C>T	c.(1120-1122)CGT>TGT	p.R374C
Pat_16	Post-Resistance	MYO1H	283446	37	12	109883364	109883364	Missense_Mutation	SNP	G	A	72	48	c.565G>A	c.(565-567)GAC>AAC	p.D189N
Pat_16	Post-Resistance	GPN3	51184	37	12	110902973	110902973	Missense_Mutation	SNP	C	T	5	414	c.95G>A	c.(94-96)CGG>CAG	p.R32Q
Pat_16	Post-Resistance	TCTN1	79600	37	12	111085668	111085668	Missense_Mutation	SNP	C	T	23	66	c.1735C>T	c.(1735-1737)CCC>TCC	p.P579S
Pat_16	Post-Resistance	SH2B3	10019	37	12	111886044	111886044	Missense_Mutation	SNP	G	A	95	60	c.1666G>A	c.(1666-1668)GAA>AAA	p.E556K
Pat_16	Post-Resistance	RASAL1	8437	37	12	113543644	113543644	Nonsense_Mutation	SNP	G	A	47	126	c.1702C>T	c.(1702-1704)CGA>TGA	p.R568*
Pat_16	Post-Resistance	MED13L	23389	37	12	116429319	116429319	Missense_Mutation	SNP	A	T	136	72	c.3440T>A	c.(3439-3441)CTT>CAT	p.L1147H
Pat_16	Post-Resistance	OASL	8638	37	12	121458536	121458536	Missense_Mutation	SNP	C	T	4	143	c.1373G>A	c.(1372-1374)GGT>GAT	p.G458D
Pat_16	Post-Resistance	CAMKK2	10645	37	12	121712291	121712292	Missense_Mutation	DNP	CC	TT	9	34	c.38_39GG>AA	c.(37-39)CGG>CAA	p.R13Q
Pat_16	Post-Resistance	WDR66	144406	37	12	122405976	122405976	Missense_Mutation	SNP	C	T	4	190	c.2672C>T	c.(2671-2673)CCG>CTG	p.P891L
Pat_16	Post-Resistance	ABCB9	23457	37	12	123444668	123444668	Missense_Mutation	SNP	G	A	5	361	c.115C>T	c.(115-117)CGC>TGC	p.R39C
Pat_16	Post-Resistance	SNRNP35	11066	37	12	123950368	123950368	Missense_Mutation	SNP	A	G	32	92	c.281A>G	c.(280-282)TAC>TGC	p.Y94C
Pat_16	Post-Resistance	ATP6V0A2	23545	37	12	124229297	124229297	Missense_Mutation	SNP	C	A	4	247	c.1480C>A	c.(1480-1482)CCA>ACA	p.P494T
Pat_16	Post-Resistance	DNAH10	196385	37	12	124297919	124297919	Nonsense_Mutation	SNP	G	A	67	215	c.2999G>A	c.(2998-3000)TGG>TAG	p.W1000*
Pat_16	Post-Resistance	TMEM132C	92293	37	12	128899844	128899844	Missense_Mutation	SNP	T	C	7	22	c.317T>C	c.(316-318)ATG>ACG	p.M106T
Pat_16	Post-Resistance	PIWIL1	9271	37	12	130839140	130839140	Missense_Mutation	SNP	G	A	72	48	c.1103G>A	c.(1102-1104)AGA>AAA	p.R368K
Pat_16	Post-Resistance	RIMBP2	23504	37	12	130883705	130883705	Missense_Mutation	SNP	T	A	135	91	c.3134A>T	c.(3133-3135)AAG>ATG	p.K1045M
Pat_16	Post-Resistance	C13orf26	122046	37	13	31513882	31513882	Missense_Mutation	SNP	C	T	5	241	c.113C>T	c.(112-114)ACG>ATG	p.T38M
Pat_16	Post-Resistance	STARD13	90627	37	13	33704332	33704332	Missense_Mutation	SNP	G	A	4	203	c.482C>T	c.(481-483)ACG>ATG	p.T161M
Pat_16	Post-Resistance	MAB21L1	4081	37	13	36049629	36049629	Missense_Mutation	SNP	T	A	53	211	c.647A>T	c.(646-648)CAC>CTC	p.H216L
Pat_16	Post-Resistance	ALG5	29880	37	13	37539733	37539733	Missense_Mutation	SNP	G	A	54	316	c.752C>T	c.(751-753)TCA>TTA	p.S251L
Pat_16	Post-Resistance	SIAH3	283514	37	13	46358171	46358171	Missense_Mutation	SNP	C	T	5	408	c.157G>A	c.(157-159)GTC>ATC	p.V53I

Pat_16	Post-Resistance	ZC3H13	23091	37	13	46541662	46541662	Missense_Mutation	SNP	G	A	101	173	c.4298C>T	c.(4297-4299)TCC>TTC	p.S1433F
Pat_16	Post-Resistance	LOC220429	220429	37	13	50466930	50466930	Missense_Mutation	SNP	C	T	35	82	c.2204C>T	c.(2203-2205)CCA>CTA	p.P735L
Pat_16	Post-Resistance	WDFY2	115825	37	13	52293396	52293396	Missense_Mutation	SNP	G	A	4	319	c.397G>A	c.(397-399)GGA>AGA	p.G133R
Pat_16	Post-Resistance	KLHL1	57626	37	13	70413125	70413125	Missense_Mutation	SNP	C	T	33	58	c.1397G>A	c.(1396-1398)GGA>GAA	p.G466E
Pat_16	Post-Resistance	DACH1	1602	37	13	72063230	72063230	Missense_Mutation	SNP	A	G	133	575	c.1621T>C	c.(1621-1623)TCT>CCT	p.S541P
Pat_16	Post-Resistance	RNF219	79596	37	13	79191193	79191193	Missense_Mutation	SNP	G	A	5	208	c.703C>T	c.(703-705)CGC>TGC	p.R235C
Pat_16	Post-Resistance	HS6ST3	266722	37	13	96743633	96743633	Nonsense_Mutation	SNP	C	T	4	91	c.517C>T	c.(517-519)CAG>TAG	p.Q173*
Pat_16	Post-Resistance	HS6ST3	266722	37	13	97484796	97484796	Missense_Mutation	SNP	G	A	4	168	c.760G>A	c.(760-762)GAG>AAG	p.E254K
Pat_16	Post-Resistance	TPP2	7174	37	13	103288670	103288670	Nonsense_Mutation	SNP	C	T	5	209	c.1606C>T	c.(1606-1608)CGA>TGA	p.R536*
Pat_16	Post-Resistance	EDDM3A	10876	37	14	21216124	21216124	Missense_Mutation	SNP	G	A	4	135	c.385G>A	c.(385-387)GTA>ATA	p.V129I
Pat_16	Post-Resistance	SALL2	6297	37	14	21991923	21991923	Missense_Mutation	SNP	G	A	4	154	c.1939C>T	c.(1939-1941)CGC>TGC	p.R647C
Pat_16	Post-Resistance	MYH7	4625	37	14	23894617	23894617	Missense_Mutation	SNP	T	G	63	94	c.2297A>C	c.(2296-2298)AAG>ACG	p.K766T
Pat_16	Post-Resistance	TGM1	7051	37	14	24724283	24724283	Missense_Mutation	SNP	G	A	4	172	c.1822C>T	c.(1822-1824)CGC>TGC	p.R608C
Pat_16	Post-Resistance	TGM1	7051	37	14	24724445	24724445	Missense_Mutation	SNP	G	A	4	191	c.1660C>T	c.(1660-1662)CGG>TGG	p.R554W
Pat_16	Post-Resistance	FBXO33	254170	37	14	39868720	39868720	Nonstop_Mutation	SNP	C	G	12	2	c.1668G>C	c.(1666-1668)TAG>TAC	p.*556Y
Pat_16	Post-Resistance	PRPF39	55015	37	14	45571853	45571853	Missense_Mutation	SNP	C	T	145	200	c.691C>T	c.(691-693)CGT>TGT	p.R231C
Pat_16	Post-Resistance	SYNE2	23224	37	14	64683071	64683071	Missense_Mutation	SNP	C	T	6	242	c.19439C>T	c.(19438-19440)CCC>CTC	p.P6480L
Pat_16	Post-Resistance	PLEKHG3	26030	37	14	65209027	65209027	Missense_Mutation	SNP	G	A	4	103	c.2792G>A	c.(2791-2793)CGC>CAC	p.R931H
Pat_16	Post-Resistance	SLC8A3	6547	37	14	70635091	70635091	Missense_Mutation	SNP	C	T	72	21	c.49G>A	c.(49-51)GGG>AGG	p.G17R
Pat_16	Post-Resistance	NUMB	8650	37	14	73753887	73753887	Missense_Mutation	SNP	G	A	5	380	c.586C>T	c.(586-588)CGT>TGT	p.R196C
Pat_16	Post-Resistance	CATSPERB	79820	37	14	92088249	92088249	Missense_Mutation	SNP	C	T	10	2	c.1963G>A	c.(1963-1965)GAG>AAG	p.E655K
Pat_16	Post-Resistance	SLC24A4	123041	37	14	92920299	92920299	Missense_Mutation	SNP	G	A	111	19	c.885G>A	c.(883-885)ATG>ATA	p.M295I
Pat_16	Post-Resistance	HSP90AA1	3320	37	14	102605674	102605675	Missense_Mutation	DNP	GG	AA	15	4	c.67_68CC>TT	c.(67-69)CCC>TTC	p.P23F
Pat_16	Post-Resistance	PPP1R13B	23368	37	14	104205122	104205122	Missense_Mutation	SNP	C	T	5	318	c.2758G>A	c.(2758-2760)GAA>AAA	p.E920K
Pat_16	Post-Resistance	MTA1	9112	37	14	105930777	105930777	Missense_Mutation	SNP	C	T	86	138	c.1217C>T	c.(1216-1218)TCT>TTT	p.S406F
Pat_16	Post-Resistance	ADAM6	8755	37	14	107087201	107087201	Splice_Site	SNP	G	A	7	22	c.5152_splice	c.e111+1	
Pat_16	Post-Resistance	OCA2	4948	37	15	28235790	28235790	Missense_Mutation	SNP	C	T	6	381	c.1048G>A	c.(1048-1050)GTG>ATG	p.V350M
Pat_16	Post-Resistance	APBA2	321	37	15	29398813	29398813	Nonsense_Mutation	SNP	C	T	4	95	c.1708C>T	c.(1708-1710)CAG>TAG	p.Q570*
Pat_16	Post-Resistance	CDAN1	146059	37	15	43024557	43024557	Missense_Mutation	SNP	G	A	4	218	c.1507C>T	c.(1507-1509)CGG>TGG	p.R503W
Pat_16	Post-Resistance	MFAP1	4236	37	15	44105192	44105192	Nonsense_Mutation	SNP	G	A	194	478	c.880C>T	c.(880-882)CGA>TGA	p.R294*
Pat_16	Post-Resistance	WDR76	79968	37	15	44127266	44127266	Missense_Mutation	SNP	C	T	25	73	c.470C>T	c.(469-471)TCG>TTG	p.S157L
Pat_16	Post-Resistance	HDC	3067	37	15	50540510	50540510	Missense_Mutation	SNP	G	A	48	176	c.1072C>T	c.(1072-1074)CGC>TGC	p.R358C
Pat_16	Post-Resistance	TRPM7	54822	37	15	50885856	50885856	Missense_Mutation	SNP	A	G	18	66	c.3566T>C	c.(3565-3567)TTT>TCT	p.F1189S
Pat_16	Post-Resistance	MYO5C	55930	37	15	52553323	52553323	Missense_Mutation	SNP	T	A	28	71	c.1049A>T	c.(1048-1050)GAG>GTG	p.E350V
Pat_16	Post-Resistance	CGNL1	84952	37	15	57730859	57730859	Missense_Mutation	SNP	C	T	107	288	c.662C>T	c.(661-663)TCC>TTC	p.S221F
Pat_16	Post-Resistance	BNIP2	663	37	15	59963387	59963387	Missense_Mutation	SNP	A	C	5	15	c.1065T>G	c.(1063-1065)GAT>GAG	p.D355E
Pat_16	Post-Resistance	NARG2	79664	37	15	60760375	60760375	Missense_Mutation	SNP	G	A	16	57	c.293C>T	c.(292-294)TCT>TTT	p.S98F
Pat_16	Post-Resistance	SNX22	79856	37	15	64446651	64446651	Missense_Mutation	SNP	G	A	123	385	c.526G>A	c.(526-528)GAT>AAT	p.D176N
Pat_16	Post-Resistance	CILP	8483	37	15	65502086	65502086	Missense_Mutation	SNP	C	T	19	86	c.8G>A	c.(7-9)GGG>GAG	p.G3E
Pat_16	Post-Resistance	HCN4	10021	37	15	73635803	73635803	Missense_Mutation	SNP	G	A	4	188	c.1132C>T	c.(1132-1134)CGC>TGC	p.R378C
Pat_16	Post-Resistance	LOXL1	4016	37	15	74235231	74235231	Missense_Mutation	SNP	A	G	210	519	c.1139A>G	c.(1138-1140)CAA>CGA	p.Q380R
Pat_16	Post-Resistance	ISLR	3671	37	15	74467929	74467929	Missense_Mutation	SNP	G	A	45	86	c.730G>A	c.(730-732)GGT>AGT	p.G244S
Pat_16	Post-Resistance	CCDC33	80125	37	15	74536345	74536345	Missense_Mutation	SNP	A	C	92	86	c.41A>C	c.(40-42)GAG>GCG	p.E14A
Pat_16	Post-Resistance	CCDC33	80125	37	15	74564051	74564051	Missense_Mutation	SNP	T	A	101	65	c.554T>A	c.(553-555)CTC>CAC	p.L185H
Pat_16	Post-Resistance	ARID3B	10620	37	15	74836597	74836597	Missense_Mutation	SNP	T	C	23	120	c.320T>C	c.(319-321)GTT>GCT	p.V107A
Pat_16	Post-Resistance	CIB2	10518	37	15	78401682	78401682	Missense_Mutation	SNP	C	T	70	64	c.241G>A	c.(241-243)GAT>AAT	p.D81N
Pat_16	Post-Resistance	ZFAND6	54469	37	15	80414108	80414108	Missense_Mutation	SNP	G	A	6	208	c.209G>A	c.(208-210)AGT>AAT	p.S70N

Pat_16	Post-Resistance	AGBL1	123624	37	15	86807702	86807702	Missense_Mutation	SNP	C	T	18	28	c.1162C>T	c.(1162-1164)CCT>TCT	p.P388S
Pat_16	Post-Resistance	RLBP1	6017	37	15	89755082	89755082	Missense_Mutation	SNP	T	A	29	81	c.576A>T	c.(574-576)GAA>GAT	p.E192D
Pat_16	Post-Resistance	SYNM	23336	37	15	99670016	99670016	Missense_Mutation	SNP	C	T	4	122	c.1451C>T	c.(1450-1452)TCG>TTG	p.S484L
Pat_16	Post-Resistance	SNRNP25	79622	37	16	105550	105550	Splice_Site	SNP	G	A	5	431	c.160_splice	c.e2+1	p.P54_splice
Pat_16	Post-Resistance	BAIAP3	8938	37	16	1397918	1397918	Missense_Mutation	SNP	G	T	4	309	c.3154G>T	c.(3154-3156)GTG>TTG	p.V1052L
Pat_16	Post-Resistance	UNKL	64718	37	16	1453342	1453342	Missense_Mutation	SNP	A	C	14	39	c.291T>G	c.(289-291)TGT>TGG	p.C97W
Pat_16	Post-Resistance	ZSCAN10	84891	37	16	3142284	3142284	Missense_Mutation	SNP	G	A	76	235	c.265C>T	c.(265-267)CGT>TGT	p.R89C
Pat_16	Post-Resistance	12-Sep	124404	37	16	4827818	4827818	Missense_Mutation	SNP	C	T	9	15	c.1057G>A	c.(1057-1059)GAT>AAT	p.D353N
Pat_16	Post-Resistance	PPL	5493	37	16	4933884	4933884	Missense_Mutation	SNP	G	A	5	347	c.4772C>T	c.(4771-4773)ACG>ATG	p.T1591M
Pat_16	Post-Resistance	CIITA	4261	37	16	10996552	10996553	Missense_Mutation	DNP	CC	TT	50	109	c.666_667CC>TT	(664-669)CTCCCT>CTTT	p.P223S
Pat_16	Post-Resistance	MKL2	57496	37	16	14334250	14334250	Missense_Mutation	SNP	C	A	181	234	c.988C>A	c.(988-990)CTC>ATC	p.L330I
Pat_16	Post-Resistance	ABCC1	4363	37	16	16230359	16230359	Missense_Mutation	SNP	C	T	74	69	c.4150C>T	c.(4150-4152)CTC>TTC	p.L1384F
Pat_16	Post-Resistance	SYT17	51760	37	16	19191808	19191808	Missense_Mutation	SNP	G	A	4	315	c.278G>A	c.(277-279)CGC>CAC	p.R93H
Pat_16	Post-Resistance	DNAH3	55567	37	16	21098244	21098244	Missense_Mutation	SNP	C	T	131	479	c.2803G>A	c.(2803-2805)GAT>AAT	p.D935N
Pat_16	Post-Resistance	HS3ST4	9951	37	16	26147178	26147178	Missense_Mutation	SNP	C	T	280	377	c.980C>T	c.(979-981)TCC>TTC	p.S327F
Pat_16	Post-Resistance	APOB48R	55911	37	16	28507353	28507353	Missense_Mutation	SNP	G	A	38	49	c.991G>A	c.(991-993)GCC>ACC	p.A331T
Pat_16	Post-Resistance	TAOK2	9344	37	16	29999080	29999080	Missense_Mutation	SNP	C	T	4	166	c.3487C>T	c.(3487-3489)CGG>TGG	p.R1163W
Pat_16	Post-Resistance	CD2BP2	10421	37	16	30365585	30365585	Missense_Mutation	SNP	G	A	145	671	c.137C>T	c.(136-138)TCT>TTT	p.S46F
Pat_16	Post-Resistance	ZNF629	23361	37	16	30794825	30794825	Missense_Mutation	SNP	G	A	4	272	c.824C>T	c.(823-825)TCG>TTG	p.S275L
Pat_16	Post-Resistance	TRIM72	493829	37	16	31230643	31230643	Missense_Mutation	SNP	G	A	65	261	c.520G>A	c.(520-522)GAG>AAG	p.E174K
Pat_16	Post-Resistance	GPT2	84706	37	16	46943833	46943833	Missense_Mutation	SNP	C	T	4	233	c.814C>T	c.(814-816)CCC>TCC	p.P272S
Pat_16	Post-Resistance	PHKB	5257	37	16	47675596	47675596	Missense_Mutation	SNP	T	C	4	153	c.1601T>C	c.(1600-1602)CTT>CCT	p.L534P
Pat_16	Post-Resistance	SLC12A3	6559	37	16	56899385	56899385	Missense_Mutation	SNP	C	T	6	357	c.238C>T	c.(238-240)CGG>TGG	p.R80W
Pat_16	Post-Resistance	CCL22	6367	37	16	57394369	57394369	Missense_Mutation	SNP	G	A	37	158	c.94G>A	c.(94-96)GAA>AAA	p.E32K
Pat_16	Post-Resistance	KIFC3	3801	37	16	57805133	57805133	Missense_Mutation	SNP	G	A	4	264	c.742C>T	c.(742-744)CGG>TGG	p.R248W
Pat_16	Post-Resistance	MMP15	4324	37	16	58079166	58079166	Missense_Mutation	SNP	G	A	12	67	c.1826G>A	c.(1825-1827)GGG>GAG	p.G609E
Pat_16	Post-Resistance	E2F4	1874	37	16	67228796	67228796	Missense_Mutation	SNP	C	T	5	282	c.721C>T	c.(721-723)CGT>TGT	p.R241C
Pat_16	Post-Resistance	ACD	65057	37	16	67694194	67694194	Missense_Mutation	SNP	G	A	15	15	c.188C>T	c.(187-189)CCG>CTG	p.P63L
Pat_16	Post-Resistance	LCAT	3931	37	16	67974220	67974220	Missense_Mutation	SNP	G	A	4	206	c.910C>T	c.(910-912)CGC>TGC	p.R304C
Pat_16	Post-Resistance	HYDIN	54768	37	16	70913367	70913367	Missense_Mutation	SNP	G	A	80	95	c.10387C>T	c.(10387-10389)CTC>TTC	p.L3463F
Pat_16	Post-Resistance	RFWD3	55159	37	16	74685992	74685992	Nonsense_Mutation	SNP	G	A	70	92	c.547C>T	c.(547-549)CAG>TAG	p.Q183*
Pat_16	Post-Resistance	CNTNAP4	85445	37	16	76461470	76461470	Missense_Mutation	SNP	G	A	45	54	c.512G>A	c.(511-513)CGA>CAA	p.R171Q
Pat_16	Post-Resistance	CNTNAP4	85445	37	16	76495952	76495952	Missense_Mutation	SNP	C	T	21	78	c.1433C>T	c.(1432-1434)CCT>CTT	p.P478L
Pat_16	Post-Resistance	MBTPS1	8720	37	16	84135312	84135312	Missense_Mutation	SNP	T	C	188	173	c.77A>G	c.(76-78)GAA>GGA	p.E26G
Pat_16	Post-Resistance	PAFAH1B1	5048	37	17	2577469	2577469	Missense_Mutation	SNP	G	A	6	195	c.787G>A	c.(787-789)GTA>ATA	p.V263I
Pat_16	Post-Resistance	CTNS	1497	37	17	3561299	3561299	Missense_Mutation	SNP	C	T	5	300	c.682C>T	c.(682-684)CGC>TGC	p.R228C
Pat_16	Post-Resistance	P2RX1	5023	37	17	3806890	3806890	Missense_Mutation	SNP	A	C	47	133	c.560T>G	c.(559-561)CTT>CGT	p.L187R
Pat_16	Post-Resistance	VMO1	284013	37	17	4688833	4688833	Missense_Mutation	SNP	G	A	33	103	c.433C>T	c.(433-435)CGC>TGC	p.R145C
Pat_16	Post-Resistance	DHX33	56919	37	17	5359375	5359375	Missense_Mutation	SNP	G	A	42	111	c.977C>T	c.(976-978)CCT>CTT	p.P326L
Pat_16	Post-Resistance	POLR2A	5430	37	17	7399591	7399591	Missense_Mutation	SNP	G	A	4	198	c.289G>A	c.(289-291)GTG>ATG	p.V97M
Pat_16	Post-Resistance	DNAH2	146754	37	17	7681635	7681635	Nonsense_Mutation	SNP	C	T	5	245	c.5389C>T	c.(5389-5391)CGA>TGA	p.R1797*
Pat_16	Post-Resistance	MYH13	8735	37	17	10206529	10206529	Missense_Mutation	SNP	C	T	315	272	c.5651G>A	c.(5650-5652)AGG>AAG	p.R1884K
Pat_16	Post-Resistance	DNAH9	1770	37	17	11622751	11622751	Missense_Mutation	SNP	C	T	86	97	c.5653C>T	c.(5653-5655)CGC>TGC	p.R1885C
Pat_16	Post-Resistance	TRIM16	10626	37	17	15532015	15532015	Missense_Mutation	SNP	A	G	14	30	c.1609T>C	c.(1609-1611)TCC>CCC	p.S537P
Pat_16	Post-Resistance	SMCR8	140775	37	17	18220451	18220451	Missense_Mutation	SNP	G	A	4	293	c.1348G>A	c.(1348-1350)GAC>AAC	p.D450N
Pat_16	Post-Resistance	PRPSAP2	5636	37	17	18814494	18814494	Missense_Mutation	SNP	G	T	4	268	c.663G>T	c.(661-663)TTG>TTT	p.L221F
Pat_16	Post-Resistance	SLC47A1	55244	37	17	19470150	19470151	Missense_Mutation	DNP	CC	TT	33	106	.1154_1155CC>T	c.(1153-1155)TCC>TTT	p.S385F

Pat_16	Post-Resistance	CYTSB	92521	37	17	20108441	20108441	Missense_Mutation	SNP	G	A	5	329	c.1079G>A	c.(1078-1080)AGT>AAT	p.S360N
Pat_16	Post-Resistance	KCNJ12	3768	37	17	21319253	21319253	Missense_Mutation	SNP	C	T	39	108	c.599C>T	c.(598-600)GCC>GTC	p.A200V
Pat_16	Post-Resistance	UNC119	9094	37	17	26874779	26874779	Missense_Mutation	SNP	C	T	5	306	c.526G>A	c.(526-528)GAC>AAC	p.D176N
Pat_16	Post-Resistance	ALDOC	230	37	17	26902152	26902152	Missense_Mutation	SNP	C	T	4	126	c.313G>A	c.(313-315)GTG>ATG	p.V105M
Pat_16	Post-Resistance	SPAG5	10615	37	17	26905522	26905522	Missense_Mutation	SNP	G	A	31	146	c.3223C>T	c.(3223-3225)CTT>TTT	p.L1075F
Pat_16	Post-Resistance	SEZ6	124925	37	17	27309030	27309030	Missense_Mutation	SNP	C	T	12	16	c.83G>A	c.(82-84)GGG>GAG	p.G28E
Pat_16	Post-Resistance	NF1	4763	37	17	29684086	29684086	Missense_Mutation	SNP	A	G	4	216	c.7847A>G	c.(7846-7848)CAG>CGG	p.Q2616R
Pat_16	Post-Resistance	UTP6	55813	37	17	30211497	30211497	Missense_Mutation	SNP	G	A	24	85	c.731C>T	c.(730-732)TCG>TTG	p.S244L
Pat_16	Post-Resistance	MMP28	79148	37	17	34093655	34093655	Missense_Mutation	SNP	G	A	13	41	c.1427C>T	c.(1426-1428)TCC>TTC	p.S476F
Pat_16	Post-Resistance	CASC3	22794	37	17	38320021	38320021	Missense_Mutation	SNP	C	T	92	211	c.1073C>T	c.(1072-1074)TCT>TTT	p.S358F
Pat_16	Post-Resistance	KRTAP9-2	83899	37	17	39383134	39383135	Nonsense_Mutation	DNP	CC	TT	111	269	c.228_229CC>TT	226-231)TGCCAG>TGTT	p.Q77*
Pat_16	Post-Resistance	KRT31	3881	37	17	39552779	39552779	Missense_Mutation	SNP	C	T	4	307	c.481G>A	c.(481-483)GGT>AGT	p.G161S
Pat_16	Post-Resistance	KRT38	8687	37	17	39594372	39594372	Missense_Mutation	SNP	C	T	4	288	c.1214G>A	c.(1213-1215)CGG>CAG	p.R405Q
Pat_16	Post-Resistance	KRT32	3882	37	17	39623524	39623524	Missense_Mutation	SNP	G	C	24	70	c.54C>G	c.(52-54)TGC>TGG	p.C18W
Pat_16	Post-Resistance	LOC90586	90586	37	17	41019611	41019611	Missense_Mutation	SNP	G	A	24	13	c.316G>A	c.(316-318)GCT>ACT	p.A106T
Pat_16	Post-Resistance	DHX8	1659	37	17	41567763	41567763	Missense_Mutation	SNP	C	T	57	49	c.239C>T	c.(238-240)TCT>TTT	p.S80F
Pat_16	Post-Resistance	MYCBPAP	84073	37	17	48595953	48595953	Missense_Mutation	SNP	G	A	86	262	c.649G>A	c.(649-651)GAA>AAA	p.E217K
Pat_16	Post-Resistance	NME1-NME2	654364	37	17	49247332	49247332	Missense_Mutation	SNP	G	A	5	276	c.683G>A	c.(682-684)CGA>CAA	p.R228Q
Pat_16	Post-Resistance	ANKFN1	162282	37	17	54450018	54450018	Missense_Mutation	SNP	G	A	53	158	c.622G>A	c.(622-624)GAA>AAA	p.E208K
Pat_16	Post-Resistance	EPX	8288	37	17	56277065	56277065	Missense_Mutation	SNP	C	T	4	220	c.1447C>T	c.(1447-1449)CGC>TGC	p.R483C
Pat_16	Post-Resistance	TRIM37	4591	37	17	57119173	57119173	Splice_Site	SNP	C	T	4	90	c.1753_splice	c.e17+1	p.G585_splice
Pat_16	Post-Resistance	BCAS3	54828	37	17	58824632	58824632	Missense_Mutation	SNP	C	T	120	294	c.395C>T	c.(394-396)CCA>CTA	p.P132L
Pat_16	Post-Resistance	TBC1D3P2	440452	37	17	60345595	60345595	Missense_Mutation	SNP	G	A	78	172	c.673C>T	c.(673-675)CAC>TAC	p.H225Y
Pat_16	Post-Resistance	SCN4A	6329	37	17	62018424	62018424	Missense_Mutation	SNP	G	A	4	172	c.5218C>T	c.(5218-5220)CGG>TGG	p.R1740W
Pat_16	Post-Resistance	ABCA8	10351	37	17	66915450	66915450	Missense_Mutation	SNP	C	T	34	91	c.1780G>A	c.(1780-1782)GAT>AAT	p.D594N
Pat_16	Post-Resistance	ABCA10	10349	37	17	67151960	67151960	Missense_Mutation	SNP	G	A	235	148	c.3562C>T	c.(3562-3564)CCA>TCA	p.P1188S
Pat_16	Post-Resistance	KCNJ16	3773	37	17	68128331	68128331	Nonsense_Mutation	SNP	C	T	4	238	c.103C>T	c.(103-105)CGA>TGA	p.R35*
Pat_16	Post-Resistance	RAB37	326624	37	17	72736931	72736931	Missense_Mutation	SNP	G	A	5	627	c.118G>A	c.(118-120)GTC>ATC	p.V40I
Pat_16	Post-Resistance	USH1G	124590	37	17	72916120	72916120	Missense_Mutation	SNP	G	A	33	43	c.811C>T	c.(811-813)CCG>TCG	p.P271S
Pat_16	Post-Resistance	PRPSAP1	5635	37	17	74324800	74324801	Missense_Mutation	DNP	GG	AA	12	44	c.778_779CC>TT	c.(778-780)CCA>TTA	p.P260L
Pat_16	Post-Resistance	ENPP7	339221	37	17	77709346	77709346	Missense_Mutation	SNP	G	A	14	53	c.904G>A	c.(904-906)GAC>AAC	p.D302N
Pat_16	Post-Resistance	RNF213	57674	37	17	78320995	78320995	Missense_Mutation	SNP	C	T	11	19	c.3079C>T	c.(3079-3081)CGT>TGT	p.R1027C
Pat_16	Post-Resistance	RPTOR	57521	37	17	78811731	78811731	Nonsense_Mutation	SNP	G	A	17	58	c.1146G>A	c.(1144-1146)TGG>TGA	p.W382*
Pat_16	Post-Resistance	GPS1	2873	37	17	80014551	80014551	Missense_Mutation	SNP	C	T	3	37	c.1175C>T	c.(1174-1176)GCC>GTC	p.A392V
Pat_16	Post-Resistance	USP14	9097	37	18	192846	192846	Missense_Mutation	SNP	G	T	5	189	c.409G>T	c.(409-411)GCA>TCA	p.A137S
Pat_16	Post-Resistance	EPB41L3	23136	37	18	5416253	5416253	Missense_Mutation	SNP	G	A	4	162	c.1631C>T	c.(1630-1632)CCG>CTG	p.P544L
Pat_16	Post-Resistance	L3MBTL4	91133	37	18	6215757	6215757	Missense_Mutation	SNP	A	T	26	44	c.862T>A	c.(862-864)TTT>ATT	p.F288I
Pat_16	Post-Resistance	ARHGAP28	79822	37	18	6894891	6894891	Splice_Site	SNP	G	A	77	62	c.1374_splice	c.e14+1	p.M458_splice
Pat_16	Post-Resistance	LAMA1	284217	37	18	6950909	6950909	Missense_Mutation	SNP	G	A	23	42	c.8269C>T	c.(8269-8271)CAT>TAT	p.H2757Y
Pat_16	Post-Resistance	PTPRM	5797	37	18	7888152	7888152	Missense_Mutation	SNP	C	T	68	139	c.245C>T	c.(244-246)GCC>GTC	p.A82V
Pat_16	Post-Resistance	NDUFV2	4729	37	18	9122540	9122540	Missense_Mutation	SNP	G	A	12	227	c.330G>A	c.(328-330)ATG>ATA	p.M110I
Pat_16	Post-Resistance	DSC3	1825	37	18	28598156	28598156	Missense_Mutation	SNP	C	T	31	39	c.1144G>A	c.(1144-1146)GAT>AAT	p.D382N
Pat_16	Post-Resistance	DSC2	1824	37	18	28662971	28662971	Missense_Mutation	SNP	A	T	37	29	c.998T>A	c.(997-999)TTT>TAT	p.F333Y
Pat_16	Post-Resistance	DSG1	1828	37	18	28914025	28914025	Missense_Mutation	SNP	G	A	46	175	c.865G>A	c.(865-867)GAG>AAG	p.E289K
Pat_16	Post-Resistance	DSG4	147409	37	18	28986205	28986205	Missense_Mutation	SNP	C	T	116	84	c.1802C>T	c.(1801-1803)GCG>GTG	p.A601V
Pat_16	Post-Resistance	DSG2	1829	37	18	29122574	29122574	Missense_Mutation	SNP	G	C	31	71	c.2093G>C	c.(2092-2094)GGA>GCA	p.G698A
Pat_16	Post-Resistance	ASXL3	80816	37	18	31318749	31318749	Missense_Mutation	SNP	A	G	34	103	c.1381A>G	c.(1381-1383)AGT>GGT	p.S461G

Pat_16	Post-Resistance	ASXL3	80816	37	18	31319227	31319227	Missense_Mutation	SNP	G	A	9	27	c.1859G>A	c.(1858-1860)GGA>GAA	p.G620E
Pat_16	Post-Resistance	TCEB3C	162699	37	18	44555339	44555339	Missense_Mutation	SNP	G	A	6	455	c.875C>T	c.(874-876)ACC>ATC	p.T292I
Pat_16	Post-Resistance	MYO5B	4645	37	18	47398601	47398601	Missense_Mutation	SNP	G	A	181	472	c.3539C>T	c.(3538-3540)GCG>GTG	p.A1180V
Pat_16	Post-Resistance	DCC	1630	37	18	50832050	50832050	Missense_Mutation	SNP	G	A	31	157	c.2014G>A	c.(2014-2016)GAA>AAA	p.E672K
Pat_16	Post-Resistance	FECH	2235	37	18	55222097	55222097	Nonsense_Mutation	SNP	G	A	69	150	c.892C>T	c.(892-894)CGA>TGA	p.R298*
Pat_16	Post-Resistance	DOK6	220164	37	18	67425073	67425073	Missense_Mutation	SNP	C	T	63	144	c.820C>T	c.(820-822)CGT>TGT	p.R274C
Pat_16	Post-Resistance	RTTN	25914	37	18	67843991	67843991	Missense_Mutation	SNP	G	A	6	408	c.1396C>T	c.(1396-1398)CTT>TTT	p.L466F
Pat_16	Post-Resistance	CDC34	997	37	19	536298	536298	Missense_Mutation	SNP	G	A	4	90	c.320G>A	c.(319-321)GGG>GAG	p.G107E
Pat_16	Post-Resistance	ABCA7	10347	37	19	1046386	1046386	Missense_Mutation	SNP	C	T	148	573	c.1603C>T	c.(1603-1605)CCG>TCG	p.P535S
Pat_16	Post-Resistance	DOT1L	84444	37	19	2226980	2226980	Missense_Mutation	SNP	C	T	25	91	c.4460C>T	c.(4459-4461)TCC>TTC	p.S1487F
Pat_16	Post-Resistance	ZNF555	148254	37	19	2853202	2853202	Missense_Mutation	SNP	C	T	8	144	c.1139C>T	c.(1138-1140)CCC>CTC	p.P380L
Pat_16	Post-Resistance	TLE2	7089	37	19	3005967	3005967	Splice_Site	SNP	C	T	31	82	c.1501_splice	c.e16-1	p.N501_splice
Pat_16	Post-Resistance	PLIN4	729359	37	19	4511993	4511993	Missense_Mutation	SNP	G	A	143	183	c.1937C>T	c.(1936-1938)GCG>GTG	p.A646V
Pat_16	Post-Resistance	EMR1	2015	37	19	6921798	6921798	Missense_Mutation	SNP	T	A	731	103	c.1695T>A	c.(1693-1695)TTT>TTA	p.F565L
Pat_16	Post-Resistance	MUC16	94025	37	19	9009311	9009312	Missense_Mutation	DNP	GG	AA	66	341	39161_39162CC>	c.(39160-39162)TCC>TTT	p.S13054F
Pat_16	Post-Resistance	MUC16	94025	37	19	9059650	9059650	Missense_Mutation	SNP	G	A	107	140	c.27796C>T	c.(27796-27798)CTC>TTC	p.L9266F
Pat_16	Post-Resistance	MUC16	94025	37	19	9068622	9068622	Missense_Mutation	SNP	G	A	90	99	c.18824C>T	c.(18823-18825)TCA>TTA	p.S6275L
Pat_16	Post-Resistance	MUC16	94025	37	19	9072288	9072288	Missense_Mutation	SNP	G	A	36	51	c.15158C>T	c.(15157-15159)TCC>TTC	p.S5053F
Pat_16	Post-Resistance	ZNF560	147741	37	19	9578016	9578016	Missense_Mutation	SNP	C	T	41	124	c.1607G>A	c.(1606-1608)CGA>CAA	p.R536Q
Pat_16	Post-Resistance	ZNF561	93134	37	19	9721330	9721330	Missense_Mutation	SNP	G	A	138	229	c.1007C>T	c.(1006-1008)CCC>CTC	p.P336L
Pat_16	Post-Resistance	COL5A3	50509	37	19	10097252	10097252	Missense_Mutation	SNP	C	T	73	253	c.2221G>A	c.(2221-2223)GAT>AAT	p.D741N
Pat_16	Post-Resistance	PPAN-P2RY11	692312	37	19	10217217	10217217	Missense_Mutation	SNP	G	A	3	5	c.59G>A	c.(58-60)CGC>CAC	p.R20H
Pat_16	Post-Resistance	CDC37	11140	37	19	10514068	10514068	Missense_Mutation	SNP	G	A	24	60	c.88C>T	c.(88-90)CGC>TGC	p.R30C
Pat_16	Post-Resistance	ZNF440	126070	37	19	11942554	11942554	Missense_Mutation	SNP	G	A	85	414	c.563G>A	c.(562-564)CGA>CAA	p.R188Q
Pat_16	Post-Resistance	ZNF844	284391	37	19	12187443	12187443	Missense_Mutation	SNP	C	G	5	451	c.1508C>G	c.(1507-1509)CCT>CGT	p.P503R
Pat_16	Post-Resistance	GCDH	2639	37	19	13007772	13007772	Missense_Mutation	SNP	G	A	6	306	c.901G>A	c.(901-903)GTG>ATG	p.V301M
Pat_16	Post-Resistance	ZSWIM4	65249	37	19	13939480	13939480	Missense_Mutation	SNP	G	A	5	642	c.2050G>A	c.(2050-2052)GTA>ATA	p.V684I
Pat_16	Post-Resistance	MED26	9441	37	19	16687703	16687703	Missense_Mutation	SNP	G	A	4	53	c.938C>T	c.(937-939)CCG>CTG	p.P313L
Pat_16	Post-Resistance	ANKLE1	126549	37	19	17394769	17394769	Missense_Mutation	SNP	C	T	202	177	c.1196C>T	c.(1195-1197)CCT>CTT	p.P399L
Pat_16	Post-Resistance	UNC13A	23025	37	19	17766699	17766699	Missense_Mutation	SNP	C	T	15	35	c.1540G>A	c.(1540-1542)GAG>AAG	p.E514K
Pat_16	Post-Resistance	ARRDC2	27106	37	19	18121461	18121461	Missense_Mutation	SNP	C	T	66	102	c.1093C>T	c.(1093-1095)CCC>TCC	p.P365S
Pat_16	Post-Resistance	SFRS14	10147	37	19	19115375	19115375	Missense_Mutation	SNP	G	A	5	502	c.2531C>T	c.(2530-2532)ACG>ATG	p.T844M
Pat_16	Post-Resistance	SF4	57794	37	19	19407930	19407930	Missense_Mutation	SNP	C	T	5	96	c.1111G>A	c.(1111-1113)GGG>AGG	p.G371R
Pat_16	Post-Resistance	ZNF253	56242	37	19	20002799	20002799	Missense_Mutation	SNP	A	T	12	512	c.743A>T	c.(742-744)AAA>ATA	p.K248I
Pat_16	Post-Resistance	ZNF253	56242	37	19	20002801	20002801	Missense_Mutation	SNP	A	G	10	528	c.745A>G	c.(745-747)ATT>GTT	p.I249V
Pat_16	Post-Resistance	ZNF93	81931	37	19	20044699	20044699	Missense_Mutation	SNP	C	T	18	136	c.935C>T	c.(934-936)CCC>CTC	p.P312L
Pat_16	Post-Resistance	ZNF626	199777	37	19	20808006	20808006	Missense_Mutation	SNP	T	C	10	352	c.677A>G	c.(676-678)GAG>GGG	p.E226G
Pat_16	Post-Resistance	ZNF85	7639	37	19	21132918	21132918	Missense_Mutation	SNP	C	T	6	292	c.1598C>T	c.(1597-1599)ACT>ATT	p.T533I
Pat_16	Post-Resistance	ZNF208	7757	37	19	22155896	22155896	Missense_Mutation	SNP	A	C	9	362	c.1640T>G	c.(1639-1641)ATT>AGT	p.I547S
Pat_16	Post-Resistance	ZNF208	7757	37	19	22157069	22157069	Missense_Mutation	SNP	G	A	63	96	c.767C>T	c.(766-768)TCC>TTC	p.S256F
Pat_16	Post-Resistance	ZNF91	7644	37	19	23544808	23544808	Missense_Mutation	SNP	C	T	7	506	c.973G>A	c.(973-975)GAA>AAA	p.E325K
Pat_16	Post-Resistance	ZNF681	148213	37	19	23927358	23927358	Missense_Mutation	SNP	G	A	148	352	c.994C>T	c.(994-996)CAT>TAT	p.H332Y
Pat_16	Post-Resistance	ZNF681	148213	37	19	23937634	23937634	Missense_Mutation	SNP	C	T	5	281	c.217G>A	c.(217-219)GAA>AAA	p.E73K
Pat_16	Post-Resistance	GPATCH1	55094	37	19	33617614	33617614	Missense_Mutation	SNP	G	A	4	216	c.2740G>A	c.(2740-2742)GTG>ATG	p.V914M
Pat_16	Post-Resistance	PDCD2L	84306	37	19	34900181	34900181	Missense_Mutation	SNP	G	A	6	314	c.452G>A	c.(451-453)AGC>AAC	p.S151N
Pat_16	Post-Resistance	LGI4	163175	37	19	35624989	35624989	Missense_Mutation	SNP	C	G	5	29	c.190G>C	c.(190-192)GTC>CTC	p.V64L
Pat_16	Post-Resistance	MLL4	9757	37	19	36219960	36219960	Missense_Mutation	SNP	G	A	5	289	c.4762G>A	c.(4762-4764)GGG>AGG	p.G1588R

Pat_16	Post-Resistance	KIRREL2	84063	37	19	36357377	36357377	Missense_Mutation	SNP	C	T	266	312	c.2110C>T	c.(2110-2112)CTC>TTC	p.L704F
Pat_16	Post-Resistance	APLP1	333	37	19	36369539	36369539	Missense_Mutation	SNP	G	A	63	99	c.1630G>A	c.(1630-1632)GAA>AAA	p.E544K
Pat_16	Post-Resistance	NFKBID	84807	37	19	36380815	36380815	Missense_Mutation	SNP	G	A	6	309	c.865C>T	c.(865-867)CGG>TGG	p.R289W
Pat_16	Post-Resistance	RYR1	6261	37	19	38939433	38939433	Missense_Mutation	SNP	C	A	19	16	c.1102C>A	c.(1102-1104)CTC>ATC	p.L368I
Pat_16	Post-Resistance	LGALS4	3960	37	19	39299478	39299478	Missense_Mutation	SNP	C	T	73	269	c.245G>A	c.(244-246)GGG>GAG	p.G82E
Pat_16	Post-Resistance	SIRT2	22933	37	19	39379771	39379771	Missense_Mutation	SNP	G	A	5	352	c.457C>T	c.(457-459)CGC>TGC	p.R153C
Pat_16	Post-Resistance	LGALS13	29124	37	19	40095879	40095879	Missense_Mutation	SNP	T	A	47	160	c.154T>A	c.(154-156)TTC>ATC	p.F52I
Pat_16	Post-Resistance	PRX	57716	37	19	40901021	40901021	Missense_Mutation	SNP	G	A	63	68	c.3238C>T	c.(3238-3240)CGT>TGT	p.R1080C
Pat_16	Post-Resistance	PRX	57716	37	19	40901635	40901635	Missense_Mutation	SNP	T	G	15	75	c.2624A>C	c.(2623-2625)AAA>ACA	p.K875T
Pat_16	Post-Resistance	CIC	23152	37	19	42794473	42794473	Missense_Mutation	SNP	C	T	4	145	c.1553C>T	c.(1552-1554)CCG>CTG	p.P518L
Pat_16	Post-Resistance	PSG8	440533	37	19	43258652	43258652	Missense_Mutation	SNP	T	C	247	297	c.1076A>G	c.(1075-1077)AAC>AGC	p.N359S
Pat_16	Post-Resistance	PSG6	5675	37	19	43529189	43529189	Nonsense_Mutation	SNP	C	T	133	431	c.102G>A	c.(100-102)TGG>TGA	p.W34*
Pat_16	Post-Resistance	CADM4	199731	37	19	44131825	44131825	Missense_Mutation	SNP	C	T	210	217	c.182G>A	c.(181-183)CGG>CAG	p.R61Q
Pat_16	Post-Resistance	ZNF225	7768	37	19	44635194	44635194	Missense_Mutation	SNP	G	A	5	422	c.427G>A	c.(427-429)GTA>ATA	p.V143I
Pat_16	Post-Resistance	DACT3	147906	37	19	47151836	47151836	Missense_Mutation	SNP	G	A	176	237	c.1793C>T	c.(1792-1794)CCC>CTC	p.P598L
Pat_16	Post-Resistance	DHX34	9704	37	19	47858488	47858488	Missense_Mutation	SNP	C	T	5	411	c.898C>T	c.(898-900)CCC>TCC	p.P300S
Pat_16	Post-Resistance	EHD2	30846	37	19	48220222	48220222	Missense_Mutation	SNP	C	T	5	317	c.353C>T	c.(352-354)CCG>CTG	p.P118L
Pat_16	Post-Resistance	GRWD1	83743	37	19	48953958	48953958	Missense_Mutation	SNP	C	T	45	145	c.718C>T	c.(718-720)CAC>TAC	p.H240Y
Pat_16	Post-Resistance	LMTK3	114783	37	19	49004787	49004787	Missense_Mutation	SNP	G	A	16	69	c.914C>T	c.(913-915)TCT>TTT	p.S305F
Pat_16	Post-Resistance	PLEKHA4	57664	37	19	49362834	49362834	Missense_Mutation	SNP	G	A	4	200	c.584C>T	c.(583-585)CCG>CTG	p.P195L
Pat_16	Post-Resistance	RUVBL2	10856	37	19	49507618	49507618	Missense_Mutation	SNP	G	A	5	345	c.208G>A	c.(208-210)GGT>AGT	p.G70S
Pat_16	Post-Resistance	ZNF473	25888	37	19	50549870	50549870	Missense_Mutation	SNP	C	T	46	157	c.2170C>T	c.(2170-2172)CAC>TAC	p.H724Y
Pat_16	Post-Resistance	LRRC4B	94030	37	19	51021739	51021739	Missense_Mutation	SNP	C	T	4	109	c.1231G>A	c.(1231-1233)GTG>ATG	p.V411M
Pat_16	Post-Resistance	SHANK1	50944	37	19	51171651	51171651	Missense_Mutation	SNP	C	A	14	23	c.3566G>T	c.(3565-3567)GGA>GTA	p.G1189V
Pat_16	Post-Resistance	ZNF175	7728	37	19	52089988	52089988	Missense_Mutation	SNP	T	C	51	41	c.404T>C	c.(403-405)TTA>TCA	p.L135S
Pat_16	Post-Resistance	ZNF611	81856	37	19	53217390	53217390	Missense_Mutation	SNP	C	T	5	439	c.68G>A	c.(67-69)CGC>CAC	p.R23H
Pat_16	Post-Resistance	ZNF677	342926	37	19	53741754	53741754	Missense_Mutation	SNP	C	T	5	41	c.226G>A	c.(226-228)GAA>AAA	p.E76K
Pat_16	Post-Resistance	ZNF525	170958	37	19	53884898	53884898	Missense_Mutation	SNP	G	A	5	234	c.958G>A	c.(958-960)GAA>AAA	p.E320K
Pat_16	Post-Resistance	DPRX	503834	37	19	54135382	54135382	Missense_Mutation	SNP	C	T	65	242	c.22C>T	c.(22-24)CGT>TGT	p.R8C
Pat_16	Post-Resistance	NLRP7	199713	37	19	55451046	55451047	Missense_Mutation	DNP	CC	TT	40	93	.1140_1141GG>A	38-1143)GGGGAG>GGA	p.E381K
Pat_16	Post-Resistance	NLRP4	147945	37	19	56373376	56373376	Missense_Mutation	SNP	T	A	52	127	c.2037T>A	c.(2035-2037)TTT>TTA	p.F679L
Pat_16	Post-Resistance	NLRP8	126205	37	19	56466396	56466396	Missense_Mutation	SNP	G	T	89	133	c.972G>T	c.(970-972)ATG>ATT	p.M324I
Pat_16	Post-Resistance	PEG3	5178	37	19	57325633	57325633	Missense_Mutation	SNP	C	T	58	185	c.4177G>A	c.(4177-4179)GAG>AAG	p.E1393K
Pat_16	Post-Resistance	PEG3	5178	37	19	57327584	57327584	Missense_Mutation	SNP	T	A	151	134	c.2226A>T	c.(2224-2226)GAA>GAT	p.E742D
Pat_16	Post-Resistance	ZNF814	730051	37	19	58384399	58384399	Missense_Mutation	SNP	A	G	5	185	c.2359T>C	c.(2359-2361)TTC>CTC	p.F787L
Pat_16	Post-Resistance	ZNF606	80095	37	19	58490987	58490987	Missense_Mutation	SNP	A	C	27	46	c.1061T>G	c.(1060-1062)TTT>TGT	p.F354C
Pat_16	Post-Resistance	TTC15	51112	37	2	3405575	3405575	Missense_Mutation	SNP	C	T	68	119	c.1075C>T	c.(1075-1077)CGC>TGC	p.R359C
Pat_16	Post-Resistance	RNF144A	9781	37	2	7170318	7170318	Missense_Mutation	SNP	G	A	4	300	c.719G>A	c.(718-720)CGG>CAG	p.R240Q
Pat_16	Post-Resistance	NBAS	51594	37	2	15506800	15506800	Missense_Mutation	SNP	G	A	6	244	c.3721C>T	c.(3721-3723)CGG>TGG	p.R1241W
Pat_16	Post-Resistance	FAM179A	165186	37	2	29225569	29225569	Missense_Mutation	SNP	G	A	24	28	c.595G>A	c.(595-597)GGG>AGG	p.G199R
Pat_16	Post-Resistance	CAPN13	92291	37	2	30977178	30977178	Missense_Mutation	SNP	T	G	28	41	c.919A>C	c.(919-921)AAA>CAA	p.K307Q
Pat_16	Post-Resistance	MAP4K3	8491	37	2	39487908	39487908	Missense_Mutation	SNP	A	T	32	28	c.2147T>A	c.(2146-2148)TTT>TAT	p.F716Y
Pat_16	Post-Resistance	AAK1	22848	37	2	69709908	69709908	Missense_Mutation	SNP	G	A	4	138	c.2402C>T	c.(2401-2403)TCT>TTT	p.S801F
Pat_16	Post-Resistance	MXD1	4084	37	2	70164473	70164473	Missense_Mutation	SNP	G	A	4	164	c.425G>A	c.(424-426)CGG>CAG	p.R142Q
Pat_16	Post-Resistance	MXD1	4084	37	2	70165315	70165315	Missense_Mutation	SNP	C	T	5	283	c.565C>T	c.(565-567)CGG>TGG	p.R189W
Pat_16	Post-Resistance	C2orf42	54980	37	2	70406670	70406670	Missense_Mutation	SNP	C	T	4	196	c.928G>A	c.(928-930)GTA>ATA	p.V310I
Pat_16	Post-Resistance	ADD2	119	37	2	70890612	70890612	Missense_Mutation	SNP	A	T	73	43	c.2126T>A	c.(2125-2127)TTC>TAC	p.F709Y

Pat_16	Post-Resistance	ADD2	119	37	2	70933534	70933534	Missense_Mutation	SNP	C	T	93	41	c.7G>A	c.(7-9)GAA>AAA	p.E3K
Pat_16	Post-Resistance	RAB11FIP5	26056	37	2	73315365	73315365	Missense_Mutation	SNP	G	A	4	232	c.1381C>T	c.(1381-1383)CGG>TGG	p.R461W
Pat_16	Post-Resistance	REG3G	130120	37	2	79254278	79254278	Missense_Mutation	SNP	G	A	76	175	c.314G>A	c.(313-315)GGG>GAG	p.G105E
Pat_16	Post-Resistance	RETSAT	54884	37	2	85581530	85581530	Missense_Mutation	SNP	G	A	68	166	c.101C>T	c.(100-102)TCC>TTC	p.S34F
Pat_16	Post-Resistance	SMYD1	150572	37	2	88396118	88396118	Missense_Mutation	SNP	G	A	132	254	c.703G>A	c.(703-705)GAG>AAG	p.E235K
Pat_16	Post-Resistance	AFF3	3899	37	2	100209977	100209978	Missense_Mutation	DNP	CC	TT	21	84	.2145_2146GG>A	43-2148)GGGGGC>GGA	p.G716S
Pat_16	Post-Resistance	RGPD4	285190	37	2	108487252	108487252	Missense_Mutation	SNP	G	A	58	176	c.2792G>A	c.(2791-2793)GGA>GAA	p.G931E
Pat_16	Post-Resistance	SULT1C4	27233	37	2	108999916	108999916	Missense_Mutation	SNP	G	A	46	158	c.565G>A	c.(565-567)GCC>ACC	p.A189T
Pat_16	Post-Resistance	EDAR	10913	37	2	109513459	109513459	Missense_Mutation	SNP	C	G	44	19	c.1251G>C	c.(1249-1251)CAG>CAC	p.Q417H
Pat_16	Post-Resistance	SH3RF3	344558	37	2	110053444	110053444	Missense_Mutation	SNP	G	A	74	141	c.1670G>A	c.(1669-1671)GGG>GAG	p.G557E
Pat_16	Post-Resistance	GPR17	2840	37	2	128408607	128408608	Nonsense_Mutation	DNP	GG	TA	56	172	c.382_383GG>TA	c.(382-384)GGG>TAG	p.G128*
Pat_16	Post-Resistance	UGGT1	56886	37	2	128884989	128884989	Missense_Mutation	SNP	G	C	32	76	c.1189G>C	c.(1189-1191)GGA>CGA	p.G397R
Pat_16	Post-Resistance	THSD7B	80731	37	2	137852453	137852453	Nonsense_Mutation	SNP	C	T	53	169	c.868C>T	c.(868-870)CAA>TAA	p.Q290*
Pat_16	Post-Resistance	THSD7B	80731	37	2	138373853	138373853	Missense_Mutation	SNP	G	A	107	396	c.3445G>A	c.(3445-3447)GAA>AAA	p.E1149K
Pat_16	Post-Resistance	LRP1B	53353	37	2	141459861	141459861	Missense_Mutation	SNP	C	T	55	145	c.6151G>A	c.(6151-6153)GAA>AAA	p.E2051K
Pat_16	Post-Resistance	LRP1B	53353	37	2	141945989	141945989	Splice_Site	SNP	C	T	12	51	c.1013_splice	c.e7+1	p.G338_splice
Pat_16	Post-Resistance	TANC1	85461	37	2	160027046	160027046	Missense_Mutation	SNP	C	T	51	135	c.1081C>T	c.(1081-1083)CCC>TCC	p.P361S
Pat_16	Post-Resistance	BAZ2B	29994	37	2	160193521	160193521	Missense_Mutation	SNP	C	T	4	246	c.5728G>A	c.(5728-5730)GCA>ACA	p.A1910T
Pat_16	Post-Resistance	SLC4A10	57282	37	2	162728844	162728844	Missense_Mutation	SNP	G	A	61	192	c.808G>A	c.(808-810)GAA>AAA	p.E270K
Pat_16	Post-Resistance	HOXD3	3232	37	2	177036364	177036364	Missense_Mutation	SNP	C	T	109	297	c.661C>T	c.(661-663)CGG>TGG	p.R221W
Pat_16	Post-Resistance	TTN	7273	37	2	179454201	179454201	Missense_Mutation	SNP	C	T	17	48	c.54547G>A	c.(54547-54549)GAA>AAA	p.E18183K
Pat_16	Post-Resistance	TTN	7273	37	2	179469452	179469452	Missense_Mutation	SNP	C	T	5	175	c.46660G>A	c.(46660-46662)GTA>ATA	p.V15554I
Pat_16	Post-Resistance	TTN	7273	37	2	179641949	179641949	Missense_Mutation	SNP	C	T	90	179	c.4741G>A	c.(4741-4743)GGT>AGT	p.G1581S
Pat_16	Post-Resistance	STAT4	6775	37	2	191937835	191937835	Missense_Mutation	SNP	T	A	109	232	c.454A>T	c.(454-456)AAC>TAC	p.N152Y
Pat_16	Post-Resistance	EEF1B2	1933	37	2	207025358	207025358	Missense_Mutation	SNP	A	G	21	359	c.127A>G	c.(127-129)AGC>GGC	p.S43G
Pat_16	Post-Resistance	ABCA12	26154	37	2	215876250	215876250	Missense_Mutation	SNP	G	A	37	110	c.2245C>T	c.(2245-2247)CCA>TCA	p.P749S
Pat_16	Post-Resistance	CXCR2	3579	37	2	219000137	219000137	Missense_Mutation	SNP	G	A	4	305	c.613G>A	c.(613-615)GCA>ACA	p.A205T
Pat_16	Post-Resistance	COL4A3	1285	37	2	228147167	228147167	Missense_Mutation	SNP	G	A	45	57	c.2575G>A	c.(2575-2577)GGA>AGA	p.G859R
Pat_16	Post-Resistance	COL4A3	1285	37	2	228168824	228168824	Missense_Mutation	SNP	G	A	17	56	c.4117G>A	c.(4117-4119)GGA>AGA	p.G1373R
Pat_16	Post-Resistance	SPHKAP	80309	37	2	228846519	228846519	Missense_Mutation	SNP	G	A	36	133	c.5017C>T	c.(5017-5019)CAT>TAT	p.H1673Y
Pat_16	Post-Resistance	SLC16A14	151473	37	2	230911393	230911393	Missense_Mutation	SNP	C	A	18	40	c.449G>T	c.(448-450)GGC>GTC	p.G150V
Pat_16	Post-Resistance	CHRND	1144	37	2	233394756	233394756	Missense_Mutation	SNP	C	T	4	282	c.727C>T	c.(727-729)CGC>TGC	p.R243C
Pat_16	Post-Resistance	USP40	55230	37	2	234442200	234442200	Missense_Mutation	SNP	C	T	73	53	c.1429G>A	c.(1429-1431)GAA>AAA	p.E477K
Pat_16	Post-Resistance	TRPM8	79054	37	2	234846100	234846100	Missense_Mutation	SNP	C	T	74	202	c.295C>T	c.(295-297)CCT>TCT	p.P99S
Pat_16	Post-Resistance	TRPM8	79054	37	2	234873271	234873271	Splice_Site	SNP	G	A	4	28	c.1750_splice	c.e14-1	p.T584_splice
Pat_16	Post-Resistance	MLPH	79083	37	2	238457876	238457876	Missense_Mutation	SNP	C	T	36	73	c.1630C>T	c.(1630-1632)CCC>TCC	p.P544S
Pat_16	Post-Resistance	TRAF3IP1	26146	37	2	239307420	239307420	Missense_Mutation	SNP	T	G	115	104	c.1936T>G	c.(1936-1938)TTA>GTA	p.L646V
Pat_16	Post-Resistance	THAP4	51078	37	2	242545816	242545817	Missense_Mutation	DNP	CC	TT	14	14	.1312_1313GG>A	c.(1312-1314)GGA>AAA	p.G438K
Pat_16	Post-Resistance	SIRPG	55423	37	20	1629761	1629761	Nonsense_Mutation	SNP	G	A	62	238	c.367C>T	c.(367-369)CGA>TGA	p.R123*
Pat_16	Post-Resistance	TGM6	343641	37	20	2411098	2411098	Missense_Mutation	SNP	G	A	89	111	c.1685G>A	c.(1684-1686)AGA>AAA	p.R562K
Pat_16	Post-Resistance	SNRPB	6628	37	20	2443296	2443296	Missense_Mutation	SNP	G	A	5	396	c.671C>T	c.(670-672)CCC>CTC	p.P224L
Pat_16	Post-Resistance	ATRN	8455	37	20	3541478	3541478	Missense_Mutation	SNP	G	A	5	343	c.1373G>A	c.(1372-1374)CGA>CAA	p.R458Q
Pat_16	Post-Resistance	C20orf94	128710	37	20	10582435	10582435	Missense_Mutation	SNP	C	T	4	209	c.373C>T	c.(373-375)CGT>TGT	p.R125C
Pat_16	Post-Resistance	BTBD3	22903	37	20	11899185	11899185	Missense_Mutation	SNP	C	T	125	496	c.262C>T	c.(262-264)CTC>TTC	p.L88F
Pat_16	Post-Resistance	CST9	128822	37	20	23584239	23584239	Missense_Mutation	SNP	A	T	42	170	c.388T>A	c.(388-390)TTT>ATT	p.F130I
Pat_16	Post-Resistance	ASXL1	171023	37	20	31023318	31023318	Missense_Mutation	SNP	C	T	29	96	c.2803C>T	c.(2803-2805)CCC>TCC	p.P935S
Pat_16	Post-Resistance	DNMT3B	1789	37	20	31368196	31368196	Missense_Mutation	SNP	G	A	4	126	c.67G>A	c.(67-69)GTC>ATC	p.V23I

Pat_16	Post-Resistance	C20orf185	359710	37	20	31657725	31657725	Missense_Mutation	SNP	C	T	7	773	c.1181C>T	c.(1180-1182)TCG>TTG	p.S394L
Pat_16	Post-Resistance	CBFA2T2	9139	37	20	32217603	32217603	Missense_Mutation	SNP	C	T	74	89	c.1138C>T	c.(1138-1140)CGT>TGT	p.R380C
Pat_16	Post-Resistance	RBM12	10137	37	20	34241449	34241449	Missense_Mutation	SNP	C	T	5	400	c.1796G>A	c.(1795-1797)CGT>CAT	p.R599H
Pat_16	Post-Resistance	PPP1R16B	26051	37	20	37524242	37524242	Missense_Mutation	SNP	T	A	36	59	c.356T>A	c.(355-357)CTG>CAG	p.L119Q
Pat_16	Post-Resistance	PLCG1	5335	37	20	39788777	39788777	Missense_Mutation	SNP	C	T	4	300	c.496C>T	c.(496-498)CGG>TGG	p.R166W
Pat_16	Post-Resistance	STK4	6789	37	20	43625841	43625841	Missense_Mutation	SNP	C	T	69	270	c.725C>T	c.(724-726)CCC>CTC	p.P242L
Pat_16	Post-Resistance	SEMG1	6406	37	20	43836962	43836962	Nonsense_Mutation	SNP	A	T	16	74	c.1024A>T	c.(1024-1026)AAG>TAG	p.K342*
Pat_16	Post-Resistance	TP53TG5	27296	37	20	44003936	44003936	Missense_Mutation	SNP	C	T	95	140	c.511G>A	c.(511-513)GGA>AGA	p.G171R
Pat_16	Post-Resistance	SLC12A5	57468	37	20	44684831	44684831	Missense_Mutation	SNP	A	G	36	139	c.2899A>G	c.(2899-2901)AAG>GAG	p.K967E
Pat_16	Post-Resistance	SNAI1	6615	37	20	48600613	48600613	Missense_Mutation	SNP	C	T	104	180	c.335C>T	c.(334-336)TCC>TTC	p.S112F
Pat_16	Post-Resistance	SALL4	57167	37	20	50407142	50407142	Missense_Mutation	SNP	G	A	47	131	c.1880C>T	c.(1879-1881)TCG>TTG	p.S627L
Pat_16	Post-Resistance	TFAP2C	7022	37	20	55208529	55208529	Missense_Mutation	SNP	C	T	32	121	c.707C>T	c.(706-708)TCT>TTT	p.S236F
Pat_16	Post-Resistance	LAMA5	3911	37	20	60885978	60885978	Missense_Mutation	SNP	G	A	47	43	c.10261C>T	.(10261-10263)CGG>TG	p.R3421W
Pat_16	Post-Resistance	DIDO1	11083	37	20	61511835	61511835	Missense_Mutation	SNP	C	T	57	87	c.5473G>A	c.(5473-5475)GGC>AGC	p.G1825S
Pat_16	Post-Resistance	KCNQ2	3785	37	20	62076642	62076642	Missense_Mutation	SNP	G	A	5	297	c.463C>T	c.(463-465)CGT>TGT	p.R155C
Pat_16	Post-Resistance	PRIC285	85441	37	20	62195457	62195457	Missense_Mutation	SNP	C	T	4	67	c.4718G>A	c.(4717-4719)CGG>CAG	p.R1573Q
Pat_16	Post-Resistance	SAMD10	140700	37	20	62608735	62608735	Missense_Mutation	SNP	C	T	5	210	c.116G>A	c.(115-117)CGG>CAG	p.R39Q
Pat_16	Post-Resistance	PCMTD2	55251	37	20	62891413	62891413	Missense_Mutation	SNP	C	T	81	138	c.95C>T	c.(94-96)GCT>GTT	p.A32V
Pat_16	Post-Resistance	TPTE	7179	37	21	10914379	10914379	Missense_Mutation	SNP	G	A	11	77	c.1340C>T	c.(1339-1341)TCA>TTA	p.S447L
Pat_16	Post-Resistance	APP	351	37	21	27254055	27254055	Missense_Mutation	SNP	G	A	5	252	c.2239C>T	c.(2239-2241)CGC>TGC	p.R747C
Pat_16	Post-Resistance	KCNJ6	3763	37	21	39087165	39087165	Missense_Mutation	SNP	C	T	94	315	c.295G>A	c.(295-297)GTT>ATT	p.V99I
Pat_16	Post-Resistance	PLAC4	191585	37	21	42551363	42551364	Missense_Mutation	DNP	AC	GG	3	91	c.192_193GT>CC	190-195)ACGTTC>ACCC	p.F65L
Pat_16	Post-Resistance	C2CD2	25966	37	21	43319324	43319325	Missense_Mutation	DNP	GG	AA	7	28	.1707_1708CC>T	1705-1710)TCCCTT>TCTT	p.L570F
Pat_16	Post-Resistance	ZNF295	49854	37	21	43411624	43411624	Missense_Mutation	SNP	A	T	60	212	c.2581T>A	c.(2581-2583)TCC>ACC	p.S861T
Pat_16	Post-Resistance	ABCG1	9619	37	21	43711687	43711687	Missense_Mutation	SNP	T	C	115	150	c.1610T>C	c.(1609-1611)TTT>TCT	p.F537S
Pat_16	Post-Resistance	SIK1	150094	37	21	44836701	44836701	Missense_Mutation	SNP	G	A	12	48	c.2273C>T	c.(2272-2274)CCC>CTC	p.P758L
Pat_16	Post-Resistance	KRTAP10-8	386681	37	21	46032217	46032217	Missense_Mutation	SNP	C	T	5	175	c.200C>T	c.(199-201)GCC>GTC	p.A67V
Pat_16	Post-Resistance	PCBP3	54039	37	21	47337538	47337538	Missense_Mutation	SNP	C	T	87	261	c.712C>T	c.(712-714)CCG>TCG	p.P238S
Pat_16	Post-Resistance	GNB1L	54584	37	22	19776285	19776285	Missense_Mutation	SNP	C	T	4	131	c.931G>A	c.(931-933)GCG>ACG	p.A311T
Pat_16	Post-Resistance	RGL4	266747	37	22	24036576	24036576	Missense_Mutation	SNP	G	A	4	180	c.955G>A	c.(955-957)GTC>ATC	p.V319I
Pat_16	Post-Resistance	GGT5	2687	37	22	24640582	24640582	Missense_Mutation	SNP	G	A	64	103	c.112C>T	c.(112-114)CCC>TCC	p.P38S
Pat_16	Post-Resistance	CRYBB2	1415	37	22	25625499	25625499	Missense_Mutation	SNP	C	T	28	62	c.403C>T	c.(403-405)CAT>TAT	p.H135Y
Pat_16	Post-Resistance	PES1	23481	37	22	30977009	30977009	Missense_Mutation	SNP	G	A	63	49	c.902C>T	c.(901-903)CCC>CTC	p.P301L
Pat_16	Post-Resistance	BPIL2	254240	37	22	32841915	32841915	Missense_Mutation	SNP	C	T	71	58	c.443G>A	c.(442-444)CGA>CAA	p.R148Q
Pat_16	Post-Resistance	RASD2	23551	37	22	35947968	35947968	Missense_Mutation	SNP	G	A	68	53	c.690G>A	c.(688-690)ATG>ATA	p.M230I
Pat_16	Post-Resistance	FOXRED2	80020	37	22	36894189	36894189	Missense_Mutation	SNP	G	A	28	63	c.1231C>T	c.(1231-1233)CGG>TGG	p.R411W
Pat_16	Post-Resistance	ELFN2	114794	37	22	37770901	37770901	Missense_Mutation	SNP	G	A	4	63	c.674C>T	c.(673-675)CCG>CTG	p.P225L
Pat_16	Post-Resistance	TRIOBP	11078	37	22	38120316	38120316	Missense_Mutation	SNP	C	T	120	617	c.1753C>T	c.(1753-1755)CCC>TCC	p.P585S
Pat_16	Post-Resistance	PDGFB	5155	37	22	39631866	39631866	Missense_Mutation	SNP	G	A	23	68	c.77C>T	c.(76-78)CCC>CTC	p.P26L
Pat_16	Post-Resistance	PARVG	64098	37	22	44583758	44583758	Nonsense_Mutation	SNP	C	T	43	96	c.247C>T	c.(247-249)CAG>TAG	p.Q83*
Pat_16	Post-Resistance	KLHDC7B	113730	37	22	50987478	50987478	Missense_Mutation	SNP	G	A	4	12	c.883G>A	c.(883-885)GGC>AGC	p.G295S
Pat_16	Post-Resistance	BRPF1	7862	37	3	9776260	9776260	Missense_Mutation	SNP	C	T	46	65	c.436C>T	c.(436-438)CCC>TCC	p.P146S
Pat_16	Post-Resistance	TMEM43	79188	37	3	14174407	14174407	Missense_Mutation	SNP	G	A	5	204	c.484G>A	c.(484-486)GAC>AAC	p.D162N
Pat_16	Post-Resistance	C3orf19	51244	37	3	14703141	14703141	Missense_Mutation	SNP	G	A	3	74	c.412G>A	c.(412-414)GGA>AGA	p.G138R
Pat_16	Post-Resistance	EAF1	85403	37	3	15471450	15471450	Missense_Mutation	SNP	C	T	54	45	c.134C>T	c.(133-135)TCC>TTC	p.S45F
Pat_16	Post-Resistance	SATB1	6304	37	3	18393533	18393533	Missense_Mutation	SNP	T	A	149	233	c.1730A>T	c.(1729-1731)CAT>CTT	p.H577L
Pat_16	Post-Resistance	KCNH8	131096	37	3	19492780	19492780	Missense_Mutation	SNP	C	T	37	43	c.1709C>T	c.(1708-1710)TCT>TTT	p.S570F

Pat_16	Post-Resistance	NEK10	152110	37	3	27213359	27213359	Missense_Mutation	SNP	A	C	20	29	c.718T>G	c.(718-720)TTA>GTA	p.L240V
Pat_16	Post-Resistance	GLB1	2720	37	3	33038614	33038614	Missense_Mutation	SNP	G	A	51	60	c.1957C>T	c.(1957-1959)CCC>TCC	p.P653S
Pat_16	Post-Resistance	STAC	6769	37	3	36484961	36484961	Missense_Mutation	SNP	G	A	25	58	c.217G>A	c.(217-219)GCA>ACA	p.A73T
Pat_16	Post-Resistance	TRANK1	9881	37	3	36873053	36873053	Missense_Mutation	SNP	A	C	9	19	c.6239T>G	c.(6238-6240)CTC>CGC	p.L2080R
Pat_16	Post-Resistance	ALS2CL	259173	37	3	46729657	46729657	Missense_Mutation	SNP	G	A	4	100	c.233C>T	c.(232-234)CCG>CTG	p.P78L
Pat_16	Post-Resistance	PTPN23	25930	37	3	47452005	47452005	Missense_Mutation	SNP	C	T	4	117	c.2717C>T	c.(2716-2718)CCC>CTC	p.P906L
Pat_16	Post-Resistance	LAMB2	3913	37	3	49163299	49163299	Missense_Mutation	SNP	G	A	103	113	c.2369C>T	c.(2368-2370)TCA>TTA	p.S790L
Pat_16	Post-Resistance	USP4	7375	37	3	49322316	49322316	Missense_Mutation	SNP	G	A	24	53	c.2237C>T	c.(2236-2238)ACT>ATT	p.T746I
Pat_16	Post-Resistance	BSN	8927	37	3	49689742	49689742	Missense_Mutation	SNP	C	T	3	35	c.2753C>T	c.(2752-2754)ACC>ATC	p.T918I
Pat_16	Post-Resistance	SEMA3F	6405	37	3	50220182	50220182	Missense_Mutation	SNP	C	T	45	69	c.869C>T	c.(868-870)CCC>CTC	p.P290L
Pat_16	Post-Resistance	SEMA3F	6405	37	3	50225363	50225363	Missense_Mutation	SNP	C	T	10	15	c.2173C>T	c.(2173-2175)CCT>TCT	p.P725S
Pat_16	Post-Resistance	CACNA2D2	9254	37	3	50421769	50421769	Splice_Site	SNP	C	T	99	205	c.511_splice	c.e6-1	p.D171_splice
Pat_16	Post-Resistance	DNAH1	25981	37	3	52397156	52397156	Missense_Mutation	SNP	C	T	27	23	c.5240C>T	c.(5239-5241)TCC>TTC	p.S1747F
Pat_16	Post-Resistance	ITIH3	3699	37	3	52831902	52831902	Missense_Mutation	SNP	G	A	6	8	c.619G>A	c.(619-621)GAC>AAC	p.D207N
Pat_16	Post-Resistance	SLMAP	7871	37	3	57898147	57898147	Missense_Mutation	SNP	G	A	4	194	c.1688G>A	c.(1687-1689)CGG>CAG	p.R563Q
Pat_16	Post-Resistance	FLNB	2317	37	3	58135678	58135678	Missense_Mutation	SNP	G	A	5	342	c.6193G>A	c.(6193-6195)GTG>ATG	p.V2065M
Pat_16	Post-Resistance	LRIG1	26018	37	3	66434654	66434654	Missense_Mutation	SNP	C	T	6	523	c.1832G>A	c.(1831-1833)CGG>CAG	p.R611Q
Pat_16	Post-Resistance	KBTBD8	84541	37	3	67058763	67058763	Missense_Mutation	SNP	G	A	53	73	c.1760G>A	c.(1759-1761)TGT>TAT	p.C587Y
Pat_16	Post-Resistance	FRMD4B	23150	37	3	69245538	69245538	Missense_Mutation	SNP	G	A	15	42	c.1102C>T	c.(1102-1104)CCT>TCT	p.P368S
Pat_16	Post-Resistance	C3orf26	84319	37	3	99879299	99879299	Missense_Mutation	SNP	C	A	3	24	c.179C>A	c.(178-180)CCA>CAA	p.P60Q
Pat_16	Post-Resistance	FAM55C	91775	37	3	101520553	101520553	Missense_Mutation	SNP	C	T	32	31	c.568C>T	c.(568-570)CCC>TCC	p.P190S
Pat_16	Post-Resistance	MYH15	22989	37	3	108117510	108117510	Missense_Mutation	SNP	C	T	72	105	c.5167G>A	c.(5167-5169)GAA>AAA	p.E1723K
Pat_16	Post-Resistance	DPPA4	55211	37	3	109049541	109049541	Missense_Mutation	SNP	A	C	35	69	c.509T>G	c.(508-510)CTT>CGT	p.L170R
Pat_16	Post-Resistance	KIAA2018	205717	37	3	113375371	113375371	Missense_Mutation	SNP	G	A	4	164	c.5158C>T	c.(5158-5160)CGT>TGT	p.R1720C
Pat_16	Post-Resistance	KIAA2018	205717	37	3	113377026	113377026	Missense_Mutation	SNP	G	A	20	32	c.3503C>T	c.(3502-3504)TCA>TTA	p.S1168L
Pat_16	Post-Resistance	POPDC2	64091	37	3	119378790	119378790	Missense_Mutation	SNP	G	A	4	232	c.481C>T	c.(481-483)CTC>TTC	p.L161F
Pat_16	Post-Resistance	ABTB1	80325	37	3	127398861	127398861	Missense_Mutation	SNP	G	A	5	314	c.1063G>A	c.(1063-1065)GTC>ATC	p.V355I
Pat_16	Post-Resistance	GATA2	2624	37	3	128204758	128204758	Missense_Mutation	SNP	G	A	17	43	c.683C>T	c.(682-684)CCC>CTC	p.P228L
Pat_16	Post-Resistance	ACPP	55	37	3	132047117	132047117	Missense_Mutation	SNP	C	T	75	53	c.127C>T	c.(127-129)CGG>TGG	p.R43W
Pat_16	Post-Resistance	BFSP2	8419	37	3	133119121	133119121	Missense_Mutation	SNP	G	A	4	81	c.194G>A	c.(193-195)TGC>TAC	p.C65Y
Pat_16	Post-Resistance	SLCO2A1	6578	37	3	133661546	133661547	Missense_Mutation	DNP	GG	AA	52	154	.1527_1528CC>T	525-1530)GTCCCC>GTT	p.P510S
Pat_16	Post-Resistance	EPHB1	2047	37	3	134851694	134851694	Missense_Mutation	SNP	G	A	29	83	c.1100G>A	c.(1099-1101)CGC>CAC	p.R367H
Pat_16	Post-Resistance	HPS3	84343	37	3	148859158	148859158	Missense_Mutation	SNP	T	C	159	301	c.961T>C	c.(961-963)TAC>CAC	p.Y321H
Pat_16	Post-Resistance	CP	1356	37	3	148939527	148939527	Nonsense_Mutation	SNP	C	T	16	53	c.53G>A	c.(52-54)TGG>TAG	p.W18*
Pat_16	Post-Resistance	B3GALNT1	8706	37	3	160803907	160803907	Missense_Mutation	SNP	A	C	13	24	c.636T>G	c.(634-636)AAT>AAG	p.N212K
Pat_16	Post-Resistance	ZBBX	79740	37	3	167016179	167016179	Missense_Mutation	SNP	A	T	38	75	c.1793T>A	c.(1792-1794)TTT>TAT	p.F598Y
Pat_16	Post-Resistance	MECOM	2122	37	3	168825731	168825731	Missense_Mutation	SNP	G	A	27	23	c.2023C>T	c.(2023-2025)CCT>TCT	p.P675S
Pat_16	Post-Resistance	PHC3	80012	37	3	169847185	169847185	Missense_Mutation	SNP	G	A	4	241	c.1039C>T	c.(1039-1041)CCC>TCC	p.P347S
Pat_16	Post-Resistance	EIF2B5	8893	37	3	183855762	183855762	Missense_Mutation	SNP	C	T	4	88	c.583C>T	c.(583-585)CGT>TGT	p.R195C
Pat_16	Post-Resistance	DVL3	1857	37	3	183882369	183882369	Missense_Mutation	SNP	G	A	5	181	c.443G>A	c.(442-444)CGG>CAG	p.R148Q
Pat_16	Post-Resistance	TBCCD1	55171	37	3	186276241	186276241	Missense_Mutation	SNP	G	A	88	200	c.457C>T	c.(457-459)CCT>TCT	p.P153S
Pat_16	Post-Resistance	TP63	8626	37	3	189582204	189582204	Missense_Mutation	SNP	G	A	36	61	c.763G>A	c.(763-765)GAG>AAG	p.E255K
Pat_16	Post-Resistance	GP5	2814	37	3	194118968	194118968	Missense_Mutation	SNP	C	T	3	54	c.44G>A	c.(43-45)CGC>CAC	p.R15H
Pat_16	Post-Resistance	LSG1	55341	37	3	194373772	194373772	Missense_Mutation	SNP	G	A	54	141	c.859C>T	c.(859-861)CCA>TCA	p.P287S
Pat_16	Post-Resistance	TFRC	7037	37	3	195785162	195785162	Missense_Mutation	SNP	A	G	146	86	c.1670T>C	c.(1669-1671)TTT>TCT	p.F557S
Pat_16	Post-Resistance	LRRC33	375387	37	3	196387690	196387690	Missense_Mutation	SNP	C	A	69	56	c.1176C>A	c.(1174-1176)CAC>CAA	p.H392Q
Pat_16	Post-Resistance	ZNF141	7700	37	4	367161	367161	Missense_Mutation	SNP	A	C	8	375	c.935A>C	c.(934-936)AAA>ACA	p.K312T

Pat_16	Post-Resistance	NOP14	8602	37	4	2946914	2946914	Missense_Mutation	SNP	C	T	3	39	c.1678G>A	c.(1678-1680)GAC>AAC	p.D560N
Pat_16	Post-Resistance	ZNF518B	85460	37	4	10444904	10444904	Missense_Mutation	SNP	G	A	25	83	c.3049C>T	c.(3049-3051)CAT>TAT	p.H1017Y
Pat_16	Post-Resistance	PPARGC1A	10891	37	4	23815598	23815598	Missense_Mutation	SNP	G	A	73	264	c.1508C>T	c.(1507-1509)TCA>TTA	p.S503L
Pat_16	Post-Resistance	DHX15	1665	37	4	24578242	24578242	Missense_Mutation	SNP	C	T	3	48	c.131G>A	c.(130-132)CGT>CAT	p.R44H
Pat_16	Post-Resistance	SEL1L3	23231	37	4	25789890	25789891	Missense_Mutation	DNP	CC	TT	118	345	.2172_2173GG>A	170-2175)ACGGAG>ACA	p.E725K
Pat_16	Post-Resistance	KLB	152831	37	4	39409123	39409123	Missense_Mutation	SNP	G	A	56	95	c.554G>A	c.(553-555)AGA>AAA	p.R185K
Pat_16	Post-Resistance	NSUN7	79730	37	4	40792702	40792702	Missense_Mutation	SNP	C	T	5	223	c.1120C>T	c.(1120-1122)CCT>TCT	p.P374S
Pat_16	Post-Resistance	KDR	3791	37	4	55976657	55976657	Missense_Mutation	SNP	C	T	61	33	c.1168G>A	c.(1168-1170)GAA>AAA	p.E390K
Pat_16	Post-Resistance	LPHN3	23284	37	4	62363041	62363041	Missense_Mutation	SNP	G	A	25	62	c.30G>A	c.(28-30)ATG>ATA	p.M10I
Pat_16	Post-Resistance	TMPRSS11B	132724	37	4	69095235	69095235	Splice_Site	SNP	C	T	20	86	c.687_splice	c.e8-1	p.K229_splice
Pat_16	Post-Resistance	SHROOM3	57619	37	4	77652072	77652072	Nonsense_Mutation	SNP	C	T	148	415	c.571C>T	c.(571-573)CAA>TAA	p.Q191*
Pat_16	Post-Resistance	FRAS1	80144	37	4	79351557	79351557	Missense_Mutation	SNP	G	A	9	41	c.4955G>A	c.(4954-4956)AGG>AAG	p.R1652K
Pat_16	Post-Resistance	GRID2	2895	37	4	94344063	94344063	Missense_Mutation	SNP	G	A	33	89	c.1489G>A	c.(1489-1491)GGA>AGA	p.G497R
Pat_16	Post-Resistance	PDHA2	5161	37	4	96761349	96761349	Missense_Mutation	SNP	A	T	39	124	c.48A>T	c.(46-48)AAA>AAT	p.K16N
Pat_16	Post-Resistance	ADH1C	126	37	4	100261800	100261800	Missense_Mutation	SNP	G	A	319	245	c.896C>T	c.(895-897)TCC>TTC	p.S299F
Pat_16	Post-Resistance	EGF	1950	37	4	110882040	110882040	Missense_Mutation	SNP	T	A	155	83	c.1084T>A	c.(1084-1086)TTT>ATT	p.F362I
Pat_16	Post-Resistance	ANK2	287	37	4	114158761	114158761	Missense_Mutation	SNP	G	A	105	291	c.676G>A	c.(676-678)GTG>ATG	p.V226M
Pat_16	Post-Resistance	PRDM5	11107	37	4	121737728	121737728	Missense_Mutation	SNP	A	G	32	84	c.745T>C	c.(745-747)TTT>CTT	p.F249L
Pat_16	Post-Resistance	ADAD1	132612	37	4	123317451	123317451	Missense_Mutation	SNP	G	A	8	44	c.643G>A	c.(643-645)GAA>AAA	p.E215K
Pat_16	Post-Resistance	NUDT6	11162	37	4	123843634	123843634	Missense_Mutation	SNP	C	T	4	95	c.94G>A	c.(94-96)GCA>ACA	p.A32T
Pat_16	Post-Resistance	FAT4	79633	37	4	126239412	126239412	Missense_Mutation	SNP	G	A	4	276	c.1846G>A	c.(1846-1848)GGA>AGA	p.G616R
Pat_16	Post-Resistance	FAT4	79633	37	4	126389676	126389676	Missense_Mutation	SNP	G	A	64	71	c.11909G>A	c.(11908-11910)GGA>GA	p.G3970E
Pat_16	Post-Resistance	C4orf29	80167	37	4	128949889	128949889	Missense_Mutation	SNP	G	A	4	266	c.959G>A	c.(958-960)CGC>CAC	p.R320H
Pat_16	Post-Resistance	NAA15	80155	37	4	140275246	140275246	Missense_Mutation	SNP	C	T	21	54	c.1081C>T	c.(1081-1083)CCC>TCC	p.P361S
Pat_16	Post-Resistance	SLC10A7	84068	37	4	147227095	147227095	Missense_Mutation	SNP	G	A	24	29	c.538C>T	c.(538-540)CCT>TCT	p.P180S
Pat_16	Post-Resistance	FHDC1	85462	37	4	153896944	153896944	Missense_Mutation	SNP	C	T	5	271	c.2501C>T	c.(2500-2502)GCC>GTC	p.A834V
Pat_16	Post-Resistance	DCHS2	54798	37	4	155237118	155237118	Missense_Mutation	SNP	G	A	26	72	c.3677C>T	c.(3676-3678)CCT>CTT	p.P1226L
Pat_16	Post-Resistance	DCHS2	54798	37	4	155241752	155241752	Missense_Mutation	SNP	C	T	5	287	c.3434G>A	c.(3433-3435)CGA>CAA	p.R1145Q
Pat_16	Post-Resistance	FGA	2243	37	4	155507586	155507586	Missense_Mutation	SNP	C	T	58	99	c.995G>A	c.(994-996)GGA>GAA	p.G332E
Pat_16	Post-Resistance	CTSO	1519	37	4	156864377	156864377	Missense_Mutation	SNP	G	A	53	127	c.175C>T	c.(175-177)CCC>TCC	p.P59S
Pat_16	Post-Resistance	TRIM60	166655	37	4	165962593	165962593	Missense_Mutation	SNP	G	A	12	40	c.1369G>A	c.(1369-1371)GAT>AAT	p.D457N
Pat_16	Post-Resistance	SPOCK3	50859	37	4	167656164	167656164	Missense_Mutation	SNP	C	T	19	49	c.1219G>A	c.(1219-1221)GAT>AAT	p.D407N
Pat_16	Post-Resistance	DDX60	55601	37	4	169206544	169206544	Missense_Mutation	SNP	C	T	17	20	c.1445G>A	c.(1444-1446)AGT>AAT	p.S482N
Pat_16	Post-Resistance	FRG1	2483	37	4	190878651	190878651	Missense_Mutation	SNP	G	A	6	232	c.531G>A	c.(529-531)ATG>ATA	p.M177I
Pat_16	Post-Resistance	PRLR	5618	37	5	35065819	35065819	Missense_Mutation	SNP	G	A	115	330	c.1241C>T	c.(1240-1242)TCA>TTA	p.S414L
Pat_16	Post-Resistance	IL7R	3575	37	5	35867469	35867469	Missense_Mutation	SNP	G	A	21	51	c.283G>A	c.(283-285)GAG>AAG	p.E95K
Pat_16	Post-Resistance	UGT3A2	167127	37	5	36036065	36036065	Missense_Mutation	SNP	G	A	4	154	c.1307C>T	c.(1306-1308)GCG>GTG	p.A436V
Pat_16	Post-Resistance	EGFLAM	133584	37	5	38370447	38370447	Missense_Mutation	SNP	G	A	86	50	c.595G>A	c.(595-597)GAC>AAC	p.D199N
Pat_16	Post-Resistance	HCN1	348980	37	5	45267196	45267196	Missense_Mutation	SNP	C	T	106	76	c.1778G>A	c.(1777-1779)CGA>CAA	p.R593Q
Pat_16	Post-Resistance	HSPB3	8988	37	5	53751759	53751759	Missense_Mutation	SNP	A	G	38	53	c.140A>G	c.(139-141)AAA>AGA	p.K47R
Pat_16	Post-Resistance	HMGCR	3156	37	5	74646107	74646107	Missense_Mutation	SNP	C	T	23	46	c.688C>T	c.(688-690)CGT>TGT	p.R230C
Pat_16	Post-Resistance	CMYA5	202333	37	5	79033696	79033696	Missense_Mutation	SNP	A	T	14	37	c.9108A>T	c.(9106-9108)GAA>GAT	p.E3036D
Pat_16	Post-Resistance	FAM172A	83989	37	5	93217337	93217337	Missense_Mutation	SNP	G	A	9	39	c.625C>T	c.(625-627)CCG>TCG	p.P209S
Pat_16	Post-Resistance	FAM81B	153643	37	5	94756087	94756087	Missense_Mutation	SNP	C	T	73	167	c.637C>T	c.(637-639)CTT>TTT	p.L213F
Pat_16	Post-Resistance	PCSK1	5122	37	5	95743978	95743978	Missense_Mutation	SNP	G	A	21	61	c.1145C>T	c.(1144-1146)TCG>TTG	p.S382L
Pat_16	Post-Resistance	CAMK4	814	37	5	110560209	110560209	Missense_Mutation	SNP	T	C	3	34	c.28T>C	c.(28-30)TCC>CCC	p.S10P
Pat_16	Post-Resistance	CAMK4	814	37	5	110819954	110819954	Missense_Mutation	SNP	A	T	41	23	c.1212A>T	c.(1210-1212)AAA>AAT	p.K404N

Pat_16	Post-Resistance	PRR16	51334	37	5	120021953	120021953	Missense_Mutation	SNP	G	A	4	138	c.464G>A	c.(463-465)CGA>CAA	p.R155Q
Pat_16	Post-Resistance	ALDH7A1	501	37	5	125930712	125930712	Missense_Mutation	SNP	C	G	28	7	c.179G>C	c.(178-180)GGA>GCA	p.G60A
Pat_16	Post-Resistance	C5orf48	389320	37	5	125968322	125968322	Missense_Mutation	SNP	G	A	34	73	c.171G>A	c.(169-171)ATG>ATA	p.M57I
Pat_16	Post-Resistance	TMEM173	340061	37	5	138857920	138857920	Missense_Mutation	SNP	G	A	4	221	c.694C>T	c.(694-696)CAT>TAT	p.H232Y
Pat_16	Post-Resistance	HARS	3035	37	5	140054286	140054286	Missense_Mutation	SNP	C	T	6	402	c.1436G>A	c.(1435-1437)CGT>CAT	p.R479H
Pat_16	Post-Resistance	PCDHA12	56137	37	5	140255958	140255958	Missense_Mutation	SNP	G	A	91	71	c.901G>A	c.(901-903)GAA>AAA	p.E301K
Pat_16	Post-Resistance	PCDHA12	56137	37	5	140256858	140256858	Missense_Mutation	SNP	T	A	46	148	c.1801T>A	c.(1801-1803)TCC>ACC	p.S601T
Pat_16	Post-Resistance	PCDHB3	56132	37	5	140480621	140480621	Missense_Mutation	SNP	T	G	48	148	c.388T>G	c.(388-390)TCT>GCT	p.S130A
Pat_16	Post-Resistance	PCDHB3	56132	37	5	140482598	140482598	Missense_Mutation	SNP	T	A	164	120	c.2365T>A	c.(2365-2367)TTC>ATC	p.F789I
Pat_16	Post-Resistance	PCDHB8	56128	37	5	140558076	140558076	Missense_Mutation	SNP	C	T	34	714	c.461C>T	c.(460-462)CCT>CTT	p.P154L
Pat_16	Post-Resistance	PCDHB8	56128	37	5	140559324	140559324	Missense_Mutation	SNP	C	T	25	226	c.1709C>T	c.(1708-1710)TCC>TTC	p.S570F
Pat_16	Post-Resistance	SLC25A2	83884	37	5	140682877	140682877	Missense_Mutation	SNP	A	G	26	62	c.556T>C	c.(556-558)TTT>CTT	p.F186L
Pat_16	Post-Resistance	PCDHGB3	56102	37	5	140751933	140751933	Missense_Mutation	SNP	G	A	4	161	c.1972G>A	c.(1972-1974)GTC>ATC	p.V658I
Pat_16	Post-Resistance	NDFIP1	80762	37	5	141511890	141511890	Missense_Mutation	SNP	C	T	199	141	c.265C>T	c.(265-267)CCT>TCT	p.P89S
Pat_16	Post-Resistance	KCTD16	57528	37	5	143853540	143853540	Missense_Mutation	SNP	G	A	14	51	c.1150G>A	c.(1150-1152)GCT>ACT	p.A384T
Pat_16	Post-Resistance	TCERG1	10915	37	5	145850279	145850279	Missense_Mutation	SNP	C	T	14	38	c.1480C>T	c.(1480-1482)CCT>TCT	p.P494S
Pat_16	Post-Resistance	HTR4	3360	37	5	147929772	147929772	Missense_Mutation	SNP	G	A	81	251	c.80C>T	c.(79-81)TCG>TTG	p.S27L
Pat_16	Post-Resistance	ABLIM3	22885	37	5	148619377	148619377	Missense_Mutation	SNP	T	C	112	233	c.1130T>C	c.(1129-1131)ATA>ACA	p.I377T
Pat_16	Post-Resistance	SLC6A7	6534	37	5	149574444	149574444	Missense_Mutation	SNP	T	G	69	149	c.187T>G	c.(187-189)TTC>GTC	p.F63V
Pat_16	Post-Resistance	ZNF300	91975	37	5	150275165	150275165	Missense_Mutation	SNP	C	T	12	75	c.1636G>A	c.(1636-1638)GAG>AAG	p.E546K
Pat_16	Post-Resistance	SLC36A1	206358	37	5	150867748	150867748	Missense_Mutation	SNP	C	T	55	40	c.1364C>T	c.(1363-1365)GCT>GTT	p.A455V
Pat_16	Post-Resistance	HAVCR2	84868	37	5	156533766	156533766	Missense_Mutation	SNP	C	T	4	275	c.266G>A	c.(265-267)CGC>CAC	p.R89H
Pat_16	Post-Resistance	CYFIP2	26999	37	5	156768085	156768085	Missense_Mutation	SNP	C	T	4	260	c.2593C>T	c.(2593-2595)CGG>TGG	p.R865W
Pat_16	Post-Resistance	ADRA1B	147	37	5	159344336	159344336	Missense_Mutation	SNP	G	A	42	111	c.424G>A	c.(424-426)GAT>AAT	p.D142N
Pat_16	Post-Resistance	CCNJL	79616	37	5	159680534	159680534	Missense_Mutation	SNP	G	A	5	217	c.1159C>T	c.(1159-1161)CCC>TCC	p.P387S
Pat_16	Post-Resistance	KCNMB1	3779	37	5	169810728	169810728	Nonsense_Mutation	SNP	C	T	50	207	c.261G>A	c.(259-261)TGG>TGA	p.W87*
Pat_16	Post-Resistance	KCNIP1	30820	37	5	170147349	170147349	Missense_Mutation	SNP	G	A	49	132	c.244G>A	c.(244-246)GAA>AAA	p.E82K
Pat_16	Post-Resistance	DDX41	51428	37	5	176939551	176939551	Missense_Mutation	SNP	G	A	27	56	c.1495C>T	c.(1495-1497)CCT>TCT	p.P499S
Pat_16	Post-Resistance	ZNF354C	30832	37	5	178505930	178505930	Missense_Mutation	SNP	G	A	41	97	c.497G>A	c.(496-498)GGG>GAG	p.G166E
Pat_16	Post-Resistance	TBC1D9B	23061	37	5	179297386	179297386	Missense_Mutation	SNP	C	T	4	250	c.2594G>A	c.(2593-2595)CGG>CAG	p.R865Q
Pat_16	Post-Resistance	MAPK9	5601	37	5	179663484	179663484	Missense_Mutation	SNP	G	A	5	311	c.1175C>T	c.(1174-1176)TCG>TTG	p.S392L
Pat_16	Post-Resistance	GFPT2	9945	37	5	179729481	179729481	Missense_Mutation	SNP	A	G	70	178	c.1946T>C	c.(1945-1947)CTG>CCG	p.L649P
Pat_16	Post-Resistance	TRIM7	81786	37	5	180622549	180622549	Missense_Mutation	SNP	G	A	38	84	c.1153C>T	c.(1153-1155)CGC>TGC	p.R385C
Pat_16	Post-Resistance	EXOC2	55770	37	6	633049	633049	Nonsense_Mutation	SNP	G	A	5	281	c.187C>T	c.(187-189)CGA>TGA	p.R63*
Pat_16	Post-Resistance	F13A1	2162	37	6	6196100	6196100	Missense_Mutation	SNP	G	A	4	213	c.1235C>T	c.(1234-1236)CCC>CTC	p.P412L
Pat_16	Post-Resistance	HIVEP1	3096	37	6	12122090	12122090	Missense_Mutation	SNP	C	T	34	113	c.2062C>T	c.(2062-2064)CCA>TCA	p.P688S
Pat_16	Post-Resistance	SLC17A3	10786	37	6	25862532	25862532	Missense_Mutation	SNP	C	T	5	223	c.232G>A	c.(232-234)GAT>AAT	p.D78N
Pat_16	Post-Resistance	ZKSCAN3	80317	37	6	28327466	28327466	Missense_Mutation	SNP	C	T	34	171	c.103C>T	c.(103-105)CCC>TCC	p.P35S
Pat_16	Post-Resistance	OR2W1	26692	37	6	29012073	29012073	Missense_Mutation	SNP	T	G	15	18	c.880A>C	c.(880-882)AAT>CAT	p.N294H
Pat_16	Post-Resistance	MOG	4340	37	6	29635420	29635420	Missense_Mutation	SNP	G	A	56	103	c.551G>A	c.(550-552)GGA>GAA	p.G184E
Pat_16	Post-Resistance	PPP1R10	5514	37	6	30574254	30574254	Missense_Mutation	SNP	G	A	4	272	c.625C>T	c.(625-627)CGT>TGT	p.R209C
Pat_16	Post-Resistance	CFB	629	37	6	31914819	31914819	Missense_Mutation	SNP	G	A	6	380	c.334G>A	c.(334-336)GGG>AGG	p.G112R
Pat_16	Post-Resistance	ZBTB22	9278	37	6	33283015	33283015	Missense_Mutation	SNP	C	T	5	201	c.1679G>A	c.(1678-1680)CGA>CAA	p.R560Q
Pat_16	Post-Resistance	KIFC1	3833	37	6	33374019	33374019	Missense_Mutation	SNP	G	A	6	553	c.1583G>A	c.(1582-1584)CGC>CAC	p.R528H
Pat_16	Post-Resistance	SCUBE3	222663	37	6	35199628	35199628	Missense_Mutation	SNP	G	A	6	269	c.461G>A	c.(460-462)CGG>CAG	p.R154Q
Pat_16	Post-Resistance	PI16	221476	37	6	36931352	36931352	Missense_Mutation	SNP	G	A	63	241	c.1234G>A	c.(1234-1236)GGT>AGT	p.G412S
Pat_16	Post-Resistance	CAPN11	11131	37	6	44144382	44144382	Missense_Mutation	SNP	G	A	4	239	c.1066G>A	c.(1066-1068)GGG>AGG	p.G356R

Pat_16	Post-Resistance	GPR116	221395	37	6	46849223	46849223	Missense_Mutation	SNP	C	T	111	137	c.783G>A	c.(781-783)ATG>ATA	p.M261I
Pat_16	Post-Resistance	TNFRSF21	27242	37	6	47254246	47254246	Missense_Mutation	SNP	G	A	4	143	c.182C>T	c.(181-183)ACC>ATC	p.T61I
Pat_16	Post-Resistance	GFRAL	389400	37	6	55196618	55196618	Missense_Mutation	SNP	G	A	59	84	c.128G>A	c.(127-129)AGA>AAA	p.R43K
Pat_16	Post-Resistance	HMGCLL1	54511	37	6	55364050	55364050	Missense_Mutation	SNP	G	A	4	302	c.680C>T	c.(679-681)CCG>CTG	p.P227L
Pat_16	Post-Resistance	ROS1	6098	37	6	117631320	117631321	Missense_Mutation	DNP	CC	TT	50	118	.6357_6358GG>A	355-6360)GGGGAA>GGA	p.E2120K
Pat_16	Post-Resistance	VNN3	55350	37	6	133055815	133055815	Missense_Mutation	SNP	A	T	34	4	c.17T>A	c.(16-18)TTT>TAT	p.F6Y
Pat_16	Post-Resistance	IPCEF1	26034	37	6	154489155	154489155	Missense_Mutation	SNP	G	A	4	280	c.1001C>T	c.(1000-1002)TCG>TTG	p.S334L
Pat_16	Post-Resistance	MICALL2	79778	37	7	1482031	1482031	Missense_Mutation	SNP	G	A	81	539	c.1508C>T	c.(1507-1509)TCG>TTG	p.S503L
Pat_16	Post-Resistance	CHST12	55501	37	7	2473175	2473175	Missense_Mutation	SNP	G	A	4	171	c.901G>A	c.(901-903)GCC>ACC	p.A301T
Pat_16	Post-Resistance	CARD11	84433	37	7	2979526	2979526	Missense_Mutation	SNP	C	T	125	293	c.721G>A	c.(721-723)GAG>AAG	p.E241K
Pat_16	Post-Resistance	KIAA0415	9907	37	7	4824677	4824677	Missense_Mutation	SNP	G	A	4	168	c.929G>A	c.(928-930)CGA>CAA	p.R310Q
Pat_16	Post-Resistance	ETV1	2115	37	7	13935508	13935508	Missense_Mutation	SNP	C	T	15	96	c.1417G>A	c.(1417-1419)GAA>AAA	p.E473K
Pat_16	Post-Resistance	AGR2	10551	37	7	16841412	16841413	Missense_Mutation	DNP	TT	CA	95	76	c.8_9AA>TG	c.(7-9)AAA>ATG	p.K3M
Pat_16	Post-Resistance	DNAH11	8701	37	7	21784183	21784183	Missense_Mutation	SNP	G	A	56	51	c.8303G>A	c.(8302-8304)AGA>AAA	p.R2768K
Pat_16	Post-Resistance	STK31	56164	37	7	23768836	23768836	Missense_Mutation	SNP	C	T	25	35	c.451C>T	c.(451-453)CCT>TCT	p.P151S
Pat_16	Post-Resistance	SKAP2	8935	37	7	26765185	26765185	Splice_Site	SNP	C	T	25	102	c.659_splice	c.e9-1	p.D220_splice
Pat_16	Post-Resistance	LOC402644	402644	37	7	28318921	28318922	Missense_Mutation	DNP	CT	TC	154	144	c.397_398AG>GA	c.(397-399)AGA>GAA	p.R133E
Pat_16	Post-Resistance	AQP1	358	37	7	30961729	30961729	Missense_Mutation	SNP	G	A	5	355	c.433G>A	c.(433-435)GGG>AGG	p.G145R
Pat_16	Post-Resistance	DPY19L2P1	554236	37	7	35163615	35163615	Missense_Mutation	SNP	C	T	38	58	c.481G>A	c.(481-483)GAC>AAC	p.D161N
Pat_16	Post-Resistance	PURB	5814	37	7	44924053	44924053	Missense_Mutation	SNP	C	T	6	591	c.895G>A	c.(895-897)GGC>AGC	p.G299S
Pat_16	Post-Resistance	VSTM2A	222008	37	7	54610419	54610419	Translation_Start_Site	SNP	T	A	89	60	c.-4T>A	c.(-6--2)TTTTG>TTATG	
Pat_16	Post-Resistance	ZNF716	441234	37	7	57529023	57529023	Missense_Mutation	SNP	T	C	7	359	c.856T>C	c.(856-858)TAC>CAC	p.Y286H
Pat_16	Post-Resistance	ZNF716	441234	37	7	57529048	57529048	Missense_Mutation	SNP	A	G	8	426	c.881A>G	c.(880-882)AAA>AGA	p.K294R
Pat_16	Post-Resistance	ZNF716	441234	37	7	57529057	57529057	Missense_Mutation	SNP	C	A	8	438	c.890C>A	c.(889-891)ACA>AAA	p.T297K
Pat_16	Post-Resistance	ZNF735	730291	37	7	63680426	63680426	Missense_Mutation	SNP	G	A	6	434	c.997G>A	c.(997-999)GCC>ACC	p.A333T
Pat_16	Post-Resistance	AUTS2	26053	37	7	70228066	70228066	Missense_Mutation	SNP	C	T	24	128	c.953C>T	c.(952-954)CCT>CTT	p.P318L
Pat_16	Post-Resistance	DTX2	113878	37	7	76132828	76132828	Missense_Mutation	SNP	G	A	4	119	c.1475G>A	c.(1474-1476)CGG>CAG	p.R492Q
Pat_16	Post-Resistance	SEMA3C	10512	37	7	80435062	80435062	Missense_Mutation	SNP	A	T	18	28	c.551T>A	c.(550-552)TTC>TAC	p.F184Y
Pat_16	Post-Resistance	HGF	3082	37	7	81372738	81372739	Nonsense_Mutation	DNP	GG	AA	157	90	c.795_796CC>TT	793-798)GGCCAG>GGTT	p.Q266*
Pat_16	Post-Resistance	DMTF1	9988	37	7	86813826	86813826	Nonsense_Mutation	SNP	C	T	4	185	c.934C>T	c.(934-936)CGA>TGA	p.R312*
Pat_16	Post-Resistance	CCDC132	55610	37	7	92970884	92970884	Missense_Mutation	SNP	C	T	49	190	c.2204C>T	c.(2203-2205)TCC>TTC	p.S735F
Pat_16	Post-Resistance	SLC25A13	10165	37	7	95751046	95751046	Nonsense_Mutation	SNP	G	A	6	466	c.1762C>T	c.(1762-1764)CGA>TGA	p.R588*
Pat_16	Post-Resistance	CYP3A5	1577	37	7	99272168	99272168	Missense_Mutation	SNP	C	T	111	115	c.206G>A	c.(205-207)GGA>GAA	p.G69E
Pat_16	Post-Resistance	ACTL6B	51412	37	7	100252698	100252698	Missense_Mutation	SNP	T	C	4	295	c.313A>G	c.(313-315)AGC>GGC	p.S105G
Pat_16	Post-Resistance	ZAN	7455	37	7	100350024	100350024	Missense_Mutation	SNP	C	T	7	413	c.2296C>T	c.(2296-2298)CCC>TCC	p.P766S
Pat_16	Post-Resistance	ZAN	7455	37	7	100350033	100350033	Missense_Mutation	SNP	T	C	7	424	c.2305T>C	c.(2305-2307)TCC>CCC	p.S769P
Pat_16	Post-Resistance	ZAN	7455	37	7	100350052	100350052	Missense_Mutation	SNP	T	C	5	450	c.2324T>C	c.(2323-2325)ATC>ACC	p.I775T
Pat_16	Post-Resistance	EPHB4	2050	37	7	100405129	100405129	Missense_Mutation	SNP	A	C	275	391	c.2192T>G	c.(2191-2193)CTT>CGT	p.L731R
Pat_16	Post-Resistance	MUC17	140453	37	7	100678520	100678520	Missense_Mutation	SNP	G	A	329	496	c.3823G>A	c.(3823-3825)GAA>AAA	p.E1275K
Pat_16	Post-Resistance	ALKBH4	54784	37	7	102100061	102100061	Missense_Mutation	SNP	C	T	6	493	c.311G>A	c.(310-312)CGG>CAG	p.R104Q
Pat_16	Post-Resistance	SLC26A3	1811	37	7	107408046	107408046	Missense_Mutation	SNP	C	T	26	54	c.2249G>A	c.(2248-2250)GGA>GAA	p.G750E
Pat_16	Post-Resistance	LAMB4	22798	37	7	107678038	107678038	Missense_Mutation	SNP	C	T	113	106	c.4474G>A	c.(4474-4476)GAA>AAA	p.E1492K
Pat_16	Post-Resistance	DOCK4	9732	37	7	111368526	111368526	Missense_Mutation	SNP	G	A	29	114	c.5705C>T	c.(5704-5706)CCG>CTG	p.P1902L
Pat_16	Post-Resistance	PPP1R3A	5506	37	7	113518058	113518058	Missense_Mutation	SNP	C	T	147	331	c.3089G>A	c.(3088-3090)GGA>GAA	p.G1030E
Pat_16	Post-Resistance	PPP1R3A	5506	37	7	113518735	113518735	Missense_Mutation	SNP	T	G	20	117	c.2412A>C	c.(2410-2412)GAA>GAC	p.E804D
Pat_16	Post-Resistance	PPP1R3A	5506	37	7	113518737	113518737	Missense_Mutation	SNP	C	T	21	114	c.2410G>A	c.(2410-2412)GAA>AAA	p.E804K
Pat_16	Post-Resistance	ING3	54556	37	7	120607624	120607624	Missense_Mutation	SNP	C	T	22	115	c.478C>T	c.(478-480)CAT>TAT	p.H160Y

Pat_16	Post-Resistance	FLNC	2318	37	7	128494697	128494697	Missense_Mutation	SNP	G	A	16	58	c.6958G>A	c.(6958-6960)GGA>AGA	p.G2320R
Pat_16	Post-Resistance	IRF5	3663	37	7	128588784	128588784	Missense_Mutation	SNP	G	A	4	283	c.1427G>A	c.(1426-1428)CGG>CAG	p.R476Q
Pat_16	Post-Resistance	FAM40B	57464	37	7	129122704	129122704	Missense_Mutation	SNP	G	A	205	220	c.2071G>A	c.(2071-2073)GCA>ACA	p.A691T
Pat_16	Post-Resistance	PLXNA4	91584	37	7	131859659	131859659	Missense_Mutation	SNP	C	T	63	363	c.3895G>A	c.(3895-3897)GAC>AAC	p.D1299N
Pat_16	Post-Resistance	AKR1B10	57016	37	7	134215537	134215537	Missense_Mutation	SNP	G	A	5	519	c.209G>A	c.(208-210)CGG>CAG	p.R70Q
Pat_16	Post-Resistance	UBN2	254048	37	7	138958812	138958812	Missense_Mutation	SNP	G	A	4	109	c.1965G>A	c.(1963-1965)ATG>ATA	p.M655I
Pat_16	Post-Resistance	JHDM1D	80853	37	7	139791679	139791679	Missense_Mutation	SNP	A	C	74	272	c.2656T>G	c.(2656-2658)TCC>GCC	p.S886A
Pat_16	Post-Resistance	BRAF	673	37	7	140453136	140453136	Missense_Mutation	SNP	A	T	120	128	c.1799T>A	c.(1798-1800)GTG>GAG	p.V600E
Pat_16	Post-Resistance	TAS2R38	5726	37	7	141673404	141673404	Missense_Mutation	SNP	C	T	158	294	c.86G>A	c.(85-87)GGG>GAG	p.G29E
Pat_16	Post-Resistance	TRYX3	136541	37	7	141952429	141952429	Missense_Mutation	SNP	T	C	77	110	c.439A>G	c.(439-441)AAA>GAA	p.K147E
Pat_16	Post-Resistance	TRPV5	56302	37	7	142626540	142626540	Missense_Mutation	SNP	C	T	5	326	c.470G>A	c.(469-471)CGC>CAC	p.R157H
Pat_16	Post-Resistance	TAS2R60	338398	37	7	143140918	143140918	Missense_Mutation	SNP	T	A	392	274	c.373T>A	c.(373-375)TTC>ATC	p.F125I
Pat_16	Post-Resistance	ACCN3	9311	37	7	150749275	150749275	Missense_Mutation	SNP	G	A	117	637	c.1409G>A	c.(1408-1410)GGA>GAA	p.G470E
Pat_16	Post-Resistance	CSMD1	64478	37	8	3216769	3216769	Missense_Mutation	SNP	G	A	137	79	c.3212C>T	c.(3211-3213)TCC>TTC	p.S1071F
Pat_16	Post-Resistance	SGK223	157285	37	8	8235459	8235459	Missense_Mutation	SNP	G	A	4	291	c.460C>T	c.(460-462)CGC>TGC	p.R154C
Pat_16	Post-Resistance	MTMR7	9108	37	8	17228656	17228656	Missense_Mutation	SNP	C	T	128	450	c.200G>A	c.(199-201)GGA>GAA	p.G67E
Pat_16	Post-Resistance	SORBS3	10174	37	8	22428730	22428730	Missense_Mutation	SNP	C	T	21	163	c.1739C>T	c.(1738-1740)ACC>ATC	p.T580I
Pat_16	Post-Resistance	SLC25A37	51312	37	8	23423681	23423681	Missense_Mutation	SNP	C	T	63	34	c.271C>T	c.(271-273)CTC>TTC	p.L91F
Pat_16	Post-Resistance	EIF4EBP1	1978	37	8	37914667	37914667	Missense_Mutation	SNP	C	T	284	132	c.214C>T	c.(214-216)CCA>TCA	p.P72S
Pat_16	Post-Resistance	GINS4	84296	37	8	41397511	41397511	Missense_Mutation	SNP	C	T	4	236	c.472C>T	c.(472-474)CTC>TTC	p.L158F
Pat_16	Post-Resistance	ANK1	286	37	8	41551520	41551520	Missense_Mutation	SNP	C	T	4	136	c.3428G>A	c.(3427-3429)CGC>CAC	p.R1143H
Pat_16	Post-Resistance	SLC20A2	6575	37	8	42294807	42294807	Missense_Mutation	SNP	G	A	39	145	c.1223C>T	c.(1222-1224)TCG>TTG	p.S408L
Pat_16	Post-Resistance	PXDNL	137902	37	8	52232512	52232512	Missense_Mutation	SNP	C	T	76	37	c.4331G>A	c.(4330-4332)GGA>GAA	p.G1444E
Pat_16	Post-Resistance	PXDNL	137902	37	8	52320945	52320946	Missense_Mutation	DNP	GG	AA	9	52	.3238_3239CC>T	c.(3238-3240)CCG>TTG	p.P1080L
Pat_16	Post-Resistance	TGS1	96764	37	8	56695312	56695312	Missense_Mutation	SNP	G	A	4	248	c.107G>A	c.(106-108)CGA>CAA	p.R36Q
Pat_16	Post-Resistance	PENK	5179	37	8	57354297	57354297	Missense_Mutation	SNP	T	A	21	95	c.338A>T	c.(337-339)AAA>ATA	p.K113I
Pat_16	Post-Resistance	CLVS1	157807	37	8	62212762	62212762	Missense_Mutation	SNP	T	C	29	129	c.376T>C	c.(376-378)TTC>CTC	p.F126L
Pat_16	Post-Resistance	PI15	51050	37	8	75757656	75757656	Missense_Mutation	SNP	C	T	79	289	c.565C>T	c.(565-567)CAT>TAT	p.H189Y
Pat_16	Post-Resistance	CA1	759	37	8	86242024	86242024	Missense_Mutation	SNP	G	A	19	21	c.563C>T	c.(562-564)TCA>TTA	p.S188L
Pat_16	Post-Resistance	REXO1L1	254958	37	8	86574444	86574444	Missense_Mutation	SNP	C	T	5	62	c.779G>A	c.(778-780)CGC>CAC	p.R260H
Pat_16	Post-Resistance	ANGPT1	284	37	8	108334328	108334328	Missense_Mutation	SNP	C	T	4	26	c.604G>A	c.(604-606)GAA>AAA	p.E202K
Pat_16	Post-Resistance	ASAP1	50807	37	8	131088611	131088611	Missense_Mutation	SNP	G	A	58	25	c.2684C>T	c.(2683-2685)CCT>CTT	p.P895L
Pat_16	Post-Resistance	ADCY8	114	37	8	131880120	131880120	Missense_Mutation	SNP	C	T	54	167	c.2182G>A	c.(2182-2184)GCA>ACA	p.A728T
Pat_16	Post-Resistance	TG	7038	37	8	133925417	133925417	Missense_Mutation	SNP	C	T	43	175	c.4285C>T	c.(4285-4287)CAC>TAC	p.H1429Y
Pat_16	Post-Resistance	DENND3	22898	37	8	142202543	142202543	Missense_Mutation	SNP	C	T	18	84	c.3253C>T	c.(3253-3255)CCT>TCT	p.P1085S
Pat_16	Post-Resistance	LYPD2	137797	37	8	143832556	143832556	Missense_Mutation	SNP	G	A	73	270	c.91C>T	c.(91-93)CCC>TCC	p.P31S
Pat_16	Post-Resistance	CYP11B1	1584	37	8	143958215	143958215	Missense_Mutation	SNP	C	T	27	14	c.682G>A	c.(682-684)GAG>AAG	p.E228K
Pat_16	Post-Resistance	ZC3H3	23144	37	8	144550663	144550663	Missense_Mutation	SNP	C	T	4	43	c.1994G>A	c.(1993-1995)CGC>CAC	p.R665H
Pat_16	Post-Resistance	GPR172A	79581	37	8	145583036	145583036	Missense_Mutation	SNP	A	G	4	97	c.83A>G	c.(82-84)AAT>AGT	p.N28S
Pat_16	Post-Resistance	FOXH1	8928	37	8	145699782	145699782	Missense_Mutation	SNP	C	T	168	72	c.937G>A	c.(937-939)GTG>ATG	p.V313M
Pat_16	Post-Resistance	GPT	2875	37	8	145730425	145730425	Missense_Mutation	SNP	G	A	4	152	c.406G>A	c.(406-408)GTG>ATG	p.V136M
Pat_16	Post-Resistance	DOCK8	81704	37	9	386341	386341	Missense_Mutation	SNP	G	A	4	159	c.2789G>A	c.(2788-2790)CGC>CAC	p.R930H
Pat_16	Post-Resistance	VCP	7415	37	9	35059143	35059143	Missense_Mutation	SNP	C	T	4	204	c.2078G>A	c.(2077-2079)CGT>CAT	p.R693H
Pat_16	Post-Resistance	FAM75A6	389730	37	9	43627096	43627096	Missense_Mutation	SNP	G	A	349	53	c.1591C>T	c.(1591-1593)CTC>TTC	p.L531F
Pat_16	Post-Resistance	RMI1	80010	37	9	86617211	86617211	Missense_Mutation	SNP	C	T	5	16	c.1310C>T	c.(1309-1311)TCC>TTC	p.S437F
Pat_16	Post-Resistance	C9orf102	375748	37	9	98691032	98691032	Missense_Mutation	SNP	C	T	5	221	c.1670C>T	c.(1669-1671)GCG>GTG	p.A557V
Pat_16	Post-Resistance	OR13C4	138804	37	9	107288820	107288820	Missense_Mutation	SNP	G	A	223	34	c.671C>T	c.(670-672)ACC>ATC	p.T224I

Pat_16	Post-Resistance	KIAA1958	158405	37	9	115336703	115336703	Missense_Mutation	SNP	C	T	4	165	c.343C>T	c.(343-345)CGG>TGG	p.R115W
Pat_16	Post-Resistance	ASTN2	23245	37	9	119858377	119858377	Missense_Mutation	SNP	C	T	128	29	c.1222G>A	c.(1222-1224)GAA>AAA	p.E408K
Pat_16	Post-Resistance	CEP110	11064	37	9	123886288	123886288	Missense_Mutation	SNP	G	A	4	112	c.1730G>A	c.(1729-1731)CGT>CAT	p.R577H
Pat_16	Post-Resistance	STOM	2040	37	9	124111550	124111550	Missense_Mutation	SNP	G	A	4	251	c.373C>T	c.(373-375)CGC>TGC	p.R125C
Pat_16	Post-Resistance	COQ4	51117	37	9	131088075	131088075	Missense_Mutation	SNP	C	T	108	23	c.317C>T	c.(316-318)TCG>TTG	p.S106L
Pat_16	Post-Resistance	SPTAN1	6709	37	9	131339474	131339475	Nonsense_Mutation	DNP	CC	TT	145	26	c.852_853CC>TT	850-855)GGCCGA>GGTT	p.R285*
Pat_16	Post-Resistance	FUBP3	8939	37	9	133506104	133506104	Missense_Mutation	SNP	C	T	3	73	c.1207C>T	c.(1207-1209)CGG>TGG	p.R403W
Pat_16	Post-Resistance	DPP7	29952	37	9	140006403	140006403	Missense_Mutation	SNP	G	A	4	87	c.1129C>T	c.(1129-1131)CTC>TTC	p.L377F
Pat_16	Post-Resistance	ANAPC2	29882	37	9	140082888	140082888	Missense_Mutation	SNP	G	A	4	43	c.97C>T	c.(97-99)CCG>TCG	p.P33S
Pat_16	Post-Resistance	SLC34A3	142680	37	9	140127244	140127244	Missense_Mutation	SNP	G	A	61	20	c.313G>A	c.(313-315)GCC>ACC	p.A105T
Pat_16	Post-Resistance	FAM9B	171483	37	X	8998366	8998366	Missense_Mutation	SNP	C	T	8	5	c.217G>A	c.(217-219)GAT>AAT	p.D73N
Pat_16	Post-Resistance	FRMPD4	9758	37	X	12712519	12712519	Missense_Mutation	SNP	T	G	68	8	c.879T>G	c.(877-879)GAT>GAG	p.D293E
Pat_16	Post-Resistance	RBBP7	5931	37	X	16870948	16870948	Missense_Mutation	SNP	G	A	6	582	c.809C>T	c.(808-810)GCG>GTG	p.A270V
Pat_16	Post-Resistance	POLA1	5422	37	X	25014054	25014054	Missense_Mutation	SNP	C	T	71	18	c.4376C>T	c.(4375-4377)GCC>GTC	p.A1459V
Pat_16	Post-Resistance	FAM47C	442444	37	X	37027345	37027345	Nonsense_Mutation	SNP	A	T	44	81	c.862A>T	c.(862-864)AAG>TAG	p.K288*
Pat_16	Post-Resistance	USP9X	8239	37	X	41029282	41029282	Nonsense_Mutation	SNP	C	T	6	346	c.2671C>T	c.(2671-2673)CGA>TGA	p.R891*
Pat_16	Post-Resistance	CLCN5	1184	37	X	49837183	49837183	Missense_Mutation	SNP	C	T	78	131	c.145C>T	c.(145-147)CAC>TAC	p.H49Y
Pat_16	Post-Resistance	MAGED2	10916	37	X	54837323	54837323	Nonsense_Mutation	SNP	C	T	3	44	c.607C>T	c.(607-609)CGA>TGA	p.R203*
Pat_16	Post-Resistance	SLC7A3	84889	37	X	70147375	70147375	Missense_Mutation	SNP	C	T	3	59	c.1142G>A	c.(1141-1143)CGC>CAC	p.R381H
Pat_16	Post-Resistance	MED12	9968	37	X	70345264	70345264	Nonsense_Mutation	SNP	C	T	4	85	c.2290C>T	c.(2290-2292)CGA>TGA	p.R764*
Pat_16	Post-Resistance	MAGEE1	57692	37	X	75649314	75649314	Missense_Mutation	SNP	T	C	3	70	c.991T>C	c.(991-993)TCC>CCC	p.S331P
Pat_16	Post-Resistance	CYLC1	1538	37	X	83129484	83129484	Missense_Mutation	SNP	G	A	18	4	c.1768G>A	c.(1768-1770)GAA>AAA	p.E590K
Pat_16	Post-Resistance	ZNF711	7552	37	X	84519283	84519283	Missense_Mutation	SNP	G	A	18	1	c.625G>A	c.(625-627)GAT>AAT	p.D209N
Pat_16	Post-Resistance	ARMCX2	9823	37	X	100911659	100911659	Missense_Mutation	SNP	C	T	5	214	c.916G>A	c.(916-918)GAA>AAA	p.E306K
Pat_16	Post-Resistance	H2BFWT	158983	37	X	103267838	103267838	Missense_Mutation	SNP	G	A	44	6	c.395C>T	c.(394-396)ACC>ATC	p.T132I
Pat_16	Post-Resistance	IL1RAPL2	26280	37	X	105011625	105011625	Missense_Mutation	SNP	G	A	139	28	c.2032G>A	c.(2032-2034)GAG>AAG	p.E678K
Pat_16	Post-Resistance	GUCY2F	2986	37	X	108719089	108719089	Missense_Mutation	SNP	C	T	146	22	c.77G>A	c.(76-78)GGC>GAC	p.G26D
Pat_16	Post-Resistance	TRPC5	7224	37	X	111095642	111095642	Missense_Mutation	SNP	C	T	180	38	c.1261G>A	c.(1261-1263)GAA>AAA	p.E421K
Pat_16	Post-Resistance	HTR2C	3358	37	X	114141526	114141526	Missense_Mutation	SNP	G	A	109	17	c.925G>A	c.(925-927)GCT>ACT	p.A309T
Pat_16	Post-Resistance	SLC6A14	11254	37	X	115586574	115586574	Nonsense_Mutation	SNP	G	A	114	152	c.1556G>A	c.(1555-1557)TGG>TAG	p.W519*
Pat_16	Post-Resistance	ODZ1	10178	37	X	123654419	123654419	Nonsense_Mutation	SNP	C	T	195	36	c.3249G>A	c.(3247-3249)TGG>TGA	p.W1083*
Pat_16	Post-Resistance	PHF6	84295	37	X	133551320	133551320	Missense_Mutation	SNP	G	A	4	91	c.956G>A	c.(955-957)CGA>CAA	p.R319Q
Pat_16	Post-Resistance	FGF13	2258	37	X	137717738	137717738	Missense_Mutation	SNP	G	A	4	193	c.481C>T	c.(481-483)CGT>TGT	p.R161C
Pat_16	Post-Resistance	GABRQ	55879	37	X	151819009	151819009	Missense_Mutation	SNP	G	A	552	85	c.867G>A	c.(865-867)ATG>ATA	p.M289I
Pat_16	Post-Resistance	IRAK1	3654	37	X	153278016	153278016	Missense_Mutation	SNP	C	G	3	66	c.2044G>C	c.(2044-2046)GAC>CAC	p.D682H
Pat_16	Post-Resistance	FAM50A	9130	37	X	153674018	153674018	Missense_Mutation	SNP	C	T	131	17	c.149C>T	c.(148-150)TCT>TTT	p.S50F
Pat_16	Post-Resistance	PLXNA3	55558	37	X	153688933	153688933	Missense_Mutation	SNP	G	A	4	175	c.410G>A	c.(409-411)CGC>CAC	p.R137H
Pat_16	Pre-Treatment	KIAA1751	85452	37	1	1920014	1920014	Missense_Mutation	SNP	C	A	36	97	c.233G>T	c.(232-234)CGG>CTG	p.R78L
Pat_16	Pre-Treatment	GPR157	80045	37	1	9164611	9164611	Missense_Mutation	SNP	G	A	18	28	c.875C>T	c.(874-876)TCT>TTT	p.S292F
Pat_16	Pre-Treatment	VPS13D	55187	37	1	12333084	12333084	Missense_Mutation	SNP	C	T	4	246	c.2128C>T	c.(2128-2130)CGG>TGG	p.R710W
Pat_16	Pre-Treatment	CLCNKA	1187	37	1	16358320	16358320	Missense_Mutation	SNP	C	T	71	39	c.1738C>T	c.(1738-1740)CCC>TCC	p.P580S
Pat_16	Pre-Treatment	NBPF3	84224	37	1	21797199	21797199	Missense_Mutation	SNP	G	A	32	36	c.418G>A	c.(418-420)GAG>AAG	p.E140K
Pat_16	Pre-Treatment	E2F2	1870	37	1	23848405	23848405	Missense_Mutation	SNP	G	A	4	148	c.502C>T	c.(502-504)CGC>TGC	p.R168C
Pat_16	Pre-Treatment	GALE	2582	37	1	24124709	24124709	Missense_Mutation	SNP	C	A	4	95	c.249G>T	c.(247-249)ATG>ATT	p.M83I
Pat_16	Pre-Treatment	SRRM1	10250	37	1	24993374	24993374	Missense_Mutation	SNP	C	A	6	171	c.1697C>A	c.(1696-1698)CCT>CAT	p.P566H
Pat_16	Pre-Treatment	SRRM1	10250	37	1	24993386	24993386	Missense_Mutation	SNP	G	T	6	166	c.1709G>T	c.(1708-1710)CGC>CTC	p.R570L
Pat_16	Pre-Treatment	UBXN11	91544	37	1	26612001	26612001	Missense_Mutation	SNP	A	T	19	39	c.806T>A	c.(805-807)TTT>TAT	p.F269Y

Pat_16	Pre-Treatment	ARID1A	8289	37	1	27107000	27107000	Missense_Mutation	SNP	C	T	54	117	c.6611C>T	c.(6610-6612)GCC>GTC	p.A2204V
Pat_16	Pre-Treatment	ZSCAN20	7579	37	1	33945010	33945010	Missense_Mutation	SNP	C	T	62	36	c.121C>T	c.(121-123)CGT>TGT	p.R41C
Pat_16	Pre-Treatment	CSMD2	114784	37	1	34285316	34285316	Missense_Mutation	SNP	C	T	3	20	c.1202G>A	c.(1201-1203)CGA>CAA	p.R401Q
Pat_16	Pre-Treatment	ZNF642	339559	37	1	40954845	40954845	Missense_Mutation	SNP	G	A	146	100	c.305G>A	c.(304-306)CGA>CAA	p.R102Q
Pat_16	Pre-Treatment	WDR65	149465	37	1	43672452	43672452	Missense_Mutation	SNP	C	T	4	231	c.1604C>T	c.(1603-1605)GCT>GTT	p.A535V
Pat_16	Pre-Treatment	C1orf175	374977	37	1	55151979	55151979	Missense_Mutation	SNP	C	T	3	65	c.2569C>T	c.(2569-2571)CGT>TGT	p.R857C
Pat_16	Pre-Treatment	C8B	732	37	1	57422517	57422517	Missense_Mutation	SNP	C	T	194	108	c.316G>A	c.(316-318)GAA>AAA	p.E106K
Pat_16	Pre-Treatment	LRRC7	57554	37	1	70493918	70493918	Missense_Mutation	SNP	C	T	116	77	c.1745C>T	c.(1744-1746)TCT>TTT	p.S582F
Pat_16	Pre-Treatment	C1orf173	127254	37	1	75065480	75065480	Missense_Mutation	SNP	T	G	264	142	c.1625A>C	c.(1624-1626)AAA>ACA	p.K542T
Pat_16	Pre-Treatment	CLCA1	1179	37	1	86951080	86951080	Missense_Mutation	SNP	A	T	69	166	c.790A>T	c.(790-792)AAT>TAT	p.N264Y
Pat_16	Pre-Treatment	SH3GLB1	51100	37	1	87208874	87208874	Nonsense_Mutation	SNP	C	T	183	198	c.1054C>T	c.(1054-1056)CAG>TAG	p.Q352*
Pat_16	Pre-Treatment	ARHGAP29	9411	37	1	94654489	94654489	Missense_Mutation	SNP	A	T	132	217	c.1585T>A	c.(1585-1587)TTT>ATT	p.F529I
Pat_16	Pre-Treatment	CD53	963	37	1	111434995	111434995	Missense_Mutation	SNP	G	A	33	85	c.92G>A	c.(91-93)GGG>GAG	p.G31E
Pat_16	Pre-Treatment	NRAS	4893	37	1	115256530	115256530	Missense_Mutation	SNP	G	T	185	532	c.181C>A	c.(181-183)CAA>AAA	p.Q61K
Pat_16	Pre-Treatment	SYCP1	6847	37	1	115469144	115469144	Missense_Mutation	SNP	G	A	29	29	c.1886G>A	c.(1885-1887)GGT>GAT	p.G629D
Pat_16	Pre-Treatment	CASQ2	845	37	1	116244011	116244011	Missense_Mutation	SNP	C	T	92	64	c.1051G>A	c.(1051-1053)GAT>AAT	p.D351N
Pat_16	Pre-Treatment	NOTCH2	4853	37	1	120467982	120467982	Missense_Mutation	SNP	G	A	6	579	c.4457C>T	c.(4456-4458)ACG>ATG	p.T1486M
Pat_16	Pre-Treatment	PDE4DIP	9659	37	1	144881505	144881505	Nonsense_Mutation	SNP	G	A	167	369	c.3691C>T	c.(3691-3693)CAG>TAG	p.Q1231*
Pat_16	Pre-Treatment	PDE4DIP	9659	37	1	145015949	145015949	Missense_Mutation	SNP	C	T	57	667	c.139G>A	c.(139-141)GAA>AAA	p.E47K
Pat_16	Pre-Treatment	NBPF10	100132406	37	1	145311785	145311785	Splice_Site	SNP	C	G	4	35	c.1854_splice	c.e14-1	p.R618_splice
Pat_16	Pre-Treatment	VPS45	11311	37	1	150064122	150064122	Missense_Mutation	SNP	G	A	5	414	c.1196G>A	c.(1195-1197)AGC>AAC	p.S399N
Pat_16	Pre-Treatment	PSMD4	5710	37	1	151238835	151238835	Missense_Mutation	SNP	G	A	5	228	c.815G>A	c.(814-816)CGC>CAC	p.R272H
Pat_16	Pre-Treatment	LCE2A	353139	37	1	152671573	152671573	Missense_Mutation	SNP	G	A	4	135	c.196G>A	c.(196-198)GGC>AGC	p.G66S
Pat_16	Pre-Treatment	KPRP	448834	37	1	152733052	152733052	Missense_Mutation	SNP	T	A	29	64	c.988T>A	c.(988-990)TCC>ACC	p.S330T
Pat_16	Pre-Treatment	DCST1	149095	37	1	155015229	155015229	Missense_Mutation	SNP	G	A	4	240	c.911G>A	c.(910-912)CGC>CAC	p.R304H
Pat_16	Pre-Treatment	INSRR	3645	37	1	156811946	156811946	Missense_Mutation	SNP	G	A	3	94	c.3355C>T	c.(3355-3357)CGC>TGC	p.R1119C
Pat_16	Pre-Treatment	FCRL3	115352	37	1	157666963	157666963	Missense_Mutation	SNP	T	G	57	28	c.811A>C	c.(811-813)AAA>CAA	p.K271Q
Pat_16	Pre-Treatment	ATP1A4	480	37	1	160141383	160141383	Missense_Mutation	SNP	T	A	245	106	c.1690T>A	c.(1690-1692)TTC>ATC	p.F564I
Pat_16	Pre-Treatment	CD244	51744	37	1	160806026	160806026	Missense_Mutation	SNP	G	A	24	70	c.868C>T	c.(868-870)CCT>TCT	p.P290S
Pat_16	Pre-Treatment	ARHGAP30	257106	37	1	161018907	161018907	Missense_Mutation	SNP	C	T	256	152	c.1904G>A	c.(1903-1905)GGA>GAA	p.G635E
Pat_16	Pre-Treatment	NOS1AP	9722	37	1	162257220	162257220	Missense_Mutation	SNP	G	T	10	140	c.264G>T	c.(262-264)AAG>AAT	p.K88N
Pat_16	Pre-Treatment	C1orf110	339512	37	1	162829392	162829392	Missense_Mutation	SNP	A	T	21	77	c.45T>A	c.(43-45)GAT>GAA	p.D15E
Pat_16	Pre-Treatment	MPZL1	9019	37	1	167757123	167757123	Missense_Mutation	SNP	G	A	239	156	c.775G>A	c.(775-777)GAG>AAG	p.E259K
Pat_16	Pre-Treatment	FMO1	2326	37	1	171254520	171254520	Missense_Mutation	SNP	G	A	52	43	c.1436G>A	c.(1435-1437)GGA>GAA	p.G479E
Pat_16	Pre-Treatment	SLC9A11	284525	37	1	173490472	173490472	Missense_Mutation	SNP	C	T	72	212	c.2707G>A	c.(2707-2709)GGA>AGA	p.G903R
Pat_16	Pre-Treatment	FAM5B	57795	37	1	177249565	177249565	Nonsense_Mutation	SNP	G	A	63	145	c.1253G>A	c.(1252-1254)TGG>TAG	p.W418*
Pat_16	Pre-Treatment	C1orf49	84066	37	1	178489831	178489831	Missense_Mutation	SNP	A	T	15	22	c.365A>T	c.(364-366)GAG>GTG	p.E122V
Pat_16	Pre-Treatment	FAM20B	9917	37	1	179013184	179013184	Missense_Mutation	SNP	G	A	4	137	c.202G>A	c.(202-204)GCC>ACC	p.A68T
Pat_16	Pre-Treatment	C1orf125	126859	37	1	179414126	179414126	Missense_Mutation	SNP	G	A	89	64	c.1585G>A	c.(1585-1587)GAG>AAG	p.E529K
Pat_16	Pre-Treatment	HMCN1	83872	37	1	186077692	186077692	Missense_Mutation	SNP	C	T	116	58	c.10952C>T	c.(10951-10953)CCT>CTT	p.P3651L
Pat_16	Pre-Treatment	CFH	3075	37	1	196684756	196684756	Missense_Mutation	SNP	G	A	215	155	c.1553G>A	c.(1552-1554)AGA>AAA	p.R518K
Pat_16	Pre-Treatment	CFHR2	3080	37	1	196918654	196918654	Missense_Mutation	SNP	C	T	24	75	c.128C>T	c.(127-129)TCC>TTC	p.S43F
Pat_16	Pre-Treatment	CFHR5	81494	37	1	196971612	196971612	Missense_Mutation	SNP	A	G	44	123	c.1148A>G	c.(1147-1149)GAA>GGA	p.E383G
Pat_16	Pre-Treatment	CRB1	23418	37	1	197446813	197446813	Missense_Mutation	SNP	C	T	29	97	c.4025C>T	c.(4024-4026)TCC>TTC	p.S1342F
Pat_16	Pre-Treatment	USH2A	7399	37	1	215956214	215956214	Missense_Mutation	SNP	C	T	4	123	c.10451G>A	c.(10450-10452)CGA>CAA	p.R3484Q
Pat_16	Pre-Treatment	SPATA17	128153	37	1	217947824	217947824	Missense_Mutation	SNP	C	T	30	77	c.668C>T	c.(667-669)GCC>GTC	p.A223V
Pat_16	Pre-Treatment	TGFB2	7042	37	1	218609479	218609479	Missense_Mutation	SNP	T	C	5	342	c.922T>C	c.(922-924)TAT>CAT	p.Y308H

Pat_16	Pre-Treatment	LYPLAL1	127018	37	1	219347239	219347239	Missense_Mutation	SNP	G	A	5	287	c.7G>A	c.(7-9)GCT>ACT	p.A3T
Pat_16	Pre-Treatment	NVL	4931	37	1	224495956	224495956	Missense_Mutation	SNP	G	A	38	84	c.352C>T	c.(352-354)CAC>TAC	p.H118Y
Pat_16	Pre-Treatment	NID1	4811	37	1	236175236	236175236	Missense_Mutation	SNP	G	A	4	313	c.2512C>T	c.(2512-2514)CGT>TGT	p.R838C
Pat_16	Pre-Treatment	ZP4	57829	37	1	238048472	238048472	Missense_Mutation	SNP	C	T	103	47	c.1304G>A	c.(1303-1305)AGG>AAG	p.R435K
Pat_16	Pre-Treatment	OPN3	23596	37	1	241767747	241767747	Missense_Mutation	SNP	C	T	4	171	c.508G>A	c.(508-510)GGA>AGA	p.G170R
Pat_16	Pre-Treatment	CNST	163882	37	1	246784866	246784866	Missense_Mutation	SNP	C	T	270	200	c.515C>T	c.(514-516)TCT>TTT	p.S172F
Pat_16	Pre-Treatment	AHCTF1	25909	37	1	247012951	247012951	Missense_Mutation	SNP	A	C	91	241	c.6357T>G	c.(6355-6357)TTT>TTG	p.F2119L
Pat_16	Pre-Treatment	OR2G6	391211	37	1	248685890	248685890	Missense_Mutation	SNP	A	G	3	48	c.943A>G	c.(943-945)AAG>GAG	p.K315E
Pat_16	Pre-Treatment	C10orf18	54906	37	10	5791697	5791697	Missense_Mutation	SNP	C	T	4	134	c.6313C>T	c.(6313-6315)CGG>TGG	p.R2105W
Pat_16	Pre-Treatment	HSPA14	51182	37	10	14881937	14881937	Missense_Mutation	SNP	G	A	5	440	c.91G>A	c.(91-93)GGT>AGT	p.G31S
Pat_16	Pre-Treatment	FAM171A1	221061	37	10	15255386	15255386	Missense_Mutation	SNP	C	T	42	56	c.2201G>A	c.(2200-2202)GGA>GAA	p.G734E
Pat_16	Pre-Treatment	ANKRD30A	91074	37	10	37430661	37430661	Missense_Mutation	SNP	G	A	49	11	c.668G>A	c.(667-669)GGA>GAA	p.G223E
Pat_16	Pre-Treatment	TMEM72	643236	37	10	45423380	45423380	Missense_Mutation	SNP	G	A	4	268	c.82G>A	c.(82-84)GTG>ATG	p.V28M
Pat_16	Pre-Treatment	PARG	8505	37	10	51093329	51093329	Missense_Mutation	SNP	C	T	4	116	c.1750G>A	c.(1750-1752)GCA>ACA	p.A584T
Pat_16	Pre-Treatment	PRKG1	5592	37	10	54048576	54048576	Missense_Mutation	SNP	A	C	71	1	c.1755A>C	c.(1753-1755)AAA>AAC	p.K585N
Pat_16	Pre-Treatment	BICC1	80114	37	10	60573673	60573673	Missense_Mutation	SNP	T	G	206	9	c.2460T>G	c.(2458-2460)AAT>AAG	p.N820K
Pat_16	Pre-Treatment	MYPN	84665	37	10	69881782	69881782	Missense_Mutation	SNP	G	A	67	4	c.587G>A	c.(586-588)AGC>AAC	p.S196N
Pat_16	Pre-Treatment	CH25H	9023	37	10	90966538	90966538	Missense_Mutation	SNP	G	A	4	219	c.512C>T	c.(511-513)ACG>ATG	p.T171M
Pat_16	Pre-Treatment	CYP2C8	1558	37	10	96824645	96824645	Missense_Mutation	SNP	T	G	196	2	c.554A>C	c.(553-555)AAA>ACA	p.K185T
Pat_16	Pre-Treatment	SLIT1	6585	37	10	98778837	98778837	Missense_Mutation	SNP	T	G	78	3	c.2774A>C	c.(2773-2775)AAG>ACG	p.K925T
Pat_16	Pre-Treatment	SEMA4G	57715	37	10	102743232	102743232	Missense_Mutation	SNP	G	A	41	34	c.1876G>A	c.(1876-1878)GAT>AAT	p.D626N
Pat_16	Pre-Treatment	POLL	27343	37	10	103342563	103342563	Missense_Mutation	SNP	A	C	143	9	c.1151T>G	c.(1150-1152)CTG>CGG	p.L384R
Pat_16	Pre-Treatment	NPM3	10360	37	10	103542027	103542027	Missense_Mutation	SNP	G	A	3	59	c.406C>T	c.(406-408)CGG>TGG	p.R136W
Pat_16	Pre-Treatment	NFKB2	4791	37	10	104156558	104156558	Missense_Mutation	SNP	G	A	5	177	c.221G>A	c.(220-222)CGA>CAA	p.R74Q
Pat_16	Pre-Treatment	PDCD11	22984	37	10	105194638	105194638	Missense_Mutation	SNP	C	T	37	33	c.3751C>T	c.(3751-3753)CCC>TCC	p.P1251S
Pat_16	Pre-Treatment	FGFR2	2263	37	10	123279680	123279680	Missense_Mutation	SNP	C	T	15	9	c.752G>A	c.(751-753)CGA>CAA	p.R251Q
Pat_16	Pre-Treatment	TACC2	10579	37	10	123845785	123845785	Missense_Mutation	SNP	C	T	91	2	c.3770C>T	c.(3769-3771)TCC>TTC	p.S1257F
Pat_16	Pre-Treatment	HTRA1	5654	37	10	124271572	124271572	Missense_Mutation	SNP	C	A	4	94	c.1265C>A	c.(1264-1266)CCA>CAA	p.P422Q
Pat_16	Pre-Treatment	LOC653544	653544	37	10	135491123	135491123	Missense_Mutation	SNP	G	A	4	19	c.734G>A	c.(733-735)GGC>GAC	p.G245D
Pat_16	Pre-Treatment	LRRC56	115399	37	11	554058	554058	Missense_Mutation	SNP	G	A	83	1	c.1411G>A	c.(1411-1413)GAC>AAC	p.D471N
Pat_16	Pre-Treatment	MUC2	4583	37	11	1101129	1101129	Missense_Mutation	SNP	G	A	37	31	c.14614G>A	c.(14614-14616)GAG>AAG	p.E4872K
Pat_16	Pre-Treatment	MUC5B	727897	37	11	1256566	1256566	Missense_Mutation	SNP	T	G	9	16	c.4780T>G	c.(4780-4782)TTC>GTC	p.F1594V
Pat_16	Pre-Treatment	MUC5B	727897	37	11	1265984	1265984	Missense_Mutation	SNP	G	A	3	86	c.9788G>A	c.(9787-9789)GGG>GAG	p.G3263E
Pat_16	Pre-Treatment	OR51B2	79345	37	11	5345040	5345040	Missense_Mutation	SNP	G	A	108	1	c.488C>T	c.(487-489)TCA>TTA	p.S163L
Pat_16	Pre-Treatment	OR51I2	390064	37	11	5475460	5475460	Missense_Mutation	SNP	G	A	4	189	c.742G>A	c.(742-744)GTA>ATA	p.V248I
Pat_16	Pre-Treatment	OR5P2	120065	37	11	7817971	7817971	Missense_Mutation	SNP	A	C	64	51	c.519T>G	c.(517-519)TTT>TTG	p.F173L
Pat_16	Pre-Treatment	PARVA	55742	37	11	12525959	12525959	Nonsense_Mutation	SNP	C	T	39	42	c.640C>T	c.(640-642)CAA>TAA	p.Q214*
Pat_16	Pre-Treatment	TCP11L1	55346	37	11	33087499	33087499	Missense_Mutation	SNP	G	A	6	334	c.1096G>A	c.(1096-1098)GAC>AAC	p.D366N
Pat_16	Pre-Treatment	EXT2	2132	37	11	44228348	44228348	Missense_Mutation	SNP	C	T	71	3	c.1501C>T	c.(1501-1503)CTC>TTC	p.L501F
Pat_16	Pre-Treatment	AMBRA1	55626	37	11	46567211	46567211	Nonsense_Mutation	SNP	C	T	151	4	c.494G>A	c.(493-495)TGG>TAG	p.W165*
Pat_16	Pre-Treatment	AMBRA1	55626	37	11	46568751	46568751	Missense_Mutation	SNP	G	A	5	267	c.290C>T	c.(289-291)ACT>ATT	p.T97I
Pat_16	Pre-Treatment	ARHGAP1	392	37	11	46702064	46702065	Nonsense_Mutation	DNP	CC	AA	94	2	c.792_793GG>TT	790-795)AGGGAG>AGTT	.264_265RE>S
Pat_16	Pre-Treatment	F2	2147	37	11	46747480	46747480	Missense_Mutation	SNP	G	A	73	39	c.631G>A	c.(631-633)GAG>AAG	p.E211K
Pat_16	Pre-Treatment	DDB2	1643	37	11	47256351	47256351	Missense_Mutation	SNP	C	T	65	2	c.746C>T	c.(745-747)GCC>GTC	p.A249V
Pat_16	Pre-Treatment	SPRYD5	84767	37	11	55653011	55653011	Missense_Mutation	SNP	G	A	3	51	c.107G>A	c.(106-108)CGG>CAG	p.R36Q
Pat_16	Pre-Treatment	OR5M9	390162	37	11	56230826	56230826	Missense_Mutation	SNP	G	A	48	1	c.52C>T	c.(52-54)CGT>TGT	p.R18C
Pat_16	Pre-Treatment	OR5B17	219965	37	11	58126355	58126355	Missense_Mutation	SNP	T	C	81	7	c.188A>G	c.(187-189)AAC>AGC	p.N63S

Pat_16	Pre-Treatment	ZFP91	80829	37	11	58380251	58380251	Nonsense_Mutation	SNP	C	T	205	6	c.925C>T	c.(925-927)CAG>TAG	p.Q309*
Pat_16	Pre-Treatment	VWCE	220001	37	11	61053800	61053800	Missense_Mutation	SNP	C	T	4	278	c.527G>A	c.(526-528)CGC>CAC	p.R176H
Pat_16	Pre-Treatment	ACTN3	89	37	11	66323694	66323694	Missense_Mutation	SNP	C	T	4	157	c.797C>T	c.(796-798)GCT>GTT	p.A266V
Pat_16	Pre-Treatment	SPTBN2	6712	37	11	66466905	66466905	Missense_Mutation	SNP	G	A	36	48	c.3748C>T	c.(3748-3750)CGG>TGG	p.R1250W
Pat_16	Pre-Treatment	ARHGEF17	9828	37	11	73073492	73073492	Missense_Mutation	SNP	C	T	8	0	c.4709C>T	c.(4708-4710)TCG>TTG	p.S1570L
Pat_16	Pre-Treatment	DNAJB13	374407	37	11	73677211	73677211	Missense_Mutation	SNP	C	T	43	1	c.521C>T	c.(520-522)ACC>ATC	p.T174I
Pat_16	Pre-Treatment	HEPHL1	341208	37	11	93754593	93754593	Missense_Mutation	SNP	G	A	63	77	c.59G>A	c.(58-60)GGG>GAG	p.G20E
Pat_16	Pre-Treatment	PDGFD	80310	37	11	103797821	103797821	Missense_Mutation	SNP	C	T	4	179	c.806G>A	c.(805-807)CGT>CAT	p.R269H
Pat_16	Pre-Treatment	GRIA4	2893	37	11	105850461	105850461	Missense_Mutation	SNP	C	T	47	0	c.2704C>T	c.(2704-2706)CCA>TCA	p.P902S
Pat_16	Pre-Treatment	APOC3	345	37	11	116701338	116701338	Missense_Mutation	SNP	C	T	3	45	c.40C>T	c.(40-42)CTC>TTC	p.L14F
Pat_16	Pre-Treatment	DSCAML1	57453	37	11	117352818	117352819	Missense_Mutation	DNP	CC	TT	46	1	.2598_2599GG>A	596-2601)AAGGAG>AAA	p.E867K
Pat_16	Pre-Treatment	RIMKLB	57494	37	12	8904628	8904628	Missense_Mutation	SNP	G	A	5	408	c.482G>A	c.(481-483)CGG>CAG	p.R161Q
Pat_16	Pre-Treatment	A2ML1	144568	37	12	8975263	8975263	Missense_Mutation	SNP	C	T	53	132	c.16C>T	c.(16-18)CTT>TTT	p.L6F
Pat_16	Pre-Treatment	GRIN2B	2904	37	12	13716732	13716732	Missense_Mutation	SNP	T	A	40	18	c.3440A>T	c.(3439-3441)GAG>GTG	p.E1147V
Pat_16	Pre-Treatment	LRMP	4033	37	12	25260897	25260898	Missense_Mutation	DNP	AT	TA	56	171	.1403_1404AT>T	c.(1402-1404)GAT>GTA	p.D468V
Pat_16	Pre-Treatment	PRKAG1	5571	37	12	49396783	49396784	Nonsense_Mutation	DNP	GG	AA	55	136	c.894_895CC>TT	892-897)CACCGA>CATT	p.R299*
Pat_16	Pre-Treatment	KRT4	3851	37	12	53202523	53202523	Missense_Mutation	SNP	C	T	30	104	c.1168G>A	c.(1168-1170)GAG>AAG	p.E390K
Pat_16	Pre-Treatment	KRT18	3875	37	12	53345602	53345602	Nonsense_Mutation	SNP	C	T	18	55	c.910C>T	c.(910-912)CAG>TAG	p.Q304*
Pat_16	Pre-Treatment	AMHR2	269	37	12	53823344	53823344	Missense_Mutation	SNP	C	T	88	48	c.1075C>T	c.(1075-1077)CCT>TCT	p.P359S
Pat_16	Pre-Treatment	KIAA0748	9840	37	12	55368225	55368225	Missense_Mutation	SNP	G	T	14	15	c.122C>A	c.(121-123)CCA>CAA	p.P41Q
Pat_16	Pre-Treatment	OR6C3	254786	37	12	55726023	55726023	Missense_Mutation	SNP	C	T	150	485	c.539C>T	c.(538-540)CCC>CTC	p.P180L
Pat_16	Pre-Treatment	CDK2	1017	37	12	56365339	56365339	Missense_Mutation	SNP	C	T	6	642	c.827C>T	c.(826-828)TCG>TTG	p.S276L
Pat_16	Pre-Treatment	IKZF4	64375	37	12	56427051	56427051	Missense_Mutation	SNP	C	T	94	203	c.943C>T	c.(943-945)CGT>TGT	p.R315C
Pat_16	Pre-Treatment	TMEM194A	23306	37	12	57453807	57453807	Missense_Mutation	SNP	G	A	4	237	c.1190C>T	c.(1189-1191)ACG>ATG	p.T397M
Pat_16	Pre-Treatment	STAT6	6778	37	12	57500077	57500077	Missense_Mutation	SNP	C	T	4	191	c.577G>A	c.(577-579)GCC>ACC	p.A193T
Pat_16	Pre-Treatment	SLC16A7	9194	37	12	60173255	60173256	Missense_Mutation	DNP	GG	AA	63	144	.1232_1233GG>A	c.(1231-1233)GGG>GAA	p.G411E
Pat_16	Pre-Treatment	C12orf56	115749	37	12	64746799	64746799	Missense_Mutation	SNP	C	T	81	79	c.290G>A	c.(289-291)AGA>AAA	p.R97K
Pat_16	Pre-Treatment	CPSF6	11052	37	12	69652691	69652691	Missense_Mutation	SNP	C	T	5	592	c.1016C>T	c.(1015-1017)CCT>CTT	p.P339L
Pat_16	Pre-Treatment	RASSF9	9182	37	12	86198724	86198724	Missense_Mutation	SNP	T	A	375	207	c.1064A>T	c.(1063-1065)AAA>ATA	p.K355I
Pat_16	Pre-Treatment	LUM	4060	37	12	91497952	91497952	Missense_Mutation	SNP	G	A	83	185	c.1007C>T	c.(1006-1008)ACT>ATT	p.T336I
Pat_16	Pre-Treatment	MYO1H	283446	37	12	109883364	109883364	Missense_Mutation	SNP	G	A	98	57	c.565G>A	c.(565-567)GAC>AAC	p.D189N
Pat_16	Pre-Treatment	TCTN1	79600	37	12	111085668	111085668	Missense_Mutation	SNP	C	T	26	83	c.1735C>T	c.(1735-1737)CCC>TCC	p.P579S
Pat_16	Pre-Treatment	SH2B3	10019	37	12	111886044	111886044	Missense_Mutation	SNP	G	A	70	34	c.1666G>A	c.(1666-1668)GAA>AAA	p.E556K
Pat_16	Pre-Treatment	RASAL1	8437	37	12	113543644	113543644	Nonsense_Mutation	SNP	G	A	40	79	c.1702C>T	c.(1702-1704)CGA>TGA	p.R568*
Pat_16	Pre-Treatment	MED13L	23389	37	12	116429319	116429319	Missense_Mutation	SNP	A	T	156	74	c.3440T>A	c.(3439-3441)CTT>CAT	p.L1147H
Pat_16	Pre-Treatment	SNRNP35	11066	37	12	123950368	123950368	Missense_Mutation	SNP	A	G	43	94	c.281A>G	c.(280-282)TAC>TGC	p.Y94C
Pat_16	Pre-Treatment	DNAH10	196385	37	12	124297919	124297919	Nonsense_Mutation	SNP	G	A	58	160	c.2999G>A	c.(2998-3000)TGG>TAG	p.W1000*
Pat_16	Pre-Treatment	TMEM132B	114795	37	12	126139119	126139119	Missense_Mutation	SNP	C	T	41	92	c.3100C>T	c.(3100-3102)CCA>TCA	p.P1034S
Pat_16	Pre-Treatment	PIWIL1	9271	37	12	130839140	130839140	Missense_Mutation	SNP	G	A	80	43	c.1103G>A	c.(1102-1104)AGA>AAA	p.R368K
Pat_16	Pre-Treatment	RIMBP2	23504	37	12	130883705	130883705	Missense_Mutation	SNP	T	A	130	80	c.3134A>T	c.(3133-3135)AAG>ATG	p.K1045M
Pat_16	Pre-Treatment	MAB21L1	4081	37	13	36049629	36049629	Missense_Mutation	SNP	T	A	93	213	c.647A>T	c.(646-648)CAC>CTC	p.H216L
Pat_16	Pre-Treatment	ALG5	29880	37	13	37539733	37539733	Missense_Mutation	SNP	G	A	81	317	c.752C>T	c.(751-753)TCA>TTA	p.S251L
Pat_16	Pre-Treatment	ZC3H13	23091	37	13	46541662	46541662	Missense_Mutation	SNP	G	A	240	245	c.4298C>T	c.(4297-4299)TCC>TTC	p.S1433F
Pat_16	Pre-Treatment	LOC220429	220429	37	13	50466930	50466930	Missense_Mutation	SNP	C	T	44	94	c.2204C>T	c.(2203-2205)CCA>CTA	p.P735L
Pat_16	Pre-Treatment	KLHL1	57626	37	13	70413125	70413125	Missense_Mutation	SNP	C	T	65	121	c.1397G>A	c.(1396-1398)GGA>GAA	p.G466E
Pat_16	Pre-Treatment	DACH1	1602	37	13	72063230	72063230	Missense_Mutation	SNP	A	G	174	650	c.1621T>C	c.(1621-1623)TCT>CCT	p.S541P
Pat_16	Pre-Treatment	ACIN1	22985	37	14	23535213	23535213	Missense_Mutation	SNP	G	A	3	61	c.2444C>T	c.(2443-2445)TCG>TTG	p.S815L

Pat_16	Pre-Treatment	MYH7	4625	37	14	23894617	23894617	Missense_Mutation	SNP	T	G	48	57	c.2297A>C	c.(2296-2298)AAG>ACG	p.K766T
Pat_16	Pre-Treatment	DHRS1	115817	37	14	24768213	24768213	Missense_Mutation	SNP	C	T	4	136	c.100G>A	c.(100-102)GTT>ATT	p.V34I
Pat_16	Pre-Treatment	BAZ1A	11177	37	14	35245523	35245523	Missense_Mutation	SNP	C	A	4	132	c.2435G>T	c.(2434-2436)AGA>ATA	p.R812I
Pat_16	Pre-Treatment	FBXO33	254170	37	14	39868720	39868720	Nonstop_Mutation	SNP	C	G	25	2	c.1668G>C	c.(1666-1668)TAG>TAC	p.*556Y
Pat_16	Pre-Treatment	PRPF39	55015	37	14	45571853	45571853	Missense_Mutation	SNP	C	T	270	285	c.691C>T	c.(691-693)CGT>TGT	p.R231C
Pat_16	Pre-Treatment	KIAA0831	22863	37	14	55844779	55844779	Missense_Mutation	SNP	C	T	3	79	c.1009G>A	c.(1009-1011)GAA>AAA	p.E337K
Pat_16	Pre-Treatment	SLC8A3	6547	37	14	70635091	70635091	Missense_Mutation	SNP	C	T	40	1	c.49G>A	c.(49-51)GGG>AGG	p.G17R
Pat_16	Pre-Treatment	CATSPERB	79820	37	14	92088249	92088249	Missense_Mutation	SNP	C	T	14	0	c.1963G>A	c.(1963-1965)GAG>AAG	p.E655K
Pat_16	Pre-Treatment	SLC24A4	123041	37	14	92920299	92920299	Missense_Mutation	SNP	G	A	54	3	c.885G>A	c.(883-885)ATG>ATA	p.M295I
Pat_16	Pre-Treatment	HSP90AA1	3320	37	14	102605674	102605675	Missense_Mutation	DNP	GG	AA	38	0	c.67_68CC>TT	c.(67-69)CCC>TTC	p.P23F
Pat_16	Pre-Treatment	ZNF839	55778	37	14	102807738	102807738	Missense_Mutation	SNP	G	A	3	84	c.1658G>A	c.(1657-1659)GGG>GAG	p.G553E
Pat_16	Pre-Treatment	CDC42BPB	9578	37	14	103406431	103406431	Missense_Mutation	SNP	G	A	3	56	c.4543C>T	c.(4543-4545)CTC>TTC	p.L1515F
Pat_16	Pre-Treatment	MTA1	9112	37	14	105930777	105930777	Missense_Mutation	SNP	C	T	57	76	c.1217C>T	c.(1216-1218)TCT>TTT	p.S406F
Pat_16	Pre-Treatment	ARHGAP11A	9824	37	15	32908542	32908542	Splice_Site	SNP	G	A	4	110	c.129_splice	c.e1+1	p.G43_splice
Pat_16	Pre-Treatment	GPR176	11245	37	15	40094145	40094145	Missense_Mutation	SNP	G	A	4	165	c.736C>T	c.(736-738)CGG>TGG	p.R246W
Pat_16	Pre-Treatment	MFAP1	4236	37	15	44105192	44105192	Nonsense_Mutation	SNP	G	A	232	537	c.880C>T	c.(880-882)CGA>TGA	p.R294*
Pat_16	Pre-Treatment	WDR76	79968	37	15	44127266	44127266	Missense_Mutation	SNP	C	T	34	75	c.470C>T	c.(469-471)TCG>TTG	p.S157L
Pat_16	Pre-Treatment	HDC	3067	37	15	50540510	50540510	Missense_Mutation	SNP	G	A	39	89	c.1072C>T	c.(1072-1074)CGC>TGC	p.R358C
Pat_16	Pre-Treatment	TRPM7	54822	37	15	50885856	50885856	Missense_Mutation	SNP	A	G	58	113	c.3566T>C	c.(3565-3567)TTT>TCT	p.F1189S
Pat_16	Pre-Treatment	MYO5C	55930	37	15	52553323	52553323	Missense_Mutation	SNP	T	A	29	57	c.1049A>T	c.(1048-1050)GAG>GTG	p.E350V
Pat_16	Pre-Treatment	CGNL1	84952	37	15	57730859	57730859	Missense_Mutation	SNP	C	T	137	251	c.662C>T	c.(661-663)TCC>TTC	p.S221F
Pat_16	Pre-Treatment	BNIP2	663	37	15	59963387	59963387	Missense_Mutation	SNP	A	C	7	15	c.1065T>G	c.(1063-1065)GAT>GAG	p.D355E
Pat_16	Pre-Treatment	NARG2	79664	37	15	60760375	60760375	Missense_Mutation	SNP	G	A	47	91	c.293C>T	c.(292-294)TCT>TTT	p.S98F
Pat_16	Pre-Treatment	SNX22	79856	37	15	64446651	64446651	Missense_Mutation	SNP	G	A	163	416	c.526G>A	c.(526-528)GAT>AAT	p.D176N
Pat_16	Pre-Treatment	CILP	8483	37	15	65502086	65502086	Missense_Mutation	SNP	C	T	37	99	c.8G>A	c.(7-9)GGG>GAG	p.G3E
Pat_16	Pre-Treatment	LOXL1	4016	37	15	74235231	74235231	Missense_Mutation	SNP	A	G	190	491	c.1139A>G	c.(1138-1140)CAA>CGA	p.Q380R
Pat_16	Pre-Treatment	ISLR	3671	37	15	74467929	74467929	Missense_Mutation	SNP	G	A	37	95	c.730G>A	c.(730-732)GGT>AGT	p.G244S
Pat_16	Pre-Treatment	CCDC33	80125	37	15	74536345	74536345	Missense_Mutation	SNP	A	C	54	73	c.41A>C	c.(40-42)GAG>GCG	p.E14A
Pat_16	Pre-Treatment	CCDC33	80125	37	15	74564051	74564051	Missense_Mutation	SNP	T	A	59	34	c.554T>A	c.(553-555)CTC>CAC	p.L185H
Pat_16	Pre-Treatment	ARID3B	10620	37	15	74836597	74836597	Missense_Mutation	SNP	T	C	45	161	c.320T>C	c.(319-321)GTT>GCT	p.V107A
Pat_16	Pre-Treatment	CIB2	10518	37	15	78401682	78401682	Missense_Mutation	SNP	C	T	64	46	c.241G>A	c.(241-243)GAT>AAT	p.D81N
Pat_16	Pre-Treatment	ZNF592	9640	37	15	85327543	85327543	Missense_Mutation	SNP	A	G	3	114	c.1637A>G	c.(1636-1638)AAG>AGG	p.K546R
Pat_16	Pre-Treatment	AGBL1	123624	37	15	86807702	86807702	Missense_Mutation	SNP	C	T	15	39	c.1162C>T	c.(1162-1164)CCT>TCT	p.P388S
Pat_16	Pre-Treatment	RLBP1	6017	37	15	89755082	89755082	Missense_Mutation	SNP	T	A	49	127	c.576A>T	c.(574-576)GAA>GAT	p.E192D
Pat_16	Pre-Treatment	AP3S2	10239	37	15	90447182	90447182	Missense_Mutation	SNP	G	A	3	88	c.335C>T	c.(334-336)ACG>ATG	p.T112M
Pat_16	Pre-Treatment	SLCO3A1	28232	37	15	92671676	92671676	Missense_Mutation	SNP	G	A	4	232	c.1469G>A	c.(1468-1470)GGC>GAC	p.G490D
Pat_16	Pre-Treatment	AXIN1	8312	37	16	347134	347134	Missense_Mutation	SNP	G	A	6	483	c.1877C>T	c.(1876-1878)GCG>GTG	p.A626V
Pat_16	Pre-Treatment	UNKL	64718	37	16	1453342	1453342	Missense_Mutation	SNP	A	C	36	31	c.291T>G	c.(289-291)TGT>TGG	p.C97W
Pat_16	Pre-Treatment	MAPK8IP3	23162	37	16	1779539	1779539	Missense_Mutation	SNP	G	A	3	54	c.562G>A	c.(562-564)GGA>AGA	p.G188R
Pat_16	Pre-Treatment	PKD1	5310	37	16	2150460	2150460	Missense_Mutation	SNP	G	A	4	84	c.9505C>T	c.(9505-9507)CGG>TGG	p.R3169W
Pat_16	Pre-Treatment	C16orf79	283870	37	16	2259985	2259985	Missense_Mutation	SNP	C	A	3	52	c.404G>T	c.(403-405)CGG>CTG	p.R135L
Pat_16	Pre-Treatment	ZSCAN10	84891	37	16	3142284	3142284	Missense_Mutation	SNP	G	A	48	154	c.265C>T	c.(265-267)CGT>TGT	p.R89C
Pat_16	Pre-Treatment	CREBBP	1387	37	16	3819305	3819305	Missense_Mutation	SNP	G	A	4	219	c.2930C>T	c.(2929-2931)TCG>TTG	p.S977L
Pat_16	Pre-Treatment	12-Sep	124404	37	16	4827818	4827818	Missense_Mutation	SNP	C	T	5	6	c.1057G>A	c.(1057-1059)GAT>AAT	p.D353N
Pat_16	Pre-Treatment	CIITA	4261	37	16	10996552	10996553	Missense_Mutation	DNP	CC	TT	74	79	c.666_667CC>TT	(664-669)CTCCCT>CTTTC	p.P223S
Pat_16	Pre-Treatment	MKL2	57496	37	16	14334250	14334250	Missense_Mutation	SNP	C	A	104	83	c.988C>A	c.(988-990)CTC>ATC	p.L330I
Pat_16	Pre-Treatment	ABCC1	4363	37	16	16230359	16230359	Missense_Mutation	SNP	C	T	36	47	c.4150C>T	c.(4150-4152)CTC>TTC	p.L1384F

Pat_16	Pre-Treatment	SMG1	23049	37	16	18937330	18937330	Missense_Mutation	SNP	T	C	3	30	c.34A>G	c.(34-36)AGC>GGC	p.S12G
Pat_16	Pre-Treatment	DNAH3	55567	37	16	21098244	21098244	Missense_Mutation	SNP	C	T	117	383	c.2803G>A	c.(2803-2805)GAT>AAT	p.D935N
Pat_16	Pre-Treatment	CACNG3	10368	37	16	24373047	24373047	Missense_Mutation	SNP	C	T	4	236	c.811C>T	c.(811-813)CCC>TCC	p.P271S
Pat_16	Pre-Treatment	HS3ST4	9951	37	16	26147178	26147178	Missense_Mutation	SNP	C	T	224	268	c.980C>T	c.(979-981)TCC>TTC	p.S327F
Pat_16	Pre-Treatment	APOB48R	55911	37	16	28507353	28507353	Missense_Mutation	SNP	G	A	32	33	c.991G>A	c.(991-993)GCC>ACC	p.A331T
Pat_16	Pre-Treatment	CD2BP2	10421	37	16	30365585	30365585	Missense_Mutation	SNP	G	A	175	662	c.137C>T	c.(136-138)TCT>TTT	p.S46F
Pat_16	Pre-Treatment	FBXL19	54620	37	16	30938732	30938732	Missense_Mutation	SNP	G	A	3	41	c.341G>A	c.(340-342)TGT>TAT	p.C114Y
Pat_16	Pre-Treatment	TRIM72	493829	37	16	31230643	31230643	Missense_Mutation	SNP	G	A	60	221	c.520G>A	c.(520-522)GAG>AAG	p.E174K
Pat_16	Pre-Treatment	ZNF267	10308	37	16	31927534	31927534	Missense_Mutation	SNP	C	G	4	186	c.1964C>G	c.(1963-1965)ACT>AGT	p.T655S
Pat_16	Pre-Treatment	ZNF267	10308	37	16	31927690	31927690	Missense_Mutation	SNP	G	A	4	199	c.2120G>A	c.(2119-2121)CGG>CAG	p.R707Q
Pat_16	Pre-Treatment	CCL22	6367	37	16	57394369	57394369	Missense_Mutation	SNP	G	A	22	120	c.94G>A	c.(94-96)GAA>AAA	p.E32K
Pat_16	Pre-Treatment	CNGB1	1258	37	16	57935297	57935297	Missense_Mutation	SNP	G	A	4	269	c.2935C>T	c.(2935-2937)CGC>TGC	p.R979C
Pat_16	Pre-Treatment	MMP15	4324	37	16	58079166	58079166	Missense_Mutation	SNP	G	A	20	70	c.1826G>A	c.(1825-1827)GGG>GAG	p.G609E
Pat_16	Pre-Treatment	ACD	65057	37	16	67694194	67694194	Missense_Mutation	SNP	G	A	20	24	c.188C>T	c.(187-189)CCG>CTG	p.P63L
Pat_16	Pre-Treatment	HYDIN	54768	37	16	70913367	70913367	Missense_Mutation	SNP	G	A	48	65	c.10387C>T	c.(10387-10389)CTC>TTC	p.L3463F
Pat_16	Pre-Treatment	RFWD3	55159	37	16	74685992	74685992	Nonsense_Mutation	SNP	G	A	89	82	c.547C>T	c.(547-549)CAG>TAG	p.Q183*
Pat_16	Pre-Treatment	CNTNAP4	85445	37	16	76461470	76461470	Missense_Mutation	SNP	G	A	58	50	c.512G>A	c.(511-513)CGA>CAA	p.R171Q
Pat_16	Pre-Treatment	CNTNAP4	85445	37	16	76495952	76495952	Missense_Mutation	SNP	C	T	28	85	c.1433C>T	c.(1432-1434)CCT>CTT	p.P478L
Pat_16	Pre-Treatment	MBTPS1	8720	37	16	84135312	84135312	Missense_Mutation	SNP	T	C	168	158	c.77A>G	c.(76-78)GAA>GGA	p.E26G
Pat_16	Pre-Treatment	ATP2C2	9914	37	16	84472866	84472866	Missense_Mutation	SNP	G	A	4	138	c.1081G>A	c.(1081-1083)GTG>ATG	p.V361M
Pat_16	Pre-Treatment	P2RX1	5023	37	17	3806890	3806890	Missense_Mutation	SNP	A	C	37	100	c.560T>G	c.(559-561)CTT>CGT	p.L187R
Pat_16	Pre-Treatment	VMO1	284013	37	17	4688833	4688833	Missense_Mutation	SNP	G	A	31	82	c.433C>T	c.(433-435)CGC>TGC	p.R145C
Pat_16	Pre-Treatment	DHX33	56919	37	17	5359375	5359375	Missense_Mutation	SNP	G	A	43	84	c.977C>T	c.(976-978)CCT>CTT	p.P326L
Pat_16	Pre-Treatment	DNAH2	146754	37	17	7643737	7643737	Splice_Site	SNP	G	A	4	312	c.1377_splice	c.e9-1	p.K459_splice
Pat_16	Pre-Treatment	CHD3	1107	37	17	7797756	7797756	Missense_Mutation	SNP	G	A	4	290	c.1099G>A	c.(1099-1101)GGG>AGG	p.G367R
Pat_16	Pre-Treatment	CHD3	1107	37	17	7807196	7807196	Missense_Mutation	SNP	G	A	4	196	c.3781G>A	c.(3781-3783)GCT>ACT	p.A1261T
Pat_16	Pre-Treatment	MYH13	8735	37	17	10206529	10206529	Missense_Mutation	SNP	C	T	209	149	c.5651G>A	c.(5650-5652)AGG>AAG	p.R1884K
Pat_16	Pre-Treatment	DNAH9	1770	37	17	11622751	11622751	Missense_Mutation	SNP	C	T	67	61	c.5653C>T	c.(5653-5655)CGC>TGC	p.R1885C
Pat_16	Pre-Treatment	TRIM16	10626	37	17	15532015	15532015	Missense_Mutation	SNP	A	G	25	36	c.1609T>C	c.(1609-1611)TCC>CCC	p.S537P
Pat_16	Pre-Treatment	TOM1L2	146691	37	17	17788064	17788064	Nonsense_Mutation	SNP	G	A	6	359	c.385C>T	c.(385-387)CGA>TGA	p.R129*
Pat_16	Pre-Treatment	SLC47A1	55244	37	17	19470150	19470151	Missense_Mutation	DNP	CC	TT	53	132	.1154_1155CC>T	c.(1153-1155)TCC>TTT	p.S385F
Pat_16	Pre-Treatment	KCNJ12	3768	37	17	21319012	21319012	Missense_Mutation	SNP	C	T	4	39	c.358C>T	c.(358-360)CGC>TGC	p.R120C
Pat_16	Pre-Treatment	KCNJ12	3768	37	17	21319253	21319253	Missense_Mutation	SNP	C	T	9	34	c.599C>T	c.(598-600)GCC>GTC	p.A200V
Pat_16	Pre-Treatment	PIGS	94005	37	17	26888548	26888548	Missense_Mutation	SNP	C	A	3	48	c.568G>T	c.(568-570)GCC>TCC	p.A190S
Pat_16	Pre-Treatment	SPAG5	10615	37	17	26905522	26905522	Missense_Mutation	SNP	G	A	84	197	c.3223C>T	c.(3223-3225)CTT>TTT	p.L1075F
Pat_16	Pre-Treatment	SEZ6	124925	37	17	27309030	27309030	Missense_Mutation	SNP	C	T	19	12	c.83G>A	c.(82-84)GGG>GAG	p.G28E
Pat_16	Pre-Treatment	UTP6	55813	37	17	30211497	30211497	Missense_Mutation	SNP	G	A	38	46	c.731C>T	c.(730-732)TCG>TTG	p.S244L
Pat_16	Pre-Treatment	MMP28	79148	37	17	34093655	34093655	Missense_Mutation	SNP	G	A	8	30	c.1427C>T	c.(1426-1428)TCC>TTC	p.S476F
Pat_16	Pre-Treatment	MYO19	80179	37	17	34861158	34861158	Missense_Mutation	SNP	G	A	4	141	c.1883C>T	c.(1882-1884)GCG>GTG	p.A628V
Pat_16	Pre-Treatment	CASC3	22794	37	17	38320021	38320021	Missense_Mutation	SNP	C	T	105	207	c.1073C>T	c.(1072-1074)TCT>TTT	p.S358F
Pat_16	Pre-Treatment	KRTAP4-11	653240	37	17	39274214	39274214	Missense_Mutation	SNP	G	C	6	91	c.354C>G	c.(352-354)AGC>AGG	p.S118R
Pat_16	Pre-Treatment	KRTAP9-2	83899	37	17	39383134	39383135	Nonsense_Mutation	DNP	CC	TT	41	96	c.228_229CC>TT	226-231)TGCCAG>TGTT	p.Q77*
Pat_16	Pre-Treatment	KRT32	3882	37	17	39623524	39623524	Missense_Mutation	SNP	G	C	12	69	c.54C>G	c.(52-54)TGC>TGG	p.C18W
Pat_16	Pre-Treatment	LOC90586	90586	37	17	41019611	41019611	Missense_Mutation	SNP	G	A	29	21	c.316G>A	c.(316-318)GCT>ACT	p.A106T
Pat_16	Pre-Treatment	DHX8	1659	37	17	41567763	41567763	Missense_Mutation	SNP	C	T	61	45	c.239C>T	c.(238-240)TCT>TTT	p.S80F
Pat_16	Pre-Treatment	SOST	50964	37	17	41832760	41832760	Missense_Mutation	SNP	G	A	3	61	c.592C>T	c.(592-594)CGC>TGC	p.R198C
Pat_16	Pre-Treatment	MYCBPAP	84073	37	17	48595953	48595953	Missense_Mutation	SNP	G	A	114	253	c.649G>A	c.(649-651)GAA>AAA	p.E217K

Pat_16	Pre-Treatment	ANKFN1	162282	37	17	54450018	54450018	Missense_Mutation	SNP	G	A	52	138	c.622G>A	c.(622-624)GAA>AAA	p.E208K
Pat_16	Pre-Treatment	TRIM25	7706	37	17	54990890	54990890	Missense_Mutation	SNP	G	A	4	147	c.460C>T	c.(460-462)CGC>TGC	p.R154C
Pat_16	Pre-Treatment	BZRAP1	9256	37	17	56387973	56387973	Missense_Mutation	SNP	G	A	4	65	c.3599C>T	c.(3598-3600)CCG>CTG	p.P1200L
Pat_16	Pre-Treatment	PPM1E	22843	37	17	57043079	57043079	Missense_Mutation	SNP	G	A	7	639	c.608G>A	c.(607-609)CGT>CAT	p.R203H
Pat_16	Pre-Treatment	BCAS3	54828	37	17	58824632	58824632	Missense_Mutation	SNP	C	T	167	517	c.395C>T	c.(394-396)CCA>CTA	p.P132L
Pat_16	Pre-Treatment	TBC1D3P2	440452	37	17	60345595	60345595	Missense_Mutation	SNP	G	A	42	119	c.673C>T	c.(673-675)CAC>TAC	p.H225Y
Pat_16	Pre-Treatment	ERN1	2081	37	17	62137857	62137857	Missense_Mutation	SNP	G	T	48	132	c.1178C>A	c.(1177-1179)GCT>GAT	p.A393D
Pat_16	Pre-Treatment	BPTF	2186	37	17	65908492	65908492	Nonsense_Mutation	SNP	C	T	4	202	c.4492C>T	c.(4492-4494)CGA>TGA	p.R1498*
Pat_16	Pre-Treatment	ABCA8	10351	37	17	66915450	66915450	Missense_Mutation	SNP	C	T	134	307	c.1780G>A	c.(1780-1782)GAT>AAT	p.D594N
Pat_16	Pre-Treatment	ABCA10	10349	37	17	67151960	67151960	Missense_Mutation	SNP	G	A	472	204	c.3562C>T	c.(3562-3564)CCA>TCA	p.P1188S
Pat_16	Pre-Treatment	USH1G	124590	37	17	72916120	72916120	Missense_Mutation	SNP	G	A	19	15	c.811C>T	c.(811-813)CCG>TCG	p.P271S
Pat_16	Pre-Treatment	PRPSAP1	5635	37	17	74324800	74324801	Missense_Mutation	DNP	GG	AA	16	58	c.778_779CC>TT	c.(778-780)CCA>TTA	p.P260L
Pat_16	Pre-Treatment	ENPP7	339221	37	17	77709346	77709346	Missense_Mutation	SNP	G	A	21	48	c.904G>A	c.(904-906)GAC>AAC	p.D302N
Pat_16	Pre-Treatment	RNF213	57674	37	17	78320995	78320995	Missense_Mutation	SNP	C	T	7	11	c.3079C>T	c.(3079-3081)CGT>TGT	p.R1027C
Pat_16	Pre-Treatment	RPTOR	57521	37	17	78811731	78811731	Nonsense_Mutation	SNP	G	A	28	53	c.1146G>A	c.(1144-1146)TGG>TGA	p.W382*
Pat_16	Pre-Treatment	L3MBTL4	91133	37	18	6215757	6215757	Missense_Mutation	SNP	A	T	34	60	c.862T>A	c.(862-864)TTT>ATT	p.F288I
Pat_16	Pre-Treatment	ARHGAP28	79822	37	18	6894891	6894891	Splice_Site	SNP	G	A	101	54	c.1374_splice	c.e14+1	p.M458_splice
Pat_16	Pre-Treatment	LAMA1	284217	37	18	6950909	6950909	Missense_Mutation	SNP	G	A	22	33	c.8269C>T	c.(8269-8271)CAT>TAT	p.H2757Y
Pat_16	Pre-Treatment	PTPRM	5797	37	18	7888152	7888152	Missense_Mutation	SNP	C	T	121	294	c.245C>T	c.(244-246)GCC>GTC	p.A82V
Pat_16	Pre-Treatment	DSC3	1825	37	18	28598156	28598156	Missense_Mutation	SNP	C	T	80	59	c.1144G>A	c.(1144-1146)GAT>AAT	p.D382N
Pat_16	Pre-Treatment	DSC2	1824	37	18	28662971	28662971	Missense_Mutation	SNP	A	T	70	29	c.998T>A	c.(997-999)TTT>TAT	p.F333Y
Pat_16	Pre-Treatment	DSG1	1828	37	18	28914025	28914025	Missense_Mutation	SNP	G	A	78	232	c.865G>A	c.(865-867)GAG>AAG	p.E289K
Pat_16	Pre-Treatment	DSG4	147409	37	18	28986205	28986205	Missense_Mutation	SNP	C	T	151	89	c.1802C>T	c.(1801-1803)GCG>GTG	p.A601V
Pat_16	Pre-Treatment	DSG2	1829	37	18	29122574	29122574	Missense_Mutation	SNP	G	C	46	102	c.2093G>C	c.(2092-2094)GGA>GCA	p.G698A
Pat_16	Pre-Treatment	ASXL3	80816	37	18	31318749	31318749	Missense_Mutation	SNP	A	G	61	139	c.1381A>G	c.(1381-1383)AGT>GGT	p.S461G
Pat_16	Pre-Treatment	ASXL3	80816	37	18	31319227	31319227	Missense_Mutation	SNP	G	A	11	30	c.1859G>A	c.(1858-1860)GGA>GAA	p.G620E
Pat_16	Pre-Treatment	TCEB3C	162699	37	18	44555339	44555339	Missense_Mutation	SNP	G	A	6	257	c.875C>T	c.(874-876)ACC>ATC	p.T292I
Pat_16	Pre-Treatment	MYO5B	4645	37	18	47398601	47398601	Missense_Mutation	SNP	G	A	174	403	c.3539C>T	c.(3538-3540)GCG>GTG	p.A1180V
Pat_16	Pre-Treatment	DCC	1630	37	18	50832050	50832050	Missense_Mutation	SNP	G	A	58	144	c.2014G>A	c.(2014-2016)GAA>AAA	p.E672K
Pat_16	Pre-Treatment	FECH	2235	37	18	55222097	55222097	Nonsense_Mutation	SNP	G	A	69	169	c.892C>T	c.(892-894)CGA>TGA	p.R298*
Pat_16	Pre-Treatment	PHLPP1	23239	37	18	60639769	60639769	Missense_Mutation	SNP	G	A	4	226	c.2047G>A	c.(2047-2049)GTG>ATG	p.V683M
Pat_16	Pre-Treatment	DOK6	220164	37	18	67425073	67425073	Missense_Mutation	SNP	C	T	62	167	c.820C>T	c.(820-822)CGT>TGT	p.R274C
Pat_16	Pre-Treatment	ATP9B	374868	37	18	77104307	77104307	Nonsense_Mutation	SNP	C	T	4	142	c.2425C>T	c.(2425-2427)CGA>TGA	p.R809*
Pat_16	Pre-Treatment	ABCA7	10347	37	19	1046386	1046386	Missense_Mutation	SNP	C	T	111	406	c.1603C>T	c.(1603-1605)CCG>TCG	p.P535S
Pat_16	Pre-Treatment	DOT1L	84444	37	19	2226980	2226980	Missense_Mutation	SNP	C	T	19	44	c.4460C>T	c.(4459-4461)TCC>TTC	p.S1487F
Pat_16	Pre-Treatment	JSRP1	126306	37	19	2254224	2254224	Missense_Mutation	SNP	G	A	6	349	c.224C>T	c.(223-225)ACC>ATC	p.T75I
Pat_16	Pre-Treatment	ZNF57	126295	37	19	2917733	2917733	Missense_Mutation	SNP	G	A	4	150	c.1114G>A	c.(1114-1116)GCC>ACC	p.A372T
Pat_16	Pre-Treatment	ZNF57	126295	37	19	2917793	2917793	Missense_Mutation	SNP	T	C	5	203	c.1174T>C	c.(1174-1176)TAT>CAT	p.Y392H
Pat_16	Pre-Treatment	ZNF57	126295	37	19	2917961	2917961	Missense_Mutation	SNP	C	T	8	239	c.1342C>T	c.(1342-1344)CAT>TAT	p.H448Y
Pat_16	Pre-Treatment	TLE2	7089	37	19	3005967	3005967	Splice_Site	SNP	C	T	23	105	c.1501_splice	c.e16-1	p.N501_splice
Pat_16	Pre-Treatment	PLIN4	729359	37	19	4511993	4511993	Missense_Mutation	SNP	G	A	66	95	c.1937C>T	c.(1936-1938)GCG>GTG	p.A646V
Pat_16	Pre-Treatment	C3	718	37	19	6713215	6713215	Missense_Mutation	SNP	C	T	3	77	c.988G>A	c.(988-990)GTC>ATC	p.V330I
Pat_16	Pre-Treatment	EMR1	2015	37	19	6921798	6921798	Missense_Mutation	SNP	T	A	54	109	c.1695T>A	c.(1693-1695)TTT>TTA	p.F565L
Pat_16	Pre-Treatment	MUC16	94025	37	19	9009311	9009312	Missense_Mutation	DNP	GG	AA	39	134	39161_39162CC>	c.(39160-39162)TCC>TTT	p.S13054F
Pat_16	Pre-Treatment	MUC16	94025	37	19	9059650	9059650	Missense_Mutation	SNP	G	A	60	62	c.27796C>T	c.(27796-27798)CTC>TTC	p.L9266F
Pat_16	Pre-Treatment	MUC16	94025	37	19	9068622	9068622	Missense_Mutation	SNP	G	A	97	95	c.18824C>T	c.(18823-18825)TCA>TTA	p.S6275L
Pat_16	Pre-Treatment	MUC16	94025	37	19	9072288	9072288	Missense_Mutation	SNP	G	A	30	36	c.15158C>T	c.(15157-15159)TCC>TTC	p.S5053F

Pat_16	Pre-Treatment	ZNF560	147741	37	19	9578016	9578016	Missense_Mutation	SNP	C	T	42	136	c.1607G>A	c.(1606-1608)CGA>CAA	p.R536Q
Pat_16	Pre-Treatment	ZNF561	93134	37	19	9721330	9721330	Missense_Mutation	SNP	G	A	146	161	c.1007C>T	c.(1006-1008)CCC>CTC	p.P336L
Pat_16	Pre-Treatment	COL5A3	50509	37	19	10097252	10097252	Missense_Mutation	SNP	C	T	29	139	c.2221G>A	c.(2221-2223)GAT>AAT	p.D741N
Pat_16	Pre-Treatment	CDC37	11140	37	19	10514068	10514068	Missense_Mutation	SNP	G	A	37	52	c.88C>T	c.(88-90)CGC>TGC	p.R30C
Pat_16	Pre-Treatment	KEAP1	9817	37	19	10610253	10610253	Missense_Mutation	SNP	G	A	4	218	c.457C>T	c.(457-459)CTC>TTC	p.L153F
Pat_16	Pre-Treatment	LPPR2	64748	37	19	11470343	11470343	Nonsense_Mutation	SNP	C	T	4	206	c.202C>T	c.(202-204)CGA>TGA	p.R68*
Pat_16	Pre-Treatment	ZNF653	115950	37	19	11597637	11597637	Missense_Mutation	SNP	G	A	8	32	c.1402C>T	c.(1402-1404)CAC>TAC	p.H468Y
Pat_16	Pre-Treatment	ZNF440	126070	37	19	11942554	11942554	Missense_Mutation	SNP	G	A	82	233	c.563G>A	c.(562-564)CGA>CAA	p.R188Q
Pat_16	Pre-Treatment	ZNF844	284391	37	19	12187307	12187307	Missense_Mutation	SNP	G	C	5	183	c.1372G>C	c.(1372-1374)GAT>CAT	p.D458H
Pat_16	Pre-Treatment	ZNF844	284391	37	19	12187502	12187502	Missense_Mutation	SNP	A	G	6	57	c.1567A>G	c.(1567-1569)AAA>GAA	p.K523E
Pat_16	Pre-Treatment	ANKLE1	126549	37	19	17394769	17394769	Missense_Mutation	SNP	C	T	128	122	c.1196C>T	c.(1195-1197)CCT>CTT	p.P399L
Pat_16	Pre-Treatment	UNC13A	23025	37	19	17766699	17766699	Missense_Mutation	SNP	C	T	18	9	c.1540G>A	c.(1540-1542)GAG>AAG	p.E514K
Pat_16	Pre-Treatment	ARRDC2	27106	37	19	18121461	18121461	Missense_Mutation	SNP	C	T	65	87	c.1093C>T	c.(1093-1095)CCC>TCC	p.P365S
Pat_16	Pre-Treatment	ZNF93	81931	37	19	20044699	20044699	Missense_Mutation	SNP	C	T	18	52	c.935C>T	c.(934-936)CCC>CTC	p.P312L
Pat_16	Pre-Treatment	ZNF626	199777	37	19	20807184	20807184	Missense_Mutation	SNP	T	C	7	190	c.1499A>G	c.(1498-1500)GAG>GGG	p.E500G
Pat_16	Pre-Treatment	ZNF208	7757	37	19	22157069	22157069	Missense_Mutation	SNP	G	A	37	36	c.767C>T	c.(766-768)TCC>TTC	p.S256F
Pat_16	Pre-Treatment	ZNF681	148213	37	19	23927358	23927358	Missense_Mutation	SNP	G	A	63	90	c.994C>T	c.(994-996)CAT>TAT	p.H332Y
Pat_16	Pre-Treatment	DPY19L3	147991	37	19	32968480	32968480	Missense_Mutation	SNP	G	A	4	197	c.1750G>A	c.(1750-1752)GGA>AGA	p.G584R
Pat_16	Pre-Treatment	PDCD2L	84306	37	19	34912539	34912539	Missense_Mutation	SNP	G	A	5	469	c.913G>A	c.(913-915)GCA>ACA	p.A305T
Pat_16	Pre-Treatment	LGI4	163175	37	19	35624989	35624989	Missense_Mutation	SNP	C	G	14	52	c.190G>C	c.(190-192)GTC>CTC	p.V64L
Pat_16	Pre-Treatment	KIRREL2	84063	37	19	36357377	36357377	Missense_Mutation	SNP	C	T	128	146	c.2110C>T	c.(2110-2112)CTC>TTC	p.L704F
Pat_16	Pre-Treatment	APLP1	333	37	19	36369539	36369539	Missense_Mutation	SNP	G	A	40	40	c.1630G>A	c.(1630-1632)GAA>AAA	p.E544K
Pat_16	Pre-Treatment	RYR1	6261	37	19	38939433	38939433	Missense_Mutation	SNP	C	A	11	22	c.1102C>A	c.(1102-1104)CTC>ATC	p.L368I
Pat_16	Pre-Treatment	LGALS4	3960	37	19	39299478	39299478	Missense_Mutation	SNP	C	T	40	128	c.245G>A	c.(244-246)GGG>GAG	p.G82E
Pat_16	Pre-Treatment	SIRT2	22933	37	19	39379771	39379771	Missense_Mutation	SNP	G	A	4	214	c.457C>T	c.(457-459)CGC>TGC	p.R153C
Pat_16	Pre-Treatment	LGALS13	29124	37	19	40095879	40095879	Missense_Mutation	SNP	T	A	30	107	c.154T>A	c.(154-156)TTC>ATC	p.F52I
Pat_16	Pre-Treatment	PRX	57716	37	19	40901021	40901021	Missense_Mutation	SNP	G	A	42	42	c.3238C>T	c.(3238-3240)CGT>TGT	p.R1080C
Pat_16	Pre-Treatment	PRX	57716	37	19	40901635	40901635	Missense_Mutation	SNP	T	G	9	57	c.2624A>C	c.(2623-2625)AAA>ACA	p.K875T
Pat_16	Pre-Treatment	DMRTC2	63946	37	19	42355736	42355736	Missense_Mutation	SNP	G	A	38	114	c.1076G>A	c.(1075-1077)CGT>CAT	p.R359H
Pat_16	Pre-Treatment	LIPE	3991	37	19	42912470	42912470	Missense_Mutation	SNP	G	A	4	199	c.1424C>T	c.(1423-1425)ACG>ATG	p.T475M
Pat_16	Pre-Treatment	PSG8	440533	37	19	43258652	43258652	Missense_Mutation	SNP	T	C	219	275	c.1076A>G	c.(1075-1077)AAC>AGC	p.N359S
Pat_16	Pre-Treatment	PSG6	5675	37	19	43529189	43529189	Nonsense_Mutation	SNP	C	T	71	253	c.102G>A	c.(100-102)TGG>TGA	p.W34*
Pat_16	Pre-Treatment	PSG4	5672	37	19	43708074	43708074	Nonsense_Mutation	SNP	C	A	6	456	c.394G>T	c.(394-396)GGA>TGA	p.G132*
Pat_16	Pre-Treatment	CADM4	199731	37	19	44131825	44131825	Missense_Mutation	SNP	C	T	196	222	c.182G>A	c.(181-183)CGG>CAG	p.R61Q
Pat_16	Pre-Treatment	DACT3	147906	37	19	47151836	47151836	Missense_Mutation	SNP	G	A	269	259	c.1793C>T	c.(1792-1794)CCC>CTC	p.P598L
Pat_16	Pre-Treatment	GRWD1	83743	37	19	48953958	48953958	Missense_Mutation	SNP	C	T	24	111	c.718C>T	c.(718-720)CAC>TAC	p.H240Y
Pat_16	Pre-Treatment	LMTK3	114783	37	19	49004787	49004787	Missense_Mutation	SNP	G	A	4	21	c.914C>T	c.(913-915)TCT>TTT	p.S305F
Pat_16	Pre-Treatment	PTH2	113091	37	19	49926533	49926533	Missense_Mutation	SNP	G	C	3	51	c.64C>G	c.(64-66)CTG>GTG	p.L22V
Pat_16	Pre-Treatment	PTOV1	53635	37	19	50361215	50361215	Missense_Mutation	SNP	G	A	5	289	c.859G>A	c.(859-861)GTG>ATG	p.V287M
Pat_16	Pre-Treatment	ZNF473	25888	37	19	50549870	50549870	Missense_Mutation	SNP	C	T	32	119	c.2170C>T	c.(2170-2172)CAC>TAC	p.H724Y
Pat_16	Pre-Treatment	SHANK1	50944	37	19	51171651	51171651	Missense_Mutation	SNP	C	A	8	24	c.3566G>T	c.(3565-3567)GGA>GTA	p.G1189V
Pat_16	Pre-Treatment	ZNF175	7728	37	19	52089988	52089988	Missense_Mutation	SNP	T	C	50	55	c.404T>C	c.(403-405)TTA>TCA	p.L135S
Pat_16	Pre-Treatment	ZNF836	162962	37	19	52659056	52659056	Missense_Mutation	SNP	T	A	6	299	c.1880A>T	c.(1879-1881)AAT>ATT	p.N627I
Pat_16	Pre-Treatment	ZNF836	162962	37	19	52659075	52659075	Missense_Mutation	SNP	C	A	6	270	c.1861G>T	c.(1861-1863)GAC>TAC	p.D621Y
Pat_16	Pre-Treatment	ZNF28	7576	37	19	53302984	53302985	Missense_Mutation	DNP	TT	GA	6	426	.2113_2114AA>T	c.(2113-2115)AAC>TCC	p.N705S
Pat_16	Pre-Treatment	ZNF677	342926	37	19	53741754	53741754	Missense_Mutation	SNP	C	T	20	98	c.226G>A	c.(226-228)GAA>AAA	p.E76K
Pat_16	Pre-Treatment	ZNF845	91664	37	19	53855364	53855364	Missense_Mutation	SNP	C	T	9	192	c.1436C>T	c.(1435-1437)ACA>ATA	p.T479I

Pat_16	Pre-Treatment	ZNF761	388561	37	19	53959137	53959137	Missense_Mutation	SNP	G	T	6	300	c.1376G>T	c.(1375-1377)CGT>CTT	p.R459L
Pat_16	Pre-Treatment	ZNF761	388561	37	19	53959151	53959151	Missense_Mutation	SNP	C	A	7	272	c.1390C>A	c.(1390-1392)CAA>AAA	p.Q464K
Pat_16	Pre-Treatment	DPRX	503834	37	19	54135382	54135382	Missense_Mutation	SNP	C	T	37	139	c.22C>T	c.(22-24)CGT>TGT	p.R8C
Pat_16	Pre-Treatment	NLRP7	199713	37	19	55451046	55451046	Missense_Mutation	SNP	C	T	11	36	c.1141G>A	c.(1141-1143)GAG>AAG	p.E381K
Pat_16	Pre-Treatment	NLRP4	147945	37	19	56373376	56373376	Missense_Mutation	SNP	T	A	28	129	c.2037T>A	c.(2035-2037)TTT>TTA	p.F679L
Pat_16	Pre-Treatment	NLRP8	126205	37	19	56466396	56466396	Missense_Mutation	SNP	G	T	59	76	c.972G>T	c.(970-972)ATG>ATT	p.M324I
Pat_16	Pre-Treatment	PEG3	5178	37	19	57325633	57325633	Missense_Mutation	SNP	C	T	40	126	c.4177G>A	c.(4177-4179)GAG>AAG	p.E1393K
Pat_16	Pre-Treatment	PEG3	5178	37	19	57327584	57327584	Missense_Mutation	SNP	T	A	145	157	c.2226A>T	c.(2224-2226)GAA>GAT	p.E742D
Pat_16	Pre-Treatment	ZNF419	79744	37	19	58005106	58005106	Missense_Mutation	SNP	C	T	7	258	c.1181C>T	c.(1180-1182)ACT>ATT	p.T394I
Pat_16	Pre-Treatment	ZNF419	79744	37	19	58005146	58005146	Missense_Mutation	SNP	C	G	7	264	c.1221C>G	c.(1219-1221)TTC>TTG	p.F407L
Pat_16	Pre-Treatment	ZNF606	80095	37	19	58490987	58490987	Missense_Mutation	SNP	A	C	73	74	c.1061T>G	c.(1060-1062)TTT>TGT	p.F354C
Pat_16	Pre-Treatment	TTC15	51112	37	2	3405575	3405575	Missense_Mutation	SNP	C	T	60	146	c.1075C>T	c.(1075-1077)CGC>TGC	p.R359C
Pat_16	Pre-Treatment	GREB1	9687	37	2	11758794	11758794	Missense_Mutation	SNP	G	A	3	67	c.3793G>A	c.(3793-3795)GTG>ATG	p.V1265M
Pat_16	Pre-Treatment	UBXN2A	165324	37	2	24199878	24199878	Missense_Mutation	SNP	G	A	4	118	c.220G>A	c.(220-222)GTC>ATC	p.V74I
Pat_16	Pre-Treatment	AGBL5	60509	37	2	27275992	27275992	Missense_Mutation	SNP	G	A	6	495	c.166G>A	c.(166-168)GTG>ATG	p.V56M
Pat_16	Pre-Treatment	FAM179A	165186	37	2	29225569	29225569	Missense_Mutation	SNP	G	A	10	46	c.595G>A	c.(595-597)GGG>AGG	p.G199R
Pat_16	Pre-Treatment	CAPN13	92291	37	2	30977178	30977178	Missense_Mutation	SNP	T	G	20	21	c.919A>C	c.(919-921)AAA>CAA	p.K307Q
Pat_16	Pre-Treatment	MAP4K3	8491	37	2	39487908	39487908	Missense_Mutation	SNP	A	T	54	36	c.2147T>A	c.(2146-2148)TTT>TAT	p.F716Y
Pat_16	Pre-Treatment	ADD2	119	37	2	70890612	70890612	Missense_Mutation	SNP	A	T	119	68	c.2126T>A	c.(2125-2127)TTC>TAC	p.F709Y
Pat_16	Pre-Treatment	ADD2	119	37	2	70933534	70933534	Missense_Mutation	SNP	C	T	90	44	c.7G>A	c.(7-9)GAA>AAA	p.E3K
Pat_16	Pre-Treatment	RAB11FIP5	26056	37	2	73315742	73315742	Missense_Mutation	SNP	G	A	3	33	c.1004C>T	c.(1003-1005)TCG>TTG	p.S335L
Pat_16	Pre-Treatment	REG3G	130120	37	2	79254278	79254278	Missense_Mutation	SNP	G	A	111	178	c.314G>A	c.(313-315)GGG>GAG	p.G105E
Pat_16	Pre-Treatment	TGOLN2	10618	37	2	85554362	85554362	Missense_Mutation	SNP	G	T	8	829	c.493C>A	c.(493-495)CCT>ACT	p.P165T
Pat_16	Pre-Treatment	TGOLN2	10618	37	2	85554367	85554367	Missense_Mutation	SNP	T	C	9	832	c.488A>G	c.(487-489)GAC>GGC	p.D163G
Pat_16	Pre-Treatment	RETSAT	54884	37	2	85581530	85581530	Missense_Mutation	SNP	G	A	110	229	c.101C>T	c.(100-102)TCC>TTC	p.S34F
Pat_16	Pre-Treatment	PTCD3	55037	37	2	86362095	86362095	Missense_Mutation	SNP	G	A	5	296	c.1763G>A	c.(1762-1764)AGA>AAA	p.R588K
Pat_16	Pre-Treatment	SMYD1	150572	37	2	88396118	88396118	Missense_Mutation	SNP	G	A	116	280	c.703G>A	c.(703-705)GAG>AAG	p.E235K
Pat_16	Pre-Treatment	KCNIP3	30818	37	2	96040928	96040928	Missense_Mutation	SNP	C	T	4	192	c.419C>T	c.(418-420)GCG>GTG	p.A140V
Pat_16	Pre-Treatment	AFF3	3899	37	2	100209977	100209978	Missense_Mutation	DNP	CC	TT	25	84	.2145_2146GG>A	43-2148)GGGGGC>GGA	p.G716S
Pat_16	Pre-Treatment	RGPD4	285190	37	2	108487252	108487252	Missense_Mutation	SNP	G	A	117	199	c.2792G>A	c.(2791-2793)GGA>GAA	p.G931E
Pat_16	Pre-Treatment	SULT1C4	27233	37	2	108999916	108999916	Missense_Mutation	SNP	G	A	46	135	c.565G>A	c.(565-567)GCC>ACC	p.A189T
Pat_16	Pre-Treatment	EDAR	10913	37	2	109513459	109513459	Missense_Mutation	SNP	C	G	39	20	c.1251G>C	c.(1249-1251)CAG>CAC	p.Q417H
Pat_16	Pre-Treatment	SH3RF3	344558	37	2	110053444	110053444	Missense_Mutation	SNP	G	A	35	95	c.1670G>A	c.(1669-1671)GGG>GAG	p.G557E
Pat_16	Pre-Treatment	GPR17	2840	37	2	128408607	128408608	Nonsense_Mutation	DNP	GG	TA	38	94	c.382_383GG>TA	c.(382-384)GGG>TAG	p.G128*
Pat_16	Pre-Treatment	UGGT1	56886	37	2	128884989	128884989	Missense_Mutation	SNP	G	C	37	95	c.1189G>C	c.(1189-1191)GGA>CGA	p.G397R
Pat_16	Pre-Treatment	THSD7B	80731	37	2	137852453	137852453	Nonsense_Mutation	SNP	C	T	56	176	c.868C>T	c.(868-870)CAA>TAA	p.Q290*
Pat_16	Pre-Treatment	THSD7B	80731	37	2	138373853	138373853	Missense_Mutation	SNP	G	A	160	347	c.3445G>A	c.(3445-3447)GAA>AAA	p.E1149K
Pat_16	Pre-Treatment	LRP1B	53353	37	2	141459861	141459861	Missense_Mutation	SNP	C	T	73	213	c.6151G>A	c.(6151-6153)GAA>AAA	p.E2051K
Pat_16	Pre-Treatment	LRP1B	53353	37	2	141945989	141945989	Splice_Site	SNP	C	T	31	96	c.1013_splice	c.e7+1	p.G338_splice
Pat_16	Pre-Treatment	NEB	4703	37	2	152394408	152394408	Missense_Mutation	SNP	G	T	6	118	c.15977C>A	c.(15976-15978)GCA>GAA	p.A5326E
Pat_16	Pre-Treatment	TANC1	85461	37	2	160027046	160027046	Missense_Mutation	SNP	C	T	35	109	c.1081C>T	c.(1081-1083)CCC>TCC	p.P361S
Pat_16	Pre-Treatment	BAZ2B	29994	37	2	160295112	160295112	Missense_Mutation	SNP	G	A	5	431	c.995C>T	c.(994-996)GCG>GTG	p.A332V
Pat_16	Pre-Treatment	SLC4A10	57282	37	2	162728844	162728844	Missense_Mutation	SNP	G	A	94	243	c.808G>A	c.(808-810)GAA>AAA	p.E270K
Pat_16	Pre-Treatment	DPP4	1803	37	2	162875301	162875301	Missense_Mutation	SNP	C	T	5	350	c.1358G>A	c.(1357-1359)AGG>AAG	p.R453K
Pat_16	Pre-Treatment	HOXD3	3232	37	2	177036364	177036364	Missense_Mutation	SNP	C	T	100	231	c.661C>T	c.(661-663)CGG>TGG	p.R221W
Pat_16	Pre-Treatment	TTN	7273	37	2	179454201	179454201	Missense_Mutation	SNP	C	T	26	68	c.54547G>A	c.(54547-54549)GAA>AAA	p.E18183K
Pat_16	Pre-Treatment	TTN	7273	37	2	179641949	179641949	Missense_Mutation	SNP	C	T	97	217	c.4741G>A	c.(4741-4743)GGT>AGT	p.G1581S

Pat_16	Pre-Treatment	DNAJC10	54431	37	2	183593668	183593668	Nonsense_Mutation	SNP	C	T	4	317	c.580C>T	c.(580-582)CGA>TGA	p.R194*
Pat_16	Pre-Treatment	STAT4	6775	37	2	191937835	191937835	Missense_Mutation	SNP	T	A	157	317	c.454A>T	c.(454-456)AAC>TAC	p.N152Y
Pat_16	Pre-Treatment	ABCA12	26154	37	2	215876250	215876250	Missense_Mutation	SNP	G	A	74	142	c.2245C>T	c.(2245-2247)CCA>TCA	p.P749S
Pat_16	Pre-Treatment	ANKZF1	55139	37	2	220099997	220099997	Missense_Mutation	SNP	C	T	4	273	c.1654C>T	c.(1654-1656)CGT>TGT	p.R552C
Pat_16	Pre-Treatment	COL4A3	1285	37	2	228147167	228147167	Missense_Mutation	SNP	G	A	125	59	c.2575G>A	c.(2575-2577)GGA>AGA	p.G859R
Pat_16	Pre-Treatment	COL4A3	1285	37	2	228168824	228168824	Missense_Mutation	SNP	G	A	26	61	c.4117G>A	c.(4117-4119)GGA>AGA	p.G1373R
Pat_16	Pre-Treatment	SPHKAP	80309	37	2	228846519	228846519	Missense_Mutation	SNP	G	A	42	114	c.5017C>T	c.(5017-5019)CAT>TAT	p.H1673Y
Pat_16	Pre-Treatment	SLC16A14	151473	37	2	230911393	230911393	Missense_Mutation	SNP	C	A	13	37	c.449G>T	c.(448-450)GGC>GTC	p.G150V
Pat_16	Pre-Treatment	USP40	55230	37	2	234442200	234442200	Missense_Mutation	SNP	C	T	127	87	c.1429G>A	c.(1429-1431)GAA>AAA	p.E477K
Pat_16	Pre-Treatment	TRPM8	79054	37	2	234846100	234846100	Missense_Mutation	SNP	C	T	80	179	c.295C>T	c.(295-297)CCT>TCT	p.P99S
Pat_16	Pre-Treatment	TRPM8	79054	37	2	234873271	234873271	Splice_Site	SNP	G	A	23	57	c.1750_splice	c.e14-1	p.T584_splice
Pat_16	Pre-Treatment	MLPH	79083	37	2	238457876	238457876	Missense_Mutation	SNP	C	T	28	63	c.1630C>T	c.(1630-1632)CCC>TCC	p.P544S
Pat_16	Pre-Treatment	TRAF3IP1	26146	37	2	239307420	239307420	Missense_Mutation	SNP	T	G	138	53	c.1936T>G	c.(1936-1938)TTA>GTA	p.L646V
Pat_16	Pre-Treatment	THAP4	51078	37	2	242545816	242545817	Missense_Mutation	DNP	CC	TT	7	10	.1312_1313GG>A	c.(1312-1314)GGA>AAA	p.G438K
Pat_16	Pre-Treatment	SIRPG	55423	37	20	1629761	1629761	Nonsense_Mutation	SNP	G	A	59	188	c.367C>T	c.(367-369)CGA>TGA	p.R123*
Pat_16	Pre-Treatment	TGM6	343641	37	20	2411098	2411098	Missense_Mutation	SNP	G	A	56	94	c.1685G>A	c.(1684-1686)AGA>AAA	p.R562K
Pat_16	Pre-Treatment	BTBD3	22903	37	20	11899185	11899185	Missense_Mutation	SNP	C	T	160	584	c.262C>T	c.(262-264)CTC>TTC	p.L88F
Pat_16	Pre-Treatment	CST9	128822	37	20	23584239	23584239	Missense_Mutation	SNP	A	T	64	155	c.388T>A	c.(388-390)TTT>ATT	p.F130I
Pat_16	Pre-Treatment	FRG1B	284802	37	20	29624093	29624093	Splice_Site	SNP	G	T	4	40	c.26_splice	c.e1+1	p.R9_splice
Pat_16	Pre-Treatment	FRG1B	284802	37	20	29625892	29625892	Missense_Mutation	SNP	T	C	5	293	c.46T>C	c.(46-48)TAT>CAT	p.Y16H
Pat_16	Pre-Treatment	ASXL1	171023	37	20	31023318	31023318	Missense_Mutation	SNP	C	T	44	137	c.2803C>T	c.(2803-2805)CCC>TCC	p.P935S
Pat_16	Pre-Treatment	CBFA2T2	9139	37	20	32217603	32217603	Missense_Mutation	SNP	C	T	69	86	c.1138C>T	c.(1138-1140)CGT>TGT	p.R380C
Pat_16	Pre-Treatment	NFS1	9054	37	20	34263049	34263049	Missense_Mutation	SNP	C	T	4	122	c.866G>A	c.(865-867)CGG>CAG	p.R289Q
Pat_16	Pre-Treatment	PPP1R16B	26051	37	20	37524242	37524242	Missense_Mutation	SNP	T	A	25	36	c.356T>A	c.(355-357)CTG>CAG	p.L119Q
Pat_16	Pre-Treatment	STK4	6789	37	20	43625841	43625841	Missense_Mutation	SNP	C	T	70	301	c.725C>T	c.(724-726)CCC>CTC	p.P242L
Pat_16	Pre-Treatment	SEMG1	6406	37	20	43836962	43836962	Nonsense_Mutation	SNP	A	T	24	58	c.1024A>T	c.(1024-1026)AAG>TAG	p.K342*
Pat_16	Pre-Treatment	TP53TG5	27296	37	20	44003936	44003936	Missense_Mutation	SNP	C	T	140	158	c.511G>A	c.(511-513)GGA>AGA	p.G171R
Pat_16	Pre-Treatment	ZSWIM3	140831	37	20	44506623	44506623	Missense_Mutation	SNP	G	A	5	211	c.1426G>A	c.(1426-1428)GCA>ACA	p.A476T
Pat_16	Pre-Treatment	SLC12A5	57468	37	20	44684831	44684831	Missense_Mutation	SNP	A	G	21	67	c.2899A>G	c.(2899-2901)AAG>GAG	p.K967E
Pat_16	Pre-Treatment	ARFGEF2	10564	37	20	47641991	47641991	Missense_Mutation	SNP	G	A	4	214	c.4897G>A	c.(4897-4899)GAG>AAG	p.E1633K
Pat_16	Pre-Treatment	SNAI1	6615	37	20	48600613	48600613	Missense_Mutation	SNP	C	T	245	302	c.335C>T	c.(334-336)TCC>TTC	p.S112F
Pat_16	Pre-Treatment	SALL4	57167	37	20	50407142	50407142	Missense_Mutation	SNP	G	A	38	133	c.1880C>T	c.(1879-1881)TCG>TTG	p.S627L
Pat_16	Pre-Treatment	TFAP2C	7022	37	20	55208529	55208529	Missense_Mutation	SNP	C	T	86	301	c.707C>T	c.(706-708)TCT>TTT	p.S236F
Pat_16	Pre-Treatment	LAMA5	3911	37	20	60885978	60885978	Missense_Mutation	SNP	G	A	20	36	c.10261C>T	.(10261-10263)CGG>TG	p.R3421W
Pat_16	Pre-Treatment	DIDO1	11083	37	20	61511835	61511835	Missense_Mutation	SNP	C	T	73	72	c.5473G>A	c.(5473-5475)GGC>AGC	p.G1825S
Pat_16	Pre-Treatment	PCMTD2	55251	37	20	62891325	62891325	Missense_Mutation	SNP	G	A	6	635	c.7G>A	c.(7-9)GGT>AGT	p.G3S
Pat_16	Pre-Treatment	PCMTD2	55251	37	20	62891413	62891413	Missense_Mutation	SNP	C	T	276	293	c.95C>T	c.(94-96)GCT>GTT	p.A32V
Pat_16	Pre-Treatment	TPTE	7179	37	21	10914379	10914379	Missense_Mutation	SNP	G	A	22	44	c.1340C>T	c.(1339-1341)TCA>TTA	p.S447L
Pat_16	Pre-Treatment	C2CD2	25966	37	21	43319324	43319325	Missense_Mutation	DNP	GG	AA	7	32	.1707_1708CC>T	1705-1710)TCCCTT>TCT	p.L570F
Pat_16	Pre-Treatment	ZNF295	49854	37	21	43411624	43411624	Missense_Mutation	SNP	A	T	68	145	c.2581T>A	c.(2581-2583)TCC>ACC	p.S861T
Pat_16	Pre-Treatment	ABCG1	9619	37	21	43711687	43711687	Missense_Mutation	SNP	T	C	16	74	c.1610T>C	c.(1609-1611)TTT>TCT	p.F537S
Pat_16	Pre-Treatment	PCBP3	54039	37	21	47337538	47337538	Missense_Mutation	SNP	C	T	106	266	c.712C>T	c.(712-714)CCG>TCG	p.P238S
Pat_16	Pre-Treatment	DIP2A	23181	37	21	47974146	47974146	Missense_Mutation	SNP	C	T	4	142	c.3095C>T	c.(3094-3096)GCT>GTT	p.A1032V
Pat_16	Pre-Treatment	GGT5	2687	37	22	24640582	24640582	Missense_Mutation	SNP	G	A	38	77	c.112C>T	c.(112-114)CCC>TCC	p.P38S
Pat_16	Pre-Treatment	PES1	23481	37	22	30977009	30977009	Missense_Mutation	SNP	G	A	69	32	c.902C>T	c.(901-903)CCC>CTC	p.P301L
Pat_16	Pre-Treatment	PISD	23761	37	22	32015741	32015741	Missense_Mutation	SNP	C	T	3	80	c.1087G>A	c.(1087-1089)GTC>ATC	p.V363I
Pat_16	Pre-Treatment	BPIL2	254240	37	22	32841915	32841915	Missense_Mutation	SNP	C	T	47	39	c.443G>A	c.(442-444)CGA>CAA	p.R148Q

Pat_16	Pre-Treatment	RASD2	23551	37	22	35947968	35947968	Missense_Mutation	SNP	G	A	42	24	c.690G>A	c.(688-690)ATG>ATA	p.M230I
Pat_16	Pre-Treatment	FOXRED2	80020	37	22	36894189	36894189	Missense_Mutation	SNP	G	A	66	111	c.1231C>T	c.(1231-1233)CGG>TGG	p.R411W
Pat_16	Pre-Treatment	TRIOBP	11078	37	22	38120316	38120316	Missense_Mutation	SNP	C	T	67	385	c.1753C>T	c.(1753-1755)CCC>TCC	p.P585S
Pat_16	Pre-Treatment	PDGFB	5155	37	22	39631866	39631866	Missense_Mutation	SNP	G	A	13	36	c.77C>T	c.(76-78)CCC>CTC	p.P26L
Pat_16	Pre-Treatment	CACNA1I	8911	37	22	40054256	40054256	Missense_Mutation	SNP	G	A	4	94	c.2092G>A	c.(2092-2094)GAC>AAC	p.D698N
Pat_16	Pre-Treatment	PARVG	64098	37	22	44583758	44583758	Nonsense_Mutation	SNP	C	T	29	44	c.247C>T	c.(247-249)CAG>TAG	p.Q83*
Pat_16	Pre-Treatment	PLXNB2	23654	37	22	50724514	50724514	Missense_Mutation	SNP	C	T	3	41	c.1891G>A	c.(1891-1893)GTG>ATG	p.V631M
Pat_16	Pre-Treatment	KLHDC7B	113730	37	22	50987478	50987478	Missense_Mutation	SNP	G	A	17	8	c.883G>A	c.(883-885)GGC>AGC	p.G295S
Pat_16	Pre-Treatment	BRPF1	7862	37	3	9776260	9776260	Missense_Mutation	SNP	C	T	26	45	c.436C>T	c.(436-438)CCC>TCC	p.P146S
Pat_16	Pre-Treatment	EAF1	85403	37	3	15471450	15471450	Missense_Mutation	SNP	C	T	74	70	c.134C>T	c.(133-135)TCC>TTC	p.S45F
Pat_16	Pre-Treatment	SATB1	6304	37	3	18393533	18393533	Missense_Mutation	SNP	T	A	212	238	c.1730A>T	c.(1729-1731)CAT>CTT	p.H577L
Pat_16	Pre-Treatment	KCNH8	131096	37	3	19492780	19492780	Missense_Mutation	SNP	C	T	83	95	c.1709C>T	c.(1708-1710)TCT>TTT	p.S570F
Pat_16	Pre-Treatment	NEK10	152110	37	3	27213359	27213359	Missense_Mutation	SNP	A	C	34	32	c.718T>G	c.(718-720)TTA>GTA	p.L240V
Pat_16	Pre-Treatment	GLB1	2720	37	3	33038614	33038614	Missense_Mutation	SNP	G	A	54	57	c.1957C>T	c.(1957-1959)CCC>TCC	p.P653S
Pat_16	Pre-Treatment	STAC	6769	37	3	36484961	36484961	Missense_Mutation	SNP	G	A	25	33	c.217G>A	c.(217-219)GCA>ACA	p.A73T
Pat_16	Pre-Treatment	TRANK1	9881	37	3	36873053	36873053	Missense_Mutation	SNP	A	C	10	16	c.6239T>G	c.(6238-6240)CTC>CGC	p.L2080R
Pat_16	Pre-Treatment	TRANK1	9881	37	3	36873507	36873507	Missense_Mutation	SNP	G	A	4	134	c.5785C>T	c.(5785-5787)CGG>TGG	p.R1929W
Pat_16	Pre-Treatment	LAMB2	3913	37	3	49163299	49163299	Missense_Mutation	SNP	G	A	71	71	c.2369C>T	c.(2368-2370)TCA>TTA	p.S790L
Pat_16	Pre-Treatment	USP4	7375	37	3	49322316	49322316	Missense_Mutation	SNP	G	A	32	27	c.2237C>T	c.(2236-2238)ACT>ATT	p.T746I
Pat_16	Pre-Treatment	SEMA3F	6405	37	3	50220182	50220182	Missense_Mutation	SNP	C	T	30	58	c.869C>T	c.(868-870)CCC>CTC	p.P290L
Pat_16	Pre-Treatment	SEMA3F	6405	37	3	50225363	50225363	Missense_Mutation	SNP	C	T	11	15	c.2173C>T	c.(2173-2175)CCT>TCT	p.P725S
Pat_16	Pre-Treatment	CACNA2D2	9254	37	3	50421769	50421769	Splice_Site	SNP	C	T	71	94	c.511_splice	c.e6-1	p.D171_splice
Pat_16	Pre-Treatment	VPRBP	9730	37	3	51500894	51500894	Splice_Site	SNP	T	C	3	106	c.188_splice	c.e5-1	p.G63_splice
Pat_16	Pre-Treatment	DNAH1	25981	37	3	52397156	52397156	Missense_Mutation	SNP	C	T	22	35	c.5240C>T	c.(5239-5241)TCC>TTC	p.S1747F
Pat_16	Pre-Treatment	ITIH3	3699	37	3	52831902	52831902	Missense_Mutation	SNP	G	A	4	11	c.619G>A	c.(619-621)GAC>AAC	p.D207N
Pat_16	Pre-Treatment	SFMBT1	51460	37	3	52940181	52940181	Missense_Mutation	SNP	C	T	4	210	c.2408G>A	c.(2407-2409)CGG>CAG	p.R803Q
Pat_16	Pre-Treatment	LRIG1	26018	37	3	66448590	66448590	Missense_Mutation	SNP	G	A	4	169	c.1250C>T	c.(1249-1251)GCG>GTG	p.A417V
Pat_16	Pre-Treatment	KBTBD8	84541	37	3	67058763	67058763	Missense_Mutation	SNP	G	A	45	84	c.1760G>A	c.(1759-1761)TGT>TAT	p.C587Y
Pat_16	Pre-Treatment	FRMD4B	23150	37	3	69245538	69245538	Missense_Mutation	SNP	G	A	46	49	c.1102C>T	c.(1102-1104)CCT>TCT	p.P368S
Pat_16	Pre-Treatment	FOXP1	27086	37	3	71008430	71008430	Missense_Mutation	SNP	C	T	4	267	c.2002G>A	c.(2002-2004)GAA>AAA	p.E668K
Pat_16	Pre-Treatment	FAM55C	91775	37	3	101520553	101520553	Missense_Mutation	SNP	C	T	58	69	c.568C>T	c.(568-570)CCC>TCC	p.P190S
Pat_16	Pre-Treatment	MYH15	22989	37	3	108117510	108117510	Missense_Mutation	SNP	C	T	94	120	c.5167G>A	c.(5167-5169)GAA>AAA	p.E1723K
Pat_16	Pre-Treatment	DPPA4	55211	37	3	109049541	109049541	Missense_Mutation	SNP	A	C	44	63	c.509T>G	c.(508-510)CTT>CGT	p.L170R
Pat_16	Pre-Treatment	KIAA2018	205717	37	3	113377026	113377026	Missense_Mutation	SNP	G	A	34	52	c.3503C>T	c.(3502-3504)TCA>TTA	p.S1168L
Pat_16	Pre-Treatment	PARP14	54625	37	3	122446777	122446777	Missense_Mutation	SNP	G	A	4	74	c.5060G>A	c.(5059-5061)GGC>GAC	p.G1687D
Pat_16	Pre-Treatment	PODXL2	50512	37	3	127358286	127358286	Missense_Mutation	SNP	G	A	4	59	c.269G>A	c.(268-270)CGG>CAG	p.R90Q
Pat_16	Pre-Treatment	GATA2	2624	37	3	128204758	128204758	Missense_Mutation	SNP	G	A	21	34	c.683C>T	c.(682-684)CCC>CTC	p.P228L
Pat_16	Pre-Treatment	IFT122	55764	37	3	129225317	129225317	Missense_Mutation	SNP	G	A	4	223	c.2716G>A	c.(2716-2718)GTG>ATG	p.V906M
Pat_16	Pre-Treatment	ACPP	55	37	3	132047117	132047117	Missense_Mutation	SNP	C	T	86	55	c.127C>T	c.(127-129)CGG>TGG	p.R43W
Pat_16	Pre-Treatment	SLCO2A1	6578	37	3	133661546	133661547	Missense_Mutation	DNP	GG	AA	60	153	.1527_1528CC>T	525-1530)GTCCCC>GTTT	p.P510S
Pat_16	Pre-Treatment	EPHB1	2047	37	3	134851694	134851694	Missense_Mutation	SNP	G	A	21	60	c.1100G>A	c.(1099-1101)CGC>CAC	p.R367H
Pat_16	Pre-Treatment	HPS3	84343	37	3	148859158	148859158	Missense_Mutation	SNP	T	C	155	303	c.961T>C	c.(961-963)TAC>CAC	p.Y321H
Pat_16	Pre-Treatment	CP	1356	37	3	148939527	148939527	Nonsense_Mutation	SNP	C	T	62	126	c.53G>A	c.(52-54)TGG>TAG	p.W18*
Pat_16	Pre-Treatment	B3GALNT1	8706	37	3	160803907	160803907	Missense_Mutation	SNP	A	C	33	61	c.636T>G	c.(634-636)AAT>AAG	p.N212K
Pat_16	Pre-Treatment	ZBBX	79740	37	3	167016179	167016179	Missense_Mutation	SNP	A	T	75	190	c.1793T>A	c.(1792-1794)TTT>TAT	p.F598Y
Pat_16	Pre-Treatment	SERPINI1	5274	37	3	167540842	167540842	Missense_Mutation	SNP	G	A	55	148	c.1048G>A	c.(1048-1050)GAA>AAA	p.E350K
Pat_16	Pre-Treatment	MECOM	2122	37	3	168825731	168825731	Missense_Mutation	SNP	G	A	67	63	c.2023C>T	c.(2023-2025)CCT>TCT	p.P675S

Pat_16	Pre-Treatment	TBCCD1	55171	37	3	186276241	186276241	Missense_Mutation	SNP	G	A	144	327	c.457C>T	c.(457-459)CCT>TCT	p.P153S
Pat_16	Pre-Treatment	TP63	8626	37	3	189582204	189582204	Missense_Mutation	SNP	G	A	28	55	c.763G>A	c.(763-765)GAG>AAG	p.E255K
Pat_16	Pre-Treatment	LSG1	55341	37	3	194373772	194373772	Missense_Mutation	SNP	G	A	57	126	c.859C>T	c.(859-861)CCA>TCA	p.P287S
Pat_16	Pre-Treatment	TFRC	7037	37	3	195785162	195785162	Missense_Mutation	SNP	A	G	150	92	c.1670T>C	c.(1669-1671)TTT>TCT	p.F557S
Pat_16	Pre-Treatment	LRRC33	375387	37	3	196387690	196387690	Missense_Mutation	SNP	C	A	84	58	c.1176C>A	c.(1174-1176)CAC>CAA	p.H392Q
Pat_16	Pre-Treatment	GAK	2580	37	4	860167	860167	Missense_Mutation	SNP	C	T	3	47	c.3028G>A	c.(3028-3030)GAC>AAC	p.D1010N
Pat_16	Pre-Treatment	HTRA3	94031	37	4	8307709	8307709	Missense_Mutation	SNP	A	G	4	129	c.1208A>G	c.(1207-1209)CAA>CGA	p.Q403R
Pat_16	Pre-Treatment	ZNF518B	85460	37	4	10444904	10444904	Missense_Mutation	SNP	G	A	32	124	c.3049C>T	c.(3049-3051)CAT>TAT	p.H1017Y
Pat_16	Pre-Treatment	PPARGC1A	10891	37	4	23815598	23815598	Missense_Mutation	SNP	G	A	82	223	c.1508C>T	c.(1507-1509)TCA>TTA	p.S503L
Pat_16	Pre-Treatment	SEL1L3	23231	37	4	25789890	25789891	Missense_Mutation	DNP	CC	TT	113	200	.2172_2173GG>A	170-2175)ACGGAG>ACA	p.E725K
Pat_16	Pre-Treatment	KLB	152831	37	4	39409123	39409123	Missense_Mutation	SNP	G	A	53	135	c.554G>A	c.(553-555)AGA>AAA	p.R185K
Pat_16	Pre-Treatment	KDR	3791	37	4	55976657	55976657	Missense_Mutation	SNP	C	T	88	43	c.1168G>A	c.(1168-1170)GAA>AAA	p.E390K
Pat_16	Pre-Treatment	LPHN3	23284	37	4	62363041	62363041	Missense_Mutation	SNP	G	A	27	92	c.30G>A	c.(28-30)ATG>ATA	p.M10I
Pat_16	Pre-Treatment	TMPRSS11B	132724	37	4	69095235	69095235	Splice_Site	SNP	C	T	36	108	c.687_splice	c.e8-1	p.K229_splice
Pat_16	Pre-Treatment	SHROOM3	57619	37	4	77652072	77652072	Nonsense_Mutation	SNP	C	T	206	446	c.571C>T	c.(571-573)CAA>TAA	p.Q191*
Pat_16	Pre-Treatment	FRAS1	80144	37	4	79351557	79351557	Missense_Mutation	SNP	G	A	15	43	c.4955G>A	c.(4954-4956)AGG>AAG	p.R1652K
Pat_16	Pre-Treatment	GRID2	2895	37	4	94344063	94344063	Missense_Mutation	SNP	G	A	32	122	c.1489G>A	c.(1489-1491)GGA>AGA	p.G497R
Pat_16	Pre-Treatment	PDHA2	5161	37	4	96761349	96761349	Missense_Mutation	SNP	A	T	50	79	c.48A>T	c.(46-48)AAA>AAT	p.K16N
Pat_16	Pre-Treatment	ADH1C	126	37	4	100261800	100261800	Missense_Mutation	SNP	G	A	364	226	c.896C>T	c.(895-897)TCC>TTC	p.S299F
Pat_16	Pre-Treatment	GAR1	54433	37	4	110743584	110743584	Missense_Mutation	SNP	G	T	5	123	c.511G>T	c.(511-513)GGT>TGT	p.G171C
Pat_16	Pre-Treatment	EGF	1950	37	4	110882040	110882040	Missense_Mutation	SNP	T	A	142	79	c.1084T>A	c.(1084-1086)TTT>ATT	p.F362I
Pat_16	Pre-Treatment	ANK2	287	37	4	114158761	114158761	Missense_Mutation	SNP	G	A	113	324	c.676G>A	c.(676-678)GTG>ATG	p.V226M
Pat_16	Pre-Treatment	ANK2	287	37	4	114263073	114263073	Splice_Site	SNP	G	A	5	174	c.4122_splice	c.e33+1	p.E1374_splice
Pat_16	Pre-Treatment	PRDM5	11107	37	4	121737728	121737728	Missense_Mutation	SNP	A	G	30	64	c.745T>C	c.(745-747)TTT>CTT	p.F249L
Pat_16	Pre-Treatment	ADAD1	132612	37	4	123317451	123317451	Missense_Mutation	SNP	G	A	31	83	c.643G>A	c.(643-645)GAA>AAA	p.E215K
Pat_16	Pre-Treatment	FAT4	79633	37	4	126389676	126389676	Missense_Mutation	SNP	G	A	163	82	c.11909G>A	c.(11908-11910)GGA>GAA	p.G3970E
Pat_16	Pre-Treatment	NAA15	80155	37	4	140275246	140275246	Missense_Mutation	SNP	C	T	53	164	c.1081C>T	c.(1081-1083)CCC>TCC	p.P361S
Pat_16	Pre-Treatment	SLC10A7	84068	37	4	147227095	147227095	Missense_Mutation	SNP	G	A	61	48	c.538C>T	c.(538-540)CCT>TCT	p.P180S
Pat_16	Pre-Treatment	DCHS2	54798	37	4	155237118	155237118	Missense_Mutation	SNP	G	A	67	136	c.3677C>T	c.(3676-3678)CCT>CTT	p.P1226L
Pat_16	Pre-Treatment	FGA	2243	37	4	155507586	155507586	Missense_Mutation	SNP	C	T	85	171	c.995G>A	c.(994-996)GGA>GAA	p.G332E
Pat_16	Pre-Treatment	CTSO	1519	37	4	156864377	156864377	Missense_Mutation	SNP	G	A	108	255	c.175C>T	c.(175-177)CCC>TCC	p.P59S
Pat_16	Pre-Treatment	TRIM60	166655	37	4	165962593	165962593	Missense_Mutation	SNP	G	A	33	64	c.1369G>A	c.(1369-1371)GAT>AAT	p.D457N
Pat_16	Pre-Treatment	SPOCK3	50859	37	4	167656164	167656164	Missense_Mutation	SNP	C	T	30	79	c.1219G>A	c.(1219-1221)GAT>AAT	p.D407N
Pat_16	Pre-Treatment	DDX60	55601	37	4	169206544	169206544	Missense_Mutation	SNP	C	T	30	25	c.1445G>A	c.(1444-1446)AGT>AAT	p.S482N
Pat_16	Pre-Treatment	C4orf41	60684	37	4	184626224	184626224	Splice_Site	SNP	G	A	4	280	c.3055_splice	c.e27+1	p.D1019_splice
Pat_16	Pre-Treatment	FRG1	2483	37	4	190878651	190878651	Missense_Mutation	SNP	G	A	14	195	c.531G>A	c.(529-531)ATG>ATA	p.M177I
Pat_16	Pre-Treatment	BRD9	65980	37	5	884073	884073	Missense_Mutation	SNP	G	A	39	98	c.946C>T	c.(946-948)CGG>TGG	p.R316W
Pat_16	Pre-Treatment	PRLR	5618	37	5	35065819	35065819	Missense_Mutation	SNP	G	A	159	403	c.1241C>T	c.(1240-1242)TCA>TTA	p.S414L
Pat_16	Pre-Treatment	IL7R	3575	37	5	35867469	35867469	Missense_Mutation	SNP	G	A	44	112	c.283G>A	c.(283-285)GAG>AAG	p.E95K
Pat_16	Pre-Treatment	EGFLAM	133584	37	5	38370447	38370447	Missense_Mutation	SNP	G	A	95	57	c.595G>A	c.(595-597)GAC>AAC	p.D199N
Pat_16	Pre-Treatment	ZNF131	7690	37	5	43161556	43161556	Missense_Mutation	SNP	G	T	4	128	c.577G>T	c.(577-579)GCC>TCC	p.A193S
Pat_16	Pre-Treatment	HCN1	348980	37	5	45267196	45267196	Missense_Mutation	SNP	C	T	152	116	c.1778G>A	c.(1777-1779)CGA>CAA	p.R593Q
Pat_16	Pre-Treatment	HSPB3	8988	37	5	53751759	53751759	Missense_Mutation	SNP	A	G	26	53	c.140A>G	c.(139-141)AAA>AGA	p.K47R
Pat_16	Pre-Treatment	PIK3R1	5295	37	5	67588966	67588966	Missense_Mutation	SNP	G	A	6	294	c.1057G>A	c.(1057-1059)GGG>AGG	p.G353R
Pat_16	Pre-Treatment	MAP1B	4131	37	5	71495673	71495673	Missense_Mutation	SNP	C	T	4	221	c.6491C>T	c.(6490-6492)CCG>CTG	p.P2164L
Pat_16	Pre-Treatment	HMGCR	3156	37	5	74646107	74646107	Missense_Mutation	SNP	C	T	29	56	c.688C>T	c.(688-690)CGT>TGT	p.R230C
Pat_16	Pre-Treatment	CMYA5	202333	37	5	79033696	79033696	Missense_Mutation	SNP	A	T	27	60	c.9108A>T	c.(9106-9108)GAA>GAT	p.E3036D

Pat_16	Pre-Treatment	SPZ1	84654	37	5	79616461	79616461	Missense_Mutation	SNP	G	C	6	242	c.427G>C	c.(427-429)GAG>CAG	p.E143Q
Pat_16	Pre-Treatment	FAM172A	83989	37	5	93217337	93217337	Missense_Mutation	SNP	G	A	36	91	c.625C>T	c.(625-627)CCG>TCG	p.P209S
Pat_16	Pre-Treatment	FAM81B	153643	37	5	94756087	94756087	Missense_Mutation	SNP	C	T	85	190	c.637C>T	c.(637-639)CTT>TTT	p.L213F
Pat_16	Pre-Treatment	PCSK1	5122	37	5	95743978	95743978	Missense_Mutation	SNP	G	A	28	70	c.1145C>T	c.(1144-1146)TCG>TTG	p.S382L
Pat_16	Pre-Treatment	CAMK4	814	37	5	110819954	110819954	Missense_Mutation	SNP	A	T	58	48	c.1212A>T	c.(1210-1212)AAA>AAT	p.K404N
Pat_16	Pre-Treatment	ALDH7A1	501	37	5	125930712	125930712	Missense_Mutation	SNP	C	G	20	15	c.179G>C	c.(178-180)GGA>GCA	p.G60A
Pat_16	Pre-Treatment	C5orf48	389320	37	5	125968322	125968322	Missense_Mutation	SNP	G	A	39	72	c.171G>A	c.(169-171)ATG>ATA	p.M57I
Pat_16	Pre-Treatment	PCDHA12	56137	37	5	140255958	140255958	Missense_Mutation	SNP	G	A	101	74	c.901G>A	c.(901-903)GAA>AAA	p.E301K
Pat_16	Pre-Treatment	PCDHA12	56137	37	5	140256858	140256858	Missense_Mutation	SNP	T	A	34	55	c.1801T>A	c.(1801-1803)TCC>ACC	p.S601T
Pat_16	Pre-Treatment	PCDHB3	56132	37	5	140480621	140480621	Missense_Mutation	SNP	T	G	49	111	c.388T>G	c.(388-390)TCT>GCT	p.S130A
Pat_16	Pre-Treatment	PCDHB3	56132	37	5	140482598	140482598	Missense_Mutation	SNP	T	A	103	62	c.2365T>A	c.(2365-2367)TTC>ATC	p.F789I
Pat_16	Pre-Treatment	PCDHB8	56128	37	5	140558076	140558076	Missense_Mutation	SNP	C	T	32	666	c.461C>T	c.(460-462)CCT>CTT	p.P154L
Pat_16	Pre-Treatment	PCDHB8	56128	37	5	140559324	140559324	Missense_Mutation	SNP	C	T	15	149	c.1709C>T	c.(1708-1710)TCC>TTC	p.S570F
Pat_16	Pre-Treatment	SLC25A2	83884	37	5	140682877	140682877	Missense_Mutation	SNP	A	G	36	50	c.556T>C	c.(556-558)TTT>CTT	p.F186L
Pat_16	Pre-Treatment	PCDHGB4	8641	37	5	140768940	140768940	Missense_Mutation	SNP	C	T	4	102	c.1489C>T	c.(1489-1491)CGG>TGG	p.R497W
Pat_16	Pre-Treatment	NDFIP1	80762	37	5	141511890	141511890	Missense_Mutation	SNP	C	T	280	171	c.265C>T	c.(265-267)CCT>TCT	p.P89S
Pat_16	Pre-Treatment	KCTD16	57528	37	5	143853540	143853540	Missense_Mutation	SNP	G	A	28	52	c.1150G>A	c.(1150-1152)GCT>ACT	p.A384T
Pat_16	Pre-Treatment	TCERG1	10915	37	5	145850279	145850279	Missense_Mutation	SNP	C	T	28	68	c.1480C>T	c.(1480-1482)CCT>TCT	p.P494S
Pat_16	Pre-Treatment	HTR4	3360	37	5	147929772	147929772	Missense_Mutation	SNP	G	A	37	112	c.80C>T	c.(79-81)TCG>TTG	p.S27L
Pat_16	Pre-Treatment	ABLIM3	22885	37	5	148619377	148619377	Missense_Mutation	SNP	T	C	75	130	c.1130T>C	c.(1129-1131)ATA>ACA	p.I377T
Pat_16	Pre-Treatment	ARHGEF37	389337	37	5	148989254	148989254	Missense_Mutation	SNP	G	A	4	183	c.454G>A	c.(454-456)GTG>ATG	p.V152M
Pat_16	Pre-Treatment	SLC6A7	6534	37	5	149574444	149574444	Missense_Mutation	SNP	T	G	55	111	c.187T>G	c.(187-189)TTC>GTC	p.F63V
Pat_16	Pre-Treatment	ZNF300	91975	37	5	150275165	150275165	Missense_Mutation	SNP	C	T	24	72	c.1636G>A	c.(1636-1638)GAG>AAG	p.E546K
Pat_16	Pre-Treatment	SLC36A1	206358	37	5	150867748	150867748	Missense_Mutation	SNP	C	T	63	37	c.1364C>T	c.(1363-1365)GCT>GTT	p.A455V
Pat_16	Pre-Treatment	GALNT10	55568	37	5	153789293	153789293	Missense_Mutation	SNP	G	A	4	313	c.1357G>A	c.(1357-1359)GTG>ATG	p.V453M
Pat_16	Pre-Treatment	ADRA1B	147	37	5	159344336	159344336	Missense_Mutation	SNP	G	A	40	66	c.424G>A	c.(424-426)GAT>AAT	p.D142N
Pat_16	Pre-Treatment	KCNMB1	3779	37	5	169810728	169810728	Nonsense_Mutation	SNP	C	T	39	108	c.261G>A	c.(259-261)TGG>TGA	p.W87*
Pat_16	Pre-Treatment	KCNIP1	30820	37	5	170147349	170147349	Missense_Mutation	SNP	G	A	48	101	c.244G>A	c.(244-246)GAA>AAA	p.E82K
Pat_16	Pre-Treatment	DDX41	51428	37	5	176939551	176939551	Missense_Mutation	SNP	G	A	30	35	c.1495C>T	c.(1495-1497)CCT>TCT	p.P499S
Pat_16	Pre-Treatment	ZNF354C	30832	37	5	178505930	178505930	Missense_Mutation	SNP	G	A	39	126	c.497G>A	c.(496-498)GGG>GAG	p.G166E
Pat_16	Pre-Treatment	GFPT2	9945	37	5	179729481	179729481	Missense_Mutation	SNP	A	G	32	76	c.1946T>C	c.(1945-1947)CTG>CCG	p.L649P
Pat_16	Pre-Treatment	TRIM7	81786	37	5	180622549	180622549	Missense_Mutation	SNP	G	A	38	128	c.1153C>T	c.(1153-1155)CGC>TGC	p.R385C
Pat_16	Pre-Treatment	WRNIP1	56897	37	6	2783738	2783738	Missense_Mutation	SNP	G	A	4	134	c.1585G>A	c.(1585-1587)GGA>AGA	p.G529R
Pat_16	Pre-Treatment	HIVEP1	3096	37	6	12122090	12122090	Missense_Mutation	SNP	C	T	23	102	c.2062C>T	c.(2062-2064)CCA>TCA	p.P688S
Pat_16	Pre-Treatment	ZKSCAN3	80317	37	6	28327466	28327466	Missense_Mutation	SNP	C	T	92	180	c.103C>T	c.(103-105)CCC>TCC	p.P35S
Pat_16	Pre-Treatment	OR2W1	26692	37	6	29012073	29012073	Missense_Mutation	SNP	T	G	20	22	c.880A>C	c.(880-882)AAT>CAT	p.N294H
Pat_16	Pre-Treatment	MOG	4340	37	6	29635420	29635420	Missense_Mutation	SNP	G	A	61	98	c.551G>A	c.(550-552)GGA>GAA	p.G184E
Pat_16	Pre-Treatment	TRIM10	10107	37	6	30122054	30122054	Missense_Mutation	SNP	T	C	3	49	c.1138A>G	c.(1138-1140)ACC>GCC	p.T380A
Pat_16	Pre-Treatment	SKIV2L	6499	37	6	31931192	31931192	Missense_Mutation	SNP	G	A	4	239	c.1406G>A	c.(1405-1407)CGG>CAG	p.R469Q
Pat_16	Pre-Treatment	TCP11	6954	37	6	35089915	35089915	Missense_Mutation	SNP	G	A	6	390	c.596C>T	c.(595-597)ACG>ATG	p.T199M
Pat_16	Pre-Treatment	BRPF3	27154	37	6	36168892	36168892	Missense_Mutation	SNP	C	T	4	220	c.793C>T	c.(793-795)CGG>TGG	p.R265W
Pat_16	Pre-Treatment	BRPF3	27154	37	6	36178156	36178156	Missense_Mutation	SNP	G	A	4	192	c.2030G>A	c.(2029-2031)CGA>CAA	p.R677Q
Pat_16	Pre-Treatment	PI16	221476	37	6	36931352	36931352	Missense_Mutation	SNP	G	A	57	236	c.1234G>A	c.(1234-1236)GGT>AGT	p.G412S
Pat_16	Pre-Treatment	GPR116	221395	37	6	46849223	46849223	Missense_Mutation	SNP	C	T	121	201	c.783G>A	c.(781-783)ATG>ATA	p.M261I
Pat_16	Pre-Treatment	GPR110	266977	37	6	46977963	46977963	Missense_Mutation	SNP	C	T	4	273	c.1208G>A	c.(1207-1209)CGG>CAG	p.R403Q
Pat_16	Pre-Treatment	GFRAL	389400	37	6	55196618	55196618	Missense_Mutation	SNP	G	A	84	111	c.128G>A	c.(127-129)AGA>AAA	p.R43K
Pat_16	Pre-Treatment	ROS1	6098	37	6	117631320	117631321	Missense_Mutation	DNP	CC	TT	79	89	.6357_6358GG>A	355-6360)GGGGAA>GGA	p.E2120K

Pat_16	Pre-Treatment	VNN3	55350	37	6	133055815	133055815	Missense_Mutation	SNP	A	T	26	2	c.17T>A	c.(16-18)TTT>TAT	p.F6Y
Pat_16	Pre-Treatment	PLG	5340	37	6	161152156	161152156	Missense_Mutation	SNP	G	A	4	95	c.1330G>A	c.(1330-1332)GTC>ATC	p.V444I
Pat_16	Pre-Treatment	MICALL2	79778	37	7	1482031	1482031	Missense_Mutation	SNP	G	A	75	288	c.1508C>T	c.(1507-1509)TCG>TTG	p.S503L
Pat_16	Pre-Treatment	CARD11	84433	37	7	2979526	2979526	Missense_Mutation	SNP	C	T	64	148	c.721G>A	c.(721-723)GAG>AAG	p.E241K
Pat_16	Pre-Treatment	ETV1	2115	37	7	13935508	13935508	Missense_Mutation	SNP	C	T	21	130	c.1417G>A	c.(1417-1419)GAA>AAA	p.E473K
Pat_16	Pre-Treatment	AGR2	10551	37	7	16841412	16841413	Missense_Mutation	DNP	TT	CA	138	128	c.8_9AA>TG	c.(7-9)AAA>ATG	p.K3M
Pat_16	Pre-Treatment	DNAH11	8701	37	7	21784183	21784183	Missense_Mutation	SNP	G	A	100	87	c.8303G>A	c.(8302-8304)AGA>AAA	p.R2768K
Pat_16	Pre-Treatment	STK31	56164	37	7	23768836	23768836	Missense_Mutation	SNP	C	T	77	59	c.451C>T	c.(451-453)CCT>TCT	p.P151S
Pat_16	Pre-Treatment	SKAP2	8935	37	7	26765185	26765185	Splice_Site	SNP	C	T	65	164	c.659_splice	c.e9-1	p.D220_splice
Pat_16	Pre-Treatment	LOC402644	402644	37	7	28318921	28318922	Missense_Mutation	DNP	CT	TC	46	52	c.397_398AG>GA	c.(397-399)AGA>GAA	p.R133E
Pat_16	Pre-Treatment	DPY19L2P1	554236	37	7	35163615	35163615	Missense_Mutation	SNP	C	T	74	109	c.481G>A	c.(481-483)GAC>AAC	p.D161N
Pat_16	Pre-Treatment	AOAH	313	37	7	36726345	36726345	Missense_Mutation	SNP	G	A	6	355	c.182C>T	c.(181-183)ACG>ATG	p.T61M
Pat_16	Pre-Treatment	HECW1	23072	37	7	43485016	43485016	Missense_Mutation	SNP	G	A	4	243	c.2245G>A	c.(2245-2247)GTA>ATA	p.V749I
Pat_16	Pre-Treatment	DBNL	28988	37	7	44092491	44092491	Missense_Mutation	SNP	G	A	4	116	c.278G>A	c.(277-279)CGG>CAG	p.R93Q
Pat_16	Pre-Treatment	RAMP3	10268	37	7	45217030	45217030	Missense_Mutation	SNP	G	A	4	242	c.181G>A	c.(181-183)GAG>AAG	p.E61K
Pat_16	Pre-Treatment	VSTM2A	222008	37	7	54610419	54610419	Translation_Start_Site	SNP	T	A	110	76	c.-4T>A	c.(-6--2)TTTTG>TTATG	
Pat_16	Pre-Treatment	AUTS2	26053	37	7	70228066	70228066	Missense_Mutation	SNP	C	T	45	65	c.953C>T	c.(952-954)CCT>CTT	p.P318L
Pat_16	Pre-Treatment	SEMA3C	10512	37	7	80435062	80435062	Missense_Mutation	SNP	A	T	66	97	c.551T>A	c.(550-552)TTC>TAC	p.F184Y
Pat_16	Pre-Treatment	HGF	3082	37	7	81372738	81372739	Nonsense_Mutation	DNP	GG	AA	202	128	c.795_796CC>TT	793-798)GGCCAG>GGTT	p.Q266*
Pat_16	Pre-Treatment	CACNA2D1	781	37	7	81689806	81689806	Nonsense_Mutation	SNP	G	A	5	621	c.817C>T	c.(817-819)CGA>TGA	p.R273*
Pat_16	Pre-Treatment	CCDC132	55610	37	7	92970884	92970884	Missense_Mutation	SNP	C	T	67	214	c.2204C>T	c.(2203-2205)TCC>TTC	p.S735F
Pat_16	Pre-Treatment	CYP3A5	1577	37	7	99272168	99272168	Missense_Mutation	SNP	C	T	125	84	c.206G>A	c.(205-207)GGA>GAA	p.G69E
Pat_16	Pre-Treatment	POP7	10248	37	7	100304533	100304533	Missense_Mutation	SNP	C	T	4	201	c.80C>T	c.(79-81)CCC>CTC	p.P27L
Pat_16	Pre-Treatment	EPHB4	2050	37	7	100405129	100405129	Missense_Mutation	SNP	A	C	116	195	c.2192T>G	c.(2191-2193)CTT>CGT	p.L731R
Pat_16	Pre-Treatment	SLC12A9	56996	37	7	100457628	100457628	Missense_Mutation	SNP	C	T	5	598	c.1099C>T	c.(1099-1101)CGC>TGC	p.R367C
Pat_16	Pre-Treatment	MUC17	140453	37	7	100678520	100678520	Missense_Mutation	SNP	G	A	351	412	c.3823G>A	c.(3823-3825)GAA>AAA	p.E1275K
Pat_16	Pre-Treatment	MUC17	140453	37	7	100681244	100681244	Missense_Mutation	SNP	A	G	6	665	c.6547A>G	c.(6547-6549)ACA>GCA	p.T2183A
Pat_16	Pre-Treatment	MUC17	140453	37	7	100681979	100681979	Missense_Mutation	SNP	G	A	10	831	c.7282G>A	c.(7282-7284)GTC>ATC	p.V2428I
Pat_16	Pre-Treatment	MUC17	140453	37	7	100684076	100684076	Missense_Mutation	SNP	A	G	6	801	c.9379A>G	c.(9379-9381)ACA>GCA	p.T3127A
Pat_16	Pre-Treatment	SLC26A3	1811	37	7	107408046	107408046	Missense_Mutation	SNP	C	T	32	108	c.2249G>A	c.(2248-2250)GGA>GAA	p.G750E
Pat_16	Pre-Treatment	LAMB4	22798	37	7	107678038	107678038	Missense_Mutation	SNP	C	T	187	128	c.4474G>A	c.(4474-4476)GAA>AAA	p.E1492K
Pat_16	Pre-Treatment	DOCK4	9732	37	7	111368526	111368526	Missense_Mutation	SNP	G	A	22	166	c.5705C>T	c.(5704-5706)CCG>CTG	p.P1902L
Pat_16	Pre-Treatment	PPP1R3A	5506	37	7	113518058	113518058	Missense_Mutation	SNP	C	T	200	455	c.3089G>A	c.(3088-3090)GGA>GAA	p.G1030E
Pat_16	Pre-Treatment	PPP1R3A	5506	37	7	113518735	113518735	Missense_Mutation	SNP	T	G	35	149	c.2412A>C	c.(2410-2412)GAA>GAC	p.E804D
Pat_16	Pre-Treatment	PPP1R3A	5506	37	7	113518737	113518737	Missense_Mutation	SNP	C	T	33	149	c.2410G>A	c.(2410-2412)GAA>AAA	p.E804K
Pat_16	Pre-Treatment	ING3	54556	37	7	120607624	120607624	Missense_Mutation	SNP	C	T	60	269	c.478C>T	c.(478-480)CAT>TAT	p.H160Y
Pat_16	Pre-Treatment	CADPS2	93664	37	7	122261558	122261558	Missense_Mutation	SNP	C	T	5	622	c.1081G>A	c.(1081-1083)GTG>ATG	p.V361M
Pat_16	Pre-Treatment	ZNF800	168850	37	7	127013577	127013577	Missense_Mutation	SNP	C	T	6	285	c.1813G>A	c.(1813-1815)GTC>ATC	p.V605I
Pat_16	Pre-Treatment	FLNC	2318	37	7	128494697	128494697	Missense_Mutation	SNP	G	A	8	55	c.6958G>A	c.(6958-6960)GGA>AGA	p.G2320R
Pat_16	Pre-Treatment	FAM40B	57464	37	7	129122704	129122704	Missense_Mutation	SNP	G	A	249	216	c.2071G>A	c.(2071-2073)GCA>ACA	p.A691T
Pat_16	Pre-Treatment	PLXNA4	91584	37	7	131859659	131859659	Missense_Mutation	SNP	C	T	38	174	c.3895G>A	c.(3895-3897)GAC>AAC	p.D1299N
Pat_16	Pre-Treatment	JHDM1D	80853	37	7	139791679	139791679	Missense_Mutation	SNP	A	C	87	319	c.2656T>G	c.(2656-2658)TCC>GCC	p.S886A
Pat_16	Pre-Treatment	BRAF	673	37	7	140453136	140453136	Missense_Mutation	SNP	A	T	229	180	c.1799T>A	c.(1798-1800)GTG>GAG	p.V600E
Pat_16	Pre-Treatment	KIAA1147	57189	37	7	141364740	141364740	Missense_Mutation	SNP	G	A	4	104	c.1067C>T	c.(1066-1068)GCT>GTT	p.A356V
Pat_16	Pre-Treatment	TAS2R38	5726	37	7	141673404	141673404	Missense_Mutation	SNP	C	T	126	181	c.86G>A	c.(85-87)GGG>GAG	p.G29E
Pat_16	Pre-Treatment	TRYX3	136541	37	7	141952429	141952429	Missense_Mutation	SNP	T	C	104	163	c.439A>G	c.(439-441)AAA>GAA	p.K147E
Pat_16	Pre-Treatment	CLCN1	1180	37	7	143029591	143029591	Missense_Mutation	SNP	G	A	5	292	c.1246G>A	c.(1246-1248)GGA>AGA	p.G416R

Pat_16	Pre-Treatment	TAS2R60	338398	37	7	143140918	143140918	Missense_Mutation	SNP	T	A	390	266	c.373T>A	c.(373-375)TTC>ATC	p.F125I
Pat_16	Pre-Treatment	ZNF425	155054	37	7	148802211	148802211	Missense_Mutation	SNP	C	A	4	191	c.752G>T	c.(751-753)TGT>TTT	p.C251F
Pat_16	Pre-Treatment	ACCN3	9311	37	7	150749275	150749275	Missense_Mutation	SNP	G	A	106	487	c.1409G>A	c.(1408-1410)GGA>GAA	p.G470E
Pat_16	Pre-Treatment	CLN8	2055	37	8	1728717	1728717	Missense_Mutation	SNP	G	A	4	208	c.845G>A	c.(844-846)CGG>CAG	p.R282Q
Pat_16	Pre-Treatment	CSMD1	64478	37	8	3216769	3216769	Missense_Mutation	SNP	G	A	175	65	c.3212C>T	c.(3211-3213)TCC>TTC	p.S1071F
Pat_16	Pre-Treatment	MTMR7	9108	37	8	17228656	17228656	Missense_Mutation	SNP	C	T	130	366	c.200G>A	c.(199-201)GGA>GAA	p.G67E
Pat_16	Pre-Treatment	PIWIL2	55124	37	8	22163488	22163488	Missense_Mutation	SNP	G	A	4	250	c.1504G>A	c.(1504-1506)GGA>AGA	p.G502R
Pat_16	Pre-Treatment	SORBS3	10174	37	8	22428730	22428730	Missense_Mutation	SNP	C	T	11	145	c.1739C>T	c.(1738-1740)ACC>ATC	p.T580I
Pat_16	Pre-Treatment	SLC25A37	51312	37	8	23423681	23423681	Missense_Mutation	SNP	C	T	76	22	c.271C>T	c.(271-273)CTC>TTC	p.L91F
Pat_16	Pre-Treatment	DOCK5	80005	37	8	25189850	25189850	Missense_Mutation	SNP	G	A	4	226	c.1987G>A	c.(1987-1989)GGA>AGA	p.G663R
Pat_16	Pre-Treatment	PTK2B	2185	37	8	27296570	27296570	Missense_Mutation	SNP	C	A	41	154	c.1666C>A	c.(1666-1668)CTG>ATG	p.L556M
Pat_16	Pre-Treatment	EIF4EBP1	1978	37	8	37914667	37914667	Missense_Mutation	SNP	C	T	366	144	c.214C>T	c.(214-216)CCA>TCA	p.P72S
Pat_16	Pre-Treatment	SLC20A2	6575	37	8	42294807	42294807	Missense_Mutation	SNP	G	A	22	69	c.1223C>T	c.(1222-1224)TCG>TTG	p.S408L
Pat_16	Pre-Treatment	PXDNL	137902	37	8	52232512	52232512	Missense_Mutation	SNP	C	T	85	30	c.4331G>A	c.(4330-4332)GGA>GAA	p.G1444E
Pat_16	Pre-Treatment	PXDNL	137902	37	8	52320945	52320946	Missense_Mutation	DNP	GG	AA	14	58	.3238_3239CC>T	c.(3238-3240)CCG>TTG	p.P1080L
Pat_16	Pre-Treatment	PENK	5179	37	8	57354297	57354297	Missense_Mutation	SNP	T	A	41	157	c.338A>T	c.(337-339)AAA>ATA	p.K113I
Pat_16	Pre-Treatment	CLVS1	157807	37	8	62212762	62212762	Missense_Mutation	SNP	T	C	56	143	c.376T>C	c.(376-378)TTC>CTC	p.F126L
Pat_16	Pre-Treatment	PI15	51050	37	8	75757656	75757656	Missense_Mutation	SNP	C	T	110	419	c.565C>T	c.(565-567)CAT>TAT	p.H189Y
Pat_16	Pre-Treatment	CA1	759	37	8	86242024	86242024	Missense_Mutation	SNP	G	A	24	30	c.563C>T	c.(562-564)TCA>TTA	p.S188L
Pat_16	Pre-Treatment	UBR5	51366	37	8	103327037	103327037	Missense_Mutation	SNP	G	A	4	207	c.1829C>T	c.(1828-1830)CCA>CTA	p.P610L
Pat_16	Pre-Treatment	ASAP1	50807	37	8	131088611	131088611	Missense_Mutation	SNP	G	A	88	45	c.2684C>T	c.(2683-2685)CCT>CTT	p.P895L
Pat_16	Pre-Treatment	ADCY8	114	37	8	131880120	131880120	Missense_Mutation	SNP	C	T	49	223	c.2182G>A	c.(2182-2184)GCA>ACA	p.A728T
Pat_16	Pre-Treatment	TG	7038	37	8	133925417	133925417	Missense_Mutation	SNP	C	T	46	177	c.4285C>T	c.(4285-4287)CAC>TAC	p.H1429Y
Pat_16	Pre-Treatment	DENND3	22898	37	8	142202543	142202543	Missense_Mutation	SNP	C	T	19	67	c.3253C>T	c.(3253-3255)CCT>TCT	p.P1085S
Pat_16	Pre-Treatment	LYPD2	137797	37	8	143832556	143832556	Missense_Mutation	SNP	G	A	38	156	c.91C>T	c.(91-93)CCC>TCC	p.P31S
Pat_16	Pre-Treatment	CYP11B1	1584	37	8	143957679	143957679	Missense_Mutation	SNP	A	T	9	51	c.932T>A	c.(931-933)CTC>CAC	p.L311H
Pat_16	Pre-Treatment	CYP11B1	1584	37	8	143958215	143958215	Missense_Mutation	SNP	C	T	21	10	c.682G>A	c.(682-684)GAG>AAG	p.E228K
Pat_16	Pre-Treatment	PYCRL	65263	37	8	144688004	144688004	Missense_Mutation	SNP	G	A	4	245	c.727C>T	c.(727-729)CGC>TGC	p.R243C
Pat_16	Pre-Treatment	FOXH1	8928	37	8	145699782	145699782	Missense_Mutation	SNP	C	T	145	57	c.937G>A	c.(937-939)GTG>ATG	p.V313M
Pat_16	Pre-Treatment	FAM75A6	389730	37	9	43627096	43627096	Missense_Mutation	SNP	G	A	267	10	c.1591C>T	c.(1591-1593)CTC>TTC	p.L531F
Pat_16	Pre-Treatment	APBA1	320	37	9	72131715	72131715	Missense_Mutation	SNP	C	T	3	31	c.412G>A	c.(412-414)GCC>ACC	p.A138T
Pat_16	Pre-Treatment	RMI1	80010	37	9	86617211	86617211	Missense_Mutation	SNP	C	T	31	23	c.1310C>T	c.(1309-1311)TCC>TTC	p.S437F
Pat_16	Pre-Treatment	C9orf89	84270	37	9	95870013	95870013	Missense_Mutation	SNP	G	A	3	53	c.65G>A	c.(64-66)CGC>CAC	p.R22H
Pat_16	Pre-Treatment	OR13C4	138804	37	9	107288820	107288820	Missense_Mutation	SNP	G	A	245	1	c.671C>T	c.(670-672)ACC>ATC	p.T224I
Pat_16	Pre-Treatment	ASTN2	23245	37	9	119858377	119858377	Missense_Mutation	SNP	C	T	124	10	c.1222G>A	c.(1222-1224)GAA>AAA	p.E408K
Pat_16	Pre-Treatment	MRRF	92399	37	9	125033270	125033270	Missense_Mutation	SNP	G	A	6	470	c.100G>A	c.(100-102)GTG>ATG	p.V34M
Pat_16	Pre-Treatment	COQ4	51117	37	9	131088075	131088075	Missense_Mutation	SNP	C	T	85	1	c.317C>T	c.(316-318)TCG>TTG	p.S106L
Pat_16	Pre-Treatment	SPTAN1	6709	37	9	131339474	131339475	Nonsense_Mutation	DNP	CC	TT	165	7	c.852_853CC>TT	850-855)GGCCGA>GGTT	p.R285*
Pat_16	Pre-Treatment	SLC34A3	142680	37	9	140127244	140127244	Missense_Mutation	SNP	G	A	52	1	c.313G>A	c.(313-315)GCC>ACC	p.A105T
Pat_16	Pre-Treatment	MXRA5	25878	37	X	3261841	3261841	Missense_Mutation	SNP	C	T	4	34	c.34G>A	c.(34-36)GTG>ATG	p.V12M
Pat_16	Pre-Treatment	FAM9B	171483	37	X	8998366	8998366	Missense_Mutation	SNP	C	T	12	1	c.217G>A	c.(217-219)GAT>AAT	p.D73N
Pat_16	Pre-Treatment	FRMPD4	9758	37	X	12712519	12712519	Missense_Mutation	SNP	T	G	112	4	c.879T>G	c.(877-879)GAT>GAG	p.D293E
Pat_16	Pre-Treatment	CDKL5	6792	37	X	18602452	18602452	Missense_Mutation	SNP	G	A	4	294	c.533G>A	c.(532-534)CGG>CAG	p.R178Q
Pat_16	Pre-Treatment	PPEF1	5475	37	X	18842202	18842202	Missense_Mutation	SNP	G	A	4	67	c.1663G>A	c.(1663-1665)GAG>AAG	p.E555K
Pat_16	Pre-Treatment	POLA1	5422	37	X	25014054	25014054	Missense_Mutation	SNP	C	T	82	5	c.4376C>T	c.(4375-4377)GCC>GTC	p.A1459V
Pat_16	Pre-Treatment	FAM47C	442444	37	X	37027345	37027345	Nonsense_Mutation	SNP	A	T	28	47	c.862A>T	c.(862-864)AAG>TAG	p.K288*
Pat_16	Pre-Treatment	GRIPAP1	56850	37	X	48846277	48846277	Missense_Mutation	SNP	G	C	3	132	c.740C>G	c.(739-741)ACA>AGA	p.T247R

Pat_16	Pre-Treatment	CLCN5	1184	37	X	49837183	49837183	Missense_Mutation	SNP	C	T	127	161	c.145C>T	c.(145-147)CAC>TAC	p.H49Y
Pat_16	Pre-Treatment	ABCB7	22	37	X	74291389	74291389	Missense_Mutation	SNP	C	T	6	389	c.1162G>A	c.(1162-1164)GGT>AGT	p.G388S
Pat_16	Pre-Treatment	CYLC1	1538	37	X	83129484	83129484	Missense_Mutation	SNP	G	A	44	0	c.1768G>A	c.(1768-1770)GAA>AAA	p.E590K
Pat_16	Pre-Treatment	ZNF711	7552	37	X	84519283	84519283	Missense_Mutation	SNP	G	A	62	1	c.625G>A	c.(625-627)GAT>AAT	p.D209N
Pat_16	Pre-Treatment	H2BFWT	158983	37	X	103267838	103267838	Missense_Mutation	SNP	G	A	44	1	c.395C>T	c.(394-396)ACC>ATC	p.T132I
Pat_16	Pre-Treatment	IL1RAPL2	26280	37	X	105011625	105011625	Missense_Mutation	SNP	G	A	174	8	c.2032G>A	c.(2032-2034)GAG>AAG	p.E678K
Pat_16	Pre-Treatment	GUCY2F	2986	37	X	108718564	108718564	Missense_Mutation	SNP	G	A	4	211	c.602C>T	c.(601-603)ACA>ATA	p.T201I
Pat_16	Pre-Treatment	GUCY2F	2986	37	X	108719089	108719089	Missense_Mutation	SNP	C	T	141	9	c.77G>A	c.(76-78)GGC>GAC	p.G26D
Pat_16	Pre-Treatment	TRPC5	7224	37	X	111095642	111095642	Missense_Mutation	SNP	C	T	188	5	c.1261G>A	c.(1261-1263)GAA>AAA	p.E421K
Pat_16	Pre-Treatment	HTR2C	3358	37	X	114141526	114141526	Missense_Mutation	SNP	G	A	160	2	c.925G>A	c.(925-927)GCT>ACT	p.A309T
Pat_16	Pre-Treatment	SLC6A14	11254	37	X	115586574	115586574	Nonsense_Mutation	SNP	G	A	168	230	c.1556G>A	c.(1555-1557)TGG>TAG	p.W519*
Pat_16	Pre-Treatment	ODZ1	10178	37	X	123654419	123654419	Nonsense_Mutation	SNP	C	T	258	7	c.3249G>A	c.(3247-3249)TGG>TGA	p.W1083*
Pat_16	Pre-Treatment	MAGEC1	9947	37	X	140995008	140995008	Missense_Mutation	SNP	G	A	9	565	c.1818G>A	c.(1816-1818)ATG>ATA	p.M606I
Pat_16	Pre-Treatment	SLITRK4	139065	37	X	142718881	142718881	Missense_Mutation	SNP	G	A	4	118	c.44C>T	c.(43-45)TCG>TTG	p.S15L
Pat_16	Pre-Treatment	GABRQ	55879	37	X	151819009	151819009	Missense_Mutation	SNP	G	A	405	15	c.867G>A	c.(865-867)ATG>ATA	p.M289I
Pat_16	Pre-Treatment	FAM50A	9130	37	X	153674018	153674018	Missense_Mutation	SNP	C	T	123	4	c.149C>T	c.(148-150)TCT>TTT	p.S50F
Pat_21	Post-Resistance	CA6	765	37	1	9022677	9022677	Missense_Mutation	SNP	G	A	41	14	c.533G>A	c.(532-534)AGC>AAC	p.S178N
Pat_21	Post-Resistance	KIAA0754	643314	37	1	39879293	39879293	Missense_Mutation	SNP	C	T	3	32	c.3356C>T	c.(3355-3357)TCC>TTC	p.S1119F
Pat_21	Post-Resistance	COL9A2	1298	37	1	40773902	40773902	Missense_Mutation	SNP	G	A	10	5	c.862C>T	c.(862-864)CGT>TGT	p.R288C
Pat_21	Post-Resistance	NBPF16	728936	37	1	148754851	148754851	Missense_Mutation	SNP	C	G	14	94	c.1507C>G	c.(1507-1509)CTG>GTG	p.L503V
Pat_21	Post-Resistance	FCER1A	2205	37	1	159277667	159277667	Missense_Mutation	SNP	G	T	10	4	c.719G>T	c.(718-720)AGG>ATG	p.R240M
Pat_21	Post-Resistance	ALOX5	240	37	10	45878120	45878120	Missense_Mutation	SNP	G	A	3	3	c.340G>A	c.(340-342)GAT>AAT	p.D114N
Pat_21	Post-Resistance	CHAT	1103	37	10	50870733	50870733	Missense_Mutation	SNP	C	T	55	17	c.1882C>T	c.(1882-1884)CGG>TGG	p.R628W
Pat_21	Post-Resistance	PRKG1	5592	37	10	54050036	54050036	Missense_Mutation	SNP	C	T	18	9	c.1903C>T	c.(1903-1905)CCT>TCT	p.P635S
Pat_21	Post-Resistance	TMEM26	219623	37	10	63170123	63170123	Missense_Mutation	SNP	C	T	14	5	c.1064G>A	c.(1063-1065)CGG>CAG	p.R355Q
Pat_21	Post-Resistance	RAB11FIP2	22841	37	10	119768573	119768573	Missense_Mutation	SNP	G	A	3	57	c.1475C>T	c.(1474-1476)ACG>ATG	p.T492M
Pat_21	Post-Resistance	PPP2R2D	55844	37	10	133754154	133754154	Missense_Mutation	SNP	G	A	9	5	c.334G>A	c.(334-336)GAA>AAA	p.E112K
Pat_21	Post-Resistance	OR51Q1	390061	37	11	5444067	5444067	Missense_Mutation	SNP	C	T	49	15	c.637C>T	c.(637-639)CCT>TCT	p.P213S
Pat_21	Post-Resistance	ZBTB39	9880	37	12	57397347	57397347	Missense_Mutation	SNP	T	A	26	8	c.1355A>T	c.(1354-1356)AAA>ATA	p.K452I
Pat_21	Post-Resistance	KIAA1370	56204	37	15	52901546	52901547	Missense_Mutation	DNP	CT	TC	60	120	.1564_1565AG>G	c.(1564-1566)AGG>GAG	p.R522E
Pat_21	Post-Resistance	PDXDC2	283970	37	16	70016259	70016259	Missense_Mutation	SNP	T	C	8	50	c.443A>G	c.(442-444)AAA>AGA	p.K148R
Pat_21	Post-Resistance	DNAH2	146754	37	17	7696425	7696425	Missense_Mutation	SNP	G	A	43	9	c.7471G>A	c.(7471-7473)GAC>AAC	p.D2491N
Pat_21	Post-Resistance	CNP	1267	37	17	40120425	40120425	Missense_Mutation	SNP	G	A	18	4	c.343G>A	c.(343-345)GAC>AAC	p.D115N
Pat_21	Post-Resistance	PHB	5245	37	17	47486767	47486767	Missense_Mutation	SNP	A	G	42	83	c.319T>C	c.(319-321)TTC>CTC	p.F107L
Pat_21	Post-Resistance	SBNO2	22904	37	19	1122996	1122996	Missense_Mutation	SNP	A	C	6	1	c.677T>G	c.(676-678)CTG>CGG	p.L226R
Pat_21	Post-Resistance	TTN	7273	37	2	179417877	179417877	Missense_Mutation	SNP	C	T	3	7	c.82046G>A	c.(82045-82047)GGA>GA	p.G27349E
Pat_21	Post-Resistance	KIF1A	547	37	2	241697894	241697894	Missense_Mutation	SNP	C	T	14	5	c.2438G>A	c.(2437-2439)CGG>CAG	p.R813Q
Pat_21	Post-Resistance	RTEL1	51750	37	20	62305428	62305428	Missense_Mutation	SNP	G	A	3	58	c.901G>A	c.(901-903)GCG>ACG	p.A301T
Pat_21	Post-Resistance	SEMA5B	54437	37	3	122630349	122630349	Missense_Mutation	SNP	G	A	7	4	c.3080C>T	c.(3079-3081)ACC>ATC	p.T1027I
Pat_21	Post-Resistance	RPL39L	116832	37	3	186838943	186838943	Missense_Mutation	SNP	A	T	5	190	c.146T>A	c.(145-147)CTG>CAG	p.L49Q
Pat_21	Post-Resistance	EVC2	132884	37	4	5578151	5578151	Missense_Mutation	SNP	C	T	5	1	c.3088G>A	c.(3088-3090)GAC>AAC	p.D1030N
Pat_21	Post-Resistance	SYNE1	23345	37	6	152443641	152443641	Missense_Mutation	SNP	G	A	40	12	c.26324C>T	c.(26323-26325)GCC>GT	p.A8775V
Pat_21	Post-Resistance	GLI3	2737	37	7	42017228	42017228	Missense_Mutation	SNP	C	T	16	18	c.1741G>A	c.(1741-1743)GAA>AAA	p.E581K
Pat_21	Post-Resistance	SEMA3E	9723	37	7	83014632	83014632	Missense_Mutation	SNP	C	T	56	50	c.1853G>A	c.(1852-1854)GGA>GAA	p.G618E
Pat_21	Post-Resistance	BRAF	673	37	7	140453136	140453136	Missense_Mutation	SNP	A	T	99	54	c.1799T>A	c.(1798-1800)GTG>GAG	p.V600E
Pat_21	Post-Resistance	MLLT3	4300	37	9	20414286	20414286	Missense_Mutation	SNP	G	T	4	43	c.558C>A	c.(556-558)AGC>AGA	p.S186R
Pat_21	Post-Resistance	TRUB2	26995	37	9	131083986	131083986	Missense_Mutation	SNP	C	T	3	6	c.133G>A	c.(133-135)GCT>ACT	p.A45T

Pat_21	Post-Resistance	TUBBP5	643224	37	9	141070950	141070950	Missense_Mutation	SNP	A	G	4	60	c.353A>G	c.(352-354)CAC>CGC	p.H118R
Pat_21	Post-Resistance	FAM48B1	100130302	37	X	24382420	24382420	Missense_Mutation	SNP	G	C	5	18	c.1543G>C	c.(1543-1545)GCT>CCT	p.A515P
Pat_21	Post-Resistance	MED12	9968	37	X	70360666	70360666	Nonsense_Mutation	SNP	C	T	4	32	c.6226C>T	c.(6226-6228)CAG>TAG	p.Q2076*
Pat_21	Post-Resistance	FLJ44635	392490	37	X	71379788	71379788	Missense_Mutation	SNP	G	A	31	8	c.109G>A	c.(109-111)GAA>AAA	p.E37K
Pat_22	Pre-Treatment	KIAA0562	9731	37	1	3755640	3755640	Missense_Mutation	SNP	G	A	4	23	c.779C>T	c.(778-780)GCC>GTC	p.A260V
Pat_22	Pre-Treatment	MFN2	9927	37	1	12066704	12066704	Missense_Mutation	SNP	C	T	4	23	c.1826C>T	c.(1825-1827)TCC>TTC	p.S609F
Pat_22	Pre-Treatment	PRAMEF11	440560	37	1	12887523	12887523	Missense_Mutation	SNP	C	T	25	116	c.334G>A	c.(334-336)GAA>AAA	p.E112K
Pat_22	Pre-Treatment	CD52	1043	37	1	26644522	26644522	Missense_Mutation	SNP	T	G	6	18	c.14T>G	c.(13-15)CTC>CGC	p.L5R
Pat_22	Pre-Treatment	SESN2	83667	37	1	28599237	28599237	Missense_Mutation	SNP	C	T	6	24	c.683C>T	c.(682-684)CCC>CTC	p.P228L
Pat_22	Pre-Treatment	SDC3	9672	37	1	31347149	31347149	Missense_Mutation	SNP	A	C	6	12	c.1157T>G	c.(1156-1158)CTC>CGC	p.L386R
Pat_22	Pre-Treatment	SPOCD1	90853	37	1	32280048	32280048	Missense_Mutation	SNP	T	C	2	4	c.887A>G	c.(886-888)CAG>CGG	p.Q296R
Pat_22	Pre-Treatment	TMEM39B	55116	37	1	32557516	32557516	Missense_Mutation	SNP	C	G	16	14	c.831C>G	c.(829-831)TTC>TTG	p.F277L
Pat_22	Pre-Treatment	CSMD2	114784	37	1	34037305	34037305	Missense_Mutation	SNP	C	T	3	23	c.7790G>A	c.(7789-7791)AGT>AAT	p.S2597N
Pat_22	Pre-Treatment	CSMD2	114784	37	1	34066469	34066469	Missense_Mutation	SNP	G	T	8	24	c.6858C>A	c.(6856-6858)TTC>TTA	p.F2286L
Pat_22	Pre-Treatment	CSMD2	114784	37	1	34158530	34158530	Missense_Mutation	SNP	C	T	10	80	c.3932G>A	c.(3931-3933)GGG>GAG	p.G1311E
Pat_22	Pre-Treatment	GRIK3	2899	37	1	37319298	37319298	Missense_Mutation	SNP	C	T	7	26	c.1130G>A	c.(1129-1131)CGA>CAA	p.R377Q
Pat_22	Pre-Treatment	HIVEP3	59269	37	1	42046859	42046859	Missense_Mutation	SNP	G	A	10	36	c.3610C>T	c.(3610-3612)CAT>TAT	p.H1204Y
Pat_22	Pre-Treatment	DEPDC1	55635	37	1	68942710	68942710	Missense_Mutation	SNP	T	C	3	15	c.2341A>G	c.(2341-2343)ACC>GCC	p.T781A
Pat_22	Pre-Treatment	GBP2	2634	37	1	89587495	89587495	Missense_Mutation	SNP	G	A	36	51	c.155C>T	c.(154-156)TCC>TTC	p.S52F
Pat_22	Pre-Treatment	SLC6A17	388662	37	1	110716639	110716639	Nonsense_Mutation	SNP	G	A	11	26	c.489G>A	c.(487-489)TGG>TGA	p.W163*
Pat_22	Pre-Treatment	NBPF7	343505	37	1	120378788	120378788	Missense_Mutation	SNP	G	A	7	17	c.958C>T	c.(958-960)CCG>TCG	p.P320S
Pat_22	Pre-Treatment	CHD1L	9557	37	1	146724319	146724319	Missense_Mutation	SNP	C	T	10	33	c.169C>T	c.(169-171)CTC>TTC	p.L57F
Pat_22	Pre-Treatment	FLG	2312	37	1	152284934	152284934	Missense_Mutation	SNP	T	C	9	38	c.2428A>G	c.(2428-2430)ACA>GCA	p.T810A
Pat_22	Pre-Treatment	ADAR	103	37	1	154574475	154574475	Missense_Mutation	SNP	C	T	4	24	c.643G>A	c.(643-645)GGT>AGT	p.G215S
Pat_22	Pre-Treatment	OR6N1	128372	37	1	158735982	158735982	Missense_Mutation	SNP	G	A	4	15	c.491C>T	c.(490-492)TCA>TTA	p.S164L
Pat_22	Pre-Treatment	TNN	63923	37	1	175086222	175086222	Missense_Mutation	SNP	G	A	7	37	c.2267G>A	c.(2266-2268)GGG>GAG	p.G756E
Pat_22	Pre-Treatment	CRB1	23418	37	1	197313530	197313530	Missense_Mutation	SNP	C	T	7	72	c.772C>T	c.(772-774)CAC>TAC	p.H258Y
Pat_22	Pre-Treatment	PTPRC	5788	37	1	198665985	198665985	Missense_Mutation	SNP	C	T	7	65	c.239C>T	c.(238-240)TCC>TTC	p.S80F
Pat_22	Pre-Treatment	CTSE	1510	37	1	206331084	206331084	Missense_Mutation	SNP	G	A	8	48	c.1090G>A	c.(1090-1092)GCT>ACT	p.A364T
Pat_22	Pre-Treatment	RASSF5	83593	37	1	206757827	206757827	Missense_Mutation	SNP	G	A	27	164	c.799G>A	c.(799-801)GAG>AAG	p.E267K
Pat_22	Pre-Treatment	CNST	163882	37	1	246810513	246810513	Missense_Mutation	SNP	C	T	4	39	c.1010C>T	c.(1009-1011)CCC>CTC	p.P337L
Pat_22	Pre-Treatment	TRIM58	25893	37	1	248039444	248039444	Missense_Mutation	SNP	G	A	3	10	c.1114G>A	c.(1114-1116)GAA>AAA	p.E372K
Pat_22	Pre-Treatment	OR2T6	254879	37	1	248551607	248551608	Missense_Mutation	DNP	GG	AA	4	40	c.698_699GG>AA	c.(697-699)GGG>GAA	p.G233E
Pat_22	Pre-Treatment	OR2T11	127077	37	1	248789853	248789853	Missense_Mutation	SNP	C	T	4	30	c.577G>A	c.(577-579)GAA>AAA	p.E193K
Pat_22	Pre-Treatment	AGAP11	119385	37	10	88768583	88768583	Missense_Mutation	SNP	G	A	4	45	c.574G>A	c.(574-576)GCA>ACA	p.A192T
Pat_22	Pre-Treatment	SLC16A12	387700	37	10	91196021	91196021	Missense_Mutation	SNP	G	A	3	16	c.994C>T	c.(994-996)CTC>TTC	p.L332F
Pat_22	Pre-Treatment	ZNF518A	9849	37	10	97918694	97918694	Missense_Mutation	SNP	T	C	4	5	c.2615T>C	c.(2614-2616)GTG>GCG	p.V872A
Pat_22	Pre-Treatment	LOXL4	84171	37	10	100017824	100017824	Nonsense_Mutation	SNP	C	T	9	21	c.1019G>A	c.(1018-1020)TGG>TAG	p.W340*
Pat_22	Pre-Treatment	SORCS3	22986	37	10	106982904	106982904	Missense_Mutation	SNP	C	T	4	16	c.2765C>T	c.(2764-2766)CCA>CTA	p.P922L
Pat_22	Pre-Treatment	PNLIP	5406	37	10	118315007	118315007	Missense_Mutation	SNP	G	A	4	33	c.799G>A	c.(799-801)GGA>AGA	p.G267R
Pat_22	Pre-Treatment	C10orf93	255352	37	10	134752184	134752184	Missense_Mutation	SNP	G	A	19	42	c.445C>T	c.(445-447)CGT>TGT	p.R149C
Pat_22	Pre-Treatment	MS4A10	341116	37	11	60561520	60561520	Missense_Mutation	SNP	C	T	3	7	c.436C>T	c.(436-438)CTC>TTC	p.L146F
Pat_22	Pre-Treatment	B3GNT1	11041	37	11	66113666	66113666	Missense_Mutation	SNP	C	G	3	21	c.1102G>C	c.(1102-1104)GAA>CAA	p.E368Q
Pat_22	Pre-Treatment	RBM4	5936	37	11	66407211	66407211	Missense_Mutation	SNP	C	T	7	36	c.29C>T	c.(28-30)CCC>CTC	p.P10L
Pat_22	Pre-Treatment	CD163	9332	37	12	7639377	7639377	Missense_Mutation	SNP	C	T	11	23	c.2176G>A	c.(2176-2178)GGT>AGT	p.G726S
Pat_22	Pre-Treatment	PHC1	1911	37	12	9089851	9089851	Missense_Mutation	SNP	G	A	2	2	c.2557G>A	c.(2557-2559)GTT>ATT	p.V853I
Pat_22	Pre-Treatment	SYT10	341359	37	12	33560007	33560007	Missense_Mutation	SNP	C	T	4	3	c.794G>A	c.(793-795)GGA>GAA	p.G265E

Pat_22	Pre-Treatment	ABCD2	225	37	12	39973341	39973341	Missense_Mutation	SNP	G	A	6	71	c.1873C>T	c.(1873-1875)CAT>TAT	p.H625Y
Pat_22	Pre-Treatment	ARID2	196528	37	12	46123701	46123701	Missense_Mutation	SNP	C	T	5	6	c.82C>T	c.(82-84)CAC>TAC	p.H28Y
Pat_22	Pre-Treatment	MLL2	8085	37	12	49426540	49426540	Missense_Mutation	SNP	G	A	2	0	c.11948C>T	c.(11947-11949)ACT>ATT	p.T3983I
Pat_22	Pre-Treatment	GCN1L1	10985	37	12	120574409	120574409	Missense_Mutation	SNP	G	A	4	20	c.6905C>T	c.(6904-6906)TCC>TTC	p.S2302F
Pat_22	Pre-Treatment	KDM2B	84678	37	12	121947683	121947683	Missense_Mutation	SNP	G	A	3	18	c.1334C>T	c.(1333-1335)TCA>TTA	p.S445L
Pat_22	Pre-Treatment	VPS33A	65082	37	12	122717499	122717499	Missense_Mutation	SNP	G	A	3	9	c.1457C>T	c.(1456-1458)TCG>TTG	p.S486L
Pat_22	Pre-Treatment	PUS1	80324	37	12	132423739	132423739	Missense_Mutation	SNP	G	A	2	2	c.463G>A	c.(463-465)GTG>ATG	p.V155M
Pat_22	Pre-Treatment	TUBA3C	7278	37	13	19748188	19748188	Missense_Mutation	SNP	G	A	6	70	c.1168C>T	c.(1168-1170)CGC>TGC	p.R390C
Pat_22	Pre-Treatment	GJB6	10804	37	13	20797118	20797118	Missense_Mutation	SNP	T	C	4	13	c.502A>G	c.(502-504)AAA>GAA	p.K168E
Pat_22	Pre-Treatment	MAPK1IP1L	93487	37	14	55529396	55529396	Missense_Mutation	SNP	C	T	4	18	c.79C>T	c.(79-81)CCT>TCT	p.P27S
Pat_22	Pre-Treatment	GPHN	10243	37	14	67432002	67432002	Missense_Mutation	SNP	C	T	6	30	c.824C>T	c.(823-825)GCT>GTT	p.A275V
Pat_22	Pre-Treatment	PCNX	22990	37	14	71429044	71429044	Missense_Mutation	SNP	A	G	6	23	c.464A>G	c.(463-465)AAC>AGC	p.N155S
Pat_22	Pre-Treatment	TTLL5	23093	37	14	76173379	76173379	Missense_Mutation	SNP	G	A	10	53	c.604G>A	c.(604-606)GAA>AAA	p.E202K
Pat_22	Pre-Treatment	RYR3	6263	37	15	33926814	33926814	Missense_Mutation	SNP	C	A	5	20	c.3055C>A	c.(3055-3057)CTG>ATG	p.L1019M
Pat_22	Pre-Treatment	BMF	90427	37	15	40398106	40398106	Missense_Mutation	SNP	C	T	12	30	c.182G>A	c.(181-183)CGA>CAA	p.R61Q
Pat_22	Pre-Treatment	PLA2G4D	283748	37	15	42363411	42363411	Missense_Mutation	SNP	T	C	2	6	c.1786A>G	c.(1786-1788)AGG>GGG	p.R596G
Pat_22	Pre-Treatment	THSD4	79875	37	15	72039374	72039374	Nonsense_Mutation	SNP	G	A	6	5	c.2234G>A	c.(2233-2235)TGG>TAG	p.W745*
Pat_22	Pre-Treatment	KIAA1024	23251	37	15	79750596	79750596	Missense_Mutation	SNP	C	T	3	13	c.2107C>T	c.(2107-2109)CTC>TTC	p.L703F
Pat_22	Pre-Treatment	FSD2	123722	37	15	83455943	83455943	Missense_Mutation	SNP	A	G	3	20	c.200T>C	c.(199-201)CTT>CCT	p.L67P
Pat_22	Pre-Treatment	RHOT2	89941	37	16	722799	722799	Missense_Mutation	SNP	T	C	10	20	c.1501T>C	c.(1501-1503)TTT>CTT	p.F501L
Pat_22	Pre-Treatment	ZNF263	10127	37	16	3339681	3339681	Missense_Mutation	SNP	A	G	13	29	c.1175A>G	c.(1174-1176)AAC>AGC	p.N392S
Pat_22	Pre-Treatment	GRIN2A	2903	37	16	9857436	9857436	Missense_Mutation	SNP	C	T	4	18	c.3965G>A	c.(3964-3966)GGA>GAA	p.G1322E
Pat_22	Pre-Treatment	ACSM5	54988	37	16	20448432	20448432	Missense_Mutation	SNP	G	A	8	27	c.1367G>A	c.(1366-1368)CGA>CAA	p.R456Q
Pat_22	Pre-Treatment	SLC5A11	115584	37	16	24921657	24921657	Missense_Mutation	SNP	G	A	5	59	c.1681G>A	c.(1681-1683)GAC>AAC	p.D561N
Pat_22	Pre-Treatment	TUBB3	10381	37	16	89989858	89989859	Missense_Mutation	DNP	GG	AA	12	16	c.49_50GG>AA	c.(49-51)GGG>AAG	p.G17K
Pat_22	Pre-Treatment	MYO15A	51168	37	17	18052101	18052101	Nonsense_Mutation	SNP	G	A	3	21	c.6791G>A	c.(6790-6792)TGG>TAG	p.W2264*
Pat_22	Pre-Treatment	ZNF286B	729288	37	17	18565486	18565486	Missense_Mutation	SNP	C	T	7	19	c.1333G>A	c.(1333-1335)GGG>AGG	p.G445R
Pat_22	Pre-Treatment	FNDC8	54752	37	17	33448915	33448915	Missense_Mutation	SNP	A	G	5	23	c.203A>G	c.(202-204)AAC>AGC	p.N68S
Pat_22	Pre-Treatment	CCL16	6360	37	17	34304696	34304696	Missense_Mutation	SNP	T	A	6	27	c.269A>T	c.(268-270)GAT>GTT	p.D90V
Pat_22	Pre-Treatment	CACNB1	782	37	17	37331531	37331531	Missense_Mutation	SNP	C	T	5	81	c.1712G>A	c.(1711-1713)CGC>CAC	p.R571H
Pat_22	Pre-Treatment	KRTAP4-2	85291	37	17	39334280	39334280	Missense_Mutation	SNP	C	A	6	86	c.137G>T	c.(136-138)TGC>TTC	p.C46F
Pat_22	Pre-Treatment	TMEM106A	113277	37	17	41365877	41365877	Missense_Mutation	SNP	C	T	3	16	c.242C>T	c.(241-243)CCC>CTC	p.P81L
Pat_22	Pre-Treatment	ARMC7	79637	37	17	73124939	73124939	Missense_Mutation	SNP	G	A	3	6	c.403G>A	c.(403-405)GAG>AAG	p.E135K
Pat_22	Pre-Treatment	MGAT5B	146664	37	17	74922812	74922812	Missense_Mutation	SNP	C	T	5	54	c.1324C>T	c.(1324-1326)CCT>TCT	p.P442S
Pat_22	Pre-Treatment	MEP1B	4225	37	18	29797884	29797884	Missense_Mutation	SNP	C	T	5	31	c.2047C>T	c.(2047-2049)CGT>TGT	p.R683C
Pat_22	Pre-Treatment	KIAA1632	57724	37	18	43493669	43493669	Splice_Site	SNP	A	G	12	63	c.3816_splice	c.e21+1	p.K1272_splice
Pat_22	Pre-Treatment	DCC	1630	37	18	50592482	50592482	Missense_Mutation	SNP	G	A	6	24	c.1207G>A	c.(1207-1209)GAA>AAA	p.E403K
Pat_22	Pre-Treatment	ALPK2	115701	37	18	56204778	56204778	Missense_Mutation	SNP	C	T	6	9	c.2641G>A	c.(2641-2643)GAC>AAC	p.D881N
Pat_22	Pre-Treatment	SEMA6B	10501	37	19	4550181	4550181	Missense_Mutation	SNP	C	T	3	13	c.1225G>A	c.(1225-1227)GTG>ATG	p.V409M
Pat_22	Pre-Treatment	FBN3	84467	37	19	8203443	8203443	Missense_Mutation	SNP	G	A	2	1	c.871C>T	c.(871-873)CGG>TGG	p.R291W
Pat_22	Pre-Treatment	MUC16	94025	37	19	9066642	9066642	Missense_Mutation	SNP	G	A	17	43	c.20804C>T	c.(20803-20805)TCC>TTC	p.S6935F
Pat_22	Pre-Treatment	MUC16	94025	37	19	9085696	9085696	Missense_Mutation	SNP	G	A	9	21	c.6119C>T	c.(6118-6120)TCC>TTC	p.S2040F
Pat_22	Pre-Treatment	NWD1	284434	37	19	16875863	16875863	Missense_Mutation	SNP	C	T	6	31	c.2270C>T	c.(2269-2271)TCC>TTC	p.S757F
Pat_22	Pre-Treatment	USHBP1	83878	37	19	17375090	17375090	Missense_Mutation	SNP	G	A	3	13	c.19C>T	c.(19-21)CGG>TGG	p.R7W
Pat_22	Pre-Treatment	PDE4C	5143	37	19	18324185	18324185	Missense_Mutation	SNP	C	T	4	15	c.1601G>A	c.(1600-1602)CGA>CAA	p.R534Q
Pat_22	Pre-Treatment	WDR62	284403	37	19	36583709	36583709	Missense_Mutation	SNP	C	T	5	53	c.2329C>T	c.(2329-2331)CCC>TCC	p.P777S
Pat_22	Pre-Treatment	FCGBP	8857	37	19	40430526	40430526	Missense_Mutation	SNP	G	A	2	3	c.1417C>T	c.(1417-1419)CGC>TGC	p.R473C

Pat_22	Pre-Treatment	NUMBL	9253	37	19	41188694	41188694	Missense_Mutation	SNP	G	A	6	29	c.338C>T	c.(337-339)TCC>TTC	p.S113F
Pat_22	Pre-Treatment	SNRPA	6626	37	19	41257328	41257328	Missense_Mutation	SNP	G	C	79	193	c.15G>C	c.(13-15)GAG>GAC	p.E5D
Pat_22	Pre-Treatment	PSG9	5678	37	19	43763240	43763241	Missense_Mutation	DNP	CC	TT	22	72	c.756_757GG>AA	754-759)AGGGAG>AGAA	p.E253K
Pat_22	Pre-Treatment	SIGLEC9	27180	37	19	51629019	51629019	Missense_Mutation	SNP	C	T	13	47	c.587C>T	c.(586-588)TCG>TTG	p.S196L
Pat_22	Pre-Treatment	SIGLEC12	89858	37	19	52002706	52002706	Missense_Mutation	SNP	C	T	7	18	c.1073G>A	c.(1072-1074)CGA>CAA	p.R358Q
Pat_22	Pre-Treatment	NLRP8	126205	37	19	56466752	56466752	Missense_Mutation	SNP	C	T	3	23	c.1328C>T	c.(1327-1329)TCC>TTC	p.S443F
Pat_22	Pre-Treatment	GPR113	165082	37	2	26534297	26534297	Missense_Mutation	SNP	C	T	12	31	c.2299G>A	c.(2299-2301)GAA>AAA	p.E767K
Pat_22	Pre-Treatment	SPTBN1	6711	37	2	54845325	54845325	Missense_Mutation	SNP	C	T	4	25	c.758C>T	c.(757-759)CCC>CTC	p.P253L
Pat_22	Pre-Treatment	TCF7L1	83439	37	2	85531407	85531407	Missense_Mutation	SNP	C	T	9	72	c.791C>T	c.(790-792)CCC>CTC	p.P264L
Pat_22	Pre-Treatment	ELMOD3	84173	37	2	85598626	85598626	Missense_Mutation	SNP	C	T	3	13	c.548C>T	c.(547-549)ACC>ATC	p.T183I
Pat_22	Pre-Treatment	PTCD3	55037	37	2	86335622	86335622	Splice_Site	SNP	G	A	9	18	c.158_splice	c.e3-1	p.G53_splice
Pat_22	Pre-Treatment	ST6GAL2	84620	37	2	107460402	107460402	Missense_Mutation	SNP	C	T	3	10	c.32G>A	c.(31-33)CGA>CAA	p.R11Q
Pat_22	Pre-Treatment	IL1B	3553	37	2	113590968	113590968	Missense_Mutation	SNP	G	A	3	11	c.284C>T	c.(283-285)CCC>CTC	p.P95L
Pat_22	Pre-Treatment	BAZ2B	29994	37	2	160310283	160310283	Missense_Mutation	SNP	G	A	4	15	c.175C>T	c.(175-177)CCG>TCG	p.P59S
Pat_22	Pre-Treatment	SCN2A	6326	37	2	166245451	166245451	Missense_Mutation	SNP	C	T	27	111	c.5135C>T	c.(5134-5136)ACC>ATC	p.T1712I
Pat_22	Pre-Treatment	TTN	7273	37	2	179472716	179472716	Missense_Mutation	SNP	C	T	6	38	c.45094G>A	c.(45094-45096)GAA>AAA	p.E15032K
Pat_22	Pre-Treatment	TTN	7273	37	2	179586756	179586756	Missense_Mutation	SNP	C	T	16	37	c.18902G>A	c.(18901-18903)CGA>CAA	p.R6301Q
Pat_22	Pre-Treatment	SDPR	8436	37	2	192700845	192700845	Missense_Mutation	SNP	G	A	24	51	c.1082C>T	c.(1081-1083)TCC>TTC	p.S361F
Pat_22	Pre-Treatment	AOX1	316	37	2	201492113	201492114	Missense_Mutation	DNP	GG	AA	8	75	.2162_2163GG>A	c.(2161-2163)AGG>AAA	p.R721K
Pat_22	Pre-Treatment	AOX1	316	37	2	201515721	201515721	Missense_Mutation	SNP	G	A	5	17	c.2872G>A	c.(2872-2874)GAA>AAA	p.E958K
Pat_22	Pre-Treatment	TTLL4	9654	37	2	219612363	219612363	Missense_Mutation	SNP	C	A	9	53	c.2293C>A	c.(2293-2295)CTG>ATG	p.L765M
Pat_22	Pre-Treatment	PAK7	57144	37	20	9538302	9538302	Missense_Mutation	SNP	G	A	5	35	c.1696C>T	c.(1696-1698)CAC>TAC	p.H566Y
Pat_22	Pre-Treatment	FAM83C	128876	37	20	33876617	33876617	Missense_Mutation	SNP	C	T	6	30	c.658G>A	c.(658-660)GAC>AAC	p.D220N
Pat_22	Pre-Treatment	RBM12	10137	37	20	34240655	34240655	Missense_Mutation	SNP	G	A	6	18	c.2590C>T	c.(2590-2592)CCC>TCC	p.P864S
Pat_22	Pre-Treatment	PPP1R16B	26051	37	20	37546830	37546830	Missense_Mutation	SNP	T	A	17	72	c.1225T>A	c.(1225-1227)TCC>ACC	p.S409T
Pat_22	Pre-Treatment	WFDC3	140686	37	20	44405770	44405770	Missense_Mutation	SNP	C	T	4	23	c.437G>A	c.(436-438)GGG>GAG	p.G146E
Pat_22	Pre-Treatment	TATDN2	9797	37	3	10320139	10320139	Missense_Mutation	SNP	C	T	20	86	c.2138C>T	c.(2137-2139)CCT>CTT	p.P713L
Pat_22	Pre-Treatment	TATDN2	9797	37	3	10320141	10320141	Missense_Mutation	SNP	C	T	20	83	c.2140C>T	c.(2140-2142)CGC>TGC	p.R714C
Pat_22	Pre-Treatment	MOBP	4336	37	3	39544031	39544031	Missense_Mutation	SNP	G	A	2	1	c.212G>A	c.(211-213)AGC>AAC	p.S71N
Pat_22	Pre-Treatment	ACOX2	8309	37	3	58510153	58510153	Missense_Mutation	SNP	C	T	8	35	c.1526G>A	c.(1525-1527)AGG>AAG	p.R509K
Pat_22	Pre-Treatment	IGSF11	152404	37	3	118623508	118623508	Missense_Mutation	SNP	G	A	5	16	c.841C>T	c.(841-843)CCT>TCT	p.P281S
Pat_22	Pre-Treatment	GPR156	165829	37	3	119886537	119886537	Missense_Mutation	SNP	G	A	4	9	c.1787C>T	c.(1786-1788)CCT>CTT	p.P596L
Pat_22	Pre-Treatment	POLQ	10721	37	3	121207124	121207124	Missense_Mutation	SNP	T	A	2	3	c.4654A>T	c.(4654-4656)AAT>TAT	p.N1552Y
Pat_22	Pre-Treatment	LRRC31	79782	37	3	169557925	169557925	Missense_Mutation	SNP	A	G	7	30	c.1504T>C	c.(1504-1506)TTT>CTT	p.F502L
Pat_22	Pre-Treatment	MUC4	4585	37	3	195507890	195507890	Missense_Mutation	SNP	G	C	2	3	c.10177C>G	c.(10177-10179)CTT>GTT	p.L3393V
Pat_22	Pre-Treatment	CORIN	10699	37	4	47746491	47746491	Missense_Mutation	SNP	A	G	13	74	c.727T>C	c.(727-729)TTT>CTT	p.F243L
Pat_22	Pre-Treatment	PTPN13	5783	37	4	87693999	87693999	Missense_Mutation	SNP	C	T	9	58	c.5237C>T	c.(5236-5238)TCC>TTC	p.S1746F
Pat_22	Pre-Treatment	NPNT	255743	37	4	106848493	106848493	Missense_Mutation	SNP	C	T	6	30	c.173C>T	c.(172-174)CCT>CTT	p.P58L
Pat_22	Pre-Treatment	BBS7	55212	37	4	122775885	122775885	Missense_Mutation	SNP	T	C	6	31	c.692A>G	c.(691-693)GAA>GGA	p.E231G
Pat_22	Pre-Treatment	INPP4B	8821	37	4	143094889	143094889	Missense_Mutation	SNP	G	C	22	34	c.1255C>G	c.(1255-1257)CAA>GAA	p.Q419E
Pat_22	Pre-Treatment	LRBA	987	37	4	151821300	151821300	Missense_Mutation	SNP	G	A	19	56	c.1825C>T	c.(1825-1827)CGG>TGG	p.R609W
Pat_22	Pre-Treatment	LRP2BP	55805	37	4	186294045	186294045	Missense_Mutation	SNP	C	T	3	23	c.768G>A	c.(766-768)ATG>ATA	p.M256I
Pat_22	Pre-Treatment	FAT1	2195	37	4	187629958	187629958	Missense_Mutation	SNP	C	T	5	17	c.1024G>A	c.(1024-1026)GGA>AGA	p.G342R
Pat_22	Pre-Treatment	CDH9	1007	37	5	26881493	26881493	Missense_Mutation	SNP	C	T	5	11	c.2122G>A	c.(2122-2124)GAA>AAA	p.E708K
Pat_22	Pre-Treatment	MARVELD2	153562	37	5	68715618	68715618	Missense_Mutation	SNP	C	T	4	26	c.406C>T	c.(406-408)CCC>TCC	p.P136S
Pat_22	Pre-Treatment	ARAP3	64411	37	5	141059845	141059845	Missense_Mutation	SNP	G	A	10	28	c.209C>T	c.(208-210)TCC>TTC	p.S70F
Pat_22	Pre-Treatment	GRXCR2	643226	37	5	145252219	145252219	Missense_Mutation	SNP	C	T	6	46	c.313G>A	c.(313-315)GAT>AAT	p.D105N

Pat_22	Pre-Treatment	GRIA1	2890	37	5	153190754	153190754	Missense_Mutation	SNP	C	T	3	14	c.2690C>T	c.(2689-2691)TCA>TTA	p.S897L
Pat_22	Pre-Treatment	DOCK2	1794	37	5	169506058	169506058	Missense_Mutation	SNP	G	A	14	29	c.5074G>A	c.(5074-5076)GAG>AAG	p.E1692K
Pat_22	Pre-Treatment	SLC22A23	63027	37	6	3324095	3324095	Missense_Mutation	SNP	G	A	6	15	c.1055C>T	c.(1054-1056)CCC>CTC	p.P352L
Pat_22	Pre-Treatment	HLA-DRB5	3127	37	6	32487267	32487267	Nonsense_Mutation	SNP	G	A	13	40	c.532C>T	c.(532-534)CAG>TAG	p.Q178*
Pat_22	Pre-Treatment	GLP1R	2740	37	6	39046097	39046097	Splice_Site	SNP	G	A	11	22	c.824_splice	c.e8-1	p.G275_splice
Pat_22	Pre-Treatment	MDFI	4188	37	6	41621284	41621284	Missense_Mutation	SNP	G	A	9	48	c.712G>A	c.(712-714)GAG>AAG	p.E238K
Pat_22	Pre-Treatment	PKHD1	5314	37	6	51947245	51947245	Missense_Mutation	SNP	G	A	17	68	c.226C>T	c.(226-228)CCC>TCC	p.P76S
Pat_22	Pre-Treatment	FAM83B	222584	37	6	54805192	54805192	Missense_Mutation	SNP	C	T	8	33	c.1423C>T	c.(1423-1425)CGC>TGC	p.R475C
Pat_22	Pre-Treatment	COL21A1	81578	37	6	56044571	56044571	Missense_Mutation	SNP	C	T	3	22	c.445G>A	c.(445-447)GAT>AAT	p.D149N
Pat_22	Pre-Treatment	ELOVL4	6785	37	6	80629160	80629160	Nonsense_Mutation	SNP	G	A	6	33	c.646C>T	c.(646-648)CGA>TGA	p.R216*
Pat_22	Pre-Treatment	RFX6	222546	37	6	117248471	117248471	Missense_Mutation	SNP	G	A	7	43	c.2167G>A	c.(2167-2169)GAG>AAG	p.E723K
Pat_22	Pre-Treatment	TXLNB	167838	37	6	139563907	139563907	Nonsense_Mutation	SNP	C	T	5	25	c.1811G>A	c.(1810-1812)TGG>TAG	p.W604*
Pat_22	Pre-Treatment	MTHFD1L	25902	37	6	151258056	151258056	Missense_Mutation	SNP	G	A	12	35	c.1373G>A	c.(1372-1374)GGA>GAA	p.G458E
Pat_22	Pre-Treatment	FTSJ2	29960	37	7	2274902	2274902	Missense_Mutation	SNP	C	T	4	16	c.596G>A	c.(595-597)AGT>AAT	p.S199N
Pat_22	Pre-Treatment	ACTB	60	37	7	5567389	5567389	Missense_Mutation	SNP	T	G	60	504	c.1118A>C	c.(1117-1119)AAA>ACA	p.K373T
Pat_22	Pre-Treatment	OGDH	4967	37	7	44715620	44715620	Missense_Mutation	SNP	C	T	16	122	c.1078C>T	c.(1078-1080)CGT>TGT	p.R360C
Pat_22	Pre-Treatment	CYP51A1	1595	37	7	91746480	91746480	Missense_Mutation	SNP	G	A	3	20	c.1229C>T	c.(1228-1230)TCT>TTT	p.S410F
Pat_22	Pre-Treatment	CYP3A4	1576	37	7	99366124	99366124	Missense_Mutation	SNP	C	T	6	48	c.523G>A	c.(523-525)GTC>ATC	p.V175I
Pat_22	Pre-Treatment	BRAF	673	37	7	140453136	140453136	Missense_Mutation	SNP	A	T	15	23	c.1799T>A	c.(1798-1800)GTG>GAG	p.V600E
Pat_22	Pre-Treatment	TAS2R60	338398	37	7	143141207	143141207	Missense_Mutation	SNP	G	A	8	12	c.662G>A	c.(661-663)GGA>GAA	p.G221E
Pat_22	Pre-Treatment	C7orf29	113763	37	7	150027766	150027766	Nonsense_Mutation	SNP	G	A	11	29	c.273G>A	c.(271-273)TGG>TGA	p.W91*
Pat_22	Pre-Treatment	CSMD1	64478	37	8	2965315	2965315	Nonsense_Mutation	SNP	G	A	3	26	c.6763C>T	c.(6763-6765)CAG>TAG	p.Q2255*
Pat_22	Pre-Treatment	DEFB136	613210	37	8	11831592	11831592	Missense_Mutation	SNP	G	A	12	68	c.91C>T	c.(91-93)CGC>TGC	p.R31C
Pat_22	Pre-Treatment	RP1	6101	37	8	55533900	55533900	Missense_Mutation	SNP	G	A	13	34	c.374G>A	c.(373-375)CGG>CAG	p.R125Q
Pat_22	Pre-Treatment	JPH1	56704	37	8	75227798	75227798	Missense_Mutation	SNP	C	G	3	25	c.437G>C	c.(436-438)AGC>ACC	p.S146T
Pat_22	Pre-Treatment	SLC7A13	157724	37	8	87241932	87241932	Missense_Mutation	SNP	C	T	17	18	c.575G>A	c.(574-576)CGA>CAA	p.R192Q
Pat_22	Pre-Treatment	ENPP2	5168	37	8	120613682	120613682	Missense_Mutation	SNP	C	T	16	98	c.854G>A	c.(853-855)AGA>AAA	p.R285K
Pat_22	Pre-Treatment	KIAA0196	9897	37	8	126051070	126051070	Splice_Site	SNP	A	G	29	37	c.3084_splice	c.e25+1	p.K1028_splice
Pat_22	Pre-Treatment	LRRC6	23639	37	8	133637582	133637582	Missense_Mutation	SNP	G	A	6	2	c.772C>T	c.(772-774)CCT>TCT	p.P258S
Pat_22	Pre-Treatment	SHARPIN	81858	37	8	145154852	145154852	Missense_Mutation	SNP	G	A	12	16	c.497C>T	c.(496-498)CCT>CTT	p.P166L
Pat_22	Pre-Treatment	ADCK5	203054	37	8	145615884	145615884	Missense_Mutation	SNP	G	A	3	10	c.280G>A	c.(280-282)GGC>AGC	p.G94S
Pat_22	Pre-Treatment	PTPRD	5789	37	9	8500886	8500886	Missense_Mutation	SNP	G	A	19	61	c.1996C>T	c.(1996-1998)CCT>TCT	p.P666S
Pat_22	Pre-Treatment	IFNA21	3452	37	9	21166224	21166224	Missense_Mutation	SNP	C	T	21	63	c.388G>A	c.(388-390)GAA>AAA	p.E130K
Pat_22	Pre-Treatment	PAX5	5079	37	9	37033987	37033987	Missense_Mutation	SNP	C	G	2	9	c.42G>C	c.(40-42)AGG>AGC	p.R14S
Pat_22	Pre-Treatment	ALDOB	229	37	9	104190778	104190778	Missense_Mutation	SNP	C	T	3	22	c.352G>A	c.(352-354)GGA>AGA	p.G118R
Pat_22	Pre-Treatment	PTPN3	5774	37	9	112195353	112195353	Nonsense_Mutation	SNP	C	T	4	16	c.764G>A	c.(763-765)TGG>TAG	p.W255*
Pat_22	Pre-Treatment	PHF19	26147	37	9	123636851	123636851	Missense_Mutation	SNP	G	A	25	54	c.169C>T	c.(169-171)CTC>TTC	p.L57F
Pat_22	Pre-Treatment	PDCL	5082	37	9	125582834	125582834	Missense_Mutation	SNP	C	T	3	26	c.436G>A	c.(436-438)GAA>AAA	p.E146K
Pat_22	Pre-Treatment	ACE2	59272	37	X	15596407	15596407	Missense_Mutation	SNP	C	T	9	32	c.1102G>A	c.(1102-1104)GAC>AAC	p.D368N
Pat_22	Pre-Treatment	BEND2	139105	37	X	18219991	18219991	Missense_Mutation	SNP	C	T	8	36	c.977G>A	c.(976-978)GGA>GAA	p.G326E
Pat_22	Pre-Treatment	ARAF	369	37	X	47429015	47429015	Missense_Mutation	SNP	G	A	3	9	c.1378G>A	c.(1378-1380)GCC>ACC	p.A460T
Pat_22	Pre-Treatment	RLIM	51132	37	X	73812068	73812068	Missense_Mutation	SNP	C	T	7	23	c.1082G>A	c.(1081-1083)GGA>GAA	p.G361E
Pat_22	Pre-Treatment	SERPINA7	6906	37	X	105278344	105278344	Missense_Mutation	SNP	G	A	5	9	c.926C>T	c.(925-927)TCC>TTC	p.S309F
Pat_22	Pre-Treatment	TBC1D8B	54885	37	X	106109164	106109164	Missense_Mutation	SNP	C	T	12	94	c.2563C>T	c.(2563-2565)CAT>TAT	p.H855Y
Pat_22	Pre-Treatment	SOX3	6658	37	X	139586325	139586325	Missense_Mutation	SNP	G	A	2	1	c.901C>T	c.(901-903)CGC>TGC	p.R301C
Pat_22	Pre-Treatment	MAGEC1	9947	37	X	140993320	140993320	Missense_Mutation	SNP	A	G	4	33	c.130A>G	c.(130-132)AGC>GGC	p.S44G
Pat_22	Pre-Treatment	AFF2	2334	37	X	147743727	147743727	Nonsense_Mutation	SNP	C	A	9	153	c.479C>A	c.(478-480)TCA>TAA	p.S160*

Pat_22	Pre-Treatment	DKC1	1736	37	X	153994523	153994523	Missense_Mutation	SNP	A	G	10	39	c.296A>G	c.(295-297)AAC>AGC	p.N99S
Pat_22	Post-Resistance	TAS1R3	83756	37	1	1269395	1269395	Missense_Mutation	SNP	C	T	21	38	c.2110C>T	c.(2110-2112)CCG>TCG	p.P704S
Pat_22	Post-Resistance	MFN2	9927	37	1	12066704	12066704	Missense_Mutation	SNP	C	T	21	116	c.1826C>T	c.(1825-1827)TCC>TTC	p.S609F
Pat_22	Post-Resistance	PRAMEF11	440560	37	1	12887523	12887523	Missense_Mutation	SNP	C	T	205	445	c.334G>A	c.(334-336)GAA>AAA	p.E112K
Pat_22	Post-Resistance	CD52	1043	37	1	26644522	26644522	Missense_Mutation	SNP	T	G	17	103	c.14T>G	c.(13-15)CTC>CGC	p.L5R
Pat_22	Post-Resistance	SESN2	83667	37	1	28599237	28599237	Missense_Mutation	SNP	C	T	25	142	c.683C>T	c.(682-684)CCC>CTC	p.P228L
Pat_22	Post-Resistance	SDC3	9672	37	1	31347149	31347149	Missense_Mutation	SNP	A	C	30	83	c.1157T>G	c.(1156-1158)CTC>CGC	p.L386R
Pat_22	Post-Resistance	TMEM39B	55116	37	1	32557516	32557516	Missense_Mutation	SNP	C	G	32	91	c.831C>G	c.(829-831)TTC>TTG	p.F277L
Pat_22	Post-Resistance	CSMD2	114784	37	1	34037305	34037305	Missense_Mutation	SNP	C	T	31	178	c.7790G>A	c.(7789-7791)AGT>AAT	p.S2597N
Pat_22	Post-Resistance	CSMD2	114784	37	1	34066469	34066469	Missense_Mutation	SNP	G	T	52	114	c.6858C>A	c.(6856-6858)TTC>TTA	p.F2286L
Pat_22	Post-Resistance	CSMD2	114784	37	1	34158530	34158530	Missense_Mutation	SNP	C	T	69	315	c.3932G>A	c.(3931-3933)GGG>GAG	p.G1311E
Pat_22	Post-Resistance	GRIK3	2899	37	1	37282732	37282732	Missense_Mutation	SNP	C	T	31	153	c.2020G>A	c.(2020-2022)GAT>AAT	p.D674N
Pat_22	Post-Resistance	GRIK3	2899	37	1	37319298	37319298	Missense_Mutation	SNP	C	T	19	178	c.1130G>A	c.(1129-1131)CGA>CAA	p.R377Q
Pat_22	Post-Resistance	C1orf175	374977	37	1	55119637	55119637	Missense_Mutation	SNP	C	A	4	155	c.1038C>A	c.(1036-1038)AGC>AGA	p.S346R
Pat_22	Post-Resistance	DEPDC1	55635	37	1	68942710	68942710	Missense_Mutation	SNP	T	C	40	98	c.2341A>G	c.(2341-2343)ACC>GCC	p.T781A
Pat_22	Post-Resistance	GBP2	2634	37	1	89587495	89587495	Missense_Mutation	SNP	G	A	126	224	c.155C>T	c.(154-156)TCC>TTC	p.S52F
Pat_22	Post-Resistance	ABCA4	24	37	1	94471119	94471119	Missense_Mutation	SNP	C	T	21	76	c.6025G>A	c.(6025-6027)GAA>AAA	p.E2009K
Pat_22	Post-Resistance	SLC6A17	388662	37	1	110716639	110716639	Nonsense_Mutation	SNP	G	A	57	120	c.489G>A	c.(487-489)TGG>TGA	p.W163*
Pat_22	Post-Resistance	C1orf88	128344	37	1	111892789	111892789	Nonsense_Mutation	SNP	G	T	5	315	c.451G>T	c.(451-453)GGA>TGA	p.G151*
Pat_22	Post-Resistance	NBPF7	343505	37	1	120378788	120378788	Missense_Mutation	SNP	G	A	56	115	c.958C>T	c.(958-960)CCG>TCG	p.P320S
Pat_22	Post-Resistance	NUDT17	200035	37	1	145588959	145588959	Missense_Mutation	SNP	C	T	3	64	c.289G>A	c.(289-291)GTC>ATC	p.V97I
Pat_22	Post-Resistance	CHD1L	9557	37	1	146724319	146724319	Missense_Mutation	SNP	C	T	79	358	c.169C>T	c.(169-171)CTC>TTC	p.L57F
Pat_22	Post-Resistance	NBPF16	728936	37	1	148753279	148753279	Missense_Mutation	SNP	G	T	9	282	c.1296G>T	c.(1294-1296)GAG>GAT	p.E432D
Pat_22	Post-Resistance	FLG	2312	37	1	152284934	152284934	Missense_Mutation	SNP	T	C	74	410	c.2428A>G	c.(2428-2430)ACA>GCA	p.T810A
Pat_22	Post-Resistance	ARHGEF11	9826	37	1	156917684	156917684	Missense_Mutation	SNP	C	A	4	86	c.2098G>T	c.(2098-2100)GAT>TAT	p.D700Y
Pat_22	Post-Resistance	TNN	63923	37	1	175086222	175086222	Missense_Mutation	SNP	G	A	49	312	c.2267G>A	c.(2266-2268)GGG>GAG	p.G756E
Pat_22	Post-Resistance	TNR	7143	37	1	175372495	175372495	Missense_Mutation	SNP	C	T	26	140	c.757G>A	c.(757-759)GAA>AAA	p.E253K
Pat_22	Post-Resistance	CFH	3075	37	1	196695999	196695999	Missense_Mutation	SNP	C	T	75	277	c.2165C>T	c.(2164-2166)TCA>TTA	p.S722L
Pat_22	Post-Resistance	CRB1	23418	37	1	197313530	197313530	Missense_Mutation	SNP	C	T	109	414	c.772C>T	c.(772-774)CAC>TAC	p.H258Y
Pat_22	Post-Resistance	PTPRC	5788	37	1	198665985	198665985	Missense_Mutation	SNP	C	T	80	461	c.239C>T	c.(238-240)TCC>TTC	p.S80F
Pat_22	Post-Resistance	GOLT1A	127845	37	1	204170779	204170779	Missense_Mutation	SNP	C	T	31	193	c.278G>A	c.(277-279)GGA>GAA	p.G93E
Pat_22	Post-Resistance	CTSE	1510	37	1	206331084	206331084	Missense_Mutation	SNP	G	A	40	352	c.1090G>A	c.(1090-1092)GCT>ACT	p.A364T
Pat_22	Post-Resistance	RASSF5	83593	37	1	206757827	206757827	Missense_Mutation	SNP	G	A	57	626	c.799G>A	c.(799-801)GAG>AAG	p.E267K
Pat_22	Post-Resistance	C1orf74	148304	37	1	209956721	209956721	Missense_Mutation	SNP	C	T	18	73	c.259G>A	c.(259-261)GAG>AAG	p.E87K
Pat_22	Post-Resistance	MIA3	375056	37	1	222825630	222825630	Missense_Mutation	SNP	C	T	66	398	c.4042C>T	c.(4042-4044)CGG>TGG	p.R1348W
Pat_22	Post-Resistance	CNST	163882	37	1	246810513	246810513	Missense_Mutation	SNP	C	T	47	271	c.1010C>T	c.(1009-1011)CCC>CTC	p.P337L
Pat_22	Post-Resistance	TRIM58	25893	37	1	248039444	248039444	Missense_Mutation	SNP	G	A	37	89	c.1114G>A	c.(1114-1116)GAA>AAA	p.E372K
Pat_22	Post-Resistance	OR2T6	254879	37	1	248551607	248551608	Missense_Mutation	DNP	GG	AA	71	243	c.698_699GG>AA	c.(697-699)GGG>GAA	p.G233E
Pat_22	Post-Resistance	OR2T11	127077	37	1	248789853	248789853	Missense_Mutation	SNP	C	T	85	188	c.577G>A	c.(577-579)GAA>AAA	p.E193K
Pat_22	Post-Resistance	ZNF692	55657	37	1	249144435	249144436	Missense_Mutation	DNP	CC	TT	19	94	.1533_1534GG>A	531-1536)CAGGCT>CAA	p.A512T
Pat_22	Post-Resistance	FBXO18	84893	37	10	5958276	5958276	Missense_Mutation	SNP	G	A	36	60	c.1645G>A	c.(1645-1647)GGA>AGA	p.G549R
Pat_22	Post-Resistance	FRMPD2	143162	37	10	49440316	49440316	Missense_Mutation	SNP	G	A	7	18	c.1010C>T	c.(1009-1011)TCC>TTC	p.S337F
Pat_22	Post-Resistance	PRF1	5551	37	10	72360448	72360448	Missense_Mutation	SNP	C	T	3	79	c.211G>A	c.(211-213)GGC>AGC	p.G71S
Pat_22	Post-Resistance	CDHR1	92211	37	10	85960421	85960421	Missense_Mutation	SNP	G	A	6	39	c.503G>A	c.(502-504)GGG>GAG	p.G168E
Pat_22	Post-Resistance	SLC16A12	387700	37	10	91196021	91196021	Missense_Mutation	SNP	G	A	35	162	c.994C>T	c.(994-996)CTC>TTC	p.L332F
Pat_22	Post-Resistance	CYP2C8	1558	37	10	96827082	96827082	Missense_Mutation	SNP	C	T	29	72	c.364G>A	c.(364-366)GAG>AAG	p.E122K
Pat_22	Post-Resistance	ZNF518A	9849	37	10	97918694	97918694	Missense_Mutation	SNP	T	C	43	55	c.2615T>C	c.(2614-2616)GTG>GCG	p.V872A

Pat_22	Post-Resistance	LOXL4	84171	37	10	100017824	100017824	Nonsense_Mutation	SNP	C	T	65	79	c.1019G>A	c.(1018-1020)TGG>TAG	p.W340*
Pat_22	Post-Resistance	SORCS3	22986	37	10	106982904	106982904	Missense_Mutation	SNP	C	T	35	90	c.2765C>T	c.(2764-2766)CCA>CTA	p.P922L
Pat_22	Post-Resistance	PNLIP	5406	37	10	118315007	118315007	Missense_Mutation	SNP	G	A	52	333	c.799G>A	c.(799-801)GGA>AGA	p.G267R
Pat_22	Post-Resistance	GLRX3	10539	37	10	131969861	131969861	Missense_Mutation	SNP	G	A	20	139	c.785G>A	c.(784-786)GGA>GAA	p.G262E
Pat_22	Post-Resistance	C10orf93	255352	37	10	134752184	134752184	Missense_Mutation	SNP	G	A	107	168	c.445C>T	c.(445-447)CGT>TGT	p.R149C
Pat_22	Post-Resistance	LOC653544	653544	37	10	135491113	135491113	Missense_Mutation	SNP	G	A	3	40	c.724G>A	c.(724-726)GCC>ACC	p.A242T
Pat_22	Post-Resistance	LRDD	55367	37	11	800594	800594	Missense_Mutation	SNP	C	T	3	73	c.1990G>A	c.(1990-1992)GAG>AAG	p.E664K
Pat_22	Post-Resistance	MS4A10	341116	37	11	60561520	60561520	Missense_Mutation	SNP	C	T	28	111	c.436C>T	c.(436-438)CTC>TTC	p.L146F
Pat_22	Post-Resistance	CPSF7	79869	37	11	61179325	61179325	Missense_Mutation	SNP	C	T	24	175	c.1169G>A	c.(1168-1170)CGT>CAT	p.R390H
Pat_22	Post-Resistance	B3GNT1	11041	37	11	66113666	66113666	Missense_Mutation	SNP	C	G	18	157	c.1102G>C	c.(1102-1104)GAA>CAA	p.E368Q
Pat_22	Post-Resistance	RBM4	5936	37	11	66407211	66407211	Missense_Mutation	SNP	C	T	59	318	c.29C>T	c.(28-30)CCC>CTC	p.P10L
Pat_22	Post-Resistance	SPTBN2	6712	37	11	66475760	66475760	Missense_Mutation	SNP	C	A	4	57	c.1202G>T	c.(1201-1203)CGG>CTG	p.R401L
Pat_22	Post-Resistance	SHANK2	22941	37	11	70333711	70333711	Missense_Mutation	SNP	G	A	17	17	c.2687C>T	c.(2686-2688)CCG>CTG	p.P896L
Pat_22	Post-Resistance	ARHGEF17	9828	37	11	73075219	73075219	Missense_Mutation	SNP	A	G	7	390	c.5336A>G	c.(5335-5337)TAT>TGT	p.Y1779C
Pat_22	Post-Resistance	MYO7A	4647	37	11	76895747	76895747	Missense_Mutation	SNP	C	T	4	37	c.3490C>T	c.(3490-3492)CGG>TGG	p.R1164W
Pat_22	Post-Resistance	HEPHL1	341208	37	11	93815680	93815680	Missense_Mutation	SNP	C	T	17	35	c.1813C>T	c.(1813-1815)CCC>TCC	p.P605S
Pat_22	Post-Resistance	ATM	472	37	11	108160328	108160328	Splice_Site	SNP	G	A	11	45	c.4237_splice	c.e29-1	p.D1413_splice
Pat_22	Post-Resistance	SIDT2	51092	37	11	117054825	117054825	Missense_Mutation	SNP	C	A	4	158	c.838C>A	c.(838-840)CTG>ATG	p.L280M
Pat_22	Post-Resistance	ST14	6768	37	11	130058088	130058088	Missense_Mutation	SNP	G	A	3	50	c.161G>A	c.(160-162)CGC>CAC	p.R54H
Pat_22	Post-Resistance	ANO2	57101	37	12	5674749	5674749	Missense_Mutation	SNP	C	T	10	37	c.2702G>A	c.(2701-2703)CGT>CAT	p.R901H
Pat_22	Post-Resistance	CD163	9332	37	12	7639377	7639377	Missense_Mutation	SNP	C	T	34	205	c.2176G>A	c.(2176-2178)GGT>AGT	p.G726S
Pat_22	Post-Resistance	PRB4	5545	37	12	11461646	11461646	Missense_Mutation	SNP	C	G	8	457	c.271G>C	c.(271-273)GGT>CGT	p.G91R
Pat_22	Post-Resistance	SYT10	341359	37	12	33560007	33560007	Missense_Mutation	SNP	C	T	25	47	c.794G>A	c.(793-795)GGA>GAA	p.G265E
Pat_22	Post-Resistance	ABCD2	225	37	12	39973341	39973341	Missense_Mutation	SNP	G	A	34	452	c.1873C>T	c.(1873-1875)CAT>TAT	p.H625Y
Pat_22	Post-Resistance	CNTN1	1272	37	12	41312557	41312557	Missense_Mutation	SNP	C	T	115	299	c.211C>T	c.(211-213)CCT>TCT	p.P71S
Pat_22	Post-Resistance	ADAMTS20	80070	37	12	43945643	43945643	Missense_Mutation	SNP	G	A	63	118	c.82C>T	c.(82-84)CCC>TCC	p.P28S
Pat_22	Post-Resistance	ARID2	196528	37	12	46123701	46123701	Missense_Mutation	SNP	C	T	17	33	c.82C>T	c.(82-84)CAC>TAC	p.H28Y
Pat_22	Post-Resistance	FAM113B	91523	37	12	47629357	47629357	Missense_Mutation	SNP	G	A	14	97	c.511G>A	c.(511-513)GAA>AAA	p.E171K
Pat_22	Post-Resistance	NCKAP1L	3071	37	12	54925961	54925962	Missense_Mutation	DNP	CC	TT	10	85	.2789_2790CC>T	c.(2788-2790)TCC>TTT	p.S930F
Pat_22	Post-Resistance	MYF6	4618	37	12	81101671	81101671	Missense_Mutation	SNP	G	A	40	103	c.173G>A	c.(172-174)GGA>GAA	p.G58E
Pat_22	Post-Resistance	LRRIQ1	84125	37	12	85492709	85492709	Missense_Mutation	SNP	C	T	35	188	c.3146C>T	c.(3145-3147)ACT>ATT	p.T1049I
Pat_22	Post-Resistance	C12orf23	90488	37	12	107360888	107360888	Splice_Site	SNP	G	T	5	109	c.-5_splice	c.e3-1	
Pat_22	Post-Resistance	TBX5	6910	37	12	114804084	114804084	Nonsense_Mutation	SNP	G	A	24	141	c.868C>T	c.(868-870)CAA>TAA	p.Q290*
Pat_22	Post-Resistance	GCN1L1	10985	37	12	120574409	120574409	Missense_Mutation	SNP	G	A	18	119	c.6905C>T	c.(6904-6906)TCC>TTC	p.S2302F
Pat_22	Post-Resistance	VPS33A	65082	37	12	122717499	122717499	Missense_Mutation	SNP	G	A	12	35	c.1457C>T	c.(1456-1458)TCG>TTG	p.S486L
Pat_22	Post-Resistance	GPR109B	8843	37	12	123200497	123200497	Missense_Mutation	SNP	G	A	3	36	c.788C>T	c.(787-789)ACG>ATG	p.T263M
Pat_22	Post-Resistance	TUBA3C	7278	37	13	19748188	19748188	Missense_Mutation	SNP	G	A	40	277	c.1168C>T	c.(1168-1170)CGC>TGC	p.R390C
Pat_22	Post-Resistance	GJB6	10804	37	13	20797118	20797118	Missense_Mutation	SNP	T	C	39	69	c.502A>G	c.(502-504)AAA>GAA	p.K168E
Pat_22	Post-Resistance	MAB21L1	4081	37	13	36050424	36050424	Translation_Start_Site	SNP	G	A	3	23	c.-148C>T	(-150--146)AACGC>AATGC	
Pat_22	Post-Resistance	SLC10A2	6555	37	13	103705031	103705031	Missense_Mutation	SNP	G	A	24	117	c.524C>T	c.(523-525)CCT>CTT	p.P175L
Pat_22	Post-Resistance	ZNF219	51222	37	14	21561080	21561080	Missense_Mutation	SNP	G	A	15	138	c.376C>T	c.(376-378)CGC>TGC	p.R126C
Pat_22	Post-Resistance	MYH7	4625	37	14	23885256	23885256	Missense_Mutation	SNP	G	A	11	66	c.4910C>T	c.(4909-4911)GCC>GTC	p.A1637V
Pat_22	Post-Resistance	MAPK1IP1L	93487	37	14	55529396	55529396	Missense_Mutation	SNP	C	T	22	111	c.79C>T	c.(79-81)CCT>TCT	p.P27S
Pat_22	Post-Resistance	LGALS3	3958	37	14	55604868	55604868	Missense_Mutation	SNP	C	T	5	31	c.124C>T	c.(124-126)CCT>TCT	p.P42S
Pat_22	Post-Resistance	PCNX	22990	37	14	71429044	71429044	Missense_Mutation	SNP	A	G	83	191	c.464A>G	c.(463-465)AAC>AGC	p.N155S
Pat_22	Post-Resistance	YLPM1	56252	37	14	75265094	75265094	Missense_Mutation	SNP	C	T	6	285	c.3094C>T	c.(3094-3096)CGG>TGG	p.R1032W
Pat_22	Post-Resistance	TTLL5	23093	37	14	76173379	76173379	Missense_Mutation	SNP	G	A	71	299	c.604G>A	c.(604-606)GAA>AAA	p.E202K

Pat_22	Post-Resistance	KIAA1409	57578	37	14	94046595	94046595	Missense_Mutation	SNP	G	A	38	158	c.2003G>A	c.(2002-2004)GGA>GAA	p.G668E
Pat_22	Post-Resistance	BCL11B	64919	37	14	99641836	99641836	Missense_Mutation	SNP	C	T	4	127	c.1337G>A	c.(1336-1338)CGG>CAG	p.R446Q
Pat_22	Post-Resistance	DYNC1H1	1778	37	14	102515854	102515854	Missense_Mutation	SNP	G	A	4	117	c.13450G>A	c.(13450-13452)GAG>AAG	p.E4484K
Pat_22	Post-Resistance	RYR3	6263	37	15	33926814	33926814	Missense_Mutation	SNP	C	A	27	118	c.3055C>A	c.(3055-3057)CTG>ATG	p.L1019M
Pat_22	Post-Resistance	BMF	90427	37	15	40398106	40398106	Missense_Mutation	SNP	C	T	33	104	c.182G>A	c.(181-183)CGA>CAA	p.R61Q
Pat_22	Post-Resistance	MGA	23269	37	15	42057138	42057138	Missense_Mutation	SNP	C	T	5	197	c.7799C>T	c.(7798-7800)CCG>CTG	p.P2600L
Pat_22	Post-Resistance	PAQR5	54852	37	15	69696009	69696009	Missense_Mutation	SNP	G	A	21	136	c.841G>A	c.(841-843)GAA>AAA	p.E281K
Pat_22	Post-Resistance	THSD4	79875	37	15	72039374	72039374	Nonsense_Mutation	SNP	G	A	10	30	c.2234G>A	c.(2233-2235)TGG>TAG	p.W745*
Pat_22	Post-Resistance	ISLR	3671	37	15	74468448	74468448	Nonsense_Mutation	SNP	C	T	10	24	c.1249C>T	c.(1249-1251)CAA>TAA	p.Q417*
Pat_22	Post-Resistance	KIAA1024	23251	37	15	79750596	79750596	Missense_Mutation	SNP	C	T	24	95	c.2107C>T	c.(2107-2109)CTC>TTC	p.L703F
Pat_22	Post-Resistance	FSD2	123722	37	15	83455943	83455943	Missense_Mutation	SNP	A	G	10	263	c.200T>C	c.(199-201)CTT>CCT	p.L67P
Pat_22	Post-Resistance	RHOT2	89941	37	16	722799	722799	Missense_Mutation	SNP	T	C	37	82	c.1501T>C	c.(1501-1503)TTT>CTT	p.F501L
Pat_22	Post-Resistance	ZNF263	10127	37	16	3339681	3339681	Missense_Mutation	SNP	A	G	82	204	c.1175A>G	c.(1174-1176)AAC>AGC	p.N392S
Pat_22	Post-Resistance	UBN1	29855	37	16	4911098	4911098	Missense_Mutation	SNP	G	A	3	44	c.1105G>A	c.(1105-1107)GCT>ACT	p.A369T
Pat_22	Post-Resistance	GRIN2A	2903	37	16	9857436	9857436	Missense_Mutation	SNP	C	T	21	155	c.3965G>A	c.(3964-3966)GGA>GAA	p.G1322E
Pat_22	Post-Resistance	ACSM5	54988	37	16	20448432	20448432	Missense_Mutation	SNP	G	A	44	239	c.1367G>A	c.(1366-1368)CGA>CAA	p.R456Q
Pat_22	Post-Resistance	ACSM2B	348158	37	16	20563586	20563586	Nonsense_Mutation	SNP	C	T	41	260	c.774G>A	c.(772-774)TGG>TGA	p.W258*
Pat_22	Post-Resistance	SLC5A11	115584	37	16	24921657	24921657	Missense_Mutation	SNP	G	A	48	251	c.1681G>A	c.(1681-1683)GAC>AAC	p.D561N
Pat_22	Post-Resistance	GTF3C1	2975	37	16	27556735	27556735	Nonsense_Mutation	SNP	G	A	40	186	c.331C>T	c.(331-333)CAG>TAG	p.Q111*
Pat_22	Post-Resistance	ESRP2	80004	37	16	68269839	68269839	Missense_Mutation	SNP	G	A	3	30	c.110C>T	c.(109-111)ACG>ATG	p.T37M
Pat_22	Post-Resistance	SMPD3	55512	37	16	68405838	68405838	Missense_Mutation	SNP	G	A	8	32	c.247C>T	c.(247-249)CTC>TTC	p.L83F
Pat_22	Post-Resistance	TERF2	7014	37	16	69390829	69390829	Missense_Mutation	SNP	C	T	6	265	c.1475G>A	c.(1474-1476)CGG>CAG	p.R492Q
Pat_22	Post-Resistance	NFAT5	10725	37	16	69727609	69727609	Missense_Mutation	SNP	T	C	6	166	c.3827T>C	c.(3826-3828)ATG>ACG	p.M1276T
Pat_22	Post-Resistance	CNTNAP4	85445	37	16	76350324	76350324	Missense_Mutation	SNP	C	T	15	90	c.100C>T	c.(100-102)CCT>TCT	p.P34S
Pat_22	Post-Resistance	FBXO31	79791	37	16	87376497	87376497	Missense_Mutation	SNP	C	T	3	50	c.718G>A	c.(718-720)GGC>AGC	p.G240S
Pat_22	Post-Resistance	MVD	4597	37	16	88723970	88723970	Missense_Mutation	SNP	G	A	4	135	c.277C>T	c.(277-279)CGG>TGG	p.R93W
Pat_22	Post-Resistance	TUBB3	10381	37	16	89989858	89989859	Missense_Mutation	DNP	GG	AA	21	65	c.49_50GG>AA	c.(49-51)GGG>AAG	p.G17K
Pat_22	Post-Resistance	CHD3	1107	37	17	7812606	7812606	Missense_Mutation	SNP	C	G	2	4	c.5540C>G	c.(5539-5541)TCC>TGC	p.S1847C
Pat_22	Post-Resistance	MYO15A	51168	37	17	18052101	18052101	Nonsense_Mutation	SNP	G	A	7	71	c.6791G>A	c.(6790-6792)TGG>TAG	p.W2264*
Pat_22	Post-Resistance	ZNF286B	729288	37	17	18565486	18565486	Missense_Mutation	SNP	C	T	150	157	c.1333G>A	c.(1333-1335)GGG>AGG	p.G445R
Pat_22	Post-Resistance	FNDC8	54752	37	17	33448915	33448915	Missense_Mutation	SNP	A	G	35	127	c.203A>G	c.(202-204)AAC>AGC	p.N68S
Pat_22	Post-Resistance	CCL16	6360	37	17	34304696	34304696	Missense_Mutation	SNP	T	A	71	194	c.269A>T	c.(268-270)GAT>GTT	p.D90V
Pat_22	Post-Resistance	ACACA	31	37	17	35614647	35614647	Missense_Mutation	SNP	C	T	47	169	c.1693G>A	c.(1693-1695)GAA>AAA	p.E565K
Pat_22	Post-Resistance	KRT39	390792	37	17	39122949	39122949	Missense_Mutation	SNP	G	A	78	485	c.160C>T	c.(160-162)CCC>TCC	p.P54S
Pat_22	Post-Resistance	TMEM106A	113277	37	17	41365877	41365877	Missense_Mutation	SNP	C	T	40	97	c.242C>T	c.(241-243)CCC>CTC	p.P81L
Pat_22	Post-Resistance	ARL17A	51326	37	17	44594548	44594548	Missense_Mutation	SNP	G	A	8	153	c.311C>T	c.(310-312)ACC>ATC	p.T104I
Pat_22	Post-Resistance	KIF2B	84643	37	17	51902342	51902342	Missense_Mutation	SNP	G	A	6	123	c.1948G>A	c.(1948-1950)GAT>AAT	p.D650N
Pat_22	Post-Resistance	TOM1L1	10040	37	17	53016382	53016382	Splice_Site	SNP	G	A	9	269	c.1130_splice	c.e11+1	p.P377_splice
Pat_22	Post-Resistance	KCNH6	81033	37	17	61622604	61622605	Missense_Mutation	DNP	GG	AA	35	85	.2670_2671GG>A	668-2673)CAGGGC>CAA	p.G891S
Pat_22	Post-Resistance	KPNA2	3838	37	17	66039997	66039997	Missense_Mutation	SNP	A	G	16	506	c.974A>G	c.(973-975)GAT>GGT	p.D325G
Pat_22	Post-Resistance	GPR142	350383	37	17	72368641	72368641	Missense_Mutation	SNP	G	A	27	180	c.1291G>A	c.(1291-1293)GAT>AAT	p.D431N
Pat_22	Post-Resistance	ARMC7	79637	37	17	73124939	73124939	Missense_Mutation	SNP	G	A	23	68	c.403G>A	c.(403-405)GAG>AAG	p.E135K
Pat_22	Post-Resistance	CDK3	1018	37	17	73999460	73999460	Missense_Mutation	SNP	A	G	3	84	c.773A>G	c.(772-774)GAG>GGG	p.E258G
Pat_22	Post-Resistance	MGAT5B	146664	37	17	74922812	74922812	Missense_Mutation	SNP	C	T	43	258	c.1324C>T	c.(1324-1326)CCT>TCT	p.P442S
Pat_22	Post-Resistance	POTEC	388468	37	18	14513663	14513663	Missense_Mutation	SNP	C	T	5	212	c.1531G>A	c.(1531-1533)GAG>AAG	p.E511K
Pat_22	Post-Resistance	POTEC	388468	37	18	14513675	14513675	Missense_Mutation	SNP	T	C	5	264	c.1519A>G	c.(1519-1521)AAA>GAA	p.K507E
Pat_22	Post-Resistance	DSG1	1828	37	18	28934903	28934903	Missense_Mutation	SNP	G	A	67	318	c.2744G>A	c.(2743-2745)AGA>AAA	p.R915K

Pat_22	Post-Resistance	MEP1B	4225	37	18	29797884	29797884	Missense_Mutation	SNP	C	T	66	174	c.2047C>T	c.(2047-2049)CGT>TGT	p.R683C
Pat_22	Post-Resistance	NOL4	8715	37	18	31537457	31537457	Missense_Mutation	SNP	C	T	7	49	c.1261G>A	c.(1261-1263)GAA>AAA	p.E421K
Pat_22	Post-Resistance	SLC39A6	25800	37	18	33694126	33694126	Missense_Mutation	SNP	C	T	5	172	c.1777G>A	c.(1777-1779)GCC>ACC	p.A593T
Pat_22	Post-Resistance	DCC	1630	37	18	50592482	50592482	Missense_Mutation	SNP	G	A	75	130	c.1207G>A	c.(1207-1209)GAA>AAA	p.E403K
Pat_22	Post-Resistance	ALPK2	115701	37	18	56204778	56204778	Missense_Mutation	SNP	C	T	37	76	c.2641G>A	c.(2641-2643)GAC>AAC	p.D881N
Pat_22	Post-Resistance	SERPINB4	6318	37	18	61328062	61328062	Missense_Mutation	SNP	T	C	30	120	c.194A>G	c.(193-195)AAC>AGC	p.N65S
Pat_22	Post-Resistance	DSEL	92126	37	18	65181856	65181856	Missense_Mutation	SNP	G	A	28	81	c.20C>T	c.(19-21)CCC>CTC	p.P7L
Pat_22	Post-Resistance	XAB2	56949	37	19	7692314	7692314	Missense_Mutation	SNP	A	C	4	24	c.337T>G	c.(337-339)TGG>GGG	p.W113G
Pat_22	Post-Resistance	MUC16	94025	37	19	9066642	9066642	Missense_Mutation	SNP	G	A	108	365	c.20804C>T	c.(20803-20805)TCC>TTC	p.S6935F
Pat_22	Post-Resistance	MUC16	94025	37	19	9085696	9085696	Missense_Mutation	SNP	G	A	95	246	c.6119C>T	c.(6118-6120)TCC>TTC	p.S2040F
Pat_22	Post-Resistance	ICAM3	3385	37	19	10449423	10449423	Missense_Mutation	SNP	C	A	4	161	c.278G>T	c.(277-279)CGG>CTG	p.R93L
Pat_22	Post-Resistance	ZNF433	163059	37	19	12126109	12126109	Missense_Mutation	SNP	C	T	32	295	c.1573G>A	c.(1573-1575)GGA>AGA	p.G525R
Pat_22	Post-Resistance	MRI1	84245	37	19	13875479	13875479	Missense_Mutation	SNP	G	A	3	61	c.77G>A	c.(76-78)CGC>CAC	p.R26H
Pat_22	Post-Resistance	NWD1	284434	37	19	16875863	16875863	Missense_Mutation	SNP	C	T	40	152	c.2270C>T	c.(2269-2271)TCC>TTC	p.S757F
Pat_22	Post-Resistance	PDE4C	5143	37	19	18324185	18324185	Missense_Mutation	SNP	C	T	18	91	c.1601G>A	c.(1600-1602)CGA>CAA	p.R534Q
Pat_22	Post-Resistance	WDR62	284403	37	19	36583709	36583709	Missense_Mutation	SNP	C	T	52	328	c.2329C>T	c.(2329-2331)CCC>TCC	p.P777S
Pat_22	Post-Resistance	NUMBL	9253	37	19	41188694	41188694	Missense_Mutation	SNP	G	A	22	174	c.338C>T	c.(337-339)TCC>TTC	p.S113F
Pat_22	Post-Resistance	SNRPA	6626	37	19	41257328	41257328	Missense_Mutation	SNP	G	C	202	563	c.15G>C	c.(13-15)GAG>GAC	p.E5D
Pat_22	Post-Resistance	PSG5	5673	37	19	43689242	43689242	Missense_Mutation	SNP	A	T	8	670	c.122T>A	c.(121-123)CTG>CAG	p.L41Q
Pat_22	Post-Resistance	PSG9	5678	37	19	43763240	43763241	Missense_Mutation	DNP	CC	TT	148	517	c.756_757GG>AA	754-759)AGGGAG>AGAA	p.E253K
Pat_22	Post-Resistance	PNMAL2	57469	37	19	46998016	46998016	Missense_Mutation	SNP	C	T	8	44	c.707G>A	c.(706-708)AGG>AAG	p.R236K
Pat_22	Post-Resistance	SLC8A2	6543	37	19	47935442	47935442	Missense_Mutation	SNP	G	C	26	78	c.2371C>G	c.(2371-2373)CTG>GTG	p.L791V
Pat_22	Post-Resistance	ACPT	93650	37	19	51293729	51293729	Missense_Mutation	SNP	C	G	3	18	c.58C>G	c.(58-60)CTG>GTG	p.L20V
Pat_22	Post-Resistance	SIGLEC9	27180	37	19	51629019	51629019	Missense_Mutation	SNP	C	T	54	208	c.587C>T	c.(586-588)TCG>TTG	p.S196L
Pat_22	Post-Resistance	SIGLEC12	89858	37	19	52002706	52002706	Missense_Mutation	SNP	C	T	31	126	c.1073G>A	c.(1072-1074)CGA>CAA	p.R358Q
Pat_22	Post-Resistance	ZNF331	55422	37	19	54080796	54080796	Missense_Mutation	SNP	G	A	26	195	c.982G>A	c.(982-984)GAA>AAA	p.E328K
Pat_22	Post-Resistance	KIR3DL1	3811	37	19	55331370	55331370	Missense_Mutation	SNP	G	T	5	311	c.558G>T	c.(556-558)ATG>ATT	p.M186I
Pat_22	Post-Resistance	NLRP8	126205	37	19	56466752	56466752	Missense_Mutation	SNP	C	T	37	241	c.1328C>T	c.(1327-1329)TCC>TTC	p.S443F
Pat_22	Post-Resistance	GPR113	165082	37	2	26534297	26534297	Missense_Mutation	SNP	C	T	117	196	c.2299G>A	c.(2299-2301)GAA>AAA	p.E767K
Pat_22	Post-Resistance	ERLEC1	27248	37	2	54028628	54028628	Missense_Mutation	SNP	G	A	7	286	c.620G>A	c.(619-621)AGA>AAA	p.R207K
Pat_22	Post-Resistance	TPRKB	51002	37	2	73959336	73959336	Missense_Mutation	SNP	C	T	25	140	c.218G>A	c.(217-219)AGA>AAA	p.R73K
Pat_22	Post-Resistance	TCF7L1	83439	37	2	85531407	85531407	Missense_Mutation	SNP	C	T	49	295	c.791C>T	c.(790-792)CCC>CTC	p.P264L
Pat_22	Post-Resistance	PTCD3	55037	37	2	86335622	86335622	Splice_Site	SNP	G	A	81	289	c.158_splice	c.e3-1	p.G53_splice
Pat_22	Post-Resistance	ST6GAL2	84620	37	2	107459497	107459497	Missense_Mutation	SNP	C	T	14	34	c.937G>A	c.(937-939)GAA>AAA	p.E313K
Pat_22	Post-Resistance	ST6GAL2	84620	37	2	107460402	107460402	Missense_Mutation	SNP	C	T	13	69	c.32G>A	c.(31-33)CGA>CAA	p.R11Q
Pat_22	Post-Resistance	IL1B	3553	37	2	113590968	113590968	Missense_Mutation	SNP	G	A	28	118	c.284C>T	c.(283-285)CCC>CTC	p.P95L
Pat_22	Post-Resistance	WDR33	55339	37	2	128467366	128467366	Missense_Mutation	SNP	G	A	39	305	c.3373C>T	c.(3373-3375)CCT>TCT	p.P1125S
Pat_22	Post-Resistance	BAZ2B	29994	37	2	160310283	160310283	Missense_Mutation	SNP	G	A	17	108	c.175C>T	c.(175-177)CCG>TCG	p.P59S
Pat_22	Post-Resistance	SCN2A	6326	37	2	166245451	166245451	Missense_Mutation	SNP	C	T	70	602	c.5135C>T	c.(5134-5136)ACC>ATC	p.T1712I
Pat_22	Post-Resistance	FASTKD1	79675	37	2	170403111	170403111	Missense_Mutation	SNP	C	T	48	251	c.1318G>A	c.(1318-1320)GAA>AAA	p.E440K
Pat_22	Post-Resistance	EVX2	344191	37	2	176945436	176945436	Missense_Mutation	SNP	G	A	4	24	c.830C>T	c.(829-831)CCC>CTC	p.P277L
Pat_22	Post-Resistance	TTN	7273	37	2	179472716	179472716	Missense_Mutation	SNP	C	T	26	224	c.45094G>A	c.(45094-45096)GAA>AAA	p.E15032K
Pat_22	Post-Resistance	TTN	7273	37	2	179586756	179586756	Missense_Mutation	SNP	C	T	134	386	c.18902G>A	c.(18901-18903)CGA>CAA	p.R6301Q
Pat_22	Post-Resistance	TTN	7273	37	2	179604201	179604201	Missense_Mutation	SNP	C	T	15	107	c.13246G>A	c.(13246-13248)GAG>AAG	p.E4416K
Pat_22	Post-Resistance	TTN	7273	37	2	179613212	179613212	Nonsense_Mutation	SNP	C	A	8	196	c.13915G>T	c.(13915-13917)GAA>TAA	p.E4639*
Pat_22	Post-Resistance	SDPR	8436	37	2	192700845	192700845	Missense_Mutation	SNP	G	A	118	284	c.1082C>T	c.(1081-1083)TCC>TTC	p.S361F
Pat_22	Post-Resistance	AOX1	316	37	2	201492113	201492114	Missense_Mutation	DNP	GG	AA	78	538	.2162_2163GG>A	c.(2161-2163)AGG>AAA	p.R721K

Pat_22	Post-Resistance	AOX1	316	37	2	201515721	201515721	Missense_Mutation	SNP	G	A	50	150	c.2872G>A	c.(2872-2874)GAA>AAA	p.E958K
Pat_22	Post-Resistance	CASP10	843	37	2	202093684	202093684	Missense_Mutation	SNP	G	A	27	62	c.1444G>A	c.(1444-1446)GAA>AAA	p.E482K
Pat_22	Post-Resistance	TTLL4	9654	37	2	219612363	219612363	Missense_Mutation	SNP	C	A	62	290	c.2293C>A	c.(2293-2295)CTG>ATG	p.L765M
Pat_22	Post-Resistance	CUL3	8452	37	2	225449690	225449690	Missense_Mutation	SNP	C	T	8	55	c.37G>A	c.(37-39)GAC>AAC	p.D13N
Pat_22	Post-Resistance	MTERFD2	130916	37	2	242035499	242035499	Missense_Mutation	SNP	C	G	4	62	c.1147G>C	c.(1147-1149)GAT>CAT	p.D383H
Pat_22	Post-Resistance	PAK7	57144	37	20	9538302	9538302	Missense_Mutation	SNP	G	A	66	175	c.1696C>T	c.(1696-1698)CAC>TAC	p.H566Y
Pat_22	Post-Resistance	ACSS1	84532	37	20	24995839	24995839	Nonsense_Mutation	SNP	C	T	13	131	c.1274G>A	c.(1273-1275)TGG>TAG	p.W425*
Pat_22	Post-Resistance	FRG1B	284802	37	20	29625941	29625941	Missense_Mutation	SNP	A	T	5	232	c.95A>T	c.(94-96)GAT>GTT	p.D32V
Pat_22	Post-Resistance	FAM83C	128876	37	20	33876617	33876617	Missense_Mutation	SNP	C	T	26	92	c.658G>A	c.(658-660)GAC>AAC	p.D220N
Pat_22	Post-Resistance	RBM12	10137	37	20	34240655	34240655	Missense_Mutation	SNP	G	A	54	153	c.2590C>T	c.(2590-2592)CCC>TCC	p.P864S
Pat_22	Post-Resistance	PPP1R16B	26051	37	20	37546830	37546830	Missense_Mutation	SNP	T	A	155	402	c.1225T>A	c.(1225-1227)TCC>ACC	p.S409T
Pat_22	Post-Resistance	WFDC3	140686	37	20	44405770	44405770	Missense_Mutation	SNP	C	T	27	131	c.437G>A	c.(436-438)GGG>GAG	p.G146E
Pat_22	Post-Resistance	CBLN4	140689	37	20	54573681	54573681	Missense_Mutation	SNP	C	T	25	185	c.538G>A	c.(538-540)GAG>AAG	p.E180K
Pat_22	Post-Resistance	CLTCL1	8218	37	22	19196557	19196557	Missense_Mutation	SNP	G	A	4	47	c.3317C>T	c.(3316-3318)GCT>GTT	p.A1106V
Pat_22	Post-Resistance	TATDN2	9797	37	3	10320139	10320139	Missense_Mutation	SNP	C	T	151	383	c.2138C>T	c.(2137-2139)CCT>CTT	p.P713L
Pat_22	Post-Resistance	TATDN2	9797	37	3	10320141	10320141	Missense_Mutation	SNP	C	T	142	374	c.2140C>T	c.(2140-2142)CGC>TGC	p.R714C
Pat_22	Post-Resistance	SYN2	6854	37	3	12182183	12182183	Missense_Mutation	SNP	G	A	10	32	c.410G>A	c.(409-411)GGA>GAA	p.G137E
Pat_22	Post-Resistance	SLC4A7	9497	37	3	27436107	27436107	Missense_Mutation	SNP	C	T	87	219	c.2992G>A	c.(2992-2994)GAA>AAA	p.E998K
Pat_22	Post-Resistance	ACOX2	8309	37	3	58510153	58510153	Missense_Mutation	SNP	C	T	32	194	c.1526G>A	c.(1525-1527)AGG>AAG	p.R509K
Pat_22	Post-Resistance	SUCLG2	8801	37	3	67451239	67451239	Missense_Mutation	SNP	C	T	4	162	c.1099G>A	c.(1099-1101)GTC>ATC	p.V367I
Pat_22	Post-Resistance	KIAA1524	57650	37	3	108300300	108300300	Missense_Mutation	SNP	G	A	34	214	c.511C>T	c.(511-513)CGG>TGG	p.R171W
Pat_22	Post-Resistance	IGSF11	152404	37	3	118623508	118623508	Missense_Mutation	SNP	G	A	75	160	c.841C>T	c.(841-843)CCT>TCT	p.P281S
Pat_22	Post-Resistance	GPR156	165829	37	3	119886537	119886537	Missense_Mutation	SNP	G	A	26	51	c.1787C>T	c.(1786-1788)CCT>CTT	p.P596L
Pat_22	Post-Resistance	POLQ	10721	37	3	121238898	121238898	Missense_Mutation	SNP	C	T	58	102	c.1288G>A	c.(1288-1290)GGA>AGA	p.G430R
Pat_22	Post-Resistance	SLC15A2	6565	37	3	121641115	121641115	Missense_Mutation	SNP	G	A	48	110	c.746G>A	c.(745-747)GGA>GAA	p.G249E
Pat_22	Post-Resistance	OSBPL11	114885	37	3	125249392	125249392	Nonsense_Mutation	SNP	C	T	11	110	c.2211G>A	c.(2209-2211)TGG>TGA	p.W737*
Pat_22	Post-Resistance	DNAJB8	165721	37	3	128181773	128181773	Missense_Mutation	SNP	C	T	10	91	c.316G>A	c.(316-318)GGC>AGC	p.G106S
Pat_22	Post-Resistance	KIAA1257	57501	37	3	128690150	128690150	Missense_Mutation	SNP	G	A	8	43	c.1148C>T	c.(1147-1149)GCC>GTC	p.A383V
Pat_22	Post-Resistance	LRRC31	79782	37	3	169557925	169557925	Missense_Mutation	SNP	A	G	87	211	c.1504T>C	c.(1504-1506)TTT>CTT	p.F502L
Pat_22	Post-Resistance	MUC4	4585	37	3	195505774	195505774	Missense_Mutation	SNP	G	T	4	21	c.12293C>A	c.(12292-12294)CCT>CAT	p.P4098H
Pat_22	Post-Resistance	PIGZ	80235	37	3	196674974	196674974	Missense_Mutation	SNP	G	A	4	82	c.794C>T	c.(793-795)GCA>GTA	p.A265V
Pat_22	Post-Resistance	DEFB131	644414	37	4	9446290	9446290	Missense_Mutation	SNP	C	T	17	101	c.31C>T	c.(31-33)CTT>TTT	p.L11F
Pat_22	Post-Resistance	SLIT2	9353	37	4	20591326	20591326	Missense_Mutation	SNP	G	A	16	93	c.3148G>A	c.(3148-3150)GAT>AAT	p.D1050N
Pat_22	Post-Resistance	ANAPC4	29945	37	4	25398350	25398350	Missense_Mutation	SNP	T	C	28	91	c.1126T>C	c.(1126-1128)TAT>CAT	p.Y376H
Pat_22	Post-Resistance	CORIN	10699	37	4	47746491	47746491	Missense_Mutation	SNP	A	G	96	490	c.727T>C	c.(727-729)TTT>CTT	p.F243L
Pat_22	Post-Resistance	CWH43	80157	37	4	49063860	49063860	Missense_Mutation	SNP	G	A	4	22	c.2053G>A	c.(2053-2055)GAA>AAA	p.E685K
Pat_22	Post-Resistance	WDFY3	23001	37	4	85678258	85678258	Missense_Mutation	SNP	C	A	6	280	c.5245G>T	c.(5245-5247)GAT>TAT	p.D1749Y
Pat_22	Post-Resistance	PTPN13	5783	37	4	87693999	87693999	Missense_Mutation	SNP	C	T	49	269	c.5237C>T	c.(5236-5238)TCC>TTC	p.S1746F
Pat_22	Post-Resistance	NPNT	255743	37	4	106848493	106848493	Missense_Mutation	SNP	C	T	32	163	c.173C>T	c.(172-174)CCT>CTT	p.P58L
Pat_22	Post-Resistance	SEC24D	9871	37	4	119727108	119727108	Missense_Mutation	SNP	A	G	4	126	c.803T>C	c.(802-804)ATC>ACC	p.I268T
Pat_22	Post-Resistance	BBS7	55212	37	4	122775885	122775885	Missense_Mutation	SNP	T	C	48	276	c.692A>G	c.(691-693)GAA>GGA	p.E231G
Pat_22	Post-Resistance	KIAA1109	84162	37	4	123122189	123122189	Missense_Mutation	SNP	G	A	5	269	c.1406G>A	c.(1405-1407)CGA>CAA	p.R469Q
Pat_22	Post-Resistance	INPP4B	8821	37	4	143094889	143094889	Missense_Mutation	SNP	G	C	171	327	c.1255C>G	c.(1255-1257)CAA>GAA	p.Q419E
Pat_22	Post-Resistance	LRBA	987	37	4	151821300	151821300	Missense_Mutation	SNP	G	A	42	217	c.1825C>T	c.(1825-1827)CGG>TGG	p.R609W
Pat_22	Post-Resistance	ETFDH	2110	37	4	159627861	159627861	Missense_Mutation	SNP	G	A	41	822	c.1549G>A	c.(1549-1551)GAC>AAC	p.D517N
Pat_22	Post-Resistance	ETFDH	2110	37	4	159627900	159627900	Missense_Mutation	SNP	G	A	23	787	c.1588G>A	c.(1588-1590)GAA>AAA	p.E530K
Pat_22	Post-Resistance	ODZ3	55714	37	4	183601472	183601472	Missense_Mutation	SNP	C	T	10	66	c.1609C>T	c.(1609-1611)CCA>TCA	p.P537S

Pat_22	Post-Resistance	LRP2BP	55805	37	4	186294045	186294045	Missense_Mutation	SNP	C	T	23	177	c.768G>A	c.(766-768)ATG>ATA	p.M256I
Pat_22	Post-Resistance	FAT1	2195	37	4	187629958	187629958	Missense_Mutation	SNP	C	T	54	217	c.1024G>A	c.(1024-1026)GGA>AGA	p.G342R
Pat_22	Post-Resistance	EXOC3	11336	37	5	453788	453788	Missense_Mutation	SNP	A	G	29	439	c.668A>G	c.(667-669)GAC>GGC	p.D223G
Pat_22	Post-Resistance	IRX1	79192	37	5	3599780	3599780	Nonsense_Mutation	SNP	C	T	19	56	c.718C>T	c.(718-720)CAG>TAG	p.Q240*
Pat_22	Post-Resistance	KIAA0947	23379	37	5	5461174	5461174	Missense_Mutation	SNP	C	T	36	316	c.1727C>T	c.(1726-1728)CCA>CTA	p.P576L
Pat_22	Post-Resistance	DNAH5	1767	37	5	13721215	13721215	Missense_Mutation	SNP	G	A	30	170	c.12173C>T	c.(12172-12174)TCC>TTC	p.S4058F
Pat_22	Post-Resistance	DNAH5	1767	37	5	13865981	13865981	Missense_Mutation	SNP	G	A	4	147	c.4151C>T	c.(4150-4152)ACA>ATA	p.T1384I
Pat_22	Post-Resistance	TRIO	7204	37	5	14401083	14401083	Missense_Mutation	SNP	G	T	5	111	c.4626G>T	c.(4624-4626)TTG>TTT	p.L1542F
Pat_22	Post-Resistance	FBXL7	23194	37	5	15928355	15928355	Missense_Mutation	SNP	G	A	5	39	c.484G>A	c.(484-486)GAG>AAG	p.E162K
Pat_22	Post-Resistance	PRDM9	56979	37	5	23527052	23527052	Missense_Mutation	SNP	C	T	5	287	c.1855C>T	c.(1855-1857)CGG>TGG	p.R619W
Pat_22	Post-Resistance	CDH9	1007	37	5	26881493	26881493	Missense_Mutation	SNP	C	T	21	157	c.2122G>A	c.(2122-2124)GAA>AAA	p.E708K
Pat_22	Post-Resistance	CDH9	1007	37	5	26902807	26902807	Missense_Mutation	SNP	G	A	9	77	c.1031C>T	c.(1030-1032)ACT>ATT	p.T344I
Pat_22	Post-Resistance	CDH6	1004	37	5	31317546	31317546	Missense_Mutation	SNP	C	T	39	191	c.1577C>T	c.(1576-1578)TCC>TTC	p.S526F
Pat_22	Post-Resistance	NPR3	4883	37	5	32712335	32712335	Missense_Mutation	SNP	C	G	4	110	c.453C>G	c.(451-453)GAC>GAG	p.D151E
Pat_22	Post-Resistance	C9	735	37	5	39315936	39315936	Missense_Mutation	SNP	G	A	12	49	c.811C>T	c.(811-813)CGG>TGG	p.R271W
Pat_22	Post-Resistance	MARVELD2	153562	37	5	68715618	68715618	Missense_Mutation	SNP	C	T	35	149	c.406C>T	c.(406-408)CCC>TCC	p.P136S
Pat_22	Post-Resistance	VCAN	1462	37	5	82833609	82833609	Missense_Mutation	SNP	C	T	21	166	c.4787C>T	c.(4786-4788)TCA>TTA	p.S1596L
Pat_22	Post-Resistance	CCNH	902	37	5	86697554	86697554	Missense_Mutation	SNP	C	T	9	70	c.725G>A	c.(724-726)AGA>AAA	p.R242K
Pat_22	Post-Resistance	TTC37	9652	37	5	94856445	94856445	Missense_Mutation	SNP	C	T	21	168	c.2089G>A	c.(2089-2091)GAA>AAA	p.E697K
Pat_22	Post-Resistance	SLCO4C1	353189	37	5	101572687	101572687	Missense_Mutation	SNP	C	T	26	92	c.2050G>A	c.(2050-2052)GGA>AGA	p.G684R
Pat_22	Post-Resistance	SLC27A6	28965	37	5	128368934	128368934	Missense_Mutation	SNP	G	A	8	104	c.1819G>A	c.(1819-1821)GAA>AAA	p.E607K
Pat_22	Post-Resistance	TRPC7	57113	37	5	135549236	135549236	Missense_Mutation	SNP	C	T	9	97	c.2473G>A	c.(2473-2475)GAA>AAA	p.E825K
Pat_22	Post-Resistance	SPOCK1	6695	37	5	136314511	136314512	Missense_Mutation	DNP	CC	TT	17	71	.1151_1152GG>A	c.(1150-1152)GGG>GAA	p.G384E
Pat_22	Post-Resistance	GFRA3	2676	37	5	137589845	137589845	Missense_Mutation	SNP	G	A	4	137	c.790C>T	c.(790-792)CGC>TGC	p.R264C
Pat_22	Post-Resistance	PCDHB1	29930	37	5	140431953	140431953	Missense_Mutation	SNP	G	A	17	56	c.898G>A	c.(898-900)GAA>AAA	p.E300K
Pat_22	Post-Resistance	PCDHB13	56123	37	5	140596049	140596049	Missense_Mutation	SNP	G	A	34	123	c.2354G>A	c.(2353-2355)GGA>GAA	p.G785E
Pat_22	Post-Resistance	PCDHB14	56122	37	5	140605428	140605428	Missense_Mutation	SNP	G	A	17	139	c.2351G>A	c.(2350-2352)GGG>GAG	p.G784E
Pat_22	Post-Resistance	PCDHGB2	56103	37	5	140740726	140740726	Missense_Mutation	SNP	G	A	23	107	c.1024G>A	c.(1024-1026)GAT>AAT	p.D342N
Pat_22	Post-Resistance	ARAP3	64411	37	5	141059845	141059845	Missense_Mutation	SNP	G	A	36	212	c.209C>T	c.(208-210)TCC>TTC	p.S70F
Pat_22	Post-Resistance	GRXCR2	643226	37	5	145252219	145252219	Missense_Mutation	SNP	C	T	39	235	c.313G>A	c.(313-315)GAT>AAT	p.D105N
Pat_22	Post-Resistance	JAKMIP2	9832	37	5	147030062	147030062	Missense_Mutation	SNP	C	T	10	92	c.676G>A	c.(676-678)GAA>AAA	p.E226K
Pat_22	Post-Resistance	FBXO38	81545	37	5	147807451	147807451	Missense_Mutation	SNP	G	T	4	97	c.2594G>T	c.(2593-2595)CGG>CTG	p.R865L
Pat_22	Post-Resistance	GRIA1	2890	37	5	153190754	153190754	Missense_Mutation	SNP	C	T	19	90	c.2690C>T	c.(2689-2691)TCA>TTA	p.S897L
Pat_22	Post-Resistance	PWWP2A	114825	37	5	159520191	159520191	Missense_Mutation	SNP	G	A	25	60	c.1466C>T	c.(1465-1467)TCT>TTT	p.S489F
Pat_22	Post-Resistance	DOCK2	1794	37	5	169506058	169506058	Missense_Mutation	SNP	G	A	36	202	c.5074G>A	c.(5074-5076)GAG>AAG	p.E1692K
Pat_22	Post-Resistance	MGAT4B	11282	37	5	179227581	179227581	Missense_Mutation	SNP	G	A	3	28	c.622C>T	c.(622-624)CAT>TAT	p.H208Y
Pat_22	Post-Resistance	SLC22A23	63027	37	6	3324095	3324095	Missense_Mutation	SNP	G	A	28	59	c.1055C>T	c.(1054-1056)CCC>CTC	p.P352L
Pat_22	Post-Resistance	CD83	9308	37	6	14131756	14131756	Missense_Mutation	SNP	G	T	4	132	c.159G>T	c.(157-159)TTG>TTT	p.L53F
Pat_22	Post-Resistance	SLC17A1	6568	37	6	25819333	25819333	Missense_Mutation	SNP	A	C	7	51	c.579T>G	c.(577-579)TGT>TGG	p.C193W
Pat_22	Post-Resistance	HLA-DRB5	3127	37	6	32487267	32487267	Nonsense_Mutation	SNP	G	A	91	223	c.532C>T	c.(532-534)CAG>TAG	p.Q178*
Pat_22	Post-Resistance	GLP1R	2740	37	6	39046097	39046097	Splice_Site	SNP	G	A	78	176	c.824_splice	c.e8-1	p.G275_splice
Pat_22	Post-Resistance	MDFI	4188	37	6	41621284	41621284	Missense_Mutation	SNP	G	A	73	243	c.712G>A	c.(712-714)GAG>AAG	p.E238K
Pat_22	Post-Resistance	PKHD1	5314	37	6	51947245	51947245	Missense_Mutation	SNP	G	A	111	379	c.226C>T	c.(226-228)CCC>TCC	p.P76S
Pat_22	Post-Resistance	FAM83B	222584	37	6	54805192	54805192	Missense_Mutation	SNP	C	T	73	294	c.1423C>T	c.(1423-1425)CGC>TGC	p.R475C
Pat_22	Post-Resistance	COL21A1	81578	37	6	56044571	56044571	Missense_Mutation	SNP	C	T	42	142	c.445G>A	c.(445-447)GAT>AAT	p.D149N
Pat_22	Post-Resistance	PHIP	55023	37	6	79700616	79700616	Missense_Mutation	SNP	G	A	20	79	c.2288C>T	c.(2287-2289)CCA>CTA	p.P763L
Pat_22	Post-Resistance	ELOVL4	6785	37	6	80629160	80629160	Nonsense_Mutation	SNP	G	A	30	214	c.646C>T	c.(646-648)CGA>TGA	p.R216*

Pat_22	Post-Resistance	ANKRD6	22881	37	6	90333759	90333759	Missense_Mutation	SNP	G	A	8	45	c.1201G>A	c.(1201-1203)GAT>AAT	p.D401N
Pat_22	Post-Resistance	ASCC3	10973	37	6	101103625	101103625	Missense_Mutation	SNP	G	A	5	308	c.2773C>T	c.(2773-2775)CGG>TGG	p.R925W
Pat_22	Post-Resistance	SCML4	256380	37	6	108071007	108071007	Missense_Mutation	SNP	C	T	4	100	c.167G>A	c.(166-168)CGG>CAG	p.R56Q
Pat_22	Post-Resistance	CDK19	23097	37	6	110935790	110935790	Missense_Mutation	SNP	G	A	16	143	c.1457C>T	c.(1456-1458)TCG>TTG	p.S486L
Pat_22	Post-Resistance	RFX6	222546	37	6	117248471	117248471	Missense_Mutation	SNP	G	A	32	220	c.2167G>A	c.(2167-2169)GAG>AAG	p.E723K
Pat_22	Post-Resistance	VGLL2	245806	37	6	117591810	117591810	Missense_Mutation	SNP	C	T	3	15	c.496C>T	c.(496-498)CAC>TAC	p.H166Y
Pat_22	Post-Resistance	MTHFD1L	25902	37	6	151258056	151258056	Missense_Mutation	SNP	G	A	52	208	c.1373G>A	c.(1372-1374)GGA>GAA	p.G458E
Pat_22	Post-Resistance	FTSJ2	29960	37	7	2274902	2274902	Missense_Mutation	SNP	C	T	22	104	c.596G>A	c.(595-597)AGT>AAT	p.S199N
Pat_22	Post-Resistance	DGKB	1607	37	7	14622749	14622749	Missense_Mutation	SNP	G	A	3	126	c.1450C>T	c.(1450-1452)CGT>TGT	p.R484C
Pat_22	Post-Resistance	ANKMY2	57037	37	7	16655443	16655443	Missense_Mutation	SNP	C	T	17	126	c.457G>A	c.(457-459)GAG>AAG	p.E153K
Pat_22	Post-Resistance	STK31	56164	37	7	23768756	23768756	Missense_Mutation	SNP	G	A	33	151	c.371G>A	c.(370-372)CGA>CAA	p.R124Q
Pat_22	Post-Resistance	GCK	2645	37	7	44228513	44228513	Missense_Mutation	SNP	C	T	6	71	c.40G>A	c.(40-42)GAG>AAG	p.E14K
Pat_22	Post-Resistance	IKZF1	10320	37	7	50450271	50450271	Missense_Mutation	SNP	C	T	4	93	c.455C>T	c.(454-456)GCC>GTC	p.A152V
Pat_22	Post-Resistance	TYW1	55253	37	7	66563692	66563692	Missense_Mutation	SNP	C	T	22	128	c.1549C>T	c.(1549-1551)CCT>TCT	p.P517S
Pat_22	Post-Resistance	GTPBP10	85865	37	7	90014367	90014367	Missense_Mutation	SNP	C	T	73	261	c.1063C>T	c.(1063-1065)CAT>TAT	p.H355Y
Pat_22	Post-Resistance	SAMD9L	219285	37	7	92762458	92762458	Missense_Mutation	SNP	C	T	6	68	c.2827G>A	c.(2827-2829)GAA>AAA	p.E943K
Pat_22	Post-Resistance	COL1A2	1278	37	7	94028379	94028379	Missense_Mutation	SNP	G	A	23	232	c.115G>A	c.(115-117)GGA>AGA	p.G39R
Pat_22	Post-Resistance	CYP3A4	1576	37	7	99366124	99366124	Missense_Mutation	SNP	C	T	41	262	c.523G>A	c.(523-525)GTC>ATC	p.V175I
Pat_22	Post-Resistance	PPP1R3A	5506	37	7	113558463	113558463	Missense_Mutation	SNP	G	A	35	125	c.589C>T	c.(589-591)CCT>TCT	p.P197S
Pat_22	Post-Resistance	C7orf58	79974	37	7	120740101	120740101	Missense_Mutation	SNP	A	G	26	170	c.871A>G	c.(871-873)ACG>GCG	p.T291A
Pat_22	Post-Resistance	BRAF	673	37	7	140453136	140453136	Missense_Mutation	SNP	A	T	394	190	c.1799T>A	c.(1798-1800)GTG>GAG	p.V600E
Pat_22	Post-Resistance	TAS2R60	338398	37	7	143141207	143141207	Missense_Mutation	SNP	G	A	120	181	c.662G>A	c.(661-663)GGA>GAA	p.G221E
Pat_22	Post-Resistance	ZNF786	136051	37	7	148768111	148768111	Missense_Mutation	SNP	G	A	4	118	c.1753C>T	c.(1753-1755)CGC>TGC	p.R585C
Pat_22	Post-Resistance	ACTR3C	653857	37	7	149983565	149983566	Missense_Mutation	DNP	TG	CA	42	131	c.361_362CA>TG	c.(361-363)CAG>TGG	p.Q121W
Pat_22	Post-Resistance	C7orf29	113763	37	7	150027766	150027766	Nonsense_Mutation	SNP	G	A	113	137	c.273G>A	c.(271-273)TGG>TGA	p.W91*
Pat_22	Post-Resistance	CSMD1	64478	37	8	2965315	2965315	Nonsense_Mutation	SNP	G	A	31	140	c.6763C>T	c.(6763-6765)CAG>TAG	p.Q2255*
Pat_22	Post-Resistance	SH2D4A	63898	37	8	19221663	19221663	Missense_Mutation	SNP	G	A	5	101	c.787G>A	c.(787-789)GGG>AGG	p.G263R
Pat_22	Post-Resistance	SCARA3	51435	37	8	27509049	27509049	Missense_Mutation	SNP	G	A	4	77	c.131G>A	c.(130-132)CGC>CAC	p.R44H
Pat_22	Post-Resistance	RP1	6101	37	8	55533900	55533900	Missense_Mutation	SNP	G	A	27	133	c.374G>A	c.(373-375)CGG>CAG	p.R125Q
Pat_22	Post-Resistance	JPH1	56704	37	8	75227798	75227798	Missense_Mutation	SNP	C	G	15	101	c.437G>C	c.(436-438)AGC>ACC	p.S146T
Pat_22	Post-Resistance	SLC7A13	157724	37	8	87241932	87241932	Missense_Mutation	SNP	C	T	215	161	c.575G>A	c.(574-576)CGA>CAA	p.R192Q
Pat_22	Post-Resistance	RBM12B	389677	37	8	94747846	94747846	Nonsense_Mutation	SNP	G	A	29	292	c.793C>T	c.(793-795)CGA>TGA	p.R265*
Pat_22	Post-Resistance	POP1	10940	37	8	99146777	99146777	Missense_Mutation	SNP	C	T	14	190	c.901C>T	c.(901-903)CCC>TCC	p.P301S
Pat_22	Post-Resistance	ABRA	137735	37	8	107781965	107781965	Missense_Mutation	SNP	G	A	55	559	c.454C>T	c.(454-456)CAC>TAC	p.H152Y
Pat_22	Post-Resistance	ENPP2	5168	37	8	120613682	120613682	Missense_Mutation	SNP	C	T	47	463	c.854G>A	c.(853-855)AGA>AAA	p.R285K
Pat_22	Post-Resistance	MTBP	27085	37	8	121528398	121528398	Missense_Mutation	SNP	C	T	4	97	c.2213C>T	c.(2212-2214)TCT>TTT	p.S738F
Pat_22	Post-Resistance	KIAA0196	9897	37	8	126051070	126051070	Splice_Site	SNP	A	G	173	207	c.3084_splice	c.e25+1	p.K1028_splice
Pat_22	Post-Resistance	LRRC6	23639	37	8	133637582	133637582	Missense_Mutation	SNP	G	A	47	61	c.772C>T	c.(772-774)CCT>TCT	p.P258S
Pat_22	Post-Resistance	SHARPIN	81858	37	8	145154852	145154852	Missense_Mutation	SNP	G	A	39	37	c.497C>T	c.(496-498)CCT>CTT	p.P166L
Pat_22	Post-Resistance	C9orf66	157983	37	9	214556	214556	Missense_Mutation	SNP	C	T	40	149	c.841G>A	c.(841-843)GAG>AAG	p.E281K
Pat_22	Post-Resistance	CDC37L1	55664	37	9	4679813	4679813	Missense_Mutation	SNP	G	C	3	80	c.46G>C	c.(46-48)GCC>CCC	p.A16P
Pat_22	Post-Resistance	RANBP6	26953	37	9	6012811	6012811	Missense_Mutation	SNP	C	A	4	139	c.2797G>T	c.(2797-2799)GCT>TCT	p.A933S
Pat_22	Post-Resistance	PTPRD	5789	37	9	8500886	8500886	Missense_Mutation	SNP	G	A	221	316	c.1996C>T	c.(1996-1998)CCT>TCT	p.P666S
Pat_22	Post-Resistance	IFNA21	3452	37	9	21166224	21166224	Missense_Mutation	SNP	C	T	210	341	c.388G>A	c.(388-390)GAA>AAA	p.E130K
Pat_22	Post-Resistance	TMEM215	401498	37	9	32784875	32784875	Missense_Mutation	SNP	G	A	5	234	c.694G>A	c.(694-696)GAG>AAG	p.E232K
Pat_22	Post-Resistance	CDK20	23552	37	9	90586181	90586182	Missense_Mutation	DNP	CC	TT	20	86	c.258_259GG>AA	(256-261)TCGGAT>TCAA	p.D87N
Pat_22	Post-Resistance	HABP4	22927	37	9	99250477	99250477	Missense_Mutation	SNP	G	A	5	205	c.1106G>A	c.(1105-1107)CGT>CAT	p.R369H

Pat_22	Post-Resistance	ALDOB	229	37	9	104190778	104190778	Missense_Mutation	SNP	C	T	39	283	c.352G>A	c.(352-354)GGA>AGA	p.G118R
Pat_22	Post-Resistance	PHF19	26147	37	9	123636851	123636851	Missense_Mutation	SNP	G	A	75	194	c.169C>T	c.(169-171)CTC>TTC	p.L57F
Pat_22	Post-Resistance	PDCL	5082	37	9	125582834	125582834	Missense_Mutation	SNP	C	T	36	173	c.436G>A	c.(436-438)GAA>AAA	p.E146K
Pat_22	Post-Resistance	RPL12	6136	37	9	130211903	130211903	Missense_Mutation	SNP	T	C	3	128	c.196A>G	c.(196-198)AAC>GAC	p.N66D
Pat_22	Post-Resistance	ACE2	59272	37	X	15596407	15596407	Missense_Mutation	SNP	C	T	41	142	c.1102G>A	c.(1102-1104)GAC>AAC	p.D368N
Pat_22	Post-Resistance	BEND2	139105	37	X	18219991	18219991	Missense_Mutation	SNP	C	T	66	200	c.977G>A	c.(976-978)GGA>GAA	p.G326E
Pat_22	Post-Resistance	MAP7D2	256714	37	X	20062607	20062607	Missense_Mutation	SNP	G	A	49	297	c.631C>T	c.(631-633)CCT>TCT	p.P211S
Pat_22	Post-Resistance	KLHL34	257240	37	X	21674138	21674138	Missense_Mutation	SNP	C	T	3	53	c.1769G>A	c.(1768-1770)CGC>CAC	p.R590H
Pat_22	Post-Resistance	FAM47C	442444	37	X	37029119	37029119	Missense_Mutation	SNP	G	A	46	195	c.2636G>A	c.(2635-2637)AGA>AAA	p.R879K
Pat_22	Post-Resistance	FAM123B	139285	37	X	63410913	63410913	Missense_Mutation	SNP	C	T	26	63	c.2254G>A	c.(2254-2256)GAA>AAA	p.E752K
Pat_22	Post-Resistance	RLIM	51132	37	X	73812068	73812068	Missense_Mutation	SNP	C	T	98	194	c.1082G>A	c.(1081-1083)GGA>GAA	p.G361E
Pat_22	Post-Resistance	SERPINA7	6906	37	X	105278344	105278344	Missense_Mutation	SNP	G	A	25	166	c.926C>T	c.(925-927)TCC>TTC	p.S309F
Pat_22	Post-Resistance	TBC1D8B	54885	37	X	106109164	106109164	Missense_Mutation	SNP	C	T	173	433	c.2563C>T	c.(2563-2565)CAT>TAT	p.H855Y
Pat_22	Post-Resistance	ALG13	79868	37	X	111003208	111003208	Missense_Mutation	SNP	A	T	4	125	c.3395A>T	c.(3394-3396)TAT>TTT	p.Y1132F
Pat_22	Post-Resistance	DOCK11	139818	37	X	117752516	117752516	Missense_Mutation	SNP	C	T	69	199	c.3296C>T	c.(3295-3297)TCA>TTA	p.S1099L
Pat_22	Post-Resistance	SLC25A5	292	37	X	118603691	118603691	Missense_Mutation	SNP	G	A	8	745	c.179G>A	c.(178-180)CGT>CAT	p.R60H
Pat_22	Post-Resistance	ACTRT1	139741	37	X	127185237	127185237	Missense_Mutation	SNP	C	T	54	142	c.949G>A	c.(949-951)GAA>AAA	p.E317K
Pat_22	Post-Resistance	XPNPEP2	7512	37	X	128881600	128881600	Missense_Mutation	SNP	G	A	20	147	c.508G>A	c.(508-510)GAT>AAT	p.D170N
Pat_22	Post-Resistance	ZNF449	203523	37	X	134494528	134494528	Missense_Mutation	SNP	C	T	26	215	c.1084C>T	c.(1084-1086)CGT>TGT	p.R362C
Pat_22	Post-Resistance	ATP11C	286410	37	X	138856954	138856954	Missense_Mutation	SNP	G	A	43	294	c.2120C>T	c.(2119-2121)ACC>ATC	p.T707I
Pat_22	Post-Resistance	MAGEC1	9947	37	X	140993455	140993455	Missense_Mutation	SNP	G	A	6	272	c.265G>A	c.(265-267)GGC>AGC	p.G89S
Pat_22	Post-Resistance	AFF2	2334	37	X	147743727	147743727	Nonsense_Mutation	SNP	C	A	84	586	c.479C>A	c.(478-480)TCA>TAA	p.S160*
Pat_22	Post-Resistance	FLNA	2316	37	X	153594547	153594547	Missense_Mutation	SNP	C	T	10	175	c.1274G>A	c.(1273-1275)GGA>GAA	p.G425E
Pat_22	Post-Resistance	DKC1	1736	37	X	153994523	153994523	Missense_Mutation	SNP	A	G	28	250	c.296A>G	c.(295-297)AAC>AGC	p.N99S
Pat_22	Post-Resistance	RAB39B	116442	37	X	154490289	154490289	Missense_Mutation	SNP	C	T	7	245	c.441G>A	c.(439-441)ATG>ATA	p.M147I
Pat_22	Post-Resistance	RAB39B	116442	37	X	154493417	154493417	Missense_Mutation	SNP	C	T	24	387	c.157G>A	c.(157-159)GAG>AAG	p.E53K
Pat_24	Pre-Treatment	NOC2L	26155	37	1	883917	883917	Missense_Mutation	SNP	C	T	4	144	c.1510G>A	c.(1510-1512)GTG>ATG	p.V504M
Pat_24	Pre-Treatment	NOC2L	26155	37	1	889226	889226	Missense_Mutation	SNP	C	T	4	80	c.824G>A	c.(823-825)CGG>CAG	p.R275Q
Pat_24	Pre-Treatment	AGRN	375790	37	1	981567	981567	Missense_Mutation	SNP	G	A	6	371	c.2833G>A	c.(2833-2835)GGC>AGC	p.G945S
Pat_24	Pre-Treatment	CALML6	163688	37	1	1848504	1848504	Missense_Mutation	SNP	G	A	4	38	c.490G>A	c.(490-492)GAC>AAC	p.D164N
Pat_24	Pre-Treatment	KIAA1751	85452	37	1	1887145	1887145	Missense_Mutation	SNP	C	T	44	74	c.2161G>A	c.(2161-2163)GAG>AAG	p.E721K
Pat_24	Pre-Treatment	MEGF6	1953	37	1	3424398	3424398	Missense_Mutation	SNP	G	A	6	234	c.1750C>T	c.(1750-1752)CGC>TGC	p.R584C
Pat_24	Pre-Treatment	CAMTA1	23261	37	1	7723494	7723494	Missense_Mutation	SNP	G	A	6	479	c.887G>A	c.(886-888)GGG>GAG	p.G296E
Pat_24	Pre-Treatment	CA6	765	37	1	9009433	9009433	Missense_Mutation	SNP	A	G	3	76	c.191A>G	c.(190-192)AAG>AGG	p.K64R
Pat_24	Pre-Treatment	UBE4B	10277	37	1	10163069	10163069	Missense_Mutation	SNP	C	T	4	135	c.499C>T	c.(499-501)CGT>TGT	p.R167C
Pat_24	Pre-Treatment	KIF1B	23095	37	1	10386389	10386389	Nonsense_Mutation	SNP	C	T	4	103	c.2896C>T	c.(2896-2898)CGA>TGA	p.R966*
Pat_24	Pre-Treatment	MASP2	10747	37	1	11087664	11087664	Missense_Mutation	SNP	C	T	46	93	c.1339G>A	c.(1339-1341)GGA>AGA	p.G447R
Pat_24	Pre-Treatment	MFN2	9927	37	1	12059138	12059138	Missense_Mutation	SNP	G	A	4	185	c.802G>A	c.(802-804)GAG>AAG	p.E268K
Pat_24	Pre-Treatment	TNFRSF8	943	37	1	12170154	12170154	Missense_Mutation	SNP	G	A	4	175	c.569G>A	c.(568-570)AGC>AAC	p.S190N
Pat_24	Pre-Treatment	VPS13D	55187	37	1	12337906	12337906	Missense_Mutation	SNP	C	T	4	215	c.4261C>T	c.(4261-4263)CGT>TGT	p.R1421C
Pat_24	Pre-Treatment	VPS13D	55187	37	1	12463904	12463904	Missense_Mutation	SNP	C	T	42	78	c.11908C>T	c.(11908-11910)CAT>TAT	p.H3970Y
Pat_24	Pre-Treatment	PRAMEF12	390999	37	1	12837729	12837729	Missense_Mutation	SNP	G	A	39	77	c.1439G>A	c.(1438-1440)GGT>GAT	p.G480D
Pat_24	Pre-Treatment	PRAMEF1	65121	37	1	12856002	12856002	Missense_Mutation	SNP	G	A	52	402	c.1282G>A	c.(1282-1284)GAG>AAG	p.E428K
Pat_24	Pre-Treatment	LOC440563	440563	37	1	13183494	13183494	Missense_Mutation	SNP	G	A	16	111	c.379C>T	c.(379-381)CCA>TCA	p.P127S
Pat_24	Pre-Treatment	ZBTB17	7709	37	1	16269047	16269047	Missense_Mutation	SNP	G	A	4	243	c.2015C>T	c.(2014-2016)GCG>GTG	p.A672V
Pat_24	Pre-Treatment	ARHGEF19	128272	37	1	16535275	16535275	Missense_Mutation	SNP	C	T	23	24	c.275G>A	c.(274-276)GGG>GAG	p.G92E
Pat_24	Pre-Treatment	ATP13A2	23400	37	1	17318253	17318253	Missense_Mutation	SNP	G	A	5	215	c.2227C>T	c.(2227-2229)CGC>TGC	p.R743C

Pat_24	Pre-Treatment	IGSF21	84966	37	1	18702857	18702857	Missense_Mutation	SNP	G	A	131	240	c.1069G>A	c.(1069-1071)GAC>AAC	p.D357N
Pat_24	Pre-Treatment	UBR4	23352	37	1	19480265	19480266	Missense_Mutation	DNP	CG	TA	4	157	.6626_6627CG>T	c.(6625-6627)GCG>GTA	p.A2209V
Pat_24	Pre-Treatment	UBR4	23352	37	1	19490771	19490771	Missense_Mutation	SNP	G	A	4	104	c.4676C>T	c.(4675-4677)GCT>GTT	p.A1559V
Pat_24	Pre-Treatment	PQLC2	54896	37	1	19651203	19651203	Missense_Mutation	SNP	G	A	4	63	c.241G>A	c.(241-243)GGA>AGA	p.G81R
Pat_24	Pre-Treatment	TMCO4	255104	37	1	20027300	20027300	Missense_Mutation	SNP	C	T	6	268	c.1343G>A	c.(1342-1344)CGG>CAG	p.R448Q
Pat_24	Pre-Treatment	PLA2G2A	5320	37	1	20302261	20302261	Missense_Mutation	SNP	G	A	4	118	c.368C>T	c.(367-369)ACG>ATG	p.T123M
Pat_24	Pre-Treatment	PLA2G2A	5320	37	1	20304963	20304963	Missense_Mutation	SNP	G	A	4	99	c.95C>T	c.(94-96)ACG>ATG	p.T32M
Pat_24	Pre-Treatment	HSPG2	3339	37	1	22168731	22168731	Splice_Site	SNP	C	T	4	138	c.9052_splice	c.e68+1	p.R3018_splice
Pat_24	Pre-Treatment	KDM1A	23028	37	1	23399805	23399805	Missense_Mutation	SNP	G	A	53	112	c.1571G>A	c.(1570-1572)AGA>AAA	p.R524K
Pat_24	Pre-Treatment	ASAP3	55616	37	1	23763960	23763960	Missense_Mutation	SNP	G	A	4	180	c.1108C>T	c.(1108-1110)CGG>TGG	p.R370W
Pat_24	Pre-Treatment	E2F2	1870	37	1	23848359	23848359	Missense_Mutation	SNP	C	T	4	183	c.548G>A	c.(547-549)CGC>CAC	p.R183H
Pat_24	Pre-Treatment	GRHL3	57822	37	1	24669436	24669436	Missense_Mutation	SNP	G	A	5	357	c.1355G>A	c.(1354-1356)CGG>CAG	p.R452Q
Pat_24	Pre-Treatment	CNKSR1	10256	37	1	26504045	26504045	Missense_Mutation	SNP	C	T	38	75	c.7C>T	c.(7-9)CCG>TCG	p.P3S
Pat_24	Pre-Treatment	WDTC1	23038	37	1	27624562	27624562	Missense_Mutation	SNP	C	T	4	201	c.1192C>T	c.(1192-1194)CTT>TTT	p.L398F
Pat_24	Pre-Treatment	GPR3	2827	37	1	27720960	27720960	Missense_Mutation	SNP	G	A	4	167	c.658G>A	c.(658-660)GTC>ATC	p.V220I
Pat_24	Pre-Treatment	MATN1	4146	37	1	31194293	31194293	Missense_Mutation	SNP	C	T	6	397	c.400G>A	c.(400-402)GAT>AAT	p.D134N
Pat_24	Pre-Treatment	NKAIN1	79570	37	1	31655401	31655401	Missense_Mutation	SNP	C	A	105	160	c.508G>T	c.(508-510)GTG>TTG	p.V170L
Pat_24	Pre-Treatment	COL16A1	1307	37	1	32163665	32163665	Missense_Mutation	SNP	G	A	5	93	c.499C>T	c.(499-501)CGT>TGT	p.R167C
Pat_24	Pre-Treatment	BAI2	576	37	1	32204495	32204495	Missense_Mutation	SNP	G	A	5	284	c.2539C>T	c.(2539-2541)CGC>TGC	p.R847C
Pat_24	Pre-Treatment	SPOCD1	90853	37	1	32262229	32262229	Missense_Mutation	SNP	G	A	6	421	c.2233C>T	c.(2233-2235)CGG>TGG	p.R745W
Pat_24	Pre-Treatment	TRIM62	55223	37	1	33613004	33613004	Missense_Mutation	SNP	G	A	4	174	c.1202C>T	c.(1201-1203)ACG>ATG	p.T401M
Pat_24	Pre-Treatment	TRIM62	55223	37	1	33625416	33625416	Missense_Mutation	SNP	C	T	5	277	c.634G>A	c.(634-636)GAG>AAG	p.E212K
Pat_24	Pre-Treatment	C1orf94	84970	37	1	34663095	34663095	Missense_Mutation	SNP	G	A	85	143	c.20G>A	c.(19-21)AGG>AAG	p.R7K
Pat_24	Pre-Treatment	EPHA10	284656	37	1	38227437	38227437	Missense_Mutation	SNP	C	T	22	48	c.490G>A	c.(490-492)GGC>AGC	p.G164S
Pat_24	Pre-Treatment	UTP11L	51118	37	1	38488443	38488443	Missense_Mutation	SNP	G	A	4	110	c.640G>A	c.(640-642)GTT>ATT	p.V214I
Pat_24	Pre-Treatment	MACF1	23499	37	1	39751063	39751063	Splice_Site	SNP	G	A	4	186	c.1368_splice	c.e14+1	p.A456_splice
Pat_24	Pre-Treatment	KIAA0754	643314	37	1	39879016	39879016	Missense_Mutation	SNP	A	G	3	61	c.3079A>G	c.(3079-3081)ACC>GCC	p.T1027A
Pat_24	Pre-Treatment	CCDC30	728621	37	1	43011243	43011243	Missense_Mutation	SNP	G	A	29	57	c.418G>A	c.(418-420)GAA>AAA	p.E140K
Pat_24	Pre-Treatment	TIE1	7075	37	1	43782919	43782919	Missense_Mutation	SNP	G	A	4	191	c.2459G>A	c.(2458-2460)CGG>CAG	p.R820Q
Pat_24	Pre-Treatment	KIAA0467	23334	37	1	43893309	43893309	Missense_Mutation	SNP	G	A	4	241	c.1010G>A	c.(1009-1011)CGG>CAG	p.R337Q
Pat_24	Pre-Treatment	KIAA0467	23334	37	1	43909464	43909464	Missense_Mutation	SNP	G	A	5	201	c.6125G>A	c.(6124-6126)CGC>CAC	p.R2042H
Pat_24	Pre-Treatment	SLC6A9	6536	37	1	44474289	44474289	Missense_Mutation	SNP	C	T	16	20	c.545G>A	c.(544-546)GGC>GAC	p.G182D
Pat_24	Pre-Treatment	DMAP1	55929	37	1	44680523	44680523	Missense_Mutation	SNP	C	T	4	167	c.346C>T	c.(346-348)CGT>TGT	p.R116C
Pat_24	Pre-Treatment	CYP4B1	1580	37	1	47283696	47283696	Missense_Mutation	SNP	C	T	90	120	c.1264C>T	c.(1264-1266)CCT>TCT	p.P422S
Pat_24	Pre-Treatment	CYP4A22	284541	37	1	47607897	47607897	Missense_Mutation	SNP	G	A	20	69	c.500G>A	c.(499-501)CGA>CAA	p.R167Q
Pat_24	Pre-Treatment	TAL1	6886	37	1	47685757	47685757	Missense_Mutation	SNP	G	A	76	114	c.631C>T	c.(631-633)CGC>TGC	p.R211C
Pat_24	Pre-Treatment	ELAVL4	1996	37	1	50610750	50610750	Missense_Mutation	SNP	G	A	5	197	c.131G>A	c.(130-132)AGC>AAC	p.S44N
Pat_24	Pre-Treatment	PODN	127435	37	1	53544158	53544158	Missense_Mutation	SNP	G	A	4	62	c.1120G>A	c.(1120-1122)GCG>ACG	p.A374T
Pat_24	Pre-Treatment	GLIS1	148979	37	1	53995598	53995598	Missense_Mutation	SNP	G	A	4	82	c.823C>T	c.(823-825)CGG>TGG	p.R275W
Pat_24	Pre-Treatment	ACOT11	26027	37	1	55065066	55065066	Missense_Mutation	SNP	G	A	6	541	c.862G>A	c.(862-864)GTG>ATG	p.V288M
Pat_24	Pre-Treatment	PARS2	25973	37	1	55224437	55224437	Missense_Mutation	SNP	C	T	5	382	c.398G>A	c.(397-399)CGG>CAG	p.R133Q
Pat_24	Pre-Treatment	JAK1	3716	37	1	65335121	65335121	Nonsense_Mutation	SNP	G	A	4	123	c.520C>T	c.(520-522)CGA>TGA	p.R174*
Pat_24	Pre-Treatment	C1orf173	127254	37	1	75065480	75065480	Missense_Mutation	SNP	T	C	50	127	c.1625A>G	c.(1624-1626)AAA>AGA	p.K542R
Pat_24	Pre-Treatment	C1orf173	127254	37	1	75072303	75072303	Missense_Mutation	SNP	C	T	71	87	c.1471G>A	c.(1471-1473)GAA>AAA	p.E491K
Pat_24	Pre-Treatment	BCL10	8915	37	1	85742019	85742019	Missense_Mutation	SNP	G	A	4	166	c.17C>T	c.(16-18)CCG>CTG	p.P6L
Pat_24	Pre-Treatment	GBP2	2634	37	1	89578223	89578223	Missense_Mutation	SNP	G	A	6	413	c.1294C>T	c.(1294-1296)CGT>TGT	p.R432C
Pat_24	Pre-Treatment	ABCA4	24	37	1	94497348	94497348	Missense_Mutation	SNP	C	T	48	63	c.4114G>A	c.(4114-4116)GAC>AAC	p.D1372N

Pat_24	Pre-Treatment	ARHGAP29	9411	37	1	94655584	94655584	Missense_Mutation	SNP	C	T	4	100	c.1337G>A	c.(1336-1338)AGT>AAT	p.S446N
Pat_24	Pre-Treatment	CNN3	1266	37	1	95363578	95363578	Missense_Mutation	SNP	G	A	6	331	c.710C>T	c.(709-711)CCG>CTG	p.P237L
Pat_24	Pre-Treatment	OLFM3	118427	37	1	102312505	102312505	Missense_Mutation	SNP	C	T	40	96	c.25G>A	c.(25-27)GGC>AGC	p.G9S
Pat_24	Pre-Treatment	COL11A1	1301	37	1	103427784	103427784	Missense_Mutation	SNP	C	T	45	104	c.3062G>A	c.(3061-3063)GGA>GAA	p.G1021E
Pat_24	Pre-Treatment	KIAA1324	57535	37	1	109741247	109741247	Missense_Mutation	SNP	G	A	4	107	c.2452G>A	c.(2452-2454)GTC>ATC	p.V818I
Pat_24	Pre-Treatment	CHI3L2	1117	37	1	111781480	111781480	Missense_Mutation	SNP	G	A	8	327	c.844G>A	c.(844-846)GTG>ATG	p.V282M
Pat_24	Pre-Treatment	MAN1A2	10905	37	1	118008992	118008992	Missense_Mutation	SNP	C	T	20	57	c.1111C>T	c.(1111-1113)CGT>TGT	p.R371C
Pat_24	Pre-Treatment	GDAP2	54834	37	1	118462964	118462964	Missense_Mutation	SNP	G	A	5	103	c.17C>T	c.(16-18)GCA>GTA	p.A6V
Pat_24	Pre-Treatment	ZNF697	90874	37	1	120166548	120166548	Missense_Mutation	SNP	C	T	4	8	c.418G>A	c.(418-420)GTA>ATA	p.V140I
Pat_24	Pre-Treatment	NBPF7	343505	37	1	120387026	120387026	Missense_Mutation	SNP	G	A	5	235	c.133C>T	c.(133-135)CGC>TGC	p.R45C
Pat_24	Pre-Treatment	NOTCH2	4853	37	1	120506280	120506280	Missense_Mutation	SNP	C	T	7	418	c.1832G>A	c.(1831-1833)TGT>TAT	p.C611Y
Pat_24	Pre-Treatment	PPIAL4G	644591	37	1	143767640	143767640	Missense_Mutation	SNP	G	A	10	563	c.209C>T	c.(208-210)CCT>CTT	p.P70L
Pat_24	Pre-Treatment	NBPF9	400818	37	1	144815950	144815950	Missense_Mutation	SNP	G	C	5	352	c.1321G>C	c.(1321-1323)GAC>CAC	p.D441H
Pat_24	Pre-Treatment	HFE2	148738	37	1	145416650	145416650	Missense_Mutation	SNP	G	A	6	130	c.995G>A	c.(994-996)CGC>CAC	p.R332H
Pat_24	Pre-Treatment	NBPF15	284565	37	1	148591264	148591264	Missense_Mutation	SNP	T	G	9	213	c.1329T>G	c.(1327-1329)TGT>TGG	p.C443W
Pat_24	Pre-Treatment	ARNT	405	37	1	150786615	150786615	Missense_Mutation	SNP	G	A	7	395	c.2051C>T	c.(2050-2052)GCC>GTC	p.A684V
Pat_24	Pre-Treatment	ARNT	405	37	1	150807020	150807020	Missense_Mutation	SNP	C	T	6	332	c.797G>A	c.(796-798)CGA>CAA	p.R266Q
Pat_24	Pre-Treatment	FLG	2312	37	1	152281475	152281475	Missense_Mutation	SNP	C	T	187	486	c.5887G>A	c.(5887-5889)GAC>AAC	p.D1963N
Pat_24	Pre-Treatment	SPRR3	6707	37	1	152975642	152975642	Missense_Mutation	SNP	G	A	26	41	c.146G>A	c.(145-147)GGA>GAA	p.G49E
Pat_24	Pre-Treatment	NPR1	4881	37	1	153660175	153660175	Missense_Mutation	SNP	G	A	5	250	c.2158G>A	c.(2158-2160)GGT>AGT	p.G720S
Pat_24	Pre-Treatment	GATAD2B	57459	37	1	153788964	153788964	Missense_Mutation	SNP	G	A	5	137	c.1001C>T	c.(1000-1002)TCG>TTG	p.S334L
Pat_24	Pre-Treatment	FLAD1	80308	37	1	154965460	154965460	Missense_Mutation	SNP	C	T	4	218	c.1711C>T	c.(1711-1713)CGT>TGT	p.R571C
Pat_24	Pre-Treatment	THBS3	7059	37	1	155172066	155172066	Missense_Mutation	SNP	G	A	5	272	c.1084C>T	c.(1084-1086)CGG>TGG	p.R362W
Pat_24	Pre-Treatment	RUSC1	23623	37	1	155292183	155292183	Missense_Mutation	SNP	C	T	4	83	c.619C>T	c.(619-621)CTC>TTC	p.L207F
Pat_24	Pre-Treatment	GON4L	54856	37	1	155734847	155734847	Missense_Mutation	SNP	C	T	5	97	c.4417G>A	c.(4417-4419)GAA>AAA	p.E1473K
Pat_24	Pre-Treatment	LMNA	4000	37	1	156105026	156105026	Missense_Mutation	SNP	G	A	4	161	c.859G>A	c.(859-861)GCT>ACT	p.A287T
Pat_24	Pre-Treatment	NTRK1	4914	37	1	156849018	156849018	Missense_Mutation	SNP	G	A	28	26	c.1910G>A	c.(1909-1911)GGG>GAG	p.G637E
Pat_24	Pre-Treatment	PEAR1	375033	37	1	156882753	156882753	Missense_Mutation	SNP	G	A	4	162	c.2401G>A	c.(2401-2403)GGC>AGC	p.G801S
Pat_24	Pre-Treatment	FCRL5	83416	37	1	157490858	157490858	Missense_Mutation	SNP	C	T	4	165	c.2464G>A	c.(2464-2466)GAC>AAC	p.D822N
Pat_24	Pre-Treatment	SPTA1	6708	37	1	158615148	158615148	Missense_Mutation	SNP	C	T	4	74	c.4024G>A	c.(4024-4026)GCT>ACT	p.A1342T
Pat_24	Pre-Treatment	HSPA7	3311	37	1	161577111	161577111	Missense_Mutation	SNP	C	T	5	107	c.1031C>T	c.(1030-1032)TCG>TTG	p.S344L
Pat_24	Pre-Treatment	POGK	57645	37	1	166819237	166819237	Missense_Mutation	SNP	G	A	4	203	c.1421G>A	c.(1420-1422)CGG>CAG	p.R474Q
Pat_24	Pre-Treatment	XCL1	6375	37	1	168549354	168549354	Nonsense_Mutation	SNP	C	T	5	346	c.115C>T	c.(115-117)CGA>TGA	p.R39*
Pat_24	Pre-Treatment	TNN	63923	37	1	175066678	175066678	Missense_Mutation	SNP	G	A	46	111	c.1714G>A	c.(1714-1716)GAG>AAG	p.E572K
Pat_24	Pre-Treatment	FAM5B	57795	37	1	177247738	177247738	Missense_Mutation	SNP	G	A	7	738	c.1052G>A	c.(1051-1053)CGG>CAG	p.R351Q
Pat_24	Pre-Treatment	ANGPTL1	9068	37	1	178834455	178834455	Missense_Mutation	SNP	G	T	4	72	c.457C>A	c.(457-459)CAA>AAA	p.Q153K
Pat_24	Pre-Treatment	PDC	5132	37	1	186418565	186418565	Missense_Mutation	SNP	C	A	5	220	c.27G>T	c.(25-27)TTG>TTT	p.L9F
Pat_24	Pre-Treatment	CRB1	23418	37	1	197446956	197446956	Nonsense_Mutation	SNP	C	T	4	224	c.4168C>T	c.(4168-4170)CGA>TGA	p.R1390*
Pat_24	Pre-Treatment	KIF14	9928	37	1	200574423	200574423	Missense_Mutation	SNP	C	T	7	130	c.1734G>A	c.(1732-1734)ATG>ATA	p.M578I
Pat_24	Pre-Treatment	KIF21B	23046	37	1	200960046	200960046	Nonsense_Mutation	SNP	G	A	4	206	c.2686C>T	c.(2686-2688)CGA>TGA	p.R896*
Pat_24	Pre-Treatment	PPFIA4	8497	37	1	203014674	203014674	Missense_Mutation	SNP	G	A	4	29	c.1286G>A	c.(1285-1287)CGG>CAG	p.R429Q
Pat_24	Pre-Treatment	PLEKHA6	22874	37	1	204210881	204210881	Missense_Mutation	SNP	G	A	107	72	c.2234C>T	c.(2233-2235)CCC>CTC	p.P745L
Pat_24	Pre-Treatment	RBBP5	5929	37	1	205070737	205070737	Missense_Mutation	SNP	C	T	6	636	c.623G>A	c.(622-624)CGG>CAG	p.R208Q
Pat_24	Pre-Treatment	TMCC2	9911	37	1	205211123	205211123	Missense_Mutation	SNP	G	A	4	168	c.698G>A	c.(697-699)GGC>GAC	p.G233D
Pat_24	Pre-Treatment	CR1L	1379	37	1	207857221	207857221	Nonsense_Mutation	SNP	C	T	4	206	c.382C>T	c.(382-384)CGA>TGA	p.R128*
Pat_24	Pre-Treatment	PLXNA2	5362	37	1	208204972	208204972	Missense_Mutation	SNP	G	A	96	152	c.5188C>T	c.(5188-5190)CAT>TAT	p.H1730Y
Pat_24	Pre-Treatment	CENPF	1063	37	1	214803896	214803896	Missense_Mutation	SNP	G	A	6	446	c.1214G>A	c.(1213-1215)CGT>CAT	p.R405H

Pat_24	Pre-Treatment	USH2A	7399	37	1	215847856	215847856	Missense_Mutation	SNP	G	A	4	155	c.13397C>T	c.(13396-13398)CCT>CTT	p.P4466L
Pat_24	Pre-Treatment	SPATA17	128153	37	1	217955597	217955597	Missense_Mutation	SNP	G	A	98	96	c.805G>A	c.(805-807)GAT>AAT	p.D269N
Pat_24	Pre-Treatment	RAB3GAP2	25782	37	1	220379276	220379276	Missense_Mutation	SNP	G	A	79	87	c.685C>T	c.(685-687)CGT>TGT	p.R229C
Pat_24	Pre-Treatment	HLX	3142	37	1	221055560	221055560	Missense_Mutation	SNP	G	A	4	138	c.827G>A	c.(826-828)CGT>CAT	p.R276H
Pat_24	Pre-Treatment	TP53BP2	7159	37	1	223990993	223990993	Missense_Mutation	SNP	G	A	7	459	c.811C>T	c.(811-813)CGC>TGC	p.R271C
Pat_24	Pre-Treatment	URB2	9816	37	1	229771796	229771796	Missense_Mutation	SNP	G	A	7	606	c.1436G>A	c.(1435-1437)CGT>CAT	p.R479H
Pat_24	Pre-Treatment	TRIM67	440730	37	1	231339738	231339738	Missense_Mutation	SNP	G	A	4	172	c.1660G>A	c.(1660-1662)GGT>AGT	p.G554S
Pat_24	Pre-Treatment	SIPA1L2	57568	37	1	232579388	232579388	Missense_Mutation	SNP	C	T	6	343	c.3397G>A	c.(3397-3399)GGC>AGC	p.G1133S
Pat_24	Pre-Treatment	SIPA1L2	57568	37	1	232600585	232600585	Splice_Site	SNP	C	T	4	156	c.2820_splice	c.e7+1	p.V940_splice
Pat_24	Pre-Treatment	PCNXL2	80003	37	1	233394278	233394278	Missense_Mutation	SNP	G	A	140	107	c.1330C>T	c.(1330-1332)CCC>TCC	p.P444S
Pat_24	Pre-Treatment	PCNXL2	80003	37	1	233394878	233394878	Missense_Mutation	SNP	C	T	4	227	c.730G>A	c.(730-732)GAG>AAG	p.E244K
Pat_24	Pre-Treatment	TARBP1	6894	37	1	234527445	234527445	Missense_Mutation	SNP	C	T	4	109	c.4744G>A	c.(4744-4746)GTT>ATT	p.V1582I
Pat_24	Pre-Treatment	OR2L8	391190	37	1	248113064	248113064	Missense_Mutation	SNP	G	A	34	99	c.905G>A	c.(904-906)CGA>CAA	p.R302Q
Pat_24	Pre-Treatment	OR2AK2	391191	37	1	248128661	248128661	Missense_Mutation	SNP	G	A	33	40	c.28G>A	c.(28-30)GAT>AAT	p.D10N
Pat_24	Pre-Treatment	OR2M5	127059	37	1	248308569	248308569	Missense_Mutation	SNP	G	A	141	127	c.120G>A	c.(118-120)ATG>ATA	p.M40I
Pat_24	Pre-Treatment	OR2M4	26245	37	1	248402801	248402801	Missense_Mutation	SNP	G	A	199	121	c.571G>A	c.(571-573)GAA>AAA	p.E191K
Pat_24	Pre-Treatment	OR2T12	127064	37	1	248458834	248458834	Missense_Mutation	SNP	A	T	120	105	c.47T>A	c.(46-48)TTT>TAT	p.F16Y
Pat_24	Pre-Treatment	ZNF692	55657	37	1	249150737	249150737	Missense_Mutation	SNP	C	T	130	103	c.500G>A	c.(499-501)AGG>AAG	p.R167K
Pat_24	Pre-Treatment	TUBB8	347688	37	10	93214	93214	Missense_Mutation	SNP	G	T	5	199	c.1118C>A	c.(1117-1119)GCC>GAC	p.A373D
Pat_24	Pre-Treatment	DIP2C	22982	37	10	409202	409202	Missense_Mutation	SNP	C	T	4	232	c.2527G>A	c.(2527-2529)GTG>ATG	p.V843M
Pat_24	Pre-Treatment	DIP2C	22982	37	10	518463	518463	Missense_Mutation	SNP	G	A	4	242	c.184C>T	c.(184-186)CGC>TGC	p.R62C
Pat_24	Pre-Treatment	ASB13	79754	37	10	5693232	5693232	Missense_Mutation	SNP	G	A	4	142	c.326C>T	c.(325-327)GCC>GTC	p.A109V
Pat_24	Pre-Treatment	IL2RA	3559	37	10	6063567	6063567	Missense_Mutation	SNP	C	T	5	200	c.457G>A	c.(457-459)GTC>ATC	p.V153I
Pat_24	Pre-Treatment	TAF3	83860	37	10	8007211	8007211	Missense_Mutation	SNP	C	T	4	88	c.1738C>T	c.(1738-1740)CTT>TTT	p.L580F
Pat_24	Pre-Treatment	TAF3	83860	37	10	8056640	8056640	Missense_Mutation	SNP	C	G	35	49	c.2716C>G	c.(2716-2718)CAG>GAG	p.Q906E
Pat_24	Pre-Treatment	FAM171A1	221061	37	10	15256371	15256371	Missense_Mutation	SNP	C	T	4	225	c.1216G>A	c.(1216-1218)GGC>AGC	p.G406S
Pat_24	Pre-Treatment	CUBN	8029	37	10	16942693	16942693	Missense_Mutation	SNP	C	T	7	383	c.8341G>A	c.(8341-8343)GTG>ATG	p.V2781M
Pat_24	Pre-Treatment	ZEB1	6935	37	10	31799637	31799637	Missense_Mutation	SNP	C	T	37	56	c.518C>T	c.(517-519)CCA>CTA	p.P173L
Pat_24	Pre-Treatment	ARHGAP12	94134	37	10	32097662	32097662	Nonsense_Mutation	SNP	G	A	6	405	c.2281C>T	c.(2281-2283)CGA>TGA	p.R761*
Pat_24	Pre-Treatment	NRP1	8829	37	10	33475384	33475384	Missense_Mutation	SNP	C	T	5	147	c.2095G>A	c.(2095-2097)GAA>AAA	p.E699K
Pat_24	Pre-Treatment	FZD8	8325	37	10	35930284	35930284	Missense_Mutation	SNP	G	A	3	36	c.74C>T	c.(73-75)GCT>GTT	p.A25V
Pat_24	Pre-Treatment	TMEM72	643236	37	10	45430515	45430515	Missense_Mutation	SNP	C	T	5	161	c.761C>T	c.(760-762)ACA>ATA	p.T254I
Pat_24	Pre-Treatment	ANUBL1	93550	37	10	46121809	46121809	Missense_Mutation	SNP	C	T	4	116	c.1462G>A	c.(1462-1464)GTG>ATG	p.V488M
Pat_24	Pre-Treatment	RBP3	5949	37	10	48382146	48382146	Missense_Mutation	SNP	C	T	48	46	c.3503G>A	c.(3502-3504)GGG>GAG	p.G1168E
Pat_24	Pre-Treatment	RBP3	5949	37	10	48382161	48382161	Missense_Mutation	SNP	C	T	4	112	c.3488G>A	c.(3487-3489)CGG>CAG	p.R1163Q
Pat_24	Pre-Treatment	C10orf71	118461	37	10	50534997	50534997	Missense_Mutation	SNP	C	T	3	32	c.2096C>T	c.(2095-2097)ACA>ATA	p.T699I
Pat_24	Pre-Treatment	CHAT	1103	37	10	50870734	50870734	Missense_Mutation	SNP	G	A	4	192	c.1883G>A	c.(1882-1884)CGG>CAG	p.R628Q
Pat_24	Pre-Treatment	AGAP7	653268	37	10	51465222	51465222	Missense_Mutation	SNP	C	T	4	194	c.1234G>A	c.(1234-1236)GTC>ATC	p.V412I
Pat_24	Pre-Treatment	ANK3	288	37	10	61829772	61829772	Missense_Mutation	SNP	C	T	25	51	c.10867G>A	c.(10867-10869)GAT>AAT	p.D3623N
Pat_24	Pre-Treatment	TMEM26	219623	37	10	63188780	63188780	Missense_Mutation	SNP	G	A	4	117	c.509C>T	c.(508-510)ACT>ATT	p.T170I
Pat_24	Pre-Treatment	NRBF2	29982	37	10	64893246	64893246	Missense_Mutation	SNP	G	A	4	135	c.16G>A	c.(16-18)GGA>AGA	p.G6R
Pat_24	Pre-Treatment	MYPN	84665	37	10	69933908	69933908	Missense_Mutation	SNP	G	A	134	159	c.2059G>A	c.(2059-2061)GAG>AAG	p.E687K
Pat_24	Pre-Treatment	UNC5B	219699	37	10	73055623	73055623	Missense_Mutation	SNP	C	T	4	126	c.2231C>T	c.(2230-2232)CCG>CTG	p.P744L
Pat_24	Pre-Treatment	ECD	11319	37	10	74894454	74894454	Missense_Mutation	SNP	A	T	4	91	c.1822T>A	c.(1822-1824)TAT>AAT	p.Y608N
Pat_24	Pre-Treatment	USP54	159195	37	10	75301233	75301233	Missense_Mutation	SNP	G	A	5	216	c.725C>T	c.(724-726)GCT>GTT	p.A242V
Pat_24	Pre-Treatment	USP54	159195	37	10	75301248	75301248	Missense_Mutation	SNP	C	T	4	225	c.710G>A	c.(709-711)CGT>CAT	p.R237H
Pat_24	Pre-Treatment	POLR3A	11128	37	10	79737362	79737362	Missense_Mutation	SNP	C	T	4	107	c.4047G>A	c.(4045-4047)ATG>ATA	p.M1349I

Pat_24	Pre-Treatment	EIF5AL1	143244	37	10	81272743	81272743	Missense_Mutation	SNP	G	A	4	176	c.338G>A	c.(337-339)CGT>CAT	p.R113H
Pat_24	Pre-Treatment	LRIT2	340745	37	10	85981954	85981954	Missense_Mutation	SNP	C	T	4	170	c.1375G>A	c.(1375-1377)GCA>ACA	p.A459T
Pat_24	Pre-Treatment	IFIT1B	439996	37	10	91143396	91143396	Missense_Mutation	SNP	G	A	4	109	c.326G>A	c.(325-327)GGC>GAC	p.G109D
Pat_24	Pre-Treatment	HELLS	3070	37	10	96348116	96348116	Missense_Mutation	SNP	G	A	4	175	c.1457G>A	c.(1456-1458)CGT>CAT	p.R486H
Pat_24	Pre-Treatment	PDLIM1	9124	37	10	96997803	96997803	Missense_Mutation	SNP	C	T	4	76	c.869G>A	c.(868-870)GGC>GAC	p.G290D
Pat_24	Pre-Treatment	DNTT	1791	37	10	98092226	98092226	Missense_Mutation	SNP	G	A	4	205	c.1232G>A	c.(1231-1233)CGT>CAT	p.R411H
Pat_24	Pre-Treatment	SLIT1	6585	37	10	98816147	98816147	Missense_Mutation	SNP	G	A	99	192	c.1232C>T	c.(1231-1233)TCC>TTC	p.S411F
Pat_24	Pre-Treatment	RRP12	23223	37	10	99140560	99140560	Missense_Mutation	SNP	C	T	4	196	c.1529G>A	c.(1528-1530)AGG>AAG	p.R510K
Pat_24	Pre-Treatment	MMS19	64210	37	10	99225675	99225675	Missense_Mutation	SNP	T	C	129	216	c.1643A>G	c.(1642-1644)CAA>CGA	p.Q548R
Pat_24	Pre-Treatment	PI4K2A	55361	37	10	99400564	99400564	Missense_Mutation	SNP	C	T	4	35	c.65C>T	c.(64-66)TCG>TTG	p.S22L
Pat_24	Pre-Treatment	SFRP5	6425	37	10	99527416	99527416	Missense_Mutation	SNP	C	T	4	144	c.809G>A	c.(808-810)CGC>CAC	p.R270H
Pat_24	Pre-Treatment	ABCC2	1244	37	10	101590187	101590187	Missense_Mutation	SNP	G	A	4	229	c.2744G>A	c.(2743-2745)CGC>CAC	p.R915H
Pat_24	Pre-Treatment	LZTS2	84445	37	10	102763861	102763861	Missense_Mutation	SNP	C	T	4	202	c.1006C>T	c.(1006-1008)CGG>TGG	p.R336W
Pat_24	Pre-Treatment	TMEM180	79847	37	10	104233583	104233583	Missense_Mutation	SNP	G	A	6	392	c.1105G>A	c.(1105-1107)GTC>ATC	p.V369I
Pat_24	Pre-Treatment	SLK	9748	37	10	105785470	105785470	Nonsense_Mutation	SNP	G	T	4	112	c.3700G>T	c.(3700-3702)GGA>TGA	p.G1234*
Pat_24	Pre-Treatment	COL17A1	1308	37	10	105836119	105836119	Missense_Mutation	SNP	G	A	4	243	c.271C>T	c.(271-273)CCC>TCC	p.P91S
Pat_24	Pre-Treatment	CCDC147	159686	37	10	106139938	106139938	Missense_Mutation	SNP	G	A	4	152	c.1325G>A	c.(1324-1326)CGT>CAT	p.R442H
Pat_24	Pre-Treatment	XPNPEP1	7511	37	10	111651581	111651581	Missense_Mutation	SNP	G	A	4	124	c.185C>T	c.(184-186)ACA>ATA	p.T62I
Pat_24	Pre-Treatment	ACSL5	51703	37	10	114173027	114173027	Missense_Mutation	SNP	C	T	86	43	c.1045C>T	c.(1045-1047)CCC>TCC	p.P349S
Pat_24	Pre-Treatment	ABLIM1	3983	37	10	116213210	116213210	Missense_Mutation	SNP	G	A	4	57	c.1474C>T	c.(1474-1476)CTC>TTC	p.L492F
Pat_24	Pre-Treatment	ABLIM1	3983	37	10	116225553	116225553	Missense_Mutation	SNP	G	A	6	227	c.1345C>T	c.(1345-1347)CGG>TGG	p.R449W
Pat_24	Pre-Treatment	ATRNL1	26033	37	10	116919972	116919972	Missense_Mutation	SNP	T	A	4	75	c.1001T>A	c.(1000-1002)CTA>CAA	p.L334Q
Pat_24	Pre-Treatment	ATRNL1	26033	37	10	117026430	117026430	Nonsense_Mutation	SNP	G	A	9	83	c.1929G>A	c.(1927-1929)TGG>TGA	p.W643*
Pat_24	Pre-Treatment	HTRA1	5654	37	10	124268285	124268285	Missense_Mutation	SNP	A	T	28	14	c.1119A>T	c.(1117-1119)AAA>AAT	p.K373N
Pat_24	Pre-Treatment	ADAM12	8038	37	10	127738226	127738226	Missense_Mutation	SNP	G	A	4	101	c.1631C>T	c.(1630-1632)GCC>GTC	p.A544V
Pat_24	Pre-Treatment	DOCK1	1793	37	10	128925979	128925979	Missense_Mutation	SNP	G	A	4	147	c.2735G>A	c.(2734-2736)CGG>CAG	p.R912Q
Pat_24	Pre-Treatment	CLRN3	119467	37	10	129690880	129690880	Missense_Mutation	SNP	G	A	98	66	c.169C>T	c.(169-171)CGT>TGT	p.R57C
Pat_24	Pre-Treatment	STK32C	282974	37	10	134041533	134041533	Missense_Mutation	SNP	G	A	3	49	c.418C>T	c.(418-420)CGG>TGG	p.R140W
Pat_24	Pre-Treatment	B4GALNT4	338707	37	11	372699	372699	Missense_Mutation	SNP	G	A	4	130	c.293G>A	c.(292-294)GGG>GAG	p.G98E
Pat_24	Pre-Treatment	PKP3	11187	37	11	397003	397003	Missense_Mutation	SNP	G	A	30	28	c.502G>A	c.(502-504)GGT>AGT	p.G168S
Pat_24	Pre-Treatment	DEAF1	10522	37	11	674732	674732	Missense_Mutation	SNP	G	A	4	195	c.1307C>T	c.(1306-1308)GCG>GTG	p.A436V
Pat_24	Pre-Treatment	KRTAP5-5	439915	37	11	1651471	1651471	Missense_Mutation	SNP	G	T	4	113	c.401G>T	c.(400-402)GGG>GTG	p.G134V
Pat_24	Pre-Treatment	KRTAP5-5	439915	37	11	1651483	1651483	Missense_Mutation	SNP	G	C	4	166	c.413G>C	c.(412-414)GGC>GCC	p.G138A
Pat_24	Pre-Treatment	ZNF195	7748	37	11	3381754	3381754	Missense_Mutation	SNP	C	G	3	63	c.484G>C	c.(484-486)GGC>CGC	p.G162R
Pat_24	Pre-Treatment	CHRNA10	57053	37	11	3690528	3690528	Missense_Mutation	SNP	G	A	4	108	c.260C>T	c.(259-261)ACA>ATA	p.T87I
Pat_24	Pre-Treatment	OR52R1	119695	37	11	4825480	4825480	Missense_Mutation	SNP	C	T	6	12	c.368G>A	c.(367-369)GGA>GAA	p.G123E
Pat_24	Pre-Treatment	OR51G2	81282	37	11	4936883	4936883	Missense_Mutation	SNP	C	T	22	27	c.11G>A	c.(10-12)GGA>GAA	p.G4E
Pat_24	Pre-Treatment	OR51B2	79345	37	11	5344923	5344923	Missense_Mutation	SNP	G	A	12	26	c.605C>T	c.(604-606)TCT>TTT	p.S202F
Pat_24	Pre-Treatment	OR51Q1	390061	37	11	5444142	5444142	Missense_Mutation	SNP	C	T	33	90	c.712C>T	c.(712-714)CGT>TGT	p.R238C
Pat_24	Pre-Treatment	FAM160A2	84067	37	11	6245114	6245114	Missense_Mutation	SNP	C	T	4	160	c.503G>A	c.(502-504)AGT>AAT	p.S168N
Pat_24	Pre-Treatment	ZNF215	7762	37	11	6962868	6962868	Missense_Mutation	SNP	G	A	4	141	c.467G>A	c.(466-468)CGA>CAA	p.R156Q
Pat_24	Pre-Treatment	SYT9	143425	37	11	7324551	7324551	Missense_Mutation	SNP	G	A	36	48	c.427G>A	c.(427-429)GGG>AGG	p.G143R
Pat_24	Pre-Treatment	OLFML1	283298	37	11	7507125	7507125	Missense_Mutation	SNP	G	A	4	142	c.19G>A	c.(19-21)GGA>AGA	p.G7R
Pat_24	Pre-Treatment	PPFIBP2	8495	37	11	7662818	7662818	Missense_Mutation	SNP	G	A	4	194	c.1484G>A	c.(1483-1485)CGG>CAG	p.R495Q
Pat_24	Pre-Treatment	OR10A3	26496	37	11	7960835	7960835	Missense_Mutation	SNP	G	A	4	189	c.233C>T	c.(232-234)ACG>ATG	p.T78M
Pat_24	Pre-Treatment	DENND5A	23258	37	11	9163614	9163614	Missense_Mutation	SNP	C	T	6	193	c.3553G>A	c.(3553-3555)GTA>ATA	p.V1185I
Pat_24	Pre-Treatment	MICAL2	9645	37	11	12229575	12229575	Missense_Mutation	SNP	C	T	6	479	c.478C>T	c.(478-480)CGC>TGC	p.R160C

Pat_24	Pre-Treatment	TEAD1	7003	37	11	12904563	12904563	Missense_Mutation	SNP	C	T	5	93	c.545C>T	c.(544-546)TCG>TTG	p.S182L
Pat_24	Pre-Treatment	ARNTL	406	37	11	13402788	13402788	Missense_Mutation	SNP	C	T	51	146	c.1604C>T	c.(1603-1605)CCA>CTA	p.P535L
Pat_24	Pre-Treatment	PIK3C2A	5286	37	11	17135987	17135987	Missense_Mutation	SNP	C	T	4	158	c.3242G>A	c.(3241-3243)CGA>CAA	p.R1081Q
Pat_24	Pre-Treatment	CSRP3	8048	37	11	19206514	19206514	Missense_Mutation	SNP	C	T	26	63	c.493G>A	c.(493-495)GAA>AAA	p.E165K
Pat_24	Pre-Treatment	CCDC34	91057	37	11	27384734	27384734	Missense_Mutation	SNP	G	A	3	17	c.8C>T	c.(7-9)GCG>GTG	p.A3V
Pat_24	Pre-Treatment	KIF18A	81930	37	11	28057807	28057807	Missense_Mutation	SNP	C	T	4	111	c.2353G>A	c.(2353-2355)GAA>AAA	p.E785K
Pat_24	Pre-Treatment	C11orf46	120534	37	11	30354450	30354450	Missense_Mutation	SNP	C	T	4	83	c.464C>T	c.(463-465)ACG>ATG	p.T155M
Pat_24	Pre-Treatment	C11orf41	25758	37	11	33565594	33565594	Missense_Mutation	SNP	G	A	5	290	c.1594G>A	c.(1594-1596)GTG>ATG	p.V532M
Pat_24	Pre-Treatment	ELF5	2001	37	11	34527196	34527196	Missense_Mutation	SNP	G	A	137	167	c.131C>T	c.(130-132)CCT>CTT	p.P44L
Pat_24	Pre-Treatment	MAPK8IP1	9479	37	11	45926796	45926796	Missense_Mutation	SNP	G	A	4	125	c.2059G>A	c.(2059-2061)GTG>ATG	p.V687M
Pat_24	Pre-Treatment	PACSIN3	29763	37	11	47199955	47199955	Missense_Mutation	SNP	T	G	42	57	c.1121A>C	c.(1120-1122)TAC>TCC	p.Y374S
Pat_24	Pre-Treatment	MADD	8567	37	11	47317128	47317128	Missense_Mutation	SNP	G	A	4	162	c.3598G>A	c.(3598-3600)GTG>ATG	p.V1200M
Pat_24	Pre-Treatment	KBTBD4	55709	37	11	47595153	47595153	Missense_Mutation	SNP	G	A	4	107	c.886C>T	c.(886-888)CGG>TGG	p.R296W
Pat_24	Pre-Treatment	NUP160	23279	37	11	47858456	47858456	Nonsense_Mutation	SNP	G	A	4	206	c.925C>T	c.(925-927)CGA>TGA	p.R309*
Pat_24	Pre-Treatment	OR4X2	119764	37	11	48267541	48267541	Missense_Mutation	SNP	A	T	5	204	c.886A>T	c.(886-888)AGG>TGG	p.R296W
Pat_24	Pre-Treatment	GLYATL1	92292	37	11	58714563	58714563	Missense_Mutation	SNP	G	A	50	101	c.3G>A	c.(1-3)ATG>ATA	p.M1I
Pat_24	Pre-Treatment	GLYATL1	92292	37	11	58723157	58723157	Missense_Mutation	SNP	G	A	32	59	c.566G>A	c.(565-567)GGG>GAG	p.G189E
Pat_24	Pre-Treatment	GLYATL1	92292	37	11	58723339	58723339	Nonsense_Mutation	SNP	C	T	4	131	c.748C>T	c.(748-750)CGA>TGA	p.R250*
Pat_24	Pre-Treatment	CD6	923	37	11	60781460	60781460	Missense_Mutation	SNP	C	T	4	186	c.1361C>T	c.(1360-1362)CCG>CTG	p.P454L
Pat_24	Pre-Treatment	CPSF7	79869	37	11	61183653	61183653	Missense_Mutation	SNP	G	A	4	136	c.889C>T	c.(889-891)CCC>TCC	p.P297S
Pat_24	Pre-Treatment	EEF1G	1937	37	11	62338516	62338516	Missense_Mutation	SNP	G	A	5	192	c.443C>T	c.(442-444)ACG>ATG	p.T148M
Pat_24	Pre-Treatment	TAF6L	10629	37	11	62543392	62543392	Missense_Mutation	SNP	A	G	3	78	c.137A>G	c.(136-138)GAG>GGG	p.E46G
Pat_24	Pre-Treatment	SLC22A8	9376	37	11	62763580	62763580	Missense_Mutation	SNP	G	A	67	92	c.806C>T	c.(805-807)TCC>TTC	p.S269F
Pat_24	Pre-Treatment	LGALS12	85329	37	11	63276320	63276320	Missense_Mutation	SNP	C	T	5	186	c.295C>T	c.(295-297)CGC>TGC	p.R99C
Pat_24	Pre-Treatment	RTN3	10313	37	11	63486611	63486611	Missense_Mutation	SNP	C	T	46	82	c.637C>T	c.(637-639)CCA>TCA	p.P213S
Pat_24	Pre-Treatment	ATG2A	23130	37	11	64662539	64662539	Missense_Mutation	SNP	G	A	4	227	c.5723C>T	c.(5722-5724)ACG>ATG	p.T1908M
Pat_24	Pre-Treatment	C11orf85	283129	37	11	64726840	64726840	Missense_Mutation	SNP	G	A	4	197	c.38C>T	c.(37-39)ACG>ATG	p.T13M
Pat_24	Pre-Treatment	ZFPL1	7542	37	11	64854809	64854809	Missense_Mutation	SNP	C	T	5	250	c.650C>T	c.(649-651)ACG>ATG	p.T217M
Pat_24	Pre-Treatment	POLA2	23649	37	11	65063436	65063436	Missense_Mutation	SNP	C	T	5	459	c.1622C>T	c.(1621-1623)CCG>CTG	p.P541L
Pat_24	Pre-Treatment	PCNXL3	399909	37	11	65385807	65385807	Missense_Mutation	SNP	G	A	4	150	c.974G>A	c.(973-975)AGC>AAC	p.S325N
Pat_24	Pre-Treatment	FIBP	9158	37	11	65651915	65651915	Missense_Mutation	SNP	G	A	4	181	c.973C>T	c.(973-975)CGG>TGG	p.R325W
Pat_24	Pre-Treatment	FOSL1	8061	37	11	65664389	65664389	Missense_Mutation	SNP	C	T	4	134	c.188G>A	c.(187-189)AGT>AAT	p.S63N
Pat_24	Pre-Treatment	B3GNT1	11041	37	11	66113576	66113576	Missense_Mutation	SNP	G	A	5	333	c.1192C>T	c.(1192-1194)CGC>TGC	p.R398C
Pat_24	Pre-Treatment	PELI3	246330	37	11	66243271	66243271	Missense_Mutation	SNP	G	A	3	46	c.1043G>A	c.(1042-1044)CGC>CAC	p.R348H
Pat_24	Pre-Treatment	CCDC87	55231	37	11	66359879	66359879	Missense_Mutation	SNP	G	A	4	57	c.608C>T	c.(607-609)ACG>ATG	p.T203M
Pat_24	Pre-Treatment	CCS	9973	37	11	66366692	66366692	Missense_Mutation	SNP	C	T	4	111	c.218C>T	c.(217-219)GCG>GTG	p.A73V
Pat_24	Pre-Treatment	PC	5091	37	11	66620239	66620239	Missense_Mutation	SNP	C	T	4	187	c.1582G>A	c.(1582-1584)GTT>ATT	p.V528I
Pat_24	Pre-Treatment	PITPNM1	9600	37	11	67270150	67270150	Missense_Mutation	SNP	C	T	4	213	c.118G>A	c.(118-120)GTG>ATG	p.V40M
Pat_24	Pre-Treatment	NUDT8	254552	37	11	67396467	67396467	Missense_Mutation	SNP	G	A	6	223	c.250C>T	c.(250-252)CGG>TGG	p.R84W
Pat_24	Pre-Treatment	LOC645332	645332	37	11	67564228	67564228	Missense_Mutation	SNP	C	T	5	132	c.236G>A	c.(235-237)AGC>AAC	p.S79N
Pat_24	Pre-Treatment	CHKA	1119	37	11	67821460	67821460	Missense_Mutation	SNP	C	T	3	50	c.1369G>A	c.(1369-1371)GTG>ATG	p.V457M
Pat_24	Pre-Treatment	LRP5	4041	37	11	68154038	68154038	Missense_Mutation	SNP	G	A	4	173	c.1270G>A	c.(1270-1272)GAC>AAC	p.D424N
Pat_24	Pre-Treatment	CPT1A	1374	37	11	68562289	68562289	Missense_Mutation	SNP	G	A	4	204	c.862C>T	c.(862-864)CGG>TGG	p.R288W
Pat_24	Pre-Treatment	MYEOV	26579	37	11	69063509	69063509	Nonsense_Mutation	SNP	C	T	4	144	c.592C>T	c.(592-594)CGA>TGA	p.R198*
Pat_24	Pre-Treatment	CTTN	2017	37	11	70263164	70263164	Missense_Mutation	SNP	G	A	7	463	c.503G>A	c.(502-504)CGA>CAA	p.R168Q
Pat_24	Pre-Treatment	DHCR7	1717	37	11	71146522	71146522	Missense_Mutation	SNP	G	A	4	128	c.1327C>T	c.(1327-1329)CGC>TGC	p.R443C
Pat_24	Pre-Treatment	PRKRIR	5612	37	11	76062369	76062369	Missense_Mutation	SNP	G	A	4	219	c.1825C>T	c.(1825-1827)CCC>TCC	p.P609S

Pat_24	Pre-Treatment	C11orf30	56946	37	11	76261033	76261033	Missense_Mutation	SNP	C	T	4	206	c.3812C>T	c.(3811-3813)TCC>TTC	p.S1271F
Pat_24	Pre-Treatment	GAB2	9846	37	11	77934697	77934697	Missense_Mutation	SNP	G	A	237	405	c.1328C>T	c.(1327-1329)TCG>TTG	p.S443L
Pat_24	Pre-Treatment	FAT3	120114	37	11	92531158	92531158	Missense_Mutation	SNP	C	T	54	127	c.4979C>T	c.(4978-4980)TCC>TTC	p.S1660F
Pat_24	Pre-Treatment	FAT3	120114	37	11	92616245	92616245	Missense_Mutation	SNP	C	T	4	165	c.12623C>T	c.(12622-12624)CCG>CTG	p.P4208L
Pat_24	Pre-Treatment	ANGPTL5	253935	37	11	101765741	101765741	Missense_Mutation	SNP	G	A	34	53	c.716C>T	c.(715-717)ACC>ATC	p.T239I
Pat_24	Pre-Treatment	GRIA4	2893	37	11	105781176	105781176	Missense_Mutation	SNP	G	A	43	57	c.1174G>A	c.(1174-1176)GAT>AAT	p.D392N
Pat_24	Pre-Treatment	PPP2R1B	5519	37	11	111625721	111625721	Missense_Mutation	SNP	G	A	4	172	c.941C>T	c.(940-942)GCT>GTT	p.A314V
Pat_24	Pre-Treatment	NCAM1	4684	37	11	113076768	113076768	Missense_Mutation	SNP	G	A	5	281	c.140G>A	c.(139-141)CGA>CAA	p.R47Q
Pat_24	Pre-Treatment	ZBTB16	7704	37	11	113934474	113934474	Missense_Mutation	SNP	G	A	4	65	c.452G>A	c.(451-453)CGG>CAG	p.R151Q
Pat_24	Pre-Treatment	ZBTB16	7704	37	11	113934735	113934735	Missense_Mutation	SNP	T	C	2	9	c.713T>C	c.(712-714)GTG>GCG	p.V238A
Pat_24	Pre-Treatment	FAM55D	54827	37	11	114453681	114453681	Missense_Mutation	SNP	T	A	85	111	c.159A>T	c.(157-159)TTA>TTT	p.L53F
Pat_24	Pre-Treatment	MLL	4297	37	11	118344458	118344458	Nonsense_Mutation	SNP	C	T	17	29	c.2584C>T	c.(2584-2586)CGA>TGA	p.R862*
Pat_24	Pre-Treatment	HINFP	25988	37	11	119004963	119004963	Missense_Mutation	SNP	G	A	4	63	c.1309G>A	c.(1309-1311)GGA>AGA	p.G437R
Pat_24	Pre-Treatment	ABCG4	64137	37	11	119029628	119029628	Missense_Mutation	SNP	G	A	4	194	c.1426G>A	c.(1426-1428)GTG>ATG	p.V476M
Pat_24	Pre-Treatment	TRIM29	23650	37	11	119991365	119991365	Missense_Mutation	SNP	G	A	4	74	c.1444C>T	c.(1444-1446)CGG>TGG	p.R482W
Pat_24	Pre-Treatment	SORL1	6653	37	11	121495971	121495971	Missense_Mutation	SNP	G	A	4	172	c.6349G>A	c.(6349-6351)GAT>AAT	p.D2117N
Pat_24	Pre-Treatment	OR10S1	219873	37	11	123848079	123848079	Missense_Mutation	SNP	G	A	16	35	c.320C>T	c.(319-321)TCC>TTC	p.S107F
Pat_24	Pre-Treatment	ROBO3	64221	37	11	124744006	124744006	Missense_Mutation	SNP	G	A	9	627	c.1825G>A	c.(1825-1827)GTG>ATG	p.V609M
Pat_24	Pre-Treatment	SNX19	399979	37	11	130775881	130775881	Missense_Mutation	SNP	C	T	4	167	c.2410G>A	c.(2410-2412)GTG>ATG	p.V804M
Pat_24	Pre-Treatment	CACNA1C	775	37	12	2719791	2719791	Missense_Mutation	SNP	G	A	6	313	c.3703G>A	c.(3703-3705)GTG>ATG	p.V1235M
Pat_24	Pre-Treatment	NTF3	4908	37	12	5603829	5603829	Missense_Mutation	SNP	C	T	7	280	c.449C>T	c.(448-450)TCG>TTG	p.S150L
Pat_24	Pre-Treatment	VWF	7450	37	12	6172182	6172182	Missense_Mutation	SNP	G	A	5	102	c.1471C>T	c.(1471-1473)CGC>TGC	p.R491C
Pat_24	Pre-Treatment	ZNF384	171017	37	12	6781600	6781600	Missense_Mutation	SNP	C	T	4	206	c.1010G>A	c.(1009-1011)CGT>CAT	p.R337H
Pat_24	Pre-Treatment	MLF2	8079	37	12	6860835	6860835	Missense_Mutation	SNP	G	A	4	228	c.188C>T	c.(187-189)GCT>GTT	p.A63V
Pat_24	Pre-Treatment	PTPN6	5777	37	12	7065712	7065712	Missense_Mutation	SNP	G	A	4	213	c.1055G>A	c.(1054-1056)CGA>CAA	p.R352Q
Pat_24	Pre-Treatment	ACSM4	341392	37	12	7479635	7479635	Missense_Mutation	SNP	C	T	12	38	c.1600C>T	c.(1600-1602)CTT>TTT	p.L534F
Pat_24	Pre-Treatment	A2M	2	37	12	9224967	9224967	Missense_Mutation	SNP	G	A	15	50	c.4091C>T	c.(4090-4092)TCC>TTC	p.S1364F
Pat_24	Pre-Treatment	PRB3	5544	37	12	11420584	11420584	Missense_Mutation	SNP	C	T	7	358	c.599G>A	c.(598-600)CGT>CAT	p.R200H
Pat_24	Pre-Treatment	RPL13AP20	387841	37	12	13028782	13028782	Missense_Mutation	SNP	G	A	4	116	c.350G>A	c.(349-351)CGG>CAG	p.R117Q
Pat_24	Pre-Treatment	GRIN2B	2904	37	12	13715812	13715812	Missense_Mutation	SNP	G	A	52	76	c.4360C>T	c.(4360-4362)CCC>TCC	p.P1454S
Pat_24	Pre-Treatment	PTPRO	5800	37	12	15742411	15742411	Missense_Mutation	SNP	A	G	126	230	c.3433A>G	c.(3433-3435)ACA>GCA	p.T1145A
Pat_24	Pre-Treatment	RECQL	5965	37	12	21624004	21624004	Missense_Mutation	SNP	T	G	3	93	c.1696A>C	c.(1696-1698)ACC>CCC	p.T566P
Pat_24	Pre-Treatment	ABCC9	10060	37	12	22068802	22068802	Nonsense_Mutation	SNP	C	A	4	54	c.616G>T	c.(616-618)GAA>TAA	p.E206*
Pat_24	Pre-Treatment	PTHLH	5744	37	12	28116642	28116642	Missense_Mutation	SNP	G	A	7	390	c.163C>T	c.(163-165)CGG>TGG	p.R55W
Pat_24	Pre-Treatment	ALG10	84920	37	12	34179675	34179675	Missense_Mutation	SNP	G	A	4	244	c.1247G>A	c.(1246-1248)CGT>CAT	p.R416H
Pat_24	Pre-Treatment	KIF21A	55605	37	12	39726893	39726893	Missense_Mutation	SNP	C	T	5	216	c.2504G>A	c.(2503-2505)CGG>CAG	p.R835Q
Pat_24	Pre-Treatment	ABCD2	225	37	12	39973341	39973341	Missense_Mutation	SNP	G	A	47	105	c.1873C>T	c.(1873-1875)CAT>TAT	p.H625Y
Pat_24	Pre-Treatment	LRRK2	120892	37	12	40758790	40758790	Missense_Mutation	SNP	G	A	4	132	c.7328G>A	c.(7327-7329)CGA>CAA	p.R2443Q
Pat_24	Pre-Treatment	PPHLN1	51535	37	12	42836514	42836514	Missense_Mutation	SNP	G	A	7	480	c.1096G>A	c.(1096-1098)GAA>AAA	p.E366K
Pat_24	Pre-Treatment	ARID2	196528	37	12	46246366	46246366	Missense_Mutation	SNP	C	T	80	117	c.4460C>T	c.(4459-4461)CCC>CTC	p.P1487L
Pat_24	Pre-Treatment	SLC38A4	55089	37	12	47181792	47181792	Missense_Mutation	SNP	C	T	19	59	c.233G>A	c.(232-234)GGA>GAA	p.G78E
Pat_24	Pre-Treatment	FAM113B	91523	37	12	47629811	47629811	Missense_Mutation	SNP	C	T	4	236	c.965C>T	c.(964-966)CCT>CTT	p.P322L
Pat_24	Pre-Treatment	RAPGEF3	10411	37	12	48144895	48144895	Missense_Mutation	SNP	C	T	3	17	c.481G>A	c.(481-483)GAA>AAA	p.E161K
Pat_24	Pre-Treatment	ADCY6	112	37	12	49176700	49176700	Missense_Mutation	SNP	G	A	4	115	c.518C>T	c.(517-519)CCC>CTC	p.P173L
Pat_24	Pre-Treatment	LMBR1L	55716	37	12	49500753	49500753	Missense_Mutation	SNP	A	G	102	210	c.148T>C	c.(148-150)TTC>CTC	p.F50L
Pat_24	Pre-Treatment	FAIM2	23017	37	12	50283310	50283310	Missense_Mutation	SNP	G	A	4	201	c.605C>T	c.(604-606)ACG>ATG	p.T202M
Pat_24	Pre-Treatment	BIN2	51411	37	12	51685932	51685932	Missense_Mutation	SNP	C	T	24	45	c.958G>A	c.(958-960)GAA>AAA	p.E320K

Pat_24	Pre-Treatment	ACVRL1	94	37	12	52309892	52309892	Missense_Mutation	SNP	G	A	6	311	c.1121G>A	c.(1120-1122)CGG>CAG	p.R374Q
Pat_24	Pre-Treatment	KRT5	3852	37	12	52911448	52911448	Missense_Mutation	SNP	C	T	5	392	c.1018G>A	c.(1018-1020)GCT>ACT	p.A340T
Pat_24	Pre-Treatment	KRT71	112802	37	12	52942532	52942532	Missense_Mutation	SNP	C	T	126	182	c.766G>A	c.(766-768)GAA>AAA	p.E256K
Pat_24	Pre-Treatment	SPRYD3	84926	37	12	53468516	53468516	Missense_Mutation	SNP	C	T	5	221	c.424G>A	c.(424-426)GGG>AGG	p.G142R
Pat_24	Pre-Treatment	ESPL1	9700	37	12	53686729	53686729	Missense_Mutation	SNP	G	A	4	107	c.6136G>A	c.(6136-6138)GTG>ATG	p.V2046M
Pat_24	Pre-Treatment	HOXC12	3228	37	12	54350232	54350232	Missense_Mutation	SNP	G	A	5	338	c.731G>A	c.(730-732)CGG>CAG	p.R244Q
Pat_24	Pre-Treatment	NCKAP1L	3071	37	12	54910702	54910702	Missense_Mutation	SNP	C	T	4	219	c.1021C>T	c.(1021-1023)CGG>TGG	p.R341W
Pat_24	Pre-Treatment	RDH16	8608	37	12	57351092	57351092	Missense_Mutation	SNP	C	T	4	102	c.155G>A	c.(154-156)CGA>CAA	p.R52Q
Pat_24	Pre-Treatment	LRP1	4035	37	12	57579368	57579368	Missense_Mutation	SNP	G	A	3	77	c.6518G>A	c.(6517-6519)CGG>CAG	p.R2173Q
Pat_24	Pre-Treatment	USP15	9958	37	12	62785105	62785105	Missense_Mutation	SNP	G	A	4	204	c.2129G>A	c.(2128-2130)CGA>CAA	p.R710Q
Pat_24	Pre-Treatment	TMEM5	10329	37	12	64202532	64202532	Missense_Mutation	SNP	C	T	4	219	c.992C>T	c.(991-993)CCG>CTG	p.P331L
Pat_24	Pre-Treatment	GNS	2799	37	12	65141685	65141685	Missense_Mutation	SNP	G	A	4	168	c.266C>T	c.(265-267)GCT>GTT	p.A89V
Pat_24	Pre-Treatment	HELB	92797	37	12	66724980	66724980	Missense_Mutation	SNP	G	A	5	171	c.2717G>A	c.(2716-2718)CGC>CAC	p.R906H
Pat_24	Pre-Treatment	CNOT2	4848	37	12	70739967	70739967	Missense_Mutation	SNP	C	T	4	125	c.1399C>T	c.(1399-1401)CGT>TGT	p.R467C
Pat_24	Pre-Treatment	THAP2	83591	37	12	72070580	72070580	Missense_Mutation	SNP	G	C	3	103	c.379G>C	c.(379-381)GCC>CCC	p.A127P
Pat_24	Pre-Treatment	NAV3	89795	37	12	78513287	78513287	Missense_Mutation	SNP	G	A	4	185	c.3311G>A	c.(3310-3312)GGG>GAG	p.G1104E
Pat_24	Pre-Treatment	SLC6A15	55117	37	12	85255559	85255559	Missense_Mutation	SNP	G	A	4	130	c.2045C>T	c.(2044-2046)CCG>CTG	p.P682L
Pat_24	Pre-Treatment	ATP2B1	490	37	12	90049560	90049560	Missense_Mutation	SNP	C	T	4	90	c.104G>A	c.(103-105)CGG>CAG	p.R35Q
Pat_24	Pre-Treatment	C12orf12	196477	37	12	91348050	91348050	Missense_Mutation	SNP	G	A	6	18	c.470C>T	c.(469-471)TCC>TTC	p.S157F
Pat_24	Pre-Treatment	PLXNC1	10154	37	12	94631525	94631525	Missense_Mutation	SNP	G	A	4	161	c.2066G>A	c.(2065-2067)CGG>CAG	p.R689Q
Pat_24	Pre-Treatment	UTP20	27340	37	12	101689336	101689336	Missense_Mutation	SNP	G	T	4	84	c.1330G>T	c.(1330-1332)GCC>TCC	p.A444S
Pat_24	Pre-Treatment	CHST11	50515	37	12	105150764	105150764	Missense_Mutation	SNP	G	A	4	144	c.242G>A	c.(241-243)CGG>CAG	p.R81Q
Pat_24	Pre-Treatment	RFX4	5992	37	12	107125991	107125991	Missense_Mutation	SNP	G	A	69	142	c.1435G>A	c.(1435-1437)GAG>AAG	p.E479K
Pat_24	Pre-Treatment	CRY1	1407	37	12	107386630	107386630	Missense_Mutation	SNP	G	A	6	280	c.1696C>T	c.(1696-1698)CGT>TGT	p.R566C
Pat_24	Pre-Treatment	PWP1	11137	37	12	108082472	108082472	Missense_Mutation	SNP	G	A	4	94	c.212G>A	c.(211-213)CGC>CAC	p.R71H
Pat_24	Pre-Treatment	FICD	11153	37	12	108912743	108912743	Missense_Mutation	SNP	G	A	4	120	c.868G>A	c.(868-870)GTG>ATG	p.V290M
Pat_24	Pre-Treatment	TMEM119	338773	37	12	108985629	108985629	Missense_Mutation	SNP	C	A	4	113	c.531G>T	c.(529-531)TTG>TTT	p.L177F
Pat_24	Pre-Treatment	DAO	1610	37	12	109278847	109278847	Missense_Mutation	SNP	G	A	5	122	c.65G>A	c.(64-66)CGC>CAC	p.R22H
Pat_24	Pre-Treatment	ACACB	32	37	12	109625846	109625846	Missense_Mutation	SNP	C	T	4	206	c.2023C>T	c.(2023-2025)CGG>TGG	p.R675W
Pat_24	Pre-Treatment	ACACB	32	37	12	109660688	109660688	Missense_Mutation	SNP	G	A	3	51	c.3763G>A	c.(3763-3765)GGC>AGC	p.G1255S
Pat_24	Pre-Treatment	TCHP	84260	37	12	110348958	110348958	Missense_Mutation	SNP	G	A	3	26	c.970G>A	c.(970-972)GAT>AAT	p.D324N
Pat_24	Pre-Treatment	ANKRD13A	88455	37	12	110456188	110456188	Missense_Mutation	SNP	C	T	4	149	c.439C>T	c.(439-441)CGC>TGC	p.R147C
Pat_24	Pre-Treatment	DDX54	79039	37	12	113601055	113601055	Missense_Mutation	SNP	G	A	4	182	c.1963C>T	c.(1963-1965)CGG>TGG	p.R655W
Pat_24	Pre-Treatment	IQCD	115811	37	12	113633648	113633648	Missense_Mutation	SNP	G	A	6	287	c.776C>T	c.(775-777)TCG>TTG	p.S259L
Pat_24	Pre-Treatment	TAOK3	51347	37	12	118636903	118636903	Missense_Mutation	SNP	C	T	4	236	c.1147G>A	c.(1147-1149)GAT>AAT	p.D383N
Pat_24	Pre-Treatment	CCDC64	92558	37	12	120436370	120436370	Nonsense_Mutation	SNP	C	T	4	140	c.475C>T	c.(475-477)CGA>TGA	p.R159*
Pat_24	Pre-Treatment	P2RX7	5027	37	12	121613228	121613228	Missense_Mutation	SNP	C	T	7	270	c.919C>T	c.(919-921)CGG>TGG	p.R307W
Pat_24	Pre-Treatment	CAMKK2	10645	37	12	121706440	121706440	Splice_Site	SNP	C	T	8	546	c.625_splice	c.e5+1	p.R209_splice
Pat_24	Pre-Treatment	TMEM120B	144404	37	12	122190101	122190101	Missense_Mutation	SNP	G	A	4	241	c.433G>A	c.(433-435)GTG>ATG	p.V145M
Pat_24	Pre-Treatment	HIP1R	9026	37	12	123346041	123346041	Missense_Mutation	SNP	G	C	3	90	c.3139G>C	c.(3139-3141)GCC>CCC	p.A1047P
Pat_24	Pre-Treatment	DNAH10	196385	37	12	124270346	124270346	Missense_Mutation	SNP	G	A	59	86	c.1101G>A	c.(1099-1101)ATG>ATA	p.M367I
Pat_24	Pre-Treatment	DNAH10	196385	37	12	124293478	124293478	Missense_Mutation	SNP	G	A	6	528	c.2768G>A	c.(2767-2769)CGG>CAG	p.R923Q
Pat_24	Pre-Treatment	AACS	65985	37	12	125626671	125626671	Missense_Mutation	SNP	G	A	5	213	c.1915G>A	c.(1915-1917)GTC>ATC	p.V639I
Pat_24	Pre-Treatment	TMEM132B	114795	37	12	126004121	126004121	Missense_Mutation	SNP	G	A	55	109	c.1228G>A	c.(1228-1230)GAG>AAG	p.E410K
Pat_24	Pre-Treatment	TMEM132D	121256	37	12	130184920	130184920	Missense_Mutation	SNP	G	A	3	51	c.403C>T	c.(403-405)CGG>TGG	p.R135W
Pat_24	Pre-Treatment	POLE	5426	37	12	133219832	133219832	Missense_Mutation	SNP	G	A	4	81	c.4529C>T	c.(4528-4530)GCA>GTA	p.A1510V
Pat_24	Pre-Treatment	PGAM5	192111	37	12	133291473	133291473	Missense_Mutation	SNP	G	A	4	236	c.221G>A	c.(220-222)CGG>CAG	p.R74Q

Pat_24	Pre-Treatment	ZNF268	10795	37	12	133727692	133727692	Translation_Start_Site	SNP	G	A	4	154	c.-972G>A	(-974--970)TCGTG>TCATG	
Pat_24	Pre-Treatment	ZNF10	7556	37	12	133732827	133732827	Nonsense_Mutation	SNP	G	A	4	94	c.995G>A	c.(994-996)TGG>TAG	p.W332*
Pat_24	Pre-Treatment	ZNF10	7556	37	12	133732959	133732959	Missense_Mutation	SNP	C	T	70	161	c.1127C>T	c.(1126-1128)CCC>CTC	p.P376L
Pat_24	Pre-Treatment	MPHOSPH8	54737	37	13	20240595	20240595	Nonsense_Mutation	SNP	C	T	5	297	c.2050C>T	c.(2050-2052)CGA>TGA	p.R684*
Pat_24	Pre-Treatment	PSPC1	55269	37	13	20356687	20356687	Missense_Mutation	SNP	G	A	4	177	c.211C>T	c.(211-213)CTC>TTC	p.L71F
Pat_24	Pre-Treatment	ATP12A	479	37	13	25262518	25262518	Missense_Mutation	SNP	C	T	8	457	c.290C>T	c.(289-291)CCT>CTT	p.P97L
Pat_24	Pre-Treatment	RNF6	6049	37	13	26789432	26789432	Missense_Mutation	SNP	C	T	6	429	c.587G>A	c.(586-588)CGA>CAA	p.R196Q
Pat_24	Pre-Treatment	MTUS2	23281	37	13	29600916	29600916	Missense_Mutation	SNP	A	G	22	36	c.2111A>G	c.(2110-2112)AAC>AGC	p.N704S
Pat_24	Pre-Treatment	STARD13	90627	37	13	33704132	33704132	Missense_Mutation	SNP	C	T	31	56	c.682G>A	c.(682-684)GTC>ATC	p.V228I
Pat_24	Pre-Treatment	TRPC4	7223	37	13	38266415	38266415	Missense_Mutation	SNP	G	A	35	74	c.955C>T	c.(955-957)CCA>TCA	p.P319S
Pat_24	Pre-Treatment	ELF1	1997	37	13	41525471	41525471	Nonsense_Mutation	SNP	G	A	4	94	c.355C>T	c.(355-357)CGA>TGA	p.R119*
Pat_24	Pre-Treatment	ATP7B	540	37	13	52524205	52524205	Missense_Mutation	SNP	C	T	4	153	c.2668G>A	c.(2668-2670)GTG>ATG	p.V890M
Pat_24	Pre-Treatment	UCHL3	7347	37	13	76141423	76141423	Missense_Mutation	SNP	G	A	5	243	c.401G>A	c.(400-402)CGA>CAA	p.R134Q
Pat_24	Pre-Treatment	LMO7	4008	37	13	76415291	76415291	Missense_Mutation	SNP	G	A	38	61	c.2930G>A	c.(2929-2931)AGG>AAG	p.R977K
Pat_24	Pre-Treatment	SPRY2	10253	37	13	80911087	80911087	Nonsense_Mutation	SNP	G	A	5	227	c.754C>T	c.(754-756)CGA>TGA	p.R252*
Pat_24	Pre-Treatment	DZIP1	22873	37	13	96239829	96239829	Missense_Mutation	SNP	C	T	6	327	c.2182G>A	c.(2182-2184)GAA>AAA	p.E728K
Pat_24	Pre-Treatment	IPO5	3843	37	13	98649834	98649834	Nonsense_Mutation	SNP	G	A	4	152	c.963G>A	c.(961-963)TGG>TGA	p.W321*
Pat_24	Pre-Treatment	NALCN	259232	37	13	101756664	101756664	Missense_Mutation	SNP	C	T	48	55	c.2871G>A	c.(2869-2871)ATG>ATA	p.M957I
Pat_24	Pre-Treatment	MYO16	23026	37	13	109661317	109661317	Missense_Mutation	SNP	G	A	65	85	c.2449G>A	c.(2449-2451)GAA>AAA	p.E817K
Pat_24	Pre-Treatment	COL4A1	1282	37	13	110835536	110835536	Missense_Mutation	SNP	G	A	14	25	c.1985C>T	c.(1984-1986)CCC>CTC	p.P662L
Pat_24	Pre-Treatment	ATP11A	23250	37	13	113527942	113527942	Missense_Mutation	SNP	C	T	4	142	c.3113C>T	c.(3112-3114)TCG>TTG	p.S1038L
Pat_24	Pre-Treatment	PROZ	8858	37	13	113826166	113826166	Missense_Mutation	SNP	G	A	4	113	c.950G>A	c.(949-951)CGG>CAG	p.R317Q
Pat_24	Pre-Treatment	OR4M1	441670	37	14	20249078	20249078	Missense_Mutation	SNP	G	A	97	136	c.597G>A	c.(595-597)ATG>ATA	p.M199I
Pat_24	Pre-Treatment	TEP1	7011	37	14	20852268	20852268	Missense_Mutation	SNP	G	A	4	178	c.3463C>T	c.(3463-3465)CGG>TGG	p.R1155W
Pat_24	Pre-Treatment	LRP10	26020	37	14	23345353	23345353	Missense_Mutation	SNP	G	C	4	226	c.1196G>C	c.(1195-1197)TGC>TCC	p.C399S
Pat_24	Pre-Treatment	ACIN1	22985	37	14	23530575	23530575	Missense_Mutation	SNP	C	T	6	279	c.3530G>A	c.(3529-3531)CGA>CAA	p.R1177Q
Pat_24	Pre-Treatment	HOMEZ	57594	37	14	23745797	23745797	Missense_Mutation	SNP	G	A	45	65	c.640C>T	c.(640-642)CCC>TCC	p.P214S
Pat_24	Pre-Treatment	CMTM5	116173	37	14	23847681	23847681	Missense_Mutation	SNP	C	T	6	442	c.250C>T	c.(250-252)CGC>TGC	p.R84C
Pat_24	Pre-Treatment	MYH7	4625	37	14	23899059	23899059	Missense_Mutation	SNP	C	T	4	132	c.1063G>A	c.(1063-1065)GCC>ACC	p.A355T
Pat_24	Pre-Treatment	JPH4	84502	37	14	24045177	24045177	Missense_Mutation	SNP	G	A	29	39	c.868C>T	c.(868-870)CGG>TGG	p.R290W
Pat_24	Pre-Treatment	LRRC16B	90668	37	14	24535670	24535670	Missense_Mutation	SNP	G	A	4	229	c.3589G>A	c.(3589-3591)GCA>ACA	p.A1197T
Pat_24	Pre-Treatment	NOVA1	4857	37	14	26949269	26949269	Nonsense_Mutation	SNP	G	A	70	121	c.361C>T	c.(361-363)CGA>TGA	p.R121*
Pat_24	Pre-Treatment	SIP1	8487	37	14	39594217	39594217	Missense_Mutation	SNP	A	T	4	205	c.541A>T	c.(541-543)AGT>TGT	p.S181C
Pat_24	Pre-Treatment	LRFN5	145581	37	14	42356643	42356643	Missense_Mutation	SNP	G	A	4	163	c.815G>A	c.(814-816)CGC>CAC	p.R272H
Pat_24	Pre-Treatment	C14orf182	283551	37	14	50472465	50472465	Missense_Mutation	SNP	C	T	7	654	c.53G>A	c.(52-54)AGG>AAG	p.R18K
Pat_24	Pre-Treatment	TRIM9	114088	37	14	51444041	51444041	Missense_Mutation	SNP	C	T	4	178	c.2101G>A	c.(2101-2103)GAC>AAC	p.D701N
Pat_24	Pre-Treatment	PELI2	57161	37	14	56763456	56763456	Missense_Mutation	SNP	G	A	4	83	c.835G>A	c.(835-837)GCC>ACC	p.A279T
Pat_24	Pre-Treatment	ARID4A	5926	37	14	58814397	58814397	Missense_Mutation	SNP	C	T	4	106	c.1205C>T	c.(1204-1206)TCG>TTG	p.S402L
Pat_24	Pre-Treatment	KCNH5	27133	37	14	63174438	63174438	Missense_Mutation	SNP	C	T	79	138	c.2755G>A	c.(2755-2757)GAG>AAG	p.E919K
Pat_24	Pre-Treatment	KCNH5	27133	37	14	63174770	63174770	Missense_Mutation	SNP	C	T	48	72	c.2423G>A	c.(2422-2424)GGA>GAA	p.G808E
Pat_24	Pre-Treatment	SYNE2	23224	37	14	64467305	64467305	Missense_Mutation	SNP	G	A	4	197	c.3506G>A	c.(3505-3507)CGC>CAC	p.R1169H
Pat_24	Pre-Treatment	SYNE2	23224	37	14	64679658	64679658	Missense_Mutation	SNP	C	T	5	191	c.18991C>T	.(18991-18993)CGC>TG	p.R6331C
Pat_24	Pre-Treatment	HSPA2	3306	37	14	65009062	65009062	Missense_Mutation	SNP	G	A	4	163	c.1495G>A	c.(1495-1497)GGT>AGT	p.G499S
Pat_24	Pre-Treatment	SPTB	6710	37	14	65240084	65240084	Missense_Mutation	SNP	C	T	6	315	c.5032G>A	c.(5032-5034)GTG>ATG	p.V1678M
Pat_24	Pre-Treatment	DCAF5	8816	37	14	69521641	69521641	Missense_Mutation	SNP	G	A	4	142	c.1762C>T	c.(1762-1764)CGG>TGG	p.R588W
Pat_24	Pre-Treatment	TMEM90A	646658	37	14	74876219	74876219	Missense_Mutation	SNP	C	T	5	7	c.229G>A	c.(229-231)GAC>AAC	p.D77N
Pat_24	Pre-Treatment	TTLL5	23093	37	14	76249729	76249729	Missense_Mutation	SNP	C	T	4	112	c.2842C>T	c.(2842-2844)CAT>TAT	p.H948Y

Pat_24	Pre-Treatment	ESRRB	2103	37	14	76928965	76928965	Missense_Mutation	SNP	C	T	5	229	c.475C>T	c.(475-477)CGC>TGC	p.R159C
Pat_24	Pre-Treatment	ANGEL1	23357	37	14	77272947	77272947	Missense_Mutation	SNP	G	A	5	155	c.1192C>T	c.(1192-1194)CGC>TGC	p.R398C
Pat_24	Pre-Treatment	GSTZ1	2954	37	14	77795544	77795544	Missense_Mutation	SNP	G	A	4	97	c.421G>A	c.(421-423)GCC>ACC	p.A141T
Pat_24	Pre-Treatment	C14orf145	145508	37	14	81372379	81372379	Missense_Mutation	SNP	C	T	4	117	c.281G>A	c.(280-282)CGT>CAT	p.R94H
Pat_24	Pre-Treatment	ZC3H14	79882	37	14	89037468	89037468	Missense_Mutation	SNP	G	A	4	155	c.235G>A	c.(235-237)GAA>AAA	p.E79K
Pat_24	Pre-Treatment	TRIP11	9321	37	14	92470806	92470806	Missense_Mutation	SNP	C	T	4	78	c.3514G>A	c.(3514-3516)GAA>AAA	p.E1172K
Pat_24	Pre-Treatment	RIN3	79890	37	14	93118751	93118751	Missense_Mutation	SNP	G	A	5	304	c.1357G>A	c.(1357-1359)GCC>ACC	p.A453T
Pat_24	Pre-Treatment	DICER1	23405	37	14	95572381	95572381	Missense_Mutation	SNP	G	A	6	371	c.2984C>T	c.(2983-2985)TCA>TTA	p.S995L
Pat_24	Pre-Treatment	CLMN	79789	37	14	95669186	95669186	Missense_Mutation	SNP	C	T	4	192	c.2500G>A	c.(2500-2502)GAC>AAC	p.D834N
Pat_24	Pre-Treatment	CYP46A1	10858	37	14	100165849	100165849	Missense_Mutation	SNP	G	A	8	587	c.329G>A	c.(328-330)CGT>CAT	p.R110H
Pat_24	Pre-Treatment	RAGE	5891	37	14	102732227	102732227	Nonsense_Mutation	SNP	G	A	5	184	c.145C>T	c.(145-147)CGA>TGA	p.R49*
Pat_24	Pre-Treatment	TDRD9	122402	37	14	104457535	104457535	Missense_Mutation	SNP	G	A	4	166	c.1154G>A	c.(1153-1155)CGA>CAA	p.R385Q
Pat_24	Pre-Treatment	KIAA0284	283638	37	14	105356013	105356013	Missense_Mutation	SNP	C	T	24	57	c.3796C>T	c.(3796-3798)CCC>TCC	p.P1266S
Pat_24	Pre-Treatment	PLD4	122618	37	14	105397256	105397256	Missense_Mutation	SNP	G	A	4	231	c.895G>A	c.(895-897)GTG>ATG	p.V299M
Pat_24	Pre-Treatment	AHNAK2	113146	37	14	105418760	105418760	Missense_Mutation	SNP	C	T	7	717	c.3028G>A	c.(3028-3030)GTA>ATA	p.V1010I
Pat_24	Pre-Treatment	NUDT14	256281	37	14	105643099	105643099	Missense_Mutation	SNP	G	A	4	220	c.200C>T	c.(199-201)GCG>GTG	p.A67V
Pat_24	Pre-Treatment	BRF1	2972	37	14	105677459	105677459	Missense_Mutation	SNP	C	T	6	329	c.1996G>A	c.(1996-1998)GAC>AAC	p.D666N
Pat_24	Pre-Treatment	GABRB3	2562	37	15	26812790	26812790	Missense_Mutation	SNP	G	A	4	144	c.773C>T	c.(772-774)ACG>ATG	p.T258M
Pat_24	Pre-Treatment	HERC2	8924	37	15	28422096	28422096	Missense_Mutation	SNP	C	T	4	115	c.9432G>A	c.(9430-9432)ATG>ATA	p.M3144I
Pat_24	Pre-Treatment	TMCO5A	145942	37	15	38229100	38229100	Missense_Mutation	SNP	G	A	35	34	c.193G>A	c.(193-195)GAG>AAG	p.E65K
Pat_24	Pre-Treatment	RASGRP1	10125	37	15	38795510	38795510	Missense_Mutation	SNP	G	T	4	90	c.1391C>A	c.(1390-1392)CCA>CAA	p.P464Q
Pat_24	Pre-Treatment	IVD	3712	37	15	40710365	40710365	Missense_Mutation	SNP	G	A	4	209	c.1184G>A	c.(1183-1185)CGC>CAC	p.R395H
Pat_24	Pre-Treatment	CASC5	57082	37	15	40933168	40933168	Missense_Mutation	SNP	G	A	6	377	c.5819G>A	c.(5818-5820)CGA>CAA	p.R1940Q
Pat_24	Pre-Treatment	MAPKBP1	23005	37	15	42115755	42115755	Missense_Mutation	SNP	C	T	4	175	c.3727C>T	c.(3727-3729)CGG>TGG	p.R1243W
Pat_24	Pre-Treatment	SPTBN5	51332	37	15	42160796	42160796	Missense_Mutation	SNP	G	A	4	198	c.5752C>T	c.(5752-5754)CGT>TGT	p.R1918C
Pat_24	Pre-Treatment	PLA2G4E	123745	37	15	42298211	42298211	Missense_Mutation	SNP	C	T	4	170	c.415G>A	c.(415-417)GTG>ATG	p.V139M
Pat_24	Pre-Treatment	CDAN1	146059	37	15	43020929	43020929	Missense_Mutation	SNP	C	T	4	156	c.2725G>A	c.(2725-2727)GGA>AGA	p.G909R
Pat_24	Pre-Treatment	TTBK2	146057	37	15	43109292	43109292	Nonsense_Mutation	SNP	G	A	4	187	c.541C>T	c.(541-543)CGA>TGA	p.R181*
Pat_24	Pre-Treatment	MAP1A	4130	37	15	43815947	43815947	Missense_Mutation	SNP	C	T	3	56	c.2276C>T	c.(2275-2277)CCG>CTG	p.P759L
Pat_24	Pre-Treatment	MAP1A	4130	37	15	43818722	43818722	Missense_Mutation	SNP	G	A	12	49	c.5051G>A	c.(5050-5052)AGG>AAG	p.R1684K
Pat_24	Pre-Treatment	CKMT1B	1159	37	15	43891417	43891418	Missense_Mutation	DNP	GG	AA	129	116	.1200_1201GG>A	198-1203)CTGGAG>CTAA	p.E401K
Pat_24	Pre-Treatment	DUOX2	50506	37	15	45388258	45388258	Missense_Mutation	SNP	C	T	63	54	c.3848G>A	c.(3847-3849)GGA>GAA	p.G1283E
Pat_24	Pre-Treatment	SEMA6D	80031	37	15	48063158	48063158	Missense_Mutation	SNP	G	A	5	165	c.2398G>A	c.(2398-2400)GCT>ACT	p.A800T
Pat_24	Pre-Treatment	CYP19A1	1588	37	15	51507369	51507369	Missense_Mutation	SNP	C	T	4	216	c.919G>A	c.(919-921)GCT>ACT	p.A307T
Pat_24	Pre-Treatment	GLDN	342035	37	15	51675633	51675633	Missense_Mutation	SNP	G	A	131	298	c.416G>A	c.(415-417)GGA>GAA	p.G139E
Pat_24	Pre-Treatment	DMXL2	23312	37	15	51756911	51756911	Missense_Mutation	SNP	C	T	4	167	c.7766G>A	c.(7765-7767)CGA>CAA	p.R2589Q
Pat_24	Pre-Treatment	MYO5C	55930	37	15	52497186	52497186	Missense_Mutation	SNP	C	T	6	112	c.4696G>A	c.(4696-4698)GGC>AGC	p.G1566S
Pat_24	Pre-Treatment	GCNT3	9245	37	15	59910924	59910924	Missense_Mutation	SNP	C	T	60	196	c.487C>T	c.(487-489)CAT>TAT	p.H163Y
Pat_24	Pre-Treatment	CILP	8483	37	15	65499120	65499120	Missense_Mutation	SNP	C	T	230	154	c.424G>A	c.(424-426)GGA>AGA	p.G142R
Pat_24	Pre-Treatment	MEGF11	84465	37	15	66262997	66262997	Missense_Mutation	SNP	C	T	16	45	c.793G>A	c.(793-795)GGG>AGG	p.G265R
Pat_24	Pre-Treatment	DIS3L	115752	37	15	66618578	66618578	Missense_Mutation	SNP	G	A	4	235	c.2077G>A	c.(2077-2079)GCC>ACC	p.A693T
Pat_24	Pre-Treatment	DIS3L	115752	37	15	66624358	66624358	Missense_Mutation	SNP	G	A	48	136	c.2681G>A	c.(2680-2682)AGG>AAG	p.R894K
Pat_24	Pre-Treatment	PIAS1	8554	37	15	68434663	68434663	Missense_Mutation	SNP	A	G	4	116	c.590A>G	c.(589-591)CAG>CGG	p.Q197R
Pat_24	Pre-Treatment	NEO1	4756	37	15	73581579	73581579	Missense_Mutation	SNP	C	T	4	114	c.3742C>T	c.(3742-3744)CCT>TCT	p.P1248S
Pat_24	Pre-Treatment	C15orf60	283677	37	15	73843396	73843396	Missense_Mutation	SNP	G	A	4	64	c.451G>A	c.(451-453)GGA>AGA	p.G151R
Pat_24	Pre-Treatment	CSK	1445	37	15	75094194	75094194	Missense_Mutation	SNP	C	T	4	120	c.1046C>T	c.(1045-1047)CCA>CTA	p.P349L
Pat_24	Pre-Treatment	LMAN1L	79748	37	15	75117900	75117900	Missense_Mutation	SNP	T	C	4	241	c.1535T>C	c.(1534-1536)CTG>CCG	p.L512P

Pat_24	Pre-Treatment	RPP25	54913	37	15	75248458	75248458	Missense_Mutation	SNP	G	A	21	38	c.467C>T	c.(466-468)CCC>CTC	p.P156L
Pat_24	Pre-Treatment	KIAA1024	23251	37	15	79749478	79749478	Missense_Mutation	SNP	G	A	6	425	c.989G>A	c.(988-990)AGC>AAC	p.S330N
Pat_24	Pre-Treatment	DET1	55070	37	15	89070830	89070830	Missense_Mutation	SNP	C	T	4	153	c.1271G>A	c.(1270-1272)CGG>CAG	p.R424Q
Pat_24	Pre-Treatment	MCTP2	55784	37	15	94841646	94841646	Missense_Mutation	SNP	C	T	16	64	c.152C>T	c.(151-153)TCT>TTT	p.S51F
Pat_24	Pre-Treatment	IGF1R	3480	37	15	99456466	99456466	Missense_Mutation	SNP	C	T	5	264	c.1783C>T	c.(1783-1785)CGT>TGT	p.R595C
Pat_24	Pre-Treatment	IGF1R	3480	37	15	99500543	99500543	Missense_Mutation	SNP	G	A	4	128	c.3976G>A	c.(3976-3978)GAG>AAG	p.E1326K
Pat_24	Pre-Treatment	SYNM	23336	37	15	99670857	99670857	Missense_Mutation	SNP	T	G	30	31	c.2292T>G	c.(2290-2292)TTT>TTG	p.F764L
Pat_24	Pre-Treatment	RHBDF1	64285	37	16	111666	111666	Missense_Mutation	SNP	C	T	4	192	c.1237G>A	c.(1237-1239)GTG>ATG	p.V413M
Pat_24	Pre-Treatment	SOLH	6650	37	16	599050	599050	Missense_Mutation	SNP	C	T	5	369	c.1507C>T	c.(1507-1509)CCC>TCC	p.P503S
Pat_24	Pre-Treatment	RHBDL1	9028	37	16	727118	727118	Missense_Mutation	SNP	G	T	4	92	c.769G>T	c.(769-771)GGG>TGG	p.G257W
Pat_24	Pre-Treatment	FBXL16	146330	37	16	744675	744675	Missense_Mutation	SNP	T	G	14	23	c.1250A>C	c.(1249-1251)CAC>CCC	p.H417P
Pat_24	Pre-Treatment	PTX4	390667	37	16	1536466	1536466	Missense_Mutation	SNP	C	T	4	88	c.896G>A	c.(895-897)CGC>CAC	p.R299H
Pat_24	Pre-Treatment	TELO2	9894	37	16	1545592	1545592	Missense_Mutation	SNP	G	A	4	202	c.581G>A	c.(580-582)CGG>CAG	p.R194Q
Pat_24	Pre-Treatment	TBL3	10607	37	16	2027116	2027116	Missense_Mutation	SNP	G	A	5	178	c.1502G>A	c.(1501-1503)CGC>CAC	p.R501H
Pat_24	Pre-Treatment	TSC2	7249	37	16	2124261	2124261	Missense_Mutation	SNP	G	A	4	131	c.2416G>A	c.(2416-2418)GTG>ATG	p.V806M
Pat_24	Pre-Treatment	TSC2	7249	37	16	2125875	2125875	Missense_Mutation	SNP	C	T	4	203	c.2621C>T	c.(2620-2622)CCG>CTG	p.P874L
Pat_24	Pre-Treatment	TSC2	7249	37	16	2138495	2138495	Missense_Mutation	SNP	C	T	4	166	c.5308C>T	c.(5308-5310)CCT>TCT	p.P1770S
Pat_24	Pre-Treatment	PKD1	5310	37	16	2140785	2140785	Missense_Mutation	SNP	G	A	4	163	c.12028C>T	c.(12028-12030)CGC>TGC	p.R4010C
Pat_24	Pre-Treatment	PKD1	5310	37	16	2152968	2152968	Missense_Mutation	SNP	T	C	4	146	c.8795A>G	c.(8794-8796)CAC>CGC	p.H2932R
Pat_24	Pre-Treatment	ABCA3	21	37	16	2354118	2354118	Missense_Mutation	SNP	G	A	5	425	c.1319C>T	c.(1318-1320)CCC>CTC	p.P440L
Pat_24	Pre-Treatment	SRRM2	23524	37	16	2817405	2817406	Missense_Mutation	DNP	CC	TT	120	178	.6876_6877CC>T	874-6879)GCCCCA>GCT	p.P2293S
Pat_24	Pre-Treatment	SRRM2	23524	37	16	2818022	2818022	Missense_Mutation	SNP	C	T	4	153	c.7493C>T	c.(7492-7494)GCC>GTC	p.A2498V
Pat_24	Pre-Treatment	ZNF213	7760	37	16	3187516	3187516	Missense_Mutation	SNP	C	T	4	189	c.235C>T	c.(235-237)CGT>TGT	p.R79C
Pat_24	Pre-Treatment	ZNF213	7760	37	16	3187633	3187633	Missense_Mutation	SNP	G	A	3	56	c.352G>A	c.(352-354)GCC>ACC	p.A118T
Pat_24	Pre-Treatment	ZNF263	10127	37	16	3340442	3340442	Missense_Mutation	SNP	C	T	4	200	c.1936C>T	c.(1936-1938)CGG>TGG	p.R646W
Pat_24	Pre-Treatment	NAT15	79903	37	16	3526288	3526288	Missense_Mutation	SNP	G	A	4	134	c.61G>A	c.(61-63)GAT>AAT	p.D21N
Pat_24	Pre-Treatment	MGRN1	23295	37	16	4721398	4721398	Missense_Mutation	SNP	C	T	4	181	c.733C>T	c.(733-735)CGG>TGG	p.R245W
Pat_24	Pre-Treatment	A2BP1	54715	37	16	7680638	7680638	Missense_Mutation	SNP	G	A	30	73	c.710G>A	c.(709-711)GGA>GAA	p.G237E
Pat_24	Pre-Treatment	TEKT5	146279	37	16	10788232	10788232	Nonsense_Mutation	SNP	G	A	136	254	c.499C>T	c.(499-501)CAG>TAG	p.Q167*
Pat_24	Pre-Treatment	CLEC16A	23274	37	16	11272395	11272395	Missense_Mutation	SNP	G	A	4	214	c.3010G>A	c.(3010-3012)GTC>ATC	p.V1004I
Pat_24	Pre-Treatment	TXNDC11	51061	37	16	11794417	11794417	Missense_Mutation	SNP	T	C	57	88	c.878A>G	c.(877-879)TAC>TGC	p.Y293C
Pat_24	Pre-Treatment	ERCC4	2072	37	16	14022037	14022037	Missense_Mutation	SNP	C	T	39	113	c.737C>T	c.(736-738)TCG>TTG	p.S246L
Pat_24	Pre-Treatment	ABCC6	368	37	16	16276744	16276744	Missense_Mutation	SNP	C	T	4	205	c.1987G>A	c.(1987-1989)GGT>AGT	p.G663S
Pat_24	Pre-Treatment	TMC7	79905	37	16	19049260	19049260	Missense_Mutation	SNP	G	A	4	188	c.1070G>A	c.(1069-1071)CGC>CAC	p.R357H
Pat_24	Pre-Treatment	ITPRIPL2	162073	37	16	19126600	19126600	Missense_Mutation	SNP	C	T	6	349	c.817C>T	c.(817-819)CGC>TGC	p.R273C
Pat_24	Pre-Treatment	SYT17	51760	37	16	19195170	19195170	Missense_Mutation	SNP	G	A	6	358	c.652G>A	c.(652-654)GAT>AAT	p.D218N
Pat_24	Pre-Treatment	IGSF6	10261	37	16	21663853	21663853	Missense_Mutation	SNP	C	T	4	158	c.67G>A	c.(67-69)GGT>AGT	p.G23S
Pat_24	Pre-Treatment	OTOA	146183	37	16	21726384	21726384	Missense_Mutation	SNP	C	T	6	554	c.1399C>T	c.(1399-1401)CGC>TGC	p.R467C
Pat_24	Pre-Treatment	POLR3E	55718	37	16	22328500	22328500	Missense_Mutation	SNP	G	A	5	244	c.838G>A	c.(838-840)GAT>AAT	p.D280N
Pat_24	Pre-Treatment	CD19	930	37	16	28944394	28944394	Missense_Mutation	SNP	G	A	66	80	c.518G>A	c.(517-519)TGT>TAT	p.C173Y
Pat_24	Pre-Treatment	SPN	6693	37	16	29675747	29675747	Missense_Mutation	SNP	C	T	4	206	c.698C>T	c.(697-699)TCT>TTT	p.S233F
Pat_24	Pre-Treatment	SEZ6L2	26470	37	16	29900013	29900013	Missense_Mutation	SNP	G	A	4	74	c.887C>T	c.(886-888)CCG>CTG	p.P296L
Pat_24	Pre-Treatment	ZNF689	115509	37	16	30616499	30616499	Missense_Mutation	SNP	G	A	4	119	c.589C>T	c.(589-591)CGG>TGG	p.R197W
Pat_24	Pre-Treatment	SETD1A	9739	37	16	30992162	30992162	Missense_Mutation	SNP	C	A	4	71	c.4684C>A	c.(4684-4686)CAG>AAG	p.Q1562K
Pat_24	Pre-Treatment	TRIM72	493829	37	16	31234180	31234180	Missense_Mutation	SNP	C	T	4	175	c.773C>T	c.(772-774)CCC>CTC	p.P258L
Pat_24	Pre-Treatment	ITGAX	3687	37	16	31393220	31393220	Missense_Mutation	SNP	G	A	49	92	c.3484G>A	c.(3484-3486)GAG>AAG	p.E1162K
Pat_24	Pre-Treatment	VPS35	55737	37	16	46714661	46714661	Missense_Mutation	SNP	G	A	4	168	c.428C>T	c.(427-429)CCC>CTC	p.P143L

Pat_24	Pre-Treatment	ZNF423	23090	37	16	49670154	49670154	Missense_Mutation	SNP	G	A	24	41	c.2909C>T	c.(2908-2910)TCG>TTG	p.S970L
Pat_24	Pre-Treatment	ADCY7	113	37	16	50324486	50324486	Missense_Mutation	SNP	C	T	41	73	c.290C>T	c.(289-291)GCG>GTG	p.A97V
Pat_24	Pre-Treatment	CES7	221223	37	16	55880509	55880509	Missense_Mutation	SNP	C	T	7	563	c.1582G>A	c.(1582-1584)GGA>AGA	p.G528R
Pat_24	Pre-Treatment	MT3	4504	37	16	56623800	56623800	Missense_Mutation	SNP	C	T	4	164	c.50C>T	c.(49-51)GCG>GTG	p.A17V
Pat_24	Pre-Treatment	SLC12A3	6559	37	16	56920388	56920388	Splice_Site	SNP	G	A	4	132	c.2037_splice	c.e16+1	p.I679_splice
Pat_24	Pre-Treatment	KIFC3	3801	37	16	57794802	57794803	Missense_Mutation	DNP	GG	AT	23	8	.2067_2068CC>A	065-2070)AGCCGC>AGA	689_690SR>R
Pat_24	Pre-Treatment	GOT2	2806	37	16	58752448	58752448	Missense_Mutation	SNP	C	T	5	286	c.580G>A	c.(580-582)GCT>ACT	p.A194T
Pat_24	Pre-Treatment	HSF4	3299	37	16	67200260	67200260	Missense_Mutation	SNP	C	T	4	120	c.523C>T	c.(523-525)CGG>TGG	p.R175W
Pat_24	Pre-Treatment	SLC9A5	6553	37	16	67304752	67304752	Missense_Mutation	SNP	C	T	4	107	c.2330C>T	c.(2329-2331)TCG>TTG	p.S777L
Pat_24	Pre-Treatment	PARD6A	50855	37	16	67695433	67695433	Missense_Mutation	SNP	C	T	5	330	c.139C>T	c.(139-141)CGG>TGG	p.R47W
Pat_24	Pre-Treatment	COG8	84342	37	16	69370596	69370596	Missense_Mutation	SNP	C	T	4	137	c.397G>A	c.(397-399)GAG>AAG	p.E133K
Pat_24	Pre-Treatment	MTSS1L	92154	37	16	70712262	70712262	Missense_Mutation	SNP	C	T	5	128	c.517G>A	c.(517-519)GAC>AAC	p.D173N
Pat_24	Pre-Treatment	HYDIN	54768	37	16	70954955	70954955	Missense_Mutation	SNP	C	T	5	174	c.7321G>A	c.(7321-7323)GAA>AAA	p.E2441K
Pat_24	Pre-Treatment	KIAA0174	9798	37	16	71955271	71955271	Missense_Mutation	SNP	C	T	4	134	c.506C>T	c.(505-507)GCC>GTC	p.A169V
Pat_24	Pre-Treatment	DHX38	9785	37	16	72139428	72139428	Missense_Mutation	SNP	G	A	4	188	c.2392G>A	c.(2392-2394)GTT>ATT	p.V798I
Pat_24	Pre-Treatment	VAT1L	57687	37	16	77850847	77850847	Missense_Mutation	SNP	G	A	68	80	c.263G>A	c.(262-264)CGA>CAA	p.R88Q
Pat_24	Pre-Treatment	SLC38A8	146167	37	16	84075678	84075678	Missense_Mutation	SNP	C	T	4	239	c.85G>A	c.(85-87)GCT>ACT	p.A29T
Pat_24	Pre-Treatment	ZCCHC14	23174	37	16	87446244	87446244	Missense_Mutation	SNP	C	T	4	158	c.1672G>A	c.(1672-1674)GCC>ACC	p.A558T
Pat_24	Pre-Treatment	CA5A	763	37	16	87969963	87969963	Nonsense_Mutation	SNP	G	A	5	277	c.94C>T	c.(94-96)CGA>TGA	p.R32*
Pat_24	Pre-Treatment	TRAPPC2L	51693	37	16	88925066	88925066	Missense_Mutation	SNP	G	A	6	461	c.73G>A	c.(73-75)GAG>AAG	p.E25K
Pat_24	Pre-Treatment	SPIRE2	84501	37	16	89916844	89916844	Missense_Mutation	SNP	G	A	3	36	c.421G>A	c.(421-423)GGC>AGC	p.G141S
Pat_24	Pre-Treatment	DEF8	54849	37	16	90027396	90027396	Missense_Mutation	SNP	G	A	5	363	c.755G>A	c.(754-756)AGC>AAC	p.S252N
Pat_24	Pre-Treatment	PRPF8	10594	37	17	1577755	1577755	Missense_Mutation	SNP	G	A	6	222	c.3280C>T	c.(3280-3282)CGC>TGC	p.R1094C
Pat_24	Pre-Treatment	SMG6	23293	37	17	2203290	2203290	Missense_Mutation	SNP	G	A	4	68	c.757C>T	c.(757-759)CGC>TGC	p.R253C
Pat_24	Pre-Treatment	SHPK	23729	37	17	3514093	3514093	Missense_Mutation	SNP	G	A	5	259	c.1198C>T	c.(1198-1200)CGG>TGG	p.R400W
Pat_24	Pre-Treatment	P2RX5	5026	37	17	3593916	3593916	Missense_Mutation	SNP	G	A	4	173	c.419C>T	c.(418-420)GCG>GTG	p.A140V
Pat_24	Pre-Treatment	ITGAE	3682	37	17	3657141	3657141	Missense_Mutation	SNP	G	A	64	107	c.1463C>T	c.(1462-1464)GCC>GTC	p.A488V
Pat_24	Pre-Treatment	GGT6	124975	37	17	4462050	4462050	Nonsense_Mutation	SNP	G	A	3	12	c.742C>T	c.(742-744)CGA>TGA	p.R248*
Pat_24	Pre-Treatment	MINK1	50488	37	17	4798370	4798370	Missense_Mutation	SNP	C	T	4	128	c.2918C>T	c.(2917-2919)GCC>GTC	p.A973V
Pat_24	Pre-Treatment	KIF1C	10749	37	17	4925960	4925960	Missense_Mutation	SNP	C	T	3	34	c.2584C>T	c.(2584-2586)CGG>TGG	p.R862W
Pat_24	Pre-Treatment	GPR172B	55065	37	17	4937566	4937566	Missense_Mutation	SNP	G	A	4	130	c.218C>T	c.(217-219)CCG>CTG	p.P73L
Pat_24	Pre-Treatment	NUP88	4927	37	17	5292182	5292182	Missense_Mutation	SNP	G	A	26	74	c.1583C>T	c.(1582-1584)TCC>TTC	p.S528F
Pat_24	Pre-Treatment	BCL6B	255877	37	17	6930888	6930888	Missense_Mutation	SNP	G	A	5	228	c.1390G>A	c.(1390-1392)GGA>AGA	p.G464R
Pat_24	Pre-Treatment	NEURL4	84461	37	17	7221108	7221108	Nonsense_Mutation	SNP	T	A	4	81	c.4204A>T	c.(4204-4206)AGA>TGA	p.R1402*
Pat_24	Pre-Treatment	TMEM102	284114	37	17	7339756	7339756	Missense_Mutation	SNP	C	T	4	147	c.458C>T	c.(457-459)ACC>ATC	p.T153I
Pat_24	Pre-Treatment	ZBTB4	57659	37	17	7366997	7366997	Missense_Mutation	SNP	G	A	4	185	c.1304C>T	c.(1303-1305)CCG>CTG	p.P435L
Pat_24	Pre-Treatment	POLR2A	5430	37	17	7401081	7401081	Missense_Mutation	SNP	C	T	4	199	c.1094C>T	c.(1093-1095)ACT>ATT	p.T365I
Pat_24	Pre-Treatment	POLR2A	5430	37	17	7404944	7404944	Nonsense_Mutation	SNP	C	T	5	260	c.2245C>T	c.(2245-2247)CGA>TGA	p.R749*
Pat_24	Pre-Treatment	DNAH2	146754	37	17	7722299	7722299	Missense_Mutation	SNP	C	T	4	55	c.10733C>T	c.(10732-10734)ACC>ATC	p.T3578I
Pat_24	Pre-Treatment	KCNAB3	9196	37	17	7826851	7826851	Missense_Mutation	SNP	G	A	4	122	c.1060C>T	c.(1060-1062)CGC>TGC	p.R354C
Pat_24	Pre-Treatment	CNTROB	116840	37	17	7851874	7851874	Missense_Mutation	SNP	G	A	4	146	c.2450G>A	c.(2449-2451)CGG>CAG	p.R817Q
Pat_24	Pre-Treatment	PIK3R5	23533	37	17	8793371	8793371	Missense_Mutation	SNP	C	T	4	128	c.730G>A	c.(730-732)GGG>AGG	p.G244R
Pat_24	Pre-Treatment	MYH8	4626	37	17	10304868	10304868	Missense_Mutation	SNP	C	T	176	287	c.2923G>A	c.(2923-2925)GAG>AAG	p.E975K
Pat_24	Pre-Treatment	MYH4	4622	37	17	10353795	10353795	Missense_Mutation	SNP	G	A	5	378	c.4156C>T	c.(4156-4158)CGC>TGC	p.R1386C
Pat_24	Pre-Treatment	MYH4	4622	37	17	10360853	10360853	Missense_Mutation	SNP	G	A	92	120	c.1781C>T	c.(1780-1782)GCC>GTC	p.A594V
Pat_24	Pre-Treatment	MYH4	4622	37	17	10364367	10364367	Missense_Mutation	SNP	G	A	4	159	c.1013C>T	c.(1012-1014)GCT>GTT	p.A338V
Pat_24	Pre-Treatment	MYH1	4619	37	17	10412834	10412834	Missense_Mutation	SNP	C	T	101	194	c.1555G>A	c.(1555-1557)GAC>AAC	p.D519N

Pat_24	Pre-Treatment	MYH2	4620	37	17	10432937	10432937	Missense_Mutation	SNP	C	T	49	94	c.3061G>A	c.(3061-3063)GAC>AAC	p.D1021N
Pat_24	Pre-Treatment	MYH3	4621	37	17	10541496	10541496	Missense_Mutation	SNP	G	A	5	155	c.3593C>T	c.(3592-3594)GCG>GTG	p.A1198V
Pat_24	Pre-Treatment	MYH3	4621	37	17	10547729	10547729	Missense_Mutation	SNP	G	A	4	187	c.1349C>T	c.(1348-1350)ACG>ATG	p.T450M
Pat_24	Pre-Treatment	DNAH9	1770	37	17	11795211	11795211	Missense_Mutation	SNP	C	T	5	432	c.11230C>T	c.(11230-11232)CGC>TGC	p.R3744C
Pat_24	Pre-Treatment	MYOCD	93649	37	17	12642601	12642601	Missense_Mutation	SNP	C	A	55	65	c.673C>A	c.(673-675)CTT>ATT	p.L225I
Pat_24	Pre-Treatment	NCOR1	9611	37	17	15978955	15978955	Missense_Mutation	SNP	G	A	5	185	c.3563C>T	c.(3562-3564)TCG>TTG	p.S1188L
Pat_24	Pre-Treatment	TRPV2	51393	37	17	16335108	16335108	Missense_Mutation	SNP	G	A	4	143	c.1598G>A	c.(1597-1599)CGG>CAG	p.R533Q
Pat_24	Pre-Treatment	RAI1	10743	37	17	17697049	17697049	Missense_Mutation	SNP	G	A	4	137	c.787G>A	c.(787-789)GTC>ATC	p.V263I
Pat_24	Pre-Treatment	SHMT1	6470	37	17	18256995	18256995	Missense_Mutation	SNP	G	A	5	321	c.233C>T	c.(232-234)CCG>CTG	p.P78L
Pat_24	Pre-Treatment	MFAP4	4239	37	17	19288418	19288418	Missense_Mutation	SNP	C	T	7	390	c.514G>A	c.(514-516)GGG>AGG	p.G172R
Pat_24	Pre-Treatment	RNF112	7732	37	17	19316944	19316944	Missense_Mutation	SNP	G	A	12	28	c.775G>A	c.(775-777)GAA>AAA	p.E259K
Pat_24	Pre-Treatment	SLC47A2	146802	37	17	19618059	19618059	Missense_Mutation	SNP	G	A	8	611	c.269C>T	c.(268-270)TCG>TTG	p.S90L
Pat_24	Pre-Treatment	ALDH3A1	218	37	17	19648378	19648378	Missense_Mutation	SNP	G	A	21	26	c.65C>T	c.(64-66)CCG>CTG	p.P22L
Pat_24	Pre-Treatment	CYTSB	92521	37	17	20163608	20163608	Splice_Site	SNP	G	A	4	74	c.2940_splice	c.e12+1	p.A980_splice
Pat_24	Pre-Treatment	SEZ6	124925	37	17	27308551	27308551	Missense_Mutation	SNP	G	A	12	26	c.562C>T	c.(562-564)CCT>TCT	p.P188S
Pat_24	Pre-Treatment	SEZ6	124925	37	17	27308970	27308970	Missense_Mutation	SNP	G	A	17	42	c.143C>T	c.(142-144)CCT>CTT	p.P48L
Pat_24	Pre-Treatment	TAOK1	57551	37	17	27861169	27861169	Missense_Mutation	SNP	C	A	4	81	c.2395C>A	c.(2395-2397)CAG>AAG	p.Q799K
Pat_24	Pre-Treatment	CPD	1362	37	17	28747972	28747972	Missense_Mutation	SNP	C	T	4	151	c.1108C>T	c.(1108-1110)CGT>TGT	p.R370C
Pat_24	Pre-Treatment	RAB11FIP4	84440	37	17	29848344	29848344	Missense_Mutation	SNP	G	A	4	95	c.724G>A	c.(724-726)GTC>ATC	p.V242I
Pat_24	Pre-Treatment	MYO1D	4642	37	17	30821877	30821877	Missense_Mutation	SNP	C	T	4	128	c.2921G>A	c.(2920-2922)GGG>GAG	p.G974E
Pat_24	Pre-Treatment	CCL18	6362	37	17	34397903	34397903	Missense_Mutation	SNP	C	T	29	76	c.164C>T	c.(163-165)CCC>CTC	p.P55L
Pat_24	Pre-Treatment	GGNBP2	79893	37	17	34937778	34937778	Missense_Mutation	SNP	C	T	39	56	c.1025C>T	c.(1024-1026)ACC>ATC	p.T342I
Pat_24	Pre-Treatment	ACACA	31	37	17	35581989	35581989	Missense_Mutation	SNP	C	T	4	136	c.3287G>A	c.(3286-3288)CGC>CAC	p.R1096H
Pat_24	Pre-Treatment	ACACA	31	37	17	35627700	35627700	Missense_Mutation	SNP	C	T	20	265	c.950G>A	c.(949-951)GGA>GAA	p.G317E
Pat_24	Pre-Treatment	MLLT6	4302	37	17	36872692	36872692	Missense_Mutation	SNP	C	T	30	35	c.1109C>T	c.(1108-1110)TCC>TTC	p.S370F
Pat_24	Pre-Treatment	FBXO47	494188	37	17	37119185	37119185	Missense_Mutation	SNP	C	T	4	171	c.94G>A	c.(94-96)GGC>AGC	p.G32S
Pat_24	Pre-Treatment	GRB7	2886	37	17	37902175	37902175	Missense_Mutation	SNP	G	A	7	644	c.1280G>A	c.(1279-1281)CGC>CAC	p.R427H
Pat_24	Pre-Treatment	CCR7	1236	37	17	38711853	38711853	Missense_Mutation	SNP	G	A	4	169	c.278C>T	c.(277-279)ACC>ATC	p.T93I
Pat_24	Pre-Treatment	KRT26	353288	37	17	38926062	38926062	Missense_Mutation	SNP	C	T	93	131	c.913G>A	c.(913-915)GAA>AAA	p.E305K
Pat_24	Pre-Treatment	KRT12	3859	37	17	39019399	39019399	Missense_Mutation	SNP	C	T	4	205	c.1292G>A	c.(1291-1293)CGC>CAC	p.R431H
Pat_24	Pre-Treatment	KRT12	3859	37	17	39023219	39023219	Missense_Mutation	SNP	C	T	4	205	c.220G>A	c.(220-222)GGA>AGA	p.G74R
Pat_24	Pre-Treatment	KRT12	3859	37	17	39023402	39023402	Missense_Mutation	SNP	G	A	5	149	c.37C>T	c.(37-39)CGC>TGC	p.R13C
Pat_24	Pre-Treatment	KRT37	8688	37	17	39580309	39580309	Missense_Mutation	SNP	C	T	4	232	c.467G>A	c.(466-468)CGT>CAT	p.R156H
Pat_24	Pre-Treatment	KRT32	3882	37	17	39616393	39616393	Missense_Mutation	SNP	G	A	4	94	c.1316C>T	c.(1315-1317)CCT>CTT	p.P439L
Pat_24	Pre-Treatment	FKBP10	60681	37	17	39973332	39973332	Missense_Mutation	SNP	G	T	4	181	c.268G>T	c.(268-270)GCC>TCC	p.A90S
Pat_24	Pre-Treatment	GHDC	84514	37	17	40344316	40344316	Missense_Mutation	SNP	C	T	4	168	c.832G>A	c.(832-834)GGG>AGG	p.G278R
Pat_24	Pre-Treatment	TUBG2	27175	37	17	40818688	40818688	Missense_Mutation	SNP	G	A	5	256	c.1226G>A	c.(1225-1227)CGT>CAT	p.R409H
Pat_24	Pre-Treatment	BRCA1	672	37	17	41209095	41209095	Nonsense_Mutation	SNP	G	A	6	393	c.5251C>T	c.(5251-5253)CGA>TGA	p.R1751*
Pat_24	Pre-Treatment	MPP3	4356	37	17	41908611	41908611	Splice_Site	SNP	C	T	5	186	c.222_splice	c.e5+1	p.D74_splice
Pat_24	Pre-Treatment	NSF	4905	37	17	44788404	44788404	Nonsense_Mutation	SNP	C	T	43	92	c.1546C>T	c.(1546-1548)CGA>TGA	p.R516*
Pat_24	Pre-Treatment	IGF2BP1	10642	37	17	47115649	47115649	Missense_Mutation	SNP	G	A	4	88	c.521G>A	c.(520-522)CGG>CAG	p.R174Q
Pat_24	Pre-Treatment	C17orf67	339210	37	17	54892231	54892231	Missense_Mutation	SNP	C	T	6	718	c.227G>A	c.(226-228)CGG>CAG	p.R76Q
Pat_24	Pre-Treatment	C17orf67	339210	37	17	54892253	54892253	Missense_Mutation	SNP	C	T	7	728	c.205G>A	c.(205-207)GGA>AGA	p.G69R
Pat_24	Pre-Treatment	OR4D2	124538	37	17	56247618	56247618	Missense_Mutation	SNP	C	T	52	77	c.602C>T	c.(601-603)TCC>TTC	p.S201F
Pat_24	Pre-Treatment	BZRAP1	9256	37	17	56389471	56389471	Missense_Mutation	SNP	G	A	4	117	c.2711C>T	c.(2710-2712)CCC>CTC	p.P904L
Pat_24	Pre-Treatment	TRIM37	4591	37	17	57157205	57157205	Missense_Mutation	SNP	C	T	65	74	c.526G>A	c.(526-528)GAT>AAT	p.D176N
Pat_24	Pre-Treatment	BCAS3	54828	37	17	59001793	59001793	Missense_Mutation	SNP	G	A	4	233	c.1019G>A	c.(1018-1020)AGT>AAT	p.S340N

Pat_24	Pre-Treatment	MED13	9969	37	17	60088302	60088302	Missense_Mutation	SNP	C	T	4	217	c.1576G>A	c.(1576-1578)GAA>AAA	p.E526K
Pat_24	Pre-Treatment	MED13	9969	37	17	60106978	60106978	Missense_Mutation	SNP	C	T	4	169	c.1207G>A	c.(1207-1209)GAA>AAA	p.E403K
Pat_24	Pre-Treatment	TBC1D3P2	440452	37	17	60348753	60348753	Missense_Mutation	SNP	C	G	4	152	c.352G>C	c.(352-354)GAG>CAG	p.E118Q
Pat_24	Pre-Treatment	ACE	1636	37	17	61555323	61555323	Missense_Mutation	SNP	C	T	3	36	c.281C>T	c.(280-282)GCG>GTG	p.A94V
Pat_24	Pre-Treatment	GH2	2689	37	17	61958766	61958766	Missense_Mutation	SNP	G	A	6	408	c.124C>T	c.(124-126)CGC>TGC	p.R42C
Pat_24	Pre-Treatment	GPR142	350383	37	17	72368171	72368171	Missense_Mutation	SNP	G	A	4	101	c.821G>A	c.(820-822)CGG>CAG	p.R274Q
Pat_24	Pre-Treatment	UNK	85451	37	17	73816091	73816091	Missense_Mutation	SNP	C	T	4	119	c.1967C>T	c.(1966-1968)CCC>CTC	p.P656L
Pat_24	Pre-Treatment	MRPL38	64978	37	17	73895736	73895736	Missense_Mutation	SNP	G	A	3	53	c.730C>T	c.(730-732)CGG>TGG	p.R244W
Pat_24	Pre-Treatment	RNF157	114804	37	17	74141393	74141393	Missense_Mutation	SNP	G	T	4	49	c.1963C>A	c.(1963-1965)CAG>AAG	p.Q655K
Pat_24	Pre-Treatment	RNF157	114804	37	17	74157728	74157728	Missense_Mutation	SNP	G	A	4	83	c.953C>T	c.(952-954)CCC>CTC	p.P318L
Pat_24	Pre-Treatment	QRICH2	84074	37	17	74289004	74289004	Missense_Mutation	SNP	G	A	8	174	c.1306C>T	c.(1306-1308)CGG>TGG	p.R436W
Pat_24	Pre-Treatment	MXRA7	439921	37	17	74673705	74673705	Missense_Mutation	SNP	C	T	6	289	c.580G>A	c.(580-582)GAC>AAC	p.D194N
Pat_24	Pre-Treatment	PGS1	9489	37	17	76394430	76394430	Missense_Mutation	SNP	G	A	4	178	c.509G>A	c.(508-510)CGA>CAA	p.R170Q
Pat_24	Pre-Treatment	LGALS3BP	3959	37	17	76972089	76972089	Missense_Mutation	SNP	C	T	15	51	c.202G>A	c.(202-204)GAG>AAG	p.E68K
Pat_24	Pre-Treatment	CANT1	124583	37	17	76989694	76989694	Missense_Mutation	SNP	G	A	4	99	c.1144C>T	c.(1144-1146)CGC>TGC	p.R382C
Pat_24	Pre-Treatment	RNF213	57674	37	17	78320284	78320284	Missense_Mutation	SNP	G	A	5	131	c.2368G>A	c.(2368-2370)GAC>AAC	p.D790N
Pat_24	Pre-Treatment	TMEM105	284186	37	17	79287722	79287722	Missense_Mutation	SNP	G	A	6	257	c.119C>T	c.(118-120)ACA>ATA	p.T40I
Pat_24	Pre-Treatment	P4HB	5034	37	17	79804327	79804327	Missense_Mutation	SNP	C	T	6	314	c.1034G>A	c.(1033-1035)CGC>CAC	p.R345H
Pat_24	Pre-Treatment	TBCD	6904	37	17	80726375	80726375	Missense_Mutation	SNP	G	A	5	307	c.515G>A	c.(514-516)GGG>GAG	p.G172E
Pat_24	Pre-Treatment	ENOSF1	55556	37	18	694292	694292	Missense_Mutation	SNP	C	T	4	194	c.352G>A	c.(352-354)GTC>ATC	p.V118I
Pat_24	Pre-Treatment	MYOM1	8736	37	18	3102547	3102547	Missense_Mutation	SNP	G	A	77	115	c.3500C>T	c.(3499-3501)TCC>TTC	p.S1167F
Pat_24	Pre-Treatment	L3MBTL4	91133	37	18	6239762	6239762	Missense_Mutation	SNP	C	T	4	206	c.662G>A	c.(661-663)CGC>CAC	p.R221H
Pat_24	Pre-Treatment	MPPE1	65258	37	18	11886762	11886762	Missense_Mutation	SNP	G	A	4	91	c.694C>T	c.(694-696)CGG>TGG	p.R232W
Pat_24	Pre-Treatment	IMPA2	3613	37	18	12009956	12009956	Missense_Mutation	SNP	C	T	101	157	c.305C>T	c.(304-306)CCC>CTC	p.P102L
Pat_24	Pre-Treatment	MEP1B	4225	37	18	29793298	29793298	Missense_Mutation	SNP	C	T	13	15	c.1355C>T	c.(1354-1356)CCA>CTA	p.P452L
Pat_24	Pre-Treatment	MEP1B	4225	37	18	29797906	29797906	Missense_Mutation	SNP	G	A	4	162	c.2069G>A	c.(2068-2070)CGA>CAA	p.R690Q
Pat_24	Pre-Treatment	ASXL3	80816	37	18	31325120	31325120	Missense_Mutation	SNP	G	A	17	25	c.5308G>A	c.(5308-5310)GGA>AGA	p.G1770R
Pat_24	Pre-Treatment	SLC14A2	8170	37	18	43212383	43212383	Missense_Mutation	SNP	C	T	5	246	c.590C>T	c.(589-591)TCG>TTG	p.S197L
Pat_24	Pre-Treatment	SLC14A2	8170	37	18	43248375	43248375	Missense_Mutation	SNP	G	A	4	115	c.1969G>A	c.(1969-1971)GTG>ATG	p.V657M
Pat_24	Pre-Treatment	PIAS2	9063	37	18	44416455	44416455	Missense_Mutation	SNP	G	A	53	93	c.1067C>T	c.(1066-1068)CCA>CTA	p.P356L
Pat_24	Pre-Treatment	MYO5B	4645	37	18	47462641	47462641	Missense_Mutation	SNP	C	T	14	21	c.1984G>A	c.(1984-1986)GAT>AAT	p.D662N
Pat_24	Pre-Treatment	ST8SIA3	51046	37	18	55021734	55021734	Missense_Mutation	SNP	G	A	4	153	c.281G>A	c.(280-282)CGG>CAG	p.R94Q
Pat_24	Pre-Treatment	CCBE1	147372	37	18	57136752	57136752	Missense_Mutation	SNP	C	T	162	231	c.353G>A	c.(352-354)CGA>CAA	p.R118Q
Pat_24	Pre-Treatment	NETO1	81832	37	18	70526196	70526196	Missense_Mutation	SNP	G	A	61	73	c.334C>T	c.(334-336)CCA>TCA	p.P112S
Pat_24	Pre-Treatment	SALL3	27164	37	18	76754380	76754380	Missense_Mutation	SNP	G	A	4	68	c.2389G>A	c.(2389-2391)GAT>AAT	p.D797N
Pat_24	Pre-Treatment	HCN2	610	37	19	613879	613879	Missense_Mutation	SNP	G	A	4	168	c.1853G>A	c.(1852-1854)CGC>CAC	p.R618H
Pat_24	Pre-Treatment	MED16	10025	37	19	885943	885943	Missense_Mutation	SNP	C	T	6	159	c.706G>A	c.(706-708)GCG>ACG	p.A236T
Pat_24	Pre-Treatment	PCSK4	54760	37	19	1488228	1488228	Missense_Mutation	SNP	C	T	4	80	c.346G>A	c.(346-348)GTG>ATG	p.V116M
Pat_24	Pre-Treatment	MBD3	53615	37	19	1581224	1581224	Missense_Mutation	SNP	C	T	4	89	c.544G>A	c.(544-546)GCC>ACC	p.A182T
Pat_24	Pre-Treatment	ATP8B3	148229	37	19	1791839	1791839	Missense_Mutation	SNP	C	T	4	129	c.2212G>A	c.(2212-2214)GAG>AAG	p.E738K
Pat_24	Pre-Treatment	FAM108A1	81926	37	19	1877576	1877576	Missense_Mutation	SNP	G	A	4	149	c.638C>T	c.(637-639)CCG>CTG	p.P213L
Pat_24	Pre-Treatment	AP3D1	8943	37	19	2116222	2116222	Missense_Mutation	SNP	G	A	4	70	c.2057C>T	c.(2056-2058)TCG>TTG	p.S686L
Pat_24	Pre-Treatment	SLC39A3	29985	37	19	2733161	2733161	Missense_Mutation	SNP	G	A	4	78	c.533C>T	c.(532-534)TCG>TTG	p.S178L
Pat_24	Pre-Treatment	NFIC	4782	37	19	3382196	3382196	Missense_Mutation	SNP	G	A	4	205	c.517G>A	c.(517-519)GTC>ATC	p.V173I
Pat_24	Pre-Treatment	LONP1	9361	37	19	5696124	5696124	Missense_Mutation	SNP	G	A	4	156	c.1954C>T	c.(1954-1956)CGT>TGT	p.R652C
Pat_24	Pre-Treatment	RANBP3	8498	37	19	5917637	5917637	Missense_Mutation	SNP	G	A	4	62	c.1688C>T	c.(1687-1689)ACG>ATG	p.T563M
Pat_24	Pre-Treatment	KHSRP	8570	37	19	6418041	6418041	Missense_Mutation	SNP	C	G	3	115	c.929G>C	c.(928-930)GGC>GCC	p.G310A

Pat_24	Pre-Treatment	SLC25A41	284427	37	19	6432116	6432116	Missense_Mutation	SNP	C	T	4	139	c.307G>A	c.(307-309)GGG>AGG	p.G103R
Pat_24	Pre-Treatment	TUBB4	10382	37	19	6495272	6495272	Missense_Mutation	SNP	C	T	5	348	c.1238G>A	c.(1237-1239)AGC>AAC	p.S413N
Pat_24	Pre-Treatment	SH2D3A	10045	37	19	6760844	6760844	Missense_Mutation	SNP	G	A	4	81	c.224C>T	c.(223-225)ACA>ATA	p.T75I
Pat_24	Pre-Treatment	ZNF557	79230	37	19	7083094	7083094	Missense_Mutation	SNP	A	G	6	169	c.611A>G	c.(610-612)AAT>AGT	p.N204S
Pat_24	Pre-Treatment	C19orf45	374877	37	19	7570268	7570268	Missense_Mutation	SNP	G	A	5	272	c.841G>A	c.(841-843)GGC>AGC	p.G281S
Pat_24	Pre-Treatment	CLEC4M	10332	37	19	7828094	7828094	Translation_Start_Site	SNP	G	A	12	34	c.-58G>A	:.(-60--56)GGGTG>GGATG	
Pat_24	Pre-Treatment	LRRC8E	80131	37	19	7965776	7965776	Missense_Mutation	SNP	G	A	4	125	c.2369G>A	c.(2368-2370)CGG>CAG	p.R790Q
Pat_24	Pre-Treatment	FBN3	84467	37	19	8188854	8188854	Missense_Mutation	SNP	C	T	19	39	c.2770G>A	c.(2770-2772)GAT>AAT	p.D924N
Pat_24	Pre-Treatment	LASS4	79603	37	19	8319406	8319406	Missense_Mutation	SNP	G	A	4	109	c.197G>A	c.(196-198)CGG>CAG	p.R66Q
Pat_24	Pre-Treatment	MYO1F	4542	37	19	8615464	8615464	Nonsense_Mutation	SNP	G	A	4	169	c.886C>T	c.(886-888)CGA>TGA	p.R296*
Pat_24	Pre-Treatment	MUC16	94025	37	19	9048291	9048291	Missense_Mutation	SNP	G	A	4	115	c.33340C>T	c.(33340-33342)CCA>TCA	p.P11114S
Pat_24	Pre-Treatment	MUC16	94025	37	19	9075747	9075747	Missense_Mutation	SNP	G	C	16	34	c.11699C>G	c.(11698-11700)TCC>TGC	p.S3900C
Pat_24	Pre-Treatment	MUC16	94025	37	19	9090637	9090637	Missense_Mutation	SNP	G	A	4	41	c.1178C>T	c.(1177-1179)CCA>CTA	p.P393L
Pat_24	Pre-Treatment	ZNF426	79088	37	19	9639976	9639976	Missense_Mutation	SNP	C	T	4	159	c.745G>A	c.(745-747)GAA>AAA	p.E249K
Pat_24	Pre-Treatment	RAVER1	125950	37	19	10439703	10439703	Missense_Mutation	SNP	G	A	3	26	c.422C>T	c.(421-423)TCG>TTG	p.S141L
Pat_24	Pre-Treatment	TYK2	7297	37	19	10465258	10465258	Missense_Mutation	SNP	G	A	4	241	c.2645C>T	c.(2644-2646)CCG>CTG	p.P882L
Pat_24	Pre-Treatment	ZNF433	163059	37	19	12127138	12127138	Missense_Mutation	SNP	G	A	4	164	c.544C>T	c.(544-546)CAT>TAT	p.H182Y
Pat_24	Pre-Treatment	MAN2B1	4125	37	19	12772187	12772187	Missense_Mutation	SNP	G	A	4	186	c.913C>T	c.(913-915)CGG>TGG	p.R305W
Pat_24	Pre-Treatment	ASNA1	439	37	19	12849338	12849338	Missense_Mutation	SNP	G	A	7	349	c.175G>A	c.(175-177)GTC>ATC	p.V59I
Pat_24	Pre-Treatment	GCDH	2639	37	19	13007041	13007041	Missense_Mutation	SNP	G	A	5	248	c.658G>A	c.(658-660)GAT>AAT	p.D220N
Pat_24	Pre-Treatment	CALR	811	37	19	13054686	13054686	Nonsense_Mutation	SNP	G	T	4	21	c.1213G>T	c.(1213-1215)GAG>TAG	p.E405*
Pat_24	Pre-Treatment	LPHN1	22859	37	19	14281565	14281565	Missense_Mutation	SNP	G	A	4	80	c.323C>T	c.(322-324)TCG>TTG	p.S108L
Pat_24	Pre-Treatment	MYO9B	4650	37	19	17317980	17317980	Missense_Mutation	SNP	G	A	4	52	c.5551G>A	c.(5551-5553)GCA>ACA	p.A1851T
Pat_24	Pre-Treatment	MAP1S	55201	37	19	17837824	17837824	Missense_Mutation	SNP	C	T	4	26	c.1631C>T	c.(1630-1632)GCA>GTA	p.A544V
Pat_24	Pre-Treatment	ARRDC2	27106	37	19	18120750	18120750	Missense_Mutation	SNP	G	A	5	78	c.751G>A	c.(751-753)GGG>AGG	p.G251R
Pat_24	Pre-Treatment	ZNF676	163223	37	19	22363213	22363213	Missense_Mutation	SNP	G	A	4	133	c.1306C>T	c.(1306-1308)CTT>TTT	p.L436F
Pat_24	Pre-Treatment	ZNF492	57615	37	19	22847739	22847739	Missense_Mutation	SNP	G	A	5	183	c.1268G>A	c.(1267-1269)TGT>TAT	p.C423Y
Pat_24	Pre-Treatment	ZNF507	22847	37	19	32844016	32844016	Nonsense_Mutation	SNP	C	T	4	148	c.280C>T	c.(280-282)CAG>TAG	p.Q94*
Pat_24	Pre-Treatment	C19orf40	91442	37	19	33464993	33464993	Missense_Mutation	SNP	G	A	4	128	c.271G>A	c.(271-273)GTT>ATT	p.V91I
Pat_24	Pre-Treatment	MLL4	9757	37	19	36214067	36214067	Nonsense_Mutation	SNP	C	T	4	154	c.2893C>T	c.(2893-2895)CGA>TGA	p.R965*
Pat_24	Pre-Treatment	APLP1	333	37	19	36368683	36368683	Missense_Mutation	SNP	G	A	4	113	c.1508G>A	c.(1507-1509)AGC>AAC	p.S503N
Pat_24	Pre-Treatment	WDR62	284403	37	19	36579954	36579954	Nonsense_Mutation	SNP	C	T	73	145	c.1783C>T	c.(1783-1785)CAG>TAG	p.Q595*
Pat_24	Pre-Treatment	WDR62	284403	37	19	36594667	36594667	Missense_Mutation	SNP	G	A	4	167	c.3922G>A	c.(3922-3924)GTG>ATG	p.V1308M
Pat_24	Pre-Treatment	ZNF146	7705	37	19	36727658	36727658	Missense_Mutation	SNP	G	A	6	145	c.316G>A	c.(316-318)GGG>AGG	p.G106R
Pat_24	Pre-Treatment	ZNF829	374899	37	19	37382503	37382503	Missense_Mutation	SNP	C	T	4	124	c.1190G>A	c.(1189-1191)CGA>CAA	p.R397Q
Pat_24	Pre-Treatment	HKR1	284459	37	19	37853872	37853872	Missense_Mutation	SNP	G	A	5	240	c.1175G>A	c.(1174-1176)CGT>CAT	p.R392H
Pat_24	Pre-Treatment	ZNF527	84503	37	19	37865129	37865129	Missense_Mutation	SNP	C	T	78	108	c.29C>T	c.(28-30)TCC>TTC	p.S10F
Pat_24	Pre-Treatment	DPF1	8193	37	19	38708452	38708452	Missense_Mutation	SNP	G	A	4	148	c.662C>T	c.(661-663)CCG>CTG	p.P221L
Pat_24	Pre-Treatment	FAM98C	147965	37	19	38896008	38896008	Missense_Mutation	SNP	C	T	4	125	c.580C>T	c.(580-582)CCC>TCC	p.P194S
Pat_24	Pre-Treatment	RYR1	6261	37	19	39013705	39013705	Missense_Mutation	SNP	G	A	12	7	c.10297G>A	:.(10297-10299)GAG>AAG	p.E3433K
Pat_24	Pre-Treatment	SIRT2	22933	37	19	39371357	39371357	Missense_Mutation	SNP	G	A	4	197	c.844C>T	c.(844-846)CGC>TGC	p.R282C
Pat_24	Pre-Treatment	FBXO17	115290	37	19	39439252	39439252	Missense_Mutation	SNP	G	A	4	227	c.416C>T	c.(415-417)CCG>CTG	p.P139L
Pat_24	Pre-Treatment	PAPL	390928	37	19	39589605	39589605	Missense_Mutation	SNP	C	T	4	99	c.328C>T	c.(328-330)CGC>TGC	p.R110C
Pat_24	Pre-Treatment	TIMM50	92609	37	19	39972542	39972542	Missense_Mutation	SNP	G	A	4	215	c.437G>A	c.(436-438)CGC>CAC	p.R146H
Pat_24	Pre-Treatment	ZNF546	339327	37	19	40519644	40519644	Missense_Mutation	SNP	T	C	54	82	c.467T>C	c.(466-468)TTG>TCG	p.L156S
Pat_24	Pre-Treatment	PRX	57716	37	19	40900066	40900066	Missense_Mutation	SNP	G	A	4	185	c.4193C>T	c.(4192-4194)GCC>GTC	p.A1398V
Pat_24	Pre-Treatment	LTBP4	8425	37	19	41129511	41129511	Missense_Mutation	SNP	G	A	4	71	c.3760G>A	c.(3760-3762)GTG>ATG	p.V1254M

Pat_24	Pre-Treatment	CYP2B7P1	1556	37	19	41442117	41442117	Missense_Mutation	SNP	C	T	44	53	c.287C>T	c.(286-288)TCT>TTT	p.S96F
Pat_24	Pre-Treatment	CYP2F1	1572	37	19	41630689	41630689	Missense_Mutation	SNP	G	A	4	39	c.1030G>A	c.(1030-1032)GCG>ACG	p.A344T
Pat_24	Pre-Treatment	BCKDHA	593	37	19	41920054	41920054	Missense_Mutation	SNP	G	A	4	124	c.476G>A	c.(475-477)CGG>CAG	p.R159Q
Pat_24	Pre-Treatment	GSK3A	2931	37	19	42736815	42736815	Missense_Mutation	SNP	G	A	4	102	c.1118C>T	c.(1117-1119)CCG>CTG	p.P373L
Pat_24	Pre-Treatment	PAFAH1B3	5050	37	19	42804331	42804331	Missense_Mutation	SNP	G	A	4	179	c.277C>T	c.(277-279)CGG>TGG	p.R93W
Pat_24	Pre-Treatment	TMEM145	284339	37	19	42827822	42827822	Missense_Mutation	SNP	G	A	4	189	c.1282G>A	c.(1282-1284)GGA>AGA	p.G428R
Pat_24	Pre-Treatment	MEGF8	1954	37	19	42847683	42847683	Missense_Mutation	SNP	G	A	4	101	c.1568G>A	c.(1567-1569)GGC>GAC	p.G523D
Pat_24	Pre-Treatment	CEACAM1	634	37	19	43025661	43025661	Missense_Mutation	SNP	G	A	6	450	c.716C>T	c.(715-717)ACC>ATC	p.T239I
Pat_24	Pre-Treatment	PSG8	440533	37	19	43259211	43259211	Missense_Mutation	SNP	C	T	57	92	c.917G>A	c.(916-918)GGA>GAA	p.G306E
Pat_24	Pre-Treatment	GIPR	2696	37	19	46180288	46180288	Missense_Mutation	SNP	G	A	5	140	c.715G>A	c.(715-717)GTC>ATC	p.V239I
Pat_24	Pre-Treatment	SYMPK	8189	37	19	46332352	46332352	Missense_Mutation	SNP	C	T	4	113	c.1861G>A	c.(1861-1863)GCC>ACC	p.A621T
Pat_24	Pre-Treatment	PNMAL1	55228	37	19	46974154	46974154	Missense_Mutation	SNP	G	A	12	55	c.139C>T	c.(139-141)CTC>TTC	p.L47F
Pat_24	Pre-Treatment	SLC1A5	6510	37	19	47280531	47280531	Missense_Mutation	SNP	G	A	4	189	c.1190C>T	c.(1189-1191)GCC>GTC	p.A397V
Pat_24	Pre-Treatment	GRLF1	2909	37	19	47424220	47424220	Missense_Mutation	SNP	G	A	4	155	c.2288G>A	c.(2287-2289)CGT>CAT	p.R763H
Pat_24	Pre-Treatment	GRLF1	2909	37	19	47440602	47440602	Missense_Mutation	SNP	G	A	4	117	c.3763G>A	c.(3763-3765)GTG>ATG	p.V1255M
Pat_24	Pre-Treatment	DHX34	9704	37	19	47882968	47882968	Missense_Mutation	SNP	C	T	130	243	c.2708C>T	c.(2707-2709)TCC>TTC	p.S903F
Pat_24	Pre-Treatment	SULT2A1	6822	37	19	48389505	48389505	Missense_Mutation	SNP	C	T	45	86	c.10G>A	c.(10-12)GAT>AAT	p.D4N
Pat_24	Pre-Treatment	FGF21	26291	37	19	49261344	49261344	Missense_Mutation	SNP	C	T	12	16	c.497C>T	c.(496-498)CCA>CTA	p.P166L
Pat_24	Pre-Treatment	BCAT2	587	37	19	49299854	49299854	Missense_Mutation	SNP	C	T	5	223	c.1046G>A	c.(1045-1047)CGA>CAA	p.R349Q
Pat_24	Pre-Treatment	BAX	581	37	19	49464149	49464149	Nonsense_Mutation	SNP	G	A	4	240	c.452G>A	c.(451-453)TGG>TAG	p.W151*
Pat_24	Pre-Treatment	CGB7	94027	37	19	49557583	49557583	Missense_Mutation	SNP	G	A	10	112	c.463C>T	c.(463-465)CCG>TCG	p.P155S
Pat_24	Pre-Treatment	CPT1C	126129	37	19	50212025	50212025	Missense_Mutation	SNP	G	A	5	332	c.1495G>A	c.(1495-1497)GGC>AGC	p.G499S
Pat_24	Pre-Treatment	SHANK1	50944	37	19	51165452	51165452	Missense_Mutation	SNP	G	A	4	88	c.6256C>T	c.(6256-6258)CCG>TCG	p.P2086S
Pat_24	Pre-Treatment	KLK15	55554	37	19	51330167	51330167	Missense_Mutation	SNP	C	T	25	36	c.448G>A	c.(448-450)GAG>AAG	p.E150K
Pat_24	Pre-Treatment	KLK5	25818	37	19	51447041	51447041	Missense_Mutation	SNP	C	T	8	22	c.728G>A	c.(727-729)GGT>GAT	p.G243D
Pat_24	Pre-Treatment	LIM2	3982	37	19	51885793	51885793	Missense_Mutation	SNP	C	T	54	117	c.204G>A	c.(202-204)ATG>ATA	p.M68I
Pat_24	Pre-Treatment	ZNF578	147660	37	19	53014551	53014551	Missense_Mutation	SNP	G	A	17	234	c.917G>A	c.(916-918)CGT>CAT	p.R306H
Pat_24	Pre-Treatment	ZNF816A	125893	37	19	53454670	53454670	Missense_Mutation	SNP	C	T	8	362	c.358G>A	c.(358-360)GTT>ATT	p.V120I
Pat_24	Pre-Treatment	VN1R2	317701	37	19	53762332	53762332	Nonsense_Mutation	SNP	G	A	37	47	c.704G>A	c.(703-705)TGG>TAG	p.W235*
Pat_24	Pre-Treatment	ZNF331	55422	37	19	54080095	54080095	Missense_Mutation	SNP	G	A	4	125	c.281G>A	c.(280-282)CGC>CAC	p.R94H
Pat_24	Pre-Treatment	LAIR1	3903	37	19	54866912	54866912	Missense_Mutation	SNP	C	T	4	234	c.829G>A	c.(829-831)GAG>AAG	p.E277K
Pat_24	Pre-Treatment	KIR2DL4	3805	37	19	55324579	55324579	Splice_Site	SNP	G	C	3	60	c.707_splice	c.e6-1	p.G236_splice
Pat_24	Pre-Treatment	NCR1	9437	37	19	55423586	55423586	Missense_Mutation	SNP	G	A	4	159	c.733G>A	c.(733-735)GAC>AAC	p.D245N
Pat_24	Pre-Treatment	PTPRH	5794	37	19	55699497	55699497	Missense_Mutation	SNP	G	T	5	311	c.2424C>A	c.(2422-2424)CAC>CAA	p.H808Q
Pat_24	Pre-Treatment	CCDC106	29903	37	19	56163871	56163871	Missense_Mutation	SNP	G	A	4	142	c.602G>A	c.(601-603)CGG>CAG	p.R201Q
Pat_24	Pre-Treatment	EPN1	29924	37	19	56190208	56190208	Missense_Mutation	SNP	G	A	4	158	c.215G>A	c.(214-216)CGT>CAT	p.R72H
Pat_24	Pre-Treatment	ZNF471	57573	37	19	57035779	57035779	Missense_Mutation	SNP	G	A	4	110	c.343G>A	c.(343-345)GGA>AGA	p.G115R
Pat_24	Pre-Treatment	PEG3	5178	37	19	57325423	57325423	Missense_Mutation	SNP	C	G	4	164	c.4387G>C	c.(4387-4389)GAA>CAA	p.E1463Q
Pat_24	Pre-Treatment	ZIM3	114026	37	19	57647082	57647082	Nonsense_Mutation	SNP	C	T	63	107	c.623G>A	c.(622-624)TGG>TAG	p.W208*
Pat_24	Pre-Treatment	ZSCAN4	201516	37	19	58189418	58189418	Missense_Mutation	SNP	C	T	63	100	c.533C>T	c.(532-534)TCC>TTC	p.S178F
Pat_24	Pre-Treatment	ZSCAN22	342945	37	19	58849872	58849872	Missense_Mutation	SNP	G	A	6	442	c.656G>A	c.(655-657)CGT>CAT	p.R219H
Pat_24	Pre-Treatment	ADAM17	6868	37	2	9676829	9676829	Missense_Mutation	SNP	A	G	101	210	c.359T>C	c.(358-360)GTT>GCT	p.V120A
Pat_24	Pre-Treatment	GEN1	348654	37	2	17946296	17946296	Missense_Mutation	SNP	T	A	69	125	c.481T>A	c.(481-483)TAT>AAT	p.Y161N
Pat_24	Pre-Treatment	NT5C1B	93034	37	2	18736717	18736717	Missense_Mutation	SNP	G	A	7	537	c.1693C>T	c.(1693-1695)CGG>TGG	p.R565W
Pat_24	Pre-Treatment	NT5C1B	93034	37	2	18765976	18765976	Missense_Mutation	SNP	G	A	12	19	c.707C>T	c.(706-708)TCG>TTG	p.S236L
Pat_24	Pre-Treatment	DPYSL5	56896	37	2	27157485	27157485	Missense_Mutation	SNP	C	T	5	351	c.830C>T	c.(829-831)ACG>ATG	p.T277M
Pat_24	Pre-Treatment	IFT172	26160	37	2	27700873	27700873	Missense_Mutation	SNP	G	A	6	474	c.1156C>T	c.(1156-1158)CGG>TGG	p.R386W

Pat_24	Pre-Treatment	PLB1	151056	37	2	28820886	28820886	Missense_Mutation	SNP	G	A	4	207	c.2336G>A	c.(2335-2337)GGC>GAC	p.G779D
Pat_24	Pre-Treatment	CRIM1	51232	37	2	36583665	36583665	Missense_Mutation	SNP	C	T	4	106	c.230C>T	c.(229-231)ACC>ATC	p.T77I
Pat_24	Pre-Treatment	GEMIN6	79833	37	2	39009011	39009011	Missense_Mutation	SNP	G	A	4	225	c.481G>A	c.(481-483)GGA>AGA	p.G161R
Pat_24	Pre-Treatment	MTA3	57504	37	2	42936069	42936069	Missense_Mutation	SNP	G	A	6	380	c.1187G>A	c.(1186-1188)CGA>CAA	p.R396Q
Pat_24	Pre-Treatment	PLEKHH2	130271	37	2	43927635	43927635	Missense_Mutation	SNP	C	T	120	176	c.1538C>T	c.(1537-1539)TCC>TTC	p.S513F
Pat_24	Pre-Treatment	ABCG8	64241	37	2	44078855	44078855	Missense_Mutation	SNP	G	A	6	184	c.455G>A	c.(454-456)CGC>CAC	p.R152H
Pat_24	Pre-Treatment	TTC7A	57217	37	2	47233086	47233086	Missense_Mutation	SNP	G	A	6	190	c.1091G>A	c.(1090-1092)CGG>CAG	p.R364Q
Pat_24	Pre-Treatment	OTX1	5013	37	2	63282733	63282733	Missense_Mutation	SNP	G	A	4	133	c.347G>A	c.(346-348)CGG>CAG	p.R116Q
Pat_24	Pre-Treatment	SLC1A4	6509	37	2	65243783	65243783	Missense_Mutation	SNP	C	T	4	135	c.1010C>T	c.(1009-1011)GCG>GTG	p.A337V
Pat_24	Pre-Treatment	APLF	200558	37	2	68753264	68753264	Missense_Mutation	SNP	G	A	4	230	c.694G>A	c.(694-696)GGA>AGA	p.G232R
Pat_24	Pre-Treatment	ARHGAP25	9938	37	2	69053237	69053237	Missense_Mutation	SNP	C	T	4	219	c.1849C>T	c.(1849-1851)CGG>TGG	p.R617W
Pat_24	Pre-Treatment	CYP26B1	56603	37	2	72362394	72362394	Missense_Mutation	SNP	C	T	4	103	c.584G>A	c.(583-585)CGG>CAG	p.R195Q
Pat_24	Pre-Treatment	ALMS1	7840	37	2	73827919	73827919	Nonsense_Mutation	SNP	G	A	4	72	c.11786G>A	c.(11785-11787)TGG>TAG	p.W3929*
Pat_24	Pre-Treatment	DQX1	165545	37	2	74751136	74751136	Missense_Mutation	SNP	G	A	4	160	c.730C>T	c.(730-732)CGG>TGG	p.R244W
Pat_24	Pre-Treatment	CTNNA2	1496	37	2	80874869	80874869	Missense_Mutation	SNP	G	A	129	204	c.2734G>A	c.(2734-2736)GAG>AAG	p.E912K
Pat_24	Pre-Treatment	MAT2A	4144	37	2	85769710	85769710	Missense_Mutation	SNP	G	A	4	173	c.791G>A	c.(790-792)CGC>CAC	p.R264H
Pat_24	Pre-Treatment	POLR1A	25885	37	2	86257434	86257434	Missense_Mutation	SNP	G	A	4	110	c.4664C>T	c.(4663-4665)GCG>GTG	p.A1555V
Pat_24	Pre-Treatment	MRPS5	64969	37	2	95774016	95774016	Nonsense_Mutation	SNP	G	A	5	167	c.541C>T	c.(541-543)CGA>TGA	p.R181*
Pat_24	Pre-Treatment	GPAT2	150763	37	2	96697836	96697836	Missense_Mutation	SNP	C	T	25	141	c.122G>A	c.(121-123)GGG>GAG	p.G41E
Pat_24	Pre-Treatment	STARD7	56910	37	2	96858130	96858130	Missense_Mutation	SNP	G	A	6	339	c.820C>T	c.(820-822)CGT>TGT	p.R274C
Pat_24	Pre-Treatment	SNRNP200	23020	37	2	96948969	96948969	Nonsense_Mutation	SNP	G	A	7	218	c.4885C>T	c.(4885-4887)CGA>TGA	p.R1629*
Pat_24	Pre-Treatment	ACTR1B	10120	37	2	98273346	98273346	Missense_Mutation	SNP	C	T	4	42	c.1106G>A	c.(1105-1107)CGT>CAT	p.R369H
Pat_24	Pre-Treatment	LYG1	129530	37	2	99907879	99907879	Missense_Mutation	SNP	G	A	14	43	c.154C>T	c.(154-156)CGT>TGT	p.R52C
Pat_24	Pre-Treatment	NPAS2	4862	37	2	101584859	101584859	Missense_Mutation	SNP	G	A	4	240	c.1024G>A	c.(1024-1026)GAG>AAG	p.E342K
Pat_24	Pre-Treatment	FHL2	2274	37	2	105979858	105979858	Missense_Mutation	SNP	C	A	5	57	c.572G>T	c.(571-573)TGC>TTC	p.C191F
Pat_24	Pre-Treatment	PSD4	23550	37	2	113950879	113950879	Missense_Mutation	SNP	G	A	56	102	c.1964G>A	c.(1963-1965)CGG>CAG	p.R655Q
Pat_24	Pre-Treatment	DPP10	57628	37	2	116548905	116548905	Missense_Mutation	SNP	G	A	4	179	c.1673G>A	c.(1672-1674)CGA>CAA	p.R558Q
Pat_24	Pre-Treatment	CNTNAP5	129684	37	2	125521709	125521709	Nonsense_Mutation	SNP	C	T	61	103	c.2515C>T	c.(2515-2517)CGA>TGA	p.R839*
Pat_24	Pre-Treatment	IWS1	55677	37	2	128250895	128250895	Missense_Mutation	SNP	G	A	4	133	c.1891C>T	c.(1891-1893)CTC>TTC	p.L631F
Pat_24	Pre-Treatment	UGGT1	56886	37	2	128848960	128848960	Missense_Mutation	SNP	C	A	3	37	c.29C>A	c.(28-30)GCG>GAG	p.A10E
Pat_24	Pre-Treatment	FAM123C	205147	37	2	131519893	131519893	Missense_Mutation	SNP	G	A	6	9	c.248G>A	c.(247-249)GGA>GAA	p.G83E
Pat_24	Pre-Treatment	PLEKHB2	55041	37	2	131904261	131904261	Missense_Mutation	SNP	G	A	6	359	c.584G>A	c.(583-585)CGA>CAA	p.R195Q
Pat_24	Pre-Treatment	NCKAP5	344148	37	2	133540573	133540573	Missense_Mutation	SNP	C	T	5	198	c.3811G>A	c.(3811-3813)GCC>ACC	p.A1271T
Pat_24	Pre-Treatment	NCKAP5	344148	37	2	133541974	133541974	Missense_Mutation	SNP	G	A	127	221	c.2410C>T	c.(2410-2412)CCT>TCT	p.P804S
Pat_24	Pre-Treatment	MGAT5	4249	37	2	135180410	135180410	Missense_Mutation	SNP	G	A	5	247	c.1714G>A	c.(1714-1716)GGG>AGG	p.G572R
Pat_24	Pre-Treatment	TMEM163	81615	37	2	135308187	135308187	Missense_Mutation	SNP	G	A	4	233	c.412C>T	c.(412-414)CGT>TGT	p.R138C
Pat_24	Pre-Treatment	LRP1B	53353	37	2	141250238	141250238	Missense_Mutation	SNP	G	A	4	102	c.9059C>T	c.(9058-9060)GCT>GTT	p.A3020V
Pat_24	Pre-Treatment	LRP1B	53353	37	2	141264467	141264467	Missense_Mutation	SNP	C	T	41	55	c.8419G>A	c.(8419-8421)GAA>AAA	p.E2807K
Pat_24	Pre-Treatment	LRP1B	53353	37	2	141946086	141946086	Missense_Mutation	SNP	C	T	4	137	c.917G>A	c.(916-918)CGG>CAG	p.R306Q
Pat_24	Pre-Treatment	ACVR1C	130399	37	2	158401119	158401119	Missense_Mutation	SNP	C	T	22	54	c.781G>A	c.(781-783)GGA>AGA	p.G261R
Pat_24	Pre-Treatment	TANC1	85461	37	2	160080770	160080770	Missense_Mutation	SNP	G	A	4	127	c.3706G>A	c.(3706-3708)GTG>ATG	p.V1236M
Pat_24	Pre-Treatment	WDSUB1	151525	37	2	160114456	160114456	Missense_Mutation	SNP	C	T	4	61	c.845G>A	c.(844-846)AGG>AAG	p.R282K
Pat_24	Pre-Treatment	SCN3A	6328	37	2	165950907	165950907	Nonsense_Mutation	SNP	G	A	135	219	c.4513C>T	c.(4513-4515)CAG>TAG	p.Q1505*
Pat_24	Pre-Treatment	SCN2A	6326	37	2	166170222	166170222	Missense_Mutation	SNP	C	T	49	82	c.1127C>T	c.(1126-1128)TCC>TTC	p.S376F
Pat_24	Pre-Treatment	CSRNP3	80034	37	2	166535587	166535587	Missense_Mutation	SNP	C	T	4	213	c.1082C>T	c.(1081-1083)ACG>ATG	p.T361M
Pat_24	Pre-Treatment	SCN1A	6323	37	2	166915126	166915126	Missense_Mutation	SNP	G	A	37	57	c.337C>T	c.(337-339)CCC>TCC	p.P113S
Pat_24	Pre-Treatment	LRP2	4036	37	2	170002377	170002377	Missense_Mutation	SNP	C	T	19	38	c.12868G>A	c.(12868-12870)GAA>AAA	p.E4290K

Pat_24	Pre-Treatment	LRP2	4036	37	2	170030528	170030528	Nonsense_Mutation	SNP	G	A	54	87	c.10915C>T	c.(10915-10917)CAG>TAG	p.Q3639*
Pat_24	Pre-Treatment	LRP2	4036	37	2	170032996	170032996	Missense_Mutation	SNP	G	A	4	87	c.10496C>T	c.(10495-10497)ACC>ATC	p.T3499I
Pat_24	Pre-Treatment	LRP2	4036	37	2	170099985	170099985	Nonsense_Mutation	SNP	G	A	5	326	c.3478C>T	c.(3478-3480)CGA>TGA	p.R1160*
Pat_24	Pre-Treatment	ITGA6	3655	37	2	173352006	173352006	Missense_Mutation	SNP	C	T	27	53	c.1985C>T	c.(1984-1986)CCA>CTA	p.P662L
Pat_24	Pre-Treatment	TTN	7273	37	2	179395188	179395188	Missense_Mutation	SNP	T	A	31	65	c.98450A>T	c.(98449-98451)AAG>ATG	p.K32817M
Pat_24	Pre-Treatment	TTN	7273	37	2	179410270	179410270	Missense_Mutation	SNP	C	T	7	615	c.87863G>A	c.(87862-87864)CGT>CAT	p.R29288H
Pat_24	Pre-Treatment	TTN	7273	37	2	179458711	179458711	Missense_Mutation	SNP	C	T	134	219	c.50705G>A	c.(50704-50706)GGT>GAT	p.G16902D
Pat_24	Pre-Treatment	CCDC141	285025	37	2	179718176	179718177	Missense_Mutation	DNP	TG	CT	80	168	.1510_1511CA>A	c.(1510-1512)CAC>AGC	p.H504S
Pat_24	Pre-Treatment	PDE1A	5136	37	2	183104982	183104982	Nonsense_Mutation	SNP	G	A	52	77	c.253C>T	c.(253-255)CAG>TAG	p.Q85*
Pat_24	Pre-Treatment	ZSWIM2	151112	37	2	187692805	187692805	Missense_Mutation	SNP	C	T	6	101	c.1808G>A	c.(1807-1809)CGA>CAA	p.R603Q
Pat_24	Pre-Treatment	ANKAR	150709	37	2	190608104	190608104	Missense_Mutation	SNP	G	A	4	53	c.3701G>A	c.(3700-3702)CGT>CAT	p.R1234H
Pat_24	Pre-Treatment	INPP1	3628	37	2	191235652	191235652	Missense_Mutation	SNP	G	A	6	540	c.724G>A	c.(724-726)GGC>AGC	p.G242S
Pat_24	Pre-Treatment	MFSD6	54842	37	2	191301809	191301809	Missense_Mutation	SNP	G	A	5	154	c.1054G>A	c.(1054-1056)GAA>AAA	p.E352K
Pat_24	Pre-Treatment	MYO1B	4430	37	2	192257872	192257872	Missense_Mutation	SNP	G	A	4	174	c.2150G>A	c.(2149-2151)GGG>GAG	p.G717E
Pat_24	Pre-Treatment	BMPR2	659	37	2	203420798	203420798	Missense_Mutation	SNP	G	A	4	145	c.2410G>A	c.(2410-2412)GTC>ATC	p.V804I
Pat_24	Pre-Treatment	PARD3B	117583	37	2	206037007	206037007	Missense_Mutation	SNP	G	A	73	210	c.1693G>A	c.(1693-1695)GAA>AAA	p.E565K
Pat_24	Pre-Treatment	NDUFS1	4719	37	2	207003231	207003231	Missense_Mutation	SNP	G	A	5	295	c.1370C>T	c.(1369-1371)TCG>TTG	p.S457L
Pat_24	Pre-Treatment	LANCL1	10314	37	2	211305413	211305413	Missense_Mutation	SNP	G	A	4	150	c.599C>T	c.(598-600)ACG>ATG	p.T200M
Pat_24	Pre-Treatment	ERBB4	2066	37	2	212578265	212578266	Missense_Mutation	DNP	GG	TT	4	99	c.991_992CC>AA	c.(991-993)CCA>AAA	p.P331K
Pat_24	Pre-Treatment	C2orf62	375307	37	2	219227554	219227554	Missense_Mutation	SNP	C	T	5	94	c.559C>T	c.(559-561)CGG>TGG	p.R187W
Pat_24	Pre-Treatment	USP37	57695	37	2	219411766	219411766	Nonsense_Mutation	SNP	G	A	4	203	c.478C>T	c.(478-480)CGA>TGA	p.R160*
Pat_24	Pre-Treatment	WNT10A	80326	37	2	219746978	219746978	Missense_Mutation	SNP	G	A	5	96	c.209G>A	c.(208-210)CGG>CAG	p.R70Q
Pat_24	Pre-Treatment	CCDC108	255101	37	2	219894331	219894331	Missense_Mutation	SNP	G	A	5	287	c.1444C>T	c.(1444-1446)CGC>TGC	p.R482C
Pat_24	Pre-Treatment	ANKZF1	55139	37	2	220098932	220098932	Missense_Mutation	SNP	C	T	11	21	c.1126C>T	c.(1126-1128)CCT>TCT	p.P376S
Pat_24	Pre-Treatment	TUBA4A	7277	37	2	220115777	220115777	Missense_Mutation	SNP	C	T	5	433	c.644G>A	c.(643-645)CGC>CAC	p.R215H
Pat_24	Pre-Treatment	KIAA1486	57624	37	2	226446729	226446729	Missense_Mutation	SNP	C	T	5	364	c.596C>T	c.(595-597)CCG>CTG	p.P199L
Pat_24	Pre-Treatment	SP140L	93349	37	2	231254663	231254663	Missense_Mutation	SNP	G	A	57	92	c.889G>A	c.(889-891)GAT>AAT	p.D297N
Pat_24	Pre-Treatment	ALPP	250	37	2	233243710	233243710	Missense_Mutation	SNP	C	T	4	175	c.106C>T	c.(106-108)CGC>TGC	p.R36C
Pat_24	Pre-Treatment	ALPP	250	37	2	233245136	233245136	Missense_Mutation	SNP	C	T	4	198	c.799C>T	c.(799-801)CGG>TGG	p.R267W
Pat_24	Pre-Treatment	GIGYF2	26058	37	2	233674449	233674449	Missense_Mutation	SNP	G	A	4	230	c.1826G>A	c.(1825-1827)CGA>CAA	p.R609Q
Pat_24	Pre-Treatment	DGKD	8527	37	2	234375783	234375783	Missense_Mutation	SNP	G	A	5	427	c.3358G>A	c.(3358-3360)GTG>ATG	p.V1120M
Pat_24	Pre-Treatment	UGT1A4	54657	37	2	234627614	234627614	Missense_Mutation	SNP	G	A	28	39	c.148G>A	c.(148-150)GAG>AAG	p.E50K
Pat_24	Pre-Treatment	TRPM8	79054	37	2	234854527	234854527	Missense_Mutation	SNP	G	A	107	187	c.727G>A	c.(727-729)GAT>AAT	p.D243N
Pat_24	Pre-Treatment	TRAF3IP1	26146	37	2	239258006	239258006	Missense_Mutation	SNP	C	T	37	87	c.1408C>T	c.(1408-1410)CGG>TGG	p.R470W
Pat_24	Pre-Treatment	TRIB3	57761	37	20	368853	368853	Missense_Mutation	SNP	C	T	4	175	c.199C>T	c.(199-201)CGT>TGT	p.R67C
Pat_24	Pre-Treatment	SIRPA	140885	37	20	1902259	1902259	Missense_Mutation	SNP	C	T	4	128	c.655C>T	c.(655-657)CGC>TGC	p.R219C
Pat_24	Pre-Treatment	SIRPA	140885	37	20	1918051	1918051	Missense_Mutation	SNP	C	T	4	136	c.1352C>T	c.(1351-1353)ACG>ATG	p.T451M
Pat_24	Pre-Treatment	TGM6	343641	37	20	2384352	2384352	Missense_Mutation	SNP	G	A	82	99	c.1219G>A	c.(1219-1221)GAT>AAT	p.D407N
Pat_24	Pre-Treatment	TMC2	117532	37	20	2575609	2575609	Nonsense_Mutation	SNP	C	T	4	229	c.1072C>T	c.(1072-1074)CGA>TGA	p.R358*
Pat_24	Pre-Treatment	IDH3B	3420	37	20	2640427	2640427	Missense_Mutation	SNP	G	A	4	114	c.928C>T	c.(928-930)CCA>TCA	p.P310S
Pat_24	Pre-Treatment	CPXM1	56265	37	20	2776427	2776427	Missense_Mutation	SNP	G	A	6	244	c.1538C>T	c.(1537-1539)ACC>ATC	p.T513I
Pat_24	Pre-Treatment	ITPA	3704	37	20	3194691	3194691	Missense_Mutation	SNP	C	T	46	80	c.250C>T	c.(250-252)CCC>TCC	p.P84S
Pat_24	Pre-Treatment	CDC25B	994	37	20	3781438	3781438	Nonsense_Mutation	SNP	C	T	29	97	c.508C>T	c.(508-510)CAG>TAG	p.Q170*
Pat_24	Pre-Treatment	HAO1	54363	37	20	7894856	7894856	Missense_Mutation	SNP	C	T	5	292	c.500G>A	c.(499-501)CGT>CAT	p.R167H
Pat_24	Pre-Treatment	PLCB4	5332	37	20	9416225	9416225	Missense_Mutation	SNP	C	T	29	45	c.2507C>T	c.(2506-2508)TCA>TTA	p.S836L
Pat_24	Pre-Treatment	BTBD3	22903	37	20	11904205	11904205	Missense_Mutation	SNP	C	T	5	161	c.1460C>T	c.(1459-1461)ACA>ATA	p.T487I
Pat_24	Pre-Treatment	XRN2	22803	37	20	21327126	21327126	Missense_Mutation	SNP	C	T	6	489	c.1603C>T	c.(1603-1605)CGT>TGT	p.R535C

Pat_24	Pre-Treatment	GZF1	64412	37	20	23350289	23350289	Missense_Mutation	SNP	C	T	6	349	c.1696C>T	c.(1696-1698)CGC>TGC	p.R566C
Pat_24	Pre-Treatment	CST9	128822	37	20	23584214	23584214	Missense_Mutation	SNP	C	T	4	110	c.413G>A	c.(412-414)TGC>TAC	p.C138Y
Pat_24	Pre-Treatment	ACSS1	84532	37	20	25002061	25002061	Missense_Mutation	SNP	C	T	4	40	c.1072G>A	c.(1072-1074)GTC>ATC	p.V358I
Pat_24	Pre-Treatment	MYLK2	85366	37	20	30408261	30408261	Missense_Mutation	SNP	G	A	50	234	c.385G>A	c.(385-387)GGC>AGC	p.G129S
Pat_24	Pre-Treatment	DNMT3B	1789	37	20	31388045	31388045	Missense_Mutation	SNP	G	A	7	642	c.1846G>A	c.(1846-1848)GTG>ATG	p.V616M
Pat_24	Pre-Treatment	ZNF341	84905	37	20	32328819	32328819	Splice_Site	SNP	G	A	4	194	c.142_splice	c.e2+1	p.D48_splice
Pat_24	Pre-Treatment	CEP250	11190	37	20	34091848	34091848	Missense_Mutation	SNP	C	T	29	25	c.5651C>T	c.(5650-5652)GCC>GTC	p.A1884V
Pat_24	Pre-Treatment	EPB41L1	2036	37	20	34782211	34782211	Missense_Mutation	SNP	G	A	4	163	c.1378G>A	c.(1378-1380)GAG>AAG	p.E460K
Pat_24	Pre-Treatment	NDRG3	57446	37	20	35282084	35282084	Missense_Mutation	SNP	G	A	4	231	c.967C>T	c.(967-969)CGG>TGG	p.R323W
Pat_24	Pre-Treatment	C20orf118	140711	37	20	35504590	35504590	Missense_Mutation	SNP	C	T	7	442	c.13C>T	c.(13-15)CGC>TGC	p.R5C
Pat_24	Pre-Treatment	SAMHD1	25939	37	20	35563559	35563559	Missense_Mutation	SNP	G	A	4	205	c.382C>T	c.(382-384)CTC>TTC	p.L128F
Pat_24	Pre-Treatment	DHX35	60625	37	20	37650576	37650576	Missense_Mutation	SNP	G	A	5	219	c.1591G>A	c.(1591-1593)GCA>ACA	p.A531T
Pat_24	Pre-Treatment	PLCG1	5335	37	20	39792036	39792036	Missense_Mutation	SNP	C	T	106	253	c.808C>T	c.(808-810)CGC>TGC	p.R270C
Pat_24	Pre-Treatment	PLCG1	5335	37	20	39797771	39797771	Missense_Mutation	SNP	G	A	4	196	c.2536G>A	c.(2536-2538)GTG>ATG	p.V846M
Pat_24	Pre-Treatment	ZHX3	23051	37	20	39830922	39830922	Missense_Mutation	SNP	C	T	7	485	c.2635G>A	c.(2635-2637)GTC>ATC	p.V879I
Pat_24	Pre-Treatment	CHD6	84181	37	20	40102096	40102096	Missense_Mutation	SNP	G	A	6	314	c.2530C>T	c.(2530-2532)CGG>TGG	p.R844W
Pat_24	Pre-Treatment	PTPRT	11122	37	20	41306788	41306788	Missense_Mutation	SNP	G	A	25	33	c.871C>T	c.(871-873)CCC>TCC	p.P291S
Pat_24	Pre-Treatment	PI3	5266	37	20	43803588	43803588	Missense_Mutation	SNP	G	A	6	290	c.25G>A	c.(25-27)GTG>ATG	p.V9M
Pat_24	Pre-Treatment	SLC12A5	57468	37	20	44676109	44676109	Missense_Mutation	SNP	G	A	60	165	c.1873G>A	c.(1873-1875)GGC>AGC	p.G625S
Pat_24	Pre-Treatment	SLC35C2	51006	37	20	44986310	44986310	Missense_Mutation	SNP	G	A	8	272	c.223C>T	c.(223-225)CGT>TGT	p.R75C
Pat_24	Pre-Treatment	SLC2A10	81031	37	20	45362445	45362445	Missense_Mutation	SNP	G	A	5	226	c.1598G>A	c.(1597-1599)AGC>AAC	p.S533N
Pat_24	Pre-Treatment	EYA2	2139	37	20	45801437	45801437	Missense_Mutation	SNP	G	A	5	323	c.1120G>A	c.(1120-1122)GTG>ATG	p.V374M
Pat_24	Pre-Treatment	ZMYND8	23613	37	20	45867738	45867738	Missense_Mutation	SNP	G	A	6	297	c.2369C>T	c.(2368-2370)CCG>CTG	p.P790L
Pat_24	Pre-Treatment	NCOA3	8202	37	20	46262366	46262366	Missense_Mutation	SNP	G	A	4	196	c.950G>A	c.(949-951)CGT>CAT	p.R317H
Pat_24	Pre-Treatment	DIDO1	11083	37	20	61511433	61511433	Missense_Mutation	SNP	G	A	289	230	c.5875C>T	c.(5875-5877)CCC>TCC	p.P1959S
Pat_24	Pre-Treatment	DIDO1	11083	37	20	61522492	61522492	Missense_Mutation	SNP	G	A	4	155	c.3361C>T	c.(3361-3363)CGC>TGC	p.R1121C
Pat_24	Pre-Treatment	DIDO1	11083	37	20	61542460	61542460	Missense_Mutation	SNP	G	A	4	178	c.505C>T	c.(505-507)CGC>TGC	p.R169C
Pat_24	Pre-Treatment	ARFGAP1	55738	37	20	61909542	61909542	Missense_Mutation	SNP	G	A	4	193	c.517G>A	c.(517-519)GGC>AGC	p.G173S
Pat_24	Pre-Treatment	EEF1A2	1917	37	20	62122041	62122041	Missense_Mutation	SNP	G	A	4	138	c.820C>T	c.(820-822)CCG>TCG	p.P274S
Pat_24	Pre-Treatment	PRPF6	24148	37	20	62657343	62657343	Missense_Mutation	SNP	G	A	5	185	c.1960G>A	c.(1960-1962)GAG>AAG	p.E654K
Pat_24	Pre-Treatment	USP25	29761	37	21	17183520	17183520	Missense_Mutation	SNP	G	A	4	238	c.922G>A	c.(922-924)GTA>ATA	p.V308I
Pat_24	Pre-Treatment	NCAM2	4685	37	21	22696705	22696705	Missense_Mutation	SNP	C	T	5	257	c.622C>T	c.(622-624)CCG>TCG	p.P208S
Pat_24	Pre-Treatment	ETS2	2114	37	21	40194704	40194704	Missense_Mutation	SNP	C	T	5	284	c.1301C>T	c.(1300-1302)TCG>TTG	p.S434L
Pat_24	Pre-Treatment	BRWD1	54014	37	21	40648100	40648100	Missense_Mutation	SNP	G	A	5	384	c.1144C>T	c.(1144-1146)CGG>TGG	p.R382W
Pat_24	Pre-Treatment	BACE2	25825	37	21	42629134	42629134	Missense_Mutation	SNP	G	A	6	246	c.1184G>A	c.(1183-1185)CGA>CAA	p.R395Q
Pat_24	Pre-Treatment	RIPK4	54101	37	21	43161465	43161465	Missense_Mutation	SNP	C	T	5	254	c.1888G>A	c.(1888-1890)GTC>ATC	p.V630I
Pat_24	Pre-Treatment	ZNF295	49854	37	21	43412883	43412883	Missense_Mutation	SNP	G	A	4	208	c.1322C>T	c.(1321-1323)TCG>TTG	p.S441L
Pat_24	Pre-Treatment	UMODL1	89766	37	21	43547286	43547286	Missense_Mutation	SNP	C	T	5	175	c.3464C>T	c.(3463-3465)ACG>ATG	p.T1155M
Pat_24	Pre-Treatment	AGPAT3	56894	37	21	45379596	45379596	Missense_Mutation	SNP	G	A	6	443	c.34G>A	c.(34-36)GTG>ATG	p.V12M
Pat_24	Pre-Treatment	PRODH	5625	37	22	18912710	18912710	Missense_Mutation	SNP	G	A	4	190	c.521C>T	c.(520-522)ACG>ATG	p.T174M
Pat_24	Pre-Treatment	ARVCF	421	37	22	19960727	19960727	Missense_Mutation	SNP	C	T	4	58	c.2353G>A	c.(2353-2355)GAA>AAA	p.E785K
Pat_24	Pre-Treatment	SMARCB1	6598	37	22	24167562	24167562	Missense_Mutation	SNP	C	T	4	147	c.946C>T	c.(946-948)CGG>TGG	p.R316W
Pat_24	Pre-Treatment	GSTT1	2952	37	22	24379432	24379432	Missense_Mutation	SNP	G	A	4	94	c.280C>T	c.(280-282)CGT>TGT	p.R94C
Pat_24	Pre-Treatment	SEZ6L	23544	37	22	26761478	26761478	Missense_Mutation	SNP	C	T	4	135	c.2740C>T	c.(2740-2742)CGC>TGC	p.R914C
Pat_24	Pre-Treatment	TBC1D10A	83874	37	22	30691727	30691727	Missense_Mutation	SNP	C	T	4	144	c.523G>A	c.(523-525)GGC>AGC	p.G175S
Pat_24	Pre-Treatment	SF3A1	10291	37	22	30735151	30735151	Missense_Mutation	SNP	C	T	6	438	c.1465G>A	c.(1465-1467)GGT>AGT	p.G489S
Pat_24	Pre-Treatment	DUSP18	150290	37	22	31059603	31059603	Missense_Mutation	SNP	C	T	4	99	c.388G>A	c.(388-390)GCC>ACC	p.A130T

Pat_24	Pre-Treatment	RFPL3	10738	37	22	32756800	32756800	Missense_Mutation	SNP	G	A	5	241	c.935G>A	c.(934-936)CGT>CAT	p.R312H
Pat_24	Pre-Treatment	C22orf28	51493	37	22	32791099	32791099	Missense_Mutation	SNP	C	T	4	169	c.1093G>A	c.(1093-1095)GGA>AGA	p.G365R
Pat_24	Pre-Treatment	MYH9	4627	37	22	36716897	36716897	Missense_Mutation	SNP	G	A	4	120	c.814C>T	c.(814-816)CGG>TGG	p.R272W
Pat_24	Pre-Treatment	EIF3D	8664	37	22	36908588	36908588	Missense_Mutation	SNP	G	A	4	180	c.1268C>T	c.(1267-1269)ACG>ATG	p.T423M
Pat_24	Pre-Treatment	CACNG2	10369	37	22	36962445	36962445	Nonsense_Mutation	SNP	G	A	4	161	c.391C>T	c.(391-393)CGA>TGA	p.R131*
Pat_24	Pre-Treatment	TRIOBP	11078	37	22	38120119	38120119	Missense_Mutation	SNP	A	G	5	277	c.1556A>G	c.(1555-1557)AAT>AGT	p.N519S
Pat_24	Pre-Treatment	TRIOBP	11078	37	22	38120359	38120359	Missense_Mutation	SNP	C	G	16	485	c.1796C>G	c.(1795-1797)ACA>AGA	p.T599R
Pat_24	Pre-Treatment	POLR2F	5435	37	22	38352793	38352793	Missense_Mutation	SNP	G	A	4	192	c.34G>A	c.(34-36)GAC>AAC	p.D12N
Pat_24	Pre-Treatment	KCNJ4	3761	37	22	38822895	38822895	Missense_Mutation	SNP	G	A	5	244	c.1243C>T	c.(1243-1245)CGG>TGG	p.R415W
Pat_24	Pre-Treatment	EP300	2033	37	22	41572528	41572528	Missense_Mutation	SNP	G	A	4	125	c.5057G>A	c.(5056-5058)TGT>TAT	p.C1686Y
Pat_24	Pre-Treatment	3-Sep	55964	37	22	42382068	42382068	Missense_Mutation	SNP	C	T	5	111	c.283C>T	c.(283-285)CGG>TGG	p.R95W
Pat_24	Pre-Treatment	NAGA	4668	37	22	42456333	42456333	Missense_Mutation	SNP	C	T	6	261	c.1186G>A	c.(1186-1188)GTG>ATG	p.V396M
Pat_24	Pre-Treatment	TBC1D22A	25771	37	22	47189519	47189519	Missense_Mutation	SNP	C	T	5	169	c.241C>T	c.(241-243)CTC>TTC	p.L81F
Pat_24	Pre-Treatment	TTLL8	164714	37	22	50470483	50470483	Missense_Mutation	SNP	G	A	4	217	c.1339C>T	c.(1339-1341)CGC>TGC	p.R447C
Pat_24	Pre-Treatment	PANX2	56666	37	22	50616139	50616139	Missense_Mutation	SNP	G	A	6	380	c.998G>A	c.(997-999)CGC>CAC	p.R333H
Pat_24	Pre-Treatment	SELO	83642	37	22	50655462	50655462	Missense_Mutation	SNP	G	A	4	102	c.1750G>A	c.(1750-1752)GTG>ATG	p.V584M
Pat_24	Pre-Treatment	MAPK12	6300	37	22	50694078	50694078	Missense_Mutation	SNP	G	A	6	438	c.737C>T	c.(736-738)CCG>CTG	p.P246L
Pat_24	Pre-Treatment	MIOX	55586	37	22	50927667	50927667	Missense_Mutation	SNP	G	A	4	55	c.529G>A	c.(529-531)GGG>AGG	p.G177R
Pat_24	Pre-Treatment	MTMR14	64419	37	3	9730640	9730640	Missense_Mutation	SNP	G	A	4	184	c.1307G>A	c.(1306-1308)CGT>CAT	p.R436H
Pat_24	Pre-Treatment	TADA3	10474	37	3	9827040	9827040	Missense_Mutation	SNP	C	T	4	211	c.880G>A	c.(880-882)GGG>AGG	p.G294R
Pat_24	Pre-Treatment	CIDEC	63924	37	3	9911632	9911632	Missense_Mutation	SNP	G	A	4	151	c.488C>T	c.(487-489)GCG>GTG	p.A163V
Pat_24	Pre-Treatment	CAND2	23066	37	3	12857393	12857393	Missense_Mutation	SNP	C	T	4	134	c.1327C>T	c.(1327-1329)CGG>TGG	p.R443W
Pat_24	Pre-Treatment	GRIP2	80852	37	3	14555822	14555822	Missense_Mutation	SNP	C	T	3	23	c.1765G>A	c.(1765-1767)GAG>AAG	p.E589K
Pat_24	Pre-Treatment	C3orf19	51244	37	3	14708937	14708937	Missense_Mutation	SNP	G	A	4	229	c.731G>A	c.(730-732)CGG>CAG	p.R244Q
Pat_24	Pre-Treatment	FGD5	152273	37	3	14939582	14939582	Missense_Mutation	SNP	G	A	6	428	c.3046G>A	c.(3046-3048)GCT>ACT	p.A1016T
Pat_24	Pre-Treatment	SH3BP5	9467	37	3	15300421	15300421	Missense_Mutation	SNP	C	T	4	114	c.806G>A	c.(805-807)CGG>CAG	p.R269Q
Pat_24	Pre-Treatment	CMTM8	152189	37	3	32398920	32398920	Missense_Mutation	SNP	C	T	108	129	c.203C>T	c.(202-204)CCC>CTC	p.P68L
Pat_24	Pre-Treatment	UBP1	7342	37	3	33438622	33438622	Missense_Mutation	SNP	C	T	4	129	c.1186G>A	c.(1186-1188)GAC>AAC	p.D396N
Pat_24	Pre-Treatment	PDCD6IP	10015	37	3	33905518	33905518	Missense_Mutation	SNP	C	T	59	99	c.2141C>T	c.(2140-2142)GCC>GTC	p.A714V
Pat_24	Pre-Treatment	STAC	6769	37	3	36545899	36545899	Missense_Mutation	SNP	G	A	47	70	c.781G>A	c.(781-783)GAA>AAA	p.E261K
Pat_24	Pre-Treatment	TRANK1	9881	37	3	36884181	36884181	Missense_Mutation	SNP	C	T	4	96	c.3430G>A	c.(3430-3432)GTT>ATT	p.V1144I
Pat_24	Pre-Treatment	DLEC1	9940	37	3	38151621	38151621	Missense_Mutation	SNP	C	T	5	154	c.3292C>T	c.(3292-3294)CTC>TTC	p.L1098F
Pat_24	Pre-Treatment	ACVR2B	93	37	3	38522951	38522951	Missense_Mutation	SNP	G	A	4	147	c.1069G>A	c.(1069-1071)GGA>AGA	p.G357R
Pat_24	Pre-Treatment	SCN10A	6336	37	3	38739931	38739931	Missense_Mutation	SNP	G	A	4	235	c.4780C>T	c.(4780-4782)CGC>TGC	p.R1594C
Pat_24	Pre-Treatment	CSRNP1	64651	37	3	39184553	39184553	Missense_Mutation	SNP	G	A	5	232	c.1763C>T	c.(1762-1764)CCG>CTG	p.P588L
Pat_24	Pre-Treatment	HIGD1A	25994	37	3	42835717	42835717	Missense_Mutation	SNP	G	A	51	86	c.29C>T	c.(28-30)CCT>CTT	p.P10L
Pat_24	Pre-Treatment	CDCP1	64866	37	3	45136959	45136959	Missense_Mutation	SNP	C	T	4	205	c.1126G>A	c.(1126-1128)GTG>ATG	p.V376M
Pat_24	Pre-Treatment	SETD2	29072	37	3	47147534	47147534	Nonsense_Mutation	SNP	G	A	4	215	c.4792C>T	c.(4792-4794)CGA>TGA	p.R1598*
Pat_24	Pre-Treatment	SETD2	29072	37	3	47164268	47164268	Nonsense_Mutation	SNP	G	A	10	29	c.1858C>T	c.(1858-1860)CGA>TGA	p.R620*
Pat_24	Pre-Treatment	KLHL18	23276	37	3	47384255	47384255	Missense_Mutation	SNP	G	A	4	122	c.1273G>A	c.(1273-1275)GTT>ATT	p.V425I
Pat_24	Pre-Treatment	PTPN23	25930	37	3	47446188	47446188	Missense_Mutation	SNP	G	A	4	161	c.206G>A	c.(205-207)CGC>CAC	p.R69H
Pat_24	Pre-Treatment	FBXW12	285231	37	3	48423472	48423472	Missense_Mutation	SNP	G	A	4	205	c.1192G>A	c.(1192-1194)GAG>AAG	p.E398K
Pat_24	Pre-Treatment	COL7A1	1294	37	3	48608389	48608389	Missense_Mutation	SNP	G	A	3	38	c.7177C>T	c.(7177-7179)CTC>TTC	p.L2393F
Pat_24	Pre-Treatment	COL7A1	1294	37	3	48629609	48629609	Missense_Mutation	SNP	G	A	5	249	c.1166C>T	c.(1165-1167)ACG>ATG	p.T389M
Pat_24	Pre-Treatment	CELSR3	1951	37	3	48663703	48663703	Missense_Mutation	SNP	G	A	4	114	c.12371C>T	c.(12370-12372)GCT>GTT	p.A4124V
Pat_24	Pre-Treatment	CELSR3	1951	37	3	48689366	48689366	Missense_Mutation	SNP	G	A	117	156	c.5867C>T	c.(5866-5868)CCA>CTA	p.P1956L
Pat_24	Pre-Treatment	C3orf62	375341	37	3	49314068	49314068	Missense_Mutation	SNP	C	G	4	180	c.238G>C	c.(238-240)GCT>CCT	p.A80P

Pat_24	Pre-Treatment	GPX1	2876	37	3	49395051	49395052	Missense_Mutation	DNP	AG	TA	22	70	c.381_382CT>TA	(379-384)GCCTTC>GCTAT	p.F128I
Pat_24	Pre-Treatment	APEH	327	37	3	49720135	49720135	Missense_Mutation	SNP	G	A	4	211	c.1849G>A	c.(1849-1851)GCC>ACC	p.A617T
Pat_24	Pre-Treatment	DOCK3	1795	37	3	51265501	51265501	Missense_Mutation	SNP	C	G	3	103	c.1629C>G	c.(1627-1629)CAC>CAG	p.H543Q
Pat_24	Pre-Treatment	DOCK3	1795	37	3	51411966	51411966	Missense_Mutation	SNP	G	A	4	90	c.5360G>A	c.(5359-5361)CGG>CAG	p.R1787Q
Pat_24	Pre-Treatment	VPRBP	9730	37	3	51458334	51458334	Missense_Mutation	SNP	G	A	149	220	c.2090C>T	c.(2089-2091)TCC>TTC	p.S697F
Pat_24	Pre-Treatment	PARP3	10039	37	3	51977511	51977511	Missense_Mutation	SNP	G	A	4	71	c.140G>A	c.(139-141)CGC>CAC	p.R47H
Pat_24	Pre-Treatment	TLR9	54106	37	3	52255447	52255447	Missense_Mutation	SNP	C	T	3	28	c.2885G>A	c.(2884-2886)CGC>CAC	p.R962H
Pat_24	Pre-Treatment	NT5DC2	64943	37	3	52559263	52559263	Missense_Mutation	SNP	C	T	4	177	c.1057G>A	c.(1057-1059)GTG>ATG	p.V353M
Pat_24	Pre-Treatment	RFT1	91869	37	3	53125938	53125938	Missense_Mutation	SNP	C	T	4	136	c.1607G>A	c.(1606-1608)CGC>CAC	p.R536H
Pat_24	Pre-Treatment	MITF	4286	37	3	69928373	69928373	Missense_Mutation	SNP	C	T	4	87	c.193C>T	c.(193-195)CGT>TGT	p.R65C
Pat_24	Pre-Treatment	CNTN3	5067	37	3	74350624	74350624	Missense_Mutation	SNP	G	A	72	147	c.2020C>T	c.(2020-2022)CGG>TGG	p.R674W
Pat_24	Pre-Treatment	ROBO2	6092	37	3	77666773	77666773	Nonsense_Mutation	SNP	C	T	55	76	c.3403C>T	c.(3403-3405)CGA>TGA	p.R1135*
Pat_24	Pre-Treatment	EPHA3	2042	37	3	89448601	89448601	Missense_Mutation	SNP	G	A	4	180	c.1565G>A	c.(1564-1566)CGC>CAC	p.R522H
Pat_24	Pre-Treatment	PROS1	5627	37	3	93646210	93646210	Missense_Mutation	SNP	G	A	4	115	c.118C>T	c.(118-120)CGT>TGT	p.R40C
Pat_24	Pre-Treatment	IMPG2	50939	37	3	100964717	100964717	Missense_Mutation	SNP	G	A	5	227	c.1472C>T	c.(1471-1473)CCG>CTG	p.P491L
Pat_24	Pre-Treatment	DRD3	1814	37	3	113866354	113866354	Missense_Mutation	SNP	C	T	88	130	c.434G>A	c.(433-435)AGC>AAC	p.S145N
Pat_24	Pre-Treatment	DRD3	1814	37	3	113890700	113890700	Missense_Mutation	SNP	T	C	64	45	c.140A>G	c.(139-141)AAT>AGT	p.N47S
Pat_24	Pre-Treatment	ZBTB20	26137	37	3	114070510	114070510	Missense_Mutation	SNP	C	T	4	139	c.415G>A	c.(415-417)GAC>AAC	p.D139N
Pat_24	Pre-Treatment	UPK1B	7348	37	3	118905613	118905613	Missense_Mutation	SNP	C	T	5	213	c.25C>T	c.(25-27)CGT>TGT	p.R9C
Pat_24	Pre-Treatment	ADPRH	141	37	3	119306475	119306475	Missense_Mutation	SNP	C	T	18	55	c.824C>T	c.(823-825)CCC>CTC	p.P275L
Pat_24	Pre-Treatment	GPR156	165829	37	3	119886477	119886477	Missense_Mutation	SNP	G	A	5	155	c.1847C>T	c.(1846-1848)GCA>GTA	p.A616V
Pat_24	Pre-Treatment	STXBP5L	9515	37	3	120760586	120760586	Missense_Mutation	SNP	A	T	6	140	c.327A>T	c.(325-327)GAA>GAT	p.E109D
Pat_24	Pre-Treatment	FBXO40	51725	37	3	121340508	121340508	Missense_Mutation	SNP	C	T	75	102	c.232C>T	c.(232-234)CGC>TGC	p.R78C
Pat_24	Pre-Treatment	FBXO40	51725	37	3	121340844	121340844	Missense_Mutation	SNP	G	A	31	48	c.568G>A	c.(568-570)GGG>AGG	p.G190R
Pat_24	Pre-Treatment	KALRN	8997	37	3	124132426	124132426	Missense_Mutation	SNP	G	A	5	169	c.2450G>A	c.(2449-2451)CGG>CAG	p.R817Q
Pat_24	Pre-Treatment	PLXNA1	5361	37	3	126735786	126735786	Splice_Site	SNP	G	A	5	203	c.3114_splice	c.e16-1	p.S1038_splice
Pat_24	Pre-Treatment	DNAJC13	23317	37	3	132235305	132235305	Missense_Mutation	SNP	C	T	4	185	c.5525C>T	c.(5524-5526)TCG>TTG	p.S1842L
Pat_24	Pre-Treatment	EPHB1	2047	37	3	134920413	134920413	Missense_Mutation	SNP	G	A	5	396	c.2228G>A	c.(2227-2229)CGG>CAG	p.R743Q
Pat_24	Pre-Treatment	MRAS	22808	37	3	138091918	138091918	Missense_Mutation	SNP	G	A	4	233	c.193G>A	c.(193-195)GTT>ATT	p.V65I
Pat_24	Pre-Treatment	ATR	545	37	3	142279165	142279165	Missense_Mutation	SNP	G	A	4	220	c.1481C>T	c.(1480-1482)GCT>GTT	p.A494V
Pat_24	Pre-Treatment	TRPC1	7220	37	3	142523009	142523009	Nonsense_Mutation	SNP	C	T	22	49	c.1948C>T	c.(1948-1950)CAG>TAG	p.Q650*
Pat_24	Pre-Treatment	HPS3	84343	37	3	148859167	148859167	Missense_Mutation	SNP	G	A	5	248	c.970G>A	c.(970-972)GGT>AGT	p.G324S
Pat_24	Pre-Treatment	CP	1356	37	3	148924003	148924003	Missense_Mutation	SNP	G	A	58	91	c.1160C>T	c.(1159-1161)CCC>CTC	p.P387L
Pat_24	Pre-Treatment	TSC22D2	9819	37	3	150128509	150128509	Missense_Mutation	SNP	C	T	3	22	c.1372C>T	c.(1372-1374)CCC>TCC	p.P458S
Pat_24	Pre-Treatment	MFSD1	64747	37	3	158520073	158520073	Missense_Mutation	SNP	G	T	4	69	c.132G>T	c.(130-132)TTG>TTT	p.L44F
Pat_24	Pre-Treatment	IFT80	57560	37	3	159995430	159995430	Missense_Mutation	SNP	G	A	4	95	c.1865C>T	c.(1864-1866)GCT>GTT	p.A622V
Pat_24	Pre-Treatment	SPATA16	83893	37	3	172737325	172737325	Missense_Mutation	SNP	G	A	131	236	c.799C>T	c.(799-801)CGT>TGT	p.R267C
Pat_24	Pre-Treatment	NLGN1	22871	37	3	173998272	173998272	Missense_Mutation	SNP	G	C	4	92	c.1651G>C	c.(1651-1653)GAC>CAC	p.D551H
Pat_24	Pre-Treatment	FXR1	8087	37	3	180685938	180685938	Missense_Mutation	SNP	G	A	5	242	c.1298G>A	c.(1297-1299)CGA>CAA	p.R433Q
Pat_24	Pre-Treatment	FXR1	8087	37	3	180688048	180688048	Missense_Mutation	SNP	G	A	6	298	c.1505G>A	c.(1504-1506)CGT>CAT	p.R502H
Pat_24	Pre-Treatment	MCF2L2	23101	37	3	183017985	183017985	Splice_Site	SNP	C	T	13	33	c.1114_splice	c.e11-1	p.E372_splice
Pat_24	Pre-Treatment	ABCC5	10057	37	3	183681340	183681340	Missense_Mutation	SNP	G	A	4	148	c.2068C>T	c.(2068-2070)CGC>TGC	p.R690C
Pat_24	Pre-Treatment	ABCF3	55324	37	3	183906749	183906749	Missense_Mutation	SNP	C	T	7	207	c.950C>T	c.(949-951)ACC>ATC	p.T317I
Pat_24	Pre-Treatment	ALG3	10195	37	3	183960623	183960623	Missense_Mutation	SNP	G	A	4	165	c.1132C>T	c.(1132-1134)CGC>TGC	p.R378C
Pat_24	Pre-Treatment	ECE2	9718	37	3	184005689	184005689	Missense_Mutation	SNP	G	A	70	112	c.1682G>A	c.(1681-1683)GGG>GAG	p.G561E
Pat_24	Pre-Treatment	EIF4G1	1981	37	3	184045071	184045071	Missense_Mutation	SNP	C	T	5	280	c.3496C>T	c.(3496-3498)CGG>TGG	p.R1166W
Pat_24	Pre-Treatment	EIF4G1	1981	37	3	184045084	184045084	Missense_Mutation	SNP	G	A	6	279	c.3509G>A	c.(3508-3510)CGT>CAT	p.R1170H

Pat_24	Pre-Treatment	CLCN2	1181	37	3	184071895	184071895	Missense_Mutation	SNP	C	T	4	93	c.1715G>A	c.(1714-1716)CGC>CAC	p.R572H
Pat_24	Pre-Treatment	KNG1	3827	37	3	186435504	186435504	Missense_Mutation	SNP	G	A	4	193	c.173G>A	c.(172-174)CGC>CAC	p.R58H
Pat_24	Pre-Treatment	LPP	4026	37	3	188477903	188477903	Missense_Mutation	SNP	C	T	4	64	c.1243C>T	c.(1243-1245)CGC>TGC	p.R415C
Pat_24	Pre-Treatment	ATP13A4	84239	37	3	193207602	193207602	Missense_Mutation	SNP	T	A	5	118	c.655A>T	c.(655-657)AGT>TGT	p.S219C
Pat_24	Pre-Treatment	LRRC33	375387	37	3	196387194	196387194	Missense_Mutation	SNP	G	A	4	132	c.680G>A	c.(679-681)CGG>CAG	p.R227Q
Pat_24	Pre-Treatment	LMLN	89782	37	3	197707212	197707212	Missense_Mutation	SNP	C	T	4	232	c.565C>T	c.(565-567)CGT>TGT	p.R189C
Pat_24	Pre-Treatment	PDE6B	5158	37	4	661780	661780	Missense_Mutation	SNP	G	A	4	168	c.2488G>A	c.(2488-2490)GTG>ATG	p.V830M
Pat_24	Pre-Treatment	CRIPAK	285464	37	4	1389048	1389048	Missense_Mutation	SNP	G	A	8	612	c.749G>A	c.(748-750)CGC>CAC	p.R250H
Pat_24	Pre-Treatment	HTT	3064	37	4	3158817	3158817	Missense_Mutation	SNP	C	T	4	103	c.3650C>T	c.(3649-3651)ACC>ATC	p.T1217I
Pat_24	Pre-Treatment	RGS12	6002	37	4	3317941	3317941	Missense_Mutation	SNP	C	T	4	172	c.44C>T	c.(43-45)CCG>CTG	p.P15L
Pat_24	Pre-Treatment	CRMP1	1400	37	4	5851178	5851178	Missense_Mutation	SNP	G	A	25	52	c.562C>T	c.(562-564)CTT>TTT	p.L188F
Pat_24	Pre-Treatment	ZNF518B	85460	37	4	10447435	10447435	Missense_Mutation	SNP	G	A	4	220	c.518C>T	c.(517-519)ACG>ATG	p.T173M
Pat_24	Pre-Treatment	LGI2	55203	37	4	25005381	25005381	Missense_Mutation	SNP	G	A	6	493	c.1330C>T	c.(1330-1332)CGG>TGG	p.R444W
Pat_24	Pre-Treatment	PCDH7	5099	37	4	30724909	30724909	Missense_Mutation	SNP	G	A	4	93	c.1865G>A	c.(1864-1866)AGC>AAC	p.S622N
Pat_24	Pre-Treatment	KLF3	51274	37	4	38698711	38698711	Missense_Mutation	SNP	C	T	27	55	c.865C>T	c.(865-867)CCC>TCC	p.P289S
Pat_24	Pre-Treatment	CHRNA9	55584	37	4	40339314	40339314	Missense_Mutation	SNP	G	A	26	47	c.298G>A	c.(298-300)GAT>AAT	p.D100N
Pat_24	Pre-Treatment	RBM47	54502	37	4	40438508	40438508	Missense_Mutation	SNP	G	A	4	217	c.1280C>T	c.(1279-1281)CCG>CTG	p.P427L
Pat_24	Pre-Treatment	UCHL1	7345	37	4	41262778	41262778	Missense_Mutation	SNP	C	T	85	150	c.289C>T	c.(289-291)CAC>TAC	p.H97Y
Pat_24	Pre-Treatment	KDR	3791	37	4	55968610	55968610	Missense_Mutation	SNP	C	T	4	139	c.2053G>A	c.(2053-2055)GAA>AAA	p.E685K
Pat_24	Pre-Treatment	SRP72	6731	37	4	57344629	57344629	Missense_Mutation	SNP	G	A	4	99	c.727G>A	c.(727-729)GAG>AAG	p.E243K
Pat_24	Pre-Treatment	UGT2B10	7365	37	4	69874623	69874623	Missense_Mutation	SNP	G	A	5	394	c.1148C>T	c.(1147-1149)TCG>TTG	p.S383L
Pat_24	Pre-Treatment	UGT2B4	7363	37	4	70355227	70355227	Missense_Mutation	SNP	G	A	6	447	c.932C>T	c.(931-933)TCG>TTG	p.S311L
Pat_24	Pre-Treatment	UGT2B4	7363	37	4	70355286	70355286	Missense_Mutation	SNP	T	A	82	147	c.873A>T	c.(871-873)GAA>GAT	p.E291D
Pat_24	Pre-Treatment	ALB	213	37	4	74280825	74280825	Missense_Mutation	SNP	G	A	65	124	c.1132G>A	c.(1132-1134)GAA>AAA	p.E378K
Pat_24	Pre-Treatment	RASSF6	166824	37	4	74459282	74459282	Missense_Mutation	SNP	C	T	67	98	c.269G>A	c.(268-270)GGA>GAA	p.G90E
Pat_24	Pre-Treatment	CXCL9	4283	37	4	76925960	76925960	Splice_Site	SNP	A	G	37	127	c.276_splice	c.e3+1	p.Q92_splice
Pat_24	Pre-Treatment	CCDC158	339965	37	4	77234386	77234386	Missense_Mutation	SNP	C	T	9	25	c.3279G>A	c.(3277-3279)ATG>ATA	p.M1093I
Pat_24	Pre-Treatment	PRKG2	5593	37	4	82061745	82061745	Nonsense_Mutation	SNP	C	A	4	137	c.1486G>T	c.(1486-1488)GAG>TAG	p.E496*
Pat_24	Pre-Treatment	HERC3	8916	37	4	89527102	89527102	Missense_Mutation	SNP	G	A	4	94	c.128G>A	c.(127-129)GGA>GAA	p.G43E
Pat_24	Pre-Treatment	GPRIN3	285513	37	4	90170964	90170964	Missense_Mutation	SNP	G	A	67	91	c.298C>T	c.(298-300)CCC>TCC	p.P100S
Pat_24	Pre-Treatment	MMRN1	22915	37	4	90857395	90857395	Missense_Mutation	SNP	C	T	14	11	c.2564C>T	c.(2563-2565)TCC>TTC	p.S855F
Pat_24	Pre-Treatment	PDLIM5	10611	37	4	95561492	95561492	Missense_Mutation	SNP	G	T	4	161	c.1174G>T	c.(1174-1176)GCT>TCT	p.A392S
Pat_24	Pre-Treatment	DDIT4L	115265	37	4	101109213	101109213	Nonsense_Mutation	SNP	G	T	6	355	c.203C>A	c.(202-204)TCA>TAA	p.S68*
Pat_24	Pre-Treatment	TET2	54790	37	4	106157378	106157378	Missense_Mutation	SNP	T	A	52	63	c.2279T>A	c.(2278-2280)TTT>TAT	p.F760Y
Pat_24	Pre-Treatment	TBCK	93627	37	4	107173160	107173160	Missense_Mutation	SNP	G	A	23	46	c.460C>T	c.(460-462)CCC>TCC	p.P154S
Pat_24	Pre-Treatment	PAPSS1	9061	37	4	108566061	108566061	Missense_Mutation	SNP	C	T	4	98	c.1403G>A	c.(1402-1404)CGT>CAT	p.R468H
Pat_24	Pre-Treatment	HADH	3033	37	4	108940781	108940781	Missense_Mutation	SNP	C	T	183	257	c.505C>T	c.(505-507)CTC>TTC	p.L169F
Pat_24	Pre-Treatment	PITX2	5308	37	4	111553619	111553619	Missense_Mutation	SNP	C	T	4	203	c.64G>A	c.(64-66)GTT>ATT	p.V22I
Pat_24	Pre-Treatment	C4orf21	55345	37	4	113540414	113540414	Missense_Mutation	SNP	C	T	4	112	c.784G>A	c.(784-786)GAA>AAA	p.E262K
Pat_24	Pre-Treatment	NDST4	64579	37	4	115767146	115767146	Missense_Mutation	SNP	C	T	35	48	c.1948G>A	c.(1948-1950)GAC>AAC	p.D650N
Pat_24	Pre-Treatment	USP53	54532	37	4	120161041	120161041	Missense_Mutation	SNP	C	T	27	40	c.127C>T	c.(127-129)CTT>TTT	p.L43F
Pat_24	Pre-Treatment	PRDM5	11107	37	4	121616280	121616280	Missense_Mutation	SNP	C	T	4	195	c.1879G>A	c.(1879-1881)GTA>ATA	p.V627I
Pat_24	Pre-Treatment	TRPC3	7222	37	4	122800914	122800914	Missense_Mutation	SNP	G	A	22	65	c.2743C>T	c.(2743-2745)CCC>TCC	p.P915S
Pat_24	Pre-Treatment	PCDH18	54510	37	4	138452779	138452779	Missense_Mutation	SNP	C	T	4	63	c.464G>A	c.(463-465)CGC>CAC	p.R155H
Pat_24	Pre-Treatment	RNF150	57484	37	4	141888839	141888839	Missense_Mutation	SNP	C	T	4	152	c.673G>A	c.(673-675)GCA>ACA	p.A225T
Pat_24	Pre-Treatment	TRIM2	23321	37	4	154197202	154197202	Missense_Mutation	SNP	G	A	4	91	c.292G>A	c.(292-294)GCT>ACT	p.A98T
Pat_24	Pre-Treatment	GLRB	2743	37	4	158091737	158091737	Missense_Mutation	SNP	T	A	57	69	c.1351T>A	c.(1351-1353)TCT>ACT	p.S451T

Pat_24	Pre-Treatment	GRIA2	2891	37	4	158282254	158282254	Missense_Mutation	SNP	G	A	4	194	c.2384G>A	c.(2383-2385)GGC>GAC	p.G795D
Pat_24	Pre-Treatment	TLL1	7092	37	4	166915607	166915607	Missense_Mutation	SNP	C	T	20	21	c.436C>T	c.(436-438)CCC>TCC	p.P146S
Pat_24	Pre-Treatment	ADAM29	11086	37	4	175898987	175898987	Missense_Mutation	SNP	C	T	7	238	c.2311C>T	c.(2311-2313)CGG>TGG	p.R771W
Pat_24	Pre-Treatment	SNX25	83891	37	4	186274751	186274751	Missense_Mutation	SNP	G	A	4	146	c.2087G>A	c.(2086-2088)CGA>CAA	p.R696Q
Pat_24	Pre-Treatment	MTNR1A	4543	37	4	187455657	187455657	Missense_Mutation	SNP	G	A	26	90	c.239C>T	c.(238-240)CCG>CTG	p.P80L
Pat_24	Pre-Treatment	EXOC3	11336	37	5	465848	465848	Missense_Mutation	SNP	G	A	4	134	c.1954G>A	c.(1954-1956)GTG>ATG	p.V652M
Pat_24	Pre-Treatment	MRPL36	64979	37	5	1798790	1798790	Missense_Mutation	SNP	C	T	5	166	c.260G>A	c.(259-261)CGG>CAG	p.R87Q
Pat_24	Pre-Treatment	CTNND2	1501	37	5	11022948	11022948	Missense_Mutation	SNP	C	T	5	97	c.2932G>A	c.(2932-2934)GCC>ACC	p.A978T
Pat_24	Pre-Treatment	CTNND2	1501	37	5	11397234	11397234	Missense_Mutation	SNP	C	A	70	37	c.521G>T	c.(520-522)AGC>ATC	p.S174I
Pat_24	Pre-Treatment	CTNND2	1501	37	5	11732369	11732369	Missense_Mutation	SNP	G	A	4	190	c.53C>T	c.(52-54)CCA>CTA	p.P18L
Pat_24	Pre-Treatment	DNAH5	1767	37	5	13864603	13864603	Missense_Mutation	SNP	G	A	4	116	c.4499C>T	c.(4498-4500)ACC>ATC	p.T1500I
Pat_24	Pre-Treatment	TRIO	7204	37	5	14280445	14280445	Missense_Mutation	SNP	C	T	5	188	c.247C>T	c.(247-249)CGT>TGT	p.R83C
Pat_24	Pre-Treatment	PRDM9	56979	37	5	23509657	23509657	Missense_Mutation	SNP	C	T	146	85	c.148C>T	c.(148-150)CGC>TGC	p.R50C
Pat_24	Pre-Treatment	PRDM9	56979	37	5	23527385	23527385	Missense_Mutation	SNP	A	C	5	263	c.2188A>C	c.(2188-2190)AGC>CGC	p.S730R
Pat_24	Pre-Treatment	PRDM9	56979	37	5	23527388	23527388	Missense_Mutation	SNP	A	G	7	280	c.2191A>G	c.(2191-2193)AAT>GAT	p.N731D
Pat_24	Pre-Treatment	MTMR12	54545	37	5	32239127	32239127	Missense_Mutation	SNP	G	A	4	134	c.1324C>T	c.(1324-1326)CGC>TGC	p.R442C
Pat_24	Pre-Treatment	SPEF2	79925	37	5	35792486	35792486	Missense_Mutation	SNP	G	A	141	140	c.4492G>A	c.(4492-4494)GTG>ATG	p.V1498M
Pat_24	Pre-Treatment	RICTOR	253260	37	5	38967280	38967280	Missense_Mutation	SNP	G	A	6	585	c.1201C>T	c.(1201-1203)CGT>TGT	p.R401C
Pat_24	Pre-Treatment	ISL1	3670	37	5	50680467	50680467	Missense_Mutation	SNP	G	A	5	379	c.121G>A	c.(121-123)GCA>ACA	p.A41T
Pat_24	Pre-Treatment	ITGA2	3673	37	5	52337982	52337982	Nonsense_Mutation	SNP	C	T	4	229	c.226C>T	c.(226-228)CGA>TGA	p.R76*
Pat_24	Pre-Treatment	ANKRD55	79722	37	5	55407572	55407572	Missense_Mutation	SNP	G	A	91	158	c.1003C>T	c.(1003-1005)CGG>TGG	p.R335W
Pat_24	Pre-Treatment	MAP3K1	4214	37	5	56178002	56178002	Missense_Mutation	SNP	C	T	4	173	c.2975C>T	c.(2974-2976)TCT>TTT	p.S992F
Pat_24	Pre-Treatment	DIMT1L	27292	37	5	61686727	61686727	Missense_Mutation	SNP	G	A	167	227	c.875C>T	c.(874-876)TCC>TTC	p.S292F
Pat_24	Pre-Treatment	MAST4	375449	37	5	66430465	66430465	Missense_Mutation	SNP	G	T	5	331	c.1774G>T	c.(1774-1776)GTG>TTG	p.V592L
Pat_24	Pre-Treatment	MAP1B	4131	37	5	71495411	71495411	Missense_Mutation	SNP	C	T	4	220	c.6229C>T	c.(6229-6231)CGT>TGT	p.R2077C
Pat_24	Pre-Treatment	RGNEF	64283	37	5	73148496	73148496	Missense_Mutation	SNP	C	T	5	305	c.1769C>T	c.(1768-1770)TCG>TTG	p.S590L
Pat_24	Pre-Treatment	HMGCR	3156	37	5	74652224	74652224	Missense_Mutation	SNP	G	A	4	226	c.1937G>A	c.(1936-1938)CGT>CAT	p.R646H
Pat_24	Pre-Treatment	AGGF1	55109	37	5	76331512	76331512	Missense_Mutation	SNP	G	A	4	144	c.460G>A	c.(460-462)GAT>AAT	p.D154N
Pat_24	Pre-Treatment	JMY	133746	37	5	78586025	78586025	Missense_Mutation	SNP	C	T	55	101	c.1288C>T	c.(1288-1290)CAC>TAC	p.H430Y
Pat_24	Pre-Treatment	JMY	133746	37	5	78586965	78586965	Missense_Mutation	SNP	G	T	4	86	c.1370G>T	c.(1369-1371)CGA>CTA	p.R457L
Pat_24	Pre-Treatment	RASA1	5921	37	5	86659278	86659278	Missense_Mutation	SNP	A	G	40	86	c.1567A>G	c.(1567-1569)AGT>GGT	p.S523G
Pat_24	Pre-Treatment	MEF2C	4208	37	5	88100420	88100420	Missense_Mutation	SNP	C	T	4	111	c.253G>A	c.(253-255)GTG>ATG	p.V85M
Pat_24	Pre-Treatment	GPR98	84059	37	5	89914946	89914946	Missense_Mutation	SNP	C	T	3	26	c.401C>T	c.(400-402)ACT>ATT	p.T134I
Pat_24	Pre-Treatment	EPB41L4A	64097	37	5	111504473	111504473	Missense_Mutation	SNP	G	A	4	225	c.1895C>T	c.(1894-1896)TCG>TTG	p.S632L
Pat_24	Pre-Treatment	APC	324	37	5	112128186	112128186	Missense_Mutation	SNP	G	A	4	180	c.689G>A	c.(688-690)CGT>CAT	p.R230H
Pat_24	Pre-Treatment	APC	324	37	5	112162892	112162892	Missense_Mutation	SNP	G	A	5	170	c.1496G>A	c.(1495-1497)CGA>CAA	p.R499Q
Pat_24	Pre-Treatment	HSD17B4	3295	37	5	118829594	118829594	Missense_Mutation	SNP	A	G	62	51	c.821A>G	c.(820-822)AAG>AGG	p.K274R
Pat_24	Pre-Treatment	CEP120	153241	37	5	122713159	122713159	Missense_Mutation	SNP	C	T	4	172	c.2267G>A	c.(2266-2268)CGT>CAT	p.R756H
Pat_24	Pre-Treatment	CHSY3	337876	37	5	129520990	129520990	Missense_Mutation	SNP	G	T	4	198	c.2155G>T	c.(2155-2157)GTT>TTT	p.V719F
Pat_24	Pre-Treatment	KIF3A	11127	37	5	132062130	132062130	Missense_Mutation	SNP	C	T	6	206	c.341G>A	c.(340-342)CGA>CAA	p.R114Q
Pat_24	Pre-Treatment	KLHL3	26249	37	5	136973018	136973018	Missense_Mutation	SNP	G	A	5	239	c.1286C>T	c.(1285-1287)ACG>ATG	p.T429M
Pat_24	Pre-Treatment	HSPA9	3313	37	5	137892552	137892552	Nonsense_Mutation	SNP	G	A	5	200	c.1732C>T	c.(1732-1734)CGA>TGA	p.R578*
Pat_24	Pre-Treatment	CXXC5	51523	37	5	139060727	139060727	Missense_Mutation	SNP	G	A	4	48	c.619G>A	c.(619-621)GAC>AAC	p.D207N
Pat_24	Pre-Treatment	SLC35A4	113829	37	5	139947436	139947436	Missense_Mutation	SNP	G	T	4	174	c.682G>T	c.(682-684)GGT>TGT	p.G228C
Pat_24	Pre-Treatment	PCDHA1	56147	37	5	140167131	140167131	Missense_Mutation	SNP	C	T	6	444	c.1256C>T	c.(1255-1257)TCG>TTG	p.S419L
Pat_24	Pre-Treatment	PCDHA1	56147	37	5	140167736	140167736	Missense_Mutation	SNP	C	T	108	218	c.1861C>T	c.(1861-1863)CCG>TCG	p.P621S
Pat_24	Pre-Treatment	PCDHA3	56145	37	5	140182649	140182649	Missense_Mutation	SNP	C	T	80	114	c.1867C>T	c.(1867-1869)CGC>TGC	p.R623C

Pat_24	Pre-Treatment	PCDHA8	56140	37	5	140222432	140222432	Missense_Mutation	SNP	C	T	5	275	c.1526C>T	c.(1525-1527)TCG>TTG	p.S509L
Pat_24	Pre-Treatment	PCDHA10	56139	37	5	140236862	140236862	Missense_Mutation	SNP	G	A	144	274	c.1229G>A	c.(1228-1230)AGC>AAC	p.S410N
Pat_24	Pre-Treatment	PCDHB1	29930	37	5	140431953	140431953	Missense_Mutation	SNP	G	A	33	49	c.898G>A	c.(898-900)GAA>AAA	p.E300K
Pat_24	Pre-Treatment	PCDHB3	56132	37	5	140481797	140481797	Missense_Mutation	SNP	G	A	60	71	c.1564G>A	c.(1564-1566)GAG>AAG	p.E522K
Pat_24	Pre-Treatment	PCDHB4	56131	37	5	140503558	140503558	Missense_Mutation	SNP	C	T	4	120	c.1978C>T	c.(1978-1980)CTC>TTC	p.L660F
Pat_24	Pre-Treatment	PCDHB6	56130	37	5	140531196	140531196	Missense_Mutation	SNP	C	T	8	411	c.1358C>T	c.(1357-1359)TCC>TTC	p.S453F
Pat_24	Pre-Treatment	PCDHB16	57717	37	5	140562543	140562543	Missense_Mutation	SNP	G	A	27	34	c.409G>A	c.(409-411)GAA>AAA	p.E137K
Pat_24	Pre-Treatment	PCDHB11	56125	37	5	140581443	140581443	Missense_Mutation	SNP	C	T	92	171	c.2096C>T	c.(2095-2097)TCG>TTG	p.S699L
Pat_24	Pre-Treatment	PCDH12	51294	37	5	141335676	141335676	Missense_Mutation	SNP	C	G	4	93	c.1741G>C	c.(1741-1743)GTG>CTG	p.V581L
Pat_24	Pre-Treatment	GRXCR2	643226	37	5	145246230	145246230	Missense_Mutation	SNP	C	T	4	147	c.398G>A	c.(397-399)CGA>CAA	p.R133Q
Pat_24	Pre-Treatment	SH3RF2	153769	37	5	145428766	145428766	Missense_Mutation	SNP	G	A	4	166	c.1280G>A	c.(1279-1281)CGA>CAA	p.R427Q
Pat_24	Pre-Treatment	SH3RF2	153769	37	5	145435672	145435672	Missense_Mutation	SNP	C	T	94	145	c.1451C>T	c.(1450-1452)TCC>TTC	p.S484F
Pat_24	Pre-Treatment	PDGFRB	5159	37	5	149510217	149510217	Nonsense_Mutation	SNP	G	A	5	333	c.1252C>T	c.(1252-1254)CGA>TGA	p.R418*
Pat_24	Pre-Treatment	RPS14	6208	37	5	149823869	149823869	Missense_Mutation	SNP	G	A	5	395	c.436C>T	c.(436-438)CGC>TGC	p.R146C
Pat_24	Pre-Treatment	FAT2	2196	37	5	150885392	150885392	Missense_Mutation	SNP	G	A	5	274	c.12784C>T	c.(12784-12786)CGC>TGC	p.R4262C
Pat_24	Pre-Treatment	PWWP2A	114825	37	5	159520099	159520099	Missense_Mutation	SNP	G	A	18	21	c.1558C>T	c.(1558-1560)CCT>TCT	p.P520S
Pat_24	Pre-Treatment	C5orf54	63920	37	5	159822493	159822493	Missense_Mutation	SNP	G	A	5	306	c.5C>T	c.(4-6)TCG>TTG	p.S2L
Pat_24	Pre-Treatment	ODZ2	57451	37	5	167631391	167631391	Missense_Mutation	SNP	G	A	23	55	c.3562G>A	c.(3562-3564)GGC>AGC	p.G1188S
Pat_24	Pre-Treatment	ODZ2	57451	37	5	167671635	167671635	Missense_Mutation	SNP	G	A	4	174	c.5704G>A	c.(5704-5706)GAG>AAG	p.E1902K
Pat_24	Pre-Treatment	SLIT3	6586	37	5	168138041	168138041	Missense_Mutation	SNP	G	A	11	25	c.2578C>T	c.(2578-2580)CAC>TAC	p.H860Y
Pat_24	Pre-Treatment	CCDC99	54908	37	5	169028394	169028394	Nonsense_Mutation	SNP	C	T	4	179	c.1435C>T	c.(1435-1437)CGA>TGA	p.R479*
Pat_24	Pre-Treatment	GPRIN1	114787	37	5	176024702	176024702	Missense_Mutation	SNP	G	A	30	58	c.2134C>T	c.(2134-2136)CCC>TCC	p.P712S
Pat_24	Pre-Treatment	SLC34A1	6569	37	5	176821059	176821059	Missense_Mutation	SNP	C	T	5	427	c.1037C>T	c.(1036-1038)CCG>CTG	p.P346L
Pat_24	Pre-Treatment	F12	2161	37	5	176832982	176832982	Missense_Mutation	SNP	G	A	5	328	c.196C>T	c.(196-198)CGG>TGG	p.R66W
Pat_24	Pre-Treatment	GRK6	2870	37	5	176860170	176860170	Missense_Mutation	SNP	G	A	5	340	c.463G>A	c.(463-465)GTG>ATG	p.V155M
Pat_24	Pre-Treatment	TMED9	54732	37	5	177020678	177020678	Missense_Mutation	SNP	G	A	5	361	c.313G>A	c.(313-315)GAG>AAG	p.E105K
Pat_24	Pre-Treatment	EXOC2	55770	37	6	564069	564069	Missense_Mutation	SNP	G	A	4	220	c.1753C>T	c.(1753-1755)CGT>TGT	p.R585C
Pat_24	Pre-Treatment	DSP	1832	37	6	7580243	7580243	Missense_Mutation	SNP	G	A	4	132	c.3820G>A	c.(3820-3822)GCC>ACC	p.A1274T
Pat_24	Pre-Treatment	TFAP2A	7020	37	6	10398877	10398877	Missense_Mutation	SNP	G	A	8	620	c.1087C>T	c.(1087-1089)CGG>TGG	p.R363W
Pat_24	Pre-Treatment	ATXN1	6310	37	6	16326632	16326632	Missense_Mutation	SNP	C	T	6	388	c.1910G>A	c.(1909-1911)CGA>CAA	p.R637Q
Pat_24	Pre-Treatment	ATXN1	6310	37	6	16328562	16328562	Translation_Start_Site	SNP	C	T	4	62	c.-20G>A	c.(-22--18)CCGTG>CCATG	
Pat_24	Pre-Treatment	BTN1A1	696	37	6	26509113	26509113	Missense_Mutation	SNP	G	A	42	43	c.1292G>A	c.(1291-1293)GGA>GAA	p.G431E
Pat_24	Pre-Treatment	HLA-G	3135	37	6	29797338	29797338	Missense_Mutation	SNP	G	A	7	289	c.763G>A	c.(763-765)GTG>ATG	p.V255M
Pat_24	Pre-Treatment	TRIM15	89870	37	6	30131474	30131474	Missense_Mutation	SNP	C	T	34	81	c.13C>T	c.(13-15)CCG>TCG	p.P5S
Pat_24	Pre-Treatment	LTB	4050	37	6	31550145	31550145	Missense_Mutation	SNP	C	T	82	53	c.50G>A	c.(49-51)GGT>GAT	p.G17D
Pat_24	Pre-Treatment	LY6G5B	58496	37	6	31639676	31639676	Nonsense_Mutation	SNP	C	T	8	501	c.223C>T	c.(223-225)CAG>TAG	p.Q75*
Pat_24	Pre-Treatment	BAT5	7920	37	6	31655035	31655035	Missense_Mutation	SNP	C	A	4	133	c.1631G>T	c.(1630-1632)TGC>TTC	p.C544F
Pat_24	Pre-Treatment	SLC44A4	80736	37	6	31846718	31846718	Missense_Mutation	SNP	C	T	7	592	c.40G>A	c.(40-42)GGG>AGG	p.G14R
Pat_24	Pre-Treatment	C4A	720	37	6	31997489	31997489	Missense_Mutation	SNP	C	T	19	55	c.3823C>T	c.(3823-3825)CAC>TAC	p.H1275Y
Pat_24	Pre-Treatment	TNXB	7148	37	6	32017964	32017964	Missense_Mutation	SNP	C	T	5	183	c.9244G>A	c.(9244-9246)GAG>AAG	p.E3082K
Pat_24	Pre-Treatment	HLA-DOB	3112	37	6	32781028	32781028	Missense_Mutation	SNP	C	T	4	167	c.787G>A	c.(787-789)GTC>ATC	p.V263I
Pat_24	Pre-Treatment	COL11A2	1302	37	6	33157226	33157226	Missense_Mutation	SNP	G	A	4	166	c.103C>T	c.(103-105)CTC>TTC	p.L35F
Pat_24	Pre-Treatment	VPS52	6293	37	6	33231874	33231874	Missense_Mutation	SNP	G	A	6	399	c.1531C>T	c.(1531-1533)CGC>TGC	p.R511C
Pat_24	Pre-Treatment	SYNGAP1	8831	37	6	33403335	33403335	Missense_Mutation	SNP	C	T	7	697	c.707C>T	c.(706-708)GCG>GTG	p.A236V
Pat_24	Pre-Treatment	C6orf125	84300	37	6	33669164	33669164	Missense_Mutation	SNP	C	T	7	372	c.172G>A	c.(172-174)GAG>AAG	p.E58K
Pat_24	Pre-Treatment	IP6K3	117283	37	6	33690697	33690697	Missense_Mutation	SNP	G	A	45	102	c.1033C>T	c.(1033-1035)CCT>TCT	p.P345S
Pat_24	Pre-Treatment	CPNE5	57699	37	6	36716016	36716016	Missense_Mutation	SNP	C	T	253	221	c.1000G>A	c.(1000-1002)GAT>AAT	p.D334N

Pat_24	Pre-Treatment	DNAH8	1769	37	6	38867551	38867551	Splice_Site	SNP	G	A	90	91	c.8413_splice	c.e60-1	p.I2805_splice
Pat_24	Pre-Treatment	CNPY3	10695	37	6	42897414	42897414	Missense_Mutation	SNP	G	A	3	35	c.106G>A	c.(106-108)GGA>AGA	p.G36R
Pat_24	Pre-Treatment	TCTE1	202500	37	6	44250280	44250280	Missense_Mutation	SNP	C	T	86	75	c.863G>A	c.(862-864)CGA>CAA	p.R288Q
Pat_24	Pre-Treatment	AARS2	57505	37	6	44269835	44269835	Missense_Mutation	SNP	G	A	4	166	c.2560C>T	c.(2560-2562)CGT>TGT	p.R854C
Pat_24	Pre-Treatment	TINAG	27283	37	6	54254619	54254619	Missense_Mutation	SNP	G	A	127	248	c.1327G>A	c.(1327-1329)GGA>AGA	p.G443R
Pat_24	Pre-Treatment	FAM83B	222584	37	6	54804664	54804664	Missense_Mutation	SNP	G	T	43	150	c.895G>T	c.(895-897)GCC>TCC	p.A299S
Pat_24	Pre-Treatment	FAM83B	222584	37	6	54806252	54806252	Missense_Mutation	SNP	C	T	18	53	c.2483C>T	c.(2482-2484)CCT>CTT	p.P828L
Pat_24	Pre-Treatment	COL19A1	1310	37	6	70878100	70878100	Missense_Mutation	SNP	G	A	4	138	c.2534G>A	c.(2533-2535)GGT>GAT	p.G845D
Pat_24	Pre-Treatment	OGFRL1	79627	37	6	72011342	72011342	Nonsense_Mutation	SNP	C	T	24	49	c.946C>T	c.(946-948)CGA>TGA	p.R316*
Pat_24	Pre-Treatment	KCNQ5	56479	37	6	73904174	73904174	Splice_Site	SNP	G	A	18	40	c.1837_splice	c.e14-1	p.V613_splice
Pat_24	Pre-Treatment	C6orf150	115004	37	6	74135186	74135186	Missense_Mutation	SNP	C	T	4	73	c.1333G>A	c.(1333-1335)GTA>ATA	p.V445I
Pat_24	Pre-Treatment	COL12A1	1303	37	6	75853037	75853037	Missense_Mutation	SNP	C	A	5	153	c.4758G>T	c.(4756-4758)TGG>TGT	p.W1586C
Pat_24	Pre-Treatment	COL12A1	1303	37	6	75875427	75875427	Missense_Mutation	SNP	A	C	89	130	c.2779T>G	c.(2779-2781)TCT>GCT	p.S927A
Pat_24	Pre-Treatment	IMPG1	3617	37	6	76660307	76660307	Missense_Mutation	SNP	C	T	18	28	c.1796G>A	c.(1795-1797)CGA>CAA	p.R599Q
Pat_24	Pre-Treatment	SH3BGRL2	83699	37	6	80383502	80383502	Missense_Mutation	SNP	G	A	4	241	c.217G>A	c.(217-219)GAC>AAC	p.D73N
Pat_24	Pre-Treatment	TTK	7272	37	6	80717681	80717681	Missense_Mutation	SNP	C	T	5	163	c.295C>T	c.(295-297)CCC>TCC	p.P99S
Pat_24	Pre-Treatment	ZNF292	23036	37	6	87965927	87965927	Missense_Mutation	SNP	C	G	3	81	c.2580C>G	c.(2578-2580)AAC>AAG	p.N860K
Pat_24	Pre-Treatment	MDN1	23195	37	6	90365626	90365626	Missense_Mutation	SNP	C	T	4	112	c.15347G>A	c.(15346-15348)CGT>CAT	p.R5116H
Pat_24	Pre-Treatment	MDN1	23195	37	6	90405631	90405631	Missense_Mutation	SNP	C	T	4	186	c.9464G>A	c.(9463-9465)CGG>CAG	p.R3155Q
Pat_24	Pre-Treatment	MDN1	23195	37	6	90463861	90463861	Missense_Mutation	SNP	G	A	4	126	c.2905C>T	c.(2905-2907)CGG>TGG	p.R969W
Pat_24	Pre-Treatment	MANEA	79694	37	6	96054174	96054174	Missense_Mutation	SNP	C	T	4	109	c.1282C>T	c.(1282-1284)CGT>TGT	p.R428C
Pat_24	Pre-Treatment	KLHL32	114792	37	6	97562088	97562088	Missense_Mutation	SNP	G	A	4	78	c.1057G>A	c.(1057-1059)GGG>AGG	p.G353R
Pat_24	Pre-Treatment	PRDM1	639	37	6	106553455	106553455	Missense_Mutation	SNP	G	A	4	160	c.1420G>A	c.(1420-1422)GGA>AGA	p.G474R
Pat_24	Pre-Treatment	MICAL1	64780	37	6	109773539	109773539	Missense_Mutation	SNP	G	A	5	425	c.742C>T	c.(742-744)CGC>TGC	p.R248C
Pat_24	Pre-Treatment	LAMA4	3910	37	6	112486417	112486417	Missense_Mutation	SNP	G	A	4	165	c.1613C>T	c.(1612-1614)GCG>GTG	p.A538V
Pat_24	Pre-Treatment	HDAC2	3066	37	6	114279863	114279863	Missense_Mutation	SNP	C	T	4	187	c.515G>A	c.(514-516)CGG>CAG	p.R172Q
Pat_24	Pre-Treatment	GPRC6A	222545	37	6	117128060	117128060	Nonsense_Mutation	SNP	G	A	26	59	c.808C>T	c.(808-810)CAG>TAG	p.Q270*
Pat_24	Pre-Treatment	RFX6	222546	37	6	117240317	117240317	Missense_Mutation	SNP	G	A	29	69	c.1040G>A	c.(1039-1041)AGA>AAA	p.R347K
Pat_24	Pre-Treatment	ROS1	6098	37	6	117609788	117609788	Missense_Mutation	SNP	T	A	29	44	c.6911A>T	c.(6910-6912)AAA>ATA	p.K2304I
Pat_24	Pre-Treatment	FAM184A	79632	37	6	119345242	119345242	Missense_Mutation	SNP	C	T	26	78	c.896G>A	c.(895-897)CGA>CAA	p.R299Q
Pat_24	Pre-Treatment	RNF217	154214	37	6	125284135	125284135	Translation_Start_Site	SNP	G	A	4	32	c.-260G>A	(-262--258)ACGTG>ACATG	
Pat_24	Pre-Treatment	PTPRK	5796	37	6	128718792	128718792	Missense_Mutation	SNP	G	A	4	158	c.142C>T	c.(142-144)CAC>TAC	p.H48Y
Pat_24	Pre-Treatment	MED23	9439	37	6	131926379	131926379	Splice_Site	SNP	C	T	4	71	c.1613_splice	c.e14+1	p.S538_splice
Pat_24	Pre-Treatment	MAP7	9053	37	6	136681893	136681893	Missense_Mutation	SNP	C	T	6	458	c.1745G>A	c.(1744-1746)CGG>CAG	p.R582Q
Pat_24	Pre-Treatment	MAP7	9053	37	6	136698940	136698940	Missense_Mutation	SNP	G	A	4	117	c.704C>T	c.(703-705)TCG>TTG	p.S235L
Pat_24	Pre-Treatment	REPS1	85021	37	6	139266690	139266690	Missense_Mutation	SNP	T	C	5	468	c.422A>G	c.(421-423)AAG>AGG	p.K141R
Pat_24	Pre-Treatment	VTA1	51534	37	6	142487422	142487422	Missense_Mutation	SNP	G	A	4	184	c.170G>A	c.(169-171)CGC>CAC	p.R57H
Pat_24	Pre-Treatment	HIVEP2	3097	37	6	143081227	143081228	Missense_Mutation	DNP	GG	AC	41	25	.6197_6198CC>G	c.(6196-6198)CCC>CGT	p.P2066R
Pat_24	Pre-Treatment	HIVEP2	3097	37	6	143092632	143092632	Missense_Mutation	SNP	G	A	4	196	c.3244C>T	c.(3244-3246)CGG>TGG	p.R1082W
Pat_24	Pre-Treatment	CNKSR3	154043	37	6	154735436	154735436	Missense_Mutation	SNP	G	A	3	60	c.1067C>T	c.(1066-1068)CCC>CTC	p.P356L
Pat_24	Pre-Treatment	SYNJ2	8871	37	6	158483177	158483177	Missense_Mutation	SNP	G	A	141	233	c.1108G>A	c.(1108-1110)GGG>AGG	p.G370R
Pat_24	Pre-Treatment	TULP4	56995	37	6	158902288	158902288	Missense_Mutation	SNP	G	A	4	49	c.1453G>A	c.(1453-1455)GTC>ATC	p.V485I
Pat_24	Pre-Treatment	FGFR1OP	11116	37	6	167438355	167438355	Missense_Mutation	SNP	G	A	4	114	c.892G>A	c.(892-894)GGA>AGA	p.G298R
Pat_24	Pre-Treatment	GPR31	2853	37	6	167570419	167570419	Nonsense_Mutation	SNP	G	A	3	49	c.901C>T	c.(901-903)CGA>TGA	p.R301*
Pat_24	Pre-Treatment	GPR146	115330	37	7	1097440	1097440	Missense_Mutation	SNP	G	A	32	102	c.289G>A	c.(289-291)GTG>ATG	p.V97M
Pat_24	Pre-Treatment	FBXL18	80028	37	7	5540381	5540381	Missense_Mutation	SNP	G	A	5	77	c.1519C>T	c.(1519-1521)CGC>TGC	p.R507C
Pat_24	Pre-Treatment	USP42	84132	37	7	6175496	6175496	Missense_Mutation	SNP	T	C	3	72	c.467T>C	c.(466-468)ATG>ACG	p.M156T

Pat_24	Pre-Treatment	ABCB5	340273	37	7	20683202	20683202	Missense_Mutation	SNP	G	A	4	140	c.625G>A	c.(625-627)GTG>ATG	p.V209M
Pat_24	Pre-Treatment	ABCB5	340273	37	7	20738102	20738102	Missense_Mutation	SNP	G	A	42	31	c.748G>A	c.(748-750)GGG>AGG	p.G250R
Pat_24	Pre-Treatment	STK31	56164	37	7	23794043	23794043	Missense_Mutation	SNP	T	C	219	122	c.1243T>C	c.(1243-1245)TGG>CGG	p.W415R
Pat_24	Pre-Treatment	CCDC129	223075	37	7	31617639	31617639	Missense_Mutation	SNP	G	A	4	121	c.761G>A	c.(760-762)GGT>GAT	p.G254D
Pat_24	Pre-Treatment	KBTBD2	25948	37	7	32909121	32909121	Missense_Mutation	SNP	G	A	6	319	c.1708C>T	c.(1708-1710)CGT>TGT	p.R570C
Pat_24	Pre-Treatment	GPR141	353345	37	7	37780815	37780815	Missense_Mutation	SNP	G	A	5	239	c.820G>A	c.(820-822)GCA>ACA	p.A274T
Pat_24	Pre-Treatment	UBE2D4	51619	37	7	43982601	43982601	Missense_Mutation	SNP	C	T	182	138	c.169C>T	c.(169-171)CCT>TCT	p.P57S
Pat_24	Pre-Treatment	DBNL	28988	37	7	44091467	44091467	Missense_Mutation	SNP	G	A	4	154	c.178G>A	c.(178-180)GGG>AGG	p.G60R
Pat_24	Pre-Treatment	AEBP1	165	37	7	44148759	44148759	Missense_Mutation	SNP	G	A	4	163	c.1072G>A	c.(1072-1074)GTG>ATG	p.V358M
Pat_24	Pre-Treatment	AEBP1	165	37	7	44151573	44151573	Missense_Mutation	SNP	G	A	6	244	c.1961G>A	c.(1960-1962)CGC>CAC	p.R654H
Pat_24	Pre-Treatment	CCM2	83605	37	7	45113987	45113987	Missense_Mutation	SNP	G	A	4	67	c.1034G>A	c.(1033-1035)AGC>AAC	p.S345N
Pat_24	Pre-Treatment	PKD1L1	168507	37	7	47898480	47898480	Missense_Mutation	SNP	C	T	4	48	c.4153G>A	c.(4153-4155)GGC>AGC	p.G1385S
Pat_24	Pre-Treatment	ABCA13	154664	37	7	48550794	48550794	Missense_Mutation	SNP	G	A	4	115	c.13639G>A	c.(13639-13641)GGA>AGA	p.G4547R
Pat_24	Pre-Treatment	COBL	23242	37	7	51152943	51152943	Missense_Mutation	SNP	G	A	4	139	c.1016C>T	c.(1015-1017)CCT>CTT	p.P339L
Pat_24	Pre-Treatment	14-Sep	346288	37	7	55886880	55886880	Missense_Mutation	SNP	C	T	20	11	c.757G>A	c.(757-759)GAA>AAA	p.E253K
Pat_24	Pre-Treatment	ZNF716	441234	37	7	57529035	57529035	Missense_Mutation	SNP	C	T	43	150	c.868C>T	c.(868-870)CAT>TAT	p.H290Y
Pat_24	Pre-Treatment	WBSCR17	64409	37	7	71130513	71130513	Missense_Mutation	SNP	C	T	89	65	c.1198C>T	c.(1198-1200)CGC>TGC	p.R400C
Pat_24	Pre-Treatment	FZD9	8326	37	7	72849278	72849278	Missense_Mutation	SNP	C	T	4	231	c.941C>T	c.(940-942)ACG>ATG	p.T314M
Pat_24	Pre-Treatment	ELN	2006	37	7	73442524	73442524	Missense_Mutation	SNP	G	A	4	139	c.7G>A	c.(7-9)GGT>AGT	p.G3S
Pat_24	Pre-Treatment	ELN	2006	37	7	73467491	73467491	Splice_Site	SNP	A	G	4	111	c.950_splice	c.e18-2	p.G317_splice
Pat_24	Pre-Treatment	LAT2	7462	37	7	73634106	73634106	Missense_Mutation	SNP	G	A	7	537	c.167G>A	c.(166-168)CGG>CAG	p.R56Q
Pat_24	Pre-Treatment	CCDC146	57639	37	7	76916860	76916860	Missense_Mutation	SNP	G	A	4	109	c.2381G>A	c.(2380-2382)GGC>GAC	p.G794D
Pat_24	Pre-Treatment	PCLO	27445	37	7	82579646	82579646	Nonsense_Mutation	SNP	G	A	114	74	c.10258C>T	c.(10258-10260)CGA>TGA	p.R3420*
Pat_24	Pre-Treatment	SEMA3D	223117	37	7	84629153	84629153	Missense_Mutation	SNP	G	A	4	83	c.1937C>T	c.(1936-1938)ACG>ATG	p.T646M
Pat_24	Pre-Treatment	ABCB4	5244	37	7	87035681	87035681	Missense_Mutation	SNP	G	A	6	467	c.3430C>T	c.(3430-3432)CGG>TGG	p.R1144W
Pat_24	Pre-Treatment	ABCB1	5243	37	7	87168601	87168601	Nonsense_Mutation	SNP	G	A	4	140	c.2380C>T	c.(2380-2382)CGA>TGA	p.R794*
Pat_24	Pre-Treatment	C7orf63	79846	37	7	89884782	89884782	Missense_Mutation	SNP	G	A	7	484	c.166G>A	c.(166-168)GAA>AAA	p.E56K
Pat_24	Pre-Treatment	CCDC132	55610	37	7	92905528	92905528	Missense_Mutation	SNP	G	A	7	503	c.853G>A	c.(853-855)GTG>ATG	p.V285M
Pat_24	Pre-Treatment	ASNS	440	37	7	97482657	97482657	Missense_Mutation	SNP	G	A	81	87	c.1280C>T	c.(1279-1281)TCC>TTC	p.S427F
Pat_24	Pre-Treatment	PTCD1	26024	37	7	99032639	99032639	Missense_Mutation	SNP	G	A	4	121	c.227C>T	c.(226-228)ACG>ATG	p.T76M
Pat_24	Pre-Treatment	ZKSCAN5	23660	37	7	99129144	99129144	Missense_Mutation	SNP	G	A	4	120	c.1792G>A	c.(1792-1794)GTC>ATC	p.V598I
Pat_24	Pre-Treatment	SPDYE3	441272	37	7	99917310	99917310	Missense_Mutation	SNP	G	A	5	450	c.338G>A	c.(337-339)CGT>CAT	p.R113H
Pat_24	Pre-Treatment	TRIM56	81844	37	7	100731159	100731159	Missense_Mutation	SNP	G	T	4	76	c.566G>T	c.(565-567)TGC>TTC	p.C189F
Pat_24	Pre-Treatment	FIS1	51024	37	7	100883161	100883161	Missense_Mutation	SNP	C	T	3	44	c.385G>A	c.(385-387)GTG>ATG	p.V129M
Pat_24	Pre-Treatment	RABL5	64792	37	7	100959806	100959806	Missense_Mutation	SNP	G	A	5	238	c.224C>T	c.(223-225)CCG>CTG	p.P75L
Pat_24	Pre-Treatment	CUX1	1523	37	7	101892248	101892248	Missense_Mutation	SNP	G	A	4	60	c.4444G>A	c.(4444-4446)GCG>ACG	p.A1482T
Pat_24	Pre-Treatment	LRWD1	222229	37	7	102107853	102107853	Missense_Mutation	SNP	C	T	4	123	c.500C>T	c.(499-501)GCG>GTG	p.A167V
Pat_24	Pre-Treatment	LAMB1	3912	37	7	107605047	107605047	Missense_Mutation	SNP	C	G	4	243	c.1648G>C	c.(1648-1650)GCC>CCC	p.A550P
Pat_24	Pre-Treatment	LAMB4	22798	37	7	107720104	107720104	Missense_Mutation	SNP	G	A	4	228	c.1829C>T	c.(1828-1830)GCT>GTT	p.A610V
Pat_24	Pre-Treatment	PNPLA8	50640	37	7	108155059	108155059	Missense_Mutation	SNP	G	A	5	315	c.877C>T	c.(877-879)CGT>TGT	p.R293C
Pat_24	Pre-Treatment	LOC407835	407835	37	7	128766867	128766867	Missense_Mutation	SNP	G	A	50	3	c.296G>A	c.(295-297)AGG>AAG	p.R99K
Pat_24	Pre-Treatment	CALD1	800	37	7	134613579	134613579	Missense_Mutation	SNP	G	A	4	171	c.146G>A	c.(145-147)CGG>CAG	p.R49Q
Pat_24	Pre-Treatment	BRAF	673	37	7	140453136	140453137	Missense_Mutation	DNP	AC	TT	224	28	c.1798_1799GT>AA	c.(1798-1800)GTG>AAG	p.V600K
Pat_24	Pre-Treatment	CLEC5A	23601	37	7	141629932	141629932	Missense_Mutation	SNP	C	T	6	365	c.539G>A	c.(538-540)CGC>CAC	p.R180H
Pat_24	Pre-Treatment	TRY6	154754	37	7	142482242	142482242	Missense_Mutation	SNP	G	A	7	185	c.622G>A	c.(622-624)GGA>AGA	p.G208R
Pat_24	Pre-Treatment	TRPV6	55503	37	7	142569711	142569711	Missense_Mutation	SNP	G	A	7	524	c.1927C>T	c.(1927-1929)CGG>TGG	p.R643W
Pat_24	Pre-Treatment	OR2F1	26211	37	7	143657455	143657455	Missense_Mutation	SNP	G	A	4	213	c.392G>A	c.(391-393)CGA>CAA	p.R131Q

Pat_24	Pre-Treatment	REPIN1	29803	37	7	150069039	150069039	Nonsense_Mutation	SNP	C	T	5	171	c.709C>T	c.(709-711)CAG>TAG	p.Q237*
Pat_24	Pre-Treatment	ZNF775	285971	37	7	150095095	150095095	Missense_Mutation	SNP	G	A	3	35	c.1526G>A	c.(1525-1527)CGC>CAC	p.R509H
Pat_24	Pre-Treatment	NOM1	64434	37	7	156752644	156752644	Missense_Mutation	SNP	G	T	5	204	c.1408G>T	c.(1408-1410)GCC>TCC	p.A470S
Pat_24	Pre-Treatment	CSMD1	64478	37	8	2820822	2820822	Missense_Mutation	SNP	C	T	7	298	c.9379G>A	c.(9379-9381)GGT>AGT	p.G3127S
Pat_24	Pre-Treatment	MFHAS1	9258	37	8	8750411	8750411	Missense_Mutation	SNP	G	A	3	30	c.158C>T	c.(157-159)TCC>TTC	p.S53F
Pat_24	Pre-Treatment	TNKS	8658	37	8	9437741	9437741	Missense_Mutation	SNP	G	A	8	313	c.746G>A	c.(745-747)GGT>GAT	p.G249D
Pat_24	Pre-Treatment	FDFT1	2222	37	8	11689096	11689096	Missense_Mutation	SNP	C	T	4	175	c.949C>T	c.(949-951)CGG>TGG	p.R317W
Pat_24	Pre-Treatment	DLC1	10395	37	8	12956977	12956977	Missense_Mutation	SNP	C	T	4	167	c.2869G>A	c.(2869-2871)GAC>AAC	p.D957N
Pat_24	Pre-Treatment	LZTS1	11178	37	8	20112631	20112631	Missense_Mutation	SNP	G	A	4	144	c.62C>T	c.(61-63)TCG>TTG	p.S21L
Pat_24	Pre-Treatment	LGI3	203190	37	8	22006155	22006155	Missense_Mutation	SNP	G	A	4	146	c.1165C>T	c.(1165-1167)CGG>TGG	p.R389W
Pat_24	Pre-Treatment	SORBS3	10174	37	8	22414417	22414417	Missense_Mutation	SNP	G	A	4	109	c.410G>A	c.(409-411)CGA>CAA	p.R137Q
Pat_24	Pre-Treatment	RHOBTB2	23221	37	8	22864881	22864881	Missense_Mutation	SNP	G	A	6	417	c.1123G>A	c.(1123-1125)GGA>AGA	p.G375R
Pat_24	Pre-Treatment	ENTPD4	9583	37	8	23297322	23297322	Missense_Mutation	SNP	C	T	5	140	c.989G>A	c.(988-990)GGC>GAC	p.G330D
Pat_24	Pre-Treatment	SLC25A37	51312	37	8	23429231	23429231	Missense_Mutation	SNP	G	A	5	116	c.880G>A	c.(880-882)GGC>AGC	p.G294S
Pat_24	Pre-Treatment	ADAM28	10863	37	8	24187570	24187570	Missense_Mutation	SNP	C	T	45	74	c.1045C>T	c.(1045-1047)CAT>TAT	p.H349Y
Pat_24	Pre-Treatment	NEFM	4741	37	8	24775894	24775894	Missense_Mutation	SNP	G	T	38	54	c.2526G>T	c.(2524-2526)AAG>AAT	p.K842N
Pat_24	Pre-Treatment	KIF13B	23303	37	8	28928049	28928049	Missense_Mutation	SNP	G	A	7	17	c.5453C>T	c.(5452-5454)CCT>CTT	p.P1818L
Pat_24	Pre-Treatment	NRG1	3084	37	8	32621523	32621523	Missense_Mutation	SNP	G	A	4	116	c.1526G>A	c.(1525-1527)AGT>AAT	p.S509N
Pat_24	Pre-Treatment	KCNU1	157855	37	8	36793199	36793199	Missense_Mutation	SNP	G	A	70	125	c.3211G>A	c.(3211-3213)GAC>AAC	p.D1071N
Pat_24	Pre-Treatment	GPR124	25960	37	8	37698701	37698701	Missense_Mutation	SNP	C	T	4	161	c.2845C>T	c.(2845-2847)CGC>TGC	p.R949C
Pat_24	Pre-Treatment	LETM2	137994	37	8	38258458	38258458	Missense_Mutation	SNP	C	T	118	165	c.730C>T	c.(730-732)CGC>TGC	p.R244C
Pat_24	Pre-Treatment	IKBKB	3551	37	8	42175254	42175254	Missense_Mutation	SNP	C	T	47	81	c.1205C>T	c.(1204-1206)TCC>TTC	p.S402F
Pat_24	Pre-Treatment	CHRNA6	8973	37	8	42611837	42611837	Missense_Mutation	SNP	G	A	68	117	c.505C>T	c.(505-507)CAT>TAT	p.H169Y
Pat_24	Pre-Treatment	KIAA0146	23514	37	8	48642011	48642011	Missense_Mutation	SNP	C	T	3	28	c.2588C>T	c.(2587-2589)GCC>GTC	p.A863V
Pat_24	Pre-Treatment	YTHDF3	253943	37	8	64099378	64099378	Missense_Mutation	SNP	T	A	4	122	c.809T>A	c.(808-810)ATA>AAA	p.I270K
Pat_24	Pre-Treatment	C8orf44	56260	37	8	67590034	67590034	Missense_Mutation	SNP	G	A	4	134	c.91G>A	c.(91-93)GAA>AAA	p.E31K
Pat_24	Pre-Treatment	C8orf34	116328	37	8	69621281	69621281	Missense_Mutation	SNP	C	T	28	45	c.1036C>T	c.(1036-1038)CAT>TAT	p.H346Y
Pat_24	Pre-Treatment	SULF1	23213	37	8	70476364	70476364	Missense_Mutation	SNP	G	A	69	95	c.154G>A	c.(154-156)GAT>AAT	p.D52N
Pat_24	Pre-Treatment	SULF1	23213	37	8	70553057	70553057	Missense_Mutation	SNP	G	A	4	75	c.2566G>A	c.(2566-2568)GGA>AGA	p.G856R
Pat_24	Pre-Treatment	RPL7	6129	37	8	74203308	74203308	Missense_Mutation	SNP	T	C	3	72	c.718A>G	c.(718-720)ATC>GTC	p.I240V
Pat_24	Pre-Treatment	JPH1	56704	37	8	75227342	75227342	Missense_Mutation	SNP	C	T	5	249	c.893G>A	c.(892-894)CGC>CAC	p.R298H
Pat_24	Pre-Treatment	TPD52	7163	37	8	80965533	80965533	Missense_Mutation	SNP	C	T	5	328	c.388G>A	c.(388-390)GTG>ATG	p.V130M
Pat_24	Pre-Treatment	ZFAND1	79752	37	8	82627077	82627077	Missense_Mutation	SNP	C	T	5	231	c.320G>A	c.(319-321)CGA>CAA	p.R107Q
Pat_24	Pre-Treatment	CA13	377677	37	8	86193501	86193501	Missense_Mutation	SNP	G	A	6	437	c.712G>A	c.(712-714)GCA>ACA	p.A238T
Pat_24	Pre-Treatment	MMP16	4325	37	8	89180150	89180150	Missense_Mutation	SNP	G	A	4	117	c.457C>T	c.(457-459)CGC>TGC	p.R153C
Pat_24	Pre-Treatment	CDH17	1015	37	8	95182723	95182723	Missense_Mutation	SNP	G	A	4	235	c.968C>T	c.(967-969)CCG>CTG	p.P323L
Pat_24	Pre-Treatment	KIAA1429	25962	37	8	95501050	95501050	Missense_Mutation	SNP	G	A	4	117	c.5323C>T	c.(5323-5325)CGT>TGT	p.R1775C
Pat_24	Pre-Treatment	INTS8	55656	37	8	95879525	95879525	Missense_Mutation	SNP	A	T	4	156	c.2374A>T	c.(2374-2376)ACA>TCA	p.T792S
Pat_24	Pre-Treatment	MATN2	4147	37	8	98991147	98991147	Missense_Mutation	SNP	G	A	4	130	c.992G>A	c.(991-993)TGT>TAT	p.C331Y
Pat_24	Pre-Treatment	KLF10	7071	37	8	103667813	103667813	Missense_Mutation	SNP	G	A	4	139	c.17C>T	c.(16-18)GCC>GTC	p.A6V
Pat_24	Pre-Treatment	ANGPT1	284	37	8	108296965	108296965	Nonsense_Mutation	SNP	G	A	4	202	c.1150C>T	c.(1150-1152)CGA>TGA	p.R384*
Pat_24	Pre-Treatment	EIF3H	8667	37	8	117671160	117671160	Missense_Mutation	SNP	C	T	4	163	c.349G>A	c.(349-351)GTG>ATG	p.V117M
Pat_24	Pre-Treatment	TNFRSF11B	4982	37	8	119945293	119945293	Missense_Mutation	SNP	C	T	4	77	c.277G>A	c.(277-279)GTC>ATC	p.V93I
Pat_24	Pre-Treatment	TAF2	6873	37	8	120814047	120814047	Missense_Mutation	SNP	G	A	37	77	c.779C>T	c.(778-780)CCA>CTA	p.P260L
Pat_24	Pre-Treatment	EFR3A	23167	37	8	132968136	132968136	Missense_Mutation	SNP	G	A	4	90	c.760G>A	c.(760-762)GTT>ATT	p.V254I
Pat_24	Pre-Treatment	KCNQ3	3786	37	8	133142113	133142113	Missense_Mutation	SNP	T	G	166	193	c.2015A>C	c.(2014-2016)AAG>ACG	p.K672T
Pat_24	Pre-Treatment	TG	7038	37	8	133881993	133881993	Missense_Mutation	SNP	G	A	4	183	c.196G>A	c.(196-198)GAC>AAC	p.D66N

Pat_24	Pre-Treatment	FAM135B	51059	37	8	139164716	139164716	Missense_Mutation	SNP	C	T	57	92	c.2002G>A	c.(2002-2004)GAA>AAA	p.E668K
Pat_24	Pre-Treatment	FAM135B	51059	37	8	139380207	139380207	Missense_Mutation	SNP	G	A	5	257	c.20C>T	c.(19-21)ACG>ATG	p.T7M
Pat_24	Pre-Treatment	GPR20	2843	37	8	142367548	142367548	Missense_Mutation	SNP	C	T	3	32	c.476G>A	c.(475-477)CGC>CAC	p.R159H
Pat_24	Pre-Treatment	LY6D	8581	37	8	143867004	143867004	Splice_Site	SNP	C	T	4	230	c.151_splice	c.e2+1	p.V51_splice
Pat_24	Pre-Treatment	CYP11B1	1584	37	8	143956699	143956699	Missense_Mutation	SNP	C	T	38	51	c.1151G>A	c.(1150-1152)CGA>CAA	p.R384Q
Pat_24	Pre-Treatment	TSTA3	7264	37	8	144698314	144698314	Missense_Mutation	SNP	C	T	6	368	c.223G>A	c.(223-225)GGC>AGC	p.G75S
Pat_24	Pre-Treatment	PLEC	5339	37	8	144993059	144993059	Missense_Mutation	SNP	G	A	5	203	c.11341C>T	c.(11341-11343)CGC>TGC	p.R3781C
Pat_24	Pre-Treatment	GPR172A	79581	37	8	145583069	145583069	Missense_Mutation	SNP	A	G	9	104	c.116A>G	c.(115-117)AAA>AGA	p.K39R
Pat_24	Pre-Treatment	KANK1	23189	37	9	712642	712642	Missense_Mutation	SNP	C	T	3	42	c.1876C>T	c.(1876-1878)CGG>TGG	p.R626W
Pat_24	Pre-Treatment	UBAP2	55833	37	9	33922757	33922757	Missense_Mutation	SNP	G	T	41	14	c.3192C>A	c.(3190-3192)TTC>TTA	p.F1064L
Pat_24	Pre-Treatment	RECK	8434	37	9	36110025	36110025	Missense_Mutation	SNP	C	T	4	143	c.1837C>T	c.(1837-1839)CGC>TGC	p.R613C
Pat_24	Pre-Treatment	ZCCHC7	84186	37	9	37304227	37304227	Missense_Mutation	SNP	C	T	4	134	c.697C>T	c.(697-699)CGG>TGG	p.R233W
Pat_24	Pre-Treatment	SMC5	23137	37	9	72893497	72893497	Missense_Mutation	SNP	C	T	86	31	c.634C>T	c.(634-636)CAC>TAC	p.H212Y
Pat_24	Pre-Treatment	TRPM6	140803	37	9	77435255	77435255	Nonsense_Mutation	SNP	G	A	86	21	c.1099C>T	c.(1099-1101)CAA>TAA	p.Q367*
Pat_24	Pre-Treatment	VPS13A	23230	37	9	79908310	79908310	Missense_Mutation	SNP	G	T	4	203	c.3393G>T	c.(3391-3393)ATG>ATT	p.M1131I
Pat_24	Pre-Treatment	KIF27	55582	37	9	86518061	86518061	Nonsense_Mutation	SNP	G	A	4	123	c.1372C>T	c.(1372-1374)CGA>TGA	p.R458*
Pat_24	Pre-Treatment	ROR2	4920	37	9	94486849	94486849	Missense_Mutation	SNP	C	T	5	134	c.1927G>A	c.(1927-1929)GCC>ACC	p.A643T
Pat_24	Pre-Treatment	COL15A1	1306	37	9	101812157	101812157	Nonsense_Mutation	SNP	C	T	5	434	c.2884C>T	c.(2884-2886)CGA>TGA	p.R962*
Pat_24	Pre-Treatment	BAAT	570	37	9	104133665	104133665	Missense_Mutation	SNP	G	A	101	29	c.22C>T	c.(22-24)CCT>TCT	p.P8S
Pat_24	Pre-Treatment	C9orf125	84302	37	9	104239242	104239242	Nonsense_Mutation	SNP	G	A	4	203	c.133C>T	c.(133-135)CGA>TGA	p.R45*
Pat_24	Pre-Treatment	ACTL7B	10880	37	9	111617367	111617367	Missense_Mutation	SNP	C	T	4	117	c.844G>A	c.(844-846)GAG>AAG	p.E282K
Pat_24	Pre-Treatment	IKBKAP	8518	37	9	111663931	111663931	Missense_Mutation	SNP	G	A	4	220	c.1885C>T	c.(1885-1887)CGC>TGC	p.R629C
Pat_24	Pre-Treatment	SVEP1	79987	37	9	113170069	113170069	Missense_Mutation	SNP	G	A	110	29	c.7811C>T	c.(7810-7812)TCC>TTC	p.S2604F
Pat_24	Pre-Treatment	C9orf84	158401	37	9	114454492	114454492	Nonsense_Mutation	SNP	C	T	92	29	c.3573G>A	c.(3571-3573)TGG>TGA	p.W1191*
Pat_24	Pre-Treatment	BSPRY	54836	37	9	116116589	116116589	Missense_Mutation	SNP	G	A	5	139	c.271G>A	c.(271-273)GTC>ATC	p.V91I
Pat_24	Pre-Treatment	C9orf43	257169	37	9	116185655	116185655	Missense_Mutation	SNP	G	A	4	122	c.533G>A	c.(532-534)CGA>CAA	p.R178Q
Pat_24	Pre-Treatment	RGS3	5998	37	9	116346450	116346450	Missense_Mutation	SNP	G	A	4	177	c.2758G>A	c.(2758-2760)GAG>AAG	p.E920K
Pat_24	Pre-Treatment	COL27A1	85301	37	9	116956726	116956726	Missense_Mutation	SNP	G	A	5	261	c.2059G>A	c.(2059-2061)GAT>AAT	p.D687N
Pat_24	Pre-Treatment	AKNA	80709	37	9	117118255	117118255	Missense_Mutation	SNP	C	T	4	128	c.3008G>A	c.(3007-3009)CGG>CAG	p.R1003Q
Pat_24	Pre-Treatment	TNC	3371	37	9	117848578	117848578	Missense_Mutation	SNP	C	T	5	403	c.1432G>A	c.(1432-1434)GGC>AGC	p.G478S
Pat_24	Pre-Treatment	ASTN2	23245	37	9	119249714	119249714	Nonsense_Mutation	SNP	G	A	4	98	c.3421C>T	c.(3421-3423)CGA>TGA	p.R1141*
Pat_24	Pre-Treatment	OR1L3	26735	37	9	125438296	125438296	Missense_Mutation	SNP	G	A	60	18	c.888G>A	c.(886-888)ATG>ATA	p.M296I
Pat_24	Pre-Treatment	PPP6C	5537	37	9	127912080	127912080	Missense_Mutation	SNP	G	A	83	10	c.790C>T	c.(790-792)CGT>TGT	p.R264C
Pat_24	Pre-Treatment	GAPVD1	26130	37	9	128083731	128083731	Missense_Mutation	SNP	C	T	83	27	c.1622C>T	c.(1621-1623)TCG>TTG	p.S541L
Pat_24	Pre-Treatment	URM1	81605	37	9	131150103	131150103	Missense_Mutation	SNP	C	T	5	375	c.115C>T	c.(115-117)CGG>TGG	p.R39W
Pat_24	Pre-Treatment	FUBP3	8939	37	9	133499049	133499049	Missense_Mutation	SNP	G	A	4	206	c.926G>A	c.(925-927)CGG>CAG	p.R309Q
Pat_24	Pre-Treatment	C9orf9	11092	37	9	135763747	135763747	Missense_Mutation	SNP	C	T	4	178	c.418C>T	c.(418-420)CTC>TTC	p.L140F
Pat_24	Pre-Treatment	C9orf7	11094	37	9	136333048	136333048	Missense_Mutation	SNP	C	T	4	107	c.326C>T	c.(325-327)GCG>GTG	p.A109V
Pat_24	Pre-Treatment	RXRA	6256	37	9	137300016	137300016	Missense_Mutation	SNP	G	A	4	205	c.301G>A	c.(301-303)GTC>ATC	p.V101I
Pat_24	Pre-Treatment	QSOX2	169714	37	9	139100978	139100978	Missense_Mutation	SNP	C	T	4	160	c.1693G>A	c.(1693-1695)GAC>AAC	p.D565N
Pat_24	Pre-Treatment	PMPCA	23203	37	9	139309021	139309021	Missense_Mutation	SNP	G	T	4	226	c.454G>T	c.(454-456)GCT>TCT	p.A152S
Pat_24	Pre-Treatment	SEC16A	9919	37	9	139366482	139366482	Missense_Mutation	SNP	C	T	4	101	c.3649G>A	c.(3649-3651)GAG>AAG	p.E1217K
Pat_24	Pre-Treatment	NOTCH1	4851	37	9	139413893	139413893	Splice_Site	SNP	G	T	4	150	c.865_splice	c.e5+1	p.G289_splice
Pat_24	Pre-Treatment	TMEM203	94107	37	9	140099601	140099601	Missense_Mutation	SNP	G	A	4	90	c.266C>T	c.(265-267)ACG>ATG	p.T89M
Pat_24	Pre-Treatment	NDOR1	27158	37	9	140110375	140110375	Missense_Mutation	SNP	G	A	4	219	c.1460G>A	c.(1459-1461)CGC>CAC	p.R487H
Pat_24	Pre-Treatment	TUBB2C	10383	37	9	140137137	140137137	Missense_Mutation	SNP	G	A	4	161	c.467G>A	c.(466-468)CGG>CAG	p.R156Q
Pat_24	Pre-Treatment	ZMYND19	116225	37	9	140477114	140477114	Missense_Mutation	SNP	G	A	5	136	c.565C>T	c.(565-567)CGC>TGC	p.R189C

Pat_24	Pre-Treatment	TUBBP5	643224	37	9	141071420	141071420	Missense_Mutation	SNP	G	A	4	97	c.823G>A	c.(823-825)GAC>AAC	p.D275N
Pat_24	Pre-Treatment	ASMTL	8623	37	X	1522283	1522283	Missense_Mutation	SNP	C	T	5	188	c.1745G>A	c.(1744-1746)GGC>GAC	p.G582D
Pat_24	Pre-Treatment	MXRA5	25878	37	X	3228314	3228314	Missense_Mutation	SNP	G	A	38	16	c.7930C>T	c.(7930-7932)CAT>TAT	p.H2644Y
Pat_24	Pre-Treatment	TLR7	51284	37	X	12903670	12903670	Missense_Mutation	SNP	C	T	77	21	c.43C>T	c.(43-45)CTT>TTT	p.L15F
Pat_24	Pre-Treatment	GLRA2	2742	37	X	14625262	14625262	Missense_Mutation	SNP	C	T	4	106	c.587C>T	c.(586-588)ACG>ATG	p.T196M
Pat_24	Pre-Treatment	ASB11	140456	37	X	15301641	15301641	Missense_Mutation	SNP	G	A	170	49	c.958C>T	c.(958-960)CTC>TTC	p.L320F
Pat_24	Pre-Treatment	PHEX	5251	37	X	22051081	22051081	Translation_Start_Site	SNP	C	T	4	158	c.-42C>T	c.(-44--40)CACGA>CATGA	
Pat_24	Pre-Treatment	FAM47C	442444	37	X	37028662	37028662	Missense_Mutation	SNP	T	C	6	57	c.2179T>C	c.(2179-2181)TGC>CGC	p.C727R
Pat_24	Pre-Treatment	SSX3	10214	37	X	48213500	48213500	Missense_Mutation	SNP	G	A	4	175	c.214C>T	c.(214-216)CGT>TGT	p.R72C
Pat_24	Pre-Treatment	OTUD5	55593	37	X	48791834	48791834	Missense_Mutation	SNP	C	T	4	115	c.977G>A	c.(976-978)CGT>CAT	p.R326H
Pat_24	Pre-Treatment	KDM5C	8242	37	X	53223862	53223862	Missense_Mutation	SNP	C	T	4	34	c.3497G>A	c.(3496-3498)CGC>CAC	p.R1166H
Pat_24	Pre-Treatment	ITIH5L	347365	37	X	54785245	54785245	Missense_Mutation	SNP	C	T	36	16	c.1262G>A	c.(1261-1263)AGG>AAG	p.R421K
Pat_24	Pre-Treatment	PFKFB1	5207	37	X	54960268	54960268	Missense_Mutation	SNP	G	A	4	61	c.1342C>T	c.(1342-1344)CGG>TGG	p.R448W
Pat_24	Pre-Treatment	EFNB1	1947	37	X	68059902	68059902	Missense_Mutation	SNP	G	A	3	40	c.599G>A	c.(598-600)GGC>GAC	p.G200D
Pat_24	Pre-Treatment	GDPD2	54857	37	X	69652895	69652895	Missense_Mutation	SNP	G	A	3	24	c.1579G>A	c.(1579-1581)GCA>ACA	p.A527T
Pat_24	Pre-Treatment	MED12	9968	37	X	70356309	70356309	Missense_Mutation	SNP	G	A	3	33	c.5204G>A	c.(5203-5205)CGC>CAC	p.R1735H
Pat_24	Pre-Treatment	ACRC	93953	37	X	70823920	70823920	Missense_Mutation	SNP	C	T	7	86	c.793C>T	c.(793-795)CCC>TCC	p.P265S
Pat_24	Pre-Treatment	NAP1L2	4674	37	X	72433673	72433673	Missense_Mutation	SNP	T	C	3	33	c.656A>G	c.(655-657)GAG>GGG	p.E219G
Pat_24	Pre-Treatment	ATP7A	538	37	X	77298875	77298875	Missense_Mutation	SNP	C	T	4	94	c.4066C>T	c.(4066-4068)CGG>TGG	p.R1356W
Pat_24	Pre-Treatment	ZMAT1	84460	37	X	101138559	101138559	Missense_Mutation	SNP	T	C	3	74	c.1327A>G	c.(1327-1329)AGG>GGG	p.R443G
Pat_24	Pre-Treatment	GPRASP1	9737	37	X	101912419	101912419	Missense_Mutation	SNP	G	A	4	97	c.3578G>A	c.(3577-3579)CGA>CAA	p.R1193Q
Pat_24	Pre-Treatment	CXorf57	55086	37	X	105912456	105912456	Missense_Mutation	SNP	G	A	4	202	c.2333G>A	c.(2332-2334)CGA>CAA	p.R778Q
Pat_24	Pre-Treatment	COL4A6	1288	37	X	107430394	107430394	Missense_Mutation	SNP	G	A	4	223	c.1886C>T	c.(1885-1887)CCC>CTC	p.P629L
Pat_24	Pre-Treatment	COL4A6	1288	37	X	107431220	107431220	Missense_Mutation	SNP	C	T	60	19	c.1628G>A	c.(1627-1629)GGA>GAA	p.G543E
Pat_24	Pre-Treatment	GUCY2F	2986	37	X	108673582	108673583	Missense_Mutation	DNP	CC	AA	5	244	.1744_1745GG>T	c.(1744-1746)GGA>TTA	p.G582L
Pat_24	Pre-Treatment	GUCY2F	2986	37	X	108673592	108673592	Nonsense_Mutation	SNP	C	A	5	212	c.1735G>T	c.(1735-1737)GGA>TGA	p.G579*
Pat_24	Pre-Treatment	TMEM164	84187	37	X	109247348	109247348	Missense_Mutation	SNP	G	A	4	147	c.346G>A	c.(346-348)GTC>ATC	p.V116I
Pat_24	Pre-Treatment	ZCCHC16	340595	37	X	111697979	111697979	Missense_Mutation	SNP	C	T	106	27	c.23C>T	c.(22-24)TCA>TTA	p.S8L
Pat_24	Pre-Treatment	CT47B1	643311	37	X	120009390	120009390	Missense_Mutation	SNP	C	G	6	110	c.135G>C	c.(133-135)ATG>ATC	p.M45I
Pat_24	Pre-Treatment	CT47B1	643311	37	X	120009393	120009393	Missense_Mutation	SNP	G	C	6	107	c.132C>G	c.(130-132)GAC>GAG	p.D44E
Pat_24	Pre-Treatment	OCRL	4952	37	X	128692706	128692706	Missense_Mutation	SNP	C	T	4	60	c.536C>T	c.(535-537)CCT>CTT	p.P179L
Pat_24	Pre-Treatment	OCRL	4952	37	X	128703359	128703359	Missense_Mutation	SNP	G	A	4	212	c.1585G>A	c.(1585-1587)GCC>ACC	p.A529T
Pat_24	Pre-Treatment	BCORL1	63035	37	X	129171402	129171402	Missense_Mutation	SNP	G	A	4	139	c.4366G>A	c.(4366-4368)GGC>AGC	p.G1456S
Pat_24	Pre-Treatment	TFDP3	51270	37	X	132351950	132351950	Missense_Mutation	SNP	C	T	4	136	c.338G>A	c.(337-339)CGT>CAT	p.R113H
Pat_24	Pre-Treatment	FAM122C	159091	37	X	133948871	133948871	Missense_Mutation	SNP	C	T	5	253	c.181C>T	c.(181-183)CGC>TGC	p.R61C
Pat_24	Pre-Treatment	ZIC3	7547	37	X	136649872	136649872	Missense_Mutation	SNP	G	A	4	174	c.1022G>A	c.(1021-1023)CGT>CAT	p.R341H
Pat_24	Pre-Treatment	FMR1	2332	37	X	147030296	147030296	Missense_Mutation	SNP	C	T	90	31	c.1831C>T	c.(1831-1833)CGT>TGT	p.R611C
Pat_24	Pre-Treatment	AFF2	2334	37	X	148072792	148072792	Missense_Mutation	SNP	G	A	5	198	c.3866G>A	c.(3865-3867)AGC>AAC	p.S1289N
Pat_24	Pre-Treatment	TMEM185A	84548	37	X	148690324	148690324	Missense_Mutation	SNP	C	T	4	212	c.413G>A	c.(412-414)AGG>AAG	p.R138K
Pat_24	Pre-Treatment	MAMLD1	10046	37	X	149639500	149639500	Missense_Mutation	SNP	C	T	4	184	c.1655C>T	c.(1654-1656)CCG>CTG	p.P552L
Pat_24	Pre-Treatment	PNMA3	29944	37	X	152226020	152226020	Missense_Mutation	SNP	G	A	4	96	c.608G>A	c.(607-609)CGG>CAG	p.R203Q
Pat_24	Pre-Treatment	HCFC1	3054	37	X	153221856	153221856	Missense_Mutation	SNP	G	A	4	82	c.2642C>T	c.(2641-2643)ACG>ATG	p.T881M
Pat_24	Post-Resistance	KIAA1751	85452	37	1	1887145	1887145	Missense_Mutation	SNP	C	T	12	96	c.2161G>A	c.(2161-2163)GAG>AAG	p.E721K
Pat_24	Post-Resistance	PLCH2	9651	37	1	2436255	2436255	Missense_Mutation	SNP	G	A	11	34	c.3854G>A	c.(3853-3855)GGG>GAG	p.G1285E
Pat_24	Post-Resistance	MASP2	10747	37	1	11087664	11087664	Missense_Mutation	SNP	C	T	32	103	c.1339G>A	c.(1339-1341)GGA>AGA	p.G447R
Pat_24	Post-Resistance	TNFRSF8	943	37	1	12195671	12195671	Splice_Site	SNP	G	A	4	132	c.1335_splice	c.e13+1	p.T445_splice
Pat_24	Post-Resistance	VPS13D	55187	37	1	12418520	12418520	Missense_Mutation	SNP	C	T	4	146	c.10004C>T	c.(10003-10005)ACG>ATG	p.T3335M

Pat_24	Post-Resistance	PRAMEF12	390999	37	1	12837729	12837729	Missense_Mutation	SNP	G	A	23	70	c.1439G>A	c.(1438-1440)GGT>GAT	p.G480D
Pat_24	Post-Resistance	PRAMEF1	65121	37	1	12856002	12856002	Missense_Mutation	SNP	G	A	32	442	c.1282G>A	c.(1282-1284)GAG>AAG	p.E428K
Pat_24	Post-Resistance	TMEM82	388595	37	1	16069565	16069566	Missense_Mutation	DNP	CC	TT	13	51	c.212_213CC>TT	c.(211-213)TCC>TTT	p.S71F
Pat_24	Post-Resistance	ARHGEF19	128272	37	1	16535275	16535275	Missense_Mutation	SNP	C	T	10	30	c.275G>A	c.(274-276)GGG>GAG	p.G92E
Pat_24	Post-Resistance	IGSF21	84966	37	1	18702857	18702857	Missense_Mutation	SNP	G	A	46	225	c.1069G>A	c.(1069-1071)GAC>AAC	p.D357N
Pat_24	Post-Resistance	CNKSR1	10256	37	1	26504045	26504045	Missense_Mutation	SNP	C	T	14	55	c.7C>T	c.(7-9)CCG>TCG	p.P3S
Pat_24	Post-Resistance	FGR	2268	37	1	27939499	27939499	Missense_Mutation	SNP	C	G	3	81	c.1516G>C	c.(1516-1518)GAG>CAG	p.E506Q
Pat_24	Post-Resistance	NKAIN1	79570	37	1	31655401	31655401	Missense_Mutation	SNP	C	A	46	182	c.508G>T	c.(508-510)GTG>TTG	p.V170L
Pat_24	Post-Resistance	ADC	113451	37	1	33559013	33559013	Missense_Mutation	SNP	G	A	4	104	c.583G>A	c.(583-585)GTG>ATG	p.V195M
Pat_24	Post-Resistance	EPHA10	284656	37	1	38227437	38227437	Missense_Mutation	SNP	C	T	6	34	c.490G>A	c.(490-492)GGC>AGC	p.G164S
Pat_24	Post-Resistance	ZMPSTE24	10269	37	1	40735746	40735746	Missense_Mutation	SNP	G	T	4	129	c.574G>T	c.(574-576)GGG>TGG	p.G192W
Pat_24	Post-Resistance	FOXJ3	22887	37	1	42730851	42730851	Nonsense_Mutation	SNP	G	A	4	109	c.379C>T	c.(379-381)CGA>TGA	p.R127*
Pat_24	Post-Resistance	CCDC30	728621	37	1	43011243	43011243	Missense_Mutation	SNP	G	A	5	26	c.418G>A	c.(418-420)GAA>AAA	p.E140K
Pat_24	Post-Resistance	YBX1	4904	37	1	43166675	43166675	Missense_Mutation	SNP	G	A	4	100	c.964G>A	c.(964-966)GGG>AGG	p.G322R
Pat_24	Post-Resistance	SLC6A9	6536	37	1	44474289	44474289	Missense_Mutation	SNP	C	T	15	47	c.545G>A	c.(544-546)GGC>GAC	p.G182D
Pat_24	Post-Resistance	CYP4B1	1580	37	1	47283696	47283696	Missense_Mutation	SNP	C	T	61	222	c.1264C>T	c.(1264-1266)CCT>TCT	p.P422S
Pat_24	Post-Resistance	TAL1	6886	37	1	47685757	47685757	Missense_Mutation	SNP	G	A	31	107	c.631C>T	c.(631-633)CGC>TGC	p.R211C
Pat_24	Post-Resistance	MAGOH	4116	37	1	53692748	53692748	Missense_Mutation	SNP	A	G	3	54	c.410T>C	c.(409-411)ATT>ACT	p.I137T
Pat_24	Post-Resistance	GLIS1	148979	37	1	53990458	53990458	Missense_Mutation	SNP	G	A	4	190	c.1060C>T	c.(1060-1062)CGT>TGT	p.R354C
Pat_24	Post-Resistance	PARS2	25973	37	1	55224360	55224360	Missense_Mutation	SNP	C	T	5	384	c.475G>A	c.(475-477)GAG>AAG	p.E159K
Pat_24	Post-Resistance	C1orf173	127254	37	1	75065480	75065480	Missense_Mutation	SNP	T	C	20	53	c.1625A>G	c.(1624-1626)AAA>AGA	p.K542R
Pat_24	Post-Resistance	C1orf173	127254	37	1	75072303	75072303	Missense_Mutation	SNP	C	T	7	50	c.1471G>A	c.(1471-1473)GAA>AAA	p.E491K
Pat_24	Post-Resistance	ABCA4	24	37	1	94497348	94497348	Missense_Mutation	SNP	C	T	16	89	c.4114G>A	c.(4114-4116)GAC>AAC	p.D1372N
Pat_24	Post-Resistance	OLFM3	118427	37	1	102312505	102312505	Missense_Mutation	SNP	C	T	17	97	c.25G>A	c.(25-27)GGC>AGC	p.G9S
Pat_24	Post-Resistance	COL11A1	1301	37	1	103427784	103427784	Missense_Mutation	SNP	C	T	16	82	c.3062G>A	c.(3061-3063)GGA>GAA	p.G1021E
Pat_24	Post-Resistance	CELSR2	1952	37	1	109805585	109805585	Missense_Mutation	SNP	G	A	3	75	c.4702G>A	c.(4702-4704)GTG>ATG	p.V1568M
Pat_24	Post-Resistance	PHTF1	10745	37	1	114254647	114254647	Missense_Mutation	SNP	C	T	4	140	c.872G>A	c.(871-873)CGT>CAT	p.R291H
Pat_24	Post-Resistance	MAN1A2	10905	37	1	118008992	118008992	Missense_Mutation	SNP	C	T	7	58	c.1111C>T	c.(1111-1113)CGT>TGT	p.R371C
Pat_24	Post-Resistance	NBPF9	400818	37	1	144621586	144621586	Missense_Mutation	SNP	C	G	7	408	c.918C>G	c.(916-918)TTC>TTG	p.F306L
Pat_24	Post-Resistance	NBPF10	100132406	37	1	145295443	145295443	Missense_Mutation	SNP	C	G	5	173	c.196C>G	c.(196-198)CTC>GTC	p.L66V
Pat_24	Post-Resistance	NBPF10	100132406	37	1	145362127	145362127	Missense_Mutation	SNP	G	T	18	371	c.9660G>T	c.(9658-9660)GAG>GAT	p.E3220D
Pat_24	Post-Resistance	BOLA1	51027	37	1	149871793	149871793	Missense_Mutation	SNP	C	T	4	113	c.181C>T	c.(181-183)CCG>TCG	p.P61S
Pat_24	Post-Resistance	FLG	2312	37	1	152281475	152281475	Missense_Mutation	SNP	C	T	63	494	c.5887G>A	c.(5887-5889)GAC>AAC	p.D1963N
Pat_24	Post-Resistance	ASH1L	55870	37	1	155448204	155448204	Missense_Mutation	SNP	C	T	4	109	c.4457G>A	c.(4456-4458)CGT>CAT	p.R1486H
Pat_24	Post-Resistance	NTRK1	4914	37	1	156849018	156849018	Missense_Mutation	SNP	G	A	8	23	c.1910G>A	c.(1909-1911)GGG>GAG	p.G637E
Pat_24	Post-Resistance	USP21	27005	37	1	161134390	161134390	Missense_Mutation	SNP	A	G	16	262	c.1372A>G	c.(1372-1374)ATC>GTC	p.I458V
Pat_24	Post-Resistance	DDR2	4921	37	1	162731044	162731044	Missense_Mutation	SNP	A	G	3	73	c.899A>G	c.(898-900)AAG>AGG	p.K300R
Pat_24	Post-Resistance	LRRC52	440699	37	1	165532978	165532978	Missense_Mutation	SNP	G	A	4	146	c.859G>A	c.(859-861)GAG>AAG	p.E287K
Pat_24	Post-Resistance	TNN	63923	37	1	175066678	175066678	Missense_Mutation	SNP	G	A	11	122	c.1714G>A	c.(1714-1716)GAG>AAG	p.E572K
Pat_24	Post-Resistance	CACNA1E	777	37	1	181745340	181745340	Nonsense_Mutation	SNP	G	A	4	128	c.5243G>A	c.(5242-5244)TGG>TAG	p.W1748*
Pat_24	Post-Resistance	LAMC1	3915	37	1	183095301	183095301	Missense_Mutation	SNP	C	T	4	184	c.2848C>T	c.(2848-2850)CGC>TGC	p.R950C
Pat_24	Post-Resistance	UBE2T	29089	37	1	202302658	202302658	Nonsense_Mutation	SNP	G	A	4	130	c.205C>T	c.(205-207)CGA>TGA	p.R69*
Pat_24	Post-Resistance	PLEKHA6	22874	37	1	204210881	204210881	Missense_Mutation	SNP	G	A	42	75	c.2234C>T	c.(2233-2235)CCC>CTC	p.P745L
Pat_24	Post-Resistance	PLXNA2	5362	37	1	208204972	208204972	Missense_Mutation	SNP	G	A	64	218	c.5188C>T	c.(5188-5190)CAT>TAT	p.H1730Y
Pat_24	Post-Resistance	CENPF	1063	37	1	214813956	214813956	Missense_Mutation	SNP	G	A	3	44	c.2275G>A	c.(2275-2277)GAA>AAA	p.E759K
Pat_24	Post-Resistance	KCTD3	51133	37	1	215775263	215775263	Missense_Mutation	SNP	C	T	29	183	c.988C>T	c.(988-990)CTT>TTT	p.L330F
Pat_24	Post-Resistance	SPATA17	128153	37	1	217955597	217955597	Missense_Mutation	SNP	G	A	70	89	c.805G>A	c.(805-807)GAT>AAT	p.D269N

Pat_24	Post-Resistance	TAF1A	9015	37	1	222750876	222750876	Missense_Mutation	SNP	C	T	4	181	c.515G>A	c.(514-516)CGG>CAG	p.R172Q
Pat_24	Post-Resistance	AGT	183	37	1	230845894	230845894	Missense_Mutation	SNP	G	A	5	158	c.703C>T	c.(703-705)CTC>TTC	p.L235F
Pat_24	Post-Resistance	PCNXL2	80003	37	1	233394278	233394278	Missense_Mutation	SNP	G	A	83	164	c.1330C>T	c.(1330-1332)CCC>TCC	p.P444S
Pat_24	Post-Resistance	OR2L8	391190	37	1	248112697	248112697	Missense_Mutation	SNP	G	A	4	191	c.538G>A	c.(538-540)GTC>ATC	p.V180I
Pat_24	Post-Resistance	OR2L8	391190	37	1	248113064	248113064	Missense_Mutation	SNP	G	A	16	99	c.905G>A	c.(904-906)CGA>CAA	p.R302Q
Pat_24	Post-Resistance	OR2AK2	391191	37	1	248128661	248128661	Missense_Mutation	SNP	G	A	15	20	c.28G>A	c.(28-30)GAT>AAT	p.D10N
Pat_24	Post-Resistance	OR2M5	127059	37	1	248308569	248308569	Missense_Mutation	SNP	G	A	67	99	c.120G>A	c.(118-120)ATG>ATA	p.M40I
Pat_24	Post-Resistance	OR2M4	26245	37	1	248402801	248402801	Missense_Mutation	SNP	G	A	74	112	c.571G>A	c.(571-573)GAA>AAA	p.E191K
Pat_24	Post-Resistance	OR2T12	127064	37	1	248458834	248458834	Missense_Mutation	SNP	A	T	46	99	c.47T>A	c.(46-48)TTT>TAT	p.F16Y
Pat_24	Post-Resistance	ZNF692	55657	37	1	249150737	249150737	Missense_Mutation	SNP	C	T	54	85	c.500G>A	c.(499-501)AGG>AAG	p.R167K
Pat_24	Post-Resistance	PITRM1	10531	37	10	3202514	3202514	Missense_Mutation	SNP	G	A	4	63	c.704C>T	c.(703-705)ACG>ATG	p.T235M
Pat_24	Post-Resistance	TAF3	83860	37	10	8056640	8056640	Missense_Mutation	SNP	C	G	9	29	c.2716C>G	c.(2716-2718)CAG>GAG	p.Q906E
Pat_24	Post-Resistance	KIAA1217	56243	37	10	24762578	24762578	Missense_Mutation	SNP	C	A	4	129	c.1268C>A	c.(1267-1269)GCA>GAA	p.A423E
Pat_24	Post-Resistance	ZEB1	6935	37	10	31799637	31799637	Missense_Mutation	SNP	C	T	15	52	c.518C>T	c.(517-519)CCA>CTA	p.P173L
Pat_24	Post-Resistance	BICC1	80114	37	10	60573728	60573728	Missense_Mutation	SNP	C	T	4	150	c.2515C>T	c.(2515-2517)CGT>TGT	p.R839C
Pat_24	Post-Resistance	MYPN	84665	37	10	69933908	69933908	Missense_Mutation	SNP	G	A	58	121	c.2059G>A	c.(2059-2061)GAG>AAG	p.E687K
Pat_24	Post-Resistance	GPR120	338557	37	10	95326521	95326521	Missense_Mutation	SNP	G	A	3	20	c.44G>A	c.(43-45)CGC>CAC	p.R15H
Pat_24	Post-Resistance	SLIT1	6585	37	10	98816147	98816147	Missense_Mutation	SNP	G	A	37	177	c.1232C>T	c.(1231-1233)TCC>TTC	p.S411F
Pat_24	Post-Resistance	RRP12	23223	37	10	99133588	99133588	Missense_Mutation	SNP	T	C	4	185	c.1862A>G	c.(1861-1863)CAG>CGG	p.Q621R
Pat_24	Post-Resistance	MMS19	64210	37	10	99225675	99225675	Missense_Mutation	SNP	T	C	61	253	c.1643A>G	c.(1642-1644)CAA>CGA	p.Q548R
Pat_24	Post-Resistance	PDZD7	79955	37	10	102783262	102783262	Missense_Mutation	SNP	C	T	4	154	c.473G>A	c.(472-474)CGC>CAC	p.R158H
Pat_24	Post-Resistance	SORCS1	114815	37	10	108536412	108536412	Missense_Mutation	SNP	T	A	4	101	c.765A>T	c.(763-765)TTA>TTT	p.L255F
Pat_24	Post-Resistance	ACSL5	51703	37	10	114173027	114173027	Missense_Mutation	SNP	C	T	26	104	c.1045C>T	c.(1045-1047)CCC>TCC	p.P349S
Pat_24	Post-Resistance	EIF3A	8661	37	10	120801755	120801756	Missense_Mutation	DNP	TG	AC	6	376	.3276_3277CA>G	274-3279)GGCATG>GGG	p.M1093L
Pat_24	Post-Resistance	HTRA1	5654	37	10	124268285	124268285	Missense_Mutation	SNP	A	T	13	25	c.1119A>T	c.(1117-1119)AAA>AAT	p.K373N
Pat_24	Post-Resistance	CLRN3	119467	37	10	129690880	129690880	Missense_Mutation	SNP	G	A	27	81	c.169C>T	c.(169-171)CGT>TGT	p.R57C
Pat_24	Post-Resistance	MGMT	4255	37	10	131565127	131565127	Missense_Mutation	SNP	G	A	4	49	c.583G>A	c.(583-585)GTG>ATG	p.V195M
Pat_24	Post-Resistance	STK32C	282974	37	10	134040349	134040349	Nonsense_Mutation	SNP	G	T	4	172	c.594C>A	c.(592-594)TGC>TGA	p.C198*
Pat_24	Post-Resistance	PKP3	11187	37	11	397003	397003	Missense_Mutation	SNP	G	A	9	38	c.502G>A	c.(502-504)GGT>AGT	p.G168S
Pat_24	Post-Resistance	CTSD	1509	37	11	1782670	1782670	Missense_Mutation	SNP	G	A	4	123	c.97C>T	c.(97-99)CGC>TGC	p.R33C
Pat_24	Post-Resistance	OR51E1	143503	37	11	4674675	4674675	Nonsense_Mutation	SNP	C	T	4	186	c.919C>T	c.(919-921)CGA>TGA	p.R307*
Pat_24	Post-Resistance	OR52R1	119695	37	11	4825480	4825480	Missense_Mutation	SNP	C	T	10	13	c.368G>A	c.(367-369)GGA>GAA	p.G123E
Pat_24	Post-Resistance	HBB	3043	37	11	5248225	5248225	Missense_Mutation	SNP	C	G	32	94	c.27G>C	c.(25-27)AAG>AAC	p.K9N
Pat_24	Post-Resistance	OR51Q1	390061	37	11	5444142	5444142	Missense_Mutation	SNP	C	T	43	127	c.712C>T	c.(712-714)CGT>TGT	p.R238C
Pat_24	Post-Resistance	SYT9	143425	37	11	7324551	7324551	Missense_Mutation	SNP	G	A	25	62	c.427G>A	c.(427-429)GGG>AGG	p.G143R
Pat_24	Post-Resistance	GALNTL4	374378	37	11	11470334	11470334	Missense_Mutation	SNP	G	A	4	62	c.385C>T	c.(385-387)CGC>TGC	p.R129C
Pat_24	Post-Resistance	ARNTL	406	37	11	13402788	13402788	Missense_Mutation	SNP	C	T	19	121	c.1604C>T	c.(1603-1605)CCA>CTA	p.P535L
Pat_24	Post-Resistance	PTPN5	84867	37	11	18759448	18759448	Missense_Mutation	SNP	G	A	4	194	c.979C>T	c.(979-981)CGG>TGG	p.R327W
Pat_24	Post-Resistance	CSRP3	8048	37	11	19206514	19206514	Missense_Mutation	SNP	C	T	5	45	c.493G>A	c.(493-495)GAA>AAA	p.E165K
Pat_24	Post-Resistance	E2F8	79733	37	11	19247042	19247042	Missense_Mutation	SNP	G	A	4	157	c.2147C>T	c.(2146-2148)CCG>CTG	p.P716L
Pat_24	Post-Resistance	E2F8	79733	37	11	19251523	19251523	Missense_Mutation	SNP	C	G	6	357	c.1371G>C	c.(1369-1371)CAG>CAC	p.Q457H
Pat_24	Post-Resistance	ELF5	2001	37	11	34527196	34527196	Missense_Mutation	SNP	G	A	81	262	c.131C>T	c.(130-132)CCT>CTT	p.P44L
Pat_24	Post-Resistance	CNTF	1270	37	11	58391688	58391688	Missense_Mutation	SNP	C	T	4	40	c.296C>T	c.(295-297)ACC>ATC	p.T99I
Pat_24	Post-Resistance	GLYATL1	92292	37	11	58714563	58714563	Missense_Mutation	SNP	G	A	21	96	c.3G>A	c.(1-3)ATG>ATA	p.M1I
Pat_24	Post-Resistance	SLC22A8	9376	37	11	62763580	62763580	Missense_Mutation	SNP	G	A	24	70	c.806C>T	c.(805-807)TCC>TTC	p.S269F
Pat_24	Post-Resistance	RTN3	10313	37	11	63486611	63486611	Missense_Mutation	SNP	C	T	12	66	c.637C>T	c.(637-639)CCA>TCA	p.P213S
Pat_24	Post-Resistance	SNX15	29907	37	11	64802547	64802547	Missense_Mutation	SNP	G	A	6	240	c.389G>A	c.(388-390)CGA>CAA	p.R130Q

Pat_24	Post-Resistance	SLC25A45	283130	37	11	65143942	65143942	Missense_Mutation	SNP	C	T	5	134	c.803G>A	c.(802-804)CGC>CAC	p.R268H
Pat_24	Post-Resistance	RIN1	9610	37	11	66102072	66102072	Missense_Mutation	SNP	G	C	2	6	c.1198C>G	c.(1198-1200)CAG>GAG	p.Q400E
Pat_24	Post-Resistance	NADSYN1	55191	37	11	71191846	71191846	Missense_Mutation	SNP	C	T	4	86	c.919C>T	c.(919-921)CTC>TTC	p.L307F
Pat_24	Post-Resistance	ARHGEF17	9828	37	11	73071384	73071384	Missense_Mutation	SNP	G	A	4	185	c.4226G>A	c.(4225-4227)CGG>CAG	p.R1409Q
Pat_24	Post-Resistance	GAB2	9846	37	11	77934697	77934697	Missense_Mutation	SNP	G	A	103	384	c.1328C>T	c.(1327-1329)TCG>TTG	p.S443L
Pat_24	Post-Resistance	NAALAD2	10003	37	11	89882229	89882229	Missense_Mutation	SNP	A	G	5	356	c.437A>G	c.(436-438)AAT>AGT	p.N146S
Pat_24	Post-Resistance	NAALAD2	10003	37	11	89882249	89882249	Missense_Mutation	SNP	G	T	6	280	c.457G>T	c.(457-459)GCT>TCT	p.A153S
Pat_24	Post-Resistance	CHORDC1	26973	37	11	89944439	89944439	Missense_Mutation	SNP	A	G	4	115	c.377T>C	c.(376-378)CTA>CCA	p.L126P
Pat_24	Post-Resistance	FAT3	120114	37	11	92531158	92531158	Missense_Mutation	SNP	C	T	71	155	c.4979C>T	c.(4978-4980)TCC>TTC	p.S1660F
Pat_24	Post-Resistance	CCDC82	79780	37	11	96117471	96117471	Missense_Mutation	SNP	A	T	4	138	c.441T>A	c.(439-441)GAT>GAA	p.D147E
Pat_24	Post-Resistance	PGR	5241	37	11	100999627	100999627	Missense_Mutation	SNP	G	A	3	55	c.175C>T	c.(175-177)CTC>TTC	p.L59F
Pat_24	Post-Resistance	ANGPTL5	253935	37	11	101765741	101765741	Missense_Mutation	SNP	G	A	10	28	c.716C>T	c.(715-717)ACC>ATC	p.T239I
Pat_24	Post-Resistance	GRIA4	2893	37	11	105781176	105781176	Missense_Mutation	SNP	G	A	31	121	c.1174G>A	c.(1174-1176)GAT>AAT	p.D392N
Pat_24	Post-Resistance	FAM55D	54827	37	11	114453681	114453681	Missense_Mutation	SNP	T	A	15	90	c.159A>T	c.(157-159)TTA>TTT	p.L53F
Pat_24	Post-Resistance	TMPRSS13	84000	37	11	117789432	117789432	Missense_Mutation	SNP	C	T	4	128	c.143G>A	c.(142-144)GGG>GAG	p.G48E
Pat_24	Post-Resistance	FOXR1	283150	37	11	118850336	118850336	Missense_Mutation	SNP	C	T	4	169	c.569C>T	c.(568-570)TCC>TTC	p.S190F
Pat_24	Post-Resistance	THYN1	29087	37	11	134120179	134120179	Missense_Mutation	SNP	C	T	6	276	c.281G>A	c.(280-282)CGT>CAT	p.R94H
Pat_24	Post-Resistance	GLB1L3	112937	37	11	134153651	134153651	Missense_Mutation	SNP	G	A	12	41	c.548G>A	c.(547-549)CGG>CAG	p.R183Q
Pat_24	Post-Resistance	KDM5A	5927	37	12	427492	427492	Nonsense_Mutation	SNP	G	A	4	157	c.2677C>T	c.(2677-2679)CGA>TGA	p.R893*
Pat_24	Post-Resistance	CHD4	1108	37	12	6707075	6707075	Missense_Mutation	SNP	C	T	4	180	c.1877G>A	c.(1876-1878)CGA>CAA	p.R626Q
Pat_24	Post-Resistance	ACSM4	341392	37	12	7479635	7479635	Missense_Mutation	SNP	C	T	3	15	c.1600C>T	c.(1600-1602)CTT>TTT	p.L534F
Pat_24	Post-Resistance	RIMKLB	57494	37	12	8866505	8866505	Missense_Mutation	SNP	C	T	4	94	c.43C>T	c.(43-45)CGT>TGT	p.R15C
Pat_24	Post-Resistance	A2M	2	37	12	9224967	9224967	Missense_Mutation	SNP	G	A	3	36	c.4091C>T	c.(4090-4092)TCC>TTC	p.S1364F
Pat_24	Post-Resistance	ETV6	2120	37	12	12022504	12022504	Missense_Mutation	SNP	C	T	130	349	c.610C>T	c.(610-612)CCC>TCC	p.P204S
Pat_24	Post-Resistance	GPRC5D	55507	37	12	13102601	13102601	Missense_Mutation	SNP	G	A	27	90	c.718C>T	c.(718-720)CCG>TCG	p.P240S
Pat_24	Post-Resistance	GRIN2B	2904	37	12	13715812	13715812	Missense_Mutation	SNP	G	A	17	72	c.4360C>T	c.(4360-4362)CCC>TCC	p.P1454S
Pat_24	Post-Resistance	GUCY2C	2984	37	12	14825883	14825883	Missense_Mutation	SNP	C	T	4	176	c.1094G>A	c.(1093-1095)GGT>GAT	p.G365D
Pat_24	Post-Resistance	PTPRO	5800	37	12	15742411	15742411	Missense_Mutation	SNP	A	G	59	267	c.3433A>G	c.(3433-3435)ACA>GCA	p.T1145A
Pat_24	Post-Resistance	GYS2	2998	37	12	21713332	21713332	Missense_Mutation	SNP	C	T	6	260	c.1157G>A	c.(1156-1158)CGA>CAA	p.R386Q
Pat_24	Post-Resistance	RASSF8	11228	37	12	26208270	26208270	Translation_Start_Site	SNP	G	A	4	109	c.-6G>A	c.(-8--4)CGGTG>CGATG	
Pat_24	Post-Resistance	ABCD2	225	37	12	39973341	39973341	Missense_Mutation	SNP	G	A	26	165	c.1873C>T	c.(1873-1875)CAT>TAT	p.H625Y
Pat_24	Post-Resistance	LRRK2	120892	37	12	40688687	40688687	Missense_Mutation	SNP	G	A	4	25	c.2849G>A	c.(2848-2850)AGA>AAA	p.R950K
Pat_24	Post-Resistance	PRICKLE1	144165	37	12	42863277	42863277	Missense_Mutation	SNP	G	A	4	106	c.359C>T	c.(358-360)GCA>GTA	p.A120V
Pat_24	Post-Resistance	ARID2	196528	37	12	46242686	46242686	Missense_Mutation	SNP	C	T	4	97	c.1648C>T	c.(1648-1650)CTC>TTC	p.L550F
Pat_24	Post-Resistance	ARID2	196528	37	12	46246366	46246366	Missense_Mutation	SNP	C	T	47	132	c.4460C>T	c.(4459-4461)CCC>CTC	p.P1487L
Pat_24	Post-Resistance	ADCY6	112	37	12	49176698	49176698	Missense_Mutation	SNP	C	T	4	105	c.520G>A	c.(520-522)GCC>ACC	p.A174T
Pat_24	Post-Resistance	LMBR1L	55716	37	12	49500753	49500753	Missense_Mutation	SNP	A	G	63	186	c.148T>C	c.(148-150)TTC>CTC	p.F50L
Pat_24	Post-Resistance	C1QL4	338761	37	12	49726938	49726938	Missense_Mutation	SNP	C	T	4	96	c.616G>A	c.(616-618)GTG>ATG	p.V206M
Pat_24	Post-Resistance	BIN2	51411	37	12	51685932	51685932	Missense_Mutation	SNP	C	T	5	31	c.958G>A	c.(958-960)GAA>AAA	p.E320K
Pat_24	Post-Resistance	SCN8A	6334	37	12	52201072	52201072	Missense_Mutation	SNP	A	T	3	6	c.5802A>T	c.(5800-5802)AAA>AAT	p.K1934N
Pat_24	Post-Resistance	KRT84	3890	37	12	52772015	52772015	Missense_Mutation	SNP	C	T	2	3	c.1606G>A	c.(1606-1608)GGA>AGA	p.G536R
Pat_24	Post-Resistance	KRT71	112802	37	12	52942532	52942532	Missense_Mutation	SNP	C	T	39	153	c.766G>A	c.(766-768)GAA>AAA	p.E256K
Pat_24	Post-Resistance	CALCOCO1	57658	37	12	54118963	54118963	Missense_Mutation	SNP	G	A	5	120	c.64C>T	c.(64-66)CGG>TGG	p.R22W
Pat_24	Post-Resistance	LRP1	4035	37	12	57588432	57588432	Missense_Mutation	SNP	C	T	4	156	c.8141C>T	c.(8140-8142)ACG>ATG	p.T2714M
Pat_24	Post-Resistance	LRP1	4035	37	12	57606018	57606018	Missense_Mutation	SNP	G	A	3	43	c.13468G>A	c.(13468-13470)GCT>ACT	p.A4490T
Pat_24	Post-Resistance	TRHDE	29953	37	12	73050751	73050751	Missense_Mutation	SNP	T	C	3	110	c.2894T>C	c.(2893-2895)GTC>GCC	p.V965A
Pat_24	Post-Resistance	CSRP2	1466	37	12	77252758	77252758	Missense_Mutation	SNP	C	T	4	89	c.556G>A	c.(556-558)GCA>ACA	p.A186T

Pat_24	Post-Resistance	SCYL2	55681	37	12	100732400	100732400	Missense_Mutation	SNP	C	T	4	153	c.2240C>T	c.(2239-2241)ACT>ATT	p.T747I
Pat_24	Post-Resistance	RFX4	5992	37	12	107125991	107125991	Missense_Mutation	SNP	G	A	34	155	c.1435G>A	c.(1435-1437)GAG>AAG	p.E479K
Pat_24	Post-Resistance	PRDM4	11108	37	12	108145294	108145294	Missense_Mutation	SNP	G	T	4	76	c.1024C>A	c.(1024-1026)CAT>AAT	p.H342N
Pat_24	Post-Resistance	USP30	84749	37	12	109519817	109519817	Missense_Mutation	SNP	G	A	6	407	c.860G>A	c.(859-861)TGT>TAT	p.C287Y
Pat_24	Post-Resistance	ACACB	32	37	12	109577470	109577470	Missense_Mutation	SNP	G	A	3	80	c.260G>A	c.(259-261)CGG>CAG	p.R87Q
Pat_24	Post-Resistance	NOS1	4842	37	12	117705897	117705897	Missense_Mutation	SNP	T	C	3	80	c.1892A>G	c.(1891-1893)AAG>AGG	p.K631R
Pat_24	Post-Resistance	GATC	283459	37	12	120894955	120894955	Missense_Mutation	SNP	G	A	4	109	c.331G>A	c.(331-333)GTG>ATG	p.V111M
Pat_24	Post-Resistance	ATP6V0A2	23545	37	12	124221795	124221795	Missense_Mutation	SNP	C	T	4	110	c.1015C>T	c.(1015-1017)CGC>TGC	p.R339C
Pat_24	Post-Resistance	DNAH10	196385	37	12	124270346	124270346	Missense_Mutation	SNP	G	A	30	132	c.1101G>A	c.(1099-1101)ATG>ATA	p.M367I
Pat_24	Post-Resistance	DHX37	57647	37	12	125441316	125441316	Nonsense_Mutation	SNP	G	A	6	269	c.2374C>T	c.(2374-2376)CGA>TGA	p.R792*
Pat_24	Post-Resistance	ZNF10	7556	37	12	133732959	133732959	Missense_Mutation	SNP	C	T	34	178	c.1127C>T	c.(1126-1128)CCC>CTC	p.P376L
Pat_24	Post-Resistance	MTUS2	23281	37	13	29600916	29600916	Missense_Mutation	SNP	A	G	9	41	c.2111A>G	c.(2110-2112)AAC>AGC	p.N704S
Pat_24	Post-Resistance	ALOX5AP	241	37	13	31330090	31330090	Missense_Mutation	SNP	C	T	4	136	c.251C>T	c.(250-252)GCG>GTG	p.A84V
Pat_24	Post-Resistance	BRCA2	675	37	13	32912568	32912568	Missense_Mutation	SNP	C	T	4	151	c.4076C>T	c.(4075-4077)ACT>ATT	p.T1359I
Pat_24	Post-Resistance	STARD13	90627	37	13	33704132	33704132	Missense_Mutation	SNP	C	T	5	68	c.682G>A	c.(682-684)GTC>ATC	p.V228I
Pat_24	Post-Resistance	ATP7B	540	37	13	52548265	52548265	Missense_Mutation	SNP	G	A	83	202	c.1091C>T	c.(1090-1092)GCC>GTC	p.A364V
Pat_24	Post-Resistance	LMO7	4008	37	13	76415291	76415291	Missense_Mutation	SNP	G	A	10	93	c.2930G>A	c.(2929-2931)AGG>AAG	p.R977K
Pat_24	Post-Resistance	IPO5	3843	37	13	98655265	98655265	Missense_Mutation	SNP	T	C	11	273	c.1471T>C	c.(1471-1473)TCC>CCC	p.S491P
Pat_24	Post-Resistance	TNFSF13B	10673	37	13	108922454	108922454	Missense_Mutation	SNP	G	A	4	183	c.211G>A	c.(211-213)GCC>ACC	p.A71T
Pat_24	Post-Resistance	MYO16	23026	37	13	109661317	109661317	Missense_Mutation	SNP	G	A	16	104	c.2449G>A	c.(2449-2451)GAA>AAA	p.E817K
Pat_24	Post-Resistance	COL4A1	1282	37	13	110835536	110835536	Missense_Mutation	SNP	G	A	6	21	c.1985C>T	c.(1984-1986)CCC>CTC	p.P662L
Pat_24	Post-Resistance	TEP1	7011	37	14	20863691	20863691	Missense_Mutation	SNP	G	A	4	80	c.1846C>T	c.(1846-1848)CGT>TGT	p.R616C
Pat_24	Post-Resistance	OSGEP	55644	37	14	20917419	20917419	Missense_Mutation	SNP	C	G	4	143	c.418G>C	c.(418-420)GCA>CCA	p.A140P
Pat_24	Post-Resistance	HOMEZ	57594	37	14	23745797	23745797	Missense_Mutation	SNP	G	A	12	61	c.640C>T	c.(640-642)CCC>TCC	p.P214S
Pat_24	Post-Resistance	JPH4	84502	37	14	24045177	24045177	Missense_Mutation	SNP	G	A	18	46	c.868C>T	c.(868-870)CGG>TGG	p.R290W
Pat_24	Post-Resistance	NOVA1	4857	37	14	26949269	26949269	Nonsense_Mutation	SNP	G	A	30	178	c.361C>T	c.(361-363)CGA>TGA	p.R121*
Pat_24	Post-Resistance	KCNH5	27133	37	14	63174438	63174438	Missense_Mutation	SNP	C	T	48	167	c.2755G>A	c.(2755-2757)GAG>AAG	p.E919K
Pat_24	Post-Resistance	KCNH5	27133	37	14	63174770	63174770	Missense_Mutation	SNP	C	T	5	42	c.2423G>A	c.(2422-2424)GGA>GAA	p.G808E
Pat_24	Post-Resistance	SPTB	6710	37	14	65270369	65270369	Missense_Mutation	SNP	G	A	4	149	c.430C>T	c.(430-432)CGC>TGC	p.R144C
Pat_24	Post-Resistance	EIF2S1	1965	37	14	67831648	67831648	Missense_Mutation	SNP	G	A	5	333	c.164G>A	c.(163-165)CGT>CAT	p.R55H
Pat_24	Post-Resistance	HEATR4	399671	37	14	73978727	73978727	Missense_Mutation	SNP	G	A	6	231	c.1541C>T	c.(1540-1542)ACC>ATC	p.T514I
Pat_24	Post-Resistance	LTBP2	4053	37	14	74971770	74971770	Missense_Mutation	SNP	G	A	4	124	c.4285C>T	c.(4285-4287)CGG>TGG	p.R1429W
Pat_24	Post-Resistance	YLPM1	56252	37	14	75230688	75230688	Missense_Mutation	SNP	C	T	3	47	c.496C>T	c.(496-498)CCC>TCC	p.P166S
Pat_24	Post-Resistance	C14orf102	55051	37	14	90759123	90759123	Missense_Mutation	SNP	C	T	6	199	c.1760G>A	c.(1759-1761)CGT>CAT	p.R587H
Pat_24	Post-Resistance	KIAA0284	283638	37	14	105353332	105353332	Missense_Mutation	SNP	C	T	4	72	c.2756C>T	c.(2755-2757)ACG>ATG	p.T919M
Pat_24	Post-Resistance	KIAA0284	283638	37	14	105356013	105356013	Missense_Mutation	SNP	C	T	12	46	c.3796C>T	c.(3796-3798)CCC>TCC	p.P1266S
Pat_24	Post-Resistance	RYR3	6263	37	15	33603253	33603253	Missense_Mutation	SNP	G	A	3	22	c.7G>A	c.(7-9)GAA>AAA	p.E3K
Pat_24	Post-Resistance	RYR3	6263	37	15	33955922	33955922	Nonsense_Mutation	SNP	C	A	3	21	c.5603C>A	c.(5602-5604)TCA>TAA	p.S1868*
Pat_24	Post-Resistance	C15orf55	256646	37	15	34646772	34646772	Missense_Mutation	SNP	G	T	4	79	c.1117G>T	c.(1117-1119)GAC>TAC	p.D373Y
Pat_24	Post-Resistance	TMCO5A	145942	37	15	38229100	38229100	Missense_Mutation	SNP	G	A	12	13	c.193G>A	c.(193-195)GAG>AAG	p.E65K
Pat_24	Post-Resistance	CASC5	57082	37	15	40951616	40951616	Missense_Mutation	SNP	G	A	4	169	c.6871G>A	c.(6871-6873)GTA>ATA	p.V2291I
Pat_24	Post-Resistance	MAP1A	4130	37	15	43816316	43816316	Missense_Mutation	SNP	C	T	4	133	c.2645C>T	c.(2644-2646)GCT>GTT	p.A882V
Pat_24	Post-Resistance	CKMT1B	1159	37	15	43891417	43891418	Missense_Mutation	DNP	GG	AA	59	108	.1200_1201GG>A	198-1203)CTGGAG>CTAA	p.E401K
Pat_24	Post-Resistance	DUOX2	50506	37	15	45388258	45388258	Missense_Mutation	SNP	C	T	15	25	c.3848G>A	c.(3847-3849)GGA>GAA	p.G1283E
Pat_24	Post-Resistance	SHF	90525	37	15	45491196	45491196	Missense_Mutation	SNP	G	A	4	14	c.77C>T	c.(76-78)CCG>CTG	p.P26L
Pat_24	Post-Resistance	CILP	8483	37	15	65499120	65499120	Missense_Mutation	SNP	C	T	107	133	c.424G>A	c.(424-426)GGA>AGA	p.G142R
Pat_24	Post-Resistance	DIS3L	115752	37	15	66624358	66624358	Missense_Mutation	SNP	G	A	5	118	c.2681G>A	c.(2680-2682)AGG>AAG	p.R894K

Pat_24	Post-Resistance	LOC645752	645752	37	15	78207888	78207888	Missense_Mutation	SNP	A	C	4	26	c.1110T>G	c.(1108-1110)AAT>AAG	p.N370K
Pat_24	Post-Resistance	C15orf42	90381	37	15	90129084	90129084	Missense_Mutation	SNP	G	A	4	170	c.1322G>A	c.(1321-1323)AGC>AAC	p.S441N
Pat_24	Post-Resistance	SYNM	23336	37	15	99670857	99670857	Missense_Mutation	SNP	T	G	19	13	c.2292T>G	c.(2290-2292)TTT>TTG	p.F764L
Pat_24	Post-Resistance	OR4F15	390649	37	15	102358732	102358732	Missense_Mutation	SNP	C	T	4	179	c.343C>T	c.(343-345)CTC>TTC	p.L115F
Pat_24	Post-Resistance	PIGQ	9091	37	16	624252	624252	Missense_Mutation	SNP	G	A	3	40	c.178G>A	c.(178-180)GTG>ATG	p.V60M
Pat_24	Post-Resistance	FBXL16	146330	37	16	744675	744675	Missense_Mutation	SNP	T	G	8	36	c.1250A>C	c.(1249-1251)CAC>CCC	p.H417P
Pat_24	Post-Resistance	PKD1	5310	37	16	2155877	2155877	Missense_Mutation	SNP	C	T	4	114	c.7852G>A	c.(7852-7854)GTG>ATG	p.V2618M
Pat_24	Post-Resistance	SRRM2	23524	37	16	2817405	2817406	Missense_Mutation	DNP	CC	TT	59	194	.6876_6877CC>T	874-6879)GCCCCA>GCT	p.P2293S
Pat_24	Post-Resistance	A2BP1	54715	37	16	7680638	7680638	Missense_Mutation	SNP	G	A	16	87	c.710G>A	c.(709-711)GGA>GAA	p.G237E
Pat_24	Post-Resistance	TEKT5	146279	37	16	10788232	10788232	Nonsense_Mutation	SNP	G	A	69	221	c.499C>T	c.(499-501)CAG>TAG	p.Q167*
Pat_24	Post-Resistance	TXNDC11	51061	37	16	11794417	11794417	Missense_Mutation	SNP	T	C	23	87	c.878A>G	c.(877-879)TAC>TGC	p.Y293C
Pat_24	Post-Resistance	ERCC4	2072	37	16	14022037	14022037	Missense_Mutation	SNP	C	T	34	118	c.737C>T	c.(736-738)TCG>TTG	p.S246L
Pat_24	Post-Resistance	SMG1	23049	37	16	18853620	18853620	Missense_Mutation	SNP	C	T	4	175	c.6376G>A	c.(6376-6378)GGA>AGA	p.G2126R
Pat_24	Post-Resistance	SMG1	23049	37	16	18937330	18937330	Missense_Mutation	SNP	T	C	6	32	c.34A>G	c.(34-36)AGC>GGC	p.S12G
Pat_24	Post-Resistance	CD19	930	37	16	28944394	28944394	Missense_Mutation	SNP	G	A	27	102	c.518G>A	c.(517-519)TGT>TAT	p.C173Y
Pat_24	Post-Resistance	TGFB1I1	7041	37	16	31487375	31487375	Missense_Mutation	SNP	G	A	5	120	c.757G>A	c.(757-759)GTT>ATT	p.V253I
Pat_24	Post-Resistance	VPS35	55737	37	16	46714661	46714661	Missense_Mutation	SNP	G	A	28	81	c.428C>T	c.(427-429)CCC>CTC	p.P143L
Pat_24	Post-Resistance	ADCY7	113	37	16	50324486	50324486	Missense_Mutation	SNP	C	T	37	67	c.290C>T	c.(289-291)GCG>GTG	p.A97V
Pat_24	Post-Resistance	KIFC3	3801	37	16	57794802	57794803	Missense_Mutation	DNP	GG	AT	7	23	.2067_2068CC>A	065-2070)AGCCGC>AGA	689_690SR>R
Pat_24	Post-Resistance	CES3	23491	37	16	67000685	67000685	Missense_Mutation	SNP	G	A	47	169	c.979G>A	c.(979-981)GAA>AAA	p.E327K
Pat_24	Post-Resistance	KCTD19	146212	37	16	67325211	67325211	Splice_Site	SNP	C	T	4	83	c.2565_splice	c.e14+1	p.W855_splice
Pat_24	Post-Resistance	THAP11	57215	37	16	67877052	67877052	Missense_Mutation	SNP	G	A	4	141	c.595G>A	c.(595-597)GCA>ACA	p.A199T
Pat_24	Post-Resistance	NRN1L	123904	37	16	67919927	67919927	Missense_Mutation	SNP	C	T	4	66	c.263C>T	c.(262-264)CCG>CTG	p.P88L
Pat_24	Post-Resistance	DHX38	9785	37	16	72133661	72133661	Missense_Mutation	SNP	G	A	4	124	c.991G>A	c.(991-993)GAG>AAG	p.E331K
Pat_24	Post-Resistance	ZFHX3	463	37	16	72991473	72991473	Missense_Mutation	SNP	C	T	5	74	c.2572G>A	c.(2572-2574)GAG>AAG	p.E858K
Pat_24	Post-Resistance	ZFHX3	463	37	16	72992655	72992655	Missense_Mutation	SNP	C	T	3	63	c.1390G>A	c.(1390-1392)GAG>AAG	p.E464K
Pat_24	Post-Resistance	VAT1L	57687	37	16	77850847	77850847	Missense_Mutation	SNP	G	A	23	122	c.263G>A	c.(262-264)CGA>CAA	p.R88Q
Pat_24	Post-Resistance	PLCG2	5336	37	16	81819769	81819769	Missense_Mutation	SNP	G	A	4	82	c.175G>A	c.(175-177)GAC>AAC	p.D59N
Pat_24	Post-Resistance	TAF1C	9013	37	16	84217086	84217086	Missense_Mutation	SNP	C	T	3	23	c.248G>A	c.(247-249)CGG>CAG	p.R83Q
Pat_24	Post-Resistance	USP10	9100	37	16	84778259	84778259	Missense_Mutation	SNP	G	C	6	39	c.172G>C	c.(172-174)GAG>CAG	p.E58Q
Pat_24	Post-Resistance	C17orf97	400566	37	17	263384	263384	Missense_Mutation	SNP	G	C	3	18	c.780G>C	c.(778-780)GAG>GAC	p.E260D
Pat_24	Post-Resistance	SLC43A2	124935	37	17	1486602	1486602	Missense_Mutation	SNP	G	A	4	165	c.1246C>T	c.(1246-1248)CGG>TGG	p.R416W
Pat_24	Post-Resistance	PRPF8	10594	37	17	1564990	1564990	Nonsense_Mutation	SNP	G	A	4	171	c.4117C>T	c.(4117-4119)CAG>TAG	p.Q1373*
Pat_24	Post-Resistance	ITGAE	3682	37	17	3657141	3657141	Missense_Mutation	SNP	G	A	22	110	c.1463C>T	c.(1462-1464)GCC>GTC	p.A488V
Pat_24	Post-Resistance	MINK1	50488	37	17	4796762	4796762	Missense_Mutation	SNP	G	A	4	70	c.2434G>A	c.(2434-2436)GAG>AAG	p.E812K
Pat_24	Post-Resistance	NUP88	4927	37	17	5292182	5292182	Missense_Mutation	SNP	G	A	13	52	c.1583C>T	c.(1582-1584)TCC>TTC	p.S528F
Pat_24	Post-Resistance	TEKT1	83659	37	17	6716271	6716271	Missense_Mutation	SNP	C	T	5	218	c.731G>A	c.(730-732)CGA>CAA	p.R244Q
Pat_24	Post-Resistance	ALOX12	239	37	17	6902059	6902059	Missense_Mutation	SNP	C	T	4	115	c.445C>T	c.(445-447)CCC>TCC	p.P149S
Pat_24	Post-Resistance	NEURL4	84461	37	17	7227426	7227426	Splice_Site	SNP	C	A	4	186	c.2062_splice	c.e11+1	p.E688_splice
Pat_24	Post-Resistance	PFAS	5198	37	17	8170932	8170932	Missense_Mutation	SNP	G	A	4	190	c.3331G>A	c.(3331-3333)GTG>ATG	p.V1111M
Pat_24	Post-Resistance	PIK3R6	146850	37	17	8736226	8736226	Missense_Mutation	SNP	G	A	4	183	c.782C>T	c.(781-783)CCC>CTC	p.P261L
Pat_24	Post-Resistance	MYH8	4626	37	17	10304868	10304868	Missense_Mutation	SNP	C	T	64	310	c.2923G>A	c.(2923-2925)GAG>AAG	p.E975K
Pat_24	Post-Resistance	MYH4	4622	37	17	10351188	10351188	Missense_Mutation	SNP	G	A	5	334	c.4912C>T	c.(4912-4914)CGC>TGC	p.R1638C
Pat_24	Post-Resistance	MYH4	4622	37	17	10360853	10360853	Missense_Mutation	SNP	G	A	39	80	c.1781C>T	c.(1780-1782)GCC>GTC	p.A594V
Pat_24	Post-Resistance	MYH1	4619	37	17	10402046	10402046	Missense_Mutation	SNP	C	T	5	279	c.4078G>A	c.(4078-4080)GAG>AAG	p.E1360K
Pat_24	Post-Resistance	MYH1	4619	37	17	10412834	10412834	Missense_Mutation	SNP	C	T	81	283	c.1555G>A	c.(1555-1557)GAC>AAC	p.D519N
Pat_24	Post-Resistance	MYH2	4620	37	17	10432937	10432937	Missense_Mutation	SNP	C	T	34	119	c.3061G>A	c.(3061-3063)GAC>AAC	p.D1021N

Pat_24	Post-Resistance	MYOCD	93649	37	17	12642601	12642601	Missense_Mutation	SNP	C	A	27	85	c.673C>A	c.(673-675)CTT>ATT	p.L225I
Pat_24	Post-Resistance	RNF112	7732	37	17	19316944	19316944	Missense_Mutation	SNP	G	A	10	47	c.775G>A	c.(775-777)GAA>AAA	p.E259K
Pat_24	Post-Resistance	ALDH3A1	218	37	17	19648378	19648378	Missense_Mutation	SNP	G	A	3	24	c.65C>T	c.(64-66)CCG>CTG	p.P22L
Pat_24	Post-Resistance	WSB1	26118	37	17	25628877	25628877	Missense_Mutation	SNP	G	A	5	329	c.104G>A	c.(103-105)CGT>CAT	p.R35H
Pat_24	Post-Resistance	SARM1	23098	37	17	26712115	26712115	Missense_Mutation	SNP	G	A	4	57	c.1451G>A	c.(1450-1452)CGC>CAC	p.R484H
Pat_24	Post-Resistance	SLC46A1	113235	37	17	26727681	26727681	Missense_Mutation	SNP	C	T	3	33	c.1267G>A	c.(1267-1269)GGG>AGG	p.G423R
Pat_24	Post-Resistance	SEZ6	124925	37	17	27308551	27308551	Missense_Mutation	SNP	G	A	11	32	c.562C>T	c.(562-564)CCT>TCT	p.P188S
Pat_24	Post-Resistance	SEZ6	124925	37	17	27308970	27308970	Missense_Mutation	SNP	G	A	13	41	c.143C>T	c.(142-144)CCT>CTT	p.P48L
Pat_24	Post-Resistance	TAOK1	57551	37	17	27829707	27829707	Missense_Mutation	SNP	G	A	7	258	c.1304G>A	c.(1303-1305)CGA>CAA	p.R435Q
Pat_24	Post-Resistance	ZNF830	91603	37	17	33289450	33289450	Missense_Mutation	SNP	G	A	4	173	c.865G>A	c.(865-867)GAA>AAA	p.E289K
Pat_24	Post-Resistance	GAS2L2	246176	37	17	34074225	34074225	Nonsense_Mutation	SNP	G	A	5	336	c.895C>T	c.(895-897)CAG>TAG	p.Q299*
Pat_24	Post-Resistance	CCL18	6362	37	17	34397903	34397903	Missense_Mutation	SNP	C	T	19	102	c.164C>T	c.(163-165)CCC>CTC	p.P55L
Pat_24	Post-Resistance	MLLT6	4302	37	17	36872692	36872692	Missense_Mutation	SNP	C	T	11	45	c.1109C>T	c.(1108-1110)TCC>TTC	p.S370F
Pat_24	Post-Resistance	GRB7	2886	37	17	37903097	37903097	Missense_Mutation	SNP	C	T	4	138	c.1546C>T	c.(1546-1548)CGC>TGC	p.R516C
Pat_24	Post-Resistance	KRT26	353288	37	17	38926062	38926062	Missense_Mutation	SNP	C	T	30	135	c.913G>A	c.(913-915)GAA>AAA	p.E305K
Pat_24	Post-Resistance	KRTAP4-7	100132476	37	17	39240742	39240742	Missense_Mutation	SNP	G	T	6	179	c.284G>T	c.(283-285)TGC>TTC	p.C95F
Pat_24	Post-Resistance	KRTAP4-12	83755	37	17	39279951	39279951	Missense_Mutation	SNP	G	A	5	213	c.424C>T	c.(424-426)CGC>TGC	p.R142C
Pat_24	Post-Resistance	SLC4A1	6521	37	17	42335041	42335041	Missense_Mutation	SNP	C	G	2	11	c.1417G>C	c.(1417-1419)GAA>CAA	p.E473Q
Pat_24	Post-Resistance	NSF	4905	37	17	44788404	44788404	Nonsense_Mutation	SNP	C	T	12	117	c.1546C>T	c.(1546-1548)CGA>TGA	p.R516*
Pat_24	Post-Resistance	SCRN2	90507	37	17	45915916	45915916	Missense_Mutation	SNP	C	T	5	362	c.919G>A	c.(919-921)GCC>ACC	p.A307T
Pat_24	Post-Resistance	SP2	6668	37	17	45994060	45994060	Missense_Mutation	SNP	G	A	4	167	c.623G>A	c.(622-624)GGC>GAC	p.G208D
Pat_24	Post-Resistance	PHB	5245	37	17	47486457	47486457	Missense_Mutation	SNP	C	T	49	48	c.457G>A	c.(457-459)GAC>AAC	p.D153N
Pat_24	Post-Resistance	MSI2	124540	37	17	55704604	55704604	Missense_Mutation	SNP	G	A	6	249	c.667G>A	c.(667-669)GTG>ATG	p.V223M
Pat_24	Post-Resistance	OR4D2	124538	37	17	56247618	56247618	Missense_Mutation	SNP	C	T	19	75	c.602C>T	c.(601-603)TCC>TTC	p.S201F
Pat_24	Post-Resistance	C17orf47	284083	37	17	56620916	56620916	Missense_Mutation	SNP	G	A	4	130	c.632C>T	c.(631-633)ACG>ATG	p.T211M
Pat_24	Post-Resistance	TRIM37	4591	37	17	57157205	57157205	Missense_Mutation	SNP	C	T	27	73	c.526G>A	c.(526-528)GAT>AAT	p.D176N
Pat_24	Post-Resistance	10-Mar	162333	37	17	60813730	60813730	Missense_Mutation	SNP	T	C	14	62	c.1499A>G	c.(1498-1500)GAC>GGC	p.D500G
Pat_24	Post-Resistance	10-Mar	162333	37	17	60821776	60821776	Nonsense_Mutation	SNP	G	A	4	182	c.496C>T	c.(496-498)CAG>TAG	p.Q166*
Pat_24	Post-Resistance	ABCA6	23460	37	17	67092389	67092389	Missense_Mutation	SNP	A	G	2	3	c.3400T>C	c.(3400-3402)TTC>CTC	p.F1134L
Pat_24	Post-Resistance	OTOP2	92736	37	17	72926856	72926856	Missense_Mutation	SNP	G	A	4	171	c.1126G>A	c.(1126-1128)GCC>ACC	p.A376T
Pat_24	Post-Resistance	MFSD11	79157	37	17	74771214	74771214	Missense_Mutation	SNP	C	T	4	169	c.1010C>T	c.(1009-1011)CCT>CTT	p.P337L
Pat_24	Post-Resistance	LGALS3BP	3959	37	17	76972089	76972089	Missense_Mutation	SNP	C	T	6	42	c.202G>A	c.(202-204)GAG>AAG	p.E68K
Pat_24	Post-Resistance	RPTOR	57521	37	17	78704421	78704421	Missense_Mutation	SNP	C	T	4	155	c.569C>T	c.(568-570)TCG>TTG	p.S190L
Pat_24	Post-Resistance	RPTOR	57521	37	17	78931496	78931496	Missense_Mutation	SNP	G	A	4	172	c.3443G>A	c.(3442-3444)CGG>CAG	p.R1148Q
Pat_24	Post-Resistance	BAIAP2	10458	37	17	79078422	79078422	Missense_Mutation	SNP	C	T	14	29	c.1175C>T	c.(1174-1176)ACC>ATC	p.T392I
Pat_24	Post-Resistance	NPLOC4	55666	37	17	79556017	79556017	Missense_Mutation	SNP	C	T	4	188	c.1234G>A	c.(1234-1236)GCC>ACC	p.A412T
Pat_24	Post-Resistance	MYOM1	8736	37	18	3102547	3102547	Missense_Mutation	SNP	G	A	17	89	c.3500C>T	c.(3499-3501)TCC>TTC	p.S1167F
Pat_24	Post-Resistance	IMPA2	3613	37	18	12009956	12009956	Missense_Mutation	SNP	C	T	43	247	c.305C>T	c.(304-306)CCC>CTC	p.P102L
Pat_24	Post-Resistance	LAMA3	3909	37	18	21492684	21492684	Missense_Mutation	SNP	C	T	4	151	c.7168C>T	c.(7168-7170)CCC>TCC	p.P2390S
Pat_24	Post-Resistance	DSC3	1825	37	18	28576937	28576937	Missense_Mutation	SNP	C	T	6	26	c.2313G>A	c.(2311-2313)ATG>ATA	p.M771I
Pat_24	Post-Resistance	MEP1B	4225	37	18	29793298	29793298	Missense_Mutation	SNP	C	T	4	20	c.1355C>T	c.(1354-1356)CCA>CTA	p.P452L
Pat_24	Post-Resistance	ASXL3	80816	37	18	31325120	31325120	Missense_Mutation	SNP	G	A	8	24	c.5308G>A	c.(5308-5310)GGA>AGA	p.G1770R
Pat_24	Post-Resistance	CCBE1	147372	37	18	57136752	57136752	Missense_Mutation	SNP	C	T	68	333	c.353G>A	c.(352-354)CGA>CAA	p.R118Q
Pat_24	Post-Resistance	KIAA1468	57614	37	18	59949677	59949677	Missense_Mutation	SNP	T	C	22	160	c.3253T>C	c.(3253-3255)TTT>CTT	p.F1085L
Pat_24	Post-Resistance	NETO1	81832	37	18	70526196	70526196	Missense_Mutation	SNP	G	A	7	68	c.334C>T	c.(334-336)CCA>TCA	p.P112S
Pat_24	Post-Resistance	PRTN3	5657	37	19	843464	843464	Missense_Mutation	SNP	C	T	3	17	c.65C>T	c.(64-66)GCT>GTT	p.A22V
Pat_24	Post-Resistance	ZNF555	148254	37	19	2853202	2853202	Missense_Mutation	SNP	C	T	5	48	c.1139C>T	c.(1138-1140)CCC>CTC	p.P380L

Pat_24	Post-Resistance	NFIC	4782	37	19	3452528	3452528	Missense_Mutation	SNP	C	T	10	723	c.1133C>T	c.(1132-1134)ACG>ATG	p.T378M
Pat_24	Post-Resistance	CLEC4M	10332	37	19	7828094	7828094	Translation_Start_Site	SNP	G	A	4	21	c.-58G>A	.(-60--56)GGGTG>GGATG	
Pat_24	Post-Resistance	FBN3	84467	37	19	8188854	8188854	Missense_Mutation	SNP	C	T	17	65	c.2770G>A	c.(2770-2772)GAT>AAT	p.D924N
Pat_24	Post-Resistance	MUC16	94025	37	19	9064995	9064995	Missense_Mutation	SNP	G	A	4	168	c.22451C>T	c.(22450-22452)ACT>ATT	p.T7484I
Pat_24	Post-Resistance	MUC16	94025	37	19	9075747	9075747	Missense_Mutation	SNP	G	C	11	26	c.11699C>G	c.(11698-11700)TCC>TGC	p.S3900C
Pat_24	Post-Resistance	COL5A3	50509	37	19	10114730	10114730	Missense_Mutation	SNP	G	A	4	192	c.686C>T	c.(685-687)CCG>CTG	p.P229L
Pat_24	Post-Resistance	FAM129C	199786	37	19	17648304	17648304	Missense_Mutation	SNP	C	G	3	124	c.640C>G	c.(640-642)CAT>GAT	p.H214D
Pat_24	Post-Resistance	PIK3R2	5296	37	19	18279920	18279920	Missense_Mutation	SNP	G	A	33	160	c.2003G>A	c.(2002-2004)TGC>TAC	p.C668Y
Pat_24	Post-Resistance	GMIP	51291	37	19	19741062	19741062	Missense_Mutation	SNP	C	T	4	114	c.2623G>A	c.(2623-2625)GGC>AGC	p.G875S
Pat_24	Post-Resistance	ZNF93	81931	37	19	20045284	20045284	Missense_Mutation	SNP	A	C	3	143	c.1520A>C	c.(1519-1521)AAA>ACA	p.K507T
Pat_24	Post-Resistance	ZNF208	7757	37	19	22155909	22155909	Missense_Mutation	SNP	C	A	4	140	c.1627G>T	c.(1627-1629)GGC>TGC	p.G543C
Pat_24	Post-Resistance	ZNF492	57615	37	19	22847739	22847739	Missense_Mutation	SNP	G	A	5	145	c.1268G>A	c.(1267-1269)TGT>TAT	p.C423Y
Pat_24	Post-Resistance	CHST8	64377	37	19	34263819	34263819	Missense_Mutation	SNP	C	T	4	90	c.1126C>T	c.(1126-1128)CGG>TGG	p.R376W
Pat_24	Post-Resistance	KIAA0355	9710	37	19	34832463	34832463	Missense_Mutation	SNP	C	T	4	159	c.1624C>T	c.(1624-1626)CGG>TGG	p.R542W
Pat_24	Post-Resistance	ATP4A	495	37	19	36049978	36049978	Missense_Mutation	SNP	G	A	9	528	c.1172C>T	c.(1171-1173)ACT>ATT	p.T391I
Pat_24	Post-Resistance	WDR62	284403	37	19	36579954	36579954	Nonsense_Mutation	SNP	C	T	44	154	c.1783C>T	c.(1783-1785)CAG>TAG	p.Q595*
Pat_24	Post-Resistance	ZNF527	84503	37	19	37865129	37865129	Missense_Mutation	SNP	C	T	28	85	c.29C>T	c.(28-30)TCC>TTC	p.S10F
Pat_24	Post-Resistance	ACTN4	81	37	19	39219688	39219688	Missense_Mutation	SNP	G	A	23	284	c.2471G>A	c.(2470-2472)GGC>GAC	p.G824D
Pat_24	Post-Resistance	ZNF546	339327	37	19	40519644	40519644	Missense_Mutation	SNP	T	C	16	48	c.467T>C	c.(466-468)TTG>TCG	p.L156S
Pat_24	Post-Resistance	CYP2B7P1	1556	37	19	41442117	41442117	Missense_Mutation	SNP	C	T	11	62	c.287C>T	c.(286-288)TCT>TTT	p.S96F
Pat_24	Post-Resistance	CYP2A13	1553	37	19	41600907	41600907	Missense_Mutation	SNP	C	T	4	191	c.1205C>T	c.(1204-1206)CCC>CTC	p.P402L
Pat_24	Post-Resistance	MEGF8	1954	37	19	42873700	42873700	Missense_Mutation	SNP	G	A	5	194	c.6458G>A	c.(6457-6459)CGC>CAC	p.R2153H
Pat_24	Post-Resistance	PSG8	440533	37	19	43259211	43259211	Missense_Mutation	SNP	C	T	13	87	c.917G>A	c.(916-918)GGA>GAA	p.G306E
Pat_24	Post-Resistance	ERCC1	2067	37	19	45923622	45923622	Missense_Mutation	SNP	C	T	4	106	c.385G>A	c.(385-387)GAC>AAC	p.D129N
Pat_24	Post-Resistance	GIPR	2696	37	19	46181236	46181236	Missense_Mutation	SNP	C	T	6	206	c.997C>T	c.(997-999)CGG>TGG	p.R333W
Pat_24	Post-Resistance	PNMAL1	55228	37	19	46974154	46974154	Missense_Mutation	SNP	G	A	12	27	c.139C>T	c.(139-141)CTC>TTC	p.L47F
Pat_24	Post-Resistance	DHX34	9704	37	19	47882968	47882968	Missense_Mutation	SNP	C	T	55	275	c.2708C>T	c.(2707-2709)TCC>TTC	p.S903F
Pat_24	Post-Resistance	SULT2A1	6822	37	19	48389505	48389505	Missense_Mutation	SNP	C	T	17	112	c.10G>A	c.(10-12)GAT>AAT	p.D4N
Pat_24	Post-Resistance	FGF21	26291	37	19	49261344	49261344	Missense_Mutation	SNP	C	T	3	14	c.497C>T	c.(496-498)CCA>CTA	p.P166L
Pat_24	Post-Resistance	PLEKHA4	57664	37	19	49363613	49363613	Missense_Mutation	SNP	T	C	3	160	c.470A>G	c.(469-471)GAC>GGC	p.D157G
Pat_24	Post-Resistance	POLD1	5424	37	19	50912813	50912813	Missense_Mutation	SNP	C	T	4	152	c.2044C>T	c.(2044-2046)CGG>TGG	p.R682W
Pat_24	Post-Resistance	MYBPC2	4606	37	19	50964863	50964863	Missense_Mutation	SNP	G	A	4	86	c.2996G>A	c.(2995-2997)GGC>GAC	p.G999D
Pat_24	Post-Resistance	KLK15	55554	37	19	51330167	51330167	Missense_Mutation	SNP	C	T	14	32	c.448G>A	c.(448-450)GAG>AAG	p.E150K
Pat_24	Post-Resistance	KLK5	25818	37	19	51447041	51447041	Missense_Mutation	SNP	C	T	6	24	c.728G>A	c.(727-729)GGT>GAT	p.G243D
Pat_24	Post-Resistance	LIM2	3982	37	19	51885793	51885793	Missense_Mutation	SNP	C	T	27	152	c.204G>A	c.(202-204)ATG>ATA	p.M68I
Pat_24	Post-Resistance	ZNF836	162962	37	19	52659470	52659470	Missense_Mutation	SNP	C	T	4	171	c.1466G>A	c.(1465-1467)CGG>CAG	p.R489Q
Pat_24	Post-Resistance	ZNF578	147660	37	19	53014551	53014551	Missense_Mutation	SNP	G	A	5	204	c.917G>A	c.(916-918)CGT>CAT	p.R306H
Pat_24	Post-Resistance	VN1R2	317701	37	19	53762332	53762332	Nonsense_Mutation	SNP	G	A	10	37	c.704G>A	c.(703-705)TGG>TAG	p.W235*
Pat_24	Post-Resistance	ZIK1	284307	37	19	58100021	58100021	Missense_Mutation	SNP	G	T	3	66	c.187G>T	c.(187-189)GTA>TTA	p.V63L
Pat_24	Post-Resistance	ZSCAN4	201516	37	19	58189418	58189418	Missense_Mutation	SNP	C	T	17	104	c.533C>T	c.(532-534)TCC>TTC	p.S178F
Pat_24	Post-Resistance	TRIM28	10155	37	19	59056878	59056878	Missense_Mutation	SNP	G	A	4	106	c.427G>A	c.(427-429)GCC>ACC	p.A143T
Pat_24	Post-Resistance	ADAM17	6868	37	2	9676829	9676829	Missense_Mutation	SNP	A	G	51	154	c.359T>C	c.(358-360)GTT>GCT	p.V120A
Pat_24	Post-Resistance	GREB1	9687	37	2	11777891	11777891	Missense_Mutation	SNP	C	T	4	176	c.5396C>T	c.(5395-5397)CCG>CTG	p.P1799L
Pat_24	Post-Resistance	GEN1	348654	37	2	17946296	17946296	Missense_Mutation	SNP	T	A	51	166	c.481T>A	c.(481-483)TAT>AAT	p.Y161N
Pat_24	Post-Resistance	PLEKHH2	130271	37	2	43927635	43927635	Missense_Mutation	SNP	C	T	64	188	c.1538C>T	c.(1537-1539)TCC>TTC	p.S513F
Pat_24	Post-Resistance	CCDC142	84865	37	2	74710339	74710339	Translation_Start_Site	SNP	G	A	4	56	c.-374C>T	.(-376--372)AACGT>AATGT	
Pat_24	Post-Resistance	REG3G	130120	37	2	79255367	79255367	Missense_Mutation	SNP	G	A	4	148	c.493G>A	c.(493-495)GCA>ACA	p.A165T

Pat_24	Post-Resistance	CTNNA2	1496	37	2	80874869	80874869	Missense_Mutation	SNP	G	A	27	83	c.2734G>A	c.(2734-2736)GAG>AAG	p.E912K
Pat_24	Post-Resistance	KDM3A	55818	37	2	86701921	86701921	Missense_Mutation	SNP	G	A	5	200	c.1747G>A	c.(1747-1749)GTG>ATG	p.V583M
Pat_24	Post-Resistance	SEMA4C	54910	37	2	97533590	97533590	Missense_Mutation	SNP	C	T	5	383	c.34G>A	c.(34-36)GCA>ACA	p.A12T
Pat_24	Post-Resistance	LYG1	129530	37	2	99907879	99907879	Missense_Mutation	SNP	G	A	12	40	c.154C>T	c.(154-156)CGT>TGT	p.R52C
Pat_24	Post-Resistance	PSD4	23550	37	2	113950879	113950879	Missense_Mutation	SNP	G	A	8	82	c.1964G>A	c.(1963-1965)CGG>CAG	p.R655Q
Pat_24	Post-Resistance	CNTNAP5	129684	37	2	125521709	125521709	Nonsense_Mutation	SNP	C	T	18	64	c.2515C>T	c.(2515-2517)CGA>TGA	p.R839*
Pat_24	Post-Resistance	MYO7B	4648	37	2	128394168	128394168	Nonsense_Mutation	SNP	C	T	3	46	c.6094C>T	c.(6094-6096)CGA>TGA	p.R2032*
Pat_24	Post-Resistance	NCKAP5	344148	37	2	133541974	133541974	Missense_Mutation	SNP	G	A	25	137	c.2410C>T	c.(2410-2412)CCT>TCT	p.P804S
Pat_24	Post-Resistance	LRP1B	53353	37	2	141264467	141264467	Missense_Mutation	SNP	C	T	33	86	c.8419G>A	c.(8419-8421)GAA>AAA	p.E2807K
Pat_24	Post-Resistance	ACVR1C	130399	37	2	158401119	158401119	Missense_Mutation	SNP	C	T	16	40	c.781G>A	c.(781-783)GGA>AGA	p.G261R
Pat_24	Post-Resistance	ITGB6	3694	37	2	161029195	161029195	Missense_Mutation	SNP	A	G	68	403	c.806T>C	c.(805-807)GTG>GCG	p.V269A
Pat_24	Post-Resistance	SCN2A	6326	37	2	166170222	166170222	Missense_Mutation	SNP	C	T	12	40	c.1127C>T	c.(1126-1128)TCC>TTC	p.S376F
Pat_24	Post-Resistance	SCN1A	6323	37	2	166915126	166915126	Missense_Mutation	SNP	G	A	17	67	c.337C>T	c.(337-339)CCC>TCC	p.P113S
Pat_24	Post-Resistance	XIRP2	129446	37	2	168106448	168106448	Missense_Mutation	SNP	C	T	4	194	c.8546C>T	c.(8545-8547)GCA>GTA	p.A2849V
Pat_24	Post-Resistance	LRP2	4036	37	2	170002377	170002377	Missense_Mutation	SNP	C	T	10	11	c.12868G>A	c.(12868-12870)GAA>AAA	p.E4290K
Pat_24	Post-Resistance	LRP2	4036	37	2	170030528	170030528	Nonsense_Mutation	SNP	G	A	30	117	c.10915C>T	c.(10915-10917)CAG>TAG	p.Q3639*
Pat_24	Post-Resistance	MYO3B	140469	37	2	171243735	171243735	Missense_Mutation	SNP	G	A	22	99	c.1494G>A	c.(1492-1494)ATG>ATA	p.M498I
Pat_24	Post-Resistance	OSBPL6	114880	37	2	179196280	179196280	Missense_Mutation	SNP	G	A	4	187	c.320G>A	c.(319-321)CGT>CAT	p.R107H
Pat_24	Post-Resistance	TTN	7273	37	2	179395188	179395188	Missense_Mutation	SNP	T	A	9	30	c.98450A>T	c.(98449-98451)AAG>ATG	p.K32817M
Pat_24	Post-Resistance	TTN	7273	37	2	179458711	179458711	Missense_Mutation	SNP	C	T	49	175	c.50705G>A	c.(50704-50706)GGT>GAT	p.G16902D
Pat_24	Post-Resistance	CCDC141	285025	37	2	179718176	179718177	Missense_Mutation	DNP	TG	CT	52	188	.1510_1511CA>A	c.(1510-1512)CAC>AGC	p.H504S
Pat_24	Post-Resistance	PDE1A	5136	37	2	183104982	183104982	Nonsense_Mutation	SNP	G	A	12	80	c.253C>T	c.(253-255)CAG>TAG	p.Q85*
Pat_24	Post-Resistance	PARD3B	117583	37	2	206037007	206037007	Missense_Mutation	SNP	G	A	32	119	c.1693G>A	c.(1693-1695)GAA>AAA	p.E565K
Pat_24	Post-Resistance	ATIC	471	37	2	216209532	216209532	Missense_Mutation	SNP	G	A	4	153	c.1258G>A	c.(1258-1260)GTA>ATA	p.V420I
Pat_24	Post-Resistance	WNT6	7475	37	2	219738322	219738322	Missense_Mutation	SNP	C	T	4	7	c.853C>T	c.(853-855)CTC>TTC	p.L285F
Pat_24	Post-Resistance	SPEG	10290	37	2	220309456	220309456	Missense_Mutation	SNP	C	T	3	37	c.470C>T	c.(469-471)ACC>ATC	p.T157I
Pat_24	Post-Resistance	ACSL3	2181	37	2	223791867	223791867	Nonsense_Mutation	SNP	C	A	4	147	c.1425C>A	c.(1423-1425)TAC>TAA	p.Y475*
Pat_24	Post-Resistance	WDFY1	57590	37	2	224763710	224763710	Missense_Mutation	SNP	G	A	5	383	c.563C>T	c.(562-564)ACG>ATG	p.T188M
Pat_24	Post-Resistance	SLC16A14	151473	37	2	230910728	230910728	Missense_Mutation	SNP	C	T	4	155	c.1114G>A	c.(1114-1116)GTC>ATC	p.V372I
Pat_24	Post-Resistance	SP140L	93349	37	2	231254663	231254663	Missense_Mutation	SNP	G	A	19	46	c.889G>A	c.(889-891)GAT>AAT	p.D297N
Pat_24	Post-Resistance	UGT1A4	54657	37	2	234627614	234627614	Missense_Mutation	SNP	G	A	5	36	c.148G>A	c.(148-150)GAG>AAG	p.E50K
Pat_24	Post-Resistance	TRPM8	79054	37	2	234854527	234854527	Missense_Mutation	SNP	G	A	69	213	c.727G>A	c.(727-729)GAT>AAT	p.D243N
Pat_24	Post-Resistance	PER2	8864	37	2	239161768	239161768	Missense_Mutation	SNP	G	A	4	102	c.2896C>T	c.(2896-2898)CGG>TGG	p.R966W
Pat_24	Post-Resistance	FARP2	9855	37	2	242423676	242423676	Missense_Mutation	SNP	A	G	18	94	c.2351A>G	c.(2350-2352)TAC>TGC	p.Y784C
Pat_24	Post-Resistance	ZCCHC3	85364	37	20	279147	279147	Missense_Mutation	SNP	G	A	4	177	c.917G>A	c.(916-918)GGG>GAG	p.G306E
Pat_24	Post-Resistance	SIRPA	140885	37	20	1895804	1895804	Missense_Mutation	SNP	G	A	4	94	c.139G>A	c.(139-141)GCT>ACT	p.A47T
Pat_24	Post-Resistance	TGM6	343641	37	20	2384352	2384352	Missense_Mutation	SNP	G	A	36	100	c.1219G>A	c.(1219-1221)GAT>AAT	p.D407N
Pat_24	Post-Resistance	ITPA	3704	37	20	3194691	3194691	Missense_Mutation	SNP	C	T	21	69	c.250C>T	c.(250-252)CCC>TCC	p.P84S
Pat_24	Post-Resistance	SLC23A2	9962	37	20	4854620	4854620	Missense_Mutation	SNP	A	C	10	128	c.1064T>G	c.(1063-1065)GTG>GGG	p.V355G
Pat_24	Post-Resistance	PLCB4	5332	37	20	9416225	9416225	Missense_Mutation	SNP	C	T	4	17	c.2507C>T	c.(2506-2508)TCA>TTA	p.S836L
Pat_24	Post-Resistance	PCSK2	5126	37	20	17434414	17434414	Missense_Mutation	SNP	G	A	4	74	c.913G>A	c.(913-915)GTG>ATG	p.V305M
Pat_24	Post-Resistance	MYLK2	85366	37	20	30408261	30408261	Missense_Mutation	SNP	G	A	13	145	c.385G>A	c.(385-387)GGC>AGC	p.G129S
Pat_24	Post-Resistance	NCOA6	23054	37	20	33337567	33337567	Missense_Mutation	SNP	C	T	4	190	c.2431G>A	c.(2431-2433)GAT>AAT	p.D811N
Pat_24	Post-Resistance	CEP250	11190	37	20	34091848	34091848	Missense_Mutation	SNP	C	T	9	32	c.5651C>T	c.(5650-5652)GCC>GTC	p.A1884V
Pat_24	Post-Resistance	PLCG1	5335	37	20	39792036	39792036	Missense_Mutation	SNP	C	T	49	149	c.808C>T	c.(808-810)CGC>TGC	p.R270C
Pat_24	Post-Resistance	PTPRT	11122	37	20	41306788	41306788	Missense_Mutation	SNP	G	A	11	16	c.871C>T	c.(871-873)CCC>TCC	p.P291S
Pat_24	Post-Resistance	TOX2	84969	37	20	42635328	42635328	Missense_Mutation	SNP	G	A	4	179	c.334G>A	c.(334-336)GGT>AGT	p.G112S

Pat_24	Post-Resistance	GDAP1L1	78997	37	20	42907720	42907720	Missense_Mutation	SNP	G	A	4	127	c.884G>A	c.(883-885)CGG>CAG	p.R295Q
Pat_24	Post-Resistance	TTPAL	79183	37	20	43109033	43109033	Missense_Mutation	SNP	G	A	6	345	c.394G>A	c.(394-396)GTG>ATG	p.V132M
Pat_24	Post-Resistance	SLC12A5	57468	37	20	44676109	44676109	Missense_Mutation	SNP	G	A	31	132	c.1873G>A	c.(1873-1875)GGC>AGC	p.G625S
Pat_24	Post-Resistance	SALL4	57167	37	20	50408315	50408315	Missense_Mutation	SNP	C	T	4	145	c.707G>A	c.(706-708)CGC>CAC	p.R236H
Pat_24	Post-Resistance	RAB22A	57403	37	20	56928332	56928332	Missense_Mutation	SNP	C	T	4	155	c.202C>T	c.(202-204)CGT>TGT	p.R68C
Pat_24	Post-Resistance	DIDO1	11083	37	20	61511433	61511433	Missense_Mutation	SNP	G	A	74	208	c.5875C>T	c.(5875-5877)CCC>TCC	p.P1959S
Pat_24	Post-Resistance	YTHDF1	54915	37	20	61833974	61833974	Missense_Mutation	SNP	C	T	4	138	c.1318G>A	c.(1318-1320)GTC>ATC	p.V440I
Pat_24	Post-Resistance	KRTAP24-1	643803	37	21	31654844	31654844	Missense_Mutation	SNP	C	T	4	181	c.407G>A	c.(406-408)CGA>CAA	p.R136Q
Pat_24	Post-Resistance	SYNJ1	8867	37	21	34012088	34012088	Missense_Mutation	SNP	G	A	4	58	c.3707C>T	c.(3706-3708)ACG>ATG	p.T1236M
Pat_24	Post-Resistance	CLIC6	54102	37	21	36042415	36042415	Missense_Mutation	SNP	A	G	4	11	c.728A>G	c.(727-729)GAG>GGG	p.E243G
Pat_24	Post-Resistance	PRDM15	63977	37	21	43248606	43248606	Missense_Mutation	SNP	C	T	9	651	c.2548G>A	c.(2548-2550)GAC>AAC	p.D850N
Pat_24	Post-Resistance	PRODH	5625	37	22	18907019	18907019	Missense_Mutation	SNP	C	T	4	74	c.1196G>A	c.(1195-1197)CGG>CAG	p.R399Q
Pat_24	Post-Resistance	TPST2	8459	37	22	26937460	26937460	Missense_Mutation	SNP	C	T	4	167	c.137G>A	c.(136-138)CGG>CAG	p.R46Q
Pat_24	Post-Resistance	CRYBB1	1414	37	22	27003893	27003893	Missense_Mutation	SNP	T	C	20	149	c.392A>G	c.(391-393)TAC>TGC	p.Y131C
Pat_24	Post-Resistance	CCDC157	550631	37	22	30768247	30768247	Missense_Mutation	SNP	G	A	3	15	c.1307G>A	c.(1306-1308)CGT>CAT	p.R436H
Pat_24	Post-Resistance	PISD	23761	37	22	32044143	32044143	Nonsense_Mutation	SNP	G	A	4	90	c.265C>T	c.(265-267)CGA>TGA	p.R89*
Pat_24	Post-Resistance	MCM5	4174	37	22	35812336	35812336	Missense_Mutation	SNP	G	A	6	501	c.1352G>A	c.(1351-1353)CGA>CAA	p.R451Q
Pat_24	Post-Resistance	TRIOBP	11078	37	22	38120359	38120359	Missense_Mutation	SNP	C	G	5	373	c.1796C>G	c.(1795-1797)ACA>AGA	p.T599R
Pat_24	Post-Resistance	ZC3H7B	23264	37	22	41752656	41752656	Missense_Mutation	SNP	A	T	6	294	c.2525A>T	c.(2524-2526)TAC>TTC	p.Y842F
Pat_24	Post-Resistance	C22orf9	23313	37	22	45599059	45599059	Missense_Mutation	SNP	C	T	7	259	c.664G>A	c.(664-666)GTG>ATG	p.V222M
Pat_24	Post-Resistance	MLC1	23209	37	22	50523291	50523291	Missense_Mutation	SNP	C	T	3	57	c.41G>A	c.(40-42)CGG>CAG	p.R14Q
Pat_24	Post-Resistance	SHANK3	85358	37	22	51121796	51121796	Missense_Mutation	SNP	G	A	4	83	c.914G>A	c.(913-915)CGT>CAT	p.R305H
Pat_24	Post-Resistance	RABL2B	11158	37	22	51208419	51208419	Missense_Mutation	SNP	G	A	7	60	c.323C>T	c.(322-324)ACC>ATC	p.T108I
Pat_24	Post-Resistance	FGD5	152273	37	3	14862356	14862356	Missense_Mutation	SNP	G	A	3	62	c.1778G>A	c.(1777-1779)GGG>GAG	p.G593E
Pat_24	Post-Resistance	ANKRD28	23243	37	3	15718494	15718494	Missense_Mutation	SNP	C	T	4	149	c.2770G>A	c.(2770-2772)GCA>ACA	p.A924T
Pat_24	Post-Resistance	CMTM8	152189	37	3	32398920	32398920	Missense_Mutation	SNP	C	T	27	115	c.203C>T	c.(202-204)CCC>CTC	p.P68L
Pat_24	Post-Resistance	CLASP2	23122	37	3	33623409	33623409	Missense_Mutation	SNP	G	A	3	77	c.2251C>T	c.(2251-2253)CGT>TGT	p.R751C
Pat_24	Post-Resistance	PDCD6IP	10015	37	3	33905518	33905518	Missense_Mutation	SNP	C	T	21	138	c.2141C>T	c.(2140-2142)GCC>GTC	p.A714V
Pat_24	Post-Resistance	HIGD1A	25994	37	3	42835717	42835717	Missense_Mutation	SNP	G	A	18	70	c.29C>T	c.(28-30)CCT>CTT	p.P10L
Pat_24	Post-Resistance	C3orf39	84892	37	3	43122095	43122095	Missense_Mutation	SNP	C	T	4	178	c.829G>A	c.(829-831)GTG>ATG	p.V277M
Pat_24	Post-Resistance	SETD2	29072	37	3	47164268	47164268	Nonsense_Mutation	SNP	G	A	4	15	c.1858C>T	c.(1858-1860)CGA>TGA	p.R620*
Pat_24	Post-Resistance	KLHL18	23276	37	3	47382099	47382099	Missense_Mutation	SNP	G	A	7	397	c.1159G>A	c.(1159-1161)GTC>ATC	p.V387I
Pat_24	Post-Resistance	CELSR3	1951	37	3	48689366	48689366	Missense_Mutation	SNP	G	A	25	134	c.5867C>T	c.(5866-5868)CCA>CTA	p.P1956L
Pat_24	Post-Resistance	GPX1	2876	37	3	49395051	49395052	Missense_Mutation	DNP	AG	TA	12	74	c.381_382CT>TA	(379-384)GCCTTC>GCTAT	p.F128I
Pat_24	Post-Resistance	AMT	275	37	3	49455262	49455262	Missense_Mutation	SNP	C	T	7	394	c.1022G>A	c.(1021-1023)GGT>GAT	p.G341D
Pat_24	Post-Resistance	DAG1	1605	37	3	49569385	49569385	Missense_Mutation	SNP	C	T	4	62	c.1441C>T	c.(1441-1443)CGC>TGC	p.R481C
Pat_24	Post-Resistance	VPRBP	9730	37	3	51458334	51458334	Missense_Mutation	SNP	G	A	85	269	c.2090C>T	c.(2089-2091)TCC>TTC	p.S697F
Pat_24	Post-Resistance	GLYCTK	132158	37	3	52324395	52324395	Nonsense_Mutation	SNP	C	T	4	67	c.37C>T	c.(37-39)CGA>TGA	p.R13*
Pat_24	Post-Resistance	TKT	7086	37	3	53263377	53263377	Missense_Mutation	SNP	G	A	4	53	c.1183C>T	c.(1183-1185)CGG>TGG	p.R395W
Pat_24	Post-Resistance	IL17RD	54756	37	3	57136608	57136608	Missense_Mutation	SNP	G	A	4	134	c.878C>T	c.(877-879)CCG>CTG	p.P293L
Pat_24	Post-Resistance	LRIG1	26018	37	3	66512898	66512898	Missense_Mutation	SNP	G	A	3	37	c.254C>T	c.(253-255)CCT>CTT	p.P85L
Pat_24	Post-Resistance	CNTN3	5067	37	3	74350624	74350624	Missense_Mutation	SNP	G	A	42	117	c.2020C>T	c.(2020-2022)CGG>TGG	p.R674W
Pat_24	Post-Resistance	ROBO2	6092	37	3	77666773	77666773	Nonsense_Mutation	SNP	C	T	28	84	c.3403C>T	c.(3403-3405)CGA>TGA	p.R1135*
Pat_24	Post-Resistance	NIT2	56954	37	3	100074045	100074045	Missense_Mutation	SNP	G	A	3	54	c.764G>A	c.(763-765)CGC>CAC	p.R255H
Pat_24	Post-Resistance	SLC9A10	285335	37	3	111950227	111950227	Missense_Mutation	SNP	C	T	3	48	c.1553G>A	c.(1552-1554)CGT>CAT	p.R518H
Pat_24	Post-Resistance	DRD3	1814	37	3	113866354	113866354	Missense_Mutation	SNP	C	T	27	125	c.434G>A	c.(433-435)AGC>AAC	p.S145N
Pat_24	Post-Resistance	DRD3	1814	37	3	113890700	113890700	Missense_Mutation	SNP	T	C	25	111	c.140A>G	c.(139-141)AAT>AGT	p.N47S

Pat_24	Post-Resistance	ADPRH	141	37	3	119306475	119306475	Missense_Mutation	SNP	C	T	20	68	c.824C>T	c.(823-825)CCC>CTC	p.P275L
Pat_24	Post-Resistance	FBXO40	51725	37	3	121340508	121340508	Missense_Mutation	SNP	C	T	37	115	c.232C>T	c.(232-234)CGC>TGC	p.R78C
Pat_24	Post-Resistance	FBXO40	51725	37	3	121340844	121340844	Missense_Mutation	SNP	G	A	8	57	c.568G>A	c.(568-570)GGG>AGG	p.G190R
Pat_24	Post-Resistance	ADCY5	111	37	3	123036955	123036955	Nonsense_Mutation	SNP	G	A	4	66	c.2266C>T	c.(2266-2268)CAG>TAG	p.Q756*
Pat_24	Post-Resistance	ALDH1L1	10840	37	3	125831722	125831722	Missense_Mutation	SNP	C	T	9	29	c.2084G>A	c.(2083-2085)GGG>GAG	p.G695E
Pat_24	Post-Resistance	TRPC1	7220	37	3	142523009	142523009	Nonsense_Mutation	SNP	C	T	9	65	c.1948C>T	c.(1948-1950)CAG>TAG	p.Q650*
Pat_24	Post-Resistance	PLSCR4	57088	37	3	145913071	145913071	Splice_Site	SNP	T	C	7	297	c.787_splice	c.e8-1	p.V263_splice
Pat_24	Post-Resistance	CP	1356	37	3	148924003	148924003	Missense_Mutation	SNP	G	A	21	91	c.1160C>T	c.(1159-1161)CCC>CTC	p.P387L
Pat_24	Post-Resistance	MED12L	116931	37	3	151085950	151085950	Missense_Mutation	SNP	C	T	4	117	c.3356C>T	c.(3355-3357)GCG>GTG	p.A1119V
Pat_24	Post-Resistance	GPR149	344758	37	3	154055985	154055985	Missense_Mutation	SNP	T	C	53	196	c.1699A>G	c.(1699-1701)ACC>GCC	p.T567A
Pat_24	Post-Resistance	GOLIM4	27333	37	3	167747592	167747592	Missense_Mutation	SNP	C	T	4	102	c.1409G>A	c.(1408-1410)CGG>CAG	p.R470Q
Pat_24	Post-Resistance	SAMD7	344658	37	3	169654162	169654162	Missense_Mutation	SNP	G	T	4	107	c.1077G>T	c.(1075-1077)TTG>TTT	p.L359F
Pat_24	Post-Resistance	FNDC3B	64778	37	3	172061890	172061890	Missense_Mutation	SNP	G	C	5	263	c.2092G>C	c.(2092-2094)GAA>CAA	p.E698Q
Pat_24	Post-Resistance	SPATA16	83893	37	3	172737325	172737325	Missense_Mutation	SNP	G	A	63	271	c.799C>T	c.(799-801)CGT>TGT	p.R267C
Pat_24	Post-Resistance	NLGN1	22871	37	3	173993297	173993297	Missense_Mutation	SNP	G	A	4	71	c.839G>A	c.(838-840)CGT>CAT	p.R280H
Pat_24	Post-Resistance	PIK3CA	5290	37	3	178936092	178936092	Missense_Mutation	SNP	A	G	4	64	c.1634A>G	c.(1633-1635)GAG>GGG	p.E545G
Pat_24	Post-Resistance	USP13	8975	37	3	179481925	179481925	Missense_Mutation	SNP	G	A	6	205	c.2228G>A	c.(2227-2229)CGA>CAA	p.R743Q
Pat_24	Post-Resistance	MCF2L2	23101	37	3	183017985	183017985	Splice_Site	SNP	C	T	8	27	c.1114_splice	c.e11-1	p.E372_splice
Pat_24	Post-Resistance	ECE2	9718	37	3	184005689	184005689	Missense_Mutation	SNP	G	A	22	61	c.1682G>A	c.(1681-1683)GGG>GAG	p.G561E
Pat_24	Post-Resistance	DGKG	1608	37	3	186006513	186006513	Missense_Mutation	SNP	T	C	3	163	c.530A>G	c.(529-531)CAG>CGG	p.Q177R
Pat_24	Post-Resistance	MUC4	4585	37	3	195515146	195515146	Missense_Mutation	SNP	G	A	2	3	c.3305C>T	c.(3304-3306)GCC>GTC	p.A1102V
Pat_24	Post-Resistance	GAK	2580	37	4	876496	876496	Missense_Mutation	SNP	C	T	4	128	c.1516G>A	c.(1516-1518)GTG>ATG	p.V506M
Pat_24	Post-Resistance	CRMP1	1400	37	4	5851178	5851178	Missense_Mutation	SNP	G	A	3	30	c.562C>T	c.(562-564)CTT>TTT	p.L188F
Pat_24	Post-Resistance	KLF3	51274	37	4	38698711	38698711	Missense_Mutation	SNP	C	T	16	43	c.865C>T	c.(865-867)CCC>TCC	p.P289S
Pat_24	Post-Resistance	CHRNA9	55584	37	4	40339314	40339314	Missense_Mutation	SNP	G	A	23	48	c.298G>A	c.(298-300)GAT>AAT	p.D100N
Pat_24	Post-Resistance	UCHL1	7345	37	4	41262778	41262778	Missense_Mutation	SNP	C	T	83	162	c.289C>T	c.(289-291)CAC>TAC	p.H97Y
Pat_24	Post-Resistance	CORIN	10699	37	4	47644003	47644003	Missense_Mutation	SNP	T	C	15	159	c.2132A>G	c.(2131-2133)CAC>CGC	p.H711R
Pat_24	Post-Resistance	KIT	3815	37	4	55604659	55604659	Missense_Mutation	SNP	G	A	4	130	c.2867G>A	c.(2866-2868)CGG>CAG	p.R956Q
Pat_24	Post-Resistance	UGT2B4	7363	37	4	70355286	70355286	Missense_Mutation	SNP	T	A	26	75	c.873A>T	c.(871-873)GAA>GAT	p.E291D
Pat_24	Post-Resistance	ALB	213	37	4	74280825	74280825	Missense_Mutation	SNP	G	A	47	160	c.1132G>A	c.(1132-1134)GAA>AAA	p.E378K
Pat_24	Post-Resistance	RASSF6	166824	37	4	74459282	74459282	Missense_Mutation	SNP	C	T	20	122	c.269G>A	c.(268-270)GGA>GAA	p.G90E
Pat_24	Post-Resistance	PF4	5196	37	4	74847200	74847200	Missense_Mutation	SNP	C	T	4	108	c.152G>A	c.(151-153)CGT>CAT	p.R51H
Pat_24	Post-Resistance	CXCL9	4283	37	4	76925960	76925960	Splice_Site	SNP	A	G	30	75	c.276_splice	c.e3+1	p.Q92_splice
Pat_24	Post-Resistance	GPRIN3	285513	37	4	90170964	90170964	Missense_Mutation	SNP	G	A	45	170	c.298C>T	c.(298-300)CCC>TCC	p.P100S
Pat_24	Post-Resistance	MMRN1	22915	37	4	90857395	90857395	Missense_Mutation	SNP	C	T	4	5	c.2564C>T	c.(2563-2565)TCC>TTC	p.S855F
Pat_24	Post-Resistance	SMARCAD1	56916	37	4	95155158	95155158	Missense_Mutation	SNP	G	A	4	65	c.422G>A	c.(421-423)AGA>AAA	p.R141K
Pat_24	Post-Resistance	TET2	54790	37	4	106157378	106157378	Missense_Mutation	SNP	T	A	16	48	c.2279T>A	c.(2278-2280)TTT>TAT	p.F760Y
Pat_24	Post-Resistance	HADH	3033	37	4	108940781	108940781	Missense_Mutation	SNP	C	T	71	362	c.505C>T	c.(505-507)CTC>TTC	p.L169F
Pat_24	Post-Resistance	NDST4	64579	37	4	115767146	115767146	Missense_Mutation	SNP	C	T	18	44	c.1948G>A	c.(1948-1950)GAC>AAC	p.D650N
Pat_24	Post-Resistance	USP53	54532	37	4	120161041	120161041	Missense_Mutation	SNP	C	T	6	22	c.127C>T	c.(127-129)CTT>TTT	p.L43F
Pat_24	Post-Resistance	TRPC3	7222	37	4	122800914	122800914	Missense_Mutation	SNP	G	A	30	111	c.2743C>T	c.(2743-2745)CCC>TCC	p.P915S
Pat_24	Post-Resistance	SFRP2	6423	37	4	154702662	154702662	Missense_Mutation	SNP	G	T	4	170	c.829C>A	c.(829-831)CAG>AAG	p.Q277K
Pat_24	Post-Resistance	PLRG1	5356	37	4	155461792	155461792	Missense_Mutation	SNP	G	A	6	325	c.893C>T	c.(892-894)CCG>CTG	p.P298L
Pat_24	Post-Resistance	GLRB	2743	37	4	158091737	158091737	Missense_Mutation	SNP	T	A	5	58	c.1351T>A	c.(1351-1353)TCT>ACT	p.S451T
Pat_24	Post-Resistance	RAPGEF2	9693	37	4	160274944	160274944	Missense_Mutation	SNP	C	A	4	153	c.3914C>A	c.(3913-3915)ACA>AAA	p.T1305K
Pat_24	Post-Resistance	TLL1	7092	37	4	166915607	166915607	Missense_Mutation	SNP	C	T	11	16	c.436C>T	c.(436-438)CCC>TCC	p.P146S
Pat_24	Post-Resistance	ACSL1	2180	37	4	185681510	185681510	Splice_Site	SNP	C	T	6	357	c.1782_splice	c.e18+1	p.Q594_splice

Pat_24	Post-Resistance	MTNR1A	4543	37	4	187455657	187455657	Missense_Mutation	SNP	G	A	18	85	c.239C>T	c.(238-240)CCG>CTG	p.P80L
Pat_24	Post-Resistance	ADAMTS16	170690	37	5	5190109	5190109	Missense_Mutation	SNP	C	A	4	188	c.1073C>A	c.(1072-1074)GCA>GAA	p.A358E
Pat_24	Post-Resistance	CTNND2	1501	37	5	10981933	10981933	Missense_Mutation	SNP	C	A	24	79	c.3369G>T	c.(3367-3369)TTG>TTT	p.L1123F
Pat_24	Post-Resistance	CTNND2	1501	37	5	11397234	11397234	Missense_Mutation	SNP	C	A	61	56	c.521G>T	c.(520-522)AGC>ATC	p.S174I
Pat_24	Post-Resistance	CDH12	1010	37	5	21854857	21854857	Missense_Mutation	SNP	G	A	4	135	c.569C>T	c.(568-570)CCG>CTG	p.P190L
Pat_24	Post-Resistance	PRDM9	56979	37	5	23509657	23509657	Missense_Mutation	SNP	C	T	40	105	c.148C>T	c.(148-150)CGC>TGC	p.R50C
Pat_24	Post-Resistance	PDZD2	23037	37	5	31983706	31983706	Missense_Mutation	SNP	C	T	6	430	c.922C>T	c.(922-924)CGC>TGC	p.R308C
Pat_24	Post-Resistance	SPEF2	79925	37	5	35792486	35792486	Missense_Mutation	SNP	G	A	77	139	c.4492G>A	c.(4492-4494)GTG>ATG	p.V1498M
Pat_24	Post-Resistance	NIPBL	25836	37	5	37022189	37022189	Nonsense_Mutation	SNP	C	T	4	152	c.5365C>T	c.(5365-5367)CGA>TGA	p.R1789*
Pat_24	Post-Resistance	NUP155	9631	37	5	37303483	37303483	Nonsense_Mutation	SNP	G	A	3	51	c.3196C>T	c.(3196-3198)CGA>TGA	p.R1066*
Pat_24	Post-Resistance	MGC42105	167359	37	5	43280506	43280506	Missense_Mutation	SNP	C	A	4	174	c.986C>A	c.(985-987)CCA>CAA	p.P329Q
Pat_24	Post-Resistance	NNT	23530	37	5	43649294	43649294	Missense_Mutation	SNP	C	T	99	450	c.1490C>T	c.(1489-1491)GCC>GTC	p.A497V
Pat_24	Post-Resistance	ANKRD55	79722	37	5	55407572	55407572	Missense_Mutation	SNP	G	A	47	110	c.1003C>T	c.(1003-1005)CGG>TGG	p.R335W
Pat_24	Post-Resistance	DIMT1L	27292	37	5	61686727	61686727	Missense_Mutation	SNP	G	A	80	326	c.875C>T	c.(874-876)TCC>TTC	p.S292F
Pat_24	Post-Resistance	JMY	133746	37	5	78586025	78586025	Missense_Mutation	SNP	C	T	16	72	c.1288C>T	c.(1288-1290)CAC>TAC	p.H430Y
Pat_24	Post-Resistance	EFNA5	1946	37	5	106722984	106722984	Missense_Mutation	SNP	G	A	4	56	c.517C>T	c.(517-519)CGT>TGT	p.R173C
Pat_24	Post-Resistance	HSD17B4	3295	37	5	118829594	118829594	Missense_Mutation	SNP	A	G	30	59	c.821A>G	c.(820-822)AAG>AGG	p.K274R
Pat_24	Post-Resistance	SLC22A5	6584	37	5	131726524	131726524	Missense_Mutation	SNP	C	T	4	165	c.1195C>T	c.(1195-1197)CGG>TGG	p.R399W
Pat_24	Post-Resistance	BRD8	10902	37	5	137500435	137500435	Missense_Mutation	SNP	C	T	4	167	c.1699G>A	c.(1699-1701)GAT>AAT	p.D567N
Pat_24	Post-Resistance	FAM53C	51307	37	5	137682559	137682559	Missense_Mutation	SNP	G	A	4	73	c.1090G>A	c.(1090-1092)GTG>ATG	p.V364M
Pat_24	Post-Resistance	PCDHA1	56147	37	5	140167736	140167736	Missense_Mutation	SNP	C	T	75	260	c.1861C>T	c.(1861-1863)CCG>TCG	p.P621S
Pat_24	Post-Resistance	PCDHA3	56145	37	5	140182649	140182649	Missense_Mutation	SNP	C	T	39	172	c.1867C>T	c.(1867-1869)CGC>TGC	p.R623C
Pat_24	Post-Resistance	PCDHA10	56139	37	5	140236862	140236862	Missense_Mutation	SNP	G	A	76	406	c.1229G>A	c.(1228-1230)AGC>AAC	p.S410N
Pat_24	Post-Resistance	PCDHB1	29930	37	5	140431953	140431953	Missense_Mutation	SNP	G	A	8	20	c.898G>A	c.(898-900)GAA>AAA	p.E300K
Pat_24	Post-Resistance	PCDHB3	56132	37	5	140481797	140481797	Missense_Mutation	SNP	G	A	18	54	c.1564G>A	c.(1564-1566)GAG>AAG	p.E522K
Pat_24	Post-Resistance	PCDHB16	57717	37	5	140562543	140562543	Missense_Mutation	SNP	G	A	15	27	c.409G>A	c.(409-411)GAA>AAA	p.E137K
Pat_24	Post-Resistance	PCDHB11	56125	37	5	140581443	140581443	Missense_Mutation	SNP	C	T	34	153	c.2096C>T	c.(2095-2097)TCG>TTG	p.S699L
Pat_24	Post-Resistance	PCDH12	51294	37	5	141334938	141334938	Missense_Mutation	SNP	G	A	4	127	c.2479C>T	c.(2479-2481)CGT>TGT	p.R827C
Pat_24	Post-Resistance	SH3RF2	153769	37	5	145435672	145435672	Missense_Mutation	SNP	C	T	39	147	c.1451C>T	c.(1450-1452)TCC>TTC	p.S484F
Pat_24	Post-Resistance	ODZ2	57451	37	5	167631391	167631391	Missense_Mutation	SNP	G	A	14	61	c.3562G>A	c.(3562-3564)GGC>AGC	p.G1188S
Pat_24	Post-Resistance	GPRIN1	114787	37	5	176024702	176024702	Missense_Mutation	SNP	G	A	11	30	c.2134C>T	c.(2134-2136)CCC>TCC	p.P712S
Pat_24	Post-Resistance	FAM193B	54540	37	5	176952013	176952013	Missense_Mutation	SNP	A	G	6	149	c.1370T>C	c.(1369-1371)TTC>TCC	p.F457S
Pat_24	Post-Resistance	HNRNPAB	3182	37	5	177636332	177636332	Missense_Mutation	SNP	G	A	8	347	c.671G>A	c.(670-672)TGT>TAT	p.C224Y
Pat_24	Post-Resistance	HNRNPH1	3187	37	5	179043960	179043960	Splice_Site	SNP	C	G	4	65	c.1118_splice	c.e11-1	p.E373_splice
Pat_24	Post-Resistance	HIVEP1	3096	37	6	12121323	12121323	Missense_Mutation	SNP	G	A	4	108	c.1295G>A	c.(1294-1296)CGA>CAA	p.R432Q
Pat_24	Post-Resistance	BTN1A1	696	37	6	26509113	26509113	Missense_Mutation	SNP	G	A	24	33	c.1292G>A	c.(1291-1293)GGA>GAA	p.G431E
Pat_24	Post-Resistance	GABBR1	2550	37	6	29589056	29589056	Missense_Mutation	SNP	C	T	4	128	c.1145G>A	c.(1144-1146)CGT>CAT	p.R382H
Pat_24	Post-Resistance	TRIM15	89870	37	6	30131474	30131474	Missense_Mutation	SNP	C	T	28	80	c.13C>T	c.(13-15)CCG>TCG	p.P5S
Pat_24	Post-Resistance	LTB	4050	37	6	31550145	31550145	Missense_Mutation	SNP	C	T	28	74	c.50G>A	c.(49-51)GGT>GAT	p.G17D
Pat_24	Post-Resistance	C4A	720	37	6	31997489	31997489	Missense_Mutation	SNP	C	T	4	52	c.3823C>T	c.(3823-3825)CAC>TAC	p.H1275Y
Pat_24	Post-Resistance	COL11A2	1302	37	6	33137639	33137639	Missense_Mutation	SNP	G	A	4	176	c.3659C>T	c.(3658-3660)TCT>TTT	p.S1220F
Pat_24	Post-Resistance	SLC39A7	7922	37	6	33169579	33169579	Missense_Mutation	SNP	C	T	4	132	c.469C>T	c.(469-471)CCC>TCC	p.P157S
Pat_24	Post-Resistance	IP6K3	117283	37	6	33690697	33690697	Missense_Mutation	SNP	G	A	23	139	c.1033C>T	c.(1033-1035)CCT>TCT	p.P345S
Pat_24	Post-Resistance	CPNE5	57699	37	6	36716016	36716016	Missense_Mutation	SNP	C	T	151	316	c.1000G>A	c.(1000-1002)GAT>AAT	p.D334N
Pat_24	Post-Resistance	DNAH8	1769	37	6	38867551	38867551	Splice_Site	SNP	G	A	25	56	c.8413_splice	c.e60-1	p.I2805_splice
Pat_24	Post-Resistance	TFEB	7942	37	6	41652383	41652383	Missense_Mutation	SNP	C	T	4	174	c.1385G>A	c.(1384-1386)AGC>AAC	p.S462N
Pat_24	Post-Resistance	SLC35B2	347734	37	6	44222697	44222697	Missense_Mutation	SNP	C	T	6	133	c.1045G>A	c.(1045-1047)GCA>ACA	p.A349T

Pat_24	Post-Resistance	TCTE1	202500	37	6	44250280	44250280	Missense_Mutation	SNP	C	T	65	117	c.863G>A	c.(862-864)CGA>CAA	p.R288Q
Pat_24	Post-Resistance	TINAG	27283	37	6	54254619	54254619	Missense_Mutation	SNP	G	A	37	208	c.1327G>A	c.(1327-1329)GGA>AGA	p.G443R
Pat_24	Post-Resistance	FAM83B	222584	37	6	54735052	54735052	Missense_Mutation	SNP	C	T	47	150	c.8C>T	c.(7-9)ACC>ATC	p.T3I
Pat_24	Post-Resistance	FAM83B	222584	37	6	54804664	54804664	Missense_Mutation	SNP	G	T	24	121	c.895G>T	c.(895-897)GCC>TCC	p.A299S
Pat_24	Post-Resistance	FAM83B	222584	37	6	54806252	54806252	Missense_Mutation	SNP	C	T	6	33	c.2483C>T	c.(2482-2484)CCT>CTT	p.P828L
Pat_24	Post-Resistance	ZNF451	26036	37	6	56999546	56999546	Missense_Mutation	SNP	G	A	4	118	c.580G>A	c.(580-582)GAT>AAT	p.D194N
Pat_24	Post-Resistance	KCNQ5	56479	37	6	73904174	73904174	Splice_Site	SNP	G	A	17	56	c.1837_splice	c.e14-1	p.V613_splice
Pat_24	Post-Resistance	MTO1	25821	37	6	74210376	74210376	Missense_Mutation	SNP	G	A	4	186	c.2072G>A	c.(2071-2073)CGA>CAA	p.R691Q
Pat_24	Post-Resistance	COL12A1	1303	37	6	75875427	75875427	Missense_Mutation	SNP	A	C	80	170	c.2779T>G	c.(2779-2781)TCT>GCT	p.S927A
Pat_24	Post-Resistance	IMPG1	3617	37	6	76660307	76660307	Missense_Mutation	SNP	C	T	11	29	c.1796G>A	c.(1795-1797)CGA>CAA	p.R599Q
Pat_24	Post-Resistance	TPBG	7162	37	6	83074982	83074982	Missense_Mutation	SNP	C	A	4	76	c.304C>A	c.(304-306)CAG>AAG	p.Q102K
Pat_24	Post-Resistance	PRSS35	167681	37	6	84233702	84233702	Missense_Mutation	SNP	G	A	5	105	c.542G>A	c.(541-543)AGT>AAT	p.S181N
Pat_24	Post-Resistance	NT5E	4907	37	6	86159912	86159912	Missense_Mutation	SNP	G	A	3	20	c.55G>A	c.(55-57)GTG>ATG	p.V19M
Pat_24	Post-Resistance	RFX6	222546	37	6	117240317	117240317	Missense_Mutation	SNP	G	A	4	38	c.1040G>A	c.(1039-1041)AGA>AAA	p.R347K
Pat_24	Post-Resistance	SERINC1	57515	37	6	122768144	122768144	Missense_Mutation	SNP	C	T	3	32	c.1001G>A	c.(1000-1002)CGT>CAT	p.R334H
Pat_24	Post-Resistance	TPD52L1	7164	37	6	125583992	125583992	Missense_Mutation	SNP	G	A	4	138	c.499G>A	c.(499-501)GGT>AGT	p.G167S
Pat_24	Post-Resistance	SLC2A12	154091	37	6	134350082	134350082	Missense_Mutation	SNP	T	C	5	104	c.881A>G	c.(880-882)CAA>CGA	p.Q294R
Pat_24	Post-Resistance	AKAP12	9590	37	6	151674214	151674214	Missense_Mutation	SNP	G	A	4	123	c.4688G>A	c.(4687-4689)CGT>CAT	p.R1563H
Pat_24	Post-Resistance	SYNE1	23345	37	6	152651941	152651941	Nonsense_Mutation	SNP	G	A	4	193	c.13879C>T	c.(13879-13881)CAG>TAG	p.Q4627*
Pat_24	Post-Resistance	FNDC1	84624	37	6	159644568	159644568	Missense_Mutation	SNP	G	A	8	14	c.775G>A	c.(775-777)GAA>AAA	p.E259K
Pat_24	Post-Resistance	LPA	4018	37	6	160961211	160961211	Missense_Mutation	SNP	A	G	3	56	c.5599T>C	c.(5599-5601)TCA>CCA	p.S1867P
Pat_24	Post-Resistance	MLLT4	4301	37	6	168352709	168352709	Missense_Mutation	SNP	G	A	3	33	c.4651G>A	c.(4651-4653)GAG>AAG	p.E1551K
Pat_24	Post-Resistance	WDR27	253769	37	6	170059581	170059581	Missense_Mutation	SNP	G	A	3	21	c.1163C>T	c.(1162-1164)TCG>TTG	p.S388L
Pat_24	Post-Resistance	INTS1	26173	37	7	1524973	1524973	Missense_Mutation	SNP	G	A	6	268	c.3109C>T	c.(3109-3111)CCT>TCT	p.P1037S
Pat_24	Post-Resistance	FSCN1	6624	37	7	5643541	5643541	Missense_Mutation	SNP	G	A	30	122	c.1159G>A	c.(1159-1161)GTG>ATG	p.V387M
Pat_24	Post-Resistance	ABCB5	340273	37	7	20738102	20738102	Missense_Mutation	SNP	G	A	21	16	c.748G>A	c.(748-750)GGG>AGG	p.G250R
Pat_24	Post-Resistance	DNAH11	8701	37	7	21600746	21600746	Missense_Mutation	SNP	T	C	6	23	c.940T>C	c.(940-942)TAT>CAT	p.Y314H
Pat_24	Post-Resistance	STK31	56164	37	7	23794043	23794043	Missense_Mutation	SNP	T	C	149	160	c.1243T>C	c.(1243-1245)TGG>CGG	p.W415R
Pat_24	Post-Resistance	GARS	2617	37	7	30651795	30651795	Missense_Mutation	SNP	C	T	4	91	c.965C>T	c.(964-966)GCT>GTT	p.A322V
Pat_24	Post-Resistance	KIAA0895	23366	37	7	36396726	36396726	Nonsense_Mutation	SNP	T	A	17	84	c.652A>T	c.(652-654)AAG>TAG	p.K218*
Pat_24	Post-Resistance	UBE2D4	51619	37	7	43982601	43982601	Missense_Mutation	SNP	C	T	82	114	c.169C>T	c.(169-171)CCT>TCT	p.P57S
Pat_24	Post-Resistance	14-Sep	346288	37	7	55886880	55886880	Missense_Mutation	SNP	C	T	4	14	c.757G>A	c.(757-759)GAA>AAA	p.E253K
Pat_24	Post-Resistance	ZNF479	90827	37	7	57187809	57187809	Missense_Mutation	SNP	T	G	16	109	c.1313A>C	c.(1312-1314)AAA>ACA	p.K438T
Pat_24	Post-Resistance	ZNF117	51351	37	7	64439050	64439050	Missense_Mutation	SNP	C	G	4	202	c.899G>C	c.(898-900)AGT>ACT	p.S300T
Pat_24	Post-Resistance	WBSCR17	64409	37	7	71130513	71130513	Missense_Mutation	SNP	C	T	88	64	c.1198C>T	c.(1198-1200)CGC>TGC	p.R400C
Pat_24	Post-Resistance	GTF2IRD1	9569	37	7	73933956	73933956	Missense_Mutation	SNP	C	T	4	52	c.823C>T	c.(823-825)CCT>TCT	p.P275S
Pat_24	Post-Resistance	PCLO	27445	37	7	82579646	82579646	Nonsense_Mutation	SNP	G	A	27	42	c.10258C>T	c.(10258-10260)CGA>TGA	p.R3420*
Pat_24	Post-Resistance	PCLO	27445	37	7	82784980	82784980	Missense_Mutation	SNP	G	A	13	22	c.977C>T	c.(976-978)CCT>CTT	p.P326L
Pat_24	Post-Resistance	ASNS	440	37	7	97482657	97482657	Missense_Mutation	SNP	G	A	29	72	c.1280C>T	c.(1279-1281)TCC>TTC	p.S427F
Pat_24	Post-Resistance	LAMB4	22798	37	7	107706339	107706339	Missense_Mutation	SNP	G	A	17	249	c.2704C>T	c.(2704-2706)CCT>TCT	p.P902S
Pat_24	Post-Resistance	CFTR	1080	37	7	117227866	117227866	Missense_Mutation	SNP	G	A	24	119	c.1658G>A	c.(1657-1659)CGA>CAA	p.R553Q
Pat_24	Post-Resistance	PTPRZ1	5803	37	7	121652413	121652413	Missense_Mutation	SNP	C	T	12	61	c.3313C>T	c.(3313-3315)CAT>TAT	p.H1105Y
Pat_24	Post-Resistance	ASB15	142685	37	7	123254602	123254602	Missense_Mutation	SNP	G	A	84	492	c.46G>A	c.(46-48)GAT>AAT	p.D16N
Pat_24	Post-Resistance	LOC407835	407835	37	7	128766867	128766867	Missense_Mutation	SNP	G	A	17	17	c.296G>A	c.(295-297)AGG>AAG	p.R99K
Pat_24	Post-Resistance	CALD1	800	37	7	134620439	134620439	Missense_Mutation	SNP	G	A	2	3	c.1309G>A	c.(1309-1311)GGA>AGA	p.G437R
Pat_24	Post-Resistance	PARP12	64761	37	7	139757737	139757737	Nonsense_Mutation	SNP	G	A	30	182	c.424C>T	c.(424-426)CAA>TAA	p.Q142*
Pat_24	Post-Resistance	BRAF	673	37	7	140453136	140453137	Missense_Mutation	DNP	AC	TT	51	75	c.1798_1799GT>A	c.(1798-1800)GTG>AAG	p.V600K

Pat_24	Post-Resistance	MGAM	8972	37	7	141731561	141731561	Missense_Mutation	SNP	C	T	19	220	c.1552C>T	c.(1552-1554)CAC>TAC	p.H518Y
Pat_24	Post-Resistance	SSPO	23145	37	7	149483200	149483200	Missense_Mutation	SNP	G	A	4	47	c.3268G>A	c.(3268-3270)GTG>ATG	p.V1090M
Pat_24	Post-Resistance	TUSC3	7991	37	8	15519763	15519763	Missense_Mutation	SNP	G	T	34	212	c.666G>T	c.(664-666)TTG>TTT	p.L222F
Pat_24	Post-Resistance	LGI3	203190	37	8	22006139	22006139	Missense_Mutation	SNP	C	T	4	124	c.1181G>A	c.(1180-1182)AGC>AAC	p.S394N
Pat_24	Post-Resistance	ADAM28	10863	37	8	24187570	24187570	Missense_Mutation	SNP	C	T	24	84	c.1045C>T	c.(1045-1047)CAT>TAT	p.H349Y
Pat_24	Post-Resistance	NEFM	4741	37	8	24775894	24775894	Missense_Mutation	SNP	G	T	6	17	c.2526G>T	c.(2524-2526)AAG>AAT	p.K842N
Pat_24	Post-Resistance	KCNU1	157855	37	8	36793199	36793199	Missense_Mutation	SNP	G	A	34	143	c.3211G>A	c.(3211-3213)GAC>AAC	p.D1071N
Pat_24	Post-Resistance	LETM2	137994	37	8	38258458	38258458	Missense_Mutation	SNP	C	T	56	200	c.730C>T	c.(730-732)CGC>TGC	p.R244C
Pat_24	Post-Resistance	IKBKB	3551	37	8	42175254	42175254	Missense_Mutation	SNP	C	T	8	66	c.1205C>T	c.(1204-1206)TCC>TTC	p.S402F
Pat_24	Post-Resistance	CHRNA6	8973	37	8	42611837	42611837	Missense_Mutation	SNP	G	A	8	70	c.505C>T	c.(505-507)CAT>TAT	p.H169Y
Pat_24	Post-Resistance	NCOA2	10499	37	8	71037031	71037031	Missense_Mutation	SNP	C	T	4	173	c.3986G>A	c.(3985-3987)CGA>CAA	p.R1329Q
Pat_24	Post-Resistance	OXR1	55074	37	8	107752610	107752610	Missense_Mutation	SNP	T	C	4	126	c.2206T>C	c.(2206-2208)TGG>CGG	p.W736R
Pat_24	Post-Resistance	SAMD12	401474	37	8	119391770	119391770	Missense_Mutation	SNP	C	T	11	81	c.492G>A	c.(490-492)ATG>ATA	p.M164I
Pat_24	Post-Resistance	TAF2	6873	37	8	120814047	120814047	Missense_Mutation	SNP	G	A	19	99	c.779C>T	c.(778-780)CCA>CTA	p.P260L
Pat_24	Post-Resistance	KCNQ3	3786	37	8	133142113	133142113	Missense_Mutation	SNP	T	G	100	213	c.2015A>C	c.(2014-2016)AAG>ACG	p.K672T
Pat_24	Post-Resistance	FAM135B	51059	37	8	139164716	139164716	Missense_Mutation	SNP	C	T	30	105	c.2002G>A	c.(2002-2004)GAA>AAA	p.E668K
Pat_24	Post-Resistance	CYP11B1	1584	37	8	143956699	143956699	Missense_Mutation	SNP	C	T	10	47	c.1151G>A	c.(1150-1152)CGA>CAA	p.R384Q
Pat_24	Post-Resistance	OPLAH	26873	37	8	145113718	145113718	Missense_Mutation	SNP	C	T	3	37	c.545G>A	c.(544-546)CGA>CAA	p.R182Q
Pat_24	Post-Resistance	ADCK5	203054	37	8	145616368	145616368	Missense_Mutation	SNP	T	C	4	129	c.578T>C	c.(577-579)CTC>CCC	p.L193P
Pat_24	Post-Resistance	APTX	54840	37	9	32989824	32989824	Missense_Mutation	SNP	C	A	4	96	c.66G>T	c.(64-66)TTG>TTT	p.L22F
Pat_24	Post-Resistance	UBAP2	55833	37	9	33922757	33922757	Missense_Mutation	SNP	G	T	29	62	c.3192C>A	c.(3190-3192)TTC>TTA	p.F1064L
Pat_24	Post-Resistance	RUSC2	9853	37	9	35561251	35561251	Nonsense_Mutation	SNP	C	T	4	100	c.4423C>T	c.(4423-4425)CGA>TGA	p.R1475*
Pat_24	Post-Resistance	APBA1	320	37	9	72131401	72131402	Missense_Mutation	DNP	GG	AA	6	40	c.725_726CC>TT	c.(724-726)TCC>TTT	p.S242F
Pat_24	Post-Resistance	SMC5	23137	37	9	72893497	72893497	Missense_Mutation	SNP	C	T	24	21	c.634C>T	c.(634-636)CAC>TAC	p.H212Y
Pat_24	Post-Resistance	TRPM6	140803	37	9	77435255	77435255	Nonsense_Mutation	SNP	G	A	28	63	c.1099C>T	c.(1099-1101)CAA>TAA	p.Q367*
Pat_24	Post-Resistance	HSD17B3	3293	37	9	99013756	99013756	Missense_Mutation	SNP	C	T	14	110	c.397G>A	c.(397-399)GGA>AGA	p.G133R
Pat_24	Post-Resistance	NR4A3	8013	37	9	102595600	102595600	Missense_Mutation	SNP	G	A	4	82	c.1118G>A	c.(1117-1119)CGT>CAT	p.R373H
Pat_24	Post-Resistance	BAAT	570	37	9	104133665	104133665	Missense_Mutation	SNP	G	A	61	72	c.22C>T	c.(22-24)CCT>TCT	p.P8S
Pat_24	Post-Resistance	ZNF462	58499	37	9	109686821	109686821	Missense_Mutation	SNP	G	A	5	81	c.628G>A	c.(628-630)GTA>ATA	p.V210I
Pat_24	Post-Resistance	C9orf6	54942	37	9	111701857	111701857	Missense_Mutation	SNP	T	A	4	41	c.437T>A	c.(436-438)GTG>GAG	p.V146E
Pat_24	Post-Resistance	C9orf6	54942	37	9	111701884	111701884	Missense_Mutation	SNP	G	A	4	51	c.464G>A	c.(463-465)AGC>AAC	p.S155N
Pat_24	Post-Resistance	SVEP1	79987	37	9	113170069	113170069	Missense_Mutation	SNP	G	A	40	66	c.7811C>T	c.(7810-7812)TCC>TTC	p.S2604F
Pat_24	Post-Resistance	KIAA0368	23392	37	9	114131428	114131428	Missense_Mutation	SNP	C	T	2	4	c.5534G>A	c.(5533-5535)CGG>CAG	p.R1845Q
Pat_24	Post-Resistance	C9orf84	158401	37	9	114454492	114454492	Nonsense_Mutation	SNP	C	T	25	47	c.3573G>A	c.(3571-3573)TGG>TGA	p.W1191*
Pat_24	Post-Resistance	AKNA	80709	37	9	117103936	117103936	Missense_Mutation	SNP	G	A	4	129	c.3944C>T	c.(3943-3945)GCG>GTG	p.A1315V
Pat_24	Post-Resistance	TRIM32	22954	37	9	119461183	119461183	Missense_Mutation	SNP	G	A	4	171	c.1162G>A	c.(1162-1164)GCT>ACT	p.A388T
Pat_24	Post-Resistance	PTGS1	5742	37	9	125154705	125154705	Missense_Mutation	SNP	C	A	4	113	c.1682C>A	c.(1681-1683)GCC>GAC	p.A561D
Pat_24	Post-Resistance	OR1L3	26735	37	9	125438296	125438296	Missense_Mutation	SNP	G	A	28	25	c.888G>A	c.(886-888)ATG>ATA	p.M296I
Pat_24	Post-Resistance	RC3H2	54542	37	9	125652627	125652627	Missense_Mutation	SNP	C	T	3	41	c.547G>A	c.(547-549)GCT>ACT	p.A183T
Pat_24	Post-Resistance	PPP6C	5537	37	9	127912080	127912080	Missense_Mutation	SNP	G	A	38	47	c.790C>T	c.(790-792)CGT>TGT	p.R264C
Pat_24	Post-Resistance	GAPVD1	26130	37	9	128083731	128083731	Missense_Mutation	SNP	C	T	24	37	c.1622C>T	c.(1621-1623)TCG>TTG	p.S541L
Pat_24	Post-Resistance	ABL1	25	37	9	133750433	133750433	Missense_Mutation	SNP	G	A	4	69	c.1264G>A	c.(1264-1266)GTC>ATC	p.V422I
Pat_24	Post-Resistance	TSC1	7248	37	9	135772721	135772721	Missense_Mutation	SNP	T	C	3	132	c.2825A>G	c.(2824-2826)CAG>CGG	p.Q942R
Pat_24	Post-Resistance	ZMYND19	116225	37	9	140477021	140477021	Nonsense_Mutation	SNP	G	A	4	177	c.658C>T	c.(658-660)CAG>TAG	p.Q220*
Pat_24	Post-Resistance	CACNA1B	774	37	9	141010104	141010104	Missense_Mutation	SNP	C	T	14	32	c.5750C>T	c.(5749-5751)TCC>TTC	p.S1917F
Pat_24	Post-Resistance	PLCXD1	55344	37	X	205453	205453	Missense_Mutation	SNP	G	A	7	371	c.181G>A	c.(181-183)GAG>AAG	p.E61K
Pat_24	Post-Resistance	PLCXD1	55344	37	X	205496	205496	Missense_Mutation	SNP	G	A	8	216	c.224G>A	c.(223-225)TGC>TAC	p.C75Y

Pat_24	Post-Resistance	MXRA5	25878	37	X	3228314	3228314	Missense_Mutation	SNP	G	A	30	38	c.7930C>T	c.(7930-7932)CAT>TAT	p.H2644Y
Pat_24	Post-Resistance	TLR7	51284	37	X	12903670	12903670	Missense_Mutation	SNP	C	T	8	36	c.43C>T	c.(43-45)CTT>TTT	p.L15F
Pat_24	Post-Resistance	ASB9	140462	37	X	15268684	15268684	Missense_Mutation	SNP	G	A	4	64	c.436C>T	c.(436-438)CAC>TAC	p.H146Y
Pat_24	Post-Resistance	ASB11	140456	37	X	15301641	15301641	Missense_Mutation	SNP	G	A	136	159	c.958C>T	c.(958-960)CTC>TTC	p.L320F
Pat_24	Post-Resistance	CDKL5	6792	37	X	18593569	18593569	Missense_Mutation	SNP	C	T	4	179	c.241C>T	c.(241-243)CGG>TGG	p.R81W
Pat_24	Post-Resistance	SSX6	280657	37	X	47969921	47969921	Missense_Mutation	SNP	T	G	5	54	c.124T>G	c.(124-126)TTC>GTC	p.F42V
Pat_24	Post-Resistance	HUWE1	10075	37	X	53587269	53587269	Missense_Mutation	SNP	A	T	4	68	c.7616T>A	c.(7615-7617)CTC>CAC	p.L2539H
Pat_24	Post-Resistance	ITIH5L	347365	37	X	54785245	54785245	Missense_Mutation	SNP	C	T	32	24	c.1262G>A	c.(1261-1263)AGG>AAG	p.R421K
Pat_24	Post-Resistance	ZMYM3	9203	37	X	70464284	70464284	Missense_Mutation	SNP	G	A	3	26	c.3148C>T	c.(3148-3150)CGG>TGG	p.R1050W
Pat_24	Post-Resistance	ACRC	93953	37	X	70823578	70823578	Missense_Mutation	SNP	G	A	4	124	c.451G>A	c.(451-453)GAC>AAC	p.D151N
Pat_24	Post-Resistance	ACRC	93953	37	X	70823920	70823920	Missense_Mutation	SNP	C	T	6	45	c.793C>T	c.(793-795)CCC>TCC	p.P265S
Pat_24	Post-Resistance	ATRX	546	37	X	76813014	76813014	Missense_Mutation	SNP	C	T	4	84	c.6607G>A	c.(6607-6609)GAG>AAG	p.E2203K
Pat_24	Post-Resistance	NOX1	27035	37	X	100117242	100117242	Missense_Mutation	SNP	C	T	5	224	c.722G>A	c.(721-723)CGC>CAC	p.R241H
Pat_24	Post-Resistance	COL4A6	1288	37	X	107431220	107431220	Missense_Mutation	SNP	C	T	9	17	c.1628G>A	c.(1627-1629)GGA>GAA	p.G543E
Pat_24	Post-Resistance	ZCCHC16	340595	37	X	111697979	111697979	Missense_Mutation	SNP	C	T	46	54	c.23C>T	c.(22-24)TCA>TTA	p.S8L
Pat_24	Post-Resistance	ZCCHC12	170261	37	X	117959245	117959245	Missense_Mutation	SNP	G	A	3	79	c.38G>A	c.(37-39)CGG>CAG	p.R13Q
Pat_24	Post-Resistance	SAGE1	55511	37	X	134991035	134991035	Missense_Mutation	SNP	C	T	4	141	c.1454C>T	c.(1453-1455)ACT>ATT	p.T485I
Pat_24	Post-Resistance	FMR1	2332	37	X	147030296	147030296	Missense_Mutation	SNP	C	T	53	64	c.1831C>T	c.(1831-1833)CGT>TGT	p.R611C
Pat_24	Post-Resistance	PCDH11Y	83259	37	Y	4968692	4968692	Missense_Mutation	SNP	G	T	4	127	c.3073G>T	c.(3073-3075)GAC>TAC	p.D1025Y
Pat_27	Post-Resistance	KIAA1751	85452	37	1	1896422	1896422	Missense_Mutation	SNP	G	A	3	55	c.1480C>T	c.(1480-1482)CGG>TGG	p.R494W
Pat_27	Post-Resistance	CAMTA1	23261	37	1	7723778	7723778	Missense_Mutation	SNP	G	A	7	192	c.1171G>A	c.(1171-1173)GGG>AGG	p.G391R
Pat_27	Post-Resistance	RAP1GAP	5909	37	1	21940167	21940167	Missense_Mutation	SNP	G	A	5	230	c.428C>T	c.(427-429)CCC>CTC	p.P143L
Pat_27	Post-Resistance	SRRM1	10250	37	1	24973198	24973198	Missense_Mutation	SNP	G	T	5	173	c.152G>T	c.(151-153)TGG>TTG	p.W51L
Pat_27	Post-Resistance	FGR	2268	37	1	27939558	27939558	Missense_Mutation	SNP	G	T	8	207	c.1457C>A	c.(1456-1458)TCC>TAC	p.S486Y
Pat_27	Post-Resistance	XKR8	55113	37	1	28293629	28293629	Missense_Mutation	SNP	C	T	6	235	c.1106C>T	c.(1105-1107)CCT>CTT	p.P369L
Pat_27	Post-Resistance	TINAGL1	64129	37	1	32051422	32051422	Missense_Mutation	SNP	C	T	3	53	c.1162C>T	c.(1162-1164)CTT>TTT	p.L388F
Pat_27	Post-Resistance	MAST2	23139	37	1	46501175	46501175	Missense_Mutation	SNP	C	T	7	219	c.4834C>T	c.(4834-4836)CCT>TCT	p.P1612S
Pat_27	Post-Resistance	BEND5	79656	37	1	49224669	49224669	Missense_Mutation	SNP	C	G	7	325	c.648G>C	c.(646-648)AAG>AAC	p.K216N
Pat_27	Post-Resistance	SERBP1	26135	37	1	67895734	67895735	Missense_Mutation	DNP	GG	AA	10	291	c.249_250CC>TT	247-252)CCCCCC>CCTT	p.P84S
Pat_27	Post-Resistance	GBP1	2633	37	1	89523902	89523902	Missense_Mutation	SNP	T	C	8	448	c.647A>G	c.(646-648)GAT>GGT	p.D216G
Pat_27	Post-Resistance	PDE4DIP	9659	37	1	144882859	144882859	Missense_Mutation	SNP	G	A	17	796	c.3160C>T	c.(3160-3162)CTT>TTT	p.L1054F
Pat_27	Post-Resistance	ANKRD35	148741	37	1	145562242	145562242	Missense_Mutation	SNP	G	A	7	169	c.1930G>A	c.(1930-1932)GAG>AAG	p.E644K
Pat_27	Post-Resistance	SNX27	81609	37	1	151665915	151665915	Nonsense_Mutation	SNP	G	T	5	273	c.1534G>T	c.(1534-1536)GAG>TAG	p.E512*
Pat_27	Post-Resistance	KPRP	448834	37	1	152733059	152733059	Missense_Mutation	SNP	C	T	9	203	c.995C>T	c.(994-996)CCG>CTG	p.P332L
Pat_27	Post-Resistance	PGLYRP3	114771	37	1	153276464	153276464	Missense_Mutation	SNP	G	A	6	125	c.398C>T	c.(397-399)GCC>GTC	p.A133V
Pat_27	Post-Resistance	ATP8B2	57198	37	1	154316912	154316912	Missense_Mutation	SNP	G	A	24	472	c.2176G>A	c.(2176-2178)GAT>AAT	p.D726N
Pat_27	Post-Resistance	SLAMF9	89886	37	1	159922198	159922198	Missense_Mutation	SNP	C	T	16	449	c.518G>A	c.(517-519)GGG>GAG	p.G173E
Pat_27	Post-Resistance	ARPC5	10092	37	1	183599639	183599639	Missense_Mutation	SNP	G	A	10	172	c.350C>T	c.(349-351)CCG>CTG	p.P117L
Pat_27	Post-Resistance	FAM129A	116496	37	1	184853830	184853830	Missense_Mutation	SNP	C	T	7	163	c.538G>A	c.(538-540)GAG>AAG	p.E180K
Pat_27	Post-Resistance	MFSD4	148808	37	1	205555175	205555175	Missense_Mutation	SNP	C	T	7	101	c.989C>T	c.(988-990)GCC>GTC	p.A330V
Pat_27	Post-Resistance	KCNK2	3776	37	1	215408276	215408276	Missense_Mutation	SNP	C	T	4	131	c.1069C>T	c.(1069-1071)CGG>TGG	p.R357W
Pat_27	Post-Resistance	USH2A	7399	37	1	215955491	215955491	Missense_Mutation	SNP	G	A	7	253	c.10633C>T	.(10633-10635)CGG>TG	p.R3545W
Pat_27	Post-Resistance	MIA3	375056	37	1	222828056	222828056	Missense_Mutation	SNP	G	A	11	333	c.4528G>A	c.(4528-4530)GAA>AAA	p.E1510K
Pat_27	Post-Resistance	OR13G1	441933	37	1	247836088	247836088	Missense_Mutation	SNP	C	T	5	103	c.256G>A	c.(256-258)GAA>AAA	p.E86K
Pat_27	Post-Resistance	ITIH2	3698	37	10	7747116	7747116	Nonsense_Mutation	SNP	C	T	11	242	c.130C>T	c.(130-132)CAA>TAA	p.Q44*
Pat_27	Post-Resistance	MBL2	4153	37	10	54527986	54527986	Missense_Mutation	SNP	C	T	22	858	c.658G>A	c.(658-660)GAA>AAA	p.E220K
Pat_27	Post-Resistance	CPN1	1369	37	10	101835676	101835676	Missense_Mutation	SNP	C	G	3	118	c.412G>C	c.(412-414)GCT>CCT	p.A138P

Pat_27	Post-Resistance	OR52K2	119774	37	11	4470906	4470906	Missense_Mutation	SNP	G	A	6	262	c.337G>A	c.(337-339)GAG>AAG	p.E113K
Pat_27	Post-Resistance	MRGPRX2	117194	37	11	19077943	19077943	Missense_Mutation	SNP	G	A	24	772	c.7C>T	c.(7-9)CCA>TCA	p.P3S
Pat_27	Post-Resistance	DEPDC7	91614	37	11	33053923	33053923	Missense_Mutation	SNP	C	T	6	133	c.1036C>T	c.(1036-1038)CTT>TTT	p.L346F
Pat_27	Post-Resistance	SLC1A2	6506	37	11	35287201	35287201	Missense_Mutation	SNP	C	T	10	432	c.1526G>A	c.(1525-1527)CGA>CAA	p.R509Q
Pat_27	Post-Resistance	OR4A15	81328	37	11	55135952	55135952	Missense_Mutation	SNP	G	A	10	228	c.593G>A	c.(592-594)GGA>GAA	p.G198E
Pat_27	Post-Resistance	OR5B17	219965	37	11	58125958	58125958	Missense_Mutation	SNP	C	G	4	147	c.585G>C	c.(583-585)TTG>TTC	p.L195F
Pat_27	Post-Resistance	POU2F3	25833	37	11	120169067	120169067	Nonsense_Mutation	SNP	C	T	9	660	c.226C>T	c.(226-228)CAA>TAA	p.Q76*
Pat_27	Post-Resistance	PRB3	5544	37	12	11420296	11420296	Missense_Mutation	SNP	C	A	13	722	c.760G>T	c.(760-762)GGT>TGT	p.G254C
Pat_27	Post-Resistance	ENDOU	8909	37	12	48110749	48110749	Missense_Mutation	SNP	C	T	11	658	c.475G>A	c.(475-477)GAA>AAA	p.E159K
Pat_27	Post-Resistance	KRT75	9119	37	12	52827961	52827961	Missense_Mutation	SNP	C	T	8	185	c.128G>A	c.(127-129)GGG>GAG	p.G43E
Pat_27	Post-Resistance	PPP1R1A	5502	37	12	54974805	54974805	Missense_Mutation	SNP	C	T	7	323	c.433G>A	c.(433-435)GAG>AAG	p.E145K
Pat_27	Post-Resistance	NEUROD4	58158	37	12	55420971	55420971	Missense_Mutation	SNP	G	A	7	213	c.748G>A	c.(748-750)GAG>AAG	p.E250K
Pat_27	Post-Resistance	DTX1	1840	37	12	113515335	113515335	Missense_Mutation	SNP	T	G	6	282	c.366T>G	c.(364-366)GAT>GAG	p.D122E
Pat_27	Post-Resistance	NOS1	4842	37	12	117691515	117691515	Missense_Mutation	SNP	G	A	9	184	c.2576C>T	c.(2575-2577)TCC>TTC	p.S859F
Pat_27	Post-Resistance	RPL21	6144	37	13	27827918	27827918	Missense_Mutation	SNP	C	T	5	205	c.5C>T	c.(4-6)ACG>ATG	p.T2M
Pat_27	Post-Resistance	NDRG2	57447	37	14	21490649	21490649	Missense_Mutation	SNP	G	A	4	72	c.125C>T	c.(124-126)TCT>TTT	p.S42F
Pat_27	Post-Resistance	KIAA1409	57578	37	14	94060164	94060164	Nonsense_Mutation	SNP	G	A	7	297	c.2640G>A	c.(2638-2640)TGG>TGA	p.W880*
Pat_27	Post-Resistance	AK7	122481	37	14	96944861	96944861	Missense_Mutation	SNP	C	T	5	309	c.1615C>T	c.(1615-1617)CCT>TCT	p.P539S
Pat_27	Post-Resistance	KIAA0284	283638	37	14	105349566	105349566	Missense_Mutation	SNP	G	A	12	422	c.772G>A	c.(772-774)GGA>AGA	p.G258R
Pat_27	Post-Resistance	GABRB3	2562	37	15	26812865	26812865	Missense_Mutation	SNP	A	G	4	230	c.698T>C	c.(697-699)CTG>CCG	p.L233P
Pat_27	Post-Resistance	CYP19A1	1588	37	15	51507941	51507941	Missense_Mutation	SNP	C	T	21	450	c.817G>A	c.(817-819)GAA>AAA	p.E273K
Pat_27	Post-Resistance	SCG3	29106	37	15	51991527	51991527	Missense_Mutation	SNP	G	A	16	330	c.997G>A	c.(997-999)GAA>AAA	p.E333K
Pat_27	Post-Resistance	ONECUT1	3175	37	15	53049970	53049970	Missense_Mutation	SNP	C	T	9	495	c.1180G>A	c.(1180-1182)GAT>AAT	p.D394N
Pat_27	Post-Resistance	CILP	8483	37	15	65489992	65489992	Missense_Mutation	SNP	T	C	8	174	c.2632A>G	c.(2632-2634)ATG>GTG	p.M878V
Pat_27	Post-Resistance	PTPN9	5780	37	15	75798062	75798062	Missense_Mutation	SNP	C	T	5	326	c.922G>A	c.(922-924)GAA>AAA	p.E308K
Pat_27	Post-Resistance	TBC1D2B	23102	37	15	78290635	78290635	Missense_Mutation	SNP	C	T	5	50	c.2759G>A	c.(2758-2760)CGA>CAA	p.R920Q
Pat_27	Post-Resistance	CTSH	1512	37	15	79228060	79228060	Missense_Mutation	SNP	C	A	4	135	c.226G>T	c.(226-228)GCT>TCT	p.A76S
Pat_27	Post-Resistance	NAGPA	51172	37	16	5083691	5083691	Missense_Mutation	SNP	C	T	3	36	c.125G>A	c.(124-126)CGC>CAC	p.R42H
Pat_27	Post-Resistance	SLC6A2	6530	37	16	55730201	55730201	Nonsense_Mutation	SNP	G	A	7	492	c.1212G>A	c.(1210-1212)TGG>TGA	p.W404*
Pat_27	Post-Resistance	HYDIN	54768	37	16	71218803	71218803	Missense_Mutation	SNP	C	T	8	375	c.226G>A	c.(226-228)GAA>AAA	p.E76K
Pat_27	Post-Resistance	WDR59	79726	37	16	74908231	74908231	Missense_Mutation	SNP	G	A	8	195	c.2801C>T	c.(2800-2802)TCG>TTG	p.S934L
Pat_27	Post-Resistance	MBTPS1	8720	37	16	84092910	84092910	Missense_Mutation	SNP	G	A	7	221	c.2828C>T	c.(2827-2829)CCC>CTC	p.P943L
Pat_27	Post-Resistance	KRT15	3866	37	17	39672221	39672221	Missense_Mutation	SNP	C	T	16	648	c.942G>A	c.(940-942)ATG>ATA	p.M314I
Pat_27	Post-Resistance	KRT9	3857	37	17	39727668	39727668	Missense_Mutation	SNP	C	T	8	284	c.577G>A	c.(577-579)GGA>AGA	p.G193R
Pat_27	Post-Resistance	BZRAP1	9256	37	17	56389844	56389844	Missense_Mutation	SNP	G	A	7	261	c.2338C>T	c.(2338-2340)CCA>TCA	p.P780S
Pat_27	Post-Resistance	INTS2	57508	37	17	59955305	59955305	Missense_Mutation	SNP	C	G	15	248	c.2423G>C	c.(2422-2424)AGA>ACA	p.R808T
Pat_27	Post-Resistance	MED13	9969	37	17	60088115	60088115	Missense_Mutation	SNP	G	C	5	153	c.1763C>G	c.(1762-1764)CCT>CGT	p.P588R
Pat_27	Post-Resistance	B3GNTL1	146712	37	17	80963044	80963044	Missense_Mutation	SNP	C	T	5	261	c.451G>A	c.(451-453)GAA>AAA	p.E151K
Pat_27	Post-Resistance	POTEC	388468	37	18	14542773	14542773	Missense_Mutation	SNP	C	T	6	317	c.373G>A	c.(373-375)GAC>AAC	p.D125N
Pat_27	Post-Resistance	DSG3	1830	37	18	29041340	29041340	Missense_Mutation	SNP	C	T	7	235	c.964C>T	c.(964-966)CCT>TCT	p.P322S
Pat_27	Post-Resistance	DCC	1630	37	18	50278595	50278595	Missense_Mutation	SNP	G	A	8	211	c.263G>A	c.(262-264)AGG>AAG	p.R88K
Pat_27	Post-Resistance	DCC	1630	37	18	50994312	50994312	Missense_Mutation	SNP	C	T	14	217	c.3668C>T	c.(3667-3669)TCG>TTG	p.S1223L
Pat_27	Post-Resistance	TCF4	6925	37	18	52942893	52942894	Missense_Mutation	DNP	GG	AA	18	829	c.745_746CC>TT	c.(745-747)CCA>TTA	p.P249L
Pat_27	Post-Resistance	CD226	10666	37	18	67563144	67563144	Missense_Mutation	SNP	C	T	9	174	c.520G>A	c.(520-522)GAC>AAC	p.D174N
Pat_27	Post-Resistance	PTPRS	5802	37	19	5212059	5212059	Missense_Mutation	SNP	C	T	4	123	c.4972G>A	c.(4972-4974)GCA>ACA	p.A1658T
Pat_27	Post-Resistance	SAFB	6294	37	19	5667829	5667829	Splice_Site	SNP	A	G	4	145	c.2552_splice	c.e20-2	p.G851_splice
Pat_27	Post-Resistance	TIMM44	10469	37	19	7999041	7999041	Missense_Mutation	SNP	G	A	8	403	c.476C>T	c.(475-477)TCG>TTG	p.S159L

Pat_27	Post-Resistance	MUC16	94025	37	19	9074278	9074278	Nonsense_Mutation	SNP	G	A	18	289	c.13168C>T	c.(13168-13170)CAA>TAA	p.Q4390*
Pat_27	Post-Resistance	ZNF559	84527	37	19	9452810	9452810	Missense_Mutation	SNP	T	C	3	112	c.683T>C	c.(682-684)CTT>CCT	p.L228P
Pat_27	Post-Resistance	SYCE2	256126	37	19	13011390	13011390	Missense_Mutation	SNP	C	T	12	157	c.379G>A	c.(379-381)GAA>AAA	p.E127K
Pat_27	Post-Resistance	LPHN1	22859	37	19	14294372	14294372	Missense_Mutation	SNP	C	T	3	36	c.43G>A	c.(43-45)GCC>ACC	p.A15T
Pat_27	Post-Resistance	NOTCH3	4854	37	19	15297763	15297763	Missense_Mutation	SNP	C	G	9	141	c.1877G>C	c.(1876-1878)AGC>ACC	p.S626T
Pat_27	Post-Resistance	OR10H5	284433	37	19	15905382	15905382	Missense_Mutation	SNP	A	C	13	202	c.524A>C	c.(523-525)CAC>CCC	p.H175P
Pat_27	Post-Resistance	OR10H5	284433	37	19	15905384	15905384	Missense_Mutation	SNP	C	T	13	203	c.526C>T	c.(526-528)CAT>TAT	p.H176Y
Pat_27	Post-Resistance	GATAD2A	54815	37	19	19616218	19616218	Nonsense_Mutation	SNP	C	T	30	531	c.1837C>T	c.(1837-1839)CAG>TAG	p.Q613*
Pat_27	Post-Resistance	ZNF93	81931	37	19	20045277	20045277	Missense_Mutation	SNP	G	A	8	395	c.1513G>A	c.(1513-1515)GGA>AGA	p.G505R
Pat_27	Post-Resistance	SUPT5H	6829	37	19	39949676	39949676	Missense_Mutation	SNP	T	C	16	571	c.421T>C	c.(421-423)TAC>CAC	p.Y141H
Pat_27	Post-Resistance	FCGBP	8857	37	19	40364210	40364210	Missense_Mutation	SNP	G	A	12	95	c.14432C>T	c.(14431-14433)CCT>CTT	p.P4811L
Pat_27	Post-Resistance	CEACAM20	125931	37	19	45024526	45024526	Missense_Mutation	SNP	G	A	4	143	c.1012C>T	c.(1012-1014)CTT>TTT	p.L338F
Pat_27	Post-Resistance	NLRP7	199713	37	19	55445975	55445975	Missense_Mutation	SNP	G	T	3	71	c.2353C>A	c.(2353-2355)CTC>ATC	p.L785I
Pat_27	Post-Resistance	MSGN1	343930	37	2	17998003	17998003	Missense_Mutation	SNP	G	A	12	192	c.218G>A	c.(217-219)GGG>GAG	p.G73E
Pat_27	Post-Resistance	PUM2	23369	37	2	20478445	20478445	Missense_Mutation	SNP	G	A	12	228	c.1856C>T	c.(1855-1857)CCA>CTA	p.P619L
Pat_27	Post-Resistance	GKN1	56287	37	2	69204869	69204869	Missense_Mutation	SNP	G	A	13	338	c.209G>A	c.(208-210)GGA>GAA	p.G70E
Pat_27	Post-Resistance	EDAR	10913	37	2	109546605	109546605	Missense_Mutation	SNP	G	A	4	135	c.145C>T	c.(145-147)CCG>TCG	p.P49S
Pat_27	Post-Resistance	YSK4	80122	37	2	135741376	135741376	Missense_Mutation	SNP	C	T	8	173	c.3092G>A	c.(3091-3093)AGG>AAG	p.R1031K
Pat_27	Post-Resistance	PLA2R1	22925	37	2	160876756	160876756	Nonsense_Mutation	SNP	C	T	6	154	c.1313G>A	c.(1312-1314)TGG>TAG	p.W438*
Pat_27	Post-Resistance	XIRP2	129446	37	2	168098359	168098359	Missense_Mutation	SNP	C	T	8	335	c.1115C>T	c.(1114-1116)TCT>TTT	p.S372F
Pat_27	Post-Resistance	KLHL23	151230	37	2	170591997	170591997	Missense_Mutation	SNP	C	T	6	220	c.473C>T	c.(472-474)TCT>TTT	p.S158F
Pat_27	Post-Resistance	TTN	7273	37	2	179610734	179610734	Missense_Mutation	SNP	G	A	30	603	c.16393C>T	c.(16393-16395)CGG>TGG	p.R5465W
Pat_27	Post-Resistance	ITGA4	3676	37	2	182399598	182399598	Missense_Mutation	SNP	T	A	6	175	c.2939T>A	c.(2938-2940)ATT>AAT	p.I980N
Pat_27	Post-Resistance	COL5A2	1290	37	2	189916194	189916194	Missense_Mutation	SNP	G	A	4	44	c.2783C>T	c.(2782-2784)CCT>CTT	p.P928L
Pat_27	Post-Resistance	MSTN	2660	37	2	190922273	190922273	Missense_Mutation	SNP	C	T	5	306	c.839G>A	c.(838-840)CGA>CAA	p.R280Q
Pat_27	Post-Resistance	SPEG	10290	37	2	220355223	220355223	Missense_Mutation	SNP	G	A	3	117	c.9014G>A	c.(9013-9015)CGG>CAG	p.R3005Q
Pat_27	Post-Resistance	UGT1A9	54600	37	2	234580881	234580881	Missense_Mutation	SNP	C	A	17	293	c.301C>A	c.(301-303)CAA>AAA	p.Q101K
Pat_27	Post-Resistance	WFDC8	90199	37	20	44187548	44187548	Missense_Mutation	SNP	C	T	10	391	c.220G>A	c.(220-222)GAA>AAA	p.E74K
Pat_27	Post-Resistance	CDH4	1002	37	20	60427833	60427833	Missense_Mutation	SNP	G	A	8	209	c.756G>A	c.(754-756)ATG>ATA	p.M252I
Pat_27	Post-Resistance	LAMA5	3911	37	20	60887335	60887335	Missense_Mutation	SNP	A	G	3	46	c.9398T>C	c.(9397-9399)CTT>CCT	p.L3133P
Pat_27	Post-Resistance	TMPRSS15	5651	37	21	19701534	19701534	Missense_Mutation	SNP	C	T	11	143	c.1732G>A	c.(1732-1734)GAT>AAT	p.D578N
Pat_27	Post-Resistance	KRTAP21-2	337978	37	21	32119361	32119361	Missense_Mutation	SNP	C	T	24	803	c.160G>A	c.(160-162)GGC>AGC	p.G54S
Pat_27	Post-Resistance	TTC3	7267	37	21	38568217	38568217	Missense_Mutation	SNP	C	T	12	99	c.5459C>T	c.(5458-5460)CCT>CTT	p.P1820L
Pat_27	Post-Resistance	SH3BGR	6450	37	21	40883652	40883652	Missense_Mutation	SNP	G	A	6	186	c.670G>A	c.(670-672)GAG>AAG	p.E224K
Pat_27	Post-Resistance	KRTAP10-10	353333	37	21	46058017	46058017	Missense_Mutation	SNP	C	T	27	477	c.683C>T	c.(682-684)TCC>TTC	p.S228F
Pat_27	Post-Resistance	SGSM1	129049	37	22	25301100	25301100	Missense_Mutation	SNP	T	C	38	685	c.2929T>C	c.(2929-2931)TAT>CAT	p.Y977H
Pat_27	Post-Resistance	TUBGCP6	85378	37	22	50678729	50678729	Missense_Mutation	SNP	G	A	4	99	c.809C>T	c.(808-810)TCC>TTC	p.S270F
Pat_27	Post-Resistance	FGD5	152273	37	3	14862841	14862841	Missense_Mutation	SNP	C	T	12	843	c.2263C>T	c.(2263-2265)CCC>TCC	p.P755S
Pat_27	Post-Resistance	LAMB2	3913	37	3	49163829	49163829	Missense_Mutation	SNP	G	A	9	231	c.2120C>T	c.(2119-2121)CCC>CTC	p.P707L
Pat_27	Post-Resistance	IMPG2	50939	37	3	100949808	100949808	Missense_Mutation	SNP	G	A	14	167	c.3415C>T	c.(3415-3417)CCC>TCC	p.P1139S
Pat_27	Post-Resistance	IMPG2	50939	37	3	100949844	100949844	Missense_Mutation	SNP	G	A	24	354	c.3379C>T	c.(3379-3381)CTT>TTT	p.L1127F
Pat_27	Post-Resistance	IFT122	55764	37	3	129233345	129233345	Missense_Mutation	SNP	C	T	21	520	c.3101C>T	c.(3100-3102)TCC>TTC	p.S1034F
Pat_27	Post-Resistance	MRPL3	11222	37	3	131188584	131188584	Missense_Mutation	SNP	G	A	7	200	c.772C>T	c.(772-774)CCT>TCT	p.P258S
Pat_27	Post-Resistance	AADACL2	344752	37	3	151475197	151475197	Missense_Mutation	SNP	G	A	11	387	c.1021G>A	c.(1021-1023)GAT>AAT	p.D341N
Pat_27	Post-Resistance	MAP3K13	9175	37	3	185169106	185169106	Missense_Mutation	SNP	C	T	7	265	c.1201C>T	c.(1201-1203)CGG>TGG	p.R401W
Pat_27	Post-Resistance	MUC4	4585	37	3	195480096	195480096	Missense_Mutation	SNP	C	T	8	279	c.14950G>A	c.(14950-14952)GGG>AGG	p.G4984R
Pat_27	Post-Resistance	LMLN	89782	37	3	197762807	197762807	Nonsense_Mutation	SNP	G	A	21	379	c.1760G>A	c.(1759-1761)TGG>TAG	p.W587*

Pat_27	Post-Resistance	RGS12	6002	37	4	3415805	3415805	Missense_Mutation	SNP	C	T	4	44	c.2027C>T	c.(2026-2028)ACG>ATG	p.T676M
Pat_27	Post-Resistance	DRD5	1816	37	4	9784941	9784941	Missense_Mutation	SNP	G	A	9	219	c.1288G>A	c.(1288-1290)GAG>AAG	p.E430K
Pat_27	Post-Resistance	KLHL8	57563	37	4	88106672	88106672	Missense_Mutation	SNP	G	A	20	431	c.496C>T	c.(496-498)CCC>TCC	p.P166S
Pat_27	Post-Resistance	FAM13A	10144	37	4	89772207	89772207	Missense_Mutation	SNP	G	A	16	471	c.971C>T	c.(970-972)TCA>TTA	p.S324L
Pat_27	Post-Resistance	ADH1A	124	37	4	100203562	100203562	Missense_Mutation	SNP	C	T	30	754	c.769G>A	c.(769-771)GAA>AAA	p.E257K
Pat_27	Post-Resistance	CENPE	1062	37	4	104059536	104059536	Missense_Mutation	SNP	C	T	10	344	c.6275G>A	c.(6274-6276)AGC>AAC	p.S2092N
Pat_27	Post-Resistance	ANK2	287	37	4	114275112	114275112	Missense_Mutation	SNP	G	A	27	540	c.5338G>A	c.(5338-5340)GAA>AAA	p.E1780K
Pat_27	Post-Resistance	GUCY1A3	2982	37	4	156634496	156634496	Missense_Mutation	SNP	G	A	7	161	c.1333G>A	c.(1333-1335)GAG>AAG	p.E445K
Pat_27	Post-Resistance	GRIA2	2891	37	4	158284132	158284132	Missense_Mutation	SNP	C	T	7	457	c.2588C>T	c.(2587-2589)TCA>TTA	p.S863L
Pat_27	Post-Resistance	AGXT2	64902	37	5	35040718	35040718	Missense_Mutation	SNP	T	C	32	421	c.139A>G	c.(139-141)AGA>GGA	p.R47G
Pat_27	Post-Resistance	NIPBL	25836	37	5	37008807	37008807	Missense_Mutation	SNP	G	A	6	285	c.4403G>A	c.(4402-4404)AGG>AAG	p.R1468K
Pat_27	Post-Resistance	HCN1	348980	37	5	45262838	45262838	Missense_Mutation	SNP	C	T	9	219	c.1858G>A	c.(1858-1860)GAA>AAA	p.E620K
Pat_27	Post-Resistance	IL6ST	3572	37	5	55250646	55250646	Missense_Mutation	SNP	T	C	30	268	c.1442A>G	c.(1441-1443)TAT>TGT	p.Y481C
Pat_27	Post-Resistance	NDUFAF2	91942	37	5	60369011	60369011	Missense_Mutation	SNP	G	A	7	247	c.187G>A	c.(187-189)GAA>AAA	p.E63K
Pat_27	Post-Resistance	ZFYVE16	9765	37	5	79732983	79732983	Missense_Mutation	SNP	C	T	23	283	c.479C>T	c.(478-480)TCC>TTC	p.S160F
Pat_27	Post-Resistance	FAM170A	340069	37	5	118970375	118970375	Missense_Mutation	SNP	G	A	8	260	c.932G>A	c.(931-933)AGG>AAG	p.R311K
Pat_27	Post-Resistance	SLC27A6	28965	37	5	128368799	128368799	Missense_Mutation	SNP	G	A	8	122	c.1684G>A	c.(1684-1686)GAA>AAA	p.E562K
Pat_27	Post-Resistance	PCDHA11	56138	37	5	140250222	140250222	Missense_Mutation	SNP	G	A	36	544	c.1534G>A	c.(1534-1536)GAG>AAG	p.E512K
Pat_27	Post-Resistance	PCDHAC1	56135	37	5	140308884	140308884	Missense_Mutation	SNP	G	A	24	610	c.2407G>A	c.(2407-2409)GGG>AGG	p.G803R
Pat_27	Post-Resistance	KIF4B	285643	37	5	154394186	154394186	Missense_Mutation	SNP	G	A	8	238	c.767G>A	c.(766-768)CGT>CAT	p.R256H
Pat_27	Post-Resistance	CYFIP2	26999	37	5	156819976	156819976	Missense_Mutation	SNP	C	T	7	211	c.3730C>T	c.(3730-3732)CCC>TCC	p.P1244S
Pat_27	Post-Resistance	LTC4S	4056	37	5	179222612	179222612	Missense_Mutation	SNP	C	T	4	150	c.86C>T	c.(85-87)GCG>GTG	p.A29V
Pat_27	Post-Resistance	CCDC90A	63933	37	6	13807199	13807199	Missense_Mutation	SNP	A	C	7	424	c.493T>G	c.(493-495)TAC>GAC	p.Y165D
Pat_27	Post-Resistance	NOTCH4	4855	37	6	32188985	32188985	Missense_Mutation	SNP	G	T	4	115	c.569C>A	c.(568-570)GCC>GAC	p.A190D
Pat_27	Post-Resistance	COL11A2	1302	37	6	33137210	33137210	Missense_Mutation	SNP	G	A	4	89	c.3748C>T	c.(3748-3750)CCA>TCA	p.P1250S
Pat_27	Post-Resistance	RNF8	9025	37	6	37348960	37348960	Missense_Mutation	SNP	C	T	14	529	c.1271C>T	c.(1270-1272)TCC>TTC	p.S424F
Pat_27	Post-Resistance	UBR2	23304	37	6	42620241	42620241	Missense_Mutation	SNP	C	A	32	713	c.2627C>A	c.(2626-2628)CCG>CAG	p.P876Q
Pat_27	Post-Resistance	TINAG	27283	37	6	54212284	54212284	Missense_Mutation	SNP	G	A	7	240	c.868G>A	c.(868-870)GAT>AAT	p.D290N
Pat_27	Post-Resistance	DSE	29940	37	6	116757093	116757093	Missense_Mutation	SNP	C	T	5	191	c.1462C>T	c.(1462-1464)CCA>TCA	p.P488S
Pat_27	Post-Resistance	NCF1	653361	37	7	74193613	74193613	Nonsense_Mutation	SNP	G	A	6	160	c.240G>A	c.(238-240)TGG>TGA	p.W80*
Pat_27	Post-Resistance	PCLO	27445	37	7	82430897	82430897	Missense_Mutation	SNP	C	T	12	136	c.14944G>A	c.(14944-14946)GGA>AGA	p.G4982R
Pat_27	Post-Resistance	TRRAP	8295	37	7	98563436	98563436	Missense_Mutation	SNP	C	T	20	226	c.7073C>T	c.(7072-7074)TCA>TTA	p.S2358L
Pat_27	Post-Resistance	RELN	5649	37	7	103294556	103294556	Missense_Mutation	SNP	G	A	10	285	c.1538C>T	c.(1537-1539)TCC>TTC	p.S513F
Pat_27	Post-Resistance	SRPK2	6733	37	7	104809704	104809704	Missense_Mutation	SNP	G	A	7	131	c.205C>T	c.(205-207)CAT>TAT	p.H69Y
Pat_27	Post-Resistance	CADPS2	93664	37	7	122091475	122091475	Missense_Mutation	SNP	T	C	11	101	c.2241A>G	c.(2239-2241)ATA>ATG	p.I747M
Pat_27	Post-Resistance	SVOPL	136306	37	7	138333801	138333801	Missense_Mutation	SNP	G	A	16	161	c.616C>T	c.(616-618)CGC>TGC	p.R206C
Pat_27	Post-Resistance	BRAF	673	37	7	140453136	140453136	Missense_Mutation	SNP	A	T	19	219	c.1799T>A	c.(1798-1800)GTG>GAG	p.V600E
Pat_27	Post-Resistance	MGAM	8972	37	7	141799414	141799414	Missense_Mutation	SNP	G	T	19	403	c.5063G>T	c.(5062-5064)GGT>GTT	p.G1688V
Pat_27	Post-Resistance	KRBA1	84626	37	7	149420968	149420968	Missense_Mutation	SNP	A	G	3	85	c.916A>G	c.(916-918)AGG>GGG	p.R306G
Pat_27	Post-Resistance	C8orf79	57604	37	8	12879537	12879537	Missense_Mutation	SNP	A	G	3	67	c.1349A>G	c.(1348-1350)AAG>AGG	p.K450R
Pat_27	Post-Resistance	ADAM7	8756	37	8	24358371	24358371	Missense_Mutation	SNP	C	T	16	432	c.2071C>T	c.(2071-2073)CGT>TGT	p.R691C
Pat_27	Post-Resistance	STAR	6770	37	8	38003511	38003511	Missense_Mutation	SNP	C	T	7	201	c.566G>A	c.(565-567)GGG>GAG	p.G189E
Pat_27	Post-Resistance	SLC20A2	6575	37	8	42302247	42302247	Missense_Mutation	SNP	G	A	4	99	c.647C>T	c.(646-648)GCC>GTC	p.A216V
Pat_27	Post-Resistance	RB1CC1	9821	37	8	53570221	53570221	Missense_Mutation	SNP	G	A	6	136	c.2168C>T	c.(2167-2169)TCA>TTA	p.S723L
Pat_27	Post-Resistance	ZFHX4	79776	37	8	77690475	77690475	Missense_Mutation	SNP	C	T	8	444	c.3047C>T	c.(3046-3048)CCC>CTC	p.P1016L
Pat_27	Post-Resistance	FAM83H	286077	37	8	144811394	144811394	Nonsense_Mutation	SNP	C	A	19	386	c.547G>T	c.(547-549)GAG>TAG	p.E183*
Pat_27	Post-Resistance	FREM1	158326	37	9	14770666	14770666	Missense_Mutation	SNP	C	T	5	167	c.4996G>A	c.(4996-4998)GAT>AAT	p.D1666N

Pat_27	Post-Resistance	TOMM5	401505	37	9	37592527	37592527	Missense_Mutation	SNP	C	G	10	246	c.3G>C	c.(1-3)ATG>ATC	p.M1I
Pat_27	Post-Resistance	TRPM6	140803	37	9	77377950	77377950	Missense_Mutation	SNP	C	T	7	189	c.3637G>A	c.(3637-3639)GAT>AAT	p.D1213N
Pat_27	Post-Resistance	IKBKAP	8518	37	9	111692162	111692162	Missense_Mutation	SNP	G	A	9	244	c.190C>T	c.(190-192)CCA>TCA	p.P64S
Pat_27	Post-Resistance	C9orf172	389813	37	9	139740328	139740328	Missense_Mutation	SNP	C	T	3	24	c.1462C>T	c.(1462-1464)CGG>TGG	p.R488W
Pat_27	Post-Resistance	C9orf172	389813	37	9	139740331	139740331	Missense_Mutation	SNP	C	T	3	22	c.1465C>T	c.(1465-1467)CGC>TGC	p.R489C
Pat_27	Post-Resistance	C9orf173	441476	37	9	140146901	140146901	Missense_Mutation	SNP	G	A	3	41	c.413G>A	c.(412-414)CGC>CAC	p.R138H
Pat_27	Post-Resistance	RBM10	8241	37	X	47030582	47030582	Missense_Mutation	SNP	G	T	6	67	c.357G>T	c.(355-357)GAG>GAT	p.E119D
Pat_27	Post-Resistance	PSMD10	5716	37	X	107331082	107331082	Missense_Mutation	SNP	T	C	14	200	c.361A>G	c.(361-363)ATC>GTC	p.I121V
Pat_27	Post-Resistance	GLUD2	2747	37	X	120183130	120183130	Missense_Mutation	SNP	G	A	14	172	c.1592G>A	c.(1591-1593)GGA>GAA	p.G531E
Pat_28	Post-Resistance	TNFRSF18	8784	37	1	1139283	1139284	Missense_Mutation	DNP	CC	TT	3	6	c.666_667GG>AA	664-669)GAGGAA>GAAA	p.E223K
Pat_28	Post-Resistance	PLCH2	9651	37	1	2418756	2418756	Missense_Mutation	SNP	C	T	14	26	c.1055C>T	c.(1054-1056)TCC>TTC	p.S352F
Pat_28	Post-Resistance	TAS1R1	80835	37	1	6631144	6631144	Missense_Mutation	SNP	G	A	82	102	c.367G>A	c.(367-369)GGG>AGG	p.G123R
Pat_28	Post-Resistance	ERRFI1	54206	37	1	8073403	8073403	Missense_Mutation	SNP	C	T	35	59	c.1256G>A	c.(1255-1257)GGA>GAA	p.G419E
Pat_28	Post-Resistance	RERE	473	37	1	8421339	8421339	Missense_Mutation	SNP	G	A	6	12	c.2228C>T	c.(2227-2229)GCT>GTT	p.A743V
Pat_28	Post-Resistance	SLC2A7	155184	37	1	9064917	9064917	Missense_Mutation	SNP	C	T	10	7	c.1214G>A	c.(1213-1215)AGG>AAG	p.R405K
Pat_28	Post-Resistance	KIF1B	23095	37	1	10356973	10356973	Missense_Mutation	SNP	G	A	31	62	c.1880G>A	c.(1879-1881)GGT>GAT	p.G627D
Pat_28	Post-Resistance	MASP2	10747	37	1	11097851	11097851	Missense_Mutation	SNP	G	A	21	50	c.907C>T	c.(907-909)CCG>TCG	p.P303S
Pat_28	Post-Resistance	PRAMEF1	65121	37	1	12856047	12856047	Missense_Mutation	SNP	G	A	100	473	c.1327G>A	c.(1327-1329)GAA>AAA	p.E443K
Pat_28	Post-Resistance	SPEN	23013	37	1	16199603	16199603	Missense_Mutation	SNP	G	A	24	40	c.376G>A	c.(376-378)GAA>AAA	p.E126K
Pat_28	Post-Resistance	ARHGEF19	128272	37	1	16528277	16528277	Missense_Mutation	SNP	C	T	9	22	c.2146G>A	c.(2146-2148)GAT>AAT	p.D716N
Pat_28	Post-Resistance	ARHGEF19	128272	37	1	16534552	16534552	Missense_Mutation	SNP	C	T	12	24	c.581G>A	c.(580-582)AGG>AAG	p.R194K
Pat_28	Post-Resistance	NBPF1	55672	37	1	16895655	16895655	Missense_Mutation	SNP	G	A	17	369	c.2527C>T	c.(2527-2529)CCT>TCT	p.P843S
Pat_28	Post-Resistance	MFAP2	4237	37	1	17304762	17304762	Missense_Mutation	SNP	C	T	5	5	c.7G>A	c.(7-9)GCT>ACT	p.A3T
Pat_28	Post-Resistance	TAS1R2	80834	37	1	19186064	19186064	Missense_Mutation	SNP	C	A	36	46	c.91G>T	c.(91-93)GGG>TGG	p.G31W
Pat_28	Post-Resistance	UBR4	23352	37	1	19412751	19412752	Missense_Mutation	DNP	GG	AA	45	46	14700_14701CC>	98-14703)GGCCGG>GG	p.R4901W
Pat_28	Post-Resistance	AKR7L	246181	37	1	19593864	19593864	Missense_Mutation	SNP	G	A	23	25	c.926C>T	c.(925-927)CCG>CTG	p.P309L
Pat_28	Post-Resistance	ALPL	249	37	1	21902301	21902301	Missense_Mutation	SNP	C	T	84	128	c.1073C>T	c.(1072-1074)GCC>GTC	p.A358V
Pat_28	Post-Resistance	ARID1A	8289	37	1	27099036	27099036	Missense_Mutation	SNP	G	A	34	50	c.3452G>A	c.(3451-3453)AGC>AAC	p.S1151N
Pat_28	Post-Resistance	WDTC1	23038	37	1	27631583	27631583	Missense_Mutation	SNP	G	A	35	35	c.1735G>A	c.(1735-1737)GAT>AAT	p.D579N
Pat_28	Post-Resistance	OPRD1	4985	37	1	29185531	29185531	Missense_Mutation	SNP	C	T	60	99	c.293C>T	c.(292-294)GCC>GTC	p.A98V
Pat_28	Post-Resistance	TINAGL1	64129	37	1	32049085	32049085	Missense_Mutation	SNP	C	T	9	4	c.491C>T	c.(490-492)GCC>GTC	p.A164V
Pat_28	Post-Resistance	TXLNA	200081	37	1	32646870	32646870	Missense_Mutation	SNP	G	A	17	5	c.197G>A	c.(196-198)GGG>GAG	p.G66E
Pat_28	Post-Resistance	PHC2	1912	37	1	33799887	33799887	Missense_Mutation	SNP	C	T	43	16	c.1562G>A	c.(1561-1563)GGG>GAG	p.G521E
Pat_28	Post-Resistance	CSMD2	114784	37	1	34174694	34174694	Missense_Mutation	SNP	G	A	51	24	c.3451C>T	c.(3451-3453)CTC>TTC	p.L1151F
Pat_28	Post-Resistance	KIAA0319L	79932	37	1	35972665	35972665	Missense_Mutation	SNP	G	A	56	19	c.214C>T	c.(214-216)CAC>TAC	p.H72Y
Pat_28	Post-Resistance	MKNK1	8569	37	1	47034147	47034147	Missense_Mutation	SNP	G	A	46	96	c.640C>T	c.(640-642)CCA>TCA	p.P214S
Pat_28	Post-Resistance	CYP4B1	1580	37	1	47279153	47279153	Splice_Site	SNP	G	A	19	56	c.496_splice	c.e5-1	p.D166_splice
Pat_28	Post-Resistance	PDE4B	5142	37	1	66838245	66838245	Missense_Mutation	SNP	C	T	21	4	c.2095C>T	c.(2095-2097)CAC>TAC	p.H699Y
Pat_28	Post-Resistance	SGIP1	84251	37	1	67142777	67142777	Missense_Mutation	SNP	G	A	41	16	c.737G>A	c.(736-738)GGA>GAA	p.G246E
Pat_28	Post-Resistance	SGIP1	84251	37	1	67185024	67185024	Missense_Mutation	SNP	C	T	35	11	c.1678C>T	c.(1678-1680)CTC>TTC	p.L560F
Pat_28	Post-Resistance	ANKRD13C	81573	37	1	70766452	70766452	Missense_Mutation	SNP	G	A	12	2	c.916C>T	c.(916-918)CAT>TAT	p.H306Y
Pat_28	Post-Resistance	HIAT1	64645	37	1	100547727	100547727	Missense_Mutation	SNP	G	A	17	8	c.1435G>A	c.(1435-1437)GAG>AAG	p.E479K
Pat_28	Post-Resistance	KIAA1324	57535	37	1	109741221	109741221	Missense_Mutation	SNP	G	A	20	9	c.2426G>A	c.(2425-2427)AGT>AAT	p.S809N
Pat_28	Post-Resistance	PROK1	84432	37	1	110998950	110998950	Missense_Mutation	SNP	G	A	19	6	c.295G>A	c.(295-297)GAC>AAC	p.D99N
Pat_28	Post-Resistance	CSDE1	7812	37	1	115261341	115261341	Missense_Mutation	SNP	G	A	38	16	c.2242C>T	c.(2242-2244)CCT>TCT	p.P748S
Pat_28	Post-Resistance	CD2	914	37	1	117311211	117311211	Missense_Mutation	SNP	C	T	24	114	c.862C>T	c.(862-864)CAT>TAT	p.H288Y
Pat_28	Post-Resistance	CD2	914	37	1	117311310	117311310	Missense_Mutation	SNP	C	T	89	289	c.961C>T	c.(961-963)CAC>TAC	p.H321Y

Pat_28	Post-Resistance	MAN1A2	10905	37	1	118035827	118035827	Nonsense_Mutation	SNP	G	A	51	257	c.1227G>A	c.(1225-1227)TGG>TGA	p.W409*
Pat_28	Post-Resistance	SPAG17	200162	37	1	118634562	118634562	Missense_Mutation	SNP	G	A	130	584	c.1237C>T	c.(1237-1239)CCA>TCA	p.P413S
Pat_28	Post-Resistance	TBX15	6913	37	1	119427795	119427795	Missense_Mutation	SNP	G	A	38	257	c.1051C>T	c.(1051-1053)CCT>TCT	p.P351S
Pat_28	Post-Resistance	NOTCH2	4853	37	1	120463021	120463021	Splice_Site	SNP	C	T	31	373	c.5311_splice	c.e30-1	p.A1771_splice
Pat_28	Post-Resistance	PDE4DIP	9659	37	1	144855760	144855760	Missense_Mutation	SNP	G	A	9	146	c.6793C>T	c.(6793-6795)CCT>TCT	p.P2265S
Pat_28	Post-Resistance	PDE4DIP	9659	37	1	144857675	144857675	Missense_Mutation	SNP	C	T	55	561	c.6379G>A	c.(6379-6381)GTC>ATC	p.V2127I
Pat_28	Post-Resistance	PDE4DIP	9659	37	1	144864232	144864232	Missense_Mutation	SNP	C	T	30	550	c.5863G>A	c.(5863-5865)GTG>ATG	p.V1955M
Pat_28	Post-Resistance	PDE4DIP	9659	37	1	145016012	145016012	Splice_Site	SNP	C	T	13	368	c.77_splice	c.e3-1	p.A26_splice
Pat_28	Post-Resistance	HFE2	148738	37	1	145416623	145416623	Missense_Mutation	SNP	C	T	39	35	c.968C>T	c.(967-969)CCA>CTA	p.P323L
Pat_28	Post-Resistance	BCL9	607	37	1	147096332	147096332	Missense_Mutation	SNP	G	A	21	59	c.3853G>A	c.(3853-3855)GGA>AGA	p.G1285R
Pat_28	Post-Resistance	ADAMTSL4	54507	37	1	150526233	150526233	Nonsense_Mutation	SNP	C	T	22	42	c.766C>T	c.(766-768)CAG>TAG	p.Q256*
Pat_28	Post-Resistance	BNIPL	149428	37	1	151018642	151018642	Splice_Site	SNP	G	A	18	46	c.1037_splice	c.e9+1	p.Q346_splice
Pat_28	Post-Resistance	POGZ	23126	37	1	151400368	151400368	Missense_Mutation	SNP	C	T	21	39	c.1009G>A	c.(1009-1011)GTG>ATG	p.V337M
Pat_28	Post-Resistance	LINGO4	339398	37	1	151773616	151773616	Missense_Mutation	SNP	G	A	43	107	c.1565C>T	c.(1564-1566)CCA>CTA	p.P522L
Pat_28	Post-Resistance	RPTN	126638	37	1	152128157	152128157	Missense_Mutation	SNP	G	A	232	606	c.1418C>T	c.(1417-1419)TCC>TTC	p.S473F
Pat_28	Post-Resistance	FLG	2312	37	1	152284826	152284826	Missense_Mutation	SNP	C	T	189	520	c.2536G>A	c.(2536-2538)GGG>AGG	p.G846R
Pat_28	Post-Resistance	S100A6	6277	37	1	153507231	153507231	Missense_Mutation	SNP	C	T	32	70	c.214G>A	c.(214-216)GAG>AAG	p.E72K
Pat_28	Post-Resistance	SLC27A3	11000	37	1	153751029	153751029	Missense_Mutation	SNP	G	A	41	115	c.1588G>A	c.(1588-1590)GGT>AGT	p.G530S
Pat_28	Post-Resistance	GATAD2B	57459	37	1	153792200	153792200	Missense_Mutation	SNP	C	T	35	94	c.347G>A	c.(346-348)CGA>CAA	p.R116Q
Pat_28	Post-Resistance	ATP8B2	57198	37	1	154315633	154315633	Missense_Mutation	SNP	G	A	27	89	c.1597G>A	c.(1597-1599)GTC>ATC	p.V533I
Pat_28	Post-Resistance	GBAP1	2630	37	1	155188242	155188242	Missense_Mutation	SNP	C	T	118	351	c.56G>A	c.(55-57)AGC>AAC	p.S19N
Pat_28	Post-Resistance	GON4L	54856	37	1	155742957	155742957	Missense_Mutation	SNP	C	T	35	127	c.2395G>A	c.(2395-2397)GCC>ACC	p.A799T
Pat_28	Post-Resistance	C1orf85	112770	37	1	156263364	156263364	Missense_Mutation	SNP	C	T	19	66	c.802G>A	c.(802-804)GAC>AAC	p.D268N
Pat_28	Post-Resistance	GPATCH4	54865	37	1	156567856	156567856	Missense_Mutation	SNP	G	A	43	177	c.319C>T	c.(319-321)CCC>TCC	p.P107S
Pat_28	Post-Resistance	ARHGEF11	9826	37	1	156907216	156907216	Missense_Mutation	SNP	C	T	12	36	c.4145G>A	c.(4144-4146)AGC>AAC	p.S1382N
Pat_28	Post-Resistance	OR10J3	441911	37	1	159283647	159283647	Missense_Mutation	SNP	G	A	41	91	c.803C>T	c.(802-804)TCC>TTC	p.S268F
Pat_28	Post-Resistance	COPA	1314	37	1	160265603	160265603	Missense_Mutation	SNP	G	C	96	94	c.2399C>G	c.(2398-2400)CCT>CGT	p.P800R
Pat_28	Post-Resistance	SLAMF7	57823	37	1	160718023	160718023	Missense_Mutation	SNP	C	T	26	59	c.95C>T	c.(94-96)TCC>TTC	p.S32F
Pat_28	Post-Resistance	SLAMF7	57823	37	1	160722024	160722024	Missense_Mutation	SNP	G	A	22	43	c.922G>A	c.(922-924)GAA>AAA	p.E308K
Pat_28	Post-Resistance	LY9	4063	37	1	160784219	160784219	Missense_Mutation	SNP	C	T	30	31	c.740C>T	c.(739-741)GCC>GTC	p.A247V
Pat_28	Post-Resistance	C1orf192	257177	37	1	161334780	161334780	Missense_Mutation	SNP	C	T	29	82	c.509G>A	c.(508-510)GGT>GAT	p.G170D
Pat_28	Post-Resistance	HSPA6	3310	37	1	161495508	161495508	Missense_Mutation	SNP	G	A	14	27	c.1060G>A	c.(1060-1062)GAC>AAC	p.D354N
Pat_28	Post-Resistance	CD247	919	37	1	167408600	167408600	Missense_Mutation	SNP	C	T	35	88	c.200G>A	c.(199-201)GGC>GAC	p.G67D
Pat_28	Post-Resistance	FMO2	2327	37	1	171165914	171165914	Missense_Mutation	SNP	C	T	100	70	c.448C>T	c.(448-450)CAC>TAC	p.H150Y
Pat_28	Post-Resistance	KLHL20	27252	37	1	173726202	173726202	Missense_Mutation	SNP	G	A	87	169	c.1055G>A	c.(1054-1056)AGC>AAC	p.S352N
Pat_28	Post-Resistance	DARS2	55157	37	1	173807354	173807354	Missense_Mutation	SNP	G	A	99	86	c.797G>A	c.(796-798)CGA>CAA	p.R266Q
Pat_28	Post-Resistance	ABL2	27	37	1	179077325	179077325	Missense_Mutation	SNP	G	T	42	110	c.3077C>A	c.(3076-3078)GCT>GAT	p.A1026D
Pat_28	Post-Resistance	XPR1	9213	37	1	180775291	180775291	Missense_Mutation	SNP	G	C	64	149	c.541G>C	c.(541-543)GAG>CAG	p.E181Q
Pat_28	Post-Resistance	DHX9	1660	37	1	182856439	182856439	Missense_Mutation	SNP	G	A	20	35	c.3683G>A	c.(3682-3684)GGC>GAC	p.G1228D
Pat_28	Post-Resistance	LAMC2	3918	37	1	183209211	183209211	Missense_Mutation	SNP	G	A	25	93	c.3106G>A	c.(3106-3108)GCA>ACA	p.A1036T
Pat_28	Post-Resistance	PRG4	10216	37	1	186277792	186277792	Missense_Mutation	SNP	C	T	76	195	c.2941C>T	c.(2941-2943)CTT>TTT	p.L981F
Pat_28	Post-Resistance	TPR	7175	37	1	186321233	186321233	Missense_Mutation	SNP	C	T	25	65	c.2344G>A	c.(2344-2346)GAA>AAA	p.E782K
Pat_28	Post-Resistance	TPR	7175	37	1	186329026	186329026	Missense_Mutation	SNP	C	T	32	101	c.1294G>A	c.(1294-1296)GCC>ACC	p.A432T
Pat_28	Post-Resistance	FAM5C	339479	37	1	190068128	190068128	Missense_Mutation	SNP	A	C	25	17	c.1321T>G	c.(1321-1323)TGC>GGC	p.C441G
Pat_28	Post-Resistance	F13B	2165	37	1	197024887	197024887	Missense_Mutation	SNP	G	A	75	213	c.1312C>T	c.(1312-1314)CGT>TGT	p.R438C
Pat_28	Post-Resistance	DENND1B	163486	37	1	197479747	197479747	Missense_Mutation	SNP	G	A	53	121	c.2111C>T	c.(2110-2112)TCG>TTG	p.S704L
Pat_28	Post-Resistance	PPFIA4	8497	37	1	203015116	203015116	Splice_Site	SNP	G	A	100	192	c.1446_splice	c.e12+1	p.Q482_splice

Pat_28	Post-Resistance	CHIT1	1118	37	1	203186259	203186259	Missense_Mutation	SNP	G	A	9	46	c.1159C>T	c.(1159-1161)CTT>TTT	p.L387F
Pat_28	Post-Resistance	LAX1	54900	37	1	203743784	203743784	Missense_Mutation	SNP	G	A	14	51	c.1172G>A	c.(1171-1173)GGC>GAC	p.G391D
Pat_28	Post-Resistance	LRRN2	10446	37	1	204587559	204587559	Missense_Mutation	SNP	G	A	9	25	c.1562C>T	c.(1561-1563)CCA>CTA	p.P521L
Pat_28	Post-Resistance	CNTN2	6900	37	1	205036253	205036253	Missense_Mutation	SNP	C	T	36	105	c.2000C>T	c.(1999-2001)GCC>GTC	p.A667V
Pat_28	Post-Resistance	TMEM81	388730	37	1	205052995	205052995	Missense_Mutation	SNP	C	T	31	79	c.454G>A	c.(454-456)GAG>AAG	p.E152K
Pat_28	Post-Resistance	C4BPA	722	37	1	207307782	207307782	Missense_Mutation	SNP	G	A	120	296	c.1118G>A	c.(1117-1119)GGT>GAT	p.G373D
Pat_28	Post-Resistance	C4BPA	722	37	1	207318040	207318040	Missense_Mutation	SNP	C	T	13	56	c.1772C>T	c.(1771-1773)TCC>TTC	p.S591F
Pat_28	Post-Resistance	CR1	1378	37	1	207737275	207737275	Missense_Mutation	SNP	C	T	84	183	c.2303C>T	c.(2302-2304)CCC>CTC	p.P768L
Pat_28	Post-Resistance	C1orf107	27042	37	1	210014251	210014251	Missense_Mutation	SNP	G	A	78	172	c.1336G>A	c.(1336-1338)GAT>AAT	p.D446N
Pat_28	Post-Resistance	RCOR3	55758	37	1	211462676	211462676	Missense_Mutation	SNP	C	T	36	88	c.703C>T	c.(703-705)CCC>TCC	p.P235S
Pat_28	Post-Resistance	RPS6KC1	26750	37	1	213415395	213415395	Missense_Mutation	SNP	C	T	64	154	c.2576C>T	c.(2575-2577)ACT>ATT	p.T859I
Pat_28	Post-Resistance	PROX1	5629	37	1	214170398	214170398	Missense_Mutation	SNP	C	T	44	113	c.520C>T	c.(520-522)CGG>TGG	p.R174W
Pat_28	Post-Resistance	USH2A	7399	37	1	215847694	215847694	Missense_Mutation	SNP	C	T	38	139	c.13559G>A	c.(13558-13560)AGT>AAT	p.S4520N
Pat_28	Post-Resistance	USH2A	7399	37	1	216465706	216465706	Missense_Mutation	SNP	G	A	11	37	c.1651C>T	c.(1651-1653)CGC>TGC	p.R551C
Pat_28	Post-Resistance	ESRRG	2104	37	1	216850709	216850709	Missense_Mutation	SNP	A	G	66	44	c.181T>C	c.(181-183)TCT>CCT	p.S61P
Pat_28	Post-Resistance	MARK1	4139	37	1	220777480	220777480	Splice_Site	SNP	G	A	48	108	c.495_splice	c.e6+1	p.Q165_splice
Pat_28	Post-Resistance	CAPN2	824	37	1	223946979	223946979	Missense_Mutation	SNP	G	A	22	80	c.1325G>A	c.(1324-1326)GGG>GAG	p.G442E
Pat_28	Post-Resistance	CDC42BPA	8476	37	1	227307504	227307504	Splice_Site	SNP	C	T	6	35	c.1647_splice	c.e12+1	p.K549_splice
Pat_28	Post-Resistance	OBSCN	84033	37	1	228431084	228431084	Missense_Mutation	SNP	G	A	18	36	c.3130G>A	c.(3130-3132)GCA>ACA	p.A1044T
Pat_28	Post-Resistance	SIPA1L2	57568	37	1	232650854	232650854	Missense_Mutation	SNP	C	T	55	152	c.232G>A	c.(232-234)GCA>ACA	p.A78T
Pat_28	Post-Resistance	GPR137B	7107	37	1	236306136	236306136	Missense_Mutation	SNP	C	T	15	50	c.214C>T	c.(214-216)CAC>TAC	p.H72Y
Pat_28	Post-Resistance	RYR2	6262	37	1	237729896	237729896	Missense_Mutation	SNP	G	A	26	23	c.3244G>A	c.(3244-3246)GGG>AGG	p.G1082R
Pat_28	Post-Resistance	RYR2	6262	37	1	237944864	237944864	Splice_Site	SNP	G	A	8	17	c.11881_splice	c.e89-1	p.D3961_splice
Pat_28	Post-Resistance	PLD5	200150	37	1	242271047	242271047	Missense_Mutation	SNP	C	T	53	111	c.1165G>A	c.(1165-1167)GAT>AAT	p.D389N
Pat_28	Post-Resistance	ZNF695	57116	37	1	247162670	247162670	Missense_Mutation	SNP	T	A	32	133	c.239A>T	c.(238-240)GAG>GTG	p.E80V
Pat_28	Post-Resistance	OR14C36	127066	37	1	248512866	248512866	Missense_Mutation	SNP	C	T	44	146	c.790C>T	c.(790-792)CCT>TCT	p.P264S
Pat_28	Post-Resistance	SH3BP5L	80851	37	1	249108722	249108722	Missense_Mutation	SNP	C	T	20	50	c.463G>A	c.(463-465)GAG>AAG	p.E155K
Pat_28	Post-Resistance	C10orf18	54906	37	10	5777482	5777482	Missense_Mutation	SNP	C	T	38	80	c.1420C>T	c.(1420-1422)CCC>TCC	p.P474S
Pat_28	Post-Resistance	FBXO18	84893	37	10	5948575	5948575	Missense_Mutation	SNP	G	A	54	68	c.733G>A	c.(733-735)GAG>AAG	p.E245K
Pat_28	Post-Resistance	CDC123	8872	37	10	12240757	12240757	Missense_Mutation	SNP	C	T	40	56	c.128C>T	c.(127-129)ACT>ATT	p.T43I
Pat_28	Post-Resistance	FAM171A1	221061	37	10	15262990	15262990	Missense_Mutation	SNP	G	A	79	91	c.824C>T	c.(823-825)GCC>GTC	p.A275V
Pat_28	Post-Resistance	CUBN	8029	37	10	16932487	16932487	Missense_Mutation	SNP	C	T	66	90	c.8638G>A	c.(8638-8640)GCC>ACC	p.A2880T
Pat_28	Post-Resistance	DNAJC1	64215	37	10	22171369	22171369	Splice_Site	SNP	C	T	9	10	c.821_splice	c.e8-1	p.K274_splice
Pat_28	Post-Resistance	MYO3A	53904	37	10	26491957	26491957	Missense_Mutation	SNP	C	T	30	33	c.4651C>T	c.(4651-4653)CCA>TCA	p.P1551S
Pat_28	Post-Resistance	ARMC4	55130	37	10	28273151	28273151	Missense_Mutation	SNP	C	T	79	104	c.644G>A	c.(643-645)GGA>GAA	p.G215E
Pat_28	Post-Resistance	ZNF438	220929	37	10	31138079	31138079	Missense_Mutation	SNP	G	A	11	19	c.1255C>T	c.(1255-1257)CCC>TCC	p.P419S
Pat_28	Post-Resistance	ITGB1	3688	37	10	33199238	33199238	Missense_Mutation	SNP	C	T	21	17	c.2077G>A	c.(2077-2079)GAG>AAG	p.E693K
Pat_28	Post-Resistance	ANK3	288	37	10	61833910	61833910	Missense_Mutation	SNP	C	G	74	22	c.6729G>C	c.(6727-6729)GAG>GAC	p.E2243D
Pat_28	Post-Resistance	LRRTM3	347731	37	10	68686729	68686729	Missense_Mutation	SNP	G	A	36	15	c.55G>A	c.(55-57)GCC>ACC	p.A19T
Pat_28	Post-Resistance	CDH23	64072	37	10	73270727	73270727	Missense_Mutation	SNP	C	T	35	15	c.305C>T	c.(304-306)ACC>ATC	p.T102I
Pat_28	Post-Resistance	CDH23	64072	37	10	73550910	73550910	Missense_Mutation	SNP	G	T	5	1	c.6071G>T	c.(6070-6072)GGT>GTT	p.G2024V
Pat_28	Post-Resistance	SEC24C	9632	37	10	75526296	75526296	Missense_Mutation	SNP	C	T	37	10	c.1796C>T	c.(1795-1797)ACC>ATC	p.T599I
Pat_28	Post-Resistance	MYST4	23522	37	10	76788642	76788642	Missense_Mutation	SNP	G	A	9	4	c.4060G>A	c.(4060-4062)GAA>AAA	p.E1354K
Pat_28	Post-Resistance	SAMD8	142891	37	10	76910581	76910581	Missense_Mutation	SNP	C	T	41	23	c.295C>T	c.(295-297)CCT>TCT	p.P99S
Pat_28	Post-Resistance	PAPSS2	9060	37	10	89503399	89503399	Splice_Site	SNP	G	A	40	16	c.1476_splice	c.e10+1	p.E492_splice
Pat_28	Post-Resistance	PANK1	53354	37	10	91353019	91353020	Missense_Mutation	DNP	GG	AA	32	10	.1545_1546CC>T	543-1548)GCCCGG>GCT	p.R516W
Pat_28	Post-Resistance	NOC3L	64318	37	10	96114731	96114731	Missense_Mutation	SNP	G	A	40	18	c.685C>T	c.(685-687)CCA>TCA	p.P229S

Pat_28	Post-Resistance	WDR11	55717	37	10	122630712	122630712	Missense_Mutation	SNP	C	T	64	24	c.1325C>T	c.(1324-1326)CCC>CTC	p.P442L
Pat_28	Post-Resistance	TACC2	10579	37	10	123971094	123971094	Missense_Mutation	SNP	C	T	53	21	c.7154C>T	c.(7153-7155)TCT>TTT	p.S2385F
Pat_28	Post-Resistance	CPXM2	119587	37	10	125514202	125514202	Missense_Mutation	SNP	C	T	57	35	c.1994G>A	c.(1993-1995)GGC>GAC	p.G665D
Pat_28	Post-Resistance	ECHS1	1892	37	10	135184208	135184208	Missense_Mutation	SNP	C	T	26	6	c.142G>A	c.(142-144)GGG>AGG	p.G48R
Pat_28	Post-Resistance	EPS8L2	64787	37	11	726925	726925	Missense_Mutation	SNP	G	A	10	10	c.2092G>A	c.(2092-2094)GAA>AAA	p.E698K
Pat_28	Post-Resistance	MUC5B	727897	37	11	1252167	1252167	Missense_Mutation	SNP	C	T	4	3	c.3449C>T	c.(3448-3450)GCC>GTC	p.A1150V
Pat_28	Post-Resistance	SYT8	90019	37	11	1858028	1858028	Missense_Mutation	SNP	C	T	15	21	c.769C>T	c.(769-771)CCC>TCC	p.P257S
Pat_28	Post-Resistance	ART1	417	37	11	3681107	3681107	Missense_Mutation	SNP	G	A	16	11	c.358G>A	c.(358-360)GCC>ACC	p.A120T
Pat_28	Post-Resistance	ART1	417	37	11	3681464	3681464	Missense_Mutation	SNP	G	A	39	44	c.715G>A	c.(715-717)GAA>AAA	p.E239K
Pat_28	Post-Resistance	UBQLNL	143630	37	11	5536746	5536746	Missense_Mutation	SNP	G	A	20	30	c.926C>T	c.(925-927)TCA>TTA	p.S309L
Pat_28	Post-Resistance	OR2AG2	338755	37	11	6789807	6789807	Missense_Mutation	SNP	G	A	15	44	c.382C>T	c.(382-384)CAT>TAT	p.H128Y
Pat_28	Post-Resistance	OVCH2	341277	37	11	7723023	7723023	Splice_Site	SNP	C	T	8	19	c.560_splice	c.e6-1	p.G187_splice
Pat_28	Post-Resistance	WEE1	7465	37	11	9603156	9603156	Missense_Mutation	SNP	C	T	35	83	c.1219C>T	c.(1219-1221)CTT>TTT	p.L407F
Pat_28	Post-Resistance	AMPD3	272	37	11	10500091	10500091	Missense_Mutation	SNP	G	A	163	252	c.240G>A	c.(238-240)ATG>ATA	p.M80I
Pat_28	Post-Resistance	CYP2R1	120227	37	11	14902114	14902114	Missense_Mutation	SNP	T	G	53	69	c.568A>C	c.(568-570)ATA>CTA	p.I190L
Pat_28	Post-Resistance	PLEKHA7	144100	37	11	16812638	16812638	Missense_Mutation	SNP	A	T	21	46	c.2854T>A	c.(2854-2856)TCT>ACT	p.S952T
Pat_28	Post-Resistance	BBOX1	8424	37	11	27077035	27077035	Missense_Mutation	SNP	C	T	41	66	c.58C>T	c.(58-60)CTC>TTC	p.L20F
Pat_28	Post-Resistance	KIF18A	81930	37	11	28090901	28090901	Missense_Mutation	SNP	C	T	37	62	c.1495G>A	c.(1495-1497)GAG>AAG	p.E499K
Pat_28	Post-Resistance	WT1	7490	37	11	32439177	32439177	Missense_Mutation	SNP	G	A	29	60	c.896C>T	c.(895-897)TCC>TTC	p.S299F
Pat_28	Post-Resistance	PDHX	8050	37	11	34953002	34953002	Missense_Mutation	SNP	G	A	24	37	c.212G>A	c.(211-213)GGA>GAA	p.G71E
Pat_28	Post-Resistance	SLC1A2	6506	37	11	35338938	35338938	Missense_Mutation	SNP	G	A	20	23	c.143C>T	c.(142-144)ACC>ATC	p.T48I
Pat_28	Post-Resistance	EXT2	2132	37	11	44148506	44148506	Splice_Site	SNP	G	A	65	79	c.1079_splice	c.e6+1	p.R360_splice
Pat_28	Post-Resistance	LRP4	4038	37	11	46897070	46897070	Missense_Mutation	SNP	G	A	36	51	c.3862C>T	c.(3862-3864)CTC>TTC	p.L1288F
Pat_28	Post-Resistance	MADD	8567	37	11	47330241	47330241	Missense_Mutation	SNP	G	A	12	14	c.3859G>A	c.(3859-3861)GGA>AGA	p.G1287R
Pat_28	Post-Resistance	OR5T3	390154	37	11	56020000	56020000	Missense_Mutation	SNP	C	T	59	115	c.325C>T	c.(325-327)CCA>TCA	p.P109S
Pat_28	Post-Resistance	RTN4RL2	349667	37	11	57243840	57243840	Missense_Mutation	SNP	C	T	5	9	c.719C>T	c.(718-720)GCC>GTC	p.A240V
Pat_28	Post-Resistance	SMTNL1	219537	37	11	57310833	57310833	Missense_Mutation	SNP	G	A	12	19	c.772G>A	c.(772-774)GAT>AAT	p.D258N
Pat_28	Post-Resistance	FADS3	3995	37	11	61646912	61646912	Missense_Mutation	SNP	G	A	7	12	c.394C>T	c.(394-396)CCC>TCC	p.P132S
Pat_28	Post-Resistance	AHNAK	79026	37	11	62291855	62291855	Missense_Mutation	SNP	C	T	17	30	c.10034G>A	c.(10033-10035)GGC>GAC	p.G3345D
Pat_28	Post-Resistance	MTA2	9219	37	11	62365541	62365541	Missense_Mutation	SNP	C	T	137	195	c.445G>A	c.(445-447)GTT>ATT	p.V149I
Pat_28	Post-Resistance	RARRES3	5920	37	11	63313688	63313688	Missense_Mutation	SNP	C	T	62	121	c.455C>T	c.(454-456)TCT>TTT	p.S152F
Pat_28	Post-Resistance	ATG2A	23130	37	11	64678361	64678361	Missense_Mutation	SNP	G	A	9	7	c.1532C>T	c.(1531-1533)ACC>ATC	p.T511I
Pat_28	Post-Resistance	SIPA1	6494	37	11	65417916	65417916	Missense_Mutation	SNP	C	T	26	34	c.2948C>T	c.(2947-2949)TCC>TTC	p.S983F
Pat_28	Post-Resistance	BRMS1	25855	37	11	66107685	66107685	Splice_Site	SNP	C	T	9	15	c.536_splice	c.e7-1	p.E179_splice
Pat_28	Post-Resistance	RBM4B	83759	37	11	66436559	66436559	Missense_Mutation	SNP	C	T	33	54	c.616G>A	c.(616-618)GGG>AGG	p.G206R
Pat_28	Post-Resistance	C2CD3	26005	37	11	73795952	73795952	Missense_Mutation	SNP	G	A	37	65	c.3974C>T	c.(3973-3975)ACA>ATA	p.T1325I
Pat_28	Post-Resistance	ODZ4	26011	37	11	78437183	78437183	Missense_Mutation	SNP	T	A	73	286	c.3491A>T	c.(3490-3492)GAC>GTC	p.D1164V
Pat_28	Post-Resistance	PCF11	51585	37	11	82880547	82880547	Missense_Mutation	SNP	G	A	16	31	c.3170G>A	c.(3169-3171)GGT>GAT	p.G1057D
Pat_28	Post-Resistance	PCF11	51585	37	11	82895760	82895760	Missense_Mutation	SNP	C	T	56	106	c.4492C>T	c.(4492-4494)CCA>TCA	p.P1498S
Pat_28	Post-Resistance	SYTL2	54843	37	11	85459318	85459318	Missense_Mutation	SNP	C	T	70	106	c.250G>A	c.(250-252)GCA>ACA	p.A84T
Pat_28	Post-Resistance	PANX1	24145	37	11	93911643	93911643	Missense_Mutation	SNP	G	A	36	55	c.430G>A	c.(430-432)GAA>AAA	p.E144K
Pat_28	Post-Resistance	CNTN5	53942	37	11	100170018	100170018	Missense_Mutation	SNP	G	A	32	38	c.2510G>A	c.(2509-2511)CGA>CAA	p.R837Q
Pat_28	Post-Resistance	MMP3	4314	37	11	102706936	102706936	Missense_Mutation	SNP	C	T	49	70	c.1355G>A	c.(1354-1356)GGA>GAA	p.G452E
Pat_28	Post-Resistance	DYNC2H1	79659	37	11	103349887	103349887	Missense_Mutation	SNP	G	A	54	94	c.12830G>A	c.(12829-12831)AGG>AAG	p.R4277K
Pat_28	Post-Resistance	PAFAH1B2	5049	37	11	117023157	117023157	Translation_Start_Site	SNP	G	A	23	38	c.-6G>A	c.(-8--4)CAGTG>CAATG	
Pat_28	Post-Resistance	SIDT2	51092	37	11	117063322	117063322	Missense_Mutation	SNP	C	T	43	81	c.2014C>T	c.(2014-2016)CTC>TTC	p.L672F
Pat_28	Post-Resistance	DSCAML1	57453	37	11	117376258	117376258	Missense_Mutation	SNP	C	T	20	40	c.2153G>A	c.(2152-2154)AGC>AAC	p.S718N

Pat_28	Post-Resistance	CD3G	917	37	11	118221377	118221377	Missense_Mutation	SNP	G	A	47	74	c.418G>A	c.(418-420)GAT>AAT	p.D140N
Pat_28	Post-Resistance	ARHGEF12	23365	37	11	120347935	120347935	Missense_Mutation	SNP	G	A	26	34	c.3373G>A	c.(3373-3375)GAC>AAC	p.D1125N
Pat_28	Post-Resistance	TECTA	7007	37	11	121008594	121008594	Missense_Mutation	SNP	G	A	19	25	c.3406G>A	c.(3406-3408)GAC>AAC	p.D1136N
Pat_28	Post-Resistance	C11orf63	79864	37	11	122830118	122830118	Missense_Mutation	SNP	G	A	47	51	c.2302G>A	c.(2302-2304)GCT>ACT	p.A768T
Pat_28	Post-Resistance	FKBP4	2288	37	12	2912344	2912344	Missense_Mutation	SNP	C	T	4	37	c.1300C>T	c.(1300-1302)CAT>TAT	p.H434Y
Pat_28	Post-Resistance	TULP3	7289	37	12	3039467	3039467	Missense_Mutation	SNP	G	A	15	70	c.448G>A	c.(448-450)GCA>ACA	p.A150T
Pat_28	Post-Resistance	ANO2	57101	37	12	5848526	5848526	Missense_Mutation	SNP	C	T	13	7	c.1379G>A	c.(1378-1380)CGA>CAA	p.R460Q
Pat_28	Post-Resistance	NOP2	4839	37	12	6666256	6666256	Missense_Mutation	SNP	T	C	13	69	c.2330A>G	c.(2329-2331)CAG>CGG	p.Q777R
Pat_28	Post-Resistance	LEPREL2	10536	37	12	6946928	6946928	Missense_Mutation	SNP	C	T	8	26	c.1744C>T	c.(1744-1746)CCA>TCA	p.P582S
Pat_28	Post-Resistance	C1S	716	37	12	7170231	7170231	Missense_Mutation	SNP	G	A	19	106	c.251G>A	c.(250-252)GGA>GAA	p.G84E
Pat_28	Post-Resistance	CD163	9332	37	12	7635975	7635975	Missense_Mutation	SNP	C	T	17	74	c.3076G>A	c.(3076-3078)GTG>ATG	p.V1026M
Pat_28	Post-Resistance	CD163	9332	37	12	7636043	7636043	Missense_Mutation	SNP	G	A	108	45	c.3008C>T	c.(3007-3009)TCT>TTT	p.S1003F
Pat_28	Post-Resistance	FAM90A1	55138	37	12	8374615	8374615	Missense_Mutation	SNP	C	T	5	36	c.1198G>A	c.(1198-1200)GAA>AAA	p.E400K
Pat_28	Post-Resistance	A2ML1	144568	37	12	9013531	9013531	Missense_Mutation	SNP	G	A	62	256	c.3319G>A	c.(3319-3321)GAG>AAG	p.E1107K
Pat_28	Post-Resistance	PHC1	1911	37	12	9087072	9087072	Missense_Mutation	SNP	C	T	12	81	c.2251C>T	c.(2251-2253)CCG>TCG	p.P751S
Pat_28	Post-Resistance	PRB1	5542	37	12	11506808	11506808	Missense_Mutation	SNP	G	A	63	522	c.229C>T	c.(229-231)CCA>TCA	p.P77S
Pat_28	Post-Resistance	LRP6	4040	37	12	12318165	12318165	Missense_Mutation	SNP	C	T	103	384	c.1610G>A	c.(1609-1611)GGA>GAA	p.G537E
Pat_28	Post-Resistance	MANSC1	54682	37	12	12483659	12483659	Missense_Mutation	SNP	C	T	17	56	c.598G>A	c.(598-600)GAA>AAA	p.E200K
Pat_28	Post-Resistance	PLBD1	79887	37	12	14659915	14659915	Missense_Mutation	SNP	C	T	63	262	c.1324G>A	c.(1324-1326)GGG>AGG	p.G442R
Pat_28	Post-Resistance	GUCY2C	2984	37	12	14794136	14794136	Missense_Mutation	SNP	C	T	38	188	c.1948G>A	c.(1948-1950)GAG>AAG	p.E650K
Pat_28	Post-Resistance	PLEKHA5	54477	37	12	19282804	19282804	Missense_Mutation	SNP	G	A	9	47	c.71G>A	c.(70-72)GGC>GAC	p.G24D
Pat_28	Post-Resistance	PLEKHA5	54477	37	12	19519010	19519010	Missense_Mutation	SNP	C	T	22	113	c.3223C>T	c.(3223-3225)CCT>TCT	p.P1075S
Pat_28	Post-Resistance	SLCO1A2	6579	37	12	21453476	21453476	Missense_Mutation	SNP	G	A	22	72	c.716C>T	c.(715-717)ACT>ATT	p.T239I
Pat_28	Post-Resistance	ETNK1	55500	37	12	22778273	22778273	Missense_Mutation	SNP	G	A	3	14	c.176G>A	c.(175-177)GGG>GAG	p.G59E
Pat_28	Post-Resistance	BCAT1	586	37	12	25047302	25047302	Nonsense_Mutation	SNP	C	T	19	57	c.186G>A	c.(184-186)TGG>TGA	p.W62*
Pat_28	Post-Resistance	MED21	9412	37	12	27180324	27180324	Missense_Mutation	SNP	G	A	89	354	c.202G>A	c.(202-204)GAC>AAC	p.D68N
Pat_28	Post-Resistance	PPFIBP1	8496	37	12	27813843	27813843	Missense_Mutation	SNP	G	A	12	70	c.931G>A	c.(931-933)GCT>ACT	p.A311T
Pat_28	Post-Resistance	PTHLH	5744	37	12	28116518	28116518	Missense_Mutation	SNP	C	T	58	274	c.287G>A	c.(286-288)GGG>GAG	p.G96E
Pat_28	Post-Resistance	CAPRIN2	65981	37	12	30881703	30881703	Missense_Mutation	SNP	C	T	89	344	c.1661G>A	c.(1660-1662)AGT>AAT	p.S554N
Pat_28	Post-Resistance	CNTN1	1272	37	12	41463763	41463763	Missense_Mutation	SNP	G	A	9	174	c.2983G>A	c.(2983-2985)GCA>ACA	p.A995T
Pat_28	Post-Resistance	NELL2	4753	37	12	44926412	44926412	Missense_Mutation	SNP	C	T	119	179	c.1756G>A	c.(1756-1758)GGC>AGC	p.G586S
Pat_28	Post-Resistance	C12orf54	121273	37	12	48888714	48888714	Missense_Mutation	SNP	G	A	66	107	c.376G>A	c.(376-378)GGA>AGA	p.G126R
Pat_28	Post-Resistance	SLC4A8	9498	37	12	51879622	51879622	Missense_Mutation	SNP	G	A	58	90	c.2224G>A	c.(2224-2226)GTG>ATG	p.V742M
Pat_28	Post-Resistance	SCN8A	6334	37	12	52100398	52100399	Missense_Mutation	DNP	CC	TT	3	8	.1534_1535CC>T	c.(1534-1536)CCC>TTC	p.P512F
Pat_28	Post-Resistance	ACVR1B	91	37	12	52377866	52377866	Missense_Mutation	SNP	G	A	21	55	c.895G>A	c.(895-897)GTG>ATG	p.V299M
Pat_28	Post-Resistance	KRT80	144501	37	12	52565292	52565292	Missense_Mutation	SNP	C	T	9	7	c.1249G>A	c.(1249-1251)GGC>AGC	p.G417S
Pat_28	Post-Resistance	TARBP2	6895	37	12	53895854	53895854	Missense_Mutation	SNP	G	A	36	68	c.109G>A	c.(109-111)GAG>AAG	p.E37K
Pat_28	Post-Resistance	RDH16	8608	37	12	57345908	57345908	Missense_Mutation	SNP	C	T	27	34	c.859G>A	c.(859-861)GCC>ACC	p.A287T
Pat_28	Post-Resistance	MYO1A	4640	37	12	57431340	57431340	Missense_Mutation	SNP	G	A	189	309	c.2047C>T	c.(2047-2049)CCC>TCC	p.P683S
Pat_28	Post-Resistance	LRP1	4035	37	12	57535237	57535237	Missense_Mutation	SNP	C	T	17	27	c.271C>T	c.(271-273)CTC>TTC	p.L91F
Pat_28	Post-Resistance	LRIG3	121227	37	12	59274590	59274590	Missense_Mutation	SNP	C	T	128	137	c.1574G>A	c.(1573-1575)AGC>AAC	p.S525N
Pat_28	Post-Resistance	SRGAP1	57522	37	12	64521485	64521485	Missense_Mutation	SNP	C	T	22	28	c.2521C>T	c.(2521-2523)CCT>TCT	p.P841S
Pat_28	Post-Resistance	PTPRR	5801	37	12	71054727	71054727	Missense_Mutation	SNP	G	A	22	27	c.1759C>T	c.(1759-1761)CAC>TAC	p.H587Y
Pat_28	Post-Resistance	TRHDE	29953	37	12	73012738	73012738	Missense_Mutation	SNP	C	T	36	59	c.2254C>T	c.(2254-2256)CTT>TTT	p.L752F
Pat_28	Post-Resistance	ACSS3	79611	37	12	81536896	81536896	Missense_Mutation	SNP	C	T	24	39	c.791C>T	c.(790-792)CCT>CTT	p.P264L
Pat_28	Post-Resistance	C12orf50	160419	37	12	88390385	88390385	Missense_Mutation	SNP	C	T	18	34	c.328G>A	c.(328-330)GAA>AAA	p.E110K
Pat_28	Post-Resistance	CCDC41	51134	37	12	94725579	94725579	Nonsense_Mutation	SNP	C	T	52	96	c.1604G>A	c.(1603-1605)TGG>TAG	p.W535*

Pat_28	Post-Resistance	HAL	3034	37	12	96384204	96384204	Nonsense_Mutation	SNP	C	T	62	86	c.822G>A	c.(820-822)TGG>TGA	p.W274*
Pat_28	Post-Resistance	BTBD11	121551	37	12	108013921	108013921	Missense_Mutation	SNP	G	A	32	62	c.2611G>A	c.(2611-2613)GAG>AAG	p.E871K
Pat_28	Post-Resistance	C12orf51	283450	37	12	112697046	112697046	Missense_Mutation	SNP	G	A	22	28	c.1601C>T	c.(1600-1602)ACT>ATT	p.T534I
Pat_28	Post-Resistance	MSI1	4440	37	12	120806035	120806035	Missense_Mutation	SNP	C	T	4	7	c.142G>A	c.(142-144)GAG>AAG	p.E48K
Pat_28	Post-Resistance	KDM2B	84678	37	12	121880111	121880111	Missense_Mutation	SNP	G	A	13	17	c.3133C>T	c.(3133-3135)CCA>TCA	p.P1045S
Pat_28	Post-Resistance	B3GNT4	79369	37	12	122690928	122690928	Missense_Mutation	SNP	G	A	24	33	c.130G>A	c.(130-132)GGC>AGC	p.G44S
Pat_28	Post-Resistance	SBNO1	55206	37	12	123789220	123789220	Missense_Mutation	SNP	G	A	12	23	c.3677C>T	c.(3676-3678)CCT>CTT	p.P1226L
Pat_28	Post-Resistance	GPR133	283383	37	12	131476909	131476909	Missense_Mutation	SNP	C	T	5	141	c.938C>T	c.(937-939)TCG>TTG	p.S313L
Pat_28	Post-Resistance	EP400	57634	37	12	132546772	132546772	Nonsense_Mutation	SNP	C	T	35	61	c.8002C>T	c.(8002-8004)CGA>TGA	p.R2668*
Pat_28	Post-Resistance	DDX51	317781	37	12	132625058	132625058	Missense_Mutation	SNP	C	T	14	23	c.1583G>A	c.(1582-1584)GGG>GAG	p.G528E
Pat_28	Post-Resistance	PARP4	143	37	13	25009030	25009030	Missense_Mutation	SNP	G	A	21	43	c.4249C>T	c.(4249-4251)CCT>TCT	p.P1417S
Pat_28	Post-Resistance	MTUS2	23281	37	13	29599727	29599727	Missense_Mutation	SNP	G	A	16	35	c.922G>A	c.(922-924)GAA>AAA	p.E308K
Pat_28	Post-Resistance	SLC7A1	6541	37	13	30091417	30091417	Missense_Mutation	SNP	G	A	22	10	c.1541C>T	c.(1540-1542)ACC>ATC	p.T514I
Pat_28	Post-Resistance	NBEA	26960	37	13	36046651	36046651	Missense_Mutation	SNP	C	T	27	68	c.6563C>T	c.(6562-6564)GCC>GTC	p.A2188V
Pat_28	Post-Resistance	FAM48A	55578	37	13	37598261	37598261	Missense_Mutation	SNP	G	A	48	122	c.1502C>T	c.(1501-1503)CCA>CTA	p.P501L
Pat_28	Post-Resistance	KIAA0564	23078	37	13	42358022	42358022	Missense_Mutation	SNP	C	T	44	140	c.2186G>A	c.(2185-2187)GGA>GAA	p.G729E
Pat_28	Post-Resistance	ENOX1	55068	37	13	43896613	43896613	Nonsense_Mutation	SNP	G	A	32	80	c.1168C>T	c.(1168-1170)CAG>TAG	p.Q390*
Pat_28	Post-Resistance	TSC22D1	8848	37	13	45148787	45148787	Missense_Mutation	SNP	C	T	79	203	c.1424G>A	c.(1423-1425)AGC>AAC	p.S475N
Pat_28	Post-Resistance	COG3	83548	37	13	46057384	46057384	Missense_Mutation	SNP	C	T	17	41	c.737C>T	c.(736-738)CCC>CTC	p.P246L
Pat_28	Post-Resistance	CPB2	1361	37	13	46632381	46632381	Missense_Mutation	SNP	G	A	162	355	c.932C>T	c.(931-933)TCA>TTA	p.S311L
Pat_28	Post-Resistance	CDADC1	81602	37	13	49841965	49841965	Missense_Mutation	SNP	C	T	13	36	c.770C>T	c.(769-771)ACT>ATT	p.T257I
Pat_28	Post-Resistance	KCNRG	283518	37	13	50594432	50594432	Missense_Mutation	SNP	G	A	27	86	c.661G>A	c.(661-663)GAA>AAA	p.E221K
Pat_28	Post-Resistance	FAM10A4	145165	37	13	50746472	50746472	Missense_Mutation	SNP	G	A	12	42	c.248G>A	c.(247-249)GGT>GAT	p.G83D
Pat_28	Post-Resistance	DIAPH3	81624	37	13	60737836	60737836	Missense_Mutation	SNP	G	A	4	15	c.65C>T	c.(64-66)CCT>CTT	p.P22L
Pat_28	Post-Resistance	DACH1	1602	37	13	72440816	72440816	Missense_Mutation	SNP	G	A	6	24	c.92C>T	c.(91-93)ACC>ATC	p.T31I
Pat_28	Post-Resistance	TBC1D4	9882	37	13	76055733	76055733	Nonsense_Mutation	SNP	C	T	8	14	c.171G>A	c.(169-171)TGG>TGA	p.W57*
Pat_28	Post-Resistance	LMO7	4008	37	13	76397878	76397878	Missense_Mutation	SNP	C	T	25	116	c.2119C>T	c.(2119-2121)CCC>TCC	p.P707S
Pat_28	Post-Resistance	MYCBP2	23077	37	13	77732175	77732175	Missense_Mutation	SNP	C	T	46	133	c.6553G>A	c.(6553-6555)GCA>ACA	p.A2185T
Pat_28	Post-Resistance	DCT	1638	37	13	95131491	95131491	Missense_Mutation	SNP	C	T	13	48	c.19G>A	c.(19-21)GGG>AGG	p.G7R
Pat_28	Post-Resistance	TM9SF2	9375	37	13	100153939	100153939	Missense_Mutation	SNP	G	A	27	50	c.79G>A	c.(79-81)GTT>ATT	p.V27I
Pat_28	Post-Resistance	UPF3A	65110	37	13	115051782	115051782	Missense_Mutation	SNP	G	A	35	69	c.427G>A	c.(427-429)GAA>AAA	p.E143K
Pat_28	Post-Resistance	RNASE11	122651	37	14	21052549	21052549	Missense_Mutation	SNP	C	T	55	140	c.85G>A	c.(85-87)GAA>AAA	p.E29K
Pat_28	Post-Resistance	RNASE2	6036	37	14	21424315	21424315	Missense_Mutation	SNP	C	T	55	143	c.385C>T	c.(385-387)CCA>TCA	p.P129S
Pat_28	Post-Resistance	RAB2B	84932	37	14	21930517	21930517	Missense_Mutation	SNP	G	A	46	155	c.535C>T	c.(535-537)CAC>TAC	p.H179Y
Pat_28	Post-Resistance	SALL2	6297	37	14	21992135	21992135	Missense_Mutation	SNP	G	A	26	37	c.1727C>T	c.(1726-1728)CCC>CTC	p.P576L
Pat_28	Post-Resistance	LRP10	26020	37	14	23346554	23346554	Missense_Mutation	SNP	G	A	67	123	c.1960G>A	c.(1960-1962)GTG>ATG	p.V654M
Pat_28	Post-Resistance	LRRC16B	90668	37	14	24524817	24524817	Missense_Mutation	SNP	A	G	44	150	c.671A>G	c.(670-672)GAC>GGC	p.D224G
Pat_28	Post-Resistance	TM9SF1	10548	37	14	24662189	24662189	Missense_Mutation	SNP	G	A	11	33	c.632C>T	c.(631-633)ACT>ATT	p.T211I
Pat_28	Post-Resistance	LTB4R2	56413	37	14	24779959	24779959	Missense_Mutation	SNP	C	T	22	48	c.182C>T	c.(181-183)GCG>GTG	p.A61V
Pat_28	Post-Resistance	NYNRIN	57523	37	14	24868469	24868469	Missense_Mutation	SNP	G	A	16	37	c.17G>A	c.(16-18)GGC>GAC	p.G6D
Pat_28	Post-Resistance	RALGAPA1	253959	37	14	36096557	36096557	Missense_Mutation	SNP	G	A	42	127	c.5078C>T	c.(5077-5079)CCT>CTT	p.P1693L
Pat_28	Post-Resistance	FOXA1	3169	37	14	38061750	38061750	Missense_Mutation	SNP	C	T	21	58	c.239G>A	c.(238-240)GGC>GAC	p.G80D
Pat_28	Post-Resistance	SEC23A	10484	37	14	39514375	39514375	Missense_Mutation	SNP	G	A	54	148	c.1891C>T	c.(1891-1893)CCA>TCA	p.P631S
Pat_28	Post-Resistance	CTAGE5	4253	37	14	39772681	39772681	Splice_Site	SNP	G	A	54	139	c.917_splice	c.e11-1	p.D306_splice
Pat_28	Post-Resistance	PRPF39	55015	37	14	45577693	45577693	Missense_Mutation	SNP	G	A	43	108	c.979G>A	c.(979-981)GAA>AAA	p.E327K
Pat_28	Post-Resistance	RPL36AL	6166	37	14	50085608	50085608	Missense_Mutation	SNP	C	T	117	287	c.215G>A	c.(214-216)TGT>TAT	p.C72Y
Pat_28	Post-Resistance	ATP5S	27109	37	14	50788309	50788309	Missense_Mutation	SNP	A	T	55	36	c.149A>T	c.(148-150)AAT>ATT	p.N50I

Pat_28	Post-Resistance	SAV1	60485	37	14	51111627	51111627	Missense_Mutation	SNP	C	T	49	141	c.641G>A	c.(640-642)AGA>AAA	p.R214K
Pat_28	Post-Resistance	NID2	22795	37	14	52508877	52508877	Missense_Mutation	SNP	C	T	74	177	c.1771G>A	c.(1771-1773)GGC>AGC	p.G591S
Pat_28	Post-Resistance	NID2	22795	37	14	52534788	52534788	Missense_Mutation	SNP	G	A	12	25	c.322C>T	c.(322-324)CCT>TCT	p.P108S
Pat_28	Post-Resistance	GPR137C	283554	37	14	53101727	53101727	Missense_Mutation	SNP	C	T	40	134	c.1184C>T	c.(1183-1185)ACT>ATT	p.T395I
Pat_28	Post-Resistance	KIAA0586	9786	37	14	58937442	58937442	Splice_Site	SNP	G	A	11	50	c.2325_splice	c.e16+1	p.K775_splice
Pat_28	Post-Resistance	SYNE2	23224	37	14	64532207	64532207	Missense_Mutation	SNP	C	T	48	123	c.10270C>T	c.(10270-10272)CTT>TTT	p.L3424F
Pat_28	Post-Resistance	SYNE2	23224	37	14	64588803	64588803	Missense_Mutation	SNP	C	T	31	75	c.13232C>T	c.(13231-13233)CCC>CTC	p.P4411L
Pat_28	Post-Resistance	C14orf50	145376	37	14	65053913	65053913	Missense_Mutation	SNP	C	T	15	44	c.713C>T	c.(712-714)TCC>TTC	p.S238F
Pat_28	Post-Resistance	PLEKHH1	57475	37	14	68028985	68028985	Missense_Mutation	SNP	G	A	3	8	c.637G>A	c.(637-639)GCA>ACA	p.A213T
Pat_28	Post-Resistance	ZFYVE26	23503	37	14	68220930	68220930	Splice_Site	SNP	C	A	8	240	c.6987_splice	c.e38-1	p.R2329_splice
Pat_28	Post-Resistance	ZFYVE26	23503	37	14	68265160	68265161	Missense_Mutation	DNP	CC	TT	29	19	.1818_1819GG>A	316-1821)GAGGGG>GAA	p.G607R
Pat_28	Post-Resistance	DNAL1	83544	37	14	74125550	74125550	Missense_Mutation	SNP	G	A	24	84	c.43G>A	c.(43-45)GAA>AAA	p.E15K
Pat_28	Post-Resistance	C14orf115	55237	37	14	74823727	74823727	Missense_Mutation	SNP	G	A	16	48	c.241G>A	c.(241-243)GGG>AGG	p.G81R
Pat_28	Post-Resistance	C14orf1	11161	37	14	76121320	76121320	Splice_Site	SNP	C	T	88	211	c.134_splice	c.e3-1	p.V45_splice
Pat_28	Post-Resistance	EML5	161436	37	14	89083215	89083215	Missense_Mutation	SNP	C	T	33	85	c.5651G>A	c.(5650-5652)GGA>GAA	p.G1884E
Pat_28	Post-Resistance	C14orf102	55051	37	14	90769076	90769076	Missense_Mutation	SNP	C	T	22	47	c.1399G>A	c.(1399-1401)GAG>AAG	p.E467K
Pat_28	Post-Resistance	TRIP11	9321	37	14	92469971	92469971	Missense_Mutation	SNP	C	T	41	116	c.4349G>A	c.(4348-4350)AGA>AAA	p.R1450K
Pat_28	Post-Resistance	KIAA1409	57578	37	14	94063753	94063753	Missense_Mutation	SNP	C	T	68	187	c.2708C>T	c.(2707-2709)ACC>ATC	p.T903I
Pat_28	Post-Resistance	DICER1	23405	37	14	95573996	95573996	Missense_Mutation	SNP	G	A	37	115	c.2753C>T	c.(2752-2754)ACA>ATA	p.T918I
Pat_28	Post-Resistance	BDKRB1	623	37	14	96730461	96730461	Nonsense_Mutation	SNP	C	T	20	49	c.442C>T	c.(442-444)CAG>TAG	p.Q148*
Pat_28	Post-Resistance	HSP90AA1	3320	37	14	102605629	102605629	Missense_Mutation	SNP	G	A	26	54	c.113C>T	c.(112-114)CCA>CTA	p.P38L
Pat_28	Post-Resistance	RAGE	5891	37	14	102698043	102698043	Splice_Site	SNP	C	T	131	334	c.981_splice	c.e10+1	p.Q327_splice
Pat_28	Post-Resistance	ZNF839	55778	37	14	102793076	102793076	Missense_Mutation	SNP	C	T	7	18	c.695C>T	c.(694-696)TCT>TTT	p.S232F
Pat_28	Post-Resistance	RCOR1	23186	37	14	103187413	103187413	Missense_Mutation	SNP	C	T	81	223	c.1114C>T	c.(1114-1116)CTT>TTT	p.L372F
Pat_28	Post-Resistance	CDC42BPB	9578	37	14	103420938	103420938	Splice_Site	SNP	C	T	11	36	c.2988_splice	c.e22+1	p.E996_splice
Pat_28	Post-Resistance	AHNAK2	113146	37	14	105415040	105415040	Missense_Mutation	SNP	C	T	32	106	c.6748G>A	c.(6748-6750)GAC>AAC	p.D2250N
Pat_28	Post-Resistance	OR4M2	390538	37	15	22368861	22368861	Missense_Mutation	SNP	G	A	37	204	c.286G>A	c.(286-288)GGA>AGA	p.G96R
Pat_28	Post-Resistance	C15orf2	23742	37	15	24924252	24924252	Missense_Mutation	SNP	G	A	30	55	c.3238G>A	c.(3238-3240)GGA>AGA	p.G1080R
Pat_28	Post-Resistance	RYR3	6263	37	15	33955831	33955831	Nonsense_Mutation	SNP	C	T	5	19	c.5512C>T	c.(5512-5514)CAG>TAG	p.Q1838*
Pat_28	Post-Resistance	SPRED1	161742	37	15	38643504	38643504	Missense_Mutation	SNP	G	A	30	37	c.974G>A	c.(973-975)CGA>CAA	p.R325Q
Pat_28	Post-Resistance	INO80	54617	37	15	41277593	41277593	Missense_Mutation	SNP	C	A	50	78	c.3864G>T	c.(3862-3864)CAG>CAT	p.Q1288H
Pat_28	Post-Resistance	MAPKBP1	23005	37	15	42110227	42110227	Missense_Mutation	SNP	G	A	87	123	c.1943G>A	c.(1942-1944)GGA>GAA	p.G648E
Pat_28	Post-Resistance	ZFP106	64397	37	15	42717193	42717193	Missense_Mutation	SNP	G	A	44	45	c.4960C>T	c.(4960-4962)CAT>TAT	p.H1654Y
Pat_28	Post-Resistance	TUBGCP4	27229	37	15	43678070	43678070	Missense_Mutation	SNP	C	T	24	44	c.805C>T	c.(805-807)CCA>TCA	p.P269S
Pat_28	Post-Resistance	CATSPER2	117155	37	15	43940142	43940142	Missense_Mutation	SNP	G	T	6	146	c.118C>A	c.(118-120)CCG>ACG	p.P40T
Pat_28	Post-Resistance	SPG11	80208	37	15	44888417	44888417	Missense_Mutation	SNP	C	T	66	83	c.4298G>A	c.(4297-4299)GGA>GAA	p.G1433E
Pat_28	Post-Resistance	DUOX1	53905	37	15	45444694	45444694	Missense_Mutation	SNP	C	T	19	32	c.3404C>T	c.(3403-3405)TCC>TTC	p.S1135F
Pat_28	Post-Resistance	SLC27A2	11001	37	15	50521152	50521152	Missense_Mutation	SNP	G	A	30	59	c.1468G>A	c.(1468-1470)GAA>AAA	p.E490K
Pat_28	Post-Resistance	GABPB1	2553	37	15	50596219	50596219	Missense_Mutation	SNP	G	A	69	97	c.220C>T	c.(220-222)CCA>TCA	p.P74S
Pat_28	Post-Resistance	GLDN	342035	37	15	51669649	51669649	Nonsense_Mutation	SNP	C	T	35	39	c.367C>T	c.(367-369)CGA>TGA	p.R123*
Pat_28	Post-Resistance	PRTG	283659	37	15	55916646	55916646	Missense_Mutation	SNP	G	A	39	34	c.2987C>T	c.(2986-2988)GCC>GTC	p.A996V
Pat_28	Post-Resistance	ZNF280D	54816	37	15	56946646	56946646	Missense_Mutation	SNP	C	T	43	68	c.2113G>A	c.(2113-2115)GAT>AAT	p.D705N
Pat_28	Post-Resistance	ZNF280D	54816	37	15	56981518	56981518	Missense_Mutation	SNP	G	A	48	93	c.650C>T	c.(649-651)TCC>TTC	p.S217F
Pat_28	Post-Resistance	SLTM	79811	37	15	59179711	59179711	Missense_Mutation	SNP	C	T	27	48	c.2404G>A	c.(2404-2406)GGG>AGG	p.G802R
Pat_28	Post-Resistance	HERC1	8925	37	15	63922787	63922787	Missense_Mutation	SNP	G	A	75	107	c.12844C>T	c.(12844-12846)CCG>TCG	p.P4282S
Pat_28	Post-Resistance	HERC1	8925	37	15	63967129	63967129	Missense_Mutation	SNP	G	A	61	88	c.7258C>T	c.(7258-7260)CAT>TAT	p.H2420Y
Pat_28	Post-Resistance	MAP2K1	5604	37	15	66735639	66735639	Missense_Mutation	SNP	G	A	44	65	c.460G>A	c.(460-462)GTC>ATC	p.V154I

Pat_28	Post-Resistance	LCTL	197021	37	15	66845518	66845518	Missense_Mutation	SNP	C	T	88	156	c.1001G>A	c.(1000-1002)GGC>GAC	p.G334D
Pat_28	Post-Resistance	PKM2	5315	37	15	72500969	72500969	Missense_Mutation	SNP	C	T	32	51	c.829G>A	c.(829-831)GTT>ATT	p.V277I
Pat_28	Post-Resistance	CELF6	60677	37	15	72612113	72612113	Missense_Mutation	SNP	C	T	3	6	c.103G>A	c.(103-105)GGT>AGT	p.G35S
Pat_28	Post-Resistance	NEO1	4756	37	15	73414991	73414991	Missense_Mutation	SNP	C	T	62	109	c.574C>T	c.(574-576)CTT>TTT	p.L192F
Pat_28	Post-Resistance	EDC3	80153	37	15	74925035	74925035	Missense_Mutation	SNP	G	A	42	59	c.1445C>T	c.(1444-1446)CCC>CTC	p.P482L
Pat_28	Post-Resistance	C15orf27	123591	37	15	76430187	76430187	Missense_Mutation	SNP	G	A	27	41	c.178G>A	c.(178-180)GCG>ACG	p.A60T
Pat_28	Post-Resistance	SH2D7	646892	37	15	78393670	78393670	Missense_Mutation	SNP	C	T	4	7	c.1075C>T	c.(1075-1077)CTC>TTC	p.L359F
Pat_28	Post-Resistance	RASGRF1	5923	37	15	79317768	79317768	Missense_Mutation	SNP	C	T	24	34	c.1430G>A	c.(1429-1431)GGG>GAG	p.G477E
Pat_28	Post-Resistance	ADAMTSL3	57188	37	15	84651298	84651298	Missense_Mutation	SNP	C	T	57	73	c.2918C>T	c.(2917-2919)GCT>GTT	p.A973V
Pat_28	Post-Resistance	ZNF592	9640	37	15	85327998	85327998	Missense_Mutation	SNP	C	T	39	57	c.2092C>T	c.(2092-2094)CCA>TCA	p.P698S
Pat_28	Post-Resistance	AKAP13	11214	37	15	86129008	86129008	Missense_Mutation	SNP	G	A	52	65	c.4115G>A	c.(4114-4116)AGC>AAC	p.S1372N
Pat_28	Post-Resistance	DET1	55070	37	15	89074920	89074920	Missense_Mutation	SNP	G	A	28	35	c.17C>T	c.(16-18)TCT>TTT	p.S6F
Pat_28	Post-Resistance	IDH2	3418	37	15	90630349	90630349	Missense_Mutation	SNP	G	A	42	64	c.962C>T	c.(961-963)GCC>GTC	p.A321V
Pat_28	Post-Resistance	IQGAP1	8826	37	15	91020018	91020018	Missense_Mutation	SNP	G	A	57	82	c.2908G>A	c.(2908-2910)GAA>AAA	p.E970K
Pat_28	Post-Resistance	CLCN7	1186	37	16	1498984	1498984	Missense_Mutation	SNP	C	T	10	21	c.1780G>A	c.(1780-1782)GGC>AGC	p.G594S
Pat_28	Post-Resistance	TSC2	7249	37	16	2115539	2115539	Missense_Mutation	SNP	C	T	69	103	c.1619C>T	c.(1618-1620)TCC>TTC	p.S540F
Pat_28	Post-Resistance	PKD1	5310	37	16	2159518	2159518	Missense_Mutation	SNP	C	T	9	5	c.5650G>A	c.(5650-5652)GAG>AAG	p.E1884K
Pat_28	Post-Resistance	SRRM2	23524	37	16	2811608	2811608	Missense_Mutation	SNP	G	A	88	123	c.1079G>A	c.(1078-1080)GGC>GAC	p.G360D
Pat_28	Post-Resistance	ZNF200	7752	37	16	3283749	3283749	Missense_Mutation	SNP	C	T	63	115	c.7G>A	c.(7-9)GCT>ACT	p.A3T
Pat_28	Post-Resistance	MEFV	4210	37	16	3293211	3293211	Missense_Mutation	SNP	C	T	20	46	c.2276G>A	c.(2275-2277)GGG>GAG	p.G759E
Pat_28	Post-Resistance	ZNF434	54925	37	16	3434791	3434791	Missense_Mutation	SNP	C	T	83	107	c.266G>A	c.(265-267)CGG>CAG	p.R89Q
Pat_28	Post-Resistance	HMOX2	3163	37	16	4557807	4557807	Missense_Mutation	SNP	C	T	35	40	c.298C>T	c.(298-300)CCC>TCC	p.P100S
Pat_28	Post-Resistance	MGRN1	23295	37	16	4732846	4732846	Missense_Mutation	SNP	C	T	19	34	c.1381C>T	c.(1381-1383)CCC>TCC	p.P461S
Pat_28	Post-Resistance	A2BP1	54715	37	16	7703847	7703847	Missense_Mutation	SNP	C	T	35	59	c.788C>T	c.(787-789)GCC>GTC	p.A263V
Pat_28	Post-Resistance	NTAN1	123803	37	16	15141408	15141408	Splice_Site	SNP	C	T	16	5	c.251_splice	c.e4-1	p.G84_splice
Pat_28	Post-Resistance	ACSM2B	348158	37	16	20563483	20563483	Missense_Mutation	SNP	G	A	78	26	c.877C>T	c.(877-879)CCA>TCA	p.P293S
Pat_28	Post-Resistance	PRKCB	5579	37	16	24196889	24196889	Splice_Site	SNP	G	A	28	9	c.1722_splice	c.e15+1	p.G574_splice
Pat_28	Post-Resistance	CORO1A	11151	37	16	30196592	30196592	Missense_Mutation	SNP	C	T	27	16	c.62C>T	c.(61-63)GCC>GTC	p.A21V
Pat_28	Post-Resistance	PRR14	78994	37	16	30666261	30666261	Missense_Mutation	SNP	C	T	37	24	c.970C>T	c.(970-972)CCT>TCT	p.P324S
Pat_28	Post-Resistance	PSKH1	5681	37	16	67942965	67942965	Missense_Mutation	SNP	G	A	23	13	c.313G>A	c.(313-315)GGC>AGC	p.G105S
Pat_28	Post-Resistance	HYDIN	54768	37	16	70891656	70891656	Missense_Mutation	SNP	G	A	18	32	c.12244C>T	c.(12244-12246)CTC>TTC	p.L4082F
Pat_28	Post-Resistance	KIAA0174	9798	37	16	71950997	71950997	Missense_Mutation	SNP	C	T	30	22	c.356C>T	c.(355-357)GCT>GTT	p.A119V
Pat_28	Post-Resistance	CNTNAP4	85445	37	16	76481969	76481970	Missense_Mutation	DNP	CC	TT	19	17	c.599_600CC>TT	c.(598-600)TCC>TTT	p.S200F
Pat_28	Post-Resistance	BCMO1	53630	37	16	81295889	81295889	Splice_Site	SNP	G	A	15	10	c.471_splice	c.e4+1	p.K157_splice
Pat_28	Post-Resistance	CDH13	1012	37	16	83159054	83159054	Missense_Mutation	SNP	C	T	16	4	c.431C>T	c.(430-432)CCC>CTC	p.P144L
Pat_28	Post-Resistance	OSGIN1	29948	37	16	83998908	83998908	Missense_Mutation	SNP	C	T	7	8	c.979C>T	c.(979-981)CTC>TTC	p.L327F
Pat_28	Post-Resistance	TCF25	22980	37	16	89965263	89965263	Missense_Mutation	SNP	C	T	14	10	c.1204C>T	c.(1204-1206)CTC>TTC	p.L402F
Pat_28	Post-Resistance	SMYD4	114826	37	17	1703574	1703574	Missense_Mutation	SNP	C	T	68	109	c.1114G>A	c.(1114-1116)GAT>AAT	p.D372N
Pat_28	Post-Resistance	ATP2A3	489	37	17	3854679	3854679	Missense_Mutation	SNP	C	T	9	50	c.329G>A	c.(328-330)CGC>CAC	p.R110H
Pat_28	Post-Resistance	ANKFY1	51479	37	17	4083052	4083052	Missense_Mutation	SNP	C	A	9	159	c.2361G>T	c.(2359-2361)CAG>CAT	p.Q787H
Pat_28	Post-Resistance	KIF1C	10749	37	17	4904580	4904580	Missense_Mutation	SNP	C	T	45	47	c.247C>T	c.(247-249)CTC>TTC	p.L83F
Pat_28	Post-Resistance	ZNF232	7775	37	17	5012856	5012856	Missense_Mutation	SNP	C	T	30	69	c.250G>A	c.(250-252)GAG>AAG	p.E84K
Pat_28	Post-Resistance	C17orf87	388325	37	17	5126713	5126713	Nonsense_Mutation	SNP	C	T	38	132	c.60G>A	c.(58-60)TGG>TGA	p.W20*
Pat_28	Post-Resistance	NLRP1	22861	37	17	5418157	5418157	Missense_Mutation	SNP	C	T	16	31	c.4339G>A	c.(4339-4341)GCC>ACC	p.A1447T
Pat_28	Post-Resistance	NEURL4	84461	37	17	7219594	7219594	Missense_Mutation	SNP	C	T	12	33	c.4537G>A	c.(4537-4539)GTG>ATG	p.V1513M
Pat_28	Post-Resistance	CHRNB1	1140	37	17	7352023	7352023	Missense_Mutation	SNP	C	T	27	39	c.736C>T	c.(736-738)CTC>TTC	p.L246F
Pat_28	Post-Resistance	WRAP53	55135	37	17	7606676	7606676	Missense_Mutation	SNP	C	T	14	26	c.1519C>T	c.(1519-1521)CAC>TAC	p.H507Y

Pat_28	Post-Resistance	ARHGEF15	22899	37	17	8222177	8222177	Missense_Mutation	SNP	C	T	137	208	c.1982C>T	c.(1981-1983)CCT>CTT	p.P661L
Pat_28	Post-Resistance	MYH13	8735	37	17	10224989	10224989	Missense_Mutation	SNP	C	T	15	28	c.2971G>A	c.(2971-2973)GAA>AAA	p.E991K
Pat_28	Post-Resistance	DNAH9	1770	37	17	11660901	11660901	Missense_Mutation	SNP	C	T	37	54	c.6887C>T	c.(6886-6888)CCT>CTT	p.P2296L
Pat_28	Post-Resistance	TRIM16	10626	37	17	15518958	15518958	Splice_Site	SNP	C	T	13	29	c.1600_splice	c.e8+1	p.E534_splice
Pat_28	Post-Resistance	CDRT1	374286	37	17	15522757	15522757	Missense_Mutation	SNP	G	A	145	232	c.70C>T	c.(70-72)CCT>TCT	p.P24S
Pat_28	Post-Resistance	NCOR1	9611	37	17	16089890	16089890	Missense_Mutation	SNP	C	T	30	46	c.220G>A	c.(220-222)GAA>AAA	p.E74K
Pat_28	Post-Resistance	CENPV	201161	37	17	16256366	16256366	Missense_Mutation	SNP	C	T	6	14	c.385G>A	c.(385-387)GCC>ACC	p.A129T
Pat_28	Post-Resistance	PEMT	10400	37	17	17415822	17415822	Splice_Site	SNP	C	T	5	15	c.355_splice	c.e4+1	p.G119_splice
Pat_28	Post-Resistance	SLC47A1	55244	37	17	19463768	19463768	Missense_Mutation	SNP	C	A	41	75	c.1068C>A	c.(1066-1068)AGC>AGA	p.S356R
Pat_28	Post-Resistance	NOS2	4843	37	17	26085933	26085933	Missense_Mutation	SNP	C	T	6	11	c.3328G>A	c.(3328-3330)GTC>ATC	p.V1110I
Pat_28	Post-Resistance	MYO18A	399687	37	17	27438824	27438824	Missense_Mutation	SNP	C	T	10	16	c.2656G>A	c.(2656-2658)GAG>AAG	p.E886K
Pat_28	Post-Resistance	SLC6A4	6532	37	17	28545256	28545256	Missense_Mutation	SNP	T	A	18	17	c.578A>T	c.(577-579)GAC>GTC	p.D193V
Pat_28	Post-Resistance	UNC45B	146862	37	17	33496857	33496857	Missense_Mutation	SNP	G	A	22	33	c.1454G>A	c.(1453-1455)GGA>GAA	p.G485E
Pat_28	Post-Resistance	GPR179	440435	37	17	36489193	36489193	Missense_Mutation	SNP	G	A	18	19	c.1978C>T	c.(1978-1980)CTT>TTT	p.L660F
Pat_28	Post-Resistance	KRT40	125115	37	17	39140422	39140422	Missense_Mutation	SNP	G	A	24	23	c.104C>T	c.(103-105)CCC>CTC	p.P35L
Pat_28	Post-Resistance	KRTAP4-5	85289	37	17	39305839	39305839	Missense_Mutation	SNP	A	T	5	92	c.181T>A	c.(181-183)TGC>AGC	p.C61S
Pat_28	Post-Resistance	STAT5A	6776	37	17	40456662	40456662	Nonsense_Mutation	SNP	C	T	62	80	c.1372C>T	c.(1372-1374)CAG>TAG	p.Q458*
Pat_28	Post-Resistance	STAT5A	6776	37	17	40458299	40458299	Missense_Mutation	SNP	C	T	48	48	c.1514C>T	c.(1513-1515)CCG>CTG	p.P505L
Pat_28	Post-Resistance	NAGLU	4669	37	17	40695604	40695604	Missense_Mutation	SNP	C	T	13	20	c.1580C>T	c.(1579-1581)ACC>ATC	p.T527I
Pat_28	Post-Resistance	WNK4	65266	37	17	40940379	40940379	Missense_Mutation	SNP	G	A	18	21	c.1994G>A	c.(1993-1995)GGG>GAG	p.G665E
Pat_28	Post-Resistance	AOC3	8639	37	17	41003494	41003494	Missense_Mutation	SNP	C	T	45	68	c.134C>T	c.(133-135)TCT>TTT	p.S45F
Pat_28	Post-Resistance	GPATCH8	23131	37	17	42474974	42474974	Missense_Mutation	SNP	C	T	39	54	c.4471G>A	c.(4471-4473)GGT>AGT	p.G1491S
Pat_28	Post-Resistance	DBF4B	80174	37	17	42828308	42828308	Missense_Mutation	SNP	C	T	16	31	c.1535C>T	c.(1534-1536)CCC>CTC	p.P512L
Pat_28	Post-Resistance	EFTUD2	9343	37	17	42937832	42937832	Missense_Mutation	SNP	C	T	5	121	c.1687G>A	c.(1687-1689)GCA>ACA	p.A563T
Pat_28	Post-Resistance	TBX21	30009	37	17	45822662	45822662	Missense_Mutation	SNP	C	T	9	16	c.1538C>T	c.(1537-1539)TCC>TTC	p.S513F
Pat_28	Post-Resistance	NFE2L1	4779	37	17	46128833	46128833	Missense_Mutation	SNP	C	T	37	59	c.353C>T	c.(352-354)CCC>CTC	p.P118L
Pat_28	Post-Resistance	AKAP1	8165	37	17	55193535	55193535	Missense_Mutation	SNP	C	T	33	50	c.2345C>T	c.(2344-2346)TCC>TTC	p.S782F
Pat_28	Post-Resistance	BZRAP1	9256	37	17	56393847	56393847	Missense_Mutation	SNP	G	A	25	34	c.1927C>T	c.(1927-1929)CCA>TCA	p.P643S
Pat_28	Post-Resistance	TANC2	26115	37	17	61499122	61499122	Missense_Mutation	SNP	G	T	30	40	c.5779G>T	c.(5779-5781)GCT>TCT	p.A1927S
Pat_28	Post-Resistance	HELZ	9931	37	17	65163817	65163817	Missense_Mutation	SNP	C	T	63	105	c.1526G>A	c.(1525-1527)GGT>GAT	p.G509D
Pat_28	Post-Resistance	BPTF	2186	37	17	65871125	65871125	Missense_Mutation	SNP	G	T	51	76	c.1853G>T	c.(1852-1854)GGA>GTA	p.G618V
Pat_28	Post-Resistance	PRKAR1A	5573	37	17	66522054	66522054	Splice_Site	SNP	G	A	20	17	c.708_splice	c.e7+1	p.M236_splice
Pat_28	Post-Resistance	ABCA8	10351	37	17	66887738	66887738	Splice_Site	SNP	C	T	25	33	c.2917_splice	c.e22-1	p.N973_splice
Pat_28	Post-Resistance	DNAI2	64446	37	17	72277988	72277988	Missense_Mutation	SNP	G	A	53	81	c.32G>A	c.(31-33)CGC>CAC	p.R11H
Pat_28	Post-Resistance	GAA	2548	37	17	78082578	78082578	Missense_Mutation	SNP	C	T	6	6	c.1277C>T	c.(1276-1278)GCC>GTC	p.A426V
Pat_28	Post-Resistance	GAA	2548	37	17	78083747	78083747	Missense_Mutation	SNP	C	T	17	34	c.1330C>T	c.(1330-1332)CCT>TCT	p.P444S
Pat_28	Post-Resistance	TBCD	6904	37	17	80887270	80887270	Missense_Mutation	SNP	C	T	9	19	c.2885C>T	c.(2884-2886)CCT>CTT	p.P962L
Pat_28	Post-Resistance	NAPG	8774	37	18	10549040	10549040	Missense_Mutation	SNP	G	A	140	203	c.742G>A	c.(742-744)GAT>AAT	p.D248N
Pat_28	Post-Resistance	ROCK1	6093	37	18	18539864	18539864	Missense_Mutation	SNP	A	T	22	37	c.3449T>A	c.(3448-3450)ATT>AAT	p.I1150N
Pat_28	Post-Resistance	CABLES1	91768	37	18	20774434	20774434	Missense_Mutation	SNP	C	T	35	47	c.940C>T	c.(940-942)CCC>TCC	p.P314S
Pat_28	Post-Resistance	CDH2	1000	37	18	25570271	25570271	Missense_Mutation	SNP	G	A	51	56	c.1388C>T	c.(1387-1389)GCT>GTT	p.A463V
Pat_28	Post-Resistance	DSC1	1823	37	18	28714042	28714042	Missense_Mutation	SNP	G	A	83	116	c.1928C>T	c.(1927-1929)TCT>TTT	p.S643F
Pat_28	Post-Resistance	C18orf34	374864	37	18	30913179	30913179	Missense_Mutation	SNP	C	T	27	52	c.838G>A	c.(838-840)GAA>AAA	p.E280K
Pat_28	Post-Resistance	C18orf21	83608	37	18	33552764	33552764	Missense_Mutation	SNP	C	T	22	30	c.73C>T	c.(73-75)CTC>TTC	p.L25F
Pat_28	Post-Resistance	TCF4	6925	37	18	52946848	52946848	Missense_Mutation	SNP	C	T	48	65	c.589G>A	c.(589-591)GAC>AAC	p.D197N
Pat_28	Post-Resistance	PHLPP1	23239	37	18	60645567	60645567	Missense_Mutation	SNP	C	T	11	29	c.2521C>T	c.(2521-2523)CCT>TCT	p.P841S
Pat_28	Post-Resistance	SERPINB7	8710	37	18	61465975	61465975	Missense_Mutation	SNP	C	T	60	109	c.592C>T	c.(592-594)CCC>TCC	p.P198S

Pat_28	Post-Resistance	FBXO15	201456	37	18	71793289	71793289	Missense_Mutation	SNP	G	A	57	87	c.605C>T	c.(604-606)ACC>ATC	p.T202I
Pat_28	Post-Resistance	CNDP2	55748	37	18	72173088	72173088	Missense_Mutation	SNP	C	T	19	19	c.209C>T	c.(208-210)CCT>CTT	p.P70L
Pat_28	Post-Resistance	PQLC1	80148	37	18	77710866	77710866	Missense_Mutation	SNP	C	T	9	11	c.61G>A	c.(61-63)GCG>ACG	p.A21T
Pat_28	Post-Resistance	ABCA7	10347	37	19	1051561	1051561	Missense_Mutation	SNP	G	A	7	4	c.2938G>A	c.(2938-2940)GAG>AAG	p.E980K
Pat_28	Post-Resistance	ADAMTSL5	339366	37	19	1510414	1510414	Missense_Mutation	SNP	C	T	8	15	c.205G>A	c.(205-207)GAA>AAA	p.E69K
Pat_28	Post-Resistance	REXO1	57455	37	19	1821560	1821561	Missense_Mutation	DNP	GG	AA	33	56	.2351_2352CC>T	c.(2350-2352)ACC>ATT	p.T784I
Pat_28	Post-Resistance	ZFR2	23217	37	19	3813925	3813925	Missense_Mutation	SNP	G	A	6	13	c.2135C>T	c.(2134-2136)TCC>TTC	p.S712F
Pat_28	Post-Resistance	DUS3L	56931	37	19	5788114	5788114	Missense_Mutation	SNP	C	T	29	29	c.1016G>A	c.(1015-1017)TGC>TAC	p.C339Y
Pat_28	Post-Resistance	LRRC8E	80131	37	19	7965235	7965235	Missense_Mutation	SNP	C	T	6	15	c.1828C>T	c.(1828-1830)CTT>TTT	p.L610F
Pat_28	Post-Resistance	MUC16	94025	37	19	9072952	9072952	Missense_Mutation	SNP	C	T	25	56	c.14494G>A	c.(14494-14496)GTT>ATT	p.V4832I
Pat_28	Post-Resistance	MUC16	94025	37	19	9088864	9088864	Missense_Mutation	SNP	G	A	138	217	c.2951C>T	c.(2950-2952)ACT>ATT	p.T984I
Pat_28	Post-Resistance	MUC16	94025	37	19	9089170	9089170	Missense_Mutation	SNP	G	A	6	14	c.2645C>T	c.(2644-2646)TCC>TTC	p.S882F
Pat_28	Post-Resistance	ZNF426	79088	37	19	9639763	9639763	Missense_Mutation	SNP	A	G	6	148	c.958T>C	c.(958-960)TCC>CCC	p.S320P
Pat_28	Post-Resistance	DNMT1	1786	37	19	10259597	10259597	Missense_Mutation	SNP	G	A	47	75	c.2635C>T	c.(2635-2637)CCT>TCT	p.P879S
Pat_28	Post-Resistance	DOCK6	57572	37	19	11333782	11333782	Missense_Mutation	SNP	C	T	14	28	c.2956G>A	c.(2956-2958)GAT>AAT	p.D986N
Pat_28	Post-Resistance	ZNF491	126069	37	19	11916832	11916832	Missense_Mutation	SNP	C	T	28	50	c.64C>T	c.(64-66)CCG>TCG	p.P22S
Pat_28	Post-Resistance	ZNF490	57474	37	19	12691426	12691426	Missense_Mutation	SNP	G	A	53	75	c.1463C>T	c.(1462-1464)TCC>TTC	p.S488F
Pat_28	Post-Resistance	SFRS14	10147	37	19	19105966	19105966	Missense_Mutation	SNP	C	T	8	14	c.3115G>A	c.(3115-3117)GAG>AAG	p.E1039K
Pat_28	Post-Resistance	NCAN	1463	37	19	19329858	19329858	Missense_Mutation	SNP	G	A	14	20	c.208G>A	c.(208-210)GCC>ACC	p.A70T
Pat_28	Post-Resistance	ZNF714	148206	37	19	21300311	21300311	Missense_Mutation	SNP	G	A	13	24	c.844G>A	c.(844-846)GAA>AAA	p.E282K
Pat_28	Post-Resistance	ZNF493	284443	37	19	21606468	21606468	Missense_Mutation	SNP	C	T	5	61	c.623C>T	c.(622-624)CCT>CTT	p.P208L
Pat_28	Post-Resistance	ZNF676	163223	37	19	22363137	22363137	Missense_Mutation	SNP	G	A	124	170	c.1382C>T	c.(1381-1383)TCC>TTC	p.S461F
Pat_28	Post-Resistance	ZNF681	148213	37	19	23927342	23927343	Missense_Mutation	DNP	GG	AA	107	176	.1009_1010CC>T	c.(1009-1011)CCC>TTC	p.P337F
Pat_28	Post-Resistance	HPN	3249	37	19	35550855	35550855	Missense_Mutation	SNP	G	A	6	2	c.368G>A	c.(367-369)GGG>GAG	p.G123E
Pat_28	Post-Resistance	ZNF567	163081	37	19	37210792	37210792	Missense_Mutation	SNP	G	A	28	10	c.1166G>A	c.(1165-1167)GGT>GAT	p.G389D
Pat_28	Post-Resistance	SHKBP1	92799	37	19	41089329	41089329	Missense_Mutation	SNP	G	A	5	1	c.986G>A	c.(985-987)AGT>AAT	p.S329N
Pat_28	Post-Resistance	CEACAM5	1048	37	19	42231273	42231273	Splice_Site	SNP	G	A	45	16	c.2145_splice	c.e9+1	
Pat_28	Post-Resistance	IRF2BP1	26145	37	19	46387621	46387621	Missense_Mutation	SNP	C	T	2	3	c.1412G>A	c.(1411-1413)CGC>CAC	p.R471H
Pat_28	Post-Resistance	LRRC4B	94030	37	19	51021106	51021106	Missense_Mutation	SNP	C	T	10	4	c.1864G>A	c.(1864-1866)GAC>AAC	p.D622N
Pat_28	Post-Resistance	KLK10	5655	37	19	51518677	51518677	Missense_Mutation	SNP	C	T	58	30	c.674G>A	c.(673-675)TGC>TAC	p.C225Y
Pat_28	Post-Resistance	TTYH1	57348	37	19	54937938	54937938	Missense_Mutation	SNP	G	A	18	9	c.727G>A	c.(727-729)GTG>ATG	p.V243M
Pat_28	Post-Resistance	SAPS1	22870	37	19	55743331	55743332	Missense_Mutation	DNP	GG	AA	7	0	.2144_2145CC>T	c.(2143-2145)ACC>ATT	p.T715I
Pat_28	Post-Resistance	NLRP9	338321	37	19	56244884	56244884	Missense_Mutation	SNP	C	T	29	17	c.313G>A	c.(313-315)GAA>AAA	p.E105K
Pat_28	Post-Resistance	NLRP8	126205	37	19	56467192	56467192	Missense_Mutation	SNP	G	A	13	8	c.1768G>A	c.(1768-1770)GTC>ATC	p.V590I
Pat_28	Post-Resistance	NLRP5	126206	37	19	56539808	56539808	Missense_Mutation	SNP	C	T	85	30	c.2209C>T	c.(2209-2211)CGG>TGG	p.R737W
Pat_28	Post-Resistance	ZNF446	55663	37	19	58991958	58991958	Nonsense_Mutation	SNP	G	A	16	5	c.1218G>A	c.(1216-1218)TGG>TGA	p.W406*
Pat_28	Post-Resistance	MZF1	7593	37	19	59073780	59073780	Missense_Mutation	SNP	C	T	11	4	c.1864G>A	c.(1864-1866)GAA>AAA	p.E622K
Pat_28	Post-Resistance	TTC15	51112	37	2	3392191	3392191	Missense_Mutation	SNP	G	A	5	5	c.797G>A	c.(796-798)CGA>CAA	p.R266Q
Pat_28	Post-Resistance	RSAD2	91543	37	2	7018278	7018278	Splice_Site	SNP	G	A	12	23	c.346_splice	c.e1+1	p.G116_splice
Pat_28	Post-Resistance	RNF144A	9781	37	2	7164519	7164519	Missense_Mutation	SNP	G	A	24	102	c.529G>A	c.(529-531)GAA>AAA	p.E177K
Pat_28	Post-Resistance	ATP6V1C2	245973	37	2	10912050	10912050	Missense_Mutation	SNP	G	A	61	90	c.556G>A	c.(556-558)GTC>ATC	p.V186I
Pat_28	Post-Resistance	NBAS	51594	37	2	15514779	15514779	Missense_Mutation	SNP	G	A	117	192	c.3656C>T	c.(3655-3657)GCC>GTC	p.A1219V
Pat_28	Post-Resistance	APOB	338	37	2	21249778	21249778	Missense_Mutation	SNP	C	T	22	37	c.2126G>A	c.(2125-2127)GGA>GAA	p.G709E
Pat_28	Post-Resistance	ADCY3	109	37	2	25141636	25141636	Missense_Mutation	SNP	C	T	27	21	c.221G>A	c.(220-222)CGC>CAC	p.R74H
Pat_28	Post-Resistance	ASXL2	55252	37	2	26029195	26029195	Missense_Mutation	SNP	G	A	9	18	c.155C>T	c.(154-156)CCT>CTT	p.P52L
Pat_28	Post-Resistance	C2orf39	92749	37	2	26676329	26676329	Missense_Mutation	SNP	G	A	3	8	c.1831G>A	c.(1831-1833)GAG>AAG	p.E611K
Pat_28	Post-Resistance	CAD	790	37	2	27447990	27447990	Missense_Mutation	SNP	G	A	29	32	c.1499G>A	c.(1498-1500)CGG>CAG	p.R500Q

Pat_28	Post-Resistance	SNX17	9784	37	2	27596970	27596970	Missense_Mutation	SNP	G	A	78	128	c.451G>A	c.(451-453)GAT>AAT	p.D151N
Pat_28	Post-Resistance	BIRC6	57448	37	2	32704593	32704593	Missense_Mutation	SNP	G	A	12	5	c.7316G>A	c.(7315-7317)GGT>GAT	p.G2439D
Pat_28	Post-Resistance	FAM98A	25940	37	2	33810001	33810001	Missense_Mutation	SNP	G	A	22	48	c.1399C>T	c.(1399-1401)CGT>TGT	p.R467C
Pat_28	Post-Resistance	FEZ2	9637	37	2	36808513	36808513	Missense_Mutation	SNP	G	A	77	24	c.554C>T	c.(553-555)CCT>CTT	p.P185L
Pat_28	Post-Resistance	MSH2	4436	37	2	47639656	47639656	Missense_Mutation	SNP	G	A	34	11	c.749G>A	c.(748-750)GGA>GAA	p.G250E
Pat_28	Post-Resistance	MSH6	2956	37	2	48030799	48030799	Missense_Mutation	SNP	G	A	58	25	c.3413G>A	c.(3412-3414)GGG>GAG	p.G1138E
Pat_28	Post-Resistance	SMEK2	57223	37	2	55806904	55806904	Missense_Mutation	SNP	C	T	15	35	c.1379G>A	c.(1378-1380)AGT>AAT	p.S460N
Pat_28	Post-Resistance	ANTXR1	84168	37	2	69472535	69472535	Missense_Mutation	SNP	C	T	7	6	c.1613C>T	c.(1612-1614)TCC>TTC	p.S538F
Pat_28	Post-Resistance	C2orf42	54980	37	2	70392231	70392231	Missense_Mutation	SNP	G	A	48	83	c.1346C>T	c.(1345-1347)ACC>ATC	p.T449I
Pat_28	Post-Resistance	MPHOSPH10	10199	37	2	71376534	71376534	Missense_Mutation	SNP	C	T	33	37	c.1847C>T	c.(1846-1848)TCG>TTG	p.S616L
Pat_28	Post-Resistance	ALMS1	7840	37	2	73679238	73679238	Missense_Mutation	SNP	G	A	23	58	c.5587G>A	c.(5587-5589)GAG>AAG	p.E1863K
Pat_28	Post-Resistance	MOGS	7841	37	2	74690347	74690347	Missense_Mutation	SNP	C	T	76	159	c.746G>A	c.(745-747)AGT>AAT	p.S249N
Pat_28	Post-Resistance	REEP1	65055	37	2	86459804	86459804	Missense_Mutation	SNP	C	T	14	27	c.539G>A	c.(538-540)GGC>GAC	p.G180D
Pat_28	Post-Resistance	EIF2AK3	9451	37	2	88885358	88885358	Splice_Site	SNP	C	T	20	38	c.1650_splice	c.e9+1	p.R550_splice
Pat_28	Post-Resistance	SNRNP200	23020	37	2	96949423	96949423	Missense_Mutation	SNP	C	T	88	123	c.4613G>A	c.(4612-4614)CGC>CAC	p.R1538H
Pat_28	Post-Resistance	IL1RL2	8808	37	2	102851660	102851660	Missense_Mutation	SNP	A	G	6	75	c.1601A>G	c.(1600-1602)TAC>TGC	p.Y534C
Pat_28	Post-Resistance	TGFBRAP1	9392	37	2	105897121	105897121	Missense_Mutation	SNP	G	A	23	29	c.1181C>T	c.(1180-1182)TCC>TTC	p.S394F
Pat_28	Post-Resistance	BUB1	699	37	2	111425401	111425401	Missense_Mutation	SNP	G	A	133	214	c.593C>T	c.(592-594)TCT>TTT	p.S198F
Pat_28	Post-Resistance	PSD4	23550	37	2	113943469	113943469	Missense_Mutation	SNP	G	A	8	7	c.1265G>A	c.(1264-1266)GGA>GAA	p.G422E
Pat_28	Post-Resistance	GLI2	2736	37	2	121747032	121747032	Missense_Mutation	SNP	G	C	10	10	c.3542G>C	c.(3541-3543)GGC>GCC	p.G1181A
Pat_28	Post-Resistance	POTEE	445582	37	2	132010515	132010515	Missense_Mutation	SNP	G	A	40	118	c.1621G>A	c.(1621-1623)GAA>AAA	p.E541K
Pat_28	Post-Resistance	RAB3GAP1	22930	37	2	135881744	135881744	Missense_Mutation	SNP	C	T	29	54	c.758C>T	c.(757-759)GCC>GTC	p.A253V
Pat_28	Post-Resistance	RAB3GAP1	22930	37	2	135911273	135911273	Missense_Mutation	SNP	G	A	71	93	c.2116G>A	c.(2116-2118)GAT>AAT	p.D706N
Pat_28	Post-Resistance	LRP1B	53353	37	2	141260598	141260598	Missense_Mutation	SNP	C	T	58	118	c.8596G>A	c.(8596-8598)GAT>AAT	p.D2866N
Pat_28	Post-Resistance	GPD2	2820	37	2	157406210	157406210	Missense_Mutation	SNP	G	A	48	83	c.752G>A	c.(751-753)AGC>AAC	p.S251N
Pat_28	Post-Resistance	FIGN	55137	37	2	164467326	164467326	Missense_Mutation	SNP	C	T	84	82	c.1016G>A	c.(1015-1017)GGC>GAC	p.G339D
Pat_28	Post-Resistance	CSRNP3	80034	37	2	166535998	166535998	Missense_Mutation	SNP	C	T	21	37	c.1493C>T	c.(1492-1494)CCC>CTC	p.P498L
Pat_28	Post-Resistance	SCN1A	6323	37	2	166904178	166904178	Nonsense_Mutation	SNP	G	A	46	61	c.1129C>T	c.(1129-1131)CGA>TGA	p.R377*
Pat_28	Post-Resistance	MYO3B	140469	37	2	171056714	171056714	Missense_Mutation	SNP	C	T	42	60	c.241C>T	c.(241-243)CAT>TAT	p.H81Y
Pat_28	Post-Resistance	RAPGEF4	11069	37	2	173853494	173853494	Missense_Mutation	SNP	C	T	6	152	c.1301C>T	c.(1300-1302)GCC>GTC	p.A434V
Pat_28	Post-Resistance	TTC30A	92104	37	2	178482813	178482813	Missense_Mutation	SNP	G	A	34	26	c.617C>T	c.(616-618)TCA>TTA	p.S206L
Pat_28	Post-Resistance	TTN	7273	37	2	179432060	179432060	Missense_Mutation	SNP	T	C	65	127	c.71095A>G	c.(71095-71097)AGA>GGA	p.R23699G
Pat_28	Post-Resistance	TTN	7273	37	2	179440406	179440406	Missense_Mutation	SNP	C	T	8	60	c.62749G>A	c.(62749-62751)GCC>ACC	p.A20917T
Pat_28	Post-Resistance	TTN	7273	37	2	179456042	179456042	Missense_Mutation	SNP	G	A	246	354	c.52706C>T	c.(52705-52707)ACC>ATC	p.T17569I
Pat_28	Post-Resistance	TTN	7273	37	2	179486387	179486387	Missense_Mutation	SNP	G	A	50	56	c.37460C>T	c.(37459-37461)TCC>TTC	p.S12487F
Pat_28	Post-Resistance	TTN	7273	37	2	179592069	179592069	Missense_Mutation	SNP	C	T	6	9	c.16291G>A	c.(16291-16293)GCC>ACC	p.A5431T
Pat_28	Post-Resistance	TTN	7273	37	2	179611769	179611769	Missense_Mutation	SNP	G	A	41	78	c.15358C>T	c.(15358-15360)CCT>TCT	p.P5120S
Pat_28	Post-Resistance	TTN	7273	37	2	179614040	179614040	Missense_Mutation	SNP	C	T	54	96	c.13087G>A	c.(13087-13089)GAG>AAG	p.E4363K
Pat_28	Post-Resistance	TTN	7273	37	2	179614208	179614208	Missense_Mutation	SNP	C	T	26	50	c.12919G>A	c.(12919-12921)GAC>AAC	p.D4307N
Pat_28	Post-Resistance	ZC3H15	55854	37	2	187371549	187371549	Missense_Mutation	SNP	C	T	77	125	c.1076C>T	c.(1075-1077)ACT>ATT	p.T359I
Pat_28	Post-Resistance	FAM171B	165215	37	2	187626412	187626412	Missense_Mutation	SNP	A	T	20	29	c.1343A>T	c.(1342-1344)GAA>GTA	p.E448V
Pat_28	Post-Resistance	STAT4	6775	37	2	191900923	191900923	Missense_Mutation	SNP	C	T	61	79	c.1537G>A	c.(1537-1539)GAT>AAT	p.D513N
Pat_28	Post-Resistance	SLC39A10	57181	37	2	196578188	196578188	Missense_Mutation	SNP	C	T	29	40	c.1607C>T	c.(1606-1608)ACA>ATA	p.T536I
Pat_28	Post-Resistance	DNAH7	56171	37	2	196718162	196718162	Missense_Mutation	SNP	C	T	45	55	c.8686G>A	c.(8686-8688)GAG>AAG	p.E2896K
Pat_28	Post-Resistance	DNAH7	56171	37	2	196746610	196746610	Missense_Mutation	SNP	C	T	62	93	c.5870G>A	c.(5869-5871)CGA>CAA	p.R1957Q
Pat_28	Post-Resistance	AOX1	316	37	2	201499552	201499552	Missense_Mutation	SNP	G	A	21	39	c.2260G>A	c.(2260-2262)GAA>AAA	p.E754K
Pat_28	Post-Resistance	NOP58	51602	37	2	203160427	203160427	Missense_Mutation	SNP	C	T	43	59	c.938C>T	c.(937-939)GCT>GTT	p.A313V

Pat_28	Post-Resistance	ALS2CR8	79800	37	2	203834727	203834727	Missense_Mutation	SNP	C	A	4	61	c.1039C>A	c.(1039-1041)CAG>AAG	p.Q347K
Pat_28	Post-Resistance	ALS2CR8	79800	37	2	203839124	203839124	Missense_Mutation	SNP	C	T	12	22	c.1399C>T	c.(1399-1401)CCA>TCA	p.P467S
Pat_28	Post-Resistance	ERBB4	2066	37	2	212285267	212285267	Missense_Mutation	SNP	C	T	25	44	c.3034G>A	c.(3034-3036)GAT>AAT	p.D1012N
Pat_28	Post-Resistance	FN1	2335	37	2	216251411	216251411	Splice_Site	SNP	C	T	25	39	c.4612_splice	c.e28+1	p.V1538_splice
Pat_28	Post-Resistance	TTLL4	9654	37	2	219617555	219617555	Missense_Mutation	SNP	G	A	87	105	c.3046G>A	c.(3046-3048)GAG>AAG	p.E1016K
Pat_28	Post-Resistance	SPEG	10290	37	2	220342638	220342638	Missense_Mutation	SNP	C	T	43	82	c.4838C>T	c.(4837-4839)TCC>TTC	p.S1613F
Pat_28	Post-Resistance	DNER	92737	37	2	230450723	230450723	Missense_Mutation	SNP	G	A	17	33	c.698C>T	c.(697-699)ACT>ATT	p.T233I
Pat_28	Post-Resistance	CAB39	51719	37	2	231663500	231663500	Missense_Mutation	SNP	G	A	27	64	c.455G>A	c.(454-456)AGA>AAA	p.R152K
Pat_28	Post-Resistance	INPP5D	3635	37	2	234085987	234085987	Missense_Mutation	SNP	C	T	46	72	c.2066C>T	c.(2065-2067)TCT>TTT	p.S689F
Pat_28	Post-Resistance	HJURP	55355	37	2	234750199	234750199	Nonsense_Mutation	SNP	C	T	32	46	c.1227G>A	c.(1225-1227)TGG>TGA	p.W409*
Pat_28	Post-Resistance	AGAP1	116987	37	2	236708027	236708027	Missense_Mutation	SNP	G	A	38	44	c.818G>A	c.(817-819)GGG>GAG	p.G273E
Pat_28	Post-Resistance	IQCA1	79781	37	2	237240009	237240009	Missense_Mutation	SNP	C	T	45	88	c.2366G>A	c.(2365-2367)AGC>AAC	p.S789N
Pat_28	Post-Resistance	SNED1	25992	37	2	242002222	242002222	Missense_Mutation	SNP	C	T	5	11	c.2272C>T	c.(2272-2274)CGG>TGG	p.R758W
Pat_28	Post-Resistance	D2HGDH	728294	37	2	242690738	242690738	Missense_Mutation	SNP	G	A	16	16	c.1075G>A	c.(1075-1077)GAG>AAG	p.E359K
Pat_28	Post-Resistance	ANGPT4	51378	37	20	855013	855013	Missense_Mutation	SNP	C	T	35	45	c.1265G>A	c.(1264-1266)AGC>AAC	p.S422N
Pat_28	Post-Resistance	IDH3B	3420	37	20	2639446	2639446	Missense_Mutation	SNP	G	A	42	75	c.1109C>T	c.(1108-1110)ACC>ATC	p.T370I
Pat_28	Post-Resistance	CHGB	1114	37	20	5903767	5903767	Missense_Mutation	SNP	A	C	13	16	c.977A>C	c.(976-978)GAC>GCC	p.D326A
Pat_28	Post-Resistance	FERMT1	55612	37	20	6077617	6077617	Missense_Mutation	SNP	C	T	162	198	c.1021G>A	c.(1021-1023)GAT>AAT	p.D341N
Pat_28	Post-Resistance	ZNF341	84905	37	20	32358002	32358002	Missense_Mutation	SNP	G	A	23	36	c.1526G>A	c.(1525-1527)GGC>GAC	p.G509D
Pat_28	Post-Resistance	GDF5	8200	37	20	34022572	34022572	Missense_Mutation	SNP	C	T	89	141	c.641G>A	c.(640-642)GGT>GAT	p.G214D
Pat_28	Post-Resistance	SLC32A1	140679	37	20	37356873	37356873	Missense_Mutation	SNP	C	T	27	35	c.1169C>T	c.(1168-1170)GCG>GTG	p.A390V
Pat_28	Post-Resistance	YWHAB	7529	37	20	43530226	43530226	Missense_Mutation	SNP	G	A	52	49	c.52G>A	c.(52-54)GCT>ACT	p.A18T
Pat_28	Post-Resistance	SPINLW1	57119	37	20	44175908	44175908	Missense_Mutation	SNP	G	A	49	75	c.89C>T	c.(88-90)CCC>CTC	p.P30L
Pat_28	Post-Resistance	UBE2C	11065	37	20	44442104	44442104	Splice_Site	SNP	G	A	58	97	c.129_splice	c.e2+1	p.M43_splice
Pat_28	Post-Resistance	NCOA3	8202	37	20	46265286	46265286	Missense_Mutation	SNP	G	A	29	47	c.2156G>A	c.(2155-2157)GGA>GAA	p.G719E
Pat_28	Post-Resistance	KCNB1	3745	37	20	47990653	47990653	Missense_Mutation	SNP	G	A	47	77	c.1444C>T	c.(1444-1446)CAC>TAC	p.H482Y
Pat_28	Post-Resistance	TMEM189-UBE2V	387522	37	20	48713345	48713345	Missense_Mutation	SNP	G	A	49	79	c.704C>T	c.(703-705)CCT>CTT	p.P235L
Pat_28	Post-Resistance	PHACTR3	116154	37	20	58420278	58420278	Missense_Mutation	SNP	G	A	32	55	c.1622G>A	c.(1621-1623)AGT>AAT	p.S541N
Pat_28	Post-Resistance	SYCP2	10388	37	20	58467061	58467061	Missense_Mutation	SNP	G	A	29	40	c.2348C>T	c.(2347-2349)TCG>TTG	p.S783L
Pat_28	Post-Resistance	TMPRSS15	5651	37	21	19698793	19698793	Missense_Mutation	SNP	C	T	115	189	c.1877G>A	c.(1876-1878)GGG>GAG	p.G626E
Pat_28	Post-Resistance	ITSN1	6453	37	21	35183343	35183343	Nonsense_Mutation	SNP	G	A	37	51	c.2384G>A	c.(2383-2385)TGG>TAG	p.W795*
Pat_28	Post-Resistance	RUNX1	861	37	21	36206779	36206779	Missense_Mutation	SNP	G	A	83	123	c.652C>T	c.(652-654)CCC>TCC	p.P218S
Pat_28	Post-Resistance	DOPEY2	9980	37	21	37591730	37591730	Missense_Mutation	SNP	G	A	29	39	c.1190G>A	c.(1189-1191)AGA>AAA	p.R397K
Pat_28	Post-Resistance	DSCAM	1826	37	21	41648105	41648105	Missense_Mutation	SNP	C	T	26	37	c.2275G>A	c.(2275-2277)GAA>AAA	p.E759K
Pat_28	Post-Resistance	DSCAM	1826	37	21	41725476	41725476	Missense_Mutation	SNP	G	A	33	62	c.850C>T	c.(850-852)CGC>TGC	p.R284C
Pat_28	Post-Resistance	RRP1	8568	37	21	45217364	45217364	Missense_Mutation	SNP	C	T	8	11	c.484C>T	c.(484-486)CCC>TCC	p.P162S
Pat_28	Post-Resistance	ITGB2	3689	37	21	46306326	46306326	Missense_Mutation	SNP	C	T	40	64	c.2267G>A	c.(2266-2268)AGC>AAC	p.S756N
Pat_28	Post-Resistance	PCNT	5116	37	21	47845764	47845764	Missense_Mutation	SNP	G	A	27	59	c.7199G>A	c.(7198-7200)CGT>CAT	p.R2400H
Pat_28	Post-Resistance	RTN4R	65078	37	22	20230523	20230523	Nonsense_Mutation	SNP	G	A	11	8	c.133C>T	c.(133-135)CAG>TAG	p.Q45*
Pat_28	Post-Resistance	SCARF2	91179	37	22	20781781	20781781	Missense_Mutation	SNP	C	T	7	15	c.1612G>A	c.(1612-1614)GGG>AGG	p.G538R
Pat_28	Post-Resistance	CCDC116	164592	37	22	21991283	21991283	Missense_Mutation	SNP	C	T	31	40	c.1766C>T	c.(1765-1767)GCC>GTC	p.A589V
Pat_28	Post-Resistance	BCR	613	37	22	23631755	23631755	Missense_Mutation	SNP	C	T	17	43	c.2654C>T	c.(2653-2655)TCG>TTG	p.S885L
Pat_28	Post-Resistance	SLC2A11	66035	37	22	24219229	24219229	Missense_Mutation	SNP	G	A	27	38	c.407G>A	c.(406-408)GGT>GAT	p.G136D
Pat_28	Post-Resistance	MYO18B	84700	37	22	26165166	26165166	Missense_Mutation	SNP	C	T	4	0	c.1283C>T	c.(1282-1284)TCG>TTG	p.S428L
Pat_28	Post-Resistance	MYO18B	84700	37	22	26224849	26224849	Missense_Mutation	SNP	G	A	18	33	c.2893G>A	c.(2893-2895)GAG>AAG	p.E965K
Pat_28	Post-Resistance	NEFH	4744	37	22	29886558	29886558	Missense_Mutation	SNP	G	A	12	26	c.2929G>A	c.(2929-2931)GAA>AAA	p.E977K
Pat_28	Post-Resistance	GCAT	23464	37	22	38211694	38211694	Missense_Mutation	SNP	C	T	38	49	c.839C>T	c.(838-840)CCC>CTC	p.P280L

Pat_28	Post-Resistance	GTPBP1	9567	37	22	39122262	39122262	Splice_Site	SNP	G	A	13	18	c.1219_splice	c.e8-1	p.G407_splice
Pat_28	Post-Resistance	SMCR7L	54471	37	22	39909855	39909855	Missense_Mutation	SNP	C	T	76	127	c.919C>T	c.(919-921)CAT>TAT	p.H307Y
Pat_28	Post-Resistance	EP300	2033	37	22	41513431	41513431	Missense_Mutation	SNP	G	A	60	99	c.335G>A	c.(334-336)AGT>AAT	p.S112N
Pat_28	Post-Resistance	NAGA	4668	37	22	42456377	42456377	Missense_Mutation	SNP	C	T	93	127	c.1142G>A	c.(1141-1143)CGA>CAA	p.R381Q
Pat_28	Post-Resistance	A4GALT	53947	37	22	43088994	43088994	Nonsense_Mutation	SNP	G	A	17	27	c.964C>T	c.(964-966)CAG>TAG	p.Q322*
Pat_28	Post-Resistance	TTLL1	25809	37	22	43464597	43464597	Splice_Site	SNP	C	T	59	99	c.323_splice	c.e5-1	p.D108_splice
Pat_28	Post-Resistance	BIK	638	37	22	43520033	43520033	Missense_Mutation	SNP	C	T	25	33	c.5C>T	c.(4-6)TCT>TTT	p.S2F
Pat_28	Post-Resistance	ATXN10	25814	37	22	46239548	46239548	Splice_Site	SNP	G	A	10	21	c.1426_splice	c.e12-1	p.*476_splice
Pat_28	Post-Resistance	WNT7B	7477	37	22	46327195	46327195	Missense_Mutation	SNP	G	A	4	6	c.353C>T	c.(352-354)GCC>GTC	p.A118V
Pat_28	Post-Resistance	LMF2	91289	37	22	50943572	50943572	Missense_Mutation	SNP	C	T	16	34	c.1168G>A	c.(1168-1170)GTG>ATG	p.V390M
Pat_28	Post-Resistance	CPNE9	151835	37	3	9759889	9759889	Missense_Mutation	SNP	C	T	13	13	c.1108C>T	c.(1108-1110)CCC>TCC	p.P370S
Pat_28	Post-Resistance	BRPF1	7862	37	3	9782600	9782600	Missense_Mutation	SNP	C	T	10	15	c.1697C>T	c.(1696-1698)TCT>TTT	p.S566F
Pat_28	Post-Resistance	IL17RE	132014	37	3	9956268	9956268	Missense_Mutation	SNP	C	T	39	61	c.1333C>T	c.(1333-1335)CTC>TTC	p.L445F
Pat_28	Post-Resistance	FANCD2	2177	37	3	10089610	10089610	Missense_Mutation	SNP	G	A	27	231	c.1288G>A	c.(1288-1290)GAT>AAT	p.D430N
Pat_28	Post-Resistance	ATP2B2	491	37	3	10379966	10379966	Missense_Mutation	SNP	G	C	28	27	c.3314C>G	c.(3313-3315)CCG>CGG	p.P1105R
Pat_28	Post-Resistance	ATP2B2	491	37	3	10452389	10452389	Nonsense_Mutation	SNP	G	A	109	169	c.310C>T	c.(310-312)CAG>TAG	p.Q104*
Pat_28	Post-Resistance	HACL1	26061	37	3	15631058	15631058	Missense_Mutation	SNP	C	T	62	88	c.370G>A	c.(370-372)GAG>AAG	p.E124K
Pat_28	Post-Resistance	GALNTL2	117248	37	3	16252690	16252690	Missense_Mutation	SNP	G	A	30	60	c.1139G>A	c.(1138-1140)GGA>GAA	p.G380E
Pat_28	Post-Resistance	GALNTL2	117248	37	3	16254176	16254176	Missense_Mutation	SNP	C	T	48	67	c.1298C>T	c.(1297-1299)ACC>ATC	p.T433I
Pat_28	Post-Resistance	ZNF385D	79750	37	3	21706425	21706425	Missense_Mutation	SNP	G	A	35	68	c.118C>T	c.(118-120)CCT>TCT	p.P40S
Pat_28	Post-Resistance	ZNF860	344787	37	3	32030630	32030630	Missense_Mutation	SNP	C	T	61	92	c.59C>T	c.(58-60)CCT>CTT	p.P20L
Pat_28	Post-Resistance	ARPP21	10777	37	3	35750489	35750489	Missense_Mutation	SNP	A	C	39	44	c.824A>C	c.(823-825)GAC>GCC	p.D275A
Pat_28	Post-Resistance	STAC	6769	37	3	36485039	36485039	Missense_Mutation	SNP	G	A	47	101	c.295G>A	c.(295-297)GCT>ACT	p.A99T
Pat_28	Post-Resistance	STAC	6769	37	3	36485042	36485042	Missense_Mutation	SNP	G	A	49	106	c.298G>A	c.(298-300)GGT>AGT	p.G100S
Pat_28	Post-Resistance	TRANK1	9881	37	3	36872900	36872900	Missense_Mutation	SNP	C	T	12	11	c.6392G>A	c.(6391-6393)AGG>AAG	p.R2131K
Pat_28	Post-Resistance	DLEC1	9940	37	3	38137409	38137409	Missense_Mutation	SNP	G	A	43	52	c.2143G>A	c.(2143-2145)GTG>ATG	p.V715M
Pat_28	Post-Resistance	MYRIP	25924	37	3	40085725	40085725	Missense_Mutation	SNP	G	A	36	72	c.295G>A	c.(295-297)GAA>AAA	p.E99K
Pat_28	Post-Resistance	ZNF35	7584	37	3	44700600	44700601	Missense_Mutation	DNP	CC	TT	36	104	c.745_746CC>TT	c.(745-747)CCC>TTC	p.P249F
Pat_28	Post-Resistance	KIF15	56992	37	3	44872502	44872502	Missense_Mutation	SNP	G	A	121	184	c.3163G>A	c.(3163-3165)GAC>AAC	p.D1055N
Pat_28	Post-Resistance	FYCO1	79443	37	3	46008670	46008670	Missense_Mutation	SNP	C	T	60	83	c.2156G>A	c.(2155-2157)TGC>TAC	p.C719Y
Pat_28	Post-Resistance	CSPG5	10675	37	3	47614300	47614301	Nonsense_Mutation	DNP	GG	AA	20	39	.1257_1258CC>T	255-1260)TTCCAG>TTTT	p.Q420*
Pat_28	Post-Resistance	TREX1	11277	37	3	48508929	48508929	Missense_Mutation	SNP	G	A	23	27	c.1040G>A	c.(1039-1041)GGT>GAT	p.G347D
Pat_28	Post-Resistance	PRKAR2A	5576	37	3	48884951	48884951	Missense_Mutation	SNP	G	A	5	3	c.79C>T	c.(79-81)CCT>TCT	p.P27S
Pat_28	Post-Resistance	QARS	5859	37	3	49140824	49140824	Missense_Mutation	SNP	A	G	63	121	c.470T>C	c.(469-471)CTG>CCG	p.L157P
Pat_28	Post-Resistance	DAG1	1605	37	3	49569597	49569597	Nonsense_Mutation	SNP	G	A	19	22	c.1653G>A	c.(1651-1653)TGG>TGA	p.W551*
Pat_28	Post-Resistance	MST1	4485	37	3	49723375	49723375	Missense_Mutation	SNP	C	T	4	25	c.1168G>A	c.(1168-1170)GAG>AAG	p.E390K
Pat_28	Post-Resistance	MON1A	84315	37	3	49948270	49948270	Missense_Mutation	SNP	C	T	19	30	c.952G>A	c.(952-954)GCG>ACG	p.A318T
Pat_28	Post-Resistance	DNAH1	25981	37	3	52360908	52360908	Splice_Site	SNP	G	A	16	17	c.738_splice	c.e5+1	p.K246_splice
Pat_28	Post-Resistance	STAB1	23166	37	3	52536099	52536099	Missense_Mutation	SNP	G	A	19	26	c.409G>A	c.(409-411)GTG>ATG	p.V137M
Pat_28	Post-Resistance	ITIH1	3697	37	3	52816017	52816017	Missense_Mutation	SNP	C	T	46	76	c.749C>T	c.(748-750)TCC>TTC	p.S250F
Pat_28	Post-Resistance	LRIG1	26018	37	3	66434613	66434613	Missense_Mutation	SNP	G	A	84	97	c.1873C>T	c.(1873-1875)CAC>TAC	p.H625Y
Pat_28	Post-Resistance	C3orf64	285203	37	3	69056913	69056913	Missense_Mutation	SNP	G	A	92	156	c.371C>T	c.(370-372)GCC>GTC	p.A124V
Pat_28	Post-Resistance	CNTN3	5067	37	3	74548880	74548880	Missense_Mutation	SNP	G	A	33	67	c.112C>T	c.(112-114)CCT>TCT	p.P38S
Pat_28	Post-Resistance	COL8A1	1295	37	3	99513844	99513844	Missense_Mutation	SNP	G	A	8	17	c.1099G>A	c.(1099-1101)GTT>ATT	p.V367I
Pat_28	Post-Resistance	PCNP	57092	37	3	101311500	101311500	Missense_Mutation	SNP	C	T	41	19	c.440C>T	c.(439-441)TCC>TTC	p.S147F
Pat_28	Post-Resistance	CEP97	79598	37	3	101484183	101484183	Missense_Mutation	SNP	A	G	140	45	c.2386A>G	c.(2386-2388)AGA>GGA	p.R796G
Pat_28	Post-Resistance	PLCXD2	257068	37	3	111427090	111427090	Missense_Mutation	SNP	G	A	61	21	c.481G>A	c.(481-483)GAT>AAT	p.D161N

Pat_28	Post-Resistance	C3orf15	89876	37	3	119445129	119445129	Missense_Mutation	SNP	A	C	14	5	c.794A>C	c.(793-795)AAG>ACG	p.K265T
Pat_28	Post-Resistance	SLC15A2	6565	37	3	121643880	121643880	Missense_Mutation	SNP	C	T	85	41	c.1124C>T	c.(1123-1125)TCA>TTA	p.S375L
Pat_28	Post-Resistance	SEC61A1	29927	37	3	127783866	127783866	Missense_Mutation	SNP	G	A	87	20	c.763G>A	c.(763-765)GTC>ATC	p.V255I
Pat_28	Post-Resistance	STAG1	10274	37	3	136141269	136141269	Missense_Mutation	SNP	C	T	61	14	c.2020G>A	c.(2020-2022)GAA>AAA	p.E674K
Pat_28	Post-Resistance	WWTR1	25937	37	3	149243815	149243815	Missense_Mutation	SNP	C	T	45	17	c.1003G>A	c.(1003-1005)GAT>AAT	p.D335N
Pat_28	Post-Resistance	IGSF10	285313	37	3	151155253	151155253	Missense_Mutation	SNP	G	A	92	28	c.7096C>T	c.(7096-7098)CCA>TCA	p.P2366S
Pat_28	Post-Resistance	C3orf79	152118	37	3	153202377	153202377	Missense_Mutation	SNP	G	A	59	36	c.32G>A	c.(31-33)AGG>AAG	p.R11K
Pat_28	Post-Resistance	NMD3	51068	37	3	160964203	160964203	Missense_Mutation	SNP	G	A	32	14	c.1097G>A	c.(1096-1098)GGA>GAA	p.G366E
Pat_28	Post-Resistance	HTR3C	170572	37	3	183772559	183772559	Missense_Mutation	SNP	G	A	39	15	c.118G>A	c.(118-120)GTT>ATT	p.V40I
Pat_28	Post-Resistance	TP63	8626	37	3	189582204	189582204	Missense_Mutation	SNP	G	A	23	57	c.763G>A	c.(763-765)GAG>AAG	p.E255K
Pat_28	Post-Resistance	SDHAP1	255812	37	3	195690273	195690274	Missense_Mutation	DNP	GG	TA	35	70	c.262_263CC>TA	c.(262-264)CCC>TAC	p.P88Y
Pat_28	Post-Resistance	PDE6B	5158	37	4	654325	654325	Missense_Mutation	SNP	G	A	14	18	c.1537G>A	c.(1537-1539)GAA>AAA	p.E513K
Pat_28	Post-Resistance	MFSD10	10227	37	4	2933320	2933320	Missense_Mutation	SNP	G	A	18	21	c.985C>T	c.(985-987)CGG>TGG	p.R329W
Pat_28	Post-Resistance	HGFAC	3083	37	4	3449646	3449646	Missense_Mutation	SNP	G	A	6	13	c.1520G>A	c.(1519-1521)GGG>GAG	p.G507E
Pat_28	Post-Resistance	OTOP1	133060	37	4	4190688	4190688	Missense_Mutation	SNP	G	A	11	104	c.1681C>T	c.(1681-1683)CCC>TCC	p.P561S
Pat_28	Post-Resistance	JAKMIP1	152789	37	4	6050637	6050637	Missense_Mutation	SNP	C	T	18	35	c.1975G>A	c.(1975-1977)GAA>AAA	p.E659K
Pat_28	Post-Resistance	MAN2B2	23324	37	4	6596460	6596460	Splice_Site	SNP	G	A	10	11	c.1057_splice	c.e7+1	p.E353_splice
Pat_28	Post-Resistance	PROM1	8842	37	4	15981017	15981017	Splice_Site	SNP	C	T	34	79	c.2582_splice	c.e25+1	p.S861_splice
Pat_28	Post-Resistance	SEPSECS	51091	37	4	25157661	25157661	Missense_Mutation	SNP	G	A	85	131	c.545C>T	c.(544-546)GCA>GTA	p.A182V
Pat_28	Post-Resistance	WDR19	57728	37	4	39216257	39216257	Missense_Mutation	SNP	G	A	46	67	c.927G>A	c.(925-927)ATG>ATA	p.M309I
Pat_28	Post-Resistance	RFC1	5981	37	4	39301676	39301677	Missense_Mutation	DNP	GG	AA	15	43	.2775_2776CC>T	773-2778)ATCCGG>ATTT	p.R926W
Pat_28	Post-Resistance	NSUN7	79730	37	4	40752969	40752969	Nonsense_Mutation	SNP	C	T	31	59	c.259C>T	c.(259-261)CAG>TAG	p.Q87*
Pat_28	Post-Resistance	KIAA1211	57482	37	4	57181815	57181815	Missense_Mutation	SNP	A	T	40	51	c.2147A>T	c.(2146-2148)AAT>ATT	p.N716I
Pat_28	Post-Resistance	UGT2A1	10941	37	4	70460343	70460343	Missense_Mutation	SNP	C	T	43	62	c.1156G>A	c.(1156-1158)GTC>ATC	p.V386I
Pat_28	Post-Resistance	SULT1E1	6783	37	4	70723320	70723320	Missense_Mutation	SNP	G	A	30	35	c.43C>T	c.(43-45)CAT>TAT	p.H15Y
Pat_28	Post-Resistance	SHROOM3	57619	37	4	77659967	77659967	Missense_Mutation	SNP	C	T	39	61	c.641C>T	c.(640-642)CCT>CTT	p.P214L
Pat_28	Post-Resistance	FRAS1	80144	37	4	79301123	79301123	Missense_Mutation	SNP	G	A	62	88	c.3536G>A	c.(3535-3537)CGT>CAT	p.R1179H
Pat_28	Post-Resistance	FRAS1	80144	37	4	79362382	79362382	Missense_Mutation	SNP	C	T	17	18	c.5596C>T	c.(5596-5598)CTC>TTC	p.L1866F
Pat_28	Post-Resistance	PAQR3	152559	37	4	79860269	79860269	Missense_Mutation	SNP	G	A	58	85	c.110C>T	c.(109-111)CCC>CTC	p.P37L
Pat_28	Post-Resistance	TMEM150C	441027	37	4	83417310	83417310	Missense_Mutation	SNP	G	A	73	76	c.274C>T	c.(274-276)CCG>TCG	p.P92S
Pat_28	Post-Resistance	SEC31A	22872	37	4	83765625	83765625	Missense_Mutation	SNP	C	T	48	27	c.2540G>A	c.(2539-2541)GGA>GAA	p.G847E
Pat_28	Post-Resistance	SEC31A	22872	37	4	83778844	83778844	Missense_Mutation	SNP	C	T	40	110	c.1700G>A	c.(1699-1701)GGG>GAG	p.G567E
Pat_28	Post-Resistance	WDFY3	23001	37	4	85678114	85678114	Missense_Mutation	SNP	G	A	151	296	c.5389C>T	c.(5389-5391)CCT>TCT	p.P1797S
Pat_28	Post-Resistance	DSPP	1834	37	4	88534072	88534072	Missense_Mutation	SNP	G	A	15	17	c.734G>A	c.(733-735)AGT>AAT	p.S245N
Pat_28	Post-Resistance	ABCG2	9429	37	4	89053785	89053785	Missense_Mutation	SNP	C	T	34	42	c.206G>A	c.(205-207)GGG>GAG	p.G69E
Pat_28	Post-Resistance	ADH1B	125	37	4	100237077	100237077	Missense_Mutation	SNP	C	T	85	200	c.545G>A	c.(544-546)GGG>GAG	p.G182E
Pat_28	Post-Resistance	CENPE	1062	37	4	104097137	104097137	Missense_Mutation	SNP	C	T	46	96	c.1459G>A	c.(1459-1461)GCA>ACA	p.A487T
Pat_28	Post-Resistance	PAPSS1	9061	37	4	108622351	108622351	Missense_Mutation	SNP	G	A	67	102	c.151C>T	c.(151-153)CGT>TGT	p.R51C
Pat_28	Post-Resistance	COL25A1	84570	37	4	109766362	109766362	Missense_Mutation	SNP	C	T	100	168	c.1561G>A	c.(1561-1563)GGT>AGT	p.G521S
Pat_28	Post-Resistance	EGF	1950	37	4	110884373	110884373	Missense_Mutation	SNP	C	T	109	189	c.1357C>T	c.(1357-1359)CCT>TCT	p.P453S
Pat_28	Post-Resistance	ANKRD50	57182	37	4	125592742	125592742	Missense_Mutation	SNP	G	A	73	119	c.1690C>T	c.(1690-1692)CTT>TTT	p.L564F
Pat_28	Post-Resistance	PCDH18	54510	37	4	138449631	138449631	Splice_Site	SNP	C	T	81	97	c.2740_splice	c.e3+1	p.A914_splice
Pat_28	Post-Resistance	FHDC1	85462	37	4	153884215	153884215	Missense_Mutation	SNP	C	T	105	133	c.962C>T	c.(961-963)TCT>TTT	p.S321F
Pat_28	Post-Resistance	DCHS2	54798	37	4	155156884	155156884	Missense_Mutation	SNP	C	T	57	78	c.7555G>A	c.(7555-7557)GTT>ATT	p.V2519I
Pat_28	Post-Resistance	RXFP1	59350	37	4	159573068	159573068	Missense_Mutation	SNP	C	T	47	83	c.2135C>T	c.(2134-2136)ACA>ATA	p.T712I
Pat_28	Post-Resistance	KLHL2	11275	37	4	166231776	166231776	Missense_Mutation	SNP	G	A	260	372	c.1111G>A	c.(1111-1113)GAT>AAT	p.D371N
Pat_28	Post-Resistance	ODZ3	55714	37	4	183675922	183675922	Missense_Mutation	SNP	G	A	43	71	c.4402G>A	c.(4402-4404)GAT>AAT	p.D1468N

Pat_28	Post-Resistance	SDHA	6389	37	5	218477	218477	Missense_Mutation	SNP	G	A	6	21	c.7G>A	c.(7-9)GGG>AGG	p.G3R
Pat_28	Post-Resistance	SLC12A7	10723	37	5	1063982	1063982	Missense_Mutation	SNP	C	T	29	56	c.2716G>A	c.(2716-2718)GCC>ACC	p.A906T
Pat_28	Post-Resistance	SLC6A3	6531	37	5	1441606	1441606	Splice_Site	SNP	C	T	9	12	c.287_splice	c.e3-1	p.G96_splice
Pat_28	Post-Resistance	KIAA0947	23379	37	5	5465026	5465026	Missense_Mutation	SNP	G	A	7	6	c.5579G>A	c.(5578-5580)AGG>AAG	p.R1860K
Pat_28	Post-Resistance	SEMA5A	9037	37	5	9202163	9202163	Missense_Mutation	SNP	G	A	33	55	c.836C>T	c.(835-837)TCC>TTC	p.S279F
Pat_28	Post-Resistance	DNAH5	1767	37	5	13807795	13807795	Missense_Mutation	SNP	C	T	6	10	c.7792G>A	c.(7792-7794)GTA>ATA	p.V2598I
Pat_28	Post-Resistance	CDH10	1008	37	5	24491808	24491808	Nonsense_Mutation	SNP	G	A	46	65	c.1753C>T	c.(1753-1755)CGA>TGA	p.R585*
Pat_28	Post-Resistance	UGT3A1	133688	37	5	35954459	35954459	Missense_Mutation	SNP	G	A	25	35	c.1417C>T	c.(1417-1419)CCC>TCC	p.P473S
Pat_28	Post-Resistance	EGFLAM	133584	37	5	38409148	38409148	Missense_Mutation	SNP	G	A	8	11	c.1291G>A	c.(1291-1293)GAA>AAA	p.E431K
Pat_28	Post-Resistance	RICTOR	253260	37	5	38953151	38953151	Missense_Mutation	SNP	C	T	72	106	c.2833G>A	c.(2833-2835)GAA>AAA	p.E945K
Pat_28	Post-Resistance	C6	729	37	5	41158798	41158798	Missense_Mutation	SNP	G	A	25	47	c.1946C>T	c.(1945-1947)CCT>CTT	p.P649L
Pat_28	Post-Resistance	HMGCS1	3157	37	5	43294211	43294211	Missense_Mutation	SNP	G	A	46	111	c.1130C>T	c.(1129-1131)TCT>TTT	p.S377F
Pat_28	Post-Resistance	GAPT	202309	37	5	57790683	57790683	Missense_Mutation	SNP	C	T	40	53	c.320C>T	c.(319-321)ACC>ATC	p.T107I
Pat_28	Post-Resistance	RGS7BP	401190	37	5	63905020	63905020	Missense_Mutation	SNP	C	T	47	67	c.715C>T	c.(715-717)CCC>TCC	p.P239S
Pat_28	Post-Resistance	PPWD1	23398	37	5	64865551	64865551	Missense_Mutation	SNP	G	A	31	57	c.392G>A	c.(391-393)AGT>AAT	p.S131N
Pat_28	Post-Resistance	MAST4	375449	37	5	66462764	66462764	Missense_Mutation	SNP	C	T	7	15	c.7190C>T	c.(7189-7191)TCC>TTC	p.S2397F
Pat_28	Post-Resistance	RGNEF	64283	37	5	73136449	73136449	Missense_Mutation	SNP	G	A	25	37	c.1291G>A	c.(1291-1293)GAA>AAA	p.E431K
Pat_28	Post-Resistance	IQGAP2	10788	37	5	75886412	75886412	Splice_Site	SNP	G	A	5	23	c.819_splice	c.e8+1	p.K273_splice
Pat_28	Post-Resistance	VCAN	1462	37	5	82815700	82815700	Missense_Mutation	SNP	G	A	68	90	c.1575G>A	c.(1573-1575)ATG>ATA	p.M525I
Pat_28	Post-Resistance	EDIL3	10085	37	5	83259133	83259133	Missense_Mutation	SNP	C	T	34	56	c.1184G>A	c.(1183-1185)GGA>GAA	p.G395E
Pat_28	Post-Resistance	GPR98	84059	37	5	90159654	90159654	Missense_Mutation	SNP	G	A	97	148	c.17836G>A	c.(17836-17838)GCA>ACA	p.A5946T
Pat_28	Post-Resistance	AQPEP	206338	37	5	115335540	115335540	Missense_Mutation	SNP	G	A	38	81	c.1456G>A	c.(1456-1458)GTG>ATG	p.V486M
Pat_28	Post-Resistance	SEMA6A	57556	37	5	115837950	115837950	Missense_Mutation	SNP	G	C	135	189	c.174C>G	c.(172-174)ATC>ATG	p.I58M
Pat_28	Post-Resistance	FAM170A	340069	37	5	118965466	118965466	Missense_Mutation	SNP	G	A	65	83	c.3G>A	c.(1-3)ATG>ATA	p.M1I
Pat_28	Post-Resistance	CSNK1G3	1456	37	5	122881506	122881506	Missense_Mutation	SNP	G	A	82	120	c.149G>A	c.(148-150)GGA>GAA	p.G50E
Pat_28	Post-Resistance	C5orf56	441108	37	5	131821956	131821956	Missense_Mutation	SNP	G	T	51	81	c.117G>T	c.(115-117)GAG>GAT	p.E39D
Pat_28	Post-Resistance	HSPA4	3308	37	5	132427028	132427028	Missense_Mutation	SNP	G	A	28	38	c.1522G>A	c.(1522-1524)GAG>AAG	p.E508K
Pat_28	Post-Resistance	TCF7	6932	37	5	133451621	133451621	Missense_Mutation	SNP	C	T	26	45	c.338C>T	c.(337-339)ACC>ATC	p.T113I
Pat_28	Post-Resistance	WNT8A	7478	37	5	137426514	137426514	Missense_Mutation	SNP	A	T	32	56	c.808A>T	c.(808-810)ACA>TCA	p.T270S
Pat_28	Post-Resistance	KIF20A	10112	37	5	137523005	137523005	Missense_Mutation	SNP	C	T	26	49	c.2576C>T	c.(2575-2577)ACC>ATC	p.T859I
Pat_28	Post-Resistance	PCDHA9	9752	37	5	140230475	140230475	Splice_Site	SNP	G	A	21	26	c.2394_splice	c.e1+1	p.K798_splice
Pat_28	Post-Resistance	PCDHA13	56136	37	5	140264182	140264182	Missense_Mutation	SNP	C	T	14	19	c.2329C>T	c.(2329-2331)CCT>TCT	p.P777S
Pat_28	Post-Resistance	PCDHB16	57717	37	5	140563779	140563779	Missense_Mutation	SNP	G	A	14	14	c.1645G>A	c.(1645-1647)GTG>ATG	p.V549M
Pat_28	Post-Resistance	PCDHGB1	56104	37	5	140730554	140730554	Missense_Mutation	SNP	G	A	49	73	c.727G>A	c.(727-729)GTA>ATA	p.V243I
Pat_28	Post-Resistance	PCDHGA5	56110	37	5	140744554	140744554	Missense_Mutation	SNP	C	A	46	64	c.657C>A	c.(655-657)GAC>GAA	p.D219E
Pat_28	Post-Resistance	PCDHGA9	56107	37	5	140783741	140783741	Nonsense_Mutation	SNP	C	T	3	6	c.1222C>T	c.(1222-1224)CAA>TAA	p.Q408*
Pat_28	Post-Resistance	PCDHGC3	5098	37	5	140857485	140857485	Missense_Mutation	SNP	G	A	14	18	c.1802G>A	c.(1801-1803)GGG>GAG	p.G601E
Pat_28	Post-Resistance	SLC26A2	1836	37	5	149357903	149357903	Missense_Mutation	SNP	G	A	67	114	c.688G>A	c.(688-690)GGA>AGA	p.G230R
Pat_28	Post-Resistance	CCDC69	26112	37	5	150581189	150581189	Missense_Mutation	SNP	C	T	44	57	c.185G>A	c.(184-186)AGA>AAA	p.R62K
Pat_28	Post-Resistance	SGCD	6444	37	5	155771587	155771587	Missense_Mutation	SNP	G	A	65	89	c.89G>A	c.(88-90)CGG>CAG	p.R30Q
Pat_28	Post-Resistance	SLIT3	6586	37	5	168098390	168098390	Missense_Mutation	SNP	C	T	17	44	c.3940G>A	c.(3940-3942)GAG>AAG	p.E1314K
Pat_28	Post-Resistance	STK10	6793	37	5	171472026	171472026	Missense_Mutation	SNP	C	T	41	53	c.2767G>A	c.(2767-2769)GCT>ACT	p.A923T
Pat_28	Post-Resistance	C5orf25	375484	37	5	175740710	175740710	Missense_Mutation	SNP	G	A	141	216	c.1694G>A	c.(1693-1695)GGG>GAG	p.G565E
Pat_28	Post-Resistance	GRM6	2916	37	5	178418532	178418532	Missense_Mutation	SNP	C	A	87	116	c.750G>T	c.(748-750)AAG>AAT	p.K250N
Pat_28	Post-Resistance	EXOC2	55770	37	6	564872	564872	Missense_Mutation	SNP	C	T	143	83	c.1501G>A	c.(1501-1503)GAT>AAT	p.D501N
Pat_28	Post-Resistance	PRPF4B	8899	37	6	4041062	4041062	Missense_Mutation	SNP	G	A	26	161	c.1469G>A	c.(1468-1470)GGT>GAT	p.G490D
Pat_28	Post-Resistance	DSP	1832	37	6	7565599	7565599	Missense_Mutation	SNP	C	T	55	240	c.785C>T	c.(784-786)TCC>TTC	p.S262F

Pat_28	Post-Resistance	SYCP2L	221711	37	6	10956431	10956431	Missense_Mutation	SNP	C	T	23	97	c.2119C>T	c.(2119-2121)CCA>TCA	p.P707S
Pat_28	Post-Resistance	JARID2	3720	37	6	15487537	15487537	Splice_Site	SNP	G	A	3	27	c.671_splice	c.e6-1	p.V224_splice
Pat_28	Post-Resistance	FAM8A1	51439	37	6	17601299	17601299	Missense_Mutation	SNP	G	A	9	18	c.659G>A	c.(658-660)AGG>AAG	p.R220K
Pat_28	Post-Resistance	NUP153	9972	37	6	17629327	17629327	Missense_Mutation	SNP	G	A	33	127	c.3103C>T	c.(3103-3105)CCT>TCT	p.P1035S
Pat_28	Post-Resistance	E2F3	1871	37	6	20402789	20402789	Missense_Mutation	SNP	G	A	4	8	c.326G>A	c.(325-327)AGA>AAA	p.R109K
Pat_28	Post-Resistance	CDKAL1	54901	37	6	21000457	21000457	Splice_Site	SNP	G	A	100	141	c.910_splice	c.e11-1	p.E304_splice
Pat_28	Post-Resistance	KIAA0319	9856	37	6	24596292	24596292	Missense_Mutation	SNP	C	T	8	36	c.610G>A	c.(610-612)GCG>ACG	p.A204T
Pat_28	Post-Resistance	HIST1H2BB	3018	37	6	26043810	26043810	Missense_Mutation	SNP	C	T	53	226	c.76G>A	c.(76-78)GAT>AAT	p.D26N
Pat_28	Post-Resistance	HIST1H4F	8361	37	6	26240940	26240940	Missense_Mutation	SNP	G	A	44	129	c.287G>A	c.(286-288)CGC>CAC	p.R96H
Pat_28	Post-Resistance	ZNF165	7718	37	6	28053992	28053992	Missense_Mutation	SNP	G	A	36	168	c.454G>A	c.(454-456)GTG>ATG	p.V152M
Pat_28	Post-Resistance	TRIM10	10107	37	6	30123507	30123507	Missense_Mutation	SNP	G	A	17	72	c.925C>T	c.(925-927)CCA>TCA	p.P309S
Pat_28	Post-Resistance	MDC1	9656	37	6	30672908	30672908	Missense_Mutation	SNP	G	A	56	225	c.4052C>T	c.(4051-4053)ACT>ATT	p.T1351I
Pat_28	Post-Resistance	PSORS1C1	170679	37	6	31107430	31107430	Missense_Mutation	SNP	C	A	13	42	c.180C>A	c.(178-180)GAC>GAA	p.D60E
Pat_28	Post-Resistance	PSORS1C1	170679	37	6	31107605	31107605	Missense_Mutation	SNP	C	T	37	102	c.355C>T	c.(355-357)CCT>TCT	p.P119S
Pat_28	Post-Resistance	LY6G6F	259215	37	6	31685358	31685358	Missense_Mutation	SNP	C	T	130	580	c.926C>T	c.(925-927)CCC>CTC	p.P309L
Pat_28	Post-Resistance	SLC44A4	80736	37	6	31833111	31833111	Missense_Mutation	SNP	G	A	110	506	c.1741C>T	c.(1741-1743)CTC>TTC	p.L581F
Pat_28	Post-Resistance	EHMT2	10919	37	6	31854650	31854650	Missense_Mutation	SNP	C	T	82	334	c.2143G>A	c.(2143-2145)GAC>AAC	p.D715N
Pat_28	Post-Resistance	CFB	629	37	6	31914225	31914225	Missense_Mutation	SNP	G	A	6	60	c.140G>A	c.(139-141)GGC>GAC	p.G47D
Pat_28	Post-Resistance	CFB	629	37	6	31919797	31919797	Missense_Mutation	SNP	G	A	111	332	c.2285G>A	c.(2284-2286)GGT>GAT	p.G762D
Pat_28	Post-Resistance	AGPAT1	10554	37	6	32139188	32139188	Missense_Mutation	SNP	C	T	22	57	c.86G>A	c.(85-87)AGC>AAC	p.S29N
Pat_28	Post-Resistance	NOTCH4	4855	37	6	32189064	32189064	Missense_Mutation	SNP	G	A	20	91	c.490C>T	c.(490-492)CCA>TCA	p.P164S
Pat_28	Post-Resistance	HLA-DQB1	3119	37	6	32629225	32629225	Missense_Mutation	SNP	G	A	11	7	c.671C>T	c.(670-672)TCT>TTT	p.S224F
Pat_28	Post-Resistance	TAP1	6890	37	6	32821391	32821391	Missense_Mutation	SNP	G	A	20	29	c.203C>T	c.(202-204)GCT>GTT	p.A68V
Pat_28	Post-Resistance	VPS52	6293	37	6	33219723	33219723	Missense_Mutation	SNP	G	A	27	73	c.1820C>T	c.(1819-1821)CCC>CTC	p.P607L
Pat_28	Post-Resistance	RPS18	6222	37	6	33243844	33243844	Splice_Site	SNP	G	A	26	73	c.291_splice	c.e4+1	p.Q97_splice
Pat_28	Post-Resistance	WDR46	9277	37	6	33256444	33256444	Missense_Mutation	SNP	G	A	35	125	c.307C>T	c.(307-309)CCC>TCC	p.P103S
Pat_28	Post-Resistance	ZBTB22	9278	37	6	33283427	33283427	Missense_Mutation	SNP	C	T	47	116	c.1267G>A	c.(1267-1269)GGC>AGC	p.G423S
Pat_28	Post-Resistance	DAXX	1616	37	6	33286845	33286845	Missense_Mutation	SNP	G	A	49	157	c.2092C>T	c.(2092-2094)CTC>TTC	p.L698F
Pat_28	Post-Resistance	ITPR3	3710	37	6	33644865	33644865	Missense_Mutation	SNP	G	A	15	61	c.3521G>A	c.(3520-3522)GGC>GAC	p.G1174D
Pat_28	Post-Resistance	HMGA1	3159	37	6	34211249	34211249	Missense_Mutation	SNP	C	T	15	68	c.224C>T	c.(223-225)ACC>ATC	p.T75I
Pat_28	Post-Resistance	ANKS1A	23294	37	6	34985363	34985363	Missense_Mutation	SNP	G	A	28	91	c.1537G>A	c.(1537-1539)GGG>AGG	p.G513R
Pat_28	Post-Resistance	CDKN1A	1026	37	6	36652219	36652219	Missense_Mutation	SNP	C	T	12	12	c.341C>T	c.(340-342)TCA>TTA	p.S114L
Pat_28	Post-Resistance	DNAH8	1769	37	6	38790697	38790697	Missense_Mutation	SNP	G	A	22	67	c.2956G>A	c.(2956-2958)GTC>ATC	p.V986I
Pat_28	Post-Resistance	DNAH8	1769	37	6	38862525	38862525	Nonsense_Mutation	SNP	C	T	28	105	c.7981C>T	c.(7981-7983)CGA>TGA	p.R2661*
Pat_28	Post-Resistance	DNAH8	1769	37	6	38917285	38917285	Missense_Mutation	SNP	G	A	51	164	c.11536G>A	c.(11536-11538)GAA>AAA	p.E3846K
Pat_28	Post-Resistance	ZNF318	24149	37	6	43316171	43316171	Missense_Mutation	SNP	G	A	70	206	c.2963C>T	c.(2962-2964)TCC>TTC	p.S988F
Pat_28	Post-Resistance	ABCC10	89845	37	6	43415624	43415624	Missense_Mutation	SNP	G	A	14	30	c.3908G>A	c.(3907-3909)CGA>CAA	p.R1303Q
Pat_28	Post-Resistance	GPR116	221395	37	6	46830722	46830722	Missense_Mutation	SNP	C	T	68	136	c.2102G>A	c.(2101-2103)GGC>GAC	p.G701D
Pat_28	Post-Resistance	C6orf138	442213	37	6	47846952	47846952	Missense_Mutation	SNP	C	T	15	49	c.1577G>A	c.(1576-1578)AGT>AAT	p.S526N
Pat_28	Post-Resistance	RHAG	6005	37	6	49586943	49586943	Missense_Mutation	SNP	A	G	65	208	c.290T>C	c.(289-291)GTA>GCA	p.V97A
Pat_28	Post-Resistance	PGK2	5232	37	6	49753930	49753930	Missense_Mutation	SNP	T	A	97	361	c.971A>T	c.(970-972)CAT>CTT	p.H324L
Pat_28	Post-Resistance	PKHD1	5314	37	6	51913410	51913410	Missense_Mutation	SNP	G	A	26	69	c.2287C>T	c.(2287-2289)CCC>TCC	p.P763S
Pat_28	Post-Resistance	PAQR8	85315	37	6	52268486	52268486	Missense_Mutation	SNP	G	A	61	197	c.475G>A	c.(475-477)GCT>ACT	p.A159T
Pat_28	Post-Resistance	ICK	22858	37	6	52880960	52880960	Missense_Mutation	SNP	G	A	53	232	c.752C>T	c.(751-753)CCC>CTC	p.P251L
Pat_28	Post-Resistance	FAM83B	222584	37	6	54735297	54735297	Missense_Mutation	SNP	G	A	66	268	c.253G>A	c.(253-255)GAT>AAT	p.D85N
Pat_28	Post-Resistance	DST	667	37	6	56496706	56496706	Missense_Mutation	SNP	C	T	61	251	c.3839G>A	c.(3838-3840)AGT>AAT	p.S1280N
Pat_28	Post-Resistance	AIM1	202	37	6	106992663	106992663	Missense_Mutation	SNP	G	A	5	1	c.3943G>A	c.(3943-3945)GAT>AAT	p.D1315N

Pat_28	Post-Resistance	FYN	2534	37	6	112035611	112035611	Missense_Mutation	SNP	C	T	32	16	c.283G>A	c.(283-285)GCA>ACA	p.A95T
Pat_28	Post-Resistance	RFPL4B	442247	37	6	112671637	112671637	Missense_Mutation	SNP	C	T	21	8	c.727C>T	c.(727-729)CCA>TCA	p.P243S
Pat_28	Post-Resistance	SAMD3	154075	37	6	130497110	130497110	Missense_Mutation	SNP	C	T	24	17	c.698G>A	c.(697-699)CGA>CAA	p.R233Q
Pat_28	Post-Resistance	GPR126	57211	37	6	142725084	142725084	Missense_Mutation	SNP	C	T	71	24	c.2101C>T	c.(2101-2103)CCA>TCA	p.P701S
Pat_28	Post-Resistance	FNDC1	84624	37	6	159654246	159654246	Missense_Mutation	SNP	C	T	5	1	c.2702C>T	c.(2701-2703)CCC>CTC	p.P901L
Pat_28	Post-Resistance	BRP44L	51660	37	6	166779481	166779481	Missense_Mutation	SNP	C	T	45	18	c.286G>A	c.(286-288)GGG>AGG	p.G96R
Pat_28	Post-Resistance	BZW2	28969	37	7	16729503	16729503	Missense_Mutation	SNP	G	A	8	41	c.623G>A	c.(622-624)AGA>AAA	p.R208K
Pat_28	Post-Resistance	HDAC9	9734	37	7	18806771	18806771	Missense_Mutation	SNP	G	A	10	18	c.2198G>A	c.(2197-2199)GGA>GAA	p.G733E
Pat_28	Post-Resistance	CCDC129	223075	37	7	31617513	31617513	Missense_Mutation	SNP	C	T	20	53	c.635C>T	c.(634-636)ACC>ATC	p.T212I
Pat_28	Post-Resistance	SFRP4	6424	37	7	37955718	37955718	Missense_Mutation	SNP	G	A	51	127	c.422C>T	c.(421-423)GCC>GTC	p.A141V
Pat_28	Post-Resistance	RAMP3	10268	37	7	45222964	45222964	Missense_Mutation	SNP	G	A	78	225	c.400G>A	c.(400-402)GCT>ACT	p.A134T
Pat_28	Post-Resistance	PKD1L1	168507	37	7	47976441	47976441	Splice_Site	SNP	A	G	19	53	c.398_splice	c.e4+1	p.R133_splice
Pat_28	Post-Resistance	ABCA13	154664	37	7	48559881	48559881	Missense_Mutation	SNP	G	A	9	47	c.14042G>A	c.(14041-14043)CGA>CAA	p.R4681Q
Pat_28	Post-Resistance	EGFR	1956	37	7	55273036	55273036	Missense_Mutation	SNP	G	A	44	145	c.3359G>A	c.(3358-3360)AGC>AAC	p.S1120N
Pat_28	Post-Resistance	ZNF716	441234	37	7	57528589	57528589	Missense_Mutation	SNP	G	A	16	87	c.422G>A	c.(421-423)GGT>GAT	p.G141D
Pat_28	Post-Resistance	ASL	435	37	7	65557607	65557607	Missense_Mutation	SNP	G	A	36	58	c.1207G>A	c.(1207-1209)GTC>ATC	p.V403I
Pat_28	Post-Resistance	SBDS	51119	37	7	66453486	66453486	Missense_Mutation	SNP	C	T	30	79	c.625G>A	c.(625-627)GTA>ATA	p.V209I
Pat_28	Post-Resistance	AUTS2	26053	37	7	69364416	69364416	Nonsense_Mutation	SNP	C	T	228	165	c.454C>T	c.(454-456)CGA>TGA	p.R152*
Pat_28	Post-Resistance	TYW1B	441250	37	7	72297543	72297543	Missense_Mutation	SNP	T	C	38	136	c.26A>G	c.(25-27)GAC>GGC	p.D9G
Pat_28	Post-Resistance	MAGI2	9863	37	7	78130964	78130964	Missense_Mutation	SNP	C	T	125	110	c.895G>A	c.(895-897)GAG>AAG	p.E299K
Pat_28	Post-Resistance	CACNA2D1	781	37	7	81641540	81641540	Missense_Mutation	SNP	C	T	44	133	c.1292G>A	c.(1291-1293)GGA>GAA	p.G431E
Pat_28	Post-Resistance	ZNF804B	219578	37	7	88962766	88962766	Missense_Mutation	SNP	G	A	27	76	c.470G>A	c.(469-471)AGA>AAA	p.R157K
Pat_28	Post-Resistance	SAMD9L	219285	37	7	92763843	92763843	Nonsense_Mutation	SNP	C	T	42	181	c.1442G>A	c.(1441-1443)TGG>TAG	p.W481*
Pat_28	Post-Resistance	COL1A2	1278	37	7	94040207	94040207	Missense_Mutation	SNP	C	T	26	80	c.1204C>T	c.(1204-1206)CCT>TCT	p.P402S
Pat_28	Post-Resistance	ASNS	440	37	7	97482371	97482371	Splice_Site	SNP	C	T	14	63	c.1476_splice	c.e12+1	p.Q492_splice
Pat_28	Post-Resistance	ARPC1A	10552	37	7	98961248	98961248	Missense_Mutation	SNP	G	A	27	63	c.1066G>A	c.(1066-1068)GAT>AAT	p.D356N
Pat_28	Post-Resistance	ZKSCAN1	7586	37	7	99621460	99621460	Missense_Mutation	SNP	G	A	27	69	c.331G>A	c.(331-333)GAG>AAG	p.E111K
Pat_28	Post-Resistance	COPS6	10980	37	7	99687039	99687039	Splice_Site	SNP	G	A	57	161	c.202_splice	c.e2+1	p.V68_splice
Pat_28	Post-Resistance	AP4M1	9179	37	7	99704099	99704099	Missense_Mutation	SNP	C	T	26	34	c.1099C>T	c.(1099-1101)CGG>TGG	p.R367W
Pat_28	Post-Resistance	GPC2	221914	37	7	99773341	99773341	Missense_Mutation	SNP	C	T	39	109	c.502G>A	c.(502-504)GCA>ACA	p.A168T
Pat_28	Post-Resistance	GPC2	221914	37	7	99773506	99773506	Missense_Mutation	SNP	C	T	15	27	c.337G>A	c.(337-339)GAG>AAG	p.E113K
Pat_28	Post-Resistance	GPC2	221914	37	7	99774815	99774815	Missense_Mutation	SNP	G	A	16	28	c.8C>T	c.(7-9)GCG>GTG	p.A3V
Pat_28	Post-Resistance	EPHB4	2050	37	7	100416159	100416159	Missense_Mutation	SNP	C	T	17	48	c.1405G>A	c.(1405-1407)GTC>ATC	p.V469I
Pat_28	Post-Resistance	SLC12A9	56996	37	7	100459495	100459495	Missense_Mutation	SNP	G	A	15	34	c.1673G>A	c.(1672-1674)GGG>GAG	p.G558E
Pat_28	Post-Resistance	CDHR3	222256	37	7	105662865	105662865	Missense_Mutation	SNP	C	T	99	300	c.2047C>T	c.(2047-2049)CCA>TCA	p.P683S
Pat_28	Post-Resistance	PRKAR2B	5577	37	7	106762448	106762448	Missense_Mutation	SNP	G	A	24	79	c.395G>A	c.(394-396)AGG>AAG	p.R132K
Pat_28	Post-Resistance	CBLL1	79872	37	7	107399303	107399303	Missense_Mutation	SNP	C	T	213	521	c.1156C>T	c.(1156-1158)CCT>TCT	p.P386S
Pat_28	Post-Resistance	LEP	3952	37	7	127894707	127894707	Missense_Mutation	SNP	G	A	10	28	c.395G>A	c.(394-396)GGG>GAG	p.G132E
Pat_28	Post-Resistance	IMPDH1	3614	37	7	128041084	128041084	Missense_Mutation	SNP	C	A	27	62	c.234G>T	c.(232-234)ATG>ATT	p.M78I
Pat_28	Post-Resistance	METTL2B	55798	37	7	128141925	128141925	Nonsense_Mutation	SNP	G	A	110	281	c.1092G>A	c.(1090-1092)TGG>TGA	p.W364*
Pat_28	Post-Resistance	IRF5	3663	37	7	128587941	128587941	Missense_Mutation	SNP	C	T	11	30	c.916C>T	c.(916-918)CCC>TCC	p.P306S
Pat_28	Post-Resistance	AHCYL2	23382	37	7	129066392	129066392	Missense_Mutation	SNP	C	T	26	68	c.1817C>T	c.(1816-1818)CCT>CTT	p.P606L
Pat_28	Post-Resistance	FAM40B	57464	37	7	129079912	129079912	Missense_Mutation	SNP	G	A	34	104	c.179G>A	c.(178-180)GGG>GAG	p.G60E
Pat_28	Post-Resistance	MKLN1	4289	37	7	131122712	131122712	Missense_Mutation	SNP	G	A	104	365	c.1129G>A	c.(1129-1131)GAT>AAT	p.D377N
Pat_28	Post-Resistance	WDR91	29062	37	7	134893671	134893671	Nonsense_Mutation	SNP	C	T	87	215	c.383G>A	c.(382-384)TGG>TAG	p.W128*
Pat_28	Post-Resistance	KIAA1549	57670	37	7	138556063	138556063	Missense_Mutation	SNP	G	A	22	73	c.4391C>T	c.(4390-4392)TCC>TTC	p.S1464F
Pat_28	Post-Resistance	BRAF	673	37	7	140453136	140453136	Missense_Mutation	SNP	A	T	102	80	c.1799T>A	c.(1798-1800)GTG>GAG	p.V600E

Pat_28	Post-Resistance	AGK	55750	37	7	141336765	141336766	Nonsense_Mutation	DNP	GG	AA	43	39	c.674_675GG>AA	c.(673-675)TGG>TAA	p.W225*
Pat_28	Post-Resistance	EPHA1	2041	37	7	143096814	143096814	Nonsense_Mutation	SNP	C	T	46	87	c.765G>A	c.(763-765)TGG>TGA	p.W255*
Pat_28	Post-Resistance	OR2A5	393046	37	7	143748032	143748032	Missense_Mutation	SNP	G	A	293	254	c.538G>A	c.(538-540)GAA>AAA	p.E180K
Pat_28	Post-Resistance	OR2A2	442361	37	7	143807483	143807483	Missense_Mutation	SNP	G	A	190	272	c.808G>A	c.(808-810)GAG>AAG	p.E270K
Pat_28	Post-Resistance	TMEM176B	28959	37	7	150488648	150488648	Missense_Mutation	SNP	C	T	22	42	c.784G>A	c.(784-786)GAG>AAG	p.E262K
Pat_28	Post-Resistance	TMEM176B	28959	37	7	150489212	150489212	Missense_Mutation	SNP	C	T	38	104	c.652G>A	c.(652-654)GTC>ATC	p.V218I
Pat_28	Post-Resistance	MLL3	58508	37	7	151945619	151945619	Missense_Mutation	SNP	C	T	54	138	c.1900G>A	c.(1900-1902)GTG>ATG	p.V634M
Pat_28	Post-Resistance	RBM33	155435	37	7	155567718	155567718	Missense_Mutation	SNP	G	A	45	93	c.3496G>A	c.(3496-3498)GCC>ACC	p.A1166T
Pat_28	Post-Resistance	CSMD1	64478	37	8	2815259	2815259	Missense_Mutation	SNP	A	G	17	15	c.9776T>C	c.(9775-9777)CTT>CCT	p.L3259P
Pat_28	Post-Resistance	DEFA6	1671	37	8	6783482	6783482	Missense_Mutation	SNP	C	T	6	21	c.76G>A	c.(76-78)GAT>AAT	p.D26N
Pat_28	Post-Resistance	USP17L2	377630	37	8	11995072	11995072	Missense_Mutation	SNP	C	T	31	36	c.1198G>A	c.(1198-1200)GAC>AAC	p.D400N
Pat_28	Post-Resistance	MSR1	4481	37	8	16012581	16012581	Missense_Mutation	SNP	C	T	22	68	c.890G>A	c.(889-891)GGT>GAT	p.G297D
Pat_28	Post-Resistance	FAM160B2	64760	37	8	21959813	21959813	Missense_Mutation	SNP	C	T	22	70	c.1979C>T	c.(1978-1980)TCC>TTC	p.S660F
Pat_28	Post-Resistance	RHOBTB2	23221	37	8	22862063	22862063	Missense_Mutation	SNP	C	T	28	69	c.116C>T	c.(115-117)ACC>ATC	p.T39I
Pat_28	Post-Resistance	STMN4	81551	37	8	27097649	27097649	Missense_Mutation	SNP	C	T	17	86	c.349G>A	c.(349-351)GCA>ACA	p.A117T
Pat_28	Post-Resistance	TEX15	56154	37	8	30694633	30694633	Missense_Mutation	SNP	G	A	100	254	c.8018C>T	c.(8017-8019)GCC>GTC	p.A2673V
Pat_28	Post-Resistance	TACC1	6867	37	8	38693693	38693693	Missense_Mutation	SNP	C	T	19	44	c.1727C>T	c.(1726-1728)TCC>TTC	p.S576F
Pat_28	Post-Resistance	ADAM18	8749	37	8	39502938	39502938	Missense_Mutation	SNP	G	A	77	196	c.991G>A	c.(991-993)GAC>AAC	p.D331N
Pat_28	Post-Resistance	DKK4	27121	37	8	42231653	42231653	Nonsense_Mutation	SNP	G	A	48	118	c.640C>T	c.(640-642)CGA>TGA	p.R214*
Pat_28	Post-Resistance	SLC20A2	6575	37	8	42296991	42296991	Missense_Mutation	SNP	C	T	34	80	c.911G>A	c.(910-912)GGC>GAC	p.G304D
Pat_28	Post-Resistance	PXDNL	137902	37	8	52336213	52336214	Missense_Mutation	DNP	GG	AA	27	81	.1716_1717CC>T	1714-1719)TTCCCT>TTTT	p.P573S
Pat_28	Post-Resistance	ST18	9705	37	8	53084562	53084562	Missense_Mutation	SNP	C	T	43	90	c.859G>A	c.(859-861)GCA>ACA	p.A287T
Pat_28	Post-Resistance	RP1	6101	37	8	55538468	55538468	Missense_Mutation	SNP	T	G	32	31	c.2026T>G	c.(2026-2028)TCT>GCT	p.S676A
Pat_28	Post-Resistance	RP1	6101	37	8	55542111	55542111	Missense_Mutation	SNP	C	T	56	163	c.5669C>T	c.(5668-5670)CCA>CTA	p.P1890L
Pat_28	Post-Resistance	SDR16C5	195814	37	8	57228786	57228786	Missense_Mutation	SNP	C	T	22	56	c.121G>A	c.(121-123)GAA>AAA	p.E41K
Pat_28	Post-Resistance	DNAJC5B	85479	37	8	66989064	66989064	Missense_Mutation	SNP	G	A	134	122	c.289G>A	c.(289-291)GAA>AAA	p.E97K
Pat_28	Post-Resistance	SLCO5A1	81796	37	8	70594532	70594532	Missense_Mutation	SNP	C	T	55	140	c.1669G>A	c.(1669-1671)GTT>ATT	p.V557I
Pat_28	Post-Resistance	SLCO5A1	81796	37	8	70744445	70744445	Missense_Mutation	SNP	G	A	15	29	c.464C>T	c.(463-465)ACC>ATC	p.T155I
Pat_28	Post-Resistance	KCNB2	9312	37	8	73849632	73849632	Missense_Mutation	SNP	G	A	27	51	c.2042G>A	c.(2041-2043)AGT>AAT	p.S681N
Pat_28	Post-Resistance	CRISPLD1	83690	37	8	75929610	75929610	Missense_Mutation	SNP	G	A	97	274	c.1052G>A	c.(1051-1053)GGC>GAC	p.G351D
Pat_28	Post-Resistance	HNF4G	3174	37	8	76456106	76456106	Missense_Mutation	SNP	C	T	33	103	c.38C>T	c.(37-39)GCT>GTT	p.A13V
Pat_28	Post-Resistance	ATP6V0D2	245972	37	8	87111316	87111316	Missense_Mutation	SNP	G	A	22	47	c.109G>A	c.(109-111)GTC>ATC	p.V37I
Pat_28	Post-Resistance	CNGB3	54714	37	8	87680246	87680246	Splice_Site	SNP	C	T	149	392	c.643_splice	c.e5+1	p.D215_splice
Pat_28	Post-Resistance	KIAA1429	25962	37	8	95547111	95547111	Missense_Mutation	SNP	G	A	36	94	c.440C>T	c.(439-441)CCA>CTA	p.P147L
Pat_28	Post-Resistance	PLEKHF2	79666	37	8	96166391	96166391	Missense_Mutation	SNP	G	A	71	208	c.119G>A	c.(118-120)GGA>GAA	p.G40E
Pat_28	Post-Resistance	RIMS2	9699	37	8	105001612	105001612	Missense_Mutation	SNP	C	T	92	273	c.2341C>T	c.(2341-2343)CGT>TGT	p.R781C
Pat_28	Post-Resistance	TRHR	7201	37	8	110100221	110100221	Nonsense_Mutation	SNP	G	A	41	105	c.480G>A	c.(478-480)TGG>TGA	p.W160*
Pat_28	Post-Resistance	CSMD3	114788	37	8	114290895	114290895	Missense_Mutation	SNP	G	A	84	195	c.440C>T	c.(439-441)ACC>ATC	p.T147I
Pat_28	Post-Resistance	FER1L6	654463	37	8	124988289	124988289	Missense_Mutation	SNP	G	A	76	170	c.835G>A	c.(835-837)GAT>AAT	p.D279N
Pat_28	Post-Resistance	TATDN1	83940	37	8	125506121	125506121	Nonsense_Mutation	SNP	C	T	52	141	c.744G>A	c.(742-744)TGG>TGA	p.W248*
Pat_28	Post-Resistance	KIAA0196	9897	37	8	126056124	126056124	Missense_Mutation	SNP	A	T	25	64	c.2793T>A	c.(2791-2793)TTT>TTA	p.F931L
Pat_28	Post-Resistance	ZFAT	57623	37	8	135614011	135614011	Missense_Mutation	SNP	G	C	15	49	c.1951C>G	c.(1951-1953)CAG>GAG	p.Q651E
Pat_28	Post-Resistance	FAM135B	51059	37	8	139163525	139163525	Missense_Mutation	SNP	G	A	21	76	c.3193C>T	c.(3193-3195)CCC>TCC	p.P1065S
Pat_28	Post-Resistance	FAM135B	51059	37	8	139165162	139165162	Nonsense_Mutation	SNP	C	T	89	223	c.1556G>A	c.(1555-1557)TGG>TAG	p.W519*
Pat_28	Post-Resistance	FAM135B	51059	37	8	139189650	139189650	Missense_Mutation	SNP	G	A	12	19	c.1043C>T	c.(1042-1044)TCT>TTT	p.S348F
Pat_28	Post-Resistance	COL22A1	169044	37	8	139856375	139856375	Missense_Mutation	SNP	C	T	68	192	c.685G>A	c.(685-687)GAA>AAA	p.E229K
Pat_28	Post-Resistance	ZNF696	79943	37	8	144378228	144378228	Missense_Mutation	SNP	G	A	3	4	c.383G>A	c.(382-384)GGC>GAC	p.G128D

Pat_28	Post-Resistance	TIGD5	84948	37	8	144681454	144681454	Missense_Mutation	SNP	G	A	8	13	c.1234G>A	c.(1234-1236)GCT>ACT	p.A412T
Pat_28	Post-Resistance	OPLAH	26873	37	8	145107071	145107071	Splice_Site	SNP	C	T	4	6	c.3461_splice	c.e24+1	p.R1154_splice
Pat_28	Post-Resistance	OPLAH	26873	37	8	145110042	145110042	Missense_Mutation	SNP	C	T	5	26	c.2299G>A	c.(2299-2301)GAG>AAG	p.E767K
Pat_28	Post-Resistance	CPSF1	29894	37	8	145622574	145622574	Missense_Mutation	SNP	C	T	3	5	c.2440G>A	c.(2440-2442)GGG>AGG	p.G814R
Pat_28	Post-Resistance	SLC39A4	55630	37	8	145640175	145640175	Nonsense_Mutation	SNP	G	A	18	57	c.910C>T	c.(910-912)CAG>TAG	p.Q304*
Pat_28	Post-Resistance	NFKBIL2	4796	37	8	145661045	145661045	Missense_Mutation	SNP	G	A	10	15	c.2771C>T	c.(2770-2772)CCC>CTC	p.P924L
Pat_28	Post-Resistance	DOCK8	81704	37	9	377127	377127	Missense_Mutation	SNP	G	A	12	15	c.2356G>A	c.(2356-2358)GAG>AAG	p.E786K
Pat_28	Post-Resistance	SMARCA2	6595	37	9	2191365	2191365	Missense_Mutation	SNP	C	T	45	52	c.4694C>T	c.(4693-4695)CCT>CTT	p.P1565L
Pat_28	Post-Resistance	GLIS3	169792	37	9	3828352	3828352	Missense_Mutation	SNP	C	T	21	21	c.2248G>A	c.(2248-2250)GCT>ACT	p.A750T
Pat_28	Post-Resistance	KIAA2026	158358	37	9	5988406	5988406	Missense_Mutation	SNP	C	T	62	98	c.733G>A	c.(733-735)GAA>AAA	p.E245K
Pat_28	Post-Resistance	PTPRD	5789	37	9	8331594	8331594	Missense_Mutation	SNP	G	A	58	97	c.5522C>T	c.(5521-5523)TCA>TTA	p.S1841L
Pat_28	Post-Resistance	PTPRD	5789	37	9	8341785	8341785	Missense_Mutation	SNP	C	T	117	166	c.4855G>A	c.(4855-4857)GAA>AAA	p.E1619K
Pat_28	Post-Resistance	DENND4C	55667	37	9	19346258	19346258	Missense_Mutation	SNP	C	T	72	85	c.2636C>T	c.(2635-2637)TCT>TTT	p.S879F
Pat_28	Post-Resistance	KIAA1797	54914	37	9	20770128	20770128	Missense_Mutation	SNP	C	T	56	71	c.797C>T	c.(796-798)ACC>ATC	p.T266I
Pat_28	Post-Resistance	NFX1	4799	37	9	33328626	33328626	Missense_Mutation	SNP	C	T	58	71	c.1954C>T	c.(1954-1956)CCA>TCA	p.P652S
Pat_28	Post-Resistance	C9orf131	138724	37	9	35043539	35043539	Missense_Mutation	SNP	C	T	34	60	c.913C>T	c.(913-915)CCC>TCC	p.P305S
Pat_28	Post-Resistance	NPR2	4882	37	9	35800782	35800782	Missense_Mutation	SNP	C	T	19	23	c.1295C>T	c.(1294-1296)CCT>CTT	p.P432L
Pat_28	Post-Resistance	ZBTB5	9925	37	9	37441572	37441572	Missense_Mutation	SNP	C	T	51	84	c.977G>A	c.(976-978)AGA>AAA	p.R326K
Pat_28	Post-Resistance	ZBTB5	9925	37	9	37442149	37442149	Nonsense_Mutation	SNP	G	A	45	74	c.400C>T	c.(400-402)CAG>TAG	p.Q134*
Pat_28	Post-Resistance	FBXO10	26267	37	9	37537505	37537505	Missense_Mutation	SNP	C	T	4	9	c.1021G>A	c.(1021-1023)GGT>AGT	p.G341S
Pat_28	Post-Resistance	CNTNAP3	79937	37	9	39133127	39133127	Missense_Mutation	SNP	C	A	3	18	c.1882G>T	c.(1882-1884)GCC>TCC	p.A628S
Pat_28	Post-Resistance	RASEF	158158	37	9	85677455	85677455	Missense_Mutation	SNP	C	T	6	8	c.328G>A	c.(328-330)GAC>AAC	p.D110N
Pat_28	Post-Resistance	SPTLC1	10558	37	9	94809516	94809516	Missense_Mutation	SNP	G	A	41	64	c.1019C>T	c.(1018-1020)TCG>TTG	p.S340L
Pat_28	Post-Resistance	ECM2	1842	37	9	95280085	95280085	Missense_Mutation	SNP	G	A	41	63	c.365C>T	c.(364-366)ACT>ATT	p.T122I
Pat_28	Post-Resistance	SUSD3	203328	37	9	95846820	95846820	Missense_Mutation	SNP	G	A	27	29	c.559G>A	c.(559-561)GAC>AAC	p.D187N
Pat_28	Post-Resistance	SLC35D2	11046	37	9	99083559	99083559	Missense_Mutation	SNP	C	T	56	98	c.979G>A	c.(979-981)GGT>AGT	p.G327S
Pat_28	Post-Resistance	TSTD2	158427	37	9	100368457	100368457	Missense_Mutation	SNP	G	A	21	37	c.922C>T	c.(922-924)CTT>TTT	p.L308F
Pat_28	Post-Resistance	TRIM14	9830	37	9	100850154	100850154	Missense_Mutation	SNP	C	G	8	5	c.927G>C	c.(925-927)TGG>TGC	p.W309C
Pat_28	Post-Resistance	TEX10	54881	37	9	103064520	103064520	Missense_Mutation	SNP	T	C	71	106	c.2743A>G	c.(2743-2745)ATC>GTC	p.I915V
Pat_28	Post-Resistance	GRIN3A	116443	37	9	104448938	104448938	Missense_Mutation	SNP	C	T	92	154	c.1244G>A	c.(1243-1245)AGC>AAC	p.S415N
Pat_28	Post-Resistance	GRIN3A	116443	37	9	104499769	104499769	Missense_Mutation	SNP	G	A	29	43	c.493C>T	c.(493-495)CCC>TCC	p.P165S
Pat_28	Post-Resistance	SVEP1	79987	37	9	113245898	113245898	Missense_Mutation	SNP	C	T	22	45	c.2006G>A	c.(2005-2007)AGC>AAC	p.S669N
Pat_28	Post-Resistance	ZFP37	7539	37	9	115805811	115805811	Missense_Mutation	SNP	C	T	80	117	c.1087G>A	c.(1087-1089)GCA>ACA	p.A363T
Pat_28	Post-Resistance	TNFSF8	944	37	9	117692611	117692611	Translation_Start_Site	SNP	C	T	9	25	c.-27G>A	c.(-29--25)AGGTG>AGATG	
Pat_28	Post-Resistance	ANGPTL2	23452	37	9	129856110	129856110	Missense_Mutation	SNP	C	T	8	103	c.913G>A	c.(913-915)GTG>ATG	p.V305M
Pat_28	Post-Resistance	PPAPDC3	84814	37	9	134183496	134183496	Missense_Mutation	SNP	C	T	10	11	c.638C>T	c.(637-639)CCC>CTC	p.P213L
Pat_28	Post-Resistance	DBH	1621	37	9	136501807	136501807	Missense_Mutation	SNP	C	T	20	29	c.314C>T	c.(313-315)ACC>ATC	p.T105I
Pat_28	Post-Resistance	COL5A1	1289	37	9	137591910	137591910	Missense_Mutation	SNP	G	A	28	22	c.433G>A	c.(433-435)GGG>AGG	p.G145R
Pat_28	Post-Resistance	FCN2	2220	37	9	137775171	137775171	Missense_Mutation	SNP	C	T	18	34	c.238C>T	c.(238-240)CCT>TCT	p.P80S
Pat_28	Post-Resistance	CARD9	64170	37	9	139265364	139265364	Missense_Mutation	SNP	C	T	4	4	c.556G>A	c.(556-558)GCC>ACC	p.A186T
Pat_28	Post-Resistance	NOTCH1	4851	37	9	139401834	139401834	Missense_Mutation	SNP	G	A	6	11	c.3566C>T	c.(3565-3567)TCC>TTC	p.S1189F
Pat_28	Post-Resistance	LCN6	158062	37	9	139640346	139640346	Missense_Mutation	SNP	C	T	38	41	c.251G>A	c.(250-252)AGT>AAT	p.S84N
Pat_28	Post-Resistance	ABCA2	20	37	9	139912032	139912032	Missense_Mutation	SNP	C	T	5	67	c.2321G>A	c.(2320-2322)GGC>GAC	p.G774D
Pat_28	Post-Resistance	DPP7	29952	37	9	140008808	140008808	Missense_Mutation	SNP	G	A	11	11	c.208C>T	c.(208-210)CCC>TCC	p.P70S
Pat_28	Post-Resistance	EHMT1	79813	37	9	140637973	140637973	Missense_Mutation	SNP	G	A	47	73	c.974G>A	c.(973-975)GGT>GAT	p.G325D
Pat_28	Post-Resistance	MXRA5	25878	37	X	3238276	3238276	Missense_Mutation	SNP	G	A	4	3	c.5450C>T	c.(5449-5451)TCC>TTC	p.S1817F
Pat_28	Post-Resistance	MXRA5	25878	37	X	3240404	3240404	Missense_Mutation	SNP	G	A	13	3	c.3322C>T	c.(3322-3324)CCA>TCA	p.P1108S

Pat_28	Post-Resistance	DDX53	168400	37	X	23020032	23020032	Missense_Mutation	SNP	C	T	28	6	c.1858C>T	c.(1858-1860)CCT>TCT	p.P620S
Pat_28	Post-Resistance	ERAS	3266	37	X	48687781	48687781	Missense_Mutation	SNP	C	T	25	6	c.248C>T	c.(247-249)ACC>ATC	p.T83I
Pat_28	Post-Resistance	NUDT11	55190	37	X	51239162	51239162	Nonsense_Mutation	SNP	C	T	9	3	c.135G>A	c.(133-135)TGG>TGA	p.W45*
Pat_28	Post-Resistance	IQSEC2	23096	37	X	53280209	53280209	Missense_Mutation	SNP	G	A	50	16	c.1549C>T	c.(1549-1551)CCC>TCC	p.P517S
Pat_28	Post-Resistance	SNX12	29934	37	X	70280897	70280897	Missense_Mutation	SNP	C	T	15	2	c.458G>A	c.(457-459)AGG>AAG	p.R153K
Pat_28	Post-Resistance	NAP1L2	4674	37	X	72434172	72434172	Missense_Mutation	SNP	C	T	29	8	c.157G>A	c.(157-159)GCT>ACT	p.A53T
Pat_28	Post-Resistance	RAB9B	51209	37	X	103080576	103080576	Nonsense_Mutation	SNP	G	A	51	11	c.139C>T	c.(139-141)CGA>TGA	p.R47*
Pat_28	Post-Resistance	IRS4	8471	37	X	107978956	107978956	Missense_Mutation	SNP	C	T	5	2	c.619G>A	c.(619-621)GGC>AGC	p.G207S
Pat_28	Post-Resistance	SMARCA1	6594	37	X	128625983	128625983	Missense_Mutation	SNP	C	T	223	38	c.1750G>A	c.(1750-1752)GCA>ACA	p.A584T
Pat_28	Post-Resistance	SAGE1	55511	37	X	134993770	134993770	Missense_Mutation	SNP	G	A	109	24	c.2179G>A	c.(2179-2181)GAG>AAG	p.E727K
Pat_28	Post-Resistance	ARHGEF6	9459	37	X	135829693	135829693	Missense_Mutation	SNP	A	G	68	14	c.308T>C	c.(307-309)CTT>CCT	p.L103P
Pat_28	Post-Resistance	RBMX	27316	37	X	135956407	135956407	Missense_Mutation	SNP	T	C	50	12	c.1070A>G	c.(1069-1071)TAC>TGC	p.Y357C
Pat_28	Post-Resistance	SPANXN3	139067	37	X	142596922	142596922	Missense_Mutation	SNP	G	A	44	8	c.148C>T	c.(148-150)CCA>TCA	p.P50S
Pat_28	Post-Resistance	HAUS7	55559	37	X	152736027	152736027	Missense_Mutation	SNP	C	T	10	2	c.19G>A	c.(19-21)GGA>AGA	p.G7R
Pat_28	Post-Resistance	FLNA	2316	37	X	153594980	153594980	Missense_Mutation	SNP	T	G	28	8	c.1015A>C	c.(1015-1017)AAC>CAC	p.N339H
Pat_28	Post-Resistance	F8	2157	37	X	154158530	154158530	Missense_Mutation	SNP	C	T	60	9	c.3535G>A	c.(3535-3537)GAC>AAC	p.D1179N
Pat_28	Post-Resistance	IL9R	3581	37	X	155235146	155235146	Splice_Site	SNP	T	C	7	21	c.781_splice	c.e6+2	p.G261_splice
Pat_28	Post-Resistance	KDM5D	8284	37	Y	21901512	21901512	Missense_Mutation	SNP	C	T	27	3	c.559G>A	c.(559-561)GAT>AAT	p.D187N
Pat_30	Pre-Treatment	C1orf127	148345	37	1	11008613	11008613	Nonsense_Mutation	SNP	G	A	4	153	c.1132C>T	c.(1132-1134)CGA>TGA	p.R378*
Pat_30	Pre-Treatment	ESPNP	284729	37	1	17023110	17023110	Missense_Mutation	SNP	G	A	6	68	c.1640C>T	c.(1639-1641)CCG>CTG	p.P547L
Pat_30	Pre-Treatment	SERINC2	347735	37	1	31902304	31902305	Missense_Mutation	DNP	CC	TT	81	320	c.944_945CC>TT	c.(943-945)CCC>CTT	p.P315L
Pat_30	Pre-Treatment	ZMYM1	79830	37	1	35579236	35579236	Missense_Mutation	SNP	T	A	38	54	c.1805T>A	c.(1804-1806)TTT>TAT	p.F602Y
Pat_30	Pre-Treatment	GUCA2B	2981	37	1	42621229	42621229	Missense_Mutation	SNP	G	A	9	452	c.301G>A	c.(301-303)GAG>AAG	p.E101K
Pat_30	Pre-Treatment	PGM1	5236	37	1	64117438	64117438	Missense_Mutation	SNP	C	T	28	90	c.1379C>T	c.(1378-1380)TCA>TTA	p.S460L
Pat_30	Pre-Treatment	CLCA4	22802	37	1	87025658	87025658	Missense_Mutation	SNP	A	G	88	148	c.203A>G	c.(202-204)GAA>GGA	p.E68G
Pat_30	Pre-Treatment	COL11A1	1301	37	1	103483375	103483375	Splice_Site	SNP	C	T	5	278	c.1413_splice	c.e11+1	p.R471_splice
Pat_30	Pre-Treatment	PTGFRN	5738	37	1	117491852	117491852	Missense_Mutation	SNP	G	A	81	324	c.871G>A	c.(871-873)GAA>AAA	p.E291K
Pat_30	Pre-Treatment	ITGA10	8515	37	1	145532599	145532599	Missense_Mutation	SNP	G	A	50	288	c.1052G>A	c.(1051-1053)GGA>GAA	p.G351E
Pat_30	Pre-Treatment	BCL9	607	37	1	147090788	147090788	Missense_Mutation	SNP	G	A	5	210	c.827G>A	c.(826-828)CGG>CAG	p.R276Q
Pat_30	Pre-Treatment	TARS2	80222	37	1	150460488	150460488	Missense_Mutation	SNP	T	C	67	192	c.221T>C	c.(220-222)GTG>GCG	p.V74A
Pat_30	Pre-Treatment	NUP210L	91181	37	1	154112300	154112300	Missense_Mutation	SNP	C	T	11	725	c.695G>A	c.(694-696)CGA>CAA	p.R232Q
Pat_30	Pre-Treatment	ADAR	103	37	1	154574328	154574328	Missense_Mutation	SNP	T	C	7	477	c.790A>G	c.(790-792)AGT>GGT	p.S264G
Pat_30	Pre-Treatment	GPATCH4	54865	37	1	156565292	156565293	Missense_Mutation	DNP	CC	TT	125	380	c.840_841GG>AA	838-843)GGGGAA>GGAA	p.E281K
Pat_30	Pre-Treatment	C1orf92	149499	37	1	156902735	156902735	Missense_Mutation	SNP	G	A	6	32	c.1654G>A	c.(1654-1656)GAT>AAT	p.D552N
Pat_30	Pre-Treatment	OR10K1	391109	37	1	158435715	158435715	Missense_Mutation	SNP	C	T	109	289	c.364C>T	c.(364-366)CGC>TGC	p.R122C
Pat_30	Pre-Treatment	SELE	6401	37	1	169698706	169698706	Missense_Mutation	SNP	C	T	45	162	c.824G>A	c.(823-825)GGA>GAA	p.G275E
Pat_30	Pre-Treatment	HMCN1	83872	37	1	185878628	185878628	Missense_Mutation	SNP	C	T	25	114	c.781C>T	c.(781-783)CGC>TGC	p.R261C
Pat_30	Pre-Treatment	F13B	2165	37	1	197026515	197026515	Missense_Mutation	SNP	C	T	70	202	c.886G>A	c.(886-888)GAA>AAA	p.E296K
Pat_30	Pre-Treatment	RAB3GAP2	25782	37	1	220338135	220338135	Missense_Mutation	SNP	G	A	3	37	c.3094C>T	c.(3094-3096)CGT>TGT	p.R1032C
Pat_30	Pre-Treatment	RHOU	58480	37	1	228879120	228879120	Missense_Mutation	SNP	A	G	108	384	c.410A>G	c.(409-411)CAG>CGG	p.Q137R
Pat_30	Pre-Treatment	EDARADD	128178	37	1	236631574	236631574	Missense_Mutation	SNP	C	T	54	147	c.263C>T	c.(262-264)CCA>CTA	p.P88L
Pat_30	Pre-Treatment	ZNF496	84838	37	1	247492847	247492847	Missense_Mutation	SNP	G	A	49	114	c.34C>T	c.(34-36)CCG>TCG	p.P12S
Pat_30	Pre-Treatment	OR2G2	81470	37	1	247752179	247752179	Missense_Mutation	SNP	G	A	47	561	c.518G>A	c.(517-519)GGG>GAG	p.G173E
Pat_30	Pre-Treatment	IL15RA	3601	37	10	6008146	6008146	Missense_Mutation	SNP	T	A	52	98	c.245A>T	c.(244-246)AAT>ATT	p.N82I
Pat_30	Pre-Treatment	FRMD4A	55691	37	10	13698788	13698788	Missense_Mutation	SNP	C	T	4	64	c.2801G>A	c.(2800-2802)CGT>CAT	p.R934H
Pat_30	Pre-Treatment	NEBL	10529	37	10	21102879	21102879	Missense_Mutation	SNP	G	A	21	116	c.2335C>T	c.(2335-2337)CAT>TAT	p.H779Y
Pat_30	Pre-Treatment	ANKRD26	22852	37	10	27366301	27366301	Missense_Mutation	SNP	G	A	57	167	c.1043C>T	c.(1042-1044)TCC>TTC	p.S348F

Pat_30	Pre-Treatment	ANK3	288	37	10	61956338	61956338	Missense_Mutation	SNP	C	G	3	78	c.1735G>C	c.(1735-1737)GAA>CAA	p.E579Q
Pat_30	Pre-Treatment	HERC4	26091	37	10	69750933	69750933	Missense_Mutation	SNP	G	A	15	37	c.1295C>T	c.(1294-1296)TCC>TTC	p.S432F
Pat_30	Pre-Treatment	PBLD	64081	37	10	70048273	70048273	Missense_Mutation	SNP	G	A	31	76	c.658C>T	c.(658-660)CCG>TCG	p.P220S
Pat_30	Pre-Treatment	CDH23	64072	37	10	73499431	73499431	Missense_Mutation	SNP	G	A	3	61	c.4390G>A	c.(4390-4392)GCG>ACG	p.A1464T
Pat_30	Pre-Treatment	ZMIZ1	57178	37	10	81060652	81060652	Nonsense_Mutation	SNP	C	T	5	289	c.1972C>T	c.(1972-1974)CAG>TAG	p.Q658*
Pat_30	Pre-Treatment	TMEM20	159371	37	10	95660637	95660637	Missense_Mutation	SNP	C	T	8	418	c.488C>T	c.(487-489)ACG>ATG	p.T163M
Pat_30	Pre-Treatment	PLCE1	51196	37	10	96028758	96028758	Missense_Mutation	SNP	C	T	40	74	c.4354C>T	c.(4354-4356)CAT>TAT	p.H1452Y
Pat_30	Pre-Treatment	CYP2C8	1558	37	10	96824642	96824642	Missense_Mutation	SNP	C	T	95	178	c.557G>A	c.(556-558)CGA>CAA	p.R186Q
Pat_30	Pre-Treatment	TLL2	7093	37	10	98192579	98192579	Missense_Mutation	SNP	C	T	15	187	c.505G>A	c.(505-507)GGA>AGA	p.G169R
Pat_30	Pre-Treatment	OR51S1	119692	37	11	4870243	4870243	Missense_Mutation	SNP	G	A	33	176	c.196C>T	c.(196-198)CCA>TCA	p.P66S
Pat_30	Pre-Treatment	OR51B6	390058	37	11	5373230	5373230	Missense_Mutation	SNP	C	T	86	216	c.493C>T	c.(493-495)CCC>TCC	p.P165S
Pat_30	Pre-Treatment	BDNF	627	37	11	27679778	27679778	Missense_Mutation	SNP	C	T	16	59	c.334G>A	c.(334-336)GAA>AAA	p.E112K
Pat_30	Pre-Treatment	TTC17	55761	37	11	43515441	43515441	Missense_Mutation	SNP	G	A	181	560	c.3413G>A	c.(3412-3414)CGG>CAG	p.R1138Q
Pat_30	Pre-Treatment	OR5D18	219438	37	11	55587153	55587153	Missense_Mutation	SNP	G	T	4	119	c.48G>T	c.(46-48)TTG>TTT	p.L16F
Pat_30	Pre-Treatment	OR8H2	390151	37	11	55872803	55872804	Missense_Mutation	DNP	GG	AA	209	626	c.285_286GG>AA	283-288)ACGGGC>ACAA	p.G96S
Pat_30	Pre-Treatment	NPAS4	266743	37	11	66192136	66192136	Missense_Mutation	SNP	C	T	45	114	c.1775C>T	c.(1774-1776)GCC>GTC	p.A592V
Pat_30	Pre-Treatment	PITPNM1	9600	37	11	67261510	67261510	Missense_Mutation	SNP	G	A	4	149	c.2891C>T	c.(2890-2892)TCG>TTG	p.S964L
Pat_30	Pre-Treatment	MYO7A	4647	37	11	76893123	76893123	Missense_Mutation	SNP	G	A	77	279	c.3031G>A	c.(3031-3033)GGG>AGG	p.G1011R
Pat_30	Pre-Treatment	NNMT	4837	37	11	114182916	114182916	Missense_Mutation	SNP	C	T	26	170	c.512C>T	c.(511-513)CCA>CTA	p.P171L
Pat_30	Pre-Treatment	PHLDB1	23187	37	11	118498561	118498561	Missense_Mutation	SNP	C	T	3	47	c.1022C>T	c.(1021-1023)GCG>GTG	p.A341V
Pat_30	Pre-Treatment	OR10G8	219869	37	11	123901051	123901051	Missense_Mutation	SNP	C	T	28	111	c.722C>T	c.(721-723)GCC>GTC	p.A241V
Pat_30	Pre-Treatment	GLB1L2	89944	37	11	134212688	134212688	Nonsense_Mutation	SNP	C	T	4	130	c.127C>T	c.(127-129)CGA>TGA	p.R43*
Pat_30	Pre-Treatment	C3AR1	719	37	12	8212106	8212106	Missense_Mutation	SNP	G	A	15	233	c.676C>T	c.(676-678)CCC>TCC	p.P226S
Pat_30	Pre-Treatment	TAS2R20	259295	37	12	11150318	11150318	Missense_Mutation	SNP	C	A	5	255	c.157G>T	c.(157-159)GTC>TTC	p.V53F
Pat_30	Pre-Treatment	SLCO1B1	10599	37	12	21391959	21391959	Missense_Mutation	SNP	G	C	24	43	c.1912G>C	c.(1912-1914)GTT>CTT	p.V638L
Pat_30	Pre-Treatment	ALG10B	144245	37	12	38714749	38714749	Missense_Mutation	SNP	G	A	44	148	c.1156G>A	c.(1156-1158)GAC>AAC	p.D386N
Pat_30	Pre-Treatment	ABCD2	225	37	12	40001403	40001403	Nonsense_Mutation	SNP	C	A	35	93	c.1234G>T	c.(1234-1236)GAG>TAG	p.E412*
Pat_30	Pre-Treatment	ANKRD33	341405	37	12	52283221	52283221	Nonsense_Mutation	SNP	C	T	34	108	c.187C>T	c.(187-189)CAG>TAG	p.Q63*
Pat_30	Pre-Treatment	KRT7	3855	37	12	52635286	52635286	Missense_Mutation	SNP	G	A	67	228	c.724G>A	c.(724-726)GAC>AAC	p.D242N
Pat_30	Pre-Treatment	KRT84	3890	37	12	52774935	52774935	Missense_Mutation	SNP	G	A	6	420	c.1132C>T	c.(1132-1134)CGG>TGG	p.R378W
Pat_30	Pre-Treatment	OR6C68	403284	37	12	55886390	55886390	Missense_Mutation	SNP	C	T	19	143	c.244C>T	c.(244-246)CCA>TCA	p.P82S
Pat_30	Pre-Treatment	DNAJC14	85406	37	12	56216235	56216235	Missense_Mutation	SNP	C	T	63	159	c.1820G>A	c.(1819-1821)GGT>GAT	p.G607D
Pat_30	Pre-Treatment	GRIP1	23426	37	12	66765581	66765581	Missense_Mutation	SNP	G	A	119	380	c.2749C>T	c.(2749-2751)CGG>TGG	p.R917W
Pat_30	Pre-Treatment	MDM1	56890	37	12	68720499	68720499	Missense_Mutation	SNP	C	G	21	72	c.436G>C	c.(436-438)GTT>CTT	p.V146L
Pat_30	Pre-Treatment	RAP1B	5908	37	12	69047982	69047982	Missense_Mutation	SNP	G	A	39	655	c.274G>A	c.(274-276)GAT>AAT	p.D92N
Pat_30	Pre-Treatment	ZDHHC17	23390	37	12	77158051	77158051	Missense_Mutation	SNP	C	T	3	48	c.35C>T	c.(34-36)GCG>GTG	p.A12V
Pat_30	Pre-Treatment	NR2C1	7181	37	12	95442888	95442888	Missense_Mutation	SNP	C	T	5	160	c.1087G>A	c.(1087-1089)GAA>AAA	p.E363K
Pat_30	Pre-Treatment	SLC25A3	5250	37	12	98992448	98992448	Missense_Mutation	SNP	C	T	5	126	c.611C>T	c.(610-612)GCT>GTT	p.A204V
Pat_30	Pre-Treatment	CKAP4	10970	37	12	106633149	106633149	Missense_Mutation	SNP	C	T	6	298	c.1462G>A	c.(1462-1464)GAG>AAG	p.E488K
Pat_30	Pre-Treatment	CIT	11113	37	12	120150494	120150494	Missense_Mutation	SNP	T	G	57	142	c.4460A>C	c.(4459-4461)CAG>CCG	p.Q1487P
Pat_30	Pre-Treatment	FLT1	2321	37	13	29002026	29002026	Missense_Mutation	SNP	G	A	80	224	c.1139C>T	c.(1138-1140)TCT>TTT	p.S380F
Pat_30	Pre-Treatment	SLC46A3	283537	37	13	29287375	29287375	Nonsense_Mutation	SNP	G	A	26	122	c.502C>T	c.(502-504)CGA>TGA	p.R168*
Pat_30	Pre-Treatment	SLAIN1	122060	37	13	78337299	78337299	Missense_Mutation	SNP	C	G	19	149	c.1225C>G	c.(1225-1227)CCT>GCT	p.P409A
Pat_30	Pre-Treatment	RBM26	64062	37	13	79940864	79940864	Missense_Mutation	SNP	G	A	4	131	c.1039C>T	c.(1039-1041)CCC>TCC	p.P347S
Pat_30	Pre-Treatment	FARP1	10160	37	13	99038039	99038039	Missense_Mutation	SNP	G	A	5	165	c.730G>A	c.(730-732)GTT>ATT	p.V244I
Pat_30	Pre-Treatment	DOCK9	23348	37	13	99567688	99567688	Missense_Mutation	SNP	C	T	19	56	c.790G>A	c.(790-792)GAC>AAC	p.D264N
Pat_30	Pre-Treatment	TPPP2	122664	37	14	21500204	21500204	Missense_Mutation	SNP	G	A	57	249	c.481G>A	c.(481-483)GGT>AGT	p.G161S

Pat_30	Pre-Treatment	IPO4	79711	37	14	24654114	24654114	Missense_Mutation	SNP	G	A	4	101	c.1481C>T	c.(1480-1482)CCC>CTC	p.P494L
Pat_30	Pre-Treatment	KCNH5	27133	37	14	63468127	63468127	Missense_Mutation	SNP	C	T	5	52	c.355G>A	c.(355-357)GAA>AAA	p.E119K
Pat_30	Pre-Treatment	SYNE2	23224	37	14	64568695	64568695	Missense_Mutation	SNP	C	T	26	141	c.12427C>T	c.(12427-12429)CTT>TTT	p.L4143F
Pat_30	Pre-Treatment	CCDC88C	440193	37	14	91779633	91779633	Missense_Mutation	SNP	G	A	5	264	c.2527C>T	c.(2527-2529)CGG>TGG	p.R843W
Pat_30	Pre-Treatment	SMEK1	55671	37	14	91929191	91929191	Missense_Mutation	SNP	T	C	40	109	c.1861A>G	c.(1861-1863)ATT>GTT	p.I621V
Pat_30	Pre-Treatment	PPP2R5C	5527	37	14	102229267	102229267	Missense_Mutation	SNP	G	A	6	29	c.53G>A	c.(52-54)GGA>GAA	p.G18E
Pat_30	Pre-Treatment	AHNAK2	113146	37	14	105421355	105421355	Missense_Mutation	SNP	G	A	9	55	c.590C>T	c.(589-591)CCA>CTA	p.P197L
Pat_30	Pre-Treatment	CHP	11261	37	15	41570983	41570983	Missense_Mutation	SNP	G	A	4	127	c.430G>A	c.(430-432)GGA>AGA	p.G144R
Pat_30	Pre-Treatment	MGA	23269	37	15	42053967	42053967	Nonsense_Mutation	SNP	C	T	5	39	c.7429C>T	c.(7429-7431)CAG>TAG	p.Q2477*
Pat_30	Pre-Treatment	MYO5A	4644	37	15	52638557	52638557	Splice_Site	SNP	C	T	7	64	c.3959_splice	c.e30+1	p.R1320_splice
Pat_30	Pre-Treatment	ARPP19	10776	37	15	52849310	52849310	Missense_Mutation	SNP	C	T	74	292	c.155G>A	c.(154-156)CGG>CAG	p.R52Q
Pat_30	Pre-Treatment	PIAS1	8554	37	15	68378810	68378810	Missense_Mutation	SNP	G	A	4	142	c.191G>A	c.(190-192)CGG>CAG	p.R64Q
Pat_30	Pre-Treatment	NOX5	79400	37	15	69341381	69341381	Missense_Mutation	SNP	C	T	14	63	c.1982C>T	c.(1981-1983)GCC>GTC	p.A661V
Pat_30	Pre-Treatment	RHCG	51458	37	15	90021130	90021130	Missense_Mutation	SNP	C	T	4	146	c.913G>A	c.(913-915)GGT>AGT	p.G305S
Pat_30	Pre-Treatment	WDR93	56964	37	15	90276361	90276361	Missense_Mutation	SNP	G	A	31	92	c.1455G>A	c.(1453-1455)ATG>ATA	p.M485I
Pat_30	Pre-Treatment	C16orf79	283870	37	16	2259391	2259391	Missense_Mutation	SNP	G	A	6	174	c.755C>T	c.(754-756)TCG>TTG	p.S252L
Pat_30	Pre-Treatment	NLRC3	197358	37	16	3614397	3614397	Missense_Mutation	SNP	C	T	37	138	c.541G>A	c.(541-543)GAT>AAT	p.D181N
Pat_30	Pre-Treatment	SRL	6345	37	16	4247914	4247914	Missense_Mutation	SNP	C	T	4	89	c.262G>A	c.(262-264)GGA>AGA	p.G88R
Pat_30	Pre-Treatment	ACSM1	116285	37	16	20636779	20636779	Missense_Mutation	SNP	G	A	48	139	c.1493C>T	c.(1492-1494)GCC>GTC	p.A498V
Pat_30	Pre-Treatment	ATXN2L	11273	37	16	28836712	28836712	Missense_Mutation	SNP	C	T	17	89	c.325C>T	c.(325-327)CCA>TCA	p.P109S
Pat_30	Pre-Treatment	PHKG2	5261	37	16	30767747	30767747	Missense_Mutation	SNP	G	A	5	245	c.707G>A	c.(706-708)CGG>CAG	p.R236Q
Pat_30	Pre-Treatment	MYLK3	91807	37	16	46744628	46744628	Missense_Mutation	SNP	C	T	90	581	c.2188G>A	c.(2188-2190)GAT>AAT	p.D730N
Pat_30	Pre-Treatment	CDH8	1006	37	16	61935302	61935302	Nonsense_Mutation	SNP	G	A	15	142	c.328C>T	c.(328-330)CAA>TAA	p.Q110*
Pat_30	Pre-Treatment	SPATA22	84690	37	17	3343629	3343629	Missense_Mutation	SNP	G	A	27	163	c.904C>T	c.(904-906)CGT>TGT	p.R302C
Pat_30	Pre-Treatment	ZZEF1	23140	37	17	3920987	3920987	Missense_Mutation	SNP	G	A	42	162	c.7679C>T	c.(7678-7680)TCG>TTG	p.S2560L
Pat_30	Pre-Treatment	CXCL16	58191	37	17	4641715	4641715	Missense_Mutation	SNP	G	A	15	76	c.346C>T	c.(346-348)CTT>TTT	p.L116F
Pat_30	Pre-Treatment	MYH8	4626	37	17	10296234	10296234	Missense_Mutation	SNP	C	T	73	252	c.5377G>A	c.(5377-5379)GTG>ATG	p.V1793M
Pat_30	Pre-Treatment	MYH4	4622	37	17	10359030	10359030	Missense_Mutation	SNP	A	G	23	98	c.2075T>C	c.(2074-2076)CTT>CCT	p.L692P
Pat_30	Pre-Treatment	MYH2	4620	37	17	10430076	10430077	Missense_Mutation	DNP	GG	AA	30	254	.4026_4027CC>T	024-4029)TCCCGC>TCT	p.R1343C
Pat_30	Pre-Treatment	KCNJ12	3768	37	17	21319348	21319348	Missense_Mutation	SNP	C	T	12	122	c.694C>T	c.(694-696)CTC>TTC	p.L232F
Pat_30	Pre-Treatment	KSR1	8844	37	17	25932605	25932605	Missense_Mutation	SNP	C	T	9	14	c.1415C>T	c.(1414-1416)CCC>CTC	p.P472L
Pat_30	Pre-Treatment	AATF	26574	37	17	35310442	35310442	Missense_Mutation	SNP	G	T	40	114	c.540G>T	c.(538-540)ATG>ATT	p.M180I
Pat_30	Pre-Treatment	SLC25A39	51629	37	17	42398503	42398503	Missense_Mutation	SNP	G	A	4	71	c.614C>T	c.(613-615)ACT>ATT	p.T205I
Pat_30	Pre-Treatment	SPOP	8405	37	17	47684692	47684692	Nonsense_Mutation	SNP	C	A	51	141	c.757G>T	c.(757-759)GAA>TAA	p.E253*
Pat_30	Pre-Treatment	BCAS3	54828	37	17	58979987	58979987	Nonsense_Mutation	SNP	C	T	146	491	c.745C>T	c.(745-747)CGA>TGA	p.R249*
Pat_30	Pre-Treatment	CACNG1	786	37	17	65051302	65051302	Missense_Mutation	SNP	G	A	5	151	c.388G>A	c.(388-390)GGG>AGG	p.G130R
Pat_30	Pre-Treatment	AFMID	125061	37	17	76200807	76200807	Missense_Mutation	SNP	G	A	4	139	c.379G>A	c.(379-381)GGC>AGC	p.G127S
Pat_30	Pre-Treatment	CBX2	84733	37	17	77758699	77758699	Missense_Mutation	SNP	C	T	52	105	c.1457C>T	c.(1456-1458)TCC>TTC	p.S486F
Pat_30	Pre-Treatment	FASN	2194	37	17	80046136	80046136	Missense_Mutation	SNP	C	T	4	117	c.2641G>A	c.(2641-2643)GAC>AAC	p.D881N
Pat_30	Pre-Treatment	LAMA1	284217	37	18	6950864	6950865	Missense_Mutation	DNP	GG	AA	61	124	.8313_8314CC>T	311-8316)GGCCGC>GGT	p.R2772C
Pat_30	Pre-Treatment	ABHD3	171586	37	18	19244083	19244083	Missense_Mutation	SNP	C	T	4	74	c.664G>A	c.(664-666)GGA>AGA	p.G222R
Pat_30	Pre-Treatment	PSMA8	143471	37	18	23713939	23713939	Nonsense_Mutation	SNP	C	T	75	184	c.10C>T	c.(10-12)CGA>TGA	p.R4*
Pat_30	Pre-Treatment	DSG1	1828	37	18	28934521	28934521	Missense_Mutation	SNP	G	A	40	175	c.2362G>A	c.(2362-2364)GAA>AAA	p.E788K
Pat_30	Pre-Treatment	KIAA1632	57724	37	18	43514816	43514816	Missense_Mutation	SNP	G	A	26	82	c.2216C>T	c.(2215-2217)TCC>TTC	p.S739F
Pat_30	Pre-Treatment	DCC	1630	37	18	50592482	50592482	Missense_Mutation	SNP	G	A	55	177	c.1207G>A	c.(1207-1209)GAA>AAA	p.E403K
Pat_30	Pre-Treatment	ALPK2	115701	37	18	56165294	56165294	Missense_Mutation	SNP	T	C	98	241	c.6283A>G	c.(6283-6285)ACG>GCG	p.T2095A
Pat_30	Pre-Treatment	CDH7	1005	37	18	63489391	63489391	Missense_Mutation	SNP	G	A	38	146	c.700G>A	c.(700-702)GAT>AAT	p.D234N

Pat_30	Pre-Treatment	ABCA7	10347	37	19	1058227	1058227	Missense_Mutation	SNP	T	A	53	111	c.5108T>A	c.(5107-5109)ATG>AAG	p.M1703K
Pat_30	Pre-Treatment	BTBD2	55643	37	19	1990755	1990755	Missense_Mutation	SNP	C	T	3	43	c.751G>A	c.(751-753)GAC>AAC	p.D251N
Pat_30	Pre-Treatment	VAV1	7409	37	19	6820829	6820830	Splice_Site	DNP	GG	AA	45	348	c.321_splice	c.e2+1	p.K107_splice
Pat_30	Pre-Treatment	MUC16	94025	37	19	9073258	9073258	Missense_Mutation	SNP	C	T	58	336	c.14188G>A	c.(14188-14190)GAC>AAC	p.D4730N
Pat_30	Pre-Treatment	DCAF15	90379	37	19	14067244	14067244	Nonsense_Mutation	SNP	C	T	9	590	c.694C>T	c.(694-696)CAG>TAG	p.Q232*
Pat_30	Pre-Treatment	ZNF208	7757	37	19	22155819	22155819	Missense_Mutation	SNP	C	T	5	196	c.1717G>A	c.(1717-1719)GCC>ACC	p.A573T
Pat_30	Pre-Treatment	ZNF565	147929	37	19	36674056	36674056	Missense_Mutation	SNP	C	T	46	147	c.812G>A	c.(811-813)AGA>AAA	p.R271K
Pat_30	Pre-Treatment	SYCN	342898	37	19	39694810	39694810	Missense_Mutation	SNP	G	A	4	87	c.85C>T	c.(85-87)CTC>TTC	p.L29F
Pat_30	Pre-Treatment	ARHGEF1	9138	37	19	42406981	42406981	Missense_Mutation	SNP	G	A	36	194	c.1671G>A	c.(1669-1671)ATG>ATA	p.M557I
Pat_30	Pre-Treatment	PSG3	5671	37	19	43243098	43243098	Missense_Mutation	SNP	C	T	51	648	c.208G>A	c.(208-210)GGG>AGG	p.G70R
Pat_30	Pre-Treatment	PTH2	113091	37	19	49926533	49926533	Missense_Mutation	SNP	G	C	5	87	c.64C>G	c.(64-66)CTG>GTG	p.L22V
Pat_30	Pre-Treatment	NKG7	4818	37	19	51875436	51875436	Missense_Mutation	SNP	T	C	9	446	c.283A>G	c.(283-285)ACC>GCC	p.T95A
Pat_30	Pre-Treatment	SIGLEC6	946	37	19	52034460	52034460	Nonsense_Mutation	SNP	C	T	16	329	c.381G>A	c.(379-381)TGG>TGA	p.W127*
Pat_30	Pre-Treatment	ZNF813	126017	37	19	53995179	53995179	Missense_Mutation	SNP	C	A	5	178	c.1693C>A	c.(1693-1695)CAC>AAC	p.H565N
Pat_30	Pre-Treatment	ZNF835	90485	37	19	57175969	57175969	Missense_Mutation	SNP	C	T	3	30	c.664G>A	c.(664-666)GGC>AGC	p.G222S
Pat_30	Pre-Treatment	ZNF497	162968	37	19	58868272	58868272	Missense_Mutation	SNP	G	A	3	34	c.730C>T	c.(730-732)CGG>TGG	p.R244W
Pat_30	Pre-Treatment	ALK	238	37	2	29497997	29497997	Missense_Mutation	SNP	G	A	23	81	c.2009C>T	c.(2008-2010)TCA>TTA	p.S670L
Pat_30	Pre-Treatment	KLRAQ1	129285	37	2	48718182	48718182	Missense_Mutation	SNP	T	C	143	392	c.1472T>C	c.(1471-1473)TTG>TCG	p.L491S
Pat_30	Pre-Treatment	ACTG2	72	37	2	74140617	74140617	Missense_Mutation	SNP	G	A	6	182	c.457G>A	c.(457-459)GTC>ATC	p.V153I
Pat_30	Pre-Treatment	SMYD1	150572	37	2	88409967	88409967	Missense_Mutation	SNP	C	T	20	55	c.1409C>T	c.(1408-1410)CCC>CTC	p.P470L
Pat_30	Pre-Treatment	MERTK	10461	37	2	112686894	112686894	Missense_Mutation	SNP	G	A	21	113	c.259G>A	c.(259-261)GAA>AAA	p.E87K
Pat_30	Pre-Treatment	ZC3H8	84524	37	2	112994195	112994195	Missense_Mutation	SNP	C	A	4	81	c.448G>T	c.(448-450)GGC>TGC	p.G150C
Pat_30	Pre-Treatment	PAX8	7849	37	2	114004371	114004371	Missense_Mutation	SNP	G	A	6	304	c.151C>T	c.(151-153)CTC>TTC	p.L51F
Pat_30	Pre-Treatment	SCTR	6344	37	2	120206299	120206299	Nonsense_Mutation	SNP	G	A	16	65	c.979C>T	c.(979-981)CAA>TAA	p.Q327*
Pat_30	Pre-Treatment	NCKAP5	344148	37	2	133541973	133541973	Missense_Mutation	SNP	G	A	79	341	c.2411C>T	c.(2410-2412)CCT>CTT	p.P804L
Pat_30	Pre-Treatment	CXCR4	7852	37	2	136873142	136873142	Missense_Mutation	SNP	T	C	5	236	c.356A>G	c.(355-357)AAC>AGC	p.N119S
Pat_30	Pre-Treatment	MBD5	55777	37	2	149227938	149227938	Missense_Mutation	SNP	C	T	84	247	c.2426C>T	c.(2425-2427)CCC>CTC	p.P809L
Pat_30	Pre-Treatment	NEB	4703	37	2	152534238	152534238	Nonsense_Mutation	SNP	C	T	34	743	c.3615G>A	c.(3613-3615)TGG>TGA	p.W1205*
Pat_30	Pre-Treatment	TANK	10010	37	2	162088049	162088049	Missense_Mutation	SNP	G	A	4	133	c.1088G>A	c.(1087-1089)CGA>CAA	p.R363Q
Pat_30	Pre-Treatment	TTN	7273	37	2	179432554	179432554	Missense_Mutation	SNP	C	T	77	313	c.70601G>A	c.(70600-70602)AGA>AAA	p.R23534K
Pat_30	Pre-Treatment	TTN	7273	37	2	179449452	179449452	Missense_Mutation	SNP	C	T	183	526	c.57212G>A	c.(57211-57213)CGA>CAA	p.R19071Q
Pat_30	Pre-Treatment	TTN	7273	37	2	179598097	179598097	Missense_Mutation	SNP	C	T	9	54	c.12191G>A	c.(12190-12192)CGA>CAA	p.R4064Q
Pat_30	Pre-Treatment	DNAH7	56171	37	2	196619064	196619064	Missense_Mutation	SNP	C	T	39	220	c.11761G>A	c.(11761-11763)GAT>AAT	p.D3921N
Pat_30	Pre-Treatment	C2orf57	165100	37	2	232458410	232458410	Missense_Mutation	SNP	C	A	116	370	c.748C>A	c.(748-750)CAC>AAC	p.H250N
Pat_30	Pre-Treatment	GAL3ST2	64090	37	2	242738570	242738570	Splice_Site	SNP	G	A	33	202	c.119_splice	c.e2+1	p.P40_splice
Pat_30	Pre-Treatment	GPCPD1	56261	37	20	5559220	5559220	Missense_Mutation	SNP	C	T	4	83	c.511G>A	c.(511-513)GAT>AAT	p.D171N
Pat_30	Pre-Treatment	LRRN4	164312	37	20	6022614	6022614	Missense_Mutation	SNP	C	T	4	118	c.1277G>A	c.(1276-1278)CGG>CAG	p.R426Q
Pat_30	Pre-Treatment	C20orf12	55184	37	20	18445978	18445978	Missense_Mutation	SNP	G	A	18	72	c.25C>T	c.(25-27)CCT>TCT	p.P9S
Pat_30	Pre-Treatment	NCOA6	23054	37	20	33330509	33330509	Missense_Mutation	SNP	G	A	4	143	c.3551C>T	c.(3550-3552)CCC>CTC	p.P1184L
Pat_30	Pre-Treatment	APCDD1L	164284	37	20	57036037	57036037	Missense_Mutation	SNP	C	T	52	170	c.1315G>A	c.(1315-1317)GAT>AAT	p.D439N
Pat_30	Pre-Treatment	GNAS	2778	37	20	57428528	57428528	Missense_Mutation	SNP	C	T	3	34	c.208C>T	c.(208-210)CCC>TCC	p.P70S
Pat_30	Pre-Treatment	TCEA2	6919	37	20	62698274	62698274	Nonsense_Mutation	SNP	C	T	4	150	c.142C>T	c.(142-144)CGA>TGA	p.R48*
Pat_30	Pre-Treatment	TPTE	7179	37	21	10941907	10941907	Splice_Site	SNP	C	T	54	624	c.795_splice	c.e14+1	p.K265_splice
Pat_30	Pre-Treatment	LIPI	149998	37	21	15558293	15558293	Missense_Mutation	SNP	C	T	32	154	c.593G>A	c.(592-594)GGA>GAA	p.G198E
Pat_30	Pre-Treatment	DYRK1A	1859	37	21	38884451	38884451	Missense_Mutation	SNP	A	G	23	148	c.1909A>G	c.(1909-1911)ACG>GCG	p.T637A
Pat_30	Pre-Treatment	DSCAM	1826	37	21	41385217	41385217	Missense_Mutation	SNP	C	T	27	59	c.5783G>A	c.(5782-5784)TGC>TAC	p.C1928Y
Pat_30	Pre-Treatment	SGSM1	129049	37	22	25251579	25251579	Missense_Mutation	SNP	G	A	4	119	c.733G>A	c.(733-735)GTG>ATG	p.V245M

Pat_30	Pre-Treatment	TFIP11	24144	37	22	26888059	26888059	Missense_Mutation	SNP	C	T	4	45	c.2434G>A	c.(2434-2436)GAC>AAC	p.D812N
Pat_30	Pre-Treatment	SFI1	9814	37	22	31976306	31976306	Nonsense_Mutation	SNP	C	T	50	93	c.1204C>T	c.(1204-1206)CAG>TAG	p.Q402*
Pat_30	Pre-Treatment	EP300	2033	37	22	41553205	41553205	Missense_Mutation	SNP	T	A	16	62	c.3294T>A	c.(3292-3294)GAT>GAA	p.D1098E
Pat_30	Pre-Treatment	PMM1	5372	37	22	41985784	41985784	Missense_Mutation	SNP	C	T	3	46	c.26G>A	c.(25-27)CGC>CAC	p.R9H
Pat_30	Pre-Treatment	TTLL12	23170	37	22	43564905	43564905	Missense_Mutation	SNP	C	T	4	46	c.1658G>A	c.(1657-1659)CGG>CAG	p.R553Q
Pat_30	Pre-Treatment	SAPS2	9701	37	22	50873444	50873444	Missense_Mutation	SNP	G	A	4	141	c.1450G>A	c.(1450-1452)GCC>ACC	p.A484T
Pat_30	Pre-Treatment	BHLHE40	8553	37	3	5025363	5025363	Missense_Mutation	SNP	G	A	55	177	c.1225G>A	c.(1225-1227)GAA>AAA	p.E409K
Pat_30	Pre-Treatment	GRIP2	80852	37	3	14545082	14545082	Missense_Mutation	SNP	C	T	8	38	c.2965G>A	c.(2965-2967)GAA>AAA	p.E989K
Pat_30	Pre-Treatment	TBC1D5	9779	37	3	17202637	17202637	Nonsense_Mutation	SNP	G	A	5	38	c.2206C>T	c.(2206-2208)CAG>TAG	p.Q736*
Pat_30	Pre-Treatment	BSN	8927	37	3	49690215	49690215	Missense_Mutation	SNP	C	T	4	86	c.3226C>T	c.(3226-3228)CGG>TGG	p.R1076W
Pat_30	Pre-Treatment	ZNF717	100131827	37	3	75790797	75790797	Missense_Mutation	SNP	C	T	4	24	c.148G>A	c.(148-150)GTG>ATG	p.V50M
Pat_30	Pre-Treatment	TOMM70A	9868	37	3	100119757	100119757	Missense_Mutation	SNP	C	T	3	15	c.37G>A	c.(37-39)GCA>ACA	p.A13T
Pat_30	Pre-Treatment	GRAMD1C	54762	37	3	113634601	113634601	Missense_Mutation	SNP	C	T	15	137	c.1006C>T	c.(1006-1008)CAT>TAT	p.H336Y
Pat_30	Pre-Treatment	SLC15A2	6565	37	3	121647961	121647961	Missense_Mutation	SNP	C	T	175	526	c.1474C>T	c.(1474-1476)CGT>TGT	p.R492C
Pat_30	Pre-Treatment	DZIP1L	199221	37	3	137786382	137786382	Missense_Mutation	SNP	G	T	4	151	c.1993C>A	c.(1993-1995)CAG>AAG	p.Q665K
Pat_30	Pre-Treatment	CPA3	1359	37	3	148600313	148600313	Missense_Mutation	SNP	C	T	9	111	c.709C>T	c.(709-711)CGT>TGT	p.R237C
Pat_30	Pre-Treatment	BCHE	590	37	3	165491217	165491217	Nonsense_Mutation	SNP	G	A	10	81	c.1762C>T	c.(1762-1764)CAA>TAA	p.Q588*
Pat_30	Pre-Treatment	EPHB3	2049	37	3	184298516	184298516	Splice_Site	SNP	G	A	10	95	c.2389_splice	c.e13-1	p.G797_splice
Pat_30	Pre-Treatment	MUC4	4585	37	3	195505774	195505774	Missense_Mutation	SNP	G	T	3	36	c.12293C>A	c.(12292-12294)CCT>CAT	p.P4098H
Pat_30	Pre-Treatment	PCYT1A	5130	37	3	195968904	195968904	Missense_Mutation	SNP	C	T	6	372	c.623G>A	c.(622-624)CGA>CAA	p.R208Q
Pat_30	Pre-Treatment	FAM53A	152877	37	4	1643193	1643193	Missense_Mutation	SNP	C	T	17	86	c.1024G>A	c.(1024-1026)GGC>AGC	p.G342S
Pat_30	Pre-Treatment	HTT	3064	37	4	3240588	3240588	Missense_Mutation	SNP	G	A	4	110	c.9104G>A	c.(9103-9105)CGG>CAG	p.R3035Q
Pat_30	Pre-Treatment	KCTD8	386617	37	4	44450237	44450237	Missense_Mutation	SNP	C	G	4	46	c.304G>C	c.(304-306)GAC>CAC	p.D102H
Pat_30	Pre-Treatment	TECRL	253017	37	4	65194260	65194260	Missense_Mutation	SNP	G	A	28	191	c.301C>T	c.(301-303)CCT>TCT	p.P101S
Pat_30	Pre-Treatment	PROL1	58503	37	4	71275623	71275623	Missense_Mutation	SNP	C	T	105	385	c.578C>T	c.(577-579)TCA>TTA	p.S193L
Pat_30	Pre-Treatment	GC	2638	37	4	72620723	72620723	Missense_Mutation	SNP	T	G	49	144	c.1136A>C	c.(1135-1137)GAA>GCA	p.E379A
Pat_30	Pre-Treatment	MYOZ2	51778	37	4	120107315	120107315	Missense_Mutation	SNP	C	T	23	116	c.755C>T	c.(754-756)CCT>CTT	p.P252L
Pat_30	Pre-Treatment	KIAA1109	84162	37	4	123280759	123280759	Missense_Mutation	SNP	C	T	54	144	c.14683C>T	c.(14683-14685)CCA>TCA	p.P4895S
Pat_30	Pre-Treatment	FAT4	79633	37	4	126336743	126336743	Missense_Mutation	SNP	G	A	75	236	c.6625G>A	c.(6625-6627)GGT>AGT	p.G2209S
Pat_30	Pre-Treatment	RWDD4A	201965	37	4	184567673	184567673	Missense_Mutation	SNP	G	A	58	221	c.499C>T	c.(499-501)CCT>TCT	p.P167S
Pat_30	Pre-Treatment	SPEF2	79925	37	5	35740060	35740060	Missense_Mutation	SNP	G	A	24	71	c.3103G>A	c.(3103-3105)GAA>AAA	p.E1035K
Pat_30	Pre-Treatment	C5orf42	65250	37	5	37169569	37169569	Missense_Mutation	SNP	G	A	4	123	c.6557C>T	c.(6556-6558)TCG>TTG	p.S2186L
Pat_30	Pre-Treatment	ITGA1	3672	37	5	52243281	52243281	Missense_Mutation	SNP	C	G	7	228	c.3485C>G	c.(3484-3486)GCA>GGA	p.A1162G
Pat_30	Pre-Treatment	CRHBP	1393	37	5	76251629	76251629	Missense_Mutation	SNP	G	A	4	145	c.485G>A	c.(484-486)CGA>CAA	p.R162Q
Pat_30	Pre-Treatment	GPR98	84059	37	5	89933639	89933639	Missense_Mutation	SNP	A	C	13	63	c.2114A>C	c.(2113-2115)GAT>GCT	p.D705A
Pat_30	Pre-Treatment	EPB41L4A	64097	37	5	111600635	111600635	Missense_Mutation	SNP	T	G	38	175	c.512A>C	c.(511-513)GAA>GCA	p.E171A
Pat_30	Pre-Treatment	PCDHB15	56121	37	5	140627305	140627305	Missense_Mutation	SNP	C	T	138	332	c.2159C>T	c.(2158-2160)GCC>GTC	p.A720V
Pat_30	Pre-Treatment	PCDHGB1	56104	37	5	140730012	140730012	Missense_Mutation	SNP	G	A	4	110	c.185G>A	c.(184-186)CGA>CAA	p.R62Q
Pat_30	Pre-Treatment	PPARGC1B	133522	37	5	149225376	149225376	Missense_Mutation	SNP	C	T	4	120	c.2870C>T	c.(2869-2871)TCT>TTT	p.S957F
Pat_30	Pre-Treatment	RARS	5917	37	5	167920965	167920965	Missense_Mutation	SNP	C	T	4	152	c.436C>T	c.(436-438)CCA>TCA	p.P146S
Pat_30	Pre-Treatment	BTNL3	10917	37	5	180419834	180419834	Missense_Mutation	SNP	C	T	4	134	c.71C>T	c.(70-72)CCG>CTG	p.P24L
Pat_30	Pre-Treatment	PHACTR1	221692	37	6	13206149	13206149	Missense_Mutation	SNP	T	G	5	325	c.767T>G	c.(766-768)CTC>CGC	p.L256R
Pat_30	Pre-Treatment	ATXN1	6310	37	6	16326801	16326801	Nonsense_Mutation	SNP	G	A	52	154	c.1741C>T	c.(1741-1743)CAG>TAG	p.Q581*
Pat_30	Pre-Treatment	ATXN1	6310	37	6	16327882	16327882	Missense_Mutation	SNP	C	A	3	45	c.660G>T	c.(658-660)CAG>CAT	p.Q220H
Pat_30	Pre-Treatment	ATXN1	6310	37	6	16327888	16327888	Missense_Mutation	SNP	C	A	3	45	c.654G>T	c.(652-654)CAG>CAT	p.Q218H
Pat_30	Pre-Treatment	CAP2	10486	37	6	17507881	17507881	Missense_Mutation	SNP	C	T	58	140	c.454C>T	c.(454-456)CCT>TCT	p.P152S
Pat_30	Pre-Treatment	OR2B6	26212	37	6	27925296	27925296	Missense_Mutation	SNP	G	A	35	106	c.278G>A	c.(277-279)AGT>AAT	p.S93N

Pat_30	Pre-Treatment	DHX16	8449	37	6	30632583	30632583	Nonsense_Mutation	SNP	C	A	26	100	c.1312G>T	c.(1312-1314)GAG>TAG	p.E438*
Pat_30	Pre-Treatment	MICB	4277	37	6	31473433	31473433	Missense_Mutation	SNP	A	G	6	303	c.110A>G	c.(109-111)CAG>CGG	p.Q37R
Pat_30	Pre-Treatment	TAP2	6891	37	6	32781530	32781530	Missense_Mutation	SNP	C	T	4	22	c.2545G>A	c.(2545-2547)GGA>AGA	p.G849R
Pat_30	Pre-Treatment	SPDEF	25803	37	6	34512187	34512187	Missense_Mutation	SNP	G	T	27	76	c.46C>A	c.(46-48)CTC>ATC	p.L16I
Pat_30	Pre-Treatment	PNPLA1	285848	37	6	36270156	36270156	Missense_Mutation	SNP	G	T	70	259	c.1294G>T	c.(1294-1296)GTG>TTG	p.V432L
Pat_30	Pre-Treatment	GLO1	2739	37	6	38650584	38650584	Missense_Mutation	SNP	C	T	4	139	c.376G>A	c.(376-378)GGT>AGT	p.G126S
Pat_30	Pre-Treatment	TREML4	285852	37	6	41204319	41204319	Nonstop_Mutation	SNP	G	T	3	34	c.602G>T	c.(601-603)TGA>TTA	p.*201L
Pat_30	Pre-Treatment	FAM83B	222584	37	6	54805310	54805310	Missense_Mutation	SNP	C	T	47	131	c.1541C>T	c.(1540-1542)TCA>TTA	p.S514L
Pat_30	Pre-Treatment	EYS	346007	37	6	66204897	66204897	Missense_Mutation	SNP	A	G	8	154	c.407T>C	c.(406-408)GTT>GCT	p.V136A
Pat_30	Pre-Treatment	KIAA0776	23376	37	6	97000377	97000377	Nonsense_Mutation	SNP	C	T	4	154	c.2005C>T	c.(2005-2007)CGA>TGA	p.R669*
Pat_30	Pre-Treatment	GOPC	57120	37	6	117642387	117642387	Missense_Mutation	SNP	C	T	64	313	c.748G>A	c.(748-750)GGC>AGC	p.G250S
Pat_30	Pre-Treatment	THSD7A	221981	37	7	11521537	11521537	Missense_Mutation	SNP	G	A	5	242	c.1895C>T	c.(1894-1896)CCG>CTG	p.P632L
Pat_30	Pre-Treatment	SNX13	23161	37	7	17908074	17908074	Nonsense_Mutation	SNP	G	A	17	49	c.793C>T	c.(793-795)CAA>TAA	p.Q265*
Pat_30	Pre-Treatment	ANLN	54443	37	7	36438918	36438918	Missense_Mutation	SNP	G	A	17	121	c.403G>A	c.(403-405)GAA>AAA	p.E135K
Pat_30	Pre-Treatment	ABCA13	154664	37	7	48280486	48280486	Missense_Mutation	SNP	G	A	38	117	c.1085G>A	c.(1084-1086)GGT>GAT	p.G362D
Pat_30	Pre-Treatment	HSPB1	3315	37	7	75933173	75933173	Missense_Mutation	SNP	G	A	58	337	c.419G>A	c.(418-420)CGG>CAG	p.R140Q
Pat_30	Pre-Treatment	CCDC146	57639	37	7	76908289	76908289	Missense_Mutation	SNP	G	A	25	47	c.1565G>A	c.(1564-1566)CGA>CAA	p.R522Q
Pat_30	Pre-Treatment	MTERF	7978	37	7	91503509	91503509	Missense_Mutation	SNP	G	A	5	269	c.599C>T	c.(598-600)GCC>GTC	p.A200V
Pat_30	Pre-Treatment	FBXL13	222235	37	7	102665589	102665589	Missense_Mutation	SNP	C	T	27	41	c.416G>A	c.(415-417)CGA>CAA	p.R139Q
Pat_30	Pre-Treatment	LAMB4	22798	37	7	107710246	107710246	Missense_Mutation	SNP	C	T	160	291	c.2209G>A	c.(2209-2211)GAA>AAA	p.E737K
Pat_30	Pre-Treatment	UBN2	254048	37	7	138968475	138968476	Missense_Mutation	DNP	CC	TT	40	252	.2824_2825CC>T	c.(2824-2826)CCA>TTA	p.P942L
Pat_30	Pre-Treatment	BRAF	673	37	7	140453136	140453136	Missense_Mutation	SNP	A	T	61	132	c.1799T>A	c.(1798-1800)GTG>GAG	p.V600E
Pat_30	Pre-Treatment	FAM131B	9715	37	7	143056833	143056833	Missense_Mutation	SNP	C	T	3	19	c.82G>A	c.(82-84)GGC>AGC	p.G28S
Pat_30	Pre-Treatment	MYOM2	9172	37	8	2017410	2017410	Missense_Mutation	SNP	G	A	30	177	c.667G>A	c.(667-669)GAC>AAC	p.D223N
Pat_30	Pre-Treatment	SNTG1	54212	37	8	51569530	51569530	Missense_Mutation	SNP	C	T	70	310	c.911C>T	c.(910-912)TCC>TTC	p.S304F
Pat_30	Pre-Treatment	SNX31	169166	37	8	101612642	101612642	Missense_Mutation	SNP	C	T	46	276	c.709G>A	c.(709-711)GCC>ACC	p.A237T
Pat_30	Pre-Treatment	LRP12	29967	37	8	105509486	105509486	Missense_Mutation	SNP	G	A	45	193	c.1294C>T	c.(1294-1296)CGC>TGC	p.R432C
Pat_30	Pre-Treatment	KCNV1	27012	37	8	110984516	110984516	Missense_Mutation	SNP	C	T	7	147	c.962G>A	c.(961-963)CGC>CAC	p.R321H
Pat_30	Pre-Treatment	ASAP1	50807	37	8	131138295	131138295	Missense_Mutation	SNP	A	C	47	134	c.1422T>G	c.(1420-1422)TGT>TGG	p.C474W
Pat_30	Pre-Treatment	ARC	23237	37	8	143694456	143694456	Missense_Mutation	SNP	T	C	5	29	c.1177A>G	c.(1177-1179)ACC>GCC	p.T393A
Pat_30	Pre-Treatment	ZNF251	90987	37	8	145947109	145947109	Missense_Mutation	SNP	C	T	23	80	c.1936G>A	c.(1936-1938)GGA>AGA	p.G646R
Pat_30	Pre-Treatment	JAK2	3717	37	9	5090739	5090739	Missense_Mutation	SNP	G	A	14	198	c.2887G>A	c.(2887-2889)GGT>AGT	p.G963S
Pat_30	Pre-Treatment	DMRTA1	63951	37	9	22447096	22447096	Missense_Mutation	SNP	G	A	12	44	c.32G>A	c.(31-33)CGA>CAA	p.R11Q
Pat_30	Pre-Treatment	SPINK4	27290	37	9	33246696	33246696	Missense_Mutation	SNP	C	T	5	273	c.185C>T	c.(184-186)ACG>ATG	p.T62M
Pat_30	Pre-Treatment	UBAP1	51271	37	9	34251508	34251508	Missense_Mutation	SNP	T	A	24	69	c.1487T>A	c.(1486-1488)ATG>AAG	p.M496K
Pat_30	Pre-Treatment	NPR2	4882	37	9	35792463	35792463	Missense_Mutation	SNP	C	T	11	75	c.58C>T	c.(58-60)CCC>TCC	p.P20S
Pat_30	Pre-Treatment	CNTNAP3	79937	37	9	39133108	39133108	Missense_Mutation	SNP	T	C	3	28	c.1901A>G	c.(1900-1902)CAG>CGG	p.Q634R
Pat_30	Pre-Treatment	FAM22F	54754	37	9	97082793	97082793	Missense_Mutation	SNP	C	G	4	72	c.1065G>C	c.(1063-1065)AAG>AAC	p.K355N
Pat_30	Pre-Treatment	COL15A1	1306	37	9	101806853	101806853	Missense_Mutation	SNP	G	A	13	150	c.2578G>A	c.(2578-2580)GAG>AAG	p.E860K
Pat_30	Pre-Treatment	ACTL7A	10881	37	9	111625872	111625872	Missense_Mutation	SNP	G	A	16	145	c.1270G>A	c.(1270-1272)GAA>AAA	p.E424K
Pat_30	Pre-Treatment	CEP110	11064	37	9	123900931	123900931	Missense_Mutation	SNP	C	T	4	138	c.2311C>T	c.(2311-2313)CTC>TTC	p.L771F
Pat_30	Pre-Treatment	DENND1A	57706	37	9	126214617	126214617	Missense_Mutation	SNP	C	T	32	106	c.1237G>A	c.(1237-1239)GGA>AGA	p.G413R
Pat_30	Pre-Treatment	PPAPDC3	84814	37	9	134165759	134165759	Nonsense_Mutation	SNP	G	A	46	302	c.375G>A	c.(373-375)TGG>TGA	p.W125*
Pat_30	Pre-Treatment	CACNA1B	774	37	9	140948459	140948459	Splice_Site	SNP	G	A	4	144	c.3968_splice	c.e26+1	p.R1323_splice
Pat_30	Pre-Treatment	ARSH	347527	37	X	2933194	2933194	Missense_Mutation	SNP	C	T	4	41	c.524C>T	c.(523-525)GCC>GTC	p.A175V
Pat_30	Pre-Treatment	CLCN4	1183	37	X	10176514	10176514	Missense_Mutation	SNP	C	T	195	570	c.1273C>T	c.(1273-1275)CCT>TCT	p.P425S
Pat_30	Pre-Treatment	ZRSR2	8233	37	X	15833978	15833978	Missense_Mutation	SNP	G	A	5	211	c.736G>A	c.(736-738)GAG>AAG	p.E246K

Pat_30	Pre-Treatment	SYAP1	94056	37	X	16761957	16761957	Missense_Mutation	SNP	C	T	172	536	c.569C>T	c.(568-570)CCT>CTT	p.P190L
Pat_30	Pre-Treatment	ZFX	7543	37	X	24229378	24229378	Missense_Mutation	SNP	C	T	130	353	c.2303C>T	c.(2302-2304)TCC>TTC	p.S768F
Pat_30	Pre-Treatment	CXorf59	286464	37	X	36162735	36162735	Missense_Mutation	SNP	G	A	34	251	c.1318G>A	c.(1318-1320)GAA>AAA	p.E440K
Pat_30	Pre-Treatment	CXorf36	79742	37	X	45011019	45011020	Missense_Mutation	DNP	GG	AA	18	109	.1179_1180CC>T	177-1182)ATCCGC>ATTT	p.R394C
Pat_30	Pre-Treatment	CHST7	56548	37	X	46433721	46433721	Missense_Mutation	SNP	G	A	23	110	c.355G>A	c.(355-357)GAA>AAA	p.E119K
Pat_30	Pre-Treatment	RBM10	8241	37	X	47030582	47030582	Missense_Mutation	SNP	G	T	4	95	c.357G>T	c.(355-357)GAG>GAT	p.E119D
Pat_30	Pre-Treatment	CCNB3	85417	37	X	50053780	50053780	Missense_Mutation	SNP	G	A	17	42	c.2611G>A	c.(2611-2613)GAG>AAG	p.E871K
Pat_30	Pre-Treatment	FGD1	2245	37	X	54481894	54481894	Missense_Mutation	SNP	C	T	4	73	c.2002G>A	c.(2002-2004)GAG>AAG	p.E668K
Pat_30	Pre-Treatment	STARD8	9754	37	X	67938434	67938434	Missense_Mutation	SNP	G	A	20	54	c.1438G>A	c.(1438-1440)GAT>AAT	p.D480N
Pat_30	Pre-Treatment	NXF5	55998	37	X	101096941	101096941	Missense_Mutation	SNP	G	A	27	376	c.56C>T	c.(55-57)CCT>CTT	p.P19L
Pat_30	Pre-Treatment	ARMCX5	64860	37	X	101857632	101857632	Missense_Mutation	SNP	C	T	33	135	c.563C>T	c.(562-564)CCT>CTT	p.P188L
Pat_30	Pre-Treatment	HCFC1	3054	37	X	153225613	153225613	Splice_Site	SNP	C	T	7	19	c.1085_splice	c.e8-1	p.E362_splice
Pat_30	Post-Resistance	PQLC2	54896	37	1	19651990	19651990	Missense_Mutation	SNP	C	T	50	59	c.296C>T	c.(295-297)ACC>ATC	p.T99I
Pat_30	Post-Resistance	ZMYM1	79830	37	1	35579236	35579236	Missense_Mutation	SNP	T	A	6	8	c.1805T>A	c.(1804-1806)TTT>TAT	p.F602Y
Pat_30	Post-Resistance	DAB1	1600	37	1	57491658	57491658	Missense_Mutation	SNP	G	A	58	95	c.782C>T	c.(781-783)CCC>CTC	p.P261L
Pat_30	Post-Resistance	PGM1	5236	37	1	64117438	64117438	Missense_Mutation	SNP	C	T	20	15	c.1379C>T	c.(1378-1380)TCA>TTA	p.S460L
Pat_30	Post-Resistance	CLCA4	22802	37	1	87025658	87025658	Missense_Mutation	SNP	A	G	35	25	c.203A>G	c.(202-204)GAA>GGA	p.E68G
Pat_30	Post-Resistance	ITGA10	8515	37	1	145532599	145532599	Missense_Mutation	SNP	G	A	51	238	c.1052G>A	c.(1051-1053)GGA>GAA	p.G351E
Pat_30	Post-Resistance	GPATCH4	54865	37	1	156565292	156565293	Missense_Mutation	DNP	CC	TT	33	166	c.840_841GG>AA	38-843)GGGGAA>GGAA	p.E281K
Pat_30	Post-Resistance	C1orf92	149499	37	1	156902735	156902735	Missense_Mutation	SNP	G	A	6	8	c.1654G>A	c.(1654-1656)GAT>AAT	p.D552N
Pat_30	Post-Resistance	OR10K1	391109	37	1	158435715	158435715	Missense_Mutation	SNP	C	T	149	67	c.364C>T	c.(364-366)CGC>TGC	p.R122C
Pat_30	Post-Resistance	SELE	6401	37	1	169698706	169698706	Missense_Mutation	SNP	C	T	10	67	c.824G>A	c.(823-825)GGA>GAA	p.G275E
Pat_30	Post-Resistance	HMCN1	83872	37	1	185878628	185878628	Missense_Mutation	SNP	C	T	25	84	c.781C>T	c.(781-783)CGC>TGC	p.R261C
Pat_30	Post-Resistance	F13B	2165	37	1	197026515	197026515	Missense_Mutation	SNP	C	T	65	38	c.886G>A	c.(886-888)GAA>AAA	p.E296K
Pat_30	Post-Resistance	RHOU	58480	37	1	228879120	228879120	Missense_Mutation	SNP	A	G	76	47	c.410A>G	c.(409-411)CAG>CGG	p.Q137R
Pat_30	Post-Resistance	EDARADD	128178	37	1	236631574	236631574	Missense_Mutation	SNP	C	T	14	45	c.263C>T	c.(262-264)CCA>CTA	p.P88L
Pat_30	Post-Resistance	ZNF695	57116	37	1	247163314	247163314	Missense_Mutation	SNP	G	T	48	109	c.66C>A	c.(64-66)GAC>GAA	p.D22E
Pat_30	Post-Resistance	ZNF496	84838	37	1	247492847	247492847	Missense_Mutation	SNP	G	A	22	74	c.34C>T	c.(34-36)CCG>TCG	p.P12S
Pat_30	Post-Resistance	IL15RA	3601	37	10	6008146	6008146	Missense_Mutation	SNP	T	A	37	10	c.245A>T	c.(244-246)AAT>ATT	p.N82I
Pat_30	Post-Resistance	ANKRD26	22852	37	10	27366301	27366301	Missense_Mutation	SNP	G	A	38	24	c.1043C>T	c.(1042-1044)TCC>TTC	p.S348F
Pat_30	Post-Resistance	HERC4	26091	37	10	69750933	69750933	Missense_Mutation	SNP	G	A	2	2	c.1295C>T	c.(1294-1296)TCC>TTC	p.S432F
Pat_30	Post-Resistance	PBLD	64081	37	10	70048273	70048273	Missense_Mutation	SNP	G	A	25	7	c.658C>T	c.(658-660)CCG>TCG	p.P220S
Pat_30	Post-Resistance	PLCE1	51196	37	10	96028758	96028758	Missense_Mutation	SNP	C	T	47	16	c.4354C>T	c.(4354-4356)CAT>TAT	p.H1452Y
Pat_30	Post-Resistance	CYP2C8	1558	37	10	96824642	96824642	Missense_Mutation	SNP	C	T	45	21	c.557G>A	c.(556-558)CGA>CAA	p.R186Q
Pat_30	Post-Resistance	LOC729020	729020	37	10	105005926	105005926	Missense_Mutation	SNP	G	A	18	235	c.173G>A	c.(172-174)CGA>CAA	p.R58Q
Pat_30	Post-Resistance	MUC2	4583	37	11	1092947	1092947	Missense_Mutation	SNP	C	T	2	0	c.11852C>T	c.(11851-11853)ACC>ATC	p.T3951I
Pat_30	Post-Resistance	OR51S1	119692	37	11	4870243	4870243	Missense_Mutation	SNP	G	A	27	73	c.196C>T	c.(196-198)CCA>TCA	p.P66S
Pat_30	Post-Resistance	OR51B6	390058	37	11	5373230	5373230	Missense_Mutation	SNP	C	T	78	61	c.493C>T	c.(493-495)CCC>TCC	p.P165S
Pat_30	Post-Resistance	BDNF	627	37	11	27679778	27679778	Missense_Mutation	SNP	C	T	9	21	c.334G>A	c.(334-336)GAA>AAA	p.E112K
Pat_30	Post-Resistance	TTC17	55761	37	11	43515441	43515441	Missense_Mutation	SNP	G	A	149	295	c.3413G>A	c.(3412-3414)CGG>CAG	p.R1138Q
Pat_30	Post-Resistance	OR8H2	390151	37	11	55872803	55872804	Missense_Mutation	DNP	GG	AA	163	333	c.285_286GG>AA	283-288)ACGGGC>ACAA	p.G96S
Pat_30	Post-Resistance	NPAS4	266743	37	11	66192136	66192136	Missense_Mutation	SNP	C	T	29	42	c.1775C>T	c.(1774-1776)GCC>GTC	p.A592V
Pat_30	Post-Resistance	MYO7A	4647	37	11	76893123	76893123	Missense_Mutation	SNP	G	A	65	161	c.3031G>A	c.(3031-3033)GGG>AGG	p.G1011R
Pat_30	Post-Resistance	NNMT	4837	37	11	114182916	114182916	Missense_Mutation	SNP	C	T	41	73	c.512C>T	c.(511-513)CCA>CTA	p.P171L
Pat_30	Post-Resistance	OR10G8	219869	37	11	123901051	123901051	Missense_Mutation	SNP	C	T	20	24	c.722C>T	c.(721-723)GCC>GTC	p.A241V
Pat_30	Post-Resistance	PRB2	653247	37	12	11546795	11546795	Missense_Mutation	SNP	G	A	9	86	c.217C>T	c.(217-219)CCT>TCT	p.P73S
Pat_30	Post-Resistance	ALG10B	144245	37	12	38714749	38714749	Missense_Mutation	SNP	G	A	21	33	c.1156G>A	c.(1156-1158)GAC>AAC	p.D386N

Pat_30	Post-Resistance	ABCD2	225	37	12	40001403	40001403	Nonsense_Mutation	SNP	C	A	9	24	c.1234G>T	c.(1234-1236)GAG>TAG	p.E412*
Pat_30	Post-Resistance	ANKRD33	341405	37	12	52283221	52283221	Nonsense_Mutation	SNP	C	T	46	51	c.187C>T	c.(187-189)CAG>TAG	p.Q63*
Pat_30	Post-Resistance	KRT7	3855	37	12	52635286	52635286	Missense_Mutation	SNP	G	A	67	86	c.724G>A	c.(724-726)GAC>AAC	p.D242N
Pat_30	Post-Resistance	OR6C68	403284	37	12	55886390	55886390	Missense_Mutation	SNP	C	T	16	31	c.244C>T	c.(244-246)CCA>TCA	p.P82S
Pat_30	Post-Resistance	DNAJC14	85406	37	12	56216235	56216235	Missense_Mutation	SNP	C	T	81	79	c.1820G>A	c.(1819-1821)GGT>GAT	p.G607D
Pat_30	Post-Resistance	GRIP1	23426	37	12	66765581	66765581	Missense_Mutation	SNP	G	A	91	128	c.2749C>T	c.(2749-2751)CGG>TGG	p.R917W
Pat_30	Post-Resistance	MDM1	56890	37	12	68720499	68720499	Missense_Mutation	SNP	C	G	25	27	c.436G>C	c.(436-438)GTT>CTT	p.V146L
Pat_30	Post-Resistance	CIT	11113	37	12	120150494	120150494	Missense_Mutation	SNP	T	G	46	50	c.4460A>C	c.(4459-4461)CAG>CCG	p.Q1487P
Pat_30	Post-Resistance	GLT1D1	144423	37	12	129431969	129431969	Missense_Mutation	SNP	C	G	35	55	c.761C>G	c.(760-762)TCT>TGT	p.S254C
Pat_30	Post-Resistance	FLT1	2321	37	13	29002026	29002026	Missense_Mutation	SNP	G	A	78	93	c.1139C>T	c.(1138-1140)TCT>TTT	p.S380F
Pat_30	Post-Resistance	SLC46A3	283537	37	13	29287375	29287375	Nonsense_Mutation	SNP	G	A	17	37	c.502C>T	c.(502-504)CGA>TGA	p.R168*
Pat_30	Post-Resistance	DOCK9	23348	37	13	99567688	99567688	Missense_Mutation	SNP	C	T	12	32	c.790G>A	c.(790-792)GAC>AAC	p.D264N
Pat_30	Post-Resistance	OR4K14	122740	37	14	20483275	20483275	Missense_Mutation	SNP	A	T	8	9	c.78T>A	c.(76-78)TTT>TTA	p.F26L
Pat_30	Post-Resistance	METT11D1	64745	37	14	21464997	21464997	Missense_Mutation	SNP	T	C	51	86	c.1319T>C	c.(1318-1320)CTT>CCT	p.L440P
Pat_30	Post-Resistance	TPPP2	122664	37	14	21500204	21500204	Missense_Mutation	SNP	G	A	65	123	c.481G>A	c.(481-483)GGT>AGT	p.G161S
Pat_30	Post-Resistance	SMEK1	55671	37	14	91929191	91929191	Missense_Mutation	SNP	T	C	26	29	c.1861A>G	c.(1861-1863)ATT>GTT	p.I621V
Pat_30	Post-Resistance	PPP2R5C	5527	37	14	102229267	102229267	Missense_Mutation	SNP	G	A	5	4	c.53G>A	c.(52-54)GGA>GAA	p.G18E
Pat_30	Post-Resistance	MGA	23269	37	15	42053967	42053967	Nonsense_Mutation	SNP	C	T	8	19	c.7429C>T	c.(7429-7431)CAG>TAG	p.Q2477*
Pat_30	Post-Resistance	ARPP19	10776	37	15	52849310	52849310	Missense_Mutation	SNP	C	T	44	64	c.155G>A	c.(154-156)CGG>CAG	p.R52Q
Pat_30	Post-Resistance	NOX5	79400	37	15	69341381	69341381	Missense_Mutation	SNP	C	T	18	17	c.1982C>T	c.(1981-1983)GCC>GTC	p.A661V
Pat_30	Post-Resistance	WDR93	56964	37	15	90276361	90276361	Missense_Mutation	SNP	G	A	20	33	c.1455G>A	c.(1453-1455)ATG>ATA	p.M485I
Pat_30	Post-Resistance	NLRC3	197358	37	16	3614397	3614397	Missense_Mutation	SNP	C	T	29	34	c.541G>A	c.(541-543)GAT>AAT	p.D181N
Pat_30	Post-Resistance	UMOD	7369	37	16	20360313	20360313	Missense_Mutation	SNP	G	C	2	5	c.310C>G	c.(310-312)CTC>GTC	p.L104V
Pat_30	Post-Resistance	ACSM1	116285	37	16	20636779	20636779	Missense_Mutation	SNP	G	A	41	49	c.1493C>T	c.(1492-1494)GCC>GTC	p.A498V
Pat_30	Post-Resistance	ATXN2L	11273	37	16	28836712	28836712	Missense_Mutation	SNP	C	T	20	33	c.325C>T	c.(325-327)CCA>TCA	p.P109S
Pat_30	Post-Resistance	ADCY7	113	37	16	50344755	50344755	Missense_Mutation	SNP	G	A	7	11	c.2318G>A	c.(2317-2319)GGC>GAC	p.G773D
Pat_30	Post-Resistance	CDH8	1006	37	16	61935302	61935302	Nonsense_Mutation	SNP	G	A	16	25	c.328C>T	c.(328-330)CAA>TAA	p.Q110*
Pat_30	Post-Resistance	ZZEF1	23140	37	17	3920987	3920987	Missense_Mutation	SNP	G	A	41	77	c.7679C>T	c.(7678-7680)TCG>TTG	p.S2560L
Pat_30	Post-Resistance	CXCL16	58191	37	17	4641715	4641715	Missense_Mutation	SNP	G	A	7	19	c.346C>T	c.(346-348)CTT>TTT	p.L116F
Pat_30	Post-Resistance	MYH8	4626	37	17	10296234	10296234	Missense_Mutation	SNP	C	T	18	36	c.5377G>A	c.(5377-5379)GTG>ATG	p.V1793M
Pat_30	Post-Resistance	MYH4	4622	37	17	10359030	10359030	Missense_Mutation	SNP	A	G	12	25	c.2075T>C	c.(2074-2076)CTT>CCT	p.L692P
Pat_30	Post-Resistance	KCNJ12	3768	37	17	21319348	21319348	Missense_Mutation	SNP	C	T	11	86	c.694C>T	c.(694-696)CTC>TTC	p.L232F
Pat_30	Post-Resistance	KSR1	8844	37	17	25932605	25932605	Missense_Mutation	SNP	C	T	5	5	c.1415C>T	c.(1414-1416)CCC>CTC	p.P472L
Pat_30	Post-Resistance	AATF	26574	37	17	35310442	35310442	Missense_Mutation	SNP	G	T	25	35	c.540G>T	c.(538-540)ATG>ATT	p.M180I
Pat_30	Post-Resistance	KRT15	3866	37	17	39674887	39674887	Missense_Mutation	SNP	T	C	107	183	c.193A>G	c.(193-195)AGG>GGG	p.R65G
Pat_30	Post-Resistance	KRT9	3857	37	17	39724810	39724810	Missense_Mutation	SNP	G	A	49	570	c.1120C>T	c.(1120-1122)CGG>TGG	p.R374W
Pat_30	Post-Resistance	SPOP	8405	37	17	47684692	47684692	Nonsense_Mutation	SNP	C	A	39	35	c.757G>T	c.(757-759)GAA>TAA	p.E253*
Pat_30	Post-Resistance	BCAS3	54828	37	17	58979987	58979987	Nonsense_Mutation	SNP	C	T	96	157	c.745C>T	c.(745-747)CGA>TGA	p.R249*
Pat_30	Post-Resistance	CBX2	84733	37	17	77758699	77758699	Missense_Mutation	SNP	C	T	47	91	c.1457C>T	c.(1456-1458)TCC>TTC	p.S486F
Pat_30	Post-Resistance	LAMA1	284217	37	18	6950864	6950865	Missense_Mutation	DNP	GG	AA	31	51	.8313_8314CC>T	311-8316)GGCCGC>GGT	p.R2772C
Pat_30	Post-Resistance	PSMA8	143471	37	18	23713939	23713939	Nonsense_Mutation	SNP	C	T	46	85	c.10C>T	c.(10-12)CGA>TGA	p.R4*
Pat_30	Post-Resistance	DSG1	1828	37	18	28934521	28934521	Missense_Mutation	SNP	G	A	30	57	c.2362G>A	c.(2362-2364)GAA>AAA	p.E788K
Pat_30	Post-Resistance	KIAA1632	57724	37	18	43514816	43514816	Missense_Mutation	SNP	G	A	20	22	c.2216C>T	c.(2215-2217)TCC>TTC	p.S739F
Pat_30	Post-Resistance	DCC	1630	37	18	50592482	50592482	Missense_Mutation	SNP	G	A	30	42	c.1207G>A	c.(1207-1209)GAA>AAA	p.E403K
Pat_30	Post-Resistance	ALPK2	115701	37	18	56165294	56165294	Missense_Mutation	SNP	T	C	55	99	c.6283A>G	c.(6283-6285)ACG>GCG	p.T2095A
Pat_30	Post-Resistance	CDH7	1005	37	18	63489391	63489391	Missense_Mutation	SNP	G	A	24	58	c.700G>A	c.(700-702)GAT>AAT	p.D234N
Pat_30	Post-Resistance	ABCA7	10347	37	19	1058227	1058227	Missense_Mutation	SNP	T	A	42	53	c.5108T>A	c.(5107-5109)ATG>AAG	p.M1703K

Pat_30	Post-Resistance	VAV1	7409	37	19	6820829	6820830	Splice_Site	DNP	GG	AA	29	72	c.321_splice	c.e2+1	p.K107_splice
Pat_30	Post-Resistance	MUC16	94025	37	19	9069841	9069841	Missense_Mutation	SNP	C	T	28	40	c.17605G>A	c.(17605-17607)GGG>AGC	p.G5869R
Pat_30	Post-Resistance	ZNF565	147929	37	19	36674056	36674056	Missense_Mutation	SNP	C	T	27	51	c.812G>A	c.(811-813)AGA>AAA	p.R271K
Pat_30	Post-Resistance	ALK	238	37	2	29497997	29497997	Missense_Mutation	SNP	G	A	10	16	c.2009C>T	c.(2008-2010)TCA>TTA	p.S670L
Pat_30	Post-Resistance	KLRAQ1	129285	37	2	48718182	48718182	Missense_Mutation	SNP	T	C	207	275	c.1472T>C	c.(1471-1473)TTG>TCG	p.L491S
Pat_30	Post-Resistance	CLEC4F	165530	37	2	71046487	71046487	Missense_Mutation	SNP	T	C	43	53	c.268A>G	c.(268-270)AAT>GAT	p.N90D
Pat_30	Post-Resistance	SMYD1	150572	37	2	88409967	88409967	Missense_Mutation	SNP	C	T	21	17	c.1409C>T	c.(1408-1410)CCC>CTC	p.P470L
Pat_30	Post-Resistance	MERTK	10461	37	2	112686894	112686894	Missense_Mutation	SNP	G	A	20	50	c.259G>A	c.(259-261)GAA>AAA	p.E87K
Pat_30	Post-Resistance	WASH2P	375260	37	2	114355129	114355129	Missense_Mutation	SNP	G	A	8	50	c.506G>A	c.(505-507)CGC>CAC	p.R169H
Pat_30	Post-Resistance	SCTR	6344	37	2	120206299	120206299	Nonsense_Mutation	SNP	G	A	4	9	c.979C>T	c.(979-981)CAA>TAA	p.Q327*
Pat_30	Post-Resistance	NCKAP5	344148	37	2	133541973	133541973	Missense_Mutation	SNP	G	A	59	99	c.2411C>T	c.(2410-2412)CCT>CTT	p.P804L
Pat_30	Post-Resistance	MBD5	55777	37	2	149227938	149227938	Missense_Mutation	SNP	C	T	60	87	c.2426C>T	c.(2425-2427)CCC>CTC	p.P809L
Pat_30	Post-Resistance	SCN1A	6323	37	2	166900378	166900378	Missense_Mutation	SNP	C	T	29	38	c.1844G>A	c.(1843-1845)GGA>GAA	p.G615E
Pat_30	Post-Resistance	TTN	7273	37	2	179432554	179432554	Missense_Mutation	SNP	C	T	20	50	c.70601G>A	c.(70600-70602)AGA>AAA	p.R23534K
Pat_30	Post-Resistance	TTN	7273	37	2	179449452	179449452	Missense_Mutation	SNP	C	T	126	221	c.57212G>A	c.(57211-57213)CGA>CAA	p.R19071Q
Pat_30	Post-Resistance	TTN	7273	37	2	179598097	179598097	Missense_Mutation	SNP	C	T	5	13	c.12191G>A	c.(12190-12192)CGA>CAA	p.R4064Q
Pat_30	Post-Resistance	DNAH7	56171	37	2	196619064	196619064	Missense_Mutation	SNP	C	T	49	63	c.11761G>A	c.(11761-11763)GAT>AAT	p.D3921N
Pat_30	Post-Resistance	C2orf57	165100	37	2	232458410	232458410	Missense_Mutation	SNP	C	A	159	177	c.748C>A	c.(748-750)CAC>AAC	p.H250N
Pat_30	Post-Resistance	APCDD1L	164284	37	20	57036037	57036037	Missense_Mutation	SNP	C	T	22	49	c.1315G>A	c.(1315-1317)GAT>AAT	p.D439N
Pat_30	Post-Resistance	TPTE	7179	37	21	10941907	10941907	Splice_Site	SNP	C	T	16	178	c.795_splice	c.e14+1	p.K265_splice
Pat_30	Post-Resistance	LIPI	149998	37	21	15558293	15558293	Missense_Mutation	SNP	C	T	18	38	c.593G>A	c.(592-594)GGA>GAA	p.G198E
Pat_30	Post-Resistance	DSCAM	1826	37	21	41385217	41385217	Missense_Mutation	SNP	C	T	11	13	c.5783G>A	c.(5782-5784)TGC>TAC	p.C1928Y
Pat_30	Post-Resistance	SFI1	9814	37	22	31976306	31976306	Nonsense_Mutation	SNP	C	T	70	8	c.1204C>T	c.(1204-1206)CAG>TAG	p.Q402*
Pat_30	Post-Resistance	GRIP2	80852	37	3	14545082	14545082	Missense_Mutation	SNP	C	T	3	2	c.2965G>A	c.(2965-2967)GAA>AAA	p.E989K
Pat_30	Post-Resistance	TBC1D5	9779	37	3	17202637	17202637	Nonsense_Mutation	SNP	G	A	16	2	c.2206C>T	c.(2206-2208)CAG>TAG	p.Q736*
Pat_30	Post-Resistance	C3orf45	132228	37	3	50323943	50323943	Missense_Mutation	SNP	C	G	2	7	c.100C>G	c.(100-102)CCA>GCA	p.P34A
Pat_30	Post-Resistance	MUC4	4585	37	3	195511283	195511283	Missense_Mutation	SNP	C	T	3	2	c.7168G>A	c.(7168-7170)GCT>ACT	p.A2390T
Pat_30	Post-Resistance	NSUN7	79730	37	4	40776320	40776320	Missense_Mutation	SNP	G	A	35	55	c.527G>A	c.(526-528)CGA>CAA	p.R176Q
Pat_30	Post-Resistance	PROL1	58503	37	4	71275623	71275623	Missense_Mutation	SNP	C	T	99	160	c.578C>T	c.(577-579)TCA>TTA	p.S193L
Pat_30	Post-Resistance	GC	2638	37	4	72620723	72620723	Missense_Mutation	SNP	T	G	29	47	c.1136A>C	c.(1135-1137)GAA>GCA	p.E379A
Pat_30	Post-Resistance	KIAA1109	84162	37	4	123280759	123280759	Missense_Mutation	SNP	C	T	22	34	c.14683C>T	c.(14683-14685)CCA>TCA	p.P4895S
Pat_30	Post-Resistance	FAT4	79633	37	4	126336743	126336743	Missense_Mutation	SNP	G	A	63	88	c.6625G>A	c.(6625-6627)GGT>AGT	p.G2209S
Pat_30	Post-Resistance	RWDD4A	201965	37	4	184567673	184567673	Missense_Mutation	SNP	G	A	44	74	c.499C>T	c.(499-501)CCT>TCT	p.P167S
Pat_30	Post-Resistance	PCDHA4	56144	37	5	140187989	140187989	Missense_Mutation	SNP	C	T	19	233	c.1217C>T	c.(1216-1218)TCG>TTG	p.S406L
Pat_30	Post-Resistance	PCDHB15	56121	37	5	140627305	140627305	Missense_Mutation	SNP	C	T	96	39	c.2159C>T	c.(2158-2160)GCC>GTC	p.A720V
Pat_30	Post-Resistance	FAT2	2196	37	5	150924239	150924239	Missense_Mutation	SNP	G	A	7	71	c.6449C>T	c.(6448-6450)ACG>ATG	p.T2150M
Pat_30	Post-Resistance	ATXN1	6310	37	6	16326801	16326801	Nonsense_Mutation	SNP	G	A	37	115	c.1741C>T	c.(1741-1743)CAG>TAG	p.Q581*
Pat_30	Post-Resistance	CAP2	10486	37	6	17507881	17507881	Missense_Mutation	SNP	C	T	17	76	c.454C>T	c.(454-456)CCT>TCT	p.P152S
Pat_30	Post-Resistance	OR2B6	26212	37	6	27925296	27925296	Missense_Mutation	SNP	G	A	16	73	c.278G>A	c.(277-279)AGT>AAT	p.S93N
Pat_30	Post-Resistance	TAP2	6891	37	6	32781530	32781530	Missense_Mutation	SNP	C	T	3	3	c.2545G>A	c.(2545-2547)GGA>AGA	p.G849R
Pat_30	Post-Resistance	SPDEF	25803	37	6	34512187	34512187	Missense_Mutation	SNP	G	T	31	98	c.46C>A	c.(46-48)CTC>ATC	p.L16I
Pat_30	Post-Resistance	PNPLA1	285848	37	6	36270156	36270156	Missense_Mutation	SNP	G	T	58	195	c.1294G>T	c.(1294-1296)GTG>TTG	p.V432L
Pat_30	Post-Resistance	GTPBP2	54676	37	6	43591778	43591778	Missense_Mutation	SNP	A	C	82	62	c.1128T>G	c.(1126-1128)AGT>AGG	p.S376R
Pat_30	Post-Resistance	FAM83B	222584	37	6	54805310	54805310	Missense_Mutation	SNP	C	T	51	32	c.1541C>T	c.(1540-1542)TCA>TTA	p.S514L
Pat_30	Post-Resistance	C7orf10	79783	37	7	40488913	40488913	Missense_Mutation	SNP	G	T	15	33	c.844G>T	c.(844-846)GTA>TTA	p.V282L
Pat_30	Post-Resistance	ABCA13	154664	37	7	48280486	48280486	Missense_Mutation	SNP	G	A	29	41	c.1085G>A	c.(1084-1086)GGT>GAT	p.G362D
Pat_30	Post-Resistance	FBXL13	222235	37	7	102665589	102665589	Missense_Mutation	SNP	C	T	10	21	c.416G>A	c.(415-417)CGA>CAA	p.R139Q

Pat_30	Post-Resistance	LAMB4	22798	37	7	107710246	107710246	Missense_Mutation	SNP	C	T	95	342	c.2209G>A	c.(2209-2211)GAA>AAA	p.E737K
Pat_30	Post-Resistance	CHRM2	1129	37	7	136699707	136699707	Missense_Mutation	SNP	C	T	25	73	c.95C>T	c.(94-96)TCC>TTC	p.S32F
Pat_30	Post-Resistance	BRAF	673	37	7	140453136	140453136	Missense_Mutation	SNP	A	T	430	142	c.1799T>A	c.(1798-1800)GTG>GAG	p.V600E
Pat_30	Post-Resistance	MYOM2	9172	37	8	2017410	2017410	Missense_Mutation	SNP	G	A	74	49	c.667G>A	c.(667-669)GAC>AAC	p.D223N
Pat_30	Post-Resistance	PPP1R3B	79660	37	8	8999115	8999115	Missense_Mutation	SNP	G	A	16	49	c.47C>T	c.(46-48)TCC>TTC	p.S16F
Pat_30	Post-Resistance	SNX31	169166	37	8	101612642	101612642	Missense_Mutation	SNP	C	T	35	54	c.709G>A	c.(709-711)GCC>ACC	p.A237T
Pat_30	Post-Resistance	LRP12	29967	37	8	105509486	105509486	Missense_Mutation	SNP	G	A	92	66	c.1294C>T	c.(1294-1296)CGC>TGC	p.R432C
Pat_30	Post-Resistance	ASAP1	50807	37	8	131138295	131138295	Missense_Mutation	SNP	A	C	64	52	c.1422T>G	c.(1420-1422)TGT>TGG	p.C474W
Pat_30	Post-Resistance	ARC	23237	37	8	143694456	143694456	Missense_Mutation	SNP	T	C	6	29	c.1177A>G	c.(1177-1179)ACC>GCC	p.T393A
Pat_30	Post-Resistance	ZNF251	90987	37	8	145947109	145947109	Missense_Mutation	SNP	C	T	16	40	c.1936G>A	c.(1936-1938)GGA>AGA	p.G646R
Pat_30	Post-Resistance	UBAP1	51271	37	9	34251508	34251508	Missense_Mutation	SNP	T	A	20	11	c.1487T>A	c.(1486-1488)ATG>AAG	p.M496K
Pat_30	Post-Resistance	TRPM6	140803	37	9	77417080	77417080	Missense_Mutation	SNP	T	C	4	0	c.1743A>G	c.(1741-1743)ATA>ATG	p.I581M
Pat_30	Post-Resistance	FLJ43950	347127	37	9	84530870	84530870	Missense_Mutation	SNP	C	T	10	3	c.791C>T	c.(790-792)TCC>TTC	p.S264F
Pat_30	Post-Resistance	DENND1A	57706	37	9	126214617	126214617	Missense_Mutation	SNP	C	T	23	7	c.1237G>A	c.(1237-1239)GGA>AGA	p.G413R
Pat_30	Post-Resistance	CLCN4	1183	37	X	10176514	10176514	Missense_Mutation	SNP	C	T	107	234	c.1273C>T	c.(1273-1275)CCT>TCT	p.P425S
Pat_30	Post-Resistance	SYAP1	94056	37	X	16761957	16761957	Missense_Mutation	SNP	C	T	169	292	c.569C>T	c.(568-570)CCT>CTT	p.P190L
Pat_30	Post-Resistance	ZFX	7543	37	X	24229378	24229378	Missense_Mutation	SNP	C	T	104	143	c.2303C>T	c.(2302-2304)TCC>TTC	p.S768F
Pat_30	Post-Resistance	SRPX	8406	37	X	38033482	38033482	Missense_Mutation	SNP	C	T	90	83	c.280G>A	c.(280-282)GAG>AAG	p.E94K
Pat_30	Post-Resistance	ZNF182	7569	37	X	47836909	47836909	Missense_Mutation	SNP	G	A	8	10	c.577C>T	c.(577-579)CAT>TAT	p.H193Y
Pat_30	Post-Resistance	CCNB3	85417	37	X	50053780	50053780	Missense_Mutation	SNP	G	A	4	9	c.2611G>A	c.(2611-2613)GAG>AAG	p.E871K
Pat_30	Post-Resistance	STARD8	9754	37	X	67938434	67938434	Missense_Mutation	SNP	G	A	23	32	c.1438G>A	c.(1438-1440)GAT>AAT	p.D480N
Pat_30	Post-Resistance	ACRC	93953	37	X	70823920	70823920	Missense_Mutation	SNP	C	T	8	59	c.793C>T	c.(793-795)CCC>TCC	p.P265S
Pat_31	Pre-Treatment	CROCC	9696	37	1	17292241	17292241	Missense_Mutation	SNP	C	T	113	60	c.4429C>T	c.(4429-4431)CCC>TCC	p.P1477S
Pat_31	Pre-Treatment	CSMD2	114784	37	1	34276445	34276445	Missense_Mutation	SNP	G	T	55	120	c.1225C>A	c.(1225-1227)CTT>ATT	p.L409I
Pat_31	Pre-Treatment	MACF1	23499	37	1	39889724	39889724	Nonsense_Mutation	SNP	C	T	104	40	c.11494C>T	c.(11494-11496)CGA>TGA	p.R3832*
Pat_31	Pre-Treatment	ZSWIM5	57643	37	1	45504680	45504680	Missense_Mutation	SNP	G	A	5	114	c.1822C>T	c.(1822-1824)CCC>TCC	p.P608S
Pat_31	Pre-Treatment	C1orf163	65260	37	1	53153418	53153418	Missense_Mutation	SNP	C	T	3	62	c.670G>A	c.(670-672)GGT>AGT	p.G224S
Pat_31	Pre-Treatment	MAGOH	4116	37	1	53692748	53692748	Missense_Mutation	SNP	A	G	3	50	c.410T>C	c.(409-411)ATT>ACT	p.I137T
Pat_31	Pre-Treatment	BSND	7809	37	1	55472863	55472863	Missense_Mutation	SNP	G	T	4	132	c.466G>T	c.(466-468)GCC>TCC	p.A156S
Pat_31	Pre-Treatment	C1orf168	199920	37	1	57258394	57258394	Missense_Mutation	SNP	G	T	13	477	c.92C>A	c.(91-93)CCA>CAA	p.P31Q
Pat_31	Pre-Treatment	CACHD1	57685	37	1	65130356	65130356	Missense_Mutation	SNP	G	T	112	53	c.2117G>T	c.(2116-2118)AGA>ATA	p.R706I
Pat_31	Pre-Treatment	AK5	26289	37	1	77806237	77806237	Missense_Mutation	SNP	A	G	3	125	c.875A>G	c.(874-876)AAG>AGG	p.K292R
Pat_31	Pre-Treatment	NBPF9	400818	37	1	144815953	144815953	Missense_Mutation	SNP	A	G	20	728	c.1324A>G	c.(1324-1326)AAT>GAT	p.N442D
Pat_31	Pre-Treatment	NBPF10	100132406	37	1	145311785	145311785	Splice_Site	SNP	C	G	10	137	c.1854_splice	c.e14-1	p.R618_splice
Pat_31	Pre-Treatment	FLG2	388698	37	1	152324164	152324164	Missense_Mutation	SNP	T	G	10	866	c.6098A>C	c.(6097-6099)TAC>TCC	p.Y2033S
Pat_31	Pre-Treatment	FLG2	388698	37	1	152326017	152326017	Missense_Mutation	SNP	C	A	10	772	c.4245G>T	c.(4243-4245)AGG>AGT	p.R1415S
Pat_31	Pre-Treatment	CRNN	49860	37	1	152382749	152382749	Missense_Mutation	SNP	G	A	12	751	c.809C>T	c.(808-810)ACC>ATC	p.T270I
Pat_31	Pre-Treatment	TRIM46	80128	37	1	155148051	155148051	Missense_Mutation	SNP	T	A	111	177	c.253T>A	c.(253-255)TCC>ACC	p.S85T
Pat_31	Pre-Treatment	TRIM46	80128	37	1	155152368	155152368	Missense_Mutation	SNP	G	A	49	121	c.1546G>A	c.(1546-1548)GAA>AAA	p.E516K
Pat_31	Pre-Treatment	FCRL2	79368	37	1	157737066	157737066	Missense_Mutation	SNP	C	T	128	189	c.1117G>A	c.(1117-1119)GGC>AGC	p.G373S
Pat_31	Pre-Treatment	SPTA1	6708	37	1	158617430	158617430	Missense_Mutation	SNP	C	T	67	116	c.3795G>A	c.(3793-3795)ATG>ATA	p.M1265I
Pat_31	Pre-Treatment	MYOC	4653	37	1	171621343	171621343	Missense_Mutation	SNP	C	T	122	175	c.409G>A	c.(409-411)GAG>AAG	p.E137K
Pat_31	Pre-Treatment	PAPPA2	60676	37	1	176738864	176738864	Missense_Mutation	SNP	G	C	16	307	c.4445G>C	c.(4444-4446)GGA>GCA	p.G1482A
Pat_31	Pre-Treatment	DDX59	83479	37	1	200619608	200619608	Missense_Mutation	SNP	A	C	75	98	c.1259T>G	c.(1258-1260)ATT>AGT	p.I420S
Pat_31	Pre-Treatment	ESRRG	2104	37	1	216850805	216850805	Nonsense_Mutation	SNP	G	A	4	96	c.85C>T	c.(85-87)CGA>TGA	p.R29*
Pat_31	Pre-Treatment	OBSCN	84033	37	1	228495004	228495004	Missense_Mutation	SNP	G	A	137	226	c.12238G>A	c.(12238-12240)GAG>AAG	p.E4080K
Pat_31	Pre-Treatment	OR2L2	26246	37	1	248201572	248201572	Missense_Mutation	SNP	G	A	188	186	c.3G>A	c.(1-3)ATG>ATA	p.M1I

Pat_31	Pre-Treatment	OR2M1P	388762	37	1	248285997	248285997	Missense_Mutation	SNP	G	C	10	683	c.560G>C	c.(559-561)GGT>GCT	p.G187A
Pat_31	Pre-Treatment	TUBAL3	79861	37	10	5436384	5436384	Missense_Mutation	SNP	C	T	8	141	c.437G>A	c.(436-438)CGA>CAA	p.R146Q
Pat_31	Pre-Treatment	FAM13C	220965	37	10	61014112	61014112	Missense_Mutation	SNP	G	T	86	267	c.1328C>A	c.(1327-1329)ACA>AAA	p.T443K
Pat_31	Pre-Treatment	CDH23	64072	37	10	73553380	73553380	Missense_Mutation	SNP	C	T	4	39	c.6695C>T	c.(6694-6696)GCT>GTT	p.A2232V
Pat_31	Pre-Treatment	NRG3	10718	37	10	84745186	84745186	Missense_Mutation	SNP	G	A	30	74	c.1916G>A	c.(1915-1917)CGA>CAA	p.R639Q
Pat_31	Pre-Treatment	PLCE1	51196	37	10	96014685	96014685	Missense_Mutation	SNP	C	T	111	579	c.3433C>T	c.(3433-3435)CCT>TCT	p.P1145S
Pat_31	Pre-Treatment	CYP2C18	1562	37	10	96495124	96495124	Missense_Mutation	SNP	G	A	101	281	c.1396G>A	c.(1396-1398)GAT>AAT	p.D466N
Pat_31	Pre-Treatment	LOC653544	653544	37	10	135491123	135491123	Missense_Mutation	SNP	G	A	4	52	c.734G>A	c.(733-735)GGC>GAC	p.G245D
Pat_31	Pre-Treatment	CDHR5	53841	37	11	618674	618674	Missense_Mutation	SNP	C	T	5	235	c.1885G>A	c.(1885-1887)GGT>AGT	p.G629S
Pat_31	Pre-Treatment	MUC2	4583	37	11	1097769	1097769	Missense_Mutation	SNP	C	A	4	100	c.13948C>A	c.(13948-13950)CAG>AAG	p.Q4650K
Pat_31	Pre-Treatment	KRTAP5-3	387266	37	11	1628952	1628952	Missense_Mutation	SNP	A	T	11	706	c.664T>A	c.(664-666)TGC>AGC	p.C222S
Pat_31	Pre-Treatment	TRIM48	79097	37	11	55035844	55035844	Missense_Mutation	SNP	T	C	6	221	c.574T>C	c.(574-576)TAC>CAC	p.Y192H
Pat_31	Pre-Treatment	AHNAK	79026	37	11	62296070	62296070	Missense_Mutation	SNP	A	G	15	781	c.5819T>C	c.(5818-5820)GTG>GCG	p.V1940A
Pat_31	Pre-Treatment	UNC93B1	81622	37	11	67767119	67767119	Missense_Mutation	SNP	C	G	6	45	c.424G>C	c.(424-426)GCT>CCT	p.A142P
Pat_31	Pre-Treatment	PDE2A	5138	37	11	72288490	72288490	Missense_Mutation	SNP	C	T	4	125	c.2764G>A	c.(2764-2766)GTG>ATG	p.V922M
Pat_31	Pre-Treatment	CNTN5	53942	37	11	100221562	100221562	Missense_Mutation	SNP	G	A	8	167	c.3160G>A	c.(3160-3162)GGA>AGA	p.G1054R
Pat_31	Pre-Treatment	TMPRSS4	56649	37	11	117984114	117984114	Missense_Mutation	SNP	G	C	41	259	c.874G>C	c.(874-876)GCC>CCC	p.A292P
Pat_31	Pre-Treatment	OR10S1	219873	37	11	123848356	123848356	Missense_Mutation	SNP	C	T	53	233	c.43G>A	c.(43-45)GAG>AAG	p.E15K
Pat_31	Pre-Treatment	CD163	9332	37	12	7639539	7639539	Missense_Mutation	SNP	C	A	49	123	c.2094G>T	c.(2092-2094)TTG>TTT	p.L698F
Pat_31	Pre-Treatment	PRB1	5542	37	12	11506690	11506690	Missense_Mutation	SNP	C	T	150	649	c.347G>A	c.(346-348)GGA>GAA	p.G116E
Pat_31	Pre-Treatment	ABCC9	10060	37	12	21981927	21981927	Missense_Mutation	SNP	G	A	167	433	c.3634C>T	c.(3634-3636)CTC>TTC	p.L1212F
Pat_31	Pre-Treatment	IPO8	10526	37	12	30790032	30790032	Missense_Mutation	SNP	T	G	94	222	c.2579A>C	c.(2578-2580)CAG>CCG	p.Q860P
Pat_31	Pre-Treatment	DDX11	1663	37	12	31237922	31237922	Missense_Mutation	SNP	G	C	4	53	c.500G>C	c.(499-501)AGA>ACA	p.R167T
Pat_31	Pre-Treatment	TUBA1B	10376	37	12	49521767	49521767	Missense_Mutation	SNP	C	T	36	409	c.1330G>A	c.(1330-1332)GGT>AGT	p.G444S
Pat_31	Pre-Treatment	SRGAP1	57522	37	12	64456773	64456773	Missense_Mutation	SNP	C	G	6	219	c.878C>G	c.(877-879)ACC>AGC	p.T293S
Pat_31	Pre-Treatment	FRS2	10818	37	12	69966038	69966038	Missense_Mutation	SNP	C	T	148	240	c.553C>T	c.(553-555)CCT>TCT	p.P185S
Pat_31	Pre-Treatment	ZMYM2	7750	37	13	20600897	20600897	Missense_Mutation	SNP	C	T	5	60	c.1730C>T	c.(1729-1731)TCA>TTA	p.S577L
Pat_31	Pre-Treatment	LHFP	10186	37	13	40175179	40175179	Missense_Mutation	SNP	G	A	291	499	c.175C>T	c.(175-177)CGG>TGG	p.R59W
Pat_31	Pre-Treatment	ERCC5	2073	37	13	103518233	103518233	Missense_Mutation	SNP	C	T	127	168	c.2171C>T	c.(2170-2172)TCG>TTG	p.S724L
Pat_31	Pre-Treatment	OR4L1	122742	37	14	20528589	20528589	Missense_Mutation	SNP	C	T	68	151	c.386C>T	c.(385-387)CCC>CTC	p.P129L
Pat_31	Pre-Treatment	PNN	5411	37	14	39645289	39645289	Nonsense_Mutation	SNP	C	T	35	68	c.121C>T	c.(121-123)CAA>TAA	p.Q41*
Pat_31	Pre-Treatment	KCNH5	27133	37	14	63174990	63174990	Nonsense_Mutation	SNP	G	A	61	86	c.2203C>T	c.(2203-2205)CAG>TAG	p.Q735*
Pat_31	Pre-Treatment	AHSA1	10598	37	14	77934803	77934803	Missense_Mutation	SNP	C	T	63	101	c.796C>T	c.(796-798)CCT>TCT	p.P266S
Pat_31	Pre-Treatment	NRXN3	9369	37	14	79117602	79117602	Missense_Mutation	SNP	G	A	143	220	c.35G>A	c.(34-36)GGA>GAA	p.G12E
Pat_31	Pre-Treatment	DEGS2	123099	37	14	100613240	100613240	Missense_Mutation	SNP	C	T	5	263	c.830G>A	c.(829-831)CGG>CAG	p.R277Q
Pat_31	Pre-Treatment	MAP2K1	5604	37	15	66727442	66727442	Missense_Mutation	SNP	T	A	215	331	c.158T>A	c.(157-159)TTT>TAT	p.F53Y
Pat_31	Pre-Treatment	PKD1	5310	37	16	2162933	2162933	Missense_Mutation	SNP	G	A	46	141	c.3017C>T	c.(3016-3018)ACC>ATC	p.T1006I
Pat_31	Pre-Treatment	ERN2	10595	37	16	23702234	23702234	Missense_Mutation	SNP	C	T	4	76	c.2843G>A	c.(2842-2844)TGC>TAC	p.C948Y
Pat_31	Pre-Treatment	ZNF267	10308	37	16	31927534	31927534	Missense_Mutation	SNP	C	G	7	353	c.1964C>G	c.(1963-1965)ACT>AGT	p.T655S
Pat_31	Pre-Treatment	SLC6A10P	386757	37	16	32890622	32890622	Missense_Mutation	SNP	T	G	6	85	c.264A>C	c.(262-264)AAA>AAC	p.K88N
Pat_31	Pre-Treatment	SLC6A10P	386757	37	16	32890639	32890639	Missense_Mutation	SNP	T	C	5	91	c.247A>G	c.(247-249)AAG>GAG	p.K83E
Pat_31	Pre-Treatment	CDH1	999	37	16	68842734	68842734	Missense_Mutation	SNP	C	T	4	94	c.670C>T	c.(670-672)CGC>TGC	p.R224C
Pat_31	Pre-Treatment	CLEC18B	497190	37	16	74446997	74446997	Missense_Mutation	SNP	G	A	35	279	c.614C>T	c.(613-615)TCG>TTG	p.S205L
Pat_31	Pre-Treatment	SPNS3	201305	37	17	4389577	4389577	Missense_Mutation	SNP	G	A	29	54	c.1234G>A	c.(1234-1236)GGC>AGC	p.G412S
Pat_31	Pre-Treatment	C17orf61	254863	37	17	7307394	7307394	Missense_Mutation	SNP	G	A	3	14	c.10C>T	c.(10-12)CCA>TCA	p.P4S
Pat_31	Pre-Treatment	C17orf74	201243	37	17	7330590	7330590	Missense_Mutation	SNP	C	T	22	97	c.1280C>T	c.(1279-1281)TCC>TTC	p.S427F
Pat_31	Pre-Treatment	MYH10	4628	37	17	8397110	8397110	Missense_Mutation	SNP	C	G	4	134	c.4057G>C	c.(4057-4059)GAG>CAG	p.E1353Q

Pat_31	Pre-Treatment	KRTAP4-7	100132476	37	17	39240745	39240745	Missense_Mutation	SNP	A	G	4	80	c.287A>G	c.(286-288)AAG>AGG	p.K96R
Pat_31	Pre-Treatment	KRTAP4-8	728224	37	17	39254013	39254013	Missense_Mutation	SNP	G	C	4	91	c.324C>G	c.(322-324)AGC>AGG	p.S108R
Pat_31	Pre-Treatment	KRTAP4-11	653240	37	17	39274150	39274150	Missense_Mutation	SNP	T	A	7	132	c.418A>T	c.(418-420)AGC>TGC	p.S140C
Pat_31	Pre-Treatment	KRTAP4-11	653240	37	17	39274214	39274214	Missense_Mutation	SNP	G	C	5	161	c.354C>G	c.(352-354)AGC>AGG	p.S118R
Pat_31	Pre-Treatment	ATP5H	10476	37	17	73035082	73035082	Missense_Mutation	SNP	T	A	61	53	c.431A>T	c.(430-432)AAA>ATA	p.K144I
Pat_31	Pre-Treatment	POTEC	388468	37	18	14513675	14513675	Missense_Mutation	SNP	T	C	6	256	c.1519A>G	c.(1519-1521)AAA>GAA	p.K507E
Pat_31	Pre-Treatment	CABLES1	91768	37	18	20716462	20716462	Missense_Mutation	SNP	G	A	3	59	c.736G>A	c.(736-738)GGA>AGA	p.G246R
Pat_31	Pre-Treatment	DCC	1630	37	18	50918172	50918172	Missense_Mutation	SNP	C	T	56	89	c.2603C>T	c.(2602-2604)TCT>TTT	p.S868F
Pat_31	Pre-Treatment	ZNF57	126295	37	19	2917807	2917807	Missense_Mutation	SNP	A	C	6	189	c.1188A>C	c.(1186-1188)CAA>CAC	p.Q396H
Pat_31	Pre-Treatment	ZNF57	126295	37	19	2917842	2917842	Missense_Mutation	SNP	G	A	9	169	c.1223G>A	c.(1222-1224)CGA>CAA	p.R408Q
Pat_31	Pre-Treatment	ZNF57	126295	37	19	2917857	2917857	Missense_Mutation	SNP	C	T	8	164	c.1238C>T	c.(1237-1239)ACG>ATG	p.T413M
Pat_31	Pre-Treatment	CD209	30835	37	19	7810766	7810766	Missense_Mutation	SNP	C	T	13	409	c.386G>A	c.(385-387)CGG>CAG	p.R129Q
Pat_31	Pre-Treatment	MUC16	94025	37	19	9059142	9059142	Missense_Mutation	SNP	G	A	102	111	c.28304C>T	c.(28303-28305)TCC>TTC	p.S9435F
Pat_31	Pre-Treatment	MUC16	94025	37	19	9066741	9066741	Missense_Mutation	SNP	G	A	124	363	c.20705C>T	c.(20704-20706)TCC>TTC	p.S6902F
Pat_31	Pre-Treatment	ZNF844	284391	37	19	12187443	12187443	Missense_Mutation	SNP	C	G	8	364	c.1508C>G	c.(1507-1509)CCT>CGT	p.P503R
Pat_31	Pre-Treatment	ZNF844	284391	37	19	12187502	12187502	Missense_Mutation	SNP	A	G	9	191	c.1567A>G	c.(1567-1569)AAA>GAA	p.K523E
Pat_31	Pre-Treatment	ZNF563	147837	37	19	12429722	12429722	Missense_Mutation	SNP	T	C	11	714	c.1117A>G	c.(1117-1119)ACG>GCG	p.T373A
Pat_31	Pre-Treatment	ZNF208	7757	37	19	22154417	22154417	Missense_Mutation	SNP	G	A	6	325	c.3035C>T	c.(3034-3036)CCC>CTC	p.P1012L
Pat_31	Pre-Treatment	ZNF599	148103	37	19	35258305	35258305	Missense_Mutation	SNP	G	A	60	39	c.157C>T	c.(157-159)CCC>TCC	p.P53S
Pat_31	Pre-Treatment	FCGBP	8857	37	19	40392568	40392568	Missense_Mutation	SNP	C	T	45	103	c.7936G>A	c.(7936-7938)GAG>AAG	p.E2646K
Pat_31	Pre-Treatment	ATF5	22809	37	19	50435732	50435732	Missense_Mutation	SNP	C	T	106	130	c.232C>T	c.(232-234)CCT>TCT	p.P78S
Pat_31	Pre-Treatment	KCNC3	3748	37	19	50823987	50823987	Missense_Mutation	SNP	G	A	4	100	c.2033C>T	c.(2032-2034)CCA>CTA	p.P678L
Pat_31	Pre-Treatment	KLK8	11202	37	19	51503311	51503311	Missense_Mutation	SNP	C	A	4	43	c.434G>T	c.(433-435)TGC>TTC	p.C145F
Pat_31	Pre-Treatment	ZNF816A	125893	37	19	53453890	53453890	Missense_Mutation	SNP	G	C	10	737	c.1138C>G	c.(1138-1140)CAG>GAG	p.Q380E
Pat_31	Pre-Treatment	ZNF17	7565	37	19	57932028	57932028	Missense_Mutation	SNP	G	A	5	271	c.1168G>A	c.(1168-1170)GAA>AAA	p.E390K
Pat_31	Pre-Treatment	ZNF749	388567	37	19	57955884	57955885	Missense_Mutation	DNP	CC	TG	6	245	.1368_1369CC>T	366-1371)CACCAG>CATG	p.Q457E
Pat_31	Pre-Treatment	ZNF551	90233	37	19	58196694	58196694	Missense_Mutation	SNP	C	T	151	194	c.98C>T	c.(97-99)TCT>TTT	p.S33F
Pat_31	Pre-Treatment	ZNF606	80095	37	19	58490292	58490292	Missense_Mutation	SNP	G	T	50	189	c.1756C>A	c.(1756-1758)CAT>AAT	p.H586N
Pat_31	Pre-Treatment	NT5C1B	93034	37	2	18768804	18768804	Missense_Mutation	SNP	C	T	9	350	c.85G>A	c.(85-87)GAA>AAA	p.E29K
Pat_31	Pre-Treatment	ZNF513	130557	37	2	27601466	27601466	Missense_Mutation	SNP	G	A	4	111	c.667C>T	c.(667-669)CGG>TGG	p.R223W
Pat_31	Pre-Treatment	MEIS1	4211	37	2	66794598	66794598	Missense_Mutation	SNP	C	T	4	152	c.979C>T	c.(979-981)CGG>TGG	p.R327W
Pat_31	Pre-Treatment	WASH2P	375260	37	2	114355998	114355998	Missense_Mutation	SNP	C	G	5	32	c.616C>G	c.(616-618)CAC>GAC	p.H206D
Pat_31	Pre-Treatment	GLI2	2736	37	2	121748042	121748042	Missense_Mutation	SNP	G	A	45	470	c.4552G>A	c.(4552-4554)GAT>AAT	p.D1518N
Pat_31	Pre-Treatment	LRP1B	53353	37	2	141208192	141208192	Nonsense_Mutation	SNP	C	T	78	207	c.10002G>A	c.(10000-10002)TGG>TGA	p.W3334*
Pat_31	Pre-Treatment	PDK1	5163	37	2	173423531	173423531	Missense_Mutation	SNP	C	T	49	132	c.292C>T	c.(292-294)CCA>TCA	p.P98S
Pat_31	Pre-Treatment	TTN	7273	37	2	179632598	179632598	Missense_Mutation	SNP	C	T	52	130	c.9359G>A	c.(9358-9360)CGG>CAG	p.R3120Q
Pat_31	Pre-Treatment	FAM171B	165215	37	2	187626849	187626849	Missense_Mutation	SNP	C	T	32	112	c.1780C>T	c.(1780-1782)CAT>TAT	p.H594Y
Pat_31	Pre-Treatment	DNAH7	56171	37	2	196737150	196737150	Missense_Mutation	SNP	C	T	169	163	c.6457G>A	c.(6457-6459)GTA>ATA	p.V2153I
Pat_31	Pre-Treatment	NOP58	51602	37	2	203165073	203165073	Missense_Mutation	SNP	C	T	44	235	c.1385C>T	c.(1384-1386)GCC>GTC	p.A462V
Pat_31	Pre-Treatment	ABCA12	26154	37	2	215876189	215876189	Missense_Mutation	SNP	G	A	49	44	c.2306C>T	c.(2305-2307)TCA>TTA	p.S769L
Pat_31	Pre-Treatment	SP140	11262	37	2	231150484	231150484	Missense_Mutation	SNP	G	A	229	252	c.1582G>A	c.(1582-1584)GGC>AGC	p.G528S
Pat_31	Pre-Treatment	NGEF	25791	37	2	233757732	233757732	Missense_Mutation	SNP	C	T	33	112	c.1018G>A	c.(1018-1020)GAG>AAG	p.E340K
Pat_31	Pre-Treatment	FRG1B	284802	37	20	29614328	29614328	Splice_Site	SNP	G	A	5	166	c.-6_splice	c.e1+1	
Pat_31	Pre-Treatment	FRG1B	284802	37	20	29625941	29625941	Missense_Mutation	SNP	A	T	6	255	c.95A>T	c.(94-96)GAT>GTT	p.D32V
Pat_31	Pre-Treatment	FRG1B	284802	37	20	29628320	29628320	Nonsense_Mutation	SNP	G	T	8	179	c.232G>T	c.(232-234)GAA>TAA	p.E78*
Pat_31	Pre-Treatment	EMILIN3	90187	37	20	39989972	39989972	Missense_Mutation	SNP	C	T	12	112	c.2237G>A	c.(2236-2238)CGG>CAG	p.R746Q
Pat_31	Pre-Treatment	SEMG2	6407	37	20	43851445	43851445	Missense_Mutation	SNP	G	C	5	244	c.1172G>C	c.(1171-1173)AGA>ACA	p.R391T

Pat_31	Pre-Treatment	PREX1	57580	37	20	47244484	47244484	Missense_Mutation	SNP	G	A	11	50	c.4784C>T	c.(4783-4785)TCC>TTC	p.S1595F
Pat_31	Pre-Treatment	PTGIS	5740	37	20	48129663	48129663	Missense_Mutation	SNP	G	A	42	158	c.1160C>T	c.(1159-1161)CCC>CTC	p.P387L
Pat_31	Pre-Treatment	TSHZ2	128553	37	20	51872447	51872447	Missense_Mutation	SNP	C	T	111	101	c.2450C>T	c.(2449-2451)CCC>CTC	p.P817L
Pat_31	Pre-Treatment	DSCR3	10311	37	21	38600029	38600029	Missense_Mutation	SNP	A	G	3	50	c.737T>C	c.(736-738)CTC>CCC	p.L246P
Pat_31	Pre-Treatment	TUBA8	51807	37	22	18604267	18604267	Missense_Mutation	SNP	G	A	5	254	c.25G>A	c.(25-27)GTG>ATG	p.V9M
Pat_31	Pre-Treatment	TRIOBP	11078	37	22	38120023	38120023	Missense_Mutation	SNP	C	T	7	355	c.1460C>T	c.(1459-1461)CCC>CTC	p.P487L
Pat_31	Pre-Treatment	SCN10A	6336	37	3	38768102	38768102	Nonsense_Mutation	SNP	C	A	56	23	c.3082G>T	c.(3082-3084)GGA>TGA	p.G1028*
Pat_31	Pre-Treatment	CCR2	729230	37	3	46401317	46401317	Missense_Mutation	SNP	C	T	61	35	c.1091C>T	c.(1090-1092)CCT>CTT	p.P364L
Pat_31	Pre-Treatment	ASB14	142686	37	3	57312490	57312490	Missense_Mutation	SNP	C	T	221	81	c.854G>A	c.(853-855)CGA>CAA	p.R285Q
Pat_31	Pre-Treatment	FLNB	2317	37	3	58116605	58116605	Missense_Mutation	SNP	C	T	20	7	c.4360C>T	c.(4360-4362)CCG>TCG	p.P1454S
Pat_31	Pre-Treatment	MCM2	4171	37	3	127325611	127325611	Missense_Mutation	SNP	C	T	179	55	c.1052C>T	c.(1051-1053)TCC>TTC	p.S351F
Pat_31	Pre-Treatment	PLXND1	23129	37	3	129277296	129277296	Missense_Mutation	SNP	G	A	17	68	c.5420C>T	c.(5419-5421)TCC>TTC	p.S1807F
Pat_31	Pre-Treatment	CLCN2	1181	37	3	184071974	184071974	Missense_Mutation	SNP	G	T	14	110	c.1636C>A	c.(1636-1638)CAG>AAG	p.Q546K
Pat_31	Pre-Treatment	ZNF595	152687	37	4	60041	60041	Missense_Mutation	SNP	C	T	38	812	c.221C>T	c.(220-222)CCC>CTC	p.P74L
Pat_31	Pre-Treatment	ZNF732	654254	37	4	265103	265104	Missense_Mutation	DNP	TG	CA	5	119	.1539_1540CA>T	537-1542)TCCACA>TCTG	p.T514A
Pat_31	Pre-Treatment	ZNF732	654254	37	4	265139	265139	Missense_Mutation	SNP	C	T	6	125	c.1504G>A	c.(1504-1506)GAA>AAA	p.E502K
Pat_31	Pre-Treatment	ZNF732	654254	37	4	265307	265307	Missense_Mutation	SNP	T	C	7	182	c.1336A>G	c.(1336-1338)AAA>GAA	p.K446E
Pat_31	Pre-Treatment	LRRC66	339977	37	4	52860901	52860901	Missense_Mutation	SNP	G	A	9	182	c.2287C>T	c.(2287-2289)CCA>TCA	p.P763S
Pat_31	Pre-Treatment	MUC7	4589	37	4	71347033	71347033	Missense_Mutation	SNP	C	T	8	678	c.572C>T	c.(571-573)GCC>GTC	p.A191V
Pat_31	Pre-Treatment	FAM13A	10144	37	4	89671023	89671023	Missense_Mutation	SNP	G	T	4	115	c.1978C>A	c.(1978-1980)CAA>AAA	p.Q660K
Pat_31	Pre-Treatment	FAT4	79633	37	4	126328170	126328170	Missense_Mutation	SNP	C	T	115	312	c.5443C>T	c.(5443-5445)CGT>TGT	p.R1815C
Pat_31	Pre-Treatment	KIAA1712	80817	37	4	175229858	175229858	Missense_Mutation	SNP	C	T	28	140	c.526C>T	c.(526-528)CGT>TGT	p.R176C
Pat_31	Pre-Treatment	ODZ3	55714	37	4	183674704	183674704	Missense_Mutation	SNP	G	A	84	105	c.3964G>A	c.(3964-3966)GAT>AAT	p.D1322N
Pat_31	Pre-Treatment	IL7R	3575	37	5	35876293	35876293	Missense_Mutation	SNP	G	A	18	72	c.1085G>A	c.(1084-1086)GGA>GAA	p.G362E
Pat_31	Pre-Treatment	SPZ1	84654	37	5	79616461	79616461	Missense_Mutation	SNP	G	C	9	255	c.427G>C	c.(427-429)GAG>CAG	p.E143Q
Pat_31	Pre-Treatment	DCP2	167227	37	5	112339673	112339673	Missense_Mutation	SNP	C	T	38	61	c.841C>T	c.(841-843)CCT>TCT	p.P281S
Pat_31	Pre-Treatment	ZSCAN16	80345	37	6	28097614	28097614	Missense_Mutation	SNP	G	C	38	131	c.933G>C	c.(931-933)CAG>CAC	p.Q311H
Pat_31	Pre-Treatment	MDC1	9656	37	6	30672941	30672941	Missense_Mutation	SNP	T	C	6	392	c.4019A>G	c.(4018-4020)CAA>CGA	p.Q1340R
Pat_31	Pre-Treatment	C6orf27	80737	37	6	31737520	31737520	Missense_Mutation	SNP	C	T	103	92	c.1249G>A	c.(1249-1251)GAT>AAT	p.D417N
Pat_31	Pre-Treatment	TNXB	7148	37	6	32021309	32021309	Missense_Mutation	SNP	C	T	20	99	c.8641G>A	c.(8641-8643)GGG>AGG	p.G2881R
Pat_31	Pre-Treatment	PEX6	5190	37	6	42936135	42936135	Missense_Mutation	SNP	C	A	4	73	c.1581G>T	c.(1579-1581)TTG>TTT	p.L527F
Pat_31	Pre-Treatment	GPR110	266977	37	6	46977531	46977531	Missense_Mutation	SNP	G	A	4	86	c.1640C>T	c.(1639-1641)GCA>GTA	p.A547V
Pat_31	Pre-Treatment	MDN1	23195	37	6	90402767	90402767	Missense_Mutation	SNP	G	C	3	93	c.9982C>G	c.(9982-9984)CAG>GAG	p.Q3328E
Pat_31	Pre-Treatment	GRIK2	2898	37	6	102307177	102307177	Missense_Mutation	SNP	C	T	13	66	c.1333C>T	c.(1333-1335)CTT>TTT	p.L445F
Pat_31	Pre-Treatment	BEND3	57673	37	6	107390596	107390596	Missense_Mutation	SNP	G	A	15	41	c.1799C>T	c.(1798-1800)TCC>TTC	p.S600F
Pat_31	Pre-Treatment	DSE	29940	37	6	116757333	116757333	Missense_Mutation	SNP	C	T	17	50	c.1702C>T	c.(1702-1704)CTT>TTT	p.L568F
Pat_31	Pre-Treatment	TULP4	56995	37	6	158924649	158924650	Missense_Mutation	DNP	CC	TT	9	187	:.3954_3955CC>T	952-3957)GTCCTC>GTTT	p.L1319F
Pat_31	Pre-Treatment	AGPAT4	56895	37	6	161587390	161587390	Missense_Mutation	SNP	G	A	45	154	c.238C>T	c.(238-240)CGC>TGC	p.R80C
Pat_31	Pre-Treatment	CHST12	55501	37	7	2473115	2473115	Missense_Mutation	SNP	C	T	18	271	c.841C>T	c.(841-843)CAC>TAC	p.H281Y
Pat_31	Pre-Treatment	THSD7A	221981	37	7	11676229	11676229	Missense_Mutation	SNP	C	T	13	102	c.550G>A	c.(550-552)GAG>AAG	p.E184K
Pat_31	Pre-Treatment	OSBPL3	26031	37	7	24854801	24854801	Nonsense_Mutation	SNP	C	T	98	190	c.2049G>A	c.(2047-2049)TGG>TGA	p.W683*
Pat_31	Pre-Treatment	MYO1G	64005	37	7	45009452	45009452	Missense_Mutation	SNP	G	A	116	192	c.1355C>T	c.(1354-1356)ACC>ATC	p.T452I
Pat_31	Pre-Treatment	MYO1G	64005	37	7	45015103	45015103	Missense_Mutation	SNP	G	A	13	103	c.544C>T	c.(544-546)CAC>TAC	p.H182Y
Pat_31	Pre-Treatment	GRB10	2887	37	7	50682492	50682492	Missense_Mutation	SNP	G	C	8	313	c.1070C>G	c.(1069-1071)CCT>CGT	p.P357R
Pat_31	Pre-Treatment	TECPR1	25851	37	7	97872840	97872840	Missense_Mutation	SNP	C	A	9	110	c.596G>T	c.(595-597)TGG>TTG	p.W199L
Pat_31	Pre-Treatment	GAL3ST4	79690	37	7	99758125	99758125	Missense_Mutation	SNP	G	A	166	335	c.887C>T	c.(886-888)TCT>TTT	p.S296F
Pat_31	Pre-Treatment	ZAN	7455	37	7	100350466	100350466	Missense_Mutation	SNP	C	T	15	776	c.2738C>T	c.(2737-2739)CCC>CTC	p.P913L

Pat_31	Pre-Treatment	SYPL1	6856	37	7	105733548	105733548	Nonsense_Mutation	SNP	C	T	5	113	c.492G>A	c.(490-492)TGG>TGA	p.W164*
Pat_31	Pre-Treatment	BRAF	673	37	7	140453136	140453136	Missense_Mutation	SNP	A	T	99	142	c.1799T>A	c.(1798-1800)GTG>GAG	p.V600E
Pat_31	Pre-Treatment	ACTR3C	653857	37	7	149983566	149983566	Nonsense_Mutation	SNP	G	A	79	201	c.361C>T	c.(361-363)CAG>TAG	p.Q121*
Pat_31	Pre-Treatment	KIF13B	23303	37	8	28980923	28980924	Missense_Mutation	DNP	GG	TA	93	189	.3438_3439CC>T	436-3441)GTCCCC>GTT	p.P1147T
Pat_31	Pre-Treatment	MYST3	7994	37	8	41798364	41798364	Missense_Mutation	SNP	C	T	269	467	c.3035G>A	c.(3034-3036)CGA>CAA	p.R1012Q
Pat_31	Pre-Treatment	OPRK1	4986	37	8	54142245	54142245	Missense_Mutation	SNP	C	T	68	87	c.755G>A	c.(754-756)CGT>CAT	p.R252H
Pat_31	Pre-Treatment	C8orf34	116328	37	8	69445300	69445300	Missense_Mutation	SNP	G	A	128	224	c.763G>A	c.(763-765)GAT>AAT	p.D255N
Pat_31	Pre-Treatment	JPH1	56704	37	8	75227565	75227565	Missense_Mutation	SNP	G	A	53	411	c.670C>T	c.(670-672)CGC>TGC	p.R224C
Pat_31	Pre-Treatment	ENPP2	5168	37	8	120629793	120629794	Missense_Mutation	DNP	GG	AA	16	108	c.489_490CC>TT	487-492)CGCCCT>CGTT	p.P164S
Pat_31	Pre-Treatment	ZNF251	90987	37	8	145947717	145947717	Missense_Mutation	SNP	C	T	118	140	c.1328G>A	c.(1327-1329)CGT>CAT	p.R443H
Pat_31	Pre-Treatment	FOXD4	2298	37	9	117809	117809	Missense_Mutation	SNP	T	A	8	400	c.311A>T	c.(310-312)AAG>ATG	p.K104M
Pat_31	Pre-Treatment	COL15A1	1306	37	9	101747945	101747945	Missense_Mutation	SNP	T	C	3	82	c.199T>C	c.(199-201)TAC>CAC	p.Y67H
Pat_31	Pre-Treatment	CYLC2	1539	37	9	105767749	105767749	Missense_Mutation	SNP	G	A	4	82	c.836G>A	c.(835-837)AGT>AAT	p.S279N
Pat_31	Pre-Treatment	ZNF462	58499	37	9	109746535	109746535	Missense_Mutation	SNP	C	T	33	167	c.6901C>T	c.(6901-6903)CGC>TGC	p.R2301C
Pat_31	Pre-Treatment	ACTL7B	10880	37	9	111617225	111617225	Missense_Mutation	SNP	G	A	4	113	c.986C>T	c.(985-987)ACG>ATG	p.T329M
Pat_31	Pre-Treatment	COL5A1	1289	37	9	137620526	137620526	Missense_Mutation	SNP	G	A	230	106	c.797G>A	c.(796-798)GGA>GAA	p.G266E
Pat_31	Pre-Treatment	ABCA2	20	37	9	139910912	139910912	Missense_Mutation	SNP	C	A	5	211	c.2932G>T	c.(2932-2934)GGC>TGC	p.G978C
Pat_31	Pre-Treatment	WAS	7454	37	X	48544334	48544334	Splice_Site	SNP	G	A	61	13	c.464_splice	c.e5-1	p.D155_splice
Pat_31	Pre-Treatment	DOCK11	139818	37	X	117722261	117722261	Missense_Mutation	SNP	G	A	97	21	c.1957G>A	c.(1957-1959)GAT>AAT	p.D653N
Pat_31	Pre-Treatment	GABRQ	55879	37	X	151821440	151821440	Missense_Mutation	SNP	G	T	21	94	c.1595G>T	c.(1594-1596)TGG>TTG	p.W532L
Pat_31	Pre-Treatment	ATP2B3	492	37	X	152813349	152813349	Missense_Mutation	SNP	G	T	4	110	c.1015G>T	c.(1015-1017)GGT>TGT	p.G339C
Pat_31	Post-Resistance	DVL1	1855	37	1	1277117	1277117	Missense_Mutation	SNP	A	G	3	49	c.535T>C	c.(535-537)TCC>CCC	p.S179P
Pat_31	Post-Resistance	PLCH2	9651	37	1	2421244	2421244	Missense_Mutation	SNP	G	A	4	141	c.1453G>A	c.(1453-1455)GAG>AAG	p.E485K
Pat_31	Post-Resistance	CHD5	26038	37	1	6190319	6190319	Missense_Mutation	SNP	G	A	4	100	c.3332C>T	c.(3331-3333)ACG>ATG	p.T1111M
Pat_31	Post-Resistance	PIK3CD	5293	37	1	9782036	9782036	Missense_Mutation	SNP	G	A	4	133	c.2059G>A	c.(2059-2061)GAA>AAA	p.E687K
Pat_31	Post-Resistance	CASZ1	54897	37	1	10699598	10699598	Missense_Mutation	SNP	C	T	4	99	c.4681G>A	c.(4681-4683)GAC>AAC	p.D1561N
Pat_31	Post-Resistance	DNAJC16	23341	37	1	15855713	15855713	Missense_Mutation	SNP	G	A	4	107	c.113G>A	c.(112-114)CGA>CAA	p.R38Q
Pat_31	Post-Resistance	NBPF1	55672	37	1	16893781	16893781	Missense_Mutation	SNP	T	G	14	657	c.2957A>C	c.(2956-2958)TAT>TCT	p.Y986S
Pat_31	Post-Resistance	CROCC	9696	37	1	17292241	17292241	Missense_Mutation	SNP	C	T	35	49	c.4429C>T	c.(4429-4431)CCC>TCC	p.P1477S
Pat_31	Post-Resistance	MYOM3	127294	37	1	24426221	24426221	Missense_Mutation	SNP	C	T	4	128	c.605G>A	c.(604-606)GGA>GAA	p.G202E
Pat_31	Post-Resistance	SRRM1	10250	37	1	24993374	24993374	Missense_Mutation	SNP	C	A	4	128	c.1697C>A	c.(1696-1698)CCT>CAT	p.P566H
Pat_31	Post-Resistance	SRRM1	10250	37	1	24993386	24993386	Missense_Mutation	SNP	G	T	4	130	c.1709G>T	c.(1708-1710)CGC>CTC	p.R570L
Pat_31	Post-Resistance	TXLNA	200081	37	1	32646954	32646954	Missense_Mutation	SNP	G	A	7	157	c.281G>A	c.(280-282)GGC>GAC	p.G94D
Pat_31	Post-Resistance	CSMD2	114784	37	1	34276445	34276445	Missense_Mutation	SNP	G	T	28	140	c.1225C>A	c.(1225-1227)CTT>ATT	p.L409I
Pat_31	Post-Resistance	MACF1	23499	37	1	39889724	39889724	Nonsense_Mutation	SNP	C	T	25	35	c.11494C>T	c.(11494-11496)CGA>TGA	p.R3832*
Pat_31	Post-Resistance	PPT1	5538	37	1	40555082	40555082	Missense_Mutation	SNP	C	T	4	152	c.536G>A	c.(535-537)CGC>CAC	p.R179H
Pat_31	Post-Resistance	ZSWIM5	57643	37	1	45504680	45504680	Missense_Mutation	SNP	G	A	21	58	c.1822C>T	c.(1822-1824)CCC>TCC	p.P608S
Pat_31	Post-Resistance	ZCCHC11	23318	37	1	52897080	52897080	Missense_Mutation	SNP	G	A	4	45	c.4313C>T	c.(4312-4314)TCC>TTC	p.S1438F
Pat_31	Post-Resistance	INADL	10207	37	1	62374107	62374107	Missense_Mutation	SNP	G	A	3	49	c.3445G>A	c.(3445-3447)GGA>AGA	p.G1149R
Pat_31	Post-Resistance	CACHD1	57685	37	1	65130356	65130356	Missense_Mutation	SNP	G	T	40	25	c.2117G>T	c.(2116-2118)AGA>ATA	p.R706I
Pat_31	Post-Resistance	KIAA1324	57535	37	1	109731772	109731772	Missense_Mutation	SNP	C	T	3	49	c.1304C>T	c.(1303-1305)ACG>ATG	p.T435M
Pat_31	Post-Resistance	NBPF9	400818	37	1	144621586	144621586	Missense_Mutation	SNP	C	G	8	516	c.918C>G	c.(916-918)TTC>TTG	p.F306L
Pat_31	Post-Resistance	HIST2H3D	653604	37	1	149785145	149785145	Missense_Mutation	SNP	G	A	4	63	c.92C>T	c.(91-93)CCG>CTG	p.P31L
Pat_31	Post-Resistance	TUFT1	7286	37	1	151535142	151535142	Missense_Mutation	SNP	G	A	4	85	c.217G>A	c.(217-219)GGA>AGA	p.G73R
Pat_31	Post-Resistance	TRIM46	80128	37	1	155148051	155148051	Missense_Mutation	SNP	T	A	118	255	c.253T>A	c.(253-255)TCC>ACC	p.S85T
Pat_31	Post-Resistance	TRIM46	80128	37	1	155152368	155152368	Missense_Mutation	SNP	G	A	51	195	c.1546G>A	c.(1546-1548)GAA>AAA	p.E516K
Pat_31	Post-Resistance	C1orf104	284618	37	1	155290636	155290636	Missense_Mutation	SNP	C	T	4	121	c.644G>A	c.(643-645)CGT>CAT	p.R215H

Pat_31	Post-Resistance	FCRL2	79368	37	1	157737066	157737066	Missense_Mutation	SNP	C	T	63	121	c.1117G>A	c.(1117-1119)GGC>AGC	p.G373S
Pat_31	Post-Resistance	SPTA1	6708	37	1	158617430	158617430	Missense_Mutation	SNP	C	T	24	68	c.3795G>A	c.(3793-3795)ATG>ATA	p.M1265I
Pat_31	Post-Resistance	CCDC19	25790	37	1	159854287	159854287	Missense_Mutation	SNP	C	T	5	243	c.836G>A	c.(835-837)CGG>CAG	p.R279Q
Pat_31	Post-Resistance	FMO2	2327	37	1	171174681	171174681	Nonsense_Mutation	SNP	C	A	4	137	c.1091C>A	c.(1090-1092)TCA>TAA	p.S364*
Pat_31	Post-Resistance	MYOC	4653	37	1	171621343	171621343	Missense_Mutation	SNP	C	T	25	37	c.409G>A	c.(409-411)GAG>AAG	p.E137K
Pat_31	Post-Resistance	HMCN1	83872	37	1	186081953	186081953	Nonsense_Mutation	SNP	C	T	6	183	c.10999C>T	c.(10999-11001)CGA>TGA	p.R3667*
Pat_31	Post-Resistance	CDC73	79577	37	1	193117030	193117030	Missense_Mutation	SNP	T	A	9	52	c.763T>A	c.(763-765)TCT>ACT	p.S255T
Pat_31	Post-Resistance	CFHR1	3078	37	1	196796100	196796100	Missense_Mutation	SNP	G	A	5	315	c.395G>A	c.(394-396)CGG>CAG	p.R132Q
Pat_31	Post-Resistance	DDX59	83479	37	1	200619608	200619608	Missense_Mutation	SNP	A	C	17	20	c.1259T>G	c.(1258-1260)ATT>AGT	p.I420S
Pat_31	Post-Resistance	DISP1	84976	37	1	223178706	223178706	Missense_Mutation	SNP	G	A	5	194	c.3967G>A	c.(3967-3969)GAG>AAG	p.E1323K
Pat_31	Post-Resistance	OBSCN	84033	37	1	228412298	228412298	Missense_Mutation	SNP	G	T	23	108	c.2792G>T	c.(2791-2793)AGC>ATC	p.S931I
Pat_31	Post-Resistance	OBSCN	84033	37	1	228495004	228495004	Missense_Mutation	SNP	G	A	71	152	c.12238G>A	c.(12238-12240)GAG>AAG	p.E4080K
Pat_31	Post-Resistance	FMN2	56776	37	1	240371474	240371474	Missense_Mutation	SNP	C	T	10	721	c.3362C>T	c.(3361-3363)CCT>CTT	p.P1121L
Pat_31	Post-Resistance	OR2L2	26246	37	1	248201572	248201572	Missense_Mutation	SNP	G	A	70	104	c.3G>A	c.(1-3)ATG>ATA	p.M1I
Pat_31	Post-Resistance	OR2T4	127074	37	1	248524937	248524937	Missense_Mutation	SNP	A	T	5	284	c.55A>T	c.(55-57)ATG>TTG	p.M19L
Pat_31	Post-Resistance	C10orf18	54906	37	10	5790354	5790354	Missense_Mutation	SNP	C	T	3	47	c.4970C>T	c.(4969-4971)ACG>ATG	p.T1657M
Pat_31	Post-Resistance	MAP3K8	1326	37	10	30736733	30736733	Missense_Mutation	SNP	G	A	4	157	c.359G>A	c.(358-360)CGT>CAT	p.R120H
Pat_31	Post-Resistance	ANKRD30A	91074	37	10	37430754	37430754	Missense_Mutation	SNP	T	C	6	35	c.761T>C	c.(760-762)GTG>GCG	p.V254A
Pat_31	Post-Resistance	FAM13C	220965	37	10	61014112	61014112	Missense_Mutation	SNP	G	T	36	180	c.1328C>A	c.(1327-1329)ACA>AAA	p.T443K
Pat_31	Post-Resistance	CTNNA3	29119	37	10	68138957	68138957	Missense_Mutation	SNP	G	A	4	160	c.1685C>T	c.(1684-1686)GCT>GTT	p.A562V
Pat_31	Post-Resistance	NRG3	10718	37	10	84745186	84745186	Missense_Mutation	SNP	G	A	7	27	c.1916G>A	c.(1915-1917)CGA>CAA	p.R639Q
Pat_31	Post-Resistance	CYP2C18	1562	37	10	96495124	96495124	Missense_Mutation	SNP	G	A	38	167	c.1396G>A	c.(1396-1398)GAT>AAT	p.D466N
Pat_31	Post-Resistance	RPL13AP6	644511	37	10	112696673	112696673	Missense_Mutation	SNP	A	G	3	59	c.319T>C	c.(319-321)TGC>CGC	p.C107R
Pat_31	Post-Resistance	KRTAP5-5	439915	37	11	1651459	1651459	Missense_Mutation	SNP	G	T	5	56	c.389G>T	c.(388-390)GGC>GTC	p.G130V
Pat_31	Post-Resistance	OSBPL5	114879	37	11	3128570	3128570	Missense_Mutation	SNP	C	T	4	124	c.982G>A	c.(982-984)GAC>AAC	p.D328N
Pat_31	Post-Resistance	OR52K2	119774	37	11	4471233	4471233	Missense_Mutation	SNP	T	A	9	161	c.664T>A	c.(664-666)TTT>ATT	p.F222I
Pat_31	Post-Resistance	OR52E2	119678	37	11	5080691	5080691	Missense_Mutation	SNP	C	T	4	91	c.167G>A	c.(166-168)AGC>AAC	p.S56N
Pat_31	Post-Resistance	ARFIP2	23647	37	11	6500104	6500104	Missense_Mutation	SNP	C	T	4	132	c.401G>A	c.(400-402)CGT>CAT	p.R134H
Pat_31	Post-Resistance	SLC6A5	9152	37	11	20673940	20673940	Missense_Mutation	SNP	G	A	4	146	c.2176G>A	c.(2176-2178)GTC>ATC	p.V726I
Pat_31	Post-Resistance	NUP160	23279	37	11	47834555	47834555	Missense_Mutation	SNP	G	A	4	60	c.1831C>T	c.(1831-1833)CGG>TGG	p.R611W
Pat_31	Post-Resistance	OR5M8	219484	37	11	56258261	56258261	Missense_Mutation	SNP	A	C	3	84	c.586T>G	c.(586-588)TTG>GTG	p.L196V
Pat_31	Post-Resistance	CCDC88B	283234	37	11	64111735	64111735	Nonsense_Mutation	SNP	G	A	4	93	c.1722G>A	c.(1720-1722)TGG>TGA	p.W574*
Pat_31	Post-Resistance	RPS6KA4	8986	37	11	64129374	64129374	Missense_Mutation	SNP	C	T	5	248	c.806C>T	c.(805-807)GCG>GTG	p.A269V
Pat_31	Post-Resistance	MUS81	80198	37	11	65632782	65632782	Missense_Mutation	SNP	G	A	4	92	c.1493G>A	c.(1492-1494)AGC>AAC	p.S498N
Pat_31	Post-Resistance	C11orf24	53838	37	11	68029495	68029495	Missense_Mutation	SNP	G	A	4	74	c.968C>T	c.(967-969)ACG>ATG	p.T323M
Pat_31	Post-Resistance	ATM	472	37	11	108168038	108168038	Missense_Mutation	SNP	T	C	3	67	c.4934T>C	c.(4933-4935)GTG>GCG	p.V1645A
Pat_31	Post-Resistance	ARHGEF12	23365	37	11	120302604	120302604	Missense_Mutation	SNP	G	A	4	107	c.908G>A	c.(907-909)AGT>AAT	p.S303N
Pat_31	Post-Resistance	SORL1	6653	37	11	121500252	121500252	Missense_Mutation	SNP	G	A	4	104	c.6625G>A	c.(6625-6627)GTC>ATC	p.V2209I
Pat_31	Post-Resistance	SIAE	54414	37	11	124507077	124507077	Nonsense_Mutation	SNP	G	A	5	258	c.1342C>T	c.(1342-1344)CGA>TGA	p.R448*
Pat_31	Post-Resistance	FGF6	2251	37	12	4554680	4554680	Missense_Mutation	SNP	C	A	4	91	c.57G>T	c.(55-57)CAG>CAT	p.Q19H
Pat_31	Post-Resistance	CD163	9332	37	12	7639539	7639539	Missense_Mutation	SNP	C	A	36	80	c.2094G>T	c.(2092-2094)TTG>TTT	p.L698F
Pat_31	Post-Resistance	PRB1	5542	37	12	11506690	11506690	Missense_Mutation	SNP	C	T	60	400	c.347G>A	c.(346-348)GGA>GAA	p.G116E
Pat_31	Post-Resistance	ABCC9	10060	37	12	21981927	21981927	Missense_Mutation	SNP	G	A	110	295	c.3634C>T	c.(3634-3636)CTC>TTC	p.L1212F
Pat_31	Post-Resistance	IPO8	10526	37	12	30790032	30790032	Missense_Mutation	SNP	T	G	73	144	c.2579A>C	c.(2578-2580)CAG>CCG	p.Q860P
Pat_31	Post-Resistance	H3F3C	440093	37	12	31944920	31944920	Missense_Mutation	SNP	G	A	4	146	c.181C>T	c.(181-183)CTC>TTC	p.L61F
Pat_31	Post-Resistance	TUBA1B	10376	37	12	49521767	49521767	Missense_Mutation	SNP	C	T	100	341	c.1330G>A	c.(1330-1332)GGT>AGT	p.G444S
Pat_31	Post-Resistance	TROAP	10024	37	12	49724486	49724486	Missense_Mutation	SNP	G	A	4	49	c.1858G>A	c.(1858-1860)GGG>AGG	p.G620R

Pat_31	Post-Resistance	TARBP2	6895	37	12	53899895	53899895	Missense_Mutation	SNP	C	T	4	114	c.1064C>T	c.(1063-1065)GCC>GTC	p.A355V
Pat_31	Post-Resistance	SRGAP1	57522	37	12	64458916	64458916	Nonsense_Mutation	SNP	C	T	4	142	c.1042C>T	c.(1042-1044)CAG>TAG	p.Q348*
Pat_31	Post-Resistance	FRS2	10818	37	12	69966038	69966038	Missense_Mutation	SNP	C	T	104	173	c.553C>T	c.(553-555)CCT>TCT	p.P185S
Pat_31	Post-Resistance	LGR5	8549	37	12	71978408	71978408	Missense_Mutation	SNP	G	C	5	318	c.2618G>C	c.(2617-2619)AGC>ACC	p.S873T
Pat_31	Post-Resistance	HSP90B1	7184	37	12	104324300	104324300	Missense_Mutation	SNP	G	A	4	126	c.7G>A	c.(7-9)GCC>ACC	p.A3T
Pat_31	Post-Resistance	CMKLR1	1240	37	12	108686070	108686070	Missense_Mutation	SNP	G	A	3	76	c.670C>T	c.(670-672)CGC>TGC	p.R224C
Pat_31	Post-Resistance	SDSL	113675	37	12	113866995	113866995	Missense_Mutation	SNP	C	T	4	151	c.245C>T	c.(244-246)GCT>GTT	p.A82V
Pat_31	Post-Resistance	LHFP	10186	37	13	40175179	40175179	Missense_Mutation	SNP	G	A	133	409	c.175C>T	c.(175-177)CGG>TGG	p.R59W
Pat_31	Post-Resistance	COG6	57511	37	13	40293485	40293485	Missense_Mutation	SNP	G	A	3	57	c.1397G>A	c.(1396-1398)CGT>CAT	p.R466H
Pat_31	Post-Resistance	ERCC5	2073	37	13	103518233	103518233	Missense_Mutation	SNP	C	T	29	95	c.2171C>T	c.(2170-2172)TCG>TTG	p.S724L
Pat_31	Post-Resistance	OR4L1	122742	37	14	20528589	20528589	Missense_Mutation	SNP	C	T	16	44	c.386C>T	c.(385-387)CCC>CTC	p.P129L
Pat_31	Post-Resistance	CHD8	57680	37	14	21868724	21868724	Missense_Mutation	SNP	C	T	3	25	c.3581G>A	c.(3580-3582)CGT>CAT	p.R1194H
Pat_31	Post-Resistance	PNN	5411	37	14	39645289	39645289	Nonsense_Mutation	SNP	C	T	22	57	c.121C>T	c.(121-123)CAA>TAA	p.Q41*
Pat_31	Post-Resistance	KCNH5	27133	37	14	63174990	63174990	Nonsense_Mutation	SNP	G	A	4	20	c.2203C>T	c.(2203-2205)CAG>TAG	p.Q735*
Pat_31	Post-Resistance	AHSA1	10598	37	14	77934803	77934803	Missense_Mutation	SNP	C	T	16	45	c.796C>T	c.(796-798)CCT>TCT	p.P266S
Pat_31	Post-Resistance	C2CD4A	145741	37	15	62359913	62359913	Missense_Mutation	SNP	C	T	6	139	c.101C>T	c.(100-102)ACC>ATC	p.T34I
Pat_31	Post-Resistance	MAP2K1	5604	37	15	66727442	66727442	Missense_Mutation	SNP	T	A	63	90	c.158T>A	c.(157-159)TTT>TAT	p.F53Y
Pat_31	Post-Resistance	C15orf39	56905	37	15	75501033	75501033	Missense_Mutation	SNP	C	T	3	52	c.2644C>T	c.(2644-2646)CGG>TGG	p.R882W
Pat_31	Post-Resistance	FURIN	5045	37	15	91422039	91422039	Missense_Mutation	SNP	G	A	4	151	c.886G>A	c.(886-888)GGG>AGG	p.G296R
Pat_31	Post-Resistance	RGMA	56963	37	15	93595495	93595495	Missense_Mutation	SNP	G	A	4	94	c.373C>T	c.(373-375)CGC>TGC	p.R125C
Pat_31	Post-Resistance	PKD1	5310	37	16	2162933	2162933	Missense_Mutation	SNP	G	A	31	162	c.3017C>T	c.(3016-3018)ACC>ATC	p.T1006I
Pat_31	Post-Resistance	GLYR1	84656	37	16	4871580	4871580	Missense_Mutation	SNP	C	T	4	95	c.700G>A	c.(700-702)GCA>ACA	p.A234T
Pat_31	Post-Resistance	KIAA0430	9665	37	16	15694351	15694351	Missense_Mutation	SNP	C	G	4	142	c.4747G>C	c.(4747-4749)GAG>CAG	p.E1583Q
Pat_31	Post-Resistance	NUP93	9688	37	16	56792560	56792560	Missense_Mutation	SNP	A	G	6	85	c.290A>G	c.(289-291)GAC>GGC	p.D97G
Pat_31	Post-Resistance	DPEP3	64180	37	16	68012486	68012486	Missense_Mutation	SNP	G	A	9	523	c.533C>T	c.(532-534)GCC>GTC	p.A178V
Pat_31	Post-Resistance	AP1G1	164	37	16	71823331	71823331	Nonsense_Mutation	SNP	G	A	29	181	c.52C>T	c.(52-54)CGA>TGA	p.R18*
Pat_31	Post-Resistance	CLEC18B	497190	37	16	74446997	74446997	Missense_Mutation	SNP	G	A	20	108	c.614C>T	c.(613-615)TCG>TTG	p.S205L
Pat_31	Post-Resistance	LDHD	197257	37	16	75148022	75148022	Missense_Mutation	SNP	C	T	4	148	c.740G>A	c.(739-741)GGC>GAC	p.G247D
Pat_31	Post-Resistance	C17orf97	400566	37	17	263384	263384	Missense_Mutation	SNP	G	C	4	33	c.780G>C	c.(778-780)GAG>GAC	p.E260D
Pat_31	Post-Resistance	SMYD4	114826	37	17	1703561	1703561	Missense_Mutation	SNP	T	C	4	181	c.1127A>G	c.(1126-1128)AAC>AGC	p.N376S
Pat_31	Post-Resistance	KIAA0664	23277	37	17	2598703	2598703	Missense_Mutation	SNP	G	A	8	208	c.2392C>T	c.(2392-2394)CGG>TGG	p.R798W
Pat_31	Post-Resistance	ATP2A3	489	37	17	3850912	3850912	Missense_Mutation	SNP	G	A	4	123	c.868C>T	c.(868-870)CGT>TGT	p.R290C
Pat_31	Post-Resistance	SPNS3	201305	37	17	4389577	4389577	Missense_Mutation	SNP	G	A	18	92	c.1234G>A	c.(1234-1236)GGC>AGC	p.G412S
Pat_31	Post-Resistance	SLC25A11	8402	37	17	4841512	4841512	Missense_Mutation	SNP	G	A	4	89	c.674C>T	c.(673-675)GCC>GTC	p.A225V
Pat_31	Post-Resistance	NLRP1	22861	37	17	5442796	5442796	Missense_Mutation	SNP	C	T	5	90	c.2809G>A	c.(2809-2811)GTT>ATT	p.V937I
Pat_31	Post-Resistance	C17orf74	201243	37	17	7330590	7330590	Missense_Mutation	SNP	C	T	19	79	c.1280C>T	c.(1279-1281)TCC>TTC	p.S427F
Pat_31	Post-Resistance	MYH13	8735	37	17	10216611	10216611	Missense_Mutation	SNP	C	T	6	345	c.4045G>A	c.(4045-4047)GAA>AAA	p.E1349K
Pat_31	Post-Resistance	SREBF1	6720	37	17	17720337	17720337	Missense_Mutation	SNP	G	A	7	200	c.1720C>T	c.(1720-1722)CCC>TCC	p.P574S
Pat_31	Post-Resistance	SLFN5	162394	37	17	33586620	33586620	Missense_Mutation	SNP	C	T	5	298	c.911C>T	c.(910-912)GCG>GTG	p.A304V
Pat_31	Post-Resistance	STARD3	10948	37	17	37809893	37809893	Missense_Mutation	SNP	C	T	4	84	c.109C>T	c.(109-111)CTT>TTT	p.L37F
Pat_31	Post-Resistance	GSDMB	55876	37	17	38068616	38068616	Missense_Mutation	SNP	G	A	4	87	c.370C>T	c.(370-372)CGG>TGG	p.R124W
Pat_31	Post-Resistance	KRT39	390792	37	17	39122910	39122910	Missense_Mutation	SNP	G	A	6	274	c.199C>T	c.(199-201)CGC>TGC	p.R67C
Pat_31	Post-Resistance	KRTAP4-8	728224	37	17	39254013	39254013	Missense_Mutation	SNP	G	C	4	119	c.324C>G	c.(322-324)AGC>AGG	p.S108R
Pat_31	Post-Resistance	KRTAP4-5	85289	37	17	39305839	39305839	Missense_Mutation	SNP	A	T	5	121	c.181T>A	c.(181-183)TGC>AGC	p.C61S
Pat_31	Post-Resistance	KRT17	3872	37	17	39780455	39780455	Missense_Mutation	SNP	G	A	5	321	c.307C>T	c.(307-309)CGT>TGT	p.R103C
Pat_31	Post-Resistance	STAT5B	6777	37	17	40359636	40359636	Missense_Mutation	SNP	G	A	6	245	c.2017C>T	c.(2017-2019)CGG>TGG	p.R673W
Pat_31	Post-Resistance	CNTNAP1	8506	37	17	40847757	40847757	Missense_Mutation	SNP	G	A	4	110	c.3211G>A	c.(3211-3213)GGT>AGT	p.G1071S

Pat_31	Post-Resistance	HDAC5	10014	37	17	42155941	42155941	Missense_Mutation	SNP	C	T	9	271	c.3256G>A	c.(3256-3258)GTG>ATG	p.V1086M
Pat_31	Post-Resistance	UTP18	51096	37	17	49343583	49343583	Nonsense_Mutation	SNP	A	T	4	93	c.496A>T	c.(496-498)AAA>TAA	p.K166*
Pat_31	Post-Resistance	ATP5H	10476	37	17	73035082	73035082	Missense_Mutation	SNP	T	A	19	16	c.431A>T	c.(430-432)AAA>ATA	p.K144I
Pat_31	Post-Resistance	EMILIN2	84034	37	18	2884967	2884967	Missense_Mutation	SNP	G	A	4	114	c.263G>A	c.(262-264)CGA>CAA	p.R88Q
Pat_31	Post-Resistance	KIAA0802	23255	37	18	8798224	8798224	Missense_Mutation	SNP	C	T	4	129	c.2371C>T	c.(2371-2373)CGG>TGG	p.R791W
Pat_31	Post-Resistance	APCDD1	147495	37	18	10471816	10471816	Missense_Mutation	SNP	G	A	4	127	c.532G>A	c.(532-534)GGG>AGG	p.G178R
Pat_31	Post-Resistance	MYO5B	4645	37	18	47352938	47352938	Missense_Mutation	SNP	A	G	4	132	c.5450T>C	c.(5449-5451)ATG>ACG	p.M1817T
Pat_31	Post-Resistance	WDR7	23335	37	18	54339789	54339789	Nonsense_Mutation	SNP	C	T	4	84	c.43C>T	c.(43-45)CGA>TGA	p.R15*
Pat_31	Post-Resistance	CNDP1	84735	37	18	72250923	72250923	Missense_Mutation	SNP	C	T	4	103	c.1436C>T	c.(1435-1437)TCG>TTG	p.S479L
Pat_31	Post-Resistance	ZNF407	55628	37	18	72344495	72344495	Missense_Mutation	SNP	G	A	3	55	c.1520G>A	c.(1519-1521)CGT>CAT	p.R507H
Pat_31	Post-Resistance	TSHZ1	10194	37	18	72998489	72998489	Missense_Mutation	SNP	T	C	4	81	c.992T>C	c.(991-993)CTG>CCG	p.L331P
Pat_31	Post-Resistance	PNPLA6	10908	37	19	7605863	7605863	Missense_Mutation	SNP	G	A	4	40	c.877G>A	c.(877-879)GTG>ATG	p.V293M
Pat_31	Post-Resistance	MUC16	94025	37	19	9059142	9059142	Missense_Mutation	SNP	G	A	15	46	c.28304C>T	c.(28303-28305)TCC>TTC	p.S9435F
Pat_31	Post-Resistance	MUC16	94025	37	19	9066741	9066741	Missense_Mutation	SNP	G	A	26	100	c.20705C>T	c.(20704-20706)TCC>TTC	p.S6902F
Pat_31	Post-Resistance	C19orf66	55337	37	19	10202839	10202839	Missense_Mutation	SNP	G	A	4	100	c.737G>A	c.(736-738)AGC>AAC	p.S246N
Pat_31	Post-Resistance	KANK2	25959	37	19	11280876	11280876	Missense_Mutation	SNP	C	T	4	125	c.2260G>A	c.(2260-2262)GTT>ATT	p.V754I
Pat_31	Post-Resistance	ACP5	54	37	19	11687174	11687174	Missense_Mutation	SNP	G	A	4	84	c.619C>T	c.(619-621)CCC>TCC	p.P207S
Pat_31	Post-Resistance	CC2D1A	54862	37	19	14031733	14031733	Missense_Mutation	SNP	A	G	3	83	c.1639A>G	c.(1639-1641)AAG>GAG	p.K547E
Pat_31	Post-Resistance	ZNF430	80264	37	19	21240459	21240459	Missense_Mutation	SNP	A	G	6	123	c.1345A>G	c.(1345-1347)ATA>GTA	p.I449V
Pat_31	Post-Resistance	ZNF430	80264	37	19	21240468	21240468	Missense_Mutation	SNP	A	T	6	134	c.1354A>T	c.(1354-1356)ACT>TCT	p.T452S
Pat_31	Post-Resistance	ZNF676	163223	37	19	22362924	22362924	Missense_Mutation	SNP	G	C	4	192	c.1595C>G	c.(1594-1596)CCC>CGC	p.P532R
Pat_31	Post-Resistance	ANKRD27	84079	37	19	33113428	33113428	Missense_Mutation	SNP	C	T	4	132	c.1727G>A	c.(1726-1728)GGC>GAC	p.G576D
Pat_31	Post-Resistance	RHPN2	85415	37	19	33493266	33493266	Missense_Mutation	SNP	G	A	4	132	c.992C>T	c.(991-993)GCG>GTG	p.A331V
Pat_31	Post-Resistance	ZNF599	148103	37	19	35258305	35258305	Missense_Mutation	SNP	G	A	22	54	c.157C>T	c.(157-159)CCC>TCC	p.P53S
Pat_31	Post-Resistance	ZNF567	163081	37	19	37211295	37211295	Missense_Mutation	SNP	G	A	4	108	c.1669G>A	c.(1669-1671)GGC>AGC	p.G557S
Pat_31	Post-Resistance	FCGBP	8857	37	19	40392568	40392568	Missense_Mutation	SNP	C	T	10	57	c.7936G>A	c.(7936-7938)GAG>AAG	p.E2646K
Pat_31	Post-Resistance	SIX5	147912	37	19	46271427	46271427	Missense_Mutation	SNP	G	A	4	54	c.676C>T	c.(676-678)CCC>TCC	p.P226S
Pat_31	Post-Resistance	PPP5C	5536	37	19	46891861	46891861	Missense_Mutation	SNP	G	A	4	45	c.1228G>A	c.(1228-1230)GTC>ATC	p.V410I
Pat_31	Post-Resistance	PRKD2	25865	37	19	47177818	47177818	Missense_Mutation	SNP	C	T	4	62	c.2599G>A	c.(2599-2601)GAC>AAC	p.D867N
Pat_31	Post-Resistance	PRKD2	25865	37	19	47197209	47197209	Nonsense_Mutation	SNP	C	T	4	77	c.1499G>A	c.(1498-1500)TGG>TAG	p.W500*
Pat_31	Post-Resistance	AP2S1	1175	37	19	47342032	47342032	Missense_Mutation	SNP	C	T	4	55	c.292G>A	c.(292-294)GTC>ATC	p.V98I
Pat_31	Post-Resistance	ATF5	22809	37	19	50435732	50435732	Missense_Mutation	SNP	C	T	35	148	c.232C>T	c.(232-234)CCT>TCT	p.P78S
Pat_31	Post-Resistance	ZNF701	55762	37	19	53086622	53086622	Missense_Mutation	SNP	C	G	5	65	c.1310C>G	c.(1309-1311)CCT>CGT	p.P437R
Pat_31	Post-Resistance	OSCAR	126014	37	19	54600311	54600311	Missense_Mutation	SNP	C	T	4	123	c.286G>A	c.(286-288)GCT>ACT	p.A96T
Pat_31	Post-Resistance	LILRA3	11026	37	19	54802518	54802518	Missense_Mutation	SNP	G	A	4	88	c.923C>T	c.(922-924)TCG>TTG	p.S308L
Pat_31	Post-Resistance	LILRA4	23547	37	19	54848270	54848270	Missense_Mutation	SNP	C	T	5	183	c.1097G>A	c.(1096-1098)CGT>CAT	p.R366H
Pat_31	Post-Resistance	NLRP2	55655	37	19	55492996	55492996	Missense_Mutation	SNP	A	T	4	55	c.409A>T	c.(409-411)ACG>TCG	p.T137S
Pat_31	Post-Resistance	ZNF551	90233	37	19	58196694	58196694	Missense_Mutation	SNP	C	T	20	54	c.98C>T	c.(97-99)TCT>TTT	p.S33F
Pat_31	Post-Resistance	ZNF606	80095	37	19	58490292	58490292	Missense_Mutation	SNP	G	T	18	56	c.1756C>A	c.(1756-1758)CAT>AAT	p.H586N
Pat_31	Post-Resistance	KHK	3795	37	2	27317458	27317458	Missense_Mutation	SNP	G	A	6	359	c.323G>A	c.(322-324)CGC>CAC	p.R108H
Pat_31	Post-Resistance	ATL2	64225	37	2	38545777	38545777	Missense_Mutation	SNP	G	A	4	57	c.503C>T	c.(502-504)GCT>GTT	p.A168V
Pat_31	Post-Resistance	ITPRIPL1	150771	37	2	96992716	96992716	Missense_Mutation	SNP	G	A	3	51	c.347G>A	c.(346-348)GGC>GAC	p.G116D
Pat_31	Post-Resistance	ANKRD39	51239	37	2	97519242	97519242	Missense_Mutation	SNP	G	T	4	96	c.304C>A	c.(304-306)CAC>AAC	p.H102N
Pat_31	Post-Resistance	SEMA4C	54910	37	2	97529774	97529774	Missense_Mutation	SNP	G	A	4	93	c.1219C>T	c.(1219-1221)CGG>TGG	p.R407W
Pat_31	Post-Resistance	GLI2	2736	37	2	121748042	121748042	Missense_Mutation	SNP	G	A	63	194	c.4552G>A	c.(4552-4554)GAT>AAT	p.D1518N
Pat_31	Post-Resistance	UGGT1	56886	37	2	128848960	128848960	Missense_Mutation	SNP	C	T	4	63	c.29C>T	c.(28-30)GCG>GTG	p.A10V
Pat_31	Post-Resistance	LRP1B	53353	37	2	141208192	141208192	Nonsense_Mutation	SNP	C	T	45	241	c.10002G>A	c.(10000-10002)TGG>TGA	p.W3334*

Pat_31	Post-Resistance	PDK1	5163	37	2	173423531	173423531	Missense_Mutation	SNP	C	T	10	66	c.292C>T	c.(292-294)CCA>TCA	p.P98S
Pat_31	Post-Resistance	TTN	7273	37	2	179611379	179611379	Missense_Mutation	SNP	C	T	4	87	c.15748G>A	.(15748-15750)GGG>AG	p.G5250R
Pat_31	Post-Resistance	TTN	7273	37	2	179632598	179632598	Missense_Mutation	SNP	C	T	18	105	c.9359G>A	c.(9358-9360)CGG>CAG	p.R3120Q
Pat_31	Post-Resistance	DNAH7	56171	37	2	196737150	196737150	Missense_Mutation	SNP	C	T	89	77	c.6457G>A	c.(6457-6459)GTA>ATA	p.V2153I
Pat_31	Post-Resistance	EEF1B2	1933	37	2	207025358	207025358	Missense_Mutation	SNP	A	G	9	490	c.127A>G	c.(127-129)AGC>GGC	p.S43G
Pat_31	Post-Resistance	ABCA12	26154	37	2	215876189	215876189	Missense_Mutation	SNP	G	A	6	7	c.2306C>T	c.(2305-2307)TCA>TTA	p.S769L
Pat_31	Post-Resistance	SP140	11262	37	2	231150484	231150484	Missense_Mutation	SNP	G	A	124	109	c.1582G>A	c.(1582-1584)GGC>AGC	p.G528S
Pat_31	Post-Resistance	CHRND	1144	37	2	233392156	233392156	Splice_Site	SNP	G	A	4	62	c.243_splice	c.e3+1	p.H81_splice
Pat_31	Post-Resistance	NGEF	25791	37	2	233757732	233757732	Missense_Mutation	SNP	C	T	31	91	c.1018G>A	c.(1018-1020)GAG>AAG	p.E340K
Pat_31	Post-Resistance	NEU2	4759	37	2	233899297	233899297	Missense_Mutation	SNP	G	A	4	105	c.673G>A	c.(673-675)GAG>AAG	p.E225K
Pat_31	Post-Resistance	COL6A3	1293	37	2	238277739	238277739	Missense_Mutation	SNP	C	T	4	76	c.4367G>A	c.(4366-4368)CGA>CAA	p.R1456Q
Pat_31	Post-Resistance	IDH3B	3420	37	20	2640783	2640783	Missense_Mutation	SNP	G	A	5	301	c.808C>T	c.(808-810)CCC>TCC	p.P270S
Pat_31	Post-Resistance	PANK2	80025	37	20	3888897	3888897	Missense_Mutation	SNP	C	T	3	29	c.953C>T	c.(952-954)GCG>GTG	p.A318V
Pat_31	Post-Resistance	C20orf103	24141	37	20	9496924	9496924	Missense_Mutation	SNP	G	A	4	116	c.391G>A	c.(391-393)GGA>AGA	p.G131R
Pat_31	Post-Resistance	RPN2	6185	37	20	35852373	35852373	Splice_Site	SNP	G	A	4	115	c.1184_splice	c.e10+1	p.R395_splice
Pat_31	Post-Resistance	RALGAPB	57148	37	20	37117167	37117167	Missense_Mutation	SNP	G	A	6	352	c.92G>A	c.(91-93)CGA>CAA	p.R31Q
Pat_31	Post-Resistance	PREX1	57580	37	20	47244484	47244484	Missense_Mutation	SNP	G	A	8	90	c.4784C>T	c.(4783-4785)TCC>TTC	p.S1595F
Pat_31	Post-Resistance	PTGIS	5740	37	20	48129663	48129663	Missense_Mutation	SNP	G	A	37	149	c.1160C>T	c.(1159-1161)CCC>CTC	p.P387L
Pat_31	Post-Resistance	TSHZ2	128553	37	20	51872447	51872447	Missense_Mutation	SNP	C	T	36	49	c.2450C>T	c.(2449-2451)CCC>CTC	p.P817L
Pat_31	Post-Resistance	PRPF6	24148	37	20	62664327	62664327	Missense_Mutation	SNP	G	A	7	231	c.2807G>A	c.(2806-2808)CGC>CAC	p.R936H
Pat_31	Post-Resistance	ADAMTS1	9510	37	21	28212314	28212314	Missense_Mutation	SNP	C	T	4	126	c.1732G>A	c.(1732-1734)GGA>AGA	p.G578R
Pat_31	Post-Resistance	CHEK2	11200	37	22	29091840	29091841	Missense_Mutation	DNP	TG	CA	4	34	.1116_1117CA>T	114-1119)TCCAAG>TCTG	p.K373E
Pat_31	Post-Resistance	SCUBE1	80274	37	22	43610107	43610107	Missense_Mutation	SNP	G	A	4	142	c.2042C>T	c.(2041-2043)TCG>TTG	p.S681L
Pat_31	Post-Resistance	PHF21B	112885	37	22	45279115	45279115	Missense_Mutation	SNP	G	A	4	149	c.1447C>T	c.(1447-1449)CGG>TGG	p.R483W
Pat_31	Post-Resistance	PLXNB2	23654	37	22	50728563	50728563	Missense_Mutation	SNP	C	T	3	40	c.451G>A	c.(451-453)GTG>ATG	p.V151M
Pat_31	Post-Resistance	HDAC11	79885	37	3	13545696	13545696	Missense_Mutation	SNP	C	T	4	66	c.752C>T	c.(751-753)CCC>CTC	p.P251L
Pat_31	Post-Resistance	SLC22A13	9390	37	3	38317807	38317807	Missense_Mutation	SNP	G	A	4	145	c.1267G>A	c.(1267-1269)GTG>ATG	p.V423M
Pat_31	Post-Resistance	SCN10A	6336	37	3	38768102	38768102	Nonsense_Mutation	SNP	C	A	12	24	c.3082G>T	c.(3082-3084)GGA>TGA	p.G1028*
Pat_31	Post-Resistance	CTNNB1	1499	37	3	41275191	41275191	Missense_Mutation	SNP	C	T	4	133	c.1357C>T	c.(1357-1359)CGG>TGG	p.R453W
Pat_31	Post-Resistance	CCR2	729230	37	3	46401317	46401317	Missense_Mutation	SNP	C	T	20	16	c.1091C>T	c.(1090-1092)CCT>CTT	p.P364L
Pat_31	Post-Resistance	CACNA1D	776	37	3	53844263	53844263	Missense_Mutation	SNP	C	T	4	162	c.6130C>T	c.(6130-6132)CCC>TCC	p.P2044S
Pat_31	Post-Resistance	ASB14	142686	37	3	57312490	57312490	Missense_Mutation	SNP	C	T	111	126	c.854G>A	c.(853-855)CGA>CAA	p.R285Q
Pat_31	Post-Resistance	FLNB	2317	37	3	58116605	58116605	Missense_Mutation	SNP	C	T	14	27	c.4360C>T	c.(4360-4362)CCG>TCG	p.P1454S
Pat_31	Post-Resistance	OR5H2	79310	37	3	98002105	98002105	Missense_Mutation	SNP	A	G	4	106	c.374A>G	c.(373-375)TAT>TGT	p.Y125C
Pat_31	Post-Resistance	FSTL1	11167	37	3	120121655	120121655	Missense_Mutation	SNP	C	T	4	162	c.805G>A	c.(805-807)GGA>AGA	p.G269R
Pat_31	Post-Resistance	MCM2	4171	37	3	127325611	127325611	Missense_Mutation	SNP	C	T	80	71	c.1052C>T	c.(1051-1053)TCC>TTC	p.S351F
Pat_31	Post-Resistance	CRIPAK	285464	37	4	1389062	1389062	Nonsense_Mutation	SNP	C	T	9	741	c.763C>T	c.(763-765)CGA>TGA	p.R255*
Pat_31	Post-Resistance	LRRC66	339977	37	4	52860901	52860901	Missense_Mutation	SNP	G	A	7	49	c.2287C>T	c.(2287-2289)CCA>TCA	p.P763S
Pat_31	Post-Resistance	TMPRSS11F	389208	37	4	68934445	68934445	Missense_Mutation	SNP	C	T	5	149	c.646G>A	c.(646-648)GGG>AGG	p.G216R
Pat_31	Post-Resistance	AFF1	4299	37	4	88055758	88055758	Missense_Mutation	SNP	G	T	5	292	c.3423G>T	c.(3421-3423)ATG>ATT	p.M1141I
Pat_31	Post-Resistance	ANK2	287	37	4	114275524	114275524	Missense_Mutation	SNP	C	T	3	35	c.5750C>T	c.(5749-5751)TCG>TTG	p.S1917L
Pat_31	Post-Resistance	FAT4	79633	37	4	126328170	126328170	Missense_Mutation	SNP	C	T	119	216	c.5443C>T	c.(5443-5445)CGT>TGT	p.R1815C
Pat_31	Post-Resistance	GRIA2	2891	37	4	158281195	158281195	Missense_Mutation	SNP	G	A	4	119	c.2191G>A	c.(2191-2193)GAG>AAG	p.E731K
Pat_31	Post-Resistance	ODZ3	55714	37	4	183674704	183674704	Missense_Mutation	SNP	G	A	21	61	c.3964G>A	c.(3964-3966)GAT>AAT	p.D1322N
Pat_31	Post-Resistance	CDH10	1008	37	5	24511590	24511590	Missense_Mutation	SNP	G	A	6	32	c.848C>T	c.(847-849)CCA>CTA	p.P283L
Pat_31	Post-Resistance	IL7R	3575	37	5	35876293	35876293	Missense_Mutation	SNP	G	A	5	46	c.1085G>A	c.(1084-1086)GGA>GAA	p.G362E
Pat_31	Post-Resistance	STARD4	134429	37	5	110837705	110837705	Nonsense_Mutation	SNP	C	T	4	102	c.237G>A	c.(235-237)TGG>TGA	p.W79*

Pat_31	Post-Resistance	DCP2	167227	37	5	112339673	112339673	Missense_Mutation	SNP	C	T	9	66	c.841C>T	c.(841-843)CCT>TCT	p.P281S
Pat_31	Post-Resistance	TRPC7	57113	37	5	135587495	135587495	Missense_Mutation	SNP	A	G	3	120	c.1418T>C	c.(1417-1419)CTA>CCA	p.L473P
Pat_31	Post-Resistance	TRPC7	57113	37	5	135692613	135692613	Missense_Mutation	SNP	C	T	4	154	c.460G>A	c.(460-462)GAC>AAC	p.D154N
Pat_31	Post-Resistance	PSD2	84249	37	5	139193118	139193118	Missense_Mutation	SNP	G	A	4	129	c.596G>A	c.(595-597)GGC>GAC	p.G199D
Pat_31	Post-Resistance	ARHGAP26	23092	37	5	142586768	142586768	Missense_Mutation	SNP	C	T	4	156	c.1994C>T	c.(1993-1995)CCG>CTG	p.P665L
Pat_31	Post-Resistance	TCOF1	6949	37	5	149772343	149772343	Missense_Mutation	SNP	C	T	3	56	c.3590C>T	c.(3589-3591)GCG>GTG	p.A1197V
Pat_31	Post-Resistance	GPRIN1	114787	37	5	176023846	176023846	Missense_Mutation	SNP	G	A	3	67	c.2990C>T	c.(2989-2991)CCG>CTG	p.P997L
Pat_31	Post-Resistance	EXOC2	55770	37	6	564149	564149	Missense_Mutation	SNP	G	A	4	98	c.1673C>T	c.(1672-1674)ACT>ATT	p.T558I
Pat_31	Post-Resistance	HIST1H4F	8361	37	6	26240762	26240762	Missense_Mutation	SNP	C	T	3	62	c.109C>T	c.(109-111)CGC>TGC	p.R37C
Pat_31	Post-Resistance	BTN2A1	11120	37	6	26460026	26460026	Missense_Mutation	SNP	G	A	4	60	c.400G>A	c.(400-402)GAT>AAT	p.D134N
Pat_31	Post-Resistance	ZSCAN16	80345	37	6	28097614	28097614	Missense_Mutation	SNP	G	C	11	60	c.933G>C	c.(931-933)CAG>CAC	p.Q311H
Pat_31	Post-Resistance	BAT2	7916	37	6	31600180	31600180	Nonsense_Mutation	SNP	C	T	4	82	c.3730C>T	c.(3730-3732)CGA>TGA	p.R1244*
Pat_31	Post-Resistance	C6orf27	80737	37	6	31737520	31737520	Missense_Mutation	SNP	C	T	47	120	c.1249G>A	c.(1249-1251)GAT>AAT	p.D417N
Pat_31	Post-Resistance	TNXB	7148	37	6	32021309	32021309	Missense_Mutation	SNP	C	T	25	92	c.8641G>A	c.(8641-8643)GGG>AGG	p.G2881R
Pat_31	Post-Resistance	PBX2	5089	37	6	32157481	32157481	Missense_Mutation	SNP	G	C	3	158	c.212C>G	c.(211-213)GCC>GGC	p.A71G
Pat_31	Post-Resistance	GRIK2	2898	37	6	102307177	102307177	Missense_Mutation	SNP	C	T	3	20	c.1333C>T	c.(1333-1335)CTT>TTT	p.L445F
Pat_31	Post-Resistance	BEND3	57673	37	6	107390596	107390596	Missense_Mutation	SNP	G	A	13	21	c.1799C>T	c.(1798-1800)TCC>TTC	p.S600F
Pat_31	Post-Resistance	TULP4	56995	37	6	158924649	158924650	Missense_Mutation	DNP	CC	TT	7	25	.3954_3955CC>T	952-3957)GTCCTC>GTTT	p.L1319F
Pat_31	Post-Resistance	FNDC1	84624	37	6	159636091	159636091	Missense_Mutation	SNP	G	A	4	133	c.575G>A	c.(574-576)CGG>CAG	p.R192Q
Pat_31	Post-Resistance	PNLDC1	154197	37	6	160240351	160240351	Nonsense_Mutation	SNP	G	A	4	129	c.1466G>A	c.(1465-1467)TGG>TAG	p.W489*
Pat_31	Post-Resistance	AGPAT4	56895	37	6	161587390	161587390	Missense_Mutation	SNP	G	A	40	99	c.238C>T	c.(238-240)CGC>TGC	p.R80C
Pat_31	Post-Resistance	OSBPL3	26031	37	7	24854801	24854801	Nonsense_Mutation	SNP	C	T	25	57	c.2049G>A	c.(2047-2049)TGG>TGA	p.W683*
Pat_31	Post-Resistance	GARS	2617	37	7	30661106	30661106	Missense_Mutation	SNP	T	A	6	204	c.1457T>A	c.(1456-1458)CTG>CAG	p.L486Q
Pat_31	Post-Resistance	MYO1G	64005	37	7	45009452	45009452	Missense_Mutation	SNP	G	A	82	222	c.1355C>T	c.(1354-1356)ACC>ATC	p.T452I
Pat_31	Post-Resistance	ZNF716	441234	37	7	57529107	57529107	Missense_Mutation	SNP	C	T	5	145	c.940C>T	c.(940-942)CAC>TAC	p.H314Y
Pat_31	Post-Resistance	ABCB1	5243	37	7	87168622	87168622	Missense_Mutation	SNP	G	A	4	136	c.2359C>T	c.(2359-2361)CGG>TGG	p.R787W
Pat_31	Post-Resistance	PPP1R9A	55607	37	7	94876803	94876803	Missense_Mutation	SNP	G	A	4	80	c.2065G>A	c.(2065-2067)GTT>ATT	p.V689I
Pat_31	Post-Resistance	SLC25A13	10165	37	7	95822414	95822414	Nonsense_Mutation	SNP	G	A	6	272	c.550C>T	c.(550-552)CGA>TGA	p.R184*
Pat_31	Post-Resistance	GAL3ST4	79690	37	7	99758125	99758125	Missense_Mutation	SNP	G	A	81	289	c.887C>T	c.(886-888)TCT>TTT	p.S296F
Pat_31	Post-Resistance	AGFG2	3268	37	7	100151115	100151115	Missense_Mutation	SNP	T	C	5	176	c.577T>C	c.(577-579)TCG>CCG	p.S193P
Pat_31	Post-Resistance	DGKI	9162	37	7	137374674	137374674	Missense_Mutation	SNP	G	A	4	152	c.476C>T	c.(475-477)CCA>CTA	p.P159L
Pat_31	Post-Resistance	BRAF	673	37	7	140453136	140453136	Missense_Mutation	SNP	A	T	59	91	c.1799T>A	c.(1798-1800)GTG>GAG	p.V600E
Pat_31	Post-Resistance	ABP1	26	37	7	150555107	150555107	Missense_Mutation	SNP	C	T	6	318	c.1549C>T	c.(1549-1551)CGC>TGC	p.R517C
Pat_31	Post-Resistance	USP17L2	377630	37	8	11995399	11995399	Missense_Mutation	SNP	G	T	7	231	c.871C>A	c.(871-873)CTT>ATT	p.L291I
Pat_31	Post-Resistance	KIF13B	23303	37	8	28980923	28980924	Missense_Mutation	DNP	GG	TA	47	162	.3438_3439CC>T	436-3441)GTCCCC>GTTA	p.P1147T
Pat_31	Post-Resistance	DDHD2	23259	37	8	38090565	38090565	Missense_Mutation	SNP	C	T	4	155	c.53C>T	c.(52-54)CCG>CTG	p.P18L
Pat_31	Post-Resistance	MYST3	7994	37	8	41798364	41798364	Missense_Mutation	SNP	C	T	166	387	c.3035G>A	c.(3034-3036)CGA>CAA	p.R1012Q
Pat_31	Post-Resistance	OPRK1	4986	37	8	54142245	54142245	Missense_Mutation	SNP	C	T	32	64	c.755G>A	c.(754-756)CGT>CAT	p.R252H
Pat_31	Post-Resistance	FAM110B	90362	37	8	59059012	59059012	Missense_Mutation	SNP	G	A	4	115	c.223G>A	c.(223-225)GTG>ATG	p.V75M
Pat_31	Post-Resistance	C8orf34	116328	37	8	69445300	69445300	Missense_Mutation	SNP	G	A	39	125	c.763G>A	c.(763-765)GAT>AAT	p.D255N
Pat_31	Post-Resistance	EIF2C2	27161	37	8	141595393	141595393	Missense_Mutation	SNP	G	A	5	260	c.40C>T	c.(40-42)CCG>TCG	p.P14S
Pat_31	Post-Resistance	PLEC	5339	37	8	144997771	144997771	Missense_Mutation	SNP	C	T	4	109	c.6737G>A	c.(6736-6738)CGG>CAG	p.R2246Q
Pat_31	Post-Resistance	ZNF251	90987	37	8	145947717	145947717	Missense_Mutation	SNP	C	T	40	39	c.1328G>A	c.(1327-1329)CGT>CAT	p.R443H
Pat_31	Post-Resistance	MLLT3	4300	37	9	20414323	20414323	Missense_Mutation	SNP	C	T	3	66	c.521G>A	c.(520-522)AGC>AAC	p.S174N
Pat_31	Post-Resistance	ELAVL2	1993	37	9	23692733	23692733	Missense_Mutation	SNP	G	A	4	154	c.902C>T	c.(901-903)GCT>GTT	p.A301V
Pat_31	Post-Resistance	BAG1	573	37	9	33261107	33261107	Missense_Mutation	SNP	C	T	4	152	c.641G>A	c.(640-642)CGG>CAG	p.R214Q
Pat_31	Post-Resistance	NFX1	4799	37	9	33313755	33313755	Missense_Mutation	SNP	G	A	5	219	c.1552G>A	c.(1552-1554)GGT>AGT	p.G518S

Pat_31	Post-Resistance	NOL6	65083	37	9	33466592	33466592	Missense_Mutation	SNP	G	A	4	126	c.2066C>T	c.(2065-2067)GCT>GTT	p.A689V
Pat_31	Post-Resistance	FAM22F	54754	37	9	97084549	97084549	Missense_Mutation	SNP	T	C	6	190	c.776A>G	c.(775-777)CAG>CGG	p.Q259R
Pat_31	Post-Resistance	STXBP1	6812	37	9	130415992	130415992	Splice_Site	SNP	A	G	3	131	c.88_splice	c.e3-2	p.V30_splice
Pat_31	Post-Resistance	SARDH	1757	37	9	136584125	136584125	Missense_Mutation	SNP	G	A	4	108	c.955C>T	c.(955-957)CTC>TTC	p.L319F
Pat_31	Post-Resistance	COL5A1	1289	37	9	137620526	137620526	Missense_Mutation	SNP	G	A	59	82	c.797G>A	c.(796-798)GGA>GAA	p.G266E
Pat_31	Post-Resistance	MID1	4281	37	X	10535412	10535412	Missense_Mutation	SNP	C	A	4	114	c.176G>T	c.(175-177)TGC>TTC	p.C59F
Pat_31	Post-Resistance	WAS	7454	37	X	48544334	48544334	Splice_Site	SNP	G	A	33	28	c.464_splice	c.e5-1	p.D155_splice
Pat_31	Post-Resistance	SPIN2A	54466	37	X	57162607	57162607	Missense_Mutation	SNP	C	T	4	146	c.424G>A	c.(424-426)GGT>AGT	p.G142S
Pat_31	Post-Resistance	ABCB7	22	37	X	74282185	74282185	Missense_Mutation	SNP	G	A	3	18	c.1913C>T	c.(1912-1914)TCG>TTG	p.S638L
Pat_31	Post-Resistance	DOCK11	139818	37	X	117722261	117722261	Missense_Mutation	SNP	G	A	27	12	c.1957G>A	c.(1957-1959)GAT>AAT	p.D653N
Pat_31	Post-Resistance	MAGEC1	9947	37	X	140994923	140994923	Missense_Mutation	SNP	A	T	5	289	c.1733A>T	c.(1732-1734)CAC>CTC	p.H578L
Pat_31	Post-Resistance	ZNF185	7739	37	X	152088906	152088906	Missense_Mutation	SNP	G	A	4	146	c.565G>A	c.(565-567)GCT>ACT	p.A189T
Pat_31	Post-Resistance	DNASE1L1	1774	37	X	153631344	153631344	Missense_Mutation	SNP	C	T	4	132	c.713G>A	c.(712-714)AGT>AAT	p.S238N
Pat_32	Pre-Treatment	CPSF3L	54973	37	1	1249252	1249252	Missense_Mutation	SNP	C	T	4	179	c.817G>A	c.(817-819)GAG>AAG	p.E273K
Pat_32	Pre-Treatment	MASP2	10747	37	1	11105485	11105485	Missense_Mutation	SNP	C	T	3	37	c.524G>A	c.(523-525)CGT>CAT	p.R175H
Pat_32	Pre-Treatment	MFN2	9927	37	1	12056305	12056305	Missense_Mutation	SNP	G	A	4	53	c.404G>A	c.(403-405)CGG>CAG	p.R135Q
Pat_32	Pre-Treatment	ARHGEF19	128272	37	1	16529023	16529023	Nonsense_Mutation	SNP	G	A	4	107	c.1954C>T	c.(1954-1956)CAG>TAG	p.Q652*
Pat_32	Pre-Treatment	IGSF21	84966	37	1	18691918	18691918	Missense_Mutation	SNP	C	A	36	67	c.742C>A	c.(742-744)CGT>AGT	p.R248S
Pat_32	Pre-Treatment	UBR4	23352	37	1	19421483	19421483	Missense_Mutation	SNP	C	T	4	173	c.13663G>A	c.(13663-13665)GGT>AGT	p.G4555S
Pat_32	Pre-Treatment	HSPG2	3339	37	1	22170750	22170750	Missense_Mutation	SNP	G	A	5	109	c.8507C>T	c.(8506-8508)TCC>TTC	p.S2836F
Pat_32	Pre-Treatment	EPHB2	2048	37	1	23239043	23239043	Missense_Mutation	SNP	G	A	4	68	c.2803G>A	c.(2803-2805)GCC>ACC	p.A935T
Pat_32	Pre-Treatment	LYPLA2	11313	37	1	24120757	24120757	Missense_Mutation	SNP	C	T	4	94	c.413C>T	c.(412-414)CCT>CTT	p.P138L
Pat_32	Pre-Treatment	SRRM1	10250	37	1	24993386	24993386	Missense_Mutation	SNP	G	T	4	117	c.1709G>T	c.(1708-1710)CGC>CTC	p.R570L
Pat_32	Pre-Treatment	RPS6KA1	6195	37	1	26883501	26883501	Missense_Mutation	SNP	C	T	4	189	c.994C>T	c.(994-996)CGT>TGT	p.R332C
Pat_32	Pre-Treatment	PIGV	55650	37	1	27121636	27121636	Missense_Mutation	SNP	G	A	5	164	c.1111G>A	c.(1111-1113)GAT>AAT	p.D371N
Pat_32	Pre-Treatment	ZDHHC18	84243	37	1	27176929	27176929	Missense_Mutation	SNP	C	T	4	188	c.784C>T	c.(784-786)CGC>TGC	p.R262C
Pat_32	Pre-Treatment	ADC	113451	37	1	33583557	33583557	Missense_Mutation	SNP	G	T	54	125	c.1084G>T	c.(1084-1086)GAT>TAT	p.D362Y
Pat_32	Pre-Treatment	PHC2	1912	37	1	33794669	33794669	Missense_Mutation	SNP	C	G	3	139	c.2224G>C	c.(2224-2226)GAT>CAT	p.D742H
Pat_32	Pre-Treatment	KIAA0319L	79932	37	1	35915994	35915994	Missense_Mutation	SNP	G	A	4	179	c.2179C>T	c.(2179-2181)CTC>TTC	p.L727F
Pat_32	Pre-Treatment	GRIK3	2899	37	1	37324831	37324831	Missense_Mutation	SNP	C	T	4	196	c.982G>A	c.(982-984)GAC>AAC	p.D328N
Pat_32	Pre-Treatment	GRIK3	2899	37	1	37356523	37356523	Missense_Mutation	SNP	T	C	3	82	c.290A>G	c.(289-291)AAG>AGG	p.K97R
Pat_32	Pre-Treatment	MACF1	23499	37	1	39788607	39788607	Missense_Mutation	SNP	C	T	6	372	c.4178C>T	c.(4177-4179)ACG>ATG	p.T1393M
Pat_32	Pre-Treatment	PABPC4	8761	37	1	40030384	40030384	Missense_Mutation	SNP	C	T	4	149	c.1307G>A	c.(1306-1308)CGC>CAC	p.R436H
Pat_32	Pre-Treatment	RIMS3	9783	37	1	41101591	41101591	Missense_Mutation	SNP	C	T	4	92	c.356G>A	c.(355-357)GGC>GAC	p.G119D
Pat_32	Pre-Treatment	KIAA0467	23334	37	1	43885615	43885615	Missense_Mutation	SNP	G	A	3	76	c.1090G>A	c.(1090-1092)GGC>AGC	p.G364S
Pat_32	Pre-Treatment	PTPRF	5792	37	1	44044559	44044559	Missense_Mutation	SNP	G	A	4	72	c.647G>A	c.(646-648)CGT>CAT	p.R216H
Pat_32	Pre-Treatment	B4GALT2	8704	37	1	44450691	44450691	Missense_Mutation	SNP	G	A	3	28	c.704G>A	c.(703-705)CGC>CAC	p.R235H
Pat_32	Pre-Treatment	RNF220	55182	37	1	44878253	44878253	Missense_Mutation	SNP	G	A	28	69	c.484G>A	c.(484-486)GAA>AAA	p.E162K
Pat_32	Pre-Treatment	AKR1A1	10327	37	1	46033655	46033655	Missense_Mutation	SNP	C	T	4	24	c.358C>T	c.(358-360)CGG>TGG	p.R120W
Pat_32	Pre-Treatment	STIL	6491	37	1	47717257	47717257	Missense_Mutation	SNP	C	T	29	67	c.3415G>A	c.(3415-3417)GAG>AAG	p.E1139K
Pat_32	Pre-Treatment	C1orf168	199920	37	1	57216756	57216756	Missense_Mutation	SNP	G	A	40	86	c.1348C>T	c.(1348-1350)CCT>TCT	p.P450S
Pat_32	Pre-Treatment	LRRC7	57554	37	1	70504985	70504985	Missense_Mutation	SNP	G	A	4	171	c.3364G>A	c.(3364-3366)GCC>ACC	p.A1122T
Pat_32	Pre-Treatment	ST6GALNAC5	81849	37	1	77528748	77528748	Missense_Mutation	SNP	C	T	4	127	c.868C>T	c.(868-870)CGC>TGC	p.R290C
Pat_32	Pre-Treatment	MCOLN3	55283	37	1	85506767	85506767	Missense_Mutation	SNP	C	A	6	246	c.322G>T	c.(322-324)GAC>TAC	p.D108Y
Pat_32	Pre-Treatment	HFM1	164045	37	1	91817167	91817167	Nonsense_Mutation	SNP	G	A	4	173	c.2011C>T	c.(2011-2013)CGA>TGA	p.R671*
Pat_32	Pre-Treatment	AMY2B	280	37	1	104116937	104116937	Missense_Mutation	SNP	G	A	7	366	c.800G>A	c.(799-801)CGG>CAG	p.R267Q
Pat_32	Pre-Treatment	CELSR2	1952	37	1	109805471	109805471	Missense_Mutation	SNP	G	T	4	170	c.4588G>T	c.(4588-4590)GAC>TAC	p.D1530Y

Pat_32	Pre-Treatment	LRIG2	9860	37	1	113662059	113662059	Missense_Mutation	SNP	C	T	3	76	c.2885C>T	c.(2884-2886)CCG>CTG	p.P962L
Pat_32	Pre-Treatment	CASQ2	845	37	1	116310966	116310966	Missense_Mutation	SNP	G	A	4	165	c.197C>T	c.(196-198)ACG>ATG	p.T66M
Pat_32	Pre-Treatment	IGSF3	3321	37	1	117150627	117150627	Missense_Mutation	SNP	C	T	4	186	c.1159G>A	c.(1159-1161)GGG>AGG	p.G387R
Pat_32	Pre-Treatment	REG4	83998	37	1	120345764	120345764	Missense_Mutation	SNP	G	A	3	28	c.92C>T	c.(91-93)GCT>GTT	p.A31V
Pat_32	Pre-Treatment	NBPF10	100132406	37	1	145325971	145325971	Missense_Mutation	SNP	G	C	10	90	c.4069G>C	c.(4069-4071)GAT>CAT	p.D1357H
Pat_32	Pre-Treatment	NBPF10	100132406	37	1	145359049	145359049	Missense_Mutation	SNP	A	G	3	30	c.9214A>G	c.(9214-9216)AAA>GAA	p.K3072E
Pat_32	Pre-Treatment	PEX11B	8799	37	1	145522734	145522734	Nonsense_Mutation	SNP	C	T	4	124	c.595C>T	c.(595-597)CGA>TGA	p.R199*
Pat_32	Pre-Treatment	NBPF15	284565	37	1	148594465	148594465	Missense_Mutation	SNP	C	T	9	433	c.1838C>T	c.(1837-1839)TCG>TTG	p.S613L
Pat_32	Pre-Treatment	LYSMD1	388695	37	1	151134363	151134363	Missense_Mutation	SNP	G	A	4	65	c.394C>T	c.(394-396)CGT>TGT	p.R132C
Pat_32	Pre-Treatment	FLG	2312	37	1	152275826	152275826	Missense_Mutation	SNP	C	T	5	272	c.11536G>A	c.(11536-11538)GGC>AGC	p.G3846S
Pat_32	Pre-Treatment	CRTC2	200186	37	1	153921815	153921815	Missense_Mutation	SNP	G	A	4	112	c.1450C>T	c.(1450-1452)CCC>TCC	p.P484S
Pat_32	Pre-Treatment	KCNN3	3782	37	1	154685948	154685948	Missense_Mutation	SNP	G	A	4	107	c.1891C>T	c.(1891-1893)CTT>TTT	p.L631F
Pat_32	Pre-Treatment	ZBTB7B	51043	37	1	154987735	154987735	Missense_Mutation	SNP	G	A	4	135	c.599G>A	c.(598-600)CGC>CAC	p.R200H
Pat_32	Pre-Treatment	PEAR1	375033	37	1	156883232	156883232	Missense_Mutation	SNP	G	A	6	38	c.2561G>A	c.(2560-2562)GGG>GAG	p.G854E
Pat_32	Pre-Treatment	SPTA1	6708	37	1	158624522	158624522	Missense_Mutation	SNP	G	A	4	75	c.2915C>T	c.(2914-2916)CCA>CTA	p.P972L
Pat_32	Pre-Treatment	SPTA1	6708	37	1	158636110	158636110	Missense_Mutation	SNP	C	T	11	80	c.2216G>A	c.(2215-2217)CGT>CAT	p.R739H
Pat_32	Pre-Treatment	ITLN1	55600	37	1	160851853	160851853	Nonsense_Mutation	SNP	C	T	4	91	c.299G>A	c.(298-300)TGG>TAG	p.W100*
Pat_32	Pre-Treatment	UHMK1	127933	37	1	162492278	162492278	Missense_Mutation	SNP	G	A	4	127	c.1198G>A	c.(1198-1200)GTG>ATG	p.V400M
Pat_32	Pre-Treatment	NUF2	83540	37	1	163297332	163297332	Nonsense_Mutation	SNP	C	T	4	167	c.178C>T	c.(178-180)CGA>TGA	p.R60*
Pat_32	Pre-Treatment	F5	2153	37	1	169510502	169510502	Missense_Mutation	SNP	G	T	8	297	c.3826C>A	c.(3826-3828)CTT>ATT	p.L1276I
Pat_32	Pre-Treatment	FAM163A	148753	37	1	179783004	179783004	Missense_Mutation	SNP	T	A	4	66	c.184T>A	c.(184-186)TGC>AGC	p.C62S
Pat_32	Pre-Treatment	SMG7	9887	37	1	183514293	183514293	Missense_Mutation	SNP	C	T	4	175	c.2216C>T	c.(2215-2217)CCT>CTT	p.P739L
Pat_32	Pre-Treatment	CFHR5	81494	37	1	196965232	196965232	Missense_Mutation	SNP	G	A	4	182	c.871G>A	c.(871-873)GTT>ATT	p.V291I
Pat_32	Pre-Treatment	ZNF281	23528	37	1	200376696	200376696	Missense_Mutation	SNP	G	A	4	140	c.2138C>T	c.(2137-2139)ACG>ATG	p.T713M
Pat_32	Pre-Treatment	ZNF281	23528	37	1	200378305	200378305	Missense_Mutation	SNP	G	A	4	124	c.529C>T	c.(529-531)CTC>TTC	p.L177F
Pat_32	Pre-Treatment	KIF14	9928	37	1	200574423	200574423	Missense_Mutation	SNP	C	T	4	93	c.1734G>A	c.(1732-1734)ATG>ATA	p.M578I
Pat_32	Pre-Treatment	RNPEP	6051	37	1	201966574	201966574	Missense_Mutation	SNP	T	C	3	89	c.982T>C	c.(982-984)TCC>CCC	p.S328P
Pat_32	Pre-Treatment	PIGR	5284	37	1	207105818	207105818	Missense_Mutation	SNP	C	T	4	105	c.1991G>A	c.(1990-1992)CGG>CAG	p.R664Q
Pat_32	Pre-Treatment	USH2A	7399	37	1	216465589	216465589	Missense_Mutation	SNP	C	A	4	176	c.1768G>T	c.(1768-1770)GTA>TTA	p.V590L
Pat_32	Pre-Treatment	HLX	3142	37	1	221053738	221053738	Missense_Mutation	SNP	G	A	4	170	c.539G>A	c.(538-540)CGC>CAC	p.R180H
Pat_32	Pre-Treatment	URB2	9816	37	1	229770776	229770776	Missense_Mutation	SNP	A	G	10	22	c.416A>G	c.(415-417)TAC>TGC	p.Y139C
Pat_32	Pre-Treatment	URB2	9816	37	1	229772521	229772521	Missense_Mutation	SNP	G	A	4	177	c.2161G>A	c.(2161-2163)GCT>ACT	p.A721T
Pat_32	Pre-Treatment	OR2T4	127074	37	1	248524937	248524937	Missense_Mutation	SNP	A	T	6	171	c.55A>T	c.(55-57)ATG>TTG	p.M19L
Pat_32	Pre-Treatment	PRPF18	8559	37	10	13658449	13658449	Missense_Mutation	SNP	G	A	52	95	c.844G>A	c.(844-846)GGT>AGT	p.G282S
Pat_32	Pre-Treatment	CUBN	8029	37	10	17107618	17107618	Missense_Mutation	SNP	G	A	6	325	c.3028C>T	c.(3028-3030)CCG>TCG	p.P1010S
Pat_32	Pre-Treatment	ANKRD30A	91074	37	10	37430754	37430754	Missense_Mutation	SNP	T	C	5	60	c.761T>C	c.(760-762)GTG>GCG	p.V254A
Pat_32	Pre-Treatment	PCDH15	65217	37	10	56106157	56106157	Nonsense_Mutation	SNP	C	A	16	48	c.562G>T	c.(562-564)GAG>TAG	p.E188*
Pat_32	Pre-Treatment	BICC1	80114	37	10	60549640	60549640	Missense_Mutation	SNP	G	A	4	178	c.994G>A	c.(994-996)GTC>ATC	p.V332I
Pat_32	Pre-Treatment	DDX50	79009	37	10	70706373	70706373	Missense_Mutation	SNP	G	A	4	188	c.2201G>A	c.(2200-2202)CGG>CAG	p.R734Q
Pat_32	Pre-Treatment	TACR2	6865	37	10	71175863	71175863	Missense_Mutation	SNP	C	T	4	46	c.217G>A	c.(217-219)GTC>ATC	p.V73I
Pat_32	Pre-Treatment	COL13A1	1305	37	10	71689832	71689832	Missense_Mutation	SNP	G	A	3	40	c.1486G>A	c.(1486-1488)GAT>AAT	p.D496N
Pat_32	Pre-Treatment	ANXA11	311	37	10	81928784	81928784	Missense_Mutation	SNP	G	A	3	29	c.502C>T	c.(502-504)CCG>TCG	p.P168S
Pat_32	Pre-Treatment	PCGF5	84333	37	10	93000338	93000338	Splice_Site	SNP	G	A	4	106	c.209_splice	c.e3+1	p.R70_splice
Pat_32	Pre-Treatment	PPP1R3C	5507	37	10	93390208	93390208	Missense_Mutation	SNP	C	T	4	153	c.430G>A	c.(430-432)GAT>AAT	p.D144N
Pat_32	Pre-Treatment	NPM3	10360	37	10	103542299	103542299	Missense_Mutation	SNP	C	T	4	55	c.260G>A	c.(259-261)CGG>CAG	p.R87Q
Pat_32	Pre-Treatment	C10orf79	80217	37	10	105967456	105967456	Missense_Mutation	SNP	C	T	4	88	c.862G>A	c.(862-864)GTA>ATA	p.V288I
Pat_32	Pre-Treatment	PDZD8	118987	37	10	119043998	119043998	Missense_Mutation	SNP	G	A	3	32	c.2246C>T	c.(2245-2247)ACG>ATG	p.T749M

Pat_32	Pre-Treatment	TACC2	10579	37	10	123844731	123844731	Missense_Mutation	SNP	C	T	3	18	c.2716C>T	c.(2716-2718)CCC>TCC	p.P906S
Pat_32	Pre-Treatment	OAT	4942	37	10	126090317	126090317	Missense_Mutation	SNP	C	T	4	67	c.992G>A	c.(991-993)CGA>CAA	p.R331Q
Pat_32	Pre-Treatment	STK32C	282974	37	10	134038745	134038745	Nonsense_Mutation	SNP	G	A	3	26	c.868C>T	c.(868-870)CGA>TGA	p.R290*
Pat_32	Pre-Treatment	TALDO1	6888	37	11	763815	763815	Missense_Mutation	SNP	G	A	5	186	c.706G>A	c.(706-708)GCC>ACC	p.A236T
Pat_32	Pre-Treatment	TRIM6-TRIM34	445372	37	11	5663725	5663725	Missense_Mutation	SNP	A	G	15	27	c.1925A>G	c.(1924-1926)CAA>CGA	p.Q642R
Pat_32	Pre-Treatment	C11orf42	160298	37	11	6231467	6231467	Nonsense_Mutation	SNP	C	T	4	162	c.460C>T	c.(460-462)CGA>TGA	p.R154*
Pat_32	Pre-Treatment	TRIM3	10612	37	11	6477868	6477868	Missense_Mutation	SNP	C	T	4	83	c.1088G>A	c.(1087-1089)CGT>CAT	p.R363H
Pat_32	Pre-Treatment	PARVA	55742	37	11	12399262	12399262	Missense_Mutation	SNP	G	A	4	20	c.68G>A	c.(67-69)CGC>CAC	p.R23H
Pat_32	Pre-Treatment	IGSF22	283284	37	11	18739598	18739598	Missense_Mutation	SNP	C	T	4	88	c.853G>A	c.(853-855)GAT>AAT	p.D285N
Pat_32	Pre-Treatment	NAV2	89797	37	11	19954827	19954827	Missense_Mutation	SNP	C	T	5	370	c.1106C>T	c.(1105-1107)TCG>TTG	p.S369L
Pat_32	Pre-Treatment	C11orf46	120534	37	11	30352529	30352529	Missense_Mutation	SNP	C	T	4	104	c.34C>T	c.(34-36)CGT>TGT	p.R12C
Pat_32	Pre-Treatment	C11orf41	25758	37	11	33566351	33566351	Missense_Mutation	SNP	G	A	3	53	c.1939G>A	c.(1939-1941)GCT>ACT	p.A647T
Pat_32	Pre-Treatment	CKAP5	9793	37	11	46772672	46772672	Missense_Mutation	SNP	C	T	4	140	c.5456G>A	c.(5455-5457)CGA>CAA	p.R1819Q
Pat_32	Pre-Treatment	ZP1	22917	37	11	60640929	60640929	Missense_Mutation	SNP	G	A	4	105	c.1322G>A	c.(1321-1323)CGG>CAG	p.R441Q
Pat_32	Pre-Treatment	LGALS12	85329	37	11	63283096	63283096	Missense_Mutation	SNP	G	A	4	71	c.775G>A	c.(775-777)GCA>ACA	p.A259T
Pat_32	Pre-Treatment	MRPL49	740	37	11	64889826	64889826	Missense_Mutation	SNP	C	T	4	62	c.8C>T	c.(7-9)GCT>GTT	p.A3V
Pat_32	Pre-Treatment	LTBP3	4054	37	11	65319749	65319749	Missense_Mutation	SNP	G	A	5	171	c.1315C>T	c.(1315-1317)CGG>TGG	p.R439W
Pat_32	Pre-Treatment	KAT5	10524	37	11	65480967	65480967	Missense_Mutation	SNP	G	A	4	123	c.434G>A	c.(433-435)CGC>CAC	p.R145H
Pat_32	Pre-Treatment	DPP3	10072	37	11	66249865	66249865	Missense_Mutation	SNP	G	A	4	88	c.194G>A	c.(193-195)CGC>CAC	p.R65H
Pat_32	Pre-Treatment	RHOD	29984	37	11	66834317	66834317	Missense_Mutation	SNP	G	A	4	86	c.329G>A	c.(328-330)CGG>CAG	p.R110Q
Pat_32	Pre-Treatment	ANKRD13D	338692	37	11	67059139	67059139	Nonsense_Mutation	SNP	C	T	4	167	c.202C>T	c.(202-204)CGA>TGA	p.R68*
Pat_32	Pre-Treatment	LRRC32	2615	37	11	76372167	76372167	Missense_Mutation	SNP	G	A	3	46	c.470C>T	c.(469-471)GCG>GTG	p.A157V
Pat_32	Pre-Treatment	CUL5	8065	37	11	107969180	107969180	Missense_Mutation	SNP	G	A	4	111	c.2072G>A	c.(2071-2073)CGT>CAT	p.R691H
Pat_32	Pre-Treatment	CEP164	22897	37	11	117232609	117232609	Missense_Mutation	SNP	G	A	4	116	c.452G>A	c.(451-453)CGA>CAA	p.R151Q
Pat_32	Pre-Treatment	MLL	4297	37	11	118376958	118376958	Missense_Mutation	SNP	G	A	4	80	c.10342G>A	c.(10342-10344)GAA>AAA	p.E3448K
Pat_32	Pre-Treatment	USP2	9099	37	11	119243682	119243682	Missense_Mutation	SNP	G	A	3	60	c.509C>T	c.(508-510)CCC>CTC	p.P170L
Pat_32	Pre-Treatment	SORL1	6653	37	11	121358825	121358825	Missense_Mutation	SNP	C	T	5	196	c.613C>T	c.(613-615)CGG>TGG	p.R205W
Pat_32	Pre-Treatment	VSIG2	23584	37	11	124621372	124621372	Missense_Mutation	SNP	C	T	4	124	c.166G>A	c.(166-168)GCC>ACC	p.A56T
Pat_32	Pre-Treatment	STT3A	3703	37	11	125481409	125481409	Missense_Mutation	SNP	G	A	4	150	c.1204G>A	c.(1204-1206)GTA>ATA	p.V402I
Pat_32	Pre-Treatment	WNT5B	81029	37	12	1755323	1755323	Missense_Mutation	SNP	G	A	4	106	c.985G>A	c.(985-987)GTG>ATG	p.V329M
Pat_32	Pre-Treatment	VWF	7450	37	12	6085278	6085278	Missense_Mutation	SNP	G	A	3	71	c.7436C>T	c.(7435-7437)TCG>TTG	p.S2479L
Pat_32	Pre-Treatment	PTPN6	5777	37	12	7069534	7069534	Missense_Mutation	SNP	G	A	4	172	c.1609G>A	c.(1609-1611)GGG>AGG	p.G537R
Pat_32	Pre-Treatment	CD163L1	283316	37	12	7528575	7528575	Missense_Mutation	SNP	G	A	4	117	c.2407C>T	c.(2407-2409)CCC>TCC	p.P803S
Pat_32	Pre-Treatment	DNM1L	10059	37	12	32866173	32866173	Missense_Mutation	SNP	G	A	4	62	c.487G>A	c.(487-489)GAG>AAG	p.E163K
Pat_32	Pre-Treatment	CNTN1	1272	37	12	41387065	41387065	Missense_Mutation	SNP	G	A	3	32	c.2107G>A	c.(2107-2109)GGT>AGT	p.G703S
Pat_32	Pre-Treatment	SFRS2IP	9169	37	12	46322549	46322549	Missense_Mutation	SNP	C	T	4	130	c.935G>A	c.(934-936)CGA>CAA	p.R312Q
Pat_32	Pre-Treatment	OR10AD1	121275	37	12	48596709	48596709	Missense_Mutation	SNP	G	A	3	37	c.367C>T	c.(367-369)CGT>TGT	p.R123C
Pat_32	Pre-Treatment	TUBA1B	10376	37	12	49521833	49521833	Missense_Mutation	SNP	G	A	6	381	c.1264C>T	c.(1264-1266)CGT>TGT	p.R422C
Pat_32	Pre-Treatment	TUBA1C	84790	37	12	49666829	49666829	Missense_Mutation	SNP	G	A	4	191	c.1169G>A	c.(1168-1170)CGC>CAC	p.R390H
Pat_32	Pre-Treatment	CSRNP2	81566	37	12	51458370	51458370	Missense_Mutation	SNP	C	T	3	51	c.791G>A	c.(790-792)CGG>CAG	p.R264Q
Pat_32	Pre-Treatment	ESPL1	9700	37	12	53683252	53683252	Missense_Mutation	SNP	G	A	4	73	c.4987G>A	c.(4987-4989)GAG>AAG	p.E1663K
Pat_32	Pre-Treatment	SP7	121340	37	12	53722199	53722199	Missense_Mutation	SNP	G	A	4	160	c.1027C>T	c.(1027-1029)CGT>TGT	p.R343C
Pat_32	Pre-Treatment	PCBP2	5094	37	12	53854853	53854853	Missense_Mutation	SNP	C	T	4	115	c.430C>T	c.(430-432)CGG>TGG	p.R144W
Pat_32	Pre-Treatment	DNAJC14	85406	37	12	56221784	56221784	Missense_Mutation	SNP	C	T	4	106	c.659G>A	c.(658-660)CGA>CAA	p.R220Q
Pat_32	Pre-Treatment	STAC3	246329	37	12	57638333	57638333	Missense_Mutation	SNP	C	T	6	374	c.793G>A	c.(793-795)GAT>AAT	p.D265N
Pat_32	Pre-Treatment	IL26	55801	37	12	68618970	68618970	Missense_Mutation	SNP	C	A	4	121	c.322G>T	c.(322-324)GTG>TTG	p.V108L
Pat_32	Pre-Treatment	LRRC10	376132	37	12	70004282	70004282	Missense_Mutation	SNP	G	A	4	83	c.337C>T	c.(337-339)CTC>TTC	p.L113F

Pat_32	Pre-Treatment	ORAI1	84876	37	12	122079355	122079355	Missense_Mutation	SNP	G	A	4	84	c.712G>A	c.(712-714)GCC>ACC	p.A238T
Pat_32	Pre-Treatment	TMEM120B	144404	37	12	122199613	122199613	Missense_Mutation	SNP	C	T	4	90	c.520C>T	c.(520-522)CGG>TGG	p.R174W
Pat_32	Pre-Treatment	RILPL1	353116	37	12	123984011	123984011	Missense_Mutation	SNP	C	T	4	135	c.533G>A	c.(532-534)CGC>CAC	p.R178H
Pat_32	Pre-Treatment	RIMBP2	23504	37	12	130912813	130912813	Missense_Mutation	SNP	C	T	19	63	c.2272G>A	c.(2272-2274)GAG>AAG	p.E758K
Pat_32	Pre-Treatment	ULK1	8408	37	12	132393323	132393323	Missense_Mutation	SNP	G	A	3	45	c.451G>A	c.(451-453)GGC>AGC	p.G151S
Pat_32	Pre-Treatment	GOLGA3	2802	37	12	133384773	133384773	Missense_Mutation	SNP	G	T	4	147	c.882C>A	c.(880-882)GAC>GAA	p.D294E
Pat_32	Pre-Treatment	MTMR6	9107	37	13	25823480	25823480	Missense_Mutation	SNP	C	T	4	131	c.1756G>A	c.(1756-1758)GAG>AAG	p.E586K
Pat_32	Pre-Treatment	RNF6	6049	37	13	26788779	26788779	Missense_Mutation	SNP	G	A	4	188	c.1240C>T	c.(1240-1242)CGG>TGG	p.R414W
Pat_32	Pre-Treatment	FREM2	341640	37	13	39263688	39263688	Missense_Mutation	SNP	G	A	4	120	c.2207G>A	c.(2206-2208)CGA>CAA	p.R736Q
Pat_32	Pre-Treatment	COG6	57511	37	13	40254159	40254159	Missense_Mutation	SNP	A	G	60	66	c.671A>G	c.(670-672)GAA>GGA	p.E224G
Pat_32	Pre-Treatment	SIAH3	283514	37	13	46358177	46358177	Missense_Mutation	SNP	G	A	4	175	c.151C>T	c.(151-153)CGC>TGC	p.R51C
Pat_32	Pre-Treatment	ZC3H13	23091	37	13	46543404	46543404	Missense_Mutation	SNP	C	T	4	102	c.3275G>A	c.(3274-3276)AGT>AAT	p.S1092N
Pat_32	Pre-Treatment	KPNA3	3839	37	13	50306795	50306795	Splice_Site	SNP	T	C	4	153	c.235_splice	c.e5-1	p.N79_splice
Pat_32	Pre-Treatment	TBC1D4	9882	37	13	75886939	75886939	Missense_Mutation	SNP	C	T	4	92	c.2318G>A	c.(2317-2319)CGG>CAG	p.R773Q
Pat_32	Pre-Treatment	FBXL3	26224	37	13	77592850	77592850	Missense_Mutation	SNP	C	T	5	187	c.356G>A	c.(355-357)AGC>AAC	p.S119N
Pat_32	Pre-Treatment	TUBGCP3	10426	37	13	113181356	113181356	Missense_Mutation	SNP	C	A	3	42	c.1455G>T	c.(1453-1455)TTG>TTT	p.L485F
Pat_32	Pre-Treatment	PCID2	55795	37	13	113838738	113838738	Missense_Mutation	SNP	C	T	4	184	c.607G>A	c.(607-609)GAT>AAT	p.D203N
Pat_32	Pre-Treatment	TMCO3	55002	37	13	114150005	114150005	Missense_Mutation	SNP	C	T	3	32	c.109C>T	c.(109-111)CGC>TGC	p.R37C
Pat_32	Pre-Treatment	GAS6	2621	37	13	114535424	114535424	Missense_Mutation	SNP	C	T	4	84	c.991G>A	c.(991-993)GAG>AAG	p.E331K
Pat_32	Pre-Treatment	TTC5	91875	37	14	20760155	20760155	Missense_Mutation	SNP	T	C	3	62	c.1190A>G	c.(1189-1191)CAG>CGG	p.Q397R
Pat_32	Pre-Treatment	RNASE4	6038	37	14	21167774	21167774	Missense_Mutation	SNP	C	T	4	196	c.244C>T	c.(244-246)CGT>TGT	p.R82C
Pat_32	Pre-Treatment	OR10G2	26534	37	14	22102833	22102833	Missense_Mutation	SNP	C	T	4	74	c.166G>A	c.(166-168)GAC>AAC	p.D56N
Pat_32	Pre-Treatment	MYH6	4624	37	14	23867937	23867937	Missense_Mutation	SNP	C	T	4	96	c.1891G>A	c.(1891-1893)GGG>AGG	p.G631R
Pat_32	Pre-Treatment	TBPL2	387332	37	14	55907239	55907239	Missense_Mutation	SNP	G	A	3	30	c.25C>T	c.(25-27)CGG>TGG	p.R9W
Pat_32	Pre-Treatment	FUT8	2530	37	14	66188556	66188556	Missense_Mutation	SNP	G	A	65	118	c.899G>A	c.(898-900)CGT>CAT	p.R300H
Pat_32	Pre-Treatment	GPHN	10243	37	14	67647580	67647580	Missense_Mutation	SNP	C	T	4	73	c.2137C>T	c.(2137-2139)CCT>TCT	p.P713S
Pat_32	Pre-Treatment	GALNTL1	57452	37	14	69795241	69795241	Missense_Mutation	SNP	G	A	4	115	c.643G>A	c.(643-645)GAA>AAA	p.E215K
Pat_32	Pre-Treatment	ADAM21P1	145241	37	14	70713408	70713408	Missense_Mutation	SNP	C	T	4	132	c.460G>A	c.(460-462)GTT>ATT	p.V154I
Pat_32	Pre-Treatment	DCAF4	26094	37	14	73413857	73413857	Missense_Mutation	SNP	C	T	4	173	c.686C>T	c.(685-687)TCG>TTG	p.S229L
Pat_32	Pre-Treatment	ABCD4	5826	37	14	74761892	74761892	Missense_Mutation	SNP	G	T	15	78	c.678C>A	c.(676-678)CAC>CAA	p.H226Q
Pat_32	Pre-Treatment	YLPM1	56252	37	14	75283295	75283295	Missense_Mutation	SNP	G	A	3	35	c.5587G>A	c.(5587-5589)GGA>AGA	p.G1863R
Pat_32	Pre-Treatment	TSHR	7253	37	14	81609547	81609547	Missense_Mutation	SNP	A	G	3	65	c.1145A>G	c.(1144-1146)GAC>GGC	p.D382G
Pat_32	Pre-Treatment	DEGS2	123099	37	14	100613207	100613207	Missense_Mutation	SNP	G	A	4	116	c.863C>T	c.(862-864)CCG>CTG	p.P288L
Pat_32	Pre-Treatment	DYNC1H1	1778	37	14	102452250	102452250	Missense_Mutation	SNP	G	A	4	109	c.1688G>A	c.(1687-1689)CGG>CAG	p.R563Q
Pat_32	Pre-Treatment	TMEM179	388021	37	14	105063337	105063337	Missense_Mutation	SNP	C	T	4	52	c.433G>A	c.(433-435)GTA>ATA	p.V145I
Pat_32	Pre-Treatment	OR4N4	283694	37	15	22382807	22382807	Missense_Mutation	SNP	G	A	57	203	c.335G>A	c.(334-336)GGA>GAA	p.G112E
Pat_32	Pre-Treatment	OR4N3P	390539	37	15	22413796	22413796	Missense_Mutation	SNP	G	A	18	317	c.95G>A	c.(94-96)GGA>GAA	p.G32E
Pat_32	Pre-Treatment	CYFIP1	23191	37	15	22929783	22929783	Missense_Mutation	SNP	G	A	4	85	c.457G>A	c.(457-459)GTG>ATG	p.V153M
Pat_32	Pre-Treatment	HERC2	8924	37	15	28525311	28525311	Missense_Mutation	SNP	G	A	4	169	c.445C>T	c.(445-447)CGC>TGC	p.R149C
Pat_32	Pre-Treatment	TRPM1	4308	37	15	31334269	31334269	Missense_Mutation	SNP	C	T	4	32	c.1906G>A	c.(1906-1908)GAA>AAA	p.E636K
Pat_32	Pre-Treatment	VPS18	57617	37	15	41191869	41191869	Missense_Mutation	SNP	G	A	4	158	c.853G>A	c.(853-855)GCC>ACC	p.A285T
Pat_32	Pre-Treatment	SQRDL	58472	37	15	45974680	45974680	Missense_Mutation	SNP	A	G	3	64	c.869A>G	c.(868-870)GAA>GGA	p.E290G
Pat_32	Pre-Treatment	FBN1	2200	37	15	48902936	48902936	Missense_Mutation	SNP	C	G	12	56	c.335G>C	c.(334-336)GGC>GCC	p.G112A
Pat_32	Pre-Treatment	RFX7	64864	37	15	56385627	56385627	Nonsense_Mutation	SNP	G	T	4	60	c.4299C>A	c.(4297-4299)TGC>TGA	p.C1433*
Pat_32	Pre-Treatment	LIPC	3990	37	15	58830636	58830636	Nonsense_Mutation	SNP	C	T	8	475	c.193C>T	c.(193-195)CGA>TGA	p.R65*
Pat_32	Pre-Treatment	HERC1	8925	37	15	63904742	63904742	Missense_Mutation	SNP	C	T	4	149	c.14108G>A	c.(14107-14109)CGA>CAA	p.R4703Q
Pat_32	Pre-Treatment	CLPX	10845	37	15	65477431	65477431	Missense_Mutation	SNP	G	A	3	34	c.61C>T	c.(61-63)CTC>TTC	p.L21F

Pat_32	Pre-Treatment	CT62	196993	37	15	71403623	71403623	Missense_Mutation	SNP	C	T	4	94	c.278G>A	c.(277-279)CGG>CAG	p.R93Q
Pat_32	Pre-Treatment	C15orf59	388135	37	15	74032746	74032746	Missense_Mutation	SNP	G	A	4	120	c.394C>T	c.(394-396)CGG>TGG	p.R132W
Pat_32	Pre-Treatment	MEX3B	84206	37	15	82336147	82336147	Missense_Mutation	SNP	C	T	4	77	c.1064G>A	c.(1063-1065)GGC>GAC	p.G355D
Pat_32	Pre-Treatment	AP3B2	8120	37	15	83333195	83333195	Missense_Mutation	SNP	C	T	4	64	c.2128G>A	c.(2128-2130)GGC>AGC	p.G710S
Pat_32	Pre-Treatment	BNC1	646	37	15	83932963	83932963	Missense_Mutation	SNP	C	T	4	93	c.1040G>A	c.(1039-1041)AGG>AAG	p.R347K
Pat_32	Pre-Treatment	IQGAP1	8826	37	15	90991828	90991828	Missense_Mutation	SNP	G	A	4	112	c.937G>A	c.(937-939)GAC>AAC	p.D313N
Pat_32	Pre-Treatment	BLM	641	37	15	91346808	91346808	Missense_Mutation	SNP	G	A	4	131	c.3416G>A	c.(3415-3417)CGA>CAA	p.R1139Q
Pat_32	Pre-Treatment	SLCO3A1	28232	37	15	92663701	92663701	Missense_Mutation	SNP	C	T	5	294	c.1016C>T	c.(1015-1017)CCG>CTG	p.P339L
Pat_32	Pre-Treatment	PCSK6	5046	37	15	101933506	101933506	Missense_Mutation	SNP	C	T	4	88	c.1120G>A	c.(1120-1122)GAG>AAG	p.E374K
Pat_32	Pre-Treatment	SOLH	6650	37	16	599035	599035	Missense_Mutation	SNP	G	A	4	146	c.1492G>A	c.(1492-1494)GAG>AAG	p.E498K
Pat_32	Pre-Treatment	MAPK8IP3	23162	37	16	1816919	1816919	Missense_Mutation	SNP	G	A	5	122	c.3032G>A	c.(3031-3033)CGT>CAT	p.R1011H
Pat_32	Pre-Treatment	MEFV	4210	37	16	3293550	3293550	Missense_Mutation	SNP	G	A	4	156	c.1937C>T	c.(1936-1938)CCG>CTG	p.P646L
Pat_32	Pre-Treatment	ATF7IP2	80063	37	16	10534245	10534245	Missense_Mutation	SNP	C	T	5	9	c.1120C>T	c.(1120-1122)CGT>TGT	p.R374C
Pat_32	Pre-Treatment	ABCC1	4363	37	16	16218725	16218725	Missense_Mutation	SNP	A	G	3	62	c.3670A>G	c.(3670-3672)AGC>GGC	p.S1224G
Pat_32	Pre-Treatment	TMC7	79905	37	16	19058479	19058479	Missense_Mutation	SNP	G	A	5	333	c.1648G>A	c.(1648-1650)GGG>AGG	p.G550R
Pat_32	Pre-Treatment	SYT17	51760	37	16	19195123	19195123	Missense_Mutation	SNP	C	T	4	192	c.605C>T	c.(604-606)ACC>ATC	p.T202I
Pat_32	Pre-Treatment	EEF2K	29904	37	16	22268217	22268217	Missense_Mutation	SNP	A	G	3	97	c.767A>G	c.(766-768)CAG>CGG	p.Q256R
Pat_32	Pre-Treatment	ATP2A1	487	37	16	28912115	28912115	Missense_Mutation	SNP	G	A	4	74	c.1978G>A	c.(1978-1980)GAC>AAC	p.D660N
Pat_32	Pre-Treatment	ATP2A1	487	37	16	28912136	28912136	Missense_Mutation	SNP	C	T	4	84	c.1999C>T	c.(1999-2001)CGG>TGG	p.R667W
Pat_32	Pre-Treatment	TBX6	6911	37	16	30100374	30100374	Missense_Mutation	SNP	G	A	5	124	c.511C>T	c.(511-513)CGT>TGT	p.R171C
Pat_32	Pre-Treatment	ZNF689	115509	37	16	30616463	30616463	Nonsense_Mutation	SNP	G	A	4	92	c.625C>T	c.(625-627)CAG>TAG	p.Q209*
Pat_32	Pre-Treatment	RNF40	9810	37	16	30783215	30783215	Missense_Mutation	SNP	G	A	4	85	c.2648G>A	c.(2647-2649)CGG>CAG	p.R883Q
Pat_32	Pre-Treatment	ABCC11	85320	37	16	48264402	48264402	Missense_Mutation	SNP	C	A	4	75	c.182G>T	c.(181-183)TGG>TTG	p.W61L
Pat_32	Pre-Treatment	MMP2	4313	37	16	55517984	55517984	Missense_Mutation	SNP	G	A	4	119	c.437G>A	c.(436-438)CGT>CAT	p.R146H
Pat_32	Pre-Treatment	CSNK2A2	1459	37	16	58208381	58208381	Missense_Mutation	SNP	G	A	3	84	c.403C>T	c.(403-405)CGG>TGG	p.R135W
Pat_32	Pre-Treatment	FHOD1	29109	37	16	67264519	67264519	Missense_Mutation	SNP	C	T	16	392	c.2843G>A	c.(2842-2844)CGC>CAC	p.R948H
Pat_32	Pre-Treatment	TPPP3	51673	37	16	67424121	67424121	Missense_Mutation	SNP	C	T	3	37	c.487G>A	c.(487-489)GCC>ACC	p.A163T
Pat_32	Pre-Treatment	GFOD2	81577	37	16	67709699	67709699	Missense_Mutation	SNP	C	T	3	75	c.517G>A	c.(517-519)GGG>AGG	p.G173R
Pat_32	Pre-Treatment	HAS3	3038	37	16	69148312	69148312	Missense_Mutation	SNP	G	A	4	152	c.805G>A	c.(805-807)GTG>ATG	p.V269M
Pat_32	Pre-Treatment	LDHD	197257	37	16	75149233	75149233	Missense_Mutation	SNP	C	T	4	190	c.190G>A	c.(190-192)GAA>AAA	p.E64K
Pat_32	Pre-Treatment	MON1B	22879	37	16	77228628	77228628	Missense_Mutation	SNP	G	A	4	86	c.872G>A	c.(871-873)CGA>CAA	p.R291Q
Pat_32	Pre-Treatment	PLCG2	5336	37	16	81960766	81960766	Missense_Mutation	SNP	G	A	4	117	c.2497G>A	c.(2497-2499)GAG>AAG	p.E833K
Pat_32	Pre-Treatment	KIAA0513	9764	37	16	85109487	85109487	Missense_Mutation	SNP	C	T	4	108	c.541C>T	c.(541-543)CTC>TTC	p.L181F
Pat_32	Pre-Treatment	MTHFSD	64779	37	16	86585659	86585659	Missense_Mutation	SNP	C	T	6	272	c.217G>A	c.(217-219)GTT>ATT	p.V73I
Pat_32	Pre-Treatment	ZCCHC14	23174	37	16	87446498	87446498	Missense_Mutation	SNP	G	A	4	101	c.1418C>T	c.(1417-1419)ACG>ATG	p.T473M
Pat_32	Pre-Treatment	PRDM7	11105	37	16	90126823	90126823	Missense_Mutation	SNP	T	G	4	138	c.1159A>C	c.(1159-1161)ATG>CTG	p.M387L
Pat_32	Pre-Treatment	SLC43A2	124935	37	17	1494599	1494599	Missense_Mutation	SNP	C	T	4	167	c.895G>A	c.(895-897)GTC>ATC	p.V299I
Pat_32	Pre-Treatment	SMYD4	114826	37	17	1703757	1703757	Missense_Mutation	SNP	C	T	4	166	c.931G>A	c.(931-933)GGA>AGA	p.G311R
Pat_32	Pre-Treatment	ITGAE	3682	37	17	3626668	3626668	Missense_Mutation	SNP	C	T	4	154	c.3151G>A	c.(3151-3153)GAA>AAA	p.E1051K
Pat_32	Pre-Treatment	ZZEF1	23140	37	17	4020367	4020367	Missense_Mutation	SNP	G	A	4	166	c.593C>T	c.(592-594)GCG>GTG	p.A198V
Pat_32	Pre-Treatment	CAMTA2	23125	37	17	4873732	4873732	Missense_Mutation	SNP	G	A	6	371	c.2908C>T	c.(2908-2910)CGG>TGG	p.R970W
Pat_32	Pre-Treatment	ALOX12B	242	37	17	7978994	7978994	Missense_Mutation	SNP	C	T	5	343	c.1573G>A	c.(1573-1575)GCA>ACA	p.A525T
Pat_32	Pre-Treatment	MYH10	4628	37	17	8439224	8439224	Missense_Mutation	SNP	A	G	3	78	c.1601T>C	c.(1600-1602)CTT>CCT	p.L534P
Pat_32	Pre-Treatment	DNAH9	1770	37	17	11572500	11572500	Missense_Mutation	SNP	G	A	4	135	c.2851G>A	c.(2851-2853)GGT>AGT	p.G951S
Pat_32	Pre-Treatment	MPRIP	23164	37	17	17053500	17053500	Missense_Mutation	SNP	G	A	5	373	c.1318G>A	c.(1318-1320)GAT>AAT	p.D440N
Pat_32	Pre-Treatment	ULK2	9706	37	17	19750148	19750148	Missense_Mutation	SNP	C	T	5	164	c.371G>A	c.(370-372)AGC>AAC	p.S124N
Pat_32	Pre-Treatment	MAP2K3	5606	37	17	21201752	21201752	Missense_Mutation	SNP	G	A	4	184	c.77G>A	c.(76-78)CGG>CAG	p.R26Q

Pat_32	Pre-Treatment	KCNJ12	3768	37	17	21318935	21318935	Missense_Mutation	SNP	C	T	4	64	c.281C>T	c.(280-282)TCC>TTC	p.S94F
Pat_32	Pre-Treatment	NF1	4763	37	17	29559745	29559745	Missense_Mutation	SNP	G	T	4	85	c.3342G>T	c.(3340-3342)TTG>TTT	p.L1114F
Pat_32	Pre-Treatment	CDK5R1	8851	37	17	30815092	30815092	Missense_Mutation	SNP	C	T	4	119	c.454C>T	c.(454-456)CTT>TTT	p.L152F
Pat_32	Pre-Treatment	MYO19	80179	37	17	34854123	34854123	Missense_Mutation	SNP	C	T	4	144	c.2744G>A	c.(2743-2745)CGA>CAA	p.R915Q
Pat_32	Pre-Treatment	CASC3	22794	37	17	38324467	38324467	Missense_Mutation	SNP	C	T	4	183	c.1762C>T	c.(1762-1764)CAC>TAC	p.H588Y
Pat_32	Pre-Treatment	CCR7	1236	37	17	38711920	38711920	Missense_Mutation	SNP	C	T	4	133	c.211G>A	c.(211-213)GTG>ATG	p.V71M
Pat_32	Pre-Treatment	KRT27	342574	37	17	38935975	38935975	Missense_Mutation	SNP	C	T	3	34	c.823G>A	c.(823-825)GCG>ACG	p.A275T
Pat_32	Pre-Treatment	KRTAP9-9	81870	37	17	39411990	39411990	Missense_Mutation	SNP	C	T	5	189	c.308C>T	c.(307-309)CCG>CTG	p.P103L
Pat_32	Pre-Treatment	KRT33B	3884	37	17	39521500	39521500	Missense_Mutation	SNP	T	C	3	86	c.803A>G	c.(802-804)TAC>TGC	p.Y268C
Pat_32	Pre-Treatment	MLX	6945	37	17	40721609	40721609	Missense_Mutation	SNP	T	A	4	85	c.623T>A	c.(622-624)CTA>CAA	p.L208Q
Pat_32	Pre-Treatment	MEOX1	4222	37	17	41719349	41719349	Missense_Mutation	SNP	C	T	4	173	c.694G>A	c.(694-696)GGT>AGT	p.G232S
Pat_32	Pre-Treatment	ZNF652	22834	37	17	47376154	47376154	Missense_Mutation	SNP	G	A	4	42	c.1442C>T	c.(1441-1443)TCG>TTG	p.S481L
Pat_32	Pre-Treatment	SPATA20	64847	37	17	48626540	48626540	Missense_Mutation	SNP	G	A	4	124	c.605G>A	c.(604-606)CGA>CAA	p.R202Q
Pat_32	Pre-Treatment	OR4D2	124538	37	17	56247506	56247506	Missense_Mutation	SNP	C	T	4	130	c.490C>T	c.(490-492)CTC>TTC	p.L164F
Pat_32	Pre-Treatment	CSH1	1442	37	17	61973503	61973503	Missense_Mutation	SNP	G	A	3	39	c.103C>T	c.(103-105)CTT>TTT	p.L35F
Pat_32	Pre-Treatment	SCN4A	6329	37	17	62019123	62019123	Missense_Mutation	SNP	C	T	4	139	c.4519G>A	c.(4519-4521)GTC>ATC	p.V1507I
Pat_32	Pre-Treatment	PLEKHM1P	440456	37	17	62781423	62781423	Missense_Mutation	SNP	G	A	4	51	c.1547C>T	c.(1546-1548)CCC>CTC	p.P516L
Pat_32	Pre-Treatment	CACNG1	786	37	17	65052344	65052344	Missense_Mutation	SNP	G	A	4	71	c.626G>A	c.(625-627)CGG>CAG	p.R209Q
Pat_32	Pre-Treatment	ABCA9	10350	37	17	66980239	66980239	Missense_Mutation	SNP	G	A	4	124	c.4457C>T	c.(4456-4458)GCG>GTG	p.A1486V
Pat_32	Pre-Treatment	KIF19	124602	37	17	72345404	72345404	Nonsense_Mutation	SNP	C	T	3	42	c.1129C>T	c.(1129-1131)CGA>TGA	p.R377*
Pat_32	Pre-Treatment	UBE2O	63893	37	17	74394972	74394972	Missense_Mutation	SNP	G	A	110	156	c.1729C>T	c.(1729-1731)CAC>TAC	p.H577Y
Pat_32	Pre-Treatment	MXRA7	439921	37	17	74673728	74673728	Missense_Mutation	SNP	G	A	4	148	c.557C>T	c.(556-558)ACG>ATG	p.T186M
Pat_32	Pre-Treatment	FOXK2	3607	37	17	80521342	80521342	Missense_Mutation	SNP	C	T	4	81	c.532C>T	c.(532-534)CAC>TAC	p.H178Y
Pat_32	Pre-Treatment	ZNF750	79755	37	17	80788214	80788214	Missense_Mutation	SNP	G	A	4	67	c.1976C>T	c.(1975-1977)CCG>CTG	p.P659L
Pat_32	Pre-Treatment	B3GNTL1	146712	37	17	80915107	80915107	Missense_Mutation	SNP	C	T	4	112	c.880G>A	c.(880-882)GTG>ATG	p.V294M
Pat_32	Pre-Treatment	EMILIN2	84034	37	18	2891084	2891084	Missense_Mutation	SNP	G	A	4	181	c.959G>A	c.(958-960)AGT>AAT	p.S320N
Pat_32	Pre-Treatment	LOC727896	727896	37	18	2946184	2946184	Missense_Mutation	SNP	C	A	4	154	c.351G>T	c.(349-351)TTG>TTT	p.L117F
Pat_32	Pre-Treatment	L3MBTL4	91133	37	18	5969427	5969427	Missense_Mutation	SNP	G	A	4	128	c.1606C>T	c.(1606-1608)CGG>TGG	p.R536W
Pat_32	Pre-Treatment	LAMA3	3909	37	18	21444806	21444806	Missense_Mutation	SNP	G	A	4	81	c.4642G>A	c.(4642-4644)GAC>AAC	p.D1548N
Pat_32	Pre-Treatment	PIAS2	9063	37	18	44426791	44426791	Missense_Mutation	SNP	G	A	3	24	c.740C>T	c.(739-741)CCG>CTG	p.P247L
Pat_32	Pre-Treatment	ZCCHC2	54877	37	18	60206998	60206998	Missense_Mutation	SNP	G	A	3	31	c.1024G>A	c.(1024-1026)GTG>ATG	p.V342M
Pat_32	Pre-Treatment	DSEL	92126	37	18	65180296	65180296	Missense_Mutation	SNP	C	T	4	85	c.1580G>A	c.(1579-1581)GGT>GAT	p.G527D
Pat_32	Pre-Treatment	CNDP2	55748	37	18	72178216	72178216	Missense_Mutation	SNP	G	A	4	54	c.625G>A	c.(625-627)GGC>AGC	p.G209S
Pat_32	Pre-Treatment	PPAP2C	8612	37	19	282265	282265	Nonsense_Mutation	SNP	G	A	4	52	c.586C>T	c.(586-588)CGA>TGA	p.R196*
Pat_32	Pre-Treatment	ZNF555	148254	37	19	2853168	2853168	Missense_Mutation	SNP	G	A	4	82	c.1105G>A	c.(1105-1107)GAA>AAA	p.E369K
Pat_32	Pre-Treatment	PIP5K1C	23396	37	19	3664846	3664846	Missense_Mutation	SNP	C	T	4	122	c.193G>A	c.(193-195)GCA>ACA	p.A65T
Pat_32	Pre-Treatment	MUC16	94025	37	19	9015707	9015707	Missense_Mutation	SNP	T	C	8	213	c.38116A>G	c.(38116-38118)ACC>GCC	p.T12706A
Pat_32	Pre-Treatment	OR7G1	125962	37	19	9226304	9226304	Missense_Mutation	SNP	G	A	4	174	c.136C>T	c.(136-138)CTC>TTC	p.L46F
Pat_32	Pre-Treatment	CDC37	11140	37	19	10506759	10506759	Missense_Mutation	SNP	C	T	4	123	c.223G>A	c.(223-225)GAG>AAG	p.E75K
Pat_32	Pre-Treatment	ELAVL3	1995	37	19	11577437	11577437	Missense_Mutation	SNP	C	T	4	72	c.215G>A	c.(214-216)CGG>CAG	p.R72Q
Pat_32	Pre-Treatment	ECSIT	51295	37	19	11618827	11618827	Missense_Mutation	SNP	G	A	4	139	c.775C>T	c.(775-777)CCC>TCC	p.P259S
Pat_32	Pre-Treatment	ZNF788	388507	37	19	12221164	12221164	Translation_Start_Site	SNP	C	T	4	154	c.-384C>T	(-386--382)GACGA>GATGA	
Pat_32	Pre-Treatment	MAST1	22983	37	19	12978321	12978321	Missense_Mutation	SNP	G	A	4	140	c.2173G>A	c.(2173-2175)GAG>AAG	p.E725K
Pat_32	Pre-Treatment	EMR2	30817	37	19	14854519	14854519	Missense_Mutation	SNP	G	A	4	149	c.2261C>T	c.(2260-2262)CCG>CTG	p.P754L
Pat_32	Pre-Treatment	NDUFA13	51079	37	19	19645867	19645867	Missense_Mutation	SNP	C	T	4	165	c.589C>T	c.(589-591)CGG>TGG	p.R197W
Pat_32	Pre-Treatment	DPY19L3	147991	37	19	32968457	32968457	Missense_Mutation	SNP	C	T	4	94	c.1727C>T	c.(1726-1728)GCG>GTG	p.A576V
Pat_32	Pre-Treatment	FXYD7	53822	37	19	35642576	35642576	Missense_Mutation	SNP	G	A	4	121	c.220G>A	c.(220-222)GCC>ACC	p.A74T

Pat_32	Pre-Treatment	FAM98C	147965	37	19	38895635	38895635	Missense_Mutation	SNP	G	A	4	176	c.437G>A	c.(436-438)GGG>GAG	p.G146E
Pat_32	Pre-Treatment	SUPT5H	6829	37	19	39949691	39949691	Missense_Mutation	SNP	G	A	4	184	c.436G>A	c.(436-438)GCC>ACC	p.A146T
Pat_32	Pre-Treatment	CEACAM4	1089	37	19	42131974	42131974	Splice_Site	SNP	C	T	4	161	c.424_splice	c.e2+1	p.Q142_splice
Pat_32	Pre-Treatment	ERF	2077	37	19	42753240	42753240	Missense_Mutation	SNP	G	A	5	61	c.1024C>T	c.(1024-1026)CCC>TCC	p.P342S
Pat_32	Pre-Treatment	LIPE	3991	37	19	42907123	42907123	Missense_Mutation	SNP	G	A	4	86	c.2603C>T	c.(2602-2604)ACG>ATG	p.T868M
Pat_32	Pre-Treatment	ZNF223	7766	37	19	44570873	44570873	Missense_Mutation	SNP	C	T	4	128	c.892C>T	c.(892-894)CGT>TGT	p.R298C
Pat_32	Pre-Treatment	PVR	5817	37	19	45157228	45157228	Missense_Mutation	SNP	G	A	4	108	c.784G>A	c.(784-786)GCC>ACC	p.A262T
Pat_32	Pre-Treatment	PRKD2	25865	37	19	47181690	47181690	Missense_Mutation	SNP	C	T	4	42	c.2301G>A	c.(2299-2301)ATG>ATA	p.M767I
Pat_32	Pre-Treatment	LMTK3	114783	37	19	49001471	49001471	Missense_Mutation	SNP	G	A	16	23	c.2942C>T	c.(2941-2943)CCC>CTC	p.P981L
Pat_32	Pre-Treatment	IL4I1	259307	37	19	50394307	50394307	Missense_Mutation	SNP	C	T	4	100	c.694G>A	c.(694-696)GTG>ATG	p.V232M
Pat_32	Pre-Treatment	ACPT	93650	37	19	51294940	51294940	Missense_Mutation	SNP	C	T	4	160	c.331C>T	c.(331-333)CGC>TGC	p.R111C
Pat_32	Pre-Treatment	KLK14	43847	37	19	51582802	51582802	Missense_Mutation	SNP	C	T	3	26	c.418G>A	c.(418-420)GGG>AGG	p.G140R
Pat_32	Pre-Treatment	SIGLEC7	27036	37	19	51649282	51649282	Missense_Mutation	SNP	C	T	4	100	c.931C>T	c.(931-933)CAC>TAC	p.H311Y
Pat_32	Pre-Treatment	SIGLEC6	946	37	19	52034213	52034213	Missense_Mutation	SNP	G	A	4	94	c.428C>T	c.(427-429)GCC>GTC	p.A143V
Pat_32	Pre-Treatment	FPR3	2359	37	19	52327161	52327161	Missense_Mutation	SNP	C	T	4	133	c.160C>T	c.(160-162)CGG>TGG	p.R54W
Pat_32	Pre-Treatment	ZNF528	84436	37	19	52918958	52918958	Missense_Mutation	SNP	G	T	5	117	c.853G>T	c.(853-855)GCA>TCA	p.A285S
Pat_32	Pre-Treatment	ZNF600	162966	37	19	53270632	53270632	Missense_Mutation	SNP	C	T	4	84	c.377G>A	c.(376-378)AGA>AAA	p.R126K
Pat_32	Pre-Treatment	ZNF320	162967	37	19	53384528	53384528	Missense_Mutation	SNP	C	T	4	171	c.851G>A	c.(850-852)CGA>CAA	p.R284Q
Pat_32	Pre-Treatment	LILRB2	10288	37	19	54783664	54783664	Missense_Mutation	SNP	G	T	18	57	c.337C>A	c.(337-339)CTG>ATG	p.L113M
Pat_32	Pre-Treatment	LILRA5	353514	37	19	54818709	54818709	Missense_Mutation	SNP	C	T	22	58	c.889G>A	c.(889-891)GCT>ACT	p.A297T
Pat_32	Pre-Treatment	LILRA2	11027	37	19	55086264	55086264	Missense_Mutation	SNP	C	T	4	128	c.419C>T	c.(418-420)ACC>ATC	p.T140I
Pat_32	Pre-Treatment	RPL28	6158	37	19	55897956	55897956	Missense_Mutation	SNP	G	A	4	140	c.100G>A	c.(100-102)GCC>ACC	p.A34T
Pat_32	Pre-Treatment	ZNF256	10172	37	19	58455313	58455313	Missense_Mutation	SNP	G	A	4	123	c.149C>T	c.(148-150)ACA>ATA	p.T50I
Pat_32	Pre-Treatment	ZNF135	7694	37	19	58574832	58574832	Missense_Mutation	SNP	C	T	4	71	c.179C>T	c.(178-180)CCG>CTG	p.P60L
Pat_32	Pre-Treatment	KCNS3	3790	37	2	18113071	18113071	Missense_Mutation	SNP	T	C	32	67	c.796T>C	c.(796-798)TTC>CTC	p.F266L
Pat_32	Pre-Treatment	MFSD2B	388931	37	2	24246538	24246538	Missense_Mutation	SNP	G	A	4	182	c.1255G>A	c.(1255-1257)GTC>ATC	p.V419I
Pat_32	Pre-Treatment	ASXL2	55252	37	2	25965173	25965173	Missense_Mutation	SNP	C	T	8	53	c.4033G>A	c.(4033-4035)GTA>ATA	p.V1345I
Pat_32	Pre-Treatment	C2orf70	339778	37	2	26798955	26798955	Missense_Mutation	SNP	G	A	4	178	c.260G>A	c.(259-261)AGC>AAC	p.S87N
Pat_32	Pre-Treatment	ABHD1	84696	37	2	27352448	27352448	Missense_Mutation	SNP	C	T	4	147	c.571C>T	c.(571-573)CGT>TGT	p.R191C
Pat_32	Pre-Treatment	C2orf16	84226	37	2	27804355	27804355	Missense_Mutation	SNP	G	A	5	244	c.4916G>A	c.(4915-4917)CGC>CAC	p.R1639H
Pat_32	Pre-Treatment	SOS1	6654	37	2	39213384	39213384	Nonsense_Mutation	SNP	G	A	4	109	c.3583C>T	c.(3583-3585)CGA>TGA	p.R1195*
Pat_32	Pre-Treatment	C2orf42	54980	37	2	70409005	70409005	Missense_Mutation	SNP	C	T	4	88	c.113G>A	c.(112-114)CGG>CAG	p.R38Q
Pat_32	Pre-Treatment	C2orf78	388960	37	2	74043857	74043857	Missense_Mutation	SNP	G	A	3	69	c.2507G>A	c.(2506-2508)CGG>CAG	p.R836Q
Pat_32	Pre-Treatment	MOGS	7841	37	2	74689115	74689115	Nonsense_Mutation	SNP	G	A	4	138	c.1801C>T	c.(1801-1803)CGA>TGA	p.R601*
Pat_32	Pre-Treatment	CCDC142	84865	37	2	74708602	74708602	Missense_Mutation	SNP	G	A	4	108	c.1085C>T	c.(1084-1086)TCG>TTG	p.S362L
Pat_32	Pre-Treatment	ADRA2B	151	37	2	96781147	96781147	Missense_Mutation	SNP	C	T	3	37	c.742G>A	c.(742-744)GGA>AGA	p.G248R
Pat_32	Pre-Treatment	IL18R1	8809	37	2	102988526	102988526	Missense_Mutation	SNP	C	T	3	55	c.416C>T	c.(415-417)ACC>ATC	p.T139I
Pat_32	Pre-Treatment	POLR1B	84172	37	2	113333092	113333092	Missense_Mutation	SNP	C	T	4	127	c.3194C>T	c.(3193-3195)TCG>TTG	p.S1065L
Pat_32	Pre-Treatment	FAM168B	130074	37	2	131813136	131813136	Missense_Mutation	SNP	G	A	4	133	c.287C>T	c.(286-288)CCG>CTG	p.P96L
Pat_32	Pre-Treatment	LYPD6	130574	37	2	150325225	150325225	Missense_Mutation	SNP	G	A	6	309	c.284G>A	c.(283-285)CGC>CAC	p.R95H
Pat_32	Pre-Treatment	NR4A2	4929	37	2	157183339	157183339	Missense_Mutation	SNP	G	A	4	182	c.1252C>T	c.(1252-1254)CGG>TGG	p.R418W
Pat_32	Pre-Treatment	FIGN	55137	37	2	164468067	164468067	Missense_Mutation	SNP	G	A	5	198	c.275C>T	c.(274-276)TCG>TTG	p.S92L
Pat_32	Pre-Treatment	OSBPL6	114880	37	2	179248776	179248776	Missense_Mutation	SNP	C	T	5	182	c.1886C>T	c.(1885-1887)GCC>GTC	p.A629V
Pat_32	Pre-Treatment	TTN	7273	37	2	179623711	179623711	Missense_Mutation	SNP	C	T	4	69	c.10303G>A	c.(10303-10305)GCT>ACT	p.A3435T
Pat_32	Pre-Treatment	TTN	7273	37	2	179640583	179640583	Missense_Mutation	SNP	C	T	4	138	c.6008G>A	c.(6007-6009)CGC>CAC	p.R2003H
Pat_32	Pre-Treatment	COL5A2	1290	37	2	189904043	189904043	Missense_Mutation	SNP	G	A	4	121	c.3880C>T	c.(3880-3882)CGC>TGC	p.R1294C
Pat_32	Pre-Treatment	PGAP1	80055	37	2	197708675	197708675	Missense_Mutation	SNP	T	C	39	55	c.2462A>G	c.(2461-2463)AAC>AGC	p.N821S

Pat_32	Pre-Treatment	C2orf69	205327	37	2	200790460	200790460	Missense_Mutation	SNP	C	T	4	187	c.1009C>T	c.(1009-1011)CGT>TGT	p.R337C
Pat_32	Pre-Treatment	PARD3B	117583	37	2	206480461	206480461	Missense_Mutation	SNP	G	A	4	85	c.3542G>A	c.(3541-3543)CGT>CAT	p.R1181H
Pat_32	Pre-Treatment	TNS1	7145	37	2	218762676	218762676	Missense_Mutation	SNP	G	A	3	28	c.13C>T	c.(13-15)CGG>TGG	p.R5W
Pat_32	Pre-Treatment	TTLL4	9654	37	2	219617532	219617532	Missense_Mutation	SNP	G	A	4	185	c.3023G>A	c.(3022-3024)CGG>CAG	p.R1008Q
Pat_32	Pre-Treatment	STK11IP	114790	37	2	220466052	220466052	Missense_Mutation	SNP	G	A	4	95	c.190G>A	c.(190-192)GGC>AGC	p.G64S
Pat_32	Pre-Treatment	GIGYF2	26058	37	2	233684688	233684688	Missense_Mutation	SNP	G	A	4	92	c.2522G>A	c.(2521-2523)CGC>CAC	p.R841H
Pat_32	Pre-Treatment	DGKD	8527	37	2	234346033	234346033	Missense_Mutation	SNP	C	T	15	46	c.830C>T	c.(829-831)TCG>TTG	p.S277L
Pat_32	Pre-Treatment	SH3BP4	23677	37	2	235950569	235950569	Missense_Mutation	SNP	G	C	3	14	c.1156G>C	c.(1156-1158)GAG>CAG	p.E386Q
Pat_32	Pre-Treatment	THAP4	51078	37	2	242542416	242542416	Missense_Mutation	SNP	G	T	4	124	c.1479C>A	c.(1477-1479)AAC>AAA	p.N493K
Pat_32	Pre-Treatment	SIRPA	140885	37	20	1902292	1902292	Missense_Mutation	SNP	G	A	7	88	c.688G>A	c.(688-690)GTG>ATG	p.V230M
Pat_32	Pre-Treatment	SIRPA	140885	37	20	1902301	1902301	Missense_Mutation	SNP	G	A	11	101	c.697G>A	c.(697-699)GTC>ATC	p.V233I
Pat_32	Pre-Treatment	TGM3	7053	37	20	2308780	2308780	Missense_Mutation	SNP	G	A	4	115	c.1102G>A	c.(1102-1104)GGC>AGC	p.G368S
Pat_32	Pre-Treatment	VPS16	64601	37	20	2845822	2845822	Missense_Mutation	SNP	G	A	4	161	c.2033G>A	c.(2032-2034)CGG>CAG	p.R678Q
Pat_32	Pre-Treatment	ProSAPiP1	9762	37	20	3145179	3145179	Missense_Mutation	SNP	G	A	4	86	c.1943C>T	c.(1942-1944)ACG>ATG	p.T648M
Pat_32	Pre-Treatment	C20orf191	149934	37	20	26084295	26084295	Missense_Mutation	SNP	C	T	3	47	c.121G>A	c.(121-123)GGA>AGA	p.G41R
Pat_32	Pre-Treatment	RBL1	5933	37	20	35635837	35635837	Missense_Mutation	SNP	C	T	4	156	c.2848G>A	c.(2848-2850)GAC>AAC	p.D950N
Pat_32	Pre-Treatment	WISP2	8839	37	20	43348589	43348589	Nonsense_Mutation	SNP	C	T	5	216	c.112C>T	c.(112-114)CGA>TGA	p.R38*
Pat_32	Pre-Treatment	PABPC1L	80336	37	20	43566707	43566707	Missense_Mutation	SNP	C	T	4	168	c.1651C>T	c.(1651-1653)CGT>TGT	p.R551C
Pat_32	Pre-Treatment	PLTP	5360	37	20	44533619	44533619	Missense_Mutation	SNP	G	A	4	194	c.844C>T	c.(844-846)CGG>TGG	p.R282W
Pat_32	Pre-Treatment	C20orf195	79025	37	20	62187846	62187846	Missense_Mutation	SNP	G	A	6	364	c.830G>A	c.(829-831)CGA>CAA	p.R277Q
Pat_32	Pre-Treatment	ZGPAT	84619	37	20	62366126	62366126	Missense_Mutation	SNP	G	A	4	138	c.1001G>A	c.(1000-1002)CGA>CAA	p.R334Q
Pat_32	Pre-Treatment	ZNF512B	57473	37	20	62593986	62593986	Nonsense_Mutation	SNP	C	T	4	46	c.2117G>A	c.(2116-2118)TGG>TAG	p.W706*
Pat_32	Pre-Treatment	DOPEY2	9980	37	21	37609674	37609674	Missense_Mutation	SNP	G	A	4	104	c.2737G>A	c.(2737-2739)GAG>AAG	p.E913K
Pat_32	Pre-Treatment	DYRK1A	1859	37	21	38862710	38862710	Missense_Mutation	SNP	C	T	4	168	c.898C>T	c.(898-900)CGC>TGC	p.R300C
Pat_32	Pre-Treatment	RIPK4	54101	37	21	43161318	43161318	Missense_Mutation	SNP	G	A	4	120	c.2035C>T	c.(2035-2037)CGC>TGC	p.R679C
Pat_32	Pre-Treatment	CBS	875	37	21	44478298	44478298	Missense_Mutation	SNP	G	A	4	128	c.1424C>T	c.(1423-1425)CCG>CTG	p.P475L
Pat_32	Pre-Treatment	RRP1	8568	37	21	45219501	45219501	Missense_Mutation	SNP	G	A	4	52	c.862G>A	c.(862-864)GAC>AAC	p.D288N
Pat_32	Pre-Treatment	ADARB1	104	37	21	46596515	46596515	Missense_Mutation	SNP	A	T	5	148	c.899A>T	c.(898-900)CAC>CTC	p.H300L
Pat_32	Pre-Treatment	DIP2A	23181	37	21	47987479	47987479	Missense_Mutation	SNP	C	T	4	143	c.4660C>T	c.(4660-4662)CGG>TGG	p.R1554W
Pat_32	Pre-Treatment	5-Sep	5413	37	22	19708173	19708173	Missense_Mutation	SNP	G	A	4	88	c.599G>A	c.(598-600)CGG>CAG	p.R200Q
Pat_32	Pre-Treatment	5-Sep	5413	37	22	19709223	19709223	Missense_Mutation	SNP	G	A	4	105	c.778G>A	c.(778-780)GTC>ATC	p.V260I
Pat_32	Pre-Treatment	TOP3B	8940	37	22	22326305	22326305	Missense_Mutation	SNP	C	T	4	163	c.328G>A	c.(328-330)GAC>AAC	p.D110N
Pat_32	Pre-Treatment	MYO18B	84700	37	22	26423222	26423222	Missense_Mutation	SNP	C	T	4	144	c.7282C>T	c.(7282-7284)CTC>TTC	p.L2428F
Pat_32	Pre-Treatment	EWSR1	2130	37	22	29684603	29684603	Nonsense_Mutation	SNP	C	T	5	137	c.802C>T	c.(802-804)CGA>TGA	p.R268*
Pat_32	Pre-Treatment	CABP7	164633	37	22	30123680	30123680	Missense_Mutation	SNP	C	T	4	140	c.139C>T	c.(139-141)CGT>TGT	p.R47C
Pat_32	Pre-Treatment	DEPDC5	9681	37	22	32198806	32198806	Nonsense_Mutation	SNP	C	T	4	182	c.1063C>T	c.(1063-1065)CAG>TAG	p.Q355*
Pat_32	Pre-Treatment	DNAJB7	150353	37	22	41257776	41257776	Missense_Mutation	SNP	C	T	5	230	c.223G>A	c.(223-225)GGA>AGA	p.G75R
Pat_32	Pre-Treatment	C22orf9	23313	37	22	45601715	45601715	Missense_Mutation	SNP	C	T	4	34	c.295G>A	c.(295-297)GAC>AAC	p.D99N
Pat_32	Pre-Treatment	GRAMD4	23151	37	22	47054119	47054119	Missense_Mutation	SNP	G	A	3	58	c.319G>A	c.(319-321)GCG>ACG	p.A107T
Pat_32	Pre-Treatment	BRD1	23774	37	22	50187865	50187865	Missense_Mutation	SNP	C	T	4	90	c.2176G>A	c.(2176-2178)GAC>AAC	p.D726N
Pat_32	Pre-Treatment	NCAPH2	29781	37	22	50954903	50954903	Missense_Mutation	SNP	G	A	4	126	c.136G>A	c.(136-138)GAA>AAA	p.E46K
Pat_32	Pre-Treatment	CPT1B	1375	37	22	51008832	51008832	Missense_Mutation	SNP	G	A	3	46	c.2032C>T	c.(2032-2034)CTC>TTC	p.L678F
Pat_32	Pre-Treatment	ITPR1	3708	37	3	4810392	4810392	Nonsense_Mutation	SNP	C	T	4	164	c.5779C>T	c.(5779-5781)CAG>TAG	p.Q1927*
Pat_32	Pre-Treatment	GRM7	2917	37	3	7503321	7503321	Missense_Mutation	SNP	G	A	5	210	c.1427G>A	c.(1426-1428)CGT>CAT	p.R476H
Pat_32	Pre-Treatment	SGOL1	151648	37	3	20216232	20216232	Missense_Mutation	SNP	G	A	4	148	c.791C>T	c.(790-792)ACG>ATG	p.T264M
Pat_32	Pre-Treatment	TGFBR2	7048	37	3	30713843	30713843	Missense_Mutation	SNP	G	A	6	373	c.1168G>A	c.(1168-1170)GAC>AAC	p.D390N
Pat_32	Pre-Treatment	CLASP2	23122	37	3	33644501	33644501	Missense_Mutation	SNP	C	T	5	11	c.1867G>A	c.(1867-1869)GTG>ATG	p.V623M

Pat_32	Pre-Treatment	TRANK1	9881	37	3	36875205	36875205	Missense_Mutation	SNP	T	A	25	47	c.4087A>T	c.(4087-4089)AAC>TAC	p.N1363Y
Pat_32	Pre-Treatment	DLEC1	9940	37	3	38163567	38163567	Nonsense_Mutation	SNP	C	T	3	26	c.5026C>T	c.(5026-5028)CAG>TAG	p.Q1676*
Pat_32	Pre-Treatment	WDR48	57599	37	3	39104667	39104667	Missense_Mutation	SNP	G	A	4	181	c.175G>A	c.(175-177)GTC>ATC	p.V59I
Pat_32	Pre-Treatment	NKTR	4820	37	3	42676768	42676768	Missense_Mutation	SNP	G	A	4	115	c.1073G>A	c.(1072-1074)AGC>AAC	p.S358N
Pat_32	Pre-Treatment	NBEAL2	23218	37	3	47049615	47049615	Missense_Mutation	SNP	G	A	4	79	c.7658G>A	c.(7657-7659)GGG>GAG	p.G2553E
Pat_32	Pre-Treatment	CELSR3	1951	37	3	48698077	48698077	Missense_Mutation	SNP	G	A	4	81	c.1991C>T	c.(1990-1992)GCT>GTT	p.A664V
Pat_32	Pre-Treatment	NDUFAF3	25915	37	3	49060595	49060595	Missense_Mutation	SNP	C	T	4	139	c.545C>T	c.(544-546)GCT>GTT	p.A182V
Pat_32	Pre-Treatment	QRICH1	54870	37	3	49094328	49094329	Missense_Mutation	DNP	CT	TG	3	50	.1304_1305AG>C	c.(1303-1305)CAG>CCA	p.Q435P
Pat_32	Pre-Treatment	GNAT1	2779	37	3	50231059	50231059	Missense_Mutation	SNP	C	A	3	70	c.412C>A	c.(412-414)CGC>AGC	p.R138S
Pat_32	Pre-Treatment	ITIH4	3700	37	3	52851074	52851074	Missense_Mutation	SNP	C	T	4	73	c.2297G>A	c.(2296-2298)GGG>GAG	p.G766E
Pat_32	Pre-Treatment	ATXN7	6314	37	3	63981293	63981293	Missense_Mutation	SNP	G	A	4	162	c.1795G>A	c.(1795-1797)GTC>ATC	p.V599I
Pat_32	Pre-Treatment	CNTN3	5067	37	3	74313619	74313619	Missense_Mutation	SNP	G	A	4	119	c.3020C>T	c.(3019-3021)TCG>TTG	p.S1007L
Pat_32	Pre-Treatment	CCDC80	151887	37	3	112358361	112358361	Missense_Mutation	SNP	C	T	4	163	c.392G>A	c.(391-393)CGT>CAT	p.R131H
Pat_32	Pre-Treatment	ARHGAP31	57514	37	3	119118063	119118063	Nonsense_Mutation	SNP	C	T	5	65	c.1024C>T	c.(1024-1026)CGA>TGA	p.R342*
Pat_32	Pre-Treatment	ARHGAP31	57514	37	3	119134452	119134452	Missense_Mutation	SNP	G	A	6	36	c.3676G>A	c.(3676-3678)GTT>ATT	p.V1226I
Pat_32	Pre-Treatment	GOLGB1	2804	37	3	121415795	121415795	Missense_Mutation	SNP	C	T	4	143	c.3560G>A	c.(3559-3561)CGC>CAC	p.R1187H
Pat_32	Pre-Treatment	SEMA5B	54437	37	3	122634464	122634464	Missense_Mutation	SNP	C	T	4	26	c.1811G>A	c.(1810-1812)CGG>CAG	p.R604Q
Pat_32	Pre-Treatment	SEMA5B	54437	37	3	122646735	122646735	Missense_Mutation	SNP	G	A	4	52	c.752C>T	c.(751-753)ACG>ATG	p.T251M
Pat_32	Pre-Treatment	AMOTL2	51421	37	3	134086424	134086424	Missense_Mutation	SNP	C	T	4	187	c.1130G>A	c.(1129-1131)AGG>AAG	p.R377K
Pat_32	Pre-Treatment	SGEF	26084	37	3	153972602	153972602	Missense_Mutation	SNP	G	A	4	192	c.2462G>A	c.(2461-2463)CGT>CAT	p.R821H
Pat_32	Pre-Treatment	WHSC1	7468	37	4	1980497	1980497	Missense_Mutation	SNP	G	A	4	93	c.3959G>A	c.(3958-3960)CGG>CAG	p.R1320Q
Pat_32	Pre-Treatment	GRK4	2868	37	4	2986281	2986281	Missense_Mutation	SNP	G	A	17	70	c.94G>A	c.(94-96)GAG>AAG	p.E32K
Pat_32	Pre-Treatment	EVC	2121	37	4	5806511	5806511	Missense_Mutation	SNP	C	T	4	127	c.2504C>T	c.(2503-2505)TCG>TTG	p.S835L
Pat_32	Pre-Treatment	ABLIM2	84448	37	4	8010776	8010776	Splice_Site	SNP	C	T	4	148	c.1377_splice	c.e14+1	p.K459_splice
Pat_32	Pre-Treatment	ZNF518B	85460	37	4	10446269	10446269	Missense_Mutation	SNP	G	A	4	60	c.1684C>T	c.(1684-1686)CCT>TCT	p.P562S
Pat_32	Pre-Treatment	GPR125	166647	37	4	22422643	22422643	Missense_Mutation	SNP	C	T	5	277	c.1675G>A	c.(1675-1677)GTG>ATG	p.V559M
Pat_32	Pre-Treatment	DHX15	1665	37	4	24572443	24572443	Nonsense_Mutation	SNP	G	A	5	63	c.535C>T	c.(535-537)CGA>TGA	p.R179*
Pat_32	Pre-Treatment	RBM47	54502	37	4	40439807	40439807	Missense_Mutation	SNP	G	C	3	72	c.1104C>G	c.(1102-1104)AAC>AAG	p.N368K
Pat_32	Pre-Treatment	LNX1	84708	37	4	54374317	54374317	Missense_Mutation	SNP	G	A	4	49	c.458C>T	c.(457-459)GCG>GTG	p.A153V
Pat_32	Pre-Treatment	AMBN	258	37	4	71471998	71471998	Missense_Mutation	SNP	G	A	4	61	c.895G>A	c.(895-897)GGC>AGC	p.G299S
Pat_32	Pre-Treatment	SLC4A4	8671	37	4	72316945	72316945	Missense_Mutation	SNP	G	T	46	191	c.1249G>T	c.(1249-1251)GGG>TGG	p.G417W
Pat_32	Pre-Treatment	FRAS1	80144	37	4	79399122	79399122	Missense_Mutation	SNP	G	A	4	59	c.8005G>A	c.(8005-8007)GAT>AAT	p.D2669N
Pat_32	Pre-Treatment	HERC5	51191	37	4	89388313	89388313	Missense_Mutation	SNP	C	T	4	143	c.1015C>T	c.(1015-1017)CCG>TCG	p.P339S
Pat_32	Pre-Treatment	TET2	54790	37	4	106157980	106157980	Missense_Mutation	SNP	G	A	4	112	c.2881G>A	c.(2881-2883)GAA>AAA	p.E961K
Pat_32	Pre-Treatment	KIAA1109	84162	37	4	123160786	123160786	Missense_Mutation	SNP	C	T	5	243	c.3949C>T	c.(3949-3951)CGT>TGT	p.R1317C
Pat_32	Pre-Treatment	TTC29	83894	37	4	147628661	147628661	Missense_Mutation	SNP	G	A	16	32	c.1373C>T	c.(1372-1374)TCA>TTA	p.S458L
Pat_32	Pre-Treatment	PET112L	5188	37	4	152601041	152601041	Missense_Mutation	SNP	G	A	4	172	c.1334C>T	c.(1333-1335)CCT>CTT	p.P445L
Pat_32	Pre-Treatment	PLRG1	5356	37	4	155459133	155459133	Missense_Mutation	SNP	G	A	4	178	c.1279C>T	c.(1279-1281)CTT>TTT	p.L427F
Pat_32	Pre-Treatment	SPATA4	132851	37	4	177114113	177114113	Nonsense_Mutation	SNP	G	A	4	100	c.463C>T	c.(463-465)CGA>TGA	p.R155*
Pat_32	Pre-Treatment	FAT1	2195	37	4	187557879	187557879	Missense_Mutation	SNP	C	T	6	315	c.3832G>A	c.(3832-3834)GAC>AAC	p.D1278N
Pat_32	Pre-Treatment	LPCAT1	79888	37	5	1489956	1489956	Missense_Mutation	SNP	G	A	8	325	c.511C>T	c.(511-513)CGG>TGG	p.R171W
Pat_32	Pre-Treatment	MRPL36	64979	37	5	1798797	1798797	Missense_Mutation	SNP	G	A	4	144	c.253C>T	c.(253-255)CGG>TGG	p.R85W
Pat_32	Pre-Treatment	DNAJC21	134218	37	5	34937509	34937509	Nonsense_Mutation	SNP	C	T	16	24	c.517C>T	c.(517-519)CGA>TGA	p.R173*
Pat_32	Pre-Treatment	NIPBL	25836	37	5	36986086	36986086	Missense_Mutation	SNP	C	T	32	69	c.2804C>T	c.(2803-2805)CCT>CTT	p.P935L
Pat_32	Pre-Treatment	EGFLAM	133584	37	5	38425067	38425067	Splice_Site	SNP	A	T	4	50	c.1685_splice	c.e13-2	p.G562_splice
Pat_32	Pre-Treatment	MAST4	375449	37	5	66459110	66459110	Missense_Mutation	SNP	G	A	4	133	c.3536G>A	c.(3535-3537)CGA>CAA	p.R1179Q
Pat_32	Pre-Treatment	RGNEF	64283	37	5	73072487	73072487	Missense_Mutation	SNP	G	A	5	256	c.806G>A	c.(805-807)CGG>CAG	p.R269Q

Pat_32	Pre-Treatment	DMGDH	29958	37	5	78347109	78347109	Splice_Site	SNP	C	T	4	123	c.745_splice	c.e5+1	p.G249_splice
Pat_32	Pre-Treatment	NR2F1	7025	37	5	92923685	92923685	Missense_Mutation	SNP	G	A	4	173	c.526G>A	c.(526-528)GGG>AGG	p.G176R
Pat_32	Pre-Treatment	CAST	831	37	5	96090398	96090398	Missense_Mutation	SNP	G	A	4	78	c.1414G>A	c.(1414-1416)GAA>AAA	p.E472K
Pat_32	Pre-Treatment	CHD1	1105	37	5	98229259	98229259	Nonsense_Mutation	SNP	G	A	4	110	c.1852C>T	c.(1852-1854)CGA>TGA	p.R618*
Pat_32	Pre-Treatment	PPIP5K2	23262	37	5	102503001	102503001	Missense_Mutation	SNP	G	A	4	136	c.2039G>A	c.(2038-2040)CGA>CAA	p.R680Q
Pat_32	Pre-Treatment	WDR36	134430	37	5	110448839	110448839	Missense_Mutation	SNP	C	T	4	132	c.1951C>T	c.(1951-1953)CTT>TTT	p.L651F
Pat_32	Pre-Treatment	ALDH7A1	501	37	5	125929071	125929071	Missense_Mutation	SNP	T	G	5	178	c.218A>C	c.(217-219)AAC>ACC	p.N73T
Pat_32	Pre-Treatment	SLC12A2	6558	37	5	127493771	127493771	Missense_Mutation	SNP	C	T	4	83	c.2390C>T	c.(2389-2391)GCT>GTT	p.A797V
Pat_32	Pre-Treatment	SLC27A6	28965	37	5	128324361	128324361	Missense_Mutation	SNP	G	T	4	127	c.754G>T	c.(754-756)GGT>TGT	p.G252C
Pat_32	Pre-Treatment	IL5	3567	37	5	131879182	131879182	Translation_Start_Site	SNP	G	A	3	63	c.-11C>T	c.(-13--9)AACGT>AATGT	
Pat_32	Pre-Treatment	TXNDC15	79770	37	5	134229210	134229210	Missense_Mutation	SNP	G	A	5	302	c.620G>A	c.(619-621)GGT>GAT	p.G207D
Pat_32	Pre-Treatment	KLHL3	26249	37	5	136969816	136969816	Missense_Mutation	SNP	G	A	3	84	c.1360C>T	c.(1360-1362)CGC>TGC	p.R454C
Pat_32	Pre-Treatment	KIF20A	10112	37	5	137519954	137519954	Missense_Mutation	SNP	G	A	5	242	c.1379G>A	c.(1378-1380)CGT>CAT	p.R460H
Pat_32	Pre-Treatment	CDC25C	995	37	5	137666711	137666711	Missense_Mutation	SNP	A	T	4	150	c.159T>A	c.(157-159)TTT>TTA	p.F53L
Pat_32	Pre-Treatment	PSD2	84249	37	5	139201522	139201522	Missense_Mutation	SNP	G	A	5	189	c.1142G>A	c.(1141-1143)CGT>CAT	p.R381H
Pat_32	Pre-Treatment	HARS2	23438	37	5	140076194	140076194	Missense_Mutation	SNP	G	A	4	78	c.821G>A	c.(820-822)TGT>TAT	p.C274Y
Pat_32	Pre-Treatment	PCDHB15	56121	37	5	140627271	140627271	Missense_Mutation	SNP	G	A	4	175	c.2125G>A	c.(2125-2127)GTG>ATG	p.V709M
Pat_32	Pre-Treatment	PCDH1	5097	37	5	141244687	141244687	Missense_Mutation	SNP	G	T	4	135	c.1209C>A	c.(1207-1209)AAC>AAA	p.N403K
Pat_32	Pre-Treatment	ANXA6	309	37	5	150498887	150498887	Missense_Mutation	SNP	C	T	4	101	c.1412G>A	c.(1411-1413)CGG>CAG	p.R471Q
Pat_32	Pre-Treatment	C5orf4	10826	37	5	154199982	154199982	Missense_Mutation	SNP	G	A	4	126	c.896C>T	c.(895-897)ACT>ATT	p.T299I
Pat_32	Pre-Treatment	TIMD4	91937	37	5	156378634	156378634	Missense_Mutation	SNP	C	T	4	121	c.568G>A	c.(568-570)GTC>ATC	p.V190I
Pat_32	Pre-Treatment	SLIT3	6586	37	5	168112718	168112718	Nonsense_Mutation	SNP	G	A	3	49	c.3529C>T	c.(3529-3531)CGA>TGA	p.R1177*
Pat_32	Pre-Treatment	BTN2A3	54718	37	6	26423221	26423221	Missense_Mutation	SNP	C	T	4	144	c.140C>T	c.(139-141)ACG>ATG	p.T47M
Pat_32	Pre-Treatment	BAT5	7920	37	6	31655427	31655427	Missense_Mutation	SNP	C	A	4	43	c.1538G>T	c.(1537-1539)TGG>TTG	p.W513L
Pat_32	Pre-Treatment	EGFL8	80864	37	6	32135716	32135716	Missense_Mutation	SNP	G	A	4	167	c.865G>A	c.(865-867)GGC>AGC	p.G289S
Pat_32	Pre-Treatment	PHF1	5252	37	6	33382064	33382064	Missense_Mutation	SNP	G	A	4	107	c.797G>A	c.(796-798)TGT>TAT	p.C266Y
Pat_32	Pre-Treatment	SCUBE3	222663	37	6	35210996	35210996	Missense_Mutation	SNP	G	A	4	52	c.1892G>A	c.(1891-1893)CGT>CAT	p.R631H
Pat_32	Pre-Treatment	FKBP5	2289	37	6	35604904	35604904	Missense_Mutation	SNP	G	A	3	70	c.137C>T	c.(136-138)ACG>ATG	p.T46M
Pat_32	Pre-Treatment	TREML1	340205	37	6	41117416	41117416	Missense_Mutation	SNP	C	T	3	54	c.862G>A	c.(862-864)GGA>AGA	p.G288R
Pat_32	Pre-Treatment	ZNF318	24149	37	6	43323731	43323731	Missense_Mutation	SNP	C	A	4	45	c.1341G>T	c.(1339-1341)CAG>CAT	p.Q447H
Pat_32	Pre-Treatment	SLC25A27	9481	37	6	46632515	46632515	Missense_Mutation	SNP	C	T	4	36	c.511C>T	c.(511-513)CGT>TGT	p.R171C
Pat_32	Pre-Treatment	TNFRSF21	27242	37	6	47253929	47253929	Missense_Mutation	SNP	G	A	5	272	c.499C>T	c.(499-501)CGG>TGG	p.R167W
Pat_32	Pre-Treatment	IL17A	3605	37	6	52054023	52054023	Missense_Mutation	SNP	G	A	4	82	c.401G>A	c.(400-402)CGG>CAG	p.R134Q
Pat_32	Pre-Treatment	MCM3	4172	37	6	52138606	52138606	Missense_Mutation	SNP	G	A	4	109	c.1483C>T	c.(1483-1485)CGG>TGG	p.R495W
Pat_32	Pre-Treatment	RARS2	57038	37	6	88229427	88229427	Splice_Site	SNP	T	A	4	54	c.1113_splice	c.e14-1	p.R371_splice
Pat_32	Pre-Treatment	HDDC2	51020	37	6	125623283	125623283	Splice_Site	SNP	C	T	3	9	c.-203_splice	c.e1-1	
Pat_32	Pre-Treatment	THEMIS	387357	37	6	128150855	128150855	Missense_Mutation	SNP	G	T	4	107	c.475C>A	c.(475-477)CAA>AAA	p.Q159K
Pat_32	Pre-Treatment	LAMA2	3908	37	6	129824276	129824276	Missense_Mutation	SNP	G	A	4	125	c.8398G>A	c.(8398-8400)GGC>AGC	p.G2800S
Pat_32	Pre-Treatment	PDE7B	27115	37	6	136476819	136476819	Missense_Mutation	SNP	G	A	4	48	c.634G>A	c.(634-636)GCA>ACA	p.A212T
Pat_32	Pre-Treatment	HECA	51696	37	6	139487505	139487505	Missense_Mutation	SNP	A	G	3	82	c.356A>G	c.(355-357)AAC>AGC	p.N119S
Pat_32	Pre-Treatment	ULBP1	80329	37	6	150290465	150290465	Missense_Mutation	SNP	G	T	5	90	c.594G>T	c.(592-594)TTG>TTT	p.L198F
Pat_32	Pre-Treatment	MTHFD1L	25902	37	6	151281463	151281463	Missense_Mutation	SNP	C	T	3	54	c.1856C>T	c.(1855-1857)ACG>ATG	p.T619M
Pat_32	Pre-Treatment	IGF2R	3482	37	6	160468929	160468929	Missense_Mutation	SNP	G	A	4	48	c.2335G>A	c.(2335-2337)GAC>AAC	p.D779N
Pat_32	Pre-Treatment	HEATR2	54919	37	7	813785	813785	Missense_Mutation	SNP	G	A	4	90	c.2032G>A	c.(2032-2034)GTG>ATG	p.V678M
Pat_32	Pre-Treatment	GPR146	115330	37	7	1097539	1097539	Missense_Mutation	SNP	G	A	4	171	c.388G>A	c.(388-390)GAG>AAG	p.E130K
Pat_32	Pre-Treatment	CHST12	55501	37	7	2473010	2473010	Missense_Mutation	SNP	G	A	5	186	c.736G>A	c.(736-738)GAC>AAC	p.D246N
Pat_32	Pre-Treatment	LFNG	3955	37	7	2565976	2565976	Missense_Mutation	SNP	G	A	4	171	c.920G>A	c.(919-921)CGC>CAC	p.R307H

Pat_32	Pre-Treatment	EIF2AK1	27102	37	7	6078293	6078293	Missense_Mutation	SNP	G	A	4	104	c.1129C>T	c.(1129-1131)CAC>TAC	p.H377Y
Pat_32	Pre-Treatment	EIF2AK1	27102	37	7	6094198	6094198	Missense_Mutation	SNP	G	A	4	151	c.256C>T	c.(256-258)CGT>TGT	p.R86C
Pat_32	Pre-Treatment	ETV1	2115	37	7	13971154	13971154	Missense_Mutation	SNP	C	T	5	96	c.775G>A	c.(775-777)GAA>AAA	p.E259K
Pat_32	Pre-Treatment	IGF2BP3	10643	37	7	23353172	23353172	Missense_Mutation	SNP	G	A	4	183	c.1496C>T	c.(1495-1497)GCT>GTT	p.A499V
Pat_32	Pre-Treatment	AVL9	23080	37	7	32609732	32609732	Missense_Mutation	SNP	G	A	6	490	c.1316G>A	c.(1315-1317)CGA>CAA	p.R439Q
Pat_32	Pre-Treatment	GCK	2645	37	7	44191932	44191932	Missense_Mutation	SNP	C	T	4	179	c.301G>A	c.(301-303)GTG>ATG	p.V101M
Pat_32	Pre-Treatment	CAMK2B	816	37	7	44294171	44294171	Missense_Mutation	SNP	G	A	4	161	c.311C>T	c.(310-312)GCG>GTG	p.A104V
Pat_32	Pre-Treatment	WBSCR17	64409	37	7	71177125	71177125	Missense_Mutation	SNP	C	G	20	77	c.1791C>G	c.(1789-1791)ATC>ATG	p.I597M
Pat_32	Pre-Treatment	SEMA3D	223117	37	7	84694808	84694808	Missense_Mutation	SNP	C	T	104	51	c.650G>A	c.(649-651)CGA>CAA	p.R217Q
Pat_32	Pre-Treatment	PON2	5445	37	7	95035519	95035519	Missense_Mutation	SNP	T	G	272	129	c.818A>C	c.(817-819)GAT>GCT	p.D273A
Pat_32	Pre-Treatment	BRI3	25798	37	7	97920524	97920524	Missense_Mutation	SNP	G	A	4	144	c.347G>A	c.(346-348)CGA>CAA	p.R116Q
Pat_32	Pre-Treatment	ZKSCAN5	23660	37	7	99129309	99129309	Nonsense_Mutation	SNP	C	T	5	162	c.1957C>T	c.(1957-1959)CGA>TGA	p.R653*
Pat_32	Pre-Treatment	C7orf43	55262	37	7	99755485	99755485	Missense_Mutation	SNP	G	T	4	163	c.488C>A	c.(487-489)CCA>CAA	p.P163Q
Pat_32	Pre-Treatment	C7orf61	402573	37	7	100061062	100061062	Missense_Mutation	SNP	G	A	5	368	c.311C>T	c.(310-312)CCG>CTG	p.P104L
Pat_32	Pre-Treatment	FBXO24	26261	37	7	100184264	100184264	Missense_Mutation	SNP	G	A	7	261	c.16G>A	c.(16-18)GTC>ATC	p.V6I
Pat_32	Pre-Treatment	MUC17	140453	37	7	100691297	100691297	Missense_Mutation	SNP	C	T	4	149	c.12436C>T	c.(12436-12438)CGC>TGC	p.R4146C
Pat_32	Pre-Treatment	MYL10	93408	37	7	101256769	101256769	Missense_Mutation	SNP	C	T	4	171	c.667G>A	c.(667-669)GAA>AAA	p.E223K
Pat_32	Pre-Treatment	ASB15	142685	37	7	123267235	123267235	Missense_Mutation	SNP	G	A	6	197	c.769G>A	c.(769-771)GAC>AAC	p.D257N
Pat_32	Pre-Treatment	TNPO3	23534	37	7	128633886	128633886	Missense_Mutation	SNP	A	T	26	157	c.1241T>A	c.(1240-1242)ATA>AAA	p.I414K
Pat_32	Pre-Treatment	ZC3HC1	51530	37	7	129668867	129668867	Nonsense_Mutation	SNP	G	A	4	77	c.496C>T	c.(496-498)CGA>TGA	p.R166*
Pat_32	Pre-Treatment	BRAF	673	37	7	140453136	140453136	Missense_Mutation	SNP	A	T	125	70	c.1799T>A	c.(1798-1800)GTG>GAG	p.V600E
Pat_32	Pre-Treatment	CLCN1	1180	37	7	143029823	143029823	Missense_Mutation	SNP	C	T	7	491	c.1258C>T	c.(1258-1260)CCC>TCC	p.P420S
Pat_32	Pre-Treatment	SSPO	23145	37	7	149474091	149474091	Missense_Mutation	SNP	G	A	4	148	c.301G>A	c.(301-303)GCC>ACC	p.A101T
Pat_32	Pre-Treatment	NOS3	4846	37	7	150707839	150707839	Missense_Mutation	SNP	G	A	4	118	c.2840G>A	c.(2839-2841)AGC>AAC	p.S947N
Pat_32	Pre-Treatment	SLC4A2	6522	37	7	150761787	150761787	Missense_Mutation	SNP	C	T	4	90	c.392C>T	c.(391-393)GCC>GTC	p.A131V
Pat_32	Pre-Treatment	PTPRN2	5799	37	7	157926656	157926656	Missense_Mutation	SNP	C	A	10	93	c.1269G>T	c.(1267-1269)ATG>ATT	p.M423I
Pat_32	Pre-Treatment	RP1L1	94137	37	8	10470173	10470173	Missense_Mutation	SNP	C	T	3	26	c.1435G>A	c.(1435-1437)GGG>AGG	p.G479R
Pat_32	Pre-Treatment	RAB11FIP1	80223	37	8	37729460	37729460	Missense_Mutation	SNP	C	T	5	188	c.2860G>A	c.(2860-2862)GAT>AAT	p.D954N
Pat_32	Pre-Treatment	TACC1	6867	37	8	38677330	38677330	Missense_Mutation	SNP	G	A	4	113	c.568G>A	c.(568-570)GCC>ACC	p.A190T
Pat_32	Pre-Treatment	IDO1	3620	37	8	39780096	39780096	Missense_Mutation	SNP	C	T	13	44	c.463C>T	c.(463-465)CGT>TGT	p.R155C
Pat_32	Pre-Treatment	LYPLA1	10434	37	8	54960666	54960666	Missense_Mutation	SNP	C	G	4	127	c.652G>C	c.(652-654)GTC>CTC	p.V218L
Pat_32	Pre-Treatment	KCNB2	9312	37	8	73850301	73850301	Missense_Mutation	SNP	G	A	5	114	c.2711G>A	c.(2710-2712)TGT>TAT	p.C904Y
Pat_32	Pre-Treatment	RPL7	6129	37	8	74203856	74203856	Missense_Mutation	SNP	G	T	4	114	c.469C>A	c.(469-471)CGT>AGT	p.R157S
Pat_32	Pre-Treatment	KLF10	7071	37	8	103663709	103663709	Missense_Mutation	SNP	G	A	31	49	c.851C>T	c.(850-852)CCT>CTT	p.P284L
Pat_32	Pre-Treatment	RIMS2	9699	37	8	105001612	105001612	Missense_Mutation	SNP	C	T	4	172	c.2341C>T	c.(2341-2343)CGT>TGT	p.R781C
Pat_32	Pre-Treatment	TMEM74	157753	37	8	109797038	109797038	Missense_Mutation	SNP	C	T	4	116	c.290G>A	c.(289-291)CGG>CAG	p.R97Q
Pat_32	Pre-Treatment	ZHX2	22882	37	8	123965305	123965305	Missense_Mutation	SNP	G	A	3	70	c.1555G>A	c.(1555-1557)GGT>AGT	p.G519S
Pat_32	Pre-Treatment	KLHL38	340359	37	8	124664685	124664685	Missense_Mutation	SNP	G	A	4	91	c.482C>T	c.(481-483)ACG>ATG	p.T161M
Pat_32	Pre-Treatment	GPR172A	79581	37	8	145583069	145583069	Missense_Mutation	SNP	A	G	3	34	c.116A>G	c.(115-117)AAA>AGA	p.K39R
Pat_32	Pre-Treatment	TEK	7010	37	9	27180258	27180258	Missense_Mutation	SNP	G	A	4	132	c.922G>A	c.(922-924)GGG>AGG	p.G308R
Pat_32	Pre-Treatment	SMU1	55234	37	9	33053233	33053233	Missense_Mutation	SNP	G	A	4	159	c.1178C>T	c.(1177-1179)ACC>ATC	p.T393I
Pat_32	Pre-Treatment	GALT	2592	37	9	34648886	34648886	Missense_Mutation	SNP	G	A	3	30	c.815G>A	c.(814-816)CGT>CAT	p.R272H
Pat_32	Pre-Treatment	TMEM2	23670	37	9	74365121	74365121	Missense_Mutation	SNP	G	A	4	169	c.169C>T	c.(169-171)CGG>TGG	p.R57W
Pat_32	Pre-Treatment	BICD2	23299	37	9	95485026	95485026	Missense_Mutation	SNP	C	T	3	55	c.518G>A	c.(517-519)CGG>CAG	p.R173Q
Pat_32	Pre-Treatment	C9orf5	23731	37	9	111819554	111819554	Missense_Mutation	SNP	G	A	4	82	c.1771C>T	c.(1771-1773)CGT>TGT	p.R591C
Pat_32	Pre-Treatment	CEP110	11064	37	9	123902994	123902994	Missense_Mutation	SNP	C	T	3	45	c.2413C>T	c.(2413-2415)CGT>TGT	p.R805C
Pat_32	Pre-Treatment	PTGS1	5742	37	9	125148833	125148833	Missense_Mutation	SNP	G	A	5	273	c.1118G>A	c.(1117-1119)CGC>CAC	p.R373H

Pat_32	Pre-Treatment	NEK6	10783	37	9	127101942	127101942	Missense_Mutation	SNP	G	A	4	137	c.715G>A	c.(715-717)GAG>AAG	p.E239K
Pat_32	Pre-Treatment	GARNL3	84253	37	9	130106529	130106529	Nonsense_Mutation	SNP	C	T	5	173	c.1267C>T	c.(1267-1269)CGA>TGA	p.R423*
Pat_32	Pre-Treatment	C9orf117	286207	37	9	130474995	130474995	Missense_Mutation	SNP	G	A	4	152	c.1145G>A	c.(1144-1146)CGC>CAC	p.R382H
Pat_32	Pre-Treatment	GOLGA2	2801	37	9	131023072	131023072	Missense_Mutation	SNP	G	A	3	26	c.1349C>T	c.(1348-1350)CCG>CTG	p.P450L
Pat_32	Pre-Treatment	RAPGEF1	2889	37	9	134514039	134514039	Missense_Mutation	SNP	C	T	5	200	c.583G>A	c.(583-585)GTG>ATG	p.V195M
Pat_32	Pre-Treatment	C9orf171	389799	37	9	135374771	135374771	Nonsense_Mutation	SNP	G	A	5	92	c.416G>A	c.(415-417)TGG>TAG	p.W139*
Pat_32	Pre-Treatment	CAMSAP1	157922	37	9	138710442	138710442	Missense_Mutation	SNP	C	T	4	60	c.3980G>A	c.(3979-3981)CGG>CAG	p.R1327Q
Pat_32	Pre-Treatment	NOTCH1	4851	37	9	139399496	139399496	Nonsense_Mutation	SNP	G	T	3	37	c.4647C>A	c.(4645-4647)TGC>TGA	p.C1549*
Pat_32	Pre-Treatment	C9orf86	55684	37	9	139734188	139734188	Missense_Mutation	SNP	G	A	4	195	c.1801G>A	c.(1801-1803)GAG>AAG	p.E601K
Pat_32	Pre-Treatment	PNPLA7	375775	37	9	140391712	140391712	Missense_Mutation	SNP	C	T	2	1	c.1865G>A	c.(1864-1866)CGC>CAC	p.R622H
Pat_32	Pre-Treatment	PLCXD1	55344	37	X	215775	215775	Missense_Mutation	SNP	G	A	4	134	c.745G>A	c.(745-747)GTG>ATG	p.V249M
Pat_32	Pre-Treatment	SFRS17A	8227	37	X	1712719	1712719	Missense_Mutation	SNP	C	T	7	377	c.364C>T	c.(364-366)CCC>TCC	p.P122S
Pat_32	Pre-Treatment	ARSE	415	37	X	2856263	2856263	Missense_Mutation	SNP	G	A	4	85	c.1162C>T	c.(1162-1164)CGC>TGC	p.R388C
Pat_32	Pre-Treatment	WWC3	55841	37	X	10085354	10085354	Missense_Mutation	SNP	G	A	4	153	c.1255G>A	c.(1255-1257)GAC>AAC	p.D419N
Pat_32	Pre-Treatment	HCCS	3052	37	X	11139086	11139086	Missense_Mutation	SNP	C	A	6	365	c.581C>A	c.(580-582)CCA>CAA	p.P194Q
Pat_32	Pre-Treatment	ARHGAP6	395	37	X	11196273	11196273	Missense_Mutation	SNP	G	A	6	142	c.1576C>T	c.(1576-1578)CTC>TTC	p.L526F
Pat_32	Pre-Treatment	OTC	5009	37	X	38260652	38260652	Missense_Mutation	SNP	C	A	19	122	c.511C>A	c.(511-513)CAG>AAG	p.Q171K
Pat_32	Pre-Treatment	RGN	9104	37	X	46949351	46949351	Missense_Mutation	SNP	G	A	4	192	c.523G>A	c.(523-525)GTG>ATG	p.V175M
Pat_32	Pre-Treatment	MAGIX	79917	37	X	49021378	49021378	Missense_Mutation	SNP	G	A	4	164	c.457G>A	c.(457-459)GTG>ATG	p.V153M
Pat_32	Pre-Treatment	SLC7A3	84889	37	X	70148757	70148757	Missense_Mutation	SNP	C	T	63	51	c.466G>A	c.(466-468)GTG>ATG	p.V156M
Pat_32	Pre-Treatment	NLGN3	54413	37	X	70387443	70387443	Missense_Mutation	SNP	C	T	4	151	c.1496C>T	c.(1495-1497)TCG>TTG	p.S499L
Pat_32	Pre-Treatment	NONO	4841	37	X	70517748	70517748	Missense_Mutation	SNP	G	A	4	66	c.1091G>A	c.(1090-1092)CGG>CAG	p.R364Q
Pat_32	Pre-Treatment	PCDH11X	27328	37	X	91133749	91133749	Missense_Mutation	SNP	G	A	4	172	c.2510G>A	c.(2509-2511)CGC>CAC	p.R837H
Pat_32	Pre-Treatment	AMOT	154796	37	X	112021870	112021870	Missense_Mutation	SNP	A	C	128	168	c.3180T>G	c.(3178-3180)AAT>AAG	p.N1060K
Pat_32	Pre-Treatment	CT47B1	643311	37	X	120009341	120009341	Missense_Mutation	SNP	C	T	6	164	c.184G>A	c.(184-186)GGG>AGG	p.G62R
Pat_32	Pre-Treatment	XPNPEP2	7512	37	X	128896706	128896706	Missense_Mutation	SNP	G	A	4	189	c.1700G>A	c.(1699-1701)CGT>CAT	p.R567H
Pat_32	Pre-Treatment	L1CAM	3897	37	X	153130303	153130303	Missense_Mutation	SNP	G	A	4	167	c.3019C>T	c.(3019-3021)CGG>TGG	p.R1007W
Pat_32	Pre-Treatment	FLNA	2316	37	X	153593066	153593066	Missense_Mutation	SNP	G	A	4	109	c.1850C>T	c.(1849-1851)TCG>TTG	p.S617L
Pat_32	Pre-Treatment	FAM50A	9130	37	X	153678271	153678271	Missense_Mutation	SNP	G	A	4	99	c.821G>A	c.(820-822)GGG>GAG	p.G274E
Pat_32	Pre-Treatment	PLXNA3	55558	37	X	153698040	153698040	Missense_Mutation	SNP	G	A	4	123	c.4708G>A	c.(4708-4710)GGT>AGT	p.G1570S
Pat_32	Post-Resistance	CPSF3L	54973	37	1	1255905	1255905	Missense_Mutation	SNP	C	T	4	225	c.131G>A	c.(130-132)CGC>CAC	p.R44H
Pat_32	Post-Resistance	PLCH2	9651	37	1	2436053	2436053	Missense_Mutation	SNP	G	A	3	46	c.3652G>A	c.(3652-3654)GAA>AAA	p.E1218K
Pat_32	Post-Resistance	PGD	5226	37	1	10471598	10471598	Missense_Mutation	SNP	G	A	4	166	c.643G>A	c.(643-645)GAG>AAG	p.E215K
Pat_32	Post-Resistance	ATP13A2	23400	37	1	17316621	17316621	Splice_Site	SNP	C	T	4	120	c.2412_splice	c.e21+1	p.K804_splice
Pat_32	Post-Resistance	IGSF21	84966	37	1	18691918	18691918	Missense_Mutation	SNP	C	A	64	145	c.742C>A	c.(742-744)CGT>AGT	p.R248S
Pat_32	Post-Resistance	MYOM3	127294	37	1	24384024	24384024	Missense_Mutation	SNP	G	A	4	107	c.4144C>T	c.(4144-4146)CGC>TGC	p.R1382C
Pat_32	Post-Resistance	NIPAL3	57185	37	1	24790611	24790611	Splice_Site	SNP	G	T	5	71	c.1021_splice	c.e11+1	p.G341_splice
Pat_32	Post-Resistance	ADC	113451	37	1	33583557	33583557	Missense_Mutation	SNP	G	T	93	242	c.1084G>T	c.(1084-1086)GAT>TAT	p.D362Y
Pat_32	Post-Resistance	CSMD2	114784	37	1	34100918	34100918	Missense_Mutation	SNP	C	T	3	45	c.4862G>A	c.(4861-4863)GGA>GAA	p.G1621E
Pat_32	Post-Resistance	ZMYM4	9202	37	1	35857903	35857903	Missense_Mutation	SNP	C	A	4	219	c.2678C>A	c.(2677-2679)GCA>GAA	p.A893E
Pat_32	Post-Resistance	C1orf50	79078	37	1	43239249	43239249	Nonsense_Mutation	SNP	C	T	4	176	c.211C>T	c.(211-213)CGA>TGA	p.R71*
Pat_32	Post-Resistance	SLC2A1	6513	37	1	43396841	43396841	Missense_Mutation	SNP	G	A	4	162	c.151C>T	c.(151-153)CGC>TGC	p.R51C
Pat_32	Post-Resistance	TIE1	7075	37	1	43785133	43785133	Missense_Mutation	SNP	C	T	5	394	c.3040C>T	c.(3040-3042)CGT>TGT	p.R1014C
Pat_32	Post-Resistance	RNF220	55182	37	1	44878253	44878253	Missense_Mutation	SNP	G	A	61	150	c.484G>A	c.(484-486)GAA>AAA	p.E162K
Pat_32	Post-Resistance	STIL	6491	37	1	47717257	47717257	Missense_Mutation	SNP	C	T	95	176	c.3415G>A	c.(3415-3417)GAG>AAG	p.E1139K
Pat_32	Post-Resistance	C1orf168	199920	37	1	57216756	57216756	Missense_Mutation	SNP	G	A	65	192	c.1348C>T	c.(1348-1350)CCT>TCT	p.P450S
Pat_32	Post-Resistance	PGM1	5236	37	1	64101904	64101904	Splice_Site	SNP	G	A	4	210	c.874_splice	c.e6-1	p.D292_splice

Pat_32	Post-Resistance	JAK1	3716	37	1	65330535	65330535	Nonsense_Mutation	SNP	C	A	5	172	c.1111G>T	c.(1111-1113)GAA>TAA	p.E371*
Pat_32	Post-Resistance	SFRS11	9295	37	1	70716106	70716106	Nonsense_Mutation	SNP	C	T	3	40	c.1177C>T	c.(1177-1179)CGA>TGA	p.R393*
Pat_32	Post-Resistance	FAM73A	374986	37	1	78326966	78326966	Missense_Mutation	SNP	G	A	4	219	c.1333G>A	c.(1333-1335)GAT>AAT	p.D445N
Pat_32	Post-Resistance	DENND2D	79961	37	1	111731865	111731865	Missense_Mutation	SNP	A	G	3	206	c.983T>C	c.(982-984)GTC>GCC	p.V328A
Pat_32	Post-Resistance	SYCP1	6847	37	1	115399208	115399208	Nonsense_Mutation	SNP	T	A	15	142	c.123T>A	c.(121-123)TGT>TGA	p.C41*
Pat_32	Post-Resistance	PGLYRP3	114771	37	1	153276341	153276341	Missense_Mutation	SNP	G	A	4	214	c.521C>T	c.(520-522)CCC>CTC	p.P174L
Pat_32	Post-Resistance	PEAR1	375033	37	1	156883232	156883232	Missense_Mutation	SNP	G	A	55	30	c.2561G>A	c.(2560-2562)GGG>GAG	p.G854E
Pat_32	Post-Resistance	SPTA1	6708	37	1	158636110	158636110	Missense_Mutation	SNP	C	T	51	185	c.2216G>A	c.(2215-2217)CGT>CAT	p.R739H
Pat_32	Post-Resistance	DDR2	4921	37	1	162731149	162731149	Missense_Mutation	SNP	C	T	4	161	c.1004C>T	c.(1003-1005)ACG>ATG	p.T335M
Pat_32	Post-Resistance	LMX1A	4009	37	1	165175236	165175236	Missense_Mutation	SNP	C	T	13	88	c.853G>A	c.(853-855)GGA>AGA	p.G285R
Pat_32	Post-Resistance	LRRC52	440699	37	1	165532788	165532788	Nonsense_Mutation	SNP	G	A	4	84	c.669G>A	c.(667-669)TGG>TGA	p.W223*
Pat_32	Post-Resistance	F5	2153	37	1	169510502	169510502	Missense_Mutation	SNP	G	T	12	482	c.3826C>A	c.(3826-3828)CTT>ATT	p.L1276I
Pat_32	Post-Resistance	PLA2G4A	5321	37	1	186880412	186880412	Missense_Mutation	SNP	T	C	33	174	c.449T>C	c.(448-450)CTG>CCG	p.L150P
Pat_32	Post-Resistance	VASH2	79805	37	1	213134526	213134526	Missense_Mutation	SNP	C	T	13	122	c.295C>T	c.(295-297)CCA>TCA	p.P99S
Pat_32	Post-Resistance	URB2	9816	37	1	229770776	229770776	Missense_Mutation	SNP	A	G	12	29	c.416A>G	c.(415-417)TAC>TGC	p.Y139C
Pat_32	Post-Resistance	TRIM67	440730	37	1	231344960	231344960	Missense_Mutation	SNP	G	A	3	46	c.2087G>A	c.(2086-2088)CGC>CAC	p.R696H
Pat_32	Post-Resistance	OR2T4	127074	37	1	248524937	248524937	Missense_Mutation	SNP	A	T	11	228	c.55A>T	c.(55-57)ATG>TTG	p.M19L
Pat_32	Post-Resistance	PRPF18	8559	37	10	13658449	13658449	Missense_Mutation	SNP	G	A	86	148	c.844G>A	c.(844-846)GGT>AGT	p.G282S
Pat_32	Post-Resistance	PTER	9317	37	10	16528567	16528567	Missense_Mutation	SNP	C	A	4	200	c.649C>A	c.(649-651)CAA>AAA	p.Q217K
Pat_32	Post-Resistance	SVIL	6840	37	10	29759388	29759388	Missense_Mutation	SNP	C	T	4	148	c.5660G>A	c.(5659-5661)CGT>CAT	p.R1887H
Pat_32	Post-Resistance	ANKRD30A	91074	37	10	37430688	37430688	Missense_Mutation	SNP	C	T	7	104	c.695C>T	c.(694-696)GCG>GTG	p.A232V
Pat_32	Post-Resistance	ANKRD30A	91074	37	10	37430754	37430754	Missense_Mutation	SNP	T	C	7	113	c.761T>C	c.(760-762)GTG>GCG	p.V254A
Pat_32	Post-Resistance	ANKRD30A	91074	37	10	37431014	37431014	Missense_Mutation	SNP	A	T	4	163	c.1021A>T	c.(1021-1023)AGT>TGT	p.S341C
Pat_32	Post-Resistance	PCDH15	65217	37	10	56106157	56106157	Nonsense_Mutation	SNP	C	A	78	132	c.562G>T	c.(562-564)GAG>TAG	p.E188*
Pat_32	Post-Resistance	CISD1	55847	37	10	60047357	60047357	Missense_Mutation	SNP	G	A	3	63	c.274G>A	c.(274-276)GAA>AAA	p.E92K
Pat_32	Post-Resistance	DLG5	9231	37	10	79576788	79576788	Missense_Mutation	SNP	C	T	4	177	c.3851G>A	c.(3850-3852)CGG>CAG	p.R1284Q
Pat_32	Post-Resistance	ZRANB1	54764	37	10	126673442	126673442	Missense_Mutation	SNP	C	T	4	144	c.2008C>T	c.(2008-2010)CGG>TGG	p.R670W
Pat_32	Post-Resistance	MKI67	4288	37	10	129902825	129902825	Missense_Mutation	SNP	G	T	20	128	c.7279C>A	c.(7279-7281)CCT>ACT	p.P2427T
Pat_32	Post-Resistance	TRIM6-TRIM34	445372	37	11	5663725	5663725	Missense_Mutation	SNP	A	G	28	50	c.1925A>G	c.(1924-1926)CAA>CGA	p.Q642R
Pat_32	Post-Resistance	ABCC8	6833	37	11	17483161	17483161	Missense_Mutation	SNP	T	A	8	70	c.791A>T	c.(790-792)CAA>CTA	p.Q264L
Pat_32	Post-Resistance	USH1C	10083	37	11	17548874	17548874	Missense_Mutation	SNP	C	T	10	91	c.392G>A	c.(391-393)GGG>GAG	p.G131E
Pat_32	Post-Resistance	CCDC86	79080	37	11	60609745	60609745	Missense_Mutation	SNP	A	T	3	23	c.148A>T	c.(148-150)AGT>TGT	p.S50C
Pat_32	Post-Resistance	PLCB3	5331	37	11	64032908	64032908	Missense_Mutation	SNP	G	A	4	93	c.2969G>A	c.(2968-2970)CGC>CAC	p.R990H
Pat_32	Post-Resistance	MAP6	4135	37	11	75319188	75319188	Missense_Mutation	SNP	C	G	3	110	c.1085G>C	c.(1084-1086)AGC>ACC	p.S362T
Pat_32	Post-Resistance	MRE11A	4361	37	11	94197342	94197342	Missense_Mutation	SNP	G	A	4	193	c.1162C>T	c.(1162-1164)CGG>TGG	p.R388W
Pat_32	Post-Resistance	CASP5	838	37	11	104872837	104872837	Missense_Mutation	SNP	G	C	4	98	c.635C>G	c.(634-636)GCT>GGT	p.A212G
Pat_32	Post-Resistance	HTR3A	3359	37	11	113856791	113856791	Missense_Mutation	SNP	G	A	46	286	c.617G>A	c.(616-618)AGG>AAG	p.R206K
Pat_32	Post-Resistance	ARHGAP32	9743	37	11	128840325	128840325	Missense_Mutation	SNP	G	A	3	135	c.4741C>T	c.(4741-4743)CGG>TGG	p.R1581W
Pat_32	Post-Resistance	LEPREL2	10536	37	12	6946600	6946600	Missense_Mutation	SNP	G	A	9	34	c.1574G>A	c.(1573-1575)GGG>GAG	p.G525E
Pat_32	Post-Resistance	PTPN6	5777	37	12	7069358	7069358	Missense_Mutation	SNP	G	A	4	92	c.1537G>A	c.(1537-1539)GCC>ACC	p.A513T
Pat_32	Post-Resistance	KLRC1	3821	37	12	10601985	10601985	Missense_Mutation	SNP	G	A	5	480	c.340C>T	c.(340-342)CGT>TGT	p.R114C
Pat_32	Post-Resistance	KIAA0528	9847	37	12	22624408	22624408	Missense_Mutation	SNP	T	A	27	160	c.2283A>T	c.(2281-2283)AAA>AAT	p.K761N
Pat_32	Post-Resistance	DHH	50846	37	12	49484169	49484169	Missense_Mutation	SNP	C	T	3	34	c.664G>A	c.(664-666)GGA>AGA	p.G222R
Pat_32	Post-Resistance	KRT73	319101	37	12	53010074	53010074	Missense_Mutation	SNP	C	G	4	105	c.538G>C	c.(538-540)GAG>CAG	p.E180Q
Pat_32	Post-Resistance	KIF5A	3798	37	12	57970140	57970140	Missense_Mutation	SNP	A	T	7	67	c.2177A>T	c.(2176-2178)AAG>ATG	p.K726M
Pat_32	Post-Resistance	XPOT	11260	37	12	64823867	64823867	Missense_Mutation	SNP	A	C	84	69	c.1776A>C	c.(1774-1776)CAA>CAC	p.Q592H
Pat_32	Post-Resistance	NAV3	89795	37	12	78513382	78513382	Missense_Mutation	SNP	C	T	4	169	c.3406C>T	c.(3406-3408)CGC>TGC	p.R1136C

Pat_32	Post-Resistance	FICD	11153	37	12	108912930	108912930	Missense_Mutation	SNP	C	T	4	139	c.1055C>T	c.(1054-1056)GCA>GTA	p.A352V
Pat_32	Post-Resistance	MMAB	326625	37	12	110011168	110011168	Missense_Mutation	SNP	C	T	3	65	c.118G>A	c.(118-120)GTG>ATG	p.V40M
Pat_32	Post-Resistance	DDX54	79039	37	12	113618782	113618782	Missense_Mutation	SNP	G	A	4	115	c.256C>T	c.(256-258)CGT>TGT	p.R86C
Pat_32	Post-Resistance	SBNO1	55206	37	12	123829937	123829937	Nonsense_Mutation	SNP	G	A	4	221	c.418C>T	c.(418-420)CGA>TGA	p.R140*
Pat_32	Post-Resistance	RIMBP2	23504	37	12	130912813	130912813	Missense_Mutation	SNP	C	T	41	82	c.2272G>A	c.(2272-2274)GAG>AAG	p.E758K
Pat_32	Post-Resistance	PDS5B	23047	37	13	33309375	33309375	Missense_Mutation	SNP	C	A	5	210	c.2314C>A	c.(2314-2316)CAT>AAT	p.H772N
Pat_32	Post-Resistance	C13orf23	80209	37	13	39586829	39586829	Missense_Mutation	SNP	C	T	3	105	c.2560G>A	c.(2560-2562)GGT>AGT	p.G854S
Pat_32	Post-Resistance	COG6	57511	37	13	40254159	40254159	Missense_Mutation	SNP	A	G	142	27	c.671A>G	c.(670-672)GAA>GGA	p.E224G
Pat_32	Post-Resistance	OR4N5	390437	37	14	20612341	20612341	Missense_Mutation	SNP	G	T	43	197	c.447G>T	c.(445-447)TGG>TGT	p.W149C
Pat_32	Post-Resistance	FLJ10357	55701	37	14	21555554	21555554	Missense_Mutation	SNP	G	A	3	50	c.4319G>A	c.(4318-4320)GGA>GAA	p.G1440E
Pat_32	Post-Resistance	CPNE6	9362	37	14	24545577	24545577	Missense_Mutation	SNP	G	A	4	153	c.1067G>A	c.(1066-1068)CGG>CAG	p.R356Q
Pat_32	Post-Resistance	IRF9	10379	37	14	24633916	24633916	Nonsense_Mutation	SNP	C	A	5	75	c.743C>A	c.(742-744)TCA>TAA	p.S248*
Pat_32	Post-Resistance	FUT8	2530	37	14	66188556	66188556	Missense_Mutation	SNP	G	A	167	110	c.899G>A	c.(898-900)CGT>CAT	p.R300H
Pat_32	Post-Resistance	DCAF5	8816	37	14	69589066	69589066	Missense_Mutation	SNP	G	A	3	76	c.226C>T	c.(226-228)CGC>TGC	p.R76C
Pat_32	Post-Resistance	KIAA0247	9766	37	14	70170201	70170201	Missense_Mutation	SNP	G	A	4	187	c.211G>A	c.(211-213)GAA>AAA	p.E71K
Pat_32	Post-Resistance	ABCD4	5826	37	14	74761892	74761892	Missense_Mutation	SNP	G	T	50	44	c.678C>A	c.(676-678)CAC>CAA	p.H226Q
Pat_32	Post-Resistance	STON2	85439	37	14	81743266	81743266	Nonsense_Mutation	SNP	G	A	4	238	c.2389C>T	c.(2389-2391)CGA>TGA	p.R797*
Pat_32	Post-Resistance	DICER1	23405	37	14	95571444	95571444	Missense_Mutation	SNP	G	A	4	163	c.3233C>T	c.(3232-3234)GCT>GTT	p.A1078V
Pat_32	Post-Resistance	BDKRB2	624	37	14	96707678	96707678	Missense_Mutation	SNP	G	A	4	74	c.1013G>A	c.(1012-1014)CGC>CAC	p.R338H
Pat_32	Post-Resistance	OR4N4	283694	37	15	22382807	22382807	Missense_Mutation	SNP	G	A	94	370	c.335G>A	c.(334-336)GGA>GAA	p.G112E
Pat_32	Post-Resistance	TJP1	7082	37	15	30019011	30019011	Missense_Mutation	SNP	C	T	5	377	c.2285G>A	c.(2284-2286)CGT>CAT	p.R762H
Pat_32	Post-Resistance	ATPBD4	89978	37	15	35830596	35830596	Missense_Mutation	SNP	G	A	4	194	c.191C>T	c.(190-192)GCA>GTA	p.A64V
Pat_32	Post-Resistance	SQRDL	58472	37	15	45965966	45965966	Missense_Mutation	SNP	G	T	30	90	c.621G>T	c.(619-621)AAG>AAT	p.K207N
Pat_32	Post-Resistance	CEP152	22995	37	15	49074424	49074424	Missense_Mutation	SNP	G	A	4	231	c.1325C>T	c.(1324-1326)TCA>TTA	p.S442L
Pat_32	Post-Resistance	ATP8B4	79895	37	15	50223378	50223378	Missense_Mutation	SNP	A	T	5	284	c.1580T>A	c.(1579-1581)GTT>GAT	p.V527D
Pat_32	Post-Resistance	SPPL2A	84888	37	15	51000002	51000002	Missense_Mutation	SNP	G	T	4	184	c.1558C>A	c.(1558-1560)CAA>AAA	p.Q520K
Pat_32	Post-Resistance	MYO5A	4644	37	15	52606331	52606331	Missense_Mutation	SNP	G	A	4	180	c.5404C>T	c.(5404-5406)CGT>TGT	p.R1802C
Pat_32	Post-Resistance	LIPC	3990	37	15	58855853	58855853	Missense_Mutation	SNP	G	A	4	140	c.1319G>A	c.(1318-1320)AGC>AAC	p.S440N
Pat_32	Post-Resistance	MAP2K1	5604	37	15	66729175	66729175	Missense_Mutation	SNP	G	T	6	217	c.383G>T	c.(382-384)GGC>GTC	p.G128V
Pat_32	Post-Resistance	NEO1	4756	37	15	73547099	73547099	Missense_Mutation	SNP	G	A	6	668	c.2021G>A	c.(2020-2022)CGA>CAA	p.R674Q
Pat_32	Post-Resistance	SNUPN	10073	37	15	75899560	75899560	Missense_Mutation	SNP	G	C	31	284	c.597C>G	c.(595-597)TGC>TGG	p.C199W
Pat_32	Post-Resistance	C15orf42	90381	37	15	90168430	90168430	Missense_Mutation	SNP	C	T	4	132	c.4889C>T	c.(4888-4890)TCC>TTC	p.S1630F
Pat_32	Post-Resistance	WASH3P	374666	37	15	102515299	102515299	Missense_Mutation	SNP	G	A	23	58	c.523G>A	c.(523-525)GGC>AGC	p.G175S
Pat_32	Post-Resistance	ATF7IP2	80063	37	16	10534245	10534245	Missense_Mutation	SNP	C	T	17	38	c.1120C>T	c.(1120-1122)CGT>TGT	p.R374C
Pat_32	Post-Resistance	TMC7	79905	37	16	19041576	19041576	Missense_Mutation	SNP	G	A	3	122	c.742G>A	c.(742-744)GGA>AGA	p.G248R
Pat_32	Post-Resistance	TMC7	79905	37	16	19049196	19049196	Missense_Mutation	SNP	G	A	12	65	c.1006G>A	c.(1006-1008)GCA>ACA	p.A336T
Pat_32	Post-Resistance	TMEM159	57146	37	16	21181846	21181846	Missense_Mutation	SNP	C	T	4	172	c.185C>T	c.(184-186)TCG>TTG	p.S62L
Pat_32	Post-Resistance	PALB2	79728	37	16	23640960	23640960	Splice_Site	SNP	C	T	4	207	c.2514_splice	c.e5+1	p.Q838_splice
Pat_32	Post-Resistance	PRKCB	5579	37	16	24196838	24196838	Missense_Mutation	SNP	G	A	4	143	c.1672G>A	c.(1672-1674)GTA>ATA	p.V558I
Pat_32	Post-Resistance	SETD1A	9739	37	16	30972675	30972675	Missense_Mutation	SNP	G	T	24	136	c.334G>T	c.(334-336)GAT>TAT	p.D112Y
Pat_32	Post-Resistance	CHD9	80205	37	16	53319528	53319528	Missense_Mutation	SNP	C	T	4	123	c.4988C>T	c.(4987-4989)CCA>CTA	p.P1663L
Pat_32	Post-Resistance	GINS3	64785	37	16	58437077	58437077	Missense_Mutation	SNP	C	T	4	191	c.262C>T	c.(262-264)CTC>TTC	p.L88F
Pat_32	Post-Resistance	CHST4	10164	37	16	71571404	71571404	Missense_Mutation	SNP	G	A	4	95	c.824G>A	c.(823-825)CGC>CAC	p.R275H
Pat_32	Post-Resistance	PRDM7	11105	37	16	90126823	90126823	Missense_Mutation	SNP	T	G	9	202	c.1159A>C	c.(1159-1161)ATG>CTG	p.M387L
Pat_32	Post-Resistance	C17orf97	400566	37	17	263584	263584	Missense_Mutation	SNP	C	T	5	54	c.980C>T	c.(979-981)ACT>ATT	p.T327I
Pat_32	Post-Resistance	USP6	9098	37	17	5042600	5042600	Missense_Mutation	SNP	G	T	4	117	c.1129G>T	c.(1129-1131)GGT>TGT	p.G377C
Pat_32	Post-Resistance	DLG4	1742	37	17	7107032	7107032	Missense_Mutation	SNP	G	A	4	127	c.443C>T	c.(442-444)GCG>GTG	p.A148V

Pat_32	Post-Resistance	GPS2	2874	37	17	7216926	7216926	Missense_Mutation	SNP	G	A	4	226	c.595C>T	c.(595-597)CCC>TCC	p.P199S
Pat_32	Post-Resistance	SEZ6	124925	37	17	27285151	27285151	Missense_Mutation	SNP	G	A	3	99	c.2116C>T	c.(2116-2118)CGC>TGC	p.R706C
Pat_32	Post-Resistance	KRT33B	3884	37	17	39525936	39525936	Missense_Mutation	SNP	G	A	4	30	c.67C>T	c.(67-69)CCC>TCC	p.P23S
Pat_32	Post-Resistance	CCDC103	388389	37	17	42979971	42979971	Missense_Mutation	SNP	G	A	3	48	c.515G>A	c.(514-516)AGC>AAC	p.S172N
Pat_32	Post-Resistance	SPAG9	9043	37	17	49072569	49072569	Missense_Mutation	SNP	C	G	3	68	c.2075G>C	c.(2074-2076)GGA>GCA	p.G692A
Pat_32	Post-Resistance	C17orf82	388407	37	17	59490015	59490015	Missense_Mutation	SNP	G	A	2	3	c.679G>A	c.(679-681)GAC>AAC	p.D227N
Pat_32	Post-Resistance	GH2	2689	37	17	61958281	61958281	Missense_Mutation	SNP	G	A	3	67	c.307C>T	c.(307-309)CGC>TGC	p.R103C
Pat_32	Post-Resistance	ABCA9	10350	37	17	67003970	67003970	Missense_Mutation	SNP	G	A	4	187	c.3365C>T	c.(3364-3366)ACA>ATA	p.T1122I
Pat_32	Post-Resistance	QRICH2	84074	37	17	74288842	74288842	Missense_Mutation	SNP	C	T	3	72	c.1468G>A	c.(1468-1470)GGT>AGT	p.G490S
Pat_32	Post-Resistance	UBE2O	63893	37	17	74394972	74394972	Missense_Mutation	SNP	G	A	132	190	c.1729C>T	c.(1729-1731)CAC>TAC	p.H577Y
Pat_32	Post-Resistance	RNF213	57674	37	17	78323706	78323706	Missense_Mutation	SNP	G	A	4	89	c.4307G>A	c.(4306-4308)CGA>CAA	p.R1436Q
Pat_32	Post-Resistance	HCN2	610	37	19	613374	613374	Missense_Mutation	SNP	A	C	4	108	c.1711A>C	c.(1711-1713)ATC>CTC	p.I571L
Pat_32	Post-Resistance	EVI5L	115704	37	19	7928427	7928427	Missense_Mutation	SNP	G	A	3	14	c.2224G>A	c.(2224-2226)GTA>ATA	p.V742I
Pat_32	Post-Resistance	FARSA	2193	37	19	13035284	13035284	Missense_Mutation	SNP	C	T	4	167	c.1252G>A	c.(1252-1254)GAG>AAG	p.E418K
Pat_32	Post-Resistance	NANOS3	342977	37	19	13988237	13988237	Missense_Mutation	SNP	G	A	3	62	c.175G>A	c.(175-177)GGA>AGA	p.G59R
Pat_32	Post-Resistance	SLC1A6	6511	37	19	15073056	15073056	Missense_Mutation	SNP	C	G	24	95	c.693G>C	c.(691-693)GAG>GAC	p.E231D
Pat_32	Post-Resistance	PDE4C	5143	37	19	18321833	18321833	Missense_Mutation	SNP	G	C	11	41	c.2045C>G	c.(2044-2046)GCC>GGC	p.A682G
Pat_32	Post-Resistance	ZNF708	7562	37	19	21476519	21476519	Missense_Mutation	SNP	T	C	5	156	c.1249A>G	c.(1249-1251)AAG>GAG	p.K417E
Pat_32	Post-Resistance	ZNF43	7594	37	19	21991550	21991550	Missense_Mutation	SNP	T	A	5	378	c.1289A>T	c.(1288-1290)GAA>GTA	p.E430V
Pat_32	Post-Resistance	ZNF208	7757	37	19	22155903	22155903	Missense_Mutation	SNP	T	C	5	290	c.1633A>G	c.(1633-1635)ACC>GCC	p.T545A
Pat_32	Post-Resistance	HPN	3249	37	19	35540274	35540274	Missense_Mutation	SNP	G	A	4	204	c.97G>A	c.(97-99)GGG>AGG	p.G33R
Pat_32	Post-Resistance	NPHS1	4868	37	19	36341266	36341266	Missense_Mutation	SNP	C	A	7	61	c.608G>T	c.(607-609)AGG>ATG	p.R203M
Pat_32	Post-Resistance	PRX	57716	37	19	40902089	40902089	Missense_Mutation	SNP	G	A	4	173	c.2170C>T	c.(2170-2172)CTC>TTC	p.L724F
Pat_32	Post-Resistance	EGLN2	112398	37	19	41292842	41292842	Translation_Start_Site	SNP	G	A	3	71	c.-275G>A	(-277--273)CCGTG>CCATG	
Pat_32	Post-Resistance	GPR77	27202	37	19	47844507	47844507	Missense_Mutation	SNP	G	A	4	105	c.451G>A	c.(451-453)GTG>ATG	p.V151M
Pat_32	Post-Resistance	LMTK3	114783	37	19	49001471	49001471	Missense_Mutation	SNP	G	A	14	37	c.2942C>T	c.(2941-2943)CCC>CTC	p.P981L
Pat_32	Post-Resistance	SIGLEC9	27180	37	19	51628446	51628446	Missense_Mutation	SNP	C	T	4	169	c.215C>T	c.(214-216)GCT>GTT	p.A72V
Pat_32	Post-Resistance	LILRB2	10288	37	19	54783664	54783664	Missense_Mutation	SNP	G	T	55	81	c.337C>A	c.(337-339)CTG>ATG	p.L113M
Pat_32	Post-Resistance	LILRA5	353514	37	19	54818709	54818709	Missense_Mutation	SNP	C	T	41	76	c.889G>A	c.(889-891)GCT>ACT	p.A297T
Pat_32	Post-Resistance	NLRP2	55655	37	19	55494663	55494663	Missense_Mutation	SNP	G	T	4	86	c.1597G>T	c.(1597-1599)GGG>TGG	p.G533W
Pat_32	Post-Resistance	ZNF460	10794	37	19	57802843	57802843	Missense_Mutation	SNP	G	A	4	134	c.934G>A	c.(934-936)GAA>AAA	p.E312K
Pat_32	Post-Resistance	MYT1L	23040	37	2	1893067	1893067	Missense_Mutation	SNP	G	T	5	143	c.2466C>A	c.(2464-2466)GAC>GAA	p.D822E
Pat_32	Post-Resistance	KIDINS220	57498	37	2	8871289	8871289	Missense_Mutation	SNP	C	T	3	73	c.4877G>A	c.(4876-4878)CGG>CAG	p.R1626Q
Pat_32	Post-Resistance	KCNS3	3790	37	2	18113071	18113071	Missense_Mutation	SNP	T	C	66	60	c.796T>C	c.(796-798)TTC>CTC	p.F266L
Pat_32	Post-Resistance	ASXL2	55252	37	2	25965173	25965173	Missense_Mutation	SNP	C	T	30	63	c.4033G>A	c.(4033-4035)GTA>ATA	p.V1345I
Pat_32	Post-Resistance	C2orf16	84226	37	2	27803797	27803797	Missense_Mutation	SNP	G	T	4	214	c.4358G>T	c.(4357-4359)CGA>CTA	p.R1453L
Pat_32	Post-Resistance	MAP4K3	8491	37	2	39515286	39515286	Missense_Mutation	SNP	G	A	4	226	c.1450C>T	c.(1450-1452)CCC>TCC	p.P484S
Pat_32	Post-Resistance	EML4	27436	37	2	42528474	42528474	Missense_Mutation	SNP	G	A	3	88	c.1583G>A	c.(1582-1584)GGG>GAG	p.G528E
Pat_32	Post-Resistance	DYSF	8291	37	2	71906211	71906211	Missense_Mutation	SNP	G	A	4	186	c.5792G>A	c.(5791-5793)CGC>CAC	p.R1931H
Pat_32	Post-Resistance	SNRNP200	23020	37	2	96964654	96964654	Missense_Mutation	SNP	G	A	4	195	c.781C>T	c.(781-783)CGG>TGG	p.R261W
Pat_32	Post-Resistance	WASH2P	375260	37	2	114355998	114355998	Missense_Mutation	SNP	C	G	7	45	c.616C>G	c.(616-618)CAC>GAC	p.H206D
Pat_32	Post-Resistance	MARCO	8685	37	2	119750748	119750748	Missense_Mutation	SNP	G	A	4	238	c.1301G>A	c.(1300-1302)CGG>CAG	p.R434Q
Pat_32	Post-Resistance	PTPN4	5775	37	2	120703991	120703991	Missense_Mutation	SNP	C	A	4	206	c.1590C>A	c.(1588-1590)TTC>TTA	p.F530L
Pat_32	Post-Resistance	CLASP1	23332	37	2	122125337	122125337	Missense_Mutation	SNP	C	T	4	76	c.3713G>A	c.(3712-3714)CGG>CAG	p.R1238Q
Pat_32	Post-Resistance	MYO7B	4648	37	2	128327430	128327430	Missense_Mutation	SNP	T	G	4	27	c.537T>G	c.(535-537)AGT>AGG	p.S179R
Pat_32	Post-Resistance	ZRANB3	84083	37	2	136072981	136072981	Missense_Mutation	SNP	G	A	3	64	c.797C>T	c.(796-798)CCC>CTC	p.P266L
Pat_32	Post-Resistance	NEB	4703	37	2	152520327	152520327	Missense_Mutation	SNP	C	G	8	106	c.5498G>C	c.(5497-5499)GGC>GCC	p.G1833A

Pat_32	Post-Resistance	DHRS9	10170	37	2	169940008	169940008	Missense_Mutation	SNP	T	G	6	156	c.483T>G	c.(481-483)AAT>AAG	p.N161K
Pat_32	Post-Resistance	PGAP1	80055	37	2	197708675	197708675	Missense_Mutation	SNP	T	C	76	119	c.2462A>G	c.(2461-2463)AAC>AGC	p.N821S
Pat_32	Post-Resistance	4-Mar	57574	37	2	217142428	217142428	Missense_Mutation	SNP	C	T	6	266	c.832G>A	c.(832-834)GGG>AGG	p.G278R
Pat_32	Post-Resistance	SMARCAL1	50485	37	2	217300060	217300060	Splice_Site	SNP	G	T	4	120	c.1486_splice	c.e9-1	p.A496_splice
Pat_32	Post-Resistance	IRS1	3667	37	2	227660463	227660463	Missense_Mutation	SNP	G	A	4	158	c.2992C>T	c.(2992-2994)CGT>TGT	p.R998C
Pat_32	Post-Resistance	CHRND	1144	37	2	233398813	233398813	Missense_Mutation	SNP	G	A	3	91	c.1220G>A	c.(1219-1221)CGG>CAG	p.R407Q
Pat_32	Post-Resistance	DGKD	8527	37	2	234346033	234346033	Missense_Mutation	SNP	C	T	36	65	c.830C>T	c.(829-831)TCG>TTG	p.S277L
Pat_32	Post-Resistance	SH3BP4	23677	37	2	235950569	235950569	Missense_Mutation	SNP	G	C	21	20	c.1156G>C	c.(1156-1158)GAG>CAG	p.E386Q
Pat_32	Post-Resistance	SIRPA	140885	37	20	1902292	1902292	Missense_Mutation	SNP	G	A	6	168	c.688G>A	c.(688-690)GTG>ATG	p.V230M
Pat_32	Post-Resistance	C20orf194	25943	37	20	3234419	3234419	Missense_Mutation	SNP	C	A	4	154	c.3374G>T	c.(3373-3375)GGC>GTC	p.G1125V
Pat_32	Post-Resistance	BFSP1	631	37	20	17495444	17495444	Missense_Mutation	SNP	C	A	4	235	c.456G>T	c.(454-456)TTG>TTT	p.L152F
Pat_32	Post-Resistance	FRG1B	284802	37	20	29625947	29625947	Missense_Mutation	SNP	T	C	7	234	c.101T>C	c.(100-102)ATT>ACT	p.I34T
Pat_32	Post-Resistance	DNMT3B	1789	37	20	31376801	31376801	Missense_Mutation	SNP	G	A	4	126	c.796G>A	c.(796-798)GAT>AAT	p.D266N
Pat_32	Post-Resistance	BPIL3	128859	37	20	31622017	31622017	Missense_Mutation	SNP	C	A	35	359	c.223C>A	c.(223-225)CCC>ACC	p.P75T
Pat_32	Post-Resistance	CDK5RAP1	51654	37	20	31984692	31984692	Missense_Mutation	SNP	G	A	24	41	c.179C>T	c.(178-180)GCT>GTT	p.A60V
Pat_32	Post-Resistance	SNTA1	6640	37	20	32000563	32000563	Missense_Mutation	SNP	C	A	3	61	c.727G>T	c.(727-729)GGT>TGT	p.G243C
Pat_32	Post-Resistance	MYH7B	57644	37	20	33585436	33585436	Missense_Mutation	SNP	G	A	4	70	c.3866G>A	c.(3865-3867)CGC>CAC	p.R1289H
Pat_32	Post-Resistance	TAF4	6874	37	20	60574083	60574083	Missense_Mutation	SNP	T	A	15	826	c.2869A>T	c.(2869-2871)AGG>TGG	p.R957W
Pat_32	Post-Resistance	OPRL1	4987	37	20	62730105	62730105	Missense_Mutation	SNP	G	A	4	100	c.1066G>A	c.(1066-1068)GTG>ATG	p.V356M
Pat_32	Post-Resistance	HUNK	30811	37	21	33346983	33346983	Missense_Mutation	SNP	C	T	28	158	c.1127C>T	c.(1126-1128)GCC>GTC	p.A376V
Pat_32	Post-Resistance	UMODL1	89766	37	21	43547170	43547170	Missense_Mutation	SNP	G	T	5	174	c.3348G>T	c.(3346-3348)ATG>ATT	p.M1116I
Pat_32	Post-Resistance	KRTAP10-1	386677	37	21	45959198	45959198	Missense_Mutation	SNP	C	G	4	55	c.836G>C	c.(835-837)CGC>CCC	p.R279P
Pat_32	Post-Resistance	PCNT	5116	37	21	47786647	47786647	Missense_Mutation	SNP	G	A	5	132	c.2758G>A	c.(2758-2760)GAG>AAG	p.E920K
Pat_32	Post-Resistance	BPIL2	254240	37	22	32841934	32841934	Missense_Mutation	SNP	C	T	4	143	c.424G>A	c.(424-426)GGT>AGT	p.G142S
Pat_32	Post-Resistance	APOL5	80831	37	22	36124797	36124797	Missense_Mutation	SNP	T	C	3	115	c.1154T>C	c.(1153-1155)GTT>GCT	p.V385A
Pat_32	Post-Resistance	TNRC6B	23112	37	22	40676091	40676091	Missense_Mutation	SNP	C	T	4	221	c.3355C>T	c.(3355-3357)CGT>TGT	p.R1119C
Pat_32	Post-Resistance	BRD1	23774	37	22	50167960	50167960	Missense_Mutation	SNP	C	T	4	177	c.3098G>A	c.(3097-3099)CGG>CAG	p.R1033Q
Pat_32	Post-Resistance	NR1D2	9975	37	3	23996244	23996244	Missense_Mutation	SNP	C	A	4	183	c.233C>A	c.(232-234)ACA>AAA	p.T78K
Pat_32	Post-Resistance	CLASP2	23122	37	3	33644501	33644501	Missense_Mutation	SNP	C	T	10	16	c.1867G>A	c.(1867-1869)GTG>ATG	p.V623M
Pat_32	Post-Resistance	TRANK1	9881	37	3	36875205	36875205	Missense_Mutation	SNP	T	A	69	50	c.4087A>T	c.(4087-4089)AAC>TAC	p.N1363Y
Pat_32	Post-Resistance	IL17RB	55540	37	3	53894255	53894255	Missense_Mutation	SNP	G	A	4	152	c.946G>A	c.(946-948)GAA>AAA	p.E316K
Pat_32	Post-Resistance	HHLA2	11148	37	3	108081229	108081229	Nonsense_Mutation	SNP	G	A	12	25	c.1044G>A	c.(1042-1044)TGG>TGA	p.W348*
Pat_32	Post-Resistance	PLXNA1	5361	37	3	126722246	126722246	Missense_Mutation	SNP	G	A	3	90	c.1382G>A	c.(1381-1383)AGC>AAC	p.S461N
Pat_32	Post-Resistance	THPO	7066	37	3	184090723	184090723	Missense_Mutation	SNP	T	C	6	28	c.640A>G	c.(640-642)ACT>GCT	p.T214A
Pat_32	Post-Resistance	PDE6B	5158	37	4	657618	657618	Missense_Mutation	SNP	G	A	15	100	c.1980G>A	c.(1978-1980)ATG>ATA	p.M660I
Pat_32	Post-Resistance	GRK4	2868	37	4	2986281	2986281	Missense_Mutation	SNP	G	A	47	155	c.94G>A	c.(94-96)GAG>AAG	p.E32K
Pat_32	Post-Resistance	BST1	683	37	4	15720550	15720550	Missense_Mutation	SNP	G	A	4	105	c.725G>A	c.(724-726)AGC>AAC	p.S242N
Pat_32	Post-Resistance	CLRN2	645104	37	4	17517017	17517017	Missense_Mutation	SNP	G	C	43	154	c.128G>C	c.(127-129)GGA>GCA	p.G43A
Pat_32	Post-Resistance	UGDH	7358	37	4	39522972	39522972	Missense_Mutation	SNP	T	A	7	265	c.161A>T	c.(160-162)GAG>GTG	p.E54V
Pat_32	Post-Resistance	USP46	64854	37	4	53468102	53468102	Missense_Mutation	SNP	G	A	4	173	c.841C>T	c.(841-843)CGG>TGG	p.R281W
Pat_32	Post-Resistance	UGT2B10	7365	37	4	69874738	69874738	Missense_Mutation	SNP	T	C	4	257	c.1033A>G	c.(1033-1035)ACA>GCA	p.T345A
Pat_32	Post-Resistance	SLC4A4	8671	37	4	72316945	72316945	Missense_Mutation	SNP	G	T	91	253	c.1249G>T	c.(1249-1251)GGG>TGG	p.G417W
Pat_32	Post-Resistance	FRAS1	80144	37	4	79284718	79284718	Missense_Mutation	SNP	G	A	4	109	c.2474G>A	c.(2473-2475)AGC>AAC	p.S825N
Pat_32	Post-Resistance	NUDT9	53343	37	4	88370382	88370382	Missense_Mutation	SNP	T	C	16	160	c.619T>C	c.(619-621)TGT>CGT	p.C207R
Pat_32	Post-Resistance	DKK2	27123	37	4	107845346	107845346	Missense_Mutation	SNP	G	A	12	111	c.545C>T	c.(544-546)CCC>CTC	p.P182L
Pat_32	Post-Resistance	PHF17	79960	37	4	129773269	129773269	Missense_Mutation	SNP	G	A	4	228	c.542G>A	c.(541-543)CGA>CAA	p.R181Q
Pat_32	Post-Resistance	SETD7	80854	37	4	140454437	140454437	Missense_Mutation	SNP	G	A	4	217	c.254C>T	c.(253-255)ACG>ATG	p.T85M

Pat_32	Post-Resistance	TTC29	83894	37	4	147628661	147628661	Missense_Mutation	SNP	G	A	76	80	c.1373C>T	c.(1372-1374)TCA>TTA	p.S458L
Pat_32	Post-Resistance	KLHL2	11275	37	4	166231897	166231897	Missense_Mutation	SNP	G	A	5	323	c.1232G>A	c.(1231-1233)AGT>AAT	p.S411N
Pat_32	Post-Resistance	SLC9A3	6550	37	5	488486	488486	Missense_Mutation	SNP	T	C	13	82	c.620A>G	c.(619-621)GAG>GGG	p.E207G
Pat_32	Post-Resistance	PRDM9	56979	37	5	23527251	23527251	Missense_Mutation	SNP	C	G	4	233	c.2054C>G	c.(2053-2055)ACA>AGA	p.T685R
Pat_32	Post-Resistance	CDH10	1008	37	5	24509674	24509674	Splice_Site	SNP	C	A	5	126	c.1256_splice	c.e7+1	p.R419_splice
Pat_32	Post-Resistance	DNAJC21	134218	37	5	34937509	34937509	Nonsense_Mutation	SNP	C	T	23	35	c.517C>T	c.(517-519)CGA>TGA	p.R173*
Pat_32	Post-Resistance	NIPBL	25836	37	5	36986086	36986086	Missense_Mutation	SNP	C	T	72	125	c.2804C>T	c.(2803-2805)CCT>CTT	p.P935L
Pat_32	Post-Resistance	MARVELD2	153562	37	5	68715915	68715915	Missense_Mutation	SNP	G	A	3	91	c.703G>A	c.(703-705)GGC>AGC	p.G235S
Pat_32	Post-Resistance	ZFYVE16	9765	37	5	79768636	79768636	Nonsense_Mutation	SNP	C	T	4	181	c.4081C>T	c.(4081-4083)CGA>TGA	p.R1361*
Pat_32	Post-Resistance	GPR98	84059	37	5	90124906	90124906	Missense_Mutation	SNP	G	A	5	315	c.16514G>A	.(16513-16515)CGG>CA	p.R5505Q
Pat_32	Post-Resistance	ANKRD32	84250	37	5	94030572	94030572	Missense_Mutation	SNP	A	G	29	176	c.2732A>G	c.(2731-2733)GAA>GGA	p.E911G
Pat_32	Post-Resistance	KDM3B	51780	37	5	137767187	137767187	Missense_Mutation	SNP	G	A	4	146	c.5144G>A	c.(5143-5145)CGC>CAC	p.R1715H
Pat_32	Post-Resistance	PPP2R2B	5521	37	5	145969713	145969713	Missense_Mutation	SNP	C	T	22	141	c.1129G>A	c.(1129-1131)GCT>ACT	p.A377T
Pat_32	Post-Resistance	ARSI	340075	37	5	149677736	149677736	Missense_Mutation	SNP	G	A	3	68	c.751C>T	c.(751-753)CGC>TGC	p.R251C
Pat_32	Post-Resistance	DBN1	1627	37	5	176884716	176884716	Missense_Mutation	SNP	C	A	3	52	c.1819G>T	c.(1819-1821)GCC>TCC	p.A607S
Pat_32	Post-Resistance	RNF130	55819	37	5	179393934	179393934	Nonsense_Mutation	SNP	G	T	4	170	c.1022C>A	c.(1021-1023)TCA>TAA	p.S341*
Pat_32	Post-Resistance	BMP6	654	37	6	7845454	7845454	Missense_Mutation	SNP	A	T	8	183	c.746A>T	c.(745-747)GAG>GTG	p.E249V
Pat_32	Post-Resistance	TRIM10	10107	37	6	30124770	30124770	Missense_Mutation	SNP	G	A	4	148	c.841C>T	c.(841-843)CGG>TGG	p.R281W
Pat_32	Post-Resistance	TRIM39	56658	37	6	30309578	30309578	Missense_Mutation	SNP	C	T	4	99	c.1099C>T	c.(1099-1101)CGG>TGG	p.R367W
Pat_32	Post-Resistance	HLA-DOA	3111	37	6	32976009	32976009	Missense_Mutation	SNP	A	G	9	33	c.112T>C	c.(112-114)TTC>CTC	p.F38L
Pat_32	Post-Resistance	CCND3	896	37	6	41904394	41904394	Missense_Mutation	SNP	G	A	4	76	c.614C>T	c.(613-615)ACG>ATG	p.T205M
Pat_32	Post-Resistance	TFAP2B	7021	37	6	50796342	50796342	Missense_Mutation	SNP	A	G	20	234	c.551A>G	c.(550-552)GAT>GGT	p.D184G
Pat_32	Post-Resistance	GCM1	8521	37	6	53010422	53010423	Missense_Mutation	DNP	AG	GT	5	183	c.8_9CT>AC	c.(7-9)CCT>CAC	p.P3H
Pat_32	Post-Resistance	RIMS1	22999	37	6	72968726	72968726	Missense_Mutation	SNP	T	C	16	157	c.2965T>C	c.(2965-2967)TCT>CCT	p.S989P
Pat_32	Post-Resistance	SMPD2	6610	37	6	109764992	109764992	Missense_Mutation	SNP	C	A	3	31	c.1156C>A	c.(1156-1158)CAG>AAG	p.Q386K
Pat_32	Post-Resistance	THEMIS	387357	37	6	128150761	128150761	Missense_Mutation	SNP	C	A	4	81	c.569G>T	c.(568-570)TGG>TTG	p.W190L
Pat_32	Post-Resistance	PHACTR2	9749	37	6	144093433	144093433	Missense_Mutation	SNP	A	T	3	67	c.1238A>T	c.(1237-1239)CAG>CTG	p.Q413L
Pat_32	Post-Resistance	TAX1BP1	8887	37	7	27839609	27839609	Missense_Mutation	SNP	A	G	17	244	c.1664A>G	c.(1663-1665)TAT>TGT	p.Y555C
Pat_32	Post-Resistance	INMT	11185	37	7	30795319	30795319	Missense_Mutation	SNP	C	T	4	111	c.644C>T	c.(643-645)GCC>GTC	p.A215V
Pat_32	Post-Resistance	WBSCR17	64409	37	7	71177125	71177125	Missense_Mutation	SNP	C	G	35	135	c.1791C>G	c.(1789-1791)ATC>ATG	p.I597M
Pat_32	Post-Resistance	CLIP2	7461	37	7	73768246	73768246	Missense_Mutation	SNP	G	A	28	487	c.715G>A	c.(715-717)GGG>AGG	p.G239R
Pat_32	Post-Resistance	SEMA3D	223117	37	7	84694808	84694808	Missense_Mutation	SNP	C	T	234	96	c.650G>A	c.(649-651)CGA>CAA	p.R217Q
Pat_32	Post-Resistance	PEX1	5189	37	7	92118669	92118669	Missense_Mutation	SNP	C	A	6	288	c.3705G>T	c.(3703-3705)ATG>ATT	p.M1235I
Pat_32	Post-Resistance	PON2	5445	37	7	95035519	95035519	Missense_Mutation	SNP	T	G	461	135	c.818A>C	c.(817-819)GAT>GCT	p.D273A
Pat_32	Post-Resistance	TRRAP	8295	37	7	98491479	98491479	Missense_Mutation	SNP	A	T	20	586	c.425A>T	c.(424-426)CAG>CTG	p.Q142L
Pat_32	Post-Resistance	ZNF498	221785	37	7	99227033	99227033	Missense_Mutation	SNP	G	A	4	143	c.1025G>A	c.(1024-1026)AGC>AAC	p.S342N
Pat_32	Post-Resistance	C7orf61	402573	37	7	100054433	100054433	Missense_Mutation	SNP	G	A	4	79	c.563C>T	c.(562-564)GCT>GTT	p.A188V
Pat_32	Post-Resistance	ZAN	7455	37	7	100350474	100350474	Missense_Mutation	SNP	T	C	19	502	c.2746T>C	c.(2746-2748)TCC>CCC	p.S916P
Pat_32	Post-Resistance	ZAN	7455	37	7	100363071	100363071	Missense_Mutation	SNP	G	A	4	86	c.4364G>A	c.(4363-4365)CGG>CAG	p.R1455Q
Pat_32	Post-Resistance	MUC17	140453	37	7	100680878	100680878	Missense_Mutation	SNP	G	A	8	626	c.6181G>A	c.(6181-6183)GGT>AGT	p.G2061S
Pat_32	Post-Resistance	DLD	1738	37	7	107557410	107557410	Splice_Site	SNP	G	T	5	150	c.1046_splice	c.e10+1	p.N349_splice
Pat_32	Post-Resistance	C7orf66	154907	37	7	108524288	108524288	Missense_Mutation	SNP	C	T	14	395	c.124G>A	c.(124-126)GCA>ACA	p.A42T
Pat_32	Post-Resistance	CAV1	857	37	7	116165101	116165101	Translation_Start_Site	SNP	C	G	18	789	c.-15C>G	c.(-17--13)ATCCA>ATGCA	
Pat_32	Post-Resistance	TNPO3	23534	37	7	128633886	128633886	Missense_Mutation	SNP	A	T	47	287	c.1241T>A	c.(1240-1242)ATA>AAA	p.I414K
Pat_32	Post-Resistance	TBXAS1	6916	37	7	139653246	139653246	Missense_Mutation	SNP	A	G	12	244	c.671A>G	c.(670-672)GAC>GGC	p.D224G
Pat_32	Post-Resistance	BRAF	673	37	7	140453136	140453136	Missense_Mutation	SNP	A	T	268	103	c.1799T>A	c.(1798-1800)GTG>GAG	p.V600E
Pat_32	Post-Resistance	PTPRN2	5799	37	7	157926656	157926656	Missense_Mutation	SNP	C	A	27	188	c.1269G>T	c.(1267-1269)ATG>ATT	p.M423I

Pat_32	Post-Resistance	IDO1	3620	37	8	39780096	39780096	Missense_Mutation	SNP	C	T	35	44	c.463C>T	c.(463-465)CGT>TGT	p.R155C
Pat_32	Post-Resistance	C8orf45	157777	37	8	67789635	67789635	Missense_Mutation	SNP	C	G	17	82	c.337C>G	c.(337-339)CTT>GTT	p.L113V
Pat_32	Post-Resistance	KLF10	7071	37	8	103663709	103663709	Missense_Mutation	SNP	G	A	49	61	c.851C>T	c.(850-852)CCT>CTT	p.P284L
Pat_32	Post-Resistance	BAALC	79870	37	8	104225179	104225179	Missense_Mutation	SNP	G	T	7	357	c.193G>T	c.(193-195)GTG>TTG	p.V65L
Pat_32	Post-Resistance	ANGPT1	284	37	8	108296965	108296965	Nonsense_Mutation	SNP	G	A	6	313	c.1150C>T	c.(1150-1152)CGA>TGA	p.R384*
Pat_32	Post-Resistance	ADCK5	203054	37	8	145616137	145616137	Missense_Mutation	SNP	G	A	3	43	c.424G>A	c.(424-426)GGG>AGG	p.G142R
Pat_32	Post-Resistance	RRAGA	10670	37	9	19050508	19050508	Missense_Mutation	SNP	C	T	6	178	c.851C>T	c.(850-852)GCG>GTG	p.A284V
Pat_32	Post-Resistance	DNAJB5	25822	37	9	34993303	34993303	Missense_Mutation	SNP	C	T	4	220	c.73C>T	c.(73-75)CGG>TGG	p.R25W
Pat_32	Post-Resistance	LOC442421	442421	37	9	66499680	66499680	Missense_Mutation	SNP	C	A	9	57	c.490C>A	c.(490-492)CCC>ACC	p.P164T
Pat_32	Post-Resistance	FLJ46321	389763	37	9	84605975	84605975	Missense_Mutation	SNP	C	T	27	89	c.590C>T	c.(589-591)CCC>CTC	p.P197L
Pat_32	Post-Resistance	ABCA1	19	37	9	107576411	107576411	Missense_Mutation	SNP	C	T	4	149	c.3889G>A	c.(3889-3891)GAC>AAC	p.D1297N
Pat_32	Post-Resistance	PAPPA	5069	37	9	119115984	119115984	Missense_Mutation	SNP	C	A	5	180	c.4259C>A	c.(4258-4260)CCA>CAA	p.P1420Q
Pat_32	Post-Resistance	PHYHD1	254295	37	9	131689386	131689386	Missense_Mutation	SNP	A	G	4	242	c.103A>G	c.(103-105)AGG>GGG	p.R35G
Pat_32	Post-Resistance	KIAA0649	9858	37	9	138376660	138376660	Missense_Mutation	SNP	G	A	4	125	c.304G>A	c.(304-306)GTT>ATT	p.V102I
Pat_32	Post-Resistance	OTC	5009	37	X	38260652	38260652	Missense_Mutation	SNP	C	A	42	227	c.511C>A	c.(511-513)CAG>AAG	p.Q171K
Pat_32	Post-Resistance	MAGED1	9500	37	X	51640657	51640657	Missense_Mutation	SNP	A	G	11	337	c.1501A>G	c.(1501-1503)ATC>GTC	p.I501V
Pat_32	Post-Resistance	SMC1A	8243	37	X	53421792	53421792	Missense_Mutation	SNP	T	C	4	218	c.2879A>G	c.(2878-2880)GAG>GGG	p.E960G
Pat_32	Post-Resistance	SLC7A3	84889	37	X	70148757	70148757	Missense_Mutation	SNP	C	T	102	91	c.466G>A	c.(466-468)GTG>ATG	p.V156M
Pat_32	Post-Resistance	ACRC	93953	37	X	70823930	70823931	Missense_Mutation	DNP	GC	AG	5	223	c.803_804GC>AG	c.(802-804)AGC>AAG	p.S268K
Pat_32	Post-Resistance	AMOT	154796	37	X	112021870	112021870	Missense_Mutation	SNP	A	C	259	246	c.3180T>G	c.(3178-3180)AAT>AAG	p.N1060K
Pat_32	Post-Resistance	TKTL1	8277	37	X	153555980	153555980	Missense_Mutation	SNP	C	T	14	365	c.1445C>T	c.(1444-1446)GCT>GTT	p.A482V
Pat_36	Post-Resistance	GNB1	2782	37	1	1721893	1721893	Nonsense_Mutation	SNP	G	A	4	99	c.640C>T	c.(640-642)CGA>TGA	p.R214*
Pat_36	Post-Resistance	CLSTN1	22883	37	1	9793532	9793532	Missense_Mutation	SNP	A	G	18	36	c.2354T>C	c.(2353-2355)TTG>TCG	p.L785S
Pat_36	Post-Resistance	CSMD2	114784	37	1	34191055	34191055	Missense_Mutation	SNP	C	T	29	44	c.2470G>A	c.(2470-2472)GGG>AGG	p.G824R
Pat_36	Post-Resistance	UROD	7389	37	1	45479419	45479419	Nonsense_Mutation	SNP	C	T	5	130	c.430C>T	c.(430-432)CGA>TGA	p.R144*
Pat_36	Post-Resistance	PCSK9	255738	37	1	55518327	55518327	Missense_Mutation	SNP	G	A	3	68	c.662G>A	c.(661-663)AGC>AAC	p.S221N
Pat_36	Post-Resistance	AP4B1	10717	37	1	114437943	114437943	Missense_Mutation	SNP	T	C	61	119	c.1964A>G	c.(1963-1965)GAC>GGC	p.D655G
Pat_36	Post-Resistance	REG4	83998	37	1	120345767	120345767	Missense_Mutation	SNP	C	G	3	65	c.89G>C	c.(88-90)TGT>TCT	p.C30S
Pat_36	Post-Resistance	NBPF10	100132406	37	1	145302695	145302695	Missense_Mutation	SNP	C	T	12	292	c.1133C>T	c.(1132-1134)ACC>ATC	p.T378I
Pat_36	Post-Resistance	NBPF10	100132406	37	1	145359049	145359049	Missense_Mutation	SNP	A	G	16	20	c.9214A>G	c.(9214-9216)AAA>GAA	p.K3072E
Pat_36	Post-Resistance	NBPF10	100132406	37	1	145362127	145362127	Missense_Mutation	SNP	G	T	6	256	c.9660G>T	c.(9658-9660)GAG>GAT	p.E3220D
Pat_36	Post-Resistance	ANKRD35	148741	37	1	145562153	145562153	Missense_Mutation	SNP	A	G	29	40	c.1841A>G	c.(1840-1842)GAG>GGG	p.E614G
Pat_36	Post-Resistance	TCHH	7062	37	1	152084627	152084627	Missense_Mutation	SNP	C	G	9	100	c.1066G>C	c.(1066-1068)GAG>CAG	p.E356Q
Pat_36	Post-Resistance	INSRR	3645	37	1	156823811	156823811	Missense_Mutation	SNP	G	A	3	53	c.370C>T	c.(370-372)CGT>TGT	p.R124C
Pat_36	Post-Resistance	F5	2153	37	1	169510502	169510502	Missense_Mutation	SNP	G	T	11	413	c.3826C>A	c.(3826-3828)CTT>ATT	p.L1276I
Pat_36	Post-Resistance	SLC9A11	284525	37	1	173494048	173494048	Missense_Mutation	SNP	C	T	88	162	c.2384G>A	c.(2383-2385)GGT>GAT	p.G795D
Pat_36	Post-Resistance	FAM5B	57795	37	1	177250597	177250597	Missense_Mutation	SNP	C	T	59	86	c.2285C>T	c.(2284-2286)TCC>TTC	p.S762F
Pat_36	Post-Resistance	CFH	3075	37	1	196709754	196709754	Missense_Mutation	SNP	C	T	66	324	c.2788C>T	c.(2788-2790)CCT>TCT	p.P930S
Pat_36	Post-Resistance	FAM58B	339521	37	1	200183175	200183175	Missense_Mutation	SNP	T	C	7	175	c.484T>C	c.(484-486)TGC>CGC	p.C162R
Pat_36	Post-Resistance	TLR5	7100	37	1	223285653	223285653	Missense_Mutation	SNP	C	T	66	265	c.721G>A	c.(721-723)GAC>AAC	p.D241N
Pat_36	Post-Resistance	BMS1	9790	37	10	43292130	43292130	Missense_Mutation	SNP	G	A	4	78	c.1438G>A	c.(1438-1440)GTT>ATT	p.V480I
Pat_36	Post-Resistance	CHAT	1103	37	10	50828610	50828610	Missense_Mutation	SNP	G	C	3	80	c.649G>C	c.(649-651)GCC>CCC	p.A217P
Pat_36	Post-Resistance	FUT11	170384	37	10	75533357	75533357	Nonsense_Mutation	SNP	G	A	3	77	c.1118G>A	c.(1117-1119)TGG>TAG	p.W373*
Pat_36	Post-Resistance	CYP2C19	1557	37	10	96540270	96540270	Missense_Mutation	SNP	C	T	176	76	c.496C>T	c.(496-498)CCC>TCC	p.P166S
Pat_36	Post-Resistance	PLEKHA1	59338	37	10	124159884	124159884	Missense_Mutation	SNP	C	T	72	40	c.224C>T	c.(223-225)CCA>CTA	p.P75L
Pat_36	Post-Resistance	HMX3	340784	37	10	124896966	124896966	Missense_Mutation	SNP	C	A	4	46	c.793C>A	c.(793-795)CAC>AAC	p.H265N
Pat_36	Post-Resistance	ADAM8	101	37	10	135085960	135085960	Missense_Mutation	SNP	G	A	4	70	c.718C>T	c.(718-720)CGG>TGG	p.R240W

Pat_36	Post-Resistance	OR4C3	256144	37	11	48347048	48347048	Missense_Mutation	SNP	C	T	14	153	c.556C>T	c.(556-558)CTC>TTC	p.L186F
Pat_36	Post-Resistance	OR5I1	10798	37	11	55703323	55703323	Missense_Mutation	SNP	G	A	30	95	c.554C>T	c.(553-555)CCC>CTC	p.P185L
Pat_36	Post-Resistance	TMEM132A	54972	37	11	60703442	60703442	Missense_Mutation	SNP	G	A	4	65	c.2135G>A	c.(2134-2136)GGT>GAT	p.G712D
Pat_36	Post-Resistance	VEGFB	7423	37	11	64004908	64004908	Missense_Mutation	SNP	C	T	4	145	c.427C>T	c.(427-429)CAC>TAC	p.H143Y
Pat_36	Post-Resistance	VEGFB	7423	37	11	64004995	64004995	Missense_Mutation	SNP	C	T	5	144	c.514C>T	c.(514-516)CCA>TCA	p.P172S
Pat_36	Post-Resistance	SF3B2	10992	37	11	65828120	65828120	Missense_Mutation	SNP	T	A	99	94	c.1697T>A	c.(1696-1698)ATC>AAC	p.I566N
Pat_36	Post-Resistance	LOC645332	645332	37	11	67564228	67564228	Missense_Mutation	SNP	C	T	4	91	c.236G>A	c.(235-237)AGC>AAC	p.S79N
Pat_36	Post-Resistance	CNTN5	53942	37	11	99715584	99715584	Missense_Mutation	SNP	A	G	129	106	c.278A>G	c.(277-279)GAA>GGA	p.E93G
Pat_36	Post-Resistance	TMPRSS13	84000	37	11	117789465	117789465	Missense_Mutation	SNP	G	C	6	120	c.110C>G	c.(109-111)GCC>GGC	p.A37G
Pat_36	Post-Resistance	CBL	867	37	11	119149421	119149421	Missense_Mutation	SNP	A	G	8	125	c.1429A>G	c.(1429-1431)AAG>GAG	p.K477E
Pat_36	Post-Resistance	CCDC15	80071	37	11	124857495	124857495	Missense_Mutation	SNP	A	C	13	504	c.1373A>C	c.(1372-1374)CAC>CCC	p.H458P
Pat_36	Post-Resistance	CD163	9332	37	12	7636205	7636205	Missense_Mutation	SNP	G	A	69	121	c.2846C>T	c.(2845-2847)TCC>TTC	p.S949F
Pat_36	Post-Resistance	PZP	5858	37	12	9346818	9346818	Missense_Mutation	SNP	C	T	45	90	c.1109G>A	c.(1108-1110)GGA>GAA	p.G370E
Pat_36	Post-Resistance	PRB4	5545	37	12	11461753	11461753	Missense_Mutation	SNP	C	T	124	208	c.164G>A	c.(163-165)GGA>GAA	p.G55E
Pat_36	Post-Resistance	LRP1	4035	37	12	57595327	57595327	Missense_Mutation	SNP	C	T	4	102	c.10393C>T	.(10393-10395)CGG>TG	p.R3465W
Pat_36	Post-Resistance	ATP2B1	490	37	12	90028875	90028875	Missense_Mutation	SNP	C	T	99	241	c.560G>A	c.(559-561)CGA>CAA	p.R187Q
Pat_36	Post-Resistance	ANKS1B	56899	37	12	100200261	100200261	Missense_Mutation	SNP	G	A	93	129	c.590C>T	c.(589-591)CCA>CTA	p.P197L
Pat_36	Post-Resistance	LOC220429	220429	37	13	50466615	50466615	Missense_Mutation	SNP	G	C	14	167	c.1889G>C	c.(1888-1890)TGT>TCT	p.C630S
Pat_36	Post-Resistance	CLEC14A	161198	37	14	38724167	38724167	Missense_Mutation	SNP	G	A	3	74	c.1061C>T	c.(1060-1062)ACG>ATG	p.T354M
Pat_36	Post-Resistance	LRFN5	145581	37	14	42360541	42360541	Missense_Mutation	SNP	G	A	172	260	c.1474G>A	c.(1474-1476)GAT>AAT	p.D492N
Pat_36	Post-Resistance	PTGER2	5732	37	14	52781426	52781426	Missense_Mutation	SNP	G	A	3	32	c.160G>A	c.(160-162)GTG>ATG	p.V54M
Pat_36	Post-Resistance	FBXO34	55030	37	14	55818498	55818498	Missense_Mutation	SNP	G	C	4	156	c.1390G>C	c.(1390-1392)GAC>CAC	p.D464H
Pat_36	Post-Resistance	CATSPERB	79820	37	14	92136192	92136192	Missense_Mutation	SNP	G	A	48	73	c.1253C>T	c.(1252-1254)CCC>CTC	p.P418L
Pat_36	Post-Resistance	ZNF839	55778	37	14	102808221	102808221	Nonsense_Mutation	SNP	C	A	4	49	c.2141C>A	c.(2140-2142)TCA>TAA	p.S714*
Pat_36	Post-Resistance	JAG2	3714	37	14	105609345	105609345	Missense_Mutation	SNP	C	T	3	32	c.3404G>A	c.(3403-3405)CGC>CAC	p.R1135H
Pat_36	Post-Resistance	CXADRP2	646243	37	15	22016334	22016334	Missense_Mutation	SNP	C	T	16	97	c.383G>A	c.(382-384)GGA>GAA	p.G128E
Pat_36	Post-Resistance	OR4N4	283694	37	15	22382615	22382615	Missense_Mutation	SNP	C	T	97	470	c.143C>T	c.(142-144)ACC>ATC	p.T48I
Pat_36	Post-Resistance	TGM5	9333	37	15	43533132	43533132	Missense_Mutation	SNP	C	T	65	82	c.919G>A	c.(919-921)GAT>AAT	p.D307N
Pat_36	Post-Resistance	CYP19A1	1588	37	15	51503039	51503039	Missense_Mutation	SNP	G	A	93	169	c.1478C>T	c.(1477-1479)ACC>ATC	p.T493I
Pat_36	Post-Resistance	DMXL2	23312	37	15	51795159	51795159	Missense_Mutation	SNP	G	A	91	107	c.2836C>T	c.(2836-2838)CCA>TCA	p.P946S
Pat_36	Post-Resistance	VPS13C	54832	37	15	62254605	62254605	Missense_Mutation	SNP	T	A	321	442	c.3568A>T	c.(3568-3570)ATT>TTT	p.I1190F
Pat_36	Post-Resistance	SMAD3	4088	37	15	67477073	67477073	Missense_Mutation	SNP	G	A	4	103	c.880G>A	c.(880-882)GTG>ATG	p.V294M
Pat_36	Post-Resistance	SCAMP5	192683	37	15	75308954	75308954	Missense_Mutation	SNP	G	A	6	175	c.157G>A	c.(157-159)GTG>ATG	p.V53M
Pat_36	Post-Resistance	NPIP	9284	37	16	15045671	15045671	Nonsense_Mutation	SNP	C	A	8	396	c.842C>A	c.(841-843)TCA>TAA	p.S281*
Pat_36	Post-Resistance	FOXF1	2294	37	16	86546572	86546572	Missense_Mutation	SNP	C	G	3	78	c.1021C>G	c.(1021-1023)CGA>GGA	p.R341G
Pat_36	Post-Resistance	NLRP1	22861	37	17	5424981	5424981	Missense_Mutation	SNP	C	T	34	26	c.3646G>A	c.(3646-3648)GGA>AGA	p.G1216R
Pat_36	Post-Resistance	CYB5D1	124637	37	17	7762832	7762832	Missense_Mutation	SNP	C	T	4	150	c.589C>T	c.(589-591)CGG>TGG	p.R197W
Pat_36	Post-Resistance	USP43	124739	37	17	9590195	9590195	Missense_Mutation	SNP	G	A	3	67	c.1322G>A	c.(1321-1323)CGC>CAC	p.R441H
Pat_36	Post-Resistance	MYH2	4620	37	17	10436824	10436824	Splice_Site	SNP	A	T	124	57	c.2304_splice	c.e20+1	p.K768_splice
Pat_36	Post-Resistance	SLC4A1	6521	37	17	42328624	42328624	Missense_Mutation	SNP	G	A	3	53	c.2558C>T	c.(2557-2559)ACG>ATG	p.T853M
Pat_36	Post-Resistance	SP2	6668	37	17	46000338	46000338	Missense_Mutation	SNP	G	A	6	202	c.1070G>A	c.(1069-1071)CGC>CAC	p.R357H
Pat_36	Post-Resistance	SGCA	6442	37	17	48252775	48252775	Missense_Mutation	SNP	C	T	4	77	c.1141C>T	c.(1141-1143)CCC>TCC	p.P381S
Pat_36	Post-Resistance	ANKFN1	162282	37	17	54534722	54534722	Missense_Mutation	SNP	T	C	69	269	c.1421T>C	c.(1420-1422)ATT>ACT	p.I474T
Pat_36	Post-Resistance	TEX2	55852	37	17	62226409	62226409	Missense_Mutation	SNP	T	G	62	89	c.3304A>C	c.(3304-3306)ATA>CTA	p.I1102L
Pat_36	Post-Resistance	CD300E	342510	37	17	72613304	72613304	Missense_Mutation	SNP	G	A	97	171	c.341C>T	c.(340-342)TCA>TTA	p.S114L
Pat_36	Post-Resistance	C19orf28	126321	37	19	3551085	3551085	Missense_Mutation	SNP	C	T	3	68	c.406G>A	c.(406-408)GTG>ATG	p.V136M
Pat_36	Post-Resistance	CD209	30835	37	19	7810766	7810766	Missense_Mutation	SNP	C	T	27	247	c.386G>A	c.(385-387)CGG>CAG	p.R129Q

Pat_36	Post-Resistance	ZNF560	147741	37	19	9578023	9578023	Missense_Mutation	SNP	G	A	53	99	c.1600C>T	c.(1600-1602)CAC>TAC	p.H534Y
Pat_36	Post-Resistance	ZNF799	90576	37	19	12501446	12501446	Missense_Mutation	SNP	T	C	13	135	c.1766A>G	c.(1765-1767)GAA>GGA	p.E589G
Pat_36	Post-Resistance	ANO8	57719	37	19	17438622	17438622	Missense_Mutation	SNP	A	G	6	150	c.2294T>C	c.(2293-2295)TTC>TCC	p.F765S
Pat_36	Post-Resistance	ZNF93	81931	37	19	20045247	20045247	Missense_Mutation	SNP	T	A	14	422	c.1483T>A	c.(1483-1485)TCC>ACC	p.S495T
Pat_36	Post-Resistance	ZNF737	100129842	37	19	20728254	20728254	Missense_Mutation	SNP	C	G	9	215	c.755G>C	c.(754-756)AGT>ACT	p.S252T
Pat_36	Post-Resistance	ZNF208	7757	37	19	22155896	22155896	Missense_Mutation	SNP	A	C	19	281	c.1640T>G	c.(1639-1641)ATT>AGT	p.I547S
Pat_36	Post-Resistance	ZNF257	113835	37	19	22271387	22271387	Missense_Mutation	SNP	C	T	41	65	c.835C>T	c.(835-837)CAT>TAT	p.H279Y
Pat_36	Post-Resistance	ZNF676	163223	37	19	22363039	22363039	Missense_Mutation	SNP	T	C	7	279	c.1480A>G	c.(1480-1482)AAA>GAA	p.K494E
Pat_36	Post-Resistance	ZNF492	57615	37	19	22847625	22847625	Missense_Mutation	SNP	G	T	10	222	c.1154G>T	c.(1153-1155)AGA>ATA	p.R385I
Pat_36	Post-Resistance	ZNF99	7652	37	19	22941036	22941036	Missense_Mutation	SNP	G	A	48	132	c.1402C>T	c.(1402-1404)CAT>TAT	p.H468Y
Pat_36	Post-Resistance	ZNF91	7644	37	19	23544808	23544808	Missense_Mutation	SNP	C	T	12	478	c.973G>A	c.(973-975)GAA>AAA	p.E325K
Pat_36	Post-Resistance	ZNF780A	284323	37	19	40580552	40580552	Missense_Mutation	SNP	T	G	27	382	c.1797A>C	c.(1795-1797)CAA>CAC	p.Q599H
Pat_36	Post-Resistance	BCL3	602	37	19	45259535	45259535	Missense_Mutation	SNP	C	T	4	96	c.457C>T	c.(457-459)CGG>TGG	p.R153W
Pat_36	Post-Resistance	ZNF160	90338	37	19	53572562	53572562	Missense_Mutation	SNP	G	A	131	264	c.1225C>T	c.(1225-1227)CGT>TGT	p.R409C
Pat_36	Post-Resistance	ZNF845	91664	37	19	53856702	53856702	Missense_Mutation	SNP	G	A	8	365	c.2774G>A	c.(2773-2775)CGT>CAT	p.R925H
Pat_36	Post-Resistance	ZNF845	91664	37	19	53856761	53856761	Missense_Mutation	SNP	T	C	8	220	c.2833T>C	c.(2833-2835)TGT>CGT	p.C945R
Pat_36	Post-Resistance	ZNF813	126017	37	19	53995130	53995130	Missense_Mutation	SNP	T	G	9	165	c.1644T>G	c.(1642-1644)GAT>GAG	p.D548E
Pat_36	Post-Resistance	LILRA1	11024	37	19	55106681	55106681	Missense_Mutation	SNP	G	A	89	177	c.475G>A	c.(475-477)GAA>AAA	p.E159K
Pat_36	Post-Resistance	AURKC	6795	37	19	57746762	57746763	Missense_Mutation	DNP	CC	TT	37	101	c.907_908CC>TT	c.(907-909)CCC>TTC	p.P303F
Pat_36	Post-Resistance	ZNF814	730051	37	19	58384315	58384315	Missense_Mutation	SNP	G	A	5	168	c.2443C>T	c.(2443-2445)CTC>TTC	p.L815F
Pat_36	Post-Resistance	BIRC6	57448	37	2	32774431	32774431	Nonsense_Mutation	SNP	C	T	102	116	c.13027C>T	c.(13027-13029)CAG>TAG	p.Q4343*
Pat_36	Post-Resistance	ARHGAP25	9938	37	2	69034596	69034596	Missense_Mutation	SNP	C	T	5	145	c.655C>T	c.(655-657)CGG>TGG	p.R219W
Pat_36	Post-Resistance	XIRP2	129446	37	2	168104981	168104981	Missense_Mutation	SNP	C	T	61	146	c.7079C>T	c.(7078-7080)TCA>TTA	p.S2360L
Pat_36	Post-Resistance	SF3B1	23451	37	2	198288653	198288653	Missense_Mutation	SNP	A	T	57	70	c.74T>A	c.(73-75)CTT>CAT	p.L25H
Pat_36	Post-Resistance	SPAG16	79582	37	2	214878736	214878736	Missense_Mutation	SNP	C	T	109	182	c.1462C>T	c.(1462-1464)CCT>TCT	p.P488S
Pat_36	Post-Resistance	PSMD1	5707	37	2	231945017	231945017	Missense_Mutation	SNP	G	A	4	102	c.1402G>A	c.(1402-1404)GCC>ACC	p.A468T
Pat_36	Post-Resistance	DGKD	8527	37	2	234350612	234350612	Missense_Mutation	SNP	G	A	5	117	c.1165G>A	c.(1165-1167)GAA>AAA	p.E389K
Pat_36	Post-Resistance	SUN5	140732	37	20	31585473	31585473	Missense_Mutation	SNP	G	A	26	63	c.361C>T	c.(361-363)CAC>TAC	p.H121Y
Pat_36	Post-Resistance	DDX27	55661	37	20	47843000	47843000	Missense_Mutation	SNP	C	T	22	116	c.727C>T	c.(727-729)CCG>TCG	p.P243S
Pat_36	Post-Resistance	PMEPA1	56937	37	20	56234616	56234616	Missense_Mutation	SNP	C	T	15	63	c.247G>A	c.(247-249)GAA>AAA	p.E83K
Pat_36	Post-Resistance	GNAS	2778	37	20	57430103	57430103	Missense_Mutation	SNP	C	T	20	63	c.1783C>T	c.(1783-1785)CGG>TGG	p.R595W
Pat_36	Post-Resistance	BAGE2	85319	37	21	11058316	11058316	Missense_Mutation	SNP	G	T	29	512	c.124C>A	c.(124-126)CAT>AAT	p.H42N
Pat_36	Post-Resistance	BAGE2	85319	37	21	11058322	11058322	Missense_Mutation	SNP	C	T	19	456	c.118G>A	c.(118-120)GAT>AAT	p.D40N
Pat_36	Post-Resistance	KRTAP10-8	386681	37	21	46032751	46032751	Missense_Mutation	SNP	G	C	3	81	c.734G>C	c.(733-735)TGC>TCC	p.C245S
Pat_36	Post-Resistance	LSS	4047	37	21	47614507	47614507	Nonsense_Mutation	SNP	C	T	3	44	c.1886G>A	c.(1885-1887)TGG>TAG	p.W629*
Pat_36	Post-Resistance	FAM83F	113828	37	22	40415904	40415904	Missense_Mutation	SNP	G	T	42	47	c.671G>T	c.(670-672)CGC>CTC	p.R224L
Pat_36	Post-Resistance	CCR3	1232	37	3	46306946	46306946	Missense_Mutation	SNP	G	T	9	518	c.297G>T	c.(295-297)TGG>TGT	p.W99C
Pat_36	Post-Resistance	TLR9	54106	37	3	52256731	52256731	Missense_Mutation	SNP	T	C	3	77	c.1601A>G	c.(1600-1602)GAC>GGC	p.D534G
Pat_36	Post-Resistance	GLT8D1	55830	37	3	52729519	52729519	Missense_Mutation	SNP	C	T	94	115	c.730G>A	c.(730-732)GGA>AGA	p.G244R
Pat_36	Post-Resistance	IGSF10	285313	37	3	151163624	151163624	Missense_Mutation	SNP	G	A	121	242	c.4145C>T	c.(4144-4146)GCC>GTC	p.A1382V
Pat_36	Post-Resistance	SLITRK3	22865	37	3	164907675	164907675	Missense_Mutation	SNP	G	A	48	106	c.944C>T	c.(943-945)TCC>TTC	p.S315F
Pat_36	Post-Resistance	TNFSF10	8743	37	3	172224614	172224614	Missense_Mutation	SNP	C	A	5	159	c.514G>T	c.(514-516)GGT>TGT	p.G172C
Pat_36	Post-Resistance	SPATA16	83893	37	3	172643172	172643172	Missense_Mutation	SNP	C	T	42	47	c.1192G>A	c.(1192-1194)GAA>AAA	p.E398K
Pat_36	Post-Resistance	EIF4G1	1981	37	3	184045020	184045020	Missense_Mutation	SNP	G	C	3	52	c.3445G>C	c.(3445-3447)GAA>CAA	p.E1149Q
Pat_36	Post-Resistance	FRYL	285527	37	4	48566058	48566058	Missense_Mutation	SNP	T	C	60	89	c.3503A>G	c.(3502-3504)AAC>AGC	p.N1168S
Pat_36	Post-Resistance	TECRL	253017	37	4	65180398	65180398	Missense_Mutation	SNP	C	A	7	180	c.519G>T	c.(517-519)GAG>GAT	p.E173D
Pat_36	Post-Resistance	ABCG2	9429	37	4	89042886	89042886	Missense_Mutation	SNP	C	T	52	93	c.590G>A	c.(589-591)GGA>GAA	p.G197E

Pat_36	Post-Resistance	TRPC3	7222	37	4	122846307	122846307	Missense_Mutation	SNP	C	T	74	87	c.1042G>A	c.(1042-1044)GAT>AAT	p.D348N
Pat_36	Post-Resistance	TLL1	7092	37	4	166914016	166914016	Missense_Mutation	SNP	G	A	33	60	c.341G>A	c.(340-342)AGG>AAG	p.R114K
Pat_36	Post-Resistance	CTNND2	1501	37	5	11022885	11022885	Missense_Mutation	SNP	C	T	38	39	c.2995G>A	c.(2995-2997)GAT>AAT	p.D999N
Pat_36	Post-Resistance	EGFLAM	133584	37	5	38350642	38350642	Missense_Mutation	SNP	C	T	115	170	c.331C>T	c.(331-333)CGT>TGT	p.R111C
Pat_36	Post-Resistance	EGFLAM	133584	37	5	38418330	38418330	Missense_Mutation	SNP	G	A	12	41	c.1657G>A	c.(1657-1659)GGA>AGA	p.G553R
Pat_36	Post-Resistance	SLIT3	6586	37	5	168176636	168176636	Missense_Mutation	SNP	G	T	44	60	c.1978C>A	c.(1978-1980)CTC>ATC	p.L660I
Pat_36	Post-Resistance	PPARD	5467	37	6	35378976	35378976	Missense_Mutation	SNP	C	T	52	185	c.112C>T	c.(112-114)CCT>TCT	p.P38S
Pat_36	Post-Resistance	SNX9	51429	37	6	158342574	158342574	Missense_Mutation	SNP	G	C	3	87	c.961G>C	c.(961-963)GAG>CAG	p.E321Q
Pat_36	Post-Resistance	HOXA2	3199	37	7	27142080	27142080	Missense_Mutation	SNP	T	A	10	389	c.40A>T	c.(40-42)AGC>TGC	p.S14C
Pat_36	Post-Resistance	CRHR2	1395	37	7	30693101	30693101	Missense_Mutation	SNP	C	T	178	101	c.1211G>A	c.(1210-1212)AGC>AAC	p.S404N
Pat_36	Post-Resistance	CCDC129	223075	37	7	31614251	31614251	Missense_Mutation	SNP	C	T	51	138	c.493C>T	c.(493-495)CCA>TCA	p.P165S
Pat_36	Post-Resistance	ZNF92	168374	37	7	64863839	64863839	Missense_Mutation	SNP	C	A	13	558	c.812C>A	c.(811-813)ACC>AAC	p.T271N
Pat_36	Post-Resistance	AUTS2	26053	37	7	70239084	70239084	Missense_Mutation	SNP	G	A	7	225	c.1901G>A	c.(1900-1902)AGG>AAG	p.R634K
Pat_36	Post-Resistance	LAMB1	3912	37	7	107626494	107626494	Missense_Mutation	SNP	C	T	19	66	c.649G>A	c.(649-651)GAA>AAA	p.E217K
Pat_36	Post-Resistance	NUP205	23165	37	7	135322742	135322742	Missense_Mutation	SNP	C	G	64	260	c.5200C>G	c.(5200-5202)CAA>GAA	p.Q1734E
Pat_36	Post-Resistance	DENND2A	27147	37	7	140221703	140221703	Missense_Mutation	SNP	A	G	66	33	c.2863T>C	c.(2863-2865)TTT>CTT	p.F955L
Pat_36	Post-Resistance	BRAF	673	37	7	140453136	140453137	Missense_Mutation	DNP	AC	TT	141	134	.1798_1799GT>A	c.(1798-1800)GTG>AAG	p.V600K
Pat_36	Post-Resistance	TRY6	154754	37	7	142481805	142481805	Missense_Mutation	SNP	G	A	186	28	c.484G>A	c.(484-486)GAC>AAC	p.D162N
Pat_36	Post-Resistance	AMAC1L2	83650	37	8	11188846	11188847	Missense_Mutation	DNP	CC	TA	121	303	c.231_232CC>TA	(229-234)TGCCTC>TGTAT	p.L78I
Pat_36	Post-Resistance	OPRK1	4986	37	8	54147645	54147645	Missense_Mutation	SNP	T	C	79	182	c.284A>G	c.(283-285)AAC>AGC	p.N95S
Pat_36	Post-Resistance	DCAF4L2	138009	37	8	88885853	88885853	Missense_Mutation	SNP	G	A	149	91	c.347C>T	c.(346-348)CCG>CTG	p.P116L
Pat_36	Post-Resistance	TAF2	6873	37	8	120800684	120800684	Missense_Mutation	SNP	G	A	44	133	c.1687C>T	c.(1687-1689)CCA>TCA	p.P563S
Pat_36	Post-Resistance	PLEC	5339	37	8	144998339	144998339	Missense_Mutation	SNP	G	A	3	59	c.6169C>T	c.(6169-6171)CGG>TGG	p.R2057W
Pat_36	Post-Resistance	ANKRD20A3	441425	37	9	67938633	67938633	Missense_Mutation	SNP	G	T	5	111	c.768G>T	c.(766-768)AAG>AAT	p.K256N
Pat_36	Post-Resistance	TLE4	7091	37	9	82333807	82333807	Missense_Mutation	SNP	C	T	118	54	c.1586C>T	c.(1585-1587)ACG>ATG	p.T529M
Pat_36	Post-Resistance	KIAA1958	158405	37	9	115422326	115422326	Missense_Mutation	SNP	G	T	4	80	c.2128G>T	c.(2128-2130)GGC>TGC	p.G710C
Pat_36	Post-Resistance	GOLGA1	2800	37	9	127651544	127651544	Missense_Mutation	SNP	C	T	3	28	c.1639G>A	c.(1639-1641)GCC>ACC	p.A547T
Pat_36	Post-Resistance	TOR1B	27348	37	9	132569576	132569576	Missense_Mutation	SNP	C	T	4	170	c.575C>T	c.(574-576)CCG>CTG	p.P192L
Pat_36	Post-Resistance	COL5A1	1289	37	9	137676874	137676874	Missense_Mutation	SNP	C	T	33	38	c.2524C>T	c.(2524-2526)CCT>TCT	p.P842S
Pat_36	Post-Resistance	MAMDC4	158056	37	9	139755051	139755051	Missense_Mutation	SNP	C	T	3	77	c.3410C>T	c.(3409-3411)CCG>CTG	p.P1137L
Pat_36	Post-Resistance	FAM47C	442444	37	X	37027190	37027190	Missense_Mutation	SNP	T	C	7	237	c.707T>C	c.(706-708)CTG>CCG	p.L236P
Pat_36	Post-Resistance	FAM47C	442444	37	X	37028699	37028699	Missense_Mutation	SNP	G	A	5	162	c.2216G>A	c.(2215-2217)CGC>CAC	p.R739H
Pat_36	Post-Resistance	SRPX	8406	37	X	38024056	38024056	Missense_Mutation	SNP	C	T	38	78	c.619G>A	c.(619-621)GAA>AAA	p.E207K
Pat_36	Post-Resistance	ACRC	93953	37	X	70823920	70823920	Missense_Mutation	SNP	C	T	8	251	c.793C>T	c.(793-795)CCC>TCC	p.P265S
Pat_36	Post-Resistance	CITED1	4435	37	X	71521743	71521743	Missense_Mutation	SNP	G	A	56	191	c.412C>T	c.(412-414)CCT>TCT	p.P138S
Pat_36	Post-Resistance	PHKA1	5255	37	X	71870239	71870239	Splice_Site	SNP	C	T	48	39	c.1324_splice	c.e13+1	p.V442_splice
Pat_36	Post-Resistance	AIFM1	9131	37	X	129290539	129290539	Nonsense_Mutation	SNP	G	A	434	335	c.145C>T	c.(145-147)CAG>TAG	p.Q49*
Pat_36	Post-Resistance	MAGEC1	9947	37	X	140994923	140994923	Missense_Mutation	SNP	A	T	14	824	c.1733A>T	c.(1732-1734)CAC>CTC	p.H578L
Pat_36	Post-Resistance	MAGEA5	4104	37	X	151283715	151283715	Missense_Mutation	SNP	C	T	51	158	c.298G>A	c.(298-300)GAC>AAC	p.D100N
Pat_37	Post-Resistance	CCDC27	148870	37	1	3677872	3677872	Missense_Mutation	SNP	C	A	3	62	c.739C>A	c.(739-741)CAG>AAG	p.Q247K
Pat_37	Post-Resistance	CASZ1	54897	37	1	10720457	10720458	Missense_Mutation	DNP	GG	AA	27	20	c.641_642CC>TT	c.(640-642)ACC>ATT	p.T214I
Pat_37	Post-Resistance	VPS13D	55187	37	1	12336563	12336563	Missense_Mutation	SNP	G	A	4	235	c.2918G>A	c.(2917-2919)CGG>CAG	p.R973Q
Pat_37	Post-Resistance	MST1P9	11223	37	1	17085609	17085609	Missense_Mutation	SNP	T	C	3	151	c.1112A>G	c.(1111-1113)AAG>AGG	p.K371R
Pat_37	Post-Resistance	PADI3	51702	37	1	17597609	17597610	Missense_Mutation	DNP	GG	TA	39	42	c.983_984GG>TA	c.(982-984)AGG>ATA	p.R328I
Pat_37	Post-Resistance	KIF17	57576	37	1	21039967	21039967	Missense_Mutation	SNP	C	A	4	114	c.460G>T	c.(460-462)GAC>TAC	p.D154Y
Pat_37	Post-Resistance	SH2D5	400745	37	1	21049335	21049335	Missense_Mutation	SNP	C	T	17	14	c.730G>A	c.(730-732)GGC>AGC	p.G244S
Pat_37	Post-Resistance	SNRNP40	9410	37	1	31740760	31740760	Missense_Mutation	SNP	C	A	5	219	c.878G>T	c.(877-879)TGG>TTG	p.W293L

Pat_37	Post-Resistance	HIVEP3	59269	37	1	42049181	42049181	Missense_Mutation	SNP	C	T	41	53	c.1288G>A	c.(1288-1290)GCC>ACC	p.A430T
Pat_37	Post-Resistance	KDM4A	9682	37	1	44137364	44137364	Missense_Mutation	SNP	C	T	4	56	c.1552C>T	c.(1552-1554)CGG>TGG	p.R518W
Pat_37	Post-Resistance	PLK3	1263	37	1	45267582	45267582	Missense_Mutation	SNP	G	A	39	32	c.631G>A	c.(631-633)GAG>AAG	p.E211K
Pat_37	Post-Resistance	EIF2B3	8891	37	1	45345603	45345603	Missense_Mutation	SNP	C	T	54	39	c.862G>A	c.(862-864)GAC>AAC	p.D288N
Pat_37	Post-Resistance	ABCA4	24	37	1	94473802	94473802	Missense_Mutation	SNP	G	A	60	41	c.5887C>T	c.(5887-5889)CGC>TGC	p.R1963C
Pat_37	Post-Resistance	TBX15	6913	37	1	119456748	119456748	Missense_Mutation	SNP	C	A	4	193	c.598G>T	c.(598-600)GGG>TGG	p.G200W
Pat_37	Post-Resistance	TBX15	6913	37	1	119466193	119466193	Nonsense_Mutation	SNP	G	A	154	166	c.409C>T	c.(409-411)CGA>TGA	p.R137*
Pat_37	Post-Resistance	RBM8A	9939	37	1	145508251	145508251	Missense_Mutation	SNP	G	A	123	280	c.172G>A	c.(172-174)GAG>AAG	p.E58K
Pat_37	Post-Resistance	NBPF16	728936	37	1	148754864	148754864	Missense_Mutation	SNP	A	G	3	118	c.1520A>G	c.(1519-1521)GAG>GGG	p.E507G
Pat_37	Post-Resistance	SPTA1	6708	37	1	158590040	158590040	Missense_Mutation	SNP	C	T	42	82	c.6337G>A	c.(6337-6339)GGT>AGT	p.G2113S
Pat_37	Post-Resistance	SPTA1	6708	37	1	158592934	158592934	Missense_Mutation	SNP	C	T	328	545	c.5959G>A	c.(5959-5961)GAG>AAG	p.E1987K
Pat_37	Post-Resistance	NCSTN	23385	37	1	160325741	160325741	Missense_Mutation	SNP	C	T	44	104	c.1544C>T	c.(1543-1545)CCC>CTC	p.P515L
Pat_37	Post-Resistance	ADCY10	55811	37	1	167823624	167823624	Missense_Mutation	SNP	C	T	85	202	c.2275G>A	c.(2275-2277)GAA>AAA	p.E759K
Pat_37	Post-Resistance	SELE	6401	37	1	169701822	169701822	Missense_Mutation	SNP	C	T	15	44	c.355G>A	c.(355-357)GAA>AAA	p.E119K
Pat_37	Post-Resistance	DNM3	26052	37	1	172002338	172002338	Missense_Mutation	SNP	C	T	18	23	c.782C>T	c.(781-783)TCC>TTC	p.S261F
Pat_37	Post-Resistance	PIGC	5279	37	1	172411623	172411623	Missense_Mutation	SNP	T	C	254	337	c.140A>G	c.(139-141)CAA>CGA	p.Q47R
Pat_37	Post-Resistance	CACNA1E	777	37	1	181705551	181705551	Missense_Mutation	SNP	A	G	34	42	c.3403A>G	c.(3403-3405)ATC>GTC	p.I1135V
Pat_37	Post-Resistance	GPR25	2848	37	1	200842308	200842308	Missense_Mutation	SNP	C	T	14	22	c.143C>T	c.(142-144)GCG>GTG	p.A48V
Pat_37	Post-Resistance	DTL	51514	37	1	212236238	212236238	Missense_Mutation	SNP	C	T	5	313	c.473C>T	c.(472-474)ACG>ATG	p.T158M
Pat_37	Post-Resistance	HHIPL2	79802	37	1	222717501	222717501	Missense_Mutation	SNP	C	T	121	293	c.352G>A	c.(352-354)GAC>AAC	p.D118N
Pat_37	Post-Resistance	SUSD4	55061	37	1	223396657	223396657	Missense_Mutation	SNP	G	A	53	135	c.1378C>T	c.(1378-1380)CCT>TCT	p.P460S
Pat_37	Post-Resistance	OBSCN	84033	37	1	228524810	228524810	Missense_Mutation	SNP	C	T	4	164	c.16643C>T	c.(16642-16644)TCG>TTG	p.S5548L
Pat_37	Post-Resistance	TAF5L	27097	37	1	229745874	229745874	Nonsense_Mutation	SNP	G	A	4	239	c.226C>T	c.(226-228)CGA>TGA	p.R76*
Pat_37	Post-Resistance	ITIH5	80760	37	10	7679199	7679199	Missense_Mutation	SNP	C	T	35	688	c.644G>A	c.(643-645)CGC>CAC	p.R215H
Pat_37	Post-Resistance	PLXDC2	84898	37	10	20453449	20453449	Missense_Mutation	SNP	G	A	146	286	c.836G>A	c.(835-837)GGA>GAA	p.G279E
Pat_37	Post-Resistance	MYO3A	53904	37	10	26305806	26305806	Missense_Mutation	SNP	C	T	124	258	c.566C>T	c.(565-567)CCG>CTG	p.P189L
Pat_37	Post-Resistance	MASTL	84930	37	10	27459701	27459701	Missense_Mutation	SNP	G	A	12	37	c.1813G>A	c.(1813-1815)GAA>AAA	p.E605K
Pat_37	Post-Resistance	MPP7	143098	37	10	28438925	28438925	Missense_Mutation	SNP	C	T	72	90	c.220G>A	c.(220-222)GCC>ACC	p.A74T
Pat_37	Post-Resistance	ZNF33B	7582	37	10	43089957	43089957	Missense_Mutation	SNP	C	T	62	195	c.441G>A	c.(439-441)ATG>ATA	p.M147I
Pat_37	Post-Resistance	PTEN	5728	37	10	89711993	89711993	Missense_Mutation	SNP	C	T	11	536	c.611C>T	c.(610-612)CCA>CTA	p.P204L
Pat_37	Post-Resistance	CRTAC1	55118	37	10	99696061	99696061	Missense_Mutation	SNP	G	A	4	83	c.287C>T	c.(286-288)GCG>GTG	p.A96V
Pat_37	Post-Resistance	C10orf81	79949	37	10	115535549	115535549	Missense_Mutation	SNP	G	A	107	85	c.955G>A	c.(955-957)GAG>AAG	p.E319K
Pat_37	Post-Resistance	EMX2	2018	37	10	119305304	119305304	Missense_Mutation	SNP	A	G	3	48	c.568A>G	c.(568-570)AGC>GGC	p.S190G
Pat_37	Post-Resistance	LOC653544	653544	37	10	135491009	135491009	Missense_Mutation	SNP	G	T	5	66	c.620G>T	c.(619-621)AGG>ATG	p.R207M
Pat_37	Post-Resistance	PHRF1	57661	37	11	598398	598398	Missense_Mutation	SNP	C	T	20	25	c.920C>T	c.(919-921)TCC>TTC	p.S307F
Pat_37	Post-Resistance	PNPLA2	57104	37	11	824073	824073	Missense_Mutation	SNP	C	T	3	57	c.995C>T	c.(994-996)ACG>ATG	p.T332M
Pat_37	Post-Resistance	TRPM5	29850	37	11	2434797	2434797	Missense_Mutation	SNP	A	C	16	31	c.1912T>G	c.(1912-1914)TGG>GGG	p.W638G
Pat_37	Post-Resistance	OR51G2	81282	37	11	4936880	4936880	Missense_Mutation	SNP	G	A	29	53	c.14C>T	c.(13-15)TCC>TTC	p.S5F
Pat_37	Post-Resistance	TUB	7275	37	11	8122119	8122119	Missense_Mutation	SNP	C	T	41	90	c.1186C>T	c.(1186-1188)CAT>TAT	p.H396Y
Pat_37	Post-Resistance	OR8J1	219477	37	11	56127862	56127862	Missense_Mutation	SNP	C	T	172	277	c.140C>T	c.(139-141)ACC>ATC	p.T47I
Pat_37	Post-Resistance	ZP1	22917	37	11	60638702	60638702	Nonsense_Mutation	SNP	C	T	39	74	c.1027C>T	c.(1027-1029)CAG>TAG	p.Q343*
Pat_37	Post-Resistance	B3GAT3	26229	37	11	62384611	62384611	Missense_Mutation	SNP	G	A	49	88	c.466C>T	c.(466-468)CGT>TGT	p.R156C
Pat_37	Post-Resistance	PCNXL3	399909	37	11	65401705	65401705	Missense_Mutation	SNP	G	A	19	23	c.4579G>A	c.(4579-4581)GAT>AAT	p.D1527N
Pat_37	Post-Resistance	SAPS3	55291	37	11	68369378	68369378	Missense_Mutation	SNP	G	A	165	343	c.2240G>A	c.(2239-2241)AGC>AAC	p.S747N
Pat_37	Post-Resistance	SHANK2	22941	37	11	70319483	70319483	Missense_Mutation	SNP	G	A	26	70	c.5041C>T	c.(5041-5043)CGC>TGC	p.R1681C
Pat_37	Post-Resistance	SYTL2	54843	37	11	85447625	85447625	Missense_Mutation	SNP	G	A	93	135	c.502C>T	c.(502-504)CCA>TCA	p.P168S
Pat_37	Post-Resistance	DYNC2H1	79659	37	11	103025334	103025334	Missense_Mutation	SNP	C	T	22	55	c.3457C>T	c.(3457-3459)CGG>TGG	p.R1153W

Pat_37	Post-Resistance	FXYD2	486	37	11	117691411	117691412	Splice_Site	DNP	CC	TT	52	53	c.177_splice	c.e5-1	p.R59_splice
Pat_37	Post-Resistance	SORL1	6653	37	11	121495820	121495820	Missense_Mutation	SNP	T	G	152	111	c.6198T>G	c.(6196-6198)AGT>AGG	p.S2066R
Pat_37	Post-Resistance	CDON	50937	37	11	125853959	125853959	Missense_Mutation	SNP	G	A	28	25	c.2803C>T	c.(2803-2805)CCT>TCT	p.P935S
Pat_37	Post-Resistance	CHD4	1108	37	12	6702280	6702280	Missense_Mutation	SNP	G	A	87	154	c.2629C>T	c.(2629-2631)CGG>TGG	p.R877W
Pat_37	Post-Resistance	MFAP5	8076	37	12	8803177	8803177	Missense_Mutation	SNP	C	T	60	104	c.256G>A	c.(256-258)GAT>AAT	p.D86N
Pat_37	Post-Resistance	PZP	5858	37	12	9353583	9353583	Missense_Mutation	SNP	G	A	95	186	c.575C>T	c.(574-576)CCC>CTC	p.P192L
Pat_37	Post-Resistance	CLEC7A	64581	37	12	10275902	10275902	Missense_Mutation	SNP	G	A	34	101	c.553C>T	c.(553-555)CGG>TGG	p.R185W
Pat_37	Post-Resistance	TAS2R42	353164	37	12	11338899	11338899	Missense_Mutation	SNP	C	G	52	69	c.645G>C	c.(643-645)AAG>AAC	p.K215N
Pat_37	Post-Resistance	GRIN2B	2904	37	12	13717171	13717171	Missense_Mutation	SNP	C	T	45	86	c.3001G>A	c.(3001-3003)GAT>AAT	p.D1001N
Pat_37	Post-Resistance	CASC1	55259	37	12	25297373	25297373	Missense_Mutation	SNP	C	T	144	331	c.910G>A	c.(910-912)GAA>AAA	p.E304K
Pat_37	Post-Resistance	MLL2	8085	37	12	49431693	49431693	Missense_Mutation	SNP	G	A	15	38	c.9446C>T	c.(9445-9447)TCC>TTC	p.S3149F
Pat_37	Post-Resistance	ACCN2	41	37	12	50473745	50473745	Missense_Mutation	SNP	G	A	6	498	c.1112G>A	c.(1111-1113)CGC>CAC	p.R371H
Pat_37	Post-Resistance	MFSD5	84975	37	12	53647014	53647014	Missense_Mutation	SNP	T	C	313	502	c.395T>C	c.(394-396)GTG>GCG	p.V132A
Pat_37	Post-Resistance	OR6C6	283365	37	12	55688866	55688866	Missense_Mutation	SNP	G	A	105	167	c.151C>T	c.(151-153)CCC>TCC	p.P51S
Pat_37	Post-Resistance	OR6C1	390321	37	12	55714592	55714592	Missense_Mutation	SNP	C	T	69	110	c.209C>T	c.(208-210)TCG>TTG	p.S70L
Pat_37	Post-Resistance	OR6C4	341418	37	12	55945126	55945126	Missense_Mutation	SNP	G	A	263	494	c.116G>A	c.(115-117)GGA>GAA	p.G39E
Pat_37	Post-Resistance	KIF5A	3798	37	12	57957903	57957903	Missense_Mutation	SNP	G	A	90	147	c.304G>A	c.(304-306)GAC>AAC	p.D102N
Pat_37	Post-Resistance	TRHDE	29953	37	12	72956777	72956777	Missense_Mutation	SNP	G	A	153	254	c.1864G>A	c.(1864-1866)GAT>AAT	p.D622N
Pat_37	Post-Resistance	PPFIA2	8499	37	12	81741397	81741397	Missense_Mutation	SNP	G	A	213	432	c.2147C>T	c.(2146-2148)TCA>TTA	p.S716L
Pat_37	Post-Resistance	C12orf12	196477	37	12	91348239	91348239	Missense_Mutation	SNP	G	A	3	59	c.281C>T	c.(280-282)CCA>CTA	p.P94L
Pat_37	Post-Resistance	ANO4	121601	37	12	101333122	101333122	Missense_Mutation	SNP	G	A	70	142	c.190G>A	c.(190-192)GAA>AAA	p.E64K
Pat_37	Post-Resistance	UTP20	27340	37	12	101680285	101680285	Nonsense_Mutation	SNP	C	A	4	203	c.513C>A	c.(511-513)TAC>TAA	p.Y171*
Pat_37	Post-Resistance	STAB2	55576	37	12	104102294	104102294	Missense_Mutation	SNP	G	A	107	187	c.4268G>A	c.(4267-4269)CGA>CAA	p.R1423Q
Pat_37	Post-Resistance	C12orf23	90488	37	12	107365098	107365098	Missense_Mutation	SNP	G	A	4	236	c.280G>A	c.(280-282)GTT>ATT	p.V94I
Pat_37	Post-Resistance	FICD	11153	37	12	108912722	108912723	Missense_Mutation	DNP	GG	AA	44	107	c.847_848GG>AA	c.(847-849)GGC>AAC	p.G283N
Pat_37	Post-Resistance	TPCN1	53373	37	12	113711397	113711398	Missense_Mutation	DNP	CC	TT	201	374	c.866_867CC>TT	c.(865-867)TCC>TTT	p.S289F
Pat_37	Post-Resistance	FBXW8	26259	37	12	117365847	117365847	Missense_Mutation	SNP	C	T	65	127	c.338C>T	c.(337-339)CCT>CTT	p.P113L
Pat_37	Post-Resistance	DIABLO	56616	37	12	122709099	122709099	Missense_Mutation	SNP	A	G	195	295	c.143T>C	c.(142-144)ATT>ACT	p.I48T
Pat_37	Post-Resistance	HIP1R	9026	37	12	123333135	123333135	Missense_Mutation	SNP	C	T	50	100	c.280C>T	c.(280-282)CTT>TTT	p.L94F
Pat_37	Post-Resistance	MTUS2	23281	37	13	29599659	29599659	Missense_Mutation	SNP	C	T	22	47	c.854C>T	c.(853-855)TCA>TTA	p.S285L
Pat_37	Post-Resistance	NBEA	26960	37	13	35806678	35806678	Missense_Mutation	SNP	C	T	7	8	c.5698C>T	c.(5698-5700)CGT>TGT	p.R1900C
Pat_37	Post-Resistance	FREM2	341640	37	13	39266402	39266402	Missense_Mutation	SNP	C	T	74	113	c.4921C>T	c.(4921-4923)CCC>TCC	p.P1641S
Pat_37	Post-Resistance	GPC5	2262	37	13	92797179	92797179	Missense_Mutation	SNP	G	A	129	250	c.1498G>A	c.(1498-1500)GAT>AAT	p.D500N
Pat_37	Post-Resistance	NALCN	259232	37	13	101910822	101910822	Missense_Mutation	SNP	C	T	48	112	c.1238G>A	c.(1237-1239)AGG>AAG	p.R413K
Pat_37	Post-Resistance	OR4N2	390429	37	14	20295764	20295764	Missense_Mutation	SNP	C	T	15	305	c.157C>T	c.(157-159)CCT>TCT	p.P53S
Pat_37	Post-Resistance	OR4L1	122742	37	14	20528650	20528650	Nonsense_Mutation	SNP	G	A	83	183	c.447G>A	c.(445-447)TGG>TGA	p.W149*
Pat_37	Post-Resistance	CHD8	57680	37	14	21861354	21861354	Missense_Mutation	SNP	G	T	4	147	c.5542C>A	c.(5542-5544)CAA>AAA	p.Q1848K
Pat_37	Post-Resistance	MYH6	4624	37	14	23854151	23854151	Missense_Mutation	SNP	C	T	47	107	c.5263G>A	c.(5263-5265)GAG>AAG	p.E1755K
Pat_37	Post-Resistance	LRRC16B	90668	37	14	24534223	24534223	Missense_Mutation	SNP	C	A	5	249	c.3137C>A	c.(3136-3138)CCA>CAA	p.P1046Q
Pat_37	Post-Resistance	LRRC16B	90668	37	14	24534241	24534241	Missense_Mutation	SNP	G	A	4	100	c.3155G>A	c.(3154-3156)CGC>CAC	p.R1052H
Pat_37	Post-Resistance	ARHGAP5	394	37	14	32562852	32562852	Missense_Mutation	SNP	C	T	200	338	c.2977C>T	c.(2977-2979)CCA>TCA	p.P993S
Pat_37	Post-Resistance	FRMD6	122786	37	14	52194536	52194536	Missense_Mutation	SNP	A	G	216	284	c.1658A>G	c.(1657-1659)AAA>AGA	p.K553R
Pat_37	Post-Resistance	MAPK1IP1L	93487	37	14	55529606	55529606	Missense_Mutation	SNP	C	T	65	134	c.289C>T	c.(289-291)CCA>TCA	p.P97S
Pat_37	Post-Resistance	DLGAP5	9787	37	14	55650429	55650429	Missense_Mutation	SNP	A	G	15	18	c.281T>C	c.(280-282)CTC>CCC	p.L94P
Pat_37	Post-Resistance	RAD51L1	5890	37	14	68934923	68934923	Missense_Mutation	SNP	C	T	118	205	c.992C>T	c.(991-993)ACC>ATC	p.T331I
Pat_37	Post-Resistance	SERPINA11	256394	37	14	94914736	94914736	Missense_Mutation	SNP	G	A	47	137	c.376C>T	c.(376-378)CTT>TTT	p.L126F
Pat_37	Post-Resistance	DIO3	1735	37	14	102028737	102028737	Missense_Mutation	SNP	C	T	35	65	c.826C>T	c.(826-828)CGG>TGG	p.R276W

Pat_37	Post-Resistance	TECPR2	9895	37	14	102874935	102874935	Nonsense_Mutation	SNP	T	A	66	139	c.459T>A	c.(457-459)TAT>TAA	p.Y153*
Pat_37	Post-Resistance	ADAM6	8755	37	14	106354443	106354443	Splice_Site	SNP	G	A	34	45	c.49316_splice	c.e3089+1	
Pat_37	Post-Resistance	UBE3A	7337	37	15	25620797	25620797	Missense_Mutation	SNP	C	G	62	123	c.185G>C	c.(184-186)CGT>CCT	p.R62P
Pat_37	Post-Resistance	GABRB3	2562	37	15	26793136	26793136	Missense_Mutation	SNP	C	T	52	84	c.1226G>A	c.(1225-1227)CGA>CAA	p.R409Q
Pat_37	Post-Resistance	C15orf55	256646	37	15	34649346	34649347	Missense_Mutation	DNP	CC	TT	35	63	.3053_3054CC>T	c.(3052-3054)TCC>TTT	p.S1018F
Pat_37	Post-Resistance	EIF2AK4	440275	37	15	40280268	40280268	Nonsense_Mutation	SNP	C	T	81	184	c.2488C>T	c.(2488-2490)CGA>TGA	p.R830*
Pat_37	Post-Resistance	C15orf57	90416	37	15	40849511	40849511	Missense_Mutation	SNP	C	T	4	214	c.305G>A	c.(304-306)CGA>CAA	p.R102Q
Pat_37	Post-Resistance	LEO1	123169	37	15	52252113	52252113	Missense_Mutation	SNP	A	T	100	156	c.1143T>A	c.(1141-1143)TTT>TTA	p.F381L
Pat_37	Post-Resistance	UNC13C	440279	37	15	54305830	54305830	Missense_Mutation	SNP	G	A	48	107	c.730G>A	c.(730-732)GAA>AAA	p.E244K
Pat_37	Post-Resistance	MAN2C1	4123	37	15	75660483	75660483	Missense_Mutation	SNP	C	T	11	8	c.158G>A	c.(157-159)AGA>AAA	p.R53K
Pat_37	Post-Resistance	ACAN	176	37	15	89416239	89416239	Missense_Mutation	SNP	C	T	24	39	c.7316C>T	c.(7315-7317)ACG>ATG	p.T2439M
Pat_37	Post-Resistance	MAN2A2	4122	37	15	91450650	91450650	Missense_Mutation	SNP	G	C	6	188	c.1121G>C	c.(1120-1122)CGC>CCC	p.R374P
Pat_37	Post-Resistance	DECR2	26063	37	16	461501	461501	Missense_Mutation	SNP	G	A	4	200	c.802G>A	c.(802-804)GAT>AAT	p.D268N
Pat_37	Post-Resistance	SOLH	6650	37	16	601598	601598	Missense_Mutation	SNP	G	A	4	80	c.2279G>A	c.(2278-2280)CGT>CAT	p.R760H
Pat_37	Post-Resistance	FLYWCH1	84256	37	16	2980449	2980449	Missense_Mutation	SNP	G	A	9	5	c.364G>A	c.(364-366)GGG>AGG	p.G122R
Pat_37	Post-Resistance	KREMEN2	79412	37	16	3016389	3016389	Missense_Mutation	SNP	G	A	69	72	c.425G>A	c.(424-426)GGC>GAC	p.G142D
Pat_37	Post-Resistance	DNASE1	1773	37	16	3706147	3706147	Missense_Mutation	SNP	G	A	5	220	c.281G>A	c.(280-282)GGA>GAA	p.G94E
Pat_37	Post-Resistance	PRKCB	5579	37	16	24231291	24231291	Missense_Mutation	SNP	A	G	3	95	c.1873A>G	c.(1873-1875)AGA>GGA	p.R625G
Pat_37	Post-Resistance	FHOD1	29109	37	16	67265090	67265090	Splice_Site	SNP	C	G	4	65	c.2667_splice	c.e17+1	p.K889_splice
Pat_37	Post-Resistance	ATP6V0D1	9114	37	16	67472954	67472954	Missense_Mutation	SNP	G	A	4	231	c.736C>T	c.(736-738)CGG>TGG	p.R246W
Pat_37	Post-Resistance	SPG7	6687	37	16	89617007	89617007	Missense_Mutation	SNP	C	G	3	87	c.1769C>G	c.(1768-1770)GCC>GGC	p.A590G
Pat_37	Post-Resistance	YWHAE	7531	37	17	1264431	1264431	Missense_Mutation	SNP	G	A	164	270	c.533C>T	c.(532-534)TCC>TTC	p.S178F
Pat_37	Post-Resistance	PITPNA	5306	37	17	1451661	1451661	Missense_Mutation	SNP	C	T	4	213	c.218G>A	c.(217-219)CGA>CAA	p.R73Q
Pat_37	Post-Resistance	SMTNL2	342527	37	17	4510744	4510744	Missense_Mutation	SNP	G	A	6	704	c.1348G>A	c.(1348-1350)GTC>ATC	p.V450I
Pat_37	Post-Resistance	MINK1	50488	37	17	4797389	4797389	Splice_Site	SNP	G	A	4	60	c.2670_splice	c.e22+1	p.R890_splice
Pat_37	Post-Resistance	CAMTA2	23125	37	17	4880437	4880438	Missense_Mutation	DNP	GG	AA	57	156	.1815_1816CC>T	813-1818)CCCCTT>CCT	p.L606F
Pat_37	Post-Resistance	TNK1	8711	37	17	7291865	7291865	Missense_Mutation	SNP	A	G	29	61	c.1633A>G	c.(1633-1635)AGC>GGC	p.S545G
Pat_37	Post-Resistance	DNAH2	146754	37	17	7727983	7727983	Missense_Mutation	SNP	C	T	167	347	c.11791C>T	c.(11791-11793)CAC>TAC	p.H3931Y
Pat_37	Post-Resistance	SPDYE4	388333	37	17	8656641	8656641	Missense_Mutation	SNP	C	T	7	21	c.652G>A	c.(652-654)GAG>AAG	p.E218K
Pat_37	Post-Resistance	TOM1L2	146691	37	17	17786101	17786101	Missense_Mutation	SNP	G	A	107	158	c.578C>T	c.(577-579)TCC>TTC	p.S193F
Pat_37	Post-Resistance	LGALS9C	654346	37	17	18387232	18387232	Missense_Mutation	SNP	G	A	90	51	c.83G>A	c.(82-84)GGA>GAA	p.G28E
Pat_37	Post-Resistance	MAPK7	5598	37	17	19284135	19284135	Missense_Mutation	SNP	C	T	3	63	c.613C>T	c.(613-615)CGT>TGT	p.R205C
Pat_37	Post-Resistance	TRAF4	9618	37	17	27075388	27075388	Missense_Mutation	SNP	C	T	3	92	c.571C>T	c.(571-573)CGC>TGC	p.R191C
Pat_37	Post-Resistance	CNTNAP1	8506	37	17	40845480	40845480	Missense_Mutation	SNP	G	A	4	159	c.2918G>A	c.(2917-2919)CGC>CAC	p.R973H
Pat_37	Post-Resistance	KIF18B	146909	37	17	43012650	43012650	Missense_Mutation	SNP	C	T	3	29	c.448G>A	c.(448-450)GAG>AAG	p.E150K
Pat_37	Post-Resistance	IGF2BP1	10642	37	17	47115636	47115636	Missense_Mutation	SNP	G	A	48	63	c.508G>A	c.(508-510)GGC>AGC	p.G170S
Pat_37	Post-Resistance	COL1A1	1277	37	17	48271376	48271377	Missense_Mutation	DNP	GG	AA	47	113	.1694_1695CC>T	c.(1693-1695)CCC>CTT	p.P565L
Pat_37	Post-Resistance	AKAP1	8165	37	17	55189933	55189933	Missense_Mutation	SNP	C	T	5	170	c.2057C>T	c.(2056-2058)CCC>CTC	p.P686L
Pat_37	Post-Resistance	RECQL5	9400	37	17	73624834	73624834	Missense_Mutation	SNP	G	A	4	87	c.2498C>T	c.(2497-2499)CCG>CTG	p.P833L
Pat_37	Post-Resistance	SPHK1	8877	37	17	74383533	74383533	Missense_Mutation	SNP	G	T	4	156	c.1021G>T	c.(1021-1023)GAT>TAT	p.D341Y
Pat_37	Post-Resistance	UBE2O	63893	37	17	74387494	74387494	Missense_Mutation	SNP	G	A	4	200	c.3409C>T	c.(3409-3411)CGG>TGG	p.R1137W
Pat_37	Post-Resistance	PCYT2	5833	37	17	79864636	79864637	Missense_Mutation	DNP	GG	AA	17	63	c.675_676CC>TT	(673-678)TTCCAC>TTTT	p.H226Y
Pat_37	Post-Resistance	LAMA3	3909	37	18	21512198	21512198	Missense_Mutation	SNP	C	T	180	293	c.8651C>T	c.(8650-8652)TCT>TTT	p.S2884F
Pat_37	Post-Resistance	SYT4	6860	37	18	40853607	40853607	Missense_Mutation	SNP	C	T	34	95	c.787G>A	c.(787-789)GGA>AGA	p.G263R
Pat_37	Post-Resistance	DCC	1630	37	18	50918076	50918076	Missense_Mutation	SNP	C	T	188	368	c.2507C>T	c.(2506-2508)TCG>TTG	p.S836L
Pat_37	Post-Resistance	DCC	1630	37	18	50994305	50994305	Missense_Mutation	SNP	G	A	71	127	c.3661G>A	c.(3661-3663)GAG>AAG	p.E1221K
Pat_37	Post-Resistance	NCLN	56926	37	19	3192594	3192594	Missense_Mutation	SNP	C	T	3	44	c.311C>T	c.(310-312)TCG>TTG	p.S104L

Pat_37	Post-Resistance	KDM4B	23030	37	19	5135389	5135390	Missense_Mutation	DNP	GG	AA	4	76	.2125_2126GG>A	c.(2125-2127)GGA>AAA	p.G709K
Pat_37	Post-Resistance	EMR1	2015	37	19	6897460	6897460	Missense_Mutation	SNP	G	A	4	158	c.416G>A	c.(415-417)AGC>AAC	p.S139N
Pat_37	Post-Resistance	KIAA1543	57662	37	19	7671277	7671277	Missense_Mutation	SNP	A	T	26	49	c.523A>T	c.(523-525)ACG>TCG	p.T175S
Pat_37	Post-Resistance	CD209	30835	37	19	7810560	7810560	Missense_Mutation	SNP	G	A	4	203	c.592C>T	c.(592-594)CGG>TGG	p.R198W
Pat_37	Post-Resistance	HNRNPM	4670	37	19	8528389	8528389	Splice_Site	SNP	G	A	5	339	c.344_splice	c.e4+1	p.A115_splice
Pat_37	Post-Resistance	ADAMTS10	81794	37	19	8645836	8645836	Nonsense_Mutation	SNP	G	A	28	78	c.3253C>T	c.(3253-3255)CAG>TAG	p.Q1085*
Pat_37	Post-Resistance	MUC16	94025	37	19	9063401	9063401	Missense_Mutation	SNP	C	A	4	163	c.24045G>T	c.(24043-24045)ATG>ATT	p.M8015I
Pat_37	Post-Resistance	COL5A3	50509	37	19	10071229	10071229	Missense_Mutation	SNP	C	T	14	271	c.5096G>A	c.(5095-5097)CGG>CAG	p.R1699Q
Pat_37	Post-Resistance	CYP4F8	11283	37	19	15734027	15734027	Missense_Mutation	SNP	C	G	74	136	c.760C>G	c.(760-762)CGG>GGG	p.R254G
Pat_37	Post-Resistance	MYO9B	4650	37	19	17213057	17213057	Missense_Mutation	SNP	C	T	7	625	c.530C>T	c.(529-531)ACG>ATG	p.T177M
Pat_37	Post-Resistance	TMEM161A	54929	37	19	19243477	19243477	Missense_Mutation	SNP	A	T	25	71	c.275T>A	c.(274-276)GTG>GAG	p.V92E
Pat_37	Post-Resistance	ZNF90	7643	37	19	20229760	20229760	Missense_Mutation	SNP	C	T	68	163	c.1397C>T	c.(1396-1398)TCA>TTA	p.S466L
Pat_37	Post-Resistance	ZNF43	7594	37	19	21992169	21992169	Missense_Mutation	SNP	T	G	4	243	c.670A>C	c.(670-672)AAT>CAT	p.N224H
Pat_37	Post-Resistance	HRC	3270	37	19	49657516	49657516	Missense_Mutation	SNP	C	T	37	31	c.979G>A	c.(979-981)GAA>AAA	p.E327K
Pat_37	Post-Resistance	KLK7	5650	37	19	51483718	51483718	Missense_Mutation	SNP	C	T	53	48	c.247G>A	c.(247-249)GAT>AAT	p.D83N
Pat_37	Post-Resistance	KLK14	43847	37	19	51582876	51582876	Missense_Mutation	SNP	G	A	4	36	c.344C>T	c.(343-345)ACG>ATG	p.T115M
Pat_37	Post-Resistance	FPR3	2359	37	19	52327004	52327004	Missense_Mutation	SNP	G	A	23	27	c.3G>A	c.(1-3)ATG>ATA	p.M1I
Pat_37	Post-Resistance	ZIM3	114026	37	19	57648292	57648292	Missense_Mutation	SNP	C	T	62	80	c.190G>A	c.(190-192)GGA>AGA	p.G64R
Pat_37	Post-Resistance	C2orf48	348738	37	2	10350701	10350701	Missense_Mutation	SNP	T	C	5	182	c.458T>C	c.(457-459)CTC>CCC	p.L153P
Pat_37	Post-Resistance	GPN1	11321	37	2	27870737	27870737	Missense_Mutation	SNP	G	T	4	120	c.1008G>T	c.(1006-1008)TTG>TTT	p.L336F
Pat_37	Post-Resistance	SRBD1	55133	37	2	45807106	45807106	Missense_Mutation	SNP	G	A	4	214	c.980C>T	c.(979-981)GCA>GTA	p.A327V
Pat_37	Post-Resistance	PROM2	150696	37	2	95953993	95953993	Missense_Mutation	SNP	C	T	90	94	c.2279C>T	c.(2278-2280)TCC>TTC	p.S760F
Pat_37	Post-Resistance	ADRA2B	151	37	2	96781752	96781752	Missense_Mutation	SNP	G	A	3	37	c.137C>T	c.(136-138)CCT>CTT	p.P46L
Pat_37	Post-Resistance	IWS1	55677	37	2	128262638	128262638	Missense_Mutation	SNP	G	A	152	105	c.841C>T	c.(841-843)CCC>TCC	p.P281S
Pat_37	Post-Resistance	KCNH7	90134	37	2	163374282	163374282	Missense_Mutation	SNP	C	T	4	144	c.850G>A	c.(850-852)GTC>ATC	p.V284I
Pat_37	Post-Resistance	TTN	7273	37	2	179463537	179463537	Missense_Mutation	SNP	T	C	6	464	c.49196A>G	c.(49195-49197)AAT>AGT	p.N16399S
Pat_37	Post-Resistance	TTN	7273	37	2	179469470	179469470	Missense_Mutation	SNP	C	T	132	106	c.46642G>A	c.(46642-46644)GAA>AAA	p.E15548K
Pat_37	Post-Resistance	PARD3B	117583	37	2	206265756	206265756	Missense_Mutation	SNP	G	A	14	6	c.2650G>A	c.(2650-2652)GAT>AAT	p.D884N
Pat_37	Post-Resistance	ABCB6	10058	37	2	220077134	220077134	Missense_Mutation	SNP	C	T	4	178	c.1943G>A	c.(1942-1944)CGA>CAA	p.R648Q
Pat_37	Post-Resistance	GPCPD1	56261	37	20	5547385	5547385	Missense_Mutation	SNP	G	A	88	158	c.1261C>T	c.(1261-1263)CGG>TGG	p.R421W
Pat_37	Post-Resistance	TM9SF4	9777	37	20	30729426	30729426	Missense_Mutation	SNP	G	A	5	368	c.356G>A	c.(355-357)CGA>CAA	p.R119Q
Pat_37	Post-Resistance	SEMG2	6407	37	20	43850512	43850512	Missense_Mutation	SNP	G	A	94	161	c.239G>A	c.(238-240)CGA>CAA	p.R80Q
Pat_37	Post-Resistance	KRTAP13-2	337959	37	21	31744194	31744194	Missense_Mutation	SNP	C	T	49	112	c.338G>A	c.(337-339)GGA>GAA	p.G113E
Pat_37	Post-Resistance	KRTAP19-5	337972	37	21	31874201	31874201	Missense_Mutation	SNP	C	T	178	402	c.208G>A	c.(208-210)GGA>AGA	p.G70R
Pat_37	Post-Resistance	IFNAR1	3454	37	21	34707922	34707922	Missense_Mutation	SNP	G	A	102	192	c.169G>A	c.(169-171)GGG>AGG	p.G57R
Pat_37	Post-Resistance	SLC37A1	54020	37	21	43979140	43979140	Missense_Mutation	SNP	C	T	28	59	c.922C>T	c.(922-924)CCC>TCC	p.P308S
Pat_37	Post-Resistance	CABIN1	23523	37	22	24466790	24466790	Missense_Mutation	SNP	G	A	168	237	c.2272G>A	c.(2272-2274)GAG>AAG	p.E758K
Pat_37	Post-Resistance	SEZ6L	23544	37	22	26692966	26692966	Missense_Mutation	SNP	G	A	33	80	c.1082G>A	c.(1081-1083)CGA>CAA	p.R361Q
Pat_37	Post-Resistance	RFPL2	10739	37	22	32587079	32587079	Missense_Mutation	SNP	C	T	115	147	c.817G>A	c.(817-819)GAG>AAG	p.E273K
Pat_37	Post-Resistance	RAC2	5880	37	22	37628869	37628869	Missense_Mutation	SNP	C	T	4	161	c.197G>A	c.(196-198)CGT>CAT	p.R66H
Pat_37	Post-Resistance	ENTHD1	150350	37	22	40140252	40140252	Missense_Mutation	SNP	G	A	42	66	c.1256C>T	c.(1255-1257)CCT>CTT	p.P419L
Pat_37	Post-Resistance	PKDREJ	10343	37	22	46657381	46657381	Missense_Mutation	SNP	T	A	75	155	c.1839A>T	c.(1837-1839)AAA>AAT	p.K613N
Pat_37	Post-Resistance	PLXNB2	23654	37	22	50716039	50716039	Missense_Mutation	SNP	G	A	5	333	c.5177C>T	c.(5176-5178)ACG>ATG	p.T1726M
Pat_37	Post-Resistance	ITPR1	3708	37	3	4730242	4730242	Missense_Mutation	SNP	G	A	15	323	c.3739G>A	c.(3739-3741)GCA>ACA	p.A1247T
Pat_37	Post-Resistance	GRIP2	80852	37	3	14583492	14583492	Missense_Mutation	SNP	G	A	3	48	c.97C>T	c.(97-99)CGC>TGC	p.R33C
Pat_37	Post-Resistance	TOP2B	7155	37	3	25665139	25665139	Missense_Mutation	SNP	A	G	67	100	c.2594T>C	c.(2593-2595)ATA>ACA	p.I865T
Pat_37	Post-Resistance	KBTBD5	131377	37	3	42729733	42729733	Missense_Mutation	SNP	G	A	4	212	c.1252G>A	c.(1252-1254)GGT>AGT	p.G418S

Pat_37	Post-Resistance	CCDC36	339834	37	3	49274018	49274018	Missense_Mutation	SNP	G	A	11	42	c.94G>A	c.(94-96)GAT>AAT	p.D32N
Pat_37	Post-Resistance	PCBP4	57060	37	3	51992163	51992163	Missense_Mutation	SNP	G	A	4	177	c.1126C>T	c.(1126-1128)CCG>TCG	p.P376S
Pat_37	Post-Resistance	TLR9	54106	37	3	52257382	52257382	Missense_Mutation	SNP	T	C	48	106	c.950A>G	c.(949-951)GAG>GGG	p.E317G
Pat_37	Post-Resistance	ITIH3	3699	37	3	52831911	52831911	Missense_Mutation	SNP	G	A	5	26	c.628G>A	c.(628-630)GGA>AGA	p.G210R
Pat_37	Post-Resistance	CACNA1D	776	37	3	53531412	53531412	Nonsense_Mutation	SNP	C	T	103	230	c.301C>T	c.(301-303)CGA>TGA	p.R101*
Pat_37	Post-Resistance	CRYBG3	131544	37	3	97662120	97662120	Missense_Mutation	SNP	G	A	40	37	c.3031G>A	c.(3031-3033)GGA>AGA	p.G1011R
Pat_37	Post-Resistance	SLC35A5	55032	37	3	112299458	112299458	Missense_Mutation	SNP	C	T	48	50	c.494C>T	c.(493-495)ACT>ATT	p.T165I
Pat_37	Post-Resistance	PLXNA1	5361	37	3	126735834	126735834	Missense_Mutation	SNP	G	A	4	160	c.3161G>A	c.(3160-3162)CGT>CAT	p.R1054H
Pat_37	Post-Resistance	COL6A6	131873	37	3	130360517	130360517	Missense_Mutation	SNP	G	A	21	13	c.5113G>A	c.(5113-5115)GAG>AAG	p.E1705K
Pat_37	Post-Resistance	ATP1B3	483	37	3	141622560	141622560	Missense_Mutation	SNP	C	T	93	55	c.208C>T	c.(208-210)CCA>TCA	p.P70S
Pat_37	Post-Resistance	IGSF10	285313	37	3	151176361	151176361	Missense_Mutation	SNP	C	T	4	147	c.137G>A	c.(136-138)CGG>CAG	p.R46Q
Pat_37	Post-Resistance	SI	6476	37	3	164741528	164741528	Missense_Mutation	SNP	G	A	54	45	c.2929C>T	c.(2929-2931)CCC>TCC	p.P977S
Pat_37	Post-Resistance	CHRD	8646	37	3	184106417	184106417	Missense_Mutation	SNP	C	T	43	52	c.2597C>T	c.(2596-2598)GCT>GTT	p.A866V
Pat_37	Post-Resistance	TPRG1	285386	37	3	188925310	188925310	Missense_Mutation	SNP	G	A	212	119	c.137G>A	c.(136-138)AGT>AAT	p.S46N
Pat_37	Post-Resistance	SLIT2	9353	37	4	20543093	20543093	Missense_Mutation	SNP	C	T	39	79	c.1994C>T	c.(1993-1995)CCT>CTT	p.P665L
Pat_37	Post-Resistance	LIMCH1	22998	37	4	41684413	41684413	Nonsense_Mutation	SNP	C	T	65	122	c.2629C>T	c.(2629-2631)CAG>TAG	p.Q877*
Pat_37	Post-Resistance	DCUN1D4	23142	37	4	52777312	52777312	Missense_Mutation	SNP	T	C	4	238	c.692T>C	c.(691-693)CTT>CCT	p.L231P
Pat_37	Post-Resistance	EREG	2069	37	4	75248388	75248388	Missense_Mutation	SNP	G	A	4	240	c.305G>A	c.(304-306)CGA>CAA	p.R102Q
Pat_37	Post-Resistance	STBD1	8987	37	4	77230595	77230595	Missense_Mutation	SNP	G	C	3	76	c.519G>C	c.(517-519)TTG>TTC	p.L173F
Pat_37	Post-Resistance	ADH6	130	37	4	100137332	100137332	Missense_Mutation	SNP	C	T	33	103	c.106G>A	c.(106-108)GAA>AAA	p.E36K
Pat_37	Post-Resistance	NHEDC2	133308	37	4	103971417	103971417	Missense_Mutation	SNP	C	T	106	193	c.565G>A	c.(565-567)GGC>AGC	p.G189S
Pat_37	Post-Resistance	NDST4	64579	37	4	115891702	115891702	Missense_Mutation	SNP	G	A	49	109	c.1105C>T	c.(1105-1107)CGG>TGG	p.R369W
Pat_37	Post-Resistance	PRSS12	8492	37	4	119239632	119239632	Missense_Mutation	SNP	C	A	27	246	c.1051G>T	c.(1051-1053)GGG>TGG	p.G351W
Pat_37	Post-Resistance	FAT4	79633	37	4	126328278	126328278	Missense_Mutation	SNP	C	T	203	346	c.5551C>T	c.(5551-5553)CCT>TCT	p.P1851S
Pat_37	Post-Resistance	RXFP1	59350	37	4	159493870	159493870	Missense_Mutation	SNP	G	A	128	273	c.70G>A	c.(70-72)GAT>AAT	p.D24N
Pat_37	Post-Resistance	RXFP1	59350	37	4	159493897	159493897	Missense_Mutation	SNP	C	T	129	250	c.97C>T	c.(97-99)CCC>TCC	p.P33S
Pat_37	Post-Resistance	FAT1	2195	37	4	187532630	187532630	Missense_Mutation	SNP	C	T	4	207	c.9763G>A	c.(9763-9765)GCA>ACA	p.A3255T
Pat_37	Post-Resistance	DNAH5	1767	37	5	13753596	13753596	Missense_Mutation	SNP	C	T	96	228	c.10618G>A	c.(10618-10620)GAT>AAT	p.D3540N
Pat_37	Post-Resistance	11-Mar	441061	37	5	16177919	16177919	Nonsense_Mutation	SNP	C	T	77	131	c.609G>A	c.(607-609)TGG>TGA	p.W203*
Pat_37	Post-Resistance	OSMR	9180	37	5	38876401	38876401	Missense_Mutation	SNP	C	T	113	178	c.172C>T	c.(172-174)CCT>TCT	p.P58S
Pat_37	Post-Resistance	C9	735	37	5	39308368	39308368	Missense_Mutation	SNP	T	C	139	196	c.1204A>G	c.(1204-1206)AAA>GAA	p.K402E
Pat_37	Post-Resistance	GHR	2690	37	5	42711394	42711394	Missense_Mutation	SNP	G	A	220	406	c.704G>A	c.(703-705)CGA>CAA	p.R235Q
Pat_37	Post-Resistance	POLK	51426	37	5	74879192	74879192	Missense_Mutation	SNP	C	T	119	103	c.1009C>T	c.(1009-1011)CCC>TCC	p.P337S
Pat_37	Post-Resistance	MEF2C	4208	37	5	88100438	88100438	Missense_Mutation	SNP	G	A	108	69	c.235C>T	c.(235-237)CGG>TGG	p.R79W
Pat_37	Post-Resistance	MEF2C	4208	37	5	88100440	88100440	Missense_Mutation	SNP	C	G	107	72	c.233G>C	c.(232-234)AGC>ACC	p.S78T
Pat_37	Post-Resistance	GPR98	84059	37	5	89981639	89981639	Missense_Mutation	SNP	C	T	28	124	c.6317C>T	c.(6316-6318)GCG>GTG	p.A2106V
Pat_37	Post-Resistance	PCDHA11	56138	37	5	140250186	140250186	Missense_Mutation	SNP	G	A	119	104	c.1498G>A	c.(1498-1500)GAC>AAC	p.D500N
Pat_37	Post-Resistance	ARAP3	64411	37	5	141041751	141041751	Missense_Mutation	SNP	G	A	5	418	c.2872C>T	c.(2872-2874)CGT>TGT	p.R958C
Pat_37	Post-Resistance	BTNL3	10917	37	5	180419833	180419833	Missense_Mutation	SNP	C	T	4	109	c.70C>T	c.(70-72)CCG>TCG	p.P24S
Pat_37	Post-Resistance	PIP5K1P1	206426	37	6	7987864	7987864	Missense_Mutation	SNP	G	T	4	107	c.1095G>T	c.(1093-1095)ATG>ATT	p.M365I
Pat_37	Post-Resistance	NUP153	9972	37	6	17616825	17616825	Missense_Mutation	SNP	C	T	16	321	c.4276G>A	c.(4276-4278)GCC>ACC	p.A1426T
Pat_37	Post-Resistance	SCAND3	114821	37	6	28543165	28543166	Missense_Mutation	DNP	CC	TT	68	165	.1316_1317GG>A	c.(1315-1317)GGG>GAA	p.G439E
Pat_37	Post-Resistance	TNXB	7148	37	6	32014050	32014050	Missense_Mutation	SNP	G	A	19	37	c.10502C>T	c.(10501-10503)ACC>ATC	p.T3501I
Pat_37	Post-Resistance	TREM1	54210	37	6	41250147	41250147	Missense_Mutation	SNP	A	G	61	91	c.392T>C	c.(391-393)TTG>TCG	p.L131S
Pat_37	Post-Resistance	MDFI	4188	37	6	41613921	41613921	Missense_Mutation	SNP	C	T	4	128	c.134C>T	c.(133-135)GCG>GTG	p.A45V
Pat_37	Post-Resistance	RUNX2	860	37	6	45399628	45399628	Missense_Mutation	SNP	G	A	207	406	c.452G>A	c.(451-453)GGG>GAG	p.G151E
Pat_37	Post-Resistance	ENPP5	59084	37	6	46135374	46135374	Missense_Mutation	SNP	G	A	90	151	c.626C>T	c.(625-627)TCA>TTA	p.S209L

Pat_37	Post-Resistance	PKHD1	5314	37	6	51892990	51892990	Missense_Mutation	SNP	G	A	227	499	c.3524C>T	c.(3523-3525)TCC>TTC	p.S1175F
Pat_37	Post-Resistance	COL9A1	1297	37	6	70966482	70966482	Missense_Mutation	SNP	G	A	26	45	c.1492C>T	c.(1492-1494)CCT>TCT	p.P498S
Pat_37	Post-Resistance	ME1	4199	37	6	84055900	84055900	Missense_Mutation	SNP	C	T	124	301	c.592G>A	c.(592-594)GAA>AAA	p.E198K
Pat_37	Post-Resistance	MDN1	23195	37	6	90409426	90409426	Missense_Mutation	SNP	G	A	62	189	c.8891C>T	c.(8890-8892)CCC>CTC	p.P2964L
Pat_37	Post-Resistance	WISP3	8838	37	6	112385967	112385967	Missense_Mutation	SNP	C	G	164	276	c.356C>G	c.(355-357)GCT>GGT	p.A119G
Pat_37	Post-Resistance	ENPP3	5169	37	6	132004258	132004258	Missense_Mutation	SNP	G	A	171	309	c.1076G>A	c.(1075-1077)CGG>CAG	p.R359Q
Pat_37	Post-Resistance	CTGF	1490	37	6	132271591	132271592	Missense_Mutation	DNP	CC	TT	93	83	c.381_382GG>AA	379-384)CTGGAC>CTAA	p.D128N
Pat_37	Post-Resistance	EYA4	2070	37	6	133767851	133767851	Missense_Mutation	SNP	C	T	99	207	c.167C>T	c.(166-168)TCT>TTT	p.S56F
Pat_37	Post-Resistance	SGK1	6446	37	6	134528571	134528571	Splice_Site	SNP	T	C	3	57	c.286_splice	c.e3-1	p.V96_splice
Pat_37	Post-Resistance	C6orf70	55780	37	6	170168250	170168250	Missense_Mutation	SNP	C	T	39	88	c.1042C>T	c.(1042-1044)CTT>TTT	p.L348F
Pat_37	Post-Resistance	IQCE	23288	37	7	2611253	2611254	Missense_Mutation	DNP	CC	TT	46	157	c.224_225CC>TT	c.(223-225)ACC>ATT	p.T75I
Pat_37	Post-Resistance	CARD11	84433	37	7	2956974	2956975	Missense_Mutation	DNP	CC	TT	11	24	.2652_2653GG>A	650-2655)CGGGTC>CGA	p.V885I
Pat_37	Post-Resistance	AIMP2	7965	37	7	6063098	6063098	Missense_Mutation	SNP	G	C	18	75	c.739G>C	c.(739-741)GGA>CGA	p.G247R
Pat_37	Post-Resistance	ISPD	729920	37	7	16348164	16348164	Missense_Mutation	SNP	G	A	26	59	c.773C>T	c.(772-774)TCA>TTA	p.S258L
Pat_37	Post-Resistance	HDAC9	9734	37	7	19015548	19015548	Missense_Mutation	SNP	G	A	50	107	c.3142G>A	c.(3142-3144)GAA>AAA	p.E1048K
Pat_37	Post-Resistance	INMT	11185	37	7	30795310	30795310	Missense_Mutation	SNP	C	T	47	100	c.635C>T	c.(634-636)TCC>TTC	p.S212F
Pat_37	Post-Resistance	CCDC129	223075	37	7	31614330	31614330	Missense_Mutation	SNP	T	A	39	103	c.572T>A	c.(571-573)ATG>AAG	p.M191K
Pat_37	Post-Resistance	C7orf16	10842	37	7	31736630	31736630	Missense_Mutation	SNP	C	T	69	158	c.287C>T	c.(286-288)CCA>CTA	p.P96L
Pat_37	Post-Resistance	PGAM2	5224	37	7	44104935	44104935	Missense_Mutation	SNP	C	T	4	230	c.194G>A	c.(193-195)CGC>CAC	p.R65H
Pat_37	Post-Resistance	NPC1L1	29881	37	7	44560420	44560420	Splice_Site	SNP	C	T	58	109	c.3081_splice	c.e14-1	.G1027_splice
Pat_37	Post-Resistance	POM121L12	285877	37	7	53103777	53103777	Missense_Mutation	SNP	C	T	33	41	c.413C>T	c.(412-414)ACC>ATC	p.T138I
Pat_37	Post-Resistance	LAT2	7462	37	7	73638115	73638115	Splice_Site	SNP	T	C	30	306	c.448_splice	c.e11+2	p.G150_splice
Pat_37	Post-Resistance	HGF	3082	37	7	81346570	81346570	Nonsense_Mutation	SNP	C	T	180	317	c.1383G>A	c.(1381-1383)TGG>TGA	p.W461*
Pat_37	Post-Resistance	DYNC1I1	1780	37	7	95726852	95726852	Missense_Mutation	SNP	C	T	121	208	c.1885C>T	c.(1885-1887)CGT>TGT	p.R629C
Pat_37	Post-Resistance	DLX6	1750	37	7	96635385	96635385	Splice_Site	SNP	G	A	5	46	c.95_splice	c.e1+1	p.H32_splice
Pat_37	Post-Resistance	PVRIG	79037	37	7	99818442	99818442	Missense_Mutation	SNP	G	T	48	65	c.656G>T	c.(655-657)TGG>TTG	p.W219L
Pat_37	Post-Resistance	SLC12A9	56996	37	7	100452361	100452361	Missense_Mutation	SNP	G	A	4	200	c.301G>A	c.(301-303)GGG>AGG	p.G101R
Pat_37	Post-Resistance	TMEM168	64418	37	7	112424369	112424369	Missense_Mutation	SNP	G	A	75	136	c.512C>T	c.(511-513)ACT>ATT	p.T171I
Pat_37	Post-Resistance	BRAF	673	37	7	140453136	140453136	Missense_Mutation	SNP	A	T	81	195	c.1799T>A	c.(1798-1800)GTG>GAG	p.V600E
Pat_37	Post-Resistance	MGAM	8972	37	7	141738413	141738413	Missense_Mutation	SNP	G	A	17	30	c.2314G>A	c.(2314-2316)GAA>AAA	p.E772K
Pat_37	Post-Resistance	TMEM176A	55365	37	7	150501930	150501930	Missense_Mutation	SNP	G	A	41	130	c.682G>A	c.(682-684)GAA>AAA	p.E228K
Pat_37	Post-Resistance	ABP1	26	37	7	150554225	150554225	Missense_Mutation	SNP	C	T	54	92	c.667C>T	c.(667-669)CAT>TAT	p.H223Y
Pat_37	Post-Resistance	ASB10	136371	37	7	150883992	150883993	Missense_Mutation	DNP	CC	TT	40	73	c.360_361GG>AA	358-363)GCGGAC>GCAA	p.D121N
Pat_37	Post-Resistance	PRKAG2	51422	37	7	151372621	151372621	Missense_Mutation	SNP	C	T	4	195	c.569G>A	c.(568-570)CGC>CAC	p.R190H
Pat_37	Post-Resistance	CSMD1	64478	37	8	3087634	3087634	Missense_Mutation	SNP	C	T	66	112	c.4276G>A	c.(4276-4278)GGA>AGA	p.G1426R
Pat_37	Post-Resistance	PSD3	23362	37	8	18729272	18729272	Missense_Mutation	SNP	G	A	28	49	c.1102C>T	c.(1102-1104)CCT>TCT	p.P368S
Pat_37	Post-Resistance	RP1	6101	37	8	55539813	55539813	Missense_Mutation	SNP	C	T	50	104	c.3371C>T	c.(3370-3372)TCA>TTA	p.S1124L
Pat_37	Post-Resistance	LYN	4067	37	8	56912099	56912100	Missense_Mutation	DNP	CC	AT	44	149	.1327_1328CC>A	c.(1327-1329)CCC>ATC	p.P443I
Pat_37	Post-Resistance	STMN2	11075	37	8	80567254	80567254	Missense_Mutation	SNP	G	A	24	164	c.437G>A	c.(436-438)CGT>CAT	p.R146H
Pat_37	Post-Resistance	DCAF4L2	138009	37	8	88886004	88886004	Missense_Mutation	SNP	G	A	104	208	c.196C>T	c.(196-198)CCC>TCC	p.P66S
Pat_37	Post-Resistance	DPY19L4	286148	37	8	95800144	95800144	Missense_Mutation	SNP	G	A	4	148	c.1871G>A	c.(1870-1872)CGA>CAA	p.R624Q
Pat_37	Post-Resistance	UBR5	51366	37	8	103306251	103306252	Missense_Mutation	DNP	CC	TT	44	85	.4280_4281GG>A	c.(4279-4281)AGG>AAA	p.R1427K
Pat_37	Post-Resistance	KCNV1	27012	37	8	110984906	110984906	Missense_Mutation	SNP	G	A	30	77	c.572C>T	c.(571-573)ACT>ATT	p.T191I
Pat_37	Post-Resistance	KCNQ3	3786	37	8	133150166	133150166	Missense_Mutation	SNP	C	T	163	279	c.1666G>A	c.(1666-1668)GAC>AAC	p.D556N
Pat_37	Post-Resistance	OPLAH	26873	37	8	145112543	145112543	Missense_Mutation	SNP	A	C	3	36	c.1230T>G	c.(1228-1230)TTT>TTG	p.F410L
Pat_37	Post-Resistance	VPS28	51160	37	8	145650178	145650178	Missense_Mutation	SNP	G	A	4	232	c.325C>T	c.(325-327)CGG>TGG	p.R109W
Pat_37	Post-Resistance	RECQL4	9401	37	8	145741403	145741403	Missense_Mutation	SNP	C	T	3	79	c.1100G>A	c.(1099-1101)CGG>CAG	p.R367Q

Pat_37	Post-Resistance	GLIS3	169792	37	9	4118619	4118619	Missense_Mutation	SNP	G	A	91	201	c.394C>T	c.(394-396)CGG>TGG	p.R132W
Pat_37	Post-Resistance	CNTLN	54875	37	9	17309195	17309195	Missense_Mutation	SNP	C	T	36	85	c.1286C>T	c.(1285-1287)TCA>TTA	p.S429L
Pat_37	Post-Resistance	TAF1L	138474	37	9	32632451	32632451	Missense_Mutation	SNP	C	T	252	445	c.3127G>A	c.(3127-3129)GAA>AAA	p.E1043K
Pat_37	Post-Resistance	UBAP2	55833	37	9	33923897	33923897	Missense_Mutation	SNP	G	T	4	202	c.2692C>A	c.(2692-2694)CAG>AAG	p.Q898K
Pat_37	Post-Resistance	TLE4	7091	37	9	82333720	82333720	Missense_Mutation	SNP	C	T	175	171	c.1499C>T	c.(1498-1500)CCC>CTC	p.P500L
Pat_37	Post-Resistance	C9orf79	286234	37	9	90503459	90503459	Missense_Mutation	SNP	G	A	42	30	c.4057G>A	c.(4057-4059)GAG>AAG	p.E1353K
Pat_37	Post-Resistance	ASTN2	23245	37	9	119739065	119739065	Splice_Site	SNP	C	T	38	41	c.1592_splice	c.e8-1	p.G531_splice
Pat_37	Post-Resistance	SFRS17A	8227	37	X	1720089	1720089	Missense_Mutation	SNP	G	A	4	235	c.1690G>A	c.(1690-1692)GAG>AAG	p.E564K
Pat_37	Post-Resistance	MAGEB16	139604	37	X	35820428	35820428	Missense_Mutation	SNP	C	T	6	5	c.115C>T	c.(115-117)CTC>TTC	p.L39F
Pat_37	Post-Resistance	RPGR	6103	37	X	38180334	38180334	Missense_Mutation	SNP	G	A	29	18	c.256C>T	c.(256-258)CCT>TCT	p.P86S
Pat_37	Post-Resistance	OTUD6A	139562	37	X	69282378	69282378	Missense_Mutation	SNP	G	A	27	16	c.4G>A	c.(4-6)GAT>AAT	p.D2N
Pat_37	Post-Resistance	PHKA1	5255	37	X	71870317	71870317	Missense_Mutation	SNP	C	T	17	9	c.1247G>A	c.(1246-1248)GGA>GAA	p.G416E
Pat_37	Post-Resistance	NRK	203447	37	X	105153465	105153465	Missense_Mutation	SNP	C	T	30	23	c.1832C>T	c.(1831-1833)CCA>CTA	p.P611L
Pat_37	Post-Resistance	COL4A5	1287	37	X	107866038	107866038	Missense_Mutation	SNP	G	A	48	24	c.2900G>A	c.(2899-2901)GGG>GAG	p.G967E
Pat_37	Post-Resistance	RENBP	5973	37	X	153208465	153208465	Missense_Mutation	SNP	G	A	3	47	c.529C>T	c.(529-531)CGG>TGG	p.R177W
Pat_40	Pre-Treatment	DVL1	1855	37	1	1271749	1271749	Missense_Mutation	SNP	C	T	4	20	c.1786G>A	c.(1786-1788)GCC>ACC	p.A596T
Pat_40	Pre-Treatment	ERRFI1	54206	37	1	8073629	8073629	Missense_Mutation	SNP	C	T	104	178	c.1030G>A	c.(1030-1032)GGG>AGG	p.G344R
Pat_40	Pre-Treatment	DFFA	1676	37	1	10532476	10532476	Missense_Mutation	SNP	C	T	15	77	c.40G>A	c.(40-42)GAG>AAG	p.E14K
Pat_40	Pre-Treatment	HSPG2	3339	37	1	22200957	22200957	Missense_Mutation	SNP	G	A	3	17	c.3598C>T	c.(3598-3600)CGG>TGG	p.R1200W
Pat_40	Pre-Treatment	IL22RA1	58985	37	1	24454633	24454633	Missense_Mutation	SNP	G	T	4	36	c.668C>A	c.(667-669)CCA>CAA	p.P223Q
Pat_40	Pre-Treatment	C1orf130	400746	37	1	24932116	24932116	Missense_Mutation	SNP	G	A	11	40	c.187G>A	c.(187-189)GAA>AAA	p.E63K
Pat_40	Pre-Treatment	AHDC1	27245	37	1	27876118	27876118	Missense_Mutation	SNP	T	G	7	99	c.2509A>C	c.(2509-2511)ACC>CCC	p.T837P
Pat_40	Pre-Treatment	LSM10	84967	37	1	36859448	36859448	Nonsense_Mutation	SNP	C	A	5	113	c.283G>T	c.(283-285)GAG>TAG	p.E95*
Pat_40	Pre-Treatment	MACF1	23499	37	1	39913514	39913514	Nonsense_Mutation	SNP	C	T	17	90	c.15241C>T	c.(15241-15243)CAG>TAG	p.Q5081*
Pat_40	Pre-Treatment	KIAA0467	23334	37	1	43893365	43893365	Missense_Mutation	SNP	G	A	3	44	c.1066G>A	c.(1066-1068)GGC>AGC	p.G356S
Pat_40	Pre-Treatment	PTPRF	5792	37	1	44069513	44069513	Missense_Mutation	SNP	G	A	4	68	c.2690G>A	c.(2689-2691)CGG>CAG	p.R897Q
Pat_40	Pre-Treatment	PLK3	1263	37	1	45266313	45266313	Missense_Mutation	SNP	C	T	2	2	c.178C>T	c.(178-180)CGC>TGC	p.R60C
Pat_40	Pre-Treatment	MAST2	23139	37	1	46495803	46495803	Missense_Mutation	SNP	C	T	4	59	c.2446C>T	c.(2446-2448)CGC>TGC	p.R816C
Pat_40	Pre-Treatment	TM2D1	83941	37	1	62175095	62175095	Missense_Mutation	SNP	C	T	13	49	c.253G>A	c.(253-255)GCA>ACA	p.A85T
Pat_40	Pre-Treatment	IL23R	149233	37	1	67635270	67635270	Missense_Mutation	SNP	C	T	45	84	c.316C>T	c.(316-318)CCC>TCC	p.P106S
Pat_40	Pre-Treatment	LRRIQ3	127255	37	1	74540468	74540468	Missense_Mutation	SNP	A	T	7	36	c.874T>A	c.(874-876)TAT>AAT	p.Y292N
Pat_40	Pre-Treatment	LHX8	431707	37	1	75626530	75626530	Nonsense_Mutation	SNP	C	T	92	159	c.1021C>T	c.(1021-1023)CAG>TAG	p.Q341*
Pat_40	Pre-Treatment	MSH4	4438	37	1	76355016	76355016	Missense_Mutation	SNP	G	A	37	60	c.2188G>A	c.(2188-2190)GAA>AAA	p.E730K
Pat_40	Pre-Treatment	LPHN2	23266	37	1	82408790	82408790	Missense_Mutation	SNP	C	T	9	59	c.535C>T	c.(535-537)CGT>TGT	p.R179C
Pat_40	Pre-Treatment	LPPR4	9890	37	1	99771489	99771489	Missense_Mutation	SNP	G	A	4	50	c.1215G>A	c.(1213-1215)ATG>ATA	p.M405I
Pat_40	Pre-Treatment	HIAT1	64645	37	1	100534099	100534099	Missense_Mutation	SNP	C	T	66	96	c.776C>T	c.(775-777)CCG>CTG	p.P259L
Pat_40	Pre-Treatment	DPH5	51611	37	1	101458271	101458271	Missense_Mutation	SNP	G	A	5	112	c.556C>T	c.(556-558)CGG>TGG	p.R186W
Pat_40	Pre-Treatment	COL11A1	1301	37	1	103488381	103488381	Missense_Mutation	SNP	C	T	10	55	c.1162G>A	c.(1162-1164)GAA>AAA	p.E388K
Pat_40	Pre-Treatment	GSTM5	2949	37	1	110255773	110255773	Missense_Mutation	SNP	G	A	16	60	c.145G>A	c.(145-147)GAA>AAA	p.E49K
Pat_40	Pre-Treatment	AMPD1	270	37	1	115229401	115229401	Nonsense_Mutation	SNP	G	A	17	91	c.346C>T	c.(346-348)CAG>TAG	p.Q116*
Pat_40	Pre-Treatment	HAO2	51179	37	1	119925542	119925542	Missense_Mutation	SNP	C	T	10	55	c.136C>T	c.(136-138)CGC>TGC	p.R46C
Pat_40	Pre-Treatment	NBPF9	400818	37	1	144823878	144823878	Missense_Mutation	SNP	A	C	9	146	c.1919A>C	c.(1918-1920)TAT>TCT	p.Y640S
Pat_40	Pre-Treatment	ANKRD34A	284615	37	1	145474041	145474041	Missense_Mutation	SNP	C	T	42	223	c.713C>T	c.(712-714)CCC>CTC	p.P238L
Pat_40	Pre-Treatment	NBPF16	728936	37	1	148753313	148753313	Missense_Mutation	SNP	T	C	13	329	c.1330T>C	c.(1330-1332)TAT>CAT	p.Y444H
Pat_40	Pre-Treatment	MCL1	4170	37	1	150551756	150551756	Missense_Mutation	SNP	G	A	2	0	c.251C>T	c.(250-252)GCC>GTC	p.A84V
Pat_40	Pre-Treatment	TCHH	7062	37	1	152084702	152084702	Missense_Mutation	SNP	G	C	6	65	c.991C>G	c.(991-993)CAG>GAG	p.Q331E
Pat_40	Pre-Treatment	HRNR	388697	37	1	152192447	152192447	Missense_Mutation	SNP	C	T	24	172	c.1658G>A	c.(1657-1659)AGG>AAG	p.R553K

Pat_40	Pre-Treatment	S100A8	6279	37	1	153363002	153363002	Missense_Mutation	SNP	C	T	137	117	c.10G>A	c.(10-12)GAG>AAG	p.E4K
Pat_40	Pre-Treatment	NPR1	4881	37	1	153656215	153656215	Splice_Site	SNP	G	A	17	40	c.1400_splice	c.e7-1	p.D467_splice
Pat_40	Pre-Treatment	FMO3	2328	37	1	171083391	171083391	Missense_Mutation	SNP	C	T	7	70	c.1072C>T	c.(1072-1074)CCT>TCT	p.P358S
Pat_40	Pre-Treatment	TNR	7143	37	1	175363013	175363014	Missense_Mutation	DNP	CC	TT	34	109	.1258_1259GG>A	c.(1258-1260)GGG>AAG	p.G420K
Pat_40	Pre-Treatment	CEP350	9857	37	1	180053225	180053225	Missense_Mutation	SNP	C	T	10	24	c.6197C>T	c.(6196-6198)TCA>TTA	p.S2066L
Pat_40	Pre-Treatment	QSOX1	5768	37	1	180165636	180165636	Nonsense_Mutation	SNP	G	T	12	72	c.1708G>T	c.(1708-1710)GAG>TAG	p.E570*
Pat_40	Pre-Treatment	CACNA1E	777	37	1	181745324	181745324	Missense_Mutation	SNP	G	A	20	137	c.5227G>A	c.(5227-5229)GAG>AAG	p.E1743K
Pat_40	Pre-Treatment	CFHR1	3078	37	1	196801125	196801125	Missense_Mutation	SNP	G	A	27	55	c.989G>A	c.(988-990)AGA>AAA	p.R330K
Pat_40	Pre-Treatment	CFHR5	81494	37	1	196964859	196964859	Missense_Mutation	SNP	C	T	36	85	c.620C>T	c.(619-621)TCA>TTA	p.S207L
Pat_40	Pre-Treatment	CAMSAP1L1	23271	37	1	200817686	200817686	Missense_Mutation	SNP	G	A	22	71	c.1822G>A	c.(1822-1824)GGT>AGT	p.G608S
Pat_40	Pre-Treatment	TIMM17A	10440	37	1	201934630	201934630	Missense_Mutation	SNP	G	A	5	78	c.389G>A	c.(388-390)GGT>GAT	p.G130D
Pat_40	Pre-Treatment	PPP1R12B	4660	37	1	202531971	202531971	Missense_Mutation	SNP	C	A	45	207	c.2573C>A	c.(2572-2574)GCC>GAC	p.A858D
Pat_40	Pre-Treatment	ADIPOR1	51094	37	1	202910727	202910727	Missense_Mutation	SNP	C	T	23	97	c.1102G>A	c.(1102-1104)GGC>AGC	p.G368S
Pat_40	Pre-Treatment	LAMB3	3914	37	1	209805978	209805978	Missense_Mutation	SNP	G	A	16	17	c.772C>T	c.(772-774)CGC>TGC	p.R258C
Pat_40	Pre-Treatment	HLX	3142	37	1	221055685	221055685	Missense_Mutation	SNP	G	A	4	38	c.952G>A	c.(952-954)GCA>ACA	p.A318T
Pat_40	Pre-Treatment	CAPN2	824	37	1	223959916	223959916	Missense_Mutation	SNP	G	A	18	91	c.2054G>A	c.(2053-2055)GGA>GAA	p.G685E
Pat_40	Pre-Treatment	LEFTY2	7044	37	1	226125308	226125308	Missense_Mutation	SNP	C	T	3	20	c.934G>A	c.(934-936)GGG>AGG	p.G312R
Pat_40	Pre-Treatment	CDC42BPA	8476	37	1	227335101	227335101	Missense_Mutation	SNP	C	T	45	160	c.853G>A	c.(853-855)GAA>AAA	p.E285K
Pat_40	Pre-Treatment	ZNF678	339500	37	1	227842427	227842427	Missense_Mutation	SNP	G	A	11	235	c.476G>A	c.(475-477)GGC>GAC	p.G159D
Pat_40	Pre-Treatment	ZNF678	339500	37	1	227842460	227842460	Missense_Mutation	SNP	A	G	12	212	c.509A>G	c.(508-510)AAC>AGC	p.N170S
Pat_40	Pre-Treatment	SDCCAG8	10806	37	1	243493952	243493952	Missense_Mutation	SNP	G	A	15	119	c.1179G>A	c.(1177-1179)ATG>ATA	p.M393I
Pat_40	Pre-Treatment	AKT3	10000	37	1	243736269	243736270	Missense_Mutation	DNP	CC	TT	13	168	c.777_778GG>AA	(775-780)TTGGAC>TTAA	p.D260N
Pat_40	Pre-Treatment	OR2M5	127059	37	1	248308997	248308997	Missense_Mutation	SNP	C	T	55	508	c.548C>T	c.(547-549)TCC>TTC	p.S183F
Pat_40	Pre-Treatment	OR2M7	391196	37	1	248487323	248487323	Missense_Mutation	SNP	G	A	87	82	c.548C>T	c.(547-549)TCC>TTC	p.S183F
Pat_40	Pre-Treatment	OR2T5	401993	37	1	248651963	248651963	Missense_Mutation	SNP	C	T	32	220	c.74C>T	c.(73-75)TCC>TTC	p.S25F
Pat_40	Pre-Treatment	MRC1	4360	37	10	18122660	18122660	Missense_Mutation	SNP	C	T	4	73	c.670C>T	c.(670-672)CCG>TCG	p.P224S
Pat_40	Pre-Treatment	BMI1	648	37	10	22618172	22618172	Nonsense_Mutation	SNP	C	T	9	25	c.682C>T	c.(682-684)CGA>TGA	p.R228*
Pat_40	Pre-Treatment	ABI1	10006	37	10	27037558	27037558	Nonsense_Mutation	SNP	G	A	4	109	c.1468C>T	c.(1468-1470)CGA>TGA	p.R490*
Pat_40	Pre-Treatment	EPC1	80314	37	10	32576138	32576138	Missense_Mutation	SNP	G	A	53	72	c.1040C>T	c.(1039-1041)TCG>TTG	p.S347L
Pat_40	Pre-Treatment	RBP3	5949	37	10	48390358	48390358	Missense_Mutation	SNP	C	T	4	25	c.520G>A	c.(520-522)GGA>AGA	p.G174R
Pat_40	Pre-Treatment	A1CF	29974	37	10	52573720	52573720	Missense_Mutation	SNP	C	T	42	57	c.1244G>A	c.(1243-1245)GGA>GAA	p.G415E
Pat_40	Pre-Treatment	PCDH15	65217	37	10	55581646	55581646	Missense_Mutation	SNP	T	G	21	119	c.5840A>C	c.(5839-5841)CAA>CCA	p.Q1947P
Pat_40	Pre-Treatment	ANK3	288	37	10	61834299	61834299	Missense_Mutation	SNP	C	T	10	44	c.6340G>A	c.(6340-6342)GAC>AAC	p.D2114N
Pat_40	Pre-Treatment	CDH23	64072	37	10	73539073	73539073	Missense_Mutation	SNP	G	A	4	60	c.5237G>A	c.(5236-5238)CGG>CAG	p.R1746Q
Pat_40	Pre-Treatment	ZMIZ1	57178	37	10	81070900	81070900	Missense_Mutation	SNP	G	A	6	83	c.3055G>A	c.(3055-3057)GGA>AGA	p.G1019R
Pat_40	Pre-Treatment	SFTPA2	729238	37	10	81318720	81318720	Missense_Mutation	SNP	T	G	36	51	c.214A>C	c.(214-216)AAT>CAT	p.N72H
Pat_40	Pre-Treatment	OPN4	94233	37	10	88417853	88417853	Missense_Mutation	SNP	A	G	31	23	c.355A>G	c.(355-357)ATG>GTG	p.M119V
Pat_40	Pre-Treatment	GLUD1	2746	37	10	88836389	88836389	Missense_Mutation	SNP	C	T	6	116	c.470G>A	c.(469-471)AGT>AAT	p.S157N
Pat_40	Pre-Treatment	ACTA2	59	37	10	90699450	90699450	Missense_Mutation	SNP	G	A	3	54	c.622C>T	c.(622-624)CGT>TGT	p.R208C
Pat_40	Pre-Treatment	MYOF	26509	37	10	95159169	95159169	Missense_Mutation	SNP	C	T	9	29	c.1201G>A	c.(1201-1203)GTT>ATT	p.V401I
Pat_40	Pre-Treatment	CYP2C19	1557	37	10	96540336	96540336	Missense_Mutation	SNP	G	A	42	114	c.562G>A	c.(562-564)GAT>AAT	p.D188N
Pat_40	Pre-Treatment	HPSE2	60495	37	10	100249833	100249833	Missense_Mutation	SNP	A	G	17	94	c.1441T>C	c.(1441-1443)TAT>CAT	p.Y481H
Pat_40	Pre-Treatment	ACSL5	51703	37	10	114173027	114173027	Missense_Mutation	SNP	C	T	19	89	c.1045C>T	c.(1045-1047)CCC>TCC	p.P349S
Pat_40	Pre-Treatment	FGFR2	2263	37	10	123245021	123245021	Missense_Mutation	SNP	C	T	15	48	c.2083G>A	c.(2083-2085)GAG>AAG	p.E695K
Pat_40	Pre-Treatment	DMBT1	1755	37	10	124392709	124392709	Missense_Mutation	SNP	G	A	46	61	c.6013G>A	c.(6013-6015)GAT>AAT	p.D2005N
Pat_40	Pre-Treatment	DOCK1	1793	37	10	129172323	129172323	Missense_Mutation	SNP	C	T	5	16	c.3457C>T	c.(3457-3459)CTT>TTT	p.L1153F
Pat_40	Pre-Treatment	CYP2E1	1571	37	10	135351354	135351354	Missense_Mutation	SNP	G	A	16	79	c.1255G>A	c.(1255-1257)GGA>AGA	p.G419R

Pat_40	Pre-Treatment	OR51G1	79324	37	11	4945065	4945065	Nonsense_Mutation	SNP	G	A	6	17	c.505C>T	c.(505-507)CAA>TAA	p.Q169*
Pat_40	Pre-Treatment	OR52A5	390054	37	11	5153391	5153391	Missense_Mutation	SNP	G	A	12	91	c.482C>T	c.(481-483)TCC>TTC	p.S161F
Pat_40	Pre-Treatment	OR51B4	79339	37	11	5322536	5322536	Missense_Mutation	SNP	G	A	7	22	c.641C>T	c.(640-642)TCT>TTT	p.S214F
Pat_40	Pre-Treatment	OR51B2	79345	37	11	5345505	5345505	Missense_Mutation	SNP	G	A	7	8	c.23C>T	c.(22-24)GCC>GTC	p.A8V
Pat_40	Pre-Treatment	UBQLN3	50613	37	11	5530502	5530502	Missense_Mutation	SNP	C	T	5	40	c.287G>A	c.(286-288)CGT>CAT	p.R96H
Pat_40	Pre-Treatment	OR56B1	387748	37	11	5758588	5758588	Missense_Mutation	SNP	C	T	151	281	c.842C>T	c.(841-843)CCA>CTA	p.P281L
Pat_40	Pre-Treatment	PPFIBP2	8495	37	11	7672168	7672168	Missense_Mutation	SNP	G	A	4	103	c.2219G>A	c.(2218-2220)CGA>CAA	p.R740Q
Pat_40	Pre-Treatment	SWAP70	23075	37	11	9749608	9749608	Missense_Mutation	SNP	G	A	15	42	c.651G>A	c.(649-651)ATG>ATA	p.M217I
Pat_40	Pre-Treatment	PLEKHA7	144100	37	11	16838766	16838767	Missense_Mutation	DNP	CC	TT	22	47	.1446_1447GG>A	44-1449)GGGGGC>GGA	p.G483S
Pat_40	Pre-Treatment	ABCC8	6833	37	11	17419984	17419984	Missense_Mutation	SNP	C	T	13	17	c.3655G>A	c.(3655-3657)GAG>AAG	p.E1219K
Pat_40	Pre-Treatment	RCN1	5954	37	11	32124946	32124946	Missense_Mutation	SNP	C	T	11	74	c.808C>T	c.(808-810)CGC>TGC	p.R270C
Pat_40	Pre-Treatment	PHF21A	51317	37	11	45959791	45959791	Missense_Mutation	SNP	G	A	4	113	c.1522C>T	c.(1522-1524)CGT>TGT	p.R508C
Pat_40	Pre-Treatment	C1QTNF4	114900	37	11	47612076	47612076	Missense_Mutation	SNP	C	T	2	2	c.287G>A	c.(286-288)CGA>CAA	p.R96Q
Pat_40	Pre-Treatment	PTPRJ	5795	37	11	48134314	48134314	Missense_Mutation	SNP	C	T	64	91	c.131C>T	c.(130-132)CCT>CTT	p.P44L
Pat_40	Pre-Treatment	TRIM48	79097	37	11	55035844	55035844	Missense_Mutation	SNP	T	C	6	142	c.574T>C	c.(574-576)TAC>CAC	p.Y192H
Pat_40	Pre-Treatment	OR4C11	219429	37	11	55371068	55371068	Missense_Mutation	SNP	G	A	18	89	c.782C>T	c.(781-783)ACC>ATC	p.T261I
Pat_40	Pre-Treatment	OR4C6	219432	37	11	55433089	55433090	Missense_Mutation	DNP	GG	AA	9	62	c.447_448GG>AA	45-450)GGGGGA>GGAA	p.G150R
Pat_40	Pre-Treatment	OR5D13	390142	37	11	55541362	55541362	Missense_Mutation	SNP	C	T	45	144	c.449C>T	c.(448-450)TCC>TTC	p.S150F
Pat_40	Pre-Treatment	OR5I1	10798	37	11	55703012	55703012	Missense_Mutation	SNP	G	A	29	43	c.865C>T	c.(865-867)CCG>TCG	p.P289S
Pat_40	Pre-Treatment	OR5M3	219482	37	11	56237733	56237733	Missense_Mutation	SNP	C	T	10	63	c.241G>A	c.(241-243)GAA>AAA	p.E81K
Pat_40	Pre-Treatment	FAM111B	374393	37	11	58892997	58892997	Missense_Mutation	SNP	C	T	70	270	c.1427C>T	c.(1426-1428)ACT>ATT	p.T476I
Pat_40	Pre-Treatment	GANAB	23193	37	11	62397931	62397931	Missense_Mutation	SNP	C	T	4	79	c.1433G>A	c.(1432-1434)CGA>CAA	p.R478Q
Pat_40	Pre-Treatment	RTN3	10313	37	11	63486769	63486769	Nonsense_Mutation	SNP	T	A	32	42	c.795T>A	c.(793-795)TAT>TAA	p.Y265*
Pat_40	Pre-Treatment	CCDC88B	283234	37	11	64118984	64118984	Missense_Mutation	SNP	G	A	2	2	c.2995G>A	c.(2995-2997)GGG>AGG	p.G999R
Pat_40	Pre-Treatment	CDC42BPG	55561	37	11	64602851	64602851	Missense_Mutation	SNP	C	T	36	216	c.1921G>A	c.(1921-1923)GAA>AAA	p.E641K
Pat_40	Pre-Treatment	LRP5	4041	37	11	68171002	68171002	Missense_Mutation	SNP	C	T	20	57	c.1636C>T	c.(1636-1638)CCG>TCG	p.P546S
Pat_40	Pre-Treatment	PHOX2A	401	37	11	71952310	71952310	Missense_Mutation	SNP	G	A	3	28	c.241C>T	c.(241-243)CCA>TCA	p.P81S
Pat_40	Pre-Treatment	USP35	57558	37	11	77921528	77921528	Missense_Mutation	SNP	C	T	19	78	c.2627C>T	c.(2626-2628)GCT>GTT	p.A876V
Pat_40	Pre-Treatment	PCF11	51585	37	11	82878325	82878325	Missense_Mutation	SNP	C	A	4	34	c.1976C>A	c.(1975-1977)GCA>GAA	p.A659E
Pat_40	Pre-Treatment	TYR	7299	37	11	88924454	88924454	Missense_Mutation	SNP	G	A	47	57	c.904G>A	c.(904-906)GGA>AGA	p.G302R
Pat_40	Pre-Treatment	DYNC2H1	79659	37	11	103306744	103306744	Missense_Mutation	SNP	G	A	4	58	c.12440G>A	c.(12439-12441)CGT>CAT	p.R4147H
Pat_40	Pre-Treatment	USP28	57646	37	11	113704150	113704150	Nonsense_Mutation	SNP	C	A	66	54	c.751G>T	c.(751-753)GAA>TAA	p.E251*
Pat_40	Pre-Treatment	PAFAH1B2	5049	37	11	117038252	117038252	Missense_Mutation	SNP	A	G	3	44	c.527A>G	c.(526-528)GAC>GGC	p.D176G
Pat_40	Pre-Treatment	B4GALNT3	283358	37	12	662410	662410	Missense_Mutation	SNP	G	A	19	101	c.1321G>A	c.(1321-1323)GAG>AAG	p.E441K
Pat_40	Pre-Treatment	CACNA1C	775	37	12	2797838	2797838	Missense_Mutation	SNP	G	A	5	32	c.6259G>A	c.(6259-6261)GGC>AGC	p.G2087S
Pat_40	Pre-Treatment	CD9	928	37	12	6344459	6344459	Missense_Mutation	SNP	C	T	17	121	c.413C>T	c.(412-414)CCC>CTC	p.P138L
Pat_40	Pre-Treatment	PLEKHG6	55200	37	12	6421516	6421517	Missense_Mutation	DNP	GG	AA	13	69	c.124_125GG>AA	c.(124-126)GGA>AAA	p.G42K
Pat_40	Pre-Treatment	TNFRSF1A	7132	37	12	6442254	6442254	Missense_Mutation	SNP	C	T	5	95	c.532G>A	c.(532-534)GAG>AAG	p.E178K
Pat_40	Pre-Treatment	VAMP1	6843	37	12	6575488	6575488	Missense_Mutation	SNP	C	T	10	45	c.32G>A	c.(31-33)GGG>GAG	p.G11E
Pat_40	Pre-Treatment	PRB3	5544	37	12	11420548	11420548	Missense_Mutation	SNP	C	T	23	139	c.635G>A	c.(634-636)GGA>GAA	p.G212E
Pat_40	Pre-Treatment	SLCO1C1	53919	37	12	20864329	20864329	Nonsense_Mutation	SNP	T	A	30	184	c.414T>A	c.(412-414)TAT>TAA	p.Y138*
Pat_40	Pre-Treatment	ABCC9	10060	37	12	22015914	22015914	Missense_Mutation	SNP	G	A	7	58	c.2312C>T	c.(2311-2313)ACT>ATT	p.T771I
Pat_40	Pre-Treatment	ADAMTS20	80070	37	12	43846171	43846171	Missense_Mutation	SNP	C	T	27	67	c.1985G>A	c.(1984-1986)GGA>GAA	p.G662E
Pat_40	Pre-Treatment	ARID2	196528	37	12	46246081	46246081	Missense_Mutation	SNP	C	T	9	48	c.4175C>T	c.(4174-4176)CCA>CTA	p.P1392L
Pat_40	Pre-Treatment	TROAP	10024	37	12	49724313	49724313	Missense_Mutation	SNP	G	T	6	46	c.1685G>T	c.(1684-1686)AGT>ATT	p.S562I
Pat_40	Pre-Treatment	TROAP	10024	37	12	49724403	49724403	Missense_Mutation	SNP	A	G	11	61	c.1775A>G	c.(1774-1776)TAC>TGC	p.Y592C
Pat_40	Pre-Treatment	KCNH3	23416	37	12	49937265	49937265	Missense_Mutation	SNP	G	A	4	91	c.787G>A	c.(787-789)GTC>ATC	p.V263I

Pat_40	Pre-Treatment	KRT75	9119	37	12	52827025	52827025	Missense_Mutation	SNP	C	A	3	33	c.510G>T	c.(508-510)TTG>TTT	p.L170F
Pat_40	Pre-Treatment	KRT6C	286887	37	12	52863452	52863452	Splice_Site	SNP	A	T	38	164	c.1424_splice	c.e7+1	p.R475_splice
Pat_40	Pre-Treatment	CSAD	51380	37	12	53565186	53565186	Missense_Mutation	SNP	C	T	4	70	c.491G>A	c.(490-492)CGC>CAC	p.R164H
Pat_40	Pre-Treatment	ITGB7	3695	37	12	53588070	53588070	Missense_Mutation	SNP	G	A	12	81	c.1220C>T	c.(1219-1221)TCT>TTT	p.S407F
Pat_40	Pre-Treatment	HOXC10	3226	37	12	54379286	54379286	Missense_Mutation	SNP	C	A	7	59	c.243C>A	c.(241-243)GAC>GAA	p.D81E
Pat_40	Pre-Treatment	ITGA5	3678	37	12	54802681	54802681	Missense_Mutation	SNP	G	A	33	90	c.641C>T	c.(640-642)ACC>ATC	p.T214I
Pat_40	Pre-Treatment	OR10A7	121364	37	12	55615268	55615268	Missense_Mutation	SNP	C	T	9	54	c.460C>T	c.(460-462)CCT>TCT	p.P154S
Pat_40	Pre-Treatment	OR6C2	341416	37	12	55846809	55846809	Missense_Mutation	SNP	G	A	36	84	c.812G>A	c.(811-813)GGA>GAA	p.G271E
Pat_40	Pre-Treatment	BAZ2A	11176	37	12	57003663	57003663	Missense_Mutation	SNP	C	T	3	34	c.1955G>A	c.(1954-1956)CGG>CAG	p.R652Q
Pat_40	Pre-Treatment	ATP5B	506	37	12	57037341	57037341	Missense_Mutation	SNP	G	A	21	113	c.638C>T	c.(637-639)ACT>ATT	p.T213I
Pat_40	Pre-Treatment	C12orf26	84190	37	12	82832521	82832521	Missense_Mutation	SNP	C	T	32	193	c.1429C>T	c.(1429-1431)CGT>TGT	p.R477C
Pat_40	Pre-Treatment	GALNT4	8693	37	12	89917357	89917358	Missense_Mutation	DNP	GG	AA	119	364	c.969_970CC>TT	.(967-972)TACCTT>TATTT	p.L324F
Pat_40	Pre-Treatment	STAB2	55576	37	12	104089415	104089415	Missense_Mutation	SNP	G	A	33	114	c.3463G>A	c.(3463-3465)GGC>AGC	p.G1155S
Pat_40	Pre-Treatment	APPL2	55198	37	12	105610863	105610863	Missense_Mutation	SNP	G	A	22	51	c.269C>T	c.(268-270)TCC>TTC	p.S90F
Pat_40	Pre-Treatment	ALKBH2	121642	37	12	109527981	109527981	Missense_Mutation	SNP	C	G	15	93	c.312G>C	c.(310-312)AAG>AAC	p.K104N
Pat_40	Pre-Treatment	ACACB	32	37	12	109577469	109577469	Missense_Mutation	SNP	C	T	5	71	c.259C>T	c.(259-261)CGG>TGG	p.R87W
Pat_40	Pre-Treatment	CUX2	23316	37	12	111758227	111758227	Missense_Mutation	SNP	C	T	3	55	c.2414C>T	c.(2413-2415)CCC>CTC	p.P805L
Pat_40	Pre-Treatment	C12orf51	283450	37	12	112657240	112657240	Missense_Mutation	SNP	G	A	5	176	c.5758C>T	c.(5758-5760)CGG>TGG	p.R1920W
Pat_40	Pre-Treatment	RPH3A	22895	37	12	113307833	113307833	Missense_Mutation	SNP	G	A	10	21	c.785G>A	c.(784-786)CGG>CAG	p.R262Q
Pat_40	Pre-Treatment	MED13L	23389	37	12	116435017	116435017	Missense_Mutation	SNP	C	T	12	82	c.2588G>A	c.(2587-2589)AGG>AAG	p.R863K
Pat_40	Pre-Treatment	KSR2	283455	37	12	118016990	118016990	Nonsense_Mutation	SNP	C	T	9	46	c.1172G>A	c.(1171-1173)TGG>TAG	p.W391*
Pat_40	Pre-Treatment	RSRC2	65117	37	12	123003404	123003404	Missense_Mutation	SNP	C	T	92	600	c.380G>A	c.(379-381)AGA>AAA	p.R127K
Pat_40	Pre-Treatment	DNAH10	196385	37	12	124288369	124288369	Missense_Mutation	SNP	C	T	8	76	c.2422C>T	c.(2422-2424)CCA>TCA	p.P808S
Pat_40	Pre-Treatment	FZD10	11211	37	12	130648985	130648985	Missense_Mutation	SNP	G	A	4	25	c.1498G>A	c.(1498-1500)GCC>ACC	p.A500T
Pat_40	Pre-Treatment	RIMBP2	23504	37	12	130919401	130919401	Missense_Mutation	SNP	C	T	15	32	c.2080G>A	c.(2080-2082)GAG>AAG	p.E694K
Pat_40	Pre-Treatment	ULK1	8408	37	12	132400462	132400462	Missense_Mutation	SNP	C	T	5	69	c.1636C>T	c.(1636-1638)CGC>TGC	p.R546C
Pat_40	Pre-Treatment	SACS	26278	37	13	23904499	23904499	Missense_Mutation	SNP	C	T	19	71	c.13516G>A	c.(13516-13518)GCT>ACT	p.A4506T
Pat_40	Pre-Treatment	FREM2	341640	37	13	39420787	39420787	Missense_Mutation	SNP	A	G	22	73	c.6097A>G	c.(6097-6099)ACG>GCG	p.T2033A
Pat_40	Pre-Treatment	ELF1	1997	37	13	41515089	41515089	Missense_Mutation	SNP	A	C	24	53	c.1224T>G	c.(1222-1224)GAT>GAG	p.D408E
Pat_40	Pre-Treatment	LOC220429	220429	37	13	50466086	50466086	Missense_Mutation	SNP	T	A	5	20	c.1360T>A	c.(1360-1362)TAC>AAC	p.Y454N
Pat_40	Pre-Treatment	OLFM4	10562	37	13	53603032	53603032	Missense_Mutation	SNP	G	A	27	85	c.61G>A	c.(61-63)GAT>AAT	p.D21N
Pat_40	Pre-Treatment	DCT	1638	37	13	95131305	95131305	Missense_Mutation	SNP	T	C	33	54	c.205A>G	c.(205-207)AGG>GGG	p.R69G
Pat_40	Pre-Treatment	DZIP1	22873	37	13	96241429	96241429	Missense_Mutation	SNP	G	A	25	58	c.2006C>T	c.(2005-2007)CCC>CTC	p.P669L
Pat_40	Pre-Treatment	SLC10A2	6555	37	13	103705031	103705031	Missense_Mutation	SNP	G	A	14	76	c.524C>T	c.(523-525)CCT>CTT	p.P175L
Pat_40	Pre-Treatment	EFNB2	1948	37	13	107145708	107145708	Missense_Mutation	SNP	A	G	14	117	c.682T>C	c.(682-684)TTT>CTT	p.F228L
Pat_40	Pre-Treatment	POTEG	404785	37	14	19553531	19553531	Missense_Mutation	SNP	G	A	10	296	c.115G>A	c.(115-117)GGC>AGC	p.G39S
Pat_40	Pre-Treatment	OR4L1	122742	37	14	20528889	20528889	Missense_Mutation	SNP	C	T	48	111	c.686C>T	c.(685-687)TCA>TTA	p.S229L
Pat_40	Pre-Treatment	TEP1	7011	37	14	20857894	20857894	Missense_Mutation	SNP	G	T	4	52	c.2340C>A	c.(2338-2340)GAC>GAA	p.D780E
Pat_40	Pre-Treatment	METTL3	56339	37	14	21969242	21969242	Missense_Mutation	SNP	G	A	10	85	c.929C>T	c.(928-930)TCT>TTT	p.S310F
Pat_40	Pre-Treatment	MYH6	4624	37	14	23855328	23855328	Nonsense_Mutation	SNP	G	A	4	57	c.4972C>T	c.(4972-4974)CAG>TAG	p.Q1658*
Pat_40	Pre-Treatment	MYH6	4624	37	14	23863057	23863057	Nonsense_Mutation	SNP	G	A	14	66	c.2746C>T	c.(2746-2748)CAG>TAG	p.Q916*
Pat_40	Pre-Treatment	MYH7	4625	37	14	23888763	23888763	Missense_Mutation	SNP	C	T	4	111	c.3782G>A	c.(3781-3783)AGC>AAC	p.S1261N
Pat_40	Pre-Treatment	FITM1	161247	37	14	24600818	24600818	Nonsense_Mutation	SNP	C	T	3	29	c.46C>T	c.(46-48)CGA>TGA	p.R16*
Pat_40	Pre-Treatment	RALGAPA1	253959	37	14	36207819	36207819	Missense_Mutation	SNP	G	A	35	95	c.1487C>T	c.(1486-1488)TCC>TTC	p.S496F
Pat_40	Pre-Treatment	PYGL	5836	37	14	51382622	51382622	Missense_Mutation	SNP	C	T	3	49	c.1160G>A	c.(1159-1161)CGC>CAC	p.R387H
Pat_40	Pre-Treatment	OTX2	5015	37	14	57272108	57272108	Missense_Mutation	SNP	C	T	6	51	c.67G>A	c.(67-69)GAC>AAC	p.D23N
Pat_40	Pre-Treatment	SPTB	6710	37	14	65246540	65246540	Missense_Mutation	SNP	C	T	4	116	c.4376G>A	c.(4375-4377)CGG>CAG	p.R1459Q

Pat_40	Pre-Treatment	SIPA1L1	26037	37	14	72128160	72128160	Missense_Mutation	SNP	C	T	30	101	c.2231C>T	c.(2230-2232)CCG>CTG	p.P744L
Pat_40	Pre-Treatment	SIPA1L1	26037	37	14	72152192	72152192	Missense_Mutation	SNP	G	A	3	28	c.3218G>A	c.(3217-3219)AGC>AAC	p.S1073N
Pat_40	Pre-Treatment	RBM25	58517	37	14	73570138	73570138	Missense_Mutation	SNP	G	A	10	25	c.1106G>A	c.(1105-1107)CGG>CAG	p.R369Q
Pat_40	Pre-Treatment	C14orf115	55237	37	14	74825074	74825074	Missense_Mutation	SNP	C	T	30	121	c.1588C>T	c.(1588-1590)CGC>TGC	p.R530C
Pat_40	Pre-Treatment	KCNK13	56659	37	14	90651187	90651187	Missense_Mutation	SNP	A	C	10	47	c.1067A>C	c.(1066-1068)AAC>ACC	p.N356T
Pat_40	Pre-Treatment	CCDC88C	440193	37	14	91780280	91780281	Missense_Mutation	DNP	CC	TT	8	34	.1879_1880GG>A	c.(1879-1881)GGG>AAG	p.G627K
Pat_40	Pre-Treatment	UBR7	55148	37	14	93686736	93686736	Nonsense_Mutation	SNP	C	T	10	221	c.1102C>T	c.(1102-1104)CAG>TAG	p.Q368*
Pat_40	Pre-Treatment	PPP2R5C	5527	37	14	102323122	102323122	Nonsense_Mutation	SNP	G	A	26	165	c.194G>A	c.(193-195)TGG>TAG	p.W65*
Pat_40	Pre-Treatment	OR4M2	390538	37	15	22368697	22368697	Missense_Mutation	SNP	G	A	107	216	c.122G>A	c.(121-123)GGA>GAA	p.G41E
Pat_40	Pre-Treatment	TJP1	7082	37	15	30008923	30008923	Missense_Mutation	SNP	C	T	15	66	c.4094G>A	c.(4093-4095)AGA>AAA	p.R1365K
Pat_40	Pre-Treatment	THBS1	7057	37	15	39886363	39886363	Missense_Mutation	SNP	C	T	4	52	c.3331C>T	c.(3331-3333)CGT>TGT	p.R1111C
Pat_40	Pre-Treatment	NDUFAF1	51103	37	15	41687083	41687083	Missense_Mutation	SNP	C	A	12	129	c.733G>T	c.(733-735)GGG>TGG	p.G245W
Pat_40	Pre-Treatment	MGA	23269	37	15	42035184	42035184	Missense_Mutation	SNP	C	T	6	38	c.5026C>T	c.(5026-5028)CCT>TCT	p.P1676S
Pat_40	Pre-Treatment	TGM7	116179	37	15	43584182	43584182	Missense_Mutation	SNP	C	T	9	36	c.553G>A	c.(553-555)GGG>AGG	p.G185R
Pat_40	Pre-Treatment	TP53BP1	7158	37	15	43748444	43748444	Missense_Mutation	SNP	C	T	4	60	c.2347G>A	c.(2347-2349)GAT>AAT	p.D783N
Pat_40	Pre-Treatment	SLC28A2	9153	37	15	45554220	45554220	Missense_Mutation	SNP	C	T	40	155	c.178C>T	c.(178-180)CGG>TGG	p.R60W
Pat_40	Pre-Treatment	PLDN	26258	37	15	45897629	45897629	Missense_Mutation	SNP	G	T	4	65	c.316G>T	c.(316-318)GCT>TCT	p.A106S
Pat_40	Pre-Treatment	NEDD4	4734	37	15	56155202	56155202	Missense_Mutation	SNP	G	A	20	72	c.1840C>T	c.(1840-1842)CCA>TCA	p.P614S
Pat_40	Pre-Treatment	ALDH1A2	8854	37	15	58284979	58284979	Missense_Mutation	SNP	C	T	52	94	c.722G>A	c.(721-723)GGA>GAA	p.G241E
Pat_40	Pre-Treatment	CCDC33	80125	37	15	74588131	74588131	Missense_Mutation	SNP	G	A	21	53	c.1132G>A	c.(1132-1134)GCT>ACT	p.A378T
Pat_40	Pre-Treatment	RPP25	54913	37	15	75248380	75248380	Missense_Mutation	SNP	G	A	3	15	c.545C>T	c.(544-546)TCC>TTC	p.S182F
Pat_40	Pre-Treatment	CSPG4	1464	37	15	75977987	75977987	Missense_Mutation	SNP	G	A	3	20	c.3845C>T	c.(3844-3846)CCG>CTG	p.P1282L
Pat_40	Pre-Treatment	ADAMTSL3	57188	37	15	84539574	84539574	Nonsense_Mutation	SNP	C	T	35	77	c.823C>T	c.(823-825)CAA>TAA	p.Q275*
Pat_40	Pre-Treatment	ZNF592	9640	37	15	85327111	85327111	Missense_Mutation	SNP	G	A	3	23	c.1205G>A	c.(1204-1206)AGT>AAT	p.S402N
Pat_40	Pre-Treatment	AGBL1	123624	37	15	86687074	86687074	Missense_Mutation	SNP	G	A	23	48	c.122G>A	c.(121-123)AGA>AAA	p.R41K
Pat_40	Pre-Treatment	WDR93	56964	37	15	90245132	90245132	Missense_Mutation	SNP	C	T	7	43	c.155C>T	c.(154-156)TCC>TTC	p.S52F
Pat_40	Pre-Treatment	IQGAP1	8826	37	15	91026618	91026618	Missense_Mutation	SNP	G	A	4	72	c.3581G>A	c.(3580-3582)CGA>CAA	p.R1194Q
Pat_40	Pre-Treatment	FAM173A	65990	37	16	772426	772426	Nonsense_Mutation	SNP	C	T	2	1	c.577C>T	c.(577-579)CGA>TGA	p.R193*
Pat_40	Pre-Treatment	C16orf42	115939	37	16	1400907	1400907	Missense_Mutation	SNP	G	A	4	52	c.427C>T	c.(427-429)CGC>TGC	p.R143C
Pat_40	Pre-Treatment	TELO2	9894	37	16	1549330	1549330	Missense_Mutation	SNP	T	A	6	22	c.929T>A	c.(928-930)CTC>CAC	p.L310H
Pat_40	Pre-Treatment	C16orf72	29035	37	16	9186816	9186816	Missense_Mutation	SNP	C	T	3	27	c.265C>T	c.(265-267)CCC>TCC	p.P89S
Pat_40	Pre-Treatment	ZC3H7A	29066	37	16	11850101	11850101	Missense_Mutation	SNP	C	T	31	184	c.2554G>A	c.(2554-2556)GAA>AAA	p.E852K
Pat_40	Pre-Treatment	C16orf88	400506	37	16	19725511	19725511	Missense_Mutation	SNP	C	T	39	146	c.847G>A	c.(847-849)GAG>AAG	p.E283K
Pat_40	Pre-Treatment	ACSM5	54988	37	16	20430616	20430616	Missense_Mutation	SNP	C	T	17	70	c.482C>T	c.(481-483)TCC>TTC	p.S161F
Pat_40	Pre-Treatment	DNAH3	55567	37	16	20994125	20994125	Nonsense_Mutation	SNP	G	A	35	65	c.7777C>T	c.(7777-7779)CAG>TAG	p.Q2593*
Pat_40	Pre-Treatment	HS3ST4	9951	37	16	26147552	26147552	Missense_Mutation	SNP	G	A	7	19	c.1354G>A	c.(1354-1356)GAA>AAA	p.E452K
Pat_40	Pre-Treatment	IL27	246778	37	16	28515273	28515273	Missense_Mutation	SNP	G	A	4	31	c.130C>T	c.(130-132)CGG>TGG	p.R44W
Pat_40	Pre-Treatment	MVP	9961	37	16	29848068	29848068	Missense_Mutation	SNP	G	A	3	43	c.698G>A	c.(697-699)CGG>CAG	p.R233Q
Pat_40	Pre-Treatment	HIRIP3	8479	37	16	30004563	30004563	Missense_Mutation	SNP	G	A	3	42	c.1636C>T	c.(1636-1638)CGT>TGT	p.R546C
Pat_40	Pre-Treatment	TGFB1I1	7041	37	16	31488207	31488207	Missense_Mutation	SNP	C	T	10	12	c.995C>T	c.(994-996)CCC>CTC	p.P332L
Pat_40	Pre-Treatment	ZNF267	10308	37	16	31927606	31927606	Missense_Mutation	SNP	G	A	7	133	c.2036G>A	c.(2035-2037)CGG>CAG	p.R679Q
Pat_40	Pre-Treatment	SALL1	6299	37	16	51172808	51172808	Missense_Mutation	SNP	G	A	17	60	c.3325C>T	c.(3325-3327)CCG>TCG	p.P1109S
Pat_40	Pre-Treatment	E2F4	1874	37	16	67228322	67228322	Missense_Mutation	SNP	G	A	3	37	c.473G>A	c.(472-474)CGG>CAG	p.R158Q
Pat_40	Pre-Treatment	RANBP10	57610	37	16	67762379	67762379	Missense_Mutation	SNP	G	A	11	74	c.1388C>T	c.(1387-1389)CCC>CTC	p.P463L
Pat_40	Pre-Treatment	NFATC3	4775	37	16	68260297	68260297	Nonsense_Mutation	SNP	C	T	8	41	c.3151C>T	c.(3151-3153)CAA>TAA	p.Q1051*
Pat_40	Pre-Treatment	CALB2	794	37	16	71419498	71419498	Missense_Mutation	SNP	G	T	4	52	c.646G>T	c.(646-648)GAC>TAC	p.D216Y
Pat_40	Pre-Treatment	ZFHX3	463	37	16	72992241	72992241	Missense_Mutation	SNP	C	T	4	30	c.1804G>A	c.(1804-1806)GCA>ACA	p.A602T

Pat_40	Pre-Treatment	CHST5	23563	37	16	75563252	75563252	Missense_Mutation	SNP	G	A	18	57	c.1031C>T	c.(1030-1032)TCG>TTG	p.S344L
Pat_40	Pre-Treatment	MLYCD	23417	37	16	83948687	83948687	Missense_Mutation	SNP	G	A	57	190	c.1075G>A	c.(1075-1077)GAA>AAA	p.E359K
Pat_40	Pre-Treatment	C17orf97	400566	37	17	263277	263277	Missense_Mutation	SNP	T	A	4	34	c.673T>A	c.(673-675)TTC>ATC	p.F225I
Pat_40	Pre-Treatment	C1QBP	708	37	17	5341507	5341507	Missense_Mutation	SNP	C	T	29	126	c.319G>A	c.(319-321)GGA>AGA	p.G107R
Pat_40	Pre-Treatment	PITPNM3	83394	37	17	6380394	6380394	Missense_Mutation	SNP	G	A	4	30	c.1040C>T	c.(1039-1041)ACC>ATC	p.T347I
Pat_40	Pre-Treatment	PITPNM3	83394	37	17	6381947	6381947	Missense_Mutation	SNP	C	T	3	20	c.697G>A	c.(697-699)GTC>ATC	p.V233I
Pat_40	Pre-Treatment	PLSCR3	57048	37	17	7296563	7296563	Missense_Mutation	SNP	G	A	2	2	c.407C>T	c.(406-408)CCG>CTG	p.P136L
Pat_40	Pre-Treatment	GUCY2D	3000	37	17	7910748	7910748	Missense_Mutation	SNP	C	T	7	112	c.1468C>T	c.(1468-1470)CGG>TGG	p.R490W
Pat_40	Pre-Treatment	ARHGEF15	22899	37	17	8222653	8222653	Missense_Mutation	SNP	G	A	34	170	c.2210G>A	c.(2209-2211)GGA>GAA	p.G737E
Pat_40	Pre-Treatment	MYOCD	93649	37	17	12626312	12626312	Missense_Mutation	SNP	A	T	35	143	c.402A>T	c.(400-402)AAA>AAT	p.K134N
Pat_40	Pre-Treatment	LGALS9	3965	37	17	25975908	25975908	Missense_Mutation	SNP	G	A	45	273	c.968G>A	c.(967-969)GGT>GAT	p.G323D
Pat_40	Pre-Treatment	SARM1	23098	37	17	26686410	26686410	Missense_Mutation	SNP	C	T	8	72	c.358C>T	c.(358-360)CGC>TGC	p.R120C
Pat_40	Pre-Treatment	SLFN11	91607	37	17	33687340	33687340	Missense_Mutation	SNP	C	T	15	101	c.1120G>A	c.(1120-1122)GGG>AGG	p.G374R
Pat_40	Pre-Treatment	GAS2L2	246176	37	17	34079495	34079495	Missense_Mutation	SNP	C	T	62	130	c.375G>A	c.(373-375)ATG>ATA	p.M125I
Pat_40	Pre-Treatment	PPP1R1B	84152	37	17	37790219	37790219	Missense_Mutation	SNP	G	A	12	77	c.325G>A	c.(325-327)GGG>AGG	p.G109R
Pat_40	Pre-Treatment	DHX40	79665	37	17	57644149	57644149	Missense_Mutation	SNP	G	A	7	37	c.274G>A	c.(274-276)GAA>AAA	p.E92K
Pat_40	Pre-Treatment	CYB561	1534	37	17	61512547	61512547	Missense_Mutation	SNP	G	A	4	101	c.463C>T	c.(463-465)CGC>TGC	p.R155C
Pat_40	Pre-Treatment	PSMD12	5718	37	17	65341882	65341882	Missense_Mutation	SNP	A	G	4	76	c.887T>C	c.(886-888)TTA>TCA	p.L296S
Pat_40	Pre-Treatment	SLC39A11	201266	37	17	70943992	70943992	Missense_Mutation	SNP	G	A	5	78	c.329C>T	c.(328-330)ACG>ATG	p.T110M
Pat_40	Pre-Treatment	QRICH2	84074	37	17	74289004	74289004	Missense_Mutation	SNP	G	A	5	128	c.1306C>T	c.(1306-1308)CGG>TGG	p.R436W
Pat_40	Pre-Treatment	TNRC6C	57690	37	17	76083091	76083091	Missense_Mutation	SNP	C	T	31	68	c.3719C>T	c.(3718-3720)TCG>TTG	p.S1240L
Pat_40	Pre-Treatment	AZI1	22994	37	17	79173231	79173231	Missense_Mutation	SNP	G	A	3	19	c.1142C>T	c.(1141-1143)TCC>TTC	p.S381F
Pat_40	Pre-Treatment	TMEM105	284186	37	17	79287596	79287596	Missense_Mutation	SNP	C	T	28	39	c.245G>A	c.(244-246)CGA>CAA	p.R82Q
Pat_40	Pre-Treatment	C17orf70	80233	37	17	79514375	79514375	Missense_Mutation	SNP	C	T	3	34	c.1733G>A	c.(1732-1734)CGG>CAG	p.R578Q
Pat_40	Pre-Treatment	DUS1L	64118	37	17	80016246	80016246	Missense_Mutation	SNP	C	T	5	56	c.1253G>A	c.(1252-1254)CGA>CAA	p.R418Q
Pat_40	Pre-Treatment	EPB41L3	23136	37	18	5406843	5406843	Missense_Mutation	SNP	G	A	6	92	c.2282C>T	c.(2281-2283)ACC>ATC	p.T761I
Pat_40	Pre-Treatment	L3MBTL4	91133	37	18	6244575	6244575	Missense_Mutation	SNP	G	A	52	150	c.232C>T	c.(232-234)CCA>TCA	p.P78S
Pat_40	Pre-Treatment	LAMA1	284217	37	18	7013833	7013833	Missense_Mutation	SNP	G	A	4	7	c.3344C>T	c.(3343-3345)ACC>ATC	p.T1115I
Pat_40	Pre-Treatment	MIB1	57534	37	18	19429266	19429266	Missense_Mutation	SNP	G	A	58	146	c.2503G>A	c.(2503-2505)GGA>AGA	p.G835R
Pat_40	Pre-Treatment	DSG4	147409	37	18	28968918	28968918	Missense_Mutation	SNP	G	A	65	133	c.454G>A	c.(454-456)GAT>AAT	p.D152N
Pat_40	Pre-Treatment	SMAD7	4092	37	18	46447797	46447797	Missense_Mutation	SNP	C	T	4	75	c.1226G>A	c.(1225-1227)CGC>CAC	p.R409H
Pat_40	Pre-Treatment	SMAD4	4089	37	18	48584806	48584806	Missense_Mutation	SNP	C	A	8	164	c.884C>A	c.(883-885)CCG>CAG	p.P295Q
Pat_40	Pre-Treatment	C18orf26	284254	37	18	52265254	52265254	Missense_Mutation	SNP	C	T	24	149	c.511C>T	c.(511-513)CCT>TCT	p.P171S
Pat_40	Pre-Treatment	CDH20	28316	37	18	59174723	59174723	Missense_Mutation	SNP	G	A	28	38	c.947G>A	c.(946-948)GGA>GAA	p.G316E
Pat_40	Pre-Treatment	CD226	10666	37	18	67614158	67614158	Missense_Mutation	SNP	G	A	10	46	c.194C>T	c.(193-195)CCT>CTT	p.P65L
Pat_40	Pre-Treatment	NETO1	81832	37	18	70423284	70423284	Missense_Mutation	SNP	C	T	23	102	c.967G>A	c.(967-969)GAA>AAA	p.E323K
Pat_40	Pre-Treatment	PRSSL1	400668	37	19	685829	685829	Missense_Mutation	SNP	C	T	2	0	c.739G>A	c.(739-741)GTG>ATG	p.V247M
Pat_40	Pre-Treatment	ABCA7	10347	37	19	1061880	1061880	Missense_Mutation	SNP	G	A	3	38	c.5563G>A	c.(5563-5565)GGC>AGC	p.G1855S
Pat_40	Pre-Treatment	S1PR4	8698	37	19	3179545	3179545	Missense_Mutation	SNP	C	T	3	19	c.755C>T	c.(754-756)ACG>ATG	p.T252M
Pat_40	Pre-Treatment	FZR1	51343	37	19	3530838	3530838	Missense_Mutation	SNP	G	A	3	21	c.703G>A	c.(703-705)GTG>ATG	p.V235M
Pat_40	Pre-Treatment	CHAF1A	10036	37	19	4428744	4428745	Missense_Mutation	DNP	CC	TT	23	34	.1461_1462CC>T	1459-1464)TTCCAT>TTTT	p.H488Y
Pat_40	Pre-Treatment	FUT3	2525	37	19	5844156	5844156	Missense_Mutation	SNP	C	T	11	58	c.695G>A	c.(694-696)GGG>GAG	p.G232E
Pat_40	Pre-Treatment	CD70	970	37	19	6586315	6586315	Missense_Mutation	SNP	G	A	4	41	c.298C>T	c.(298-300)CGT>TGT	p.R100C
Pat_40	Pre-Treatment	CD209	30835	37	19	7810698	7810698	Missense_Mutation	SNP	A	G	12	164	c.454T>C	c.(454-456)TGG>CGG	p.W152R
Pat_40	Pre-Treatment	TIMM44	10469	37	19	7993024	7993024	Nonsense_Mutation	SNP	G	A	3	25	c.1066C>T	c.(1066-1068)CAG>TAG	p.Q356*
Pat_40	Pre-Treatment	RAB11B	9230	37	19	8464792	8464792	Missense_Mutation	SNP	C	T	4	59	c.86C>T	c.(85-87)TCG>TTG	p.S29L
Pat_40	Pre-Treatment	MUC16	94025	37	19	9046043	9046043	Missense_Mutation	SNP	G	A	69	114	c.35588C>T	c.(35587-35589)CCA>CTA	p.P11863L

Pat_40	Pre-Treatment	MUC16	94025	37	19	9049653	9049653	Missense_Mutation	SNP	C	T	8	68	c.31978G>A	c.(31978-31980)GGG>AGC	p.G10660R
Pat_40	Pre-Treatment	MUC16	94025	37	19	9056776	9056776	Missense_Mutation	SNP	G	A	11	25	c.30670C>T	c.(30670-30672)CCA>TCA	p.P10224S
Pat_40	Pre-Treatment	MUC16	94025	37	19	9060955	9060955	Missense_Mutation	SNP	G	A	19	90	c.26491C>T	c.(26491-26493)CCT>TCT	p.P8831S
Pat_40	Pre-Treatment	MUC16	94025	37	19	9082516	9082516	Missense_Mutation	SNP	A	T	94	185	c.9299T>A	c.(9298-9300)ATT>AAT	p.I3100N
Pat_40	Pre-Treatment	MUC16	94025	37	19	9087347	9087347	Missense_Mutation	SNP	G	A	33	165	c.4468C>T	c.(4468-4470)CCA>TCA	p.P1490S
Pat_40	Pre-Treatment	ZNF700	90592	37	19	12060645	12060645	Missense_Mutation	SNP	T	A	16	315	c.1806T>A	c.(1804-1806)AGT>AGA	p.S602R
Pat_40	Pre-Treatment	ZNF700	90592	37	19	12060647	12060647	Missense_Mutation	SNP	G	C	10	317	c.1808G>C	c.(1807-1809)TGT>TCT	p.C603S
Pat_40	Pre-Treatment	ZNF443	10224	37	19	12542283	12542283	Missense_Mutation	SNP	A	G	19	262	c.703T>C	c.(703-705)TCT>CCT	p.S235P
Pat_40	Pre-Treatment	OR7C2	26658	37	19	15053205	15053205	Missense_Mutation	SNP	G	A	8	48	c.905G>A	c.(904-906)AGA>AAA	p.R302K
Pat_40	Pre-Treatment	OR10H1	26539	37	19	15918436	15918436	Missense_Mutation	SNP	G	A	25	33	c.412C>T	c.(412-414)CCG>TCG	p.P138S
Pat_40	Pre-Treatment	CPAMD8	27151	37	19	17049247	17049247	Missense_Mutation	SNP	C	T	15	25	c.2944G>A	c.(2944-2946)GTC>ATC	p.V982I
Pat_40	Pre-Treatment	SLC5A5	6528	37	19	17992969	17992969	Missense_Mutation	SNP	G	A	4	100	c.1183G>A	c.(1183-1185)GGA>AGA	p.G395R
Pat_40	Pre-Treatment	ZNF14	7561	37	19	19822928	19822928	Missense_Mutation	SNP	C	T	18	102	c.1162G>A	c.(1162-1164)GAG>AAG	p.E388K
Pat_40	Pre-Treatment	ZNF93	81931	37	19	20044933	20044933	Missense_Mutation	SNP	T	G	7	200	c.1169T>G	c.(1168-1170)GTT>GGT	p.V390G
Pat_40	Pre-Treatment	ZNF737	100129842	37	19	20728170	20728170	Missense_Mutation	SNP	G	C	8	171	c.839C>G	c.(838-840)ACT>AGT	p.T280S
Pat_40	Pre-Treatment	ZNF737	100129842	37	19	20728189	20728189	Missense_Mutation	SNP	T	C	6	149	c.820A>G	c.(820-822)ACA>GCA	p.T274A
Pat_40	Pre-Treatment	ZNF85	7639	37	19	21132437	21132437	Missense_Mutation	SNP	G	A	5	100	c.1117G>A	c.(1117-1119)GAA>AAA	p.E373K
Pat_40	Pre-Treatment	ZNF714	148206	37	19	21300738	21300738	Missense_Mutation	SNP	T	C	10	203	c.1271T>C	c.(1270-1272)CTC>CCC	p.L424P
Pat_40	Pre-Treatment	ZNF100	163227	37	19	21909650	21909650	Missense_Mutation	SNP	C	G	10	287	c.1464G>C	c.(1462-1464)GAG>GAC	p.E488D
Pat_40	Pre-Treatment	ZNF208	7757	37	19	22154826	22154826	Missense_Mutation	SNP	C	T	21	151	c.2626G>A	c.(2626-2628)GAA>AAA	p.E876K
Pat_40	Pre-Treatment	ZNF208	7757	37	19	22157163	22157163	Missense_Mutation	SNP	C	T	41	110	c.673G>A	c.(673-675)GGA>AGA	p.G225R
Pat_40	Pre-Treatment	ZNF99	7652	37	19	22941372	22941372	Missense_Mutation	SNP	G	A	16	76	c.1066C>T	c.(1066-1068)CAT>TAT	p.H356Y
Pat_40	Pre-Treatment	ZNF91	7644	37	19	23544783	23544783	Missense_Mutation	SNP	C	T	12	268	c.998G>A	c.(997-999)CGT>CAT	p.R333H
Pat_40	Pre-Treatment	ZNF675	171392	37	19	23836431	23836431	Missense_Mutation	SNP	C	T	7	211	c.1304G>A	c.(1303-1305)CGA>CAA	p.R435Q
Pat_40	Pre-Treatment	ZNF681	148213	37	19	23926839	23926839	Missense_Mutation	SNP	A	G	12	212	c.1513T>C	c.(1513-1515)TCC>CCC	p.S505P
Pat_40	Pre-Treatment	ZNF536	9745	37	19	31039065	31039065	Missense_Mutation	SNP	G	A	8	50	c.2539G>A	c.(2539-2541)GGA>AGA	p.G847R
Pat_40	Pre-Treatment	RHPN2	85415	37	19	33470912	33470912	Missense_Mutation	SNP	G	A	8	56	c.2051C>T	c.(2050-2052)TCT>TTT	p.S684F
Pat_40	Pre-Treatment	SLC7A10	56301	37	19	33702192	33702192	Missense_Mutation	SNP	G	A	7	43	c.955C>T	c.(955-957)CCT>TCT	p.P319S
Pat_40	Pre-Treatment	PEPD	5184	37	19	34003584	34003584	Missense_Mutation	SNP	G	A	3	15	c.116C>T	c.(115-117)GCT>GTT	p.A39V
Pat_40	Pre-Treatment	FFAR2	2867	37	19	35940779	35940779	Missense_Mutation	SNP	G	A	3	38	c.163G>A	c.(163-165)GAC>AAC	p.D55N
Pat_40	Pre-Treatment	ZNF420	147923	37	19	37619580	37619580	Missense_Mutation	SNP	G	A	16	98	c.1687G>A	c.(1687-1689)GAA>AAA	p.E563K
Pat_40	Pre-Treatment	ZNF527	84503	37	19	37871191	37871191	Missense_Mutation	SNP	C	T	8	49	c.173C>T	c.(172-174)TCT>TTT	p.S58F
Pat_40	Pre-Treatment	AKT2	208	37	19	40739784	40739784	Missense_Mutation	SNP	C	T	4	66	c.1441G>A	c.(1441-1443)GAG>AAG	p.E481K
Pat_40	Pre-Treatment	PRX	57716	37	19	40900057	40900057	Missense_Mutation	SNP	G	A	10	75	c.4202C>T	c.(4201-4203)TCC>TTC	p.S1401F
Pat_40	Pre-Treatment	ZNF574	64763	37	19	42583483	42583483	Missense_Mutation	SNP	C	T	12	52	c.725C>T	c.(724-726)CCC>CTC	p.P242L
Pat_40	Pre-Treatment	PAFAH1B3	5050	37	19	42801403	42801403	Missense_Mutation	SNP	C	T	5	59	c.523G>A	c.(523-525)GAC>AAC	p.D175N
Pat_40	Pre-Treatment	PRR19	284338	37	19	42814720	42814720	Missense_Mutation	SNP	C	T	29	139	c.899C>T	c.(898-900)CCC>CTC	p.P300L
Pat_40	Pre-Treatment	BCL3	602	37	19	45260400	45260400	Missense_Mutation	SNP	C	T	2	1	c.646C>T	c.(646-648)CGC>TGC	p.R216C
Pat_40	Pre-Treatment	DMPK	1760	37	19	46283155	46283155	Missense_Mutation	SNP	G	A	5	24	c.163C>T	c.(163-165)CGG>TGG	p.R55W
Pat_40	Pre-Treatment	PNMAL2	57469	37	19	46997818	46997818	Missense_Mutation	SNP	G	A	8	33	c.905C>T	c.(904-906)CCG>CTG	p.P302L
Pat_40	Pre-Treatment	BCAT2	587	37	19	49302959	49302959	Missense_Mutation	SNP	C	T	3	8	c.668G>A	c.(667-669)GGC>GAC	p.G223D
Pat_40	Pre-Treatment	KLK1	3816	37	19	51326967	51326967	Missense_Mutation	SNP	C	T	14	50	c.38G>A	c.(37-39)GGG>GAG	p.G13E
Pat_40	Pre-Treatment	CD33	945	37	19	51729242	51729242	Missense_Mutation	SNP	C	T	5	73	c.602C>T	c.(601-603)CCA>CTA	p.P201L
Pat_40	Pre-Treatment	FPR1	2357	37	19	52249241	52249241	Missense_Mutation	SNP	G	A	51	298	c.1007C>T	c.(1006-1008)ACC>ATC	p.T336I
Pat_40	Pre-Treatment	ZNF350	59348	37	19	52468403	52468403	Missense_Mutation	SNP	C	T	13	74	c.1303G>A	c.(1303-1305)GAA>AAA	p.E435K
Pat_40	Pre-Treatment	ZNF480	147657	37	19	52825082	52825082	Missense_Mutation	SNP	A	C	17	85	c.579A>C	c.(577-579)GAA>GAC	p.E193D
Pat_40	Pre-Treatment	ZNF701	55762	37	19	53086622	53086622	Missense_Mutation	SNP	C	G	4	83	c.1310C>G	c.(1309-1311)CCT>CGT	p.P437R

Pat_40	Pre-Treatment	ZNF611	81856	37	19	53208494	53208494	Missense_Mutation	SNP	C	T	15	513	c.1814G>A	c.(1813-1815)CGC>CAC	p.R605H
Pat_40	Pre-Treatment	ZNF28	7576	37	19	53302941	53302941	Nonstop_Mutation	SNP	T	G	25	261	c.2157A>C	c.(2155-2157)TGA>TGC	p.*719C
Pat_40	Pre-Treatment	NLRP2	55655	37	19	55497572	55497572	Missense_Mutation	SNP	G	A	20	34	c.2255G>A	c.(2254-2256)CGA>CAA	p.R752Q
Pat_40	Pre-Treatment	NLRP2	55655	37	19	55502033	55502033	Missense_Mutation	SNP	A	C	18	64	c.2701A>C	c.(2701-2703)ACC>CCC	p.T901P
Pat_40	Pre-Treatment	NAT14	57106	37	19	55997836	55997836	Missense_Mutation	SNP	T	C	2	0	c.134T>C	c.(133-135)CTG>CCG	p.L45P
Pat_40	Pre-Treatment	NLRP11	204801	37	19	56321318	56321318	Missense_Mutation	SNP	C	T	7	30	c.658G>A	c.(658-660)GAT>AAT	p.D220N
Pat_40	Pre-Treatment	NLRP5	126206	37	19	56539203	56539203	Missense_Mutation	SNP	C	T	5	18	c.1604C>T	c.(1603-1605)GCT>GTT	p.A535V
Pat_40	Pre-Treatment	GALP	85569	37	19	56696603	56696603	Missense_Mutation	SNP	G	A	16	71	c.315G>A	c.(313-315)ATG>ATA	p.M105I
Pat_40	Pre-Treatment	ZNF835	90485	37	19	57175768	57175768	Missense_Mutation	SNP	G	A	3	12	c.865C>T	c.(865-867)CGC>TGC	p.R289C
Pat_40	Pre-Treatment	ZIM3	114026	37	19	57646333	57646333	Missense_Mutation	SNP	C	T	19	127	c.1372G>A	c.(1372-1374)GAC>AAC	p.D458N
Pat_40	Pre-Treatment	DUXA	503835	37	19	57666725	57666725	Nonsense_Mutation	SNP	G	A	8	23	c.454C>T	c.(454-456)CGA>TGA	p.R152*
Pat_40	Pre-Treatment	ZNF776	284309	37	19	58265885	58265885	Missense_Mutation	SNP	G	A	5	117	c.1387G>A	c.(1387-1389)GGA>AGA	p.G463R
Pat_40	Pre-Treatment	TRIM28	10155	37	19	59060116	59060116	Missense_Mutation	SNP	G	A	3	33	c.1333G>A	c.(1333-1335)GTG>ATG	p.V445M
Pat_40	Pre-Treatment	MYT1L	23040	37	2	1926835	1926835	Missense_Mutation	SNP	C	T	20	91	c.706G>A	c.(706-708)GAT>AAT	p.D236N
Pat_40	Pre-Treatment	KCNF1	3754	37	2	11053364	11053364	Missense_Mutation	SNP	C	T	4	26	c.812C>T	c.(811-813)ACG>ATG	p.T271M
Pat_40	Pre-Treatment	NT5C1B	93034	37	2	18758129	18758129	Missense_Mutation	SNP	C	T	21	101	c.1234G>A	c.(1234-1236)GGA>AGA	p.G412R
Pat_40	Pre-Treatment	APOB	338	37	2	21229243	21229243	Missense_Mutation	SNP	A	C	17	67	c.10497T>G	c.(10495-10497)GAT>GAG	p.D3499E
Pat_40	Pre-Treatment	APOB	338	37	2	21231815	21231815	Missense_Mutation	SNP	G	A	22	148	c.7925C>T	c.(7924-7926)CCA>CTA	p.P2642L
Pat_40	Pre-Treatment	EMILIN1	11117	37	2	27306645	27306645	Missense_Mutation	SNP	C	T	4	54	c.2206C>T	c.(2206-2208)CGG>TGG	p.R736W
Pat_40	Pre-Treatment	FOSL2	2355	37	2	28635035	28635035	Missense_Mutation	SNP	C	T	5	27	c.701C>T	c.(700-702)TCG>TTG	p.S234L
Pat_40	Pre-Treatment	C2orf56	55471	37	2	37473259	37473259	Missense_Mutation	SNP	C	T	26	128	c.857C>T	c.(856-858)TCT>TTT	p.S286F
Pat_40	Pre-Treatment	C2orf56	55471	37	2	37473261	37473261	Nonsense_Mutation	SNP	C	T	26	124	c.859C>T	c.(859-861)CAA>TAA	p.Q287*
Pat_40	Pre-Treatment	SPTBN1	6711	37	2	54876239	54876239	Missense_Mutation	SNP	G	A	5	122	c.5114G>A	c.(5113-5115)CGG>CAG	p.R1705Q
Pat_40	Pre-Treatment	ANTXR1	84168	37	2	69304577	69304577	Missense_Mutation	SNP	C	T	45	244	c.599C>T	c.(598-600)CCC>CTC	p.P200L
Pat_40	Pre-Treatment	MPHOSPH10	10199	37	2	71360620	71360620	Missense_Mutation	SNP	G	A	12	55	c.682G>A	c.(682-684)GAT>AAT	p.D228N
Pat_40	Pre-Treatment	DYSF	8291	37	2	71901417	71901417	Missense_Mutation	SNP	G	A	25	48	c.5758G>A	c.(5758-5760)GAT>AAT	p.D1920N
Pat_40	Pre-Treatment	WDR54	84058	37	2	74652245	74652245	Missense_Mutation	SNP	G	A	3	33	c.679G>A	c.(679-681)GCA>ACA	p.A227T
Pat_40	Pre-Treatment	C2orf68	388969	37	2	85839056	85839056	Missense_Mutation	SNP	G	A	3	45	c.52C>T	c.(52-54)CGG>TGG	p.R18W
Pat_40	Pre-Treatment	TMEM127	55654	37	2	96919611	96919611	Missense_Mutation	SNP	C	T	3	23	c.652G>A	c.(652-654)GAG>AAG	p.E218K
Pat_40	Pre-Treatment	CIAO1	9391	37	2	96936947	96936947	Missense_Mutation	SNP	C	T	12	87	c.878C>T	c.(877-879)TCC>TTC	p.S293F
Pat_40	Pre-Treatment	ANAPC1	64682	37	2	112583383	112583383	Missense_Mutation	SNP	G	A	13	75	c.2675C>T	c.(2674-2676)TCC>TTC	p.S892F
Pat_40	Pre-Treatment	C2orf76	130355	37	2	120069246	120069246	Missense_Mutation	SNP	C	T	12	36	c.256G>A	c.(256-258)GAA>AAA	p.E86K
Pat_40	Pre-Treatment	GLI2	2736	37	2	121708942	121708942	Missense_Mutation	SNP	G	A	22	36	c.378G>A	c.(376-378)ATG>ATA	p.M126I
Pat_40	Pre-Treatment	LIMS2	55679	37	2	128412421	128412421	Missense_Mutation	SNP	G	A	13	69	c.221C>T	c.(220-222)CCG>CTG	p.P74L
Pat_40	Pre-Treatment	NCKAP5	344148	37	2	133541812	133541812	Missense_Mutation	SNP	C	T	21	75	c.2572G>A	c.(2572-2574)GAA>AAA	p.E858K
Pat_40	Pre-Treatment	LCT	3938	37	2	136575471	136575471	Missense_Mutation	SNP	G	A	20	116	c.1147C>T	c.(1147-1149)CCT>TCT	p.P383S
Pat_40	Pre-Treatment	THSD7B	80731	37	2	138434125	138434125	Missense_Mutation	SNP	C	T	5	30	c.4684C>T	c.(4684-4686)CCC>TCC	p.P1562S
Pat_40	Pre-Treatment	LRP1B	53353	37	2	140995735	140995735	Missense_Mutation	SNP	T	C	36	138	c.13546A>G	c.(13546-13548)ATA>GTA	p.I4516V
Pat_40	Pre-Treatment	PABPC1P2	728773	37	2	147345742	147345742	Missense_Mutation	SNP	G	A	3	21	c.202G>A	c.(202-204)GCT>ACT	p.A68T
Pat_40	Pre-Treatment	GALNT13	114805	37	2	155157995	155157995	Missense_Mutation	SNP	C	T	48	214	c.1049C>T	c.(1048-1050)CCA>CTA	p.P350L
Pat_40	Pre-Treatment	KCNJ3	3760	37	2	155711754	155711754	Missense_Mutation	SNP	G	A	7	24	c.1435G>A	c.(1435-1437)GGA>AGA	p.G479R
Pat_40	Pre-Treatment	GPD2	2820	37	2	157369987	157369987	Missense_Mutation	SNP	G	A	3	54	c.640G>A	c.(640-642)GGA>AGA	p.G214R
Pat_40	Pre-Treatment	IFIH1	64135	37	2	163130442	163130442	Missense_Mutation	SNP	C	T	18	32	c.2317G>A	c.(2317-2319)GAA>AAA	p.E773K
Pat_40	Pre-Treatment	SCN1A	6323	37	2	166892572	166892572	Missense_Mutation	SNP	C	T	37	203	c.3382G>A	c.(3382-3384)GAA>AAA	p.E1128K
Pat_40	Pre-Treatment	XIRP2	129446	37	2	168100354	168100354	Missense_Mutation	SNP	G	A	15	90	c.2452G>A	c.(2452-2454)GAG>AAG	p.E818K
Pat_40	Pre-Treatment	B3GALT1	8708	37	2	168726108	168726108	Missense_Mutation	SNP	C	T	14	22	c.559C>T	c.(559-561)CTT>TTT	p.L187F
Pat_40	Pre-Treatment	SPC25	57405	37	2	169745932	169745932	Missense_Mutation	SNP	C	T	24	83	c.98G>A	c.(97-99)AGA>AAA	p.R33K

Pat_40	Pre-Treatment	LRP2	4036	37	2	170070368	170070368	Missense_Mutation	SNP	T	A	8	49	c.5839A>T	c.(5839-5841)AAC>TAC	p.N1947Y
Pat_40	Pre-Treatment	SLC25A12	8604	37	2	172712353	172712353	Missense_Mutation	SNP	C	T	58	374	c.316G>A	c.(316-318)GTG>ATG	p.V106M
Pat_40	Pre-Treatment	TTN	7273	37	2	179452825	179452825	Missense_Mutation	SNP	C	T	21	99	c.55605G>A	c.(55603-55605)ATG>ATA	p.M18535I
Pat_40	Pre-Treatment	TTN	7273	37	2	179454489	179454489	Missense_Mutation	SNP	C	T	43	218	c.54259G>A	c.(54259-54261)GAA>AAA	p.E18087K
Pat_40	Pre-Treatment	TTN	7273	37	2	179457199	179457199	Missense_Mutation	SNP	G	A	108	226	c.51829C>T	c.(51829-51831)CGT>TGT	p.R17277C
Pat_40	Pre-Treatment	TTN	7273	37	2	179464431	179464431	Missense_Mutation	SNP	G	A	15	108	c.48493C>T	c.(48493-48495)CTC>TTC	p.L16165F
Pat_40	Pre-Treatment	TTN	7273	37	2	179592468	179592468	Missense_Mutation	SNP	C	T	113	179	c.16105G>A	c.(16105-16107)GAA>AAA	p.E5369K
Pat_40	Pre-Treatment	TTN	7273	37	2	179592569	179592569	Missense_Mutation	SNP	T	C	7	24	c.16004A>G	c.(16003-16005)AAA>AGA	p.K5335R
Pat_40	Pre-Treatment	ZNF804A	91752	37	2	185798364	185798364	Missense_Mutation	SNP	G	A	17	82	c.290G>A	c.(289-291)CGA>CAA	p.R97Q
Pat_40	Pre-Treatment	CALCRL	10203	37	2	188245239	188245239	Nonsense_Mutation	SNP	C	T	128	244	c.363G>A	c.(361-363)TGG>TGA	p.W121*
Pat_40	Pre-Treatment	DNAH7	56171	37	2	196722260	196722260	Missense_Mutation	SNP	A	C	17	74	c.8255T>G	c.(8254-8256)CTT>CGT	p.L2752R
Pat_40	Pre-Treatment	DNAH7	56171	37	2	196729430	196729430	Nonsense_Mutation	SNP	G	A	20	82	c.6949C>T	c.(6949-6951)CGA>TGA	p.R2317*
Pat_40	Pre-Treatment	DNAH7	56171	37	2	196746544	196746544	Missense_Mutation	SNP	C	T	27	163	c.5936G>A	c.(5935-5937)GGA>GAA	p.G1979E
Pat_40	Pre-Treatment	HECW2	57520	37	2	197185066	197185066	Missense_Mutation	SNP	C	T	3	16	c.982G>A	c.(982-984)GAA>AAA	p.E328K
Pat_40	Pre-Treatment	BMPR2	659	37	2	203417586	203417586	Missense_Mutation	SNP	A	G	70	80	c.1561A>G	c.(1561-1563)ATG>GTG	p.M521V
Pat_40	Pre-Treatment	ABI2	10152	37	2	204292046	204292046	Missense_Mutation	SNP	G	A	3	54	c.1513G>A	c.(1513-1515)GTT>ATT	p.V505I
Pat_40	Pre-Treatment	EEF1B2	1933	37	2	207025358	207025358	Missense_Mutation	SNP	A	G	8	214	c.127A>G	c.(127-129)AGC>GGC	p.S43G
Pat_40	Pre-Treatment	ERBB4	2066	37	2	212587120	212587120	Missense_Mutation	SNP	G	A	13	66	c.881C>T	c.(880-882)CCA>CTA	p.P294L
Pat_40	Pre-Treatment	RQCD1	9125	37	2	219449406	219449406	Missense_Mutation	SNP	C	T	128	233	c.392C>T	c.(391-393)CCC>CTC	p.P131L
Pat_40	Pre-Treatment	ZNF142	7701	37	2	219521014	219521014	Missense_Mutation	SNP	G	A	4	59	c.139C>T	c.(139-141)CGG>TGG	p.R47W
Pat_40	Pre-Treatment	ECEL1	9427	37	2	233347583	233347583	Missense_Mutation	SNP	G	A	42	189	c.1663C>T	c.(1663-1665)CGG>TGG	p.R555W
Pat_40	Pre-Treatment	GIGYF2	26058	37	2	233655585	233655585	Missense_Mutation	SNP	T	C	22	106	c.890T>C	c.(889-891)ATG>ACG	p.M297T
Pat_40	Pre-Treatment	GPR35	2859	37	2	241569694	241569694	Missense_Mutation	SNP	G	A	4	17	c.325G>A	c.(325-327)GCC>ACC	p.A109T
Pat_40	Pre-Treatment	BOK	666	37	2	242501765	242501765	Missense_Mutation	SNP	G	A	4	48	c.223G>A	c.(223-225)GAT>AAT	p.D75N
Pat_40	Pre-Treatment	THAP4	51078	37	2	242573324	242573324	Missense_Mutation	SNP	G	A	24	105	c.248C>T	c.(247-249)TCC>TTC	p.S83F
Pat_40	Pre-Treatment	TGM6	343641	37	20	2377248	2377248	Missense_Mutation	SNP	C	T	13	31	c.521C>T	c.(520-522)GCC>GTC	p.A174V
Pat_40	Pre-Treatment	PAK7	57144	37	20	9560919	9560919	Missense_Mutation	SNP	G	A	51	72	c.863C>T	c.(862-864)TCA>TTA	p.S288L
Pat_40	Pre-Treatment	PAK7	57144	37	20	9561263	9561263	Missense_Mutation	SNP	C	T	68	128	c.519G>A	c.(517-519)ATG>ATA	p.M173I
Pat_40	Pre-Treatment	OVOL2	58495	37	20	18022253	18022253	Missense_Mutation	SNP	T	C	3	50	c.436A>G	c.(436-438)AGA>GGA	p.R146G
Pat_40	Pre-Treatment	POLR3F	10621	37	20	18453489	18453489	Nonsense_Mutation	SNP	C	T	38	70	c.184C>T	c.(184-186)CAG>TAG	p.Q62*
Pat_40	Pre-Treatment	THBD	7056	37	20	23028806	23028806	Missense_Mutation	SNP	C	T	4	48	c.1336G>A	c.(1336-1338)GAA>AAA	p.E446K
Pat_40	Pre-Treatment	NINL	22981	37	20	25456929	25456929	Missense_Mutation	SNP	G	A	4	54	c.2998C>T	c.(2998-3000)CGG>TGG	p.R1000W
Pat_40	Pre-Treatment	TPX2	22974	37	20	30382317	30382317	Missense_Mutation	SNP	G	A	47	123	c.1799G>A	c.(1798-1800)AGA>AAA	p.R600K
Pat_40	Pre-Treatment	ASXL1	171023	37	20	31017234	31017234	Missense_Mutation	SNP	G	A	20	71	c.565G>A	c.(565-567)GGG>AGG	p.G189R
Pat_40	Pre-Treatment	C20orf186	149954	37	20	31671216	31671217	Missense_Mutation	DNP	CC	TT	17	130	c.213_214CC>TT	211-216)CCCCCC>CCTT	p.P72S
Pat_40	Pre-Treatment	E2F1	1869	37	20	32267679	32267679	Missense_Mutation	SNP	C	T	4	69	c.454G>A	c.(454-456)GAC>AAC	p.D152N
Pat_40	Pre-Treatment	EPB41L1	2036	37	20	34797782	34797782	Nonsense_Mutation	SNP	C	T	4	17	c.2041C>T	c.(2041-2043)CGA>TGA	p.R681*
Pat_40	Pre-Treatment	RIMS4	140730	37	20	43384905	43384905	Missense_Mutation	SNP	G	A	15	47	c.680C>T	c.(679-681)ACC>ATC	p.T227I
Pat_40	Pre-Treatment	PI3	5266	37	20	43803639	43803639	Missense_Mutation	SNP	G	A	3	51	c.76G>A	c.(76-78)GGA>AGA	p.G26R
Pat_40	Pre-Treatment	EEF1A2	1917	37	20	62122040	62122040	Missense_Mutation	SNP	G	A	3	28	c.821C>T	c.(820-822)CCG>CTG	p.P274L
Pat_40	Pre-Treatment	ZGPAT	84619	37	20	62340299	62340299	Missense_Mutation	SNP	G	A	4	30	c.367G>A	c.(367-369)GGA>AGA	p.G123R
Pat_40	Pre-Treatment	USP25	29761	37	21	17214827	17214827	Missense_Mutation	SNP	G	A	32	172	c.2305G>A	c.(2305-2307)GAA>AAA	p.E769K
Pat_40	Pre-Treatment	C21orf59	56683	37	21	33982292	33982292	Missense_Mutation	SNP	C	T	13	54	c.163G>A	c.(163-165)GGC>AGC	p.G55S
Pat_40	Pre-Treatment	IL10RB	3588	37	21	34652102	34652102	Missense_Mutation	SNP	C	T	55	117	c.377C>T	c.(376-378)TCT>TTT	p.S126F
Pat_40	Pre-Treatment	KCNJ15	3772	37	21	39672159	39672159	Missense_Mutation	SNP	G	A	23	109	c.976G>A	c.(976-978)GAT>AAT	p.D326N
Pat_40	Pre-Treatment	DSCAM	1826	37	21	41719737	41719737	Missense_Mutation	SNP	C	T	40	291	c.1070G>A	c.(1069-1071)GGA>GAA	p.G357E
Pat_40	Pre-Treatment	RIPK4	54101	37	21	43166796	43166796	Missense_Mutation	SNP	G	A	3	39	c.809C>T	c.(808-810)CCG>CTG	p.P270L

Pat_40	Pre-Treatment	PTTG1IP	754	37	21	46275124	46275124	Splice_Site	SNP	C	T	9	20	c.496_splice	c.e5+1	p.G166_splice
Pat_40	Pre-Treatment	MICAL3	57553	37	22	18370094	18370094	Missense_Mutation	SNP	G	A	23	10	c.1999C>T	c.(1999-2001)CCC>TCC	p.P667S
Pat_40	Pre-Treatment	PRODH	5625	37	22	18912573	18912573	Missense_Mutation	SNP	C	T	3	27	c.658G>A	c.(658-660)GAA>AAA	p.E220K
Pat_40	Pre-Treatment	CLTCL1	8218	37	22	19170950	19170950	Missense_Mutation	SNP	A	T	15	32	c.4780T>A	c.(4780-4782)TTG>ATG	p.L1594M
Pat_40	Pre-Treatment	ZDHHC8	29801	37	22	20126835	20126835	Nonsense_Mutation	SNP	C	T	4	86	c.223C>T	c.(223-225)CGA>TGA	p.R75*
Pat_40	Pre-Treatment	BCR	613	37	22	23610637	23610637	Missense_Mutation	SNP	G	A	15	6	c.1795G>A	c.(1795-1797)GGA>AGA	p.G599R
Pat_40	Pre-Treatment	NEFH	4744	37	22	29885686	29885686	Missense_Mutation	SNP	C	A	10	102	c.2057C>A	c.(2056-2058)GCA>GAA	p.A686E
Pat_40	Pre-Treatment	PATZ1	23598	37	22	31741521	31741521	Missense_Mutation	SNP	C	T	4	46	c.68G>A	c.(67-69)AGC>AAC	p.S23N
Pat_40	Pre-Treatment	CSF2RB	1439	37	22	37322150	37322150	Missense_Mutation	SNP	G	A	4	80	c.322G>A	c.(322-324)GTT>ATT	p.V108I
Pat_40	Pre-Treatment	SSTR3	6753	37	22	37603517	37603517	Nonsense_Mutation	SNP	C	T	15	12	c.326G>A	c.(325-327)TGG>TAG	p.W109*
Pat_40	Pre-Treatment	TRIOBP	11078	37	22	38120359	38120359	Missense_Mutation	SNP	C	G	12	319	c.1796C>G	c.(1795-1797)ACA>AGA	p.T599R
Pat_40	Pre-Treatment	H1F0	3005	37	22	38201896	38201897	Nonsense_Mutation	DNP	GA	AT	15	35	c.345_346GA>AT	343-348)AAGAAG>AAATA	p.K116*
Pat_40	Pre-Treatment	BAIAP2L2	80115	37	22	38494156	38494156	Missense_Mutation	SNP	G	A	4	46	c.379C>T	c.(379-381)CGC>TGC	p.R127C
Pat_40	Pre-Treatment	PARVB	29780	37	22	44495969	44495969	Missense_Mutation	SNP	C	T	14	75	c.239C>T	c.(238-240)TCC>TTC	p.S80F
Pat_40	Pre-Treatment	WNT7B	7477	37	22	46345908	46345908	Missense_Mutation	SNP	C	T	31	37	c.190G>A	c.(190-192)GAG>AAG	p.E64K
Pat_40	Pre-Treatment	CELSR1	9620	37	22	46792517	46792517	Missense_Mutation	SNP	G	A	13	21	c.5828C>T	c.(5827-5829)CCG>CTG	p.P1943L
Pat_40	Pre-Treatment	PLXNB2	23654	37	22	50715060	50715060	Missense_Mutation	SNP	G	A	14	74	c.5335C>T	c.(5335-5337)CGG>TGG	p.R1779W
Pat_40	Pre-Treatment	SBF1	6305	37	22	50900836	50900836	Missense_Mutation	SNP	G	A	4	108	c.2194C>T	c.(2194-2196)CGC>TGC	p.R732C
Pat_40	Pre-Treatment	MIOX	55586	37	22	50925884	50925884	Missense_Mutation	SNP	G	A	3	52	c.86G>A	c.(85-87)CGG>CAG	p.R29Q
Pat_40	Pre-Treatment	CNTN6	27255	37	3	1367579	1367579	Missense_Mutation	SNP	G	A	12	52	c.1027G>A	c.(1027-1029)GGA>AGA	p.G343R
Pat_40	Pre-Treatment	GHRL	51738	37	3	10331857	10331857	Missense_Mutation	SNP	G	A	3	16	c.8C>T	c.(7-9)TCC>TTC	p.S3F
Pat_40	Pre-Treatment	HRH1	3269	37	3	11301460	11301460	Missense_Mutation	SNP	G	A	4	12	c.737G>A	c.(736-738)GGG>GAG	p.G246E
Pat_40	Pre-Treatment	CAND2	23066	37	3	12858191	12858191	Missense_Mutation	SNP	T	C	20	43	c.1760T>C	c.(1759-1761)GTG>GCG	p.V587A
Pat_40	Pre-Treatment	PLCL2	23228	37	3	17053134	17053134	Missense_Mutation	SNP	T	A	12	22	c.2272T>A	c.(2272-2274)TTT>ATT	p.F758I
Pat_40	Pre-Treatment	LRRC3B	116135	37	3	26751248	26751248	Missense_Mutation	SNP	C	T	21	65	c.85C>T	c.(85-87)CAT>TAT	p.H29Y
Pat_40	Pre-Treatment	SCN5A	6331	37	3	38648165	38648165	Nonsense_Mutation	SNP	G	A	4	6	c.1135C>T	c.(1135-1137)CAG>TAG	p.Q379*
Pat_40	Pre-Treatment	SCN10A	6336	37	3	38793820	38793820	Missense_Mutation	SNP	G	A	3	29	c.1645C>T	c.(1645-1647)CTC>TTC	p.L549F
Pat_40	Pre-Treatment	CTNNB1	1499	37	3	41266137	41266137	Missense_Mutation	SNP	C	T	14	47	c.134C>T	c.(133-135)TCT>TTT	p.S45F
Pat_40	Pre-Treatment	CXCR6	10663	37	3	45988860	45988860	Missense_Mutation	SNP	G	A	8	19	c.887G>A	c.(886-888)CGA>CAA	p.R296Q
Pat_40	Pre-Treatment	CCR3	1232	37	3	46307479	46307479	Missense_Mutation	SNP	A	G	20	60	c.830A>G	c.(829-831)AAG>AGG	p.K277R
Pat_40	Pre-Treatment	SCAP	22937	37	3	47476586	47476586	Missense_Mutation	SNP	A	C	16	43	c.164T>G	c.(163-165)GTG>GGG	p.V55G
Pat_40	Pre-Treatment	PLXNB1	5364	37	3	48459905	48459905	Missense_Mutation	SNP	A	G	6	6	c.3002T>C	c.(3001-3003)CTG>CCG	p.L1001P
Pat_40	Pre-Treatment	PLXNB1	5364	37	3	48461146	48461146	Missense_Mutation	SNP	G	A	6	0	c.2549C>T	c.(2548-2550)CCC>CTC	p.P850L
Pat_40	Pre-Treatment	CELSR3	1951	37	3	48698392	48698392	Missense_Mutation	SNP	C	T	3	11	c.1676G>A	c.(1675-1677)CGC>CAC	p.R559H
Pat_40	Pre-Treatment	LAMB2	3913	37	3	49163916	49163916	Missense_Mutation	SNP	G	A	23	47	c.2033C>T	c.(2032-2034)CCT>CTT	p.P678L
Pat_40	Pre-Treatment	GNAT1	2779	37	3	50229208	50229208	Missense_Mutation	SNP	A	G	3	27	c.50A>G	c.(49-51)AAG>AGG	p.K17R
Pat_40	Pre-Treatment	DOCK3	1795	37	3	51395405	51395405	Missense_Mutation	SNP	G	T	14	93	c.4781G>T	c.(4780-4782)GGA>GTA	p.G1594V
Pat_40	Pre-Treatment	DOCK3	1795	37	3	51418581	51418582	Missense_Mutation	DNP	CC	TT	9	41	.5684_5685CC>TT	c.(5683-5685)TCC>TTT	p.S1895F
Pat_40	Pre-Treatment	CACNA1D	776	37	3	53781378	53781378	Missense_Mutation	SNP	C	T	24	83	c.3217C>T	c.(3217-3219)CGT>TGT	p.R1073C
Pat_40	Pre-Treatment	CACNA2D3	55799	37	3	54615870	54615870	Missense_Mutation	SNP	G	A	12	41	c.929G>A	c.(928-930)GGA>GAA	p.G310E
Pat_40	Pre-Treatment	PXK	54899	37	3	58410506	58410506	Missense_Mutation	SNP	C	T	79	67	c.1556C>T	c.(1555-1557)CCA>CTA	p.P519L
Pat_40	Pre-Treatment	CNTN3	5067	37	3	74315713	74315713	Missense_Mutation	SNP	C	T	39	617	c.2905G>A	c.(2905-2907)GAC>AAC	p.D969N
Pat_40	Pre-Treatment	PROS1	5627	37	3	93624748	93624748	Missense_Mutation	SNP	A	C	19	63	c.481T>G	c.(481-483)TGC>GGC	p.C161G
Pat_40	Pre-Treatment	CD96	10225	37	3	111325559	111325559	Missense_Mutation	SNP	C	T	19	93	c.1148C>T	c.(1147-1149)TCC>TTC	p.S383F
Pat_40	Pre-Treatment	PLXNA1	5361	37	3	126735849	126735849	Missense_Mutation	SNP	G	A	4	61	c.3176G>A	c.(3175-3177)CGG>CAG	p.R1059Q
Pat_40	Pre-Treatment	MBD4	8930	37	3	129155742	129155742	Missense_Mutation	SNP	C	T	34	120	c.745G>A	c.(745-747)GGA>AGA	p.G249R
Pat_40	Pre-Treatment	PLXND1	23129	37	3	129305046	129305046	Missense_Mutation	SNP	C	T	3	11	c.1690G>A	c.(1690-1692)GCC>ACC	p.A564T

Pat_40	Pre-Treatment	NMNAT3	349565	37	3	139297817	139297817	Missense_Mutation	SNP	G	C	4	36	c.190C>G	c.(190-192)CGA>GGA	p.R64G
Pat_40	Pre-Treatment	AADACL2	344752	37	3	151475240	151475240	Missense_Mutation	SNP	G	A	13	68	c.1064G>A	c.(1063-1065)CGA>CAA	p.R355Q
Pat_40	Pre-Treatment	FNDC3B	64778	37	3	171965431	171965432	Missense_Mutation	DNP	CC	TT	47	250	c.373_374CC>TT	c.(373-375)CCC>TTC	p.P125F
Pat_40	Pre-Treatment	FNDC3B	64778	37	3	172115059	172115059	Missense_Mutation	SNP	G	A	20	47	c.3409G>A	c.(3409-3411)GAG>AAG	p.E1137K
Pat_40	Pre-Treatment	AP2M1	1173	37	3	183899833	183899833	Missense_Mutation	SNP	G	A	4	17	c.961G>A	c.(961-963)GAG>AAG	p.E321K
Pat_40	Pre-Treatment	ABCF3	55324	37	3	183910456	183910456	Missense_Mutation	SNP	G	A	5	11	c.1637G>A	c.(1636-1638)CGG>CAG	p.R546Q
Pat_40	Pre-Treatment	KNG1	3827	37	3	186460082	186460082	Missense_Mutation	SNP	G	A	5	86	c.1897G>A	c.(1897-1899)GAA>AAA	p.E633K
Pat_40	Pre-Treatment	C3orf59	151963	37	3	192516621	192516621	Missense_Mutation	SNP	G	A	8	13	c.1030C>T	c.(1030-1032)CCT>TCT	p.P344S
Pat_40	Pre-Treatment	ZNF721	170960	37	4	435639	435639	Missense_Mutation	SNP	T	C	8	140	c.2617A>G	c.(2617-2619)ACC>GCC	p.T873A
Pat_40	Pre-Treatment	ZNF721	170960	37	4	436514	436514	Missense_Mutation	SNP	C	T	38	173	c.1742G>A	c.(1741-1743)GGA>GAA	p.G581E
Pat_40	Pre-Treatment	ZNF721	170960	37	4	437319	437319	Missense_Mutation	SNP	C	T	8	217	c.937G>A	c.(937-939)GCC>ACC	p.A313T
Pat_40	Pre-Treatment	GAK	2580	37	4	843819	843819	Missense_Mutation	SNP	C	T	2	3	c.3695G>A	c.(3694-3696)CGG>CAG	p.R1232Q
Pat_40	Pre-Treatment	CRMP1	1400	37	4	5843131	5843131	Missense_Mutation	SNP	C	T	54	228	c.715G>A	c.(715-717)GCC>ACC	p.A239T
Pat_40	Pre-Treatment	JAKMIP1	152789	37	4	6066645	6066645	Missense_Mutation	SNP	C	T	20	38	c.1393G>A	c.(1393-1395)GAC>AAC	p.D465N
Pat_40	Pre-Treatment	AFAP1	60312	37	4	7770626	7770626	Missense_Mutation	SNP	C	T	22	58	c.2111G>A	c.(2110-2112)AGC>AAC	p.S704N
Pat_40	Pre-Treatment	BOD1L	259282	37	4	13602199	13602199	Missense_Mutation	SNP	T	C	3	22	c.6325A>G	c.(6325-6327)AGA>GGA	p.R2109G
Pat_40	Pre-Treatment	CPEB2	132864	37	4	15063811	15063811	Missense_Mutation	SNP	C	T	71	252	c.1469C>T	c.(1468-1470)TCC>TTC	p.S490F
Pat_40	Pre-Treatment	RBPJ	3516	37	4	26431526	26431526	Missense_Mutation	SNP	C	T	5	38	c.934C>T	c.(934-936)CCA>TCA	p.P312S
Pat_40	Pre-Treatment	GUF1	60558	37	4	44691864	44691864	Missense_Mutation	SNP	G	A	23	108	c.1207G>A	c.(1207-1209)GGA>AGA	p.G403R
Pat_40	Pre-Treatment	REST	5978	37	4	57797744	57797744	Missense_Mutation	SNP	C	T	4	56	c.2720C>T	c.(2719-2721)CCT>CTT	p.P907L
Pat_40	Pre-Treatment	UGT2B28	54490	37	4	70146351	70146351	Missense_Mutation	SNP	G	A	44	203	c.133G>A	c.(133-135)GAG>AAG	p.E45K
Pat_40	Pre-Treatment	UGT2B28	54490	37	4	70146547	70146547	Missense_Mutation	SNP	C	T	30	124	c.329C>T	c.(328-330)TCA>TTA	p.S110L
Pat_40	Pre-Treatment	ALB	213	37	4	74285291	74285291	Missense_Mutation	SNP	G	A	40	84	c.1720G>A	c.(1720-1722)GAT>AAT	p.D574N
Pat_40	Pre-Treatment	CCDC158	339965	37	4	77292635	77292635	Missense_Mutation	SNP	G	A	4	90	c.1084C>T	c.(1084-1086)CGG>TGG	p.R362W
Pat_40	Pre-Treatment	FRAS1	80144	37	4	79301056	79301056	Missense_Mutation	SNP	G	A	32	47	c.3469G>A	c.(3469-3471)GGA>AGA	p.G1157R
Pat_40	Pre-Treatment	BMP3	651	37	4	81967248	81967248	Missense_Mutation	SNP	G	A	59	95	c.673G>A	c.(673-675)GGA>AGA	p.G225R
Pat_40	Pre-Treatment	ADH1B	125	37	4	100232022	100232022	Missense_Mutation	SNP	C	T	36	162	c.1003G>A	c.(1003-1005)GAT>AAT	p.D335N
Pat_40	Pre-Treatment	ADH7	131	37	4	100349774	100349774	Missense_Mutation	SNP	C	T	45	183	c.170G>A	c.(169-171)GGA>GAA	p.G57E
Pat_40	Pre-Treatment	EGF	1950	37	4	110883099	110883099	Missense_Mutation	SNP	C	T	76	155	c.1270C>T	c.(1270-1272)CCT>TCT	p.P424S
Pat_40	Pre-Treatment	EGF	1950	37	4	110884429	110884430	Missense_Mutation	DNP	GG	AA	47	102	.1413_1414GG>A	411-1416)CTGGAT>CTAA	p.D472N
Pat_40	Pre-Treatment	LARP7	51574	37	4	113568238	113568238	Missense_Mutation	SNP	C	T	34	117	c.601C>T	c.(601-603)CCT>TCT	p.P201S
Pat_40	Pre-Treatment	TBC1D9	23158	37	4	141590792	141590792	Missense_Mutation	SNP	T	C	7	29	c.1433A>G	c.(1432-1434)AAA>AGA	p.K478R
Pat_40	Pre-Treatment	MAB21L2	10586	37	4	151504863	151504863	Missense_Mutation	SNP	G	A	7	24	c.682G>A	c.(682-684)GAC>AAC	p.D228N
Pat_40	Pre-Treatment	TLR2	7097	37	4	154625141	154625141	Missense_Mutation	SNP	C	T	27	23	c.1082C>T	c.(1081-1083)TCA>TTA	p.S361L
Pat_40	Pre-Treatment	RBM46	166863	37	4	155719334	155719334	Missense_Mutation	SNP	C	T	9	95	c.523C>T	c.(523-525)CCA>TCA	p.P175S
Pat_40	Pre-Treatment	GUCY1A3	2982	37	4	156618119	156618119	Missense_Mutation	SNP	G	A	7	42	c.100G>A	c.(100-102)GCA>ACA	p.A34T
Pat_40	Pre-Treatment	GRIA2	2891	37	4	158284078	158284078	Missense_Mutation	SNP	G	A	19	83	c.2534G>A	c.(2533-2535)CGA>CAA	p.R845Q
Pat_40	Pre-Treatment	TLL1	7092	37	4	166963247	166963247	Missense_Mutation	SNP	C	T	43	205	c.1330C>T	c.(1330-1332)CGT>TGT	p.R444C
Pat_40	Pre-Treatment	NEK1	4750	37	4	170506576	170506576	Missense_Mutation	SNP	C	T	4	36	c.731G>A	c.(730-732)AGG>AAG	p.R244K
Pat_40	Pre-Treatment	C4orf41	60684	37	4	184598649	184598649	Missense_Mutation	SNP	G	A	21	152	c.773G>A	c.(772-774)AGA>AAA	p.R258K
Pat_40	Pre-Treatment	FAT1	2195	37	4	187541333	187541333	Missense_Mutation	SNP	G	A	21	56	c.6407C>T	c.(6406-6408)TCA>TTA	p.S2136L
Pat_40	Pre-Treatment	ADAMTS16	170690	37	5	5262860	5262860	Missense_Mutation	SNP	G	A	19	74	c.2753G>A	c.(2752-2754)GGG>GAG	p.G918E
Pat_40	Pre-Treatment	FASTKD3	79072	37	5	7859553	7859553	Missense_Mutation	SNP	C	T	8	46	c.1984G>A	c.(1984-1986)GAA>AAA	p.E662K
Pat_40	Pre-Treatment	MTRR	4552	37	5	7892881	7892881	Missense_Mutation	SNP	A	G	91	141	c.1493A>G	c.(1492-1494)AAC>AGC	p.N498S
Pat_40	Pre-Treatment	DNAH5	1767	37	5	13700913	13700913	Nonsense_Mutation	SNP	C	T	67	101	c.13559G>A	c.(13558-13560)TGG>TAG	p.W4520*
Pat_40	Pre-Treatment	PRDM9	56979	37	5	23526999	23526999	Missense_Mutation	SNP	C	T	6	142	c.1802C>T	c.(1801-1803)ACA>ATA	p.T601I
Pat_40	Pre-Treatment	PRDM9	56979	37	5	23527083	23527083	Missense_Mutation	SNP	G	C	6	94	c.1886G>C	c.(1885-1887)AGA>ACA	p.R629T

Pat_40	Pre-Treatment	GOLPH3	64083	37	5	32126541	32126541	Missense_Mutation	SNP	C	G	47	102	c.674G>C	c.(673-675)TGG>TCG	p.W225S
Pat_40	Pre-Treatment	ADAMTS12	81792	37	5	33637805	33637805	Missense_Mutation	SNP	G	A	4	72	c.1765C>T	c.(1765-1767)CGC>TGC	p.R589C
Pat_40	Pre-Treatment	C9	735	37	5	39311479	39311479	Missense_Mutation	SNP	C	T	8	72	c.871G>A	c.(871-873)GAA>AAA	p.E291K
Pat_40	Pre-Treatment	ITGA1	3672	37	5	52221138	52221138	Missense_Mutation	SNP	G	A	17	82	c.2434G>A	c.(2434-2436)GAA>AAA	p.E812K
Pat_40	Pre-Treatment	DDX4	54514	37	5	55110910	55110910	Missense_Mutation	SNP	C	T	46	195	c.1897C>T	c.(1897-1899)CGT>TGT	p.R633C
Pat_40	Pre-Treatment	F2RL1	2150	37	5	76128587	76128587	Missense_Mutation	SNP	G	A	25	112	c.155G>A	c.(154-156)GGA>GAA	p.G52E
Pat_40	Pre-Treatment	GPR98	84059	37	5	89990494	89990494	Missense_Mutation	SNP	G	A	8	27	c.7921G>A	c.(7921-7923)GGA>AGA	p.G2641R
Pat_40	Pre-Treatment	MCTP1	79772	37	5	94204141	94204141	Missense_Mutation	SNP	A	C	10	60	c.2333T>G	c.(2332-2334)TTT>TGT	p.F778C
Pat_40	Pre-Treatment	WDR36	134430	37	5	110439905	110439905	Missense_Mutation	SNP	C	T	3	56	c.928C>T	c.(928-930)CCA>TCA	p.P310S
Pat_40	Pre-Treatment	EPB41L4A	64097	37	5	111545588	111545588	Splice_Site	SNP	C	T	33	56	c.1178_splice	c.e13+1	p.S393_splice
Pat_40	Pre-Treatment	FAM170A	340069	37	5	118969746	118969746	Missense_Mutation	SNP	T	G	45	44	c.303T>G	c.(301-303)CAT>CAG	p.H101Q
Pat_40	Pre-Treatment	FTMT	94033	37	5	121188229	121188229	Missense_Mutation	SNP	G	A	15	117	c.571G>A	c.(571-573)GAT>AAT	p.D191N
Pat_40	Pre-Treatment	P4HA2	8974	37	5	131545009	131545009	Missense_Mutation	SNP	C	A	54	105	c.725G>T	c.(724-726)CGA>CTA	p.R242L
Pat_40	Pre-Treatment	KIF3A	11127	37	5	132037886	132037886	Missense_Mutation	SNP	C	T	13	81	c.1696G>A	c.(1696-1698)GAA>AAA	p.E566K
Pat_40	Pre-Treatment	TIFAB	497189	37	5	134785386	134785386	Missense_Mutation	SNP	C	T	24	89	c.244G>A	c.(244-246)GGC>AGC	p.G82S
Pat_40	Pre-Treatment	KLHL3	26249	37	5	136974690	136974691	Missense_Mutation	DNP	CC	TT	13	51	.1170_1171GG>A	168-1173)GCGGTG>GCA	p.V391M
Pat_40	Pre-Treatment	ANKHD1-EIF4EBP	404734	37	5	139906028	139906028	Missense_Mutation	SNP	G	A	4	107	c.4940G>A	c.(4939-4941)CGA>CAA	p.R1647Q
Pat_40	Pre-Treatment	PCDHA2	56146	37	5	140175006	140175006	Missense_Mutation	SNP	C	T	24	28	c.457C>T	c.(457-459)CCT>TCT	p.P153S
Pat_40	Pre-Treatment	PCDHA3	56145	37	5	140182748	140182748	Missense_Mutation	SNP	G	A	20	72	c.1966G>A	c.(1966-1968)GAA>AAA	p.E656K
Pat_40	Pre-Treatment	PCDHA4	56144	37	5	140187721	140187721	Missense_Mutation	SNP	G	A	29	114	c.949G>A	c.(949-951)GAA>AAA	p.E317K
Pat_40	Pre-Treatment	PCDHA5	56143	37	5	140202835	140202835	Missense_Mutation	SNP	C	T	17	83	c.1475C>T	c.(1474-1476)TCG>TTG	p.S492L
Pat_40	Pre-Treatment	PCDHA10	56139	37	5	140237555	140237555	Missense_Mutation	SNP	C	T	9	14	c.1922C>T	c.(1921-1923)TCG>TTG	p.S641L
Pat_40	Pre-Treatment	PCDHB6	56130	37	5	140530709	140530709	Missense_Mutation	SNP	G	A	53	79	c.871G>A	c.(871-873)GAA>AAA	p.E291K
Pat_40	Pre-Treatment	PCDHB6	56130	37	5	140531786	140531786	Missense_Mutation	SNP	C	T	4	44	c.1948C>T	c.(1948-1950)CGC>TGC	p.R650C
Pat_40	Pre-Treatment	PCDHGB2	56103	37	5	140741165	140741165	Missense_Mutation	SNP	C	T	19	31	c.1463C>T	c.(1462-1464)TCC>TTC	p.S488F
Pat_40	Pre-Treatment	PCDHGB3	56102	37	5	140750571	140750571	Missense_Mutation	SNP	G	A	11	23	c.610G>A	c.(610-612)GAG>AAG	p.E204K
Pat_40	Pre-Treatment	ARHGAP26	23092	37	5	142311641	142311641	Missense_Mutation	SNP	C	T	26	123	c.1058C>T	c.(1057-1059)TCG>TTG	p.S353L
Pat_40	Pre-Treatment	FBXO38	81545	37	5	147778639	147778639	Missense_Mutation	SNP	G	A	18	76	c.206G>A	c.(205-207)CGA>CAA	p.R69Q
Pat_40	Pre-Treatment	SLC36A2	153201	37	5	150704953	150704953	Missense_Mutation	SNP	C	T	7	41	c.904G>A	c.(904-906)GGA>AGA	p.G302R
Pat_40	Pre-Treatment	PWWP2A	114825	37	5	159520269	159520269	Missense_Mutation	SNP	T	C	4	59	c.1388A>G	c.(1387-1389)CAG>CGG	p.Q463R
Pat_40	Pre-Treatment	CCDC99	54908	37	5	169015538	169015538	Nonsense_Mutation	SNP	C	T	22	94	c.118C>T	c.(118-120)CAA>TAA	p.Q40*
Pat_40	Pre-Treatment	CPLX2	10814	37	5	175305922	175305922	Missense_Mutation	SNP	G	A	3	21	c.43G>A	c.(43-45)GAC>AAC	p.D15N
Pat_40	Pre-Treatment	NSD1	64324	37	5	176631253	176631253	Missense_Mutation	SNP	G	A	14	52	c.1196G>A	c.(1195-1197)AGG>AAG	p.R399K
Pat_40	Pre-Treatment	DOK3	79930	37	5	176931802	176931802	Missense_Mutation	SNP	C	T	6	45	c.755G>A	c.(754-756)GGC>GAC	p.G252D
Pat_40	Pre-Treatment	BTNL3	10917	37	5	180424335	180424335	Missense_Mutation	SNP	G	A	7	42	c.520G>A	c.(520-522)GAT>AAT	p.D174N
Pat_40	Pre-Treatment	BTNL3	10917	37	5	180432588	180432588	Missense_Mutation	SNP	C	T	50	51	c.1117C>T	c.(1117-1119)CCC>TCC	p.P373S
Pat_40	Pre-Treatment	GNB2L1	10399	37	5	180666075	180666075	Missense_Mutation	SNP	C	T	38	210	c.628G>A	c.(628-630)GGA>AGA	p.G210R
Pat_40	Pre-Treatment	EXOC2	55770	37	6	572614	572614	Missense_Mutation	SNP	G	A	17	40	c.1349C>T	c.(1348-1350)GCC>GTC	p.A450V
Pat_40	Pre-Treatment	RANBP9	10048	37	6	13634740	13634741	Missense_Mutation	DNP	CC	TT	23	47	.1717_1718GG>A	c.(1717-1719)GGA>AAA	p.G573K
Pat_40	Pre-Treatment	NUP153	9972	37	6	17675825	17675825	Missense_Mutation	SNP	C	T	10	68	c.511G>A	c.(511-513)GAT>AAT	p.D171N
Pat_40	Pre-Treatment	GPLD1	2822	37	6	24445860	24445860	Missense_Mutation	SNP	C	T	29	50	c.1934G>A	c.(1933-1935)GGG>GAG	p.G645E
Pat_40	Pre-Treatment	HIST1H2BC	8347	37	6	26123919	26123919	Missense_Mutation	SNP	C	T	28	132	c.214G>A	c.(214-216)GAG>AAG	p.E72K
Pat_40	Pre-Treatment	BTN3A3	10384	37	6	26445976	26445976	Missense_Mutation	SNP	G	A	3	52	c.478G>A	c.(478-480)GGA>AGA	p.G160R
Pat_40	Pre-Treatment	TRIM15	89870	37	6	30131681	30131681	Missense_Mutation	SNP	C	T	3	30	c.220C>T	c.(220-222)CCC>TCC	p.P74S
Pat_40	Pre-Treatment	HLA-B	3106	37	6	31322904	31322904	Missense_Mutation	SNP	A	T	28	114	c.992T>A	c.(991-993)ATG>AAG	p.M331K
Pat_40	Pre-Treatment	MSH5	4439	37	6	31727727	31727727	Missense_Mutation	SNP	C	T	8	13	c.1660C>T	c.(1660-1662)CTT>TTT	p.L554F
Pat_40	Pre-Treatment	C6orf27	80737	37	6	31735258	31735259	Missense_Mutation	DNP	GG	AA	6	25	.1669_1670CC>T	c.(1669-1671)CCT>TTT	p.P557F

Pat_40	Pre-Treatment	BRD2	6046	37	6	32947723	32947723	Missense_Mutation	SNP	A	T	4	51	c.1960A>T	c.(1960-1962)ATC>TTC	p.I654F
Pat_40	Pre-Treatment	ZNF318	24149	37	6	43323693	43323693	Missense_Mutation	SNP	G	A	10	54	c.1379C>T	c.(1378-1380)CCC>CTC	p.P460L
Pat_40	Pre-Treatment	CAPN11	11131	37	6	44144035	44144035	Missense_Mutation	SNP	C	T	19	106	c.961C>T	c.(961-963)CCC>TCC	p.P321S
Pat_40	Pre-Treatment	RCAN2	10231	37	6	46214583	46214583	Missense_Mutation	SNP	G	A	9	84	c.335C>T	c.(334-336)TCG>TTG	p.S112L
Pat_40	Pre-Treatment	TINAG	27283	37	6	54173703	54173703	Missense_Mutation	SNP	G	A	24	66	c.355G>A	c.(355-357)GGT>AGT	p.G119S
Pat_40	Pre-Treatment	DST	667	37	6	56347614	56347614	Missense_Mutation	SNP	C	T	4	87	c.14912G>A	c.(14911-14913)CGA>CAA	p.R4971Q
Pat_40	Pre-Treatment	BAI3	577	37	6	69665943	69665943	Missense_Mutation	SNP	C	T	13	75	c.1223C>T	c.(1222-1224)TCG>TTG	p.S408L
Pat_40	Pre-Treatment	FAM135A	57579	37	6	71238035	71238035	Missense_Mutation	SNP	C	T	28	62	c.3655C>T	c.(3655-3657)CCT>TCT	p.P1219S
Pat_40	Pre-Treatment	FAM135A	57579	37	6	71266500	71266500	Missense_Mutation	SNP	C	T	21	116	c.4276C>T	c.(4276-4278)CGC>TGC	p.R1426C
Pat_40	Pre-Treatment	FILIP1	27145	37	6	76022621	76022621	Missense_Mutation	SNP	C	T	31	55	c.2927G>A	c.(2926-2928)CGA>CAA	p.R976Q
Pat_40	Pre-Treatment	PRSS35	167681	37	6	84234328	84234328	Missense_Mutation	SNP	C	T	13	32	c.1168C>T	c.(1168-1170)CGC>TGC	p.R390C
Pat_40	Pre-Treatment	LAMA4	3910	37	6	112476887	112476887	Missense_Mutation	SNP	C	T	60	139	c.1839G>A	c.(1837-1839)ATG>ATA	p.M613I
Pat_40	Pre-Treatment	ROS1	6098	37	6	117662453	117662453	Missense_Mutation	SNP	C	T	29	106	c.4924G>A	c.(4924-4926)GAA>AAA	p.E1642K
Pat_40	Pre-Treatment	FAM184A	79632	37	6	119295618	119295618	Missense_Mutation	SNP	C	T	40	171	c.2890G>A	c.(2890-2892)GAA>AAA	p.E964K
Pat_40	Pre-Treatment	VNN2	8875	37	6	133078678	133078678	Missense_Mutation	SNP	C	T	12	105	c.221G>A	c.(220-222)CGA>CAA	p.R74Q
Pat_40	Pre-Treatment	BCLAF1	9774	37	6	136599171	136599171	Missense_Mutation	SNP	C	T	4	39	c.848G>A	c.(847-849)CGA>CAA	p.R283Q
Pat_40	Pre-Treatment	SHPRH	257218	37	6	146276260	146276260	Missense_Mutation	SNP	G	A	18	67	c.199C>T	c.(199-201)CAC>TAC	p.H67Y
Pat_40	Pre-Treatment	ZBTB2	57621	37	6	151687684	151687684	Missense_Mutation	SNP	C	T	14	32	c.517G>A	c.(517-519)GAG>AAG	p.E173K
Pat_40	Pre-Treatment	TULP4	56995	37	6	158923439	158923439	Missense_Mutation	SNP	C	T	16	70	c.2744C>T	c.(2743-2745)ACC>ATC	p.T915I
Pat_40	Pre-Treatment	LPA	4018	37	6	160978522	160978522	Nonsense_Mutation	SNP	C	T	22	104	c.4713G>A	c.(4711-4713)TGG>TGA	p.W1571*
Pat_40	Pre-Treatment	LPA	4018	37	6	161020605	161020605	Missense_Mutation	SNP	C	T	116	339	c.3214G>A	c.(3214-3216)GGA>AGA	p.G1072R
Pat_40	Pre-Treatment	PLG	5340	37	6	161143526	161143526	Missense_Mutation	SNP	G	A	72	213	c.1183G>A	c.(1183-1185)GGA>AGA	p.G395R
Pat_40	Pre-Treatment	MAD1L1	8379	37	7	2188787	2188787	Missense_Mutation	SNP	C	T	6	37	c.1073G>A	c.(1072-1074)AGC>AAC	p.S358N
Pat_40	Pre-Treatment	AMZ1	155185	37	7	2740383	2740383	Missense_Mutation	SNP	C	T	23	63	c.298C>T	c.(298-300)CCG>TCG	p.P100S
Pat_40	Pre-Treatment	SLC29A4	222962	37	7	5338625	5338625	Missense_Mutation	SNP	C	T	5	56	c.889C>T	c.(889-891)CCA>TCA	p.P297S
Pat_40	Pre-Treatment	HDAC9	9734	37	7	18625110	18625110	Missense_Mutation	SNP	C	T	4	51	c.229C>T	c.(229-231)CGG>TGG	p.R77W
Pat_40	Pre-Treatment	MACC1	346389	37	7	20199595	20199595	Missense_Mutation	SNP	G	A	8	63	c.389C>T	c.(388-390)TCC>TTC	p.S130F
Pat_40	Pre-Treatment	DNAH11	8701	37	7	21747399	21747399	Missense_Mutation	SNP	C	T	23	57	c.6650C>T	c.(6649-6651)ACA>ATA	p.T2217I
Pat_40	Pre-Treatment	FAM188B	84182	37	7	30831178	30831178	Missense_Mutation	SNP	C	T	12	53	c.1061C>T	c.(1060-1062)CCC>CTC	p.P354L
Pat_40	Pre-Treatment	CCDC129	223075	37	7	31682490	31682490	Missense_Mutation	SNP	G	A	12	103	c.1506G>A	c.(1504-1506)ATG>ATA	p.M502I
Pat_40	Pre-Treatment	PDE1C	5137	37	7	31877577	31877577	Missense_Mutation	SNP	C	T	89	185	c.989G>A	c.(988-990)CGA>CAA	p.R330Q
Pat_40	Pre-Treatment	BMPER	168667	37	7	34097762	34097762	Missense_Mutation	SNP	G	A	21	56	c.1019G>A	c.(1018-1020)AGT>AAT	p.S340N
Pat_40	Pre-Treatment	CDK13	8621	37	7	40038988	40038988	Nonsense_Mutation	SNP	A	T	13	66	c.2071A>T	c.(2071-2073)AAA>TAA	p.K691*
Pat_40	Pre-Treatment	ZNF713	349075	37	7	55990859	55990859	Missense_Mutation	SNP	C	T	37	118	c.53C>T	c.(52-54)TCA>TTA	p.S18L
Pat_40	Pre-Treatment	ZNF107	51427	37	7	64167982	64167982	Missense_Mutation	SNP	C	T	20	118	c.1300C>T	c.(1300-1302)CAT>TAT	p.H434Y
Pat_40	Pre-Treatment	SPDYE5	442590	37	7	75130895	75130895	Missense_Mutation	SNP	C	T	26	361	c.770C>T	c.(769-771)CCG>CTG	p.P257L
Pat_40	Pre-Treatment	SPDYE5	442590	37	7	75130970	75130970	Missense_Mutation	SNP	T	C	10	226	c.845T>C	c.(844-846)CTG>CCG	p.L282P
Pat_40	Pre-Treatment	HIP1	3092	37	7	75184825	75184825	Nonsense_Mutation	SNP	G	A	3	24	c.1858C>T	c.(1858-1860)CGA>TGA	p.R620*
Pat_40	Pre-Treatment	FGL2	10875	37	7	76825822	76825822	Missense_Mutation	SNP	C	T	39	197	c.1094G>A	c.(1093-1095)CGA>CAA	p.R365Q
Pat_40	Pre-Treatment	PCLO	27445	37	7	82583350	82583350	Missense_Mutation	SNP	C	T	61	152	c.6919G>A	c.(6919-6921)GAA>AAA	p.E2307K
Pat_40	Pre-Treatment	PCLO	27445	37	7	82585683	82585683	Missense_Mutation	SNP	C	T	14	66	c.4586G>A	c.(4585-4587)CGA>CAA	p.R1529Q
Pat_40	Pre-Treatment	ABCB1	5243	37	7	87175289	87175289	Missense_Mutation	SNP	G	A	58	148	c.1777C>T	c.(1777-1779)CGT>TGT	p.R593C
Pat_40	Pre-Treatment	CYP3A43	64816	37	7	99453321	99453321	Missense_Mutation	SNP	C	A	3	34	c.778C>A	c.(778-780)CGC>AGC	p.R260S
Pat_40	Pre-Treatment	ZAN	7455	37	7	100349941	100349941	Missense_Mutation	SNP	C	T	8	193	c.2213C>T	c.(2212-2214)CCC>CTC	p.P738L
Pat_40	Pre-Treatment	RELN	5649	37	7	103206794	103206794	Missense_Mutation	SNP	C	T	9	122	c.4813G>A	c.(4813-4815)GGA>AGA	p.G1605R
Pat_40	Pre-Treatment	PPP1R3A	5506	37	7	113519829	113519829	Missense_Mutation	SNP	C	T	30	141	c.1318G>A	c.(1318-1320)GAT>AAT	p.D440N
Pat_40	Pre-Treatment	FOXP2	93986	37	7	114292325	114292325	Missense_Mutation	SNP	G	A	101	84	c.1162G>A	c.(1162-1164)GTG>ATG	p.V388M

Pat_40	Pre-Treatment	CFTR	1080	37	7	117232308	117232308	Missense_Mutation	SNP	A	T	10	73	c.2087A>T	c.(2086-2088)AAA>ATA	p.K696I
Pat_40	Pre-Treatment	SLC13A1	6561	37	7	122759211	122759211	Missense_Mutation	SNP	A	C	19	42	c.1436T>G	c.(1435-1437)TTG>TGG	p.L479W
Pat_40	Pre-Treatment	ZNF800	168850	37	7	127013826	127013826	Missense_Mutation	SNP	G	A	19	109	c.1564C>T	c.(1564-1566)CCT>TCT	p.P522S
Pat_40	Pre-Treatment	TSPAN33	340348	37	7	128806635	128806635	Missense_Mutation	SNP	G	A	84	81	c.476G>A	c.(475-477)GGG>GAG	p.G159E
Pat_40	Pre-Treatment	BRAF	673	37	7	140453136	140453136	Missense_Mutation	SNP	A	T	97	63	c.1799T>A	c.(1798-1800)GTG>GAG	p.V600E
Pat_40	Pre-Treatment	KEL	3792	37	7	142640960	142640961	Missense_Mutation	DNP	CC	TT	6	34	.1501_1502GG>A	c.(1501-1503)GGA>AAA	p.G501K
Pat_40	Pre-Treatment	TAS2R41	259287	37	7	143175722	143175722	Missense_Mutation	SNP	G	A	29	146	c.757G>A	c.(757-759)GAT>AAT	p.D253N
Pat_40	Pre-Treatment	LOC441294	441294	37	7	143270156	143270156	Missense_Mutation	SNP	C	T	14	298	c.1246C>T	c.(1246-1248)CTT>TTT	p.L416F
Pat_40	Pre-Treatment	ZNF777	27153	37	7	149129013	149129013	Missense_Mutation	SNP	C	T	3	31	c.2350G>A	c.(2350-2352)GGC>AGC	p.G784S
Pat_40	Pre-Treatment	REPIN1	29803	37	7	150068497	150068497	Missense_Mutation	SNP	C	T	2	1	c.167C>T	c.(166-168)GCC>GTC	p.A56V
Pat_40	Pre-Treatment	MLL3	58508	37	7	151879283	151879283	Missense_Mutation	SNP	T	A	14	93	c.5662A>T	c.(5662-5664)AAC>TAC	p.N1888Y
Pat_40	Pre-Treatment	MLL3	58508	37	7	151919131	151919131	Missense_Mutation	SNP	C	T	49	270	c.3454G>A	c.(3454-3456)GAA>AAA	p.E1152K
Pat_40	Pre-Treatment	CSMD1	64478	37	8	2824251	2824251	Missense_Mutation	SNP	G	A	5	40	c.8944C>T	c.(8944-8946)CCT>TCT	p.P2982S
Pat_40	Pre-Treatment	CSMD1	64478	37	8	3081309	3081309	Missense_Mutation	SNP	C	T	32	95	c.4429G>A	c.(4429-4431)GAA>AAA	p.E1477K
Pat_40	Pre-Treatment	XPO7	23039	37	8	21857050	21857050	Missense_Mutation	SNP	T	G	56	214	c.2647T>G	c.(2647-2649)TAC>GAC	p.Y883D
Pat_40	Pre-Treatment	LGI3	203190	37	8	22013937	22013937	Missense_Mutation	SNP	G	A	2	1	c.119C>T	c.(118-120)CCG>CTG	p.P40L
Pat_40	Pre-Treatment	TNFRSF10A	8797	37	8	23049398	23049398	Missense_Mutation	SNP	C	T	45	89	c.1216G>A	c.(1216-1218)GAT>AAT	p.D406N
Pat_40	Pre-Treatment	ADAM7	8756	37	8	24324428	24324428	Missense_Mutation	SNP	C	T	27	194	c.506C>T	c.(505-507)TCC>TTC	p.S169F
Pat_40	Pre-Treatment	DDHD2	23259	37	8	38092070	38092070	Missense_Mutation	SNP	C	T	28	169	c.379C>T	c.(379-381)CCC>TCC	p.P127S
Pat_40	Pre-Treatment	POLB	5423	37	8	42227383	42227383	Nonsense_Mutation	SNP	C	T	10	48	c.790C>T	c.(790-792)CAG>TAG	p.Q264*
Pat_40	Pre-Treatment	SNAI2	6591	37	8	49832783	49832783	Missense_Mutation	SNP	G	C	20	145	c.297C>G	c.(295-297)CAC>CAG	p.H99Q
Pat_40	Pre-Treatment	PXDNL	137902	37	8	52320967	52320967	Missense_Mutation	SNP	C	T	23	16	c.3217G>A	c.(3217-3219)GAA>AAA	p.E1073K
Pat_40	Pre-Treatment	RP1	6101	37	8	55537556	55537557	Nonsense_Mutation	DNP	AG	TA	19	45	.1114_1115AG>T	c.(1114-1116)AGA>TAA	p.R372*
Pat_40	Pre-Treatment	RP1	6101	37	8	55539350	55539350	Missense_Mutation	SNP	G	A	34	41	c.2908G>A	c.(2908-2910)GAA>AAA	p.E970K
Pat_40	Pre-Treatment	CYP7B1	9420	37	8	65527628	65527628	Missense_Mutation	SNP	G	A	21	161	c.1012C>T	c.(1012-1014)CCC>TCC	p.P338S
Pat_40	Pre-Treatment	CPA6	57094	37	8	68346290	68346290	Missense_Mutation	SNP	G	A	25	299	c.1024C>T	c.(1024-1026)CCC>TCC	p.P342S
Pat_40	Pre-Treatment	PREX2	80243	37	8	69028131	69028131	Missense_Mutation	SNP	C	T	53	348	c.3290C>T	c.(3289-3291)TCT>TTT	p.S1097F
Pat_40	Pre-Treatment	HNF4G	3174	37	8	76470899	76470899	Missense_Mutation	SNP	G	A	39	342	c.739G>A	c.(739-741)GAT>AAT	p.D247N
Pat_40	Pre-Treatment	C8orf47	203111	37	8	99102024	99102024	Missense_Mutation	SNP	G	A	7	60	c.779G>A	c.(778-780)AGA>AAA	p.R260K
Pat_40	Pre-Treatment	STK3	6788	37	8	99718703	99718703	Missense_Mutation	SNP	G	A	31	24	c.676C>T	c.(676-678)CCA>TCA	p.P226S
Pat_40	Pre-Treatment	RIMS2	9699	37	8	104987692	104987692	Missense_Mutation	SNP	G	A	12	98	c.2219G>A	c.(2218-2220)GGA>GAA	p.G740E
Pat_40	Pre-Treatment	RIMS2	9699	37	8	105263859	105263859	Missense_Mutation	SNP	G	A	133	131	c.3915G>A	c.(3913-3915)ATG>ATA	p.M1305I
Pat_40	Pre-Treatment	FAM83H	286077	37	8	144808878	144808878	Missense_Mutation	SNP	G	A	3	7	c.2753C>T	c.(2752-2754)CCC>CTC	p.P918L
Pat_40	Pre-Treatment	OPLAH	26873	37	8	145113548	145113548	Missense_Mutation	SNP	C	G	7	18	c.634G>C	c.(634-636)GGC>CGC	p.G212R
Pat_40	Pre-Treatment	GPT	2875	37	8	145730651	145730651	Missense_Mutation	SNP	C	T	3	5	c.518C>T	c.(517-519)GCC>GTC	p.A173V
Pat_40	Pre-Treatment	PTPRD	5789	37	9	8636785	8636785	Missense_Mutation	SNP	A	T	45	41	c.124T>A	c.(124-126)TCT>ACT	p.S42T
Pat_40	Pre-Treatment	MPDZ	8777	37	9	13217180	13217180	Missense_Mutation	SNP	C	A	13	10	c.1200G>T	c.(1198-1200)TTG>TTT	p.L400F
Pat_40	Pre-Treatment	C9orf23	138716	37	9	34611158	34611158	Missense_Mutation	SNP	G	A	4	93	c.136C>T	c.(136-138)CGG>TGG	p.R46W
Pat_40	Pre-Treatment	SHB	6461	37	9	38016038	38016038	Missense_Mutation	SNP	C	T	36	81	c.808G>A	c.(808-810)GAG>AAG	p.E270K
Pat_40	Pre-Treatment	LOC442421	442421	37	9	66499716	66499716	Missense_Mutation	SNP	A	G	6	69	c.526A>G	c.(526-528)AAT>GAT	p.N176D
Pat_40	Pre-Treatment	IARS	3376	37	9	95025293	95025293	Missense_Mutation	SNP	G	A	4	53	c.1745C>T	c.(1744-1746)CCG>CTG	p.P582L
Pat_40	Pre-Treatment	WNK2	65268	37	9	96054935	96054935	Missense_Mutation	SNP	C	T	2	2	c.5299C>T	c.(5299-5301)CGG>TGG	p.R1767W
Pat_40	Pre-Treatment	C9orf156	51531	37	9	100672706	100672706	Missense_Mutation	SNP	C	T	3	46	c.602G>A	c.(601-603)CGA>CAA	p.R201Q
Pat_40	Pre-Treatment	STX17	55014	37	9	102730759	102730759	Missense_Mutation	SNP	T	C	4	71	c.713T>C	c.(712-714)CTC>CCC	p.L238P
Pat_40	Pre-Treatment	OR1N1	138883	37	9	125288794	125288794	Missense_Mutation	SNP	G	A	15	36	c.779C>T	c.(778-780)CCT>CTT	p.P260L
Pat_40	Pre-Treatment	SLC2A8	29988	37	9	130167241	130167241	Missense_Mutation	SNP	C	T	15	57	c.1121C>T	c.(1120-1122)GCC>GTC	p.A374V
Pat_40	Pre-Treatment	C9orf78	51759	37	9	132594217	132594217	Missense_Mutation	SNP	G	A	28	102	c.302C>T	c.(301-303)TCG>TTG	p.S101L

Pat_40	Pre-Treatment	FIBCD1	84929	37	9	133780759	133780759	Missense_Mutation	SNP	C	T	3	24	c.988G>A	c.(988-990)GAG>AAG	p.E330K
Pat_40	Pre-Treatment	RAPGEF1	2889	37	9	134514084	134514084	Missense_Mutation	SNP	C	T	27	87	c.538G>A	c.(538-540)GAA>AAA	p.E180K
Pat_40	Pre-Treatment	COL5A1	1289	37	9	137582859	137582859	Missense_Mutation	SNP	C	T	16	40	c.211C>T	c.(211-213)CCG>TCG	p.P71S
Pat_40	Pre-Treatment	SEC16A	9919	37	9	139370230	139370230	Missense_Mutation	SNP	G	A	2	1	c.1838C>T	c.(1837-1839)CCG>CTG	p.P613L
Pat_40	Pre-Treatment	C9orf172	389813	37	9	139740194	139740194	Missense_Mutation	SNP	G	A	2	1	c.1328G>A	c.(1327-1329)CGC>CAC	p.R443H
Pat_40	Pre-Treatment	FBXW5	54461	37	9	139836762	139836762	Missense_Mutation	SNP	G	A	2	3	c.832C>T	c.(832-834)CGC>TGC	p.R278C
Pat_40	Pre-Treatment	TPRN	286262	37	9	140087077	140087077	Missense_Mutation	SNP	C	T	9	15	c.1609G>A	c.(1609-1611)GAG>AAG	p.E537K
Pat_40	Pre-Treatment	TUBB2C	10383	37	9	140137584	140137585	Missense_Mutation	DNP	CC	TT	17	61	c.914_915CC>TT	c.(913-915)CCC>CTT	p.P305L
Pat_40	Pre-Treatment	NLGN4X	57502	37	X	5810998	5810998	Missense_Mutation	SNP	T	A	35	160	c.2311A>T	c.(2311-2313)ATC>TTC	p.I771F
Pat_40	Pre-Treatment	KAL1	3730	37	X	8553380	8553380	Nonsense_Mutation	SNP	G	A	5	101	c.784C>T	c.(784-786)CGA>TGA	p.R262*
Pat_40	Pre-Treatment	TLR7	51284	37	X	12903805	12903805	Missense_Mutation	SNP	C	T	48	144	c.178C>T	c.(178-180)CCT>TCT	p.P60S
Pat_40	Pre-Treatment	TCEANC	170082	37	X	13681166	13681166	Missense_Mutation	SNP	T	C	55	207	c.539T>C	c.(538-540)CTT>CCT	p.L180P
Pat_40	Pre-Treatment	KLHL15	80311	37	X	24024498	24024498	Missense_Mutation	SNP	G	A	18	122	c.313C>T	c.(313-315)CTT>TTT	p.L105F
Pat_40	Pre-Treatment	DCAF8L2	347442	37	X	27766412	27766412	Missense_Mutation	SNP	G	A	7	14	c.1400G>A	c.(1399-1401)AGA>AAA	p.R467K
Pat_40	Pre-Treatment	MAGEB1	4112	37	X	30269469	30269469	Missense_Mutation	SNP	G	A	20	95	c.859G>A	c.(859-861)GAG>AAG	p.E287K
Pat_40	Pre-Treatment	DMD	1756	37	X	32361316	32361316	Missense_Mutation	SNP	A	T	28	86	c.5674T>A	c.(5674-5676)TGC>AGC	p.C1892S
Pat_40	Pre-Treatment	CXorf22	170063	37	X	35974281	35974281	Missense_Mutation	SNP	G	A	17	43	c.1378G>A	c.(1378-1380)GAA>AAA	p.E460K
Pat_40	Pre-Treatment	FAM47C	442444	37	X	37027156	37027156	Missense_Mutation	SNP	C	G	4	50	c.673C>G	c.(673-675)CAG>GAG	p.Q225E
Pat_40	Pre-Treatment	OTC	5009	37	X	38212016	38212016	Nonsense_Mutation	SNP	C	T	23	72	c.67C>T	c.(67-69)CGA>TGA	p.R23*
Pat_40	Pre-Treatment	MED14	9282	37	X	40518681	40518681	Missense_Mutation	SNP	C	T	15	51	c.3863G>A	c.(3862-3864)AGA>AAA	p.R1288K
Pat_40	Pre-Treatment	RBM10	8241	37	X	47045530	47045530	Missense_Mutation	SNP	C	G	9	46	c.2497C>G	c.(2497-2499)CCC>GCC	p.P833A
Pat_40	Pre-Treatment	HUWE1	10075	37	X	53619528	53619528	Nonsense_Mutation	SNP	G	A	3	33	c.3802C>T	c.(3802-3804)CGA>TGA	p.R1268*
Pat_40	Pre-Treatment	ITIH5L	347365	37	X	54823498	54823498	Missense_Mutation	SNP	G	A	11	71	c.134C>T	c.(133-135)ACG>ATG	p.T45M
Pat_40	Pre-Treatment	TRO	7216	37	X	54949440	54949440	Missense_Mutation	SNP	C	T	16	43	c.475C>T	c.(475-477)CAT>TAT	p.H159Y
Pat_40	Pre-Treatment	SPIN4	139886	37	X	62570220	62570220	Missense_Mutation	SNP	G	A	19	182	c.479C>T	c.(478-480)CCT>CTT	p.P160L
Pat_40	Pre-Treatment	PJA1	64219	37	X	68381748	68381748	Missense_Mutation	SNP	C	T	12	95	c.1334G>A	c.(1333-1335)CGA>CAA	p.R445Q
Pat_40	Pre-Treatment	FOXO4	4303	37	X	70321239	70321239	Missense_Mutation	SNP	G	C	3	50	c.1159G>C	c.(1159-1161)GAT>CAT	p.D387H
Pat_40	Pre-Treatment	ACRC	93953	37	X	70823920	70823920	Missense_Mutation	SNP	C	T	8	119	c.793C>T	c.(793-795)CCC>TCC	p.P265S
Pat_40	Pre-Treatment	ACRC	93953	37	X	70823950	70823950	Missense_Mutation	SNP	C	T	7	145	c.823C>T	c.(823-825)CCC>TCC	p.P275S
Pat_40	Pre-Treatment	ACRC	93953	37	X	70823960	70823961	Missense_Mutation	DNP	GC	AG	6	160	c.833_834GC>AG	c.(832-834)AGC>AAG	p.S278K
Pat_40	Pre-Treatment	ABCB7	22	37	X	74273345	74273345	Missense_Mutation	SNP	T	C	10	20	c.2119A>G	c.(2119-2121)ACA>GCA	p.T707A
Pat_40	Pre-Treatment	MAGEE1	57692	37	X	75648828	75648828	Missense_Mutation	SNP	G	A	4	53	c.505G>A	c.(505-507)GGT>AGT	p.G169S
Pat_40	Pre-Treatment	ATRX	546	37	X	76907828	76907828	Missense_Mutation	SNP	C	T	3	26	c.4333G>A	c.(4333-4335)GAA>AAA	p.E1445K
Pat_40	Pre-Treatment	DACH2	117154	37	X	85403846	85403846	Missense_Mutation	SNP	C	A	18	94	c.222C>A	c.(220-222)CAC>CAA	p.H74Q
Pat_40	Pre-Treatment	RAB40A	142684	37	X	102754855	102754855	Missense_Mutation	SNP	G	A	10	60	c.830C>T	c.(829-831)TCT>TTT	p.S277F
Pat_40	Pre-Treatment	NRK	203447	37	X	105152811	105152811	Missense_Mutation	SNP	G	A	10	48	c.1178G>A	c.(1177-1179)AGG>AAG	p.R393K
Pat_40	Pre-Treatment	COL4A5	1287	37	X	107865120	107865120	Missense_Mutation	SNP	A	T	18	22	c.2765A>T	c.(2764-2766)AAA>ATA	p.K922I
Pat_40	Pre-Treatment	SLC6A14	11254	37	X	115588809	115588809	Missense_Mutation	SNP	G	A	47	210	c.1649G>A	c.(1648-1650)AGA>AAA	p.R550K
Pat_40	Pre-Treatment	KIAA1210	57481	37	X	118223262	118223262	Missense_Mutation	SNP	G	A	3	30	c.1931C>T	c.(1930-1932)TCC>TTC	p.S644F
Pat_40	Pre-Treatment	KIAA1210	57481	37	X	118227657	118227657	Missense_Mutation	SNP	C	T	10	68	c.1456G>A	c.(1456-1458)GAA>AAA	p.E486K
Pat_40	Pre-Treatment	THOC2	57187	37	X	122774460	122774460	Missense_Mutation	SNP	C	T	31	149	c.1675G>A	c.(1675-1677)GAA>AAA	p.E559K
Pat_40	Pre-Treatment	ODZ1	10178	37	X	123514532	123514532	Missense_Mutation	SNP	C	T	114	210	c.8032G>A	c.(8032-8034)GAA>AAA	p.E2678K
Pat_40	Pre-Treatment	USP26	83844	37	X	132159788	132159788	Missense_Mutation	SNP	C	A	9	131	c.2461G>T	c.(2461-2463)GAT>TAT	p.D821Y
Pat_40	Pre-Treatment	USP26	83844	37	X	132159790	132159790	Missense_Mutation	SNP	C	A	9	123	c.2459G>T	c.(2458-2460)GGA>GTA	p.G820V
Pat_40	Pre-Treatment	GPR112	139378	37	X	135430610	135430610	Missense_Mutation	SNP	C	T	34	181	c.4745C>T	c.(4744-4746)TCC>TTC	p.S1582F
Pat_40	Pre-Treatment	ATP11C	286410	37	X	138870439	138870439	Missense_Mutation	SNP	C	T	19	107	c.1441G>A	c.(1441-1443)GAT>AAT	p.D481N
Pat_40	Pre-Treatment	SPANXN2	494119	37	X	142795287	142795287	Missense_Mutation	SNP	A	G	15	164	c.391T>C	c.(391-393)TCT>CCT	p.S131P

Pat_40	Pre-Treatment	SPANXN2	494119	37	X	142795326	142795326	Missense_Mutation	SNP	A	C	8	152	c.352T>G	c.(352-354)TCT>GCT	p.S118A
Pat_40	Pre-Treatment	SPANXN1	494118	37	X	144337239	144337239	Nonsense_Mutation	SNP	A	T	24	50	c.124A>T	c.(124-126)AAG>TAG	p.K42*
Pat_40	Pre-Treatment	MAGEA12	4111	37	X	151900242	151900242	Missense_Mutation	SNP	C	T	38	132	c.559G>A	c.(559-561)GAT>AAT	p.D187N
Pat_40	Pre-Treatment	MPP1	4354	37	X	154011765	154011765	Missense_Mutation	SNP	G	A	6	32	c.883C>T	c.(883-885)CGC>TGC	p.R295C
Pat_40	Pre-Treatment	RAB39B	116442	37	X	154490329	154490329	Missense_Mutation	SNP	G	T	25	104	c.401C>A	c.(400-402)ACT>AAT	p.T134N
Pat_40	Post-Resistance	ARHGEF16	27237	37	1	3394445	3394445	Missense_Mutation	SNP	C	G	3	98	c.1480C>G	c.(1480-1482)CCA>GCA	p.P494A
Pat_40	Post-Resistance	CAMTA1	23261	37	1	7721851	7721851	Missense_Mutation	SNP	G	A	3	44	c.730G>A	c.(730-732)GTG>ATG	p.V244M
Pat_40	Post-Resistance	ERRFI1	54206	37	1	8073629	8073629	Missense_Mutation	SNP	C	T	324	181	c.1030G>A	c.(1030-1032)GGG>AGG	p.G344R
Pat_40	Post-Resistance	DFFA	1676	37	1	10532476	10532476	Missense_Mutation	SNP	C	T	51	135	c.40G>A	c.(40-42)GAG>AAG	p.E14K
Pat_40	Post-Resistance	C1orf130	400746	37	1	24932116	24932116	Missense_Mutation	SNP	G	A	22	68	c.187G>A	c.(187-189)GAA>AAA	p.E63K
Pat_40	Post-Resistance	CATSPER4	378807	37	1	26517249	26517249	Missense_Mutation	SNP	C	T	6	33	c.131C>T	c.(130-132)CCC>CTC	p.P44L
Pat_40	Post-Resistance	AHDC1	27245	37	1	27876118	27876118	Missense_Mutation	SNP	T	G	26	77	c.2509A>C	c.(2509-2511)ACC>CCC	p.T837P
Pat_40	Post-Resistance	PHC2	1912	37	1	33820513	33820513	Missense_Mutation	SNP	C	T	4	95	c.1318G>A	c.(1318-1320)GTG>ATG	p.V440M
Pat_40	Post-Resistance	COL8A2	1296	37	1	36563643	36563643	Missense_Mutation	SNP	G	A	3	12	c.1639C>T	c.(1639-1641)CCC>TCC	p.P547S
Pat_40	Post-Resistance	POU3F1	5453	37	1	38511393	38511393	Missense_Mutation	SNP	C	G	4	17	c.1023G>C	c.(1021-1023)AAG>AAC	p.K341N
Pat_40	Post-Resistance	MACF1	23499	37	1	39913514	39913514	Nonsense_Mutation	SNP	C	T	28	163	c.15241C>T	c.(15241-15243)CAG>TAG	p.Q5081*
Pat_40	Post-Resistance	TIE1	7075	37	1	43773118	43773118	Missense_Mutation	SNP	G	A	3	37	c.788G>A	c.(787-789)CGT>CAT	p.R263H
Pat_40	Post-Resistance	TM2D1	83941	37	1	62175095	62175095	Missense_Mutation	SNP	C	T	33	96	c.253G>A	c.(253-255)GCA>ACA	p.A85T
Pat_40	Post-Resistance	IL23R	149233	37	1	67635270	67635270	Missense_Mutation	SNP	C	T	124	117	c.316C>T	c.(316-318)CCC>TCC	p.P106S
Pat_40	Post-Resistance	LRRIQ3	127255	37	1	74540468	74540468	Missense_Mutation	SNP	A	T	29	59	c.874T>A	c.(874-876)TAT>AAT	p.Y292N
Pat_40	Post-Resistance	LHX8	431707	37	1	75626530	75626530	Nonsense_Mutation	SNP	C	T	249	187	c.1021C>T	c.(1021-1023)CAG>TAG	p.Q341*
Pat_40	Post-Resistance	MSH4	4438	37	1	76355016	76355016	Missense_Mutation	SNP	G	A	105	69	c.2188G>A	c.(2188-2190)GAA>AAA	p.E730K
Pat_40	Post-Resistance	LPHN2	23266	37	1	82408790	82408790	Missense_Mutation	SNP	C	T	39	87	c.535C>T	c.(535-537)CGT>TGT	p.R179C
Pat_40	Post-Resistance	HIAT1	64645	37	1	100534099	100534099	Missense_Mutation	SNP	C	T	145	109	c.776C>T	c.(775-777)CCG>CTG	p.P259L
Pat_40	Post-Resistance	COL11A1	1301	37	1	103488381	103488381	Missense_Mutation	SNP	C	T	20	71	c.1162G>A	c.(1162-1164)GAA>AAA	p.E388K
Pat_40	Post-Resistance	GSTM5	2949	37	1	110255773	110255773	Missense_Mutation	SNP	G	A	11	83	c.145G>A	c.(145-147)GAA>AAA	p.E49K
Pat_40	Post-Resistance	AMPD1	270	37	1	115229401	115229401	Nonsense_Mutation	SNP	G	A	49	106	c.346C>T	c.(346-348)CAG>TAG	p.Q116*
Pat_40	Post-Resistance	NRAS	4893	37	1	115256530	115256530	Missense_Mutation	SNP	G	T	69	438	c.181C>A	c.(181-183)CAA>AAA	p.Q61K
Pat_40	Post-Resistance	HAO2	51179	37	1	119925542	119925542	Missense_Mutation	SNP	C	T	37	101	c.136C>T	c.(136-138)CGC>TGC	p.R46C
Pat_40	Post-Resistance	NBPF9	400818	37	1	144220816	144220816	Missense_Mutation	SNP	A	G	7	384	c.2189A>G	c.(2188-2190)GAG>GGG	p.E730G
Pat_40	Post-Resistance	ANKRD34A	284615	37	1	145474041	145474041	Missense_Mutation	SNP	C	T	85	302	c.713C>T	c.(712-714)CCC>CTC	p.P238L
Pat_40	Post-Resistance	NBPF16	728936	37	1	148753298	148753298	Missense_Mutation	SNP	T	C	11	302	c.1315T>C	c.(1315-1317)TCA>CCA	p.S439P
Pat_40	Post-Resistance	NBPF16	728936	37	1	148753317	148753317	Missense_Mutation	SNP	C	T	9	409	c.1334C>T	c.(1333-1335)TCG>TTG	p.S445L
Pat_40	Post-Resistance	TCHH	7062	37	1	152084702	152084702	Missense_Mutation	SNP	G	C	3	91	c.991C>G	c.(991-993)CAG>GAG	p.Q331E
Pat_40	Post-Resistance	HRNR	388697	37	1	152192447	152192447	Missense_Mutation	SNP	C	T	51	255	c.1658G>A	c.(1657-1659)AGG>AAG	p.R553K
Pat_40	Post-Resistance	FLG	2312	37	1	152284699	152284699	Missense_Mutation	SNP	C	T	257	97	c.2663G>A	c.(2662-2664)GGA>GAA	p.G888E
Pat_40	Post-Resistance	S100A8	6279	37	1	153363002	153363002	Missense_Mutation	SNP	C	T	330	131	c.10G>A	c.(10-12)GAG>AAG	p.E4K
Pat_40	Post-Resistance	S100A16	140576	37	1	153580138	153580138	Missense_Mutation	SNP	G	A	4	139	c.184C>T	c.(184-186)CTC>TTC	p.L62F
Pat_40	Post-Resistance	NPR1	4881	37	1	153656215	153656215	Splice_Site	SNP	G	A	49	71	c.1400_splice	c.e7-1	p.D467_splice
Pat_40	Post-Resistance	F5	2153	37	1	169510220	169510220	Missense_Mutation	SNP	G	A	12	598	c.4108C>T	c.(4108-4110)CTC>TTC	p.L1370F
Pat_40	Post-Resistance	F5	2153	37	1	169510259	169510259	Missense_Mutation	SNP	G	T	10	616	c.4069C>A	c.(4069-4071)CTT>ATT	p.L1357I
Pat_40	Post-Resistance	PRRX1	5396	37	1	170633409	170633409	Missense_Mutation	SNP	G	A	4	59	c.50G>A	c.(49-51)GGC>GAC	p.G17D
Pat_40	Post-Resistance	FMO3	2328	37	1	171083391	171083391	Missense_Mutation	SNP	C	T	37	119	c.1072C>T	c.(1072-1074)CCT>TCT	p.P358S
Pat_40	Post-Resistance	TNR	7143	37	1	175363013	175363014	Missense_Mutation	DNP	CC	TT	60	157	.1258_1259GG>A	c.(1258-1260)GGG>AAG	p.G420K
Pat_40	Post-Resistance	FAM20B	9917	37	1	179041241	179041241	Missense_Mutation	SNP	G	A	3	80	c.1192G>A	c.(1192-1194)GTA>ATA	p.V398I
Pat_40	Post-Resistance	CEP350	9857	37	1	180053225	180053225	Missense_Mutation	SNP	C	T	38	10	c.6197C>T	c.(6196-6198)TCA>TTA	p.S2066L
Pat_40	Post-Resistance	QSOX1	5768	37	1	180165636	180165636	Nonsense_Mutation	SNP	G	T	14	91	c.1708G>T	c.(1708-1710)GAG>TAG	p.E570*

Pat_40	Post-Resistance	CACNA1E	777	37	1	181745324	181745324	Missense_Mutation	SNP	G	A	56	227	c.5227G>A	c.(5227-5229)GAG>AAG	p.E1743K
Pat_40	Post-Resistance	CFHR1	3078	37	1	196801125	196801125	Missense_Mutation	SNP	G	A	136	54	c.989G>A	c.(988-990)AGA>AAA	p.R330K
Pat_40	Post-Resistance	CFHR5	81494	37	1	196964859	196964859	Missense_Mutation	SNP	C	T	116	139	c.620C>T	c.(619-621)TCA>TTA	p.S207L
Pat_40	Post-Resistance	CAMSAP1L1	23271	37	1	200817686	200817686	Missense_Mutation	SNP	G	A	64	137	c.1822G>A	c.(1822-1824)GGT>AGT	p.G608S
Pat_40	Post-Resistance	PPP1R12B	4660	37	1	202531971	202531971	Missense_Mutation	SNP	C	A	108	424	c.2573C>A	c.(2572-2574)GCC>GAC	p.A858D
Pat_40	Post-Resistance	ADIPOR1	51094	37	1	202910727	202910727	Missense_Mutation	SNP	C	T	40	156	c.1102G>A	c.(1102-1104)GGC>AGC	p.G368S
Pat_40	Post-Resistance	PLXNA2	5362	37	1	208252741	208252741	Missense_Mutation	SNP	G	A	5	26	c.2450C>T	c.(2449-2451)GCC>GTC	p.A817V
Pat_40	Post-Resistance	LAMB3	3914	37	1	209805978	209805978	Missense_Mutation	SNP	G	A	44	26	c.772C>T	c.(772-774)CGC>TGC	p.R258C
Pat_40	Post-Resistance	CAPN2	824	37	1	223959916	223959916	Missense_Mutation	SNP	G	A	43	161	c.2054G>A	c.(2053-2055)GGA>GAA	p.G685E
Pat_40	Post-Resistance	LEFTY2	7044	37	1	226125308	226125308	Missense_Mutation	SNP	C	T	35	14	c.934G>A	c.(934-936)GGG>AGG	p.G312R
Pat_40	Post-Resistance	CDC42BPA	8476	37	1	227335101	227335101	Missense_Mutation	SNP	C	T	117	344	c.853G>A	c.(853-855)GAA>AAA	p.E285K
Pat_40	Post-Resistance	GPR137B	7107	37	1	236306031	236306031	Missense_Mutation	SNP	G	A	3	65	c.109G>A	c.(109-111)GTG>ATG	p.V37M
Pat_40	Post-Resistance	SDCCAG8	10806	37	1	243493952	243493952	Missense_Mutation	SNP	G	A	20	134	c.1179G>A	c.(1177-1179)ATG>ATA	p.M393I
Pat_40	Post-Resistance	SDCCAG8	10806	37	1	243652386	243652386	Nonsense_Mutation	SNP	C	T	3	33	c.2056C>T	c.(2056-2058)CAG>TAG	p.Q686*
Pat_40	Post-Resistance	AKT3	10000	37	1	243736269	243736270	Missense_Mutation	DNP	CC	TT	16	259	c.777_778GG>AA	(775-780)TTGGAC>TTAA	p.D260N
Pat_40	Post-Resistance	OR2M5	127059	37	1	248308997	248308997	Missense_Mutation	SNP	C	T	128	574	c.548C>T	c.(547-549)TCC>TTC	p.S183F
Pat_40	Post-Resistance	OR2M7	391196	37	1	248487323	248487323	Missense_Mutation	SNP	G	A	210	94	c.548C>T	c.(547-549)TCC>TTC	p.S183F
Pat_40	Post-Resistance	DIP2C	22982	37	10	460041	460041	Missense_Mutation	SNP	G	A	4	87	c.869C>T	c.(868-870)CCG>CTG	p.P290L
Pat_40	Post-Resistance	BMI1	648	37	10	22618172	22618172	Nonsense_Mutation	SNP	C	T	25	31	c.682C>T	c.(682-684)CGA>TGA	p.R228*
Pat_40	Post-Resistance	KIAA1217	56243	37	10	24762649	24762649	Missense_Mutation	SNP	G	A	4	98	c.1339G>A	c.(1339-1341)GAA>AAA	p.E447K
Pat_40	Post-Resistance	EPC1	80314	37	10	32576138	32576138	Missense_Mutation	SNP	G	A	123	21	c.1040C>T	c.(1039-1041)TCG>TTG	p.S347L
Pat_40	Post-Resistance	ANKRD30A	91074	37	10	37430910	37430910	Missense_Mutation	SNP	C	T	5	94	c.917C>T	c.(916-918)ACG>ATG	p.T306M
Pat_40	Post-Resistance	ANKRD30A	91074	37	10	37431050	37431050	Missense_Mutation	SNP	G	C	9	111	c.1057G>C	c.(1057-1059)GCA>CCA	p.A353P
Pat_40	Post-Resistance	RBP3	5949	37	10	48390358	48390358	Missense_Mutation	SNP	C	T	13	8	c.520G>A	c.(520-522)GGA>AGA	p.G174R
Pat_40	Post-Resistance	A1CF	29974	37	10	52573720	52573720	Missense_Mutation	SNP	C	T	109	31	c.1244G>A	c.(1243-1245)GGA>GAA	p.G415E
Pat_40	Post-Resistance	PCDH15	65217	37	10	55581646	55581646	Missense_Mutation	SNP	T	G	80	98	c.5840A>C	c.(5839-5841)CAA>CCA	p.Q1947P
Pat_40	Post-Resistance	ANK3	288	37	10	61834299	61834299	Missense_Mutation	SNP	C	T	18	27	c.6340G>A	c.(6340-6342)GAC>AAC	p.D2114N
Pat_40	Post-Resistance	SFTPA2	729238	37	10	81318720	81318720	Missense_Mutation	SNP	T	G	90	16	c.214A>C	c.(214-216)AAT>CAT	p.N72H
Pat_40	Post-Resistance	OPN4	94233	37	10	88417853	88417853	Missense_Mutation	SNP	A	G	19	2	c.355A>G	c.(355-357)ATG>GTG	p.M119V
Pat_40	Post-Resistance	KIF20B	9585	37	10	91522528	91522528	Missense_Mutation	SNP	G	A	4	101	c.4925G>A	c.(4924-4926)TGT>TAT	p.C1642Y
Pat_40	Post-Resistance	MYOF	26509	37	10	95159169	95159169	Missense_Mutation	SNP	C	T	12	31	c.1201G>A	c.(1201-1203)GTT>ATT	p.V401I
Pat_40	Post-Resistance	CYP2C19	1557	37	10	96540336	96540336	Missense_Mutation	SNP	G	A	80	111	c.562G>A	c.(562-564)GAT>AAT	p.D188N
Pat_40	Post-Resistance	HPSE2	60495	37	10	100249833	100249833	Missense_Mutation	SNP	A	G	103	125	c.1441T>C	c.(1441-1443)TAT>CAT	p.Y481H
Pat_40	Post-Resistance	CALHM2	51063	37	10	105209250	105209250	Nonsense_Mutation	SNP	G	T	4	49	c.449C>A	c.(448-450)TCA>TAA	p.S150*
Pat_40	Post-Resistance	ACSL5	51703	37	10	114173027	114173027	Missense_Mutation	SNP	C	T	93	68	c.1045C>T	c.(1045-1047)CCC>TCC	p.P349S
Pat_40	Post-Resistance	WDR11	55717	37	10	122646253	122646253	Missense_Mutation	SNP	C	T	4	64	c.2026C>T	c.(2026-2028)CGG>TGG	p.R676W
Pat_40	Post-Resistance	FGFR2	2263	37	10	123245021	123245021	Missense_Mutation	SNP	C	T	41	10	c.2083G>A	c.(2083-2085)GAG>AAG	p.E695K
Pat_40	Post-Resistance	DMBT1	1755	37	10	124392709	124392709	Missense_Mutation	SNP	G	A	104	21	c.6013G>A	c.(6013-6015)GAT>AAT	p.D2005N
Pat_40	Post-Resistance	DOCK1	1793	37	10	129172323	129172323	Missense_Mutation	SNP	C	T	8	13	c.3457C>T	c.(3457-3459)CTT>TTT	p.L1153F
Pat_40	Post-Resistance	KNDC1	85442	37	10	135010625	135010625	Missense_Mutation	SNP	G	A	3	33	c.1798G>A	c.(1798-1800)GCT>ACT	p.A600T
Pat_40	Post-Resistance	CYP2E1	1571	37	10	135351354	135351354	Missense_Mutation	SNP	G	A	17	113	c.1255G>A	c.(1255-1257)GGA>AGA	p.G419R
Pat_40	Post-Resistance	CDHR5	53841	37	11	618833	618833	Missense_Mutation	SNP	G	C	4	123	c.1726C>G	c.(1726-1728)CCA>GCA	p.P576A
Pat_40	Post-Resistance	MUC2	4583	37	11	1095290	1095290	Missense_Mutation	SNP	C	T	3	57	c.13196C>T	c.(13195-13197)ACG>ATG	p.T4399M
Pat_40	Post-Resistance	OR51G1	79324	37	11	4945065	4945065	Nonsense_Mutation	SNP	G	A	26	43	c.505C>T	c.(505-507)CAA>TAA	p.Q169*
Pat_40	Post-Resistance	OR52A5	390054	37	11	5153391	5153391	Missense_Mutation	SNP	G	A	77	147	c.482C>T	c.(481-483)TCC>TTC	p.S161F
Pat_40	Post-Resistance	OR51B4	79339	37	11	5322536	5322536	Missense_Mutation	SNP	G	A	24	44	c.641C>T	c.(640-642)TCT>TTT	p.S214F
Pat_40	Post-Resistance	OR51B2	79345	37	11	5345505	5345505	Missense_Mutation	SNP	G	A	20	23	c.23C>T	c.(22-24)GCC>GTC	p.A8V

Pat_40	Post-Resistance	OR56B1	387748	37	11	5758164	5758164	Missense_Mutation	SNP	C	T	45	79	c.418C>T	c.(418-420)CGC>TGC	p.R140C
Pat_40	Post-Resistance	OR56B1	387748	37	11	5758588	5758588	Missense_Mutation	SNP	C	T	350	372	c.842C>T	c.(841-843)CCA>CTA	p.P281L
Pat_40	Post-Resistance	SWAP70	23075	37	11	9749608	9749608	Missense_Mutation	SNP	G	A	23	68	c.651G>A	c.(649-651)ATG>ATA	p.M217I
Pat_40	Post-Resistance	PLEKHA7	144100	37	11	16838766	16838767	Missense_Mutation	DNP	CC	TT	78	64	.1446_1447GG>A	44-1449)GGGGGC>GGA	p.G483S
Pat_40	Post-Resistance	ABCC8	6833	37	11	17419984	17419984	Missense_Mutation	SNP	C	T	15	12	c.3655G>A	c.(3655-3657)GAG>AAG	p.E1219K
Pat_40	Post-Resistance	MRGPRX2	117194	37	11	19077222	19077222	Nonsense_Mutation	SNP	C	T	21	60	c.728G>A	c.(727-729)TGG>TAG	p.W243*
Pat_40	Post-Resistance	RCN1	5954	37	11	32124946	32124946	Missense_Mutation	SNP	C	T	42	80	c.808C>T	c.(808-810)CGC>TGC	p.R270C
Pat_40	Post-Resistance	PTPRJ	5795	37	11	48134314	48134314	Missense_Mutation	SNP	C	T	205	119	c.131C>T	c.(130-132)CCT>CTT	p.P44L
Pat_40	Post-Resistance	OR4C11	219429	37	11	55371068	55371068	Missense_Mutation	SNP	G	A	11	151	c.782C>T	c.(781-783)ACC>ATC	p.T261I
Pat_40	Post-Resistance	OR4C6	219432	37	11	55433089	55433090	Missense_Mutation	DNP	GG	AA	40	119	c.447_448GG>AA	45-450)GGGGGA>GGAA	p.G150R
Pat_40	Post-Resistance	OR5D13	390142	37	11	55541362	55541362	Missense_Mutation	SNP	C	T	81	215	c.449C>T	c.(448-450)TCC>TTC	p.S150F
Pat_40	Post-Resistance	OR5I1	10798	37	11	55703012	55703012	Missense_Mutation	SNP	G	A	87	64	c.865C>T	c.(865-867)CCG>TCG	p.P289S
Pat_40	Post-Resistance	OR5M3	219482	37	11	56237733	56237733	Missense_Mutation	SNP	C	T	44	117	c.241G>A	c.(241-243)GAA>AAA	p.E81K
Pat_40	Post-Resistance	FAM111B	374393	37	11	58892997	58892997	Missense_Mutation	SNP	C	T	138	441	c.1427C>T	c.(1426-1428)ACT>ATT	p.T476I
Pat_40	Post-Resistance	GPR44	11251	37	11	60620688	60620688	Missense_Mutation	SNP	G	A	9	40	c.508C>T	c.(508-510)CGG>TGG	p.R170W
Pat_40	Post-Resistance	RTN3	10313	37	11	63486769	63486769	Nonsense_Mutation	SNP	T	A	56	28	c.795T>A	c.(793-795)TAT>TAA	p.Y265*
Pat_40	Post-Resistance	C11orf20	25858	37	11	64070987	64070987	Missense_Mutation	SNP	C	T	4	47	c.386C>T	c.(385-387)GCG>GTG	p.A129V
Pat_40	Post-Resistance	CCDC88B	283234	37	11	64118984	64118984	Missense_Mutation	SNP	G	A	2	4	c.2995G>A	c.(2995-2997)GGG>AGG	p.G999R
Pat_40	Post-Resistance	CDC42BPG	55561	37	11	64602851	64602851	Missense_Mutation	SNP	C	T	84	225	c.1921G>A	c.(1921-1923)GAA>AAA	p.E641K
Pat_40	Post-Resistance	LRP5	4041	37	11	68171002	68171002	Missense_Mutation	SNP	C	T	16	86	c.1636C>T	c.(1636-1638)CCG>TCG	p.P546S
Pat_40	Post-Resistance	USP35	57558	37	11	77921528	77921528	Missense_Mutation	SNP	C	T	52	124	c.2627C>T	c.(2626-2628)GCT>GTT	p.A876V
Pat_40	Post-Resistance	PCF11	51585	37	11	82876987	82876987	Missense_Mutation	SNP	G	A	11	12	c.1048G>A	c.(1048-1050)GAA>AAA	p.E350K
Pat_40	Post-Resistance	TYR	7299	37	11	88924454	88924454	Missense_Mutation	SNP	G	A	181	26	c.904G>A	c.(904-906)GGA>AGA	p.G302R
Pat_40	Post-Resistance	GUCY1A2	2977	37	11	106810823	106810823	Missense_Mutation	SNP	C	T	6	134	c.569G>A	c.(568-570)CGA>CAA	p.R190Q
Pat_40	Post-Resistance	C11orf92	399948	37	11	111167004	111167004	Missense_Mutation	SNP	T	A	18	59	c.200A>T	c.(199-201)AAG>ATG	p.K67M
Pat_40	Post-Resistance	USP28	57646	37	11	113704150	113704150	Nonsense_Mutation	SNP	C	A	149	25	c.751G>T	c.(751-753)GAA>TAA	p.E251*
Pat_40	Post-Resistance	PAFAH1B2	5049	37	11	117038252	117038252	Missense_Mutation	SNP	A	G	26	54	c.527A>G	c.(526-528)GAC>GGC	p.D176G
Pat_40	Post-Resistance	PAFAH1B2	5049	37	11	117038293	117038293	Missense_Mutation	SNP	G	A	4	86	c.568G>A	c.(568-570)GAC>AAC	p.D190N
Pat_40	Post-Resistance	TECTA	7007	37	11	120989347	120989347	Missense_Mutation	SNP	G	A	4	82	c.1123G>A	c.(1123-1125)GTC>ATC	p.V375I
Pat_40	Post-Resistance	ARHGAP32	9743	37	11	128963533	128963533	Missense_Mutation	SNP	C	T	3	75	c.472G>A	c.(472-474)GTG>ATG	p.V158M
Pat_40	Post-Resistance	KDM5A	5927	37	12	432896	432896	Missense_Mutation	SNP	G	A	12	275	c.2020C>T	c.(2020-2022)CGG>TGG	p.R674W
Pat_40	Post-Resistance	B4GALNT3	283358	37	12	662410	662410	Missense_Mutation	SNP	G	A	34	150	c.1321G>A	c.(1321-1323)GAG>AAG	p.E441K
Pat_40	Post-Resistance	CACNA1C	775	37	12	2797838	2797838	Missense_Mutation	SNP	G	A	9	46	c.6259G>A	c.(6259-6261)GGC>AGC	p.G2087S
Pat_40	Post-Resistance	CD9	928	37	12	6344459	6344459	Missense_Mutation	SNP	C	T	30	192	c.413C>T	c.(412-414)CCC>CTC	p.P138L
Pat_40	Post-Resistance	PLEKHG6	55200	37	12	6421516	6421517	Missense_Mutation	DNP	GG	AA	30	126	c.124_125GG>AA	c.(124-126)GGA>AAA	p.G42K
Pat_40	Post-Resistance	SCNN1A	6337	37	12	6472790	6472790	Missense_Mutation	SNP	G	A	4	10	c.503C>T	c.(502-504)ACC>ATC	p.T168I
Pat_40	Post-Resistance	VAMP1	6843	37	12	6575488	6575488	Missense_Mutation	SNP	C	T	25	90	c.32G>A	c.(31-33)GGG>GAG	p.G11E
Pat_40	Post-Resistance	PRB3	5544	37	12	11420548	11420548	Missense_Mutation	SNP	C	T	49	187	c.635G>A	c.(634-636)GGA>GAA	p.G212E
Pat_40	Post-Resistance	PRB1	5542	37	12	11506835	11506835	Missense_Mutation	SNP	G	A	6	157	c.202C>T	c.(202-204)CCT>TCT	p.P68S
Pat_40	Post-Resistance	SLCO1C1	53919	37	12	20864329	20864329	Nonsense_Mutation	SNP	T	A	64	293	c.414T>A	c.(412-414)TAT>TAA	p.Y138*
Pat_40	Post-Resistance	ABCC9	10060	37	12	22015914	22015914	Missense_Mutation	SNP	G	A	28	97	c.2312C>T	c.(2311-2313)ACT>ATT	p.T771I
Pat_40	Post-Resistance	ADAMTS20	80070	37	12	43846171	43846171	Missense_Mutation	SNP	C	T	79	127	c.1985G>A	c.(1984-1986)GGA>GAA	p.G662E
Pat_40	Post-Resistance	ARID2	196528	37	12	46246081	46246081	Missense_Mutation	SNP	C	T	25	100	c.4175C>T	c.(4174-4176)CCA>CTA	p.P1392L
Pat_40	Post-Resistance	MLL2	8085	37	12	49431867	49431867	Missense_Mutation	SNP	G	T	3	33	c.9272C>A	c.(9271-9273)CCA>CAA	p.P3091Q
Pat_40	Post-Resistance	PRPH	5630	37	12	49691287	49691287	Missense_Mutation	SNP	C	T	5	92	c.1144C>T	c.(1144-1146)CTC>TTC	p.L382F
Pat_40	Post-Resistance	KCNH3	23416	37	12	49951191	49951191	Missense_Mutation	SNP	C	T	4	38	c.2707C>T	c.(2707-2709)CGC>TGC	p.R903C
Pat_40	Post-Resistance	KRT6B	3854	37	12	52841560	52841560	Splice_Site	SNP	A	T	53	185	c.1424_splice	c.e7+1	p.R475_splice

Pat_40	Post-Resistance	KRT6C	286887	37	12	52863452	52863452	Splice_Site	SNP	A	T	69	282	c.1424_splice	c.e7+1	p.R475_splice
Pat_40	Post-Resistance	ITGB7	3695	37	12	53588070	53588070	Missense_Mutation	SNP	G	A	28	167	c.1220C>T	c.(1219-1221)TCT>TTT	p.S407F
Pat_40	Post-Resistance	HOXC10	3226	37	12	54379286	54379286	Missense_Mutation	SNP	C	A	31	143	c.243C>A	c.(241-243)GAC>GAA	p.D81E
Pat_40	Post-Resistance	ITGA5	3678	37	12	54802681	54802681	Missense_Mutation	SNP	G	A	50	87	c.641C>T	c.(640-642)ACC>ATC	p.T214I
Pat_40	Post-Resistance	OR10A7	121364	37	12	55615268	55615268	Missense_Mutation	SNP	C	T	15	107	c.460C>T	c.(460-462)CCT>TCT	p.P154S
Pat_40	Post-Resistance	OR6C2	341416	37	12	55846809	55846809	Missense_Mutation	SNP	G	A	55	80	c.812G>A	c.(811-813)GGA>GAA	p.G271E
Pat_40	Post-Resistance	ATP5B	506	37	12	57037341	57037341	Missense_Mutation	SNP	G	A	44	160	c.638C>T	c.(637-639)ACT>ATT	p.T213I
Pat_40	Post-Resistance	C12orf26	84190	37	12	82832521	82832521	Missense_Mutation	SNP	C	T	68	210	c.1429C>T	c.(1429-1431)CGT>TGT	p.R477C
Pat_40	Post-Resistance	GALNT4	8693	37	12	89917357	89917358	Missense_Mutation	DNP	GG	AA	255	340	c.969_970CC>TT	.(967-972)TACCTT>TATTT	p.L324F
Pat_40	Post-Resistance	STAB2	55576	37	12	104089415	104089415	Missense_Mutation	SNP	G	A	75	147	c.3463G>A	c.(3463-3465)GGC>AGC	p.G1155S
Pat_40	Post-Resistance	TXNRD1	7296	37	12	104645313	104645313	Missense_Mutation	SNP	C	T	3	48	c.100C>T	c.(100-102)CAT>TAT	p.H34Y
Pat_40	Post-Resistance	APPL2	55198	37	12	105610863	105610863	Missense_Mutation	SNP	G	A	30	79	c.269C>T	c.(268-270)TCC>TTC	p.S90F
Pat_40	Post-Resistance	ALKBH2	121642	37	12	109527981	109527981	Missense_Mutation	SNP	C	G	19	97	c.312G>C	c.(310-312)AAG>AAC	p.K104N
Pat_40	Post-Resistance	RPH3A	22895	37	12	113307833	113307833	Missense_Mutation	SNP	G	A	23	21	c.785G>A	c.(784-786)CGG>CAG	p.R262Q
Pat_40	Post-Resistance	MED13L	23389	37	12	116435017	116435017	Missense_Mutation	SNP	C	T	28	104	c.2588G>A	c.(2587-2589)AGG>AAG	p.R863K
Pat_40	Post-Resistance	KSR2	283455	37	12	118016990	118016990	Nonsense_Mutation	SNP	C	T	15	51	c.1172G>A	c.(1171-1173)TGG>TAG	p.W391*
Pat_40	Post-Resistance	KDM2B	84678	37	12	121947645	121947645	Missense_Mutation	SNP	C	T	3	83	c.1372G>A	c.(1372-1374)GGG>AGG	p.G458R
Pat_40	Post-Resistance	RSRC2	65117	37	12	123003404	123003404	Missense_Mutation	SNP	C	T	125	633	c.380G>A	c.(379-381)AGA>AAA	p.R127K
Pat_40	Post-Resistance	DNAH10	196385	37	12	124288369	124288369	Missense_Mutation	SNP	C	T	17	124	c.2422C>T	c.(2422-2424)CCA>TCA	p.P808S
Pat_40	Post-Resistance	ZNF664	144348	37	12	124497079	124497079	Missense_Mutation	SNP	C	A	33	291	c.388C>A	c.(388-390)CTT>ATT	p.L130I
Pat_40	Post-Resistance	FZD10	11211	37	12	130648985	130648985	Missense_Mutation	SNP	G	A	8	28	c.1498G>A	c.(1498-1500)GCC>ACC	p.A500T
Pat_40	Post-Resistance	RIMBP2	23504	37	12	130919401	130919401	Missense_Mutation	SNP	C	T	15	29	c.2080G>A	c.(2080-2082)GAG>AAG	p.E694K
Pat_40	Post-Resistance	ULK1	8408	37	12	132393324	132393324	Missense_Mutation	SNP	G	A	4	80	c.452G>A	c.(451-453)GGC>GAC	p.G151D
Pat_40	Post-Resistance	SACS	26278	37	13	23904499	23904499	Missense_Mutation	SNP	C	T	81	143	c.13516G>A	c.(13516-13518)GCT>ACT	p.A4506T
Pat_40	Post-Resistance	FLT3	2322	37	13	28608541	28608541	Missense_Mutation	SNP	G	A	32	51	c.1601C>T	c.(1600-1602)CCC>CTC	p.P534L
Pat_40	Post-Resistance	ALOX5AP	241	37	13	31309800	31309800	Missense_Mutation	SNP	G	A	3	60	c.58G>A	c.(58-60)GTG>ATG	p.V20M
Pat_40	Post-Resistance	TRPC4	7223	37	13	38225576	38225576	Nonsense_Mutation	SNP	C	T	50	80	c.1905G>A	c.(1903-1905)TGG>TGA	p.W635*
Pat_40	Post-Resistance	FREM2	341640	37	13	39420787	39420787	Missense_Mutation	SNP	A	G	89	125	c.6097A>G	c.(6097-6099)ACG>GCG	p.T2033A
Pat_40	Post-Resistance	ELF1	1997	37	13	41515089	41515089	Missense_Mutation	SNP	A	C	42	89	c.1224T>G	c.(1222-1224)GAT>GAG	p.D408E
Pat_40	Post-Resistance	LOC220429	220429	37	13	50466086	50466086	Missense_Mutation	SNP	T	A	10	14	c.1360T>A	c.(1360-1362)TAC>AAC	p.Y454N
Pat_40	Post-Resistance	OLFM4	10562	37	13	53603032	53603032	Missense_Mutation	SNP	G	A	55	84	c.61G>A	c.(61-63)GAT>AAT	p.D21N
Pat_40	Post-Resistance	DCT	1638	37	13	95131305	95131305	Missense_Mutation	SNP	T	C	112	62	c.205A>G	c.(205-207)AGG>GGG	p.R69G
Pat_40	Post-Resistance	DZIP1	22873	37	13	96241429	96241429	Missense_Mutation	SNP	G	A	57	49	c.2006C>T	c.(2005-2007)CCC>CTC	p.P669L
Pat_40	Post-Resistance	SLC10A2	6555	37	13	103705031	103705031	Missense_Mutation	SNP	G	A	45	113	c.524C>T	c.(523-525)CCT>CTT	p.P175L
Pat_40	Post-Resistance	EFNB2	1948	37	13	107145708	107145708	Missense_Mutation	SNP	A	G	53	116	c.682T>C	c.(682-684)TTT>CTT	p.F228L
Pat_40	Post-Resistance	TNFSF13B	10673	37	13	108922751	108922751	Missense_Mutation	SNP	G	A	4	168	c.403G>A	c.(403-405)GTT>ATT	p.V135I
Pat_40	Post-Resistance	OR4L1	122742	37	14	20528889	20528889	Missense_Mutation	SNP	C	T	90	117	c.686C>T	c.(685-687)TCA>TTA	p.S229L
Pat_40	Post-Resistance	METTL3	56339	37	14	21969242	21969242	Missense_Mutation	SNP	G	A	42	108	c.929C>T	c.(928-930)TCT>TTT	p.S310F
Pat_40	Post-Resistance	MYH6	4624	37	14	23863057	23863057	Nonsense_Mutation	SNP	G	A	19	78	c.2746C>T	c.(2746-2748)CAG>TAG	p.Q916*
Pat_40	Post-Resistance	RALGAPA1	253959	37	14	36207819	36207819	Missense_Mutation	SNP	G	A	141	126	c.1487C>T	c.(1486-1488)TCC>TTC	p.S496F
Pat_40	Post-Resistance	NID2	22795	37	14	52520862	52520862	Missense_Mutation	SNP	C	G	24	53	c.945G>C	c.(943-945)TTG>TTC	p.L315F
Pat_40	Post-Resistance	OTX2	5015	37	14	57272108	57272108	Missense_Mutation	SNP	C	T	27	85	c.67G>A	c.(67-69)GAC>AAC	p.D23N
Pat_40	Post-Resistance	GPR135	64582	37	14	59930927	59930927	Missense_Mutation	SNP	C	T	3	32	c.1018G>A	c.(1018-1020)GTC>ATC	p.V340I
Pat_40	Post-Resistance	SIPA1L1	26037	37	14	72128160	72128160	Missense_Mutation	SNP	C	T	19	155	c.2231C>T	c.(2230-2232)CCG>CTG	p.P744L
Pat_40	Post-Resistance	RBM25	58517	37	14	73570138	73570138	Missense_Mutation	SNP	G	A	17	47	c.1106G>A	c.(1105-1107)CGG>CAG	p.R369Q
Pat_40	Post-Resistance	C14orf115	55237	37	14	74825074	74825074	Missense_Mutation	SNP	C	T	78	85	c.1588C>T	c.(1588-1590)CGC>TGC	p.R530C
Pat_40	Post-Resistance	KCNK13	56659	37	14	90651187	90651187	Missense_Mutation	SNP	A	C	6	80	c.1067A>C	c.(1066-1068)AAC>ACC	p.N356T

Pat_40	Post-Resistance	RPS6KA5	9252	37	14	91409424	91409424	Missense_Mutation	SNP	C	T	54	152	c.616G>A	c.(616-618)GAA>AAA	p.E206K
Pat_40	Post-Resistance	CCDC88C	440193	37	14	91780280	91780281	Missense_Mutation	DNP	CC	TT	4	47	.1879_1880GG>A	c.(1879-1881)GGG>AAG	p.G627K
Pat_40	Post-Resistance	BTBD7	55727	37	14	93712382	93712382	Missense_Mutation	SNP	C	T	4	169	c.2372G>A	c.(2371-2373)CGT>CAT	p.R791H
Pat_40	Post-Resistance	PPP2R5C	5527	37	14	102323122	102323122	Nonsense_Mutation	SNP	G	A	38	343	c.194G>A	c.(193-195)TGG>TAG	p.W65*
Pat_40	Post-Resistance	OR4M2	390538	37	15	22368697	22368697	Missense_Mutation	SNP	G	A	204	311	c.122G>A	c.(121-123)GGA>GAA	p.G41E
Pat_40	Post-Resistance	TJP1	7082	37	15	30008923	30008923	Missense_Mutation	SNP	C	T	26	83	c.4094G>A	c.(4093-4095)AGA>AAA	p.R1365K
Pat_40	Post-Resistance	RPUSD2	27079	37	15	40866150	40866150	Missense_Mutation	SNP	C	T	34	170	c.1328C>T	c.(1327-1329)ACG>ATG	p.T443M
Pat_40	Post-Resistance	NDUFAF1	51103	37	15	41687083	41687083	Missense_Mutation	SNP	C	A	37	145	c.733G>T	c.(733-735)GGG>TGG	p.G245W
Pat_40	Post-Resistance	MGA	23269	37	15	42035184	42035184	Missense_Mutation	SNP	C	T	5	92	c.5026C>T	c.(5026-5028)CCT>TCT	p.P1676S
Pat_40	Post-Resistance	TGM7	116179	37	15	43584182	43584182	Missense_Mutation	SNP	C	T	24	78	c.553G>A	c.(553-555)GGG>AGG	p.G185R
Pat_40	Post-Resistance	TP53BP1	7158	37	15	43748444	43748444	Missense_Mutation	SNP	C	T	20	44	c.2347G>A	c.(2347-2349)GAT>AAT	p.D783N
Pat_40	Post-Resistance	SLC28A2	9153	37	15	45554220	45554220	Missense_Mutation	SNP	C	T	53	206	c.178C>T	c.(178-180)CGG>TGG	p.R60W
Pat_40	Post-Resistance	NEDD4	4734	37	15	56155202	56155202	Missense_Mutation	SNP	G	A	53	117	c.1840C>T	c.(1840-1842)CCA>TCA	p.P614S
Pat_40	Post-Resistance	RFX7	64864	37	15	56395783	56395783	Missense_Mutation	SNP	C	T	3	49	c.487G>A	c.(487-489)GCA>ACA	p.A163T
Pat_40	Post-Resistance	ALDH1A2	8854	37	15	58284979	58284979	Missense_Mutation	SNP	C	T	89	87	c.722G>A	c.(721-723)GGA>GAA	p.G241E
Pat_40	Post-Resistance	TLN2	83660	37	15	63097925	63097925	Missense_Mutation	SNP	G	A	4	140	c.6604G>A	c.(6604-6606)GTG>ATG	p.V2202M
Pat_40	Post-Resistance	CCDC33	80125	37	15	74588131	74588131	Missense_Mutation	SNP	G	A	49	37	c.1132G>A	c.(1132-1134)GCT>ACT	p.A378T
Pat_40	Post-Resistance	IL16	3603	37	15	81558097	81558097	Missense_Mutation	SNP	G	C	7	51	c.519G>C	c.(517-519)AGG>AGC	p.R173S
Pat_40	Post-Resistance	WHAMM	123720	37	15	83485576	83485576	Missense_Mutation	SNP	A	G	2	9	c.916A>G	c.(916-918)ACA>GCA	p.T306A
Pat_40	Post-Resistance	ADAMTSL3	57188	37	15	84539574	84539574	Nonsense_Mutation	SNP	C	T	43	73	c.823C>T	c.(823-825)CAA>TAA	p.Q275*
Pat_40	Post-Resistance	AGBL1	123624	37	15	86687074	86687074	Missense_Mutation	SNP	G	A	25	42	c.122G>A	c.(121-123)AGA>AAA	p.R41K
Pat_40	Post-Resistance	WDR93	56964	37	15	90245132	90245132	Missense_Mutation	SNP	C	T	17	48	c.155C>T	c.(154-156)TCC>TTC	p.S52F
Pat_40	Post-Resistance	TELO2	9894	37	16	1549330	1549330	Missense_Mutation	SNP	T	A	9	30	c.929T>A	c.(928-930)CTC>CAC	p.L310H
Pat_40	Post-Resistance	TXNDC11	51061	37	16	11785884	11785884	Missense_Mutation	SNP	G	A	3	70	c.1243C>T	c.(1243-1245)CGT>TGT	p.R415C
Pat_40	Post-Resistance	ZC3H7A	29066	37	16	11850101	11850101	Missense_Mutation	SNP	C	T	48	216	c.2554G>A	c.(2554-2556)GAA>AAA	p.E852K
Pat_40	Post-Resistance	C16orf88	400506	37	16	19721878	19721878	Missense_Mutation	SNP	C	T	4	140	c.1018G>A	c.(1018-1020)GAT>AAT	p.D340N
Pat_40	Post-Resistance	C16orf88	400506	37	16	19725511	19725511	Missense_Mutation	SNP	C	T	42	126	c.847G>A	c.(847-849)GAG>AAG	p.E283K
Pat_40	Post-Resistance	ACSM5	54988	37	16	20430616	20430616	Missense_Mutation	SNP	C	T	28	73	c.482C>T	c.(481-483)TCC>TTC	p.S161F
Pat_40	Post-Resistance	DNAH3	55567	37	16	20994125	20994125	Nonsense_Mutation	SNP	G	A	96	52	c.7777C>T	c.(7777-7779)CAG>TAG	p.Q2593*
Pat_40	Post-Resistance	HS3ST4	9951	37	16	26147552	26147552	Missense_Mutation	SNP	G	A	8	31	c.1354G>A	c.(1354-1356)GAA>AAA	p.E452K
Pat_40	Post-Resistance	IL27	246778	37	16	28515273	28515273	Missense_Mutation	SNP	G	A	6	34	c.130C>T	c.(130-132)CGG>TGG	p.R44W
Pat_40	Post-Resistance	ATP2A1	487	37	16	28900230	28900230	Missense_Mutation	SNP	G	A	10	431	c.1051G>A	c.(1051-1053)GAC>AAC	p.D351N
Pat_40	Post-Resistance	MVP	9961	37	16	29853121	29853121	Missense_Mutation	SNP	G	A	4	67	c.1396G>A	c.(1396-1398)GCT>ACT	p.A466T
Pat_40	Post-Resistance	ASPHD1	253982	37	16	29916256	29916256	Missense_Mutation	SNP	G	A	28	81	c.1033G>A	c.(1033-1035)GAC>AAC	p.D345N
Pat_40	Post-Resistance	TGFB1I1	7041	37	16	31488207	31488207	Missense_Mutation	SNP	C	T	13	8	c.995C>T	c.(994-996)CCC>CTC	p.P332L
Pat_40	Post-Resistance	ZNF267	10308	37	16	31927613	31927613	Missense_Mutation	SNP	A	T	6	270	c.2043A>T	c.(2041-2043)AGA>AGT	p.R681S
Pat_40	Post-Resistance	SALL1	6299	37	16	51172808	51172808	Missense_Mutation	SNP	G	A	27	70	c.3325C>T	c.(3325-3327)CCG>TCG	p.P1109S
Pat_40	Post-Resistance	CETP	1071	37	16	57005960	57005960	Missense_Mutation	SNP	G	A	4	87	c.715G>A	c.(715-717)GTC>ATC	p.V239I
Pat_40	Post-Resistance	TMEM208	29100	37	16	67262984	67262984	Nonsense_Mutation	SNP	C	T	3	60	c.490C>T	c.(490-492)CGA>TGA	p.R164*
Pat_40	Post-Resistance	FHOD1	29109	37	16	67266028	67266028	Missense_Mutation	SNP	C	T	4	93	c.2116G>A	c.(2116-2118)GGC>AGC	p.G706S
Pat_40	Post-Resistance	FAM65A	79567	37	16	67577052	67577052	Missense_Mutation	SNP	G	A	4	26	c.2423G>A	c.(2422-2424)AGG>AAG	p.R808K
Pat_40	Post-Resistance	RANBP10	57610	37	16	67762379	67762379	Missense_Mutation	SNP	G	A	19	50	c.1388C>T	c.(1387-1389)CCC>CTC	p.P463L
Pat_40	Post-Resistance	NFATC3	4775	37	16	68260296	68260297	Nonsense_Mutation	DNP	CC	TT	24	81	.3150_3151CC>T	148-3153)TCCCAA>TCTT	p.Q1051*
Pat_40	Post-Resistance	CHST5	23563	37	16	75563252	75563252	Missense_Mutation	SNP	G	A	59	37	c.1031C>T	c.(1030-1032)TCG>TTG	p.S344L
Pat_40	Post-Resistance	MLYCD	23417	37	16	83948687	83948687	Missense_Mutation	SNP	G	A	81	215	c.1075G>A	c.(1075-1077)GAA>AAA	p.E359K
Pat_40	Post-Resistance	KLHL36	79786	37	16	84691170	84691170	Missense_Mutation	SNP	G	A	4	79	c.757G>A	c.(757-759)GTG>ATG	p.V253M
Pat_40	Post-Resistance	TRPV3	162514	37	17	3422088	3422088	Missense_Mutation	SNP	C	T	3	48	c.1867G>A	c.(1867-1869)GGC>AGC	p.G623S

Pat_40	Post-Resistance	P2RX1	5023	37	17	3801803	3801803	Missense_Mutation	SNP	C	T	3	60	c.1007G>A	c.(1006-1008)GGC>GAC	p.G336D
Pat_40	Post-Resistance	MINK1	50488	37	17	4796834	4796834	Missense_Mutation	SNP	G	A	4	24	c.2506G>A	c.(2506-2508)GAC>AAC	p.D836N
Pat_40	Post-Resistance	C1QBP	708	37	17	5341507	5341507	Missense_Mutation	SNP	C	T	63	224	c.319G>A	c.(319-321)GGA>AGA	p.G107R
Pat_40	Post-Resistance	PITPNM3	83394	37	17	6380394	6380394	Missense_Mutation	SNP	G	A	11	22	c.1040C>T	c.(1039-1041)ACC>ATC	p.T347I
Pat_40	Post-Resistance	DNAH2	146754	37	17	7722666	7722666	Missense_Mutation	SNP	G	A	4	90	c.10955G>A	c.(10954-10956)AGC>AAC	p.S3652N
Pat_40	Post-Resistance	ARHGEF15	22899	37	17	8222653	8222653	Missense_Mutation	SNP	G	A	91	213	c.2210G>A	c.(2209-2211)GGA>GAA	p.G737E
Pat_40	Post-Resistance	MYOCD	93649	37	17	12626312	12626312	Missense_Mutation	SNP	A	T	60	166	c.402A>T	c.(400-402)AAA>AAT	p.K134N
Pat_40	Post-Resistance	RAI1	10743	37	17	17701574	17701574	Missense_Mutation	SNP	C	T	6	2	c.5312C>T	c.(5311-5313)ACC>ATC	p.T1771I
Pat_40	Post-Resistance	LGALS9	3965	37	17	25975908	25975908	Missense_Mutation	SNP	G	A	103	300	c.968G>A	c.(967-969)GGT>GAT	p.G323D
Pat_40	Post-Resistance	SARM1	23098	37	17	26686410	26686410	Missense_Mutation	SNP	C	T	28	141	c.358C>T	c.(358-360)CGC>TGC	p.R120C
Pat_40	Post-Resistance	SLFN11	91607	37	17	33687340	33687340	Missense_Mutation	SNP	C	T	26	100	c.1120G>A	c.(1120-1122)GGG>AGG	p.G374R
Pat_40	Post-Resistance	RASL10B	91608	37	17	34062220	34062220	Missense_Mutation	SNP	G	A	3	70	c.17G>A	c.(16-18)CGG>CAG	p.R6Q
Pat_40	Post-Resistance	GAS2L2	246176	37	17	34079495	34079495	Missense_Mutation	SNP	C	T	125	116	c.375G>A	c.(373-375)ATG>ATA	p.M125I
Pat_40	Post-Resistance	GPR179	440435	37	17	36492965	36492965	Missense_Mutation	SNP	C	T	7	12	c.1123G>A	c.(1123-1125)GAA>AAA	p.E375K
Pat_40	Post-Resistance	PPP1R1B	84152	37	17	37790219	37790219	Missense_Mutation	SNP	G	A	33	86	c.325G>A	c.(325-327)GGG>AGG	p.G109R
Pat_40	Post-Resistance	PLCD3	113026	37	17	43190532	43190532	Missense_Mutation	SNP	C	T	3	39	c.2089G>A	c.(2089-2091)GCA>ACA	p.A697T
Pat_40	Post-Resistance	TBKBP1	9755	37	17	45776096	45776096	Missense_Mutation	SNP	G	T	9	41	c.589G>T	c.(589-591)GAC>TAC	p.D197Y
Pat_40	Post-Resistance	DHX40	79665	37	17	57644149	57644149	Missense_Mutation	SNP	G	A	21	107	c.274G>A	c.(274-276)GAA>AAA	p.E92K
Pat_40	Post-Resistance	CYB561	1534	37	17	61513475	61513475	Missense_Mutation	SNP	G	A	5	108	c.241C>T	c.(241-243)CGC>TGC	p.R81C
Pat_40	Post-Resistance	SDK2	54549	37	17	71415426	71415426	Missense_Mutation	SNP	G	A	3	35	c.2065C>T	c.(2065-2067)CCC>TCC	p.P689S
Pat_40	Post-Resistance	TSEN54	283989	37	17	73519416	73519416	Missense_Mutation	SNP	G	A	6	191	c.1313G>A	c.(1312-1314)CGG>CAG	p.R438Q
Pat_40	Post-Resistance	TNRC6C	57690	37	17	76083091	76083091	Missense_Mutation	SNP	C	T	96	80	c.3719C>T	c.(3718-3720)TCG>TTG	p.S1240L
Pat_40	Post-Resistance	TMEM105	284186	37	17	79287596	79287596	Missense_Mutation	SNP	C	T	72	45	c.245G>A	c.(244-246)CGA>CAA	p.R82Q
Pat_40	Post-Resistance	USP14	9097	37	18	163321	163322	Nonsense_Mutation	DNP	GG	AA	4	16	c.30_31GG>AA	.(28-33)TGGGGA>TGAAG	p.10_11WG>*F
Pat_40	Post-Resistance	L3MBTL4	91133	37	18	6244575	6244575	Missense_Mutation	SNP	G	A	209	185	c.232C>T	c.(232-234)CCA>TCA	p.P78S
Pat_40	Post-Resistance	LAMA1	284217	37	18	7013833	7013833	Missense_Mutation	SNP	G	A	20	17	c.3344C>T	c.(3343-3345)ACC>ATC	p.T1115I
Pat_40	Post-Resistance	MIB1	57534	37	18	19429266	19429266	Missense_Mutation	SNP	G	A	125	163	c.2503G>A	c.(2503-2505)GGA>AGA	p.G835R
Pat_40	Post-Resistance	CABLES1	91768	37	18	20817209	20817209	Missense_Mutation	SNP	G	A	26	101	c.1446G>A	c.(1444-1446)ATG>ATA	p.M482I
Pat_40	Post-Resistance	DSG4	147409	37	18	28968918	28968918	Missense_Mutation	SNP	G	A	72	175	c.454G>A	c.(454-456)GAT>AAT	p.D152N
Pat_40	Post-Resistance	C18orf26	284254	37	18	52265254	52265254	Missense_Mutation	SNP	C	T	43	160	c.511C>T	c.(511-513)CCT>TCT	p.P171S
Pat_40	Post-Resistance	CDH20	28316	37	18	59174723	59174723	Missense_Mutation	SNP	G	A	56	51	c.947G>A	c.(946-948)GGA>GAA	p.G316E
Pat_40	Post-Resistance	CD226	10666	37	18	67614158	67614158	Missense_Mutation	SNP	G	A	12	59	c.194C>T	c.(193-195)CCT>CTT	p.P65L
Pat_40	Post-Resistance	NETO1	81832	37	18	70423284	70423284	Missense_Mutation	SNP	C	T	40	155	c.967G>A	c.(967-969)GAA>AAA	p.E323K
Pat_40	Post-Resistance	C19orf26	255057	37	19	1231025	1231025	Missense_Mutation	SNP	G	C	3	8	c.1211C>G	c.(1210-1212)CCC>CGC	p.P404R
Pat_40	Post-Resistance	SLC39A3	29985	37	19	2737177	2737177	Missense_Mutation	SNP	C	T	5	92	c.79G>A	c.(79-81)GTG>ATG	p.V27M
Pat_40	Post-Resistance	GNA11	2767	37	19	3113418	3113418	Missense_Mutation	SNP	G	A	3	37	c.412G>A	c.(412-414)GAC>AAC	p.D138N
Pat_40	Post-Resistance	CHAF1A	10036	37	19	4428744	4428745	Missense_Mutation	DNP	CC	TT	28	58	c.1461_1462CC>T	1459-1464)TTCCAT>TTTT	p.H488Y
Pat_40	Post-Resistance	LRG1	116844	37	19	4538773	4538773	Missense_Mutation	SNP	C	T	3	74	c.223G>A	c.(223-225)GTG>ATG	p.V75M
Pat_40	Post-Resistance	PTPRS	5802	37	19	5220014	5220014	Missense_Mutation	SNP	C	T	4	165	c.3701G>A	c.(3700-3702)CGG>CAG	p.R1234Q
Pat_40	Post-Resistance	FUT3	2525	37	19	5844156	5844156	Missense_Mutation	SNP	C	T	35	69	c.695G>A	c.(694-696)GGG>GAG	p.G232E
Pat_40	Post-Resistance	SLC25A41	284427	37	19	6433610	6433610	Missense_Mutation	SNP	G	A	4	89	c.95C>T	c.(94-96)CCC>CTC	p.P32L
Pat_40	Post-Resistance	MYO1F	4542	37	19	8587588	8587588	Nonsense_Mutation	SNP	G	A	3	67	c.2980C>T	c.(2980-2982)CGA>TGA	p.R994*
Pat_40	Post-Resistance	MUC16	94025	37	19	9045677	9045677	Missense_Mutation	SNP	G	A	4	69	c.35954C>T	c.(35953-35955)CCC>CTC	p.P11985L
Pat_40	Post-Resistance	MUC16	94025	37	19	9046043	9046043	Missense_Mutation	SNP	G	A	115	80	c.35588C>T	c.(35587-35589)CCA>CTA	p.P11863L
Pat_40	Post-Resistance	MUC16	94025	37	19	9049653	9049653	Missense_Mutation	SNP	C	T	15	80	c.31978G>A	c.(31978-31980)GGG>AGC	p.G10660R
Pat_40	Post-Resistance	MUC16	94025	37	19	9056776	9056776	Missense_Mutation	SNP	G	A	55	28	c.30670C>T	c.(30670-30672)CCA>TCA	p.P10224S
Pat_40	Post-Resistance	MUC16	94025	37	19	9060955	9060955	Missense_Mutation	SNP	G	A	28	108	c.26491C>T	c.(26491-26493)CCT>TCT	p.P8831S

Pat_40	Post-Resistance	MUC16	94025	37	19	9063550	9063550	Missense_Mutation	SNP	C	T	9	27	c.23896G>A	c.(23896-23898)GAA>AAA	p.E7966K
Pat_40	Post-Resistance	MUC16	94025	37	19	9082516	9082516	Missense_Mutation	SNP	A	T	221	149	c.9299T>A	c.(9298-9300)ATT>AAT	p.I3100N
Pat_40	Post-Resistance	MUC16	94025	37	19	9087347	9087347	Missense_Mutation	SNP	G	A	94	243	c.4468C>T	c.(4468-4470)CCA>TCA	p.P1490S
Pat_40	Post-Resistance	OR7D2	162998	37	19	9297215	9297215	Missense_Mutation	SNP	G	A	26	73	c.758G>A	c.(757-759)GGG>GAG	p.G253E
Pat_40	Post-Resistance	ZNF700	90592	37	19	12060645	12060645	Missense_Mutation	SNP	T	A	13	521	c.1806T>A	c.(1804-1806)AGT>AGA	p.S602R
Pat_40	Post-Resistance	ZNF700	90592	37	19	12060647	12060647	Missense_Mutation	SNP	G	C	9	511	c.1808G>C	c.(1807-1809)TGT>TCT	p.C603S
Pat_40	Post-Resistance	ZNF878	729747	37	19	12155282	12155282	Missense_Mutation	SNP	C	T	27	148	c.1075G>A	c.(1075-1077)GAG>AAG	p.E359K
Pat_40	Post-Resistance	ZNF443	10224	37	19	12542142	12542142	Missense_Mutation	SNP	T	C	9	367	c.844A>G	c.(844-846)AAA>GAA	p.K282E
Pat_40	Post-Resistance	OR7C2	26658	37	19	15053205	15053205	Missense_Mutation	SNP	G	A	19	54	c.905G>A	c.(904-906)AGA>AAA	p.R302K
Pat_40	Post-Resistance	SLC1A6	6511	37	19	15061164	15061164	Missense_Mutation	SNP	G	A	33	88	c.1538C>T	c.(1537-1539)TCA>TTA	p.S513L
Pat_40	Post-Resistance	RASAL3	64926	37	19	15572101	15572101	Nonsense_Mutation	SNP	G	A	13	21	c.472C>T	c.(472-474)CGA>TGA	p.R158*
Pat_40	Post-Resistance	OR10H1	26539	37	19	15918436	15918436	Missense_Mutation	SNP	G	A	42	35	c.412C>T	c.(412-414)CCG>TCG	p.P138S
Pat_40	Post-Resistance	CPAMD8	27151	37	19	17049247	17049247	Missense_Mutation	SNP	C	T	31	21	c.2944G>A	c.(2944-2946)GTC>ATC	p.V982I
Pat_40	Post-Resistance	ZNF14	7561	37	19	19822928	19822928	Missense_Mutation	SNP	C	T	39	122	c.1162G>A	c.(1162-1164)GAG>AAG	p.E388K
Pat_40	Post-Resistance	ZNF93	81931	37	19	20045254	20045254	Missense_Mutation	SNP	C	T	14	314	c.1490C>T	c.(1489-1491)ACT>ATT	p.T497I
Pat_40	Post-Resistance	ZNF93	81931	37	19	20045277	20045277	Missense_Mutation	SNP	G	A	10	328	c.1513G>A	c.(1513-1515)GGA>AGA	p.G505R
Pat_40	Post-Resistance	ZNF429	353088	37	19	21720411	21720411	Missense_Mutation	SNP	T	A	8	221	c.1556T>A	c.(1555-1557)ATC>AAC	p.I519N
Pat_40	Post-Resistance	ZNF429	353088	37	19	21720414	21720414	Missense_Mutation	SNP	T	G	8	225	c.1559T>G	c.(1558-1560)CTG>CGG	p.L520R
Pat_40	Post-Resistance	ZNF208	7757	37	19	22154826	22154826	Missense_Mutation	SNP	C	T	62	197	c.2626G>A	c.(2626-2628)GAA>AAA	p.E876K
Pat_40	Post-Resistance	ZNF208	7757	37	19	22155896	22155896	Missense_Mutation	SNP	A	C	13	279	c.1640T>G	c.(1639-1641)ATT>AGT	p.I547S
Pat_40	Post-Resistance	ZNF208	7757	37	19	22157163	22157163	Missense_Mutation	SNP	C	T	85	78	c.673G>A	c.(673-675)GGA>AGA	p.G225R
Pat_40	Post-Resistance	ZNF99	7652	37	19	22941372	22941372	Missense_Mutation	SNP	G	A	27	73	c.1066C>T	c.(1066-1068)CAT>TAT	p.H356Y
Pat_40	Post-Resistance	ZNF91	7644	37	19	23544724	23544724	Missense_Mutation	SNP	T	C	13	136	c.1057A>G	c.(1057-1059)AAA>GAA	p.K353E
Pat_40	Post-Resistance	ZNF91	7644	37	19	23544783	23544783	Missense_Mutation	SNP	C	T	15	383	c.998G>A	c.(997-999)CGT>CAT	p.R333H
Pat_40	Post-Resistance	ZNF536	9745	37	19	31039065	31039065	Missense_Mutation	SNP	G	A	20	75	c.2539G>A	c.(2539-2541)GGA>AGA	p.G847R
Pat_40	Post-Resistance	RHPN2	85415	37	19	33470912	33470912	Missense_Mutation	SNP	G	A	22	70	c.2051C>T	c.(2050-2052)TCT>TTT	p.S684F
Pat_40	Post-Resistance	SLC7A10	56301	37	19	33702192	33702192	Missense_Mutation	SNP	G	A	20	65	c.955C>T	c.(955-957)CCT>TCT	p.P319S
Pat_40	Post-Resistance	KIRREL2	84063	37	19	36350402	36350402	Missense_Mutation	SNP	C	T	4	50	c.542C>T	c.(541-543)ACC>ATC	p.T181I
Pat_40	Post-Resistance	ZNF420	147923	37	19	37619580	37619580	Missense_Mutation	SNP	G	A	35	119	c.1687G>A	c.(1687-1689)GAA>AAA	p.E563K
Pat_40	Post-Resistance	ZNF383	163087	37	19	37726939	37726939	Nonsense_Mutation	SNP	G	A	32	152	c.195G>A	c.(193-195)TGG>TGA	p.W65*
Pat_40	Post-Resistance	ZNF527	84503	37	19	37871191	37871191	Missense_Mutation	SNP	C	T	35	63	c.173C>T	c.(172-174)TCT>TTT	p.S58F
Pat_40	Post-Resistance	SIPA1L3	23094	37	19	38652944	38652944	Missense_Mutation	SNP	G	A	4	55	c.3713G>A	c.(3712-3714)AGC>AAC	p.S1238N
Pat_40	Post-Resistance	MAP3K10	4294	37	19	40698501	40698501	Missense_Mutation	SNP	G	A	4	66	c.563G>A	c.(562-564)GGT>GAT	p.G188D
Pat_40	Post-Resistance	PRX	57716	37	19	40900057	40900057	Missense_Mutation	SNP	G	A	25	65	c.4202C>T	c.(4201-4203)TCC>TTC	p.S1401F
Pat_40	Post-Resistance	LTBP4	8425	37	19	41128336	41128336	Missense_Mutation	SNP	C	T	2	3	c.3449C>T	c.(3448-3450)CCT>CTT	p.P1150L
Pat_40	Post-Resistance	ZNF574	64763	37	19	42583483	42583483	Missense_Mutation	SNP	C	T	14	88	c.725C>T	c.(724-726)CCC>CTC	p.P242L
Pat_40	Post-Resistance	PRR19	284338	37	19	42814720	42814720	Missense_Mutation	SNP	C	T	45	164	c.899C>T	c.(898-900)CCC>CTC	p.P300L
Pat_40	Post-Resistance	DMPK	1760	37	19	46283155	46283155	Missense_Mutation	SNP	G	A	10	26	c.163C>T	c.(163-165)CGG>TGG	p.R55W
Pat_40	Post-Resistance	SYMPK	8189	37	19	46330823	46330823	Missense_Mutation	SNP	C	T	3	70	c.2126G>A	c.(2125-2127)CGC>CAC	p.R709H
Pat_40	Post-Resistance	PNMAL2	57469	37	19	46997818	46997818	Missense_Mutation	SNP	G	A	14	28	c.905C>T	c.(904-906)CCG>CTG	p.P302L
Pat_40	Post-Resistance	BCAT2	587	37	19	49302959	49302959	Missense_Mutation	SNP	C	T	7	10	c.668G>A	c.(667-669)GGC>GAC	p.G223D
Pat_40	Post-Resistance	PPFIA3	8541	37	19	49649230	49649230	Missense_Mutation	SNP	G	A	5	193	c.2776G>A	c.(2776-2778)GAG>AAG	p.E926K
Pat_40	Post-Resistance	KLK1	3816	37	19	51326967	51326967	Missense_Mutation	SNP	C	T	35	57	c.38G>A	c.(37-39)GGG>GAG	p.G13E
Pat_40	Post-Resistance	KLK3	354	37	19	51359627	51359627	Missense_Mutation	SNP	G	A	5	175	c.178G>A	c.(178-180)GTC>ATC	p.V60I
Pat_40	Post-Resistance	CD33	945	37	19	51729242	51729242	Missense_Mutation	SNP	C	T	18	71	c.602C>T	c.(601-603)CCA>CTA	p.P201L
Pat_40	Post-Resistance	FPR1	2357	37	19	52249241	52249241	Missense_Mutation	SNP	G	A	93	327	c.1007C>T	c.(1006-1008)ACC>ATC	p.T336I
Pat_40	Post-Resistance	ZNF649	65251	37	19	52394619	52394619	Missense_Mutation	SNP	T	C	4	132	c.770A>G	c.(769-771)AAA>AGA	p.K257R

Pat_40	Post-Resistance	ZNF350	59348	37	19	52468403	52468403	Missense_Mutation	SNP	C	T	37	115	c.1303G>A	c.(1303-1305)GAA>AAA	p.E435K
Pat_40	Post-Resistance	ZNF480	147657	37	19	52825082	52825082	Missense_Mutation	SNP	A	C	43	102	c.579A>C	c.(577-579)GAA>GAC	p.E193D
Pat_40	Post-Resistance	LAIR1	3903	37	19	54868145	54868145	Missense_Mutation	SNP	G	A	3	87	c.538C>T	c.(538-540)CTC>TTC	p.L180F
Pat_40	Post-Resistance	LENG8	114823	37	19	54967876	54967876	Missense_Mutation	SNP	C	T	3	14	c.1396C>T	c.(1396-1398)CCG>TCG	p.P466S
Pat_40	Post-Resistance	NLRP2	55655	37	19	55497572	55497572	Missense_Mutation	SNP	G	A	59	33	c.2255G>A	c.(2254-2256)CGA>CAA	p.R752Q
Pat_40	Post-Resistance	NLRP2	55655	37	19	55502033	55502033	Missense_Mutation	SNP	A	C	39	54	c.2701A>C	c.(2701-2703)ACC>CCC	p.T901P
Pat_40	Post-Resistance	NLRP11	204801	37	19	56321318	56321318	Missense_Mutation	SNP	C	T	20	53	c.658G>A	c.(658-660)GAT>AAT	p.D220N
Pat_40	Post-Resistance	NLRP5	126206	37	19	56539203	56539203	Missense_Mutation	SNP	C	T	35	18	c.1604C>T	c.(1603-1605)GCT>GTT	p.A535V
Pat_40	Post-Resistance	GALP	85569	37	19	56696603	56696603	Missense_Mutation	SNP	G	A	37	91	c.315G>A	c.(313-315)ATG>ATA	p.M105I
Pat_40	Post-Resistance	ZIM3	114026	37	19	57646333	57646333	Missense_Mutation	SNP	C	T	45	163	c.1372G>A	c.(1372-1374)GAC>AAC	p.D458N
Pat_40	Post-Resistance	DUXA	503835	37	19	57666725	57666725	Nonsense_Mutation	SNP	G	A	5	6	c.454C>T	c.(454-456)CGA>TGA	p.R152*
Pat_40	Post-Resistance	PXDN	7837	37	2	1647244	1647244	Missense_Mutation	SNP	C	T	4	142	c.3848G>A	c.(3847-3849)CGG>CAG	p.R1283Q
Pat_40	Post-Resistance	MYT1L	23040	37	2	1926835	1926835	Missense_Mutation	SNP	C	T	51	109	c.706G>A	c.(706-708)GAT>AAT	p.D236N
Pat_40	Post-Resistance	COLEC11	78989	37	2	3691415	3691415	Missense_Mutation	SNP	G	A	3	36	c.523G>A	c.(523-525)GGC>AGC	p.G175S
Pat_40	Post-Resistance	ITGB1BP1	9270	37	2	9558775	9558775	Missense_Mutation	SNP	C	T	10	723	c.52G>A	c.(52-54)GAA>AAA	p.E18K
Pat_40	Post-Resistance	NT5C1B	93034	37	2	18758129	18758129	Missense_Mutation	SNP	C	T	67	124	c.1234G>A	c.(1234-1236)GGA>AGA	p.G412R
Pat_40	Post-Resistance	APOB	338	37	2	21229243	21229243	Missense_Mutation	SNP	A	C	39	91	c.10497T>G	c.(10495-10497)GAT>GAG	p.D3499E
Pat_40	Post-Resistance	APOB	338	37	2	21231815	21231815	Missense_Mutation	SNP	G	A	53	154	c.7925C>T	c.(7924-7926)CCA>CTA	p.P2642L
Pat_40	Post-Resistance	KRTCAP3	200634	37	2	27666104	27666104	Missense_Mutation	SNP	G	A	4	30	c.437G>A	c.(436-438)GGG>GAG	p.G146E
Pat_40	Post-Resistance	HEATR5B	54497	37	2	37276944	37276944	Missense_Mutation	SNP	G	A	4	56	c.2548C>T	c.(2548-2550)CGT>TGT	p.R850C
Pat_40	Post-Resistance	C2orf56	55471	37	2	37473259	37473259	Missense_Mutation	SNP	C	T	87	270	c.857C>T	c.(856-858)TCT>TTT	p.S286F
Pat_40	Post-Resistance	C2orf56	55471	37	2	37473261	37473261	Nonsense_Mutation	SNP	C	T	85	273	c.859C>T	c.(859-861)CAA>TAA	p.Q287*
Pat_40	Post-Resistance	ANTXR1	84168	37	2	69304577	69304577	Missense_Mutation	SNP	C	T	108	309	c.599C>T	c.(598-600)CCC>CTC	p.P200L
Pat_40	Post-Resistance	ATP6V1B1	525	37	2	71190758	71190758	Missense_Mutation	SNP	G	A	4	144	c.1117G>A	c.(1117-1119)GTG>ATG	p.V373M
Pat_40	Post-Resistance	MPHOSPH10	10199	37	2	71360620	71360620	Missense_Mutation	SNP	G	A	25	85	c.682G>A	c.(682-684)GAT>AAT	p.D228N
Pat_40	Post-Resistance	DYSF	8291	37	2	71901417	71901417	Missense_Mutation	SNP	G	A	52	49	c.5758G>A	c.(5758-5760)GAT>AAT	p.D1920N
Pat_40	Post-Resistance	KCNIP3	30818	37	2	96048160	96048160	Missense_Mutation	SNP	G	T	4	43	c.591G>T	c.(589-591)ATG>ATT	p.M197I
Pat_40	Post-Resistance	CIAO1	9391	37	2	96936947	96936947	Missense_Mutation	SNP	C	T	51	125	c.878C>T	c.(877-879)TCC>TTC	p.S293F
Pat_40	Post-Resistance	SNRNP200	23020	37	2	96952204	96952204	Missense_Mutation	SNP	G	A	3	81	c.3848C>T	c.(3847-3849)CCT>CTT	p.P1283L
Pat_40	Post-Resistance	INPP4A	3631	37	2	99152605	99152605	Missense_Mutation	SNP	G	T	19	67	c.401G>T	c.(400-402)GGC>GTC	p.G134V
Pat_40	Post-Resistance	MALL	7851	37	2	110873353	110873353	Missense_Mutation	SNP	G	A	2	6	c.17C>T	c.(16-18)CCG>CTG	p.P6L
Pat_40	Post-Resistance	ANAPC1	64682	37	2	112583383	112583383	Missense_Mutation	SNP	G	A	43	85	c.2675C>T	c.(2674-2676)TCC>TTC	p.S892F
Pat_40	Post-Resistance	GLI2	2736	37	2	121708942	121708942	Missense_Mutation	SNP	G	A	61	52	c.378G>A	c.(376-378)ATG>ATA	p.M126I
Pat_40	Post-Resistance	CNTNAP5	129684	37	2	124979303	124979303	Missense_Mutation	SNP	C	T	4	85	c.104C>T	c.(103-105)GCA>GTA	p.A35V
Pat_40	Post-Resistance	LIMS2	55679	37	2	128412421	128412421	Missense_Mutation	SNP	G	A	25	86	c.221C>T	c.(220-222)CCG>CTG	p.P74L
Pat_40	Post-Resistance	NCKAP5	344148	37	2	133541515	133541515	Missense_Mutation	SNP	C	T	7	7	c.2869G>A	c.(2869-2871)GAA>AAA	p.E957K
Pat_40	Post-Resistance	NCKAP5	344148	37	2	133541812	133541812	Missense_Mutation	SNP	C	T	30	56	c.2572G>A	c.(2572-2574)GAA>AAA	p.E858K
Pat_40	Post-Resistance	LCT	3938	37	2	136575471	136575471	Missense_Mutation	SNP	G	A	47	118	c.1147C>T	c.(1147-1149)CCT>TCT	p.P383S
Pat_40	Post-Resistance	THSD7B	80731	37	2	138434125	138434125	Missense_Mutation	SNP	C	T	6	18	c.4684C>T	c.(4684-4686)CCC>TCC	p.P1562S
Pat_40	Post-Resistance	LRP1B	53353	37	2	140995735	140995735	Missense_Mutation	SNP	T	C	68	201	c.13546A>G	c.(13546-13548)ATA>GTA	p.I4516V
Pat_40	Post-Resistance	PABPC1P2	728773	37	2	147345742	147345742	Missense_Mutation	SNP	G	A	3	14	c.202G>A	c.(202-204)GCT>ACT	p.A68T
Pat_40	Post-Resistance	GALNT13	114805	37	2	155157995	155157995	Missense_Mutation	SNP	C	T	67	360	c.1049C>T	c.(1048-1050)CCA>CTA	p.P350L
Pat_40	Post-Resistance	UPP2	151531	37	2	158971625	158971625	Missense_Mutation	SNP	G	A	5	164	c.193G>A	c.(193-195)GGT>AGT	p.G65S
Pat_40	Post-Resistance	IFIH1	64135	37	2	163130442	163130442	Missense_Mutation	SNP	C	T	39	34	c.2317G>A	c.(2317-2319)GAA>AAA	p.E773K
Pat_40	Post-Resistance	SCN1A	6323	37	2	166892572	166892572	Missense_Mutation	SNP	C	T	101	296	c.3382G>A	c.(3382-3384)GAA>AAA	p.E1128K
Pat_40	Post-Resistance	XIRP2	129446	37	2	168100354	168100354	Missense_Mutation	SNP	G	A	56	117	c.2452G>A	c.(2452-2454)GAG>AAG	p.E818K
Pat_40	Post-Resistance	B3GALT1	8708	37	2	168726108	168726108	Missense_Mutation	SNP	C	T	29	21	c.559C>T	c.(559-561)CTT>TTT	p.L187F

Pat_40	Post-Resistance	SPC25	57405	37	2	169745932	169745932	Missense_Mutation	SNP	C	T	45	160	c.98G>A	c.(97-99)AGA>AAA	p.R33K
Pat_40	Post-Resistance	LRP2	4036	37	2	170070368	170070368	Missense_Mutation	SNP	T	A	26	77	c.5839A>T	c.(5839-5841)AAC>TAC	p.N1947Y
Pat_40	Post-Resistance	SLC25A12	8604	37	2	172712353	172712353	Missense_Mutation	SNP	C	T	145	431	c.316G>A	c.(316-318)GTG>ATG	p.V106M
Pat_40	Post-Resistance	TTN	7273	37	2	179452825	179452825	Missense_Mutation	SNP	C	T	68	142	c.55605G>A	c.(55603-55605)ATG>ATA	p.M18535I
Pat_40	Post-Resistance	TTN	7273	37	2	179454489	179454489	Missense_Mutation	SNP	C	T	126	259	c.54259G>A	c.(54259-54261)GAA>AAA	p.E18087K
Pat_40	Post-Resistance	TTN	7273	37	2	179457199	179457199	Missense_Mutation	SNP	G	A	207	214	c.51829C>T	c.(51829-51831)CGT>TGT	p.R17277C
Pat_40	Post-Resistance	TTN	7273	37	2	179464431	179464431	Missense_Mutation	SNP	G	A	32	142	c.48493C>T	c.(48493-48495)CTC>TTC	p.L16165F
Pat_40	Post-Resistance	TTN	7273	37	2	179592468	179592468	Missense_Mutation	SNP	C	T	239	198	c.16105G>A	c.(16105-16107)GAA>AAA	p.E5369K
Pat_40	Post-Resistance	TTN	7273	37	2	179592569	179592569	Missense_Mutation	SNP	T	C	14	18	c.16004A>G	c.(16003-16005)AAA>AGA	p.K5335R
Pat_40	Post-Resistance	TTN	7273	37	2	179600590	179600590	Missense_Mutation	SNP	A	T	4	105	c.10851T>A	c.(10849-10851)GAT>GAA	p.D3617E
Pat_40	Post-Resistance	ZNF804A	91752	37	2	185798364	185798364	Missense_Mutation	SNP	G	A	28	84	c.290G>A	c.(289-291)CGA>CAA	p.R97Q
Pat_40	Post-Resistance	CALCRL	10203	37	2	188245239	188245239	Nonsense_Mutation	SNP	C	T	327	322	c.363G>A	c.(361-363)TGG>TGA	p.W121*
Pat_40	Post-Resistance	COL3A1	1281	37	2	189860512	189860512	Missense_Mutation	SNP	T	C	3	4	c.1604T>C	c.(1603-1605)ATG>ACG	p.M535T
Pat_40	Post-Resistance	DNAH7	56171	37	2	196722260	196722260	Missense_Mutation	SNP	A	C	34	77	c.8255T>G	c.(8254-8256)CTT>CGT	p.L2752R
Pat_40	Post-Resistance	DNAH7	56171	37	2	196729430	196729430	Nonsense_Mutation	SNP	G	A	56	136	c.6949C>T	c.(6949-6951)CGA>TGA	p.R2317*
Pat_40	Post-Resistance	DNAH7	56171	37	2	196746544	196746544	Missense_Mutation	SNP	C	T	106	236	c.5936G>A	c.(5935-5937)GGA>GAA	p.G1979E
Pat_40	Post-Resistance	BMPR2	659	37	2	203417586	203417586	Missense_Mutation	SNP	A	G	131	108	c.1561A>G	c.(1561-1563)ATG>GTG	p.M521V
Pat_40	Post-Resistance	EEF1B2	1933	37	2	207025358	207025358	Missense_Mutation	SNP	A	G	9	379	c.127A>G	c.(127-129)AGC>GGC	p.S43G
Pat_40	Post-Resistance	ZDBF2	57683	37	2	207173258	207173258	Missense_Mutation	SNP	C	T	28	143	c.4006C>T	c.(4006-4008)CCT>TCT	p.P1336S
Pat_40	Post-Resistance	ACADL	33	37	2	211085509	211085509	Missense_Mutation	SNP	C	T	10	10	c.95G>A	c.(94-96)GGG>GAG	p.G32E
Pat_40	Post-Resistance	ERBB4	2066	37	2	212587120	212587120	Missense_Mutation	SNP	G	A	43	98	c.881C>T	c.(880-882)CCA>CTA	p.P294L
Pat_40	Post-Resistance	TNS1	7145	37	2	218750535	218750535	Missense_Mutation	SNP	G	A	40	71	c.673C>T	c.(673-675)CCA>TCA	p.P225S
Pat_40	Post-Resistance	RQCD1	9125	37	2	219449406	219449406	Missense_Mutation	SNP	C	T	311	225	c.392C>T	c.(391-393)CCC>CTC	p.P131L
Pat_40	Post-Resistance	OBSL1	23363	37	2	220434979	220434980	Missense_Mutation	DNP	CC	TT	5	20	c.975_976GG>AA	973-978)GCGGGC>GCAA	p.G326S
Pat_40	Post-Resistance	COL4A3	1285	37	2	228142267	228142267	Missense_Mutation	SNP	A	G	4	4	c.2123A>G	c.(2122-2124)AAG>AGG	p.K708R
Pat_40	Post-Resistance	ECEL1	9427	37	2	233347583	233347583	Missense_Mutation	SNP	G	A	102	188	c.1663C>T	c.(1663-1665)CGG>TGG	p.R555W
Pat_40	Post-Resistance	GIGYF2	26058	37	2	233655585	233655585	Missense_Mutation	SNP	T	C	76	122	c.890T>C	c.(889-891)ATG>ACG	p.M297T
Pat_40	Post-Resistance	SNED1	25992	37	2	241974013	241974013	Missense_Mutation	SNP	G	A	3	61	c.671G>A	c.(670-672)CGT>CAT	p.R224H
Pat_40	Post-Resistance	BOK	666	37	2	242501765	242501765	Missense_Mutation	SNP	G	A	27	42	c.223G>A	c.(223-225)GAT>AAT	p.D75N
Pat_40	Post-Resistance	THAP4	51078	37	2	242573324	242573324	Missense_Mutation	SNP	G	A	30	154	c.248C>T	c.(247-249)TCC>TTC	p.S83F
Pat_40	Post-Resistance	TGM6	343641	37	20	2377248	2377248	Missense_Mutation	SNP	C	T	38	40	c.521C>T	c.(520-522)GCC>GTC	p.A174V
Pat_40	Post-Resistance	VPS16	64601	37	20	2842708	2842708	Missense_Mutation	SNP	G	A	4	56	c.1003G>A	c.(1003-1005)GAG>AAG	p.E335K
Pat_40	Post-Resistance	LRRN4	164312	37	20	6031588	6031588	Missense_Mutation	SNP	G	A	3	56	c.697C>T	c.(697-699)CTC>TTC	p.L233F
Pat_40	Post-Resistance	PAK7	57144	37	20	9560919	9560919	Missense_Mutation	SNP	G	A	110	121	c.863C>T	c.(862-864)TCA>TTA	p.S288L
Pat_40	Post-Resistance	PAK7	57144	37	20	9561263	9561263	Missense_Mutation	SNP	C	T	159	228	c.519G>A	c.(517-519)ATG>ATA	p.M173I
Pat_40	Post-Resistance	POLR3F	10621	37	20	18453489	18453489	Nonsense_Mutation	SNP	C	T	60	65	c.184C>T	c.(184-186)CAG>TAG	p.Q62*
Pat_40	Post-Resistance	TPX2	22974	37	20	30382317	30382317	Missense_Mutation	SNP	G	A	101	209	c.1799G>A	c.(1798-1800)AGA>AAA	p.R600K
Pat_40	Post-Resistance	ASXL1	171023	37	20	31017234	31017234	Missense_Mutation	SNP	G	A	52	78	c.565G>A	c.(565-567)GGG>AGG	p.G189R
Pat_40	Post-Resistance	C20orf186	149954	37	20	31671216	31671217	Missense_Mutation	DNP	CC	TT	62	175	c.213_214CC>TT	211-216)CCCCCC>CCTT	p.P72S
Pat_40	Post-Resistance	EPB41L1	2036	37	20	34797782	34797782	Nonsense_Mutation	SNP	C	T	8	18	c.2041C>T	c.(2041-2043)CGA>TGA	p.R681*
Pat_40	Post-Resistance	MYBL2	4605	37	20	42315498	42315498	Missense_Mutation	SNP	G	A	4	83	c.286G>A	c.(286-288)GAG>AAG	p.E96K
Pat_40	Post-Resistance	HNF4A	3172	37	20	43052879	43052879	Missense_Mutation	SNP	G	A	4	64	c.1114G>A	c.(1114-1116)GAG>AAG	p.E372K
Pat_40	Post-Resistance	RIMS4	140730	37	20	43384905	43384905	Missense_Mutation	SNP	G	A	33	46	c.680C>T	c.(679-681)ACC>ATC	p.T227I
Pat_40	Post-Resistance	CASS4	57091	37	20	55026876	55026876	Missense_Mutation	SNP	G	T	27	166	c.644G>T	c.(643-645)GGG>GTG	p.G215V
Pat_40	Post-Resistance	PRPF6	24148	37	20	62659922	62659922	Missense_Mutation	SNP	G	A	5	112	c.2431G>A	c.(2431-2433)GGT>AGT	p.G811S
Pat_40	Post-Resistance	USP25	29761	37	21	17214827	17214827	Missense_Mutation	SNP	G	A	56	234	c.2305G>A	c.(2305-2307)GAA>AAA	p.E769K
Pat_40	Post-Resistance	C21orf59	56683	37	21	33982292	33982292	Missense_Mutation	SNP	C	T	27	101	c.163G>A	c.(163-165)GGC>AGC	p.G55S

Pat_40	Post-Resistance	SYNJ1	8867	37	21	34014274	34014274	Missense_Mutation	SNP	G	A	4	94	c.3637C>T	c.(3637-3639)CGC>TGC	p.R1213C
Pat_40	Post-Resistance	IL10RB	3588	37	21	34652102	34652102	Missense_Mutation	SNP	C	T	150	220	c.377C>T	c.(376-378)TCT>TTT	p.S126F
Pat_40	Post-Resistance	KCNJ15	3772	37	21	39672159	39672159	Missense_Mutation	SNP	G	A	54	112	c.976G>A	c.(976-978)GAT>AAT	p.D326N
Pat_40	Post-Resistance	DSCAM	1826	37	21	41719737	41719737	Missense_Mutation	SNP	C	T	122	393	c.1070G>A	c.(1069-1071)GGA>GAA	p.G357E
Pat_40	Post-Resistance	TRAPPC10	7109	37	21	45518395	45518395	Missense_Mutation	SNP	C	T	37	178	c.3326C>T	c.(3325-3327)TCG>TTG	p.S1109L
Pat_40	Post-Resistance	PTTG1IP	754	37	21	46275124	46275124	Splice_Site	SNP	C	T	23	39	c.496_splice	c.e5+1	p.G166_splice
Pat_40	Post-Resistance	FTCD	10841	37	21	47570044	47570044	Missense_Mutation	SNP	G	A	3	37	c.895C>T	c.(895-897)CGG>TGG	p.R299W
Pat_40	Post-Resistance	MICAL3	57553	37	22	18370094	18370094	Missense_Mutation	SNP	G	A	37	8	c.1999C>T	c.(1999-2001)CCC>TCC	p.P667S
Pat_40	Post-Resistance	DGCR2	9993	37	22	19050757	19050757	Missense_Mutation	SNP	G	A	3	104	c.583C>T	c.(583-585)CGG>TGG	p.R195W
Pat_40	Post-Resistance	DGCR2	9993	37	22	19055633	19055633	Missense_Mutation	SNP	G	A	4	100	c.308C>T	c.(307-309)GCG>GTG	p.A103V
Pat_40	Post-Resistance	CLTCL1	8218	37	22	19170950	19170950	Missense_Mutation	SNP	A	T	18	46	c.4780T>A	c.(4780-4782)TTG>ATG	p.L1594M
Pat_40	Post-Resistance	BCR	613	37	22	23610637	23610637	Missense_Mutation	SNP	G	A	38	4	c.1795G>A	c.(1795-1797)GGA>AGA	p.G599R
Pat_40	Post-Resistance	VPREB3	29802	37	22	24095239	24095239	Nonsense_Mutation	SNP	G	A	4	109	c.196C>T	c.(196-198)CGA>TGA	p.R66*
Pat_40	Post-Resistance	CHEK2	11200	37	22	29091840	29091841	Missense_Mutation	DNP	TG	CA	17	98	.1116_1117CA>TC	114-1119)TCCAAG>TCTG	p.K373E
Pat_40	Post-Resistance	CCDC157	550631	37	22	30772567	30772567	Missense_Mutation	SNP	T	C	7	397	c.2092T>C	c.(2092-2094)TCT>CCT	p.S698P
Pat_40	Post-Resistance	SYN3	8224	37	22	32992686	32992686	Missense_Mutation	SNP	C	T	5	99	c.748G>A	c.(748-750)GGA>AGA	p.G250R
Pat_40	Post-Resistance	IFT27	11020	37	22	37159046	37159046	Missense_Mutation	SNP	C	T	3	87	c.364G>A	c.(364-366)GGG>AGG	p.G122R
Pat_40	Post-Resistance	SSTR3	6753	37	22	37603516	37603517	Nonsense_Mutation	DNP	CC	TT	40	9	c.326_327GG>AA	c.(325-327)TGG>TAA	p.W109*
Pat_40	Post-Resistance	TRIOBP	11078	37	22	38120290	38120290	Missense_Mutation	SNP	G	C	8	376	c.1727G>C	c.(1726-1728)AGA>ACA	p.R576T
Pat_40	Post-Resistance	H1F0	3005	37	22	38201896	38201897	Nonsense_Mutation	DNP	GA	AT	22	64	c.345_346GA>AT	343-348)AAGAAG>AAATA	p.K116*
Pat_40	Post-Resistance	EP300	2033	37	22	41573548	41573548	Missense_Mutation	SNP	G	A	4	115	c.5833G>A	c.(5833-5835)GTG>ATG	p.V1945M
Pat_40	Post-Resistance	ZC3H7B	23264	37	22	41721779	41721779	Missense_Mutation	SNP	C	T	3	60	c.142C>T	c.(142-144)CGG>TGG	p.R48W
Pat_40	Post-Resistance	PARVB	29780	37	22	44495969	44495969	Missense_Mutation	SNP	C	T	35	99	c.239C>T	c.(238-240)TCC>TTC	p.S80F
Pat_40	Post-Resistance	WNT7B	7477	37	22	46345908	46345908	Missense_Mutation	SNP	C	T	48	42	c.190G>A	c.(190-192)GAG>AAG	p.E64K
Pat_40	Post-Resistance	CELSR1	9620	37	22	46792517	46792517	Missense_Mutation	SNP	G	A	40	7	c.5828C>T	c.(5827-5829)CCG>CTG	p.P1943L
Pat_40	Post-Resistance	PLXNB2	23654	37	22	50715060	50715060	Missense_Mutation	SNP	G	A	60	42	c.5335C>T	c.(5335-5337)CGG>TGG	p.R1779W
Pat_40	Post-Resistance	CNTN6	27255	37	3	1367579	1367579	Missense_Mutation	SNP	G	A	49	57	c.1027G>A	c.(1027-1029)GGA>AGA	p.G343R
Pat_40	Post-Resistance	HRH1	3269	37	3	11301460	11301460	Missense_Mutation	SNP	G	A	5	13	c.737G>A	c.(736-738)GGG>GAG	p.G246E
Pat_40	Post-Resistance	CAND2	23066	37	3	12858191	12858191	Missense_Mutation	SNP	T	C	24	58	c.1760T>C	c.(1759-1761)GTG>GCG	p.V587A
Pat_40	Post-Resistance	NUP210	23225	37	3	13461569	13461569	Missense_Mutation	SNP	C	T	4	6	c.158G>A	c.(157-159)TGC>TAC	p.C53Y
Pat_40	Post-Resistance	PLCL2	23228	37	3	17053134	17053134	Missense_Mutation	SNP	T	A	25	32	c.2272T>A	c.(2272-2274)TTT>ATT	p.F758I
Pat_40	Post-Resistance	LRRC3B	116135	37	3	26751248	26751248	Missense_Mutation	SNP	C	T	44	84	c.85C>T	c.(85-87)CAT>TAT	p.H29Y
Pat_40	Post-Resistance	DYNC1LI1	51143	37	3	32571119	32571119	Nonsense_Mutation	SNP	G	A	3	55	c.1219C>T	c.(1219-1221)CGA>TGA	p.R407*
Pat_40	Post-Resistance	GLB1	2720	37	3	33087713	33087713	Missense_Mutation	SNP	G	A	4	96	c.967C>T	c.(967-969)CCC>TCC	p.P323S
Pat_40	Post-Resistance	SCN5A	6331	37	3	38648165	38648165	Nonsense_Mutation	SNP	G	A	7	3	c.1135C>T	c.(1135-1137)CAG>TAG	p.Q379*
Pat_40	Post-Resistance	SCN10A	6336	37	3	38793820	38793820	Missense_Mutation	SNP	G	A	19	18	c.1645C>T	c.(1645-1647)CTC>TTC	p.L549F
Pat_40	Post-Resistance	CTNNB1	1499	37	3	41266137	41266137	Missense_Mutation	SNP	C	T	22	64	c.134C>T	c.(133-135)TCT>TTT	p.S45F
Pat_40	Post-Resistance	CXCR6	10663	37	3	45988860	45988860	Missense_Mutation	SNP	G	A	16	28	c.887G>A	c.(886-888)CGA>CAA	p.R296Q
Pat_40	Post-Resistance	CCR3	1232	37	3	46307479	46307479	Missense_Mutation	SNP	A	G	31	47	c.830A>G	c.(829-831)AAG>AGG	p.K277R
Pat_40	Post-Resistance	PTH1R	5745	37	3	46939575	46939575	Nonsense_Mutation	SNP	C	T	4	89	c.436C>T	c.(436-438)CGA>TGA	p.R146*
Pat_40	Post-Resistance	SCAP	22937	37	3	47476586	47476586	Missense_Mutation	SNP	A	C	37	59	c.164T>G	c.(163-165)GTG>GGG	p.V55G
Pat_40	Post-Resistance	PLXNB1	5364	37	3	48459905	48459905	Missense_Mutation	SNP	A	G	10	17	c.3002T>C	c.(3001-3003)CTG>CCG	p.L1001P
Pat_40	Post-Resistance	PLXNB1	5364	37	3	48465923	48465923	Missense_Mutation	SNP	G	A	2	4	c.98C>T	c.(97-99)ACG>ATG	p.T33M
Pat_40	Post-Resistance	LAMB2	3913	37	3	49163916	49163916	Missense_Mutation	SNP	G	A	43	36	c.2033C>T	c.(2032-2034)CCT>CTT	p.P678L
Pat_40	Post-Resistance	DOCK3	1795	37	3	51395405	51395405	Missense_Mutation	SNP	G	T	48	84	c.4781G>T	c.(4780-4782)GGA>GTA	p.G1594V
Pat_40	Post-Resistance	DOCK3	1795	37	3	51418581	51418582	Missense_Mutation	DNP	CC	TT	22	49	.5684_5685CC>TT	c.(5683-5685)TCC>TTT	p.S1895F
Pat_40	Post-Resistance	ITIH4	3700	37	3	52850994	52850994	Missense_Mutation	SNP	A	G	3	94	c.2377T>C	c.(2377-2379)TGG>CGG	p.W793R

Pat_40	Post-Resistance	TKT	7086	37	3	53263409	53263409	Missense_Mutation	SNP	G	A	9	10	c.1151C>T	c.(1150-1152)CCC>CTC	p.P384L
Pat_40	Post-Resistance	CACNA1D	776	37	3	53781378	53781378	Missense_Mutation	SNP	C	T	71	76	c.3217C>T	c.(3217-3219)CGT>TGT	p.R1073C
Pat_40	Post-Resistance	CACNA2D3	55799	37	3	54615870	54615870	Missense_Mutation	SNP	G	A	26	25	c.929G>A	c.(928-930)GGA>GAA	p.G310E
Pat_40	Post-Resistance	C3orf63	23272	37	3	56680705	56680705	Missense_Mutation	SNP	A	G	32	85	c.2060T>C	c.(2059-2061)TTA>TCA	p.L687S
Pat_40	Post-Resistance	PXK	54899	37	3	58410506	58410506	Missense_Mutation	SNP	C	T	757	32	c.1556C>T	c.(1555-1557)CCA>CTA	p.P519L
Pat_40	Post-Resistance	CNTN3	5067	37	3	74315713	74315713	Missense_Mutation	SNP	C	T	41	876	c.2905G>A	c.(2905-2907)GAC>AAC	p.D969N
Pat_40	Post-Resistance	PROS1	5627	37	3	93624748	93624748	Missense_Mutation	SNP	A	C	25	63	c.481T>G	c.(481-483)TGC>GGC	p.C161G
Pat_40	Post-Resistance	IMPG2	50939	37	3	100962459	100962459	Nonsense_Mutation	SNP	G	A	15	10	c.2716C>T	c.(2716-2718)CGA>TGA	p.R906*
Pat_40	Post-Resistance	CD96	10225	37	3	111325559	111325559	Missense_Mutation	SNP	C	T	88	124	c.1148C>T	c.(1147-1149)TCC>TTC	p.S383F
Pat_40	Post-Resistance	MBD4	8930	37	3	129155742	129155742	Missense_Mutation	SNP	C	T	52	101	c.745G>A	c.(745-747)GGA>AGA	p.G249R
Pat_40	Post-Resistance	NMNAT3	349565	37	3	139297817	139297817	Missense_Mutation	SNP	G	C	15	34	c.190C>G	c.(190-192)CGA>GGA	p.R64G
Pat_40	Post-Resistance	AADACL2	344752	37	3	151475240	151475240	Missense_Mutation	SNP	G	A	56	91	c.1064G>A	c.(1063-1065)CGA>CAA	p.R355Q
Pat_40	Post-Resistance	SLITRK3	22865	37	3	164905945	164905945	Missense_Mutation	SNP	G	A	10	13	c.2674C>T	c.(2674-2676)CCT>TCT	p.P892S
Pat_40	Post-Resistance	FNDC3B	64778	37	3	171965431	171965432	Missense_Mutation	DNP	CC	TT	126	264	c.373_374CC>TT	c.(373-375)CCC>TTC	p.P125F
Pat_40	Post-Resistance	FNDC3B	64778	37	3	172115059	172115059	Missense_Mutation	SNP	G	A	35	66	c.3409G>A	c.(3409-3411)GAG>AAG	p.E1137K
Pat_40	Post-Resistance	KLHL6	89857	37	3	183273180	183273180	Missense_Mutation	SNP	C	T	4	207	c.262G>A	c.(262-264)GTG>ATG	p.V88M
Pat_40	Post-Resistance	ABCF3	55324	37	3	183910456	183910456	Missense_Mutation	SNP	G	A	11	14	c.1637G>A	c.(1636-1638)CGG>CAG	p.R546Q
Pat_40	Post-Resistance	C3orf59	151963	37	3	192516621	192516621	Missense_Mutation	SNP	G	A	13	29	c.1030C>T	c.(1030-1032)CCT>TCT	p.P344S
Pat_40	Post-Resistance	C3orf59	151963	37	3	192517362	192517362	Missense_Mutation	SNP	C	T	4	99	c.289G>A	c.(289-291)GTG>ATG	p.V97M
Pat_40	Post-Resistance	ZNF721	170960	37	4	436514	436514	Missense_Mutation	SNP	C	T	65	302	c.1742G>A	c.(1741-1743)GGA>GAA	p.G581E
Pat_40	Post-Resistance	ZNF721	170960	37	4	436658	436658	Missense_Mutation	SNP	A	T	12	373	c.1598T>A	c.(1597-1599)GTA>GAA	p.V533E
Pat_40	Post-Resistance	PIGG	54872	37	4	502757	502757	Missense_Mutation	SNP	C	T	24	59	c.899C>T	c.(898-900)CCC>CTC	p.P300L
Pat_40	Post-Resistance	FAM193A	8603	37	4	2696821	2696821	Missense_Mutation	SNP	G	A	5	177	c.2368G>A	c.(2368-2370)GAC>AAC	p.D790N
Pat_40	Post-Resistance	ADD1	118	37	4	2906492	2906492	Missense_Mutation	SNP	G	T	10	202	c.1163G>T	c.(1162-1164)GGC>GTC	p.G388V
Pat_40	Post-Resistance	HTT	3064	37	4	3208651	3208651	Missense_Mutation	SNP	C	T	4	104	c.6022C>T	c.(6022-6024)CGC>TGC	p.R2008C
Pat_40	Post-Resistance	EVC2	132884	37	4	5624469	5624469	Missense_Mutation	SNP	G	T	4	61	c.2296C>A	c.(2296-2298)CGT>AGT	p.R766S
Pat_40	Post-Resistance	CRMP1	1400	37	4	5843131	5843131	Missense_Mutation	SNP	C	T	98	283	c.715G>A	c.(715-717)GCC>ACC	p.A239T
Pat_40	Post-Resistance	JAKMIP1	152789	37	4	6066645	6066645	Missense_Mutation	SNP	C	T	46	37	c.1393G>A	c.(1393-1395)GAC>AAC	p.D465N
Pat_40	Post-Resistance	WFS1	7466	37	4	6303478	6303478	Nonsense_Mutation	SNP	C	A	66	243	c.1956C>A	c.(1954-1956)TAC>TAA	p.Y652*
Pat_40	Post-Resistance	AFAP1	60312	37	4	7770626	7770626	Missense_Mutation	SNP	C	T	30	97	c.2111G>A	c.(2110-2112)AGC>AAC	p.S704N
Pat_40	Post-Resistance	CPEB2	132864	37	4	15063811	15063811	Missense_Mutation	SNP	C	T	167	518	c.1469C>T	c.(1468-1470)TCC>TTC	p.S490F
Pat_40	Post-Resistance	RBPJ	3516	37	4	26431526	26431526	Missense_Mutation	SNP	C	T	10	33	c.934C>T	c.(934-936)CCA>TCA	p.P312S
Pat_40	Post-Resistance	GUF1	60558	37	4	44691864	44691864	Missense_Mutation	SNP	G	A	44	111	c.1207G>A	c.(1207-1209)GGA>AGA	p.G403R
Pat_40	Post-Resistance	UGT2B28	54490	37	4	70146351	70146351	Missense_Mutation	SNP	G	A	150	338	c.133G>A	c.(133-135)GAG>AAG	p.E45K
Pat_40	Post-Resistance	UGT2B28	54490	37	4	70146547	70146547	Missense_Mutation	SNP	C	T	49	177	c.329C>T	c.(328-330)TCA>TTA	p.S110L
Pat_40	Post-Resistance	ALB	213	37	4	74285291	74285291	Missense_Mutation	SNP	G	A	81	61	c.1720G>A	c.(1720-1722)GAT>AAT	p.D574N
Pat_40	Post-Resistance	FRAS1	80144	37	4	79301056	79301056	Missense_Mutation	SNP	G	A	43	53	c.3469G>A	c.(3469-3471)GGA>AGA	p.G1157R
Pat_40	Post-Resistance	BMP2K	55589	37	4	79832861	79832861	Missense_Mutation	SNP	G	T	65	256	c.3160G>T	c.(3160-3162)GAT>TAT	p.D1054Y
Pat_40	Post-Resistance	BMP3	651	37	4	81967248	81967248	Missense_Mutation	SNP	G	A	127	93	c.673G>A	c.(673-675)GGA>AGA	p.G225R
Pat_40	Post-Resistance	RASGEF1B	153020	37	4	82378748	82378748	Missense_Mutation	SNP	T	A	25	252	c.205A>T	c.(205-207)AGT>TGT	p.S69C
Pat_40	Post-Resistance	HPSE	10855	37	4	84230632	84230632	Missense_Mutation	SNP	G	A	5	195	c.907C>T	c.(907-909)CGG>TGG	p.R303W
Pat_40	Post-Resistance	ADH1B	125	37	4	100232022	100232022	Missense_Mutation	SNP	C	T	78	250	c.1003G>A	c.(1003-1005)GAT>AAT	p.D335N
Pat_40	Post-Resistance	ADH7	131	37	4	100349774	100349774	Missense_Mutation	SNP	C	T	131	324	c.170G>A	c.(169-171)GGA>GAA	p.G57E
Pat_40	Post-Resistance	CENPE	1062	37	4	104072535	104072535	Splice_Site	SNP	C	T	7	14	c.3238_splice	c.e26-1	p.T1080_splice
Pat_40	Post-Resistance	EGF	1950	37	4	110883099	110883099	Missense_Mutation	SNP	C	T	218	159	c.1270C>T	c.(1270-1272)CCT>TCT	p.P424S
Pat_40	Post-Resistance	EGF	1950	37	4	110884429	110884430	Missense_Mutation	DNP	GG	AA	109	129	.1413_1414GG>A	411-1416)CTGGAT>CTA	p.D472N
Pat_40	Post-Resistance	LARP7	51574	37	4	113568238	113568238	Missense_Mutation	SNP	C	T	49	182	c.601C>T	c.(601-603)CCT>TCT	p.P201S

Pat_40	Post-Resistance	PHF17	79960	37	4	129773398	129773398	Missense_Mutation	SNP	A	G	14	148	c.671A>G	c.(670-672)GAC>GGC	p.D224G
Pat_40	Post-Resistance	TBC1D9	23158	37	4	141590792	141590792	Missense_Mutation	SNP	T	C	14	43	c.1433A>G	c.(1432-1434)AAA>AGA	p.K478R
Pat_40	Post-Resistance	MAB21L2	10586	37	4	151504863	151504863	Missense_Mutation	SNP	G	A	51	37	c.682G>A	c.(682-684)GAC>AAC	p.D228N
Pat_40	Post-Resistance	TLR2	7097	37	4	154625141	154625141	Missense_Mutation	SNP	C	T	30	34	c.1082C>T	c.(1081-1083)TCA>TTA	p.S361L
Pat_40	Post-Resistance	RBM46	166863	37	4	155719334	155719334	Missense_Mutation	SNP	C	T	47	136	c.523C>T	c.(523-525)CCA>TCA	p.P175S
Pat_40	Post-Resistance	GUCY1A3	2982	37	4	156618119	156618119	Missense_Mutation	SNP	G	A	19	53	c.100G>A	c.(100-102)GCA>ACA	p.A34T
Pat_40	Post-Resistance	GRIA2	2891	37	4	158284078	158284078	Missense_Mutation	SNP	G	A	42	148	c.2534G>A	c.(2533-2535)CGA>CAA	p.R845Q
Pat_40	Post-Resistance	TLL1	7092	37	4	166963247	166963247	Missense_Mutation	SNP	C	T	94	267	c.1330C>T	c.(1330-1332)CGT>TGT	p.R444C
Pat_40	Post-Resistance	DDX60	55601	37	4	169227743	169227743	Nonsense_Mutation	SNP	C	T	42	203	c.393G>A	c.(391-393)TGG>TGA	p.W131*
Pat_40	Post-Resistance	PALLD	23022	37	4	169630191	169630191	Missense_Mutation	SNP	C	A	18	275	c.1514C>A	c.(1513-1515)ACC>AAC	p.T505N
Pat_40	Post-Resistance	NEK1	4750	37	4	170506576	170506576	Missense_Mutation	SNP	C	T	25	48	c.731G>A	c.(730-732)AGG>AAG	p.R244K
Pat_40	Post-Resistance	C4orf41	60684	37	4	184598649	184598649	Missense_Mutation	SNP	G	A	66	192	c.773G>A	c.(772-774)AGA>AAA	p.R258K
Pat_40	Post-Resistance	FAT1	2195	37	4	187541333	187541333	Missense_Mutation	SNP	G	A	35	105	c.6407C>T	c.(6406-6408)TCA>TTA	p.S2136L
Pat_40	Post-Resistance	AHRR	57491	37	5	433016	433016	Missense_Mutation	SNP	C	A	3	5	c.1132C>A	c.(1132-1134)CTC>ATC	p.L378I
Pat_40	Post-Resistance	ADAMTS16	170690	37	5	5262860	5262860	Missense_Mutation	SNP	G	A	41	109	c.2753G>A	c.(2752-2754)GGG>GAG	p.G918E
Pat_40	Post-Resistance	FASTKD3	79072	37	5	7859553	7859553	Missense_Mutation	SNP	C	T	37	73	c.1984G>A	c.(1984-1986)GAA>AAA	p.E662K
Pat_40	Post-Resistance	MTRR	4552	37	5	7892881	7892881	Missense_Mutation	SNP	A	G	286	188	c.1493A>G	c.(1492-1494)AAC>AGC	p.N498S
Pat_40	Post-Resistance	DNAH5	1767	37	5	13700913	13700913	Nonsense_Mutation	SNP	C	T	151	133	c.13559G>A	c.(13558-13560)TGG>TAG	p.W4520*
Pat_40	Post-Resistance	DNAH5	1767	37	5	13823473	13823473	Missense_Mutation	SNP	C	T	18	58	c.6586G>A	c.(6586-6588)GAG>AAG	p.E2196K
Pat_40	Post-Resistance	GOLPH3	64083	37	5	32126541	32126541	Missense_Mutation	SNP	C	G	101	106	c.674G>C	c.(673-675)TGG>TCG	p.W225S
Pat_40	Post-Resistance	C9	735	37	5	39311479	39311479	Missense_Mutation	SNP	C	T	44	85	c.871G>A	c.(871-873)GAA>AAA	p.E291K
Pat_40	Post-Resistance	ITGA1	3672	37	5	52221138	52221138	Missense_Mutation	SNP	G	A	38	126	c.2434G>A	c.(2434-2436)GAA>AAA	p.E812K
Pat_40	Post-Resistance	DDX4	54514	37	5	55110910	55110910	Missense_Mutation	SNP	C	T	116	296	c.1897C>T	c.(1897-1899)CGT>TGT	p.R633C
Pat_40	Post-Resistance	F2RL1	2150	37	5	76128587	76128587	Missense_Mutation	SNP	G	A	53	120	c.155G>A	c.(154-156)GGA>GAA	p.G52E
Pat_40	Post-Resistance	GPR98	84059	37	5	89990494	89990494	Missense_Mutation	SNP	G	A	48	37	c.7921G>A	c.(7921-7923)GGA>AGA	p.G2641R
Pat_40	Post-Resistance	MCTP1	79772	37	5	94204141	94204141	Missense_Mutation	SNP	A	C	47	84	c.2333T>G	c.(2332-2334)TTT>TGT	p.F778C
Pat_40	Post-Resistance	EPB41L4A	64097	37	5	111545588	111545588	Splice_Site	SNP	C	T	63	63	c.1178_splice	c.e13+1	p.S393_splice
Pat_40	Post-Resistance	MCC	4163	37	5	112824014	112824014	Missense_Mutation	SNP	C	T	3	44	c.98G>A	c.(97-99)AGC>AAC	p.S33N
Pat_40	Post-Resistance	FAM170A	340069	37	5	118969746	118969746	Missense_Mutation	SNP	T	G	67	58	c.303T>G	c.(301-303)CAT>CAG	p.H101Q
Pat_40	Post-Resistance	FTMT	94033	37	5	121188229	121188229	Missense_Mutation	SNP	G	A	64	178	c.571G>A	c.(571-573)GAT>AAT	p.D191N
Pat_40	Post-Resistance	P4HA2	8974	37	5	131545009	131545009	Missense_Mutation	SNP	C	A	93	75	c.725G>T	c.(724-726)CGA>CTA	p.R242L
Pat_40	Post-Resistance	KIF3A	11127	37	5	132037886	132037886	Missense_Mutation	SNP	C	T	54	143	c.1696G>A	c.(1696-1698)GAA>AAA	p.E566K
Pat_40	Post-Resistance	TIFAB	497189	37	5	134785386	134785386	Missense_Mutation	SNP	C	T	61	113	c.244G>A	c.(244-246)GGC>AGC	p.G82S
Pat_40	Post-Resistance	KLHL3	26249	37	5	136974690	136974691	Missense_Mutation	DNP	CC	TT	23	65	.1170_1171GG>A	168-1173)GCGGTG>GCA	p.V391M
Pat_40	Post-Resistance	PCDHA2	56146	37	5	140175006	140175006	Missense_Mutation	SNP	C	T	43	24	c.457C>T	c.(457-459)CCT>TCT	p.P153S
Pat_40	Post-Resistance	PCDHA3	56145	37	5	140182748	140182748	Missense_Mutation	SNP	G	A	30	75	c.1966G>A	c.(1966-1968)GAA>AAA	p.E656K
Pat_40	Post-Resistance	PCDHA4	56144	37	5	140187721	140187721	Missense_Mutation	SNP	G	A	45	140	c.949G>A	c.(949-951)GAA>AAA	p.E317K
Pat_40	Post-Resistance	PCDHA5	56143	37	5	140202835	140202835	Missense_Mutation	SNP	C	T	39	85	c.1475C>T	c.(1474-1476)TCG>TTG	p.S492L
Pat_40	Post-Resistance	PCDHA10	56139	37	5	140237555	140237555	Missense_Mutation	SNP	C	T	25	15	c.1922C>T	c.(1921-1923)TCG>TTG	p.S641L
Pat_40	Post-Resistance	PCDHB6	56130	37	5	140530709	140530709	Missense_Mutation	SNP	G	A	100	76	c.871G>A	c.(871-873)GAA>AAA	p.E291K
Pat_40	Post-Resistance	PCDHB6	56130	37	5	140531786	140531786	Missense_Mutation	SNP	C	T	9	54	c.1948C>T	c.(1948-1950)CGC>TGC	p.R650C
Pat_40	Post-Resistance	PCDHGB2	56103	37	5	140741165	140741165	Missense_Mutation	SNP	C	T	28	20	c.1463C>T	c.(1462-1464)TCC>TTC	p.S488F
Pat_40	Post-Resistance	PCDHGB3	56102	37	5	140750571	140750571	Missense_Mutation	SNP	G	A	36	23	c.610G>A	c.(610-612)GAG>AAG	p.E204K
Pat_40	Post-Resistance	PCDHGA8	9708	37	5	140773695	140773695	Missense_Mutation	SNP	G	A	3	70	c.1315G>A	c.(1315-1317)GCT>ACT	p.A439T
Pat_40	Post-Resistance	PCDHGC5	56097	37	5	140869774	140869774	Missense_Mutation	SNP	C	T	3	61	c.967C>T	c.(967-969)CGT>TGT	p.R323C
Pat_40	Post-Resistance	ARHGAP26	23092	37	5	142311641	142311641	Missense_Mutation	SNP	C	T	50	168	c.1058C>T	c.(1057-1059)TCG>TTG	p.S353L
Pat_40	Post-Resistance	FBXO38	81545	37	5	147778639	147778639	Missense_Mutation	SNP	G	A	89	144	c.206G>A	c.(205-207)CGA>CAA	p.R69Q

Pat_40	Post-Resistance	CSF1R	1436	37	5	149460399	149460399	Missense_Mutation	SNP	C	T	3	27	c.238G>A	c.(238-240)GGG>AGG	p.G80R
Pat_40	Post-Resistance	SLC36A2	153201	37	5	150704953	150704953	Missense_Mutation	SNP	C	T	25	40	c.904G>A	c.(904-906)GGA>AGA	p.G302R
Pat_40	Post-Resistance	SLIT3	6586	37	5	168135006	168135006	Missense_Mutation	SNP	C	T	4	79	c.2819G>A	c.(2818-2820)CGC>CAC	p.R940H
Pat_40	Post-Resistance	CCDC99	54908	37	5	169015538	169015538	Nonsense_Mutation	SNP	C	T	53	179	c.118C>T	c.(118-120)CAA>TAA	p.Q40*
Pat_40	Post-Resistance	DOCK2	1794	37	5	169461444	169461444	Missense_Mutation	SNP	C	T	5	139	c.3509C>T	c.(3508-3510)TCG>TTG	p.S1170L
Pat_40	Post-Resistance	CPLX2	10814	37	5	175305922	175305922	Missense_Mutation	SNP	G	A	12	31	c.43G>A	c.(43-45)GAC>AAC	p.D15N
Pat_40	Post-Resistance	NSD1	64324	37	5	176631253	176631253	Missense_Mutation	SNP	G	A	29	69	c.1196G>A	c.(1195-1197)AGG>AAG	p.R399K
Pat_40	Post-Resistance	DOK3	79930	37	5	176931802	176931802	Missense_Mutation	SNP	C	T	14	35	c.755G>A	c.(754-756)GGC>GAC	p.G252D
Pat_40	Post-Resistance	BTNL8	79908	37	5	180377053	180377053	Missense_Mutation	SNP	G	A	16	66	c.1012G>A	c.(1012-1014)GCA>ACA	p.A338T
Pat_40	Post-Resistance	BTNL3	10917	37	5	180424335	180424335	Missense_Mutation	SNP	G	A	13	50	c.520G>A	c.(520-522)GAT>AAT	p.D174N
Pat_40	Post-Resistance	BTNL3	10917	37	5	180432588	180432588	Missense_Mutation	SNP	C	T	89	51	c.1117C>T	c.(1117-1119)CCC>TCC	p.P373S
Pat_40	Post-Resistance	GNB2L1	10399	37	5	180666075	180666075	Missense_Mutation	SNP	C	T	138	270	c.628G>A	c.(628-630)GGA>AGA	p.G210R
Pat_40	Post-Resistance	EXOC2	55770	37	6	572614	572614	Missense_Mutation	SNP	G	A	56	65	c.1349C>T	c.(1348-1350)GCC>GTC	p.A450V
Pat_40	Post-Resistance	WRNIP1	56897	37	6	2766550	2766550	Missense_Mutation	SNP	C	T	3	52	c.694C>T	c.(694-696)CGT>TGT	p.R232C
Pat_40	Post-Resistance	RANBP9	10048	37	6	13634740	13634741	Missense_Mutation	DNP	CC	TT	66	80	.1717_1718GG>A	c.(1717-1719)GGA>AAA	p.G573K
Pat_40	Post-Resistance	NUP153	9972	37	6	17675825	17675825	Missense_Mutation	SNP	C	T	33	128	c.511G>A	c.(511-513)GAT>AAT	p.D171N
Pat_40	Post-Resistance	CDKAL1	54901	37	6	21201495	21201495	Missense_Mutation	SNP	G	T	8	172	c.1538G>T	c.(1537-1539)GGT>GTT	p.G513V
Pat_40	Post-Resistance	GPLD1	2822	37	6	24445860	24445860	Missense_Mutation	SNP	C	T	50	62	c.1934G>A	c.(1933-1935)GGG>GAG	p.G645E
Pat_40	Post-Resistance	HIST1H2BC	8347	37	6	26123919	26123919	Missense_Mutation	SNP	C	T	219	313	c.214G>A	c.(214-216)GAG>AAG	p.E72K
Pat_40	Post-Resistance	OR5V1	81696	37	6	29323822	29323822	Missense_Mutation	SNP	T	A	27	332	c.151A>T	c.(151-153)ACT>TCT	p.T51S
Pat_40	Post-Resistance	CCHCR1	54535	37	6	31124662	31124662	Missense_Mutation	SNP	T	C	4	149	c.76A>G	c.(76-78)AGA>GGA	p.R26G
Pat_40	Post-Resistance	HLA-B	3106	37	6	31322904	31322904	Missense_Mutation	SNP	A	T	79	145	c.992T>A	c.(991-993)ATG>AAG	p.M331K
Pat_40	Post-Resistance	MSH5	4439	37	6	31727727	31727727	Missense_Mutation	SNP	C	T	15	30	c.1660C>T	c.(1660-1662)CTT>TTT	p.L554F
Pat_40	Post-Resistance	C6orf27	80737	37	6	31735258	31735259	Missense_Mutation	DNP	GG	AA	23	70	.1669_1670CC>T	c.(1669-1671)CCT>TTT	p.P557F
Pat_40	Post-Resistance	PBX2	5089	37	6	32157623	32157623	Missense_Mutation	SNP	C	T	7	15	c.70G>A	c.(70-72)GAG>AAG	p.E24K
Pat_40	Post-Resistance	ZNF318	24149	37	6	43323693	43323693	Missense_Mutation	SNP	G	A	28	120	c.1379C>T	c.(1378-1380)CCC>CTC	p.P460L
Pat_40	Post-Resistance	CAPN11	11131	37	6	44144035	44144035	Missense_Mutation	SNP	C	T	76	143	c.961C>T	c.(961-963)CCC>TCC	p.P321S
Pat_40	Post-Resistance	RCAN2	10231	37	6	46214583	46214583	Missense_Mutation	SNP	G	A	36	121	c.335C>T	c.(334-336)TCG>TTG	p.S112L
Pat_40	Post-Resistance	GPR116	221395	37	6	46827142	46827142	Missense_Mutation	SNP	G	A	41	88	c.2498C>T	c.(2497-2499)TCC>TTC	p.S833F
Pat_40	Post-Resistance	GSTA1	2938	37	6	52658965	52658965	Missense_Mutation	SNP	G	C	31	465	c.372C>G	c.(370-372)ATC>ATG	p.I124M
Pat_40	Post-Resistance	TINAG	27283	37	6	54173703	54173703	Missense_Mutation	SNP	G	A	93	86	c.355G>A	c.(355-357)GGT>AGT	p.G119S
Pat_40	Post-Resistance	BAI3	577	37	6	69665943	69665943	Missense_Mutation	SNP	C	T	29	81	c.1223C>T	c.(1222-1224)TCG>TTG	p.S408L
Pat_40	Post-Resistance	FAM135A	57579	37	6	71238035	71238035	Missense_Mutation	SNP	C	T	75	74	c.3655C>T	c.(3655-3657)CCT>TCT	p.P1219S
Pat_40	Post-Resistance	FAM135A	57579	37	6	71266500	71266500	Missense_Mutation	SNP	C	T	81	147	c.4276C>T	c.(4276-4278)CGC>TGC	p.R1426C
Pat_40	Post-Resistance	COL12A1	1303	37	6	75822998	75822998	Missense_Mutation	SNP	C	A	57	266	c.7872G>T	c.(7870-7872)AAG>AAT	p.K2624N
Pat_40	Post-Resistance	FILIP1	27145	37	6	76022621	76022621	Missense_Mutation	SNP	C	T	64	58	c.2927G>A	c.(2926-2928)CGA>CAA	p.R976Q
Pat_40	Post-Resistance	PRSS35	167681	37	6	84234328	84234328	Missense_Mutation	SNP	C	T	46	29	c.1168C>T	c.(1168-1170)CGC>TGC	p.R390C
Pat_40	Post-Resistance	GRIK2	2898	37	6	102503320	102503320	Missense_Mutation	SNP	C	A	35	98	c.2427C>A	c.(2425-2427)AGC>AGA	p.S809R
Pat_40	Post-Resistance	LAMA4	3910	37	6	112476887	112476887	Missense_Mutation	SNP	C	T	168	160	c.1839G>A	c.(1837-1839)ATG>ATA	p.M613I
Pat_40	Post-Resistance	ROS1	6098	37	6	117662453	117662453	Missense_Mutation	SNP	C	T	73	94	c.4924G>A	c.(4924-4926)GAA>AAA	p.E1642K
Pat_40	Post-Resistance	FAM184A	79632	37	6	119295618	119295618	Missense_Mutation	SNP	C	T	102	187	c.2890G>A	c.(2890-2892)GAA>AAA	p.E964K
Pat_40	Post-Resistance	VNN2	8875	37	6	133078678	133078678	Missense_Mutation	SNP	C	T	57	124	c.221G>A	c.(220-222)CGA>CAA	p.R74Q
Pat_40	Post-Resistance	BCLAF1	9774	37	6	136599171	136599171	Missense_Mutation	SNP	C	T	11	54	c.848G>A	c.(847-849)CGA>CAA	p.R283Q
Pat_40	Post-Resistance	MAP7	9053	37	6	136683834	136683834	Missense_Mutation	SNP	G	T	3	22	c.1280C>A	c.(1279-1281)CCA>CAA	p.P427Q
Pat_40	Post-Resistance	SHPRH	257218	37	6	146276260	146276260	Missense_Mutation	SNP	G	A	48	74	c.199C>T	c.(199-201)CAC>TAC	p.H67Y
Pat_40	Post-Resistance	ZBTB2	57621	37	6	151687684	151687684	Missense_Mutation	SNP	C	T	26	27	c.517G>A	c.(517-519)GAG>AAG	p.E173K
Pat_40	Post-Resistance	TULP4	56995	37	6	158923439	158923439	Missense_Mutation	SNP	C	T	28	42	c.2744C>T	c.(2743-2745)ACC>ATC	p.T915I

Pat_40	Post-Resistance	IGF2R	3482	37	6	160455485	160455485	Nonsense_Mutation	SNP	G	T	4	132	c.1246G>T	c.(1246-1248)GGA>TGA	p.G416*
Pat_40	Post-Resistance	IGF2R	3482	37	6	160511078	160511078	Missense_Mutation	SNP	G	A	3	73	c.6598G>A	c.(6598-6600)GAT>AAT	p.D2200N
Pat_40	Post-Resistance	LPA	4018	37	6	160978522	160978522	Nonsense_Mutation	SNP	C	T	56	82	c.4713G>A	c.(4711-4713)TGG>TGA	p.W1571*
Pat_40	Post-Resistance	LPA	4018	37	6	161020605	161020605	Missense_Mutation	SNP	C	T	218	303	c.3214G>A	c.(3214-3216)GGA>AGA	p.G1072R
Pat_40	Post-Resistance	PLG	5340	37	6	161143526	161143526	Missense_Mutation	SNP	G	A	162	226	c.1183G>A	c.(1183-1185)GGA>AGA	p.G395R
Pat_40	Post-Resistance	THBS2	7058	37	6	169629684	169629684	Missense_Mutation	SNP	C	T	5	174	c.2242G>A	c.(2242-2244)GGT>AGT	p.G748S
Pat_40	Post-Resistance	AMZ1	155185	37	7	2740383	2740383	Missense_Mutation	SNP	C	T	33	40	c.298C>T	c.(298-300)CCG>TCG	p.P100S
Pat_40	Post-Resistance	PHF14	9678	37	7	11209061	11209061	Missense_Mutation	SNP	G	A	6	20	c.2791G>A	c.(2791-2793)GAA>AAA	p.E931K
Pat_40	Post-Resistance	TMEM106B	54664	37	7	12258147	12258147	Missense_Mutation	SNP	C	T	5	190	c.281C>T	c.(280-282)ACA>ATA	p.T94I
Pat_40	Post-Resistance	MACC1	346389	37	7	20199595	20199595	Missense_Mutation	SNP	G	A	33	86	c.389C>T	c.(388-390)TCC>TTC	p.S130F
Pat_40	Post-Resistance	DNAH11	8701	37	7	21747399	21747399	Missense_Mutation	SNP	C	T	61	84	c.6650C>T	c.(6649-6651)ACA>ATA	p.T2217I
Pat_40	Post-Resistance	FAM188B	84182	37	7	30831178	30831178	Missense_Mutation	SNP	C	T	26	43	c.1061C>T	c.(1060-1062)CCC>CTC	p.P354L
Pat_40	Post-Resistance	CCDC129	223075	37	7	31682490	31682490	Missense_Mutation	SNP	G	A	35	130	c.1506G>A	c.(1504-1506)ATG>ATA	p.M502I
Pat_40	Post-Resistance	PDE1C	5137	37	7	31877577	31877577	Missense_Mutation	SNP	C	T	202	291	c.989G>A	c.(988-990)CGA>CAA	p.R330Q
Pat_40	Post-Resistance	BMPER	168667	37	7	34097762	34097762	Missense_Mutation	SNP	G	A	78	108	c.1019G>A	c.(1018-1020)AGT>AAT	p.S340N
Pat_40	Post-Resistance	CDK13	8621	37	7	40038988	40038988	Nonsense_Mutation	SNP	A	T	26	109	c.2071A>T	c.(2071-2073)AAA>TAA	p.K691*
Pat_40	Post-Resistance	ZNF713	349075	37	7	55990859	55990859	Missense_Mutation	SNP	C	T	89	151	c.53C>T	c.(52-54)TCA>TTA	p.S18L
Pat_40	Post-Resistance	ZNF479	90827	37	7	57187788	57187788	Missense_Mutation	SNP	G	A	8	332	c.1334C>T	c.(1333-1335)GCC>GTC	p.A445V
Pat_40	Post-Resistance	ZNF107	51427	37	7	64167982	64167982	Missense_Mutation	SNP	C	T	36	167	c.1300C>T	c.(1300-1302)CAT>TAT	p.H434Y
Pat_40	Post-Resistance	HIP1	3092	37	7	75189170	75189170	Missense_Mutation	SNP	G	T	3	43	c.1241C>A	c.(1240-1242)GCA>GAA	p.A414E
Pat_40	Post-Resistance	FGL2	10875	37	7	76825822	76825822	Missense_Mutation	SNP	C	T	73	337	c.1094G>A	c.(1093-1095)CGA>CAA	p.R365Q
Pat_40	Post-Resistance	PCLO	27445	37	7	82583350	82583350	Missense_Mutation	SNP	C	T	112	148	c.6919G>A	c.(6919-6921)GAA>AAA	p.E2307K
Pat_40	Post-Resistance	PCLO	27445	37	7	82585683	82585683	Missense_Mutation	SNP	C	T	20	58	c.4586G>A	c.(4585-4587)CGA>CAA	p.R1529Q
Pat_40	Post-Resistance	ABCB1	5243	37	7	87160681	87160681	Missense_Mutation	SNP	C	T	68	519	c.2614G>A	c.(2614-2616)GGA>AGA	p.G872R
Pat_40	Post-Resistance	ABCB1	5243	37	7	87175289	87175289	Missense_Mutation	SNP	G	A	136	227	c.1777C>T	c.(1777-1779)CGT>TGT	p.R593C
Pat_40	Post-Resistance	ZAN	7455	37	7	100349941	100349941	Missense_Mutation	SNP	C	T	7	157	c.2213C>T	c.(2212-2214)CCC>CTC	p.P738L
Pat_40	Post-Resistance	RELN	5649	37	7	103206793	103206794	Missense_Mutation	DNP	CC	TT	45	218	.4813_4814GG>A	c.(4813-4815)GGA>AAA	p.G1605K
Pat_40	Post-Resistance	PPP1R3A	5506	37	7	113519829	113519829	Missense_Mutation	SNP	C	T	74	258	c.1318G>A	c.(1318-1320)GAT>AAT	p.D440N
Pat_40	Post-Resistance	FOXP2	93986	37	7	114292325	114292325	Missense_Mutation	SNP	G	A	319	30	c.1162G>A	c.(1162-1164)GTG>ATG	p.V388M
Pat_40	Post-Resistance	CFTR	1080	37	7	117232308	117232308	Missense_Mutation	SNP	A	T	18	69	c.2087A>T	c.(2086-2088)AAA>ATA	p.K696I
Pat_40	Post-Resistance	SLC13A1	6561	37	7	122759211	122759211	Missense_Mutation	SNP	A	C	31	106	c.1436T>G	c.(1435-1437)TTG>TGG	p.L479W
Pat_40	Post-Resistance	ZNF800	168850	37	7	127013826	127013826	Missense_Mutation	SNP	G	A	57	260	c.1564C>T	c.(1564-1566)CCT>TCT	p.P522S
Pat_40	Post-Resistance	TSPAN33	340348	37	7	128806635	128806635	Missense_Mutation	SNP	G	A	302	22	c.476G>A	c.(475-477)GGG>GAG	p.G159E
Pat_40	Post-Resistance	DGKI	9162	37	7	137080445	137080445	Splice_Site	SNP	T	A	4	99	c.2982_splice	c.e33-1	p.T994_splice
Pat_40	Post-Resistance	BRAF	673	37	7	140453136	140453136	Missense_Mutation	SNP	A	T	311	34	c.1799T>A	c.(1798-1800)GTG>GAG	p.V600E
Pat_40	Post-Resistance	KEL	3792	37	7	142640960	142640961	Missense_Mutation	DNP	CC	TT	6	45	.1501_1502GG>A	c.(1501-1503)GGA>AAA	p.G501K
Pat_40	Post-Resistance	TAS2R41	259287	37	7	143175722	143175722	Missense_Mutation	SNP	G	A	48	230	c.757G>A	c.(757-759)GAT>AAT	p.D253N
Pat_40	Post-Resistance	LOC441294	441294	37	7	143270156	143270156	Missense_Mutation	SNP	C	T	26	326	c.1246C>T	c.(1246-1248)CTT>TTT	p.L416F
Pat_40	Post-Resistance	ZNF282	8427	37	7	148895647	148895647	Missense_Mutation	SNP	G	A	4	100	c.388G>A	c.(388-390)GAG>AAG	p.E130K
Pat_40	Post-Resistance	ZNF777	27153	37	7	149152312	149152312	Missense_Mutation	SNP	A	G	17	107	c.802T>C	c.(802-804)TGG>CGG	p.W268R
Pat_40	Post-Resistance	C7orf29	113763	37	7	150027503	150027503	Missense_Mutation	SNP	C	T	4	178	c.10C>T	c.(10-12)CGC>TGC	p.R4C
Pat_40	Post-Resistance	MLL3	58508	37	7	151879283	151879283	Missense_Mutation	SNP	T	A	56	187	c.5662A>T	c.(5662-5664)AAC>TAC	p.N1888Y
Pat_40	Post-Resistance	MLL3	58508	37	7	151919131	151919131	Missense_Mutation	SNP	C	T	90	446	c.3454G>A	c.(3454-3456)GAA>AAA	p.E1152K
Pat_40	Post-Resistance	CSMD1	64478	37	8	2824251	2824251	Missense_Mutation	SNP	G	A	26	49	c.8944C>T	c.(8944-8946)CCT>TCT	p.P2982S
Pat_40	Post-Resistance	CSMD1	64478	37	8	3081309	3081309	Missense_Mutation	SNP	C	T	52	96	c.4429G>A	c.(4429-4431)GAA>AAA	p.E1477K
Pat_40	Post-Resistance	CSMD1	64478	37	8	3224730	3224730	Missense_Mutation	SNP	G	A	8	18	c.2942C>T	c.(2941-2943)TCC>TTC	p.S981F
Pat_40	Post-Resistance	XPO7	23039	37	8	21857050	21857050	Missense_Mutation	SNP	T	G	96	155	c.2647T>G	c.(2647-2649)TAC>GAC	p.Y883D

Pat_40	Post-Resistance	TNFRSF10A	8797	37	8	23049398	23049398	Missense_Mutation	SNP	C	T	74	122	c.1216G>A	c.(1216-1218)GAT>AAT	p.D406N
Pat_40	Post-Resistance	ADAM7	8756	37	8	24324428	24324428	Missense_Mutation	SNP	C	T	99	158	c.506C>T	c.(505-507)TCC>TTC	p.S169F
Pat_40	Post-Resistance	NEFM	4741	37	8	24775836	24775836	Missense_Mutation	SNP	G	A	9	9	c.2468G>A	c.(2467-2469)AGG>AAG	p.R823K
Pat_40	Post-Resistance	DDHD2	23259	37	8	38092070	38092070	Missense_Mutation	SNP	C	T	109	149	c.379C>T	c.(379-381)CCC>TCC	p.P127S
Pat_40	Post-Resistance	SNAI2	6591	37	8	49832783	49832783	Missense_Mutation	SNP	G	C	44	257	c.297C>G	c.(295-297)CAC>CAG	p.H99Q
Pat_40	Post-Resistance	PXDNL	137902	37	8	52320967	52320967	Missense_Mutation	SNP	C	T	48	7	c.3217G>A	c.(3217-3219)GAA>AAA	p.E1073K
Pat_40	Post-Resistance	RP1	6101	37	8	55537556	55537557	Nonsense_Mutation	DNP	AG	TA	64	55	.1114_1115AG>T	c.(1114-1116)AGA>TAA	p.R372*
Pat_40	Post-Resistance	RP1	6101	37	8	55539350	55539350	Missense_Mutation	SNP	G	A	141	42	c.2908G>A	c.(2908-2910)GAA>AAA	p.E970K
Pat_40	Post-Resistance	RP1	6101	37	8	55542726	55542726	Missense_Mutation	SNP	A	G	8	310	c.6284A>G	c.(6283-6285)TAC>TGC	p.Y2095C
Pat_40	Post-Resistance	CYP7B1	9420	37	8	65527628	65527628	Missense_Mutation	SNP	G	A	43	402	c.1012C>T	c.(1012-1014)CCC>TCC	p.P338S
Pat_40	Post-Resistance	VCPIP1	80124	37	8	67579161	67579161	Missense_Mutation	SNP	C	A	4	22	c.33G>T	c.(31-33)TTG>TTT	p.L11F
Pat_40	Post-Resistance	CPA6	57094	37	8	68346290	68346290	Missense_Mutation	SNP	G	A	90	565	c.1024C>T	c.(1024-1026)CCC>TCC	p.P342S
Pat_40	Post-Resistance	PREX2	80243	37	8	69028131	69028131	Missense_Mutation	SNP	C	T	96	553	c.3290C>T	c.(3289-3291)TCT>TTT	p.S1097F
Pat_40	Post-Resistance	RPL7	6129	37	8	74203316	74203316	Missense_Mutation	SNP	T	C	4	178	c.710A>G	c.(709-711)GAG>GGG	p.E237G
Pat_40	Post-Resistance	HNF4G	3174	37	8	76470899	76470899	Missense_Mutation	SNP	G	A	63	543	c.739G>A	c.(739-741)GAT>AAT	p.D247N
Pat_40	Post-Resistance	HEY1	23462	37	8	80677704	80677705	Missense_Mutation	DNP	CC	TT	6	85	c.633_634GG>AA	631-636)ACGGAA>ACAA	p.E212K
Pat_40	Post-Resistance	C8orf47	203111	37	8	99102024	99102024	Missense_Mutation	SNP	G	A	9	121	c.779G>A	c.(778-780)AGA>AAA	p.R260K
Pat_40	Post-Resistance	STK3	6788	37	8	99718703	99718703	Missense_Mutation	SNP	G	A	93	31	c.676C>T	c.(676-678)CCA>TCA	p.P226S
Pat_40	Post-Resistance	RIMS2	9699	37	8	104987692	104987692	Missense_Mutation	SNP	G	A	30	270	c.2219G>A	c.(2218-2220)GGA>GAA	p.G740E
Pat_40	Post-Resistance	RIMS2	9699	37	8	105263859	105263859	Missense_Mutation	SNP	G	A	315	253	c.3915G>A	c.(3913-3915)ATG>ATA	p.M1305I
Pat_40	Post-Resistance	NRBP2	340371	37	8	144920908	144920908	Missense_Mutation	SNP	C	T	4	54	c.784G>A	c.(784-786)GTC>ATC	p.V262I
Pat_40	Post-Resistance	PTPRD	5789	37	9	8636785	8636785	Missense_Mutation	SNP	A	T	130	14	c.124T>A	c.(124-126)TCT>ACT	p.S42T
Pat_40	Post-Resistance	MPDZ	8777	37	9	13217180	13217180	Missense_Mutation	SNP	C	A	24	4	c.1200G>T	c.(1198-1200)TTG>TTT	p.L400F
Pat_40	Post-Resistance	UNC13B	10497	37	9	35313966	35313966	Missense_Mutation	SNP	G	T	23	207	c.1147G>T	c.(1147-1149)GTT>TTT	p.V383F
Pat_40	Post-Resistance	SHB	6461	37	9	38016038	38016038	Missense_Mutation	SNP	C	T	84	34	c.808G>A	c.(808-810)GAG>AAG	p.E270K
Pat_40	Post-Resistance	LOC442421	442421	37	9	66499716	66499716	Missense_Mutation	SNP	A	G	8	114	c.526A>G	c.(526-528)AAT>GAT	p.N176D
Pat_40	Post-Resistance	CENPP	401541	37	9	95373672	95373672	Missense_Mutation	SNP	C	T	8	17	c.641C>T	c.(640-642)CCA>CTA	p.P214L
Pat_40	Post-Resistance	SNX30	401548	37	9	115567122	115567122	Missense_Mutation	SNP	C	T	5	195	c.223C>T	c.(223-225)CTC>TTC	p.L75F
Pat_40	Post-Resistance	OR1N1	138883	37	9	125288794	125288794	Missense_Mutation	SNP	G	A	64	8	c.779C>T	c.(778-780)CCT>CTT	p.P260L
Pat_40	Post-Resistance	HSPA5	3309	37	9	128003071	128003071	Missense_Mutation	SNP	C	T	3	87	c.238G>A	c.(238-240)GCC>ACC	p.A80T
Pat_40	Post-Resistance	ANGPTL2	23452	37	9	129856164	129856164	Missense_Mutation	SNP	C	T	3	98	c.859G>A	c.(859-861)GAC>AAC	p.D287N
Pat_40	Post-Resistance	SLC2A8	29988	37	9	130167241	130167241	Missense_Mutation	SNP	C	T	15	41	c.1121C>T	c.(1120-1122)GCC>GTC	p.A374V
Pat_40	Post-Resistance	LRSAM1	90678	37	9	130241696	130241696	Missense_Mutation	SNP	G	A	3	65	c.815G>A	c.(814-816)CGG>CAG	p.R272Q
Pat_40	Post-Resistance	C9orf78	51759	37	9	132594217	132594217	Missense_Mutation	SNP	G	A	80	102	c.302C>T	c.(301-303)TCG>TTG	p.S101L
Pat_40	Post-Resistance	RAPGEF1	2889	37	9	134514084	134514084	Missense_Mutation	SNP	C	T	60	95	c.538G>A	c.(538-540)GAA>AAA	p.E180K
Pat_40	Post-Resistance	WDR5	11091	37	9	137007527	137007527	Missense_Mutation	SNP	C	T	38	38	c.427C>T	c.(427-429)CTT>TTT	p.L143F
Pat_40	Post-Resistance	COL5A1	1289	37	9	137582859	137582859	Missense_Mutation	SNP	C	T	17	17	c.211C>T	c.(211-213)CCG>TCG	p.P71S
Pat_40	Post-Resistance	NOTCH1	4851	37	9	139413213	139413213	Missense_Mutation	SNP	C	T	3	50	c.929G>A	c.(928-930)GGG>GAG	p.G310E
Pat_40	Post-Resistance	TPRN	286262	37	9	140087077	140087077	Missense_Mutation	SNP	C	T	13	10	c.1609G>A	c.(1609-1611)GAG>AAG	p.E537K
Pat_40	Post-Resistance	TUBB2C	10383	37	9	140137584	140137585	Missense_Mutation	DNP	CC	TT	55	54	c.914_915CC>TT	c.(913-915)CCC>CTT	p.P305L
Pat_40	Post-Resistance	NLGN4X	57502	37	X	5810998	5810998	Missense_Mutation	SNP	T	A	59	205	c.2311A>T	c.(2311-2313)ATC>TTC	p.I771F
Pat_40	Post-Resistance	TLR7	51284	37	X	12903805	12903805	Missense_Mutation	SNP	C	T	159	179	c.178C>T	c.(178-180)CCT>TCT	p.P60S
Pat_40	Post-Resistance	TCEANC	170082	37	X	13681166	13681166	Missense_Mutation	SNP	T	C	180	312	c.539T>C	c.(538-540)CTT>CCT	p.L180P
Pat_40	Post-Resistance	KLHL15	80311	37	X	24024498	24024498	Missense_Mutation	SNP	G	A	53	216	c.313C>T	c.(313-315)CTT>TTT	p.L105F
Pat_40	Post-Resistance	DCAF8L2	347442	37	X	27766412	27766412	Missense_Mutation	SNP	G	A	29	33	c.1400G>A	c.(1399-1401)AGA>AAA	p.R467K
Pat_40	Post-Resistance	MAGEB1	4112	37	X	30269469	30269469	Missense_Mutation	SNP	G	A	61	94	c.859G>A	c.(859-861)GAG>AAG	p.E287K
Pat_40	Post-Resistance	DMD	1756	37	X	32361316	32361316	Missense_Mutation	SNP	A	T	58	142	c.5674T>A	c.(5674-5676)TGC>AGC	p.C1892S

Pat_40	Post-Resistance	CXorf22	170063	37	X	35974281	35974281	Missense_Mutation	SNP	G	A	39	59	c.1378G>A	c.(1378-1380)GAA>AAA	p.E460K
Pat_40	Post-Resistance	OTC	5009	37	X	38212016	38212016	Nonsense_Mutation	SNP	C	T	76	93	c.67C>T	c.(67-69)CGA>TGA	p.R23*
Pat_40	Post-Resistance	MED14	9282	37	X	40518681	40518681	Missense_Mutation	SNP	C	T	49	62	c.3863G>A	c.(3862-3864)AGA>AAA	p.R1288K
Pat_40	Post-Resistance	RBM10	8241	37	X	47045530	47045530	Missense_Mutation	SNP	C	G	25	44	c.2497C>G	c.(2497-2499)CCC>GCC	p.P833A
Pat_40	Post-Resistance	LOC100133957	100133957	37	X	47518383	47518384	Missense_Mutation	DNP	CT	AA	26	69	c.59_60CT>AA	c.(58-60)CCT>CAA	p.P20Q
Pat_40	Post-Resistance	ZNF81	347344	37	X	47774499	47774499	Missense_Mutation	SNP	C	T	25	35	c.454C>T	c.(454-456)CGC>TGC	p.R152C
Pat_40	Post-Resistance	CACNA1F	778	37	X	49066097	49066097	Missense_Mutation	SNP	C	T	5	23	c.4846G>A	c.(4846-4848)GCC>ACC	p.A1616T
Pat_40	Post-Resistance	ITIH5L	347365	37	X	54823498	54823498	Missense_Mutation	SNP	G	A	36	52	c.134C>T	c.(133-135)ACG>ATG	p.T45M
Pat_40	Post-Resistance	TRO	7216	37	X	54949440	54949440	Missense_Mutation	SNP	C	T	19	45	c.475C>T	c.(475-477)CAT>TAT	p.H159Y
Pat_40	Post-Resistance	SPIN4	139886	37	X	62570220	62570220	Missense_Mutation	SNP	G	A	78	229	c.479C>T	c.(478-480)CCT>CTT	p.P160L
Pat_40	Post-Resistance	PJA1	64219	37	X	68381748	68381748	Missense_Mutation	SNP	C	T	28	107	c.1334G>A	c.(1333-1335)CGA>CAA	p.R445Q
Pat_40	Post-Resistance	ACRC	93953	37	X	70823920	70823920	Missense_Mutation	SNP	C	T	6	137	c.793C>T	c.(793-795)CCC>TCC	p.P265S
Pat_40	Post-Resistance	KIAA2022	340533	37	X	73963813	73963813	Missense_Mutation	SNP	C	T	6	7	c.579G>A	c.(577-579)ATG>ATA	p.M193I
Pat_40	Post-Resistance	ABCB7	22	37	X	74273345	74273345	Missense_Mutation	SNP	T	C	12	8	c.2119A>G	c.(2119-2121)ACA>GCA	p.T707A
Pat_40	Post-Resistance	DACH2	117154	37	X	85403846	85403846	Missense_Mutation	SNP	C	A	30	127	c.222C>A	c.(220-222)CAC>CAA	p.H74Q
Pat_40	Post-Resistance	RAB40A	142684	37	X	102754855	102754855	Missense_Mutation	SNP	G	A	21	54	c.830C>T	c.(829-831)TCT>TTT	p.S277F
Pat_40	Post-Resistance	NRK	203447	37	X	105152811	105152811	Missense_Mutation	SNP	G	A	24	64	c.1178G>A	c.(1177-1179)AGG>AAG	p.R393K
Pat_40	Post-Resistance	COL4A5	1287	37	X	107865120	107865120	Missense_Mutation	SNP	A	T	32	38	c.2765A>T	c.(2764-2766)AAA>ATA	p.K922I
Pat_40	Post-Resistance	SLC6A14	11254	37	X	115588809	115588809	Missense_Mutation	SNP	G	A	170	375	c.1649G>A	c.(1648-1650)AGA>AAA	p.R550K
Pat_40	Post-Resistance	KIAA1210	57481	37	X	118223262	118223262	Missense_Mutation	SNP	G	A	16	39	c.1931C>T	c.(1930-1932)TCC>TTC	p.S644F
Pat_40	Post-Resistance	KIAA1210	57481	37	X	118227657	118227657	Missense_Mutation	SNP	C	T	11	55	c.1456G>A	c.(1456-1458)GAA>AAA	p.E486K
Pat_40	Post-Resistance	THOC2	57187	37	X	122774460	122774460	Missense_Mutation	SNP	C	T	84	212	c.1675G>A	c.(1675-1677)GAA>AAA	p.E559K
Pat_40	Post-Resistance	ODZ1	10178	37	X	123514532	123514532	Missense_Mutation	SNP	C	T	198	210	c.8032G>A	c.(8032-8034)GAA>AAA	p.E2678K
Pat_40	Post-Resistance	USP26	83844	37	X	132159788	132159788	Missense_Mutation	SNP	C	A	28	99	c.2461G>T	c.(2461-2463)GAT>TAT	p.D821Y
Pat_40	Post-Resistance	USP26	83844	37	X	132159790	132159790	Missense_Mutation	SNP	C	A	24	93	c.2459G>T	c.(2458-2460)GGA>GTA	p.G820V
Pat_40	Post-Resistance	GPR112	139378	37	X	135430610	135430610	Missense_Mutation	SNP	C	T	70	172	c.4745C>T	c.(4744-4746)TCC>TTC	p.S1582F
Pat_40	Post-Resistance	ATP11C	286410	37	X	138870439	138870439	Missense_Mutation	SNP	C	T	66	104	c.1441G>A	c.(1441-1443)GAT>AAT	p.D481N
Pat_40	Post-Resistance	MAGEC1	9947	37	X	140994583	140994583	Nonsense_Mutation	SNP	A	T	8	179	c.1393A>T	c.(1393-1395)AGA>TGA	p.R465*
Pat_40	Post-Resistance	MAGEC1	9947	37	X	140994585	140994585	Missense_Mutation	SNP	A	T	9	186	c.1395A>T	c.(1393-1395)AGA>AGT	p.R465S
Pat_40	Post-Resistance	SPANXN1	494118	37	X	144337239	144337239	Nonsense_Mutation	SNP	A	T	57	38	c.124A>T	c.(124-126)AAG>TAG	p.K42*
Pat_40	Post-Resistance	MAGEA12	4111	37	X	151900242	151900242	Missense_Mutation	SNP	C	T	88	124	c.559G>A	c.(559-561)GAT>AAT	p.D187N
Pat_40	Post-Resistance	SRPK3	26576	37	X	153049213	153049213	Missense_Mutation	SNP	G	A	3	34	c.781G>A	c.(781-783)GGT>AGT	p.G261S
Pat_40	Post-Resistance	MPP1	4354	37	X	154011765	154011765	Missense_Mutation	SNP	G	A	26	49	c.883C>T	c.(883-885)CGC>TGC	p.R295C
Pat_40	Post-Resistance	RAB39B	116442	37	X	154490329	154490329	Missense_Mutation	SNP	G	T	66	131	c.401C>A	c.(400-402)ACT>AAT	p.T134N
Pat_41	Pre-Treatment	CHD5	26038	37	1	6166767	6166767	Missense_Mutation	SNP	C	T	4	84	c.5651G>A	c.(5650-5652)CGC>CAC	p.R1884H
Pat_41	Pre-Treatment	TAS1R1	80835	37	1	6634701	6634701	Missense_Mutation	SNP	C	T	4	173	c.509C>T	c.(508-510)GCG>GTG	p.A170V
Pat_41	Pre-Treatment	ENO1	2023	37	1	8924017	8924017	Missense_Mutation	SNP	C	T	8	612	c.1000G>A	c.(1000-1002)GAG>AAG	p.E334K
Pat_41	Pre-Treatment	VPS13D	55187	37	1	12368580	12368580	Missense_Mutation	SNP	G	A	5	449	c.6532G>A	c.(6532-6534)GCA>ACA	p.A2178T
Pat_41	Pre-Treatment	EPHA2	1969	37	1	16475418	16475418	Missense_Mutation	SNP	C	T	5	197	c.278G>A	c.(277-279)CGT>CAT	p.R93H
Pat_41	Pre-Treatment	MST1P9	11223	37	1	17085865	17085865	Missense_Mutation	SNP	A	G	3	61	c.956T>C	c.(955-957)CTC>CCC	p.L319P
Pat_41	Pre-Treatment	ALDH4A1	8659	37	1	19201071	19201071	Missense_Mutation	SNP	C	T	4	200	c.1465G>A	c.(1465-1467)GTC>ATC	p.V489I
Pat_41	Pre-Treatment	HSPG2	3339	37	1	22188296	22188296	Missense_Mutation	SNP	G	A	4	58	c.4909C>T	c.(4909-4911)CGC>TGC	p.R1637C
Pat_41	Pre-Treatment	C1orf172	126695	37	1	27277919	27277919	Missense_Mutation	SNP	C	T	5	35	c.953G>A	c.(952-954)GGT>GAT	p.G318D
Pat_41	Pre-Treatment	TFAP2E	339488	37	1	36054105	36054105	Missense_Mutation	SNP	C	T	6	338	c.737C>T	c.(736-738)TCG>TTG	p.S246L
Pat_41	Pre-Treatment	KIAA0754	643314	37	1	39879806	39879806	Missense_Mutation	SNP	T	C	3	43	c.3869T>C	c.(3868-3870)CTA>CCA	p.L1290P
Pat_41	Pre-Treatment	KIAA0754	643314	37	1	39879817	39879817	Missense_Mutation	SNP	G	A	4	37	c.3880G>A	c.(3880-3882)GCC>ACC	p.A1294T
Pat_41	Pre-Treatment	CYP4B1	1580	37	1	47282803	47282803	Missense_Mutation	SNP	G	A	4	121	c.1154G>A	c.(1153-1155)CGC>CAC	p.R385H

Pat_41	Pre-Treatment	ELAVL4	1996	37	1	50610767	50610767	Missense_Mutation	SNP	G	A	4	225	c.148G>A	c.(148-150)GTC>ATC	p.V50I
Pat_41	Pre-Treatment	ZCCHC11	23318	37	1	52991639	52991639	Missense_Mutation	SNP	G	A	5	447	c.314C>T	c.(313-315)CCG>CTG	p.P105L
Pat_41	Pre-Treatment	KANK4	163782	37	1	62737205	62737205	Missense_Mutation	SNP	G	A	4	234	c.1957C>T	c.(1957-1959)CGT>TGT	p.R653C
Pat_41	Pre-Treatment	JAK1	3716	37	1	65312338	65312338	Missense_Mutation	SNP	C	T	4	71	c.1981G>A	c.(1981-1983)GTG>ATG	p.V661M
Pat_41	Pre-Treatment	ST6GALNAC3	256435	37	1	76779652	76779652	Missense_Mutation	SNP	C	T	15	154	c.181C>T	c.(181-183)CAC>TAC	p.H61Y
Pat_41	Pre-Treatment	CELSR2	1952	37	1	109812339	109812339	Missense_Mutation	SNP	C	T	4	191	c.7004C>T	c.(7003-7005)TCG>TTG	p.S2335L
Pat_41	Pre-Treatment	PSMA5	5686	37	1	109957975	109957975	Missense_Mutation	SNP	G	A	6	165	c.107C>T	c.(106-108)ACA>ATA	p.T36I
Pat_41	Pre-Treatment	ECM1	1893	37	1	150484015	150484015	Missense_Mutation	SNP	A	G	4	94	c.791A>G	c.(790-792)GAG>GGG	p.E264G
Pat_41	Pre-Treatment	FLG2	388698	37	1	152324407	152324407	Missense_Mutation	SNP	C	G	7	683	c.5855G>C	c.(5854-5856)GGA>GCA	p.G1952A
Pat_41	Pre-Treatment	INTS3	65123	37	1	153723712	153723713	Missense_Mutation	DNP	AC	TT	5	102	c.726_727AC>TT	724-729)GAACGG>GATT	242_243ER>D
Pat_41	Pre-Treatment	MUC1	4582	37	1	155159796	155159796	Missense_Mutation	SNP	G	A	4	174	c.883C>T	c.(883-885)CGG>TGG	p.R295W
Pat_41	Pre-Treatment	ISG20L2	81875	37	1	156697269	156697269	Missense_Mutation	SNP	G	A	15	203	c.176C>T	c.(175-177)TCA>TTA	p.S59L
Pat_41	Pre-Treatment	OR10K1	391109	37	1	158435419	158435419	Missense_Mutation	SNP	T	A	10	120	c.68T>A	c.(67-69)CTG>CAG	p.L23Q
Pat_41	Pre-Treatment	SPTA1	6708	37	1	158621161	158621161	Missense_Mutation	SNP	C	T	5	477	c.3473G>A	c.(3472-3474)CGG>CAG	p.R1158Q
Pat_41	Pre-Treatment	DARC	2532	37	1	159175495	159175495	Missense_Mutation	SNP	G	A	6	459	c.266G>A	c.(265-267)CGC>CAC	p.R89H
Pat_41	Pre-Treatment	CRP	1401	37	1	159683792	159683793	Missense_Mutation	DNP	CC	TT	8	157	c.197_198GG>AA	c.(196-198)GGG>GAA	p.G66E
Pat_41	Pre-Treatment	USP21	27005	37	1	161134655	161134655	Missense_Mutation	SNP	C	T	15	266	c.1415C>T	c.(1414-1416)TCC>TTC	p.S472F
Pat_41	Pre-Treatment	PTPRC	5788	37	1	198671552	198671552	Missense_Mutation	SNP	C	T	35	564	c.470C>T	c.(469-471)CCT>CTT	p.P157L
Pat_41	Pre-Treatment	PPP1R12B	4660	37	1	202462390	202462390	Missense_Mutation	SNP	C	T	5	54	c.2090C>T	c.(2089-2091)CCA>CTA	p.P697L
Pat_41	Pre-Treatment	ZC3H11A	9877	37	1	203821508	203821508	Nonsense_Mutation	SNP	C	G	4	90	c.2414C>G	c.(2413-2415)TCA>TGA	p.S805*
Pat_41	Pre-Treatment	SDCCAG8	10806	37	1	243589838	243589838	Missense_Mutation	SNP	G	A	4	190	c.1963G>A	c.(1963-1965)GTA>ATA	p.V655I
Pat_41	Pre-Treatment	DIP2C	22982	37	10	532401	532401	Missense_Mutation	SNP	G	A	4	167	c.155C>T	c.(154-156)CCG>CTG	p.P52L
Pat_41	Pre-Treatment	A1CF	29974	37	10	52603882	52603882	Missense_Mutation	SNP	C	T	14	86	c.100G>A	c.(100-102)GAA>AAA	p.E34K
Pat_41	Pre-Treatment	CTNNA3	29119	37	10	68940163	68940163	Missense_Mutation	SNP	G	A	5	185	c.959C>T	c.(958-960)ACG>ATG	p.T320M
Pat_41	Pre-Treatment	TSPAN15	23555	37	10	71244945	71244945	Missense_Mutation	SNP	G	A	5	234	c.331G>A	c.(331-333)GTG>ATG	p.V111M
Pat_41	Pre-Treatment	DLG5	9231	37	10	79579739	79579739	Missense_Mutation	SNP	G	A	5	166	c.3440C>T	c.(3439-3441)CCG>CTG	p.P1147L
Pat_41	Pre-Treatment	MYOF	26509	37	10	95093597	95093597	Missense_Mutation	SNP	G	A	4	100	c.4637C>T	c.(4636-4638)CCT>CTT	p.P1546L
Pat_41	Pre-Treatment	PIPSL	266971	37	10	95719498	95719498	Missense_Mutation	SNP	G	C	3	75	c.1656C>G	c.(1654-1656)GAC>GAG	p.D552E
Pat_41	Pre-Treatment	MMS19	64210	37	10	99238117	99238117	Missense_Mutation	SNP	G	A	4	36	c.292C>T	c.(292-294)CGG>TGG	p.R98W
Pat_41	Pre-Treatment	DNMBP	23268	37	10	101657896	101657896	Missense_Mutation	SNP	G	A	4	222	c.2867C>T	c.(2866-2868)GCG>GTG	p.A956V
Pat_41	Pre-Treatment	POLL	27343	37	10	103339574	103339574	Missense_Mutation	SNP	C	T	3	74	c.1364G>A	c.(1363-1365)GGG>GAG	p.G455E
Pat_41	Pre-Treatment	CUEDC2	79004	37	10	104184887	104184887	Missense_Mutation	SNP	G	T	4	98	c.59C>A	c.(58-60)CCG>CAG	p.P20Q
Pat_41	Pre-Treatment	RPL13AP6	644511	37	10	112696573	112696573	Missense_Mutation	SNP	T	C	4	38	c.419A>G	c.(418-420)CAC>CGC	p.H140R
Pat_41	Pre-Treatment	TACC2	10579	37	10	123842859	123842859	Missense_Mutation	SNP	G	A	4	200	c.844G>A	c.(844-846)GCC>ACC	p.A282T
Pat_41	Pre-Treatment	CUZD1	50624	37	10	124596466	124596466	Missense_Mutation	SNP	G	A	10	235	c.698C>T	c.(697-699)ACT>ATT	p.T233I
Pat_41	Pre-Treatment	B4GALNT4	338707	37	11	380355	380355	Missense_Mutation	SNP	G	A	4	148	c.2779G>A	c.(2779-2781)GGC>AGC	p.G927S
Pat_41	Pre-Treatment	RNH1	6050	37	11	500626	500626	Missense_Mutation	SNP	G	A	16	92	c.130C>T	c.(130-132)CGG>TGG	p.R44W
Pat_41	Pre-Treatment	MUC6	4588	37	11	1019280	1019280	Missense_Mutation	SNP	G	A	3	41	c.4025C>T	c.(4024-4026)ACG>ATG	p.T1342M
Pat_41	Pre-Treatment	MUC6	4588	37	11	1020252	1020252	Missense_Mutation	SNP	G	A	4	60	c.3646C>T	c.(3646-3648)CGG>TGG	p.R1216W
Pat_41	Pre-Treatment	MUC5B	727897	37	11	1271468	1271468	Missense_Mutation	SNP	C	T	7	282	c.14777C>T	c.(14776-14778)CCG>CTG	p.P4926L
Pat_41	Pre-Treatment	MUC5B	727897	37	11	1271471	1271471	Missense_Mutation	SNP	G	C	7	269	c.14780G>C	c.(14779-14781)AGC>ACC	p.S4927T
Pat_41	Pre-Treatment	MUC5B	727897	37	11	1272554	1272554	Missense_Mutation	SNP	C	T	6	307	c.15410C>T	c.(15409-15411)ACG>ATG	p.T5137M
Pat_41	Pre-Treatment	UBQLNL	143630	37	11	5537331	5537331	Missense_Mutation	SNP	C	T	4	148	c.341G>A	c.(340-342)CGG>CAG	p.R114Q
Pat_41	Pre-Treatment	OR52E4	390081	37	11	5905799	5905799	Missense_Mutation	SNP	G	A	11	226	c.277G>A	c.(277-279)GAG>AAG	p.E93K
Pat_41	Pre-Treatment	MPPED2	744	37	11	30433088	30433088	Missense_Mutation	SNP	G	A	4	207	c.812C>T	c.(811-813)TCG>TTG	p.S271L
Pat_41	Pre-Treatment	PTPRJ	5795	37	11	48149416	48149416	Missense_Mutation	SNP	C	T	6	367	c.1178C>T	c.(1177-1179)TCG>TTG	p.S393L
Pat_41	Pre-Treatment	MAP4K2	5871	37	11	64566894	64566894	Missense_Mutation	SNP	G	A	9	233	c.1052C>T	c.(1051-1053)CCG>CTG	p.P351L

Pat_41	Pre-Treatment	CHKA	1119	37	11	67842270	67842270	Missense_Mutation	SNP	C	T	4	124	c.544G>A	c.(544-546)GTT>ATT	p.V182I
Pat_41	Pre-Treatment	ATM	472	37	11	108235884	108235884	Missense_Mutation	SNP	G	A	17	220	c.8926G>A	c.(8926-8928)GAT>AAT	p.D2976N
Pat_41	Pre-Treatment	BCL9L	283149	37	11	118772324	118772324	Missense_Mutation	SNP	G	A	4	217	c.2128C>T	c.(2128-2130)CGG>TGG	p.R710W
Pat_41	Pre-Treatment	KIRREL3	84623	37	11	126314916	126314916	Missense_Mutation	SNP	G	A	4	172	c.1210C>T	c.(1210-1212)CGT>TGT	p.R404C
Pat_41	Pre-Treatment	WNK1	65125	37	12	1005396	1005396	Missense_Mutation	SNP	C	T	7	104	c.5743C>T	c.(5743-5745)CCT>TCT	p.P1915S
Pat_41	Pre-Treatment	MRPL51	51258	37	12	6601441	6601441	Missense_Mutation	SNP	C	T	6	343	c.383G>A	c.(382-384)CGA>CAA	p.R128Q
Pat_41	Pre-Treatment	LRRC23	10233	37	12	7022090	7022090	Nonsense_Mutation	SNP	C	T	7	512	c.955C>T	c.(955-957)CGA>TGA	p.R319*
Pat_41	Pre-Treatment	SLCO1B1	10599	37	12	21370086	21370086	Missense_Mutation	SNP	G	A	4	226	c.1531G>A	c.(1531-1533)GGT>AGT	p.G511S
Pat_41	Pre-Treatment	ITPR2	3709	37	12	26553126	26553126	Missense_Mutation	SNP	C	T	5	428	c.7465G>A	c.(7465-7467)GTG>ATG	p.V2489M
Pat_41	Pre-Treatment	DDX11	1663	37	12	31237922	31237922	Missense_Mutation	SNP	G	C	6	43	c.500G>C	c.(499-501)AGA>ACA	p.R167T
Pat_41	Pre-Treatment	DDX11	1663	37	12	31256617	31256617	Missense_Mutation	SNP	T	C	6	168	c.2638T>C	c.(2638-2640)TGT>CGT	p.C880R
Pat_41	Pre-Treatment	SFRS2IP	9169	37	12	46345434	46345434	Missense_Mutation	SNP	T	C	21	268	c.296A>G	c.(295-297)AAG>AGG	p.K99R
Pat_41	Pre-Treatment	KCNH3	23416	37	12	49948198	49948198	Missense_Mutation	SNP	C	T	4	229	c.1997C>T	c.(1996-1998)ACG>ATG	p.T666M
Pat_41	Pre-Treatment	DIP2B	57609	37	12	51128860	51128860	Missense_Mutation	SNP	C	T	5	191	c.4048C>T	c.(4048-4050)CGT>TGT	p.R1350C
Pat_41	Pre-Treatment	NR4A1	3164	37	12	52448795	52448795	Missense_Mutation	SNP	C	T	6	341	c.683C>T	c.(682-684)ACG>ATG	p.T228M
Pat_41	Pre-Treatment	KRT73	319101	37	12	53003040	53003040	Missense_Mutation	SNP	C	T	4	228	c.1357G>A	c.(1357-1359)GTG>ATG	p.V453M
Pat_41	Pre-Treatment	NCKAP1L	3071	37	12	54894338	54894338	Missense_Mutation	SNP	C	T	5	415	c.235C>T	c.(235-237)CGT>TGT	p.R79C
Pat_41	Pre-Treatment	NCKAP1L	3071	37	12	54917676	54917676	Missense_Mutation	SNP	G	A	5	194	c.2092G>A	c.(2092-2094)GTG>ATG	p.V698M
Pat_41	Pre-Treatment	OR6C1	390321	37	12	55714592	55714592	Missense_Mutation	SNP	C	T	15	137	c.209C>T	c.(208-210)TCG>TTG	p.S70L
Pat_41	Pre-Treatment	BAZ2A	11176	37	12	56994000	56994000	Missense_Mutation	SNP	C	T	4	38	c.4883G>A	c.(4882-4884)GGC>GAC	p.G1628D
Pat_41	Pre-Treatment	SHMT2	6472	37	12	57627789	57627789	Missense_Mutation	SNP	C	T	5	219	c.1283C>T	c.(1282-1284)GCC>GTC	p.A428V
Pat_41	Pre-Treatment	PPM1H	57460	37	12	63042293	63042293	Missense_Mutation	SNP	T	A	4	209	c.1521A>T	c.(1519-1521)TTA>TTT	p.L507F
Pat_41	Pre-Treatment	C12orf26	84190	37	12	82780698	82780698	Missense_Mutation	SNP	T	A	28	337	c.376T>A	c.(376-378)TTT>ATT	p.F126I
Pat_41	Pre-Treatment	CDK17	5128	37	12	96674618	96674618	Missense_Mutation	SNP	G	A	4	150	c.1502C>T	c.(1501-1503)CCG>CTG	p.P501L
Pat_41	Pre-Treatment	GCN1L1	10985	37	12	120595667	120595667	Missense_Mutation	SNP	C	T	4	67	c.3073G>A	c.(3073-3075)GGG>AGG	p.G1025R
Pat_41	Pre-Treatment	KDM2B	84678	37	12	122016778	122016778	Missense_Mutation	SNP	C	T	4	176	c.200G>A	c.(199-201)GGC>GAC	p.G67D
Pat_41	Pre-Treatment	NCOR2	9612	37	12	124957628	124957628	Missense_Mutation	SNP	G	A	4	151	c.461C>T	c.(460-462)CCG>CTG	p.P154L
Pat_41	Pre-Treatment	EP400	57634	37	12	132445261	132445261	Missense_Mutation	SNP	A	C	7	40	c.97A>C	c.(97-99)AAC>CAC	p.N33H
Pat_41	Pre-Treatment	DDX51	317781	37	12	132624223	132624223	Missense_Mutation	SNP	G	A	5	82	c.1931C>T	c.(1930-1932)CCT>CTT	p.P644L
Pat_41	Pre-Treatment	MPHOSPH8	54737	37	13	20221066	20221066	Missense_Mutation	SNP	G	A	6	476	c.853G>A	c.(853-855)GAC>AAC	p.D285N
Pat_41	Pre-Treatment	RASL11A	387496	37	13	27847209	27847209	Missense_Mutation	SNP	G	A	4	218	c.307G>A	c.(307-309)GTG>ATG	p.V103M
Pat_41	Pre-Treatment	SLC25A30	253512	37	13	45980097	45980097	Missense_Mutation	SNP	C	T	4	120	c.228G>A	c.(226-228)ATG>ATA	p.M76I
Pat_41	Pre-Treatment	ATP11A	23250	37	13	113508684	113508684	Missense_Mutation	SNP	G	A	4	96	c.2083G>A	c.(2083-2085)GCG>ACG	p.A695T
Pat_41	Pre-Treatment	MCF2L	23263	37	13	113730403	113730403	Missense_Mutation	SNP	G	C	6	67	c.1603G>C	c.(1603-1605)GAA>CAA	p.E535Q
Pat_41	Pre-Treatment	P704P	641455	37	14	20020008	20020008	Missense_Mutation	SNP	C	G	6	607	c.213G>C	c.(211-213)TGG>TGC	p.W71C
Pat_41	Pre-Treatment	P704P	641455	37	14	20020013	20020013	Missense_Mutation	SNP	G	C	6	550	c.208C>G	c.(208-210)CCC>GCC	p.P70A
Pat_41	Pre-Treatment	MYH6	4624	37	14	23855654	23855654	Missense_Mutation	SNP	C	T	5	294	c.4829G>A	c.(4828-4830)CGC>CAC	p.R1610H
Pat_41	Pre-Treatment	COCH	1690	37	14	31355068	31355068	Missense_Mutation	SNP	G	A	5	245	c.1027G>A	c.(1027-1029)GTA>ATA	p.V343I
Pat_41	Pre-Treatment	STRN3	29966	37	14	31380279	31380279	Missense_Mutation	SNP	G	A	4	230	c.1688C>T	c.(1687-1689)CCG>CTG	p.P563L
Pat_41	Pre-Treatment	HECTD1	25831	37	14	31642515	31642515	Nonsense_Mutation	SNP	G	A	7	446	c.1003C>T	c.(1003-1005)CGA>TGA	p.R335*
Pat_41	Pre-Treatment	C14orf179	112752	37	14	76455273	76455273	Missense_Mutation	SNP	G	A	5	232	c.100G>A	c.(100-102)GAG>AAG	p.E34K
Pat_41	Pre-Treatment	TECPR2	9895	37	14	102900744	102900744	Missense_Mutation	SNP	C	A	4	139	c.1590C>A	c.(1588-1590)TTC>TTA	p.F530L
Pat_41	Pre-Treatment	CDC42BPB	9578	37	14	103447186	103447186	Missense_Mutation	SNP	G	A	4	156	c.1064C>T	c.(1063-1065)GCA>GTA	p.A355V
Pat_41	Pre-Treatment	AKT1	207	37	14	105243030	105243030	Missense_Mutation	SNP	C	T	6	195	c.253G>A	c.(253-255)GAA>AAA	p.E85K
Pat_41	Pre-Treatment	AHNAK2	113146	37	14	105420232	105420232	Missense_Mutation	SNP	G	A	4	152	c.1556C>T	c.(1555-1557)GCG>GTG	p.A519V
Pat_41	Pre-Treatment	PACS2	23241	37	14	105836206	105836206	Missense_Mutation	SNP	C	G	3	43	c.770C>G	c.(769-771)GCG>GGG	p.A257G
Pat_41	Pre-Treatment	ADAM6	8755	37	14	106573144	106573144	Splice_Site	SNP	T	A	4	86	c.29299_splice	c.e1363-1	

Pat_41	Pre-Treatment	HERC2	8924	37	15	28377842	28377842	Missense_Mutation	SNP	C	T	4	147	c.12365G>A	.(12364-12366)CGG>CA	p.R4122Q
Pat_41	Pre-Treatment	C15orf55	256646	37	15	34642939	34642939	Missense_Mutation	SNP	A	G	8	121	c.760A>G	c.(760-762)ACT>GCT	p.T254A
Pat_41	Pre-Treatment	AQR	9716	37	15	35202473	35202473	Missense_Mutation	SNP	C	T	4	196	c.1526G>A	c.(1525-1527)CGA>CAA	p.R509Q
Pat_41	Pre-Treatment	BUB1B	701	37	15	40477780	40477780	Missense_Mutation	SNP	C	T	4	220	c.995C>T	c.(994-996)GCT>GTT	p.A332V
Pat_41	Pre-Treatment	ULK3	25989	37	15	75134640	75134640	Missense_Mutation	SNP	A	T	13	135	c.224T>A	c.(223-225)GTG>GAG	p.V75E
Pat_41	Pre-Treatment	ADAMTSL3	57188	37	15	84442357	84442357	Missense_Mutation	SNP	G	A	4	162	c.272G>A	c.(271-273)TGT>TAT	p.C91Y
Pat_41	Pre-Treatment	POLG	5428	37	15	89861811	89861811	Missense_Mutation	SNP	C	T	8	248	c.3443G>A	c.(3442-3444)CGC>CAC	p.R1148H
Pat_41	Pre-Treatment	POLG	5428	37	15	89864150	89864150	Missense_Mutation	SNP	C	T	4	148	c.2828G>A	c.(2827-2829)CGT>CAT	p.R943H
Pat_41	Pre-Treatment	NPRL3	8131	37	16	162729	162729	Missense_Mutation	SNP	G	A	4	63	c.439C>T	c.(439-441)CGT>TGT	p.R147C
Pat_41	Pre-Treatment	MSLNL	401827	37	16	830799	830799	Missense_Mutation	SNP	T	G	6	393	c.202A>C	c.(202-204)ACC>CCC	p.T68P
Pat_41	Pre-Treatment	RPUSD1	113000	37	16	836138	836138	Missense_Mutation	SNP	C	T	4	74	c.751G>A	c.(751-753)GTG>ATG	p.V251M
Pat_41	Pre-Treatment	PTX4	390667	37	16	1537647	1537647	Missense_Mutation	SNP	G	A	3	45	c.451C>T	c.(451-453)CGC>TGC	p.R151C
Pat_41	Pre-Treatment	ABCA3	21	37	16	2369709	2369709	Missense_Mutation	SNP	G	A	4	117	c.746C>T	c.(745-747)CCG>CTG	p.P249L
Pat_41	Pre-Treatment	NTN3	4917	37	16	2522489	2522489	Missense_Mutation	SNP	C	T	4	103	c.787C>T	c.(787-789)CGG>TGG	p.R263W
Pat_41	Pre-Treatment	CORO7	79585	37	16	4414276	4414276	Splice_Site	SNP	C	T	3	24	c.1275_splice	c.e14+1	p.S425_splice
Pat_41	Pre-Treatment	ABAT	18	37	16	8866748	8866748	Missense_Mutation	SNP	C	T	13	105	c.928C>T	c.(928-930)CGG>TGG	p.R310W
Pat_41	Pre-Treatment	UMOD	7369	37	16	20357602	20357602	Missense_Mutation	SNP	G	A	4	195	c.1028C>T	c.(1027-1029)TCG>TTG	p.S343L
Pat_41	Pre-Treatment	RBBP6	5930	37	16	24580584	24580584	Missense_Mutation	SNP	A	T	13	182	c.2573A>T	c.(2572-2574)GAG>GTG	p.E858V
Pat_41	Pre-Treatment	IL4R	3566	37	16	27374931	27374931	Missense_Mutation	SNP	C	T	4	95	c.2258C>T	c.(2257-2259)TCG>TTG	p.S753L
Pat_41	Pre-Treatment	ZNF267	10308	37	16	31927690	31927690	Missense_Mutation	SNP	G	A	5	249	c.2120G>A	c.(2119-2121)CGG>CAG	p.R707Q
Pat_41	Pre-Treatment	ZNF267	10308	37	16	31927702	31927702	Missense_Mutation	SNP	G	C	5	253	c.2132G>C	c.(2131-2133)AGT>ACT	p.S711T
Pat_41	Pre-Treatment	SLC6A10P	386757	37	16	32890622	32890622	Missense_Mutation	SNP	T	G	4	73	c.264A>C	c.(262-264)AAA>AAC	p.K88N
Pat_41	Pre-Treatment	ZNF423	23090	37	16	49660102	49660102	Missense_Mutation	SNP	G	A	40	363	c.3556C>T	c.(3556-3558)CAC>TAC	p.H1186Y
Pat_41	Pre-Treatment	NOD2	64127	37	16	50744988	50744988	Missense_Mutation	SNP	C	T	4	186	c.1166C>T	c.(1165-1167)ACG>ATG	p.T389M
Pat_41	Pre-Treatment	NUP93	9688	37	16	56832442	56832442	Missense_Mutation	SNP	C	T	4	145	c.352C>T	c.(352-354)CGG>TGG	p.R118W
Pat_41	Pre-Treatment	NQO1	1728	37	16	69746963	69746963	Missense_Mutation	SNP	C	T	6	650	c.487G>A	c.(487-489)GGG>AGG	p.G163R
Pat_41	Pre-Treatment	WWOX	51741	37	16	78466647	78466647	Missense_Mutation	SNP	A	G	32	490	c.1054A>G	c.(1054-1056)ATG>GTG	p.M352V
Pat_41	Pre-Treatment	PKD1L2	114780	37	16	81181855	81181855	Missense_Mutation	SNP	G	A	4	109	c.4861C>T	c.(4861-4863)CGG>TGG	p.R1621W
Pat_41	Pre-Treatment	GAN	8139	37	16	81399016	81399016	Missense_Mutation	SNP	C	T	5	356	c.1435C>T	c.(1435-1437)CGT>TGT	p.R479C
Pat_41	Pre-Treatment	KLHL36	79786	37	16	84690665	84690665	Missense_Mutation	SNP	G	C	3	90	c.252G>C	c.(250-252)CAG>CAC	p.Q84H
Pat_41	Pre-Treatment	PRDM7	11105	37	16	90126823	90126823	Missense_Mutation	SNP	T	G	5	165	c.1159A>C	c.(1159-1161)ATG>CTG	p.M387L
Pat_41	Pre-Treatment	SMG6	23293	37	17	2203337	2203337	Missense_Mutation	SNP	C	T	4	141	c.710G>A	c.(709-711)AGG>AAG	p.R237K
Pat_41	Pre-Treatment	ANKFY1	51479	37	17	4074017	4074017	Missense_Mutation	SNP	C	T	4	163	c.3278G>A	c.(3277-3279)CGA>CAA	p.R1093Q
Pat_41	Pre-Treatment	POLR2A	5430	37	17	7401483	7401483	Missense_Mutation	SNP	G	A	4	141	c.1289G>A	c.(1288-1290)CGT>CAT	p.R430H
Pat_41	Pre-Treatment	TP53	7157	37	17	7577139	7577139	Missense_Mutation	SNP	G	C	5	29	c.799C>G	c.(799-801)CGG>GGG	p.R267G
Pat_41	Pre-Treatment	NLK	51701	37	17	26495646	26495646	Missense_Mutation	SNP	G	A	5	209	c.1010G>A	c.(1009-1011)CGA>CAA	p.R337Q
Pat_41	Pre-Treatment	CORO6	84940	37	17	27943849	27943849	Missense_Mutation	SNP	C	T	8	272	c.875G>A	c.(874-876)CGG>CAG	p.R292Q
Pat_41	Pre-Treatment	MLLT6	4302	37	17	36863766	36863766	Missense_Mutation	SNP	G	A	4	202	c.217G>A	c.(217-219)GGG>AGG	p.G73R
Pat_41	Pre-Treatment	KRT28	162605	37	17	38953286	38953286	Missense_Mutation	SNP	G	A	4	88	c.860C>T	c.(859-861)TCG>TTG	p.S287L
Pat_41	Pre-Treatment	KRTAP4-11	653240	37	17	39274310	39274311	Missense_Mutation	DNP	CT	TC	4	162	c.257_258AG>GA	c.(256-258)AAG>AGA	p.K86R
Pat_41	Pre-Treatment	HOXB3	3213	37	17	46628349	46628349	Missense_Mutation	SNP	G	A	5	461	c.643C>T	c.(643-645)CGG>TGG	p.R215W
Pat_41	Pre-Treatment	LRRC59	55379	37	17	48465438	48465438	Missense_Mutation	SNP	C	T	6	419	c.485G>A	c.(484-486)CGG>CAG	p.R162Q
Pat_41	Pre-Treatment	RNF43	54894	37	17	56435252	56435252	Missense_Mutation	SNP	C	T	4	166	c.1885G>A	c.(1885-1887)GCC>ACC	p.A629T
Pat_41	Pre-Treatment	TNRC6C	57690	37	17	76047011	76047011	Missense_Mutation	SNP	G	A	4	184	c.1868G>A	c.(1867-1869)AGT>AAT	p.S623N
Pat_41	Pre-Treatment	RPTOR	57521	37	17	78933974	78933974	Missense_Mutation	SNP	G	A	5	113	c.3574G>A	c.(3574-3576)GTC>ATC	p.V1192I
Pat_41	Pre-Treatment	EMILIN2	84034	37	18	2885114	2885114	Missense_Mutation	SNP	G	A	11	174	c.410G>A	c.(409-411)CGA>CAA	p.R137Q
Pat_41	Pre-Treatment	DLGAP1	9229	37	18	3879678	3879678	Missense_Mutation	SNP	G	A	15	249	c.391C>T	c.(391-393)CGC>TGC	p.R131C

Pat_41	Pre-Treatment	CEP192	55125	37	18	13055903	13055903	Missense_Mutation	SNP	C	T	10	153	c.3314C>T	c.(3313-3315)TCA>TTA	p.S1105L
Pat_41	Pre-Treatment	ASXL3	80816	37	18	31251776	31251776	Missense_Mutation	SNP	C	T	4	69	c.661C>T	c.(661-663)CCC>TCC	p.P221S
Pat_41	Pre-Treatment	ZBTB7C	201501	37	18	45556097	45556097	Missense_Mutation	SNP	C	T	3	27	c.1394G>A	c.(1393-1395)CGC>CAC	p.R465H
Pat_41	Pre-Treatment	MYO5B	4645	37	18	47500907	47500907	Missense_Mutation	SNP	G	A	5	363	c.1135C>T	c.(1135-1137)CGC>TGC	p.R379C
Pat_41	Pre-Treatment	CTDP1	9150	37	18	77513743	77513743	Missense_Mutation	SNP	G	A	4	70	c.2839G>A	c.(2839-2841)GAC>AAC	p.D947N
Pat_41	Pre-Treatment	ZNF556	80032	37	19	2877321	2877321	Missense_Mutation	SNP	G	A	4	112	c.365G>A	c.(364-366)CGT>CAT	p.R122H
Pat_41	Pre-Treatment	NCLN	56926	37	19	3207456	3207456	Missense_Mutation	SNP	G	A	4	219	c.1621G>A	c.(1621-1623)GTG>ATG	p.V541M
Pat_41	Pre-Treatment	STAP2	55620	37	19	4325471	4325471	Missense_Mutation	SNP	G	A	5	275	c.901C>T	c.(901-903)CCC>TCC	p.P301S
Pat_41	Pre-Treatment	PLIN4	729359	37	19	4511094	4511094	Missense_Mutation	SNP	C	T	4	139	c.2836G>A	c.(2836-2838)GCT>ACT	p.A946T
Pat_41	Pre-Treatment	KIAA1543	57662	37	19	7675610	7675610	Missense_Mutation	SNP	G	A	5	228	c.925G>A	c.(925-927)GAG>AAG	p.E309K
Pat_41	Pre-Treatment	MUC16	94025	37	19	9045743	9045743	Missense_Mutation	SNP	C	T	4	137	c.35888G>A	c.(35887-35889)AGT>AAT	p.S11963N
Pat_41	Pre-Treatment	MUC16	94025	37	19	9084835	9084835	Missense_Mutation	SNP	G	A	6	76	c.6980C>T	c.(6979-6981)TCC>TTC	p.S2327F
Pat_41	Pre-Treatment	ZNF564	163050	37	19	12638407	12638407	Missense_Mutation	SNP	G	A	6	383	c.515C>T	c.(514-516)CCG>CTG	p.P172L
Pat_41	Pre-Treatment	FBXW9	84261	37	19	12805466	12805466	Missense_Mutation	SNP	G	A	4	94	c.590C>T	c.(589-591)ACG>ATG	p.T197M
Pat_41	Pre-Treatment	SYDE1	85360	37	19	15224616	15224616	Missense_Mutation	SNP	G	A	6	426	c.2050G>A	c.(2050-2052)GAG>AAG	p.E684K
Pat_41	Pre-Treatment	ILVBL	10994	37	19	15228714	15228714	Nonsense_Mutation	SNP	C	T	14	152	c.1164G>A	c.(1162-1164)TGG>TGA	p.W388*
Pat_41	Pre-Treatment	TMEM38A	79041	37	19	16791303	16791303	Missense_Mutation	SNP	G	A	6	431	c.377G>A	c.(376-378)CGA>CAA	p.R126Q
Pat_41	Pre-Treatment	FAM129C	199786	37	19	17654201	17654201	Missense_Mutation	SNP	G	A	5	321	c.1498G>A	c.(1498-1500)GCT>ACT	p.A500T
Pat_41	Pre-Treatment	ZNF626	199777	37	19	20808006	20808006	Missense_Mutation	SNP	T	C	7	403	c.677A>G	c.(676-678)GAG>GGG	p.E226G
Pat_41	Pre-Treatment	ZNF493	284443	37	19	21606468	21606468	Missense_Mutation	SNP	C	T	4	172	c.623C>T	c.(622-624)CCT>CTT	p.P208L
Pat_41	Pre-Treatment	ZNF91	7644	37	19	23544783	23544783	Missense_Mutation	SNP	C	T	8	537	c.998G>A	c.(997-999)CGT>CAT	p.R333H
Pat_41	Pre-Treatment	HAUS5	23354	37	19	36110393	36110393	Missense_Mutation	SNP	G	A	3	38	c.1247G>A	c.(1246-1248)CGG>CAG	p.R416Q
Pat_41	Pre-Treatment	IL28B	282617	37	19	39735086	39735086	Missense_Mutation	SNP	G	A	3	31	c.229C>T	c.(229-231)CCC>TCC	p.P77S
Pat_41	Pre-Treatment	ZNF780B	163131	37	19	40541297	40541297	Missense_Mutation	SNP	C	T	6	300	c.1469G>A	c.(1468-1470)CGA>CAA	p.R490Q
Pat_41	Pre-Treatment	CCDC97	90324	37	19	41828519	41828519	Missense_Mutation	SNP	G	A	5	310	c.931G>A	c.(931-933)GAC>AAC	p.D311N
Pat_41	Pre-Treatment	PSG3	5671	37	19	43234208	43234208	Missense_Mutation	SNP	G	A	5	425	c.710C>T	c.(709-711)CCG>CTG	p.P237L
Pat_41	Pre-Treatment	PSG5	5673	37	19	43689023	43689023	Missense_Mutation	SNP	C	A	54	757	c.341G>T	c.(340-342)CGG>CTG	p.R114L
Pat_41	Pre-Treatment	SYMPK	8189	37	19	46338422	46338422	Missense_Mutation	SNP	G	A	4	188	c.1307C>T	c.(1306-1308)CCC>CTC	p.P436L
Pat_41	Pre-Treatment	CRX	1406	37	19	48339605	48339605	Missense_Mutation	SNP	G	A	4	144	c.206G>A	c.(205-207)CGT>CAT	p.R69H
Pat_41	Pre-Treatment	PPFIA3	8541	37	19	49637315	49637315	Missense_Mutation	SNP	G	A	5	260	c.1270G>A	c.(1270-1272)GAT>AAT	p.D424N
Pat_41	Pre-Treatment	AP2A1	160	37	19	50270427	50270427	Missense_Mutation	SNP	C	T	4	144	c.37C>T	c.(37-39)CTC>TTC	p.L13F
Pat_41	Pre-Treatment	ZNF649	65251	37	19	52394736	52394736	Missense_Mutation	SNP	T	C	4	233	c.653A>G	c.(652-654)AAG>AGG	p.K218R
Pat_41	Pre-Treatment	ZNF578	147660	37	19	53014551	53014551	Missense_Mutation	SNP	G	A	7	393	c.917G>A	c.(916-918)CGT>CAT	p.R306H
Pat_41	Pre-Treatment	ZNF845	91664	37	19	53856702	53856702	Missense_Mutation	SNP	G	A	9	264	c.2774G>A	c.(2773-2775)CGT>CAT	p.R925H
Pat_41	Pre-Treatment	ZNF845	91664	37	19	53856761	53856761	Missense_Mutation	SNP	T	C	6	180	c.2833T>C	c.(2833-2835)TGT>CGT	p.C945R
Pat_41	Pre-Treatment	LILRA3	11026	37	19	54802193	54802193	Missense_Mutation	SNP	G	A	3	67	c.995C>T	c.(994-996)CCG>CTG	p.P332L
Pat_41	Pre-Treatment	ZBTB45	84878	37	19	59028425	59028425	Nonsense_Mutation	SNP	G	A	5	472	c.616C>T	c.(616-618)CGA>TGA	p.R206*
Pat_41	Pre-Treatment	PDIA6	10130	37	2	10942730	10942730	Missense_Mutation	SNP	C	A	14	226	c.56G>T	c.(55-57)GGT>GTT	p.G19V
Pat_41	Pre-Treatment	KIF3C	3797	37	2	26204170	26204170	Missense_Mutation	SNP	C	T	4	169	c.617G>A	c.(616-618)AGC>AAC	p.S206N
Pat_41	Pre-Treatment	GPR113	165082	37	2	26537309	26537309	Missense_Mutation	SNP	C	T	4	123	c.1105G>A	c.(1105-1107)GCC>ACC	p.A369T
Pat_41	Pre-Treatment	SEMA4F	10505	37	2	74889932	74889932	Missense_Mutation	SNP	G	A	8	293	c.530G>A	c.(529-531)CGG>CAG	p.R177Q
Pat_41	Pre-Treatment	VWA3B	200403	37	2	98866818	98866818	Missense_Mutation	SNP	A	C	18	157	c.2711A>C	c.(2710-2712)AAG>ACG	p.K904T
Pat_41	Pre-Treatment	MAP4K4	9448	37	2	102486786	102486786	Missense_Mutation	SNP	C	T	3	46	c.2426C>T	c.(2425-2427)ACG>ATG	p.T809M
Pat_41	Pre-Treatment	ZC3H6	376940	37	2	113089358	113089358	Missense_Mutation	SNP	G	A	4	213	c.2863G>A	c.(2863-2865)GGT>AGT	p.G955S
Pat_41	Pre-Treatment	POLR1B	84172	37	2	113333019	113333019	Missense_Mutation	SNP	G	A	22	267	c.3121G>A	c.(3121-3123)GAA>AAA	p.E1041K
Pat_41	Pre-Treatment	TMEM177	80775	37	2	120439210	120439210	Missense_Mutation	SNP	C	T	4	124	c.781C>T	c.(781-783)CGC>TGC	p.R261C
Pat_41	Pre-Treatment	POTEF	728378	37	2	130877802	130877802	Missense_Mutation	SNP	T	C	6	680	c.287A>G	c.(286-288)AAC>AGC	p.N96S

Pat_41	Pre-Treatment	NEB	4703	37	2	152426597	152426597	Missense_Mutation	SNP	C	T	4	27	c.12325G>A	c.(12325-12327)GAT>AAT	p.D4109N
Pat_41	Pre-Treatment	LY75	4065	37	2	160690699	160690699	Missense_Mutation	SNP	G	A	16	224	c.3697C>T	c.(3697-3699)CCA>TCA	p.P1233S
Pat_41	Pre-Treatment	COL3A1	1281	37	2	189873777	189873777	Missense_Mutation	SNP	C	T	5	322	c.3653C>T	c.(3652-3654)CCG>CTG	p.P1218L
Pat_41	Pre-Treatment	DNAH7	56171	37	2	196801470	196801470	Missense_Mutation	SNP	C	T	4	108	c.3125G>A	c.(3124-3126)AGG>AAG	p.R1042K
Pat_41	Pre-Treatment	FN1	2335	37	2	216236954	216236954	Missense_Mutation	SNP	G	A	12	126	c.6392C>T	c.(6391-6393)TCT>TTT	p.S2131F
Pat_41	Pre-Treatment	NCL	4691	37	2	232319964	232319964	Nonsense_Mutation	SNP	G	A	4	192	c.2071C>T	c.(2071-2073)CGA>TGA	p.R691*
Pat_41	Pre-Treatment	ALPP	250	37	2	233244579	233244579	Missense_Mutation	SNP	C	T	4	127	c.590C>T	c.(589-591)CCT>CTT	p.P197L
Pat_41	Pre-Treatment	COL6A3	1293	37	2	238243521	238243521	Missense_Mutation	SNP	G	A	4	241	c.8977C>T	c.(8977-8979)CGT>TGT	p.R2993C
Pat_41	Pre-Treatment	OR6B2	389090	37	2	240969130	240969131	Missense_Mutation	DNP	AG	GA	4	105	c.716_717CT>TC	c.(715-717)TCT>TTC	p.S239F
Pat_41	Pre-Treatment	SNAP25	6616	37	20	10279933	10279933	Missense_Mutation	SNP	G	A	34	604	c.425G>A	c.(424-426)CGA>CAA	p.R142Q
Pat_41	Pre-Treatment	GGTLC1	92086	37	20	23966333	23966333	Missense_Mutation	SNP	C	T	5	305	c.502G>A	c.(502-504)GTC>ATC	p.V168I
Pat_41	Pre-Treatment	PTPRT	11122	37	20	40790038	40790038	Missense_Mutation	SNP	G	A	4	227	c.2636C>T	c.(2635-2637)ACG>ATG	p.T879M
Pat_41	Pre-Treatment	LAMA5	3911	37	20	60927114	60927114	Missense_Mutation	SNP	C	T	4	79	c.709G>A	c.(709-711)GGA>AGA	p.G237R
Pat_41	Pre-Treatment	DIDO1	11083	37	20	61542508	61542508	Missense_Mutation	SNP	C	T	4	161	c.457G>A	c.(457-459)GAT>AAT	p.D153N
Pat_41	Pre-Treatment	KRTAP10-7	386675	37	21	46021245	46021245	Missense_Mutation	SNP	G	A	9	703	c.709G>A	c.(709-711)GTC>ATC	p.V237I
Pat_41	Pre-Treatment	MCM3AP	8888	37	21	47703734	47703734	Missense_Mutation	SNP	G	A	4	193	c.1238C>T	c.(1237-1239)CCG>CTG	p.P413L
Pat_41	Pre-Treatment	PI4KA	5297	37	22	21087345	21087345	Missense_Mutation	SNP	C	T	4	87	c.4028G>A	c.(4027-4029)CGT>CAT	p.R1343H
Pat_41	Pre-Treatment	ZNF70	7621	37	22	24086331	24086331	Missense_Mutation	SNP	C	T	4	233	c.997G>A	c.(997-999)GAG>AAG	p.E333K
Pat_41	Pre-Treatment	SLC2A11	66035	37	22	24226594	24226594	Missense_Mutation	SNP	G	A	4	124	c.1268G>A	c.(1267-1269)GGC>GAC	p.G423D
Pat_41	Pre-Treatment	SSTR3	6753	37	22	37602887	37602887	Missense_Mutation	SNP	C	T	4	159	c.956G>A	c.(955-957)CGC>CAC	p.R319H
Pat_41	Pre-Treatment	MGAT3	4248	37	22	39884335	39884335	Missense_Mutation	SNP	T	C	5	308	c.983T>C	c.(982-984)CTT>CCT	p.L328P
Pat_41	Pre-Treatment	MEI1	150365	37	22	42172199	42172199	Missense_Mutation	SNP	G	A	5	130	c.2638G>A	c.(2638-2640)GGT>AGT	p.G880S
Pat_41	Pre-Treatment	ZNF860	344787	37	3	32031962	32031962	Missense_Mutation	SNP	A	G	22	437	c.1391A>G	c.(1390-1392)CAT>CGT	p.H464R
Pat_41	Pre-Treatment	TRANK1	9881	37	3	36871069	36871069	Missense_Mutation	SNP	C	T	5	175	c.7013G>A	c.(7012-7014)CGC>CAC	p.R2338H
Pat_41	Pre-Treatment	MST1R	4486	37	3	49940664	49940664	Missense_Mutation	SNP	G	A	20	205	c.379C>T	c.(379-381)CCC>TCC	p.P127S
Pat_41	Pre-Treatment	GNAI2	2771	37	3	50293707	50293707	Missense_Mutation	SNP	C	T	4	171	c.548C>T	c.(547-549)ACG>ATG	p.T183M
Pat_41	Pre-Treatment	GRM2	2912	37	3	51749086	51749086	Missense_Mutation	SNP	C	T	4	127	c.1297C>T	c.(1297-1299)CGC>TGC	p.R433C
Pat_41	Pre-Treatment	TLR9	54106	37	3	52263753	52263753	Missense_Mutation	SNP	C	T	4	116	c.218G>A	c.(217-219)CGA>CAA	p.R73Q
Pat_41	Pre-Treatment	MAGI1	9223	37	3	66023736	66023736	Missense_Mutation	SNP	C	T	5	355	c.248G>A	c.(247-249)CGC>CAC	p.R83H
Pat_41	Pre-Treatment	UBA3	9039	37	3	69112237	69112237	Missense_Mutation	SNP	G	A	5	220	c.589C>T	c.(589-591)CCT>TCT	p.P197S
Pat_41	Pre-Treatment	FAM86D	692099	37	3	75476581	75476581	Missense_Mutation	SNP	C	T	3	48	c.484G>A	c.(484-486)GCA>ACA	p.A162T
Pat_41	Pre-Treatment	ABI3BP	25890	37	3	100489784	100489784	Missense_Mutation	SNP	C	T	4	191	c.2411G>A	c.(2410-2412)CGA>CAA	p.R804Q
Pat_41	Pre-Treatment	PLXND1	23129	37	3	129290536	129290536	Missense_Mutation	SNP	G	A	4	213	c.3229C>T	c.(3229-3231)CGC>TGC	p.R1077C
Pat_41	Pre-Treatment	TMCC1	23023	37	3	129370592	129370592	Missense_Mutation	SNP	T	A	4	156	c.1694A>T	c.(1693-1695)CAG>CTG	p.Q565L
Pat_41	Pre-Treatment	C3orf57	165679	37	3	161064020	161064020	Missense_Mutation	SNP	C	T	9	163	c.92G>A	c.(91-93)CGA>CAA	p.R31Q
Pat_41	Pre-Treatment	ACTL6A	86	37	3	179291252	179291252	Missense_Mutation	SNP	G	A	4	114	c.373G>A	c.(373-375)GCA>ACA	p.A125T
Pat_41	Pre-Treatment	ALG3	10195	37	3	183961676	183961676	Missense_Mutation	SNP	G	A	3	49	c.835C>T	c.(835-837)CTC>TTC	p.L279F
Pat_41	Pre-Treatment	EIF4G1	1981	37	3	184042681	184042681	Missense_Mutation	SNP	C	T	4	218	c.2635C>T	c.(2635-2637)CGC>TGC	p.R879C
Pat_41	Pre-Treatment	EPHB3	2049	37	3	184298637	184298637	Nonsense_Mutation	SNP	C	T	4	210	c.2509C>T	c.(2509-2511)CGA>TGA	p.R837*
Pat_41	Pre-Treatment	TBC1D14	57533	37	4	7026952	7026952	Missense_Mutation	SNP	C	T	4	126	c.1979C>T	c.(1978-1980)ACG>ATG	p.T660M
Pat_41	Pre-Treatment	SORCS2	57537	37	4	7725544	7725544	Missense_Mutation	SNP	C	T	4	138	c.2545C>T	c.(2545-2547)CGC>TGC	p.R849C
Pat_41	Pre-Treatment	PCDH7	5099	37	4	30726141	30726141	Missense_Mutation	SNP	G	A	4	150	c.3097G>A	c.(3097-3099)GCA>ACA	p.A1033T
Pat_41	Pre-Treatment	LIMCH1	22998	37	4	41684416	41684416	Missense_Mutation	SNP	G	C	8	135	c.2632G>C	c.(2632-2634)GGA>CGA	p.G878R
Pat_41	Pre-Treatment	MUC7	4589	37	4	71346978	71346978	Missense_Mutation	SNP	T	C	6	622	c.517T>C	c.(517-519)TCT>CCT	p.S173P
Pat_41	Pre-Treatment	KIAA1109	84162	37	4	123167965	123167965	Missense_Mutation	SNP	G	A	4	234	c.5312G>A	c.(5311-5313)AGA>AAA	p.R1771K
Pat_41	Pre-Treatment	GAB1	2549	37	4	144387286	144387286	Missense_Mutation	SNP	G	A	5	345	c.1834G>A	c.(1834-1836)GGA>AGA	p.G612R
Pat_41	Pre-Treatment	TIGD4	201798	37	4	153691826	153691826	Missense_Mutation	SNP	G	A	6	388	c.331C>T	c.(331-333)CGT>TGT	p.R111C

Pat_41	Pre-Treatment	ETFDH	2110	37	4	159627981	159627981	Missense_Mutation	SNP	G	A	5	193	c.1669G>A	c.(1669-1671)GAG>AAG	p.E557K
Pat_41	Pre-Treatment	FAT1	2195	37	4	187542860	187542860	Missense_Mutation	SNP	C	T	4	70	c.4880G>A	c.(4879-4881)CGA>CAA	p.R1627Q
Pat_41	Pre-Treatment	ADAMTS16	170690	37	5	5242271	5242271	Missense_Mutation	SNP	G	A	4	104	c.2629G>A	c.(2629-2631)GTG>ATG	p.V877M
Pat_41	Pre-Treatment	MED10	84246	37	5	6372626	6372626	Missense_Mutation	SNP	G	T	4	154	c.398C>A	c.(397-399)CCG>CAG	p.P133Q
Pat_41	Pre-Treatment	PRDM9	56979	37	5	23527083	23527083	Missense_Mutation	SNP	G	C	4	190	c.1886G>C	c.(1885-1887)AGA>ACA	p.R629T
Pat_41	Pre-Treatment	MSH3	4437	37	5	79966006	79966006	Missense_Mutation	SNP	C	T	4	151	c.670C>T	c.(670-672)CGG>TGG	p.R224W
Pat_41	Pre-Treatment	MBLAC2	153364	37	5	89757012	89757012	Missense_Mutation	SNP	C	T	4	81	c.812G>A	c.(811-813)CGT>CAT	p.R271H
Pat_41	Pre-Treatment	GPR98	84059	37	5	90074707	90074707	Missense_Mutation	SNP	G	C	34	418	c.12875G>C	c.(12874-12876)AGT>ACT	p.S4292T
Pat_41	Pre-Treatment	GPR98	84059	37	5	90106705	90106705	Missense_Mutation	SNP	G	A	20	122	c.15628G>A	c.(15628-15630)GTA>ATA	p.V5210I
Pat_41	Pre-Treatment	3-Mar	115123	37	5	126253769	126253769	Missense_Mutation	SNP	C	T	4	154	c.95G>A	c.(94-96)AGC>AAC	p.S32N
Pat_41	Pre-Treatment	FBN2	2201	37	5	127710438	127710438	Missense_Mutation	SNP	C	G	6	84	c.1978G>C	c.(1978-1980)GAT>CAT	p.D660H
Pat_41	Pre-Treatment	FBN2	2201	37	5	127744405	127744405	Missense_Mutation	SNP	C	T	4	127	c.1040G>A	c.(1039-1041)CGT>CAT	p.R347H
Pat_41	Pre-Treatment	FSTL4	23105	37	5	132652206	132652206	Missense_Mutation	SNP	A	C	6	107	c.548T>G	c.(547-549)TTC>TGC	p.F183C
Pat_41	Pre-Treatment	SPOCK1	6695	37	5	136448165	136448165	Missense_Mutation	SNP	C	A	4	181	c.433G>T	c.(433-435)GCC>TCC	p.A145S
Pat_41	Pre-Treatment	PCDHAC2	56134	37	5	140362082	140362082	Missense_Mutation	SNP	G	C	6	132	c.2647G>C	c.(2647-2649)GGC>CGC	p.G883R
Pat_41	Pre-Treatment	PCDHGA6	56109	37	5	140754753	140754753	Missense_Mutation	SNP	T	C	4	228	c.1103T>C	c.(1102-1104)CTT>CCT	p.L368P
Pat_41	Pre-Treatment	SH3PXD2B	285590	37	5	171833335	171833335	Missense_Mutation	SNP	G	A	26	366	c.178C>T	c.(178-180)CCC>TCC	p.P60S
Pat_41	Pre-Treatment	CCHCR1	54535	37	6	31113476	31113476	Missense_Mutation	SNP	G	A	4	174	c.1423C>T	c.(1423-1425)CGG>TGG	p.R475W
Pat_41	Pre-Treatment	MICB	4277	37	6	31474904	31474904	Missense_Mutation	SNP	G	A	4	128	c.719G>A	c.(718-720)CGT>CAT	p.R240H
Pat_41	Pre-Treatment	TNXB	7148	37	6	32049975	32049975	Nonsense_Mutation	SNP	G	A	4	31	c.3574C>T	c.(3574-3576)CAG>TAG	p.Q1192*
Pat_41	Pre-Treatment	KIFC1	3833	37	6	33372825	33372825	Missense_Mutation	SNP	G	A	4	230	c.953G>A	c.(952-954)CGC>CAC	p.R318H
Pat_41	Pre-Treatment	TCTE1	202500	37	6	44254149	44254149	Missense_Mutation	SNP	C	T	4	166	c.398G>A	c.(397-399)CGC>CAC	p.R133H
Pat_41	Pre-Treatment	BAI3	577	37	6	69772890	69772890	Missense_Mutation	SNP	G	A	5	302	c.2398G>A	c.(2398-2400)GAT>AAT	p.D800N
Pat_41	Pre-Treatment	C6orf165	154313	37	6	88127995	88127995	Missense_Mutation	SNP	G	A	4	182	c.701G>A	c.(700-702)CGG>CAG	p.R234Q
Pat_41	Pre-Treatment	DSE	29940	37	6	116720546	116720546	Missense_Mutation	SNP	A	G	13	144	c.133A>G	c.(133-135)ATG>GTG	p.M45V
Pat_41	Pre-Treatment	EZR	7430	37	6	159188399	159188399	Missense_Mutation	SNP	G	A	5	254	c.1490C>T	c.(1489-1491)ACG>ATG	p.T497M
Pat_41	Pre-Treatment	WTAP	9589	37	6	160164786	160164786	Nonsense_Mutation	SNP	C	T	5	155	c.235C>T	c.(235-237)CGA>TGA	p.R79*
Pat_41	Pre-Treatment	FAM120B	84498	37	6	170626797	170626797	Missense_Mutation	SNP	A	G	4	192	c.319A>G	c.(319-321)AAG>GAG	p.K107E
Pat_41	Pre-Treatment	INTS1	26173	37	7	1542717	1542717	Missense_Mutation	SNP	G	A	4	104	c.169C>T	c.(169-171)CGC>TGC	p.R57C
Pat_41	Pre-Treatment	TTYH3	80727	37	7	2696113	2696113	Missense_Mutation	SNP	G	A	4	168	c.1195G>A	c.(1195-1197)GCC>ACC	p.A399T
Pat_41	Pre-Treatment	USP42	84132	37	7	6193668	6193668	Missense_Mutation	SNP	C	T	4	183	c.2483C>T	c.(2482-2484)GCG>GTG	p.A828V
Pat_41	Pre-Treatment	ZDHHC4	55146	37	7	6628363	6628363	Missense_Mutation	SNP	C	A	4	212	c.857C>A	c.(856-858)ACT>AAT	p.T286N
Pat_41	Pre-Treatment	TMEM195	392636	37	7	15433792	15433793	Missense_Mutation	DNP	GG	AA	8	193	c.621_622CC>TT	(619-624)AACCTT>AATTT	p.L208F
Pat_41	Pre-Treatment	ZMIZ2	83637	37	7	44806206	44806206	Missense_Mutation	SNP	G	A	4	104	c.2599G>A	c.(2599-2601)GTG>ATG	p.V867M
Pat_41	Pre-Treatment	ZNF727	442319	37	7	63538806	63538806	Missense_Mutation	SNP	C	G	6	118	c.1379C>G	c.(1378-1380)ACC>AGC	p.T460S
Pat_41	Pre-Treatment	CCDC146	57639	37	7	76891535	76891535	Nonsense_Mutation	SNP	C	T	5	190	c.1084C>T	c.(1084-1086)CGA>TGA	p.R362*
Pat_41	Pre-Treatment	POT1	25913	37	7	124464120	124464120	Missense_Mutation	SNP	G	A	4	125	c.1801C>T	c.(1801-1803)CCG>TCG	p.P601S
Pat_41	Pre-Treatment	UBE3C	9690	37	7	156963025	156963025	Missense_Mutation	SNP	C	T	9	427	c.223C>T	c.(223-225)CGC>TGC	p.R75C
Pat_41	Pre-Treatment	FBXO25	26260	37	8	413124	413124	Missense_Mutation	SNP	C	T	5	372	c.961C>T	c.(961-963)CGG>TGG	p.R321W
Pat_41	Pre-Treatment	MTMR9	66036	37	8	11172484	11172484	Nonsense_Mutation	SNP	C	T	22	181	c.1024C>T	c.(1024-1026)CAG>TAG	p.Q342*
Pat_41	Pre-Treatment	ADAMDEC1	27299	37	8	24257743	24257743	Missense_Mutation	SNP	C	T	4	155	c.1072C>T	c.(1072-1074)CTT>TTT	p.L358F
Pat_41	Pre-Treatment	PURG	29942	37	8	30889512	30889512	Missense_Mutation	SNP	C	T	15	150	c.787G>A	c.(787-789)GAG>AAG	p.E263K
Pat_41	Pre-Treatment	CHD7	55636	37	8	61764739	61764739	Missense_Mutation	SNP	C	T	5	199	c.5827C>T	c.(5827-5829)CGG>TGG	p.R1943W
Pat_41	Pre-Treatment	SLC10A5	347051	37	8	82607156	82607156	Missense_Mutation	SNP	C	T	7	93	c.52G>A	c.(52-54)GAA>AAA	p.E18K
Pat_41	Pre-Treatment	HAS2	3037	37	8	122641376	122641377	Nonsense_Mutation	DNP	GG	AA	47	460	c.204_205CC>TT	202-207)CACCGA>CATT	p.R69*
Pat_41	Pre-Treatment	MTSS1	9788	37	8	125601951	125601951	Missense_Mutation	SNP	C	T	5	410	c.295G>A	c.(295-297)GCT>ACT	p.A99T
Pat_41	Pre-Treatment	FAM135B	51059	37	8	139160771	139160771	Missense_Mutation	SNP	C	T	4	197	c.3440G>A	c.(3439-3441)GGC>GAC	p.G1147D

Pat_41	Pre-Treatment	TOP1MT	116447	37	8	144407583	144407583	Missense_Mutation	SNP	C	T	4	121	c.604G>A	c.(604-606)GAC>AAC	p.D202N
Pat_41	Pre-Treatment	TSTA3	7264	37	8	144695735	144695735	Missense_Mutation	SNP	C	T	3	53	c.769G>A	c.(769-771)GAG>AAG	p.E257K
Pat_41	Pre-Treatment	CCL27	10850	37	9	34662059	34662059	Missense_Mutation	SNP	C	T	6	254	c.221G>A	c.(220-222)CGC>CAC	p.R74H
Pat_41	Pre-Treatment	TMEM2	23670	37	9	74319553	74319553	Missense_Mutation	SNP	G	A	4	203	c.3152C>T	c.(3151-3153)CCG>CTG	p.P1051L
Pat_41	Pre-Treatment	FAM75C1	441452	37	9	90536665	90536665	Missense_Mutation	SNP	G	A	7	362	c.1843G>A	c.(1843-1845)GTA>ATA	p.V615I
Pat_41	Pre-Treatment	LPAR1	1902	37	9	113637878	113637878	Missense_Mutation	SNP	C	T	21	197	c.918G>A	c.(916-918)ATG>ATA	p.M306I
Pat_41	Pre-Treatment	TLR4	7099	37	9	120476765	120476765	Missense_Mutation	SNP	C	T	4	152	c.2359C>T	c.(2359-2361)CGC>TGC	p.R787C
Pat_41	Pre-Treatment	OR1N1	138883	37	9	125288851	125288851	Missense_Mutation	SNP	G	A	9	117	c.722C>T	c.(721-723)TCC>TTC	p.S241F
Pat_41	Pre-Treatment	ODF2	4957	37	9	131233716	131233716	Missense_Mutation	SNP	G	A	5	247	c.550G>A	c.(550-552)GAG>AAG	p.E184K
Pat_41	Pre-Treatment	GBGT1	26301	37	9	136029595	136029595	Missense_Mutation	SNP	C	T	4	140	c.413G>A	c.(412-414)CGT>CAT	p.R138H
Pat_41	Pre-Treatment	COL5A1	1289	37	9	137591886	137591886	Missense_Mutation	SNP	G	A	4	105	c.409G>A	c.(409-411)GTC>ATC	p.V137I
Pat_41	Pre-Treatment	NELF	26012	37	9	140347597	140347597	Missense_Mutation	SNP	C	T	4	99	c.958G>A	c.(958-960)GAG>AAG	p.E320K
Pat_41	Pre-Treatment	ASB11	140456	37	X	15301701	15301701	Missense_Mutation	SNP	C	T	6	443	c.898G>A	c.(898-900)GGT>AGT	p.G300S
Pat_41	Pre-Treatment	NHS	4810	37	X	17750562	17750562	Missense_Mutation	SNP	G	A	5	292	c.4871G>A	c.(4870-4872)CGT>CAT	p.R1624H
Pat_41	Pre-Treatment	MAP7D2	256714	37	X	20033394	20033394	Missense_Mutation	SNP	C	T	5	306	c.1573G>A	c.(1573-1575)GAG>AAG	p.E525K
Pat_41	Pre-Treatment	RPS6KA6	27330	37	X	83402002	83402002	Missense_Mutation	SNP	A	C	19	158	c.405T>G	c.(403-405)ATT>ATG	p.I135M
Pat_41	Pre-Treatment	MCART6	401612	37	X	103349910	103349910	Missense_Mutation	SNP	C	T	5	109	c.31G>A	c.(31-33)GAG>AAG	p.E11K
Pat_41	Post-Resistance	AGRN	375790	37	1	957839	957839	Missense_Mutation	SNP	G	A	5	171	c.460G>A	c.(460-462)GAA>AAA	p.E154K
Pat_41	Post-Resistance	SDF4	51150	37	1	1154193	1154193	Missense_Mutation	SNP	C	T	5	193	c.692G>A	c.(691-693)CGG>CAG	p.R231Q
Pat_41	Post-Resistance	TAS1R3	83756	37	1	1268373	1268373	Missense_Mutation	SNP	G	A	7	43	c.1348G>A	c.(1348-1350)GTG>ATG	p.V450M
Pat_41	Post-Resistance	TAS1R3	83756	37	1	1269318	1269318	Missense_Mutation	SNP	G	A	7	65	c.2033G>A	c.(2032-2034)GGG>GAG	p.G678E
Pat_41	Post-Resistance	CCNL2	81669	37	1	1322823	1322823	Missense_Mutation	SNP	C	T	10	100	c.1351G>A	c.(1351-1353)GAC>AAC	p.D451N
Pat_41	Post-Resistance	MIB2	142678	37	1	1559324	1559324	Missense_Mutation	SNP	C	T	12	33	c.592C>T	c.(592-594)CCT>TCT	p.P198S
Pat_41	Post-Resistance	MIB2	142678	37	1	1562727	1562727	Missense_Mutation	SNP	G	A	9	121	c.1600G>A	c.(1600-1602)GGC>AGC	p.G534S
Pat_41	Post-Resistance	CDK11B	984	37	1	1653122	1653122	Missense_Mutation	SNP	G	A	6	60	c.140C>T	c.(139-141)TCC>TTC	p.S47F
Pat_41	Post-Resistance	TNFRSF14	8764	37	1	2492081	2492081	Missense_Mutation	SNP	C	T	6	52	c.479C>T	c.(478-480)ACC>ATC	p.T160I
Pat_41	Post-Resistance	TP73	7161	37	1	3624249	3624249	Missense_Mutation	SNP	C	T	15	77	c.323C>T	c.(322-324)ACC>ATC	p.T108I
Pat_41	Post-Resistance	LRRC47	57470	37	1	3703477	3703477	Missense_Mutation	SNP	C	T	6	13	c.1013G>A	c.(1012-1014)GGG>GAG	p.G338E
Pat_41	Post-Resistance	KIAA0562	9731	37	1	3755608	3755608	Missense_Mutation	SNP	C	T	18	254	c.811G>A	c.(811-813)GAG>AAG	p.E271K
Pat_41	Post-Resistance	KIAA0562	9731	37	1	3765275	3765275	Missense_Mutation	SNP	G	A	10	84	c.184C>T	c.(184-186)CTT>TTT	p.L62F
Pat_41	Post-Resistance	AJAP1	55966	37	1	4772045	4772045	Missense_Mutation	SNP	C	T	19	253	c.115C>T	c.(115-117)CCC>TCC	p.P39S
Pat_41	Post-Resistance	AJAP1	55966	37	1	4772072	4772072	Missense_Mutation	SNP	C	T	8	123	c.142C>T	c.(142-144)CCG>TCG	p.P48S
Pat_41	Post-Resistance	RPL22	6146	37	1	6253111	6253111	Nonsense_Mutation	SNP	G	A	11	212	c.121C>T	c.(121-123)CAG>TAG	p.Q41*
Pat_41	Post-Resistance	ESPN	83715	37	1	6504683	6504683	Missense_Mutation	SNP	C	T	11	275	c.1133C>T	c.(1132-1134)TCC>TTC	p.S378F
Pat_41	Post-Resistance	TAS1R1	80835	37	1	6635378	6635378	Missense_Mutation	SNP	G	A	13	90	c.1186G>A	c.(1186-1188)GTG>ATG	p.V396M
Pat_41	Post-Resistance	ZBTB48	3104	37	1	6640677	6640677	Missense_Mutation	SNP	G	A	7	91	c.8G>A	c.(7-9)GGC>GAC	p.G3D
Pat_41	Post-Resistance	PHF13	148479	37	1	6680248	6680248	Missense_Mutation	SNP	C	T	4	74	c.527C>T	c.(526-528)CCC>CTC	p.P176L
Pat_41	Post-Resistance	PER3	8863	37	1	7887280	7887280	Missense_Mutation	SNP	G	A	13	115	c.2267G>A	c.(2266-2268)GGC>GAC	p.G756D
Pat_41	Post-Resistance	PER3	8863	37	1	7887297	7887297	Missense_Mutation	SNP	G	A	11	126	c.2284G>A	c.(2284-2286)GGA>AGA	p.G762R
Pat_41	Post-Resistance	PER3	8863	37	1	7887696	7887696	Missense_Mutation	SNP	C	T	13	167	c.2683C>T	c.(2683-2685)CCT>TCT	p.P895S
Pat_41	Post-Resistance	ERRFI1	54206	37	1	8075578	8075578	Nonsense_Mutation	SNP	C	T	16	611	c.102G>A	c.(100-102)TGG>TGA	p.W34*
Pat_41	Post-Resistance	RERE	473	37	1	8420002	8420002	Missense_Mutation	SNP	G	A	6	169	c.3440C>T	c.(3439-3441)ACA>ATA	p.T1147I
Pat_41	Post-Resistance	RERE	473	37	1	8425920	8425920	Missense_Mutation	SNP	C	T	13	235	c.1399G>A	c.(1399-1401)GCG>ACG	p.A467T
Pat_41	Post-Resistance	RERE	473	37	1	8616586	8616586	Nonsense_Mutation	SNP	G	A	13	514	c.673C>T	c.(673-675)CGA>TGA	p.R225*
Pat_41	Post-Resistance	RERE	473	37	1	8674729	8674729	Missense_Mutation	SNP	G	A	16	317	c.413C>T	c.(412-414)GCC>GTC	p.A138V
Pat_41	Post-Resistance	ENO1	2023	37	1	8926451	8926451	Missense_Mutation	SNP	C	T	20	282	c.554G>A	c.(553-555)GGA>GAA	p.G185E
Pat_41	Post-Resistance	UBE4B	10277	37	1	10197139	10197139	Missense_Mutation	SNP	C	T	35	143	c.2239C>T	c.(2239-2241)CCA>TCA	p.P747S

Pat_41	Post-Resistance	KIF1B	23095	37	1	10357072	10357072	Missense_Mutation	SNP	C	T	12	143	c.1979C>T	c.(1978-1980)ACA>ATA	p.T660I
Pat_41	Post-Resistance	KIF1B	23095	37	1	10383982	10383982	Missense_Mutation	SNP	C	T	39	296	c.2399C>T	c.(2398-2400)TCC>TTC	p.S800F
Pat_41	Post-Resistance	PGD	5226	37	1	10459183	10459183	Splice_Site	SNP	G	A	7	79	c.8_splice	c.e1+1	p.Q3_splice
Pat_41	Post-Resistance	PGD	5226	37	1	10460522	10460522	Missense_Mutation	SNP	G	A	17	153	c.157G>A	c.(157-159)GTG>ATG	p.V53M
Pat_41	Post-Resistance	CORT	1325	37	1	10510162	10510162	Missense_Mutation	SNP	G	A	11	209	c.32G>A	c.(31-33)GGC>GAC	p.G11D
Pat_41	Post-Resistance	C1orf127	148345	37	1	11008707	11008707	Nonsense_Mutation	SNP	C	T	12	105	c.1038G>A	c.(1036-1038)TGG>TGA	p.W346*
Pat_41	Post-Resistance	EXOSC10	5394	37	1	11147617	11147617	Missense_Mutation	SNP	G	A	25	497	c.977C>T	c.(976-978)ACC>ATC	p.T326I
Pat_41	Post-Resistance	EXOSC10	5394	37	1	11159836	11159836	Missense_Mutation	SNP	G	T	11	94	c.53C>A	c.(52-54)ACC>AAC	p.T18N
Pat_41	Post-Resistance	MTOR	2475	37	1	11169738	11169738	Missense_Mutation	SNP	C	T	34	171	c.7415G>A	c.(7414-7416)GGG>GAG	p.G2472E
Pat_41	Post-Resistance	ANGPTL7	10218	37	1	11254552	11254552	Missense_Mutation	SNP	G	A	28	457	c.707G>A	c.(706-708)AGC>AAC	p.S236N
Pat_41	Post-Resistance	MTOR	2475	37	1	11264622	11264622	Missense_Mutation	SNP	C	T	33	356	c.3940G>A	c.(3940-3942)GCC>ACC	p.A1314T
Pat_41	Post-Resistance	PTCHD2	57540	37	1	11586751	11586751	Missense_Mutation	SNP	C	T	40	220	c.2657C>T	c.(2656-2658)GCT>GTT	p.A886V
Pat_41	Post-Resistance	PTCHD2	57540	37	1	11591714	11591714	Missense_Mutation	SNP	G	A	6	59	c.3322G>A	c.(3322-3324)GCA>ACA	p.A1108T
Pat_41	Post-Resistance	PTCHD2	57540	37	1	11595687	11595687	Missense_Mutation	SNP	C	T	8	132	c.3802C>T	c.(3802-3804)CCC>TCC	p.P1268S
Pat_41	Post-Resistance	CLCN6	1185	37	1	11894605	11894605	Missense_Mutation	SNP	G	A	14	182	c.1751G>A	c.(1750-1752)GGC>GAC	p.G584D
Pat_41	Post-Resistance	KIAA2013	90231	37	1	11983300	11983300	Missense_Mutation	SNP	G	A	4	27	c.1280C>T	c.(1279-1281)TCT>TTT	p.S427F
Pat_41	Post-Resistance	PLOD1	5351	37	1	12030823	12030823	Missense_Mutation	SNP	G	A	15	120	c.1852G>A	c.(1852-1854)GAG>AAG	p.E618K
Pat_41	Post-Resistance	MFN2	9927	37	1	12061576	12061576	Missense_Mutation	SNP	C	T	9	33	c.935C>T	c.(934-936)GCC>GTC	p.A312V
Pat_41	Post-Resistance	MFN2	9927	37	1	12064581	12064581	Missense_Mutation	SNP	G	A	23	316	c.1303G>A	c.(1303-1305)GCC>ACC	p.A435T
Pat_41	Post-Resistance	TNFRSF8	943	37	1	12202385	12202386	Missense_Mutation	DNP	AC	GT	4	21	.1585_1586AC>G	c.(1585-1587)ACC>GTC	p.T529V
Pat_41	Post-Resistance	VPS13D	55187	37	1	12337031	12337031	Missense_Mutation	SNP	C	T	12	15	c.3386C>T	c.(3385-3387)TCC>TTC	p.S1129F
Pat_41	Post-Resistance	VPS13D	55187	37	1	12337883	12337883	Missense_Mutation	SNP	G	A	13	114	c.4238G>A	c.(4237-4239)GGA>GAA	p.G1413E
Pat_41	Post-Resistance	VPS13D	55187	37	1	12439601	12439601	Missense_Mutation	SNP	G	A	18	339	c.11141G>A	c.(11140-11142)AGT>AAT	p.S3714N
Pat_41	Post-Resistance	PRAMEF4	400735	37	1	12943177	12943177	Missense_Mutation	SNP	C	A	15	265	c.39G>T	c.(37-39)GAG>GAT	p.E13D
Pat_41	Post-Resistance	PRAMEF14	729528	37	1	13669128	13669128	Missense_Mutation	SNP	G	A	23	223	c.1058C>T	c.(1057-1059)ACC>ATC	p.T353I
Pat_41	Post-Resistance	PRDM2	7799	37	1	14105534	14105534	Missense_Mutation	SNP	G	A	5	86	c.1244G>A	c.(1243-1245)GGG>GAG	p.G415E
Pat_41	Post-Resistance	CELA2A	63036	37	1	15793896	15793896	Missense_Mutation	SNP	C	T	11	119	c.655C>T	c.(655-657)CCA>TCA	p.P219S
Pat_41	Post-Resistance	CELA2B	51032	37	1	15807599	15807599	Missense_Mutation	SNP	C	A	17	263	c.136C>A	c.(136-138)CTG>ATG	p.L46M
Pat_41	Post-Resistance	DNAJC16	23341	37	1	15863277	15863277	Nonsense_Mutation	SNP	G	A	5	173	c.542G>A	c.(541-543)TGG>TAG	p.W181*
Pat_41	Post-Resistance	DNAJC16	23341	37	1	15873296	15873296	Missense_Mutation	SNP	G	A	25	138	c.794G>A	c.(793-795)GGC>GAC	p.G265D
Pat_41	Post-Resistance	DNAJC16	23341	37	1	15894367	15894367	Missense_Mutation	SNP	C	T	45	340	c.2044C>T	c.(2044-2046)CCA>TCA	p.P682S
Pat_41	Post-Resistance	FBLIM1	54751	37	1	16091651	16091651	Missense_Mutation	SNP	G	A	5	16	c.173G>A	c.(172-174)GGG>GAG	p.G58E
Pat_41	Post-Resistance	FBLIM1	54751	37	1	16111082	16111082	Missense_Mutation	SNP	G	A	29	296	c.1048G>A	c.(1048-1050)GGC>AGC	p.G350S
Pat_41	Post-Resistance	SPEN	23013	37	1	16199556	16199556	Missense_Mutation	SNP	G	A	7	144	c.329G>A	c.(328-330)GGT>GAT	p.G110D
Pat_41	Post-Resistance	HSPB7	27129	37	1	16344421	16344421	Missense_Mutation	SNP	C	T	6	50	c.38G>A	c.(37-39)AGA>AAA	p.R13K
Pat_41	Post-Resistance	CLCNKA	1187	37	1	16359707	16359707	Missense_Mutation	SNP	G	A	37	524	c.1972G>A	c.(1972-1974)GTG>ATG	p.V658M
Pat_41	Post-Resistance	NECAP2	55707	37	1	16782376	16782376	Missense_Mutation	SNP	C	T	13	99	c.731C>T	c.(730-732)ACC>ATC	p.T244I
Pat_41	Post-Resistance	CROCC	9696	37	1	17280827	17280827	Missense_Mutation	SNP	C	T	4	77	c.3296C>T	c.(3295-3297)GCC>GTC	p.A1099V
Pat_41	Post-Resistance	MFAP2	4237	37	1	17302186	17302186	Missense_Mutation	SNP	G	A	9	87	c.326C>T	c.(325-327)TCC>TTC	p.S109F
Pat_41	Post-Resistance	ATP13A2	23400	37	1	17318267	17318267	Missense_Mutation	SNP	G	A	22	157	c.2213C>T	c.(2212-2214)GCT>GTT	p.A738V
Pat_41	Post-Resistance	ATP13A2	23400	37	1	17332032	17332032	Missense_Mutation	SNP	C	T	16	85	c.125G>A	c.(124-126)GGC>GAC	p.G42D
Pat_41	Post-Resistance	ATP13A2	23400	37	1	17332252	17332252	Missense_Mutation	SNP	C	T	5	10	c.32G>A	c.(31-33)AGC>AAC	p.S11N
Pat_41	Post-Resistance	PADI2	11240	37	1	17396618	17396618	Missense_Mutation	SNP	C	T	6	98	c.1729G>A	c.(1729-1731)GAG>AAG	p.E577K
Pat_41	Post-Resistance	PADI2	11240	37	1	17402220	17402220	Missense_Mutation	SNP	C	T	7	310	c.1409G>A	c.(1408-1410)GGC>GAC	p.G470D
Pat_41	Post-Resistance	PADI3	51702	37	1	17603144	17603144	Missense_Mutation	SNP	G	A	11	86	c.1438G>A	c.(1438-1440)GCC>ACC	p.A480T
Pat_41	Post-Resistance	PAX7	5081	37	1	19027178	19027178	Missense_Mutation	SNP	G	A	5	138	c.818G>A	c.(817-819)CGT>CAT	p.R273H
Pat_41	Post-Resistance	KIAA0090	23065	37	1	19570460	19570460	Missense_Mutation	SNP	C	T	30	199	c.270G>A	c.(268-270)ATG>ATA	p.M90I

Pat_41	Post-Resistance	AKR7L	246181	37	1	19593943	19593943	Missense_Mutation	SNP	C	T	11	131	c.847G>A	c.(847-849)GAC>AAC	p.D283N
Pat_41	Post-Resistance	CAPZB	832	37	1	19705143	19705143	Missense_Mutation	SNP	G	A	8	68	c.307C>T	c.(307-309)CCA>TCA	p.P103S
Pat_41	Post-Resistance	HTR6	3362	37	1	20005526	20005526	Missense_Mutation	SNP	G	A	4	82	c.988G>A	c.(988-990)GCG>ACG	p.A330T
Pat_41	Post-Resistance	OTUD3	23252	37	1	20216981	20216981	Missense_Mutation	SNP	G	A	20	562	c.325G>A	c.(325-327)GAT>AAT	p.D109N
Pat_41	Post-Resistance	OTUD3	23252	37	1	20220894	20220894	Missense_Mutation	SNP	G	A	23	202	c.404G>A	c.(403-405)GGC>GAC	p.G135D
Pat_41	Post-Resistance	PINK1	65018	37	1	20964533	20964533	Missense_Mutation	SNP	C	T	4	55	c.586C>T	c.(586-588)CCA>TCA	p.P196S
Pat_41	Post-Resistance	PINK1	65018	37	1	20975600	20975600	Missense_Mutation	SNP	G	A	5	18	c.1364G>A	c.(1363-1365)GGC>GAC	p.G455D
Pat_41	Post-Resistance	KIF17	57576	37	1	21014275	21014275	Missense_Mutation	SNP	G	A	16	154	c.1544C>T	c.(1543-1545)ACT>ATT	p.T515I
Pat_41	Post-Resistance	EIF4G3	8672	37	1	21205934	21205934	Missense_Mutation	SNP	C	T	41	737	c.2336G>A	c.(2335-2337)GGA>GAA	p.G779E
Pat_41	Post-Resistance	EIF4G3	8672	37	1	21226436	21226436	Missense_Mutation	SNP	G	A	8	145	c.1585C>T	c.(1585-1587)CTT>TTT	p.L529F
Pat_41	Post-Resistance	NBPF3	84224	37	1	21798133	21798133	Missense_Mutation	SNP	G	A	34	409	c.518G>A	c.(517-519)AGA>AAA	p.R173K
Pat_41	Post-Resistance	LDLRAD2	401944	37	1	22138997	22138997	Missense_Mutation	SNP	C	T	7	79	c.53C>T	c.(52-54)GCA>GTA	p.A18V
Pat_41	Post-Resistance	HSPG2	3339	37	1	22201443	22201444	Missense_Mutation	DNP	GG	AA	30	25	.3354_3355CC>T	352-3357)GACCCC>GATT	p.P1119S
Pat_41	Post-Resistance	HSPG2	3339	37	1	22214512	22214512	Missense_Mutation	SNP	T	C	5	77	c.622A>G	c.(622-624)AGC>GGC	p.S208G
Pat_41	Post-Resistance	CDC42	998	37	1	22413183	22413183	Missense_Mutation	SNP	C	T	10	422	c.310C>T	c.(310-312)CAC>TAC	p.H104Y
Pat_41	Post-Resistance	ZBTB40	9923	37	1	22818024	22818024	Missense_Mutation	SNP	G	A	7	157	c.829G>A	c.(829-831)GAG>AAG	p.E277K
Pat_41	Post-Resistance	ZBTB40	9923	37	1	22834619	22834619	Missense_Mutation	SNP	G	A	4	75	c.1486G>A	c.(1486-1488)GGA>AGA	p.G496R
Pat_41	Post-Resistance	EPHB2	2048	37	1	23233205	23233205	Missense_Mutation	SNP	G	A	6	72	c.1891G>A	c.(1891-1893)GAG>AAG	p.E631K
Pat_41	Post-Resistance	ZNF436	80818	37	1	23688598	23688598	Missense_Mutation	SNP	C	T	23	213	c.1277G>A	c.(1276-1278)GGT>GAT	p.G426D
Pat_41	Post-Resistance	ZNF436	80818	37	1	23689360	23689360	Missense_Mutation	SNP	C	T	7	191	c.515G>A	c.(514-516)GGA>GAA	p.G172E
Pat_41	Post-Resistance	E2F2	1870	37	1	23848503	23848503	Missense_Mutation	SNP	C	T	14	184	c.404G>A	c.(403-405)GGG>GAG	p.G135E
Pat_41	Post-Resistance	LYPLA2	11313	37	1	24120984	24120984	Missense_Mutation	SNP	C	T	4	79	c.539C>T	c.(538-540)CCC>CTC	p.P180L
Pat_41	Post-Resistance	C1orf130	400746	37	1	24921982	24921982	Missense_Mutation	SNP	G	A	8	121	c.61G>A	c.(61-63)GGA>AGA	p.G21R
Pat_41	Post-Resistance	TMEM57	55219	37	1	25818024	25818024	Missense_Mutation	SNP	G	A	15	121	c.1741G>A	c.(1741-1743)GAC>AAC	p.D581N
Pat_41	Post-Resistance	MAN1C1	57134	37	1	26080020	26080020	Missense_Mutation	SNP	G	A	16	102	c.880G>A	c.(880-882)GCG>ACG	p.A294T
Pat_41	Post-Resistance	MAN1C1	57134	37	1	26104735	26104735	Missense_Mutation	SNP	C	T	6	45	c.1397C>T	c.(1396-1398)GCC>GTC	p.A466V
Pat_41	Post-Resistance	C1orf135	79000	37	1	26161653	26161653	Missense_Mutation	SNP	G	A	20	266	c.905C>T	c.(904-906)ACT>ATT	p.T302I
Pat_41	Post-Resistance	ZNF593	51042	37	1	26497181	26497181	Missense_Mutation	SNP	G	A	8	161	c.379G>A	c.(379-381)GTC>ATC	p.V127I
Pat_41	Post-Resistance	CNKSR1	10256	37	1	26515939	26515939	Missense_Mutation	SNP	C	T	8	91	c.2063C>T	c.(2062-2064)TCC>TTC	p.S688F
Pat_41	Post-Resistance	UBXN11	91544	37	1	26628190	26628190	Missense_Mutation	SNP	C	T	12	78	c.95G>A	c.(94-96)GGA>GAA	p.G32E
Pat_41	Post-Resistance	NR0B2	8431	37	1	27238395	27238395	Missense_Mutation	SNP	G	A	16	248	c.715C>T	c.(715-717)CCT>TCT	p.P239S
Pat_41	Post-Resistance	C1orf172	126695	37	1	27277919	27277919	Missense_Mutation	SNP	C	T	21	21	c.953G>A	c.(952-954)GGT>GAT	p.G318D
Pat_41	Post-Resistance	FGR	2268	37	1	27948098	27948098	Missense_Mutation	SNP	C	T	26	190	c.400G>A	c.(400-402)GCC>ACC	p.A134T
Pat_41	Post-Resistance	STX12	23673	37	1	28148833	28148833	Missense_Mutation	SNP	C	T	13	351	c.824C>T	c.(823-825)ACG>ATG	p.T275M
Pat_41	Post-Resistance	PPP1R8	5511	37	1	28167569	28167569	Missense_Mutation	SNP	C	T	10	441	c.316C>T	c.(316-318)CCT>TCT	p.P106S
Pat_41	Post-Resistance	C1orf38	9473	37	1	28212407	28212407	Missense_Mutation	SNP	C	T	19	139	c.1906C>T	c.(1906-1908)CTT>TTT	p.L636F
Pat_41	Post-Resistance	SMPDL3B	27293	37	1	28282459	28282459	Splice_Site	SNP	G	A	5	76	c.872_splice	c.e7-1	p.G291_splice
Pat_41	Post-Resistance	XKR8	55113	37	1	28293040	28293040	Missense_Mutation	SNP	G	A	6	164	c.517G>A	c.(517-519)GGC>AGC	p.G173S
Pat_41	Post-Resistance	XKR8	55113	37	1	28293258	28293258	Nonsense_Mutation	SNP	G	A	5	46	c.735G>A	c.(733-735)TGG>TGA	p.W245*
Pat_41	Post-Resistance	EYA3	2140	37	1	28362061	28362061	Missense_Mutation	SNP	G	A	25	516	c.355C>T	c.(355-357)CCT>TCT	p.P119S
Pat_41	Post-Resistance	RCC1	1104	37	1	28863271	28863271	Missense_Mutation	SNP	G	A	23	165	c.950G>A	c.(949-951)AGC>AAC	p.S317N
Pat_41	Post-Resistance	EPB41	2035	37	1	29379747	29379747	Missense_Mutation	SNP	G	A	15	189	c.1768G>A	c.(1768-1770)GAA>AAA	p.E590K
Pat_41	Post-Resistance	MECR	51102	37	1	29528490	29528490	Missense_Mutation	SNP	C	T	57	415	c.721G>A	c.(721-723)GAG>AAG	p.E241K
Pat_41	Post-Resistance	PTPRU	10076	37	1	29647228	29647228	Missense_Mutation	SNP	C	T	13	132	c.3749C>T	c.(3748-3750)ACC>ATC	p.T1250I
Pat_41	Post-Resistance	LAPTM5	7805	37	1	31206764	31206764	Missense_Mutation	SNP	C	T	9	60	c.700G>A	c.(700-702)GTG>ATG	p.V234M
Pat_41	Post-Resistance	PUM1	9698	37	1	31440139	31440139	Missense_Mutation	SNP	G	A	17	239	c.1664C>T	c.(1663-1665)CCT>CTT	p.P555L
Pat_41	Post-Resistance	PUM1	9698	37	1	31441205	31441205	Missense_Mutation	SNP	C	T	5	190	c.1641G>A	c.(1639-1641)ATG>ATA	p.M547I

Pat_41	Post-Resistance	PUM1	9698	37	1	31454168	31454168	Missense_Mutation	SNP	G	A	5	162	c.1243C>T	c.(1243-1245)CCG>TCG	p.P415S
Pat_41	Post-Resistance	SNRNP40	9410	37	1	31766101	31766101	Missense_Mutation	SNP	G	A	26	155	c.236C>T	c.(235-237)TCC>TTC	p.S79F
Pat_41	Post-Resistance	COL16A1	1307	37	1	32148591	32148591	Missense_Mutation	SNP	C	T	8	61	c.2482G>A	c.(2482-2484)GTG>ATG	p.V828M
Pat_41	Post-Resistance	COL16A1	1307	37	1	32155377	32155377	Missense_Mutation	SNP	G	A	16	109	c.1585C>T	c.(1585-1587)CCC>TCC	p.P529S
Pat_41	Post-Resistance	COL16A1	1307	37	1	32157658	32157658	Missense_Mutation	SNP	C	T	15	169	c.1205G>A	c.(1204-1206)GGC>GAC	p.G402D
Pat_41	Post-Resistance	BAI2	576	37	1	32196445	32196445	Missense_Mutation	SNP	G	A	16	164	c.4336C>T	c.(4336-4338)CCT>TCT	p.P1446S
Pat_41	Post-Resistance	CCDC28B	79140	37	1	32669792	32669792	Missense_Mutation	SNP	G	A	12	146	c.337G>A	c.(337-339)GAA>AAA	p.E113K
Pat_41	Post-Resistance	LCK	3932	37	1	32742054	32742054	Missense_Mutation	SNP	C	T	5	49	c.748C>T	c.(748-750)CGG>TGG	p.R250W
Pat_41	Post-Resistance	HDAC1	3065	37	1	32790131	32790131	Missense_Mutation	SNP	A	C	10	446	c.332A>C	c.(331-333)CAG>CCG	p.Q111P
Pat_41	Post-Resistance	KIAA1522	57648	37	1	33236888	33236888	Missense_Mutation	SNP	G	A	7	151	c.1931G>A	c.(1930-1932)AGT>AAT	p.S644N
Pat_41	Post-Resistance	KIAA1522	57648	37	1	33237295	33237295	Missense_Mutation	SNP	C	T	10	89	c.2338C>T	c.(2338-2340)CCG>TCG	p.P780S
Pat_41	Post-Resistance	YARS	8565	37	1	33248080	33248080	Missense_Mutation	SNP	G	A	7	116	c.967C>T	c.(967-969)CCA>TCA	p.P323S
Pat_41	Post-Resistance	ZNF362	149076	37	1	33745785	33745785	Missense_Mutation	SNP	G	A	45	375	c.410G>A	c.(409-411)GGC>GAC	p.G137D
Pat_41	Post-Resistance	ZNF362	149076	37	1	33745887	33745887	Missense_Mutation	SNP	C	T	11	332	c.512C>T	c.(511-513)CCT>CTT	p.P171L
Pat_41	Post-Resistance	PHC2	1912	37	1	33833029	33833029	Missense_Mutation	SNP	C	T	13	261	c.664G>A	c.(664-666)GTA>ATA	p.V222I
Pat_41	Post-Resistance	CSMD2	114784	37	1	34204766	34204766	Nonsense_Mutation	SNP	C	T	3	17	c.2223G>A	c.(2221-2223)TGG>TGA	p.W741*
Pat_41	Post-Resistance	CSMD2	114784	37	1	34401462	34401462	Missense_Mutation	SNP	C	T	34	232	c.491G>A	c.(490-492)AGC>AAC	p.S164N
Pat_41	Post-Resistance	DLGAP3	58512	37	1	35365280	35365280	Missense_Mutation	SNP	G	A	17	225	c.1376C>T	c.(1375-1377)ACC>ATC	p.T459I
Pat_41	Post-Resistance	ZMYM1	79830	37	1	35577723	35577723	Missense_Mutation	SNP	A	G	6	222	c.1138A>G	c.(1138-1140)ATT>GTT	p.I380V
Pat_41	Post-Resistance	ZMYM1	79830	37	1	35578630	35578630	Missense_Mutation	SNP	C	T	5	143	c.1199C>T	c.(1198-1200)ACG>ATG	p.T400M
Pat_41	Post-Resistance	ZMYM4	9202	37	1	35847190	35847190	Missense_Mutation	SNP	G	A	43	423	c.1400G>A	c.(1399-1401)TGC>TAC	p.C467Y
Pat_41	Post-Resistance	NCDN	23154	37	1	36030965	36030965	Missense_Mutation	SNP	G	A	23	83	c.1891G>A	c.(1891-1893)GCC>ACC	p.A631T
Pat_41	Post-Resistance	CLSPN	63967	37	1	36215406	36215406	Missense_Mutation	SNP	C	T	12	65	c.2035G>A	c.(2035-2037)GAA>AAA	p.E679K
Pat_41	Post-Resistance	CLSPN	63967	37	1	36225942	36225942	Splice_Site	SNP	C	T	5	96	c.1579_splice	c.e8+1	p.E527_splice
Pat_41	Post-Resistance	EIF2C1	26523	37	1	36381006	36381006	Nonsense_Mutation	SNP	C	T	19	430	c.1891C>T	c.(1891-1893)CGA>TGA	p.R631*
Pat_41	Post-Resistance	ADPRHL2	54936	37	1	36557313	36557313	Missense_Mutation	SNP	G	A	5	124	c.403G>A	c.(403-405)GTC>ATC	p.V135I
Pat_41	Post-Resistance	MAP7D1	55700	37	1	36636617	36636617	Missense_Mutation	SNP	G	A	11	234	c.92G>A	c.(91-93)GGT>GAT	p.G31D
Pat_41	Post-Resistance	MACF1	23499	37	1	39696859	39696859	Translation_Start_Site	SNP	C	T	44	693	c.-50C>T	c.(-52--48)AACGG>AATGG	
Pat_41	Post-Resistance	MACF1	23499	37	1	39752983	39752983	Missense_Mutation	SNP	G	A	13	321	c.1549G>A	c.(1549-1551)GTC>ATC	p.V517I
Pat_41	Post-Resistance	MACF1	23499	37	1	39776656	39776656	Missense_Mutation	SNP	G	A	9	218	c.3269G>A	c.(3268-3270)AGG>AAG	p.R1090K
Pat_41	Post-Resistance	MACF1	23499	37	1	39806597	39806597	Missense_Mutation	SNP	G	A	28	138	c.5873G>A	c.(5872-5874)AGC>AAC	p.S1958N
Pat_41	Post-Resistance	MACF1	23499	37	1	39827140	39827140	Missense_Mutation	SNP	G	A	27	381	c.7882G>A	c.(7882-7884)GGC>AGC	p.G2628S
Pat_41	Post-Resistance	KIAA0754	643314	37	1	39879016	39879016	Missense_Mutation	SNP	A	G	3	36	c.3079A>G	c.(3079-3081)ACC>GCC	p.T1027A
Pat_41	Post-Resistance	KIAA0754	643314	37	1	39879250	39879250	Missense_Mutation	SNP	A	G	7	20	c.3313A>G	c.(3313-3315)ACC>GCC	p.T1105A
Pat_41	Post-Resistance	MACF1	23499	37	1	39898297	39898297	Nonsense_Mutation	SNP	C	T	14	107	c.12748C>T	c.(12748-12750)CAG>TAG	p.Q4250*
Pat_41	Post-Resistance	MACF1	23499	37	1	39906787	39906787	Missense_Mutation	SNP	G	A	13	70	c.13889G>A	c.(13888-13890)AGC>AAC	p.S4630N
Pat_41	Post-Resistance	PABPC4	8761	37	1	40035636	40035636	Missense_Mutation	SNP	G	A	19	187	c.542C>T	c.(541-543)GCT>GTT	p.A181V
Pat_41	Post-Resistance	PABPC4	8761	37	1	40041641	40041641	Translation_Start_Site	SNP	C	T	5	27	c.-17G>A	c.(-19--15)GGGTG>GGATG	
Pat_41	Post-Resistance	PPIE	10450	37	1	40207050	40207050	Missense_Mutation	SNP	G	A	30	342	c.143G>A	c.(142-144)GGA>GAA	p.G48E
Pat_41	Post-Resistance	MYCL1	4610	37	1	40366805	40366805	Missense_Mutation	SNP	G	A	4	18	c.302C>T	c.(301-303)GCC>GTC	p.A101V
Pat_41	Post-Resistance	MFSD2A	84879	37	1	40431657	40431657	Missense_Mutation	SNP	A	G	4	135	c.724A>G	c.(724-726)ACA>GCA	p.T242A
Pat_41	Post-Resistance	PPT1	5538	37	1	40542513	40542513	Splice_Site	SNP	C	T	13	175	c.798_splice	c.e8+1	p.Q266_splice
Pat_41	Post-Resistance	RLF	6018	37	1	40702766	40702766	Missense_Mutation	SNP	G	A	12	327	c.2392G>A	c.(2392-2394)GAT>AAT	p.D798N
Pat_41	Post-Resistance	ZNF684	127396	37	1	41012864	41012864	Missense_Mutation	SNP	C	T	13	141	c.869C>T	c.(868-870)TCC>TTC	p.S290F
Pat_41	Post-Resistance	HIVEP3	59269	37	1	41979218	41979218	Missense_Mutation	SNP	C	T	4	41	c.5674G>A	c.(5674-5676)GCA>ACA	p.A1892T
Pat_41	Post-Resistance	FOXJ3	22887	37	1	42671492	42671492	Missense_Mutation	SNP	C	T	11	163	c.571G>A	c.(571-573)GAG>AAG	p.E191K
Pat_41	Post-Resistance	PPCS	79717	37	1	42925484	42925484	Missense_Mutation	SNP	G	A	11	254	c.823G>A	c.(823-825)GAA>AAA	p.E275K

Pat_41	Post-Resistance	LEPRE1	64175	37	1	43232591	43232591	Missense_Mutation	SNP	C	T	9	181	c.52G>A	c.(52-54)GCT>ACT	p.A18T
Pat_41	Post-Resistance	ERMAP	114625	37	1	43308506	43308506	Missense_Mutation	SNP	C	T	7	60	c.1031C>T	c.(1030-1032)TCC>TTC	p.S344F
Pat_41	Post-Resistance	SLC2A1	6513	37	1	43393347	43393347	Missense_Mutation	SNP	C	T	7	57	c.1207G>A	c.(1207-1209)GCC>ACC	p.A403T
Pat_41	Post-Resistance	EBNA1BP2	10969	37	1	43630345	43630345	Missense_Mutation	SNP	C	T	5	57	c.839G>A	c.(838-840)GGC>GAC	p.G280D
Pat_41	Post-Resistance	WDR65	149465	37	1	43672465	43672465	Nonsense_Mutation	SNP	G	A	13	241	c.1617G>A	c.(1615-1617)TGG>TGA	p.W539*
Pat_41	Post-Resistance	WDR65	149465	37	1	43675684	43675684	Missense_Mutation	SNP	C	T	34	163	c.2026C>T	c.(2026-2028)CTT>TTT	p.L676F
Pat_41	Post-Resistance	TMEM125	128218	37	1	43738856	43738856	Missense_Mutation	SNP	G	A	6	55	c.463G>A	c.(463-465)GCT>ACT	p.A155T
Pat_41	Post-Resistance	MPL	4352	37	1	43805047	43805047	Missense_Mutation	SNP	G	A	5	102	c.497G>A	c.(496-498)AGG>AAG	p.R166K
Pat_41	Post-Resistance	KIAA0467	23334	37	1	43908520	43908520	Missense_Mutation	SNP	G	A	33	174	c.5485G>A	c.(5485-5487)GAA>AAA	p.E1829K
Pat_41	Post-Resistance	KIAA0467	23334	37	1	43908599	43908599	Missense_Mutation	SNP	G	A	7	87	c.5564G>A	c.(5563-5565)GGG>GAG	p.G1855E
Pat_41	Post-Resistance	PTPRF	5792	37	1	44057183	44057183	Missense_Mutation	SNP	G	A	4	32	c.1490G>A	c.(1489-1491)GGC>GAC	p.G497D
Pat_41	Post-Resistance	PTPRF	5792	37	1	44069683	44069683	Missense_Mutation	SNP	G	A	7	123	c.2860G>A	c.(2860-2862)GTG>ATG	p.V954M
Pat_41	Post-Resistance	PTPRF	5792	37	1	44084726	44084726	Missense_Mutation	SNP	C	T	8	128	c.4499C>T	c.(4498-4500)TCC>TTC	p.S1500F
Pat_41	Post-Resistance	SLC6A9	6536	37	1	44474134	44474134	Missense_Mutation	SNP	C	T	9	128	c.700G>A	c.(700-702)GAC>AAC	p.D234N
Pat_41	Post-Resistance	SLC6A9	6536	37	1	44482780	44482780	Missense_Mutation	SNP	G	A	5	77	c.26C>T	c.(25-27)GCG>GTG	p.A9V
Pat_41	Post-Resistance	KLF17	128209	37	1	44596372	44596372	Missense_Mutation	SNP	C	T	8	137	c.1114C>T	c.(1114-1116)CCA>TCA	p.P372S
Pat_41	Post-Resistance	DMAP1	55929	37	1	44684067	44684067	Missense_Mutation	SNP	C	T	14	323	c.478C>T	c.(478-480)CTC>TTC	p.L160F
Pat_41	Post-Resistance	KIF2C	11004	37	1	45206657	45206657	Missense_Mutation	SNP	G	A	6	150	c.143G>A	c.(142-144)GGA>GAA	p.G48E
Pat_41	Post-Resistance	PLK3	1263	37	1	45268722	45268722	Missense_Mutation	SNP	G	A	4	117	c.845G>A	c.(844-846)AGC>AAC	p.S282N
Pat_41	Post-Resistance	PLK3	1263	37	1	45270380	45270380	Missense_Mutation	SNP	C	T	41	634	c.1564C>T	c.(1564-1566)CCC>TCC	p.P522S
Pat_41	Post-Resistance	PTCH2	8643	37	1	45292305	45292305	Missense_Mutation	SNP	G	A	4	21	c.2831C>T	c.(2830-2832)GCC>GTC	p.A944V
Pat_41	Post-Resistance	ZSWIM5	57643	37	1	45501794	45501794	Missense_Mutation	SNP	T	G	6	87	c.2072A>C	c.(2071-2073)CAG>CCG	p.Q691P
Pat_41	Post-Resistance	HPDL	84842	37	1	45793335	45793335	Missense_Mutation	SNP	G	A	4	104	c.515G>A	c.(514-516)AGC>AAC	p.S172N
Pat_41	Post-Resistance	MAST2	23139	37	1	46501709	46501709	Missense_Mutation	SNP	G	A	5	146	c.5368G>A	c.(5368-5370)GTT>ATT	p.V1790I
Pat_41	Post-Resistance	PIK3R3	8503	37	1	46509370	46509370	Missense_Mutation	SNP	G	A	12	266	c.1361C>T	c.(1360-1362)GCA>GTA	p.A454V
Pat_41	Post-Resistance	DMBX1	127343	37	1	46976784	46976784	Missense_Mutation	SNP	C	T	157	170	c.526C>T	c.(526-528)CCT>TCT	p.P176S
Pat_41	Post-Resistance	MOBKL2C	148932	37	1	47075807	47075807	Missense_Mutation	SNP	A	G	7	213	c.488T>C	c.(487-489)GTC>GCC	p.V163A
Pat_41	Post-Resistance	CYP4Z1	199974	37	1	47571916	47571916	Missense_Mutation	SNP	G	A	27	114	c.1184G>A	c.(1183-1185)GGA>GAA	p.G395E
Pat_41	Post-Resistance	FOXE3	2301	37	1	47882381	47882381	Missense_Mutation	SNP	G	A	12	224	c.394G>A	c.(394-396)GTG>ATG	p.V132M
Pat_41	Post-Resistance	SLC5A9	200010	37	1	48699363	48699363	Missense_Mutation	SNP	G	A	11	104	c.1070G>A	c.(1069-1071)AGA>AAA	p.R357K
Pat_41	Post-Resistance	SLC5A9	200010	37	1	48701532	48701532	Missense_Mutation	SNP	G	A	10	153	c.1273G>A	c.(1273-1275)GAG>AAG	p.E425K
Pat_41	Post-Resistance	SPATA6	54558	37	1	48764422	48764422	Missense_Mutation	SNP	G	A	14	203	c.1430C>T	c.(1429-1431)GCC>GTC	p.A477V
Pat_41	Post-Resistance	FAF1	11124	37	1	51204547	51204547	Missense_Mutation	SNP	G	A	9	209	c.539C>T	c.(538-540)TCT>TTT	p.S180F
Pat_41	Post-Resistance	CDKN2C	1031	37	1	51436056	51436056	Missense_Mutation	SNP	G	A	4	61	c.16G>A	c.(16-18)GGG>AGG	p.G6R
Pat_41	Post-Resistance	OSBPL9	114883	37	1	52231608	52231608	Missense_Mutation	SNP	C	T	11	155	c.893C>T	c.(892-894)GCT>GTT	p.A298V
Pat_41	Post-Resistance	RAB3B	5865	37	1	52399097	52399097	Missense_Mutation	SNP	G	A	15	178	c.365C>T	c.(364-366)ACC>ATC	p.T122I
Pat_41	Post-Resistance	KTI12	112970	37	1	52498737	52498737	Missense_Mutation	SNP	C	T	10	43	c.697G>A	c.(697-699)GTG>ATG	p.V233M
Pat_41	Post-Resistance	KTI12	112970	37	1	52498898	52498898	Missense_Mutation	SNP	G	A	13	156	c.536C>T	c.(535-537)TCC>TTC	p.S179F
Pat_41	Post-Resistance	ZFYVE9	9372	37	1	52703852	52703852	Missense_Mutation	SNP	G	A	35	727	c.763G>A	c.(763-765)GAC>AAC	p.D255N
Pat_41	Post-Resistance	FAM159A	348378	37	1	53122521	53122521	Missense_Mutation	SNP	C	T	8	153	c.382C>T	c.(382-384)CCA>TCA	p.P128S
Pat_41	Post-Resistance	ZYG11B	79699	37	1	53237373	53237373	Missense_Mutation	SNP	G	A	31	218	c.878G>A	c.(877-879)AGC>AAC	p.S293N
Pat_41	Post-Resistance	PODN	127435	37	1	53543381	53543381	Missense_Mutation	SNP	C	T	22	373	c.907C>T	c.(907-909)CCG>TCG	p.P303S
Pat_41	Post-Resistance	C1orf123	54987	37	1	53684085	53684085	Splice_Site	SNP	C	T	17	297	c.229_splice	c.e4+1	p.E77_splice
Pat_41	Post-Resistance	LRP8	7804	37	1	53726227	53726227	Missense_Mutation	SNP	A	T	25	288	c.1965T>A	c.(1963-1965)AAT>AAA	p.N655K
Pat_41	Post-Resistance	CDCP2	200008	37	1	54605260	54605260	Missense_Mutation	SNP	G	A	7	49	c.1283C>T	c.(1282-1284)CCC>CTC	p.P428L
Pat_41	Post-Resistance	C1orf175	374977	37	1	55118771	55118771	Missense_Mutation	SNP	G	A	6	122	c.172G>A	c.(172-174)GTT>ATT	p.V58I
Pat_41	Post-Resistance	USP24	23358	37	1	55561066	55561066	Missense_Mutation	SNP	T	G	4	46	c.5585A>C	c.(5584-5586)AAC>ACC	p.N1862T

Pat_41	Post-Resistance	PRKAA2	5563	37	1	57111134	57111134	Missense_Mutation	SNP	G	A	4	20	c.74G>A	c.(73-75)GGC>GAC	p.G25D
Pat_41	Post-Resistance	C1orf168	199920	37	1	57185911	57185911	Missense_Mutation	SNP	T	C	30	129	c.2066A>G	c.(2065-2067)GAA>GGA	p.E689G
Pat_41	Post-Resistance	C8A	731	37	1	57372418	57372418	Missense_Mutation	SNP	G	A	10	143	c.1175G>A	c.(1174-1176)GGA>GAA	p.G392E
Pat_41	Post-Resistance	DAB1	1600	37	1	57480825	57480825	Missense_Mutation	SNP	C	T	6	118	c.1175G>A	c.(1174-1176)GGC>GAC	p.G392D
Pat_41	Post-Resistance	DAB1	1600	37	1	57491682	57491682	Missense_Mutation	SNP	G	A	12	263	c.758C>T	c.(757-759)TCC>TTC	p.S253F
Pat_41	Post-Resistance	MYSM1	114803	37	1	59142648	59142648	Missense_Mutation	SNP	C	T	11	314	c.1340G>A	c.(1339-1341)GGA>GAA	p.G447E
Pat_41	Post-Resistance	HOOK1	51361	37	1	60325957	60325957	Missense_Mutation	SNP	G	A	38	552	c.1489G>A	c.(1489-1491)GAA>AAA	p.E497K
Pat_41	Post-Resistance	HOOK1	51361	37	1	60330918	60330918	Splice_Site	SNP	G	A	7	72	c.1744_splice	c.e19+1	p.V582_splice
Pat_41	Post-Resistance	C1orf87	127795	37	1	60505689	60505689	Missense_Mutation	SNP	G	A	9	62	c.647C>T	c.(646-648)TCT>TTT	p.S216F
Pat_41	Post-Resistance	INADL	10207	37	1	62253469	62253469	Missense_Mutation	SNP	G	A	10	142	c.893G>A	c.(892-894)GGC>GAC	p.G298D
Pat_41	Post-Resistance	CACHD1	57685	37	1	65157210	65157210	Missense_Mutation	SNP	C	T	8	168	c.3638C>T	c.(3637-3639)GCC>GTC	p.A1213V
Pat_41	Post-Resistance	DNAJC6	9829	37	1	65860607	65860607	Missense_Mutation	SNP	C	T	15	170	c.1759C>T	c.(1759-1761)CCT>TCT	p.P587S
Pat_41	Post-Resistance	DNAJC6	9829	37	1	65871719	65871719	Missense_Mutation	SNP	G	A	13	132	c.2223G>A	c.(2221-2223)ATG>ATA	p.M741I
Pat_41	Post-Resistance	PDE4B	5142	37	1	66384379	66384379	Nonsense_Mutation	SNP	G	T	8	122	c.142G>T	c.(142-144)GGA>TGA	p.G48*
Pat_41	Post-Resistance	TCTEX1D1	200132	37	1	67236072	67236072	Missense_Mutation	SNP	C	T	50	345	c.122C>T	c.(121-123)TCT>TTT	p.S41F
Pat_41	Post-Resistance	WDR78	79819	37	1	67299760	67299760	Missense_Mutation	SNP	C	T	22	92	c.1805G>A	c.(1804-1806)GGA>GAA	p.G602E
Pat_41	Post-Resistance	WDR78	79819	37	1	67299805	67299805	Missense_Mutation	SNP	G	A	11	77	c.1760C>T	c.(1759-1761)CCT>CTT	p.P587L
Pat_41	Post-Resistance	MIER1	57708	37	1	67425406	67425406	Missense_Mutation	SNP	C	T	29	143	c.679C>T	c.(679-681)CCA>TCA	p.P227S
Pat_41	Post-Resistance	SLC35D1	23169	37	1	67470040	67470040	Missense_Mutation	SNP	C	T	9	305	c.1051G>A	c.(1051-1053)GGG>AGG	p.G351R
Pat_41	Post-Resistance	SLC35D1	23169	37	1	67519582	67519582	Missense_Mutation	SNP	C	T	5	58	c.115G>A	c.(115-117)GTG>ATG	p.V39M
Pat_41	Post-Resistance	IL23R	149233	37	1	67724160	67724160	Splice_Site	SNP	G	A	4	174	c.1240_splice	c.e11-1	p.E414_splice
Pat_41	Post-Resistance	SERBP1	26135	37	1	67880913	67880913	Missense_Mutation	SNP	C	T	19	134	c.1106G>A	c.(1105-1107)GGC>GAC	p.G369D
Pat_41	Post-Resistance	DEPDC1	55635	37	1	68947788	68947788	Missense_Mutation	SNP	G	A	10	105	c.1703C>T	c.(1702-1704)ACA>ATA	p.T568I
Pat_41	Post-Resistance	FPGT	8790	37	1	74670431	74670431	Missense_Mutation	SNP	G	A	8	112	c.700G>A	c.(700-702)GAA>AAA	p.E234K
Pat_41	Post-Resistance	TNNI3K	51086	37	1	74701803	74701803	Missense_Mutation	SNP	G	A	12	94	c.58G>A	c.(58-60)GTC>ATC	p.V20I
Pat_41	Post-Resistance	C1orf173	127254	37	1	75037060	75037060	Missense_Mutation	SNP	C	T	10	202	c.4334G>A	c.(4333-4335)GGA>GAA	p.G1445E
Pat_41	Post-Resistance	C1orf173	127254	37	1	75037804	75037804	Missense_Mutation	SNP	G	A	25	236	c.3590C>T	c.(3589-3591)TCC>TTC	p.S1197F
Pat_41	Post-Resistance	C1orf173	127254	37	1	75038600	75038600	Missense_Mutation	SNP	C	T	27	181	c.2794G>A	c.(2794-2796)GAG>AAG	p.E932K
Pat_41	Post-Resistance	SLC44A5	204962	37	1	75672389	75672389	Missense_Mutation	SNP	C	T	8	213	c.2063G>A	c.(2062-2064)AGA>AAA	p.R688K
Pat_41	Post-Resistance	MSH4	4438	37	1	76346936	76346936	Missense_Mutation	SNP	T	C	12	181	c.1787T>C	c.(1786-1788)GTG>GCG	p.V596A
Pat_41	Post-Resistance	ST6GALNAC3	256435	37	1	76779652	76779652	Missense_Mutation	SNP	C	T	55	66	c.181C>T	c.(181-183)CAC>TAC	p.H61Y
Pat_41	Post-Resistance	PIGK	10026	37	1	77627084	77627084	Missense_Mutation	SNP	G	A	12	110	c.709C>T	c.(709-711)CCT>TCT	p.P237S
Pat_41	Post-Resistance	FUBP1	8880	37	1	78444637	78444637	Missense_Mutation	SNP	C	T	7	53	c.52G>A	c.(52-54)GGT>AGT	p.G18S
Pat_41	Post-Resistance	GIPC2	54810	37	1	78601393	78601393	Missense_Mutation	SNP	G	A	7	154	c.914G>A	c.(913-915)GGA>GAA	p.G305E
Pat_41	Post-Resistance	IFI44L	10964	37	1	79101047	79101047	Missense_Mutation	SNP	G	A	11	235	c.749G>A	c.(748-750)GGA>GAA	p.G250E
Pat_41	Post-Resistance	ELTD1	64123	37	1	79387426	79387426	Missense_Mutation	SNP	G	A	5	124	c.1129C>T	c.(1129-1131)CCT>TCT	p.P377S
Pat_41	Post-Resistance	LPHN2	23266	37	1	82431862	82431862	Missense_Mutation	SNP	G	A	30	166	c.2087G>A	c.(2086-2088)AGG>AAG	p.R696K
Pat_41	Post-Resistance	CTBS	1486	37	1	85039948	85039948	Missense_Mutation	SNP	G	A	4	18	c.151C>T	c.(151-153)CCG>TCG	p.P51S
Pat_41	Post-Resistance	SSX2IP	117178	37	1	85130099	85130099	Splice_Site	SNP	C	T	6	237	c.673_splice	c.e7+1	p.A225_splice
Pat_41	Post-Resistance	MCOLN3	55283	37	1	85510881	85510881	Missense_Mutation	SNP	C	T	19	102	c.163G>A	c.(163-165)GCT>ACT	p.A55T
Pat_41	Post-Resistance	DDAH1	23576	37	1	85787205	85787205	Missense_Mutation	SNP	G	A	8	103	c.788C>T	c.(787-789)TCT>TTT	p.S263F
Pat_41	Post-Resistance	COL24A1	255631	37	1	86313446	86313446	Missense_Mutation	SNP	C	T	4	105	c.3364G>A	c.(3364-3366)GGA>AGA	p.G1122R
Pat_41	Post-Resistance	CLCA1	1179	37	1	86965618	86965618	Missense_Mutation	SNP	G	A	49	345	c.2635G>A	c.(2635-2637)GAA>AAA	p.E879K
Pat_41	Post-Resistance	CLCA1	1179	37	1	86965625	86965625	Missense_Mutation	SNP	C	T	55	313	c.2642C>T	c.(2641-2643)TCT>TTT	p.S881F
Pat_41	Post-Resistance	GBP1	2633	37	1	89522803	89522803	Missense_Mutation	SNP	C	T	24	194	c.889G>A	c.(889-891)GTG>ATG	p.V297M
Pat_41	Post-Resistance	GBP2	2634	37	1	89579779	89579779	Missense_Mutation	SNP	C	T	66	248	c.1069G>A	c.(1069-1071)GAC>AAC	p.D357N
Pat_41	Post-Resistance	GBP7	388646	37	1	89613341	89613341	Missense_Mutation	SNP	G	A	25	202	c.1274C>T	c.(1273-1275)ACT>ATT	p.T425I

Pat_41	Post-Resistance	GBP6	163351	37	1	89843986	89843986	Missense_Mutation	SNP	G	A	42	316	c.439G>A	c.(439-441)GAG>AAG	p.E147K
Pat_41	Post-Resistance	LRRC8B	23507	37	1	90049189	90049189	Missense_Mutation	SNP	G	A	8	161	c.980G>A	c.(979-981)GGT>GAT	p.G327D
Pat_41	Post-Resistance	ZNF644	84146	37	1	91403258	91403258	Missense_Mutation	SNP	G	A	25	207	c.3472C>T	c.(3472-3474)CCA>TCA	p.P1158S
Pat_41	Post-Resistance	BTBD8	284697	37	1	92604938	92604938	Missense_Mutation	SNP	C	T	10	211	c.784C>T	c.(784-786)CAT>TAT	p.H262Y
Pat_41	Post-Resistance	BTBD8	284697	37	1	92604954	92604954	Missense_Mutation	SNP	G	A	10	190	c.800G>A	c.(799-801)GGA>GAA	p.G267E
Pat_41	Post-Resistance	MTF2	22823	37	1	93594945	93594945	Missense_Mutation	SNP	G	A	14	223	c.1100G>A	c.(1099-1101)GGA>GAA	p.G367E
Pat_41	Post-Resistance	MTF2	22823	37	1	93594972	93594972	Missense_Mutation	SNP	G	A	19	241	c.1127G>A	c.(1126-1128)GGC>GAC	p.G376D
Pat_41	Post-Resistance	CCDC18	343099	37	1	93646148	93646148	Missense_Mutation	SNP	G	A	7	112	c.61G>A	c.(61-63)GCT>ACT	p.A21T
Pat_41	Post-Resistance	FNBP1L	54874	37	1	93988987	93988987	Missense_Mutation	SNP	C	T	7	65	c.281C>T	c.(280-282)GCG>GTG	p.A94V
Pat_41	Post-Resistance	ABCA4	24	37	1	94502814	94502814	Missense_Mutation	SNP	G	A	13	181	c.3700C>T	c.(3700-3702)CCA>TCA	p.P1234S
Pat_41	Post-Resistance	ARHGAP29	9411	37	1	94640149	94640149	Missense_Mutation	SNP	G	A	10	227	c.3062C>T	c.(3061-3063)CCT>CTT	p.P1021L
Pat_41	Post-Resistance	RWDD3	25950	37	1	95710043	95710043	Missense_Mutation	SNP	G	A	19	184	c.362G>A	c.(361-363)GGC>GAC	p.G121D
Pat_41	Post-Resistance	DPYD	1806	37	1	97658624	97658624	Splice_Site	SNP	C	T	9	173	c.2622_splice	c.e20+1	p.K874_splice
Pat_41	Post-Resistance	LPPR5	163404	37	1	99380362	99380362	Missense_Mutation	SNP	C	T	7	147	c.913G>A	c.(913-915)GAA>AAA	p.E305K
Pat_41	Post-Resistance	LPPR4	9890	37	1	99764654	99764654	Missense_Mutation	SNP	G	A	22	218	c.602G>A	c.(601-603)GGA>GAA	p.G201E
Pat_41	Post-Resistance	FRRS1	391059	37	1	100203679	100203679	Missense_Mutation	SNP	C	T	20	351	c.722G>A	c.(721-723)GGC>GAC	p.G241D
Pat_41	Post-Resistance	SLC35A3	23443	37	1	100464904	100464904	Missense_Mutation	SNP	G	A	34	192	c.275G>A	c.(274-276)GGG>GAG	p.G92E
Pat_41	Post-Resistance	SLC35A3	23443	37	1	100488006	100488006	Missense_Mutation	SNP	C	T	4	123	c.952C>T	c.(952-954)CCT>TCT	p.P318S
Pat_41	Post-Resistance	SASS6	163786	37	1	100584644	100584644	Missense_Mutation	SNP	G	A	4	85	c.599C>T	c.(598-600)GCG>GTG	p.A200V
Pat_41	Post-Resistance	DBT	1629	37	1	100672153	100672153	Missense_Mutation	SNP	C	T	20	481	c.1057G>A	c.(1057-1059)GGT>AGT	p.G353S
Pat_41	Post-Resistance	VAV3	10451	37	1	108247184	108247184	Missense_Mutation	SNP	C	T	16	256	c.1693G>A	c.(1693-1695)GTT>ATT	p.V565I
Pat_41	Post-Resistance	C1orf59	113802	37	1	109192835	109192835	Missense_Mutation	SNP	C	T	17	322	c.754G>A	c.(754-756)GCT>ACT	p.A252T
Pat_41	Post-Resistance	WDR47	22911	37	1	109524409	109524409	Missense_Mutation	SNP	C	T	35	314	c.2344G>A	c.(2344-2346)GAT>AAT	p.D782N
Pat_41	Post-Resistance	KIAA1324	57535	37	1	109704625	109704625	Missense_Mutation	SNP	G	A	6	127	c.263G>A	c.(262-264)GGC>GAC	p.G88D
Pat_41	Post-Resistance	CELSR2	1952	37	1	109793887	109793887	Missense_Mutation	SNP	G	A	5	108	c.1186G>A	c.(1186-1188)GCC>ACC	p.A396T
Pat_41	Post-Resistance	CELSR2	1952	37	1	109803751	109803751	Missense_Mutation	SNP	G	A	8	232	c.4046G>A	c.(4045-4047)GGC>GAC	p.G1349D
Pat_41	Post-Resistance	CELSR2	1952	37	1	109804176	109804176	Missense_Mutation	SNP	G	A	7	297	c.4223G>A	c.(4222-4224)GGG>GAG	p.G1408E
Pat_41	Post-Resistance	CELSR2	1952	37	1	109812092	109812092	Missense_Mutation	SNP	G	A	5	61	c.6859G>A	c.(6859-6861)GTC>ATC	p.V2287I
Pat_41	Post-Resistance	CELSR2	1952	37	1	109814127	109814127	Missense_Mutation	SNP	G	A	16	210	c.7796G>A	c.(7795-7797)TGC>TAC	p.C2599Y
Pat_41	Post-Resistance	AMIGO1	57463	37	1	110051098	110051098	Missense_Mutation	SNP	A	C	17	180	c.437T>G	c.(436-438)ATC>AGC	p.I146S
Pat_41	Post-Resistance	GSTM2	2946	37	1	110224435	110224435	Missense_Mutation	SNP	C	T	8	104	c.572C>T	c.(571-573)TCC>TTC	p.S191F
Pat_41	Post-Resistance	EPS8L3	79574	37	1	110301901	110301901	Missense_Mutation	SNP	G	A	31	583	c.364C>T	c.(364-366)CCA>TCA	p.P122S
Pat_41	Post-Resistance	FAM40A	85369	37	1	110584222	110584222	Missense_Mutation	SNP	G	A	15	158	c.715G>A	c.(715-717)GCT>ACT	p.A239T
Pat_41	Post-Resistance	SLC6A17	388662	37	1	110738259	110738259	Missense_Mutation	SNP	C	T	10	191	c.1544C>T	c.(1543-1545)TCC>TTC	p.S515F
Pat_41	Post-Resistance	RBM15	64783	37	1	110884155	110884155	Missense_Mutation	SNP	G	A	6	153	c.2128G>A	c.(2128-2130)GAG>AAG	p.E710K
Pat_41	Post-Resistance	SLC16A4	9122	37	1	110919577	110919577	Missense_Mutation	SNP	C	T	16	78	c.1237G>A	c.(1237-1239)GTA>ATA	p.V413I
Pat_41	Post-Resistance	SLC16A4	9122	37	1	110921759	110921759	Missense_Mutation	SNP	C	T	9	332	c.746G>A	c.(745-747)AGC>AAC	p.S249N
Pat_41	Post-Resistance	KCNA10	3744	37	1	111060116	111060116	Missense_Mutation	SNP	G	A	9	45	c.1294C>T	c.(1294-1296)CCA>TCA	p.P432S
Pat_41	Post-Resistance	KCNA3	3738	37	1	111216162	111216162	Missense_Mutation	SNP	G	A	27	47	c.1270C>T	c.(1270-1272)CCC>TCC	p.P424S
Pat_41	Post-Resistance	C1orf103	55791	37	1	111492639	111492639	Missense_Mutation	SNP	G	A	5	116	c.1703C>T	c.(1702-1704)GCT>GTT	p.A568V
Pat_41	Post-Resistance	C1orf103	55791	37	1	111495306	111495306	Missense_Mutation	SNP	G	A	10	138	c.200C>T	c.(199-201)GCT>GTT	p.A67V
Pat_41	Post-Resistance	CEPT1	10390	37	1	111702080	111702080	Missense_Mutation	SNP	G	A	17	271	c.418G>A	c.(418-420)GCA>ACA	p.A140T
Pat_41	Post-Resistance	CHI3L2	1117	37	1	111778665	111778665	Missense_Mutation	SNP	C	T	32	489	c.625C>T	c.(625-627)CTC>TTC	p.L209F
Pat_41	Post-Resistance	CHIA	27159	37	1	111860652	111860652	Missense_Mutation	SNP	C	T	11	141	c.650C>T	c.(649-651)TCC>TTC	p.S217F
Pat_41	Post-Resistance	OVGP1	5016	37	1	111957946	111957946	Missense_Mutation	SNP	G	A	7	112	c.1177C>T	c.(1177-1179)CCA>TCA	p.P393S
Pat_41	Post-Resistance	OVGP1	5016	37	1	111966292	111966292	Missense_Mutation	SNP	T	C	21	173	c.356A>G	c.(355-357)AAG>AGG	p.K119R
Pat_41	Post-Resistance	ATP5F1	515	37	1	112002095	112002095	Missense_Mutation	SNP	C	T	8	176	c.530C>T	c.(529-531)GCT>GTT	p.A177V

Pat_41	Post-Resistance	DDX20	11218	37	1	112308860	112308860	Missense_Mutation	SNP	G	A	5	112	c.1814G>A	c.(1813-1815)GGG>GAG	p.G605E
Pat_41	Post-Resistance	MOV10	4343	37	1	113231577	113231577	Missense_Mutation	SNP	G	A	22	152	c.158G>A	c.(157-159)GGC>GAC	p.G53D
Pat_41	Post-Resistance	MOV10	4343	37	1	113232218	113232218	Missense_Mutation	SNP	C	T	36	394	c.523C>T	c.(523-525)CCC>TCC	p.P175S
Pat_41	Post-Resistance	MOV10	4343	37	1	113232266	113232266	Missense_Mutation	SNP	G	A	11	126	c.571G>A	c.(571-573)GGC>AGC	p.G191S
Pat_41	Post-Resistance	PPM1J	333926	37	1	113253130	113253130	Missense_Mutation	SNP	G	A	10	178	c.1322C>T	c.(1321-1323)GCC>GTC	p.A441V
Pat_41	Post-Resistance	FAM19A3	284467	37	1	113266686	113266686	Missense_Mutation	SNP	G	A	11	78	c.317G>A	c.(316-318)GGG>GAG	p.G106E
Pat_41	Post-Resistance	HIPK1	204851	37	1	114499792	114499792	Missense_Mutation	SNP	C	T	32	278	c.1639C>T	c.(1639-1641)CAC>TAC	p.H547Y
Pat_41	Post-Resistance	HIPK1	204851	37	1	114505028	114505028	Missense_Mutation	SNP	C	T	19	187	c.2071C>T	c.(2071-2073)CCA>TCA	p.P691S
Pat_41	Post-Resistance	HIPK1	204851	37	1	114508860	114508860	Missense_Mutation	SNP	G	A	17	80	c.2347G>A	c.(2347-2349)GCC>ACC	p.A783T
Pat_41	Post-Resistance	TRIM33	51592	37	1	114948110	114948110	Missense_Mutation	SNP	C	T	39	641	c.2690G>A	c.(2689-2691)GGA>GAA	p.G897E
Pat_41	Post-Resistance	AMPD1	270	37	1	115215853	115215853	Missense_Mutation	SNP	C	T	29	206	c.2126G>A	c.(2125-2127)GGC>GAC	p.G709D
Pat_41	Post-Resistance	AMPD1	270	37	1	115216529	115216529	Splice_Site	SNP	C	T	126	238	c.1974_splice	c.e14+1	p.K658_splice
Pat_41	Post-Resistance	NRAS	4893	37	1	115256529	115256529	Missense_Mutation	SNP	T	C	27	681	c.182A>G	c.(181-183)CAA>CGA	p.Q61R
Pat_41	Post-Resistance	NRAS	4893	37	1	115256538	115256538	Missense_Mutation	SNP	G	A	261	449	c.173C>T	c.(172-174)ACA>ATA	p.T58I
Pat_41	Post-Resistance	CSDE1	7812	37	1	115261250	115261250	Missense_Mutation	SNP	C	T	16	232	c.2333G>A	c.(2332-2334)GGA>GAA	p.G778E
Pat_41	Post-Resistance	CSDE1	7812	37	1	115263285	115263285	Missense_Mutation	SNP	C	T	22	443	c.1927G>A	c.(1927-1929)GGG>AGG	p.G643R
Pat_41	Post-Resistance	VANGL1	81839	37	1	116206309	116206309	Missense_Mutation	SNP	G	A	95	189	c.232G>A	c.(232-234)GCC>ACC	p.A78T
Pat_41	Post-Resistance	VANGL1	81839	37	1	116206471	116206471	Missense_Mutation	SNP	C	T	11	71	c.394C>T	c.(394-396)CTT>TTT	p.L132F
Pat_41	Post-Resistance	VANGL1	81839	37	1	116226583	116226583	Missense_Mutation	SNP	C	T	51	374	c.965C>T	c.(964-966)ACT>ATT	p.T322I
Pat_41	Post-Resistance	IGSF3	3321	37	1	117146321	117146321	Missense_Mutation	SNP	C	T	17	447	c.1549G>A	c.(1549-1551)GTG>ATG	p.V517M
Pat_41	Post-Resistance	IGSF3	3321	37	1	117158986	117158986	Missense_Mutation	SNP	C	T	6	277	c.137G>A	c.(136-138)GGC>GAC	p.G46D
Pat_41	Post-Resistance	CD101	9398	37	1	117556219	117556219	Missense_Mutation	SNP	G	A	65	69	c.1033G>A	c.(1033-1035)GCA>ACA	p.A345T
Pat_41	Post-Resistance	TTF2	8458	37	1	117617599	117617599	Missense_Mutation	SNP	G	T	6	285	c.393G>T	c.(391-393)AAG>AAT	p.K131N
Pat_41	Post-Resistance	TTF2	8458	37	1	117633200	117633200	Missense_Mutation	SNP	C	T	21	199	c.2543C>T	c.(2542-2544)TCT>TTT	p.S848F
Pat_41	Post-Resistance	TRIM45	80263	37	1	117654973	117654973	Missense_Mutation	SNP	C	T	70	112	c.1697G>A	c.(1696-1698)GGT>GAT	p.G566D
Pat_41	Post-Resistance	TRIM45	80263	37	1	117660679	117660679	Missense_Mutation	SNP	G	A	11	338	c.1199C>T	c.(1198-1200)GCC>GTC	p.A400V
Pat_41	Post-Resistance	TRIM45	80263	37	1	117663750	117663750	Missense_Mutation	SNP	C	T	17	148	c.74G>A	c.(73-75)GGC>GAC	p.G25D
Pat_41	Post-Resistance	SPAG17	200162	37	1	118535096	118535096	Missense_Mutation	SNP	G	A	10	303	c.5354C>T	c.(5353-5355)TCC>TTC	p.S1785F
Pat_41	Post-Resistance	SPAG17	200162	37	1	118644362	118644362	Splice_Site	SNP	C	T	6	156	c.634_splice	c.e5+1	p.D212_splice
Pat_41	Post-Resistance	TBX15	6913	37	1	119427477	119427477	Missense_Mutation	SNP	C	T	7	89	c.1369G>A	c.(1369-1371)GAG>AAG	p.E457K
Pat_41	Post-Resistance	TBX15	6913	37	1	119427938	119427938	Missense_Mutation	SNP	G	A	4	81	c.908C>T	c.(907-909)GCC>GTC	p.A303V
Pat_41	Post-Resistance	WARS2	10352	37	1	119619077	119619077	Missense_Mutation	SNP	G	A	11	204	c.244C>T	c.(244-246)CCC>TCC	p.P82S
Pat_41	Post-Resistance	HMGCS2	3158	37	1	120300046	120300046	Missense_Mutation	SNP	G	A	18	157	c.866C>T	c.(865-867)CCC>CTC	p.P289L
Pat_41	Post-Resistance	NOTCH2	4853	37	1	120458965	120458965	Missense_Mutation	SNP	T	C	13	157	c.6380A>G	c.(6379-6381)AAG>AGG	p.K2127R
Pat_41	Post-Resistance	PDE4DIP	9659	37	1	144879561	144879561	Missense_Mutation	SNP	A	G	3	40	c.3889T>C	c.(3889-3891)TGT>CGT	p.C1297R
Pat_41	Post-Resistance	PDE4DIP	9659	37	1	144886128	144886128	Missense_Mutation	SNP	C	T	9	108	c.3106G>A	c.(3106-3108)GAA>AAA	p.E1036K
Pat_41	Post-Resistance	PDE4DIP	9659	37	1	144892575	144892575	Missense_Mutation	SNP	C	T	11	425	c.2830G>A	c.(2830-2832)GAT>AAT	p.D944N
Pat_41	Post-Resistance	PDE4DIP	9659	37	1	144906091	144906091	Missense_Mutation	SNP	C	T	18	261	c.2542G>A	c.(2542-2544)GGT>AGT	p.G848S
Pat_41	Post-Resistance	PDE4DIP	9659	37	1	144917498	144917498	Splice_Site	SNP	C	T	22	791	c.1605_splice	c.e12+1	p.Q535_splice
Pat_41	Post-Resistance	LIX1L	128077	37	1	145492269	145492269	Missense_Mutation	SNP	C	T	12	352	c.491C>T	c.(490-492)GCT>GTT	p.A164V
Pat_41	Post-Resistance	RBM8A	9939	37	1	145508953	145508953	Missense_Mutation	SNP	C	T	8	77	c.380C>T	c.(379-381)GCC>GTC	p.A127V
Pat_41	Post-Resistance	POLR3C	10623	37	1	145606342	145606342	Missense_Mutation	SNP	G	A	43	243	c.611C>T	c.(610-612)TCA>TTA	p.S204L
Pat_41	Post-Resistance	POLR3C	10623	37	1	145608177	145608177	Missense_Mutation	SNP	G	A	11	247	c.520C>T	c.(520-522)CCA>TCA	p.P174S
Pat_41	Post-Resistance	LOC728989	728989	37	1	146496484	146496484	Splice_Site	SNP	C	T	13	31	c.17_splice	c.e2-1	p.D6_splice
Pat_41	Post-Resistance	PDIA3P	171423	37	1	146649927	146649927	Missense_Mutation	SNP	C	T	16	234	c.235C>T	c.(235-237)CCA>TCA	p.P79S
Pat_41	Post-Resistance	BCL9	607	37	1	147094189	147094189	Missense_Mutation	SNP	C	T	12	527	c.3020C>T	c.(3019-3021)TCT>TTT	p.S1007F
Pat_41	Post-Resistance	GJA5	2702	37	1	147230524	147230524	Missense_Mutation	SNP	G	A	18	163	c.823C>T	c.(823-825)CCT>TCT	p.P275S

Pat_41	Post-Resistance	NBPF14	25832	37	1	148015766	148015766	Missense_Mutation	SNP	G	A	16	397	c.865C>T	c.(865-867)CCT>TCT	p.P289S
Pat_41	Post-Resistance	LOC200030	200030	37	1	148342473	148342473	Missense_Mutation	SNP	G	A	40	691	c.563C>T	c.(562-564)CCC>CTC	p.P188L
Pat_41	Post-Resistance	HIST2H2BF	440689	37	1	149783685	149783685	Missense_Mutation	SNP	G	A	21	254	c.194C>T	c.(193-195)TCC>TTC	p.S65F
Pat_41	Post-Resistance	SV2A	9900	37	1	149885365	149885365	Missense_Mutation	SNP	C	T	6	159	c.28G>A	c.(28-30)GCT>ACT	p.A10T
Pat_41	Post-Resistance	OTUD7B	56957	37	1	149916315	149916315	Missense_Mutation	SNP	C	T	14	210	c.1973G>A	c.(1972-1974)GGG>GAG	p.G658E
Pat_41	Post-Resistance	OTUD7B	56957	37	1	149916928	149916928	Missense_Mutation	SNP	C	T	10	73	c.1360G>A	c.(1360-1362)GCT>ACT	p.A454T
Pat_41	Post-Resistance	VPS45	11311	37	1	150082640	150082640	Missense_Mutation	SNP	G	A	18	92	c.1523G>A	c.(1522-1524)GGA>GAA	p.G508E
Pat_41	Post-Resistance	C1orf51	148523	37	1	150259056	150259056	Missense_Mutation	SNP	C	T	45	231	c.848C>T	c.(847-849)CCT>CTT	p.P283L
Pat_41	Post-Resistance	RPRD2	23248	37	1	150444176	150444176	Missense_Mutation	SNP	G	A	83	424	c.2752G>A	c.(2752-2754)GTA>ATA	p.V918I
Pat_41	Post-Resistance	RPRD2	23248	37	1	150444887	150444887	Missense_Mutation	SNP	G	A	6	64	c.3463G>A	c.(3463-3465)GGC>AGC	p.G1155S
Pat_41	Post-Resistance	TARS2	80222	37	1	150469355	150469355	Missense_Mutation	SNP	G	A	5	70	c.991G>A	c.(991-993)GTG>ATG	p.V331M
Pat_41	Post-Resistance	ECM1	1893	37	1	150482181	150482181	Missense_Mutation	SNP	C	T	18	325	c.166C>T	c.(166-168)CCC>TCC	p.P56S
Pat_41	Post-Resistance	MCL1	4170	37	1	150549889	150549889	Missense_Mutation	SNP	C	T	100	653	c.1015G>A	c.(1015-1017)GCT>ACT	p.A339T
Pat_41	Post-Resistance	ANXA9	8416	37	1	150967112	150967112	Missense_Mutation	SNP	C	G	39	291	c.912C>G	c.(910-912)GAC>GAG	p.D304E
Pat_41	Post-Resistance	MLLT11	10962	37	1	151039951	151039951	Missense_Mutation	SNP	C	T	22	460	c.251C>T	c.(250-252)TCC>TTC	p.S84F
Pat_41	Post-Resistance	SEMA6C	10500	37	1	151107673	151107673	Missense_Mutation	SNP	G	A	5	91	c.1546C>T	c.(1546-1548)CTC>TTC	p.L516F
Pat_41	Post-Resistance	LYSMD1	388695	37	1	151133381	151133381	Missense_Mutation	SNP	C	T	19	329	c.661G>A	c.(661-663)GAG>AAG	p.E221K
Pat_41	Post-Resistance	PIP5K1A	8394	37	1	151210722	151210722	Missense_Mutation	SNP	G	A	5	153	c.1210G>A	c.(1210-1212)GAC>AAC	p.D404N
Pat_41	Post-Resistance	SELENBP1	8991	37	1	151339246	151339246	Missense_Mutation	SNP	C	T	30	331	c.616G>A	c.(616-618)GCT>ACT	p.A206T
Pat_41	Post-Resistance	SELENBP1	8991	37	1	151341550	151341550	Missense_Mutation	SNP	G	A	5	139	c.290C>T	c.(289-291)CCC>CTC	p.P97L
Pat_41	Post-Resistance	POGZ	23126	37	1	151400683	151400683	Missense_Mutation	SNP	G	A	15	203	c.775C>T	c.(775-777)CCC>TCC	p.P259S
Pat_41	Post-Resistance	CGN	57530	37	1	151508765	151508765	Missense_Mutation	SNP	G	A	16	137	c.3250G>A	c.(3250-3252)GAA>AAA	p.E1084K
Pat_41	Post-Resistance	CGN	57530	37	1	151509224	151509224	Missense_Mutation	SNP	G	A	9	114	c.3325G>A	c.(3325-3327)GCT>ACT	p.A1109T
Pat_41	Post-Resistance	SNX27	81609	37	1	151611384	151611384	Missense_Mutation	SNP	G	A	5	258	c.332G>A	c.(331-333)GGG>GAG	p.G111E
Pat_41	Post-Resistance	SNX27	81609	37	1	151630880	151630880	Missense_Mutation	SNP	G	A	15	158	c.713G>A	c.(712-714)GGA>GAA	p.G238E
Pat_41	Post-Resistance	TDRKH	11022	37	1	151752463	151752463	Missense_Mutation	SNP	G	A	12	158	c.385C>T	c.(385-387)CTT>TTT	p.L129F
Pat_41	Post-Resistance	LINGO4	339398	37	1	151773413	151773413	Missense_Mutation	SNP	C	T	5	114	c.1768G>A	c.(1768-1770)GCC>ACC	p.A590T
Pat_41	Post-Resistance	LINGO4	339398	37	1	151773935	151773935	Nonsense_Mutation	SNP	G	A	4	120	c.1246C>T	c.(1246-1248)CGA>TGA	p.R416*
Pat_41	Post-Resistance	LINGO4	339398	37	1	151774058	151774058	Missense_Mutation	SNP	G	A	5	58	c.1123C>T	c.(1123-1125)CAC>TAC	p.H375Y
Pat_41	Post-Resistance	LINGO4	339398	37	1	151774919	151774919	Missense_Mutation	SNP	C	T	6	31	c.262G>A	c.(262-264)GAA>AAA	p.E88K
Pat_41	Post-Resistance	S100A11	6282	37	1	152005164	152005164	Missense_Mutation	SNP	C	T	7	78	c.292G>A	c.(292-294)GCT>ACT	p.A98T
Pat_41	Post-Resistance	TCHH	7062	37	1	152081093	152081093	Missense_Mutation	SNP	G	A	7	50	c.4600C>T	c.(4600-4602)CTC>TTC	p.L1534F
Pat_41	Post-Resistance	TCHH	7062	37	1	152084165	152084165	Missense_Mutation	SNP	C	T	5	82	c.1528G>A	c.(1528-1530)GAG>AAG	p.E510K
Pat_41	Post-Resistance	RPTN	126638	37	1	152127456	152127456	Missense_Mutation	SNP	C	T	40	335	c.2119G>A	c.(2119-2121)GAA>AAA	p.E707K
Pat_41	Post-Resistance	HRNR	388697	37	1	152187617	152187617	Missense_Mutation	SNP	C	T	15	828	c.6488G>A	c.(6487-6489)GGG>GAG	p.G2163E
Pat_41	Post-Resistance	FLG	2312	37	1	152276792	152276792	Missense_Mutation	SNP	C	T	27	397	c.10570G>A	c.(10570-10572)GGA>AGA	p.G3524R
Pat_41	Post-Resistance	FLG	2312	37	1	152277097	152277097	Missense_Mutation	SNP	G	A	8	299	c.10265C>T	c.(10264-10266)TCC>TTC	p.S3422F
Pat_41	Post-Resistance	FLG	2312	37	1	152283904	152283904	Missense_Mutation	SNP	G	A	9	325	c.3458C>T	c.(3457-3459)TCC>TTC	p.S1153F
Pat_41	Post-Resistance	FLG	2312	37	1	152284948	152284948	Missense_Mutation	SNP	G	A	15	309	c.2414C>T	c.(2413-2415)TCC>TTC	p.S805F
Pat_41	Post-Resistance	FLG	2312	37	1	152285591	152285591	Missense_Mutation	SNP	C	T	33	464	c.1771G>A	c.(1771-1773)GCT>ACT	p.A591T
Pat_41	Post-Resistance	FLG2	388698	37	1	152325436	152325436	Missense_Mutation	SNP	G	A	13	505	c.4826C>T	c.(4825-4827)CCA>CTA	p.P1609L
Pat_41	Post-Resistance	FLG2	388698	37	1	152325865	152325865	Missense_Mutation	SNP	C	T	39	675	c.4397G>A	c.(4396-4398)GGA>GAA	p.G1466E
Pat_41	Post-Resistance	FLG2	388698	37	1	152327749	152327749	Missense_Mutation	SNP	G	A	51	745	c.2513C>T	c.(2512-2514)TCT>TTT	p.S838F
Pat_41	Post-Resistance	FLG2	388698	37	1	152329195	152329195	Missense_Mutation	SNP	C	T	33	114	c.1067G>A	c.(1066-1068)GGA>GAA	p.G356E
Pat_41	Post-Resistance	CRNN	49860	37	1	152384655	152384655	Missense_Mutation	SNP	C	T	23	141	c.55G>A	c.(55-57)GCA>ACA	p.A19T
Pat_41	Post-Resistance	KPRP	448834	37	1	152732125	152732125	Missense_Mutation	SNP	C	T	16	233	c.61C>T	c.(61-63)CCC>TCC	p.P21S
Pat_41	Post-Resistance	SPRR1B	6699	37	1	153005056	153005056	Missense_Mutation	SNP	C	T	16	280	c.235C>T	c.(235-237)CCA>TCA	p.P79S

Pat_41	Post-Resistance	SPRR2G	6706	37	1	153122457	153122457	Missense_Mutation	SNP	C	T	12	179	c.130G>A	c.(130-132)GAG>AAG	p.E44K
Pat_41	Post-Resistance	S100A7A	338324	37	1	153391778	153391778	Missense_Mutation	SNP	G	A	7	55	c.299G>A	c.(298-300)AGC>AAC	p.S100N
Pat_41	Post-Resistance	INTS3	65123	37	1	153701196	153701196	Missense_Mutation	SNP	G	A	6	97	c.86G>A	c.(85-87)GGA>GAA	p.G29E
Pat_41	Post-Resistance	INTS3	65123	37	1	153723712	153723713	Missense_Mutation	DNP	AC	TT	50	89	c.726_727AC>TT	724-729)GAACGG>GATT	(242_243ER>D
Pat_41	Post-Resistance	INTS3	65123	37	1	153735307	153735307	Missense_Mutation	SNP	G	T	16	155	c.1620G>T	c.(1618-1620)GAG>GAT	p.E540D
Pat_41	Post-Resistance	GATAD2B	57459	37	1	153788820	153788820	Missense_Mutation	SNP	C	T	16	240	c.1145G>A	c.(1144-1146)AGT>AAT	p.S382N
Pat_41	Post-Resistance	NUP210L	91181	37	1	153994680	153994680	Missense_Mutation	SNP	G	A	16	219	c.4438C>T	c.(4438-4440)CAT>TAT	p.H1480Y
Pat_41	Post-Resistance	NUP210L	91181	37	1	154098842	154098842	Missense_Mutation	SNP	C	T	8	271	c.1283G>A	c.(1282-1284)GGT>GAT	p.G428D
Pat_41	Post-Resistance	NUP210L	91181	37	1	154113906	154113906	Splice_Site	SNP	C	T	20	244	c.566_splice	c.e4+1	p.R189_splice
Pat_41	Post-Resistance	UBAP2L	9898	37	1	154207702	154207702	Missense_Mutation	SNP	C	T	7	29	c.479C>T	c.(478-480)ACC>ATC	p.T160I
Pat_41	Post-Resistance	HAX1	10456	37	1	154247728	154247728	Missense_Mutation	SNP	C	T	6	105	c.655C>T	c.(655-657)CCA>TCA	p.P219S
Pat_41	Post-Resistance	SHE	126669	37	1	154461626	154461626	Missense_Mutation	SNP	G	A	7	66	c.925C>T	c.(925-927)CCC>TCC	p.P309S
Pat_41	Post-Resistance	SHE	126669	37	1	154473961	154473961	Missense_Mutation	SNP	G	A	10	69	c.542C>T	c.(541-543)TCC>TTC	p.S181F
Pat_41	Post-Resistance	UBE2Q1	55585	37	1	154524445	154524445	Missense_Mutation	SNP	G	A	7	106	c.977C>T	c.(976-978)CCC>CTC	p.P326L
Pat_41	Post-Resistance	ADAR	103	37	1	154574774	154574774	Missense_Mutation	SNP	C	T	13	57	c.344G>A	c.(343-345)GGC>GAC	p.G115D
Pat_41	Post-Resistance	KCNN3	3782	37	1	154794630	154794630	Missense_Mutation	SNP	G	A	8	104	c.964C>T	c.(964-966)CTT>TTT	p.L322F
Pat_41	Post-Resistance	PBXIP1	57326	37	1	154918265	154918265	Missense_Mutation	SNP	C	T	13	81	c.1885G>A	c.(1885-1887)GCT>ACT	p.A629T
Pat_41	Post-Resistance	PBXIP1	57326	37	1	154919237	154919237	Missense_Mutation	SNP	C	T	5	41	c.913G>A	c.(913-915)GGG>AGG	p.G305R
Pat_41	Post-Resistance	SHC1	6464	37	1	154938680	154938680	Missense_Mutation	SNP	G	A	7	74	c.1210C>T	c.(1210-1212)CCA>TCA	p.P404S
Pat_41	Post-Resistance	FLAD1	80308	37	1	154962075	154962075	Missense_Mutation	SNP	C	T	20	134	c.1157C>T	c.(1156-1158)ACC>ATC	p.T386I
Pat_41	Post-Resistance	ADAM15	8751	37	1	155029544	155029544	Missense_Mutation	SNP	C	T	5	52	c.1115C>T	c.(1114-1116)CCA>CTA	p.P372L
Pat_41	Post-Resistance	TRIM46	80128	37	1	155147944	155147944	Missense_Mutation	SNP	C	T	6	227	c.146C>T	c.(145-147)ACC>ATC	p.T49I
Pat_41	Post-Resistance	THBS3	7059	37	1	155165886	155165886	Missense_Mutation	SNP	C	T	12	235	c.2704G>A	c.(2704-2706)GCG>ACG	p.A902T
Pat_41	Post-Resistance	CLK2	1196	37	1	155233104	155233104	Missense_Mutation	SNP	T	A	9	107	c.1405A>T	c.(1405-1407)ACC>TCC	p.T469S
Pat_41	Post-Resistance	PKLR	5313	37	1	155265054	155265054	Missense_Mutation	SNP	C	T	5	241	c.547G>A	c.(547-549)GTG>ATG	p.V183M
Pat_41	Post-Resistance	ASH1L	55870	37	1	155311810	155311810	Missense_Mutation	SNP	G	A	17	365	c.8392C>T	c.(8392-8394)CAC>TAC	p.H2798Y
Pat_41	Post-Resistance	ASH1L	55870	37	1	155448141	155448141	Missense_Mutation	SNP	G	A	4	79	c.4520C>T	c.(4519-4521)TCC>TTC	p.S1507F
Pat_41	Post-Resistance	ASH1L	55870	37	1	155448984	155448984	Missense_Mutation	SNP	G	A	8	268	c.3677C>T	c.(3676-3678)TCT>TTT	p.S1226F
Pat_41	Post-Resistance	ASH1L	55870	37	1	155450143	155450143	Missense_Mutation	SNP	C	T	5	82	c.2518G>A	c.(2518-2520)GAA>AAA	p.E840K
Pat_41	Post-Resistance	ASH1L	55870	37	1	155491252	155491252	Missense_Mutation	SNP	C	T	15	294	c.59G>A	c.(58-60)AGA>AAA	p.R20K
Pat_41	Post-Resistance	MSTO1	55154	37	1	155582276	155582276	Missense_Mutation	SNP	G	A	19	167	c.881G>A	c.(880-882)AGC>AAC	p.S294N
Pat_41	Post-Resistance	GON4L	54856	37	1	155735525	155735525	Missense_Mutation	SNP	G	A	10	83	c.3739C>T	c.(3739-3741)CCC>TCC	p.P1247S
Pat_41	Post-Resistance	ARHGEF2	9181	37	1	155920227	155920227	Missense_Mutation	SNP	G	A	9	191	c.2750C>T	c.(2749-2751)TCT>TTT	p.S917F
Pat_41	Post-Resistance	ARHGEF2	9181	37	1	155936257	155936257	Missense_Mutation	SNP	G	A	36	251	c.290C>T	c.(289-291)GCC>GTC	p.A97V
Pat_41	Post-Resistance	UBQLN4	56893	37	1	156012620	156012620	Missense_Mutation	SNP	G	A	5	27	c.1211C>T	c.(1210-1212)CCC>CTC	p.P404L
Pat_41	Post-Resistance	LMNA	4000	37	1	156105913	156105913	Splice_Site	SNP	G	A	5	70	c.1157_splice	c.e6+1	p.R386_splice
Pat_41	Post-Resistance	PAQR6	79957	37	1	156215990	156215990	Missense_Mutation	SNP	C	T	5	124	c.103G>A	c.(103-105)GCT>ACT	p.A35T
Pat_41	Post-Resistance	APOA1BP	128240	37	1	156563845	156563845	Missense_Mutation	SNP	C	T	13	320	c.836C>T	c.(835-837)CCT>CTT	p.P279L
Pat_41	Post-Resistance	GPATCH4	54865	37	1	156565333	156565333	Missense_Mutation	SNP	C	T	27	240	c.800G>A	c.(799-801)GGG>GAG	p.G267E
Pat_41	Post-Resistance	ISG20L2	81875	37	1	156697269	156697269	Missense_Mutation	SNP	G	A	24	37	c.176C>T	c.(175-177)TCA>TTA	p.S59L
Pat_41	Post-Resistance	MRPL24	79590	37	1	156707878	156707878	Missense_Mutation	SNP	G	A	4	129	c.328C>T	c.(328-330)CCT>TCT	p.P110S
Pat_41	Post-Resistance	MRPL24	79590	37	1	156708343	156708343	Missense_Mutation	SNP	C	T	13	218	c.154G>A	c.(154-156)GAA>AAA	p.E52K
Pat_41	Post-Resistance	INSRR	3645	37	1	156823618	156823618	Missense_Mutation	SNP	C	T	9	118	c.563G>A	c.(562-564)GGT>GAT	p.G188D
Pat_41	Post-Resistance	NTRK1	4914	37	1	156845344	156845344	Missense_Mutation	SNP	G	A	14	151	c.1387G>A	c.(1387-1389)GCC>ACC	p.A463T
Pat_41	Post-Resistance	C1orf92	149499	37	1	156897544	156897544	Missense_Mutation	SNP	C	T	4	64	c.842C>T	c.(841-843)TCC>TTC	p.S281F
Pat_41	Post-Resistance	ETV3	2117	37	1	157103937	157103937	Missense_Mutation	SNP	G	A	9	181	c.367C>T	c.(367-369)CCC>TCC	p.P123S
Pat_41	Post-Resistance	FCRL4	83417	37	1	157556215	157556215	Missense_Mutation	SNP	G	A	11	131	c.878C>T	c.(877-879)ACC>ATC	p.T293I

Pat_41	Post-Resistance	FCRL2	79368	37	1	157718718	157718718	Missense_Mutation	SNP	G	A	13	166	c.1340C>T	c.(1339-1341)ACC>ATC	p.T447I
Pat_41	Post-Resistance	FCRL1	115350	37	1	157771365	157771365	Missense_Mutation	SNP	G	A	5	89	c.889C>T	c.(889-891)CCT>TCT	p.P297S
Pat_41	Post-Resistance	KIRREL	55243	37	1	158059292	158059292	Missense_Mutation	SNP	G	A	6	101	c.1045G>A	c.(1045-1047)GTC>ATC	p.V349I
Pat_41	Post-Resistance	KIRREL	55243	37	1	158061185	158061185	Missense_Mutation	SNP	C	T	7	274	c.1310C>T	c.(1309-1311)ACC>ATC	p.T437I
Pat_41	Post-Resistance	OR10K1	391109	37	1	158435419	158435419	Missense_Mutation	SNP	T	A	19	41	c.68T>A	c.(67-69)CTG>CAG	p.L23Q
Pat_41	Post-Resistance	OR10R2	343406	37	1	158449836	158449836	Missense_Mutation	SNP	G	A	10	124	c.169G>A	c.(169-171)GTC>ATC	p.V57I
Pat_41	Post-Resistance	SPTA1	6708	37	1	158582744	158582744	Missense_Mutation	SNP	A	G	4	84	c.6997T>C	c.(6997-6999)TAT>CAT	p.Y2333H
Pat_41	Post-Resistance	SPTA1	6708	37	1	158651378	158651378	Missense_Mutation	SNP	G	A	29	299	c.470C>T	c.(469-471)GCC>GTC	p.A157V
Pat_41	Post-Resistance	AIM2	9447	37	1	159043148	159043148	Missense_Mutation	SNP	C	T	11	124	c.142G>A	c.(142-144)GTA>ATA	p.V48I
Pat_41	Post-Resistance	DARC	2532	37	1	159176016	159176016	Missense_Mutation	SNP	G	A	4	95	c.787G>A	c.(787-789)GAT>AAT	p.D263N
Pat_41	Post-Resistance	CRP	1401	37	1	159683792	159683793	Missense_Mutation	DNP	CC	TT	69	102	c.197_198GG>AA	c.(196-198)GGG>GAA	p.G66E
Pat_41	Post-Resistance	VSIG8	391123	37	1	159827708	159827708	Missense_Mutation	SNP	C	T	13	67	c.479G>A	c.(478-480)GGC>GAC	p.G160D
Pat_41	Post-Resistance	CCDC19	25790	37	1	159862980	159862980	Missense_Mutation	SNP	C	T	10	120	c.119G>A	c.(118-120)GGA>GAA	p.G40E
Pat_41	Post-Resistance	COPA	1314	37	1	160261641	160261641	Missense_Mutation	SNP	C	T	85	452	c.3226G>A	c.(3226-3228)GAG>AAG	p.E1076K
Pat_41	Post-Resistance	NCSTN	23385	37	1	160328042	160328042	Missense_Mutation	SNP	C	T	7	94	c.2111C>T	c.(2110-2112)CCA>CTA	p.P704L
Pat_41	Post-Resistance	LY9	4063	37	1	160786503	160786503	Missense_Mutation	SNP	C	T	17	99	c.1192C>T	c.(1192-1194)CCG>TCG	p.P398S
Pat_41	Post-Resistance	USF1	7391	37	1	161010461	161010461	Splice_Site	SNP	C	T	6	97	c.620_splice	c.e9-1	p.V207_splice
Pat_41	Post-Resistance	USF1	7391	37	1	161012650	161012650	Missense_Mutation	SNP	C	T	25	381	c.31G>A	c.(31-33)GAA>AAA	p.E11K
Pat_41	Post-Resistance	ARHGAP30	257106	37	1	161021425	161021425	Missense_Mutation	SNP	C	T	10	64	c.1099G>A	c.(1099-1101)GCA>ACA	p.A367T
Pat_41	Post-Resistance	KLHDC9	126823	37	1	161069216	161069216	Missense_Mutation	SNP	G	A	5	70	c.608G>A	c.(607-609)GGT>GAT	p.G203D
Pat_41	Post-Resistance	PPOX	5498	37	1	161140923	161140923	Missense_Mutation	SNP	G	A	29	275	c.1391G>A	c.(1390-1392)CGC>CAC	p.R464H
Pat_41	Post-Resistance	B4GALT3	8703	37	1	161145700	161145700	Missense_Mutation	SNP	G	A	22	159	c.151C>T	c.(151-153)CCT>TCT	p.P51S
Pat_41	Post-Resistance	B4GALT3	8703	37	1	161145798	161145798	Missense_Mutation	SNP	G	A	16	192	c.53C>T	c.(52-54)TCC>TTC	p.S18F
Pat_41	Post-Resistance	NDUFS2	4720	37	1	161183505	161183505	Missense_Mutation	SNP	C	T	16	199	c.1279C>T	c.(1279-1281)CCT>TCT	p.P427S
Pat_41	Post-Resistance	PCP4L1	654790	37	1	161254224	161254224	Missense_Mutation	SNP	G	A	7	41	c.160G>A	c.(160-162)GGC>AGC	p.G54S
Pat_41	Post-Resistance	C1orf192	257177	37	1	161337654	161337654	Missense_Mutation	SNP	G	A	18	290	c.5C>T	c.(4-6)GCC>GTC	p.A2V
Pat_41	Post-Resistance	FCGR2A	2212	37	1	161476138	161476138	Missense_Mutation	SNP	G	A	16	285	c.121G>A	c.(121-123)GCT>ACT	p.A41T
Pat_41	Post-Resistance	FCGR2A	2212	37	1	161480714	161480714	Missense_Mutation	SNP	C	T	82	578	c.710C>T	c.(709-711)GCC>GTC	p.A237V
Pat_41	Post-Resistance	FCGR2C	9103	37	1	161569489	161569489	Missense_Mutation	SNP	G	A	14	85	c.868G>A	c.(868-870)GCT>ACT	p.A290T
Pat_41	Post-Resistance	FCGR2B	2213	37	1	161641275	161641275	Missense_Mutation	SNP	G	A	13	164	c.227G>A	c.(226-228)AGC>AAC	p.S76N
Pat_41	Post-Resistance	PBX1	5087	37	1	164776807	164776807	Missense_Mutation	SNP	G	A	62	287	c.730G>A	c.(730-732)GCG>ACG	p.A244T
Pat_41	Post-Resistance	ILDR2	387597	37	1	166904616	166904616	Missense_Mutation	SNP	G	A	5	139	c.802C>T	c.(802-804)CCC>TCC	p.P268S
Pat_41	Post-Resistance	MAEL	84944	37	1	166973459	166973459	Missense_Mutation	SNP	G	A	61	147	c.566G>A	c.(565-567)GGG>GAG	p.G189E
Pat_41	Post-Resistance	POU2F1	5451	37	1	167341226	167341226	Missense_Mutation	SNP	G	A	37	513	c.286G>A	c.(286-288)GCC>ACC	p.A96T
Pat_41	Post-Resistance	ADCY10	55811	37	1	167805716	167805716	Missense_Mutation	SNP	G	A	10	192	c.3140C>T	c.(3139-3141)ACA>ATA	p.T1047I
Pat_41	Post-Resistance	SLC19A2	10560	37	1	169439360	169439360	Missense_Mutation	SNP	G	A	28	194	c.872C>T	c.(871-873)TCC>TTC	p.S291F
Pat_41	Post-Resistance	F5	2153	37	1	169493067	169493067	Missense_Mutation	SNP	G	A	23	402	c.5864C>T	c.(5863-5865)GCA>GTA	p.A1955V
Pat_41	Post-Resistance	F5	2153	37	1	169510897	169510897	Missense_Mutation	SNP	G	A	44	281	c.3431C>T	c.(3430-3432)CCC>CTC	p.P1144L
Pat_41	Post-Resistance	F5	2153	37	1	169511764	169511764	Missense_Mutation	SNP	C	T	11	240	c.2564G>A	c.(2563-2565)GGA>GAA	p.G855E
Pat_41	Post-Resistance	SELE	6401	37	1	169696574	169696574	Missense_Mutation	SNP	G	A	23	100	c.1561C>T	c.(1561-1563)CCT>TCT	p.P521S
Pat_41	Post-Resistance	C1orf112	55732	37	1	169801648	169801648	Splice_Site	SNP	G	A	7	260	c.1539_splice	c.e17+1	p.Q513_splice
Pat_41	Post-Resistance	SCYL3	57147	37	1	169822897	169822897	Nonsense_Mutation	SNP	C	T	27	465	c.2186G>A	c.(2185-2187)TGG>TAG	p.W729*
Pat_41	Post-Resistance	BAT2L2	23215	37	1	171510135	171510135	Missense_Mutation	SNP	G	A	9	82	c.3524G>A	c.(3523-3525)AGA>AAA	p.R1175K
Pat_41	Post-Resistance	BAT2L2	23215	37	1	171511112	171511112	Missense_Mutation	SNP	G	A	13	153	c.4501G>A	c.(4501-4503)GAA>AAA	p.E1501K
Pat_41	Post-Resistance	BAT2L2	23215	37	1	171527198	171527198	Missense_Mutation	SNP	C	T	14	322	c.5941C>T	c.(5941-5943)CCA>TCA	p.P1981S
Pat_41	Post-Resistance	CENPL	91687	37	1	173769605	173769605	Missense_Mutation	SNP	G	A	10	71	c.1016C>T	c.(1015-1017)GCA>GTA	p.A339V
Pat_41	Post-Resistance	DARS2	55157	37	1	173822936	173822936	Missense_Mutation	SNP	C	T	16	264	c.1567C>T	c.(1567-1569)CGT>TGT	p.R523C

Pat_41	Post-Resistance	SERPINC1	462	37	1	173876629	173876629	Missense_Mutation	SNP	C	T	73	355	c.1177G>A	c.(1177-1179)GAC>AAC	p.D393N
Pat_41	Post-Resistance	SERPINC1	462	37	1	173878981	173878981	Missense_Mutation	SNP	C	T	14	162	c.862G>A	c.(862-864)GGC>AGC	p.G288S
Pat_41	Post-Resistance	RC3H1	149041	37	1	173933204	173933204	Missense_Mutation	SNP	C	T	9	141	c.1738G>A	c.(1738-1740)GGT>AGT	p.G580S
Pat_41	Post-Resistance	RABGAP1L	9910	37	1	174221712	174221712	Missense_Mutation	SNP	G	A	14	132	c.970G>A	c.(970-972)GAA>AAA	p.E324K
Pat_41	Post-Resistance	CACYBP	27101	37	1	174976316	174976316	Missense_Mutation	SNP	G	A	26	223	c.415G>A	c.(415-417)GAA>AAA	p.E139K
Pat_41	Post-Resistance	TNR	7143	37	1	175304895	175304895	Missense_Mutation	SNP	C	T	13	419	c.3583G>A	c.(3583-3585)GCT>ACT	p.A1195T
Pat_41	Post-Resistance	TNR	7143	37	1	175323620	175323620	Missense_Mutation	SNP	C	T	16	145	c.3289G>A	c.(3289-3291)GAG>AAG	p.E1097K
Pat_41	Post-Resistance	PAPPA2	60676	37	1	176525967	176525967	Missense_Mutation	SNP	C	T	10	139	c.509C>T	c.(508-510)GCC>GTC	p.A170V
Pat_41	Post-Resistance	PAPPA2	60676	37	1	176563933	176563933	Missense_Mutation	SNP	C	T	39	140	c.1193C>T	c.(1192-1194)CCC>CTC	p.P398L
Pat_41	Post-Resistance	PAPPA2	60676	37	1	176668608	176668608	Missense_Mutation	SNP	C	T	14	111	c.3119C>T	c.(3118-3120)CCC>CTC	p.P1040L
Pat_41	Post-Resistance	ASTN1	460	37	1	176918351	176918351	Missense_Mutation	SNP	G	A	17	253	c.2024C>T	c.(2023-2025)CCC>CTC	p.P675L
Pat_41	Post-Resistance	RASAL2	9462	37	1	178442367	178442367	Missense_Mutation	SNP	G	A	7	142	c.3413G>A	c.(3412-3414)AGC>AAC	p.S1138N
Pat_41	Post-Resistance	ANGPTL1	9068	37	1	178820378	178820378	Nonsense_Mutation	SNP	C	T	25	200	c.1362G>A	c.(1360-1362)TGG>TGA	p.W454*
Pat_41	Post-Resistance	C1orf125	126859	37	1	179347827	179347827	Missense_Mutation	SNP	G	A	18	242	c.430G>A	c.(430-432)GCA>ACA	p.A144T
Pat_41	Post-Resistance	C1orf125	126859	37	1	179363073	179363073	Missense_Mutation	SNP	G	A	44	374	c.899G>A	c.(898-900)CGG>CAG	p.R300Q
Pat_41	Post-Resistance	TDRD5	163589	37	1	179604997	179604997	Missense_Mutation	SNP	C	T	12	212	c.1495C>T	c.(1495-1497)CTC>TTC	p.L499F
Pat_41	Post-Resistance	KIAA1614	57710	37	1	180905430	180905430	Nonsense_Mutation	SNP	G	A	10	90	c.2385G>A	c.(2383-2385)TGG>TGA	p.W795*
Pat_41	Post-Resistance	RNASEL	6041	37	1	182553275	182553275	Missense_Mutation	SNP	C	T	13	200	c.1507G>A	c.(1507-1509)GAT>AAT	p.D503N
Pat_41	Post-Resistance	RGS16	6004	37	1	182569471	182569471	Missense_Mutation	SNP	C	T	5	211	c.565G>A	c.(565-567)GCC>ACC	p.A189T
Pat_41	Post-Resistance	RGS8	85397	37	1	182635155	182635155	Missense_Mutation	SNP	C	T	21	180	c.142G>A	c.(142-144)GAA>AAA	p.E48K
Pat_41	Post-Resistance	NPL	80896	37	1	182791321	182791321	Missense_Mutation	SNP	C	T	7	73	c.725C>T	c.(724-726)GCC>GTC	p.A242V
Pat_41	Post-Resistance	DHX9	1660	37	1	182821367	182821367	Splice_Site	SNP	G	A	7	119	c.253_splice	c.e4-1	p.V85_splice
Pat_41	Post-Resistance	SMG7	9887	37	1	183515189	183515189	Missense_Mutation	SNP	A	G	8	203	c.2459A>G	c.(2458-2460)TAC>TGC	p.Y820C
Pat_41	Post-Resistance	SMG7	9887	37	1	183521038	183521038	Missense_Mutation	SNP	G	A	11	188	c.3386G>A	c.(3385-3387)GGA>GAA	p.G1129E
Pat_41	Post-Resistance	RGL1	23179	37	1	183816833	183816833	Missense_Mutation	SNP	C	T	7	114	c.272C>T	c.(271-273)ACC>ATC	p.T91I
Pat_41	Post-Resistance	IVNS1ABP	10625	37	1	185277946	185277946	Missense_Mutation	SNP	C	T	82	520	c.343G>A	c.(343-345)GAT>AAT	p.D115N
Pat_41	Post-Resistance	HMCN1	83872	37	1	185939535	185939535	Missense_Mutation	SNP	G	A	19	310	c.2281G>A	c.(2281-2283)GAA>AAA	p.E761K
Pat_41	Post-Resistance	HMCN1	83872	37	1	185951441	185951441	Missense_Mutation	SNP	G	A	26	372	c.2710G>A	c.(2710-2712)GGA>AGA	p.G904R
Pat_41	Post-Resistance	HMCN1	83872	37	1	185976273	185976273	Missense_Mutation	SNP	G	A	7	76	c.4489G>A	c.(4489-4491)GGC>AGC	p.G1497S
Pat_41	Post-Resistance	HMCN1	83872	37	1	186055459	186055459	Missense_Mutation	SNP	C	T	14	221	c.8966C>T	c.(8965-8967)TCT>TTT	p.S2989F
Pat_41	Post-Resistance	HMCN1	83872	37	1	186059961	186059961	Missense_Mutation	SNP	G	A	20	343	c.9799G>A	c.(9799-9801)GTC>ATC	p.V3267I
Pat_41	Post-Resistance	HMCN1	83872	37	1	186158693	186158693	Missense_Mutation	SNP	C	T	31	210	c.16591C>T	c.(16591-16593)CCA>TCA	p.P5531S
Pat_41	Post-Resistance	PRG4	10216	37	1	186269222	186269222	Splice_Site	SNP	G	A	13	117	c.77_splice	c.e3-1	p.D26_splice
Pat_41	Post-Resistance	PRG4	10216	37	1	186277079	186277079	Missense_Mutation	SNP	C	T	9	132	c.2228C>T	c.(2227-2229)TCC>TTC	p.S743F
Pat_41	Post-Resistance	PRG4	10216	37	1	186277960	186277960	Missense_Mutation	SNP	C	T	10	39	c.3109C>T	c.(3109-3111)CCA>TCA	p.P1037S
Pat_41	Post-Resistance	CFHR3	10878	37	1	196748402	196748402	Missense_Mutation	SNP	G	A	9	114	c.169G>A	c.(169-171)GAA>AAA	p.E57K
Pat_41	Post-Resistance	CFHR2	3080	37	1	196918584	196918584	Splice_Site	SNP	G	A	4	43	c.59_splice	c.e2-1	p.A20_splice
Pat_41	Post-Resistance	ASPM	259266	37	1	197062351	197062351	Missense_Mutation	SNP	C	T	13	305	c.9125G>A	c.(9124-9126)GGA>GAA	p.G3042E
Pat_41	Post-Resistance	PTPRC	5788	37	1	198665870	198665870	Missense_Mutation	SNP	C	T	25	508	c.124C>T	c.(124-126)CCA>TCA	p.P42S
Pat_41	Post-Resistance	PTPRC	5788	37	1	198671552	198671552	Missense_Mutation	SNP	C	T	157	239	c.470C>T	c.(469-471)CCT>CTT	p.P157L
Pat_41	Post-Resistance	PTPRC	5788	37	1	198719669	198719669	Missense_Mutation	SNP	G	A	8	164	c.3115G>A	c.(3115-3117)GAG>AAG	p.E1039K
Pat_41	Post-Resistance	FAM58B	339521	37	1	200182828	200182828	Missense_Mutation	SNP	G	A	19	108	c.137G>A	c.(136-138)GGG>GAG	p.G46E
Pat_41	Post-Resistance	ZNF281	23528	37	1	200378092	200378092	Missense_Mutation	SNP	C	T	5	146	c.742G>A	c.(742-744)GAT>AAT	p.D248N
Pat_41	Post-Resistance	KIF14	9928	37	1	200561223	200561223	Missense_Mutation	SNP	A	G	30	306	c.2798T>C	c.(2797-2799)ATG>ACG	p.M933T
Pat_41	Post-Resistance	KIF14	9928	37	1	200575908	200575908	Missense_Mutation	SNP	G	A	68	461	c.1573C>T	c.(1573-1575)CCT>TCT	p.P525S
Pat_41	Post-Resistance	C1orf106	55765	37	1	200860739	200860739	Missense_Mutation	SNP	G	A	6	54	c.71G>A	c.(70-72)GGA>GAA	p.G24E
Pat_41	Post-Resistance	KIF21B	23046	37	1	200948781	200948781	Missense_Mutation	SNP	G	A	17	673	c.4042C>T	c.(4042-4044)CCC>TCC	p.P1348S

Pat_41	Post-Resistance	KIF21B	23046	37	1	200973529	200973529	Missense_Mutation	SNP	G	A	4	18	c.955C>T	c.(955-957)CAC>TAC	p.H319Y
Pat_41	Post-Resistance	NAV1	89796	37	1	201778357	201778357	Missense_Mutation	SNP	G	A	29	392	c.4264G>A	c.(4264-4266)GTG>ATG	p.V1422M
Pat_41	Post-Resistance	NAV1	89796	37	1	201781751	201781751	Missense_Mutation	SNP	C	T	23	312	c.5174C>T	c.(5173-5175)ACC>ATC	p.T1725I
Pat_41	Post-Resistance	RNPEP	6051	37	1	201958137	201958137	Missense_Mutation	SNP	C	T	22	280	c.553C>T	c.(553-555)CCT>TCT	p.P185S
Pat_41	Post-Resistance	ELF3	1999	37	1	201981217	201981217	Missense_Mutation	SNP	G	A	22	68	c.296G>A	c.(295-297)GGC>GAC	p.G99D
Pat_41	Post-Resistance	LGR6	59352	37	1	202287248	202287248	Missense_Mutation	SNP	G	A	8	64	c.1817G>A	c.(1816-1818)GGC>GAC	p.G606D
Pat_41	Post-Resistance	PPP1R12B	4660	37	1	202462390	202462390	Missense_Mutation	SNP	C	T	11	19	c.2090C>T	c.(2089-2091)CCA>CTA	p.P697L
Pat_41	Post-Resistance	SYT2	127833	37	1	202569487	202569487	Missense_Mutation	SNP	G	A	8	128	c.917C>T	c.(916-918)TCA>TTA	p.S306L
Pat_41	Post-Resistance	CYB5R1	51706	37	1	202935712	202935712	Missense_Mutation	SNP	G	A	15	111	c.182C>T	c.(181-183)ACC>ATC	p.T61I
Pat_41	Post-Resistance	CHI3L1	1116	37	1	203148936	203148936	Missense_Mutation	SNP	C	T	20	149	c.964G>A	c.(964-966)GGC>AGC	p.G322S
Pat_41	Post-Resistance	FMOD	2331	37	1	203316579	203316579	Missense_Mutation	SNP	G	A	29	191	c.820C>T	c.(820-822)CGG>TGG	p.R274W
Pat_41	Post-Resistance	FMOD	2331	37	1	203317272	203317272	Missense_Mutation	SNP	C	T	8	76	c.127G>A	c.(127-129)GAC>AAC	p.D43N
Pat_41	Post-Resistance	ATP2B4	493	37	1	203672848	203672848	Missense_Mutation	SNP	G	A	11	133	c.1006G>A	c.(1006-1008)GAA>AAA	p.E336K
Pat_41	Post-Resistance	ATP2B4	493	37	1	203682323	203682323	Missense_Mutation	SNP	C	T	17	496	c.2242C>T	c.(2242-2244)CCT>TCT	p.P748S
Pat_41	Post-Resistance	ATP2B4	493	37	1	203683341	203683341	Missense_Mutation	SNP	C	T	31	406	c.2342C>T	c.(2341-2343)GCT>GTT	p.A781V
Pat_41	Post-Resistance	ATP2B4	493	37	1	203690430	203690430	Missense_Mutation	SNP	C	T	4	113	c.2704C>T	c.(2704-2706)CGG>TGG	p.R902W
Pat_41	Post-Resistance	SOX13	9580	37	1	204083684	204083684	Nonsense_Mutation	SNP	G	A	9	155	c.369G>A	c.(367-369)TGG>TGA	p.W123*
Pat_41	Post-Resistance	PIK3C2B	5287	37	1	204418348	204418348	Missense_Mutation	SNP	G	A	5	31	c.2311C>T	c.(2311-2313)CCT>TCT	p.P771S
Pat_41	Post-Resistance	CDK18	5129	37	1	205492348	205492348	Missense_Mutation	SNP	C	T	5	43	c.53C>T	c.(52-54)CCC>CTC	p.P18L
Pat_41	Post-Resistance	MFSD4	148808	37	1	205569545	205569545	Missense_Mutation	SNP	G	A	14	99	c.1501G>A	c.(1501-1503)GAC>AAC	p.D501N
Pat_41	Post-Resistance	SLC45A3	85414	37	1	205628444	205628444	Missense_Mutation	SNP	G	A	11	165	c.1580C>T	c.(1579-1581)GCC>GTC	p.A527V
Pat_41	Post-Resistance	SLC41A1	254428	37	1	205767092	205767092	Missense_Mutation	SNP	G	A	8	106	c.932C>T	c.(931-933)GCC>GTC	p.A311V
Pat_41	Post-Resistance	C1orf116	79098	37	1	207196099	207196099	Missense_Mutation	SNP	G	A	4	53	c.1010C>T	c.(1009-1011)TCC>TTC	p.S337F
Pat_41	Post-Resistance	CD55	1604	37	1	207495876	207495876	Missense_Mutation	SNP	G	A	15	187	c.250G>A	c.(250-252)GGC>AGC	p.G84S
Pat_41	Post-Resistance	CR2	1380	37	1	207642514	207642514	Missense_Mutation	SNP	C	T	31	483	c.754C>T	c.(754-756)CCT>TCT	p.P252S
Pat_41	Post-Resistance	PLXNA2	5362	37	1	208217993	208217993	Missense_Mutation	SNP	C	T	9	66	c.3734G>A	c.(3733-3735)GGC>GAC	p.G1245D
Pat_41	Post-Resistance	PLXNA2	5362	37	1	208390682	208390682	Missense_Mutation	SNP	G	A	18	383	c.586C>T	c.(586-588)CCG>TCG	p.P196S
Pat_41	Post-Resistance	LAMB3	3914	37	1	209797251	209797251	Missense_Mutation	SNP	C	T	15	111	c.2071G>A	c.(2071-2073)GGT>AGT	p.G691S
Pat_41	Post-Resistance	LPGAT1	9926	37	1	211923371	211923371	Missense_Mutation	SNP	C	T	8	138	c.983G>A	c.(982-984)GGC>GAC	p.G328D
Pat_41	Post-Resistance	TMEM206	55248	37	1	212538715	212538715	Missense_Mutation	SNP	C	T	17	268	c.895G>A	c.(895-897)GTC>ATC	p.V299I
Pat_41	Post-Resistance	ANGEL2	90806	37	1	213170601	213170601	Missense_Mutation	SNP	G	A	11	253	c.1379C>T	c.(1378-1380)CCT>CTT	p.P460L
Pat_41	Post-Resistance	ANGEL2	90806	37	1	213188986	213188986	Missense_Mutation	SNP	C	T	12	215	c.28G>A	c.(28-30)GGC>AGC	p.G10S
Pat_41	Post-Resistance	RPS6KC1	26750	37	1	213415575	213415575	Missense_Mutation	SNP	C	T	14	292	c.2756C>T	c.(2755-2757)GCT>GTT	p.A919V
Pat_41	Post-Resistance	CENPF	1063	37	1	214787102	214787102	Missense_Mutation	SNP	G	A	8	107	c.5G>A	c.(4-6)AGC>AAC	p.S2N
Pat_41	Post-Resistance	CENPF	1063	37	1	214794119	214794119	Missense_Mutation	SNP	C	T	37	177	c.695C>T	c.(694-696)TCT>TTT	p.S232F
Pat_41	Post-Resistance	CENPF	1063	37	1	214818053	214818053	Missense_Mutation	SNP	G	A	8	91	c.5140G>A	c.(5140-5142)GCA>ACA	p.A1714T
Pat_41	Post-Resistance	CENPF	1063	37	1	214836955	214836955	Missense_Mutation	SNP	C	T	5	146	c.9163C>T	c.(9163-9165)CCA>TCA	p.P3055S
Pat_41	Post-Resistance	USH2A	7399	37	1	216011345	216011345	Missense_Mutation	SNP	C	T	26	334	c.9359G>A	c.(9358-9360)GGC>GAC	p.G3120D
Pat_41	Post-Resistance	USH2A	7399	37	1	216074176	216074176	Missense_Mutation	SNP	G	A	12	186	c.7372C>T	c.(7372-7374)CCA>TCA	p.P2458S
Pat_41	Post-Resistance	USH2A	7399	37	1	216246236	216246236	Missense_Mutation	SNP	C	T	19	450	c.5852G>A	c.(5851-5853)GGA>GAA	p.G1951E
Pat_41	Post-Resistance	USH2A	7399	37	1	216260094	216260094	Missense_Mutation	SNP	G	A	4	134	c.4954C>T	c.(4954-4956)CCG>TCG	p.P1652S
Pat_41	Post-Resistance	USH2A	7399	37	1	216262426	216262426	Missense_Mutation	SNP	C	T	31	207	c.4814G>A	c.(4813-4815)GGA>GAA	p.G1605E
Pat_41	Post-Resistance	USH2A	7399	37	1	216370001	216370001	Nonsense_Mutation	SNP	C	T	5	137	c.4145G>A	c.(4144-4146)TGG>TAG	p.W1382*
Pat_41	Post-Resistance	USH2A	7399	37	1	216380702	216380702	Missense_Mutation	SNP	G	A	33	222	c.3229C>T	c.(3229-3231)CCT>TCT	p.P1077S
Pat_41	Post-Resistance	USH2A	7399	37	1	216498829	216498829	Missense_Mutation	SNP	G	A	73	111	c.961C>T	c.(961-963)CCT>TCT	p.P321S
Pat_41	Post-Resistance	GPATCH2	55105	37	1	217793198	217793198	Missense_Mutation	SNP	C	T	5	181	c.700G>A	c.(700-702)GAA>AAA	p.E234K
Pat_41	Post-Resistance	GPATCH2	55105	37	1	217793841	217793841	Nonsense_Mutation	SNP	C	T	8	73	c.57G>A	c.(55-57)TGG>TGA	p.W19*

Pat_41	Post-Resistance	EPRS	2058	37	1	220146740	220146740	Missense_Mutation	SNP	C	T	4	108	c.4084G>A	c.(4084-4086)GGA>AGA	p.G1362R
Pat_41	Post-Resistance	EPRS	2058	37	1	220192341	220192341	Missense_Mutation	SNP	G	A	56	380	c.1430C>T	c.(1429-1431)GCT>GTT	p.A477V
Pat_41	Post-Resistance	MARK1	4139	37	1	220791990	220791990	Nonsense_Mutation	SNP	C	T	36	160	c.802C>T	c.(802-804)CGA>TGA	p.R268*
Pat_41	Post-Resistance	MARK1	4139	37	1	220826621	220826621	Missense_Mutation	SNP	G	A	20	226	c.1915G>A	c.(1915-1917)GGT>AGT	p.G639S
Pat_41	Post-Resistance	HHIPL2	79802	37	1	222711990	222711990	Missense_Mutation	SNP	C	T	8	88	c.1577G>A	c.(1576-1578)GGT>GAT	p.G526D
Pat_41	Post-Resistance	MIA3	375056	37	1	222805585	222805585	Missense_Mutation	SNP	C	T	8	243	c.3248C>T	c.(3247-3249)ACC>ATC	p.T1083I
Pat_41	Post-Resistance	MIA3	375056	37	1	222827755	222827755	Missense_Mutation	SNP	G	A	5	113	c.4402G>A	c.(4402-4404)GAA>AAA	p.E1468K
Pat_41	Post-Resistance	C1orf58	148362	37	1	222895852	222895852	Missense_Mutation	SNP	G	A	4	99	c.397G>A	c.(397-399)GAA>AAA	p.E133K
Pat_41	Post-Resistance	DISP1	84976	37	1	223116199	223116199	Missense_Mutation	SNP	G	A	19	254	c.34G>A	c.(34-36)GTT>ATT	p.V12I
Pat_41	Post-Resistance	DISP1	84976	37	1	223165415	223165415	Nonsense_Mutation	SNP	G	A	15	174	c.852G>A	c.(850-852)TGG>TGA	p.W284*
Pat_41	Post-Resistance	DISP1	84976	37	1	223179114	223179114	Missense_Mutation	SNP	G	A	9	146	c.4375G>A	c.(4375-4377)GAA>AAA	p.E1459K
Pat_41	Post-Resistance	C1orf65	164127	37	1	223567494	223567494	Missense_Mutation	SNP	C	T	6	169	c.677C>T	c.(676-678)TCC>TTC	p.S226F
Pat_41	Post-Resistance	CAPN2	824	37	1	223931838	223931838	Missense_Mutation	SNP	C	T	14	135	c.344C>T	c.(343-345)ACC>ATC	p.T115I
Pat_41	Post-Resistance	LBR	3930	37	1	225599038	225599038	Splice_Site	SNP	C	T	19	263	c.1188_splice	c.e9+1	p.W396_splice
Pat_41	Post-Resistance	ENAH	55740	37	1	225702590	225702590	Missense_Mutation	SNP	C	T	15	142	c.926G>A	c.(925-927)GGA>GAA	p.G309E
Pat_41	Post-Resistance	ENAH	55740	37	1	225754977	225754977	Missense_Mutation	SNP	C	T	50	643	c.145G>A	c.(145-147)GTG>ATG	p.V49M
Pat_41	Post-Resistance	LEFTY1	10637	37	1	226111406	226111406	Missense_Mutation	SNP	G	A	9	165	c.133C>T	c.(133-135)CTC>TTC	p.L45F
Pat_41	Post-Resistance	C1orf55	163859	37	1	226175658	226175658	Missense_Mutation	SNP	G	A	8	113	c.1073C>T	c.(1072-1074)GCA>GTA	p.A358V
Pat_41	Post-Resistance	ACBD3	64746	37	1	226353612	226353612	Missense_Mutation	SNP	G	A	28	129	c.376C>T	c.(376-378)CCA>TCA	p.P126S
Pat_41	Post-Resistance	ITPKB	3707	37	1	226836382	226836382	Missense_Mutation	SNP	C	T	47	188	c.2023G>A	c.(2023-2025)GGA>AGA	p.G675R
Pat_41	Post-Resistance	CDC42BPA	8476	37	1	227221050	227221050	Missense_Mutation	SNP	T	C	4	150	c.3438A>G	c.(3436-3438)ATA>ATG	p.I1146M
Pat_41	Post-Resistance	SNAP47	116841	37	1	227946862	227946862	Missense_Mutation	SNP	G	A	4	116	c.799G>A	c.(799-801)GAG>AAG	p.E267K
Pat_41	Post-Resistance	OBSCN	84033	37	1	228437677	228437677	Missense_Mutation	SNP	G	A	11	193	c.4045G>A	c.(4045-4047)GTG>ATG	p.V1349M
Pat_41	Post-Resistance	OBSCN	84033	37	1	228523926	228523926	Missense_Mutation	SNP	G	A	7	219	c.16492G>A	.(16492-16494)GGG>AG	p.G5498R
Pat_41	Post-Resistance	HIST3H3	8290	37	1	228612633	228612633	Missense_Mutation	SNP	G	A	14	198	c.394C>T	c.(394-396)CGC>TGC	p.R132C
Pat_41	Post-Resistance	C1orf96	126731	37	1	229461116	229461116	Missense_Mutation	SNP	C	T	7	49	c.679G>A	c.(679-681)GAA>AAA	p.E227K
Pat_41	Post-Resistance	C1orf96	126731	37	1	229478092	229478092	Missense_Mutation	SNP	C	T	3	23	c.121G>A	c.(121-123)GAG>AAG	p.E41K
Pat_41	Post-Resistance	ACTA1	58	37	1	229567578	229567578	Missense_Mutation	SNP	C	T	26	343	c.880G>A	c.(880-882)GAC>AAC	p.D294N
Pat_41	Post-Resistance	NUP133	55746	37	1	229635550	229635550	Missense_Mutation	SNP	C	T	17	144	c.529G>A	c.(529-531)GTT>ATT	p.V177I
Pat_41	Post-Resistance	URB2	9816	37	1	229773334	229773334	Missense_Mutation	SNP	C	T	4	24	c.2974C>T	c.(2974-2976)CCC>TCC	p.P992S
Pat_41	Post-Resistance	PGBD5	79605	37	1	230486717	230486717	Missense_Mutation	SNP	C	T	18	170	c.674G>A	c.(673-675)GGC>GAC	p.G225D
Pat_41	Post-Resistance	CAPN9	10753	37	1	230931004	230931004	Missense_Mutation	SNP	G	A	4	51	c.1966G>A	c.(1966-1968)GTC>ATC	p.V656I
Pat_41	Post-Resistance	C1orf198	84886	37	1	230979617	230979617	Missense_Mutation	SNP	G	A	7	232	c.410C>T	c.(409-411)GCC>GTC	p.A137V
Pat_41	Post-Resistance	TRIM67	440730	37	1	231335990	231335990	Missense_Mutation	SNP	T	C	6	195	c.1360T>C	c.(1360-1362)TCC>CCC	p.S454P
Pat_41	Post-Resistance	GNPAT	8443	37	1	231386830	231386830	Missense_Mutation	SNP	C	T	10	175	c.202C>T	c.(202-204)CCA>TCA	p.P68S
Pat_41	Post-Resistance	SIPA1L2	57568	37	1	232539293	232539293	Missense_Mutation	SNP	G	A	16	77	c.4841C>T	c.(4840-4842)ACC>ATC	p.T1614I
Pat_41	Post-Resistance	SIPA1L2	57568	37	1	232564275	232564275	Missense_Mutation	SNP	G	A	10	238	c.4292C>T	c.(4291-4293)ACT>ATT	p.T1431I
Pat_41	Post-Resistance	SIPA1L2	57568	37	1	232568171	232568171	Missense_Mutation	SNP	T	C	18	148	c.4078A>G	c.(4078-4080)AGT>GGT	p.S1360G
Pat_41	Post-Resistance	KIAA1383	54627	37	1	232942168	232942168	Missense_Mutation	SNP	C	T	12	133	c.1399C>T	c.(1399-1401)CCT>TCT	p.P467S
Pat_41	Post-Resistance	KIAA1383	54627	37	1	232942258	232942258	Missense_Mutation	SNP	C	T	15	60	c.1489C>T	c.(1489-1491)CCA>TCA	p.P497S
Pat_41	Post-Resistance	PCNXL2	80003	37	1	233122245	233122245	Missense_Mutation	SNP	C	T	3	18	c.5833G>A	c.(5833-5835)GCG>ACG	p.A1945T
Pat_41	Post-Resistance	PCNXL2	80003	37	1	233136119	233136119	Missense_Mutation	SNP	C	T	8	304	c.5260G>A	c.(5260-5262)GAC>AAC	p.D1754N
Pat_41	Post-Resistance	KIAA1804	84451	37	1	233507862	233507862	Missense_Mutation	SNP	C	T	28	163	c.1631C>T	c.(1630-1632)CCC>CTC	p.P544L
Pat_41	Post-Resistance	KCNK1	3775	37	1	233750260	233750260	Missense_Mutation	SNP	C	T	5	40	c.343C>T	c.(343-345)CTC>TTC	p.L115F
Pat_41	Post-Resistance	IRF2BP2	359948	37	1	234743275	234743275	Missense_Mutation	SNP	G	A	32	522	c.1372C>T	c.(1372-1374)CCG>TCG	p.P458S
Pat_41	Post-Resistance	ARID4B	51742	37	1	235345619	235345619	Missense_Mutation	SNP	T	C	33	71	c.2615A>G	c.(2614-2616)AAG>AGG	p.K872R
Pat_41	Post-Resistance	ARID4B	51742	37	1	235386549	235386549	Missense_Mutation	SNP	G	A	13	130	c.997C>T	c.(997-999)CTT>TTT	p.L333F

Pat_41	Post-Resistance	LYST	1130	37	1	235866153	235866153	Missense_Mutation	SNP	G	A	31	470	c.10268C>T	c.(10267-10269)CCT>CTT	p.P3423L
Pat_41	Post-Resistance	LYST	1130	37	1	235872510	235872510	Missense_Mutation	SNP	G	A	16	180	c.10024C>T	c.(10024-10026)CGG>TGC	p.R3342W
Pat_41	Post-Resistance	LYST	1130	37	1	235904850	235904850	Missense_Mutation	SNP	G	A	13	115	c.8230C>T	c.(8230-8232)CTT>TTT	p.L2744F
Pat_41	Post-Resistance	LYST	1130	37	1	235922474	235922474	Missense_Mutation	SNP	G	A	5	125	c.6679C>T	c.(6679-6681)CCT>TCT	p.P2227S
Pat_41	Post-Resistance	LYST	1130	37	1	235929378	235929378	Splice_Site	SNP	C	T	15	336	c.6121_splice	c.e21+1	p.D2041_splice
Pat_41	Post-Resistance	LYST	1130	37	1	235969930	235969930	Missense_Mutation	SNP	C	T	40	606	c.2506G>A	c.(2506-2508)GTT>ATT	p.V836I
Pat_41	Post-Resistance	EDARADD	128178	37	1	236645720	236645720	Missense_Mutation	SNP	G	A	10	212	c.419G>A	c.(418-420)AGG>AAG	p.R140K
Pat_41	Post-Resistance	RYR2	6262	37	1	237777469	237777469	Missense_Mutation	SNP	G	A	4	108	c.5041G>A	c.(5041-5043)GAT>AAT	p.D1681N
Pat_41	Post-Resistance	RYR2	6262	37	1	237780746	237780746	Missense_Mutation	SNP	C	T	30	220	c.5876C>T	c.(5875-5877)GCC>GTC	p.A1959V
Pat_41	Post-Resistance	ZP4	57829	37	1	238048125	238048125	Missense_Mutation	SNP	G	A	27	140	c.1334C>T	c.(1333-1335)TCA>TTA	p.S445L
Pat_41	Post-Resistance	FMN2	56776	37	1	240371090	240371090	Missense_Mutation	SNP	C	T	12	259	c.2978C>T	c.(2977-2979)CCC>CTC	p.P993L
Pat_41	Post-Resistance	FMN2	56776	37	1	240421333	240421333	Splice_Site	SNP	G	A	5	85	c.4153_splice	c.e7+1	p.A1385_splice
Pat_41	Post-Resistance	FH	2271	37	1	241680504	241680504	Missense_Mutation	SNP	C	T	22	364	c.245G>A	c.(244-246)GGA>GAA	p.G82E
Pat_41	Post-Resistance	MAP1LC3C	440738	37	1	242161877	242161877	Missense_Mutation	SNP	C	T	29	129	c.160G>A	c.(160-162)GAC>AAC	p.D54N
Pat_41	Post-Resistance	CEP170	9859	37	1	243327952	243327952	Missense_Mutation	SNP	G	A	14	120	c.3310C>T	c.(3310-3312)CGC>TGC	p.R1104C
Pat_41	Post-Resistance	C1orf101	257044	37	1	244640891	244640891	Missense_Mutation	SNP	G	A	30	491	c.163G>A	c.(163-165)GAA>AAA	p.E55K
Pat_41	Post-Resistance	C1orf101	257044	37	1	244756696	244756696	Splice_Site	SNP	G	A	8	172	c.2190_splice	c.e16-1	p.K730_splice
Pat_41	Post-Resistance	HNRNPU	3192	37	1	245023714	245023714	Missense_Mutation	SNP	C	T	19	128	c.940G>A	c.(940-942)GAG>AAG	p.E314K
Pat_41	Post-Resistance	KIF26B	55083	37	1	245766051	245766051	Missense_Mutation	SNP	C	T	5	234	c.1523C>T	c.(1522-1524)GCC>GTC	p.A508V
Pat_41	Post-Resistance	KIF26B	55083	37	1	245862193	245862193	Missense_Mutation	SNP	C	T	6	77	c.6032C>T	c.(6031-6033)GCC>GTC	p.A2011V
Pat_41	Post-Resistance	SMYD3	64754	37	1	246021912	246021912	Missense_Mutation	SNP	G	A	22	186	c.962C>T	c.(961-963)CCC>CTC	p.P321L
Pat_41	Post-Resistance	TFB2M	64216	37	1	246729173	246729173	Missense_Mutation	SNP	C	T	20	213	c.268G>A	c.(268-270)GGA>AGA	p.G90R
Pat_41	Post-Resistance	AHCTF1	25909	37	1	247013349	247013349	Missense_Mutation	SNP	C	T	10	81	c.5959G>A	c.(5959-5961)GGA>AGA	p.G1987R
Pat_41	Post-Resistance	OR13G1	441933	37	1	247835739	247835739	Missense_Mutation	SNP	G	A	8	121	c.605C>T	c.(604-606)ACC>ATC	p.T202I
Pat_41	Post-Resistance	OR6F1	343169	37	1	247875184	247875184	Missense_Mutation	SNP	G	A	7	162	c.874C>T	c.(874-876)CTT>TTT	p.L292F
Pat_41	Post-Resistance	OR2M5	127059	37	1	248308496	248308496	Missense_Mutation	SNP	G	A	17	417	c.47G>A	c.(46-48)GGA>GAA	p.G16E
Pat_41	Post-Resistance	OR2M4	26245	37	1	248402768	248402768	Missense_Mutation	SNP	G	A	15	314	c.538G>A	c.(538-540)GAT>AAT	p.D180N
Pat_41	Post-Resistance	OR2M4	26245	37	1	248402786	248402786	Missense_Mutation	SNP	C	T	15	320	c.556C>T	c.(556-558)CCT>TCT	p.P186S
Pat_41	Post-Resistance	OR2T4	127074	37	1	248524908	248524908	Missense_Mutation	SNP	G	A	6	163	c.26G>A	c.(25-27)AGC>AAC	p.S9N
Pat_41	Post-Resistance	OR2T3	343173	37	1	248636994	248636994	Missense_Mutation	SNP	G	A	4	98	c.343G>A	c.(343-345)GCT>ACT	p.A115T
Pat_41	Post-Resistance	OR2G6	391211	37	1	248685462	248685462	Missense_Mutation	SNP	G	A	13	118	c.515G>A	c.(514-516)CGC>CAC	p.R172H
Pat_41	Post-Resistance	DIP2C	22982	37	10	410400	410400	Missense_Mutation	SNP	C	T	17	108	c.2391G>A	c.(2389-2391)ATG>ATA	p.M797I
Pat_41	Post-Resistance	KLF6	1316	37	10	3827122	3827122	Missense_Mutation	SNP	C	T	8	49	c.85G>A	c.(85-87)GAG>AAG	p.E29K
Pat_41	Post-Resistance	UCN3	114131	37	10	5415733	5415733	Missense_Mutation	SNP	G	A	20	66	c.50G>A	c.(49-51)GGC>GAC	p.G17D
Pat_41	Post-Resistance	NET1	10276	37	10	5495479	5495479	Missense_Mutation	SNP	C	T	40	231	c.724C>T	c.(724-726)CCT>TCT	p.P242S
Pat_41	Post-Resistance	C10orf18	54906	37	10	5803267	5803267	Missense_Mutation	SNP	C	T	14	137	c.7007C>T	c.(7006-7008)GCA>GTA	p.A2336V
Pat_41	Post-Resistance	USP6NL	9712	37	10	11505396	11505396	Missense_Mutation	SNP	C	T	27	136	c.1531G>A	c.(1531-1533)GCG>ACG	p.A511T
Pat_41	Post-Resistance	USP6NL	9712	37	10	11505675	11505675	Missense_Mutation	SNP	G	A	4	26	c.1252C>T	c.(1252-1254)CCC>TCC	p.P418S
Pat_41	Post-Resistance	UPF2	26019	37	10	12071162	12071162	Missense_Mutation	SNP	C	T	9	88	c.727G>A	c.(727-729)GTC>ATC	p.V243I
Pat_41	Post-Resistance	CDC123	8872	37	10	12292309	12292309	Splice_Site	SNP	G	A	9	70	c.985_splice	c.e13-1	p.K329_splice
Pat_41	Post-Resistance	FAM107B	83641	37	10	14563275	14563275	Missense_Mutation	SNP	C	T	26	55	c.310G>A	c.(310-312)GAG>AAG	p.E104K
Pat_41	Post-Resistance	SUV39H2	79723	37	10	14944497	14944497	Missense_Mutation	SNP	G	A	12	45	c.1039G>A	c.(1039-1041)GGT>AGT	p.G347S
Pat_41	Post-Resistance	DCLRE1C	64421	37	10	14976425	14976425	Missense_Mutation	SNP	C	T	46	322	c.632G>A	c.(631-633)GGC>GAC	p.G211D
Pat_41	Post-Resistance	RSU1	6251	37	10	16737067	16737067	Missense_Mutation	SNP	C	A	4	136	c.686G>T	c.(685-687)GGC>GTC	p.G229V
Pat_41	Post-Resistance	CUBN	8029	37	10	16975248	16975248	Missense_Mutation	SNP	G	A	18	47	c.5962C>T	c.(5962-5964)CCC>TCC	p.P1988S
Pat_41	Post-Resistance	CUBN	8029	37	10	17146516	17146516	Missense_Mutation	SNP	G	A	13	68	c.1319C>T	c.(1318-1320)CCC>CTC	p.P440L
Pat_41	Post-Resistance	TRDMT1	1787	37	10	17210858	17210858	Missense_Mutation	SNP	G	A	19	64	c.233C>T	c.(232-234)CCC>CTC	p.P78L

Pat_41	Post-Resistance	VIM	7431	37	10	17271902	17271902	Missense_Mutation	SNP	G	A	8	31	c.481G>A	c.(481-483)GTG>ATG	p.V161M
Pat_41	Post-Resistance	SLC39A12	221074	37	10	18280107	18280107	Missense_Mutation	SNP	C	T	4	39	c.1297C>T	c.(1297-1299)CCA>TCA	p.P433S
Pat_41	Post-Resistance	CACNB2	783	37	10	18690890	18690890	Missense_Mutation	SNP	C	T	13	50	c.251C>T	c.(250-252)TCC>TTC	p.S84F
Pat_41	Post-Resistance	NEBL	10529	37	10	21117503	21117503	Missense_Mutation	SNP	G	A	14	48	c.1732C>T	c.(1732-1734)CCT>TCT	p.P578S
Pat_41	Post-Resistance	ARMC3	219681	37	10	23321789	23321789	Splice_Site	SNP	G	A	11	42	c.2247_splice	c.e18-1	p.K749_splice
Pat_41	Post-Resistance	KIAA1217	56243	37	10	24762385	24762385	Missense_Mutation	SNP	C	T	10	91	c.1075C>T	c.(1075-1077)CCC>TCC	p.P359S
Pat_41	Post-Resistance	GPR158	57512	37	10	25464869	25464869	Missense_Mutation	SNP	G	A	8	29	c.520G>A	c.(520-522)GCG>ACG	p.A174T
Pat_41	Post-Resistance	MYO3A	53904	37	10	26446321	26446321	Missense_Mutation	SNP	A	G	12	114	c.2876A>G	c.(2875-2877)CAG>CGG	p.Q959R
Pat_41	Post-Resistance	ANKRD26	22852	37	10	27301983	27301983	Missense_Mutation	SNP	C	T	9	65	c.4778G>A	c.(4777-4779)AGC>AAC	p.S1593N
Pat_41	Post-Resistance	ANKRD26	22852	37	10	27389230	27389230	Missense_Mutation	SNP	C	T	4	7	c.26G>A	c.(25-27)GGC>GAC	p.G9D
Pat_41	Post-Resistance	YME1L1	10730	37	10	27400938	27400938	Missense_Mutation	SNP	C	T	17	155	c.2290G>A	c.(2290-2292)GTT>ATT	p.V764I
Pat_41	Post-Resistance	LOC387646	387646	37	10	27539046	27539046	Missense_Mutation	SNP	G	A	3	47	c.347C>T	c.(346-348)CCT>CTT	p.P116L
Pat_41	Post-Resistance	PTCHD3	374308	37	10	27703106	27703106	Missense_Mutation	SNP	G	A	31	141	c.74C>T	c.(73-75)ACC>ATC	p.T25I
Pat_41	Post-Resistance	LYZL1	84569	37	10	29599945	29599945	Missense_Mutation	SNP	G	A	16	234	c.542G>A	c.(541-543)GGC>GAC	p.G181D
Pat_41	Post-Resistance	MTPAP	55149	37	10	30611359	30611359	Missense_Mutation	SNP	G	A	9	89	c.1180C>T	c.(1180-1182)CCT>TCT	p.P394S
Pat_41	Post-Resistance	LYZL2	119180	37	10	30915129	30915129	Missense_Mutation	SNP	C	T	6	75	c.341G>A	c.(340-342)GGC>GAC	p.G114D
Pat_41	Post-Resistance	ARHGAP12	94134	37	10	32132425	32132425	Nonsense_Mutation	SNP	C	T	16	108	c.1260G>A	c.(1258-1260)TGG>TGA	p.W420*
Pat_41	Post-Resistance	KIF5B	3799	37	10	32310198	32310198	Missense_Mutation	SNP	C	T	7	67	c.2050G>A	c.(2050-2052)GAA>AAA	p.E684K
Pat_41	Post-Resistance	EPC1	80314	37	10	32560834	32560834	Missense_Mutation	SNP	C	T	5	20	c.2086G>A	c.(2086-2088)GGC>AGC	p.G696S
Pat_41	Post-Resistance	PARD3	56288	37	10	34400110	34400110	Missense_Mutation	SNP	G	A	9	53	c.4058C>T	c.(4057-4059)CCC>CTC	p.P1353L
Pat_41	Post-Resistance	ANKRD30A	91074	37	10	37430948	37430948	Missense_Mutation	SNP	C	G	7	83	c.955C>G	c.(955-957)CCA>GCA	p.P319A
Pat_41	Post-Resistance	ANKRD30A	91074	37	10	37508134	37508134	Missense_Mutation	SNP	G	A	8	188	c.3326G>A	c.(3325-3327)AGT>AAT	p.S1109N
Pat_41	Post-Resistance	ZNF33A	7581	37	10	38344166	38344166	Missense_Mutation	SNP	C	T	17	62	c.1111C>T	c.(1111-1113)CTC>TTC	p.L371F
Pat_41	Post-Resistance	ZNF33B	7582	37	10	43089722	43089722	Missense_Mutation	SNP	C	T	36	121	c.676G>A	c.(676-678)GAA>AAA	p.E226K
Pat_41	Post-Resistance	RASGEF1A	221002	37	10	43694401	43694401	Missense_Mutation	SNP	C	T	10	79	c.1012G>A	c.(1012-1014)GCC>ACC	p.A338T
Pat_41	Post-Resistance	ZNF239	8187	37	10	44052878	44052878	Missense_Mutation	SNP	C	T	13	44	c.650G>A	c.(649-651)AGT>AAT	p.S217N
Pat_41	Post-Resistance	GDF2	2658	37	10	48413825	48413825	Missense_Mutation	SNP	G	A	5	57	c.1043C>T	c.(1042-1044)CCC>CTC	p.P348L
Pat_41	Post-Resistance	ARHGAP22	58504	37	10	49667836	49667836	Missense_Mutation	SNP	G	A	4	95	c.550C>T	c.(550-552)CGG>TGG	p.R184W
Pat_41	Post-Resistance	C10orf71	118461	37	10	50531089	50531089	Missense_Mutation	SNP	C	T	5	17	c.499C>T	c.(499-501)CCT>TCT	p.P167S
Pat_41	Post-Resistance	A1CF	29974	37	10	52603882	52603882	Missense_Mutation	SNP	C	T	47	7	c.100G>A	c.(100-102)GAA>AAA	p.E34K
Pat_41	Post-Resistance	DKK1	22943	37	10	54074202	54074202	Missense_Mutation	SNP	C	T	29	68	c.8C>T	c.(7-9)GCT>GTT	p.A3V
Pat_41	Post-Resistance	PCDH15	65217	37	10	55626560	55626560	Missense_Mutation	SNP	G	A	6	95	c.3559C>T	c.(3559-3561)CCA>TCA	p.P1187S
Pat_41	Post-Resistance	ZWINT	11130	37	10	58118627	58118627	Missense_Mutation	SNP	C	T	16	106	c.562G>A	c.(562-564)GTG>ATG	p.V188M
Pat_41	Post-Resistance	BICC1	80114	37	10	60556281	60556281	Missense_Mutation	SNP	G	A	13	16	c.1361G>A	c.(1360-1362)GGA>GAA	p.G454E
Pat_41	Post-Resistance	ANK3	288	37	10	61836191	61836191	Missense_Mutation	SNP	C	T	7	44	c.4448G>A	c.(4447-4449)GGA>GAA	p.G1483E
Pat_41	Post-Resistance	ANK3	288	37	10	61965594	61965594	Missense_Mutation	SNP	C	T	10	91	c.1249G>A	c.(1249-1251)GAA>AAA	p.E417K
Pat_41	Post-Resistance	ARID5B	84159	37	10	63810682	63810682	Missense_Mutation	SNP	C	T	18	205	c.769C>T	c.(769-771)CCA>TCA	p.P257S
Pat_41	Post-Resistance	ADO	84890	37	10	64565459	64565459	Missense_Mutation	SNP	C	T	6	21	c.640C>T	c.(640-642)CCG>TCG	p.P214S
Pat_41	Post-Resistance	EGR2	1959	37	10	64575632	64575632	Missense_Mutation	SNP	C	T	6	16	c.158G>A	c.(157-159)GGA>GAA	p.G53E
Pat_41	Post-Resistance	CTNNA3	29119	37	10	69299332	69299332	Missense_Mutation	SNP	C	T	11	75	c.388G>A	c.(388-390)GCT>ACT	p.A130T
Pat_41	Post-Resistance	DNAJC12	56521	37	10	69583081	69583081	Missense_Mutation	SNP	G	A	4	69	c.148C>T	c.(148-150)CCC>TCC	p.P50S
Pat_41	Post-Resistance	MYPN	84665	37	10	69934232	69934232	Missense_Mutation	SNP	C	T	4	59	c.2383C>T	c.(2383-2385)CCA>TCA	p.P795S
Pat_41	Post-Resistance	DNA2	1763	37	10	70178897	70178897	Missense_Mutation	SNP	A	G	7	51	c.3119T>C	c.(3118-3120)TTG>TCG	p.L1040S
Pat_41	Post-Resistance	DDX50	79009	37	10	70706156	70706156	Missense_Mutation	SNP	C	T	12	108	c.1984C>T	c.(1984-1986)CCT>TCT	p.P662S
Pat_41	Post-Resistance	HKDC1	80201	37	10	70992797	70992797	Missense_Mutation	SNP	G	A	7	37	c.403G>A	c.(403-405)GCA>ACA	p.A135T
Pat_41	Post-Resistance	HKDC1	80201	37	10	71008289	71008289	Missense_Mutation	SNP	G	A	3	19	c.1375G>A	c.(1375-1377)GTG>ATG	p.V459M
Pat_41	Post-Resistance	HK1	3098	37	10	71139668	71139668	Missense_Mutation	SNP	T	C	11	147	c.1082T>C	c.(1081-1083)GTG>GCG	p.V361A

Pat_41	Post-Resistance	HK1	3098	37	10	71151947	71151947	Missense_Mutation	SNP	G	A	19	117	c.2102G>A	c.(2101-2103)GGG>GAG	p.G701E
Pat_41	Post-Resistance	COL13A1	1305	37	10	71677064	71677064	Missense_Mutation	SNP	G	A	3	26	c.971G>A	c.(970-972)GGG>GAG	p.G324E
Pat_41	Post-Resistance	NODAL	4838	37	10	72192822	72192822	Missense_Mutation	SNP	G	A	7	150	c.914C>T	c.(913-915)CCC>CTC	p.P305L
Pat_41	Post-Resistance	DNAJB12	54788	37	10	74104768	74104768	Missense_Mutation	SNP	C	T	42	303	c.353G>A	c.(352-354)GGT>GAT	p.G118D
Pat_41	Post-Resistance	NUDT13	25961	37	10	74884888	74884888	Missense_Mutation	SNP	C	T	14	99	c.478C>T	c.(478-480)CTC>TTC	p.L160F
Pat_41	Post-Resistance	USP54	159195	37	10	75276288	75276288	Missense_Mutation	SNP	C	T	9	105	c.3896G>A	c.(3895-3897)AGA>AAA	p.R1299K
Pat_41	Post-Resistance	MYOZ1	58529	37	10	75393725	75393725	Missense_Mutation	SNP	C	T	24	57	c.601G>A	c.(601-603)GAA>AAA	p.E201K
Pat_41	Post-Resistance	MYOZ1	58529	37	10	75394274	75394274	Missense_Mutation	SNP	G	A	14	99	c.470C>T	c.(469-471)GCT>GTT	p.A157V
Pat_41	Post-Resistance	PLAU	5328	37	10	75674575	75674575	Missense_Mutation	SNP	C	T	9	47	c.871C>T	c.(871-873)CCA>TCA	p.P291S
Pat_41	Post-Resistance	AP3M1	26985	37	10	75889711	75889711	Missense_Mutation	SNP	G	A	17	47	c.623C>T	c.(622-624)GCT>GTT	p.A208V
Pat_41	Post-Resistance	MYST4	23522	37	10	76603178	76603178	Missense_Mutation	SNP	C	T	18	64	c.563C>T	c.(562-564)CCC>CTC	p.P188L
Pat_41	Post-Resistance	DUSP13	51207	37	10	76868815	76868815	Missense_Mutation	SNP	G	A	6	58	c.101C>T	c.(100-102)TCT>TTT	p.S34F
Pat_41	Post-Resistance	VDAC2	7417	37	10	76978928	76978928	Nonsense_Mutation	SNP	G	A	7	111	c.258G>A	c.(256-258)TGG>TGA	p.W86*
Pat_41	Post-Resistance	POLR3A	11128	37	10	79753058	79753058	Missense_Mutation	SNP	C	T	8	68	c.2684G>A	c.(2683-2685)GGC>GAC	p.G895D
Pat_41	Post-Resistance	NRG3	10718	37	10	84733566	84733566	Missense_Mutation	SNP	C	T	17	144	c.1307C>T	c.(1306-1308)CCT>CTT	p.P436L
Pat_41	Post-Resistance	OPN4	94233	37	10	88415939	88415939	Missense_Mutation	SNP	G	A	5	53	c.172G>A	c.(172-174)GTC>ATC	p.V58I
Pat_41	Post-Resistance	LIPF	8513	37	10	90429695	90429695	Missense_Mutation	SNP	C	T	35	353	c.524C>T	c.(523-525)ACC>ATC	p.T175I
Pat_41	Post-Resistance	STAMBPL1	57559	37	10	90674416	90674416	Splice_Site	SNP	G	A	19	20	c.903_splice	c.e7+1	p.L301_splice
Pat_41	Post-Resistance	ANKRD1	27063	37	10	92672669	92672669	Missense_Mutation	SNP	C	T	44	300	c.914G>A	c.(913-915)AGC>AAC	p.S305N
Pat_41	Post-Resistance	BTAF1	9044	37	10	93713506	93713506	Missense_Mutation	SNP	G	A	22	147	c.577G>A	c.(577-579)GCT>ACT	p.A193T
Pat_41	Post-Resistance	BTAF1	9044	37	10	93773718	93773718	Missense_Mutation	SNP	G	A	8	129	c.4516G>A	c.(4516-4518)GAA>AAA	p.E1506K
Pat_41	Post-Resistance	PIPSL	266971	37	10	95719353	95719353	Missense_Mutation	SNP	G	A	3	7	c.1801C>T	c.(1801-1803)CCG>TCG	p.P601S
Pat_41	Post-Resistance	SORBS1	10580	37	10	97158873	97158873	Missense_Mutation	SNP	C	A	8	65	c.1059G>T	c.(1057-1059)AAG>AAT	p.K353N
Pat_41	Post-Resistance	TM9SF3	56889	37	10	98321767	98321767	Missense_Mutation	SNP	C	T	12	118	c.550G>A	c.(550-552)GTT>ATT	p.V184I
Pat_41	Post-Resistance	SLIT1	6585	37	10	98802757	98802757	Missense_Mutation	SNP	G	A	6	41	c.2065C>T	c.(2065-2067)CGC>TGC	p.R689C
Pat_41	Post-Resistance	SLIT1	6585	37	10	98807477	98807477	Missense_Mutation	SNP	G	A	9	102	c.1604C>T	c.(1603-1605)CCT>CTT	p.P535L
Pat_41	Post-Resistance	ZDHHC16	84287	37	10	99216604	99216604	Missense_Mutation	SNP	C	T	12	42	c.1090C>T	c.(1090-1092)CCT>TCT	p.P364S
Pat_41	Post-Resistance	CRTAC1	55118	37	10	99655716	99655716	Missense_Mutation	SNP	C	T	42	84	c.1243G>A	c.(1243-1245)GAC>AAC	p.D415N
Pat_41	Post-Resistance	CWF19L1	55280	37	10	102006574	102006574	Missense_Mutation	SNP	C	T	18	41	c.827G>A	c.(826-828)GGA>GAA	p.G276E
Pat_41	Post-Resistance	BLOC1S2	282991	37	10	102045956	102045956	Missense_Mutation	SNP	C	T	8	53	c.70G>A	c.(70-72)GAG>AAG	p.E24K
Pat_41	Post-Resistance	SCD	6319	37	10	102107962	102107962	Missense_Mutation	SNP	C	T	9	72	c.169C>T	c.(169-171)CCC>TCC	p.P57S
Pat_41	Post-Resistance	WNT8B	7479	37	10	102241690	102241690	Missense_Mutation	SNP	G	A	10	50	c.389G>A	c.(388-390)GGA>GAA	p.G130E
Pat_41	Post-Resistance	NDUFB8	4714	37	10	102289560	102289560	Missense_Mutation	SNP	C	T	12	73	c.49G>A	c.(49-51)GCA>ACA	p.A17T
Pat_41	Post-Resistance	HIF1AN	55662	37	10	102300469	102300469	Nonsense_Mutation	SNP	G	A	9	79	c.507G>A	c.(505-507)TGG>TGA	p.W169*
Pat_41	Post-Resistance	PDZD7	79955	37	10	102778003	102778003	Missense_Mutation	SNP	C	T	3	69	c.1375G>A	c.(1375-1377)GGT>AGT	p.G459S
Pat_41	Post-Resistance	POLL	27343	37	10	103339574	103339574	Missense_Mutation	SNP	C	T	26	0	c.1364G>A	c.(1363-1365)GGG>GAG	p.G455E
Pat_41	Post-Resistance	MGEA5	10724	37	10	103546243	103546243	Missense_Mutation	SNP	G	A	28	92	c.2716C>T	c.(2716-2718)CCA>TCA	p.P906S
Pat_41	Post-Resistance	MGEA5	10724	37	10	103559090	103559090	Missense_Mutation	SNP	G	T	4	85	c.1318C>A	c.(1318-1320)CAG>AAG	p.Q440K
Pat_41	Post-Resistance	KCNIP2	30819	37	10	103588911	103588911	Missense_Mutation	SNP	G	A	12	107	c.269C>T	c.(268-270)CCT>CTT	p.P90L
Pat_41	Post-Resistance	HPS6	79803	37	10	103826571	103826571	Missense_Mutation	SNP	C	T	6	54	c.1340C>T	c.(1339-1341)CCC>CTC	p.P447L
Pat_41	Post-Resistance	PPRC1	23082	37	10	103907092	103907092	Missense_Mutation	SNP	C	T	7	75	c.4343C>T	c.(4342-4344)TCT>TTT	p.S1448F
Pat_41	Post-Resistance	ELOVL3	83401	37	10	103986333	103986333	Missense_Mutation	SNP	G	A	13	89	c.28G>A	c.(28-30)GAA>AAA	p.E10K
Pat_41	Post-Resistance	GBF1	8729	37	10	104111600	104111600	Missense_Mutation	SNP	G	A	8	54	c.415G>A	c.(415-417)GTT>ATT	p.V139I
Pat_41	Post-Resistance	GBF1	8729	37	10	104141903	104141903	Missense_Mutation	SNP	C	T	9	53	c.5390C>T	c.(5389-5391)CCC>CTC	p.P1797L
Pat_41	Post-Resistance	NFKB2	4791	37	10	104156537	104156537	Missense_Mutation	SNP	G	A	7	100	c.200G>A	c.(199-201)GGT>GAT	p.G67D
Pat_41	Post-Resistance	NFKB2	4791	37	10	104158595	104158595	Missense_Mutation	SNP	C	T	3	13	c.1091C>T	c.(1090-1092)GCC>GTC	p.A364V
Pat_41	Post-Resistance	PSD	5662	37	10	104176267	104176267	Missense_Mutation	SNP	G	A	4	20	c.529C>T	c.(529-531)CCG>TCG	p.P177S

Pat_41	Post-Resistance	NT5C2	22978	37	10	104852961	104852961	Missense_Mutation	SNP	C	T	4	132	c.1094G>A	c.(1093-1095)GGG>GAG	p.G365E
Pat_41	Post-Resistance	SORCS3	22986	37	10	106976824	106976824	Missense_Mutation	SNP	C	T	30	106	c.2678C>T	c.(2677-2679)GCC>GTC	p.A893V
Pat_41	Post-Resistance	SORCS1	114815	37	10	108923950	108923950	Missense_Mutation	SNP	C	T	3	40	c.335G>A	c.(334-336)GGA>GAA	p.G112E
Pat_41	Post-Resistance	ADD3	120	37	10	111876017	111876017	Missense_Mutation	SNP	G	A	11	117	c.335G>A	c.(334-336)AGT>AAT	p.S112N
Pat_41	Post-Resistance	SMC3	9126	37	10	112350822	112350822	Missense_Mutation	SNP	C	T	33	74	c.1744C>T	c.(1744-1746)CCT>TCT	p.P582S
Pat_41	Post-Resistance	PDCD4	27250	37	10	112641189	112641189	Missense_Mutation	SNP	G	A	11	156	c.242G>A	c.(241-243)GGG>GAG	p.G81E
Pat_41	Post-Resistance	ACSL5	51703	37	10	114168182	114168182	Nonsense_Mutation	SNP	G	A	48	130	c.435G>A	c.(433-435)TGG>TGA	p.W145*
Pat_41	Post-Resistance	ABLIM1	3983	37	10	116196119	116196119	Missense_Mutation	SNP	G	A	5	76	c.2237C>T	c.(2236-2238)CCT>CTT	p.P746L
Pat_41	Post-Resistance	C10orf84	63877	37	10	120095065	120095065	Splice_Site	SNP	C	T	16	42	c.322_splice	c.e4+1	p.D108_splice
Pat_41	Post-Resistance	FAM45A	404636	37	10	120867497	120867497	Missense_Mutation	SNP	G	A	18	132	c.73G>A	c.(73-75)GAA>AAA	p.E25K
Pat_41	Post-Resistance	SFXN4	119559	37	10	120917556	120917556	Missense_Mutation	SNP	G	A	12	123	c.379C>T	c.(379-381)CCA>TCA	p.P127S
Pat_41	Post-Resistance	GRK5	2869	37	10	121207758	121207758	Missense_Mutation	SNP	C	T	28	87	c.1390C>T	c.(1390-1392)CCC>TCC	p.P464S
Pat_41	Post-Resistance	INPP5F	22876	37	10	121586205	121586205	Missense_Mutation	SNP	C	T	17	105	c.2312C>T	c.(2311-2313)GCC>GTC	p.A771V
Pat_41	Post-Resistance	DMBT1	1755	37	10	124351902	124351902	Missense_Mutation	SNP	C	T	80	172	c.2291C>T	c.(2290-2292)ACC>ATC	p.T764I
Pat_41	Post-Resistance	DMBT1	1755	37	10	124351968	124351968	Missense_Mutation	SNP	C	T	22	147	c.2357C>T	c.(2356-2358)GCC>GTC	p.A786V
Pat_41	Post-Resistance	CUZD1	50624	37	10	124596466	124596466	Missense_Mutation	SNP	G	A	113	37	c.698C>T	c.(697-699)ACT>ATT	p.T233I
Pat_41	Post-Resistance	LHPP	64077	37	10	126172851	126172851	Missense_Mutation	SNP	T	C	6	88	c.269T>C	c.(268-270)ATC>ACC	p.I90T
Pat_41	Post-Resistance	DHX32	55760	37	10	127525392	127525392	Missense_Mutation	SNP	C	T	15	92	c.2096G>A	c.(2095-2097)AGT>AAT	p.S699N
Pat_41	Post-Resistance	DHX32	55760	37	10	127529566	127529566	Splice_Site	SNP	C	T	8	17	c.1544_splice	c.e8-1	p.A515_splice
Pat_41	Post-Resistance	ADAM12	8038	37	10	127843809	127843809	Missense_Mutation	SNP	G	A	38	349	c.326C>T	c.(325-327)GCT>GTT	p.A109V
Pat_41	Post-Resistance	DOCK1	1793	37	10	129172401	129172401	Missense_Mutation	SNP	G	A	5	24	c.3535G>A	c.(3535-3537)GAA>AAA	p.E1179K
Pat_41	Post-Resistance	DOCK1	1793	37	10	129224261	129224261	Missense_Mutation	SNP	G	A	28	211	c.4837G>A	c.(4837-4839)GGC>AGC	p.G1613S
Pat_41	Post-Resistance	MKI67	4288	37	10	129913827	129913827	Missense_Mutation	SNP	C	T	8	67	c.845G>A	c.(844-846)GGG>GAG	p.G282E
Pat_41	Post-Resistance	STK32C	282974	37	10	134145201	134145201	Missense_Mutation	SNP	C	T	11	63	c.40G>A	c.(40-42)GGC>AGC	p.G14S
Pat_41	Post-Resistance	FRG2B	441581	37	10	135440209	135440209	Missense_Mutation	SNP	G	A	15	401	c.38C>T	c.(37-39)TCC>TTC	p.S13F
Pat_41	Post-Resistance	SCGB1C1	147199	37	11	193798	193798	Missense_Mutation	SNP	G	A	4	49	c.142G>A	c.(142-144)GGG>AGG	p.G48R
Pat_41	Post-Resistance	B4GALNT4	338707	37	11	375477	375477	Missense_Mutation	SNP	C	T	58	312	c.800C>T	c.(799-801)CCC>CTC	p.P267L
Pat_41	Post-Resistance	RNH1	6050	37	11	499857	499857	Missense_Mutation	SNP	C	T	4	96	c.415G>A	c.(415-417)GAC>AAC	p.D139N
Pat_41	Post-Resistance	RNH1	6050	37	11	500626	500626	Missense_Mutation	SNP	G	A	40	69	c.130C>T	c.(130-132)CGG>TGG	p.R44W
Pat_41	Post-Resistance	PHRF1	57661	37	11	597524	597524	Missense_Mutation	SNP	G	A	10	60	c.848G>A	c.(847-849)AGA>AAA	p.R283K
Pat_41	Post-Resistance	PHRF1	57661	37	11	607705	607705	Missense_Mutation	SNP	C	T	3	6	c.2249C>T	c.(2248-2250)CCC>CTC	p.P750L
Pat_41	Post-Resistance	CDHR5	53841	37	11	618767	618767	Missense_Mutation	SNP	C	T	5	199	c.1792G>A	c.(1792-1794)GGT>AGT	p.G598S
Pat_41	Post-Resistance	DRD4	1815	37	11	640481	640481	Missense_Mutation	SNP	C	T	12	115	c.1138C>T	c.(1138-1140)CGG>TGG	p.R380W
Pat_41	Post-Resistance	TALDO1	6888	37	11	763505	763505	Missense_Mutation	SNP	C	A	13	150	c.623C>A	c.(622-624)CCC>CAC	p.P208H
Pat_41	Post-Resistance	EFCAB4A	283229	37	11	831296	831296	Splice_Site	SNP	G	A	6	77	c.1025_splice	c.e8+1	p.R342_splice
Pat_41	Post-Resistance	TSPAN4	7106	37	11	862698	862698	Missense_Mutation	SNP	G	A	6	56	c.212G>A	c.(211-213)GGC>GAC	p.G71D
Pat_41	Post-Resistance	MUC6	4588	37	11	1017910	1017910	Missense_Mutation	SNP	C	T	16	475	c.4891G>A	c.(4891-4893)GTC>ATC	p.V1631I
Pat_41	Post-Resistance	MUC6	4588	37	11	1019409	1019409	Missense_Mutation	SNP	G	A	21	195	c.3896C>T	c.(3895-3897)CCC>CTC	p.P1299L
Pat_41	Post-Resistance	MUC5B	727897	37	11	1247931	1247931	Missense_Mutation	SNP	C	T	4	53	c.2254C>T	c.(2254-2256)CCT>TCT	p.P752S
Pat_41	Post-Resistance	MUC5B	727897	37	11	1271468	1271468	Missense_Mutation	SNP	C	T	5	157	c.14777C>T	c.(14776-14778)CCG>CTG	p.P4926L
Pat_41	Post-Resistance	SYT8	90019	37	11	1857722	1857722	Missense_Mutation	SNP	G	A	3	7	c.626G>A	c.(625-627)GGG>GAG	p.G209E
Pat_41	Post-Resistance	LSP1	4046	37	11	1908085	1908085	Missense_Mutation	SNP	C	T	10	69	c.841C>T	c.(841-843)CCG>TCG	p.P281S
Pat_41	Post-Resistance	ZNF195	7748	37	11	3380555	3380555	Nonsense_Mutation	SNP	C	T	10	160	c.1683G>A	c.(1681-1683)TGG>TGA	p.W561*
Pat_41	Post-Resistance	CHRNA10	57053	37	11	3688647	3688647	Missense_Mutation	SNP	G	A	5	38	c.710C>T	c.(709-711)GCC>GTC	p.A237V
Pat_41	Post-Resistance	NUP98	4928	37	11	3714493	3714493	Missense_Mutation	SNP	C	T	15	261	c.4280G>A	c.(4279-4281)AGG>AAG	p.R1427K
Pat_41	Post-Resistance	NUP98	4928	37	11	3797200	3797200	Missense_Mutation	SNP	G	A	19	306	c.407C>T	c.(406-408)ACC>ATC	p.T136I
Pat_41	Post-Resistance	STIM1	6786	37	11	4104112	4104112	Missense_Mutation	SNP	G	A	9	65	c.1138G>A	c.(1138-1140)GCT>ACT	p.A380T

Pat_41	Post-Resistance	OR52I1	390037	37	11	4616149	4616149	Missense_Mutation	SNP	C	T	23	323	c.881C>T	c.(880-882)CCC>CTC	p.P294L
Pat_41	Post-Resistance	OR52I1	390037	37	11	4616208	4616208	Missense_Mutation	SNP	C	T	13	276	c.940C>T	c.(940-942)CAC>TAC	p.H314Y
Pat_41	Post-Resistance	MMP26	56547	37	11	5011001	5011001	Missense_Mutation	SNP	G	A	10	123	c.223G>A	c.(223-225)GCT>ACT	p.A75T
Pat_41	Post-Resistance	OR51V1	283111	37	11	5221782	5221782	Missense_Mutation	SNP	C	T	12	316	c.149G>A	c.(148-150)GGC>GAC	p.G50D
Pat_41	Post-Resistance	OR51Q1	390061	37	11	5443989	5443989	Missense_Mutation	SNP	A	G	6	213	c.559A>G	c.(559-561)ATC>GTC	p.I187V
Pat_41	Post-Resistance	UBQLN3	50613	37	11	5529393	5529393	Missense_Mutation	SNP	C	T	4	55	c.1396G>A	c.(1396-1398)GCA>ACA	p.A466T
Pat_41	Post-Resistance	OR52E4	390081	37	11	5905799	5905799	Missense_Mutation	SNP	G	A	80	107	c.277G>A	c.(277-279)GAG>AAG	p.E93K
Pat_41	Post-Resistance	OR56A4	120793	37	11	6023409	6023409	Missense_Mutation	SNP	G	A	14	45	c.970C>T	c.(970-972)CCT>TCT	p.P324S
Pat_41	Post-Resistance	DNHD1	144132	37	11	6592105	6592105	Missense_Mutation	SNP	G	A	6	170	c.13363G>A	c.(13363-13365)GAT>AAT	p.D4455N
Pat_41	Post-Resistance	ILK	3611	37	11	6629392	6629392	Missense_Mutation	SNP	C	T	18	262	c.206C>T	c.(205-207)ACC>ATC	p.T69I
Pat_41	Post-Resistance	DCHS1	8642	37	11	6643131	6643131	Missense_Mutation	SNP	G	A	4	39	c.9776C>T	c.(9775-9777)TCT>TTT	p.S3259F
Pat_41	Post-Resistance	DCHS1	8642	37	11	6643339	6643339	Missense_Mutation	SNP	C	T	5	91	c.9568G>A	c.(9568-9570)GCT>ACT	p.A3190T
Pat_41	Post-Resistance	OR10A5	144124	37	11	6867203	6867203	Missense_Mutation	SNP	G	A	4	86	c.290G>A	c.(289-291)GGC>GAC	p.G97D
Pat_41	Post-Resistance	OR2D3	120775	37	11	6943121	6943121	Missense_Mutation	SNP	G	A	29	149	c.889G>A	c.(889-891)GTG>ATG	p.V297M
Pat_41	Post-Resistance	NLRP14	338323	37	11	7065164	7065164	Missense_Mutation	SNP	C	T	8	184	c.1907C>T	c.(1906-1908)ACT>ATT	p.T636I
Pat_41	Post-Resistance	PPFIBP2	8495	37	11	7652158	7652158	Missense_Mutation	SNP	C	T	15	247	c.967C>T	c.(967-969)CCT>TCT	p.P323S
Pat_41	Post-Resistance	OR5P3	120066	37	11	7846759	7846759	Missense_Mutation	SNP	G	A	15	240	c.761C>T	c.(760-762)ACC>ATC	p.T254I
Pat_41	Post-Resistance	SCUBE2	57758	37	11	9042672	9042672	Missense_Mutation	SNP	C	T	16	219	c.2920G>A	c.(2920-2922)GAG>AAG	p.E974K
Pat_41	Post-Resistance	SCUBE2	57758	37	11	9055305	9055305	Missense_Mutation	SNP	C	T	4	120	c.1954G>A	c.(1954-1956)GAA>AAA	p.E652K
Pat_41	Post-Resistance	SWAP70	23075	37	11	9769469	9769469	Missense_Mutation	SNP	G	A	21	211	c.1420G>A	c.(1420-1422)GCC>ACC	p.A474T
Pat_41	Post-Resistance	SBF2	81846	37	11	10064425	10064425	Missense_Mutation	SNP	C	T	20	310	c.245G>A	c.(244-246)TGC>TAC	p.C82Y
Pat_41	Post-Resistance	AMPD3	272	37	11	10503679	10503679	Missense_Mutation	SNP	G	A	25	330	c.496G>A	c.(496-498)GCG>ACG	p.A166T
Pat_41	Post-Resistance	USP47	55031	37	11	11963920	11963920	Missense_Mutation	SNP	G	A	27	371	c.2412G>A	c.(2410-2412)ATG>ATA	p.M804I
Pat_41	Post-Resistance	DKK3	27122	37	11	11989941	11989941	Splice_Site	SNP	C	T	9	106	c.528_splice	c.e4+1	p.M176_splice
Pat_41	Post-Resistance	MICAL2	9645	37	11	12225923	12225923	Missense_Mutation	SNP	C	T	43	273	c.391C>T	c.(391-393)CCT>TCT	p.P131S
Pat_41	Post-Resistance	MICAL2	9645	37	11	12244255	12244255	Missense_Mutation	SNP	C	T	5	108	c.1414C>T	c.(1414-1416)CCA>TCA	p.P472S
Pat_41	Post-Resistance	MICAL2	9645	37	11	12277227	12277227	Missense_Mutation	SNP	C	T	9	105	c.2885C>T	c.(2884-2886)GCA>GTA	p.A962V
Pat_41	Post-Resistance	ARNTL	406	37	11	13395658	13395658	Missense_Mutation	SNP	G	A	21	151	c.1084G>A	c.(1084-1086)GCA>ACA	p.A362T
Pat_41	Post-Resistance	BTBD10	84280	37	11	13410679	13410679	Missense_Mutation	SNP	G	A	5	25	c.1127C>T	c.(1126-1128)ACC>ATC	p.T376I
Pat_41	Post-Resistance	PDE3B	5140	37	11	14825489	14825489	Splice_Site	SNP	G	A	11	67	c.1416_splice	c.e5-1	p.S472_splice
Pat_41	Post-Resistance	PIK3C2A	5286	37	11	17170266	17170266	Missense_Mutation	SNP	C	T	18	144	c.1396G>A	c.(1396-1398)GAT>AAT	p.D466N
Pat_41	Post-Resistance	ABCC8	6833	37	11	17428954	17428954	Missense_Mutation	SNP	G	A	5	176	c.2867C>T	c.(2866-2868)TCT>TTT	p.S956F
Pat_41	Post-Resistance	ABCC8	6833	37	11	17452463	17452463	Missense_Mutation	SNP	G	A	4	90	c.1715C>T	c.(1714-1716)TCG>TTG	p.S572L
Pat_41	Post-Resistance	USH1C	10083	37	11	17553037	17553037	Missense_Mutation	SNP	G	A	6	78	c.157C>T	c.(157-159)CCC>TCC	p.P53S
Pat_41	Post-Resistance	HPS5	11234	37	11	18309185	18309185	Missense_Mutation	SNP	G	A	5	151	c.2614C>T	c.(2614-2616)CCA>TCA	p.P872S
Pat_41	Post-Resistance	UEVLD	55293	37	11	18566169	18566169	Splice_Site	SNP	C	T	8	452	c.1060_splice	c.e9+1	p.V354_splice
Pat_41	Post-Resistance	TMEM86A	144110	37	11	18723324	18723324	Missense_Mutation	SNP	G	A	11	68	c.491G>A	c.(490-492)GGG>GAG	p.G164E
Pat_41	Post-Resistance	ZDHHC13	54503	37	11	19197497	19197497	Missense_Mutation	SNP	G	A	29	368	c.1859G>A	c.(1858-1860)CGC>CAC	p.R620H
Pat_41	Post-Resistance	NAV2	89797	37	11	19954803	19954803	Missense_Mutation	SNP	C	T	16	552	c.1082C>T	c.(1081-1083)ACC>ATC	p.T361I
Pat_41	Post-Resistance	NAV2	89797	37	11	20129210	20129210	Missense_Mutation	SNP	G	A	131	645	c.6851G>A	c.(6850-6852)GGC>GAC	p.G2284D
Pat_41	Post-Resistance	SLC6A5	9152	37	11	20648329	20648329	Missense_Mutation	SNP	G	A	11	181	c.1336G>A	c.(1336-1338)GCT>ACT	p.A446T
Pat_41	Post-Resistance	NELL1	4745	37	11	21135228	21135228	Missense_Mutation	SNP	G	A	33	343	c.1394G>A	c.(1393-1395)GGA>GAA	p.G465E
Pat_41	Post-Resistance	ANO5	203859	37	11	22249029	22249029	Missense_Mutation	SNP	C	T	26	225	c.545C>T	c.(544-546)CCC>CTC	p.P182L
Pat_41	Post-Resistance	SLC17A6	57084	37	11	22360113	22360113	Missense_Mutation	SNP	G	A	7	102	c.34G>A	c.(34-36)GGA>AGA	p.G12R
Pat_41	Post-Resistance	FANCF	2188	37	11	22646594	22646594	Missense_Mutation	SNP	G	A	14	195	c.763C>T	c.(763-765)CTC>TTC	p.L255F
Pat_41	Post-Resistance	LUZP2	338645	37	11	24759789	24759789	Missense_Mutation	SNP	G	A	5	57	c.274G>A	c.(274-276)GAG>AAG	p.E92K
Pat_41	Post-Resistance	LGR4	55366	37	11	27389985	27389985	Missense_Mutation	SNP	G	A	9	146	c.2285C>T	c.(2284-2286)CCT>CTT	p.P762L

Pat_41	Post-Resistance	KIF18A	81930	37	11	28080523	28080523	Missense_Mutation	SNP	G	A	78	428	c.1898C>T	c.(1897-1899)TCT>TTT	p.S633F
Pat_41	Post-Resistance	KIF18A	81930	37	11	28116299	28116299	Missense_Mutation	SNP	C	T	66	339	c.374G>A	c.(373-375)GGA>GAA	p.G125E
Pat_41	Post-Resistance	MPPED2	744	37	11	30516958	30516958	Missense_Mutation	SNP	C	T	16	184	c.421G>A	c.(421-423)GTG>ATG	p.V141M
Pat_41	Post-Resistance	IMMP1L	196294	37	11	31484777	31484777	Missense_Mutation	SNP	G	A	17	211	c.47C>T	c.(46-48)ACT>ATT	p.T16I
Pat_41	Post-Resistance	QSER1	79832	37	11	32954948	32954948	Missense_Mutation	SNP	C	T	15	212	c.1757C>T	c.(1756-1758)TCT>TTT	p.S586F
Pat_41	Post-Resistance	DEPDC7	91614	37	11	33047225	33047225	Missense_Mutation	SNP	C	T	15	129	c.94C>T	c.(94-96)CCA>TCA	p.P32S
Pat_41	Post-Resistance	TCP11L1	55346	37	11	33065407	33065407	Missense_Mutation	SNP	G	A	28	559	c.88G>A	c.(88-90)GAA>AAA	p.E30K
Pat_41	Post-Resistance	CSTF3	1479	37	11	33106835	33106835	Missense_Mutation	SNP	G	A	9	79	c.1952C>T	c.(1951-1953)ACT>ATT	p.T651I
Pat_41	Post-Resistance	CSTF3	1479	37	11	33118472	33118472	Missense_Mutation	SNP	C	T	6	86	c.1181G>A	c.(1180-1182)GGA>GAA	p.G394E
Pat_41	Post-Resistance	HIPK3	10114	37	11	33369738	33369738	Nonsense_Mutation	SNP	G	A	5	87	c.2333G>A	c.(2332-2334)TGG>TAG	p.W778*
Pat_41	Post-Resistance	C11orf41	25758	37	11	33564178	33564178	Missense_Mutation	SNP	C	T	16	149	c.178C>T	c.(178-180)CCT>TCT	p.P60S
Pat_41	Post-Resistance	ABTB2	25841	37	11	34378509	34378509	Missense_Mutation	SNP	C	T	3	13	c.64G>A	c.(64-66)GGT>AGT	p.G22S
Pat_41	Post-Resistance	SLC1A2	6506	37	11	35282502	35282502	Missense_Mutation	SNP	G	A	11	164	c.1664C>T	c.(1663-1665)GCA>GTA	p.A555V
Pat_41	Post-Resistance	SLC1A2	6506	37	11	35302498	35302498	Missense_Mutation	SNP	C	T	14	50	c.1337G>A	c.(1336-1338)GGG>GAG	p.G446E
Pat_41	Post-Resistance	PAMR1	25891	37	11	35454164	35454164	Nonsense_Mutation	SNP	C	A	3	17	c.1903G>T	c.(1903-1905)GAG>TAG	p.E635*
Pat_41	Post-Resistance	COMMD9	29099	37	11	36302296	36302296	Missense_Mutation	SNP	G	A	21	179	c.143C>T	c.(142-144)TCC>TTC	p.S48F
Pat_41	Post-Resistance	RAG1	5896	37	11	36595272	36595272	Missense_Mutation	SNP	C	T	9	58	c.418C>T	c.(418-420)CTT>TTT	p.L140F
Pat_41	Post-Resistance	RAG1	5896	37	11	36597564	36597564	Missense_Mutation	SNP	G	A	8	100	c.2710G>A	c.(2710-2712)GAG>AAG	p.E904K
Pat_41	Post-Resistance	RAG2	5897	37	11	36614172	36614172	Missense_Mutation	SNP	G	A	11	57	c.1547C>T	c.(1546-1548)CCT>CTT	p.P516L
Pat_41	Post-Resistance	LRRC4C	57689	37	11	40136126	40136126	Missense_Mutation	SNP	C	T	9	151	c.1717G>A	c.(1717-1719)GAT>AAT	p.D573N
Pat_41	Post-Resistance	TTC17	55761	37	11	43513648	43513648	Missense_Mutation	SNP	G	A	24	321	c.3229G>A	c.(3229-3231)GCA>ACA	p.A1077T
Pat_41	Post-Resistance	SLC35C1	55343	37	11	45827888	45827888	Splice_Site	SNP	G	A	5	41	c.535_splice	c.e1+1	p.G179_splice
Pat_41	Post-Resistance	CREB3L1	90993	37	11	46338979	46338979	Missense_Mutation	SNP	G	A	13	103	c.1199G>A	c.(1198-1200)GGC>GAC	p.G400D
Pat_41	Post-Resistance	AMBRA1	55626	37	11	46563502	46563502	Missense_Mutation	SNP	G	A	42	194	c.2065C>T	c.(2065-2067)CTC>TTC	p.L689F
Pat_41	Post-Resistance	AMBRA1	55626	37	11	46564479	46564479	Missense_Mutation	SNP	C	T	45	237	c.1088G>A	c.(1087-1089)GGC>GAC	p.G363D
Pat_41	Post-Resistance	AMBRA1	55626	37	11	46564888	46564888	Missense_Mutation	SNP	C	T	7	148	c.679G>A	c.(679-681)GCC>ACC	p.A227T
Pat_41	Post-Resistance	CKAP5	9793	37	11	46829663	46829663	Missense_Mutation	SNP	G	A	9	143	c.896C>T	c.(895-897)GCC>GTC	p.A299V
Pat_41	Post-Resistance	MADD	8567	37	11	47303271	47303271	Missense_Mutation	SNP	G	A	13	105	c.1436G>A	c.(1435-1437)GGC>GAC	p.G479D
Pat_41	Post-Resistance	MYBPC3	4607	37	11	47353709	47353709	Missense_Mutation	SNP	G	A	4	68	c.3728C>T	c.(3727-3729)CCC>CTC	p.P1243L
Pat_41	Post-Resistance	MYBPC3	4607	37	11	47353809	47353809	Missense_Mutation	SNP	G	A	9	86	c.3628C>T	c.(3628-3630)CCC>TCC	p.P1210S
Pat_41	Post-Resistance	SLC39A13	91252	37	11	47435155	47435155	Missense_Mutation	SNP	G	A	17	88	c.653G>A	c.(652-654)GGC>GAC	p.G218D
Pat_41	Post-Resistance	PSMC3	5702	37	11	47440466	47440466	Missense_Mutation	SNP	C	T	5	68	c.1240G>A	c.(1240-1242)GAG>AAG	p.E414K
Pat_41	Post-Resistance	PSMC3	5702	37	11	47445695	47445695	Missense_Mutation	SNP	G	A	14	262	c.493C>T	c.(493-495)CCC>TCC	p.P165S
Pat_41	Post-Resistance	AGBL2	79841	37	11	47711872	47711872	Missense_Mutation	SNP	G	A	14	135	c.1387C>T	c.(1387-1389)CCT>TCT	p.P463S
Pat_41	Post-Resistance	FNBP4	23360	37	11	47786906	47786906	Missense_Mutation	SNP	C	T	16	264	c.229G>A	c.(229-231)GAA>AAA	p.E77K
Pat_41	Post-Resistance	NUP160	23279	37	11	47869834	47869834	Missense_Mutation	SNP	C	T	6	128	c.139G>A	c.(139-141)GAG>AAG	p.E47K
Pat_41	Post-Resistance	FOLH1	2346	37	11	49204764	49204764	Missense_Mutation	SNP	G	A	17	145	c.857C>T	c.(856-858)GCT>GTT	p.A286V
Pat_41	Post-Resistance	OR4C13	283092	37	11	49974380	49974380	Missense_Mutation	SNP	C	A	4	120	c.406C>A	c.(406-408)CAG>AAG	p.Q136K
Pat_41	Post-Resistance	OR4C11	219429	37	11	55371495	55371495	Missense_Mutation	SNP	C	T	12	69	c.355G>A	c.(355-357)GAT>AAT	p.D119N
Pat_41	Post-Resistance	OR8H2	390151	37	11	55872874	55872874	Missense_Mutation	SNP	C	T	28	358	c.356C>T	c.(355-357)GCC>GTC	p.A119V
Pat_41	Post-Resistance	OR8K3	219473	37	11	56086182	56086182	Missense_Mutation	SNP	G	A	7	190	c.400G>A	c.(400-402)GTA>ATA	p.V134I
Pat_41	Post-Resistance	OR5M11	219487	37	11	56310081	56310081	Missense_Mutation	SNP	G	A	10	113	c.653C>T	c.(652-654)GCC>GTC	p.A218V
Pat_41	Post-Resistance	TNKS1BP1	85456	37	11	57076871	57076871	Missense_Mutation	SNP	C	T	18	214	c.3314G>A	c.(3313-3315)GGG>GAG	p.G1105E
Pat_41	Post-Resistance	TNKS1BP1	85456	37	11	57088045	57088045	Missense_Mutation	SNP	C	T	7	43	c.236G>A	c.(235-237)AGG>AAG	p.R79K
Pat_41	Post-Resistance	SLC43A1	8501	37	11	57259305	57259305	Missense_Mutation	SNP	G	A	7	63	c.902C>T	c.(901-903)TCC>TTC	p.S301F
Pat_41	Post-Resistance	UBE2L6	9246	37	11	57322020	57322020	Missense_Mutation	SNP	A	G	11	423	c.200T>C	c.(199-201)ATG>ACG	p.M67T
Pat_41	Post-Resistance	CLP1	10978	37	11	57428648	57428648	Missense_Mutation	SNP	C	T	22	279	c.1018C>T	c.(1018-1020)CCT>TCT	p.P340S

Pat_41	Post-Resistance	ZDHHC5	25921	37	11	57463461	57463461	Missense_Mutation	SNP	G	A	23	88	c.955G>A	c.(955-957)GAC>AAC	p.D319N
Pat_41	Post-Resistance	CTNND1	1500	37	11	57571197	57571197	Missense_Mutation	SNP	G	A	6	88	c.1525G>A	c.(1525-1527)GAG>AAG	p.E509K
Pat_41	Post-Resistance	OR6Q1	219952	37	11	57799031	57799031	Missense_Mutation	SNP	G	A	10	187	c.607G>A	c.(607-609)GAT>AAT	p.D203N
Pat_41	Post-Resistance	OR5B2	390190	37	11	58190191	58190191	Missense_Mutation	SNP	C	T	17	119	c.544G>A	c.(544-546)GTC>ATC	p.V182I
Pat_41	Post-Resistance	FAM111A	63901	37	11	58920286	58920286	Missense_Mutation	SNP	C	T	10	405	c.1145C>T	c.(1144-1146)ACT>ATT	p.T382I
Pat_41	Post-Resistance	MPEG1	219972	37	11	58979621	58979621	Missense_Mutation	SNP	C	T	4	72	c.718G>A	c.(718-720)GCT>ACT	p.A240T
Pat_41	Post-Resistance	OR5A2	219981	37	11	59189969	59189969	Missense_Mutation	SNP	C	T	7	78	c.458G>A	c.(457-459)GGA>GAA	p.G153E
Pat_41	Post-Resistance	ZP1	22917	37	11	60637136	60637136	Missense_Mutation	SNP	G	A	10	113	c.445G>A	c.(445-447)GCA>ACA	p.A149T
Pat_41	Post-Resistance	ZP1	22917	37	11	60641136	60641136	Missense_Mutation	SNP	C	T	21	180	c.1460C>T	c.(1459-1461)ACC>ATC	p.T487I
Pat_41	Post-Resistance	TMEM109	79073	37	11	60689264	60689264	Missense_Mutation	SNP	G	A	19	167	c.359G>A	c.(358-360)GGC>GAC	p.G120D
Pat_41	Post-Resistance	CD5	921	37	11	60889344	60889344	Missense_Mutation	SNP	G	T	9	116	c.1067G>T	c.(1066-1068)AGA>ATA	p.R356I
Pat_41	Post-Resistance	C11orf9	745	37	11	61536761	61536761	Missense_Mutation	SNP	G	A	5	23	c.428G>A	c.(427-429)GGC>GAC	p.G143D
Pat_41	Post-Resistance	C11orf9	745	37	11	61553601	61553601	Missense_Mutation	SNP	C	T	5	114	c.3442C>T	c.(3442-3444)CGC>TGC	p.R1148C
Pat_41	Post-Resistance	AHNAK	79026	37	11	62287166	62287166	Missense_Mutation	SNP	G	A	13	84	c.14723C>T	c.(14722-14724)TCG>TTG	p.S4908L
Pat_41	Post-Resistance	AHNAK	79026	37	11	62287578	62287578	Missense_Mutation	SNP	C	T	67	408	c.14311G>A	c.(14311-14313)GTT>ATT	p.V4771I
Pat_41	Post-Resistance	AHNAK	79026	37	11	62294080	62294080	Missense_Mutation	SNP	T	G	9	395	c.7809A>C	c.(7807-7809)AAA>AAC	p.K2603N
Pat_41	Post-Resistance	AHNAK	79026	37	11	62294327	62294327	Missense_Mutation	SNP	G	A	62	433	c.7562C>T	c.(7561-7563)CCT>CTT	p.P2521L
Pat_41	Post-Resistance	AHNAK	79026	37	11	62294675	62294675	Missense_Mutation	SNP	T	C	4	53	c.7214A>G	c.(7213-7215)GAT>GGT	p.D2405G
Pat_41	Post-Resistance	AHNAK	79026	37	11	62295483	62295483	Missense_Mutation	SNP	C	T	10	510	c.6406G>A	c.(6406-6408)GAT>AAT	p.D2136N
Pat_41	Post-Resistance	AHNAK	79026	37	11	62300864	62300864	Missense_Mutation	SNP	C	T	5	128	c.1025G>A	c.(1024-1026)GGC>GAC	p.G342D
Pat_41	Post-Resistance	AHNAK	79026	37	11	62300970	62300970	Missense_Mutation	SNP	G	A	9	132	c.919C>T	c.(919-921)CCC>TCC	p.P307S
Pat_41	Post-Resistance	ROM1	6094	37	11	62380819	62380819	Nonsense_Mutation	SNP	G	A	5	13	c.66G>A	c.(64-66)TGG>TGA	p.W22*
Pat_41	Post-Resistance	GANAB	23193	37	11	62400135	62400135	Missense_Mutation	SNP	G	A	47	489	c.898C>T	c.(898-900)CCT>TCT	p.P300S
Pat_41	Post-Resistance	GANAB	23193	37	11	62402383	62402383	Missense_Mutation	SNP	C	T	17	244	c.470G>A	c.(469-471)CGC>CAC	p.R157H
Pat_41	Post-Resistance	INTS5	80789	37	11	62414839	62414839	Missense_Mutation	SNP	C	T	11	153	c.2713G>A	c.(2713-2715)GAG>AAG	p.E905K
Pat_41	Post-Resistance	POLR2G	5436	37	11	62532658	62532658	Missense_Mutation	SNP	G	A	14	276	c.287G>A	c.(286-288)GGA>GAA	p.G96E
Pat_41	Post-Resistance	TAF6L	10629	37	11	62545577	62545577	Missense_Mutation	SNP	G	A	7	100	c.362G>A	c.(361-363)GGC>GAC	p.G121D
Pat_41	Post-Resistance	SLC3A2	6520	37	11	62655947	62655947	Nonsense_Mutation	SNP	C	T	8	193	c.1675C>T	c.(1675-1677)CAG>TAG	p.Q559*
Pat_41	Post-Resistance	SLC22A8	9376	37	11	62762217	62762217	Missense_Mutation	SNP	C	T	5	64	c.1013G>A	c.(1012-1014)GGT>GAT	p.G338D
Pat_41	Post-Resistance	SLC22A25	387601	37	11	62985134	62985134	Missense_Mutation	SNP	G	A	8	86	c.580C>T	c.(580-582)CCC>TCC	p.P194S
Pat_41	Post-Resistance	RARRES3	5920	37	11	63312342	63312342	Missense_Mutation	SNP	G	A	26	436	c.368G>A	c.(367-369)GGC>GAC	p.G123D
Pat_41	Post-Resistance	ATL3	25923	37	11	63396870	63396870	Missense_Mutation	SNP	G	A	9	105	c.1547C>T	c.(1546-1548)TCT>TTT	p.S516F
Pat_41	Post-Resistance	ATL3	25923	37	11	63400536	63400536	Missense_Mutation	SNP	C	T	13	133	c.1069G>A	c.(1069-1071)GCC>ACC	p.A357T
Pat_41	Post-Resistance	RTN3	10313	37	11	63517562	63517562	Missense_Mutation	SNP	G	A	5	25	c.2630G>A	c.(2629-2631)AGT>AAT	p.S877N
Pat_41	Post-Resistance	C11orf84	144097	37	11	63586454	63586454	Missense_Mutation	SNP	G	A	3	41	c.914G>A	c.(913-915)CGG>CAG	p.R305Q
Pat_41	Post-Resistance	MARK2	2011	37	11	63672516	63672516	Splice_Site	SNP	G	A	34	182	c.1934_splice	c.e16+1	p.R645_splice
Pat_41	Post-Resistance	RCOR2	283248	37	11	63681590	63681590	Missense_Mutation	SNP	C	T	6	99	c.727G>A	c.(727-729)GTC>ATC	p.V243I
Pat_41	Post-Resistance	PLCB3	5331	37	11	64025948	64025948	Missense_Mutation	SNP	G	A	5	26	c.1016G>A	c.(1015-1017)GGG>GAG	p.G339E
Pat_41	Post-Resistance	PLCB3	5331	37	11	64029423	64029423	Splice_Site	SNP	G	A	17	190	c.1914_splice	c.e17-1	p.E638_splice
Pat_41	Post-Resistance	PRDX5	25824	37	11	64087243	64087243	Missense_Mutation	SNP	G	A	21	265	c.209G>A	c.(208-210)GGG>GAG	p.G70E
Pat_41	Post-Resistance	NRXN2	9379	37	11	64453251	64453251	Missense_Mutation	SNP	G	A	17	258	c.1019C>T	c.(1018-1020)TCC>TTC	p.S340F
Pat_41	Post-Resistance	SF1	7536	37	11	64543988	64543988	Nonsense_Mutation	SNP	G	A	7	132	c.142C>T	c.(142-144)CAA>TAA	p.Q48*
Pat_41	Post-Resistance	SF1	7536	37	11	64544006	64544006	Missense_Mutation	SNP	G	A	11	143	c.124C>T	c.(124-126)CCT>TCT	p.P42S
Pat_41	Post-Resistance	CDC42BPG	55561	37	11	64600104	64600104	Missense_Mutation	SNP	C	A	4	122	c.2977G>T	c.(2977-2979)GGG>TGG	p.G993W
Pat_41	Post-Resistance	CDC42BPG	55561	37	11	64609299	64609299	Missense_Mutation	SNP	C	T	5	69	c.238G>A	c.(238-240)GGA>AGA	p.G80R
Pat_41	Post-Resistance	EHD1	10938	37	11	64645605	64645605	Missense_Mutation	SNP	C	T	7	48	c.332G>A	c.(331-333)GGC>GAC	p.G111D
Pat_41	Post-Resistance	ATG2A	23130	37	11	64668527	64668527	Missense_Mutation	SNP	G	A	4	21	c.4157C>T	c.(4156-4158)CCC>CTC	p.P1386L

Pat_41	Post-Resistance	SAC3D1	29901	37	11	64811748	64811748	Missense_Mutation	SNP	C	T	7	143	c.626C>T	c.(625-627)GCC>GTC	p.A209V
Pat_41	Post-Resistance	CDCA5	113130	37	11	64847030	64847030	Missense_Mutation	SNP	G	A	7	35	c.473C>T	c.(472-474)TCC>TTC	p.S158F
Pat_41	Post-Resistance	C11orf2	738	37	11	64875941	64875941	Missense_Mutation	SNP	G	A	4	22	c.998G>A	c.(997-999)GGT>GAT	p.G333D
Pat_41	Post-Resistance	SLC25A45	283130	37	11	65144006	65144006	Missense_Mutation	SNP	C	T	8	286	c.739G>A	c.(739-741)GTG>ATG	p.V247M
Pat_41	Post-Resistance	SLC25A45	283130	37	11	65144292	65144292	Missense_Mutation	SNP	G	A	47	608	c.595C>T	c.(595-597)CCC>TCC	p.P199S
Pat_41	Post-Resistance	SIPA1	6494	37	11	65417614	65417614	Missense_Mutation	SNP	C	T	11	166	c.2854C>T	c.(2854-2856)CCC>TCC	p.P952S
Pat_41	Post-Resistance	SIPA1	6494	37	11	65417939	65417939	Missense_Mutation	SNP	G	A	5	44	c.2971G>A	c.(2971-2973)GAC>AAC	p.D991N
Pat_41	Post-Resistance	RELA	5970	37	11	65423216	65423216	Missense_Mutation	SNP	G	A	5	93	c.976C>T	c.(976-978)CCT>TCT	p.P326S
Pat_41	Post-Resistance	KAT5	10524	37	11	65482350	65482350	Missense_Mutation	SNP	C	T	8	152	c.899C>T	c.(898-900)TCC>TTC	p.S300F
Pat_41	Post-Resistance	DKFZp761E198	91056	37	11	65545809	65545809	Missense_Mutation	SNP	G	A	3	36	c.1984C>T	c.(1984-1986)CGC>TGC	p.R662C
Pat_41	Post-Resistance	SF3B2	10992	37	11	65826355	65826355	Missense_Mutation	SNP	G	A	4	66	c.1021G>A	c.(1021-1023)GGG>AGG	p.G341R
Pat_41	Post-Resistance	PACS1	55690	37	11	65988665	65988665	Missense_Mutation	SNP	G	A	17	226	c.1240G>A	c.(1240-1242)GAG>AAG	p.E414K
Pat_41	Post-Resistance	TMEM151A	256472	37	11	66061887	66061887	Missense_Mutation	SNP	C	T	3	20	c.170C>T	c.(169-171)GCC>GTC	p.A57V
Pat_41	Post-Resistance	CD248	57124	37	11	66083718	66083718	Missense_Mutation	SNP	C	T	4	50	c.781G>A	c.(781-783)GGC>AGC	p.G261S
Pat_41	Post-Resistance	B3GNT1	11041	37	11	66114284	66114284	Missense_Mutation	SNP	C	T	18	234	c.733G>A	c.(733-735)GAT>AAT	p.D245N
Pat_41	Post-Resistance	PELI3	246330	37	11	66235712	66235712	Missense_Mutation	SNP	G	A	24	171	c.113G>A	c.(112-114)GGC>GAC	p.G38D
Pat_41	Post-Resistance	DPP3	10072	37	11	66272120	66272120	Missense_Mutation	SNP	C	T	32	128	c.1916C>T	c.(1915-1917)GCC>GTC	p.A639V
Pat_41	Post-Resistance	CCDC87	55231	37	11	66360360	66360360	Missense_Mutation	SNP	G	A	8	37	c.127C>T	c.(127-129)CGG>TGG	p.R43W
Pat_41	Post-Resistance	RBM4	5936	37	11	66411212	66411212	Missense_Mutation	SNP	C	T	15	79	c.704C>T	c.(703-705)GCA>GTA	p.A235V
Pat_41	Post-Resistance	SPTBN2	6712	37	11	66454493	66454493	Nonsense_Mutation	SNP	G	A	28	162	c.6868C>T	c.(6868-6870)CGA>TGA	p.R2290*
Pat_41	Post-Resistance	C11orf80	79703	37	11	66555658	66555658	Missense_Mutation	SNP	C	T	15	182	c.551C>T	c.(550-552)TCT>TTT	p.S184F
Pat_41	Post-Resistance	C11orf80	79703	37	11	66571561	66571561	Missense_Mutation	SNP	G	A	28	467	c.938G>A	c.(937-939)GGC>GAC	p.G313D
Pat_41	Post-Resistance	RCE1	9986	37	11	66613400	66613400	Missense_Mutation	SNP	C	T	9	203	c.824C>T	c.(823-825)GCC>GTC	p.A275V
Pat_41	Post-Resistance	PC	5091	37	11	66617225	66617225	Missense_Mutation	SNP	C	T	5	110	c.3004G>A	c.(3004-3006)GTG>ATG	p.V1002M
Pat_41	Post-Resistance	ADRBK1	156	37	11	67046932	67046932	Missense_Mutation	SNP	C	T	6	110	c.308C>T	c.(307-309)GCC>GTC	p.A103V
Pat_41	Post-Resistance	RAD9A	5883	37	11	67160165	67160165	Missense_Mutation	SNP	C	T	30	214	c.146C>T	c.(145-147)GCC>GTC	p.A49V
Pat_41	Post-Resistance	PITPNM1	9600	37	11	67267787	67267787	Missense_Mutation	SNP	G	A	47	246	c.746C>T	c.(745-747)GCT>GTT	p.A249V
Pat_41	Post-Resistance	C11orf24	53838	37	11	68029831	68029831	Missense_Mutation	SNP	G	A	11	144	c.632C>T	c.(631-633)GCC>GTC	p.A211V
Pat_41	Post-Resistance	LRP5	4041	37	11	68174207	68174207	Missense_Mutation	SNP	G	A	7	41	c.2017G>A	c.(2017-2019)GGC>AGC	p.G673S
Pat_41	Post-Resistance	SAPS3	55291	37	11	68367812	68367812	Missense_Mutation	SNP	C	T	6	275	c.2042C>T	c.(2041-2043)CCC>CTC	p.P681L
Pat_41	Post-Resistance	IGHMBP2	3508	37	11	68675720	68675720	Missense_Mutation	SNP	C	T	21	164	c.364C>T	c.(364-366)CAC>TAC	p.H122Y
Pat_41	Post-Resistance	TPCN2	219931	37	11	68825148	68825148	Missense_Mutation	SNP	C	T	14	137	c.532C>T	c.(532-534)CTC>TTC	p.L178F
Pat_41	Post-Resistance	ANO1	55107	37	11	70028704	70028704	Missense_Mutation	SNP	A	G	5	89	c.2500A>G	c.(2500-2502)ACC>GCC	p.T834A
Pat_41	Post-Resistance	PPFIA1	8500	37	11	70194417	70194417	Missense_Mutation	SNP	C	T	50	470	c.2054C>T	c.(2053-2055)CCT>CTT	p.P685L
Pat_41	Post-Resistance	SHANK2	22941	37	11	70331537	70331537	Missense_Mutation	SNP	C	T	5	79	c.4861G>A	c.(4861-4863)GCA>ACA	p.A1621T
Pat_41	Post-Resistance	SHANK2	22941	37	11	70332164	70332164	Missense_Mutation	SNP	G	A	18	73	c.4234C>T	c.(4234-4236)CCT>TCT	p.P1412S
Pat_41	Post-Resistance	SHANK2	22941	37	11	70505982	70505982	Missense_Mutation	SNP	C	T	7	64	c.2012G>A	c.(2011-2013)GGT>GAT	p.G671D
Pat_41	Post-Resistance	NADSYN1	55191	37	11	71169538	71169538	Missense_Mutation	SNP	G	A	30	136	c.211G>A	c.(211-213)GCG>ACG	p.A71T
Pat_41	Post-Resistance	NUMA1	4926	37	11	71715350	71715350	Missense_Mutation	SNP	G	A	12	105	c.6044C>T	c.(6043-6045)ACT>ATT	p.T2015I
Pat_41	Post-Resistance	NUMA1	4926	37	11	71715858	71715858	Missense_Mutation	SNP	G	A	4	20	c.5834C>T	c.(5833-5835)TCC>TTC	p.S1945F
Pat_41	Post-Resistance	INPPL1	3636	37	11	71948415	71948415	Missense_Mutation	SNP	G	A	12	121	c.3127G>A	c.(3127-3129)GAG>AAG	p.E1043K
Pat_41	Post-Resistance	CLPB	81570	37	11	72084016	72084016	Missense_Mutation	SNP	C	A	13	292	c.689G>T	c.(688-690)TGG>TTG	p.W230L
Pat_41	Post-Resistance	ARAP1	116985	37	11	72407682	72407682	Missense_Mutation	SNP	C	T	8	68	c.3184G>A	c.(3184-3186)GAG>AAG	p.E1062K
Pat_41	Post-Resistance	ARHGEF17	9828	37	11	73022621	73022621	Missense_Mutation	SNP	C	T	10	127	c.2938C>T	c.(2938-2940)CCC>TCC	p.P980S
Pat_41	Post-Resistance	C2CD3	26005	37	11	73811664	73811664	Missense_Mutation	SNP	C	T	7	85	c.2638G>A	c.(2638-2640)GTA>ATA	p.V880I
Pat_41	Post-Resistance	PGM2L1	283209	37	11	74054003	74054003	Missense_Mutation	SNP	C	T	24	422	c.1369G>A	c.(1369-1371)GTT>ATT	p.V457I
Pat_41	Post-Resistance	GDPD5	81544	37	11	75160621	75160621	Missense_Mutation	SNP	G	A	7	23	c.509C>T	c.(508-510)GCA>GTA	p.A170V

Pat_41	Post-Resistance	MAP6	4135	37	11	75298411	75298411	Missense_Mutation	SNP	G	A	10	90	c.2135C>T	c.(2134-2136)TCC>TTC	p.S712F
Pat_41	Post-Resistance	UVRAG	7405	37	11	75827011	75827011	Missense_Mutation	SNP	C	T	7	162	c.1349C>T	c.(1348-1350)ACC>ATC	p.T450I
Pat_41	Post-Resistance	PRKRIR	5612	37	11	76063133	76063133	Missense_Mutation	SNP	G	A	15	233	c.1061C>T	c.(1060-1062)GCT>GTT	p.A354V
Pat_41	Post-Resistance	C11orf30	56946	37	11	76183846	76183846	Missense_Mutation	SNP	C	T	20	371	c.1070C>T	c.(1069-1071)TCC>TTC	p.S357F
Pat_41	Post-Resistance	LRRC32	2615	37	11	76370955	76370955	Missense_Mutation	SNP	G	A	5	20	c.1682C>T	c.(1681-1683)ACC>ATC	p.T561I
Pat_41	Post-Resistance	AQP11	282679	37	11	77301255	77301255	Missense_Mutation	SNP	C	T	5	103	c.218C>T	c.(217-219)GCG>GTG	p.A73V
Pat_41	Post-Resistance	RSF1	51773	37	11	77413346	77413346	Missense_Mutation	SNP	C	T	5	86	c.928G>A	c.(928-930)GAA>AAA	p.E310K
Pat_41	Post-Resistance	USP35	57558	37	11	77911777	77911777	Missense_Mutation	SNP	G	A	4	46	c.1120G>A	c.(1120-1122)GCG>ACG	p.A374T
Pat_41	Post-Resistance	GAB2	9846	37	11	77937766	77937766	Missense_Mutation	SNP	C	T	5	70	c.952G>A	c.(952-954)GCC>ACC	p.A318T
Pat_41	Post-Resistance	C11orf82	220042	37	11	82644551	82644551	Missense_Mutation	SNP	C	T	23	166	c.2171C>T	c.(2170-2172)TCT>TTT	p.S724F
Pat_41	Post-Resistance	PCF11	51585	37	11	82882888	82882888	Missense_Mutation	SNP	C	T	15	189	c.3689C>T	c.(3688-3690)GCT>GTT	p.A1230V
Pat_41	Post-Resistance	DLG2	1740	37	11	83252779	83252779	Missense_Mutation	SNP	C	T	18	158	c.1748G>A	c.(1747-1749)AGA>AAA	p.R583K
Pat_41	Post-Resistance	CREBZF	58487	37	11	85375129	85375129	Missense_Mutation	SNP	C	T	31	571	c.791G>A	c.(790-792)AGT>AAT	p.S264N
Pat_41	Post-Resistance	CCDC83	220047	37	11	85610046	85610046	Nonsense_Mutation	SNP	G	A	14	128	c.660G>A	c.(658-660)TGG>TGA	p.W220*
Pat_41	Post-Resistance	PICALM	8301	37	11	85712202	85712202	Splice_Site	SNP	C	T	9	323	c.894_splice	c.e10-1	p.R298_splice
Pat_41	Post-Resistance	PRSS23	11098	37	11	86519167	86519167	Missense_Mutation	SNP	C	T	8	167	c.482C>T	c.(481-483)ACC>ATC	p.T161I
Pat_41	Post-Resistance	FZD4	8322	37	11	86663026	86663026	Missense_Mutation	SNP	G	A	4	41	c.772C>T	c.(772-774)CTC>TTC	p.L258F
Pat_41	Post-Resistance	TYR	7299	37	11	89028403	89028403	Missense_Mutation	SNP	G	A	10	87	c.1459G>A	c.(1459-1461)GTC>ATC	p.V487I
Pat_41	Post-Resistance	NOX4	50507	37	11	89075338	89075338	Missense_Mutation	SNP	C	T	24	168	c.1241G>A	c.(1240-1242)GGA>GAA	p.G414E
Pat_41	Post-Resistance	FAT3	120114	37	11	92087958	92087958	Missense_Mutation	SNP	C	T	9	145	c.2680C>T	c.(2680-2682)CGG>TGG	p.R894W
Pat_41	Post-Resistance	FAT3	120114	37	11	92088525	92088525	Missense_Mutation	SNP	A	G	15	137	c.3247A>G	c.(3247-3249)AGG>GGG	p.R1083G
Pat_41	Post-Resistance	FAT3	120114	37	11	92531452	92531452	Missense_Mutation	SNP	A	G	3	70	c.5273A>G	c.(5272-5274)CAG>CGG	p.Q1758R
Pat_41	Post-Resistance	FAT3	120114	37	11	92616434	92616434	Missense_Mutation	SNP	C	T	24	254	c.12812C>T	c.(12811-12813)CCC>CTC	p.P4271L
Pat_41	Post-Resistance	FAT3	120114	37	11	92624253	92624253	Nonsense_Mutation	SNP	G	T	3	55	c.13648G>T	c.(13648-13650)GAG>TAG	p.E4550*
Pat_41	Post-Resistance	MRE11A	4361	37	11	94209570	94209570	Splice_Site	SNP	C	T	10	107	c.545_splice	c.e7-1	p.G182_splice
Pat_41	Post-Resistance	KDM4D	55693	37	11	94731499	94731499	Missense_Mutation	SNP	G	A	11	70	c.963G>A	c.(961-963)ATG>ATA	p.M321I
Pat_41	Post-Resistance	SFRS2B	10929	37	11	94800803	94800803	Missense_Mutation	SNP	G	A	5	4	c.413G>A	c.(412-414)GGT>GAT	p.G138D
Pat_41	Post-Resistance	SESN3	143686	37	11	94923022	94923022	Missense_Mutation	SNP	G	A	16	229	c.446C>T	c.(445-447)CCA>CTA	p.P149L
Pat_41	Post-Resistance	FAM76B	143684	37	11	95509103	95509103	Missense_Mutation	SNP	T	C	8	82	c.913A>G	c.(913-915)ACT>GCT	p.T305A
Pat_41	Post-Resistance	FAM76B	143684	37	11	95512806	95512806	Missense_Mutation	SNP	C	A	11	269	c.657G>T	c.(655-657)AAG>AAT	p.K219N
Pat_41	Post-Resistance	JRKL	8690	37	11	96125326	96125326	Missense_Mutation	SNP	G	A	9	191	c.1513G>A	c.(1513-1515)GTA>ATA	p.V505I
Pat_41	Post-Resistance	CNTN5	53942	37	11	100126494	100126494	Missense_Mutation	SNP	C	T	22	163	c.2008C>T	c.(2008-2010)CCC>TCC	p.P670S
Pat_41	Post-Resistance	CNTN5	53942	37	11	100179193	100179193	Missense_Mutation	SNP	G	A	9	59	c.2723G>A	c.(2722-2724)GGA>GAA	p.G908E
Pat_41	Post-Resistance	PGR	5241	37	11	100922221	100922221	Missense_Mutation	SNP	C	T	17	202	c.2291G>A	c.(2290-2292)GGA>GAA	p.G764E
Pat_41	Post-Resistance	YAP1	10413	37	11	102076672	102076672	Missense_Mutation	SNP	C	T	13	178	c.851C>T	c.(850-852)CCC>CTC	p.P284L
Pat_41	Post-Resistance	BIRC3	330	37	11	102195460	102195460	Missense_Mutation	SNP	G	A	6	194	c.220G>A	c.(220-222)GAT>AAT	p.D74N
Pat_41	Post-Resistance	MMP8	4317	37	11	102593314	102593314	Missense_Mutation	SNP	C	T	25	294	c.193G>A	c.(193-195)GAA>AAA	p.E65K
Pat_41	Post-Resistance	MMP13	4322	37	11	102820942	102820942	Missense_Mutation	SNP	C	T	11	446	c.814G>A	c.(814-816)GAC>AAC	p.D272N
Pat_41	Post-Resistance	DYNC2H1	79659	37	11	103006658	103006658	Missense_Mutation	SNP	C	T	10	67	c.2555C>T	c.(2554-2556)GCT>GTT	p.A852V
Pat_41	Post-Resistance	DYNC2H1	79659	37	11	103070077	103070077	Missense_Mutation	SNP	G	A	17	143	c.7960G>A	c.(7960-7962)GCA>ACA	p.A2654T
Pat_41	Post-Resistance	PDGFD	80310	37	11	103797716	103797716	Missense_Mutation	SNP	C	T	10	89	c.911G>A	c.(910-912)GGA>GAA	p.G304E
Pat_41	Post-Resistance	CASP5	838	37	11	104878026	104878026	Missense_Mutation	SNP	C	T	15	89	c.217G>A	c.(217-219)GAA>AAA	p.E73K
Pat_41	Post-Resistance	CASP1	834	37	11	104897633	104897633	Missense_Mutation	SNP	C	T	17	223	c.1052G>A	c.(1051-1053)GGA>GAA	p.G351E
Pat_41	Post-Resistance	CARD16	114769	37	11	104915346	104915346	Missense_Mutation	SNP	G	A	90	596	c.47C>T	c.(46-48)TCC>TTC	p.S16F
Pat_41	Post-Resistance	GRIA4	2893	37	11	105797547	105797547	Missense_Mutation	SNP	C	T	6	287	c.1928C>T	c.(1927-1929)GCT>GTT	p.A643V
Pat_41	Post-Resistance	AASDHPPT	60496	37	11	105961310	105961310	Missense_Mutation	SNP	C	T	10	196	c.436C>T	c.(436-438)CAT>TAT	p.H146Y
Pat_41	Post-Resistance	GUCY1A2	2977	37	11	106647210	106647210	Missense_Mutation	SNP	C	T	3	39	c.1791G>A	c.(1789-1791)ATG>ATA	p.M597I

Pat_41	Post-Resistance	CWF19L2	143884	37	11	107205636	107205636	Missense_Mutation	SNP	C	T	17	149	c.2410G>A	c.(2410-2412)GAT>AAT	p.D804N
Pat_41	Post-Resistance	SLC35F2	54733	37	11	107686665	107686665	Missense_Mutation	SNP	C	T	12	107	c.137G>A	c.(136-138)GGT>GAT	p.G46D
Pat_41	Post-Resistance	NPAT	4863	37	11	108032511	108032511	Missense_Mutation	SNP	G	A	4	32	c.3302C>T	c.(3301-3303)CCC>CTC	p.P1101L
Pat_41	Post-Resistance	ATM	472	37	11	108235884	108235884	Missense_Mutation	SNP	G	A	56	102	c.8926G>A	c.(8926-8928)GAT>AAT	p.D2976N
Pat_41	Post-Resistance	EXPH5	23086	37	11	108383046	108383046	Missense_Mutation	SNP	C	T	7	88	c.3188G>A	c.(3187-3189)GGG>GAG	p.G1063E
Pat_41	Post-Resistance	RDX	5962	37	11	110135599	110135599	Missense_Mutation	SNP	C	T	16	156	c.97G>A	c.(97-99)GTG>ATG	p.V33M
Pat_41	Post-Resistance	BTG4	54766	37	11	111365997	111365997	Missense_Mutation	SNP	G	A	12	202	c.553C>T	c.(553-555)CCC>TCC	p.P185S
Pat_41	Post-Resistance	C11orf88	399949	37	11	111407547	111407547	Missense_Mutation	SNP	G	A	21	136	c.505G>A	c.(505-507)GAC>AAC	p.D169N
Pat_41	Post-Resistance	FDXACB1	91893	37	11	111745660	111745660	Missense_Mutation	SNP	C	T	4	122	c.1861G>A	c.(1861-1863)GTT>ATT	p.V621I
Pat_41	Post-Resistance	DLAT	1737	37	11	111914190	111914190	Missense_Mutation	SNP	G	A	31	509	c.1130G>A	c.(1129-1131)GGG>GAG	p.G377E
Pat_41	Post-Resistance	DLAT	1737	37	11	111930682	111930682	Missense_Mutation	SNP	C	T	10	48	c.1570C>T	c.(1570-1572)CCT>TCT	p.P524S
Pat_41	Post-Resistance	PIH1D2	120379	37	11	111941916	111941916	Missense_Mutation	SNP	C	T	21	396	c.393G>A	c.(391-393)ATG>ATA	p.M131I
Pat_41	Post-Resistance	TMPRSS5	80975	37	11	113569713	113569713	Missense_Mutation	SNP	G	A	4	20	c.242C>T	c.(241-243)TCC>TTC	p.S81F
Pat_41	Post-Resistance	USP28	57646	37	11	113699951	113699951	Missense_Mutation	SNP	G	A	6	188	c.1027C>T	c.(1027-1029)CCC>TCC	p.P343S
Pat_41	Post-Resistance	HTR3B	9177	37	11	113780103	113780103	Missense_Mutation	SNP	G	A	11	142	c.139G>A	c.(139-141)GTG>ATG	p.V47M
Pat_41	Post-Resistance	ZBTB16	7704	37	11	114121087	114121087	Missense_Mutation	SNP	C	T	16	169	c.1832C>T	c.(1831-1833)TCC>TTC	p.S611F
Pat_41	Post-Resistance	FAM55A	120400	37	11	114401213	114401213	Missense_Mutation	SNP	C	T	9	88	c.91G>A	c.(91-93)GAG>AAG	p.E31K
Pat_41	Post-Resistance	CADM1	23705	37	11	115099967	115099967	Missense_Mutation	SNP	G	A	8	223	c.587C>T	c.(586-588)TCA>TTA	p.S196L
Pat_41	Post-Resistance	BUD13	84811	37	11	116628632	116628632	Missense_Mutation	SNP	C	T	15	96	c.1534G>A	c.(1534-1536)GAG>AAG	p.E512K
Pat_41	Post-Resistance	BUD13	84811	37	11	116640903	116640903	Missense_Mutation	SNP	G	A	39	123	c.179C>T	c.(178-180)GCT>GTT	p.A60V
Pat_41	Post-Resistance	SIK3	23387	37	11	116718272	116718272	Missense_Mutation	SNP	C	T	19	407	c.3554G>A	c.(3553-3555)AGC>AAC	p.S1185N
Pat_41	Post-Resistance	SIK3	23387	37	11	116728588	116728588	Missense_Mutation	SNP	C	T	6	142	c.3275G>A	c.(3274-3276)GGG>GAG	p.G1092E
Pat_41	Post-Resistance	SIK3	23387	37	11	116730309	116730309	Missense_Mutation	SNP	A	T	16	90	c.2119T>A	c.(2119-2121)TCT>ACT	p.S707T
Pat_41	Post-Resistance	SIK3	23387	37	11	116744298	116744298	Missense_Mutation	SNP	G	A	10	57	c.1462C>T	c.(1462-1464)CTT>TTT	p.L488F
Pat_41	Post-Resistance	SIDT2	51092	37	11	117062698	117062698	Missense_Mutation	SNP	G	A	11	220	c.1840G>A	c.(1840-1842)GCC>ACC	p.A614T
Pat_41	Post-Resistance	PCSK7	9159	37	11	117089857	117089857	Nonsense_Mutation	SNP	C	T	4	49	c.1347G>A	c.(1345-1347)TGG>TGA	p.W449*
Pat_41	Post-Resistance	PCSK7	9159	37	11	117100259	117100259	Missense_Mutation	SNP	G	A	17	113	c.302C>T	c.(301-303)CCT>CTT	p.P101L
Pat_41	Post-Resistance	RNF214	257160	37	11	117109585	117109585	Missense_Mutation	SNP	G	A	4	79	c.376G>A	c.(376-378)GAG>AAG	p.E126K
Pat_41	Post-Resistance	BACE1	23621	37	11	117162498	117162498	Missense_Mutation	SNP	C	T	5	207	c.872G>A	c.(871-873)GGC>GAC	p.G291D
Pat_41	Post-Resistance	CEP164	22897	37	11	117263215	117263215	Missense_Mutation	SNP	G	A	6	34	c.2365G>A	c.(2365-2367)GTC>ATC	p.V789I
Pat_41	Post-Resistance	CEP164	22897	37	11	117280574	117280574	Missense_Mutation	SNP	C	T	5	159	c.3989C>T	c.(3988-3990)ACG>ATG	p.T1330M
Pat_41	Post-Resistance	CEP164	22897	37	11	117282626	117282626	Missense_Mutation	SNP	C	T	9	51	c.4279C>T	c.(4279-4281)CCC>TCC	p.P1427S
Pat_41	Post-Resistance	DSCAML1	57453	37	11	117306485	117306485	Missense_Mutation	SNP	C	T	7	176	c.4931G>A	c.(4930-4932)GGT>GAT	p.G1644D
Pat_41	Post-Resistance	TMPRSS13	84000	37	11	117789142	117789142	Missense_Mutation	SNP	C	T	8	86	c.433G>A	c.(433-435)GCC>ACC	p.A145T
Pat_41	Post-Resistance	AMICA1	120425	37	11	118081393	118081393	Missense_Mutation	SNP	C	T	16	273	c.233G>A	c.(232-234)AGT>AAT	p.S78N
Pat_41	Post-Resistance	CD3D	915	37	11	118211164	118211164	Missense_Mutation	SNP	G	A	23	109	c.200C>T	c.(199-201)CCA>CTA	p.P67L
Pat_41	Post-Resistance	UBE4A	9354	37	11	118263519	118263519	Missense_Mutation	SNP	C	T	59	285	c.2983C>T	c.(2983-2985)CCC>TCC	p.P995S
Pat_41	Post-Resistance	MLL	4297	37	11	118344806	118344806	Missense_Mutation	SNP	C	T	8	43	c.2932C>T	c.(2932-2934)CCA>TCA	p.P978S
Pat_41	Post-Resistance	MLL	4297	37	11	118348697	118348697	Missense_Mutation	SNP	C	T	48	669	c.3350C>T	c.(3349-3351)GCT>GTT	p.A1117V
Pat_41	Post-Resistance	MLL	4297	37	11	118373572	118373572	Missense_Mutation	SNP	C	T	17	162	c.6956C>T	c.(6955-6957)TCT>TTT	p.S2319F
Pat_41	Post-Resistance	IFT46	56912	37	11	118425302	118425302	Missense_Mutation	SNP	C	T	23	114	c.355G>A	c.(355-357)GTC>ATC	p.V119I
Pat_41	Post-Resistance	VPS11	55823	37	11	118938614	118938614	Missense_Mutation	SNP	C	T	3	30	c.80C>T	c.(79-81)GCC>GTC	p.A27V
Pat_41	Post-Resistance	NLRX1	79671	37	11	119043648	119043648	Missense_Mutation	SNP	C	T	7	148	c.179C>T	c.(178-180)GCT>GTT	p.A60V
Pat_41	Post-Resistance	NLRX1	79671	37	11	119045592	119045592	Missense_Mutation	SNP	G	A	4	90	c.1280G>A	c.(1279-1281)CGA>CAA	p.R427Q
Pat_41	Post-Resistance	MCAM	4162	37	11	119182805	119182805	Missense_Mutation	SNP	G	A	9	72	c.1100C>T	c.(1099-1101)GCA>GTA	p.A367V
Pat_41	Post-Resistance	RNF26	79102	37	11	119206316	119206316	Missense_Mutation	SNP	C	T	8	58	c.484C>T	c.(484-486)CTC>TTC	p.L162F
Pat_41	Post-Resistance	TRIM29	23650	37	11	119996552	119996552	Missense_Mutation	SNP	G	A	13	101	c.1180C>T	c.(1180-1182)CCC>TCC	p.P394S

Pat_41	Post-Resistance	TECTA	7007	37	11	121008283	121008283	Missense_Mutation	SNP	C	T	15	72	c.3095C>T	c.(3094-3096)ACG>ATG	p.T1032M
Pat_41	Post-Resistance	TECTA	7007	37	11	121016279	121016279	Missense_Mutation	SNP	C	T	43	520	c.3559C>T	c.(3559-3561)CTC>TTC	p.L1187F
Pat_41	Post-Resistance	SC5DL	6309	37	11	121175190	121175190	Missense_Mutation	SNP	G	A	27	163	c.331G>A	c.(331-333)GAG>AAG	p.E111K
Pat_41	Post-Resistance	BLID	414899	37	11	121986317	121986317	Missense_Mutation	SNP	G	A	15	127	c.314C>T	c.(313-315)GCT>GTT	p.A105V
Pat_41	Post-Resistance	UBASH3B	84959	37	11	122671960	122671960	Nonsense_Mutation	SNP	G	A	98	543	c.1515G>A	c.(1513-1515)TGG>TGA	p.W505*
Pat_41	Post-Resistance	UBASH3B	84959	37	11	122677152	122677152	Missense_Mutation	SNP	G	A	16	139	c.1630G>A	c.(1630-1632)GAA>AAA	p.E544K
Pat_41	Post-Resistance	HSPA8	3312	37	11	122931842	122931842	Missense_Mutation	SNP	G	A	9	154	c.191C>T	c.(190-192)ACC>ATC	p.T64I
Pat_41	Post-Resistance	GRAMD1B	57476	37	11	123465538	123465538	Missense_Mutation	SNP	G	A	17	112	c.436G>A	c.(436-438)GAA>AAA	p.E146K
Pat_41	Post-Resistance	OR6M1	390261	37	11	123676504	123676504	Missense_Mutation	SNP	G	A	12	60	c.554C>T	c.(553-555)GCC>GTC	p.A185V
Pat_41	Post-Resistance	OR10G4	390264	37	11	123886700	123886700	Missense_Mutation	SNP	G	A	49	462	c.419G>A	c.(418-420)TGT>TAT	p.C140Y
Pat_41	Post-Resistance	OR8D2	283160	37	11	124190047	124190047	Missense_Mutation	SNP	C	T	15	287	c.47G>A	c.(46-48)GGC>GAC	p.G16D
Pat_41	Post-Resistance	ROBO4	54538	37	11	124761435	124761435	Missense_Mutation	SNP	G	A	18	87	c.1708C>T	c.(1708-1710)CCC>TCC	p.P570S
Pat_41	Post-Resistance	PKNOX2	63876	37	11	125280141	125280141	Missense_Mutation	SNP	C	T	36	231	c.638C>T	c.(637-639)CCC>CTC	p.P213L
Pat_41	Post-Resistance	DCPS	28960	37	11	126208245	126208245	Missense_Mutation	SNP	C	T	22	148	c.587C>T	c.(586-588)CCC>CTC	p.P196L
Pat_41	Post-Resistance	KIRREL3	84623	37	11	126299174	126299174	Missense_Mutation	SNP	C	T	13	53	c.1706G>A	c.(1705-1707)GGT>GAT	p.G569D
Pat_41	Post-Resistance	FLI1	2313	37	11	128680431	128680431	Missense_Mutation	SNP	G	A	11	34	c.907G>A	c.(907-909)GAG>AAG	p.E303K
Pat_41	Post-Resistance	FLI1	2313	37	11	128680488	128680488	Missense_Mutation	SNP	G	A	5	53	c.964G>A	c.(964-966)GGC>AGC	p.G322S
Pat_41	Post-Resistance	KCNJ5	3762	37	11	128781857	128781857	Missense_Mutation	SNP	T	G	14	137	c.689T>G	c.(688-690)GTG>GGG	p.V230G
Pat_41	Post-Resistance	ARHGAP32	9743	37	11	128844534	128844534	Missense_Mutation	SNP	C	T	13	161	c.2516G>A	c.(2515-2517)GGT>GAT	p.G839D
Pat_41	Post-Resistance	TMEM45B	120224	37	11	129727230	129727230	Missense_Mutation	SNP	C	T	21	230	c.593C>T	c.(592-594)CCT>CTT	p.P198L
Pat_41	Post-Resistance	NFRKB	4798	37	11	129744763	129744763	Missense_Mutation	SNP	C	T	12	202	c.1903G>A	c.(1903-1905)GAT>AAT	p.D635N
Pat_41	Post-Resistance	NFRKB	4798	37	11	129754679	129754679	Missense_Mutation	SNP	C	T	6	125	c.703G>A	c.(703-705)GTG>ATG	p.V235M
Pat_41	Post-Resistance	APLP2	334	37	11	129990604	129990604	Missense_Mutation	SNP	G	A	4	86	c.407G>A	c.(406-408)GGT>GAT	p.G136D
Pat_41	Post-Resistance	SNX19	399979	37	11	130775944	130775944	Missense_Mutation	SNP	G	A	6	106	c.2347C>T	c.(2347-2349)CCA>TCA	p.P783S
Pat_41	Post-Resistance	JAM3	83700	37	11	134019041	134019041	Missense_Mutation	SNP	G	A	20	116	c.1033G>A	c.(1033-1035)GGC>AGC	p.G345S
Pat_41	Post-Resistance	THYN1	29087	37	11	134122734	134122734	Missense_Mutation	SNP	C	T	12	131	c.43G>A	c.(43-45)GAC>AAC	p.D15N
Pat_41	Post-Resistance	GLB1L2	89944	37	11	134239737	134239737	Missense_Mutation	SNP	G	A	7	179	c.1066G>A	c.(1066-1068)GCC>ACC	p.A356T
Pat_41	Post-Resistance	GLB1L2	89944	37	11	134240951	134240951	Missense_Mutation	SNP	G	A	14	189	c.1265G>A	c.(1264-1266)GGG>GAG	p.G422E
Pat_41	Post-Resistance	IQSEC3	440073	37	12	266719	266719	Missense_Mutation	SNP	G	A	42	303	c.1393G>A	c.(1393-1395)GAA>AAA	p.E465K
Pat_41	Post-Resistance	SLC6A12	6539	37	12	318973	318973	Nonsense_Mutation	SNP	C	T	19	349	c.180G>A	c.(178-180)TGG>TGA	p.W60*
Pat_41	Post-Resistance	KDM5A	5927	37	12	463271	463271	Missense_Mutation	SNP	C	T	10	202	c.1000G>A	c.(1000-1002)GAC>AAC	p.D334N
Pat_41	Post-Resistance	B4GALNT3	283358	37	12	665987	665987	Missense_Mutation	SNP	G	A	4	73	c.2335G>A	c.(2335-2337)GGT>AGT	p.G779S
Pat_41	Post-Resistance	WNK1	65125	37	12	988967	988967	Missense_Mutation	SNP	G	A	9	219	c.2602G>A	c.(2602-2604)GGC>AGC	p.G868S
Pat_41	Post-Resistance	WNK1	65125	37	12	992952	992952	Missense_Mutation	SNP	G	A	33	164	c.3676G>A	c.(3676-3678)GAG>AAG	p.E1226K
Pat_41	Post-Resistance	WNK1	65125	37	12	993365	993365	Missense_Mutation	SNP	G	A	22	379	c.3800G>A	c.(3799-3801)CGA>CAA	p.R1267Q
Pat_41	Post-Resistance	WNK1	65125	37	12	1005396	1005396	Missense_Mutation	SNP	C	T	28	44	c.5743C>T	c.(5743-5745)CCT>TCT	p.P1915S
Pat_41	Post-Resistance	ADIPOR2	79602	37	12	1889700	1889700	Missense_Mutation	SNP	G	A	9	173	c.547G>A	c.(547-549)GTC>ATC	p.V183I
Pat_41	Post-Resistance	LRTM2	654429	37	12	1940232	1940232	Missense_Mutation	SNP	C	T	7	226	c.199C>T	c.(199-201)CCC>TCC	p.P67S
Pat_41	Post-Resistance	FOXM1	2305	37	12	2983554	2983554	Missense_Mutation	SNP	C	T	13	140	c.91G>A	c.(91-93)GAA>AAA	p.E31K
Pat_41	Post-Resistance	TULP3	7289	37	12	3048509	3048509	Missense_Mutation	SNP	G	A	23	447	c.1228G>A	c.(1228-1230)GCA>ACA	p.A410T
Pat_41	Post-Resistance	C12orf4	57102	37	12	4634694	4634694	Nonsense_Mutation	SNP	G	A	26	363	c.562C>T	c.(562-564)CAA>TAA	p.Q188*
Pat_41	Post-Resistance	KCNA5	3741	37	12	5154839	5154839	Missense_Mutation	SNP	C	T	13	146	c.1526C>T	c.(1525-1527)GCC>GTC	p.A509V
Pat_41	Post-Resistance	ANO2	57101	37	12	5848527	5848527	Nonsense_Mutation	SNP	G	A	7	22	c.1378C>T	c.(1378-1380)CGA>TGA	p.R460*
Pat_41	Post-Resistance	VWF	7450	37	12	6204741	6204741	Missense_Mutation	SNP	G	A	5	151	c.542C>T	c.(541-543)ACC>ATC	p.T181I
Pat_41	Post-Resistance	CD9	928	37	12	6309670	6309670	Missense_Mutation	SNP	C	T	8	152	c.5C>T	c.(4-6)CCG>CTG	p.P2L
Pat_41	Post-Resistance	SCNN1A	6337	37	12	6472649	6472649	Missense_Mutation	SNP	G	A	4	66	c.644C>T	c.(643-645)CCC>CTC	p.P215L
Pat_41	Post-Resistance	LTBR	4055	37	12	6497621	6497621	Missense_Mutation	SNP	C	T	6	187	c.725C>T	c.(724-726)ACC>ATC	p.T242I

Pat_41	Post-Resistance	NCAPD2	9918	37	12	6639978	6639978	Missense_Mutation	SNP	C	T	13	135	c.3959C>T	c.(3958-3960)TCC>TTC	p.S1320F
Pat_41	Post-Resistance	CHD4	1108	37	12	6708980	6708980	Missense_Mutation	SNP	G	A	19	171	c.1441C>T	c.(1441-1443)CCA>TCA	p.P481S
Pat_41	Post-Resistance	CHD4	1108	37	12	6710674	6710674	Missense_Mutation	SNP	G	A	33	614	c.580C>T	c.(580-582)CCC>TCC	p.P194S
Pat_41	Post-Resistance	CHD4	1108	37	12	6710932	6710932	Missense_Mutation	SNP	C	T	16	292	c.439G>A	c.(439-441)GAG>AAG	p.E147K
Pat_41	Post-Resistance	LPAR5	57121	37	12	6729382	6729382	Missense_Mutation	SNP	C	T	5	30	c.1033G>A	c.(1033-1035)GAT>AAT	p.D345N
Pat_41	Post-Resistance	LPAR5	57121	37	12	6729589	6729589	Missense_Mutation	SNP	G	A	4	28	c.826C>T	c.(826-828)CGC>TGC	p.R276C
Pat_41	Post-Resistance	C12orf53	196500	37	12	6806564	6806564	Missense_Mutation	SNP	G	A	13	99	c.412C>T	c.(412-414)CTC>TTC	p.L138F
Pat_41	Post-Resistance	COPS7A	50813	37	12	6839618	6839618	Missense_Mutation	SNP	G	A	5	263	c.581G>A	c.(580-582)CGT>CAT	p.R194H
Pat_41	Post-Resistance	LAG3	3902	37	12	6882474	6882474	Missense_Mutation	SNP	G	A	8	123	c.175G>A	c.(175-177)GCA>ACA	p.A59T
Pat_41	Post-Resistance	GNB3	2784	37	12	6952852	6952852	Missense_Mutation	SNP	G	A	8	95	c.487G>A	c.(487-489)GAC>AAC	p.D163N
Pat_41	Post-Resistance	USP5	8078	37	12	6961416	6961416	Missense_Mutation	SNP	G	A	4	59	c.73G>A	c.(73-75)GTC>ATC	p.V25I
Pat_41	Post-Resistance	USP5	8078	37	12	6968699	6968699	Missense_Mutation	SNP	C	T	23	185	c.1124C>T	c.(1123-1125)ACC>ATC	p.T375I
Pat_41	Post-Resistance	USP5	8078	37	12	6971706	6971706	Nonsense_Mutation	SNP	G	A	14	199	c.1746G>A	c.(1744-1746)TGG>TGA	p.W582*
Pat_41	Post-Resistance	PTPN6	5777	37	12	7064827	7064827	Missense_Mutation	SNP	T	C	6	152	c.752T>C	c.(751-753)TTG>TCG	p.L251S
Pat_41	Post-Resistance	PHB2	11331	37	12	7076922	7076922	Missense_Mutation	SNP	C	T	53	178	c.628G>A	c.(628-630)GCC>ACC	p.A210T
Pat_41	Post-Resistance	C1R	715	37	12	7244047	7244047	Splice_Site	SNP	C	T	4	11	c.231_splice	c.e2+1	p.K77_splice
Pat_41	Post-Resistance	CD163L1	283316	37	12	7527238	7527238	Missense_Mutation	SNP	G	A	8	117	c.3209C>T	c.(3208-3210)GCC>GTC	p.A1070V
Pat_41	Post-Resistance	C3AR1	719	37	12	8212427	8212427	Missense_Mutation	SNP	C	T	14	245	c.355G>A	c.(355-357)GAT>AAT	p.D119N
Pat_41	Post-Resistance	A2ML1	144568	37	12	9009850	9009850	Missense_Mutation	SNP	C	T	26	258	c.2939C>T	c.(2938-2940)CCC>CTC	p.P980L
Pat_41	Post-Resistance	A2ML1	144568	37	12	9016534	9016534	Missense_Mutation	SNP	C	T	12	87	c.3647C>T	c.(3646-3648)GCG>GTG	p.A1216V
Pat_41	Post-Resistance	DDX12	440081	37	12	9572580	9572580	Missense_Mutation	SNP	C	T	9	48	c.2369G>A	c.(2368-2370)GGC>GAC	p.G790D
Pat_41	Post-Resistance	DDX12	440081	37	12	9572644	9572644	Missense_Mutation	SNP	C	T	7	63	c.2305G>A	c.(2305-2307)GCC>ACC	p.A769T
Pat_41	Post-Resistance	CLEC2D	29121	37	12	9822341	9822341	Missense_Mutation	SNP	G	A	22	224	c.11G>A	c.(10-12)AGT>AAT	p.S4N
Pat_41	Post-Resistance	KLRC3	3823	37	12	10588566	10588566	Missense_Mutation	SNP	G	A	22	392	c.20C>T	c.(19-21)ACC>ATC	p.T7I
Pat_41	Post-Resistance	STYK1	55359	37	12	10787209	10787209	Missense_Mutation	SNP	C	T	13	192	c.9G>A	c.(7-9)ATG>ATA	p.M3I
Pat_41	Post-Resistance	CSDA	8531	37	12	10853922	10853922	Missense_Mutation	SNP	G	A	13	152	c.1084C>T	c.(1084-1086)CCT>TCT	p.P362S
Pat_41	Post-Resistance	PRH1	5554	37	12	11036753	11036753	Missense_Mutation	SNP	C	T	4	91	c.64G>A	c.(64-66)GAT>AAT	p.D22N
Pat_41	Post-Resistance	TAS2R50	259296	37	12	11138991	11138991	Missense_Mutation	SNP	C	T	67	314	c.469G>A	c.(469-471)GAA>AAA	p.E157K
Pat_41	Post-Resistance	PRB3	5544	37	12	11420846	11420846	Missense_Mutation	SNP	G	A	12	258	c.337C>T	c.(337-339)CCC>TCC	p.P113S
Pat_41	Post-Resistance	PRB1	5542	37	12	11506618	11506618	Missense_Mutation	SNP	C	T	9	219	c.419G>A	c.(418-420)GGA>GAA	p.G140E
Pat_41	Post-Resistance	BCL2L14	79370	37	12	12240209	12240209	Missense_Mutation	SNP	C	T	49	174	c.496C>T	c.(496-498)CCA>TCA	p.P166S
Pat_41	Post-Resistance	LRP6	4040	37	12	12303821	12303821	Nonsense_Mutation	SNP	C	T	35	492	c.2943G>A	c.(2941-2943)TGG>TGA	p.W981*
Pat_41	Post-Resistance	LRP6	4040	37	12	12312002	12312002	Missense_Mutation	SNP	C	T	11	120	c.2552G>A	c.(2551-2553)AGC>AAC	p.S851N
Pat_41	Post-Resistance	LRP6	4040	37	12	12312776	12312776	Missense_Mutation	SNP	G	A	8	296	c.2402C>T	c.(2401-2403)GCT>GTT	p.A801V
Pat_41	Post-Resistance	MANSC1	54682	37	12	12491408	12491408	Missense_Mutation	SNP	C	T	38	252	c.310G>A	c.(310-312)GAA>AAA	p.E104K
Pat_41	Post-Resistance	GPR19	2842	37	12	12815333	12815333	Missense_Mutation	SNP	G	A	9	342	c.50C>T	c.(49-51)CCT>CTT	p.P17L
Pat_41	Post-Resistance	GRIN2B	2904	37	12	13906731	13906731	Missense_Mutation	SNP	G	T	12	174	c.530C>A	c.(529-531)CCT>CAT	p.P177H
Pat_41	Post-Resistance	ATF7IP	55729	37	12	14577424	14577424	Missense_Mutation	SNP	G	A	35	228	c.575G>A	c.(574-576)GGT>GAT	p.G192D
Pat_41	Post-Resistance	PLBD1	79887	37	12	14659170	14659170	Missense_Mutation	SNP	G	A	4	96	c.1405C>T	c.(1405-1407)CCC>TCC	p.P469S
Pat_41	Post-Resistance	AEBP2	121536	37	12	19646756	19646756	Missense_Mutation	SNP	C	T	13	88	c.1010C>T	c.(1009-1011)GCC>GTC	p.A337V
Pat_41	Post-Resistance	SLCO1C1	53919	37	12	20874932	20874932	Missense_Mutation	SNP	G	A	9	83	c.970G>A	c.(970-972)GAC>AAC	p.D324N
Pat_41	Post-Resistance	SLCO1A2	6579	37	12	21422693	21422693	Missense_Mutation	SNP	T	C	17	96	c.1802A>G	c.(1801-1803)TAC>TGC	p.Y601C
Pat_41	Post-Resistance	ABCC9	10060	37	12	21965085	21965085	Missense_Mutation	SNP	A	T	15	143	c.4109T>A	c.(4108-4110)ATT>AAT	p.I1370N
Pat_41	Post-Resistance	CMAS	55907	37	12	22218169	22218169	Missense_Mutation	SNP	G	A	20	260	c.1229G>A	c.(1228-1230)GGC>GAC	p.G410D
Pat_41	Post-Resistance	ST8SIA1	6489	37	12	22354896	22354896	Missense_Mutation	SNP	G	A	5	149	c.661C>T	c.(661-663)CCT>TCT	p.P221S
Pat_41	Post-Resistance	KIAA0528	9847	37	12	22622643	22622643	Missense_Mutation	SNP	C	T	8	144	c.2533G>A	c.(2533-2535)GCC>ACC	p.A845T
Pat_41	Post-Resistance	KIAA0528	9847	37	12	22688216	22688216	Nonsense_Mutation	SNP	C	T	32	185	c.153G>A	c.(151-153)TGG>TGA	p.W51*

Pat_41	Post-Resistance	LRMP	4033	37	12	25257380	25257380	Missense_Mutation	SNP	G	A	7	149	c.1132G>A	c.(1132-1134)GAA>AAA	p.E378K
Pat_41	Post-Resistance	CASC1	55259	37	12	25300020	25300020	Missense_Mutation	SNP	C	T	6	220	c.586G>A	c.(586-588)GAT>AAT	p.D196N
Pat_41	Post-Resistance	SSPN	8082	37	12	26383863	26383863	Missense_Mutation	SNP	C	T	28	394	c.586C>T	c.(586-588)CTC>TTC	p.L196F
Pat_41	Post-Resistance	SSPN	8082	37	12	26383956	26383956	Missense_Mutation	SNP	G	A	17	105	c.679G>A	c.(679-681)GGT>AGT	p.G227S
Pat_41	Post-Resistance	ITPR2	3709	37	12	26492338	26492338	Missense_Mutation	SNP	G	A	9	185	c.8098C>T	c.(8098-8100)CCA>TCA	p.P2700S
Pat_41	Post-Resistance	FAR2	55711	37	12	29462124	29462124	Nonsense_Mutation	SNP	G	A	33	346	c.729G>A	c.(727-729)TGG>TGA	p.W243*
Pat_41	Post-Resistance	ERGIC2	51290	37	12	29519860	29519860	Missense_Mutation	SNP	C	T	14	111	c.283G>A	c.(283-285)GAT>AAT	p.D95N
Pat_41	Post-Resistance	TMTC1	83857	37	12	29669397	29669397	Missense_Mutation	SNP	C	T	21	120	c.1868G>A	c.(1867-1869)GGT>GAT	p.G623D
Pat_41	Post-Resistance	DENND5B	160518	37	12	31551174	31551174	Missense_Mutation	SNP	G	A	4	50	c.3191C>T	c.(3190-3192)CCC>CTC	p.P1064L
Pat_41	Post-Resistance	DENND5B	160518	37	12	31632982	31632982	Missense_Mutation	SNP	C	T	10	134	c.445G>A	c.(445-447)GCT>ACT	p.A149T
Pat_41	Post-Resistance	CPNE8	144402	37	12	39047769	39047769	Missense_Mutation	SNP	G	A	18	82	c.1610C>T	c.(1609-1611)TCC>TTC	p.S537F
Pat_41	Post-Resistance	CPNE8	144402	37	12	39233743	39233743	Missense_Mutation	SNP	G	A	7	49	c.305C>T	c.(304-306)TCA>TTA	p.S102L
Pat_41	Post-Resistance	KIF21A	55605	37	12	39716617	39716617	Missense_Mutation	SNP	G	A	44	508	c.3524C>T	c.(3523-3525)ACT>ATT	p.T1175I
Pat_41	Post-Resistance	ABCD2	225	37	12	40012802	40012802	Missense_Mutation	SNP	G	A	8	255	c.616C>T	c.(616-618)CCT>TCT	p.P206S
Pat_41	Post-Resistance	PDZRN4	29951	37	12	41966971	41966971	Missense_Mutation	SNP	C	T	14	281	c.1793C>T	c.(1792-1794)ACC>ATC	p.T598I
Pat_41	Post-Resistance	PPHLN1	51535	37	12	42778756	42778756	Missense_Mutation	SNP	G	A	19	231	c.526G>A	c.(526-528)GGT>AGT	p.G176S
Pat_41	Post-Resistance	PPHLN1	51535	37	12	42836476	42836476	Missense_Mutation	SNP	C	T	33	686	c.1058C>T	c.(1057-1059)CCT>CTT	p.P353L
Pat_41	Post-Resistance	ADAMTS20	80070	37	12	43824267	43824267	Missense_Mutation	SNP	G	A	12	128	c.3269C>T	c.(3268-3270)ACC>ATC	p.T1090I
Pat_41	Post-Resistance	PUS7L	83448	37	12	44148787	44148787	Missense_Mutation	SNP	C	T	10	77	c.262G>A	c.(262-264)GTT>ATT	p.V88I
Pat_41	Post-Resistance	SFRS2IP	9169	37	12	46321186	46321186	Missense_Mutation	SNP	C	A	14	239	c.2298G>T	c.(2296-2298)AAG>AAT	p.K766N
Pat_41	Post-Resistance	SFRS2IP	9169	37	12	46345434	46345434	Missense_Mutation	SNP	T	C	141	161	c.296A>G	c.(295-297)AAG>AGG	p.K99R
Pat_41	Post-Resistance	SLC38A2	54407	37	12	46760858	46760858	Splice_Site	SNP	C	T	26	110	c.481_splice	c.e6+1	p.A161_splice
Pat_41	Post-Resistance	SLC38A2	54407	37	12	46764585	46764585	Missense_Mutation	SNP	C	T	6	93	c.172G>A	c.(172-174)GGG>AGG	p.G58R
Pat_41	Post-Resistance	AMIGO2	347902	37	12	47472676	47472676	Missense_Mutation	SNP	G	A	12	158	c.110C>T	c.(109-111)GCC>GTC	p.A37V
Pat_41	Post-Resistance	RPAP3	79657	37	12	48063889	48063889	Splice_Site	SNP	C	T	18	349	c.1526_splice	c.e13+1	p.Q509_splice
Pat_41	Post-Resistance	COL2A1	1280	37	12	48389081	48389081	Missense_Mutation	SNP	C	T	22	132	c.719G>A	c.(718-720)GGT>GAT	p.G240D
Pat_41	Post-Resistance	COL2A1	1280	37	12	48389699	48389699	Missense_Mutation	SNP	G	A	4	59	c.613C>T	c.(613-615)CCC>TCC	p.P205S
Pat_41	Post-Resistance	COL2A1	1280	37	12	48393815	48393815	Missense_Mutation	SNP	C	T	13	128	c.179G>A	c.(178-180)GGG>GAG	p.G60E
Pat_41	Post-Resistance	PFKM	5213	37	12	48529077	48529077	Missense_Mutation	SNP	G	A	16	133	c.847G>A	c.(847-849)GTG>ATG	p.V283M
Pat_41	Post-Resistance	ZNF641	121274	37	12	48736877	48736877	Missense_Mutation	SNP	G	A	12	278	c.1196C>T	c.(1195-1197)CCC>CTC	p.P399L
Pat_41	Post-Resistance	ZNF641	121274	37	12	48737394	48737394	Missense_Mutation	SNP	C	T	4	45	c.679G>A	c.(679-681)GAT>AAT	p.D227N
Pat_41	Post-Resistance	LALBA	3906	37	12	48963721	48963721	Missense_Mutation	SNP	G	A	4	65	c.83C>T	c.(82-84)TCC>TTC	p.S28F
Pat_41	Post-Resistance	CCNT1	904	37	12	49099637	49099637	Missense_Mutation	SNP	C	G	27	141	c.286G>C	c.(286-288)GAG>CAG	p.E96Q
Pat_41	Post-Resistance	ADCY6	112	37	12	49170302	49170302	Missense_Mutation	SNP	A	G	5	190	c.1444T>C	c.(1444-1446)TGC>CGC	p.C482R
Pat_41	Post-Resistance	CCDC65	85478	37	12	49312652	49312652	Missense_Mutation	SNP	C	T	11	105	c.992C>T	c.(991-993)GCC>GTC	p.A331V
Pat_41	Post-Resistance	PRKAG1	5571	37	12	49399244	49399244	Splice_Site	SNP	C	T	12	61	c.250_splice	c.e4+1	p.G84_splice
Pat_41	Post-Resistance	MLL2	8085	37	12	49431087	49431087	Missense_Mutation	SNP	G	A	4	46	c.10052C>T	c.(10051-10053)TCC>TTC	p.S3351F
Pat_41	Post-Resistance	RHEBL1	121268	37	12	49462827	49462827	Missense_Mutation	SNP	C	T	48	356	c.115G>A	c.(115-117)GTG>ATG	p.V39M
Pat_41	Post-Resistance	LMBR1L	55716	37	12	49496286	49496286	Missense_Mutation	SNP	G	A	15	235	c.734C>T	c.(733-735)GCC>GTC	p.A245V
Pat_41	Post-Resistance	TUBA1C	84790	37	12	49663372	49663372	Missense_Mutation	SNP	G	A	24	290	c.128G>A	c.(127-129)GGG>GAG	p.G43E
Pat_41	Post-Resistance	PRPH	5630	37	12	49690690	49690690	Missense_Mutation	SNP	G	A	3	26	c.721G>A	c.(721-723)GTG>ATG	p.V241M
Pat_41	Post-Resistance	TROAP	10024	37	12	49719410	49719410	Missense_Mutation	SNP	G	A	6	129	c.464G>A	c.(463-465)GGA>GAA	p.G155E
Pat_41	Post-Resistance	SPATS2	65244	37	12	49918587	49918587	Missense_Mutation	SNP	C	T	49	236	c.1234C>T	c.(1234-1236)CTT>TTT	p.L412F
Pat_41	Post-Resistance	FAM186B	84070	37	12	49994386	49994386	Missense_Mutation	SNP	G	A	7	110	c.1037C>T	c.(1036-1038)ACC>ATC	p.T346I
Pat_41	Post-Resistance	NCKAP5L	57701	37	12	50189167	50189167	Missense_Mutation	SNP	C	T	7	38	c.2476G>A	c.(2476-2478)GTG>ATG	p.V826M
Pat_41	Post-Resistance	AQP5	362	37	12	50356024	50356024	Missense_Mutation	SNP	C	T	4	34	c.224C>T	c.(223-225)GCC>GTC	p.A75V
Pat_41	Post-Resistance	AQP5	362	37	12	50357426	50357426	Missense_Mutation	SNP	G	A	6	115	c.515G>A	c.(514-516)GGC>GAC	p.G172D

Pat_41	Post-Resistance	RACGAP1	29127	37	12	50385802	50385802	Missense_Mutation	SNP	G	A	23	282	c.1693C>T	c.(1693-1695)CCA>TCA	p.P565S
Pat_41	Post-Resistance	ACCN2	41	37	12	50472758	50472758	Missense_Mutation	SNP	C	T	27	115	c.1046C>T	c.(1045-1047)GCT>GTT	p.A349V
Pat_41	Post-Resistance	LIMA1	51474	37	12	50571778	50571778	Missense_Mutation	SNP	C	T	9	151	c.1349G>A	c.(1348-1350)GGC>GAC	p.G450D
Pat_41	Post-Resistance	LIMA1	51474	37	12	50625483	50625483	Missense_Mutation	SNP	C	T	13	131	c.130G>A	c.(130-132)GCA>ACA	p.A44T
Pat_41	Post-Resistance	DIP2B	57609	37	12	51100366	51100366	Missense_Mutation	SNP	G	A	25	427	c.2452G>A	c.(2452-2454)GTT>ATT	p.V818I
Pat_41	Post-Resistance	ATF1	466	37	12	51189692	51189692	Missense_Mutation	SNP	G	A	4	53	c.94G>A	c.(94-96)GTA>ATA	p.V32I
Pat_41	Post-Resistance	SLC11A2	4891	37	12	51393137	51393137	Missense_Mutation	SNP	C	T	7	181	c.598G>A	c.(598-600)GAC>AAC	p.D200N
Pat_41	Post-Resistance	LETMD1	25875	37	12	51442260	51442260	Missense_Mutation	SNP	C	T	7	152	c.121C>T	c.(121-123)CGG>TGG	p.R41W
Pat_41	Post-Resistance	TFCP2	7024	37	12	51510112	51510112	Missense_Mutation	SNP	C	T	21	143	c.443G>A	c.(442-444)AGA>AAA	p.R148K
Pat_41	Post-Resistance	TFCP2	7024	37	12	51510129	51510129	Nonsense_Mutation	SNP	C	T	16	202	c.426G>A	c.(424-426)TGG>TGA	p.W142*
Pat_41	Post-Resistance	POU6F1	5463	37	12	51586239	51586239	Missense_Mutation	SNP	G	A	8	152	c.265C>T	c.(265-267)CCC>TCC	p.P89S
Pat_41	Post-Resistance	SCN8A	6334	37	12	52056803	52056803	Missense_Mutation	SNP	A	G	9	141	c.202A>G	c.(202-204)ATC>GTC	p.I68V
Pat_41	Post-Resistance	SCN8A	6334	37	12	52093499	52093499	Nonsense_Mutation	SNP	G	A	10	73	c.852G>A	c.(850-852)TGG>TGA	p.W284*
Pat_41	Post-Resistance	NR4A1	3164	37	12	52435692	52435692	Missense_Mutation	SNP	G	A	4	27	c.16G>A	c.(16-18)GCC>ACC	p.A6T
Pat_41	Post-Resistance	NR4A1	3164	37	12	52448711	52448711	Missense_Mutation	SNP	C	T	10	187	c.599C>T	c.(598-600)CCC>CTC	p.P200L
Pat_41	Post-Resistance	NR4A1	3164	37	12	52451006	52451006	Missense_Mutation	SNP	G	A	9	59	c.1324G>A	c.(1324-1326)GCC>ACC	p.A442T
Pat_41	Post-Resistance	KRT80	144501	37	12	52566100	52566100	Nonsense_Mutation	SNP	G	A	5	113	c.1060C>T	c.(1060-1062)CAG>TAG	p.Q354*
Pat_41	Post-Resistance	KRT81	3887	37	12	52681471	52681471	Missense_Mutation	SNP	C	T	10	63	c.935G>A	c.(934-936)GGG>GAG	p.G312E
Pat_41	Post-Resistance	KRT86	3892	37	12	52695765	52695765	Missense_Mutation	SNP	C	T	14	66	c.65C>T	c.(64-66)CCC>CTC	p.P22L
Pat_41	Post-Resistance	KRT83	3889	37	12	52712989	52712989	Missense_Mutation	SNP	C	T	27	416	c.544G>A	c.(544-546)GCC>ACC	p.A182T
Pat_41	Post-Resistance	KRT83	3889	37	12	52714836	52714836	Missense_Mutation	SNP	G	A	8	231	c.284C>T	c.(283-285)CCC>CTC	p.P95L
Pat_41	Post-Resistance	KRT84	3890	37	12	52776824	52776824	Missense_Mutation	SNP	C	T	17	301	c.781G>A	c.(781-783)GCC>ACC	p.A261T
Pat_41	Post-Resistance	KRT75	9119	37	12	52818464	52818464	Missense_Mutation	SNP	C	T	5	83	c.1493G>A	c.(1492-1494)GGG>GAG	p.G498E
Pat_41	Post-Resistance	KRT5	3852	37	12	52913627	52913627	Missense_Mutation	SNP	G	A	7	89	c.454C>T	c.(454-456)CCC>TCC	p.P152S
Pat_41	Post-Resistance	KRT72	140807	37	12	52986179	52986179	Splice_Site	SNP	C	T	6	67	c.798_splice	c.e4+1	p.G266_splice
Pat_41	Post-Resistance	KRT73	319101	37	12	53004580	53004580	Missense_Mutation	SNP	G	A	8	85	c.1150C>T	c.(1150-1152)CGG>TGG	p.R384W
Pat_41	Post-Resistance	TENC1	23371	37	12	53451359	53451359	Missense_Mutation	SNP	G	A	59	514	c.854G>A	c.(853-855)AGC>AAC	p.S285N
Pat_41	Post-Resistance	TENC1	23371	37	12	53454959	53454959	Missense_Mutation	SNP	G	A	15	184	c.3269G>A	c.(3268-3270)GGC>GAC	p.G1090D
Pat_41	Post-Resistance	ESPL1	9700	37	12	53666582	53666582	Missense_Mutation	SNP	C	T	6	91	c.1447C>T	c.(1447-1449)CTC>TTC	p.L483F
Pat_41	Post-Resistance	ESPL1	9700	37	12	53680497	53680497	Missense_Mutation	SNP	C	T	6	26	c.3977C>T	c.(3976-3978)GCT>GTT	p.A1326V
Pat_41	Post-Resistance	SP1	6667	37	12	53776440	53776440	Missense_Mutation	SNP	C	T	14	142	c.709C>T	c.(709-711)CCC>TCC	p.P237S
Pat_41	Post-Resistance	MAP3K12	7786	37	12	53876945	53876945	Missense_Mutation	SNP	G	A	5	106	c.1543C>T	c.(1543-1545)CTC>TTC	p.L515F
Pat_41	Post-Resistance	ATF7	11016	37	12	53911103	53911103	Missense_Mutation	SNP	G	A	3	23	c.1303C>T	c.(1303-1305)CCA>TCA	p.P435S
Pat_41	Post-Resistance	ATF7	11016	37	12	53926943	53926943	Splice_Site	SNP	C	T	4	68	c.693_splice	c.e6+1	p.S231_splice
Pat_41	Post-Resistance	HNRNPA1	3178	37	12	54677677	54677677	Missense_Mutation	SNP	G	A	17	232	c.989G>A	c.(988-990)GGA>GAA	p.G330E
Pat_41	Post-Resistance	ZNF385A	25946	37	12	54767846	54767846	Missense_Mutation	SNP	C	T	10	50	c.272G>A	c.(271-273)AGA>AAA	p.R91K
Pat_41	Post-Resistance	ITGA5	3678	37	12	54793695	54793695	Missense_Mutation	SNP	G	A	12	157	c.2680C>T	c.(2680-2682)CGG>TGG	p.R894W
Pat_41	Post-Resistance	ITGA5	3678	37	12	54797521	54797521	Missense_Mutation	SNP	C	T	6	72	c.1664G>A	c.(1663-1665)GGA>GAA	p.G555E
Pat_41	Post-Resistance	OR6C1	390321	37	12	55714592	55714592	Missense_Mutation	SNP	C	T	28	34	c.209C>T	c.(208-210)TCG>TTG	p.S70L
Pat_41	Post-Resistance	OR6C3	254786	37	12	55725953	55725953	Missense_Mutation	SNP	C	T	32	366	c.469C>T	c.(469-471)CTT>TTT	p.L157F
Pat_41	Post-Resistance	OR6C3	254786	37	12	55726266	55726266	Missense_Mutation	SNP	C	T	6	41	c.782C>T	c.(781-783)GCA>GTA	p.A261V
Pat_41	Post-Resistance	OR6C65	403282	37	12	55794818	55794818	Missense_Mutation	SNP	C	T	28	435	c.506C>T	c.(505-507)TCC>TTC	p.S169F
Pat_41	Post-Resistance	OR10P1	121130	37	12	56030910	56030910	Missense_Mutation	SNP	C	T	11	113	c.235C>T	c.(235-237)CCC>TCC	p.P79S
Pat_41	Post-Resistance	DNAJC14	85406	37	12	56216410	56216410	Missense_Mutation	SNP	C	T	15	270	c.1741G>A	c.(1741-1743)GGC>AGC	p.G581S
Pat_41	Post-Resistance	SUOX	6821	37	12	56398807	56398807	Missense_Mutation	SNP	C	T	22	182	c.1634C>T	c.(1633-1635)CCA>CTA	p.P545L
Pat_41	Post-Resistance	ESYT1	23344	37	12	56522413	56522413	Missense_Mutation	SNP	G	A	7	29	c.310G>A	c.(310-312)GCA>ACA	p.A104T
Pat_41	Post-Resistance	ESYT1	23344	37	12	56526022	56526022	Missense_Mutation	SNP	C	T	43	551	c.890C>T	c.(889-891)TCC>TTC	p.S297F

Pat_41	Post-Resistance	SMARCC2	6601	37	12	56572780	56572780	Splice_Site	SNP	C	T	9	77	c.1141_splice	c.e12+1	p.D381_splice
Pat_41	Post-Resistance	SLC39A5	283375	37	12	56629058	56629058	Missense_Mutation	SNP	C	T	15	84	c.752C>T	c.(751-753)GCC>GTC	p.A251V
Pat_41	Post-Resistance	ANKRD52	283373	37	12	56648691	56648691	Missense_Mutation	SNP	C	T	15	168	c.508G>A	c.(508-510)GAC>AAC	p.D170N
Pat_41	Post-Resistance	PAN2	9924	37	12	56721357	56721357	Missense_Mutation	SNP	C	T	13	158	c.710G>A	c.(709-711)GGA>GAA	p.G237E
Pat_41	Post-Resistance	GLS2	27165	37	12	56872924	56872924	Missense_Mutation	SNP	C	T	4	116	c.446G>A	c.(445-447)CGA>CAA	p.R149Q
Pat_41	Post-Resistance	BAZ2A	11176	37	12	56996577	56996577	Missense_Mutation	SNP	C	T	5	63	c.3350G>A	c.(3349-3351)GGT>GAT	p.G1117D
Pat_41	Post-Resistance	ATP5B	506	37	12	57036294	57036294	Missense_Mutation	SNP	G	A	24	151	c.1022C>T	c.(1021-1023)ACT>ATT	p.T341I
Pat_41	Post-Resistance	STAT6	6778	37	12	57496686	57496686	Missense_Mutation	SNP	C	T	19	100	c.1231G>A	c.(1231-1233)GTG>ATG	p.V411M
Pat_41	Post-Resistance	LRP1	4035	37	12	57574222	57574222	Missense_Mutation	SNP	G	A	13	130	c.5346G>A	c.(5344-5346)ATG>ATA	p.M1782I
Pat_41	Post-Resistance	LRP1	4035	37	12	57593076	57593076	Missense_Mutation	SNP	C	T	45	313	c.9758C>T	c.(9757-9759)TCC>TTC	p.S3253F
Pat_41	Post-Resistance	LRP1	4035	37	12	57594589	57594589	Missense_Mutation	SNP	G	A	26	170	c.10216G>A	c.(10216-10218)GCC>ACC	p.A3406T
Pat_41	Post-Resistance	SHMT2	6472	37	12	57626991	57626991	Missense_Mutation	SNP	G	A	6	91	c.886G>A	c.(886-888)GTG>ATG	p.V296M
Pat_41	Post-Resistance	GLI1	2735	37	12	57861780	57861780	Missense_Mutation	SNP	C	T	6	48	c.1081C>T	c.(1081-1083)CCG>TCG	p.P361S
Pat_41	Post-Resistance	KIF5A	3798	37	12	57944134	57944134	Missense_Mutation	SNP	G	A	9	130	c.80G>A	c.(79-81)GGA>GAA	p.G27E
Pat_41	Post-Resistance	DTX3	196403	37	12	58002510	58002510	Missense_Mutation	SNP	G	A	5	79	c.958G>A	c.(958-960)GGA>AGA	p.G320R
Pat_41	Post-Resistance	AGAP2	116986	37	12	58129185	58129185	Nonsense_Mutation	SNP	C	T	11	62	c.1194G>A	c.(1192-1194)TGG>TGA	p.W398*
Pat_41	Post-Resistance	TSPAN31	6302	37	12	58139615	58139615	Missense_Mutation	SNP	G	A	49	191	c.151G>A	c.(151-153)GCT>ACT	p.A51T
Pat_41	Post-Resistance	CDK4	1019	37	12	58144505	58144505	Missense_Mutation	SNP	G	A	10	264	c.566C>T	c.(565-567)TCC>TTC	p.S189F
Pat_41	Post-Resistance	9-Mar	92979	37	12	58151912	58151912	Missense_Mutation	SNP	G	A	25	126	c.535G>A	c.(535-537)GTC>ATC	p.V179I
Pat_41	Post-Resistance	XRCC6BP1	91419	37	12	58350489	58350489	Missense_Mutation	SNP	C	T	6	145	c.557C>T	c.(556-558)GCC>GTC	p.A186V
Pat_41	Post-Resistance	LRIG3	121227	37	12	59274444	59274444	Missense_Mutation	SNP	C	T	18	151	c.1720G>A	c.(1720-1722)GCC>ACC	p.A574T
Pat_41	Post-Resistance	SLC16A7	9194	37	12	60098595	60098595	Missense_Mutation	SNP	C	T	4	39	c.13C>T	c.(13-15)CCA>TCA	p.P5S
Pat_41	Post-Resistance	USP15	9958	37	12	62777862	62777862	Missense_Mutation	SNP	G	A	7	129	c.1252G>A	c.(1252-1254)GTT>ATT	p.V418I
Pat_41	Post-Resistance	USP15	9958	37	12	62783460	62783460	Missense_Mutation	SNP	G	A	7	384	c.1633G>A	c.(1633-1635)GAA>AAA	p.E545K
Pat_41	Post-Resistance	MON2	23041	37	12	62946851	62946851	Missense_Mutation	SNP	C	T	27	325	c.3107C>T	c.(3106-3108)CCC>CTC	p.P1036L
Pat_41	Post-Resistance	PPM1H	57460	37	12	63114045	63114045	Missense_Mutation	SNP	C	T	24	126	c.979G>A	c.(979-981)GGA>AGA	p.G327R
Pat_41	Post-Resistance	PPM1H	57460	37	12	63195703	63195703	Missense_Mutation	SNP	C	T	6	55	c.649G>A	c.(649-651)GGG>AGG	p.G217R
Pat_41	Post-Resistance	SRGAP1	57522	37	12	64472840	64472840	Missense_Mutation	SNP	C	T	20	212	c.1267C>T	c.(1267-1269)CCC>TCC	p.P423S
Pat_41	Post-Resistance	TBK1	29110	37	12	64858132	64858132	Missense_Mutation	SNP	G	A	8	91	c.247G>A	c.(247-249)GTA>ATA	p.V83I
Pat_41	Post-Resistance	TBK1	29110	37	12	64875671	64875671	Missense_Mutation	SNP	G	A	17	215	c.862G>A	c.(862-864)GAT>AAT	p.D288N
Pat_41	Post-Resistance	LEMD3	23592	37	12	65609824	65609824	Splice_Site	SNP	G	A	16	141	c.1627_splice	c.e3+1	p.G543_splice
Pat_41	Post-Resistance	LEMD3	23592	37	12	65639671	65639671	Missense_Mutation	SNP	G	A	7	253	c.2524G>A	c.(2524-2526)GAA>AAA	p.E842K
Pat_41	Post-Resistance	MSRB3	253827	37	12	65857031	65857031	Missense_Mutation	SNP	G	A	15	124	c.508G>A	c.(508-510)GAT>AAT	p.D170N
Pat_41	Post-Resistance	TMBIM4	51643	37	12	66546107	66546107	Missense_Mutation	SNP	C	T	13	200	c.256G>A	c.(256-258)GCG>ACG	p.A86T
Pat_41	Post-Resistance	GRIP1	23426	37	12	66773093	66773093	Missense_Mutation	SNP	C	T	36	487	c.2432G>A	c.(2431-2433)AGT>AAT	p.S811N
Pat_41	Post-Resistance	CAND1	55832	37	12	67698469	67698469	Missense_Mutation	SNP	G	A	7	80	c.1378G>A	c.(1378-1380)GAG>AAG	p.E460K
Pat_41	Post-Resistance	CAND1	55832	37	12	67705555	67705555	Missense_Mutation	SNP	C	T	70	317	c.3443C>T	c.(3442-3444)CCA>CTA	p.P1148L
Pat_41	Post-Resistance	DYRK2	8445	37	12	68050997	68050997	Missense_Mutation	SNP	C	T	21	178	c.310C>T	c.(310-312)CTC>TTC	p.L104F
Pat_41	Post-Resistance	NUP107	57122	37	12	69128526	69128526	Missense_Mutation	SNP	G	A	8	90	c.2301G>A	c.(2299-2301)ATG>ATA	p.M767I
Pat_41	Post-Resistance	LYZ	4069	37	12	69746066	69746066	Missense_Mutation	SNP	G	A	22	231	c.368G>A	c.(367-369)GGC>GAC	p.G123D
Pat_41	Post-Resistance	RAB3IP	117177	37	12	70189072	70189072	Missense_Mutation	SNP	G	A	4	76	c.884G>A	c.(883-885)GGC>GAC	p.G295D
Pat_41	Post-Resistance	CNOT2	4848	37	12	70724165	70724165	Missense_Mutation	SNP	G	A	7	290	c.485G>A	c.(484-486)GGG>GAG	p.G162E
Pat_41	Post-Resistance	PTPRR	5801	37	12	71139697	71139697	Missense_Mutation	SNP	A	G	6	90	c.908T>C	c.(907-909)GTG>GCG	p.V303A
Pat_41	Post-Resistance	TPH2	121278	37	12	72372795	72372795	Missense_Mutation	SNP	G	A	30	326	c.869G>A	c.(868-870)GGA>GAA	p.G290E
Pat_41	Post-Resistance	TRHDE	29953	37	12	72771880	72771880	Missense_Mutation	SNP	C	T	32	165	c.1159C>T	c.(1159-1161)CCC>TCC	p.P387S
Pat_41	Post-Resistance	PHLDA1	22822	37	12	76424788	76424788	Missense_Mutation	SNP	C	T	18	138	c.734G>A	c.(733-735)CGC>CAC	p.R245H
Pat_41	Post-Resistance	BBS10	79738	37	12	76740260	76740260	Missense_Mutation	SNP	G	A	8	321	c.1505C>T	c.(1504-1506)ACA>ATA	p.T502I

Pat_41	Post-Resistance	ZDHHC17	23390	37	12	77220718	77220718	Missense_Mutation	SNP	C	T	22	125	c.928C>T	c.(928-930)CCT>TCT	p.P310S
Pat_41	Post-Resistance	NAV3	89795	37	12	78571464	78571464	Missense_Mutation	SNP	C	T	6	131	c.5362C>T	c.(5362-5364)CGG>TGG	p.R1788W
Pat_41	Post-Resistance	PPP1R12A	4659	37	12	80199528	80199528	Missense_Mutation	SNP	G	A	4	55	c.1844C>T	c.(1843-1845)GCT>GTT	p.A615V
Pat_41	Post-Resistance	PPFIA2	8499	37	12	81688815	81688815	Splice_Site	SNP	C	T	12	87	c.2725_splice	c.e24-1	p.L909_splice
Pat_41	Post-Resistance	C12orf26	84190	37	12	82780698	82780698	Missense_Mutation	SNP	T	A	153	177	c.376T>A	c.(376-378)TTT>ATT	p.F126I
Pat_41	Post-Resistance	RASSF9	9182	37	12	86199624	86199624	Missense_Mutation	SNP	G	A	13	205	c.164C>T	c.(163-165)GCT>GTT	p.A55V
Pat_41	Post-Resistance	GALNT4	8693	37	12	89917699	89917699	Missense_Mutation	SNP	C	T	55	224	c.628G>A	c.(628-630)GCC>ACC	p.A210T
Pat_41	Post-Resistance	ATP2B1	490	37	12	89995107	89995107	Missense_Mutation	SNP	C	T	18	245	c.3164G>A	c.(3163-3165)GGC>GAC	p.G1055D
Pat_41	Post-Resistance	ATP2B1	490	37	12	90010785	90010785	Missense_Mutation	SNP	C	T	5	138	c.1861G>A	c.(1861-1863)GCA>ACA	p.A621T
Pat_41	Post-Resistance	ATP2B1	490	37	12	90024380	90024380	Missense_Mutation	SNP	G	A	11	178	c.830C>T	c.(829-831)GCT>GTT	p.A277V
Pat_41	Post-Resistance	ATP2B1	490	37	12	90028936	90028936	Missense_Mutation	SNP	C	T	26	346	c.499G>A	c.(499-501)GTG>ATG	p.V167M
Pat_41	Post-Resistance	KERA	11081	37	12	91449398	91449398	Missense_Mutation	SNP	C	T	16	166	c.661G>A	c.(661-663)GAC>AAC	p.D221N
Pat_41	Post-Resistance	DCN	1634	37	12	91546915	91546915	Missense_Mutation	SNP	C	T	16	270	c.704G>A	c.(703-705)AGA>AAA	p.R235K
Pat_41	Post-Resistance	EEA1	8411	37	12	93171859	93171859	Missense_Mutation	SNP	C	T	36	403	c.3751G>A	c.(3751-3753)GGC>AGC	p.G1251S
Pat_41	Post-Resistance	NUDT4	11163	37	12	93789271	93789271	Missense_Mutation	SNP	G	A	7	115	c.217G>A	c.(217-219)GTC>ATC	p.V73I
Pat_41	Post-Resistance	PLXNC1	10154	37	12	94543726	94543726	Missense_Mutation	SNP	G	A	3	4	c.979G>A	c.(979-981)GCG>ACG	p.A327T
Pat_41	Post-Resistance	PLXNC1	10154	37	12	94603365	94603365	Splice_Site	SNP	G	A	8	298	c.1440_splice	c.e5-1	p.R480_splice
Pat_41	Post-Resistance	LTA4H	4048	37	12	96397692	96397692	Missense_Mutation	SNP	G	A	8	92	c.1537C>T	c.(1537-1539)CTT>TTT	p.L513F
Pat_41	Post-Resistance	ELK3	2004	37	12	96617354	96617354	Missense_Mutation	SNP	G	A	15	221	c.10G>A	c.(10-12)GCA>ACA	p.A4T
Pat_41	Post-Resistance	TMPO	7112	37	12	98921775	98921775	Missense_Mutation	SNP	C	T	17	201	c.391C>T	c.(391-393)CCT>TCT	p.P131S
Pat_41	Post-Resistance	APAF1	317	37	12	99071301	99071301	Missense_Mutation	SNP	C	T	12	192	c.1892C>T	c.(1891-1893)GCT>GTT	p.A631V
Pat_41	Post-Resistance	ANKS1B	56899	37	12	100377906	100377906	Missense_Mutation	SNP	G	A	14	142	c.110C>T	c.(109-111)CCC>CTC	p.P37L
Pat_41	Post-Resistance	UHRF1BP1L	23074	37	12	100491142	100491142	Splice_Site	SNP	C	T	4	85	c.669_splice	c.e6+1	p.R223_splice
Pat_41	Post-Resistance	UTP20	27340	37	12	101764222	101764222	Missense_Mutation	SNP	C	T	23	243	c.6568C>T	c.(6568-6570)CTT>TTT	p.L2190F
Pat_41	Post-Resistance	MYBPC1	4604	37	12	102054971	102054971	Missense_Mutation	SNP	G	A	9	78	c.1888G>A	c.(1888-1890)GAG>AAG	p.E630K
Pat_41	Post-Resistance	GNPTAB	79158	37	12	102158533	102158533	Missense_Mutation	SNP	C	T	18	123	c.2162G>A	c.(2161-2163)GGA>GAA	p.G721E
Pat_41	Post-Resistance	GNPTAB	79158	37	12	102158638	102158638	Missense_Mutation	SNP	G	A	4	31	c.2057C>T	c.(2056-2058)ACA>ATA	p.T686I
Pat_41	Post-Resistance	CCDC53	51019	37	12	102433677	102433677	Missense_Mutation	SNP	C	T	34	472	c.404G>A	c.(403-405)AGA>AAA	p.R135K
Pat_41	Post-Resistance	C12orf48	55010	37	12	102572470	102572470	Missense_Mutation	SNP	C	T	16	62	c.1106C>T	c.(1105-1107)ACC>ATC	p.T369I
Pat_41	Post-Resistance	IGF1	3479	37	12	102813330	102813330	Missense_Mutation	SNP	G	A	14	178	c.359C>T	c.(358-360)TCT>TTT	p.S120F
Pat_41	Post-Resistance	STAB2	55576	37	12	104138951	104138951	Missense_Mutation	SNP	C	T	14	114	c.6032C>T	c.(6031-6033)CCC>CTC	p.P2011L
Pat_41	Post-Resistance	HSP90B1	7184	37	12	104336961	104336961	Missense_Mutation	SNP	G	A	7	88	c.1754G>A	c.(1753-1755)GGG>GAG	p.G585E
Pat_41	Post-Resistance	TDG	6996	37	12	104373816	104373816	Missense_Mutation	SNP	C	T	6	83	c.374C>T	c.(373-375)CCC>CTC	p.P125L
Pat_41	Post-Resistance	KIAA1033	23325	37	12	105512246	105512246	Missense_Mutation	SNP	G	A	45	226	c.458G>A	c.(457-459)AGG>AAG	p.R153K
Pat_41	Post-Resistance	NUAK1	9891	37	12	106532346	106532346	Missense_Mutation	SNP	C	T	3	21	c.86G>A	c.(85-87)GGG>GAG	p.G29E
Pat_41	Post-Resistance	CKAP4	10970	37	12	106633769	106633769	Missense_Mutation	SNP	C	T	12	212	c.842G>A	c.(841-843)GGG>GAG	p.G281E
Pat_41	Post-Resistance	TCP11L2	255394	37	12	106740111	106740111	Missense_Mutation	SNP	C	T	3	38	c.1363C>T	c.(1363-1365)CCT>TCT	p.P455S
Pat_41	Post-Resistance	POLR3B	55703	37	12	106889833	106889833	Missense_Mutation	SNP	G	A	8	546	c.2714G>A	c.(2713-2715)GGT>GAT	p.G905D
Pat_41	Post-Resistance	RFX4	5992	37	12	107126012	107126012	Missense_Mutation	SNP	G	A	10	212	c.1456G>A	c.(1456-1458)GGA>AGA	p.G486R
Pat_41	Post-Resistance	RFX4	5992	37	12	107141349	107141349	Missense_Mutation	SNP	C	T	12	195	c.1768C>T	c.(1768-1770)CCA>TCA	p.P590S
Pat_41	Post-Resistance	SART3	9733	37	12	108932789	108932789	Missense_Mutation	SNP	C	T	5	238	c.983G>A	c.(982-984)CGC>CAC	p.R328H
Pat_41	Post-Resistance	ISCU	23479	37	12	108959182	108959182	Missense_Mutation	SNP	C	T	16	165	c.314C>T	c.(313-315)GCC>GTC	p.A105V
Pat_41	Post-Resistance	USP30	84749	37	12	109523716	109523716	Missense_Mutation	SNP	G	A	4	42	c.1534G>A	c.(1534-1536)GAG>AAG	p.E512K
Pat_41	Post-Resistance	ACACB	32	37	12	109677720	109677720	Missense_Mutation	SNP	C	T	11	182	c.4748C>T	c.(4747-4749)ACC>ATC	p.T1583I
Pat_41	Post-Resistance	TCHP	84260	37	12	110352355	110352355	Missense_Mutation	SNP	G	A	11	40	c.1243G>A	c.(1243-1245)GTG>ATG	p.V415M
Pat_41	Post-Resistance	ANAPC7	51434	37	12	110826391	110826391	Missense_Mutation	SNP	C	T	16	167	c.548G>A	c.(547-549)GGT>GAT	p.G183D
Pat_41	Post-Resistance	RAD9B	144715	37	12	110957645	110957645	Missense_Mutation	SNP	A	G	6	71	c.814A>G	c.(814-816)ATT>GTT	p.I272V

Pat_41	Post-Resistance	ACAD10	80724	37	12	112187060	112187060	Missense_Mutation	SNP	G	A	21	77	c.2728G>A	c.(2728-2730)GCC>ACC	p.A910T
Pat_41	Post-Resistance	ALDH2	217	37	12	112236000	112236000	Missense_Mutation	SNP	C	T	18	146	c.1202C>T	c.(1201-1203)ACT>ATT	p.T401I
Pat_41	Post-Resistance	TRAFD1	10906	37	12	112589871	112589871	Missense_Mutation	SNP	C	T	20	329	c.1546C>T	c.(1546-1548)CCT>TCT	p.P516S
Pat_41	Post-Resistance	TPCN1	53373	37	12	113724826	113724826	Missense_Mutation	SNP	G	A	7	165	c.1561G>A	c.(1561-1563)GGA>AGA	p.G521R
Pat_41	Post-Resistance	TPCN1	53373	37	12	113733789	113733789	Missense_Mutation	SNP	G	A	5	14	c.2359G>A	c.(2359-2361)GAG>AAG	p.E787K
Pat_41	Post-Resistance	SLC24A6	80024	37	12	113748104	113748104	Missense_Mutation	SNP	C	T	13	160	c.1192G>A	c.(1192-1194)GGC>AGC	p.G398S
Pat_41	Post-Resistance	RBM19	9904	37	12	114390340	114390340	Missense_Mutation	SNP	C	T	31	146	c.977G>A	c.(976-978)AGA>AAA	p.R326K
Pat_41	Post-Resistance	MED13L	23389	37	12	116424196	116424196	Missense_Mutation	SNP	C	T	13	85	c.4213G>A	c.(4213-4215)GAG>AAG	p.E1405K
Pat_41	Post-Resistance	FBXW8	26259	37	12	117426562	117426562	Missense_Mutation	SNP	C	T	21	327	c.1127C>T	c.(1126-1128)TCC>TTC	p.S376F
Pat_41	Post-Resistance	TESC	54997	37	12	117494657	117494657	Missense_Mutation	SNP	G	A	10	205	c.322C>T	c.(322-324)CTC>TTC	p.L108F
Pat_41	Post-Resistance	FBXO21	23014	37	12	117604702	117604702	Splice_Site	SNP	C	T	12	189	c.1193_splice	c.e8+1	p.R398_splice
Pat_41	Post-Resistance	NOS1	4842	37	12	117672499	117672499	Missense_Mutation	SNP	C	T	4	40	c.3106G>A	c.(3106-3108)GAC>AAC	p.D1036N
Pat_41	Post-Resistance	WSB2	55884	37	12	118474207	118474207	Missense_Mutation	SNP	C	T	42	236	c.769G>A	c.(769-771)GCT>ACT	p.A257T
Pat_41	Post-Resistance	CCDC60	160777	37	12	119909831	119909831	Missense_Mutation	SNP	G	A	4	119	c.203G>A	c.(202-204)GGA>GAA	p.G68E
Pat_41	Post-Resistance	CCDC64	92558	37	12	120499613	120499613	Missense_Mutation	SNP	G	A	9	49	c.745G>A	c.(745-747)GAG>AAG	p.E249K
Pat_41	Post-Resistance	GCN1L1	10985	37	12	120580442	120580442	Missense_Mutation	SNP	C	T	5	109	c.5698G>A	c.(5698-5700)GTG>ATG	p.V1900M
Pat_41	Post-Resistance	GCN1L1	10985	37	12	120580635	120580635	Missense_Mutation	SNP	G	A	32	148	c.5606C>T	c.(5605-5607)TCC>TTC	p.S1869F
Pat_41	Post-Resistance	GCN1L1	10985	37	12	120582137	120582137	Missense_Mutation	SNP	C	T	13	114	c.5468G>A	c.(5467-5469)GGC>GAC	p.G1823D
Pat_41	Post-Resistance	GCN1L1	10985	37	12	120597757	120597757	Missense_Mutation	SNP	G	A	12	117	c.2621C>T	c.(2620-2622)ACC>ATC	p.T874I
Pat_41	Post-Resistance	GCN1L1	10985	37	12	120599745	120599745	Missense_Mutation	SNP	C	T	12	94	c.2281G>A	c.(2281-2283)GAG>AAG	p.E761K
Pat_41	Post-Resistance	RNF10	9921	37	12	120995259	120995259	Missense_Mutation	SNP	G	A	7	203	c.820G>A	c.(820-822)GAT>AAT	p.D274N
Pat_41	Post-Resistance	POP5	51367	37	12	121017705	121017705	Missense_Mutation	SNP	G	A	13	127	c.185C>T	c.(184-186)ACT>ATT	p.T62I
Pat_41	Post-Resistance	ACADS	35	37	12	121177223	121177223	Missense_Mutation	SNP	G	A	4	37	c.1211G>A	c.(1210-1212)GGG>GAG	p.G404E
Pat_41	Post-Resistance	OASL	8638	37	12	121458612	121458612	Missense_Mutation	SNP	C	T	40	52	c.1297G>A	c.(1297-1299)GAG>AAG	p.E433K
Pat_41	Post-Resistance	P2RX7	5027	37	12	121603916	121603916	Missense_Mutation	SNP	C	T	35	384	c.670C>T	c.(670-672)CCA>TCA	p.P224S
Pat_41	Post-Resistance	CAMKK2	10645	37	12	121691153	121691153	Missense_Mutation	SNP	G	A	12	110	c.1030C>T	c.(1030-1032)CTC>TTC	p.L344F
Pat_41	Post-Resistance	CAMKK2	10645	37	12	121712148	121712148	Missense_Mutation	SNP	C	T	19	69	c.182G>A	c.(181-183)GGC>GAC	p.G61D
Pat_41	Post-Resistance	ANAPC5	51433	37	12	121783808	121783808	Missense_Mutation	SNP	C	T	11	78	c.424G>A	c.(424-426)GCC>ACC	p.A142T
Pat_41	Post-Resistance	KDM2B	84678	37	12	121881913	121881913	Missense_Mutation	SNP	C	T	8	136	c.2353G>A	c.(2353-2355)GTG>ATG	p.V785M
Pat_41	Post-Resistance	HPD	3242	37	12	122287697	122287697	Splice_Site	SNP	C	T	5	53	c.415_splice	c.e8-1	p.Y139_splice
Pat_41	Post-Resistance	HPD	3242	37	12	122294229	122294229	Splice_Site	SNP	C	T	10	157	c.324_splice	c.e6+1	p.Q108_splice
Pat_41	Post-Resistance	PSMD9	5715	37	12	122326772	122326772	Missense_Mutation	SNP	G	A	4	4	c.10G>A	c.(10-12)GAG>AAG	p.E4K
Pat_41	Post-Resistance	VPS33A	65082	37	12	122727031	122727031	Missense_Mutation	SNP	C	T	5	102	c.994G>A	c.(994-996)GGG>AGG	p.G332R
Pat_41	Post-Resistance	ZCCHC8	55596	37	12	122958637	122958637	Missense_Mutation	SNP	C	T	8	62	c.1531G>A	c.(1531-1533)GAT>AAT	p.D511N
Pat_41	Post-Resistance	ABCB9	23457	37	12	123444595	123444595	Missense_Mutation	SNP	C	T	10	104	c.188G>A	c.(187-189)GGA>GAA	p.G63E
Pat_41	Post-Resistance	SBNO1	55206	37	12	123810879	123810879	Nonsense_Mutation	SNP	C	T	32	198	c.1695G>A	c.(1693-1695)TGG>TGA	p.W565*
Pat_41	Post-Resistance	EIF2B1	1967	37	12	124111643	124111643	Missense_Mutation	SNP	C	T	37	286	c.430G>A	c.(430-432)GCC>ACC	p.A144T
Pat_41	Post-Resistance	DNAH10	196385	37	12	124289517	124289517	Missense_Mutation	SNP	C	T	8	112	c.2563C>T	c.(2563-2565)CCC>TCC	p.P855S
Pat_41	Post-Resistance	DNAH10	196385	37	12	124352080	124352080	Missense_Mutation	SNP	G	A	4	48	c.6880G>A	c.(6880-6882)GAA>AAA	p.E2294K
Pat_41	Post-Resistance	CCDC92	80212	37	12	124427987	124427987	Missense_Mutation	SNP	C	T	26	292	c.88G>A	c.(88-90)GCA>ACA	p.A30T
Pat_41	Post-Resistance	NCOR2	9612	37	12	124941668	124941668	Missense_Mutation	SNP	C	T	16	30	c.746G>A	c.(745-747)GGG>GAG	p.G249E
Pat_41	Post-Resistance	NCOR2	9612	37	12	124950813	124950813	Missense_Mutation	SNP	G	A	4	95	c.611C>T	c.(610-612)GCT>GTT	p.A204V
Pat_41	Post-Resistance	NCOR2	9612	37	12	124970986	124970986	Splice_Site	SNP	C	T	4	31	c.233_splice	c.e2+1	p.R78_splice
Pat_41	Post-Resistance	DHX37	57647	37	12	125457048	125457048	Splice_Site	SNP	C	T	22	283	c.1077_splice	c.e7+1	p.K359_splice
Pat_41	Post-Resistance	TMEM132B	114795	37	12	125834801	125834801	Missense_Mutation	SNP	G	A	59	412	c.856G>A	c.(856-858)GTA>ATA	p.V286I
Pat_41	Post-Resistance	SFRS8	6433	37	12	132237821	132237821	Missense_Mutation	SNP	C	T	15	251	c.1235C>T	c.(1234-1236)GCC>GTC	p.A412V
Pat_41	Post-Resistance	SFRS8	6433	37	12	132237830	132237830	Missense_Mutation	SNP	C	T	23	215	c.1244C>T	c.(1243-1245)CCT>CTT	p.P415L

Pat_41	Post-Resistance	DDX51	317781	37	12	132624223	132624223	Missense_Mutation	SNP	G	A	23	21	c.1931C>T	c.(1930-1932)CCT>CTT	p.P644L
Pat_41	Post-Resistance	POLE	5426	37	12	133219913	133219913	Missense_Mutation	SNP	C	T	10	97	c.4448G>A	c.(4447-4449)AGT>AAT	p.S1483N
Pat_41	Post-Resistance	POLE	5426	37	12	133226345	133226345	Missense_Mutation	SNP	C	T	6	95	c.3713G>A	c.(3712-3714)AGC>AAC	p.S1238N
Pat_41	Post-Resistance	POLE	5426	37	12	133235987	133235987	Missense_Mutation	SNP	C	T	13	86	c.3169G>A	c.(3169-3171)GCA>ACA	p.A1057T
Pat_41	Post-Resistance	POLE	5426	37	12	133238271	133238271	Splice_Site	SNP	C	T	11	153	c.2707_splice	c.e24-1	p.E903_splice
Pat_41	Post-Resistance	PGAM5	192111	37	12	133294030	133294030	Missense_Mutation	SNP	G	A	4	47	c.376G>A	c.(376-378)GAG>AAG	p.E126K
Pat_41	Post-Resistance	ANKLE2	23141	37	12	133324818	133324818	Missense_Mutation	SNP	G	A	5	112	c.947C>T	c.(946-948)GCT>GTT	p.A316V
Pat_41	Post-Resistance	GOLGA3	2802	37	12	133359063	133359063	Missense_Mutation	SNP	C	T	6	59	c.3284G>A	c.(3283-3285)GGC>GAC	p.G1095D
Pat_41	Post-Resistance	TUBA3C	7278	37	13	19751504	19751504	Missense_Mutation	SNP	C	T	14	190	c.619G>A	c.(619-621)GAA>AAA	p.E207K
Pat_41	Post-Resistance	PSPC1	55269	37	13	20356848	20356848	Missense_Mutation	SNP	G	A	7	88	c.50C>T	c.(49-51)GCC>GTC	p.A17V
Pat_41	Post-Resistance	ZMYM5	9205	37	13	20411908	20411908	Missense_Mutation	SNP	G	A	5	115	c.926C>T	c.(925-927)TCC>TTC	p.S309F
Pat_41	Post-Resistance	ZMYM5	9205	37	13	20426275	20426275	Missense_Mutation	SNP	G	A	115	605	c.46C>T	c.(46-48)CCT>TCT	p.P16S
Pat_41	Post-Resistance	ZMYM2	7750	37	13	20577074	20577074	Missense_Mutation	SNP	C	T	21	278	c.932C>T	c.(931-933)CCT>CTT	p.P311L
Pat_41	Post-Resistance	XPO4	64328	37	13	21476858	21476858	Missense_Mutation	SNP	C	T	6	26	c.20G>A	c.(19-21)GGG>GAG	p.G7E
Pat_41	Post-Resistance	SGCG	6445	37	13	23894876	23894876	Missense_Mutation	SNP	C	T	4	122	c.679C>T	c.(679-681)CTT>TTT	p.L227F
Pat_41	Post-Resistance	SACS	26278	37	13	23905090	23905090	Missense_Mutation	SNP	C	T	9	259	c.12925G>A	c.(12925-12927)GAA>AAA	p.E4309K
Pat_41	Post-Resistance	SACS	26278	37	13	23905651	23905651	Missense_Mutation	SNP	C	T	10	398	c.12364G>A	c.(12364-12366)GCT>ACT	p.A4122T
Pat_41	Post-Resistance	SACS	26278	37	13	23909083	23909083	Missense_Mutation	SNP	C	T	11	250	c.8932G>A	c.(8932-8934)GTG>ATG	p.V2978M
Pat_41	Post-Resistance	SACS	26278	37	13	23910426	23910426	Missense_Mutation	SNP	C	T	8	237	c.7589G>A	c.(7588-7590)AGC>AAC	p.S2530N
Pat_41	Post-Resistance	SACS	26278	37	13	23911068	23911068	Missense_Mutation	SNP	G	A	11	516	c.6947C>T	c.(6946-6948)ACC>ATC	p.T2316I
Pat_41	Post-Resistance	MIPEP	4285	37	13	24411810	24411810	Missense_Mutation	SNP	G	A	26	474	c.1424C>T	c.(1423-1425)CCC>CTC	p.P475L
Pat_41	Post-Resistance	PARP4	143	37	13	25023855	25023855	Splice_Site	SNP	C	T	7	149	c.3114_splice	c.e25+1	.Q1038_splice
Pat_41	Post-Resistance	ATP12A	479	37	13	25265219	25265219	Missense_Mutation	SNP	C	T	18	83	c.899C>T	c.(898-900)GCC>GTC	p.A300V
Pat_41	Post-Resistance	CENPJ	55835	37	13	25479958	25479958	Missense_Mutation	SNP	G	A	21	280	c.2218C>T	c.(2218-2220)CCT>TCT	p.P740S
Pat_41	Post-Resistance	PABPC3	5042	37	13	25670469	25670469	Missense_Mutation	SNP	G	A	15	270	c.133G>A	c.(133-135)GAC>AAC	p.D45N
Pat_41	Post-Resistance	FAM123A	219287	37	13	25744127	25744127	Missense_Mutation	SNP	C	T	4	90	c.1631G>A	c.(1630-1632)GGC>GAC	p.G544D
Pat_41	Post-Resistance	FAM123A	219287	37	13	25744190	25744191	Missense_Mutation	DNP	CC	TT	7	189	.1567_1568GG>A	c.(1567-1569)GGC>AAC	p.G523N
Pat_41	Post-Resistance	ATP8A2	51761	37	13	26116129	26116129	Missense_Mutation	SNP	G	A	34	239	c.724G>A	c.(724-726)GGG>AGG	p.G242R
Pat_41	Post-Resistance	RNF6	6049	37	13	26789003	26789003	Missense_Mutation	SNP	C	T	8	240	c.1016G>A	c.(1015-1017)AGA>AAA	p.R339K
Pat_41	Post-Resistance	CDK8	1024	37	13	26974611	26974611	Missense_Mutation	SNP	G	A	23	627	c.955G>A	c.(955-957)GAC>AAC	p.D319N
Pat_41	Post-Resistance	LNX2	222484	37	13	28127475	28127475	Missense_Mutation	SNP	G	A	29	381	c.1648C>T	c.(1648-1650)CTT>TTT	p.L550F
Pat_41	Post-Resistance	POLR1D	51082	37	13	28222587	28222587	Missense_Mutation	SNP	G	A	7	77	c.98G>A	c.(97-99)GGT>GAT	p.G33D
Pat_41	Post-Resistance	CDX2	1045	37	13	28537367	28537367	Missense_Mutation	SNP	C	T	7	149	c.827G>A	c.(826-828)AGA>AAA	p.R276K
Pat_41	Post-Resistance	FLT3	2322	37	13	28592707	28592707	Missense_Mutation	SNP	G	A	17	327	c.2438C>T	c.(2437-2439)GCC>GTC	p.A813V
Pat_41	Post-Resistance	FLT3	2322	37	13	28623803	28623803	Missense_Mutation	SNP	G	A	12	348	c.851C>T	c.(850-852)ACC>ATC	p.T284I
Pat_41	Post-Resistance	FLT1	2321	37	13	28877396	28877396	Missense_Mutation	SNP	A	G	22	379	c.3925T>C	c.(3925-3927)TAC>CAC	p.Y1309H
Pat_41	Post-Resistance	MTUS2	23281	37	13	29600285	29600285	Missense_Mutation	SNP	C	T	6	124	c.1480C>T	c.(1480-1482)CCT>TCT	p.P494S
Pat_41	Post-Resistance	MTUS2	23281	37	13	29600633	29600633	Missense_Mutation	SNP	C	T	6	115	c.1828C>T	c.(1828-1830)CCT>TCT	p.P610S
Pat_41	Post-Resistance	USPL1	10208	37	13	31205029	31205029	Missense_Mutation	SNP	G	A	20	160	c.286G>A	c.(286-288)GAA>AAA	p.E96K
Pat_41	Post-Resistance	USPL1	10208	37	13	31205454	31205454	Nonsense_Mutation	SNP	G	A	23	629	c.711G>A	c.(709-711)TGG>TGA	p.W237*
Pat_41	Post-Resistance	USPL1	10208	37	13	31231754	31231754	Missense_Mutation	SNP	C	T	19	268	c.1540C>T	c.(1540-1542)CTT>TTT	p.L514F
Pat_41	Post-Resistance	HSPH1	10808	37	13	31719741	31719741	Missense_Mutation	SNP	C	T	6	199	c.1543G>A	c.(1543-1545)GAG>AAG	p.E515K
Pat_41	Post-Resistance	HSPH1	10808	37	13	31722586	31722586	Missense_Mutation	SNP	C	T	18	412	c.1169G>A	c.(1168-1170)AGA>AAA	p.R390K
Pat_41	Post-Resistance	B3GALTL	145173	37	13	31848749	31848749	Missense_Mutation	SNP	C	T	10	307	c.764C>T	c.(763-765)TCT>TTT	p.S255F
Pat_41	Post-Resistance	FRY	10129	37	13	32768380	32768380	Missense_Mutation	SNP	C	T	15	313	c.3692C>T	c.(3691-3693)TCC>TTC	p.S1231F
Pat_41	Post-Resistance	FRY	10129	37	13	32808710	32808710	Splice_Site	SNP	G	A	31	267	c.5528_splice	c.e42-1	.G1843_splice
Pat_41	Post-Resistance	BRCA2	675	37	13	32944629	32944629	Missense_Mutation	SNP	C	T	15	331	c.8422C>T	c.(8422-8424)CTT>TTT	p.L2808F

Pat_41	Post-Resistance	BRCA2	675	37	13	32950872	32950872	Missense_Mutation	SNP	G	A	7	251	c.8698G>A	c.(8698-8700)GAT>AAT	p.D2900N
Pat_41	Post-Resistance	PDS5B	23047	37	13	33225940	33225940	Splice_Site	SNP	G	A	7	62	c.109_splice	c.e3-1	p.M37_splice
Pat_41	Post-Resistance	KL	9365	37	13	33629252	33629252	Missense_Mutation	SNP	C	T	14	333	c.1399C>T	c.(1399-1401)CAC>TAC	p.H467Y
Pat_41	Post-Resistance	STARD13	90627	37	13	33685998	33685998	Missense_Mutation	SNP	G	A	5	131	c.2524C>T	c.(2524-2526)CCA>TCA	p.P842S
Pat_41	Post-Resistance	RFC3	5983	37	13	34404101	34404101	Missense_Mutation	SNP	C	T	25	463	c.520C>T	c.(520-522)CCT>TCT	p.P174S
Pat_41	Post-Resistance	MAB21L1	4081	37	13	36049687	36049687	Missense_Mutation	SNP	G	A	9	280	c.589C>T	c.(589-591)CCC>TCC	p.P197S
Pat_41	Post-Resistance	NBEA	26960	37	13	36141093	36141093	Missense_Mutation	SNP	C	T	7	363	c.6974C>T	c.(6973-6975)ACC>ATC	p.T2325I
Pat_41	Post-Resistance	DCLK1	9201	37	13	36445414	36445414	Missense_Mutation	SNP	G	A	37	186	c.887C>T	c.(886-888)ACC>ATC	p.T296I
Pat_41	Post-Resistance	DCLK1	9201	37	13	36686043	36686043	Missense_Mutation	SNP	C	T	12	222	c.686G>A	c.(685-687)GGA>GAA	p.G229E
Pat_41	Post-Resistance	CCNA1	8900	37	13	37011860	37011860	Missense_Mutation	SNP	C	T	14	74	c.392C>T	c.(391-393)CCC>CTC	p.P131L
Pat_41	Post-Resistance	CCNA1	8900	37	13	37016395	37016395	Missense_Mutation	SNP	C	T	33	284	c.1300C>T	c.(1300-1302)CCC>TCC	p.P434S
Pat_41	Post-Resistance	SMAD9	4093	37	13	37453675	37453675	Missense_Mutation	SNP	G	A	10	57	c.152C>T	c.(151-153)GCC>GTC	p.A51V
Pat_41	Post-Resistance	TRPC4	7223	37	13	38211071	38211071	Missense_Mutation	SNP	G	A	8	130	c.2903C>T	c.(2902-2904)ACC>ATC	p.T968I
Pat_41	Post-Resistance	FREM2	341640	37	13	39265781	39265781	Missense_Mutation	SNP	G	A	20	305	c.4300G>A	c.(4300-4302)GGT>AGT	p.G1434S
Pat_41	Post-Resistance	FREM2	341640	37	13	39425180	39425180	Missense_Mutation	SNP	C	T	14	186	c.6677C>T	c.(6676-6678)TCT>TTT	p.S2226F
Pat_41	Post-Resistance	COG6	57511	37	13	40273640	40273640	Missense_Mutation	SNP	G	A	9	191	c.1169G>A	c.(1168-1170)GGT>GAT	p.G390D
Pat_41	Post-Resistance	SLC25A15	10166	37	13	41373452	41373452	Splice_Site	SNP	G	A	13	156	c.314_splice	c.e3+1	p.S105_splice
Pat_41	Post-Resistance	KBTBD6	89890	37	13	41704716	41704716	Nonsense_Mutation	SNP	C	T	20	150	c.1932G>A	c.(1930-1932)TGG>TGA	p.W644*
Pat_41	Post-Resistance	KIAA0564	23078	37	13	42144619	42144619	Missense_Mutation	SNP	C	T	42	174	c.5594G>A	c.(5593-5595)GGT>GAT	p.G1865D
Pat_41	Post-Resistance	KIAA0564	23078	37	13	42357951	42357951	Missense_Mutation	SNP	G	A	9	183	c.2257C>T	c.(2257-2259)CTT>TTT	p.L753F
Pat_41	Post-Resistance	KIAA0564	23078	37	13	42361635	42361635	Missense_Mutation	SNP	G	A	11	187	c.2108C>T	c.(2107-2109)GCA>GTA	p.A703V
Pat_41	Post-Resistance	KIAA0564	23078	37	13	42460141	42460141	Missense_Mutation	SNP	G	A	4	47	c.890C>T	c.(889-891)GCC>GTC	p.A297V
Pat_41	Post-Resistance	DGKH	160851	37	13	42740744	42740744	Missense_Mutation	SNP	G	A	14	187	c.1052G>A	c.(1051-1053)CGT>CAT	p.R351H
Pat_41	Post-Resistance	DGKH	160851	37	13	42783164	42783164	Missense_Mutation	SNP	G	A	19	168	c.2671G>A	c.(2671-2673)GCA>ACA	p.A891T
Pat_41	Post-Resistance	TNFSF11	8600	37	13	43155355	43155355	Missense_Mutation	SNP	G	A	11	123	c.313G>A	c.(313-315)GAG>AAG	p.E105K
Pat_41	Post-Resistance	SERP2	387923	37	13	44953819	44953819	Missense_Mutation	SNP	G	A	10	371	c.127G>A	c.(127-129)GCA>ACA	p.A43T
Pat_41	Post-Resistance	NUFIP1	26747	37	13	45563534	45563534	Missense_Mutation	SNP	C	T	5	54	c.38G>A	c.(37-39)GGG>GAG	p.G13E
Pat_41	Post-Resistance	TPT1	7178	37	13	45914846	45914846	Splice_Site	SNP	C	T	5	110	c.102_splice	c.e2+1	p.K34_splice
Pat_41	Post-Resistance	TPT1	7178	37	13	45914851	45914851	Missense_Mutation	SNP	C	T	5	115	c.98G>A	c.(97-99)GGG>GAG	p.G33E
Pat_41	Post-Resistance	TPT1	7178	37	13	45914861	45914861	Missense_Mutation	SNP	C	T	5	128	c.88G>A	c.(88-90)GAG>AAG	p.E30K
Pat_41	Post-Resistance	COG3	83548	37	13	46039337	46039337	Missense_Mutation	SNP	C	T	10	65	c.166C>T	c.(166-168)CCA>TCA	p.P56S
Pat_41	Post-Resistance	ZC3H13	23091	37	13	46542124	46542124	Missense_Mutation	SNP	G	A	56	357	c.3836C>T	c.(3835-3837)TCT>TTT	p.S1279F
Pat_41	Post-Resistance	ZC3H13	23091	37	13	46543375	46543375	Missense_Mutation	SNP	G	A	6	73	c.3304C>T	c.(3304-3306)CCT>TCT	p.P1102S
Pat_41	Post-Resistance	LCP1	3936	37	13	46705015	46705015	Missense_Mutation	SNP	C	T	42	201	c.1685G>A	c.(1684-1686)GGT>GAT	p.G562D
Pat_41	Post-Resistance	C13orf18	80183	37	13	46946234	46946234	Missense_Mutation	SNP	C	T	10	67	c.377G>A	c.(376-378)AGC>AAC	p.S126N
Pat_41	Post-Resistance	ITM2B	9445	37	13	48828005	48828005	Missense_Mutation	SNP	G	A	28	258	c.179G>A	c.(178-180)GGA>GAA	p.G60E
Pat_41	Post-Resistance	LPAR6	10161	37	13	48986036	48986036	Missense_Mutation	SNP	G	A	3	35	c.524C>T	c.(523-525)GCC>GTC	p.A175V
Pat_41	Post-Resistance	RCBTB2	1102	37	13	49084793	49084793	Missense_Mutation	SNP	G	A	20	381	c.898C>T	c.(898-900)CCT>TCT	p.P300S
Pat_41	Post-Resistance	FNDC3A	22862	37	13	49705348	49705348	Missense_Mutation	SNP	G	A	30	471	c.328G>A	c.(328-330)GTT>ATT	p.V110I
Pat_41	Post-Resistance	FNDC3A	22862	37	13	49771876	49771876	Missense_Mutation	SNP	G	A	19	129	c.2356G>A	c.(2356-2358)GGA>AGA	p.G786R
Pat_41	Post-Resistance	CAB39L	81617	37	13	49885120	49885120	Missense_Mutation	SNP	C	T	19	354	c.844G>A	c.(844-846)GCC>ACC	p.A282T
Pat_41	Post-Resistance	PHF11	51131	37	13	50102755	50102755	Missense_Mutation	SNP	G	A	7	96	c.950G>A	c.(949-951)AGA>AAA	p.R317K
Pat_41	Post-Resistance	ATP7B	540	37	13	52513243	52513243	Missense_Mutation	SNP	C	T	14	269	c.3643G>A	c.(3643-3645)GAC>AAC	p.D1215N
Pat_41	Post-Resistance	UTP14C	9724	37	13	52602995	52602995	Missense_Mutation	SNP	G	A	8	96	c.55G>A	c.(55-57)GTG>ATG	p.V19M
Pat_41	Post-Resistance	UTP14C	9724	37	13	52604220	52604220	Missense_Mutation	SNP	C	T	6	66	c.1280C>T	c.(1279-1281)TCC>TTC	p.S427F
Pat_41	Post-Resistance	NEK5	341676	37	13	52646166	52646166	Missense_Mutation	SNP	C	T	8	70	c.1838G>A	c.(1837-1839)GGC>GAC	p.G613D
Pat_41	Post-Resistance	LECT1	11061	37	13	53282696	53282696	Missense_Mutation	SNP	G	A	8	86	c.764C>T	c.(763-765)GCC>GTC	p.A255V

Pat_41	Post-Resistance	PCDH8	5100	37	13	53422450	53422450	Missense_Mutation	SNP	G	A	9	164	c.122C>T	c.(121-123)GCC>GTC	p.A41V
Pat_41	Post-Resistance	PCDH20	64881	37	13	61987784	61987784	Missense_Mutation	SNP	C	T	6	39	c.448G>A	c.(448-450)GAG>AAG	p.E150K
Pat_41	Post-Resistance	DACH1	1602	37	13	72049847	72049847	Missense_Mutation	SNP	C	T	36	634	c.2005G>A	c.(2005-2007)GTC>ATC	p.V669I
Pat_41	Post-Resistance	KLF5	688	37	13	73636627	73636627	Missense_Mutation	SNP	C	T	10	184	c.890C>T	c.(889-891)GCC>GTC	p.A297V
Pat_41	Post-Resistance	TBC1D4	9882	37	13	75861071	75861071	Missense_Mutation	SNP	C	T	13	178	c.3754G>A	c.(3754-3756)GAA>AAA	p.E1252K
Pat_41	Post-Resistance	TBC1D4	9882	37	13	75915639	75915639	Missense_Mutation	SNP	C	T	6	98	c.1493G>A	c.(1492-1494)AGA>AAA	p.R498K
Pat_41	Post-Resistance	LMO7	4008	37	13	76379781	76379781	Missense_Mutation	SNP	C	T	32	601	c.382C>T	c.(382-384)CCA>TCA	p.P128S
Pat_41	Post-Resistance	LMO7	4008	37	13	76395650	76395650	Missense_Mutation	SNP	C	T	6	161	c.1846C>T	c.(1846-1848)CGG>TGG	p.R616W
Pat_41	Post-Resistance	LMO7	4008	37	13	76430682	76430682	Missense_Mutation	SNP	G	A	6	315	c.4003G>A	c.(4003-4005)GAG>AAG	p.E1335K
Pat_41	Post-Resistance	MYCBP2	23077	37	13	77656037	77656037	Missense_Mutation	SNP	C	T	6	390	c.11014G>A	c.(11014-11016)GAT>AAT	p.D3672N
Pat_41	Post-Resistance	MYCBP2	23077	37	13	77672108	77672108	Missense_Mutation	SNP	G	A	8	66	c.9067C>T	c.(9067-9069)CTT>TTT	p.L3023F
Pat_41	Post-Resistance	MYCBP2	23077	37	13	77739436	77739436	Missense_Mutation	SNP	C	T	15	88	c.6317G>A	c.(6316-6318)GGA>GAA	p.G2106E
Pat_41	Post-Resistance	MYCBP2	23077	37	13	77825286	77825286	Missense_Mutation	SNP	C	T	7	113	c.2267G>A	c.(2266-2268)GGG>GAG	p.G756E
Pat_41	Post-Resistance	SCEL	8796	37	13	78163334	78163334	Missense_Mutation	SNP	C	T	21	238	c.601C>T	c.(601-603)CCT>TCT	p.P201S
Pat_41	Post-Resistance	SLITRK6	84189	37	13	86368273	86368273	Missense_Mutation	SNP	G	A	6	124	c.2371C>T	c.(2371-2373)CCT>TCT	p.P791S
Pat_41	Post-Resistance	SLITRK5	26050	37	13	88328385	88328385	Missense_Mutation	SNP	G	A	8	270	c.742G>A	c.(742-744)GAT>AAT	p.D248N
Pat_41	Post-Resistance	SLITRK5	26050	37	13	88328767	88328767	Missense_Mutation	SNP	C	T	21	137	c.1124C>T	c.(1123-1125)CCC>CTC	p.P375L
Pat_41	Post-Resistance	ABCC4	10257	37	13	95673857	95673857	Missense_Mutation	SNP	G	A	34	242	c.3950C>T	c.(3949-3951)ACC>ATC	p.T1317I
Pat_41	Post-Resistance	ABCC4	10257	37	13	95725537	95725537	Missense_Mutation	SNP	C	T	25	164	c.2939G>A	c.(2938-2940)GGT>GAT	p.G980D
Pat_41	Post-Resistance	UGGT2	55757	37	13	96536846	96536846	Missense_Mutation	SNP	G	A	9	174	c.3127C>T	c.(3127-3129)CCT>TCT	p.P1043S
Pat_41	Post-Resistance	UGGT2	55757	37	13	96638618	96638618	Missense_Mutation	SNP	C	T	25	131	c.1000G>A	c.(1000-1002)GAC>AAC	p.D334N
Pat_41	Post-Resistance	OXGR1	27199	37	13	97639130	97639130	Missense_Mutation	SNP	G	A	15	230	c.884C>T	c.(883-885)ACC>ATC	p.T295I
Pat_41	Post-Resistance	OXGR1	27199	37	13	97639230	97639230	Missense_Mutation	SNP	C	T	10	126	c.784G>A	c.(784-786)GTC>ATC	p.V262I
Pat_41	Post-Resistance	FARP1	10160	37	13	99092246	99092246	Missense_Mutation	SNP	C	T	20	387	c.2465C>T	c.(2464-2466)CCC>CTC	p.P822L
Pat_41	Post-Resistance	DOCK9	23348	37	13	99535386	99535386	Splice_Site	SNP	C	T	5	24	c.2473_splice	c.e23-1	p.D825_splice
Pat_41	Post-Resistance	DOCK9	23348	37	13	99537337	99537337	Missense_Mutation	SNP	G	A	7	113	c.2273C>T	c.(2272-2274)TCC>TTC	p.S758F
Pat_41	Post-Resistance	DOCK9	23348	37	13	99554091	99554091	Missense_Mutation	SNP	G	A	4	33	c.1447C>T	c.(1447-1449)CTT>TTT	p.L483F
Pat_41	Post-Resistance	DOCK9	23348	37	13	99567691	99567691	Missense_Mutation	SNP	C	T	3	59	c.787G>A	c.(787-789)GCA>ACA	p.A263T
Pat_41	Post-Resistance	ZIC2	7546	37	13	100634962	100634962	Missense_Mutation	SNP	G	A	6	38	c.644G>A	c.(643-645)GGC>GAC	p.G215D
Pat_41	Post-Resistance	TMTC4	84899	37	13	101277863	101277863	Missense_Mutation	SNP	C	T	5	168	c.1705G>A	c.(1705-1707)GCA>ACA	p.A569T
Pat_41	Post-Resistance	TMTC4	84899	37	13	101287166	101287166	Missense_Mutation	SNP	C	T	5	202	c.1342G>A	c.(1342-1344)GGA>AGA	p.G448R
Pat_41	Post-Resistance	TMTC4	84899	37	13	101289856	101289856	Missense_Mutation	SNP	G	A	29	219	c.878C>T	c.(877-879)ACG>ATG	p.T293M
Pat_41	Post-Resistance	TPP2	7174	37	13	103309439	103309439	Missense_Mutation	SNP	C	T	9	179	c.2986C>T	c.(2986-2988)CCA>TCA	p.P996S
Pat_41	Post-Resistance	C13orf39	196541	37	13	103339383	103339383	Missense_Mutation	SNP	C	T	10	119	c.307G>A	c.(307-309)GAG>AAG	p.E103K
Pat_41	Post-Resistance	SLC10A2	6555	37	13	103718402	103718402	Nonsense_Mutation	SNP	C	T	19	136	c.198G>A	c.(196-198)TGG>TGA	p.W66*
Pat_41	Post-Resistance	FAM155A	728215	37	13	108518842	108518842	Missense_Mutation	SNP	C	T	18	355	c.103G>A	c.(103-105)GCT>ACT	p.A35T
Pat_41	Post-Resistance	COL4A1	1282	37	13	110833727	110833727	Missense_Mutation	SNP	C	T	5	20	c.2105G>A	c.(2104-2106)GGC>GAC	p.G702D
Pat_41	Post-Resistance	COL4A1	1282	37	13	110847454	110847454	Missense_Mutation	SNP	C	T	4	87	c.1297G>A	c.(1297-1299)GAA>AAA	p.E433K
Pat_41	Post-Resistance	COL4A1	1282	37	13	110863993	110863993	Splice_Site	SNP	C	T	4	135	c.468_splice	c.e8+1	p.K156_splice
Pat_41	Post-Resistance	ING1	3621	37	13	111368182	111368182	Missense_Mutation	SNP	G	A	5	35	c.392G>A	c.(391-393)AGC>AAC	p.S131N
Pat_41	Post-Resistance	MCF2L	23263	37	13	113730403	113730403	Missense_Mutation	SNP	G	C	29	28	c.1603G>C	c.(1603-1605)GAA>CAA	p.E535Q
Pat_41	Post-Resistance	CUL4A	8451	37	13	113907510	113907510	Splice_Site	SNP	G	A	6	109	c.1752_splice	c.e17+1	p.E584_splice
Pat_41	Post-Resistance	FAM70B	348013	37	13	114507949	114507949	Missense_Mutation	SNP	G	A	4	47	c.761G>A	c.(760-762)CGC>CAC	p.R254H
Pat_41	Post-Resistance	GAS6	2621	37	13	114531521	114531521	Missense_Mutation	SNP	G	A	24	92	c.1307C>T	c.(1306-1308)CCT>CTT	p.P436L
Pat_41	Post-Resistance	POTEG	404785	37	14	19553531	19553531	Missense_Mutation	SNP	G	A	13	248	c.115G>A	c.(115-117)GGC>AGC	p.G39S
Pat_41	Post-Resistance	P704P	641455	37	14	20020008	20020008	Missense_Mutation	SNP	C	G	9	531	c.213G>C	c.(211-213)TGG>TGC	p.W71C
Pat_41	Post-Resistance	OR4K13	390433	37	14	20502229	20502229	Missense_Mutation	SNP	G	A	8	140	c.689C>T	c.(688-690)GCT>GTT	p.A230V

Pat_41	Post-Resistance	OR4K13	390433	37	14	20502748	20502748	Missense_Mutation	SNP	G	A	7	104	c.170C>T	c.(169-171)ACA>ATA	p.T57I
Pat_41	Post-Resistance	TEP1	7011	37	14	20839657	20839657	Missense_Mutation	SNP	G	A	21	361	c.7211C>T	c.(7210-7212)TCT>TTT	p.S2404F
Pat_41	Post-Resistance	TEP1	7011	37	14	20859138	20859138	Missense_Mutation	SNP	C	T	42	187	c.2215G>A	c.(2215-2217)GGC>AGC	p.G739S
Pat_41	Post-Resistance	TEP1	7011	37	14	20859195	20859195	Missense_Mutation	SNP	C	T	11	171	c.2158G>A	c.(2158-2160)GAC>AAC	p.D720N
Pat_41	Post-Resistance	TEP1	7011	37	14	20876360	20876360	Missense_Mutation	SNP	T	C	6	205	c.239A>G	c.(238-240)CAG>CGG	p.Q80R
Pat_41	Post-Resistance	TEP1	7011	37	14	20876416	20876416	Missense_Mutation	SNP	C	T	26	88	c.183G>A	c.(181-183)ATG>ATA	p.M61I
Pat_41	Post-Resistance	APEX1	328	37	14	20924902	20924902	Missense_Mutation	SNP	C	T	6	191	c.322C>T	c.(322-324)CTT>TTT	p.L108F
Pat_41	Post-Resistance	PNP	4860	37	14	20942959	20942959	Missense_Mutation	SNP	C	T	3	52	c.313C>T	c.(313-315)CTT>TTT	p.L105F
Pat_41	Post-Resistance	RNASE9	390443	37	14	21024667	21024667	Missense_Mutation	SNP	G	A	12	45	c.562C>T	c.(562-564)CCA>TCA	p.P188S
Pat_41	Post-Resistance	RNASE4	6038	37	14	21167940	21167940	Missense_Mutation	SNP	G	A	37	462	c.410G>A	c.(409-411)GGT>GAT	p.G137D
Pat_41	Post-Resistance	METT11D1	64745	37	14	21458680	21458680	Missense_Mutation	SNP	G	A	14	187	c.287G>A	c.(286-288)AGC>AAC	p.S96N
Pat_41	Post-Resistance	METT11D1	64745	37	14	21464991	21464991	Missense_Mutation	SNP	C	T	6	177	c.1313C>T	c.(1312-1314)CCT>CTT	p.P438L
Pat_41	Post-Resistance	TPPP2	122664	37	14	21500117	21500117	Missense_Mutation	SNP	G	A	9	195	c.394G>A	c.(394-396)GAG>AAG	p.E132K
Pat_41	Post-Resistance	FLJ10357	55701	37	14	21548928	21548928	Missense_Mutation	SNP	G	A	10	88	c.2483G>A	c.(2482-2484)AGC>AAC	p.S828N
Pat_41	Post-Resistance	TOX4	9878	37	14	21960997	21960997	Missense_Mutation	SNP	G	A	21	305	c.1222G>A	c.(1222-1224)GCT>ACT	p.A408T
Pat_41	Post-Resistance	OR4E2	26686	37	14	22133916	22133916	Missense_Mutation	SNP	C	T	6	123	c.620C>T	c.(619-621)TCC>TTC	p.S207F
Pat_41	Post-Resistance	SLC7A7	9056	37	14	23243585	23243585	Missense_Mutation	SNP	G	A	20	291	c.1223C>T	c.(1222-1224)CCT>CTT	p.P408L
Pat_41	Post-Resistance	PSMB11	122706	37	14	23511780	23511780	Missense_Mutation	SNP	G	A	7	179	c.346G>A	c.(346-348)GAA>AAA	p.E116K
Pat_41	Post-Resistance	ACIN1	22985	37	14	23530758	23530758	Missense_Mutation	SNP	G	A	4	50	c.3347C>T	c.(3346-3348)CCC>CTC	p.P1116L
Pat_41	Post-Resistance	ACIN1	22985	37	14	23547399	23547399	Missense_Mutation	SNP	G	A	42	553	c.2258C>T	c.(2257-2259)ACC>ATC	p.T753I
Pat_41	Post-Resistance	ACIN1	22985	37	14	23549793	23549793	Missense_Mutation	SNP	C	T	11	205	c.925G>A	c.(925-927)GAA>AAA	p.E309K
Pat_41	Post-Resistance	EFS	10278	37	14	23829034	23829034	Missense_Mutation	SNP	G	A	5	115	c.653C>T	c.(652-654)GCT>GTT	p.A218V
Pat_41	Post-Resistance	MYH6	4624	37	14	23858711	23858711	Missense_Mutation	SNP	G	A	5	65	c.3869C>T	c.(3868-3870)GCC>GTC	p.A1290V
Pat_41	Post-Resistance	THTPA	79178	37	14	24026265	24026265	Missense_Mutation	SNP	G	A	10	209	c.299G>A	c.(298-300)GGC>GAC	p.G100D
Pat_41	Post-Resistance	DHRS4L1	728635	37	14	24507086	24507086	Missense_Mutation	SNP	G	A	6	17	c.263G>A	c.(262-264)TGC>TAC	p.C88Y
Pat_41	Post-Resistance	LRRC16B	90668	37	14	24534948	24534948	Missense_Mutation	SNP	G	A	21	227	c.3514G>A	c.(3514-3516)GGG>AGG	p.G1172R
Pat_41	Post-Resistance	DCAF11	80344	37	14	24586528	24586528	Missense_Mutation	SNP	G	A	20	115	c.337G>A	c.(337-339)GTG>ATG	p.V113M
Pat_41	Post-Resistance	DCAF11	80344	37	14	24592252	24592252	Nonsense_Mutation	SNP	G	A	5	230	c.1472G>A	c.(1471-1473)TGG>TAG	p.W491*
Pat_41	Post-Resistance	FAM158A	51016	37	14	24610461	24610461	Missense_Mutation	SNP	G	A	48	223	c.53C>T	c.(52-54)GCT>GTT	p.A18V
Pat_41	Post-Resistance	RNF31	55072	37	14	24619482	24619482	Missense_Mutation	SNP	G	A	10	64	c.1022G>A	c.(1021-1023)GGA>GAA	p.G341E
Pat_41	Post-Resistance	REC8	9985	37	14	24648087	24648087	Missense_Mutation	SNP	G	A	20	224	c.1168G>A	c.(1168-1170)GAA>AAA	p.E390K
Pat_41	Post-Resistance	IPO4	79711	37	14	24651230	24651230	Missense_Mutation	SNP	G	A	6	75	c.2738C>T	c.(2737-2739)CCC>CTC	p.P913L
Pat_41	Post-Resistance	IPO4	79711	37	14	24652682	24652682	Missense_Mutation	SNP	C	T	7	30	c.2101G>A	c.(2101-2103)GAA>AAA	p.E701K
Pat_41	Post-Resistance	IPO4	79711	37	14	24655388	24655388	Missense_Mutation	SNP	C	T	24	291	c.1006G>A	c.(1006-1008)GTT>ATT	p.V336I
Pat_41	Post-Resistance	TGM1	7051	37	14	24731474	24731474	Missense_Mutation	SNP	G	A	13	158	c.85C>T	c.(85-87)CCA>TCA	p.P29S
Pat_41	Post-Resistance	RABGGTA	5875	37	14	24735669	24735669	Missense_Mutation	SNP	G	A	17	202	c.1522C>T	c.(1522-1524)CCC>TCC	p.P508S
Pat_41	Post-Resistance	CIDEB	27141	37	14	24776591	24776591	Missense_Mutation	SNP	C	T	15	174	c.172G>A	c.(172-174)GAG>AAG	p.E58K
Pat_41	Post-Resistance	LTB4R2	56413	37	14	24780820	24780820	Missense_Mutation	SNP	G	A	6	98	c.1043G>A	c.(1042-1044)GGC>GAC	p.G348D
Pat_41	Post-Resistance	NYNRIN	57523	37	14	24884569	24884569	Missense_Mutation	SNP	G	A	13	78	c.3614G>A	c.(3613-3615)GGG>GAG	p.G1205E
Pat_41	Post-Resistance	GZMB	3002	37	14	25101204	25101204	Missense_Mutation	SNP	C	T	18	205	c.460G>A	c.(460-462)GGA>AGA	p.G154R
Pat_41	Post-Resistance	NOVA1	4857	37	14	26918111	26918111	Missense_Mutation	SNP	G	A	35	298	c.578C>T	c.(577-579)ACT>ATT	p.T193I
Pat_41	Post-Resistance	SCFD1	23256	37	14	31119857	31119857	Splice_Site	SNP	G	A	9	132	c.755_splice	c.e9+1	p.S252_splice
Pat_41	Post-Resistance	SCFD1	23256	37	14	31169453	31169453	Missense_Mutation	SNP	G	A	32	199	c.1399G>A	c.(1399-1401)GCA>ACA	p.A467T
Pat_41	Post-Resistance	HEATR5A	25938	37	14	31787492	31787492	Missense_Mutation	SNP	C	T	25	425	c.3097G>A	c.(3097-3099)GCA>ACA	p.A1033T
Pat_41	Post-Resistance	AKAP6	9472	37	14	33004938	33004938	Missense_Mutation	SNP	G	A	12	132	c.503G>A	c.(502-504)GGT>GAT	p.G168D
Pat_41	Post-Resistance	AKAP6	9472	37	14	33204888	33204888	Missense_Mutation	SNP	G	A	4	76	c.3172G>A	c.(3172-3174)GAC>AAC	p.D1058N
Pat_41	Post-Resistance	AKAP6	9472	37	14	33293569	33293569	Missense_Mutation	SNP	G	A	14	83	c.6550G>A	c.(6550-6552)GAA>AAA	p.E2184K

Pat_41	Post-Resistance	NPAS3	64067	37	14	33684482	33684482	Missense_Mutation	SNP	C	T	29	257	c.235C>T	c.(235-237)CCT>TCT	p.P79S
Pat_41	Post-Resistance	EGLN3	112399	37	14	34419841	34419841	Missense_Mutation	SNP	C	T	6	51	c.118G>A	c.(118-120)GGC>AGC	p.G40S
Pat_41	Post-Resistance	BAZ1A	11177	37	14	35331464	35331464	Missense_Mutation	SNP	G	A	96	387	c.178C>T	c.(178-180)CCT>TCT	p.P60S
Pat_41	Post-Resistance	FAM177A1	283635	37	14	35522625	35522625	Missense_Mutation	SNP	G	A	40	286	c.238G>A	c.(238-240)GAG>AAG	p.E80K
Pat_41	Post-Resistance	RALGAPA1	253959	37	14	36230200	36230200	Missense_Mutation	SNP	C	T	4	20	c.382G>A	c.(382-384)GGT>AGT	p.G128S
Pat_41	Post-Resistance	NKX2-1	7080	37	14	36987148	36987148	Missense_Mutation	SNP	T	C	5	2	c.451A>G	c.(451-453)AAG>GAG	p.K151E
Pat_41	Post-Resistance	PAX9	5083	37	14	37132609	37132609	Missense_Mutation	SNP	C	T	6	47	c.512C>T	c.(511-513)GCC>GTC	p.A171V
Pat_41	Post-Resistance	SLC25A21	89874	37	14	37180638	37180638	Nonsense_Mutation	SNP	C	T	5	88	c.488G>A	c.(487-489)TGG>TAG	p.W163*
Pat_41	Post-Resistance	CTAGE5	4253	37	14	39819370	39819370	Missense_Mutation	SNP	C	T	76	407	c.2317C>T	c.(2317-2319)CCC>TCC	p.P773S
Pat_41	Post-Resistance	FAM179B	23116	37	14	45496510	45496510	Missense_Mutation	SNP	G	A	30	356	c.3337G>A	c.(3337-3339)GGA>AGA	p.G1113R
Pat_41	Post-Resistance	FANCM	57697	37	14	45636294	45636294	Missense_Mutation	SNP	C	T	6	230	c.1930C>T	c.(1930-1932)CAT>TAT	p.H644Y
Pat_41	Post-Resistance	C14orf106	55320	37	14	45679592	45679592	Missense_Mutation	SNP	G	A	11	85	c.3143C>T	c.(3142-3144)TCT>TTT	p.S1048F
Pat_41	Post-Resistance	MDGA2	161357	37	14	47342764	47342764	Missense_Mutation	SNP	G	A	6	245	c.2417C>T	c.(2416-2418)CCC>CTC	p.P806L
Pat_41	Post-Resistance	RPL36AL	6166	37	14	50085540	50085540	Missense_Mutation	SNP	C	T	7	317	c.283G>A	c.(283-285)GGA>AGA	p.G95R
Pat_41	Post-Resistance	C14orf138	79609	37	14	50582884	50582884	Missense_Mutation	SNP	C	T	11	291	c.280G>A	c.(280-282)GTC>ATC	p.V94I
Pat_41	Post-Resistance	SOS2	6655	37	14	50585072	50585072	Missense_Mutation	SNP	G	A	5	162	c.3989C>T	c.(3988-3990)ACT>ATT	p.T1330I
Pat_41	Post-Resistance	NIN	51199	37	14	51224387	51224387	Missense_Mutation	SNP	C	T	14	251	c.3361G>A	c.(3361-3363)GAA>AAA	p.E1121K
Pat_41	Post-Resistance	NIN	51199	37	14	51228576	51228576	Missense_Mutation	SNP	C	T	13	306	c.1828G>A	c.(1828-1830)GTC>ATC	p.V610I
Pat_41	Post-Resistance	TRIM9	114088	37	14	51492006	51492006	Missense_Mutation	SNP	G	A	43	616	c.895C>T	c.(895-897)CGC>TGC	p.R299C
Pat_41	Post-Resistance	FRMD6	122786	37	14	52174941	52174941	Missense_Mutation	SNP	G	A	5	107	c.704G>A	c.(703-705)AGA>AAA	p.R235K
Pat_41	Post-Resistance	PTGER2	5732	37	14	52781508	52781508	Missense_Mutation	SNP	G	A	9	57	c.242G>A	c.(241-243)GGG>GAG	p.G81E
Pat_41	Post-Resistance	GNPNAT1	64841	37	14	53250203	53250203	Missense_Mutation	SNP	C	T	11	115	c.155G>A	c.(154-156)GGT>GAT	p.G52D
Pat_41	Post-Resistance	DDHD1	80821	37	14	53529728	53529728	Missense_Mutation	SNP	G	A	33	372	c.1699C>T	c.(1699-1701)CCT>TCT	p.P567S
Pat_41	Post-Resistance	BMP4	652	37	14	54417499	54417499	Missense_Mutation	SNP	G	A	8	56	c.478C>T	c.(478-480)CTC>TTC	p.L160F
Pat_41	Post-Resistance	SAMD4A	23034	37	14	55255652	55255652	Missense_Mutation	SNP	C	T	14	160	c.2144C>T	c.(2143-2145)TCC>TTC	p.S715F
Pat_41	Post-Resistance	WDHD1	11169	37	14	55477026	55477026	Splice_Site	SNP	C	T	20	287	c.341_splice	c.e4+1	p.S114_splice
Pat_41	Post-Resistance	WDHD1	11169	37	14	55480289	55480289	Missense_Mutation	SNP	C	T	17	237	c.103G>A	c.(103-105)GGT>AGT	p.G35S
Pat_41	Post-Resistance	KIAA0831	22863	37	14	55847290	55847290	Splice_Site	SNP	C	T	12	232	c.995_splice	c.e7+1	p.S332_splice
Pat_41	Post-Resistance	NAA30	122830	37	14	57857757	57857757	Missense_Mutation	SNP	C	T	4	6	c.82C>T	c.(82-84)CCC>TCC	p.P28S
Pat_41	Post-Resistance	C14orf105	55195	37	14	57948309	57948309	Nonsense_Mutation	SNP	G	A	19	285	c.463C>T	c.(463-465)CAA>TAA	p.Q155*
Pat_41	Post-Resistance	C14orf105	55195	37	14	57960247	57960247	Missense_Mutation	SNP	G	A	21	251	c.187C>T	c.(187-189)CCT>TCT	p.P63S
Pat_41	Post-Resistance	ARID4A	5926	37	14	58814531	58814531	Missense_Mutation	SNP	C	T	13	184	c.1339C>T	c.(1339-1341)CCT>TCT	p.P447S
Pat_41	Post-Resistance	C14orf135	64430	37	14	60581747	60581747	Missense_Mutation	SNP	C	T	9	98	c.223C>T	c.(223-225)CCA>TCA	p.P75S
Pat_41	Post-Resistance	C14orf39	317761	37	14	60936330	60936330	Missense_Mutation	SNP	G	A	23	240	c.596C>T	c.(595-597)GCC>GTC	p.A199V
Pat_41	Post-Resistance	SIX1	6495	37	14	61113141	61113141	Missense_Mutation	SNP	C	T	9	164	c.715G>A	c.(715-717)GGC>AGC	p.G239S
Pat_41	Post-Resistance	MNAT1	4331	37	14	61285492	61285492	Missense_Mutation	SNP	C	T	12	220	c.614C>T	c.(613-615)TCT>TTT	p.S205F
Pat_41	Post-Resistance	TRMT5	57570	37	14	61442231	61442231	Missense_Mutation	SNP	G	A	14	221	c.1406C>T	c.(1405-1407)CCT>CTT	p.P469L
Pat_41	Post-Resistance	TRMT5	57570	37	14	61446390	61446390	Missense_Mutation	SNP	G	A	21	400	c.226C>T	c.(226-228)CCT>TCT	p.P76S
Pat_41	Post-Resistance	SLC38A6	145389	37	14	61517308	61517308	Missense_Mutation	SNP	G	A	16	176	c.1004G>A	c.(1003-1005)TGC>TAC	p.C335Y
Pat_41	Post-Resistance	PRKCH	5583	37	14	61920000	61920000	Missense_Mutation	SNP	G	A	33	215	c.889G>A	c.(889-891)GTA>ATA	p.V297I
Pat_41	Post-Resistance	GPHB5	122876	37	14	63784554	63784554	Missense_Mutation	SNP	C	T	4	44	c.10G>A	c.(10-12)GCA>ACA	p.A4T
Pat_41	Post-Resistance	SYNE2	23224	37	14	64518670	64518670	Missense_Mutation	SNP	C	T	27	215	c.8039C>T	c.(8038-8040)TCT>TTT	p.S2680F
Pat_41	Post-Resistance	SYNE2	23224	37	14	64560166	64560166	Missense_Mutation	SNP	C	T	68	504	c.12076C>T	c.(12076-12078)CCA>TCA	p.P4026S
Pat_41	Post-Resistance	SYNE2	23224	37	14	64676163	64676163	Missense_Mutation	SNP	G	A	13	56	c.18407G>A	c.(18406-18408)CGC>CAC	p.R6136H
Pat_41	Post-Resistance	MTHFD1	4522	37	14	64894107	64894107	Missense_Mutation	SNP	G	A	19	178	c.1180G>A	c.(1180-1182)GTG>ATG	p.V394M
Pat_41	Post-Resistance	HSPA2	3306	37	14	65009020	65009020	Missense_Mutation	SNP	G	A	7	95	c.1453G>A	c.(1453-1455)GCC>ACC	p.A485T
Pat_41	Post-Resistance	C14orf50	145376	37	14	65019531	65019531	Splice_Site	SNP	G	A	16	153	c.135_splice	c.e3-1	p.R45_splice

Pat_41	Post-Resistance	C14orf50	145376	37	14	65054832	65054832	Missense_Mutation	SNP	G	A	5	180	c.901G>A	c.(901-903)GCA>ACA	p.A301T
Pat_41	Post-Resistance	PLEKHG3	26030	37	14	65208274	65208274	Missense_Mutation	SNP	G	A	4	105	c.2039G>A	c.(2038-2040)AGC>AAC	p.S680N
Pat_41	Post-Resistance	SPTB	6710	37	14	65234389	65234389	Missense_Mutation	SNP	G	A	6	151	c.6211C>T	c.(6211-6213)CCC>TCC	p.P2071S
Pat_41	Post-Resistance	SPTB	6710	37	14	65263411	65263411	Missense_Mutation	SNP	G	A	7	80	c.1205C>T	c.(1204-1206)GCT>GTT	p.A402V
Pat_41	Post-Resistance	GPHN	10243	37	14	67626201	67626201	Missense_Mutation	SNP	C	T	31	321	c.1807C>T	c.(1807-1809)CCA>TCA	p.P603S
Pat_41	Post-Resistance	GPHN	10243	37	14	67647637	67647637	Missense_Mutation	SNP	G	A	9	187	c.2194G>A	c.(2194-2196)GTC>ATC	p.V732I
Pat_41	Post-Resistance	RDH12	145226	37	14	68195941	68195941	Missense_Mutation	SNP	G	A	93	368	c.692G>A	c.(691-693)GGC>GAC	p.G231D
Pat_41	Post-Resistance	ZFYVE26	23503	37	14	68233124	68233124	Missense_Mutation	SNP	T	C	11	262	c.5831A>G	c.(5830-5832)CAC>CGC	p.H1944R
Pat_41	Post-Resistance	ZFYVE26	23503	37	14	68256267	68256267	Missense_Mutation	SNP	G	A	16	251	c.2804C>T	c.(2803-2805)ACC>ATC	p.T935I
Pat_41	Post-Resistance	ZFYVE26	23503	37	14	68273324	68273324	Missense_Mutation	SNP	C	T	14	147	c.955G>A	c.(955-957)GCT>ACT	p.A319T
Pat_41	Post-Resistance	RAD51L1	5890	37	14	68331819	68331819	Missense_Mutation	SNP	G	A	7	165	c.415G>A	c.(415-417)GTG>ATG	p.V139M
Pat_41	Post-Resistance	ZFP36L1	677	37	14	69256443	69256443	Missense_Mutation	SNP	G	A	14	153	c.824C>T	c.(823-825)ACC>ATC	p.T275I
Pat_41	Post-Resistance	GALNTL1	57452	37	14	69787567	69787567	Missense_Mutation	SNP	G	A	5	143	c.317G>A	c.(316-318)CGG>CAG	p.R106Q
Pat_41	Post-Resistance	ADAM21	8747	37	14	70924713	70924713	Missense_Mutation	SNP	C	T	5	137	c.497C>T	c.(496-498)ACA>ATA	p.T166I
Pat_41	Post-Resistance	MAP3K9	4293	37	14	71227752	71227752	Missense_Mutation	SNP	G	A	28	345	c.968C>T	c.(967-969)GCC>GTC	p.A323V
Pat_41	Post-Resistance	PCNX	22990	37	14	71443928	71443928	Missense_Mutation	SNP	G	A	20	157	c.874G>A	c.(874-876)GCT>ACT	p.A292T
Pat_41	Post-Resistance	PCNX	22990	37	14	71492934	71492934	Missense_Mutation	SNP	C	T	4	109	c.3284C>T	c.(3283-3285)ACC>ATC	p.T1095I
Pat_41	Post-Resistance	PCNX	22990	37	14	71575321	71575321	Missense_Mutation	SNP	G	A	8	237	c.6302G>A	c.(6301-6303)GGC>GAC	p.G2101D
Pat_41	Post-Resistance	SIPA1L1	26037	37	14	72172002	72172002	Missense_Mutation	SNP	G	A	45	261	c.3773G>A	c.(3772-3774)GGG>GAG	p.G1258E
Pat_41	Post-Resistance	SIPA1L1	26037	37	14	72176117	72176117	Missense_Mutation	SNP	G	A	26	224	c.4007G>A	c.(4006-4008)AGC>AAC	p.S1336N
Pat_41	Post-Resistance	SIPA1L1	26037	37	14	72176140	72176140	Missense_Mutation	SNP	G	A	41	136	c.4030G>A	c.(4030-4032)GGG>AGG	p.G1344R
Pat_41	Post-Resistance	RGS6	9628	37	14	72936756	72936756	Nonsense_Mutation	SNP	G	A	18	169	c.501G>A	c.(499-501)TGG>TGA	p.W167*
Pat_41	Post-Resistance	ZFYVE1	53349	37	14	73437604	73437604	Missense_Mutation	SNP	G	A	10	75	c.2320C>T	c.(2320-2322)CCC>TCC	p.P774S
Pat_41	Post-Resistance	ZFYVE1	53349	37	14	73440794	73440794	Missense_Mutation	SNP	G	A	14	200	c.2095C>T	c.(2095-2097)CCA>TCA	p.P699S
Pat_41	Post-Resistance	RBM25	58517	37	14	73576052	73576052	Missense_Mutation	SNP	G	A	11	168	c.1544G>A	c.(1543-1545)GGA>GAA	p.G515E
Pat_41	Post-Resistance	ACOT1	641371	37	14	74008335	74008335	Missense_Mutation	SNP	C	T	28	240	c.596C>T	c.(595-597)ACC>ATC	p.T199I
Pat_41	Post-Resistance	C14orf43	91748	37	14	74196600	74196600	Missense_Mutation	SNP	G	A	10	122	c.1838C>T	c.(1837-1839)ACC>ATC	p.T613I
Pat_41	Post-Resistance	FAM161B	145483	37	14	74404361	74404361	Missense_Mutation	SNP	C	T	14	298	c.1609G>A	c.(1609-1611)GAG>AAG	p.E537K
Pat_41	Post-Resistance	VSX2	338917	37	14	74726396	74726396	Missense_Mutation	SNP	C	T	12	188	c.671C>T	c.(670-672)GCC>GTC	p.A224V
Pat_41	Post-Resistance	YLPM1	56252	37	14	75230492	75230492	Nonsense_Mutation	SNP	G	A	5	122	c.300G>A	c.(298-300)TGG>TGA	p.W100*
Pat_41	Post-Resistance	YLPM1	56252	37	14	75283760	75283760	Missense_Mutation	SNP	G	A	3	64	c.5812G>A	c.(5812-5814)GTT>ATT	p.V1938I
Pat_41	Post-Resistance	PROX2	283571	37	14	75329567	75329567	Missense_Mutation	SNP	G	A	16	81	c.971C>T	c.(970-972)CCC>CTC	p.P324L
Pat_41	Post-Resistance	DLST	1743	37	14	75360128	75360128	Splice_Site	SNP	G	A	10	195	c.672_splice	c.e9+1	p.R224_splice
Pat_41	Post-Resistance	EIF2B2	8892	37	14	75470313	75470313	Missense_Mutation	SNP	C	T	7	185	c.344C>T	c.(343-345)TCC>TTC	p.S115F
Pat_41	Post-Resistance	NEK9	91754	37	14	75558055	75558055	Missense_Mutation	SNP	C	T	10	136	c.2360G>A	c.(2359-2361)GGA>GAA	p.G787E
Pat_41	Post-Resistance	BATF	10538	37	14	76013009	76013009	Missense_Mutation	SNP	C	T	7	16	c.373C>T	c.(373-375)CCC>TCC	p.P125S
Pat_41	Post-Resistance	FLVCR2	55640	37	14	76112793	76112793	Missense_Mutation	SNP	C	T	6	123	c.1559C>T	c.(1558-1560)GCT>GTT	p.A520V
Pat_41	Post-Resistance	C14orf118	55668	37	14	76642970	76642970	Missense_Mutation	SNP	C	T	14	223	c.989C>T	c.(988-990)ACC>ATC	p.T330I
Pat_41	Post-Resistance	KIAA1737	85457	37	14	77580174	77580174	Missense_Mutation	SNP	G	A	10	84	c.713G>A	c.(712-714)GGA>GAA	p.G238E
Pat_41	Post-Resistance	SPTLC2	9517	37	14	78021671	78021671	Missense_Mutation	SNP	G	A	25	374	c.1148C>T	c.(1147-1149)GCT>GTT	p.A383V
Pat_41	Post-Resistance	C14orf156	81892	37	14	78177234	78177234	Missense_Mutation	SNP	C	T	8	293	c.151C>T	c.(151-153)CCT>TCT	p.P51S
Pat_41	Post-Resistance	SNW1	22938	37	14	78189609	78189609	Missense_Mutation	SNP	C	T	22	229	c.1045G>A	c.(1045-1047)GCA>ACA	p.A349T
Pat_41	Post-Resistance	NRXN3	9369	37	14	79432716	79432716	Missense_Mutation	SNP	G	A	17	397	c.1625G>A	c.(1624-1626)GGC>GAC	p.G542D
Pat_41	Post-Resistance	STON2	85439	37	14	81837504	81837504	Nonsense_Mutation	SNP	C	T	7	170	c.399G>A	c.(397-399)TGG>TGA	p.W133*
Pat_41	Post-Resistance	GALC	2581	37	14	88407853	88407853	Missense_Mutation	SNP	C	T	11	445	c.1720G>A	c.(1720-1722)GGA>AGA	p.G574R
Pat_41	Post-Resistance	GALC	2581	37	14	88454487	88454487	Splice_Site	SNP	C	T	28	221	c.328_splice	c.e3+1	p.D110_splice
Pat_41	Post-Resistance	PTPN21	11099	37	14	88946585	88946585	Missense_Mutation	SNP	G	A	10	87	c.1190C>T	c.(1189-1191)GCA>GTA	p.A397V

Pat_41	Post-Resistance	TDP1	55775	37	14	90450989	90450989	Nonsense_Mutation	SNP	G	A	18	319	c.1014G>A	c.(1012-1014)TGG>TGA	p.W338*
Pat_41	Post-Resistance	C14orf102	55051	37	14	90778814	90778814	Missense_Mutation	SNP	C	T	8	266	c.481G>A	c.(481-483)GAA>AAA	p.E161K
Pat_41	Post-Resistance	C14orf102	55051	37	14	90778817	90778817	Missense_Mutation	SNP	C	T	20	248	c.478G>A	c.(478-480)GGA>AGA	p.G160R
Pat_41	Post-Resistance	CATSPERB	79820	37	14	92126274	92126274	Missense_Mutation	SNP	G	A	15	133	c.1339C>T	c.(1339-1341)CAT>TAT	p.H447Y
Pat_41	Post-Resistance	TC2N	123036	37	14	92258724	92258724	Missense_Mutation	SNP	G	A	16	262	c.1034C>T	c.(1033-1035)CCT>CTT	p.P345L
Pat_41	Post-Resistance	FBLN5	10516	37	14	92347741	92347741	Missense_Mutation	SNP	C	T	16	218	c.884G>A	c.(883-885)AGG>AAG	p.R295K
Pat_41	Post-Resistance	TRIP11	9321	37	14	92480721	92480721	Missense_Mutation	SNP	C	T	8	99	c.1024G>A	c.(1024-1026)GAA>AAA	p.E342K
Pat_41	Post-Resistance	ATXN3	4287	37	14	92530756	92530756	Missense_Mutation	SNP	C	T	20	265	c.994G>A	c.(994-996)GAT>AAT	p.D332N
Pat_41	Post-Resistance	SLC24A4	123041	37	14	92953035	92953035	Missense_Mutation	SNP	G	A	4	132	c.1397G>A	c.(1396-1398)GGG>GAG	p.G466E
Pat_41	Post-Resistance	RIN3	79890	37	14	93142951	93142951	Missense_Mutation	SNP	G	A	5	66	c.2467G>A	c.(2467-2469)GGT>AGT	p.G823S
Pat_41	Post-Resistance	UBR7	55148	37	14	93686745	93686745	Missense_Mutation	SNP	G	A	26	304	c.1111G>A	c.(1111-1113)GAA>AAA	p.E371K
Pat_41	Post-Resistance	KIAA1409	57578	37	14	94069654	94069654	Missense_Mutation	SNP	G	A	31	175	c.3113G>A	c.(3112-3114)CGC>CAC	p.R1038H
Pat_41	Post-Resistance	KIAA1409	57578	37	14	94120289	94120289	Missense_Mutation	SNP	G	A	26	487	c.5852G>A	c.(5851-5853)GGG>GAG	p.G1951E
Pat_41	Post-Resistance	ASB2	51676	37	14	94420818	94420818	Missense_Mutation	SNP	G	A	7	82	c.179C>T	c.(178-180)CCC>CTC	p.P60L
Pat_41	Post-Resistance	DDX24	57062	37	14	94528586	94528586	Missense_Mutation	SNP	C	T	6	248	c.1100G>A	c.(1099-1101)GGA>GAA	p.G367E
Pat_41	Post-Resistance	PPP4R4	57718	37	14	94733334	94733334	Missense_Mutation	SNP	G	A	18	149	c.2417G>A	c.(2416-2418)GGG>GAG	p.G806E
Pat_41	Post-Resistance	SERPINA6	866	37	14	94770892	94770892	Missense_Mutation	SNP	C	T	23	106	c.1081G>A	c.(1081-1083)GCT>ACT	p.A361T
Pat_41	Post-Resistance	SERPINA6	866	37	14	94780820	94780820	Missense_Mutation	SNP	C	T	7	104	c.166G>A	c.(166-168)GCC>ACC	p.A56T
Pat_41	Post-Resistance	SERPINA11	256394	37	14	94915078	94915078	Missense_Mutation	SNP	C	T	10	101	c.34G>A	c.(34-36)GGG>AGG	p.G12R
Pat_41	Post-Resistance	DICER1	23405	37	14	95570047	95570047	Missense_Mutation	SNP	G	A	45	177	c.3686C>T	c.(3685-3687)CCC>CTC	p.P1229L
Pat_41	Post-Resistance	DICER1	23405	37	14	95570392	95570392	Missense_Mutation	SNP	G	A	6	59	c.3341C>T	c.(3340-3342)TCT>TTT	p.S1114F
Pat_41	Post-Resistance	TCL1A	8115	37	14	96178636	96178636	Missense_Mutation	SNP	G	A	13	130	c.218C>T	c.(217-219)CCT>CTT	p.P73L
Pat_41	Post-Resistance	ATG2B	55102	37	14	96781490	96781490	Splice_Site	SNP	C	T	6	107	c.3642_splice	c.e23+1	p.Q1214_splice
Pat_41	Post-Resistance	C14orf129	51527	37	14	96848664	96848664	Missense_Mutation	SNP	G	A	8	345	c.80G>A	c.(79-81)GGA>GAA	p.G27E
Pat_41	Post-Resistance	AK7	122481	37	14	96924474	96924474	Missense_Mutation	SNP	G	A	6	60	c.1282G>A	c.(1282-1284)GAA>AAA	p.E428K
Pat_41	Post-Resistance	PAPOLA	10914	37	14	96994315	96994315	Missense_Mutation	SNP	T	C	28	422	c.467T>C	c.(466-468)GTT>GCT	p.V156A
Pat_41	Post-Resistance	SETD3	84193	37	14	99880270	99880270	Missense_Mutation	SNP	G	A	9	146	c.677C>T	c.(676-678)ACC>ATC	p.T226I
Pat_41	Post-Resistance	C14orf68	283600	37	14	100795750	100795750	Nonsense_Mutation	SNP	G	A	19	219	c.695G>A	c.(694-696)TGG>TAG	p.W232*
Pat_41	Post-Resistance	DYNC1H1	1778	37	14	102469268	102469268	Missense_Mutation	SNP	G	A	4	92	c.4849G>A	c.(4849-4851)GAA>AAA	p.E1617K
Pat_41	Post-Resistance	DYNC1H1	1778	37	14	102481607	102481607	Missense_Mutation	SNP	G	A	6	49	c.7180G>A	c.(7180-7182)GCA>ACA	p.A2394T
Pat_41	Post-Resistance	HSP90AA1	3320	37	14	102548063	102548063	Missense_Mutation	SNP	C	T	35	388	c.2185G>A	c.(2185-2187)GAA>AAA	p.E729K
Pat_41	Post-Resistance	TECPR2	9895	37	14	102901274	102901274	Missense_Mutation	SNP	G	A	5	96	c.2120G>A	c.(2119-2121)GGT>GAT	p.G707D
Pat_41	Post-Resistance	TRAF3	7187	37	14	103371855	103371855	Missense_Mutation	SNP	G	A	15	234	c.1441G>A	c.(1441-1443)GAA>AAA	p.E481K
Pat_41	Post-Resistance	CDC42BPB	9578	37	14	103404464	103404464	Missense_Mutation	SNP	G	A	32	204	c.4981C>T	c.(4981-4983)CCA>TCA	p.P1661S
Pat_41	Post-Resistance	BAG5	9529	37	14	104027231	104027231	Missense_Mutation	SNP	G	A	19	343	c.271C>T	c.(271-273)CGG>TGG	p.R91W
Pat_41	Post-Resistance	KLC1	3831	37	14	104038036	104038036	Missense_Mutation	SNP	C	T	16	225	c.200C>T	c.(199-201)CCT>CTT	p.P67L
Pat_41	Post-Resistance	ZFYVE21	79038	37	14	104195517	104195517	Missense_Mutation	SNP	G	A	13	54	c.524G>A	c.(523-525)GGA>GAA	p.G175E
Pat_41	Post-Resistance	AHNAK2	113146	37	14	105405604	105405604	Missense_Mutation	SNP	G	A	4	87	c.16184C>T	c.(16183-16185)TCC>TTC	p.S5395F
Pat_41	Post-Resistance	AHNAK2	113146	37	14	105411634	105411634	Missense_Mutation	SNP	G	A	25	125	c.10154C>T	c.(10153-10155)GCT>GTT	p.A3385V
Pat_41	Post-Resistance	AHNAK2	113146	37	14	105414474	105414474	Missense_Mutation	SNP	C	T	10	176	c.7314G>A	c.(7312-7314)ATG>ATA	p.M2438I
Pat_41	Post-Resistance	AHNAK2	113146	37	14	105414536	105414536	Missense_Mutation	SNP	C	T	9	154	c.7252G>A	c.(7252-7254)GGC>AGC	p.G2418S
Pat_41	Post-Resistance	AHNAK2	113146	37	14	105414764	105414764	Missense_Mutation	SNP	C	T	24	277	c.7024G>A	c.(7024-7026)GAT>AAT	p.D2342N
Pat_41	Post-Resistance	AHNAK2	113146	37	14	105417320	105417320	Missense_Mutation	SNP	C	T	78	422	c.4468G>A	c.(4468-4470)GAC>AAC	p.D1490N
Pat_41	Post-Resistance	CDCA4	55038	37	14	105478184	105478184	Missense_Mutation	SNP	G	A	27	148	c.83C>T	c.(82-84)TCC>TTC	p.S28F
Pat_41	Post-Resistance	NUDT14	256281	37	14	105643073	105643073	Missense_Mutation	SNP	C	T	6	185	c.226G>A	c.(226-228)GGG>AGG	p.G76R
Pat_41	Post-Resistance	PACS2	23241	37	14	105846131	105846131	Missense_Mutation	SNP	C	T	25	135	c.1015C>T	c.(1015-1017)CAC>TAC	p.H339Y
Pat_41	Post-Resistance	OR4M2	390538	37	15	22368615	22368615	Missense_Mutation	SNP	C	T	17	233	c.40C>T	c.(40-42)CTC>TTC	p.L14F

Pat_41	Post-Resistance	TUBGCP5	114791	37	15	22848242	22848242	Missense_Mutation	SNP	C	T	7	73	c.832C>T	c.(832-834)CTT>TTT	p.L278F
Pat_41	Post-Resistance	SNRPN	6638	37	15	25221514	25221514	Missense_Mutation	SNP	G	A	8	209	c.218G>A	c.(217-219)CGT>CAT	p.R73H
Pat_41	Post-Resistance	SNRPN	6638	37	15	25222934	25222934	Missense_Mutation	SNP	C	T	7	133	c.430C>T	c.(430-432)CCA>TCA	p.P144S
Pat_41	Post-Resistance	ATP10A	57194	37	15	25981245	25981245	Missense_Mutation	SNP	C	T	12	160	c.698G>A	c.(697-699)TGC>TAC	p.C233Y
Pat_41	Post-Resistance	OCA2	4948	37	15	28202856	28202856	Nonsense_Mutation	SNP	C	T	9	70	c.1662G>A	c.(1660-1662)TGG>TGA	p.W554*
Pat_41	Post-Resistance	HERC2	8924	37	15	28422190	28422190	Missense_Mutation	SNP	G	A	8	90	c.9338C>T	c.(9337-9339)GCC>GTC	p.A3113V
Pat_41	Post-Resistance	HERC2	8924	37	15	28474855	28474855	Missense_Mutation	SNP	C	T	8	436	c.4948G>A	c.(4948-4950)GAT>AAT	p.D1650N
Pat_41	Post-Resistance	APBA2	321	37	15	29346358	29346358	Missense_Mutation	SNP	C	T	39	178	c.271C>T	c.(271-273)CCT>TCT	p.P91S
Pat_41	Post-Resistance	APBA2	321	37	15	29346562	29346562	Missense_Mutation	SNP	G	A	7	75	c.475G>A	c.(475-477)GAC>AAC	p.D159N
Pat_41	Post-Resistance	TJP1	7082	37	15	30012903	30012903	Missense_Mutation	SNP	C	T	11	90	c.2422G>A	c.(2422-2424)GCT>ACT	p.A808T
Pat_41	Post-Resistance	MTMR10	54893	37	15	31234238	31234238	Missense_Mutation	SNP	G	A	22	352	c.1769C>T	c.(1768-1770)GCC>GTC	p.A590V
Pat_41	Post-Resistance	ARHGAP11A	9824	37	15	32908495	32908495	Missense_Mutation	SNP	G	A	10	48	c.83G>A	c.(82-84)GGG>GAG	p.G28E
Pat_41	Post-Resistance	RYR3	6263	37	15	33842432	33842432	Missense_Mutation	SNP	C	T	5	48	c.887C>T	c.(886-888)GCC>GTC	p.A296V
Pat_41	Post-Resistance	RYR3	6263	37	15	33855095	33855095	Missense_Mutation	SNP	C	T	6	63	c.1030C>T	c.(1030-1032)CCA>TCA	p.P344S
Pat_41	Post-Resistance	RYR3	6263	37	15	33916169	33916169	Missense_Mutation	SNP	C	T	72	282	c.2519C>T	c.(2518-2520)ACC>ATC	p.T840I
Pat_41	Post-Resistance	RYR3	6263	37	15	33916180	33916180	Missense_Mutation	SNP	C	T	43	350	c.2530C>T	c.(2530-2532)CTC>TTC	p.L844F
Pat_41	Post-Resistance	RYR3	6263	37	15	34133026	34133026	Missense_Mutation	SNP	G	A	15	84	c.12979G>A	c.(12979-12981)GCA>ACA	p.A4327T
Pat_41	Post-Resistance	TMEM85	51234	37	15	34520009	34520009	Missense_Mutation	SNP	C	T	9	147	c.317C>T	c.(316-318)GCC>GTC	p.A106V
Pat_41	Post-Resistance	SLC12A6	9990	37	15	34533510	34533510	Missense_Mutation	SNP	G	A	5	179	c.2191C>T	c.(2191-2193)CGT>TGT	p.R731C
Pat_41	Post-Resistance	C15orf55	256646	37	15	34642915	34642915	Missense_Mutation	SNP	C	T	4	113	c.736C>T	c.(736-738)CGT>TGT	p.R246C
Pat_41	Post-Resistance	C15orf55	256646	37	15	34642939	34642939	Missense_Mutation	SNP	A	G	65	78	c.760A>G	c.(760-762)ACT>GCT	p.T254A
Pat_41	Post-Resistance	C15orf55	256646	37	15	34647827	34647827	Missense_Mutation	SNP	C	T	8	53	c.1534C>T	c.(1534-1536)CCT>TCT	p.P512S
Pat_41	Post-Resistance	C15orf55	256646	37	15	34648920	34648920	Missense_Mutation	SNP	C	T	12	35	c.2627C>T	c.(2626-2628)TCC>TTC	p.S876F
Pat_41	Post-Resistance	FAM98B	283742	37	15	38757556	38757556	Missense_Mutation	SNP	G	A	4	110	c.304G>A	c.(304-306)GAT>AAT	p.D102N
Pat_41	Post-Resistance	EIF2AK4	440275	37	15	40265849	40265849	Missense_Mutation	SNP	G	A	36	316	c.1717G>A	c.(1717-1719)GCT>ACT	p.A573T
Pat_41	Post-Resistance	BUB1B	701	37	15	40494795	40494795	Missense_Mutation	SNP	C	T	22	456	c.1634C>T	c.(1633-1635)CCT>CTT	p.P545L
Pat_41	Post-Resistance	BUB1B	701	37	15	40498511	40498511	Missense_Mutation	SNP	C	T	6	119	c.1861C>T	c.(1861-1863)CCT>TCT	p.P621S
Pat_41	Post-Resistance	BUB1B	701	37	15	40505561	40505561	Missense_Mutation	SNP	C	T	13	128	c.2564C>T	c.(2563-2565)ACC>ATC	p.T855I
Pat_41	Post-Resistance	PAK6	56924	37	15	40558338	40558338	Missense_Mutation	SNP	G	A	7	32	c.500G>A	c.(499-501)CGG>CAG	p.R167Q
Pat_41	Post-Resistance	DISP2	85455	37	15	40659601	40659601	Missense_Mutation	SNP	G	A	15	515	c.1288G>A	c.(1288-1290)GTG>ATG	p.V430M
Pat_41	Post-Resistance	DISP2	85455	37	15	40662506	40662506	Missense_Mutation	SNP	G	A	6	113	c.4193G>A	c.(4192-4194)GGC>GAC	p.G1398D
Pat_41	Post-Resistance	CHST14	113189	37	15	40764301	40764301	Missense_Mutation	SNP	G	A	5	103	c.889G>A	c.(889-891)GGC>AGC	p.G297S
Pat_41	Post-Resistance	CASC5	57082	37	15	40916810	40916810	Missense_Mutation	SNP	C	T	8	118	c.4426C>T	c.(4426-4428)CCT>TCT	p.P1476S
Pat_41	Post-Resistance	EXD1	161829	37	15	41476314	41476314	Missense_Mutation	SNP	C	T	16	171	c.1360G>A	c.(1360-1362)GAA>AAA	p.E454K
Pat_41	Post-Resistance	EXD1	161829	37	15	41487977	41487977	Missense_Mutation	SNP	G	A	7	63	c.542C>T	c.(541-543)ACA>ATA	p.T181I
Pat_41	Post-Resistance	RTF1	23168	37	15	41763531	41763531	Missense_Mutation	SNP	G	A	7	205	c.1187G>A	c.(1186-1188)AGC>AAC	p.S396N
Pat_41	Post-Resistance	RPAP1	26015	37	15	41814373	41814373	Missense_Mutation	SNP	G	A	7	53	c.2818C>T	c.(2818-2820)CTC>TTC	p.L940F
Pat_41	Post-Resistance	RPAP1	26015	37	15	41822178	41822178	Splice_Site	SNP	C	T	5	45	c.944_splice	c.e8-1	p.A315_splice
Pat_41	Post-Resistance	TYRO3	7301	37	15	41861190	41861190	Missense_Mutation	SNP	C	T	10	116	c.1222C>T	c.(1222-1224)CCA>TCA	p.P408S
Pat_41	Post-Resistance	MGA	23269	37	15	42003155	42003155	Missense_Mutation	SNP	G	A	71	425	c.2692G>A	c.(2692-2694)GCA>ACA	p.A898T
Pat_41	Post-Resistance	MAPKBP1	23005	37	15	42105184	42105184	Missense_Mutation	SNP	C	T	16	216	c.704C>T	c.(703-705)ACT>ATT	p.T235I
Pat_41	Post-Resistance	JMJD7-PLA2G4B	8681	37	15	42136691	42136691	Missense_Mutation	SNP	C	T	16	97	c.902C>T	c.(901-903)GCC>GTC	p.A301V
Pat_41	Post-Resistance	SPTBN5	51332	37	15	42166131	42166131	Missense_Mutation	SNP	C	T	9	54	c.4697G>A	c.(4696-4698)TGC>TAC	p.C1566Y
Pat_41	Post-Resistance	PLA2G4E	123745	37	15	42278083	42278083	Missense_Mutation	SNP	G	A	5	22	c.2069C>T	c.(2068-2070)GCC>GTC	p.A690V
Pat_41	Post-Resistance	TMEM87A	25963	37	15	42523457	42523457	Missense_Mutation	SNP	G	A	22	113	c.1064C>T	c.(1063-1065)GCC>GTC	p.A355V
Pat_41	Post-Resistance	TMEM87A	25963	37	15	42556401	42556401	Missense_Mutation	SNP	C	T	6	39	c.292G>A	c.(292-294)GCA>ACA	p.A98T
Pat_41	Post-Resistance	ZFP106	64397	37	15	42730815	42730815	Missense_Mutation	SNP	G	A	3	68	c.4526C>T	c.(4525-4527)TCT>TTT	p.S1509F

Pat_41	Post-Resistance	ZFP106	64397	37	15	42742210	42742210	Missense_Mutation	SNP	C	T	11	145	c.2191G>A	c.(2191-2193)GAT>AAT	p.D731N
Pat_41	Post-Resistance	CDAN1	146059	37	15	43028515	43028515	Missense_Mutation	SNP	G	A	5	37	c.554C>T	c.(553-555)CCC>CTC	p.P185L
Pat_41	Post-Resistance	UBR1	197131	37	15	43347061	43347061	Missense_Mutation	SNP	C	T	20	139	c.1318G>A	c.(1318-1320)GTC>ATC	p.V440I
Pat_41	Post-Resistance	UBR1	197131	37	15	43351996	43351996	Missense_Mutation	SNP	G	A	22	114	c.889C>T	c.(889-891)CCA>TCA	p.P297S
Pat_41	Post-Resistance	UBR1	197131	37	15	43367242	43367242	Missense_Mutation	SNP	C	T	78	330	c.463G>A	c.(463-465)GAG>AAG	p.E155K
Pat_41	Post-Resistance	TP53BP1	7158	37	15	43739659	43739659	Missense_Mutation	SNP	G	A	5	77	c.2726C>T	c.(2725-2727)CCT>CTT	p.P909L
Pat_41	Post-Resistance	STRC	161497	37	15	43892271	43892271	Missense_Mutation	SNP	G	A	4	97	c.5126C>T	c.(5125-5127)ACC>ATC	p.T1709I
Pat_41	Post-Resistance	PDIA3	2923	37	15	44038801	44038801	Missense_Mutation	SNP	G	A	11	76	c.64G>A	c.(64-66)GCC>ACC	p.A22T
Pat_41	Post-Resistance	PDIA3	2923	37	15	44058135	44058135	Missense_Mutation	SNP	G	A	15	119	c.770G>A	c.(769-771)GGC>GAC	p.G257D
Pat_41	Post-Resistance	SERINC4	619189	37	15	44089112	44089112	Missense_Mutation	SNP	C	T	36	303	c.139G>A	c.(139-141)GCT>ACT	p.A47T
Pat_41	Post-Resistance	C15orf63	25764	37	15	44092969	44092969	Missense_Mutation	SNP	C	T	4	45	c.173C>T	c.(172-174)TCC>TTC	p.S58F
Pat_41	Post-Resistance	MFAP1	4236	37	15	44097432	44097432	Missense_Mutation	SNP	G	A	5	143	c.1180C>T	c.(1180-1182)CTT>TTT	p.L394F
Pat_41	Post-Resistance	SPG11	80208	37	15	44865859	44865859	Nonsense_Mutation	SNP	G	A	5	55	c.6091C>T	c.(6091-6093)CGA>TGA	p.R2031*
Pat_41	Post-Resistance	SPG11	80208	37	15	44951346	44951346	Missense_Mutation	SNP	C	T	9	305	c.598G>A	c.(598-600)GTG>ATG	p.V200M
Pat_41	Post-Resistance	DUOX2	50506	37	15	45404102	45404102	Missense_Mutation	SNP	G	A	5	58	c.377C>T	c.(376-378)GCC>GTC	p.A126V
Pat_41	Post-Resistance	DUOX1	53905	37	15	45448032	45448032	Missense_Mutation	SNP	G	A	15	259	c.3607G>A	c.(3607-3609)GCC>ACC	p.A1203T
Pat_41	Post-Resistance	MYEF2	50804	37	15	48450388	48450388	Missense_Mutation	SNP	G	A	6	145	c.905C>T	c.(904-906)CCT>CTT	p.P302L
Pat_41	Post-Resistance	SLC12A1	6557	37	15	48539187	48539187	Missense_Mutation	SNP	C	T	8	626	c.1534C>T	c.(1534-1536)CTT>TTT	p.L512F
Pat_41	Post-Resistance	FBN1	2200	37	15	48714178	48714178	Missense_Mutation	SNP	C	T	26	117	c.7541G>A	c.(7540-7542)GGA>GAA	p.G2514E
Pat_41	Post-Resistance	FBN1	2200	37	15	48808499	48808499	Missense_Mutation	SNP	G	A	8	163	c.1208C>T	c.(1207-1209)CCC>CTC	p.P403L
Pat_41	Post-Resistance	CEP152	22995	37	15	49030589	49030589	Missense_Mutation	SNP	C	T	35	449	c.4822G>A	c.(4822-4824)GCT>ACT	p.A1608T
Pat_41	Post-Resistance	CEP152	22995	37	15	49054863	49054863	Missense_Mutation	SNP	C	T	6	73	c.2287G>A	c.(2287-2289)GAA>AAA	p.E763K
Pat_41	Post-Resistance	SHC4	399694	37	15	49127160	49127160	Missense_Mutation	SNP	G	A	4	32	c.1543C>T	c.(1543-1545)CCA>TCA	p.P515S
Pat_41	Post-Resistance	SECISBP2L	9728	37	15	49301504	49301504	Missense_Mutation	SNP	G	A	35	279	c.1936C>T	c.(1936-1938)CCT>TCT	p.P646S
Pat_41	Post-Resistance	SPPL2A	84888	37	15	51039816	51039816	Missense_Mutation	SNP	C	T	11	179	c.460G>A	c.(460-462)GAT>AAT	p.D154N
Pat_41	Post-Resistance	AP4E1	23431	37	15	51223077	51223077	Missense_Mutation	SNP	C	T	13	162	c.778C>T	c.(778-780)CCA>TCA	p.P260S
Pat_41	Post-Resistance	AP4E1	23431	37	15	51250845	51250845	Missense_Mutation	SNP	A	G	57	195	c.1705A>G	c.(1705-1707)AAT>GAT	p.N569D
Pat_41	Post-Resistance	CYP19A1	1588	37	15	51503123	51503123	Missense_Mutation	SNP	C	T	14	175	c.1394G>A	c.(1393-1395)GGA>GAA	p.G465E
Pat_41	Post-Resistance	CYP19A1	1588	37	15	51504669	51504669	Missense_Mutation	SNP	C	T	8	223	c.1111G>A	c.(1111-1113)GAC>AAC	p.D371N
Pat_41	Post-Resistance	GLDN	342035	37	15	51693888	51693888	Missense_Mutation	SNP	G	A	5	82	c.1126G>A	c.(1126-1128)GTT>ATT	p.V376I
Pat_41	Post-Resistance	TMOD2	29767	37	15	52090395	52090395	Missense_Mutation	SNP	C	T	3	36	c.734C>T	c.(733-735)GCT>GTT	p.A245V
Pat_41	Post-Resistance	TMOD2	29767	37	15	52100629	52100629	Missense_Mutation	SNP	G	A	8	200	c.1034G>A	c.(1033-1035)AGA>AAA	p.R345K
Pat_41	Post-Resistance	MYO5C	55930	37	15	52506800	52506800	Missense_Mutation	SNP	C	T	6	45	c.4042G>A	c.(4042-4044)GCC>ACC	p.A1348T
Pat_41	Post-Resistance	MYO5C	55930	37	15	52521391	52521391	Missense_Mutation	SNP	C	T	31	232	c.3146G>A	c.(3145-3147)GGG>GAG	p.G1049E
Pat_41	Post-Resistance	ONECUT1	3175	37	15	53081177	53081177	Missense_Mutation	SNP	G	A	4	106	c.905C>T	c.(904-906)ACC>ATC	p.T302I
Pat_41	Post-Resistance	UNC13C	440279	37	15	54542591	54542591	Missense_Mutation	SNP	G	A	15	118	c.3397G>A	c.(3397-3399)GTG>ATG	p.V1133M
Pat_41	Post-Resistance	PYGO1	26108	37	15	55838474	55838474	Missense_Mutation	SNP	G	A	11	560	c.1007C>T	c.(1006-1008)TCT>TTT	p.S336F
Pat_41	Post-Resistance	ZNF280D	54816	37	15	56961124	56961124	Missense_Mutation	SNP	C	T	19	297	c.1442G>A	c.(1441-1443)AGG>AAG	p.R481K
Pat_41	Post-Resistance	ALDH1A2	8854	37	15	58302858	58302858	Missense_Mutation	SNP	G	A	29	112	c.482C>T	c.(481-483)ACC>ATC	p.T161I
Pat_41	Post-Resistance	CCNB2	9133	37	15	59406644	59406644	Missense_Mutation	SNP	G	A	15	74	c.269G>A	c.(268-270)GGT>GAT	p.G90D
Pat_41	Post-Resistance	NARG2	79664	37	15	60770197	60770197	Translation_Start_Site	SNP	C	T	11	195	c.-20G>A	c.(-22--18)GAGTG>GAATG	
Pat_41	Post-Resistance	VPS13C	54832	37	15	62242617	62242617	Splice_Site	SNP	C	T	34	202	c.4537_splice	c.e41-1	p.A1513_splice
Pat_41	Post-Resistance	VPS13C	54832	37	15	62253795	62253795	Missense_Mutation	SNP	G	A	13	78	c.3901C>T	c.(3901-3903)CTT>TTT	p.L1301F
Pat_41	Post-Resistance	VPS13C	54832	37	15	62259578	62259578	Missense_Mutation	SNP	C	T	4	110	c.2980G>A	c.(2980-2982)GAG>AAG	p.E994K
Pat_41	Post-Resistance	TLN2	83660	37	15	62967473	62967473	Missense_Mutation	SNP	C	T	18	172	c.910C>T	c.(910-912)CTC>TTC	p.L304F
Pat_41	Post-Resistance	TLN2	83660	37	15	63131181	63131181	Splice_Site	SNP	G	A	10	225	c.7500_splice	c.e55+1	p.Q2500_splice
Pat_41	Post-Resistance	HERC1	8925	37	15	63904493	63904493	Missense_Mutation	SNP	G	A	3	42	c.14357C>T	c.(14356-14358)ACT>ATT	p.T4786I

Pat_41	Post-Resistance	HERC1	8925	37	15	63986511	63986511	Missense_Mutation	SNP	C	T	6	29	c.5480G>A	c.(5479-5481)GGG>GAG	p.G1827E
Pat_41	Post-Resistance	HERC1	8925	37	15	64041612	64041612	Missense_Mutation	SNP	C	T	114	507	c.2173G>A	c.(2173-2175)GCT>ACT	p.A725T
Pat_41	Post-Resistance	DAPK2	23604	37	15	64204397	64204397	Splice_Site	SNP	C	T	36	170	c.859_splice	c.e10-1	p.P287_splice
Pat_41	Post-Resistance	DAPK2	23604	37	15	64218255	64218255	Nonsense_Mutation	SNP	G	A	28	148	c.697C>T	c.(697-699)CAG>TAG	p.Q233*
Pat_41	Post-Resistance	ZNF609	23060	37	15	64915161	64915161	Missense_Mutation	SNP	G	A	10	88	c.883G>A	c.(883-885)GCT>ACT	p.A295T
Pat_41	Post-Resistance	ZNF609	23060	37	15	64973514	64973514	Missense_Mutation	SNP	C	T	36	592	c.4169C>T	c.(4168-4170)TCT>TTT	p.S1390F
Pat_41	Post-Resistance	PIF1	80119	37	15	65112045	65112045	Splice_Site	SNP	C	T	6	34	c.1333_splice	c.e8+1	p.G445_splice
Pat_41	Post-Resistance	SPG21	51324	37	15	65262548	65262548	Missense_Mutation	SNP	C	T	20	154	c.465G>A	c.(463-465)ATG>ATA	p.M155I
Pat_41	Post-Resistance	OSTBETA	123264	37	15	65345356	65345356	Missense_Mutation	SNP	G	A	8	22	c.241G>A	c.(241-243)GAT>AAT	p.D81N
Pat_41	Post-Resistance	CLPX	10845	37	15	65447338	65447338	Missense_Mutation	SNP	C	T	25	99	c.1393G>A	c.(1393-1395)GAA>AAA	p.E465K
Pat_41	Post-Resistance	IGDCC4	57722	37	15	65686851	65686851	Missense_Mutation	SNP	G	A	4	118	c.1612C>T	c.(1612-1614)CCC>TCC	p.P538S
Pat_41	Post-Resistance	IGDCC4	57722	37	15	65703556	65703556	Missense_Mutation	SNP	C	T	7	90	c.223G>A	c.(223-225)GAT>AAT	p.D75N
Pat_41	Post-Resistance	C15orf44	81556	37	15	65899703	65899703	Missense_Mutation	SNP	C	T	19	89	c.16G>A	c.(16-18)GTA>ATA	p.V6I
Pat_41	Post-Resistance	DENND4A	10260	37	15	65989644	65989644	Nonsense_Mutation	SNP	G	A	24	121	c.2779C>T	c.(2779-2781)CAA>TAA	p.Q927*
Pat_41	Post-Resistance	MEGF11	84465	37	15	66210399	66210399	Missense_Mutation	SNP	G	A	12	82	c.1991C>T	c.(1990-1992)GCC>GTC	p.A664V
Pat_41	Post-Resistance	MAP2K1	5604	37	15	66727463	66727463	Missense_Mutation	SNP	T	A	24	320	c.179T>A	c.(178-180)GTG>GAG	p.V60E
Pat_41	Post-Resistance	SMAD3	4088	37	15	67358595	67358595	Missense_Mutation	SNP	G	A	5	49	c.103G>A	c.(103-105)GTC>ATC	p.V35I
Pat_41	Post-Resistance	IQCH	64799	37	15	67649682	67649682	Splice_Site	SNP	G	A	6	166	c.638_splice	c.e7-1	p.A213_splice
Pat_41	Post-Resistance	PIAS1	8554	37	15	68466133	68466133	Missense_Mutation	SNP	G	A	12	82	c.1072G>A	c.(1072-1074)GAC>AAC	p.D358N
Pat_41	Post-Resistance	FEM1B	10116	37	15	68583233	68583233	Missense_Mutation	SNP	C	T	28	382	c.1537C>T	c.(1537-1539)CTT>TTT	p.L513F
Pat_41	Post-Resistance	CORO2B	10391	37	15	69006908	69006908	Missense_Mutation	SNP	C	T	32	173	c.776C>T	c.(775-777)TCC>TTC	p.S259F
Pat_41	Post-Resistance	CORO2B	10391	37	15	69006925	69006925	Missense_Mutation	SNP	G	A	16	251	c.793G>A	c.(793-795)GAG>AAG	p.E265K
Pat_41	Post-Resistance	TLE3	7090	37	15	70351756	70351756	Missense_Mutation	SNP	G	A	14	33	c.758C>T	c.(757-759)TCC>TTC	p.S253F
Pat_41	Post-Resistance	THSD4	79875	37	15	71535088	71535088	Missense_Mutation	SNP	C	T	14	143	c.565C>T	c.(565-567)CTC>TTC	p.L189F
Pat_41	Post-Resistance	THSD4	79875	37	15	72037505	72037505	Missense_Mutation	SNP	G	A	38	379	c.1967G>A	c.(1966-1968)AGT>AAT	p.S656N
Pat_41	Post-Resistance	THSD4	79875	37	15	72050323	72050323	Missense_Mutation	SNP	G	A	17	99	c.2498G>A	c.(2497-2499)GGC>GAC	p.G833D
Pat_41	Post-Resistance	MYO9A	4649	37	15	72154922	72154922	Missense_Mutation	SNP	C	T	20	226	c.6010G>A	c.(6010-6012)GCC>ACC	p.A2004T
Pat_41	Post-Resistance	MYO9A	4649	37	15	72190435	72190435	Missense_Mutation	SNP	C	T	8	124	c.4409G>A	c.(4408-4410)GGA>GAA	p.G1470E
Pat_41	Post-Resistance	MYO9A	4649	37	15	72193596	72193596	Nonsense_Mutation	SNP	C	T	14	139	c.3086G>A	c.(3085-3087)TGG>TAG	p.W1029*
Pat_41	Post-Resistance	MYO9A	4649	37	15	72227775	72227775	Missense_Mutation	SNP	C	T	18	169	c.2429G>A	c.(2428-2430)AGA>AAA	p.R810K
Pat_41	Post-Resistance	MYO9A	4649	37	15	72338085	72338085	Missense_Mutation	SNP	C	T	10	131	c.820G>A	c.(820-822)GGA>AGA	p.G274R
Pat_41	Post-Resistance	PKM2	5315	37	15	72511407	72511407	Missense_Mutation	SNP	G	A	14	201	c.32C>T	c.(31-33)GCC>GTC	p.A11V
Pat_41	Post-Resistance	PARP6	56965	37	15	72552862	72552862	Missense_Mutation	SNP	G	A	22	292	c.713C>T	c.(712-714)CCT>CTT	p.P238L
Pat_41	Post-Resistance	ADPGK	83440	37	15	73064173	73064173	Missense_Mutation	SNP	C	T	10	105	c.473G>A	c.(472-474)GGA>GAA	p.G158E
Pat_41	Post-Resistance	NEO1	4756	37	15	73590859	73590859	Missense_Mutation	SNP	C	T	21	192	c.4072C>T	c.(4072-4074)CCA>TCA	p.P1358S
Pat_41	Post-Resistance	CD276	80381	37	15	74001997	74001997	Missense_Mutation	SNP	G	A	4	112	c.1513G>A	c.(1513-1515)GAC>AAC	p.D505N
Pat_41	Post-Resistance	PML	5371	37	15	74336714	74336714	Missense_Mutation	SNP	C	T	17	51	c.2014C>T	c.(2014-2016)CCT>TCT	p.P672S
Pat_41	Post-Resistance	STRA6	64220	37	15	74483219	74483219	Missense_Mutation	SNP	C	T	6	93	c.889G>A	c.(889-891)GTG>ATG	p.V297M
Pat_41	Post-Resistance	SEMA7A	8482	37	15	74703085	74703085	Nonsense_Mutation	SNP	C	T	3	37	c.1881G>A	c.(1879-1881)TGG>TGA	p.W627*
Pat_41	Post-Resistance	ARID3B	10620	37	15	74836480	74836480	Missense_Mutation	SNP	C	T	4	101	c.203C>T	c.(202-204)CCC>CTC	p.P68L
Pat_41	Post-Resistance	ULK3	25989	37	15	75134640	75134640	Missense_Mutation	SNP	A	T	29	48	c.224T>A	c.(223-225)GTG>GAG	p.V75E
Pat_41	Post-Resistance	NEIL1	79661	37	15	75641568	75641568	Missense_Mutation	SNP	C	T	13	73	c.322C>T	c.(322-324)CCC>TCC	p.P108S
Pat_41	Post-Resistance	MAN2C1	4123	37	15	75649222	75649222	Missense_Mutation	SNP	C	T	16	132	c.2569G>A	c.(2569-2571)GAT>AAT	p.D857N
Pat_41	Post-Resistance	CSPG4	1464	37	15	75968751	75968751	Missense_Mutation	SNP	C	T	8	113	c.6109G>A	c.(6109-6111)GCC>ACC	p.A2037T
Pat_41	Post-Resistance	CSPG4	1464	37	15	75970054	75970054	Nonsense_Mutation	SNP	C	T	48	270	c.5124G>A	c.(5122-5124)TGG>TGA	p.W1708*
Pat_41	Post-Resistance	C15orf27	123591	37	15	76467899	76467899	Splice_Site	SNP	G	A	5	64	c.653_splice	c.e8-1	p.A218_splice
Pat_41	Post-Resistance	ETFA	2108	37	15	76576148	76576148	Missense_Mutation	SNP	C	T	5	84	c.683G>A	c.(682-684)GGA>GAA	p.G228E

Pat_41	Post-Resistance	RCN2	5955	37	15	77239805	77239805	Missense_Mutation	SNP	G	A	10	195	c.605G>A	c.(604-606)GGT>GAT	p.G202D
Pat_41	Post-Resistance	HMG20A	10363	37	15	77750772	77750772	Missense_Mutation	SNP	C	T	22	118	c.23C>T	c.(22-24)TCC>TTC	p.S8F
Pat_41	Post-Resistance	LINGO1	84894	37	15	77907294	77907294	Missense_Mutation	SNP	C	T	3	32	c.955G>A	c.(955-957)GTG>ATG	p.V319M
Pat_41	Post-Resistance	TBC1D2B	23102	37	15	78305252	78305252	Missense_Mutation	SNP	G	A	10	68	c.2183C>T	c.(2182-2184)ACC>ATC	p.T728I
Pat_41	Post-Resistance	ACSBG1	23205	37	15	78486346	78486346	Missense_Mutation	SNP	G	A	4	102	c.470C>T	c.(469-471)GCC>GTC	p.A157V
Pat_41	Post-Resistance	MORF4L1	10933	37	15	79177389	79177389	Missense_Mutation	SNP	G	A	8	160	c.236G>A	c.(235-237)GGA>GAA	p.G79E
Pat_41	Post-Resistance	FAH	2184	37	15	80452789	80452789	Missense_Mutation	SNP	C	T	26	147	c.352C>T	c.(352-354)CCA>TCA	p.P118S
Pat_41	Post-Resistance	KIAA1199	57214	37	15	81234254	81234254	Missense_Mutation	SNP	G	A	5	75	c.3472G>A	c.(3472-3474)GGC>AGC	p.G1158S
Pat_41	Post-Resistance	C15orf26	161502	37	15	81440695	81440695	Missense_Mutation	SNP	G	A	10	224	c.727G>A	c.(727-729)GAG>AAG	p.E243K
Pat_41	Post-Resistance	IL16	3603	37	15	81582852	81582852	Missense_Mutation	SNP	G	A	5	68	c.1391G>A	c.(1390-1392)GGA>GAA	p.G464E
Pat_41	Post-Resistance	IL16	3603	37	15	81592083	81592083	Missense_Mutation	SNP	C	T	6	120	c.2416C>T	c.(2416-2418)CCA>TCA	p.P806S
Pat_41	Post-Resistance	IL16	3603	37	15	81593774	81593774	Missense_Mutation	SNP	C	T	5	89	c.3239C>T	c.(3238-3240)TCC>TTC	p.S1080F
Pat_41	Post-Resistance	IL16	3603	37	15	81601023	81601023	Missense_Mutation	SNP	C	T	13	120	c.3883C>T	c.(3883-3885)CTC>TTC	p.L1295F
Pat_41	Post-Resistance	STARD5	80765	37	15	81614753	81614753	Missense_Mutation	SNP	G	A	22	271	c.278C>T	c.(277-279)ACT>ATT	p.T93I
Pat_41	Post-Resistance	FAM154B	283726	37	15	82555224	82555224	Missense_Mutation	SNP	G	A	5	9	c.4G>A	c.(4-6)GGA>AGA	p.G2R
Pat_41	Post-Resistance	FAM154B	283726	37	15	82574472	82574472	Missense_Mutation	SNP	C	T	7	101	c.266C>T	c.(265-267)GCT>GTT	p.A89V
Pat_41	Post-Resistance	BTBD1	53339	37	15	83718861	83718861	Missense_Mutation	SNP	C	T	16	185	c.628G>A	c.(628-630)GCA>ACA	p.A210T
Pat_41	Post-Resistance	ZNF592	9640	37	15	85326544	85326544	Missense_Mutation	SNP	G	A	5	81	c.638G>A	c.(637-639)GGG>GAG	p.G213E
Pat_41	Post-Resistance	ALPK3	57538	37	15	85407795	85407795	Missense_Mutation	SNP	C	T	7	67	c.5228C>T	c.(5227-5229)CCG>CTG	p.P1743L
Pat_41	Post-Resistance	PDE8A	5151	37	15	85666332	85666332	Missense_Mutation	SNP	G	A	25	202	c.1993G>A	c.(1993-1995)GTC>ATC	p.V665I
Pat_41	Post-Resistance	AKAP13	11214	37	15	86123382	86123382	Missense_Mutation	SNP	G	A	48	194	c.2083G>A	c.(2083-2085)GCA>ACA	p.A695T
Pat_41	Post-Resistance	AKAP13	11214	37	15	86125252	86125252	Missense_Mutation	SNP	C	T	5	150	c.3953C>T	c.(3952-3954)GCC>GTC	p.A1318V
Pat_41	Post-Resistance	AKAP13	11214	37	15	86198921	86198921	Missense_Mutation	SNP	G	A	12	108	c.4648G>A	c.(4648-4650)GTC>ATC	p.V1550I
Pat_41	Post-Resistance	KLHL25	64410	37	15	86312573	86312573	Missense_Mutation	SNP	C	T	8	81	c.469G>A	c.(469-471)GAC>AAC	p.D157N
Pat_41	Post-Resistance	NTRK3	4916	37	15	88472468	88472468	Missense_Mutation	SNP	C	T	17	180	c.2087G>A	c.(2086-2088)GGG>GAG	p.G696E
Pat_41	Post-Resistance	DET1	55070	37	15	89056328	89056328	Missense_Mutation	SNP	C	T	8	43	c.1507G>A	c.(1507-1509)GCG>ACG	p.A503T
Pat_41	Post-Resistance	AEN	64782	37	15	89169838	89169838	Missense_Mutation	SNP	C	T	13	416	c.398C>T	c.(397-399)TCC>TTC	p.S133F
Pat_41	Post-Resistance	FANCI	55215	37	15	89804815	89804815	Splice_Site	SNP	G	A	22	256	c.289_splice	c.e5-1	p.A97_splice
Pat_41	Post-Resistance	FANCI	55215	37	15	89820021	89820021	Missense_Mutation	SNP	G	A	4	136	c.1192G>A	c.(1192-1194)GTT>ATT	p.V398I
Pat_41	Post-Resistance	C15orf42	90381	37	15	90161420	90161420	Missense_Mutation	SNP	G	A	11	448	c.2998G>A	c.(2998-3000)GAG>AAG	p.E1000K
Pat_41	Post-Resistance	C15orf42	90381	37	15	90167155	90167155	Missense_Mutation	SNP	G	A	14	184	c.3614G>A	c.(3613-3615)GGG>GAG	p.G1205E
Pat_41	Post-Resistance	C15orf42	90381	37	15	90168430	90168430	Missense_Mutation	SNP	C	T	5	80	c.4889C>T	c.(4888-4890)TCC>TTC	p.S1630F
Pat_41	Post-Resistance	ANPEP	290	37	15	90348690	90348690	Missense_Mutation	SNP	C	T	4	41	c.619G>A	c.(619-621)GTG>ATG	p.V207M
Pat_41	Post-Resistance	IDH2	3418	37	15	90631606	90631606	Missense_Mutation	SNP	C	T	8	201	c.663G>A	c.(661-663)ATG>ATA	p.M221I
Pat_41	Post-Resistance	IQGAP1	8826	37	15	90984917	90984917	Splice_Site	SNP	G	A	4	96	c.828_splice	c.e8+1	p.R276_splice
Pat_41	Post-Resistance	IQGAP1	8826	37	15	90996028	90996028	Missense_Mutation	SNP	T	A	17	264	c.1184T>A	c.(1183-1185)ATT>AAT	p.I395N
Pat_41	Post-Resistance	UNC45A	55898	37	15	91491911	91491911	Missense_Mutation	SNP	G	A	5	112	c.1765G>A	c.(1765-1767)GTG>ATG	p.V589M
Pat_41	Post-Resistance	SV2B	9899	37	15	91803625	91803625	Missense_Mutation	SNP	G	A	14	117	c.994G>A	c.(994-996)GAG>AAG	p.E332K
Pat_41	Post-Resistance	CHD2	1106	37	15	93528792	93528792	Missense_Mutation	SNP	C	T	7	149	c.3302C>T	c.(3301-3303)TCT>TTT	p.S1101F
Pat_41	Post-Resistance	CHD2	1106	37	15	93558139	93558139	Missense_Mutation	SNP	G	A	12	170	c.4906G>A	c.(4906-4908)GAT>AAT	p.D1636N
Pat_41	Post-Resistance	IGF1R	3480	37	15	99459931	99459931	Missense_Mutation	SNP	G	A	9	87	c.2027G>A	c.(2026-2028)GGC>GAC	p.G676D
Pat_41	Post-Resistance	IGF1R	3480	37	15	99478132	99478132	Missense_Mutation	SNP	G	A	16	93	c.3036G>A	c.(3034-3036)ATG>ATA	p.M1012I
Pat_41	Post-Resistance	SYNM	23336	37	15	99670421	99670421	Missense_Mutation	SNP	G	A	6	44	c.1856G>A	c.(1855-1857)AGG>AAG	p.R619K
Pat_41	Post-Resistance	SYNM	23336	37	15	99672538	99672538	Missense_Mutation	SNP	G	A	44	215	c.3973G>A	c.(3973-3975)GTT>ATT	p.V1325I
Pat_41	Post-Resistance	ADAMTS17	170691	37	15	100636666	100636666	Missense_Mutation	SNP	C	A	23	206	c.2032G>T	c.(2032-2034)GGC>TGC	p.G678C
Pat_41	Post-Resistance	ALDH1A3	220	37	15	101434188	101434188	Nonsense_Mutation	SNP	G	A	9	268	c.567G>A	c.(565-567)TGG>TGA	p.W189*
Pat_41	Post-Resistance	LRRK1	79705	37	15	101552327	101552327	Missense_Mutation	SNP	C	T	14	192	c.1396C>T	c.(1396-1398)CCC>TCC	p.P466S

Pat_41	Post-Resistance	LRRK1	79705	37	15	101566179	101566179	Missense_Mutation	SNP	C	T	19	108	c.2242C>T	c.(2242-2244)CCA>TCA	p.P748S
Pat_41	Post-Resistance	LRRK1	79705	37	15	101606055	101606055	Missense_Mutation	SNP	C	T	5	92	c.5413C>T	c.(5413-5415)CCA>TCA	p.P1805S
Pat_41	Post-Resistance	NPRL3	8131	37	16	142724	142724	Splice_Site	SNP	C	T	14	84	c.1032_splice	c.e11-1	p.L344_splice
Pat_41	Post-Resistance	TMEM8A	58986	37	16	427422	427422	Missense_Mutation	SNP	C	T	4	53	c.463G>A	c.(463-465)GTG>ATG	p.V155M
Pat_41	Post-Resistance	PIGQ	9091	37	16	633095	633095	Missense_Mutation	SNP	G	A	4	66	c.1744G>A	c.(1744-1746)GGG>AGG	p.G582R
Pat_41	Post-Resistance	WDR90	197335	37	16	700070	700070	Missense_Mutation	SNP	G	A	20	411	c.182G>A	c.(181-183)AGC>AAC	p.S61N
Pat_41	Post-Resistance	WDR90	197335	37	16	708906	708906	Missense_Mutation	SNP	G	A	5	184	c.2906G>A	c.(2905-2907)GGC>GAC	p.G969D
Pat_41	Post-Resistance	WDR90	197335	37	16	716059	716059	Missense_Mutation	SNP	C	T	5	195	c.4544C>T	c.(4543-4545)ACG>ATG	p.T1515M
Pat_41	Post-Resistance	CCDC78	124093	37	16	773876	773876	Missense_Mutation	SNP	C	T	3	12	c.1114G>A	c.(1114-1116)GGG>AGG	p.G372R
Pat_41	Post-Resistance	MSLN	10232	37	16	816980	816980	Missense_Mutation	SNP	C	T	5	62	c.1493C>T	c.(1492-1494)TCC>TTC	p.S498F
Pat_41	Post-Resistance	PRR25	388199	37	16	855624	855624	Missense_Mutation	SNP	G	A	4	34	c.182G>A	c.(181-183)AGC>AAC	p.S61N
Pat_41	Post-Resistance	C1QTNF8	390664	37	16	1144721	1144721	Missense_Mutation	SNP	G	A	9	56	c.202C>T	c.(202-204)CTC>TTC	p.L68F
Pat_41	Post-Resistance	BAIAP3	8938	37	16	1397964	1397964	Missense_Mutation	SNP	G	A	23	244	c.3200G>A	c.(3199-3201)AGG>AAG	p.R1067K
Pat_41	Post-Resistance	MAPK8IP3	23162	37	16	1797255	1797255	Missense_Mutation	SNP	G	A	6	102	c.970G>A	c.(970-972)GAG>AAG	p.E324K
Pat_41	Post-Resistance	EME2	197342	37	16	1825622	1825622	Missense_Mutation	SNP	C	T	7	106	c.869C>T	c.(868-870)TCT>TTT	p.S290F
Pat_41	Post-Resistance	EME2	197342	37	16	1826204	1826204	Missense_Mutation	SNP	G	A	9	166	c.1300G>A	c.(1300-1302)GCC>ACC	p.A434T
Pat_41	Post-Resistance	NUBP2	10101	37	16	1837746	1837746	Missense_Mutation	SNP	C	T	19	120	c.403C>T	c.(403-405)CCG>TCG	p.P135S
Pat_41	Post-Resistance	HAGH	3029	37	16	1872338	1872338	Missense_Mutation	SNP	C	T	15	197	c.277G>A	c.(277-279)GTG>ATG	p.V93M
Pat_41	Post-Resistance	C16orf73	254528	37	16	1891834	1891834	Missense_Mutation	SNP	C	T	8	105	c.1021G>A	c.(1021-1023)GTT>ATT	p.V341I
Pat_41	Post-Resistance	RPL3L	6123	37	16	1995618	1995618	Missense_Mutation	SNP	G	A	5	121	c.1049C>T	c.(1048-1050)TCC>TTC	p.S350F
Pat_41	Post-Resistance	SLC9A3R2	9351	37	16	2087564	2087564	Missense_Mutation	SNP	C	T	7	43	c.818C>T	c.(817-819)TCC>TTC	p.S273F
Pat_41	Post-Resistance	SLC9A3R2	9351	37	16	2087952	2087952	Nonsense_Mutation	SNP	G	A	4	45	c.981G>A	c.(979-981)TGG>TGA	p.W327*
Pat_41	Post-Resistance	MLST8	64223	37	16	2258289	2258289	Missense_Mutation	SNP	G	A	26	383	c.652G>A	c.(652-654)GCC>ACC	p.A218T
Pat_41	Post-Resistance	RNPS1	10921	37	16	2305604	2305604	Missense_Mutation	SNP	G	A	4	118	c.800C>T	c.(799-801)CCC>CTC	p.P267L
Pat_41	Post-Resistance	TBC1D24	57465	37	16	2548309	2548309	Missense_Mutation	SNP	G	A	4	32	c.1054G>A	c.(1054-1056)GAC>AAC	p.D352N
Pat_41	Post-Resistance	SRRM2	23524	37	16	2816014	2816014	Missense_Mutation	SNP	G	A	10	62	c.5485G>A	c.(5485-5487)GAA>AAA	p.E1829K
Pat_41	Post-Resistance	SRRM2	23524	37	16	2819233	2819233	Nonsense_Mutation	SNP	C	T	25	211	c.7969C>T	c.(7969-7971)CAG>TAG	p.Q2657*
Pat_41	Post-Resistance	TCEB2	6923	37	16	2822016	2822016	Missense_Mutation	SNP	C	T	11	62	c.332G>A	c.(331-333)AGT>AAT	p.S111N
Pat_41	Post-Resistance	PRSS22	64063	37	16	2906134	2906134	Missense_Mutation	SNP	C	T	7	99	c.230G>A	c.(229-231)GGT>GAT	p.G77D
Pat_41	Post-Resistance	FLYWCH1	84256	37	16	2983538	2983538	Nonsense_Mutation	SNP	C	T	4	48	c.1204C>T	c.(1204-1206)CAG>TAG	p.Q402*
Pat_41	Post-Resistance	PAQR4	124222	37	16	3021518	3021518	Missense_Mutation	SNP	G	A	35	148	c.391G>A	c.(391-393)GCC>ACC	p.A131T
Pat_41	Post-Resistance	CCDC64B	146439	37	16	3079737	3079737	Missense_Mutation	SNP	C	T	3	4	c.766G>A	c.(766-768)GAA>AAA	p.E256K
Pat_41	Post-Resistance	ZNF205	7755	37	16	3165426	3165426	Missense_Mutation	SNP	C	T	30	102	c.128C>T	c.(127-129)ACT>ATT	p.T43I
Pat_41	Post-Resistance	OR1F1	4992	37	16	3254437	3254437	Missense_Mutation	SNP	G	A	16	285	c.191G>A	c.(190-192)AGC>AAC	p.S64N
Pat_41	Post-Resistance	ZNF200	7752	37	16	3283734	3283734	Missense_Mutation	SNP	G	A	24	258	c.22C>T	c.(22-24)CCT>TCT	p.P8S
Pat_41	Post-Resistance	TIGD7	91151	37	16	3350395	3350395	Missense_Mutation	SNP	C	T	18	225	c.220G>A	c.(220-222)GGA>AGA	p.G74R
Pat_41	Post-Resistance	ZNF174	7727	37	16	3454425	3454425	Splice_Site	SNP	G	A	14	225	c.403_splice	c.e2-1	p.V135_splice
Pat_41	Post-Resistance	NAT15	79903	37	16	3533585	3533585	Missense_Mutation	SNP	C	T	4	62	c.560C>T	c.(559-561)CCC>CTC	p.P187L
Pat_41	Post-Resistance	NLRC3	197358	37	16	3614586	3614586	Missense_Mutation	SNP	G	A	10	73	c.352C>T	c.(352-354)CCC>TCC	p.P118S
Pat_41	Post-Resistance	CREBBP	1387	37	16	3781408	3781408	Missense_Mutation	SNP	C	T	3	25	c.4957G>A	c.(4957-4959)GAC>AAC	p.D1653N
Pat_41	Post-Resistance	CREBBP	1387	37	16	3820797	3820797	Missense_Mutation	SNP	G	A	7	82	c.2654C>T	c.(2653-2655)CCC>CTC	p.P885L
Pat_41	Post-Resistance	CREBBP	1387	37	16	3843581	3843581	Missense_Mutation	SNP	G	A	8	134	c.1022C>T	c.(1021-1023)GCA>GTA	p.A341V
Pat_41	Post-Resistance	ADCY9	115	37	16	4016216	4016216	Missense_Mutation	SNP	C	T	14	306	c.3622G>A	c.(3622-3624)GTG>ATG	p.V1208M
Pat_41	Post-Resistance	GLIS2	84662	37	16	4382336	4382336	Missense_Mutation	SNP	G	A	3	47	c.55G>A	c.(55-57)GCG>ACG	p.A19T
Pat_41	Post-Resistance	NMRAL1	57407	37	16	4511851	4511851	Missense_Mutation	SNP	C	T	22	285	c.830G>A	c.(829-831)AGA>AAA	p.R277K
Pat_41	Post-Resistance	HMOX2	3163	37	16	4557882	4557882	Missense_Mutation	SNP	G	A	5	34	c.373G>A	c.(373-375)GTG>ATG	p.V125M
Pat_41	Post-Resistance	MGRN1	23295	37	16	4731713	4731713	Missense_Mutation	SNP	G	A	15	85	c.1294G>A	c.(1294-1296)GCT>ACT	p.A432T

Pat_41	Post-Resistance	MGRN1	23295	37	16	4733883	4733883	Missense_Mutation	SNP	G	A	5	60	c.1568G>A	c.(1567-1569)AGC>AAC	p.S523N
Pat_41	Post-Resistance	ANKS3	124401	37	16	4755113	4755113	Missense_Mutation	SNP	G	A	17	140	c.851C>T	c.(850-852)GCC>GTC	p.A284V
Pat_41	Post-Resistance	ANKS3	124401	37	16	4776659	4776659	Splice_Site	SNP	C	T	7	97	c.491_splice	c.e5+1	p.R164_splice
Pat_41	Post-Resistance	ANKS3	124401	37	16	4776766	4776766	Missense_Mutation	SNP	C	T	19	74	c.385G>A	c.(385-387)GAA>AAA	p.E129K
Pat_41	Post-Resistance	GLYR1	84656	37	16	4861639	4861639	Missense_Mutation	SNP	C	T	9	72	c.1447G>A	c.(1447-1449)GAC>AAC	p.D483N
Pat_41	Post-Resistance	UBN1	29855	37	16	4925341	4925341	Missense_Mutation	SNP	C	T	5	156	c.2930C>T	c.(2929-2931)TCC>TTC	p.S977F
Pat_41	Post-Resistance	PPL	5493	37	16	4934980	4934980	Missense_Mutation	SNP	C	T	4	18	c.3676G>A	c.(3676-3678)GTG>ATG	p.V1226M
Pat_41	Post-Resistance	PPL	5493	37	16	4937225	4937225	Missense_Mutation	SNP	C	T	7	267	c.2518G>A	c.(2518-2520)GCA>ACA	p.A840T
Pat_41	Post-Resistance	A2BP1	54715	37	16	7568356	7568356	Missense_Mutation	SNP	G	A	44	356	c.235G>A	c.(235-237)GAC>AAC	p.D79N
Pat_41	Post-Resistance	ABAT	18	37	16	8866748	8866748	Missense_Mutation	SNP	C	T	49	48	c.928C>T	c.(928-930)CGG>TGG	p.R310W
Pat_41	Post-Resistance	USP7	7874	37	16	8998314	8998314	Missense_Mutation	SNP	G	A	10	91	c.1682C>T	c.(1681-1683)GCC>GTC	p.A561V
Pat_41	Post-Resistance	GRIN2A	2903	37	16	10032359	10032359	Missense_Mutation	SNP	G	A	7	148	c.464C>T	c.(463-465)GCC>GTC	p.A155V
Pat_41	Post-Resistance	ATF7IP2	80063	37	16	10524713	10524713	Missense_Mutation	SNP	C	T	3	64	c.236C>T	c.(235-237)TCT>TTT	p.S79F
Pat_41	Post-Resistance	NUBP1	4682	37	16	10851733	10851733	Missense_Mutation	SNP	T	C	104	124	c.455T>C	c.(454-456)ATG>ACG	p.M152T
Pat_41	Post-Resistance	CIITA	4261	37	16	10989537	10989537	Missense_Mutation	SNP	G	A	8	157	c.211G>A	c.(211-213)GAC>AAC	p.D71N
Pat_41	Post-Resistance	CIITA	4261	37	16	10997657	10997657	Missense_Mutation	SNP	C	T	34	202	c.842C>T	c.(841-843)CCA>CTA	p.P281L
Pat_41	Post-Resistance	CIITA	4261	37	16	11001028	11001028	Missense_Mutation	SNP	C	T	4	9	c.1679C>T	c.(1678-1680)GCC>GTC	p.A560V
Pat_41	Post-Resistance	CLEC16A	23274	37	16	11096938	11096938	Missense_Mutation	SNP	C	T	3	39	c.1079C>T	c.(1078-1080)CCC>CTC	p.P360L
Pat_41	Post-Resistance	CLEC16A	23274	37	16	11260257	11260257	Missense_Mutation	SNP	C	T	5	90	c.2654C>T	c.(2653-2655)GCC>GTC	p.A885V
Pat_41	Post-Resistance	GSPT1	2935	37	16	11981536	11981536	Missense_Mutation	SNP	G	A	16	253	c.434C>T	c.(433-435)GCC>GTC	p.A145V
Pat_41	Post-Resistance	ERCC4	2072	37	16	14029291	14029291	Missense_Mutation	SNP	C	T	4	78	c.1502C>T	c.(1501-1503)CCT>CTT	p.P501L
Pat_41	Post-Resistance	ERCC4	2072	37	16	14031696	14031696	Missense_Mutation	SNP	G	A	11	132	c.1885G>A	c.(1885-1887)GCT>ACT	p.A629T
Pat_41	Post-Resistance	MKL2	57496	37	16	14354874	14354874	Missense_Mutation	SNP	C	T	36	365	c.2873C>T	c.(2872-2874)CCC>CTC	p.P958L
Pat_41	Post-Resistance	KIAA0430	9665	37	16	15711297	15711297	Missense_Mutation	SNP	G	A	22	44	c.2816C>T	c.(2815-2817)CCC>CTC	p.P939L
Pat_41	Post-Resistance	NDE1	54820	37	16	15771806	15771806	Missense_Mutation	SNP	G	A	15	222	c.386G>A	c.(385-387)CGC>CAC	p.R129H
Pat_41	Post-Resistance	NDE1	54820	37	16	15790678	15790678	Missense_Mutation	SNP	G	A	17	113	c.908G>A	c.(907-909)AGA>AAA	p.R303K
Pat_41	Post-Resistance	ABCC1	4363	37	16	16110374	16110374	Missense_Mutation	SNP	C	T	25	440	c.511C>T	c.(511-513)CGT>TGT	p.R171C
Pat_41	Post-Resistance	ABCC1	4363	37	16	16208623	16208623	Missense_Mutation	SNP	G	A	11	95	c.3080G>A	c.(3079-3081)GGG>GAG	p.G1027E
Pat_41	Post-Resistance	XYLT1	64131	37	16	17353093	17353093	Missense_Mutation	SNP	C	T	18	300	c.665G>A	c.(664-666)AGA>AAA	p.R222K
Pat_41	Post-Resistance	TMC7	79905	37	16	19047075	19047075	Missense_Mutation	SNP	G	A	9	300	c.935G>A	c.(934-936)GGC>GAC	p.G312D
Pat_41	Post-Resistance	SYT17	51760	37	16	19191802	19191802	Missense_Mutation	SNP	G	A	11	163	c.272G>A	c.(271-273)GGA>GAA	p.G91E
Pat_41	Post-Resistance	TMC5	79838	37	16	19483534	19483534	Missense_Mutation	SNP	C	T	6	88	c.1907C>T	c.(1906-1908)GCC>GTC	p.A636V
Pat_41	Post-Resistance	C16orf62	57020	37	16	19621688	19621688	Missense_Mutation	SNP	G	A	13	153	c.974G>A	c.(973-975)GGG>GAG	p.G325E
Pat_41	Post-Resistance	IQCK	124152	37	16	19775207	19775207	Missense_Mutation	SNP	C	T	18	300	c.512C>T	c.(511-513)ACT>ATT	p.T171I
Pat_41	Post-Resistance	UMOD	7369	37	16	20357498	20357498	Missense_Mutation	SNP	C	T	6	67	c.1132G>A	c.(1132-1134)GTG>ATG	p.V378M
Pat_41	Post-Resistance	ERI2	112479	37	16	20814927	20814927	Missense_Mutation	SNP	G	A	5	90	c.89C>T	c.(88-90)TCC>TTC	p.S30F
Pat_41	Post-Resistance	DCUN1D3	123879	37	16	20873643	20873643	Missense_Mutation	SNP	C	T	14	306	c.218G>A	c.(217-219)GGA>GAA	p.G73E
Pat_41	Post-Resistance	DNAH3	55567	37	16	20944756	20944756	Missense_Mutation	SNP	C	T	6	104	c.12071G>A	c.(12070-12072)GGT>GAT	p.G4024D
Pat_41	Post-Resistance	DNAH3	55567	37	16	21038385	21038385	Missense_Mutation	SNP	G	A	22	163	c.5504C>T	c.(5503-5505)GCC>GTC	p.A1835V
Pat_41	Post-Resistance	ZP2	7783	37	16	21221037	21221037	Missense_Mutation	SNP	C	T	11	146	c.245G>A	c.(244-246)GGT>GAT	p.G82D
Pat_41	Post-Resistance	ANKS4B	257629	37	16	21261140	21261140	Missense_Mutation	SNP	G	A	27	93	c.253G>A	c.(253-255)GTC>ATC	p.V85I
Pat_41	Post-Resistance	OTOA	146183	37	16	21771817	21771817	Missense_Mutation	SNP	C	T	7	106	c.3376C>T	c.(3376-3378)CTT>TTT	p.L1126F
Pat_41	Post-Resistance	PDZD9	255762	37	16	21995620	21995620	Missense_Mutation	SNP	C	T	126	653	c.577G>A	c.(577-579)GGT>AGT	p.G193S
Pat_41	Post-Resistance	SCNN1B	6338	37	16	23360152	23360152	Missense_Mutation	SNP	G	A	7	61	c.232G>A	c.(232-234)GAG>AAG	p.E78K
Pat_41	Post-Resistance	SCNN1B	6338	37	16	23388525	23388525	Missense_Mutation	SNP	G	A	6	77	c.1310G>A	c.(1309-1311)AGA>AAA	p.R437K
Pat_41	Post-Resistance	EARS2	124454	37	16	23568562	23568562	Missense_Mutation	SNP	C	T	9	39	c.103G>A	c.(103-105)GTT>ATT	p.V35I
Pat_41	Post-Resistance	PLK1	5347	37	16	23692258	23692258	Missense_Mutation	SNP	G	A	23	248	c.601G>A	c.(601-603)GTC>ATC	p.V201I

Pat_41	Post-Resistance	RBBP6	5930	37	16	24574823	24574823	Splice_Site	SNP	G	A	20	178	c.1465_splice	c.e12+1	p.G489_splice
Pat_41	Post-Resistance	RBBP6	5930	37	16	24578789	24578789	Missense_Mutation	SNP	G	A	6	306	c.1915G>A	c.(1915-1917)GAA>AAA	p.E639K
Pat_41	Post-Resistance	RBBP6	5930	37	16	24580584	24580584	Missense_Mutation	SNP	A	T	69	66	c.2573A>T	c.(2572-2574)GAG>GTG	p.E858V
Pat_41	Post-Resistance	RBBP6	5930	37	16	24581717	24581717	Missense_Mutation	SNP	G	A	6	100	c.3706G>A	c.(3706-3708)GAG>AAG	p.E1236K
Pat_41	Post-Resistance	TNRC6A	27327	37	16	24801456	24801456	Missense_Mutation	SNP	G	A	5	71	c.1493G>A	c.(1492-1494)GGT>GAT	p.G498D
Pat_41	Post-Resistance	TNRC6A	27327	37	16	24802535	24802535	Missense_Mutation	SNP	G	A	5	83	c.2572G>A	c.(2572-2574)GGA>AGA	p.G858R
Pat_41	Post-Resistance	TNRC6A	27327	37	16	24809245	24809245	Missense_Mutation	SNP	C	T	6	118	c.3652C>T	c.(3652-3654)CCA>TCA	p.P1218S
Pat_41	Post-Resistance	TNRC6A	27327	37	16	24828149	24828149	Missense_Mutation	SNP	G	A	26	285	c.4844G>A	c.(4843-4845)GGT>GAT	p.G1615D
Pat_41	Post-Resistance	TNRC6A	27327	37	16	24834914	24834914	Missense_Mutation	SNP	C	T	24	346	c.5675C>T	c.(5674-5676)TCC>TTC	p.S1892F
Pat_41	Post-Resistance	AQP8	343	37	16	25228522	25228522	Missense_Mutation	SNP	G	A	8	422	c.16G>A	c.(16-18)GCC>ACC	p.A6T
Pat_41	Post-Resistance	AQP8	343	37	16	25238444	25238444	Missense_Mutation	SNP	G	A	11	137	c.658G>A	c.(658-660)GTG>ATG	p.V220M
Pat_41	Post-Resistance	ZKSCAN2	342357	37	16	25258673	25258673	Missense_Mutation	SNP	C	T	4	106	c.844G>A	c.(844-846)GAA>AAA	p.E282K
Pat_41	Post-Resistance	C16orf82	162083	37	16	27078584	27078584	Missense_Mutation	SNP	G	A	3	22	c.268G>A	c.(268-270)GGG>AGG	p.G90R
Pat_41	Post-Resistance	JMJD5	79831	37	16	27230300	27230300	Missense_Mutation	SNP	G	A	7	285	c.862G>A	c.(862-864)GAC>AAC	p.D288N
Pat_41	Post-Resistance	IL21R	50615	37	16	27460078	27460078	Missense_Mutation	SNP	G	A	12	105	c.1091G>A	c.(1090-1092)AGT>AAT	p.S364N
Pat_41	Post-Resistance	GTF3C1	2975	37	16	27506155	27506155	Missense_Mutation	SNP	C	T	5	132	c.2707G>A	c.(2707-2709)GCT>ACT	p.A903T
Pat_41	Post-Resistance	KIAA0556	23247	37	16	27772814	27772814	Missense_Mutation	SNP	G	A	8	147	c.3712G>A	c.(3712-3714)GGC>AGC	p.G1238S
Pat_41	Post-Resistance	ATXN2L	11273	37	16	28836973	28836973	Missense_Mutation	SNP	G	A	33	503	c.365G>A	c.(364-366)AGA>AAA	p.R122K
Pat_41	Post-Resistance	ATXN2L	11273	37	16	28843565	28843565	Missense_Mutation	SNP	C	T	9	135	c.1361C>T	c.(1360-1362)GCC>GTC	p.A454V
Pat_41	Post-Resistance	ATXN2L	11273	37	16	28844809	28844809	Missense_Mutation	SNP	A	G	13	104	c.2005A>G	c.(2005-2007)ACA>GCA	p.T669A
Pat_41	Post-Resistance	TUFM	7284	37	16	28856355	28856355	Missense_Mutation	SNP	G	A	4	80	c.436C>T	c.(436-438)CCC>TCC	p.P146S
Pat_41	Post-Resistance	SH2B1	25970	37	16	28884792	28884792	Missense_Mutation	SNP	C	T	20	76	c.1922C>T	c.(1921-1923)CCC>CTC	p.P641L
Pat_41	Post-Resistance	RABEP2	79874	37	16	28925906	28925906	Missense_Mutation	SNP	C	T	5	28	c.545G>A	c.(544-546)AGA>AAA	p.R182K
Pat_41	Post-Resistance	CD19	930	37	16	28948978	28948978	Missense_Mutation	SNP	C	T	14	122	c.1406C>T	c.(1405-1407)ACC>ATC	p.T469I
Pat_41	Post-Resistance	C16orf53	79447	37	16	29830875	29830875	Splice_Site	SNP	G	A	89	498	c.566_splice	c.e3-1	p.G189_splice
Pat_41	Post-Resistance	MVP	9961	37	16	29848044	29848044	Missense_Mutation	SNP	C	T	5	140	c.674C>T	c.(673-675)ACA>ATA	p.T225I
Pat_41	Post-Resistance	SEZ6L2	26470	37	16	29884904	29884904	Missense_Mutation	SNP	C	T	16	90	c.2251G>A	c.(2251-2253)GAC>AAC	p.D751N
Pat_41	Post-Resistance	TAOK2	9344	37	16	29994887	29994887	Missense_Mutation	SNP	C	T	20	756	c.1324C>T	c.(1324-1326)CCT>TCT	p.P442S
Pat_41	Post-Resistance	ITGAL	3683	37	16	30500468	30500468	Missense_Mutation	SNP	C	T	12	84	c.1072C>T	c.(1072-1074)CTC>TTC	p.L358F
Pat_41	Post-Resistance	ZNF747	65988	37	16	30544408	30544408	Missense_Mutation	SNP	G	A	6	83	c.548C>T	c.(547-549)ACC>ATC	p.T183I
Pat_41	Post-Resistance	ZNF785	146540	37	16	30593963	30593963	Missense_Mutation	SNP	G	A	18	187	c.1136C>T	c.(1135-1137)TCA>TTA	p.S379L
Pat_41	Post-Resistance	SRCAP	10847	37	16	30749754	30749754	Missense_Mutation	SNP	G	A	21	148	c.8393G>A	c.(8392-8394)GGG>GAG	p.G2798E
Pat_41	Post-Resistance	ORAI3	93129	37	16	30964596	30964596	Missense_Mutation	SNP	G	A	10	150	c.319G>A	c.(319-321)GCT>ACT	p.A107T
Pat_41	Post-Resistance	SETD1A	9739	37	16	30975478	30975478	Missense_Mutation	SNP	G	A	27	216	c.703G>A	c.(703-705)GGC>AGC	p.G235S
Pat_41	Post-Resistance	ZNF646	9726	37	16	31092837	31092837	Missense_Mutation	SNP	G	A	33	255	c.5192G>A	c.(5191-5193)CGC>CAC	p.R1731H
Pat_41	Post-Resistance	BCKDK	10295	37	16	31120731	31120731	Missense_Mutation	SNP	G	A	5	37	c.187G>A	c.(187-189)GCG>ACG	p.A63T
Pat_41	Post-Resistance	PRSS36	146547	37	16	31152070	31152070	Missense_Mutation	SNP	G	A	9	105	c.1910C>T	c.(1909-1911)TCT>TTT	p.S637F
Pat_41	Post-Resistance	ITGAX	3687	37	16	31374356	31374356	Missense_Mutation	SNP	C	T	15	73	c.1460C>T	c.(1459-1461)ACC>ATC	p.T487I
Pat_41	Post-Resistance	ITGAX	3687	37	16	31383814	31383814	Missense_Mutation	SNP	G	A	6	23	c.2276G>A	c.(2275-2277)AGA>AAA	p.R759K
Pat_41	Post-Resistance	SLC6A10P	386757	37	16	32890984	32890984	Missense_Mutation	SNP	G	A	7	80	c.70C>T	c.(70-72)CTC>TTC	p.L24F
Pat_41	Post-Resistance	SHCBP1	79801	37	16	46652201	46652201	Missense_Mutation	SNP	C	T	9	63	c.187G>A	c.(187-189)GGA>AGA	p.G63R
Pat_41	Post-Resistance	VPS35	55737	37	16	46712869	46712869	Missense_Mutation	SNP	C	T	18	395	c.706G>A	c.(706-708)GAA>AAA	p.E236K
Pat_41	Post-Resistance	ORC6L	23594	37	16	46724994	46724994	Missense_Mutation	SNP	G	A	17	177	c.157G>A	c.(157-159)GAC>AAC	p.D53N
Pat_41	Post-Resistance	ITFG1	81533	37	16	47462714	47462714	Splice_Site	SNP	C	T	20	310	c.655_splice	c.e6+1	p.D219_splice
Pat_41	Post-Resistance	PHKB	5257	37	16	47581441	47581441	Missense_Mutation	SNP	G	A	16	138	c.692G>A	c.(691-693)AGC>AAC	p.S231N
Pat_41	Post-Resistance	ABCC12	94160	37	16	48121981	48121981	Missense_Mutation	SNP	C	T	6	92	c.3491G>A	c.(3490-3492)GGA>GAA	p.G1164E
Pat_41	Post-Resistance	ZNF423	23090	37	16	49660102	49660102	Missense_Mutation	SNP	G	A	159	282	c.3556C>T	c.(3556-3558)CAC>TAC	p.H1186Y

Pat_41	Post-Resistance	ZNF423	23090	37	16	49672465	49672465	Missense_Mutation	SNP	C	T	4	49	c.598G>A	c.(598-600)GAG>AAG	p.E200K
Pat_41	Post-Resistance	ZNF423	23090	37	16	49856580	49856580	Splice_Site	SNP	C	T	10	174	c.16_splice	c.e2+1	p.V6_splice
Pat_41	Post-Resistance	HEATR3	55027	37	16	50104158	50104158	Missense_Mutation	SNP	G	A	23	168	c.469G>A	c.(469-471)GAG>AAG	p.E157K
Pat_41	Post-Resistance	BRD7	29117	37	16	50367507	50367507	Missense_Mutation	SNP	G	A	41	674	c.989C>T	c.(988-990)ACC>ATC	p.T330I
Pat_41	Post-Resistance	NKD1	85407	37	16	50583351	50583351	Missense_Mutation	SNP	G	A	5	54	c.77G>A	c.(76-78)AGC>AAC	p.S26N
Pat_41	Post-Resistance	CYLD	1540	37	16	50813809	50813809	Missense_Mutation	SNP	C	T	4	82	c.1372C>T	c.(1372-1374)CCA>TCA	p.P458S
Pat_41	Post-Resistance	CYLD	1540	37	16	50818352	50818352	Missense_Mutation	SNP	C	T	8	108	c.1939C>T	c.(1939-1941)CCT>TCT	p.P647S
Pat_41	Post-Resistance	TOX3	27324	37	16	52484245	52484245	Missense_Mutation	SNP	C	T	8	168	c.622G>A	c.(622-624)GCC>ACC	p.A208T
Pat_41	Post-Resistance	CHD9	80205	37	16	53358307	53358307	Missense_Mutation	SNP	A	G	10	171	c.8194A>G	c.(8194-8196)ACA>GCA	p.T2732A
Pat_41	Post-Resistance	IRX5	10265	37	16	54966409	54966409	Splice_Site	SNP	G	A	9	134	c.250_splice	c.e2-1	p.G84_splice
Pat_41	Post-Resistance	NLRC5	84166	37	16	57111875	57111875	Missense_Mutation	SNP	G	A	7	55	c.5024G>A	c.(5023-5025)GGG>GAG	p.G1675E
Pat_41	Post-Resistance	RSPRY1	89970	37	16	57238692	57238692	Missense_Mutation	SNP	G	A	19	389	c.122G>A	c.(121-123)GGT>GAT	p.G41D
Pat_41	Post-Resistance	ARL2BP	23568	37	16	57284322	57284322	Splice_Site	SNP	G	A	7	206	c.294_splice	c.e5-1	p.Q98_splice
Pat_41	Post-Resistance	CCDC102A	92922	37	16	57546774	57546774	Missense_Mutation	SNP	C	T	7	144	c.1532G>A	c.(1531-1533)AGG>AAG	p.R511K
Pat_41	Post-Resistance	CCDC135	84229	37	16	57732829	57732829	Missense_Mutation	SNP	G	A	10	529	c.271G>A	c.(271-273)GAG>AAG	p.E91K
Pat_41	Post-Resistance	CCDC135	84229	37	16	57738809	57738809	Missense_Mutation	SNP	G	A	10	69	c.721G>A	c.(721-723)GTG>ATG	p.V241M
Pat_41	Post-Resistance	KIFC3	3801	37	16	57794222	57794222	Missense_Mutation	SNP	C	T	4	71	c.2339G>A	c.(2338-2340)GGG>GAG	p.G780E
Pat_41	Post-Resistance	KIFC3	3801	37	16	57796052	57796052	Missense_Mutation	SNP	C	T	4	93	c.1748G>A	c.(1747-1749)AGG>AAG	p.R583K
Pat_41	Post-Resistance	CNGB1	1258	37	16	57994760	57994760	Missense_Mutation	SNP	G	A	4	54	c.518C>T	c.(517-519)CCC>CTC	p.P173L
Pat_41	Post-Resistance	CNGB1	1258	37	16	57996888	57996889	Missense_Mutation	DNP	TC	CT	9	93	c.370_371GA>AG	c.(370-372)GAC>AGC	p.D124S
Pat_41	Post-Resistance	CNOT1	23019	37	16	58576436	58576436	Missense_Mutation	SNP	C	T	51	679	c.4471G>A	c.(4471-4473)GCA>ACA	p.A1491T
Pat_41	Post-Resistance	CNOT1	23019	37	16	58576463	58576463	Missense_Mutation	SNP	G	A	82	492	c.4444C>T	c.(4444-4446)CCA>TCA	p.P1482S
Pat_41	Post-Resistance	SLC38A7	55238	37	16	58709939	58709939	Missense_Mutation	SNP	G	A	8	68	c.788C>T	c.(787-789)CCC>CTC	p.P263L
Pat_41	Post-Resistance	GOT2	2806	37	16	58757759	58757759	Missense_Mutation	SNP	C	T	11	117	c.137G>A	c.(136-138)GGA>GAA	p.G46E
Pat_41	Post-Resistance	CDH8	1006	37	16	61687646	61687646	Missense_Mutation	SNP	C	T	6	48	c.2266G>A	c.(2266-2268)GCT>ACT	p.A756T
Pat_41	Post-Resistance	CDH11	1009	37	16	64981616	64981616	Missense_Mutation	SNP	C	T	20	140	c.2281G>A	c.(2281-2283)GCC>ACC	p.A761T
Pat_41	Post-Resistance	CDH11	1009	37	16	65025839	65025839	Splice_Site	SNP	C	T	8	175	c.644_splice	c.e6-1	p.G215_splice
Pat_41	Post-Resistance	CDH5	1003	37	16	66436942	66436942	Missense_Mutation	SNP	C	T	3	21	c.2225C>T	c.(2224-2226)TCC>TTC	p.S742F
Pat_41	Post-Resistance	CMTM1	113540	37	16	66612897	66612897	Missense_Mutation	SNP	C	T	5	111	c.503C>T	c.(502-504)CCC>CTC	p.P168L
Pat_41	Post-Resistance	CMTM4	146223	37	16	66657389	66657389	Missense_Mutation	SNP	C	T	5	57	c.380G>A	c.(379-381)GGA>GAA	p.G127E
Pat_41	Post-Resistance	DYNC1LI2	1783	37	16	66776499	66776499	Missense_Mutation	SNP	G	A	32	136	c.371C>T	c.(370-372)TCT>TTT	p.S124F
Pat_41	Post-Resistance	C16orf70	80262	37	16	67174447	67174447	Missense_Mutation	SNP	G	A	7	255	c.829G>A	c.(829-831)GTT>ATT	p.V277I
Pat_41	Post-Resistance	KCTD19	146212	37	16	67325617	67325617	Missense_Mutation	SNP	C	T	10	169	c.2342G>A	c.(2341-2343)AGC>AAC	p.S781N
Pat_41	Post-Resistance	TPPP3	51673	37	16	67424120	67424120	Missense_Mutation	SNP	G	A	14	47	c.488C>T	c.(487-489)GCC>GTC	p.A163V
Pat_41	Post-Resistance	FAM65A	79567	37	16	67576319	67576319	Missense_Mutation	SNP	C	T	52	688	c.1690C>T	c.(1690-1692)CCC>TCC	p.P564S
Pat_41	Post-Resistance	FAM65A	79567	37	16	67576449	67576449	Missense_Mutation	SNP	C	T	53	708	c.1820C>T	c.(1819-1821)CCT>CTT	p.P607L
Pat_41	Post-Resistance	FAM65A	79567	37	16	67579764	67579764	Splice_Site	SNP	G	A	5	58	c.3447_splice	c.e19+1	p.R1149_splice
Pat_41	Post-Resistance	RLTPR	146206	37	16	67685847	67685847	Missense_Mutation	SNP	G	A	23	209	c.2612G>A	c.(2611-2613)GGG>GAG	p.G871E
Pat_41	Post-Resistance	RANBP10	57610	37	16	67778202	67778202	Missense_Mutation	SNP	C	T	8	141	c.557G>A	c.(556-558)GGC>GAC	p.G186D
Pat_41	Post-Resistance	NRN1L	123904	37	16	67918850	67918850	Missense_Mutation	SNP	C	T	14	91	c.44C>T	c.(43-45)CCC>CTC	p.P15L
Pat_41	Post-Resistance	PSMB10	5699	37	16	67969912	67969912	Missense_Mutation	SNP	G	A	5	72	c.337C>T	c.(337-339)CCC>TCC	p.P113S
Pat_41	Post-Resistance	PSMB10	5699	37	16	67970375	67970375	Missense_Mutation	SNP	C	T	5	56	c.70G>A	c.(70-72)GAA>AAA	p.E24K
Pat_41	Post-Resistance	SLC12A4	6560	37	16	67980907	67980907	Missense_Mutation	SNP	G	A	4	53	c.2174C>T	c.(2173-2175)ACC>ATC	p.T725I
Pat_41	Post-Resistance	DDX28	55794	37	16	68055722	68055722	Missense_Mutation	SNP	C	T	4	77	c.1384G>A	c.(1384-1386)GAC>AAC	p.D462N
Pat_41	Post-Resistance	NFATC3	4775	37	16	68200898	68200898	Missense_Mutation	SNP	C	T	22	347	c.1754C>T	c.(1753-1755)GCC>GTC	p.A585V
Pat_41	Post-Resistance	ESRP2	80004	37	16	68267964	68267964	Missense_Mutation	SNP	G	A	13	62	c.374C>T	c.(373-375)CCC>CTC	p.P125L
Pat_41	Post-Resistance	ESRP2	80004	37	16	68267998	68267998	Missense_Mutation	SNP	C	T	5	32	c.340G>A	c.(340-342)GTG>ATG	p.V114M

Pat_41	Post-Resistance	SLC7A6	9057	37	16	68331224	68331224	Missense_Mutation	SNP	C	T	4	89	c.1541C>T	c.(1540-1542)ACT>ATT	p.T514I
Pat_41	Post-Resistance	SLC7A6OS	84138	37	16	68344687	68344687	Missense_Mutation	SNP	C	T	22	151	c.143G>A	c.(142-144)AGA>AAA	p.R48K
Pat_41	Post-Resistance	PRMT7	54496	37	16	68373735	68373735	Missense_Mutation	SNP	G	A	31	128	c.791G>A	c.(790-792)AGC>AAC	p.S264N
Pat_41	Post-Resistance	CIRH1A	84916	37	16	69184788	69184788	Missense_Mutation	SNP	G	A	34	157	c.983G>A	c.(982-984)CGA>CAA	p.R328Q
Pat_41	Post-Resistance	TMED6	146456	37	16	69381804	69381804	Missense_Mutation	SNP	G	A	116	337	c.376C>T	c.(376-378)CAC>TAC	p.H126Y
Pat_41	Post-Resistance	CYB5B	80777	37	16	69482030	69482030	Missense_Mutation	SNP	C	T	22	330	c.316C>T	c.(316-318)CCT>TCT	p.P106S
Pat_41	Post-Resistance	NFAT5	10725	37	16	69726828	69726828	Missense_Mutation	SNP	G	A	26	176	c.3046G>A	c.(3046-3048)GAC>AAC	p.D1016N
Pat_41	Post-Resistance	WWP2	11060	37	16	69832662	69832662	Missense_Mutation	SNP	C	T	9	326	c.148C>T	c.(148-150)CCC>TCC	p.P50S
Pat_41	Post-Resistance	CLEC18A	348174	37	16	69988328	69988328	Missense_Mutation	SNP	C	T	5	41	c.308C>T	c.(307-309)ACC>ATC	p.T103I
Pat_41	Post-Resistance	PDPR	55066	37	16	70177414	70177414	Missense_Mutation	SNP	C	T	7	120	c.1607C>T	c.(1606-1608)TCC>TTC	p.S536F
Pat_41	Post-Resistance	DDX19A	55308	37	16	70400544	70400544	Missense_Mutation	SNP	G	A	8	91	c.800G>A	c.(799-801)TGC>TAC	p.C267Y
Pat_41	Post-Resistance	ST3GAL2	6483	37	16	70422372	70422372	Missense_Mutation	SNP	C	T	25	322	c.611G>A	c.(610-612)AGT>AAT	p.S204N
Pat_41	Post-Resistance	FUK	197258	37	16	70500038	70500038	Nonsense_Mutation	SNP	C	T	6	182	c.289C>T	c.(289-291)CGA>TGA	p.R97*
Pat_41	Post-Resistance	FUK	197258	37	16	70501825	70501825	Missense_Mutation	SNP	G	A	23	166	c.619G>A	c.(619-621)GCA>ACA	p.A207T
Pat_41	Post-Resistance	SF3B3	23450	37	16	70562835	70562835	Missense_Mutation	SNP	G	A	6	180	c.130G>A	c.(130-132)GAC>AAC	p.D44N
Pat_41	Post-Resistance	VAC14	55697	37	16	70778362	70778362	Missense_Mutation	SNP	G	A	9	88	c.1492C>T	c.(1492-1494)CCC>TCC	p.P498S
Pat_41	Post-Resistance	HYDIN	54768	37	16	70841859	70841859	Missense_Mutation	SNP	C	T	21	166	c.14987G>A	c.(14986-14988)GGT>GAT	p.G4996D
Pat_41	Post-Resistance	HYDIN	54768	37	16	70908211	70908211	Missense_Mutation	SNP	C	T	12	413	c.10942G>A	c.(10942-10944)GCA>ACA	p.A3648T
Pat_41	Post-Resistance	CALB2	794	37	16	71406125	71406125	Missense_Mutation	SNP	C	T	5	88	c.164C>T	c.(163-165)TCT>TTT	p.S55F
Pat_41	Post-Resistance	ZNF19	7567	37	16	71512186	71512186	Nonsense_Mutation	SNP	C	T	15	95	c.219G>A	c.(217-219)TGG>TGA	p.W73*
Pat_41	Post-Resistance	AP1G1	164	37	16	71779145	71779145	Missense_Mutation	SNP	C	T	6	111	c.1901G>A	c.(1900-1902)GGA>GAA	p.G634E
Pat_41	Post-Resistance	AP1G1	164	37	16	71783825	71783825	Missense_Mutation	SNP	C	T	34	610	c.1469G>A	c.(1468-1470)GGC>GAC	p.G490D
Pat_41	Post-Resistance	ZNF821	55565	37	16	71898940	71898940	Missense_Mutation	SNP	C	T	23	468	c.178G>A	c.(178-180)GGT>AGT	p.G60S
Pat_41	Post-Resistance	KIAA0174	9798	37	16	71950374	71950374	Missense_Mutation	SNP	C	T	13	170	c.137C>T	c.(136-138)GCC>GTC	p.A46V
Pat_41	Post-Resistance	ZFHX3	463	37	16	72827214	72827214	Missense_Mutation	SNP	G	A	14	252	c.9367C>T	c.(9367-9369)CCT>TCT	p.P3123S
Pat_41	Post-Resistance	ZFHX3	463	37	16	72827669	72827669	Missense_Mutation	SNP	G	A	10	115	c.8912C>T	c.(8911-8913)CCC>CTC	p.P2971L
Pat_41	Post-Resistance	ZFHX3	463	37	16	72845508	72845508	Missense_Mutation	SNP	C	T	4	60	c.3832G>A	c.(3832-3834)GCA>ACA	p.A1278T
Pat_41	Post-Resistance	CLEC18B	497190	37	16	74443750	74443750	Missense_Mutation	SNP	C	T	4	135	c.1238G>A	c.(1237-1239)GGG>GAG	p.G413E
Pat_41	Post-Resistance	GLG1	2734	37	16	74528714	74528714	Missense_Mutation	SNP	C	T	12	190	c.994G>A	c.(994-996)GGC>AGC	p.G332S
Pat_41	Post-Resistance	LDHD	197257	37	16	75148802	75148802	Missense_Mutation	SNP	G	A	8	59	c.392C>T	c.(391-393)TCT>TTT	p.S131F
Pat_41	Post-Resistance	BCAR1	9564	37	16	75269059	75269059	Missense_Mutation	SNP	C	T	15	20	c.1738G>A	c.(1738-1740)GTG>ATG	p.V580M
Pat_41	Post-Resistance	ADAT1	23536	37	16	75646733	75646733	Missense_Mutation	SNP	G	A	7	116	c.451C>T	c.(451-453)CTT>TTT	p.L151F
Pat_41	Post-Resistance	ADAMTS18	170692	37	16	77393255	77393255	Missense_Mutation	SNP	G	A	9	134	c.1282C>T	c.(1282-1284)CTT>TTT	p.L428F
Pat_41	Post-Resistance	WWOX	51741	37	16	78466647	78466647	Missense_Mutation	SNP	A	G	265	258	c.1054A>G	c.(1054-1056)ATG>GTG	p.M352V
Pat_41	Post-Resistance	CDYL2	124359	37	16	80718975	80718975	Missense_Mutation	SNP	G	A	45	137	c.76C>T	c.(76-78)CTT>TTT	p.L26F
Pat_41	Post-Resistance	C16orf46	123775	37	16	81095064	81095064	Missense_Mutation	SNP	C	T	4	102	c.890G>A	c.(889-891)CGC>CAC	p.R297H
Pat_41	Post-Resistance	PKD1L2	114780	37	16	81134798	81134798	Missense_Mutation	SNP	C	T	6	52	c.7310G>A	c.(7309-7311)AGC>AAC	p.S2437N
Pat_41	Post-Resistance	PKD1L2	114780	37	16	81209334	81209334	Missense_Mutation	SNP	G	A	10	75	c.2459C>T	c.(2458-2460)CCT>CTT	p.P820L
Pat_41	Post-Resistance	BCMO1	53630	37	16	81272557	81272557	Missense_Mutation	SNP	C	T	5	68	c.44C>T	c.(43-45)CCT>CTT	p.P15L
Pat_41	Post-Resistance	GAN	8139	37	16	81398963	81398963	Missense_Mutation	SNP	C	T	14	185	c.1382C>T	c.(1381-1383)GCG>GTG	p.A461V
Pat_41	Post-Resistance	PLCG2	5336	37	16	81979856	81979856	Missense_Mutation	SNP	G	A	11	91	c.3558G>A	c.(3556-3558)ATG>ATA	p.M1186I
Pat_41	Post-Resistance	SDR42E1	93517	37	16	82033150	82033150	Nonsense_Mutation	SNP	G	A	33	134	c.748C>T	c.(748-750)CAG>TAG	p.Q250*
Pat_41	Post-Resistance	CDH13	1012	37	16	82892060	82892060	Missense_Mutation	SNP	G	A	15	50	c.139G>A	c.(139-141)GAC>AAC	p.D47N
Pat_41	Post-Resistance	HSDL1	83693	37	16	84163634	84163634	Missense_Mutation	SNP	C	T	24	67	c.623G>A	c.(622-624)TGC>TAC	p.C208Y
Pat_41	Post-Resistance	LRRC50	123872	37	16	84203504	84203504	Missense_Mutation	SNP	C	T	5	60	c.1070C>T	c.(1069-1071)GCC>GTC	p.A357V
Pat_41	Post-Resistance	LRRC50	123872	37	16	84205881	84205881	Missense_Mutation	SNP	C	T	4	32	c.1544C>T	c.(1543-1545)GCT>GTT	p.A515V
Pat_41	Post-Resistance	CRISPLD2	83716	37	16	84879430	84879430	Nonsense_Mutation	SNP	G	A	15	68	c.279G>A	c.(277-279)TGG>TGA	p.W93*

Pat_41	Post-Resistance	ZDHHC7	55625	37	16	85010020	85010020	Missense_Mutation	SNP	G	A	14	30	c.856C>T	c.(856-858)CCC>TCC	p.P286S
Pat_41	Post-Resistance	IRF8	3394	37	16	85952185	85952185	Missense_Mutation	SNP	C	T	4	14	c.764C>T	c.(763-765)GCC>GTC	p.A255V
Pat_41	Post-Resistance	MTHFSD	64779	37	16	86575392	86575392	Missense_Mutation	SNP	C	T	4	57	c.592G>A	c.(592-594)GAC>AAC	p.D198N
Pat_41	Post-Resistance	FBXO31	79791	37	16	87380785	87380785	Missense_Mutation	SNP	C	T	28	288	c.484G>A	c.(484-486)GTG>ATG	p.V162M
Pat_41	Post-Resistance	ZCCHC14	23174	37	16	87448055	87448055	Missense_Mutation	SNP	C	T	16	96	c.1157G>A	c.(1156-1158)GGG>GAG	p.G386E
Pat_41	Post-Resistance	GALNS	2588	37	16	88902257	88902257	Missense_Mutation	SNP	C	T	5	31	c.634G>A	c.(634-636)GAA>AAA	p.E212K
Pat_41	Post-Resistance	PRDM7	11105	37	16	90126753	90126753	Missense_Mutation	SNP	C	T	9	56	c.1229G>A	c.(1228-1230)GGA>GAA	p.G410E
Pat_41	Post-Resistance	PRDM7	11105	37	16	90126823	90126823	Missense_Mutation	SNP	T	G	9	127	c.1159A>C	c.(1159-1161)ATG>CTG	p.M387L
Pat_41	Post-Resistance	RNMTL1	55178	37	17	694896	694896	Missense_Mutation	SNP	G	A	5	141	c.850G>A	c.(850-852)GTC>ATC	p.V284I
Pat_41	Post-Resistance	RNMTL1	55178	37	17	694905	694905	Missense_Mutation	SNP	G	A	19	131	c.859G>A	c.(859-861)GCT>ACT	p.A287T
Pat_41	Post-Resistance	INPP5K	51763	37	17	1399391	1399391	Missense_Mutation	SNP	C	T	24	115	c.1253G>A	c.(1252-1254)AGT>AAT	p.S418N
Pat_41	Post-Resistance	INPP5K	51763	37	17	1411456	1411456	Missense_Mutation	SNP	C	T	65	460	c.619G>A	c.(619-621)GAA>AAA	p.E207K
Pat_41	Post-Resistance	PITPNA	5306	37	17	1442186	1442186	Missense_Mutation	SNP	C	T	21	77	c.433G>A	c.(433-435)GAT>AAT	p.D145N
Pat_41	Post-Resistance	PRPF8	10594	37	17	1557147	1557147	Missense_Mutation	SNP	C	T	38	183	c.6151G>A	c.(6151-6153)GGC>AGC	p.G2051S
Pat_41	Post-Resistance	OR1A2	26189	37	17	3101255	3101255	Missense_Mutation	SNP	C	T	15	96	c.443C>T	c.(442-444)TCT>TTT	p.S148F
Pat_41	Post-Resistance	OR1E2	8388	37	17	3336178	3336178	Missense_Mutation	SNP	G	A	8	46	c.958C>T	c.(958-960)CCC>TCC	p.P320S
Pat_41	Post-Resistance	TRPV1	7442	37	17	3483784	3483784	Missense_Mutation	SNP	G	A	7	216	c.1514C>T	c.(1513-1515)ACC>ATC	p.T505I
Pat_41	Post-Resistance	ITGAE	3682	37	17	3643153	3643153	Missense_Mutation	SNP	C	T	12	91	c.2468G>A	c.(2467-2469)TGC>TAC	p.C823Y
Pat_41	Post-Resistance	ZZEF1	23140	37	17	3984678	3984678	Missense_Mutation	SNP	C	T	45	161	c.2821G>A	c.(2821-2823)GCT>ACT	p.A941T
Pat_41	Post-Resistance	MYBBP1A	10514	37	17	4446207	4446207	Splice_Site	SNP	C	T	6	27	c.2892_splice	c.e20+1	p.Q964_splice
Pat_41	Post-Resistance	MYBBP1A	10514	37	17	4449005	4449005	Missense_Mutation	SNP	A	G	2	2	c.1973T>C	c.(1972-1974)CTG>CCG	p.L658P
Pat_41	Post-Resistance	SMTNL2	342527	37	17	4495686	4495686	Missense_Mutation	SNP	G	A	12	85	c.430G>A	c.(430-432)GAG>AAG	p.E144K
Pat_41	Post-Resistance	VMO1	284013	37	17	4688820	4688820	Missense_Mutation	SNP	C	T	9	59	c.446G>A	c.(445-447)GGC>GAC	p.G149D
Pat_41	Post-Resistance	CHRNE	1145	37	17	4805992	4805992	Missense_Mutation	SNP	C	T	19	137	c.113G>A	c.(112-114)GGA>GAA	p.G38E
Pat_41	Post-Resistance	SLC25A11	8402	37	17	4842369	4842369	Missense_Mutation	SNP	C	A	4	104	c.234G>T	c.(232-234)AGG>AGT	p.R78S
Pat_41	Post-Resistance	KIF1C	10749	37	17	4907332	4907332	Missense_Mutation	SNP	G	A	12	126	c.904G>A	c.(904-906)GAC>AAC	p.D302N
Pat_41	Post-Resistance	KIF1C	10749	37	17	4923900	4923900	Missense_Mutation	SNP	G	A	7	63	c.1864G>A	c.(1864-1866)GTC>ATC	p.V622I
Pat_41	Post-Resistance	ZNF232	7775	37	17	5009466	5009466	Missense_Mutation	SNP	G	A	26	139	c.907C>T	c.(907-909)CCC>TCC	p.P303S
Pat_41	Post-Resistance	NUP88	4927	37	17	5319903	5319903	Missense_Mutation	SNP	C	T	13	55	c.397G>A	c.(397-399)GTA>ATA	p.V133I
Pat_41	Post-Resistance	KIAA0753	9851	37	17	6499486	6499486	Missense_Mutation	SNP	C	T	39	231	c.2350G>A	c.(2350-2352)GAG>AAG	p.E784K
Pat_41	Post-Resistance	KIAA0753	9851	37	17	6531482	6531482	Missense_Mutation	SNP	C	T	7	31	c.673G>A	c.(673-675)GAA>AAA	p.E225K
Pat_41	Post-Resistance	ALOX12	239	37	17	6908616	6908616	Missense_Mutation	SNP	C	T	40	404	c.1202C>T	c.(1201-1203)ACC>ATC	p.T401I
Pat_41	Post-Resistance	SLC16A13	201232	37	17	6939775	6939775	Missense_Mutation	SNP	C	T	4	38	c.74C>T	c.(73-75)GCG>GTG	p.A25V
Pat_41	Post-Resistance	DLG4	1742	37	17	7111554	7111554	Missense_Mutation	SNP	T	C	11	86	c.164A>G	c.(163-165)TAC>TGC	p.Y55C
Pat_41	Post-Resistance	YBX2	51087	37	17	7193698	7193698	Missense_Mutation	SNP	G	A	4	32	c.616C>T	c.(616-618)CCT>TCT	p.P206S
Pat_41	Post-Resistance	NEURL4	84461	37	17	7228960	7228960	Missense_Mutation	SNP	C	T	10	80	c.1366G>A	c.(1366-1368)GGA>AGA	p.G456R
Pat_41	Post-Resistance	TMEM95	339168	37	17	7259219	7259219	Missense_Mutation	SNP	C	T	11	42	c.289C>T	c.(289-291)CCT>TCT	p.P97S
Pat_41	Post-Resistance	NLGN2	57555	37	17	7315493	7315493	Missense_Mutation	SNP	C	T	11	88	c.475C>T	c.(475-477)CGT>TGT	p.R159C
Pat_41	Post-Resistance	C17orf74	201243	37	17	7329740	7329740	Missense_Mutation	SNP	C	T	9	8	c.430C>T	c.(430-432)CGG>TGG	p.R144W
Pat_41	Post-Resistance	C17orf74	201243	37	17	7330495	7330495	Nonsense_Mutation	SNP	G	A	9	24	c.1185G>A	c.(1183-1185)TGG>TGA	p.W395*
Pat_41	Post-Resistance	CHRNB1	1140	37	17	7350188	7350188	Missense_Mutation	SNP	G	A	9	86	c.280G>A	c.(280-282)GAG>AAG	p.E94K
Pat_41	Post-Resistance	ZBTB4	57659	37	17	7369423	7369423	Missense_Mutation	SNP	G	A	3	40	c.698C>T	c.(697-699)CCC>CTC	p.P233L
Pat_41	Post-Resistance	TP53	7157	37	17	7577139	7577139	Missense_Mutation	SNP	G	C	10	2	c.799C>G	c.(799-801)CGG>GGG	p.R267G
Pat_41	Post-Resistance	EFNB3	1949	37	17	7611403	7611403	Missense_Mutation	SNP	G	A	28	86	c.250G>A	c.(250-252)GTA>ATA	p.V84I
Pat_41	Post-Resistance	LSMD1	84316	37	17	7760087	7760087	Missense_Mutation	SNP	C	T	15	137	c.340G>A	c.(340-342)GTG>ATG	p.V114M
Pat_41	Post-Resistance	GUCY2D	3000	37	17	7915632	7915632	Nonsense_Mutation	SNP	G	A	5	56	c.1920G>A	c.(1918-1920)TGG>TGA	p.W640*
Pat_41	Post-Resistance	PFAS	5198	37	17	8160203	8160203	Missense_Mutation	SNP	G	A	17	115	c.997G>A	c.(997-999)GAT>AAT	p.D333N

Pat_41	Post-Resistance	MYH10	4628	37	17	8396255	8396255	Missense_Mutation	SNP	C	T	9	19	c.4204G>A	c.(4204-4206)GAG>AAG	p.E1402K
Pat_41	Post-Resistance	MFSD6L	162387	37	17	8702098	8702098	Missense_Mutation	SNP	C	T	12	103	c.341G>A	c.(340-342)GGC>GAC	p.G114D
Pat_41	Post-Resistance	GLP2R	9340	37	17	9757914	9757914	Missense_Mutation	SNP	C	T	42	96	c.607C>T	c.(607-609)CTT>TTT	p.L203F
Pat_41	Post-Resistance	MYH13	8735	37	17	10216655	10216655	Missense_Mutation	SNP	G	A	13	152	c.4001C>T	c.(4000-4002)GCG>GTG	p.A1334V
Pat_41	Post-Resistance	MYH8	4626	37	17	10318659	10318659	Missense_Mutation	SNP	C	T	22	119	c.691G>A	c.(691-693)GAG>AAG	p.E231K
Pat_41	Post-Resistance	MYH1	4619	37	17	10408209	10408209	Missense_Mutation	SNP	G	A	9	41	c.2609C>T	c.(2608-2610)ACC>ATC	p.T870I
Pat_41	Post-Resistance	MYH1	4619	37	17	10408751	10408751	Missense_Mutation	SNP	C	T	11	78	c.2252G>A	c.(2251-2253)GGG>GAG	p.G751E
Pat_41	Post-Resistance	MYH3	4621	37	17	10535165	10535165	Missense_Mutation	SNP	C	T	26	43	c.5125G>A	c.(5125-5127)GAC>AAC	p.D1709N
Pat_41	Post-Resistance	DNAH9	1770	37	17	11666845	11666845	Missense_Mutation	SNP	C	T	15	85	c.7084C>T	c.(7084-7086)CCT>TCT	p.P2362S
Pat_41	Post-Resistance	DNAH9	1770	37	17	11774922	11774922	Missense_Mutation	SNP	G	A	17	125	c.10061G>A	c.(10060-10062)GGA>GAA	p.G3354E
Pat_41	Post-Resistance	ZNF18	7566	37	17	11895783	11895783	Missense_Mutation	SNP	C	T	6	114	c.364G>A	c.(364-366)GAC>AAC	p.D122N
Pat_41	Post-Resistance	TRPV2	51393	37	17	16325966	16325966	Missense_Mutation	SNP	G	A	5	53	c.388G>A	c.(388-390)GGA>AGA	p.G130R
Pat_41	Post-Resistance	ZNF624	57547	37	17	16527271	16527271	Missense_Mutation	SNP	C	T	4	25	c.929G>A	c.(928-930)GGG>GAG	p.G310E
Pat_41	Post-Resistance	FLCN	201163	37	17	17117006	17117006	Missense_Mutation	SNP	G	A	4	122	c.1703C>T	c.(1702-1704)ACG>ATG	p.T568M
Pat_41	Post-Resistance	RASD1	51655	37	17	17399332	17399332	Missense_Mutation	SNP	G	A	20	92	c.164C>T	c.(163-165)CCT>CTT	p.P55L
Pat_41	Post-Resistance	SREBF1	6720	37	17	17722535	17722535	Missense_Mutation	SNP	C	T	12	79	c.860G>A	c.(859-861)GGC>GAC	p.G287D
Pat_41	Post-Resistance	TOM1L2	146691	37	17	17786143	17786143	Missense_Mutation	SNP	G	A	18	71	c.536C>T	c.(535-537)CCC>CTC	p.P179L
Pat_41	Post-Resistance	FLII	2314	37	17	18157489	18157489	Missense_Mutation	SNP	G	A	14	3	c.583C>T	c.(583-585)CCA>TCA	p.P195S
Pat_41	Post-Resistance	SMCR7	125170	37	17	18166111	18166111	Missense_Mutation	SNP	C	T	6	49	c.77C>T	c.(76-78)GCC>GTC	p.A26V
Pat_41	Post-Resistance	KCNJ12	3768	37	17	21319175	21319175	Missense_Mutation	SNP	C	T	4	109	c.521C>T	c.(520-522)TCC>TTC	p.S174F
Pat_41	Post-Resistance	NLK	51701	37	17	26495580	26495580	Missense_Mutation	SNP	G	A	21	190	c.944G>A	c.(943-945)AGC>AAC	p.S315N
Pat_41	Post-Resistance	IFT20	90410	37	17	26658936	26658936	Missense_Mutation	SNP	C	T	19	90	c.76G>A	c.(76-78)GTT>ATT	p.V26I
Pat_41	Post-Resistance	PIGS	94005	37	17	26898185	26898185	Missense_Mutation	SNP	G	A	5	48	c.56C>T	c.(55-57)GCC>GTC	p.A19V
Pat_41	Post-Resistance	SPAG5	10615	37	17	26904721	26904721	Missense_Mutation	SNP	C	T	9	40	c.3578G>A	c.(3577-3579)AGC>AAC	p.S1193N
Pat_41	Post-Resistance	KIAA0100	9703	37	17	26961666	26961666	Missense_Mutation	SNP	G	A	34	67	c.2939C>T	c.(2938-2940)TCC>TTC	p.S980F
Pat_41	Post-Resistance	TRAF4	9618	37	17	27076479	27076479	Missense_Mutation	SNP	G	A	4	39	c.1297G>A	c.(1297-1299)GGC>AGC	p.G433S
Pat_41	Post-Resistance	SEZ6	124925	37	17	27286811	27286811	Missense_Mutation	SNP	C	T	16	17	c.1676G>A	c.(1675-1677)TGC>TAC	p.C559Y
Pat_41	Post-Resistance	NUFIP2	57532	37	17	27613053	27613053	Nonsense_Mutation	SNP	C	T	18	89	c.1959G>A	c.(1957-1959)TGG>TGA	p.W653*
Pat_41	Post-Resistance	GIT1	28964	37	17	27902114	27902114	Missense_Mutation	SNP	C	T	4	73	c.2056G>A	c.(2056-2058)GCC>ACC	p.A686T
Pat_41	Post-Resistance	GIT1	28964	37	17	27905368	27905368	Missense_Mutation	SNP	C	T	7	65	c.832G>A	c.(832-834)GAA>AAA	p.E278K
Pat_41	Post-Resistance	CPD	1362	37	17	28788905	28788905	Missense_Mutation	SNP	G	A	9	111	c.3641G>A	c.(3640-3642)GGA>GAA	p.G1214E
Pat_41	Post-Resistance	C17orf79	55352	37	17	30183833	30183833	Missense_Mutation	SNP	C	T	37	575	c.151G>A	c.(151-153)GCT>ACT	p.A51T
Pat_41	Post-Resistance	CCL1	6346	37	17	32690113	32690113	Missense_Mutation	SNP	C	T	12	97	c.68G>A	c.(67-69)AGC>AAC	p.S23N
Pat_41	Post-Resistance	FNDC8	54752	37	17	33456546	33456546	Missense_Mutation	SNP	C	T	15	60	c.691C>T	c.(691-693)CGT>TGT	p.R231C
Pat_41	Post-Resistance	NLE1	54475	37	17	33464882	33464882	Missense_Mutation	SNP	G	A	9	41	c.488C>T	c.(487-489)TCC>TTC	p.S163F
Pat_41	Post-Resistance	UNC45B	146862	37	17	33513459	33513459	Missense_Mutation	SNP	G	A	9	35	c.2677G>A	c.(2677-2679)GAG>AAG	p.E893K
Pat_41	Post-Resistance	PEX12	5193	37	17	33904063	33904063	Missense_Mutation	SNP	G	A	18	153	c.674C>T	c.(673-675)GCC>GTC	p.A225V
Pat_41	Post-Resistance	PEX12	5193	37	17	33904112	33904112	Nonsense_Mutation	SNP	G	A	40	237	c.625C>T	c.(625-627)CAA>TAA	p.Q209*
Pat_41	Post-Resistance	RASL10B	91608	37	17	34067433	34067433	Nonsense_Mutation	SNP	G	A	12	28	c.222G>A	c.(220-222)TGG>TGA	p.W74*
Pat_41	Post-Resistance	ACACA	31	37	17	35518748	35518748	Missense_Mutation	SNP	C	T	20	212	c.5185G>A	c.(5185-5187)GAA>AAA	p.E1729K
Pat_41	Post-Resistance	C17orf78	284099	37	17	35736233	35736233	Missense_Mutation	SNP	G	A	7	158	c.304G>A	c.(304-306)GCT>ACT	p.A102T
Pat_41	Post-Resistance	GPR179	440435	37	17	36491997	36491997	Missense_Mutation	SNP	C	T	21	112	c.1258G>A	c.(1258-1260)GAA>AAA	p.E420K
Pat_41	Post-Resistance	FBXO47	494188	37	17	37118187	37118187	Missense_Mutation	SNP	G	A	9	95	c.295C>T	c.(295-297)CTT>TTT	p.L99F
Pat_41	Post-Resistance	TCAP	8557	37	17	37821691	37821691	Missense_Mutation	SNP	G	A	5	47	c.79G>A	c.(79-81)GAT>AAT	p.D27N
Pat_41	Post-Resistance	IKZF3	22806	37	17	37944619	37944619	Missense_Mutation	SNP	G	A	4	47	c.601C>T	c.(601-603)CCC>TCC	p.P201S
Pat_41	Post-Resistance	ORMDL3	94103	37	17	38080447	38080447	Missense_Mutation	SNP	C	T	24	153	c.10G>A	c.(10-12)GGC>AGC	p.G4S
Pat_41	Post-Resistance	MED24	9862	37	17	38183655	38183655	Missense_Mutation	SNP	G	A	5	27	c.1511C>T	c.(1510-1512)GCC>GTC	p.A504V

Pat_41	Post-Resistance	KRT39	390792	37	17	39122976	39122976	Nonsense_Mutation	SNP	G	A	12	155	c.133C>T	c.(133-135)CAA>TAA	p.Q45*
Pat_41	Post-Resistance	KRTAP1-5	83895	37	17	39183247	39183247	Missense_Mutation	SNP	C	T	9	68	c.161G>A	c.(160-162)GGG>GAG	p.G54E
Pat_41	Post-Resistance	KRTAP4-9	100132386	37	17	39262049	39262049	Missense_Mutation	SNP	C	T	6	45	c.409C>T	c.(409-411)CCC>TCC	p.P137S
Pat_41	Post-Resistance	KRTAP4-5	85289	37	17	39305892	39305892	Missense_Mutation	SNP	G	A	4	101	c.128C>T	c.(127-129)CCC>CTC	p.P43L
Pat_41	Post-Resistance	KRTAP4-3	85290	37	17	39323934	39323934	Missense_Mutation	SNP	C	T	4	31	c.491G>A	c.(490-492)TGC>TAC	p.C164Y
Pat_41	Post-Resistance	KRT31	3881	37	17	39550386	39550386	Missense_Mutation	SNP	C	T	4	92	c.1133G>A	c.(1132-1134)TGC>TAC	p.C378Y
Pat_41	Post-Resistance	KRT37	8688	37	17	39580664	39580664	Missense_Mutation	SNP	C	T	5	65	c.112G>A	c.(112-114)GCC>ACC	p.A38T
Pat_41	Post-Resistance	KRT32	3882	37	17	39616408	39616408	Missense_Mutation	SNP	C	T	5	42	c.1301G>A	c.(1300-1302)CGC>CAC	p.R434H
Pat_41	Post-Resistance	KRT32	3882	37	17	39619212	39619212	Missense_Mutation	SNP	C	T	4	100	c.1087G>A	c.(1087-1089)GCC>ACC	p.A363T
Pat_41	Post-Resistance	SC65	10609	37	17	39963047	39963047	Splice_Site	SNP	C	T	4	20	c.1146_splice	c.e6+1	p.E382_splice
Pat_41	Post-Resistance	DHX58	79132	37	17	40262862	40262862	Missense_Mutation	SNP	C	T	15	150	c.440G>A	c.(439-441)AGC>AAC	p.S147N
Pat_41	Post-Resistance	KAT2A	2648	37	17	40273054	40273054	Missense_Mutation	SNP	C	T	3	13	c.269G>A	c.(268-270)AGG>AAG	p.R90K
Pat_41	Post-Resistance	RAB5C	5878	37	17	40278824	40278824	Missense_Mutation	SNP	C	T	18	269	c.484G>A	c.(484-486)GAG>AAG	p.E162K
Pat_41	Post-Resistance	KCNH4	23415	37	17	40318534	40318534	Missense_Mutation	SNP	C	T	13	94	c.1621G>A	c.(1621-1623)GCT>ACT	p.A541T
Pat_41	Post-Resistance	FAM134C	162427	37	17	40761296	40761296	Missense_Mutation	SNP	C	T	6	18	c.47G>A	c.(46-48)GGG>GAG	p.G16E
Pat_41	Post-Resistance	TUBG2	27175	37	17	40818461	40818461	Missense_Mutation	SNP	G	A	26	85	c.1117G>A	c.(1117-1119)GTC>ATC	p.V373I
Pat_41	Post-Resistance	CNTNAP1	8506	37	17	40845338	40845338	Missense_Mutation	SNP	C	T	13	71	c.2776C>T	c.(2776-2778)CCC>TCC	p.P926S
Pat_41	Post-Resistance	DHX8	1659	37	17	41585294	41585294	Missense_Mutation	SNP	C	T	23	71	c.2227C>T	c.(2227-2229)CCA>TCA	p.P743S
Pat_41	Post-Resistance	MPP2	4355	37	17	41955302	41955302	Missense_Mutation	SNP	C	T	14	48	c.1667G>A	c.(1666-1668)GGC>GAC	p.G556D
Pat_41	Post-Resistance	FZD2	2535	37	17	42635786	42635786	Missense_Mutation	SNP	G	A	5	62	c.730G>A	c.(730-732)GCG>ACG	p.A244T
Pat_41	Post-Resistance	GFAP	2670	37	17	42992644	42992644	Missense_Mutation	SNP	C	T	9	47	c.211G>A	c.(211-213)GCA>ACA	p.A71T
Pat_41	Post-Resistance	MAPT	4137	37	17	44061231	44061231	Missense_Mutation	SNP	C	T	8	44	c.1061C>T	c.(1060-1062)CCC>CTC	p.P354L
Pat_41	Post-Resistance	MAPT	4137	37	17	44073905	44073905	Missense_Mutation	SNP	C	T	8	18	c.1648C>T	c.(1648-1650)CCC>TCC	p.P550S
Pat_41	Post-Resistance	NSF	4905	37	17	44803982	44803982	Splice_Site	SNP	G	A	22	256	c.1828_splice	c.e16+1	p.D610_splice
Pat_41	Post-Resistance	C17orf57	124989	37	17	45452260	45452260	Missense_Mutation	SNP	C	T	13	35	c.1300C>T	c.(1300-1302)CCA>TCA	p.P434S
Pat_41	Post-Resistance	KPNB1	3837	37	17	45735929	45735929	Missense_Mutation	SNP	G	A	9	74	c.539G>A	c.(538-540)GGG>GAG	p.G180E
Pat_41	Post-Resistance	KPNB1	3837	37	17	45757887	45757887	Missense_Mutation	SNP	G	A	5	186	c.2482G>A	c.(2482-2484)GCA>ACA	p.A828T
Pat_41	Post-Resistance	TBX21	30009	37	17	45820554	45820554	Missense_Mutation	SNP	C	T	5	43	c.764C>T	c.(763-765)ACC>ATC	p.T255I
Pat_41	Post-Resistance	COPZ2	51226	37	17	46105876	46105876	Missense_Mutation	SNP	C	T	8	20	c.547G>A	c.(547-549)GCA>ACA	p.A183T
Pat_41	Post-Resistance	HOXB2	3212	37	17	46620540	46620540	Missense_Mutation	SNP	C	T	13	58	c.961G>A	c.(961-963)GGC>AGC	p.G321S
Pat_41	Post-Resistance	HOXB3	3213	37	17	46627886	46627886	Missense_Mutation	SNP	G	A	4	6	c.1106C>T	c.(1105-1107)TCC>TTC	p.S369F
Pat_41	Post-Resistance	CALCOCO2	10241	37	17	46933509	46933509	Missense_Mutation	SNP	C	T	9	54	c.968C>T	c.(967-969)GCT>GTT	p.A323V
Pat_41	Post-Resistance	IGF2BP1	10642	37	17	47118754	47118754	Missense_Mutation	SNP	C	T	14	30	c.833C>T	c.(832-834)CCC>CTC	p.P278L
Pat_41	Post-Resistance	ZNF652	22834	37	17	47394681	47394681	Missense_Mutation	SNP	C	T	12	83	c.407G>A	c.(406-408)GGT>GAT	p.G136D
Pat_41	Post-Resistance	COL1A1	1277	37	17	48276792	48276792	Missense_Mutation	SNP	G	A	6	11	c.356C>T	c.(355-357)CCC>CTC	p.P119L
Pat_41	Post-Resistance	RSAD1	55316	37	17	48557041	48557041	Missense_Mutation	SNP	C	T	5	74	c.187C>T	c.(187-189)CCT>TCT	p.P63S
Pat_41	Post-Resistance	MYCBPAP	84073	37	17	48606386	48606386	Missense_Mutation	SNP	C	T	8	99	c.2690C>T	c.(2689-2691)CCC>CTC	p.P897L
Pat_41	Post-Resistance	EPN3	55040	37	17	48618939	48618939	Missense_Mutation	SNP	C	T	12	35	c.1469C>T	c.(1468-1470)GCC>GTC	p.A490V
Pat_41	Post-Resistance	ABCC3	8714	37	17	48752818	48752818	Missense_Mutation	SNP	G	A	5	44	c.2695G>A	c.(2695-2697)GTC>ATC	p.V899I
Pat_41	Post-Resistance	ANKRD40	91369	37	17	48777117	48777117	Missense_Mutation	SNP	C	T	16	37	c.421G>A	c.(421-423)GCC>ACC	p.A141T
Pat_41	Post-Resistance	WFIKKN2	124857	37	17	48918031	48918031	Missense_Mutation	SNP	G	A	7	32	c.1382G>A	c.(1381-1383)AGC>AAC	p.S461N
Pat_41	Post-Resistance	SPAG9	9043	37	17	49118995	49118995	Missense_Mutation	SNP	G	A	10	123	c.608C>T	c.(607-609)TCA>TTA	p.S203L
Pat_41	Post-Resistance	NME1-NME2	654364	37	17	49231736	49231736	Missense_Mutation	SNP	T	C	4	97	c.2T>C	c.(1-3)ATG>ACG	p.M1T
Pat_41	Post-Resistance	STXBP4	252983	37	17	53150348	53150348	Missense_Mutation	SNP	G	A	34	87	c.1099G>A	c.(1099-1101)GAA>AAA	p.E367K
Pat_41	Post-Resistance	PRR11	55771	37	17	57270974	57270974	Missense_Mutation	SNP	C	T	9	72	c.524C>T	c.(523-525)CCC>CTC	p.P175L
Pat_41	Post-Resistance	PTRH2	51651	37	17	57774879	57774879	Missense_Mutation	SNP	C	T	8	67	c.461G>A	c.(460-462)GGC>GAC	p.G154D
Pat_41	Post-Resistance	RPS6KB1	6198	37	17	57990133	57990133	Missense_Mutation	SNP	C	T	23	284	c.280C>T	c.(280-282)CTT>TTT	p.L94F

Pat_41	Post-Resistance	RPS6KB1	6198	37	17	58013613	58013613	Missense_Mutation	SNP	G	A	17	102	c.1016G>A	c.(1015-1017)GGT>GAT	p.G339D
Pat_41	Post-Resistance	RPS6KB1	6198	37	17	58018279	58018279	Missense_Mutation	SNP	G	A	18	127	c.1202G>A	c.(1201-1203)AGT>AAT	p.S401N
Pat_41	Post-Resistance	RNFT1	51136	37	17	58040217	58040217	Missense_Mutation	SNP	C	T	20	120	c.485G>A	c.(484-486)AGC>AAC	p.S162N
Pat_41	Post-Resistance	PPM1D	8493	37	17	58740647	58740647	Missense_Mutation	SNP	C	T	21	48	c.1552C>T	c.(1552-1554)CCT>TCT	p.P518S
Pat_41	Post-Resistance	BCAS3	54828	37	17	59445709	59445709	Missense_Mutation	SNP	C	T	19	165	c.2492C>T	c.(2491-2493)ACC>ATC	p.T831I
Pat_41	Post-Resistance	C17orf82	388407	37	17	59489518	59489518	Missense_Mutation	SNP	C	T	3	4	c.182C>T	c.(181-183)CCC>CTC	p.P61L
Pat_41	Post-Resistance	INTS2	57508	37	17	59989332	59989332	Missense_Mutation	SNP	G	A	16	134	c.773C>T	c.(772-774)CCT>CTT	p.P258L
Pat_41	Post-Resistance	METTL2A	339175	37	17	60526017	60526017	Missense_Mutation	SNP	G	A	17	199	c.1064G>A	c.(1063-1065)GGA>GAA	p.G355E
Pat_41	Post-Resistance	DCAF7	10238	37	17	61662613	61662613	Missense_Mutation	SNP	C	T	32	138	c.779C>T	c.(778-780)GCC>GTC	p.A260V
Pat_41	Post-Resistance	ERN1	2081	37	17	62142568	62142568	Splice_Site	SNP	C	T	5	18	c.921_splice	c.e9+1	p.V307_splice
Pat_41	Post-Resistance	SMURF2	64750	37	17	62589560	62589560	Missense_Mutation	SNP	C	T	42	123	c.332G>A	c.(331-333)GGT>GAT	p.G111D
Pat_41	Post-Resistance	PLEKHM1P	440456	37	17	62793381	62793381	Splice_Site	SNP	C	T	5	14	c.1068_splice	c.e7+1	p.P356_splice
Pat_41	Post-Resistance	LRRC37A3	374819	37	17	62855682	62855682	Missense_Mutation	SNP	G	A	6	248	c.4582C>T	c.(4582-4584)CTC>TTC	p.L1528F
Pat_41	Post-Resistance	AXIN2	8313	37	17	63554534	63554534	Missense_Mutation	SNP	C	T	15	56	c.205G>A	c.(205-207)GCA>ACA	p.A69T
Pat_41	Post-Resistance	CACNG4	27092	37	17	65027112	65027112	Missense_Mutation	SNP	C	T	17	113	c.976C>T	c.(976-978)CCT>TCT	p.P326S
Pat_41	Post-Resistance	CACNG1	786	37	17	65040852	65040852	Missense_Mutation	SNP	G	A	7	167	c.76G>A	c.(76-78)GCC>ACC	p.A26T
Pat_41	Post-Resistance	PITPNC1	26207	37	17	65688789	65688789	Missense_Mutation	SNP	C	T	21	320	c.784C>T	c.(784-786)CCC>TCC	p.P262S
Pat_41	Post-Resistance	NOL11	25926	37	17	65733697	65733697	Missense_Mutation	SNP	C	T	29	312	c.1292C>T	c.(1291-1293)ACT>ATT	p.T431I
Pat_41	Post-Resistance	BPTF	2186	37	17	65909084	65909084	Missense_Mutation	SNP	G	A	5	93	c.5084G>A	c.(5083-5085)AGA>AAA	p.R1695K
Pat_41	Post-Resistance	ARSG	22901	37	17	66381213	66381213	Missense_Mutation	SNP	C	T	24	302	c.991C>T	c.(991-993)CCA>TCA	p.P331S
Pat_41	Post-Resistance	WIPI1	55062	37	17	66430733	66430733	Missense_Mutation	SNP	C	T	8	94	c.656G>A	c.(655-657)GGG>GAG	p.G219E
Pat_41	Post-Resistance	PRKAR1A	5573	37	17	66525098	66525098	Missense_Mutation	SNP	G	A	17	240	c.857G>A	c.(856-858)GGA>GAA	p.G286E
Pat_41	Post-Resistance	ABCA9	10350	37	17	67012509	67012509	Missense_Mutation	SNP	C	T	32	248	c.2924G>A	c.(2923-2925)TGT>TAT	p.C975Y
Pat_41	Post-Resistance	ABCA10	10349	37	17	67145193	67145193	Missense_Mutation	SNP	G	A	23	343	c.4514C>T	c.(4513-4515)TCT>TTT	p.S1505F
Pat_41	Post-Resistance	MAP2K6	5608	37	17	67515454	67515454	Missense_Mutation	SNP	C	T	5	194	c.247C>T	c.(247-249)CGG>TGG	p.R83W
Pat_41	Post-Resistance	DNAI2	64446	37	17	72306255	72306255	Missense_Mutation	SNP	C	T	3	37	c.1447C>T	c.(1447-1449)CCT>TCT	p.P483S
Pat_41	Post-Resistance	GPRC5C	55890	37	17	72443045	72443045	Missense_Mutation	SNP	G	A	9	99	c.1204G>A	c.(1204-1206)GGC>AGC	p.G402S
Pat_41	Post-Resistance	RAB37	326624	37	17	72667766	72667766	Missense_Mutation	SNP	G	A	7	96	c.41G>A	c.(40-42)GGC>GAC	p.G14D
Pat_41	Post-Resistance	TMEM104	54868	37	17	72832612	72832612	Missense_Mutation	SNP	G	A	3	64	c.1277G>A	c.(1276-1278)GGG>GAG	p.G426E
Pat_41	Post-Resistance	GRIN2C	2905	37	17	72840518	72840518	Missense_Mutation	SNP	C	T	23	93	c.2480G>A	c.(2479-2481)GGG>GAG	p.G827E
Pat_41	Post-Resistance	FDXR	2232	37	17	72861921	72861921	Missense_Mutation	SNP	C	T	11	64	c.529G>A	c.(529-531)GAC>AAC	p.D177N
Pat_41	Post-Resistance	OTOP2	92736	37	17	72926818	72926818	Missense_Mutation	SNP	C	T	11	134	c.1088C>T	c.(1087-1089)CCC>CTC	p.P363L
Pat_41	Post-Resistance	SLC16A5	9121	37	17	73089912	73089912	Missense_Mutation	SNP	G	A	28	219	c.181G>A	c.(181-183)GCT>ACT	p.A61T
Pat_41	Post-Resistance	SLC16A5	9121	37	17	73094133	73094133	Missense_Mutation	SNP	G	A	10	108	c.200G>A	c.(199-201)GGG>GAG	p.G67E
Pat_41	Post-Resistance	GGA3	23163	37	17	73242797	73242797	Missense_Mutation	SNP	C	T	9	129	c.121G>A	c.(121-123)GAA>AAA	p.E41K
Pat_41	Post-Resistance	LLGL2	3993	37	17	73566246	73566246	Missense_Mutation	SNP	C	T	3	5	c.1784C>T	c.(1783-1785)GCC>GTC	p.A595V
Pat_41	Post-Resistance	RECQL5	9400	37	17	73625116	73625116	Missense_Mutation	SNP	C	T	4	42	c.2387G>A	c.(2386-2388)GGA>GAA	p.G796E
Pat_41	Post-Resistance	UNK	85451	37	17	73780812	73780812	Missense_Mutation	SNP	G	A	21	162	c.79G>A	c.(79-81)GAC>AAC	p.D27N
Pat_41	Post-Resistance	UNC13D	201294	37	17	73827364	73827364	Missense_Mutation	SNP	C	T	9	80	c.2513G>A	c.(2512-2514)AGC>AAC	p.S838N
Pat_41	Post-Resistance	TRIM47	91107	37	17	73871127	73871127	Missense_Mutation	SNP	C	T	25	158	c.1354G>A	c.(1354-1356)GTG>ATG	p.V452M
Pat_41	Post-Resistance	FBF1	85302	37	17	73910115	73910115	Missense_Mutation	SNP	T	C	4	18	c.2963A>G	c.(2962-2964)TAC>TGC	p.Y988C
Pat_41	Post-Resistance	FBF1	85302	37	17	73926110	73926110	Missense_Mutation	SNP	C	T	3	21	c.205G>A	c.(205-207)GCA>ACA	p.A69T
Pat_41	Post-Resistance	EVPL	2125	37	17	74008108	74008108	Missense_Mutation	SNP	C	A	3	35	c.2436G>T	c.(2434-2436)CAG>CAT	p.Q812H
Pat_41	Post-Resistance	EXOC7	23265	37	17	74080606	74080606	Missense_Mutation	SNP	C	T	6	74	c.1921G>A	c.(1921-1923)GGA>AGA	p.G641R
Pat_41	Post-Resistance	EXOC7	23265	37	17	74097787	74097787	Missense_Mutation	SNP	C	T	22	301	c.284G>A	c.(283-285)AGT>AAT	p.S95N
Pat_41	Post-Resistance	FOXJ1	2302	37	17	74134153	74134153	Missense_Mutation	SNP	G	A	4	101	c.547C>T	c.(547-549)CCT>TCT	p.P183S
Pat_41	Post-Resistance	RNF157	114804	37	17	74150376	74150376	Missense_Mutation	SNP	G	A	7	284	c.1798C>T	c.(1798-1800)CCC>TCC	p.P600S

Pat_41	Post-Resistance	FAM100B	283991	37	17	74266309	74266309	Missense_Mutation	SNP	C	T	20	189	c.218C>T	c.(217-219)CCC>CTC	p.P73L
Pat_41	Post-Resistance	QRICH2	84074	37	17	74271977	74271977	Missense_Mutation	SNP	C	T	15	58	c.4907G>A	c.(4906-4908)AGG>AAG	p.R1636K
Pat_41	Post-Resistance	QRICH2	84074	37	17	74287704	74287704	Missense_Mutation	SNP	C	T	19	185	c.2606G>A	c.(2605-2607)GGT>GAT	p.G869D
Pat_41	Post-Resistance	UBE2O	63893	37	17	74393939	74393939	Missense_Mutation	SNP	C	T	23	221	c.2056G>A	c.(2056-2058)GTC>ATC	p.V686I
Pat_41	Post-Resistance	RHBDF2	79651	37	17	74467899	74467899	Missense_Mutation	SNP	C	T	5	23	c.2387G>A	c.(2386-2388)AGC>AAC	p.S796N
Pat_41	Post-Resistance	TNRC6C	57690	37	17	76045785	76045785	Missense_Mutation	SNP	G	A	50	404	c.642G>A	c.(640-642)ATG>ATA	p.M214I
Pat_41	Post-Resistance	TMC8	147138	37	17	76134118	76134118	Nonsense_Mutation	SNP	G	A	5	108	c.1382G>A	c.(1381-1383)TGG>TAG	p.W461*
Pat_41	Post-Resistance	SOCS3	9021	37	17	76354629	76354629	Missense_Mutation	SNP	G	A	6	173	c.548C>T	c.(547-549)TCC>TTC	p.S183F
Pat_41	Post-Resistance	DNAH17	8632	37	17	76447667	76447667	Missense_Mutation	SNP	G	A	60	252	c.1618C>T	c.(1618-1620)CCA>TCA	p.P540S
Pat_41	Post-Resistance	DNAH17	8632	37	17	76459036	76459036	Missense_Mutation	SNP	C	T	18	72	c.64G>A	c.(64-66)GAG>AAG	p.E22K
Pat_41	Post-Resistance	USP36	57602	37	17	76799789	76799789	Missense_Mutation	SNP	G	A	3	36	c.2488C>T	c.(2488-2490)CCA>TCA	p.P830S
Pat_41	Post-Resistance	USP36	57602	37	17	76809938	76809938	Nonsense_Mutation	SNP	C	T	16	136	c.1182G>A	c.(1180-1182)TGG>TGA	p.W394*
Pat_41	Post-Resistance	CANT1	124583	37	17	76993359	76993359	Missense_Mutation	SNP	C	T	45	300	c.346G>A	c.(346-348)GAG>AAG	p.E116K
Pat_41	Post-Resistance	ENPP7	339221	37	17	77709013	77709013	Missense_Mutation	SNP	G	A	8	102	c.571G>A	c.(571-573)GTC>ATC	p.V191I
Pat_41	Post-Resistance	CBX4	8535	37	17	77807985	77807985	Missense_Mutation	SNP	C	T	4	31	c.1456G>A	c.(1456-1458)GAG>AAG	p.E486K
Pat_41	Post-Resistance	CCDC40	55036	37	17	78023713	78023713	Missense_Mutation	SNP	G	A	7	67	c.864G>A	c.(862-864)ATG>ATA	p.M288I
Pat_41	Post-Resistance	CCDC40	55036	37	17	78023718	78023718	Missense_Mutation	SNP	G	A	8	70	c.869G>A	c.(868-870)AGA>AAA	p.R290K
Pat_41	Post-Resistance	RPTOR	57521	37	17	78865520	78865520	Missense_Mutation	SNP	G	A	25	465	c.1984G>A	c.(1984-1986)GAG>AAG	p.E662K
Pat_41	Post-Resistance	RPTOR	57521	37	17	78897397	78897397	Missense_Mutation	SNP	C	T	3	46	c.2732C>T	c.(2731-2733)CCC>CTC	p.P911L
Pat_41	Post-Resistance	BAIAP2	10458	37	17	79082309	79082309	Missense_Mutation	SNP	G	A	9	102	c.1535G>A	c.(1534-1536)AGG>AAG	p.R512K
Pat_41	Post-Resistance	AZI1	22994	37	17	79176097	79176097	Missense_Mutation	SNP	G	A	12	136	c.731C>T	c.(730-732)ACT>ATT	p.T244I
Pat_41	Post-Resistance	TMEM105	284186	37	17	79287501	79287501	Missense_Mutation	SNP	C	T	6	182	c.340G>A	c.(340-342)GTG>ATG	p.V114M
Pat_41	Post-Resistance	ACTG1	71	37	17	79478405	79478405	Missense_Mutation	SNP	G	A	11	294	c.611C>T	c.(610-612)GCC>GTC	p.A204V
Pat_41	Post-Resistance	HGS	9146	37	17	79660976	79660976	Missense_Mutation	SNP	G	A	7	67	c.917G>A	c.(916-918)AGC>AAC	p.S306N
Pat_41	Post-Resistance	HGS	9146	37	17	79661961	79661962	Missense_Mutation	DNP	GG	AA	12	212	c.983_984GG>AA	c.(982-984)CGG>CAA	p.R328Q
Pat_41	Post-Resistance	P4HB	5034	37	17	79804397	79804397	Missense_Mutation	SNP	C	T	6	120	c.964G>A	c.(964-966)GAG>AAG	p.E322K
Pat_41	Post-Resistance	THOC4	10189	37	17	79846247	79846247	Missense_Mutation	SNP	C	T	5	48	c.650G>A	c.(649-651)GGT>GAT	p.G217D
Pat_41	Post-Resistance	ANAPC11	51529	37	17	79852387	79852387	Missense_Mutation	SNP	G	A	29	276	c.34G>A	c.(34-36)GCC>ACC	p.A12T
Pat_41	Post-Resistance	PYCR1	5831	37	17	79892993	79892993	Missense_Mutation	SNP	C	T	6	54	c.349G>A	c.(349-351)GTC>ATC	p.V117I
Pat_41	Post-Resistance	GPS1	2873	37	17	80012628	80012628	Missense_Mutation	SNP	C	T	15	74	c.563C>T	c.(562-564)GCC>GTC	p.A188V
Pat_41	Post-Resistance	SECTM1	6398	37	17	80282536	80282536	Missense_Mutation	SNP	C	T	5	82	c.325G>A	c.(325-327)GAC>AAC	p.D109N
Pat_41	Post-Resistance	HEXDC	284004	37	17	80395080	80395080	Missense_Mutation	SNP	C	T	13	400	c.740C>T	c.(739-741)CCG>CTG	p.P247L
Pat_41	Post-Resistance	HEXDC	284004	37	17	80397523	80397523	Missense_Mutation	SNP	G	A	40	233	c.916G>A	c.(916-918)GTG>ATG	p.V306M
Pat_41	Post-Resistance	NARF	26502	37	17	80441612	80441612	Missense_Mutation	SNP	G	A	8	199	c.790G>A	c.(790-792)GAG>AAG	p.E264K
Pat_41	Post-Resistance	FN3KRP	79672	37	17	80674738	80674738	Missense_Mutation	SNP	G	A	9	151	c.107G>A	c.(106-108)GGA>GAA	p.G36E
Pat_41	Post-Resistance	METRNL	284207	37	17	81043197	81043197	Missense_Mutation	SNP	C	T	9	189	c.554C>T	c.(553-555)TCT>TTT	p.S185F
Pat_41	Post-Resistance	METRNL	284207	37	17	81052055	81052055	Missense_Mutation	SNP	C	T	13	242	c.671C>T	c.(670-672)GCC>GTC	p.A224V
Pat_41	Post-Resistance	CLUL1	27098	37	18	627217	627217	Missense_Mutation	SNP	G	A	37	432	c.544G>A	c.(544-546)GAT>AAT	p.D182N
Pat_41	Post-Resistance	METTL4	64863	37	18	2554742	2554742	Missense_Mutation	SNP	C	T	5	48	c.755G>A	c.(754-756)GGA>GAA	p.G252E
Pat_41	Post-Resistance	NDC80	10403	37	18	2577833	2577833	Missense_Mutation	SNP	G	A	25	230	c.268G>A	c.(268-270)GCA>ACA	p.A90T
Pat_41	Post-Resistance	EMILIN2	84034	37	18	2885114	2885114	Missense_Mutation	SNP	G	A	60	48	c.410G>A	c.(409-411)CGA>CAA	p.R137Q
Pat_41	Post-Resistance	EMILIN2	84034	37	18	2891675	2891675	Missense_Mutation	SNP	G	A	8	92	c.1550G>A	c.(1549-1551)AGT>AAT	p.S517N
Pat_41	Post-Resistance	MYOM1	8736	37	18	3168976	3168976	Missense_Mutation	SNP	C	T	6	44	c.1178G>A	c.(1177-1179)GGT>GAT	p.G393D
Pat_41	Post-Resistance	DLGAP1	9229	37	18	3879678	3879678	Missense_Mutation	SNP	G	A	114	177	c.391C>T	c.(391-393)CGC>TGC	p.R131C
Pat_41	Post-Resistance	EPB41L3	23136	37	18	5433986	5433986	Missense_Mutation	SNP	C	T	42	398	c.740G>A	c.(739-741)AGC>AAC	p.S247N
Pat_41	Post-Resistance	ARHGAP28	79822	37	18	6868197	6868197	Missense_Mutation	SNP	C	T	28	178	c.244C>T	c.(244-246)CCG>TCG	p.P82S
Pat_41	Post-Resistance	LAMA1	284217	37	18	6943402	6943402	Splice_Site	SNP	C	T	5	106	c.8845_splice	c.e62-1	p.V2949_splice

Pat_41	Post-Resistance	LAMA1	284217	37	18	6950780	6950780	Splice_Site	SNP	C	T	10	214	c.8397_splice	c.e58+1	p.T2799_splice
Pat_41	Post-Resistance	KIAA0802	23255	37	18	8819025	8819025	Missense_Mutation	SNP	T	C	6	141	c.2924T>C	c.(2923-2925)GTT>GCT	p.V975A
Pat_41	Post-Resistance	ANKRD12	23253	37	18	9256993	9256993	Missense_Mutation	SNP	C	T	4	135	c.3728C>T	c.(3727-3729)TCC>TTC	p.S1243F
Pat_41	Post-Resistance	VAPA	9218	37	18	9950446	9950446	Missense_Mutation	SNP	C	T	16	203	c.472C>T	c.(472-474)CCT>TCT	p.P158S
Pat_41	Post-Resistance	CEP192	55125	37	18	13049213	13049213	Missense_Mutation	SNP	C	T	22	135	c.2423C>T	c.(2422-2424)ACT>ATT	p.T808I
Pat_41	Post-Resistance	CEP192	55125	37	18	13052932	13052932	Missense_Mutation	SNP	C	T	72	417	c.3032C>T	c.(3031-3033)TCC>TTC	p.S1011F
Pat_41	Post-Resistance	CEP192	55125	37	18	13055903	13055903	Missense_Mutation	SNP	C	T	29	41	c.3314C>T	c.(3313-3315)TCA>TTA	p.S1105L
Pat_41	Post-Resistance	C18orf19	125228	37	18	13681685	13681685	Missense_Mutation	SNP	C	T	12	160	c.392G>A	c.(391-393)AGA>AAA	p.R131K
Pat_41	Post-Resistance	RNMT	8731	37	18	13741509	13741509	Missense_Mutation	SNP	G	A	12	289	c.793G>A	c.(793-795)GAA>AAA	p.E265K
Pat_41	Post-Resistance	POTEC	388468	37	18	14542790	14542790	Missense_Mutation	SNP	G	A	7	178	c.356C>T	c.(355-357)GCT>GTT	p.A119V
Pat_41	Post-Resistance	ANKRD30B	374860	37	18	14752654	14752654	Missense_Mutation	SNP	G	A	12	46	c.311G>A	c.(310-312)GGC>GAC	p.G104D
Pat_41	Post-Resistance	ROCK1	6093	37	18	18622532	18622532	Missense_Mutation	SNP	G	A	39	249	c.814C>T	c.(814-816)CTT>TTT	p.L272F
Pat_41	Post-Resistance	CTAGE1	64693	37	18	19996309	19996309	Missense_Mutation	SNP	C	T	5	276	c.1466G>A	c.(1465-1467)GGT>GAT	p.G489D
Pat_41	Post-Resistance	CTAGE1	64693	37	18	19996346	19996346	Missense_Mutation	SNP	G	A	5	166	c.1429C>T	c.(1429-1431)CCA>TCA	p.P477S
Pat_41	Post-Resistance	CABLES1	91768	37	18	20774501	20774501	Missense_Mutation	SNP	G	A	12	166	c.1007G>A	c.(1006-1008)GGC>GAC	p.G336D
Pat_41	Post-Resistance	RIOK3	8780	37	18	21056969	21056969	Splice_Site	SNP	G	A	11	148	c.1174_splice	c.e10-1	p.L392_splice
Pat_41	Post-Resistance	NPC1	4864	37	18	21118549	21118549	Missense_Mutation	SNP	G	A	17	260	c.2998C>T	c.(2998-3000)CCC>TCC	p.P1000S
Pat_41	Post-Resistance	NPC1	4864	37	18	21136332	21136332	Missense_Mutation	SNP	G	A	5	40	c.1201C>T	c.(1201-1203)CCT>TCT	p.P401S
Pat_41	Post-Resistance	NPC1	4864	37	18	21153480	21153480	Missense_Mutation	SNP	C	T	38	446	c.116G>A	c.(115-117)AGG>AAG	p.R39K
Pat_41	Post-Resistance	TTC39C	125488	37	18	21649143	21649143	Missense_Mutation	SNP	C	T	16	340	c.368C>T	c.(367-369)CCC>CTC	p.P123L
Pat_41	Post-Resistance	ZNF521	25925	37	18	22805060	22805060	Missense_Mutation	SNP	G	A	9	159	c.2822C>T	c.(2821-2823)TCC>TTC	p.S941F
Pat_41	Post-Resistance	ZNF521	25925	37	18	22806363	22806363	Missense_Mutation	SNP	C	T	13	149	c.1519G>A	c.(1519-1521)GCT>ACT	p.A507T
Pat_41	Post-Resistance	KCTD1	284252	37	18	24081090	24081090	Missense_Mutation	SNP	C	T	9	158	c.110G>A	c.(109-111)GGC>GAC	p.G37D
Pat_41	Post-Resistance	CDH2	1000	37	18	25589790	25589790	Missense_Mutation	SNP	G	A	13	147	c.593C>T	c.(592-594)ACT>ATT	p.T198I
Pat_41	Post-Resistance	DSC2	1824	37	18	28659833	28659833	Missense_Mutation	SNP	G	A	26	158	c.1643C>T	c.(1642-1644)ACA>ATA	p.T548I
Pat_41	Post-Resistance	DSC2	1824	37	18	28669488	28669488	Missense_Mutation	SNP	G	A	6	91	c.544C>T	c.(544-546)CCT>TCT	p.P182S
Pat_41	Post-Resistance	DSG1	1828	37	18	28910000	28910000	Splice_Site	SNP	G	A	15	142	c.517_splice	c.e5+1	p.N173_splice
Pat_41	Post-Resistance	DSG3	1830	37	18	29027850	29027850	Missense_Mutation	SNP	C	T	5	80	c.10C>T	c.(10-12)CTC>TTC	p.L4F
Pat_41	Post-Resistance	TTR	7276	37	18	29178567	29178567	Missense_Mutation	SNP	T	C	20	340	c.373T>C	c.(373-375)TAC>CAC	p.Y125H
Pat_41	Post-Resistance	RNF138	51444	37	18	29706735	29706735	Missense_Mutation	SNP	G	A	27	177	c.641G>A	c.(640-642)AGA>AAA	p.R214K
Pat_41	Post-Resistance	ASXL3	80816	37	18	31251776	31251776	Missense_Mutation	SNP	C	T	21	29	c.661C>T	c.(661-663)CCC>TCC	p.P221S
Pat_41	Post-Resistance	ASXL3	80816	37	18	31325625	31325625	Missense_Mutation	SNP	C	T	3	28	c.5813C>T	c.(5812-5814)GCC>GTC	p.A1938V
Pat_41	Post-Resistance	DTNA	1837	37	18	32345951	32345951	Missense_Mutation	SNP	C	T	18	194	c.94C>T	c.(94-96)CTC>TTC	p.L32F
Pat_41	Post-Resistance	ZNF24	7572	37	18	32917477	32917477	Missense_Mutation	SNP	C	T	12	212	c.826G>A	c.(826-828)GAG>AAG	p.E276K
Pat_41	Post-Resistance	GALNT1	2589	37	18	33271108	33271108	Missense_Mutation	SNP	G	A	7	184	c.1111G>A	c.(1111-1113)GAA>AAA	p.E371K
Pat_41	Post-Resistance	MOCOS	55034	37	18	33780034	33780034	Missense_Mutation	SNP	C	T	14	132	c.688C>T	c.(688-690)CCT>TCT	p.P230S
Pat_41	Post-Resistance	SLC14A1	6563	37	18	43328362	43328362	Missense_Mutation	SNP	G	A	34	370	c.968G>A	c.(967-969)GGA>GAA	p.G323E
Pat_41	Post-Resistance	KIAA1632	57724	37	18	43534415	43534415	Missense_Mutation	SNP	C	T	34	267	c.953G>A	c.(952-954)TGC>TAC	p.C318Y
Pat_41	Post-Resistance	HDHD2	84064	37	18	44656699	44656699	Missense_Mutation	SNP	C	T	32	180	c.311G>A	c.(310-312)GGA>GAA	p.G104E
Pat_41	Post-Resistance	MYO5B	4645	37	18	47379941	47379941	Missense_Mutation	SNP	C	T	15	95	c.4099G>A	c.(4099-4101)GCC>ACC	p.A1367T
Pat_41	Post-Resistance	CCDC11	220136	37	18	47769387	47769387	Missense_Mutation	SNP	C	T	17	285	c.1096G>A	c.(1096-1098)GAA>AAA	p.E366K
Pat_41	Post-Resistance	MBD1	4152	37	18	47799063	47799063	Missense_Mutation	SNP	C	T	23	623	c.1762G>A	c.(1762-1764)GCA>ACA	p.A588T
Pat_41	Post-Resistance	CXXC1	30827	37	18	47810355	47810355	Missense_Mutation	SNP	C	T	11	190	c.1322G>A	c.(1321-1323)CGC>CAC	p.R441H
Pat_41	Post-Resistance	CXXC1	30827	37	18	47811184	47811184	Missense_Mutation	SNP	G	A	7	131	c.938C>T	c.(937-939)TCC>TTC	p.S313F
Pat_41	Post-Resistance	MAPK4	5596	37	18	48190423	48190423	Missense_Mutation	SNP	G	A	8	177	c.95G>A	c.(94-96)GGT>GAT	p.G32D
Pat_41	Post-Resistance	MAPK4	5596	37	18	48248397	48248397	Missense_Mutation	SNP	C	T	5	42	c.781C>T	c.(781-783)CCT>TCT	p.P261S
Pat_41	Post-Resistance	MRO	83876	37	18	48327762	48327762	Missense_Mutation	SNP	G	A	55	191	c.542C>T	c.(541-543)TCC>TTC	p.S181F

Pat_41	Post-Resistance	DCC	1630	37	18	50592443	50592443	Missense_Mutation	SNP	G	A	17	236	c.1168G>A	c.(1168-1170)GTG>ATG	p.V390M
Pat_41	Post-Resistance	DCC	1630	37	18	51025758	51025758	Missense_Mutation	SNP	C	T	17	335	c.3989C>T	c.(3988-3990)ACC>ATC	p.T1330I
Pat_41	Post-Resistance	C18orf54	162681	37	18	51888064	51888064	Missense_Mutation	SNP	G	A	8	121	c.335G>A	c.(334-336)AGA>AAA	p.R112K
Pat_41	Post-Resistance	TCF4	6925	37	18	53131311	53131311	Missense_Mutation	SNP	G	A	27	343	c.203C>T	c.(202-204)TCC>TTC	p.S68F
Pat_41	Post-Resistance	TXNL1	9352	37	18	54281660	54281660	Missense_Mutation	SNP	C	T	7	162	c.730G>A	c.(730-732)GTA>ATA	p.V244I
Pat_41	Post-Resistance	WDR7	23335	37	18	54363622	54363622	Missense_Mutation	SNP	G	A	16	250	c.1507G>A	c.(1507-1509)GAA>AAA	p.E503K
Pat_41	Post-Resistance	WDR7	23335	37	18	54398829	54398829	Splice_Site	SNP	G	A	7	118	c.1989_splice	c.e14+1	p.K663_splice
Pat_41	Post-Resistance	WDR7	23335	37	18	54448804	54448804	Missense_Mutation	SNP	G	A	9	91	c.3107G>A	c.(3106-3108)AGA>AAA	p.R1036K
Pat_41	Post-Resistance	NARS	4677	37	18	55287847	55287847	Missense_Mutation	SNP	G	A	33	217	c.47C>T	c.(46-48)GCC>GTC	p.A16V
Pat_41	Post-Resistance	ALPK2	115701	37	18	56204126	56204126	Missense_Mutation	SNP	T	C	18	362	c.3293A>G	c.(3292-3294)AAT>AGT	p.N1098S
Pat_41	Post-Resistance	ALPK2	115701	37	18	56205078	56205078	Missense_Mutation	SNP	G	A	4	127	c.2341C>T	c.(2341-2343)CCC>TCC	p.P781S
Pat_41	Post-Resistance	ALPK2	115701	37	18	56247083	56247083	Missense_Mutation	SNP	C	T	18	256	c.925G>A	c.(925-927)GAA>AAA	p.E309K
Pat_41	Post-Resistance	ZNF532	55205	37	18	56585646	56585646	Nonsense_Mutation	SNP	C	T	14	85	c.127C>T	c.(127-129)CAG>TAG	p.Q43*
Pat_41	Post-Resistance	ZNF532	55205	37	18	56586991	56586991	Missense_Mutation	SNP	G	A	6	54	c.1472G>A	c.(1471-1473)AGC>AAC	p.S491N
Pat_41	Post-Resistance	ZNF532	55205	37	18	56606750	56606750	Missense_Mutation	SNP	G	A	18	304	c.2602G>A	c.(2602-2604)GTC>ATC	p.V868I
Pat_41	Post-Resistance	LMAN1	3998	37	18	57026292	57026292	Missense_Mutation	SNP	C	T	11	160	c.185G>A	c.(184-186)GGG>GAG	p.G62E
Pat_41	Post-Resistance	CCBE1	147372	37	18	57134012	57134012	Missense_Mutation	SNP	C	T	28	415	c.512G>A	c.(511-513)GGG>GAG	p.G171E
Pat_41	Post-Resistance	MC4R	4160	37	18	58038721	58038721	Missense_Mutation	SNP	G	A	9	199	c.862C>T	c.(862-864)CTC>TTC	p.L288F
Pat_41	Post-Resistance	CDH20	28316	37	18	59167622	59167622	Missense_Mutation	SNP	C	T	13	207	c.548C>T	c.(547-549)TCC>TTC	p.S183F
Pat_41	Post-Resistance	ZCCHC2	54877	37	18	60227835	60227835	Missense_Mutation	SNP	C	T	13	233	c.1508C>T	c.(1507-1509)GCC>GTC	p.A503V
Pat_41	Post-Resistance	SERPINB13	5275	37	18	61256932	61256932	Missense_Mutation	SNP	G	A	8	61	c.208G>A	c.(208-210)GCT>ACT	p.A70T
Pat_41	Post-Resistance	SERPINB13	5275	37	18	61262408	61262408	Missense_Mutation	SNP	G	A	20	176	c.761G>A	c.(760-762)GGC>GAC	p.G254D
Pat_41	Post-Resistance	CDH7	1005	37	18	63526179	63526179	Missense_Mutation	SNP	G	A	7	84	c.1391G>A	c.(1390-1392)GGA>GAA	p.G464E
Pat_41	Post-Resistance	CDH19	28513	37	18	64172386	64172386	Missense_Mutation	SNP	C	T	23	316	c.1982G>A	c.(1981-1983)AGT>AAT	p.S661N
Pat_41	Post-Resistance	DSEL	92126	37	18	65181334	65181334	Missense_Mutation	SNP	C	T	11	81	c.542G>A	c.(541-543)GGC>GAC	p.G181D
Pat_41	Post-Resistance	TMX3	54495	37	18	66351458	66351458	Missense_Mutation	SNP	C	T	11	111	c.817G>A	c.(817-819)GTT>ATT	p.V273I
Pat_41	Post-Resistance	NETO1	81832	37	18	70532440	70532440	Missense_Mutation	SNP	G	A	4	23	c.65C>T	c.(64-66)GCA>GTA	p.A22V
Pat_41	Post-Resistance	ZNF407	55628	37	18	72343232	72343232	Missense_Mutation	SNP	C	T	11	76	c.257C>T	c.(256-258)TCT>TTT	p.S86F
Pat_41	Post-Resistance	ZNF407	55628	37	18	72589198	72589198	Nonsense_Mutation	SNP	G	A	13	41	c.4923G>A	c.(4921-4923)TGG>TGA	p.W1641*
Pat_41	Post-Resistance	ZNF236	7776	37	18	74625807	74625807	Missense_Mutation	SNP	G	A	20	65	c.3008G>A	c.(3007-3009)GGC>GAC	p.G1003D
Pat_41	Post-Resistance	SALL3	27164	37	18	76753535	76753535	Missense_Mutation	SNP	G	A	3	20	c.1544G>A	c.(1543-1545)AGC>AAC	p.S515N
Pat_41	Post-Resistance	ADNP2	22850	37	18	77891008	77891008	Missense_Mutation	SNP	G	A	10	20	c.131G>A	c.(130-132)GGA>GAA	p.G44E
Pat_41	Post-Resistance	PPAP2C	8612	37	19	282238	282238	Missense_Mutation	SNP	C	T	20	44	c.613G>A	c.(613-615)GCC>ACC	p.A205T
Pat_41	Post-Resistance	PALM	5064	37	19	746516	746516	Missense_Mutation	SNP	G	A	3	23	c.866G>A	c.(865-867)GGG>GAG	p.G289E
Pat_41	Post-Resistance	LPPR3	79948	37	19	814885	814885	Splice_Site	SNP	C	T	15	64	c.599_splice	c.e5+1	p.R200_splice
Pat_41	Post-Resistance	UQCR11	10975	37	19	1599554	1599554	Missense_Mutation	SNP	G	T	3	58	c.56C>A	c.(55-57)CCG>CAG	p.P19Q
Pat_41	Post-Resistance	ATP8B3	148229	37	19	1795962	1795962	Missense_Mutation	SNP	C	T	9	23	c.1967G>A	c.(1966-1968)TGC>TAC	p.C656Y
Pat_41	Post-Resistance	MKNK2	2872	37	19	2039752	2039752	Missense_Mutation	SNP	C	T	5	16	c.1258G>A	c.(1258-1260)GGG>AGG	p.G420R
Pat_41	Post-Resistance	ZNF554	115196	37	19	2834596	2834596	Missense_Mutation	SNP	G	A	8	78	c.1363G>A	c.(1363-1365)GAG>AAG	p.E455K
Pat_41	Post-Resistance	PIP5K1C	23396	37	19	3644084	3644084	Splice_Site	SNP	C	T	18	68	c.1510_splice	c.e12+1	p.G504_splice
Pat_41	Post-Resistance	CHAF1A	10036	37	19	4433262	4433262	Missense_Mutation	SNP	G	A	4	106	c.2399G>A	c.(2398-2400)CGG>CAG	p.R800Q
Pat_41	Post-Resistance	PLIN5	440503	37	19	4523680	4523680	Missense_Mutation	SNP	C	T	24	180	c.1252G>A	c.(1252-1254)GCC>ACC	p.A418T
Pat_41	Post-Resistance	C19orf10	56005	37	19	4660005	4660005	Missense_Mutation	SNP	G	A	11	97	c.380C>T	c.(379-381)GCA>GTA	p.A127V
Pat_41	Post-Resistance	FEM1A	55527	37	19	4792581	4792581	Missense_Mutation	SNP	C	T	7	72	c.715C>T	c.(715-717)CCC>TCC	p.P239S
Pat_41	Post-Resistance	PTPRS	5802	37	19	5231452	5231452	Missense_Mutation	SNP	G	A	4	57	c.2024C>T	c.(2023-2025)CCC>CTC	p.P675L
Pat_41	Post-Resistance	SAFB2	9667	37	19	5587339	5587339	Missense_Mutation	SNP	C	T	8	21	c.2777G>A	c.(2776-2778)GGA>GAA	p.G926E
Pat_41	Post-Resistance	ACER1	125981	37	19	6309807	6309807	Missense_Mutation	SNP	A	G	12	29	c.389T>C	c.(388-390)GTC>GCC	p.V130A

Pat_41	Post-Resistance	CLPP	8192	37	19	6362493	6362493	Missense_Mutation	SNP	C	T	14	91	c.307C>T	c.(307-309)CTC>TTC	p.L103F
Pat_41	Post-Resistance	C3	718	37	19	6719238	6719238	Missense_Mutation	SNP	C	T	8	156	c.251G>A	c.(250-252)GGC>GAC	p.G84D
Pat_41	Post-Resistance	TRIP10	9322	37	19	6746515	6746515	Missense_Mutation	SNP	G	A	4	133	c.1205G>A	c.(1204-1206)CGG>CAG	p.R402Q
Pat_41	Post-Resistance	INSR	3643	37	19	7184645	7184645	Missense_Mutation	SNP	C	T	3	21	c.656G>A	c.(655-657)TGC>TAC	p.C219Y
Pat_41	Post-Resistance	PNPLA6	10908	37	19	7600838	7600838	Missense_Mutation	SNP	G	A	5	14	c.191G>A	c.(190-192)GGG>GAG	p.G64E
Pat_41	Post-Resistance	CD209	30835	37	19	7810835	7810835	Missense_Mutation	SNP	T	C	6	105	c.317A>G	c.(316-318)CAG>CGG	p.Q106R
Pat_41	Post-Resistance	FBN3	84467	37	19	8159329	8159329	Splice_Site	SNP	C	T	4	22	c.5905_splice	c.e46+1	p.D1969_splice
Pat_41	Post-Resistance	FBN3	84467	37	19	8203338	8203338	Missense_Mutation	SNP	C	T	3	30	c.976G>A	c.(976-978)GCA>ACA	p.A326T
Pat_41	Post-Resistance	2-Mar	51257	37	19	8491579	8491579	Missense_Mutation	SNP	C	T	3	41	c.263C>T	c.(262-264)GCC>GTC	p.A88V
Pat_41	Post-Resistance	HNRNPM	4670	37	19	8539129	8539129	Splice_Site	SNP	G	A	5	119	c.1120_splice	c.e12+1	p.E374_splice
Pat_41	Post-Resistance	OR2Z1	284383	37	19	8841526	8841526	Missense_Mutation	SNP	C	T	22	45	c.136C>T	c.(136-138)CTC>TTC	p.L46F
Pat_41	Post-Resistance	OR2Z1	284383	37	19	8842192	8842192	Missense_Mutation	SNP	C	T	4	64	c.802C>T	c.(802-804)CCA>TCA	p.P268S
Pat_41	Post-Resistance	MUC16	94025	37	19	9009710	9009710	Missense_Mutation	SNP	C	T	21	127	c.39016G>A	c.(39016-39018)GCT>ACT	p.A13006T
Pat_41	Post-Resistance	MUC16	94025	37	19	9061564	9061564	Missense_Mutation	SNP	C	T	12	48	c.25882G>A	c.(25882-25884)GCC>ACC	p.A8628T
Pat_41	Post-Resistance	MUC16	94025	37	19	9065791	9065791	Missense_Mutation	SNP	C	T	6	119	c.21655G>A	c.(21655-21657)GAG>AAG	p.E7219K
Pat_41	Post-Resistance	MUC16	94025	37	19	9069555	9069555	Missense_Mutation	SNP	C	T	5	34	c.17891G>A	c.(17890-17892)GGC>GAC	p.G5964D
Pat_41	Post-Resistance	MUC16	94025	37	19	9082631	9082631	Missense_Mutation	SNP	C	T	12	50	c.9184G>A	c.(9184-9186)GCA>ACA	p.A3062T
Pat_41	Post-Resistance	MUC16	94025	37	19	9083483	9083483	Missense_Mutation	SNP	C	T	3	15	c.8332G>A	c.(8332-8334)GCT>ACT	p.A2778T
Pat_41	Post-Resistance	MUC16	94025	37	19	9084835	9084835	Missense_Mutation	SNP	G	A	27	7	c.6980C>T	c.(6979-6981)TCC>TTC	p.S2327F
Pat_41	Post-Resistance	MUC16	94025	37	19	9084874	9084874	Missense_Mutation	SNP	C	T	9	28	c.6941G>A	c.(6940-6942)GGA>GAA	p.G2314E
Pat_41	Post-Resistance	MUC16	94025	37	19	9091478	9091478	Missense_Mutation	SNP	G	A	16	97	c.337C>T	c.(337-339)CCC>TCC	p.P113S
Pat_41	Post-Resistance	ZNF317	57693	37	19	9271786	9271786	Missense_Mutation	SNP	C	T	3	32	c.1465C>T	c.(1465-1467)CGG>TGG	p.R489W
Pat_41	Post-Resistance	ZNF559	84527	37	19	9453635	9453635	Missense_Mutation	SNP	C	T	25	52	c.1508C>T	c.(1507-1509)ACT>ATT	p.T503I
Pat_41	Post-Resistance	ZNF560	147741	37	19	9578040	9578040	Missense_Mutation	SNP	G	A	10	60	c.1583C>T	c.(1582-1584)TCT>TTT	p.S528F
Pat_41	Post-Resistance	ZNF560	147741	37	19	9578698	9578698	Missense_Mutation	SNP	C	T	29	74	c.925G>A	c.(925-927)GCA>ACA	p.A309T
Pat_41	Post-Resistance	ZNF846	162993	37	19	9874060	9874060	Missense_Mutation	SNP	C	T	20	323	c.40G>A	c.(40-42)GCT>ACT	p.A14T
Pat_41	Post-Resistance	COL5A3	50509	37	19	10100032	10100032	Missense_Mutation	SNP	C	T	4	13	c.2057G>A	c.(2056-2058)GGA>GAA	p.G686E
Pat_41	Post-Resistance	TYK2	7297	37	19	10478786	10478786	Missense_Mutation	SNP	G	A	5	31	c.410C>T	c.(409-411)ACA>ATA	p.T137I
Pat_41	Post-Resistance	CDC37	11140	37	19	10504024	10504024	Missense_Mutation	SNP	C	T	10	72	c.820G>A	c.(820-822)GCC>ACC	p.A274T
Pat_41	Post-Resistance	PDE4A	5141	37	19	10574509	10574509	Missense_Mutation	SNP	C	T	63	164	c.1784C>T	c.(1783-1785)CCC>CTC	p.P595L
Pat_41	Post-Resistance	ILF3	3609	37	19	10782072	10782072	Missense_Mutation	SNP	G	A	67	155	c.272G>A	c.(271-273)GGA>GAA	p.G91E
Pat_41	Post-Resistance	TMED1	11018	37	19	10945621	10945621	Missense_Mutation	SNP	C	T	22	262	c.454G>A	c.(454-456)GAG>AAG	p.E152K
Pat_41	Post-Resistance	SMARCA4	6597	37	19	11141409	11141409	Missense_Mutation	SNP	C	T	11	26	c.3386C>T	c.(3385-3387)ACC>ATC	p.T1129I
Pat_41	Post-Resistance	TSPAN16	26526	37	19	11422815	11422815	Missense_Mutation	SNP	G	A	5	12	c.604G>A	c.(604-606)GGC>AGC	p.G202S
Pat_41	Post-Resistance	RGL3	57139	37	19	11527509	11527509	Splice_Site	SNP	C	T	9	87	c.371_splice	c.e3+1	p.G124_splice
Pat_41	Post-Resistance	ZNF700	90592	37	19	12060645	12060645	Missense_Mutation	SNP	T	A	7	304	c.1806T>A	c.(1804-1806)AGT>AGA	p.S602R
Pat_41	Post-Resistance	ZNF763	284390	37	19	12087898	12087898	Missense_Mutation	SNP	G	A	16	161	c.49G>A	c.(49-51)GAG>AAG	p.E17K
Pat_41	Post-Resistance	ZNF563	147837	37	19	12429458	12429458	Missense_Mutation	SNP	G	A	17	116	c.1381C>T	c.(1381-1383)CCC>TCC	p.P461S
Pat_41	Post-Resistance	ZNF791	163049	37	19	12739658	12739658	Missense_Mutation	SNP	C	T	8	133	c.1315C>T	c.(1315-1317)CCT>TCT	p.P439S
Pat_41	Post-Resistance	MAST1	22983	37	19	12962965	12962965	Missense_Mutation	SNP	G	A	26	81	c.913G>A	c.(913-915)GCG>ACG	p.A305T
Pat_41	Post-Resistance	CALR	811	37	19	13049584	13049584	Missense_Mutation	SNP	G	A	4	13	c.91G>A	c.(91-93)GAC>AAC	p.D31N
Pat_41	Post-Resistance	NACC1	112939	37	19	13249071	13249071	Missense_Mutation	SNP	G	A	36	172	c.1435G>A	c.(1435-1437)GTC>ATC	p.V479I
Pat_41	Post-Resistance	CACNA1A	773	37	19	13394121	13394121	Missense_Mutation	SNP	G	T	4	52	c.3785C>A	c.(3784-3786)GCC>GAC	p.A1262D
Pat_41	Post-Resistance	ZSWIM4	65249	37	19	13928045	13928045	Missense_Mutation	SNP	G	A	25	80	c.1196G>A	c.(1195-1197)GGC>GAC	p.G399D
Pat_41	Post-Resistance	ZSWIM4	65249	37	19	13936397	13936397	Missense_Mutation	SNP	C	T	11	131	c.1898C>T	c.(1897-1899)TCC>TTC	p.S633F
Pat_41	Post-Resistance	NANOS3	342977	37	19	13988237	13988237	Missense_Mutation	SNP	G	A	4	130	c.175G>A	c.(175-177)GGA>AGA	p.G59R
Pat_41	Post-Resistance	C19orf57	79173	37	19	14000681	14000681	Missense_Mutation	SNP	C	T	6	76	c.988G>A	c.(988-990)GGA>AGA	p.G330R

Pat_41	Post-Resistance	CC2D1A	54862	37	19	14029357	14029357	Missense_Mutation	SNP	C	T	5	170	c.914C>T	c.(913-915)CCC>CTC	p.P305L
Pat_41	Post-Resistance	CC2D1A	54862	37	19	14031688	14031688	Missense_Mutation	SNP	C	T	14	232	c.1594C>T	c.(1594-1596)CCT>TCT	p.P532S
Pat_41	Post-Resistance	CC2D1A	54862	37	19	14040256	14040256	Splice_Site	SNP	G	A	14	307	c.2583_splice	c.e25+1	p.K861_splice
Pat_41	Post-Resistance	RFX1	5989	37	19	14094327	14094327	Missense_Mutation	SNP	C	T	5	62	c.400G>A	c.(400-402)GTG>ATG	p.V134M
Pat_41	Post-Resistance	IL27RA	9466	37	19	14150325	14150325	Missense_Mutation	SNP	C	T	20	414	c.224C>T	c.(223-225)TCC>TTC	p.S75F
Pat_41	Post-Resistance	IL27RA	9466	37	19	14150354	14150354	Missense_Mutation	SNP	G	A	16	460	c.253G>A	c.(253-255)GCC>ACC	p.A85T
Pat_41	Post-Resistance	IL27RA	9466	37	19	14157140	14157140	Missense_Mutation	SNP	G	A	14	278	c.943G>A	c.(943-945)GTC>ATC	p.V315I
Pat_41	Post-Resistance	IL27RA	9466	37	19	14157257	14157257	Missense_Mutation	SNP	C	T	20	206	c.968C>T	c.(967-969)CCC>CTC	p.P323L
Pat_41	Post-Resistance	DNAJB1	3337	37	19	14627750	14627750	Missense_Mutation	SNP	C	T	12	276	c.320G>A	c.(319-321)GGT>GAT	p.G107D
Pat_41	Post-Resistance	EMR2	30817	37	19	14854260	14854260	Missense_Mutation	SNP	G	A	33	633	c.2435C>T	c.(2434-2436)GCT>GTT	p.A812V
Pat_41	Post-Resistance	OR7C1	26664	37	19	14910029	14910029	Missense_Mutation	SNP	C	T	10	243	c.920G>A	c.(919-921)AGG>AAG	p.R307K
Pat_41	Post-Resistance	SYDE1	85360	37	19	15224542	15224542	Missense_Mutation	SNP	G	A	7	170	c.1976G>A	c.(1975-1977)GGG>GAG	p.G659E
Pat_41	Post-Resistance	ILVBL	10994	37	19	15228714	15228714	Nonsense_Mutation	SNP	C	T	55	105	c.1164G>A	c.(1162-1164)TGG>TGA	p.W388*
Pat_41	Post-Resistance	NOTCH3	4854	37	19	15297975	15297975	Missense_Mutation	SNP	C	T	7	63	c.1781G>A	c.(1780-1782)GGC>GAC	p.G594D
Pat_41	Post-Resistance	AKAP8L	26993	37	19	15512311	15512311	Missense_Mutation	SNP	C	T	13	65	c.466G>A	c.(466-468)GCC>ACC	p.A156T
Pat_41	Post-Resistance	RASAL3	64926	37	19	15569407	15569407	Missense_Mutation	SNP	C	T	3	38	c.722G>A	c.(721-723)GGT>GAT	p.G241D
Pat_41	Post-Resistance	CYP4F12	66002	37	19	15807283	15807283	Missense_Mutation	SNP	G	A	18	365	c.1358G>A	c.(1357-1359)AGG>AAG	p.R453K
Pat_41	Post-Resistance	OR10H2	26538	37	19	15839353	15839353	Missense_Mutation	SNP	C	T	6	117	c.500C>T	c.(499-501)ACT>ATT	p.T167I
Pat_41	Post-Resistance	OR10H5	284433	37	19	15905699	15905699	Missense_Mutation	SNP	G	A	8	59	c.841G>A	c.(841-843)GTC>ATC	p.V281I
Pat_41	Post-Resistance	CYP4F2	8529	37	19	16000439	16000439	Missense_Mutation	SNP	C	T	24	202	c.712G>A	c.(712-714)GAG>AAG	p.E238K
Pat_41	Post-Resistance	TPM4	7171	37	19	16204358	16204358	Missense_Mutation	SNP	G	A	13	159	c.544G>A	c.(544-546)GAG>AAG	p.E182K
Pat_41	Post-Resistance	CIB3	117286	37	19	16280518	16280518	Missense_Mutation	SNP	G	A	9	63	c.121C>T	c.(121-123)CTC>TTC	p.L41F
Pat_41	Post-Resistance	AP1M1	8907	37	19	16319915	16319915	Missense_Mutation	SNP	C	T	13	153	c.473C>T	c.(472-474)TCC>TTC	p.S158F
Pat_41	Post-Resistance	EPS15L1	58513	37	19	16496996	16496996	Missense_Mutation	SNP	G	A	5	75	c.2150C>T	c.(2149-2151)TCC>TTC	p.S717F
Pat_41	Post-Resistance	CHERP	10523	37	19	16632398	16632398	Missense_Mutation	SNP	C	T	7	38	c.2048G>A	c.(2047-2049)AGC>AAC	p.S683N
Pat_41	Post-Resistance	CHERP	10523	37	19	16638953	16638953	Missense_Mutation	SNP	G	A	7	135	c.1243C>T	c.(1243-1245)CCA>TCA	p.P415S
Pat_41	Post-Resistance	CHERP	10523	37	19	16639054	16639054	Missense_Mutation	SNP	G	A	5	92	c.1142C>T	c.(1141-1143)CCT>CTT	p.P381L
Pat_41	Post-Resistance	SLC35E1	79939	37	19	16664575	16664575	Missense_Mutation	SNP	C	T	26	441	c.1148G>A	c.(1147-1149)GGC>GAC	p.G383D
Pat_41	Post-Resistance	CPAMD8	27151	37	19	17015321	17015321	Missense_Mutation	SNP	C	T	15	103	c.4210G>A	c.(4210-4212)GAC>AAC	p.D1404N
Pat_41	Post-Resistance	CPAMD8	27151	37	19	17115144	17115144	Nonsense_Mutation	SNP	C	T	17	66	c.753G>A	c.(751-753)TGG>TGA	p.W251*
Pat_41	Post-Resistance	USHBP1	83878	37	19	17367318	17367318	Missense_Mutation	SNP	C	T	4	130	c.1432G>A	c.(1432-1434)GAG>AAG	p.E478K
Pat_41	Post-Resistance	SLC27A1	376497	37	19	17597766	17597766	Missense_Mutation	SNP	G	A	3	22	c.562G>A	c.(562-564)GCG>ACG	p.A188T
Pat_41	Post-Resistance	SLC27A1	376497	37	19	17608082	17608082	Missense_Mutation	SNP	G	A	4	109	c.1015G>A	c.(1015-1017)GAG>AAG	p.E339K
Pat_41	Post-Resistance	JAK3	3718	37	19	17949128	17949128	Nonsense_Mutation	SNP	G	A	7	252	c.1513C>T	c.(1513-1515)CAA>TAA	p.Q505*
Pat_41	Post-Resistance	SLC5A5	6528	37	19	17986872	17986872	Missense_Mutation	SNP	G	A	9	179	c.655G>A	c.(655-657)GTG>ATG	p.V219M
Pat_41	Post-Resistance	SLC5A5	6528	37	19	17988645	17988645	Missense_Mutation	SNP	C	T	18	198	c.812C>T	c.(811-813)GCT>GTT	p.A271V
Pat_41	Post-Resistance	ARRDC2	27106	37	19	18120711	18120711	Missense_Mutation	SNP	G	A	6	75	c.712G>A	c.(712-714)GCA>ACA	p.A238T
Pat_41	Post-Resistance	ARRDC2	27106	37	19	18120741	18120741	Missense_Mutation	SNP	G	A	4	55	c.742G>A	c.(742-744)GTG>ATG	p.V248M
Pat_41	Post-Resistance	ARRDC2	27106	37	19	18121024	18121024	Missense_Mutation	SNP	G	A	7	190	c.869G>A	c.(868-870)GGA>GAA	p.G290E
Pat_41	Post-Resistance	MAST3	23031	37	19	18246595	18246595	Missense_Mutation	SNP	C	T	3	22	c.1829C>T	c.(1828-1830)GCC>GTC	p.A610V
Pat_41	Post-Resistance	MAST3	23031	37	19	18260483	18260483	Missense_Mutation	SNP	G	A	4	138	c.3877G>A	c.(3877-3879)GTG>ATG	p.V1293M
Pat_41	Post-Resistance	MPV17L2	84769	37	19	18304706	18304706	Missense_Mutation	SNP	C	T	36	237	c.220C>T	c.(220-222)CCC>TCC	p.P74S
Pat_41	Post-Resistance	LRRC25	126364	37	19	18507019	18507019	Missense_Mutation	SNP	G	A	9	222	c.755C>T	c.(754-756)GCC>GTC	p.A252V
Pat_41	Post-Resistance	FKBP8	23770	37	19	18648560	18648560	Missense_Mutation	SNP	C	T	20	153	c.793G>A	c.(793-795)GCA>ACA	p.A265T
Pat_41	Post-Resistance	CRTC1	23373	37	19	18888085	18888085	Missense_Mutation	SNP	C	T	49	612	c.1798C>T	c.(1798-1800)CTC>TTC	p.L600F
Pat_41	Post-Resistance	SFRS14	10147	37	19	19115455	19115455	Nonsense_Mutation	SNP	C	T	7	102	c.2451G>A	c.(2449-2451)TGG>TGA	p.W817*
Pat_41	Post-Resistance	SFRS14	10147	37	19	19135659	19135659	Missense_Mutation	SNP	C	T	17	174	c.1498G>A	c.(1498-1500)GAA>AAA	p.E500K

Pat_41	Post-Resistance	GATAD2A	54815	37	19	19576357	19576357	Missense_Mutation	SNP	C	T	4	44	c.203C>T	c.(202-204)GCC>GTC	p.A68V
Pat_41	Post-Resistance	GATAD2A	54815	37	19	19603465	19603465	Missense_Mutation	SNP	G	A	9	194	c.478G>A	c.(478-480)GTG>ATG	p.V160M
Pat_41	Post-Resistance	GMIP	51291	37	19	19751151	19751151	Missense_Mutation	SNP	C	T	26	136	c.383G>A	c.(382-384)AGC>AAC	p.S128N
Pat_41	Post-Resistance	ZNF253	56242	37	19	19989407	19989407	Missense_Mutation	SNP	G	A	7	196	c.121G>A	c.(121-123)GTC>ATC	p.V41I
Pat_41	Post-Resistance	ZNF93	81931	37	19	20044608	20044608	Missense_Mutation	SNP	G	A	7	261	c.844G>A	c.(844-846)GAG>AAG	p.E282K
Pat_41	Post-Resistance	ZNF93	81931	37	19	20045277	20045277	Missense_Mutation	SNP	G	A	8	311	c.1513G>A	c.(1513-1515)GGA>AGA	p.G505R
Pat_41	Post-Resistance	ZNF93	81931	37	19	20045454	20045454	Missense_Mutation	SNP	C	T	4	87	c.1690C>T	c.(1690-1692)CCT>TCT	p.P564S
Pat_41	Post-Resistance	ZNF90	7643	37	19	20229964	20229964	Missense_Mutation	SNP	C	A	6	154	c.1601C>A	c.(1600-1602)GCG>GAG	p.A534E
Pat_41	Post-Resistance	ZNF737	100129842	37	19	20728179	20728179	Missense_Mutation	SNP	A	T	6	210	c.830T>A	c.(829-831)ATA>AAA	p.I277K
Pat_41	Post-Resistance	ZNF626	199777	37	19	20807706	20807706	Missense_Mutation	SNP	T	G	5	228	c.977A>C	c.(976-978)TAT>TCT	p.Y326S
Pat_41	Post-Resistance	ZNF714	148206	37	19	21300738	21300738	Missense_Mutation	SNP	T	C	16	239	c.1271T>C	c.(1270-1272)CTC>CCC	p.L424P
Pat_41	Post-Resistance	ZNF493	284443	37	19	21605856	21605856	Missense_Mutation	SNP	G	A	25	310	c.11G>A	c.(10-12)TGT>TAT	p.C4Y
Pat_41	Post-Resistance	ZNF493	284443	37	19	21606876	21606876	Missense_Mutation	SNP	G	A	5	147	c.1031G>A	c.(1030-1032)CGA>CAA	p.R344Q
Pat_41	Post-Resistance	ZNF493	284443	37	19	21606988	21606988	Missense_Mutation	SNP	A	G	7	126	c.1143A>G	c.(1141-1143)ATA>ATG	p.I381M
Pat_41	Post-Resistance	ZNF43	7594	37	19	21991191	21991191	Missense_Mutation	SNP	A	T	6	237	c.1648T>A	c.(1648-1650)TTC>ATC	p.F550I
Pat_41	Post-Resistance	ZNF208	7757	37	19	22155626	22155626	Missense_Mutation	SNP	G	A	12	243	c.1910C>T	c.(1909-1911)ACT>ATT	p.T637I
Pat_41	Post-Resistance	ZNF208	7757	37	19	22155891	22155891	Missense_Mutation	SNP	C	T	12	265	c.1645G>A	c.(1645-1647)GTC>ATC	p.V549I
Pat_41	Post-Resistance	ZNF208	7757	37	19	22155975	22155975	Missense_Mutation	SNP	C	T	32	209	c.1561G>A	c.(1561-1563)GTC>ATC	p.V521I
Pat_41	Post-Resistance	ZNF208	7757	37	19	22156034	22156034	Missense_Mutation	SNP	C	T	7	123	c.1502G>A	c.(1501-1503)AGA>AAA	p.R501K
Pat_41	Post-Resistance	ZNF208	7757	37	19	22170068	22170068	Missense_Mutation	SNP	C	T	10	159	c.176G>A	c.(175-177)GGA>GAA	p.G59E
Pat_41	Post-Resistance	ZNF98	148198	37	19	22574676	22574676	Missense_Mutation	SNP	A	C	7	110	c.1361T>G	c.(1360-1362)ATA>AGA	p.I454R
Pat_41	Post-Resistance	ZNF99	7652	37	19	22939472	22939472	Missense_Mutation	SNP	A	G	5	150	c.2699T>C	c.(2698-2700)TTC>TCC	p.F900S
Pat_41	Post-Resistance	ZNF91	7644	37	19	23544073	23544073	Missense_Mutation	SNP	C	T	5	82	c.1708G>A	c.(1708-1710)GGA>AGA	p.G570R
Pat_41	Post-Resistance	ZNF675	171392	37	19	23836350	23836350	Missense_Mutation	SNP	A	T	7	102	c.1385T>A	c.(1384-1386)ATC>AAC	p.I462N
Pat_41	Post-Resistance	ZNF681	148213	37	19	23926839	23926839	Missense_Mutation	SNP	A	G	13	212	c.1513T>C	c.(1513-1515)TCC>CCC	p.S505P
Pat_41	Post-Resistance	ZNF681	148213	37	19	23927181	23927181	Missense_Mutation	SNP	C	T	22	395	c.1171G>A	c.(1171-1173)GAG>AAG	p.E391K
Pat_41	Post-Resistance	ZNF536	9745	37	19	31025778	31025778	Missense_Mutation	SNP	C	T	55	287	c.2195C>T	c.(2194-2196)TCT>TTT	p.S732F
Pat_41	Post-Resistance	ZNF507	22847	37	19	32844671	32844671	Missense_Mutation	SNP	G	A	41	619	c.935G>A	c.(934-936)AGT>AAT	p.S312N
Pat_41	Post-Resistance	DPY19L3	147991	37	19	32923625	32923625	Missense_Mutation	SNP	G	A	7	138	c.241G>A	c.(241-243)GTG>ATG	p.V81M
Pat_41	Post-Resistance	RHPN2	85415	37	19	33502637	33502637	Missense_Mutation	SNP	C	T	10	118	c.541G>A	c.(541-543)GTC>ATC	p.V181I
Pat_41	Post-Resistance	WDR88	126248	37	19	33639799	33639799	Missense_Mutation	SNP	C	T	4	66	c.662C>T	c.(661-663)ACC>ATC	p.T221I
Pat_41	Post-Resistance	CHST8	64377	37	19	34180267	34180267	Missense_Mutation	SNP	C	T	10	177	c.100C>T	c.(100-102)CCT>TCT	p.P34S
Pat_41	Post-Resistance	KCTD15	79047	37	19	34297820	34297820	Nonsense_Mutation	SNP	C	T	6	163	c.295C>T	c.(295-297)CAA>TAA	p.Q99*
Pat_41	Post-Resistance	KCTD15	79047	37	19	34297905	34297905	Missense_Mutation	SNP	A	T	6	138	c.380A>T	c.(379-381)GAC>GTC	p.D127V
Pat_41	Post-Resistance	KIAA0355	9710	37	19	34832863	34832863	Missense_Mutation	SNP	C	T	7	119	c.2024C>T	c.(2023-2025)GCC>GTC	p.A675V
Pat_41	Post-Resistance	KIAA0355	9710	37	19	34832977	34832977	Missense_Mutation	SNP	C	T	22	207	c.2138C>T	c.(2137-2139)CCC>CTC	p.P713L
Pat_41	Post-Resistance	KIAA0355	9710	37	19	34833273	34833273	Missense_Mutation	SNP	G	A	47	313	c.2434G>A	c.(2434-2436)GGA>AGA	p.G812R
Pat_41	Post-Resistance	PDCD2L	84306	37	19	34900385	34900385	Missense_Mutation	SNP	G	A	17	126	c.656G>A	c.(655-657)GGC>GAC	p.G219D
Pat_41	Post-Resistance	UBA2	10054	37	19	34942921	34942921	Missense_Mutation	SNP	C	T	8	65	c.907C>T	c.(907-909)CCC>TCC	p.P303S
Pat_41	Post-Resistance	ZNF599	148103	37	19	35250222	35250222	Missense_Mutation	SNP	G	A	15	223	c.1484C>T	c.(1483-1485)ACT>ATT	p.T495I
Pat_41	Post-Resistance	ZNF30	90075	37	19	35435233	35435233	Missense_Mutation	SNP	C	T	9	154	c.1363C>T	c.(1363-1365)CCC>TCC	p.P455S
Pat_41	Post-Resistance	GRAMD1A	57655	37	19	35505283	35505283	Missense_Mutation	SNP	G	A	6	86	c.1061G>A	c.(1060-1062)GGG>GAG	p.G354E
Pat_41	Post-Resistance	USF2	7392	37	19	35760507	35760507	Missense_Mutation	SNP	G	A	6	45	c.133G>A	c.(133-135)GAG>AAG	p.E45K
Pat_41	Post-Resistance	CD22	933	37	19	35828853	35828853	Missense_Mutation	SNP	G	A	7	97	c.914G>A	c.(913-915)GGG>GAG	p.G305E
Pat_41	Post-Resistance	SBSN	374897	37	19	36015792	36015792	Missense_Mutation	SNP	C	T	4	55	c.644G>A	c.(643-645)GGA>GAA	p.G215E
Pat_41	Post-Resistance	ETV2	2116	37	19	36133387	36133387	Missense_Mutation	SNP	G	A	16	79	c.25G>A	c.(25-27)GCA>ACA	p.A9T
Pat_41	Post-Resistance	ARHGAP33	115703	37	19	36276138	36276138	Missense_Mutation	SNP	G	A	5	50	c.1769G>A	c.(1768-1770)AGC>AAC	p.S590N

Pat_41	Post-Resistance	ARHGAP33	115703	37	19	36278765	36278765	Missense_Mutation	SNP	C	T	4	49	c.2815C>T	c.(2815-2817)CCC>TCC	p.P939S
Pat_41	Post-Resistance	NPHS1	4868	37	19	36317527	36317527	Nonsense_Mutation	SNP	C	T	6	105	c.3615G>A	c.(3613-3615)TGG>TGA	p.W1205*
Pat_41	Post-Resistance	NPHS1	4868	37	19	36333362	36333362	Missense_Mutation	SNP	C	T	18	170	c.2425G>A	c.(2425-2427)GCC>ACC	p.A809T
Pat_41	Post-Resistance	ZFP82	284406	37	19	36884856	36884856	Missense_Mutation	SNP	C	T	13	92	c.386G>A	c.(385-387)GGA>GAA	p.G129E
Pat_41	Post-Resistance	ZNF260	339324	37	19	37005543	37005543	Missense_Mutation	SNP	C	T	6	142	c.598G>A	c.(598-600)GCT>ACT	p.A200T
Pat_41	Post-Resistance	ZNF461	92283	37	19	37129761	37129761	Missense_Mutation	SNP	G	A	23	174	c.1486C>T	c.(1486-1488)CCC>TCC	p.P496S
Pat_41	Post-Resistance	ZNF790	388536	37	19	37310041	37310041	Missense_Mutation	SNP	G	A	8	107	c.1205C>T	c.(1204-1206)GCC>GTC	p.A402V
Pat_41	Post-Resistance	ZNF345	25850	37	19	37368684	37368684	Missense_Mutation	SNP	G	A	8	192	c.952G>A	c.(952-954)GAG>AAG	p.E318K
Pat_41	Post-Resistance	ZNF571	51276	37	19	38074980	38074980	Missense_Mutation	SNP	C	T	22	349	c.28G>A	c.(28-30)GAT>AAT	p.D10N
Pat_41	Post-Resistance	ZNF607	84775	37	19	38190232	38190232	Missense_Mutation	SNP	C	T	16	60	c.800G>A	c.(799-801)GGC>GAC	p.G267D
Pat_41	Post-Resistance	ZNF573	126231	37	19	38262270	38262270	Missense_Mutation	SNP	C	T	13	266	c.136G>A	c.(136-138)GAC>AAC	p.D46N
Pat_41	Post-Resistance	YIF1B	90522	37	19	38798276	38798276	Missense_Mutation	SNP	G	A	12	147	c.656C>T	c.(655-657)ACC>ATC	p.T219I
Pat_41	Post-Resistance	FAM98C	147965	37	19	38899394	38899394	Missense_Mutation	SNP	C	T	15	105	c.922C>T	c.(922-924)CTT>TTT	p.L308F
Pat_41	Post-Resistance	RYR1	6261	37	19	38934424	38934424	Missense_Mutation	SNP	G	A	8	153	c.412G>A	c.(412-414)GAG>AAG	p.E138K
Pat_41	Post-Resistance	RYR1	6261	37	19	38958349	38958349	Missense_Mutation	SNP	C	T	12	153	c.3278C>T	c.(3277-3279)GCA>GTA	p.A1093V
Pat_41	Post-Resistance	RYR1	6261	37	19	38985033	38985033	Missense_Mutation	SNP	G	A	4	60	c.6316G>A	c.(6316-6318)GCC>ACC	p.A2106T
Pat_41	Post-Resistance	RYR1	6261	37	19	38997495	38997495	Missense_Mutation	SNP	C	T	16	64	c.8719C>T	c.(8719-8721)CCC>TCC	p.P2907S
Pat_41	Post-Resistance	EIF3K	27335	37	19	39123287	39123287	Nonsense_Mutation	SNP	G	A	12	67	c.468G>A	c.(466-468)TGG>TGA	p.W156*
Pat_41	Post-Resistance	ACTN4	81	37	19	39219729	39219729	Missense_Mutation	SNP	G	A	15	282	c.2512G>A	c.(2512-2514)GAG>AAG	p.E838K
Pat_41	Post-Resistance	ECH1	1891	37	19	39306955	39306955	Missense_Mutation	SNP	C	T	7	72	c.700G>A	c.(700-702)GCT>ACT	p.A234T
Pat_41	Post-Resistance	RINL	126432	37	19	39362299	39362299	Missense_Mutation	SNP	C	T	12	170	c.97G>A	c.(97-99)GAT>AAT	p.D33N
Pat_41	Post-Resistance	SIRT2	22933	37	19	39384083	39384083	Missense_Mutation	SNP	C	T	10	90	c.197G>A	c.(196-198)GGG>GAG	p.G66E
Pat_41	Post-Resistance	NFKBIB	4793	37	19	39395761	39395761	Splice_Site	SNP	G	A	13	194	c.285_splice	c.e2+1	p.Q95_splice
Pat_41	Post-Resistance	PAPL	390928	37	19	39590911	39590911	Missense_Mutation	SNP	G	A	14	211	c.550G>A	c.(550-552)GAT>AAT	p.D184N
Pat_41	Post-Resistance	IL28B	282617	37	19	39735086	39735086	Missense_Mutation	SNP	G	A	18	21	c.229C>T	c.(229-231)CCC>TCC	p.P77S
Pat_41	Post-Resistance	IL29	282618	37	19	39787066	39787066	Missense_Mutation	SNP	C	T	38	198	c.5C>T	c.(4-6)GCT>GTT	p.A2V
Pat_41	Post-Resistance	PLEKHG2	64857	37	19	39908303	39908303	Missense_Mutation	SNP	C	T	6	69	c.853C>T	c.(853-855)CGC>TGC	p.R285C
Pat_41	Post-Resistance	PLEKHG2	64857	37	19	39914454	39914454	Missense_Mutation	SNP	G	A	4	55	c.2681G>A	c.(2680-2682)GGT>GAT	p.G894D
Pat_41	Post-Resistance	TIMM50	92609	37	19	39978722	39978722	Missense_Mutation	SNP	G	A	16	330	c.1027G>A	c.(1027-1029)GAC>AAC	p.D343N
Pat_41	Post-Resistance	FCGBP	8857	37	19	40357760	40357760	Missense_Mutation	SNP	C	T	10	57	c.15553G>A	c.(15553-15555)GTA>ATA	p.V5185I
Pat_41	Post-Resistance	FCGBP	8857	37	19	40384065	40384065	Missense_Mutation	SNP	C	T	6	170	c.9545G>A	c.(9544-9546)GGC>GAC	p.G3182D
Pat_41	Post-Resistance	FCGBP	8857	37	19	40423988	40423988	Missense_Mutation	SNP	C	T	11	108	c.2215G>A	c.(2215-2217)GCC>ACC	p.A739T
Pat_41	Post-Resistance	ZNF546	339327	37	19	40520195	40520195	Missense_Mutation	SNP	C	T	12	95	c.1018C>T	c.(1018-1020)CTT>TTT	p.L340F
Pat_41	Post-Resistance	ZNF780A	284323	37	19	40581774	40581774	Missense_Mutation	SNP	G	A	5	249	c.575C>T	c.(574-576)CCC>CTC	p.P192L
Pat_41	Post-Resistance	C19orf47	126526	37	19	40832322	40832322	Missense_Mutation	SNP	C	T	7	96	c.622G>A	c.(622-624)GAG>AAG	p.E208K
Pat_41	Post-Resistance	PLD3	23646	37	19	40882551	40882551	Missense_Mutation	SNP	C	T	35	191	c.1055C>T	c.(1054-1056)GCC>GTC	p.A352V
Pat_41	Post-Resistance	HIPK4	147746	37	19	40886664	40886664	Missense_Mutation	SNP	G	A	7	72	c.1234C>T	c.(1234-1236)CCC>TCC	p.P412S
Pat_41	Post-Resistance	HIPK4	147746	37	19	40886789	40886789	Missense_Mutation	SNP	C	T	14	155	c.1109G>A	c.(1108-1110)CGC>CAC	p.R370H
Pat_41	Post-Resistance	HIPK4	147746	37	19	40889961	40889961	Missense_Mutation	SNP	G	A	16	86	c.551C>T	c.(550-552)CCT>CTT	p.P184L
Pat_41	Post-Resistance	SPTBN4	57731	37	19	41076387	41076387	Missense_Mutation	SNP	A	G	6	79	c.7072A>G	c.(7072-7074)AAC>GAC	p.N2358D
Pat_41	Post-Resistance	ITPKC	80271	37	19	41243624	41243624	Missense_Mutation	SNP	G	A	21	221	c.1798G>A	c.(1798-1800)GAA>AAA	p.E600K
Pat_41	Post-Resistance	CYP2A6	1548	37	19	41350653	41350653	Missense_Mutation	SNP	C	T	12	160	c.1186G>A	c.(1186-1188)GGC>AGC	p.G396S
Pat_41	Post-Resistance	CYP2A7	1549	37	19	41383877	41383877	Missense_Mutation	SNP	C	T	12	101	c.853G>A	c.(853-855)GAG>AAG	p.E285K
Pat_41	Post-Resistance	CYP2A7	1549	37	19	41386092	41386092	Missense_Mutation	SNP	G	A	9	62	c.551C>T	c.(550-552)TCC>TTC	p.S184F
Pat_41	Post-Resistance	CYP2B6	1555	37	19	41510291	41510291	Missense_Mutation	SNP	G	A	6	49	c.424G>A	c.(424-426)GTG>ATG	p.V142M
Pat_41	Post-Resistance	CYP2A13	1553	37	19	41595951	41595951	Splice_Site	SNP	G	A	4	45	c.344_splice	c.e3-1	p.G115_splice
Pat_41	Post-Resistance	CYP2S1	29785	37	19	41703762	41703762	Missense_Mutation	SNP	G	A	7	16	c.422G>A	c.(421-423)GGG>GAG	p.G141E

Pat_41	Post-Resistance	CYP2S1	29785	37	19	41707216	41707216	Missense_Mutation	SNP	G	A	20	349	c.915G>A	c.(913-915)ATG>ATA	p.M305I
Pat_41	Post-Resistance	AXL	558	37	19	41765687	41765687	Missense_Mutation	SNP	C	T	9	79	c.2563C>T	c.(2563-2565)CTC>TTC	p.L855F
Pat_41	Post-Resistance	B9D2	80776	37	19	41869415	41869415	Missense_Mutation	SNP	C	T	8	122	c.10G>A	c.(10-12)GTG>ATG	p.V4M
Pat_41	Post-Resistance	BCKDHA	593	37	19	41884272	41884272	Missense_Mutation	SNP	G	A	7	107	c.58G>A	c.(58-60)GAG>AAG	p.E20K
Pat_41	Post-Resistance	CEACAM5	1048	37	19	42224059	42224059	Missense_Mutation	SNP	C	T	17	231	c.1703C>T	c.(1702-1704)GCC>GTC	p.A568V
Pat_41	Post-Resistance	ATP1A3	478	37	19	42474550	42474550	Missense_Mutation	SNP	C	T	5	73	c.2408G>A	c.(2407-2409)GGC>GAC	p.G803D
Pat_41	Post-Resistance	GRIK5	2901	37	19	42510015	42510015	Missense_Mutation	SNP	C	T	3	40	c.2123G>A	c.(2122-2124)GGC>GAC	p.G708D
Pat_41	Post-Resistance	GRIK5	2901	37	19	42510823	42510823	Missense_Mutation	SNP	C	T	3	52	c.2011G>A	c.(2011-2013)GCC>ACC	p.A671T
Pat_41	Post-Resistance	ZNF574	64763	37	19	42583899	42583899	Missense_Mutation	SNP	G	A	4	55	c.1141G>A	c.(1141-1143)GCC>ACC	p.A381T
Pat_41	Post-Resistance	POU2F2	5452	37	19	42598025	42598025	Missense_Mutation	SNP	C	T	15	295	c.1154G>A	c.(1153-1155)GGG>GAG	p.G385E
Pat_41	Post-Resistance	POU2F2	5452	37	19	42600332	42600332	Missense_Mutation	SNP	C	T	5	64	c.565G>A	c.(565-567)GAG>AAG	p.E189K
Pat_41	Post-Resistance	ZNF526	116115	37	19	42728907	42728907	Missense_Mutation	SNP	C	T	8	109	c.352C>T	c.(352-354)CTC>TTC	p.L118F
Pat_41	Post-Resistance	ERF	2077	37	19	42754672	42754672	Missense_Mutation	SNP	C	T	7	56	c.68G>A	c.(67-69)GGC>GAC	p.G23D
Pat_41	Post-Resistance	CIC	23152	37	19	42795519	42795519	Missense_Mutation	SNP	C	T	7	102	c.2599C>T	c.(2599-2601)CCA>TCA	p.P867S
Pat_41	Post-Resistance	TMEM145	284339	37	19	42821922	42821922	Missense_Mutation	SNP	G	A	14	101	c.962G>A	c.(961-963)GGA>GAA	p.G321E
Pat_41	Post-Resistance	TMEM145	284339	37	19	42824573	42824573	Missense_Mutation	SNP	C	T	7	50	c.1178C>T	c.(1177-1179)GCC>GTC	p.A393V
Pat_41	Post-Resistance	CEACAM8	1088	37	19	43087426	43087426	Missense_Mutation	SNP	C	T	18	138	c.1022G>A	c.(1021-1023)GGA>GAA	p.G341E
Pat_41	Post-Resistance	PSG5	5673	37	19	43679396	43679396	Missense_Mutation	SNP	C	T	25	198	c.935G>A	c.(934-936)AGC>AAC	p.S312N
Pat_41	Post-Resistance	PSG5	5673	37	19	43689023	43689023	Missense_Mutation	SNP	C	A	287	317	c.341G>T	c.(340-342)CGG>CTG	p.R114L
Pat_41	Post-Resistance	XRCC1	7515	37	19	44050783	44050783	Missense_Mutation	SNP	G	A	14	250	c.1390C>T	c.(1390-1392)CTC>TTC	p.L464F
Pat_41	Post-Resistance	KCNN4	3783	37	19	44273891	44273891	Missense_Mutation	SNP	C	T	19	316	c.910G>A	c.(910-912)GAT>AAT	p.D304N
Pat_41	Post-Resistance	LYPD5	284348	37	19	44303051	44303051	Missense_Mutation	SNP	G	A	4	10	c.283C>T	c.(283-285)CCA>TCA	p.P95S
Pat_41	Post-Resistance	ZNF283	284349	37	19	44351576	44351576	Missense_Mutation	SNP	G	A	18	226	c.823G>A	c.(823-825)GGA>AGA	p.G275R
Pat_41	Post-Resistance	ZNF404	342908	37	19	44376924	44376924	Missense_Mutation	SNP	C	T	4	26	c.1433G>A	c.(1432-1434)GGT>GAT	p.G478D
Pat_41	Post-Resistance	ZNF45	7596	37	19	44418989	44418989	Missense_Mutation	SNP	G	A	26	474	c.599C>T	c.(598-600)GCC>GTC	p.A200V
Pat_41	Post-Resistance	ZNF222	7673	37	19	44536302	44536302	Missense_Mutation	SNP	G	A	21	441	c.475G>A	c.(475-477)GCC>ACC	p.A159T
Pat_41	Post-Resistance	ZNF222	7673	37	19	44537091	44537091	Missense_Mutation	SNP	G	A	20	100	c.1264G>A	c.(1264-1266)GAA>AAA	p.E422K
Pat_41	Post-Resistance	ZNF225	7768	37	19	44636500	44636500	Missense_Mutation	SNP	G	A	19	133	c.1733G>A	c.(1732-1734)AGC>AAC	p.S578N
Pat_41	Post-Resistance	ZNF226	7769	37	19	44681461	44681461	Nonsense_Mutation	SNP	G	A	22	166	c.2046G>A	c.(2044-2046)TGG>TGA	p.W682*
Pat_41	Post-Resistance	CEACAM20	125931	37	19	45017289	45017289	Missense_Mutation	SNP	C	T	4	110	c.1369G>A	c.(1369-1371)GCT>ACT	p.A457T
Pat_41	Post-Resistance	CEACAM20	125931	37	19	45021256	45021256	Missense_Mutation	SNP	C	T	6	144	c.1060G>A	c.(1060-1062)GAG>AAG	p.E354K
Pat_41	Post-Resistance	CBLC	23624	37	19	45284568	45284568	Missense_Mutation	SNP	G	A	9	226	c.605G>A	c.(604-606)TGC>TAC	p.C202Y
Pat_41	Post-Resistance	CBLC	23624	37	19	45295727	45295727	Missense_Mutation	SNP	C	T	7	93	c.1093C>T	c.(1093-1095)CCG>TCG	p.P365S
Pat_41	Post-Resistance	BCAM	4059	37	19	45322748	45322748	Splice_Site	SNP	G	A	16	106	c.1618_splice	c.e12+1	p.V540_splice
Pat_41	Post-Resistance	CKM	1158	37	19	45815178	45815178	Missense_Mutation	SNP	G	A	13	111	c.482C>T	c.(481-483)GCT>GTT	p.A161V
Pat_41	Post-Resistance	CKM	1158	37	19	45818854	45818854	Missense_Mutation	SNP	C	T	8	63	c.350G>A	c.(349-351)GGT>GAT	p.G117D
Pat_41	Post-Resistance	KLC3	147700	37	19	45850774	45850774	Missense_Mutation	SNP	G	A	4	101	c.559G>A	c.(559-561)GGT>AGT	p.G187S
Pat_41	Post-Resistance	KLC3	147700	37	19	45852840	45852840	Missense_Mutation	SNP	G	A	13	67	c.1123G>A	c.(1123-1125)GCC>ACC	p.A375T
Pat_41	Post-Resistance	PPP1R13L	10848	37	19	45889405	45889405	Missense_Mutation	SNP	G	A	3	14	c.1849C>T	c.(1849-1851)CCG>TCG	p.P617S
Pat_41	Post-Resistance	CD3EAP	10849	37	19	45912202	45912202	Missense_Mutation	SNP	C	T	9	187	c.976C>T	c.(976-978)CCT>TCT	p.P326S
Pat_41	Post-Resistance	GPR4	2828	37	19	46094106	46094106	Missense_Mutation	SNP	C	T	12	123	c.1019G>A	c.(1018-1020)GGC>GAC	p.G340D
Pat_41	Post-Resistance	EML2	24139	37	19	46119804	46119804	Missense_Mutation	SNP	A	G	4	94	c.1424T>C	c.(1423-1425)CTG>CCG	p.L475P
Pat_41	Post-Resistance	SYMPK	8189	37	19	46324653	46324653	Missense_Mutation	SNP	G	A	10	93	c.2882C>T	c.(2881-2883)TCC>TTC	p.S961F
Pat_41	Post-Resistance	SYMPK	8189	37	19	46332303	46332303	Missense_Mutation	SNP	C	T	15	80	c.1910G>A	c.(1909-1911)GGC>GAC	p.G637D
Pat_41	Post-Resistance	SYMPK	8189	37	19	46338461	46338461	Missense_Mutation	SNP	G	A	8	145	c.1268C>T	c.(1267-1269)CCC>CTC	p.P423L
Pat_41	Post-Resistance	SYMPK	8189	37	19	46347405	46347405	Missense_Mutation	SNP	C	T	10	250	c.730G>A	c.(730-732)GTG>ATG	p.V244M
Pat_41	Post-Resistance	FOXA3	3171	37	19	46375649	46375649	Missense_Mutation	SNP	C	T	20	367	c.386C>T	c.(385-387)GCC>GTC	p.A129V

Pat_41	Post-Resistance	NOVA2	4858	37	19	46443231	46443231	Missense_Mutation	SNP	C	T	12	91	c.1369G>A	c.(1369-1371)GTC>ATC	p.V457I
Pat_41	Post-Resistance	PPP5C	5536	37	19	46850457	46850457	Missense_Mutation	SNP	C	T	4	22	c.104C>T	c.(103-105)GCC>GTC	p.A35V
Pat_41	Post-Resistance	CCDC8	83987	37	19	46915017	46915018	Missense_Mutation	DNP	CC	GG	7	223	.1050_1051GG>C	48-1053)GAGGAG>GAC	350_351EE>D
Pat_41	Post-Resistance	STRN4	29888	37	19	47236348	47236348	Missense_Mutation	SNP	G	A	4	45	c.685C>T	c.(685-687)CTC>TTC	p.L229F
Pat_41	Post-Resistance	GRLF1	2909	37	19	47422582	47422582	Missense_Mutation	SNP	C	T	4	58	c.650C>T	c.(649-651)GCC>GTC	p.A217V
Pat_41	Post-Resistance	BBC3	27113	37	19	47725147	47725147	Missense_Mutation	SNP	G	A	5	62	c.494C>T	c.(493-495)CCC>CTC	p.P165L
Pat_41	Post-Resistance	C5AR1	728	37	19	47823581	47823581	Missense_Mutation	SNP	C	T	11	113	c.547C>T	c.(547-549)CCA>TCA	p.P183S
Pat_41	Post-Resistance	DHX34	9704	37	19	47879317	47879317	Missense_Mutation	SNP	C	T	10	76	c.2444C>T	c.(2443-2445)CCC>CTC	p.P815L
Pat_41	Post-Resistance	SLC8A2	6543	37	19	47941153	47941153	Missense_Mutation	SNP	C	T	9	197	c.1963G>A	c.(1963-1965)GAG>AAG	p.E655K
Pat_41	Post-Resistance	EHD2	30846	37	19	48221837	48221837	Missense_Mutation	SNP	C	T	6	35	c.476C>T	c.(475-477)TCG>TTG	p.S159L
Pat_41	Post-Resistance	EHD2	30846	37	19	48229413	48229413	Nonsense_Mutation	SNP	C	T	4	28	c.847C>T	c.(847-849)CAG>TAG	p.Q283*
Pat_41	Post-Resistance	GLTSCR2	29997	37	19	48253530	48253530	Missense_Mutation	SNP	C	T	10	69	c.385C>T	c.(385-387)CCT>TCT	p.P129S
Pat_41	Post-Resistance	PLA2G4C	8605	37	19	48556253	48556253	Splice_Site	SNP	C	T	5	148	c.1580_splice	c.e16+1	p.G527_splice
Pat_41	Post-Resistance	CARD8	22900	37	19	48725012	48725012	Missense_Mutation	SNP	G	A	9	102	c.818C>T	c.(817-819)TCT>TTT	p.S273F
Pat_41	Post-Resistance	KDELR1	10945	37	19	48892866	48892866	Missense_Mutation	SNP	C	T	8	109	c.295G>A	c.(295-297)GTC>ATC	p.V99I
Pat_41	Post-Resistance	SPHK2	56848	37	19	49132000	49132000	Missense_Mutation	SNP	G	A	16	290	c.935G>A	c.(934-936)GGT>GAT	p.G312D
Pat_41	Post-Resistance	CA11	770	37	19	49143086	49143086	Missense_Mutation	SNP	G	A	17	340	c.526C>T	c.(526-528)CGC>TGC	p.R176C
Pat_41	Post-Resistance	FUT1	2523	37	19	49254351	49254351	Missense_Mutation	SNP	C	T	11	97	c.188G>A	c.(187-189)GGC>GAC	p.G63D
Pat_41	Post-Resistance	HRC	3270	37	19	49657944	49657944	Missense_Mutation	SNP	C	T	10	118	c.551G>A	c.(550-552)GGC>GAC	p.G184D
Pat_41	Post-Resistance	TRPM4	54795	37	19	49671229	49671229	Missense_Mutation	SNP	G	A	13	296	c.323G>A	c.(322-324)CGC>CAC	p.R108H
Pat_41	Post-Resistance	TRPM4	54795	37	19	49671238	49671238	Missense_Mutation	SNP	G	A	5	276	c.332G>A	c.(331-333)GGC>GAC	p.G111D
Pat_41	Post-Resistance	TRPM4	54795	37	19	49684701	49684701	Missense_Mutation	SNP	G	A	10	120	c.1246G>A	c.(1246-1248)GGG>AGG	p.G416R
Pat_41	Post-Resistance	TRPM4	54795	37	19	49691902	49691902	Missense_Mutation	SNP	C	T	10	83	c.1748C>T	c.(1747-1749)TCC>TTC	p.S583F
Pat_41	Post-Resistance	PIH1D1	55011	37	19	49952756	49952756	Missense_Mutation	SNP	C	T	13	168	c.313G>A	c.(313-315)GAG>AAG	p.E105K
Pat_41	Post-Resistance	RPL13A	23521	37	19	49993768	49993768	Missense_Mutation	SNP	C	T	6	169	c.191C>T	c.(190-192)ACC>ATC	p.T64I
Pat_41	Post-Resistance	PRR12	57479	37	19	50098041	50098041	Missense_Mutation	SNP	C	T	7	38	c.449C>T	c.(448-450)GCT>GTT	p.A150V
Pat_41	Post-Resistance	NR1H2	7376	37	19	50880894	50880894	Missense_Mutation	SNP	C	T	31	217	c.32C>T	c.(31-33)ACC>ATC	p.T11I
Pat_41	Post-Resistance	NR1H2	7376	37	19	50882377	50882377	Missense_Mutation	SNP	C	T	13	205	c.869C>T	c.(868-870)CCT>CTT	p.P290L
Pat_41	Post-Resistance	GPR32	2854	37	19	51274188	51274188	Missense_Mutation	SNP	G	A	5	74	c.331G>A	c.(331-333)GAG>AAG	p.E111K
Pat_41	Post-Resistance	KLK10	5655	37	19	51519411	51519411	Missense_Mutation	SNP	G	A	3	25	c.271C>T	c.(271-273)CCA>TCA	p.P91S
Pat_41	Post-Resistance	SIGLEC7	27036	37	19	51656411	51656411	Missense_Mutation	SNP	C	T	16	149	c.1313C>T	c.(1312-1314)GCA>GTA	p.A438V
Pat_41	Post-Resistance	C19orf75	284369	37	19	51770758	51770758	Missense_Mutation	SNP	C	T	11	143	c.542C>T	c.(541-543)GCC>GTC	p.A181V
Pat_41	Post-Resistance	SIGLEC8	27181	37	19	51957998	51957998	Missense_Mutation	SNP	G	A	6	222	c.1088C>T	c.(1087-1089)GCA>GTA	p.A363V
Pat_41	Post-Resistance	ZNF175	7728	37	19	52090251	52090251	Missense_Mutation	SNP	C	T	6	166	c.667C>T	c.(667-669)CTT>TTT	p.L223F
Pat_41	Post-Resistance	ZNF649	65251	37	19	52394077	52394077	Missense_Mutation	SNP	C	T	34	314	c.1312G>A	c.(1312-1314)GCT>ACT	p.A438T
Pat_41	Post-Resistance	ZNF649	65251	37	19	52394413	52394413	Missense_Mutation	SNP	C	T	9	152	c.976G>A	c.(976-978)GGC>AGC	p.G326S
Pat_41	Post-Resistance	ZNF649	65251	37	19	52394703	52394703	Missense_Mutation	SNP	C	T	6	160	c.686G>A	c.(685-687)AGA>AAA	p.R229K
Pat_41	Post-Resistance	ZNF649	65251	37	19	52399808	52399808	Missense_Mutation	SNP	C	T	18	211	c.155G>A	c.(154-156)GGC>GAC	p.G52D
Pat_41	Post-Resistance	ZNF350	59348	37	19	52468819	52468819	Missense_Mutation	SNP	C	T	8	157	c.887G>A	c.(886-888)GGA>GAA	p.G296E
Pat_41	Post-Resistance	ZNF615	284370	37	19	52497574	52497574	Missense_Mutation	SNP	C	T	26	205	c.755G>A	c.(754-756)AGA>AAA	p.R252K
Pat_41	Post-Resistance	ZNF880	400713	37	19	52876433	52876433	Nonsense_Mutation	SNP	C	T	14	229	c.82C>T	c.(82-84)CAG>TAG	p.Q28*
Pat_41	Post-Resistance	ZNF880	400713	37	19	52887427	52887427	Missense_Mutation	SNP	A	T	3	42	c.594A>T	c.(592-594)AGA>AGT	p.R198S
Pat_41	Post-Resistance	ZNF528	84436	37	19	52919495	52919495	Missense_Mutation	SNP	C	T	7	106	c.1390C>T	c.(1390-1392)CCT>TCT	p.P464S
Pat_41	Post-Resistance	ZNF534	147658	37	19	52942391	52942391	Missense_Mutation	SNP	A	C	4	92	c.1717A>C	c.(1717-1719)AGT>CGT	p.S573R
Pat_41	Post-Resistance	ZNF808	388558	37	19	53057109	53057109	Missense_Mutation	SNP	C	T	29	432	c.940C>T	c.(940-942)CCT>TCT	p.P314S
Pat_41	Post-Resistance	ZNF808	388558	37	19	53058514	53058514	Missense_Mutation	SNP	G	A	35	576	c.2345G>A	c.(2344-2346)CGT>CAT	p.R782H
Pat_41	Post-Resistance	ZNF701	55762	37	19	53086538	53086538	Missense_Mutation	SNP	G	C	5	144	c.1226G>C	c.(1225-1227)CGT>CCT	p.R409P

Pat_41	Post-Resistance	ZNF83	55769	37	19	53116509	53116509	Missense_Mutation	SNP	C	T	8	147	c.1309G>A	c.(1309-1311)GTC>ATC	p.V437I
Pat_41	Post-Resistance	ZNF347	84671	37	19	53644931	53644931	Missense_Mutation	SNP	C	T	13	218	c.1150G>A	c.(1150-1152)GCT>ACT	p.A384T
Pat_41	Post-Resistance	ZNF347	84671	37	19	53645156	53645156	Missense_Mutation	SNP	C	T	49	358	c.925G>A	c.(925-927)GTG>ATG	p.V309M
Pat_41	Post-Resistance	ZNF347	84671	37	19	53645558	53645558	Missense_Mutation	SNP	C	T	8	84	c.523G>A	c.(523-525)GCA>ACA	p.A175T
Pat_41	Post-Resistance	ZNF665	79788	37	19	53668095	53668095	Missense_Mutation	SNP	C	T	57	323	c.1648G>A	c.(1648-1650)GTC>ATC	p.V550I
Pat_41	Post-Resistance	ZNF665	79788	37	19	53669192	53669192	Missense_Mutation	SNP	C	T	27	247	c.551G>A	c.(550-552)GGC>GAC	p.G184D
Pat_41	Post-Resistance	BIRC8	112401	37	19	53793477	53793477	Missense_Mutation	SNP	G	A	7	53	c.151C>T	c.(151-153)CCC>TCC	p.P51S
Pat_41	Post-Resistance	ZNF845	91664	37	19	53856669	53856669	Missense_Mutation	SNP	C	T	5	255	c.2741C>T	c.(2740-2742)CCT>CTT	p.P914L
Pat_41	Post-Resistance	ZNF845	91664	37	19	53856702	53856702	Missense_Mutation	SNP	G	A	9	243	c.2774G>A	c.(2773-2775)CGT>CAT	p.R925H
Pat_41	Post-Resistance	ZNF845	91664	37	19	53856761	53856761	Missense_Mutation	SNP	T	C	8	131	c.2833T>C	c.(2833-2835)TGT>CGT	p.C945R
Pat_41	Post-Resistance	ZNF761	388561	37	19	53958365	53958365	Missense_Mutation	SNP	C	T	7	189	c.604C>T	c.(604-606)CTC>TTC	p.L202F
Pat_41	Post-Resistance	ZNF761	388561	37	19	53959854	53959854	Missense_Mutation	SNP	A	C	10	286	c.2093A>C	c.(2092-2094)AAC>ACC	p.N698T
Pat_41	Post-Resistance	ZNF813	126017	37	19	53994037	53994037	Missense_Mutation	SNP	C	T	28	199	c.551C>T	c.(550-552)CCC>CTC	p.P184L
Pat_41	Post-Resistance	ZNF813	126017	37	19	53995104	53995105	Missense_Mutation	DNP	CA	TG	6	122	.1618_1619CA>T	c.(1618-1620)CAT>TGT	p.H540C
Pat_41	Post-Resistance	NLRP12	91662	37	19	54313193	54313193	Missense_Mutation	SNP	G	A	11	44	c.1720C>T	c.(1720-1722)CAC>TAC	p.H574Y
Pat_41	Post-Resistance	MYADM	91663	37	19	54377265	54377265	Missense_Mutation	SNP	G	A	3	25	c.482G>A	c.(481-483)CGG>CAG	p.R161Q
Pat_41	Post-Resistance	PRKCG	5582	37	19	54404004	54404004	Splice_Site	SNP	G	A	59	488	c.1575_splice	c.e14+1	p.E525_splice
Pat_41	Post-Resistance	CNOT3	4849	37	19	54656680	54656680	Missense_Mutation	SNP	G	A	46	382	c.1981G>A	c.(1981-1983)GAA>AAA	p.E661K
Pat_41	Post-Resistance	LILRB3	11025	37	19	54726003	54726003	Splice_Site	SNP	C	T	4	53	c.356_splice	c.e4-1	p.G119_splice
Pat_41	Post-Resistance	LILRA3	11026	37	19	54803139	54803139	Missense_Mutation	SNP	C	T	12	49	c.538G>A	c.(538-540)GCC>ACC	p.A180T
Pat_41	Post-Resistance	LENG8	114823	37	19	54963881	54963881	Missense_Mutation	SNP	T	C	10	315	c.265T>C	c.(265-267)TGG>CGG	p.W89R
Pat_41	Post-Resistance	LILRB4	11006	37	19	55177346	55177346	Missense_Mutation	SNP	C	T	3	63	c.838C>T	c.(838-840)CTC>TTC	p.L280F
Pat_41	Post-Resistance	KIR2DL4	3805	37	19	55316292	55316292	Missense_Mutation	SNP	G	A	4	43	c.121G>A	c.(121-123)GTG>ATG	p.V41M
Pat_41	Post-Resistance	RDH13	112724	37	19	55558826	55558826	Missense_Mutation	SNP	G	A	6	20	c.689C>T	c.(688-690)CCC>CTC	p.P230L
Pat_41	Post-Resistance	BRSK1	84446	37	19	55805413	55805413	Missense_Mutation	SNP	C	T	14	398	c.487C>T	c.(487-489)CTT>TTT	p.L163F
Pat_41	Post-Resistance	SBK2	646643	37	19	56041138	56041138	Missense_Mutation	SNP	C	T	7	85	c.1009G>A	c.(1009-1011)GAG>AAG	p.E337K
Pat_41	Post-Resistance	ZNF524	147807	37	19	56113672	56113672	Missense_Mutation	SNP	C	T	3	10	c.194C>T	c.(193-195)CCA>CTA	p.P65L
Pat_41	Post-Resistance	NLRP11	204801	37	19	56320832	56320832	Missense_Mutation	SNP	C	T	40	168	c.1144G>A	c.(1144-1146)GCT>ACT	p.A382T
Pat_41	Post-Resistance	ZNF582	147948	37	19	56896420	56896420	Nonsense_Mutation	SNP	C	T	20	444	c.366G>A	c.(364-366)TGG>TGA	p.W122*
Pat_41	Post-Resistance	ZNF583	147949	37	19	56934484	56934484	Missense_Mutation	SNP	G	A	18	231	c.457G>A	c.(457-459)GTT>ATT	p.V153I
Pat_41	Post-Resistance	ZNF471	57573	37	19	57037178	57037178	Missense_Mutation	SNP	G	A	7	96	c.1742G>A	c.(1741-1743)AGT>AAT	p.S581N
Pat_41	Post-Resistance	ZNF71	58491	37	19	57133428	57133428	Missense_Mutation	SNP	T	C	7	179	c.773T>C	c.(772-774)ATC>ACC	p.I258T
Pat_41	Post-Resistance	ZNF71	58491	37	19	57133431	57133431	Missense_Mutation	SNP	T	A	7	181	c.776T>A	c.(775-777)GTG>GAG	p.V259E
Pat_41	Post-Resistance	PEG3	5178	37	19	57328186	57328186	Missense_Mutation	SNP	C	T	12	273	c.1624G>A	c.(1624-1626)GAA>AAA	p.E542K
Pat_41	Post-Resistance	AURKC	6795	37	19	57743435	57743435	Missense_Mutation	SNP	C	T	3	48	c.139C>T	c.(139-141)CGT>TGT	p.R47C
Pat_41	Post-Resistance	ZNF304	57343	37	19	57868567	57868567	Missense_Mutation	SNP	G	A	16	140	c.1330G>A	c.(1330-1332)GCA>ACA	p.A444T
Pat_41	Post-Resistance	ZNF17	7565	37	19	57931018	57931018	Missense_Mutation	SNP	C	T	7	81	c.158C>T	c.(157-159)GCC>GTC	p.A53V
Pat_41	Post-Resistance	ZNF419	79744	37	19	58004332	58004332	Missense_Mutation	SNP	C	T	4	51	c.407C>T	c.(406-408)CCC>CTC	p.P136L
Pat_41	Post-Resistance	ZNF416	55659	37	19	58084370	58084370	Missense_Mutation	SNP	C	T	23	110	c.902G>A	c.(901-903)GGT>GAT	p.G301D
Pat_41	Post-Resistance	ZNF134	7693	37	19	58132739	58132739	Missense_Mutation	SNP	C	T	16	715	c.1252C>T	c.(1252-1254)CAC>TAC	p.H418Y
Pat_41	Post-Resistance	ZSCAN4	201516	37	19	58187859	58187859	Missense_Mutation	SNP	G	A	13	91	c.346G>A	c.(346-348)GAG>AAG	p.E116K
Pat_41	Post-Resistance	ZNF551	90233	37	19	58196637	58196637	Missense_Mutation	SNP	C	T	11	141	c.41C>T	c.(40-42)ACC>ATC	p.T14I
Pat_41	Post-Resistance	ZNF671	79891	37	19	58234633	58234633	Missense_Mutation	SNP	G	A	23	215	c.214C>T	c.(214-216)CTT>TTT	p.L72F
Pat_41	Post-Resistance	ZNF776	284309	37	19	58265369	58265369	Missense_Mutation	SNP	C	T	10	325	c.871C>T	c.(871-873)CCT>TCT	p.P291S
Pat_41	Post-Resistance	ZNF776	284309	37	19	58265885	58265885	Missense_Mutation	SNP	G	A	5	192	c.1387G>A	c.(1387-1389)GGA>AGA	p.G463R
Pat_41	Post-Resistance	ZNF586	54807	37	19	58290602	58290602	Missense_Mutation	SNP	C	T	20	181	c.647C>T	c.(646-648)GCT>GTT	p.A216V
Pat_41	Post-Resistance	ZNF418	147686	37	19	58437684	58437684	Missense_Mutation	SNP	C	T	41	217	c.1865G>A	c.(1864-1866)AGC>AAC	p.S622N

Pat_41	Post-Resistance	ZNF418	147686	37	19	58438011	58438011	Missense_Mutation	SNP	C	T	23	296	c.1538G>A	c.(1537-1539)AGT>AAT	p.S513N
Pat_41	Post-Resistance	ZNF544	27300	37	19	58772991	58772991	Missense_Mutation	SNP	C	T	4	72	c.1019C>T	c.(1018-1020)TCT>TTT	p.S340F
Pat_41	Post-Resistance	ZSCAN22	342945	37	19	58850304	58850304	Missense_Mutation	SNP	G	A	10	195	c.1088G>A	c.(1087-1089)CGC>CAC	p.R363H
Pat_41	Post-Resistance	ZBTB45	84878	37	19	59028301	59028301	Missense_Mutation	SNP	G	A	14	293	c.740C>T	c.(739-741)GCT>GTT	p.A247V
Pat_41	Post-Resistance	TRIM28	10155	37	19	59059749	59059749	Missense_Mutation	SNP	C	T	17	67	c.1190C>T	c.(1189-1191)GCC>GTC	p.A397V
Pat_41	Post-Resistance	UBE2M	9040	37	19	59067682	59067682	Splice_Site	SNP	C	T	36	171	c.411_splice	c.e5+1	p.L137_splice
Pat_41	Post-Resistance	SH3YL1	26751	37	2	231169	231169	Missense_Mutation	SNP	C	T	4	13	c.556G>A	c.(556-558)GCT>ACT	p.A186T
Pat_41	Post-Resistance	TPO	7173	37	2	1507750	1507750	Missense_Mutation	SNP	C	T	12	70	c.2417C>T	c.(2416-2418)CCC>CTC	p.P806L
Pat_41	Post-Resistance	PXDN	7837	37	2	1670036	1670036	Missense_Mutation	SNP	G	A	5	83	c.1241C>T	c.(1240-1242)GCG>GTG	p.A414V
Pat_41	Post-Resistance	CMPK2	129607	37	2	7001358	7001358	Nonsense_Mutation	SNP	C	A	4	125	c.949G>T	c.(949-951)GAA>TAA	p.E317*
Pat_41	Post-Resistance	KIDINS220	57498	37	2	8888060	8888060	Missense_Mutation	SNP	G	A	11	221	c.3485C>T	c.(3484-3486)CCA>CTA	p.P1162L
Pat_41	Post-Resistance	KIDINS220	57498	37	2	8926455	8926455	Missense_Mutation	SNP	C	T	31	320	c.1820G>A	c.(1819-1821)AGT>AAT	p.S607N
Pat_41	Post-Resistance	ASAP2	8853	37	2	9484745	9484745	Missense_Mutation	SNP	C	T	15	209	c.934C>T	c.(934-936)CTC>TTC	p.L312F
Pat_41	Post-Resistance	IAH1	285148	37	2	9621510	9621510	Nonsense_Mutation	SNP	C	T	4	118	c.379C>T	c.(379-381)CGA>TGA	p.R127*
Pat_41	Post-Resistance	TAF1B	9014	37	2	10008460	10008460	Missense_Mutation	SNP	G	A	7	136	c.455G>A	c.(454-456)AGT>AAT	p.S152N
Pat_41	Post-Resistance	PDIA6	10130	37	2	10942730	10942730	Missense_Mutation	SNP	C	A	71	120	c.56G>T	c.(55-57)GGT>GTT	p.G19V
Pat_41	Post-Resistance	E2F6	1876	37	2	11587752	11587752	Splice_Site	SNP	C	T	8	236	c.799_splice	c.e6+1	p.E267_splice
Pat_41	Post-Resistance	GREB1	9687	37	2	11702678	11702678	Missense_Mutation	SNP	C	T	14	185	c.247C>T	c.(247-249)CCT>TCT	p.P83S
Pat_41	Post-Resistance	GREB1	9687	37	2	11720832	11720832	Missense_Mutation	SNP	C	T	13	436	c.775C>T	c.(775-777)CCA>TCA	p.P259S
Pat_41	Post-Resistance	GREB1	9687	37	2	11728961	11728961	Missense_Mutation	SNP	G	A	57	282	c.1249G>A	c.(1249-1251)GTC>ATC	p.V417I
Pat_41	Post-Resistance	GREB1	9687	37	2	11735461	11735461	Missense_Mutation	SNP	G	A	9	101	c.1781G>A	c.(1780-1782)GGG>GAG	p.G594E
Pat_41	Post-Resistance	GREB1	9687	37	2	11756826	11756826	Missense_Mutation	SNP	C	T	9	148	c.3392C>T	c.(3391-3393)TCC>TTC	p.S1131F
Pat_41	Post-Resistance	FAM84A	151354	37	2	14774290	14774290	Missense_Mutation	SNP	C	T	4	30	c.187C>T	c.(187-189)CCC>TCC	p.P63S
Pat_41	Post-Resistance	NBAS	51594	37	2	15378686	15378686	Missense_Mutation	SNP	G	A	8	49	c.5849C>T	c.(5848-5850)ACC>ATC	p.T1950I
Pat_41	Post-Resistance	NBAS	51594	37	2	15470778	15470778	Missense_Mutation	SNP	C	T	24	256	c.4291G>A	c.(4291-4293)GCC>ACC	p.A1431T
Pat_41	Post-Resistance	MYCN	4613	37	2	16086074	16086074	Missense_Mutation	SNP	C	T	10	174	c.1250C>T	c.(1249-1251)GCC>GTC	p.A417V
Pat_41	Post-Resistance	RAD51AP2	729475	37	2	17699318	17699318	Missense_Mutation	SNP	C	T	9	134	c.365G>A	c.(364-366)AGT>AAT	p.S122N
Pat_41	Post-Resistance	SMC6	79677	37	2	17847700	17847700	Missense_Mutation	SNP	G	A	5	59	c.3148C>T	c.(3148-3150)CCT>TCT	p.P1050S
Pat_41	Post-Resistance	OSR1	130497	37	2	19552052	19552052	Missense_Mutation	SNP	G	A	4	61	c.785C>T	c.(784-786)TCC>TTC	p.S262F
Pat_41	Post-Resistance	PUM2	23369	37	2	20460228	20460228	Splice_Site	SNP	C	T	7	150	c.2226_splice	c.e14-1	p.R742_splice
Pat_41	Post-Resistance	PUM2	23369	37	2	20512172	20512172	Missense_Mutation	SNP	G	A	13	123	c.173C>T	c.(172-174)TCC>TTC	p.S58F
Pat_41	Post-Resistance	APOB	338	37	2	21225030	21225030	Missense_Mutation	SNP	G	A	13	76	c.13264C>T	c.(13264-13266)CAT>TAT	p.H4422Y
Pat_41	Post-Resistance	APOB	338	37	2	21236115	21236115	Missense_Mutation	SNP	G	A	56	460	c.4133C>T	c.(4132-4134)ACC>ATC	p.T1378I
Pat_41	Post-Resistance	APOB	338	37	2	21237399	21237399	Missense_Mutation	SNP	G	A	17	64	c.3763C>T	c.(3763-3765)CTC>TTC	p.L1255F
Pat_41	Post-Resistance	APOB	338	37	2	21252786	21252786	Missense_Mutation	SNP	G	A	23	257	c.1454C>T	c.(1453-1455)ACC>ATC	p.T485I
Pat_41	Post-Resistance	ATAD2B	54454	37	2	23985186	23985186	Missense_Mutation	SNP	G	A	7	82	c.3287C>T	c.(3286-3288)CCT>CTT	p.P1096L
Pat_41	Post-Resistance	ATAD2B	54454	37	2	24021016	24021016	Missense_Mutation	SNP	G	A	3	12	c.2632C>T	c.(2632-2634)CCT>TCT	p.P878S
Pat_41	Post-Resistance	ATAD2B	54454	37	2	24051809	24051809	Missense_Mutation	SNP	C	T	7	113	c.1729G>A	c.(1729-1731)GCA>ACA	p.A577T
Pat_41	Post-Resistance	ITSN2	50618	37	2	24432880	24432880	Missense_Mutation	SNP	G	A	10	128	c.4280C>T	c.(4279-4281)ACC>ATC	p.T1427I
Pat_41	Post-Resistance	NCOA1	8648	37	2	24881548	24881548	Missense_Mutation	SNP	T	C	18	195	c.2T>C	c.(1-3)ATG>ACG	p.M1T
Pat_41	Post-Resistance	NCOA1	8648	37	2	24951236	24951236	Missense_Mutation	SNP	G	A	21	102	c.2777G>A	c.(2776-2778)AGA>AAA	p.R926K
Pat_41	Post-Resistance	NCOA1	8648	37	2	24974860	24974860	Missense_Mutation	SNP	C	T	4	102	c.3716C>T	c.(3715-3717)CCC>CTC	p.P1239L
Pat_41	Post-Resistance	ADCY3	109	37	2	25064427	25064427	Missense_Mutation	SNP	C	T	3	27	c.1066G>A	c.(1066-1068)GCT>ACT	p.A356T
Pat_41	Post-Resistance	DNAJC27	51277	37	2	25170549	25170549	Missense_Mutation	SNP	C	T	21	202	c.758G>A	c.(757-759)GGC>GAC	p.G253D
Pat_41	Post-Resistance	DNMT3A	1788	37	2	25463208	25463208	Missense_Mutation	SNP	C	T	18	219	c.2285G>A	c.(2284-2286)GGC>GAC	p.G762D
Pat_41	Post-Resistance	ASXL2	55252	37	2	25964976	25964976	Nonsense_Mutation	SNP	G	T	5	272	c.4230C>A	c.(4228-4230)TGC>TGA	p.C1410*
Pat_41	Post-Resistance	ASXL2	55252	37	2	25982365	25982365	Missense_Mutation	SNP	C	T	19	312	c.925G>A	c.(925-927)GAG>AAG	p.E309K

Pat_41	Post-Resistance	ASXL2	55252	37	2	25990505	25990505	Missense_Mutation	SNP	G	A	5	93	c.722C>T	c.(721-723)ACT>ATT	p.T241I
Pat_41	Post-Resistance	ASXL2	55252	37	2	25994346	25994346	Missense_Mutation	SNP	G	A	17	180	c.467C>T	c.(466-468)TCT>TTT	p.S156F
Pat_41	Post-Resistance	KIF3C	3797	37	2	26204432	26204432	Missense_Mutation	SNP	C	T	19	198	c.355G>A	c.(355-357)GTC>ATC	p.V119I
Pat_41	Post-Resistance	HADHB	3032	37	2	26507065	26507065	Missense_Mutation	SNP	C	T	12	243	c.1142C>T	c.(1141-1143)GCT>GTT	p.A381V
Pat_41	Post-Resistance	GPR113	165082	37	2	26534851	26534851	Missense_Mutation	SNP	G	A	3	48	c.1745C>T	c.(1744-1746)ACT>ATT	p.T582I
Pat_41	Post-Resistance	OTOF	9381	37	2	26725265	26725265	Missense_Mutation	SNP	G	A	14	53	c.613C>T	c.(613-615)CTT>TTT	p.L205F
Pat_41	Post-Resistance	DPYSL5	56896	37	2	27157511	27157511	Nonsense_Mutation	SNP	C	T	46	574	c.856C>T	c.(856-858)CAG>TAG	p.Q286*
Pat_41	Post-Resistance	TMEM214	54867	37	2	27259431	27259431	Missense_Mutation	SNP	G	A	12	215	c.797G>A	c.(796-798)GGT>GAT	p.G266D
Pat_41	Post-Resistance	PREB	10113	37	2	27354608	27354608	Missense_Mutation	SNP	G	A	20	301	c.1091C>T	c.(1090-1092)TCC>TTC	p.S364F
Pat_41	Post-Resistance	CAD	790	37	2	27444165	27444165	Missense_Mutation	SNP	C	T	7	94	c.302C>T	c.(301-303)ACC>ATC	p.T101I
Pat_41	Post-Resistance	CAD	790	37	2	27447329	27447329	Missense_Mutation	SNP	G	A	10	114	c.1225G>A	c.(1225-1227)GCT>ACT	p.A409T
Pat_41	Post-Resistance	CAD	790	37	2	27465599	27465599	Missense_Mutation	SNP	C	T	24	202	c.6334C>T	c.(6334-6336)CCA>TCA	p.P2112S
Pat_41	Post-Resistance	SNX17	9784	37	2	27598548	27598548	Missense_Mutation	SNP	G	A	8	113	c.950G>A	c.(949-951)CGC>CAC	p.R317H
Pat_41	Post-Resistance	NRBP1	29959	37	2	27664656	27664656	Missense_Mutation	SNP	G	A	45	253	c.1585G>A	c.(1585-1587)GCC>ACC	p.A529T
Pat_41	Post-Resistance	IFT172	26160	37	2	27677269	27677269	Missense_Mutation	SNP	G	A	7	220	c.3482C>T	c.(3481-3483)GCT>GTT	p.A1161V
Pat_41	Post-Resistance	FNDC4	64838	37	2	27716802	27716802	Missense_Mutation	SNP	C	T	14	204	c.449G>A	c.(448-450)AGC>AAC	p.S150N
Pat_41	Post-Resistance	GCKR	2646	37	2	27746206	27746206	Missense_Mutation	SNP	C	T	8	49	c.1778C>T	c.(1777-1779)GCA>GTA	p.A593V
Pat_41	Post-Resistance	C2orf16	84226	37	2	27804067	27804067	Missense_Mutation	SNP	G	A	21	209	c.4628G>A	c.(4627-4629)AGC>AAC	p.S1543N
Pat_41	Post-Resistance	C2orf16	84226	37	2	27804870	27804870	Missense_Mutation	SNP	G	A	27	199	c.5431G>A	c.(5431-5433)GAG>AAG	p.E1811K
Pat_41	Post-Resistance	ZNF512	84450	37	2	27822521	27822521	Missense_Mutation	SNP	C	T	8	73	c.349C>T	c.(349-351)CCT>TCT	p.P117S
Pat_41	Post-Resistance	SUPT7L	9913	37	2	27878382	27878382	Missense_Mutation	SNP	C	T	7	108	c.832G>A	c.(832-834)GAA>AAA	p.E278K
Pat_41	Post-Resistance	PLB1	151056	37	2	28801018	28801018	Missense_Mutation	SNP	A	G	4	96	c.1478A>G	c.(1477-1479)AAT>AGT	p.N493S
Pat_41	Post-Resistance	PLB1	151056	37	2	28825688	28825688	Missense_Mutation	SNP	G	A	19	182	c.2674G>A	c.(2674-2676)GTG>ATG	p.V892M
Pat_41	Post-Resistance	PLB1	151056	37	2	28841216	28841216	Missense_Mutation	SNP	C	T	67	492	c.3265C>T	c.(3265-3267)CTC>TTC	p.L1089F
Pat_41	Post-Resistance	CLIP4	79745	37	2	29344297	29344297	Missense_Mutation	SNP	C	T	12	146	c.43C>T	c.(43-45)CCT>TCT	p.P15S
Pat_41	Post-Resistance	CLIP4	79745	37	2	29354184	29354184	Missense_Mutation	SNP	C	T	8	179	c.194C>T	c.(193-195)ACT>ATT	p.T65I
Pat_41	Post-Resistance	ALK	238	37	2	29416599	29416599	Missense_Mutation	SNP	C	T	17	216	c.4354G>A	c.(4354-4356)GCT>ACT	p.A1452T
Pat_41	Post-Resistance	ALK	238	37	2	29446380	29446380	Missense_Mutation	SNP	G	A	15	74	c.3187C>T	c.(3187-3189)CAC>TAC	p.H1063Y
Pat_41	Post-Resistance	ALK	238	37	2	29917868	29917868	Missense_Mutation	SNP	C	T	12	176	c.800G>A	c.(799-801)AGC>AAC	p.S267N
Pat_41	Post-Resistance	MEMO1	51072	37	2	32108531	32108531	Missense_Mutation	SNP	C	T	45	374	c.581G>A	c.(580-582)GGT>GAT	p.G194D
Pat_41	Post-Resistance	NLRC4	58484	37	2	32474873	32474873	Missense_Mutation	SNP	G	A	6	81	c.2060C>T	c.(2059-2061)GCC>GTC	p.A687V
Pat_41	Post-Resistance	NLRC4	58484	37	2	32475537	32475537	Missense_Mutation	SNP	C	T	13	169	c.1396G>A	c.(1396-1398)GAG>AAG	p.E466K
Pat_41	Post-Resistance	BIRC6	57448	37	2	32641130	32641130	Missense_Mutation	SNP	C	T	21	69	c.2771C>T	c.(2770-2772)GCC>GTC	p.A924V
Pat_41	Post-Resistance	BIRC6	57448	37	2	32715153	32715153	Missense_Mutation	SNP	C	T	33	574	c.8141C>T	c.(8140-8142)ACT>ATT	p.T2714I
Pat_41	Post-Resistance	LTBP1	4052	37	2	33246023	33246023	Nonsense_Mutation	SNP	C	T	45	567	c.613C>T	c.(613-615)CAA>TAA	p.Q205*
Pat_41	Post-Resistance	LTBP1	4052	37	2	33335776	33335776	Missense_Mutation	SNP	C	T	7	234	c.991C>T	c.(991-993)CCT>TCT	p.P331S
Pat_41	Post-Resistance	LTBP1	4052	37	2	33359917	33359917	Missense_Mutation	SNP	C	T	13	143	c.1091C>T	c.(1090-1092)ACC>ATC	p.T364I
Pat_41	Post-Resistance	FAM98A	25940	37	2	33810177	33810177	Missense_Mutation	SNP	C	T	38	202	c.1223G>A	c.(1222-1224)GGC>GAC	p.G408D
Pat_41	Post-Resistance	FAM98A	25940	37	2	33817276	33817276	Missense_Mutation	SNP	T	G	24	363	c.208A>C	c.(208-210)AGT>CGT	p.S70R
Pat_41	Post-Resistance	VIT	5212	37	2	36982107	36982107	Missense_Mutation	SNP	G	A	9	292	c.319G>A	c.(319-321)GTT>ATT	p.V107I
Pat_41	Post-Resistance	CEBPZ	10153	37	2	37443458	37443458	Splice_Site	SNP	C	T	8	105	c.2311_splice	c.e7+1	p.E771_splice
Pat_41	Post-Resistance	CDC42EP3	10602	37	2	37873007	37873007	Missense_Mutation	SNP	G	A	9	133	c.724C>T	c.(724-726)CTT>TTT	p.L242F
Pat_41	Post-Resistance	CDC42EP3	10602	37	2	37873370	37873370	Missense_Mutation	SNP	G	A	7	100	c.361C>T	c.(361-363)CCC>TCC	p.P121S
Pat_41	Post-Resistance	SOS1	6654	37	2	39213279	39213279	Missense_Mutation	SNP	G	T	22	189	c.3688C>A	c.(3688-3690)CCA>ACA	p.P1230T
Pat_41	Post-Resistance	SOS1	6654	37	2	39224083	39224083	Missense_Mutation	SNP	G	A	13	272	c.3061C>T	c.(3061-3063)CCT>TCT	p.P1021S
Pat_41	Post-Resistance	MAP4K3	8491	37	2	39553381	39553381	Missense_Mutation	SNP	C	T	29	488	c.568G>A	c.(568-570)GGT>AGT	p.G190S
Pat_41	Post-Resistance	SLC8A1	6546	37	2	40392083	40392083	Missense_Mutation	SNP	C	T	26	257	c.2080G>A	c.(2080-2082)GAG>AAG	p.E694K

Pat_41	Post-Resistance	SLC8A1	6546	37	2	40656072	40656072	Missense_Mutation	SNP	G	A	24	253	c.1349C>T	c.(1348-1350)ACA>ATA	p.T450I
Pat_41	Post-Resistance	EML4	27436	37	2	42508017	42508017	Missense_Mutation	SNP	G	A	20	95	c.695G>A	c.(694-696)CGC>CAC	p.R232H
Pat_41	Post-Resistance	LOC728819	728819	37	2	43902939	43902939	Missense_Mutation	SNP	C	T	24	426	c.523G>A	c.(523-525)GAC>AAC	p.D175N
Pat_41	Post-Resistance	PLEKHH2	130271	37	2	43939514	43939514	Missense_Mutation	SNP	C	T	4	115	c.2452C>T	c.(2452-2454)CTC>TTC	p.L818F
Pat_41	Post-Resistance	LRPPRC	10128	37	2	44176749	44176749	Missense_Mutation	SNP	C	T	19	141	c.1727G>A	c.(1726-1728)GGA>GAA	p.G576E
Pat_41	Post-Resistance	PPM1B	5495	37	2	44428835	44428835	Missense_Mutation	SNP	C	T	9	337	c.497C>T	c.(496-498)ACC>ATC	p.T166I
Pat_41	Post-Resistance	SLC3A1	6519	37	2	44541007	44541007	Missense_Mutation	SNP	G	A	7	177	c.1534G>A	c.(1534-1536)GAC>AAC	p.D512N
Pat_41	Post-Resistance	PREPL	9581	37	2	44553948	44553948	Missense_Mutation	SNP	G	A	4	111	c.1649C>T	c.(1648-1650)CCA>CTA	p.P550L
Pat_41	Post-Resistance	PRKCE	5581	37	2	46378189	46378189	Missense_Mutation	SNP	G	A	5	60	c.1741G>A	c.(1741-1743)GAG>AAG	p.E581K
Pat_41	Post-Resistance	RHOQ	23433	37	2	46770261	46770261	Missense_Mutation	SNP	C	T	25	261	c.76C>T	c.(76-78)CTC>TTC	p.L26F
Pat_41	Post-Resistance	MSH2	4436	37	2	47643505	47643505	Missense_Mutation	SNP	G	T	18	260	c.1013G>T	c.(1012-1014)GGA>GTA	p.G338V
Pat_41	Post-Resistance	KCNK12	56660	37	2	47748459	47748459	Missense_Mutation	SNP	G	A	4	24	c.880C>T	c.(880-882)CTC>TTC	p.L294F
Pat_41	Post-Resistance	MSH6	2956	37	2	48018065	48018065	Splice_Site	SNP	G	A	24	168	c.261_splice	c.e2-1	p.S87_splice
Pat_41	Post-Resistance	FOXN2	3344	37	2	48600496	48600496	Missense_Mutation	SNP	G	A	31	130	c.769G>A	c.(769-771)GAA>AAA	p.E257K
Pat_41	Post-Resistance	KLRAQ1	129285	37	2	48688296	48688296	Missense_Mutation	SNP	C	T	4	88	c.619C>T	c.(619-621)CTT>TTT	p.L207F
Pat_41	Post-Resistance	STON1-GTF2A1L	286749	37	2	48808655	48808655	Missense_Mutation	SNP	G	A	6	91	c.883G>A	c.(883-885)GGA>AGA	p.G295R
Pat_41	Post-Resistance	LHCGR	3973	37	2	48915873	48915873	Missense_Mutation	SNP	C	T	20	222	c.1063G>A	c.(1063-1065)GAT>AAT	p.D355N
Pat_41	Post-Resistance	FSHR	2492	37	2	49191017	49191017	Missense_Mutation	SNP	C	T	18	464	c.943G>A	c.(943-945)GCA>ACA	p.A315T
Pat_41	Post-Resistance	CHAC2	494143	37	2	53995144	53995144	Missense_Mutation	SNP	G	A	16	140	c.121G>A	c.(121-123)GGG>AGG	p.G41R
Pat_41	Post-Resistance	ERLEC1	27248	37	2	54040096	54040096	Missense_Mutation	SNP	G	A	5	175	c.1112G>A	c.(1111-1113)AGT>AAT	p.S371N
Pat_41	Post-Resistance	SPTBN1	6711	37	2	54858180	54858180	Missense_Mutation	SNP	C	T	17	220	c.2996C>T	c.(2995-2997)ACC>ATC	p.T999I
Pat_41	Post-Resistance	SPTBN1	6711	37	2	54880977	54880977	Nonsense_Mutation	SNP	C	T	8	63	c.5809C>T	c.(5809-5811)CAG>TAG	p.Q1937*
Pat_41	Post-Resistance	CCDC88A	55704	37	2	55518866	55518866	Missense_Mutation	SNP	C	T	9	160	c.5594G>A	c.(5593-5595)AGG>AAG	p.R1865K
Pat_41	Post-Resistance	CCDC88A	55704	37	2	55522765	55522765	Missense_Mutation	SNP	G	A	13	384	c.5516C>T	c.(5515-5517)GCT>GTT	p.A1839V
Pat_41	Post-Resistance	CCDC88A	55704	37	2	55522802	55522802	Missense_Mutation	SNP	C	T	23	475	c.5479G>A	c.(5479-5481)GAC>AAC	p.D1827N
Pat_41	Post-Resistance	PAPOLG	64895	37	2	61014666	61014666	Nonsense_Mutation	SNP	G	A	29	118	c.1307G>A	c.(1306-1308)TGG>TAG	p.W436*
Pat_41	Post-Resistance	PAPOLG	64895	37	2	61022111	61022111	Missense_Mutation	SNP	G	A	7	245	c.2068G>A	c.(2068-2070)GGA>AGA	p.G690R
Pat_41	Post-Resistance	REL	5966	37	2	61149357	61149357	Missense_Mutation	SNP	G	A	16	166	c.1547G>A	c.(1546-1548)AGC>AAC	p.S516N
Pat_41	Post-Resistance	PUS10	150962	37	2	61175236	61175236	Missense_Mutation	SNP	C	T	41	464	c.1393G>A	c.(1393-1395)GAG>AAG	p.E465K
Pat_41	Post-Resistance	USP34	9736	37	2	61524004	61524004	Nonsense_Mutation	SNP	C	T	34	512	c.4185G>A	c.(4183-4185)TGG>TGA	p.W1395*
Pat_41	Post-Resistance	B3GNT2	10678	37	2	62449597	62449597	Missense_Mutation	SNP	C	T	43	784	c.242C>T	c.(241-243)ACG>ATG	p.T81M
Pat_41	Post-Resistance	B3GNT2	10678	37	2	62449728	62449728	Missense_Mutation	SNP	T	C	33	371	c.373T>C	c.(373-375)TGC>CGC	p.C125R
Pat_41	Post-Resistance	EHBP1	23301	37	2	63176236	63176236	Missense_Mutation	SNP	C	T	8	110	c.2360C>T	c.(2359-2361)TCT>TTT	p.S787F
Pat_41	Post-Resistance	C2orf86	51057	37	2	63660953	63660953	Missense_Mutation	SNP	G	A	30	131	c.751C>T	c.(751-753)CCT>TCT	p.P251S
Pat_41	Post-Resistance	UGP2	7360	37	2	64114737	64114737	Missense_Mutation	SNP	C	T	33	425	c.1273C>T	c.(1273-1275)CCT>TCT	p.P425S
Pat_41	Post-Resistance	AFTPH	54812	37	2	64800203	64800203	Splice_Site	SNP	G	A	14	203	c.2394_splice	c.e5+1	p.Q798_splice
Pat_41	Post-Resistance	WDR92	116143	37	2	68384458	68384458	Missense_Mutation	SNP	C	T	21	146	c.118G>A	c.(118-120)GCA>ACA	p.A40T
Pat_41	Post-Resistance	PNO1	56902	37	2	68385656	68385656	Missense_Mutation	SNP	A	T	11	152	c.352A>T	c.(352-354)ATC>TTC	p.I118F
Pat_41	Post-Resistance	PNO1	56902	37	2	68389753	68389753	Missense_Mutation	SNP	C	T	15	426	c.578C>T	c.(577-579)ACC>ATC	p.T193I
Pat_41	Post-Resistance	ARHGAP25	9938	37	2	69049701	69049701	Missense_Mutation	SNP	C	T	9	165	c.1427C>T	c.(1426-1428)GCT>GTT	p.A476V
Pat_41	Post-Resistance	PCBP1	5093	37	2	70315398	70315398	Nonsense_Mutation	SNP	C	T	33	119	c.523C>T	c.(523-525)CAA>TAA	p.Q175*
Pat_41	Post-Resistance	TIA1	7072	37	2	70442564	70442564	Missense_Mutation	SNP	C	T	11	198	c.827G>A	c.(826-828)GGT>GAT	p.G276D
Pat_41	Post-Resistance	CLEC4F	165530	37	2	71044113	71044113	Nonsense_Mutation	SNP	G	A	38	256	c.400C>T	c.(400-402)CAG>TAG	p.Q134*
Pat_41	Post-Resistance	TEX261	113419	37	2	71221839	71221839	Missense_Mutation	SNP	C	T	6	39	c.49G>A	c.(49-51)GCC>ACC	p.A17T
Pat_41	Post-Resistance	MPHOSPH10	10199	37	2	71360278	71360278	Missense_Mutation	SNP	G	A	6	73	c.340G>A	c.(340-342)GAA>AAA	p.E114K
Pat_41	Post-Resistance	MPHOSPH10	10199	37	2	71368380	71368380	Missense_Mutation	SNP	C	T	6	211	c.1327C>T	c.(1327-1329)CGT>TGT	p.R443C
Pat_41	Post-Resistance	ZNF638	27332	37	2	71576166	71576166	Missense_Mutation	SNP	C	T	16	109	c.82C>T	c.(82-84)CCA>TCA	p.P28S

Pat_41	Post-Resistance	ZNF638	27332	37	2	71623280	71623280	Missense_Mutation	SNP	G	A	11	141	c.2387G>A	c.(2386-2388)GGA>GAA	p.G796E
Pat_41	Post-Resistance	ZNF638	27332	37	2	71627260	71627260	Missense_Mutation	SNP	C	T	4	123	c.2606C>T	c.(2605-2607)ACC>ATC	p.T869I
Pat_41	Post-Resistance	RAB11FIP5	26056	37	2	73315638	73315638	Missense_Mutation	SNP	C	T	19	66	c.1108G>A	c.(1108-1110)GCT>ACT	p.A370T
Pat_41	Post-Resistance	CCT7	10574	37	2	73467624	73467624	Missense_Mutation	SNP	C	T	5	110	c.220C>T	c.(220-222)CCT>TCT	p.P74S
Pat_41	Post-Resistance	FBXO41	150726	37	2	73490957	73490957	Missense_Mutation	SNP	C	T	7	40	c.2107G>A	c.(2107-2109)GGC>AGC	p.G703S
Pat_41	Post-Resistance	ALMS1	7840	37	2	73762077	73762077	Splice_Site	SNP	G	A	49	489	c.9910_splice	c.e14+1	p.G3304_splice
Pat_41	Post-Resistance	ALMS1	7840	37	2	73800181	73800181	Missense_Mutation	SNP	G	A	15	102	c.11180G>A	c.(11179-11181)GGT>GAT	p.G3727D
Pat_41	Post-Resistance	DUSP11	8446	37	2	73989876	73989876	Missense_Mutation	SNP	G	A	15	187	c.1046C>T	c.(1045-1047)GCC>GTC	p.A349V
Pat_41	Post-Resistance	ACTG2	72	37	2	74136264	74136264	Missense_Mutation	SNP	C	T	23	311	c.449C>T	c.(448-450)ACA>ATA	p.T150I
Pat_41	Post-Resistance	TET3	200424	37	2	74275025	74275025	Missense_Mutation	SNP	G	A	5	21	c.1576G>A	c.(1576-1578)GAA>AAA	p.E526K
Pat_41	Post-Resistance	SLC4A5	57835	37	2	74542125	74542125	Missense_Mutation	SNP	C	T	18	333	c.26G>A	c.(25-27)GGG>GAG	p.G9E
Pat_41	Post-Resistance	DCTN1	1639	37	2	74590452	74590452	Missense_Mutation	SNP	G	A	5	38	c.3314C>T	c.(3313-3315)TCC>TTC	p.S1105F
Pat_41	Post-Resistance	DCTN1	1639	37	2	74597318	74597318	Missense_Mutation	SNP	C	T	11	70	c.1282G>A	c.(1282-1284)GAG>AAG	p.E428K
Pat_41	Post-Resistance	RTKN	6242	37	2	74656046	74656046	Missense_Mutation	SNP	G	A	8	160	c.779C>T	c.(778-780)GCT>GTT	p.A260V
Pat_41	Post-Resistance	INO80B	83444	37	2	74683256	74683256	Missense_Mutation	SNP	C	T	7	94	c.397C>T	c.(397-399)CCA>TCA	p.P133S
Pat_41	Post-Resistance	LOXL3	84695	37	2	74761253	74761253	Missense_Mutation	SNP	C	T	27	102	c.2050G>A	c.(2050-2052)GTG>ATG	p.V684M
Pat_41	Post-Resistance	LOXL3	84695	37	2	74762821	74762821	Missense_Mutation	SNP	G	A	7	46	c.1310C>T	c.(1309-1311)CCT>CTT	p.P437L
Pat_41	Post-Resistance	DOK1	1796	37	2	74784033	74784033	Missense_Mutation	SNP	C	T	28	488	c.1238C>T	c.(1237-1239)CCC>CTC	p.P413L
Pat_41	Post-Resistance	HK2	3099	37	2	75094799	75094799	Missense_Mutation	SNP	C	T	57	656	c.263C>T	c.(262-264)ACC>ATC	p.T88I
Pat_41	Post-Resistance	TGOLN2	10618	37	2	85553665	85553665	Missense_Mutation	SNP	G	A	32	245	c.1190C>T	c.(1189-1191)GCT>GTT	p.A397V
Pat_41	Post-Resistance	RETSAT	54884	37	2	85577249	85577249	Missense_Mutation	SNP	G	A	25	188	c.713C>T	c.(712-714)TCC>TTC	p.S238F
Pat_41	Post-Resistance	USP39	10713	37	2	85850775	85850775	Missense_Mutation	SNP	G	A	44	650	c.440G>A	c.(439-441)GGT>GAT	p.G147D
Pat_41	Post-Resistance	POLR1A	25885	37	2	86297328	86297328	Missense_Mutation	SNP	G	A	13	96	c.1679C>T	c.(1678-1680)TCC>TTC	p.S560F
Pat_41	Post-Resistance	KDM3A	55818	37	2	86701976	86701976	Missense_Mutation	SNP	G	A	50	362	c.1802G>A	c.(1801-1803)GGC>GAC	p.G601D
Pat_41	Post-Resistance	KDM3A	55818	37	2	86707369	86707369	Missense_Mutation	SNP	G	A	11	82	c.2396G>A	c.(2395-2397)GGT>GAT	p.G799D
Pat_41	Post-Resistance	VPS24	51652	37	2	86756464	86756464	Missense_Mutation	SNP	C	T	21	232	c.163G>A	c.(163-165)GGC>AGC	p.G55S
Pat_41	Post-Resistance	VPS24	51652	37	2	86790432	86790432	Missense_Mutation	SNP	C	T	50	553	c.40G>A	c.(40-42)GAA>AAA	p.E14K
Pat_41	Post-Resistance	RNF103	7844	37	2	86831817	86831817	Missense_Mutation	SNP	C	T	9	89	c.1207G>A	c.(1207-1209)GCT>ACT	p.A403T
Pat_41	Post-Resistance	TEKT4	150483	37	2	95540645	95540645	Missense_Mutation	SNP	G	A	5	15	c.838G>A	c.(838-840)GAC>AAC	p.D280N
Pat_41	Post-Resistance	ZNF514	84874	37	2	95818919	95818919	Missense_Mutation	SNP	C	T	21	209	c.80G>A	c.(79-81)AGG>AAG	p.R27K
Pat_41	Post-Resistance	FAHD2A	51011	37	2	96071313	96071313	Missense_Mutation	SNP	G	A	6	98	c.7G>A	c.(7-9)GTG>ATG	p.V3M
Pat_41	Post-Resistance	FER1L5	90342	37	2	97370253	97370253	Missense_Mutation	SNP	C	T	19	243	c.6106C>T	c.(6106-6108)CCC>TCC	p.P2036S
Pat_41	Post-Resistance	SEMA4C	54910	37	2	97527532	97527532	Missense_Mutation	SNP	G	A	10	65	c.1543C>T	c.(1543-1545)CCC>TCC	p.P515S
Pat_41	Post-Resistance	VWA3B	200403	37	2	98866818	98866818	Missense_Mutation	SNP	A	C	68	89	c.2711A>C	c.(2710-2712)AAG>ACG	p.K904T
Pat_41	Post-Resistance	UNC50	25972	37	2	99232764	99232764	Missense_Mutation	SNP	C	T	36	205	c.496C>T	c.(496-498)CCA>TCA	p.P166S
Pat_41	Post-Resistance	MGAT4A	11320	37	2	99291564	99291564	Missense_Mutation	SNP	G	A	12	143	c.337C>T	c.(337-339)CCT>TCT	p.P113S
Pat_41	Post-Resistance	TSGA10	80705	37	2	99651772	99651772	Missense_Mutation	SNP	C	T	16	107	c.1535G>A	c.(1534-1536)AGG>AAG	p.R512K
Pat_41	Post-Resistance	EIF5B	9669	37	2	99980878	99980878	Missense_Mutation	SNP	G	A	23	372	c.1282G>A	c.(1282-1284)GCT>ACT	p.A428T
Pat_41	Post-Resistance	EIF5B	9669	37	2	99995860	99995860	Missense_Mutation	SNP	C	T	9	121	c.2030C>T	c.(2029-2031)GCT>GTT	p.A677V
Pat_41	Post-Resistance	REV1	51455	37	2	100065967	100065967	Splice_Site	SNP	C	T	4	63	c.182_splice	c.e4-1	p.D61_splice
Pat_41	Post-Resistance	CREG2	200407	37	2	102000094	102000094	Missense_Mutation	SNP	G	A	9	75	c.512C>T	c.(511-513)CCT>CTT	p.P171L
Pat_41	Post-Resistance	IL1RL2	8808	37	2	102851396	102851396	Missense_Mutation	SNP	G	A	18	145	c.1337G>A	c.(1336-1338)AGG>AAG	p.R446K
Pat_41	Post-Resistance	IL18RAP	8807	37	2	103063647	103063647	Missense_Mutation	SNP	G	A	14	522	c.1190G>A	c.(1189-1191)AGC>AAC	p.S397N
Pat_41	Post-Resistance	SLC9A2	6549	37	2	103274281	103274281	Missense_Mutation	SNP	G	A	46	433	c.548G>A	c.(547-549)GGC>GAC	p.G183D
Pat_41	Post-Resistance	SLC9A2	6549	37	2	103324775	103324775	Missense_Mutation	SNP	G	A	50	257	c.2266G>A	c.(2266-2268)GGC>AGC	p.G756S
Pat_41	Post-Resistance	TMEM182	130827	37	2	103379073	103379073	Missense_Mutation	SNP	G	A	22	192	c.160G>A	c.(160-162)GGG>AGG	p.G54R
Pat_41	Post-Resistance	C2orf49	79074	37	2	105959681	105959681	Splice_Site	SNP	G	A	8	38	c.642_splice	c.e3+1	p.M214_splice

Pat_41	Post-Resistance	UXS1	80146	37	2	106739425	106739425	Splice_Site	SNP	C	T	9	195	c.744_splice	c.e9+1	p.Q248_splice
Pat_41	Post-Resistance	RGPD3	653489	37	2	107041181	107041181	Missense_Mutation	SNP	C	T	103	424	c.3242G>A	c.(3241-3243)GGC>GAC	p.G1081D
Pat_41	Post-Resistance	ST6GAL2	84620	37	2	107459547	107459547	Missense_Mutation	SNP	C	T	4	24	c.887G>A	c.(886-888)TGC>TAC	p.C296Y
Pat_41	Post-Resistance	ST6GAL2	84620	37	2	107460014	107460014	Nonsense_Mutation	SNP	C	T	22	219	c.420G>A	c.(418-420)TGG>TGA	p.W140*
Pat_41	Post-Resistance	RGPD4	285190	37	2	108488208	108488208	Missense_Mutation	SNP	G	A	54	420	c.3748G>A	c.(3748-3750)GAT>AAT	p.D1250N
Pat_41	Post-Resistance	RGPD4	285190	37	2	108488274	108488274	Missense_Mutation	SNP	C	T	38	426	c.3814C>T	c.(3814-3816)CCA>TCA	p.P1272S
Pat_41	Post-Resistance	SULT1C3	442038	37	2	108875240	108875240	Missense_Mutation	SNP	G	A	18	172	c.577G>A	c.(577-579)GAC>AAC	p.D193N
Pat_41	Post-Resistance	GCC2	9648	37	2	109086800	109086800	Missense_Mutation	SNP	G	A	7	39	c.1015G>A	c.(1015-1017)GAT>AAT	p.D339N
Pat_41	Post-Resistance	GCC2	9648	37	2	109087679	109087679	Missense_Mutation	SNP	G	A	15	186	c.1894G>A	c.(1894-1896)GAG>AAG	p.E632K
Pat_41	Post-Resistance	RANBP2	5903	37	2	109383056	109383056	Missense_Mutation	SNP	G	A	32	506	c.6061G>A	c.(6061-6063)GAA>AAA	p.E2021K
Pat_41	Post-Resistance	RANBP2	5903	37	2	109384545	109384545	Missense_Mutation	SNP	G	A	14	599	c.7550G>A	c.(7549-7551)GGT>GAT	p.G2517D
Pat_41	Post-Resistance	RANBP2	5903	37	2	109399254	109399254	Missense_Mutation	SNP	G	A	22	306	c.9305G>A	c.(9304-9306)GGA>GAA	p.G3102E
Pat_41	Post-Resistance	CCDC138	165055	37	2	109404537	109404537	Missense_Mutation	SNP	C	T	8	70	c.143C>T	c.(142-144)ACC>ATC	p.T48I
Pat_41	Post-Resistance	NPHP1	4867	37	2	110926131	110926131	Splice_Site	SNP	C	T	3	54	c.523_splice	c.e6-1	p.K175_splice
Pat_41	Post-Resistance	ANAPC1	64682	37	2	112615898	112615898	Missense_Mutation	SNP	G	A	6	129	c.1343C>T	c.(1342-1344)TCC>TTC	p.S448F
Pat_41	Post-Resistance	MERTK	10461	37	2	112751934	112751934	Missense_Mutation	SNP	G	A	25	245	c.1403G>A	c.(1402-1404)GGA>GAA	p.G468E
Pat_41	Post-Resistance	TMEM87B	84910	37	2	112843588	112843588	Missense_Mutation	SNP	G	A	5	53	c.845G>A	c.(844-846)GGC>GAC	p.G282D
Pat_41	Post-Resistance	POLR1B	84172	37	2	113305001	113305001	Missense_Mutation	SNP	G	A	12	242	c.349G>A	c.(349-351)GAT>AAT	p.D117N
Pat_41	Post-Resistance	POLR1B	84172	37	2	113316891	113316891	Missense_Mutation	SNP	C	T	82	461	c.1352C>T	c.(1351-1353)TCT>TTT	p.S451F
Pat_41	Post-Resistance	POLR1B	84172	37	2	113333019	113333019	Missense_Mutation	SNP	G	A	82	161	c.3121G>A	c.(3121-3123)GAA>AAA	p.E1041K
Pat_41	Post-Resistance	PSD4	23550	37	2	113942976	113942976	Missense_Mutation	SNP	G	A	24	96	c.1208G>A	c.(1207-1209)GGT>GAT	p.G403D
Pat_41	Post-Resistance	PSD4	23550	37	2	113955140	113955140	Splice_Site	SNP	G	A	4	91	c.2387_splice	c.e13-1	p.T796_splice
Pat_41	Post-Resistance	DPP10	57628	37	2	116599842	116599842	Missense_Mutation	SNP	G	A	5	125	c.2312G>A	c.(2311-2313)AGC>AAC	p.S771N
Pat_41	Post-Resistance	DDX18	8886	37	2	118583129	118583129	Missense_Mutation	SNP	C	T	51	180	c.1475C>T	c.(1474-1476)CCT>CTT	p.P492L
Pat_41	Post-Resistance	MARCO	8685	37	2	119739968	119739968	Missense_Mutation	SNP	G	A	9	101	c.1045G>A	c.(1045-1047)GGA>AGA	p.G349R
Pat_41	Post-Resistance	TMEM37	140738	37	2	120194496	120194496	Missense_Mutation	SNP	G	A	3	42	c.53G>A	c.(52-54)CGC>CAC	p.R18H
Pat_41	Post-Resistance	TMEM37	140738	37	2	120194946	120194946	Missense_Mutation	SNP	C	T	29	422	c.503C>T	c.(502-504)GCC>GTC	p.A168V
Pat_41	Post-Resistance	SCTR	6344	37	2	120252123	120252123	Missense_Mutation	SNP	G	A	10	115	c.74C>T	c.(73-75)ACT>ATT	p.T25I
Pat_41	Post-Resistance	TMEM177	80775	37	2	120438577	120438577	Missense_Mutation	SNP	C	T	12	222	c.148C>T	c.(148-150)CCT>TCT	p.P50S
Pat_41	Post-Resistance	PTPN4	5775	37	2	120643453	120643453	Missense_Mutation	SNP	G	A	11	192	c.670G>A	c.(670-672)GCA>ACA	p.A224T
Pat_41	Post-Resistance	EPB41L5	57669	37	2	120776715	120776715	Missense_Mutation	SNP	G	A	70	615	c.55G>A	c.(55-57)GAG>AAG	p.E19K
Pat_41	Post-Resistance	EPB41L5	57669	37	2	120776841	120776841	Splice_Site	SNP	G	A	23	304	c.180_splice	c.e2+1	p.P60_splice
Pat_41	Post-Resistance	GLI2	2736	37	2	121747352	121747352	Missense_Mutation	SNP	G	A	8	69	c.3862G>A	c.(3862-3864)GTG>ATG	p.V1288M
Pat_41	Post-Resistance	TFCP2L1	29842	37	2	122006620	122006620	Missense_Mutation	SNP	G	A	4	34	c.335C>T	c.(334-336)ACG>ATG	p.T112M
Pat_41	Post-Resistance	TFCP2L1	29842	37	2	122038726	122038726	Missense_Mutation	SNP	G	A	23	156	c.184C>T	c.(184-186)CAT>TAT	p.H62Y
Pat_41	Post-Resistance	MKI67IP	84365	37	2	122485887	122485887	Missense_Mutation	SNP	G	A	9	70	c.670C>T	c.(670-672)CCT>TCT	p.P224S
Pat_41	Post-Resistance	CNTNAP5	129684	37	2	124999929	124999929	Missense_Mutation	SNP	G	A	8	108	c.340G>A	c.(340-342)GGA>AGA	p.G114R
Pat_41	Post-Resistance	GYPC	2995	37	2	127453576	127453576	Missense_Mutation	SNP	G	A	47	335	c.245G>A	c.(244-246)CGC>CAC	p.R82H
Pat_41	Post-Resistance	BIN1	274	37	2	127864485	127864485	Missense_Mutation	SNP	C	T	4	76	c.35G>A	c.(34-36)GGA>GAA	p.G12E
Pat_41	Post-Resistance	CYP27C1	339761	37	2	127957069	127957069	Missense_Mutation	SNP	C	T	15	48	c.435G>A	c.(433-435)ATG>ATA	p.M145I
Pat_41	Post-Resistance	ERCC3	2071	37	2	128044527	128044527	Missense_Mutation	SNP	C	T	18	193	c.1094G>A	c.(1093-1095)GGC>GAC	p.G365D
Pat_41	Post-Resistance	IWS1	55677	37	2	128250895	128250895	Missense_Mutation	SNP	G	A	4	132	c.1891C>T	c.(1891-1893)CTC>TTC	p.L631F
Pat_41	Post-Resistance	MYO7B	4648	37	2	128384589	128384589	Nonsense_Mutation	SNP	C	T	6	37	c.4177C>T	c.(4177-4179)CGA>TGA	p.R1393*
Pat_41	Post-Resistance	WDR33	55339	37	2	128477840	128477840	Missense_Mutation	SNP	G	A	21	172	c.1759C>T	c.(1759-1761)CCT>TCT	p.P587S
Pat_41	Post-Resistance	RAB6C	84084	37	2	130738091	130738091	Nonsense_Mutation	SNP	C	T	42	440	c.403C>T	c.(403-405)CAA>TAA	p.Q135*
Pat_41	Post-Resistance	POTEF	728378	37	2	130877782	130877782	Missense_Mutation	SNP	A	G	12	299	c.307T>C	c.(307-309)TGC>CGC	p.C103R
Pat_41	Post-Resistance	ARHGEF4	50649	37	2	131798881	131798881	Missense_Mutation	SNP	C	T	33	251	c.1183C>T	c.(1183-1185)CTC>TTC	p.L395F

Pat_41	Post-Resistance	PLEKHB2	55041	37	2	131888310	131888310	Missense_Mutation	SNP	C	T	5	74	c.310C>T	c.(310-312)CTC>TTC	p.L104F
Pat_41	Post-Resistance	TUBA3D	113457	37	2	132237838	132237838	Missense_Mutation	SNP	C	T	12	302	c.572C>T	c.(571-573)ACC>ATC	p.T191I
Pat_41	Post-Resistance	GPR39	2863	37	2	133174850	133174850	Missense_Mutation	SNP	G	A	15	171	c.235G>A	c.(235-237)GAC>AAC	p.D79N
Pat_41	Post-Resistance	LYPD1	116372	37	2	133426065	133426065	Missense_Mutation	SNP	A	G	7	69	c.98T>C	c.(97-99)CTG>CCG	p.L33P
Pat_41	Post-Resistance	NCKAP5	344148	37	2	133486419	133486419	Nonsense_Mutation	SNP	C	T	30	308	c.5550G>A	c.(5548-5550)TGG>TGA	p.W1850*
Pat_41	Post-Resistance	YSK4	80122	37	2	135738500	135738500	Missense_Mutation	SNP	C	T	12	72	c.3811G>A	c.(3811-3813)GAC>AAC	p.D1271N
Pat_41	Post-Resistance	RAB3GAP1	22930	37	2	135809891	135809891	Missense_Mutation	SNP	G	A	9	40	c.14G>A	c.(13-15)AGT>AAT	p.S5N
Pat_41	Post-Resistance	DARS	1615	37	2	136668717	136668717	Missense_Mutation	SNP	C	T	8	106	c.1406G>A	c.(1405-1407)GGA>GAA	p.G469E
Pat_41	Post-Resistance	THSD7B	80731	37	2	137852567	137852567	Missense_Mutation	SNP	C	T	9	37	c.982C>T	c.(982-984)CCA>TCA	p.P328S
Pat_41	Post-Resistance	ACVR2A	92	37	2	148677894	148677894	Missense_Mutation	SNP	C	T	12	148	c.1058C>T	c.(1057-1059)GCA>GTA	p.A353V
Pat_41	Post-Resistance	MBD5	55777	37	2	149247133	149247133	Missense_Mutation	SNP	G	A	14	146	c.3233G>A	c.(3232-3234)GGT>GAT	p.G1078D
Pat_41	Post-Resistance	EPC2	26122	37	2	149520303	149520303	Missense_Mutation	SNP	G	A	6	47	c.880G>A	c.(880-882)GAG>AAG	p.E294K
Pat_41	Post-Resistance	RIF1	55183	37	2	152273165	152273165	Missense_Mutation	SNP	C	T	42	698	c.371C>T	c.(370-372)TCT>TTT	p.S124F
Pat_41	Post-Resistance	RIF1	55183	37	2	152322461	152322461	Missense_Mutation	SNP	G	A	4	82	c.6427G>A	c.(6427-6429)GCA>ACA	p.A2143T
Pat_41	Post-Resistance	NEB	4703	37	2	152409277	152409277	Missense_Mutation	SNP	G	A	7	62	c.14642C>T	c.(14641-14643)GCT>GTT	p.A4881V
Pat_41	Post-Resistance	NEB	4703	37	2	152426597	152426597	Missense_Mutation	SNP	C	T	12	24	c.12325G>A	c.(12325-12327)GAT>AAT	p.D4109N
Pat_41	Post-Resistance	CACNB4	785	37	2	152739806	152739806	Missense_Mutation	SNP	C	T	23	349	c.226G>A	c.(226-228)GAG>AAG	p.E76K
Pat_41	Post-Resistance	PRPF40A	55660	37	2	153535943	153535943	Missense_Mutation	SNP	G	A	4	10	c.581C>T	c.(580-582)TCT>TTT	p.S194F
Pat_41	Post-Resistance	GPD2	2820	37	2	157414034	157414034	Missense_Mutation	SNP	G	A	10	145	c.1105G>A	c.(1105-1107)GAA>AAA	p.E369K
Pat_41	Post-Resistance	ACVR1	90	37	2	158617440	158617440	Missense_Mutation	SNP	C	T	6	99	c.1216G>A	c.(1216-1218)GCC>ACC	p.A406T
Pat_41	Post-Resistance	DAPL1	92196	37	2	159663569	159663569	Missense_Mutation	SNP	C	T	7	135	c.149C>T	c.(148-150)GCC>GTC	p.A50V
Pat_41	Post-Resistance	TANC1	85461	37	2	160053240	160053240	Missense_Mutation	SNP	C	T	7	177	c.3101C>T	c.(3100-3102)ACC>ATC	p.T1034I
Pat_41	Post-Resistance	TANC1	85461	37	2	160076253	160076253	Missense_Mutation	SNP	G	A	14	98	c.3553G>A	c.(3553-3555)GCT>ACT	p.A1185T
Pat_41	Post-Resistance	WDSUB1	151525	37	2	160139436	160139436	Missense_Mutation	SNP	G	A	5	140	c.145C>T	c.(145-147)CCA>TCA	p.P49S
Pat_41	Post-Resistance	7-Mar	64844	37	2	160599612	160599612	Missense_Mutation	SNP	C	T	9	254	c.194C>T	c.(193-195)GCA>GTA	p.A65V
Pat_41	Post-Resistance	LY75	4065	37	2	160663489	160663489	Missense_Mutation	SNP	G	A	12	204	c.4985C>T	c.(4984-4986)CCT>CTT	p.P1662L
Pat_41	Post-Resistance	LY75	4065	37	2	160690699	160690699	Missense_Mutation	SNP	G	A	99	156	c.3697C>T	c.(3697-3699)CCA>TCA	p.P1233S
Pat_41	Post-Resistance	ITGB6	3694	37	2	160958260	160958260	Missense_Mutation	SNP	G	A	5	90	c.2354C>T	c.(2353-2355)TCC>TTC	p.S785F
Pat_41	Post-Resistance	IFIH1	64135	37	2	163133374	163133374	Missense_Mutation	SNP	C	T	16	251	c.2127G>A	c.(2125-2127)ATG>ATA	p.M709I
Pat_41	Post-Resistance	IFIH1	64135	37	2	163137899	163137899	Missense_Mutation	SNP	G	A	18	225	c.1463C>T	c.(1462-1464)ACA>ATA	p.T488I
Pat_41	Post-Resistance	COBLL1	22837	37	2	165550903	165550903	Missense_Mutation	SNP	C	T	7	109	c.3314G>A	c.(3313-3315)AGT>AAT	p.S1105N
Pat_41	Post-Resistance	SLC38A11	151258	37	2	165765269	165765269	Missense_Mutation	SNP	C	T	9	215	c.808G>A	c.(808-810)GTG>ATG	p.V270M
Pat_41	Post-Resistance	SCN3A	6328	37	2	165994501	165994501	Missense_Mutation	SNP	G	A	19	250	c.2279C>T	c.(2278-2280)CCA>CTA	p.P760L
Pat_41	Post-Resistance	SCN3A	6328	37	2	165996042	165996042	Missense_Mutation	SNP	G	A	13	196	c.2096C>T	c.(2095-2097)TCC>TTC	p.S699F
Pat_41	Post-Resistance	SCN2A	6326	37	2	166170192	166170192	Missense_Mutation	SNP	G	A	25	160	c.1097G>A	c.(1096-1098)AGC>AAC	p.S366N
Pat_41	Post-Resistance	SCN2A	6326	37	2	166179958	166179958	Missense_Mutation	SNP	C	T	11	83	c.1964C>T	c.(1963-1965)TCC>TTC	p.S655F
Pat_41	Post-Resistance	SCN2A	6326	37	2	166245950	166245950	Missense_Mutation	SNP	G	C	6	125	c.5634G>C	c.(5632-5634)CAG>CAC	p.Q1878H
Pat_41	Post-Resistance	CSRNP3	80034	37	2	166535401	166535401	Missense_Mutation	SNP	G	A	26	164	c.896G>A	c.(895-897)AGT>AAT	p.S299N
Pat_41	Post-Resistance	SCN1A	6323	37	2	166915152	166915152	Missense_Mutation	SNP	G	A	15	116	c.311C>T	c.(310-312)GCC>GTC	p.A104V
Pat_41	Post-Resistance	SCN9A	6335	37	2	167056222	167056222	Missense_Mutation	SNP	C	T	30	280	c.4894G>A	c.(4894-4896)GCG>ACG	p.A1632T
Pat_41	Post-Resistance	NOSTRIN	115677	37	2	169711956	169711956	Missense_Mutation	SNP	C	T	4	46	c.950C>T	c.(949-951)TCA>TTA	p.S317L
Pat_41	Post-Resistance	ABCB11	8647	37	2	169874631	169874631	Missense_Mutation	SNP	G	A	5	122	c.5C>T	c.(4-6)TCT>TTT	p.S2F
Pat_41	Post-Resistance	LRP2	4036	37	2	170026233	170026233	Missense_Mutation	SNP	C	T	30	399	c.11476G>A	c.(11476-11478)GCG>ACG	p.A3826T
Pat_41	Post-Resistance	LRP2	4036	37	2	170096163	170096163	Missense_Mutation	SNP	C	T	16	149	c.4168G>A	c.(4168-4170)GAC>AAC	p.D1390N
Pat_41	Post-Resistance	UBR3	130507	37	2	170843250	170843250	Missense_Mutation	SNP	C	T	18	268	c.3730C>T	c.(3730-3732)CCC>TCC	p.P1244S
Pat_41	Post-Resistance	MYO3B	140469	37	2	171356256	171356256	Missense_Mutation	SNP	G	A	11	136	c.3227G>A	c.(3226-3228)GGA>GAA	p.G1076E
Pat_41	Post-Resistance	MYO3B	140469	37	2	171356268	171356268	Missense_Mutation	SNP	A	G	15	120	c.3239A>G	c.(3238-3240)TAC>TGC	p.Y1080C

Pat_41	Post-Resistance	MAP1D	254042	37	2	172926384	172926384	Splice_Site	SNP	G	A	22	352	c.198_splice	c.e2+1	p.K66_splice
Pat_41	Post-Resistance	MAP1D	254042	37	2	172935770	172935770	Missense_Mutation	SNP	C	T	5	32	c.676C>T	c.(676-678)CCC>TCC	p.P226S
Pat_41	Post-Resistance	DLX2	1746	37	2	172965299	172965299	Missense_Mutation	SNP	G	A	9	104	c.959C>T	c.(958-960)GCC>GTC	p.A320V
Pat_41	Post-Resistance	SP3	6670	37	2	174820032	174820032	Missense_Mutation	SNP	G	A	14	106	c.1208C>T	c.(1207-1209)TCT>TTT	p.S403F
Pat_41	Post-Resistance	GPR155	151556	37	2	175311340	175311340	Missense_Mutation	SNP	G	A	10	139	c.2012C>T	c.(2011-2013)GCT>GTT	p.A671V
Pat_41	Post-Resistance	GPR155	151556	37	2	175333744	175333744	Missense_Mutation	SNP	C	T	5	253	c.1078G>A	c.(1078-1080)GTT>ATT	p.V360I
Pat_41	Post-Resistance	MTX2	10651	37	2	177188121	177188121	Missense_Mutation	SNP	C	T	10	242	c.137C>T	c.(136-138)GCC>GTC	p.A46V
Pat_41	Post-Resistance	RBM45	129831	37	2	178977382	178977382	Missense_Mutation	SNP	C	T	9	80	c.109C>T	c.(109-111)CCT>TCT	p.P37S
Pat_41	Post-Resistance	OSBPL6	114880	37	2	179213954	179213954	Missense_Mutation	SNP	C	T	50	545	c.991C>T	c.(991-993)CCT>TCT	p.P331S
Pat_41	Post-Resistance	DFNB59	494513	37	2	179323262	179323262	Missense_Mutation	SNP	C	T	7	98	c.575C>T	c.(574-576)CCC>CTC	p.P192L
Pat_41	Post-Resistance	TTN	7273	37	2	179396353	179396353	Missense_Mutation	SNP	G	A	5	57	c.97285C>T	c.(97285-97287)CTC>TTC	p.L32429F
Pat_41	Post-Resistance	TTN	7273	37	2	179399496	179399496	Missense_Mutation	SNP	G	A	4	50	c.94142C>T	c.(94141-94143)ACC>ATC	p.T31381I
Pat_41	Post-Resistance	TTN	7273	37	2	179404897	179404897	Missense_Mutation	SNP	G	A	58	578	c.90292C>T	c.(90292-90294)CCT>TCT	p.P30098S
Pat_41	Post-Resistance	TTN	7273	37	2	179425690	179425690	Missense_Mutation	SNP	G	A	5	110	c.77465C>T	c.(77464-77466)TCC>TTC	p.S25822F
Pat_41	Post-Resistance	TTN	7273	37	2	179431165	179431165	Missense_Mutation	SNP	G	A	12	273	c.71990C>T	c.(71989-71991)GCC>GTC	p.A23997V
Pat_41	Post-Resistance	TTN	7273	37	2	179441092	179441092	Missense_Mutation	SNP	G	A	10	44	c.62063C>T	c.(62062-62064)TCT>TTT	p.S20688F
Pat_41	Post-Resistance	TTN	7273	37	2	179482973	179482973	Missense_Mutation	SNP	C	T	47	460	c.39508G>A	c.(39508-39510)GTT>ATT	p.V13170I
Pat_41	Post-Resistance	TTN	7273	37	2	179495564	179495564	Nonsense_Mutation	SNP	C	T	7	210	c.36417G>A	c.(36415-36417)TGG>TGA	p.W12139*
Pat_41	Post-Resistance	TTN	7273	37	2	179516255	179516255	Missense_Mutation	SNP	C	T	5	42	c.32170G>A	c.(32170-32172)GTG>ATG	p.V10724M
Pat_41	Post-Resistance	TTN	7273	37	2	179544687	179544687	Missense_Mutation	SNP	C	T	10	56	c.29782G>A	c.(29782-29784)GAG>AAG	p.E9928K
Pat_41	Post-Resistance	TTN	7273	37	2	179575875	179575875	Missense_Mutation	SNP	G	A	28	188	c.24356C>T	c.(24355-24357)ACT>ATT	p.T8119I
Pat_41	Post-Resistance	TTN	7273	37	2	179578665	179578665	Missense_Mutation	SNP	G	A	5	94	c.22988C>T	c.(22987-22989)CCT>CTT	p.P7663L
Pat_41	Post-Resistance	TTN	7273	37	2	179586661	179586661	Missense_Mutation	SNP	C	T	29	156	c.18997G>A	c.(18997-18999)GTA>ATA	p.V6333I
Pat_41	Post-Resistance	TTN	7273	37	2	179594477	179594477	Missense_Mutation	SNP	G	A	20	205	c.14771C>T	c.(14770-14772)GCC>GTC	p.A4924V
Pat_41	Post-Resistance	TTN	7273	37	2	179611780	179611780	Missense_Mutation	SNP	C	T	13	137	c.15347G>A	c.(15346-15348)AGA>AAA	p.R5116K
Pat_41	Post-Resistance	TTN	7273	37	2	179638404	179638404	Missense_Mutation	SNP	G	A	29	171	c.7379C>T	c.(7378-7380)ACC>ATC	p.T2460I
Pat_41	Post-Resistance	TTN	7273	37	2	179643629	179643629	Missense_Mutation	SNP	G	A	17	104	c.4180C>T	c.(4180-4182)CCC>TCC	p.P1394S
Pat_41	Post-Resistance	TTN	7273	37	2	179644795	179644795	Missense_Mutation	SNP	C	T	4	69	c.3661G>A	c.(3661-3663)GAA>AAA	p.E1221K
Pat_41	Post-Resistance	ITGA4	3676	37	2	182359509	182359509	Nonsense_Mutation	SNP	C	T	68	305	c.1309C>T	c.(1309-1311)CAA>TAA	p.Q437*
Pat_41	Post-Resistance	NCKAP1	10787	37	2	183792864	183792864	Missense_Mutation	SNP	C	T	28	181	c.3161G>A	c.(3160-3162)CGT>CAT	p.R1054H
Pat_41	Post-Resistance	NCKAP1	10787	37	2	183817944	183817944	Missense_Mutation	SNP	C	T	21	121	c.2269G>A	c.(2269-2271)GTG>ATG	p.V757M
Pat_41	Post-Resistance	ITGAV	3685	37	2	187519436	187519436	Splice_Site	SNP	G	A	4	107	c.1564_splice	c.e16+1	p.N522_splice
Pat_41	Post-Resistance	FAM171B	165215	37	2	187627083	187627083	Missense_Mutation	SNP	G	A	15	118	c.2014G>A	c.(2014-2016)GCC>ACC	p.A672T
Pat_41	Post-Resistance	COL3A1	1281	37	2	189849566	189849566	Missense_Mutation	SNP	G	A	11	314	c.160G>A	c.(160-162)GTC>ATC	p.V54I
Pat_41	Post-Resistance	COL3A1	1281	37	2	189868140	189868140	Missense_Mutation	SNP	C	T	8	84	c.2557C>T	c.(2557-2559)CCT>TCT	p.P853S
Pat_41	Post-Resistance	SLC40A1	30061	37	2	190436512	190436512	Missense_Mutation	SNP	G	A	38	335	c.443C>T	c.(442-444)ACT>ATT	p.T148I
Pat_41	Post-Resistance	ASNSD1	54529	37	2	190532629	190532629	Missense_Mutation	SNP	G	A	54	315	c.1604G>A	c.(1603-1605)GGT>GAT	p.G535D
Pat_41	Post-Resistance	ANKAR	150709	37	2	190593096	190593096	Missense_Mutation	SNP	G	A	19	83	c.2768G>A	c.(2767-2769)AGC>AAC	p.S923N
Pat_41	Post-Resistance	INPP1	3628	37	2	191235635	191235635	Missense_Mutation	SNP	C	T	8	446	c.707C>T	c.(706-708)ACC>ATC	p.T236I
Pat_41	Post-Resistance	STAT1	6772	37	2	191844559	191844559	Missense_Mutation	SNP	G	A	13	53	c.1666C>T	c.(1666-1668)CTT>TTT	p.L556F
Pat_41	Post-Resistance	MYO1B	4430	37	2	192256880	192256880	Missense_Mutation	SNP	G	A	7	160	c.2029G>A	c.(2029-2031)GAA>AAA	p.E677K
Pat_41	Post-Resistance	OBFC2A	64859	37	2	192548984	192548984	Missense_Mutation	SNP	T	C	32	319	c.407T>C	c.(406-408)ATG>ACG	p.M136T
Pat_41	Post-Resistance	SDPR	8436	37	2	192711237	192711237	Missense_Mutation	SNP	C	T	4	78	c.415G>A	c.(415-417)GTG>ATG	p.V139M
Pat_41	Post-Resistance	TMEFF2	23671	37	2	192863893	192863893	Missense_Mutation	SNP	G	A	21	107	c.578C>T	c.(577-579)CCC>CTC	p.P193L
Pat_41	Post-Resistance	DNAH7	56171	37	2	196726664	196726664	Missense_Mutation	SNP	G	A	10	79	c.7513C>T	c.(7513-7515)CCT>TCT	p.P2505S
Pat_41	Post-Resistance	DNAH7	56171	37	2	196851812	196851812	Missense_Mutation	SNP	C	T	7	96	c.1732G>A	c.(1732-1734)GAT>AAT	p.D578N
Pat_41	Post-Resistance	DNAH7	56171	37	2	196889208	196889208	Missense_Mutation	SNP	G	A	4	27	c.688C>T	c.(688-690)CCT>TCT	p.P230S

Pat_41	Post-Resistance	GTF3C3	9330	37	2	197645291	197645291	Missense_Mutation	SNP	G	A	15	239	c.1210C>T	c.(1210-1212)CCA>TCA	p.P404S
Pat_41	Post-Resistance	GTF3C3	9330	37	2	197654056	197654056	Nonsense_Mutation	SNP	C	T	5	76	c.765G>A	c.(763-765)TGG>TGA	p.W255*
Pat_41	Post-Resistance	MOBKL3	25843	37	2	198404858	198404858	Missense_Mutation	SNP	G	A	10	120	c.248G>A	c.(247-249)GGA>GAA	p.G83E
Pat_41	Post-Resistance	RFTN2	130132	37	2	198436751	198436751	Missense_Mutation	SNP	G	A	8	112	c.1487C>T	c.(1486-1488)ACT>ATT	p.T496I
Pat_41	Post-Resistance	MARS2	92935	37	2	198571186	198571186	Missense_Mutation	SNP	G	A	53	585	c.1057G>A	c.(1057-1059)GGC>AGC	p.G353S
Pat_41	Post-Resistance	PLCL1	5334	37	2	198948668	198948668	Missense_Mutation	SNP	G	A	6	33	c.427G>A	c.(427-429)GCT>ACT	p.A143T
Pat_41	Post-Resistance	SGOL2	151246	37	2	201434502	201434502	Missense_Mutation	SNP	C	T	26	185	c.590C>T	c.(589-591)CCT>CTT	p.P197L
Pat_41	Post-Resistance	SGOL2	151246	37	2	201436499	201436499	Missense_Mutation	SNP	C	T	27	607	c.1430C>T	c.(1429-1431)ACT>ATT	p.T477I
Pat_41	Post-Resistance	AOX1	316	37	2	201485445	201485445	Missense_Mutation	SNP	G	A	16	156	c.1777G>A	c.(1777-1779)GCC>ACC	p.A593T
Pat_41	Post-Resistance	AOX1	316	37	2	201499601	201499601	Missense_Mutation	SNP	A	G	4	107	c.2309A>G	c.(2308-2310)GAT>GGT	p.D770G
Pat_41	Post-Resistance	ORC2L	4999	37	2	201802656	201802656	Missense_Mutation	SNP	G	A	20	102	c.487C>T	c.(487-489)CCT>TCT	p.P163S
Pat_41	Post-Resistance	CASP10	843	37	2	202072858	202072858	Missense_Mutation	SNP	C	T	16	70	c.874C>T	c.(874-876)CAC>TAC	p.H292Y
Pat_41	Post-Resistance	TRAK2	66008	37	2	202264105	202264105	Missense_Mutation	SNP	C	T	6	134	c.475G>A	c.(475-477)GAT>AAT	p.D159N
Pat_41	Post-Resistance	TRAK2	66008	37	2	202265811	202265811	Missense_Mutation	SNP	C	T	21	258	c.293G>A	c.(292-294)GGC>GAC	p.G98D
Pat_41	Post-Resistance	MPP4	58538	37	2	202545629	202545629	Nonsense_Mutation	SNP	C	T	3	43	c.861G>A	c.(859-861)TGG>TGA	p.W287*
Pat_41	Post-Resistance	ALS2	57679	37	2	202574734	202574734	Missense_Mutation	SNP	C	T	16	192	c.4150G>A	c.(4150-4152)GGC>AGC	p.G1384S
Pat_41	Post-Resistance	ALS2	57679	37	2	202591410	202591410	Nonsense_Mutation	SNP	C	T	4	88	c.3159G>A	c.(3157-3159)TGG>TGA	p.W1053*
Pat_41	Post-Resistance	ALS2	57679	37	2	202611318	202611318	Missense_Mutation	SNP	T	G	8	384	c.1969A>C	c.(1969-1971)AAG>CAG	p.K657Q
Pat_41	Post-Resistance	CDK15	65061	37	2	202687532	202687532	Missense_Mutation	SNP	C	T	24	223	c.449C>T	c.(448-450)GCT>GTT	p.A150V
Pat_41	Post-Resistance	CDK15	65061	37	2	202700468	202700468	Missense_Mutation	SNP	C	T	20	188	c.833C>T	c.(832-834)TCC>TTC	p.S278F
Pat_41	Post-Resistance	FZD7	8324	37	2	202899702	202899702	Missense_Mutation	SNP	C	T	31	169	c.332C>T	c.(331-333)ACC>ATC	p.T111I
Pat_41	Post-Resistance	FZD7	8324	37	2	202899716	202899716	Missense_Mutation	SNP	G	A	5	189	c.346G>A	c.(346-348)GCC>ACC	p.A116T
Pat_41	Post-Resistance	FZD7	8324	37	2	202899836	202899836	Missense_Mutation	SNP	G	A	9	55	c.466G>A	c.(466-468)GCG>ACG	p.A156T
Pat_41	Post-Resistance	BMPR2	659	37	2	203420052	203420052	Missense_Mutation	SNP	C	T	31	117	c.1664C>T	c.(1663-1665)TCT>TTT	p.S555F
Pat_41	Post-Resistance	FAM117B	150864	37	2	203624030	203624030	Missense_Mutation	SNP	G	A	5	123	c.1405G>A	c.(1405-1407)GAA>AAA	p.E469K
Pat_41	Post-Resistance	ALS2CR8	79800	37	2	203846332	203846332	Missense_Mutation	SNP	G	A	21	111	c.1613G>A	c.(1612-1614)GGT>GAT	p.G538D
Pat_41	Post-Resistance	ALS2CR8	79800	37	2	203846937	203846937	Missense_Mutation	SNP	G	A	12	128	c.1832G>A	c.(1831-1833)GGT>GAT	p.G611D
Pat_41	Post-Resistance	RAPH1	65059	37	2	204305305	204305305	Missense_Mutation	SNP	G	A	30	134	c.2608C>T	c.(2608-2610)CCA>TCA	p.P870S
Pat_41	Post-Resistance	RAPH1	65059	37	2	204305682	204305682	Missense_Mutation	SNP	G	A	21	240	c.2231C>T	c.(2230-2232)CCT>CTT	p.P744L
Pat_41	Post-Resistance	PARD3B	117583	37	2	205989104	205989104	Missense_Mutation	SNP	C	T	24	183	c.1219C>T	c.(1219-1221)CCC>TCC	p.P407S
Pat_41	Post-Resistance	NRP2	8828	37	2	206607930	206607930	Missense_Mutation	SNP	C	T	38	485	c.1295C>T	c.(1294-1296)GCT>GTT	p.A432V
Pat_41	Post-Resistance	GPR1	2825	37	2	207041418	207041418	Missense_Mutation	SNP	G	A	12	101	c.554C>T	c.(553-555)ACT>ATT	p.T185I
Pat_41	Post-Resistance	LOC200726	200726	37	2	207509225	207509225	Missense_Mutation	SNP	G	A	10	62	c.265G>A	c.(265-267)GCA>ACA	p.A89T
Pat_41	Post-Resistance	PIKFYVE	200576	37	2	209191008	209191008	Missense_Mutation	SNP	G	A	5	77	c.3473G>A	c.(3472-3474)AGA>AAA	p.R1158K
Pat_41	Post-Resistance	PTH2R	5746	37	2	209358014	209358014	Nonsense_Mutation	SNP	G	A	10	95	c.1283G>A	c.(1282-1284)TGG>TAG	p.W428*
Pat_41	Post-Resistance	MAP2	4133	37	2	210558884	210558884	Missense_Mutation	SNP	C	T	4	35	c.1990C>T	c.(1990-1992)CCA>TCA	p.P664S
Pat_41	Post-Resistance	MAP2	4133	37	2	210574835	210574835	Missense_Mutation	SNP	G	A	8	131	c.4930G>A	c.(4930-4932)GTC>ATC	p.V1644I
Pat_41	Post-Resistance	C2orf67	151050	37	2	211018438	211018438	Missense_Mutation	SNP	G	A	37	286	c.869C>T	c.(868-870)ACT>ATT	p.T290I
Pat_41	Post-Resistance	CPS1	1373	37	2	211464095	211464095	Splice_Site	SNP	G	A	6	155	c.1360_splice	c.e14-1	p.E454_splice
Pat_41	Post-Resistance	CPS1	1373	37	2	211476989	211476989	Missense_Mutation	SNP	G	A	18	265	c.2540G>A	c.(2539-2541)AGC>AAC	p.S847N
Pat_41	Post-Resistance	SPAG16	79582	37	2	215274959	215274959	Missense_Mutation	SNP	G	A	23	286	c.1816G>A	c.(1816-1818)GCA>ACA	p.A606T
Pat_41	Post-Resistance	BARD1	580	37	2	215674215	215674215	Missense_Mutation	SNP	C	T	3	13	c.79G>A	c.(79-81)GAA>AAA	p.E27K
Pat_41	Post-Resistance	FN1	2335	37	2	216236805	216236805	Missense_Mutation	SNP	G	A	19	106	c.6541C>T	c.(6541-6543)CCC>TCC	p.P2181S
Pat_41	Post-Resistance	FN1	2335	37	2	216236954	216236954	Missense_Mutation	SNP	G	A	53	85	c.6392C>T	c.(6391-6393)TCT>TTT	p.S2131F
Pat_41	Post-Resistance	FN1	2335	37	2	216257783	216257783	Missense_Mutation	SNP	C	T	8	108	c.3940G>A	c.(3940-3942)GAT>AAT	p.D1314N
Pat_41	Post-Resistance	PNKD	25953	37	2	219206769	219206769	Missense_Mutation	SNP	G	A	9	79	c.683G>A	c.(682-684)GGC>GAC	p.G228D
Pat_41	Post-Resistance	SLC11A1	6556	37	2	219257753	219257753	Missense_Mutation	SNP	G	A	11	131	c.1214G>A	c.(1213-1215)CGC>CAC	p.R405H

Pat_41	Post-Resistance	USP37	57695	37	2	219328071	219328071	Missense_Mutation	SNP	C	T	23	90	c.2485G>A	c.(2485-2487)GAA>AAA	p.E829K
Pat_41	Post-Resistance	USP37	57695	37	2	219423307	219423307	Missense_Mutation	SNP	C	T	39	221	c.70G>A	c.(70-72)GAA>AAA	p.E24K
Pat_41	Post-Resistance	ZNF142	7701	37	2	219507247	219507247	Missense_Mutation	SNP	G	A	9	93	c.3992C>T	c.(3991-3993)TCC>TTC	p.S1331F
Pat_41	Post-Resistance	STK36	27148	37	2	219559006	219559006	Missense_Mutation	SNP	G	A	47	238	c.2356G>A	c.(2356-2358)GAC>AAC	p.D786N
Pat_41	Post-Resistance	STK36	27148	37	2	219563988	219563988	Missense_Mutation	SNP	G	A	27	69	c.3721G>A	c.(3721-3723)GCA>ACA	p.A1241T
Pat_41	Post-Resistance	TTLL4	9654	37	2	219602830	219602830	Missense_Mutation	SNP	G	A	18	117	c.431G>A	c.(430-432)AGC>AAC	p.S144N
Pat_41	Post-Resistance	TTLL4	9654	37	2	219603268	219603268	Missense_Mutation	SNP	C	T	22	432	c.869C>T	c.(868-870)GCT>GTT	p.A290V
Pat_41	Post-Resistance	PRKAG3	53632	37	2	219691750	219691750	Nonsense_Mutation	SNP	G	A	53	296	c.1069C>T	c.(1069-1071)CGA>TGA	p.R357*
Pat_41	Post-Resistance	WNT10A	80326	37	2	219747031	219747031	Missense_Mutation	SNP	G	A	8	144	c.262G>A	c.(262-264)GGC>AGC	p.G88S
Pat_41	Post-Resistance	CCDC108	255101	37	2	219895848	219895848	Missense_Mutation	SNP	C	T	6	6	c.995G>A	c.(994-996)AGC>AAC	p.S332N
Pat_41	Post-Resistance	ABCB6	10058	37	2	220075486	220075486	Missense_Mutation	SNP	C	T	4	131	c.2203G>A	c.(2203-2205)GTC>ATC	p.V735I
Pat_41	Post-Resistance	ATG9A	79065	37	2	220087033	220087033	Missense_Mutation	SNP	G	A	5	194	c.1988C>T	c.(1987-1989)GCG>GTG	p.A663V
Pat_41	Post-Resistance	ANKZF1	55139	37	2	220095062	220095062	Missense_Mutation	SNP	G	A	7	60	c.83G>A	c.(82-84)GGC>GAC	p.G28D
Pat_41	Post-Resistance	PTPRN	5798	37	2	220155547	220155547	Splice_Site	SNP	C	T	9	129	c.2794_splice	c.e21+1	p.G932_splice
Pat_41	Post-Resistance	PTPRN	5798	37	2	220164831	220164831	Missense_Mutation	SNP	G	A	12	65	c.1312C>T	c.(1312-1314)CCC>TCC	p.P438S
Pat_41	Post-Resistance	SPEG	10290	37	2	220338478	220338478	Missense_Mutation	SNP	G	A	47	269	c.4300G>A	c.(4300-4302)GCC>ACC	p.A1434T
Pat_41	Post-Resistance	SPEG	10290	37	2	220350095	220350095	Missense_Mutation	SNP	G	A	3	69	c.7637G>A	c.(7636-7638)CGC>CAC	p.R2546H
Pat_41	Post-Resistance	SPEG	10290	37	2	220356934	220356934	Missense_Mutation	SNP	C	T	6	81	c.9563C>T	c.(9562-9564)TCC>TTC	p.S3188F
Pat_41	Post-Resistance	ACCN4	55515	37	2	220380015	220380015	Missense_Mutation	SNP	G	A	18	91	c.950G>A	c.(949-951)AGC>AAC	p.S317N
Pat_41	Post-Resistance	OBSL1	23363	37	2	220421305	220421305	Missense_Mutation	SNP	G	A	4	66	c.4207C>T	c.(4207-4209)CCC>TCC	p.P1403S
Pat_41	Post-Resistance	MRPL44	65080	37	2	224824261	224824261	Missense_Mutation	SNP	C	T	41	327	c.190C>T	c.(190-192)CCG>TCG	p.P64S
Pat_41	Post-Resistance	SERPINE2	5270	37	2	224866547	224866547	Missense_Mutation	SNP	G	A	21	207	c.71C>T	c.(70-72)CCT>CTT	p.P24L
Pat_41	Post-Resistance	DOCK10	55619	37	2	225659648	225659648	Missense_Mutation	SNP	G	A	24	390	c.5102C>T	c.(5101-5103)ACC>ATC	p.T1701I
Pat_41	Post-Resistance	DOCK10	55619	37	2	225706558	225706558	Missense_Mutation	SNP	G	A	38	395	c.2624C>T	c.(2623-2625)TCT>TTT	p.S875F
Pat_41	Post-Resistance	IRS1	3667	37	2	227661668	227661668	Missense_Mutation	SNP	C	T	4	59	c.1787G>A	c.(1786-1788)GGG>GAG	p.G596E
Pat_41	Post-Resistance	COL4A4	1286	37	2	227953439	227953439	Missense_Mutation	SNP	C	T	7	32	c.1553G>A	c.(1552-1554)GGG>GAG	p.G518E
Pat_41	Post-Resistance	COL4A4	1286	37	2	227983386	227983386	Missense_Mutation	SNP	C	T	5	112	c.464G>A	c.(463-465)GGA>GAA	p.G155E
Pat_41	Post-Resistance	COL4A3	1285	37	2	228110679	228110679	Missense_Mutation	SNP	G	A	9	163	c.334G>A	c.(334-336)GGC>AGC	p.G112S
Pat_41	Post-Resistance	COL4A3	1285	37	2	228175595	228175595	Missense_Mutation	SNP	G	A	10	140	c.4859G>A	c.(4858-4860)GGA>GAA	p.G1620E
Pat_41	Post-Resistance	AGFG1	3267	37	2	228384668	228384668	Missense_Mutation	SNP	G	A	17	58	c.266G>A	c.(265-267)TGT>TAT	p.C89Y
Pat_41	Post-Resistance	AGFG1	3267	37	2	228398316	228398316	Missense_Mutation	SNP	C	T	17	253	c.866C>T	c.(865-867)CCC>CTC	p.P289L
Pat_41	Post-Resistance	SLC19A3	80704	37	2	228563653	228563653	Missense_Mutation	SNP	C	T	17	99	c.778G>A	c.(778-780)GAC>AAC	p.D260N
Pat_41	Post-Resistance	SLC19A3	80704	37	2	228563779	228563779	Missense_Mutation	SNP	C	T	3	14	c.652G>A	c.(652-654)GAG>AAG	p.E218K
Pat_41	Post-Resistance	WDR69	164781	37	2	228750112	228750112	Missense_Mutation	SNP	C	T	6	170	c.86C>T	c.(85-87)TCC>TTC	p.S29F
Pat_41	Post-Resistance	TRIP12	9320	37	2	230643186	230643186	Missense_Mutation	SNP	C	T	15	290	c.5102G>A	c.(5101-5103)GGA>GAA	p.G1701E
Pat_41	Post-Resistance	TRIP12	9320	37	2	230656612	230656612	Missense_Mutation	SNP	G	A	32	484	c.4160C>T	c.(4159-4161)GCT>GTT	p.A1387V
Pat_41	Post-Resistance	SP110	3431	37	2	231076211	231076211	Missense_Mutation	SNP	G	A	8	76	c.725C>T	c.(724-726)CCC>CTC	p.P242L
Pat_41	Post-Resistance	SP100	6672	37	2	231282365	231282365	Missense_Mutation	SNP	G	A	62	352	c.92G>A	c.(91-93)AGC>AAC	p.S31N
Pat_41	Post-Resistance	ITM2C	81618	37	2	231740489	231740489	Missense_Mutation	SNP	G	A	37	427	c.416G>A	c.(415-417)GGT>GAT	p.G139D
Pat_41	Post-Resistance	ARMC9	80210	37	2	232137775	232137775	Nonsense_Mutation	SNP	C	T	35	194	c.1318C>T	c.(1318-1320)CAG>TAG	p.Q440*
Pat_41	Post-Resistance	C2orf52	151477	37	2	232373844	232373844	Missense_Mutation	SNP	C	T	27	214	c.247G>A	c.(247-249)GGG>AGG	p.G83R
Pat_41	Post-Resistance	C2orf52	151477	37	2	232373910	232373910	Nonsense_Mutation	SNP	G	A	71	314	c.181C>T	c.(181-183)CAG>TAG	p.Q61*
Pat_41	Post-Resistance	DIS3L2	129563	37	2	233001350	233001350	Missense_Mutation	SNP	G	A	15	285	c.871G>A	c.(871-873)GCA>ACA	p.A291T
Pat_41	Post-Resistance	CHRND	1144	37	2	233399032	233399032	Missense_Mutation	SNP	G	A	5	78	c.1351G>A	c.(1351-1353)GAC>AAC	p.D451N
Pat_41	Post-Resistance	GIGYF2	26058	37	2	233709136	233709136	Missense_Mutation	SNP	C	T	11	147	c.3157C>T	c.(3157-3159)CCT>TCT	p.P1053S
Pat_41	Post-Resistance	NGEF	25791	37	2	233839419	233839419	Missense_Mutation	SNP	C	T	10	134	c.182G>A	c.(181-183)AGA>AAA	p.R61K
Pat_41	Post-Resistance	DGKD	8527	37	2	234375787	234375787	Missense_Mutation	SNP	C	T	16	276	c.3362C>T	c.(3361-3363)ACC>ATC	p.T1121I

Pat_41	Post-Resistance	USP40	55230	37	2	234465553	234465553	Missense_Mutation	SNP	G	A	5	110	c.494C>T	c.(493-495)ACC>ATC	p.T165I
Pat_41	Post-Resistance	UGT1A6	54578	37	2	234602384	234602384	Missense_Mutation	SNP	C	T	67	320	c.734C>T	c.(733-735)ACC>ATC	p.T245I
Pat_41	Post-Resistance	UGT1A4	54657	37	2	234627602	234627602	Missense_Mutation	SNP	G	A	5	53	c.136G>A	c.(136-138)GAG>AAG	p.E46K
Pat_41	Post-Resistance	UGT1A1	54658	37	2	234669559	234669559	Missense_Mutation	SNP	G	A	25	265	c.626G>A	c.(625-627)CGG>CAG	p.R209Q
Pat_41	Post-Resistance	HJURP	55355	37	2	234750429	234750429	Missense_Mutation	SNP	C	T	4	35	c.997G>A	c.(997-999)GGG>AGG	p.G333R
Pat_41	Post-Resistance	COL6A3	1293	37	2	238234284	238234284	Missense_Mutation	SNP	C	T	21	192	c.9412G>A	c.(9412-9414)GCA>ACA	p.A3138T
Pat_41	Post-Resistance	COL6A3	1293	37	2	238253297	238253297	Missense_Mutation	SNP	G	A	7	76	c.7364C>T	c.(7363-7365)ACC>ATC	p.T2455I
Pat_41	Post-Resistance	COL6A3	1293	37	2	238280506	238280506	Missense_Mutation	SNP	G	A	13	113	c.4154C>T	c.(4153-4155)CCC>CTC	p.P1385L
Pat_41	Post-Resistance	LRRFIP1	9208	37	2	238668762	238668762	Missense_Mutation	SNP	C	T	9	102	c.803C>T	c.(802-804)ACC>ATC	p.T268I
Pat_41	Post-Resistance	ASB1	51665	37	2	239353257	239353257	Missense_Mutation	SNP	G	A	10	89	c.769G>A	c.(769-771)GTA>ATA	p.V257I
Pat_41	Post-Resistance	ANKMY1	51281	37	2	241421640	241421640	Missense_Mutation	SNP	G	A	15	31	c.2578C>T	c.(2578-2580)CCC>TCC	p.P860S
Pat_41	Post-Resistance	SNED1	25992	37	2	242021733	242021733	Missense_Mutation	SNP	G	A	13	129	c.4075G>A	c.(4075-4077)GAG>AAG	p.E1359K
Pat_41	Post-Resistance	PASK	23178	37	2	242065707	242065707	Missense_Mutation	SNP	G	A	7	95	c.2623C>T	c.(2623-2625)CCC>TCC	p.P875S
Pat_41	Post-Resistance	ANO7	50636	37	2	242138798	242138798	Missense_Mutation	SNP	G	A	18	41	c.539G>A	c.(538-540)TGC>TAC	p.C180Y
Pat_41	Post-Resistance	ANO7	50636	37	2	242162649	242162649	Nonsense_Mutation	SNP	G	A	28	248	c.2532G>A	c.(2530-2532)TGG>TGA	p.W844*
Pat_41	Post-Resistance	HDLBP	3069	37	2	242169102	242169102	Missense_Mutation	SNP	C	T	5	12	c.3721G>A	c.(3721-3723)GCT>ACT	p.A1241T
Pat_41	Post-Resistance	2-Sep	4735	37	2	242275509	242275509	Missense_Mutation	SNP	G	A	9	55	c.337G>A	c.(337-339)GAT>AAT	p.D113N
Pat_41	Post-Resistance	FARP2	9855	37	2	242402876	242402876	Missense_Mutation	SNP	G	A	6	81	c.1804G>A	c.(1804-1806)GCA>ACA	p.A602T
Pat_41	Post-Resistance	THAP4	51078	37	2	242573291	242573291	Missense_Mutation	SNP	G	A	28	87	c.281C>T	c.(280-282)GCT>GTT	p.A94V
Pat_41	Post-Resistance	PDCD1	5133	37	2	242794415	242794415	Missense_Mutation	SNP	C	T	13	10	c.527G>A	c.(526-528)GGC>GAC	p.G176D
Pat_41	Post-Resistance	DEFB129	140881	37	20	210243	210243	Missense_Mutation	SNP	C	T	6	209	c.383C>T	c.(382-384)GCC>GTC	p.A128V
Pat_41	Post-Resistance	PSMF1	9491	37	20	1099469	1099469	Missense_Mutation	SNP	G	A	10	98	c.53G>A	c.(52-54)AGG>AAG	p.R18K
Pat_41	Post-Resistance	PSMF1	9491	37	20	1145117	1145117	Missense_Mutation	SNP	C	T	9	187	c.761C>T	c.(760-762)CCC>CTC	p.P254L
Pat_41	Post-Resistance	SNPH	9751	37	20	1285635	1285635	Missense_Mutation	SNP	A	G	18	206	c.422A>G	c.(421-423)GAG>GGG	p.E141G
Pat_41	Post-Resistance	SIRPG	55423	37	20	1616139	1616139	Nonsense_Mutation	SNP	C	T	10	187	c.855G>A	c.(853-855)TGG>TGA	p.W285*
Pat_41	Post-Resistance	SIRPG	55423	37	20	1616227	1616227	Missense_Mutation	SNP	A	G	18	33	c.767T>C	c.(766-768)GTT>GCT	p.V256A
Pat_41	Post-Resistance	SIRPA	140885	37	20	1895915	1895915	Missense_Mutation	SNP	G	A	9	89	c.250G>A	c.(250-252)GAA>AAA	p.E84K
Pat_41	Post-Resistance	TMC2	117532	37	20	2591183	2591183	Missense_Mutation	SNP	C	T	6	129	c.1532C>T	c.(1531-1533)GCA>GTA	p.A511V
Pat_41	Post-Resistance	IDH3B	3420	37	20	2641366	2641366	Missense_Mutation	SNP	C	T	33	143	c.508G>A	c.(508-510)GAG>AAG	p.E170K
Pat_41	Post-Resistance	VPS16	64601	37	20	2845854	2845854	Missense_Mutation	SNP	G	A	24	153	c.2065G>A	c.(2065-2067)GGC>AGC	p.G689S
Pat_41	Post-Resistance	C20orf194	25943	37	20	3245087	3245087	Missense_Mutation	SNP	C	T	8	78	c.2870G>A	c.(2869-2871)GGC>GAC	p.G957D
Pat_41	Post-Resistance	C20orf194	25943	37	20	3297413	3297413	Missense_Mutation	SNP	G	A	18	133	c.1496C>T	c.(1495-1497)TCC>TTC	p.S499F
Pat_41	Post-Resistance	ATRN	8455	37	20	3543933	3543933	Missense_Mutation	SNP	G	A	43	315	c.1709G>A	c.(1708-1710)GGA>GAA	p.G570E
Pat_41	Post-Resistance	C20orf27	54976	37	20	3735088	3735088	Missense_Mutation	SNP	C	T	15	200	c.380G>A	c.(379-381)GGC>GAC	p.G127D
Pat_41	Post-Resistance	CENPB	1059	37	20	3765656	3765656	Missense_Mutation	SNP	G	A	16	102	c.1475C>T	c.(1474-1476)GCC>GTC	p.A492V
Pat_41	Post-Resistance	CDC25B	994	37	20	3785265	3785265	Missense_Mutation	SNP	C	T	25	423	c.1540C>T	c.(1540-1542)CTC>TTC	p.L514F
Pat_41	Post-Resistance	CDS2	8760	37	20	5155911	5155911	Missense_Mutation	SNP	G	A	14	327	c.277G>A	c.(277-279)GTT>ATT	p.V93I
Pat_41	Post-Resistance	MCM8	84515	37	20	5974160	5974160	Missense_Mutation	SNP	G	A	8	137	c.2249G>A	c.(2248-2250)GGA>GAA	p.G750E
Pat_41	Post-Resistance	BMP2	650	37	20	6759129	6759129	Missense_Mutation	SNP	G	A	9	142	c.584G>A	c.(583-585)AGG>AAG	p.R195K
Pat_41	Post-Resistance	PLCB4	5332	37	20	9351932	9351932	Missense_Mutation	SNP	C	T	32	188	c.575C>T	c.(574-576)CCC>CTC	p.P192L
Pat_41	Post-Resistance	PLCB4	5332	37	20	9374316	9374316	Missense_Mutation	SNP	G	A	8	67	c.1405G>A	c.(1405-1407)GTT>ATT	p.V469I
Pat_41	Post-Resistance	PAK7	57144	37	20	9543635	9543635	Missense_Mutation	SNP	C	T	15	464	c.1519G>A	c.(1519-1521)GTT>ATT	p.V507I
Pat_41	Post-Resistance	SNAP25	6616	37	20	10279933	10279933	Missense_Mutation	SNP	G	A	190	280	c.425G>A	c.(424-426)CGA>CAA	p.R142Q
Pat_41	Post-Resistance	JAG1	182	37	20	10637056	10637056	Missense_Mutation	SNP	C	T	9	151	c.745G>A	c.(745-747)GGT>AGT	p.G249S
Pat_41	Post-Resistance	SPTLC3	55304	37	20	13098233	13098233	Missense_Mutation	SNP	C	T	27	151	c.1013C>T	c.(1012-1014)GCT>GTT	p.A338V
Pat_41	Post-Resistance	TASP1	55617	37	20	13398114	13398114	Missense_Mutation	SNP	G	A	21	140	c.1151C>T	c.(1150-1152)GCC>GTC	p.A384V
Pat_41	Post-Resistance	TASP1	55617	37	20	13605867	13605867	Missense_Mutation	SNP	C	T	20	289	c.178G>A	c.(178-180)GAG>AAG	p.E60K

Pat_41	Post-Resistance	FLRT3	23767	37	20	14306531	14306531	Missense_Mutation	SNP	G	A	7	148	c.1622C>T	c.(1621-1623)ACC>ATC	p.T541I
Pat_41	Post-Resistance	MACROD2	140733	37	20	15967795	15967795	Missense_Mutation	SNP	G	A	9	81	c.1145G>A	c.(1144-1146)GGT>GAT	p.G382D
Pat_41	Post-Resistance	KIF16B	55614	37	20	16359631	16359631	Missense_Mutation	SNP	C	T	6	100	c.3016G>A	c.(3016-3018)GAG>AAG	p.E1006K
Pat_41	Post-Resistance	RRBP1	6238	37	20	17614165	17614165	Missense_Mutation	SNP	C	T	5	64	c.8G>A	c.(7-9)AGC>AAC	p.S3N
Pat_41	Post-Resistance	SNX5	27131	37	20	17932164	17932164	Missense_Mutation	SNP	C	T	17	216	c.589G>A	c.(589-591)GTC>ATC	p.V197I
Pat_41	Post-Resistance	OVOL2	58495	37	20	18022295	18022295	Missense_Mutation	SNP	G	A	5	103	c.394C>T	c.(394-396)CGC>TGC	p.R132C
Pat_41	Post-Resistance	C20orf26	26074	37	20	20150016	20150016	Missense_Mutation	SNP	C	T	10	320	c.1297C>T	c.(1297-1299)CTC>TTC	p.L433F
Pat_41	Post-Resistance	CST5	1473	37	20	23856908	23856908	Missense_Mutation	SNP	C	T	5	41	c.346G>A	c.(346-348)GAA>AAA	p.E116K
Pat_41	Post-Resistance	C20orf3	57136	37	20	24964612	24964612	Missense_Mutation	SNP	C	T	8	149	c.139G>A	c.(139-141)GCT>ACT	p.A47T
Pat_41	Post-Resistance	PYGB	5834	37	20	25249831	25249831	Missense_Mutation	SNP	G	A	10	81	c.412G>A	c.(412-414)GGG>AGG	p.G138R
Pat_41	Post-Resistance	PYGB	5834	37	20	25261584	25261584	Splice_Site	SNP	G	A	20	222	c.1240_splice	c.e11-1	p.H414_splice
Pat_41	Post-Resistance	NINL	22981	37	20	25443114	25443114	Missense_Mutation	SNP	C	T	7	304	c.3487G>A	c.(3487-3489)GCT>ACT	p.A1163T
Pat_41	Post-Resistance	NINL	22981	37	20	25478877	25478877	Missense_Mutation	SNP	C	T	7	56	c.1138G>A	c.(1138-1140)GCC>ACC	p.A380T
Pat_41	Post-Resistance	DEFB123	245936	37	20	30037835	30037835	Missense_Mutation	SNP	G	A	14	201	c.62G>A	c.(61-63)GGC>GAC	p.G21D
Pat_41	Post-Resistance	BCL2L1	598	37	20	30309813	30309813	Missense_Mutation	SNP	C	T	5	259	c.209G>A	c.(208-210)GGC>GAC	p.G70D
Pat_41	Post-Resistance	TPX2	22974	37	20	30366746	30366746	Missense_Mutation	SNP	C	T	7	171	c.1013C>T	c.(1012-1014)ACC>ATC	p.T338I
Pat_41	Post-Resistance	MYLK2	85366	37	20	30409498	30409498	Missense_Mutation	SNP	C	T	40	321	c.730C>T	c.(730-732)CTC>TTC	p.L244F
Pat_41	Post-Resistance	C20orf160	140706	37	20	30610479	30610479	Missense_Mutation	SNP	C	T	10	249	c.950C>T	c.(949-951)TCC>TTC	p.S317F
Pat_41	Post-Resistance	TM9SF4	9777	37	20	30729625	30729625	Missense_Mutation	SNP	G	A	8	308	c.455G>A	c.(454-456)AGC>AAC	p.S152N
Pat_41	Post-Resistance	KIF3B	9371	37	20	30915391	30915391	Missense_Mutation	SNP	C	T	21	254	c.1895C>T	c.(1894-1896)GCC>GTC	p.A632V
Pat_41	Post-Resistance	ASXL1	171023	37	20	31023022	31023022	Missense_Mutation	SNP	C	T	37	430	c.2507C>T	c.(2506-2508)ACT>ATT	p.T836I
Pat_41	Post-Resistance	ASXL1	171023	37	20	31023360	31023360	Missense_Mutation	SNP	G	A	8	119	c.2845G>A	c.(2845-2847)GGT>AGT	p.G949S
Pat_41	Post-Resistance	DNMT3B	1789	37	20	31380463	31380463	Missense_Mutation	SNP	C	T	27	151	c.953C>T	c.(952-954)CCC>CTC	p.P318L
Pat_41	Post-Resistance	CDK5RAP1	51654	37	20	31954712	31954712	Missense_Mutation	SNP	C	T	6	268	c.1537G>A	c.(1537-1539)GCC>ACC	p.A513T
Pat_41	Post-Resistance	CHMP4B	128866	37	20	32436417	32436417	Missense_Mutation	SNP	C	T	16	90	c.335C>T	c.(334-336)GCC>GTC	p.A112V
Pat_41	Post-Resistance	CHMP4B	128866	37	20	32439907	32439907	Missense_Mutation	SNP	G	A	18	110	c.508G>A	c.(508-510)GAA>AAA	p.E170K
Pat_41	Post-Resistance	AHCY	191	37	20	32880221	32880221	Missense_Mutation	SNP	C	T	6	119	c.388G>A	c.(388-390)GAC>AAC	p.D130N
Pat_41	Post-Resistance	NCOA6	23054	37	20	33330006	33330006	Missense_Mutation	SNP	G	A	15	77	c.4054C>T	c.(4054-4056)CCT>TCT	p.P1352S
Pat_41	Post-Resistance	MYH7B	57644	37	20	33575479	33575479	Splice_Site	SNP	G	A	8	229	c.1392_splice	c.e15+1	p.Q464_splice
Pat_41	Post-Resistance	MYH7B	57644	37	20	33575943	33575943	Nonsense_Mutation	SNP	C	T	9	217	c.1591C>T	c.(1591-1593)CAG>TAG	p.Q531*
Pat_41	Post-Resistance	MYH7B	57644	37	20	33584554	33584554	Missense_Mutation	SNP	C	T	5	70	c.3385C>T	c.(3385-3387)CTC>TTC	p.L1129F
Pat_41	Post-Resistance	CEP250	11190	37	20	34060642	34060642	Missense_Mutation	SNP	C	T	45	230	c.1195C>T	c.(1195-1197)CGC>TGC	p.R399C
Pat_41	Post-Resistance	SPAG4	6676	37	20	34205157	34205157	Missense_Mutation	SNP	T	C	4	35	c.404T>C	c.(403-405)TTT>TCT	p.F135S
Pat_41	Post-Resistance	NFS1	9054	37	20	34278370	34278370	Missense_Mutation	SNP	G	A	20	394	c.526C>T	c.(526-528)CTC>TTC	p.L176F
Pat_41	Post-Resistance	RBM39	9584	37	20	34313043	34313043	Missense_Mutation	SNP	C	T	13	366	c.451G>A	c.(451-453)GAT>AAT	p.D151N
Pat_41	Post-Resistance	PHF20	51230	37	20	34526750	34526750	Missense_Mutation	SNP	C	T	10	45	c.2432C>T	c.(2431-2433)ACT>ATT	p.T811I
Pat_41	Post-Resistance	C20orf152	140894	37	20	34599169	34599169	Missense_Mutation	SNP	G	A	9	132	c.1259G>A	c.(1258-1260)GGA>GAA	p.G420E
Pat_41	Post-Resistance	EPB41L1	2036	37	20	34763533	34763533	Missense_Mutation	SNP	C	T	5	88	c.238C>T	c.(238-240)CCC>TCC	p.P80S
Pat_41	Post-Resistance	DLGAP4	22839	37	20	35060295	35060295	Missense_Mutation	SNP	C	T	7	30	c.175C>T	c.(175-177)CCC>TCC	p.P59S
Pat_41	Post-Resistance	SLA2	84174	37	20	35242722	35242722	Nonsense_Mutation	SNP	C	T	9	290	c.651G>A	c.(649-651)TGG>TGA	p.W217*
Pat_41	Post-Resistance	SAMHD1	25939	37	20	35547790	35547790	Missense_Mutation	SNP	C	T	13	205	c.829G>A	c.(829-831)GAA>AAA	p.E277K
Pat_41	Post-Resistance	RBL1	5933	37	20	35695224	35695224	Missense_Mutation	SNP	G	A	13	224	c.749C>T	c.(748-750)GCT>GTT	p.A250V
Pat_41	Post-Resistance	C20orf132	140699	37	20	35749312	35749312	Missense_Mutation	SNP	G	A	4	95	c.2134C>T	c.(2134-2136)CTC>TTC	p.L712F
Pat_41	Post-Resistance	C20orf132	140699	37	20	35776234	35776234	Missense_Mutation	SNP	C	T	12	38	c.1183G>A	c.(1183-1185)GCT>ACT	p.A395T
Pat_41	Post-Resistance	KIAA0406	9675	37	20	36625327	36625327	Missense_Mutation	SNP	C	T	15	162	c.2822G>A	c.(2821-2823)GGT>GAT	p.G941D
Pat_41	Post-Resistance	KIAA0406	9675	37	20	36631125	36631125	Missense_Mutation	SNP	C	T	32	231	c.2557G>A	c.(2557-2559)GAG>AAG	p.E853K
Pat_41	Post-Resistance	RPRD1B	58490	37	20	36685990	36685990	Missense_Mutation	SNP	G	A	8	138	c.472G>A	c.(472-474)GAT>AAT	p.D158N

Pat_41	Post-Resistance	TGM2	7052	37	20	36775133	36775133	Missense_Mutation	SNP	G	A	10	117	c.845C>T	c.(844-846)GCC>GTC	p.A282V
Pat_41	Post-Resistance	KIAA1755	85449	37	20	36841505	36841505	Missense_Mutation	SNP	C	T	4	35	c.3542G>A	c.(3541-3543)GGG>GAG	p.G1181E
Pat_41	Post-Resistance	KIAA1755	85449	37	20	36845824	36845824	Missense_Mutation	SNP	G	A	3	20	c.2732C>T	c.(2731-2733)GCT>GTT	p.A911V
Pat_41	Post-Resistance	LBP	3929	37	20	36975013	36975013	Missense_Mutation	SNP	G	A	11	98	c.94G>A	c.(94-96)GCC>ACC	p.A32T
Pat_41	Post-Resistance	RALGAPB	57148	37	20	37153503	37153503	Missense_Mutation	SNP	C	T	66	418	c.1702C>T	c.(1702-1704)CCT>TCT	p.P568S
Pat_41	Post-Resistance	ACTR5	79913	37	20	37394896	37394896	Missense_Mutation	SNP	G	A	12	158	c.1309G>A	c.(1309-1311)GCA>ACA	p.A437T
Pat_41	Post-Resistance	ACTR5	79913	37	20	37396174	37396174	Missense_Mutation	SNP	C	T	18	232	c.1501C>T	c.(1501-1503)CCT>TCT	p.P501S
Pat_41	Post-Resistance	DHX35	60625	37	20	37634870	37634870	Missense_Mutation	SNP	C	T	40	722	c.1093C>T	c.(1093-1095)CTC>TTC	p.L365F
Pat_41	Post-Resistance	DHX35	60625	37	20	37647476	37647476	Missense_Mutation	SNP	C	T	42	681	c.1432C>T	c.(1432-1434)CCG>TCG	p.P478S
Pat_41	Post-Resistance	PLCG1	5335	37	20	39794436	39794436	Missense_Mutation	SNP	C	T	6	131	c.1769C>T	c.(1768-1770)ACC>ATC	p.T590I
Pat_41	Post-Resistance	ZHX3	23051	37	20	39831193	39831193	Nonsense_Mutation	SNP	C	T	8	485	c.2364G>A	c.(2362-2364)TGG>TGA	p.W788*
Pat_41	Post-Resistance	ZHX3	23051	37	20	39832329	39832329	Missense_Mutation	SNP	G	A	15	449	c.1228C>T	c.(1228-1230)CTT>TTT	p.L410F
Pat_41	Post-Resistance	LPIN3	64900	37	20	39986971	39986971	Missense_Mutation	SNP	G	A	9	78	c.2287G>A	c.(2287-2289)GCC>ACC	p.A763T
Pat_41	Post-Resistance	EMILIN3	90187	37	20	39990030	39990030	Missense_Mutation	SNP	G	A	5	55	c.2179C>T	c.(2179-2181)CAT>TAT	p.H727Y
Pat_41	Post-Resistance	CHD6	84181	37	20	40116325	40116325	Missense_Mutation	SNP	C	T	10	112	c.1981G>A	c.(1981-1983)GAT>AAT	p.D661N
Pat_41	Post-Resistance	PTPRT	11122	37	20	40733309	40733309	Missense_Mutation	SNP	C	T	22	273	c.3440G>A	c.(3439-3441)GGC>GAC	p.G1147D
Pat_41	Post-Resistance	PTPRT	11122	37	20	41101188	41101188	Missense_Mutation	SNP	G	A	8	82	c.1168C>T	c.(1168-1170)CCA>TCA	p.P390S
Pat_41	Post-Resistance	PTPRT	11122	37	20	41306536	41306536	Missense_Mutation	SNP	G	A	5	94	c.1123C>T	c.(1123-1125)CCT>TCT	p.P375S
Pat_41	Post-Resistance	SFRS6	6431	37	20	42089549	42089549	Missense_Mutation	SNP	G	A	12	231	c.881G>A	c.(880-882)AGA>AAA	p.R294K
Pat_41	Post-Resistance	SGK2	10110	37	20	42195097	42195097	Missense_Mutation	SNP	C	T	29	267	c.142C>T	c.(142-144)CTC>TTC	p.L48F
Pat_41	Post-Resistance	SGK2	10110	37	20	42195107	42195107	Missense_Mutation	SNP	C	T	14	277	c.152C>T	c.(151-153)CCC>CTC	p.P51L
Pat_41	Post-Resistance	SGK2	10110	37	20	42199281	42199281	Missense_Mutation	SNP	C	T	15	189	c.565C>T	c.(565-567)CGC>TGC	p.R189C
Pat_41	Post-Resistance	MYBL2	4605	37	20	42344713	42344713	Missense_Mutation	SNP	C	T	15	279	c.2089C>T	c.(2089-2091)CTC>TTC	p.L697F
Pat_41	Post-Resistance	JPH2	57158	37	20	42744483	42744483	Missense_Mutation	SNP	C	T	3	21	c.1832G>A	c.(1831-1833)GGC>GAC	p.G611D
Pat_41	Post-Resistance	GDAP1L1	78997	37	20	42907898	42907898	Missense_Mutation	SNP	G	T	7	160	c.1062G>T	c.(1060-1062)ATG>ATT	p.M354I
Pat_41	Post-Resistance	SERINC3	10955	37	20	43150567	43150567	Missense_Mutation	SNP	G	A	13	112	c.26C>T	c.(25-27)TCC>TTC	p.S9F
Pat_41	Post-Resistance	ADA	100	37	20	43257697	43257697	Missense_Mutation	SNP	G	A	9	314	c.209C>T	c.(208-210)CCT>CTT	p.P70L
Pat_41	Post-Resistance	RIMS4	140730	37	20	43384893	43384893	Missense_Mutation	SNP	C	T	10	107	c.692G>A	c.(691-693)GGC>GAC	p.G231D
Pat_41	Post-Resistance	PABPC1L	80336	37	20	43559221	43559221	Missense_Mutation	SNP	G	A	10	395	c.1093G>A	c.(1093-1095)GTG>ATG	p.V365M
Pat_41	Post-Resistance	WFDC3	140686	37	20	44418584	44418584	Missense_Mutation	SNP	C	T	10	202	c.31G>A	c.(31-33)GCA>ACA	p.A11T
Pat_41	Post-Resistance	TNNC2	7125	37	20	44452716	44452716	Missense_Mutation	SNP	G	A	33	354	c.365C>T	c.(364-366)GCC>GTC	p.A122V
Pat_41	Post-Resistance	ZSWIM3	140831	37	20	44506821	44506821	Missense_Mutation	SNP	G	A	8	142	c.1624G>A	c.(1624-1626)GTT>ATT	p.V542I
Pat_41	Post-Resistance	NEURL2	140825	37	20	44519150	44519150	Missense_Mutation	SNP	C	T	16	217	c.481G>A	c.(481-483)GGC>AGC	p.G161S
Pat_41	Post-Resistance	PCIF1	63935	37	20	44575921	44575921	Missense_Mutation	SNP	C	T	25	262	c.1727C>T	c.(1726-1728)CCG>CTG	p.P576L
Pat_41	Post-Resistance	ZNF335	63925	37	20	44596415	44596415	Missense_Mutation	SNP	C	T	8	212	c.772G>A	c.(772-774)GCC>ACC	p.A258T
Pat_41	Post-Resistance	CD40	958	37	20	44756812	44756812	Missense_Mutation	SNP	C	T	11	201	c.595C>T	c.(595-597)CCC>TCC	p.P199S
Pat_41	Post-Resistance	ELMO2	63916	37	20	45003204	45003204	Missense_Mutation	SNP	C	T	11	201	c.1141G>A	c.(1141-1143)GCT>ACT	p.A381T
Pat_41	Post-Resistance	ZNF334	55713	37	20	45130777	45130777	Missense_Mutation	SNP	C	T	7	346	c.1201G>A	c.(1201-1203)GGG>AGG	p.G401R
Pat_41	Post-Resistance	SLC2A10	81031	37	20	45354285	45354285	Missense_Mutation	SNP	G	A	18	92	c.610G>A	c.(610-612)GGT>AGT	p.G204S
Pat_41	Post-Resistance	EYA2	2139	37	20	45618758	45618758	Missense_Mutation	SNP	G	A	7	93	c.109G>A	c.(109-111)GGC>AGC	p.G37S
Pat_41	Post-Resistance	ZMYND8	23613	37	20	45905538	45905538	Missense_Mutation	SNP	C	T	6	110	c.940G>A	c.(940-942)GCC>ACC	p.A314T
Pat_41	Post-Resistance	ZMYND8	23613	37	20	45976600	45976600	Missense_Mutation	SNP	C	T	18	485	c.25G>A	c.(25-27)GAT>AAT	p.D9N
Pat_41	Post-Resistance	NCOA3	8202	37	20	46271001	46271001	Missense_Mutation	SNP	C	T	12	285	c.3125C>T	c.(3124-3126)TCC>TTC	p.S1042F
Pat_41	Post-Resistance	PREX1	57580	37	20	47256399	47256399	Missense_Mutation	SNP	C	T	6	359	c.3809G>A	c.(3808-3810)GGC>GAC	p.G1270D
Pat_41	Post-Resistance	PREX1	57580	37	20	47317290	47317290	Splice_Site	SNP	C	T	13	286	c.917_splice	c.e7+1	p.R306_splice
Pat_41	Post-Resistance	ARFGEF2	10564	37	20	47630164	47630164	Missense_Mutation	SNP	G	A	15	134	c.3982G>A	c.(3982-3984)GGC>AGC	p.G1328S
Pat_41	Post-Resistance	CSE1L	1434	37	20	47682952	47682952	Nonsense_Mutation	SNP	G	A	15	366	c.381G>A	c.(379-381)TGG>TGA	p.W127*

Pat_41	Post-Resistance	CSE1L	1434	37	20	47691980	47691980	Missense_Mutation	SNP	C	T	21	213	c.1258C>T	c.(1258-1260)CCA>TCA	p.P420S
Pat_41	Post-Resistance	DDX27	55661	37	20	47839962	47839962	Missense_Mutation	SNP	C	T	12	295	c.551C>T	c.(550-552)ACC>ATC	p.T184I
Pat_41	Post-Resistance	ZNFX1	57169	37	20	47864502	47864502	Missense_Mutation	SNP	C	T	28	199	c.5059G>A	c.(5059-5061)GAG>AAG	p.E1687K
Pat_41	Post-Resistance	PTPN1	5770	37	20	49196374	49196374	Nonsense_Mutation	SNP	G	A	5	160	c.999G>A	c.(997-999)TGG>TGA	p.W333*
Pat_41	Post-Resistance	FAM65C	140876	37	20	49214229	49214229	Missense_Mutation	SNP	C	T	4	38	c.1666G>A	c.(1666-1668)GAG>AAG	p.E556K
Pat_41	Post-Resistance	ZFP64	55734	37	20	50776736	50776736	Missense_Mutation	SNP	G	A	36	283	c.689C>T	c.(688-690)CCC>CTC	p.P230L
Pat_41	Post-Resistance	ZNF217	7764	37	20	52193402	52193402	Missense_Mutation	SNP	G	A	7	213	c.1901C>T	c.(1900-1902)ACT>ATT	p.T634I
Pat_41	Post-Resistance	ZNF217	7764	37	20	52198432	52198432	Missense_Mutation	SNP	C	T	5	247	c.934G>A	c.(934-936)GAA>AAA	p.E312K
Pat_41	Post-Resistance	ZNF217	7764	37	20	52199177	52199177	Missense_Mutation	SNP	C	T	16	261	c.189G>A	c.(187-189)ATG>ATA	p.M63I
Pat_41	Post-Resistance	CYP24A1	1591	37	20	52775661	52775661	Missense_Mutation	SNP	G	A	28	230	c.992C>T	c.(991-993)ACA>ATA	p.T331I
Pat_41	Post-Resistance	CBLN4	140689	37	20	54579029	54579029	Missense_Mutation	SNP	C	T	7	83	c.199G>A	c.(199-201)GCC>ACC	p.A67T
Pat_41	Post-Resistance	MC3R	4159	37	20	54823949	54823949	Missense_Mutation	SNP	G	A	40	289	c.50G>A	c.(49-51)GGC>GAC	p.G17D
Pat_41	Post-Resistance	CSTF1	1477	37	20	54978748	54978748	Missense_Mutation	SNP	G	A	32	684	c.1261G>A	c.(1261-1263)GCG>ACG	p.A421T
Pat_41	Post-Resistance	C20orf43	51507	37	20	55093268	55093268	Missense_Mutation	SNP	C	T	11	310	c.868C>T	c.(868-870)CGC>TGC	p.R290C
Pat_41	Post-Resistance	SPO11	23626	37	20	55909080	55909080	Nonsense_Mutation	SNP	C	T	12	246	c.439C>T	c.(439-441)CAG>TAG	p.Q147*
Pat_41	Post-Resistance	RAE1	8480	37	20	55931523	55931523	Missense_Mutation	SNP	G	A	6	106	c.217G>A	c.(217-219)GAC>AAC	p.D73N
Pat_41	Post-Resistance	CTCFL	140690	37	20	56078514	56078514	Nonsense_Mutation	SNP	C	T	16	298	c.1818G>A	c.(1816-1818)TGG>TGA	p.W606*
Pat_41	Post-Resistance	CTCFL	140690	37	20	56078519	56078519	Missense_Mutation	SNP	C	T	7	309	c.1813G>A	c.(1813-1815)GGA>AGA	p.G605R
Pat_41	Post-Resistance	CTCFL	140690	37	20	56099144	56099144	Missense_Mutation	SNP	C	T	24	610	c.118G>A	c.(118-120)GAC>AAC	p.D40N
Pat_41	Post-Resistance	ZBP1	81030	37	20	56185397	56185397	Missense_Mutation	SNP	C	T	8	259	c.901G>A	c.(901-903)GCT>ACT	p.A301T
Pat_41	Post-Resistance	PMEPA1	56937	37	20	56227483	56227483	Missense_Mutation	SNP	G	A	4	57	c.490C>T	c.(490-492)CCC>TCC	p.P164S
Pat_41	Post-Resistance	STX16	8675	37	20	57227168	57227168	Missense_Mutation	SNP	C	T	31	144	c.106C>T	c.(106-108)CCT>TCT	p.P36S
Pat_41	Post-Resistance	GNAS	2778	37	20	57478605	57478605	Nonsense_Mutation	SNP	C	T	10	203	c.2206C>T	c.(2206-2208)CAG>TAG	p.Q736*
Pat_41	Post-Resistance	TH1L	51497	37	20	57564660	57564660	Missense_Mutation	SNP	G	A	11	435	c.649G>A	c.(649-651)GAA>AAA	p.E217K
Pat_41	Post-Resistance	ZNF831	128611	37	20	57767386	57767386	Missense_Mutation	SNP	G	A	3	39	c.1312G>A	c.(1312-1314)GGC>AGC	p.G438S
Pat_41	Post-Resistance	EDN3	1908	37	20	57876763	57876763	Nonsense_Mutation	SNP	G	A	21	289	c.351G>A	c.(349-351)TGG>TGA	p.W117*
Pat_41	Post-Resistance	PPP1R3D	5509	37	20	58514517	58514517	Missense_Mutation	SNP	G	A	9	111	c.470C>T	c.(469-471)CCC>CTC	p.P157L
Pat_41	Post-Resistance	CDH4	1002	37	20	60504676	60504676	Missense_Mutation	SNP	C	T	14	68	c.2015C>T	c.(2014-2016)GCC>GTC	p.A672V
Pat_41	Post-Resistance	C20orf200	253868	37	20	61143493	61143493	Missense_Mutation	SNP	G	A	7	107	c.355C>T	c.(355-357)CCG>TCG	p.P119S
Pat_41	Post-Resistance	C20orf200	253868	37	20	61143684	61143684	Missense_Mutation	SNP	C	T	8	124	c.164G>A	c.(163-165)AGG>AAG	p.R55K
Pat_41	Post-Resistance	SLCO4A1	28231	37	20	61292419	61292419	Missense_Mutation	SNP	C	T	5	186	c.1013C>T	c.(1012-1014)TCC>TTC	p.S338F
Pat_41	Post-Resistance	DIDO1	11083	37	20	61511454	61511454	Missense_Mutation	SNP	C	T	5	245	c.5854G>A	c.(5854-5856)GCG>ACG	p.A1952T
Pat_41	Post-Resistance	SLC17A9	63910	37	20	61595601	61595601	Missense_Mutation	SNP	C	T	28	465	c.844C>T	c.(844-846)CCT>TCT	p.P282S
Pat_41	Post-Resistance	ARFGAP1	55738	37	20	61907923	61907923	Missense_Mutation	SNP	G	A	8	98	c.262G>A	c.(262-264)GAG>AAG	p.E88K
Pat_41	Post-Resistance	EEF1A2	1917	37	20	62129076	62129076	Missense_Mutation	SNP	C	T	14	255	c.41G>A	c.(40-42)GGC>GAC	p.G14D
Pat_41	Post-Resistance	TPD52L2	7165	37	20	62507201	62507201	Nonsense_Mutation	SNP	G	A	12	274	c.347G>A	c.(346-348)TGG>TAG	p.W116*
Pat_41	Post-Resistance	UCKL1	54963	37	20	62571373	62571373	Missense_Mutation	SNP	C	T	4	98	c.1603G>A	c.(1603-1605)GTC>ATC	p.V535I
Pat_41	Post-Resistance	ZNF512B	57473	37	20	62597849	62597849	Missense_Mutation	SNP	C	T	54	693	c.679G>A	c.(679-681)GCC>ACC	p.A227T
Pat_41	Post-Resistance	TCEA2	6919	37	20	62698350	62698350	Missense_Mutation	SNP	T	C	7	60	c.218T>C	c.(217-219)ATC>ACC	p.I73T
Pat_41	Post-Resistance	OPRL1	4987	37	20	62729860	62729860	Missense_Mutation	SNP	G	A	4	41	c.821G>A	c.(820-822)GGC>GAC	p.G274D
Pat_41	Post-Resistance	MYT1	4661	37	20	62839670	62839670	Missense_Mutation	SNP	C	T	4	114	c.1121C>T	c.(1120-1122)ACC>ATC	p.T374I
Pat_41	Post-Resistance	PCMTD2	55251	37	20	62891376	62891376	Missense_Mutation	SNP	G	A	5	190	c.58G>A	c.(58-60)GAA>AAA	p.E20K
Pat_41	Post-Resistance	TPTE	7179	37	21	10910378	10910378	Missense_Mutation	SNP	C	T	7	431	c.1378G>A	c.(1378-1380)GAC>AAC	p.D460N
Pat_41	Post-Resistance	TPTE	7179	37	21	10933860	10933860	Missense_Mutation	SNP	C	T	15	695	c.1019G>A	c.(1018-1020)GGA>GAA	p.G340E
Pat_41	Post-Resistance	LIPI	149998	37	21	15537681	15537681	Missense_Mutation	SNP	C	T	20	129	c.827G>A	c.(826-828)AGA>AAA	p.R276K
Pat_41	Post-Resistance	RNF160	26046	37	21	30304959	30304959	Missense_Mutation	SNP	C	T	22	335	c.5041G>A	c.(5041-5043)GTA>ATA	p.V1681I
Pat_41	Post-Resistance	C21orf7	56911	37	21	30458185	30458185	Missense_Mutation	SNP	G	A	16	304	c.4G>A	c.(4-6)GTT>ATT	p.V2I

Pat_41	Post-Resistance	BACH1	571	37	21	30714988	30714988	Missense_Mutation	SNP	C	T	25	190	c.2045C>T	c.(2044-2046)CCC>CTC	p.P682L
Pat_41	Post-Resistance	GRIK1	2897	37	21	30959845	30959845	Missense_Mutation	SNP	G	A	12	44	c.1634C>T	c.(1633-1635)TCC>TTC	p.S545F
Pat_41	Post-Resistance	KRTAP19-4	337971	37	21	31869256	31869256	Missense_Mutation	SNP	C	T	14	419	c.173G>A	c.(172-174)GGA>GAA	p.G58E
Pat_41	Post-Resistance	SFRS15	57466	37	21	33064678	33064678	Missense_Mutation	SNP	G	A	8	210	c.1598C>T	c.(1597-1599)CCA>CTA	p.P533L
Pat_41	Post-Resistance	C21orf63	59271	37	21	33825767	33825767	Missense_Mutation	SNP	C	T	4	24	c.308C>T	c.(307-309)GCC>GTC	p.A103V
Pat_41	Post-Resistance	SYNJ1	8867	37	21	34018840	34018840	Missense_Mutation	SNP	C	T	9	195	c.3227G>A	c.(3226-3228)GGC>GAC	p.G1076D
Pat_41	Post-Resistance	GCFC1	94104	37	21	34117134	34117134	Missense_Mutation	SNP	G	A	8	263	c.2159C>T	c.(2158-2160)TCA>TTA	p.S720L
Pat_41	Post-Resistance	GCFC1	94104	37	21	34117208	34117208	Missense_Mutation	SNP	C	T	12	102	c.2085G>A	c.(2083-2085)ATG>ATA	p.M695I
Pat_41	Post-Resistance	GCFC1	94104	37	21	34134467	34134467	Missense_Mutation	SNP	G	A	25	295	c.811C>T	c.(811-813)CGC>TGC	p.R271C
Pat_41	Post-Resistance	GART	2618	37	21	34892715	34892715	Missense_Mutation	SNP	G	A	38	169	c.1658C>T	c.(1657-1659)GCT>GTT	p.A553V
Pat_41	Post-Resistance	GART	2618	37	21	34900841	34900841	Missense_Mutation	SNP	C	T	43	223	c.881G>A	c.(880-882)GGT>GAT	p.G294D
Pat_41	Post-Resistance	DONSON	29980	37	21	34954276	34954276	Missense_Mutation	SNP	C	T	7	163	c.1132G>A	c.(1132-1134)GAC>AAC	p.D378N
Pat_41	Post-Resistance	DONSON	29980	37	21	34958319	34958319	Missense_Mutation	SNP	T	C	16	216	c.571A>G	c.(571-573)AGG>GGG	p.R191G
Pat_41	Post-Resistance	CRYZL1	9946	37	21	34974587	34974587	Missense_Mutation	SNP	C	T	8	259	c.530G>A	c.(529-531)TGC>TAC	p.C177Y
Pat_41	Post-Resistance	ITSN1	6453	37	21	35127655	35127655	Missense_Mutation	SNP	G	A	11	140	c.677G>A	c.(676-678)AGG>AAG	p.R226K
Pat_41	Post-Resistance	ITSN1	6453	37	21	35183468	35183468	Missense_Mutation	SNP	G	A	40	309	c.2509G>A	c.(2509-2511)GCA>ACA	p.A837T
Pat_41	Post-Resistance	ITSN1	6453	37	21	35255878	35255878	Missense_Mutation	SNP	G	A	10	235	c.4579G>A	c.(4579-4581)GTA>ATA	p.V1527I
Pat_41	Post-Resistance	SETD4	54093	37	21	37418152	37418152	Missense_Mutation	SNP	G	A	19	262	c.454C>T	c.(454-456)CCC>TCC	p.P152S
Pat_41	Post-Resistance	DOPEY2	9980	37	21	37600023	37600023	Missense_Mutation	SNP	G	A	6	86	c.1513G>A	c.(1513-1515)GTG>ATG	p.V505M
Pat_41	Post-Resistance	MORC3	23515	37	21	37713822	37713822	Missense_Mutation	SNP	C	T	14	185	c.734C>T	c.(733-735)CCT>CTT	p.P245L
Pat_41	Post-Resistance	CHAF1B	8208	37	21	37785376	37785376	Missense_Mutation	SNP	C	T	5	121	c.1256C>T	c.(1255-1257)ACC>ATC	p.T419I
Pat_41	Post-Resistance	DSCR6	53820	37	21	38390460	38390460	Missense_Mutation	SNP	C	T	10	129	c.526C>T	c.(526-528)CCT>TCT	p.P176S
Pat_41	Post-Resistance	TTC3	7267	37	21	38525381	38525381	Nonsense_Mutation	SNP	G	A	18	300	c.2544G>A	c.(2542-2544)TGG>TGA	p.W848*
Pat_41	Post-Resistance	TTC3	7267	37	21	38538301	38538301	Missense_Mutation	SNP	C	T	16	170	c.3785C>T	c.(3784-3786)TCT>TTT	p.S1262F
Pat_41	Post-Resistance	TTC3	7267	37	21	38538357	38538357	Missense_Mutation	SNP	C	T	17	223	c.3841C>T	c.(3841-3843)CCA>TCA	p.P1281S
Pat_41	Post-Resistance	DSCR3	10311	37	21	38610871	38610871	Missense_Mutation	SNP	G	A	28	430	c.241C>T	c.(241-243)CCG>TCG	p.P81S
Pat_41	Post-Resistance	KCNJ6	3763	37	21	38997688	38997688	Missense_Mutation	SNP	C	T	13	91	c.1045G>A	c.(1045-1047)GTT>ATT	p.V349I
Pat_41	Post-Resistance	ERG	2078	37	21	39755693	39755693	Missense_Mutation	SNP	G	A	8	126	c.1093C>T	c.(1093-1095)CCC>TCC	p.P365S
Pat_41	Post-Resistance	BRWD1	54014	37	21	40571024	40571024	Missense_Mutation	SNP	G	A	26	291	c.5318C>T	c.(5317-5319)GCT>GTT	p.A1773V
Pat_41	Post-Resistance	BRWD1	54014	37	21	40597076	40597076	Missense_Mutation	SNP	C	T	34	543	c.3256G>A	c.(3256-3258)GTG>ATG	p.V1086M
Pat_41	Post-Resistance	DSCAM	1826	37	21	41427723	41427723	Missense_Mutation	SNP	G	A	67	345	c.4964C>T	c.(4963-4965)ACC>ATC	p.T1655I
Pat_41	Post-Resistance	DSCAM	1826	37	21	41648185	41648185	Missense_Mutation	SNP	G	A	5	73	c.2195C>T	c.(2194-2196)CCC>CTC	p.P732L
Pat_41	Post-Resistance	MX2	4600	37	21	42748852	42748852	Missense_Mutation	SNP	C	T	5	173	c.19C>T	c.(19-21)CCT>TCT	p.P7S
Pat_41	Post-Resistance	MX1	4599	37	21	42817957	42817957	Missense_Mutation	SNP	G	A	9	133	c.1162G>A	c.(1162-1164)GCT>ACT	p.A388T
Pat_41	Post-Resistance	RIPK4	54101	37	21	43187057	43187057	Missense_Mutation	SNP	C	T	4	114	c.145G>A	c.(145-147)GCC>ACC	p.A49T
Pat_41	Post-Resistance	PRDM15	63977	37	21	43222894	43222894	Missense_Mutation	SNP	G	A	48	288	c.4019C>T	c.(4018-4020)TCC>TTC	p.S1340F
Pat_41	Post-Resistance	PRDM15	63977	37	21	43274852	43274852	Missense_Mutation	SNP	G	A	4	78	c.1459C>T	c.(1459-1461)CGG>TGG	p.R487W
Pat_41	Post-Resistance	PRDM15	63977	37	21	43279771	43279771	Missense_Mutation	SNP	G	A	4	93	c.961C>T	c.(961-963)CAC>TAC	p.H321Y
Pat_41	Post-Resistance	C2CD2	25966	37	21	43309243	43309243	Missense_Mutation	SNP	G	A	4	69	c.2081C>T	c.(2080-2082)CCC>CTC	p.P694L
Pat_41	Post-Resistance	ZNF295	49854	37	21	43413526	43413526	Missense_Mutation	SNP	C	T	4	114	c.679G>A	c.(679-681)GAT>AAT	p.D227N
Pat_41	Post-Resistance	ZNF295	49854	37	21	43413639	43413639	Missense_Mutation	SNP	G	A	37	457	c.566C>T	c.(565-567)CCA>CTA	p.P189L
Pat_41	Post-Resistance	TMPRSS3	64699	37	21	43795859	43795859	Missense_Mutation	SNP	G	A	9	186	c.1313C>T	c.(1312-1314)ACC>ATC	p.T438I
Pat_41	Post-Resistance	SLC37A1	54020	37	21	43955661	43955661	Splice_Site	SNP	G	A	31	161	c.350_splice	c.e6+1	p.S117_splice
Pat_41	Post-Resistance	WDR4	10785	37	21	44270239	44270239	Nonsense_Mutation	SNP	G	A	4	57	c.1159C>T	c.(1159-1161)CAG>TAG	p.Q387*
Pat_41	Post-Resistance	SIK1	150094	37	21	44838403	44838403	Missense_Mutation	SNP	G	A	8	67	c.1481C>T	c.(1480-1482)TCC>TTC	p.S494F
Pat_41	Post-Resistance	SIK1	150094	37	21	44845286	44845286	Splice_Site	SNP	C	T	10	134	c.273_splice	c.e3+1	p.Q91_splice
Pat_41	Post-Resistance	TRAPPC10	7109	37	21	45494238	45494238	Missense_Mutation	SNP	G	A	13	221	c.1072G>A	c.(1072-1074)GTG>ATG	p.V358M

Pat_41	Post-Resistance	PWP2	5822	37	21	45547828	45547828	Missense_Mutation	SNP	C	T	12	154	c.2156C>T	c.(2155-2157)GCC>GTC	p.A719V
Pat_41	Post-Resistance	C21orf33	8209	37	21	45555968	45555968	Missense_Mutation	SNP	G	A	5	42	c.221G>A	c.(220-222)GGG>GAG	p.G74E
Pat_41	Post-Resistance	AIRE	326	37	21	45716315	45716315	Missense_Mutation	SNP	C	T	5	123	c.1553C>T	c.(1552-1554)TCC>TTC	p.S518F
Pat_41	Post-Resistance	KRTAP10-4	386672	37	21	45993670	45993670	Missense_Mutation	SNP	G	A	25	218	c.35G>A	c.(34-36)AGC>AAC	p.S12N
Pat_41	Post-Resistance	KRTAP10-4	386672	37	21	45993688	45993688	Missense_Mutation	SNP	G	A	27	142	c.53G>A	c.(52-54)GGT>GAT	p.G18D
Pat_41	Post-Resistance	KRTAP10-4	386672	37	21	45994705	45994705	Missense_Mutation	SNP	C	T	7	327	c.1070C>T	c.(1069-1071)CCC>CTC	p.P357L
Pat_41	Post-Resistance	KRTAP10-6	386674	37	21	46011464	46011464	Missense_Mutation	SNP	G	A	13	246	c.902C>T	c.(901-903)TCC>TTC	p.S301F
Pat_41	Post-Resistance	PTTG1IP	754	37	21	46281144	46281144	Missense_Mutation	SNP	C	T	13	88	c.211G>A	c.(211-213)GTT>ATT	p.V71I
Pat_41	Post-Resistance	ADARB1	104	37	21	46624559	46624559	Missense_Mutation	SNP	A	G	5	167	c.1775A>G	c.(1774-1776)CAC>CGC	p.H592R
Pat_41	Post-Resistance	POFUT2	23275	37	21	46689858	46689858	Missense_Mutation	SNP	C	T	6	128	c.908G>A	c.(907-909)AGA>AAA	p.R303K
Pat_41	Post-Resistance	COL6A1	1291	37	21	47410909	47410909	Missense_Mutation	SNP	C	T	3	41	c.1073C>T	c.(1072-1074)CCT>CTT	p.P358L
Pat_41	Post-Resistance	MCM3AP	8888	37	21	47656826	47656826	Missense_Mutation	SNP	G	A	13	210	c.5701C>T	c.(5701-5703)CCC>TCC	p.P1901S
Pat_41	Post-Resistance	C21orf58	54058	37	21	47731445	47731445	Missense_Mutation	SNP	G	A	9	35	c.646C>T	c.(646-648)CCT>TCT	p.P216S
Pat_41	Post-Resistance	PCNT	5116	37	21	47773939	47773939	Missense_Mutation	SNP	G	A	4	55	c.1718G>A	c.(1717-1719)GGA>GAA	p.G573E
Pat_41	Post-Resistance	PCNT	5116	37	21	47776987	47776987	Missense_Mutation	SNP	G	A	5	68	c.2035G>A	c.(2035-2037)GTG>ATG	p.V679M
Pat_41	Post-Resistance	PCNT	5116	37	21	47809325	47809325	Missense_Mutation	SNP	G	A	3	24	c.3819G>A	c.(3817-3819)ATG>ATA	p.M1273I
Pat_41	Post-Resistance	DIP2A	23181	37	21	47969737	47969737	Missense_Mutation	SNP	C	T	72	452	c.2576C>T	c.(2575-2577)GCT>GTT	p.A859V
Pat_41	Post-Resistance	S100B	6285	37	21	48019416	48019416	Missense_Mutation	SNP	C	T	16	161	c.139G>A	c.(139-141)GAA>AAA	p.E47K
Pat_41	Post-Resistance	PRMT2	3275	37	21	48068433	48068433	Nonsense_Mutation	SNP	C	T	24	164	c.391C>T	c.(391-393)CAG>TAG	p.Q131*
Pat_41	Post-Resistance	OR11H1	81061	37	22	16449638	16449638	Missense_Mutation	SNP	C	T	12	397	c.167G>A	c.(166-168)GGG>GAG	p.G56E
Pat_41	Post-Resistance	GAB4	128954	37	22	17449205	17449205	Missense_Mutation	SNP	C	T	10	186	c.1006G>A	c.(1006-1008)GGA>AGA	p.G336R
Pat_41	Post-Resistance	CECR2	27443	37	22	18028668	18028668	Missense_Mutation	SNP	C	T	5	89	c.3625C>T	c.(3625-3627)CCC>TCC	p.P1209S
Pat_41	Post-Resistance	MICAL3	57553	37	22	18273773	18273773	Missense_Mutation	SNP	C	T	8	59	c.5815G>A	c.(5815-5817)GCA>ACA	p.A1939T
Pat_41	Post-Resistance	MICAL3	57553	37	22	18387479	18387479	Missense_Mutation	SNP	G	A	66	425	c.391C>T	c.(391-393)CCA>TCA	p.P131S
Pat_41	Post-Resistance	HIRA	7290	37	22	19394767	19394767	Missense_Mutation	SNP	C	T	17	229	c.242G>A	c.(241-243)AGT>AAT	p.S81N
Pat_41	Post-Resistance	DGCR8	54487	37	22	20079038	20079038	Missense_Mutation	SNP	G	A	44	491	c.1387G>A	c.(1387-1389)GAG>AAG	p.E463K
Pat_41	Post-Resistance	DGCR8	54487	37	22	20080365	20080365	Missense_Mutation	SNP	C	T	7	272	c.1640C>T	c.(1639-1641)ACC>ATC	p.T547I
Pat_41	Post-Resistance	ZDHHC8	29801	37	22	20127387	20127387	Missense_Mutation	SNP	G	A	5	34	c.529G>A	c.(529-531)GGG>AGG	p.G177R
Pat_41	Post-Resistance	ZDHHC8	29801	37	22	20127394	20127394	Missense_Mutation	SNP	G	A	3	38	c.536G>A	c.(535-537)GGA>GAA	p.G179E
Pat_41	Post-Resistance	DGCR6L	85359	37	22	20302927	20302927	Missense_Mutation	SNP	C	T	6	106	c.445G>A	c.(445-447)GTG>ATG	p.V149M
Pat_41	Post-Resistance	PI4KA	5297	37	22	21081565	21081565	Missense_Mutation	SNP	G	A	8	75	c.4720C>T	c.(4720-4722)CCT>TCT	p.P1574S
Pat_41	Post-Resistance	PI4KA	5297	37	22	21115619	21115619	Missense_Mutation	SNP	C	T	8	120	c.2590G>A	c.(2590-2592)GAT>AAT	p.D864N
Pat_41	Post-Resistance	SERPIND1	3053	37	22	21133718	21133718	Missense_Mutation	SNP	C	T	6	17	c.118C>T	c.(118-120)CCC>TCC	p.P40S
Pat_41	Post-Resistance	SNAP29	9342	37	22	21235390	21235390	Missense_Mutation	SNP	G	A	7	99	c.488G>A	c.(487-489)AGC>AAC	p.S163N
Pat_41	Post-Resistance	CCDC116	164592	37	22	21988818	21988818	Missense_Mutation	SNP	G	A	5	31	c.580G>A	c.(580-582)GAG>AAG	p.E194K
Pat_41	Post-Resistance	RGL4	266747	37	22	24035981	24035981	Missense_Mutation	SNP	G	T	5	161	c.732G>T	c.(730-732)TTG>TTT	p.L244F
Pat_41	Post-Resistance	SLC2A11	66035	37	22	24226914	24226914	Missense_Mutation	SNP	C	T	9	103	c.1369C>T	c.(1369-1371)CCT>TCT	p.P457S
Pat_41	Post-Resistance	CABIN1	23523	37	22	24432610	24432610	Missense_Mutation	SNP	C	T	6	247	c.77C>T	c.(76-78)ACC>ATC	p.T26I
Pat_41	Post-Resistance	CABIN1	23523	37	22	24463064	24463064	Missense_Mutation	SNP	G	A	18	89	c.2164G>A	c.(2164-2166)GAC>AAC	p.D722N
Pat_41	Post-Resistance	CYTSA	23384	37	22	24718563	24718563	Missense_Mutation	SNP	G	A	8	36	c.1615G>A	c.(1615-1617)GAA>AAA	p.E539K
Pat_41	Post-Resistance	MYO18B	84700	37	22	26239830	26239830	Missense_Mutation	SNP	G	A	3	19	c.3337G>A	c.(3337-3339)GAT>AAT	p.D1113N
Pat_41	Post-Resistance	MYO18B	84700	37	22	26423258	26423258	Missense_Mutation	SNP	G	A	10	231	c.7318G>A	c.(7318-7320)GAC>AAC	p.D2440N
Pat_41	Post-Resistance	HPS4	89781	37	22	26861420	26861420	Splice_Site	SNP	C	T	10	141	c.803_splice	c.e10+1	p.R268_splice
Pat_41	Post-Resistance	HPS4	89781	37	22	26861434	26861434	Missense_Mutation	SNP	C	T	16	180	c.790G>A	c.(790-792)GAA>AAA	p.E264K
Pat_41	Post-Resistance	SRRD	402055	37	22	26884440	26884440	Missense_Mutation	SNP	C	T	16	182	c.595C>T	c.(595-597)CTC>TTC	p.L199F
Pat_41	Post-Resistance	CCDC117	150275	37	22	29169756	29169756	Missense_Mutation	SNP	G	A	16	181	c.229G>A	c.(229-231)GAG>AAG	p.E77K
Pat_41	Post-Resistance	ZNRF3	84133	37	22	29445419	29445419	Missense_Mutation	SNP	G	A	5	105	c.950G>A	c.(949-951)CGC>CAC	p.R317H

Pat_41	Post-Resistance	NF2	4771	37	22	30054177	30054177	Splice_Site	SNP	G	A	9	125	c.600_splice	c.e7-1	p.R200_splice
Pat_41	Post-Resistance	ASCC2	84164	37	22	30189353	30189353	Missense_Mutation	SNP	G	A	9	57	c.1915C>T	c.(1915-1917)CGC>TGC	p.R639C
Pat_41	Post-Resistance	SF3A1	10291	37	22	30731676	30731676	Nonsense_Mutation	SNP	G	A	16	222	c.2173C>T	c.(2173-2175)CAG>TAG	p.Q725*
Pat_41	Post-Resistance	SF3A1	10291	37	22	30738296	30738296	Missense_Mutation	SNP	C	T	6	31	c.770G>A	c.(769-771)AGG>AAG	p.R257K
Pat_41	Post-Resistance	SF3A1	10291	37	22	30741179	30741179	Missense_Mutation	SNP	C	T	11	113	c.394G>A	c.(394-396)GTC>ATC	p.V132I
Pat_41	Post-Resistance	CCDC157	550631	37	22	30762185	30762185	Missense_Mutation	SNP	C	T	14	272	c.196C>T	c.(196-198)CCC>TCC	p.P66S
Pat_41	Post-Resistance	MORC2	22880	37	22	31330977	31330977	Missense_Mutation	SNP	C	T	6	24	c.1798G>A	c.(1798-1800)GCC>ACC	p.A600T
Pat_41	Post-Resistance	INPP5J	27124	37	22	31529938	31529938	Missense_Mutation	SNP	G	A	8	87	c.2554G>A	c.(2554-2556)GAC>AAC	p.D852N
Pat_41	Post-Resistance	PATZ1	23598	37	22	31723196	31723196	Missense_Mutation	SNP	G	A	8	108	c.1745C>T	c.(1744-1746)GCC>GTC	p.A582V
Pat_41	Post-Resistance	EIF4ENIF1	56478	37	22	31843443	31843443	Missense_Mutation	SNP	C	T	17	165	c.1957G>A	c.(1957-1959)GTG>ATG	p.V653M
Pat_41	Post-Resistance	SFI1	9814	37	22	31924693	31924693	Missense_Mutation	SNP	C	T	15	61	c.110C>T	c.(109-111)GCA>GTA	p.A37V
Pat_41	Post-Resistance	SFI1	9814	37	22	31957301	31957301	Nonsense_Mutation	SNP	C	T	9	135	c.688C>T	c.(688-690)CGA>TGA	p.R230*
Pat_41	Post-Resistance	C22orf28	51493	37	22	32789949	32789949	Missense_Mutation	SNP	G	A	16	207	c.1220C>T	c.(1219-1221)ACC>ATC	p.T407I
Pat_41	Post-Resistance	FBXO7	25793	37	22	32880106	32880106	Missense_Mutation	SNP	C	T	22	276	c.640C>T	c.(640-642)CCT>TCT	p.P214S
Pat_41	Post-Resistance	LARGE	9215	37	22	34046631	34046631	Missense_Mutation	SNP	G	A	8	91	c.130C>T	c.(130-132)CCG>TCG	p.P44S
Pat_41	Post-Resistance	RASD2	23551	37	22	35948051	35948051	Missense_Mutation	SNP	G	A	16	93	c.773G>A	c.(772-774)CGT>CAT	p.R258H
Pat_41	Post-Resistance	MB	4151	37	22	36006948	36006948	Missense_Mutation	SNP	G	A	4	47	c.301C>T	c.(301-303)CCC>TCC	p.P101S
Pat_41	Post-Resistance	APOL2	23780	37	22	36629202	36629202	Missense_Mutation	SNP	G	A	44	268	c.7C>T	c.(7-9)CCA>TCA	p.P3S
Pat_41	Post-Resistance	MYH9	4627	37	22	36684330	36684330	Missense_Mutation	SNP	C	T	9	148	c.4900G>A	c.(4900-4902)GAC>AAC	p.D1634N
Pat_41	Post-Resistance	IL2RB	3560	37	22	37535186	37535186	Missense_Mutation	SNP	G	A	8	91	c.359C>T	c.(358-360)GCC>GTC	p.A120V
Pat_41	Post-Resistance	CYTH4	27128	37	22	37705337	37705337	Missense_Mutation	SNP	G	A	18	258	c.781G>A	c.(781-783)GAC>AAC	p.D261N
Pat_41	Post-Resistance	TRIOBP	11078	37	22	38120212	38120212	Missense_Mutation	SNP	C	G	6	356	c.1649C>G	c.(1648-1650)ACA>AGA	p.T550R
Pat_41	Post-Resistance	TRIOBP	11078	37	22	38120290	38120290	Missense_Mutation	SNP	G	C	6	235	c.1727G>C	c.(1726-1728)AGA>ACA	p.R576T
Pat_41	Post-Resistance	TRIOBP	11078	37	22	38120296	38120296	Missense_Mutation	SNP	C	T	11	252	c.1733C>T	c.(1732-1734)TCC>TTC	p.S578F
Pat_41	Post-Resistance	TRIOBP	11078	37	22	38121418	38121418	Missense_Mutation	SNP	C	T	36	361	c.2855C>T	c.(2854-2856)CCC>CTC	p.P952L
Pat_41	Post-Resistance	GALR3	8484	37	22	38219532	38219532	Missense_Mutation	SNP	C	T	4	50	c.119C>T	c.(118-120)GCA>GTA	p.A40V
Pat_41	Post-Resistance	PICK1	9463	37	22	38468589	38468589	Missense_Mutation	SNP	G	A	19	153	c.662G>A	c.(661-663)GGC>GAC	p.G221D
Pat_41	Post-Resistance	KCNJ4	3761	37	22	38824159	38824159	Translation_Start_Site	SNP	C	T	12	125	c.-21G>A	c.(-23--19)AGGTG>AGATG	
Pat_41	Post-Resistance	APOBEC3B	9582	37	22	39385461	39385461	Splice_Site	SNP	G	A	7	60	c.570_splice	c.e5-1	p.R190_splice
Pat_41	Post-Resistance	PDGFB	5155	37	22	39621852	39621852	Missense_Mutation	SNP	G	A	5	50	c.602C>T	c.(601-603)GCC>GTC	p.A201V
Pat_41	Post-Resistance	CACNA1I	8911	37	22	40061886	40061886	Missense_Mutation	SNP	C	T	30	231	c.3979C>T	c.(3979-3981)CTC>TTC	p.L1327F
Pat_41	Post-Resistance	CACNA1I	8911	37	22	40061913	40061913	Missense_Mutation	SNP	C	A	5	222	c.4006C>A	c.(4006-4008)CTG>ATG	p.L1336M
Pat_41	Post-Resistance	TNRC6B	23112	37	22	40711366	40711366	Nonsense_Mutation	SNP	G	A	12	163	c.4758G>A	c.(4756-4758)TGG>TGA	p.W1586*
Pat_41	Post-Resistance	ADSL	158	37	22	40760884	40760884	Missense_Mutation	SNP	G	A	6	185	c.1192G>A	c.(1192-1194)GAT>AAT	p.D398N
Pat_41	Post-Resistance	MKL1	57591	37	22	40815348	40815348	Missense_Mutation	SNP	G	A	7	77	c.1094C>T	c.(1093-1095)CCT>CTT	p.P365L
Pat_41	Post-Resistance	XRCC6	2547	37	22	42049664	42049664	Missense_Mutation	SNP	G	A	25	134	c.1261G>A	c.(1261-1263)GAT>AAT	p.D421N
Pat_41	Post-Resistance	CENPM	79019	37	22	42343100	42343100	Translation_Start_Site	SNP	G	A	3	30	c.-19C>T	c.(-21--17)AACGG>AATGG	
Pat_41	Post-Resistance	3-Sep	55964	37	22	42390326	42390326	Missense_Mutation	SNP	C	T	7	168	c.898C>T	c.(898-900)CTT>TTT	p.L300F
Pat_41	Post-Resistance	TCF20	6942	37	22	42607342	42607342	Missense_Mutation	SNP	C	T	8	123	c.3970G>A	c.(3970-3972)GAT>AAT	p.D1324N
Pat_41	Post-Resistance	ARFGAP3	26286	37	22	43195130	43195130	Missense_Mutation	SNP	G	A	18	303	c.1448C>T	c.(1447-1449)CCC>CTC	p.P483L
Pat_41	Post-Resistance	ARFGAP3	26286	37	22	43230267	43230267	Missense_Mutation	SNP	G	A	48	459	c.458C>T	c.(457-459)GCC>GTC	p.A153V
Pat_41	Post-Resistance	EFCAB6	64800	37	22	43986065	43986065	Missense_Mutation	SNP	G	A	11	148	c.2921C>T	c.(2920-2922)ACC>ATC	p.T974I
Pat_41	Post-Resistance	PHF21B	112885	37	22	45309824	45309824	Nonsense_Mutation	SNP	G	A	18	244	c.709C>T	c.(709-711)CAA>TAA	p.Q237*
Pat_41	Post-Resistance	GTSE1	51512	37	22	46704322	46704322	Missense_Mutation	SNP	C	T	27	314	c.244C>T	c.(244-246)CCC>TCC	p.P82S
Pat_41	Post-Resistance	GTSE1	51512	37	22	46725279	46725279	Missense_Mutation	SNP	G	A	20	301	c.1951G>A	c.(1951-1953)GAA>AAA	p.E651K
Pat_41	Post-Resistance	CELSR1	9620	37	22	46835245	46835245	Missense_Mutation	SNP	C	T	4	132	c.4247G>A	c.(4246-4248)GGC>GAC	p.G1416D
Pat_41	Post-Resistance	CELSR1	9620	37	22	46931300	46931300	Missense_Mutation	SNP	C	T	3	44	c.1768G>A	c.(1768-1770)GTG>ATG	p.V590M

Pat_41	Post-Resistance	CELSR1	9620	37	22	46931672	46931672	Missense_Mutation	SNP	C	T	6	110	c.1396G>A	c.(1396-1398)GTC>ATC	p.V466I
Pat_41	Post-Resistance	TBC1D22A	25771	37	22	47287172	47287172	Missense_Mutation	SNP	C	T	11	63	c.719C>T	c.(718-720)CCC>CTC	p.P240L
Pat_41	Post-Resistance	BRD1	23774	37	22	50170699	50170699	Missense_Mutation	SNP	G	A	5	98	c.2711C>T	c.(2710-2712)GCG>GTG	p.A904V
Pat_41	Post-Resistance	BRD1	23774	37	22	50217766	50217766	Missense_Mutation	SNP	G	A	7	74	c.200C>T	c.(199-201)GCT>GTT	p.A67V
Pat_41	Post-Resistance	ALG12	79087	37	22	50307401	50307401	Missense_Mutation	SNP	C	T	7	111	c.13G>A	c.(13-15)GGG>AGG	p.G5R
Pat_41	Post-Resistance	CRELD2	79174	37	22	50320917	50320917	Missense_Mutation	SNP	G	A	25	287	c.1024G>A	c.(1024-1026)GAA>AAA	p.E342K
Pat_41	Post-Resistance	SELO	83642	37	22	50649175	50649175	Missense_Mutation	SNP	G	A	6	85	c.1186G>A	c.(1186-1188)GAA>AAA	p.E396K
Pat_41	Post-Resistance	TUBGCP6	85378	37	22	50660114	50660114	Missense_Mutation	SNP	C	T	4	98	c.2674G>A	c.(2674-2676)GAC>AAC	p.D892N
Pat_41	Post-Resistance	TUBGCP6	85378	37	22	50682668	50682668	Missense_Mutation	SNP	G	A	18	170	c.221C>T	c.(220-222)TCC>TTC	p.S74F
Pat_41	Post-Resistance	MAPK11	5600	37	22	50703885	50703885	Missense_Mutation	SNP	C	T	9	112	c.880G>A	c.(880-882)GAC>AAC	p.D294N
Pat_41	Post-Resistance	MAPK11	5600	37	22	50705022	50705022	Missense_Mutation	SNP	C	T	5	87	c.629G>A	c.(628-630)GGC>GAC	p.G210D
Pat_41	Post-Resistance	PLXNB2	23654	37	22	50716313	50716313	Missense_Mutation	SNP	C	T	5	98	c.5017G>A	c.(5017-5019)GAA>AAA	p.E1673K
Pat_41	Post-Resistance	PLXNB2	23654	37	22	50717332	50717332	Missense_Mutation	SNP	G	A	3	55	c.4498C>T	c.(4498-4500)CGT>TGT	p.R1500C
Pat_41	Post-Resistance	PLXNB2	23654	37	22	50721230	50721230	Missense_Mutation	SNP	C	T	7	50	c.2897G>A	c.(2896-2898)GGG>GAG	p.G966E
Pat_41	Post-Resistance	SAPS2	9701	37	22	50876607	50876607	Missense_Mutation	SNP	G	A	12	180	c.1844G>A	c.(1843-1845)AGC>AAC	p.S615N
Pat_41	Post-Resistance	SBF1	6305	37	22	50899024	50899024	Missense_Mutation	SNP	C	T	20	191	c.3085G>A	c.(3085-3087)GGC>AGC	p.G1029S
Pat_41	Post-Resistance	SBF1	6305	37	22	50900531	50900531	Missense_Mutation	SNP	G	A	18	111	c.2414C>T	c.(2413-2415)GCC>GTC	p.A805V
Pat_41	Post-Resistance	MIOX	55586	37	22	50928211	50928211	Missense_Mutation	SNP	C	T	14	250	c.784C>T	c.(784-786)CCG>TCG	p.P262S
Pat_41	Post-Resistance	ODF3B	440836	37	22	50968920	50968920	Missense_Mutation	SNP	C	T	3	16	c.751G>A	c.(751-753)GCG>ACG	p.A251T
Pat_41	Post-Resistance	CPT1B	1375	37	22	51014526	51014526	Missense_Mutation	SNP	C	T	7	117	c.715G>A	c.(715-717)GAA>AAA	p.E239K
Pat_41	Post-Resistance	CPT1B	1375	37	22	51015819	51015819	Missense_Mutation	SNP	G	A	7	94	c.215C>T	c.(214-216)TCC>TTC	p.S72F
Pat_41	Post-Resistance	ITPR1	3708	37	3	4702715	4702715	Missense_Mutation	SNP	G	A	6	44	c.1195G>A	c.(1195-1197)GTT>ATT	p.V399I
Pat_41	Post-Resistance	ITPR1	3708	37	3	4704808	4704808	Missense_Mutation	SNP	G	A	9	68	c.1472G>A	c.(1471-1473)GGT>GAT	p.G491D
Pat_41	Post-Resistance	ITPR1	3708	37	3	4723047	4723047	Splice_Site	SNP	G	A	13	61	c.3080_splice	c.e26-1	p.G1027_splice
Pat_41	Post-Resistance	BHLHE40	8553	37	3	5024833	5024833	Missense_Mutation	SNP	G	A	34	174	c.695G>A	c.(694-696)GGG>GAG	p.G232E
Pat_41	Post-Resistance	SETD5	55209	37	3	9482218	9482218	Nonsense_Mutation	SNP	C	T	6	72	c.646C>T	c.(646-648)CAG>TAG	p.Q216*
Pat_41	Post-Resistance	TADA3	10474	37	3	9832961	9832961	Missense_Mutation	SNP	G	A	11	72	c.190C>T	c.(190-192)CTT>TTT	p.L64F
Pat_41	Post-Resistance	CIDEC	63924	37	3	9911976	9911976	Missense_Mutation	SNP	G	A	13	80	c.238C>T	c.(238-240)CCC>TCC	p.P80S
Pat_41	Post-Resistance	JAGN1	84522	37	3	9934738	9934738	Missense_Mutation	SNP	C	T	6	26	c.229C>T	c.(229-231)CCG>TCG	p.P77S
Pat_41	Post-Resistance	PRRT3	285368	37	3	9990915	9990915	Missense_Mutation	SNP	C	A	7	64	c.885G>T	c.(883-885)GAG>GAT	p.E295D
Pat_41	Post-Resistance	TATDN2	9797	37	3	10312178	10312178	Missense_Mutation	SNP	G	A	11	97	c.1312G>A	c.(1312-1314)GAG>AAG	p.E438K
Pat_41	Post-Resistance	ATP2B2	491	37	3	10387112	10387112	Missense_Mutation	SNP	C	T	10	34	c.2659G>A	c.(2659-2661)GTG>ATG	p.V887M
Pat_41	Post-Resistance	TSEN2	80746	37	3	12560606	12560606	Missense_Mutation	SNP	C	T	6	87	c.1009C>T	c.(1009-1011)CCC>TCC	p.P337S
Pat_41	Post-Resistance	TSEN2	80746	37	3	12573097	12573097	Missense_Mutation	SNP	C	T	6	61	c.1277C>T	c.(1276-1278)CCC>CTC	p.P426L
Pat_41	Post-Resistance	NUP210	23225	37	3	13383264	13383264	Missense_Mutation	SNP	G	A	8	78	c.3212C>T	c.(3211-3213)GCC>GTC	p.A1071V
Pat_41	Post-Resistance	NUP210	23225	37	3	13429877	13429877	Missense_Mutation	SNP	C	T	5	27	c.610G>A	c.(610-612)GAC>AAC	p.D204N
Pat_41	Post-Resistance	RFTN1	23180	37	3	16419321	16419321	Missense_Mutation	SNP	C	T	17	39	c.730G>A	c.(730-732)GGA>AGA	p.G244R
Pat_41	Post-Resistance	KCNH8	131096	37	3	19389238	19389238	Missense_Mutation	SNP	G	A	8	78	c.592G>A	c.(592-594)GCA>ACA	p.A198T
Pat_41	Post-Resistance	RAB5A	5868	37	3	19992545	19992545	Missense_Mutation	SNP	C	T	5	148	c.155C>T	c.(154-156)ACC>ATC	p.T52I
Pat_41	Post-Resistance	SGOL1	151648	37	3	20216343	20216343	Missense_Mutation	SNP	C	T	32	109	c.680G>A	c.(679-681)GGA>GAA	p.G227E
Pat_41	Post-Resistance	UBE2E1	7324	37	3	23930708	23930708	Missense_Mutation	SNP	G	A	20	113	c.442G>A	c.(442-444)GTC>ATC	p.V148I
Pat_41	Post-Resistance	NKIRAS1	28512	37	3	23942517	23942517	Missense_Mutation	SNP	C	T	14	205	c.118G>A	c.(118-120)GAA>AAA	p.E40K
Pat_41	Post-Resistance	NR1D2	9975	37	3	23996028	23996028	Missense_Mutation	SNP	G	A	23	122	c.17G>A	c.(16-18)GGA>GAA	p.G6E
Pat_41	Post-Resistance	SLC4A7	9497	37	3	27444754	27444754	Missense_Mutation	SNP	C	T	32	121	c.2170G>A	c.(2170-2172)GAA>AAA	p.E724K
Pat_41	Post-Resistance	ZNF860	344787	37	3	32032046	32032046	Missense_Mutation	SNP	G	A	26	334	c.1475G>A	c.(1474-1476)CGT>CAT	p.R492H
Pat_41	Post-Resistance	CMTM7	112616	37	3	32493951	32493951	Missense_Mutation	SNP	T	C	22	193	c.500T>C	c.(499-501)GTA>GCA	p.V167A
Pat_41	Post-Resistance	DYNC1LI1	51143	37	3	32576067	32576067	Nonsense_Mutation	SNP	G	A	6	61	c.904C>T	c.(904-906)CAG>TAG	p.Q302*

Pat_41	Post-Resistance	UBP1	7342	37	3	33458275	33458275	Missense_Mutation	SNP	G	A	38	148	c.317C>T	c.(316-318)CCT>CTT	p.P106L
Pat_41	Post-Resistance	UBP1	7342	37	3	33467192	33467192	Missense_Mutation	SNP	C	T	7	53	c.155G>A	c.(154-156)AGC>AAC	p.S52N
Pat_41	Post-Resistance	UBP1	7342	37	3	33467217	33467217	Missense_Mutation	SNP	G	A	25	51	c.130C>T	c.(130-132)CCC>TCC	p.P44S
Pat_41	Post-Resistance	PDCD6IP	10015	37	3	33887037	33887037	Missense_Mutation	SNP	C	T	6	195	c.1598C>T	c.(1597-1599)GCC>GTC	p.A533V
Pat_41	Post-Resistance	MLH1	4292	37	3	37045965	37045965	Missense_Mutation	SNP	G	A	93	81	c.380G>A	c.(379-381)AGA>AAA	p.R127K
Pat_41	Post-Resistance	MLH1	4292	37	3	37081748	37081748	Nonsense_Mutation	SNP	C	T	33	128	c.1630C>T	c.(1630-1632)CAA>TAA	p.Q544*
Pat_41	Post-Resistance	ACAA1	30	37	3	38168066	38168066	Missense_Mutation	SNP	C	T	10	62	c.752G>A	c.(751-753)AGC>AAC	p.S251N
Pat_41	Post-Resistance	ACAA1	30	37	3	38173086	38173086	Splice_Site	SNP	C	T	6	76	c.446_splice	c.e5+1	p.G149_splice
Pat_41	Post-Resistance	SLC22A13	9390	37	3	38316202	38316202	Missense_Mutation	SNP	C	T	10	71	c.590C>T	c.(589-591)GCT>GTT	p.A197V
Pat_41	Post-Resistance	SCN5A	6331	37	3	38595943	38595943	Missense_Mutation	SNP	A	G	6	103	c.4640T>C	c.(4639-4641)GTG>GCG	p.V1547A
Pat_41	Post-Resistance	SCN5A	6331	37	3	38627264	38627264	Missense_Mutation	SNP	G	A	8	114	c.2705C>T	c.(2704-2706)ACC>ATC	p.T902I
Pat_41	Post-Resistance	SCN10A	6336	37	3	38738979	38738979	Missense_Mutation	SNP	G	A	9	194	c.5732C>T	c.(5731-5733)ACT>ATT	p.T1911I
Pat_41	Post-Resistance	WDR48	57599	37	3	39104625	39104625	Missense_Mutation	SNP	C	T	30	170	c.133C>T	c.(133-135)CTT>TTT	p.L45F
Pat_41	Post-Resistance	GORASP1	64689	37	3	39139810	39139810	Missense_Mutation	SNP	C	T	20	132	c.1240G>A	c.(1240-1242)GAA>AAA	p.E414K
Pat_41	Post-Resistance	CSRNP1	64651	37	3	39184674	39184674	Missense_Mutation	SNP	C	T	20	43	c.1642G>A	c.(1642-1644)GCC>ACC	p.A548T
Pat_41	Post-Resistance	ZNF619	285267	37	3	40528516	40528516	Missense_Mutation	SNP	C	T	10	92	c.635C>T	c.(634-636)ACC>ATC	p.T212I
Pat_41	Post-Resistance	CTNNB1	1499	37	3	41266201	41266201	Nonsense_Mutation	SNP	G	A	4	72	c.198G>A	c.(196-198)TGG>TGA	p.W66*
Pat_41	Post-Resistance	ULK4	54986	37	3	41977324	41977324	Missense_Mutation	SNP	C	T	7	109	c.347G>A	c.(346-348)GGC>GAC	p.G116D
Pat_41	Post-Resistance	NKTR	4820	37	3	42672739	42672739	Missense_Mutation	SNP	G	A	3	50	c.481G>A	c.(481-483)GCA>ACA	p.A161T
Pat_41	Post-Resistance	HHATL	57467	37	3	42739750	42739750	Missense_Mutation	SNP	C	T	31	97	c.577G>A	c.(577-579)GAG>AAG	p.E193K
Pat_41	Post-Resistance	CCDC13	152206	37	3	42781266	42781266	Missense_Mutation	SNP	G	A	27	63	c.1024C>T	c.(1024-1026)CTT>TTT	p.L342F
Pat_41	Post-Resistance	C3orf39	84892	37	3	43122413	43122413	Missense_Mutation	SNP	C	T	16	44	c.511G>A	c.(511-513)GAC>AAC	p.D171N
Pat_41	Post-Resistance	ZNF445	353274	37	3	44488854	44488854	Missense_Mutation	SNP	G	A	15	28	c.2309C>T	c.(2308-2310)GCC>GTC	p.A770V
Pat_41	Post-Resistance	ZNF445	353274	37	3	44489930	44489930	Missense_Mutation	SNP	T	G	6	55	c.1233A>C	c.(1231-1233)GAA>GAC	p.E411D
Pat_41	Post-Resistance	ZNF167	55888	37	3	44612067	44612067	Missense_Mutation	SNP	C	T	8	94	c.1465C>T	c.(1465-1467)CAT>TAT	p.H489Y
Pat_41	Post-Resistance	ZNF501	115560	37	3	44775975	44775975	Missense_Mutation	SNP	C	T	7	121	c.62C>T	c.(61-63)CCT>CTT	p.P21L
Pat_41	Post-Resistance	KIF15	56992	37	3	44803231	44803231	Translation_Start_Site	SNP	C	T	3	8	c.-126C>T	.(-128--124)AACGT>AATGT	
Pat_41	Post-Resistance	KIF15	56992	37	3	44822385	44822385	Missense_Mutation	SNP	C	T	22	211	c.332C>T	c.(331-333)ACT>ATT	p.T111I
Pat_41	Post-Resistance	KIF15	56992	37	3	44839050	44839050	Missense_Mutation	SNP	G	A	21	57	c.857G>A	c.(856-858)GGT>GAT	p.G286D
Pat_41	Post-Resistance	CDCP1	64866	37	3	45153724	45153724	Missense_Mutation	SNP	G	A	61	155	c.506C>T	c.(505-507)GCC>GTC	p.A169V
Pat_41	Post-Resistance	LARS2	23395	37	3	45458999	45458999	Missense_Mutation	SNP	C	T	25	163	c.389C>T	c.(388-390)GCT>GTT	p.A130V
Pat_41	Post-Resistance	LIMD1	8994	37	3	45636997	45636997	Missense_Mutation	SNP	C	T	19	41	c.626C>T	c.(625-627)CCT>CTT	p.P209L
Pat_41	Post-Resistance	FYCO1	79443	37	3	45996748	45996748	Missense_Mutation	SNP	C	T	37	302	c.3937G>A	c.(3937-3939)GCT>ACT	p.A1313T
Pat_41	Post-Resistance	CCR2	729230	37	3	46399356	46399356	Missense_Mutation	SNP	G	A	15	373	c.338G>A	c.(337-339)TGC>TAC	p.C113Y
Pat_41	Post-Resistance	PTH1R	5745	37	3	46939953	46939953	Missense_Mutation	SNP	C	T	15	52	c.629C>T	c.(628-630)GCC>GTC	p.A210V
Pat_41	Post-Resistance	SETD2	29072	37	3	47125676	47125676	Missense_Mutation	SNP	C	T	18	143	c.5594G>A	c.(5593-5595)AGC>AAC	p.S1865N
Pat_41	Post-Resistance	SETD2	29072	37	3	47144843	47144843	Missense_Mutation	SNP	G	A	59	164	c.4910C>T	c.(4909-4911)ACC>ATC	p.T1637I
Pat_41	Post-Resistance	SETD2	29072	37	3	47163062	47163062	Missense_Mutation	SNP	C	T	21	128	c.3064G>A	c.(3064-3066)GAC>AAC	p.D1022N
Pat_41	Post-Resistance	KLHL18	23276	37	3	47382136	47382136	Missense_Mutation	SNP	C	T	6	176	c.1196C>T	c.(1195-1197)TCC>TTC	p.S399F
Pat_41	Post-Resistance	PTPN23	25930	37	3	47453591	47453591	Missense_Mutation	SNP	C	T	6	58	c.4081C>T	c.(4081-4083)CCC>TCC	p.P1361S
Pat_41	Post-Resistance	ZNF589	51385	37	3	48310166	48310166	Missense_Mutation	SNP	G	A	14	128	c.985G>A	c.(985-987)GAG>AAG	p.E329K
Pat_41	Post-Resistance	COL7A1	1294	37	3	48623653	48623653	Missense_Mutation	SNP	C	T	22	177	c.3577G>A	c.(3577-3579)GCT>ACT	p.A1193T
Pat_41	Post-Resistance	CELSR3	1951	37	3	48677720	48677720	Missense_Mutation	SNP	C	T	4	70	c.9298G>A	c.(9298-9300)GGG>AGG	p.G3100R
Pat_41	Post-Resistance	QARS	5859	37	3	49137393	49137393	Splice_Site	SNP	C	T	17	85	c.1295_splice	c.e14+1	p.W432_splice
Pat_41	Post-Resistance	QARS	5859	37	3	49141139	49141139	Missense_Mutation	SNP	C	T	6	17	c.376G>A	c.(376-378)GTG>ATG	p.V126M
Pat_41	Post-Resistance	LAMB2	3913	37	3	49160681	49160681	Missense_Mutation	SNP	C	T	22	165	c.4108G>A	c.(4108-4110)GCA>ACA	p.A1370T
Pat_41	Post-Resistance	KLHDC8B	200942	37	3	49212225	49212225	Missense_Mutation	SNP	G	A	3	24	c.592G>A	c.(592-594)GAG>AAG	p.E198K

Pat_41	Post-Resistance	LOC646498	646498	37	3	49227385	49227385	Missense_Mutation	SNP	A	G	13	232	c.37T>C	c.(37-39)TCC>CCC	p.S13P
Pat_41	Post-Resistance	DAG1	1605	37	3	49568864	49568864	Missense_Mutation	SNP	C	T	5	104	c.920C>T	c.(919-921)CCC>CTC	p.P307L
Pat_41	Post-Resistance	APEH	327	37	3	49718663	49718663	Missense_Mutation	SNP	G	A	12	45	c.1429G>A	c.(1429-1431)GTG>ATG	p.V477M
Pat_41	Post-Resistance	RNF123	63891	37	3	49740160	49740160	Missense_Mutation	SNP	C	T	37	281	c.1724C>T	c.(1723-1725)TCC>TTC	p.S575F
Pat_41	Post-Resistance	AMIGO3	386724	37	3	49756430	49756430	Missense_Mutation	SNP	G	A	26	89	c.469C>T	c.(469-471)CGC>TGC	p.R157C
Pat_41	Post-Resistance	MST1R	4486	37	3	49924853	49924853	Missense_Mutation	SNP	C	T	20	85	c.4090G>A	c.(4090-4092)GGC>AGC	p.G1364S
Pat_41	Post-Resistance	MST1R	4486	37	3	49940664	49940664	Missense_Mutation	SNP	G	A	57	16	c.379C>T	c.(379-381)CCC>TCC	p.P127S
Pat_41	Post-Resistance	MON1A	84315	37	3	49949136	49949136	Missense_Mutation	SNP	C	T	13	54	c.727G>A	c.(727-729)GAT>AAT	p.D243N
Pat_41	Post-Resistance	SEMA3F	6405	37	3	50211674	50211674	Missense_Mutation	SNP	G	A	11	29	c.347G>A	c.(346-348)GGG>GAG	p.G116E
Pat_41	Post-Resistance	SEMA3B	7869	37	3	50311816	50311816	Missense_Mutation	SNP	C	T	16	149	c.1160C>T	c.(1159-1161)ACC>ATC	p.T387I
Pat_41	Post-Resistance	CACNA2D2	9254	37	3	50403578	50403578	Missense_Mutation	SNP	C	T	12	88	c.2747G>A	c.(2746-2748)AGT>AAT	p.S916N
Pat_41	Post-Resistance	MAPKAPK3	7867	37	3	50677846	50677846	Missense_Mutation	SNP	A	C	24	185	c.269A>C	c.(268-270)CAG>CCG	p.Q90P
Pat_41	Post-Resistance	DOCK3	1795	37	3	51127763	51127763	Missense_Mutation	SNP	G	A	4	6	c.694G>A	c.(694-696)GAT>AAT	p.D232N
Pat_41	Post-Resistance	RBM15B	29890	37	3	51430158	51430158	Missense_Mutation	SNP	G	A	20	91	c.1328G>A	c.(1327-1329)AGC>AAC	p.S443N
Pat_41	Post-Resistance	RBM15B	29890	37	3	51430191	51430191	Missense_Mutation	SNP	G	A	23	41	c.1361G>A	c.(1360-1362)AGC>AAC	p.S454N
Pat_41	Post-Resistance	VPRBP	9730	37	3	51457803	51457803	Missense_Mutation	SNP	G	A	11	52	c.2621C>T	c.(2620-2622)GCT>GTT	p.A874V
Pat_41	Post-Resistance	GRM2	2912	37	3	51747282	51747282	Missense_Mutation	SNP	G	A	9	36	c.1244G>A	c.(1243-1245)GGG>GAG	p.G415E
Pat_41	Post-Resistance	GRM2	2912	37	3	51749819	51749819	Missense_Mutation	SNP	C	T	8	19	c.2030C>T	c.(2029-2031)GCC>GTC	p.A677V
Pat_41	Post-Resistance	IQCF3	401067	37	3	51864522	51864522	Missense_Mutation	SNP	C	T	3	18	c.170C>T	c.(169-171)GCC>GTC	p.A57V
Pat_41	Post-Resistance	PCBP4	57060	37	3	51993271	51993271	Missense_Mutation	SNP	G	A	5	28	c.674C>T	c.(673-675)CCC>CTC	p.P225L
Pat_41	Post-Resistance	POC1A	25886	37	3	52172229	52172229	Missense_Mutation	SNP	C	T	6	80	c.769G>A	c.(769-771)GAC>AAC	p.D257N
Pat_41	Post-Resistance	ALAS1	211	37	3	52238853	52238853	Missense_Mutation	SNP	C	T	7	112	c.722C>T	c.(721-723)ACC>ATC	p.T241I
Pat_41	Post-Resistance	TLR9	54106	37	3	52257056	52257056	Missense_Mutation	SNP	G	A	4	132	c.1276C>T	c.(1276-1278)CGC>TGC	p.R426C
Pat_41	Post-Resistance	DNAH1	25981	37	3	52426949	52426949	Missense_Mutation	SNP	C	T	27	162	c.10382C>T	c.(10381-10383)TCC>TTC	p.S3461F
Pat_41	Post-Resistance	STAB1	23166	37	3	52543996	52543996	Missense_Mutation	SNP	G	A	4	66	c.2458G>A	c.(2458-2460)GGG>AGG	p.G820R
Pat_41	Post-Resistance	STAB1	23166	37	3	52548421	52548421	Missense_Mutation	SNP	C	T	12	90	c.3587C>T	c.(3586-3588)GCC>GTC	p.A1196V
Pat_41	Post-Resistance	STAB1	23166	37	3	52554689	52554689	Missense_Mutation	SNP	C	T	13	143	c.5681C>T	c.(5680-5682)CCC>CTC	p.P1894L
Pat_41	Post-Resistance	PBRM1	55193	37	3	52597379	52597379	Missense_Mutation	SNP	C	T	8	46	c.4006G>A	c.(4006-4008)GTC>ATC	p.V1336I
Pat_41	Post-Resistance	PBRM1	55193	37	3	52620524	52620524	Missense_Mutation	SNP	C	T	18	129	c.3304G>A	c.(3304-3306)GCA>ACA	p.A1102T
Pat_41	Post-Resistance	GLT8D1	55830	37	3	52729233	52729233	Missense_Mutation	SNP	C	T	5	259	c.898G>A	c.(898-900)GAT>AAT	p.D300N
Pat_41	Post-Resistance	ITIH4	3700	37	3	52855115	52855115	Missense_Mutation	SNP	G	A	17	172	c.1571C>T	c.(1570-1572)TCC>TTC	p.S524F
Pat_41	Post-Resistance	CACNA2D3	55799	37	3	54798245	54798245	Missense_Mutation	SNP	G	A	17	549	c.1247G>A	c.(1246-1248)GGA>GAA	p.G416E
Pat_41	Post-Resistance	LRTM1	57408	37	3	54952686	54952686	Missense_Mutation	SNP	C	T	5	199	c.838G>A	c.(838-840)GCC>ACC	p.A280T
Pat_41	Post-Resistance	CACNA2D3	55799	37	3	55107555	55107555	Missense_Mutation	SNP	C	T	33	170	c.3071C>T	c.(3070-3072)CCC>CTC	p.P1024L
Pat_41	Post-Resistance	CCDC66	285331	37	3	56650082	56650082	Splice_Site	SNP	G	A	10	382	c.1843_splice	c.e13+1	p.D615_splice
Pat_41	Post-Resistance	C3orf63	23272	37	3	56667301	56667301	Missense_Mutation	SNP	G	A	23	378	c.3335C>T	c.(3334-3336)ACT>ATT	p.T1112I
Pat_41	Post-Resistance	IL17RD	54756	37	3	57132071	57132071	Missense_Mutation	SNP	C	T	7	65	c.1660G>A	c.(1660-1662)GAC>AAC	p.D554N
Pat_41	Post-Resistance	APPL1	26060	37	3	57303657	57303657	Missense_Mutation	SNP	G	A	29	368	c.2072G>A	c.(2071-2073)AGC>AAC	p.S691N
Pat_41	Post-Resistance	FLNB	2317	37	3	58083621	58083621	Missense_Mutation	SNP	G	A	5	119	c.1064G>A	c.(1063-1065)AGT>AAT	p.S355N
Pat_41	Post-Resistance	FLNB	2317	37	3	58104698	58104698	Missense_Mutation	SNP	C	T	22	252	c.2845C>T	c.(2845-2847)CTC>TTC	p.L949F
Pat_41	Post-Resistance	FLNB	2317	37	3	58110221	58110221	Missense_Mutation	SNP	C	T	6	129	c.3887C>T	c.(3886-3888)CCC>CTC	p.P1296L
Pat_41	Post-Resistance	PXK	54899	37	3	58398639	58398639	Missense_Mutation	SNP	G	A	18	388	c.1477G>A	c.(1477-1479)GCC>ACC	p.A493T
Pat_41	Post-Resistance	CADPS	8618	37	3	62739376	62739376	Missense_Mutation	SNP	C	T	16	108	c.628G>A	c.(628-630)GTC>ATC	p.V210I
Pat_41	Post-Resistance	ATXN7	6314	37	3	63973979	63973979	Missense_Mutation	SNP	C	T	5	142	c.1340C>T	c.(1339-1341)CCT>CTT	p.P447L
Pat_41	Post-Resistance	PSMD6	9861	37	3	63999166	63999166	Missense_Mutation	SNP	G	A	32	330	c.944C>T	c.(943-945)ACC>ATC	p.T315I
Pat_41	Post-Resistance	ADAMTS9	56999	37	3	64589614	64589614	Missense_Mutation	SNP	G	A	26	247	c.3731C>T	c.(3730-3732)GCC>GTC	p.A1244V
Pat_41	Post-Resistance	ADAMTS9	56999	37	3	64601700	64601700	Missense_Mutation	SNP	C	T	25	492	c.2960G>A	c.(2959-2961)AGC>AAC	p.S987N

Pat_41	Post-Resistance	MAGI1	9223	37	3	65377002	65377002	Missense_Mutation	SNP	C	T	11	100	c.2231G>A	c.(2230-2232)AGT>AAT	p.S744N
Pat_41	Post-Resistance	LMOD3	56203	37	3	69168233	69168233	Missense_Mutation	SNP	C	T	19	196	c.1273G>A	c.(1273-1275)GGG>AGG	p.G425R
Pat_41	Post-Resistance	FRMD4B	23150	37	3	69362662	69362662	Missense_Mutation	SNP	C	T	5	28	c.169G>A	c.(169-171)GAA>AAA	p.E57K
Pat_41	Post-Resistance	FOXP1	27086	37	3	71021743	71021743	Missense_Mutation	SNP	C	T	10	463	c.1615G>A	c.(1615-1617)GTA>ATA	p.V539I
Pat_41	Post-Resistance	SHQ1	55164	37	3	72799569	72799569	Missense_Mutation	SNP	C	T	6	121	c.1600G>A	c.(1600-1602)GTG>ATG	p.V534M
Pat_41	Post-Resistance	FLJ10213	55096	37	3	73111963	73111963	Missense_Mutation	SNP	G	A	104	535	c.731G>A	c.(730-732)AGC>AAC	p.S244N
Pat_41	Post-Resistance	PDZRN3	23024	37	3	73432809	73432809	Missense_Mutation	SNP	C	T	6	156	c.2908G>A	c.(2908-2910)GGG>AGG	p.G970R
Pat_41	Post-Resistance	ROBO2	6092	37	3	77526715	77526715	Missense_Mutation	SNP	G	A	6	76	c.539G>A	c.(538-540)AGA>AAA	p.R180K
Pat_41	Post-Resistance	ROBO1	6091	37	3	78663797	78663797	Splice_Site	SNP	C	T	4	96	c.4435_splice	c.e28+1	p.D1479_splice
Pat_41	Post-Resistance	ROBO1	6091	37	3	78667175	78667175	Missense_Mutation	SNP	G	A	6	89	c.3892C>T	c.(3892-3894)CCT>TCT	p.P1298S
Pat_41	Post-Resistance	ROBO1	6091	37	3	78680405	78680405	Missense_Mutation	SNP	C	T	5	92	c.3532G>A	c.(3532-3534)GGT>AGT	p.G1178S
Pat_41	Post-Resistance	POU1F1	5449	37	3	87309106	87309106	Missense_Mutation	SNP	C	T	5	168	c.814G>A	c.(814-816)GTG>ATG	p.V272M
Pat_41	Post-Resistance	HTR1F	3355	37	3	88040911	88040911	Missense_Mutation	SNP	C	T	9	76	c.1012C>T	c.(1012-1014)CTC>TTC	p.L338F
Pat_41	Post-Resistance	PROS1	5627	37	3	93619768	93619768	Missense_Mutation	SNP	C	T	3	22	c.607G>A	c.(607-609)GAT>AAT	p.D203N
Pat_41	Post-Resistance	ARL13B	200894	37	3	93772088	93772088	Missense_Mutation	SNP	C	T	10	125	c.1268C>T	c.(1267-1269)GCT>GTT	p.A423V
Pat_41	Post-Resistance	DHFRL1	200895	37	3	93780286	93780286	Missense_Mutation	SNP	G	A	27	268	c.70C>T	c.(70-72)CCC>TCC	p.P24S
Pat_41	Post-Resistance	EPHA6	285220	37	3	97356825	97356825	Missense_Mutation	SNP	G	A	13	186	c.2683G>A	c.(2683-2685)GCT>ACT	p.A895T
Pat_41	Post-Resistance	ST3GAL6	10402	37	3	98507174	98507174	Missense_Mutation	SNP	C	T	20	138	c.623C>T	c.(622-624)ACT>ATT	p.T208I
Pat_41	Post-Resistance	DCBLD2	131566	37	3	98518310	98518310	Missense_Mutation	SNP	G	A	70	417	c.2234C>T	c.(2233-2235)CCA>CTA	p.P745L
Pat_41	Post-Resistance	C3orf26	84319	37	3	99891191	99891191	Missense_Mutation	SNP	G	A	9	119	c.611G>A	c.(610-612)CGT>CAT	p.R204H
Pat_41	Post-Resistance	TBC1D23	55773	37	3	100018107	100018107	Missense_Mutation	SNP	G	A	9	151	c.1024G>A	c.(1024-1026)GAT>AAT	p.D342N
Pat_41	Post-Resistance	NIT2	56954	37	3	100067673	100067673	Missense_Mutation	SNP	G	A	7	56	c.532G>A	c.(532-534)GCT>ACT	p.A178T
Pat_41	Post-Resistance	NIT2	56954	37	3	100073671	100073671	Missense_Mutation	SNP	G	A	13	139	c.739G>A	c.(739-741)GAC>AAC	p.D247N
Pat_41	Post-Resistance	ABI3BP	25890	37	3	100621470	100621470	Missense_Mutation	SNP	G	A	4	68	c.341C>T	c.(340-342)TCA>TTA	p.S114L
Pat_41	Post-Resistance	SENP7	57337	37	3	101044800	101044800	Missense_Mutation	SNP	C	T	56	338	c.3140G>A	c.(3139-3141)GGC>GAC	p.G1047D
Pat_41	Post-Resistance	SENP7	57337	37	3	101177827	101177827	Missense_Mutation	SNP	G	A	25	458	c.256C>T	c.(256-258)CCT>TCT	p.P86S
Pat_41	Post-Resistance	CEP97	79598	37	3	101443551	101443551	Missense_Mutation	SNP	C	T	5	141	c.31C>T	c.(31-33)CCT>TCT	p.P11S
Pat_41	Post-Resistance	NFKBIZ	64332	37	3	101571756	101571756	Missense_Mutation	SNP	G	A	17	267	c.487G>A	c.(487-489)GGG>AGG	p.G163R
Pat_41	Post-Resistance	ALCAM	214	37	3	105252457	105252457	Missense_Mutation	SNP	G	A	11	183	c.470G>A	c.(469-471)TGC>TAC	p.C157Y
Pat_41	Post-Resistance	CBLB	868	37	3	105378031	105378031	Missense_Mutation	SNP	C	T	10	115	c.2732G>A	c.(2731-2733)CGC>CAC	p.R911H
Pat_41	Post-Resistance	CBLB	868	37	3	105459350	105459350	Missense_Mutation	SNP	C	T	6	235	c.971G>A	c.(970-972)AGC>AAC	p.S324N
Pat_41	Post-Resistance	MYH15	22989	37	3	108103629	108103629	Missense_Mutation	SNP	C	T	11	101	c.5596G>A	c.(5596-5598)GCA>ACA	p.A1866T
Pat_41	Post-Resistance	MYH15	22989	37	3	108129642	108129642	Missense_Mutation	SNP	C	T	4	50	c.4343G>A	c.(4342-4344)CGC>CAC	p.R1448H
Pat_41	Post-Resistance	KIAA1524	57650	37	3	108288376	108288376	Missense_Mutation	SNP	G	A	10	86	c.973C>T	c.(973-975)CCA>TCA	p.P325S
Pat_41	Post-Resistance	CD96	10225	37	3	111325595	111325595	Missense_Mutation	SNP	C	T	13	347	c.1184C>T	c.(1183-1185)ACC>ATC	p.T395I
Pat_41	Post-Resistance	TAGLN3	29114	37	3	111719686	111719686	Missense_Mutation	SNP	C	T	6	243	c.248C>T	c.(247-249)TCA>TTA	p.S83L
Pat_41	Post-Resistance	SLC9A10	285335	37	3	111918221	111918221	Missense_Mutation	SNP	C	T	5	104	c.2470G>A	c.(2470-2472)GCT>ACT	p.A824T
Pat_41	Post-Resistance	SLC9A10	285335	37	3	111988919	111988919	Missense_Mutation	SNP	C	T	9	112	c.619G>A	c.(619-621)GAG>AAG	p.E207K
Pat_41	Post-Resistance	SLC9A10	285335	37	3	111999631	111999631	Splice_Site	SNP	C	T	5	83	c.89_splice	c.e3-1	p.A30_splice
Pat_41	Post-Resistance	CCDC80	151887	37	3	112349098	112349098	Missense_Mutation	SNP	C	T	26	311	c.1897G>A	c.(1897-1899)GCT>ACT	p.A633T
Pat_41	Post-Resistance	CCDC80	151887	37	3	112356931	112356931	Missense_Mutation	SNP	G	A	36	340	c.1822C>T	c.(1822-1824)CCC>TCC	p.P608S
Pat_41	Post-Resistance	BOC	91653	37	3	112969573	112969573	Missense_Mutation	SNP	C	T	5	85	c.269C>T	c.(268-270)ACC>ATC	p.T90I
Pat_41	Post-Resistance	CCDC52	152185	37	3	113172702	113172702	Missense_Mutation	SNP	G	A	4	138	c.1753C>T	c.(1753-1755)CCT>TCT	p.P585S
Pat_41	Post-Resistance	CCDC52	152185	37	3	113212965	113212965	Nonsense_Mutation	SNP	G	A	7	132	c.316C>T	c.(316-318)CAA>TAA	p.Q106*
Pat_41	Post-Resistance	KIAA2018	205717	37	3	113375055	113375055	Missense_Mutation	SNP	G	T	6	189	c.5474C>A	c.(5473-5475)GCC>GAC	p.A1825D
Pat_41	Post-Resistance	KIAA2018	205717	37	3	113375784	113375784	Missense_Mutation	SNP	G	A	7	73	c.4745C>T	c.(4744-4746)CCT>CTT	p.P1582L
Pat_41	Post-Resistance	KIAA2018	205717	37	3	113379561	113379561	Missense_Mutation	SNP	C	T	14	82	c.968G>A	c.(967-969)AGC>AAC	p.S323N

Pat_41	Post-Resistance	KIAA1407	57577	37	3	113775306	113775306	Missense_Mutation	SNP	A	G	15	237	c.8T>C	c.(7-9)CTG>CCG	p.L3P
Pat_41	Post-Resistance	IGSF11	152404	37	3	118621687	118621687	Missense_Mutation	SNP	G	A	27	386	c.976C>T	c.(976-978)CCA>TCA	p.P326S
Pat_41	Post-Resistance	ARHGAP31	57514	37	3	119132904	119132904	Missense_Mutation	SNP	C	T	9	51	c.2128C>T	c.(2128-2130)CCA>TCA	p.P710S
Pat_41	Post-Resistance	TMEM39A	55254	37	3	119180854	119180854	Missense_Mutation	SNP	G	A	11	118	c.68C>T	c.(67-69)ACT>ATT	p.T23I
Pat_41	Post-Resistance	GTF2E1	2960	37	3	120495464	120495464	Missense_Mutation	SNP	G	A	6	139	c.845G>A	c.(844-846)AGA>AAA	p.R282K
Pat_41	Post-Resistance	GTF2E1	2960	37	3	120499893	120499893	Missense_Mutation	SNP	G	A	4	57	c.896G>A	c.(895-897)GGC>GAC	p.G299D
Pat_41	Post-Resistance	HCLS1	3059	37	3	121353262	121353262	Missense_Mutation	SNP	G	A	10	48	c.695C>T	c.(694-696)TCT>TTT	p.S232F
Pat_41	Post-Resistance	GOLGB1	2804	37	3	121415064	121415064	Missense_Mutation	SNP	C	T	6	58	c.4291G>A	c.(4291-4293)GAA>AAA	p.E1431K
Pat_41	Post-Resistance	CASR	846	37	3	121976185	121976185	Missense_Mutation	SNP	G	A	5	147	c.443G>A	c.(442-444)GGC>GAC	p.G148D
Pat_41	Post-Resistance	DTX3L	151636	37	3	122283428	122283428	Missense_Mutation	SNP	G	A	19	176	c.155G>A	c.(154-156)GGC>GAC	p.G52D
Pat_41	Post-Resistance	PARP14	54625	37	3	122437289	122437289	Missense_Mutation	SNP	G	A	25	211	c.4291G>A	c.(4291-4293)GTG>ATG	p.V1431M
Pat_41	Post-Resistance	ADCY5	111	37	3	123022988	123022988	Missense_Mutation	SNP	G	A	6	103	c.2485C>T	c.(2485-2487)CGG>TGG	p.R829W
Pat_41	Post-Resistance	ADCY5	111	37	3	123166400	123166400	Nonsense_Mutation	SNP	C	T	3	24	c.993G>A	c.(991-993)TGG>TGA	p.W331*
Pat_41	Post-Resistance	KALRN	8997	37	3	124196182	124196182	Splice_Site	SNP	G	A	8	161	c.4185_splice	c.e27+1	p.D1395_splice
Pat_41	Post-Resistance	KALRN	8997	37	3	124351368	124351368	Missense_Mutation	SNP	C	T	8	107	c.5278C>T	c.(5278-5280)CCC>TCC	p.P1760S
Pat_41	Post-Resistance	KALRN	8997	37	3	124438283	124438283	Missense_Mutation	SNP	G	A	20	237	c.8927G>A	c.(8926-8928)AGC>AAC	p.S2976N
Pat_41	Post-Resistance	ITGB5	3693	37	3	124560267	124560267	Missense_Mutation	SNP	C	T	5	114	c.743G>A	c.(742-744)GGG>GAG	p.G248E
Pat_41	Post-Resistance	HEG1	57493	37	3	124731685	124731685	Missense_Mutation	SNP	C	T	11	112	c.2738G>A	c.(2737-2739)GGA>GAA	p.G913E
Pat_41	Post-Resistance	SLC12A8	84561	37	3	124826453	124826453	Missense_Mutation	SNP	G	A	9	118	c.1577C>T	c.(1576-1578)GCC>GTC	p.A526V
Pat_41	Post-Resistance	ZNF148	7707	37	3	124951726	124951726	Missense_Mutation	SNP	C	T	44	234	c.1844G>A	c.(1843-1845)AGA>AAA	p.R615K
Pat_41	Post-Resistance	CCDC37	348807	37	3	126139060	126139060	Missense_Mutation	SNP	G	A	5	95	c.1070G>A	c.(1069-1071)GGC>GAC	p.G357D
Pat_41	Post-Resistance	CCDC37	348807	37	3	126142406	126142406	Missense_Mutation	SNP	T	G	9	87	c.1205T>G	c.(1204-1206)CTG>CGG	p.L402R
Pat_41	Post-Resistance	PLXNA1	5361	37	3	126749146	126749146	Missense_Mutation	SNP	G	A	9	205	c.5053G>A	c.(5053-5055)GGC>AGC	p.G1685S
Pat_41	Post-Resistance	RUVBL1	8607	37	3	127842528	127842528	Missense_Mutation	SNP	G	A	10	136	c.40C>T	c.(40-42)CGC>TGC	p.R14C
Pat_41	Post-Resistance	EEFSEC	60678	37	3	128060472	128060472	Missense_Mutation	SNP	G	A	5	26	c.1183G>A	c.(1183-1185)GAC>AAC	p.D395N
Pat_41	Post-Resistance	RAB7A	7879	37	3	128525231	128525231	Missense_Mutation	SNP	G	A	7	318	c.197G>A	c.(196-198)GGA>GAA	p.G66E
Pat_41	Post-Resistance	ACAD9	28976	37	3	128622923	128622923	Missense_Mutation	SNP	C	T	10	201	c.977C>T	c.(976-978)GCC>GTC	p.A326V
Pat_41	Post-Resistance	CNBP	7555	37	3	128890366	128890366	Missense_Mutation	SNP	G	A	12	132	c.140C>T	c.(139-141)TCC>TTC	p.S47F
Pat_41	Post-Resistance	COPG	22820	37	3	128973582	128973582	Missense_Mutation	SNP	C	T	7	90	c.395C>T	c.(394-396)ACT>ATT	p.T132I
Pat_41	Post-Resistance	COPG	22820	37	3	128987397	128987397	Missense_Mutation	SNP	T	C	5	240	c.1708T>C	c.(1708-1710)TCA>CCA	p.S570P
Pat_41	Post-Resistance	COPG	22820	37	3	128996146	128996146	Missense_Mutation	SNP	G	A	6	406	c.2504G>A	c.(2503-2505)CGG>CAG	p.R835Q
Pat_41	Post-Resistance	MBD4	8930	37	3	129151389	129151389	Missense_Mutation	SNP	C	T	20	531	c.1622G>A	c.(1621-1623)GGC>GAC	p.G541D
Pat_41	Post-Resistance	IFT122	55764	37	3	129218874	129218874	Missense_Mutation	SNP	G	A	10	220	c.2338G>A	c.(2338-2340)GCC>ACC	p.A780T
Pat_41	Post-Resistance	IFT122	55764	37	3	129231201	129231201	Missense_Mutation	SNP	C	T	17	515	c.2933C>T	c.(2932-2934)TCC>TTC	p.S978F
Pat_41	Post-Resistance	RHO	6010	37	3	129251376	129251376	Missense_Mutation	SNP	G	A	8	88	c.697G>A	c.(697-699)GCC>ACC	p.A233T
Pat_41	Post-Resistance	PLXND1	23129	37	3	129278518	129278518	Missense_Mutation	SNP	C	T	6	231	c.5242G>A	c.(5242-5244)GCT>ACT	p.A1748T
Pat_41	Post-Resistance	PLXND1	23129	37	3	129290547	129290547	Missense_Mutation	SNP	G	A	24	243	c.3218C>T	c.(3217-3219)GCC>GTC	p.A1073V
Pat_41	Post-Resistance	PLXND1	23129	37	3	129304838	129304838	Missense_Mutation	SNP	A	G	155	273	c.1808T>C	c.(1807-1809)ATG>ACG	p.M603T
Pat_41	Post-Resistance	COL6A6	131873	37	3	130282226	130282226	Missense_Mutation	SNP	G	A	8	44	c.379G>A	c.(379-381)GAC>AAC	p.D127N
Pat_41	Post-Resistance	COL6A6	131873	37	3	130300551	130300551	Missense_Mutation	SNP	G	A	6	89	c.3694G>A	c.(3694-3696)GGC>AGC	p.G1232S
Pat_41	Post-Resistance	PIK3R4	30849	37	3	130452517	130452517	Missense_Mutation	SNP	G	A	13	211	c.1325C>T	c.(1324-1326)ACC>ATC	p.T442I
Pat_41	Post-Resistance	ATP2C1	27032	37	3	130686196	130686196	Missense_Mutation	SNP	C	T	5	201	c.1241C>T	c.(1240-1242)GCT>GTT	p.A414V
Pat_41	Post-Resistance	DNAJC13	23317	37	3	132226150	132226150	Missense_Mutation	SNP	G	A	9	244	c.5068G>A	c.(5068-5070)GAG>AAG	p.E1690K
Pat_41	Post-Resistance	NPHP3	27031	37	3	132403444	132403444	Missense_Mutation	SNP	G	A	6	113	c.3524C>T	c.(3523-3525)TCT>TTT	p.S1175F
Pat_41	Post-Resistance	NPHP3	27031	37	3	132407549	132407549	Missense_Mutation	SNP	G	A	23	446	c.3070C>T	c.(3070-3072)CCA>TCA	p.P1024S
Pat_41	Post-Resistance	NPHP3	27031	37	3	132420320	132420320	Missense_Mutation	SNP	C	T	4	121	c.1582G>A	c.(1582-1584)GTG>ATG	p.V528M
Pat_41	Post-Resistance	NPHP3	27031	37	3	132424642	132424642	Missense_Mutation	SNP	C	T	5	128	c.1292G>A	c.(1291-1293)GGA>GAA	p.G431E

Pat_41	Post-Resistance	NPHP3	27031	37	3	132427061	132427061	Missense_Mutation	SNP	G	A	9	206	c.1159C>T	c.(1159-1161)CCT>TCT	p.P387S
Pat_41	Post-Resistance	BFSP2	8419	37	3	133119157	133119157	Missense_Mutation	SNP	C	T	16	81	c.230C>T	c.(229-231)GCC>GTC	p.A77V
Pat_41	Post-Resistance	BFSP2	8419	37	3	133191402	133191402	Missense_Mutation	SNP	G	A	3	31	c.1237G>A	c.(1237-1239)GAG>AAG	p.E413K
Pat_41	Post-Resistance	CDV3	55573	37	3	133305512	133305512	Missense_Mutation	SNP	G	A	7	222	c.572G>A	c.(571-573)AGT>AAT	p.S191N
Pat_41	Post-Resistance	SRPRB	58477	37	3	133526666	133526666	Missense_Mutation	SNP	G	A	41	359	c.326G>A	c.(325-327)AGG>AAG	p.R109K
Pat_41	Post-Resistance	SLCO2A1	6578	37	3	133664028	133664028	Missense_Mutation	SNP	C	T	26	528	c.1372G>A	c.(1372-1374)GTC>ATC	p.V458I
Pat_41	Post-Resistance	AMOTL2	51421	37	3	134077483	134077483	Missense_Mutation	SNP	C	T	8	80	c.2354G>A	c.(2353-2355)AGC>AAC	p.S785N
Pat_41	Post-Resistance	EPHB1	2047	37	3	134670736	134670736	Missense_Mutation	SNP	C	T	18	388	c.647C>T	c.(646-648)ACA>ATA	p.T216I
Pat_41	Post-Resistance	MSL2	55167	37	3	135870860	135870860	Missense_Mutation	SNP	G	A	5	166	c.863C>T	c.(862-864)CCT>CTT	p.P288L
Pat_41	Post-Resistance	MSL2	55167	37	3	135913882	135913882	Missense_Mutation	SNP	G	A	49	467	c.74C>T	c.(73-75)CCC>CTC	p.P25L
Pat_41	Post-Resistance	PCCB	5096	37	3	136019912	136019912	Missense_Mutation	SNP	G	A	10	212	c.925G>A	c.(925-927)GAA>AAA	p.E309K
Pat_41	Post-Resistance	STAG1	10274	37	3	136096591	136096591	Missense_Mutation	SNP	C	T	20	261	c.2281G>A	c.(2281-2283)GAT>AAT	p.D761N
Pat_41	Post-Resistance	IL20RB	53833	37	3	136710799	136710799	Missense_Mutation	SNP	G	A	16	110	c.551G>A	c.(550-552)AGG>AAG	p.R184K
Pat_41	Post-Resistance	DZIP1L	199221	37	3	137822620	137822620	Missense_Mutation	SNP	C	T	6	97	c.194G>A	c.(193-195)TGC>TAC	p.C65Y
Pat_41	Post-Resistance	ESYT3	83850	37	3	138187543	138187543	Missense_Mutation	SNP	G	A	20	273	c.1355G>A	c.(1354-1356)AGT>AAT	p.S452N
Pat_41	Post-Resistance	ESYT3	83850	37	3	138188347	138188347	Splice_Site	SNP	G	A	7	152	c.1503_splice	c.e15+1	p.K501_splice
Pat_41	Post-Resistance	CEP70	80321	37	3	138213904	138213904	Missense_Mutation	SNP	C	T	7	44	c.1747G>A	c.(1747-1749)GAT>AAT	p.D583N
Pat_41	Post-Resistance	FAIM	55179	37	3	138351772	138351772	Missense_Mutation	SNP	G	A	15	178	c.391G>A	c.(391-393)GGT>AGT	p.G131S
Pat_41	Post-Resistance	FAIM	55179	37	3	138351839	138351839	Missense_Mutation	SNP	C	T	11	210	c.458C>T	c.(457-459)GCT>GTT	p.A153V
Pat_41	Post-Resistance	PIK3CB	5291	37	3	138374254	138374254	Missense_Mutation	SNP	C	T	22	207	c.3190G>A	c.(3190-3192)GTT>ATT	p.V1064I
Pat_41	Post-Resistance	PRR23B	389151	37	3	138738911	138738911	Missense_Mutation	SNP	C	T	5	60	c.593G>A	c.(592-594)TGT>TAT	p.C198Y
Pat_41	Post-Resistance	NMNAT3	349565	37	3	139280028	139280028	Missense_Mutation	SNP	G	A	5	66	c.583C>T	c.(583-585)CCT>TCT	p.P195S
Pat_41	Post-Resistance	SLC25A36	55186	37	3	140675386	140675386	Missense_Mutation	SNP	G	A	6	71	c.59G>A	c.(58-60)GGA>GAA	p.G20E
Pat_41	Post-Resistance	ZBTB38	253461	37	3	141163769	141163769	Missense_Mutation	SNP	G	A	5	97	c.2539G>A	c.(2539-2541)GCC>ACC	p.A847T
Pat_41	Post-Resistance	GRK7	131890	37	3	141535653	141535653	Missense_Mutation	SNP	C	T	26	342	c.1423C>T	c.(1423-1425)CCT>TCT	p.P475S
Pat_41	Post-Resistance	XRN1	54464	37	3	142051319	142051319	Missense_Mutation	SNP	G	A	10	84	c.4117C>T	c.(4117-4119)CAT>TAT	p.H1373Y
Pat_41	Post-Resistance	XRN1	54464	37	3	142151675	142151675	Missense_Mutation	SNP	G	A	17	186	c.136C>T	c.(136-138)CCT>TCT	p.P46S
Pat_41	Post-Resistance	ATR	545	37	3	142185236	142185236	Missense_Mutation	SNP	G	A	18	246	c.6827C>T	c.(6826-6828)ACC>ATC	p.T2276I
Pat_41	Post-Resistance	ATR	545	37	3	142215363	142215363	Splice_Site	SNP	C	T	17	281	c.5739_splice	c.e34-1	p.R1913_splice
Pat_41	Post-Resistance	PCOLCE2	26577	37	3	142539878	142539878	Missense_Mutation	SNP	C	T	26	182	c.959G>A	c.(958-960)GGC>GAC	p.G320D
Pat_41	Post-Resistance	SLC9A9	285195	37	3	143185984	143185984	Missense_Mutation	SNP	G	A	13	212	c.1364C>T	c.(1363-1365)TCT>TTT	p.S455F
Pat_41	Post-Resistance	PLOD2	5352	37	3	145788906	145788906	Missense_Mutation	SNP	G	A	4	129	c.1981C>T	c.(1981-1983)CGT>TGT	p.R661C
Pat_41	Post-Resistance	PLOD2	5352	37	3	145789114	145789114	Missense_Mutation	SNP	C	T	22	239	c.1882G>A	c.(1882-1884)GAG>AAG	p.E628K
Pat_41	Post-Resistance	ZIC4	84107	37	3	147113714	147113714	Missense_Mutation	SNP	G	A	27	140	c.613C>T	c.(613-615)CCT>TCT	p.P205S
Pat_41	Post-Resistance	CPA3	1359	37	3	148583288	148583288	Missense_Mutation	SNP	G	A	5	105	c.97G>A	c.(97-99)GAT>AAT	p.D33N
Pat_41	Post-Resistance	HPS3	84343	37	3	148889920	148889920	Missense_Mutation	SNP	G	A	16	197	c.2926G>A	c.(2926-2928)GAT>AAT	p.D976N
Pat_41	Post-Resistance	CP	1356	37	3	148924006	148924006	Missense_Mutation	SNP	G	A	8	204	c.1157C>T	c.(1156-1158)GCT>GTT	p.A386V
Pat_41	Post-Resistance	TM4SF4	7104	37	3	149205491	149205491	Missense_Mutation	SNP	G	A	21	110	c.350G>A	c.(349-351)GGT>GAT	p.G117D
Pat_41	Post-Resistance	EIF2A	83939	37	3	150285708	150285708	Missense_Mutation	SNP	G	A	8	206	c.569G>A	c.(568-570)GGA>GAA	p.G190E
Pat_41	Post-Resistance	FAM194A	131831	37	3	150404085	150404085	Missense_Mutation	SNP	C	T	8	164	c.610G>A	c.(610-612)GAA>AAA	p.E204K
Pat_41	Post-Resistance	SIAH2	6478	37	3	150480554	150480554	Missense_Mutation	SNP	G	A	4	21	c.83C>T	c.(82-84)TCC>TTC	p.S28F
Pat_41	Post-Resistance	CLRN1	7401	37	3	150645781	150645781	Missense_Mutation	SNP	G	A	17	125	c.641C>T	c.(640-642)CCT>CTT	p.P214L
Pat_41	Post-Resistance	MED12L	116931	37	3	150845669	150845669	Missense_Mutation	SNP	C	T	5	105	c.454C>T	c.(454-456)CCA>TCA	p.P152S
Pat_41	Post-Resistance	MED12L	116931	37	3	150845718	150845718	Missense_Mutation	SNP	C	T	7	116	c.503C>T	c.(502-504)TCT>TTT	p.S168F
Pat_41	Post-Resistance	MED12L	116931	37	3	150911329	150911329	Missense_Mutation	SNP	G	A	11	177	c.2021G>A	c.(2020-2022)GGC>GAC	p.G674D
Pat_41	Post-Resistance	MED12L	116931	37	3	151105767	151105767	Missense_Mutation	SNP	C	T	5	160	c.5153C>T	c.(5152-5154)CCC>CTC	p.P1718L
Pat_41	Post-Resistance	MED12L	116931	37	3	151129190	151129190	Missense_Mutation	SNP	C	T	17	379	c.5930C>T	c.(5929-5931)TCC>TTC	p.S1977F

Pat_41	Post-Resistance	IGSF10	285313	37	3	151161217	151161217	Missense_Mutation	SNP	C	T	5	68	c.5518G>A	c.(5518-5520)GCA>ACA	p.A1840T
Pat_41	Post-Resistance	IGSF10	285313	37	3	151163246	151163246	Missense_Mutation	SNP	G	A	10	280	c.4523C>T	c.(4522-4524)TCC>TTC	p.S1508F
Pat_41	Post-Resistance	IGSF10	285313	37	3	151171274	151171274	Missense_Mutation	SNP	C	T	11	117	c.613G>A	c.(613-615)GTC>ATC	p.V205I
Pat_41	Post-Resistance	PLCH1	23007	37	3	155203205	155203205	Missense_Mutation	SNP	C	T	21	108	c.2938G>A	c.(2938-2940)GCT>ACT	p.A980T
Pat_41	Post-Resistance	PTX3	5806	37	3	157160721	157160721	Missense_Mutation	SNP	G	A	9	66	c.1099G>A	c.(1099-1101)GGA>AGA	p.G367R
Pat_41	Post-Resistance	IL12A	3592	37	3	159710853	159710853	Missense_Mutation	SNP	G	A	46	100	c.319G>A	c.(319-321)GAT>AAT	p.D107N
Pat_41	Post-Resistance	SMC4	10051	37	3	160120605	160120605	Missense_Mutation	SNP	G	A	23	80	c.460G>A	c.(460-462)GAC>AAC	p.D154N
Pat_41	Post-Resistance	C3orf57	165679	37	3	161064020	161064020	Missense_Mutation	SNP	C	T	83	17	c.92G>A	c.(91-93)CGA>CAA	p.R31Q
Pat_41	Post-Resistance	SI	6476	37	3	164792327	164792327	Missense_Mutation	SNP	G	A	11	31	c.247C>T	c.(247-249)CCA>TCA	p.P83S
Pat_41	Post-Resistance	MECOM	2122	37	3	168833693	168833693	Missense_Mutation	SNP	C	T	11	93	c.1403G>A	c.(1402-1404)GGA>GAA	p.G468E
Pat_41	Post-Resistance	SLC7A14	57709	37	3	170198641	170198641	Missense_Mutation	SNP	G	A	12	75	c.1430C>T	c.(1429-1431)GCC>GTC	p.A477V
Pat_41	Post-Resistance	TNIK	23043	37	3	170846532	170846532	Missense_Mutation	SNP	G	A	6	97	c.1744C>T	c.(1744-1746)CCC>TCC	p.P582S
Pat_41	Post-Resistance	NLGN1	22871	37	3	173525539	173525539	Missense_Mutation	SNP	C	T	28	99	c.563C>T	c.(562-564)ACT>ATT	p.T188I
Pat_41	Post-Resistance	TBL1XR1	79718	37	3	176769495	176769495	Missense_Mutation	SNP	C	T	9	35	c.224G>A	c.(223-225)GGT>GAT	p.G75D
Pat_41	Post-Resistance	MRPL47	57129	37	3	179322315	179322315	Missense_Mutation	SNP	C	T	22	130	c.98G>A	c.(97-99)GGG>GAG	p.G33E
Pat_41	Post-Resistance	NDUFB5	4711	37	3	179336299	179336299	Missense_Mutation	SNP	G	A	9	44	c.439G>A	c.(439-441)GCT>ACT	p.A147T
Pat_41	Post-Resistance	FXR1	8087	37	3	180685964	180685964	Missense_Mutation	SNP	C	T	18	87	c.1324C>T	c.(1324-1326)CCA>TCA	p.P442S
Pat_41	Post-Resistance	KLHL24	54800	37	3	183368160	183368160	Missense_Mutation	SNP	G	A	4	63	c.16G>A	c.(16-18)GGA>AGA	p.G6R
Pat_41	Post-Resistance	DVL3	1857	37	3	183882109	183882109	Missense_Mutation	SNP	C	T	13	115	c.286C>T	c.(286-288)CCA>TCA	p.P96S
Pat_41	Post-Resistance	FAM131A	131408	37	3	184059806	184059806	Missense_Mutation	SNP	C	T	17	144	c.185C>T	c.(184-186)TCC>TTC	p.S62F
Pat_41	Post-Resistance	FAM131A	131408	37	3	184062559	184062559	Missense_Mutation	SNP	C	T	14	102	c.809C>T	c.(808-810)GCC>GTC	p.A270V
Pat_41	Post-Resistance	CLCN2	1181	37	3	184076859	184076859	Missense_Mutation	SNP	G	A	6	41	c.124C>T	c.(124-126)CGC>TGC	p.R42C
Pat_41	Post-Resistance	EPHB3	2049	37	3	184297322	184297322	Missense_Mutation	SNP	C	T	16	54	c.1859C>T	c.(1858-1860)GCT>GTT	p.A620V
Pat_41	Post-Resistance	MAP3K13	9175	37	3	185167687	185167687	Splice_Site	SNP	G	A	32	217	c.1011_splice	c.e7-1	p.W337_splice
Pat_41	Post-Resistance	DGKG	1608	37	3	185993402	185993402	Missense_Mutation	SNP	G	A	19	51	c.844C>T	c.(844-846)CCA>TCA	p.P282S
Pat_41	Post-Resistance	FETUB	26998	37	3	186360306	186360306	Missense_Mutation	SNP	G	A	5	91	c.383G>A	c.(382-384)AGA>AAA	p.R128K
Pat_41	Post-Resistance	EIF4A2	1974	37	3	186502795	186502795	Missense_Mutation	SNP	G	A	8	213	c.253G>A	c.(253-255)GCC>ACC	p.A85T
Pat_41	Post-Resistance	CLDN1	9076	37	3	190039851	190039851	Missense_Mutation	SNP	C	T	31	80	c.145G>A	c.(145-147)GGG>AGG	p.G49R
Pat_41	Post-Resistance	FGF12	2257	37	3	192125817	192125817	Missense_Mutation	SNP	G	A	8	233	c.196C>T	c.(196-198)CCA>TCA	p.P66S
Pat_41	Post-Resistance	ATP13A4	84239	37	3	193210705	193210705	Splice_Site	SNP	C	T	27	163	c.533_splice	c.e5+1	p.R178_splice
Pat_41	Post-Resistance	GP5	2814	37	3	194118947	194118947	Missense_Mutation	SNP	G	A	5	41	c.65C>T	c.(64-66)CCG>CTG	p.P22L
Pat_41	Post-Resistance	ATP13A3	79572	37	3	194162080	194162080	Missense_Mutation	SNP	C	T	14	210	c.1670G>A	c.(1669-1671)GGT>GAT	p.G557D
Pat_41	Post-Resistance	MUC20	200958	37	3	195452822	195452822	Missense_Mutation	SNP	G	A	4	90	c.835G>A	c.(835-837)GTG>ATG	p.V279M
Pat_41	Post-Resistance	TFRC	7037	37	3	195778890	195778890	Missense_Mutation	SNP	C	T	10	95	c.2206G>A	c.(2206-2208)GCT>ACT	p.A736T
Pat_41	Post-Resistance	RNF168	165918	37	3	196210677	196210677	Missense_Mutation	SNP	C	T	15	233	c.644G>A	c.(643-645)AGT>AAT	p.S215N
Pat_41	Post-Resistance	LRRC33	375387	37	3	196387643	196387643	Missense_Mutation	SNP	G	A	9	128	c.1129G>A	c.(1129-1131)GCG>ACG	p.A377T
Pat_41	Post-Resistance	LRRC33	375387	37	3	196388160	196388160	Missense_Mutation	SNP	C	T	20	101	c.1646C>T	c.(1645-1647)ACC>ATC	p.T549I
Pat_41	Post-Resistance	LRRC33	375387	37	3	196388457	196388457	Missense_Mutation	SNP	T	C	15	177	c.1943T>C	c.(1942-1944)CTG>CCG	p.L648P
Pat_41	Post-Resistance	SENP5	205564	37	3	196612242	196612242	Missense_Mutation	SNP	C	T	8	76	c.190C>T	c.(190-192)CTT>TTT	p.L64F
Pat_41	Post-Resistance	SENP5	205564	37	3	196613553	196613553	Missense_Mutation	SNP	G	A	9	92	c.1501G>A	c.(1501-1503)GTC>ATC	p.V501I
Pat_41	Post-Resistance	KIAA0226	9711	37	3	197402064	197402064	Missense_Mutation	SNP	C	T	8	89	c.2744G>A	c.(2743-2745)TGT>TAT	p.C915Y
Pat_41	Post-Resistance	KIAA0226	9711	37	3	197408178	197408178	Missense_Mutation	SNP	T	C	18	249	c.2252A>G	c.(2251-2253)CAC>CGC	p.H751R
Pat_41	Post-Resistance	KIAA0226	9711	37	3	197409434	197409434	Missense_Mutation	SNP	G	A	6	162	c.2033C>T	c.(2032-2034)GCT>GTT	p.A678V
Pat_41	Post-Resistance	LRCH3	84859	37	3	197562680	197562680	Missense_Mutation	SNP	G	A	25	386	c.1238G>A	c.(1237-1239)CGA>CAA	p.R413Q
Pat_41	Post-Resistance	ZNF595	152687	37	4	86829	86829	Missense_Mutation	SNP	C	T	15	199	c.1435C>T	c.(1435-1437)CCC>TCC	p.P479S
Pat_41	Post-Resistance	ZNF141	7700	37	4	367245	367245	Missense_Mutation	SNP	C	A	8	331	c.1019C>A	c.(1018-1020)ACA>AAA	p.T340K
Pat_41	Post-Resistance	ABCA11P	79963	37	4	420613	420613	Missense_Mutation	SNP	G	A	11	125	c.293C>T	c.(292-294)ACT>ATT	p.T98I

Pat_41	Post-Resistance	ZNF721	170960	37	4	437330	437330	Missense_Mutation	SNP	A	T	9	374	c.926T>A	c.(925-927)GTA>GAA	p.V309E
Pat_41	Post-Resistance	PIGG	54872	37	4	514955	514955	Missense_Mutation	SNP	C	T	8	112	c.1225C>T	c.(1225-1227)CTC>TTC	p.L409F
Pat_41	Post-Resistance	PIGG	54872	37	4	524535	524535	Splice_Site	SNP	G	A	10	215	c.2571_splice	c.e11+1	p.Q857_splice
Pat_41	Post-Resistance	MFSD7	84179	37	4	678282	678282	Missense_Mutation	SNP	C	T	8	134	c.833G>A	c.(832-834)GGC>GAC	p.G278D
Pat_41	Post-Resistance	GAK	2580	37	4	871402	871402	Splice_Site	SNP	C	T	11	92	c.1856_splice	c.e16+1	p.R619_splice
Pat_41	Post-Resistance	DGKQ	1609	37	4	956927	956927	Missense_Mutation	SNP	C	T	3	12	c.1886G>A	c.(1885-1887)GGG>GAG	p.G629E
Pat_41	Post-Resistance	SLC26A1	10861	37	4	982930	982930	Missense_Mutation	SNP	C	A	6	8	c.1797G>T	c.(1795-1797)AGG>AGT	p.R599S
Pat_41	Post-Resistance	LETM1	3954	37	4	1843078	1843078	Missense_Mutation	SNP	C	T	4	54	c.590G>A	c.(589-591)AGG>AAG	p.R197K
Pat_41	Post-Resistance	POLN	353497	37	4	2082718	2082718	Missense_Mutation	SNP	G	A	13	355	c.2354C>T	c.(2353-2355)ACT>ATT	p.T785I
Pat_41	Post-Resistance	HAUS3	79441	37	4	2242433	2242433	Missense_Mutation	SNP	G	A	9	186	c.241C>T	c.(241-243)CTT>TTT	p.L81F
Pat_41	Post-Resistance	ADD1	118	37	4	2930165	2930165	Missense_Mutation	SNP	C	T	9	248	c.2129C>T	c.(2128-2130)TCT>TTT	p.S710F
Pat_41	Post-Resistance	HTT	3064	37	4	3123027	3123027	Nonsense_Mutation	SNP	C	T	8	214	c.1147C>T	c.(1147-1149)CAG>TAG	p.Q383*
Pat_41	Post-Resistance	HTT	3064	37	4	3123111	3123111	Missense_Mutation	SNP	G	A	13	140	c.1231G>A	c.(1231-1233)GAG>AAG	p.E411K
Pat_41	Post-Resistance	HTT	3064	37	4	3137689	3137689	Missense_Mutation	SNP	A	G	4	128	c.2698A>G	c.(2698-2700)ACA>GCA	p.T900A
Pat_41	Post-Resistance	HTT	3064	37	4	3189471	3189471	Missense_Mutation	SNP	C	T	7	213	c.5089C>T	c.(5089-5091)CGT>TGT	p.R1697C
Pat_41	Post-Resistance	HTT	3064	37	4	3221987	3221987	Nonsense_Mutation	SNP	C	T	20	187	c.7327C>T	c.(7327-7329)CAG>TAG	p.Q2443*
Pat_41	Post-Resistance	HTT	3064	37	4	3225190	3225190	Missense_Mutation	SNP	G	A	7	144	c.7534G>A	c.(7534-7536)GTG>ATG	p.V2512M
Pat_41	Post-Resistance	DOK7	285489	37	4	3495224	3495224	Missense_Mutation	SNP	C	T	7	29	c.1511C>T	c.(1510-1512)CCT>CTT	p.P504L
Pat_41	Post-Resistance	OTOP1	133060	37	4	4214714	4214714	Missense_Mutation	SNP	C	T	12	172	c.421G>A	c.(421-423)GCA>ACA	p.A141T
Pat_41	Post-Resistance	ZBTB49	166793	37	4	4304317	4304317	Missense_Mutation	SNP	G	A	40	385	c.754G>A	c.(754-756)GTA>ATA	p.V252I
Pat_41	Post-Resistance	ZBTB49	166793	37	4	4317446	4317446	Splice_Site	SNP	G	A	6	61	c.1459_splice	c.e6+1	p.G487_splice
Pat_41	Post-Resistance	CYTL1	54360	37	4	5018664	5018664	Missense_Mutation	SNP	C	T	7	498	c.226G>A	c.(226-228)GAC>AAC	p.D76N
Pat_41	Post-Resistance	EVC2	132884	37	4	5624502	5624502	Nonsense_Mutation	SNP	G	A	4	83	c.2263C>T	c.(2263-2265)CAG>TAG	p.Q755*
Pat_41	Post-Resistance	EVC	2121	37	4	5754687	5754687	Missense_Mutation	SNP	C	T	4	41	c.1223C>T	c.(1222-1224)GCT>GTT	p.A408V
Pat_41	Post-Resistance	EVC	2121	37	4	5798859	5798859	Missense_Mutation	SNP	G	A	7	139	c.1997G>A	c.(1996-1998)GGG>GAG	p.G666E
Pat_41	Post-Resistance	MAN2B2	23324	37	4	6598927	6598927	Missense_Mutation	SNP	G	A	11	211	c.1145G>A	c.(1144-1146)GGG>GAG	p.G382E
Pat_41	Post-Resistance	KIAA0232	9778	37	4	6863389	6863389	Missense_Mutation	SNP	G	A	37	172	c.1280G>A	c.(1279-1281)AGA>AAA	p.R427K
Pat_41	Post-Resistance	KIAA0232	9778	37	4	6863529	6863529	Missense_Mutation	SNP	C	T	13	186	c.1420C>T	c.(1420-1422)CCT>TCT	p.P474S
Pat_41	Post-Resistance	CCDC96	257236	37	4	7043644	7043644	Missense_Mutation	SNP	G	A	23	283	c.1022C>T	c.(1021-1023)GCC>GTC	p.A341V
Pat_41	Post-Resistance	SH3TC1	54436	37	4	8220014	8220014	Missense_Mutation	SNP	C	T	10	74	c.856C>T	c.(856-858)CCC>TCC	p.P286S
Pat_41	Post-Resistance	HS3ST1	9957	37	4	11400774	11400774	Missense_Mutation	SNP	G	A	35	327	c.856C>T	c.(856-858)CAC>TAC	p.H286Y
Pat_41	Post-Resistance	HS3ST1	9957	37	4	11401460	11401460	Missense_Mutation	SNP	G	A	6	47	c.170C>T	c.(169-171)ACC>ATC	p.T57I
Pat_41	Post-Resistance	RAB28	9364	37	4	13383114	13383114	Splice_Site	SNP	C	T	7	140	c.495_splice	c.e5+1	p.S165_splice
Pat_41	Post-Resistance	BOD1L	259282	37	4	13604302	13604302	Missense_Mutation	SNP	C	T	17	150	c.4222G>A	c.(4222-4224)GAC>AAC	p.D1408N
Pat_41	Post-Resistance	BOD1L	259282	37	4	13617083	13617083	Missense_Mutation	SNP	C	T	12	148	c.412G>A	c.(412-414)GTT>ATT	p.V138I
Pat_41	Post-Resistance	CC2D2A	57545	37	4	15587859	15587859	Missense_Mutation	SNP	G	A	27	451	c.4055G>A	c.(4054-4056)AGC>AAC	p.S1352N
Pat_41	Post-Resistance	MED28	80306	37	4	17616332	17616332	Missense_Mutation	SNP	G	A	5	39	c.55G>A	c.(55-57)GCC>ACC	p.A19T
Pat_41	Post-Resistance	NCAPG	64151	37	4	17841784	17841784	Missense_Mutation	SNP	G	A	16	178	c.2719G>A	c.(2719-2721)GCA>ACA	p.A907T
Pat_41	Post-Resistance	SLIT2	9353	37	4	20569002	20569002	Missense_Mutation	SNP	G	A	22	267	c.2843G>A	c.(2842-2844)GGT>GAT	p.G948D
Pat_41	Post-Resistance	GPR125	166647	37	4	22390103	22390103	Missense_Mutation	SNP	C	T	8	142	c.3191G>A	c.(3190-3192)GGA>GAA	p.G1064E
Pat_41	Post-Resistance	GPR125	166647	37	4	22394222	22394222	Missense_Mutation	SNP	G	A	12	140	c.2573C>T	c.(2572-2574)GCT>GTT	p.A858V
Pat_41	Post-Resistance	PPARGC1A	10891	37	4	23833375	23833375	Splice_Site	SNP	C	T	14	180	c.235_splice	c.e3-1	p.K79_splice
Pat_41	Post-Resistance	LGI2	55203	37	4	25005407	25005407	Missense_Mutation	SNP	G	A	47	610	c.1304C>T	c.(1303-1305)TCC>TTC	p.S435F
Pat_41	Post-Resistance	PCDH7	5099	37	4	30725308	30725308	Missense_Mutation	SNP	C	T	24	211	c.2264C>T	c.(2263-2265)CCT>CTT	p.P755L
Pat_41	Post-Resistance	PCDH7	5099	37	4	30921959	30921959	Missense_Mutation	SNP	G	A	14	171	c.3359G>A	c.(3358-3360)GGC>GAC	p.G1120D
Pat_41	Post-Resistance	PCDH7	5099	37	4	31144257	31144257	Missense_Mutation	SNP	G	A	6	149	c.3530G>A	c.(3529-3531)AGC>AAC	p.S1177N
Pat_41	Post-Resistance	TBC1D1	23216	37	4	38046089	38046089	Missense_Mutation	SNP	C	T	9	144	c.1520C>T	c.(1519-1521)TCT>TTT	p.S507F

Pat_41	Post-Resistance	TLR10	81793	37	4	38776620	38776620	Missense_Mutation	SNP	G	A	6	165	c.592C>T	c.(592-594)CCA>TCA	p.P198S
Pat_41	Post-Resistance	FAM114A1	92689	37	4	38880025	38880025	Missense_Mutation	SNP	C	T	8	220	c.326C>T	c.(325-327)CCC>CTC	p.P109L
Pat_41	Post-Resistance	KLHL5	51088	37	4	39109203	39109203	Missense_Mutation	SNP	G	A	11	219	c.1678G>A	c.(1678-1680)GAA>AAA	p.E560K
Pat_41	Post-Resistance	WDR19	57728	37	4	39184184	39184184	Splice_Site	SNP	G	A	7	68	c.6_splice	c.e1+1	p.K2_splice
Pat_41	Post-Resistance	WDR19	57728	37	4	39217532	39217532	Missense_Mutation	SNP	G	A	9	113	c.1033G>A	c.(1033-1035)GTT>ATT	p.V345I
Pat_41	Post-Resistance	WDR19	57728	37	4	39233548	39233548	Missense_Mutation	SNP	G	A	26	345	c.2114G>A	c.(2113-2115)GGC>GAC	p.G705D
Pat_41	Post-Resistance	WDR19	57728	37	4	39269615	39269615	Missense_Mutation	SNP	G	A	7	26	c.3262G>A	c.(3262-3264)GAT>AAT	p.D1088N
Pat_41	Post-Resistance	RFC1	5981	37	4	39306496	39306496	Missense_Mutation	SNP	C	T	113	642	c.2051G>A	c.(2050-2052)AGC>AAC	p.S684N
Pat_41	Post-Resistance	UGDH	7358	37	4	39512134	39512134	Missense_Mutation	SNP	C	T	31	125	c.502G>A	c.(502-504)GCC>ACC	p.A168T
Pat_41	Post-Resistance	LIMCH1	22998	37	4	41664924	41664924	Missense_Mutation	SNP	G	A	4	112	c.2059G>A	c.(2059-2061)GAT>AAT	p.D687N
Pat_41	Post-Resistance	LIMCH1	22998	37	4	41684416	41684416	Missense_Mutation	SNP	G	C	53	62	c.2632G>C	c.(2632-2634)GGA>CGA	p.G878R
Pat_41	Post-Resistance	SLC30A9	10463	37	4	41992727	41992727	Missense_Mutation	SNP	G	A	3	37	c.59G>A	c.(58-60)CGG>CAG	p.R20Q
Pat_41	Post-Resistance	SHISA3	152573	37	4	42403227	42403227	Missense_Mutation	SNP	C	T	18	230	c.476C>T	c.(475-477)TCC>TTC	p.S159F
Pat_41	Post-Resistance	GABRG1	2565	37	4	46043100	46043100	Missense_Mutation	SNP	G	A	10	139	c.1303C>T	c.(1303-1305)CGC>TGC	p.R435C
Pat_41	Post-Resistance	GABRG1	2565	37	4	46060350	46060350	Missense_Mutation	SNP	C	T	5	96	c.800G>A	c.(799-801)AGC>AAC	p.S267N
Pat_41	Post-Resistance	ATP10D	57205	37	4	47538510	47538510	Missense_Mutation	SNP	C	T	80	334	c.1072C>T	c.(1072-1074)CCT>TCT	p.P358S
Pat_41	Post-Resistance	ATP10D	57205	37	4	47560009	47560009	Missense_Mutation	SNP	C	T	6	65	c.2153C>T	c.(2152-2154)GCC>GTC	p.A718V
Pat_41	Post-Resistance	NFXL1	152518	37	4	47850221	47850221	Missense_Mutation	SNP	C	T	26	247	c.2695G>A	c.(2695-2697)GTT>ATT	p.V899I
Pat_41	Post-Resistance	NIPAL1	152519	37	4	48027108	48027108	Missense_Mutation	SNP	C	T	15	194	c.70C>T	c.(70-72)CCA>TCA	p.P24S
Pat_41	Post-Resistance	NIPAL1	152519	37	4	48037013	48037013	Missense_Mutation	SNP	G	A	12	181	c.577G>A	c.(577-579)GAA>AAA	p.E193K
Pat_41	Post-Resistance	FRYL	285527	37	4	48503750	48503750	Missense_Mutation	SNP	C	T	15	269	c.8482G>A	c.(8482-8484)GAA>AAA	p.E2828K
Pat_41	Post-Resistance	FRYL	285527	37	4	48523199	48523199	Missense_Mutation	SNP	G	A	5	112	c.7555C>T	c.(7555-7557)CCA>TCA	p.P2519S
Pat_41	Post-Resistance	FRYL	285527	37	4	48537729	48537729	Missense_Mutation	SNP	T	C	14	151	c.6509A>G	c.(6508-6510)TAC>TGC	p.Y2170C
Pat_41	Post-Resistance	OCIAD1	54940	37	4	48859335	48859335	Missense_Mutation	SNP	C	T	10	146	c.653C>T	c.(652-654)ACT>ATT	p.T218I
Pat_41	Post-Resistance	CWH43	80157	37	4	49032865	49032865	Missense_Mutation	SNP	G	A	9	108	c.1396G>A	c.(1396-1398)GAG>AAG	p.E466K
Pat_41	Post-Resistance	LRRC66	339977	37	4	52861488	52861488	Missense_Mutation	SNP	C	T	16	170	c.1700G>A	c.(1699-1701)GGC>GAC	p.G567D
Pat_41	Post-Resistance	LRRC66	339977	37	4	52861713	52861713	Missense_Mutation	SNP	C	T	34	137	c.1475G>A	c.(1474-1476)GGG>GAG	p.G492E
Pat_41	Post-Resistance	LNX1	84708	37	4	54344908	54344908	Missense_Mutation	SNP	G	A	5	51	c.1487C>T	c.(1486-1488)CCC>CTC	p.P496L
Pat_41	Post-Resistance	LNX1	84708	37	4	54362405	54362405	Missense_Mutation	SNP	T	C	15	76	c.1135A>G	c.(1135-1137)AGC>GGC	p.S379G
Pat_41	Post-Resistance	PDGFRA	5156	37	4	55127445	55127445	Missense_Mutation	SNP	G	A	51	471	c.233G>A	c.(232-234)AGC>AAC	p.S78N
Pat_41	Post-Resistance	KIAA1211	57482	37	4	57173741	57173741	Missense_Mutation	SNP	C	T	30	104	c.161C>T	c.(160-162)CCC>CTC	p.P54L
Pat_41	Post-Resistance	KIAA1211	57482	37	4	57181769	57181769	Missense_Mutation	SNP	G	A	7	259	c.2101G>A	c.(2101-2103)GGC>AGC	p.G701S
Pat_41	Post-Resistance	KIAA1211	57482	37	4	57193878	57193878	Missense_Mutation	SNP	G	A	50	537	c.3610G>A	c.(3610-3612)GAT>AAT	p.D1204N
Pat_41	Post-Resistance	PPAT	5471	37	4	57267627	57267627	Missense_Mutation	SNP	G	A	14	73	c.755C>T	c.(754-756)CCT>CTT	p.P252L
Pat_41	Post-Resistance	PAICS	10606	37	4	57312960	57312960	Missense_Mutation	SNP	C	T	4	25	c.314C>T	c.(313-315)ACT>ATT	p.T105I
Pat_41	Post-Resistance	C4orf14	84273	37	4	57830661	57830661	Missense_Mutation	SNP	C	T	23	276	c.1796G>A	c.(1795-1797)GGA>GAA	p.G599E
Pat_41	Post-Resistance	UBA6	55236	37	4	68490716	68490716	Missense_Mutation	SNP	C	T	4	108	c.2708G>A	c.(2707-2709)GGC>GAC	p.G903D
Pat_41	Post-Resistance	UGT2B7	7364	37	4	69968562	69968562	Missense_Mutation	SNP	G	A	18	451	c.908G>A	c.(907-909)GGT>GAT	p.G303D
Pat_41	Post-Resistance	STATH	6779	37	4	70866607	70866607	Missense_Mutation	SNP	C	T	28	415	c.130C>T	c.(130-132)CCA>TCA	p.P44S
Pat_41	Post-Resistance	MUC7	4589	37	4	71347018	71347018	Missense_Mutation	SNP	C	A	10	598	c.557C>A	c.(556-558)CCA>CAA	p.P186Q
Pat_41	Post-Resistance	AMBN	258	37	4	71472004	71472004	Missense_Mutation	SNP	G	A	3	38	c.901G>A	c.(901-903)GAC>AAC	p.D301N
Pat_41	Post-Resistance	ENAM	10117	37	4	71509592	71509592	Missense_Mutation	SNP	C	T	10	90	c.2449C>T	c.(2449-2451)CTT>TTT	p.L817F
Pat_41	Post-Resistance	GRSF1	2926	37	4	71698066	71698066	Missense_Mutation	SNP	G	A	13	192	c.772C>T	c.(772-774)CCT>TCT	p.P258S
Pat_41	Post-Resistance	GC	2638	37	4	72618237	72618237	Missense_Mutation	SNP	C	T	24	84	c.1393G>A	c.(1393-1395)GAG>AAG	p.E465K
Pat_41	Post-Resistance	ADAMTS3	9508	37	4	73433114	73433114	Missense_Mutation	SNP	C	T	8	91	c.74G>A	c.(73-75)GGT>GAT	p.G25D
Pat_41	Post-Resistance	ANKRD17	26057	37	4	73956714	73956714	Missense_Mutation	SNP	G	A	30	228	c.6631C>T	c.(6631-6633)CCT>TCT	p.P2211S
Pat_41	Post-Resistance	EREG	2069	37	4	75246757	75246757	Missense_Mutation	SNP	G	A	26	295	c.181G>A	c.(181-183)GCT>ACT	p.A61T

Pat_41	Post-Resistance	USO1	8615	37	4	76714968	76714968	Missense_Mutation	SNP	G	A	8	131	c.1366G>A	c.(1366-1368)GAA>AAA	p.E456K
Pat_41	Post-Resistance	USO1	8615	37	4	76733470	76733470	Missense_Mutation	SNP	C	T	4	20	c.2741C>T	c.(2740-2742)GCC>GTC	p.A914V
Pat_41	Post-Resistance	PPEF2	5470	37	4	76797517	76797517	Missense_Mutation	SNP	C	T	8	47	c.1243G>A	c.(1243-1245)GAG>AAG	p.E415K
Pat_41	Post-Resistance	SDAD1	55153	37	4	76882236	76882236	Missense_Mutation	SNP	G	A	13	224	c.1301C>T	c.(1300-1302)ACT>ATT	p.T434I
Pat_41	Post-Resistance	SDAD1	55153	37	4	76903090	76903090	Missense_Mutation	SNP	G	A	23	108	c.191C>T	c.(190-192)GCA>GTA	p.A64V
Pat_41	Post-Resistance	STBD1	8987	37	4	77231062	77231062	Missense_Mutation	SNP	G	A	13	171	c.986G>A	c.(985-987)GGG>GAG	p.G329E
Pat_41	Post-Resistance	FRAS1	80144	37	4	79202565	79202565	Missense_Mutation	SNP	C	T	4	46	c.1085C>T	c.(1084-1086)GCT>GTT	p.A362V
Pat_41	Post-Resistance	FRAS1	80144	37	4	79240129	79240129	Missense_Mutation	SNP	G	A	12	403	c.2126G>A	c.(2125-2127)GGC>GAC	p.G709D
Pat_41	Post-Resistance	BMP2K	55589	37	4	79763592	79763592	Missense_Mutation	SNP	C	T	7	156	c.457C>T	c.(457-459)CCA>TCA	p.P153S
Pat_41	Post-Resistance	BMP2K	55589	37	4	79786842	79786842	Missense_Mutation	SNP	C	T	16	266	c.1199C>T	c.(1198-1200)GCT>GTT	p.A400V
Pat_41	Post-Resistance	NAA11	84779	37	4	80246532	80246532	Missense_Mutation	SNP	C	T	12	35	c.500G>A	c.(499-501)GGC>GAC	p.G167D
Pat_41	Post-Resistance	GK2	2712	37	4	80327742	80327742	Missense_Mutation	SNP	C	T	7	81	c.1613G>A	c.(1612-1614)AGT>AAT	p.S538N
Pat_41	Post-Resistance	SEC31A	22872	37	4	83800048	83800048	Missense_Mutation	SNP	C	T	10	73	c.237G>A	c.(235-237)ATG>ATA	p.M79I
Pat_41	Post-Resistance	FAM175A	84142	37	4	84383770	84383770	Missense_Mutation	SNP	C	T	37	390	c.1082G>A	c.(1081-1083)CGG>CAG	p.R361Q
Pat_41	Post-Resistance	WDFY3	23001	37	4	85598446	85598446	Missense_Mutation	SNP	C	T	7	97	c.10363G>A	c.(10363-10365)GAA>AAA	p.E3455K
Pat_41	Post-Resistance	WDFY3	23001	37	4	85612927	85612927	Missense_Mutation	SNP	G	A	5	27	c.9061C>T	c.(9061-9063)CCT>TCT	p.P3021S
Pat_41	Post-Resistance	WDFY3	23001	37	4	85630100	85630100	Missense_Mutation	SNP	G	A	14	177	c.8179C>T	c.(8179-8181)CCT>TCT	p.P2727S
Pat_41	Post-Resistance	WDFY3	23001	37	4	85687151	85687151	Missense_Mutation	SNP	C	T	30	339	c.5000G>A	c.(4999-5001)GGT>GAT	p.G1667D
Pat_41	Post-Resistance	WDFY3	23001	37	4	85715759	85715759	Nonsense_Mutation	SNP	G	A	37	520	c.3400C>T	c.(3400-3402)CAA>TAA	p.Q1134*
Pat_41	Post-Resistance	WDFY3	23001	37	4	85729487	85729487	Missense_Mutation	SNP	C	T	21	268	c.2429G>A	c.(2428-2430)AGG>AAG	p.R810K
Pat_41	Post-Resistance	AFF1	4299	37	4	87968735	87968735	Nonsense_Mutation	SNP	C	T	15	188	c.1027C>T	c.(1027-1029)CAG>TAG	p.Q343*
Pat_41	Post-Resistance	AFF1	4299	37	4	88036399	88036399	Missense_Mutation	SNP	G	A	3	18	c.2393G>A	c.(2392-2394)AGC>AAC	p.S798N
Pat_41	Post-Resistance	AFF1	4299	37	4	88048794	88048794	Splice_Site	SNP	G	A	10	133	c.2883_splice	c.e15-1	p.K961_splice
Pat_41	Post-Resistance	HSD17B13	345275	37	4	88235098	88235098	Missense_Mutation	SNP	G	A	17	166	c.572C>T	c.(571-573)GCC>GTC	p.A191V
Pat_41	Post-Resistance	HSD17B11	51170	37	4	88261676	88261676	Missense_Mutation	SNP	G	A	5	57	c.778C>T	c.(778-780)CCA>TCA	p.P260S
Pat_41	Post-Resistance	HSD17B11	51170	37	4	88293907	88293907	Missense_Mutation	SNP	C	T	8	239	c.511G>A	c.(511-513)GCT>ACT	p.A171T
Pat_41	Post-Resistance	DMP1	1758	37	4	88584093	88584093	Missense_Mutation	SNP	G	A	43	449	c.1163G>A	c.(1162-1164)AGC>AAC	p.S388N
Pat_41	Post-Resistance	MEPE	56955	37	4	88767513	88767513	Missense_Mutation	SNP	C	T	23	430	c.1493C>T	c.(1492-1494)TCC>TTC	p.S498F
Pat_41	Post-Resistance	HERC6	55008	37	4	89363442	89363442	Missense_Mutation	SNP	G	A	9	57	c.2899G>A	c.(2899-2901)GTA>ATA	p.V967I
Pat_41	Post-Resistance	HERC5	51191	37	4	89407357	89407357	Missense_Mutation	SNP	G	A	43	253	c.1829G>A	c.(1828-1830)AGG>AAG	p.R610K
Pat_41	Post-Resistance	TIGD2	166815	37	4	90034868	90034868	Missense_Mutation	SNP	C	T	4	125	c.743C>T	c.(742-744)ACA>ATA	p.T248I
Pat_41	Post-Resistance	SMARCAD1	56916	37	4	95173991	95173991	Missense_Mutation	SNP	G	A	11	142	c.1114G>A	c.(1114-1116)GAG>AAG	p.E372K
Pat_41	Post-Resistance	ADH7	131	37	4	100341758	100341758	Missense_Mutation	SNP	C	T	4	124	c.793G>A	c.(793-795)GTG>ATG	p.V265M
Pat_41	Post-Resistance	PPP3CA	5530	37	4	101953423	101953423	Splice_Site	SNP	C	T	5	76	c.1339_splice	c.e12+1	p.A447_splice
Pat_41	Post-Resistance	BANK1	55024	37	4	102783822	102783822	Splice_Site	SNP	G	A	4	66	c.763_splice	c.e4+1	p.E255_splice
Pat_41	Post-Resistance	BANK1	55024	37	4	102981511	102981511	Nonsense_Mutation	SNP	C	T	15	188	c.2113C>T	c.(2113-2115)CAG>TAG	p.Q705*
Pat_41	Post-Resistance	NFKB1	4790	37	4	103534660	103534660	Missense_Mutation	SNP	G	A	7	91	c.2668G>A	c.(2668-2670)GCA>ACA	p.A890T
Pat_41	Post-Resistance	NFKB1	4790	37	4	103537695	103537695	Missense_Mutation	SNP	C	T	8	118	c.2851C>T	c.(2851-2853)CTC>TTC	p.L951F
Pat_41	Post-Resistance	INTS12	57117	37	4	106621110	106621110	Missense_Mutation	SNP	C	T	19	359	c.53G>A	c.(52-54)GGT>GAT	p.G18D
Pat_41	Post-Resistance	GSTCD	79807	37	4	106647965	106647965	Missense_Mutation	SNP	G	A	20	242	c.1124G>A	c.(1123-1125)AGA>AAA	p.R375K
Pat_41	Post-Resistance	PAPSS1	9061	37	4	108574760	108574760	Nonsense_Mutation	SNP	C	T	8	119	c.1124G>A	c.(1123-1125)TGG>TAG	p.W375*
Pat_41	Post-Resistance	GAR1	54433	37	4	110737478	110737478	Missense_Mutation	SNP	G	A	26	142	c.158G>A	c.(157-159)GGT>GAT	p.G53D
Pat_41	Post-Resistance	ENPEP	2028	37	4	111463931	111463931	Missense_Mutation	SNP	C	T	17	206	c.1832C>T	c.(1831-1833)CCT>CTT	p.P611L
Pat_41	Post-Resistance	C4orf21	55345	37	4	113508775	113508775	Nonsense_Mutation	SNP	C	T	4	97	c.3438G>A	c.(3436-3438)TGG>TGA	p.W1146*
Pat_41	Post-Resistance	C4orf21	55345	37	4	113539521	113539521	Nonsense_Mutation	SNP	C	T	15	295	c.1677G>A	c.(1675-1677)TGG>TGA	p.W559*
Pat_41	Post-Resistance	LARP7	51574	37	4	113567786	113567786	Missense_Mutation	SNP	G	A	3	25	c.346G>A	c.(346-348)GGG>AGG	p.G116R
Pat_41	Post-Resistance	LARP7	51574	37	4	113575292	113575292	Missense_Mutation	SNP	G	A	7	163	c.1645G>A	c.(1645-1647)GAA>AAA	p.E549K

Pat_41	Post-Resistance	ANK2	287	37	4	114274530	114274530	Missense_Mutation	SNP	G	A	8	101	c.4756G>A	c.(4756-4758)GGA>AGA	p.G1586R
Pat_41	Post-Resistance	ANK2	287	37	4	114278005	114278005	Missense_Mutation	SNP	C	T	8	96	c.8231C>T	c.(8230-8232)GCT>GTT	p.A2744V
Pat_41	Post-Resistance	ANK2	287	37	4	114278824	114278824	Missense_Mutation	SNP	C	T	26	268	c.9050C>T	c.(9049-9051)CCT>CTT	p.P3017L
Pat_41	Post-Resistance	CAMK2D	817	37	4	114378559	114378559	Nonsense_Mutation	SNP	C	T	17	417	c.1365G>A	c.(1363-1365)TGG>TGA	p.W455*
Pat_41	Post-Resistance	PRSS12	8492	37	4	119259448	119259448	Missense_Mutation	SNP	C	T	13	154	c.524G>A	c.(523-525)GGC>GAC	p.G175D
Pat_41	Post-Resistance	SEC24D	9871	37	4	119678893	119678893	Missense_Mutation	SNP	C	T	5	65	c.1404G>A	c.(1402-1404)ATG>ATA	p.M468I
Pat_41	Post-Resistance	SEC24D	9871	37	4	119686070	119686070	Missense_Mutation	SNP	G	A	20	90	c.1183C>T	c.(1183-1185)CCA>TCA	p.P395S
Pat_41	Post-Resistance	SEC24D	9871	37	4	119736851	119736851	Missense_Mutation	SNP	G	A	22	60	c.428C>T	c.(427-429)CCC>CTC	p.P143L
Pat_41	Post-Resistance	MYOZ2	51778	37	4	120107252	120107252	Missense_Mutation	SNP	C	T	15	161	c.692C>T	c.(691-693)TCC>TTC	p.S231F
Pat_41	Post-Resistance	PDE5A	8654	37	4	120474796	120474796	Nonsense_Mutation	SNP	C	T	8	114	c.1305G>A	c.(1303-1305)TGG>TGA	p.W435*
Pat_41	Post-Resistance	QRFPR	84109	37	4	122254103	122254103	Missense_Mutation	SNP	G	A	20	116	c.670C>T	c.(670-672)CTC>TTC	p.L224F
Pat_41	Post-Resistance	TRPC3	7222	37	4	122833127	122833127	Missense_Mutation	SNP	G	A	24	305	c.1463C>T	c.(1462-1464)CCC>CTC	p.P488L
Pat_41	Post-Resistance	KIAA1109	84162	37	4	123264711	123264711	Missense_Mutation	SNP	G	A	14	170	c.12499G>A	c.(12499-12501)GCA>ACA	p.A4167T
Pat_41	Post-Resistance	KIAA1109	84162	37	4	123277779	123277779	Missense_Mutation	SNP	C	T	24	314	c.14504C>T	c.(14503-14505)GCC>GTC	p.A4835V
Pat_41	Post-Resistance	ADAD1	132612	37	4	123333760	123333760	Missense_Mutation	SNP	G	A	10	222	c.1045G>A	c.(1045-1047)GCA>ACA	p.A349T
Pat_41	Post-Resistance	SPATA5	166378	37	4	123977570	123977570	Missense_Mutation	SNP	G	A	7	67	c.2108G>A	c.(2107-2109)GGT>GAT	p.G703D
Pat_41	Post-Resistance	ANKRD50	57182	37	4	125631177	125631177	Missense_Mutation	SNP	T	G	5	170	c.490A>C	c.(490-492)AAC>CAC	p.N164H
Pat_41	Post-Resistance	FAT4	79633	37	4	126373138	126373138	Missense_Mutation	SNP	C	T	16	90	c.10967C>T	c.(10966-10968)ACC>ATC	p.T3656I
Pat_41	Post-Resistance	FAT4	79633	37	4	126373635	126373635	Missense_Mutation	SNP	G	A	4	59	c.11464G>A	c.(11464-11466)GCT>ACT	p.A3822T
Pat_41	Post-Resistance	FAT4	79633	37	4	126373893	126373893	Missense_Mutation	SNP	C	T	18	110	c.11722C>T	c.(11722-11724)CCT>TCT	p.P3908S
Pat_41	Post-Resistance	HSPA4L	22824	37	4	128719766	128719766	Missense_Mutation	SNP	C	T	20	185	c.331C>T	c.(331-333)CCT>TCT	p.P111S
Pat_41	Post-Resistance	SCLT1	132320	37	4	129924948	129924948	Missense_Mutation	SNP	G	A	12	480	c.374C>T	c.(373-375)GCA>GTA	p.A125V
Pat_41	Post-Resistance	C4orf49	84709	37	4	140188063	140188063	Missense_Mutation	SNP	G	A	29	334	c.413C>T	c.(412-414)GCC>GTC	p.A138V
Pat_41	Post-Resistance	CLGN	1047	37	4	141317301	141317301	Missense_Mutation	SNP	G	A	23	789	c.943C>T	c.(943-945)CTT>TTT	p.L315F
Pat_41	Post-Resistance	TBC1D9	23158	37	4	141590810	141590810	Missense_Mutation	SNP	G	A	16	203	c.1415C>T	c.(1414-1416)CCC>CTC	p.P472L
Pat_41	Post-Resistance	TBC1D9	23158	37	4	141590867	141590867	Missense_Mutation	SNP	C	T	6	190	c.1358G>A	c.(1357-1359)GGC>GAC	p.G453D
Pat_41	Post-Resistance	INPP4B	8821	37	4	143324156	143324156	Missense_Mutation	SNP	G	A	13	216	c.307C>T	c.(307-309)CCC>TCC	p.P103S
Pat_41	Post-Resistance	USP38	84640	37	4	144133521	144133521	Nonsense_Mutation	SNP	G	A	29	246	c.1548G>A	c.(1546-1548)TGG>TGA	p.W516*
Pat_41	Post-Resistance	USP38	84640	37	4	144135257	144135257	Missense_Mutation	SNP	C	T	10	80	c.2128C>T	c.(2128-2130)CCA>TCA	p.P710S
Pat_41	Post-Resistance	HHIP	64399	37	4	145627791	145627791	Missense_Mutation	SNP	C	T	4	65	c.940C>T	c.(940-942)CCT>TCT	p.P314S
Pat_41	Post-Resistance	HHIP	64399	37	4	145628315	145628315	Missense_Mutation	SNP	G	A	16	67	c.1060G>A	c.(1060-1062)GGA>AGA	p.G354R
Pat_41	Post-Resistance	MMAA	166785	37	4	146560602	146560602	Missense_Mutation	SNP	C	T	5	88	c.311C>T	c.(310-312)GCC>GTC	p.A104V
Pat_41	Post-Resistance	ZNF827	152485	37	4	146744579	146744579	Missense_Mutation	SNP	G	A	15	177	c.2378C>T	c.(2377-2379)GCT>GTT	p.A793V
Pat_41	Post-Resistance	TTC29	83894	37	4	147824811	147824811	Nonsense_Mutation	SNP	C	T	5	22	c.471G>A	c.(469-471)TGG>TGA	p.W157*
Pat_41	Post-Resistance	PRMT10	90826	37	4	148582127	148582127	Missense_Mutation	SNP	G	A	32	145	c.1016C>T	c.(1015-1017)GCT>GTT	p.A339V
Pat_41	Post-Resistance	LRBA	987	37	4	151242487	151242487	Missense_Mutation	SNP	C	T	10	106	c.7519G>A	c.(7519-7521)GAT>AAT	p.D2507N
Pat_41	Post-Resistance	LRBA	987	37	4	151773974	151773974	Missense_Mutation	SNP	C	T	11	80	c.2888G>A	c.(2887-2889)AGG>AAG	p.R963K
Pat_41	Post-Resistance	LRBA	987	37	4	151837635	151837635	Missense_Mutation	SNP	C	T	18	59	c.812G>A	c.(811-813)GGA>GAA	p.G271E
Pat_41	Post-Resistance	SH3D19	152503	37	4	152069099	152069099	Missense_Mutation	SNP	C	T	4	70	c.1217G>A	c.(1216-1218)GGA>GAA	p.G406E
Pat_41	Post-Resistance	PET112L	5188	37	4	152638156	152638156	Missense_Mutation	SNP	G	A	44	248	c.512C>T	c.(511-513)GCA>GTA	p.A171V
Pat_41	Post-Resistance	PET112L	5188	37	4	152679997	152679997	Missense_Mutation	SNP	G	A	19	370	c.254C>T	c.(253-255)TCT>TTT	p.S85F
Pat_41	Post-Resistance	FHDC1	85462	37	4	153874667	153874667	Missense_Mutation	SNP	C	T	19	178	c.515C>T	c.(514-516)GCA>GTA	p.A172V
Pat_41	Post-Resistance	FHDC1	85462	37	4	153896179	153896179	Missense_Mutation	SNP	C	T	4	37	c.1736C>T	c.(1735-1737)GCC>GTC	p.A579V
Pat_41	Post-Resistance	FHDC1	85462	37	4	153896457	153896457	Missense_Mutation	SNP	G	A	7	37	c.2014G>A	c.(2014-2016)GAG>AAG	p.E672K
Pat_41	Post-Resistance	MND1	84057	37	4	154318389	154318389	Missense_Mutation	SNP	G	A	5	82	c.370G>A	c.(370-372)GCA>ACA	p.A124T
Pat_41	Post-Resistance	KIAA0922	23240	37	4	154555385	154555385	Missense_Mutation	SNP	G	A	25	417	c.4367G>A	c.(4366-4368)AGC>AAC	p.S1456N
Pat_41	Post-Resistance	KIAA0922	23240	37	4	154557691	154557691	Missense_Mutation	SNP	C	T	26	206	c.4793C>T	c.(4792-4794)CCA>CTA	p.P1598L

Pat_41	Post-Resistance	DCHS2	54798	37	4	155254493	155254493	Missense_Mutation	SNP	C	T	26	185	c.1370G>A	c.(1369-1371)AGC>AAC	p.S457N
Pat_41	Post-Resistance	DCHS2	54798	37	4	155305552	155305552	Missense_Mutation	SNP	C	T	12	64	c.202G>A	c.(202-204)GAA>AAA	p.E68K
Pat_41	Post-Resistance	FGB	2244	37	4	155488861	155488861	Missense_Mutation	SNP	G	A	18	216	c.607G>A	c.(607-609)GAA>AAA	p.E203K
Pat_41	Post-Resistance	FGA	2243	37	4	155507724	155507724	Missense_Mutation	SNP	G	A	8	72	c.857C>T	c.(856-858)CCC>CTC	p.P286L
Pat_41	Post-Resistance	FGG	2266	37	4	155528006	155528006	Missense_Mutation	SNP	T	A	9	308	c.980A>T	c.(979-981)GAC>GTC	p.D327V
Pat_41	Post-Resistance	CTSO	1519	37	4	156864349	156864349	Missense_Mutation	SNP	C	T	24	343	c.203G>A	c.(202-204)GGA>GAA	p.G68E
Pat_41	Post-Resistance	GLRB	2743	37	4	158057829	158057829	Missense_Mutation	SNP	G	A	11	139	c.506G>A	c.(505-507)GGA>GAA	p.G169E
Pat_41	Post-Resistance	GRIA2	2891	37	4	158281249	158281249	Missense_Mutation	SNP	G	A	13	149	c.2245G>A	c.(2245-2247)GAT>AAT	p.D749N
Pat_41	Post-Resistance	RXFP1	59350	37	4	159569708	159569708	Missense_Mutation	SNP	G	A	15	68	c.1814G>A	c.(1813-1815)AGT>AAT	p.S605N
Pat_41	Post-Resistance	ETFDH	2110	37	4	159606330	159606330	Missense_Mutation	SNP	G	A	28	269	c.565G>A	c.(565-567)GCC>ACC	p.A189T
Pat_41	Post-Resistance	PPID	5481	37	4	159638217	159638217	Missense_Mutation	SNP	C	T	17	343	c.469G>A	c.(469-471)GGA>AGA	p.G157R
Pat_41	Post-Resistance	C4orf45	152940	37	4	159836345	159836345	Missense_Mutation	SNP	G	A	6	34	c.523C>T	c.(523-525)CCG>TCG	p.P175S
Pat_41	Post-Resistance	RAPGEF2	9693	37	4	160225608	160225608	Missense_Mutation	SNP	C	T	36	261	c.175C>T	c.(175-177)CTT>TTT	p.L59F
Pat_41	Post-Resistance	GK3P	2713	37	4	166200742	166200742	Missense_Mutation	SNP	C	T	20	80	c.56G>A	c.(55-57)GGC>GAC	p.G19D
Pat_41	Post-Resistance	KLHL2	11275	37	4	166235280	166235280	Missense_Mutation	SNP	G	A	34	310	c.1571G>A	c.(1570-1572)AGA>AAA	p.R524K
Pat_41	Post-Resistance	ANXA10	11199	37	4	169049259	169049259	Missense_Mutation	SNP	C	T	5	161	c.43C>T	c.(43-45)CCC>TCC	p.P15S
Pat_41	Post-Resistance	ANXA10	11199	37	4	169105717	169105717	Missense_Mutation	SNP	G	A	7	120	c.791G>A	c.(790-792)GGT>GAT	p.G264D
Pat_41	Post-Resistance	PALLD	23022	37	4	169589448	169589448	Missense_Mutation	SNP	C	T	14	131	c.1016C>T	c.(1015-1017)ACA>ATA	p.T339I
Pat_41	Post-Resistance	SH3RF1	57630	37	4	170042042	170042042	Nonsense_Mutation	SNP	C	T	17	123	c.1445G>A	c.(1444-1446)TGG>TAG	p.W482*
Pat_41	Post-Resistance	GALNTL6	442117	37	4	173803945	173803945	Missense_Mutation	SNP	C	T	9	244	c.928C>T	c.(928-930)CCT>TCT	p.P310S
Pat_41	Post-Resistance	HMGB2	3148	37	4	174254268	174254268	Missense_Mutation	SNP	C	T	12	138	c.248G>A	c.(247-249)GGT>GAT	p.G83D
Pat_41	Post-Resistance	SAP30	8819	37	4	174294545	174294545	Missense_Mutation	SNP	G	A	5	41	c.320G>A	c.(319-321)AGG>AAG	p.R107K
Pat_41	Post-Resistance	HAND2	9464	37	4	174448483	174448483	Missense_Mutation	SNP	G	A	31	154	c.599C>T	c.(598-600)ACC>ATC	p.T200I
Pat_41	Post-Resistance	MORF4	10934	37	4	174537275	174537275	Missense_Mutation	SNP	G	A	7	295	c.520C>T	c.(520-522)CAT>TAT	p.H174Y
Pat_41	Post-Resistance	KIAA1712	80817	37	4	175225510	175225510	Missense_Mutation	SNP	C	T	7	124	c.497C>T	c.(496-498)ACC>ATC	p.T166I
Pat_41	Post-Resistance	GPM6A	2823	37	4	176622841	176622841	Missense_Mutation	SNP	C	T	15	535	c.115G>A	c.(115-117)GGT>AGT	p.G39S
Pat_41	Post-Resistance	WDR17	116966	37	4	177098240	177098240	Missense_Mutation	SNP	C	T	12	260	c.3598C>T	c.(3598-3600)CCT>TCT	p.P1200S
Pat_41	Post-Resistance	ODZ3	55714	37	4	183696262	183696262	Missense_Mutation	SNP	G	A	8	118	c.5260G>A	c.(5260-5262)GAG>AAG	p.E1754K
Pat_41	Post-Resistance	IRF2	3660	37	4	185309964	185309964	Missense_Mutation	SNP	C	T	11	114	c.998G>A	c.(997-999)AGC>AAC	p.S333N
Pat_41	Post-Resistance	IRF2	3660	37	4	185339698	185339698	Missense_Mutation	SNP	G	A	14	161	c.352C>T	c.(352-354)CCT>TCT	p.P118S
Pat_41	Post-Resistance	HELT	391723	37	4	185941613	185941613	Missense_Mutation	SNP	C	T	5	32	c.671C>T	c.(670-672)TCG>TTG	p.S224L
Pat_41	Post-Resistance	LRP2BP	55805	37	4	186291963	186291963	Missense_Mutation	SNP	G	A	28	119	c.809C>T	c.(808-810)GCT>GTT	p.A270V
Pat_41	Post-Resistance	UFSP2	55325	37	4	186336886	186336886	Missense_Mutation	SNP	C	T	14	219	c.469G>A	c.(469-471)GCT>ACT	p.A157T
Pat_41	Post-Resistance	SORBS2	8470	37	4	186545621	186545621	Missense_Mutation	SNP	G	A	15	150	c.950C>T	c.(949-951)TCC>TTC	p.S317F
Pat_41	Post-Resistance	FAT1	2195	37	4	187540874	187540874	Missense_Mutation	SNP	G	A	14	140	c.6866C>T	c.(6865-6867)GCG>GTG	p.A2289V
Pat_41	Post-Resistance	FAT1	2195	37	4	187541709	187541709	Missense_Mutation	SNP	G	A	38	382	c.6031C>T	c.(6031-6033)CCT>TCT	p.P2011S
Pat_41	Post-Resistance	FAT1	2195	37	4	187584680	187584680	Missense_Mutation	SNP	G	A	18	145	c.3353C>T	c.(3352-3354)CCT>CTT	p.P1118L
Pat_41	Post-Resistance	SDHA	6389	37	5	230999	230999	Missense_Mutation	SNP	G	A	9	336	c.779G>A	c.(778-780)GGG>GAG	p.G260E
Pat_41	Post-Resistance	AHRR	57491	37	5	424037	424037	Missense_Mutation	SNP	C	T	10	158	c.665C>T	c.(664-666)ACC>ATC	p.T222I
Pat_41	Post-Resistance	AHRR	57491	37	5	434254	434254	Missense_Mutation	SNP	C	T	5	206	c.1465C>T	c.(1465-1467)CCC>TCC	p.P489S
Pat_41	Post-Resistance	SLC9A3	6550	37	5	484708	484708	Missense_Mutation	SNP	G	A	10	104	c.859C>T	c.(859-861)CCC>TCC	p.P287S
Pat_41	Post-Resistance	SLC9A3	6550	37	5	492022	492022	Missense_Mutation	SNP	C	T	4	50	c.376G>A	c.(376-378)GAC>AAC	p.D126N
Pat_41	Post-Resistance	CEP72	55722	37	5	644435	644435	Missense_Mutation	SNP	G	A	10	236	c.1561G>A	c.(1561-1563)GAT>AAT	p.D521N
Pat_41	Post-Resistance	TPPP	11076	37	5	665227	665227	Missense_Mutation	SNP	C	T	5	91	c.650G>A	c.(649-651)GGG>GAG	p.G217E
Pat_41	Post-Resistance	TERT	7015	37	5	1278860	1278860	Missense_Mutation	SNP	C	T	22	299	c.2182G>A	c.(2182-2184)GTC>ATC	p.V728I
Pat_41	Post-Resistance	IRX4	50805	37	5	1879867	1879867	Missense_Mutation	SNP	C	T	11	83	c.487G>A	c.(487-489)GAG>AAG	p.E163K
Pat_41	Post-Resistance	IRX2	153572	37	5	2749547	2749547	Missense_Mutation	SNP	C	T	3	21	c.604G>A	c.(604-606)GAG>AAG	p.E202K

Pat_41	Post-Resistance	ADAMTS16	170690	37	5	5190184	5190184	Missense_Mutation	SNP	C	T	24	117	c.1148C>T	c.(1147-1149)GCC>GTC	p.A383V
Pat_41	Post-Resistance	NSUN2	54888	37	5	6607428	6607428	Missense_Mutation	SNP	G	A	25	164	c.1393C>T	c.(1393-1395)CCC>TCC	p.P465S
Pat_41	Post-Resistance	CMBL	134147	37	5	10288642	10288642	Splice_Site	SNP	C	T	8	48	c.216_splice	c.e3-1	p.T72_splice
Pat_41	Post-Resistance	6-Mar	10299	37	5	10394222	10394222	Nonsense_Mutation	SNP	G	A	9	96	c.795G>A	c.(793-795)TGG>TGA	p.W265*
Pat_41	Post-Resistance	CTNND2	1501	37	5	10981913	10981913	Missense_Mutation	SNP	G	A	22	392	c.3389C>T	c.(3388-3390)GCG>GTG	p.A1130V
Pat_41	Post-Resistance	TRIO	7204	37	5	14291188	14291188	Missense_Mutation	SNP	G	A	25	141	c.904G>A	c.(904-906)GCG>ACG	p.A302T
Pat_41	Post-Resistance	TRIO	7204	37	5	14480082	14480082	Missense_Mutation	SNP	C	T	7	189	c.6298C>T	c.(6298-6300)CCA>TCA	p.P2100S
Pat_41	Post-Resistance	TRIO	7204	37	5	14482853	14482853	Missense_Mutation	SNP	C	T	15	273	c.6628C>T	c.(6628-6630)CCG>TCG	p.P2210S
Pat_41	Post-Resistance	FAM105A	54491	37	5	14609067	14609067	Missense_Mutation	SNP	C	T	29	194	c.838C>T	c.(838-840)CCT>TCT	p.P280S
Pat_41	Post-Resistance	ANKH	56172	37	5	14758707	14758707	Missense_Mutation	SNP	G	A	11	148	c.314C>T	c.(313-315)GCT>GTT	p.A105V
Pat_41	Post-Resistance	ZNF622	90441	37	5	16465521	16465521	Missense_Mutation	SNP	T	A	5	169	c.254A>T	c.(253-255)CAC>CTC	p.H85L
Pat_41	Post-Resistance	FAM134B	54463	37	5	16475203	16475203	Missense_Mutation	SNP	C	T	14	212	c.1141G>A	c.(1141-1143)GAC>AAC	p.D381N
Pat_41	Post-Resistance	CDH6	1004	37	5	31302272	31302272	Missense_Mutation	SNP	G	A	10	65	c.866G>A	c.(865-867)AGA>AAA	p.R289K
Pat_41	Post-Resistance	ZFR	51663	37	5	32397416	32397416	Missense_Mutation	SNP	C	T	19	177	c.1742G>A	c.(1741-1743)CGG>CAG	p.R581Q
Pat_41	Post-Resistance	ADAMTS12	81792	37	5	33546283	33546283	Missense_Mutation	SNP	C	T	5	47	c.4327G>A	c.(4327-4329)GTT>ATT	p.V1443I
Pat_41	Post-Resistance	ADAMTS12	81792	37	5	33577237	33577237	Missense_Mutation	SNP	C	T	8	256	c.2894G>A	c.(2893-2895)CGG>CAG	p.R965Q
Pat_41	Post-Resistance	TTC23L	153657	37	5	34869071	34869071	Missense_Mutation	SNP	C	T	3	49	c.902C>T	c.(901-903)GCG>GTG	p.A301V
Pat_41	Post-Resistance	AGXT2	64902	37	5	35039589	35039589	Missense_Mutation	SNP	C	T	18	63	c.202G>A	c.(202-204)GAA>AAA	p.E68K
Pat_41	Post-Resistance	PRLR	5618	37	5	35066060	35066060	Missense_Mutation	SNP	G	A	15	91	c.1000C>T	c.(1000-1002)CCA>TCA	p.P334S
Pat_41	Post-Resistance	PRLR	5618	37	5	35066123	35066123	Missense_Mutation	SNP	C	T	9	104	c.937G>A	c.(937-939)GAG>AAG	p.E313K
Pat_41	Post-Resistance	SPEF2	79925	37	5	35793295	35793295	Missense_Mutation	SNP	C	T	8	185	c.4589C>T	c.(4588-4590)TCC>TTC	p.S1530F
Pat_41	Post-Resistance	SLC1A3	6507	37	5	36671250	36671250	Missense_Mutation	SNP	C	T	5	131	c.439C>T	c.(439-441)CCT>TCT	p.P147S
Pat_41	Post-Resistance	NIPBL	25836	37	5	36985800	36985800	Missense_Mutation	SNP	G	A	6	97	c.2518G>A	c.(2518-2520)GTT>ATT	p.V840I
Pat_41	Post-Resistance	NIPBL	25836	37	5	37045695	37045695	Missense_Mutation	SNP	G	A	73	343	c.6494G>A	c.(6493-6495)AGC>AAC	p.S2165N
Pat_41	Post-Resistance	C5orf42	65250	37	5	37187861	37187861	Missense_Mutation	SNP	C	T	7	82	c.3895G>A	c.(3895-3897)GCA>ACA	p.A1299T
Pat_41	Post-Resistance	WDR70	55100	37	5	37438051	37438051	Missense_Mutation	SNP	C	T	17	65	c.520C>T	c.(520-522)CAT>TAT	p.H174Y
Pat_41	Post-Resistance	LIFR	3977	37	5	38484947	38484947	Missense_Mutation	SNP	G	A	5	129	c.2521C>T	c.(2521-2523)CTC>TTC	p.L841F
Pat_41	Post-Resistance	LIFR	3977	37	5	38510653	38510653	Missense_Mutation	SNP	G	A	13	117	c.904C>T	c.(904-906)CGT>TGT	p.R302C
Pat_41	Post-Resistance	RICTOR	253260	37	5	38942952	38942952	Missense_Mutation	SNP	C	T	11	100	c.5035G>A	c.(5035-5037)GAT>AAT	p.D1679N
Pat_41	Post-Resistance	PTGER4	5734	37	5	40691880	40691880	Splice_Site	SNP	G	A	6	146	c.868_splice	c.e3-1	p.V290_splice
Pat_41	Post-Resistance	OXCT1	5019	37	5	41842795	41842795	Missense_Mutation	SNP	G	A	15	393	c.653C>T	c.(652-654)GCA>GTA	p.A218V
Pat_41	Post-Resistance	ZNF131	7690	37	5	43175095	43175095	Missense_Mutation	SNP	G	A	15	148	c.1732G>A	c.(1732-1734)GAG>AAG	p.E578K
Pat_41	Post-Resistance	HMGCS1	3157	37	5	43294962	43294962	Missense_Mutation	SNP	C	T	8	100	c.907G>A	c.(907-909)GAT>AAT	p.D303N
Pat_41	Post-Resistance	PARP8	79668	37	5	50059055	50059055	Missense_Mutation	SNP	G	A	6	103	c.497G>A	c.(496-498)GGG>GAG	p.G166E
Pat_41	Post-Resistance	PELO	53918	37	5	52096686	52096686	Missense_Mutation	SNP	C	T	8	97	c.458C>T	c.(457-459)ACT>ATT	p.T153I
Pat_41	Post-Resistance	ITGA2	3673	37	5	52340912	52340912	Missense_Mutation	SNP	G	A	7	171	c.377G>A	c.(376-378)GGA>GAA	p.G126E
Pat_41	Post-Resistance	ITGA2	3673	37	5	52358731	52358731	Missense_Mutation	SNP	G	A	4	86	c.1574G>A	c.(1573-1575)GGA>GAA	p.G525E
Pat_41	Post-Resistance	ITGA2	3673	37	5	52367835	52367835	Missense_Mutation	SNP	G	A	4	101	c.2303G>A	c.(2302-2304)AGC>AAC	p.S768N
Pat_41	Post-Resistance	HSPB3	8988	37	5	53751731	53751731	Missense_Mutation	SNP	C	T	4	92	c.112C>T	c.(112-114)CCT>TCT	p.P38S
Pat_41	Post-Resistance	SNX18	112574	37	5	53839089	53839089	Missense_Mutation	SNP	G	A	18	287	c.1702G>A	c.(1702-1704)GAT>AAT	p.D568N
Pat_41	Post-Resistance	DHX29	54505	37	5	54562988	54562988	Missense_Mutation	SNP	C	T	17	187	c.3503G>A	c.(3502-3504)AGA>AAA	p.R1168K
Pat_41	Post-Resistance	DHX29	54505	37	5	54563554	54563554	Missense_Mutation	SNP	C	T	45	359	c.3391G>A	c.(3391-3393)GCG>ACG	p.A1131T
Pat_41	Post-Resistance	DHX29	54505	37	5	54570732	54570732	Missense_Mutation	SNP	A	C	24	290	c.2534T>G	c.(2533-2535)ATC>AGC	p.I845S
Pat_41	Post-Resistance	DHX29	54505	37	5	54593151	54593151	Missense_Mutation	SNP	C	T	8	196	c.337G>A	c.(337-339)GGA>AGA	p.G113R
Pat_41	Post-Resistance	SLC38A9	153129	37	5	54948533	54948533	Missense_Mutation	SNP	C	T	14	78	c.776G>A	c.(775-777)GGG>GAG	p.G259E
Pat_41	Post-Resistance	IL6ST	3572	37	5	55237200	55237200	Missense_Mutation	SNP	C	T	46	314	c.2467G>A	c.(2467-2469)GAA>AAA	p.E823K
Pat_41	Post-Resistance	MAP3K1	4214	37	5	56184123	56184123	Missense_Mutation	SNP	C	T	12	145	c.4328C>T	c.(4327-4329)GCT>GTT	p.A1443V

Pat_41	Post-Resistance	C5orf43	643155	37	5	60455907	60455907	Missense_Mutation	SNP	G	A	14	176	c.92C>T	c.(91-93)ACT>ATT	p.T31I
Pat_41	Post-Resistance	PPWD1	23398	37	5	64867940	64867940	Missense_Mutation	SNP	G	A	9	154	c.796G>A	c.(796-798)GAA>AAA	p.E266K
Pat_41	Post-Resistance	C5orf44	80006	37	5	64933539	64933539	Missense_Mutation	SNP	G	A	3	58	c.232G>A	c.(232-234)GAG>AAG	p.E78K
Pat_41	Post-Resistance	SGTB	54557	37	5	65016567	65016567	Missense_Mutation	SNP	G	A	9	289	c.68C>T	c.(67-69)ACT>ATT	p.T23I
Pat_41	Post-Resistance	ERBB2IP	55914	37	5	65346625	65346625	Missense_Mutation	SNP	A	T	10	199	c.1918A>T	c.(1918-1920)ACA>TCA	p.T640S
Pat_41	Post-Resistance	SFRS12	140890	37	5	65458045	65458045	Missense_Mutation	SNP	C	T	6	171	c.172C>T	c.(172-174)CCT>TCT	p.P58S
Pat_41	Post-Resistance	SFRS12	140890	37	5	65458097	65458097	Missense_Mutation	SNP	C	T	3	41	c.224C>T	c.(223-225)TCC>TTC	p.S75F
Pat_41	Post-Resistance	CDK7	1022	37	5	68568800	68568800	Missense_Mutation	SNP	G	A	12	171	c.796G>A	c.(796-798)GAC>AAC	p.D266N
Pat_41	Post-Resistance	RAD17	5884	37	5	68682092	68682092	Missense_Mutation	SNP	C	T	14	171	c.817C>T	c.(817-819)CCC>TCC	p.P273S
Pat_41	Post-Resistance	RAD17	5884	37	5	68689015	68689015	Missense_Mutation	SNP	T	C	13	214	c.1256T>C	c.(1255-1257)TTG>TCG	p.L419S
Pat_41	Post-Resistance	MARVELD2	153562	37	5	68715289	68715289	Missense_Mutation	SNP	C	T	17	63	c.77C>T	c.(76-78)ACC>ATC	p.T26I
Pat_41	Post-Resistance	GTF2H2C	728340	37	5	68875685	68875685	Missense_Mutation	SNP	C	T	7	378	c.751C>T	c.(751-753)CGT>TGT	p.R251C
Pat_41	Post-Resistance	BDP1	55814	37	5	70819765	70819765	Splice_Site	SNP	G	A	22	268	c.5388_splice	c.e25-1	p.S1796_splice
Pat_41	Post-Resistance	MAP1B	4131	37	5	71495073	71495073	Missense_Mutation	SNP	C	T	5	71	c.5891C>T	c.(5890-5892)ACC>ATC	p.T1964I
Pat_41	Post-Resistance	TNPO1	3842	37	5	72189277	72189277	Missense_Mutation	SNP	G	A	11	91	c.1970G>A	c.(1969-1971)AGT>AAT	p.S657N
Pat_41	Post-Resistance	BTF3	689	37	5	72801044	72801044	Missense_Mutation	SNP	C	T	14	159	c.602C>T	c.(601-603)TCC>TTC	p.S201F
Pat_41	Post-Resistance	RGNEF	64283	37	5	73136341	73136341	Missense_Mutation	SNP	G	A	17	134	c.1183G>A	c.(1183-1185)GGA>AGA	p.G395R
Pat_41	Post-Resistance	HMGCR	3156	37	5	74639678	74639678	Missense_Mutation	SNP	G	A	10	143	c.166G>A	c.(166-168)GAT>AAT	p.D56N
Pat_41	Post-Resistance	COL4A3BP	10087	37	5	74677889	74677889	Missense_Mutation	SNP	G	A	4	88	c.1502C>T	c.(1501-1503)GCT>GTT	p.A501V
Pat_41	Post-Resistance	COL4A3BP	10087	37	5	74721224	74721224	Missense_Mutation	SNP	G	A	34	208	c.557C>T	c.(556-558)GCT>GTT	p.A186V
Pat_41	Post-Resistance	POLK	51426	37	5	74842834	74842834	Splice_Site	SNP	G	A	14	222	c.-12_splice	c.e2-1	
Pat_41	Post-Resistance	POLK	51426	37	5	74879196	74879196	Missense_Mutation	SNP	A	G	21	204	c.1013A>G	c.(1012-1014)AAT>AGT	p.N338S
Pat_41	Post-Resistance	IQGAP2	10788	37	5	75906892	75906892	Missense_Mutation	SNP	C	T	10	99	c.1405C>T	c.(1405-1407)CCT>TCT	p.P469S
Pat_41	Post-Resistance	IQGAP2	10788	37	5	75970386	75970386	Missense_Mutation	SNP	G	A	7	80	c.3379G>A	c.(3379-3381)GGA>AGA	p.G1127R
Pat_41	Post-Resistance	F2RL1	2150	37	5	76129178	76129178	Missense_Mutation	SNP	G	A	4	84	c.746G>A	c.(745-747)GGG>GAG	p.G249E
Pat_41	Post-Resistance	AGGF1	55109	37	5	76355529	76355529	Missense_Mutation	SNP	G	A	4	137	c.1805G>A	c.(1804-1806)GGA>GAA	p.G602E
Pat_41	Post-Resistance	AP3B1	8546	37	5	77423912	77423912	Missense_Mutation	SNP	G	A	7	183	c.1910C>T	c.(1909-1911)TCT>TTT	p.S637F
Pat_41	Post-Resistance	BHMT	635	37	5	78416243	78416243	Missense_Mutation	SNP	C	T	20	82	c.356C>T	c.(355-357)GCA>GTA	p.A119V
Pat_41	Post-Resistance	CMYA5	202333	37	5	79031151	79031151	Missense_Mutation	SNP	G	A	7	61	c.6563G>A	c.(6562-6564)GGA>GAA	p.G2188E
Pat_41	Post-Resistance	CMYA5	202333	37	5	79032029	79032029	Missense_Mutation	SNP	G	A	9	59	c.7441G>A	c.(7441-7443)GCC>ACC	p.A2481T
Pat_41	Post-Resistance	MTX3	345778	37	5	79279605	79279605	Missense_Mutation	SNP	G	A	12	174	c.841C>T	c.(841-843)CTT>TTT	p.L281F
Pat_41	Post-Resistance	SERINC5	256987	37	5	79473176	79473176	Missense_Mutation	SNP	C	T	14	150	c.418G>A	c.(418-420)GGA>AGA	p.G140R
Pat_41	Post-Resistance	ZFYVE16	9765	37	5	79733583	79733583	Missense_Mutation	SNP	C	T	14	206	c.1079C>T	c.(1078-1080)TCC>TTC	p.S360F
Pat_41	Post-Resistance	ANKRD34B	340120	37	5	79854305	79854305	Missense_Mutation	SNP	C	T	7	47	c.1534G>A	c.(1534-1536)GTA>ATA	p.V512I
Pat_41	Post-Resistance	RASGRF2	5924	37	5	80381703	80381703	Missense_Mutation	SNP	C	T	10	124	c.1244C>T	c.(1243-1245)GCC>GTC	p.A415V
Pat_41	Post-Resistance	ACOT12	134526	37	5	80643708	80643708	Missense_Mutation	SNP	C	T	38	548	c.538G>A	c.(538-540)GGC>AGC	p.G180S
Pat_41	Post-Resistance	SSBP2	23635	37	5	80738527	80738527	Missense_Mutation	SNP	C	T	19	124	c.794G>A	c.(793-795)GGT>GAT	p.G265D
Pat_41	Post-Resistance	ATP6AP1L	92270	37	5	81608459	81608459	Missense_Mutation	SNP	C	T	31	417	c.161C>T	c.(160-162)TCC>TTC	p.S54F
Pat_41	Post-Resistance	VCAN	1462	37	5	82816521	82816521	Missense_Mutation	SNP	C	T	21	157	c.2396C>T	c.(2395-2397)ACT>ATT	p.T799I
Pat_41	Post-Resistance	VCAN	1462	37	5	82834788	82834788	Missense_Mutation	SNP	C	T	7	109	c.5966C>T	c.(5965-5967)CCC>CTC	p.P1989L
Pat_41	Post-Resistance	LYSMD3	116068	37	5	89814746	89814746	Missense_Mutation	SNP	C	T	24	208	c.811G>A	c.(811-813)GAA>AAA	p.E271K
Pat_41	Post-Resistance	GPR98	84059	37	5	89938716	89938716	Missense_Mutation	SNP	C	T	39	205	c.2411C>T	c.(2410-2412)TCC>TTC	p.S804F
Pat_41	Post-Resistance	GPR98	84059	37	5	90001249	90001249	Missense_Mutation	SNP	G	A	54	419	c.8419G>A	c.(8419-8421)GCT>ACT	p.A2807T
Pat_41	Post-Resistance	GPR98	84059	37	5	90059198	90059198	Missense_Mutation	SNP	G	A	5	52	c.12197G>A	c.(12196-12198)GGA>GAA	p.G4066E
Pat_41	Post-Resistance	GPR98	84059	37	5	90074707	90074707	Missense_Mutation	SNP	G	C	155	316	c.12875G>C	c.(12874-12876)AGT>ACT	p.S4292T
Pat_41	Post-Resistance	GPR98	84059	37	5	90079082	90079082	Missense_Mutation	SNP	C	T	7	78	c.13373C>T	c.(13372-13374)ACC>ATC	p.T4458I
Pat_41	Post-Resistance	GPR98	84059	37	5	90106705	90106705	Missense_Mutation	SNP	G	A	45	86	c.15628G>A	c.(15628-15630)GTA>ATA	p.V5210I

Pat_41	Post-Resistance	GPR98	84059	37	5	90398082	90398082	Nonsense_Mutation	SNP	G	A	6	65	c.18357G>A	c.(18355-18357)TGG>TGA	p.W6119*
Pat_41	Post-Resistance	C5orf36	285600	37	5	93856004	93856004	Missense_Mutation	SNP	C	T	18	209	c.919G>A	c.(919-921)GTT>ATT	p.V307I
Pat_41	Post-Resistance	ELL2	22936	37	5	95226932	95226932	Missense_Mutation	SNP	C	T	16	140	c.1636G>A	c.(1636-1638)GAT>AAT	p.D546N
Pat_41	Post-Resistance	ELL2	22936	37	5	95234357	95234357	Missense_Mutation	SNP	G	A	7	183	c.1112C>T	c.(1111-1113)GCC>GTC	p.A371V
Pat_41	Post-Resistance	ERAP1	51752	37	5	96139274	96139274	Missense_Mutation	SNP	G	A	14	85	c.356C>T	c.(355-357)CCC>CTC	p.P119L
Pat_41	Post-Resistance	LNPEP	4012	37	5	96315082	96315082	Missense_Mutation	SNP	G	A	6	93	c.260G>A	c.(259-261)GGC>GAC	p.G87D
Pat_41	Post-Resistance	CHD1	1105	37	5	98205478	98205478	Missense_Mutation	SNP	A	G	7	55	c.4087T>C	c.(4087-4089)TCT>CCT	p.S1363P
Pat_41	Post-Resistance	CHD1	1105	37	5	98234106	98234106	Missense_Mutation	SNP	G	A	4	92	c.1219C>T	c.(1219-1221)CCT>TCT	p.P407S
Pat_41	Post-Resistance	PPIP5K2	23262	37	5	102508940	102508940	Missense_Mutation	SNP	C	T	25	140	c.2368C>T	c.(2368-2370)CTT>TTT	p.L790F
Pat_41	Post-Resistance	NUDT12	83594	37	5	102894955	102894955	Missense_Mutation	SNP	C	T	7	92	c.421G>A	c.(421-423)GCT>ACT	p.A141T
Pat_41	Post-Resistance	FBXL17	64839	37	5	107700632	107700632	Missense_Mutation	SNP	G	A	18	223	c.1181C>T	c.(1180-1182)TCT>TTT	p.S394F
Pat_41	Post-Resistance	FER	2241	37	5	108168579	108168579	Missense_Mutation	SNP	G	A	24	346	c.316G>A	c.(316-318)GAC>AAC	p.D106N
Pat_41	Post-Resistance	PJA2	9867	37	5	108698712	108698712	Missense_Mutation	SNP	G	A	6	267	c.1481C>T	c.(1480-1482)TCC>TTC	p.S494F
Pat_41	Post-Resistance	PJA2	9867	37	5	108714877	108714877	Missense_Mutation	SNP	G	A	6	221	c.311C>T	c.(310-312)ACT>ATT	p.T104I
Pat_41	Post-Resistance	CAMK4	814	37	5	110560343	110560343	Splice_Site	SNP	G	A	8	18	c.161_splice	c.e2+1	p.R54_splice
Pat_41	Post-Resistance	APC	324	37	5	112173495	112173495	Missense_Mutation	SNP	C	T	3	56	c.2204C>T	c.(2203-2205)GCG>GTG	p.A735V
Pat_41	Post-Resistance	YTHDC2	64848	37	5	112849752	112849752	Missense_Mutation	SNP	G	A	8	47	c.160G>A	c.(160-162)GAG>AAG	p.E54K
Pat_41	Post-Resistance	KCNN2	3781	37	5	113831790	113831790	Missense_Mutation	SNP	G	A	22	240	c.1651G>A	c.(1651-1653)GTC>ATC	p.V551I
Pat_41	Post-Resistance	PGGT1B	5229	37	5	114572085	114572085	Splice_Site	SNP	A	G	12	253	c.612_splice	c.e5+1	p.M204_splice
Pat_41	Post-Resistance	PGGT1B	5229	37	5	114572154	114572154	Missense_Mutation	SNP	C	T	19	190	c.545G>A	c.(544-546)TGC>TAC	p.C182Y
Pat_41	Post-Resistance	TMED7-TICAM2	100302736	37	5	114916389	114916389	Missense_Mutation	SNP	G	A	20	119	c.565C>T	c.(565-567)CTC>TTC	p.L189F
Pat_41	Post-Resistance	CDO1	1036	37	5	115151991	115151991	Missense_Mutation	SNP	G	A	16	184	c.104C>T	c.(103-105)GCC>GTC	p.A35V
Pat_41	Post-Resistance	SEMA6A	57556	37	5	115783136	115783136	Missense_Mutation	SNP	G	A	23	263	c.2266C>T	c.(2266-2268)CCC>TCC	p.P756S
Pat_41	Post-Resistance	DTWD2	285605	37	5	118274985	118274985	Missense_Mutation	SNP	C	T	8	75	c.310G>A	c.(310-312)GAA>AAA	p.E104K
Pat_41	Post-Resistance	DMXL1	1657	37	5	118484967	118484967	Missense_Mutation	SNP	G	A	5	87	c.3445G>A	c.(3445-3447)GAC>AAC	p.D1149N
Pat_41	Post-Resistance	DMXL1	1657	37	5	118485163	118485163	Missense_Mutation	SNP	C	T	39	199	c.3641C>T	c.(3640-3642)CCT>CTT	p.P1214L
Pat_41	Post-Resistance	DMXL1	1657	37	5	118582832	118582832	Missense_Mutation	SNP	G	A	17	166	c.9002G>A	c.(9001-9003)GGA>GAA	p.G3001E
Pat_41	Post-Resistance	HSD17B4	3295	37	5	118860969	118860969	Missense_Mutation	SNP	C	T	5	191	c.1562C>T	c.(1561-1563)GCT>GTT	p.A521V
Pat_41	Post-Resistance	PRR16	51334	37	5	120022208	120022208	Missense_Mutation	SNP	C	T	4	74	c.719C>T	c.(718-720)CCA>CTA	p.P240L
Pat_41	Post-Resistance	SNX2	6643	37	5	122131019	122131019	Missense_Mutation	SNP	C	T	16	221	c.167C>T	c.(166-168)TCC>TTC	p.S56F
Pat_41	Post-Resistance	CEP120	153241	37	5	122682380	122682380	Missense_Mutation	SNP	G	A	21	276	c.2794C>T	c.(2794-2796)CCC>TCC	p.P932S
Pat_41	Post-Resistance	CEP120	153241	37	5	122725741	122725741	Missense_Mutation	SNP	G	A	8	144	c.1132C>T	c.(1132-1134)CCA>TCA	p.P378S
Pat_41	Post-Resistance	LMNB1	4001	37	5	126145924	126145924	Missense_Mutation	SNP	C	T	15	206	c.695C>T	c.(694-696)TCT>TTT	p.S232F
Pat_41	Post-Resistance	3-Mar	115123	37	5	126253836	126253836	Missense_Mutation	SNP	G	A	9	86	c.28C>T	c.(28-30)CCC>TCC	p.P10S
Pat_41	Post-Resistance	PRRC1	133619	37	5	126859233	126859233	Missense_Mutation	SNP	G	A	6	140	c.62G>A	c.(61-63)GGG>GAG	p.G21E
Pat_41	Post-Resistance	SLC12A2	6558	37	5	127520164	127520164	Missense_Mutation	SNP	G	A	12	72	c.3406G>A	c.(3406-3408)GAT>AAT	p.D1136N
Pat_41	Post-Resistance	FBN2	2201	37	5	127710438	127710438	Missense_Mutation	SNP	C	G	20	41	c.1978G>C	c.(1978-1980)GAT>CAT	p.D660H
Pat_41	Post-Resistance	ADAMTS19	171019	37	5	129015481	129015481	Missense_Mutation	SNP	C	T	5	208	c.2513C>T	c.(2512-2514)TCT>TTT	p.S838F
Pat_41	Post-Resistance	ADAMTS19	171019	37	5	129070718	129070718	Missense_Mutation	SNP	G	A	22	222	c.3388G>A	c.(3388-3390)GAA>AAA	p.E1130K
Pat_41	Post-Resistance	CHSY3	337876	37	5	129519976	129519976	Missense_Mutation	SNP	G	A	23	195	c.1141G>A	c.(1141-1143)GAC>AAC	p.D381N
Pat_41	Post-Resistance	CHSY3	337876	37	5	129520694	129520694	Missense_Mutation	SNP	A	G	6	64	c.1859A>G	c.(1858-1860)AAA>AGA	p.K620R
Pat_41	Post-Resistance	CHSY3	337876	37	5	129520885	129520885	Missense_Mutation	SNP	G	A	4	46	c.2050G>A	c.(2050-2052)GCA>ACA	p.A684T
Pat_41	Post-Resistance	RAPGEF6	51735	37	5	130769267	130769267	Missense_Mutation	SNP	C	T	30	161	c.3830G>A	c.(3829-3831)AGC>AAC	p.S1277N
Pat_41	Post-Resistance	FNIP1	96459	37	5	131046307	131046307	Missense_Mutation	SNP	G	A	7	71	c.670C>T	c.(670-672)CCG>TCG	p.P224S
Pat_41	Post-Resistance	IL3	3562	37	5	131398222	131398222	Missense_Mutation	SNP	C	A	35	444	c.298C>A	c.(298-300)CTC>ATC	p.L100I
Pat_41	Post-Resistance	SLC22A5	6584	37	5	131722845	131722845	Splice_Site	SNP	T	C	38	629	c.951_splice	c.e5+2	p.E317_splice
Pat_41	Post-Resistance	SLC22A5	6584	37	5	131724664	131724664	Missense_Mutation	SNP	C	T	10	202	c.1003C>T	c.(1003-1005)CTT>TTT	p.L335F

Pat_41	Post-Resistance	C5orf56	441108	37	5	131796323	131796323	Missense_Mutation	SNP	C	T	27	261	c.158C>T	c.(157-159)TCC>TTC	p.S53F
Pat_41	Post-Resistance	IRF1	3659	37	5	131821384	131821384	Missense_Mutation	SNP	C	T	16	172	c.692G>A	c.(691-693)GGG>GAG	p.G231E
Pat_41	Post-Resistance	IL4	3565	37	5	132009806	132009806	Missense_Mutation	SNP	G	A	13	428	c.64G>A	c.(64-66)GTC>ATC	p.V22I
Pat_41	Post-Resistance	8-Sep	23176	37	5	132099397	132099397	Splice_Site	SNP	C	T	40	301	c.534_splice	c.e4+1	p.K178_splice
Pat_41	Post-Resistance	AFF4	27125	37	5	132232233	132232233	Missense_Mutation	SNP	C	T	16	80	c.2089G>A	c.(2089-2091)GAA>AAA	p.E697K
Pat_41	Post-Resistance	FSTL4	23105	37	5	132560976	132560976	Missense_Mutation	SNP	G	A	18	279	c.1178C>T	c.(1177-1179)GCC>GTC	p.A393V
Pat_41	Post-Resistance	FSTL4	23105	37	5	132652206	132652206	Missense_Mutation	SNP	A	C	23	48	c.548T>G	c.(547-549)TTC>TGC	p.F183C
Pat_41	Post-Resistance	CDKL3	51265	37	5	133634380	133634380	Missense_Mutation	SNP	C	T	16	156	c.1741G>A	c.(1741-1743)GGG>AGG	p.G581R
Pat_41	Post-Resistance	PHF15	23338	37	5	133895530	133895530	Missense_Mutation	SNP	C	T	11	73	c.322C>T	c.(322-324)CCA>TCA	p.P108S
Pat_41	Post-Resistance	SEC24A	10802	37	5	134059317	134059317	Missense_Mutation	SNP	C	T	36	223	c.3124C>T	c.(3124-3126)CTT>TTT	p.L1042F
Pat_41	Post-Resistance	CAMLG	819	37	5	134086557	134086557	Missense_Mutation	SNP	G	A	8	159	c.808G>A	c.(808-810)GTC>ATC	p.V270I
Pat_41	Post-Resistance	DDX46	9879	37	5	134131783	134131783	Missense_Mutation	SNP	G	A	24	109	c.1897G>A	c.(1897-1899)GAT>AAT	p.D633N
Pat_41	Post-Resistance	PITX1	5307	37	5	134366967	134366967	Missense_Mutation	SNP	C	T	4	44	c.401G>A	c.(400-402)CGG>CAG	p.R134Q
Pat_41	Post-Resistance	NEUROG1	4762	37	5	134870695	134870695	Missense_Mutation	SNP	G	A	6	55	c.686C>T	c.(685-687)ACA>ATA	p.T229I
Pat_41	Post-Resistance	LOC153328	153328	37	5	135188482	135188482	Missense_Mutation	SNP	G	T	3	30	c.393G>T	c.(391-393)TTG>TTT	p.L131F
Pat_41	Post-Resistance	PKD2L2	27039	37	5	137228247	137228247	Missense_Mutation	SNP	C	T	17	218	c.212C>T	c.(211-213)CCT>CTT	p.P71L
Pat_41	Post-Resistance	BRD8	10902	37	5	137500585	137500585	Missense_Mutation	SNP	G	A	9	114	c.1549C>T	c.(1549-1551)CCA>TCA	p.P517S
Pat_41	Post-Resistance	KIF20A	10112	37	5	137518302	137518302	Missense_Mutation	SNP	C	T	8	85	c.542C>T	c.(541-543)CCC>CTC	p.P181L
Pat_41	Post-Resistance	CDC23	8697	37	5	137528045	137528045	Missense_Mutation	SNP	C	T	6	144	c.1199G>A	c.(1198-1200)AGA>AAA	p.R400K
Pat_41	Post-Resistance	CDC23	8697	37	5	137528052	137528052	Missense_Mutation	SNP	C	T	5	148	c.1192G>A	c.(1192-1194)GAC>AAC	p.D398N
Pat_41	Post-Resistance	FAM53C	51307	37	5	137681153	137681153	Missense_Mutation	SNP	C	T	10	166	c.776C>T	c.(775-777)CCC>CTC	p.P259L
Pat_41	Post-Resistance	REEP2	51308	37	5	137781166	137781166	Missense_Mutation	SNP	C	T	7	128	c.569C>T	c.(568-570)CCT>CTT	p.P190L
Pat_41	Post-Resistance	CTNNA1	1495	37	5	138260240	138260240	Missense_Mutation	SNP	C	T	12	91	c.1588C>T	c.(1588-1590)CTC>TTC	p.L530F
Pat_41	Post-Resistance	SIL1	64374	37	5	138386626	138386626	Splice_Site	SNP	C	T	19	108	c.353_splice	c.e3+1	p.R118_splice
Pat_41	Post-Resistance	TMEM173	340061	37	5	138858040	138858040	Missense_Mutation	SNP	C	T	67	473	c.574G>A	c.(574-576)GGT>AGT	p.G192S
Pat_41	Post-Resistance	NKHD1-EIF4EBP	404734	37	5	139864709	139864709	Missense_Mutation	SNP	C	T	10	180	c.1874C>T	c.(1873-1875)GCC>GTC	p.A625V
Pat_41	Post-Resistance	NKHD1-EIF4EBP	404734	37	5	139909283	139909283	Missense_Mutation	SNP	G	A	21	273	c.6752G>A	c.(6751-6753)GGT>GAT	p.G2251D
Pat_41	Post-Resistance	APBB3	10307	37	5	139940050	139940050	Missense_Mutation	SNP	G	A	4	98	c.1087C>T	c.(1087-1089)CCT>TCT	p.P363S
Pat_41	Post-Resistance	APBB3	10307	37	5	139940065	139940065	Missense_Mutation	SNP	G	A	4	68	c.1072C>T	c.(1072-1074)CCA>TCA	p.P358S
Pat_41	Post-Resistance	IK	3550	37	5	140037215	140037215	Missense_Mutation	SNP	C	T	30	159	c.878C>T	c.(877-879)ACC>ATC	p.T293I
Pat_41	Post-Resistance	WDR55	54853	37	5	140044597	140044597	Missense_Mutation	SNP	G	A	5	40	c.100G>A	c.(100-102)GAC>AAC	p.D34N
Pat_41	Post-Resistance	DND1	373863	37	5	140050913	140050913	Missense_Mutation	SNP	C	T	18	154	c.1027G>A	c.(1027-1029)GCT>ACT	p.A343T
Pat_41	Post-Resistance	HARS	3035	37	5	140056370	140056370	Missense_Mutation	SNP	C	T	5	218	c.1063G>A	c.(1063-1065)GGC>AGC	p.G355S
Pat_41	Post-Resistance	HARS2	23438	37	5	140076166	140076166	Missense_Mutation	SNP	G	A	5	141	c.793G>A	c.(793-795)GCT>ACT	p.A265T
Pat_41	Post-Resistance	PCDHA12	56137	37	5	140256900	140256900	Missense_Mutation	SNP	G	A	8	212	c.1843G>A	c.(1843-1845)GCG>ACG	p.A615T
Pat_41	Post-Resistance	PCDHAC2	56134	37	5	140362082	140362082	Missense_Mutation	SNP	G	C	70	74	c.2647G>C	c.(2647-2649)GGC>CGC	p.G883R
Pat_41	Post-Resistance	PCDHB4	56131	37	5	140502320	140502320	Missense_Mutation	SNP	G	A	19	136	c.740G>A	c.(739-741)GGG>GAG	p.G247E
Pat_41	Post-Resistance	PCDHB7	56129	37	5	140553110	140553110	Missense_Mutation	SNP	G	A	9	70	c.694G>A	c.(694-696)GTT>ATT	p.V232I
Pat_41	Post-Resistance	PCDHB7	56129	37	5	140553204	140553204	Missense_Mutation	SNP	C	T	17	75	c.788C>T	c.(787-789)TCC>TTC	p.S263F
Pat_41	Post-Resistance	PCDHB8	56128	37	5	140558060	140558060	Missense_Mutation	SNP	C	T	11	190	c.445C>T	c.(445-447)CCT>TCT	p.P149S
Pat_41	Post-Resistance	PCDHB9	56127	37	5	140568333	140568333	Missense_Mutation	SNP	G	A	18	395	c.1442G>A	c.(1441-1443)GGC>GAC	p.G481D
Pat_41	Post-Resistance	PCDHB12	56124	37	5	140589471	140589471	Missense_Mutation	SNP	C	T	10	62	c.992C>T	c.(991-993)TCT>TTT	p.S331F
Pat_41	Post-Resistance	SLC25A2	83884	37	5	140682748	140682748	Missense_Mutation	SNP	G	A	8	130	c.685C>T	c.(685-687)CCA>TCA	p.P229S
Pat_41	Post-Resistance	PCDHGA1	56114	37	5	140711560	140711560	Missense_Mutation	SNP	C	T	11	100	c.1309C>T	c.(1309-1311)CAC>TAC	p.H437Y
Pat_41	Post-Resistance	PCDHGA2	56113	37	5	140720640	140720640	Missense_Mutation	SNP	C	T	49	265	c.2102C>T	c.(2101-2103)TCC>TTC	p.S701F
Pat_41	Post-Resistance	PCDHGA3	56112	37	5	140724288	140724288	Missense_Mutation	SNP	G	A	12	122	c.688G>A	c.(688-690)GTG>ATG	p.V230M
Pat_41	Post-Resistance	PCDHGA3	56112	37	5	140725009	140725009	Missense_Mutation	SNP	C	T	20	159	c.1409C>T	c.(1408-1410)TCC>TTC	p.S470F

Pat_41	Post-Resistance	PCDHGB2	56103	37	5	140740664	140740664	Missense_Mutation	SNP	C	T	6	47	c.962C>T	c.(961-963)GCA>GTA	p.A321V
Pat_41	Post-Resistance	PCDHGB4	8641	37	5	140768607	140768607	Missense_Mutation	SNP	G	A	5	95	c.1156G>A	c.(1156-1158)GGT>AGT	p.G386S
Pat_41	Post-Resistance	PCDHGA10	56106	37	5	140794520	140794520	Missense_Mutation	SNP	C	T	46	252	c.1778C>T	c.(1777-1779)ACC>ATC	p.T593I
Pat_41	Post-Resistance	PCDHGB7	56099	37	5	140799446	140799446	Missense_Mutation	SNP	G	A	23	134	c.2020G>A	c.(2020-2022)GAT>AAT	p.D674N
Pat_41	Post-Resistance	PCDHGB8P	56120	37	5	140807703	140807703	Missense_Mutation	SNP	G	A	5	66	c.1492G>A	c.(1492-1494)GGG>AGG	p.G498R
Pat_41	Post-Resistance	PCDHGC4	56098	37	5	140865107	140865107	Missense_Mutation	SNP	A	G	15	221	c.367A>G	c.(367-369)ATC>GTC	p.I123V
Pat_41	Post-Resistance	PCDHGC5	56097	37	5	140869495	140869495	Missense_Mutation	SNP	G	A	26	225	c.688G>A	c.(688-690)GTC>ATC	p.V230I
Pat_41	Post-Resistance	PCDH1	5097	37	5	141244410	141244410	Missense_Mutation	SNP	C	T	50	258	c.1486G>A	c.(1486-1488)GTG>ATG	p.V496M
Pat_41	Post-Resistance	PCDH12	51294	37	5	141335744	141335744	Missense_Mutation	SNP	G	A	11	119	c.1673C>T	c.(1672-1674)GCC>GTC	p.A558V
Pat_41	Post-Resistance	PCDH12	51294	37	5	141335892	141335892	Missense_Mutation	SNP	C	T	19	106	c.1525G>A	c.(1525-1527)GCT>ACT	p.A509T
Pat_41	Post-Resistance	PCDH12	51294	37	5	141336072	141336072	Nonsense_Mutation	SNP	G	A	9	219	c.1345C>T	c.(1345-1347)CAG>TAG	p.Q449*
Pat_41	Post-Resistance	GNPDA1	10007	37	5	141385892	141385892	Splice_Site	SNP	C	T	14	78	c.227_splice	c.e3-1	p.G76_splice
Pat_41	Post-Resistance	NR3C1	2908	37	5	142779602	142779602	Missense_Mutation	SNP	G	A	20	342	c.803C>T	c.(802-804)CCC>CTC	p.P268L
Pat_41	Post-Resistance	YIPF5	81555	37	5	143545124	143545124	Missense_Mutation	SNP	G	A	55	339	c.155C>T	c.(154-156)CCT>CTT	p.P52L
Pat_41	Post-Resistance	KCTD16	57528	37	5	143853291	143853291	Missense_Mutation	SNP	G	A	14	162	c.901G>A	c.(901-903)GGG>AGG	p.G301R
Pat_41	Post-Resistance	LARS	51520	37	5	145512537	145512537	Missense_Mutation	SNP	C	T	16	148	c.2320G>A	c.(2320-2322)GTG>ATG	p.V774M
Pat_41	Post-Resistance	LARS	51520	37	5	145522435	145522435	Missense_Mutation	SNP	C	T	4	61	c.2090G>A	c.(2089-2091)AGT>AAT	p.S697N
Pat_41	Post-Resistance	LARS	51520	37	5	145547779	145547779	Missense_Mutation	SNP	G	A	18	103	c.344C>T	c.(343-345)CCT>CTT	p.P115L
Pat_41	Post-Resistance	TCERG1	10915	37	5	145849152	145849152	Missense_Mutation	SNP	C	T	48	657	c.1244C>T	c.(1243-1245)CCC>CTC	p.P415L
Pat_41	Post-Resistance	GPR151	134391	37	5	145894924	145894924	Missense_Mutation	SNP	C	T	7	122	c.753G>A	c.(751-753)ATG>ATA	p.M251I
Pat_41	Post-Resistance	SH3TC2	79628	37	5	148421162	148421162	Missense_Mutation	SNP	G	A	16	176	c.548C>T	c.(547-549)GCC>GTC	p.A183V
Pat_41	Post-Resistance	ABLIM3	22885	37	5	148624443	148624443	Splice_Site	SNP	G	A	21	234	c.1352_splice	c.e16-1	p.G451_splice
Pat_41	Post-Resistance	CSNK1A1	1452	37	5	148929726	148929726	Missense_Mutation	SNP	C	T	19	274	c.142G>A	c.(142-144)GAA>AAA	p.E48K
Pat_41	Post-Resistance	PPARGC1B	133522	37	5	149206399	149206399	Missense_Mutation	SNP	C	T	14	167	c.416C>T	c.(415-417)GCC>GTC	p.A139V
Pat_41	Post-Resistance	PPARGC1B	133522	37	5	149212247	149212247	Missense_Mutation	SNP	C	T	28	440	c.611C>T	c.(610-612)CCC>CTC	p.P204L
Pat_41	Post-Resistance	PPARGC1B	133522	37	5	149216308	149216308	Missense_Mutation	SNP	C	T	13	293	c.2290C>T	c.(2290-2292)CTC>TTC	p.L764F
Pat_41	Post-Resistance	CSF1R	1436	37	5	149433666	149433666	Missense_Mutation	SNP	G	A	26	102	c.2885C>T	c.(2884-2886)CCC>CTC	p.P962L
Pat_41	Post-Resistance	CSF1R	1436	37	5	149449526	149449526	Missense_Mutation	SNP	C	T	5	123	c.1420G>A	c.(1420-1422)GTT>ATT	p.V474I
Pat_41	Post-Resistance	PDGFRB	5159	37	5	149515324	149515324	Missense_Mutation	SNP	G	A	5	39	c.158C>T	c.(157-159)ACC>ATC	p.T53I
Pat_41	Post-Resistance	CAMK2A	815	37	5	149602774	149602774	Missense_Mutation	SNP	G	A	8	68	c.1211C>T	c.(1210-1212)TCC>TTC	p.S404F
Pat_41	Post-Resistance	ARSI	340075	37	5	149677591	149677591	Missense_Mutation	SNP	C	T	7	122	c.896G>A	c.(895-897)GGT>GAT	p.G299D
Pat_41	Post-Resistance	TCOF1	6949	37	5	149755468	149755468	Missense_Mutation	SNP	C	T	4	39	c.1889C>T	c.(1888-1890)GCT>GTT	p.A630V
Pat_41	Post-Resistance	TCOF1	6949	37	5	149758876	149758876	Missense_Mutation	SNP	G	A	12	110	c.2563G>A	c.(2563-2565)GCT>ACT	p.A855T
Pat_41	Post-Resistance	RBM22	55696	37	5	150075153	150075153	Missense_Mutation	SNP	G	A	16	173	c.661C>T	c.(661-663)CCT>TCT	p.P221S
Pat_41	Post-Resistance	RBM22	55696	37	5	150075165	150075165	Missense_Mutation	SNP	C	T	17	134	c.649G>A	c.(649-651)GCT>ACT	p.A217T
Pat_41	Post-Resistance	GPX3	2878	37	5	150406470	150406470	Missense_Mutation	SNP	C	T	23	135	c.251C>T	c.(250-252)GCA>GTA	p.A84V
Pat_41	Post-Resistance	ANXA6	309	37	5	150496699	150496699	Missense_Mutation	SNP	C	T	9	71	c.1561G>A	c.(1561-1563)GAA>AAA	p.E521K
Pat_41	Post-Resistance	ANXA6	309	37	5	150516883	150516883	Splice_Site	SNP	C	T	10	35	c.319_splice	c.e6-1	p.G107_splice
Pat_41	Post-Resistance	FAT2	2196	37	5	150886780	150886780	Missense_Mutation	SNP	G	A	22	208	c.12452C>T	c.(12451-12453)GCT>GTT	p.A4151V
Pat_41	Post-Resistance	FAT2	2196	37	5	150900978	150900978	Missense_Mutation	SNP	G	A	12	157	c.11176C>T	c.(11176-11178)CCC>TCC	p.P3726S
Pat_41	Post-Resistance	FAT2	2196	37	5	150923484	150923484	Nonsense_Mutation	SNP	G	A	3	40	c.7204C>T	c.(7204-7206)CAG>TAG	p.Q2402*
Pat_41	Post-Resistance	FAT2	2196	37	5	150947235	150947235	Missense_Mutation	SNP	G	A	7	91	c.1258C>T	c.(1258-1260)CTC>TTC	p.L420F
Pat_41	Post-Resistance	G3BP1	10146	37	5	151166204	151166204	Missense_Mutation	SNP	C	T	59	374	c.23C>T	c.(22-24)CCC>CTC	p.P8L
Pat_41	Post-Resistance	GRIA1	2890	37	5	153078544	153078544	Missense_Mutation	SNP	C	T	9	112	c.1363C>T	c.(1363-1365)CGT>TGT	p.R455C
Pat_41	Post-Resistance	FAM114A2	10827	37	5	153382525	153382525	Missense_Mutation	SNP	C	T	10	129	c.998G>A	c.(997-999)AGA>AAA	p.R333K
Pat_41	Post-Resistance	FAM114A2	10827	37	5	153409129	153409129	Missense_Mutation	SNP	C	T	9	42	c.415G>A	c.(415-417)GCC>ACC	p.A139T
Pat_41	Post-Resistance	GALNT10	55568	37	5	153789203	153789203	Nonsense_Mutation	SNP	C	T	11	121	c.1267C>T	c.(1267-1269)CAG>TAG	p.Q423*

Pat_41	Post-Resistance	LARP1	23367	37	5	154183836	154183836	Missense_Mutation	SNP	C	T	7	364	c.2515C>T	c.(2515-2517)CGT>TGT	p.R839C
Pat_41	Post-Resistance	GEMIN5	25929	37	5	154282236	154282236	Missense_Mutation	SNP	C	T	42	176	c.2729G>A	c.(2728-2730)GGA>GAA	p.G910E
Pat_41	Post-Resistance	KIF4B	285643	37	5	154393943	154393943	Missense_Mutation	SNP	G	A	17	363	c.524G>A	c.(523-525)GGA>GAA	p.G175E
Pat_41	Post-Resistance	KIF4B	285643	37	5	154396685	154396685	Missense_Mutation	SNP	C	T	10	68	c.3266C>T	c.(3265-3267)TCC>TTC	p.S1089F
Pat_41	Post-Resistance	PPP1R2P3	153743	37	5	156278129	156278129	Missense_Mutation	SNP	G	A	13	153	c.556G>A	c.(556-558)GAA>AAA	p.E186K
Pat_41	Post-Resistance	HAVCR1	26762	37	5	156479456	156479456	Missense_Mutation	SNP	G	A	42	628	c.589C>T	c.(589-591)CCA>TCA	p.P197S
Pat_41	Post-Resistance	CYFIP2	26999	37	5	156760384	156760384	Missense_Mutation	SNP	C	T	38	609	c.2315C>T	c.(2314-2316)TCT>TTT	p.S772F
Pat_41	Post-Resistance	ADAM19	8728	37	5	156991397	156991397	Missense_Mutation	SNP	C	T	4	127	c.235G>A	c.(235-237)GAC>AAC	p.D79N
Pat_41	Post-Resistance	SOX30	11063	37	5	157078471	157078471	Missense_Mutation	SNP	C	T	13	238	c.616G>A	c.(616-618)GCC>ACC	p.A206T
Pat_41	Post-Resistance	RNF145	153830	37	5	158630538	158630538	Missense_Mutation	SNP	C	T	38	223	c.88G>A	c.(88-90)GAT>AAT	p.D30N
Pat_41	Post-Resistance	CCNJL	79616	37	5	159680569	159680569	Missense_Mutation	SNP	C	T	9	76	c.1124G>A	c.(1123-1125)GGC>GAC	p.G375D
Pat_41	Post-Resistance	ATP10B	23120	37	5	159996596	159996596	Missense_Mutation	SNP	G	A	12	200	c.3845C>T	c.(3844-3846)CCC>CTC	p.P1282L
Pat_41	Post-Resistance	GABRG2	2566	37	5	161569169	161569169	Splice_Site	SNP	G	T	26	402	c.770_splice	c.e7-1	p.G257_splice
Pat_41	Post-Resistance	ODZ2	57451	37	5	167420131	167420131	Missense_Mutation	SNP	C	T	14	107	c.1130C>T	c.(1129-1131)GCC>GTC	p.A377V
Pat_41	Post-Resistance	ODZ2	57451	37	5	167645925	167645925	Missense_Mutation	SNP	C	T	18	219	c.5002C>T	c.(5002-5004)CTT>TTT	p.L1668F
Pat_41	Post-Resistance	ODZ2	57451	37	5	167655066	167655066	Missense_Mutation	SNP	C	G	5	64	c.5424C>G	c.(5422-5424)AAC>AAG	p.N1808K
Pat_41	Post-Resistance	WWC1	23286	37	5	167881036	167881036	Missense_Mutation	SNP	G	T	12	89	c.2589G>T	c.(2587-2589)GAG>GAT	p.E863D
Pat_41	Post-Resistance	WWC1	23286	37	5	167882439	167882439	Missense_Mutation	SNP	C	T	19	220	c.2737C>T	c.(2737-2739)CCG>TCG	p.P913S
Pat_41	Post-Resistance	SLIT3	6586	37	5	168127629	168127629	Missense_Mutation	SNP	C	T	7	130	c.2900G>A	c.(2899-2901)GGA>GAA	p.G967E
Pat_41	Post-Resistance	DOCK2	1794	37	5	169502991	169502991	Missense_Mutation	SNP	G	A	12	150	c.4769G>A	c.(4768-4770)AGG>AAG	p.R1590K
Pat_41	Post-Resistance	TLX3	30012	37	5	170737360	170737360	Missense_Mutation	SNP	G	A	3	38	c.628G>A	c.(628-630)GTC>ATC	p.V210I
Pat_41	Post-Resistance	FGF18	8817	37	5	170863256	170863256	Missense_Mutation	SNP	G	A	6	29	c.229G>A	c.(229-231)GGC>AGC	p.G77S
Pat_41	Post-Resistance	STK10	6793	37	5	171554401	171554401	Missense_Mutation	SNP	C	T	21	84	c.346G>A	c.(346-348)GGA>AGA	p.G116R
Pat_41	Post-Resistance	SH3PXD2B	285590	37	5	171773171	171773171	Missense_Mutation	SNP	C	T	16	251	c.1157G>A	c.(1156-1158)GGC>GAC	p.G386D
Pat_41	Post-Resistance	SH3PXD2B	285590	37	5	171833335	171833335	Missense_Mutation	SNP	G	A	145	199	c.178C>T	c.(178-180)CCC>TCC	p.P60S
Pat_41	Post-Resistance	C5orf41	153222	37	5	172535810	172535810	Missense_Mutation	SNP	G	A	14	178	c.1406G>A	c.(1405-1407)GGC>GAC	p.G469D
Pat_41	Post-Resistance	CPEB4	80315	37	5	173317682	173317682	Missense_Mutation	SNP	G	A	9	184	c.946G>A	c.(946-948)GAT>AAT	p.D316N
Pat_41	Post-Resistance	KIAA1191	57179	37	5	175774742	175774742	Missense_Mutation	SNP	G	A	5	132	c.779C>T	c.(778-780)GCC>GTC	p.A260V
Pat_41	Post-Resistance	HIGD2A	192286	37	5	175816374	175816374	Missense_Mutation	SNP	C	T	18	260	c.197C>T	c.(196-198)TCC>TTC	p.S66F
Pat_41	Post-Resistance	GPRIN1	114787	37	5	176026667	176026667	Missense_Mutation	SNP	G	A	23	80	c.169C>T	c.(169-171)CCC>TCC	p.P57S
Pat_41	Post-Resistance	HK3	3101	37	5	176317706	176317706	Missense_Mutation	SNP	C	T	63	263	c.560G>A	c.(559-561)GGT>GAT	p.G187D
Pat_41	Post-Resistance	UIMC1	51720	37	5	176332440	176332440	Missense_Mutation	SNP	G	A	12	138	c.2003C>T	c.(2002-2004)TCT>TTT	p.S668F
Pat_41	Post-Resistance	NSD1	64324	37	5	176639013	176639013	Missense_Mutation	SNP	G	A	5	157	c.3613G>A	c.(3613-3615)GAG>AAG	p.E1205K
Pat_41	Post-Resistance	NSD1	64324	37	5	176721018	176721018	Missense_Mutation	SNP	G	A	20	63	c.6649G>A	c.(6649-6651)GAG>AAG	p.E2217K
Pat_41	Post-Resistance	FAM153A	285596	37	5	177164096	177164096	Missense_Mutation	SNP	C	T	7	89	c.349G>A	c.(349-351)GAG>AAG	p.E117K
Pat_41	Post-Resistance	N4BP3	23138	37	5	177546868	177546868	Missense_Mutation	SNP	G	A	32	183	c.284G>A	c.(283-285)GGT>GAT	p.G95D
Pat_41	Post-Resistance	C5orf45	51149	37	5	179268973	179268973	Missense_Mutation	SNP	C	T	15	333	c.383G>A	c.(382-384)AGC>AAC	p.S128N
Pat_41	Post-Resistance	BTNL8	79908	37	5	180338356	180338356	Missense_Mutation	SNP	C	T	17	638	c.415C>T	c.(415-417)CTC>TTC	p.L139F
Pat_41	Post-Resistance	BTNL9	153579	37	5	180483007	180483007	Missense_Mutation	SNP	G	A	13	256	c.947G>A	c.(946-948)GGC>GAC	p.G316D
Pat_41	Post-Resistance	TRIM41	90933	37	5	180661740	180661740	Missense_Mutation	SNP	C	T	8	94	c.1858C>T	c.(1858-1860)CTC>TTC	p.L620F
Pat_41	Post-Resistance	TRIM52	84851	37	5	180687240	180687240	Missense_Mutation	SNP	C	T	9	158	c.575G>A	c.(574-576)CGT>CAT	p.R192H
Pat_41	Post-Resistance	TRIM52	84851	37	5	180687601	180687601	Missense_Mutation	SNP	C	T	20	143	c.214G>A	c.(214-216)GTG>ATG	p.V72M
Pat_41	Post-Resistance	EXOC2	55770	37	6	553885	553885	Missense_Mutation	SNP	C	T	29	174	c.2090G>A	c.(2089-2091)GGA>GAA	p.G697E
Pat_41	Post-Resistance	EXOC2	55770	37	6	592521	592521	Nonsense_Mutation	SNP	C	T	8	173	c.1140G>A	c.(1138-1140)TGG>TGA	p.W380*
Pat_41	Post-Resistance	EXOC2	55770	37	6	637749	637749	Missense_Mutation	SNP	C	T	18	312	c.70G>A	c.(70-72)GTC>ATC	p.V24I
Pat_41	Post-Resistance	FOXF2	2295	37	6	1390673	1390673	Missense_Mutation	SNP	G	A	22	121	c.491G>A	c.(490-492)GGC>GAC	p.G164D
Pat_41	Post-Resistance	MYLK4	340156	37	6	2679604	2679604	Missense_Mutation	SNP	G	A	39	601	c.797C>T	c.(796-798)ACC>ATC	p.T266I

Pat_41	Post-Resistance	SERPINB1	1992	37	6	2836113	2836113	Missense_Mutation	SNP	C	T	4	116	c.712G>A	c.(712-714)GAC>AAC	p.D238N
Pat_41	Post-Resistance	SERPINB1	1992	37	6	2836377	2836377	Missense_Mutation	SNP	C	T	9	461	c.532G>A	c.(532-534)GAA>AAA	p.E178K
Pat_41	Post-Resistance	SERPINB9	5272	37	6	2892117	2892117	Missense_Mutation	SNP	C	T	7	119	c.673G>A	c.(673-675)GAG>AAG	p.E225K
Pat_41	Post-Resistance	SERPINB6	5269	37	6	2948668	2948668	Missense_Mutation	SNP	G	A	13	68	c.995C>T	c.(994-996)GCC>GTC	p.A332V
Pat_41	Post-Resistance	SLC22A23	63027	37	6	3273552	3273552	Missense_Mutation	SNP	G	A	9	186	c.1798C>T	c.(1798-1800)CAC>TAC	p.H600Y
Pat_41	Post-Resistance	C6orf146	222826	37	6	4074813	4074813	Missense_Mutation	SNP	C	T	8	176	c.143G>A	c.(142-144)GGT>GAT	p.G48D
Pat_41	Post-Resistance	LY86	9450	37	6	6654829	6654829	Missense_Mutation	SNP	C	T	24	127	c.458C>T	c.(457-459)GCC>GTC	p.A153V
Pat_41	Post-Resistance	RIOK1	83732	37	6	7413164	7413164	Missense_Mutation	SNP	G	A	6	132	c.1432G>A	c.(1432-1434)GGA>AGA	p.G478R
Pat_41	Post-Resistance	DSP	1832	37	6	7585744	7585744	Missense_Mutation	SNP	C	T	13	59	c.8249C>T	c.(8248-8250)GCC>GTC	p.A2750V
Pat_41	Post-Resistance	DSP	1832	37	6	7586038	7586038	Missense_Mutation	SNP	G	A	13	131	c.8543G>A	c.(8542-8544)GGA>GAA	p.G2848E
Pat_41	Post-Resistance	SNRNP48	154007	37	6	7606305	7606305	Missense_Mutation	SNP	C	T	12	345	c.848C>T	c.(847-849)TCT>TTT	p.S283F
Pat_41	Post-Resistance	HIVEP1	3096	37	6	12122729	12122729	Missense_Mutation	SNP	G	A	8	202	c.2701G>A	c.(2701-2703)GCC>ACC	p.A901T
Pat_41	Post-Resistance	HIVEP1	3096	37	6	12131064	12131064	Missense_Mutation	SNP	G	A	12	193	c.6274G>A	c.(6274-6276)GAA>AAA	p.E2092K
Pat_41	Post-Resistance	HIVEP1	3096	37	6	12162014	12162014	Missense_Mutation	SNP	C	T	23	196	c.6830C>T	c.(6829-6831)GCC>GTC	p.A2277V
Pat_41	Post-Resistance	TBC1D7	51256	37	6	13321219	13321219	Missense_Mutation	SNP	G	A	41	674	c.302C>T	c.(301-303)GCC>GTC	p.A101V
Pat_41	Post-Resistance	C6orf114	85411	37	6	13470469	13470469	Missense_Mutation	SNP	G	A	13	85	c.44C>T	c.(43-45)GCC>GTC	p.A15V
Pat_41	Post-Resistance	RNF182	221687	37	6	13977756	13977756	Missense_Mutation	SNP	G	A	4	82	c.406G>A	c.(406-408)GTG>ATG	p.V136M
Pat_41	Post-Resistance	JARID2	3720	37	6	15487685	15487685	Missense_Mutation	SNP	C	T	26	171	c.818C>T	c.(817-819)GCC>GTC	p.A273V
Pat_41	Post-Resistance	DTNBP1	84062	37	6	15533578	15533578	Missense_Mutation	SNP	G	A	13	298	c.560C>T	c.(559-561)ACC>ATC	p.T187I
Pat_41	Post-Resistance	ATXN1	6310	37	6	16307041	16307041	Missense_Mutation	SNP	C	T	14	208	c.1967G>A	c.(1966-1968)GGC>GAC	p.G656D
Pat_41	Post-Resistance	NUP153	9972	37	6	17626279	17626279	Missense_Mutation	SNP	G	A	6	120	c.3661C>T	c.(3661-3663)CCA>TCA	p.P1221S
Pat_41	Post-Resistance	NUP153	9972	37	6	17629443	17629443	Missense_Mutation	SNP	G	A	5	50	c.2987C>T	c.(2986-2988)ACT>ATT	p.T996I
Pat_41	Post-Resistance	KDM1B	221656	37	6	18197453	18197453	Missense_Mutation	SNP	G	A	4	38	c.526G>A	c.(526-528)GAC>AAC	p.D176N
Pat_41	Post-Resistance	CDKAL1	54901	37	6	20546595	20546595	Missense_Mutation	SNP	C	T	20	320	c.14C>T	c.(13-15)TCC>TTC	p.S5F
Pat_41	Post-Resistance	KIAA0319	9856	37	6	24596114	24596114	Missense_Mutation	SNP	C	T	47	509	c.788G>A	c.(787-789)AGC>AAC	p.S263N
Pat_41	Post-Resistance	TRIM38	10475	37	6	25967132	25967132	Missense_Mutation	SNP	C	T	15	293	c.382C>T	c.(382-384)CTT>TTT	p.L128F
Pat_41	Post-Resistance	HIST1H1A	3024	37	6	26017440	26017440	Missense_Mutation	SNP	G	A	9	186	c.521C>T	c.(520-522)ACT>ATT	p.T174I
Pat_41	Post-Resistance	HIST1H3D	8351	37	6	26197156	26197156	Missense_Mutation	SNP	G	A	30	411	c.323C>T	c.(322-324)ACC>ATC	p.T108I
Pat_41	Post-Resistance	PRSS16	10279	37	6	27220684	27220684	Missense_Mutation	SNP	G	A	32	388	c.1106G>A	c.(1105-1107)GGT>GAT	p.G369D
Pat_41	Post-Resistance	ZNF391	346157	37	6	27369215	27369215	Missense_Mutation	SNP	A	G	19	106	c.1066A>G	c.(1066-1068)ACT>GCT	p.T356A
Pat_41	Post-Resistance	HIST1H2AK	8330	37	6	27806095	27806095	Missense_Mutation	SNP	C	T	13	229	c.23G>A	c.(22-24)GGC>GAC	p.G8D
Pat_41	Post-Resistance	HIST1H1B	3009	37	6	27834956	27834956	Missense_Mutation	SNP	C	T	23	109	c.352G>A	c.(352-354)GAA>AAA	p.E118K
Pat_41	Post-Resistance	PGBD1	84547	37	6	28251930	28251930	Missense_Mutation	SNP	G	A	25	419	c.340G>A	c.(340-342)GAG>AAG	p.E114K
Pat_41	Post-Resistance	PGBD1	84547	37	6	28269811	28269811	Missense_Mutation	SNP	C	T	12	146	c.2180C>T	c.(2179-2181)TCC>TTC	p.S727F
Pat_41	Post-Resistance	ZNF323	64288	37	6	28297458	28297458	Missense_Mutation	SNP	C	T	42	235	c.3G>A	c.(1-3)ATG>ATA	p.M1I
Pat_41	Post-Resistance	ZKSCAN3	80317	37	6	28333227	28333227	Missense_Mutation	SNP	G	A	5	149	c.782G>A	c.(781-783)AGG>AAG	p.R261K
Pat_41	Post-Resistance	ZNF311	282890	37	6	28963251	28963251	Missense_Mutation	SNP	C	T	13	106	c.1528G>A	c.(1528-1530)GAT>AAT	p.D510N
Pat_41	Post-Resistance	OR2H1	26716	37	6	29430081	29430081	Missense_Mutation	SNP	G	A	30	390	c.535G>A	c.(535-537)GTC>ATC	p.V179I
Pat_41	Post-Resistance	GABBR1	2550	37	6	29577084	29577084	Missense_Mutation	SNP	G	A	24	61	c.1781C>T	c.(1780-1782)TCC>TTC	p.S594F
Pat_41	Post-Resistance	GABBR1	2550	37	6	29588918	29588918	Missense_Mutation	SNP	A	G	13	191	c.1283T>C	c.(1282-1284)GTC>GCC	p.V428A
Pat_41	Post-Resistance	GABBR1	2550	37	6	29595301	29595301	Missense_Mutation	SNP	G	A	4	57	c.619C>T	c.(619-621)CCG>TCG	p.P207S
Pat_41	Post-Resistance	HLA-G	3135	37	6	29795664	29795664	Missense_Mutation	SNP	G	A	10	87	c.43G>A	c.(43-45)GGG>AGG	p.G15R
Pat_41	Post-Resistance	HLA-H	3136	37	6	29856286	29856286	Missense_Mutation	SNP	C	T	15	124	c.281C>T	c.(280-282)CCC>CTC	p.P94L
Pat_41	Post-Resistance	TRIM10	10107	37	6	30122087	30122087	Missense_Mutation	SNP	C	T	5	47	c.1105G>A	c.(1105-1107)GTG>ATG	p.V369M
Pat_41	Post-Resistance	TRIM15	89870	37	6	30131822	30131822	Missense_Mutation	SNP	G	A	12	111	c.361G>A	c.(361-363)GAG>AAG	p.E121K
Pat_41	Post-Resistance	TRIM39	56658	37	6	30307703	30307703	Missense_Mutation	SNP	G	A	9	99	c.799G>A	c.(799-801)GAA>AAA	p.E267K
Pat_41	Post-Resistance	TRIM39	56658	37	6	30308331	30308331	Missense_Mutation	SNP	G	A	14	239	c.943G>A	c.(943-945)GAA>AAA	p.E315K

Pat_41	Post-Resistance	TRIM39	56658	37	6	30309749	30309749	Missense_Mutation	SNP	C	T	14	130	c.1270C>T	c.(1270-1272)CCT>TCT	p.P424S
Pat_41	Post-Resistance	C6orf136	221545	37	6	30617539	30617539	Missense_Mutation	SNP	G	A	40	259	c.277G>A	c.(277-279)GAG>AAG	p.E93K
Pat_41	Post-Resistance	DHX16	8449	37	6	30640513	30640513	Missense_Mutation	SNP	G	A	11	117	c.106C>T	c.(106-108)CGC>TGC	p.R36C
Pat_41	Post-Resistance	MDC1	9656	37	6	30672593	30672593	Missense_Mutation	SNP	T	A	14	235	c.4367A>T	c.(4366-4368)CAG>CTG	p.Q1456L
Pat_41	Post-Resistance	MDC1	9656	37	6	30681789	30681789	Missense_Mutation	SNP	G	A	5	90	c.308C>T	c.(307-309)CCT>CTT	p.P103L
Pat_41	Post-Resistance	DDR1	780	37	6	30856724	30856724	Missense_Mutation	SNP	T	C	6	253	c.125T>C	c.(124-126)ATC>ACC	p.I42T
Pat_41	Post-Resistance	DDR1	780	37	6	30860155	30860155	Missense_Mutation	SNP	C	T	5	49	c.935C>T	c.(934-936)GCC>GTC	p.A312V
Pat_41	Post-Resistance	GTF2H4	2968	37	6	30879272	30879272	Missense_Mutation	SNP	G	A	11	264	c.737G>A	c.(736-738)GGC>GAC	p.G246D
Pat_41	Post-Resistance	VARS2	57176	37	6	30892294	30892294	Missense_Mutation	SNP	C	T	4	56	c.2630C>T	c.(2629-2631)GCC>GTC	p.A877V
Pat_41	Post-Resistance	C6orf15	29113	37	6	31079240	31079240	Missense_Mutation	SNP	C	T	9	49	c.896G>A	c.(895-897)GGA>GAA	p.G299E
Pat_41	Post-Resistance	CCHCR1	54535	37	6	31118537	31118537	Missense_Mutation	SNP	C	T	24	298	c.799G>A	c.(799-801)GAA>AAA	p.E267K
Pat_41	Post-Resistance	TCF19	6941	37	6	31129226	31129226	Missense_Mutation	SNP	A	G	9	232	c.241A>G	c.(241-243)ACT>GCT	p.T81A
Pat_41	Post-Resistance	MICB	4277	37	6	31474987	31474987	Missense_Mutation	SNP	G	A	8	81	c.802G>A	c.(802-804)GTG>ATG	p.V268M
Pat_41	Post-Resistance	MICB	4277	37	6	31475045	31475045	Missense_Mutation	SNP	G	A	4	106	c.860G>A	c.(859-861)AGC>AAC	p.S287N
Pat_41	Post-Resistance	LTA	4049	37	6	31540715	31540715	Missense_Mutation	SNP	G	A	6	89	c.110G>A	c.(109-111)GGT>GAT	p.G37D
Pat_41	Post-Resistance	LTA	4049	37	6	31540721	31540721	Missense_Mutation	SNP	G	A	8	116	c.116G>A	c.(115-117)GGC>GAC	p.G39D
Pat_41	Post-Resistance	BAT2	7916	37	6	31596016	31596016	Missense_Mutation	SNP	G	A	10	66	c.1765G>A	c.(1765-1767)GTG>ATG	p.V589M
Pat_41	Post-Resistance	BAT2	7916	37	6	31599025	31599025	Missense_Mutation	SNP	C	T	20	77	c.2575C>T	c.(2575-2577)CCA>TCA	p.P859S
Pat_41	Post-Resistance	BAT3	7917	37	6	31615534	31615534	Missense_Mutation	SNP	C	T	21	319	c.640G>A	c.(640-642)GTA>ATA	p.V214I
Pat_41	Post-Resistance	C6orf47	57827	37	6	31627214	31627214	Missense_Mutation	SNP	C	T	13	177	c.511G>A	c.(511-513)GGC>AGC	p.G171S
Pat_41	Post-Resistance	BAT5	7920	37	6	31668790	31668790	Missense_Mutation	SNP	G	A	7	175	c.272C>T	c.(271-273)TCC>TTC	p.S91F
Pat_41	Post-Resistance	LY6G6F	259215	37	6	31678132	31678132	Missense_Mutation	SNP	C	T	40	540	c.806C>T	c.(805-807)GCC>GTC	p.A269V
Pat_41	Post-Resistance	DDAH2	23564	37	6	31695340	31695340	Missense_Mutation	SNP	C	T	19	403	c.721G>A	c.(721-723)GAT>AAT	p.D241N
Pat_41	Post-Resistance	DDAH2	23564	37	6	31695400	31695400	Missense_Mutation	SNP	G	A	48	208	c.661C>T	c.(661-663)CTC>TTC	p.L221F
Pat_41	Post-Resistance	VARS	7407	37	6	31760581	31760581	Missense_Mutation	SNP	C	T	6	94	c.614G>A	c.(613-615)GGA>GAA	p.G205E
Pat_41	Post-Resistance	HSPA1A	3303	37	6	31785170	31785170	Missense_Mutation	SNP	C	T	5	32	c.1637C>T	c.(1636-1638)GCC>GTC	p.A546V
Pat_41	Post-Resistance	NEU1	4758	37	6	31829962	31829962	Missense_Mutation	SNP	G	A	9	93	c.166C>T	c.(166-168)CCG>TCG	p.P56S
Pat_41	Post-Resistance	SLC44A4	80736	37	6	31832501	31832501	Missense_Mutation	SNP	C	T	9	96	c.1939G>A	c.(1939-1941)GGG>AGG	p.G647R
Pat_41	Post-Resistance	CFB	629	37	6	31917040	31917040	Missense_Mutation	SNP	G	T	9	112	c.1189G>T	c.(1189-1191)GAC>TAC	p.D397Y
Pat_41	Post-Resistance	RDBP	7936	37	6	31922602	31922602	Missense_Mutation	SNP	C	T	41	266	c.472G>A	c.(472-474)GCT>ACT	p.A158T
Pat_41	Post-Resistance	TNXB	7148	37	6	32032682	32032682	Missense_Mutation	SNP	C	T	4	71	c.6757G>A	c.(6757-6759)GAG>AAG	p.E2253K
Pat_41	Post-Resistance	TNXB	7148	37	6	32036433	32036433	Missense_Mutation	SNP	G	A	6	94	c.5954C>T	c.(5953-5955)CCC>CTC	p.P1985L
Pat_41	Post-Resistance	TNXB	7148	37	6	32049975	32049975	Nonsense_Mutation	SNP	G	A	15	16	c.3574C>T	c.(3574-3576)CAG>TAG	p.Q1192*
Pat_41	Post-Resistance	TNXB	7148	37	6	32063792	32063792	Missense_Mutation	SNP	C	T	16	107	c.1838G>A	c.(1837-1839)AGT>AAT	p.S613N
Pat_41	Post-Resistance	GPSM3	63940	37	6	32159259	32159259	Missense_Mutation	SNP	G	A	5	115	c.367C>T	c.(367-369)CGG>TGG	p.R123W
Pat_41	Post-Resistance	TAP2	6891	37	6	32784671	32784671	Missense_Mutation	SNP	C	T	7	180	c.1991G>A	c.(1990-1992)GGA>GAA	p.G664E
Pat_41	Post-Resistance	PSMB8	5696	37	6	32809307	32809307	Splice_Site	SNP	C	T	8	200	c.742_splice	c.e5+1	p.M248_splice
Pat_41	Post-Resistance	PSMB8	5696	37	6	32809940	32809940	Missense_Mutation	SNP	C	T	14	209	c.508G>A	c.(508-510)GGC>AGC	p.G170S
Pat_41	Post-Resistance	HLA-DPA1	3113	37	6	33036530	33036530	Missense_Mutation	SNP	G	A	21	166	c.680C>T	c.(679-681)GCC>GTC	p.A227V
Pat_41	Post-Resistance	COL11A2	1302	37	6	33131493	33131493	Missense_Mutation	SNP	C	T	25	69	c.5173G>A	c.(5173-5175)GGA>AGA	p.G1725R
Pat_41	Post-Resistance	COL11A2	1302	37	6	33144527	33144527	Missense_Mutation	SNP	C	T	12	35	c.2086G>A	c.(2086-2088)GAA>AAA	p.E696K
Pat_41	Post-Resistance	RXRB	6257	37	6	33165539	33165539	Missense_Mutation	SNP	C	T	3	66	c.820G>A	c.(820-822)GCG>ACG	p.A274T
Pat_41	Post-Resistance	RXRB	6257	37	6	33166147	33166147	Missense_Mutation	SNP	G	A	37	290	c.578C>T	c.(577-579)CCC>CTC	p.P193L
Pat_41	Post-Resistance	SLC39A7	7922	37	6	33169260	33169260	Missense_Mutation	SNP	G	A	12	245	c.238G>A	c.(238-240)GAC>AAC	p.D80N
Pat_41	Post-Resistance	VPS52	6293	37	6	33236299	33236299	Missense_Mutation	SNP	C	T	7	168	c.676G>A	c.(676-678)GTG>ATG	p.V226M
Pat_41	Post-Resistance	TAPBP	6892	37	6	33271992	33271992	Missense_Mutation	SNP	G	A	7	106	c.1213C>T	c.(1213-1215)CTT>TTT	p.L405F
Pat_41	Post-Resistance	DAXX	1616	37	6	33288156	33288156	Splice_Site	SNP	C	T	12	129	c.1251_splice	c.e4+1	p.E417_splice

Pat_41	Post-Resistance	DAXX	1616	37	6	33288677	33288677	Missense_Mutation	SNP	G	A	16	137	c.875C>T	c.(874-876)GCT>GTT	p.A292V
Pat_41	Post-Resistance	PHF1	5252	37	6	33381232	33381232	Missense_Mutation	SNP	G	A	6	76	c.485G>A	c.(484-486)GGT>GAT	p.G162D
Pat_41	Post-Resistance	ITPR3	3710	37	6	33643499	33643499	Missense_Mutation	SNP	G	A	5	180	c.3148G>A	c.(3148-3150)GAG>AAG	p.E1050K
Pat_41	Post-Resistance	ITPR3	3710	37	6	33648444	33648444	Missense_Mutation	SNP	G	A	17	215	c.4463G>A	c.(4462-4464)AGC>AAC	p.S1488N
Pat_41	Post-Resistance	ITPR3	3710	37	6	33653298	33653298	Missense_Mutation	SNP	C	T	6	18	c.5470C>T	c.(5470-5472)CCC>TCC	p.P1824S
Pat_41	Post-Resistance	LEMD2	221496	37	6	33756811	33756811	Missense_Mutation	SNP	C	T	11	62	c.83G>A	c.(82-84)CGG>CAG	p.R28Q
Pat_41	Post-Resistance	PACSIN1	29993	37	6	34497237	34497237	Missense_Mutation	SNP	G	A	7	131	c.520G>A	c.(520-522)GAG>AAG	p.E174K
Pat_41	Post-Resistance	UHRF1BP1	54887	37	6	34826973	34826973	Missense_Mutation	SNP	G	A	4	48	c.2840G>A	c.(2839-2841)AGG>AAG	p.R947K
Pat_41	Post-Resistance	UHRF1BP1	54887	37	6	34850779	34850779	Splice_Site	SNP	G	A	4	50	c.4570_splice	c.e22-1	
Pat_41	Post-Resistance	TCP11	6954	37	6	35087097	35087097	Missense_Mutation	SNP	C	T	31	141	c.1226G>A	c.(1225-1227)GGC>GAC	p.G409D
Pat_41	Post-Resistance	TCP11	6954	37	6	35088424	35088424	Splice_Site	SNP	C	T	4	35	c.755_splice	c.e7-1	p.S252_splice
Pat_41	Post-Resistance	SCUBE3	222663	37	6	35209404	35209404	Missense_Mutation	SNP	T	C	11	229	c.1280T>C	c.(1279-1281)CTG>CCG	p.L427P
Pat_41	Post-Resistance	DEF6	50619	37	6	35289140	35289140	Missense_Mutation	SNP	G	A	7	101	c.1849G>A	c.(1849-1851)GCT>ACT	p.A617T
Pat_41	Post-Resistance	FANCE	2178	37	6	35427148	35427148	Missense_Mutation	SNP	C	T	10	246	c.1154C>T	c.(1153-1155)ACT>ATT	p.T385I
Pat_41	Post-Resistance	FKBP5	2289	37	6	35558986	35558986	Missense_Mutation	SNP	C	T	18	103	c.677G>A	c.(676-678)GGA>GAA	p.G226E
Pat_41	Post-Resistance	LHFPL5	222662	37	6	35773572	35773572	Missense_Mutation	SNP	C	T	27	393	c.125C>T	c.(124-126)GCC>GTC	p.A42V
Pat_41	Post-Resistance	SRPK1	6732	37	6	35837616	35837616	Missense_Mutation	SNP	C	T	61	422	c.1054G>A	c.(1054-1056)GCA>ACA	p.A352T
Pat_41	Post-Resistance	SLC26A8	116369	37	6	35980092	35980092	Nonsense_Mutation	SNP	C	T	29	115	c.246G>A	c.(244-246)TGG>TGA	p.W82*
Pat_41	Post-Resistance	MAPK14	1432	37	6	36040661	36040661	Missense_Mutation	SNP	C	T	15	105	c.317C>T	c.(316-318)ACC>ATC	p.T106I
Pat_41	Post-Resistance	MAPK13	5603	37	6	36106190	36106190	Missense_Mutation	SNP	C	T	4	109	c.731C>T	c.(730-732)ACG>ATG	p.T244M
Pat_41	Post-Resistance	BRPF3	27154	37	6	36178288	36178288	Missense_Mutation	SNP	G	A	12	83	c.2162G>A	c.(2161-2163)CGC>CAC	p.R721H
Pat_41	Post-Resistance	BRPF3	27154	37	6	36181732	36181732	Missense_Mutation	SNP	C	T	20	103	c.2558C>T	c.(2557-2559)CCC>CTC	p.P853L
Pat_41	Post-Resistance	PNPLA1	285848	37	6	36270015	36270015	Missense_Mutation	SNP	C	T	28	251	c.1153C>T	c.(1153-1155)CCT>TCT	p.P385S
Pat_41	Post-Resistance	STK38	11329	37	6	36483240	36483240	Missense_Mutation	SNP	C	T	17	156	c.544G>A	c.(544-546)GAC>AAC	p.D182N
Pat_41	Post-Resistance	CDKN1A	1026	37	6	36652012	36652012	Missense_Mutation	SNP	C	T	20	122	c.134C>T	c.(133-135)GCC>GTC	p.A45V
Pat_41	Post-Resistance	PI16	221476	37	6	36931691	36931691	Missense_Mutation	SNP	C	T	5	55	c.1363C>T	c.(1363-1365)CCT>TCT	p.P455S
Pat_41	Post-Resistance	TBC1D22B	55633	37	6	37249996	37249996	Nonsense_Mutation	SNP	C	T	8	217	c.457C>T	c.(457-459)CAA>TAA	p.Q153*
Pat_41	Post-Resistance	FTSJD2	23070	37	6	37443943	37443943	Missense_Mutation	SNP	C	T	27	237	c.2078C>T	c.(2077-2079)CCT>CTT	p.P693L
Pat_41	Post-Resistance	BTBD9	114781	37	6	38142775	38142775	Missense_Mutation	SNP	G	A	6	337	c.1825C>T	c.(1825-1827)CGG>TGG	p.R609W
Pat_41	Post-Resistance	DNAH8	1769	37	6	38879353	38879353	Missense_Mutation	SNP	A	G	3	77	c.9199A>G	c.(9199-9201)ATG>GTG	p.M3067V
Pat_41	Post-Resistance	DNAH8	1769	37	6	38881726	38881726	Missense_Mutation	SNP	G	A	6	60	c.9310G>A	c.(9310-9312)GAA>AAA	p.E3104K
Pat_41	Post-Resistance	DNAH8	1769	37	6	38885845	38885845	Missense_Mutation	SNP	G	A	19	166	c.9802G>A	c.(9802-9804)GCT>ACT	p.A3268T
Pat_41	Post-Resistance	DNAH8	1769	37	6	38941554	38941554	Missense_Mutation	SNP	G	A	12	106	c.11992G>A	c.(11992-11994)GAG>AAG	p.E3998K
Pat_41	Post-Resistance	DNAH8	1769	37	6	38998080	38998080	Missense_Mutation	SNP	C	T	16	180	c.13385C>T	c.(13384-13386)ACC>ATC	p.T4462I
Pat_41	Post-Resistance	DNAH8	1769	37	6	38998148	38998148	Missense_Mutation	SNP	C	T	17	135	c.13453C>T	c.(13453-13455)CTT>TTT	p.L4485F
Pat_41	Post-Resistance	GLP1R	2740	37	6	39046128	39046128	Missense_Mutation	SNP	G	A	9	221	c.854G>A	c.(853-855)GGC>GAC	p.G285D
Pat_41	Post-Resistance	GLP1R	2740	37	6	39046924	39046924	Missense_Mutation	SNP	G	A	9	360	c.991G>A	c.(991-993)GTG>ATG	p.V331M
Pat_41	Post-Resistance	KCNK16	83795	37	6	39285729	39285729	Splice_Site	SNP	C	T	5	30	c.329_splice	c.e3-1	p.G110_splice
Pat_41	Post-Resistance	DAAM2	23500	37	6	39843120	39843120	Missense_Mutation	SNP	G	A	30	418	c.1177G>A	c.(1177-1179)GGC>AGC	p.G393S
Pat_41	Post-Resistance	MOCS1	4337	37	6	39893527	39893527	Missense_Mutation	SNP	C	T	15	100	c.313G>A	c.(313-315)GAG>AAG	p.E105K
Pat_41	Post-Resistance	NFYA	4800	37	6	41062193	41062193	Missense_Mutation	SNP	G	A	14	223	c.947G>A	c.(946-948)GGA>GAA	p.G316E
Pat_41	Post-Resistance	TRERF1	55809	37	6	42237117	42237117	Missense_Mutation	SNP	G	A	7	113	c.212C>T	c.(211-213)TCC>TTC	p.S71F
Pat_41	Post-Resistance	PRPH2	5961	37	6	42672326	42672326	Missense_Mutation	SNP	C	T	14	221	c.605G>A	c.(604-606)GGG>GAG	p.G202E
Pat_41	Post-Resistance	KIAA0240	23506	37	6	42833126	42833126	Missense_Mutation	SNP	G	A	68	421	c.3182G>A	c.(3181-3183)GGT>GAT	p.G1061D
Pat_41	Post-Resistance	CUL7	9820	37	6	43014327	43014327	Nonsense_Mutation	SNP	G	A	4	91	c.2410C>T	c.(2410-2412)CAG>TAG	p.Q804*
Pat_41	Post-Resistance	CUL7	9820	37	6	43019191	43019191	Missense_Mutation	SNP	G	A	27	139	c.748C>T	c.(748-750)CTC>TTC	p.L250F
Pat_41	Post-Resistance	PTK7	5754	37	6	43096754	43096754	Missense_Mutation	SNP	C	T	14	125	c.119C>T	c.(118-120)TCC>TTC	p.S40F

Pat_41	Post-Resistance	PTK7	5754	37	6	43111196	43111196	Missense_Mutation	SNP	C	T	26	147	c.2089C>T	c.(2089-2091)CCC>TCC	p.P697S
Pat_41	Post-Resistance	PTK7	5754	37	6	43126554	43126554	Splice_Site	SNP	G	A	4	27	c.2722_splice	c.e18-1	p.V908_splice
Pat_41	Post-Resistance	CUL9	23113	37	6	43171173	43171173	Missense_Mutation	SNP	G	A	17	227	c.3868G>A	c.(3868-3870)GTT>ATT	p.V1290I
Pat_41	Post-Resistance	TTBK1	84630	37	6	43220597	43220597	Missense_Mutation	SNP	G	A	16	240	c.229G>A	c.(229-231)GAG>AAG	p.E77K
Pat_41	Post-Resistance	TTBK1	84630	37	6	43226906	43226906	Missense_Mutation	SNP	G	A	17	135	c.1147G>A	c.(1147-1149)GGC>AGC	p.G383S
Pat_41	Post-Resistance	ZNF318	24149	37	6	43307112	43307112	Missense_Mutation	SNP	G	A	25	70	c.4624C>T	c.(4624-4626)CTC>TTC	p.L1542F
Pat_41	Post-Resistance	ZNF318	24149	37	6	43307505	43307505	Missense_Mutation	SNP	C	T	21	87	c.4231G>A	c.(4231-4233)GGA>AGA	p.G1411R
Pat_41	Post-Resistance	ZNF318	24149	37	6	43316061	43316061	Splice_Site	SNP	C	T	22	127	c.3072_splice	c.e6+1	p.K1024_splice
Pat_41	Post-Resistance	ABCC10	89845	37	6	43400078	43400078	Nonsense_Mutation	SNP	G	A	12	57	c.360G>A	c.(358-360)TGG>TGA	p.W120*
Pat_41	Post-Resistance	YIPF3	25844	37	6	43483384	43483384	Missense_Mutation	SNP	A	C	8	175	c.344T>G	c.(343-345)ATC>AGC	p.I115S
Pat_41	Post-Resistance	POLH	5429	37	6	43572476	43572476	Splice_Site	SNP	G	A	9	189	c.1008_splice	c.e8+1	p.Q336_splice
Pat_41	Post-Resistance	HSP90AB1	3326	37	6	44221050	44221050	Missense_Mutation	SNP	G	A	48	783	c.2000G>A	c.(1999-2001)GGC>GAC	p.G667D
Pat_41	Post-Resistance	AARS2	57505	37	6	44274997	44274997	Missense_Mutation	SNP	C	T	6	83	c.1029G>A	c.(1027-1029)ATG>ATA	p.M343I
Pat_41	Post-Resistance	ENPP4	22875	37	6	46111307	46111307	Missense_Mutation	SNP	G	A	25	457	c.1292G>A	c.(1291-1293)AGA>AAA	p.R431K
Pat_41	Post-Resistance	ENPP5	59084	37	6	46135583	46135583	Nonsense_Mutation	SNP	C	T	14	255	c.417G>A	c.(415-417)TGG>TGA	p.W139*
Pat_41	Post-Resistance	TDRD6	221400	37	6	46657517	46657517	Missense_Mutation	SNP	G	A	24	281	c.1652G>A	c.(1651-1653)GGT>GAT	p.G551D
Pat_41	Post-Resistance	PLA2G7	7941	37	6	46684800	46684800	Missense_Mutation	SNP	G	A	19	327	c.143C>T	c.(142-144)GCT>GTT	p.A48V
Pat_41	Post-Resistance	GPR116	221395	37	6	46826579	46826579	Missense_Mutation	SNP	C	T	4	91	c.3061G>A	c.(3061-3063)GGC>AGC	p.G1021S
Pat_41	Post-Resistance	GPR116	221395	37	6	46826769	46826769	Nonsense_Mutation	SNP	C	T	11	218	c.2871G>A	c.(2869-2871)TGG>TGA	p.W957*
Pat_41	Post-Resistance	GPR116	221395	37	6	46836787	46836787	Missense_Mutation	SNP	C	T	5	73	c.1454G>A	c.(1453-1455)GGA>GAA	p.G485E
Pat_41	Post-Resistance	TNFRSF21	27242	37	6	47253680	47253680	Missense_Mutation	SNP	C	T	13	44	c.748G>A	c.(748-750)GGC>AGC	p.G250S
Pat_41	Post-Resistance	GPR111	222611	37	6	47646772	47646772	Missense_Mutation	SNP	C	T	20	107	c.373C>T	c.(373-375)CCA>TCA	p.P125S
Pat_41	Post-Resistance	CRISP2	7180	37	6	49667525	49667525	Missense_Mutation	SNP	C	T	12	155	c.263G>A	c.(262-264)CGC>CAC	p.R88H
Pat_41	Post-Resistance	TFAP2D	83741	37	6	50740386	50740386	Missense_Mutation	SNP	G	A	11	229	c.1168G>A	c.(1168-1170)GCA>ACA	p.A390T
Pat_41	Post-Resistance	PKHD1	5314	37	6	51612717	51612717	Missense_Mutation	SNP	G	A	9	159	c.9697C>T	c.(9697-9699)CCC>TCC	p.P3233S
Pat_41	Post-Resistance	PKHD1	5314	37	6	51875247	51875247	Missense_Mutation	SNP	C	T	9	171	c.5611G>A	c.(5611-5613)GAA>AAA	p.E1871K
Pat_41	Post-Resistance	PKHD1	5314	37	6	51889519	51889519	Missense_Mutation	SNP	C	T	13	51	c.5089G>A	c.(5089-5091)GGT>AGT	p.G1697S
Pat_41	Post-Resistance	PKHD1	5314	37	6	51913308	51913308	Missense_Mutation	SNP	G	A	35	297	c.2389C>T	c.(2389-2391)CCT>TCT	p.P797S
Pat_41	Post-Resistance	PKHD1	5314	37	6	51923254	51923254	Missense_Mutation	SNP	C	T	22	282	c.1379G>A	c.(1378-1380)GGG>GAG	p.G460E
Pat_41	Post-Resistance	PKHD1	5314	37	6	51924779	51924779	Missense_Mutation	SNP	C	T	29	194	c.1180G>A	c.(1180-1182)GCA>ACA	p.A394T
Pat_41	Post-Resistance	MCM3	4172	37	6	52141130	52141130	Missense_Mutation	SNP	C	T	11	124	c.1310G>A	c.(1309-1311)GGC>GAC	p.G437D
Pat_41	Post-Resistance	EFHC1	114327	37	6	52319001	52319001	Missense_Mutation	SNP	G	A	21	349	c.832G>A	c.(832-834)GTC>ATC	p.V278I
Pat_41	Post-Resistance	TRAM2	9697	37	6	52372379	52372379	Missense_Mutation	SNP	C	T	9	116	c.598G>A	c.(598-600)GTG>ATG	p.V200M
Pat_41	Post-Resistance	GSTA3	2940	37	6	52768479	52768479	Missense_Mutation	SNP	C	T	20	153	c.134G>A	c.(133-135)AGA>AAA	p.R45K
Pat_41	Post-Resistance	ICK	22858	37	6	52905955	52905955	Missense_Mutation	SNP	C	T	10	285	c.80G>A	c.(79-81)GGG>GAG	p.G27E
Pat_41	Post-Resistance	HMGCLL1	54511	37	6	55304335	55304335	Missense_Mutation	SNP	G	A	20	247	c.908C>T	c.(907-909)TCC>TTC	p.S303F
Pat_41	Post-Resistance	DST	667	37	6	56323951	56323951	Missense_Mutation	SNP	G	A	7	85	c.16880C>T	c.(16879-16881)TCC>TTC	p.S5627F
Pat_41	Post-Resistance	DST	667	37	6	56366452	56366452	Missense_Mutation	SNP	C	T	21	176	c.13249G>A	c.(13249-13251)GAA>AAA	p.E4417K
Pat_41	Post-Resistance	DST	667	37	6	56425130	56425130	Missense_Mutation	SNP	G	A	7	56	c.8045C>T	c.(8044-8046)CCT>CTT	p.P2682L
Pat_41	Post-Resistance	KIAA1586	57691	37	6	56917809	56917809	Missense_Mutation	SNP	G	T	10	307	c.512G>T	c.(511-513)GGA>GTA	p.G171V
Pat_41	Post-Resistance	PHF3	23469	37	6	64390030	64390030	Missense_Mutation	SNP	C	T	21	390	c.374C>T	c.(373-375)TCT>TTT	p.S125F
Pat_41	Post-Resistance	PHF3	23469	37	6	64422708	64422708	Missense_Mutation	SNP	G	A	6	138	c.5224G>A	c.(5224-5226)GAT>AAT	p.D1742N
Pat_41	Post-Resistance	COL19A1	1310	37	6	70873248	70873248	Missense_Mutation	SNP	G	A	9	85	c.2360G>A	c.(2359-2361)AGA>AAA	p.R787K
Pat_41	Post-Resistance	COL19A1	1310	37	6	70873263	70873263	Missense_Mutation	SNP	G	A	5	85	c.2375G>A	c.(2374-2376)GGT>GAT	p.G792D
Pat_41	Post-Resistance	COL19A1	1310	37	6	70897807	70897807	Missense_Mutation	SNP	G	A	8	99	c.2885G>A	c.(2884-2886)GGC>GAC	p.G962D
Pat_41	Post-Resistance	COL9A1	1297	37	6	70944555	70944555	Missense_Mutation	SNP	G	A	5	54	c.2201C>T	c.(2200-2202)CCC>CTC	p.P734L
Pat_41	Post-Resistance	COL9A1	1297	37	6	70980033	70980033	Missense_Mutation	SNP	C	T	5	126	c.1181G>A	c.(1180-1182)GGC>GAC	p.G394D

Pat_41	Post-Resistance	SMAP1	60682	37	6	71567732	71567732	Missense_Mutation	SNP	G	A	10	128	c.1069G>A	c.(1069-1071)GGA>AGA	p.G357R
Pat_41	Post-Resistance	RIMS1	22999	37	6	73043413	73043413	Missense_Mutation	SNP	G	A	4	25	c.4241G>A	c.(4240-4242)AGC>AAC	p.S1414N
Pat_41	Post-Resistance	KCNQ5	56479	37	6	73821047	73821047	Missense_Mutation	SNP	G	A	9	74	c.1046G>A	c.(1045-1047)GGT>GAT	p.G349D
Pat_41	Post-Resistance	COL12A1	1303	37	6	75838026	75838026	Missense_Mutation	SNP	C	T	19	269	c.6326G>A	c.(6325-6327)GGA>GAA	p.G2109E
Pat_41	Post-Resistance	COL12A1	1303	37	6	75893101	75893101	Missense_Mutation	SNP	G	A	61	302	c.1556C>T	c.(1555-1557)ACT>ATT	p.T519I
Pat_41	Post-Resistance	FILIP1	27145	37	6	76024752	76024752	Nonsense_Mutation	SNP	G	A	21	264	c.796C>T	c.(796-798)CAG>TAG	p.Q266*
Pat_41	Post-Resistance	SENP6	26054	37	6	76425110	76425110	Missense_Mutation	SNP	C	T	19	391	c.3139C>T	c.(3139-3141)CTC>TTC	p.L1047F
Pat_41	Post-Resistance	MYO6	4646	37	6	76538267	76538267	Missense_Mutation	SNP	G	A	8	188	c.198G>A	c.(196-198)ATG>ATA	p.M66I
Pat_41	Post-Resistance	MYO6	4646	37	6	76572354	76572354	Missense_Mutation	SNP	G	A	17	94	c.1588G>A	c.(1588-1590)GAT>AAT	p.D530N
Pat_41	Post-Resistance	MYO6	4646	37	6	76618239	76618239	Missense_Mutation	SNP	G	A	14	182	c.3307G>A	c.(3307-3309)GAA>AAA	p.E1103K
Pat_41	Post-Resistance	HMGN3	9324	37	6	79924715	79924715	Missense_Mutation	SNP	C	T	15	98	c.40G>A	c.(40-42)GAT>AAT	p.D14N
Pat_41	Post-Resistance	BCKDHB	594	37	6	80878691	80878691	Missense_Mutation	SNP	G	A	7	57	c.577G>A	c.(577-579)GCT>ACT	p.A193T
Pat_41	Post-Resistance	IBTK	25998	37	6	82912293	82912293	Missense_Mutation	SNP	G	A	30	272	c.2681C>T	c.(2680-2682)TCT>TTT	p.S894F
Pat_41	Post-Resistance	TPBG	7162	37	6	83075178	83075178	Missense_Mutation	SNP	C	T	37	221	c.500C>T	c.(499-501)GCC>GTC	p.A167V
Pat_41	Post-Resistance	RWDD2A	112611	37	6	83905771	83905771	Missense_Mutation	SNP	C	T	5	79	c.659C>T	c.(658-660)TCC>TTC	p.S220F
Pat_41	Post-Resistance	SNAP91	9892	37	6	84290226	84290226	Missense_Mutation	SNP	C	T	52	110	c.2242G>A	c.(2242-2244)GCA>ACA	p.A748T
Pat_41	Post-Resistance	ZNF292	23036	37	6	87970656	87970656	Missense_Mutation	SNP	G	A	3	24	c.7309G>A	c.(7309-7311)GAA>AAA	p.E2437K
Pat_41	Post-Resistance	GJB7	375519	37	6	87994516	87994516	Missense_Mutation	SNP	C	T	10	158	c.115G>A	c.(115-117)GCA>ACA	p.A39T
Pat_41	Post-Resistance	C6orf165	154313	37	6	88173913	88173913	Missense_Mutation	SNP	G	A	15	46	c.1814G>A	c.(1813-1815)AGC>AAC	p.S605N
Pat_41	Post-Resistance	SLC35A1	10559	37	6	88187175	88187175	Missense_Mutation	SNP	G	A	5	107	c.112G>A	c.(112-114)GAC>AAC	p.D38N
Pat_41	Post-Resistance	UBE2J1	51465	37	6	90053466	90053466	Missense_Mutation	SNP	C	T	3	37	c.41G>A	c.(40-42)CGT>CAT	p.R14H
Pat_41	Post-Resistance	MDN1	23195	37	6	90359807	90359807	Missense_Mutation	SNP	C	T	52	107	c.16142G>A	c.(16141-16143)CGC>CAC	p.R5381H
Pat_41	Post-Resistance	MDN1	23195	37	6	90359833	90359833	Nonsense_Mutation	SNP	C	T	20	104	c.16116G>A	c.(16114-16116)TGG>TGA	p.W5372*
Pat_41	Post-Resistance	MDN1	23195	37	6	90365584	90365584	Missense_Mutation	SNP	G	A	13	79	c.15389C>T	c.(15388-15390)GCC>GTC	p.A5130V
Pat_41	Post-Resistance	EPHA7	2045	37	6	93964405	93964405	Missense_Mutation	SNP	G	A	7	250	c.2492C>T	c.(2491-2493)TCT>TTT	p.S831F
Pat_41	Post-Resistance	FUT9	10690	37	6	96651915	96651915	Missense_Mutation	SNP	C	T	8	29	c.884C>T	c.(883-885)CCC>CTC	p.P295L
Pat_41	Post-Resistance	C6orf167	253714	37	6	97677017	97677017	Missense_Mutation	SNP	C	T	7	52	c.1792G>A	c.(1792-1794)GCT>ACT	p.A598T
Pat_41	Post-Resistance	USP45	85015	37	6	99912955	99912955	Splice_Site	SNP	C	T	7	42	c.1164_splice	c.e12+1	p.R388_splice
Pat_41	Post-Resistance	SIM1	6492	37	6	100838517	100838517	Missense_Mutation	SNP	G	A	32	78	c.2021C>T	c.(2020-2022)GCT>GTT	p.A674V
Pat_41	Post-Resistance	SIM1	6492	37	6	100895230	100895230	Nonsense_Mutation	SNP	C	T	9	51	c.912G>A	c.(910-912)TGG>TGA	p.W304*
Pat_41	Post-Resistance	AIM1	202	37	6	107006431	107006431	Missense_Mutation	SNP	C	T	4	111	c.4562C>T	c.(4561-4563)GCA>GTA	p.A1521V
Pat_41	Post-Resistance	QRSL1	55278	37	6	107100368	107100368	Missense_Mutation	SNP	G	A	26	94	c.760G>A	c.(760-762)GAC>AAC	p.D254N
Pat_41	Post-Resistance	SOBP	55084	37	6	107955643	107955643	Missense_Mutation	SNP	C	T	6	52	c.1595C>T	c.(1594-1596)CCC>CTC	p.P532L
Pat_41	Post-Resistance	SESN1	27244	37	6	109323539	109323539	Missense_Mutation	SNP	C	T	23	65	c.110G>A	c.(109-111)GGC>GAC	p.G37D
Pat_41	Post-Resistance	SLC22A16	85413	37	6	110777942	110777942	Missense_Mutation	SNP	C	T	27	209	c.332G>A	c.(331-333)AGT>AAT	p.S111N
Pat_41	Post-Resistance	CDK19	23097	37	6	110942440	110942440	Missense_Mutation	SNP	C	T	8	45	c.1244G>A	c.(1243-1245)GGG>GAG	p.G415E
Pat_41	Post-Resistance	REV3L	5980	37	6	111670513	111670513	Missense_Mutation	SNP	C	T	30	113	c.7327G>A	c.(7327-7329)GCT>ACT	p.A2443T
Pat_41	Post-Resistance	REV3L	5980	37	6	111710320	111710320	Missense_Mutation	SNP	G	A	48	144	c.851C>T	c.(850-852)CCT>CTT	p.P284L
Pat_41	Post-Resistance	TRAF3IP2	10758	37	6	111912557	111912557	Missense_Mutation	SNP	G	A	7	30	c.733C>T	c.(733-735)CCA>TCA	p.P245S
Pat_41	Post-Resistance	LAMA4	3910	37	6	112476148	112476148	Missense_Mutation	SNP	G	A	4	85	c.1961C>T	c.(1960-1962)GCG>GTG	p.A654V
Pat_41	Post-Resistance	DSE	29940	37	6	116720546	116720546	Missense_Mutation	SNP	A	G	52	6	c.133A>G	c.(133-135)ATG>GTG	p.M45V
Pat_41	Post-Resistance	RWDD1	51389	37	6	116910006	116910006	Missense_Mutation	SNP	C	T	15	73	c.272C>T	c.(271-273)GCT>GTT	p.A91V
Pat_41	Post-Resistance	RWDD1	51389	37	6	116914232	116914232	Missense_Mutation	SNP	C	T	12	99	c.700C>T	c.(700-702)CCT>TCT	p.P234S
Pat_41	Post-Resistance	RFX6	222546	37	6	117250125	117250125	Missense_Mutation	SNP	C	T	23	136	c.2602C>T	c.(2602-2604)CCA>TCA	p.P868S
Pat_41	Post-Resistance	C6orf170	221322	37	6	121544399	121544399	Missense_Mutation	SNP	C	T	18	63	c.2464G>A	c.(2464-2466)GTC>ATC	p.V822I
Pat_41	Post-Resistance	GJA1	2697	37	6	121768171	121768171	Missense_Mutation	SNP	G	T	4	43	c.178G>T	c.(178-180)GGT>TGT	p.G60C
Pat_41	Post-Resistance	HSF2	3298	37	6	122743976	122743976	Missense_Mutation	SNP	G	A	6	91	c.944G>A	c.(943-945)GGC>GAC	p.G315D

Pat_41	Post-Resistance	NCOA7	135112	37	6	126242132	126242132	Missense_Mutation	SNP	G	A	21	107	c.2288G>A	c.(2287-2289)AGC>AAC	p.S763N
Pat_41	Post-Resistance	ARHGAP18	93663	37	6	129905244	129905244	Missense_Mutation	SNP	T	C	4	72	c.1727A>G	c.(1726-1728)CAG>CGG	p.Q576R
Pat_41	Post-Resistance	EPB41L2	2037	37	6	131206241	131206241	Missense_Mutation	SNP	C	T	12	221	c.1828G>A	c.(1828-1830)GGA>AGA	p.G610R
Pat_41	Post-Resistance	EPB41L2	2037	37	6	131215562	131215562	Missense_Mutation	SNP	G	A	6	228	c.1409C>T	c.(1408-1410)ACC>ATC	p.T470I
Pat_41	Post-Resistance	AKAP7	9465	37	6	131602750	131602750	Missense_Mutation	SNP	G	A	12	55	c.199G>A	c.(199-201)GCT>ACT	p.A67T
Pat_41	Post-Resistance	MED23	9439	37	6	131926429	131926429	Missense_Mutation	SNP	G	A	7	78	c.1564C>T	c.(1564-1566)CCC>TCC	p.P522S
Pat_41	Post-Resistance	MED23	9439	37	6	131929121	131929121	Missense_Mutation	SNP	C	T	9	90	c.1168G>A	c.(1168-1170)GCT>ACT	p.A390T
Pat_41	Post-Resistance	ENPP3	5169	37	6	132047335	132047335	Nonsense_Mutation	SNP	C	T	15	121	c.1948C>T	c.(1948-1950)CAG>TAG	p.Q650*
Pat_41	Post-Resistance	TAAR2	9287	37	6	132938716	132938716	Missense_Mutation	SNP	C	T	6	79	c.629G>A	c.(628-630)GGG>GAG	p.G210E
Pat_41	Post-Resistance	VNN1	8876	37	6	133005556	133005556	Missense_Mutation	SNP	G	A	13	157	c.1277C>T	c.(1276-1278)TCC>TTC	p.S426F
Pat_41	Post-Resistance	EYA4	2070	37	6	133849899	133849899	Missense_Mutation	SNP	G	A	21	418	c.1876G>A	c.(1876-1878)GAC>AAC	p.D626N
Pat_41	Post-Resistance	TCF21	6943	37	6	134210849	134210849	Missense_Mutation	SNP	C	T	28	159	c.314C>T	c.(313-315)ACC>ATC	p.T105I
Pat_41	Post-Resistance	HBS1L	10767	37	6	135318631	135318631	Missense_Mutation	SNP	C	T	15	132	c.703G>A	c.(703-705)GTG>ATG	p.V235M
Pat_41	Post-Resistance	MYB	4602	37	6	135515596	135515596	Missense_Mutation	SNP	C	T	7	60	c.946C>T	c.(946-948)CCA>TCA	p.P316S
Pat_41	Post-Resistance	BCLAF1	9774	37	6	136582453	136582453	Missense_Mutation	SNP	C	T	19	148	c.2707G>A	c.(2707-2709)GAG>AAG	p.E903K
Pat_41	Post-Resistance	MAP7	9053	37	6	136742895	136742895	Missense_Mutation	SNP	C	T	9	86	c.110G>A	c.(109-111)AGC>AAC	p.S37N
Pat_41	Post-Resistance	MAP3K5	4217	37	6	136935302	136935302	Missense_Mutation	SNP	G	A	5	60	c.2273C>T	c.(2272-2274)CCT>CTT	p.P758L
Pat_41	Post-Resistance	IL22RA2	116379	37	6	137476092	137476092	Missense_Mutation	SNP	G	A	18	122	c.458C>T	c.(457-459)ACT>ATT	p.T153I
Pat_41	Post-Resistance	IL22RA2	116379	37	6	137477929	137477929	Missense_Mutation	SNP	G	A	22	136	c.260C>T	c.(259-261)TCT>TTT	p.S87F
Pat_41	Post-Resistance	OLIG3	167826	37	6	137814884	137814884	Missense_Mutation	SNP	C	T	6	29	c.424G>A	c.(424-426)GAG>AAG	p.E142K
Pat_41	Post-Resistance	TNFAIP3	7128	37	6	138196877	138196877	Missense_Mutation	SNP	C	T	10	193	c.539C>T	c.(538-540)CCC>CTC	p.P180L
Pat_41	Post-Resistance	KIAA1244	57221	37	6	138584656	138584656	Missense_Mutation	SNP	C	T	3	27	c.2036C>T	c.(2035-2037)TCC>TTC	p.S679F
Pat_41	Post-Resistance	GPR126	57211	37	6	142688820	142688820	Missense_Mutation	SNP	C	T	4	63	c.218C>T	c.(217-219)GCC>GTC	p.A73V
Pat_41	Post-Resistance	HIVEP2	3097	37	6	143089518	143089518	Splice_Site	SNP	C	T	29	245	c.5342_splice	c.e6+1	p.G1781_splice
Pat_41	Post-Resistance	HIVEP2	3097	37	6	143094096	143094096	Missense_Mutation	SNP	C	T	17	148	c.1780G>A	c.(1780-1782)GCG>ACG	p.A594T
Pat_41	Post-Resistance	AIG1	51390	37	6	143458050	143458050	Missense_Mutation	SNP	G	A	15	140	c.220G>A	c.(220-222)GAG>AAG	p.E74K
Pat_41	Post-Resistance	PHACTR2	9749	37	6	144081633	144081633	Missense_Mutation	SNP	C	T	6	2	c.517C>T	c.(517-519)CCT>TCT	p.P173S
Pat_41	Post-Resistance	PHACTR2	9749	37	6	144081723	144081723	Nonsense_Mutation	SNP	C	T	30	91	c.607C>T	c.(607-609)CAG>TAG	p.Q203*
Pat_41	Post-Resistance	SHPRH	257218	37	6	146275869	146275869	Missense_Mutation	SNP	C	T	19	63	c.590G>A	c.(589-591)AGA>AAA	p.R197K
Pat_41	Post-Resistance	SHPRH	257218	37	6	146276256	146276256	Missense_Mutation	SNP	C	T	11	61	c.203G>A	c.(202-204)AGA>AAA	p.R68K
Pat_41	Post-Resistance	SASH1	23328	37	6	148711373	148711373	Missense_Mutation	SNP	G	A	3	13	c.260G>A	c.(259-261)CGG>CAG	p.R87Q
Pat_41	Post-Resistance	PCMT1	5110	37	6	150117584	150117584	Missense_Mutation	SNP	C	T	30	118	c.626C>T	c.(625-627)GCC>GTC	p.A209V
Pat_41	Post-Resistance	AKAP12	9590	37	6	151670613	151670613	Missense_Mutation	SNP	G	A	27	101	c.1087G>A	c.(1087-1089)GAA>AAA	p.E363K
Pat_41	Post-Resistance	RMND1	55005	37	6	151766870	151766870	Missense_Mutation	SNP	C	T	4	58	c.77G>A	c.(76-78)GGT>GAT	p.G26D
Pat_41	Post-Resistance	SYNE1	23345	37	6	152497620	152497620	Missense_Mutation	SNP	C	T	25	232	c.23536G>A	c.(23536-23538)GCC>ACC	p.A7846T
Pat_41	Post-Resistance	SYNE1	23345	37	6	152542003	152542003	Missense_Mutation	SNP	C	T	28	213	c.21835G>A	c.(21835-21837)GTT>ATT	p.V7279I
Pat_41	Post-Resistance	SYNE1	23345	37	6	152651401	152651401	Missense_Mutation	SNP	C	T	12	27	c.14419G>A	c.(14419-14421)GAA>AAA	p.E4807K
Pat_41	Post-Resistance	SYNE1	23345	37	6	152725448	152725448	Missense_Mutation	SNP	G	A	16	93	c.6725C>T	c.(6724-6726)TCT>TTT	p.S2242F
Pat_41	Post-Resistance	TFB1M	51106	37	6	155581535	155581535	Splice_Site	SNP	C	T	22	85	c.667_splice	c.e6-1	p.V223_splice
Pat_41	Post-Resistance	ARID1B	57492	37	6	157502166	157502166	Missense_Mutation	SNP	C	T	9	42	c.3145C>T	c.(3145-3147)CCA>TCA	p.P1049S
Pat_41	Post-Resistance	ARID1B	57492	37	6	157502238	157502238	Missense_Mutation	SNP	C	T	12	58	c.3217C>T	c.(3217-3219)CCT>TCT	p.P1073S
Pat_41	Post-Resistance	ARID1B	57492	37	6	157519985	157519985	Missense_Mutation	SNP	C	T	13	31	c.4000C>T	c.(4000-4002)CCC>TCC	p.P1334S
Pat_41	Post-Resistance	ARID1B	57492	37	6	157527697	157527697	Missense_Mutation	SNP	C	T	36	313	c.5368C>T	c.(5368-5370)CGT>TGT	p.R1790C
Pat_41	Post-Resistance	SERAC1	84947	37	6	158571497	158571497	Missense_Mutation	SNP	C	T	4	37	c.253G>A	c.(253-255)GGA>AGA	p.G85R
Pat_41	Post-Resistance	TMEM181	57583	37	6	159029496	159029496	Splice_Site	SNP	G	A	25	207	c.1215_splice	c.e9+1	p.Q405_splice
Pat_41	Post-Resistance	SYTL3	94120	37	6	159184350	159184350	Missense_Mutation	SNP	C	T	9	102	c.1532C>T	c.(1531-1533)CCA>CTA	p.P511L
Pat_41	Post-Resistance	ACAT2	39	37	6	160197211	160197211	Missense_Mutation	SNP	C	T	11	99	c.664C>T	c.(664-666)CCT>TCT	p.P222S

Pat_41	Post-Resistance	PNLDC1	154197	37	6	160240050	160240050	Missense_Mutation	SNP	G	A	6	97	c.1297G>A	c.(1297-1299)GTC>ATC	p.V433I
Pat_41	Post-Resistance	IGF2R	3482	37	6	160484638	160484638	Missense_Mutation	SNP	C	T	4	34	c.3862C>T	c.(3862-3864)CCG>TCG	p.P1288S
Pat_41	Post-Resistance	LPA	4018	37	6	160999554	160999554	Splice_Site	SNP	C	T	23	67	c.4471_splice	c.e28+1	p.A1491_splice
Pat_41	Post-Resistance	TTLL2	83887	37	6	167754397	167754397	Missense_Mutation	SNP	G	A	22	177	c.1009G>A	c.(1009-1011)GAC>AAC	p.D337N
Pat_41	Post-Resistance	KIF25	3834	37	6	168430266	168430266	Missense_Mutation	SNP	A	C	3	94	c.1A>C	c.(1-3)ATG>CTG	p.M1L
Pat_41	Post-Resistance	THBS2	7058	37	6	169640546	169640546	Splice_Site	SNP	C	T	10	87	c.1032_splice	c.e7+1	p.K344_splice
Pat_41	Post-Resistance	WDR27	253769	37	6	170060792	170060792	Missense_Mutation	SNP	T	C	6	74	c.1096A>G	c.(1096-1098)AAC>GAC	p.N366D
Pat_41	Post-Resistance	TBP	6908	37	6	170870889	170870889	Missense_Mutation	SNP	C	T	7	310	c.65C>T	c.(64-66)ACT>ATT	p.T22I
Pat_41	Post-Resistance	TBP	6908	37	6	170880559	170880559	Missense_Mutation	SNP	C	T	12	63	c.907C>T	c.(907-909)CTT>TTT	p.L303F
Pat_41	Post-Resistance	PDCD2	5134	37	6	170887992	170887992	Missense_Mutation	SNP	C	T	14	112	c.829G>A	c.(829-831)GAT>AAT	p.D277N
Pat_41	Post-Resistance	FAM20C	56975	37	7	195733	195733	Splice_Site	SNP	G	A	8	147	c.784_splice	c.e2+1	p.A262_splice
Pat_41	Post-Resistance	C7orf50	84310	37	7	1037352	1037352	Missense_Mutation	SNP	G	A	20	81	c.494C>T	c.(493-495)GCC>GTC	p.A165V
Pat_41	Post-Resistance	INTS1	26173	37	7	1512800	1512800	Missense_Mutation	SNP	C	T	15	76	c.5978G>A	c.(5977-5979)AGT>AAT	p.S1993N
Pat_41	Post-Resistance	TMEM184A	202915	37	7	1586805	1586805	Missense_Mutation	SNP	G	A	3	38	c.1025C>T	c.(1024-1026)CCC>CTC	p.P342L
Pat_41	Post-Resistance	MAD1L1	8379	37	7	2054240	2054240	Missense_Mutation	SNP	T	C	13	68	c.1256A>G	c.(1255-1257)GAC>GGC	p.D419G
Pat_41	Post-Resistance	EIF3B	8662	37	7	2409142	2409142	Missense_Mutation	SNP	C	T	20	323	c.1439C>T	c.(1438-1440)GCC>GTC	p.A480V
Pat_41	Post-Resistance	TTYH3	80727	37	7	2686850	2686850	Missense_Mutation	SNP	G	T	3	38	c.368G>T	c.(367-369)CGC>CTC	p.R123L
Pat_41	Post-Resistance	TTYH3	80727	37	7	2698650	2698650	Splice_Site	SNP	G	A	11	277	c.1500_splice	c.e13+1	p.S500_splice
Pat_41	Post-Resistance	CARD11	84433	37	7	2962947	2962947	Missense_Mutation	SNP	G	A	4	97	c.1961C>T	c.(1960-1962)ACC>ATC	p.T654I
Pat_41	Post-Resistance	CARD11	84433	37	7	2979526	2979526	Missense_Mutation	SNP	C	T	10	215	c.721G>A	c.(721-723)GAG>AAG	p.E241K
Pat_41	Post-Resistance	SDK1	221935	37	7	4185505	4185505	Nonsense_Mutation	SNP	G	A	13	84	c.4380G>A	c.(4378-4380)TGG>TGA	p.W1460*
Pat_41	Post-Resistance	KIAA0415	9907	37	7	4825967	4825967	Missense_Mutation	SNP	G	A	5	177	c.1219G>A	c.(1219-1221)GCC>ACC	p.A407T
Pat_41	Post-Resistance	RADIL	55698	37	7	4856943	4856943	Missense_Mutation	SNP	C	T	5	89	c.1655G>A	c.(1654-1656)AGC>AAC	p.S552N
Pat_41	Post-Resistance	TNRC18	84629	37	7	5355635	5355635	Missense_Mutation	SNP	T	C	15	72	c.6814A>G	c.(6814-6816)ATC>GTC	p.I2272V
Pat_41	Post-Resistance	RNF216	54476	37	7	5662589	5662589	Missense_Mutation	SNP	G	A	18	249	c.2503C>T	c.(2503-2505)CCC>TCC	p.P835S
Pat_41	Post-Resistance	PMS2	5395	37	7	6042224	6042224	Missense_Mutation	SNP	T	C	93	563	c.397A>G	c.(397-399)ACT>GCT	p.T133A
Pat_41	Post-Resistance	PMS2	5395	37	7	6043405	6043405	Missense_Mutation	SNP	G	A	23	146	c.269C>T	c.(268-270)TCT>TTT	p.S90F
Pat_41	Post-Resistance	PMS2	5395	37	7	6045630	6045630	Missense_Mutation	SNP	T	G	14	546	c.56A>C	c.(55-57)GAT>GCT	p.D19A
Pat_41	Post-Resistance	USP42	84132	37	7	6189806	6189806	Missense_Mutation	SNP	C	T	7	47	c.1979C>T	c.(1978-1980)GCT>GTT	p.A660V
Pat_41	Post-Resistance	USP42	84132	37	7	6193634	6193634	Missense_Mutation	SNP	G	A	4	109	c.2449G>A	c.(2449-2451)GAC>AAC	p.D817N
Pat_41	Post-Resistance	USP42	84132	37	7	6196570	6196570	Missense_Mutation	SNP	G	A	5	31	c.3827G>A	c.(3826-3828)GGC>GAC	p.G1276D
Pat_41	Post-Resistance	C7orf70	84792	37	7	6370391	6370391	Missense_Mutation	SNP	C	T	6	108	c.395G>A	c.(394-396)GGA>GAA	p.G132E
Pat_41	Post-Resistance	DAGLB	221955	37	7	6449592	6449592	Missense_Mutation	SNP	C	T	15	356	c.1895G>A	c.(1894-1896)GGT>GAT	p.G632D
Pat_41	Post-Resistance	DAGLB	221955	37	7	6474499	6474499	Missense_Mutation	SNP	C	T	30	428	c.572G>A	c.(571-573)AGC>AAC	p.S191N
Pat_41	Post-Resistance	MIOS	54468	37	7	7613064	7613064	Missense_Mutation	SNP	C	T	14	432	c.958C>T	c.(958-960)CCT>TCT	p.P320S
Pat_41	Post-Resistance	ICA1	3382	37	7	8167583	8167583	Missense_Mutation	SNP	G	A	6	160	c.1250C>T	c.(1249-1251)CCC>CTC	p.P417L
Pat_41	Post-Resistance	PHF14	9678	37	7	11076259	11076259	Missense_Mutation	SNP	G	A	14	100	c.1817G>A	c.(1816-1818)GGA>GAA	p.G606E
Pat_41	Post-Resistance	PHF14	9678	37	7	11101648	11101648	Missense_Mutation	SNP	G	A	5	41	c.2590G>A	c.(2590-2592)GCT>ACT	p.A864T
Pat_41	Post-Resistance	THSD7A	221981	37	7	11418814	11418814	Missense_Mutation	SNP	G	A	42	168	c.4684C>T	c.(4684-4686)CCC>TCC	p.P1562S
Pat_41	Post-Resistance	THSD7A	221981	37	7	11676199	11676199	Missense_Mutation	SNP	C	T	6	100	c.580G>A	c.(580-582)GAT>AAT	p.D194N
Pat_41	Post-Resistance	TMEM195	392636	37	7	15433792	15433793	Missense_Mutation	DNP	GG	AA	109	141	c.621_622CC>TT	(619-624)AACCTT>AATTT	p.L208F
Pat_41	Post-Resistance	ANKMY2	57037	37	7	16642096	16642096	Nonsense_Mutation	SNP	C	T	37	215	c.1050G>A	c.(1048-1050)TGG>TGA	p.W350*
Pat_41	Post-Resistance	AHR	196	37	7	17382575	17382575	Missense_Mutation	SNP	C	T	30	155	c.2434C>T	c.(2434-2436)CCA>TCA	p.P812S
Pat_41	Post-Resistance	HDAC9	9734	37	7	18706005	18706005	Missense_Mutation	SNP	G	A	5	53	c.1628G>A	c.(1627-1629)GGG>GAG	p.G543E
Pat_41	Post-Resistance	ITGB8	3696	37	7	20406758	20406758	Missense_Mutation	SNP	G	A	13	231	c.337G>A	c.(337-339)GAA>AAA	p.E113K
Pat_41	Post-Resistance	DNAH11	8701	37	7	21744166	21744166	Missense_Mutation	SNP	A	T	4	116	c.6409A>T	c.(6409-6411)AGG>TGG	p.R2137W
Pat_41	Post-Resistance	DNAH11	8701	37	7	21788281	21788281	Missense_Mutation	SNP	C	T	13	95	c.8615C>T	c.(8614-8616)TCC>TTC	p.S2872F

Pat_41	Post-Resistance	DNAH11	8701	37	7	21920430	21920430	Nonsense_Mutation	SNP	G	A	11	86	c.12327G>A	c.(12325-12327)TGG>TGA	p.W4109*
Pat_41	Post-Resistance	RAPGEF5	9771	37	7	22194192	22194192	Missense_Mutation	SNP	G	A	7	217	c.1208C>T	c.(1207-1209)TCC>TTC	p.S403F
Pat_41	Post-Resistance	NUPL2	11097	37	7	23240257	23240257	Missense_Mutation	SNP	C	T	26	371	c.1165C>T	c.(1165-1167)CCC>TCC	p.P389S
Pat_41	Post-Resistance	NUPL2	11097	37	7	23240312	23240312	Missense_Mutation	SNP	C	T	8	102	c.1220C>T	c.(1219-1221)ACT>ATT	p.T407I
Pat_41	Post-Resistance	IGF2BP3	10643	37	7	23352079	23352079	Missense_Mutation	SNP	C	T	7	67	c.1642G>A	c.(1642-1644)GTT>ATT	p.V548I
Pat_41	Post-Resistance	IGF2BP3	10643	37	7	23357275	23357275	Missense_Mutation	SNP	G	A	19	338	c.1378C>T	c.(1378-1380)CCA>TCA	p.P460S
Pat_41	Post-Resistance	CLK2P	1197	37	7	23624917	23624917	Missense_Mutation	SNP	C	T	20	200	c.580G>A	c.(580-582)GAT>AAT	p.D194N
Pat_41	Post-Resistance	C7orf46	340277	37	7	23731120	23731120	Missense_Mutation	SNP	C	A	35	302	c.542C>A	c.(541-543)CCA>CAA	p.P181Q
Pat_41	Post-Resistance	C7orf46	340277	37	7	23737882	23737882	Missense_Mutation	SNP	G	A	7	383	c.709G>A	c.(709-711)GCA>ACA	p.A237T
Pat_41	Post-Resistance	C7orf46	340277	37	7	23740488	23740488	Splice_Site	SNP	G	A	17	219	c.828_splice	c.e6+1	p.R276_splice
Pat_41	Post-Resistance	OSBPL3	26031	37	7	24901388	24901388	Missense_Mutation	SNP	C	T	7	139	c.871G>A	c.(871-873)GTC>ATC	p.V291I
Pat_41	Post-Resistance	CBX3	11335	37	7	26251312	26251312	Missense_Mutation	SNP	C	T	8	251	c.361C>T	c.(361-363)CTT>TTT	p.L121F
Pat_41	Post-Resistance	SKAP2	8935	37	7	26765179	26765179	Missense_Mutation	SNP	C	T	4	88	c.664G>A	c.(664-666)GAA>AAA	p.E222K
Pat_41	Post-Resistance	HOXA1	3198	37	7	27135161	27135161	Missense_Mutation	SNP	G	A	12	170	c.371C>T	c.(370-372)CCC>CTC	p.P124L
Pat_41	Post-Resistance	HOXA2	3199	37	7	27142064	27142064	Missense_Mutation	SNP	G	A	20	385	c.56C>T	c.(55-57)GCT>GTT	p.A19V
Pat_41	Post-Resistance	HOXA6	3203	37	7	27185506	27185506	Missense_Mutation	SNP	C	T	16	160	c.473G>A	c.(472-474)GGC>GAC	p.G158D
Pat_41	Post-Resistance	HIBADH	11112	37	7	27565940	27565940	Missense_Mutation	SNP	G	A	7	62	c.904C>T	c.(904-906)CTT>TTT	p.L302F
Pat_41	Post-Resistance	CREB5	9586	37	7	28547246	28547246	Missense_Mutation	SNP	C	T	12	467	c.182C>T	c.(181-183)ACC>ATC	p.T61I
Pat_41	Post-Resistance	CPVL	54504	37	7	29070228	29070228	Missense_Mutation	SNP	C	T	45	570	c.1285G>A	c.(1285-1287)GCT>ACT	p.A429T
Pat_41	Post-Resistance	CHN2	1124	37	7	29539497	29539497	Missense_Mutation	SNP	G	A	5	239	c.754G>A	c.(754-756)GTA>ATA	p.V252I
Pat_41	Post-Resistance	WIPF3	644150	37	7	29928987	29928987	Missense_Mutation	SNP	C	T	7	126	c.1315C>T	c.(1315-1317)CCA>TCA	p.P439S
Pat_41	Post-Resistance	AQP1	358	37	7	30951784	30951784	Missense_Mutation	SNP	G	A	7	161	c.260G>A	c.(259-261)TGC>TAC	p.C87Y
Pat_41	Post-Resistance	PDE1C	5137	37	7	31904613	31904613	Missense_Mutation	SNP	C	T	12	131	c.693G>A	c.(691-693)ATG>ATA	p.M231I
Pat_41	Post-Resistance	FKBP9	11328	37	7	33020054	33020054	Missense_Mutation	SNP	C	T	31	348	c.782C>T	c.(781-783)TCC>TTC	p.S261F
Pat_41	Post-Resistance	EEPD1	80820	37	7	36194114	36194114	Missense_Mutation	SNP	G	A	28	195	c.181G>A	c.(181-183)GCA>ACA	p.A61T
Pat_41	Post-Resistance	EEPD1	80820	37	7	36194759	36194759	Missense_Mutation	SNP	G	A	8	100	c.826G>A	c.(826-828)GCC>ACC	p.A276T
Pat_41	Post-Resistance	ANLN	54443	37	7	36438964	36438964	Missense_Mutation	SNP	C	T	7	157	c.449C>T	c.(448-450)GCA>GTA	p.A150V
Pat_41	Post-Resistance	ANLN	54443	37	7	36450314	36450314	Splice_Site	SNP	G	A	26	401	c.1287_splice	c.e6+1	p.Q429_splice
Pat_41	Post-Resistance	ELMO1	9844	37	7	37252945	37252945	Missense_Mutation	SNP	C	T	10	237	c.949G>A	c.(949-951)GAC>AAC	p.D317N
Pat_41	Post-Resistance	STARD3NL	83930	37	7	38256888	38256888	Missense_Mutation	SNP	G	A	5	131	c.535G>A	c.(535-537)GAA>AAA	p.E179K
Pat_41	Post-Resistance	POU6F2	11281	37	7	39243911	39243911	Missense_Mutation	SNP	C	T	21	126	c.268C>T	c.(268-270)CCA>TCA	p.P90S
Pat_41	Post-Resistance	RALA	5898	37	7	39730128	39730128	Missense_Mutation	SNP	G	A	7	155	c.262G>A	c.(262-264)GGG>AGG	p.G88R
Pat_41	Post-Resistance	C7orf10	79783	37	7	40789033	40789033	Missense_Mutation	SNP	G	A	8	222	c.1090G>A	c.(1090-1092)GTA>ATA	p.V364I
Pat_41	Post-Resistance	C7orf10	79783	37	7	40899963	40899963	Missense_Mutation	SNP	C	T	41	478	c.1202C>T	c.(1201-1203)CCC>CTC	p.P401L
Pat_41	Post-Resistance	GLI3	2737	37	7	42063207	42063207	Missense_Mutation	SNP	C	T	5	77	c.1357G>A	c.(1357-1359)GAA>AAA	p.E453K
Pat_41	Post-Resistance	GLI3	2737	37	7	42065985	42065985	Missense_Mutation	SNP	G	A	4	58	c.1055C>T	c.(1054-1056)TCC>TTC	p.S352F
Pat_41	Post-Resistance	C7orf25	79020	37	7	42949470	42949470	Missense_Mutation	SNP	G	A	7	106	c.1030C>T	c.(1030-1032)CGT>TGT	p.R344C
Pat_41	Post-Resistance	C7orf25	79020	37	7	42950138	42950138	Missense_Mutation	SNP	C	T	17	218	c.362G>A	c.(361-363)GGC>GAC	p.G121D
Pat_41	Post-Resistance	POLD2	5425	37	7	44157597	44157597	Missense_Mutation	SNP	G	A	32	197	c.287C>T	c.(286-288)ACT>ATT	p.T96I
Pat_41	Post-Resistance	TMED4	222068	37	7	44620754	44620754	Missense_Mutation	SNP	G	A	10	149	c.472C>T	c.(472-474)CTC>TTC	p.L158F
Pat_41	Post-Resistance	ZMIZ2	83637	37	7	44806248	44806248	Missense_Mutation	SNP	G	A	4	53	c.2641G>A	c.(2641-2643)GAA>AAA	p.E881K
Pat_41	Post-Resistance	PURB	5814	37	7	44924157	44924157	Missense_Mutation	SNP	G	A	18	233	c.791C>T	c.(790-792)GCC>GTC	p.A264V
Pat_41	Post-Resistance	MYO1G	64005	37	7	45009350	45009350	Missense_Mutation	SNP	G	A	9	246	c.1457C>T	c.(1456-1458)ACC>ATC	p.T486I
Pat_41	Post-Resistance	ADCY1	107	37	7	45614510	45614510	Missense_Mutation	SNP	G	A	4	76	c.368G>A	c.(367-369)GGC>GAC	p.G123D
Pat_41	Post-Resistance	PKD1L1	168507	37	7	47894505	47894505	Missense_Mutation	SNP	C	T	45	513	c.4834G>A	c.(4834-4836)GCA>ACA	p.A1612T
Pat_41	Post-Resistance	ABCA13	154664	37	7	48287983	48287983	Missense_Mutation	SNP	C	T	51	417	c.1807C>T	c.(1807-1809)CCC>TCC	p.P603S
Pat_41	Post-Resistance	GRB10	2887	37	7	50673084	50673084	Missense_Mutation	SNP	G	A	11	124	c.1292C>T	c.(1291-1293)TCC>TTC	p.S431F

Pat_41	Post-Resistance	COBL	23242	37	7	51096946	51096946	Missense_Mutation	SNP	G	A	9	82	c.1847C>T	c.(1846-1848)TCT>TTT	p.S616F
Pat_41	Post-Resistance	EGFR	1956	37	7	55220293	55220293	Missense_Mutation	SNP	C	T	78	153	c.683C>T	c.(682-684)CCC>CTC	p.P228L
Pat_41	Post-Resistance	ZNF479	90827	37	7	57187686	57187686	Missense_Mutation	SNP	G	A	17	181	c.1436C>T	c.(1435-1437)ACC>ATC	p.T479I
Pat_41	Post-Resistance	ZNF716	441234	37	7	57529068	57529068	Missense_Mutation	SNP	T	C	6	242	c.901T>C	c.(901-903)TGT>CGT	p.C301R
Pat_41	Post-Resistance	ZNF679	168417	37	7	63727184	63727184	Nonsense_Mutation	SNP	G	A	5	112	c.1173G>A	c.(1171-1173)TGG>TGA	p.W391*
Pat_41	Post-Resistance	ASL	435	37	7	65552326	65552326	Missense_Mutation	SNP	C	T	9	146	c.608C>T	c.(607-609)GCC>GTC	p.A203V
Pat_41	Post-Resistance	POM121	9883	37	7	72413675	72413675	Missense_Mutation	SNP	G	A	15	36	c.3143G>A	c.(3142-3144)GGC>GAC	p.G1048D
Pat_41	Post-Resistance	NCF1B	654816	37	7	72639965	72639965	Missense_Mutation	SNP	G	A	7	243	c.196G>A	c.(196-198)GGC>AGC	p.G66S
Pat_41	Post-Resistance	BAZ1B	9031	37	7	72892541	72892541	Missense_Mutation	SNP	G	A	12	194	c.1250C>T	c.(1249-1251)TCC>TTC	p.S417F
Pat_41	Post-Resistance	STX1A	6804	37	7	73118149	73118149	Missense_Mutation	SNP	G	A	13	68	c.476C>T	c.(475-477)ACC>ATC	p.T159I
Pat_41	Post-Resistance	CLIP2	7461	37	7	73752811	73752811	Missense_Mutation	SNP	C	T	6	49	c.155C>T	c.(154-156)TCC>TTC	p.S52F
Pat_41	Post-Resistance	GTF2IRD1	9569	37	7	73973250	73973250	Missense_Mutation	SNP	C	T	4	95	c.2212C>T	c.(2212-2214)CCC>TCC	p.P738S
Pat_41	Post-Resistance	TRIM74	378108	37	7	75034352	75034352	Nonsense_Mutation	SNP	G	A	8	93	c.726G>A	c.(724-726)TGG>TGA	p.W242*
Pat_41	Post-Resistance	POR	5447	37	7	75612839	75612839	Missense_Mutation	SNP	C	T	17	118	c.832C>T	c.(832-834)CCC>TCC	p.P278S
Pat_41	Post-Resistance	UPK3B	80761	37	7	76140051	76140051	Missense_Mutation	SNP	C	A	3	24	c.82C>A	c.(82-84)CTG>ATG	p.L28M
Pat_41	Post-Resistance	UPK3B	80761	37	7	76143388	76143388	Missense_Mutation	SNP	G	A	6	184	c.751G>A	c.(751-753)GCG>ACG	p.A251T
Pat_41	Post-Resistance	MAGI2	9863	37	7	77764430	77764430	Missense_Mutation	SNP	C	T	32	220	c.2939G>A	c.(2938-2940)GGC>GAC	p.G980D
Pat_41	Post-Resistance	GNAI1	2770	37	7	79833051	79833051	Missense_Mutation	SNP	C	T	21	216	c.493C>T	c.(493-495)CCA>TCA	p.P165S
Pat_41	Post-Resistance	SEMA3C	10512	37	7	80387731	80387731	Missense_Mutation	SNP	G	A	20	327	c.1559C>T	c.(1558-1560)GCC>GTC	p.A520V
Pat_41	Post-Resistance	PCLO	27445	37	7	82451814	82451814	Missense_Mutation	SNP	G	A	15	519	c.14788C>T	c.(14788-14790)CCA>TCA	p.P4930S
Pat_41	Post-Resistance	PCLO	27445	37	7	82579001	82579001	Missense_Mutation	SNP	C	T	21	230	c.10903G>A	c.(10903-10905)GCC>ACC	p.A3635T
Pat_41	Post-Resistance	SEMA3E	9723	37	7	83014750	83014750	Splice_Site	SNP	C	T	44	434	c.1736_splice	c.e16-1	p.G579_splice
Pat_41	Post-Resistance	DMTF1	9988	37	7	86824069	86824069	Missense_Mutation	SNP	C	T	27	256	c.2098C>T	c.(2098-2100)CCT>TCT	p.P700S
Pat_41	Post-Resistance	C7orf23	79161	37	7	86827279	86827279	Missense_Mutation	SNP	C	T	59	515	c.212G>A	c.(211-213)AGT>AAT	p.S71N
Pat_41	Post-Resistance	C7orf23	79161	37	7	86827362	86827362	Splice_Site	SNP	C	T	21	278	c.130_splice	c.e3-1	p.V44_splice
Pat_41	Post-Resistance	CROT	54677	37	7	87011233	87011233	Missense_Mutation	SNP	C	T	6	138	c.986C>T	c.(985-987)CCT>CTT	p.P329L
Pat_41	Post-Resistance	ABCB1	5243	37	7	87183123	87183123	Missense_Mutation	SNP	G	A	20	332	c.953C>T	c.(952-954)ACC>ATC	p.T318I
Pat_41	Post-Resistance	ABCB1	5243	37	7	87225093	87225093	Missense_Mutation	SNP	C	T	9	245	c.106G>A	c.(106-108)GTA>ATA	p.V36I
Pat_41	Post-Resistance	DBF4	10926	37	7	87514318	87514318	Missense_Mutation	SNP	G	A	11	115	c.244G>A	c.(244-246)GAT>AAT	p.D82N
Pat_41	Post-Resistance	ADAM22	53616	37	7	87704955	87704955	Missense_Mutation	SNP	C	T	11	260	c.338C>T	c.(337-339)TCT>TTT	p.S113F
Pat_41	Post-Resistance	ADAM22	53616	37	7	87785270	87785270	Missense_Mutation	SNP	G	A	8	421	c.1856G>A	c.(1855-1857)GGT>GAT	p.G619D
Pat_41	Post-Resistance	SRI	6717	37	7	87838663	87838663	Missense_Mutation	SNP	C	T	8	215	c.502G>A	c.(502-504)GCT>ACT	p.A168T
Pat_41	Post-Resistance	C7orf63	79846	37	7	89903303	89903303	Missense_Mutation	SNP	C	T	6	76	c.863C>T	c.(862-864)GCT>GTT	p.A288V
Pat_41	Post-Resistance	GTPBP10	85865	37	7	90014364	90014364	Missense_Mutation	SNP	C	T	27	473	c.1060C>T	c.(1060-1062)CTT>TTT	p.L354F
Pat_41	Post-Resistance	CLDN12	9069	37	7	90042445	90042445	Missense_Mutation	SNP	T	A	31	361	c.455T>A	c.(454-456)ATC>AAC	p.I152N
Pat_41	Post-Resistance	AKAP9	10142	37	7	91668009	91668009	Missense_Mutation	SNP	C	T	34	364	c.4615C>T	c.(4615-4617)CCA>TCA	p.P1539S
Pat_41	Post-Resistance	AKAP9	10142	37	7	91674387	91674387	Missense_Mutation	SNP	C	T	14	393	c.5228C>T	c.(5227-5229)GCA>GTA	p.A1743V
Pat_41	Post-Resistance	AKAP9	10142	37	7	91690647	91690647	Missense_Mutation	SNP	C	T	26	305	c.5675C>T	c.(5674-5676)TCC>TTC	p.S1892F
Pat_41	Post-Resistance	AKAP9	10142	37	7	91736646	91736646	Missense_Mutation	SNP	G	A	12	344	c.11456G>A	c.(11455-11457)GGG>GAG	p.G3819E
Pat_41	Post-Resistance	PEX1	5189	37	7	92147353	92147353	Missense_Mutation	SNP	G	A	8	95	c.476C>T	c.(475-477)GCA>GTA	p.A159V
Pat_41	Post-Resistance	SAMD9	54809	37	7	92731132	92731132	Nonsense_Mutation	SNP	G	A	22	444	c.4279C>T	c.(4279-4281)CAG>TAG	p.Q1427*
Pat_41	Post-Resistance	SAMD9	54809	37	7	92733004	92733004	Missense_Mutation	SNP	C	T	30	247	c.2407G>A	c.(2407-2409)GAA>AAA	p.E803K
Pat_41	Post-Resistance	SAMD9L	219285	37	7	92762127	92762127	Missense_Mutation	SNP	G	A	6	321	c.3158C>T	c.(3157-3159)ACT>ATT	p.T1053I
Pat_41	Post-Resistance	CCDC132	55610	37	7	92935281	92935281	Missense_Mutation	SNP	G	A	32	443	c.1594G>A	c.(1594-1596)GAT>AAT	p.D532N
Pat_41	Post-Resistance	CCDC132	55610	37	7	92940543	92940543	Missense_Mutation	SNP	C	T	64	568	c.1814C>T	c.(1813-1815)CCT>CTT	p.P605L
Pat_41	Post-Resistance	CALCR	799	37	7	93090240	93090240	Missense_Mutation	SNP	C	T	15	300	c.643G>A	c.(643-645)GTA>ATA	p.V215I
Pat_41	Post-Resistance	BET1	10282	37	7	93628543	93628543	Missense_Mutation	SNP	C	T	21	179	c.83G>A	c.(82-84)TGT>TAT	p.C28Y

Pat_41	Post-Resistance	COL1A2	1278	37	7	94037541	94037541	Missense_Mutation	SNP	G	A	4	119	c.686G>A	c.(685-687)GGC>GAC	p.G229D
Pat_41	Post-Resistance	PON1	5444	37	7	94944760	94944760	Missense_Mutation	SNP	G	A	11	193	c.244C>T	c.(244-246)CCT>TCT	p.P82S
Pat_41	Post-Resistance	ASB4	51666	37	7	95115471	95115471	Splice_Site	SNP	G	A	21	272	c.187_splice	c.e1+1	p.G63_splice
Pat_41	Post-Resistance	LMTK2	22853	37	7	97822521	97822521	Missense_Mutation	SNP	G	A	21	307	c.2744G>A	c.(2743-2745)GGG>GAG	p.G915E
Pat_41	Post-Resistance	LMTK2	22853	37	7	97822571	97822571	Missense_Mutation	SNP	G	A	19	309	c.2794G>A	c.(2794-2796)GAA>AAA	p.E932K
Pat_41	Post-Resistance	TECPR1	25851	37	7	97851059	97851059	Missense_Mutation	SNP	C	T	9	152	c.3071G>A	c.(3070-3072)TGC>TAC	p.C1024Y
Pat_41	Post-Resistance	TECPR1	25851	37	7	97862970	97862970	Missense_Mutation	SNP	C	T	5	161	c.1435G>A	c.(1435-1437)GCC>ACC	p.A479T
Pat_41	Post-Resistance	TRRAP	8295	37	7	98515090	98515090	Missense_Mutation	SNP	G	A	10	165	c.2410G>A	c.(2410-2412)GAC>AAC	p.D804N
Pat_41	Post-Resistance	TRRAP	8295	37	7	98527726	98527726	Missense_Mutation	SNP	C	T	5	206	c.3290C>T	c.(3289-3291)GCT>GTT	p.A1097V
Pat_41	Post-Resistance	TRRAP	8295	37	7	98564710	98564710	Missense_Mutation	SNP	C	T	10	179	c.7202C>T	c.(7201-7203)ACT>ATT	p.T2401I
Pat_41	Post-Resistance	TRRAP	8295	37	7	98606051	98606051	Missense_Mutation	SNP	C	T	15	564	c.10763C>T	c.(10762-10764)CCC>CTC	p.P3588L
Pat_41	Post-Resistance	SMURF1	57154	37	7	98643330	98643330	Missense_Mutation	SNP	C	T	19	239	c.1325G>A	c.(1324-1326)GGT>GAT	p.G442D
Pat_41	Post-Resistance	SMURF1	57154	37	7	98645402	98645402	Missense_Mutation	SNP	C	T	11	368	c.1135G>A	c.(1135-1137)GTC>ATC	p.V379I
Pat_41	Post-Resistance	SMURF1	57154	37	7	98654839	98654839	Missense_Mutation	SNP	C	T	30	684	c.392G>A	c.(391-393)GGC>GAC	p.G131D
Pat_41	Post-Resistance	ARPC1A	10552	37	7	98946500	98946500	Missense_Mutation	SNP	C	T	27	384	c.418C>T	c.(418-420)CCG>TCG	p.P140S
Pat_41	Post-Resistance	ARPC1A	10552	37	7	98956034	98956034	Missense_Mutation	SNP	C	T	7	274	c.785C>T	c.(784-786)GCT>GTT	p.A262V
Pat_41	Post-Resistance	PTCD1	26024	37	7	99030947	99030947	Missense_Mutation	SNP	C	T	37	541	c.548G>A	c.(547-549)TGC>TAC	p.C183Y
Pat_41	Post-Resistance	ZNF789	285989	37	7	99077329	99077329	Missense_Mutation	SNP	G	A	12	235	c.70G>A	c.(70-72)GAG>AAG	p.E24K
Pat_41	Post-Resistance	CYP3A5	1577	37	7	99247830	99247830	Missense_Mutation	SNP	C	T	54	481	c.1279G>A	c.(1279-1281)GAT>AAT	p.D427N
Pat_41	Post-Resistance	CYP3A5	1577	37	7	99261613	99261613	Missense_Mutation	SNP	C	T	19	166	c.776G>A	c.(775-777)AGT>AAT	p.S259N
Pat_41	Post-Resistance	CYP3A7	1551	37	7	99314831	99314831	Missense_Mutation	SNP	C	T	12	386	c.490G>A	c.(490-492)GCA>ACA	p.A164T
Pat_41	Post-Resistance	CYP3A43	64816	37	7	99445199	99445199	Missense_Mutation	SNP	C	T	11	237	c.407C>T	c.(406-408)GCT>GTT	p.A136V
Pat_41	Post-Resistance	CYP3A43	64816	37	7	99447177	99447177	Missense_Mutation	SNP	G	A	6	275	c.530G>A	c.(529-531)GGG>GAG	p.G177E
Pat_41	Post-Resistance	GJC3	349149	37	7	99527119	99527119	Missense_Mutation	SNP	C	T	6	209	c.125G>A	c.(124-126)GGA>GAA	p.G42E
Pat_41	Post-Resistance	GJC3	349149	37	7	99527156	99527156	Missense_Mutation	SNP	C	T	13	91	c.88G>A	c.(88-90)GGA>AGA	p.G30R
Pat_41	Post-Resistance	AZGP1	563	37	7	99569368	99569368	Splice_Site	SNP	C	T	11	332	c.337_splice	c.e2+1	p.G113_splice
Pat_41	Post-Resistance	ZKSCAN1	7586	37	7	99631096	99631096	Missense_Mutation	SNP	C	T	4	43	c.968C>T	c.(967-969)ACC>ATC	p.T323I
Pat_41	Post-Resistance	MCM7	4176	37	7	99696317	99696317	Missense_Mutation	SNP	G	A	15	167	c.604C>T	c.(604-606)CCT>TCT	p.P202S
Pat_41	Post-Resistance	AP4M1	9179	37	7	99699520	99699520	Missense_Mutation	SNP	G	A	11	152	c.76G>A	c.(76-78)GGC>AGC	p.G26S
Pat_41	Post-Resistance	AP4M1	9179	37	7	99701032	99701032	Missense_Mutation	SNP	G	A	10	219	c.352G>A	c.(352-354)GAC>AAC	p.D118N
Pat_41	Post-Resistance	GPC2	221914	37	7	99773257	99773257	Missense_Mutation	SNP	C	T	3	58	c.586G>A	c.(586-588)GCC>ACC	p.A196T
Pat_41	Post-Resistance	STAG3	10734	37	7	99798462	99798462	Missense_Mutation	SNP	C	T	12	208	c.1931C>T	c.(1930-1932)GCT>GTT	p.A644V
Pat_41	Post-Resistance	STAG3	10734	37	7	99808640	99808640	Missense_Mutation	SNP	C	T	5	177	c.3245C>T	c.(3244-3246)GCC>GTC	p.A1082V
Pat_41	Post-Resistance	MEPCE	56257	37	7	100028425	100028425	Missense_Mutation	SNP	C	T	28	738	c.784C>T	c.(784-786)CGG>TGG	p.R262W
Pat_41	Post-Resistance	TSC22D4	81628	37	7	100074905	100074905	Missense_Mutation	SNP	C	T	10	207	c.757G>A	c.(757-759)GGG>AGG	p.G253R
Pat_41	Post-Resistance	AGFG2	3268	37	7	100153284	100153284	Missense_Mutation	SNP	G	A	6	224	c.803G>A	c.(802-804)GGC>GAC	p.G268D
Pat_41	Post-Resistance	LRCH4	4034	37	7	100180040	100180040	Missense_Mutation	SNP	C	T	9	112	c.263G>A	c.(262-264)TGC>TAC	p.C88Y
Pat_41	Post-Resistance	TFR2	7036	37	7	100230916	100230916	Missense_Mutation	SNP	C	T	10	123	c.662G>A	c.(661-663)GGA>GAA	p.G221E
Pat_41	Post-Resistance	GIGYF1	64599	37	7	100284410	100284410	Missense_Mutation	SNP	G	A	5	41	c.556C>T	c.(556-558)CCA>TCA	p.P186S
Pat_41	Post-Resistance	ZAN	7455	37	7	100350706	100350706	Missense_Mutation	SNP	C	T	13	371	c.2978C>T	c.(2977-2979)CCC>CTC	p.P993L
Pat_41	Post-Resistance	SLC12A9	56996	37	7	100457825	100457825	Missense_Mutation	SNP	G	A	11	61	c.1189G>A	c.(1189-1191)GCT>ACT	p.A397T
Pat_41	Post-Resistance	MUC17	140453	37	7	100679202	100679202	Missense_Mutation	SNP	C	T	30	605	c.4505C>T	c.(4504-4506)ACC>ATC	p.T1502I
Pat_41	Post-Resistance	MUC17	140453	37	7	100680999	100680999	Missense_Mutation	SNP	G	A	30	712	c.6302G>A	c.(6301-6303)AGT>AAT	p.S2101N
Pat_41	Post-Resistance	MUC17	140453	37	7	100682754	100682754	Missense_Mutation	SNP	C	T	13	806	c.8057C>T	c.(8056-8058)ACT>ATT	p.T2686I
Pat_41	Post-Resistance	MUC17	140453	37	7	100683071	100683071	Missense_Mutation	SNP	C	T	27	750	c.8374C>T	c.(8374-8376)CCT>TCT	p.P2792S
Pat_41	Post-Resistance	MUC17	140453	37	7	100683423	100683423	Missense_Mutation	SNP	C	T	27	764	c.8726C>T	c.(8725-8727)TCT>TTT	p.S2909F
Pat_41	Post-Resistance	MUC17	140453	37	7	100695189	100695189	Missense_Mutation	SNP	C	T	16	396	c.13049C>T	c.(13048-13050)TCC>TTC	p.S4350F

Pat_41	Post-Resistance	TRIM56	81844	37	7	100732323	100732323	Missense_Mutation	SNP	G	A	10	254	c.1730G>A	c.(1729-1731)GGC>GAC	p.G577D
Pat_41	Post-Resistance	PLOD3	8985	37	7	100855182	100855182	Missense_Mutation	SNP	C	T	4	46	c.1177G>A	c.(1177-1179)GCC>ACC	p.A393T
Pat_41	Post-Resistance	ZNHIT1	10467	37	7	100866973	100866973	Missense_Mutation	SNP	G	A	7	139	c.293G>A	c.(292-294)GGC>GAC	p.G98D
Pat_41	Post-Resistance	CUX1	1523	37	7	101843453	101843453	Splice_Site	SNP	G	A	5	78	c.2062_splice	c.e17+1	p.A688_splice
Pat_41	Post-Resistance	LRWD1	222229	37	7	102106607	102106607	Missense_Mutation	SNP	G	A	9	214	c.322G>A	c.(322-324)GAC>AAC	p.D108N
Pat_41	Post-Resistance	FBXL13	222235	37	7	102553582	102553582	Missense_Mutation	SNP	C	T	6	197	c.959G>A	c.(958-960)GGG>GAG	p.G320E
Pat_41	Post-Resistance	DPY19L2P2	349152	37	7	102825941	102825941	Missense_Mutation	SNP	C	T	42	264	c.1054G>A	c.(1054-1056)GCT>ACT	p.A352T
Pat_41	Post-Resistance	PMPCB	9512	37	7	102939942	102939942	Missense_Mutation	SNP	G	A	15	328	c.293G>A	c.(292-294)GGA>GAA	p.G98E
Pat_41	Post-Resistance	SLC26A5	375611	37	7	103018221	103018221	Missense_Mutation	SNP	G	A	44	283	c.1811C>T	c.(1810-1812)GCT>GTT	p.A604V
Pat_41	Post-Resistance	RELN	5649	37	7	103393659	103393659	Missense_Mutation	SNP	G	A	8	335	c.547C>T	c.(547-549)CCA>TCA	p.P183S
Pat_41	Post-Resistance	ORC5L	5001	37	7	103807252	103807252	Missense_Mutation	SNP	G	A	10	277	c.958C>T	c.(958-960)CCA>TCA	p.P320S
Pat_41	Post-Resistance	LHFPL3	375612	37	7	103969607	103969607	Missense_Mutation	SNP	C	T	8	134	c.380C>T	c.(379-381)ACC>ATC	p.T127I
Pat_41	Post-Resistance	MLL5	55904	37	7	104742023	104742023	Missense_Mutation	SNP	C	T	7	163	c.1874C>T	c.(1873-1875)GCT>GTT	p.A625V
Pat_41	Post-Resistance	MLL5	55904	37	7	104753127	104753127	Nonsense_Mutation	SNP	C	T	15	589	c.4924C>T	c.(4924-4926)CAA>TAA	p.Q1642*
Pat_41	Post-Resistance	PUS7	54517	37	7	105143011	105143011	Missense_Mutation	SNP	C	T	7	107	c.586G>A	c.(586-588)GTT>ATT	p.V196I
Pat_41	Post-Resistance	PUS7	54517	37	7	105146464	105146464	Missense_Mutation	SNP	C	T	9	278	c.523G>A	c.(523-525)GAA>AAA	p.E175K
Pat_41	Post-Resistance	SYPL1	6856	37	7	105752618	105752618	Missense_Mutation	SNP	C	T	5	101	c.91G>A	c.(91-93)GAG>AAG	p.E31K
Pat_41	Post-Resistance	PIK3CG	5294	37	7	106508716	106508716	Missense_Mutation	SNP	C	T	40	449	c.710C>T	c.(709-711)CCC>CTC	p.P237L
Pat_41	Post-Resistance	PIK3CG	5294	37	7	106509321	106509321	Missense_Mutation	SNP	C	T	5	207	c.1315C>T	c.(1315-1317)CCA>TCA	p.P439S
Pat_41	Post-Resistance	COG5	10466	37	7	107188745	107188745	Missense_Mutation	SNP	C	T	23	734	c.418G>A	c.(418-420)GCT>ACT	p.A140T
Pat_41	Post-Resistance	DUS4L	11062	37	7	107215727	107215727	Missense_Mutation	SNP	C	T	6	203	c.451C>T	c.(451-453)CCT>TCT	p.P151S
Pat_41	Post-Resistance	SLC26A4	5172	37	7	107314726	107314726	Missense_Mutation	SNP	C	T	16	462	c.533C>T	c.(532-534)ACT>ATT	p.T178I
Pat_41	Post-Resistance	SLC26A4	5172	37	7	107315403	107315403	Missense_Mutation	SNP	G	A	47	443	c.614G>A	c.(613-615)GGC>GAC	p.G205D
Pat_41	Post-Resistance	CBLL1	79872	37	7	107398769	107398769	Missense_Mutation	SNP	C	T	25	623	c.622C>T	c.(622-624)CCT>TCT	p.P208S
Pat_41	Post-Resistance	CBLL1	79872	37	7	107399240	107399240	Missense_Mutation	SNP	C	T	21	774	c.1093C>T	c.(1093-1095)CCT>TCT	p.P365S
Pat_41	Post-Resistance	SLC26A3	1811	37	7	107423462	107423462	Missense_Mutation	SNP	C	T	81	491	c.1196G>A	c.(1195-1197)AGA>AAA	p.R399K
Pat_41	Post-Resistance	SLC26A3	1811	37	7	107432319	107432319	Missense_Mutation	SNP	G	A	25	390	c.338C>T	c.(337-339)GCC>GTC	p.A113V
Pat_41	Post-Resistance	LAMB1	3912	37	7	107615483	107615483	Missense_Mutation	SNP	C	T	22	277	c.1430G>A	c.(1429-1431)GGT>GAT	p.G477D
Pat_41	Post-Resistance	LAMB4	22798	37	7	107696131	107696131	Missense_Mutation	SNP	G	A	6	93	c.3701C>T	c.(3700-3702)CCT>CTT	p.P1234L
Pat_41	Post-Resistance	THAP5	168451	37	7	108205072	108205072	Missense_Mutation	SNP	G	A	34	353	c.751C>T	c.(751-753)CCA>TCA	p.P251S
Pat_41	Post-Resistance	DNAJB9	4189	37	7	108213565	108213565	Missense_Mutation	SNP	G	A	15	269	c.440G>A	c.(439-441)GGT>GAT	p.G147D
Pat_41	Post-Resistance	LRRN3	54674	37	7	110764299	110764299	Missense_Mutation	SNP	G	A	6	160	c.1471G>A	c.(1471-1473)GGG>AGG	p.G491R
Pat_41	Post-Resistance	DOCK4	9732	37	7	111379221	111379221	Missense_Mutation	SNP	G	A	18	295	c.5174C>T	c.(5173-5175)GCC>GTC	p.A1725V
Pat_41	Post-Resistance	DOCK4	9732	37	7	111381153	111381153	Missense_Mutation	SNP	C	T	8	461	c.5010G>A	c.(5008-5010)ATG>ATA	p.M1670I
Pat_41	Post-Resistance	DOCK4	9732	37	7	111484938	111484938	Missense_Mutation	SNP	C	T	33	206	c.2617G>A	c.(2617-2619)GAG>AAG	p.E873K
Pat_41	Post-Resistance	DOCK4	9732	37	7	111617186	111617186	Splice_Site	SNP	C	T	8	124	c.701_splice	c.e8+1	p.S234_splice
Pat_41	Post-Resistance	IFRD1	3475	37	7	112102181	112102181	Nonsense_Mutation	SNP	G	A	7	443	c.744G>A	c.(742-744)TGG>TGA	p.W248*
Pat_41	Post-Resistance	TFEC	22797	37	7	115594691	115594691	Missense_Mutation	SNP	C	T	12	112	c.388G>A	c.(388-390)GAC>AAC	p.D130N
Pat_41	Post-Resistance	WNT2	7472	37	7	116955306	116955306	Missense_Mutation	SNP	G	A	10	204	c.407C>T	c.(406-408)TCC>TTC	p.S136F
Pat_41	Post-Resistance	CFTR	1080	37	7	117254688	117254688	Missense_Mutation	SNP	G	A	14	461	c.3389G>A	c.(3388-3390)GGT>GAT	p.G1130D
Pat_41	Post-Resistance	CTTNBP2	83992	37	7	117432428	117432428	Missense_Mutation	SNP	G	T	4	97	c.822C>A	c.(820-822)GAC>GAA	p.D274E
Pat_41	Post-Resistance	ANKRD7	56311	37	7	117876878	117876878	Missense_Mutation	SNP	C	T	30	469	c.610C>T	c.(610-612)CCA>TCA	p.P204S
Pat_41	Post-Resistance	KCND2	3751	37	7	119914895	119914895	Missense_Mutation	SNP	C	T	74	476	c.209C>T	c.(208-210)TCT>TTT	p.S70F
Pat_41	Post-Resistance	KCND2	3751	37	7	119915042	119915042	Missense_Mutation	SNP	T	C	31	580	c.356T>C	c.(355-357)CTG>CCG	p.L119P
Pat_41	Post-Resistance	ING3	54556	37	7	120608117	120608117	Missense_Mutation	SNP	C	T	5	124	c.686C>T	c.(685-687)GCT>GTT	p.A229V
Pat_41	Post-Resistance	C7orf58	79974	37	7	120935675	120935675	Missense_Mutation	SNP	G	A	14	350	c.3050G>A	c.(3049-3051)AGC>AAC	p.S1017N
Pat_41	Post-Resistance	PTPRZ1	5803	37	7	121653814	121653814	Missense_Mutation	SNP	G	A	48	260	c.4714G>A	c.(4714-4716)GAC>AAC	p.D1572N

Pat_41	Post-Resistance	PTPRZ1	5803	37	7	121653847	121653847	Missense_Mutation	SNP	G	A	31	542	c.4747G>A	c.(4747-4749)GCA>ACA	p.A1583T
Pat_41	Post-Resistance	PTPRZ1	5803	37	7	121691519	121691519	Missense_Mutation	SNP	C	T	19	391	c.6122C>T	c.(6121-6123)TCT>TTT	p.S2041F
Pat_41	Post-Resistance	AASS	10157	37	7	121726122	121726122	Missense_Mutation	SNP	C	T	9	437	c.2128G>A	c.(2128-2130)GAG>AAG	p.E710K
Pat_41	Post-Resistance	FEZF1	389549	37	7	121942272	121942272	Missense_Mutation	SNP	G	A	34	269	c.1207C>T	c.(1207-1209)CCC>TCC	p.P403S
Pat_41	Post-Resistance	TAS2R16	50833	37	7	122635189	122635189	Missense_Mutation	SNP	G	A	48	336	c.500C>T	c.(499-501)ACT>ATT	p.T167I
Pat_41	Post-Resistance	IQUB	154865	37	7	123097539	123097539	Missense_Mutation	SNP	C	T	28	776	c.2089G>A	c.(2089-2091)GTC>ATC	p.V697I
Pat_41	Post-Resistance	IQUB	154865	37	7	123142718	123142718	Missense_Mutation	SNP	G	A	5	205	c.956C>T	c.(955-957)ACT>ATT	p.T319I
Pat_41	Post-Resistance	LMOD2	442721	37	7	123302785	123302785	Missense_Mutation	SNP	G	A	10	266	c.1145G>A	c.(1144-1146)AGA>AAA	p.R382K
Pat_41	Post-Resistance	SPAM1	6677	37	7	123593991	123593991	Missense_Mutation	SNP	C	T	9	345	c.367C>T	c.(367-369)CAT>TAT	p.H123Y
Pat_41	Post-Resistance	SPAM1	6677	37	7	123595115	123595115	Missense_Mutation	SNP	G	A	57	455	c.1019G>A	c.(1018-1020)GGA>GAA	p.G340E
Pat_41	Post-Resistance	POT1	25913	37	7	124503616	124503616	Missense_Mutation	SNP	C	T	8	163	c.334G>A	c.(334-336)GCC>ACC	p.A112T
Pat_41	Post-Resistance	GRM8	2918	37	7	126882871	126882871	Missense_Mutation	SNP	C	T	13	217	c.388G>A	c.(388-390)GAT>AAT	p.D130N
Pat_41	Post-Resistance	ZNF800	168850	37	7	127013448	127013448	Missense_Mutation	SNP	G	A	4	89	c.1942C>T	c.(1942-1944)CCT>TCT	p.P648S
Pat_41	Post-Resistance	PAX4	5078	37	7	127253864	127253864	Missense_Mutation	SNP	C	T	20	166	c.484G>A	c.(484-486)GGC>AGC	p.G162S
Pat_41	Post-Resistance	SND1	27044	37	7	127569307	127569307	Missense_Mutation	SNP	G	A	44	299	c.1594G>A	c.(1594-1596)GAA>AAA	p.E532K
Pat_41	Post-Resistance	RBM28	55131	37	7	127955018	127955018	Missense_Mutation	SNP	G	A	8	251	c.1844C>T	c.(1843-1845)CCT>CTT	p.P615L
Pat_41	Post-Resistance	IMPDH1	3614	37	7	128040569	128040569	Missense_Mutation	SNP	C	T	6	86	c.349G>A	c.(349-351)GAC>AAC	p.D117N
Pat_41	Post-Resistance	CALU	813	37	7	128398946	128398946	Missense_Mutation	SNP	G	A	8	526	c.437G>A	c.(436-438)GGA>GAA	p.G146E
Pat_41	Post-Resistance	OPN1SW	611	37	7	128415045	128415045	Nonsense_Mutation	SNP	C	T	14	193	c.516G>A	c.(514-516)TGG>TGA	p.W172*
Pat_41	Post-Resistance	FLNC	2318	37	7	128480646	128480646	Missense_Mutation	SNP	G	A	24	450	c.1594G>A	c.(1594-1596)GTG>ATG	p.V532M
Pat_41	Post-Resistance	FLNC	2318	37	7	128481563	128481563	Missense_Mutation	SNP	C	T	17	397	c.2063C>T	c.(2062-2064)GCT>GTT	p.A688V
Pat_41	Post-Resistance	FLNC	2318	37	7	128483512	128483512	Missense_Mutation	SNP	G	A	6	115	c.2692G>A	c.(2692-2694)GGC>AGC	p.G898S
Pat_41	Post-Resistance	FLNC	2318	37	7	128496677	128496677	Missense_Mutation	SNP	G	A	5	106	c.7357G>A	c.(7357-7359)GAG>AAG	p.E2453K
Pat_41	Post-Resistance	IRF5	3663	37	7	128586043	128586043	Missense_Mutation	SNP	C	T	5	160	c.340C>T	c.(340-342)CCC>TCC	p.P114S
Pat_41	Post-Resistance	TNPO3	23534	37	7	128694821	128694821	Missense_Mutation	SNP	C	T	7	93	c.4G>A	c.(4-6)GAA>AAA	p.E2K
Pat_41	Post-Resistance	SMO	6608	37	7	128851543	128851543	Missense_Mutation	SNP	C	T	9	221	c.1868C>T	c.(1867-1869)ACC>ATC	p.T623I
Pat_41	Post-Resistance	AHCYL2	23382	37	7	129066405	129066405	Splice_Site	SNP	G	A	8	89	c.1829_splice	c.e16+1	p.R610_splice
Pat_41	Post-Resistance	ZC3HC1	51530	37	7	129658530	129658530	Nonsense_Mutation	SNP	G	A	53	380	c.1483C>T	c.(1483-1485)CAG>TAG	p.Q495*
Pat_41	Post-Resistance	KLHDC10	23008	37	7	129769366	129769366	Missense_Mutation	SNP	C	T	16	237	c.1069C>T	c.(1069-1071)CCA>TCA	p.P357S
Pat_41	Post-Resistance	TMEM209	84928	37	7	129841722	129841722	Missense_Mutation	SNP	C	T	4	136	c.541G>A	c.(541-543)GTG>ATG	p.V181M
Pat_41	Post-Resistance	CPA4	51200	37	7	129944382	129944382	Missense_Mutation	SNP	G	A	8	448	c.449G>A	c.(448-450)GGA>GAA	p.G150E
Pat_41	Post-Resistance	CPA1	1357	37	7	130023625	130023625	Missense_Mutation	SNP	C	T	6	296	c.686C>T	c.(685-687)ACG>ATG	p.T229M
Pat_41	Post-Resistance	PLXNA4	91584	37	7	132193067	132193067	Missense_Mutation	SNP	G	A	11	56	c.386C>T	c.(385-387)GCC>GTC	p.A129V
Pat_41	Post-Resistance	AKR1B10	57016	37	7	134225822	134225822	Missense_Mutation	SNP	C	T	9	106	c.932C>T	c.(931-933)CCC>CTC	p.P311L
Pat_41	Post-Resistance	AKR1B15	441282	37	7	134256425	134256425	Missense_Mutation	SNP	G	A	12	362	c.505G>A	c.(505-507)GCC>ACC	p.A169T
Pat_41	Post-Resistance	BPGM	669	37	7	134346389	134346389	Nonsense_Mutation	SNP	C	T	6	168	c.130C>T	c.(130-132)CAA>TAA	p.Q44*
Pat_41	Post-Resistance	CNOT4	4850	37	7	135047690	135047690	Missense_Mutation	SNP	G	A	30	723	c.2089C>T	c.(2089-2091)CCC>TCC	p.P697S
Pat_41	Post-Resistance	SLC13A4	26266	37	7	135368912	135368912	Missense_Mutation	SNP	G	A	21	157	c.1703C>T	c.(1702-1704)GCC>GTC	p.A568V
Pat_41	Post-Resistance	LUZP6	767558	37	7	135614697	135614697	Missense_Mutation	SNP	C	T	73	556	c.334G>A	c.(334-336)GCA>ACA	p.A112T
Pat_41	Post-Resistance	DGKI	9162	37	7	137271908	137271908	Missense_Mutation	SNP	G	A	7	279	c.1360C>T	c.(1360-1362)CCT>TCT	p.P454S
Pat_41	Post-Resistance	AKR1D1	6718	37	7	137791435	137791435	Missense_Mutation	SNP	C	T	19	357	c.661C>T	c.(661-663)CCT>TCT	p.P221S
Pat_41	Post-Resistance	ATP6V0A4	50617	37	7	138432246	138432246	Missense_Mutation	SNP	C	T	5	112	c.1244G>A	c.(1243-1245)GGA>GAA	p.G415E
Pat_41	Post-Resistance	ATP6V0A4	50617	37	7	138437504	138437504	Missense_Mutation	SNP	C	T	10	219	c.895G>A	c.(895-897)GTG>ATG	p.V299M
Pat_41	Post-Resistance	KIAA1549	57670	37	7	138603546	138603546	Missense_Mutation	SNP	C	T	4	56	c.826G>A	c.(826-828)GGT>AGT	p.G276S
Pat_41	Post-Resistance	ZC3HAV1	56829	37	7	138768753	138768753	Missense_Mutation	SNP	C	T	6	131	c.470G>A	c.(469-471)GGT>GAT	p.G157D
Pat_41	Post-Resistance	UBN2	254048	37	7	138969256	138969256	Missense_Mutation	SNP	C	T	10	258	c.3605C>T	c.(3604-3606)CCA>CTA	p.P1202L
Pat_41	Post-Resistance	LUC7L2	51631	37	7	139030283	139030283	Missense_Mutation	SNP	C	T	11	176	c.175C>T	c.(175-177)CTT>TTT	p.L59F

Pat_41	Post-Resistance	LUC7L2	51631	37	7	139102364	139102364	Missense_Mutation	SNP	G	A	12	489	c.890G>A	c.(889-891)CGG>CAG	p.R297Q
Pat_41	Post-Resistance	JHDM1D	80853	37	7	139796441	139796441	Missense_Mutation	SNP	C	T	23	339	c.2288G>A	c.(2287-2289)AGA>AAA	p.R763K
Pat_41	Post-Resistance	JHDM1D	80853	37	7	139810984	139810984	Missense_Mutation	SNP	G	A	7	116	c.1339C>T	c.(1339-1341)CTT>TTT	p.L447F
Pat_41	Post-Resistance	BRAF	673	37	7	140439683	140439683	Missense_Mutation	SNP	G	A	5	95	c.2056C>T	c.(2056-2058)CCA>TCA	p.P686S
Pat_41	Post-Resistance	BRAF	673	37	7	140453136	140453136	Missense_Mutation	SNP	A	T	260	18	c.1799T>A	c.(1798-1800)GTG>GAG	p.V600E
Pat_41	Post-Resistance	BRAF	673	37	7	140476715	140476715	Missense_Mutation	SNP	A	G	11	373	c.1691T>C	c.(1690-1692)ATG>ACG	p.M564T
Pat_41	Post-Resistance	MRPS33	51650	37	7	140710402	140710402	Missense_Mutation	SNP	A	G	22	633	c.32T>C	c.(31-33)ATG>ACG	p.M11T
Pat_41	Post-Resistance	WEE2	494551	37	7	141414144	141414144	Missense_Mutation	SNP	C	T	6	96	c.478C>T	c.(478-480)CCA>TCA	p.P160S
Pat_41	Post-Resistance	WEE2	494551	37	7	141422958	141422958	Missense_Mutation	SNP	C	T	9	339	c.905C>T	c.(904-906)TCT>TTT	p.S302F
Pat_41	Post-Resistance	WEE2	494551	37	7	141427132	141427132	Missense_Mutation	SNP	G	A	37	440	c.1421G>A	c.(1420-1422)AGA>AAA	p.R474K
Pat_41	Post-Resistance	TAS2R4	50832	37	7	141478958	141478958	Missense_Mutation	SNP	G	A	7	121	c.670G>A	c.(670-672)GCT>ACT	p.A224T
Pat_41	Post-Resistance	PRSS37	136242	37	7	141540827	141540827	Missense_Mutation	SNP	C	T	62	432	c.23G>A	c.(22-24)GGT>GAT	p.G8D
Pat_41	Post-Resistance	MGAM	8972	37	7	141805680	141805680	Missense_Mutation	SNP	A	G	7	382	c.5563A>G	c.(5563-5565)AGC>GGC	p.S1855G
Pat_41	Post-Resistance	TRY6	154754	37	7	142480022	142480022	Missense_Mutation	SNP	C	T	36	570	c.154C>T	c.(154-156)CTC>TTC	p.L52F
Pat_41	Post-Resistance	TRY6	154754	37	7	142481270	142481270	Missense_Mutation	SNP	C	T	30	324	c.344C>T	c.(343-345)ACA>ATA	p.T115I
Pat_41	Post-Resistance	EPHB6	2051	37	7	142568053	142568053	Nonsense_Mutation	SNP	G	A	9	408	c.2694G>A	c.(2692-2694)TGG>TGA	p.W898*
Pat_41	Post-Resistance	TRPV6	55503	37	7	142573566	142573566	Missense_Mutation	SNP	G	A	21	220	c.854C>T	c.(853-855)TCC>TTC	p.S285F
Pat_41	Post-Resistance	C7orf34	135927	37	7	142636707	142636707	Missense_Mutation	SNP	G	A	5	95	c.64G>A	c.(64-66)GTG>ATG	p.V22M
Pat_41	Post-Resistance	OR6V1	346517	37	7	142749823	142749823	Missense_Mutation	SNP	G	A	10	215	c.386G>A	c.(385-387)CGC>CAC	p.R129H
Pat_41	Post-Resistance	OR6V1	346517	37	7	142750170	142750170	Missense_Mutation	SNP	C	G	36	257	c.733C>G	c.(733-735)CTG>GTG	p.L245V
Pat_41	Post-Resistance	TAS2R39	259285	37	7	142880944	142880944	Missense_Mutation	SNP	C	T	5	239	c.433C>T	c.(433-435)CCC>TCC	p.P145S
Pat_41	Post-Resistance	TAS2R40	259286	37	7	142920027	142920027	Missense_Mutation	SNP	G	A	16	361	c.856G>A	c.(856-858)GCT>ACT	p.A286T
Pat_41	Post-Resistance	GSTK1	373156	37	7	142965883	142965883	Missense_Mutation	SNP	G	A	11	169	c.634G>A	c.(634-636)GAG>AAG	p.E212K
Pat_41	Post-Resistance	CLCN1	1180	37	7	143036392	143036392	Missense_Mutation	SNP	G	A	23	407	c.1448G>A	c.(1447-1449)GGC>GAC	p.G483D
Pat_41	Post-Resistance	FAM131B	9715	37	7	143056055	143056055	Missense_Mutation	SNP	C	T	7	140	c.247G>A	c.(247-249)GCC>ACC	p.A83T
Pat_41	Post-Resistance	ZYX	7791	37	7	143085929	143085929	Missense_Mutation	SNP	G	A	8	220	c.1384G>A	c.(1384-1386)GCC>ACC	p.A462T
Pat_41	Post-Resistance	FAM115C	285966	37	7	143421678	143421678	Missense_Mutation	SNP	C	T	4	23	c.2393C>T	c.(2392-2394)GCC>GTC	p.A798V
Pat_41	Post-Resistance	FAM115A	9747	37	7	143573641	143573641	Missense_Mutation	SNP	G	A	9	155	c.61C>T	c.(61-63)CCC>TCC	p.P21S
Pat_41	Post-Resistance	OR2F2	135948	37	7	143632797	143632797	Missense_Mutation	SNP	G	A	8	192	c.472G>A	c.(472-474)GTG>ATG	p.V158M
Pat_41	Post-Resistance	OR2F1	26211	37	7	143657961	143657961	Missense_Mutation	SNP	G	A	15	214	c.898G>A	c.(898-900)GCC>ACC	p.A300T
Pat_41	Post-Resistance	ARHGEF5	7984	37	7	144075960	144075960	Splice_Site	SNP	G	A	14	347	c.4636_splice	c.e14+1	.G1546_splice
Pat_41	Post-Resistance	CUL1	8454	37	7	148427162	148427162	Translation_Start_Site	SNP	C	A	16	423	c.-52C>A	.(-54--50)AGCTG>AGATG	
Pat_41	Post-Resistance	CUL1	8454	37	7	148454172	148454172	Missense_Mutation	SNP	C	T	16	531	c.413C>T	c.(412-414)GCC>GTC	p.A138V
Pat_41	Post-Resistance	EZH2	2146	37	7	148512598	148512598	Missense_Mutation	SNP	C	T	18	456	c.1531G>A	c.(1531-1533)GAC>AAC	p.D511N
Pat_41	Post-Resistance	EZH2	2146	37	7	148544387	148544387	Missense_Mutation	SNP	C	T	72	734	c.4G>A	c.(4-6)GGC>AGC	p.G2S
Pat_41	Post-Resistance	ZNF425	155054	37	7	148802082	148802082	Missense_Mutation	SNP	C	T	9	94	c.881G>A	c.(880-882)TGT>TAT	p.C294Y
Pat_41	Post-Resistance	ZNF425	155054	37	7	148809285	148809285	Missense_Mutation	SNP	C	T	16	296	c.248G>A	c.(247-249)AGC>AAC	p.S83N
Pat_41	Post-Resistance	ZNF425	155054	37	7	148815350	148815350	Missense_Mutation	SNP	C	T	32	349	c.109G>A	c.(109-111)GAG>AAG	p.E37K
Pat_41	Post-Resistance	ZNF398	57541	37	7	148851154	148851154	Missense_Mutation	SNP	G	A	7	257	c.142G>A	c.(142-144)GCC>ACC	p.A48T
Pat_41	Post-Resistance	ZNF777	27153	37	7	149133753	149133753	Missense_Mutation	SNP	G	A	5	157	c.1252C>T	c.(1252-1254)CCA>TCA	p.P418S
Pat_41	Post-Resistance	ZNF862	643641	37	7	149556569	149556569	Nonsense_Mutation	SNP	G	A	8	58	c.1176G>A	c.(1174-1176)TGG>TGA	p.W392*
Pat_41	Post-Resistance	ZNF775	285971	37	7	150094991	150094992	Missense_Mutation	DNP	CC	TT	6	130	.1422_1423CC>T	420-1425)TACCCG>TATT	p.P475S
Pat_41	Post-Resistance	GIMAP8	155038	37	7	150167948	150167948	Missense_Mutation	SNP	G	A	12	184	c.668G>A	c.(667-669)GGA>GAA	p.G223E
Pat_41	Post-Resistance	GIMAP4	55303	37	7	150269490	150269490	Missense_Mutation	SNP	C	T	14	138	c.332C>T	c.(331-333)TCC>TTC	p.S111F
Pat_41	Post-Resistance	GIMAP1	170575	37	7	150417432	150417432	Missense_Mutation	SNP	G	A	9	117	c.340G>A	c.(340-342)GCG>ACG	p.A114T
Pat_41	Post-Resistance	NOS3	4846	37	7	150703991	150703991	Missense_Mutation	SNP	G	A	22	217	c.1835G>A	c.(1834-1836)CGC>CAC	p.R612H
Pat_41	Post-Resistance	ACCN3	9311	37	7	150747649	150747649	Missense_Mutation	SNP	G	A	19	193	c.767G>A	c.(766-768)GGG>GAG	p.G256E

Pat_41	Post-Resistance	SLC4A2	6522	37	7	150761690	150761690	Missense_Mutation	SNP	C	T	33	285	c.295C>T	c.(295-297)CCC>TCC	p.P99S
Pat_41	Post-Resistance	SLC4A2	6522	37	7	150763962	150763962	Missense_Mutation	SNP	G	A	6	66	c.848G>A	c.(847-849)GGG>GAG	p.G283E
Pat_41	Post-Resistance	ABCF2	10061	37	7	150921903	150921903	Missense_Mutation	SNP	T	C	7	217	c.326A>G	c.(325-327)AAC>AGC	p.N109S
Pat_41	Post-Resistance	SMARCD3	6604	37	7	150939647	150939647	Missense_Mutation	SNP	G	A	11	381	c.499C>T	c.(499-501)CCT>TCT	p.P167S
Pat_41	Post-Resistance	RHEB	6009	37	7	151181827	151181827	Missense_Mutation	SNP	C	T	9	398	c.188G>A	c.(187-189)GGG>GAG	p.G63E
Pat_41	Post-Resistance	MLL3	58508	37	7	151851351	151851351	Splice_Site	SNP	C	T	16	145	c.12139_splice	c.e47+1	p.S4047_splice
Pat_41	Post-Resistance	MLL3	58508	37	7	151879505	151879505	Missense_Mutation	SNP	G	A	32	759	c.5440C>T	c.(5440-5442)CCT>TCT	p.P1814S
Pat_41	Post-Resistance	MLL3	58508	37	7	151884799	151884799	Splice_Site	SNP	C	T	6	279	c.4793_splice	c.e32+1	p.R1598_splice
Pat_41	Post-Resistance	DPP6	1804	37	7	154595584	154595584	Missense_Mutation	SNP	G	A	9	182	c.1418G>A	c.(1417-1419)AGC>AAC	p.S473N
Pat_41	Post-Resistance	INSIG1	3638	37	7	155093396	155093396	Missense_Mutation	SNP	G	A	18	426	c.533G>A	c.(532-534)AGT>AAT	p.S178N
Pat_41	Post-Resistance	RBM33	155435	37	7	155473567	155473567	Missense_Mutation	SNP	G	A	19	128	c.532G>A	c.(532-534)GAC>AAC	p.D178N
Pat_41	Post-Resistance	NOM1	64434	37	7	156746904	156746904	Missense_Mutation	SNP	C	T	10	199	c.1220C>T	c.(1219-1221)GCC>GTC	p.A407V
Pat_41	Post-Resistance	NOM1	64434	37	7	156754844	156754844	Splice_Site	SNP	G	A	17	555	c.1633_splice	c.e5-1	p.I545_splice
Pat_41	Post-Resistance	UBE3C	9690	37	7	157000567	157000567	Missense_Mutation	SNP	A	G	9	142	c.1747A>G	c.(1747-1749)ACT>GCT	p.T583A
Pat_41	Post-Resistance	UBE3C	9690	37	7	157049658	157049658	Missense_Mutation	SNP	G	A	7	312	c.3001G>A	c.(3001-3003)GAA>AAA	p.E1001K
Pat_41	Post-Resistance	NCAPG2	54892	37	7	158457348	158457348	Missense_Mutation	SNP	G	A	15	121	c.1574C>T	c.(1573-1575)TCT>TTT	p.S525F
Pat_41	Post-Resistance	ZNF596	169270	37	8	195811	195811	Missense_Mutation	SNP	C	T	5	31	c.964C>T	c.(964-966)CTT>TTT	p.L322F
Pat_41	Post-Resistance	ARHGEF10	9639	37	8	1851528	1851528	Missense_Mutation	SNP	G	A	7	187	c.1732G>A	c.(1732-1734)GAG>AAG	p.E578K
Pat_41	Post-Resistance	ARHGEF10	9639	37	8	1853773	1853773	Missense_Mutation	SNP	G	A	21	351	c.1858G>A	c.(1858-1860)GAT>AAT	p.D620N
Pat_41	Post-Resistance	MYOM2	9172	37	8	2005865	2005865	Missense_Mutation	SNP	C	T	6	157	c.527C>T	c.(526-528)ACC>ATC	p.T176I
Pat_41	Post-Resistance	MYOM2	9172	37	8	2089063	2089063	Splice_Site	SNP	G	A	16	215	c.3965_splice	c.e34-1	p.A1322_splice
Pat_41	Post-Resistance	CSMD1	64478	37	8	2830795	2830795	Missense_Mutation	SNP	G	A	26	603	c.8770C>T	c.(8770-8772)CCG>TCG	p.P2924S
Pat_41	Post-Resistance	CSMD1	64478	37	8	3165912	3165912	Missense_Mutation	SNP	C	T	7	132	c.3748G>A	c.(3748-3750)GCC>ACC	p.A1250T
Pat_41	Post-Resistance	CSMD1	64478	37	8	3889615	3889615	Missense_Mutation	SNP	G	A	8	52	c.422C>T	c.(421-423)CCT>CTT	p.P141L
Pat_41	Post-Resistance	MCPH1	79648	37	8	6302747	6302747	Missense_Mutation	SNP	G	A	10	124	c.1504G>A	c.(1504-1506)GCC>ACC	p.A502T
Pat_41	Post-Resistance	SGK223	157285	37	8	8176743	8176743	Missense_Mutation	SNP	C	T	11	144	c.3142G>A	c.(3142-3144)GAC>AAC	p.D1048N
Pat_41	Post-Resistance	SGK223	157285	37	8	8234750	8234750	Missense_Mutation	SNP	C	T	10	30	c.1169G>A	c.(1168-1170)GGG>GAG	p.G390E
Pat_41	Post-Resistance	TNKS	8658	37	8	9623824	9623824	Missense_Mutation	SNP	C	T	43	246	c.3629C>T	c.(3628-3630)GCC>GTC	p.A1210V
Pat_41	Post-Resistance	RP1L1	94137	37	8	10466636	10466636	Missense_Mutation	SNP	G	A	6	55	c.4972C>T	c.(4972-4974)CCC>TCC	p.P1658S
Pat_41	Post-Resistance	RP1L1	94137	37	8	10468205	10468205	Missense_Mutation	SNP	G	A	12	124	c.3403C>T	c.(3403-3405)CCT>TCT	p.P1135S
Pat_41	Post-Resistance	MTMR9	66036	37	8	11172484	11172484	Nonsense_Mutation	SNP	C	T	124	101	c.1024C>T	c.(1024-1026)CAG>TAG	p.Q342*
Pat_41	Post-Resistance	AMAC1L2	83650	37	8	11189118	11189118	Missense_Mutation	SNP	G	A	23	427	c.503G>A	c.(502-504)GGA>GAA	p.G168E
Pat_41	Post-Resistance	FAM167A	83648	37	8	11301799	11301799	Missense_Mutation	SNP	G	A	9	106	c.122C>T	c.(121-123)ACC>ATC	p.T41I
Pat_41	Post-Resistance	BLK	640	37	8	11400822	11400822	Missense_Mutation	SNP	C	T	5	101	c.89C>T	c.(88-90)GCC>GTC	p.A30V
Pat_41	Post-Resistance	GATA4	2626	37	8	11614533	11614533	Missense_Mutation	SNP	C	T	19	353	c.1087C>T	c.(1087-1089)CCC>TCC	p.P363S
Pat_41	Post-Resistance	FDFT1	2222	37	8	11660420	11660420	Missense_Mutation	SNP	G	A	10	94	c.79G>A	c.(79-81)GTG>ATG	p.V27M
Pat_41	Post-Resistance	USP17L2	377630	37	8	11994816	11994816	Missense_Mutation	SNP	G	A	15	181	c.1454C>T	c.(1453-1455)TCC>TTC	p.S485F
Pat_41	Post-Resistance	TUSC3	7991	37	8	15605895	15605895	Missense_Mutation	SNP	G	A	13	191	c.949G>A	c.(949-951)GTG>ATG	p.V317M
Pat_41	Post-Resistance	EFHA2	286097	37	8	16962981	16962981	Missense_Mutation	SNP	G	A	4	54	c.1145G>A	c.(1144-1146)GGA>GAA	p.G382E
Pat_41	Post-Resistance	SLC7A2	6542	37	8	17415833	17415833	Missense_Mutation	SNP	G	A	13	112	c.1225G>A	c.(1225-1227)GCG>ACG	p.A409T
Pat_41	Post-Resistance	PDGFRL	5157	37	8	17486196	17486196	Missense_Mutation	SNP	C	T	15	178	c.706C>T	c.(706-708)CCT>TCT	p.P236S
Pat_41	Post-Resistance	MTUS1	57509	37	8	17581330	17581330	Missense_Mutation	SNP	G	A	8	329	c.2300C>T	c.(2299-2301)TCC>TTC	p.S767F
Pat_41	Post-Resistance	PCM1	5108	37	8	17804812	17804812	Missense_Mutation	SNP	G	A	26	447	c.901G>A	c.(901-903)GCT>ACT	p.A301T
Pat_41	Post-Resistance	PCM1	5108	37	8	17814921	17814921	Missense_Mutation	SNP	C	T	8	258	c.1795C>T	c.(1795-1797)CCT>TCT	p.P599S
Pat_41	Post-Resistance	ASAH1	427	37	8	17918954	17918954	Nonsense_Mutation	SNP	C	T	19	217	c.717G>A	c.(715-717)TGG>TGA	p.W239*
Pat_41	Post-Resistance	NAT2	10	37	8	18257965	18257965	Missense_Mutation	SNP	G	A	20	85	c.452G>A	c.(451-453)TGC>TAC	p.C151Y
Pat_41	Post-Resistance	LZTS1	11178	37	8	20107711	20107711	Missense_Mutation	SNP	C	T	13	170	c.1313G>A	c.(1312-1314)GGC>GAC	p.G438D

Pat_41	Post-Resistance	DOK2	9046	37	8	21768189	21768189	Missense_Mutation	SNP	C	T	12	81	c.613G>A	c.(613-615)GAC>AAC	p.D205N
Pat_41	Post-Resistance	EPB49	2039	37	8	21927705	21927705	Missense_Mutation	SNP	G	A	16	344	c.464G>A	c.(463-465)GGC>GAC	p.G155D
Pat_41	Post-Resistance	HR	55806	37	8	21980040	21980040	Missense_Mutation	SNP	G	A	7	54	c.2087C>T	c.(2086-2088)GCC>GTC	p.A696V
Pat_41	Post-Resistance	HR	55806	37	8	21984894	21984894	Missense_Mutation	SNP	C	T	13	96	c.1061G>A	c.(1060-1062)GGA>GAA	p.G354E
Pat_41	Post-Resistance	POLR3D	661	37	8	22105687	22105687	Missense_Mutation	SNP	G	A	4	78	c.382G>A	c.(382-384)GAT>AAT	p.D128N
Pat_41	Post-Resistance	PPP3CC	5533	37	8	22385005	22385005	Nonsense_Mutation	SNP	G	A	32	378	c.1044G>A	c.(1042-1044)TGG>TGA	p.W348*
Pat_41	Post-Resistance	SORBS3	10174	37	8	22424218	22424218	Missense_Mutation	SNP	G	A	6	117	c.1135G>A	c.(1135-1137)GAG>AAG	p.E379K
Pat_41	Post-Resistance	EGR3	1960	37	8	22550325	22550325	Missense_Mutation	SNP	G	A	7	214	c.133C>T	c.(133-135)CAT>TAT	p.H45Y
Pat_41	Post-Resistance	RHOBTB2	23221	37	8	22868064	22868064	Missense_Mutation	SNP	A	G	12	436	c.1634A>G	c.(1633-1635)TAC>TGC	p.Y545C
Pat_41	Post-Resistance	CHMP7	91782	37	8	23106878	23106878	Missense_Mutation	SNP	C	T	4	71	c.455C>T	c.(454-456)GCT>GTT	p.A152V
Pat_41	Post-Resistance	LOXL2	4017	37	8	23156381	23156381	Missense_Mutation	SNP	C	T	12	185	c.2213G>A	c.(2212-2214)GGC>GAC	p.G738D
Pat_41	Post-Resistance	LOXL2	4017	37	8	23225765	23225765	Missense_Mutation	SNP	G	A	15	112	c.100C>T	c.(100-102)CCC>TCC	p.P34S
Pat_41	Post-Resistance	SLC25A37	51312	37	8	23429241	23429241	Missense_Mutation	SNP	G	A	10	108	c.890G>A	c.(889-891)GGC>GAC	p.G297D
Pat_41	Post-Resistance	ADAM28	10863	37	8	24209561	24209561	Missense_Mutation	SNP	C	T	6	161	c.2240C>T	c.(2239-2241)TCT>TTT	p.S747F
Pat_41	Post-Resistance	NEFL	4747	37	8	24811169	24811169	Missense_Mutation	SNP	C	T	9	247	c.1310G>A	c.(1309-1311)CGC>CAC	p.R437H
Pat_41	Post-Resistance	DOCK5	80005	37	8	25174634	25174634	Missense_Mutation	SNP	G	A	34	650	c.1430G>A	c.(1429-1431)GGC>GAC	p.G477D
Pat_41	Post-Resistance	PPP2R2A	5520	37	8	26218626	26218626	Missense_Mutation	SNP	G	A	21	354	c.596G>A	c.(595-597)CGG>CAG	p.R199Q
Pat_41	Post-Resistance	PNMA2	10687	37	8	26365578	26365578	Missense_Mutation	SNP	C	T	4	72	c.694G>A	c.(694-696)GAG>AAG	p.E232K
Pat_41	Post-Resistance	DPYSL2	1808	37	8	26484171	26484171	Missense_Mutation	SNP	C	T	31	208	c.517C>T	c.(517-519)CGC>TGC	p.R173C
Pat_41	Post-Resistance	DPYSL2	1808	37	8	26509827	26509827	Missense_Mutation	SNP	G	A	13	140	c.1336G>A	c.(1336-1338)GTC>ATC	p.V446I
Pat_41	Post-Resistance	DPYSL2	1808	37	8	26510899	26510899	Missense_Mutation	SNP	G	A	31	402	c.1613G>A	c.(1612-1614)GGA>GAA	p.G538E
Pat_41	Post-Resistance	CLU	1191	37	8	27463878	27463878	Missense_Mutation	SNP	C	T	6	129	c.410G>A	c.(409-411)GGC>GAC	p.G137D
Pat_41	Post-Resistance	SCARA3	51435	37	8	27509117	27509117	Missense_Mutation	SNP	G	A	19	180	c.199G>A	c.(199-201)GTG>ATG	p.V67M
Pat_41	Post-Resistance	ESCO2	157570	37	8	27634013	27634013	Missense_Mutation	SNP	C	T	11	108	c.188C>T	c.(187-189)ACT>ATT	p.T63I
Pat_41	Post-Resistance	ZNF395	55893	37	8	28217209	28217209	Missense_Mutation	SNP	C	T	15	61	c.373G>A	c.(373-375)GCA>ACA	p.A125T
Pat_41	Post-Resistance	FZD3	7976	37	8	28384768	28384768	Nonsense_Mutation	SNP	G	A	16	269	c.491G>A	c.(490-492)TGG>TAG	p.W164*
Pat_41	Post-Resistance	INTS9	55756	37	8	28635392	28635392	Missense_Mutation	SNP	G	A	11	105	c.1349C>T	c.(1348-1350)ACC>ATC	p.T450I
Pat_41	Post-Resistance	TMEM66	51669	37	8	29931557	29931557	Missense_Mutation	SNP	G	A	7	192	c.118C>T	c.(118-120)CGG>TGG	p.R40W
Pat_41	Post-Resistance	RBPMS	11030	37	8	30361818	30361818	Missense_Mutation	SNP	C	T	27	478	c.262C>T	c.(262-264)CCT>TCT	p.P88S
Pat_41	Post-Resistance	TEX15	56154	37	8	30706455	30706455	Missense_Mutation	SNP	G	A	5	157	c.79C>T	c.(79-81)CTT>TTT	p.L27F
Pat_41	Post-Resistance	PURG	29942	37	8	30889512	30889512	Missense_Mutation	SNP	C	T	38	63	c.787G>A	c.(787-789)GAG>AAG	p.E263K
Pat_41	Post-Resistance	ERLIN2	11160	37	8	37607115	37607115	Missense_Mutation	SNP	G	A	32	244	c.463G>A	c.(463-465)GAC>AAC	p.D155N
Pat_41	Post-Resistance	GPR124	25960	37	8	37690531	37690531	Nonsense_Mutation	SNP	G	A	24	472	c.1101G>A	c.(1099-1101)TGG>TGA	p.W367*
Pat_41	Post-Resistance	GPR124	25960	37	8	37698647	37698647	Missense_Mutation	SNP	C	T	15	301	c.2791C>T	c.(2791-2793)CCT>TCT	p.P931S
Pat_41	Post-Resistance	RAB11FIP1	80223	37	8	37730678	37730678	Missense_Mutation	SNP	C	T	7	89	c.1642G>A	c.(1642-1644)GCG>ACG	p.A548T
Pat_41	Post-Resistance	ASH2L	9070	37	8	37978591	37978591	Nonsense_Mutation	SNP	G	A	14	256	c.1089G>A	c.(1087-1089)TGG>TGA	p.W363*
Pat_41	Post-Resistance	BAG4	9530	37	8	38067931	38067931	Missense_Mutation	SNP	G	A	5	68	c.1294G>A	c.(1294-1296)GAC>AAC	p.D432N
Pat_41	Post-Resistance	PPAPDC1B	84513	37	8	38125418	38125418	Missense_Mutation	SNP	C	T	11	281	c.335G>A	c.(334-336)GGG>GAG	p.G112E
Pat_41	Post-Resistance	WHSC1L1	54904	37	8	38148031	38148031	Missense_Mutation	SNP	G	A	27	499	c.3080C>T	c.(3079-3081)GCT>GTT	p.A1027V
Pat_41	Post-Resistance	FGFR1	2260	37	8	38272147	38272147	Missense_Mutation	SNP	C	T	13	209	c.1978G>A	c.(1978-1980)GGC>AGC	p.G660S
Pat_41	Post-Resistance	RNF5P1	286140	37	8	38458435	38458435	Missense_Mutation	SNP	G	A	6	63	c.284C>T	c.(283-285)CCC>CTC	p.P95L
Pat_41	Post-Resistance	HTRA4	203100	37	8	38831861	38831861	Missense_Mutation	SNP	C	T	6	69	c.79C>T	c.(79-81)CTC>TTC	p.L27F
Pat_41	Post-Resistance	HTRA4	203100	37	8	38840022	38840022	Missense_Mutation	SNP	G	A	8	179	c.1120G>A	c.(1120-1122)GCG>ACG	p.A374T
Pat_41	Post-Resistance	ADAM32	203102	37	8	39044437	39044437	Missense_Mutation	SNP	G	A	13	138	c.925G>A	c.(925-927)GAG>AAG	p.E309K
Pat_41	Post-Resistance	AGPAT6	137964	37	8	41467272	41467272	Missense_Mutation	SNP	C	T	16	271	c.334C>T	c.(334-336)CTC>TTC	p.L112F
Pat_41	Post-Resistance	AP3M2	10947	37	8	42015612	42015612	Missense_Mutation	SNP	G	A	32	218	c.427G>A	c.(427-429)GTT>ATT	p.V143I
Pat_41	Post-Resistance	PLAT	5327	37	8	42046545	42046545	Nonsense_Mutation	SNP	G	A	42	485	c.160C>T	c.(160-162)CAG>TAG	p.Q54*

Pat_41	Post-Resistance	SLC20A2	6575	37	8	42297133	42297133	Missense_Mutation	SNP	C	T	4	133	c.769G>A	c.(769-771)GAC>AAC	p.D257N
Pat_41	Post-Resistance	CHRNB3	1142	37	8	42587433	42587433	Missense_Mutation	SNP	A	G	47	366	c.983A>G	c.(982-984)TAC>TGC	p.Y328C
Pat_41	Post-Resistance	RNF170	81790	37	8	42711321	42711321	Missense_Mutation	SNP	G	A	9	216	c.758C>T	c.(757-759)ACC>ATC	p.T253I
Pat_41	Post-Resistance	FNTA	2339	37	8	42940318	42940318	Missense_Mutation	SNP	G	A	4	69	c.1033G>A	c.(1033-1035)GCT>ACT	p.A345T
Pat_41	Post-Resistance	KIAA0146	23514	37	8	48614415	48614415	Missense_Mutation	SNP	G	A	28	464	c.1906G>A	c.(1906-1908)GAC>AAC	p.D636N
Pat_41	Post-Resistance	KIAA0146	23514	37	8	48625377	48625377	Missense_Mutation	SNP	G	A	15	251	c.2131G>A	c.(2131-2133)GCA>ACA	p.A711T
Pat_41	Post-Resistance	KIAA0146	23514	37	8	48626086	48626086	Missense_Mutation	SNP	C	T	18	247	c.2224C>T	c.(2224-2226)CTT>TTT	p.L742F
Pat_41	Post-Resistance	KIAA0146	23514	37	8	48626174	48626174	Missense_Mutation	SNP	C	T	9	164	c.2312C>T	c.(2311-2313)ACA>ATA	p.T771I
Pat_41	Post-Resistance	PRKDC	5591	37	8	48690356	48690356	Missense_Mutation	SNP	C	T	11	191	c.11933G>A	c.(11932-11934)GGC>GAC	p.G3978D
Pat_41	Post-Resistance	PRKDC	5591	37	8	48866432	48866432	Missense_Mutation	SNP	G	A	5	21	c.556C>T	c.(556-558)CCT>TCT	p.P186S
Pat_41	Post-Resistance	RB1CC1	9821	37	8	53568656	53568656	Missense_Mutation	SNP	C	T	9	109	c.3733G>A	c.(3733-3735)GCC>ACC	p.A1245T
Pat_41	Post-Resistance	LYPLA1	10434	37	8	54963590	54963590	Missense_Mutation	SNP	C	T	11	606	c.621G>A	c.(619-621)ATG>ATA	p.M207I
Pat_41	Post-Resistance	LYPLA1	10434	37	8	54974859	54974859	Missense_Mutation	SNP	C	T	10	163	c.241G>A	c.(241-243)GAT>AAT	p.D81N
Pat_41	Post-Resistance	MRPL15	29088	37	8	55049973	55049973	Missense_Mutation	SNP	G	A	22	134	c.409G>A	c.(409-411)GGT>AGT	p.G137S
Pat_41	Post-Resistance	MRPL15	29088	37	8	55055224	55055224	Missense_Mutation	SNP	G	A	4	105	c.431G>A	c.(430-432)GGT>GAT	p.G144D
Pat_41	Post-Resistance	RP1	6101	37	8	55541286	55541286	Missense_Mutation	SNP	G	A	27	235	c.4844G>A	c.(4843-4845)GGC>GAC	p.G1615D
Pat_41	Post-Resistance	TGS1	96764	37	8	56698347	56698347	Missense_Mutation	SNP	G	A	13	204	c.236G>A	c.(235-237)GGC>GAC	p.G79D
Pat_41	Post-Resistance	PLAG1	5324	37	8	57078812	57078812	Missense_Mutation	SNP	G	A	53	453	c.1493C>T	c.(1492-1494)GCT>GTT	p.A498V
Pat_41	Post-Resistance	PLAG1	5324	37	8	57079254	57079254	Missense_Mutation	SNP	G	A	13	359	c.1051C>T	c.(1051-1053)CCA>TCA	p.P351S
Pat_41	Post-Resistance	SDR16C5	195814	37	8	57221564	57221564	Missense_Mutation	SNP	G	A	6	139	c.488C>T	c.(487-489)GCT>GTT	p.A163V
Pat_41	Post-Resistance	SDR16C5	195814	37	8	57228653	57228653	Missense_Mutation	SNP	C	T	7	283	c.254G>A	c.(253-255)CGG>CAG	p.R85Q
Pat_41	Post-Resistance	IMPAD1	54928	37	8	57878851	57878851	Missense_Mutation	SNP	G	A	10	198	c.707C>T	c.(706-708)ACC>ATC	p.T236I
Pat_41	Post-Resistance	CYP7A1	1581	37	8	59411012	59411012	Missense_Mutation	SNP	G	A	30	547	c.97C>T	c.(97-99)CCT>TCT	p.P33S
Pat_41	Post-Resistance	NSMAF	8439	37	8	59500237	59500237	Missense_Mutation	SNP	C	A	10	205	c.2235G>T	c.(2233-2235)GAG>GAT	p.E745D
Pat_41	Post-Resistance	GGH	8836	37	8	63936638	63936638	Splice_Site	SNP	C	T	10	109	c.606_splice	c.e6+1	p.K202_splice
Pat_41	Post-Resistance	GGH	8836	37	8	63939739	63939739	Splice_Site	SNP	C	T	8	182	c.360_splice	c.e4+1	p.Q120_splice
Pat_41	Post-Resistance	YTHDF3	253943	37	8	64100128	64100128	Missense_Mutation	SNP	G	A	26	40	c.1559G>A	c.(1558-1560)CGC>CAC	p.R520H
Pat_41	Post-Resistance	DNAJC5B	85479	37	8	67012241	67012241	Missense_Mutation	SNP	C	T	14	105	c.575C>T	c.(574-576)TCT>TTT	p.S192F
Pat_41	Post-Resistance	TRIM55	84675	37	8	67040644	67040644	Missense_Mutation	SNP	G	A	13	362	c.274G>A	c.(274-276)GTA>ATA	p.V92I
Pat_41	Post-Resistance	VCPIP1	80124	37	8	67578206	67578206	Missense_Mutation	SNP	C	T	19	190	c.988G>A	c.(988-990)GAG>AAG	p.E330K
Pat_41	Post-Resistance	CSPP1	79848	37	8	68015300	68015300	Missense_Mutation	SNP	C	T	6	208	c.1084C>T	c.(1084-1086)CCT>TCT	p.P362S
Pat_41	Post-Resistance	CSPP1	79848	37	8	68031010	68031010	Missense_Mutation	SNP	G	A	13	210	c.1741G>A	c.(1741-1743)GCT>ACT	p.A581T
Pat_41	Post-Resistance	CSPP1	79848	37	8	68107721	68107721	Missense_Mutation	SNP	G	A	21	244	c.3664G>A	c.(3664-3666)GAA>AAA	p.E1222K
Pat_41	Post-Resistance	ARFGEF1	10565	37	8	68130264	68130264	Missense_Mutation	SNP	G	A	14	309	c.4448C>T	c.(4447-4449)GCT>GTT	p.A1483V
Pat_41	Post-Resistance	ARFGEF1	10565	37	8	68130312	68130312	Missense_Mutation	SNP	G	A	37	232	c.4400C>T	c.(4399-4401)ACT>ATT	p.T1467I
Pat_41	Post-Resistance	ARFGEF1	10565	37	8	68179613	68179613	Nonsense_Mutation	SNP	C	T	20	333	c.1637G>A	c.(1636-1638)TGG>TAG	p.W546*
Pat_41	Post-Resistance	CPA6	57094	37	8	68340293	68340293	Missense_Mutation	SNP	G	A	8	192	c.1115C>T	c.(1114-1116)TCC>TTC	p.S372F
Pat_41	Post-Resistance	SULF1	23213	37	8	70476235	70476235	Missense_Mutation	SNP	G	A	21	250	c.25G>A	c.(25-27)GTT>ATT	p.V9I
Pat_41	Post-Resistance	SULF1	23213	37	8	70501307	70501307	Missense_Mutation	SNP	C	T	6	149	c.665C>T	c.(664-666)GCT>GTT	p.A222V
Pat_41	Post-Resistance	SLCO5A1	81796	37	8	70617279	70617279	Missense_Mutation	SNP	G	A	16	285	c.1609C>T	c.(1609-1611)CCT>TCT	p.P537S
Pat_41	Post-Resistance	PRDM14	63978	37	8	70981642	70981642	Missense_Mutation	SNP	G	A	9	138	c.454C>T	c.(454-456)CCG>TCG	p.P152S
Pat_41	Post-Resistance	PRDM14	63978	37	8	70981662	70981662	Missense_Mutation	SNP	C	T	8	138	c.434G>A	c.(433-435)GGA>GAA	p.G145E
Pat_41	Post-Resistance	LACTB2	51110	37	8	71550135	71550135	Missense_Mutation	SNP	C	T	11	79	c.827G>A	c.(826-828)AGC>AAC	p.S276N
Pat_41	Post-Resistance	XKR9	389668	37	8	71646393	71646393	Missense_Mutation	SNP	C	T	6	62	c.856C>T	c.(856-858)CCA>TCA	p.P286S
Pat_41	Post-Resistance	EYA1	2138	37	8	72123426	72123426	Missense_Mutation	SNP	C	T	12	344	c.1663G>A	c.(1663-1665)GGA>AGA	p.G555R
Pat_41	Post-Resistance	TRPA1	8989	37	8	72973868	72973868	Missense_Mutation	SNP	C	T	24	314	c.936G>A	c.(934-936)ATG>ATA	p.M312I
Pat_41	Post-Resistance	TRPA1	8989	37	8	72973983	72973983	Missense_Mutation	SNP	G	A	6	162	c.821C>T	c.(820-822)ACA>ATA	p.T274I

Pat_41	Post-Resistance	KCNB2	9312	37	8	73480201	73480201	Missense_Mutation	SNP	G	A	7	80	c.232G>A	c.(232-234)GAC>AAC	p.D78N
Pat_41	Post-Resistance	RPL7	6129	37	8	74204077	74204077	Missense_Mutation	SNP	C	T	15	217	c.359G>A	c.(358-360)GGA>GAA	p.G120E
Pat_41	Post-Resistance	STAU2	27067	37	8	74600967	74600967	Missense_Mutation	SNP	C	T	48	387	c.196G>A	c.(196-198)GCC>ACC	p.A66T
Pat_41	Post-Resistance	TMEM70	54968	37	8	74891055	74891055	Missense_Mutation	SNP	G	A	25	237	c.275G>A	c.(274-276)GGA>GAA	p.G92E
Pat_41	Post-Resistance	ZFHX4	79776	37	8	77618080	77618080	Missense_Mutation	SNP	C	T	10	158	c.1757C>T	c.(1756-1758)GCC>GTC	p.A586V
Pat_41	Post-Resistance	ZFHX4	79776	37	8	77763770	77763770	Missense_Mutation	SNP	C	T	7	92	c.4478C>T	c.(4477-4479)TCT>TTT	p.S1493F
Pat_41	Post-Resistance	ZFHX4	79776	37	8	77766995	77766995	Missense_Mutation	SNP	C	T	4	46	c.7703C>T	c.(7702-7704)ACC>ATC	p.T2568I
Pat_41	Post-Resistance	ZNF704	619279	37	8	81577201	81577201	Missense_Mutation	SNP	G	A	14	236	c.776C>T	c.(775-777)TCC>TTC	p.S259F
Pat_41	Post-Resistance	PAG1	55824	37	8	81897456	81897456	Missense_Mutation	SNP	G	A	24	126	c.431C>T	c.(430-432)ACC>ATC	p.T144I
Pat_41	Post-Resistance	FABP12	646486	37	8	82441810	82441810	Missense_Mutation	SNP	C	T	9	74	c.109G>A	c.(109-111)GCA>ACA	p.A37T
Pat_41	Post-Resistance	SLC10A5	347051	37	8	82607156	82607156	Missense_Mutation	SNP	C	T	24	29	c.52G>A	c.(52-54)GAA>AAA	p.E18K
Pat_41	Post-Resistance	CA1	759	37	8	86244782	86244782	Splice_Site	SNP	C	T	6	142	c.451_splice	c.e7-1	p.V151_splice
Pat_41	Post-Resistance	WWP1	11059	37	8	87437514	87437514	Missense_Mutation	SNP	C	T	7	170	c.1124C>T	c.(1123-1125)ACC>ATC	p.T375I
Pat_41	Post-Resistance	CNGB3	54714	37	8	87656054	87656054	Missense_Mutation	SNP	G	A	18	296	c.1103C>T	c.(1102-1104)GCC>GTC	p.A368V
Pat_41	Post-Resistance	DCAF4L2	138009	37	8	88885197	88885197	Missense_Mutation	SNP	C	T	6	104	c.1003G>A	c.(1003-1005)GAC>AAC	p.D335N
Pat_41	Post-Resistance	DCAF4L2	138009	37	8	88885309	88885309	Nonsense_Mutation	SNP	C	T	13	258	c.891G>A	c.(889-891)TGG>TGA	p.W297*
Pat_41	Post-Resistance	MMP16	4325	37	8	89209469	89209469	Missense_Mutation	SNP	C	T	14	211	c.199G>A	c.(199-201)GAG>AAG	p.E67K
Pat_41	Post-Resistance	TMEM55A	55529	37	8	92052878	92052878	Missense_Mutation	SNP	G	A	9	159	c.100C>T	c.(100-102)CCC>TCC	p.P34S
Pat_41	Post-Resistance	SLC26A7	115111	37	8	92330549	92330549	Missense_Mutation	SNP	G	A	9	280	c.583G>A	c.(583-585)GTC>ATC	p.V195I
Pat_41	Post-Resistance	RUNX1T1	862	37	8	92982981	92982981	Missense_Mutation	SNP	C	T	10	120	c.1444G>A	c.(1444-1446)GAG>AAG	p.E482K
Pat_41	Post-Resistance	RUNX1T1	862	37	8	92983014	92983014	Missense_Mutation	SNP	C	T	5	117	c.1411G>A	c.(1411-1413)GCG>ACG	p.A471T
Pat_41	Post-Resistance	RBM12B	389677	37	8	94746603	94746603	Missense_Mutation	SNP	G	A	19	185	c.2036C>T	c.(2035-2037)CCA>CTA	p.P679L
Pat_41	Post-Resistance	RBM12B	389677	37	8	94747366	94747366	Missense_Mutation	SNP	G	A	14	278	c.1273C>T	c.(1273-1275)CTT>TTT	p.L425F
Pat_41	Post-Resistance	TMEM67	91147	37	8	94798514	94798514	Missense_Mutation	SNP	G	A	14	238	c.1352G>A	c.(1351-1353)CGA>CAA	p.R451Q
Pat_41	Post-Resistance	TMEM67	91147	37	8	94798541	94798541	Missense_Mutation	SNP	G	A	18	200	c.1379G>A	c.(1378-1380)AGA>AAA	p.R460K
Pat_41	Post-Resistance	KIAA1429	25962	37	8	95523736	95523736	Missense_Mutation	SNP	C	T	10	202	c.3067G>A	c.(3067-3069)GGT>AGT	p.G1023S
Pat_41	Post-Resistance	KIAA1429	25962	37	8	95547100	95547100	Missense_Mutation	SNP	G	A	15	145	c.451C>T	c.(451-453)CCA>TCA	p.P151S
Pat_41	Post-Resistance	INTS8	55656	37	8	95853759	95853759	Missense_Mutation	SNP	G	A	34	405	c.1058G>A	c.(1057-1059)AGT>AAT	p.S353N
Pat_41	Post-Resistance	MTERFD1	51001	37	8	97258116	97258116	Missense_Mutation	SNP	C	T	14	292	c.869G>A	c.(868-870)AGT>AAT	p.S290N
Pat_41	Post-Resistance	PGCP	10404	37	8	98155400	98155400	Missense_Mutation	SNP	C	T	9	127	c.1408C>T	c.(1408-1410)CCT>TCT	p.P470S
Pat_41	Post-Resistance	HRSP12	10247	37	8	99118553	99118553	Missense_Mutation	SNP	G	A	10	207	c.173C>T	c.(172-174)GCT>GTT	p.A58V
Pat_41	Post-Resistance	POP1	10940	37	8	99148764	99148764	Missense_Mutation	SNP	G	A	65	523	c.1066G>A	c.(1066-1068)GCT>ACT	p.A356T
Pat_41	Post-Resistance	STK3	6788	37	8	99761557	99761557	Missense_Mutation	SNP	C	T	8	390	c.298G>A	c.(298-300)GAG>AAG	p.E100K
Pat_41	Post-Resistance	VPS13B	157680	37	8	100494001	100494001	Missense_Mutation	SNP	C	T	14	131	c.3841C>T	c.(3841-3843)CCA>TCA	p.P1281S
Pat_41	Post-Resistance	VPS13B	157680	37	8	100871565	100871565	Missense_Mutation	SNP	G	T	9	108	c.10976G>T	c.(10975-10977)AGC>ATC	p.S3659I
Pat_41	Post-Resistance	VPS13B	157680	37	8	100871666	100871666	Missense_Mutation	SNP	G	A	16	82	c.11077G>A	c.(11077-11079)GTC>ATC	p.V3693I
Pat_41	Post-Resistance	RGS22	26166	37	8	101074878	101074878	Nonsense_Mutation	SNP	C	T	5	86	c.1455G>A	c.(1453-1455)TGG>TGA	p.W485*
Pat_41	Post-Resistance	FBXO43	286151	37	8	101153190	101153190	Missense_Mutation	SNP	G	A	14	238	c.1292C>T	c.(1291-1293)ACC>ATC	p.T431I
Pat_41	Post-Resistance	RNF19A	25897	37	8	101271296	101271296	Missense_Mutation	SNP	C	T	11	420	c.2005G>A	c.(2005-2007)GCA>ACA	p.A669T
Pat_41	Post-Resistance	PABPC1	26986	37	8	101724600	101724600	Missense_Mutation	SNP	G	A	16	687	c.962C>T	c.(961-963)ACT>ATT	p.T321I
Pat_41	Post-Resistance	ZNF706	51123	37	8	102213926	102213926	Missense_Mutation	SNP	G	A	6	174	c.44C>T	c.(43-45)GCC>GTC	p.A15V
Pat_41	Post-Resistance	GRHL2	79977	37	8	102555642	102555642	Missense_Mutation	SNP	G	A	28	143	c.194G>A	c.(193-195)GGC>GAC	p.G65D
Pat_41	Post-Resistance	NCALD	83988	37	8	102731503	102731503	Missense_Mutation	SNP	C	T	8	307	c.355G>A	c.(355-357)GCA>ACA	p.A119T
Pat_41	Post-Resistance	RRM2B	50484	37	8	103236342	103236342	Missense_Mutation	SNP	G	A	13	169	c.482C>T	c.(481-483)ACC>ATC	p.T161I
Pat_41	Post-Resistance	UBR5	51366	37	8	103279234	103279234	Missense_Mutation	SNP	C	T	17	166	c.7363G>A	c.(7363-7365)GAA>AAA	p.E2455K
Pat_41	Post-Resistance	UBR5	51366	37	8	103297454	103297454	Missense_Mutation	SNP	C	T	11	206	c.5597G>A	c.(5596-5598)GGA>GAA	p.G1866E
Pat_41	Post-Resistance	UBR5	51366	37	8	103326043	103326043	Missense_Mutation	SNP	G	A	11	191	c.1996C>T	c.(1996-1998)CCT>TCT	p.P666S

Pat_41	Post-Resistance	ATP6V1C1	528	37	8	104053185	104053185	Missense_Mutation	SNP	C	T	15	338	c.121C>T	c.(121-123)CCT>TCT	p.P41S
Pat_41	Post-Resistance	FZD6	8323	37	8	104340583	104340583	Missense_Mutation	SNP	G	A	12	198	c.1480G>A	c.(1480-1482)GTT>ATT	p.V494I
Pat_41	Post-Resistance	SLC25A32	81034	37	8	104419914	104419914	Missense_Mutation	SNP	C	T	13	365	c.253G>A	c.(253-255)GTA>ATA	p.V85I
Pat_41	Post-Resistance	DCAF13	25879	37	8	104453777	104453777	Missense_Mutation	SNP	G	A	25	324	c.1637G>A	c.(1636-1638)CGA>CAA	p.R546Q
Pat_41	Post-Resistance	RIMS2	9699	37	8	105026742	105026742	Missense_Mutation	SNP	C	T	11	206	c.2453C>T	c.(2452-2454)CCT>CTT	p.P818L
Pat_41	Post-Resistance	LRP12	29967	37	8	105503247	105503247	Missense_Mutation	SNP	C	T	9	153	c.2234G>A	c.(2233-2235)GGA>GAA	p.G745E
Pat_41	Post-Resistance	LRP12	29967	37	8	105510163	105510163	Missense_Mutation	SNP	G	A	25	600	c.617C>T	c.(616-618)CCT>CTT	p.P206L
Pat_41	Post-Resistance	ZFPM2	23414	37	8	106456570	106456570	Missense_Mutation	SNP	G	A	13	73	c.262G>A	c.(262-264)GGG>AGG	p.G88R
Pat_41	Post-Resistance	PKHD1L1	93035	37	8	110425717	110425717	Missense_Mutation	SNP	G	A	6	42	c.2303G>A	c.(2302-2304)AGC>AAC	p.S768N
Pat_41	Post-Resistance	PKHD1L1	93035	37	8	110457317	110457317	Missense_Mutation	SNP	C	T	16	223	c.5219C>T	c.(5218-5220)ACC>ATC	p.T1740I
Pat_41	Post-Resistance	PKHD1L1	93035	37	8	110477106	110477106	Missense_Mutation	SNP	G	A	9	50	c.8045G>A	c.(8044-8046)GGA>GAA	p.G2682E
Pat_41	Post-Resistance	EBAG9	9166	37	8	110569213	110569213	Missense_Mutation	SNP	G	A	14	70	c.371G>A	c.(370-372)AGC>AAC	p.S124N
Pat_41	Post-Resistance	TRPS1	7227	37	8	116426877	116426877	Missense_Mutation	SNP	G	A	17	266	c.3220C>T	c.(3220-3222)CCT>TCT	p.P1074S
Pat_41	Post-Resistance	TRPS1	7227	37	8	116427012	116427012	Missense_Mutation	SNP	G	A	4	109	c.3085C>T	c.(3085-3087)CAC>TAC	p.H1029Y
Pat_41	Post-Resistance	EIF3H	8667	37	8	117668154	117668154	Nonsense_Mutation	SNP	C	T	23	229	c.648G>A	c.(646-648)TGG>TGA	p.W216*
Pat_41	Post-Resistance	EIF3H	8667	37	8	117738276	117738276	Missense_Mutation	SNP	C	T	9	299	c.268G>A	c.(268-270)GAT>AAT	p.D90N
Pat_41	Post-Resistance	RAD21	5885	37	8	117864201	117864201	Missense_Mutation	SNP	C	T	33	434	c.1456G>A	c.(1456-1458)GAG>AAG	p.E486K
Pat_41	Post-Resistance	SLC30A8	169026	37	8	118159291	118159291	Missense_Mutation	SNP	C	T	30	269	c.170C>T	c.(169-171)TCC>TTC	p.S57F
Pat_41	Post-Resistance	SLC30A8	169026	37	8	118183402	118183402	Missense_Mutation	SNP	C	T	9	471	c.959C>T	c.(958-960)GCT>GTT	p.A320V
Pat_41	Post-Resistance	EXT1	2131	37	8	119122876	119122876	Missense_Mutation	SNP	G	A	9	123	c.410C>T	c.(409-411)GCC>GTC	p.A137V
Pat_41	Post-Resistance	ENPP2	5168	37	8	120650688	120650688	Missense_Mutation	SNP	C	T	27	497	c.113G>A	c.(112-114)GGA>GAA	p.G38E
Pat_41	Post-Resistance	TAF2	6873	37	8	120795872	120795872	Missense_Mutation	SNP	C	T	19	92	c.1861G>A	c.(1861-1863)GCT>ACT	p.A621T
Pat_41	Post-Resistance	TAF2	6873	37	8	120809305	120809305	Missense_Mutation	SNP	G	A	13	144	c.1016C>T	c.(1015-1017)ACA>ATA	p.T339I
Pat_41	Post-Resistance	DSCC1	79075	37	8	120854069	120854069	Missense_Mutation	SNP	G	A	27	178	c.889C>T	c.(889-891)CCT>TCT	p.P297S
Pat_41	Post-Resistance	COL14A1	7373	37	8	121219269	121219269	Missense_Mutation	SNP	C	T	4	76	c.1127C>T	c.(1126-1128)GCC>GTC	p.A376V
Pat_41	Post-Resistance	MTBP	27085	37	8	121458681	121458681	Missense_Mutation	SNP	G	A	9	303	c.127G>A	c.(127-129)GCA>ACA	p.A43T
Pat_41	Post-Resistance	MTBP	27085	37	8	121535549	121535549	Nonsense_Mutation	SNP	G	A	18	477	c.2688G>A	c.(2686-2688)TGG>TGA	p.W896*
Pat_41	Post-Resistance	HAS2	3037	37	8	122626858	122626858	Missense_Mutation	SNP	C	T	66	455	c.1150G>A	c.(1150-1152)GGA>AGA	p.G384R
Pat_41	Post-Resistance	HAS2	3037	37	8	122641376	122641377	Nonsense_Mutation	DNP	GG	AA	131	148	c.204_205CC>TT	202-207)CACCGA>CATT	p.R69*
Pat_41	Post-Resistance	HAS2	3037	37	8	122641581	122641581	Splice_Site	SNP	C	T	6	163	c.1_splice	c.e2-1	p.M1_splice
Pat_41	Post-Resistance	ZHX2	22882	37	8	123965971	123965971	Missense_Mutation	SNP	G	A	11	157	c.2221G>A	c.(2221-2223)GAC>AAC	p.D741N
Pat_41	Post-Resistance	WDR67	93594	37	8	124113180	124113180	Missense_Mutation	SNP	C	T	13	191	c.965C>T	c.(964-966)GCA>GTA	p.A322V
Pat_41	Post-Resistance	FAM91A1	157769	37	8	124799566	124799566	Missense_Mutation	SNP	T	A	20	402	c.1144T>A	c.(1144-1146)TTT>ATT	p.F382I
Pat_41	Post-Resistance	RNF139	11236	37	8	125498239	125498239	Missense_Mutation	SNP	G	A	23	193	c.349G>A	c.(349-351)GAG>AAG	p.E117K
Pat_41	Post-Resistance	RNF139	11236	37	8	125499364	125499364	Missense_Mutation	SNP	G	A	7	367	c.1474G>A	c.(1474-1476)GGA>AGA	p.G492R
Pat_41	Post-Resistance	NDUFB9	4715	37	8	125559341	125559341	Missense_Mutation	SNP	G	A	12	374	c.395G>A	c.(394-396)AGC>AAC	p.S132N
Pat_41	Post-Resistance	ZNF572	137209	37	8	125988797	125988797	Missense_Mutation	SNP	G	A	19	134	c.287G>A	c.(286-288)GGA>GAA	p.G96E
Pat_41	Post-Resistance	ZNF572	137209	37	8	125989117	125989117	Missense_Mutation	SNP	C	T	18	272	c.607C>T	c.(607-609)CTT>TTT	p.L203F
Pat_41	Post-Resistance	KIAA0196	9897	37	8	126085397	126085397	Missense_Mutation	SNP	G	A	27	171	c.1148C>T	c.(1147-1149)TCA>TTA	p.S383L
Pat_41	Post-Resistance	MYC	4609	37	8	128751046	128751046	Missense_Mutation	SNP	G	A	10	90	c.583G>A	c.(583-585)GAT>AAT	p.D195N
Pat_41	Post-Resistance	FAM49B	51571	37	8	130864442	130864442	Missense_Mutation	SNP	G	A	17	199	c.599C>T	c.(598-600)ACC>ATC	p.T200I
Pat_41	Post-Resistance	ASAP1	50807	37	8	131070323	131070323	Splice_Site	SNP	C	T	7	125	c.3193_splice	c.e28-1	.G1065_splice
Pat_41	Post-Resistance	ADCY8	114	37	8	131880179	131880179	Missense_Mutation	SNP	C	T	28	126	c.2123G>A	c.(2122-2124)AGG>AAG	p.R708K
Pat_41	Post-Resistance	EFR3A	23167	37	8	132971875	132971875	Missense_Mutation	SNP	G	A	6	152	c.820G>A	c.(820-822)GTT>ATT	p.V274I
Pat_41	Post-Resistance	EFR3A	23167	37	8	133014911	133014911	Missense_Mutation	SNP	G	T	10	108	c.2268G>T	c.(2266-2268)CAG>CAT	p.Q756H
Pat_41	Post-Resistance	PHF20L1	51105	37	8	133827045	133827045	Missense_Mutation	SNP	C	T	18	365	c.1094C>T	c.(1093-1095)CCC>CTC	p.P365L
Pat_41	Post-Resistance	TG	7038	37	8	134125739	134125739	Missense_Mutation	SNP	G	A	14	134	c.7646G>A	c.(7645-7647)GGC>GAC	p.G2549D

Pat_41	Post-Resistance	WISP1	8840	37	8	134237642	134237642	Missense_Mutation	SNP	G	A	49	346	c.620G>A	c.(619-621)GGT>GAT	p.G207D
Pat_41	Post-Resistance	ST3GAL1	6482	37	8	134477115	134477115	Missense_Mutation	SNP	C	T	24	348	c.589G>A	c.(589-591)GAG>AAG	p.E197K
Pat_41	Post-Resistance	ZFAT	57623	37	8	135577626	135577626	Missense_Mutation	SNP	C	T	16	190	c.2926G>A	c.(2926-2928)GCC>ACC	p.A976T
Pat_41	Post-Resistance	COL22A1	169044	37	8	139606439	139606439	Missense_Mutation	SNP	C	T	4	69	c.4436G>A	c.(4435-4437)AGA>AAA	p.R1479K
Pat_41	Post-Resistance	COL22A1	169044	37	8	139703116	139703116	Missense_Mutation	SNP	C	T	5	61	c.2756G>A	c.(2755-2757)GGT>GAT	p.G919D
Pat_41	Post-Resistance	TRAPPC9	83696	37	8	141461088	141461088	Missense_Mutation	SNP	G	A	12	120	c.385C>T	c.(385-387)CGC>TGC	p.R129C
Pat_41	Post-Resistance	PTK2	5747	37	8	141712714	141712714	Nonsense_Mutation	SNP	C	T	20	387	c.2322G>A	c.(2320-2322)TGG>TGA	p.W774*
Pat_41	Post-Resistance	DENND3	22898	37	8	142146714	142146714	Translation_Start_Site	SNP	G	A	4	25	c.-31G>A	c.(-33--29)CGGTG>CGATG	
Pat_41	Post-Resistance	DENND3	22898	37	8	142176489	142176489	Splice_Site	SNP	G	A	4	109	c.1513_splice	c.e12+1	p.V505_splice
Pat_41	Post-Resistance	TSNARE1	203062	37	8	143425575	143425575	Missense_Mutation	SNP	C	T	15	241	c.497G>A	c.(496-498)CGC>CAC	p.R166H
Pat_41	Post-Resistance	TSNARE1	203062	37	8	143427211	143427211	Missense_Mutation	SNP	G	A	8	204	c.131C>T	c.(130-132)CCC>CTC	p.P44L
Pat_41	Post-Resistance	BAI1	575	37	8	143603435	143603435	Missense_Mutation	SNP	G	T	3	53	c.3134G>T	c.(3133-3135)CGG>CTG	p.R1045L
Pat_41	Post-Resistance	GML	2765	37	8	143921857	143921857	Missense_Mutation	SNP	C	T	5	87	c.4C>T	c.(4-6)CTC>TTC	p.L2F
Pat_41	Post-Resistance	CYP11B1	1584	37	8	143961144	143961144	Missense_Mutation	SNP	G	A	9	38	c.86C>T	c.(85-87)GCC>GTC	p.A29V
Pat_41	Post-Resistance	GLI4	2738	37	8	144358607	144358607	Missense_Mutation	SNP	C	T	8	145	c.764C>T	c.(763-765)ACG>ATG	p.T255M
Pat_41	Post-Resistance	FAM83H	286077	37	8	144808356	144808356	Missense_Mutation	SNP	G	A	3	46	c.3275C>T	c.(3274-3276)GCC>GTC	p.A1092V
Pat_41	Post-Resistance	EPPK1	83481	37	8	144943070	144943070	Missense_Mutation	SNP	C	T	15	60	c.4352G>A	c.(4351-4353)AGG>AAG	p.R1451K
Pat_41	Post-Resistance	PLEC	5339	37	8	144990973	144990973	Missense_Mutation	SNP	C	T	6	147	c.13427G>A	c.(13426-13428)GGC>GAC	p.G4476D
Pat_41	Post-Resistance	PLEC	5339	37	8	144997775	144997775	Missense_Mutation	SNP	G	A	9	53	c.6733C>T	c.(6733-6735)CGG>TGG	p.R2245W
Pat_41	Post-Resistance	PLEC	5339	37	8	145012819	145012819	Missense_Mutation	SNP	C	T	16	311	c.565G>A	c.(565-567)GTC>ATC	p.V189I
Pat_41	Post-Resistance	GRINA	2907	37	8	145065764	145065764	Missense_Mutation	SNP	C	T	7	196	c.373C>T	c.(373-375)CCT>TCT	p.P125S
Pat_41	Post-Resistance	OPLAH	26873	37	8	145111352	145111352	Missense_Mutation	SNP	C	T	4	26	c.1919G>A	c.(1918-1920)GGC>GAC	p.G640D
Pat_41	Post-Resistance	OPLAH	26873	37	8	145111358	145111358	Missense_Mutation	SNP	C	T	3	24	c.1913G>A	c.(1912-1914)GGC>GAC	p.G638D
Pat_41	Post-Resistance	GPAA1	8733	37	8	145139502	145139502	Missense_Mutation	SNP	G	A	12	136	c.1000G>A	c.(1000-1002)GCA>ACA	p.A334T
Pat_41	Post-Resistance	SHARPIN	81858	37	8	145154251	145154251	Missense_Mutation	SNP	G	A	6	113	c.851C>T	c.(850-852)GCC>GTC	p.A284V
Pat_41	Post-Resistance	HEATR7A	727957	37	8	145245825	145245825	Missense_Mutation	SNP	G	A	5	36	c.701G>A	c.(700-702)AGT>AAT	p.S234N
Pat_41	Post-Resistance	HEATR7A	727957	37	8	145247237	145247237	Missense_Mutation	SNP	C	T	4	27	c.881C>T	c.(880-882)GCT>GTT	p.A294V
Pat_41	Post-Resistance	HSF1	3297	37	8	145537564	145537564	Missense_Mutation	SNP	G	A	13	257	c.1304G>A	c.(1303-1305)AGC>AAC	p.S435N
Pat_41	Post-Resistance	DGAT1	8694	37	8	145541660	145541660	Missense_Mutation	SNP	C	T	16	100	c.772G>A	c.(772-774)GCC>ACC	p.A258T
Pat_41	Post-Resistance	FBXL6	26233	37	8	145580576	145580576	Splice_Site	SNP	C	T	5	61	c.772_splice	c.e5-1	p.V258_splice
Pat_41	Post-Resistance	ADCK5	203054	37	8	145616060	145616060	Missense_Mutation	SNP	G	A	15	153	c.347G>A	c.(346-348)AGC>AAC	p.S116N
Pat_41	Post-Resistance	CPSF1	29894	37	8	145623961	145623961	Missense_Mutation	SNP	C	T	22	260	c.1706G>A	c.(1705-1707)GGC>GAC	p.G569D
Pat_41	Post-Resistance	CPSF1	29894	37	8	145624695	145624695	Missense_Mutation	SNP	C	T	9	151	c.1363G>A	c.(1363-1365)GGA>AGA	p.G455R
Pat_41	Post-Resistance	NFKBIL2	4796	37	8	145661985	145661985	Missense_Mutation	SNP	G	A	6	38	c.1970C>T	c.(1969-1971)GCC>GTC	p.A657V
Pat_41	Post-Resistance	NFKBIL2	4796	37	8	145665547	145665547	Missense_Mutation	SNP	G	A	6	122	c.1337C>T	c.(1336-1338)CCC>CTC	p.P446L
Pat_41	Post-Resistance	GPT	2875	37	8	145730175	145730175	Missense_Mutation	SNP	C	T	42	617	c.274C>T	c.(274-276)CCT>TCT	p.P92S
Pat_41	Post-Resistance	LRRC14	9684	37	8	145746452	145746452	Missense_Mutation	SNP	G	A	15	104	c.1072G>A	c.(1072-1074)GGT>AGT	p.G358S
Pat_41	Post-Resistance	ZNF34	80778	37	8	146003512	146003512	Missense_Mutation	SNP	G	A	4	89	c.134C>T	c.(133-135)TCC>TTC	p.S45F
Pat_41	Post-Resistance	ZNF7	7553	37	8	146067688	146067688	Missense_Mutation	SNP	G	A	7	134	c.1196G>A	c.(1195-1197)AGC>AAC	p.S399N
Pat_41	Post-Resistance	ZNF7	7553	37	8	146068449	146068449	Nonsense_Mutation	SNP	C	T	9	165	c.1957C>T	c.(1957-1959)CAG>TAG	p.Q653*
Pat_41	Post-Resistance	ZNF250	58500	37	8	146107292	146107292	Missense_Mutation	SNP	C	T	11	222	c.1291G>A	c.(1291-1293)GCC>ACC	p.A431T
Pat_41	Post-Resistance	FOXD4	2298	37	9	117939	117939	Missense_Mutation	SNP	C	T	7	62	c.181G>A	c.(181-183)GGC>AGC	p.G61S
Pat_41	Post-Resistance	DOCK8	81704	37	9	428399	428399	Missense_Mutation	SNP	G	A	11	85	c.4376G>A	c.(4375-4377)GGA>GAA	p.G1459E
Pat_41	Post-Resistance	KANK1	23189	37	9	711024	711024	Nonsense_Mutation	SNP	G	A	12	74	c.258G>A	c.(256-258)TGG>TGA	p.W86*
Pat_41	Post-Resistance	KANK1	23189	37	9	738385	738385	Missense_Mutation	SNP	C	T	34	82	c.3434C>T	c.(3433-3435)GCC>GTC	p.A1145V
Pat_41	Post-Resistance	KIAA0020	9933	37	9	2837362	2837362	Missense_Mutation	SNP	G	A	3	34	c.122C>T	c.(121-123)GCT>GTT	p.A41V
Pat_41	Post-Resistance	RFX3	5991	37	9	3346713	3346713	Missense_Mutation	SNP	C	T	18	170	c.169G>A	c.(169-171)GTG>ATG	p.V57M

Pat_41	Post-Resistance	RCL1	10171	37	9	4844622	4844622	Missense_Mutation	SNP	G	A	33	135	c.808G>A	c.(808-810)GTA>ATA	p.V270I
Pat_41	Post-Resistance	ERMP1	79956	37	9	5810154	5810154	Missense_Mutation	SNP	G	A	22	211	c.1405C>T	c.(1405-1407)CTC>TTC	p.L469F
Pat_41	Post-Resistance	KIAA2026	158358	37	9	6007224	6007224	Missense_Mutation	SNP	C	T	24	151	c.564G>A	c.(562-564)ATG>ATA	p.M188I
Pat_41	Post-Resistance	KDM4C	23081	37	9	7103728	7103728	Missense_Mutation	SNP	C	T	27	81	c.2468C>T	c.(2467-2469)GCC>GTC	p.A823V
Pat_41	Post-Resistance	PTPRD	5789	37	9	8500931	8500931	Missense_Mutation	SNP	C	T	47	195	c.1951G>A	c.(1951-1953)GCA>ACA	p.A651T
Pat_41	Post-Resistance	MPDZ	8777	37	9	13221445	13221445	Missense_Mutation	SNP	C	T	9	91	c.802G>A	c.(802-804)GGA>AGA	p.G268R
Pat_41	Post-Resistance	C9orf93	203238	37	9	15678820	15678820	Missense_Mutation	SNP	G	A	3	13	c.1141G>A	c.(1141-1143)GTA>ATA	p.V381I
Pat_41	Post-Resistance	DENND4C	55667	37	9	19360267	19360267	Missense_Mutation	SNP	C	T	23	151	c.4331C>T	c.(4330-4332)CCT>CTT	p.P1444L
Pat_41	Post-Resistance	ACER2	340485	37	9	19450551	19450551	Missense_Mutation	SNP	C	T	25	54	c.745C>T	c.(745-747)CCC>TCC	p.P249S
Pat_41	Post-Resistance	SLC24A2	25769	37	9	19786422	19786422	Missense_Mutation	SNP	G	A	4	50	c.443C>T	c.(442-444)GCC>GTC	p.A148V
Pat_41	Post-Resistance	MLLT3	4300	37	9	20363517	20363517	Missense_Mutation	SNP	C	T	11	63	c.1288G>A	c.(1288-1290)GAA>AAA	p.E430K
Pat_41	Post-Resistance	IFNA16	3449	37	9	21216814	21216814	Nonsense_Mutation	SNP	C	T	69	480	c.491G>A	c.(490-492)TGG>TAG	p.W164*
Pat_41	Post-Resistance	DMRTA1	63951	37	9	22451101	22451101	Nonsense_Mutation	SNP	C	T	13	88	c.706C>T	c.(706-708)CAA>TAA	p.Q236*
Pat_41	Post-Resistance	C9orf72	203228	37	9	27562426	27562426	Missense_Mutation	SNP	C	T	24	160	c.553G>A	c.(553-555)GAA>AAA	p.E185K
Pat_41	Post-Resistance	C9orf72	203228	37	9	27566773	27566773	Missense_Mutation	SNP	G	A	36	81	c.346C>T	c.(346-348)CTT>TTT	p.L116F
Pat_41	Post-Resistance	NOL6	65083	37	9	33469208	33469208	Missense_Mutation	SNP	C	T	12	57	c.859G>A	c.(859-861)GAT>AAT	p.D287N
Pat_41	Post-Resistance	UBAP2	55833	37	9	33922537	33922537	Missense_Mutation	SNP	G	A	4	21	c.3325C>T	c.(3325-3327)CCT>TCT	p.P1109S
Pat_41	Post-Resistance	DCAF12	25853	37	9	34093419	34093419	Missense_Mutation	SNP	G	A	4	69	c.889C>T	c.(889-891)CGT>TGT	p.R297C
Pat_41	Post-Resistance	IL11RA	3590	37	9	34657458	34657458	Missense_Mutation	SNP	C	T	6	50	c.520C>T	c.(520-522)CCC>TCC	p.P174S
Pat_41	Post-Resistance	C9orf131	138724	37	9	35043155	35043155	Missense_Mutation	SNP	C	T	5	54	c.529C>T	c.(529-531)CCT>TCT	p.P177S
Pat_41	Post-Resistance	C9orf131	138724	37	9	35043738	35043738	Missense_Mutation	SNP	C	T	14	78	c.1112C>T	c.(1111-1113)ACC>ATC	p.T371I
Pat_41	Post-Resistance	C9orf131	138724	37	9	35044205	35044205	Missense_Mutation	SNP	C	T	54	200	c.1579C>T	c.(1579-1581)CCA>TCA	p.P527S
Pat_41	Post-Resistance	C9orf131	138724	37	9	35044316	35044316	Missense_Mutation	SNP	C	T	19	145	c.1690C>T	c.(1690-1692)CCA>TCA	p.P564S
Pat_41	Post-Resistance	CD72	971	37	9	35611800	35611800	Splice_Site	SNP	C	T	24	56	c.950_splice	c.e7+1	p.R317_splice
Pat_41	Post-Resistance	CA9	768	37	9	35680970	35680970	Missense_Mutation	SNP	C	T	9	134	c.1328C>T	c.(1327-1329)ACC>ATC	p.T443I
Pat_41	Post-Resistance	NPR2	4882	37	9	35800146	35800146	Missense_Mutation	SNP	G	A	11	147	c.1115G>A	c.(1114-1116)AGA>AAA	p.R372K
Pat_41	Post-Resistance	CLTA	1211	37	9	36199075	36199075	Missense_Mutation	SNP	G	A	39	105	c.355G>A	c.(355-357)GAA>AAA	p.E119K
Pat_41	Post-Resistance	POLR1E	64425	37	9	37503099	37503099	Missense_Mutation	SNP	C	T	6	30	c.1346C>T	c.(1345-1347)GCC>GTC	p.A449V
Pat_41	Post-Resistance	PIP5K1B	8395	37	9	71532542	71532542	Missense_Mutation	SNP	G	A	31	121	c.850G>A	c.(850-852)GAG>AAG	p.E284K
Pat_41	Post-Resistance	VPS13A	23230	37	9	79952399	79952399	Nonsense_Mutation	SNP	G	A	15	136	c.6324G>A	c.(6322-6324)TGG>TGA	p.W2108*
Pat_41	Post-Resistance	CEP78	84131	37	9	80861630	80861630	Missense_Mutation	SNP	C	T	15	69	c.824C>T	c.(823-825)GCT>GTT	p.A275V
Pat_41	Post-Resistance	TLE4	7091	37	9	82333666	82333666	Missense_Mutation	SNP	G	A	9	45	c.1445G>A	c.(1444-1446)GGT>GAT	p.G482D
Pat_41	Post-Resistance	RASEF	158158	37	9	85605342	85605342	Missense_Mutation	SNP	C	T	6	195	c.2081G>A	c.(2080-2082)GGT>GAT	p.G694D
Pat_41	Post-Resistance	UBQLN1	29979	37	9	86297946	86297946	Missense_Mutation	SNP	G	A	14	132	c.368C>T	c.(367-369)GCT>GTT	p.A123V
Pat_41	Post-Resistance	GKAP1	80318	37	9	86383767	86383767	Missense_Mutation	SNP	C	T	5	55	c.704G>A	c.(703-705)GGA>GAA	p.G235E
Pat_41	Post-Resistance	KIF27	55582	37	9	86452059	86452059	Missense_Mutation	SNP	G	A	8	73	c.4063C>T	c.(4063-4065)CCT>TCT	p.P1355S
Pat_41	Post-Resistance	C9orf64	84267	37	9	86571229	86571229	Missense_Mutation	SNP	C	T	11	27	c.187G>A	c.(187-189)GCC>ACC	p.A63T
Pat_41	Post-Resistance	RMI1	80010	37	9	86616913	86616913	Missense_Mutation	SNP	C	T	7	33	c.1012C>T	c.(1012-1014)CCA>TCA	p.P338S
Pat_41	Post-Resistance	DAPK1	1612	37	9	90263777	90263777	Missense_Mutation	SNP	C	T	21	170	c.1411C>T	c.(1411-1413)CCC>TCC	p.P471S
Pat_41	Post-Resistance	CTSL3	392360	37	9	90401723	90401723	Missense_Mutation	SNP	G	A	18	58	c.575G>A	c.(574-576)GGT>GAT	p.G192D
Pat_41	Post-Resistance	SECISBP2	79048	37	9	91943656	91943656	Missense_Mutation	SNP	C	T	7	104	c.656C>T	c.(655-657)ACC>ATC	p.T219I
Pat_41	Post-Resistance	SEMA4D	10507	37	9	92003963	92003963	Splice_Site	SNP	C	T	10	29	c.775_splice	c.e12-1	p.G259_splice
Pat_41	Post-Resistance	SYK	6850	37	9	93640016	93640016	Missense_Mutation	SNP	G	A	5	89	c.1345G>A	c.(1345-1347)GAG>AAG	p.E449K
Pat_41	Post-Resistance	ROR2	4920	37	9	94486207	94486207	Missense_Mutation	SNP	G	A	6	53	c.2569C>T	c.(2569-2571)CCC>TCC	p.P857S
Pat_41	Post-Resistance	ROR2	4920	37	9	94519784	94519784	Missense_Mutation	SNP	G	A	3	40	c.233C>T	c.(232-234)ACG>ATG	p.T78M
Pat_41	Post-Resistance	SPTLC1	10558	37	9	94797091	94797091	Splice_Site	SNP	C	T	19	112	c.1328_splice	c.e14+1	p.S443_splice
Pat_41	Post-Resistance	WNK2	65268	37	9	95993352	95993352	Missense_Mutation	SNP	C	T	72	142	c.1037C>T	c.(1036-1038)GCC>GTC	p.A346V

Pat_41	Post-Resistance	ZNF169	169841	37	9	97054659	97054659	Missense_Mutation	SNP	A	G	31	103	c.70A>G	c.(70-72)ACC>GCC	p.T24A
Pat_41	Post-Resistance	C9orf3	84909	37	9	97522426	97522426	Missense_Mutation	SNP	C	T	7	321	c.361C>T	c.(361-363)CAT>TAT	p.H121Y
Pat_41	Post-Resistance	PTCH1	5727	37	9	98209459	98209459	Missense_Mutation	SNP	G	A	8	17	c.4079C>T	c.(4078-4080)TCC>TTC	p.S1360F
Pat_41	Post-Resistance	CDC14B	8555	37	9	99327738	99327738	Missense_Mutation	SNP	C	T	23	203	c.188G>A	c.(187-189)AGC>AAC	p.S63N
Pat_41	Post-Resistance	TDRD7	23424	37	9	100190809	100190809	Missense_Mutation	SNP	G	A	18	58	c.62G>A	c.(61-63)GGA>GAA	p.G21E
Pat_41	Post-Resistance	TDRD7	23424	37	9	100222550	100222550	Missense_Mutation	SNP	G	A	5	50	c.946G>A	c.(946-948)GTA>ATA	p.V316I
Pat_41	Post-Resistance	TBC1D2	55357	37	9	100963810	100963810	Missense_Mutation	SNP	C	T	11	87	c.2408G>A	c.(2407-2409)AGC>AAC	p.S803N
Pat_41	Post-Resistance	ANKS6	203286	37	9	101552434	101552434	Missense_Mutation	SNP	C	T	22	85	c.814G>A	c.(814-816)GAC>AAC	p.D272N
Pat_41	Post-Resistance	STX17	55014	37	9	102730902	102730902	Missense_Mutation	SNP	C	T	6	91	c.856C>T	c.(856-858)CTC>TTC	p.L286F
Pat_41	Post-Resistance	LPPR1	54886	37	9	104075216	104075216	Missense_Mutation	SNP	T	A	275	37	c.773T>A	c.(772-774)ATT>AAT	p.I258N
Pat_41	Post-Resistance	MRPL50	54534	37	9	104153098	104153098	Missense_Mutation	SNP	C	T	10	56	c.127G>A	c.(127-129)GAA>AAA	p.E43K
Pat_41	Post-Resistance	SMC2	10592	37	9	106901489	106901489	Missense_Mutation	SNP	G	A	9	74	c.3487G>A	c.(3487-3489)GAT>AAT	p.D1163N
Pat_41	Post-Resistance	OR13C9	286362	37	9	107380046	107380046	Missense_Mutation	SNP	C	T	14	131	c.440G>A	c.(439-441)GGG>GAG	p.G147E
Pat_41	Post-Resistance	ABCA1	19	37	9	107562184	107562184	Missense_Mutation	SNP	T	C	3	99	c.4859A>G	c.(4858-4860)AAG>AGG	p.K1620R
Pat_41	Post-Resistance	ZNF462	58499	37	9	109765657	109765657	Missense_Mutation	SNP	G	A	9	45	c.7139G>A	c.(7138-7140)AGC>AAC	p.S2380N
Pat_41	Post-Resistance	CTNNAL1	8727	37	9	111706289	111706289	Missense_Mutation	SNP	C	T	5	140	c.1894G>A	c.(1894-1896)GCA>ACA	p.A632T
Pat_41	Post-Resistance	C9orf5	23731	37	9	111822716	111822716	Missense_Mutation	SNP	C	T	29	69	c.1640G>A	c.(1639-1641)GGA>GAA	p.G547E
Pat_41	Post-Resistance	SVEP1	79987	37	9	113192285	113192285	Splice_Site	SNP	C	T	20	67	c.5531_splice	c.e34-1	p.A1844_splice
Pat_41	Post-Resistance	LPAR1	1902	37	9	113637878	113637878	Missense_Mutation	SNP	C	T	92	22	c.918G>A	c.(916-918)ATG>ATA	p.M306I
Pat_41	Post-Resistance	KIAA0368	23392	37	9	114134762	114134762	Missense_Mutation	SNP	G	A	20	139	c.5009C>T	c.(5008-5010)TCC>TTC	p.S1670F
Pat_41	Post-Resistance	UGCG	7357	37	9	114695126	114695126	Missense_Mutation	SNP	C	T	28	85	c.1034C>T	c.(1033-1035)TCA>TTA	p.S345L
Pat_41	Post-Resistance	ALAD	210	37	9	116155769	116155769	Missense_Mutation	SNP	G	A	6	66	c.71C>T	c.(70-72)ACC>ATC	p.T24I
Pat_41	Post-Resistance	C9orf43	257169	37	9	116185634	116185634	Missense_Mutation	SNP	G	A	20	48	c.512G>A	c.(511-513)GGA>GAA	p.G171E
Pat_41	Post-Resistance	RGS3	5998	37	9	116224012	116224012	Missense_Mutation	SNP	C	T	9	93	c.106C>T	c.(106-108)CCC>TCC	p.P36S
Pat_41	Post-Resistance	AMBP	259	37	9	116838957	116838957	Missense_Mutation	SNP	C	T	20	80	c.181G>A	c.(181-183)GAC>AAC	p.D61N
Pat_41	Post-Resistance	COL27A1	85301	37	9	116967403	116967403	Missense_Mutation	SNP	C	T	10	90	c.2146C>T	c.(2146-2148)CCG>TCG	p.P716S
Pat_41	Post-Resistance	COL27A1	85301	37	9	116999979	116999979	Missense_Mutation	SNP	G	A	6	53	c.2711G>A	c.(2710-2712)GGG>GAG	p.G904E
Pat_41	Post-Resistance	COL27A1	85301	37	9	117062942	117062942	Missense_Mutation	SNP	G	A	7	20	c.4676G>A	c.(4675-4677)GGC>GAC	p.G1559D
Pat_41	Post-Resistance	AKNA	80709	37	9	117106084	117106084	Splice_Site	SNP	C	T	5	40	c.3662_splice	c.e18-1	p.G1221_splice
Pat_41	Post-Resistance	DFNB31	25861	37	9	117166342	117166342	Missense_Mutation	SNP	G	A	5	32	c.2252C>T	c.(2251-2253)TCC>TTC	p.S751F
Pat_41	Post-Resistance	ASTN2	23245	37	9	119413883	119413883	Missense_Mutation	SNP	C	T	10	83	c.2996G>A	c.(2995-2997)AGC>AAC	p.S999N
Pat_41	Post-Resistance	TRIM32	22954	37	9	119460041	119460041	Missense_Mutation	SNP	C	T	9	51	c.20C>T	c.(19-21)TCT>TTT	p.S7F
Pat_41	Post-Resistance	C5	727	37	9	123739097	123739097	Missense_Mutation	SNP	C	T	9	121	c.3745G>A	c.(3745-3747)GAA>AAA	p.E1249K
Pat_41	Post-Resistance	C5	727	37	9	123770685	123770685	Splice_Site	SNP	C	T	40	90	c.2348_splice	c.e18+1	p.R783_splice
Pat_41	Post-Resistance	C5	727	37	9	123777506	123777506	Missense_Mutation	SNP	C	T	3	63	c.2030G>A	c.(2029-2031)AGA>AAA	p.R677K
Pat_41	Post-Resistance	C5	727	37	9	123778579	123778579	Missense_Mutation	SNP	C	T	25	130	c.1949G>A	c.(1948-1950)GGA>GAA	p.G650E
Pat_41	Post-Resistance	CEP110	11064	37	9	123920340	123920340	Missense_Mutation	SNP	G	A	4	44	c.4717G>A	c.(4717-4719)GTG>ATG	p.V1573M
Pat_41	Post-Resistance	OR1J1	347168	37	9	125239683	125239683	Missense_Mutation	SNP	G	A	12	22	c.523C>T	c.(523-525)CCT>TCT	p.P175S
Pat_41	Post-Resistance	OR1N1	138883	37	9	125288851	125288851	Missense_Mutation	SNP	G	A	50	10	c.722C>T	c.(721-723)TCC>TTC	p.S241F
Pat_41	Post-Resistance	OR1L3	26735	37	9	125437417	125437417	Missense_Mutation	SNP	G	A	4	135	c.9G>A	c.(7-9)ATG>ATA	p.M3I
Pat_41	Post-Resistance	OR1L4	254973	37	9	125486969	125486969	Missense_Mutation	SNP	G	A	21	237	c.701G>A	c.(700-702)GGG>GAG	p.G234E
Pat_41	Post-Resistance	OR5C1	392391	37	9	125551815	125551815	Missense_Mutation	SNP	C	T	4	54	c.604C>T	c.(604-606)CTT>TTT	p.L202F
Pat_41	Post-Resistance	SCAI	286205	37	9	127733699	127733699	Missense_Mutation	SNP	T	C	12	81	c.1624A>G	c.(1624-1626)ACA>GCA	p.T542A
Pat_41	Post-Resistance	HSPA5	3309	37	9	128003049	128003049	Missense_Mutation	SNP	T	C	22	130	c.260A>G	c.(259-261)AAC>AGC	p.N87S
Pat_41	Post-Resistance	RALGPS1	9649	37	9	129728169	129728169	Missense_Mutation	SNP	C	T	15	125	c.104C>T	c.(103-105)GCC>GTC	p.A35V
Pat_41	Post-Resistance	LRSAM1	90678	37	9	130236172	130236172	Missense_Mutation	SNP	C	T	4	61	c.712C>T	c.(712-714)CCC>TCC	p.P238S
Pat_41	Post-Resistance	FAM129B	64855	37	9	130286123	130286123	Missense_Mutation	SNP	T	A	33	69	c.424A>T	c.(424-426)ACC>TCC	p.T142S

Pat_41	Post-Resistance	ST6GALNAC6	30815	37	9	130652997	130652997	Missense_Mutation	SNP	G	A	15	69	c.623C>T	c.(622-624)CCC>CTC	p.P208L
Pat_41	Post-Resistance	ST6GALNAC4	27090	37	9	130672239	130672239	Missense_Mutation	SNP	C	T	4	33	c.710G>A	c.(709-711)AGC>AAC	p.S237N
Pat_41	Post-Resistance	DPM2	8818	37	9	130699801	130699801	Missense_Mutation	SNP	G	A	4	20	c.5C>T	c.(4-6)GCC>GTC	p.A2V
Pat_41	Post-Resistance	PTGES2	80142	37	9	130885987	130885987	Missense_Mutation	SNP	G	A	5	57	c.680C>T	c.(679-681)GCC>GTC	p.A227V
Pat_41	Post-Resistance	CIZ1	25792	37	9	130931372	130931372	Missense_Mutation	SNP	C	T	8	184	c.2254G>A	c.(2254-2256)GAT>AAT	p.D752N
Pat_41	Post-Resistance	GOLGA2	2801	37	9	131022360	131022360	Missense_Mutation	SNP	C	T	10	40	c.1786G>A	c.(1786-1788)GAA>AAA	p.E596K
Pat_41	Post-Resistance	CERCAM	51148	37	9	131191057	131191057	Missense_Mutation	SNP	C	T	14	78	c.908C>T	c.(907-909)GCC>GTC	p.A303V
Pat_41	Post-Resistance	DOLK	22845	37	9	131708828	131708828	Missense_Mutation	SNP	G	A	4	48	c.755C>T	c.(754-756)ACC>ATC	p.T252I
Pat_41	Post-Resistance	CRAT	1384	37	9	131860302	131860302	Missense_Mutation	SNP	G	A	26	103	c.1454C>T	c.(1453-1455)TCC>TTC	p.S485F
Pat_41	Post-Resistance	LAMC3	10319	37	9	133917032	133917032	Missense_Mutation	SNP	C	T	10	33	c.1292C>T	c.(1291-1293)ACT>ATT	p.T431I
Pat_41	Post-Resistance	NUP214	8021	37	9	134073823	134073823	Missense_Mutation	SNP	C	T	24	111	c.4942C>T	c.(4942-4944)CCT>TCT	p.P1648S
Pat_41	Post-Resistance	BAT2L1	84726	37	9	134353234	134353234	Missense_Mutation	SNP	C	T	3	22	c.4510C>T	c.(4510-4512)CCC>TCC	p.P1504S
Pat_41	Post-Resistance	BAT2L1	84726	37	9	134362594	134362594	Missense_Mutation	SNP	C	T	7	42	c.5897C>T	c.(5896-5898)TCT>TTT	p.S1966F
Pat_41	Post-Resistance	RAPGEF1	2889	37	9	134458071	134458071	Missense_Mutation	SNP	T	C	6	104	c.2875A>G	c.(2875-2877)ACA>GCA	p.T959A
Pat_41	Post-Resistance	SETX	23064	37	9	135202229	135202229	Missense_Mutation	SNP	G	A	7	127	c.4756C>T	c.(4756-4758)CCT>TCT	p.P1586S
Pat_41	Post-Resistance	MED22	6837	37	9	136211178	136211178	Missense_Mutation	SNP	C	T	7	44	c.215G>A	c.(214-216)GGC>GAC	p.G72D
Pat_41	Post-Resistance	SURF1	6834	37	9	136221547	136221547	Missense_Mutation	SNP	C	A	20	311	c.290G>T	c.(289-291)AGA>ATA	p.R97I
Pat_41	Post-Resistance	SARDH	1757	37	9	136568051	136568051	Missense_Mutation	SNP	G	A	5	42	c.1655C>T	c.(1654-1656)CCC>CTC	p.P552L
Pat_41	Post-Resistance	SARDH	1757	37	9	136597637	136597637	Missense_Mutation	SNP	C	T	66	178	c.418G>A	c.(418-420)GAG>AAG	p.E140K
Pat_41	Post-Resistance	BRD3	8019	37	9	136913400	136913400	Missense_Mutation	SNP	C	A	6	25	c.891G>T	c.(889-891)GAG>GAT	p.E297D
Pat_41	Post-Resistance	BRD3	8019	37	9	136913488	136913488	Missense_Mutation	SNP	G	A	6	34	c.803C>T	c.(802-804)TCA>TTA	p.S268L
Pat_41	Post-Resistance	WDR5	11091	37	9	137005070	137005070	Missense_Mutation	SNP	C	T	15	54	c.71C>T	c.(70-72)ACT>ATT	p.T24I
Pat_41	Post-Resistance	COL5A1	1289	37	9	137693854	137693854	Splice_Site	SNP	G	A	4	47	c.3006_splice	c.e38+1	p.Q1002_splice
Pat_41	Post-Resistance	KCNT1	57582	37	9	138651556	138651556	Missense_Mutation	SNP	G	A	9	27	c.886G>A	c.(886-888)GGC>AGC	p.G296S
Pat_41	Post-Resistance	CAMSAP1	157922	37	9	138712831	138712831	Missense_Mutation	SNP	G	A	3	7	c.3676C>T	c.(3676-3678)CCT>TCT	p.P1226S
Pat_41	Post-Resistance	CAMSAP1	157922	37	9	138716676	138716676	Missense_Mutation	SNP	C	T	6	19	c.1274G>A	c.(1273-1275)AGA>AAA	p.R425K
Pat_41	Post-Resistance	SEC16A	9919	37	9	139369229	139369229	Missense_Mutation	SNP	C	T	4	92	c.2839G>A	c.(2839-2841)GCA>ACA	p.A947T
Pat_41	Post-Resistance	SEC16A	9919	37	9	139370783	139370783	Missense_Mutation	SNP	G	A	11	36	c.1285C>T	c.(1285-1287)CCA>TCA	p.P429S
Pat_41	Post-Resistance	NOTCH1	4851	37	9	139391956	139391956	Missense_Mutation	SNP	C	T	3	30	c.6235G>A	c.(6235-6237)GTG>ATG	p.V2079M
Pat_41	Post-Resistance	MAMDC4	158056	37	9	139752008	139752008	Missense_Mutation	SNP	C	T	20	44	c.2296C>T	c.(2296-2298)CCA>TCA	p.P766S
Pat_41	Post-Resistance	NPDC1	56654	37	9	139934304	139934304	Missense_Mutation	SNP	C	T	7	49	c.898G>A	c.(898-900)GAG>AAG	p.E300K
Pat_41	Post-Resistance	DPP7	29952	37	9	140006162	140006162	Missense_Mutation	SNP	C	T	9	47	c.1252G>A	c.(1252-1254)GAC>AAC	p.D418N
Pat_41	Post-Resistance	ANAPC2	29882	37	9	140077608	140077608	Missense_Mutation	SNP	C	T	7	98	c.1255G>A	c.(1255-1257)GTG>ATG	p.V419M
Pat_41	Post-Resistance	PNPLA7	375775	37	9	140358901	140358901	Missense_Mutation	SNP	G	A	18	87	c.2972C>T	c.(2971-2973)ACG>ATG	p.T991M
Pat_41	Post-Resistance	ARRDC1	92714	37	9	140508073	140508073	Missense_Mutation	SNP	C	T	38	41	c.287C>T	c.(286-288)GCA>GTA	p.A96V
Pat_41	Post-Resistance	ARRDC1	92714	37	9	140509416	140509416	Missense_Mutation	SNP	C	T	5	73	c.1201C>T	c.(1201-1203)CTT>TTT	p.L401F
Pat_41	Post-Resistance	CACNA1B	774	37	9	140777284	140777284	Missense_Mutation	SNP	C	T	15	172	c.479C>T	c.(478-480)TCT>TTT	p.S160F
Pat_41	Post-Resistance	CSF2RA	1438	37	X	1424364	1424364	Missense_Mutation	SNP	C	T	37	165	c.1069C>T	c.(1069-1071)CCG>TCG	p.P357S
Pat_41	Post-Resistance	SLC25A6	293	37	X	1508422	1508422	Missense_Mutation	SNP	C	T	75	306	c.310G>A	c.(310-312)GAC>AAC	p.D104N
Pat_41	Post-Resistance	ZBED1	9189	37	X	2407863	2407863	Nonsense_Mutation	SNP	G	A	22	104	c.898C>T	c.(898-900)CAG>TAG	p.Q300*
Pat_41	Post-Resistance	CD99	4267	37	X	2641376	2641376	Missense_Mutation	SNP	G	A	13	234	c.332G>A	c.(331-333)GGA>GAA	p.G111E
Pat_41	Post-Resistance	ARSH	347527	37	X	2931166	2931166	Missense_Mutation	SNP	C	T	11	220	c.293C>T	c.(292-294)ACT>ATT	p.T98I
Pat_41	Post-Resistance	ARSF	416	37	X	3021821	3021821	Missense_Mutation	SNP	G	A	24	184	c.1121G>A	c.(1120-1122)GGC>GAC	p.G374D
Pat_41	Post-Resistance	ARSF	416	37	X	3030389	3030389	Missense_Mutation	SNP	C	T	12	138	c.1565C>T	c.(1564-1566)GCC>GTC	p.A522V
Pat_41	Post-Resistance	MXRA5	25878	37	X	3238810	3238810	Missense_Mutation	SNP	G	A	19	353	c.4916C>T	c.(4915-4917)CCT>CTT	p.P1639L
Pat_41	Post-Resistance	MXRA5	25878	37	X	3238838	3238838	Missense_Mutation	SNP	A	G	28	235	c.4888T>C	c.(4888-4890)TCC>CCC	p.S1630P
Pat_41	Post-Resistance	SHROOM2	357	37	X	9862532	9862532	Missense_Mutation	SNP	G	A	15	112	c.584G>A	c.(583-585)AGC>AAC	p.S195N

Pat_41	Post-Resistance	SHROOM2	357	37	X	9863421	9863421	Nonsense_Mutation	SNP	G	A	3	12	c.1473G>A	c.(1471-1473)TGG>TGA	p.W491*
Pat_41	Post-Resistance	WWC3	55841	37	X	10085264	10085264	Missense_Mutation	SNP	G	A	16	129	c.1165G>A	c.(1165-1167)GTC>ATC	p.V389I
Pat_41	Post-Resistance	WWC3	55841	37	X	10085394	10085394	Missense_Mutation	SNP	G	A	4	81	c.1295G>A	c.(1294-1296)GGC>GAC	p.G432D
Pat_41	Post-Resistance	AMELX	265	37	X	11316809	11316809	Missense_Mutation	SNP	C	T	38	507	c.286C>T	c.(286-288)CCC>TCC	p.P96S
Pat_41	Post-Resistance	MSL3	10943	37	X	11793181	11793181	Missense_Mutation	SNP	C	T	25	144	c.1549C>T	c.(1549-1551)CCC>TCC	p.P517S
Pat_41	Post-Resistance	ATXN3L	92552	37	X	13337953	13337953	Missense_Mutation	SNP	G	A	30	291	c.101C>T	c.(100-102)GCC>GTC	p.A34V
Pat_41	Post-Resistance	OFD1	8481	37	X	13756972	13756972	Missense_Mutation	SNP	C	T	7	235	c.320C>T	c.(319-321)ACT>ATT	p.T107I
Pat_41	Post-Resistance	GLRA2	2742	37	X	14708949	14708949	Missense_Mutation	SNP	C	T	14	206	c.1048C>T	c.(1048-1050)CGC>TGC	p.R350C
Pat_41	Post-Resistance	PIR	8544	37	X	15477779	15477779	Splice_Site	SNP	C	T	49	786	c.273_splice	c.e4+1	p.Q91_splice
Pat_41	Post-Resistance	ACE2	59272	37	X	15582271	15582271	Missense_Mutation	SNP	G	A	34	402	c.2185C>T	c.(2185-2187)CCA>TCA	p.P729S
Pat_41	Post-Resistance	ACE2	59272	37	X	15589806	15589806	Missense_Mutation	SNP	G	A	43	236	c.1778C>T	c.(1777-1779)ACC>ATC	p.T593I
Pat_41	Post-Resistance	ZRSR2	8233	37	X	15840977	15840977	Missense_Mutation	SNP	G	A	14	143	c.1061G>A	c.(1060-1062)GGC>GAC	p.G354D
Pat_41	Post-Resistance	NHS	4810	37	X	17739693	17739693	Missense_Mutation	SNP	G	A	18	240	c.985G>A	c.(985-987)GAG>AAG	p.E329K
Pat_41	Post-Resistance	NHS	4810	37	X	17745815	17745815	Missense_Mutation	SNP	G	A	23	261	c.3526G>A	c.(3526-3528)GAC>AAC	p.D1176N
Pat_41	Post-Resistance	NHS	4810	37	X	17750444	17750444	Missense_Mutation	SNP	G	A	14	158	c.4753G>A	c.(4753-4755)GCC>ACC	p.A1585T
Pat_41	Post-Resistance	RAI2	10742	37	X	17819827	17819827	Missense_Mutation	SNP	G	A	7	81	c.304C>T	c.(304-306)CCA>TCA	p.P102S
Pat_41	Post-Resistance	SCML2	10389	37	X	18343086	18343086	Missense_Mutation	SNP	A	G	6	157	c.103T>C	c.(103-105)TGG>CGG	p.W35R
Pat_41	Post-Resistance	CDKL5	6792	37	X	18622915	18622915	Missense_Mutation	SNP	G	A	74	365	c.1871G>A	c.(1870-1872)GGC>GAC	p.G624D
Pat_41	Post-Resistance	GPR64	10149	37	X	19054078	19054078	Missense_Mutation	SNP	G	A	31	293	c.244C>T	c.(244-246)CTC>TTC	p.L82F
Pat_41	Post-Resistance	CXorf23	256643	37	X	19954004	19954004	Nonsense_Mutation	SNP	G	A	32	446	c.1786C>T	c.(1786-1788)CAG>TAG	p.Q596*
Pat_41	Post-Resistance	RPS6KA3	6197	37	X	20206014	20206014	Missense_Mutation	SNP	C	T	15	399	c.706G>A	c.(706-708)GCT>ACT	p.A236T
Pat_41	Post-Resistance	CNKSR2	22866	37	X	21450862	21450862	Missense_Mutation	SNP	C	T	38	420	c.361C>T	c.(361-363)CCA>TCA	p.P121S
Pat_41	Post-Resistance	PHEX	5251	37	X	22132611	22132611	Nonsense_Mutation	SNP	G	A	8	239	c.1209G>A	c.(1207-1209)TGG>TGA	p.W403*
Pat_41	Post-Resistance	ZFX	7543	37	X	24226463	24226463	Missense_Mutation	SNP	C	T	15	138	c.1069C>T	c.(1069-1071)CCG>TCG	p.P357S
Pat_41	Post-Resistance	ZFX	7543	37	X	24229398	24229398	Missense_Mutation	SNP	C	T	10	309	c.2323C>T	c.(2323-2325)CCT>TCT	p.P775S
Pat_41	Post-Resistance	FAM48B2	170067	37	X	24330676	24330676	Nonsense_Mutation	SNP	G	A	7	157	c.757C>T	c.(757-759)CAG>TAG	p.Q253*
Pat_41	Post-Resistance	POLA1	5422	37	X	24735451	24735451	Missense_Mutation	SNP	G	A	8	128	c.733G>A	c.(733-735)GGG>AGG	p.G245R
Pat_41	Post-Resistance	POLA1	5422	37	X	24760138	24760138	Missense_Mutation	SNP	G	A	16	264	c.2348G>A	c.(2347-2349)GGA>GAA	p.G783E
Pat_41	Post-Resistance	MAGEB6	158809	37	X	26212043	26212043	Missense_Mutation	SNP	G	A	4	59	c.80G>A	c.(79-81)GGT>GAT	p.G27D
Pat_41	Post-Resistance	DCAF8L1	139425	37	X	27998457	27998457	Missense_Mutation	SNP	T	C	5	108	c.995A>G	c.(994-996)GAT>GGT	p.D332G
Pat_41	Post-Resistance	CXorf21	80231	37	X	30578037	30578037	Missense_Mutation	SNP	A	G	5	142	c.436T>C	c.(436-438)TCT>CCT	p.S146P
Pat_41	Post-Resistance	CXorf21	80231	37	X	30578411	30578411	Missense_Mutation	SNP	G	A	8	73	c.62C>T	c.(61-63)GCC>GTC	p.A21V
Pat_41	Post-Resistance	DMD	1756	37	X	32383153	32383153	Nonsense_Mutation	SNP	C	T	11	191	c.5009G>A	c.(5008-5010)TGG>TAG	p.W1670*
Pat_41	Post-Resistance	CXorf59	286464	37	X	36156093	36156093	Missense_Mutation	SNP	G	A	7	88	c.1064G>A	c.(1063-1065)AGA>AAA	p.R355K
Pat_41	Post-Resistance	FAM47C	442444	37	X	37027907	37027907	Missense_Mutation	SNP	G	A	7	109	c.1424G>A	c.(1423-1425)TGC>TAC	p.C475Y
Pat_41	Post-Resistance	FAM47C	442444	37	X	37028134	37028134	Missense_Mutation	SNP	C	T	7	175	c.1651C>T	c.(1651-1653)CCT>TCT	p.P551S
Pat_41	Post-Resistance	FAM47C	442444	37	X	37028662	37028662	Missense_Mutation	SNP	T	C	6	90	c.2179T>C	c.(2179-2181)TGC>CGC	p.C727R
Pat_41	Post-Resistance	FAM47C	442444	37	X	37028708	37028708	Missense_Mutation	SNP	C	T	6	111	c.2225C>T	c.(2224-2226)CCT>CTT	p.P742L
Pat_41	Post-Resistance	LANCL3	347404	37	X	37431196	37431196	Missense_Mutation	SNP	G	A	5	6	c.73G>A	c.(73-75)GAG>AAG	p.E25K
Pat_41	Post-Resistance	BCOR	54880	37	X	39934241	39934241	Missense_Mutation	SNP	G	A	8	72	c.358C>T	c.(358-360)CCA>TCA	p.P120S
Pat_41	Post-Resistance	ATP6AP2	10159	37	X	40450564	40450564	Missense_Mutation	SNP	G	A	14	195	c.247G>A	c.(247-249)GTG>ATG	p.V83M
Pat_41	Post-Resistance	USP9X	8239	37	X	41002601	41002601	Missense_Mutation	SNP	C	T	4	60	c.1219C>T	c.(1219-1221)CCA>TCA	p.P407S
Pat_41	Post-Resistance	USP9X	8239	37	X	41027288	41027288	Missense_Mutation	SNP	C	T	53	298	c.2453C>T	c.(2452-2454)TCT>TTT	p.S818F
Pat_41	Post-Resistance	DDX3X	1654	37	X	41203334	41203334	Missense_Mutation	SNP	G	A	4	65	c.817G>A	c.(817-819)GCA>ACA	p.A273T
Pat_41	Post-Resistance	DDX3X	1654	37	X	41205761	41205761	Missense_Mutation	SNP	G	A	7	339	c.1501G>A	c.(1501-1503)GCA>ACA	p.A501T
Pat_41	Post-Resistance	GPR34	2857	37	X	41555440	41555440	Missense_Mutation	SNP	G	A	12	110	c.554G>A	c.(553-555)GGA>GAA	p.G185E
Pat_41	Post-Resistance	MAOA	4128	37	X	43603621	43603621	Missense_Mutation	SNP	C	T	4	103	c.1445C>T	c.(1444-1446)CCA>CTA	p.P482L

Pat_41	Post-Resistance	SLC9A7	84679	37	X	46532013	46532013	Missense_Mutation	SNP	C	T	10	189	c.653G>A	c.(652-654)GGG>GAG	p.G218E
Pat_41	Post-Resistance	RP2	6102	37	X	46713343	46713343	Missense_Mutation	SNP	C	T	7	112	c.535C>T	c.(535-537)CCT>TCT	p.P179S
Pat_41	Post-Resistance	ZNF157	7712	37	X	47271863	47271863	Missense_Mutation	SNP	G	A	8	107	c.391G>A	c.(391-393)GAT>AAT	p.D131N
Pat_41	Post-Resistance	ZNF41	7592	37	X	47307520	47307520	Missense_Mutation	SNP	G	A	11	98	c.1775C>T	c.(1774-1776)CCC>CTC	p.P592L
Pat_41	Post-Resistance	CFP	5199	37	X	47486897	47486897	Missense_Mutation	SNP	C	T	4	57	c.547G>A	c.(547-549)GCC>ACC	p.A183T
Pat_41	Post-Resistance	ELK1	2002	37	X	47497422	47497422	Missense_Mutation	SNP	C	T	5	50	c.814G>A	c.(814-816)GCC>ACC	p.A272T
Pat_41	Post-Resistance	SLC38A5	92745	37	X	48326126	48326126	Missense_Mutation	SNP	G	A	3	32	c.100C>T	c.(100-102)CCT>TCT	p.P34S
Pat_41	Post-Resistance	FTSJ1	24140	37	X	48340040	48340040	Missense_Mutation	SNP	G	A	5	73	c.592G>A	c.(592-594)GGC>AGC	p.G198S
Pat_41	Post-Resistance	TBC1D25	4943	37	X	48419014	48419014	Missense_Mutation	SNP	C	T	8	95	c.1718C>T	c.(1717-1719)CCC>CTC	p.P573L
Pat_41	Post-Resistance	WDR13	64743	37	X	48460595	48460595	Splice_Site	SNP	G	A	4	105	c.1154_splice	c.e8+1	p.R385_splice
Pat_41	Post-Resistance	WAS	7454	37	X	48542276	48542276	Missense_Mutation	SNP	G	A	4	76	c.34G>A	c.(34-36)GGC>AGC	p.G12S
Pat_41	Post-Resistance	SUV39H1	6839	37	X	48559067	48559067	Missense_Mutation	SNP	G	A	15	102	c.751G>A	c.(751-753)GAT>AAT	p.D251N
Pat_41	Post-Resistance	PQBP1	10084	37	X	48759548	48759548	Missense_Mutation	SNP	G	A	12	89	c.331G>A	c.(331-333)GAC>AAC	p.D111N
Pat_41	Post-Resistance	CCDC120	90060	37	X	48920089	48920089	Missense_Mutation	SNP	G	A	3	11	c.140G>A	c.(139-141)AGC>AAC	p.S47N
Pat_41	Post-Resistance	PRICKLE3	4007	37	X	49035625	49035625	Missense_Mutation	SNP	G	A	4	71	c.539C>T	c.(538-540)ACC>ATC	p.T180I
Pat_41	Post-Resistance	SYP	6855	37	X	49048118	49048118	Missense_Mutation	SNP	G	A	5	13	c.718C>T	c.(718-720)CCC>TCC	p.P240S
Pat_41	Post-Resistance	FOXP3	50943	37	X	49113934	49113934	Missense_Mutation	SNP	G	T	7	26	c.404C>A	c.(403-405)ACC>AAC	p.T135N
Pat_41	Post-Resistance	PPP1R3F	89801	37	X	49142746	49142746	Missense_Mutation	SNP	C	T	3	46	c.1594C>T	c.(1594-1596)CGC>TGC	p.R532C
Pat_41	Post-Resistance	GAGE2A	729447	37	X	49355903	49355903	Missense_Mutation	SNP	G	A	41	620	c.185G>A	c.(184-186)GGA>GAA	p.G62E
Pat_41	Post-Resistance	CCNB3	85417	37	X	50053127	50053127	Missense_Mutation	SNP	C	T	5	71	c.1958C>T	c.(1957-1959)TCC>TTC	p.S653F
Pat_41	Post-Resistance	MAGED1	9500	37	X	51639671	51639671	Missense_Mutation	SNP	G	A	4	57	c.920G>A	c.(919-921)GGC>GAC	p.G307D
Pat_41	Post-Resistance	XAGE5	170627	37	X	52841618	52841618	Missense_Mutation	SNP	C	T	71	388	c.28C>T	c.(28-30)CCA>TCA	p.P10S
Pat_41	Post-Resistance	KDM5C	8242	37	X	53222411	53222411	Missense_Mutation	SNP	C	T	3	63	c.4421G>A	c.(4420-4422)CGA>CAA	p.R1474Q
Pat_41	Post-Resistance	KDM5C	8242	37	X	53228300	53228300	Missense_Mutation	SNP	G	A	36	182	c.2102C>T	c.(2101-2103)CCA>CTA	p.P701L
Pat_41	Post-Resistance	SMC1A	8243	37	X	53407569	53407569	Missense_Mutation	SNP	G	A	5	50	c.3590C>T	c.(3589-3591)GCC>GTC	p.A1197V
Pat_41	Post-Resistance	SMC1A	8243	37	X	53432762	53432762	Nonsense_Mutation	SNP	G	A	10	42	c.1672C>T	c.(1672-1674)CAG>TAG	p.Q558*
Pat_41	Post-Resistance	RIBC1	158787	37	X	53455500	53455500	Nonsense_Mutation	SNP	C	T	20	53	c.469C>T	c.(469-471)CAG>TAG	p.Q157*
Pat_41	Post-Resistance	HUWE1	10075	37	X	53561490	53561490	Missense_Mutation	SNP	G	A	27	141	c.12818C>T	c.(12817-12819)TCC>TTC	p.S4273F
Pat_41	Post-Resistance	HUWE1	10075	37	X	53566717	53566717	Missense_Mutation	SNP	G	A	18	51	c.11533C>T	c.(11533-11535)CCC>TCC	p.P3845S
Pat_41	Post-Resistance	FAM120C	54954	37	X	54117836	54117836	Missense_Mutation	SNP	C	T	4	113	c.2336G>A	c.(2335-2337)GGC>GAC	p.G779D
Pat_41	Post-Resistance	WNK3	65267	37	X	54224765	54224765	Missense_Mutation	SNP	G	A	5	35	c.5224C>T	c.(5224-5226)CCT>TCT	p.P1742S
Pat_41	Post-Resistance	WNK3	65267	37	X	54334405	54334405	Missense_Mutation	SNP	G	A	26	267	c.1039C>T	c.(1039-1041)CCT>TCT	p.P347S
Pat_41	Post-Resistance	GNL3L	54552	37	X	54578319	54578319	Missense_Mutation	SNP	G	A	18	105	c.1093G>A	c.(1093-1095)GCA>ACA	p.A365T
Pat_41	Post-Resistance	ITIH5L	347365	37	X	54785182	54785182	Missense_Mutation	SNP	G	A	4	33	c.1325C>T	c.(1324-1326)TCC>TTC	p.S442F
Pat_41	Post-Resistance	FAAH2	158584	37	X	57407425	57407425	Missense_Mutation	SNP	C	T	7	112	c.959C>T	c.(958-960)TCC>TTC	p.S320F
Pat_41	Post-Resistance	MTMR8	55613	37	X	63557195	63557195	Missense_Mutation	SNP	C	T	8	89	c.1054G>A	c.(1054-1056)GCT>ACT	p.A352T
Pat_41	Post-Resistance	LAS1L	81887	37	X	64744016	64744016	Missense_Mutation	SNP	G	A	6	58	c.1220C>T	c.(1219-1221)CCA>CTA	p.P407L
Pat_41	Post-Resistance	MSN	4478	37	X	64949432	64949432	Missense_Mutation	SNP	G	A	16	122	c.325G>A	c.(325-327)GGC>AGC	p.G109S
Pat_41	Post-Resistance	VSIG4	11326	37	X	65253510	65253510	Missense_Mutation	SNP	G	A	13	133	c.218C>T	c.(217-219)TCT>TTT	p.S73F
Pat_41	Post-Resistance	OPHN1	4983	37	X	67430060	67430060	Missense_Mutation	SNP	G	T	5	58	c.767C>A	c.(766-768)GCT>GAT	p.A256D
Pat_41	Post-Resistance	PJA1	64219	37	X	68381658	68381658	Missense_Mutation	SNP	C	T	49	368	c.1424G>A	c.(1423-1425)GGG>GAG	p.G475E
Pat_41	Post-Resistance	PJA1	64219	37	X	68382516	68382516	Missense_Mutation	SNP	C	T	4	17	c.566G>A	c.(565-567)AGA>AAA	p.R189K
Pat_41	Post-Resistance	KIF4A	24137	37	X	69510387	69510387	Missense_Mutation	SNP	G	A	13	47	c.79G>A	c.(79-81)GGC>AGC	p.G27S
Pat_41	Post-Resistance	KIF4A	24137	37	X	69563595	69563595	Missense_Mutation	SNP	C	T	9	124	c.1309C>T	c.(1309-1311)CTC>TTC	p.L437F
Pat_41	Post-Resistance	DLG3	1741	37	X	69719025	69719025	Splice_Site	SNP	G	A	7	54	c.1871_splice	c.e15-1	p.I624_splice
Pat_41	Post-Resistance	FOXO4	4303	37	X	70321153	70321153	Missense_Mutation	SNP	G	A	4	28	c.1073G>A	c.(1072-1074)GGG>GAG	p.G358E
Pat_41	Post-Resistance	CXorf65	158830	37	X	70324618	70324618	Splice_Site	SNP	C	T	10	199	c.319_splice	c.e4+1	p.V107_splice

Pat_41	Post-Resistance	MED12	9968	37	X	70356132	70356132	Missense_Mutation	SNP	G	A	8	83	c.5027G>A	c.(5026-5028)GGT>GAT	p.G1676D
Pat_41	Post-Resistance	NLGN3	54413	37	X	70389546	70389546	Missense_Mutation	SNP	G	A	8	37	c.2086G>A	c.(2086-2088)GCC>ACC	p.A696T
Pat_41	Post-Resistance	ZMYM3	9203	37	X	70467360	70467360	Missense_Mutation	SNP	C	T	5	42	c.2149G>A	c.(2149-2151)GCT>ACT	p.A717T
Pat_41	Post-Resistance	ITGB1BP2	26548	37	X	70524453	70524453	Missense_Mutation	SNP	G	A	4	57	c.815G>A	c.(814-816)GGG>GAG	p.G272E
Pat_41	Post-Resistance	TAF1	6872	37	X	70618504	70618504	Missense_Mutation	SNP	C	T	4	63	c.3700C>T	c.(3700-3702)CTT>TTT	p.L1234F
Pat_41	Post-Resistance	TAF1	6872	37	X	70679537	70679537	Missense_Mutation	SNP	G	A	30	199	c.5197G>A	c.(5197-5199)GAA>AAA	p.E1733K
Pat_41	Post-Resistance	OGT	8473	37	X	70767761	70767761	Missense_Mutation	SNP	G	A	21	395	c.536G>A	c.(535-537)TGT>TAT	p.C179Y
Pat_41	Post-Resistance	OGT	8473	37	X	70775894	70775894	Missense_Mutation	SNP	G	A	27	350	c.1015G>A	c.(1015-1017)GAA>AAA	p.E339K
Pat_41	Post-Resistance	ACRC	93953	37	X	70823920	70823920	Missense_Mutation	SNP	C	T	17	156	c.793C>T	c.(793-795)CCC>TCC	p.P265S
Pat_41	Post-Resistance	ACRC	93953	37	X	70823950	70823950	Missense_Mutation	SNP	C	T	5	202	c.823C>T	c.(823-825)CCC>TCC	p.P275S
Pat_41	Post-Resistance	ACRC	93953	37	X	70823960	70823961	Missense_Mutation	DNP	GC	AG	7	226	c.833_834GC>AG	c.(832-834)AGC>AAG	p.S278K
Pat_41	Post-Resistance	ACRC	93953	37	X	70830569	70830569	Missense_Mutation	SNP	G	A	16	50	c.1650G>A	c.(1648-1650)ATG>ATA	p.M550I
Pat_41	Post-Resistance	CXCR3	2833	37	X	70837269	70837269	Missense_Mutation	SNP	G	A	3	45	c.53C>T	c.(52-54)GCC>GTC	p.A18V
Pat_41	Post-Resistance	ERCC6L	54821	37	X	71425492	71425492	Missense_Mutation	SNP	C	T	24	139	c.3125G>A	c.(3124-3126)AGC>AAC	p.S1042N
Pat_41	Post-Resistance	RPS4X	6191	37	X	71492601	71492601	Missense_Mutation	SNP	G	A	15	150	c.712C>T	c.(712-714)CTT>TTT	p.L238F
Pat_41	Post-Resistance	PHKA1	5255	37	X	71840649	71840649	Missense_Mutation	SNP	C	T	13	122	c.2063G>A	c.(2062-2064)CGG>CAG	p.R688Q
Pat_41	Post-Resistance	MAGEE1	57692	37	X	75649929	75649929	Missense_Mutation	SNP	G	A	5	42	c.1606G>A	c.(1606-1608)GCA>ACA	p.A536T
Pat_41	Post-Resistance	PGAM4	441531	37	X	77224618	77224618	Missense_Mutation	SNP	G	A	13	110	c.518C>T	c.(517-519)CCC>CTC	p.P173L
Pat_41	Post-Resistance	LPAR4	2846	37	X	78011400	78011400	Missense_Mutation	SNP	C	T	11	222	c.1034C>T	c.(1033-1035)TCC>TTC	p.S345F
Pat_41	Post-Resistance	LPAR4	2846	37	X	78011423	78011423	Missense_Mutation	SNP	G	A	19	177	c.1057G>A	c.(1057-1059)GTG>ATG	p.V353M
Pat_41	Post-Resistance	BRWD3	254065	37	X	79999541	79999541	Missense_Mutation	SNP	G	A	20	76	c.803C>T	c.(802-804)ACT>ATT	p.T268I
Pat_41	Post-Resistance	SH3BGRL	6451	37	X	80532622	80532622	Missense_Mutation	SNP	G	A	21	85	c.185G>A	c.(184-186)GGT>GAT	p.G62D
Pat_41	Post-Resistance	RPS6KA6	27330	37	X	83402002	83402002	Missense_Mutation	SNP	A	C	159	24	c.405T>G	c.(403-405)ATT>ATG	p.I135M
Pat_41	Post-Resistance	HDX	139324	37	X	83723587	83723587	Missense_Mutation	SNP	C	T	10	148	c.1144G>A	c.(1144-1146)GCA>ACA	p.A382T
Pat_41	Post-Resistance	POF1B	79983	37	X	84600891	84600891	Missense_Mutation	SNP	C	T	89	501	c.698G>A	c.(697-699)AGT>AAT	p.S233N
Pat_41	Post-Resistance	DACH2	117154	37	X	85969707	85969707	Missense_Mutation	SNP	G	A	36	162	c.1088G>A	c.(1087-1089)GGT>GAT	p.G363D
Pat_41	Post-Resistance	RPA4	29935	37	X	96139881	96139881	Missense_Mutation	SNP	G	A	16	220	c.572G>A	c.(571-573)GGG>GAG	p.G191E
Pat_41	Post-Resistance	PCDH19	57526	37	X	99551804	99551804	Missense_Mutation	SNP	G	A	11	181	c.2918C>T	c.(2917-2919)CCC>CTC	p.P973L
Pat_41	Post-Resistance	NOX1	27035	37	X	100117507	100117507	Missense_Mutation	SNP	G	A	24	578	c.545C>T	c.(544-546)ACA>ATA	p.T182I
Pat_41	Post-Resistance	CENPI	2491	37	X	100403022	100403022	Missense_Mutation	SNP	C	T	6	309	c.1966C>T	c.(1966-1968)CCC>TCC	p.P656S
Pat_41	Post-Resistance	DRP2	1821	37	X	100513423	100513423	Missense_Mutation	SNP	C	T	3	14	c.2516C>T	c.(2515-2517)GCC>GTC	p.A839V
Pat_41	Post-Resistance	TAF7L	54457	37	X	100533088	100533088	Missense_Mutation	SNP	C	T	5	220	c.784G>A	c.(784-786)GAA>AAA	p.E262K
Pat_41	Post-Resistance	BTK	695	37	X	100611144	100611144	Missense_Mutation	SNP	C	T	20	202	c.1462G>A	c.(1462-1464)GAG>AAG	p.E488K
Pat_41	Post-Resistance	ARMCX2	9823	37	X	100911455	100911455	Missense_Mutation	SNP	G	A	7	73	c.1120C>T	c.(1120-1122)CCC>TCC	p.P374S
Pat_41	Post-Resistance	ARMCX2	9823	37	X	100912304	100912304	Missense_Mutation	SNP	C	T	6	55	c.271G>A	c.(271-273)GAC>AAC	p.D91N
Pat_41	Post-Resistance	ZMAT1	84460	37	X	101138643	101138643	Missense_Mutation	SNP	C	T	4	130	c.1243G>A	c.(1243-1245)GTC>ATC	p.V415I
Pat_41	Post-Resistance	ARMCX5	64860	37	X	101857806	101857806	Missense_Mutation	SNP	G	A	14	77	c.737G>A	c.(736-738)GGA>GAA	p.G246E
Pat_41	Post-Resistance	ARMCX5	64860	37	X	101858195	101858195	Missense_Mutation	SNP	G	A	40	188	c.1126G>A	c.(1126-1128)GTG>ATG	p.V376M
Pat_41	Post-Resistance	GPRASP1	9737	37	X	101911416	101911416	Missense_Mutation	SNP	G	A	14	113	c.2575G>A	c.(2575-2577)GGA>AGA	p.G859R
Pat_41	Post-Resistance	GPRASP2	114928	37	X	101969910	101969910	Missense_Mutation	SNP	C	T	9	173	c.113C>T	c.(112-114)CCC>CTC	p.P38L
Pat_41	Post-Resistance	BHLHB9	80823	37	X	102004992	102004992	Missense_Mutation	SNP	G	A	12	113	c.1069G>A	c.(1069-1071)GCC>ACC	p.A357T
Pat_41	Post-Resistance	BHLHB9	80823	37	X	102005388	102005388	Missense_Mutation	SNP	G	A	33	403	c.1465G>A	c.(1465-1467)GCA>ACA	p.A489T
Pat_41	Post-Resistance	TCEAL5	340543	37	X	102528993	102528993	Missense_Mutation	SNP	C	T	6	116	c.499G>A	c.(499-501)GGT>AGT	p.G167S
Pat_41	Post-Resistance	GLRA4	441509	37	X	102978793	102978793	Missense_Mutation	SNP	G	A	13	71	c.568C>T	c.(568-570)CTT>TTT	p.L190F
Pat_41	Post-Resistance	MCART6	401612	37	X	103349910	103349910	Missense_Mutation	SNP	C	T	70	3	c.31G>A	c.(31-33)GAG>AAG	p.E11K
Pat_41	Post-Resistance	MUM1L1	139221	37	X	105449736	105449736	Missense_Mutation	SNP	G	A	8	101	c.311G>A	c.(310-312)AGT>AAT	p.S104N
Pat_41	Post-Resistance	TBC1D8B	54885	37	X	106066546	106066546	Missense_Mutation	SNP	G	A	33	188	c.677G>A	c.(676-678)GGA>GAA	p.G226E

Pat_41	Post-Resistance	RBM41	55285	37	X	106358597	106358597	Missense_Mutation	SNP	C	T	29	303	c.508G>A	c.(508-510)GCT>ACT	p.A170T
Pat_41	Post-Resistance	NUP62CL	54830	37	X	106391040	106391040	Splice_Site	SNP	C	T	34	183	c.531_splice	c.e8-1	p.I177_splice
Pat_41	Post-Resistance	PSMD10	5716	37	X	107331203	107331203	Missense_Mutation	SNP	C	T	55	531	c.340G>A	c.(340-342)GCT>ACT	p.A114T
Pat_41	Post-Resistance	COL4A6	1288	37	X	107418412	107418412	Missense_Mutation	SNP	G	A	16	365	c.2867C>T	c.(2866-2868)CCT>CTT	p.P956L
Pat_41	Post-Resistance	COL4A6	1288	37	X	107430395	107430395	Missense_Mutation	SNP	G	T	25	475	c.1885C>A	c.(1885-1887)CCC>ACC	p.P629T
Pat_41	Post-Resistance	COL4A5	1287	37	X	107924124	107924124	Missense_Mutation	SNP	G	A	21	409	c.4025G>A	c.(4024-4026)GGA>GAA	p.G1342E
Pat_41	Post-Resistance	IRS4	8471	37	X	107979483	107979483	Missense_Mutation	SNP	G	A	13	80	c.92C>T	c.(91-93)ACC>ATC	p.T31I
Pat_41	Post-Resistance	GUCY2F	2986	37	X	108625390	108625390	Missense_Mutation	SNP	C	T	100	443	c.3107G>A	c.(3106-3108)AGT>AAT	p.S1036N
Pat_41	Post-Resistance	ACSL4	2182	37	X	108926546	108926546	Missense_Mutation	SNP	C	T	38	417	c.170G>A	c.(169-171)AGT>AAT	p.S57N
Pat_41	Post-Resistance	RGAG1	57529	37	X	109695158	109695158	Missense_Mutation	SNP	C	T	12	265	c.1313C>T	c.(1312-1314)ACC>ATC	p.T438I
Pat_41	Post-Resistance	CHRDL1	91851	37	X	109964741	109964741	Missense_Mutation	SNP	C	T	13	284	c.319G>A	c.(319-321)GTG>ATG	p.V107M
Pat_41	Post-Resistance	ALG13	79868	37	X	110970674	110970674	Splice_Site	SNP	G	A	6	25	c.2090_splice	c.e17+1	p.R697_splice
Pat_41	Post-Resistance	LHFPL1	340596	37	X	111914526	111914526	Nonsense_Mutation	SNP	G	C	24	354	c.93C>G	c.(91-93)TAC>TAG	p.Y31*
Pat_41	Post-Resistance	PLS3	5358	37	X	114856629	114856629	Missense_Mutation	SNP	C	T	51	234	c.145C>T	c.(145-147)CCA>TCA	p.P49S
Pat_41	Post-Resistance	AGTR2	186	37	X	115303837	115303838	Missense_Mutation	DNP	AC	GT	12	226	c.304_305AC>GT	c.(304-306)ACC>GTC	p.T102V
Pat_41	Post-Resistance	KLHL13	90293	37	X	117043960	117043960	Missense_Mutation	SNP	G	A	45	280	c.670C>T	c.(670-672)CCT>TCT	p.P224S
Pat_41	Post-Resistance	WDR44	54521	37	X	117577637	117577637	Nonsense_Mutation	SNP	G	A	37	155	c.2499G>A	c.(2497-2499)TGG>TGA	p.W833*
Pat_41	Post-Resistance	DOCK11	139818	37	X	117700109	117700109	Missense_Mutation	SNP	G	A	27	141	c.835G>A	c.(835-837)GTT>ATT	p.V279I
Pat_41	Post-Resistance	DOCK11	139818	37	X	117707929	117707929	Missense_Mutation	SNP	C	T	9	171	c.1337C>T	c.(1336-1338)CCC>CTC	p.P446L
Pat_41	Post-Resistance	DOCK11	139818	37	X	117809980	117809980	Missense_Mutation	SNP	G	A	3	29	c.5281G>A	c.(5281-5283)GGC>AGC	p.G1761S
Pat_41	Post-Resistance	LONRF3	79836	37	X	118148200	118148200	Missense_Mutation	SNP	G	A	50	422	c.2005G>A	c.(2005-2007)GGA>AGA	p.G669R
Pat_41	Post-Resistance	ATP1B4	23439	37	X	119500562	119500562	Nonsense_Mutation	SNP	G	A	6	115	c.246G>A	c.(244-246)TGG>TGA	p.W82*
Pat_41	Post-Resistance	C1GALT1C1	29071	37	X	119760514	119760514	Missense_Mutation	SNP	C	T	9	64	c.508G>A	c.(508-510)GGC>AGC	p.G170S
Pat_41	Post-Resistance	GRIA3	2892	37	X	122598771	122598771	Missense_Mutation	SNP	C	T	18	243	c.2132C>T	c.(2131-2133)CCA>CTA	p.P711L
Pat_41	Post-Resistance	STAG2	10735	37	X	123229247	123229247	Missense_Mutation	SNP	G	A	7	269	c.3620G>A	c.(3619-3621)AGA>AAA	p.R1207K
Pat_41	Post-Resistance	ODZ1	10178	37	X	123517525	123517525	Missense_Mutation	SNP	T	C	17	262	c.7235A>G	c.(7234-7236)TAC>TGC	p.Y2412C
Pat_41	Post-Resistance	ODZ1	10178	37	X	123556304	123556304	Missense_Mutation	SNP	G	A	6	172	c.4268C>T	c.(4267-4269)TCC>TTC	p.S1423F
Pat_41	Post-Resistance	ODZ1	10178	37	X	123838968	123838968	Missense_Mutation	SNP	C	T	55	455	c.910G>A	c.(910-912)GCC>ACC	p.A304T
Pat_41	Post-Resistance	DCAF12L2	340578	37	X	125298880	125298880	Missense_Mutation	SNP	G	A	10	68	c.1028C>T	c.(1027-1029)CCC>CTC	p.P343L
Pat_41	Post-Resistance	ACTRT1	139741	37	X	127185299	127185299	Missense_Mutation	SNP	G	A	17	215	c.887C>T	c.(886-888)GCA>GTA	p.A296V
Pat_41	Post-Resistance	ACTRT1	139741	37	X	127185414	127185414	Missense_Mutation	SNP	C	T	25	277	c.772G>A	c.(772-774)GTG>ATG	p.V258M
Pat_41	Post-Resistance	SMARCA1	6594	37	X	128614788	128614788	Missense_Mutation	SNP	G	A	15	54	c.2332C>T	c.(2332-2334)CCA>TCA	p.P778S
Pat_41	Post-Resistance	ZDHHC9	51114	37	X	128975782	128975782	Missense_Mutation	SNP	C	T	45	206	c.140G>A	c.(139-141)GGG>GAG	p.G47E
Pat_41	Post-Resistance	ELF4	2000	37	X	129201460	129201460	Missense_Mutation	SNP	G	A	4	107	c.1228C>T	c.(1228-1230)CCC>TCC	p.P410S
Pat_41	Post-Resistance	SLC25A14	9016	37	X	129499537	129499537	Missense_Mutation	SNP	G	A	52	165	c.742G>A	c.(742-744)GCT>ACT	p.A248T
Pat_41	Post-Resistance	RBMX2	51634	37	X	129546445	129546445	Missense_Mutation	SNP	G	A	13	148	c.592G>A	c.(592-594)GAT>AAT	p.D198N
Pat_41	Post-Resistance	ENOX2	10495	37	X	129803996	129803996	Missense_Mutation	SNP	G	A	15	237	c.724C>T	c.(724-726)CCC>TCC	p.P242S
Pat_41	Post-Resistance	IGSF1	3547	37	X	130417206	130417206	Missense_Mutation	SNP	G	A	6	117	c.700C>T	c.(700-702)CCT>TCT	p.P234S
Pat_41	Post-Resistance	TFDP3	51270	37	X	132352019	132352019	Missense_Mutation	SNP	G	A	22	145	c.269C>T	c.(268-270)TCC>TTC	p.S90F
Pat_41	Post-Resistance	FAM127B	26071	37	X	134185895	134185895	Missense_Mutation	SNP	G	A	5	104	c.244C>T	c.(244-246)CCC>TCC	p.P82S
Pat_41	Post-Resistance	FAM127B	26071	37	X	134186057	134186057	Missense_Mutation	SNP	G	A	15	280	c.82C>T	c.(82-84)CCC>TCC	p.P28S
Pat_41	Post-Resistance	BRS3	680	37	X	135574292	135574292	Missense_Mutation	SNP	T	A	40	471	c.958T>A	c.(958-960)TTC>ATC	p.F320I
Pat_41	Post-Resistance	ARHGEF6	9459	37	X	135814317	135814317	Missense_Mutation	SNP	G	A	3	46	c.676C>T	c.(676-678)CCA>TCA	p.P226S
Pat_41	Post-Resistance	GPR101	83550	37	X	136112666	136112666	Missense_Mutation	SNP	G	A	25	112	c.1168C>T	c.(1168-1170)CCC>TCC	p.P390S
Pat_41	Post-Resistance	GPR101	83550	37	X	136112783	136112783	Missense_Mutation	SNP	C	T	31	220	c.1051G>A	c.(1051-1053)GAT>AAT	p.D351N
Pat_41	Post-Resistance	ZIC3	7547	37	X	136649563	136649563	Missense_Mutation	SNP	C	T	5	61	c.713C>T	c.(712-714)GCC>GTC	p.A238V
Pat_41	Post-Resistance	CDR1	1038	37	X	139866528	139866528	Missense_Mutation	SNP	C	T	10	365	c.4G>A	c.(4-6)GCT>ACT	p.A2T

Pat_41	Post-Resistance	MAGEC1	9947	37	X	140995972	140995972	Missense_Mutation	SNP	C	T	12	359	c.2782C>T	c.(2782-2784)CCT>TCT	p.P928S
Pat_41	Post-Resistance	FMR1NB	158521	37	X	147106459	147106459	Missense_Mutation	SNP	A	G	18	147	c.707A>G	c.(706-708)AAG>AGG	p.K236R
Pat_41	Post-Resistance	AFF2	2334	37	X	147744131	147744131	Nonsense_Mutation	SNP	C	T	36	254	c.883C>T	c.(883-885)CAG>TAG	p.Q295*
Pat_41	Post-Resistance	AFF2	2334	37	X	148044294	148044294	Missense_Mutation	SNP	C	T	4	95	c.2740C>T	c.(2740-2742)CCT>TCT	p.P914S
Pat_41	Post-Resistance	IDS	3423	37	X	148564719	148564719	Missense_Mutation	SNP	A	G	3	122	c.1211T>C	c.(1210-1212)GTG>GCG	p.V404A
Pat_41	Post-Resistance	CXorf40A	91966	37	X	148628300	148628300	Missense_Mutation	SNP	G	A	4	41	c.269G>A	c.(268-270)GGG>GAG	p.G90E
Pat_41	Post-Resistance	CXorf40B	541578	37	X	149102028	149102028	Missense_Mutation	SNP	G	A	7	39	c.65C>T	c.(64-66)ACT>ATT	p.T22I
Pat_41	Post-Resistance	HMGB3	3149	37	X	150156340	150156340	Missense_Mutation	SNP	G	A	4	51	c.556G>A	c.(556-558)GAA>AAA	p.E186K
Pat_41	Post-Resistance	PNMA5	114824	37	X	152158908	152158908	Missense_Mutation	SNP	G	A	7	111	c.1235C>T	c.(1234-1236)CCC>CTC	p.P412L
Pat_41	Post-Resistance	MAGEA1	4100	37	X	152482965	152482965	Missense_Mutation	SNP	G	A	4	71	c.46C>T	c.(46-48)CTT>TTT	p.L16F
Pat_41	Post-Resistance	ZNF275	10838	37	X	152612435	152612435	Missense_Mutation	SNP	G	A	6	86	c.292G>A	c.(292-294)GAA>AAA	p.E98K
Pat_41	Post-Resistance	BGN	633	37	X	152772563	152772563	Missense_Mutation	SNP	C	T	6	16	c.829C>T	c.(829-831)CCC>TCC	p.P277S
Pat_41	Post-Resistance	BGN	633	37	X	152773823	152773823	Missense_Mutation	SNP	C	T	4	132	c.1027C>T	c.(1027-1029)CCC>TCC	p.P343S
Pat_41	Post-Resistance	ATP2B3	492	37	X	152823634	152823634	Missense_Mutation	SNP	C	T	6	216	c.2498C>T	c.(2497-2499)ACC>ATC	p.T833I
Pat_41	Post-Resistance	ATP2B3	492	37	X	152845520	152845520	Missense_Mutation	SNP	G	A	92	344	c.3427G>A	c.(3427-3429)GCC>ACC	p.A1143T
Pat_41	Post-Resistance	DUSP9	1852	37	X	152915026	152915026	Missense_Mutation	SNP	C	T	55	316	c.713C>T	c.(712-714)CCC>CTC	p.P238L
Pat_41	Post-Resistance	PLXNB3	5365	37	X	153035389	153035389	Missense_Mutation	SNP	G	A	5	33	c.1624G>A	c.(1624-1626)GGC>AGC	p.G542S
Pat_41	Post-Resistance	PLXNB3	5365	37	X	153040816	153040816	Missense_Mutation	SNP	C	T	6	62	c.4292C>T	c.(4291-4293)GCG>GTG	p.A1431V
Pat_41	Post-Resistance	PLXNB3	5365	37	X	153041597	153041597	Missense_Mutation	SNP	G	A	5	33	c.4657G>A	c.(4657-4659)GAG>AAG	p.E1553K
Pat_41	Post-Resistance	PLXNB3	5365	37	X	153043904	153043904	Missense_Mutation	SNP	C	T	4	71	c.5528C>T	c.(5527-5529)TCT>TTT	p.S1843F
Pat_41	Post-Resistance	SRPK3	26576	37	X	153050556	153050556	Missense_Mutation	SNP	G	A	5	75	c.1447G>A	c.(1447-1449)GAG>AAG	p.E483K
Pat_41	Post-Resistance	L1CAM	3897	37	X	153130159	153130159	Missense_Mutation	SNP	C	T	9	164	c.3047G>A	c.(3046-3048)GGG>GAG	p.G1016E
Pat_41	Post-Resistance	L1CAM	3897	37	X	153130447	153130447	Missense_Mutation	SNP	C	T	9	176	c.2875G>A	c.(2875-2877)GAT>AAT	p.D959N
Pat_41	Post-Resistance	L1CAM	3897	37	X	153134326	153134326	Missense_Mutation	SNP	G	A	45	446	c.1349C>T	c.(1348-1350)GCC>GTC	p.A450V
Pat_41	Post-Resistance	ARHGAP4	393	37	X	153186600	153186600	Missense_Mutation	SNP	C	T	3	11	c.448G>A	c.(448-450)GAG>AAG	p.E150K
Pat_41	Post-Resistance	HCFC1	3054	37	X	153220945	153220945	Missense_Mutation	SNP	C	T	5	81	c.2905G>A	c.(2905-2907)GTG>ATG	p.V969M
Pat_41	Post-Resistance	HCFC1	3054	37	X	153224816	153224816	Missense_Mutation	SNP	C	T	11	446	c.1571G>A	c.(1570-1572)CGG>CAG	p.R524Q
Pat_41	Post-Resistance	TMEM187	8269	37	X	153247619	153247619	Missense_Mutation	SNP	G	A	16	289	c.106G>A	c.(106-108)GGC>AGC	p.G36S
Pat_41	Post-Resistance	MECP2	4204	37	X	153296025	153296025	Missense_Mutation	SNP	C	T	17	129	c.1254G>A	c.(1252-1254)ATG>ATA	p.M418I
Pat_41	Post-Resistance	OPN1LW	5956	37	X	153421817	153421817	Missense_Mutation	SNP	G	A	32	226	c.793G>A	c.(793-795)GAA>AAA	p.E265K
Pat_41	Post-Resistance	TKTL1	8277	37	X	153557940	153557940	Missense_Mutation	SNP	G	A	31	267	c.1693G>A	c.(1693-1695)GGA>AGA	p.G565R
Pat_41	Post-Resistance	FLNA	2316	37	X	153581793	153581793	Missense_Mutation	SNP	C	T	6	102	c.5893G>A	c.(5893-5895)GTC>ATC	p.V1965I
Pat_41	Post-Resistance	FLNA	2316	37	X	153594823	153594823	Missense_Mutation	SNP	C	T	9	45	c.1081G>A	c.(1081-1083)GCT>ACT	p.A361T
Pat_41	Post-Resistance	RPL10	6134	37	X	153627728	153627728	Missense_Mutation	SNP	G	A	22	414	c.73G>A	c.(73-75)GGT>AGT	p.G25S
Pat_41	Post-Resistance	RPL10	6134	37	X	153631631	153631631	Missense_Mutation	SNP	G	A	9	236	c.295G>A	c.(295-297)GAC>AAC	p.D99N
Pat_41	Post-Resistance	PLXNA3	55558	37	X	153690615	153690615	Missense_Mutation	SNP	G	A	10	97	c.1282G>A	c.(1282-1284)GTC>ATC	p.V428I
Pat_41	Post-Resistance	CTAG2	30848	37	X	153880816	153880816	Missense_Mutation	SNP	C	T	5	113	c.359G>A	c.(358-360)GGG>GAG	p.G120E
Pat_41	Post-Resistance	MPP1	4354	37	X	154014612	154014612	Missense_Mutation	SNP	C	T	11	770	c.544G>A	c.(544-546)GCG>ACG	p.A182T
Pat_41	Post-Resistance	F8	2157	37	X	154176005	154176005	Missense_Mutation	SNP	C	T	27	287	c.2081G>A	c.(2080-2082)GGA>GAA	p.G694E
Pat_41	Post-Resistance	F8	2157	37	X	154225280	154225280	Missense_Mutation	SNP	G	A	27	533	c.356C>T	c.(355-357)GCT>GTT	p.A119V
Pat_41	Post-Resistance	F8	2157	37	X	154225304	154225304	Missense_Mutation	SNP	G	A	21	599	c.332C>T	c.(331-333)GCT>GTT	p.A111V
Pat_41	Post-Resistance	SPRY3	10251	37	X	155003630	155003630	Missense_Mutation	SNP	G	A	15	194	c.97G>A	c.(97-99)GCC>ACC	p.A33T
Pat_44	Pre-Treatment	CAMTA1	23261	37	1	7805007	7805007	Missense_Mutation	SNP	C	T	21	32	c.4295C>T	c.(4294-4296)ACC>ATC	p.T1432I
Pat_44	Pre-Treatment	PRAMEF4	400735	37	1	12942930	12942930	Missense_Mutation	SNP	G	A	4	32	c.286C>T	c.(286-288)CGT>TGT	p.R96C
Pat_44	Pre-Treatment	UBR4	23352	37	1	19439223	19439223	Missense_Mutation	SNP	G	A	89	210	c.11596C>T	c.(11596-11598)CAC>TAC	p.H3866Y
Pat_44	Pre-Treatment	EPHA10	284656	37	1	38185631	38185631	Missense_Mutation	SNP	C	T	16	25	c.2512G>A	c.(2512-2514)GAG>AAG	p.E838K
Pat_44	Pre-Treatment	PTCH2	8643	37	1	45296644	45296644	Missense_Mutation	SNP	G	A	4	9	c.689C>T	c.(688-690)TCC>TTC	p.S230F

Pat_44	Pre-Treatment	DAB1	1600	37	1	57480934	57480934	Missense_Mutation	SNP	T	C	16	31	c.1066A>G	c.(1066-1068)ACT>GCT	p.T356A
Pat_44	Pre-Treatment	FNDC7	163479	37	1	109270469	109270469	Missense_Mutation	SNP	C	T	28	90	c.1151C>T	c.(1150-1152)TCC>TTC	p.S384F
Pat_44	Pre-Treatment	FAM40A	85369	37	1	110590491	110590491	Missense_Mutation	SNP	C	T	2	1	c.1661C>T	c.(1660-1662)CCC>CTC	p.P554L
Pat_44	Pre-Treatment	DENND2C	163259	37	1	115143490	115143490	Missense_Mutation	SNP	G	A	11	11	c.1907C>T	c.(1906-1908)CCT>CTT	p.P636L
Pat_44	Pre-Treatment	OTUD7B	56957	37	1	149915985	149915985	Missense_Mutation	SNP	G	A	3	8	c.2303C>T	c.(2302-2304)CCC>CTC	p.P768L
Pat_44	Pre-Treatment	FLG2	388698	37	1	152325707	152325707	Missense_Mutation	SNP	C	T	73	185	c.4555G>A	c.(4555-4557)GGA>AGA	p.G1519R
Pat_44	Pre-Treatment	FCRL3	115352	37	1	157665283	157665283	Missense_Mutation	SNP	C	T	8	23	c.1247G>A	c.(1246-1248)CGA>CAA	p.R416Q
Pat_44	Pre-Treatment	KIRREL	55243	37	1	158064813	158064813	Missense_Mutation	SNP	C	T	5	13	c.2177C>T	c.(2176-2178)CCC>CTC	p.P726L
Pat_44	Pre-Treatment	CD1C	911	37	1	158261127	158261127	Missense_Mutation	SNP	C	T	10	23	c.265C>T	c.(265-267)CGT>TGT	p.R89C
Pat_44	Pre-Treatment	LY9	4063	37	1	160769588	160769588	Missense_Mutation	SNP	G	A	5	26	c.170G>A	c.(169-171)GGG>GAG	p.G57E
Pat_44	Pre-Treatment	C1orf112	55732	37	1	169806207	169806207	Missense_Mutation	SNP	G	A	11	49	c.1679G>A	c.(1678-1680)AGG>AAG	p.R560K
Pat_44	Pre-Treatment	TNR	7143	37	1	175375790	175375790	Missense_Mutation	SNP	G	A	15	38	c.61C>T	c.(61-63)CTT>TTT	p.L21F
Pat_44	Pre-Treatment	FAM163A	148753	37	1	179782945	179782945	Missense_Mutation	SNP	T	C	6	18	c.125T>C	c.(124-126)GTT>GCT	p.V42A
Pat_44	Pre-Treatment	RNASEL	6041	37	1	182555806	182555806	Missense_Mutation	SNP	C	T	23	32	c.136G>A	c.(136-138)GAA>AAA	p.E46K
Pat_44	Pre-Treatment	SLC30A10	55532	37	1	220088927	220088927	Missense_Mutation	SNP	C	T	8	39	c.1322G>A	c.(1321-1323)GGA>GAA	p.G441E
Pat_44	Pre-Treatment	ZNF695	57116	37	1	247150500	247150500	Missense_Mutation	SNP	A	T	4	32	c.1317T>A	c.(1315-1317)GAT>GAA	p.D439E
Pat_44	Pre-Treatment	PRKCQ	5588	37	10	6470194	6470194	Missense_Mutation	SNP	G	A	4	36	c.2096C>T	c.(2095-2097)CCC>CTC	p.P699L
Pat_44	Pre-Treatment	PLXDC2	84898	37	10	20335828	20335828	Nonsense_Mutation	SNP	C	T	9	65	c.355C>T	c.(355-357)CGA>TGA	p.R119*
Pat_44	Pre-Treatment	PLXDC2	84898	37	10	20506391	20506391	Missense_Mutation	SNP	G	A	10	6	c.1159G>A	c.(1159-1161)GAA>AAA	p.E387K
Pat_44	Pre-Treatment	NEBL	10529	37	10	21120192	21120192	Missense_Mutation	SNP	C	T	5	15	c.1604G>A	c.(1603-1605)GGA>GAA	p.G535E
Pat_44	Pre-Treatment	ANKRD30A	91074	37	10	37431050	37431050	Missense_Mutation	SNP	G	C	4	12	c.1057G>C	c.(1057-1059)GCA>CCA	p.A353P
Pat_44	Pre-Treatment	SGMS1	259230	37	10	52103400	52103400	Nonsense_Mutation	SNP	G	A	2	1	c.475C>T	c.(475-477)CGA>TGA	p.R159*
Pat_44	Pre-Treatment	PTEN	5728	37	10	89690846	89690846	Missense_Mutation	SNP	G	C	15	29	c.253G>C	c.(253-255)GTT>CTT	p.V85L
Pat_44	Pre-Treatment	LIPN	643418	37	10	90521203	90521203	Missense_Mutation	SNP	G	A	18	20	c.41G>A	c.(40-42)GGA>GAA	p.G14E
Pat_44	Pre-Treatment	CDHR5	53841	37	11	618833	618833	Missense_Mutation	SNP	G	C	4	30	c.1726C>G	c.(1726-1728)CCA>GCA	p.P576A
Pat_44	Pre-Treatment	C11orf49	79096	37	11	47185766	47185766	Missense_Mutation	SNP	C	T	2	0	c.944C>T	c.(943-945)CCG>CTG	p.P315L
Pat_44	Pre-Treatment	MED17	9440	37	11	93523785	93523785	Missense_Mutation	SNP	G	A	23	39	c.463G>A	c.(463-465)GGA>AGA	p.G155R
Pat_44	Pre-Treatment	OR8D1	283159	37	11	124180013	124180013	Missense_Mutation	SNP	G	A	4	3	c.650C>T	c.(649-651)TCC>TTC	p.S217F
Pat_44	Pre-Treatment	C3AR1	719	37	12	8211934	8211934	Missense_Mutation	SNP	A	G	6	8	c.848T>C	c.(847-849)CTG>CCG	p.L283P
Pat_44	Pre-Treatment	PRB2	653247	37	12	11546795	11546795	Missense_Mutation	SNP	G	A	4	21	c.217C>T	c.(217-219)CCT>TCT	p.P73S
Pat_44	Pre-Treatment	RERG	85004	37	12	15262420	15262420	Missense_Mutation	SNP	C	T	111	227	c.224G>A	c.(223-225)CGA>CAA	p.R75Q
Pat_44	Pre-Treatment	PKP2	5318	37	12	33021868	33021868	Missense_Mutation	SNP	C	T	17	37	c.1163G>A	c.(1162-1164)CGG>CAG	p.R388Q
Pat_44	Pre-Treatment	KIF21A	55605	37	12	39760186	39760186	Missense_Mutation	SNP	C	T	7	29	c.869G>A	c.(868-870)AGG>AAG	p.R290K
Pat_44	Pre-Treatment	KRT83	3889	37	12	52710275	52710275	Missense_Mutation	SNP	C	T	10	16	c.1018G>A	c.(1018-1020)GAG>AAG	p.E340K
Pat_44	Pre-Treatment	ARHGAP9	64333	37	12	57870685	57870685	Missense_Mutation	SNP	C	T	12	11	c.1145G>A	c.(1144-1146)CGA>CAA	p.R382Q
Pat_44	Pre-Treatment	CAND1	55832	37	12	67699646	67699646	Missense_Mutation	SNP	C	T	26	40	c.2198C>T	c.(2197-2199)TCC>TTC	p.S733F
Pat_44	Pre-Treatment	TMCC3	57458	37	12	94975900	94975900	Missense_Mutation	SNP	G	A	12	25	c.493C>T	c.(493-495)CGC>TGC	p.R165C
Pat_44	Pre-Treatment	ACTR6	64431	37	12	100601549	100601549	Missense_Mutation	SNP	G	A	3	22	c.364G>A	c.(364-366)GTA>ATA	p.V122I
Pat_44	Pre-Treatment	TMEM132D	121256	37	12	129559291	129559291	Missense_Mutation	SNP	C	T	21	27	c.2429G>A	c.(2428-2430)AGA>AAA	p.R810K
Pat_44	Pre-Treatment	FZD10	11211	37	12	130648391	130648391	Missense_Mutation	SNP	G	A	4	16	c.904G>A	c.(904-906)GAG>AAG	p.E302K
Pat_44	Pre-Treatment	SUGT1	10910	37	13	53236839	53236839	Splice_Site	SNP	T	C	19	27	c.478_splice	c.e7+2	p.G160_splice
Pat_44	Pre-Treatment	P704P	641455	37	14	20019914	20019914	Missense_Mutation	SNP	A	G	9	84	c.307T>C	c.(307-309)TGC>CGC	p.C103R
Pat_44	Pre-Treatment	OR4E2	26686	37	14	22133489	22133489	Missense_Mutation	SNP	A	C	26	86	c.193A>C	c.(193-195)AAT>CAT	p.N65H
Pat_44	Pre-Treatment	KIAA1409	57578	37	14	94088434	94088434	Missense_Mutation	SNP	G	A	21	44	c.4390G>A	c.(4390-4392)GAA>AAA	p.E1464K
Pat_44	Pre-Treatment	EVL	51466	37	14	100589879	100589879	Missense_Mutation	SNP	C	T	8	9	c.356C>T	c.(355-357)CCC>CTC	p.P119L
Pat_44	Pre-Treatment	AHNAK2	113146	37	14	105418834	105418834	Missense_Mutation	SNP	G	A	70	252	c.2954C>T	c.(2953-2955)TCC>TTC	p.S985F
Pat_44	Pre-Treatment	OR4M2	390538	37	15	22369141	22369141	Missense_Mutation	SNP	G	T	11	40	c.566G>T	c.(565-567)TGT>TTT	p.C189F

Pat_44	Pre-Treatment	DUOX2	50506	37	15	45396472	45396472	Missense_Mutation	SNP	G	T	2	0	c.2426C>A	c.(2425-2427)GCC>GAC	p.A809D
Pat_44	Pre-Treatment	CILP	8483	37	15	65496872	65496872	Missense_Mutation	SNP	G	A	3	16	c.653C>T	c.(652-654)GCC>GTC	p.A218V
Pat_44	Pre-Treatment	C15orf39	56905	37	15	75498897	75498897	Missense_Mutation	SNP	G	A	9	22	c.508G>A	c.(508-510)GCT>ACT	p.A170T
Pat_44	Pre-Treatment	ADAMTSL3	57188	37	15	84373159	84373159	Missense_Mutation	SNP	C	T	6	29	c.88C>T	c.(88-90)CCT>TCT	p.P30S
Pat_44	Pre-Treatment	ADAMTSL3	57188	37	15	84651288	84651288	Missense_Mutation	SNP	C	T	8	48	c.2908C>T	c.(2908-2910)CAT>TAT	p.H970Y
Pat_44	Pre-Treatment	RGMA	56963	37	15	93588419	93588419	Missense_Mutation	SNP	C	T	2	2	c.1162G>A	c.(1162-1164)GTG>ATG	p.V388M
Pat_44	Pre-Treatment	OR1F1	4992	37	16	3254951	3254951	Nonsense_Mutation	SNP	G	A	8	16	c.705G>A	c.(703-705)TGG>TGA	p.W235*
Pat_44	Pre-Treatment	A2BP1	54715	37	16	7568201	7568201	Missense_Mutation	SNP	C	T	11	74	c.80C>T	c.(79-81)TCG>TTG	p.S27L
Pat_44	Pre-Treatment	TMC5	79838	37	16	19451548	19451548	Missense_Mutation	SNP	C	T	4	25	c.188C>T	c.(187-189)CCA>CTA	p.P63L
Pat_44	Pre-Treatment	SEZ6L2	26470	37	16	29907064	29907064	Missense_Mutation	SNP	G	A	5	16	c.629C>T	c.(628-630)CCT>CTT	p.P210L
Pat_44	Pre-Treatment	NUDT21	11051	37	16	56473646	56473646	Nonsense_Mutation	SNP	G	A	24	96	c.394C>T	c.(394-396)CAG>TAG	p.Q132*
Pat_44	Pre-Treatment	NDRG4	65009	37	16	58538102	58538102	Missense_Mutation	SNP	G	A	11	38	c.172G>A	c.(172-174)GAG>AAG	p.E58K
Pat_44	Pre-Treatment	ADAT1	23536	37	16	75646166	75646166	Missense_Mutation	SNP	C	T	9	18	c.1018G>A	c.(1018-1020)GCC>ACC	p.A340T
Pat_44	Pre-Treatment	VAT1L	57687	37	16	77822748	77822748	Missense_Mutation	SNP	C	T	2	2	c.169C>T	c.(169-171)CGG>TGG	p.R57W
Pat_44	Pre-Treatment	PKD1L2	114780	37	16	81232607	81232607	Missense_Mutation	SNP	C	A	7	11	c.1203G>T	c.(1201-1203)AAG>AAT	p.K401N
Pat_44	Pre-Treatment	KIAA0182	23199	37	16	85667541	85667541	Missense_Mutation	SNP	C	T	3	21	c.29C>T	c.(28-30)TCC>TTC	p.S10F
Pat_44	Pre-Treatment	PRDM7	11105	37	16	90126823	90126823	Missense_Mutation	SNP	T	G	5	49	c.1159A>C	c.(1159-1161)ATG>CTG	p.M387L
Pat_44	Pre-Treatment	PRDM7	11105	37	16	90126912	90126912	Missense_Mutation	SNP	G	T	6	48	c.1070C>A	c.(1069-1071)TCT>TAT	p.S357Y
Pat_44	Pre-Treatment	DNAH2	146754	37	17	7704907	7704907	Missense_Mutation	SNP	G	A	21	120	c.8711G>A	c.(8710-8712)CGC>CAC	p.R2904H
Pat_44	Pre-Treatment	PER1	5187	37	17	8047057	8047057	Missense_Mutation	SNP	G	A	3	14	c.2599C>T	c.(2599-2601)CCC>TCC	p.P867S
Pat_44	Pre-Treatment	MYH4	4622	37	17	10358351	10358351	Missense_Mutation	SNP	C	T	10	23	c.2342G>A	c.(2341-2343)CGA>CAA	p.R781Q
Pat_44	Pre-Treatment	TMEM98	26022	37	17	31263453	31263453	Missense_Mutation	SNP	G	T	4	26	c.401G>T	c.(400-402)CGG>CTG	p.R134L
Pat_44	Pre-Treatment	KRTAP3-3	85293	37	17	39150276	39150276	Missense_Mutation	SNP	G	A	8	115	c.74C>T	c.(73-75)TCC>TTC	p.S25F
Pat_44	Pre-Treatment	KRTAP3-2	83897	37	17	39156032	39156032	Missense_Mutation	SNP	G	A	20	115	c.74C>T	c.(73-75)TCC>TTC	p.S25F
Pat_44	Pre-Treatment	KRTAP4-4	84616	37	17	39316759	39316759	Missense_Mutation	SNP	T	C	10	113	c.185A>G	c.(184-186)CAC>CGC	p.H62R
Pat_44	Pre-Treatment	FZD2	2535	37	17	42636236	42636236	Missense_Mutation	SNP	G	A	13	25	c.1180G>A	c.(1180-1182)GAC>AAC	p.D394N
Pat_44	Pre-Treatment	SPATA20	64847	37	17	48625781	48625781	Missense_Mutation	SNP	A	G	6	12	c.215A>G	c.(214-216)TAC>TGC	p.Y72C
Pat_44	Pre-Treatment	KIF2B	84643	37	17	51900764	51900764	Missense_Mutation	SNP	C	A	3	17	c.370C>A	c.(370-372)CAA>AAA	p.Q124K
Pat_44	Pre-Treatment	MRC2	9902	37	17	60741911	60741911	Missense_Mutation	SNP	C	T	4	20	c.121C>T	c.(121-123)CCC>TCC	p.P41S
Pat_44	Pre-Treatment	ZBTB7C	201501	37	18	45567019	45567019	Missense_Mutation	SNP	C	T	2	2	c.460G>A	c.(460-462)GAA>AAA	p.E154K
Pat_44	Pre-Treatment	SERPINB4	6318	37	18	61305069	61305069	Missense_Mutation	SNP	C	T	4	22	c.1057G>A	c.(1057-1059)GAA>AAA	p.E353K
Pat_44	Pre-Treatment	ZNF556	80032	37	19	2877745	2877745	Missense_Mutation	SNP	C	G	5	11	c.789C>G	c.(787-789)CAC>CAG	p.H263Q
Pat_44	Pre-Treatment	2-Mar	51257	37	19	8495569	8495569	Missense_Mutation	SNP	G	A	24	48	c.400G>A	c.(400-402)GAG>AAG	p.E134K
Pat_44	Pre-Treatment	MUC16	94025	37	19	9071943	9071943	Missense_Mutation	SNP	G	A	31	77	c.15503C>T	c.(15502-15504)TCA>TTA	p.S5168L
Pat_44	Pre-Treatment	MUC16	94025	37	19	9076723	9076723	Missense_Mutation	SNP	T	C	10	22	c.10723A>G	c.(10723-10725)ACT>GCT	p.T3575A
Pat_44	Pre-Treatment	ZNF878	729747	37	19	12155757	12155757	Missense_Mutation	SNP	C	A	12	64	c.600G>T	c.(598-600)AGG>AGT	p.R200S
Pat_44	Pre-Treatment	ZNF799	90576	37	19	12501446	12501446	Missense_Mutation	SNP	T	C	5	6	c.1766A>G	c.(1765-1767)GAA>GGA	p.E589G
Pat_44	Pre-Treatment	ANO8	57719	37	19	17439459	17439459	Missense_Mutation	SNP	C	T	2	2	c.1738G>A	c.(1738-1740)GGC>AGC	p.G580S
Pat_44	Pre-Treatment	ZNF93	81931	37	19	20044933	20044933	Missense_Mutation	SNP	T	G	6	35	c.1169T>G	c.(1168-1170)GTT>GGT	p.V390G
Pat_44	Pre-Treatment	ZNF626	199777	37	19	20808006	20808006	Missense_Mutation	SNP	T	C	7	40	c.677A>G	c.(676-678)GAG>GGG	p.E226G
Pat_44	Pre-Treatment	ZNF257	113835	37	19	22271366	22271366	Missense_Mutation	SNP	A	C	3	15	c.814A>C	c.(814-816)ATT>CTT	p.I272L
Pat_44	Pre-Treatment	ZNF675	171392	37	19	23836350	23836350	Missense_Mutation	SNP	A	T	6	14	c.1385T>A	c.(1384-1386)ATC>AAC	p.I462N
Pat_44	Pre-Treatment	ZNF540	163255	37	19	38090627	38090627	Missense_Mutation	SNP	A	G	3	33	c.110A>G	c.(109-111)GAG>GGG	p.E37G
Pat_44	Pre-Treatment	RYR1	6261	37	19	38990289	38990289	Missense_Mutation	SNP	G	A	4	21	c.7042G>A	c.(7042-7044)GAG>AAG	p.E2348K
Pat_44	Pre-Treatment	ZNF780A	284323	37	19	40580552	40580552	Missense_Mutation	SNP	T	G	6	47	c.1797A>C	c.(1795-1797)CAA>CAC	p.Q599H
Pat_44	Pre-Treatment	PSG4	5672	37	19	43697536	43697536	Nonsense_Mutation	SNP	C	T	17	14	c.1248G>A	c.(1246-1248)TGG>TGA	p.W416*
Pat_44	Pre-Treatment	BCL3	602	37	19	45262002	45262002	Missense_Mutation	SNP	A	G	2	5	c.1081A>G	c.(1081-1083)AAG>GAG	p.K361E

Pat_44	Pre-Treatment	CCDC8	83987	37	19	46914959	46914959	Missense_Mutation	SNP	T	C	4	33	c.1109A>G	c.(1108-1110)GAG>GGG	p.E370G
Pat_44	Pre-Treatment	NAPSB	256236	37	19	50837578	50837578	Missense_Mutation	SNP	C	T	12	16	c.238G>A	c.(238-240)GAT>AAT	p.D80N
Pat_44	Pre-Treatment	NR1H2	7376	37	19	50882034	50882034	Missense_Mutation	SNP	C	T	12	58	c.731C>T	c.(730-732)TCC>TTC	p.S244F
Pat_44	Pre-Treatment	ZNF649	65251	37	19	52394652	52394652	Missense_Mutation	SNP	C	T	4	17	c.737G>A	c.(736-738)AGG>AAG	p.R246K
Pat_44	Pre-Treatment	LILRA6	79168	37	19	54745739	54745739	Missense_Mutation	SNP	G	A	10	86	c.371C>T	c.(370-372)CCC>CTC	p.P124L
Pat_44	Pre-Treatment	LILRA1	11024	37	19	55107864	55107864	Missense_Mutation	SNP	C	T	20	55	c.1169C>T	c.(1168-1170)GCC>GTC	p.A390V
Pat_44	Pre-Treatment	RDH13	112724	37	19	55560029	55560029	Missense_Mutation	SNP	A	C	19	27	c.443T>G	c.(442-444)CTG>CGG	p.L148R
Pat_44	Pre-Treatment	TNNI3	7137	37	19	55666144	55666144	Missense_Mutation	SNP	C	T	3	15	c.337G>A	c.(337-339)GAC>AAC	p.D113N
Pat_44	Pre-Treatment	KIF3C	3797	37	2	26177197	26177197	Missense_Mutation	SNP	T	C	5	6	c.1828A>G	c.(1828-1830)ATC>GTC	p.I610V
Pat_44	Pre-Treatment	C2orf16	84226	37	2	27804477	27804477	Missense_Mutation	SNP	G	A	7	61	c.5038G>A	c.(5038-5040)GGT>AGT	p.G1680S
Pat_44	Pre-Treatment	NRXN1	9378	37	2	50850687	50850687	Missense_Mutation	SNP	G	A	6	32	c.998C>T	c.(997-999)CCC>CTC	p.P333L
Pat_44	Pre-Treatment	PTCD3	55037	37	2	86333474	86333474	Missense_Mutation	SNP	G	A	6	55	c.104G>A	c.(103-105)AGA>AAA	p.R35K
Pat_44	Pre-Treatment	MGAT4A	11320	37	2	99279513	99279513	Missense_Mutation	SNP	C	T	8	18	c.533G>A	c.(532-534)GGA>GAA	p.G178E
Pat_44	Pre-Treatment	PSD4	23550	37	2	113955150	113955150	Missense_Mutation	SNP	G	A	3	18	c.2396G>A	c.(2395-2397)GGC>GAC	p.G799D
Pat_44	Pre-Treatment	POTEF	728378	37	2	130877782	130877782	Missense_Mutation	SNP	A	G	6	64	c.307T>C	c.(307-309)TGC>CGC	p.C103R
Pat_44	Pre-Treatment	LRP1B	53353	37	2	141143575	141143575	Missense_Mutation	SNP	T	G	12	8	c.10418A>C	c.(10417-10419)AAA>ACA	p.K3473T
Pat_44	Pre-Treatment	ACVR1C	130399	37	2	158443750	158443750	Missense_Mutation	SNP	C	T	39	41	c.253G>A	c.(253-255)GAA>AAA	p.E85K
Pat_44	Pre-Treatment	BAZ2B	29994	37	2	160295582	160295582	Missense_Mutation	SNP	C	T	4	6	c.838G>A	c.(838-840)GAA>AAA	p.E280K
Pat_44	Pre-Treatment	SCN1A	6323	37	2	166848048	166848048	Missense_Mutation	SNP	T	G	10	23	c.5704A>C	c.(5704-5706)AAA>CAA	p.K1902Q
Pat_44	Pre-Treatment	TTN	7273	37	2	179437213	179437213	Missense_Mutation	SNP	G	A	4	3	c.65942C>T	c.(65941-65943)TCA>TTA	p.S21981L
Pat_44	Pre-Treatment	TTN	7273	37	2	179472521	179472521	Missense_Mutation	SNP	C	T	25	57	c.45289G>A	c.(45289-45291)GAA>AAA	p.E15097K
Pat_44	Pre-Treatment	TTN	7273	37	2	179483347	179483347	Missense_Mutation	SNP	C	T	6	36	c.39226G>A	c.(39226-39228)GGA>AGA	p.G13076R
Pat_44	Pre-Treatment	TTN	7273	37	2	179633436	179633436	Missense_Mutation	SNP	C	T	13	31	c.9127G>A	c.(9127-9129)GGA>AGA	p.G3043R
Pat_44	Pre-Treatment	COL5A2	1290	37	2	189943814	189943814	Missense_Mutation	SNP	C	T	6	17	c.980G>A	c.(979-981)GGT>GAT	p.G327D
Pat_44	Pre-Treatment	FZD7	8324	37	2	202899662	202899662	Missense_Mutation	SNP	C	T	4	34	c.292C>T	c.(292-294)CTC>TTC	p.L98F
Pat_44	Pre-Treatment	NOP58	51602	37	2	203139870	203139870	Missense_Mutation	SNP	G	A	3	10	c.80G>A	c.(79-81)AGT>AAT	p.S27N
Pat_44	Pre-Treatment	WNT10A	80326	37	2	219754939	219754939	Missense_Mutation	SNP	G	A	6	10	c.610G>A	c.(610-612)GGC>AGC	p.G204S
Pat_44	Pre-Treatment	DES	1674	37	2	220285045	220285045	Missense_Mutation	SNP	T	C	3	8	c.712T>C	c.(712-714)TTC>CTC	p.F238L
Pat_44	Pre-Treatment	INPP5D	3635	37	2	233990491	233990491	Missense_Mutation	SNP	G	A	7	15	c.386G>A	c.(385-387)AGA>AAA	p.R129K
Pat_44	Pre-Treatment	TGM3	7053	37	20	2291763	2291763	Nonsense_Mutation	SNP	G	A	6	45	c.528G>A	c.(526-528)TGG>TGA	p.W176*
Pat_44	Pre-Treatment	MYH7B	57644	37	20	33586367	33586367	Missense_Mutation	SNP	C	T	3	13	c.4054C>T	c.(4054-4056)CGT>TGT	p.R1352C
Pat_44	Pre-Treatment	DLGAP4	22839	37	20	35155384	35155384	Missense_Mutation	SNP	A	G	4	23	c.2920A>G	c.(2920-2922)AGC>GGC	p.S974G
Pat_44	Pre-Treatment	KCNB1	3745	37	20	47990401	47990401	Missense_Mutation	SNP	G	A	7	14	c.1696C>T	c.(1696-1698)CCC>TCC	p.P566S
Pat_44	Pre-Treatment	RTEL1	51750	37	20	62305428	62305428	Missense_Mutation	SNP	G	A	3	14	c.901G>A	c.(901-903)GCG>ACG	p.A301T
Pat_44	Pre-Treatment	ADARB1	104	37	21	46604892	46604892	Missense_Mutation	SNP	T	A	12	36	c.1571T>A	c.(1570-1572)ATA>AAA	p.I524K
Pat_44	Pre-Treatment	TXNRD2	10587	37	22	19864642	19864642	Missense_Mutation	SNP	C	T	3	9	c.1561G>A	c.(1561-1563)GGC>AGC	p.G521S
Pat_44	Pre-Treatment	EP300	2033	37	22	41551082	41551082	Missense_Mutation	SNP	C	T	29	69	c.3226C>T	c.(3226-3228)CGT>TGT	p.R1076C
Pat_44	Pre-Treatment	CPT1B	1375	37	22	51012763	51012763	Splice_Site	SNP	C	T	3	12	c.970_splice	c.e8+1	p.D324_splice
Pat_44	Pre-Treatment	THUMPD3	25917	37	3	9406849	9406849	Missense_Mutation	SNP	G	C	2	10	c.97G>C	c.(97-99)GAA>CAA	p.E33Q
Pat_44	Pre-Treatment	IRAK2	3656	37	3	10242054	10242054	Nonsense_Mutation	SNP	G	A	7	48	c.279G>A	c.(277-279)TGG>TGA	p.W93*
Pat_44	Pre-Treatment	GHRL	51738	37	3	10331851	10331851	Missense_Mutation	SNP	C	T	6	8	c.14G>A	c.(13-15)GGG>GAG	p.G5E
Pat_44	Pre-Treatment	ARPP21	10777	37	3	35729262	35729262	Missense_Mutation	SNP	C	T	3	7	c.293C>T	c.(292-294)TCC>TTC	p.S98F
Pat_44	Pre-Treatment	UBA7	7318	37	3	49849440	49849440	Missense_Mutation	SNP	C	T	12	21	c.802G>A	c.(802-804)GAC>AAC	p.D268N
Pat_44	Pre-Treatment	PRICKLE2	166336	37	3	64084864	64084864	Missense_Mutation	SNP	G	A	5	27	c.2398C>T	c.(2398-2400)CGC>TGC	p.R800C
Pat_44	Pre-Treatment	ADAMTS9	56999	37	3	64527257	64527257	Missense_Mutation	SNP	T	A	23	47	c.5237A>T	c.(5236-5238)AAA>ATA	p.K1746I
Pat_44	Pre-Treatment	CADM2	253559	37	3	85935366	85935367	Missense_Mutation	DNP	GG	AA	5	22	c.391_392GG>AA	c.(391-393)GGA>AAA	p.G131K
Pat_44	Pre-Treatment	NEK11	79858	37	3	130889665	130889665	Missense_Mutation	SNP	C	A	16	78	c.1333C>A	c.(1333-1335)CCT>ACT	p.P445T

Pat_44	Pre-Treatment	IGSF10	285313	37	3	151161504	151161504	Missense_Mutation	SNP	G	A	4	17	c.5231C>T	c.(5230-5232)CCT>CTT	p.P1744L
Pat_44	Pre-Treatment	UBXN7	26043	37	3	196083689	196083689	Missense_Mutation	SNP	C	T	6	7	c.1337G>A	c.(1336-1338)GGA>GAA	p.G446E
Pat_44	Pre-Treatment	CPLX1	10815	37	4	786295	786295	Missense_Mutation	SNP	C	T	2	1	c.133G>A	c.(133-135)GAG>AAG	p.E45K
Pat_44	Pre-Treatment	SLC10A4	201780	37	4	48485582	48485582	Missense_Mutation	SNP	G	A	2	1	c.4G>A	c.(4-6)GAC>AAC	p.D2N
Pat_44	Pre-Treatment	ALB	213	37	4	74276060	74276060	Missense_Mutation	SNP	C	T	7	41	c.647C>T	c.(646-648)TCG>TTG	p.S216L
Pat_44	Pre-Treatment	AIMP1	9255	37	4	107258144	107258144	Missense_Mutation	SNP	C	T	23	33	c.722C>T	c.(721-723)CCT>CTT	p.P241L
Pat_44	Pre-Treatment	DCHS2	54798	37	4	155191120	155191120	Missense_Mutation	SNP	T	G	5	20	c.5144A>C	c.(5143-5145)CAG>CCG	p.Q1715P
Pat_44	Pre-Treatment	ADAMTS16	170690	37	5	5318284	5318284	Missense_Mutation	SNP	C	A	2	0	c.3449C>A	c.(3448-3450)TCC>TAC	p.S1150Y
Pat_44	Pre-Treatment	PRDM9	56979	37	5	23527167	23527167	Missense_Mutation	SNP	G	C	4	31	c.1970G>C	c.(1969-1971)AGA>ACA	p.R657T
Pat_44	Pre-Treatment	ANKRD34B	340120	37	5	79854737	79854737	Missense_Mutation	SNP	G	A	3	2	c.1102C>T	c.(1102-1104)CAC>TAC	p.H368Y
Pat_44	Pre-Treatment	SEC24A	10802	37	5	134011777	134011777	Missense_Mutation	SNP	C	T	8	16	c.1216C>T	c.(1216-1218)CCT>TCT	p.P406S
Pat_44	Pre-Treatment	PCDHB7	56129	37	5	140554361	140554361	Missense_Mutation	SNP	G	A	5	14	c.1945G>A	c.(1945-1947)GAG>AAG	p.E649K
Pat_44	Pre-Treatment	PCDHB16	57717	37	5	140563942	140563942	Missense_Mutation	SNP	C	T	37	35	c.1808C>T	c.(1807-1809)TCG>TTG	p.S603L
Pat_44	Pre-Treatment	F13A1	2162	37	6	6222398	6222398	Missense_Mutation	SNP	C	T	8	26	c.980G>A	c.(979-981)CGA>CAA	p.R327Q
Pat_44	Pre-Treatment	SCAND3	114821	37	6	28543412	28543412	Missense_Mutation	SNP	G	A	7	27	c.1070C>T	c.(1069-1071)TCA>TTA	p.S357L
Pat_44	Pre-Treatment	HLA-DRB1	3123	37	6	32549440	32549440	Nonsense_Mutation	SNP	C	T	15	73	c.546G>A	c.(544-546)TGG>TGA	p.W182*
Pat_44	Pre-Treatment	BRD2	6046	37	6	32945615	32945615	Missense_Mutation	SNP	C	T	15	17	c.1411C>T	c.(1411-1413)CCT>TCT	p.P471S
Pat_44	Pre-Treatment	DNAH8	1769	37	6	38980336	38980336	Missense_Mutation	SNP	G	A	11	50	c.12986G>A	c.(12985-12987)AGA>AAA	p.R4329K
Pat_44	Pre-Treatment	CUL7	9820	37	6	43018716	43018716	Missense_Mutation	SNP	G	A	44	109	c.1223C>T	c.(1222-1224)CCT>CTT	p.P408L
Pat_44	Pre-Treatment	ENPP5	59084	37	6	46129128	46129128	Missense_Mutation	SNP	G	A	4	18	c.1369C>T	c.(1369-1371)CAC>TAC	p.H457Y
Pat_44	Pre-Treatment	ENPP5	59084	37	6	46133259	46133259	Missense_Mutation	SNP	G	A	7	18	c.871C>T	c.(871-873)CCT>TCT	p.P291S
Pat_44	Pre-Treatment	CRISP1	167	37	6	49819748	49819748	Missense_Mutation	SNP	C	T	5	26	c.161G>A	c.(160-162)AGA>AAA	p.R54K
Pat_44	Pre-Treatment	TRMT11	60487	37	6	126317137	126317137	Missense_Mutation	SNP	C	T	10	24	c.163C>T	c.(163-165)CCC>TCC	p.P55S
Pat_44	Pre-Treatment	ENPP1	5167	37	6	132206128	132206128	Missense_Mutation	SNP	G	A	6	13	c.2369G>A	c.(2368-2370)GGT>GAT	p.G790D
Pat_44	Pre-Treatment	NOX3	50508	37	6	155732380	155732380	Missense_Mutation	SNP	G	A	6	26	c.1423C>T	c.(1423-1425)CAT>TAT	p.H475Y
Pat_44	Pre-Treatment	SDK1	221935	37	7	4152925	4152925	Nonsense_Mutation	SNP	C	T	6	62	c.3439C>T	c.(3439-3441)CGA>TGA	p.R1147*
Pat_44	Pre-Treatment	DGKB	1607	37	7	14758205	14758205	Missense_Mutation	SNP	G	A	7	33	c.428C>T	c.(427-429)TCT>TTT	p.S143F
Pat_44	Pre-Treatment	DNAH11	8701	37	7	21906088	21906088	Missense_Mutation	SNP	G	A	25	55	c.11518G>A	c.(11518-11520)GCA>ACA	p.A3840T
Pat_44	Pre-Treatment	ZNF92	168374	37	7	64863839	64863840	Missense_Mutation	DNP	CC	AT	9	85	c.812_813CC>AT	c.(811-813)ACC>AAT	p.T271N
Pat_44	Pre-Treatment	PCLO	27445	37	7	82595241	82595241	Missense_Mutation	SNP	C	T	4	10	c.3863G>A	c.(3862-3864)GGG>GAG	p.G1288E
Pat_44	Pre-Treatment	NPTX2	4885	37	7	98249123	98249123	Missense_Mutation	SNP	G	A	4	10	c.595G>A	c.(595-597)GAG>AAG	p.E199K
Pat_44	Pre-Treatment	NPTX2	4885	37	7	98257909	98257909	Missense_Mutation	SNP	G	A	3	2	c.1264G>A	c.(1264-1266)GAG>AAG	p.E422K
Pat_44	Pre-Treatment	GIGYF1	64599	37	7	100282236	100282236	Missense_Mutation	SNP	G	A	17	27	c.1466C>T	c.(1465-1467)CCC>CTC	p.P489L
Pat_44	Pre-Treatment	MUC17	140453	37	7	100677456	100677456	Missense_Mutation	SNP	G	A	94	280	c.2759G>A	c.(2758-2760)GGG>GAG	p.G920E
Pat_44	Pre-Treatment	MUC17	140453	37	7	100684305	100684305	Missense_Mutation	SNP	C	T	92	186	c.9608C>T	c.(9607-9609)TCA>TTA	p.S3203L
Pat_44	Pre-Treatment	FOXP2	93986	37	7	114284742	114284742	Missense_Mutation	SNP	C	T	5	16	c.992C>T	c.(991-993)TCG>TTG	p.S331L
Pat_44	Pre-Treatment	SLC35B4	84912	37	7	133981162	133981162	Missense_Mutation	SNP	G	A	4	30	c.730C>T	c.(730-732)CTC>TTC	p.L244F
Pat_44	Pre-Treatment	KIAA1549	57670	37	7	138556030	138556030	Missense_Mutation	SNP	G	A	5	21	c.4424C>T	c.(4423-4425)CCC>CTC	p.P1475L
Pat_44	Pre-Treatment	UBN2	254048	37	7	138957074	138957074	Missense_Mutation	SNP	C	T	3	16	c.1603C>T	c.(1603-1605)CGT>TGT	p.R535C
Pat_44	Pre-Treatment	BRAF	673	37	7	140453136	140453136	Missense_Mutation	SNP	A	T	12	29	c.1799T>A	c.(1798-1800)GTG>GAG	p.V600E
Pat_44	Pre-Treatment	TMEM176A	55365	37	7	150499363	150499363	Missense_Mutation	SNP	G	A	8	17	c.235G>A	c.(235-237)GAC>AAC	p.D79N
Pat_44	Pre-Treatment	MLL3	58508	37	7	151896402	151896402	Missense_Mutation	SNP	A	C	12	26	c.4235T>G	c.(4234-4236)CTT>CGT	p.L1412R
Pat_44	Pre-Treatment	RP1L1	94137	37	8	10466059	10466059	Missense_Mutation	SNP	C	T	6	32	c.5549G>A	c.(5548-5550)GGT>GAT	p.G1850D
Pat_44	Pre-Treatment	HR	55806	37	8	21978651	21978651	Missense_Mutation	SNP	G	A	30	53	c.2294C>T	c.(2293-2295)ACC>ATC	p.T765I
Pat_44	Pre-Treatment	ADAM28	10863	37	8	24181463	24181463	Nonsense_Mutation	SNP	G	A	11	10	c.837G>A	c.(835-837)TGG>TGA	p.W279*
Pat_44	Pre-Treatment	CA8	767	37	8	61144872	61144872	Missense_Mutation	SNP	C	T	63	245	c.484G>A	c.(484-486)GGA>AGA	p.G162R
Pat_44	Pre-Treatment	PREX2	80243	37	8	68965372	68965372	Nonsense_Mutation	SNP	G	A	15	69	c.984G>A	c.(982-984)TGG>TGA	p.W328*

Pat_44	Pre-Treatment	C8orf34	116328	37	8	69699772	69699772	Splice_Site	SNP	G	A	4	36	c.1291_splice	c.e12+1	p.R431_splice
Pat_44	Pre-Treatment	NACAP1	83955	37	8	102381492	102381492	Missense_Mutation	SNP	A	G	12	62	c.355A>G	c.(355-357)ACA>GCA	p.T119A
Pat_44	Pre-Treatment	ZFPM2	23414	37	8	106811077	106811077	Missense_Mutation	SNP	G	A	103	57	c.865G>A	c.(865-867)GAC>AAC	p.D289N
Pat_44	Pre-Treatment	CSMD3	114788	37	8	113697683	113697683	Nonsense_Mutation	SNP	G	A	117	59	c.2434C>T	c.(2434-2436)CAG>TAG	p.Q812*
Pat_44	Pre-Treatment	MAPK15	225689	37	8	144801568	144801568	Missense_Mutation	SNP	C	T	4	36	c.637C>T	c.(637-639)CGG>TGG	p.R213W
Pat_44	Pre-Treatment	RFX3	5991	37	9	3257189	3257189	Missense_Mutation	SNP	G	A	9	6	c.1616C>T	c.(1615-1617)TCC>TTC	p.S539F
Pat_44	Pre-Treatment	PTPRD	5789	37	9	8319881	8319881	Nonsense_Mutation	SNP	G	A	14	18	c.5620C>T	c.(5620-5622)CAG>TAG	p.Q1874*
Pat_44	Pre-Treatment	LINGO2	158038	37	9	27950023	27950023	Missense_Mutation	SNP	A	C	13	15	c.647T>G	c.(646-648)ATG>AGG	p.M216R
Pat_44	Pre-Treatment	C9orf79	286234	37	9	90498092	90498092	Missense_Mutation	SNP	G	A	2	1	c.286G>A	c.(286-288)GGG>AGG	p.G96R
Pat_44	Pre-Treatment	RBM18	92400	37	9	125023747	125023747	Missense_Mutation	SNP	G	A	3	7	c.25C>T	c.(25-27)CCC>TCC	p.P9S
Pat_44	Pre-Treatment	ZER1	10444	37	9	131513520	131513520	Missense_Mutation	SNP	C	T	11	8	c.1066G>A	c.(1066-1068)GTG>ATG	p.V356M
Pat_44	Pre-Treatment	RNF208	727800	37	9	140115622	140115622	Missense_Mutation	SNP	C	T	3	7	c.43G>A	c.(43-45)GGC>AGC	p.G15S
Pat_44	Pre-Treatment	SPANXN5	494197	37	X	52825650	52825650	Missense_Mutation	SNP	C	T	10	3	c.97G>A	c.(97-99)GAC>AAC	p.D33N
Pat_44	Pre-Treatment	TEX11	56159	37	X	69825324	69825324	Missense_Mutation	SNP	C	T	15	10	c.2039G>A	c.(2038-2040)CGG>CAG	p.R680Q
Pat_44	Pre-Treatment	ACRC	93953	37	X	70823916	70823916	Missense_Mutation	SNP	A	T	7	19	c.789A>T	c.(787-789)GAA>GAT	p.E263D
Pat_44	Pre-Treatment	ACRC	93953	37	X	70823918	70823918	Missense_Mutation	SNP	C	T	7	18	c.791C>T	c.(790-792)GCT>GTT	p.A264V
Pat_44	Pre-Treatment	CYLC1	1538	37	X	83128420	83128420	Missense_Mutation	SNP	C	T	4	6	c.704C>T	c.(703-705)TCA>TTA	p.S235L
Pat_44	Pre-Treatment	SATL1	340562	37	X	84363364	84363364	Missense_Mutation	SNP	C	T	4	35	c.611G>A	c.(610-612)AGC>AAC	p.S204N
Pat_44	Pre-Treatment	SRPX2	27286	37	X	99921932	99921932	Splice_Site	SNP	T	A	2	6	c.961_splice	c.e8+2	p.P321_splice
Pat_44	Pre-Treatment	GPRASP2	114928	37	X	101969946	101969946	Missense_Mutation	SNP	C	T	3	17	c.149C>T	c.(148-150)CCC>CTC	p.P50L
Pat_44	Pre-Treatment	SPANXN2	494119	37	X	142795358	142795358	Missense_Mutation	SNP	C	T	28	20	c.320G>A	c.(319-321)GGA>GAA	p.G107E
Pat_44	Pre-Treatment	GPR50	9248	37	X	150348653	150348653	Missense_Mutation	SNP	C	T	17	32	c.598C>T	c.(598-600)CCT>TCT	p.P200S
Pat_44	Pre-Treatment	MAGEA1	4100	37	X	152482755	152482755	Missense_Mutation	SNP	C	T	8	7	c.256G>A	c.(256-258)GAG>AAG	p.E86K
Pat_44	Pre-Treatment	ZFY	7544	37	Y	2844779	2844779	Missense_Mutation	SNP	G	A	2	0	c.997G>A	c.(997-999)GCA>ACA	p.A333T
Pat_44	Post-Resistance	DVL1	1855	37	1	1271820	1271820	Missense_Mutation	SNP	G	A	4	38	c.1715C>T	c.(1714-1716)GCT>GTT	p.A572V
Pat_44	Post-Resistance	RNF207	388591	37	1	6272420	6272420	Missense_Mutation	SNP	G	A	4	100	c.1426G>A	c.(1426-1428)GTG>ATG	p.V476M
Pat_44	Post-Resistance	TNFRSF9	3604	37	1	7997775	7997775	Missense_Mutation	SNP	G	A	4	160	c.388C>T	c.(388-390)CGT>TGT	p.R130C
Pat_44	Post-Resistance	H6PD	9563	37	1	9324162	9324162	Missense_Mutation	SNP	C	T	3	43	c.1610C>T	c.(1609-1611)GCC>GTC	p.A537V
Pat_44	Post-Resistance	CLSTN1	22883	37	1	9815188	9815188	Missense_Mutation	SNP	C	T	4	120	c.424G>A	c.(424-426)GTG>ATG	p.V142M
Pat_44	Post-Resistance	TARDBP	23435	37	1	11073983	11073983	Missense_Mutation	SNP	G	T	4	174	c.199G>T	c.(199-201)GGC>TGC	p.G67C
Pat_44	Post-Resistance	TAS1R2	80834	37	1	19175984	19175984	Missense_Mutation	SNP	G	A	4	116	c.1318C>T	c.(1318-1320)CCG>TCG	p.P440S
Pat_44	Post-Resistance	EPHA8	2046	37	1	22924331	22924331	Missense_Mutation	SNP	G	A	5	116	c.2093G>A	c.(2092-2094)CGC>CAC	p.R698H
Pat_44	Post-Resistance	CCDC21	64793	37	1	26582163	26582163	Missense_Mutation	SNP	G	A	4	138	c.710G>A	c.(709-711)CGG>CAG	p.R237Q
Pat_44	Post-Resistance	WDTC1	23038	37	1	27621115	27621115	Missense_Mutation	SNP	G	A	4	62	c.868G>A	c.(868-870)GAA>AAA	p.E290K
Pat_44	Post-Resistance	TMEM222	84065	37	1	27660733	27660733	Missense_Mutation	SNP	C	T	4	153	c.500C>T	c.(499-501)ACG>ATG	p.T167M
Pat_44	Post-Resistance	TMEM200B	399474	37	1	29447653	29447653	Missense_Mutation	SNP	C	T	3	41	c.688G>A	c.(688-690)GGG>AGG	p.G230R
Pat_44	Post-Resistance	COL16A1	1307	37	1	32122645	32122645	Missense_Mutation	SNP	C	T	4	228	c.4045G>A	c.(4045-4047)GCT>ACT	p.A1349T
Pat_44	Post-Resistance	PABPC4	8761	37	1	40030188	40030188	Missense_Mutation	SNP	G	A	4	191	c.1360C>T	c.(1360-1362)CGC>TGC	p.R454C
Pat_44	Post-Resistance	ZNF684	127396	37	1	41007374	41007374	Missense_Mutation	SNP	G	A	4	53	c.230G>A	c.(229-231)AGC>AAC	p.S77N
Pat_44	Post-Resistance	KIAA0467	23334	37	1	43909271	43909271	Missense_Mutation	SNP	C	T	3	32	c.5932C>T	c.(5932-5934)CGC>TGC	p.R1978C
Pat_44	Post-Resistance	ZSWIM5	57643	37	1	45484542	45484542	Missense_Mutation	SNP	G	A	4	71	c.3142C>T	c.(3142-3144)CTC>TTC	p.L1048F
Pat_44	Post-Resistance	C1orf175	374977	37	1	55172183	55172183	Missense_Mutation	SNP	C	T	4	172	c.3640C>T	c.(3640-3642)CTC>TTC	p.L1214F
Pat_44	Post-Resistance	INADL	10207	37	1	62594540	62594540	Missense_Mutation	SNP	G	A	5	351	c.5194G>A	c.(5194-5196)GGG>AGG	p.G1732R
Pat_44	Post-Resistance	SGIP1	84251	37	1	67145406	67145406	Missense_Mutation	SNP	G	A	5	279	c.785G>A	c.(784-786)CGA>CAA	p.R262Q
Pat_44	Post-Resistance	IL12RB2	3595	37	1	67793971	67793971	Nonsense_Mutation	SNP	G	T	6	392	c.568G>T	c.(568-570)GAA>TAA	p.E190*
Pat_44	Post-Resistance	LPHN2	23266	37	1	82409013	82409013	Missense_Mutation	SNP	C	T	4	166	c.758C>T	c.(757-759)ACC>ATC	p.T253I
Pat_44	Post-Resistance	DPYD	1806	37	1	98187146	98187146	Missense_Mutation	SNP	G	A	4	193	c.403C>T	c.(403-405)CTT>TTT	p.L135F

Pat_44	Post-Resistance	AP4B1	10717	37	1	114438057	114438057	Missense_Mutation	SNP	G	A	4	132	c.1850C>T	c.(1849-1851)GCC>GTC	p.A617V
Pat_44	Post-Resistance	AMPD1	270	37	1	115231293	115231293	Missense_Mutation	SNP	C	T	5	229	c.104G>A	c.(103-105)CGT>CAT	p.R35H
Pat_44	Post-Resistance	NOTCH2NL	388677	37	1	145281653	145281653	Missense_Mutation	SNP	G	A	5	297	c.583G>A	c.(583-585)GGC>AGC	p.G195S
Pat_44	Post-Resistance	TCHH	7062	37	1	152082220	152082220	Missense_Mutation	SNP	G	C	3	54	c.3473C>G	c.(3472-3474)CCG>CGG	p.P1158R
Pat_44	Post-Resistance	CRNN	49860	37	1	152382873	152382873	Missense_Mutation	SNP	C	T	5	269	c.685G>A	c.(685-687)GGA>AGA	p.G229R
Pat_44	Post-Resistance	KPRP	448834	37	1	152732734	152732734	Missense_Mutation	SNP	C	T	4	196	c.670C>T	c.(670-672)CGG>TGG	p.R224W
Pat_44	Post-Resistance	HCN3	57657	37	1	155253804	155253804	Missense_Mutation	SNP	C	T	4	176	c.748C>T	c.(748-750)CGC>TGC	p.R250C
Pat_44	Post-Resistance	IGSF9	57549	37	1	159906306	159906306	Missense_Mutation	SNP	C	T	4	144	c.556G>A	c.(556-558)GTG>ATG	p.V186M
Pat_44	Post-Resistance	PBX1	5087	37	1	164781327	164781327	Missense_Mutation	SNP	C	T	4	131	c.938C>T	c.(937-939)GCT>GTT	p.A313V
Pat_44	Post-Resistance	F5	2153	37	1	169510571	169510571	Missense_Mutation	SNP	G	A	6	313	c.3757C>T	c.(3757-3759)CTC>TTC	p.L1253F
Pat_44	Post-Resistance	MYOC	4653	37	1	171605481	171605481	Missense_Mutation	SNP	C	T	4	134	c.1099G>A	c.(1099-1101)GGA>AGA	p.G367R
Pat_44	Post-Resistance	ZBTB37	84614	37	1	173839887	173839887	Missense_Mutation	SNP	G	A	5	141	c.524G>A	c.(523-525)CGA>CAA	p.R175Q
Pat_44	Post-Resistance	HMCN1	83872	37	1	185984537	185984537	Missense_Mutation	SNP	C	T	4	130	c.4877C>T	c.(4876-4878)ACT>ATT	p.T1626I
Pat_44	Post-Resistance	PRG4	10216	37	1	186276274	186276274	Missense_Mutation	SNP	G	T	6	84	c.1423G>T	c.(1423-1425)GCA>TCA	p.A475S
Pat_44	Post-Resistance	CFHR4	10877	37	1	196871608	196871608	Missense_Mutation	SNP	G	A	4	222	c.119G>A	c.(118-120)CGT>CAT	p.R40H
Pat_44	Post-Resistance	KIF14	9928	37	1	200574423	200574423	Missense_Mutation	SNP	C	G	4	103	c.1734G>C	c.(1732-1734)ATG>ATC	p.M578I
Pat_44	Post-Resistance	CAMSAP1L1	23271	37	1	200816783	200816783	Missense_Mutation	SNP	C	T	4	89	c.1241C>T	c.(1240-1242)TCT>TTT	p.S414F
Pat_44	Post-Resistance	KIF21B	23046	37	1	200943915	200943915	Missense_Mutation	SNP	C	T	4	167	c.4741G>A	c.(4741-4743)GGT>AGT	p.G1581S
Pat_44	Post-Resistance	KIF21B	23046	37	1	200954057	200954057	Missense_Mutation	SNP	G	A	6	182	c.3733C>T	c.(3733-3735)CGG>TGG	p.R1245W
Pat_44	Post-Resistance	CACNA1S	779	37	1	201047107	201047107	Missense_Mutation	SNP	C	T	4	148	c.1519G>A	c.(1519-1521)GGT>AGT	p.G507S
Pat_44	Post-Resistance	LGR6	59352	37	1	202205106	202205106	Missense_Mutation	SNP	C	T	3	62	c.413C>T	c.(412-414)CCG>CTG	p.P138L
Pat_44	Post-Resistance	PPP1R12B	4660	37	1	202411616	202411616	Missense_Mutation	SNP	G	A	4	108	c.1583G>A	c.(1582-1584)CGG>CAG	p.R528Q
Pat_44	Post-Resistance	PPP1R12B	4660	37	1	202532031	202532031	Missense_Mutation	SNP	G	A	5	177	c.2633G>A	c.(2632-2634)AGC>AAC	p.S878N
Pat_44	Post-Resistance	ADIPOR1	51094	37	1	202920072	202920072	Missense_Mutation	SNP	C	T	4	237	c.127G>A	c.(127-129)GCC>ACC	p.A43T
Pat_44	Post-Resistance	CR1L	1379	37	1	207874932	207874932	Missense_Mutation	SNP	G	A	6	281	c.1297G>A	c.(1297-1299)GGA>AGA	p.G433R
Pat_44	Post-Resistance	USH2A	7399	37	1	216595602	216595602	Missense_Mutation	SNP	G	A	4	106	c.77C>T	c.(76-78)GCT>GTT	p.A26V
Pat_44	Post-Resistance	C1orf55	163859	37	1	226175973	226175973	Missense_Mutation	SNP	C	T	6	291	c.758G>A	c.(757-759)AGC>AAC	p.S253N
Pat_44	Post-Resistance	GJC2	57165	37	1	228346178	228346178	Missense_Mutation	SNP	G	A	4	153	c.719G>A	c.(718-720)CGA>CAA	p.R240Q
Pat_44	Post-Resistance	OBSCN	84033	37	1	228553829	228553829	Missense_Mutation	SNP	C	T	4	117	c.19118C>T	c.(19117-19119)ACG>ATG	p.T6373M
Pat_44	Post-Resistance	HIST3H3	8290	37	1	228612899	228612899	Missense_Mutation	SNP	C	T	4	147	c.128G>A	c.(127-129)CGG>CAG	p.R43Q
Pat_44	Post-Resistance	GALNT2	2590	37	1	230379054	230379054	Missense_Mutation	SNP	C	T	5	189	c.610C>T	c.(610-612)CTC>TTC	p.L204F
Pat_44	Post-Resistance	EDARADD	128178	37	1	236645918	236645918	Missense_Mutation	SNP	G	A	4	153	c.617G>A	c.(616-618)CGG>CAG	p.R206Q
Pat_44	Post-Resistance	CEP170	9859	37	1	243388551	243388551	Missense_Mutation	SNP	C	T	4	51	c.32G>A	c.(31-33)AGT>AAT	p.S11N
Pat_44	Post-Resistance	C1orf100	200159	37	1	244538721	244538721	Missense_Mutation	SNP	G	A	4	125	c.104G>A	c.(103-105)GGG>GAG	p.G35E
Pat_44	Post-Resistance	KIF26B	55083	37	1	245704194	245704194	Missense_Mutation	SNP	C	T	4	107	c.1292C>T	c.(1291-1293)GCC>GTC	p.A431V
Pat_44	Post-Resistance	OR2G2	81470	37	1	247752034	247752034	Missense_Mutation	SNP	C	T	6	363	c.373C>T	c.(373-375)CGC>TGC	p.R125C
Pat_44	Post-Resistance	OR2T4	127074	37	1	248524908	248524908	Missense_Mutation	SNP	G	A	6	114	c.26G>A	c.(25-27)AGC>AAC	p.S9N
Pat_44	Post-Resistance	OR2T4	127074	37	1	248524937	248524937	Missense_Mutation	SNP	A	T	8	128	c.55A>T	c.(55-57)ATG>TTG	p.M19L
Pat_44	Post-Resistance	PGBD2	267002	37	1	249212035	249212035	Missense_Mutation	SNP	G	A	4	102	c.1252G>A	c.(1252-1254)GTG>ATG	p.V418M
Pat_44	Post-Resistance	C10orf18	54906	37	10	5788743	5788743	Missense_Mutation	SNP	G	A	4	178	c.3359G>A	c.(3358-3360)GGC>GAC	p.G1120D
Pat_44	Post-Resistance	PRKCQ	5588	37	10	6539181	6539181	Splice_Site	SNP	C	T	4	186	c.574_splice	c.e6+1	p.Q192_splice
Pat_44	Post-Resistance	ECHDC3	79746	37	10	11791562	11791562	Missense_Mutation	SNP	C	T	4	146	c.361C>T	c.(361-363)CAT>TAT	p.H121Y
Pat_44	Post-Resistance	BEND7	222389	37	10	13541865	13541865	Missense_Mutation	SNP	G	A	4	53	c.205C>T	c.(205-207)CCG>TCG	p.P69S
Pat_44	Post-Resistance	ANKRD26	22852	37	10	27368041	27368041	Missense_Mutation	SNP	C	T	4	122	c.790G>A	c.(790-792)GAA>AAA	p.E264K
Pat_44	Post-Resistance	MKX	283078	37	10	27964213	27964213	Missense_Mutation	SNP	G	A	5	198	c.1004C>T	c.(1003-1005)TCG>TTG	p.S335L
Pat_44	Post-Resistance	SVIL	6840	37	10	29782322	29782322	Splice_Site	SNP	T	A	4	74	c.3842_splice	c.e21-1	p.V1281_splice
Pat_44	Post-Resistance	KIAA1462	57608	37	10	30317428	30317428	Missense_Mutation	SNP	C	T	5	153	c.1649G>A	c.(1648-1650)AGC>AAC	p.S550N

Pat_44	Post-Resistance	ANKRD30A	91074	37	10	37430754	37430754	Missense_Mutation	SNP	T	C	11	86	c.761T>C	c.(760-762)GTG>GCG	p.V254A
Pat_44	Post-Resistance	ATOH7	220202	37	10	69991119	69991119	Missense_Mutation	SNP	G	A	4	48	c.316C>T	c.(316-318)CGG>TGG	p.R106W
Pat_44	Post-Resistance	DNA2	1763	37	10	70182463	70182463	Missense_Mutation	SNP	C	T	3	47	c.2651G>A	c.(2650-2652)CGT>CAT	p.R884H
Pat_44	Post-Resistance	DDX21	9188	37	10	70737388	70737388	Missense_Mutation	SNP	G	A	4	108	c.1846G>A	c.(1846-1848)GCC>ACC	p.A616T
Pat_44	Post-Resistance	SUPV3L1	6832	37	10	70956825	70956825	Missense_Mutation	SNP	G	A	4	209	c.1009G>A	c.(1009-1011)GGG>AGG	p.G337R
Pat_44	Post-Resistance	GRID1	2894	37	10	87379700	87379700	Missense_Mutation	SNP	C	T	4	147	c.2284G>A	c.(2284-2286)GGC>AGC	p.G762S
Pat_44	Post-Resistance	CYP2C8	1558	37	10	96818190	96818190	Nonsense_Mutation	SNP	G	A	5	147	c.721C>T	c.(721-723)CGA>TGA	p.R241*
Pat_44	Post-Resistance	PSD	5662	37	10	104163019	104163019	Missense_Mutation	SNP	G	A	3	29	c.3013C>T	c.(3013-3015)CGG>TGG	p.R1005W
Pat_44	Post-Resistance	MKI67	4288	37	10	129910469	129910469	Nonsense_Mutation	SNP	G	A	4	172	c.1897C>T	c.(1897-1899)CGA>TGA	p.R633*
Pat_44	Post-Resistance	KNDC1	85442	37	10	135027499	135027499	Missense_Mutation	SNP	C	T	4	129	c.4550C>T	c.(4549-4551)TCG>TTG	p.S1517L
Pat_44	Post-Resistance	PHRF1	57661	37	11	607537	607537	Missense_Mutation	SNP	G	A	4	168	c.2081G>A	c.(2080-2082)CGG>CAG	p.R694Q
Pat_44	Post-Resistance	CDHR5	53841	37	11	619577	619577	Missense_Mutation	SNP	G	A	4	57	c.1190C>T	c.(1189-1191)TCG>TTG	p.S397L
Pat_44	Post-Resistance	OR51B4	79339	37	11	5322800	5322800	Missense_Mutation	SNP	G	A	6	305	c.377C>T	c.(376-378)CCA>CTA	p.P126L
Pat_44	Post-Resistance	SPTY2D1	144108	37	11	18637412	18637412	Missense_Mutation	SNP	C	T	6	130	c.409G>A	c.(409-411)GCA>ACA	p.A137T
Pat_44	Post-Resistance	MRGPRX2	117194	37	11	19077579	19077579	Missense_Mutation	SNP	C	T	4	203	c.371G>A	c.(370-372)AGC>AAC	p.S124N
Pat_44	Post-Resistance	PRDM11	56981	37	11	45246079	45246079	Missense_Mutation	SNP	G	A	5	187	c.1156G>A	c.(1156-1158)GGT>AGT	p.G386S
Pat_44	Post-Resistance	F2	2147	37	11	46745005	46745005	Missense_Mutation	SNP	G	A	4	102	c.496G>A	c.(496-498)GGA>AGA	p.G166R
Pat_44	Post-Resistance	MYBPC3	4607	37	11	47356686	47356686	Missense_Mutation	SNP	C	T	4	44	c.2812G>A	c.(2812-2814)GCC>ACC	p.A938T
Pat_44	Post-Resistance	CNTF	1270	37	11	58391958	58391958	Missense_Mutation	SNP	G	A	4	88	c.566G>A	c.(565-567)CGT>CAT	p.R189H
Pat_44	Post-Resistance	DAK	26007	37	11	61113919	61113919	Missense_Mutation	SNP	G	A	4	184	c.1672G>A	c.(1672-1674)GGG>AGG	p.G558R
Pat_44	Post-Resistance	STIP1	10963	37	11	63965415	63965415	Missense_Mutation	SNP	G	A	4	213	c.992G>A	c.(991-993)CGA>CAA	p.R331Q
Pat_44	Post-Resistance	RPS6KB2	6199	37	11	67198881	67198881	Missense_Mutation	SNP	G	A	4	192	c.352G>A	c.(352-354)GCT>ACT	p.A118T
Pat_44	Post-Resistance	SUV420H1	51111	37	11	67925969	67925969	Missense_Mutation	SNP	C	T	3	36	c.1844G>A	c.(1843-1845)CGA>CAA	p.R615Q
Pat_44	Post-Resistance	CREBZF	58487	37	11	85375234	85375234	Missense_Mutation	SNP	A	T	6	239	c.686T>A	c.(685-687)GTG>GAG	p.V229E
Pat_44	Post-Resistance	FAT3	120114	37	11	92088309	92088309	Missense_Mutation	SNP	C	T	3	64	c.3031C>T	c.(3031-3033)CGG>TGG	p.R1011W
Pat_44	Post-Resistance	MMP27	64066	37	11	102573794	102573794	Missense_Mutation	SNP	C	T	4	169	c.397G>A	c.(397-399)GAA>AAA	p.E133K
Pat_44	Post-Resistance	DYNC2H1	79659	37	11	103049787	103049787	Missense_Mutation	SNP	A	G	3	128	c.6172A>G	c.(6172-6174)ATT>GTT	p.I2058V
Pat_44	Post-Resistance	CASP1	834	37	11	104904952	104904952	Missense_Mutation	SNP	G	A	5	226	c.257C>T	c.(256-258)ACG>ATG	p.T86M
Pat_44	Post-Resistance	POU2AF1	5450	37	11	111228204	111228204	Missense_Mutation	SNP	G	A	4	89	c.422C>T	c.(421-423)ACC>ATC	p.T141I
Pat_44	Post-Resistance	BACE1	23621	37	11	117167631	117167631	Missense_Mutation	SNP	G	A	5	172	c.308C>T	c.(307-309)GCT>GTT	p.A103V
Pat_44	Post-Resistance	CDON	50937	37	11	125864887	125864887	Missense_Mutation	SNP	G	A	4	143	c.2423C>T	c.(2422-2424)TCA>TTA	p.S808L
Pat_44	Post-Resistance	ERC1	23085	37	12	1137358	1137358	Missense_Mutation	SNP	C	T	5	206	c.289C>T	c.(289-291)CGT>TGT	p.R97C
Pat_44	Post-Resistance	TAPBPL	55080	37	12	6567939	6567939	Missense_Mutation	SNP	G	A	4	61	c.1033G>A	c.(1033-1035)GCC>ACC	p.A345T
Pat_44	Post-Resistance	PZP	5858	37	12	9345287	9345287	Missense_Mutation	SNP	C	T	4	114	c.1303G>A	c.(1303-1305)GAA>AAA	p.E435K
Pat_44	Post-Resistance	PRB4	5545	37	12	11461682	11461682	Missense_Mutation	SNP	C	G	7	501	c.235G>C	c.(235-237)GAA>CAA	p.E79Q
Pat_44	Post-Resistance	SLCO1B1	10599	37	12	21377737	21377737	Missense_Mutation	SNP	G	A	5	224	c.1829G>A	c.(1828-1830)CGT>CAT	p.R610H
Pat_44	Post-Resistance	CAPRIN2	65981	37	12	30886568	30886568	Missense_Mutation	SNP	G	A	4	153	c.887C>T	c.(886-888)ACG>ATG	p.T296M
Pat_44	Post-Resistance	ABCD2	225	37	12	39980088	39980088	Missense_Mutation	SNP	G	C	3	153	c.1658C>G	c.(1657-1659)TCT>TGT	p.S553C
Pat_44	Post-Resistance	SLC2A13	114134	37	12	40265629	40265629	Missense_Mutation	SNP	C	T	4	178	c.1169G>A	c.(1168-1170)CGC>CAC	p.R390H
Pat_44	Post-Resistance	PPHLN1	51535	37	12	42729721	42729721	Missense_Mutation	SNP	G	A	5	193	c.17G>A	c.(16-18)CGA>CAA	p.R6Q
Pat_44	Post-Resistance	ADAMTS20	80070	37	12	43769235	43769235	Missense_Mutation	SNP	C	T	4	125	c.5393G>A	c.(5392-5394)GGA>GAA	p.G1798E
Pat_44	Post-Resistance	KRT5	3852	37	12	52913972	52913972	Missense_Mutation	SNP	G	A	4	156	c.109C>T	c.(109-111)CGG>TGG	p.R37W
Pat_44	Post-Resistance	EIF4B	1975	37	12	53410370	53410370	Missense_Mutation	SNP	G	A	4	106	c.127G>A	c.(127-129)GAA>AAA	p.E43K
Pat_44	Post-Resistance	ATF7	11016	37	12	53910973	53910973	Missense_Mutation	SNP	G	A	4	201	c.1433C>T	c.(1432-1434)CCG>CTG	p.P478L
Pat_44	Post-Resistance	OR6C70	390327	37	12	55863565	55863565	Missense_Mutation	SNP	G	A	4	132	c.358C>T	c.(358-360)CGC>TGC	p.R120C
Pat_44	Post-Resistance	ITGA7	3679	37	12	56094174	56094174	Missense_Mutation	SNP	G	A	4	155	c.674C>T	c.(673-675)ACG>ATG	p.T225M
Pat_44	Post-Resistance	LRP1	4035	37	12	57591091	57591091	Missense_Mutation	SNP	C	T	6	433	c.9086C>T	c.(9085-9087)CCG>CTG	p.P3029L

Pat_44	Post-Resistance	KIF5A	3798	37	12	57963893	57963893	Missense_Mutation	SNP	G	A	3	27	c.1241G>A	c.(1240-1242)CGG>CAG	p.R414Q
Pat_44	Post-Resistance	PPFIA2	8499	37	12	81741473	81741473	Missense_Mutation	SNP	C	T	4	198	c.2071G>A	c.(2071-2073)GAA>AAA	p.E691K
Pat_44	Post-Resistance	KERA	11081	37	12	91445232	91445232	Missense_Mutation	SNP	C	T	4	93	c.950G>A	c.(949-951)AGT>AAT	p.S317N
Pat_44	Post-Resistance	UBE3B	89910	37	12	109959040	109959040	Missense_Mutation	SNP	G	A	4	211	c.2164G>A	c.(2164-2166)GAA>AAA	p.E722K
Pat_44	Post-Resistance	ABCB9	23457	37	12	123430679	123430679	Missense_Mutation	SNP	C	T	4	95	c.1144G>A	c.(1144-1146)GCC>ACC	p.A382T
Pat_44	Post-Resistance	CDK2AP1	8099	37	12	123749848	123749848	Missense_Mutation	SNP	G	A	4	110	c.175C>T	c.(175-177)CCC>TCC	p.P59S
Pat_44	Post-Resistance	NCOR2	9612	37	12	124821355	124821355	Missense_Mutation	SNP	C	T	5	90	c.6089G>A	c.(6088-6090)CGG>CAG	p.R2030Q
Pat_44	Post-Resistance	MMP17	4326	37	12	132335520	132335520	Missense_Mutation	SNP	G	A	4	64	c.1513G>A	c.(1513-1515)GAG>AAG	p.E505K
Pat_44	Post-Resistance	CHFR	55743	37	12	133438077	133438077	Missense_Mutation	SNP	G	A	4	96	c.763C>T	c.(763-765)CCC>TCC	p.P255S
Pat_44	Post-Resistance	KIAA0564	23078	37	13	42439903	42439903	Missense_Mutation	SNP	C	T	4	131	c.1394G>A	c.(1393-1395)GGA>GAA	p.G465E
Pat_44	Post-Resistance	CPB2	1361	37	13	46632333	46632333	Missense_Mutation	SNP	C	T	4	210	c.980G>A	c.(979-981)AGC>AAC	p.S327N
Pat_44	Post-Resistance	ATP7B	540	37	13	52515217	52515217	Missense_Mutation	SNP	C	T	4	142	c.3556G>A	c.(3556-3558)GGT>AGT	p.G1186S
Pat_44	Post-Resistance	ATP11A	23250	37	13	113473681	113473681	Missense_Mutation	SNP	G	A	6	221	c.634G>A	c.(634-636)GCC>ACC	p.A212T
Pat_44	Post-Resistance	ATP11A	23250	37	13	113485726	113485726	Missense_Mutation	SNP	C	A	4	155	c.1259C>A	c.(1258-1260)ACG>AAG	p.T420K
Pat_44	Post-Resistance	OR4M1	441670	37	14	20248846	20248846	Missense_Mutation	SNP	G	A	6	454	c.365G>A	c.(364-366)CGC>CAC	p.R122H
Pat_44	Post-Resistance	OR10G2	26534	37	14	22102815	22102815	Missense_Mutation	SNP	G	A	4	112	c.184C>T	c.(184-186)CGC>TGC	p.R62C
Pat_44	Post-Resistance	REC8	9985	37	14	24647390	24647390	Nonsense_Mutation	SNP	C	T	5	124	c.958C>T	c.(958-960)CAG>TAG	p.Q320*
Pat_44	Post-Resistance	MDP1	145553	37	14	24684770	24684770	Missense_Mutation	SNP	G	A	6	463	c.197C>T	c.(196-198)GCG>GTG	p.A66V
Pat_44	Post-Resistance	TGM1	7051	37	14	24727849	24727849	Missense_Mutation	SNP	G	A	4	137	c.1190C>T	c.(1189-1191)ACT>ATT	p.T397I
Pat_44	Post-Resistance	NID2	22795	37	14	52481816	52481816	Missense_Mutation	SNP	C	T	4	38	c.3206G>A	c.(3205-3207)AGA>AAA	p.R1069K
Pat_44	Post-Resistance	KIAA0831	22863	37	14	55836558	55836558	Missense_Mutation	SNP	C	T	4	101	c.1258G>A	c.(1258-1260)GGA>AGA	p.G420R
Pat_44	Post-Resistance	C14orf37	145407	37	14	58471800	58471800	Missense_Mutation	SNP	C	T	4	148	c.2222G>A	c.(2221-2223)CGA>CAA	p.R741Q
Pat_44	Post-Resistance	KIAA0586	9786	37	14	58949374	58949374	Missense_Mutation	SNP	G	A	4	159	c.2860G>A	c.(2860-2862)GGT>AGT	p.G954S
Pat_44	Post-Resistance	RTN1	6252	37	14	60072171	60072171	Missense_Mutation	SNP	G	A	4	105	c.2027C>T	c.(2026-2028)ACG>ATG	p.T676M
Pat_44	Post-Resistance	SPTB	6710	37	14	65237808	65237808	Missense_Mutation	SNP	C	T	5	347	c.5593G>A	c.(5593-5595)GCA>ACA	p.A1865T
Pat_44	Post-Resistance	YLPM1	56252	37	14	75265245	75265245	Missense_Mutation	SNP	G	A	4	103	c.3245G>A	c.(3244-3246)GGG>GAG	p.G1082E
Pat_44	Post-Resistance	GPR65	8477	37	14	88477274	88477274	Missense_Mutation	SNP	G	A	4	144	c.83G>A	c.(82-84)AGC>AAC	p.S28N
Pat_44	Post-Resistance	BCL11B	64919	37	14	99641023	99641023	Missense_Mutation	SNP	G	A	3	16	c.2150C>T	c.(2149-2151)GCG>GTG	p.A717V
Pat_44	Post-Resistance	BCL11B	64919	37	14	99723849	99723849	Missense_Mutation	SNP	G	A	4	171	c.386C>T	c.(385-387)TCA>TTA	p.S129L
Pat_44	Post-Resistance	RAGE	5891	37	14	102695832	102695832	Missense_Mutation	SNP	C	T	4	130	c.1144G>A	c.(1144-1146)GTG>ATG	p.V382M
Pat_44	Post-Resistance	RYR3	6263	37	15	34018665	34018665	Missense_Mutation	SNP	G	A	3	17	c.6991G>A	c.(6991-6993)GGG>AGG	p.G2331R
Pat_44	Post-Resistance	RASGRP1	10125	37	15	38791042	38791042	Missense_Mutation	SNP	C	T	4	198	c.1826G>A	c.(1825-1827)GGG>GAG	p.G609E
Pat_44	Post-Resistance	THBS1	7057	37	15	39882090	39882090	Missense_Mutation	SNP	G	A	4	92	c.2011G>A	c.(2011-2013)GAC>AAC	p.D671N
Pat_44	Post-Resistance	MGA	23269	37	15	41961330	41961330	Missense_Mutation	SNP	G	A	4	189	c.238G>A	c.(238-240)GAT>AAT	p.D80N
Pat_44	Post-Resistance	EHD4	30844	37	15	42192955	42192955	Missense_Mutation	SNP	G	A	4	65	c.1514C>T	c.(1513-1515)GCG>GTG	p.A505V
Pat_44	Post-Resistance	VPS39	23339	37	15	42461978	42461978	Missense_Mutation	SNP	G	A	4	127	c.1210C>T	c.(1210-1212)CTC>TTC	p.L404F
Pat_44	Post-Resistance	MYO1E	4643	37	15	59487726	59487726	Missense_Mutation	SNP	G	A	4	210	c.1739C>T	c.(1738-1740)ACG>ATG	p.T580M
Pat_44	Post-Resistance	TLN2	83660	37	15	62942372	62942372	Missense_Mutation	SNP	C	T	4	162	c.226C>T	c.(226-228)CGG>TGG	p.R76W
Pat_44	Post-Resistance	TLN2	83660	37	15	62991013	62991013	Missense_Mutation	SNP	G	A	4	137	c.1534G>A	c.(1534-1536)GCC>ACC	p.A512T
Pat_44	Post-Resistance	USP3	9960	37	15	63848880	63848880	Missense_Mutation	SNP	C	T	3	26	c.383C>T	c.(382-384)GCT>GTT	p.A128V
Pat_44	Post-Resistance	C15orf59	388135	37	15	74032707	74032707	Missense_Mutation	SNP	C	T	4	74	c.433G>A	c.(433-435)GGC>AGC	p.G145S
Pat_44	Post-Resistance	CLK3	1198	37	15	74912408	74912408	Missense_Mutation	SNP	C	T	4	194	c.655C>T	c.(655-657)CGG>TGG	p.R219W
Pat_44	Post-Resistance	CYP1A1	1543	37	15	75014747	75014747	Missense_Mutation	SNP	C	T	4	102	c.692G>A	c.(691-693)GGA>GAA	p.G231E
Pat_44	Post-Resistance	DET1	55070	37	15	89070848	89070848	Missense_Mutation	SNP	G	C	4	115	c.1253C>G	c.(1252-1254)GCA>GGA	p.A418G
Pat_44	Post-Resistance	AP3S2	10239	37	15	90451601	90451601	Missense_Mutation	SNP	C	T	4	88	c.212G>A	c.(211-213)CGC>CAC	p.R71H
Pat_44	Post-Resistance	C16orf59	80178	37	16	2512205	2512205	Missense_Mutation	SNP	G	A	4	149	c.715G>A	c.(715-717)GCC>ACC	p.A239T
Pat_44	Post-Resistance	THOC6	79228	37	16	3075788	3075788	Missense_Mutation	SNP	C	T	4	78	c.119C>T	c.(118-120)GCG>GTG	p.A40V

Pat_44	Post-Resistance	ZSCAN10	84891	37	16	3140123	3140123	Missense_Mutation	SNP	C	T	4	48	c.1147G>A	c.(1147-1149)GGC>AGC	p.G383S
Pat_44	Post-Resistance	DNAJA3	9093	37	16	4496917	4496917	Missense_Mutation	SNP	G	A	4	84	c.1027G>A	c.(1027-1029)GGC>AGC	p.G343S
Pat_44	Post-Resistance	ABCC6P1	653190	37	16	18597216	18597216	Missense_Mutation	SNP	C	T	5	130	c.580C>T	c.(580-582)CGG>TGG	p.R194W
Pat_44	Post-Resistance	COQ7	10229	37	16	19083411	19083411	Missense_Mutation	SNP	G	A	4	171	c.235G>A	c.(235-237)GTC>ATC	p.V79I
Pat_44	Post-Resistance	UMOD	7369	37	16	20355365	20355365	Missense_Mutation	SNP	C	T	4	61	c.1312G>A	c.(1312-1314)GCC>ACC	p.A438T
Pat_44	Post-Resistance	ACSM1	116285	37	16	20682922	20682922	Missense_Mutation	SNP	C	T	4	91	c.683G>A	c.(682-684)GGG>GAG	p.G228E
Pat_44	Post-Resistance	SULT1A1	6817	37	16	28618125	28618125	Missense_Mutation	SNP	C	T	4	230	c.551G>A	c.(550-552)CGC>CAC	p.R184H
Pat_44	Post-Resistance	ZNF629	23361	37	16	30794877	30794877	Missense_Mutation	SNP	C	T	4	110	c.772G>A	c.(772-774)GGC>AGC	p.G258S
Pat_44	Post-Resistance	TRIM72	493829	37	16	31230631	31230631	Missense_Mutation	SNP	G	A	4	200	c.508G>A	c.(508-510)GGG>AGG	p.G170R
Pat_44	Post-Resistance	ORC6L	23594	37	16	46729982	46729982	Missense_Mutation	SNP	G	A	4	111	c.616G>A	c.(616-618)GAA>AAA	p.E206K
Pat_44	Post-Resistance	ABCC12	94160	37	16	48145704	48145704	Nonsense_Mutation	SNP	G	A	4	214	c.2107C>T	c.(2107-2109)CGA>TGA	p.R703*
Pat_44	Post-Resistance	CNOT1	23019	37	16	58554896	58554896	Missense_Mutation	SNP	G	A	5	214	c.7097C>T	c.(7096-7098)GCC>GTC	p.A2366V
Pat_44	Post-Resistance	CDH8	1006	37	16	61687612	61687612	Missense_Mutation	SNP	G	A	5	87	c.2300C>T	c.(2299-2301)TCA>TTA	p.S767L
Pat_44	Post-Resistance	CDH11	1009	37	16	64981667	64981667	Missense_Mutation	SNP	C	T	4	112	c.2230G>A	c.(2230-2232)GGT>AGT	p.G744S
Pat_44	Post-Resistance	RLTPR	146206	37	16	67690199	67690199	Missense_Mutation	SNP	G	A	4	212	c.3811G>A	c.(3811-3813)GCT>ACT	p.A1271T
Pat_44	Post-Resistance	TAT	6898	37	16	71602163	71602163	Nonsense_Mutation	SNP	G	A	4	63	c.1249C>T	c.(1249-1251)CGA>TGA	p.R417*
Pat_44	Post-Resistance	PMFBP1	83449	37	16	72173243	72173243	Missense_Mutation	SNP	G	A	5	112	c.863C>T	c.(862-864)ACA>ATA	p.T288I
Pat_44	Post-Resistance	PSMD7	5713	37	16	74336162	74336162	Missense_Mutation	SNP	C	T	4	200	c.410C>T	c.(409-411)GCG>GTG	p.A137V
Pat_44	Post-Resistance	HSD17B2	3294	37	16	82131796	82131796	Missense_Mutation	SNP	C	T	4	185	c.919C>T	c.(919-921)CTC>TTC	p.L307F
Pat_44	Post-Resistance	PRDM7	11105	37	16	90126823	90126823	Missense_Mutation	SNP	T	G	7	135	c.1159A>C	c.(1159-1161)ATG>CTG	p.M387L
Pat_44	Post-Resistance	FAM101B	359845	37	17	293163	293163	Missense_Mutation	SNP	C	T	4	96	c.227G>A	c.(226-228)CGC>CAC	p.R76H
Pat_44	Post-Resistance	SERPINF2	5345	37	17	1657484	1657484	Missense_Mutation	SNP	G	A	6	228	c.1132G>A	c.(1132-1134)GTG>ATG	p.V378M
Pat_44	Post-Resistance	OR3A4	390756	37	17	3214529	3214529	Missense_Mutation	SNP	G	A	4	203	c.925G>A	c.(925-927)GAT>AAT	p.D309N
Pat_44	Post-Resistance	ATP2A3	489	37	17	3850810	3850810	Missense_Mutation	SNP	G	A	4	123	c.970C>T	c.(970-972)CGG>TGG	p.R324W
Pat_44	Post-Resistance	ATP2A3	489	37	17	3854563	3854563	Missense_Mutation	SNP	C	T	5	59	c.445G>A	c.(445-447)GAC>AAC	p.D149N
Pat_44	Post-Resistance	DHX33	56919	37	17	5358585	5358585	Missense_Mutation	SNP	G	A	4	178	c.1042C>T	c.(1042-1044)CGC>TGC	p.R348C
Pat_44	Post-Resistance	C17orf81	23587	37	17	7156274	7156274	Missense_Mutation	SNP	G	A	4	167	c.193G>A	c.(193-195)GAG>AAG	p.E65K
Pat_44	Post-Resistance	SAT2	112483	37	17	7530306	7530306	Missense_Mutation	SNP	G	A	4	135	c.259C>T	c.(259-261)CGC>TGC	p.R87C
Pat_44	Post-Resistance	MYH4	4622	37	17	10363399	10363399	Missense_Mutation	SNP	G	A	6	433	c.1286C>T	c.(1285-1287)GCT>GTT	p.A429V
Pat_44	Post-Resistance	TEKT3	64518	37	17	15234435	15234435	Nonsense_Mutation	SNP	C	T	4	93	c.468G>A	c.(466-468)TGG>TGA	p.W156*
Pat_44	Post-Resistance	KCNJ12	3768	37	17	21318691	21318691	Missense_Mutation	SNP	G	A	4	109	c.37G>A	c.(37-39)GTG>ATG	p.V13M
Pat_44	Post-Resistance	TAOK1	57551	37	17	27869789	27869789	Missense_Mutation	SNP	G	A	4	120	c.2755G>A	c.(2755-2757)GGA>AGA	p.G919R
Pat_44	Post-Resistance	ACCN1	40	37	17	31439018	31439018	Missense_Mutation	SNP	G	A	4	171	c.623C>T	c.(622-624)ACG>ATG	p.T208M
Pat_44	Post-Resistance	SLFN13	146857	37	17	33769098	33769098	Missense_Mutation	SNP	G	A	4	169	c.1406C>T	c.(1405-1407)ACC>ATC	p.T469I
Pat_44	Post-Resistance	MYO19	80179	37	17	34854231	34854231	Missense_Mutation	SNP	C	T	4	170	c.2636G>A	c.(2635-2637)AGC>AAC	p.S879N
Pat_44	Post-Resistance	ACACA	31	37	17	35508300	35508300	Missense_Mutation	SNP	C	T	4	62	c.5383G>A	c.(5383-5385)GAG>AAG	p.E1795K
Pat_44	Post-Resistance	KRT40	125115	37	17	39140251	39140251	Missense_Mutation	SNP	G	A	7	371	c.275C>T	c.(274-276)ACG>ATG	p.T92M
Pat_44	Post-Resistance	STAT3	6774	37	17	40485716	40485716	Missense_Mutation	SNP	C	T	4	131	c.1024G>A	c.(1024-1026)GGC>AGC	p.G342S
Pat_44	Post-Resistance	AOC2	314	37	17	40997683	40997683	Missense_Mutation	SNP	G	A	5	210	c.1040G>A	c.(1039-1041)CGG>CAG	p.R347Q
Pat_44	Post-Resistance	AOC3	8639	37	17	41003382	41003382	Missense_Mutation	SNP	G	A	5	328	c.22G>A	c.(22-24)GTG>ATG	p.V8M
Pat_44	Post-Resistance	BRCA1	672	37	17	41201142	41201142	Missense_Mutation	SNP	C	T	4	65	c.5402G>A	c.(5401-5403)GGC>GAC	p.G1801D
Pat_44	Post-Resistance	BRCA1	672	37	17	41209094	41209094	Missense_Mutation	SNP	C	T	4	240	c.5252G>A	c.(5251-5253)CGA>CAA	p.R1751Q
Pat_44	Post-Resistance	SLC4A1	6521	37	17	42336626	42336626	Missense_Mutation	SNP	G	A	4	46	c.781C>T	c.(781-783)CCT>TCT	p.P261S
Pat_44	Post-Resistance	DBF4B	80174	37	17	42807343	42807343	Missense_Mutation	SNP	G	A	4	134	c.296G>A	c.(295-297)AGC>AAC	p.S99N
Pat_44	Post-Resistance	OSBPL7	114881	37	17	45885746	45885746	Missense_Mutation	SNP	C	T	4	135	c.2440G>A	c.(2440-2442)GGG>AGG	p.G814R
Pat_44	Post-Resistance	ACSF2	80221	37	17	48551148	48551148	Missense_Mutation	SNP	C	T	5	250	c.1598C>T	c.(1597-1599)CCG>CTG	p.P533L
Pat_44	Post-Resistance	RGS9	8787	37	17	63221522	63221522	Missense_Mutation	SNP	C	T	4	135	c.1810C>T	c.(1810-1812)CCT>TCT	p.P604S

Pat_44	Post-Resistance	USH1G	124590	37	17	72916242	72916242	Missense_Mutation	SNP	G	A	4	49	c.689C>T	c.(688-690)ACC>ATC	p.T230I
Pat_44	Post-Resistance	CASKIN2	57513	37	17	73498246	73498246	Missense_Mutation	SNP	G	A	4	157	c.2909C>T	c.(2908-2910)CCG>CTG	p.P970L
Pat_44	Post-Resistance	PRPSAP1	5635	37	17	74307751	74307751	Missense_Mutation	SNP	C	T	4	165	c.1030G>A	c.(1030-1032)GTT>ATT	p.V344I
Pat_44	Post-Resistance	SPHK1	8877	37	17	74383333	74383333	Missense_Mutation	SNP	C	T	4	25	c.821C>T	c.(820-822)GCT>GTT	p.A274V
Pat_44	Post-Resistance	RHBDF2	79651	37	17	74472931	74472931	Missense_Mutation	SNP	C	T	2	2	c.1183G>A	c.(1183-1185)GAG>AAG	p.E395K
Pat_44	Post-Resistance	MGAT5B	146664	37	17	74922744	74922744	Missense_Mutation	SNP	C	T	4	139	c.1256C>T	c.(1255-1257)ACG>ATG	p.T419M
Pat_44	Post-Resistance	RNF213	57674	37	17	78353466	78353466	Missense_Mutation	SNP	C	T	4	237	c.7811C>T	c.(7810-7812)CCG>CTG	p.P2604L
Pat_44	Post-Resistance	RPTOR	57521	37	17	78867626	78867626	Missense_Mutation	SNP	C	T	4	164	c.2362C>T	c.(2362-2364)CGC>TGC	p.R788C
Pat_44	Post-Resistance	AZI1	22994	37	17	79163585	79163585	Missense_Mutation	SNP	G	A	5	232	c.3236C>T	c.(3235-3237)ACG>ATG	p.T1079M
Pat_44	Post-Resistance	SIRT7	51547	37	17	79872523	79872523	Missense_Mutation	SNP	G	A	4	141	c.536C>T	c.(535-537)CCG>CTG	p.P179L
Pat_44	Post-Resistance	UTS2R	2837	37	17	80332865	80332865	Missense_Mutation	SNP	G	A	4	13	c.665G>A	c.(664-666)GGG>GAG	p.G222E
Pat_44	Post-Resistance	L3MBTL4	91133	37	18	6093472	6093472	Missense_Mutation	SNP	C	T	4	191	c.1255G>A	c.(1255-1257)GAT>AAT	p.D419N
Pat_44	Post-Resistance	LAMA1	284217	37	18	7023295	7023295	Missense_Mutation	SNP	G	A	5	130	c.2569C>T	c.(2569-2571)CCC>TCC	p.P857S
Pat_44	Post-Resistance	RAB12	201475	37	18	8633230	8633230	Missense_Mutation	SNP	T	A	5	162	c.331T>A	c.(331-333)TAT>AAT	p.Y111N
Pat_44	Post-Resistance	ANKRD12	23253	37	18	9258637	9258637	Missense_Mutation	SNP	G	A	5	117	c.5372G>A	c.(5371-5373)CGT>CAT	p.R1791H
Pat_44	Post-Resistance	FAM38B	63895	37	18	10675247	10675247	Missense_Mutation	SNP	G	A	4	87	c.1652C>T	c.(1651-1653)CCT>CTT	p.P551L
Pat_44	Post-Resistance	MPPE1	65258	37	18	11886734	11886734	Missense_Mutation	SNP	G	A	3	65	c.722C>T	c.(721-723)ACG>ATG	p.T241M
Pat_44	Post-Resistance	C18orf1	753	37	18	13621212	13621212	Missense_Mutation	SNP	C	T	4	118	c.278C>T	c.(277-279)ACG>ATG	p.T93M
Pat_44	Post-Resistance	DTNA	1837	37	18	32345949	32345949	Missense_Mutation	SNP	G	A	4	174	c.92G>A	c.(91-93)CGA>CAA	p.R31Q
Pat_44	Post-Resistance	DTNA	1837	37	18	32374168	32374168	Nonsense_Mutation	SNP	C	T	5	273	c.316C>T	c.(316-318)CAG>TAG	p.Q106*
Pat_44	Post-Resistance	MYO5B	4645	37	18	47462691	47462691	Missense_Mutation	SNP	T	C	2	10	c.1934A>G	c.(1933-1935)GAG>GGG	p.E645G
Pat_44	Post-Resistance	MBD2	8932	37	18	51731393	51731393	Missense_Mutation	SNP	C	T	5	284	c.677G>A	c.(676-678)CGA>CAA	p.R226Q
Pat_44	Post-Resistance	FECH	2235	37	18	55238716	55238716	Missense_Mutation	SNP	C	T	4	228	c.371G>A	c.(370-372)CGC>CAC	p.R124H
Pat_44	Post-Resistance	KIAA1468	57614	37	18	59854865	59854865	Missense_Mutation	SNP	G	A	4	164	c.127G>A	c.(127-129)GCC>ACC	p.A43T
Pat_44	Post-Resistance	RTTN	25914	37	18	67755290	67755290	Missense_Mutation	SNP	C	T	5	180	c.4237G>A	c.(4237-4239)GGG>AGG	p.G1413R
Pat_44	Post-Resistance	ZNF407	55628	37	18	72347621	72347621	Missense_Mutation	SNP	G	A	6	257	c.4646G>A	c.(4645-4647)AGC>AAC	p.S1549N
Pat_44	Post-Resistance	NFATC1	4772	37	18	77211046	77211046	Missense_Mutation	SNP	G	A	7	322	c.1682G>A	c.(1681-1683)CGG>CAG	p.R561Q
Pat_44	Post-Resistance	SHC2	25759	37	19	440898	440898	Missense_Mutation	SNP	C	T	4	196	c.503G>A	c.(502-504)CGC>CAC	p.R168H
Pat_44	Post-Resistance	HCN2	610	37	19	613374	613374	Missense_Mutation	SNP	A	C	3	83	c.1711A>C	c.(1711-1713)ATC>CTC	p.I571L
Pat_44	Post-Resistance	C19orf22	91300	37	19	900092	900092	Missense_Mutation	SNP	C	T	4	90	c.530G>A	c.(529-531)CGA>CAA	p.R177Q
Pat_44	Post-Resistance	MUM1	84939	37	19	1360146	1360146	Missense_Mutation	SNP	G	A	4	70	c.226G>A	c.(226-228)GAG>AAG	p.E76K
Pat_44	Post-Resistance	TCF3	6929	37	19	1622133	1622133	Missense_Mutation	SNP	G	A	4	17	c.742C>T	c.(742-744)CCC>TCC	p.P248S
Pat_44	Post-Resistance	S1PR4	8698	37	19	3179824	3179824	Missense_Mutation	SNP	A	T	4	69	c.1034A>T	c.(1033-1035)CAC>CTC	p.H345L
Pat_44	Post-Resistance	ATCAY	85300	37	19	3907767	3907767	Missense_Mutation	SNP	G	A	4	130	c.394G>A	c.(394-396)GGG>AGG	p.G132R
Pat_44	Post-Resistance	ZNF557	79230	37	19	7083178	7083178	Missense_Mutation	SNP	G	A	5	141	c.695G>A	c.(694-696)AGT>AAT	p.S232N
Pat_44	Post-Resistance	MUC16	94025	37	19	9060720	9060720	Missense_Mutation	SNP	G	A	4	191	c.26726C>T	c.(26725-26727)CCT>CTT	p.P8909L
Pat_44	Post-Resistance	ZNF177	7730	37	19	9492142	9492142	Missense_Mutation	SNP	G	A	5	296	c.655G>A	c.(655-657)GAT>AAT	p.D219N
Pat_44	Post-Resistance	ZNF878	729747	37	19	12155693	12155693	Missense_Mutation	SNP	G	C	6	446	c.664C>G	c.(664-666)CAG>GAG	p.Q222E
Pat_44	Post-Resistance	BEST2	54831	37	19	12866976	12866976	Missense_Mutation	SNP	G	A	5	285	c.970G>A	c.(970-972)GAG>AAG	p.E324K
Pat_44	Post-Resistance	NFIX	4784	37	19	13136063	13136063	Missense_Mutation	SNP	G	A	5	131	c.280G>A	c.(280-282)GAG>AAG	p.E94K
Pat_44	Post-Resistance	CASP14	23581	37	19	15164697	15164697	Missense_Mutation	SNP	G	A	4	131	c.331G>A	c.(331-333)GCC>ACC	p.A111T
Pat_44	Post-Resistance	WIZ	58525	37	19	15535181	15535181	Missense_Mutation	SNP	G	A	4	119	c.2560C>T	c.(2560-2562)CGC>TGC	p.R854C
Pat_44	Post-Resistance	IL12RB1	3594	37	19	18197581	18197581	Missense_Mutation	SNP	G	A	3	29	c.53C>T	c.(52-54)TCC>TTC	p.S18F
Pat_44	Post-Resistance	ZNF626	199777	37	19	20808006	20808006	Missense_Mutation	SNP	T	C	10	200	c.677A>G	c.(676-678)GAG>GGG	p.E226G
Pat_44	Post-Resistance	ZNF99	7652	37	19	22939400	22939400	Missense_Mutation	SNP	G	C	7	160	c.2771C>G	c.(2770-2772)GCT>GGT	p.A924G
Pat_44	Post-Resistance	MLL4	9757	37	19	36212330	36212330	Missense_Mutation	SNP	G	A	3	40	c.2081G>A	c.(2080-2082)CGG>CAG	p.R694Q
Pat_44	Post-Resistance	COX7A1	1346	37	19	36642623	36642623	Missense_Mutation	SNP	G	A	3	26	c.50C>T	c.(49-51)ACC>ATC	p.T17I

Pat_44	Post-Resistance	RYR1	6261	37	19	39019018	39019018	Missense_Mutation	SNP	G	A	4	216	c.10897G>A	c.(10897-10899)GTG>ATG	p.V3633M
Pat_44	Post-Resistance	AKT2	208	37	19	40741933	40741933	Missense_Mutation	SNP	G	A	4	122	c.1039C>T	c.(1039-1041)CGC>TGC	p.R347C
Pat_44	Post-Resistance	SPTBN4	57731	37	19	41007935	41007935	Missense_Mutation	SNP	G	A	4	114	c.892G>A	c.(892-894)GGG>AGG	p.G298R
Pat_44	Post-Resistance	ERF	2077	37	19	42753743	42753743	Missense_Mutation	SNP	G	A	4	144	c.521C>T	c.(520-522)TCG>TTG	p.S174L
Pat_44	Post-Resistance	TEX101	83639	37	19	43922496	43922496	Missense_Mutation	SNP	G	A	4	194	c.697G>A	c.(697-699)GGG>AGG	p.G233R
Pat_44	Post-Resistance	CD3EAP	10849	37	19	45912475	45912475	Missense_Mutation	SNP	G	A	4	40	c.1249G>A	c.(1249-1251)GCT>ACT	p.A417T
Pat_44	Post-Resistance	ERCC1	2067	37	19	45917271	45917271	Missense_Mutation	SNP	C	T	5	100	c.724G>A	c.(724-726)GTG>ATG	p.V242M
Pat_44	Post-Resistance	SYMPK	8189	37	19	46345703	46345703	Missense_Mutation	SNP	G	A	4	202	c.892C>T	c.(892-894)CGT>TGT	p.R298C
Pat_44	Post-Resistance	GYS1	2997	37	19	49484803	49484803	Missense_Mutation	SNP	C	T	4	64	c.1153G>A	c.(1153-1155)GTG>ATG	p.V385M
Pat_44	Post-Resistance	HRC	3270	37	19	49656843	49656843	Missense_Mutation	SNP	C	T	3	21	c.1652G>A	c.(1651-1653)AGG>AAG	p.R551K
Pat_44	Post-Resistance	KLK3	354	37	19	51359603	51359603	Missense_Mutation	SNP	G	A	7	236	c.154G>A	c.(154-156)GGT>AGT	p.G52S
Pat_44	Post-Resistance	FPR2	2358	37	19	52272221	52272221	Missense_Mutation	SNP	G	A	5	272	c.310G>A	c.(310-312)GTG>ATG	p.V104M
Pat_44	Post-Resistance	ZNF649	65251	37	19	52394769	52394769	Missense_Mutation	SNP	A	C	4	80	c.620T>G	c.(619-621)GTG>GGG	p.V207G
Pat_44	Post-Resistance	ZNF534	147658	37	19	52942191	52942191	Missense_Mutation	SNP	T	C	3	66	c.1517T>C	c.(1516-1518)CTT>CCT	p.L506P
Pat_44	Post-Resistance	ZNF534	147658	37	19	52942308	52942308	Missense_Mutation	SNP	G	A	4	76	c.1634G>A	c.(1633-1635)CGT>CAT	p.R545H
Pat_44	Post-Resistance	LILRA3	11026	37	19	54802530	54802530	Missense_Mutation	SNP	G	A	5	126	c.911C>T	c.(910-912)TCC>TTC	p.S304F
Pat_44	Post-Resistance	LILRA2	11027	37	19	55085974	55085974	Missense_Mutation	SNP	G	A	4	132	c.277G>A	c.(277-279)GGG>AGG	p.G93R
Pat_44	Post-Resistance	ZNF776	284309	37	19	58265928	58265928	Missense_Mutation	SNP	G	A	7	153	c.1430G>A	c.(1429-1431)CGA>CAA	p.R477Q
Pat_44	Post-Resistance	CHMP2A	27243	37	19	59063796	59063796	Missense_Mutation	SNP	G	A	4	95	c.178C>T	c.(178-180)CGC>TGC	p.R60C
Pat_44	Post-Resistance	RNF144A	9781	37	2	7164576	7164576	Missense_Mutation	SNP	G	A	4	113	c.586G>A	c.(586-588)GAA>AAA	p.E196K
Pat_44	Post-Resistance	LAPTM4A	9741	37	2	20240746	20240746	Missense_Mutation	SNP	C	A	6	222	c.138G>T	c.(136-138)TTG>TTT	p.L46F
Pat_44	Post-Resistance	ITSN2	50618	37	2	24480820	24480820	Missense_Mutation	SNP	C	T	5	213	c.2825G>A	c.(2824-2826)GGA>GAA	p.G942E
Pat_44	Post-Resistance	CENPA	1058	37	2	27015046	27015046	Missense_Mutation	SNP	G	A	4	51	c.148G>A	c.(148-150)GAG>AAG	p.E50K
Pat_44	Post-Resistance	LCLAT1	253558	37	2	30682522	30682522	Nonsense_Mutation	SNP	G	A	5	389	c.44G>A	c.(43-45)TGG>TAG	p.W15*
Pat_44	Post-Resistance	BIRC6	57448	37	2	32756472	32756472	Missense_Mutation	SNP	G	A	4	144	c.12145G>A	c.(12145-12147)GGT>AGT	p.G4049S
Pat_44	Post-Resistance	ABCG8	64241	37	2	44079980	44079980	Missense_Mutation	SNP	C	T	4	181	c.937C>T	c.(937-939)CGC>TGC	p.R313C
Pat_44	Post-Resistance	USP34	9736	37	2	61441818	61441818	Missense_Mutation	SNP	G	A	4	120	c.8059C>T	c.(8059-8061)CTT>TTT	p.L2687F
Pat_44	Post-Resistance	USP34	9736	37	2	61493200	61493200	Missense_Mutation	SNP	C	T	4	180	c.5536G>A	c.(5536-5538)GAT>AAT	p.D1846N
Pat_44	Post-Resistance	GFPT1	2673	37	2	69565679	69565679	Missense_Mutation	SNP	C	T	4	188	c.1168G>A	c.(1168-1170)GAG>AAG	p.E390K
Pat_44	Post-Resistance	DYSF	8291	37	2	71795377	71795377	Missense_Mutation	SNP	G	A	8	636	c.2719G>A	c.(2719-2721)GTC>ATC	p.V907I
Pat_44	Post-Resistance	SFXN5	94097	37	2	73228695	73228695	Missense_Mutation	SNP	G	A	4	78	c.370C>T	c.(370-372)CTC>TTC	p.L124F
Pat_44	Post-Resistance	IMMT	10989	37	2	86393643	86393643	Missense_Mutation	SNP	C	T	5	142	c.780G>A	c.(778-780)ATG>ATA	p.M260I
Pat_44	Post-Resistance	KIAA1310	55683	37	2	97267994	97267994	Missense_Mutation	SNP	G	A	5	34	c.2341C>T	c.(2341-2343)CCT>TCT	p.P781S
Pat_44	Post-Resistance	ZC3H6	376940	37	2	113082075	113082075	Missense_Mutation	SNP	G	A	4	45	c.1687G>A	c.(1687-1689)GTA>ATA	p.V563I
Pat_44	Post-Resistance	POTEF	728378	37	2	130877782	130877782	Missense_Mutation	SNP	A	G	14	269	c.307T>C	c.(307-309)TGC>CGC	p.C103R
Pat_44	Post-Resistance	PTPN18	26469	37	2	131128815	131128815	Missense_Mutation	SNP	C	T	4	116	c.968C>T	c.(967-969)CCC>CTC	p.P323L
Pat_44	Post-Resistance	GPR39	2863	37	2	133175270	133175270	Missense_Mutation	SNP	G	A	5	121	c.655G>A	c.(655-657)GTG>ATG	p.V219M
Pat_44	Post-Resistance	NCKAP5	344148	37	2	133486432	133486432	Missense_Mutation	SNP	G	A	6	293	c.5537C>T	c.(5536-5538)CCG>CTG	p.P1846L
Pat_44	Post-Resistance	MCM6	4175	37	2	136615478	136615478	Missense_Mutation	SNP	C	T	4	142	c.1459G>A	c.(1459-1461)GCA>ACA	p.A487T
Pat_44	Post-Resistance	EPC2	26122	37	2	149528439	149528439	Missense_Mutation	SNP	C	T	5	224	c.1309C>T	c.(1309-1311)CTT>TTT	p.L437F
Pat_44	Post-Resistance	NEB	4703	37	2	152581387	152581387	Missense_Mutation	SNP	G	A	4	107	c.491C>T	c.(490-492)TCG>TTG	p.S164L
Pat_44	Post-Resistance	BAZ2B	29994	37	2	160269014	160269014	Missense_Mutation	SNP	G	A	4	100	c.2509C>T	c.(2509-2511)CGT>TGT	p.R837C
Pat_44	Post-Resistance	RBMS1	5937	37	2	161135124	161135124	Missense_Mutation	SNP	G	A	4	77	c.997C>T	c.(997-999)CCC>TCC	p.P333S
Pat_44	Post-Resistance	GCA	25801	37	2	163215596	163215596	Missense_Mutation	SNP	G	A	5	274	c.497G>A	c.(496-498)CGT>CAT	p.R166H
Pat_44	Post-Resistance	ABCB11	8647	37	2	169780296	169780296	Missense_Mutation	SNP	G	A	4	160	c.3802C>T	c.(3802-3804)CGG>TGG	p.R1268W
Pat_44	Post-Resistance	TTN	7273	37	2	179481213	179481213	Nonsense_Mutation	SNP	C	T	6	456	c.40601G>A	c.(40600-40602)TGG>TAG	p.W13534*
Pat_44	Post-Resistance	TTN	7273	37	2	179599451	179599451	Missense_Mutation	SNP	G	A	5	348	c.11468C>T	c.(11467-11469)ACT>ATT	p.T3823I

Pat_44	Post-Resistance	SESTD1	91404	37	2	180011158	180011158	Missense_Mutation	SNP	G	A	4	159	c.608C>T	c.(607-609)TCG>TTG	p.S203L
Pat_44	Post-Resistance	COL3A1	1281	37	2	189876393	189876393	Nonsense_Mutation	SNP	C	T	4	210	c.4294C>T	c.(4294-4296)CGA>TGA	p.R1432*
Pat_44	Post-Resistance	COL5A2	1290	37	2	189921752	189921752	Missense_Mutation	SNP	C	T	4	156	c.2338G>A	c.(2338-2340)GGT>AGT	p.G780S
Pat_44	Post-Resistance	STAT4	6775	37	2	191940952	191940952	Splice_Site	SNP	C	T	4	167	c.372_splice	c.e4+1	p.Q124_splice
Pat_44	Post-Resistance	SATB2	23314	37	2	200213711	200213711	Missense_Mutation	SNP	C	T	4	158	c.886G>A	c.(886-888)GGT>AGT	p.G296S
Pat_44	Post-Resistance	ZDBF2	57683	37	2	207171443	207171443	Missense_Mutation	SNP	C	T	4	109	c.2191C>T	c.(2191-2193)CTT>TTT	p.L731F
Pat_44	Post-Resistance	ADAM23	8745	37	2	207431970	207431970	Missense_Mutation	SNP	C	T	5	178	c.1418C>T	c.(1417-1419)TCA>TTA	p.S473L
Pat_44	Post-Resistance	PLCD4	84812	37	2	219499249	219499249	Missense_Mutation	SNP	G	A	4	153	c.1792G>A	c.(1792-1794)GGC>AGC	p.G598S
Pat_44	Post-Resistance	ZNF142	7701	37	2	219508114	219508114	Missense_Mutation	SNP	G	A	4	121	c.3125C>T	c.(3124-3126)ACC>ATC	p.T1042I
Pat_44	Post-Resistance	STK36	27148	37	2	219559039	219559039	Missense_Mutation	SNP	G	A	4	242	c.2389G>A	c.(2389-2391)GTC>ATC	p.V797I
Pat_44	Post-Resistance	ABCB6	10058	37	2	220075504	220075504	Missense_Mutation	SNP	C	T	4	82	c.2185G>A	c.(2185-2187)GGC>AGC	p.G729S
Pat_44	Post-Resistance	SP100	6672	37	2	231405602	231405602	Missense_Mutation	SNP	G	A	6	296	c.2222G>A	c.(2221-2223)AGT>AAT	p.S741N
Pat_44	Post-Resistance	NGEF	25791	37	2	233757690	233757690	Missense_Mutation	SNP	G	A	4	164	c.1060C>T	c.(1060-1062)CGT>TGT	p.R354C
Pat_44	Post-Resistance	PPP1R7	5510	37	2	242122110	242122110	Missense_Mutation	SNP	G	A	4	76	c.955G>A	c.(955-957)GGA>AGA	p.G319R
Pat_44	Post-Resistance	SIRPG	55423	37	20	1616242	1616242	Missense_Mutation	SNP	G	A	3	61	c.752C>T	c.(751-753)CCA>CTA	p.P251L
Pat_44	Post-Resistance	ATRN	8455	37	20	3571942	3571942	Missense_Mutation	SNP	G	A	5	257	c.3311G>A	c.(3310-3312)GGG>GAG	p.G1104E
Pat_44	Post-Resistance	ATRN	8455	37	20	3575197	3575197	Missense_Mutation	SNP	G	A	4	182	c.3394G>A	c.(3394-3396)GTC>ATC	p.V1132I
Pat_44	Post-Resistance	PCSK2	5126	37	20	17339005	17339005	Nonsense_Mutation	SNP	C	T	4	158	c.316C>T	c.(316-318)CGA>TGA	p.R106*
Pat_44	Post-Resistance	CBFA2T2	9139	37	20	32217661	32217661	Missense_Mutation	SNP	C	T	4	60	c.1196C>T	c.(1195-1197)ACG>ATG	p.T399M
Pat_44	Post-Resistance	GSS	2937	37	20	33530388	33530388	Missense_Mutation	SNP	G	A	4	101	c.394C>T	c.(394-396)CGC>TGC	p.R132C
Pat_44	Post-Resistance	PROCR	10544	37	20	33764184	33764184	Missense_Mutation	SNP	G	A	4	238	c.536G>A	c.(535-537)CGG>CAG	p.R179Q
Pat_44	Post-Resistance	CHD6	84181	37	20	40143496	40143496	Missense_Mutation	SNP	G	A	4	100	c.650C>T	c.(649-651)ACG>ATG	p.T217M
Pat_44	Post-Resistance	DDX27	55661	37	20	47860213	47860213	Missense_Mutation	SNP	G	A	4	121	c.2345G>A	c.(2344-2346)CGA>CAA	p.R782Q
Pat_44	Post-Resistance	PTPN1	5770	37	20	49196301	49196301	Missense_Mutation	SNP	C	T	4	159	c.926C>T	c.(925-927)CCT>CTT	p.P309L
Pat_44	Post-Resistance	FAM65C	140876	37	20	49212784	49212784	Missense_Mutation	SNP	G	A	6	190	c.1795C>T	c.(1795-1797)CCC>TCC	p.P599S
Pat_44	Post-Resistance	CYP24A1	1591	37	20	52779318	52779318	Missense_Mutation	SNP	G	A	4	85	c.928C>T	c.(928-930)CGG>TGG	p.R310W
Pat_44	Post-Resistance	STX16	8675	37	20	57244455	57244455	Missense_Mutation	SNP	G	A	3	35	c.502G>A	c.(502-504)GCC>ACC	p.A168T
Pat_44	Post-Resistance	TCFL5	10732	37	20	61492676	61492676	Missense_Mutation	SNP	G	A	3	17	c.347C>T	c.(346-348)GCC>GTC	p.A116V
Pat_44	Post-Resistance	KCNQ2	3785	37	20	62046309	62046309	Missense_Mutation	SNP	C	T	5	136	c.1472G>A	c.(1471-1473)CGG>CAG	p.R491Q
Pat_44	Post-Resistance	RGS19	10287	37	20	62705333	62705333	Missense_Mutation	SNP	G	A	4	169	c.527C>T	c.(526-528)ACG>ATG	p.T176M
Pat_44	Post-Resistance	MRPL39	54148	37	21	26958036	26958036	Missense_Mutation	SNP	C	T	4	153	c.1000G>A	c.(1000-1002)GAA>AAA	p.E334K
Pat_44	Post-Resistance	BACH1	571	37	21	30714987	30714987	Missense_Mutation	SNP	C	T	4	145	c.2044C>T	c.(2044-2046)CCC>TCC	p.P682S
Pat_44	Post-Resistance	KCNJ6	3763	37	21	39087081	39087081	Missense_Mutation	SNP	G	A	4	129	c.379C>T	c.(379-381)CCC>TCC	p.P127S
Pat_44	Post-Resistance	TRAPPC10	7109	37	21	45523267	45523267	Missense_Mutation	SNP	C	T	3	33	c.3635C>T	c.(3634-3636)TCG>TTG	p.S1212L
Pat_44	Post-Resistance	KRTAP10-1	386677	37	21	45959208	45959208	Missense_Mutation	SNP	C	T	4	67	c.826G>A	c.(826-828)GCG>ACG	p.A276T
Pat_44	Post-Resistance	KRTAP10-3	386682	37	21	45978063	45978063	Missense_Mutation	SNP	G	A	4	149	c.536C>T	c.(535-537)GCC>GTC	p.A179V
Pat_44	Post-Resistance	KRTAP10-4	386672	37	21	45994249	45994249	Missense_Mutation	SNP	C	T	4	100	c.614C>T	c.(613-615)ACG>ATG	p.T205M
Pat_44	Post-Resistance	HIRA	7290	37	22	19385557	19385557	Missense_Mutation	SNP	C	T	4	76	c.451G>A	c.(451-453)GTG>ATG	p.V151M
Pat_44	Post-Resistance	PPIL2	23759	37	22	22029404	22029404	Missense_Mutation	SNP	G	A	4	134	c.295G>A	c.(295-297)GGG>AGG	p.G99R
Pat_44	Post-Resistance	DUSP18	150290	37	22	31059759	31059759	Missense_Mutation	SNP	G	A	4	106	c.232C>T	c.(232-234)CGT>TGT	p.R78C
Pat_44	Post-Resistance	LIMK2	3985	37	22	31663886	31663886	Missense_Mutation	SNP	G	A	4	116	c.1253G>A	c.(1252-1254)CGC>CAC	p.R418H
Pat_44	Post-Resistance	SFI1	9814	37	22	32009138	32009138	Missense_Mutation	SNP	G	A	5	32	c.2501G>A	c.(2500-2502)AGG>AAG	p.R834K
Pat_44	Post-Resistance	SSTR3	6753	37	22	37603625	37603625	Missense_Mutation	SNP	G	A	4	144	c.218C>T	c.(217-219)ACG>ATG	p.T73M
Pat_44	Post-Resistance	ELFN2	114794	37	22	37771192	37771192	Missense_Mutation	SNP	C	T	3	50	c.383G>A	c.(382-384)CGC>CAC	p.R128H
Pat_44	Post-Resistance	TRIOBP	11078	37	22	38120290	38120290	Missense_Mutation	SNP	G	C	10	445	c.1727G>C	c.(1726-1728)AGA>ACA	p.R576T
Pat_44	Post-Resistance	TRIOBP	11078	37	22	38120359	38120359	Missense_Mutation	SNP	C	G	9	474	c.1796C>G	c.(1795-1797)ACA>AGA	p.T599R
Pat_44	Post-Resistance	TRIOBP	11078	37	22	38120596	38120596	Missense_Mutation	SNP	T	A	4	99	c.2033T>A	c.(2032-2034)CTA>CAA	p.L678Q

Pat_44	Post-Resistance	ADSL	158	37	22	40760954	40760954	Missense_Mutation	SNP	A	G	5	243	c.1262A>G	c.(1261-1263)AAT>AGT	p.N421S
Pat_44	Post-Resistance	SCUBE1	80274	37	22	43625140	43625140	Missense_Mutation	SNP	G	A	4	85	c.1022C>T	c.(1021-1023)CCG>CTG	p.P341L
Pat_44	Post-Resistance	MPPED1	758	37	22	43898598	43898598	Missense_Mutation	SNP	G	A	6	200	c.823G>A	c.(823-825)GTC>ATC	p.V275I
Pat_44	Post-Resistance	RIBC2	26150	37	22	45813680	45813680	Missense_Mutation	SNP	G	A	4	109	c.395G>A	c.(394-396)CGG>CAG	p.R132Q
Pat_44	Post-Resistance	TRABD	80305	37	22	50636361	50636361	Missense_Mutation	SNP	G	A	4	135	c.781G>A	c.(781-783)GTC>ATC	p.V261I
Pat_44	Post-Resistance	TUBGCP6	85378	37	22	50659166	50659166	Missense_Mutation	SNP	T	C	5	104	c.3622A>G	c.(3622-3624)ACC>GCC	p.T1208A
Pat_44	Post-Resistance	MAPK12	6300	37	22	50694090	50694090	Missense_Mutation	SNP	G	A	5	185	c.725C>T	c.(724-726)ACG>ATG	p.T242M
Pat_44	Post-Resistance	LMF2	91289	37	22	50942257	50942257	Missense_Mutation	SNP	G	A	4	148	c.1795C>T	c.(1795-1797)CTC>TTC	p.L599F
Pat_44	Post-Resistance	CHL1	10752	37	3	391214	391214	Missense_Mutation	SNP	G	A	6	338	c.973G>A	c.(973-975)GTT>ATT	p.V325I
Pat_44	Post-Resistance	SRGAP3	9901	37	3	9036109	9036109	Missense_Mutation	SNP	G	A	4	203	c.2326C>T	c.(2326-2328)CGC>TGC	p.R776C
Pat_44	Post-Resistance	CPNE9	151835	37	3	9746653	9746653	Missense_Mutation	SNP	G	A	4	42	c.235G>A	c.(235-237)GAA>AAA	p.E79K
Pat_44	Post-Resistance	CRELD1	78987	37	3	9982711	9982711	Splice_Site	SNP	G	A	4	88	c.637_splice	c.e6+1	p.A213_splice
Pat_44	Post-Resistance	KCNH8	131096	37	3	19190216	19190216	Missense_Mutation	SNP	C	T	4	236	c.5C>T	c.(4-6)CCG>CTG	p.P2L
Pat_44	Post-Resistance	OXSM	54995	37	3	25832705	25832705	Missense_Mutation	SNP	G	A	4	216	c.194G>A	c.(193-195)CGT>CAT	p.R65H
Pat_44	Post-Resistance	DCLK3	85443	37	3	36779024	36779024	Missense_Mutation	SNP	C	T	4	158	c.1127G>A	c.(1126-1128)CGC>CAC	p.R376H
Pat_44	Post-Resistance	ITGA9	3680	37	3	37523026	37523026	Missense_Mutation	SNP	C	T	5	112	c.472C>T	c.(472-474)CCC>TCC	p.P158S
Pat_44	Post-Resistance	DLEC1	9940	37	3	38139274	38139274	Missense_Mutation	SNP	G	T	4	62	c.2605G>T	c.(2605-2607)GGT>TGT	p.G869C
Pat_44	Post-Resistance	LTF	4057	37	3	46480833	46480833	Missense_Mutation	SNP	C	T	4	194	c.1862G>A	c.(1861-1863)CGG>CAG	p.R621Q
Pat_44	Post-Resistance	PLXNB1	5364	37	3	48457802	48457802	Missense_Mutation	SNP	C	T	4	172	c.3433G>A	c.(3433-3435)GTG>ATG	p.V1145M
Pat_44	Post-Resistance	COL7A1	1294	37	3	48615945	48615945	Missense_Mutation	SNP	G	A	3	20	c.5428C>T	c.(5428-5430)CTT>TTT	p.L1810F
Pat_44	Post-Resistance	BSN	8927	37	3	49693768	49693768	Missense_Mutation	SNP	G	A	4	187	c.6779G>A	c.(6778-6780)CGC>CAC	p.R2260H
Pat_44	Post-Resistance	GMPPB	29925	37	3	49760087	49760087	Missense_Mutation	SNP	G	A	4	66	c.503C>T	c.(502-504)TCC>TTC	p.S168F
Pat_44	Post-Resistance	C3orf54	389119	37	3	49842317	49842317	Missense_Mutation	SNP	C	T	5	196	c.761C>T	c.(760-762)CCT>CTT	p.P254L
Pat_44	Post-Resistance	CAMKV	79012	37	3	49898933	49898933	Missense_Mutation	SNP	C	T	4	78	c.380G>A	c.(379-381)CGG>CAG	p.R127Q
Pat_44	Post-Resistance	MST1R	4486	37	3	49936581	49936581	Missense_Mutation	SNP	G	A	4	155	c.1346C>T	c.(1345-1347)ACT>ATT	p.T449I
Pat_44	Post-Resistance	SEMA3F	6405	37	3	50219837	50219837	Splice_Site	SNP	G	A	4	207	c.763_splice	c.e8+1	p.D255_splice
Pat_44	Post-Resistance	RAD54L2	23132	37	3	51667774	51667774	Missense_Mutation	SNP	C	T	4	96	c.1007C>T	c.(1006-1008)CCG>CTG	p.P336L
Pat_44	Post-Resistance	STAB1	23166	37	3	52536244	52536244	Missense_Mutation	SNP	G	A	4	82	c.487G>A	c.(487-489)GTG>ATG	p.V163M
Pat_44	Post-Resistance	PRKCD	5580	37	3	53226233	53226233	Missense_Mutation	SNP	C	T	4	94	c.1982C>T	c.(1981-1983)GCT>GTT	p.A661V
Pat_44	Post-Resistance	CCDC66	285331	37	3	56627639	56627639	Missense_Mutation	SNP	G	C	3	76	c.1189G>C	c.(1189-1191)GAC>CAC	p.D397H
Pat_44	Post-Resistance	SLMAP	7871	37	3	57847758	57847758	Missense_Mutation	SNP	C	T	6	168	c.911C>T	c.(910-912)GCC>GTC	p.A304V
Pat_44	Post-Resistance	CADPS	8618	37	3	62570894	62570894	Nonsense_Mutation	SNP	G	A	4	213	c.1543C>T	c.(1543-1545)CGA>TGA	p.R515*
Pat_44	Post-Resistance	ADAMTS9	56999	37	3	64527080	64527080	Missense_Mutation	SNP	G	A	4	218	c.5303C>T	c.(5302-5304)GCG>GTG	p.A1768V
Pat_44	Post-Resistance	TMF1	7110	37	3	69097282	69097282	Missense_Mutation	SNP	C	T	5	184	c.574G>A	c.(574-576)GTA>ATA	p.V192I
Pat_44	Post-Resistance	FOXP1	27086	37	3	71015123	71015123	Missense_Mutation	SNP	G	A	6	374	c.1807C>T	c.(1807-1809)CGG>TGG	p.R603W
Pat_44	Post-Resistance	CLDND1	56650	37	3	98235555	98235555	Missense_Mutation	SNP	G	A	5	140	c.710C>T	c.(709-711)GCT>GTT	p.A237V
Pat_44	Post-Resistance	IMPG2	50939	37	3	100976394	100976394	Missense_Mutation	SNP	C	A	5	235	c.1132G>T	c.(1132-1134)GAT>TAT	p.D378Y
Pat_44	Post-Resistance	SEMA5B	54437	37	3	122680068	122680068	Missense_Mutation	SNP	C	T	5	95	c.43G>A	c.(43-45)GTC>ATC	p.V15I
Pat_44	Post-Resistance	ADCY5	111	37	3	123003523	123003523	Missense_Mutation	SNP	C	T	6	364	c.3718G>A	c.(3718-3720)GTG>ATG	p.V1240M
Pat_44	Post-Resistance	MUC13	56667	37	3	124646640	124646640	Missense_Mutation	SNP	G	A	6	228	c.250C>T	c.(250-252)CCT>TCT	p.P84S
Pat_44	Post-Resistance	COPG	22820	37	3	128976643	128976643	Missense_Mutation	SNP	G	A	5	311	c.811G>A	c.(811-813)GCC>ACC	p.A271T
Pat_44	Post-Resistance	PLS1	5357	37	3	142413338	142413338	Missense_Mutation	SNP	G	A	4	207	c.1205G>A	c.(1204-1206)CGG>CAG	p.R402Q
Pat_44	Post-Resistance	TM4SF18	116441	37	3	149051160	149051160	Missense_Mutation	SNP	G	A	6	84	c.10C>T	c.(10-12)CGG>TGG	p.R4W
Pat_44	Post-Resistance	GPR160	26996	37	3	169802385	169802385	Nonsense_Mutation	SNP	C	T	4	119	c.625C>T	c.(625-627)CAG>TAG	p.Q209*
Pat_44	Post-Resistance	NDUFB5	4711	37	3	179322646	179322646	Missense_Mutation	SNP	G	A	4	31	c.43G>A	c.(43-45)GTG>ATG	p.V15M
Pat_44	Post-Resistance	PEX5L	51555	37	3	179529629	179529629	Missense_Mutation	SNP	C	T	5	212	c.1114G>A	c.(1114-1116)GAG>AAG	p.E372K
Pat_44	Post-Resistance	MCF2L2	23101	37	3	183029470	183029470	Missense_Mutation	SNP	G	A	6	311	c.844C>T	c.(844-846)CTC>TTC	p.L282F

Pat_44	Post-Resistance	EIF4G1	1981	37	3	184039630	184039630	Missense_Mutation	SNP	G	A	6	439	c.1258G>A	c.(1258-1260)GAG>AAG	p.E420K
Pat_44	Post-Resistance	EHHADH	1962	37	3	184922411	184922411	Missense_Mutation	SNP	G	A	4	194	c.703C>T	c.(703-705)CGT>TGT	p.R235C
Pat_44	Post-Resistance	MUC4	4585	37	3	195511778	195511778	Missense_Mutation	SNP	G	C	5	9	c.6673C>G	c.(6673-6675)CTT>GTT	p.L2225V
Pat_44	Post-Resistance	PIGX	54965	37	3	196449387	196449387	Missense_Mutation	SNP	C	T	6	296	c.155C>T	c.(154-156)CCG>CTG	p.P52L
Pat_44	Post-Resistance	HTT	3064	37	4	3208355	3208355	Missense_Mutation	SNP	G	A	4	96	c.5857G>A	c.(5857-5859)GGC>AGC	p.G1953S
Pat_44	Post-Resistance	CCDC96	257236	37	4	7043201	7043201	Missense_Mutation	SNP	G	A	4	159	c.1465C>T	c.(1465-1467)CGG>TGG	p.R489W
Pat_44	Post-Resistance	GPR78	27201	37	4	8589002	8589002	Missense_Mutation	SNP	A	G	4	204	c.1004A>G	c.(1003-1005)CAG>CGG	p.Q335R
Pat_44	Post-Resistance	SLIT2	9353	37	4	20597399	20597399	Missense_Mutation	SNP	G	A	5	363	c.3262G>A	c.(3262-3264)GGA>AGA	p.G1088R
Pat_44	Post-Resistance	FRYL	285527	37	4	48542805	48542805	Missense_Mutation	SNP	G	A	4	157	c.5860C>T	c.(5860-5862)CGG>TGG	p.R1954W
Pat_44	Post-Resistance	KDR	3791	37	4	55955042	55955042	Missense_Mutation	SNP	G	A	4	67	c.3503C>T	c.(3502-3504)GCT>GTT	p.A1168V
Pat_44	Post-Resistance	UGT2B4	7363	37	4	70346495	70346495	Missense_Mutation	SNP	C	T	6	452	c.1444G>A	c.(1444-1446)GAC>AAC	p.D482N
Pat_44	Post-Resistance	AFM	173	37	4	74350000	74350000	Missense_Mutation	SNP	G	A	4	155	c.163G>A	c.(163-165)GTT>ATT	p.V55I
Pat_44	Post-Resistance	BTC	685	37	4	75681097	75681097	Missense_Mutation	SNP	C	T	5	208	c.253G>A	c.(253-255)GTG>ATG	p.V85M
Pat_44	Post-Resistance	PRDM8	56978	37	4	81124579	81124579	Missense_Mutation	SNP	G	A	3	38	c.1963G>A	c.(1963-1965)GAG>AAG	p.E655K
Pat_44	Post-Resistance	HPSE	10855	37	4	84227444	84227444	Missense_Mutation	SNP	G	A	4	161	c.1118C>T	c.(1117-1119)GCC>GTC	p.A373V
Pat_44	Post-Resistance	PDHA2	5161	37	4	96761395	96761395	Missense_Mutation	SNP	G	A	4	62	c.94G>A	c.(94-96)GCT>ACT	p.A32T
Pat_44	Post-Resistance	SPRY1	10252	37	4	124323405	124323405	Missense_Mutation	SNP	C	T	4	163	c.659C>T	c.(658-660)ACC>ATC	p.T220I
Pat_44	Post-Resistance	PLK4	10733	37	4	128807661	128807661	Missense_Mutation	SNP	C	T	4	123	c.1136C>T	c.(1135-1137)TCT>TTT	p.S379F
Pat_44	Post-Resistance	HHIP	64399	37	4	145655991	145655991	Missense_Mutation	SNP	C	T	4	129	c.1859C>T	c.(1858-1860)ACG>ATG	p.T620M
Pat_44	Post-Resistance	NR3C2	4306	37	4	149356701	149356701	Missense_Mutation	SNP	C	T	4	92	c.1312G>A	c.(1312-1314)GGC>AGC	p.G438S
Pat_44	Post-Resistance	MAP9	79884	37	4	156281477	156281477	Missense_Mutation	SNP	G	A	4	104	c.893C>T	c.(892-894)GCA>GTA	p.A298V
Pat_44	Post-Resistance	PALLD	23022	37	4	169846223	169846223	Missense_Mutation	SNP	G	A	4	117	c.3352G>A	c.(3352-3354)GTT>ATT	p.V1118I
Pat_44	Post-Resistance	CLCN3	1182	37	4	170613332	170613332	Missense_Mutation	SNP	C	T	4	219	c.797C>T	c.(796-798)ACC>ATC	p.T266I
Pat_44	Post-Resistance	FAT1	2195	37	4	187540997	187540997	Missense_Mutation	SNP	G	A	4	161	c.6743C>T	c.(6742-6744)CCG>CTG	p.P2248L
Pat_44	Post-Resistance	CEP72	55722	37	5	637644	637644	Missense_Mutation	SNP	C	T	4	96	c.917C>T	c.(916-918)ACC>ATC	p.T306I
Pat_44	Post-Resistance	NKD2	85409	37	5	1038460	1038460	Missense_Mutation	SNP	A	C	2	3	c.1328A>C	c.(1327-1329)CAC>CCC	p.H443P
Pat_44	Post-Resistance	ADAMTS16	170690	37	5	5303769	5303769	Missense_Mutation	SNP	C	A	4	68	c.3076C>A	c.(3076-3078)CCC>ACC	p.P1026T
Pat_44	Post-Resistance	SEMA5A	9037	37	5	9063104	9063104	Missense_Mutation	SNP	G	A	4	139	c.2413C>T	c.(2413-2415)CGG>TGG	p.R805W
Pat_44	Post-Resistance	CTNND2	1501	37	5	11018111	11018111	Missense_Mutation	SNP	C	T	4	145	c.3059G>A	c.(3058-3060)CGA>CAA	p.R1020Q
Pat_44	Post-Resistance	CTNND2	1501	37	5	11023077	11023077	Nonsense_Mutation	SNP	G	A	4	81	c.2803C>T	c.(2803-2805)CGA>TGA	p.R935*
Pat_44	Post-Resistance	DNAH5	1767	37	5	13737439	13737439	Missense_Mutation	SNP	C	T	4	165	c.11377G>A	c.(11377-11379)GAG>AAG	p.E3793K
Pat_44	Post-Resistance	PDZD2	23037	37	5	32058041	32058041	Missense_Mutation	SNP	C	T	4	203	c.2032C>T	c.(2032-2034)CTC>TTC	p.L678F
Pat_44	Post-Resistance	C9	735	37	5	39342204	39342204	Missense_Mutation	SNP	G	A	4	188	c.172C>T	c.(172-174)CTC>TTC	p.L58F
Pat_44	Post-Resistance	GZMA	3001	37	5	54403740	54403740	Missense_Mutation	SNP	G	A	4	181	c.334G>A	c.(334-336)GAA>AAA	p.E112K
Pat_44	Post-Resistance	RGNEF	64283	37	5	73193828	73193828	Missense_Mutation	SNP	G	A	3	32	c.3883G>A	c.(3883-3885)GCC>ACC	p.A1295T
Pat_44	Post-Resistance	IQGAP2	10788	37	5	75998398	75998398	Missense_Mutation	SNP	G	A	4	110	c.4597G>A	c.(4597-4599)GTG>ATG	p.V1533M
Pat_44	Post-Resistance	ARSB	411	37	5	78076321	78076321	Missense_Mutation	SNP	G	A	4	133	c.1501C>T	c.(1501-1503)CGC>TGC	p.R501C
Pat_44	Post-Resistance	DMGDH	29958	37	5	78338269	78338269	Nonsense_Mutation	SNP	G	A	4	163	c.1030C>T	c.(1030-1032)CGA>TGA	p.R344*
Pat_44	Post-Resistance	THBS4	7060	37	5	79374926	79374926	Missense_Mutation	SNP	C	T	4	140	c.2356C>T	c.(2356-2358)CAT>TAT	p.H786Y
Pat_44	Post-Resistance	PCSK1	5122	37	5	95759156	95759156	Missense_Mutation	SNP	G	A	5	111	c.404C>T	c.(403-405)ACC>ATC	p.T135I
Pat_44	Post-Resistance	PRRC1	133619	37	5	126860489	126860489	Missense_Mutation	SNP	C	T	6	405	c.370C>T	c.(370-372)CCC>TCC	p.P124S
Pat_44	Post-Resistance	PCDHA8	56140	37	5	140221559	140221559	Missense_Mutation	SNP	G	A	4	102	c.653G>A	c.(652-654)GGC>GAC	p.G218D
Pat_44	Post-Resistance	WWC1	23286	37	5	167882478	167882478	Missense_Mutation	SNP	C	T	7	242	c.2776C>T	c.(2776-2778)CGC>TGC	p.R926C
Pat_44	Post-Resistance	STK10	6793	37	5	171520450	171520450	Missense_Mutation	SNP	G	A	4	119	c.1520C>T	c.(1519-1521)TCG>TTG	p.S507L
Pat_44	Post-Resistance	CPEB4	80315	37	5	173370044	173370044	Missense_Mutation	SNP	G	A	5	207	c.1274G>A	c.(1273-1275)CGA>CAA	p.R425Q
Pat_44	Post-Resistance	FGFR4	2264	37	5	176519689	176519689	Missense_Mutation	SNP	C	T	4	144	c.961C>T	c.(961-963)CGG>TGG	p.R321W
Pat_44	Post-Resistance	NHP2	55651	37	5	177577981	177577981	Missense_Mutation	SNP	C	G	4	238	c.244G>C	c.(244-246)GCA>CCA	p.A82P

Pat_44	Post-Resistance	COL23A1	91522	37	5	177683382	177683382	Missense_Mutation	SNP	C	T	3	28	c.854G>A	c.(853-855)CGA>CAA	p.R285Q
Pat_44	Post-Resistance	C5orf45	51149	37	5	179264450	179264450	Nonsense_Mutation	SNP	G	A	5	283	c.973C>T	c.(973-975)CGA>TGA	p.R325*
Pat_44	Post-Resistance	MYLK4	340156	37	6	2678592	2678592	Missense_Mutation	SNP	G	A	4	190	c.902C>T	c.(901-903)TCG>TTG	p.S301L
Pat_44	Post-Resistance	GCM2	9247	37	6	10877576	10877576	Missense_Mutation	SNP	C	T	3	85	c.140G>A	c.(139-141)CGC>CAC	p.R47H
Pat_44	Post-Resistance	HIST1H2AD	3013	37	6	26199413	26199413	Missense_Mutation	SNP	G	A	3	31	c.59C>T	c.(58-60)TCG>TTG	p.S20L
Pat_44	Post-Resistance	BTN1A1	696	37	6	26508798	26508798	Missense_Mutation	SNP	G	A	5	299	c.977G>A	c.(976-978)CGA>CAA	p.R326Q
Pat_44	Post-Resistance	MDC1	9656	37	6	30672288	30672288	Missense_Mutation	SNP	C	A	5	153	c.4672G>T	c.(4672-4674)GGC>TGC	p.G1558C
Pat_44	Post-Resistance	BAT1	7919	37	6	31498907	31498907	Nonsense_Mutation	SNP	G	A	4	139	c.1045C>T	c.(1045-1047)CGA>TGA	p.R349*
Pat_44	Post-Resistance	SKIV2L	6499	37	6	31929327	31929327	Missense_Mutation	SNP	G	A	4	106	c.793G>A	c.(793-795)GCG>ACG	p.A265T
Pat_44	Post-Resistance	SKIV2L	6499	37	6	31932075	31932075	Missense_Mutation	SNP	C	T	4	94	c.1927C>T	c.(1927-1929)CTC>TTC	p.L643F
Pat_44	Post-Resistance	EGFL8	80864	37	6	32134938	32134938	Missense_Mutation	SNP	G	A	4	162	c.505G>A	c.(505-507)GGC>AGC	p.G169S
Pat_44	Post-Resistance	HLA-DMA	3108	37	6	32918577	32918577	Missense_Mutation	SNP	G	A	5	200	c.92C>T	c.(91-93)CCT>CTT	p.P31L
Pat_44	Post-Resistance	TEAD3	7005	37	6	35454289	35454289	Missense_Mutation	SNP	G	A	4	100	c.151C>T	c.(151-153)CCG>TCG	p.P51S
Pat_44	Post-Resistance	KCNK17	89822	37	6	39267504	39267504	Missense_Mutation	SNP	G	A	4	154	c.698C>T	c.(697-699)CCC>CTC	p.P233L
Pat_44	Post-Resistance	UNC5CL	222643	37	6	40999485	40999485	Missense_Mutation	SNP	C	T	4	182	c.1054G>A	c.(1054-1056)GAT>AAT	p.D352N
Pat_44	Post-Resistance	TREM2	54209	37	6	41129150	41129150	Missense_Mutation	SNP	C	T	4	128	c.242G>A	c.(241-243)AGC>AAC	p.S81N
Pat_44	Post-Resistance	PEX6	5190	37	6	42932612	42932612	Nonsense_Mutation	SNP	G	A	4	156	c.2722C>T	c.(2722-2724)CAG>TAG	p.Q908*
Pat_44	Post-Resistance	TTBK1	84630	37	6	43221397	43221397	Missense_Mutation	SNP	C	A	4	28	c.422C>A	c.(421-423)TCC>TAC	p.S141Y
Pat_44	Post-Resistance	TCTE1	202500	37	6	44253853	44253853	Missense_Mutation	SNP	C	T	4	194	c.694G>A	c.(694-696)GAT>AAT	p.D232N
Pat_44	Post-Resistance	MUT	4594	37	6	49426989	49426989	Missense_Mutation	SNP	G	A	4	63	c.191C>T	c.(190-192)CCG>CTG	p.P64L
Pat_44	Post-Resistance	GSTA3	2940	37	6	52762685	52762685	Missense_Mutation	SNP	C	T	5	180	c.484G>A	c.(484-486)GAA>AAA	p.E162K
Pat_44	Post-Resistance	GCM1	8521	37	6	52998936	52998936	Missense_Mutation	SNP	C	T	8	270	c.262G>A	c.(262-264)GCA>ACA	p.A88T
Pat_44	Post-Resistance	FAM83B	222584	37	6	54805208	54805208	Missense_Mutation	SNP	G	A	8	355	c.1439G>A	c.(1438-1440)CGA>CAA	p.R480Q
Pat_44	Post-Resistance	RIMS1	22999	37	6	73110297	73110297	Missense_Mutation	SNP	G	A	4	234	c.4960G>A	c.(4960-4962)GGA>AGA	p.G1654R
Pat_44	Post-Resistance	COL12A1	1303	37	6	75844499	75844499	Missense_Mutation	SNP	C	T	5	208	c.5467G>A	c.(5467-5469)GTA>ATA	p.V1823I
Pat_44	Post-Resistance	RRAGD	58528	37	6	90089954	90089954	Missense_Mutation	SNP	G	T	5	271	c.577C>A	c.(577-579)CAA>AAA	p.Q193K
Pat_44	Post-Resistance	BEND3	57673	37	6	107390255	107390255	Missense_Mutation	SNP	G	A	5	207	c.2140C>T	c.(2140-2142)CCG>TCG	p.P714S
Pat_44	Post-Resistance	REV3L	5980	37	6	111680156	111680156	Missense_Mutation	SNP	G	A	5	239	c.6941C>T	c.(6940-6942)CCG>CTG	p.P2314L
Pat_44	Post-Resistance	DSE	29940	37	6	116720742	116720742	Missense_Mutation	SNP	C	T	5	98	c.329C>T	c.(328-330)GCA>GTA	p.A110V
Pat_44	Post-Resistance	EYA4	2070	37	6	133802609	133802609	Missense_Mutation	SNP	G	A	4	193	c.979G>A	c.(979-981)GAT>AAT	p.D327N
Pat_44	Post-Resistance	MAP7	9053	37	6	136677864	136677864	Missense_Mutation	SNP	C	T	4	105	c.1981G>A	c.(1981-1983)GTT>ATT	p.V661I
Pat_44	Post-Resistance	PLAGL1	5325	37	6	144263033	144263033	Missense_Mutation	SNP	G	C	3	53	c.920C>G	c.(919-921)TCT>TGT	p.S307C
Pat_44	Post-Resistance	GRM1	2911	37	6	146350780	146350780	Missense_Mutation	SNP	G	A	4	128	c.127G>A	c.(127-129)GGA>AGA	p.G43R
Pat_44	Post-Resistance	GRM1	2911	37	6	146755453	146755453	Missense_Mutation	SNP	G	A	4	141	c.3106G>A	c.(3106-3108)GGA>AGA	p.G1036R
Pat_44	Post-Resistance	SASH1	23328	37	6	148711291	148711291	Missense_Mutation	SNP	G	A	5	340	c.178G>A	c.(178-180)GAT>AAT	p.D60N
Pat_44	Post-Resistance	NUP43	348995	37	6	150057610	150057610	Missense_Mutation	SNP	C	T	4	86	c.787G>A	c.(787-789)GAA>AAA	p.E263K
Pat_44	Post-Resistance	MTHFD1L	25902	37	6	151281429	151281429	Missense_Mutation	SNP	G	A	4	230	c.1822G>A	c.(1822-1824)GTG>ATG	p.V608M
Pat_44	Post-Resistance	TIAM2	26230	37	6	155458470	155458470	Missense_Mutation	SNP	G	A	6	341	c.1354G>A	c.(1354-1356)GAT>AAT	p.D452N
Pat_44	Post-Resistance	SERAC1	84947	37	6	158535847	158535847	Missense_Mutation	SNP	G	A	5	271	c.1658C>T	c.(1657-1659)TCG>TTG	p.S553L
Pat_44	Post-Resistance	RSPH3	83861	37	6	159398793	159398793	Missense_Mutation	SNP	G	A	5	226	c.1460C>T	c.(1459-1461)CCT>CTT	p.P487L
Pat_44	Post-Resistance	GPER	2852	37	7	1131797	1131797	Missense_Mutation	SNP	G	A	5	134	c.433G>A	c.(433-435)GTC>ATC	p.V145I
Pat_44	Post-Resistance	SCIN	85477	37	7	12664737	12664737	Missense_Mutation	SNP	G	A	4	42	c.862G>A	c.(862-864)GGG>AGG	p.G288R
Pat_44	Post-Resistance	ABCB5	340273	37	7	20766690	20766690	Missense_Mutation	SNP	C	T	4	151	c.1318C>T	c.(1318-1320)CGT>TGT	p.R440C
Pat_44	Post-Resistance	DNAH11	8701	37	7	21603969	21603969	Missense_Mutation	SNP	G	A	3	78	c.1148G>A	c.(1147-1149)CGG>CAG	p.R383Q
Pat_44	Post-Resistance	TRA2A	29896	37	7	23556103	23556103	Missense_Mutation	SNP	C	T	4	160	c.215G>A	c.(214-216)AGA>AAA	p.R72K
Pat_44	Post-Resistance	DPY19L2P1	554236	37	7	35144260	35144260	Missense_Mutation	SNP	C	T	4	79	c.848G>A	c.(847-849)CGA>CAA	p.R283Q
Pat_44	Post-Resistance	IGFBP1	3484	37	7	45930257	45930257	Missense_Mutation	SNP	G	A	4	103	c.460G>A	c.(460-462)GCC>ACC	p.A154T

Pat_44	Post-Resistance	PKD1L1	168507	37	7	47969091	47969091	Missense_Mutation	SNP	G	A	4	56	c.770C>T	c.(769-771)ACC>ATC	p.T257I
Pat_44	Post-Resistance	ZNF735	730291	37	7	63680322	63680322	Missense_Mutation	SNP	A	C	4	176	c.893A>C	c.(892-894)AAA>ACA	p.K298T
Pat_44	Post-Resistance	C7orf42	55069	37	7	66410200	66410200	Missense_Mutation	SNP	G	A	5	258	c.397G>A	c.(397-399)GTC>ATC	p.V133I
Pat_44	Post-Resistance	FKBP6	8468	37	7	72744261	72744261	Missense_Mutation	SNP	C	T	4	187	c.374C>T	c.(373-375)CCC>CTC	p.P125L
Pat_44	Post-Resistance	FKBP6	8468	37	7	72744270	72744270	Missense_Mutation	SNP	C	T	4	206	c.383C>T	c.(382-384)CCC>CTC	p.P128L
Pat_44	Post-Resistance	POR	5447	37	7	75612905	75612905	Missense_Mutation	SNP	G	A	6	317	c.898G>A	c.(898-900)GAG>AAG	p.E300K
Pat_44	Post-Resistance	DTX2	113878	37	7	76132897	76132897	Missense_Mutation	SNP	G	A	4	53	c.1544G>A	c.(1543-1545)GGT>GAT	p.G515D
Pat_44	Post-Resistance	ABCB1	5243	37	7	87160669	87160669	Missense_Mutation	SNP	T	C	5	282	c.2626A>G	c.(2626-2628)ATG>GTG	p.M876V
Pat_44	Post-Resistance	STEAP4	79689	37	7	87912078	87912078	Missense_Mutation	SNP	G	A	4	166	c.862C>T	c.(862-864)CTT>TTT	p.L288F
Pat_44	Post-Resistance	DYNC1I1	1780	37	7	95614264	95614264	Missense_Mutation	SNP	G	A	4	232	c.769G>A	c.(769-771)GGC>AGC	p.G257S
Pat_44	Post-Resistance	BRI3	25798	37	7	97920521	97920521	Missense_Mutation	SNP	G	A	4	71	c.344G>A	c.(343-345)CGA>CAA	p.R115Q
Pat_44	Post-Resistance	PILRA	29992	37	7	99995510	99995510	Missense_Mutation	SNP	C	T	4	206	c.682C>T	c.(682-684)CGG>TGG	p.R228W
Pat_44	Post-Resistance	ZAN	7455	37	7	100361687	100361687	Missense_Mutation	SNP	G	A	4	125	c.4135G>A	c.(4135-4137)GAC>AAC	p.D1379N
Pat_44	Post-Resistance	EPHB4	2050	37	7	100404041	100404041	Splice_Site	SNP	C	T	4	129	c.2484_splice	c.e14+1	p.D828_splice
Pat_44	Post-Resistance	PSMC2	5701	37	7	103008167	103008167	Missense_Mutation	SNP	C	T	4	102	c.1055C>T	c.(1054-1056)ACC>ATC	p.T352I
Pat_44	Post-Resistance	CDHR3	222256	37	7	105645010	105645010	Missense_Mutation	SNP	C	T	4	97	c.929C>T	c.(928-930)ACC>ATC	p.T310I
Pat_44	Post-Resistance	LAMB4	22798	37	7	107732813	107732813	Missense_Mutation	SNP	C	G	4	126	c.1519G>C	c.(1519-1521)GAC>CAC	p.D507H
Pat_44	Post-Resistance	SPAM1	6677	37	7	123595094	123595094	Missense_Mutation	SNP	C	T	6	349	c.998C>T	c.(997-999)GCT>GTT	p.A333V
Pat_44	Post-Resistance	IRF5	3663	37	7	128588332	128588332	Missense_Mutation	SNP	G	A	4	97	c.1219G>A	c.(1219-1221)GAA>AAA	p.E407K
Pat_44	Post-Resistance	PLXNA4	91584	37	7	131831448	131831448	Missense_Mutation	SNP	G	A	5	297	c.4876C>T	c.(4876-4878)CGG>TGG	p.R1626W
Pat_44	Post-Resistance	TRIM24	8805	37	7	138223473	138223473	Missense_Mutation	SNP	G	T	4	192	c.1068G>T	c.(1066-1068)TTG>TTT	p.L356F
Pat_44	Post-Resistance	TRIM24	8805	37	7	138269680	138269680	Missense_Mutation	SNP	G	A	4	115	c.3137G>A	c.(3136-3138)CGC>CAC	p.R1046H
Pat_44	Post-Resistance	KIAA1549	57670	37	7	138603918	138603918	Missense_Mutation	SNP	C	T	6	406	c.454G>A	c.(454-456)GTC>ATC	p.V152I
Pat_44	Post-Resistance	PRSS1	5644	37	7	142460762	142460762	Missense_Mutation	SNP	G	A	4	95	c.635G>A	c.(634-636)GGA>GAA	p.G212E
Pat_44	Post-Resistance	OR6V1	346517	37	7	142749903	142749903	Missense_Mutation	SNP	C	T	4	160	c.466C>T	c.(466-468)CCC>TCC	p.P156S
Pat_44	Post-Resistance	ZYX	7791	37	7	143085594	143085594	Missense_Mutation	SNP	G	A	4	103	c.1157G>A	c.(1156-1158)CGA>CAA	p.R386Q
Pat_44	Post-Resistance	ZNF786	136051	37	7	148767871	148767871	Missense_Mutation	SNP	C	T	4	121	c.1993G>A	c.(1993-1995)GAG>AAG	p.E665K
Pat_44	Post-Resistance	WDR86	349136	37	7	151082210	151082210	Missense_Mutation	SNP	G	A	3	55	c.826C>T	c.(826-828)CGC>TGC	p.R276C
Pat_44	Post-Resistance	DLGAP2	9228	37	8	1497104	1497104	Missense_Mutation	SNP	C	T	4	78	c.245C>T	c.(244-246)CCG>CTG	p.P82L
Pat_44	Post-Resistance	FGF20	26281	37	8	16850642	16850642	Missense_Mutation	SNP	G	A	5	129	c.575C>T	c.(574-576)CCT>CTT	p.P192L
Pat_44	Post-Resistance	XPO7	23039	37	8	21848421	21848421	Missense_Mutation	SNP	G	A	6	462	c.2032G>A	c.(2032-2034)GTG>ATG	p.V678M
Pat_44	Post-Resistance	LGI3	203190	37	8	22005857	22005857	Missense_Mutation	SNP	G	A	4	43	c.1463C>T	c.(1462-1464)TCC>TTC	p.S488F
Pat_44	Post-Resistance	BMP1	649	37	8	22067071	22067071	Missense_Mutation	SNP	G	A	4	234	c.2689G>A	c.(2689-2691)GAG>AAG	p.E897K
Pat_44	Post-Resistance	RHOBTB2	23221	37	8	22864257	22864257	Missense_Mutation	SNP	G	A	4	72	c.499G>A	c.(499-501)GAA>AAA	p.E167K
Pat_44	Post-Resistance	PTK2B	2185	37	8	27311809	27311809	Splice_Site	SNP	G	A	3	29	c.2733_splice	c.e34+1	p.K911_splice
Pat_44	Post-Resistance	GPR124	25960	37	8	37690527	37690527	Splice_Site	SNP	G	A	7	362	c.1098_splice	c.e9-1	p.R366_splice
Pat_44	Post-Resistance	JPH1	56704	37	8	75157194	75157194	Missense_Mutation	SNP	G	A	5	182	c.1475C>T	c.(1474-1476)GCG>GTG	p.A492V
Pat_44	Post-Resistance	WWP1	11059	37	8	87473549	87473549	Missense_Mutation	SNP	G	A	5	198	c.2596G>A	c.(2596-2598)GGA>AGA	p.G866R
Pat_44	Post-Resistance	RBM12B	389677	37	8	94748493	94748493	Missense_Mutation	SNP	G	A	4	89	c.146C>T	c.(145-147)ACA>ATA	p.T49I
Pat_44	Post-Resistance	TMEM67	91147	37	8	94777638	94777638	Missense_Mutation	SNP	G	A	4	146	c.511G>A	c.(511-513)GTC>ATC	p.V171I
Pat_44	Post-Resistance	GRHL2	79977	37	8	102505011	102505011	Missense_Mutation	SNP	C	T	4	154	c.14C>T	c.(13-15)TCG>TTG	p.S5L
Pat_44	Post-Resistance	CSMD3	114788	37	8	113668416	113668416	Missense_Mutation	SNP	G	A	4	116	c.2971C>T	c.(2971-2973)CGT>TGT	p.R991C
Pat_44	Post-Resistance	CSMD3	114788	37	8	113668487	113668487	Missense_Mutation	SNP	C	T	4	126	c.2900G>A	c.(2899-2901)GGC>GAC	p.G967D
Pat_44	Post-Resistance	COLEC10	10584	37	8	120079546	120079546	Missense_Mutation	SNP	G	A	4	94	c.26G>A	c.(25-27)CGA>CAA	p.R9Q
Pat_44	Post-Resistance	OC90	729330	37	8	133062080	133062080	Nonsense_Mutation	SNP	G	A	5	232	c.37C>T	c.(37-39)CAG>TAG	p.Q13*
Pat_44	Post-Resistance	TG	7038	37	8	133900673	133900673	Missense_Mutation	SNP	G	A	3	39	c.2621G>A	c.(2620-2622)GGC>GAC	p.G874D
Pat_44	Post-Resistance	NDRG1	10397	37	8	134260140	134260140	Missense_Mutation	SNP	C	T	4	244	c.785G>A	c.(784-786)AGC>AAC	p.S262N

Pat_44	Post-Resistance	BAI1	575	37	8	143602201	143602201	Missense_Mutation	SNP	G	A	4	83	c.2939G>A	c.(2938-2940)CGT>CAT	p.R980H
Pat_44	Post-Resistance	EPPK1	83481	37	8	144940844	144940844	Missense_Mutation	SNP	G	A	5	282	c.6578C>T	c.(6577-6579)ACG>ATG	p.T2193M
Pat_44	Post-Resistance	EPPK1	83481	37	8	144943152	144943152	Missense_Mutation	SNP	C	T	4	143	c.4270G>A	c.(4270-4272)GAC>AAC	p.D1424N
Pat_44	Post-Resistance	KIAA2026	158358	37	9	5922299	5922299	Missense_Mutation	SNP	C	T	5	133	c.3697G>A	c.(3697-3699)GGT>AGT	p.G1233S
Pat_44	Post-Resistance	UHRF2	115426	37	9	6506075	6506075	Missense_Mutation	SNP	C	T	4	148	c.2305C>T	c.(2305-2307)CCT>TCT	p.P769S
Pat_44	Post-Resistance	GLDC	2731	37	9	6554754	6554754	Missense_Mutation	SNP	C	T	3	49	c.2230G>A	c.(2230-2232)GGG>AGG	p.G744R
Pat_44	Post-Resistance	OR2S2	56656	37	9	35957483	35957483	Missense_Mutation	SNP	C	T	5	147	c.613G>A	c.(613-615)GTG>ATG	p.V205M
Pat_44	Post-Resistance	PAX5	5079	37	9	36923376	36923376	Missense_Mutation	SNP	G	A	4	168	c.886C>T	c.(886-888)CCG>TCG	p.P296S
Pat_44	Post-Resistance	RG9MTD3	158234	37	9	37769975	37769975	Missense_Mutation	SNP	C	T	5	412	c.611C>T	c.(610-612)CCC>CTC	p.P204L
Pat_44	Post-Resistance	VPS13A	23230	37	9	79996953	79996953	Missense_Mutation	SNP	G	A	4	107	c.9139G>A	c.(9139-9141)GTT>ATT	p.V3047I
Pat_44	Post-Resistance	DAPK1	1612	37	9	90322028	90322028	Missense_Mutation	SNP	G	A	4	112	c.4042G>A	c.(4042-4044)GGG>AGG	p.G1348R
Pat_44	Post-Resistance	SEMA4D	10507	37	9	92020266	92020266	Missense_Mutation	SNP	C	T	4	84	c.106G>A	c.(106-108)GAG>AAG	p.E36K
Pat_44	Post-Resistance	CDC14B	8555	37	9	99296754	99296754	Missense_Mutation	SNP	C	T	4	160	c.698G>A	c.(697-699)AGA>AAA	p.R233K
Pat_44	Post-Resistance	NCBP1	4686	37	9	100426677	100426677	Missense_Mutation	SNP	C	T	4	206	c.1853C>T	c.(1852-1854)GCC>GTC	p.A618V
Pat_44	Post-Resistance	TBC1D2	55357	37	9	100963825	100963825	Missense_Mutation	SNP	G	A	4	188	c.2393C>T	c.(2392-2394)GCG>GTG	p.A798V
Pat_44	Post-Resistance	ZNF462	58499	37	9	109746677	109746677	Missense_Mutation	SNP	G	A	4	145	c.7043G>A	c.(7042-7044)CGG>CAG	p.R2348Q
Pat_44	Post-Resistance	RAD23B	5887	37	9	110073982	110073982	Missense_Mutation	SNP	C	T	4	119	c.517C>T	c.(517-519)CGG>TGG	p.R173W
Pat_44	Post-Resistance	ZNF483	158399	37	9	114304755	114304755	Missense_Mutation	SNP	C	A	4	49	c.1540C>A	c.(1540-1542)CAG>AAG	p.Q514K
Pat_44	Post-Resistance	ORM1	5004	37	9	117086085	117086085	Missense_Mutation	SNP	G	A	4	82	c.257G>A	c.(256-258)CGA>CAA	p.R86Q
Pat_44	Post-Resistance	ASTN2	23245	37	9	119903655	119903655	Missense_Mutation	SNP	G	A	4	108	c.1118C>T	c.(1117-1119)CCC>CTC	p.P373L
Pat_44	Post-Resistance	C5	727	37	9	123724984	123724984	Missense_Mutation	SNP	G	A	5	422	c.4469C>T	c.(4468-4470)CCT>CTT	p.P1490L
Pat_44	Post-Resistance	SCAI	286205	37	9	127733949	127733949	Splice_Site	SNP	C	T	6	428	c.1573_splice	c.e16+1	p.D525_splice
Pat_44	Post-Resistance	CDK9	1025	37	9	130550841	130550841	Missense_Mutation	SNP	C	T	2	2	c.623C>T	c.(622-624)CCC>CTC	p.P208L
Pat_44	Post-Resistance	CIZ1	25792	37	9	130938655	130938655	Missense_Mutation	SNP	G	A	4	193	c.1918C>T	c.(1918-1920)CGG>TGG	p.R640W
Pat_44	Post-Resistance	CAMSAP1	157922	37	9	138703415	138703415	Missense_Mutation	SNP	G	A	4	23	c.4549C>T	c.(4549-4551)CGT>TGT	p.R1517C
Pat_44	Post-Resistance	CTPS2	56474	37	X	16716382	16716382	Missense_Mutation	SNP	C	T	6	282	c.415G>A	c.(415-417)GAG>AAG	p.E139K
Pat_44	Post-Resistance	YY2	404281	37	X	21875236	21875236	Missense_Mutation	SNP	G	A	5	187	c.634G>A	c.(634-636)GAG>AAG	p.E212K
Pat_44	Post-Resistance	DCAF8L1	139425	37	X	27998611	27998611	Missense_Mutation	SNP	G	A	3	64	c.841C>T	c.(841-843)CGT>TGT	p.R281C
Pat_44	Post-Resistance	OTUD5	55593	37	X	48792014	48792014	Missense_Mutation	SNP	G	A	4	67	c.880C>T	c.(880-882)CGT>TGT	p.R294C
Pat_44	Post-Resistance	PFKFB1	5207	37	X	54982667	54982667	Missense_Mutation	SNP	C	T	3	66	c.557G>A	c.(556-558)CGG>CAG	p.R186Q
Pat_44	Post-Resistance	RAB40A	142684	37	X	102755651	102755651	Missense_Mutation	SNP	C	A	4	89	c.34G>T	c.(34-36)GAC>TAC	p.D12Y
Pat_44	Post-Resistance	RAB40A	142684	37	X	102755657	102755657	Missense_Mutation	SNP	C	T	4	78	c.28G>A	c.(28-30)GCC>ACC	p.A10T
Pat_44	Post-Resistance	VGLL1	51442	37	X	135630918	135630918	Missense_Mutation	SNP	G	A	7	170	c.385G>A	c.(385-387)GAG>AAG	p.E129K
Pat_44	Post-Resistance	MAGEC1	9947	37	X	140994583	140994583	Nonsense_Mutation	SNP	A	T	5	120	c.1393A>T	c.(1393-1395)AGA>TGA	p.R465*
Pat_44	Post-Resistance	MAGEC1	9947	37	X	140994923	140994923	Missense_Mutation	SNP	A	T	7	287	c.1733A>T	c.(1732-1734)CAC>CTC	p.H578L
Pat_44	Post-Resistance	SPANXN2	494119	37	X	142795287	142795287	Missense_Mutation	SNP	A	G	12	112	c.391T>C	c.(391-393)TCT>CCT	p.S131P
Pat_44	Post-Resistance	MTM1	4534	37	X	149839923	149839923	Missense_Mutation	SNP	G	A	4	54	c.1667G>A	c.(1666-1668)CGT>CAT	p.R556H
Pat_44	Post-Resistance	SLC6A8	6535	37	X	152959631	152959631	Missense_Mutation	SNP	C	T	4	75	c.1301C>T	c.(1300-1302)CCG>CTG	p.P434L
Pat_44	Post-Resistance	USP9Y	8287	37	Y	14922709	14922709	Missense_Mutation	SNP	G	A	4	66	c.4195G>A	c.(4195-4197)GAA>AAA	p.E1399K
Pat_45	Pre-Treatment	AGRN	375790	37	1	957741	957741	Missense_Mutation	SNP	C	T	5	93	c.362C>T	c.(361-363)CCC>CTC	p.P121L
Pat_45	Pre-Treatment	NADK	65220	37	1	1688674	1688674	Missense_Mutation	SNP	C	A	43	71	c.339G>T	c.(337-339)ATG>ATT	p.M113I
Pat_45	Pre-Treatment	ENO1	2023	37	1	8930542	8930542	Missense_Mutation	SNP	T	C	18	64	c.209A>G	c.(208-210)AAT>AGT	p.N70S
Pat_45	Pre-Treatment	MTOR	2475	37	1	11186732	11186732	Missense_Mutation	SNP	G	A	4	94	c.6473C>T	c.(6472-6474)CCG>CTG	p.P2158L
Pat_45	Pre-Treatment	LOC440563	440563	37	1	13183290	13183290	Missense_Mutation	SNP	C	T	60	287	c.583G>A	c.(583-585)GAT>AAT	p.D195N
Pat_45	Pre-Treatment	FBLIM1	54751	37	1	16091650	16091650	Missense_Mutation	SNP	G	A	3	17	c.172G>A	c.(172-174)GGG>AGG	p.G58R
Pat_45	Pre-Treatment	SPEN	23013	37	1	16260971	16260971	Missense_Mutation	SNP	G	A	4	73	c.8236G>A	c.(8236-8238)GTT>ATT	p.V2746I
Pat_45	Pre-Treatment	ZBTB17	7709	37	1	16271646	16271646	Missense_Mutation	SNP	T	C	2	8	c.713A>G	c.(712-714)GAG>GGG	p.E238G

Pat_45	Pre-Treatment	CLCNKB	1188	37	1	16372118	16372118	Missense_Mutation	SNP	C	A	3	37	c.166C>A	c.(166-168)CTC>ATC	p.L56I
Pat_45	Pre-Treatment	EPHA2	1969	37	1	16458313	16458313	Missense_Mutation	SNP	T	C	3	42	c.2378A>G	c.(2377-2379)AAG>AGG	p.K793R
Pat_45	Pre-Treatment	FBXO42	54455	37	1	16577955	16577955	Missense_Mutation	SNP	G	A	3	23	c.1364C>T	c.(1363-1365)TCT>TTT	p.S455F
Pat_45	Pre-Treatment	PADI2	11240	37	1	17420088	17420088	Missense_Mutation	SNP	C	T	4	108	c.503G>A	c.(502-504)CGT>CAT	p.R168H
Pat_45	Pre-Treatment	PADI1	29943	37	1	17550188	17550188	Missense_Mutation	SNP	G	A	3	30	c.346G>A	c.(346-348)GAT>AAT	p.D116N
Pat_45	Pre-Treatment	UBR4	23352	37	1	19404519	19404519	Missense_Mutation	SNP	G	A	11	87	c.15275C>T	c.(15274-15276)TCT>TTT	p.S5092F
Pat_45	Pre-Treatment	UBR4	23352	37	1	19474509	19474509	Missense_Mutation	SNP	C	T	4	117	c.7607G>A	c.(7606-7608)CGC>CAC	p.R2536H
Pat_45	Pre-Treatment	UBR4	23352	37	1	19504038	19504038	Missense_Mutation	SNP	G	A	6	244	c.2554C>T	c.(2554-2556)CCG>TCG	p.P852S
Pat_45	Pre-Treatment	RNF186	54546	37	1	20141465	20141465	Missense_Mutation	SNP	G	A	4	62	c.130C>T	c.(130-132)CGG>TGG	p.R44W
Pat_45	Pre-Treatment	C1orf63	57035	37	1	25573127	25573127	Missense_Mutation	SNP	G	A	3	36	c.328C>T	c.(328-330)CGG>TGG	p.R110W
Pat_45	Pre-Treatment	LDLRAP1	26119	37	1	25889602	25889602	Missense_Mutation	SNP	G	A	4	125	c.574G>A	c.(574-576)GTC>ATC	p.V192I
Pat_45	Pre-Treatment	SESN2	83667	37	1	28598946	28598946	Missense_Mutation	SNP	G	A	4	88	c.506G>A	c.(505-507)CGG>CAG	p.R169Q
Pat_45	Pre-Treatment	ZSCAN20	7579	37	1	33959999	33959999	Nonsense_Mutation	SNP	G	A	4	104	c.2055G>A	c.(2053-2055)TGG>TGA	p.W685*
Pat_45	Pre-Treatment	CSMD2	114784	37	1	34006125	34006125	Missense_Mutation	SNP	G	A	4	71	c.9199C>T	c.(9199-9201)CCT>TCT	p.P3067S
Pat_45	Pre-Treatment	EIF2C1	26523	37	1	36358825	36358825	Missense_Mutation	SNP	C	T	10	97	c.458C>T	c.(457-459)CCC>CTC	p.P153L
Pat_45	Pre-Treatment	KIAA0754	643314	37	1	39879817	39879817	Missense_Mutation	SNP	G	A	3	11	c.3880G>A	c.(3880-3882)GCC>ACC	p.A1294T
Pat_45	Pre-Treatment	ZNF691	51058	37	1	43317387	43317387	Missense_Mutation	SNP	G	A	5	153	c.839G>A	c.(838-840)CGG>CAG	p.R280Q
Pat_45	Pre-Treatment	FAM151A	338094	37	1	55076117	55076117	Missense_Mutation	SNP	C	T	4	97	c.1052G>A	c.(1051-1053)GGC>GAC	p.G351D
Pat_45	Pre-Treatment	USP24	23358	37	1	55567369	55567369	Missense_Mutation	SNP	G	A	4	67	c.4553C>T	c.(4552-4554)CCC>CTC	p.P1518L
Pat_45	Pre-Treatment	USP24	23358	37	1	55590162	55590162	Missense_Mutation	SNP	C	T	4	38	c.3620G>A	c.(3619-3621)CGA>CAA	p.R1207Q
Pat_45	Pre-Treatment	LRRC8D	55144	37	1	90401185	90401185	Missense_Mutation	SNP	C	T	42	156	c.2558C>T	c.(2557-2559)CCC>CTC	p.P853L
Pat_45	Pre-Treatment	C1orf146	388649	37	1	92707815	92707815	Missense_Mutation	SNP	G	A	36	190	c.113G>A	c.(112-114)CGA>CAA	p.R38Q
Pat_45	Pre-Treatment	CDC14A	8556	37	1	100964760	100964760	Missense_Mutation	SNP	G	A	4	123	c.1697G>A	c.(1696-1698)CGA>CAA	p.R566Q
Pat_45	Pre-Treatment	SORT1	6272	37	1	109869773	109869773	Missense_Mutation	SNP	C	T	15	104	c.1484G>A	c.(1483-1485)GGG>GAG	p.G495E
Pat_45	Pre-Treatment	RBM15	64783	37	1	110882755	110882755	Missense_Mutation	SNP	G	A	4	107	c.728G>A	c.(727-729)CGG>CAG	p.R243Q
Pat_45	Pre-Treatment	PTGFRN	5738	37	1	117527332	117527332	Missense_Mutation	SNP	C	T	4	62	c.2198C>T	c.(2197-2199)GCG>GTG	p.A733V
Pat_45	Pre-Treatment	NBPF10	100132406	37	1	145360576	145360576	Missense_Mutation	SNP	T	A	11	81	c.9426T>A	c.(9424-9426)GAT>GAA	p.D3142E
Pat_45	Pre-Treatment	ANKRD35	148741	37	1	145560154	145560154	Missense_Mutation	SNP	G	A	4	61	c.640G>A	c.(640-642)GCT>ACT	p.A214T
Pat_45	Pre-Treatment	CTSS	1520	37	1	150730438	150730438	Missense_Mutation	SNP	G	A	3	60	c.145C>T	c.(145-147)CGT>TGT	p.R49C
Pat_45	Pre-Treatment	ZNF687	57592	37	1	151260469	151260469	Missense_Mutation	SNP	C	T	4	86	c.1702C>T	c.(1702-1704)CGC>TGC	p.R568C
Pat_45	Pre-Treatment	CRNN	49860	37	1	152382821	152382821	Missense_Mutation	SNP	C	T	4	125	c.737G>A	c.(736-738)AGC>AAC	p.S246N
Pat_45	Pre-Treatment	DENND4B	9909	37	1	153912212	153912212	Missense_Mutation	SNP	G	A	3	47	c.1672C>T	c.(1672-1674)CGC>TGC	p.R558C
Pat_45	Pre-Treatment	C1orf43	25912	37	1	154180096	154180096	Nonsense_Mutation	SNP	G	A	4	103	c.595C>T	c.(595-597)CGA>TGA	p.R199*
Pat_45	Pre-Treatment	HAX1	10456	37	1	154247935	154247935	Missense_Mutation	SNP	G	A	6	272	c.730G>A	c.(730-732)GAA>AAA	p.E244K
Pat_45	Pre-Treatment	GON4L	54856	37	1	155764858	155764858	Missense_Mutation	SNP	C	T	4	151	c.1730G>A	c.(1729-1731)CGG>CAG	p.R577Q
Pat_45	Pre-Treatment	INSRR	3645	37	1	156816443	156816443	Missense_Mutation	SNP	C	T	4	46	c.1678G>A	c.(1678-1680)GTG>ATG	p.V560M
Pat_45	Pre-Treatment	FCRL5	83416	37	1	157512843	157512843	Missense_Mutation	SNP	G	A	4	70	c.929C>T	c.(928-930)ACC>ATC	p.T310I
Pat_45	Pre-Treatment	FCRL1	115350	37	1	157776892	157776892	Missense_Mutation	SNP	C	T	33	86	c.52G>A	c.(52-54)GAG>AAG	p.E18K
Pat_45	Pre-Treatment	OR10T2	128360	37	1	158368742	158368742	Missense_Mutation	SNP	G	A	3	44	c.515C>T	c.(514-516)CCC>CTC	p.P172L
Pat_45	Pre-Treatment	CRP	1401	37	1	159683787	159683787	Missense_Mutation	SNP	C	T	19	107	c.203G>A	c.(202-204)AGT>AAT	p.S68N
Pat_45	Pre-Treatment	ARHGAP30	257106	37	1	161021356	161021356	Nonsense_Mutation	SNP	G	A	4	103	c.1168C>T	c.(1168-1170)CGA>TGA	p.R390*
Pat_45	Pre-Treatment	RGS5	8490	37	1	163122354	163122354	Missense_Mutation	SNP	C	T	225	307	c.370G>A	c.(370-372)GAG>AAG	p.E124K
Pat_45	Pre-Treatment	DUSP27	92235	37	1	167096607	167096607	Missense_Mutation	SNP	C	T	4	113	c.2239C>T	c.(2239-2241)CGC>TGC	p.R747C
Pat_45	Pre-Treatment	RC3H1	149041	37	1	173907863	173907864	Missense_Mutation	DNP	GG	AA	8	156	.3397_3398CC>T	c.(3397-3399)CCT>TTT	p.P1133F
Pat_45	Pre-Treatment	TNN	63923	37	1	175087853	175087853	Missense_Mutation	SNP	G	A	4	93	c.2543G>A	c.(2542-2544)AGC>AAC	p.S848N
Pat_45	Pre-Treatment	ASTN1	460	37	1	176853559	176853559	Missense_Mutation	SNP	G	A	5	104	c.3142C>T	c.(3142-3144)CCA>TCA	p.P1048S
Pat_45	Pre-Treatment	CACNA1E	777	37	1	181690901	181690901	Missense_Mutation	SNP	C	T	4	90	c.1964C>T	c.(1963-1965)ACG>ATG	p.T655M

Pat_45	Pre-Treatment	RNASEL	6041	37	1	182555277	182555277	Missense_Mutation	SNP	G	A	4	81	c.665C>T	c.(664-666)ACG>ATG	p.T222M
Pat_45	Pre-Treatment	FAM129A	116496	37	1	184777287	184777287	Missense_Mutation	SNP	C	T	6	157	c.1256G>A	c.(1255-1257)CGC>CAC	p.R419H
Pat_45	Pre-Treatment	DENND1B	163486	37	1	197479988	197479988	Missense_Mutation	SNP	G	A	4	98	c.1870C>T	c.(1870-1872)CCT>TCT	p.P624S
Pat_45	Pre-Treatment	SHISA4	149345	37	1	201860675	201860675	Missense_Mutation	SNP	C	T	53	63	c.526C>T	c.(526-528)CCC>TCC	p.P176S
Pat_45	Pre-Treatment	MDM4	4194	37	1	204515928	204515928	Missense_Mutation	SNP	A	G	3	92	c.826A>G	c.(826-828)ATT>GTT	p.I276V
Pat_45	Pre-Treatment	DSTYK	25778	37	1	205156710	205156710	Missense_Mutation	SNP	T	C	14	70	c.490A>G	c.(490-492)AGC>GGC	p.S164G
Pat_45	Pre-Treatment	CR1	1378	37	1	207758068	207758068	Missense_Mutation	SNP	G	A	25	152	c.4027G>A	c.(4027-4029)GGA>AGA	p.G1343R
Pat_45	Pre-Treatment	RCOR3	55758	37	1	211487015	211487015	Missense_Mutation	SNP	C	T	17	128	c.1393C>T	c.(1393-1395)CGT>TGT	p.R465C
Pat_45	Pre-Treatment	TMEM63A	9725	37	1	226044656	226044656	Missense_Mutation	SNP	G	A	4	51	c.1439C>T	c.(1438-1440)CCC>CTC	p.P480L
Pat_45	Pre-Treatment	LEFTY2	7044	37	1	226128594	226128594	Nonsense_Mutation	SNP	G	A	9	32	c.247C>T	c.(247-249)CGA>TGA	p.R83*
Pat_45	Pre-Treatment	TRIM67	440730	37	1	231335945	231335945	Missense_Mutation	SNP	G	A	5	209	c.1315G>A	c.(1315-1317)GGA>AGA	p.G439R
Pat_45	Pre-Treatment	NID1	4811	37	1	236157029	236157029	Missense_Mutation	SNP	C	T	6	23	c.2671G>A	c.(2671-2673)GGC>AGC	p.G891S
Pat_45	Pre-Treatment	OR2G6	391211	37	1	248684984	248684984	Missense_Mutation	SNP	C	T	59	117	c.37C>T	c.(37-39)CTT>TTT	p.L13F
Pat_45	Pre-Treatment	DIP2C	22982	37	10	518453	518453	Missense_Mutation	SNP	G	A	4	88	c.194C>T	c.(193-195)CCT>CTT	p.P65L
Pat_45	Pre-Treatment	TUBAL3	79861	37	10	5437346	5437346	Missense_Mutation	SNP	G	A	34	94	c.340C>T	c.(340-342)CGT>TGT	p.R114C
Pat_45	Pre-Treatment	C10orf18	54906	37	10	5781863	5781863	Missense_Mutation	SNP	G	A	4	108	c.1730G>A	c.(1729-1731)CGA>CAA	p.R577Q
Pat_45	Pre-Treatment	KIAA1217	56243	37	10	24820827	24820827	Missense_Mutation	SNP	C	T	4	62	c.3151C>T	c.(3151-3153)CCT>TCT	p.P1051S
Pat_45	Pre-Treatment	ARHGAP22	58504	37	10	49658349	49658349	Missense_Mutation	SNP	G	A	2	4	c.1823C>T	c.(1822-1824)GCC>GTC	p.A608V
Pat_45	Pre-Treatment	RHOBTB1	9886	37	10	62671193	62671193	Nonsense_Mutation	SNP	G	T	6	128	c.108C>A	c.(106-108)TGC>TGA	p.C36*
Pat_45	Pre-Treatment	ARID5B	84159	37	10	63851728	63851728	Missense_Mutation	SNP	C	T	5	100	c.2506C>T	c.(2506-2508)CAT>TAT	p.H836Y
Pat_45	Pre-Treatment	CYP2C18	1562	37	10	96447632	96447632	Missense_Mutation	SNP	G	A	33	86	c.274G>A	c.(274-276)GAG>AAG	p.E92K
Pat_45	Pre-Treatment	CYP2C8	1558	37	10	96802652	96802652	Missense_Mutation	SNP	G	A	31	64	c.1144C>T	c.(1144-1146)CCC>TCC	p.P382S
Pat_45	Pre-Treatment	C10orf2	56652	37	10	102747987	102747987	Missense_Mutation	SNP	G	A	4	60	c.20G>A	c.(19-21)AGT>AAT	p.S7N
Pat_45	Pre-Treatment	TRIM8	81603	37	10	104416597	104416597	Missense_Mutation	SNP	C	T	4	96	c.1142C>T	c.(1141-1143)ACG>ATG	p.T381M
Pat_45	Pre-Treatment	GSTO1	9446	37	10	106014944	106014944	Missense_Mutation	SNP	C	T	3	70	c.58C>T	c.(58-60)CCG>TCG	p.P20S
Pat_45	Pre-Treatment	CCDC147	159686	37	10	106118145	106118145	Missense_Mutation	SNP	T	C	27	48	c.56T>C	c.(55-57)ATG>ACG	p.M19T
Pat_45	Pre-Treatment	TDRD1	56165	37	10	115985820	115985820	Missense_Mutation	SNP	G	T	4	133	c.3020G>T	c.(3019-3021)TGG>TTG	p.W1007L
Pat_45	Pre-Treatment	GPR26	2849	37	10	125434408	125434408	Missense_Mutation	SNP	G	A	4	15	c.743G>A	c.(742-744)GGG>GAG	p.G248E
Pat_45	Pre-Treatment	PKP3	11187	37	11	397603	397603	Missense_Mutation	SNP	G	A	4	55	c.1009G>A	c.(1009-1011)GTG>ATG	p.V337M
Pat_45	Pre-Treatment	SYT8	90019	37	11	1856367	1856367	Missense_Mutation	SNP	C	T	3	33	c.74C>T	c.(73-75)CCG>CTG	p.P25L
Pat_45	Pre-Treatment	OSBPL5	114879	37	11	3128545	3128545	Missense_Mutation	SNP	G	A	3	51	c.1007C>T	c.(1006-1008)CCG>CTG	p.P336L
Pat_45	Pre-Treatment	NUP98	4928	37	11	3792977	3792977	Splice_Site	SNP	C	T	4	88	c.784_splice	c.e7+1	p.S262_splice
Pat_45	Pre-Treatment	OR52B2	255725	37	11	6191508	6191508	Missense_Mutation	SNP	G	A	21	31	c.49C>T	c.(49-51)CCT>TCT	p.P17S
Pat_45	Pre-Treatment	SMPD1	6609	37	11	6415448	6415448	Missense_Mutation	SNP	G	A	4	102	c.1507G>A	c.(1507-1509)GAT>AAT	p.D503N
Pat_45	Pre-Treatment	TRIM3	10612	37	11	6478003	6478003	Missense_Mutation	SNP	G	A	4	50	c.953C>T	c.(952-954)ACG>ATG	p.T318M
Pat_45	Pre-Treatment	MICAL2	9645	37	11	12183950	12183950	Missense_Mutation	SNP	C	T	4	101	c.248C>T	c.(247-249)TCG>TTG	p.S83L
Pat_45	Pre-Treatment	ABCC8	6833	37	11	17482154	17482154	Missense_Mutation	SNP	G	A	4	58	c.892C>T	c.(892-894)CGC>TGC	p.R298C
Pat_45	Pre-Treatment	IGSF22	283284	37	11	18737158	18737158	Nonsense_Mutation	SNP	C	T	4	109	c.1352G>A	c.(1351-1353)TGG>TAG	p.W451*
Pat_45	Pre-Treatment	GAS2	2620	37	11	22696432	22696432	Missense_Mutation	SNP	G	A	12	68	c.17G>A	c.(16-18)AGC>AAC	p.S6N
Pat_45	Pre-Treatment	SLC5A12	159963	37	11	26743146	26743146	Missense_Mutation	SNP	C	T	3	50	c.116G>A	c.(115-117)CGA>CAA	p.R39Q
Pat_45	Pre-Treatment	CAPRIN1	4076	37	11	34107903	34107903	Missense_Mutation	SNP	G	A	4	131	c.1174G>A	c.(1174-1176)GCA>ACA	p.A392T
Pat_45	Pre-Treatment	CAT	847	37	11	34478267	34478267	Missense_Mutation	SNP	G	A	5	219	c.959G>A	c.(958-960)CGG>CAG	p.R320Q
Pat_45	Pre-Treatment	SLC35C1	55343	37	11	45832791	45832791	Missense_Mutation	SNP	T	C	2	4	c.1000T>C	c.(1000-1002)TCC>CCC	p.S334P
Pat_45	Pre-Treatment	PTPRJ	5795	37	11	48185942	48185942	Missense_Mutation	SNP	G	A	4	49	c.3730G>A	c.(3730-3732)GGA>AGA	p.G1244R
Pat_45	Pre-Treatment	OR5M1	390168	37	11	56380431	56380432	Missense_Mutation	DNP	GG	AA	7	57	c.547_548CC>TT	c.(547-549)CCT>TTT	p.P183F
Pat_45	Pre-Treatment	OR9G9	504191	37	11	56468324	56468324	Missense_Mutation	SNP	A	T	6	150	c.461A>T	c.(460-462)AAC>ATC	p.N154I
Pat_45	Pre-Treatment	SSRP1	6749	37	11	57099626	57099626	Missense_Mutation	SNP	C	T	4	123	c.1001G>A	c.(1000-1002)GGG>GAG	p.G334E

Pat_45	Pre-Treatment	CTNND1	1500	37	11	57564344	57564344	Missense_Mutation	SNP	C	T	35	161	c.836C>T	c.(835-837)CCT>CTT	p.P279L
Pat_45	Pre-Treatment	OR5B17	219965	37	11	58126271	58126271	Missense_Mutation	SNP	G	A	9	53	c.272C>T	c.(271-273)TCC>TTC	p.S91F
Pat_45	Pre-Treatment	MTA2	9219	37	11	62366009	62366009	Missense_Mutation	SNP	G	A	7	413	c.293C>T	c.(292-294)CCA>CTA	p.P98L
Pat_45	Pre-Treatment	UBXN1	51035	37	11	62444096	62444096	Missense_Mutation	SNP	G	A	2	3	c.860C>T	c.(859-861)GCT>GTT	p.A287V
Pat_45	Pre-Treatment	DPF2	5977	37	11	65108977	65108977	Nonsense_Mutation	SNP	C	T	4	110	c.409C>T	c.(409-411)CGA>TGA	p.R137*
Pat_45	Pre-Treatment	RBM14	10432	37	11	66393948	66393948	Missense_Mutation	SNP	C	T	4	98	c.1819C>T	c.(1819-1821)CGT>TGT	p.R607C
Pat_45	Pre-Treatment	SYT12	91683	37	11	66807334	66807334	Missense_Mutation	SNP	G	A	3	61	c.281G>A	c.(280-282)CGC>CAC	p.R94H
Pat_45	Pre-Treatment	ACY3	91703	37	11	67410203	67410203	Missense_Mutation	SNP	C	T	4	90	c.952G>A	c.(952-954)GCT>ACT	p.A318T
Pat_45	Pre-Treatment	CHKA	1119	37	11	67842213	67842213	Missense_Mutation	SNP	G	A	32	114	c.601C>T	c.(601-603)CCC>TCC	p.P201S
Pat_45	Pre-Treatment	ARHGEF17	9828	37	11	73076914	73076914	Missense_Mutation	SNP	G	A	3	43	c.5917G>A	c.(5917-5919)GTC>ATC	p.V1973I
Pat_45	Pre-Treatment	RELT	84957	37	11	73101611	73101611	Missense_Mutation	SNP	C	T	22	85	c.61C>T	c.(61-63)CTC>TTC	p.L21F
Pat_45	Pre-Treatment	RELT	84957	37	11	73106179	73106179	Missense_Mutation	SNP	C	T	4	71	c.1094C>T	c.(1093-1095)TCT>TTT	p.S365F
Pat_45	Pre-Treatment	ARRB1	408	37	11	74994459	74994459	Missense_Mutation	SNP	G	A	6	29	c.226C>T	c.(226-228)CGC>TGC	p.R76C
Pat_45	Pre-Treatment	HEPHL1	341208	37	11	93800692	93800692	Missense_Mutation	SNP	C	T	18	125	c.839C>T	c.(838-840)CCG>CTG	p.P280L
Pat_45	Pre-Treatment	HTR3A	3359	37	11	113853870	113853870	Missense_Mutation	SNP	C	T	4	96	c.421C>T	c.(421-423)CCG>TCG	p.P141S
Pat_45	Pre-Treatment	IL10RA	3587	37	11	117860281	117860281	Missense_Mutation	SNP	G	A	4	62	c.313G>A	c.(313-315)GGC>AGC	p.G105S
Pat_45	Pre-Treatment	C2CD2L	9854	37	11	118983554	118983554	Nonsense_Mutation	SNP	C	T	4	107	c.1357C>T	c.(1357-1359)CAG>TAG	p.Q453*
Pat_45	Pre-Treatment	C11orf63	79864	37	11	122756805	122756805	Missense_Mutation	SNP	G	A	5	235	c.248G>A	c.(247-249)GGA>GAA	p.G83E
Pat_45	Pre-Treatment	VWA5A	4013	37	11	124015943	124015943	Splice_Site	SNP	G	A	4	81	c.2155_splice	c.e18-1	p.L719_splice
Pat_45	Pre-Treatment	OR8B2	26595	37	11	124252879	124252879	Missense_Mutation	SNP	C	T	14	50	c.361G>A	c.(361-363)GAT>AAT	p.D121N
Pat_45	Pre-Treatment	VSIG2	23584	37	11	124621425	124621425	Missense_Mutation	SNP	C	T	3	48	c.113G>A	c.(112-114)GGG>GAG	p.G38E
Pat_45	Pre-Treatment	CCDC15	80071	37	11	124857870	124857870	Missense_Mutation	SNP	A	G	6	264	c.1748A>G	c.(1747-1749)CAG>CGG	p.Q583R
Pat_45	Pre-Treatment	WNK1	65125	37	12	970285	970285	Missense_Mutation	SNP	G	A	5	205	c.1727G>A	c.(1726-1728)CGG>CAG	p.R576Q
Pat_45	Pre-Treatment	WNK1	65125	37	12	970384	970384	Missense_Mutation	SNP	C	T	4	104	c.1826C>T	c.(1825-1827)GCT>GTT	p.A609V
Pat_45	Pre-Treatment	CACNA2D4	93589	37	12	1910248	1910249	Missense_Mutation	DNP	GG	TT	25	28	.2828_2829CC>A	c.(2827-2829)CCC>CAA	p.P943Q
Pat_45	Pre-Treatment	PRB1	5542	37	12	11506208	11506208	Missense_Mutation	SNP	G	A	59	73	c.829C>T	c.(829-831)CCT>TCT	p.P277S
Pat_45	Pre-Treatment	PRB2	653247	37	12	11546195	11546195	Missense_Mutation	SNP	T	G	4	62	c.817A>C	c.(817-819)AAA>CAA	p.K273Q
Pat_45	Pre-Treatment	PLEKHA5	54477	37	12	19514631	19514631	Missense_Mutation	SNP	T	A	4	85	c.3101T>A	c.(3100-3102)GTT>GAT	p.V1034D
Pat_45	Pre-Treatment	PDE3A	5139	37	12	20807046	20807046	Missense_Mutation	SNP	G	A	4	56	c.3091G>A	c.(3091-3093)GAT>AAT	p.D1031N
Pat_45	Pre-Treatment	SLCO1B3	28234	37	12	21030726	21030726	Missense_Mutation	SNP	A	G	8	113	c.991A>G	c.(991-993)AGC>GGC	p.S331G
Pat_45	Pre-Treatment	PKP2	5318	37	12	32955384	32955384	Missense_Mutation	SNP	G	A	135	133	c.2252C>T	c.(2251-2253)TCG>TTG	p.S751L
Pat_45	Pre-Treatment	PKP2	5318	37	12	33021871	33021871	Missense_Mutation	SNP	G	A	4	136	c.1160C>T	c.(1159-1161)GCT>GTT	p.A387V
Pat_45	Pre-Treatment	FAM113B	91523	37	12	47629951	47629951	Missense_Mutation	SNP	G	A	4	117	c.1105G>A	c.(1105-1107)GTC>ATC	p.V369I
Pat_45	Pre-Treatment	COL2A1	1280	37	12	48376648	48376648	Missense_Mutation	SNP	C	T	3	61	c.2176G>A	c.(2176-2178)GGC>AGC	p.G726S
Pat_45	Pre-Treatment	SPATS2	65244	37	12	49893916	49893916	Missense_Mutation	SNP	G	A	4	58	c.767G>A	c.(766-768)CGA>CAA	p.R256Q
Pat_45	Pre-Treatment	SPATS2	65244	37	12	49919815	49919815	Missense_Mutation	SNP	G	A	3	68	c.1415G>A	c.(1414-1416)AGT>AAT	p.S472N
Pat_45	Pre-Treatment	POU6F1	5463	37	12	51586223	51586223	Missense_Mutation	SNP	G	A	25	49	c.281C>T	c.(280-282)CCC>CTC	p.P94L
Pat_45	Pre-Treatment	SCN8A	6334	37	12	52056612	52056612	Missense_Mutation	SNP	G	A	5	168	c.11G>A	c.(10-12)CGG>CAG	p.R4Q
Pat_45	Pre-Treatment	SMARCC2	6601	37	12	56558236	56558236	Missense_Mutation	SNP	G	A	4	99	c.3419C>T	c.(3418-3420)GCG>GTG	p.A1140V
Pat_45	Pre-Treatment	SMARCC2	6601	37	12	56574800	56574800	Missense_Mutation	SNP	G	A	4	93	c.1042C>T	c.(1042-1044)CCA>TCA	p.P348S
Pat_45	Pre-Treatment	PAN2	9924	37	12	56712197	56712197	Missense_Mutation	SNP	G	A	4	82	c.3398C>T	c.(3397-3399)ACC>ATC	p.T1133I
Pat_45	Pre-Treatment	TIMELESS	8914	37	12	56824014	56824014	Missense_Mutation	SNP	G	A	4	65	c.961C>T	c.(961-963)CGT>TGT	p.R321C
Pat_45	Pre-Treatment	NT5DC3	51559	37	12	104187760	104187760	Missense_Mutation	SNP	C	T	5	185	c.769G>A	c.(769-771)GTC>ATC	p.V257I
Pat_45	Pre-Treatment	NUAK1	9891	37	12	106461685	106461685	Missense_Mutation	SNP	C	T	3	78	c.881G>A	c.(880-882)CGG>CAG	p.R294Q
Pat_45	Pre-Treatment	SART3	9733	37	12	108920304	108920304	Missense_Mutation	SNP	C	T	4	84	c.1942G>A	c.(1942-1944)GAG>AAG	p.E648K
Pat_45	Pre-Treatment	DAO	1610	37	12	109278786	109278786	Missense_Mutation	SNP	C	T	3	56	c.4C>T	c.(4-6)CGT>TGT	p.R2C
Pat_45	Pre-Treatment	ACACB	32	37	12	109623454	109623454	Missense_Mutation	SNP	T	G	24	28	c.1889T>G	c.(1888-1890)GTG>GGG	p.V630G

Pat_45	Pre-Treatment	ATP2A2	488	37	12	110784091	110784091	Missense_Mutation	SNP	C	T	3	34	c.2945C>T	c.(2944-2946)ACG>ATG	p.T982M
Pat_45	Pre-Treatment	IQCD	115811	37	12	113645722	113645722	Missense_Mutation	SNP	C	T	4	120	c.250G>A	c.(250-252)GGG>AGG	p.G84R
Pat_45	Pre-Treatment	ACADS	35	37	12	121174813	121174813	Missense_Mutation	SNP	C	T	2	4	c.235C>T	c.(235-237)CTT>TTT	p.L79F
Pat_45	Pre-Treatment	KDM2B	84678	37	12	121880476	121880476	Missense_Mutation	SNP	C	T	2	3	c.2768G>A	c.(2767-2769)GGG>GAG	p.G923E
Pat_45	Pre-Treatment	VPS33A	65082	37	12	122745944	122745944	Missense_Mutation	SNP	C	T	4	120	c.347G>A	c.(346-348)CGC>CAC	p.R116H
Pat_45	Pre-Treatment	VPS37B	79720	37	12	123355437	123355437	Missense_Mutation	SNP	C	T	4	109	c.283G>A	c.(283-285)GAC>AAC	p.D95N
Pat_45	Pre-Treatment	DHX37	57647	37	12	125455913	125455913	Missense_Mutation	SNP	C	T	4	32	c.1126G>A	c.(1126-1128)GAG>AAG	p.E376K
Pat_45	Pre-Treatment	MTIF3	219402	37	13	28014482	28014482	Missense_Mutation	SNP	G	A	4	111	c.104C>T	c.(103-105)GCA>GTA	p.A35V
Pat_45	Pre-Treatment	POLR1D	51082	37	13	28239855	28239855	Missense_Mutation	SNP	G	T	27	43	c.134G>T	c.(133-135)AGA>ATA	p.R45I
Pat_45	Pre-Treatment	STARD13	90627	37	13	33704351	33704351	Missense_Mutation	SNP	G	A	24	56	c.463C>T	c.(463-465)CGT>TGT	p.R155C
Pat_45	Pre-Treatment	FREM2	341640	37	13	39264041	39264041	Missense_Mutation	SNP	G	A	4	83	c.2560G>A	c.(2560-2562)GTG>ATG	p.V854M
Pat_45	Pre-Treatment	NEK5	341676	37	13	52639613	52639613	Missense_Mutation	SNP	G	A	4	123	c.2057C>T	c.(2056-2058)TCT>TTT	p.S686F
Pat_45	Pre-Treatment	DCT	1638	37	13	95131376	95131376	Missense_Mutation	SNP	C	T	10	57	c.134G>A	c.(133-135)GGT>GAT	p.G45D
Pat_45	Pre-Treatment	GPR18	2841	37	13	99907672	99907672	Missense_Mutation	SNP	G	A	4	112	c.455C>T	c.(454-456)ACG>ATG	p.T152M
Pat_45	Pre-Treatment	SLC10A2	6555	37	13	103703661	103703661	Missense_Mutation	SNP	G	A	43	71	c.707C>T	c.(706-708)GCG>GTG	p.A236V
Pat_45	Pre-Treatment	MYO16	23026	37	13	109793674	109793675	Missense_Mutation	DNP	GG	AA	10	14	.5048_5049GG>A	c.(5047-5049)AGG>AAA	p.R1683K
Pat_45	Pre-Treatment	COL4A1	1282	37	13	110839513	110839513	Missense_Mutation	SNP	G	A	5	221	c.1700C>T	c.(1699-1701)CCG>CTG	p.P567L
Pat_45	Pre-Treatment	OR4K14	122740	37	14	20483294	20483294	Missense_Mutation	SNP	G	A	28	84	c.59C>T	c.(58-60)TCA>TTA	p.S20L
Pat_45	Pre-Treatment	RNASE11	122651	37	14	21052064	21052064	Missense_Mutation	SNP	C	T	4	110	c.570G>A	c.(568-570)ATG>ATA	p.M190I
Pat_45	Pre-Treatment	ACIN1	22985	37	14	23530699	23530699	Missense_Mutation	SNP	G	A	5	187	c.3406C>T	c.(3406-3408)CGG>TGG	p.R1136W
Pat_45	Pre-Treatment	FSCB	84075	37	14	44975115	44975115	Missense_Mutation	SNP	G	T	32	72	c.1076C>A	c.(1075-1077)CCT>CAT	p.P359H
Pat_45	Pre-Treatment	POLE2	5427	37	14	50140840	50140840	Splice_Site	SNP	C	T	10	655	c.417_splice	c.e5+1	p.Q139_splice
Pat_45	Pre-Treatment	POLE2	5427	37	14	50140909	50140909	Missense_Mutation	SNP	G	A	133	300	c.349C>T	c.(349-351)CCA>TCA	p.P117S
Pat_45	Pre-Treatment	DACT1	51339	37	14	59113551	59113551	Missense_Mutation	SNP	C	T	4	113	c.2210C>T	c.(2209-2211)ACC>ATC	p.T737I
Pat_45	Pre-Treatment	GPHB5	122876	37	14	63779784	63779784	Missense_Mutation	SNP	C	T	3	15	c.250G>A	c.(250-252)GTA>ATA	p.V84I
Pat_45	Pre-Treatment	SYNE2	23224	37	14	64586214	64586214	Missense_Mutation	SNP	G	A	4	131	c.12910G>A	c.(12910-12912)GAT>AAT	p.D4304N
Pat_45	Pre-Treatment	SMOC1	64093	37	14	70490077	70490077	Missense_Mutation	SNP	C	T	5	219	c.1204C>T	c.(1204-1206)CGG>TGG	p.R402W
Pat_45	Pre-Treatment	TMEM63C	57156	37	14	77715198	77715198	Missense_Mutation	SNP	C	T	14	65	c.1853C>T	c.(1852-1854)CCC>CTC	p.P618L
Pat_45	Pre-Treatment	C14orf102	55051	37	14	90778814	90778814	Missense_Mutation	SNP	C	T	5	198	c.481G>A	c.(481-483)GAA>AAA	p.E161K
Pat_45	Pre-Treatment	CATSPERB	79820	37	14	92157893	92157893	Missense_Mutation	SNP	T	A	66	130	c.838A>T	c.(838-840)AGG>TGG	p.R280W
Pat_45	Pre-Treatment	MOAP1	64112	37	14	93650424	93650424	Missense_Mutation	SNP	A	C	7	242	c.164T>G	c.(163-165)ATG>AGG	p.M55R
Pat_45	Pre-Treatment	ATG2B	55102	37	14	96752132	96752132	Missense_Mutation	SNP	C	T	4	135	c.6197G>A	c.(6196-6198)CGG>CAG	p.R2066Q
Pat_45	Pre-Treatment	MARK3	4140	37	14	103932728	103932728	Missense_Mutation	SNP	C	T	4	118	c.946C>T	c.(946-948)CTC>TTC	p.L316F
Pat_45	Pre-Treatment	AHNAK2	113146	37	14	105413426	105413426	Missense_Mutation	SNP	C	T	4	135	c.8362G>A	c.(8362-8364)GCA>ACA	p.A2788T
Pat_45	Pre-Treatment	C15orf2	23742	37	15	24922887	24922887	Missense_Mutation	SNP	C	T	17	62	c.1873C>T	c.(1873-1875)CCA>TCA	p.P625S
Pat_45	Pre-Treatment	BMF	90427	37	15	40396431	40396431	Nonsense_Mutation	SNP	G	A	6	407	c.403C>T	c.(403-405)CGA>TGA	p.R135*
Pat_45	Pre-Treatment	BAHD1	22893	37	15	40756213	40756213	Missense_Mutation	SNP	G	A	3	36	c.1969G>A	c.(1969-1971)GAG>AAG	p.E657K
Pat_45	Pre-Treatment	SPTBN5	51332	37	15	42155949	42155949	Missense_Mutation	SNP	C	T	4	127	c.6997G>A	c.(6997-6999)GTG>ATG	p.V2333M
Pat_45	Pre-Treatment	SPG11	80208	37	15	44892732	44892732	Missense_Mutation	SNP	G	A	8	323	c.3619C>T	c.(3619-3621)CGG>TGG	p.R1207W
Pat_45	Pre-Treatment	SQRDL	58472	37	15	45983208	45983208	Missense_Mutation	SNP	T	A	62	151	c.1333T>A	c.(1333-1335)TTT>ATT	p.F445I
Pat_45	Pre-Treatment	C15orf33	196951	37	15	49800512	49800512	Nonsense_Mutation	SNP	C	T	18	86	c.908G>A	c.(907-909)TGG>TAG	p.W303*
Pat_45	Pre-Treatment	CYP19A1	1588	37	15	51520084	51520084	Nonsense_Mutation	SNP	G	A	60	138	c.343C>T	c.(343-345)CGA>TGA	p.R115*
Pat_45	Pre-Treatment	FAM81A	145773	37	15	59784573	59784573	Missense_Mutation	SNP	G	A	3	52	c.398G>A	c.(397-399)CGA>CAA	p.R133Q
Pat_45	Pre-Treatment	VPS13C	54832	37	15	62160902	62160902	Missense_Mutation	SNP	G	A	4	93	c.10819C>T	c.(10819-10821)CGT>TGT	p.R3607C
Pat_45	Pre-Treatment	USP3	9960	37	15	63862770	63862771	Missense_Mutation	DNP	GT	AA	50	170	c.900_901GT>AA	898-903)AAGTGT>AAAA	p.C301S
Pat_45	Pre-Treatment	PIAS1	8554	37	15	68466136	68466136	Missense_Mutation	SNP	G	A	4	71	c.1075G>A	c.(1075-1077)GCA>ACA	p.A359T
Pat_45	Pre-Treatment	PARP6	56965	37	15	72543226	72543226	Missense_Mutation	SNP	G	A	3	51	c.1378C>T	c.(1378-1380)CGG>TGG	p.R460W

Pat_45	Pre-Treatment	CYP1A1	1543	37	15	75014865	75014865	Missense_Mutation	SNP	C	T	4	71	c.574G>A	c.(574-576)GTA>ATA	p.V192I
Pat_45	Pre-Treatment	SNX33	257364	37	15	75949506	75949506	Missense_Mutation	SNP	C	T	5	183	c.1675C>T	c.(1675-1677)CGG>TGG	p.R559W
Pat_45	Pre-Treatment	LOC645752	645752	37	15	78211546	78211546	Missense_Mutation	SNP	G	A	39	71	c.221C>T	c.(220-222)TCC>TTC	p.S74F
Pat_45	Pre-Treatment	KIAA1024	23251	37	15	79755620	79755620	Missense_Mutation	SNP	G	A	4	69	c.2510G>A	c.(2509-2511)CGG>CAG	p.R837Q
Pat_45	Pre-Treatment	TM6SF1	53346	37	15	83776476	83776476	Missense_Mutation	SNP	C	T	4	14	c.44C>T	c.(43-45)TCG>TTG	p.S15L
Pat_45	Pre-Treatment	BNC1	646	37	15	83932330	83932330	Missense_Mutation	SNP	C	T	23	43	c.1673G>A	c.(1672-1674)AGA>AAA	p.R558K
Pat_45	Pre-Treatment	ADAMTSL3	57188	37	15	84566671	84566671	Missense_Mutation	SNP	G	A	39	83	c.1529G>A	c.(1528-1530)GGA>GAA	p.G510E
Pat_45	Pre-Treatment	ACAN	176	37	15	89400555	89400555	Missense_Mutation	SNP	C	T	6	31	c.4739C>T	c.(4738-4740)GCT>GTT	p.A1580V
Pat_45	Pre-Treatment	MFGE8	4240	37	15	89444955	89444955	Missense_Mutation	SNP	G	A	12	41	c.697C>T	c.(697-699)CCC>TCC	p.P233S
Pat_45	Pre-Treatment	TTLL13	440307	37	15	90802123	90802123	Missense_Mutation	SNP	G	A	4	131	c.1316G>A	c.(1315-1317)CGG>CAG	p.R439Q
Pat_45	Pre-Treatment	WASH3P	374666	37	15	102515299	102515299	Missense_Mutation	SNP	G	A	3	20	c.523G>A	c.(523-525)GGC>AGC	p.G175S
Pat_45	Pre-Treatment	MRPL28	10573	37	16	420112	420112	Missense_Mutation	SNP	C	T	2	4	c.107G>A	c.(106-108)CGG>CAG	p.R36Q
Pat_45	Pre-Treatment	SOLH	6650	37	16	597460	597460	Missense_Mutation	SNP	G	A	2	0	c.622G>A	c.(622-624)GGT>AGT	p.G208S
Pat_45	Pre-Treatment	NDUFB10	4716	37	16	2011166	2011166	Missense_Mutation	SNP	G	A	4	44	c.143G>A	c.(142-144)CGG>CAG	p.R48Q
Pat_45	Pre-Treatment	PKD1	5310	37	16	2167572	2167572	Missense_Mutation	SNP	G	T	2	0	c.1303C>A	c.(1303-1305)CAG>AAG	p.Q435K
Pat_45	Pre-Treatment	ZNF205	7755	37	16	3165844	3165844	Missense_Mutation	SNP	C	T	4	20	c.286C>T	c.(286-288)CGG>TGG	p.R96W
Pat_45	Pre-Treatment	CLUAP1	23059	37	16	3554783	3554783	Missense_Mutation	SNP	C	T	4	137	c.86C>T	c.(85-87)ACA>ATA	p.T29I
Pat_45	Pre-Treatment	CLUAP1	23059	37	16	3562394	3562394	Missense_Mutation	SNP	G	T	4	84	c.411G>T	c.(409-411)TTG>TTT	p.L137F
Pat_45	Pre-Treatment	KIAA0430	9665	37	16	15729949	15729949	Missense_Mutation	SNP	G	A	6	301	c.395C>T	c.(394-396)CCG>CTG	p.P132L
Pat_45	Pre-Treatment	GTF3C1	2975	37	16	27475716	27475716	Missense_Mutation	SNP	C	T	3	87	c.5797G>A	c.(5797-5799)GGT>AGT	p.G1933S
Pat_45	Pre-Treatment	SETD1A	9739	37	16	30976033	30976033	Missense_Mutation	SNP	T	C	3	71	c.970T>C	c.(970-972)TCC>CCC	p.S324P
Pat_45	Pre-Treatment	NUP93	9688	37	16	56782307	56782307	Missense_Mutation	SNP	C	T	3	45	c.148C>T	c.(148-150)CGC>TGC	p.R50C
Pat_45	Pre-Treatment	NLRC5	84166	37	16	57088981	57088981	Missense_Mutation	SNP	G	A	5	82	c.3634G>A	c.(3634-3636)GAG>AAG	p.E1212K
Pat_45	Pre-Treatment	CDH8	1006	37	16	61858972	61858972	Missense_Mutation	SNP	G	A	5	110	c.779C>T	c.(778-780)ACG>ATG	p.T260M
Pat_45	Pre-Treatment	CES2	8824	37	16	66973139	66973139	Missense_Mutation	SNP	G	A	4	104	c.493G>A	c.(493-495)GCA>ACA	p.A165T
Pat_45	Pre-Treatment	LRRC50	123872	37	16	84182710	84182710	Missense_Mutation	SNP	G	A	4	133	c.223G>A	c.(223-225)GCA>ACA	p.A75T
Pat_45	Pre-Treatment	ABR	29	37	17	1028606	1028606	Missense_Mutation	SNP	G	A	4	47	c.158C>T	c.(157-159)TCG>TTG	p.S53L
Pat_45	Pre-Treatment	PAFAH1B1	5048	37	17	2577437	2577437	Missense_Mutation	SNP	G	A	4	121	c.755G>A	c.(754-756)TGT>TAT	p.C252Y
Pat_45	Pre-Treatment	OR3A1	4994	37	17	3195798	3195798	Nonsense_Mutation	SNP	G	A	3	55	c.79C>T	c.(79-81)CAG>TAG	p.Q27*
Pat_45	Pre-Treatment	OR3A3	8392	37	17	3324354	3324354	Missense_Mutation	SNP	G	A	4	137	c.493G>A	c.(493-495)GCA>ACA	p.A165T
Pat_45	Pre-Treatment	C17orf74	201243	37	17	7329824	7329824	Nonsense_Mutation	SNP	C	T	4	97	c.514C>T	c.(514-516)CGA>TGA	p.R172*
Pat_45	Pre-Treatment	MYH10	4628	37	17	8424195	8424195	Splice_Site	SNP	C	T	4	82	c.2180_splice	c.e17+1	p.R727_splice
Pat_45	Pre-Treatment	MYH8	4626	37	17	10307736	10307736	Missense_Mutation	SNP	C	T	4	83	c.2599G>A	c.(2599-2601)GCC>ACC	p.A867T
Pat_45	Pre-Treatment	ELAC2	60528	37	17	12899865	12899865	Missense_Mutation	SNP	G	A	3	60	c.1658C>T	c.(1657-1659)ACG>ATG	p.T553M
Pat_45	Pre-Treatment	EVI2B	2124	37	17	29631910	29631910	Missense_Mutation	SNP	C	T	4	79	c.718G>A	c.(718-720)GGT>AGT	p.G240S
Pat_45	Pre-Treatment	AP2B1	163	37	17	33977594	33977594	Missense_Mutation	SNP	C	T	4	84	c.1582C>T	c.(1582-1584)CGC>TGC	p.R528C
Pat_45	Pre-Treatment	GGNBP2	79893	37	17	34945798	34945798	Missense_Mutation	SNP	G	A	5	188	c.2051G>A	c.(2050-2052)AGG>AAG	p.R684K
Pat_45	Pre-Treatment	SMARCE1	6605	37	17	38787103	38787103	Missense_Mutation	SNP	C	T	3	72	c.890G>A	c.(889-891)CGC>CAC	p.R297H
Pat_45	Pre-Treatment	KRT23	25984	37	17	39092582	39092582	Missense_Mutation	SNP	C	T	4	118	c.274G>A	c.(274-276)GCC>ACC	p.A92T
Pat_45	Pre-Treatment	KRT33A	3883	37	17	39502820	39502820	Missense_Mutation	SNP	G	A	4	81	c.977C>T	c.(976-978)GCG>GTG	p.A326V
Pat_45	Pre-Treatment	JUP	3728	37	17	39681184	39681184	Missense_Mutation	SNP	C	T	49	55	c.1060G>A	c.(1060-1062)GAT>AAT	p.D354N
Pat_45	Pre-Treatment	KCNH4	23415	37	17	40323967	40323967	Missense_Mutation	SNP	A	G	2	4	c.1034T>C	c.(1033-1035)CTG>CCG	p.L345P
Pat_45	Pre-Treatment	KCNH4	23415	37	17	40330137	40330137	Missense_Mutation	SNP	C	T	29	45	c.566G>A	c.(565-567)GGA>GAA	p.G189E
Pat_45	Pre-Treatment	BRCA1	672	37	17	41228590	41228590	Nonsense_Mutation	SNP	G	A	4	112	c.4399C>T	c.(4399-4401)CAG>TAG	p.Q1467*
Pat_45	Pre-Treatment	CDC27	996	37	17	45219248	45219248	Missense_Mutation	SNP	C	T	11	354	c.1522G>A	c.(1522-1524)GCC>ACC	p.A508T
Pat_45	Pre-Treatment	KPNB1	3837	37	17	45755440	45755440	Missense_Mutation	SNP	C	T	5	203	c.2132C>T	c.(2131-2133)CCG>CTG	p.P711L
Pat_45	Pre-Treatment	CBX1	10951	37	17	46153428	46153428	Missense_Mutation	SNP	G	A	3	49	c.253C>T	c.(253-255)CGC>TGC	p.R85C

Pat_45	Pre-Treatment	B4GALNT2	124872	37	17	47247085	47247085	Missense_Mutation	SNP	G	A	3	19	c.1696G>A	c.(1696-1698)GCA>ACA	p.A566T
Pat_45	Pre-Treatment	CA4	762	37	17	58234829	58234829	Missense_Mutation	SNP	G	A	3	57	c.310G>A	c.(310-312)GGA>AGA	p.G104R
Pat_45	Pre-Treatment	DDX42	11325	37	17	61886234	61886234	Missense_Mutation	SNP	G	A	6	254	c.1078G>A	c.(1078-1080)GTA>ATA	p.V360I
Pat_45	Pre-Treatment	HELZ	9931	37	17	65214908	65214908	Nonsense_Mutation	SNP	T	A	3	87	c.13A>T	c.(13-15)AGA>TGA	p.R5*
Pat_45	Pre-Treatment	NUP85	79902	37	17	73208149	73208149	Missense_Mutation	SNP	A	G	3	110	c.353A>G	c.(352-354)CAG>CGG	p.Q118R
Pat_45	Pre-Treatment	EVPL	2125	37	17	74005546	74005546	Missense_Mutation	SNP	G	A	3	51	c.3740C>T	c.(3739-3741)ACG>ATG	p.T1247M
Pat_45	Pre-Treatment	EVPL	2125	37	17	74019694	74019694	Missense_Mutation	SNP	C	G	2	4	c.240G>C	c.(238-240)CAG>CAC	p.Q80H
Pat_45	Pre-Treatment	CARD14	79092	37	17	78163634	78163634	Missense_Mutation	SNP	G	A	3	23	c.926G>A	c.(925-927)CGG>CAG	p.R309Q
Pat_45	Pre-Treatment	FLJ35220	284131	37	17	78402411	78402411	Nonsense_Mutation	SNP	C	T	2	2	c.730C>T	c.(730-732)CGA>TGA	p.R244*
Pat_45	Pre-Treatment	DLGAP1	9229	37	18	3582121	3582121	Missense_Mutation	SNP	C	T	4	110	c.1717G>A	c.(1717-1719)GGA>AGA	p.G573R
Pat_45	Pre-Treatment	CABLES1	91768	37	18	20815983	20815983	Missense_Mutation	SNP	G	A	3	93	c.1310G>A	c.(1309-1311)CGG>CAG	p.R437Q
Pat_45	Pre-Treatment	KIAA1012	22878	37	18	29447422	29447422	Missense_Mutation	SNP	T	G	27	83	c.2406A>C	c.(2404-2406)GAA>GAC	p.E802D
Pat_45	Pre-Treatment	DTNA	1837	37	18	32335949	32335949	Missense_Mutation	SNP	A	C	4	78	c.9A>C	c.(7-9)GAA>GAC	p.E3D
Pat_45	Pre-Treatment	SLC14A2	8170	37	18	43219790	43219790	Missense_Mutation	SNP	C	T	3	65	c.923C>T	c.(922-924)GCT>GTT	p.A308V
Pat_45	Pre-Treatment	PSTPIP2	9050	37	18	43579439	43579439	Missense_Mutation	SNP	C	T	4	131	c.479G>A	c.(478-480)CGG>CAG	p.R160Q
Pat_45	Pre-Treatment	MYO5B	4645	37	18	47432958	47432958	Nonsense_Mutation	SNP	G	A	17	36	c.2245C>T	c.(2245-2247)CGA>TGA	p.R749*
Pat_45	Pre-Treatment	ALPK2	115701	37	18	56247145	56247145	Missense_Mutation	SNP	C	G	9	36	c.863G>C	c.(862-864)AGT>ACT	p.S288T
Pat_45	Pre-Treatment	CDH7	1005	37	18	63511183	63511183	Missense_Mutation	SNP	G	A	23	95	c.1117G>A	c.(1117-1119)GAG>AAG	p.E373K
Pat_45	Pre-Treatment	CBLN2	147381	37	18	70205419	70205419	Missense_Mutation	SNP	G	A	18	48	c.667C>T	c.(667-669)CCT>TCT	p.P223S
Pat_45	Pre-Treatment	NETO1	81832	37	18	70450954	70450954	Missense_Mutation	SNP	C	T	33	175	c.827G>A	c.(826-828)CGA>CAA	p.R276Q
Pat_45	Pre-Treatment	CNDP2	55748	37	18	72185827	72185827	Missense_Mutation	SNP	G	A	4	103	c.1162G>A	c.(1162-1164)GAC>AAC	p.D388N
Pat_45	Pre-Treatment	BTBD2	55643	37	19	1997440	1997440	Missense_Mutation	SNP	C	T	4	112	c.430G>A	c.(430-432)GCC>ACC	p.A144T
Pat_45	Pre-Treatment	PIP5K1C	23396	37	19	3642933	3642933	Missense_Mutation	SNP	G	A	6	89	c.1654C>T	c.(1654-1656)CGC>TGC	p.R552C
Pat_45	Pre-Treatment	CHAF1A	10036	37	19	4409310	4409310	Missense_Mutation	SNP	C	T	16	68	c.514C>T	c.(514-516)CCT>TCT	p.P172S
Pat_45	Pre-Treatment	TNFSF14	8740	37	19	6669966	6669966	Missense_Mutation	SNP	C	T	33	173	c.115G>A	c.(115-117)GGT>AGT	p.G39S
Pat_45	Pre-Treatment	INSR	3643	37	19	7122913	7122913	Missense_Mutation	SNP	G	A	2	2	c.3346C>T	c.(3346-3348)CGT>TGT	p.R1116C
Pat_45	Pre-Treatment	CLEC4G	339390	37	19	7794279	7794279	Nonsense_Mutation	SNP	C	T	6	4	c.855G>A	c.(853-855)TGG>TGA	p.W285*
Pat_45	Pre-Treatment	KANK3	256949	37	19	8389972	8389972	Missense_Mutation	SNP	C	T	3	18	c.1945G>A	c.(1945-1947)GAG>AAG	p.E649K
Pat_45	Pre-Treatment	MUC16	94025	37	19	9068846	9068846	Missense_Mutation	SNP	C	T	25	66	c.18600G>A	c.(18598-18600)ATG>ATA	p.M6200I
Pat_45	Pre-Treatment	ZNF426	79088	37	19	9639255	9639255	Missense_Mutation	SNP	C	T	5	203	c.1466G>A	c.(1465-1467)AGT>AAT	p.S489N
Pat_45	Pre-Treatment	ZNF625	90589	37	19	12256929	12256929	Missense_Mutation	SNP	G	A	30	43	c.104C>T	c.(103-105)TCA>TTA	p.S35L
Pat_45	Pre-Treatment	IL27RA	9466	37	19	14161617	14161617	Missense_Mutation	SNP	C	T	3	38	c.1450C>T	c.(1450-1452)CCC>TCC	p.P484S
Pat_45	Pre-Treatment	CD97	976	37	19	14517213	14517213	Missense_Mutation	SNP	G	A	2	1	c.1892G>A	c.(1891-1893)AGC>AAC	p.S631N
Pat_45	Pre-Treatment	LOC100130932	100130932	37	19	14600293	14600293	Missense_Mutation	SNP	C	T	4	95	c.94C>T	c.(94-96)CGG>TGG	p.R32W
Pat_45	Pre-Treatment	C19orf44	84167	37	19	16612191	16612191	Missense_Mutation	SNP	G	T	4	84	c.588G>T	c.(586-588)TTG>TTT	p.L196F
Pat_45	Pre-Treatment	NWD1	284434	37	19	16902281	16902281	Missense_Mutation	SNP	G	A	3	12	c.3061G>A	c.(3061-3063)GAT>AAT	p.D1021N
Pat_45	Pre-Treatment	NWD1	284434	37	19	16908590	16908590	Missense_Mutation	SNP	C	T	5	159	c.3352C>T	c.(3352-3354)CGC>TGC	p.R1118C
Pat_45	Pre-Treatment	GLT25D1	79709	37	19	17671237	17671237	Missense_Mutation	SNP	T	C	3	82	c.452T>C	c.(451-453)CTG>CCG	p.L151P
Pat_45	Pre-Treatment	MAP1S	55201	37	19	17837868	17837868	Missense_Mutation	SNP	G	A	2	3	c.1675G>A	c.(1675-1677)GCA>ACA	p.A559T
Pat_45	Pre-Treatment	PDE4C	5143	37	19	18322645	18322645	Missense_Mutation	SNP	C	T	13	68	c.1715G>A	c.(1714-1716)GGA>GAA	p.G572E
Pat_45	Pre-Treatment	LOC284441	284441	37	19	20369281	20369281	Missense_Mutation	SNP	G	A	51	175	c.74G>A	c.(73-75)CGA>CAA	p.R25Q
Pat_45	Pre-Treatment	ZNF493	284443	37	19	21606988	21606988	Missense_Mutation	SNP	A	G	5	204	c.1143A>G	c.(1141-1143)ATA>ATG	p.I381M
Pat_45	Pre-Treatment	ZNF208	7757	37	19	22155282	22155282	Missense_Mutation	SNP	T	C	4	184	c.2254A>G	c.(2254-2256)AAG>GAG	p.K752E
Pat_45	Pre-Treatment	RGS9BP	388531	37	19	33167684	33167684	Missense_Mutation	SNP	G	A	2	3	c.515G>A	c.(514-516)CGC>CAC	p.R172H
Pat_45	Pre-Treatment	GRAMD1A	57655	37	19	35500079	35500079	Missense_Mutation	SNP	G	A	4	111	c.65G>A	c.(64-66)CGG>CAG	p.R22Q
Pat_45	Pre-Treatment	ZNF568	374900	37	19	37441709	37441709	Missense_Mutation	SNP	C	T	10	52	c.1654C>T	c.(1654-1656)CAT>TAT	p.H552Y
Pat_45	Pre-Treatment	RYR1	6261	37	19	38942437	38942437	Missense_Mutation	SNP	G	A	3	52	c.1156G>A	c.(1156-1158)GCA>ACA	p.A386T

Pat_45	Pre-Treatment	GMFG	9535	37	19	39819654	39819654	Missense_Mutation	SNP	C	T	4	103	c.343G>A	c.(343-345)GCA>ACA	p.A115T
Pat_45	Pre-Treatment	BLVRB	645	37	19	40964341	40964341	Missense_Mutation	SNP	G	A	4	14	c.191C>T	c.(190-192)ACC>ATC	p.T64I
Pat_45	Pre-Treatment	NUMBL	9253	37	19	41188842	41188842	Missense_Mutation	SNP	C	T	4	108	c.281G>A	c.(280-282)CGG>CAG	p.R94Q
Pat_45	Pre-Treatment	CYP2S1	29785	37	19	41704369	41704369	Missense_Mutation	SNP	C	T	4	91	c.496C>T	c.(496-498)CGC>TGC	p.R166C
Pat_45	Pre-Treatment	ARHGEF1	9138	37	19	42408220	42408220	Missense_Mutation	SNP	G	A	4	72	c.1951G>A	c.(1951-1953)GAG>AAG	p.E651K
Pat_45	Pre-Treatment	ZNF223	7766	37	19	44570909	44570909	Missense_Mutation	SNP	C	T	32	143	c.928C>T	c.(928-930)CAC>TAC	p.H310Y
Pat_45	Pre-Treatment	APOC2	344	37	19	45451740	45451740	Missense_Mutation	SNP	G	A	3	81	c.5G>A	c.(4-6)GGC>GAC	p.G2D
Pat_45	Pre-Treatment	MARK4	57787	37	19	45790890	45790890	Missense_Mutation	SNP	C	T	4	23	c.1462C>T	c.(1462-1464)CCA>TCA	p.P488S
Pat_45	Pre-Treatment	GRLF1	2909	37	19	47424681	47424681	Missense_Mutation	SNP	G	A	5	221	c.2749G>A	c.(2749-2751)GGA>AGA	p.G917R
Pat_45	Pre-Treatment	DHX34	9704	37	19	47856634	47856634	Missense_Mutation	SNP	G	A	4	116	c.347G>A	c.(346-348)CGG>CAG	p.R116Q
Pat_45	Pre-Treatment	GLTSCR1	29998	37	19	48183493	48183493	Missense_Mutation	SNP	G	A	2	0	c.1066G>A	c.(1066-1068)GCG>ACG	p.A356T
Pat_45	Pre-Treatment	IZUMO1	284359	37	19	49248955	49248955	Missense_Mutation	SNP	C	T	31	148	c.162G>A	c.(160-162)ATG>ATA	p.M54I
Pat_45	Pre-Treatment	GYS1	2997	37	19	49494681	49494681	Missense_Mutation	SNP	C	T	5	274	c.178G>A	c.(178-180)GAC>AAC	p.D60N
Pat_45	Pre-Treatment	PRR12	57479	37	19	50105048	50105048	Missense_Mutation	SNP	C	T	6	23	c.4646C>T	c.(4645-4647)GCC>GTC	p.A1549V
Pat_45	Pre-Treatment	SIGLEC11	114132	37	19	50462331	50462331	Missense_Mutation	SNP	G	A	3	40	c.1061C>T	c.(1060-1062)CCT>CTT	p.P354L
Pat_45	Pre-Treatment	MYBPC2	4606	37	19	50962555	50962555	Missense_Mutation	SNP	G	A	3	24	c.2783G>A	c.(2782-2784)CGC>CAC	p.R928H
Pat_45	Pre-Treatment	KLK15	55554	37	19	51329900	51329900	Missense_Mutation	SNP	C	T	3	69	c.595G>A	c.(595-597)GGC>AGC	p.G199S
Pat_45	Pre-Treatment	HAS1	3036	37	19	52220383	52220383	Missense_Mutation	SNP	C	T	26	76	c.766G>A	c.(766-768)GAG>AAG	p.E256K
Pat_45	Pre-Treatment	ZNF616	90317	37	19	52618799	52618799	Missense_Mutation	SNP	G	A	5	247	c.1618C>T	c.(1618-1620)CGG>TGG	p.R540W
Pat_45	Pre-Treatment	ZNF160	90338	37	19	53589523	53589524	Missense_Mutation	DNP	GG	AA	23	63	c.6_7CC>TT	c.(4-9)GCCCTT>GCTTTT	p.L3F
Pat_45	Pre-Treatment	DPRX	503834	37	19	54140183	54140183	Missense_Mutation	SNP	G	A	5	157	c.517G>A	c.(517-519)GCT>ACT	p.A173T
Pat_45	Pre-Treatment	CACNG7	59284	37	19	54418696	54418696	Missense_Mutation	SNP	G	A	4	94	c.361G>A	c.(361-363)GGC>AGC	p.G121S
Pat_45	Pre-Treatment	RPS9	6203	37	19	54711307	54711307	Missense_Mutation	SNP	G	A	4	85	c.449G>A	c.(448-450)CGC>CAC	p.R150H
Pat_45	Pre-Treatment	LILRA1	11024	37	19	55106729	55106729	Missense_Mutation	SNP	C	T	25	104	c.523C>T	c.(523-525)CAT>TAT	p.H175Y
Pat_45	Pre-Treatment	LILRB1	10859	37	19	55146735	55146735	Missense_Mutation	SNP	G	A	16	57	c.1585G>A	c.(1585-1587)GAA>AAA	p.E529K
Pat_45	Pre-Treatment	KIR2DS4	3809	37	19	55354347	55354347	Missense_Mutation	SNP	C	T	107	181	c.689C>T	c.(688-690)TCA>TTA	p.S230L
Pat_45	Pre-Treatment	BRSK1	84446	37	19	55800943	55800943	Missense_Mutation	SNP	G	A	4	97	c.413G>A	c.(412-414)CGC>CAC	p.R138H
Pat_45	Pre-Treatment	CCDC106	29903	37	19	56160423	56160423	Missense_Mutation	SNP	G	A	4	110	c.11G>A	c.(10-12)CGG>CAG	p.R4Q
Pat_45	Pre-Treatment	NLRP11	204801	37	19	56307518	56307518	Missense_Mutation	SNP	G	A	5	164	c.2270C>T	c.(2269-2271)CCG>CTG	p.P757L
Pat_45	Pre-Treatment	NLRP4	147945	37	19	56363558	56363558	Missense_Mutation	SNP	G	A	8	47	c.112G>A	c.(112-114)GAA>AAA	p.E38K
Pat_45	Pre-Treatment	NLRP4	147945	37	19	56372838	56372838	Missense_Mutation	SNP	G	A	3	58	c.1943G>A	c.(1942-1944)AGC>AAC	p.S648N
Pat_45	Pre-Treatment	NLRP5	126206	37	19	56539247	56539247	Missense_Mutation	SNP	G	A	8	7	c.1648G>A	c.(1648-1650)GAC>AAC	p.D550N
Pat_45	Pre-Treatment	KIDINS220	57498	37	2	8934045	8934045	Missense_Mutation	SNP	G	A	44	95	c.1171C>T	c.(1171-1173)CCC>TCC	p.P391S
Pat_45	Pre-Treatment	GREB1	9687	37	2	11767162	11767162	Missense_Mutation	SNP	G	A	3	48	c.4381G>A	c.(4381-4383)GCA>ACA	p.A1461T
Pat_45	Pre-Treatment	LPIN1	23175	37	2	11955254	11955254	Missense_Mutation	SNP	G	A	3	73	c.2182G>A	c.(2182-2184)GGG>AGG	p.G728R
Pat_45	Pre-Treatment	MATN3	4148	37	2	20205796	20205796	Nonsense_Mutation	SNP	G	A	20	40	c.499C>T	c.(499-501)CAG>TAG	p.Q167*
Pat_45	Pre-Treatment	ATAD2B	54454	37	2	23980810	23980810	Missense_Mutation	SNP	C	T	3	82	c.3556G>A	c.(3556-3558)GTA>ATA	p.V1186I
Pat_45	Pre-Treatment	NCOA1	8648	37	2	24964714	24964714	Missense_Mutation	SNP	G	A	3	56	c.3365G>A	c.(3364-3366)CGA>CAA	p.R1122Q
Pat_45	Pre-Treatment	C2orf70	339778	37	2	26800463	26800463	Missense_Mutation	SNP	G	A	4	61	c.428G>A	c.(427-429)AGG>AAG	p.R143K
Pat_45	Pre-Treatment	DPYSL5	56896	37	2	27121425	27121425	Missense_Mutation	SNP	G	A	4	135	c.58G>A	c.(58-60)GAT>AAT	p.D20N
Pat_45	Pre-Treatment	ABHD1	84696	37	2	27352478	27352478	Missense_Mutation	SNP	G	A	4	36	c.601G>A	c.(601-603)GGC>AGC	p.G201S
Pat_45	Pre-Treatment	C2orf16	84226	37	2	27803008	27803008	Missense_Mutation	SNP	G	A	10	67	c.3569G>A	c.(3568-3570)CGG>CAG	p.R1190Q
Pat_45	Pre-Treatment	SLC4A1AP	22950	37	2	27900620	27900620	Missense_Mutation	SNP	C	T	31	108	c.1592C>T	c.(1591-1593)CCA>CTA	p.P531L
Pat_45	Pre-Treatment	CEP68	23177	37	2	65299218	65299218	Nonsense_Mutation	SNP	C	T	4	87	c.988C>T	c.(988-990)CAG>TAG	p.Q330*
Pat_45	Pre-Treatment	SEMA4F	10505	37	2	74902386	74902386	Missense_Mutation	SNP	G	A	4	79	c.1247G>A	c.(1246-1248)AGG>AAG	p.R416K
Pat_45	Pre-Treatment	FLJ40330	645784	37	2	89082281	89082281	Splice_Site	SNP	T	C	3	136	c.397_splice	c.e3+2	
Pat_45	Pre-Treatment	ASTL	431705	37	2	96798324	96798324	Missense_Mutation	SNP	C	T	4	89	c.592G>A	c.(592-594)GAC>AAC	p.D198N

Pat_45	Pre-Treatment	ST6GAL2	84620	37	2	107459979	107459979	Missense_Mutation	SNP	G	A	4	133	c.455C>T	c.(454-456)TCC>TTC	p.S152F
Pat_45	Pre-Treatment	POTEE	445582	37	2	132020967	132020967	Missense_Mutation	SNP	G	A	9	48	c.1939G>A	c.(1939-1941)GAA>AAA	p.E647K
Pat_45	Pre-Treatment	GPR39	2863	37	2	133174679	133174679	Missense_Mutation	SNP	G	A	4	87	c.64G>A	c.(64-66)GAG>AAG	p.E22K
Pat_45	Pre-Treatment	ZRANB3	84083	37	2	136033282	136033282	Missense_Mutation	SNP	T	C	21	59	c.1010A>G	c.(1009-1011)GAT>GGT	p.D337G
Pat_45	Pre-Treatment	CACNB4	785	37	2	152739875	152739875	Missense_Mutation	SNP	C	T	36	164	c.157G>A	c.(157-159)GAT>AAT	p.D53N
Pat_45	Pre-Treatment	NOSTRIN	115677	37	2	169716093	169716093	Missense_Mutation	SNP	A	C	58	154	c.1125A>C	c.(1123-1125)CAA>CAC	p.Q375H
Pat_45	Pre-Treatment	LRP2	4036	37	2	170062971	170062971	Missense_Mutation	SNP	G	A	4	94	c.7259C>T	c.(7258-7260)ACT>ATT	p.T2420I
Pat_45	Pre-Treatment	GPR155	151556	37	2	175346273	175346273	Missense_Mutation	SNP	G	A	57	465	c.412C>T	c.(412-414)CCT>TCT	p.P138S
Pat_45	Pre-Treatment	TTN	7273	37	2	179459373	179459373	Missense_Mutation	SNP	G	A	5	138	c.50144C>T	c.(50143-50145)ACT>ATT	p.T16715I
Pat_45	Pre-Treatment	TTN	7273	37	2	179469836	179469836	Missense_Mutation	SNP	C	T	5	141	c.46364G>A	c.(46363-46365)CGA>CAA	p.R15455Q
Pat_45	Pre-Treatment	TTN	7273	37	2	179614255	179614255	Missense_Mutation	SNP	G	A	27	85	c.12872C>T	c.(12871-12873)GCT>GTT	p.A4291V
Pat_45	Pre-Treatment	CERKL	375298	37	2	182430229	182430229	Missense_Mutation	SNP	C	T	7	369	c.686G>A	c.(685-687)CGG>CAG	p.R229Q
Pat_45	Pre-Treatment	NAB1	4664	37	2	191524260	191524260	Missense_Mutation	SNP	G	T	4	97	c.358G>T	c.(358-360)GCC>TCC	p.A120S
Pat_45	Pre-Treatment	SDPR	8436	37	2	192701344	192701344	Missense_Mutation	SNP	C	T	14	32	c.583G>A	c.(583-585)GAA>AAA	p.E195K
Pat_45	Pre-Treatment	AOX1	316	37	2	201527615	201527616	Missense_Mutation	DNP	GG	AA	50	152	.3466_3467GG>A	c.(3466-3468)GGC>AAC	p.G1156N
Pat_45	Pre-Treatment	NOP58	51602	37	2	203149129	203149129	Missense_Mutation	SNP	G	A	4	129	c.359G>A	c.(358-360)CGT>CAT	p.R120H
Pat_45	Pre-Treatment	DYTN	391475	37	2	207564538	207564538	Missense_Mutation	SNP	G	A	3	59	c.632C>T	c.(631-633)CCG>CTG	p.P211L
Pat_45	Pre-Treatment	ABCA12	26154	37	2	215875192	215875192	Missense_Mutation	SNP	G	A	4	54	c.2335C>T	c.(2335-2337)CCA>TCA	p.P779S
Pat_45	Pre-Treatment	CXCR2	3579	37	2	219000231	219000231	Missense_Mutation	SNP	G	A	5	264	c.707G>A	c.(706-708)CGT>CAT	p.R236H
Pat_45	Pre-Treatment	COL4A4	1286	37	2	227973581	227973581	Missense_Mutation	SNP	G	A	3	34	c.661C>T	c.(661-663)CCT>TCT	p.P221S
Pat_45	Pre-Treatment	PSMD1	5707	37	2	231948392	231948392	Missense_Mutation	SNP	G	A	4	137	c.1637G>A	c.(1636-1638)CGT>CAT	p.R546H
Pat_45	Pre-Treatment	HDAC4	9759	37	2	240016726	240016726	Missense_Mutation	SNP	G	A	4	127	c.2245C>T	c.(2245-2247)CTC>TTC	p.L749F
Pat_45	Pre-Treatment	ATG4B	23192	37	2	242590687	242590687	Missense_Mutation	SNP	G	A	3	25	c.121G>A	c.(121-123)GAG>AAG	p.E41K
Pat_45	Pre-Treatment	TRIB3	57761	37	20	372154	372155	Missense_Mutation	DNP	AC	TT	7	18	c.515_516AC>TT	c.(514-516)CAC>CTT	p.H172L
Pat_45	Pre-Treatment	SIRPG	55423	37	20	1616833	1616833	Splice_Site	SNP	C	T	3	55	c.748_splice	c.e3+1	p.V250_splice
Pat_45	Pre-Treatment	FASTKD5	60493	37	20	3127727	3127727	Missense_Mutation	SNP	G	A	5	76	c.1990C>T	c.(1990-1992)CCT>TCT	p.P664S
Pat_45	Pre-Treatment	JAG1	182	37	20	10630918	10630918	Nonsense_Mutation	SNP	C	T	24	74	c.1211G>A	c.(1210-1212)TGG>TAG	p.W404*
Pat_45	Pre-Treatment	CD93	22918	37	20	23065529	23065529	Missense_Mutation	SNP	G	A	4	74	c.1301C>T	c.(1300-1302)CCG>CTG	p.P434L
Pat_45	Pre-Treatment	PLUNC	51297	37	20	31829222	31829222	Missense_Mutation	SNP	G	A	125	245	c.613G>A	c.(613-615)GAC>AAC	p.D205N
Pat_45	Pre-Treatment	NCOA6	23054	37	20	33337708	33337708	Missense_Mutation	SNP	C	T	3	60	c.2290G>A	c.(2290-2292)GGA>AGA	p.G764R
Pat_45	Pre-Treatment	RALGAPB	57148	37	20	37126006	37126006	Missense_Mutation	SNP	G	A	4	113	c.400G>A	c.(400-402)GGT>AGT	p.G134S
Pat_45	Pre-Treatment	ADA	100	37	20	43255157	43255157	Missense_Mutation	SNP	C	T	4	76	c.302G>A	c.(301-303)CGG>CAG	p.R101Q
Pat_45	Pre-Treatment	SLC35C2	51006	37	20	44987058	44987058	Missense_Mutation	SNP	C	T	4	120	c.88G>A	c.(88-90)GGC>AGC	p.G30S
Pat_45	Pre-Treatment	PHACTR3	116154	37	20	58318169	58318169	Missense_Mutation	SNP	G	A	37	94	c.126G>A	c.(124-126)ATG>ATA	p.M42I
Pat_45	Pre-Treatment	PHACTR3	116154	37	20	58342267	58342267	Missense_Mutation	SNP	G	A	27	37	c.568G>A	c.(568-570)GAA>AAA	p.E190K
Pat_45	Pre-Treatment	DIDO1	11083	37	20	61510767	61510767	Missense_Mutation	SNP	G	A	2	2	c.6541C>T	c.(6541-6543)CGC>TGC	p.R2181C
Pat_45	Pre-Treatment	TIAM1	7074	37	21	32513700	32513700	Missense_Mutation	SNP	G	A	4	85	c.3598C>T	c.(3598-3600)CTC>TTC	p.L1200F
Pat_45	Pre-Treatment	TIAM1	7074	37	21	32595763	32595763	Missense_Mutation	SNP	C	T	70	175	c.1954G>A	c.(1954-1956)GGC>AGC	p.G652S
Pat_45	Pre-Treatment	DYRK1A	1859	37	21	38845021	38845021	Missense_Mutation	SNP	C	T	5	169	c.46C>T	c.(46-48)CGG>TGG	p.R16W
Pat_45	Pre-Treatment	BRWD1	54014	37	21	40582064	40582064	Missense_Mutation	SNP	C	T	29	98	c.4054G>A	c.(4054-4056)GAT>AAT	p.D1352N
Pat_45	Pre-Treatment	COL18A1	80781	37	21	46930009	46930009	Missense_Mutation	SNP	C	T	2	1	c.4763C>T	c.(4762-4764)TCA>TTA	p.S1588L
Pat_45	Pre-Treatment	PCNT	5116	37	21	47754455	47754455	Missense_Mutation	SNP	C	T	4	77	c.412C>T	c.(412-414)CAC>TAC	p.H138Y
Pat_45	Pre-Treatment	CECR6	27439	37	22	17600757	17600757	Missense_Mutation	SNP	G	A	2	1	c.1261C>T	c.(1261-1263)CCC>TCC	p.P421S
Pat_45	Pre-Treatment	CECR5	27440	37	22	17624015	17624015	Missense_Mutation	SNP	G	A	21	40	c.544C>T	c.(544-546)CCG>TCG	p.P182S
Pat_45	Pre-Treatment	TBX1	6899	37	22	19766821	19766821	Missense_Mutation	SNP	G	A	4	61	c.1088G>A	c.(1087-1089)AGG>AAG	p.R363K
Pat_45	Pre-Treatment	ZDHHC8	29801	37	22	20128852	20128852	Missense_Mutation	SNP	G	A	3	31	c.1007G>A	c.(1006-1008)GGC>GAC	p.G336D
Pat_45	Pre-Treatment	RTDR1	27156	37	22	23401726	23401726	Missense_Mutation	SNP	C	T	4	57	c.961G>A	c.(961-963)GTG>ATG	p.V321M

Pat_45	Pre-Treatment	BCR	613	37	22	23631788	23631788	Missense_Mutation	SNP	C	T	7	38	c.2687C>T	c.(2686-2688)CCG>CTG	p.P896L
Pat_45	Pre-Treatment	ZNF70	7621	37	22	24086387	24086387	Missense_Mutation	SNP	C	T	4	103	c.941G>A	c.(940-942)GGG>GAG	p.G314E
Pat_45	Pre-Treatment	MYO18B	84700	37	22	26400684	26400684	Missense_Mutation	SNP	G	A	13	45	c.6333G>A	c.(6331-6333)ATG>ATA	p.M2111I
Pat_45	Pre-Treatment	SEZ6L	23544	37	22	26688759	26688759	Missense_Mutation	SNP	C	T	3	15	c.482C>T	c.(481-483)ACG>ATG	p.T161M
Pat_45	Pre-Treatment	HPS4	89781	37	22	26854482	26854482	Missense_Mutation	SNP	C	A	3	48	c.1775G>T	c.(1774-1776)AGG>ATG	p.R592M
Pat_45	Pre-Treatment	KREMEN1	83999	37	22	29537939	29537939	Missense_Mutation	SNP	C	T	4	124	c.1267C>T	c.(1267-1269)CGT>TGT	p.R423C
Pat_45	Pre-Treatment	AP1B1	162	37	22	29746040	29746040	Missense_Mutation	SNP	G	A	6	167	c.1255C>T	c.(1255-1257)CGC>TGC	p.R419C
Pat_45	Pre-Treatment	OSBP2	23762	37	22	31289161	31289161	Nonsense_Mutation	SNP	G	A	4	35	c.1922G>A	c.(1921-1923)TGG>TAG	p.W641*
Pat_45	Pre-Treatment	SFI1	9814	37	22	31946325	31946325	Missense_Mutation	SNP	G	A	3	42	c.535G>A	c.(535-537)GAG>AAG	p.E179K
Pat_45	Pre-Treatment	MYH9	4627	37	22	36714329	36714329	Missense_Mutation	SNP	C	T	6	309	c.1150G>A	c.(1150-1152)GAT>AAT	p.D384N
Pat_45	Pre-Treatment	TMPRSS6	164656	37	22	37466570	37466570	Missense_Mutation	SNP	C	T	4	94	c.1822G>A	c.(1822-1824)GCT>ACT	p.A608T
Pat_45	Pre-Treatment	TAB1	10454	37	22	39811633	39811633	Missense_Mutation	SNP	C	T	12	28	c.299C>T	c.(298-300)GCC>GTC	p.A100V
Pat_45	Pre-Treatment	MPPED1	758	37	22	43870764	43870764	Missense_Mutation	SNP	G	C	3	100	c.555G>C	c.(553-555)CAG>CAC	p.Q185H
Pat_45	Pre-Treatment	UPK3A	7380	37	22	45685025	45685025	Splice_Site	SNP	G	A	4	128	c.571_splice	c.e4+1	p.L191_splice
Pat_45	Pre-Treatment	PKDREJ	10343	37	22	46654188	46654188	Missense_Mutation	SNP	C	T	4	122	c.5032G>A	c.(5032-5034)GTC>ATC	p.V1678I
Pat_45	Pre-Treatment	JAGN1	84522	37	3	9934877	9934877	Missense_Mutation	SNP	T	G	89	69	c.368T>G	c.(367-369)TTC>TGC	p.F123C
Pat_45	Pre-Treatment	IQSEC1	9922	37	3	12962047	12962047	Missense_Mutation	SNP	G	A	4	78	c.1945C>T	c.(1945-1947)CCA>TCA	p.P649S
Pat_45	Pre-Treatment	PLCL2	23228	37	3	17131387	17131387	Missense_Mutation	SNP	G	A	3	52	c.3343G>A	c.(3343-3345)GAT>AAT	p.D1115N
Pat_45	Pre-Treatment	DLEC1	9940	37	3	38158478	38158478	Missense_Mutation	SNP	G	A	3	45	c.4192G>A	c.(4192-4194)GGG>AGG	p.G1398R
Pat_45	Pre-Treatment	COL7A1	1294	37	3	48607707	48607707	Splice_Site	SNP	C	T	3	35	c.7440_splice	c.e97+1	p.R2480_splice
Pat_45	Pre-Treatment	QARS	5859	37	3	49133496	49133496	Missense_Mutation	SNP	G	A	4	42	c.2294C>T	c.(2293-2295)ACT>ATT	p.T765I
Pat_45	Pre-Treatment	GPX1	2876	37	3	49395482	49395482	Missense_Mutation	SNP	G	C	6	20	c.230C>G	c.(229-231)CCG>CGG	p.P77R
Pat_45	Pre-Treatment	DAG1	1605	37	3	49569062	49569062	Missense_Mutation	SNP	G	A	4	107	c.1118G>A	c.(1117-1119)CGA>CAA	p.R373Q
Pat_45	Pre-Treatment	RBM5	10181	37	3	50155830	50155830	Missense_Mutation	SNP	G	A	4	48	c.2389G>A	c.(2389-2391)GAT>AAT	p.D797N
Pat_45	Pre-Treatment	TLR9	54106	37	3	52255324	52255324	Missense_Mutation	SNP	C	T	3	24	c.3008G>A	c.(3007-3009)CGC>CAC	p.R1003H
Pat_45	Pre-Treatment	TWF2	11344	37	3	52265154	52265154	Missense_Mutation	SNP	G	A	4	59	c.472C>T	c.(472-474)CGC>TGC	p.R158C
Pat_45	Pre-Treatment	PRKCD	5580	37	3	53217169	53217169	Missense_Mutation	SNP	G	A	4	66	c.604G>A	c.(604-606)GAC>AAC	p.D202N
Pat_45	Pre-Treatment	FLNB	2317	37	3	58108856	58108856	Missense_Mutation	SNP	G	A	4	104	c.3163G>A	c.(3163-3165)GTG>ATG	p.V1055M
Pat_45	Pre-Treatment	ATXN7	6314	37	3	63981842	63981842	Missense_Mutation	SNP	G	A	4	127	c.2344G>A	c.(2344-2346)GGG>AGG	p.G782R
Pat_45	Pre-Treatment	ADCY5	111	37	3	123166474	123166474	Missense_Mutation	SNP	C	T	2	0	c.919G>A	c.(919-921)GCC>ACC	p.A307T
Pat_45	Pre-Treatment	SLC12A8	84561	37	3	124909229	124909229	Missense_Mutation	SNP	C	T	4	115	c.188G>A	c.(187-189)GGC>GAC	p.G63D
Pat_45	Pre-Treatment	MCM2	4171	37	3	127325110	127325110	Missense_Mutation	SNP	G	A	5	152	c.823G>A	c.(823-825)GAC>AAC	p.D275N
Pat_45	Pre-Treatment	ZBTB38	253461	37	3	141163272	141163272	Missense_Mutation	SNP	C	T	5	138	c.2042C>T	c.(2041-2043)GCT>GTT	p.A681V
Pat_45	Pre-Treatment	RNF13	11342	37	3	149613348	149613348	Splice_Site	SNP	G	A	5	189	c.409_splice	c.e6+1	p.I137_splice
Pat_45	Pre-Treatment	GPR87	53836	37	3	151011986	151011986	Missense_Mutation	SNP	G	A	8	361	c.1048C>T	c.(1048-1050)CGC>TGC	p.R350C
Pat_45	Pre-Treatment	C3orf55	152078	37	3	157289043	157289043	Missense_Mutation	SNP	G	A	3	40	c.161G>A	c.(160-162)GGA>GAA	p.G54E
Pat_45	Pre-Treatment	ARPM1	84517	37	3	169486133	169486133	Missense_Mutation	SNP	G	A	4	76	c.206C>T	c.(205-207)CCA>CTA	p.P69L
Pat_45	Pre-Treatment	THPO	7066	37	3	184090434	184090434	Missense_Mutation	SNP	G	A	4	72	c.929C>T	c.(928-930)CCA>CTA	p.P310L
Pat_45	Pre-Treatment	GP5	2814	37	3	194118791	194118791	Missense_Mutation	SNP	G	A	30	36	c.221C>T	c.(220-222)ACC>ATC	p.T74I
Pat_45	Pre-Treatment	MUC4	4585	37	3	195512117	195512117	Missense_Mutation	SNP	C	G	5	4	c.6334G>C	c.(6334-6336)GCT>CCT	p.A2112P
Pat_45	Pre-Treatment	PCYT1A	5130	37	3	195965671	195965671	Missense_Mutation	SNP	G	A	7	18	c.992C>T	c.(991-993)TCC>TTC	p.S331F
Pat_45	Pre-Treatment	FGFR3	2261	37	4	1805525	1805525	Missense_Mutation	SNP	G	A	3	34	c.1037G>A	c.(1036-1038)GGG>GAG	p.G346E
Pat_45	Pre-Treatment	RGS12	6002	37	4	3415832	3415832	Missense_Mutation	SNP	G	A	2	2	c.2054G>A	c.(2053-2055)AGC>AAC	p.S685N
Pat_45	Pre-Treatment	HGFAC	3083	37	4	3444502	3444502	Missense_Mutation	SNP	C	T	5	83	c.161C>T	c.(160-162)GCG>GTG	p.A54V
Pat_45	Pre-Treatment	ZBTB49	166793	37	4	4322555	4322555	Missense_Mutation	SNP	G	A	3	30	c.1810G>A	c.(1810-1812)GAG>AAG	p.E604K
Pat_45	Pre-Treatment	PSAPL1	768239	37	4	7435406	7435406	Missense_Mutation	SNP	T	C	2	6	c.1201A>G	c.(1201-1203)AGG>GGG	p.R401G
Pat_45	Pre-Treatment	TLR1	7096	37	4	38798346	38798346	Nonsense_Mutation	SNP	G	A	167	259	c.2107C>T	c.(2107-2109)CAG>TAG	p.Q703*

Pat_45	Pre-Treatment	RFC1	5981	37	4	39297270	39297270	Missense_Mutation	SNP	C	T	4	105	c.2921G>A	c.(2920-2922)CGT>CAT	p.R974H
Pat_45	Pre-Treatment	ATP8A1	10396	37	4	42454025	42454025	Missense_Mutation	SNP	A	G	3	49	c.2869T>C	c.(2869-2871)TGG>CGG	p.W957R
Pat_45	Pre-Treatment	RASSF6	166824	37	4	74450977	74450977	Missense_Mutation	SNP	T	C	4	86	c.583A>G	c.(583-585)AGG>GGG	p.R195G
Pat_45	Pre-Treatment	LIN54	132660	37	4	83861083	83861083	Missense_Mutation	SNP	G	A	5	215	c.1201C>T	c.(1201-1203)CGG>TGG	p.R401W
Pat_45	Pre-Treatment	PPM1K	152926	37	4	89199310	89199310	Missense_Mutation	SNP	C	T	4	79	c.426G>A	c.(424-426)ATG>ATA	p.M142I
Pat_45	Pre-Treatment	NDST3	9348	37	4	119064828	119064828	Missense_Mutation	SNP	G	A	3	59	c.1528G>A	c.(1528-1530)GTC>ATC	p.V510I
Pat_45	Pre-Treatment	FAT4	79633	37	4	126240061	126240061	Missense_Mutation	SNP	C	T	4	99	c.2495C>T	c.(2494-2496)ACT>ATT	p.T832I
Pat_45	Pre-Treatment	GLRB	2743	37	4	158091830	158091830	Missense_Mutation	SNP	C	T	8	180	c.1444C>T	c.(1444-1446)CCT>TCT	p.P482S
Pat_45	Pre-Treatment	NPY5R	4889	37	4	164272176	164272176	Missense_Mutation	SNP	G	A	13	132	c.751G>A	c.(751-753)GAA>AAA	p.E251K
Pat_45	Pre-Treatment	ANP32C	23520	37	4	165118166	165118166	Missense_Mutation	SNP	C	T	25	39	c.698G>A	c.(697-699)CGA>CAA	p.R233Q
Pat_45	Pre-Treatment	GK3P	2713	37	4	166199849	166199849	Missense_Mutation	SNP	C	T	5	210	c.949G>A	c.(949-951)GCT>ACT	p.A317T
Pat_45	Pre-Treatment	TLL1	7092	37	4	166915635	166915635	Missense_Mutation	SNP	G	T	12	38	c.464G>T	c.(463-465)AGA>ATA	p.R155I
Pat_45	Pre-Treatment	FAM149A	25854	37	4	187088231	187088231	Missense_Mutation	SNP	G	A	4	42	c.1274G>A	c.(1273-1275)AGC>AAC	p.S425N
Pat_45	Pre-Treatment	CYP4V2	285440	37	4	187118110	187118110	Missense_Mutation	SNP	C	T	4	107	c.430C>T	c.(430-432)CGC>TGC	p.R144C
Pat_45	Pre-Treatment	NKD2	85409	37	5	1038318	1038318	Missense_Mutation	SNP	C	T	2	2	c.1186C>T	c.(1186-1188)CTC>TTC	p.L396F
Pat_45	Pre-Treatment	TERT	7015	37	5	1282710	1282710	Missense_Mutation	SNP	G	A	3	24	c.1603C>T	c.(1603-1605)CGT>TGT	p.R535C
Pat_45	Pre-Treatment	SLC6A3	6531	37	5	1406365	1406365	Missense_Mutation	SNP	C	T	4	63	c.1537G>A	c.(1537-1539)GGG>AGG	p.G513R
Pat_45	Pre-Treatment	CTNND2	1501	37	5	11346553	11346553	Missense_Mutation	SNP	C	T	4	129	c.1559G>A	c.(1558-1560)GGC>GAC	p.G520D
Pat_45	Pre-Treatment	PRDM9	56979	37	5	23526999	23526999	Missense_Mutation	SNP	C	T	4	111	c.1802C>T	c.(1801-1803)ACA>ATA	p.T601I
Pat_45	Pre-Treatment	C6	729	37	5	41159253	41159253	Missense_Mutation	SNP	C	T	48	137	c.1787G>A	c.(1786-1788)CGA>CAA	p.R596Q
Pat_45	Pre-Treatment	BDP1	55814	37	5	70818718	70818718	Missense_Mutation	SNP	G	A	4	89	c.5329G>A	c.(5329-5331)GTA>ATA	p.V1777I
Pat_45	Pre-Treatment	CMYA5	202333	37	5	79034609	79034609	Missense_Mutation	SNP	C	T	6	52	c.10021C>T	c.(10021-10023)CCA>TCA	p.P3341S
Pat_45	Pre-Treatment	VCAN	1462	37	5	82834931	82834931	Missense_Mutation	SNP	G	A	4	39	c.6109G>A	c.(6109-6111)GCT>ACT	p.A2037T
Pat_45	Pre-Treatment	SLCO6A1	133482	37	5	101813557	101813557	Missense_Mutation	SNP	C	T	47	139	c.625G>A	c.(625-627)GAA>AAA	p.E209K
Pat_45	Pre-Treatment	TRPC7	57113	37	5	135561775	135561775	Missense_Mutation	SNP	C	T	3	16	c.2206G>A	c.(2206-2208)GCC>ACC	p.A736T
Pat_45	Pre-Treatment	PCDHA6	56142	37	5	140209564	140209564	Missense_Mutation	SNP	G	A	4	62	c.1888G>A	c.(1888-1890)GAG>AAG	p.E630K
Pat_45	Pre-Treatment	PCDHGA1	56114	37	5	140712640	140712640	Missense_Mutation	SNP	T	A	29	35	c.2389T>A	c.(2389-2391)TTA>ATA	p.L797I
Pat_45	Pre-Treatment	HDAC3	8841	37	5	141009255	141009255	Missense_Mutation	SNP	G	A	4	134	c.472C>T	c.(472-474)CTC>TTC	p.L158F
Pat_45	Pre-Treatment	FCHSD1	89848	37	5	141024239	141024239	Missense_Mutation	SNP	C	T	4	81	c.1543G>A	c.(1543-1545)GAG>AAG	p.E515K
Pat_45	Pre-Treatment	PCDH1	5097	37	5	141242829	141242829	Missense_Mutation	SNP	G	A	21	37	c.3067C>T	c.(3067-3069)CGC>TGC	p.R1023C
Pat_45	Pre-Treatment	SH3RF2	153769	37	5	145439449	145439449	Missense_Mutation	SNP	C	T	18	50	c.1576C>T	c.(1576-1578)CTC>TTC	p.L526F
Pat_45	Pre-Treatment	DPYSL3	1809	37	5	146781115	146781115	Missense_Mutation	SNP	G	A	9	25	c.956C>T	c.(955-957)TCC>TTC	p.S319F
Pat_45	Pre-Treatment	FBXO38	81545	37	5	147806803	147806803	Missense_Mutation	SNP	G	A	4	68	c.1946G>A	c.(1945-1947)CGA>CAA	p.R649Q
Pat_45	Pre-Treatment	PPARGC1B	133522	37	5	149212805	149212805	Missense_Mutation	SNP	C	T	3	46	c.1169C>T	c.(1168-1170)TCG>TTG	p.S390L
Pat_45	Pre-Treatment	FAT2	2196	37	5	150921921	150921921	Missense_Mutation	SNP	C	T	13	187	c.8767G>A	c.(8767-8769)GAA>AAA	p.E2923K
Pat_45	Pre-Treatment	TIMD4	91937	37	5	156381747	156381747	Missense_Mutation	SNP	C	T	4	62	c.79G>A	c.(79-81)GTT>ATT	p.V27I
Pat_45	Pre-Treatment	ADAM19	8728	37	5	156929917	156929917	Missense_Mutation	SNP	C	T	24	96	c.1202G>A	c.(1201-1203)GGA>GAA	p.G401E
Pat_45	Pre-Treatment	DOCK2	1794	37	5	169116299	169116299	Missense_Mutation	SNP	G	A	23	97	c.805G>A	c.(805-807)GAG>AAG	p.E269K
Pat_45	Pre-Treatment	CNOT6	57472	37	5	179998353	179998353	Missense_Mutation	SNP	G	A	4	88	c.1382G>A	c.(1381-1383)AGG>AAG	p.R461K
Pat_45	Pre-Treatment	PIP5K1P1	206426	37	6	7987158	7987158	Missense_Mutation	SNP	C	T	4	97	c.389C>T	c.(388-390)GCG>GTG	p.A130V
Pat_45	Pre-Treatment	GFOD1	54438	37	6	13486885	13486885	Missense_Mutation	SNP	C	T	4	38	c.238G>A	c.(238-240)GCT>ACT	p.A80T
Pat_45	Pre-Treatment	JARID2	3720	37	6	15501269	15501269	Missense_Mutation	SNP	C	T	4	36	c.2077C>T	c.(2077-2079)CGG>TGG	p.R693W
Pat_45	Pre-Treatment	CAP2	10486	37	6	17551741	17551741	Missense_Mutation	SNP	G	T	4	127	c.1256G>T	c.(1255-1257)TGC>TTC	p.C419F
Pat_45	Pre-Treatment	DCDC2	51473	37	6	24174966	24174966	Missense_Mutation	SNP	C	T	5	122	c.1423G>A	c.(1423-1425)GTG>ATG	p.V475M
Pat_45	Pre-Treatment	SLC17A1	6568	37	6	25826840	25826840	Missense_Mutation	SNP	C	A	3	22	c.56G>T	c.(55-57)CGC>CTC	p.R19L
Pat_45	Pre-Treatment	OR12D2	26529	37	6	29365320	29365320	Missense_Mutation	SNP	C	T	32	182	c.844C>T	c.(844-846)CCT>TCT	p.P282S
Pat_45	Pre-Treatment	DPCR1	135656	37	6	30919836	30919837	Missense_Mutation	DNP	GG	AA	23	91	.3595_3596GG>A	c.(3595-3597)GGG>AAG	p.G1199K

Pat_45	Pre-Treatment	PSORS1C1	170679	37	6	31106510	31106510	Missense_Mutation	SNP	G	A	5	159	c.121G>A	c.(121-123)GTT>ATT	p.V41I
Pat_45	Pre-Treatment	SLC39A7	7922	37	6	33170780	33170780	Missense_Mutation	SNP	G	A	6	351	c.1034G>A	c.(1033-1035)CGG>CAG	p.R345Q
Pat_45	Pre-Treatment	KIFC1	3833	37	6	33374184	33374184	Missense_Mutation	SNP	G	A	4	69	c.1748G>A	c.(1747-1749)CGG>CAG	p.R583Q
Pat_45	Pre-Treatment	C6orf106	64771	37	6	34614410	34614410	Missense_Mutation	SNP	C	T	4	123	c.479G>A	c.(478-480)CGG>CAG	p.R160Q
Pat_45	Pre-Treatment	TREML4	285852	37	6	41196184	41196184	Missense_Mutation	SNP	C	A	3	23	c.19C>A	c.(19-21)CAC>AAC	p.H7N
Pat_45	Pre-Treatment	PRPH2	5961	37	6	42689774	42689774	Missense_Mutation	SNP	G	A	3	32	c.299C>T	c.(298-300)CCG>CTG	p.P100L
Pat_45	Pre-Treatment	TCTE1	202500	37	6	44254138	44254138	Missense_Mutation	SNP	G	T	4	41	c.409C>A	c.(409-411)CAT>AAT	p.H137N
Pat_45	Pre-Treatment	EYS	346007	37	6	66204958	66204958	Missense_Mutation	SNP	G	T	4	131	c.346C>A	c.(346-348)CAA>AAA	p.Q116K
Pat_45	Pre-Treatment	IMPG1	3617	37	6	76713637	76713637	Missense_Mutation	SNP	G	A	25	92	c.1166C>T	c.(1165-1167)CCT>CTT	p.P389L
Pat_45	Pre-Treatment	BVES	11149	37	6	105573398	105573398	Missense_Mutation	SNP	C	T	5	272	c.407G>A	c.(406-408)CGT>CAT	p.R136H
Pat_45	Pre-Treatment	FAM26E	254228	37	6	116833142	116833142	Missense_Mutation	SNP	C	T	4	112	c.283C>T	c.(283-285)CGT>TGT	p.R95C
Pat_45	Pre-Treatment	ROS1	6098	37	6	117724427	117724427	Missense_Mutation	SNP	G	A	3	54	c.452C>T	c.(451-453)CCG>CTG	p.P151L
Pat_45	Pre-Treatment	IL20RA	53832	37	6	137330594	137330594	Missense_Mutation	SNP	C	T	19	79	c.439G>A	c.(439-441)GAT>AAT	p.D147N
Pat_45	Pre-Treatment	SYNE1	23345	37	6	152765647	152765647	Missense_Mutation	SNP	C	T	20	78	c.3736G>A	c.(3736-3738)GAA>AAA	p.E1246K
Pat_45	Pre-Treatment	RNASET2	8635	37	6	167366005	167366005	Missense_Mutation	SNP	C	T	28	91	c.118G>A	c.(118-120)GTT>ATT	p.V40I
Pat_45	Pre-Treatment	MICALL2	79778	37	7	1481914	1481914	Missense_Mutation	SNP	G	A	14	10	c.1625C>T	c.(1624-1626)TCC>TTC	p.S542F
Pat_45	Pre-Treatment	PMS2	5395	37	7	6026810	6026810	Missense_Mutation	SNP	G	A	4	92	c.1586C>T	c.(1585-1587)TCG>TTG	p.S529L
Pat_45	Pre-Treatment	ZNF853	54753	37	7	6662322	6662322	Missense_Mutation	SNP	G	A	2	2	c.1700G>A	c.(1699-1701)CGA>CAA	p.R567Q
Pat_45	Pre-Treatment	NXPH1	30010	37	7	8790885	8790885	Missense_Mutation	SNP	G	A	4	98	c.302G>A	c.(301-303)CGG>CAG	p.R101Q
Pat_45	Pre-Treatment	TRA2A	29896	37	7	23552565	23552565	Missense_Mutation	SNP	C	T	28	191	c.473G>A	c.(472-474)CGA>CAA	p.R158Q
Pat_45	Pre-Treatment	CLK2P	1197	37	7	23625138	23625138	Missense_Mutation	SNP	C	T	4	85	c.359G>A	c.(358-360)CGA>CAA	p.R120Q
Pat_45	Pre-Treatment	HOXA11	3207	37	7	27222585	27222585	Missense_Mutation	SNP	G	A	6	133	c.772C>T	c.(772-774)CGG>TGG	p.R258W
Pat_45	Pre-Treatment	CPVL	54504	37	7	29126138	29126138	Missense_Mutation	SNP	G	A	115	113	c.571C>T	c.(571-573)CCT>TCT	p.P191S
Pat_45	Pre-Treatment	CHN2	1124	37	7	29535581	29535581	Missense_Mutation	SNP	G	T	4	106	c.668G>T	c.(667-669)CGA>CTA	p.R223L
Pat_45	Pre-Treatment	DPY19L1	23333	37	7	35013211	35013211	Missense_Mutation	SNP	G	A	3	73	c.610C>T	c.(610-612)CGT>TGT	p.R204C
Pat_45	Pre-Treatment	MYO1G	64005	37	7	45002693	45002693	Missense_Mutation	SNP	C	T	2	0	c.2776G>A	c.(2776-2778)GAC>AAC	p.D926N
Pat_45	Pre-Treatment	IGFBP3	3486	37	7	45956840	45956840	Missense_Mutation	SNP	G	A	29	246	c.602C>T	c.(601-603)TCC>TTC	p.S201F
Pat_45	Pre-Treatment	TYW1B	441250	37	7	72081656	72081656	Splice_Site	SNP	C	T	5	183	c.1785_splice	c.e16+1	p.K595_splice
Pat_45	Pre-Treatment	ELN	2006	37	7	73458236	73458236	Missense_Mutation	SNP	G	A	3	21	c.455G>A	c.(454-456)GGT>GAT	p.G152D
Pat_45	Pre-Treatment	ELN	2006	37	7	73458239	73458239	Missense_Mutation	SNP	G	C	3	21	c.458G>C	c.(457-459)GGC>GCC	p.G153A
Pat_45	Pre-Treatment	LIMK1	3984	37	7	73521482	73521482	Missense_Mutation	SNP	G	A	3	31	c.1024G>A	c.(1024-1026)GGG>AGG	p.G342R
Pat_45	Pre-Treatment	PCLO	27445	37	7	82430898	82430898	Missense_Mutation	SNP	C	T	46	57	c.14943G>A	c.(14941-14943)ATG>ATA	p.M4981I
Pat_45	Pre-Treatment	PCLO	27445	37	7	82584325	82584325	Missense_Mutation	SNP	C	T	22	254	c.5944G>A	c.(5944-5946)GGA>AGA	p.G1982R
Pat_45	Pre-Treatment	ABCB4	5244	37	7	87037363	87037363	Missense_Mutation	SNP	G	A	6	219	c.3269C>T	c.(3268-3270)GCG>GTG	p.A1090V
Pat_45	Pre-Treatment	SRI	6717	37	7	87846436	87846436	Splice_Site	SNP	C	T	5	266	c.205_splice	c.e3+1	p.P69_splice
Pat_45	Pre-Treatment	STEAP2	261729	37	7	89854678	89854678	Missense_Mutation	SNP	C	G	114	109	c.282C>G	c.(280-282)CAC>CAG	p.H94Q
Pat_45	Pre-Treatment	AP4M1	9179	37	7	99701259	99701259	Missense_Mutation	SNP	A	G	215	194	c.487A>G	c.(487-489)AAA>GAA	p.K163E
Pat_45	Pre-Treatment	MUC17	140453	37	7	100683878	100683878	Missense_Mutation	SNP	C	T	87	435	c.9181C>T	c.(9181-9183)CCT>TCT	p.P3061S
Pat_45	Pre-Treatment	RELN	5649	37	7	103244910	103244910	Missense_Mutation	SNP	C	T	6	163	c.3029G>A	c.(3028-3030)CGC>CAC	p.R1010H
Pat_45	Pre-Treatment	DLD	1738	37	7	107556059	107556059	Missense_Mutation	SNP	C	T	109	93	c.793C>T	c.(793-795)CTT>TTT	p.L265F
Pat_45	Pre-Treatment	IRF5	3663	37	7	128586065	128586065	Missense_Mutation	SNP	G	A	5	58	c.362G>A	c.(361-363)TGC>TAC	p.C121Y
Pat_45	Pre-Treatment	BRAF	673	37	7	140453136	140453136	Missense_Mutation	SNP	A	T	114	105	c.1799T>A	c.(1798-1800)GTG>GAG	p.V600E
Pat_45	Pre-Treatment	CNTNAP2	26047	37	7	146805370	146805370	Missense_Mutation	SNP	G	A	56	48	c.682G>A	c.(682-684)GGA>AGA	p.G228R
Pat_45	Pre-Treatment	SSPO	23145	37	7	149477982	149477982	Missense_Mutation	SNP	G	A	3	26	c.1753G>A	c.(1753-1755)GGT>AGT	p.G585S
Pat_45	Pre-Treatment	SSPO	23145	37	7	149500187	149500187	Missense_Mutation	SNP	G	A	2	0	c.7813G>A	c.(7813-7815)GGC>AGC	p.G2605S
Pat_45	Pre-Treatment	GALNTL5	168391	37	7	151664473	151664473	Missense_Mutation	SNP	C	T	3	30	c.142C>T	c.(142-144)CCT>TCT	p.P48S
Pat_45	Pre-Treatment	VIPR2	7434	37	7	158935207	158935207	Missense_Mutation	SNP	G	A	158	102	c.82C>T	c.(82-84)CAT>TAT	p.H28Y

Pat_45	Pre-Treatment	DEFA4	1669	37	8	6794369	6794369	Missense_Mutation	SNP	C	T	3	19	c.53G>A	c.(52-54)CGG>CAG	p.R18Q
Pat_45	Pre-Treatment	PINX1	54984	37	8	10677719	10677719	Missense_Mutation	SNP	C	T	4	84	c.455G>A	c.(454-456)AGT>AAT	p.S152N
Pat_45	Pre-Treatment	SH2D4A	63898	37	8	19231157	19231157	Missense_Mutation	SNP	C	T	4	93	c.1034C>T	c.(1033-1035)GCC>GTC	p.A345V
Pat_45	Pre-Treatment	REEP4	80346	37	8	21996301	21996301	Missense_Mutation	SNP	G	A	3	56	c.559C>T	c.(559-561)CGG>TGG	p.R187W
Pat_45	Pre-Treatment	LOXL2	4017	37	8	23159641	23159641	Missense_Mutation	SNP	C	T	35	27	c.2032G>A	c.(2032-2034)GAT>AAT	p.D678N
Pat_45	Pre-Treatment	NEFL	4747	37	8	24813629	24813629	Missense_Mutation	SNP	C	T	2	2	c.401G>A	c.(400-402)CGC>CAC	p.R134H
Pat_45	Pre-Treatment	PTK2B	2185	37	8	27297754	27297754	Missense_Mutation	SNP	C	T	3	31	c.1835C>T	c.(1834-1836)GCC>GTC	p.A612V
Pat_45	Pre-Treatment	C8orf41	80185	37	8	33357868	33357868	Missense_Mutation	SNP	C	T	3	99	c.1400G>A	c.(1399-1401)CGC>CAC	p.R467H
Pat_45	Pre-Treatment	GPR124	25960	37	8	37693220	37693220	Missense_Mutation	SNP	C	T	4	87	c.1982C>T	c.(1981-1983)TCC>TTC	p.S661F
Pat_45	Pre-Treatment	ADRB3	155	37	8	37823923	37823923	Missense_Mutation	SNP	G	T	2	0	c.65C>A	c.(64-66)CCC>CAC	p.P22H
Pat_45	Pre-Treatment	WHSC1L1	54904	37	8	38146018	38146018	Missense_Mutation	SNP	C	T	4	132	c.3488G>A	c.(3487-3489)AGG>AAG	p.R1163K
Pat_45	Pre-Treatment	IKBKB	3551	37	8	42178346	42178346	Missense_Mutation	SNP	G	A	4	97	c.1672G>A	c.(1672-1674)GGA>AGA	p.G558R
Pat_45	Pre-Treatment	PRKDC	5591	37	8	48746808	48746808	Missense_Mutation	SNP	C	A	5	276	c.8101G>T	c.(8101-8103)GGG>TGG	p.G2701W
Pat_45	Pre-Treatment	ST18	9705	37	8	53079523	53079523	Missense_Mutation	SNP	C	T	83	137	c.1093G>A	c.(1093-1095)GAG>AAG	p.E365K
Pat_45	Pre-Treatment	TMEM68	137695	37	8	56663561	56663561	Missense_Mutation	SNP	G	A	75	127	c.649C>T	c.(649-651)CGC>TGC	p.R217C
Pat_45	Pre-Treatment	CYP7B1	9420	37	8	65527628	65527628	Missense_Mutation	SNP	G	A	32	138	c.1012C>T	c.(1012-1014)CCC>TCC	p.P338S
Pat_45	Pre-Treatment	PTDSS1	9791	37	8	97321851	97321851	Splice_Site	SNP	G	A	4	118	c.1073_splice	c.e9+1	p.G358_splice
Pat_45	Pre-Treatment	RGS22	26166	37	8	100994197	100994197	Missense_Mutation	SNP	C	T	126	248	c.3328G>A	c.(3328-3330)GAG>AAG	p.E1110K
Pat_45	Pre-Treatment	ZHX1	11244	37	8	124267180	124267180	Missense_Mutation	SNP	C	T	6	345	c.1007G>A	c.(1006-1008)CGT>CAT	p.R336H
Pat_45	Pre-Treatment	ZNF572	137209	37	8	125988764	125988764	Missense_Mutation	SNP	C	T	58	78	c.254C>T	c.(253-255)TCC>TTC	p.S85F
Pat_45	Pre-Treatment	BAI1	575	37	8	143561116	143561116	Missense_Mutation	SNP	G	A	3	41	c.1789G>A	c.(1789-1791)GGA>AGA	p.G597R
Pat_45	Pre-Treatment	KIFC2	90990	37	8	145694113	145694113	Missense_Mutation	SNP	C	T	4	113	c.1009C>T	c.(1009-1011)CGG>TGG	p.R337W
Pat_45	Pre-Treatment	MFSD3	113655	37	8	145736372	145736372	Splice_Site	SNP	A	G	2	6	c.1066_splice	c.e5-2	p.A356_splice
Pat_45	Pre-Treatment	CER1	9350	37	9	14722231	14722231	Missense_Mutation	SNP	C	T	19	35	c.440G>A	c.(439-441)GGG>GAG	p.G147E
Pat_45	Pre-Treatment	FREM1	158326	37	9	14776179	14776179	Missense_Mutation	SNP	G	A	3	48	c.4465C>T	c.(4465-4467)CGG>TGG	p.R1489W
Pat_45	Pre-Treatment	FREM1	158326	37	9	14859270	14859270	Missense_Mutation	SNP	C	T	4	138	c.542G>A	c.(541-543)CGG>CAG	p.R181Q
Pat_45	Pre-Treatment	C9orf93	203238	37	9	15623350	15623350	Missense_Mutation	SNP	G	A	7	411	c.761G>A	c.(760-762)CGA>CAA	p.R254Q
Pat_45	Pre-Treatment	FANCG	2189	37	9	35078250	35078250	Missense_Mutation	SNP	G	A	4	71	c.398C>T	c.(397-399)CCG>CTG	p.P133L
Pat_45	Pre-Treatment	FRMPD1	22844	37	9	37733588	37733588	Nonsense_Mutation	SNP	C	T	4	47	c.1114C>T	c.(1114-1116)CGA>TGA	p.R372*
Pat_45	Pre-Treatment	FLJ43859	389761	37	9	84547469	84547469	Missense_Mutation	SNP	C	T	26	21	c.2393C>T	c.(2392-2394)TCT>TTT	p.S798F
Pat_45	Pre-Treatment	SLC28A3	64078	37	9	86905169	86905169	Missense_Mutation	SNP	G	A	31	36	c.1049C>T	c.(1048-1050)CCA>CTA	p.P350L
Pat_45	Pre-Treatment	CDK20	23552	37	9	90584248	90584248	Missense_Mutation	SNP	G	A	4	51	c.704C>T	c.(703-705)CCG>CTG	p.P235L
Pat_45	Pre-Treatment	ANKRD19	138649	37	9	95576241	95576241	Missense_Mutation	SNP	C	T	4	100	c.407C>T	c.(406-408)ACT>ATT	p.T136I
Pat_45	Pre-Treatment	OR2K2	26248	37	9	114090194	114090194	Missense_Mutation	SNP	C	T	3	56	c.520G>A	c.(520-522)GAT>AAT	p.D174N
Pat_45	Pre-Treatment	PTGR1	22949	37	9	114337092	114337092	Missense_Mutation	SNP	C	T	3	93	c.682G>A	c.(682-684)GGC>AGC	p.G228S
Pat_45	Pre-Treatment	OR1J1	347168	37	9	125240181	125240181	Missense_Mutation	SNP	C	T	4	93	c.25G>A	c.(25-27)GTG>ATG	p.V9M
Pat_45	Pre-Treatment	AK1	203	37	9	130635040	130635040	Missense_Mutation	SNP	C	T	3	46	c.136G>A	c.(136-138)GAG>AAG	p.E46K
Pat_45	Pre-Treatment	NUP188	23511	37	9	131731770	131731770	Missense_Mutation	SNP	G	A	4	55	c.889G>A	c.(889-891)GCG>ACG	p.A297T
Pat_45	Pre-Treatment	C9orf106	414318	37	9	132084535	132084536	Nonsense_Mutation	DNP	GG	AA	24	27	c.443_444GG>AA	c.(442-444)TGG>TAA	p.W148*
Pat_45	Pre-Treatment	BRD3	8019	37	9	136915644	136915644	Missense_Mutation	SNP	G	A	4	51	c.566C>T	c.(565-567)ACC>ATC	p.T189I
Pat_45	Pre-Treatment	C9orf142	286257	37	9	139887380	139887380	Missense_Mutation	SNP	G	A	4	99	c.184G>A	c.(184-186)GCC>ACC	p.A62T
Pat_45	Pre-Treatment	ABCA2	20	37	9	139907164	139907164	Missense_Mutation	SNP	C	T	3	22	c.5078G>A	c.(5077-5079)CGG>CAG	p.R1693Q
Pat_45	Pre-Treatment	PLCXD1	55344	37	X	209850	209850	Missense_Mutation	SNP	G	A	4	66	c.698G>A	c.(697-699)CGA>CAA	p.R233Q
Pat_45	Pre-Treatment	ARSF	416	37	X	3002349	3002349	Missense_Mutation	SNP	G	A	4	110	c.472G>A	c.(472-474)GGG>AGG	p.G158R
Pat_45	Pre-Treatment	SHROOM2	357	37	X	9862984	9862984	Missense_Mutation	SNP	G	A	3	8	c.1036G>A	c.(1036-1038)GCA>ACA	p.A346T
Pat_45	Pre-Treatment	SH3KBP1	30011	37	X	19568187	19568187	Missense_Mutation	SNP	C	A	4	53	c.1399G>T	c.(1399-1401)GAC>TAC	p.D467Y
Pat_45	Pre-Treatment	KLHL34	257240	37	X	21675800	21675800	Missense_Mutation	SNP	T	C	2	5	c.107A>G	c.(106-108)GAG>GGG	p.E36G

Pat_45	Pre-Treatment	FAM47C	442444	37	X	37027957	37027957	Missense_Mutation	SNP	G	A	28	33	c.1474G>A	c.(1474-1476)GAC>AAC	p.D492N
Pat_45	Pre-Treatment	SYTL5	94122	37	X	37985840	37985840	Splice_Site	SNP	G	A	17	15	c.2051_splice	c.e18-1	p.G684_splice
Pat_45	Pre-Treatment	DGKK	139189	37	X	50213400	50213400	Missense_Mutation	SNP	G	A	4	73	c.278C>T	c.(277-279)CCG>CTG	p.P93L
Pat_45	Pre-Treatment	GSPT2	23708	37	X	51487156	51487156	Missense_Mutation	SNP	C	A	3	11	c.434C>A	c.(433-435)GCC>GAC	p.A145D
Pat_45	Pre-Treatment	GPR173	54328	37	X	53106351	53106351	Missense_Mutation	SNP	C	G	2	10	c.548C>G	c.(547-549)GCC>GGC	p.A183G
Pat_45	Pre-Treatment	PFKFB1	5207	37	X	54960267	54960267	Missense_Mutation	SNP	C	T	3	26	c.1343G>A	c.(1342-1344)CGG>CAG	p.R448Q
Pat_45	Pre-Treatment	NONO	4841	37	X	70514153	70514153	Missense_Mutation	SNP	G	A	23	11	c.425G>A	c.(424-426)CGC>CAC	p.R142H
Pat_45	Pre-Treatment	P2RY10	27334	37	X	78216429	78216429	Missense_Mutation	SNP	C	T	33	39	c.412C>T	c.(412-414)CCC>TCC	p.P138S
Pat_45	Pre-Treatment	MUM1L1	139221	37	X	105451229	105451229	Missense_Mutation	SNP	G	A	4	28	c.1804G>A	c.(1804-1806)GAT>AAT	p.D602N
Pat_45	Pre-Treatment	RGAG1	57529	37	X	109697032	109697032	Missense_Mutation	SNP	G	A	3	38	c.3187G>A	c.(3187-3189)GCC>ACC	p.A1063T
Pat_45	Pre-Treatment	PGRMC1	10857	37	X	118370342	118370342	Missense_Mutation	SNP	G	A	4	25	c.16G>A	c.(16-18)GTG>ATG	p.V6M
Pat_45	Pre-Treatment	CDR1	1038	37	X	139866323	139866323	Missense_Mutation	SNP	G	A	4	67	c.209C>T	c.(208-210)TCG>TTG	p.S70L
Pat_45	Pre-Treatment	MAGEC1	9947	37	X	140994163	140994163	Nonsense_Mutation	SNP	A	T	4	109	c.973A>T	c.(973-975)AGA>TGA	p.R325*
Pat_45	Pre-Treatment	SLITRK4	139065	37	X	142716578	142716578	Missense_Mutation	SNP	C	T	49	39	c.2347G>A	c.(2347-2349)GAA>AAA	p.E783K
Pat_45	Pre-Treatment	CNGA2	1260	37	X	150912089	150912089	Missense_Mutation	SNP	G	A	29	34	c.1114G>A	c.(1114-1116)GGC>AGC	p.G372S
Pat_45	Pre-Treatment	GABRQ	55879	37	X	151820196	151820196	Missense_Mutation	SNP	G	A	20	16	c.1109G>A	c.(1108-1110)AGA>AAA	p.R370K
Pat_45	Pre-Treatment	PLXNB3	5365	37	X	153036336	153036336	Nonsense_Mutation	SNP	C	T	4	40	c.2134C>T	c.(2134-2136)CGA>TGA	p.R712*
Pat_45	Pre-Treatment	DKC1	1736	37	X	153997469	153997469	Missense_Mutation	SNP	C	T	6	172	c.799C>T	c.(799-801)CTT>TTT	p.L267F
Pat_45	Pre-Treatment	NLGN4Y	22829	37	Y	16734114	16734114	Missense_Mutation	SNP	A	T	4	89	c.115A>T	c.(115-117)ATT>TTT	p.I39F
Pat_45	Post-Resistance	CPSF3L	54973	37	1	1249214	1249214	Nonsense_Mutation	SNP	C	T	11	153	c.855G>A	c.(853-855)TGG>TGA	p.W285*
Pat_45	Post-Resistance	DVL1	1855	37	1	1273814	1273814	Missense_Mutation	SNP	C	T	15	87	c.1267G>A	c.(1267-1269)GCG>ACG	p.A423T
Pat_45	Post-Resistance	NADK	65220	37	1	1688674	1688674	Missense_Mutation	SNP	C	A	56	208	c.339G>T	c.(337-339)ATG>ATT	p.M113I
Pat_45	Post-Resistance	LRRC47	57470	37	1	3703658	3703658	Missense_Mutation	SNP	C	T	11	85	c.832G>A	c.(832-834)GAA>AAA	p.E278K
Pat_45	Post-Resistance	NPHP4	261734	37	1	5923966	5923966	Missense_Mutation	SNP	C	T	4	117	c.4124G>A	c.(4123-4125)AGA>AAA	p.R1375K
Pat_45	Post-Resistance	CHD5	26038	37	1	6191691	6191691	Missense_Mutation	SNP	C	T	4	47	c.3262G>A	c.(3262-3264)GCC>ACC	p.A1088T
Pat_45	Post-Resistance	ICMT	23463	37	1	6292105	6292105	Missense_Mutation	SNP	C	T	6	65	c.529G>A	c.(529-531)GCC>ACC	p.A177T
Pat_45	Post-Resistance	CAMTA1	23261	37	1	7731074	7731074	Missense_Mutation	SNP	G	A	22	219	c.2756G>A	c.(2755-2757)GGG>GAG	p.G919E
Pat_45	Post-Resistance	RERE	473	37	1	8418946	8418946	Missense_Mutation	SNP	G	A	15	111	c.3649C>T	c.(3649-3651)CTC>TTC	p.L1217F
Pat_45	Post-Resistance	RERE	473	37	1	8425964	8425964	Missense_Mutation	SNP	C	T	8	171	c.1355G>A	c.(1354-1356)AGG>AAG	p.R452K
Pat_45	Post-Resistance	SLC2A5	6518	37	1	9098084	9098084	Splice_Site	SNP	C	T	4	50	c.1175_splice	c.e11-1	p.S392_splice
Pat_45	Post-Resistance	EXOSC10	5394	37	1	11132159	11132159	Missense_Mutation	SNP	C	T	12	148	c.2227G>A	c.(2227-2229)GCA>ACA	p.A743T
Pat_45	Post-Resistance	EXOSC10	5394	37	1	11155912	11155912	Missense_Mutation	SNP	C	T	33	352	c.275G>A	c.(274-276)GGG>GAG	p.G92E
Pat_45	Post-Resistance	MTHFR	4524	37	1	11854785	11854785	Splice_Site	SNP	C	T	47	465	c.1166_splice	c.e7+1	p.W389_splice
Pat_45	Post-Resistance	LOC440563	440563	37	1	13183290	13183290	Missense_Mutation	SNP	C	T	27	279	c.583G>A	c.(583-585)GAT>AAT	p.D195N
Pat_45	Post-Resistance	PRDM2	7799	37	1	14107415	14107415	Missense_Mutation	SNP	C	T	13	118	c.3125C>T	c.(3124-3126)TCT>TTT	p.S1042F
Pat_45	Post-Resistance	PRDM2	7799	37	1	14142945	14142945	Missense_Mutation	SNP	G	A	4	158	c.5060G>A	c.(5059-5061)CGA>CAA	p.R1687Q
Pat_45	Post-Resistance	CELA2B	51032	37	1	15812407	15812407	Missense_Mutation	SNP	C	T	21	196	c.505C>T	c.(505-507)CTC>TTC	p.L169F
Pat_45	Post-Resistance	SPEN	23013	37	1	16259910	16259910	Missense_Mutation	SNP	C	T	4	100	c.7175C>T	c.(7174-7176)TCC>TTC	p.S2392F
Pat_45	Post-Resistance	RCC2	55920	37	1	17747230	17747230	Missense_Mutation	SNP	C	T	3	43	c.839G>A	c.(838-840)TGC>TAC	p.C280Y
Pat_45	Post-Resistance	TAS1R2	80834	37	1	19166727	19166727	Missense_Mutation	SNP	G	A	9	142	c.1886C>T	c.(1885-1887)ACC>ATC	p.T629I
Pat_45	Post-Resistance	UBR4	23352	37	1	19404519	19404519	Missense_Mutation	SNP	G	A	12	107	c.15275C>T	c.(15274-15276)TCT>TTT	p.S5092F
Pat_45	Post-Resistance	UBR4	23352	37	1	19488940	19488940	Missense_Mutation	SNP	C	T	22	270	c.4930G>A	c.(4930-4932)GAG>AAG	p.E1644K
Pat_45	Post-Resistance	CAPZB	832	37	1	19810694	19810694	Missense_Mutation	SNP	G	A	12	35	c.80C>T	c.(79-81)CCC>CTC	p.P27L
Pat_45	Post-Resistance	KIF17	57576	37	1	21014062	21014062	Missense_Mutation	SNP	G	A	3	30	c.1757C>T	c.(1756-1758)GCT>GTT	p.A586V
Pat_45	Post-Resistance	ECE1	1889	37	1	21616607	21616607	Missense_Mutation	SNP	C	T	6	38	c.94G>A	c.(94-96)GTG>ATG	p.V32M
Pat_45	Post-Resistance	HSPG2	3339	37	1	22161264	22161264	Missense_Mutation	SNP	G	A	9	133	c.10628C>T	c.(10627-10629)GCC>GTC	p.A3543V
Pat_45	Post-Resistance	HSPG2	3339	37	1	22176677	22176677	Missense_Mutation	SNP	C	T	13	178	c.7303G>A	c.(7303-7305)GTC>ATC	p.V2435I

Pat_45	Post-Resistance	AIM1L	55057	37	1	26663745	26663745	Missense_Mutation	SNP	G	A	13	150	c.635C>T	c.(634-636)ACG>ATG	p.T212M
Pat_45	Post-Resistance	OPRD1	4985	37	1	29185675	29185675	Missense_Mutation	SNP	G	A	4	128	c.437G>A	c.(436-438)CGC>CAC	p.R146H
Pat_45	Post-Resistance	SFRS4	6429	37	1	29475127	29475127	Missense_Mutation	SNP	C	T	36	530	c.1280G>A	c.(1279-1281)GGT>GAT	p.G427D
Pat_45	Post-Resistance	SDC3	9672	37	1	31347342	31347342	Missense_Mutation	SNP	C	T	25	295	c.964G>A	c.(964-966)GAA>AAA	p.E322K
Pat_45	Post-Resistance	KPNA6	23633	37	1	32625032	32625032	Missense_Mutation	SNP	C	T	21	153	c.458C>T	c.(457-459)GCC>GTC	p.A153V
Pat_45	Post-Resistance	RBBP4	5928	37	1	33138423	33138423	Missense_Mutation	SNP	C	T	3	65	c.1133C>T	c.(1132-1134)TCT>TTT	p.S378F
Pat_45	Post-Resistance	KIAA1522	57648	37	1	33236897	33236897	Missense_Mutation	SNP	C	T	16	182	c.1940C>T	c.(1939-1941)TCC>TTC	p.S647F
Pat_45	Post-Resistance	RNF19B	127544	37	1	33411136	33411136	Missense_Mutation	SNP	C	T	21	222	c.1243G>A	c.(1243-1245)GTT>ATT	p.V415I
Pat_45	Post-Resistance	PHC2	1912	37	1	33794740	33794740	Missense_Mutation	SNP	C	T	5	75	c.2153G>A	c.(2152-2154)GGC>GAC	p.G718D
Pat_45	Post-Resistance	PHC2	1912	37	1	33795814	33795814	Splice_Site	SNP	C	T	10	117	c.2004_splice	c.e12-1	p.R668_splice
Pat_45	Post-Resistance	EIF2C4	192670	37	1	36297685	36297685	Missense_Mutation	SNP	C	T	10	144	c.1144C>T	c.(1144-1146)CCT>TCT	p.P382S
Pat_45	Post-Resistance	EIF2C1	26523	37	1	36358825	36358825	Missense_Mutation	SNP	C	T	13	78	c.458C>T	c.(457-459)CCC>CTC	p.P153L
Pat_45	Post-Resistance	THRAP3	9967	37	1	36755055	36755055	Missense_Mutation	SNP	C	T	5	68	c.1435C>T	c.(1435-1437)CCA>TCA	p.P479S
Pat_45	Post-Resistance	GNL2	29889	37	1	38033897	38033897	Missense_Mutation	SNP	C	T	4	70	c.1930G>A	c.(1930-1932)GAA>AAA	p.E644K
Pat_45	Post-Resistance	RRAGC	64121	37	1	39322646	39322646	Missense_Mutation	SNP	C	T	14	190	c.346G>A	c.(346-348)GAT>AAT	p.D116N
Pat_45	Post-Resistance	ZMPSTE24	10269	37	1	40758286	40758286	Missense_Mutation	SNP	C	T	6	129	c.1373C>T	c.(1372-1374)TCT>TTT	p.S458F
Pat_45	Post-Resistance	KIAA0467	23334	37	1	43914296	43914296	Missense_Mutation	SNP	C	T	13	248	c.7286C>T	c.(7285-7287)TCC>TTC	p.S2429F
Pat_45	Post-Resistance	KDM4A	9682	37	1	44134971	44134971	Splice_Site	SNP	G	A	16	188	c.1363_splice	c.e10+1	p.D455_splice
Pat_45	Post-Resistance	ATP6V0B	533	37	1	44442463	44442463	Missense_Mutation	SNP	C	T	5	102	c.367C>T	c.(367-369)CCC>TCC	p.P123S
Pat_45	Post-Resistance	PTCH2	8643	37	1	45288187	45288187	Missense_Mutation	SNP	C	T	5	48	c.3512G>A	c.(3511-3513)GGT>GAT	p.G1171D
Pat_45	Post-Resistance	TOE1	114034	37	1	45808589	45808589	Missense_Mutation	SNP	G	A	7	59	c.827G>A	c.(826-828)AGC>AAC	p.S276N
Pat_45	Post-Resistance	POMGNT1	55624	37	1	46661548	46661548	Missense_Mutation	SNP	C	T	4	53	c.469G>A	c.(469-471)GAT>AAT	p.D157N
Pat_45	Post-Resistance	NSUN4	387338	37	1	46810621	46810621	Missense_Mutation	SNP	C	T	11	92	c.242C>T	c.(241-243)GCT>GTT	p.A81V
Pat_45	Post-Resistance	STIL	6491	37	1	47759130	47759130	Missense_Mutation	SNP	C	T	5	82	c.872G>A	c.(871-873)AGG>AAG	p.R291K
Pat_45	Post-Resistance	PRPF38A	84950	37	1	52882346	52882346	Missense_Mutation	SNP	G	A	4	75	c.923G>A	c.(922-924)CGG>CAG	p.R308Q
Pat_45	Post-Resistance	FAM159A	348378	37	1	53122707	53122707	Missense_Mutation	SNP	C	T	21	265	c.568C>T	c.(568-570)CCA>TCA	p.P190S
Pat_45	Post-Resistance	C1orf175	374977	37	1	55158132	55158132	Missense_Mutation	SNP	G	A	9	93	c.2747G>A	c.(2746-2748)AGG>AAG	p.R916K
Pat_45	Post-Resistance	C1orf177	163747	37	1	55280672	55280672	Missense_Mutation	SNP	G	A	30	319	c.1010G>A	c.(1009-1011)GGG>GAG	p.G337E
Pat_45	Post-Resistance	C8B	732	37	1	57417785	57417785	Missense_Mutation	SNP	G	A	10	195	c.602C>T	c.(601-603)TCC>TTC	p.S201F
Pat_45	Post-Resistance	OMA1	115209	37	1	58999681	58999681	Missense_Mutation	SNP	G	A	18	175	c.955C>T	c.(955-957)CAT>TAT	p.H319Y
Pat_45	Post-Resistance	KANK4	163782	37	1	62740559	62740559	Missense_Mutation	SNP	A	C	16	236	c.217T>G	c.(217-219)TTC>GTC	p.F73V
Pat_45	Post-Resistance	DOCK7	85440	37	1	63099209	63099209	Missense_Mutation	SNP	G	A	10	184	c.1076C>T	c.(1075-1077)GCA>GTA	p.A359V
Pat_45	Post-Resistance	CACHD1	57685	37	1	65141144	65141144	Missense_Mutation	SNP	C	T	10	206	c.2635C>T	c.(2635-2637)CCA>TCA	p.P879S
Pat_45	Post-Resistance	DNAJC6	9829	37	1	65851433	65851433	Missense_Mutation	SNP	C	T	13	130	c.668C>T	c.(667-669)CCC>CTC	p.P223L
Pat_45	Post-Resistance	RPE65	6121	37	1	68897205	68897205	Missense_Mutation	SNP	C	T	5	57	c.1192G>A	c.(1192-1194)GAC>AAC	p.D398N
Pat_45	Post-Resistance	C1orf173	127254	37	1	75055372	75055372	Missense_Mutation	SNP	C	T	17	317	c.2119G>A	c.(2119-2121)GAA>AAA	p.E707K
Pat_45	Post-Resistance	RBMXL1	494115	37	1	89448975	89448975	Missense_Mutation	SNP	C	T	23	230	c.535G>A	c.(535-537)GGA>AGA	p.G179R
Pat_45	Post-Resistance	RBMXL1	494115	37	1	89449215	89449215	Missense_Mutation	SNP	G	A	5	77	c.295C>T	c.(295-297)CCT>TCT	p.P99S
Pat_45	Post-Resistance	GBP6	163351	37	1	89850898	89850898	Missense_Mutation	SNP	C	T	8	164	c.1772C>T	c.(1771-1773)CCC>CTC	p.P591L
Pat_45	Post-Resistance	LRRC8D	55144	37	1	90401185	90401185	Missense_Mutation	SNP	C	T	7	71	c.2558C>T	c.(2557-2559)CCC>CTC	p.P853L
Pat_45	Post-Resistance	ZNF644	84146	37	1	91403554	91403554	Missense_Mutation	SNP	C	T	5	108	c.3176G>A	c.(3175-3177)GGC>GAC	p.G1059D
Pat_45	Post-Resistance	C1orf146	388649	37	1	92707815	92707815	Missense_Mutation	SNP	G	A	9	103	c.113G>A	c.(112-114)CGA>CAA	p.R38Q
Pat_45	Post-Resistance	COL11A1	1301	37	1	103400666	103400666	Missense_Mutation	SNP	G	A	4	44	c.3442C>T	c.(3442-3444)CCT>TCT	p.P1148S
Pat_45	Post-Resistance	COL11A1	1301	37	1	103471401	103471401	Missense_Mutation	SNP	C	G	21	233	c.1838G>C	c.(1837-1839)GGT>GCT	p.G613A
Pat_45	Post-Resistance	CLCC1	23155	37	1	109486509	109486509	Missense_Mutation	SNP	C	A	6	85	c.510G>T	c.(508-510)TGG>TGT	p.W170C
Pat_45	Post-Resistance	CYB561D1	284613	37	1	110038705	110038705	Missense_Mutation	SNP	G	A	15	229	c.514G>A	c.(514-516)GTG>ATG	p.V172M
Pat_45	Post-Resistance	KCNA3	3738	37	1	111215826	111215826	Missense_Mutation	SNP	C	T	5	93	c.1606G>A	c.(1606-1608)GGT>AGT	p.G536S

Pat_45	Post-Resistance	C1orf183	55924	37	1	112269948	112269948	Missense_Mutation	SNP	C	T	14	232	c.536G>A	c.(535-537)GGG>GAG	p.G179E
Pat_45	Post-Resistance	ATP1A1	476	37	1	116932123	116932123	Missense_Mutation	SNP	C	T	18	262	c.817C>T	c.(817-819)CTT>TTT	p.L273F
Pat_45	Post-Resistance	TRIM45	80263	37	1	117661336	117661336	Missense_Mutation	SNP	C	T	13	222	c.542G>A	c.(541-543)GGC>GAC	p.G181D
Pat_45	Post-Resistance	VTCN1	79679	37	1	117690383	117690383	Missense_Mutation	SNP	C	T	10	146	c.746G>A	c.(745-747)AGT>AAT	p.S249N
Pat_45	Post-Resistance	SPAG17	200162	37	1	118623853	118623853	Missense_Mutation	SNP	G	A	15	108	c.2080C>T	c.(2080-2082)CCT>TCT	p.P694S
Pat_45	Post-Resistance	ANXA9	8416	37	1	150967749	150967749	Missense_Mutation	SNP	G	A	28	240	c.989G>A	c.(988-990)GGG>GAG	p.G330E
Pat_45	Post-Resistance	PRUNE	58497	37	1	151001398	151001398	Missense_Mutation	SNP	C	T	3	81	c.911C>T	c.(910-912)CCC>CTC	p.P304L
Pat_45	Post-Resistance	ZNF687	57592	37	1	151263588	151263588	Missense_Mutation	SNP	G	A	7	108	c.3617G>A	c.(3616-3618)GGC>GAC	p.G1206D
Pat_45	Post-Resistance	POGZ	23126	37	1	151400607	151400607	Missense_Mutation	SNP	G	A	11	178	c.851C>T	c.(850-852)CCC>CTC	p.P284L
Pat_45	Post-Resistance	POGZ	23126	37	1	151414616	151414616	Missense_Mutation	SNP	C	T	3	46	c.65G>A	c.(64-66)AGT>AAT	p.S22N
Pat_45	Post-Resistance	LINGO4	339398	37	1	151774244	151774244	Missense_Mutation	SNP	T	G	6	54	c.937A>C	c.(937-939)ACC>CCC	p.T313P
Pat_45	Post-Resistance	TCHH	7062	37	1	152082827	152082827	Missense_Mutation	SNP	G	A	18	177	c.2866C>T	c.(2866-2868)CGG>TGG	p.R956W
Pat_45	Post-Resistance	FLG	2312	37	1	152280643	152280643	Missense_Mutation	SNP	C	T	35	453	c.6719G>A	c.(6718-6720)GGA>GAA	p.G2240E
Pat_45	Post-Resistance	FLG2	388698	37	1	152323162	152323162	Missense_Mutation	SNP	C	T	22	131	c.7100G>A	c.(7099-7101)AGC>AAC	p.S2367N
Pat_45	Post-Resistance	JTB	10899	37	1	153948353	153948353	Missense_Mutation	SNP	C	T	6	103	c.233G>A	c.(232-234)GGA>GAA	p.G78E
Pat_45	Post-Resistance	TPM3	7170	37	1	154148619	154148619	Missense_Mutation	SNP	C	T	9	123	c.349G>A	c.(349-351)GCT>ACT	p.A117T
Pat_45	Post-Resistance	ATP8B2	57198	37	1	154317127	154317127	Missense_Mutation	SNP	G	A	8	204	c.2251G>A	c.(2251-2253)GAG>AAG	p.E751K
Pat_45	Post-Resistance	ADAR	103	37	1	154574907	154574907	Missense_Mutation	SNP	G	A	18	142	c.211C>T	c.(211-213)CTC>TTC	p.L71F
Pat_45	Post-Resistance	PYGO2	90780	37	1	154932226	154932226	Missense_Mutation	SNP	C	T	6	51	c.250G>A	c.(250-252)GCC>ACC	p.A84T
Pat_45	Post-Resistance	TRIM46	80128	37	1	155156527	155156527	Missense_Mutation	SNP	T	G	3	69	c.2141T>G	c.(2140-2142)TTG>TGG	p.L714W
Pat_45	Post-Resistance	THBS3	7059	37	1	155172189	155172189	Missense_Mutation	SNP	C	T	13	158	c.961G>A	c.(961-963)GCT>ACT	p.A321T
Pat_45	Post-Resistance	SCAMP3	10067	37	1	155230154	155230154	Missense_Mutation	SNP	C	T	11	110	c.355G>A	c.(355-357)GAG>AAG	p.E119K
Pat_45	Post-Resistance	SLC25A44	9673	37	1	156169645	156169645	Missense_Mutation	SNP	G	A	12	158	c.7G>A	c.(7-9)GAC>AAC	p.D3N
Pat_45	Post-Resistance	SMG5	23381	37	1	156222745	156222745	Missense_Mutation	SNP	G	A	4	29	c.2627C>T	c.(2626-2628)ACC>ATC	p.T876I
Pat_45	Post-Resistance	C1orf85	112770	37	1	156263853	156263853	Missense_Mutation	SNP	C	T	13	239	c.754G>A	c.(754-756)GAG>AAG	p.E252K
Pat_45	Post-Resistance	GPATCH4	54865	37	1	156568241	156568241	Missense_Mutation	SNP	C	T	25	399	c.140G>A	c.(139-141)AGG>AAG	p.R47K
Pat_45	Post-Resistance	FCRL1	115350	37	1	157776892	157776892	Missense_Mutation	SNP	C	T	29	114	c.52G>A	c.(52-54)GAG>AAG	p.E18K
Pat_45	Post-Resistance	CD1D	912	37	1	158151334	158151334	Missense_Mutation	SNP	G	A	24	249	c.151G>A	c.(151-153)GGG>AGG	p.G51R
Pat_45	Post-Resistance	CRP	1401	37	1	159683787	159683787	Missense_Mutation	SNP	C	T	13	133	c.203G>A	c.(202-204)AGT>AAT	p.S68N
Pat_45	Post-Resistance	ATP1A2	477	37	1	160105688	160105688	Missense_Mutation	SNP	C	T	21	288	c.2344C>T	c.(2344-2346)CCC>TCC	p.P782S
Pat_45	Post-Resistance	NCSTN	23385	37	1	160322963	160322963	Missense_Mutation	SNP	C	T	6	122	c.1115C>T	c.(1114-1116)ACT>ATT	p.T372I
Pat_45	Post-Resistance	DEDD	9191	37	1	161093674	161093674	Missense_Mutation	SNP	C	T	16	125	c.388G>A	c.(388-390)GCC>ACC	p.A130T
Pat_45	Post-Resistance	USP21	27005	37	1	161130993	161130993	Missense_Mutation	SNP	C	T	4	74	c.563C>T	c.(562-564)GCC>GTC	p.A188V
Pat_45	Post-Resistance	PPOX	5498	37	1	161138303	161138303	Missense_Mutation	SNP	C	T	7	107	c.553C>T	c.(553-555)CCC>TCC	p.P185S
Pat_45	Post-Resistance	RGS5	8490	37	1	163122354	163122354	Missense_Mutation	SNP	C	T	136	272	c.370G>A	c.(370-372)GAG>AAG	p.E124K
Pat_45	Post-Resistance	ILDR2	387597	37	1	166927029	166927029	Missense_Mutation	SNP	C	T	14	107	c.356G>A	c.(355-357)GGC>GAC	p.G119D
Pat_45	Post-Resistance	POU2F1	5451	37	1	167381247	167381247	Missense_Mutation	SNP	C	T	9	156	c.1538C>T	c.(1537-1539)CCT>CTT	p.P513L
Pat_45	Post-Resistance	MPZL1	9019	37	1	167745386	167745386	Missense_Mutation	SNP	C	T	6	121	c.691C>T	c.(691-693)CCT>TCT	p.P231S
Pat_45	Post-Resistance	F5	2153	37	1	169510571	169510571	Missense_Mutation	SNP	G	A	9	298	c.3757C>T	c.(3757-3759)CTC>TTC	p.L1253F
Pat_45	Post-Resistance	FMO1	2326	37	1	171251362	171251362	Missense_Mutation	SNP	C	T	3	81	c.1073C>T	c.(1072-1074)CCT>CTT	p.P358L
Pat_45	Post-Resistance	METTL13	51603	37	1	171756938	171756938	Missense_Mutation	SNP	C	T	8	96	c.1177C>T	c.(1177-1179)CCC>TCC	p.P393S
Pat_45	Post-Resistance	KLHL20	27252	37	1	173685205	173685205	Missense_Mutation	SNP	G	A	15	142	c.23G>A	c.(22-24)AGG>AAG	p.R8K
Pat_45	Post-Resistance	RC3H1	149041	37	1	173931173	173931173	Missense_Mutation	SNP	G	A	6	72	c.1892C>T	c.(1891-1893)GCT>GTT	p.A631V
Pat_45	Post-Resistance	TOR1AIP1	26092	37	1	179886668	179886668	Missense_Mutation	SNP	C	T	26	161	c.1046C>T	c.(1045-1047)TCT>TTT	p.S349F
Pat_45	Post-Resistance	TOR1AIP1	26092	37	1	179887234	179887234	Missense_Mutation	SNP	G	A	13	106	c.1612G>A	c.(1612-1614)GTC>ATC	p.V538I
Pat_45	Post-Resistance	CEP350	9857	37	1	180080214	180080214	Missense_Mutation	SNP	G	A	4	67	c.9272G>A	c.(9271-9273)GGG>GAG	p.G3091E
Pat_45	Post-Resistance	LAMC1	3915	37	1	183111888	183111888	Missense_Mutation	SNP	C	T	17	106	c.4793C>T	c.(4792-4794)TCT>TTT	p.S1598F

Pat_45	Post-Resistance	HMCN1	83872	37	1	186064584	186064584	Missense_Mutation	SNP	G	A	15	106	c.10504G>A	c.(10504-10506)GGA>AG	p.G3502R
Pat_45	Post-Resistance	CAMSAP1L1	23271	37	1	200817176	200817176	Missense_Mutation	SNP	G	A	4	54	c.1312G>A	c.(1312-1314)GTA>ATA	p.V438I
Pat_45	Post-Resistance	NAV1	89796	37	1	201786372	201786372	Missense_Mutation	SNP	G	A	4	84	c.5488G>A	c.(5488-5490)GTC>ATC	p.V1830I
Pat_45	Post-Resistance	SHISA4	149345	37	1	201860675	201860675	Missense_Mutation	SNP	C	T	48	146	c.526C>T	c.(526-528)CCC>TCC	p.P176S
Pat_45	Post-Resistance	TIMM17A	10440	37	1	201934587	201934587	Missense_Mutation	SNP	G	A	14	66	c.346G>A	c.(346-348)GCC>ACC	p.A116T
Pat_45	Post-Resistance	RNPEP	6051	37	1	201958602	201958602	Missense_Mutation	SNP	C	T	12	166	c.680C>T	c.(679-681)CCC>CTC	p.P227L
Pat_45	Post-Resistance	LGR6	59352	37	1	202278202	202278202	Missense_Mutation	SNP	C	T	19	138	c.1304C>T	c.(1303-1305)ACC>ATC	p.T435I
Pat_45	Post-Resistance	ZC3H11A	9877	37	1	203821489	203821489	Missense_Mutation	SNP	G	A	4	65	c.2395G>A	c.(2395-2397)GAC>AAC	p.D799N
Pat_45	Post-Resistance	LRRN2	10446	37	1	204587326	204587326	Missense_Mutation	SNP	C	T	6	30	c.1795G>A	c.(1795-1797)GTG>ATG	p.V599M
Pat_45	Post-Resistance	DSTYK	25778	37	1	205156710	205156710	Missense_Mutation	SNP	T	C	5	64	c.490A>G	c.(490-492)AGC>GGC	p.S164G
Pat_45	Post-Resistance	SLC26A9	115019	37	1	205890972	205890972	Missense_Mutation	SNP	C	T	4	45	c.1777G>A	c.(1777-1779)GTC>ATC	p.V593I
Pat_45	Post-Resistance	CR1	1378	37	1	207758068	207758068	Missense_Mutation	SNP	G	A	8	149	c.4027G>A	c.(4027-4029)GGA>AGA	p.G1343R
Pat_45	Post-Resistance	LAMB3	3914	37	1	209799042	209799042	Missense_Mutation	SNP	C	T	13	117	c.1927G>A	c.(1927-1929)GTC>ATC	p.V643I
Pat_45	Post-Resistance	TRAF3IP3	80342	37	1	209954799	209954799	Missense_Mutation	SNP	C	T	7	101	c.1559C>T	c.(1558-1560)CCC>CTC	p.P520L
Pat_45	Post-Resistance	RCOR3	55758	37	1	211487015	211487015	Missense_Mutation	SNP	C	T	16	195	c.1393C>T	c.(1393-1395)CGT>TGT	p.R465C
Pat_45	Post-Resistance	DTL	51514	37	1	212238342	212238342	Nonsense_Mutation	SNP	C	T	11	131	c.610C>T	c.(610-612)CAG>TAG	p.Q204*
Pat_45	Post-Resistance	BPNT1	10380	37	1	220236290	220236290	Missense_Mutation	SNP	G	A	9	91	c.481C>T	c.(481-483)CCA>TCA	p.P161S
Pat_45	Post-Resistance	MARK1	4139	37	1	220805650	220805650	Missense_Mutation	SNP	C	T	4	54	c.1117C>T	c.(1117-1119)CCT>TCT	p.P373S
Pat_45	Post-Resistance	AIDA	64853	37	1	222843496	222843496	Missense_Mutation	SNP	G	A	5	113	c.803C>T	c.(802-804)CCT>CTT	p.P268L
Pat_45	Post-Resistance	DISP1	84976	37	1	223156444	223156444	Missense_Mutation	SNP	C	T	5	61	c.532C>T	c.(532-534)CCA>TCA	p.P178S
Pat_45	Post-Resistance	NVL	4931	37	1	224505589	224505589	Missense_Mutation	SNP	C	T	3	57	c.175G>A	c.(175-177)GTA>ATA	p.V59I
Pat_45	Post-Resistance	PYCR2	29920	37	1	226108178	226108178	Missense_Mutation	SNP	C	T	6	59	c.940G>A	c.(940-942)GCC>ACC	p.A314T
Pat_45	Post-Resistance	LEFTY2	7044	37	1	226128594	226128594	Nonsense_Mutation	SNP	G	A	11	182	c.247C>T	c.(247-249)CGA>TGA	p.R83*
Pat_45	Post-Resistance	ACBD3	64746	37	1	226340062	226340062	Missense_Mutation	SNP	G	A	37	294	c.1349C>T	c.(1348-1350)TCC>TTC	p.S450F
Pat_45	Post-Resistance	JMJD4	65094	37	1	227921201	227921201	Missense_Mutation	SNP	G	A	13	63	c.874C>T	c.(874-876)CTT>TTT	p.L292F
Pat_45	Post-Resistance	OBSCN	84033	37	1	228509232	228509232	Missense_Mutation	SNP	G	A	4	38	c.14690G>A	c.(14689-14691)GGG>GA	p.G4897E
Pat_45	Post-Resistance	TRIM17	51127	37	1	228602724	228602724	Missense_Mutation	SNP	G	A	7	65	c.50C>T	c.(49-51)TCC>TTC	p.S17F
Pat_45	Post-Resistance	URB2	9816	37	1	229772338	229772338	Missense_Mutation	SNP	G	A	14	346	c.1978G>A	c.(1978-1980)GAG>AAG	p.E660K
Pat_45	Post-Resistance	C1orf124	83932	37	1	231487140	231487140	Missense_Mutation	SNP	G	A	3	46	c.541G>A	c.(541-543)GGC>AGC	p.G181S
Pat_45	Post-Resistance	KIAA1383	54627	37	1	232942466	232942466	Missense_Mutation	SNP	C	T	4	58	c.1697C>T	c.(1696-1698)GCC>GTC	p.A566V
Pat_45	Post-Resistance	PCNXL2	80003	37	1	233395048	233395048	Missense_Mutation	SNP	G	A	3	20	c.560C>T	c.(559-561)TCT>TTT	p.S187F
Pat_45	Post-Resistance	RBM34	23029	37	1	235299373	235299373	Missense_Mutation	SNP	C	T	3	43	c.865G>A	c.(865-867)GTT>ATT	p.V289I
Pat_45	Post-Resistance	ARID4B	51742	37	1	235416125	235416125	Splice_Site	SNP	C	T	9	73	c.275_splice	c.e6-1	p.V92_splice
Pat_45	Post-Resistance	LYST	1130	37	1	235972151	235972151	Missense_Mutation	SNP	C	T	6	48	c.1967G>A	c.(1966-1968)GGA>GAA	p.G656E
Pat_45	Post-Resistance	LYST	1130	37	1	235993582	235993582	Missense_Mutation	SNP	G	A	14	113	c.136C>T	c.(136-138)CTT>TTT	p.L46F
Pat_45	Post-Resistance	NID1	4811	37	1	236157029	236157029	Missense_Mutation	SNP	C	T	14	35	c.2671G>A	c.(2671-2673)GGC>AGC	p.G891S
Pat_45	Post-Resistance	RYR2	6262	37	1	237897032	237897032	Missense_Mutation	SNP	G	T	3	34	c.11067G>T	c.(11065-11067)ATG>ATT	p.M3689I
Pat_45	Post-Resistance	FMN2	56776	37	1	240255995	240255995	Missense_Mutation	SNP	C	T	3	38	c.586C>T	c.(586-588)CTT>TTT	p.L196F
Pat_45	Post-Resistance	SMYD3	64754	37	1	246490624	246490624	Missense_Mutation	SNP	G	A	4	17	c.410C>T	c.(409-411)ACT>ATT	p.T137I
Pat_45	Post-Resistance	OR2T2	401992	37	1	248616438	248616438	Missense_Mutation	SNP	T	C	4	151	c.340T>C	c.(340-342)TTC>CTC	p.F114L
Pat_45	Post-Resistance	OR2G6	391211	37	1	248684984	248684984	Missense_Mutation	SNP	C	T	30	114	c.37C>T	c.(37-39)CTT>TTT	p.L13F
Pat_45	Post-Resistance	TUBAL3	79861	37	10	5437346	5437346	Missense_Mutation	SNP	G	A	61	266	c.340C>T	c.(340-342)CGT>TGT	p.R114C
Pat_45	Post-Resistance	FAM107B	83641	37	10	14816530	14816530	Missense_Mutation	SNP	C	T	3	68	c.133G>A	c.(133-135)GTG>ATG	p.V45M
Pat_45	Post-Resistance	SUV39H2	79723	37	10	14939349	14939349	Missense_Mutation	SNP	G	A	6	102	c.502G>A	c.(502-504)GAA>AAA	p.E168K
Pat_45	Post-Resistance	PLXDC2	84898	37	10	20436832	20436832	Splice_Site	SNP	G	A	5	48	c.783_splice	c.e6+1	p.E261_splice
Pat_45	Post-Resistance	PTCHD3	374308	37	10	27702690	27702690	Missense_Mutation	SNP	C	T	15	207	c.490G>A	c.(490-492)GAG>AAG	p.E164K
Pat_45	Post-Resistance	ZNF438	220929	37	10	31138702	31138702	Missense_Mutation	SNP	T	A	4	51	c.632A>T	c.(631-633)CAT>CTT	p.H211L

Pat_45	Post-Resistance	ANKRD30A	91074	37	10	37430754	37430754	Missense_Mutation	SNP	T	C	9	77	c.761T>C	c.(760-762)GTG>GCG	p.V254A
Pat_45	Post-Resistance	BMS1	9790	37	10	43289384	43289384	Missense_Mutation	SNP	G	A	13	48	c.1174G>A	c.(1174-1176)GTG>ATG	p.V392M
Pat_45	Post-Resistance	RET	5979	37	10	43604641	43604641	Missense_Mutation	SNP	C	T	11	73	c.1226C>T	c.(1225-1227)TCC>TTC	p.S409F
Pat_45	Post-Resistance	NCOA4	8031	37	10	51582809	51582809	Missense_Mutation	SNP	G	A	5	55	c.584G>A	c.(583-585)GGT>GAT	p.G195D
Pat_45	Post-Resistance	EGR2	1959	37	10	64575768	64575768	Missense_Mutation	SNP	C	T	66	453	c.22G>A	c.(22-24)GAC>AAC	p.D8N
Pat_45	Post-Resistance	CTNNA3	29119	37	10	67829190	67829190	Missense_Mutation	SNP	C	T	9	69	c.2035G>A	c.(2035-2037)GAT>AAT	p.D679N
Pat_45	Post-Resistance	RUFY2	55680	37	10	70161376	70161376	Splice_Site	SNP	C	T	13	127	c.401_splice	c.e3+1	p.K134_splice
Pat_45	Post-Resistance	TET1	80312	37	10	70333230	70333230	Missense_Mutation	SNP	C	T	46	185	c.1135C>T	c.(1135-1137)CCT>TCT	p.P379S
Pat_45	Post-Resistance	DDX50	79009	37	10	70672975	70672975	Missense_Mutation	SNP	G	A	4	77	c.697G>A	c.(697-699)GAT>AAT	p.D233N
Pat_45	Post-Resistance	VPS26A	9559	37	10	70892711	70892711	Missense_Mutation	SNP	G	A	8	47	c.61G>A	c.(61-63)GGG>AGG	p.G21R
Pat_45	Post-Resistance	DDIT4	54541	37	10	74034141	74034141	Missense_Mutation	SNP	C	T	6	84	c.167C>T	c.(166-168)TCC>TTC	p.S56F
Pat_45	Post-Resistance	USP54	159195	37	10	75276534	75276534	Missense_Mutation	SNP	C	T	9	183	c.3650G>A	c.(3649-3651)GGT>GAT	p.G1217D
Pat_45	Post-Resistance	DLG5	9231	37	10	79554698	79554698	Missense_Mutation	SNP	C	T	16	52	c.5455G>A	c.(5455-5457)GAC>AAC	p.D1819N
Pat_45	Post-Resistance	SFTPD	6441	37	10	81697744	81697744	Missense_Mutation	SNP	G	A	16	394	c.992C>T	c.(991-993)TCC>TTC	p.S331F
Pat_45	Post-Resistance	HHEX	3087	37	10	94452275	94452275	Missense_Mutation	SNP	C	T	4	59	c.512C>T	c.(511-513)GCC>GTC	p.A171V
Pat_45	Post-Resistance	CYP2C18	1562	37	10	96447632	96447632	Missense_Mutation	SNP	G	A	17	100	c.274G>A	c.(274-276)GAG>AAG	p.E92K
Pat_45	Post-Resistance	CYP2C8	1558	37	10	96802652	96802652	Missense_Mutation	SNP	G	A	24	99	c.1144C>T	c.(1144-1146)CCC>TCC	p.P382S
Pat_45	Post-Resistance	RRP12	23223	37	10	99126308	99126308	Missense_Mutation	SNP	C	T	4	87	c.3286G>A	c.(3286-3288)GAG>AAG	p.E1096K
Pat_45	Post-Resistance	RRP12	23223	37	10	99139485	99139485	Missense_Mutation	SNP	G	A	16	89	c.1576C>T	c.(1576-1578)CCC>TCC	p.P526S
Pat_45	Post-Resistance	MMS19	64210	37	10	99222430	99222430	Missense_Mutation	SNP	G	A	3	47	c.1922C>T	c.(1921-1923)CCC>CTC	p.P641L
Pat_45	Post-Resistance	SEMA4G	57715	37	10	102740727	102740727	Missense_Mutation	SNP	C	T	14	115	c.1616C>T	c.(1615-1617)ACC>ATC	p.T539I
Pat_45	Post-Resistance	TRIM8	81603	37	10	104416851	104416851	Missense_Mutation	SNP	C	T	14	161	c.1396C>T	c.(1396-1398)CTC>TTC	p.L466F
Pat_45	Post-Resistance	SH3PXD2A	9644	37	10	105495501	105495501	Missense_Mutation	SNP	C	T	22	287	c.295G>A	c.(295-297)GAA>AAA	p.E99K
Pat_45	Post-Resistance	SLK	9748	37	10	105761973	105761973	Missense_Mutation	SNP	C	T	13	112	c.1037C>T	c.(1036-1038)GCC>GTC	p.A346V
Pat_45	Post-Resistance	CCDC147	159686	37	10	106118145	106118145	Missense_Mutation	SNP	T	C	7	35	c.56T>C	c.(55-57)ATG>ACG	p.M19T
Pat_45	Post-Resistance	BAG3	9531	37	10	121432104	121432104	Missense_Mutation	SNP	G	A	20	76	c.845G>A	c.(844-846)AGG>AAG	p.R282K
Pat_45	Post-Resistance	INPP5F	22876	37	10	121586180	121586180	Missense_Mutation	SNP	A	G	9	114	c.2287A>G	c.(2287-2289)AGG>GGG	p.R763G
Pat_45	Post-Resistance	C10orf119	79892	37	10	121608956	121608956	Missense_Mutation	SNP	C	T	6	52	c.707G>A	c.(706-708)GGC>GAC	p.G236D
Pat_45	Post-Resistance	DHX32	55760	37	10	127527686	127527686	Missense_Mutation	SNP	C	T	15	103	c.1765G>A	c.(1765-1767)GCT>ACT	p.A589T
Pat_45	Post-Resistance	ADAM12	8038	37	10	127727947	127727947	Missense_Mutation	SNP	G	A	6	104	c.2165C>T	c.(2164-2166)GCT>GTT	p.A722V
Pat_45	Post-Resistance	MKI67	4288	37	10	129907471	129907471	Missense_Mutation	SNP	G	A	19	258	c.2633C>T	c.(2632-2634)TCT>TTT	p.S878F
Pat_45	Post-Resistance	BNIP3	664	37	10	133786587	133786587	Missense_Mutation	SNP	C	T	37	250	c.233G>A	c.(232-234)AGG>AAG	p.R78K
Pat_45	Post-Resistance	JAKMIP3	282973	37	10	133967314	133967314	Missense_Mutation	SNP	G	A	14	363	c.2119G>A	c.(2119-2121)GAT>AAT	p.D707N
Pat_45	Post-Resistance	JAKMIP3	282973	37	10	133967483	133967483	Nonsense_Mutation	SNP	C	T	9	129	c.2203C>T	c.(2203-2205)CAG>TAG	p.Q735*
Pat_45	Post-Resistance	PAOX	196743	37	10	135195101	135195101	Missense_Mutation	SNP	C	T	10	160	c.806C>T	c.(805-807)TCG>TTG	p.S269L
Pat_45	Post-Resistance	PTDSS2	81490	37	11	460260	460260	Missense_Mutation	SNP	C	T	7	104	c.256C>T	c.(256-258)CCT>TCT	p.P86S
Pat_45	Post-Resistance	MUC2	4583	37	11	1080524	1080524	Missense_Mutation	SNP	G	T	3	30	c.1166G>T	c.(1165-1167)GGC>GTC	p.G389V
Pat_45	Post-Resistance	MUC5B	727897	37	11	1162355	1162355	Missense_Mutation	SNP	G	A	6	58	c.1864G>A	c.(1864-1866)GAG>AAG	p.E622K
Pat_45	Post-Resistance	CD81	975	37	11	2398786	2398786	Missense_Mutation	SNP	G	A	3	15	c.7G>A	c.(7-9)GTG>ATG	p.V3M
Pat_45	Post-Resistance	OR51T1	401665	37	11	4903401	4903401	Missense_Mutation	SNP	C	T	8	74	c.353C>T	c.(352-354)GCC>GTC	p.A118V
Pat_45	Post-Resistance	OR51A7	119687	37	11	4929446	4929446	Missense_Mutation	SNP	C	T	13	124	c.847C>T	c.(847-849)CCG>TCG	p.P283S
Pat_45	Post-Resistance	OR51M1	390059	37	11	5411211	5411211	Missense_Mutation	SNP	G	A	10	124	c.583G>A	c.(583-585)GAA>AAA	p.E195K
Pat_45	Post-Resistance	OR52B2	255725	37	11	6191508	6191508	Missense_Mutation	SNP	G	A	10	33	c.49C>T	c.(49-51)CCT>TCT	p.P17S
Pat_45	Post-Resistance	SBF2	81846	37	11	10052627	10052627	Missense_Mutation	SNP	C	T	19	159	c.370G>A	c.(370-372)GTA>ATA	p.V124I
Pat_45	Post-Resistance	SLC5A12	159963	37	11	26692673	26692673	Missense_Mutation	SNP	C	T	10	174	c.1833G>A	c.(1831-1833)ATG>ATA	p.M611I
Pat_45	Post-Resistance	RCN1	5954	37	11	32119901	32119901	Missense_Mutation	SNP	C	T	7	64	c.454C>T	c.(454-456)CCC>TCC	p.P152S
Pat_45	Post-Resistance	CRY2	1408	37	11	45882416	45882416	Missense_Mutation	SNP	G	A	7	132	c.548G>A	c.(547-549)GGG>GAG	p.G183E

Pat_45	Post-Resistance	KIAA0652	9776	37	11	46665911	46665911	Splice_Site	SNP	G	A	8	142	c.69_splice	c.e3+1	p.K23_splice
Pat_45	Post-Resistance	MADD	8567	37	11	47303958	47303958	Missense_Mutation	SNP	C	T	9	145	c.1496C>T	c.(1495-1497)TCC>TTC	p.S499F
Pat_45	Post-Resistance	OR5M11	219487	37	11	56310465	56310465	Missense_Mutation	SNP	G	A	4	45	c.269C>T	c.(268-270)ACC>ATC	p.T90I
Pat_45	Post-Resistance	UBE2L6	9246	37	11	57321972	57321972	Missense_Mutation	SNP	C	T	34	259	c.248G>A	c.(247-249)GGA>GAA	p.G83E
Pat_45	Post-Resistance	CTNND1	1500	37	11	57564110	57564110	Missense_Mutation	SNP	C	T	19	226	c.602C>T	c.(601-603)ACC>ATC	p.T201I
Pat_45	Post-Resistance	MS4A14	84689	37	11	60170449	60170449	Missense_Mutation	SNP	C	T	18	224	c.383C>T	c.(382-384)ACC>ATC	p.T128I
Pat_45	Post-Resistance	MS4A1	931	37	11	60229888	60229888	Missense_Mutation	SNP	C	G	3	55	c.41C>G	c.(40-42)GCA>GGA	p.A14G
Pat_45	Post-Resistance	CD6	923	37	11	60785844	60785844	Missense_Mutation	SNP	G	A	4	27	c.1921G>A	c.(1921-1923)GAG>AAG	p.E641K
Pat_45	Post-Resistance	AHNAK	79026	37	11	62292183	62292183	Missense_Mutation	SNP	C	T	4	48	c.9706G>A	c.(9706-9708)GAG>AAG	p.E3236K
Pat_45	Post-Resistance	MAP4K2	5871	37	11	64564631	64564631	Missense_Mutation	SNP	C	T	15	65	c.1310G>A	c.(1309-1311)AGC>AAC	p.S437N
Pat_45	Post-Resistance	CDCA5	113130	37	11	64846868	64846868	Missense_Mutation	SNP	G	A	17	110	c.635C>T	c.(634-636)CCC>CTC	p.P212L
Pat_45	Post-Resistance	FRMD8	83786	37	11	65168298	65168298	Missense_Mutation	SNP	G	A	9	144	c.1031G>A	c.(1030-1032)GGC>GAC	p.G344D
Pat_45	Post-Resistance	KDM2A	22992	37	11	67020958	67020958	Nonsense_Mutation	SNP	G	A	26	262	c.2967G>A	c.(2965-2967)TGG>TGA	p.W989*
Pat_45	Post-Resistance	LRP5	4041	37	11	68216419	68216419	Missense_Mutation	SNP	C	T	14	135	c.4729C>T	c.(4729-4731)CCC>TCC	p.P1577S
Pat_45	Post-Resistance	SHANK2	22941	37	11	70319218	70319218	Missense_Mutation	SNP	A	T	25	107	c.5306T>A	c.(5305-5307)CTG>CAG	p.L1769Q
Pat_45	Post-Resistance	ARHGEF17	9828	37	11	73022424	73022424	Missense_Mutation	SNP	C	T	12	135	c.2741C>T	c.(2740-2742)TCC>TTC	p.S914F
Pat_45	Post-Resistance	RELT	84957	37	11	73101611	73101611	Missense_Mutation	SNP	C	T	68	221	c.61C>T	c.(61-63)CTC>TTC	p.L21F
Pat_45	Post-Resistance	SLCO2B1	11309	37	11	74880368	74880368	Missense_Mutation	SNP	G	A	11	198	c.599G>A	c.(598-600)GGC>GAC	p.G200D
Pat_45	Post-Resistance	INTS4	92105	37	11	77672136	77672136	Missense_Mutation	SNP	G	A	14	148	c.520C>T	c.(520-522)CTT>TTT	p.L174F
Pat_45	Post-Resistance	PCF11	51585	37	11	82878306	82878306	Missense_Mutation	SNP	C	T	8	45	c.1957C>T	c.(1957-1959)CCT>TCT	p.P653S
Pat_45	Post-Resistance	PCF11	51585	37	11	82879547	82879547	Missense_Mutation	SNP	C	T	9	121	c.2170C>T	c.(2170-2172)CCA>TCA	p.P724S
Pat_45	Post-Resistance	PCF11	51585	37	11	82879997	82879997	Missense_Mutation	SNP	G	A	5	119	c.2620G>A	c.(2620-2622)GGT>AGT	p.G874S
Pat_45	Post-Resistance	C11orf73	51501	37	11	86055741	86055741	Missense_Mutation	SNP	C	T	19	133	c.517C>T	c.(517-519)CCG>TCG	p.P173S
Pat_45	Post-Resistance	FAT3	120114	37	11	92495281	92495281	Missense_Mutation	SNP	C	T	4	68	c.3929C>T	c.(3928-3930)ACT>ATT	p.T1310I
Pat_45	Post-Resistance	FAT3	120114	37	11	92531755	92531755	Missense_Mutation	SNP	C	T	6	54	c.5576C>T	c.(5575-5577)CCC>CTC	p.P1859L
Pat_45	Post-Resistance	HEPHL1	341208	37	11	93800692	93800692	Missense_Mutation	SNP	C	T	23	117	c.839C>T	c.(838-840)CCG>CTG	p.P280L
Pat_45	Post-Resistance	ENDOD1	23052	37	11	94862237	94862237	Missense_Mutation	SNP	G	A	3	22	c.997G>A	c.(997-999)GGC>AGC	p.G333S
Pat_45	Post-Resistance	KIAA1826	84437	37	11	105881565	105881565	Missense_Mutation	SNP	C	T	3	59	c.80G>A	c.(79-81)AGG>AAG	p.R27K
Pat_45	Post-Resistance	EXPH5	23086	37	11	108385480	108385480	Missense_Mutation	SNP	G	A	5	91	c.754C>T	c.(754-756)CAT>TAT	p.H252Y
Pat_45	Post-Resistance	NCAM1	4684	37	11	113146084	113146084	Missense_Mutation	SNP	C	T	4	50	c.257C>T	c.(256-258)ACA>ATA	p.T86I
Pat_45	Post-Resistance	MLL	4297	37	11	118343168	118343168	Missense_Mutation	SNP	G	A	11	160	c.1294G>A	c.(1294-1296)GAG>AAG	p.E432K
Pat_45	Post-Resistance	BCL9L	283149	37	11	118779096	118779096	Missense_Mutation	SNP	C	T	16	94	c.295G>A	c.(295-297)GCA>ACA	p.A99T
Pat_45	Post-Resistance	TRAPPC4	51399	37	11	118892596	118892596	Missense_Mutation	SNP	G	A	5	97	c.581G>A	c.(580-582)AGG>AAG	p.R194K
Pat_45	Post-Resistance	TRIM29	23650	37	11	119996597	119996597	Missense_Mutation	SNP	C	T	7	44	c.1135G>A	c.(1135-1137)GAA>AAA	p.E379K
Pat_45	Post-Resistance	TRIM29	23650	37	11	120008183	120008183	Missense_Mutation	SNP	G	A	3	35	c.557C>T	c.(556-558)TCC>TTC	p.S186F
Pat_45	Post-Resistance	TECTA	7007	37	11	120996474	120996474	Missense_Mutation	SNP	G	A	15	118	c.1667G>A	c.(1666-1668)AGT>AAT	p.S556N
Pat_45	Post-Resistance	CCDC15	80071	37	11	124857828	124857828	Missense_Mutation	SNP	T	A	7	253	c.1706T>A	c.(1705-1707)GTT>GAT	p.V569D
Pat_45	Post-Resistance	CCDC15	80071	37	11	124857870	124857870	Missense_Mutation	SNP	A	G	6	182	c.1748A>G	c.(1747-1749)CAG>CGG	p.Q583R
Pat_45	Post-Resistance	VPS26B	112936	37	11	134095156	134095156	Missense_Mutation	SNP	C	T	17	186	c.140C>T	c.(139-141)TCC>TTC	p.S47F
Pat_45	Post-Resistance	B4GALNT3	283358	37	12	663104	663104	Missense_Mutation	SNP	A	G	3	52	c.2015A>G	c.(2014-2016)GAG>GGG	p.E672G
Pat_45	Post-Resistance	RAD52	5893	37	12	1025632	1025632	Missense_Mutation	SNP	G	A	4	29	c.743C>T	c.(742-744)GCC>GTC	p.A248V
Pat_45	Post-Resistance	CACNA2D4	93589	37	12	1910248	1910249	Missense_Mutation	DNP	GG	TT	7	90	.2828_2829CC>A	c.(2827-2829)CCC>CAA	p.P943Q
Pat_45	Post-Resistance	TNFRSF1A	7132	37	12	6442535	6442535	Missense_Mutation	SNP	G	A	3	29	c.470C>T	c.(469-471)TCC>TTC	p.S157F
Pat_45	Post-Resistance	KLRC1	3821	37	12	10601919	10601919	Missense_Mutation	SNP	C	T	16	188	c.406G>A	c.(406-408)GAA>AAA	p.E136K
Pat_45	Post-Resistance	PRB1	5542	37	12	11506208	11506208	Missense_Mutation	SNP	G	A	51	199	c.829C>T	c.(829-831)CCT>TCT	p.P277S
Pat_45	Post-Resistance	LRP6	4040	37	12	12284989	12284989	Missense_Mutation	SNP	G	A	14	105	c.3736C>T	c.(3736-3738)CCT>TCT	p.P1246S
Pat_45	Post-Resistance	PKP2	5318	37	12	32955384	32955384	Missense_Mutation	SNP	G	A	65	250	c.2252C>T	c.(2251-2253)TCG>TTG	p.S751L

Pat_45	Post-Resistance	IRAK4	51135	37	12	44180314	44180314	Missense_Mutation	SNP	G	A	7	56	c.1301G>A	c.(1300-1302)AGT>AAT	p.S434N
Pat_45	Post-Resistance	MLL2	8085	37	12	49440495	49440495	Missense_Mutation	SNP	G	A	12	77	c.4315C>T	c.(4315-4317)CCC>TCC	p.P1439S
Pat_45	Post-Resistance	TROAP	10024	37	12	49724304	49724304	Missense_Mutation	SNP	G	A	6	54	c.1676G>A	c.(1675-1677)TGC>TAC	p.C559Y
Pat_45	Post-Resistance	TROAP	10024	37	12	49724313	49724313	Missense_Mutation	SNP	G	T	8	54	c.1685G>T	c.(1684-1686)AGT>ATT	p.S562I
Pat_45	Post-Resistance	POU6F1	5463	37	12	51586223	51586223	Missense_Mutation	SNP	G	A	23	103	c.281C>T	c.(280-282)CCC>CTC	p.P94L
Pat_45	Post-Resistance	NR4A1	3164	37	12	52448671	52448671	Missense_Mutation	SNP	C	T	13	95	c.559C>T	c.(559-561)CCA>TCA	p.P187S
Pat_45	Post-Resistance	NCKAP1L	3071	37	12	54911672	54911672	Missense_Mutation	SNP	C	T	11	132	c.1288C>T	c.(1288-1290)CTT>TTT	p.L430F
Pat_45	Post-Resistance	OR6C6	283365	37	12	55688542	55688542	Missense_Mutation	SNP	C	T	14	53	c.475G>A	c.(475-477)GTC>ATC	p.V159I
Pat_45	Post-Resistance	DGKA	1606	37	12	56334729	56334729	Missense_Mutation	SNP	G	A	10	46	c.1066G>A	c.(1066-1068)GAT>AAT	p.D356N
Pat_45	Post-Resistance	MYL6B	140465	37	12	56551482	56551482	Missense_Mutation	SNP	C	T	6	50	c.599C>T	c.(598-600)GCC>GTC	p.A200V
Pat_45	Post-Resistance	MARS	4141	37	12	57906711	57906711	Missense_Mutation	SNP	C	T	19	191	c.1931C>T	c.(1930-1932)TCT>TTT	p.S644F
Pat_45	Post-Resistance	PIP4K2C	79837	37	12	57995103	57995103	Missense_Mutation	SNP	C	T	6	49	c.1157C>T	c.(1156-1158)GCT>GTT	p.A386V
Pat_45	Post-Resistance	RPSAP52	204010	37	12	66152134	66152134	Missense_Mutation	SNP	G	A	4	7	c.389C>T	c.(388-390)GCT>GTT	p.A130V
Pat_45	Post-Resistance	SLC35E3	55508	37	12	69141800	69141800	Missense_Mutation	SNP	G	A	10	109	c.493G>A	c.(493-495)GTT>ATT	p.V165I
Pat_45	Post-Resistance	KCNMB4	27345	37	12	70824296	70824296	Missense_Mutation	SNP	G	A	20	178	c.496G>A	c.(496-498)GAT>AAT	p.D166N
Pat_45	Post-Resistance	NAV3	89795	37	12	78515772	78515772	Missense_Mutation	SNP	G	A	8	38	c.3802G>A	c.(3802-3804)GGT>AGT	p.G1268S
Pat_45	Post-Resistance	CCDC59	29080	37	12	82746994	82746994	Missense_Mutation	SNP	T	C	3	70	c.662A>G	c.(661-663)AAG>AGG	p.K221R
Pat_45	Post-Resistance	DUSP6	1848	37	12	89745728	89745728	Missense_Mutation	SNP	C	T	3	45	c.89G>A	c.(88-90)GGC>GAC	p.G30D
Pat_45	Post-Resistance	ELK3	2004	37	12	96617480	96617480	Missense_Mutation	SNP	G	A	6	52	c.136G>A	c.(136-138)GGA>AGA	p.G46R
Pat_45	Post-Resistance	NFYB	4801	37	12	104520010	104520010	Missense_Mutation	SNP	C	G	2	4	c.113G>C	c.(112-114)AGC>ACC	p.S38T
Pat_45	Post-Resistance	ACACB	32	37	12	109623454	109623454	Missense_Mutation	SNP	T	G	20	62	c.1889T>G	c.(1888-1890)GTG>GGG	p.V630G
Pat_45	Post-Resistance	FBXW8	26259	37	12	117426471	117426471	Nonsense_Mutation	SNP	C	T	28	266	c.1036C>T	c.(1036-1038)CAG>TAG	p.Q346*
Pat_45	Post-Resistance	NOS1	4842	37	12	117718614	117718614	Nonsense_Mutation	SNP	C	T	5	46	c.1440G>A	c.(1438-1440)TGG>TGA	p.W480*
Pat_45	Post-Resistance	KSR2	283455	37	12	117977643	117977643	Missense_Mutation	SNP	G	A	15	121	c.1481C>T	c.(1480-1482)TCC>TTC	p.S494F
Pat_45	Post-Resistance	EP400	57634	37	12	132466850	132466850	Missense_Mutation	SNP	G	A	17	136	c.1756G>A	c.(1756-1758)GCC>ACC	p.A586T
Pat_45	Post-Resistance	POLE	5426	37	12	133226409	133226409	Missense_Mutation	SNP	G	A	6	34	c.3649C>T	c.(3649-3651)CTC>TTC	p.L1217F
Pat_45	Post-Resistance	POLR1D	51082	37	13	28239855	28239855	Missense_Mutation	SNP	G	T	4	43	c.134G>T	c.(133-135)AGA>ATA	p.R45I
Pat_45	Post-Resistance	B3GALTL	145173	37	13	31835207	31835207	Missense_Mutation	SNP	C	T	5	55	c.584C>T	c.(583-585)CCA>CTA	p.P195L
Pat_45	Post-Resistance	NBEA	26960	37	13	35632956	35632956	Missense_Mutation	SNP	C	T	3	36	c.1195C>T	c.(1195-1197)CCA>TCA	p.P399S
Pat_45	Post-Resistance	CSNK1A1L	122011	37	13	37678426	37678426	Missense_Mutation	SNP	G	A	16	165	c.968C>T	c.(967-969)ACA>ATA	p.T323I
Pat_45	Post-Resistance	CSNK1A1L	122011	37	13	37678453	37678453	Missense_Mutation	SNP	C	T	13	198	c.941G>A	c.(940-942)GGG>GAG	p.G314E
Pat_45	Post-Resistance	FREM2	341640	37	13	39265691	39265691	Missense_Mutation	SNP	C	T	14	150	c.4210C>T	c.(4210-4212)CCC>TCC	p.P1404S
Pat_45	Post-Resistance	NAA16	79612	37	13	41932505	41932505	Missense_Mutation	SNP	G	A	11	131	c.1153G>A	c.(1153-1155)GAT>AAT	p.D385N
Pat_45	Post-Resistance	EPSTI1	94240	37	13	43462438	43462438	Missense_Mutation	SNP	G	A	13	55	c.1181C>T	c.(1180-1182)CCT>CTT	p.P394L
Pat_45	Post-Resistance	KIAA1704	55425	37	13	45602022	45602022	Missense_Mutation	SNP	C	T	5	66	c.907C>T	c.(907-909)CGT>TGT	p.R303C
Pat_45	Post-Resistance	LPAR6	10161	37	13	48986500	48986500	Nonsense_Mutation	SNP	A	T	4	73	c.60T>A	c.(58-60)TAT>TAA	p.Y20*
Pat_45	Post-Resistance	SETDB2	83852	37	13	50057041	50057041	Missense_Mutation	SNP	C	T	7	55	c.1361C>T	c.(1360-1362)ACT>ATT	p.T454I
Pat_45	Post-Resistance	KCNRG	283518	37	13	50590158	50590158	Missense_Mutation	SNP	G	A	12	115	c.529G>A	c.(529-531)GTT>ATT	p.V177I
Pat_45	Post-Resistance	CKAP2	26586	37	13	53049104	53049104	Missense_Mutation	SNP	G	A	9	56	c.1880G>A	c.(1879-1881)CGT>CAT	p.R627H
Pat_45	Post-Resistance	DACH1	1602	37	13	72049279	72049279	Missense_Mutation	SNP	T	C	10	90	c.2077A>G	c.(2077-2079)ATA>GTA	p.I693V
Pat_45	Post-Resistance	PIBF1	10464	37	13	73357692	73357692	Missense_Mutation	SNP	G	A	9	115	c.85G>A	c.(85-87)GTT>ATT	p.V29I
Pat_45	Post-Resistance	TBC1D4	9882	37	13	75880586	75880586	Missense_Mutation	SNP	G	A	4	83	c.2615C>T	c.(2614-2616)TCC>TTC	p.S872F
Pat_45	Post-Resistance	SCEL	8796	37	13	78178522	78178522	Missense_Mutation	SNP	G	A	6	103	c.1129G>A	c.(1129-1131)GAT>AAT	p.D377N
Pat_45	Post-Resistance	SLITRK1	114798	37	13	84453844	84453844	Missense_Mutation	SNP	G	A	10	116	c.1799C>T	c.(1798-1800)GCG>GTG	p.A600V
Pat_45	Post-Resistance	SLITRK6	84189	37	13	86368348	86368348	Missense_Mutation	SNP	G	A	7	81	c.2296C>T	c.(2296-2298)CTT>TTT	p.L766F
Pat_45	Post-Resistance	GPC5	2262	37	13	92408617	92408617	Missense_Mutation	SNP	A	G	12	97	c.1223A>G	c.(1222-1224)AAT>AGT	p.N408S
Pat_45	Post-Resistance	MBNL2	10150	37	13	97986545	97986545	Missense_Mutation	SNP	G	A	8	104	c.190G>A	c.(190-192)GAG>AAG	p.E64K

Pat_45	Post-Resistance	SLC10A2	6555	37	13	103703661	103703661	Missense_Mutation	SNP	G	A	14	80	c.707C>T	c.(706-708)GCG>GTG	p.A236V
Pat_45	Post-Resistance	SLC10A2	6555	37	13	103703743	103703743	Missense_Mutation	SNP	C	T	6	51	c.625G>A	c.(625-627)GCT>ACT	p.A209T
Pat_45	Post-Resistance	GRK1	6011	37	13	114322374	114322374	Missense_Mutation	SNP	C	T	4	31	c.673C>T	c.(673-675)CGG>TGG	p.R225W
Pat_45	Post-Resistance	OR4Q3	441669	37	14	20216025	20216025	Missense_Mutation	SNP	C	T	5	60	c.439C>T	c.(439-441)CTT>TTT	p.L147F
Pat_45	Post-Resistance	TEP1	7011	37	14	20852822	20852822	Missense_Mutation	SNP	G	A	18	239	c.3158C>T	c.(3157-3159)GCC>GTC	p.A1053V
Pat_45	Post-Resistance	OR6S1	341799	37	14	21109394	21109394	Missense_Mutation	SNP	C	T	4	71	c.457G>A	c.(457-459)GGG>AGG	p.G153R
Pat_45	Post-Resistance	CHD8	57680	37	14	21883732	21883732	Splice_Site	SNP	C	T	6	66	c.1131_splice	c.e7+1	p.E377_splice
Pat_45	Post-Resistance	TOX4	9878	37	14	21960767	21960767	Nonsense_Mutation	SNP	C	A	13	148	c.992C>A	c.(991-993)TCA>TAA	p.S331*
Pat_45	Post-Resistance	DHRS2	10202	37	14	24108123	24108123	Missense_Mutation	SNP	C	T	10	160	c.50C>T	c.(49-51)GCT>GTT	p.A17V
Pat_45	Post-Resistance	NFATC4	4776	37	14	24841655	24841655	Missense_Mutation	SNP	C	T	7	128	c.1205C>T	c.(1204-1206)GCC>GTC	p.A402V
Pat_45	Post-Resistance	ARHGAP5	394	37	14	32562267	32562267	Missense_Mutation	SNP	C	T	5	147	c.2392C>T	c.(2392-2394)CCC>TCC	p.P798S
Pat_45	Post-Resistance	FSCB	84075	37	14	44975115	44975115	Missense_Mutation	SNP	G	T	22	84	c.1076C>A	c.(1075-1077)CCT>CAT	p.P359H
Pat_45	Post-Resistance	FANCM	57697	37	14	45636294	45636294	Missense_Mutation	SNP	C	T	8	135	c.1930C>T	c.(1930-1932)CAT>TAT	p.H644Y
Pat_45	Post-Resistance	FANCM	57697	37	14	45658350	45658350	Missense_Mutation	SNP	C	T	22	244	c.5125C>T	c.(5125-5127)CCT>TCT	p.P1709S
Pat_45	Post-Resistance	POLE2	5427	37	14	50140909	50140909	Missense_Mutation	SNP	G	A	96	278	c.349C>T	c.(349-351)CCA>TCA	p.P117S
Pat_45	Post-Resistance	KLHDC2	23588	37	14	50238352	50238352	Missense_Mutation	SNP	G	A	12	74	c.194G>A	c.(193-195)AGA>AAA	p.R65K
Pat_45	Post-Resistance	ARF6	382	37	14	50360936	50360936	Missense_Mutation	SNP	G	A	6	62	c.482G>A	c.(481-483)GGA>GAA	p.G161E
Pat_45	Post-Resistance	CDKL1	8814	37	14	50807897	50807897	Missense_Mutation	SNP	G	A	12	129	c.2524C>T	c.(2524-2526)CCT>TCT	p.P842S
Pat_45	Post-Resistance	NID2	22795	37	14	52493928	52493928	Nonsense_Mutation	SNP	G	A	5	45	c.2665C>T	c.(2665-2667)CAG>TAG	p.Q889*
Pat_45	Post-Resistance	TXNDC16	57544	37	14	52948991	52948991	Missense_Mutation	SNP	C	T	7	85	c.1269G>A	c.(1267-1269)ATG>ATA	p.M423I
Pat_45	Post-Resistance	RTN1	6252	37	14	60213121	60213121	Missense_Mutation	SNP	G	A	3	66	c.320C>T	c.(319-321)TCT>TTT	p.S107F
Pat_45	Post-Resistance	TRMT5	57570	37	14	61446257	61446257	Missense_Mutation	SNP	C	T	17	198	c.359G>A	c.(358-360)CGC>CAC	p.R120H
Pat_45	Post-Resistance	SYNE2	23224	37	14	64522818	64522818	Missense_Mutation	SNP	G	A	8	47	c.9901G>A	c.(9901-9903)GAG>AAG	p.E3301K
Pat_45	Post-Resistance	ZBTB25	7597	37	14	64957244	64957244	Missense_Mutation	SNP	G	A	8	171	c.8C>T	c.(7-9)ACT>ATT	p.T3I
Pat_45	Post-Resistance	VTI1B	10490	37	14	68141101	68141101	Missense_Mutation	SNP	C	T	6	23	c.106G>A	c.(106-108)GCG>ACG	p.A36T
Pat_45	Post-Resistance	ACOT4	122970	37	14	74062158	74062158	Missense_Mutation	SNP	C	T	10	97	c.1066C>T	c.(1066-1068)CCT>TCT	p.P356S
Pat_45	Post-Resistance	C14orf115	55237	37	14	74824727	74824727	Missense_Mutation	SNP	C	T	6	131	c.1241C>T	c.(1240-1242)TCC>TTC	p.S414F
Pat_45	Post-Resistance	MLH3	27030	37	14	75513393	75513393	Missense_Mutation	SNP	C	T	17	116	c.2966G>A	c.(2965-2967)AGA>AAA	p.R989K
Pat_45	Post-Resistance	FAM164C	79696	37	14	75537559	75537559	Missense_Mutation	SNP	G	A	29	288	c.283G>A	c.(283-285)GAT>AAT	p.D95N
Pat_45	Post-Resistance	NEK9	91754	37	14	75553876	75553876	Missense_Mutation	SNP	G	A	8	129	c.2662C>T	c.(2662-2664)CCT>TCT	p.P888S
Pat_45	Post-Resistance	TMEM63C	57156	37	14	77715198	77715198	Missense_Mutation	SNP	C	T	9	210	c.1853C>T	c.(1852-1854)CCC>CTC	p.P618L
Pat_45	Post-Resistance	KCNK10	54207	37	14	88652225	88652225	Missense_Mutation	SNP	C	T	13	87	c.1271G>A	c.(1270-1272)CGC>CAC	p.R424H
Pat_45	Post-Resistance	C14orf159	80017	37	14	91639748	91639748	Missense_Mutation	SNP	G	A	3	39	c.557G>A	c.(556-558)GGT>GAT	p.G186D
Pat_45	Post-Resistance	CATSPERB	79820	37	14	92157893	92157893	Missense_Mutation	SNP	T	A	7	111	c.838A>T	c.(838-840)AGG>TGG	p.R280W
Pat_45	Post-Resistance	TRIP11	9321	37	14	92436129	92436129	Missense_Mutation	SNP	G	A	9	117	c.5828C>T	c.(5827-5829)CCC>CTC	p.P1943L
Pat_45	Post-Resistance	DDX24	57062	37	14	94528964	94528964	Missense_Mutation	SNP	C	T	19	105	c.722G>A	c.(721-723)AGT>AAT	p.S241N
Pat_45	Post-Resistance	ATG2B	55102	37	14	96783538	96783538	Missense_Mutation	SNP	G	A	6	76	c.3154C>T	c.(3154-3156)CTC>TTC	p.L1052F
Pat_45	Post-Resistance	PPP2R5C	5527	37	14	102276373	102276373	Missense_Mutation	SNP	G	A	6	63	c.94G>A	c.(94-96)GAT>AAT	p.D32N
Pat_45	Post-Resistance	DYNC1H1	1778	37	14	102482379	102482379	Missense_Mutation	SNP	C	T	3	46	c.7429C>T	c.(7429-7431)CCC>TCC	p.P2477S
Pat_45	Post-Resistance	RAGE	5891	37	14	102695823	102695823	Missense_Mutation	SNP	G	A	18	185	c.1153C>T	c.(1153-1155)CCC>TCC	p.P385S
Pat_45	Post-Resistance	PPP1R13B	23368	37	14	104206385	104206385	Missense_Mutation	SNP	C	T	16	127	c.2368G>A	c.(2368-2370)GAT>AAT	p.D790N
Pat_45	Post-Resistance	C15orf2	23742	37	15	24922887	24922887	Missense_Mutation	SNP	C	T	9	61	c.1873C>T	c.(1873-1875)CCA>TCA	p.P625S
Pat_45	Post-Resistance	HERC2	8924	37	15	28501415	28501415	Missense_Mutation	SNP	C	T	6	42	c.2566G>A	c.(2566-2568)GGT>AGT	p.G856S
Pat_45	Post-Resistance	RYR3	6263	37	15	34064312	34064312	Missense_Mutation	SNP	C	T	5	50	c.9008C>T	c.(9007-9009)TCC>TTC	p.S3003F
Pat_45	Post-Resistance	C15orf55	256646	37	15	34648760	34648760	Missense_Mutation	SNP	G	A	8	75	c.2467G>A	c.(2467-2469)GAA>AAA	p.E823K
Pat_45	Post-Resistance	RAD51	5888	37	15	40990990	40990990	Missense_Mutation	SNP	G	A	6	115	c.34G>A	c.(34-36)GAT>AAT	p.D12N
Pat_45	Post-Resistance	VPS18	57617	37	15	41191546	41191546	Missense_Mutation	SNP	G	A	8	144	c.530G>A	c.(529-531)AGC>AAC	p.S177N

Pat_45	Post-Resistance	INO80	54617	37	15	41377602	41377602	Missense_Mutation	SNP	C	T	23	125	c.838G>A	c.(838-840)GTA>ATA	p.V280I
Pat_45	Post-Resistance	STRC	161497	37	15	43895526	43895526	Missense_Mutation	SNP	C	T	7	55	c.4459G>A	c.(4459-4461)GAC>AAC	p.D1487N
Pat_45	Post-Resistance	SQRDL	58472	37	15	45983208	45983208	Missense_Mutation	SNP	T	A	20	241	c.1333T>A	c.(1333-1335)TTT>ATT	p.F445I
Pat_45	Post-Resistance	FBN1	2200	37	15	48707754	48707754	Missense_Mutation	SNP	C	T	10	138	c.8030G>A	c.(8029-8031)GGT>GAT	p.G2677D
Pat_45	Post-Resistance	C15orf33	196951	37	15	49800512	49800512	Nonsense_Mutation	SNP	C	T	5	57	c.908G>A	c.(907-909)TGG>TAG	p.W303*
Pat_45	Post-Resistance	TMOD3	29766	37	15	52192472	52192472	Missense_Mutation	SNP	G	A	7	52	c.856G>A	c.(856-858)GCA>ACA	p.A286T
Pat_45	Post-Resistance	SLTM	79811	37	15	59179486	59179486	Missense_Mutation	SNP	G	A	14	131	c.2629C>T	c.(2629-2631)CCT>TCT	p.P877S
Pat_45	Post-Resistance	ANXA2	302	37	15	60674586	60674586	Missense_Mutation	SNP	C	T	7	79	c.103G>A	c.(103-105)GCT>ACT	p.A35T
Pat_45	Post-Resistance	USP3	9960	37	15	63862770	63862771	Missense_Mutation	DNP	GT	AA	12	201	c.900_901GT>AA	898-903)AAGTGT>AAAA	p.C301S
Pat_45	Post-Resistance	CLPX	10845	37	15	65450171	65450171	Nonsense_Mutation	SNP	G	A	6	116	c.970C>T	c.(970-972)CAG>TAG	p.Q324*
Pat_45	Post-Resistance	CILP	8483	37	15	65490358	65490358	Missense_Mutation	SNP	C	T	14	223	c.2266G>A	c.(2266-2268)GTG>ATG	p.V756M
Pat_45	Post-Resistance	AAGAB	79719	37	15	67528320	67528320	Missense_Mutation	SNP	C	T	12	154	c.448G>A	c.(448-450)GAT>AAT	p.D150N
Pat_45	Post-Resistance	CALML4	91860	37	15	68497780	68497780	Translation_Start_Site	SNP	C	T	3	14	c.-65G>A	c.(-67--63)AGGTG>AGATG	
Pat_45	Post-Resistance	PARP6	56965	37	15	72559163	72559163	Missense_Mutation	SNP	C	T	10	79	c.4G>A	c.(4-6)GAC>AAC	p.D2N
Pat_45	Post-Resistance	CSK	1445	37	15	75094136	75094136	Missense_Mutation	SNP	G	A	6	96	c.988G>A	c.(988-990)GTC>ATC	p.V330I
Pat_45	Post-Resistance	CSK	1445	37	15	75094706	75094706	Missense_Mutation	SNP	G	A	13	105	c.1205G>A	c.(1204-1206)GGC>GAC	p.G402D
Pat_45	Post-Resistance	MAN2C1	4123	37	15	75654258	75654258	Missense_Mutation	SNP	C	T	21	268	c.1039G>A	c.(1039-1041)GTG>ATG	p.V347M
Pat_45	Post-Resistance	LOC645752	645752	37	15	78211546	78211546	Missense_Mutation	SNP	G	A	19	218	c.221C>T	c.(220-222)TCC>TTC	p.S74F
Pat_45	Post-Resistance	EFTUD1	79631	37	15	82532887	82532887	Missense_Mutation	SNP	C	T	12	109	c.388G>A	c.(388-390)GTT>ATT	p.V130I
Pat_45	Post-Resistance	BNC1	646	37	15	83932330	83932330	Missense_Mutation	SNP	C	T	15	78	c.1673G>A	c.(1672-1674)AGA>AAA	p.R558K
Pat_45	Post-Resistance	ADAMTSL3	57188	37	15	84566671	84566671	Missense_Mutation	SNP	G	A	28	121	c.1529G>A	c.(1528-1530)GGA>GAA	p.G510E
Pat_45	Post-Resistance	ACAN	176	37	15	89400555	89400555	Missense_Mutation	SNP	C	T	4	45	c.4739C>T	c.(4738-4740)GCT>GTT	p.A1580V
Pat_45	Post-Resistance	MFGE8	4240	37	15	89444955	89444955	Missense_Mutation	SNP	G	A	8	53	c.697C>T	c.(697-699)CCC>TCC	p.P233S
Pat_45	Post-Resistance	MAN2A2	4122	37	15	91453374	91453374	Missense_Mutation	SNP	G	A	11	178	c.1429G>A	c.(1429-1431)GTG>ATG	p.V477M
Pat_45	Post-Resistance	CHD2	1106	37	15	93480792	93480792	Missense_Mutation	SNP	G	A	5	54	c.488G>A	c.(487-489)GGC>GAC	p.G163D
Pat_45	Post-Resistance	CHD2	1106	37	15	93528866	93528866	Missense_Mutation	SNP	G	A	18	263	c.3376G>A	c.(3376-3378)GAC>AAC	p.D1126N
Pat_45	Post-Resistance	NR2F2	7026	37	15	96877589	96877589	Missense_Mutation	SNP	G	A	19	191	c.727G>A	c.(727-729)GCC>ACC	p.A243T
Pat_45	Post-Resistance	OR4F15	390649	37	15	102359125	102359125	Missense_Mutation	SNP	G	A	20	208	c.736G>A	c.(736-738)GTG>ATG	p.V246M
Pat_45	Post-Resistance	WASH3P	374666	37	15	102515299	102515299	Missense_Mutation	SNP	G	A	5	58	c.523G>A	c.(523-525)GGC>AGC	p.G175S
Pat_45	Post-Resistance	NUBP2	10101	37	16	1836628	1836628	Missense_Mutation	SNP	C	T	7	99	c.107C>T	c.(106-108)GCC>GTC	p.A36V
Pat_45	Post-Resistance	GFER	2671	37	16	2035982	2035982	Missense_Mutation	SNP	G	A	15	177	c.571G>A	c.(571-573)GTG>ATG	p.V191M
Pat_45	Post-Resistance	CCNF	899	37	16	2499328	2499328	Missense_Mutation	SNP	C	T	9	88	c.1264C>T	c.(1264-1266)CCT>TCT	p.P422S
Pat_45	Post-Resistance	CCNF	899	37	16	2503258	2503258	Missense_Mutation	SNP	C	T	18	161	c.1535C>T	c.(1534-1536)GCC>GTC	p.A512V
Pat_45	Post-Resistance	MEFV	4210	37	16	3298929	3298929	Missense_Mutation	SNP	C	T	16	204	c.1336G>A	c.(1336-1338)GAG>AAG	p.E446K
Pat_45	Post-Resistance	ZNF75A	7627	37	16	3367588	3367588	Missense_Mutation	SNP	C	T	5	70	c.610C>T	c.(610-612)CTT>TTT	p.L204F
Pat_45	Post-Resistance	PPL	5493	37	16	4934485	4934485	Missense_Mutation	SNP	G	A	3	28	c.4171C>T	c.(4171-4173)CGG>TGG	p.R1391W
Pat_45	Post-Resistance	C16orf68	79091	37	16	8736343	8736343	Missense_Mutation	SNP	G	A	64	618	c.931G>A	c.(931-933)GAT>AAT	p.D311N
Pat_45	Post-Resistance	GRIN2A	2903	37	16	9857353	9857353	Missense_Mutation	SNP	C	T	4	21	c.4048G>A	c.(4048-4050)GAC>AAC	p.D1350N
Pat_45	Post-Resistance	TEKT5	146279	37	16	10729774	10729774	Missense_Mutation	SNP	G	A	20	264	c.1088C>T	c.(1087-1089)ACG>ATG	p.T363M
Pat_45	Post-Resistance	MKL2	57496	37	16	14346301	14346301	Missense_Mutation	SNP	C	T	8	107	c.2645C>T	c.(2644-2646)CCC>CTC	p.P882L
Pat_45	Post-Resistance	XYLT1	64131	37	16	17352853	17352853	Missense_Mutation	SNP	G	A	10	58	c.905C>T	c.(904-906)CCC>CTC	p.P302L
Pat_45	Post-Resistance	TMC5	79838	37	16	19498639	19498639	Missense_Mutation	SNP	C	T	8	85	c.2564C>T	c.(2563-2565)ACC>ATC	p.T855I
Pat_45	Post-Resistance	TMC5	79838	37	16	19505632	19505632	Missense_Mutation	SNP	G	A	16	181	c.2875G>A	c.(2875-2877)GAT>AAT	p.D959N
Pat_45	Post-Resistance	ACSM1	116285	37	16	20651829	20651829	Missense_Mutation	SNP	C	T	15	186	c.1070G>A	c.(1069-1071)AGA>AAA	p.R357K
Pat_45	Post-Resistance	DNAH3	55567	37	16	21014460	21014460	Missense_Mutation	SNP	G	A	11	138	c.6092C>T	c.(6091-6093)ACC>ATC	p.T2031I
Pat_45	Post-Resistance	ZKSCAN2	342357	37	16	25268154	25268154	Missense_Mutation	SNP	C	T	7	124	c.295G>A	c.(295-297)GAG>AAG	p.E99K
Pat_45	Post-Resistance	KIAA0556	23247	37	16	27640058	27640058	Missense_Mutation	SNP	G	A	10	150	c.217G>A	c.(217-219)GTC>ATC	p.V73I

Pat_45	Post-Resistance	XPO6	23214	37	16	28118864	28118864	Missense_Mutation	SNP	G	A	7	120	c.2476C>T	c.(2476-2478)CCA>TCA	p.P826S
Pat_45	Post-Resistance	SULT1A1	6817	37	16	28617503	28617503	Missense_Mutation	SNP	C	T	5	74	c.649G>A	c.(649-651)GAG>AAG	p.E217K
Pat_45	Post-Resistance	CORO1A	11151	37	16	30199809	30199809	Missense_Mutation	SNP	C	T	5	42	c.1193C>T	c.(1192-1194)CCC>CTC	p.P398L
Pat_45	Post-Resistance	SRCAP	10847	37	16	30749948	30749948	Missense_Mutation	SNP	C	T	8	67	c.8587C>T	c.(8587-8589)CCC>TCC	p.P2863S
Pat_45	Post-Resistance	SETD1A	9739	37	16	30991419	30991419	Missense_Mutation	SNP	G	A	10	96	c.4312G>A	c.(4312-4314)GAG>AAG	p.E1438K
Pat_45	Post-Resistance	ARMC5	79798	37	16	31473563	31473563	Missense_Mutation	SNP	C	T	5	70	c.695C>T	c.(694-696)GCC>GTC	p.A232V
Pat_45	Post-Resistance	NETO2	81831	37	16	47162401	47162401	Missense_Mutation	SNP	C	T	39	237	c.316G>A	c.(316-318)GAA>AAA	p.E106K
Pat_45	Post-Resistance	IRX6	79190	37	16	55361274	55361274	Missense_Mutation	SNP	T	C	4	42	c.370T>C	c.(370-372)TAT>CAT	p.Y124H
Pat_45	Post-Resistance	CES7	221223	37	16	55886795	55886795	Missense_Mutation	SNP	C	T	9	89	c.1271G>A	c.(1270-1272)AGA>AAA	p.R424K
Pat_45	Post-Resistance	COQ9	57017	37	16	57485117	57485117	Missense_Mutation	SNP	C	T	7	131	c.239C>T	c.(238-240)CCC>CTC	p.P80L
Pat_45	Post-Resistance	CCDC113	29070	37	16	58286740	58286740	Missense_Mutation	SNP	G	A	6	108	c.211G>A	c.(211-213)GCA>ACA	p.A71T
Pat_45	Post-Resistance	NDRG4	65009	37	16	58540345	58540345	Missense_Mutation	SNP	G	A	27	387	c.427G>A	c.(427-429)GGC>AGC	p.G143S
Pat_45	Post-Resistance	DYNC1LI2	1783	37	16	66759746	66759746	Missense_Mutation	SNP	T	A	21	248	c.1363A>T	c.(1363-1365)ACA>TCA	p.T455S
Pat_45	Post-Resistance	DYNC1LI2	1783	37	16	66764028	66764028	Missense_Mutation	SNP	G	A	9	61	c.1028C>T	c.(1027-1029)CCT>CTT	p.P343L
Pat_45	Post-Resistance	TPPP3	51673	37	16	67424207	67424207	Missense_Mutation	SNP	G	A	29	242	c.401C>T	c.(400-402)TCC>TTC	p.S134F
Pat_45	Post-Resistance	TPPP3	51673	37	16	67424399	67424399	Missense_Mutation	SNP	C	T	20	93	c.325G>A	c.(325-327)GCC>ACC	p.A109T
Pat_45	Post-Resistance	DUS2L	54920	37	16	68072032	68072032	Missense_Mutation	SNP	G	A	3	48	c.106G>A	c.(106-108)GCG>ACG	p.A36T
Pat_45	Post-Resistance	PRMT7	54496	37	16	68358650	68358650	Missense_Mutation	SNP	C	T	11	103	c.197C>T	c.(196-198)GCC>GTC	p.A66V
Pat_45	Post-Resistance	AARS	16	37	16	70289630	70289630	Splice_Site	SNP	C	T	6	67	c.2286_splice	c.e16+1	p.K762_splice
Pat_45	Post-Resistance	DHX38	9785	37	16	72134474	72134474	Missense_Mutation	SNP	G	A	7	104	c.1256G>A	c.(1255-1257)GGG>GAG	p.G419E
Pat_45	Post-Resistance	PKD1L2	114780	37	16	81232276	81232276	Missense_Mutation	SNP	G	A	4	50	c.1534C>T	c.(1534-1536)CCG>TCG	p.P512S
Pat_45	Post-Resistance	PKD1L2	114780	37	16	81236132	81236132	Nonsense_Mutation	SNP	C	T	23	169	c.1116G>A	c.(1114-1116)TGG>TGA	p.W372*
Pat_45	Post-Resistance	GAN	8139	37	16	81388232	81388232	Missense_Mutation	SNP	G	A	8	132	c.505G>A	c.(505-507)GAA>AAA	p.E169K
Pat_45	Post-Resistance	CDH13	1012	37	16	83817005	83817005	Missense_Mutation	SNP	G	A	19	188	c.2062G>A	c.(2062-2064)GAC>AAC	p.D688N
Pat_45	Post-Resistance	KCNG4	93107	37	16	84270361	84270361	Missense_Mutation	SNP	G	A	7	64	c.731C>T	c.(730-732)CCC>CTC	p.P244L
Pat_45	Post-Resistance	ZCCHC14	23174	37	16	87446222	87446222	Missense_Mutation	SNP	G	A	4	92	c.1694C>T	c.(1693-1695)GCG>GTG	p.A565V
Pat_45	Post-Resistance	BANP	54971	37	16	88039791	88039791	Missense_Mutation	SNP	G	A	25	267	c.548G>A	c.(547-549)AGC>AAC	p.S183N
Pat_45	Post-Resistance	GALNS	2588	37	16	88904029	88904029	Splice_Site	SNP	C	T	12	65	c.566_splice	c.e5+1	p.R189_splice
Pat_45	Post-Resistance	ANKRD11	29123	37	16	89351391	89351391	Missense_Mutation	SNP	G	A	11	72	c.1559C>T	c.(1558-1560)GCC>GTC	p.A520V
Pat_45	Post-Resistance	SPG7	6687	37	16	89590593	89590593	Missense_Mutation	SNP	G	A	41	438	c.556G>A	c.(556-558)GTG>ATG	p.V186M
Pat_45	Post-Resistance	SPG7	6687	37	16	89592849	89592849	Missense_Mutation	SNP	C	T	14	204	c.731C>T	c.(730-732)TCC>TTC	p.S244F
Pat_45	Post-Resistance	FANCA	2175	37	16	89846307	89846307	Missense_Mutation	SNP	C	T	5	108	c.1685G>A	c.(1684-1686)GGG>GAG	p.G562E
Pat_45	Post-Resistance	TUBB3	10381	37	16	89999944	89999944	Missense_Mutation	SNP	G	A	22	415	c.235G>A	c.(235-237)GGG>AGG	p.G79R
Pat_45	Post-Resistance	VPS53	55275	37	17	463814	463814	Splice_Site	SNP	C	T	5	90	c.1557_splice	c.e15-1	p.K519_splice
Pat_45	Post-Resistance	FAM57A	79850	37	17	644578	644578	Missense_Mutation	SNP	G	A	5	118	c.542G>A	c.(541-543)GGA>GAA	p.G181E
Pat_45	Post-Resistance	GLOD4	51031	37	17	680108	680108	Missense_Mutation	SNP	C	T	5	137	c.306G>A	c.(304-306)ATG>ATA	p.M102I
Pat_45	Post-Resistance	NXN	64359	37	17	704256	704256	Missense_Mutation	SNP	G	A	11	91	c.1241C>T	c.(1240-1242)ACC>ATC	p.T414I
Pat_45	Post-Resistance	PITPNA	5306	37	17	1456434	1456434	Missense_Mutation	SNP	C	T	7	100	c.61G>A	c.(61-63)GGG>AGG	p.G21R
Pat_45	Post-Resistance	SGSM2	9905	37	17	2267426	2267426	Missense_Mutation	SNP	C	T	9	78	c.881C>T	c.(880-882)ACC>ATC	p.T294I
Pat_45	Post-Resistance	SGSM2	9905	37	17	2278882	2278882	Missense_Mutation	SNP	G	A	23	232	c.2062G>A	c.(2062-2064)GGC>AGC	p.G688S
Pat_45	Post-Resistance	ZNF232	7775	37	17	5009592	5009592	Nonsense_Mutation	SNP	G	A	9	122	c.781C>T	c.(781-783)CAG>TAG	p.Q261*
Pat_45	Post-Resistance	SLC2A4	6517	37	17	7186892	7186892	Missense_Mutation	SNP	C	T	5	96	c.251C>T	c.(250-252)TCC>TTC	p.S84F
Pat_45	Post-Resistance	ZBTB4	57659	37	17	7365485	7365485	Missense_Mutation	SNP	C	T	34	371	c.2816G>A	c.(2815-2817)AGT>AAT	p.S939N
Pat_45	Post-Resistance	DNAH2	146754	37	17	7708601	7708601	Missense_Mutation	SNP	G	A	4	78	c.9332G>A	c.(9331-9333)GGA>GAA	p.G3111E
Pat_45	Post-Resistance	CNTROB	116840	37	17	7836545	7836545	Missense_Mutation	SNP	G	A	12	88	c.148G>A	c.(148-150)GCC>ACC	p.A50T
Pat_45	Post-Resistance	PFAS	5198	37	17	8167572	8167572	Missense_Mutation	SNP	G	A	7	100	c.1834G>A	c.(1834-1836)GGC>AGC	p.G612S
Pat_45	Post-Resistance	SLC25A35	399512	37	17	8194176	8194176	Missense_Mutation	SNP	G	A	15	206	c.713C>T	c.(712-714)ACA>ATA	p.T238I

Pat_45	Post-Resistance	MFSD6L	162387	37	17	8701883	8701883	Missense_Mutation	SNP	G	A	13	136	c.556C>T	c.(556-558)CTC>TTC	p.L186F
Pat_45	Post-Resistance	MYH4	4622	37	17	10358931	10358931	Missense_Mutation	SNP	C	T	8	81	c.2174G>A	c.(2173-2175)AGA>AAA	p.R725K
Pat_45	Post-Resistance	MYH2	4620	37	17	10443351	10443351	Missense_Mutation	SNP	T	G	8	70	c.1041A>C	c.(1039-1041)GAA>GAC	p.E347D
Pat_45	Post-Resistance	PMP22	5376	37	17	15134286	15134286	Missense_Mutation	SNP	G	A	7	94	c.431C>T	c.(430-432)CCC>CTC	p.P144L
Pat_45	Post-Resistance	NCOR1	9611	37	17	16062073	16062073	Splice_Site	SNP	C	T	5	43	c.732_splice	c.e6+1	p.R244_splice
Pat_45	Post-Resistance	RAI1	10743	37	17	17700796	17700796	Missense_Mutation	SNP	G	A	3	22	c.4534G>A	c.(4534-4536)GAG>AAG	p.E1512K
Pat_45	Post-Resistance	TOM1L2	146691	37	17	17783002	17783002	Missense_Mutation	SNP	G	A	22	183	c.716C>T	c.(715-717)TCT>TTT	p.S239F
Pat_45	Post-Resistance	FAM83G	644815	37	17	18874838	18874838	Missense_Mutation	SNP	G	A	12	216	c.2306C>T	c.(2305-2307)CCC>CTC	p.P769L
Pat_45	Post-Resistance	TMEM11	8834	37	17	21101711	21101711	Missense_Mutation	SNP	T	C	28	255	c.505A>G	c.(505-507)AGA>GGA	p.R169G
Pat_45	Post-Resistance	NOS2	4843	37	17	26089953	26089953	Missense_Mutation	SNP	C	T	4	9	c.2671G>A	c.(2671-2673)GTG>ATG	p.V891M
Pat_45	Post-Resistance	KIAA0100	9703	37	17	26948005	26948005	Splice_Site	SNP	C	T	6	125	c.5242_splice	c.e28+1	.G1748_splice
Pat_45	Post-Resistance	CORO6	84940	37	17	27943988	27943988	Missense_Mutation	SNP	G	A	25	364	c.826C>T	c.(826-828)CCC>TCC	p.P276S
Pat_45	Post-Resistance	CPD	1362	37	17	28782441	28782441	Missense_Mutation	SNP	G	A	5	81	c.3290G>A	c.(3289-3291)GGT>GAT	p.G1097D
Pat_45	Post-Resistance	SRCIN1	80725	37	17	36705372	36705372	Missense_Mutation	SNP	A	G	3	56	c.3037T>C	c.(3037-3039)TTC>CTC	p.F1013L
Pat_45	Post-Resistance	MLLT6	4302	37	17	36865819	36865819	Missense_Mutation	SNP	C	A	4	66	c.543C>A	c.(541-543)TTC>TTA	p.F181L
Pat_45	Post-Resistance	STARD3	10948	37	17	37813294	37813294	Missense_Mutation	SNP	G	A	17	117	c.253G>A	c.(253-255)GAG>AAG	p.E85K
Pat_45	Post-Resistance	GSDMB	55876	37	17	38073346	38073346	Missense_Mutation	SNP	G	A	4	55	c.224C>T	c.(223-225)TCT>TTT	p.S75F
Pat_45	Post-Resistance	KRTAP4-8	728224	37	17	39254021	39254021	Missense_Mutation	SNP	C	T	5	108	c.316G>A	c.(316-318)GTG>ATG	p.V106M
Pat_45	Post-Resistance	KRT33B	3884	37	17	39521507	39521507	Nonsense_Mutation	SNP	G	A	19	97	c.796C>T	c.(796-798)CAG>TAG	p.Q266*
Pat_45	Post-Resistance	JUP	3728	37	17	39681184	39681184	Missense_Mutation	SNP	C	T	34	165	c.1060G>A	c.(1060-1062)GAT>AAT	p.D354N
Pat_45	Post-Resistance	KCNH4	23415	37	17	40330137	40330137	Missense_Mutation	SNP	C	T	21	109	c.566G>A	c.(565-567)GGA>GAA	p.G189E
Pat_45	Post-Resistance	EZH1	2145	37	17	40857150	40857150	Missense_Mutation	SNP	C	T	7	97	c.1891G>A	c.(1891-1893)GAG>AAG	p.E631K
Pat_45	Post-Resistance	AOC2	314	37	17	41001247	41001247	Missense_Mutation	SNP	C	T	20	125	c.1733C>T	c.(1732-1734)CCC>CTC	p.P578L
Pat_45	Post-Resistance	TMUB2	79089	37	17	42268104	42268104	Missense_Mutation	SNP	G	A	18	126	c.838G>A	c.(838-840)GTG>ATG	p.V280M
Pat_45	Post-Resistance	FZD2	2535	37	17	42635313	42635313	Missense_Mutation	SNP	C	T	22	143	c.257C>T	c.(256-258)CCC>CTC	p.P86L
Pat_45	Post-Resistance	KIF18B	146909	37	17	43009061	43009061	Missense_Mutation	SNP	C	T	17	119	c.1462G>A	c.(1462-1464)GCA>ACA	p.A488T
Pat_45	Post-Resistance	COL1A1	1277	37	17	48265937	48265937	Missense_Mutation	SNP	G	A	9	78	c.3161C>T	c.(3160-3162)CCT>CTT	p.P1054L
Pat_45	Post-Resistance	ABCC3	8714	37	17	48738451	48738451	Missense_Mutation	SNP	C	T	3	50	c.974C>T	c.(973-975)TCC>TTC	p.S325F
Pat_45	Post-Resistance	ABCC3	8714	37	17	48746761	48746761	Missense_Mutation	SNP	C	T	7	66	c.2113C>T	c.(2113-2115)CTT>TTT	p.L705F
Pat_45	Post-Resistance	CA10	56934	37	17	50235132	50235132	Nonsense_Mutation	SNP	C	T	16	185	c.15G>A	c.(13-15)TGG>TGA	p.W5*
Pat_45	Post-Resistance	AKAP1	8165	37	17	55194225	55194225	Missense_Mutation	SNP	G	A	39	349	c.2437G>A	c.(2437-2439)GAC>AAC	p.D813N
Pat_45	Post-Resistance	CUEDC1	404093	37	17	55943873	55943873	Missense_Mutation	SNP	G	A	6	132	c.1126C>T	c.(1126-1128)CCC>TCC	p.P376S
Pat_45	Post-Resistance	EPX	8288	37	17	56280680	56280680	Splice_Site	SNP	G	A	10	86	c.1946_splice	c.e11+1	p.R649_splice
Pat_45	Post-Resistance	MKS1	54903	37	17	56288382	56288382	Missense_Mutation	SNP	G	A	17	151	c.917C>T	c.(916-918)ACT>ATT	p.T306I
Pat_45	Post-Resistance	4-Sep	5414	37	17	56598662	56598662	Missense_Mutation	SNP	C	T	18	239	c.1067G>A	c.(1066-1068)AGA>AAA	p.R356K
Pat_45	Post-Resistance	TEX14	56155	37	17	56692603	56692603	Missense_Mutation	SNP	C	T	17	300	c.889G>A	c.(889-891)GAA>AAA	p.E297K
Pat_45	Post-Resistance	BRIP1	83990	37	17	59886064	59886064	Missense_Mutation	SNP	C	T	5	97	c.682G>A	c.(682-684)GAG>AAG	p.E228K
Pat_45	Post-Resistance	10-Mar	162333	37	17	60837289	60837289	Missense_Mutation	SNP	G	A	19	122	c.289C>T	c.(289-291)CCA>TCA	p.P97S
Pat_45	Post-Resistance	CYB561	1534	37	17	61511927	61511927	Missense_Mutation	SNP	C	T	10	104	c.592G>A	c.(592-594)GGT>AGT	p.G198S
Pat_45	Post-Resistance	SMARCD2	6603	37	17	61910707	61910707	Missense_Mutation	SNP	G	A	8	91	c.1391C>T	c.(1390-1392)CCC>CTC	p.P464L
Pat_45	Post-Resistance	ERN1	2081	37	17	62141418	62141418	Missense_Mutation	SNP	C	T	7	101	c.1015G>A	c.(1015-1017)GAC>AAC	p.D339N
Pat_45	Post-Resistance	SMURF2	64750	37	17	62589678	62589678	Missense_Mutation	SNP	A	G	5	80	c.214T>C	c.(214-216)TCT>CCT	p.S72P
Pat_45	Post-Resistance	BPTF	2186	37	17	65862656	65862656	Missense_Mutation	SNP	G	A	8	253	c.1513G>A	c.(1513-1515)GAC>AAC	p.D505N
Pat_45	Post-Resistance	BPTF	2186	37	17	65908567	65908567	Missense_Mutation	SNP	C	T	10	157	c.4567C>T	c.(4567-4569)CCA>TCA	p.P1523S
Pat_45	Post-Resistance	ABCA8	10351	37	17	66881375	66881375	Missense_Mutation	SNP	G	T	6	85	c.3391C>A	c.(3391-3393)CCT>ACT	p.P1131T
Pat_45	Post-Resistance	NAT9	26151	37	17	72768417	72768417	Splice_Site	SNP	C	T	14	83	c.335_splice	c.e5-1	p.E112_splice
Pat_45	Post-Resistance	UNC13D	201294	37	17	73836610	73836610	Missense_Mutation	SNP	C	T	13	225	c.731G>A	c.(730-732)GGG>GAG	p.G244E

Pat_45	Post-Resistance	SRP68	6730	37	17	74060188	74060188	Missense_Mutation	SNP	C	T	9	164	c.430G>A	c.(430-432)GAA>AAA	p.E144K
Pat_45	Post-Resistance	MXRA7	439921	37	17	74673774	74673774	Missense_Mutation	SNP	C	T	7	92	c.511G>A	c.(511-513)GAA>AAA	p.E171K
Pat_45	Post-Resistance	DNAH17	8632	37	17	76449428	76449428	Missense_Mutation	SNP	C	T	4	36	c.1526G>A	c.(1525-1527)GGA>GAA	p.G509E
Pat_45	Post-Resistance	RNF213	57674	37	17	78350185	78350185	Missense_Mutation	SNP	G	A	36	289	c.7489G>A	c.(7489-7491)GAC>AAC	p.D2497N
Pat_45	Post-Resistance	RPTOR	57521	37	17	78931423	78931423	Splice_Site	SNP	G	A	14	137	c.3371_splice	c.e29-1	p.G1124_splice
Pat_45	Post-Resistance	BAHCC1	57597	37	17	79429032	79429032	Missense_Mutation	SNP	C	T	5	45	c.7343C>T	c.(7342-7344)CCC>CTC	p.P2448L
Pat_45	Post-Resistance	FASN	2194	37	17	80037376	80037376	Missense_Mutation	SNP	C	T	5	122	c.7255G>A	c.(7255-7257)GCG>ACG	p.A2419T
Pat_45	Post-Resistance	FOXK2	3607	37	17	80521306	80521306	Missense_Mutation	SNP	G	A	5	59	c.496G>A	c.(496-498)GAG>AAG	p.E166K
Pat_45	Post-Resistance	TBCD	6904	37	17	80758775	80758775	Missense_Mutation	SNP	C	T	6	161	c.853C>T	c.(853-855)CTC>TTC	p.L285F
Pat_45	Post-Resistance	EPB41L3	23136	37	18	5424310	5424310	Missense_Mutation	SNP	C	T	44	204	c.1114G>A	c.(1114-1116)GCT>ACT	p.A372T
Pat_45	Post-Resistance	LAMA3	3909	37	18	21293980	21293980	Missense_Mutation	SNP	C	T	12	98	c.391C>T	c.(391-393)CCC>TCC	p.P131S
Pat_45	Post-Resistance	CABYR	26256	37	18	21736420	21736420	Missense_Mutation	SNP	C	T	3	37	c.955C>T	c.(955-957)CCT>TCT	p.P319S
Pat_45	Post-Resistance	TAF4B	6875	37	18	23865876	23865876	Missense_Mutation	SNP	C	T	23	167	c.1003C>T	c.(1003-1005)CCT>TCT	p.P335S
Pat_45	Post-Resistance	MAPRE2	10982	37	18	32706945	32706945	Missense_Mutation	SNP	G	A	13	112	c.644G>A	c.(643-645)GGA>GAA	p.G215E
Pat_45	Post-Resistance	SETBP1	26040	37	18	42618459	42618459	Missense_Mutation	SNP	G	A	16	58	c.4010G>A	c.(4009-4011)AGT>AAT	p.S1337N
Pat_45	Post-Resistance	ATP5A1	498	37	18	43666117	43666117	Missense_Mutation	SNP	C	T	13	145	c.1391G>A	c.(1390-1392)GGC>GAC	p.G464D
Pat_45	Post-Resistance	MRO	83876	37	18	48331529	48331529	Missense_Mutation	SNP	C	T	8	49	c.424G>A	c.(424-426)GAT>AAT	p.D142N
Pat_45	Post-Resistance	MEX3C	51320	37	18	48703571	48703571	Missense_Mutation	SNP	G	A	7	109	c.1130C>T	c.(1129-1131)CCT>CTT	p.P377L
Pat_45	Post-Resistance	POLI	11201	37	18	51807109	51807109	Missense_Mutation	SNP	C	T	24	287	c.632C>T	c.(631-633)GCC>GTC	p.A211V
Pat_45	Post-Resistance	ALPK2	115701	37	18	56247145	56247145	Missense_Mutation	SNP	C	G	12	28	c.863G>C	c.(862-864)AGT>ACT	p.S288T
Pat_45	Post-Resistance	CBLN2	147381	37	18	70205419	70205419	Missense_Mutation	SNP	G	A	23	71	c.667C>T	c.(667-669)CCT>TCT	p.P223S
Pat_45	Post-Resistance	POLRMT	5442	37	19	630154	630154	Missense_Mutation	SNP	C	T	20	199	c.208G>A	c.(208-210)GTG>ATG	p.V70M
Pat_45	Post-Resistance	FSTL3	10272	37	19	677879	677879	Missense_Mutation	SNP	C	T	17	220	c.191C>T	c.(190-192)TCC>TTC	p.S64F
Pat_45	Post-Resistance	AES	166	37	19	3061231	3061231	Missense_Mutation	SNP	G	A	24	210	c.52C>T	c.(52-54)CTC>TTC	p.L18F
Pat_45	Post-Resistance	MAP2K2	5605	37	19	4117617	4117617	Missense_Mutation	SNP	C	T	5	80	c.103G>A	c.(103-105)GTG>ATG	p.V35M
Pat_45	Post-Resistance	CHAF1A	10036	37	19	4409310	4409310	Missense_Mutation	SNP	C	T	23	91	c.514C>T	c.(514-516)CCT>TCT	p.P172S
Pat_45	Post-Resistance	FEM1A	55527	37	19	4793832	4793832	Missense_Mutation	SNP	G	A	6	32	c.1966G>A	c.(1966-1968)GGC>AGC	p.G656S
Pat_45	Post-Resistance	UHRF1	29128	37	19	4930828	4930828	Missense_Mutation	SNP	G	A	14	93	c.509G>A	c.(508-510)TGC>TAC	p.C170Y
Pat_45	Post-Resistance	SAFB2	9667	37	19	5613531	5613531	Missense_Mutation	SNP	C	T	16	95	c.551G>A	c.(550-552)GGG>GAG	p.G184E
Pat_45	Post-Resistance	DENND1C	79958	37	19	6468925	6468925	Missense_Mutation	SNP	C	T	6	26	c.1447G>A	c.(1447-1449)GCC>ACC	p.A483T
Pat_45	Post-Resistance	TNFSF14	8740	37	19	6669966	6669966	Missense_Mutation	SNP	C	T	67	500	c.115G>A	c.(115-117)GGT>AGT	p.G39S
Pat_45	Post-Resistance	EMR1	2015	37	19	6935082	6935082	Missense_Mutation	SNP	G	A	6	102	c.2374G>A	c.(2374-2376)GAC>AAC	p.D792N
Pat_45	Post-Resistance	KIAA1543	57662	37	19	7676884	7676884	Missense_Mutation	SNP	C	T	14	108	c.1505C>T	c.(1504-1506)CCC>CTC	p.P502L
Pat_45	Post-Resistance	CLEC4G	339390	37	19	7794279	7794279	Nonsense_Mutation	SNP	C	T	5	62	c.855G>A	c.(853-855)TGG>TGA	p.W285*
Pat_45	Post-Resistance	CLEC4M	10332	37	19	7830868	7830868	Missense_Mutation	SNP	C	G	7	104	c.490C>G	c.(490-492)CGG>GGG	p.R164G
Pat_45	Post-Resistance	FBN3	84467	37	19	8201157	8201157	Missense_Mutation	SNP	C	T	6	109	c.1382G>A	c.(1381-1383)GGT>GAT	p.G461D
Pat_45	Post-Resistance	MYO1F	4542	37	19	8595223	8595223	Missense_Mutation	SNP	C	T	43	439	c.2185G>A	c.(2185-2187)GAG>AAG	p.E729K
Pat_45	Post-Resistance	MBD3L1	85509	37	19	8953482	8953482	Missense_Mutation	SNP	C	T	8	69	c.128C>T	c.(127-129)ACA>ATA	p.T43I
Pat_45	Post-Resistance	MUC16	94025	37	19	9047922	9047922	Missense_Mutation	SNP	A	G	9	29	c.33709T>C	c.(33709-33711)TCA>CCA	p.S11237P
Pat_45	Post-Resistance	MUC16	94025	37	19	9060132	9060132	Missense_Mutation	SNP	C	T	10	119	c.27314G>A	c.(27313-27315)GGG>GA	p.G9105E
Pat_45	Post-Resistance	MUC16	94025	37	19	9060313	9060313	Missense_Mutation	SNP	C	T	3	50	c.27133G>A	c.(27133-27135)GGA>AGA	p.G9045R
Pat_45	Post-Resistance	MUC16	94025	37	19	9065926	9065926	Missense_Mutation	SNP	C	T	16	133	c.21520G>A	c.(21520-21522)GCT>ACT	p.A7174T
Pat_45	Post-Resistance	MUC16	94025	37	19	9068846	9068846	Missense_Mutation	SNP	C	T	6	100	c.18600G>A	c.(18598-18600)ATG>ATA	p.M6200I
Pat_45	Post-Resistance	COL5A3	50509	37	19	10106275	10106275	Missense_Mutation	SNP	C	T	9	44	c.1552G>A	c.(1552-1554)GGA>AGA	p.G518R
Pat_45	Post-Resistance	EIF3G	8666	37	19	10227834	10227834	Missense_Mutation	SNP	C	A	4	68	c.331G>T	c.(331-333)GAC>TAC	p.D111Y
Pat_45	Post-Resistance	DOCK6	57572	37	19	11325258	11325258	Missense_Mutation	SNP	C	T	9	159	c.4174G>A	c.(4174-4176)GTT>ATT	p.V1392I
Pat_45	Post-Resistance	ZNF627	199692	37	19	11728403	11728403	Missense_Mutation	SNP	C	T	9	137	c.1085C>T	c.(1084-1086)CCC>CTC	p.P362L

Pat_45	Post-Resistance	ZNF433	163059	37	19	12127446	12127446	Missense_Mutation	SNP	C	T	8	41	c.236G>A	c.(235-237)GGT>GAT	p.G79D
Pat_45	Post-Resistance	ZNF625	90589	37	19	12256929	12256929	Missense_Mutation	SNP	G	A	9	55	c.104C>T	c.(103-105)TCA>TTA	p.S35L
Pat_45	Post-Resistance	HOOK2	29911	37	19	12876642	12876642	Splice_Site	SNP	C	T	13	84	c.1605_splice	c.e17+1	p.I535_splice
Pat_45	Post-Resistance	ZNF333	84449	37	19	14829206	14829206	Missense_Mutation	SNP	C	T	10	87	c.1067C>T	c.(1066-1068)CCC>CTC	p.P356L
Pat_45	Post-Resistance	HSH2D	84941	37	19	16263420	16263420	Missense_Mutation	SNP	C	T	4	27	c.184C>T	c.(184-186)CAC>TAC	p.H62Y
Pat_45	Post-Resistance	FAM129C	199786	37	19	17653030	17653030	Missense_Mutation	SNP	G	A	22	286	c.1349G>A	c.(1348-1350)GGG>GAG	p.G450E
Pat_45	Post-Resistance	SLC5A5	6528	37	19	17985541	17985541	Splice_Site	SNP	G	A	8	57	c.543_splice	c.e4+1	p.V181_splice
Pat_45	Post-Resistance	PDE4C	5143	37	19	18322645	18322645	Missense_Mutation	SNP	C	T	15	178	c.1715G>A	c.(1714-1716)GGA>GAA	p.G572E
Pat_45	Post-Resistance	NCAN	1463	37	19	19329961	19329961	Missense_Mutation	SNP	C	G	7	53	c.311C>G	c.(310-312)GCC>GGC	p.A104G
Pat_45	Post-Resistance	KIAA0892	23383	37	19	19458167	19458167	Missense_Mutation	SNP	C	A	4	95	c.1300C>A	c.(1300-1302)CAA>AAA	p.Q434K
Pat_45	Post-Resistance	GMIP	51291	37	19	19745992	19745992	Missense_Mutation	SNP	C	T	3	17	c.1591G>A	c.(1591-1593)GAG>AAG	p.E531K
Pat_45	Post-Resistance	LOC284441	284441	37	19	20369281	20369281	Missense_Mutation	SNP	G	A	19	124	c.74G>A	c.(73-75)CGA>CAA	p.R25Q
Pat_45	Post-Resistance	ZNF99	7652	37	19	22940567	22940567	Missense_Mutation	SNP	C	T	5	122	c.1871G>A	c.(1870-1872)AGC>AAC	p.S624N
Pat_45	Post-Resistance	ANKRD27	84079	37	19	33095326	33095326	Missense_Mutation	SNP	C	T	4	31	c.2498G>A	c.(2497-2499)GGG>GAG	p.G833E
Pat_45	Post-Resistance	WDR88	126248	37	19	33623100	33623100	Missense_Mutation	SNP	C	T	7	44	c.25C>T	c.(25-27)CCG>TCG	p.P9S
Pat_45	Post-Resistance	ARHGAP33	115703	37	19	36278595	36278595	Missense_Mutation	SNP	C	T	10	138	c.2645C>T	c.(2644-2646)CCC>CTC	p.P882L
Pat_45	Post-Resistance	NPHS1	4868	37	19	36322248	36322248	Missense_Mutation	SNP	C	T	12	111	c.3337G>A	c.(3337-3339)GAA>AAA	p.E1113K
Pat_45	Post-Resistance	THAP8	199745	37	19	36530347	36530347	Missense_Mutation	SNP	C	T	4	6	c.550G>A	c.(550-552)GTG>ATG	p.V184M
Pat_45	Post-Resistance	ZNF529	57711	37	19	37038249	37038249	Missense_Mutation	SNP	C	T	19	124	c.1211G>A	c.(1210-1212)AGA>AAA	p.R404K
Pat_45	Post-Resistance	DPF1	8193	37	19	38703019	38703019	Missense_Mutation	SNP	C	T	5	52	c.973G>A	c.(973-975)GCG>ACG	p.A325T
Pat_45	Post-Resistance	ZFP36	7538	37	19	39899095	39899095	Missense_Mutation	SNP	C	T	6	105	c.737C>T	c.(736-738)ACC>ATC	p.T246I
Pat_45	Post-Resistance	PRX	57716	37	19	40902065	40902065	Missense_Mutation	SNP	C	T	18	211	c.2194G>A	c.(2194-2196)GTG>ATG	p.V732M
Pat_45	Post-Resistance	BLVRB	645	37	19	40964341	40964341	Missense_Mutation	SNP	G	A	6	27	c.191C>T	c.(190-192)ACC>ATC	p.T64I
Pat_45	Post-Resistance	EGLN2	112398	37	19	41307219	41307219	Missense_Mutation	SNP	C	T	9	50	c.742C>T	c.(742-744)CCA>TCA	p.P248S
Pat_45	Post-Resistance	CYP2A7	1549	37	19	41387952	41387952	Missense_Mutation	SNP	C	T	4	61	c.164G>A	c.(163-165)TGT>TAT	p.C55Y
Pat_45	Post-Resistance	CYP2S1	29785	37	19	41700570	41700570	Missense_Mutation	SNP	G	A	11	104	c.299G>A	c.(298-300)GGC>GAC	p.G100D
Pat_45	Post-Resistance	ZNF526	116115	37	19	42729087	42729087	Missense_Mutation	SNP	C	T	19	247	c.532C>T	c.(532-534)CCT>TCT	p.P178S
Pat_45	Post-Resistance	ERF	2077	37	19	42753810	42753810	Missense_Mutation	SNP	C	T	9	74	c.454G>A	c.(454-456)GTG>ATG	p.V152M
Pat_45	Post-Resistance	ZNF223	7766	37	19	44570909	44570909	Missense_Mutation	SNP	C	T	17	139	c.928C>T	c.(928-930)CAC>TAC	p.H310Y
Pat_45	Post-Resistance	ZNF285	26974	37	19	44891638	44891638	Missense_Mutation	SNP	C	T	10	93	c.769G>A	c.(769-771)GAA>AAA	p.E257K
Pat_45	Post-Resistance	ZNF229	7772	37	19	44934304	44934304	Missense_Mutation	SNP	C	T	6	139	c.652G>A	c.(652-654)GAT>AAT	p.D218N
Pat_45	Post-Resistance	PVRL2	5819	37	19	45377175	45377175	Missense_Mutation	SNP	C	T	31	256	c.778C>T	c.(778-780)CCT>TCT	p.P260S
Pat_45	Post-Resistance	PPP1R13L	10848	37	19	45901355	45901355	Missense_Mutation	SNP	C	T	4	126	c.106G>A	c.(106-108)GCG>ACG	p.A36T
Pat_45	Post-Resistance	SYMPK	8189	37	19	46345570	46345570	Missense_Mutation	SNP	C	T	18	174	c.1025G>A	c.(1024-1026)AGC>AAC	p.S342N
Pat_45	Post-Resistance	NANOS2	339345	37	19	46417719	46417719	Nonsense_Mutation	SNP	G	C	5	160	c.233C>G	c.(232-234)TCA>TGA	p.S78*
Pat_45	Post-Resistance	NOVA2	4858	37	19	46457133	46457133	Missense_Mutation	SNP	C	T	12	194	c.301G>A	c.(301-303)GAG>AAG	p.E101K
Pat_45	Post-Resistance	STRN4	29888	37	19	47234041	47234041	Missense_Mutation	SNP	C	T	17	215	c.827G>A	c.(826-828)AGC>AAC	p.S276N
Pat_45	Post-Resistance	DHX34	9704	37	19	47884166	47884166	Missense_Mutation	SNP	C	T	20	185	c.3076C>T	c.(3076-3078)CTC>TTC	p.L1026F
Pat_45	Post-Resistance	NAPA	8775	37	19	47996392	47996392	Missense_Mutation	SNP	C	T	7	77	c.460G>A	c.(460-462)GGC>AGC	p.G154S
Pat_45	Post-Resistance	LIG1	3978	37	19	48636316	48636316	Missense_Mutation	SNP	C	T	31	328	c.1648G>A	c.(1648-1650)GGC>AGC	p.G550S
Pat_45	Post-Resistance	IZUMO1	284359	37	19	49248930	49248930	Missense_Mutation	SNP	C	T	13	153	c.187G>A	c.(187-189)GAT>AAT	p.D63N
Pat_45	Post-Resistance	SNRNP70	6625	37	19	49611533	49611533	Missense_Mutation	SNP	C	T	6	12	c.1147C>T	c.(1147-1149)CGG>TGG	p.R383W
Pat_45	Post-Resistance	PTH2	113091	37	19	49926533	49926533	Missense_Mutation	SNP	G	C	4	50	c.64C>G	c.(64-66)CTG>GTG	p.L22V
Pat_45	Post-Resistance	PRR12	57479	37	19	50105048	50105048	Missense_Mutation	SNP	C	T	15	39	c.4646C>T	c.(4645-4647)GCC>GTC	p.A1549V
Pat_45	Post-Resistance	ZNF473	25888	37	19	50549141	50549141	Missense_Mutation	SNP	C	A	4	29	c.1441C>A	c.(1441-1443)CAC>AAC	p.H481N
Pat_45	Post-Resistance	HAS1	3036	37	19	52220383	52220383	Missense_Mutation	SNP	C	T	19	241	c.766G>A	c.(766-768)GAG>AAG	p.E256K
Pat_45	Post-Resistance	ZNF649	65251	37	19	52394652	52394652	Missense_Mutation	SNP	C	T	5	124	c.737G>A	c.(736-738)AGG>AAG	p.R246K

Pat_45	Post-Resistance	ZNF160	90338	37	19	53589523	53589524	Missense_Mutation	DNP	GG	AA	12	69	c.6_7CC>TT	c.(4-9)GCCCTT>GCTTTT	p.L3F
Pat_45	Post-Resistance	NLRP12	91662	37	19	54327171	54327171	Nonsense_Mutation	SNP	C	T	19	227	c.258G>A	c.(256-258)TGG>TGA	p.W86*
Pat_45	Post-Resistance	PRPF31	26121	37	19	54626908	54626908	Missense_Mutation	SNP	G	A	16	160	c.496G>A	c.(496-498)GTC>ATC	p.V166I
Pat_45	Post-Resistance	LILRA1	11024	37	19	55106729	55106729	Missense_Mutation	SNP	C	T	27	185	c.523C>T	c.(523-525)CAT>TAT	p.H175Y
Pat_45	Post-Resistance	LILRB1	10859	37	19	55146735	55146735	Missense_Mutation	SNP	G	A	31	98	c.1585G>A	c.(1585-1587)GAA>AAA	p.E529K
Pat_45	Post-Resistance	KIR2DS4	3809	37	19	55354347	55354347	Missense_Mutation	SNP	C	T	59	280	c.689C>T	c.(688-690)TCA>TTA	p.S230L
Pat_45	Post-Resistance	NLRP2	55655	37	19	55493601	55493601	Missense_Mutation	SNP	A	G	14	142	c.535A>G	c.(535-537)AGC>GGC	p.S179G
Pat_45	Post-Resistance	RDH13	112724	37	19	55559706	55559706	Missense_Mutation	SNP	G	A	3	63	c.649C>T	c.(649-651)CGG>TGG	p.R217W
Pat_45	Post-Resistance	NLRP9	338321	37	19	56243836	56243836	Missense_Mutation	SNP	G	A	25	217	c.1361C>T	c.(1360-1362)GCC>GTC	p.A454V
Pat_45	Post-Resistance	NLRP4	147945	37	19	56363558	56363558	Missense_Mutation	SNP	G	A	4	46	c.112G>A	c.(112-114)GAA>AAA	p.E38K
Pat_45	Post-Resistance	ZSCAN5A	79149	37	19	56736364	56736364	Missense_Mutation	SNP	G	A	6	92	c.52C>T	c.(52-54)CCT>TCT	p.P18S
Pat_45	Post-Resistance	ZNF134	7693	37	19	58131554	58131554	Missense_Mutation	SNP	G	A	12	75	c.67G>A	c.(67-69)GAG>AAG	p.E23K
Pat_45	Post-Resistance	ZNF551	90233	37	19	58199447	58199447	Missense_Mutation	SNP	C	T	11	198	c.1756C>T	c.(1756-1758)CTC>TTC	p.L586F
Pat_45	Post-Resistance	ZNF606	80095	37	19	58499962	58499962	Splice_Site	SNP	C	T	11	221	c.304_splice	c.e5+1	p.G102_splice
Pat_45	Post-Resistance	SH3YL1	26751	37	2	218899	218899	Missense_Mutation	SNP	G	A	6	125	c.941C>T	c.(940-942)TCA>TTA	p.S314L
Pat_45	Post-Resistance	SOX11	6664	37	2	5833455	5833455	Missense_Mutation	SNP	G	A	7	83	c.602G>A	c.(601-603)GGC>GAC	p.G201D
Pat_45	Post-Resistance	ADAM17	6868	37	2	9658100	9658100	Missense_Mutation	SNP	C	T	4	77	c.1121G>A	c.(1120-1122)GGG>GAG	p.G374E
Pat_45	Post-Resistance	GEN1	348654	37	2	17961301	17961301	Missense_Mutation	SNP	G	A	4	35	c.1321G>A	c.(1321-1323)GAA>AAA	p.E441K
Pat_45	Post-Resistance	APOB	338	37	2	21229484	21229484	Missense_Mutation	SNP	T	G	23	194	c.10256A>C	c.(10255-10257)AAA>ACA	p.K3419T
Pat_45	Post-Resistance	GPR113	165082	37	2	26534707	26534707	Missense_Mutation	SNP	C	A	4	32	c.1889G>T	c.(1888-1890)CGG>CTG	p.R630L
Pat_45	Post-Resistance	ABHD1	84696	37	2	27351878	27351878	Missense_Mutation	SNP	G	A	15	118	c.341G>A	c.(340-342)AGC>AAC	p.S114N
Pat_45	Post-Resistance	C2orf16	84226	37	2	27803008	27803008	Missense_Mutation	SNP	G	A	15	25	c.3569G>A	c.(3568-3570)CGG>CAG	p.R1190Q
Pat_45	Post-Resistance	PPP1CB	5500	37	2	29006802	29006802	Missense_Mutation	SNP	C	G	9	78	c.550C>G	c.(550-552)CAG>GAG	p.Q184E
Pat_45	Post-Resistance	LCLAT1	253558	37	2	30863202	30863202	Missense_Mutation	SNP	G	A	19	169	c.962G>A	c.(961-963)GGG>GAG	p.G321E
Pat_45	Post-Resistance	NLRC4	58484	37	2	32477565	32477565	Missense_Mutation	SNP	C	T	12	91	c.185G>A	c.(184-186)GGT>GAT	p.G62D
Pat_45	Post-Resistance	STRN	6801	37	2	37105140	37105140	Missense_Mutation	SNP	C	T	9	196	c.1217G>A	c.(1216-1218)GGA>GAA	p.G406E
Pat_45	Post-Resistance	HEATR5B	54497	37	2	37229562	37229562	Missense_Mutation	SNP	G	A	12	257	c.5204C>T	c.(5203-5205)TCA>TTA	p.S1735L
Pat_45	Post-Resistance	HEATR5B	54497	37	2	37310493	37310493	Missense_Mutation	SNP	C	T	8	107	c.65G>A	c.(64-66)AGA>AAA	p.R22K
Pat_45	Post-Resistance	C2orf56	55471	37	2	37464930	37464930	Missense_Mutation	SNP	A	G	3	74	c.328A>G	c.(328-330)ATG>GTG	p.M110V
Pat_45	Post-Resistance	DHX57	90957	37	2	39095553	39095553	Translation_Start_Site	SNP	C	T	9	81	c.-5G>A	c.(-7--3)AGGTG>AGATG	
Pat_45	Post-Resistance	SOS1	6654	37	2	39278325	39278325	Missense_Mutation	SNP	G	A	9	53	c.824C>T	c.(823-825)CCC>CTC	p.P275L
Pat_45	Post-Resistance	SLC8A1	6546	37	2	40342508	40342508	Missense_Mutation	SNP	T	C	19	105	c.2807A>G	c.(2806-2808)GAG>GGG	p.E936G
Pat_45	Post-Resistance	SRBD1	55133	37	2	45774743	45774743	Missense_Mutation	SNP	G	A	4	52	c.1684C>T	c.(1684-1686)CTT>TTT	p.L562F
Pat_45	Post-Resistance	FOXN2	3344	37	2	48602224	48602224	Missense_Mutation	SNP	G	A	5	60	c.938G>A	c.(937-939)CGT>CAT	p.R313H
Pat_45	Post-Resistance	KIAA1841	84542	37	2	61331003	61331003	Missense_Mutation	SNP	G	A	9	55	c.1381G>A	c.(1381-1383)GAC>AAC	p.D461N
Pat_45	Post-Resistance	VPS54	51542	37	2	64208875	64208875	Missense_Mutation	SNP	C	T	11	180	c.283G>A	c.(283-285)GGA>AGA	p.G95R
Pat_45	Post-Resistance	CEP68	23177	37	2	65299512	65299512	Missense_Mutation	SNP	G	A	8	46	c.1282G>A	c.(1282-1284)GGC>AGC	p.G428S
Pat_45	Post-Resistance	AAK1	22848	37	2	69747977	69747977	Missense_Mutation	SNP	G	A	29	400	c.1199C>T	c.(1198-1200)CCT>CTT	p.P400L
Pat_45	Post-Resistance	LRRTM4	80059	37	2	77746529	77746529	Missense_Mutation	SNP	G	T	4	38	c.466C>A	c.(466-468)CTT>ATT	p.L156I
Pat_45	Post-Resistance	MITD1	129531	37	2	99786018	99786018	Missense_Mutation	SNP	G	A	8	68	c.649C>T	c.(649-651)CCA>TCA	p.P217S
Pat_45	Post-Resistance	EIF5B	9669	37	2	99992981	99992981	Nonsense_Mutation	SNP	C	A	4	61	c.1724C>A	c.(1723-1725)TCA>TAA	p.S575*
Pat_45	Post-Resistance	REV1	51455	37	2	100022421	100022421	Missense_Mutation	SNP	C	T	20	133	c.2762G>A	c.(2761-2763)AGT>AAT	p.S921N
Pat_45	Post-Resistance	REV1	51455	37	2	100027328	100027328	Missense_Mutation	SNP	G	A	4	29	c.2174C>T	c.(2173-2175)CCA>CTA	p.P725L
Pat_45	Post-Resistance	RGPD3	653489	37	2	107029693	107029693	Missense_Mutation	SNP	C	T	13	166	c.5113G>A	c.(5113-5115)GTG>ATG	p.V1705M
Pat_45	Post-Resistance	10-Sep	151011	37	2	110322024	110322024	Missense_Mutation	SNP	G	A	14	73	c.947C>T	c.(946-948)ACC>ATC	p.T316I
Pat_45	Post-Resistance	POLR1B	84172	37	2	113325662	113325662	Missense_Mutation	SNP	C	T	17	153	c.1865C>T	c.(1864-1866)CCT>CTT	p.P622L
Pat_45	Post-Resistance	DPP10	57628	37	2	116548883	116548883	Missense_Mutation	SNP	C	T	5	116	c.1651C>T	c.(1651-1653)CTT>TTT	p.L551F

Pat_45	Post-Resistance	TMEM37	140738	37	2	120194856	120194856	Missense_Mutation	SNP	C	T	22	221	c.413C>T	c.(412-414)TCC>TTC	p.S138F
Pat_45	Post-Resistance	RALB	5899	37	2	121043609	121043609	Missense_Mutation	SNP	G	A	11	101	c.274G>A	c.(274-276)GTG>ATG	p.V92M
Pat_45	Post-Resistance	RAB3GAP1	22930	37	2	135926254	135926254	Missense_Mutation	SNP	C	T	19	228	c.2849C>T	c.(2848-2850)CCC>CTC	p.P950L
Pat_45	Post-Resistance	ZRANB3	84083	37	2	136033282	136033282	Missense_Mutation	SNP	T	C	3	43	c.1010A>G	c.(1009-1011)GAT>GGT	p.D337G
Pat_45	Post-Resistance	LRP1B	53353	37	2	141274541	141274541	Missense_Mutation	SNP	C	T	8	83	c.8066G>A	c.(8065-8067)TGT>TAT	p.C2689Y
Pat_45	Post-Resistance	STAM2	10254	37	2	153006704	153006704	Missense_Mutation	SNP	C	T	3	39	c.80G>A	c.(79-81)AGT>AAT	p.S27N
Pat_45	Post-Resistance	TANC1	85461	37	2	160035675	160035675	Splice_Site	SNP	G	A	13	87	c.2510_splice	c.e14+1	p.R837_splice
Pat_45	Post-Resistance	LY75	4065	37	2	160673338	160673338	Nonsense_Mutation	SNP	C	T	4	99	c.4359G>A	c.(4357-4359)TGG>TGA	p.W1453*
Pat_45	Post-Resistance	NOSTRIN	115677	37	2	169716093	169716093	Missense_Mutation	SNP	A	C	45	115	c.1125A>C	c.(1123-1125)CAA>CAC	p.Q375H
Pat_45	Post-Resistance	LRP2	4036	37	2	170115628	170115628	Missense_Mutation	SNP	C	T	28	224	c.2420G>A	c.(2419-2421)AGT>AAT	p.S807N
Pat_45	Post-Resistance	GORASP2	26003	37	2	171806783	171806783	Missense_Mutation	SNP	G	A	9	100	c.418G>A	c.(418-420)GAT>AAT	p.D140N
Pat_45	Post-Resistance	TLK1	9874	37	2	171902700	171902700	Missense_Mutation	SNP	G	A	18	208	c.1153C>T	c.(1153-1155)CCA>TCA	p.P385S
Pat_45	Post-Resistance	OSBPL6	114880	37	2	179260211	179260211	Nonsense_Mutation	SNP	G	A	4	40	c.2730G>A	c.(2728-2730)TGG>TGA	p.W910*
Pat_45	Post-Resistance	TTN	7273	37	2	179395254	179395254	Missense_Mutation	SNP	C	T	9	122	c.98384G>A	c.(98383-98385)GGT>GAT	p.G32795D
Pat_45	Post-Resistance	TTN	7273	37	2	179417575	179417575	Missense_Mutation	SNP	G	A	7	21	c.82348C>T	c.(82348-82350)CCC>TCC	p.P27450S
Pat_45	Post-Resistance	TTN	7273	37	2	179429729	179429729	Nonsense_Mutation	SNP	G	A	30	297	c.73426C>T	c.(73426-73428)CAG>TAG	p.Q24476*
Pat_45	Post-Resistance	TTN	7273	37	2	179430083	179430083	Missense_Mutation	SNP	C	T	20	196	c.73072G>A	c.(73072-73074)GTA>ATA	p.V24358I
Pat_45	Post-Resistance	TTN	7273	37	2	179460390	179460390	Missense_Mutation	SNP	A	T	3	24	c.49987T>A	c.(49987-49989)TGG>AGG	p.W16663R
Pat_45	Post-Resistance	TTN	7273	37	2	179614255	179614255	Missense_Mutation	SNP	G	A	6	53	c.12872C>T	c.(12871-12873)GCT>GTT	p.A4291V
Pat_45	Post-Resistance	CCDC141	285025	37	2	179720088	179720088	Missense_Mutation	SNP	C	T	13	133	c.1321G>A	c.(1321-1323)GAG>AAG	p.E441K
Pat_45	Post-Resistance	UBE2E3	10477	37	2	181846938	181846938	Missense_Mutation	SNP	G	A	11	165	c.169G>A	c.(169-171)GCT>ACT	p.A57T
Pat_45	Post-Resistance	STAT1	6772	37	2	191862613	191862613	Missense_Mutation	SNP	G	A	7	77	c.754C>T	c.(754-756)CCC>TCC	p.P252S
Pat_45	Post-Resistance	STAT4	6775	37	2	191919238	191919238	Missense_Mutation	SNP	C	T	7	165	c.1229G>A	c.(1228-1230)AGT>AAT	p.S410N
Pat_45	Post-Resistance	ANKRD44	91526	37	2	197873681	197873681	Missense_Mutation	SNP	C	T	41	336	c.1924G>A	c.(1924-1926)GAT>AAT	p.D642N
Pat_45	Post-Resistance	AOX1	316	37	2	201527615	201527616	Missense_Mutation	DNP	GG	AA	54	134	.3466_3467GG>A	c.(3466-3468)GGC>AAC	p.G1156N
Pat_45	Post-Resistance	CLK1	1195	37	2	201725959	201725959	Splice_Site	SNP	A	C	21	156	c.390_splice	c.e3+1	p.G130_splice
Pat_45	Post-Resistance	NOP58	51602	37	2	203149177	203149177	Missense_Mutation	SNP	C	T	13	189	c.407C>T	c.(406-408)GCA>GTA	p.A136V
Pat_45	Post-Resistance	RAPH1	65059	37	2	204354593	204354593	Missense_Mutation	SNP	G	A	6	106	c.446C>T	c.(445-447)GCC>GTC	p.A149V
Pat_45	Post-Resistance	ZDBF2	57683	37	2	207171504	207171504	Missense_Mutation	SNP	C	T	35	318	c.2252C>T	c.(2251-2253)ACT>ATT	p.T751I
Pat_45	Post-Resistance	PIKFYVE	200576	37	2	209141477	209141477	Missense_Mutation	SNP	C	T	7	81	c.364C>T	c.(364-366)CCT>TCT	p.P122S
Pat_45	Post-Resistance	PIKFYVE	200576	37	2	209192986	209192986	Missense_Mutation	SNP	G	A	14	189	c.3701G>A	c.(3700-3702)AGT>AAT	p.S1234N
Pat_45	Post-Resistance	FN1	2335	37	2	216247040	216247040	Missense_Mutation	SNP	C	T	5	46	c.5059G>A	c.(5059-5061)GAA>AAA	p.E1687K
Pat_45	Post-Resistance	C2orf62	375307	37	2	219232544	219232544	Missense_Mutation	SNP	G	A	5	87	c.1021G>A	c.(1021-1023)GAG>AAG	p.E341K
Pat_45	Post-Resistance	CTDSP1	58190	37	2	219268087	219268087	Missense_Mutation	SNP	G	A	8	151	c.604G>A	c.(604-606)GTG>ATG	p.V202M
Pat_45	Post-Resistance	IHH	3549	37	2	219922361	219922361	Missense_Mutation	SNP	C	T	13	234	c.371G>A	c.(370-372)GGT>GAT	p.G124D
Pat_45	Post-Resistance	PAX3	5077	37	2	223158951	223158951	Missense_Mutation	SNP	C	T	6	143	c.521G>A	c.(520-522)AGG>AAG	p.R174K
Pat_45	Post-Resistance	FARSB	10056	37	2	223489056	223489056	Missense_Mutation	SNP	C	T	7	100	c.1105G>A	c.(1105-1107)GCT>ACT	p.A369T
Pat_45	Post-Resistance	IRS1	3667	37	2	227662737	227662737	Missense_Mutation	SNP	C	T	46	297	c.718G>A	c.(718-720)GTG>ATG	p.V240M
Pat_45	Post-Resistance	TM4SF20	79853	37	2	228228469	228228469	Missense_Mutation	SNP	C	T	25	197	c.661G>A	c.(661-663)GTC>ATC	p.V221I
Pat_45	Post-Resistance	TRIP12	9320	37	2	230723748	230723748	Missense_Mutation	SNP	G	A	5	66	c.641C>T	c.(640-642)TCC>TTC	p.S214F
Pat_45	Post-Resistance	CHRND	1144	37	2	233392997	233392997	Nonsense_Mutation	SNP	G	A	9	130	c.269G>A	c.(268-270)TGG>TAG	p.W90*
Pat_45	Post-Resistance	NGEF	25791	37	2	233839413	233839413	Missense_Mutation	SNP	G	A	13	207	c.188C>T	c.(187-189)TCC>TTC	p.S63F
Pat_45	Post-Resistance	UGT1A4	54657	37	2	234628115	234628115	Missense_Mutation	SNP	C	T	15	149	c.649C>T	c.(649-651)CCT>TCT	p.P217S
Pat_45	Post-Resistance	HDAC4	9759	37	2	240055965	240055965	Missense_Mutation	SNP	G	A	6	82	c.1270C>T	c.(1270-1272)CCG>TCG	p.P424S
Pat_45	Post-Resistance	ANKMY1	51281	37	2	241465744	241465744	Missense_Mutation	SNP	C	T	4	69	c.805G>A	c.(805-807)GAA>AAA	p.E269K
Pat_45	Post-Resistance	TRIB3	57761	37	20	372154	372155	Missense_Mutation	DNP	AC	TT	16	60	c.515_516AC>TT	c.(514-516)CAC>CTT	p.H172L
Pat_45	Post-Resistance	PTPRA	5786	37	20	2945518	2945518	Missense_Mutation	SNP	G	A	7	83	c.85G>A	c.(85-87)GTA>ATA	p.V29I

Pat_45	Post-Resistance	CENPB	1059	37	20	3766517	3766517	Missense_Mutation	SNP	G	A	13	217	c.614C>T	c.(613-615)CCC>CTC	p.P205L
Pat_45	Post-Resistance	PLCB4	5332	37	20	9388579	9388579	Missense_Mutation	SNP	G	A	17	99	c.1627G>A	c.(1627-1629)GAA>AAA	p.E543K
Pat_45	Post-Resistance	PAK7	57144	37	20	9520162	9520162	Missense_Mutation	SNP	C	T	19	232	c.2107G>A	c.(2107-2109)GCA>ACA	p.A703T
Pat_45	Post-Resistance	PCSK2	5126	37	20	17437086	17437086	Missense_Mutation	SNP	G	A	11	154	c.1195G>A	c.(1195-1197)GAG>AAG	p.E399K
Pat_45	Post-Resistance	DSTN	11034	37	20	17581578	17581578	Missense_Mutation	SNP	C	T	5	148	c.199C>T	c.(199-201)CCT>TCT	p.P67S
Pat_45	Post-Resistance	CSRP2BP	57325	37	20	18143302	18143302	Missense_Mutation	SNP	C	T	4	18	c.1384C>T	c.(1384-1386)CCC>TCC	p.P462S
Pat_45	Post-Resistance	GGTLC1	92086	37	20	23967244	23967244	Missense_Mutation	SNP	G	A	9	190	c.5C>T	c.(4-6)ACC>ATC	p.T2I
Pat_45	Post-Resistance	TM9SF4	9777	37	20	30720825	30720825	Missense_Mutation	SNP	C	T	7	82	c.25C>T	c.(25-27)CCG>TCG	p.P9S
Pat_45	Post-Resistance	POFUT1	23509	37	20	30803181	30803181	Missense_Mutation	SNP	C	T	13	248	c.356C>T	c.(355-357)CCT>CTT	p.P119L
Pat_45	Post-Resistance	KIF3B	9371	37	20	30897723	30897723	Missense_Mutation	SNP	G	A	16	111	c.143G>A	c.(142-144)GGG>GAG	p.G48E
Pat_45	Post-Resistance	ASXL1	171023	37	20	31023018	31023018	Missense_Mutation	SNP	C	T	18	330	c.2503C>T	c.(2503-2505)CCC>TCC	p.P835S
Pat_45	Post-Resistance	PLUNC	51297	37	20	31829222	31829222	Missense_Mutation	SNP	G	A	150	367	c.613G>A	c.(613-615)GAC>AAC	p.D205N
Pat_45	Post-Resistance	ZNF341	84905	37	20	32354746	32354746	Missense_Mutation	SNP	G	A	32	486	c.1312G>A	c.(1312-1314)GTG>ATG	p.V438M
Pat_45	Post-Resistance	CHMP4B	128866	37	20	32439895	32439895	Missense_Mutation	SNP	G	A	7	134	c.496G>A	c.(496-498)GCG>ACG	p.A166T
Pat_45	Post-Resistance	ITCH	83737	37	20	32981665	32981665	Missense_Mutation	SNP	G	A	15	266	c.48G>A	c.(46-48)ATG>ATA	p.M16I
Pat_45	Post-Resistance	MYH7B	57644	37	20	33582006	33582006	Nonsense_Mutation	SNP	G	A	21	251	c.2628G>A	c.(2626-2628)TGG>TGA	p.W876*
Pat_45	Post-Resistance	TRPC4AP	26133	37	20	33590986	33590986	Missense_Mutation	SNP	G	A	11	104	c.2357C>T	c.(2356-2358)CCC>CTC	p.P786L
Pat_45	Post-Resistance	PROCR	10544	37	20	33762622	33762622	Missense_Mutation	SNP	C	T	8	67	c.188C>T	c.(187-189)ACC>ATC	p.T63I
Pat_45	Post-Resistance	SPAG4	6676	37	20	34207230	34207230	Missense_Mutation	SNP	G	A	11	132	c.907G>A	c.(907-909)GAG>AAG	p.E303K
Pat_45	Post-Resistance	C20orf4	25980	37	20	34828112	34828112	Missense_Mutation	SNP	G	A	9	140	c.322G>A	c.(322-324)GTG>ATG	p.V108M
Pat_45	Post-Resistance	RBL1	5933	37	20	35672611	35672611	Missense_Mutation	SNP	C	T	11	131	c.1648G>A	c.(1648-1650)GAC>AAC	p.D550N
Pat_45	Post-Resistance	TGM2	7052	37	20	36766698	36766698	Missense_Mutation	SNP	G	A	4	79	c.1432C>T	c.(1432-1434)CGT>TGT	p.R478C
Pat_45	Post-Resistance	KCNS1	3787	37	20	43723747	43723747	Missense_Mutation	SNP	C	T	5	84	c.1345G>A	c.(1345-1347)GTA>ATA	p.V449I
Pat_45	Post-Resistance	CTSA	5476	37	20	44521067	44521067	Missense_Mutation	SNP	G	A	6	125	c.388G>A	c.(388-390)GCT>ACT	p.A130T
Pat_45	Post-Resistance	ZNF335	63925	37	20	44582362	44582362	Missense_Mutation	SNP	C	T	11	96	c.2668G>A	c.(2668-2670)GAG>AAG	p.E890K
Pat_45	Post-Resistance	LOC100131496	100131496	37	20	45947671	45947671	Missense_Mutation	SNP	G	A	4	15	c.307G>A	c.(307-309)GGA>AGA	p.G103R
Pat_45	Post-Resistance	NCOA3	8202	37	20	46268767	46268767	Missense_Mutation	SNP	G	A	13	105	c.3052G>A	c.(3052-3054)GAA>AAA	p.E1018K
Pat_45	Post-Resistance	ZNFX1	57169	37	20	47865036	47865036	Missense_Mutation	SNP	G	A	5	117	c.4525C>T	c.(4525-4527)CCC>TCC	p.P1509S
Pat_45	Post-Resistance	SLC9A8	23315	37	20	48461621	48461621	Missense_Mutation	SNP	C	T	6	143	c.397C>T	c.(397-399)CCT>TCT	p.P133S
Pat_45	Post-Resistance	PARD6B	84612	37	20	49354424	49354424	Missense_Mutation	SNP	G	A	9	94	c.97G>A	c.(97-99)GAA>AAA	p.E33K
Pat_45	Post-Resistance	SALL4	57167	37	20	50401212	50401212	Missense_Mutation	SNP	C	T	8	146	c.2754G>A	c.(2752-2754)ATG>ATA	p.M918I
Pat_45	Post-Resistance	TH1L	51497	37	20	57562780	57562780	Missense_Mutation	SNP	G	A	5	158	c.331G>A	c.(331-333)GTT>ATT	p.V111I
Pat_45	Post-Resistance	PHACTR3	116154	37	20	58318169	58318169	Missense_Mutation	SNP	G	A	11	206	c.126G>A	c.(124-126)ATG>ATA	p.M42I
Pat_45	Post-Resistance	PHACTR3	116154	37	20	58342267	58342267	Missense_Mutation	SNP	G	A	14	59	c.568G>A	c.(568-570)GAA>AAA	p.E190K
Pat_45	Post-Resistance	DIDO1	11083	37	20	61511262	61511262	Missense_Mutation	SNP	G	A	7	93	c.6046C>T	c.(6046-6048)CCG>TCG	p.P2016S
Pat_45	Post-Resistance	SAMD10	140700	37	20	62607045	62607045	Missense_Mutation	SNP	C	T	17	334	c.586G>A	c.(586-588)GCT>ACT	p.A196T
Pat_45	Post-Resistance	CXADR	1525	37	21	18924121	18924121	Missense_Mutation	SNP	G	A	3	35	c.265G>A	c.(265-267)GGC>AGC	p.G89S
Pat_45	Post-Resistance	ADAMTS1	9510	37	21	28214939	28214939	Missense_Mutation	SNP	C	T	6	75	c.796G>A	c.(796-798)GCA>ACA	p.A266T
Pat_45	Post-Resistance	RNF160	26046	37	21	30339429	30339429	Missense_Mutation	SNP	C	T	7	45	c.1522G>A	c.(1522-1524)GAA>AAA	p.E508K
Pat_45	Post-Resistance	RNF160	26046	37	21	30359174	30359174	Nonsense_Mutation	SNP	G	A	7	106	c.262C>T	c.(262-264)CAG>TAG	p.Q88*
Pat_45	Post-Resistance	KRTAP27-1	643812	37	21	31709754	31709754	Missense_Mutation	SNP	C	T	19	174	c.233G>A	c.(232-234)AGT>AAT	p.S78N
Pat_45	Post-Resistance	KRTAP13-1	140258	37	21	31768730	31768730	Missense_Mutation	SNP	C	T	9	64	c.326C>T	c.(325-327)TCC>TTC	p.S109F
Pat_45	Post-Resistance	TIAM1	7074	37	21	32595763	32595763	Missense_Mutation	SNP	C	T	24	148	c.1954G>A	c.(1954-1956)GGC>AGC	p.G652S
Pat_45	Post-Resistance	ITSN1	6453	37	21	35093554	35093554	Missense_Mutation	SNP	C	T	6	80	c.100C>T	c.(100-102)CCA>TCA	p.P34S
Pat_45	Post-Resistance	MORC3	23515	37	21	37705988	37705988	Nonsense_Mutation	SNP	G	A	15	140	c.84G>A	c.(82-84)TGG>TGA	p.W28*
Pat_45	Post-Resistance	KCNJ6	3763	37	21	39086672	39086672	Missense_Mutation	SNP	C	T	17	197	c.788G>A	c.(787-789)GGG>GAG	p.G263E
Pat_45	Post-Resistance	BRWD1	54014	37	21	40582064	40582064	Missense_Mutation	SNP	C	T	4	36	c.4054G>A	c.(4054-4056)GAT>AAT	p.D1352N

Pat_45	Post-Resistance	DSCAM	1826	37	21	41434798	41434798	Missense_Mutation	SNP	C	T	4	66	c.4917G>A	c.(4915-4917)ATG>ATA	p.M1639I
Pat_45	Post-Resistance	TMPRSS3	64699	37	21	43795965	43795965	Missense_Mutation	SNP	C	T	12	298	c.1207G>A	c.(1207-1209)GGG>AGG	p.G403R
Pat_45	Post-Resistance	PFKL	5211	37	21	45741675	45741675	Missense_Mutation	SNP	C	T	4	146	c.1255C>T	c.(1255-1257)CGC>TGC	p.R419C
Pat_45	Post-Resistance	ITGB2	3689	37	21	46314884	46314884	Splice_Site	SNP	A	T	4	35	c.1083_splice	c.e8+1	p.N361_splice
Pat_45	Post-Resistance	MCM3AP	8888	37	21	47704228	47704228	Nonsense_Mutation	SNP	G	A	17	147	c.973C>T	c.(973-975)CGA>TGA	p.R325*
Pat_45	Post-Resistance	IL17RA	23765	37	22	17581326	17581326	Missense_Mutation	SNP	C	T	15	171	c.505C>T	c.(505-507)CCT>TCT	p.P169S
Pat_45	Post-Resistance	CECR5	27440	37	22	17624015	17624015	Missense_Mutation	SNP	G	A	30	66	c.544C>T	c.(544-546)CCG>TCG	p.P182S
Pat_45	Post-Resistance	PEX26	55670	37	22	18568025	18568025	Splice_Site	SNP	G	A	5	111	c.814_splice	c.e5+1	p.A272_splice
Pat_45	Post-Resistance	DGCR2	9993	37	22	19052491	19052491	Missense_Mutation	SNP	C	T	10	124	c.418G>A	c.(418-420)GAT>AAT	p.D140N
Pat_45	Post-Resistance	TSSK2	23617	37	22	19119823	19119823	Missense_Mutation	SNP	G	A	10	148	c.911G>A	c.(910-912)GGC>GAC	p.G304D
Pat_45	Post-Resistance	C22orf25	128989	37	22	20043498	20043498	Missense_Mutation	SNP	G	A	3	86	c.413G>A	c.(412-414)GGG>GAG	p.G138E
Pat_45	Post-Resistance	DGCR6L	85359	37	22	20303659	20303659	Nonsense_Mutation	SNP	G	A	4	43	c.355C>T	c.(355-357)CAG>TAG	p.Q119*
Pat_45	Post-Resistance	THAP7	80764	37	22	21354362	21354362	Missense_Mutation	SNP	G	A	9	27	c.737C>T	c.(736-738)GCA>GTA	p.A246V
Pat_45	Post-Resistance	BCR	613	37	22	23631788	23631788	Missense_Mutation	SNP	C	T	7	82	c.2687C>T	c.(2686-2688)CCG>CTG	p.P896L
Pat_45	Post-Resistance	CABIN1	23523	37	22	24439465	24439465	Missense_Mutation	SNP	G	A	8	145	c.445G>A	c.(445-447)GAA>AAA	p.E149K
Pat_45	Post-Resistance	MYO18B	84700	37	22	26400684	26400684	Missense_Mutation	SNP	G	A	14	44	c.6333G>A	c.(6331-6333)ATG>ATA	p.M2111I
Pat_45	Post-Resistance	EMID1	129080	37	22	29639435	29639435	Missense_Mutation	SNP	G	A	3	30	c.1070G>A	c.(1069-1071)GGG>GAG	p.G357E
Pat_45	Post-Resistance	AP1B1	162	37	22	29737718	29737718	Missense_Mutation	SNP	C	T	8	174	c.1568G>A	c.(1567-1569)GGC>GAC	p.G523D
Pat_45	Post-Resistance	PES1	23481	37	22	30977037	30977037	Missense_Mutation	SNP	C	T	15	161	c.874G>A	c.(874-876)GAG>AAG	p.E292K
Pat_45	Post-Resistance	C22orf30	253143	37	22	32072839	32072839	Nonsense_Mutation	SNP	C	T	4	13	c.5742G>A	c.(5740-5742)TGG>TGA	p.W1914*
Pat_45	Post-Resistance	RFPL2	10739	37	22	32598380	32598380	Missense_Mutation	SNP	A	T	3	20	c.59T>A	c.(58-60)CTA>CAA	p.L20Q
Pat_45	Post-Resistance	APOL3	80833	37	22	36537525	36537525	Missense_Mutation	SNP	G	A	7	53	c.932C>T	c.(931-933)ACC>ATC	p.T311I
Pat_45	Post-Resistance	CYTH4	27128	37	22	37696979	37696979	Missense_Mutation	SNP	G	A	5	61	c.466G>A	c.(466-468)GAG>AAG	p.E156K
Pat_45	Post-Resistance	ELFN2	114794	37	22	37770265	37770265	Missense_Mutation	SNP	G	A	18	193	c.1310C>T	c.(1309-1311)ACC>ATC	p.T437I
Pat_45	Post-Resistance	GCAT	23464	37	22	38212714	38212714	Missense_Mutation	SNP	G	A	7	107	c.1249G>A	c.(1249-1251)GCA>ACA	p.A417T
Pat_45	Post-Resistance	EIF3L	51386	37	22	38271944	38271944	Missense_Mutation	SNP	G	A	13	184	c.1003G>A	c.(1003-1005)GTC>ATC	p.V335I
Pat_45	Post-Resistance	CSNK1E	1454	37	22	38694940	38694940	Splice_Site	SNP	C	T	10	191	c.737_splice	c.e7-1	p.S246_splice
Pat_45	Post-Resistance	TAB1	10454	37	22	39811633	39811633	Missense_Mutation	SNP	C	T	8	27	c.299C>T	c.(298-300)GCC>GTC	p.A100V
Pat_45	Post-Resistance	EP300	2033	37	22	41551116	41551116	Missense_Mutation	SNP	C	T	19	303	c.3260C>T	c.(3259-3261)CCT>CTT	p.P1087L
Pat_45	Post-Resistance	EP300	2033	37	22	41568579	41568579	Missense_Mutation	SNP	C	A	4	71	c.4529C>A	c.(4528-4530)CCC>CAC	p.P1510H
Pat_45	Post-Resistance	TTLL12	23170	37	22	43570251	43570251	Missense_Mutation	SNP	G	A	19	419	c.1193C>T	c.(1192-1194)CCC>CTC	p.P398L
Pat_45	Post-Resistance	SAMM50	25813	37	22	44371954	44371954	Missense_Mutation	SNP	G	A	10	51	c.668G>A	c.(667-669)AGC>AAC	p.S223N
Pat_45	Post-Resistance	KIAA1644	85352	37	22	44681567	44681567	Missense_Mutation	SNP	C	T	28	494	c.340G>A	c.(340-342)GTT>ATT	p.V114I
Pat_45	Post-Resistance	SMC1B	27127	37	22	45802707	45802707	Missense_Mutation	SNP	C	T	7	104	c.338G>A	c.(337-339)AGT>AAT	p.S113N
Pat_45	Post-Resistance	PKDREJ	10343	37	22	46653096	46653096	Missense_Mutation	SNP	C	T	11	82	c.6124G>A	c.(6124-6126)GCA>ACA	p.A2042T
Pat_45	Post-Resistance	CELSR1	9620	37	22	46761158	46761158	Missense_Mutation	SNP	C	T	8	86	c.8524G>A	c.(8524-8526)GCC>ACC	p.A2842T
Pat_45	Post-Resistance	GRAMD4	23151	37	22	47059038	47059038	Missense_Mutation	SNP	G	A	10	273	c.568G>A	c.(568-570)GTG>ATG	p.V190M
Pat_45	Post-Resistance	TBC1D22A	25771	37	22	47189600	47189600	Missense_Mutation	SNP	C	T	3	34	c.322C>T	c.(322-324)CGG>TGG	p.R108W
Pat_45	Post-Resistance	TBC1D22A	25771	37	22	47433095	47433095	Splice_Site	SNP	G	A	9	135	c.1329_splice	c.e11+1	p.Q443_splice
Pat_45	Post-Resistance	SELO	83642	37	22	50655449	50655449	Nonsense_Mutation	SNP	G	A	5	48	c.1737G>A	c.(1735-1737)TGG>TGA	p.W579*
Pat_45	Post-Resistance	TUBGCP6	85378	37	22	50664784	50664784	Missense_Mutation	SNP	C	T	4	36	c.1625G>A	c.(1624-1626)AGC>AAC	p.S542N
Pat_45	Post-Resistance	SBF1	6305	37	22	50900379	50900379	Missense_Mutation	SNP	G	A	10	138	c.2566C>T	c.(2566-2568)CCA>TCA	p.P856S
Pat_45	Post-Resistance	NCAPH2	29781	37	22	50961482	50961482	Missense_Mutation	SNP	G	A	3	36	c.1564G>A	c.(1564-1566)GAC>AAC	p.D522N
Pat_45	Post-Resistance	KLHDC7B	113730	37	22	50988037	50988037	Missense_Mutation	SNP	G	A	14	242	c.1442G>A	c.(1441-1443)AGC>AAC	p.S481N
Pat_45	Post-Resistance	MAPK8IP2	23542	37	22	51040276	51040276	Missense_Mutation	SNP	G	A	15	165	c.124G>A	c.(124-126)GAT>AAT	p.D42N
Pat_45	Post-Resistance	ARSA	410	37	22	51065175	51065175	Missense_Mutation	SNP	G	A	8	132	c.692C>T	c.(691-693)CCT>CTT	p.P231L
Pat_45	Post-Resistance	JAGN1	84522	37	3	9934877	9934877	Missense_Mutation	SNP	T	G	42	105	c.368T>G	c.(367-369)TTC>TGC	p.F123C

Pat_45	Post-Resistance	IL17RE	132014	37	3	9955689	9955689	Missense_Mutation	SNP	G	A	25	144	c.1277G>A	c.(1276-1278)AGG>AAG	p.R426K
Pat_45	Post-Resistance	PRRT3	285368	37	3	9990456	9990456	Missense_Mutation	SNP	C	T	93	273	c.1157G>A	c.(1156-1158)GGG>GAG	p.G386E
Pat_45	Post-Resistance	SLC6A11	6538	37	3	10974933	10974933	Missense_Mutation	SNP	G	A	42	140	c.1468G>A	c.(1468-1470)GTG>ATG	p.V490M
Pat_45	Post-Resistance	NR2C2	7182	37	3	15071868	15071868	Missense_Mutation	SNP	G	A	21	131	c.1019G>A	c.(1018-1020)GGA>GAA	p.G340E
Pat_45	Post-Resistance	SATB1	6304	37	3	18390738	18390738	Missense_Mutation	SNP	G	A	17	119	c.2216C>T	c.(2215-2217)ACC>ATC	p.T739I
Pat_45	Post-Resistance	NR1D2	9975	37	3	24018876	24018876	Missense_Mutation	SNP	C	T	6	64	c.1706C>T	c.(1705-1707)TCT>TTT	p.S569F
Pat_45	Post-Resistance	ZNF860	344787	37	3	32030852	32030852	Missense_Mutation	SNP	G	A	6	67	c.281G>A	c.(280-282)AGT>AAT	p.S94N
Pat_45	Post-Resistance	CCR4	1233	37	3	32995173	32995173	Missense_Mutation	SNP	C	T	15	138	c.259C>T	c.(259-261)CTC>TTC	p.L87F
Pat_45	Post-Resistance	CCR4	1233	37	3	32995716	32995716	Missense_Mutation	SNP	G	A	5	29	c.802G>A	c.(802-804)GTG>ATG	p.V268M
Pat_45	Post-Resistance	SUSD5	26032	37	3	33194245	33194245	Missense_Mutation	SNP	C	T	8	82	c.1879G>A	c.(1879-1881)GAG>AAG	p.E627K
Pat_45	Post-Resistance	TRAK1	22906	37	3	42167035	42167035	Missense_Mutation	SNP	C	T	9	165	c.215C>T	c.(214-216)ACA>ATA	p.T72I
Pat_45	Post-Resistance	CCK	885	37	3	42304972	42304972	Missense_Mutation	SNP	C	T	10	84	c.151G>A	c.(151-153)GAT>AAT	p.D51N
Pat_45	Post-Resistance	PRSS42	339906	37	3	46875079	46875080	Missense_Mutation	DNP	CC	TT	4	15	c.301_302GG>AA	c.(301-303)GGC>AAC	p.G101N
Pat_45	Post-Resistance	PTPN23	25930	37	3	47449932	47449932	Missense_Mutation	SNP	C	T	6	140	c.1282C>T	c.(1282-1284)CTC>TTC	p.L428F
Pat_45	Post-Resistance	ATRIP	84126	37	3	48506294	48506294	Missense_Mutation	SNP	C	T	6	92	c.2120C>T	c.(2119-2121)CCC>CTC	p.P707L
Pat_45	Post-Resistance	GPX1	2876	37	3	49395482	49395482	Missense_Mutation	SNP	G	C	8	52	c.230C>G	c.(229-231)CCG>CGG	p.P77R
Pat_45	Post-Resistance	MST1R	4486	37	3	49940688	49940688	Missense_Mutation	SNP	C	T	18	201	c.355G>A	c.(355-357)GAC>AAC	p.D119N
Pat_45	Post-Resistance	RBM6	10180	37	3	50091825	50091825	Missense_Mutation	SNP	G	A	50	280	c.1690G>A	c.(1690-1692)GAA>AAA	p.E564K
Pat_45	Post-Resistance	ZMYND10	51364	37	3	50380390	50380390	Missense_Mutation	SNP	A	C	17	69	c.659T>G	c.(658-660)GTG>GGG	p.V220G
Pat_45	Post-Resistance	VPRBP	9730	37	3	51457233	51457233	Missense_Mutation	SNP	C	T	6	130	c.3191G>A	c.(3190-3192)GGA>GAA	p.G1064E
Pat_45	Post-Resistance	RRP9	9136	37	3	51975498	51975498	Missense_Mutation	SNP	C	T	14	172	c.97G>A	c.(97-99)GCG>ACG	p.A33T
Pat_45	Post-Resistance	GLYCTK	132158	37	3	52327063	52327063	Missense_Mutation	SNP	G	A	4	69	c.1493G>A	c.(1492-1494)GGT>GAT	p.G498D
Pat_45	Post-Resistance	ITIH4	3700	37	3	52852164	52852164	Missense_Mutation	SNP	C	T	3	31	c.2200G>A	c.(2200-2202)GCC>ACC	p.A734T
Pat_45	Post-Resistance	ITIH4	3700	37	3	52858272	52858272	Missense_Mutation	SNP	C	T	25	147	c.1105G>A	c.(1105-1107)GAG>AAG	p.E369K
Pat_45	Post-Resistance	PDE12	201626	37	3	57542926	57542926	Missense_Mutation	SNP	C	T	13	180	c.820C>T	c.(820-822)CCT>TCT	p.P274S
Pat_45	Post-Resistance	PRICKLE2	166336	37	3	64085592	64085592	Missense_Mutation	SNP	G	A	14	94	c.1670C>T	c.(1669-1671)GCT>GTT	p.A557V
Pat_45	Post-Resistance	SHQ1	55164	37	3	72799667	72799667	Missense_Mutation	SNP	G	A	26	140	c.1502C>T	c.(1501-1503)GCC>GTC	p.A501V
Pat_45	Post-Resistance	CRYBG3	131544	37	3	97605517	97605517	Missense_Mutation	SNP	C	T	7	159	c.1351C>T	c.(1351-1353)CCA>TCA	p.P451S
Pat_45	Post-Resistance	CRYBG3	131544	37	3	97618108	97618108	Splice_Site	SNP	G	A	13	93	c.2127_splice	c.e11+1	p.L709_splice
Pat_45	Post-Resistance	ABI3BP	25890	37	3	100583726	100583726	Missense_Mutation	SNP	G	C	3	26	c.1035C>G	c.(1033-1035)AGC>AGG	p.S345R
Pat_45	Post-Resistance	ZBTB20	26137	37	3	114070071	114070071	Missense_Mutation	SNP	G	A	5	50	c.854C>T	c.(853-855)CCC>CTC	p.P285L
Pat_45	Post-Resistance	UPK1B	7348	37	3	118906641	118906641	Missense_Mutation	SNP	C	T	7	246	c.89C>T	c.(88-90)ACT>ATT	p.T30I
Pat_45	Post-Resistance	COL6A6	131873	37	3	130286992	130286992	Missense_Mutation	SNP	G	A	15	145	c.1945G>A	c.(1945-1947)GTG>ATG	p.V649M
Pat_45	Post-Resistance	PIK3CB	5291	37	3	138376531	138376531	Splice_Site	SNP	C	T	5	153	c.2942_splice	c.e20+1	p.R981_splice
Pat_45	Post-Resistance	HPS3	84343	37	3	148858052	148858052	Missense_Mutation	SNP	G	A	6	148	c.479G>A	c.(478-480)AGT>AAT	p.S160N
Pat_45	Post-Resistance	TSC22D2	9819	37	3	150128888	150128888	Missense_Mutation	SNP	C	T	8	252	c.1751C>T	c.(1750-1752)ACC>ATC	p.T584I
Pat_45	Post-Resistance	IFT80	57560	37	3	160083830	160083830	Splice_Site	SNP	C	T	7	97	c.549_splice	c.e6+1	p.Q183_splice
Pat_45	Post-Resistance	FNDC3B	64778	37	3	172013211	172013211	Missense_Mutation	SNP	C	T	15	187	c.908C>T	c.(907-909)TCC>TTC	p.S303F
Pat_45	Post-Resistance	FNDC3B	64778	37	3	172096107	172096107	Missense_Mutation	SNP	G	A	17	91	c.3056G>A	c.(3055-3057)AGA>AAA	p.R1019K
Pat_45	Post-Resistance	MFN1	55669	37	3	179093027	179093027	Missense_Mutation	SNP	C	T	4	32	c.995C>T	c.(994-996)GCA>GTA	p.A332V
Pat_45	Post-Resistance	CCDC39	339829	37	3	180397136	180397136	Nonsense_Mutation	SNP	C	T	48	322	c.33G>A	c.(31-33)TGG>TGA	p.W11*
Pat_45	Post-Resistance	DVL3	1857	37	3	183888163	183888163	Missense_Mutation	SNP	C	T	4	36	c.1771C>T	c.(1771-1773)CCG>TCG	p.P591S
Pat_45	Post-Resistance	CHRD	8646	37	3	184101121	184101121	Missense_Mutation	SNP	G	A	15	138	c.1235G>A	c.(1234-1236)GGG>GAG	p.G412E
Pat_45	Post-Resistance	MAP3K13	9175	37	3	185146547	185146547	Missense_Mutation	SNP	G	A	3	69	c.178G>A	c.(178-180)GTG>ATG	p.V60M
Pat_45	Post-Resistance	OPA1	4976	37	3	193372664	193372664	Nonsense_Mutation	SNP	C	T	5	38	c.1861C>T	c.(1861-1863)CAA>TAA	p.Q621*
Pat_45	Post-Resistance	CPN2	1370	37	3	194062028	194062028	Nonsense_Mutation	SNP	C	T	31	306	c.1404G>A	c.(1402-1404)TGG>TGA	p.W468*
Pat_45	Post-Resistance	GP5	2814	37	3	194118791	194118791	Missense_Mutation	SNP	G	A	40	115	c.221C>T	c.(220-222)ACC>ATC	p.T74I

Pat_45	Post-Resistance	ATP13A3	79572	37	3	194167679	194167679	Missense_Mutation	SNP	G	A	18	174	c.1474C>T	c.(1474-1476)CTC>TTC	p.L492F
Pat_45	Post-Resistance	MUC4	4585	37	3	195510155	195510155	Missense_Mutation	SNP	C	T	4	4	c.7912G>A	c.(7912-7914)GCC>ACC	p.A2638T
Pat_45	Post-Resistance	MUC4	4585	37	3	195510158	195510158	Missense_Mutation	SNP	G	C	4	4	c.7909C>G	c.(7909-7911)CAC>GAC	p.H2637D
Pat_45	Post-Resistance	MUC4	4585	37	3	195512606	195512606	Missense_Mutation	SNP	G	C	2	7	c.5845C>G	c.(5845-5847)CAC>GAC	p.H1949D
Pat_45	Post-Resistance	MUC4	4585	37	3	195513758	195513758	Missense_Mutation	SNP	G	C	2	1	c.4693C>G	c.(4693-4695)CAC>GAC	p.H1565D
Pat_45	Post-Resistance	PCYT1A	5130	37	3	195965671	195965671	Missense_Mutation	SNP	G	A	7	25	c.992C>T	c.(991-993)TCC>TTC	p.S331F
Pat_45	Post-Resistance	CRIPAK	285464	37	4	1389416	1389416	Missense_Mutation	SNP	C	T	58	623	c.1117C>T	c.(1117-1119)CCG>TCG	p.P373S
Pat_45	Post-Resistance	FGFR3	2261	37	4	1805525	1805525	Missense_Mutation	SNP	G	A	13	111	c.1037G>A	c.(1036-1038)GGG>GAG	p.G346E
Pat_45	Post-Resistance	POLN	353497	37	4	2158580	2158580	Missense_Mutation	SNP	C	T	13	65	c.1666G>A	c.(1666-1668)GGC>AGC	p.G556S
Pat_45	Post-Resistance	MAN2B2	23324	37	4	6622960	6622960	Missense_Mutation	SNP	C	T	7	165	c.2978C>T	c.(2977-2979)ACC>ATC	p.T993I
Pat_45	Post-Resistance	TAPT1	202018	37	4	16215429	16215429	Missense_Mutation	SNP	C	T	4	31	c.292G>A	c.(292-294)GTA>ATA	p.V98I
Pat_45	Post-Resistance	GPR125	166647	37	4	22463390	22463390	Missense_Mutation	SNP	G	A	9	112	c.371C>T	c.(370-372)GCC>GTC	p.A124V
Pat_45	Post-Resistance	PPARGC1A	10891	37	4	23815650	23815650	Missense_Mutation	SNP	C	T	15	213	c.1456G>A	c.(1456-1458)GAC>AAC	p.D486N
Pat_45	Post-Resistance	ANAPC4	29945	37	4	25391808	25391808	Missense_Mutation	SNP	C	T	4	66	c.566C>T	c.(565-567)GCT>GTT	p.A189V
Pat_45	Post-Resistance	TLR1	7096	37	4	38798346	38798346	Nonsense_Mutation	SNP	G	A	91	292	c.2107C>T	c.(2107-2109)CAG>TAG	p.Q703*
Pat_45	Post-Resistance	KLB	152831	37	4	39448261	39448261	Missense_Mutation	SNP	G	A	18	221	c.1915G>A	c.(1915-1917)GTC>ATC	p.V639I
Pat_45	Post-Resistance	SCFD2	152579	37	4	54231780	54231780	Missense_Mutation	SNP	G	A	3	58	c.329C>T	c.(328-330)GCT>GTT	p.A110V
Pat_45	Post-Resistance	REST	5978	37	4	57777025	57777025	Missense_Mutation	SNP	C	T	9	95	c.221C>T	c.(220-222)GCA>GTA	p.A74V
Pat_45	Post-Resistance	EPHA5	2044	37	4	66509128	66509128	Missense_Mutation	SNP	G	A	4	54	c.199C>T	c.(199-201)CGC>TGC	p.R67C
Pat_45	Post-Resistance	ALB	213	37	4	74280829	74280829	Missense_Mutation	SNP	C	T	10	118	c.1136C>T	c.(1135-1137)ACC>ATC	p.T379I
Pat_45	Post-Resistance	BMP2K	55589	37	4	79792088	79792088	Missense_Mutation	SNP	G	C	3	41	c.1383G>C	c.(1381-1383)CAG>CAC	p.Q461H
Pat_45	Post-Resistance	CDS1	1040	37	4	85566381	85566381	Missense_Mutation	SNP	G	T	4	54	c.1159G>T	c.(1159-1161)GCA>TCA	p.A387S
Pat_45	Post-Resistance	DDIT4L	115265	37	4	101108841	101108841	Missense_Mutation	SNP	C	T	5	24	c.575G>A	c.(574-576)GGG>GAG	p.G192E
Pat_45	Post-Resistance	CENPE	1062	37	4	104059588	104059588	Missense_Mutation	SNP	C	T	9	161	c.6223G>A	c.(6223-6225)GTA>ATA	p.V2075I
Pat_45	Post-Resistance	OSTC	58505	37	4	109571893	109571893	Missense_Mutation	SNP	C	T	10	97	c.82C>T	c.(82-84)CCG>TCG	p.P28S
Pat_45	Post-Resistance	PCDH18	54510	37	4	138442490	138442490	Missense_Mutation	SNP	G	A	7	79	c.3101C>T	c.(3100-3102)TCC>TTC	p.S1034F
Pat_45	Post-Resistance	ZNF827	152485	37	4	146813483	146813483	Missense_Mutation	SNP	A	G	3	56	c.1178T>C	c.(1177-1179)ATG>ACG	p.M393T
Pat_45	Post-Resistance	GLRB	2743	37	4	158091830	158091830	Missense_Mutation	SNP	C	T	6	62	c.1444C>T	c.(1444-1446)CCT>TCT	p.P482S
Pat_45	Post-Resistance	NPY5R	4889	37	4	164272176	164272176	Missense_Mutation	SNP	G	A	4	56	c.751G>A	c.(751-753)GAA>AAA	p.E251K
Pat_45	Post-Resistance	WDR17	116966	37	4	177056421	177056421	Missense_Mutation	SNP	G	A	3	48	c.1333G>A	c.(1333-1335)GCT>ACT	p.A445T
Pat_45	Post-Resistance	ACSL1	2180	37	4	185689574	185689574	Missense_Mutation	SNP	C	T	17	186	c.1024G>A	c.(1024-1026)GGA>AGA	p.G342R
Pat_45	Post-Resistance	TERT	7015	37	5	1254567	1254567	Nonsense_Mutation	SNP	G	A	4	58	c.3211C>T	c.(3211-3213)CAG>TAG	p.Q1071*
Pat_45	Post-Resistance	KIAA0947	23379	37	5	5461116	5461116	Missense_Mutation	SNP	G	A	19	170	c.1669G>A	c.(1669-1671)GGA>AGA	p.G557R
Pat_45	Post-Resistance	FASTKD3	79072	37	5	7867464	7867464	Missense_Mutation	SNP	C	T	6	104	c.733G>A	c.(733-735)GGT>AGT	p.G245S
Pat_45	Post-Resistance	SLC45A2	51151	37	5	33963920	33963920	Missense_Mutation	SNP	G	A	7	91	c.764C>T	c.(763-765)CCT>CTT	p.P255L
Pat_45	Post-Resistance	DAB2	1601	37	5	39376959	39376959	Missense_Mutation	SNP	C	T	6	43	c.1930G>A	c.(1930-1932)GGG>AGG	p.G644R
Pat_45	Post-Resistance	C6	729	37	5	41159253	41159253	Missense_Mutation	SNP	C	T	21	162	c.1787G>A	c.(1786-1788)CGA>CAA	p.R596Q
Pat_45	Post-Resistance	PAIP1	10605	37	5	43547961	43547961	Missense_Mutation	SNP	C	T	7	53	c.490G>A	c.(490-492)GAT>AAT	p.D164N
Pat_45	Post-Resistance	SNX18	112574	37	5	53815262	53815262	Missense_Mutation	SNP	G	A	3	37	c.1480G>A	c.(1480-1482)GCC>ACC	p.A494T
Pat_45	Post-Resistance	MRPS27	23107	37	5	71519541	71519541	Missense_Mutation	SNP	G	A	15	174	c.974C>T	c.(973-975)TCC>TTC	p.S325F
Pat_45	Post-Resistance	CMYA5	202333	37	5	79034609	79034609	Missense_Mutation	SNP	C	T	7	61	c.10021C>T	c.(10021-10023)CCA>TCA	p.P3341S
Pat_45	Post-Resistance	VCAN	1462	37	5	82815315	82815315	Missense_Mutation	SNP	C	T	21	176	c.1190C>T	c.(1189-1191)CCC>CTC	p.P397L
Pat_45	Post-Resistance	EDIL3	10085	37	5	83402649	83402649	Splice_Site	SNP	C	T	10	50	c.470_splice	c.e6-1	p.K157_splice
Pat_45	Post-Resistance	POLR3G	10622	37	5	89781490	89781490	Missense_Mutation	SNP	C	T	8	82	c.106C>T	c.(106-108)CCA>TCA	p.P36S
Pat_45	Post-Resistance	CHD1	1105	37	5	98232902	98232902	Nonsense_Mutation	SNP	C	T	6	66	c.1488G>A	c.(1486-1488)TGG>TGA	p.W496*
Pat_45	Post-Resistance	TMED7-TICAM2	100302736	37	5	114916719	114916719	Missense_Mutation	SNP	G	A	14	281	c.235C>T	c.(235-237)CTC>TTC	p.L79F
Pat_45	Post-Resistance	DMXL1	1657	37	5	118556765	118556765	Missense_Mutation	SNP	G	A	4	6	c.8203G>A	c.(8203-8205)GGA>AGA	p.G2735R

Pat_45	Post-Resistance	ZNF608	57507	37	5	124079830	124079830	Missense_Mutation	SNP	C	T	13	207	c.853G>A	c.(853-855)GAA>AAA	p.E285K
Pat_45	Post-Resistance	RAPGEF6	51735	37	5	130840357	130840357	Missense_Mutation	SNP	C	T	7	195	c.1216G>A	c.(1216-1218)GAC>AAC	p.D406N
Pat_45	Post-Resistance	SHROOM1	134549	37	5	132160884	132160884	Missense_Mutation	SNP	C	T	3	34	c.949G>A	c.(949-951)GGA>AGA	p.G317R
Pat_45	Post-Resistance	PHF15	23338	37	5	133895593	133895593	Missense_Mutation	SNP	C	T	10	32	c.385C>T	c.(385-387)CCT>TCT	p.P129S
Pat_45	Post-Resistance	SEC24A	10802	37	5	134022544	134022544	Missense_Mutation	SNP	C	T	11	129	c.1556C>T	c.(1555-1557)ACT>ATT	p.T519I
Pat_45	Post-Resistance	BRD8	10902	37	5	137503704	137503704	Missense_Mutation	SNP	C	T	11	173	c.706G>A	c.(706-708)GTA>ATA	p.V236I
Pat_45	Post-Resistance	APBB3	10307	37	5	139943395	139943395	Missense_Mutation	SNP	C	T	5	65	c.155G>A	c.(154-156)GGT>GAT	p.G52D
Pat_45	Post-Resistance	HARS	3035	37	5	140062774	140062774	Missense_Mutation	SNP	C	T	14	113	c.211G>A	c.(211-213)GCA>ACA	p.A71T
Pat_45	Post-Resistance	PCDHGA1	56114	37	5	140712640	140712640	Missense_Mutation	SNP	T	A	31	73	c.2389T>A	c.(2389-2391)TTA>ATA	p.L797I
Pat_45	Post-Resistance	PCDHGA10	56106	37	5	140794780	140794780	Missense_Mutation	SNP	G	A	7	194	c.2038G>A	c.(2038-2040)GGC>AGC	p.G680S
Pat_45	Post-Resistance	PCDH1	5097	37	5	141242829	141242829	Missense_Mutation	SNP	G	A	29	114	c.3067C>T	c.(3067-3069)CGC>TGC	p.R1023C
Pat_45	Post-Resistance	LARS	51520	37	5	145543896	145543896	Missense_Mutation	SNP	C	T	9	96	c.571G>A	c.(571-573)GAT>AAT	p.D191N
Pat_45	Post-Resistance	TCERG1	10915	37	5	145849230	145849230	Missense_Mutation	SNP	C	T	12	117	c.1322C>T	c.(1321-1323)GCA>GTA	p.A441V
Pat_45	Post-Resistance	DPYSL3	1809	37	5	146781115	146781115	Missense_Mutation	SNP	G	A	8	33	c.956C>T	c.(955-957)TCC>TTC	p.S319F
Pat_45	Post-Resistance	AFAP1L1	134265	37	5	148689631	148689631	Missense_Mutation	SNP	C	T	6	87	c.860C>T	c.(859-861)ACC>ATC	p.T287I
Pat_45	Post-Resistance	GRPEL2	134266	37	5	148727920	148727920	Missense_Mutation	SNP	C	T	10	131	c.163C>T	c.(163-165)CCC>TCC	p.P55S
Pat_45	Post-Resistance	PDGFRB	5159	37	5	149509499	149509499	Missense_Mutation	SNP	C	T	15	211	c.1400G>A	c.(1399-1401)GGG>GAG	p.G467E
Pat_45	Post-Resistance	GRIA1	2890	37	5	153085424	153085424	Nonsense_Mutation	SNP	G	A	19	167	c.1620G>A	c.(1618-1620)TGG>TGA	p.W540*
Pat_45	Post-Resistance	LARP1	23367	37	5	154181715	154181715	Missense_Mutation	SNP	C	T	6	149	c.1865C>T	c.(1864-1866)ACC>ATC	p.T622I
Pat_45	Post-Resistance	ADAM19	8728	37	5	156929917	156929917	Missense_Mutation	SNP	C	T	14	158	c.1202G>A	c.(1201-1203)GGA>GAA	p.G401E
Pat_45	Post-Resistance	ODZ2	57451	37	5	167420127	167420127	Missense_Mutation	SNP	G	T	5	76	c.1126G>T	c.(1126-1128)GCT>TCT	p.A376S
Pat_45	Post-Resistance	DOCK2	1794	37	5	169116299	169116299	Missense_Mutation	SNP	G	A	21	102	c.805G>A	c.(805-807)GAG>AAG	p.E269K
Pat_45	Post-Resistance	NKX2-5	1482	37	5	172659607	172659607	Missense_Mutation	SNP	C	T	5	106	c.940G>A	c.(940-942)GGA>AGA	p.G314R
Pat_45	Post-Resistance	NOP16	51491	37	5	175811276	175811276	Missense_Mutation	SNP	C	T	6	51	c.493G>A	c.(493-495)GAC>AAC	p.D165N
Pat_45	Post-Resistance	HK3	3101	37	5	176318460	176318460	Missense_Mutation	SNP	C	T	4	85	c.188G>A	c.(187-189)AGG>AAG	p.R63K
Pat_45	Post-Resistance	N4BP3	23138	37	5	177547296	177547296	Missense_Mutation	SNP	C	T	4	22	c.448C>T	c.(448-450)CAC>TAC	p.H150Y
Pat_45	Post-Resistance	ZNF454	285676	37	5	178392343	178392343	Missense_Mutation	SNP	C	T	9	42	c.938C>T	c.(937-939)GCA>GTA	p.A313V
Pat_45	Post-Resistance	ADAMTS2	9509	37	5	178541068	178541068	Missense_Mutation	SNP	C	T	6	88	c.3436G>A	c.(3436-3438)GCC>ACC	p.A1146T
Pat_45	Post-Resistance	MAPK9	5601	37	5	179676072	179676072	Missense_Mutation	SNP	C	T	12	118	c.517G>A	c.(517-519)GCC>ACC	p.A173T
Pat_45	Post-Resistance	GFPT2	9945	37	5	179729496	179729496	Missense_Mutation	SNP	C	T	11	85	c.1931G>A	c.(1930-1932)TGC>TAC	p.C644Y
Pat_45	Post-Resistance	WRNIP1	56897	37	6	2779496	2779496	Splice_Site	SNP	G	A	9	103	c.1257_splice	c.e4-1	p.E419_splice
Pat_45	Post-Resistance	DSP	1832	37	6	7581491	7581491	Missense_Mutation	SNP	G	A	15	40	c.5068G>A	c.(5068-5070)GAA>AAA	p.E1690K
Pat_45	Post-Resistance	SLC35B3	51000	37	6	8415190	8415190	Missense_Mutation	SNP	T	C	5	63	c.1006A>G	c.(1006-1008)ATG>GTG	p.M336V
Pat_45	Post-Resistance	PHACTR1	221692	37	6	13230391	13230391	Missense_Mutation	SNP	G	A	6	30	c.1357G>A	c.(1357-1359)GAG>AAG	p.E453K
Pat_45	Post-Resistance	NOL7	51406	37	6	13618326	13618326	Missense_Mutation	SNP	G	A	3	49	c.455G>A	c.(454-456)GGA>GAA	p.G152E
Pat_45	Post-Resistance	NUP153	9972	37	6	17665474	17665474	Missense_Mutation	SNP	C	T	3	48	c.1211G>A	c.(1210-1212)TGC>TAC	p.C404Y
Pat_45	Post-Resistance	KIF13A	63971	37	6	17764861	17764861	Missense_Mutation	SNP	G	A	3	69	c.4898C>T	c.(4897-4899)ACC>ATC	p.T1633I
Pat_45	Post-Resistance	KIF13A	63971	37	6	17796918	17796918	Missense_Mutation	SNP	G	A	68	313	c.2924C>T	c.(2923-2925)ACA>ATA	p.T975I
Pat_45	Post-Resistance	MBOAT1	154141	37	6	20144547	20144547	Splice_Site	SNP	C	T	4	37	c.324_splice	c.e4-1	p.R108_splice
Pat_45	Post-Resistance	HIST1H3H	8357	37	6	27777876	27777876	Missense_Mutation	SNP	C	T	24	150	c.25C>T	c.(25-27)CGC>TGC	p.R9C
Pat_45	Post-Resistance	SCAND3	114821	37	6	28541481	28541481	Missense_Mutation	SNP	C	T	11	28	c.2185G>A	c.(2185-2187)GTT>ATT	p.V729I
Pat_45	Post-Resistance	OR12D2	26529	37	6	29365320	29365320	Missense_Mutation	SNP	C	T	16	182	c.844C>T	c.(844-846)CCT>TCT	p.P282S
Pat_45	Post-Resistance	OR2H1	26716	37	6	29429587	29429587	Missense_Mutation	SNP	G	A	11	202	c.41G>A	c.(40-42)GGC>GAC	p.G14D
Pat_45	Post-Resistance	ZFP57	346171	37	6	29641408	29641408	Missense_Mutation	SNP	C	T	4	83	c.480G>A	c.(478-480)ATG>ATA	p.M160I
Pat_45	Post-Resistance	RNF39	80352	37	6	30039054	30039054	Missense_Mutation	SNP	C	T	4	34	c.1097G>A	c.(1096-1098)CGC>CAC	p.R366H
Pat_45	Post-Resistance	MDC1	9656	37	6	30673605	30673605	Missense_Mutation	SNP	G	A	15	169	c.3355C>T	c.(3355-3357)CCA>TCA	p.P1119S
Pat_45	Post-Resistance	DPCR1	135656	37	6	30919836	30919837	Missense_Mutation	DNP	GG	AA	25	161	.3595_3596GG>A	c.(3595-3597)GGG>AAG	p.G1199K

Pat_45	Post-Resistance	C6orf47	57827	37	6	31627519	31627519	Missense_Mutation	SNP	G	A	8	72	c.206C>T	c.(205-207)GCT>GTT	p.A69V
Pat_45	Post-Resistance	SKIV2L	6499	37	6	31927814	31927814	Missense_Mutation	SNP	C	T	5	140	c.154C>T	c.(154-156)CCA>TCA	p.P52S
Pat_45	Post-Resistance	EGFL8	80864	37	6	32134274	32134274	Splice_Site	SNP	G	A	13	139	c.102_splice	c.e3-1	p.S34_splice
Pat_45	Post-Resistance	EGFL8	80864	37	6	32135002	32135002	Missense_Mutation	SNP	C	T	9	18	c.569C>T	c.(568-570)CCC>CTC	p.P190L
Pat_45	Post-Resistance	COL11A2	1302	37	6	33131507	33131507	Missense_Mutation	SNP	G	A	3	81	c.5159C>T	c.(5158-5160)GCC>GTC	p.A1720V
Pat_45	Post-Resistance	ITPR3	3710	37	6	33653432	33653432	Missense_Mutation	SNP	C	T	12	70	c.5495C>T	c.(5494-5496)TCC>TTC	p.S1832F
Pat_45	Post-Resistance	SNRPC	6631	37	6	34741322	34741322	Missense_Mutation	SNP	C	T	18	122	c.455C>T	c.(454-456)CCC>CTC	p.P152L
Pat_45	Post-Resistance	MAPK14	1432	37	6	36076195	36076195	Missense_Mutation	SNP	C	T	6	87	c.1054C>T	c.(1054-1056)CCC>TCC	p.P352S
Pat_45	Post-Resistance	C6orf129	154467	37	6	37450997	37450997	Missense_Mutation	SNP	G	A	7	92	c.259C>T	c.(259-261)CTC>TTC	p.L87F
Pat_45	Post-Resistance	FOXP4	116113	37	6	41562730	41562730	Splice_Site	SNP	G	A	6	101	c.1658_splice	c.e14+1	p.G553_splice
Pat_45	Post-Resistance	FRS3	10817	37	6	41740697	41740697	Missense_Mutation	SNP	C	T	6	56	c.254G>A	c.(253-255)GGA>GAA	p.G85E
Pat_45	Post-Resistance	KIAA0240	23506	37	6	42832724	42832724	Missense_Mutation	SNP	C	T	11	41	c.2780C>T	c.(2779-2781)CCT>CTT	p.P927L
Pat_45	Post-Resistance	MEA1	4201	37	6	42980663	42980663	Splice_Site	SNP	C	T	10	119	c.406_splice	c.e3+1	p.E136_splice
Pat_45	Post-Resistance	SLC22A7	10864	37	6	43270099	43270099	Missense_Mutation	SNP	G	A	3	36	c.1223G>A	c.(1222-1224)GGG>GAG	p.G408E
Pat_45	Post-Resistance	POLH	5429	37	6	43581870	43581870	Missense_Mutation	SNP	G	A	27	169	c.1718G>A	c.(1717-1719)GGG>GAG	p.G573E
Pat_45	Post-Resistance	SLC29A1	2030	37	6	44197670	44197670	Missense_Mutation	SNP	G	A	10	88	c.341G>A	c.(340-342)GGC>GAC	p.G114D
Pat_45	Post-Resistance	SUPT3H	8464	37	6	44921114	44921114	Missense_Mutation	SNP	G	A	4	60	c.767C>T	c.(766-768)ACC>ATC	p.T256I
Pat_45	Post-Resistance	DEFB114	245928	37	6	49928058	49928058	Missense_Mutation	SNP	G	A	9	54	c.157C>T	c.(157-159)CCA>TCA	p.P53S
Pat_45	Post-Resistance	PKHD1	5314	37	6	51887733	51887733	Missense_Mutation	SNP	C	T	10	79	c.5246G>A	c.(5245-5247)GGT>GAT	p.G1749D
Pat_45	Post-Resistance	PKHD1	5314	37	6	51915024	51915024	Missense_Mutation	SNP	G	A	29	113	c.2210C>T	c.(2209-2211)TCC>TTC	p.S737F
Pat_45	Post-Resistance	BMP5	653	37	6	55739516	55739516	Missense_Mutation	SNP	C	T	10	135	c.148G>A	c.(148-150)GAA>AAA	p.E50K
Pat_45	Post-Resistance	RAB23	51715	37	6	57061387	57061387	Missense_Mutation	SNP	G	A	9	26	c.259C>T	c.(259-261)CTC>TTC	p.L87F
Pat_45	Post-Resistance	B3GAT2	135152	37	6	71665784	71665784	Missense_Mutation	SNP	C	G	4	37	c.349G>C	c.(349-351)GAG>CAG	p.E117Q
Pat_45	Post-Resistance	DDX43	55510	37	6	74104827	74104827	Missense_Mutation	SNP	G	A	9	22	c.199G>A	c.(199-201)GAA>AAA	p.E67K
Pat_45	Post-Resistance	MYO6	4646	37	6	76576283	76576283	Missense_Mutation	SNP	G	A	8	97	c.1715G>A	c.(1714-1716)AGA>AAA	p.R572K
Pat_45	Post-Resistance	TBX18	9096	37	6	85470015	85470015	Missense_Mutation	SNP	T	C	6	36	c.557A>G	c.(556-558)TAC>TGC	p.Y186C
Pat_45	Post-Resistance	SLC35A1	10559	37	6	88218174	88218174	Missense_Mutation	SNP	C	T	4	60	c.611C>T	c.(610-612)ACT>ATT	p.T204I
Pat_45	Post-Resistance	MDN1	23195	37	6	90402676	90402676	Missense_Mutation	SNP	C	T	4	34	c.10073G>A	.(10072-10074)GGG>GA	p.G3358E
Pat_45	Post-Resistance	MDN1	23195	37	6	90442434	90442434	Missense_Mutation	SNP	C	T	11	219	c.4784G>A	c.(4783-4785)GGC>GAC	p.G1595D
Pat_45	Post-Resistance	CASP8AP2	9994	37	6	90572776	90572776	Missense_Mutation	SNP	G	A	9	127	c.1348G>A	c.(1348-1350)GAA>AAA	p.E450K
Pat_45	Post-Resistance	EPHA7	2045	37	6	94120359	94120359	Missense_Mutation	SNP	C	T	4	93	c.692G>A	c.(691-693)CGA>CAA	p.R231Q
Pat_45	Post-Resistance	FUT9	10690	37	6	96651776	96651776	Missense_Mutation	SNP	C	T	5	9	c.745C>T	c.(745-747)CAC>TAC	p.H249Y
Pat_45	Post-Resistance	MCHR2	84539	37	6	100368874	100368874	Missense_Mutation	SNP	C	T	9	139	c.965G>A	c.(964-966)AGA>AAA	p.R322K
Pat_45	Post-Resistance	ZUFSP	221302	37	6	116973256	116973256	Missense_Mutation	SNP	C	T	12	183	c.1061G>A	c.(1060-1062)GGC>GAC	p.G354D
Pat_45	Post-Resistance	RFX6	222546	37	6	117198650	117198650	Missense_Mutation	SNP	C	G	2	8	c.212C>G	c.(211-213)GCA>GGA	p.A71G
Pat_45	Post-Resistance	ROS1	6098	37	6	117687247	117687247	Missense_Mutation	SNP	G	A	12	173	c.2804C>T	c.(2803-2805)CCC>CTC	p.P935L
Pat_45	Post-Resistance	PTPRK	5796	37	6	128388705	128388705	Missense_Mutation	SNP	C	T	4	64	c.2116G>A	c.(2116-2118)GGA>AGA	p.G706R
Pat_45	Post-Resistance	PTPRK	5796	37	6	128643216	128643216	Missense_Mutation	SNP	C	T	4	80	c.463G>A	c.(463-465)GCA>ACA	p.A155T
Pat_45	Post-Resistance	LAMA2	3908	37	6	129748927	129748927	Missense_Mutation	SNP	G	A	14	151	c.5896G>A	c.(5896-5898)GAT>AAT	p.D1966N
Pat_45	Post-Resistance	TMEM200A	114801	37	6	130762616	130762616	Missense_Mutation	SNP	C	T	6	86	c.1049C>T	c.(1048-1050)TCC>TTC	p.S350F
Pat_45	Post-Resistance	EPB41L2	2037	37	6	131216109	131216109	Missense_Mutation	SNP	C	T	9	114	c.1387G>A	c.(1387-1389)GAG>AAG	p.E463K
Pat_45	Post-Resistance	MOXD1	26002	37	6	132645128	132645128	Missense_Mutation	SNP	G	C	9	109	c.1055C>G	c.(1054-1056)CCT>CGT	p.P352R
Pat_45	Post-Resistance	SGK1	6446	37	6	134491980	134491980	Missense_Mutation	SNP	G	A	11	129	c.1112C>T	c.(1111-1113)CCT>CTT	p.P371L
Pat_45	Post-Resistance	IFNGR1	3459	37	6	137527318	137527318	Missense_Mutation	SNP	C	T	8	220	c.328G>A	c.(328-330)GAA>AAA	p.E110K
Pat_45	Post-Resistance	TNFAIP3	7128	37	6	138196132	138196132	Missense_Mutation	SNP	C	T	20	253	c.446C>T	c.(445-447)TCT>TTT	p.S149F
Pat_45	Post-Resistance	HIVEP2	3097	37	6	143093718	143093718	Missense_Mutation	SNP	G	A	7	89	c.2158C>T	c.(2158-2160)CCT>TCT	p.P720S
Pat_45	Post-Resistance	HIVEP2	3097	37	6	143094717	143094717	Missense_Mutation	SNP	G	A	14	205	c.1159C>T	c.(1159-1161)CTT>TTT	p.L387F

Pat_45	Post-Resistance	UTRN	7402	37	6	144750798	144750798	Missense_Mutation	SNP	C	T	10	80	c.776C>T	c.(775-777)ACC>ATC	p.T259I
Pat_45	Post-Resistance	FBXO30	84085	37	6	146126061	146126061	Missense_Mutation	SNP	C	T	4	66	c.1481G>A	c.(1480-1482)AGT>AAT	p.S494N
Pat_45	Post-Resistance	FBXO30	84085	37	6	146126272	146126272	Missense_Mutation	SNP	C	T	20	220	c.1270G>A	c.(1270-1272)GAT>AAT	p.D424N
Pat_45	Post-Resistance	NUP43	348995	37	6	150048310	150048310	Missense_Mutation	SNP	G	A	4	22	c.938C>T	c.(937-939)TCT>TTT	p.S313F
Pat_45	Post-Resistance	SYNE1	23345	37	6	152657990	152657990	Missense_Mutation	SNP	C	T	10	158	c.12514G>A	c.(12514-12516)GTT>ATT	p.V4172I
Pat_45	Post-Resistance	SYNE1	23345	37	6	152674397	152674397	Splice_Site	SNP	C	T	17	302	c.11253_splice	c.e69+1	p.E3751_splice
Pat_45	Post-Resistance	SYNE1	23345	37	6	152697944	152697944	Missense_Mutation	SNP	C	T	5	90	c.9113G>A	c.(9112-9114)GGA>GAA	p.G3038E
Pat_45	Post-Resistance	SYNE1	23345	37	6	152706859	152706859	Missense_Mutation	SNP	C	T	27	167	c.8602G>A	c.(8602-8604)GAT>AAT	p.D2868N
Pat_45	Post-Resistance	SYNE1	23345	37	6	152749434	152749434	Missense_Mutation	SNP	C	T	22	226	c.4882G>A	c.(4882-4884)GAG>AAG	p.E1628K
Pat_45	Post-Resistance	TIAM2	26230	37	6	155450689	155450689	Nonsense_Mutation	SNP	C	A	4	56	c.332C>A	c.(331-333)TCA>TAA	p.S111*
Pat_45	Post-Resistance	TULP4	56995	37	6	158923406	158923406	Missense_Mutation	SNP	G	A	28	327	c.2711G>A	c.(2710-2712)CGC>CAC	p.R904H
Pat_45	Post-Resistance	RSPH3	83861	37	6	159414948	159414948	Missense_Mutation	SNP	G	A	3	18	c.553C>T	c.(553-555)CCT>TCT	p.P185S
Pat_45	Post-Resistance	WTAP	9589	37	6	160176300	160176300	Missense_Mutation	SNP	C	T	10	78	c.848C>T	c.(847-849)TCC>TTC	p.S283F
Pat_45	Post-Resistance	SLC22A3	6581	37	6	160769498	160769498	Missense_Mutation	SNP	G	A	6	64	c.47G>A	c.(46-48)CGC>CAC	p.R16H
Pat_45	Post-Resistance	PLG	5340	37	6	161127530	161127530	Missense_Mutation	SNP	A	C	9	176	c.141A>C	c.(139-141)GAA>GAC	p.E47D
Pat_45	Post-Resistance	MAP3K4	4216	37	6	161455329	161455329	Missense_Mutation	SNP	C	T	6	96	c.191C>T	c.(190-192)CCT>CTT	p.P64L
Pat_45	Post-Resistance	RNASET2	8635	37	6	167366005	167366005	Missense_Mutation	SNP	C	T	26	88	c.118G>A	c.(118-120)GTT>ATT	p.V40I
Pat_45	Post-Resistance	THBS2	7058	37	6	169637792	169637792	Missense_Mutation	SNP	C	T	15	211	c.1228G>A	c.(1228-1230)GTC>ATC	p.V410I
Pat_45	Post-Resistance	FAM120B	84498	37	6	170627298	170627298	Missense_Mutation	SNP	G	A	5	64	c.820G>A	c.(820-822)GTT>ATT	p.V274I
Pat_45	Post-Resistance	GPER	2852	37	7	1132472	1132472	Missense_Mutation	SNP	A	G	3	75	c.1108A>G	c.(1108-1110)AGG>GGG	p.R370G
Pat_45	Post-Resistance	MICALL2	79778	37	7	1481914	1481914	Missense_Mutation	SNP	G	A	20	93	c.1625C>T	c.(1624-1626)TCC>TTC	p.S542F
Pat_45	Post-Resistance	INTS1	26173	37	7	1542537	1542537	Missense_Mutation	SNP	C	T	41	243	c.349G>A	c.(349-351)GTG>ATG	p.V117M
Pat_45	Post-Resistance	C7orf27	221927	37	7	2578065	2578065	Missense_Mutation	SNP	C	T	8	157	c.2104G>A	c.(2104-2106)GAC>AAC	p.D702N
Pat_45	Post-Resistance	SDK1	221935	37	7	4089031	4089031	Missense_Mutation	SNP	C	T	21	185	c.2654C>T	c.(2653-2655)ACC>ATC	p.T885I
Pat_45	Post-Resistance	TNRC18	84629	37	7	5399064	5399064	Missense_Mutation	SNP	C	T	32	429	c.4798G>A	c.(4798-4800)GAT>AAT	p.D1600N
Pat_45	Post-Resistance	ACTB	60	37	7	5568970	5568970	Missense_Mutation	SNP	C	T	10	186	c.185G>A	c.(184-186)AGA>AAA	p.R62K
Pat_45	Post-Resistance	C7orf70	84792	37	7	6370608	6370608	Missense_Mutation	SNP	C	T	9	95	c.178G>A	c.(178-180)GCA>ACA	p.A60T
Pat_45	Post-Resistance	GLCCI1	113263	37	7	8009030	8009030	Missense_Mutation	SNP	C	T	3	10	c.49C>T	c.(49-51)CAT>TAT	p.H17Y
Pat_45	Post-Resistance	HDAC9	9734	37	7	18788643	18788643	Missense_Mutation	SNP	C	T	8	68	c.1916C>T	c.(1915-1917)CCC>CTC	p.P639L
Pat_45	Post-Resistance	MACC1	346389	37	7	20199746	20199746	Missense_Mutation	SNP	C	T	7	97	c.238G>A	c.(238-240)GAC>AAC	p.D80N
Pat_45	Post-Resistance	SP4	6671	37	7	21469306	21469306	Missense_Mutation	SNP	G	A	33	169	c.523G>A	c.(523-525)GAA>AAA	p.E175K
Pat_45	Post-Resistance	SP4	6671	37	7	21469960	21469960	Missense_Mutation	SNP	C	T	5	87	c.1177C>T	c.(1177-1179)CTT>TTT	p.L393F
Pat_45	Post-Resistance	DNAH11	8701	37	7	21934611	21934611	Missense_Mutation	SNP	C	T	5	75	c.13064C>T	c.(13063-13065)GCC>GTC	p.A4355V
Pat_45	Post-Resistance	NUPL2	11097	37	7	23240326	23240326	Missense_Mutation	SNP	C	T	4	74	c.1234C>T	c.(1234-1236)CCA>TCA	p.P412S
Pat_45	Post-Resistance	TRA2A	29896	37	7	23552565	23552565	Missense_Mutation	SNP	C	T	50	144	c.473G>A	c.(472-474)CGA>CAA	p.R158Q
Pat_45	Post-Resistance	OSBPL3	26031	37	7	24874119	24874119	Missense_Mutation	SNP	G	A	8	162	c.1732C>T	c.(1732-1734)CCC>TCC	p.P578S
Pat_45	Post-Resistance	HOXA3	3200	37	7	27148306	27148306	Missense_Mutation	SNP	C	T	5	71	c.560G>A	c.(559-561)GGG>GAG	p.G187E
Pat_45	Post-Resistance	CPVL	54504	37	7	29126138	29126138	Missense_Mutation	SNP	G	A	3	60	c.571C>T	c.(571-573)CCT>TCT	p.P191S
Pat_45	Post-Resistance	PDE1C	5137	37	7	31876811	31876811	Missense_Mutation	SNP	C	T	4	100	c.1186G>A	c.(1186-1188)GAG>AAG	p.E396K
Pat_45	Post-Resistance	DPY19L1	23333	37	7	34971314	34971314	Nonsense_Mutation	SNP	C	T	3	17	c.1899G>A	c.(1897-1899)TGG>TGA	p.W633*
Pat_45	Post-Resistance	KIAA0895	23366	37	7	36370620	36370620	Missense_Mutation	SNP	C	T	7	161	c.1375G>A	c.(1375-1377)GAC>AAC	p.D459N
Pat_45	Post-Resistance	ANLN	54443	37	7	36459802	36459802	Missense_Mutation	SNP	G	A	18	90	c.1894G>A	c.(1894-1896)GAA>AAA	p.E632K
Pat_45	Post-Resistance	TARP	445347	37	7	38305096	38305096	Missense_Mutation	SNP	G	A	15	131	c.611C>T	c.(610-612)ACC>ATC	p.T204I
Pat_45	Post-Resistance	TARP	445347	37	7	38305106	38305106	Missense_Mutation	SNP	C	G	15	136	c.601G>C	c.(601-603)GAG>CAG	p.E201Q
Pat_45	Post-Resistance	AMPH	273	37	7	38424515	38424515	Nonsense_Mutation	SNP	C	T	9	92	c.1992G>A	c.(1990-1992)TGG>TGA	p.W664*
Pat_45	Post-Resistance	MRPL32	64983	37	7	42974574	42974574	Missense_Mutation	SNP	G	A	7	142	c.151G>A	c.(151-153)GGC>AGC	p.G51S
Pat_45	Post-Resistance	HECW1	23072	37	7	43508660	43508660	Missense_Mutation	SNP	G	A	33	499	c.3055G>A	c.(3055-3057)GAA>AAA	p.E1019K

Pat_45	Post-Resistance	BLVRA	644	37	7	43843320	43843320	Missense_Mutation	SNP	G	A	24	379	c.506G>A	c.(505-507)GGC>GAC	p.G169D
Pat_45	Post-Resistance	YKT6	10652	37	7	44245993	44245993	Missense_Mutation	SNP	G	T	4	84	c.197G>T	c.(196-198)TGC>TTC	p.C66F
Pat_45	Post-Resistance	NPC1L1	29881	37	7	44575965	44575965	Missense_Mutation	SNP	C	T	11	101	c.1744G>A	c.(1744-1746)GGG>AGG	p.G582R
Pat_45	Post-Resistance	OGDH	4967	37	7	44713485	44713485	Nonsense_Mutation	SNP	C	T	9	192	c.733C>T	c.(733-735)CAG>TAG	p.Q245*
Pat_45	Post-Resistance	MYO1G	64005	37	7	45005743	45005743	Missense_Mutation	SNP	G	A	11	73	c.2086C>T	c.(2086-2088)CCC>TCC	p.P696S
Pat_45	Post-Resistance	MYO1G	64005	37	7	45005830	45005830	Missense_Mutation	SNP	C	T	3	26	c.1999G>A	c.(1999-2001)GAC>AAC	p.D667N
Pat_45	Post-Resistance	CCM2	83605	37	7	45078002	45078002	Missense_Mutation	SNP	G	A	22	252	c.181G>A	c.(181-183)GAC>AAC	p.D61N
Pat_45	Post-Resistance	TBRG4	9238	37	7	45145221	45145221	Missense_Mutation	SNP	G	A	9	142	c.554C>T	c.(553-555)GCC>GTC	p.A185V
Pat_45	Post-Resistance	IGFBP3	3486	37	7	45956840	45956840	Missense_Mutation	SNP	G	A	67	222	c.602C>T	c.(601-603)TCC>TTC	p.S201F
Pat_45	Post-Resistance	POM121	9883	37	7	72398999	72398999	Missense_Mutation	SNP	C	T	6	120	c.1099C>T	c.(1099-1101)CCT>TCT	p.P367S
Pat_45	Post-Resistance	ELN	2006	37	7	73481094	73481094	Missense_Mutation	SNP	C	T	8	108	c.2137C>T	c.(2137-2139)CCC>TCC	p.P713S
Pat_45	Post-Resistance	UPK3B	80761	37	7	76143347	76143347	Missense_Mutation	SNP	G	A	16	120	c.710G>A	c.(709-711)GGC>GAC	p.G237D
Pat_45	Post-Resistance	HGF	3082	37	7	81332055	81332055	Missense_Mutation	SNP	G	A	5	70	c.2029C>T	c.(2029-2031)CTT>TTT	p.L677F
Pat_45	Post-Resistance	PCLO	27445	37	7	82584325	82584325	Missense_Mutation	SNP	C	T	11	127	c.5944G>A	c.(5944-5946)GGA>AGA	p.G1982R
Pat_45	Post-Resistance	ZNF804B	219578	37	7	88964874	88964874	Missense_Mutation	SNP	G	A	4	54	c.2578G>A	c.(2578-2580)GAG>AAG	p.E860K
Pat_45	Post-Resistance	STEAP2	261729	37	7	89854678	89854678	Missense_Mutation	SNP	C	G	20	43	c.282C>G	c.(280-282)CAC>CAG	p.H94Q
Pat_45	Post-Resistance	AKAP9	10142	37	7	91674350	91674350	Missense_Mutation	SNP	C	T	6	79	c.5191C>T	c.(5191-5193)CTT>TTT	p.L1731F
Pat_45	Post-Resistance	COL1A2	1278	37	7	94034535	94034535	Missense_Mutation	SNP	C	T	8	78	c.457C>T	c.(457-459)CCT>TCT	p.P153S
Pat_45	Post-Resistance	COL1A2	1278	37	7	94054955	94054955	Missense_Mutation	SNP	G	A	12	141	c.2815G>A	c.(2815-2817)GAT>AAT	p.D939N
Pat_45	Post-Resistance	BAIAP2L1	55971	37	7	97946539	97946539	Missense_Mutation	SNP	C	T	28	208	c.478G>A	c.(478-480)GAA>AAA	p.E160K
Pat_45	Post-Resistance	TRRAP	8295	37	7	98567775	98567775	Missense_Mutation	SNP	C	T	18	176	c.7532C>T	c.(7531-7533)ACC>ATC	p.T2511I
Pat_45	Post-Resistance	AP4M1	9179	37	7	99701259	99701259	Missense_Mutation	SNP	A	G	96	439	c.487A>G	c.(487-489)AAA>GAA	p.K163E
Pat_45	Post-Resistance	GPC2	221914	37	7	99769443	99769443	Missense_Mutation	SNP	C	T	4	11	c.1129G>A	c.(1129-1131)GAG>AAG	p.E377K
Pat_45	Post-Resistance	STAG3	10734	37	7	99783872	99783872	Missense_Mutation	SNP	G	A	8	172	c.386G>A	c.(385-387)GGA>GAA	p.G129E
Pat_45	Post-Resistance	EPHB4	2050	37	7	100417784	100417784	Missense_Mutation	SNP	G	A	6	157	c.943C>T	c.(943-945)CCC>TCC	p.P315S
Pat_45	Post-Resistance	SRRT	51593	37	7	100484762	100484762	Missense_Mutation	SNP	G	A	31	331	c.1916G>A	c.(1915-1917)CGC>CAC	p.R639H
Pat_45	Post-Resistance	C7orf52	375607	37	7	100817952	100817952	Missense_Mutation	SNP	G	A	9	108	c.137C>T	c.(136-138)CCT>CTT	p.P46L
Pat_45	Post-Resistance	FIS1	51024	37	7	100883103	100883103	Missense_Mutation	SNP	G	A	3	26	c.443C>T	c.(442-444)TCC>TTC	p.S148F
Pat_45	Post-Resistance	DLD	1738	37	7	107556059	107556059	Missense_Mutation	SNP	C	T	10	55	c.793C>T	c.(793-795)CTT>TTT	p.L265F
Pat_45	Post-Resistance	NRCAM	4897	37	7	107864205	107864205	Missense_Mutation	SNP	C	T	11	85	c.854G>A	c.(853-855)GGA>GAA	p.G285E
Pat_45	Post-Resistance	GCC1	79571	37	7	127224651	127224651	Missense_Mutation	SNP	C	T	11	129	c.586G>A	c.(586-588)GAC>AAC	p.D196N
Pat_45	Post-Resistance	SND1	27044	37	7	127528066	127528066	Splice_Site	SNP	G	A	5	36	c.1454_splice	c.e13+1	p.R485_splice
Pat_45	Post-Resistance	ZC3HC1	51530	37	7	129680862	129680862	Missense_Mutation	SNP	T	C	28	307	c.338A>G	c.(337-339)GAT>GGT	p.D113G
Pat_45	Post-Resistance	MKLN1	4289	37	7	131012692	131012692	Missense_Mutation	SNP	G	A	8	61	c.34G>A	c.(34-36)GAG>AAG	p.E12K
Pat_45	Post-Resistance	WDR91	29062	37	7	134894507	134894507	Missense_Mutation	SNP	C	T	11	111	c.124G>A	c.(124-126)GTG>ATG	p.V42M
Pat_45	Post-Resistance	HIPK2	28996	37	7	139285224	139285224	Missense_Mutation	SNP	G	A	3	78	c.2374C>T	c.(2374-2376)CGG>TGG	p.R792W
Pat_45	Post-Resistance	SLC37A3	84255	37	7	140043279	140043279	Missense_Mutation	SNP	C	T	14	130	c.1259G>A	c.(1258-1260)AGT>AAT	p.S420N
Pat_45	Post-Resistance	BRAF	673	37	7	140453136	140453136	Missense_Mutation	SNP	A	T	22	126	c.1799T>A	c.(1798-1800)GTG>GAG	p.V600E
Pat_45	Post-Resistance	TAS2R39	259285	37	7	142880801	142880801	Missense_Mutation	SNP	G	A	7	73	c.290G>A	c.(289-291)AGC>AAC	p.S97N
Pat_45	Post-Resistance	CNTNAP2	26047	37	7	146805370	146805370	Missense_Mutation	SNP	G	A	6	48	c.682G>A	c.(682-684)GGA>AGA	p.G228R
Pat_45	Post-Resistance	ZNF398	57541	37	7	148875956	148875956	Missense_Mutation	SNP	G	A	34	351	c.992G>A	c.(991-993)AGC>AAC	p.S331N
Pat_45	Post-Resistance	SLC4A2	6522	37	7	150772839	150772839	Missense_Mutation	SNP	C	T	12	136	c.3448C>T	c.(3448-3450)CCA>TCA	p.P1150S
Pat_45	Post-Resistance	FASTK	10922	37	7	150776776	150776776	Missense_Mutation	SNP	G	A	4	9	c.316C>T	c.(316-318)CCC>TCC	p.P106S
Pat_45	Post-Resistance	SMARCD3	6604	37	7	150936564	150936564	Missense_Mutation	SNP	C	T	6	77	c.1316G>A	c.(1315-1317)GGC>GAC	p.G439D
Pat_45	Post-Resistance	MLL3	58508	37	7	151949172	151949172	Nonsense_Mutation	SNP	C	T	3	48	c.1473G>A	c.(1471-1473)TGG>TGA	p.W491*
Pat_45	Post-Resistance	RBM33	155435	37	7	155559213	155559213	Missense_Mutation	SNP	G	A	7	64	c.3239G>A	c.(3238-3240)CGC>CAC	p.R1080H
Pat_45	Post-Resistance	LMBR1	64327	37	7	156480739	156480739	Missense_Mutation	SNP	G	A	4	77	c.1372C>T	c.(1372-1374)CTT>TTT	p.L458F

Pat_45	Post-Resistance	WDR60	55112	37	7	158705727	158705727	Missense_Mutation	SNP	G	A	5	64	c.1642G>A	c.(1642-1644)GAA>AAA	p.E548K
Pat_45	Post-Resistance	VIPR2	7434	37	7	158935207	158935207	Missense_Mutation	SNP	G	A	42	142	c.82C>T	c.(82-84)CAT>TAT	p.H28Y
Pat_45	Post-Resistance	CSMD1	64478	37	8	3165990	3165990	Missense_Mutation	SNP	G	A	4	66	c.3670C>T	c.(3670-3672)CCT>TCT	p.P1224S
Pat_45	Post-Resistance	SPAG11A	653423	37	8	7718227	7718227	Missense_Mutation	SNP	C	T	6	58	c.406C>T	c.(406-408)CTT>TTT	p.L136F
Pat_45	Post-Resistance	MTMR9	66036	37	8	11172574	11172574	Splice_Site	SNP	G	A	12	146	c.1113_splice	c.e7+1	p.Q371_splice
Pat_45	Post-Resistance	BLK	640	37	8	11412326	11412326	Missense_Mutation	SNP	G	T	3	35	c.547G>T	c.(547-549)GAT>TAT	p.D183Y
Pat_45	Post-Resistance	KIAA1967	57805	37	8	22476205	22476205	Missense_Mutation	SNP	G	A	9	113	c.2296G>A	c.(2296-2298)GGC>AGC	p.G766S
Pat_45	Post-Resistance	TNFRSF10C	8794	37	8	22974339	22974339	Missense_Mutation	SNP	C	T	8	210	c.575C>T	c.(574-576)CCA>CTA	p.P192L
Pat_45	Post-Resistance	LOXL2	4017	37	8	23159641	23159641	Missense_Mutation	SNP	C	T	18	74	c.2032G>A	c.(2032-2034)GAT>AAT	p.D678N
Pat_45	Post-Resistance	INTS9	55756	37	8	28669866	28669866	Missense_Mutation	SNP	G	A	7	101	c.722C>T	c.(721-723)TCC>TTC	p.S241F
Pat_45	Post-Resistance	RBPMS	11030	37	8	30336847	30336847	Missense_Mutation	SNP	G	A	7	83	c.200G>A	c.(199-201)AGT>AAT	p.S67N
Pat_45	Post-Resistance	NRG1	3084	37	8	32621567	32621567	Missense_Mutation	SNP	G	A	9	43	c.1570G>A	c.(1570-1572)GAG>AAG	p.E524K
Pat_45	Post-Resistance	KCNU1	157855	37	8	36698455	36698455	Missense_Mutation	SNP	G	A	8	60	c.1637G>A	c.(1636-1638)TGC>TAC	p.C546Y
Pat_45	Post-Resistance	ST18	9705	37	8	53079523	53079523	Missense_Mutation	SNP	C	T	62	176	c.1093G>A	c.(1093-1095)GAG>AAG	p.E365K
Pat_45	Post-Resistance	CYP7A1	1581	37	8	59412636	59412636	Missense_Mutation	SNP	A	C	15	130	c.22T>G	c.(22-24)TGG>GGG	p.W8G
Pat_45	Post-Resistance	RRS1	23212	37	8	67341997	67341997	Missense_Mutation	SNP	G	A	4	54	c.631G>A	c.(631-633)GGA>AGA	p.G211R
Pat_45	Post-Resistance	STAU2	27067	37	8	74516017	74516017	Missense_Mutation	SNP	C	T	6	124	c.973G>A	c.(973-975)GAT>AAT	p.D325N
Pat_45	Post-Resistance	TPD52	7163	37	8	81083675	81083675	Missense_Mutation	SNP	C	T	14	100	c.4G>A	c.(4-6)GAC>AAC	p.D2N
Pat_45	Post-Resistance	PAG1	55824	37	8	81897532	81897532	Nonsense_Mutation	SNP	G	A	4	49	c.355C>T	c.(355-357)CAG>TAG	p.Q119*
Pat_45	Post-Resistance	CA2	760	37	8	86385937	86385937	Missense_Mutation	SNP	C	T	4	62	c.248C>T	c.(247-249)CCC>CTC	p.P83L
Pat_45	Post-Resistance	SLC7A13	157724	37	8	87242161	87242161	Missense_Mutation	SNP	C	A	4	42	c.346G>T	c.(346-348)GCT>TCT	p.A116S
Pat_45	Post-Resistance	WWP1	11059	37	8	87410658	87410658	Missense_Mutation	SNP	G	A	7	112	c.422G>A	c.(421-423)GGA>GAA	p.G141E
Pat_45	Post-Resistance	WWP1	11059	37	8	87470245	87470245	Nonsense_Mutation	SNP	G	A	9	89	c.2490G>A	c.(2488-2490)TGG>TGA	p.W830*
Pat_45	Post-Resistance	NBN	4683	37	8	90965603	90965603	Missense_Mutation	SNP	G	A	16	197	c.1714C>T	c.(1714-1716)CCA>TCA	p.P572S
Pat_45	Post-Resistance	RAD54B	25788	37	8	95390536	95390536	Missense_Mutation	SNP	G	A	3	36	c.2387C>T	c.(2386-2388)ACC>ATC	p.T796I
Pat_45	Post-Resistance	KIAA1429	25962	37	8	95524296	95524296	Missense_Mutation	SNP	G	A	6	70	c.2773C>T	c.(2773-2775)CCA>TCA	p.P925S
Pat_45	Post-Resistance	PGCP	10404	37	8	97797264	97797264	Missense_Mutation	SNP	G	T	4	75	c.139G>T	c.(139-141)GCT>TCT	p.A47S
Pat_45	Post-Resistance	VPS13B	157680	37	8	100847784	100847784	Missense_Mutation	SNP	G	A	9	83	c.9835G>A	c.(9835-9837)GTT>ATT	p.V3279I
Pat_45	Post-Resistance	RGS22	26166	37	8	100994197	100994197	Missense_Mutation	SNP	C	T	67	212	c.3328G>A	c.(3328-3330)GAG>AAG	p.E1110K
Pat_45	Post-Resistance	UBR5	51366	37	8	103299718	103299718	Missense_Mutation	SNP	C	T	4	63	c.4900G>A	c.(4900-4902)GAT>AAT	p.D1634N
Pat_45	Post-Resistance	TRHR	7201	37	8	110100014	110100014	Nonsense_Mutation	SNP	G	A	8	84	c.273G>A	c.(271-273)TGG>TGA	p.W91*
Pat_45	Post-Resistance	CSMD3	114788	37	8	113702210	113702210	Missense_Mutation	SNP	G	A	27	214	c.2042C>T	c.(2041-2043)TCT>TTT	p.S681F
Pat_45	Post-Resistance	UTP23	84294	37	8	117783815	117783815	Missense_Mutation	SNP	G	A	16	97	c.484G>A	c.(484-486)GAG>AAG	p.E162K
Pat_45	Post-Resistance	COLEC10	10584	37	8	120101985	120101985	Missense_Mutation	SNP	C	A	3	38	c.215C>A	c.(214-216)CCG>CAG	p.P72Q
Pat_45	Post-Resistance	FER1L6	654463	37	8	125110043	125110043	Missense_Mutation	SNP	C	T	7	103	c.4802C>T	c.(4801-4803)ACC>ATC	p.T1601I
Pat_45	Post-Resistance	MTSS1	9788	37	8	125565661	125565661	Missense_Mutation	SNP	G	A	5	82	c.1840C>T	c.(1840-1842)CCC>TCC	p.P614S
Pat_45	Post-Resistance	ZNF572	137209	37	8	125988764	125988764	Missense_Mutation	SNP	C	T	29	61	c.254C>T	c.(253-255)TCC>TTC	p.S85F
Pat_45	Post-Resistance	OC90	729330	37	8	133041415	133041415	Missense_Mutation	SNP	G	T	10	154	c.1043C>A	c.(1042-1044)TCC>TAC	p.S348Y
Pat_45	Post-Resistance	TG	7038	37	8	133880359	133880359	Splice_Site	SNP	G	A	11	101	c.68_splice	c.e2-1	p.E23_splice
Pat_45	Post-Resistance	TG	7038	37	8	133975250	133975250	Missense_Mutation	SNP	G	A	32	380	c.5479G>A	c.(5479-5481)GGG>AGG	p.G1827R
Pat_45	Post-Resistance	WISP1	8840	37	8	134225378	134225378	Missense_Mutation	SNP	T	C	13	185	c.341T>C	c.(340-342)GTG>GCG	p.V114A
Pat_45	Post-Resistance	PTK2	5747	37	8	141900685	141900685	Missense_Mutation	SNP	G	A	8	77	c.152C>T	c.(151-153)ACC>ATC	p.T51I
Pat_45	Post-Resistance	PLEC	5339	37	8	144991270	144991270	Missense_Mutation	SNP	G	A	8	177	c.13130C>T	c.(13129-13131)GCC>GTC	p.A4377V
Pat_45	Post-Resistance	CYC1	1537	37	8	145152194	145152194	Nonsense_Mutation	SNP	G	A	6	161	c.933G>A	c.(931-933)TGG>TGA	p.W311*
Pat_45	Post-Resistance	KIFC2	90990	37	8	145694125	145694125	Missense_Mutation	SNP	G	A	26	363	c.1021G>A	c.(1021-1023)GCC>ACC	p.A341T
Pat_45	Post-Resistance	MFSD3	113655	37	8	145736051	145736051	Missense_Mutation	SNP	G	A	13	156	c.901G>A	c.(901-903)GTC>ATC	p.V301I
Pat_45	Post-Resistance	SMARCA2	6595	37	9	2088558	2088558	Missense_Mutation	SNP	G	A	14	143	c.2828G>A	c.(2827-2829)AGA>AAA	p.R943K

Pat_45	Post-Resistance	CDC37L1	55664	37	9	4685105	4685105	Missense_Mutation	SNP	G	A	11	206	c.361G>A	c.(361-363)GAG>AAG	p.E121K
Pat_45	Post-Resistance	KDM4C	23081	37	9	7011727	7011727	Missense_Mutation	SNP	G	A	16	99	c.1816G>A	c.(1816-1818)GAA>AAA	p.E606K
Pat_45	Post-Resistance	CER1	9350	37	9	14722231	14722231	Missense_Mutation	SNP	C	T	48	38	c.440G>A	c.(439-441)GGG>GAG	p.G147E
Pat_45	Post-Resistance	C9orf93	203238	37	9	15727867	15727867	Missense_Mutation	SNP	G	A	6	69	c.1693G>A	c.(1693-1695)GAG>AAG	p.E565K
Pat_45	Post-Resistance	CNTLN	54875	37	9	17394971	17394971	Missense_Mutation	SNP	G	A	8	160	c.2519G>A	c.(2518-2520)GGT>GAT	p.G840D
Pat_45	Post-Resistance	ADAMTSL1	92949	37	9	18680380	18680380	Missense_Mutation	SNP	T	C	4	128	c.1207T>C	c.(1207-1209)TGT>CGT	p.C403R
Pat_45	Post-Resistance	ADAMTSL1	92949	37	9	18887904	18887904	Missense_Mutation	SNP	G	A	8	107	c.4325G>A	c.(4324-4326)GGA>GAA	p.G1442E
Pat_45	Post-Resistance	KIAA1797	54914	37	9	20874716	20874716	Missense_Mutation	SNP	G	A	24	155	c.2227G>A	c.(2227-2229)GAC>AAC	p.D743N
Pat_45	Post-Resistance	NFX1	4799	37	9	33294937	33294937	Missense_Mutation	SNP	C	A	6	133	c.545C>A	c.(544-546)CCA>CAA	p.P182Q
Pat_45	Post-Resistance	PRSS3	5646	37	9	33799038	33799038	Missense_Mutation	SNP	G	A	32	203	c.775G>A	c.(775-777)GGC>AGC	p.G259S
Pat_45	Post-Resistance	IL11RA	3590	37	9	34658567	34658567	Missense_Mutation	SNP	C	T	26	242	c.697C>T	c.(697-699)CCC>TCC	p.P233S
Pat_45	Post-Resistance	C9orf131	138724	37	9	35043635	35043635	Missense_Mutation	SNP	G	A	102	570	c.1009G>A	c.(1009-1011)GAG>AAG	p.E337K
Pat_45	Post-Resistance	FANCG	2189	37	9	35074927	35074927	Missense_Mutation	SNP	G	A	9	155	c.1633C>T	c.(1633-1635)CCA>TCA	p.P545S
Pat_45	Post-Resistance	KIAA1539	80256	37	9	35105788	35105788	Missense_Mutation	SNP	G	A	6	123	c.1354C>T	c.(1354-1356)CCT>TCT	p.P452S
Pat_45	Post-Resistance	SIT1	27240	37	9	35650798	35650798	Missense_Mutation	SNP	G	A	16	69	c.53C>T	c.(52-54)TCT>TTT	p.S18F
Pat_45	Post-Resistance	NPR2	4882	37	9	35809204	35809204	Missense_Mutation	SNP	G	A	32	239	c.3038G>A	c.(3037-3039)GGA>GAA	p.G1013E
Pat_45	Post-Resistance	RG9MTD3	158234	37	9	37770711	37770711	Missense_Mutation	SNP	G	A	6	78	c.695G>A	c.(694-696)GGG>GAG	p.G232E
Pat_45	Post-Resistance	FAM75A6	389730	37	9	43627693	43627693	Missense_Mutation	SNP	C	T	20	245	c.994G>A	c.(994-996)GTC>ATC	p.V332I
Pat_45	Post-Resistance	PCSK5	5125	37	9	78710854	78710854	Missense_Mutation	SNP	G	A	12	124	c.943G>A	c.(943-945)GGA>AGA	p.G315R
Pat_45	Post-Resistance	TLE4	7091	37	9	82335034	82335034	Missense_Mutation	SNP	G	A	9	92	c.1739G>A	c.(1738-1740)AGT>AAT	p.S580N
Pat_45	Post-Resistance	FLJ43859	389761	37	9	84547469	84547469	Missense_Mutation	SNP	C	T	19	43	c.2393C>T	c.(2392-2394)TCT>TTT	p.S798F
Pat_45	Post-Resistance	KIF27	55582	37	9	86482625	86482625	Missense_Mutation	SNP	C	T	3	12	c.2908G>A	c.(2908-2910)GAA>AAA	p.E970K
Pat_45	Post-Resistance	SLC28A3	64078	37	9	86905169	86905170	Missense_Mutation	DNP	GG	AA	13	36	.1048_1049CC>T	c.(1048-1050)CCA>TTA	p.P350L
Pat_45	Post-Resistance	ZCCHC6	79670	37	9	88943368	88943368	Missense_Mutation	SNP	G	A	16	136	c.1495C>T	c.(1495-1497)CTT>TTT	p.L499F
Pat_45	Post-Resistance	CTSL3	392360	37	9	90401734	90401734	Missense_Mutation	SNP	G	A	8	49	c.586G>A	c.(586-588)GAT>AAT	p.D196N
Pat_45	Post-Resistance	FAM75C1	441452	37	9	90536719	90536719	Missense_Mutation	SNP	G	A	12	185	c.1897G>A	c.(1897-1899)GCC>ACC	p.A633T
Pat_45	Post-Resistance	SYK	6850	37	9	93606427	93606427	Missense_Mutation	SNP	G	A	6	115	c.247G>A	c.(247-249)GCC>ACC	p.A83T
Pat_45	Post-Resistance	FANCC	2176	37	9	97934336	97934336	Missense_Mutation	SNP	G	A	4	23	c.439C>T	c.(439-441)CCT>TCT	p.P147S
Pat_45	Post-Resistance	TBC1D2	55357	37	9	100995767	100995767	Missense_Mutation	SNP	C	T	17	175	c.712G>A	c.(712-714)GAA>AAA	p.E238K
Pat_45	Post-Resistance	TEX10	54881	37	9	103064526	103064526	Missense_Mutation	SNP	C	T	4	163	c.2737G>A	c.(2737-2739)GTG>ATG	p.V913M
Pat_45	Post-Resistance	TEX10	54881	37	9	103109477	103109477	Missense_Mutation	SNP	G	A	4	115	c.392C>T	c.(391-393)GCT>GTT	p.A131V
Pat_45	Post-Resistance	NIPSNAP3B	55335	37	9	107535175	107535175	Missense_Mutation	SNP	G	A	4	9	c.653G>A	c.(652-654)AGA>AAA	p.R218K
Pat_45	Post-Resistance	SLC44A1	23446	37	9	108123535	108123535	Missense_Mutation	SNP	C	T	11	58	c.824C>T	c.(823-825)ACT>ATT	p.T275I
Pat_45	Post-Resistance	IKBKAP	8518	37	9	111681145	111681145	Missense_Mutation	SNP	G	A	24	208	c.686C>T	c.(685-687)GCT>GTT	p.A229V
Pat_45	Post-Resistance	C9orf84	158401	37	9	114454022	114454022	Missense_Mutation	SNP	C	T	11	71	c.4043G>A	c.(4042-4044)AGT>AAT	p.S1348N
Pat_45	Post-Resistance	PDCL	5082	37	9	125582773	125582773	Missense_Mutation	SNP	C	T	9	86	c.497G>A	c.(496-498)AGT>AAT	p.S166N
Pat_45	Post-Resistance	RC3H2	54542	37	9	125616490	125616490	Missense_Mutation	SNP	C	T	12	136	c.2956G>A	c.(2956-2958)GAC>AAC	p.D986N
Pat_45	Post-Resistance	SCAI	286205	37	9	127715148	127715148	Missense_Mutation	SNP	C	T	18	48	c.1759G>A	c.(1759-1761)GAA>AAA	p.E587K
Pat_45	Post-Resistance	LMX1B	4010	37	9	129453302	129453302	Missense_Mutation	SNP	G	A	4	36	c.445G>A	c.(445-447)GAG>AAG	p.E149K
Pat_45	Post-Resistance	LRRC8A	56262	37	9	131670351	131670351	Missense_Mutation	SNP	C	T	14	240	c.908C>T	c.(907-909)ACG>ATG	p.T303M
Pat_45	Post-Resistance	LRRC8A	56262	37	9	131678465	131678465	Missense_Mutation	SNP	G	A	9	71	c.2248G>A	c.(2248-2250)GTG>ATG	p.V750M
Pat_45	Post-Resistance	PHYHD1	254295	37	9	131689422	131689422	Missense_Mutation	SNP	C	T	14	134	c.139C>T	c.(139-141)CTC>TTC	p.L47F
Pat_45	Post-Resistance	C9orf106	414318	37	9	132084535	132084536	Nonsense_Mutation	DNP	GG	AA	12	68	c.443_444GG>AA	c.(442-444)TGG>TAA	p.W148*
Pat_45	Post-Resistance	USP20	10868	37	9	132637729	132637729	Missense_Mutation	SNP	C	T	5	49	c.2189C>T	c.(2188-2190)ACC>ATC	p.T730I
Pat_45	Post-Resistance	QRFP	347148	37	9	133768837	133768837	Missense_Mutation	SNP	C	T	10	97	c.389G>A	c.(388-390)AGC>AAC	p.S130N
Pat_45	Post-Resistance	UCK1	83549	37	9	134400446	134400446	Missense_Mutation	SNP	G	A	11	71	c.815C>T	c.(814-816)TCC>TTC	p.S272F
Pat_45	Post-Resistance	RAPGEF1	2889	37	9	134504052	134504052	Missense_Mutation	SNP	G	A	13	165	c.850C>T	c.(850-852)CCA>TCA	p.P284S

Pat_45	Post-Resistance	COBRA1	25920	37	9	140166617	140166617	Missense_Mutation	SNP	C	T	7	93	c.1430C>T	c.(1429-1431)GCC>GTC	p.A477V
Pat_45	Post-Resistance	MXRA5	25878	37	X	3242864	3242864	Missense_Mutation	SNP	T	C	3	70	c.862A>G	c.(862-864)AGG>GGG	p.R288G
Pat_45	Post-Resistance	FRMPD4	9758	37	X	12627905	12627905	Missense_Mutation	SNP	C	T	15	92	c.224C>T	c.(223-225)GCT>GTT	p.A75V
Pat_45	Post-Resistance	TMSL3	7117	37	X	12994901	12994901	Missense_Mutation	SNP	G	A	13	66	c.106G>A	c.(106-108)GAA>AAA	p.E36K
Pat_45	Post-Resistance	BMX	660	37	X	15548143	15548143	Missense_Mutation	SNP	G	A	8	47	c.932G>A	c.(931-933)AGA>AAA	p.R311K
Pat_45	Post-Resistance	BEND2	139105	37	X	18220021	18220021	Missense_Mutation	SNP	G	A	6	62	c.947C>T	c.(946-948)ACT>ATT	p.T316I
Pat_45	Post-Resistance	PHKA2	5256	37	X	18972475	18972475	Missense_Mutation	SNP	C	T	4	59	c.134G>A	c.(133-135)CGG>CAG	p.R45Q
Pat_45	Post-Resistance	KLHL15	80311	37	X	24024119	24024119	Missense_Mutation	SNP	C	T	27	192	c.692G>A	c.(691-693)AGC>AAC	p.S231N
Pat_45	Post-Resistance	ARX	170302	37	X	25025475	25025475	Missense_Mutation	SNP	G	A	4	2	c.1201C>T	c.(1201-1203)CCG>TCG	p.P401S
Pat_45	Post-Resistance	MAGEB4	4115	37	X	30260383	30260383	Missense_Mutation	SNP	C	T	3	9	c.131C>T	c.(130-132)TCT>TTT	p.S44F
Pat_45	Post-Resistance	NR0B1	190	37	X	30327347	30327347	Missense_Mutation	SNP	T	A	4	28	c.134A>T	c.(133-135)GAT>GTT	p.D45V
Pat_45	Post-Resistance	DMD	1756	37	X	32536238	32536238	Missense_Mutation	SNP	C	T	3	18	c.2179G>A	c.(2179-2181)GAT>AAT	p.D727N
Pat_45	Post-Resistance	FAM47C	442444	37	X	37027957	37027957	Missense_Mutation	SNP	G	A	33	93	c.1474G>A	c.(1474-1476)GAC>AAC	p.D492N
Pat_45	Post-Resistance	SYTL5	94122	37	X	37985840	37985840	Splice_Site	SNP	G	A	4	21	c.2051_splice	c.e18-1	p.G684_splice
Pat_45	Post-Resistance	ZNF630	57232	37	X	47919846	47919846	Nonsense_Mutation	SNP	G	T	4	67	c.221C>A	c.(220-222)TCA>TAA	p.S74*
Pat_45	Post-Resistance	HDAC6	10013	37	X	48663864	48663864	Missense_Mutation	SNP	C	T	11	37	c.331C>T	c.(331-333)CGG>TGG	p.R111W
Pat_45	Post-Resistance	CCNB3	85417	37	X	50052401	50052401	Missense_Mutation	SNP	A	C	6	31	c.1232A>C	c.(1231-1233)AAG>ACG	p.K411T
Pat_45	Post-Resistance	SMC1A	8243	37	X	53423146	53423146	Splice_Site	SNP	C	T	13	110	c.2862_splice	c.e18+1	p.E954_splice
Pat_45	Post-Resistance	SMC1A	8243	37	X	53432032	53432032	Missense_Mutation	SNP	G	A	3	10	c.2108C>T	c.(2107-2109)TCT>TTT	p.S703F
Pat_45	Post-Resistance	P2RY4	5030	37	X	69479234	69479234	Missense_Mutation	SNP	C	T	4	14	c.241G>A	c.(241-243)GAC>AAC	p.D81N
Pat_45	Post-Resistance	ARR3	407	37	X	69500635	69500635	Missense_Mutation	SNP	C	T	21	76	c.1033C>T	c.(1033-1035)CCC>TCC	p.P345S
Pat_45	Post-Resistance	NONO	4841	37	X	70514153	70514153	Missense_Mutation	SNP	G	A	9	48	c.425G>A	c.(424-426)CGC>CAC	p.R142H
Pat_45	Post-Resistance	MAGT1	84061	37	X	77130979	77130979	Missense_Mutation	SNP	G	A	42	219	c.314C>T	c.(313-315)TCC>TTC	p.S105F
Pat_45	Post-Resistance	P2RY10	27334	37	X	78216429	78216429	Missense_Mutation	SNP	C	T	19	53	c.412C>T	c.(412-414)CCC>TCC	p.P138S
Pat_45	Post-Resistance	PABPC5	140886	37	X	90691465	90691465	Missense_Mutation	SNP	A	G	3	3	c.889A>G	c.(889-891)AGT>GGT	p.S297G
Pat_45	Post-Resistance	RPA4	29935	37	X	96139680	96139680	Missense_Mutation	SNP	A	G	11	54	c.371A>G	c.(370-372)TAT>TGT	p.Y124C
Pat_45	Post-Resistance	TRMT2B	79979	37	X	100297070	100297070	Missense_Mutation	SNP	G	T	4	47	c.209C>A	c.(208-210)CCA>CAA	p.P70Q
Pat_45	Post-Resistance	ARMCX3	51566	37	X	100880118	100880118	Missense_Mutation	SNP	G	A	12	83	c.149G>A	c.(148-150)GGG>GAG	p.G50E
Pat_45	Post-Resistance	TSC22D3	1831	37	X	106957870	106957870	Missense_Mutation	SNP	G	A	31	153	c.284C>T	c.(283-285)ACC>ATC	p.T95I
Pat_45	Post-Resistance	ALG13	79868	37	X	110951413	110951413	Missense_Mutation	SNP	C	T	5	56	c.542C>T	c.(541-543)ACC>ATC	p.T181I
Pat_45	Post-Resistance	IL13RA2	3598	37	X	114248393	114248393	Missense_Mutation	SNP	G	A	8	25	c.460C>T	c.(460-462)CTC>TTC	p.L154F
Pat_45	Post-Resistance	LONRF3	79836	37	X	118145821	118145821	Missense_Mutation	SNP	C	T	20	183	c.1696C>T	c.(1696-1698)CCC>TCC	p.P566S
Pat_45	Post-Resistance	GPR119	139760	37	X	129519028	129519028	Missense_Mutation	SNP	C	T	12	79	c.394G>A	c.(394-396)GTG>ATG	p.V132M
Pat_45	Post-Resistance	ENOX2	10495	37	X	129822959	129822959	Missense_Mutation	SNP	A	G	5	25	c.218T>C	c.(217-219)ATT>ACT	p.I73T
Pat_45	Post-Resistance	GPR101	83550	37	X	136113427	136113427	Missense_Mutation	SNP	G	A	4	28	c.407C>T	c.(406-408)CCT>CTT	p.P136L
Pat_45	Post-Resistance	MAGEC3	139081	37	X	140985596	140985596	Missense_Mutation	SNP	C	T	6	65	c.1910C>T	c.(1909-1911)TCC>TTC	p.S637F
Pat_45	Post-Resistance	SLITRK4	139065	37	X	142716578	142716578	Missense_Mutation	SNP	C	T	16	53	c.2347G>A	c.(2347-2349)GAA>AAA	p.E783K
Pat_45	Post-Resistance	FMR1	2332	37	X	147024783	147024783	Missense_Mutation	SNP	G	A	6	81	c.1408G>A	c.(1408-1410)GGT>AGT	p.G470S
Pat_45	Post-Resistance	CNGA2	1260	37	X	150912089	150912089	Missense_Mutation	SNP	G	A	24	44	c.1114G>A	c.(1114-1116)GGC>AGC	p.G372S
Pat_45	Post-Resistance	GABRQ	55879	37	X	151820196	151820196	Missense_Mutation	SNP	G	A	17	35	c.1109G>A	c.(1108-1110)AGA>AAA	p.R370K
Pat_45	Post-Resistance	ZNF185	7739	37	X	152097165	152097165	Missense_Mutation	SNP	G	A	10	74	c.874G>A	c.(874-876)GCA>ACA	p.A292T
Pat_45	Post-Resistance	HCFC1	3054	37	X	153221674	153221674	Missense_Mutation	SNP	C	T	19	88	c.2824G>A	c.(2824-2826)GGC>AGC	p.G942S
Pat_45	Post-Resistance	FAM3A	60343	37	X	153735805	153735805	Missense_Mutation	SNP	C	A	4	54	c.402G>T	c.(400-402)TTG>TTT	p.L134F
Pat_45	Post-Resistance	G6PD	2539	37	X	153761790	153761790	Splice_Site	SNP	C	T	7	82	c.864_splice	c.e8+1	p.K288_splice
Pat_45	Post-Resistance	IKBKG	8517	37	X	153780386	153780386	Missense_Mutation	SNP	G	A	3	15	c.169G>A	c.(169-171)GAG>AAG	p.E57K
Pat_45	Post-Resistance	NLGN4Y	22829	37	Y	16734333	16734333	Nonsense_Mutation	SNP	C	T	3	56	c.334C>T	c.(334-336)CAG>TAG	p.Q112*
Pat_51	Pre-Treatment	HSPG2	3339	37	1	22191343	22191343	Missense_Mutation	SNP	G	A	9	0	c.4619C>T	c.(4618-4620)TCC>TTC	p.S1540F

Pat_51	Pre-Treatment	GJB3	2707	37	1	35250527	35250527	Missense_Mutation	SNP	C	T	21	33	c.164C>T	c.(163-165)ACC>ATC	p.T55I
Pat_51	Pre-Treatment	NBPF10	100132406	37	1	145327548	145327548	Missense_Mutation	SNP	A	G	3	6	c.4330A>G	c.(4330-4332)AAT>GAT	p.N1444D
Pat_51	Pre-Treatment	FLG	2312	37	1	152278987	152278987	Missense_Mutation	SNP	G	A	209	436	c.8375C>T	c.(8374-8376)TCA>TTA	p.S2792L
Pat_51	Pre-Treatment	OR10J3	441911	37	1	159284407	159284407	Missense_Mutation	SNP	C	T	136	144	c.43G>A	c.(43-45)GAA>AAA	p.E15K
Pat_51	Pre-Treatment	PPOX	5498	37	1	161138337	161138337	Missense_Mutation	SNP	C	T	21	28	c.587C>T	c.(586-588)TCC>TTC	p.S196F
Pat_51	Pre-Treatment	RGS13	6003	37	1	192628516	192628516	Missense_Mutation	SNP	G	A	23	26	c.343G>A	c.(343-345)GAA>AAA	p.E115K
Pat_51	Pre-Treatment	IGFN1	91156	37	1	201190783	201190784	Missense_Mutation	DNP	GG	AA	19	28	.1590_1591GG>A	588-1593)GAGGGC>GAA	p.G531S
Pat_51	Pre-Treatment	CR2	1380	37	1	207644114	207644115	Missense_Mutation	DNP	GG	AA	12	25	.1255_1256GG>A	c.(1255-1257)GGG>AAG	p.G419K
Pat_51	Pre-Treatment	OR11L1	391189	37	1	248004661	248004661	Missense_Mutation	SNP	C	T	56	81	c.538G>A	c.(538-540)GAC>AAC	p.D180N
Pat_51	Pre-Treatment	OR2M2	391194	37	1	248343390	248343390	Missense_Mutation	SNP	T	A	8	295	c.103T>A	c.(103-105)TTT>ATT	p.F35I
Pat_51	Pre-Treatment	KLF6	1316	37	10	3827122	3827122	Nonsense_Mutation	SNP	C	A	20	3	c.85G>T	c.(85-87)GAG>TAG	p.E29*
Pat_51	Pre-Treatment	OR56B4	196335	37	11	6129583	6129583	Missense_Mutation	SNP	G	A	61	75	c.575G>A	c.(574-576)AGC>AAC	p.S192N
Pat_51	Pre-Treatment	OR5AK2	390181	37	11	56756815	56756815	Missense_Mutation	SNP	C	T	56	61	c.427C>T	c.(427-429)CGT>TGT	p.R143C
Pat_51	Pre-Treatment	FAT3	120114	37	11	92525957	92525957	Nonsense_Mutation	SNP	C	T	55	63	c.4636C>T	c.(4636-4638)CGA>TGA	p.R1546*
Pat_51	Pre-Treatment	CNTN5	53942	37	11	100169975	100169975	Missense_Mutation	SNP	G	A	7	21	c.2467G>A	c.(2467-2469)GAA>AAA	p.E823K
Pat_51	Pre-Treatment	HYOU1	10525	37	11	118918666	118918666	Missense_Mutation	SNP	A	G	14	14	c.2503T>C	c.(2503-2505)TTC>CTC	p.F835L
Pat_51	Pre-Treatment	KIRREL3	84623	37	11	126319042	126319042	Missense_Mutation	SNP	G	A	4	140	c.859C>T	c.(859-861)CGG>TGG	p.R287W
Pat_51	Pre-Treatment	KRT73	319101	37	12	53011971	53011971	Missense_Mutation	SNP	A	G	67	75	c.338T>C	c.(337-339)CTC>CCC	p.L113P
Pat_51	Pre-Treatment	CCDC38	120935	37	12	96284649	96284649	Missense_Mutation	SNP	C	T	18	28	c.832G>A	c.(832-834)GTC>ATC	p.V278I
Pat_51	Pre-Treatment	KIAA1033	23325	37	12	105531672	105531672	Missense_Mutation	SNP	G	C	13	23	c.1335G>C	c.(1333-1335)TTG>TTC	p.L445F
Pat_51	Pre-Treatment	FOXN4	121643	37	12	109717706	109717706	Missense_Mutation	SNP	C	T	17	21	c.1324G>A	c.(1324-1326)GGA>AGA	p.G442R
Pat_51	Pre-Treatment	MTUS2	23281	37	13	29855909	29855909	Missense_Mutation	SNP	G	A	24	24	c.2743G>A	c.(2743-2745)GGG>AGG	p.G915R
Pat_51	Pre-Treatment	PCDH9	5101	37	13	67800080	67800080	Missense_Mutation	SNP	G	C	73	66	c.2493C>G	c.(2491-2493)TTC>TTG	p.F831L
Pat_51	Pre-Treatment	TSHR	7253	37	14	81610614	81610614	Missense_Mutation	SNP	G	A	41	58	c.2212G>A	c.(2212-2214)GTC>ATC	p.V738I
Pat_51	Pre-Treatment	ACTC1	70	37	15	35083365	35083365	Missense_Mutation	SNP	G	A	122	152	c.940C>T	c.(940-942)CGT>TGT	p.R314C
Pat_51	Pre-Treatment	MAPKBP1	23005	37	15	42110235	42110235	Missense_Mutation	SNP	A	C	71	105	c.1951A>C	c.(1951-1953)AAG>CAG	p.K651Q
Pat_51	Pre-Treatment	TRPM7	54822	37	15	50904804	50904804	Missense_Mutation	SNP	C	T	37	48	c.1993G>A	c.(1993-1995)GAA>AAA	p.E665K
Pat_51	Pre-Treatment	SLTM	79811	37	15	59185100	59185100	Nonsense_Mutation	SNP	G	A	28	48	c.1894C>T	c.(1894-1896)CGA>TGA	p.R632*
Pat_51	Pre-Treatment	TLE3	7090	37	15	70351756	70351756	Missense_Mutation	SNP	G	A	5	9	c.758C>T	c.(757-759)TCC>TTC	p.S253F
Pat_51	Pre-Treatment	BNC1	646	37	15	83931721	83931721	Missense_Mutation	SNP	G	A	9	15	c.2282C>T	c.(2281-2283)TCC>TTC	p.S761F
Pat_51	Pre-Treatment	TSC2	7249	37	16	2126529	2126529	Missense_Mutation	SNP	C	T	29	40	c.2780C>T	c.(2779-2781)ACC>ATC	p.T927I
Pat_51	Pre-Treatment	ZNF213	7760	37	16	3187444	3187444	Missense_Mutation	SNP	G	A	26	33	c.163G>A	c.(163-165)GAT>AAT	p.D55N
Pat_51	Pre-Treatment	PALB2	79728	37	16	23641487	23641487	Missense_Mutation	SNP	C	T	57	68	c.1988G>A	c.(1987-1989)CGC>CAC	p.R663H
Pat_51	Pre-Treatment	SLC6A10P	386757	37	16	32890622	32890622	Missense_Mutation	SNP	T	G	4	30	c.264A>C	c.(262-264)AAA>AAC	p.K88N
Pat_51	Pre-Treatment	SPG7	6687	37	16	89620266	89620266	Missense_Mutation	SNP	G	A	27	32	c.2001G>A	c.(1999-2001)ATG>ATA	p.M667I
Pat_51	Pre-Treatment	OR1D2	4991	37	17	2995395	2995395	Missense_Mutation	SNP	G	A	41	59	c.896C>T	c.(895-897)GCT>GTT	p.A299V
Pat_51	Pre-Treatment	SPACA3	124912	37	17	31324480	31324480	Missense_Mutation	SNP	C	A	62	95	c.520C>A	c.(520-522)CTC>ATC	p.L174I
Pat_51	Pre-Treatment	KRTAP4-11	653240	37	17	39274150	39274150	Missense_Mutation	SNP	T	A	3	51	c.418A>T	c.(418-420)AGC>TGC	p.S140C
Pat_51	Pre-Treatment	SOST	50964	37	17	41836054	41836054	Missense_Mutation	SNP	C	T	45	53	c.56G>A	c.(55-57)CGT>CAT	p.R19H
Pat_51	Pre-Treatment	DCAF7	10238	37	17	61661011	61661011	Missense_Mutation	SNP	C	T	35	57	c.676C>T	c.(676-678)CGC>TGC	p.R226C
Pat_51	Pre-Treatment	GH2	2689	37	17	61959155	61959155	Missense_Mutation	SNP	C	T	4	70	c.7G>A	c.(7-9)GCA>ACA	p.A3T
Pat_51	Pre-Treatment	PIP5K1C	23396	37	19	3645974	3645974	Missense_Mutation	SNP	G	A	26	42	c.1343C>T	c.(1342-1344)TCC>TTC	p.S448F
Pat_51	Pre-Treatment	MUC16	94025	37	19	9066157	9066157	Missense_Mutation	SNP	G	A	31	32	c.21289C>T	c.(21289-21291)CCT>TCT	p.P7097S
Pat_51	Pre-Treatment	MUC16	94025	37	19	9072645	9072645	Missense_Mutation	SNP	G	A	54	52	c.14801C>T	c.(14800-14802)TCC>TTC	p.S4934F
Pat_51	Pre-Treatment	PLVAP	83483	37	19	17471613	17471613	Missense_Mutation	SNP	G	A	18	18	c.1208C>T	c.(1207-1209)CCC>CTC	p.P403L
Pat_51	Pre-Treatment	ZNF420	147923	37	19	37619143	37619143	Missense_Mutation	SNP	A	G	32	55	c.1250A>G	c.(1249-1251)AAA>AGA	p.K417R
Pat_51	Pre-Treatment	RASGRP4	115727	37	19	38910865	38910865	Missense_Mutation	SNP	C	T	7	5	c.415G>A	c.(415-417)GAT>AAT	p.D139N

Pat_51	Pre-Treatment	ZNF180	7733	37	19	45004265	45004265	Missense_Mutation	SNP	C	T	80	126	c.28G>A	c.(28-30)GAA>AAA	p.E10K
Pat_51	Pre-Treatment	PTH2	113091	37	19	49926533	49926533	Missense_Mutation	SNP	G	C	3	25	c.64C>G	c.(64-66)CTG>GTG	p.L22V
Pat_51	Pre-Treatment	SIGLEC7	27036	37	19	51649293	51649293	Missense_Mutation	SNP	T	G	43	49	c.942T>G	c.(940-942)GAT>GAG	p.D314E
Pat_51	Pre-Treatment	LILRA2	11027	37	19	55098770	55098770	Missense_Mutation	SNP	C	T	22	40	c.1409C>T	c.(1408-1410)GCT>GTT	p.A470V
Pat_51	Pre-Treatment	ZSCAN4	201516	37	19	58189852	58189852	Missense_Mutation	SNP	G	A	39	45	c.881G>A	c.(880-882)GGA>GAA	p.G294E
Pat_51	Pre-Treatment	ZNF512	84450	37	2	27822870	27822870	Missense_Mutation	SNP	C	T	15	23	c.407C>T	c.(406-408)CCC>CTC	p.P136L
Pat_51	Pre-Treatment	LTBP1	4052	37	2	33447173	33447173	Missense_Mutation	SNP	G	A	25	34	c.1831G>A	c.(1831-1833)GAA>AAA	p.E611K
Pat_51	Pre-Treatment	YSK4	80122	37	2	135738878	135738878	Missense_Mutation	SNP	C	T	41	49	c.3433G>A	c.(3433-3435)GGT>AGT	p.G1145S
Pat_51	Pre-Treatment	NGEF	25791	37	2	233834974	233834974	Missense_Mutation	SNP	C	T	22	35	c.333G>A	c.(331-333)ATG>ATA	p.M111I
Pat_51	Pre-Treatment	ESF1	51575	37	20	13763660	13763660	Missense_Mutation	SNP	G	A	38	34	c.127C>T	c.(127-129)CAT>TAT	p.H43Y
Pat_51	Pre-Treatment	FRG1B	284802	37	20	29625877	29625877	Missense_Mutation	SNP	G	A	3	83	c.31G>A	c.(31-33)GCC>ACC	p.A11T
Pat_51	Pre-Treatment	TFF1	7031	37	21	43783499	43783499	Missense_Mutation	SNP	G	A	20	14	c.103C>T	c.(103-105)CCC>TCC	p.P35S
Pat_51	Pre-Treatment	DAZL	1618	37	3	16640102	16640102	Missense_Mutation	SNP	T	C	3	143	c.7A>G	c.(7-9)ACT>GCT	p.T3A
Pat_51	Pre-Treatment	KIAA2018	205717	37	3	113377321	113377321	Missense_Mutation	SNP	C	A	46	52	c.3208G>T	c.(3208-3210)GAT>TAT	p.D1070Y
Pat_51	Pre-Treatment	TMCC1	23023	37	3	129370592	129370592	Missense_Mutation	SNP	T	A	3	60	c.1694A>T	c.(1693-1695)CAG>CTG	p.Q565L
Pat_51	Pre-Treatment	MED12L	116931	37	3	150911394	150911394	Missense_Mutation	SNP	C	T	27	52	c.2086C>T	c.(2086-2088)CCA>TCA	p.P696S
Pat_51	Pre-Treatment	FAM193A	8603	37	4	2661349	2661349	Missense_Mutation	SNP	C	T	25	39	c.581C>T	c.(580-582)TCG>TTG	p.S194L
Pat_51	Pre-Treatment	CPZ	8532	37	4	8621123	8621123	Missense_Mutation	SNP	A	C	13	27	c.1738A>C	c.(1738-1740)ATT>CTT	p.I580L
Pat_51	Pre-Treatment	UGT2B4	7363	37	4	70360952	70360952	Missense_Mutation	SNP	T	A	20	45	c.628A>T	c.(628-630)AGG>TGG	p.R210W
Pat_51	Pre-Treatment	FNIP2	57600	37	4	159789968	159789968	Missense_Mutation	SNP	C	T	36	65	c.2180C>T	c.(2179-2181)CCA>CTA	p.P727L
Pat_51	Pre-Treatment	NEK1	4750	37	4	170429410	170429410	Missense_Mutation	SNP	G	A	5	10	c.1738C>T	c.(1738-1740)CGT>TGT	p.R580C
Pat_51	Pre-Treatment	C7	730	37	5	40972649	40972649	Missense_Mutation	SNP	G	A	58	92	c.2027G>A	c.(2026-2028)AGC>AAC	p.S676N
Pat_51	Pre-Treatment	SLCO6A1	133482	37	5	101709070	101709070	Missense_Mutation	SNP	C	T	22	27	c.2146G>A	c.(2146-2148)GAA>AAA	p.E716K
Pat_51	Pre-Treatment	SNCAIP	9627	37	5	121786290	121786290	Missense_Mutation	SNP	C	T	96	91	c.1748C>T	c.(1747-1749)TCT>TTT	p.S583F
Pat_51	Pre-Treatment	RBM24	221662	37	6	17283145	17283145	Missense_Mutation	SNP	G	A	20	25	c.278G>A	c.(277-279)AGG>AAG	p.R93K
Pat_51	Pre-Treatment	BAT1	7919	37	6	31504459	31504459	Missense_Mutation	SNP	A	C	6	36	c.434T>G	c.(433-435)GTT>GGT	p.V145G
Pat_51	Pre-Treatment	ZNF318	24149	37	6	43305131	43305131	Missense_Mutation	SNP	G	A	11	21	c.6605C>T	c.(6604-6606)TCC>TTC	p.S2202F
Pat_51	Pre-Treatment	RHAG	6005	37	6	49582513	49582513	Missense_Mutation	SNP	G	A	60	63	c.694C>T	c.(694-696)CCT>TCT	p.P232S
Pat_51	Pre-Treatment	PRSS35	167681	37	6	84233578	84233578	Missense_Mutation	SNP	A	G	47	52	c.418A>G	c.(418-420)ACC>GCC	p.T140A
Pat_51	Pre-Treatment	ESR1	2099	37	6	152201874	152201874	Missense_Mutation	SNP	G	T	22	28	c.728G>T	c.(727-729)CGC>CTC	p.R243L
Pat_51	Pre-Treatment	MAP3K4	4216	37	6	161470424	161470424	Missense_Mutation	SNP	C	G	22	32	c.1120C>G	c.(1120-1122)CTT>GTT	p.L374V
Pat_51	Pre-Treatment	MMD2	221938	37	7	4949648	4949648	Missense_Mutation	SNP	C	T	57	51	c.473G>A	c.(472-474)GGG>GAG	p.G158E
Pat_51	Pre-Treatment	STAG3	10734	37	7	99798578	99798578	Missense_Mutation	SNP	G	A	28	48	c.2047G>A	c.(2047-2049)GAA>AAA	p.E683K
Pat_51	Pre-Treatment	CREB3L2	64764	37	7	137586118	137586118	Missense_Mutation	SNP	A	G	15	15	c.1025T>C	c.(1024-1026)GTT>GCT	p.V342A
Pat_51	Pre-Treatment	BRAF	673	37	7	140453136	140453136	Missense_Mutation	SNP	A	T	25	43	c.1799T>A	c.(1798-1800)GTG>GAG	p.V600E
Pat_51	Pre-Treatment	RP1L1	94137	37	8	10469284	10469284	Missense_Mutation	SNP	G	A	40	27	c.2324C>T	c.(2323-2325)CCC>CTC	p.P775L
Pat_51	Pre-Treatment	RP1	6101	37	8	55537629	55537629	Missense_Mutation	SNP	G	A	16	35	c.1187G>A	c.(1186-1188)CGA>CAA	p.R396Q
Pat_51	Pre-Treatment	SDR16C5	195814	37	8	57218208	57218208	Nonsense_Mutation	SNP	T	A	16	21	c.784A>T	c.(784-786)AAA>TAA	p.K262*
Pat_51	Pre-Treatment	WWP1	11059	37	8	87414307	87414307	Missense_Mutation	SNP	A	G	4	105	c.599A>G	c.(598-600)CAA>CGA	p.Q200R
Pat_51	Pre-Treatment	UBR5	51366	37	8	103335705	103335705	Missense_Mutation	SNP	G	A	8	22	c.1618C>T	c.(1618-1620)CCT>TCT	p.P540S
Pat_51	Pre-Treatment	TMEM2	23670	37	9	74349902	74349902	Missense_Mutation	SNP	G	A	21	41	c.1213C>T	c.(1213-1215)CTT>TTT	p.L405F
Pat_51	Pre-Treatment	FLJ46321	389763	37	9	84606143	84606143	Missense_Mutation	SNP	T	C	180	182	c.758T>C	c.(757-759)ATT>ACT	p.I253T
Pat_51	Pre-Treatment	GRIN3A	116443	37	9	104390553	104390553	Missense_Mutation	SNP	C	T	24	1	c.2483G>A	c.(2482-2484)GGA>GAA	p.G828E
Pat_51	Pre-Treatment	GBGT1	26301	37	9	136029277	136029277	Missense_Mutation	SNP	C	T	32	44	c.731G>A	c.(730-732)AGG>AAG	p.R244K
Pat_51	Pre-Treatment	CACNA1B	774	37	9	141016272	141016272	Missense_Mutation	SNP	G	A	36	35	c.6841G>A	c.(6841-6843)GAG>AAG	p.E2281K
Pat_51	Pre-Treatment	MXRA5	25878	37	X	3239827	3239827	Missense_Mutation	SNP	C	T	37	1	c.3899G>A	c.(3898-3900)AGA>AAA	p.R1300K
Pat_51	Pre-Treatment	CCNB3	85417	37	X	50028219	50028219	Missense_Mutation	SNP	C	T	35	3	c.56C>T	c.(55-57)TCC>TTC	p.S19F

Pat_51	Pre-Treatment	NXF3	56000	37	X	102334770	102334770	Nonsense_Mutation	SNP	G	A	51	4	c.1081C>T	c.(1081-1083)CGA>TGA	p.R361*
Pat_53	Pre-Treatment	UBR4	23352	37	1	19403389	19403389	Missense_Mutation	SNP	G	A	16	132	c.15332C>T	c.(15331-15333)CCT>CTT	p.P5111L
Pat_53	Pre-Treatment	KIF17	57576	37	1	20996934	20996934	Missense_Mutation	SNP	C	T	18	199	c.2773G>A	c.(2773-2775)GAC>AAC	p.D925N
Pat_53	Pre-Treatment	NBPF9	400818	37	1	144220807	144220807	Missense_Mutation	SNP	A	C	57	521	c.2180A>C	c.(2179-2181)GAT>GCT	p.D727A
Pat_53	Pre-Treatment	RFX5	5993	37	1	151315152	151315152	Missense_Mutation	SNP	T	C	79	736	c.1361A>G	c.(1360-1362)GAT>GGT	p.D454G
Pat_53	Pre-Treatment	TCHH	7062	37	1	152082304	152082304	Missense_Mutation	SNP	T	G	6	251	c.3389A>C	c.(3388-3390)AAG>ACG	p.K1130T
Pat_53	Pre-Treatment	FLG2	388698	37	1	152326043	152326043	Nonsense_Mutation	SNP	C	A	7	454	c.4219G>T	c.(4219-4221)GGA>TGA	p.G1407*
Pat_53	Pre-Treatment	CRNN	49860	37	1	152382519	152382519	Missense_Mutation	SNP	T	C	5	314	c.1039A>G	c.(1039-1041)ACT>GCT	p.T347A
Pat_53	Pre-Treatment	KLHDC8A	55220	37	1	205312401	205312401	Missense_Mutation	SNP	C	T	6	323	c.332G>A	c.(331-333)AGC>AAC	p.S111N
Pat_53	Pre-Treatment	OR2M5	127059	37	1	248308943	248308943	Missense_Mutation	SNP	C	T	51	675	c.494C>T	c.(493-495)TCC>TTC	p.S165F
Pat_53	Pre-Treatment	C10orf10	11067	37	10	45472884	45472884	Missense_Mutation	SNP	G	A	4	165	c.595C>T	c.(595-597)CTC>TTC	p.L199F
Pat_53	Pre-Treatment	ADAM12	8038	37	10	127724774	127724774	Missense_Mutation	SNP	G	A	4	88	c.2479C>T	c.(2479-2481)CGT>TGT	p.R827C
Pat_53	Pre-Treatment	MUC5B	727897	37	11	1272638	1272639	Missense_Mutation	DNP	GG	AA	45	231	15494_15495GG>	c.(15493-15495)GGG>GA	p.G5165E
Pat_53	Pre-Treatment	KRTAP5-4	387267	37	11	1642989	1642989	Missense_Mutation	SNP	C	A	20	135	c.473G>T	c.(472-474)GGC>GTC	p.G158V
Pat_53	Pre-Treatment	NAV2	89797	37	11	20122579	20122579	Missense_Mutation	SNP	G	A	6	340	c.6287G>A	c.(6286-6288)CGG>CAG	p.R2096Q
Pat_53	Pre-Treatment	MPEG1	219972	37	11	58980051	58980051	Missense_Mutation	SNP	C	T	43	286	c.288G>A	c.(286-288)ATG>ATA	p.M96I
Pat_53	Pre-Treatment	FADS1	3992	37	11	61580759	61580759	Nonsense_Mutation	SNP	C	A	7	482	c.442G>T	c.(442-444)GGA>TGA	p.G148*
Pat_53	Pre-Treatment	AHNAK	79026	37	11	62296070	62296070	Missense_Mutation	SNP	A	G	9	787	c.5819T>C	c.(5818-5820)GTG>GCG	p.V1940A
Pat_53	Pre-Treatment	RARRES3	5920	37	11	63312329	63312329	Missense_Mutation	SNP	C	A	8	649	c.355C>A	c.(355-357)CAG>AAG	p.Q119K
Pat_53	Pre-Treatment	PRB2	653247	37	12	11546150	11546150	Missense_Mutation	SNP	G	C	8	402	c.862C>G	c.(862-864)CCA>GCA	p.P288A
Pat_53	Pre-Treatment	GJB6	10804	37	13	20797589	20797589	Missense_Mutation	SNP	C	A	6	471	c.31G>T	c.(31-33)GGG>TGG	p.G11W
Pat_53	Pre-Treatment	PABPC3	5042	37	13	25670736	25670736	Missense_Mutation	SNP	G	A	47	436	c.400G>A	c.(400-402)GAA>AAA	p.E134K
Pat_53	Pre-Treatment	LOC220429	220429	37	13	50466749	50466749	Missense_Mutation	SNP	C	G	6	677	c.2023C>G	c.(2023-2025)CCT>GCT	p.P675A
Pat_53	Pre-Treatment	TSSK4	283629	37	14	24675730	24675730	Missense_Mutation	SNP	C	T	6	228	c.241C>T	c.(241-243)CGG>TGG	p.R81W
Pat_53	Pre-Treatment	SRP54	6729	37	14	35465931	35465931	Missense_Mutation	SNP	C	T	29	420	c.16C>T	c.(16-18)CTT>TTT	p.L6F
Pat_53	Pre-Treatment	AHNAK2	113146	37	14	105413888	105413888	Missense_Mutation	SNP	G	T	7	481	c.7900C>A	c.(7900-7902)CTG>ATG	p.L2634M
Pat_53	Pre-Treatment	ADAM6	8755	37	14	106993798	106993798	Splice_Site	SNP	C	T	23	609	c.8648_splice	c.e187+1	
Pat_53	Pre-Treatment	OR4N3P	390539	37	15	22413810	22413810	Missense_Mutation	SNP	G	C	6	297	c.109G>C	c.(109-111)GTG>CTG	p.V37L
Pat_53	Pre-Treatment	CYP1A2	1544	37	15	75042102	75042102	Missense_Mutation	SNP	C	T	78	368	c.23C>T	c.(22-24)CCC>CTC	p.P8L
Pat_53	Pre-Treatment	CHRNB4	1143	37	15	78921974	78921974	Missense_Mutation	SNP	C	T	29	136	c.673G>A	c.(673-675)GAC>AAC	p.D225N
Pat_53	Pre-Treatment	ZNF267	10308	37	16	31927522	31927522	Missense_Mutation	SNP	A	G	7	375	c.1952A>G	c.(1951-1953)CAG>CGG	p.Q651R
Pat_53	Pre-Treatment	NOD2	64127	37	16	50733419	50733419	Missense_Mutation	SNP	G	A	100	589	c.94G>A	c.(94-96)GAG>AAG	p.E32K
Pat_53	Pre-Treatment	KRTAP9-8	83901	37	17	39394482	39394482	Missense_Mutation	SNP	T	C	7	174	c.179T>C	c.(178-180)ATC>ACC	p.I60T
Pat_53	Pre-Treatment	STAT5B	6777	37	17	40370266	40370266	Missense_Mutation	SNP	C	T	6	211	c.1072G>A	c.(1072-1074)GGG>AGG	p.G358R
Pat_53	Pre-Treatment	GOSR2	9570	37	17	45009435	45009435	Missense_Mutation	SNP	G	T	6	474	c.206G>T	c.(205-207)CGG>CTG	p.R69L
Pat_53	Pre-Treatment	ZNF700	90592	37	19	12060571	12060571	Missense_Mutation	SNP	C	A	8	673	c.1732C>A	c.(1732-1734)CAC>AAC	p.H578N
Pat_53	Pre-Treatment	ZNF844	284391	37	19	12187443	12187443	Missense_Mutation	SNP	C	G	8	378	c.1508C>G	c.(1507-1509)CCT>CGT	p.P503R
Pat_53	Pre-Treatment	ZNF563	147837	37	19	12429554	12429554	Missense_Mutation	SNP	C	T	9	548	c.1285G>A	c.(1285-1287)GCG>ACG	p.A429T
Pat_53	Pre-Treatment	ZNF563	147837	37	19	12429722	12429722	Missense_Mutation	SNP	T	C	11	619	c.1117A>G	c.(1117-1119)ACG>GCG	p.T373A
Pat_53	Pre-Treatment	ZNF443	10224	37	19	12542283	12542283	Missense_Mutation	SNP	A	G	7	585	c.703T>C	c.(703-705)TCT>CCT	p.S235P
Pat_53	Pre-Treatment	ZNF564	163050	37	19	12637723	12637723	Missense_Mutation	SNP	C	T	9	535	c.1199G>A	c.(1198-1200)AGA>AAA	p.R400K
Pat_53	Pre-Treatment	ZNF93	81931	37	19	20045196	20045196	Missense_Mutation	SNP	G	A	7	582	c.1432G>A	c.(1432-1434)GAG>AAG	p.E478K
Pat_53	Pre-Treatment	PRX	57716	37	19	40902620	40902620	Missense_Mutation	SNP	G	C	9	404	c.1639C>G	c.(1639-1641)CAG>GAG	p.Q547E
Pat_53	Pre-Treatment	ZNF28	7576	37	19	53302985	53302985	Missense_Mutation	SNP	T	A	7	653	c.2113A>T	c.(2113-2115)AAC>TAC	p.N705Y
Pat_53	Pre-Treatment	ZNF816A	125893	37	19	53453890	53453890	Missense_Mutation	SNP	G	C	8	744	c.1138C>G	c.(1138-1140)CAG>GAG	p.Q380E
Pat_53	Pre-Treatment	ZNF845	91664	37	19	53855197	53855197	Missense_Mutation	SNP	G	A	11	647	c.1269G>A	c.(1267-1269)ATG>ATA	p.M423I
Pat_53	Pre-Treatment	ZNF761	388561	37	19	53959137	53959137	Missense_Mutation	SNP	G	T	5	350	c.1376G>T	c.(1375-1377)CGT>CTT	p.R459L

Pat_53	Pre-Treatment	FLJ40330	645784	37	2	89084114	89084114	Splice_Site	SNP	G	A	17	368	c.471_splice	c.e5-1	
Pat_53	Pre-Treatment	LRP2	4036	37	2	170065986	170065986	Missense_Mutation	SNP	C	T	6	448	c.6446G>A	c.(6445-6447)GGT>GAT	p.G2149D
Pat_53	Pre-Treatment	FRG1B	284802	37	20	29628251	29628251	Missense_Mutation	SNP	A	G	33	507	c.163A>G	c.(163-165)AAT>GAT	p.N55D
Pat_53	Pre-Treatment	FRG1B	284802	37	20	29628278	29628278	Missense_Mutation	SNP	G	A	8	390	c.190G>A	c.(190-192)GCA>ACA	p.A64T
Pat_53	Pre-Treatment	FRG1B	284802	37	20	29628299	29628300	Missense_Mutation	DNP	AG	GA	6	279	c.211_212AG>GA	c.(211-213)AGT>GAT	p.S71D
Pat_53	Pre-Treatment	CRYZL1	9946	37	21	34963478	34963478	Missense_Mutation	SNP	C	A	6	446	c.940G>T	c.(940-942)GGT>TGT	p.G314C
Pat_53	Pre-Treatment	ADORA2A	135	37	22	24836601	24836601	Missense_Mutation	SNP	G	T	6	422	c.383G>T	c.(382-384)TGC>TTC	p.C128F
Pat_53	Pre-Treatment	NEFH	4744	37	22	29885739	29885739	Missense_Mutation	SNP	T	A	8	351	c.2110T>A	c.(2110-2112)TCC>ACC	p.S704T
Pat_53	Pre-Treatment	TRIOBP	11078	37	22	38122252	38122252	Missense_Mutation	SNP	C	A	5	200	c.3689C>A	c.(3688-3690)CCC>CAC	p.P1230H
Pat_53	Pre-Treatment	LHFPL4	375323	37	3	9547827	9547827	Missense_Mutation	SNP	C	T	4	146	c.467G>A	c.(466-468)CGG>CAG	p.R156Q
Pat_53	Pre-Treatment	CELSR3	1951	37	3	48677168	48677168	Missense_Mutation	SNP	C	A	6	176	c.9850G>T	c.(9850-9852)GGG>TGG	p.G3284W
Pat_53	Pre-Treatment	ACOX2	8309	37	3	58516196	58516196	Missense_Mutation	SNP	G	A	25	130	c.989C>T	c.(988-990)CCC>CTC	p.P330L
Pat_53	Pre-Treatment	CLSTN2	64084	37	3	140275377	140275377	Missense_Mutation	SNP	C	T	36	434	c.1697C>T	c.(1696-1698)TCC>TTC	p.S566F
Pat_53	Pre-Treatment	ZNF141	7700	37	4	367194	367194	Missense_Mutation	SNP	C	T	8	534	c.968C>T	c.(967-969)TCC>TTC	p.S323F
Pat_53	Pre-Treatment	ZNF721	170960	37	4	435639	435639	Missense_Mutation	SNP	T	C	5	290	c.2617A>G	c.(2617-2619)ACC>GCC	p.T873A
Pat_53	Pre-Treatment	MAB21L2	10586	37	4	151504675	151504675	Missense_Mutation	SNP	G	A	6	263	c.494G>A	c.(493-495)CGC>CAC	p.R165H
Pat_53	Pre-Treatment	SPEF2	79925	37	5	35792480	35792480	Missense_Mutation	SNP	G	A	6	345	c.4486G>A	c.(4486-4488)GAT>AAT	p.D1496N
Pat_53	Pre-Treatment	ANKHD1-EIF4EBP	404734	37	5	139887525	139887525	Missense_Mutation	SNP	G	A	6	252	c.3707G>A	c.(3706-3708)CGA>CAA	p.R1236Q
Pat_53	Pre-Treatment	STK10	6793	37	5	171523561	171523561	Missense_Mutation	SNP	G	A	57	344	c.874C>T	c.(874-876)CCC>TCC	p.P292S
Pat_53	Pre-Treatment	FLT4	2324	37	5	180057000	180057000	Missense_Mutation	SNP	C	T	7	88	c.619G>A	c.(619-621)GAG>AAG	p.E207K
Pat_53	Pre-Treatment	MDC1	9656	37	6	30673208	30673208	Missense_Mutation	SNP	T	C	7	541	c.3752A>G	c.(3751-3753)CAG>CGG	p.Q1251R
Pat_53	Pre-Treatment	BCLAF1	9774	37	6	136597052	136597052	Missense_Mutation	SNP	C	T	60	639	c.1611G>A	c.(1609-1611)ATG>ATA	p.M537I
Pat_53	Pre-Treatment	HECW1	23072	37	7	43477632	43477632	Missense_Mutation	SNP	G	A	7	480	c.832G>A	c.(832-834)GTG>ATG	p.V278M
Pat_53	Pre-Treatment	ZNF479	90827	37	7	57187809	57187809	Missense_Mutation	SNP	T	G	10	228	c.1313A>C	c.(1312-1314)AAA>ACA	p.K438T
Pat_53	Pre-Treatment	SMURF1	57154	37	7	98652449	98652449	Missense_Mutation	SNP	G	A	6	388	c.443C>T	c.(442-444)TCG>TTG	p.S148L
Pat_53	Pre-Treatment	FBXO24	26261	37	7	100187616	100187616	Missense_Mutation	SNP	C	T	38	150	c.56C>T	c.(55-57)CCT>CTT	p.P19L
Pat_53	Pre-Treatment	ZAN	7455	37	7	100350361	100350361	Missense_Mutation	SNP	T	C	7	577	c.2633T>C	c.(2632-2634)CTC>CCC	p.L878P
Pat_53	Pre-Treatment	MUC17	140453	37	7	100682094	100682094	Missense_Mutation	SNP	C	T	10	884	c.7397C>T	c.(7396-7398)ACG>ATG	p.T2466M
Pat_53	Pre-Treatment	MUC17	140453	37	7	100682156	100682156	Missense_Mutation	SNP	A	G	10	866	c.7459A>G	c.(7459-7461)ATG>GTG	p.M2487V
Pat_53	Pre-Treatment	MUC17	140453	37	7	100682158	100682158	Missense_Mutation	SNP	G	C	9	868	c.7461G>C	c.(7459-7461)ATG>ATC	p.M2487I
Pat_53	Pre-Treatment	CPA1	1357	37	7	130027693	130027693	Nonsense_Mutation	SNP	G	A	153	672	c.1101G>A	c.(1099-1101)TGG>TGA	p.W367*
Pat_53	Pre-Treatment	TRIM24	8805	37	7	138252271	138252271	Missense_Mutation	SNP	C	T	70	411	c.1576C>T	c.(1576-1578)CCC>TCC	p.P526S
Pat_53	Pre-Treatment	MTMR7	9108	37	8	17157633	17157633	Missense_Mutation	SNP	C	T	6	483	c.1721G>A	c.(1720-1722)AGC>AAC	p.S574N
Pat_53	Pre-Treatment	IFNA14	3448	37	9	21239652	21239652	Missense_Mutation	SNP	T	C	6	232	c.283A>G	c.(283-285)AAC>GAC	p.N95D
Pat_53	Pre-Treatment	LOC442421	442421	37	9	66499794	66499795	Missense_Mutation	DNP	CG	TA	8	168	c.604_605CG>TA	c.(604-606)CGC>TAC	p.R202Y
Pat_53	Pre-Treatment	TMC1	117531	37	9	75407222	75407222	Missense_Mutation	SNP	C	A	7	593	c.1520C>A	c.(1519-1521)CCT>CAT	p.P507H
Pat_53	Pre-Treatment	FRMPD4	9758	37	X	12632978	12632978	Missense_Mutation	SNP	G	A	61	73	c.400G>A	c.(400-402)GAG>AAG	p.E134K
Pat_53	Post-Resistance	NADK	65220	37	1	1688735	1688735	Missense_Mutation	SNP	G	A	4	225	c.278C>T	c.(277-279)CCC>CTC	p.P93L
Pat_53	Post-Resistance	RERE	473	37	1	8716366	8716366	Translation_Start_Site	SNP	C	T	6	532	c.-9G>A	c.(-11--7)ACGTG>ACATG	
Pat_53	Post-Resistance	PRDM2	7799	37	1	14106496	14106496	Missense_Mutation	SNP	C	T	4	179	c.2206C>T	c.(2206-2208)CGG>TGG	p.R736W
Pat_53	Post-Resistance	PRDM2	7799	37	1	14107241	14107241	Missense_Mutation	SNP	C	T	4	158	c.2951C>T	c.(2950-2952)ACT>ATT	p.T984I
Pat_53	Post-Resistance	PRDM2	7799	37	1	14108153	14108153	Missense_Mutation	SNP	G	A	5	233	c.3863G>A	c.(3862-3864)CGA>CAA	p.R1288Q
Pat_53	Post-Resistance	ZBTB17	7709	37	1	16269655	16269655	Missense_Mutation	SNP	G	A	4	183	c.1732C>T	c.(1732-1734)CGC>TGC	p.R578C
Pat_53	Post-Resistance	UBR4	23352	37	1	19403389	19403389	Missense_Mutation	SNP	G	A	26	87	c.15332C>T	c.(15331-15333)CCT>CTT	p.P5111L
Pat_53	Post-Resistance	KIF17	57576	37	1	20996934	20996934	Missense_Mutation	SNP	C	T	40	105	c.2773G>A	c.(2773-2775)GAC>AAC	p.D925N
Pat_53	Post-Resistance	EPHB2	2048	37	1	23234492	23234492	Missense_Mutation	SNP	G	A	4	262	c.2183G>A	c.(2182-2184)CGG>CAG	p.R728Q
Pat_53	Post-Resistance	HMGCL	3155	37	1	24140679	24140679	Splice_Site	SNP	C	T	4	166	c.497_splice	c.e5+1	p.G166_splice

Pat_53	Post-Resistance	AHDC1	27245	37	1	27878176	27878176	Nonsense_Mutation	SNP	G	A	4	144	c.451C>T	c.(451-453)CGA>TGA	p.R151*
Pat_53	Post-Resistance	SESN2	83667	37	1	28599131	28599131	Missense_Mutation	SNP	G	A	4	210	c.577G>A	c.(577-579)GAG>AAG	p.E193K
Pat_53	Post-Resistance	RRAGC	64121	37	1	39321428	39321428	Missense_Mutation	SNP	C	T	4	313	c.593G>A	c.(592-594)AGG>AAG	p.R198K
Pat_53	Post-Resistance	MACF1	23499	37	1	39929341	39929341	Missense_Mutation	SNP	G	A	4	192	c.17065G>A	c.(17065-17067)GGA>AG	p.G5689R
Pat_53	Post-Resistance	HEYL	26508	37	1	40095904	40095904	Missense_Mutation	SNP	C	T	4	171	c.308G>A	c.(307-309)GGG>GAG	p.G103E
Pat_53	Post-Resistance	STIL	6491	37	1	47746263	47746263	Missense_Mutation	SNP	C	T	5	369	c.1867G>A	c.(1867-1869)GCA>ACA	p.A623T
Pat_53	Post-Resistance	SPATA6	54558	37	1	48865097	48865097	Missense_Mutation	SNP	G	A	5	246	c.706C>T	c.(706-708)CGG>TGG	p.R236W
Pat_53	Post-Resistance	ACADM	34	37	1	76190498	76190498	Missense_Mutation	SNP	G	A	4	144	c.26G>A	c.(25-27)TGC>TAC	p.C9Y
Pat_53	Post-Resistance	DNAJB4	11080	37	1	78479056	78479056	Missense_Mutation	SNP	G	A	4	195	c.533G>A	c.(532-534)CGG>CAG	p.R178Q
Pat_53	Post-Resistance	ZNF326	284695	37	1	90470571	90470571	Missense_Mutation	SNP	G	A	4	291	c.71G>A	c.(70-72)CGT>CAT	p.R24H
Pat_53	Post-Resistance	VCAM1	7412	37	1	101198204	101198204	Missense_Mutation	SNP	G	A	5	356	c.1756G>A	c.(1756-1758)GGA>AGA	p.G586R
Pat_53	Post-Resistance	AMIGO1	57463	37	1	110050069	110050069	Missense_Mutation	SNP	G	A	4	207	c.1466C>T	c.(1465-1467)ACG>ATG	p.T489M
Pat_53	Post-Resistance	KCND3	3752	37	1	112319846	112319846	Missense_Mutation	SNP	C	T	4	139	c.1568G>A	c.(1567-1569)AGT>AAT	p.S523N
Pat_53	Post-Resistance	MAGI3	260425	37	1	114184609	114184609	Missense_Mutation	SNP	G	T	4	144	c.1437G>T	c.(1435-1437)TTG>TTT	p.L479F
Pat_53	Post-Resistance	AMPD1	270	37	1	115220030	115220030	Missense_Mutation	SNP	C	A	4	82	c.1330G>T	c.(1330-1332)GTC>TTC	p.V444F
Pat_53	Post-Resistance	NBPF9	400818	37	1	144220807	144220807	Missense_Mutation	SNP	A	C	106	438	c.2180A>C	c.(2179-2181)GAT>GCT	p.D727A
Pat_53	Post-Resistance	NBPF9	400818	37	1	144220816	144220816	Missense_Mutation	SNP	A	G	5	515	c.2189A>G	c.(2188-2190)GAG>GGG	p.E730G
Pat_53	Post-Resistance	NBPF10	100132406	37	1	145299808	145299808	Missense_Mutation	SNP	T	C	25	365	c.857T>C	c.(856-858)ATG>ACG	p.M286T
Pat_53	Post-Resistance	NBPF10	100132406	37	1	145311932	145311932	Missense_Mutation	SNP	G	A	4	249	c.2000G>A	c.(1999-2001)CGT>CAT	p.R667H
Pat_53	Post-Resistance	BCL9	607	37	1	147086304	147086304	Missense_Mutation	SNP	C	T	4	172	c.449C>T	c.(448-450)GCC>GTC	p.A150V
Pat_53	Post-Resistance	NBPF14	25832	37	1	148008610	148008610	Missense_Mutation	SNP	G	T	8	448	c.1978C>A	c.(1978-1980)CAA>AAA	p.Q660K
Pat_53	Post-Resistance	ANP32E	81611	37	1	150193030	150193030	Missense_Mutation	SNP	C	T	5	558	c.770G>A	c.(769-771)CGA>CAA	p.R257Q
Pat_53	Post-Resistance	C1orf51	148523	37	1	150255844	150255844	Missense_Mutation	SNP	G	A	4	316	c.167G>A	c.(166-168)CGG>CAG	p.R56Q
Pat_53	Post-Resistance	RFX5	5993	37	1	151315152	151315152	Missense_Mutation	SNP	T	C	112	506	c.1361A>G	c.(1360-1362)GAT>GGT	p.D454G
Pat_53	Post-Resistance	POGZ	23126	37	1	151403146	151403146	Missense_Mutation	SNP	G	A	9	679	c.455C>T	c.(454-456)ACG>ATG	p.T152M
Pat_53	Post-Resistance	IL6R	3570	37	1	154437810	154437810	Missense_Mutation	SNP	G	A	4	205	c.1361G>A	c.(1360-1362)CGG>CAG	p.R454Q
Pat_53	Post-Resistance	ADAR	103	37	1	154574328	154574328	Missense_Mutation	SNP	T	C	4	230	c.790A>G	c.(790-792)AGT>GGT	p.S264G
Pat_53	Post-Resistance	SHC1	6464	37	1	154940681	154940681	Missense_Mutation	SNP	G	A	7	760	c.803C>T	c.(802-804)CCG>CTG	p.P268L
Pat_53	Post-Resistance	SEMA4A	64218	37	1	156128201	156128201	Missense_Mutation	SNP	G	A	5	406	c.386G>A	c.(385-387)CGT>CAT	p.R129H
Pat_53	Post-Resistance	CCT3	7203	37	1	156303425	156303425	Nonsense_Mutation	SNP	G	A	4	202	c.217C>T	c.(217-219)CAG>TAG	p.Q73*
Pat_53	Post-Resistance	IQGAP3	128239	37	1	156534434	156534434	Missense_Mutation	SNP	C	T	4	251	c.410G>A	c.(409-411)CGG>CAG	p.R137Q
Pat_53	Post-Resistance	DCAF8	50717	37	1	160209573	160209573	Missense_Mutation	SNP	C	T	4	134	c.637G>A	c.(637-639)GAT>AAT	p.D213N
Pat_53	Post-Resistance	DUSP12	11266	37	1	161722902	161722902	Missense_Mutation	SNP	C	T	4	305	c.712C>T	c.(712-714)CGT>TGT	p.R238C
Pat_53	Post-Resistance	KLHL20	27252	37	1	173726157	173726157	Missense_Mutation	SNP	G	A	4	187	c.1010G>A	c.(1009-1011)CGA>CAA	p.R337Q
Pat_53	Post-Resistance	TNR	7143	37	1	175332855	175332855	Missense_Mutation	SNP	C	T	4	118	c.2696G>A	c.(2695-2697)CGA>CAA	p.R899Q
Pat_53	Post-Resistance	PRG4	10216	37	1	186276044	186276044	Missense_Mutation	SNP	C	A	4	158	c.1193C>A	c.(1192-1194)CCC>CAC	p.P398H
Pat_53	Post-Resistance	TNNI1	7135	37	1	201382215	201382215	Missense_Mutation	SNP	A	G	4	409	c.224T>C	c.(223-225)GTG>GCG	p.V75A
Pat_53	Post-Resistance	RNPEP	6051	37	1	201970811	201970811	Nonsense_Mutation	SNP	C	T	4	242	c.1342C>T	c.(1342-1344)CGA>TGA	p.R448*
Pat_53	Post-Resistance	ELK4	2005	37	1	205589339	205589339	Missense_Mutation	SNP	C	T	5	311	c.835G>A	c.(835-837)GAC>AAC	p.D279N
Pat_53	Post-Resistance	TP53BP2	7159	37	1	223989835	223989835	Missense_Mutation	SNP	G	A	4	161	c.1208C>T	c.(1207-1209)GCT>GTT	p.A403V
Pat_53	Post-Resistance	WDR64	128025	37	1	241958569	241958569	Missense_Mutation	SNP	G	A	4	235	c.1687G>A	c.(1687-1689)GGC>AGC	p.G563S
Pat_53	Post-Resistance	OR2M5	127059	37	1	248308943	248308943	Missense_Mutation	SNP	C	T	44	362	c.494C>T	c.(493-495)TCC>TTC	p.S165F
Pat_53	Post-Resistance	PFKP	5214	37	10	3175465	3175465	Missense_Mutation	SNP	G	A	4	253	c.1981G>A	c.(1981-1983)GTG>ATG	p.V661M
Pat_53	Post-Resistance	ATP5C1	509	37	10	7844778	7844778	Missense_Mutation	SNP	C	A	4	205	c.851C>A	c.(850-852)ACA>AAA	p.T284K
Pat_53	Post-Resistance	BMI1	648	37	10	22615385	22615385	Nonsense_Mutation	SNP	C	T	4	255	c.7C>T	c.(7-9)CGA>TGA	p.R3*
Pat_53	Post-Resistance	SVIL	6840	37	10	29813424	29813424	Missense_Mutation	SNP	C	T	4	177	c.2563G>A	c.(2563-2565)GTC>ATC	p.V855I
Pat_53	Post-Resistance	EPC1	80314	37	10	32573670	32573670	Missense_Mutation	SNP	C	T	4	142	c.1700G>A	c.(1699-1701)AGT>AAT	p.S567N

Pat_53	Post-Resistance	ITGB1	3688	37	10	33200813	33200813	Splice_Site	SNP	C	T	4	247	c.1708_splice	c.e12+1	p.G570_splice
Pat_53	Post-Resistance	TTC18	118491	37	10	75051010	75051010	Missense_Mutation	SNP	G	A	4	120	c.2423C>T	c.(2422-2424)ACA>ATA	p.T808I
Pat_53	Post-Resistance	ZMIZ1	57178	37	10	81061895	81061895	Missense_Mutation	SNP	G	A	4	252	c.2051G>A	c.(2050-2052)CGG>CAG	p.R684Q
Pat_53	Post-Resistance	AGAP11	119385	37	10	88761494	88761494	Splice_Site	SNP	G	A	4	150	c.14_splice	c.e9+1	p.S5_splice
Pat_53	Post-Resistance	PI4K2A	55361	37	10	99433423	99433423	Missense_Mutation	SNP	G	A	5	265	c.1364G>A	c.(1363-1365)CGT>CAT	p.R455H
Pat_53	Post-Resistance	ABLIM1	3983	37	10	116247739	116247739	Missense_Mutation	SNP	G	A	5	351	c.1019C>T	c.(1018-1020)ACG>ATG	p.T340M
Pat_53	Post-Resistance	ABLIM1	3983	37	10	116331094	116331094	Missense_Mutation	SNP	G	A	4	85	c.635C>T	c.(634-636)CCG>CTG	p.P212L
Pat_53	Post-Resistance	MKI67	4288	37	10	129905132	129905132	Missense_Mutation	SNP	C	T	4	256	c.4972G>A	c.(4972-4974)GAG>AAG	p.E1658K
Pat_53	Post-Resistance	ATHL1	80162	37	11	294633	294633	Missense_Mutation	SNP	G	A	6	284	c.2098G>A	c.(2098-2100)GAG>AAG	p.E700K
Pat_53	Post-Resistance	SLC25A22	79751	37	11	792330	792330	Missense_Mutation	SNP	G	A	4	138	c.716C>T	c.(715-717)GCC>GTC	p.A239V
Pat_53	Post-Resistance	MUC6	4588	37	11	1017592	1017592	Nonsense_Mutation	SNP	G	A	6	538	c.5209C>T	c.(5209-5211)CGA>TGA	p.R1737*
Pat_53	Post-Resistance	MUC5B	727897	37	11	1264181	1264181	Missense_Mutation	SNP	C	T	4	192	c.8150C>T	c.(8149-8151)ACC>ATC	p.T2717I
Pat_53	Post-Resistance	MUC5B	727897	37	11	1272638	1272639	Missense_Mutation	DNP	GG	AA	25	117	15494_15495GG>	c.(15493-15495)GGG>GA	p.G5165E
Pat_53	Post-Resistance	KRTAP5-4	387267	37	11	1642989	1642989	Missense_Mutation	SNP	C	A	50	157	c.473G>T	c.(472-474)GGC>GTC	p.G158V
Pat_53	Post-Resistance	TRIM5	85363	37	11	5686299	5686299	Missense_Mutation	SNP	C	T	4	242	c.1222G>A	c.(1222-1224)GTT>ATT	p.V408I
Pat_53	Post-Resistance	ARFGAP2	84364	37	11	47192980	47192980	Missense_Mutation	SNP	C	T	4	230	c.938G>A	c.(937-939)CGA>CAA	p.R313Q
Pat_53	Post-Resistance	OR8H3	390152	37	11	55890222	55890222	Missense_Mutation	SNP	C	T	4	170	c.374C>T	c.(373-375)GCG>GTG	p.A125V
Pat_53	Post-Resistance	OR5M10	390167	37	11	56344321	56344321	Missense_Mutation	SNP	G	A	5	304	c.877C>T	c.(877-879)CGG>TGG	p.R293W
Pat_53	Post-Resistance	ZDHHC5	25921	37	11	57456099	57456099	Nonsense_Mutation	SNP	C	T	4	146	c.346C>T	c.(346-348)CGA>TGA	p.R116*
Pat_53	Post-Resistance	MPEG1	219972	37	11	58980051	58980051	Missense_Mutation	SNP	C	T	46	144	c.288G>A	c.(286-288)ATG>ATA	p.M96I
Pat_53	Post-Resistance	OR4D10	390197	37	11	59245656	59245656	Missense_Mutation	SNP	G	A	4	230	c.754G>A	c.(754-756)GTG>ATG	p.V252M
Pat_53	Post-Resistance	SF1	7536	37	11	64534431	64534431	Missense_Mutation	SNP	G	A	4	199	c.1523C>T	c.(1522-1524)CCG>CTG	p.P508L
Pat_53	Post-Resistance	MEN1	4221	37	11	64575113	64575113	Missense_Mutation	SNP	G	A	4	179	c.709C>T	c.(709-711)CGC>TGC	p.R237C
Pat_53	Post-Resistance	POLA2	23649	37	11	65048467	65048467	Missense_Mutation	SNP	C	T	4	147	c.749C>T	c.(748-750)CCT>CTT	p.P250L
Pat_53	Post-Resistance	RBM4B	83759	37	11	66444243	66444243	Missense_Mutation	SNP	G	A	5	467	c.308C>T	c.(307-309)CCG>CTG	p.P103L
Pat_53	Post-Resistance	PPFIA1	8500	37	11	70221060	70221060	Nonsense_Mutation	SNP	G	A	4	118	c.3176G>A	c.(3175-3177)TGG>TAG	p.W1059*
Pat_53	Post-Resistance	ATG16L2	89849	37	11	72539448	72539448	Missense_Mutation	SNP	C	T	6	159	c.1517C>T	c.(1516-1518)ACC>ATC	p.T506I
Pat_53	Post-Resistance	HINFP	25988	37	11	119003254	119003254	Missense_Mutation	SNP	G	A	4	107	c.725G>A	c.(724-726)CGG>CAG	p.R242Q
Pat_53	Post-Resistance	RNF26	79102	37	11	119206068	119206068	Missense_Mutation	SNP	G	A	4	206	c.236G>A	c.(235-237)GGC>GAC	p.G79D
Pat_53	Post-Resistance	STT3A	3703	37	11	125476253	125476253	Missense_Mutation	SNP	G	A	4	222	c.673G>A	c.(673-675)GTG>ATG	p.V225M
Pat_53	Post-Resistance	ST3GAL4	6484	37	11	126277530	126277530	Splice_Site	SNP	G	A	7	261	c.341_splice	c.e6+1	p.S114_splice
Pat_53	Post-Resistance	USP5	8078	37	12	6965951	6965951	Missense_Mutation	SNP	G	A	4	190	c.665G>A	c.(664-666)CGC>CAC	p.R222H
Pat_53	Post-Resistance	USP5	8078	37	12	6973901	6973901	Missense_Mutation	SNP	C	T	4	154	c.2260C>T	c.(2260-2262)CGG>TGG	p.R754W
Pat_53	Post-Resistance	C3AR1	719	37	12	8212381	8212381	Missense_Mutation	SNP	C	T	4	115	c.401G>A	c.(400-402)CGC>CAC	p.R134H
Pat_53	Post-Resistance	PRB2	653247	37	12	11546150	11546150	Missense_Mutation	SNP	G	C	8	207	c.862C>G	c.(862-864)CCA>GCA	p.P288A
Pat_53	Post-Resistance	PPFIBP1	8496	37	12	27832514	27832514	Missense_Mutation	SNP	C	T	5	347	c.1726C>T	c.(1726-1728)CCG>TCG	p.P576S
Pat_53	Post-Resistance	IPO8	10526	37	12	30792654	30792654	Missense_Mutation	SNP	C	T	4	144	c.2284G>A	c.(2284-2286)GTT>ATT	p.V762I
Pat_53	Post-Resistance	PPHLN1	51535	37	12	42836505	42836505	Missense_Mutation	SNP	G	A	5	428	c.1087G>A	c.(1087-1089)GGA>AGA	p.G363R
Pat_53	Post-Resistance	SLC4A8	9498	37	12	51856106	51856106	Missense_Mutation	SNP	G	A	6	169	c.1114G>A	c.(1114-1116)GTA>ATA	p.V372I
Pat_53	Post-Resistance	AAAS	8086	37	12	53702572	53702572	Nonsense_Mutation	SNP	G	A	4	308	c.1024C>T	c.(1024-1026)CGA>TGA	p.R342*
Pat_53	Post-Resistance	HNRNPA1	3178	37	12	54675657	54675657	Missense_Mutation	SNP	G	A	4	180	c.211G>A	c.(211-213)GCT>ACT	p.A71T
Pat_53	Post-Resistance	SUOX	6821	37	12	56398758	56398758	Nonsense_Mutation	SNP	C	T	7	414	c.1585C>T	c.(1585-1587)CGA>TGA	p.R529*
Pat_53	Post-Resistance	ERBB3	2065	37	12	56480329	56480329	Missense_Mutation	SNP	G	A	4	199	c.436G>A	c.(436-438)GGT>AGT	p.G146S
Pat_53	Post-Resistance	SMARCC2	6601	37	12	56567575	56567575	Nonsense_Mutation	SNP	G	A	4	175	c.1555C>T	c.(1555-1557)CGA>TGA	p.R519*
Pat_53	Post-Resistance	CS	1431	37	12	56676220	56676220	Missense_Mutation	SNP	C	T	4	96	c.572G>A	c.(571-573)CGA>CAA	p.R191Q
Pat_53	Post-Resistance	MARS	4141	37	12	57894139	57894139	Missense_Mutation	SNP	G	A	5	508	c.1127G>A	c.(1126-1128)CGA>CAA	p.R376Q
Pat_53	Post-Resistance	AGAP2	116986	37	12	58124305	58124305	Missense_Mutation	SNP	G	A	4	306	c.2401C>T	c.(2401-2403)CGG>TGG	p.R801W

Pat_53	Post-Resistance	MON2	23041	37	12	62861015	62861015	Missense_Mutation	SNP	G	A	4	227	c.28G>A	c.(28-30)GTG>ATG	p.V10M
Pat_53	Post-Resistance	C12orf23	90488	37	12	107364940	107364940	Missense_Mutation	SNP	G	A	5	233	c.122G>A	c.(121-123)GGT>GAT	p.G41D
Pat_53	Post-Resistance	ACACB	32	37	12	109577535	109577535	Missense_Mutation	SNP	G	A	4	262	c.325G>A	c.(325-327)GCA>ACA	p.A109T
Pat_53	Post-Resistance	SH2B3	10019	37	12	111885287	111885287	Missense_Mutation	SNP	G	A	4	125	c.1175G>A	c.(1174-1176)CGG>CAG	p.R392Q
Pat_53	Post-Resistance	C12orf51	283450	37	12	112690233	112690233	Missense_Mutation	SNP	C	T	4	167	c.2281G>A	c.(2281-2283)GCT>ACT	p.A761T
Pat_53	Post-Resistance	GCN1L1	10985	37	12	120576584	120576584	Missense_Mutation	SNP	G	A	4	191	c.6071C>T	c.(6070-6072)GCG>GTG	p.A2024V
Pat_53	Post-Resistance	EP400	57634	37	12	132534880	132534880	Missense_Mutation	SNP	C	T	4	111	c.7213C>T	c.(7213-7215)CGT>TGT	p.R2405C
Pat_53	Post-Resistance	PABPC3	5042	37	13	25670736	25670736	Missense_Mutation	SNP	G	A	24	193	c.400G>A	c.(400-402)GAA>AAA	p.E134K
Pat_53	Post-Resistance	FREM2	341640	37	13	39265178	39265178	Missense_Mutation	SNP	C	T	4	266	c.3697C>T	c.(3697-3699)CCC>TCC	p.P1233S
Pat_53	Post-Resistance	COG3	83548	37	13	46083902	46083902	Missense_Mutation	SNP	C	T	5	446	c.1670C>T	c.(1669-1671)ACG>ATG	p.T557M
Pat_53	Post-Resistance	RB1	5925	37	13	49033845	49033845	Missense_Mutation	SNP	G	A	4	217	c.1982G>A	c.(1981-1983)CGG>CAG	p.R661Q
Pat_53	Post-Resistance	MYCBP2	23077	37	13	77657273	77657273	Missense_Mutation	SNP	C	T	4	236	c.10816G>A	c.(10816-10818)GAA>AAA	p.E3606K
Pat_53	Post-Resistance	ERCC5	2073	37	13	103518190	103518190	Missense_Mutation	SNP	G	A	4	89	c.2128G>A	c.(2128-2130)GTG>ATG	p.V710M
Pat_53	Post-Resistance	TUBGCP3	10426	37	13	113223532	113223532	Missense_Mutation	SNP	C	A	4	124	c.118G>T	c.(118-120)GGC>TGC	p.G40C
Pat_53	Post-Resistance	POTEG	404785	37	14	19553531	19553531	Missense_Mutation	SNP	G	A	6	190	c.115G>A	c.(115-117)GGC>AGC	p.G39S
Pat_53	Post-Resistance	POTEG	404785	37	14	19553678	19553678	Missense_Mutation	SNP	G	A	4	180	c.262G>A	c.(262-264)GAC>AAC	p.D88N
Pat_53	Post-Resistance	RNASE4	6038	37	14	21167919	21167919	Missense_Mutation	SNP	G	A	4	199	c.389G>A	c.(388-390)CGT>CAT	p.R130H
Pat_53	Post-Resistance	RBM23	55147	37	14	23374630	23374630	Missense_Mutation	SNP	C	T	4	185	c.488G>A	c.(487-489)CGT>CAT	p.R163H
Pat_53	Post-Resistance	CDH24	64403	37	14	23523420	23523420	Missense_Mutation	SNP	C	T	5	152	c.902G>A	c.(901-903)GGG>GAG	p.G301E
Pat_53	Post-Resistance	SRP54	6729	37	14	35465931	35465931	Missense_Mutation	SNP	C	T	57	227	c.16C>T	c.(16-18)CTT>TTT	p.L6F
Pat_53	Post-Resistance	FAM179B	23116	37	14	45475280	45475280	Missense_Mutation	SNP	G	A	4	197	c.2714G>A	c.(2713-2715)CGA>CAA	p.R905Q
Pat_53	Post-Resistance	NID2	22795	37	14	52478368	52478368	Missense_Mutation	SNP	G	A	6	259	c.3454C>T	c.(3454-3456)CGG>TGG	p.R1152W
Pat_53	Post-Resistance	SAMD4A	23034	37	14	55226903	55226903	Missense_Mutation	SNP	C	T	4	344	c.1198C>T	c.(1198-1200)CGC>TGC	p.R400C
Pat_53	Post-Resistance	DAAM1	23002	37	14	59791097	59791097	Missense_Mutation	SNP	G	A	4	179	c.914G>A	c.(913-915)CGC>CAC	p.R305H
Pat_53	Post-Resistance	RDH12	145226	37	14	68195943	68195943	Missense_Mutation	SNP	G	A	4	184	c.694G>A	c.(694-696)GTC>ATC	p.V232I
Pat_53	Post-Resistance	SLC39A9	55334	37	14	69925110	69925110	Missense_Mutation	SNP	G	A	4	338	c.724G>A	c.(724-726)GCC>ACC	p.A242T
Pat_53	Post-Resistance	SMOC1	64093	37	14	70490078	70490078	Missense_Mutation	SNP	G	A	4	201	c.1205G>A	c.(1204-1206)CGG>CAG	p.R402Q
Pat_53	Post-Resistance	LTBP2	4053	37	14	74968216	74968216	Missense_Mutation	SNP	G	A	4	111	c.5248C>T	c.(5248-5250)CGC>TGC	p.R1750C
Pat_53	Post-Resistance	C14orf179	112752	37	14	76548694	76548694	Missense_Mutation	SNP	G	A	5	260	c.352G>A	c.(352-354)GTG>ATG	p.V118M
Pat_53	Post-Resistance	SNW1	22938	37	14	78187145	78187145	Missense_Mutation	SNP	C	T	4	139	c.1157G>A	c.(1156-1158)CGG>CAG	p.R386Q
Pat_53	Post-Resistance	PSMC1	5700	37	14	90735856	90735856	Nonsense_Mutation	SNP	C	T	4	185	c.997C>T	c.(997-999)CGA>TGA	p.R333*
Pat_53	Post-Resistance	OTUB2	78990	37	14	94510327	94510327	Missense_Mutation	SNP	C	T	4	291	c.229C>T	c.(229-231)CGC>TGC	p.R77C
Pat_53	Post-Resistance	PAPOLA	10914	37	14	97009136	97009136	Nonsense_Mutation	SNP	C	T	4	337	c.1195C>T	c.(1195-1197)CGA>TGA	p.R399*
Pat_53	Post-Resistance	AHNAK2	113146	37	14	105413410	105413410	Missense_Mutation	SNP	G	A	88	208	c.8378C>T	c.(8377-8379)GCG>GTG	p.A2793V
Pat_53	Post-Resistance	AHNAK2	113146	37	14	105420169	105420169	Missense_Mutation	SNP	C	T	4	160	c.1619G>A	c.(1618-1620)GGC>GAC	p.G540D
Pat_53	Post-Resistance	ADAM6	8755	37	14	106993798	106993798	Splice_Site	SNP	C	T	14	223	c.8648_splice	c.e187+1	
Pat_53	Post-Resistance	GABRB3	2562	37	15	26793203	26793203	Missense_Mutation	SNP	C	T	4	196	c.1159G>A	c.(1159-1161)GAT>AAT	p.D387N
Pat_53	Post-Resistance	HERC2	8924	37	15	28386902	28386902	Missense_Mutation	SNP	C	T	5	452	c.11791G>A	c.(11791-11793)GAA>AAA	p.E3931K
Pat_53	Post-Resistance	CHAC1	79094	37	15	41247791	41247791	Missense_Mutation	SNP	C	T	4	185	c.614C>T	c.(613-615)ACG>ATG	p.T205M
Pat_53	Post-Resistance	TYRO3	7301	37	15	41864643	41864643	Missense_Mutation	SNP	G	A	5	265	c.1756G>A	c.(1756-1758)GTA>ATA	p.V586I
Pat_53	Post-Resistance	WDR76	79968	37	15	44131850	44131850	Missense_Mutation	SNP	G	A	5	613	c.656G>A	c.(655-657)CGA>CAA	p.R219Q
Pat_53	Post-Resistance	MYEF2	50804	37	15	48443760	48443760	Missense_Mutation	SNP	G	A	5	538	c.1216C>T	c.(1216-1218)CGT>TGT	p.R406C
Pat_53	Post-Resistance	RFX7	64864	37	15	56386649	56386649	Missense_Mutation	SNP	G	A	5	170	c.3277C>T	c.(3277-3279)CGT>TGT	p.R1093C
Pat_53	Post-Resistance	SLTM	79811	37	15	59179507	59179507	Missense_Mutation	SNP	G	A	4	155	c.2608C>T	c.(2608-2610)CCT>TCT	p.P870S
Pat_53	Post-Resistance	VPS13C	54832	37	15	62165483	62165483	Nonsense_Mutation	SNP	C	A	6	541	c.10540G>T	c.(10540-10542)GGA>TGA	p.G3514*
Pat_53	Post-Resistance	NEO1	4756	37	15	73575382	73575382	Missense_Mutation	SNP	G	A	5	411	c.3340G>A	c.(3340-3342)GTC>ATC	p.V1114I
Pat_53	Post-Resistance	CYP1A2	1544	37	15	75042102	75042102	Missense_Mutation	SNP	C	T	112	228	c.23C>T	c.(22-24)CCC>CTC	p.P8L

Pat_53	Post-Resistance	CHRNB4	1143	37	15	78921974	78921974	Missense_Mutation	SNP	C	T	44	107	c.673G>A	c.(673-675)GAC>AAC	p.D225N
Pat_53	Post-Resistance	STARD5	80765	37	15	81605677	81605677	Missense_Mutation	SNP	C	T	6	262	c.562G>A	c.(562-564)GTG>ATG	p.V188M
Pat_53	Post-Resistance	WHAMM	123720	37	15	83499373	83499373	Missense_Mutation	SNP	G	A	5	560	c.1664G>A	c.(1663-1665)CGA>CAA	p.R555Q
Pat_53	Post-Resistance	AKAP13	11214	37	15	86122195	86122195	Missense_Mutation	SNP	C	T	4	353	c.896C>T	c.(895-897)CCC>CTC	p.P299L
Pat_53	Post-Resistance	ZNF710	374655	37	15	90616474	90616474	Missense_Mutation	SNP	G	A	5	229	c.1630G>A	c.(1630-1632)GTG>ATG	p.V544M
Pat_53	Post-Resistance	TSC2	7249	37	16	2111902	2111902	Missense_Mutation	SNP	G	A	4	94	c.1150G>A	c.(1150-1152)GTC>ATC	p.V384I
Pat_53	Post-Resistance	ZNF205	7755	37	16	3170105	3170105	Missense_Mutation	SNP	G	A	4	240	c.1444G>A	c.(1444-1446)GGC>AGC	p.G482S
Pat_53	Post-Resistance	ALG1	56052	37	16	5125428	5125428	Missense_Mutation	SNP	G	A	4	302	c.430G>A	c.(430-432)GTG>ATG	p.V144M
Pat_53	Post-Resistance	ALG1	56052	37	16	5127505	5127505	Missense_Mutation	SNP	G	A	4	192	c.599G>A	c.(598-600)CGA>CAA	p.R200Q
Pat_53	Post-Resistance	C16orf62	57020	37	16	19639050	19639050	Missense_Mutation	SNP	C	T	4	213	c.1306C>T	c.(1306-1308)CGG>TGG	p.R436W
Pat_53	Post-Resistance	UBFD1	56061	37	16	23569565	23569565	Missense_Mutation	SNP	G	A	4	217	c.320G>A	c.(319-321)GGC>GAC	p.G107D
Pat_53	Post-Resistance	DNAJA2	10294	37	16	47005303	47005303	Missense_Mutation	SNP	C	T	6	259	c.320G>A	c.(319-321)CGA>CAA	p.R107Q
Pat_53	Post-Resistance	HEATR3	55027	37	16	50102702	50102702	Missense_Mutation	SNP	C	T	6	481	c.323C>T	c.(322-324)GCT>GTT	p.A108V
Pat_53	Post-Resistance	NOD2	64127	37	16	50733419	50733419	Missense_Mutation	SNP	G	A	212	419	c.94G>A	c.(94-96)GAG>AAG	p.E32K
Pat_53	Post-Resistance	KIFC3	3801	37	16	57805333	57805333	Missense_Mutation	SNP	C	T	4	246	c.542G>A	c.(541-543)CGT>CAT	p.R181H
Pat_53	Post-Resistance	CDH5	1003	37	16	66426076	66426076	Missense_Mutation	SNP	T	C	4	301	c.1007T>C	c.(1006-1008)ATC>ACC	p.I336T
Pat_53	Post-Resistance	ZNF23	7571	37	16	71483003	71483003	Missense_Mutation	SNP	C	T	5	194	c.925G>A	c.(925-927)GAG>AAG	p.E309K
Pat_53	Post-Resistance	ZNF19	7567	37	16	71509686	71509686	Missense_Mutation	SNP	G	A	4	312	c.764C>T	c.(763-765)ACG>ATG	p.T255M
Pat_53	Post-Resistance	HSDL1	83693	37	16	84163719	84163719	Missense_Mutation	SNP	C	T	4	287	c.538G>A	c.(538-540)GCC>ACC	p.A180T
Pat_53	Post-Resistance	CRISPLD2	83716	37	16	84922899	84922899	Missense_Mutation	SNP	G	A	5	366	c.1369G>A	c.(1369-1371)GTG>ATG	p.V457M
Pat_53	Post-Resistance	FANCA	2175	37	16	89818580	89818580	Missense_Mutation	SNP	C	T	6	573	c.3032G>A	c.(3031-3033)CGC>CAC	p.R1011H
Pat_53	Post-Resistance	VPS53	55275	37	17	456619	456619	Splice_Site	SNP	C	T	4	163	c.1787_splice	c.e16+1	p.T596_splice
Pat_53	Post-Resistance	INPP5K	51763	37	17	1401247	1401247	Missense_Mutation	SNP	C	T	4	264	c.946G>A	c.(946-948)GGC>AGC	p.G316S
Pat_53	Post-Resistance	EIF4A1	1973	37	17	7481670	7481670	Missense_Mutation	SNP	G	A	6	536	c.1087G>A	c.(1087-1089)GGT>AGT	p.G363S
Pat_53	Post-Resistance	MPDU1	9526	37	17	7487199	7487199	Missense_Mutation	SNP	G	A	5	568	c.19G>A	c.(19-21)GGA>AGA	p.G7R
Pat_53	Post-Resistance	CYB5D1	124637	37	17	7761979	7761979	Missense_Mutation	SNP	G	A	5	239	c.293G>A	c.(292-294)GGC>GAC	p.G98D
Pat_53	Post-Resistance	CHD3	1107	37	17	7814172	7814172	Missense_Mutation	SNP	C	T	5	288	c.5762C>T	c.(5761-5763)CCG>CTG	p.P1921L
Pat_53	Post-Resistance	PMP22	5376	37	17	15134242	15134242	Missense_Mutation	SNP	G	A	4	179	c.475C>T	c.(475-477)CGC>TGC	p.R159C
Pat_53	Post-Resistance	ADORA2B	136	37	17	15878627	15878627	Missense_Mutation	SNP	G	A	5	222	c.970G>A	c.(970-972)GTA>ATA	p.V324I
Pat_53	Post-Resistance	DRG2	1819	37	17	18001674	18001674	Splice_Site	SNP	G	A	5	186	c.315_splice	c.e3+1	p.E105_splice
Pat_53	Post-Resistance	MYO15A	51168	37	17	18054816	18054816	Missense_Mutation	SNP	C	T	4	159	c.7762C>T	c.(7762-7764)CGG>TGG	p.R2588W
Pat_53	Post-Resistance	KSR1	8844	37	17	25931710	25931710	Missense_Mutation	SNP	G	A	4	159	c.1225G>A	c.(1225-1227)GAT>AAT	p.D409N
Pat_53	Post-Resistance	GOSR1	9527	37	17	28849323	28849323	Missense_Mutation	SNP	G	A	5	471	c.680G>A	c.(679-681)CGG>CAG	p.R227Q
Pat_53	Post-Resistance	C17orf79	55352	37	17	30179888	30179888	Missense_Mutation	SNP	C	T	4	315	c.328G>A	c.(328-330)GAT>AAT	p.D110N
Pat_53	Post-Resistance	TAF15	8148	37	17	34171973	34171973	Missense_Mutation	SNP	G	A	4	161	c.1670G>A	c.(1669-1671)GGC>GAC	p.G557D
Pat_53	Post-Resistance	ACACA	31	37	17	35545405	35545405	Missense_Mutation	SNP	G	A	4	121	c.4477C>T	c.(4477-4479)CGG>TGG	p.R1493W
Pat_53	Post-Resistance	RPL19	6143	37	17	37360818	37360818	Missense_Mutation	SNP	C	G	4	222	c.508C>G	c.(508-510)CGC>GGC	p.R170G
Pat_53	Post-Resistance	GRB7	2886	37	17	37898595	37898595	Missense_Mutation	SNP	C	T	10	202	c.41C>T	c.(40-42)CCG>CTG	p.P14L
Pat_53	Post-Resistance	KRTAP4-1	85285	37	17	39340740	39340740	Missense_Mutation	SNP	G	A	4	153	c.310C>T	c.(310-312)CGT>TGT	p.R104C
Pat_53	Post-Resistance	KRT17	3872	37	17	39777910	39777910	Missense_Mutation	SNP	G	A	4	128	c.769C>T	c.(769-771)CGT>TGT	p.R257C
Pat_53	Post-Resistance	EIF1	10209	37	17	39846374	39846374	Missense_Mutation	SNP	C	T	4	313	c.230C>T	c.(229-231)CCG>CTG	p.P77L
Pat_53	Post-Resistance	KAT2A	2648	37	17	40266944	40266944	Missense_Mutation	SNP	G	A	4	268	c.1985C>T	c.(1984-1986)ACG>ATG	p.T662M
Pat_53	Post-Resistance	WNK4	65266	37	17	40940169	40940169	Missense_Mutation	SNP	C	T	5	444	c.1885C>T	c.(1885-1887)CGT>TGT	p.R629C
Pat_53	Post-Resistance	AARSD1	80755	37	17	41131448	41131448	Missense_Mutation	SNP	C	T	5	644	c.265G>A	c.(265-267)GAT>AAT	p.D89N
Pat_53	Post-Resistance	NMT1	4836	37	17	43181221	43181221	Missense_Mutation	SNP	G	A	6	363	c.1309G>A	c.(1309-1311)GAC>AAC	p.D437N
Pat_53	Post-Resistance	COL1A1	1277	37	17	48264166	48264166	Missense_Mutation	SNP	G	A	4	238	c.3649C>T	c.(3649-3651)CGG>TGG	p.R1217W
Pat_53	Post-Resistance	INTS2	57508	37	17	59989419	59989419	Missense_Mutation	SNP	A	G	5	375	c.686T>C	c.(685-687)CTG>CCG	p.L229P

Pat_53	Post-Resistance	SCN4A	6329	37	17	62034631	62034631	Missense_Mutation	SNP	C	A	4	125	c.2267G>T	c.(2266-2268)CGC>CTC	p.R756L
Pat_53	Post-Resistance	BPTF	2186	37	17	65850575	65850575	Missense_Mutation	SNP	G	A	6	614	c.1133G>A	c.(1132-1134)CGA>CAA	p.R378Q
Pat_53	Post-Resistance	RECQL5	9400	37	17	73659025	73659025	Missense_Mutation	SNP	G	A	5	467	c.305C>T	c.(304-306)TCG>TTG	p.S102L
Pat_53	Post-Resistance	DNAH17	8632	37	17	76455237	76455237	Missense_Mutation	SNP	G	A	6	352	c.707C>T	c.(706-708)ACG>ATG	p.T236M
Pat_53	Post-Resistance	METTL4	64863	37	18	2566965	2566965	Missense_Mutation	SNP	C	T	4	205	c.251G>A	c.(250-252)CGA>CAA	p.R84Q
Pat_53	Post-Resistance	ANKRD12	23253	37	18	9258861	9258861	Missense_Mutation	SNP	G	A	4	201	c.5596G>A	c.(5596-5598)GAA>AAA	p.E1866K
Pat_53	Post-Resistance	TXNDC2	84203	37	18	9887461	9887461	Missense_Mutation	SNP	A	C	5	195	c.985A>C	c.(985-987)ATC>CTC	p.I329L
Pat_53	Post-Resistance	MBD2	8932	37	18	51715341	51715341	Missense_Mutation	SNP	G	A	6	427	c.743C>T	c.(742-744)ACA>ATA	p.T248I
Pat_53	Post-Resistance	ALPK2	115701	37	18	56171336	56171336	Missense_Mutation	SNP	G	A	4	230	c.6074C>T	c.(6073-6075)CCG>CTG	p.P2025L
Pat_53	Post-Resistance	ZNF532	55205	37	18	56586013	56586013	Missense_Mutation	SNP	C	T	4	216	c.494C>T	c.(493-495)ACG>ATG	p.T165M
Pat_53	Post-Resistance	C19orf36	113177	37	19	2098101	2098101	Missense_Mutation	SNP	G	A	6	314	c.448G>A	c.(448-450)GTC>ATC	p.V150I
Pat_53	Post-Resistance	NFIC	4782	37	19	3381836	3381836	Missense_Mutation	SNP	G	A	4	198	c.157G>A	c.(157-159)GAG>AAG	p.E53K
Pat_53	Post-Resistance	KDM4B	23030	37	19	5032995	5032995	Missense_Mutation	SNP	G	A	4	122	c.94G>A	c.(94-96)GTG>ATG	p.V32M
Pat_53	Post-Resistance	CD209	30835	37	19	7810766	7810766	Missense_Mutation	SNP	C	T	6	166	c.386G>A	c.(385-387)CGG>CAG	p.R129Q
Pat_53	Post-Resistance	LPPR2	64748	37	19	11474862	11474862	Nonsense_Mutation	SNP	C	T	5	164	c.973C>T	c.(973-975)CGA>TGA	p.R325*
Pat_53	Post-Resistance	ZNF440	126070	37	19	11943142	11943142	Missense_Mutation	SNP	G	A	4	153	c.1151G>A	c.(1150-1152)CGA>CAA	p.R384Q
Pat_53	Post-Resistance	ZNF844	284391	37	19	12187475	12187475	Missense_Mutation	SNP	C	G	4	179	c.1540C>G	c.(1540-1542)CAT>GAT	p.H514D
Pat_53	Post-Resistance	NFIX	4784	37	19	13183923	13183923	Missense_Mutation	SNP	G	A	4	183	c.646G>A	c.(646-648)GGG>AGG	p.G216R
Pat_53	Post-Resistance	EMR3	84658	37	19	14765803	14765803	Missense_Mutation	SNP	C	T	4	117	c.568G>A	c.(568-570)GAT>AAT	p.D190N
Pat_53	Post-Resistance	IL12RB1	3594	37	19	18186628	18186628	Nonsense_Mutation	SNP	G	A	4	88	c.631C>T	c.(631-633)CGA>TGA	p.R211*
Pat_53	Post-Resistance	PDE4C	5143	37	19	18322649	18322649	Missense_Mutation	SNP	G	T	4	87	c.1711C>A	c.(1711-1713)CAG>AAG	p.Q571K
Pat_53	Post-Resistance	ZNF737	100129842	37	19	20727799	20727799	Missense_Mutation	SNP	C	T	4	112	c.1210G>A	c.(1210-1212)GAA>AAA	p.E404K
Pat_53	Post-Resistance	ZNF681	148213	37	19	23926839	23926839	Missense_Mutation	SNP	A	G	4	191	c.1513T>C	c.(1513-1515)TCC>CCC	p.S505P
Pat_53	Post-Resistance	CD22	933	37	19	35831831	35831831	Nonsense_Mutation	SNP	C	T	4	101	c.1297C>T	c.(1297-1299)CGA>TGA	p.R433*
Pat_53	Post-Resistance	GAPDHS	26330	37	19	36034584	36034584	Missense_Mutation	SNP	C	T	4	158	c.911C>T	c.(910-912)GCG>GTG	p.A304V
Pat_53	Post-Resistance	ATP4A	495	37	19	36046487	36046487	Missense_Mutation	SNP	G	A	3	47	c.2012C>T	c.(2011-2013)GCC>GTC	p.A671V
Pat_53	Post-Resistance	WDR62	284403	37	19	36583665	36583665	Missense_Mutation	SNP	G	A	5	152	c.2285G>A	c.(2284-2286)CGG>CAG	p.R762Q
Pat_53	Post-Resistance	ZNF780A	284323	37	19	40580552	40580552	Missense_Mutation	SNP	T	G	4	212	c.1797A>C	c.(1795-1797)CAA>CAC	p.Q599H
Pat_53	Post-Resistance	CEACAM1	634	37	19	43026222	43026222	Missense_Mutation	SNP	G	A	6	388	c.557C>T	c.(556-558)CCG>CTG	p.P186L
Pat_53	Post-Resistance	XRCC1	7515	37	19	44047618	44047618	Nonsense_Mutation	SNP	G	A	4	136	c.1828C>T	c.(1828-1830)CGA>TGA	p.R610*
Pat_53	Post-Resistance	GRIN2D	2906	37	19	48922505	48922505	Missense_Mutation	SNP	G	A	4	133	c.1750G>A	c.(1750-1752)GCC>ACC	p.A584T
Pat_53	Post-Resistance	TEAD2	8463	37	19	49850484	49850484	Missense_Mutation	SNP	C	T	5	422	c.872G>A	c.(871-873)CGT>CAT	p.R291H
Pat_53	Post-Resistance	POLD1	5424	37	19	50906786	50906786	Missense_Mutation	SNP	G	A	4	162	c.1174G>A	c.(1174-1176)GTG>ATG	p.V392M
Pat_53	Post-Resistance	ZNF665	79788	37	19	53668482	53668482	Nonsense_Mutation	SNP	G	A	4	130	c.1261C>T	c.(1261-1263)CGA>TGA	p.R421*
Pat_53	Post-Resistance	ZNF761	388561	37	19	53958879	53958879	Missense_Mutation	SNP	A	G	9	469	c.1118A>G	c.(1117-1119)CAT>CGT	p.H373R
Pat_53	Post-Resistance	ZNF761	388561	37	19	53959275	53959275	Missense_Mutation	SNP	G	A	4	240	c.1514G>A	c.(1513-1515)CGG>CAG	p.R505Q
Pat_53	Post-Resistance	LILRA4	23547	37	19	54848178	54848178	Missense_Mutation	SNP	C	T	4	221	c.1189G>A	c.(1189-1191)GGC>AGC	p.G397S
Pat_53	Post-Resistance	ZNF419	79744	37	19	58005172	58005172	Missense_Mutation	SNP	G	A	4	196	c.1247G>A	c.(1246-1248)AGA>AAA	p.R416K
Pat_53	Post-Resistance	PXDN	7837	37	2	1652010	1652010	Missense_Mutation	SNP	G	A	4	306	c.3542C>T	c.(3541-3543)GCG>GTG	p.A1181V
Pat_53	Post-Resistance	WDR35	57539	37	2	20138033	20138033	Nonsense_Mutation	SNP	G	A	4	214	c.2089C>T	c.(2089-2091)CGA>TGA	p.R697*
Pat_53	Post-Resistance	CENPA	1058	37	2	27016113	27016113	Missense_Mutation	SNP	G	A	7	286	c.389G>A	c.(388-390)CGG>CAG	p.R130Q
Pat_53	Post-Resistance	IFT172	26160	37	2	27672622	27672622	Missense_Mutation	SNP	C	T	4	219	c.4096G>A	c.(4096-4098)GAT>AAT	p.D1366N
Pat_53	Post-Resistance	MTA3	57504	37	2	42936069	42936069	Missense_Mutation	SNP	G	A	4	409	c.1187G>A	c.(1186-1188)CGA>CAA	p.R396Q
Pat_53	Post-Resistance	PPM1B	5495	37	2	44428405	44428405	Missense_Mutation	SNP	C	T	5	318	c.67C>T	c.(67-69)CGT>TGT	p.R23C
Pat_53	Post-Resistance	PAPOLG	64895	37	2	61021162	61021162	Missense_Mutation	SNP	G	A	6	253	c.1825G>A	c.(1825-1827)GTA>ATA	p.V609I
Pat_53	Post-Resistance	ADD2	119	37	2	70890681	70890681	Missense_Mutation	SNP	G	A	4	297	c.2057C>T	c.(2056-2058)TCG>TTG	p.S686L
Pat_53	Post-Resistance	LMAN2L	81562	37	2	97403690	97403690	Missense_Mutation	SNP	C	T	4	180	c.302G>A	c.(301-303)CGG>CAG	p.R101Q

Pat_53	Post-Resistance	CNGA3	1261	37	2	99012913	99012913	Missense_Mutation	SNP	G	A	4	69	c.1280G>A	c.(1279-1281)CGC>CAC	p.R427H
Pat_53	Post-Resistance	C2orf29	55571	37	2	101881385	101881385	Missense_Mutation	SNP	C	T	6	184	c.911C>T	c.(910-912)ACG>ATG	p.T304M
Pat_53	Post-Resistance	FHL2	2274	37	2	106002910	106002910	Missense_Mutation	SNP	G	A	4	134	c.64C>T	c.(64-66)CGG>TGG	p.R22W
Pat_53	Post-Resistance	RGPD3	653489	37	2	107049425	107049425	Missense_Mutation	SNP	A	C	15	111	c.2435T>G	c.(2434-2436)CTG>CGG	p.L812R
Pat_53	Post-Resistance	ST6GAL2	84620	37	2	107460025	107460025	Nonsense_Mutation	SNP	G	A	4	130	c.409C>T	c.(409-411)CAG>TAG	p.Q137*
Pat_53	Post-Resistance	SULT1C2	6819	37	2	108910750	108910750	Nonsense_Mutation	SNP	C	T	4	173	c.217C>T	c.(217-219)CGA>TGA	p.R73*
Pat_53	Post-Resistance	DARS	1615	37	2	136736874	136736874	Missense_Mutation	SNP	G	A	6	514	c.187C>T	c.(187-189)CGT>TGT	p.R63C
Pat_53	Post-Resistance	SPOPL	339745	37	2	139322536	139322536	Missense_Mutation	SNP	G	A	4	150	c.1007G>A	c.(1006-1008)TGT>TAT	p.C336Y
Pat_53	Post-Resistance	STAM2	10254	37	2	153001437	153001437	Missense_Mutation	SNP	G	A	5	287	c.482C>T	c.(481-483)TCG>TTG	p.S161L
Pat_53	Post-Resistance	ITGB6	3694	37	2	160983112	160983112	Missense_Mutation	SNP	C	T	4	108	c.1661G>A	c.(1660-1662)GGT>GAT	p.G554D
Pat_53	Post-Resistance	GAD1	2571	37	2	171686090	171686090	Missense_Mutation	SNP	G	A	4	232	c.251G>A	c.(250-252)CGG>CAG	p.R84Q
Pat_53	Post-Resistance	GPR155	151556	37	2	175301062	175301062	Missense_Mutation	SNP	G	A	4	333	c.2395C>T	c.(2395-2397)CGT>TGT	p.R799C
Pat_53	Post-Resistance	GPR155	151556	37	2	175301077	175301077	Missense_Mutation	SNP	C	T	4	281	c.2380G>A	c.(2380-2382)GGC>AGC	p.G794S
Pat_53	Post-Resistance	ATF2	1386	37	2	175986196	175986196	Missense_Mutation	SNP	G	A	5	142	c.175C>T	c.(175-177)CGT>TGT	p.R59C
Pat_53	Post-Resistance	TTN	7273	37	2	179422707	179422707	Missense_Mutation	SNP	G	A	5	208	c.79670C>T	c.(79669-79671)ACA>ATA	p.T26557I
Pat_53	Post-Resistance	TTN	7273	37	2	179430305	179430305	Missense_Mutation	SNP	G	A	4	320	c.72850C>T	c.(72850-72852)CGT>TGT	p.R24284C
Pat_53	Post-Resistance	TTN	7273	37	2	179481497	179481497	Missense_Mutation	SNP	C	T	4	300	c.40415G>A	c.(40414-40416)CGT>CAT	p.R13472H
Pat_53	Post-Resistance	GULP1	51454	37	2	189342436	189342436	Missense_Mutation	SNP	C	T	4	327	c.7C>T	c.(7-9)CGT>TGT	p.R3C
Pat_53	Post-Resistance	MAP2	4133	37	2	210545509	210545509	Missense_Mutation	SNP	C	T	7	626	c.412C>T	c.(412-414)CCC>TCC	p.P138S
Pat_53	Post-Resistance	TTLL4	9654	37	2	219617568	219617568	Missense_Mutation	SNP	G	A	4	265	c.3059G>A	c.(3058-3060)CGT>CAT	p.R1020H
Pat_53	Post-Resistance	PTPRN	5798	37	2	220164074	220164074	Missense_Mutation	SNP	C	T	4	127	c.1556G>A	c.(1555-1557)CGG>CAG	p.R519Q
Pat_53	Post-Resistance	EPHA4	2043	37	2	222428870	222428870	Missense_Mutation	SNP	C	T	4	170	c.404G>A	c.(403-405)CGT>CAT	p.R135H
Pat_53	Post-Resistance	DGKD	8527	37	2	234365876	234365876	Nonsense_Mutation	SNP	C	T	4	165	c.2482C>T	c.(2482-2484)CGA>TGA	p.R828*
Pat_53	Post-Resistance	CRNKL1	51340	37	20	20026049	20026049	Missense_Mutation	SNP	C	T	6	385	c.1187G>A	c.(1186-1188)CGG>CAG	p.R396Q
Pat_53	Post-Resistance	ZNF337	26152	37	20	25657503	25657503	Missense_Mutation	SNP	C	T	5	386	c.421G>A	c.(421-423)GTA>ATA	p.V141I
Pat_53	Post-Resistance	FRG1B	284802	37	20	29628243	29628243	Missense_Mutation	SNP	T	C	23	397	c.155T>C	c.(154-156)TTG>TCG	p.L52S
Pat_53	Post-Resistance	FRG1B	284802	37	20	29628245	29628245	Missense_Mutation	SNP	G	A	24	398	c.157G>A	c.(157-159)GCC>ACC	p.A53T
Pat_53	Post-Resistance	FRG1B	284802	37	20	29628251	29628251	Missense_Mutation	SNP	A	G	51	370	c.163A>G	c.(163-165)AAT>GAT	p.N55D
Pat_53	Post-Resistance	FRG1B	284802	37	20	29628278	29628278	Missense_Mutation	SNP	G	A	9	296	c.190G>A	c.(190-192)GCA>ACA	p.A64T
Pat_53	Post-Resistance	FRG1B	284802	37	20	29628299	29628300	Missense_Mutation	DNP	AG	GA	6	234	c.211_212AG>GA	c.(211-213)AGT>GAT	p.S71D
Pat_53	Post-Resistance	RBM12	10137	37	20	34241449	34241449	Missense_Mutation	SNP	C	T	5	426	c.1796G>A	c.(1795-1797)CGT>CAT	p.R599H
Pat_53	Post-Resistance	PHF20	51230	37	20	34515765	34515765	Missense_Mutation	SNP	G	A	4	329	c.2068G>A	c.(2068-2070)GAG>AAG	p.E690K
Pat_53	Post-Resistance	NPEPL1	79716	37	20	57273776	57273776	Missense_Mutation	SNP	G	A	4	176	c.544G>A	c.(544-546)GCC>ACC	p.A182T
Pat_53	Post-Resistance	SYCP2	10388	37	20	58491593	58491593	Missense_Mutation	SNP	C	T	4	228	c.461G>A	c.(460-462)CGC>CAC	p.R154H
Pat_53	Post-Resistance	SYNJ1	8867	37	21	34067441	34067441	Nonsense_Mutation	SNP	G	A	5	512	c.748C>T	c.(748-750)CGA>TGA	p.R250*
Pat_53	Post-Resistance	GART	2618	37	21	34876757	34876757	Missense_Mutation	SNP	C	T	5	319	c.2803G>A	c.(2803-2805)GGA>AGA	p.G935R
Pat_53	Post-Resistance	DOPEY2	9980	37	21	37623566	37623566	Missense_Mutation	SNP	G	A	5	251	c.5105G>A	c.(5104-5106)CGT>CAT	p.R1702H
Pat_53	Post-Resistance	ZNF295	49854	37	21	43411870	43411870	Missense_Mutation	SNP	C	T	7	608	c.2335G>A	c.(2335-2337)GAG>AAG	p.E779K
Pat_53	Post-Resistance	UMODL1	89766	37	21	43547924	43547924	Missense_Mutation	SNP	G	A	4	216	c.3673G>A	c.(3673-3675)GGA>AGA	p.G1225R
Pat_53	Post-Resistance	COL6A2	1292	37	21	47546100	47546100	Missense_Mutation	SNP	G	A	5	524	c.2371G>A	c.(2371-2373)GAC>AAC	p.D791N
Pat_53	Post-Resistance	PCNT	5116	37	21	47754470	47754470	Missense_Mutation	SNP	C	T	4	120	c.427C>T	c.(427-429)CGT>TGT	p.R143C
Pat_53	Post-Resistance	CECR2	27443	37	22	17976569	17976569	Missense_Mutation	SNP	G	A	4	172	c.230G>A	c.(229-231)CGA>CAA	p.R77Q
Pat_53	Post-Resistance	HIRA	7290	37	22	19363214	19363214	Missense_Mutation	SNP	C	T	4	174	c.1715G>A	c.(1714-1716)CGG>CAG	p.R572Q
Pat_53	Post-Resistance	CABIN1	23523	37	22	24494110	24494110	Missense_Mutation	SNP	G	A	4	206	c.4072G>A	c.(4072-4074)GAT>AAT	p.D1358N
Pat_53	Post-Resistance	NEFH	4744	37	22	29885686	29885686	Missense_Mutation	SNP	C	A	7	200	c.2057C>A	c.(2056-2058)GCA>GAA	p.A686E
Pat_53	Post-Resistance	GAL3ST1	9514	37	22	30951785	30951785	Missense_Mutation	SNP	G	A	4	130	c.427C>T	c.(427-429)CGC>TGC	p.R143C
Pat_53	Post-Resistance	ELFN2	114794	37	22	37769986	37769986	Missense_Mutation	SNP	G	A	4	139	c.1589C>T	c.(1588-1590)TCG>TTG	p.S530L

Pat_53	Post-Resistance	TRIOBP	11078	37	22	38120676	38120676	Missense_Mutation	SNP	G	A	4	246	c.2113G>A	c.(2113-2115)GAT>AAT	p.D705N
Pat_53	Post-Resistance	TRIOBP	11078	37	22	38120707	38120707	Missense_Mutation	SNP	C	T	6	243	c.2144C>T	c.(2143-2145)ACC>ATC	p.T715I
Pat_53	Post-Resistance	GTPBP1	9567	37	22	39122093	39122093	Missense_Mutation	SNP	C	T	4	210	c.1156C>T	c.(1156-1158)CGC>TGC	p.R386C
Pat_53	Post-Resistance	SGSM3	27352	37	22	40803286	40803286	Missense_Mutation	SNP	G	A	4	102	c.1322G>A	c.(1321-1323)CGC>CAC	p.R441H
Pat_53	Post-Resistance	ZFYVE20	64145	37	3	15115678	15115678	Missense_Mutation	SNP	G	A	4	193	c.1966C>T	c.(1966-1968)CGC>TGC	p.R656C
Pat_53	Post-Resistance	GPD1L	23171	37	3	32200501	32200501	Missense_Mutation	SNP	C	T	4	168	c.752C>T	c.(751-753)ACA>ATA	p.T251I
Pat_53	Post-Resistance	SLC25A38	54977	37	3	39437955	39437955	Missense_Mutation	SNP	G	A	4	270	c.859G>A	c.(859-861)GCA>ACA	p.A287T
Pat_53	Post-Resistance	CELSR3	1951	37	3	48667109	48667109	Missense_Mutation	SNP	G	A	4	121	c.11780C>T	c.(11779-11781)ACG>ATG	p.T3927M
Pat_53	Post-Resistance	QARS	5859	37	3	49136550	49136550	Missense_Mutation	SNP	G	A	4	209	c.1751C>T	c.(1750-1752)GCT>GTT	p.A584V
Pat_53	Post-Resistance	CCDC36	339834	37	3	49294693	49294693	Missense_Mutation	SNP	G	A	5	361	c.1763G>A	c.(1762-1764)AGC>AAC	p.S588N
Pat_53	Post-Resistance	BSN	8927	37	3	49690290	49690290	Missense_Mutation	SNP	G	A	4	139	c.3301G>A	c.(3301-3303)GAG>AAG	p.E1101K
Pat_53	Post-Resistance	RNF123	63891	37	3	49740085	49740085	Missense_Mutation	SNP	C	T	5	229	c.1649C>T	c.(1648-1650)CCC>CTC	p.P550L
Pat_53	Post-Resistance	GNAI2	2771	37	3	50295019	50295019	Missense_Mutation	SNP	C	T	4	134	c.965C>T	c.(964-966)ACG>ATG	p.T322M
Pat_53	Post-Resistance	ACOX2	8309	37	3	58516196	58516196	Missense_Mutation	SNP	G	A	55	66	c.989C>T	c.(988-990)CCC>CTC	p.P330L
Pat_53	Post-Resistance	MINA	84864	37	3	97686164	97686164	Missense_Mutation	SNP	G	A	5	548	c.274C>T	c.(274-276)CGG>TGG	p.R92W
Pat_53	Post-Resistance	BOC	91653	37	3	112991448	112991448	Missense_Mutation	SNP	G	A	5	119	c.859G>A	c.(859-861)GAC>AAC	p.D287N
Pat_53	Post-Resistance	ILDR1	286676	37	3	121720591	121720591	Splice_Site	SNP	C	T	4	306	c.499_splice	c.e4+1	p.H167_splice
Pat_53	Post-Resistance	TMCC1	23023	37	3	129370347	129370347	Missense_Mutation	SNP	G	A	4	242	c.1939C>T	c.(1939-1941)CGG>TGG	p.R647W
Pat_53	Post-Resistance	TF	7018	37	3	133485208	133485208	Missense_Mutation	SNP	G	A	4	256	c.1417G>A	c.(1417-1419)GTT>ATT	p.V473I
Pat_53	Post-Resistance	PIK3CB	5291	37	3	138409921	138409921	Missense_Mutation	SNP	C	A	5	364	c.1957G>T	c.(1957-1959)GAT>TAT	p.D653Y
Pat_53	Post-Resistance	CLSTN2	64084	37	3	140275377	140275377	Missense_Mutation	SNP	C	T	37	181	c.1697C>T	c.(1696-1698)TCC>TTC	p.S566F
Pat_53	Post-Resistance	SLC25A36	55186	37	3	140675488	140675488	Missense_Mutation	SNP	C	T	5	285	c.161C>T	c.(160-162)GCC>GTC	p.A54V
Pat_53	Post-Resistance	GMPS	8833	37	3	155623981	155623981	Missense_Mutation	SNP	C	T	5	235	c.455C>T	c.(454-456)ACA>ATA	p.T152I
Pat_53	Post-Resistance	CCNL1	57018	37	3	156869994	156869994	Missense_Mutation	SNP	G	A	5	444	c.646C>T	c.(646-648)CGT>TGT	p.R216C
Pat_53	Post-Resistance	FNDC3B	64778	37	3	172061944	172061944	Missense_Mutation	SNP	G	A	5	332	c.2146G>A	c.(2146-2148)GTA>ATA	p.V716I
Pat_53	Post-Resistance	EIF4G1	1981	37	3	184042052	184042052	Nonsense_Mutation	SNP	C	T	4	273	c.2536C>T	c.(2536-2538)CGA>TGA	p.R846*
Pat_53	Post-Resistance	DGKG	1608	37	3	185906038	185906038	Missense_Mutation	SNP	C	T	6	198	c.2048G>A	c.(2047-2049)AGC>AAC	p.S683N
Pat_53	Post-Resistance	DGKG	1608	37	3	186006595	186006595	Missense_Mutation	SNP	G	A	5	489	c.448C>T	c.(448-450)CGG>TGG	p.R150W
Pat_53	Post-Resistance	EIF4A2	1974	37	3	186501409	186501409	Missense_Mutation	SNP	G	T	5	370	c.10G>T	c.(10-12)GGC>TGC	p.G4C
Pat_53	Post-Resistance	RNF168	165918	37	3	196198977	196198977	Missense_Mutation	SNP	G	A	5	248	c.1429C>T	c.(1429-1431)CGC>TGC	p.R477C
Pat_53	Post-Resistance	LMLN	89782	37	3	197717540	197717540	Missense_Mutation	SNP	G	A	4	228	c.1040G>A	c.(1039-1041)CGT>CAT	p.R347H
Pat_53	Post-Resistance	ZNF721	170960	37	4	435653	435653	Missense_Mutation	SNP	C	T	8	176	c.2603G>A	c.(2602-2604)GGA>GAA	p.G868E
Pat_53	Post-Resistance	LETM1	3954	37	4	1824831	1824831	Missense_Mutation	SNP	C	T	4	183	c.1360G>A	c.(1360-1362)GAG>AAG	p.E454K
Pat_53	Post-Resistance	NOP14	8602	37	4	2940976	2940976	Nonsense_Mutation	SNP	G	A	5	349	c.2413C>T	c.(2413-2415)CGA>TGA	p.R805*
Pat_53	Post-Resistance	HTT	3064	37	4	3148660	3148660	Missense_Mutation	SNP	G	A	6	692	c.3286G>A	c.(3286-3288)GGA>AGA	p.G1096R
Pat_53	Post-Resistance	S100P	6286	37	4	6698758	6698758	Missense_Mutation	SNP	G	A	4	252	c.277G>A	c.(277-279)GGA>AGA	p.G93R
Pat_53	Post-Resistance	CPEB2	132864	37	4	15063882	15063882	Missense_Mutation	SNP	C	T	5	507	c.1540C>T	c.(1540-1542)CGT>TGT	p.R514C
Pat_53	Post-Resistance	SLIT2	9353	37	4	20490504	20490504	Missense_Mutation	SNP	G	A	4	362	c.674G>A	c.(673-675)CGC>CAC	p.R225H
Pat_53	Post-Resistance	DHX15	1665	37	4	24534590	24534590	Missense_Mutation	SNP	C	T	6	507	c.1997G>A	c.(1996-1998)CGA>CAA	p.R666Q
Pat_53	Post-Resistance	STIM2	57620	37	4	27019557	27019557	Nonsense_Mutation	SNP	C	T	6	669	c.1999C>T	c.(1999-2001)CGA>TGA	p.R667*
Pat_53	Post-Resistance	TBC1D1	23216	37	4	38016194	38016194	Missense_Mutation	SNP	G	A	4	218	c.482G>A	c.(481-483)TGC>TAC	p.C161Y
Pat_53	Post-Resistance	TLR6	10333	37	4	38829218	38829218	Missense_Mutation	SNP	C	T	5	239	c.1877G>A	c.(1876-1878)CGC>CAC	p.R626H
Pat_53	Post-Resistance	CHRNA9	55584	37	4	40351405	40351405	Missense_Mutation	SNP	C	T	4	114	c.872C>T	c.(871-873)CCG>CTG	p.P291L
Pat_53	Post-Resistance	NSUN7	79730	37	4	40752936	40752936	Missense_Mutation	SNP	C	T	4	109	c.226C>T	c.(226-228)CGG>TGG	p.R76W
Pat_53	Post-Resistance	RUFY3	22902	37	4	71659525	71659525	Missense_Mutation	SNP	G	A	4	123	c.1361G>A	c.(1360-1362)CGC>CAC	p.R454H
Pat_53	Post-Resistance	RASGEF1B	153020	37	4	82380611	82380611	Nonsense_Mutation	SNP	G	A	4	94	c.52C>T	c.(52-54)CGA>TGA	p.R18*
Pat_53	Post-Resistance	PTPN13	5783	37	4	87730992	87730992	Missense_Mutation	SNP	C	T	4	125	c.7154C>T	c.(7153-7155)CCA>CTA	p.P2385L

Pat_53	Post-Resistance	HPGDS	27306	37	4	95223361	95223361	Missense_Mutation	SNP	G	A	5	276	c.371C>T	c.(370-372)GCG>GTG	p.A124V
Pat_53	Post-Resistance	C4orf17	84103	37	4	100434366	100434366	Splice_Site	SNP	G	A	4	172	c.127_splice	c.e2+1	p.G43_splice
Pat_53	Post-Resistance	GLRA3	8001	37	4	175565136	175565136	Missense_Mutation	SNP	G	A	4	183	c.1196C>T	c.(1195-1197)ACT>ATT	p.T399I
Pat_53	Post-Resistance	PAPD7	11044	37	5	6748658	6748658	Missense_Mutation	SNP	C	T	6	406	c.791C>T	c.(790-792)GCT>GTT	p.A264V
Pat_53	Post-Resistance	6-Mar	10299	37	5	10426548	10426548	Missense_Mutation	SNP	G	A	7	546	c.2420G>A	c.(2419-2421)CGT>CAT	p.R807H
Pat_53	Post-Resistance	SLC30A5	64924	37	5	68423862	68423862	Missense_Mutation	SNP	G	A	5	307	c.2030G>A	c.(2029-2031)CGA>CAA	p.R677Q
Pat_53	Post-Resistance	ZNF366	167465	37	5	71752332	71752332	Missense_Mutation	SNP	G	A	5	321	c.1423C>T	c.(1423-1425)CGC>TGC	p.R475C
Pat_53	Post-Resistance	MCTP1	79772	37	5	94248663	94248663	Missense_Mutation	SNP	G	A	5	429	c.1369C>T	c.(1369-1371)CGC>TGC	p.R457C
Pat_53	Post-Resistance	STARD4	134429	37	5	110835597	110835597	Missense_Mutation	SNP	C	T	4	230	c.605G>A	c.(604-606)CGA>CAA	p.R202Q
Pat_53	Post-Resistance	PPP2CA	5515	37	5	133534796	133534796	Missense_Mutation	SNP	C	T	4	89	c.838G>A	c.(838-840)GAT>AAT	p.D280N
Pat_53	Post-Resistance	PHF15	23338	37	5	133887748	133887748	Missense_Mutation	SNP	C	T	4	211	c.160C>T	c.(160-162)CGG>TGG	p.R54W
Pat_53	Post-Resistance	UBE2D2	7322	37	5	138994515	138994515	Nonsense_Mutation	SNP	C	T	6	423	c.268C>T	c.(268-270)CGA>TGA	p.R90*
Pat_53	Post-Resistance	PCDHB13	56123	37	5	140595178	140595178	Missense_Mutation	SNP	G	A	5	189	c.1483G>A	c.(1483-1485)GAC>AAC	p.D495N
Pat_53	Post-Resistance	PCDHGB2	56103	37	5	140741032	140741032	Missense_Mutation	SNP	G	A	4	181	c.1330G>A	c.(1330-1332)GAC>AAC	p.D444N
Pat_53	Post-Resistance	PCDHGA5	56110	37	5	140745615	140745615	Missense_Mutation	SNP	C	T	4	159	c.1718C>T	c.(1717-1719)ACG>ATG	p.T573M
Pat_53	Post-Resistance	DIAPH1	1729	37	5	140960344	140960344	Missense_Mutation	SNP	G	A	5	243	c.791C>T	c.(790-792)TCT>TTT	p.S264F
Pat_53	Post-Resistance	DIAPH1	1729	37	5	140966665	140966665	Nonsense_Mutation	SNP	G	A	5	215	c.244C>T	c.(244-246)CAG>TAG	p.Q82*
Pat_53	Post-Resistance	FCHSD1	89848	37	5	141029015	141029015	Missense_Mutation	SNP	G	A	5	445	c.322C>T	c.(322-324)CGT>TGT	p.R108C
Pat_53	Post-Resistance	RBM27	54439	37	5	145609417	145609417	Missense_Mutation	SNP	G	A	7	357	c.533G>A	c.(532-534)CGC>CAC	p.R178H
Pat_53	Post-Resistance	TCERG1	10915	37	5	145843321	145843321	Missense_Mutation	SNP	G	A	5	367	c.1100G>A	c.(1099-1101)CGT>CAT	p.R367H
Pat_53	Post-Resistance	JAKMIP2	9832	37	5	147019206	147019206	Nonsense_Mutation	SNP	G	A	8	664	c.1519C>T	c.(1519-1521)CGA>TGA	p.R507*
Pat_53	Post-Resistance	ADRB2	154	37	5	148206770	148206770	Missense_Mutation	SNP	G	A	4	280	c.376G>A	c.(376-378)GTG>ATG	p.V126M
Pat_53	Post-Resistance	CSF1R	1436	37	5	149456998	149456998	Missense_Mutation	SNP	G	A	4	233	c.730C>T	c.(730-732)CTC>TTC	p.L244F
Pat_53	Post-Resistance	FAT2	2196	37	5	150885392	150885392	Missense_Mutation	SNP	G	A	4	205	c.12784C>T	c.(12784-12786)CGC>TGC	p.R4262C
Pat_53	Post-Resistance	CYFIP2	26999	37	5	156746911	156746911	Missense_Mutation	SNP	C	T	4	329	c.1498C>T	c.(1498-1500)CGG>TGG	p.R500W
Pat_53	Post-Resistance	ODZ2	57451	37	5	167645361	167645361	Missense_Mutation	SNP	T	C	4	158	c.4438T>C	c.(4438-4440)TAC>CAC	p.Y1480H
Pat_53	Post-Resistance	ODZ2	57451	37	5	167645661	167645661	Missense_Mutation	SNP	G	A	4	207	c.4738G>A	c.(4738-4740)GGA>AGA	p.G1580R
Pat_53	Post-Resistance	DOCK2	1794	37	5	169138991	169138991	Missense_Mutation	SNP	G	A	4	163	c.1535G>A	c.(1534-1536)CGA>CAA	p.R512Q
Pat_53	Post-Resistance	DOCK2	1794	37	5	169138996	169138996	Missense_Mutation	SNP	C	T	4	163	c.1540C>T	c.(1540-1542)CGG>TGG	p.R514W
Pat_53	Post-Resistance	STK10	6793	37	5	171523561	171523561	Missense_Mutation	SNP	G	A	89	254	c.874C>T	c.(874-876)CCC>TCC	p.P292S
Pat_53	Post-Resistance	SFXN1	94081	37	5	174938494	174938494	Missense_Mutation	SNP	G	A	5	470	c.475G>A	c.(475-477)GTA>ATA	p.V159I
Pat_53	Post-Resistance	MAML1	9794	37	5	179195951	179195951	Missense_Mutation	SNP	A	G	13	244	c.1832A>G	c.(1831-1833)TAT>TGT	p.Y611C
Pat_53	Post-Resistance	MAML1	9794	37	5	179200916	179200916	Missense_Mutation	SNP	G	A	4	232	c.2089G>A	c.(2089-2091)GGC>AGC	p.G697S
Pat_53	Post-Resistance	DSP	1832	37	6	7586049	7586049	Missense_Mutation	SNP	G	A	4	147	c.8554G>A	c.(8554-8556)GCC>ACC	p.A2852T
Pat_53	Post-Resistance	TRIM10	10107	37	6	30126280	30126280	Missense_Mutation	SNP	G	A	6	595	c.652C>T	c.(652-654)CGG>TGG	p.R218W
Pat_53	Post-Resistance	DDR1	780	37	6	30857068	30857068	Missense_Mutation	SNP	G	A	4	171	c.278G>A	c.(277-279)CGA>CAA	p.R93Q
Pat_53	Post-Resistance	VARS2	57176	37	6	30886666	30886666	Missense_Mutation	SNP	G	A	4	170	c.1048G>A	c.(1048-1050)GTT>ATT	p.V350I
Pat_53	Post-Resistance	VARS2	57176	37	6	30887548	30887548	Missense_Mutation	SNP	G	A	6	585	c.1088G>A	c.(1087-1089)CGA>CAA	p.R363Q
Pat_53	Post-Resistance	C6orf27	80737	37	6	31735444	31735444	Missense_Mutation	SNP	G	A	6	365	c.1591C>T	c.(1591-1593)CGG>TGG	p.R531W
Pat_53	Post-Resistance	HSPA1L	3305	37	6	31778194	31778194	Missense_Mutation	SNP	C	T	6	697	c.1556G>A	c.(1555-1557)CGC>CAC	p.R519H
Pat_53	Post-Resistance	ATF6B	1388	37	6	32093933	32093933	Missense_Mutation	SNP	C	T	4	283	c.439G>A	c.(439-441)GTC>ATC	p.V147I
Pat_53	Post-Resistance	BYSL	705	37	6	41900193	41900193	Missense_Mutation	SNP	C	T	4	206	c.1063C>T	c.(1063-1065)CGG>TGG	p.R355W
Pat_53	Post-Resistance	TRERF1	55809	37	6	42236862	42236862	Missense_Mutation	SNP	C	T	4	350	c.467G>A	c.(466-468)CGA>CAA	p.R156Q
Pat_53	Post-Resistance	TRERF1	55809	37	6	42236889	42236889	Missense_Mutation	SNP	G	A	6	416	c.440C>T	c.(439-441)ACC>ATC	p.T147I
Pat_53	Post-Resistance	EFHC1	114327	37	6	52317558	52317558	Nonsense_Mutation	SNP	C	T	4	364	c.646C>T	c.(646-648)CGA>TGA	p.R216*
Pat_53	Post-Resistance	MANEA	79694	37	6	96054018	96054018	Nonsense_Mutation	SNP	C	T	4	157	c.1126C>T	c.(1126-1128)CGA>TGA	p.R376*
Pat_53	Post-Resistance	GJA1	2697	37	6	121768889	121768889	Missense_Mutation	SNP	G	T	4	120	c.896G>T	c.(895-897)CGC>CTC	p.R299L

Pat_53	Post-Resistance	RNF217	154214	37	6	125397950	125397950	Missense_Mutation	SNP	C	T	4	201	c.553C>T	c.(553-555)CGC>TGC	p.R185C
Pat_53	Post-Resistance	ARG1	383	37	6	131903856	131903856	Splice_Site	SNP	G	A	4	108	c.560_splice	c.e5+1	p.H187_splice
Pat_53	Post-Resistance	TAAR8	83551	37	6	132874313	132874313	Missense_Mutation	SNP	C	T	4	262	c.482C>T	c.(481-483)ACG>ATG	p.T161M
Pat_53	Post-Resistance	BCLAF1	9774	37	6	136597052	136597052	Missense_Mutation	SNP	C	T	54	367	c.1611G>A	c.(1609-1611)ATG>ATA	p.M537I
Pat_53	Post-Resistance	BCLAF1	9774	37	6	136599354	136599354	Missense_Mutation	SNP	C	T	4	268	c.665G>A	c.(664-666)AGT>AAT	p.S222N
Pat_53	Post-Resistance	SYNE1	23345	37	6	152621904	152621904	Missense_Mutation	SNP	G	A	4	123	c.17554C>T	c.(17554-17556)CGC>TGC	p.R5852C
Pat_53	Post-Resistance	MAS1	4142	37	6	160328255	160328255	Missense_Mutation	SNP	G	A	5	231	c.268G>A	c.(268-270)GAC>AAC	p.D90N
Pat_53	Post-Resistance	SLC22A2	6582	37	6	160664672	160664672	Missense_Mutation	SNP	C	T	4	153	c.1211G>A	c.(1210-1212)CGT>CAT	p.R404H
Pat_53	Post-Resistance	AGPAT4	56895	37	6	161560486	161560486	Missense_Mutation	SNP	G	A	4	153	c.1010C>T	c.(1009-1011)ACG>ATG	p.T337M
Pat_53	Post-Resistance	MLLT4	4301	37	6	168344148	168344148	Missense_Mutation	SNP	C	A	4	148	c.3208C>A	c.(3208-3210)CAG>AAG	p.Q1070K
Pat_53	Post-Resistance	MIOS	54468	37	7	7625425	7625425	Missense_Mutation	SNP	G	A	5	515	c.1807G>A	c.(1807-1809)GAT>AAT	p.D603N
Pat_53	Post-Resistance	PRPS1L1	221823	37	7	18067261	18067261	Missense_Mutation	SNP	G	A	5	629	c.145C>T	c.(145-147)CGT>TGT	p.R49C
Pat_53	Post-Resistance	DNAH11	8701	37	7	21940631	21940631	Missense_Mutation	SNP	G	A	6	431	c.13331G>A	c.(13330-13332)CGC>CAC	p.R4444H
Pat_53	Post-Resistance	GLI3	2737	37	7	42088134	42088134	Missense_Mutation	SNP	G	A	4	270	c.635C>T	c.(634-636)TCG>TTG	p.S212L
Pat_53	Post-Resistance	POLD2	5425	37	7	44157660	44157660	Missense_Mutation	SNP	C	T	4	94	c.224G>A	c.(223-225)AGT>AAT	p.S75N
Pat_53	Post-Resistance	DDC	1644	37	7	50611650	50611650	Missense_Mutation	SNP	G	A	4	218	c.134C>T	c.(133-135)GCT>GTT	p.A45V
Pat_53	Post-Resistance	COBL	23242	37	7	51096824	51096824	Missense_Mutation	SNP	C	T	4	225	c.1969G>A	c.(1969-1971)GGG>AGG	p.G657R
Pat_53	Post-Resistance	ZNF479	90827	37	7	57187725	57187725	Missense_Mutation	SNP	G	T	11	357	c.1397C>A	c.(1396-1398)ACA>AAA	p.T466K
Pat_53	Post-Resistance	ZNF92	168374	37	7	64863755	64863756	Missense_Mutation	DNP	AT	CC	9	479	c.728_729AT>CC	c.(727-729)AAT>ACC	p.N243T
Pat_53	Post-Resistance	ZNF92	168374	37	7	64863830	64863830	Missense_Mutation	SNP	G	A	6	570	c.803G>A	c.(802-804)CGG>CAG	p.R268Q
Pat_53	Post-Resistance	RHBDD2	57414	37	7	75517395	75517395	Missense_Mutation	SNP	G	A	4	234	c.823G>A	c.(823-825)GCC>ACC	p.A275T
Pat_53	Post-Resistance	ZNF804B	219578	37	7	88962859	88962859	Missense_Mutation	SNP	G	A	4	195	c.563G>A	c.(562-564)CGA>CAA	p.R188Q
Pat_53	Post-Resistance	C7orf63	79846	37	7	89894641	89894641	Missense_Mutation	SNP	C	T	6	529	c.383C>T	c.(382-384)TCG>TTG	p.S128L
Pat_53	Post-Resistance	PEX1	5189	37	7	92131236	92131236	Missense_Mutation	SNP	C	T	6	399	c.2384G>A	c.(2383-2385)CGA>CAA	p.R795Q
Pat_53	Post-Resistance	DYNC1I1	1780	37	7	95665055	95665055	Missense_Mutation	SNP	G	A	6	487	c.1406G>A	c.(1405-1407)CGT>CAT	p.R469H
Pat_53	Post-Resistance	PTCD1	26024	37	7	99021441	99021441	Missense_Mutation	SNP	C	T	5	382	c.1877G>A	c.(1876-1878)CGC>CAC	p.R626H
Pat_53	Post-Resistance	PTCD1	26024	37	7	99032459	99032459	Missense_Mutation	SNP	G	A	5	482	c.407C>T	c.(406-408)CCG>CTG	p.P136L
Pat_53	Post-Resistance	FBXO24	26261	37	7	100187616	100187616	Missense_Mutation	SNP	C	T	77	153	c.56C>T	c.(55-57)CCT>CTT	p.P19L
Pat_53	Post-Resistance	GIGYF1	64599	37	7	100284665	100284665	Missense_Mutation	SNP	C	T	4	251	c.487G>A	c.(487-489)GAG>AAG	p.E163K
Pat_53	Post-Resistance	ZAN	7455	37	7	100349878	100349878	Missense_Mutation	SNP	C	T	5	406	c.2150C>T	c.(2149-2151)CCC>CTC	p.P717L
Pat_53	Post-Resistance	RBM28	55131	37	7	127950869	127950869	Missense_Mutation	SNP	C	T	5	288	c.2261G>A	c.(2260-2262)AGC>AAC	p.S754N
Pat_53	Post-Resistance	AHCYL2	23382	37	7	129066314	129066314	Missense_Mutation	SNP	C	T	4	162	c.1739C>T	c.(1738-1740)ACC>ATC	p.T580I
Pat_53	Post-Resistance	CPA1	1357	37	7	130027693	130027693	Nonsense_Mutation	SNP	G	A	288	401	c.1101G>A	c.(1099-1101)TGG>TGA	p.W367*
Pat_53	Post-Resistance	MKLN1	4289	37	7	131122671	131122671	Missense_Mutation	SNP	G	A	6	529	c.1088G>A	c.(1087-1089)CGT>CAT	p.R363H
Pat_53	Post-Resistance	PLXNA4	91584	37	7	131832704	131832704	Missense_Mutation	SNP	C	T	4	133	c.4819G>A	c.(4819-4821)GCA>ACA	p.A1607T
Pat_53	Post-Resistance	NUP205	23165	37	7	135312771	135312771	Missense_Mutation	SNP	G	A	6	552	c.4844G>A	c.(4843-4845)CGC>CAC	p.R1615H
Pat_53	Post-Resistance	SLC13A4	26266	37	7	135391022	135391022	Missense_Mutation	SNP	G	A	4	100	c.392C>T	c.(391-393)ACC>ATC	p.T131I
Pat_53	Post-Resistance	TRIM24	8805	37	7	138252271	138252271	Missense_Mutation	SNP	C	T	203	269	c.1576C>T	c.(1576-1578)CCC>TCC	p.P526S
Pat_53	Post-Resistance	DENND2A	27147	37	7	140287471	140287471	Missense_Mutation	SNP	C	T	4	275	c.1105G>A	c.(1105-1107)GTC>ATC	p.V369I
Pat_53	Post-Resistance	UBE3C	9690	37	7	156974362	156974362	Missense_Mutation	SNP	C	T	5	330	c.767C>T	c.(766-768)GCG>GTG	p.A256V
Pat_53	Post-Resistance	RP1L1	94137	37	8	10466059	10466059	Missense_Mutation	SNP	C	T	5	377	c.5549G>A	c.(5548-5550)GGT>GAT	p.G1850D
Pat_53	Post-Resistance	FDFT1	2222	37	8	11687816	11687816	Missense_Mutation	SNP	G	A	4	275	c.766G>A	c.(766-768)GTG>ATG	p.V256M
Pat_53	Post-Resistance	ENTPD4	9583	37	8	23306367	23306367	Missense_Mutation	SNP	G	A	5	412	c.94C>T	c.(94-96)CGC>TGC	p.R32C
Pat_53	Post-Resistance	KCTD9	54793	37	8	25293759	25293759	Nonsense_Mutation	SNP	G	A	5	369	c.655C>T	c.(655-657)CGA>TGA	p.R219*
Pat_53	Post-Resistance	EXTL3	2137	37	8	28595080	28595080	Missense_Mutation	SNP	G	A	4	226	c.2321G>A	c.(2320-2322)CGT>CAT	p.R774H
Pat_53	Post-Resistance	FGFR1	2260	37	8	38272338	38272338	Missense_Mutation	SNP	G	A	4	166	c.1936C>T	c.(1936-1938)CGG>TGG	p.R646W
Pat_53	Post-Resistance	ATP6V0D2	245972	37	8	87162459	87162459	Missense_Mutation	SNP	G	A	4	207	c.758G>A	c.(757-759)CGG>CAG	p.R253Q

Pat_53	Post-Resistance	DCAF13	25879	37	8	104433227	104433227	Missense_Mutation	SNP	C	T	5	222	c.751C>T	c.(751-753)CGG>TGG	p.R251W
Pat_53	Post-Resistance	OXR1	55074	37	8	107726086	107726086	Missense_Mutation	SNP	G	A	5	492	c.1832G>A	c.(1831-1833)AGT>AAT	p.S611N
Pat_53	Post-Resistance	EIF3E	3646	37	8	109226887	109226887	Missense_Mutation	SNP	C	T	4	278	c.1010G>A	c.(1009-1011)CGT>CAT	p.R337H
Pat_53	Post-Resistance	GSDMC	56169	37	8	130789733	130789733	Missense_Mutation	SNP	C	T	4	270	c.101G>A	c.(100-102)CGT>CAT	p.R34H
Pat_53	Post-Resistance	PLEC	5339	37	8	145011179	145011179	Missense_Mutation	SNP	C	A	4	169	c.814G>T	c.(814-816)GGC>TGC	p.G272C
Pat_53	Post-Resistance	GRINA	2907	37	8	145066134	145066134	Missense_Mutation	SNP	G	A	4	315	c.581G>A	c.(580-582)CGG>CAG	p.R194Q
Pat_53	Post-Resistance	SPATC1	375686	37	8	145095844	145095844	Missense_Mutation	SNP	G	A	4	160	c.1142G>A	c.(1141-1143)TGT>TAT	p.C381Y
Pat_53	Post-Resistance	HSF1	3297	37	8	145532616	145532616	Missense_Mutation	SNP	G	A	4	182	c.142G>A	c.(142-144)GAC>AAC	p.D48N
Pat_53	Post-Resistance	CPSF1	29894	37	8	145624179	145624179	Missense_Mutation	SNP	C	T	4	190	c.1628G>A	c.(1627-1629)CGT>CAT	p.R543H
Pat_53	Post-Resistance	ZNF250	58500	37	8	146112263	146112263	Missense_Mutation	SNP	G	A	4	223	c.323C>T	c.(322-324)ACA>ATA	p.T108I
Pat_53	Post-Resistance	IFNA14	3448	37	9	21239652	21239652	Missense_Mutation	SNP	T	C	11	142	c.283A>G	c.(283-285)AAC>GAC	p.N95D
Pat_53	Post-Resistance	IFNA2	3440	37	9	21384947	21384947	Missense_Mutation	SNP	C	T	5	172	c.382G>A	c.(382-384)GTG>ATG	p.V128M
Pat_53	Post-Resistance	DCTN3	11258	37	9	34618733	34618733	Missense_Mutation	SNP	G	T	4	181	c.121C>A	c.(121-123)CAG>AAG	p.Q41K
Pat_53	Post-Resistance	IL11RA	3590	37	9	34660865	34660865	Missense_Mutation	SNP	G	A	6	438	c.1184G>A	c.(1183-1185)CGG>CAG	p.R395Q
Pat_53	Post-Resistance	UNC13B	10497	37	9	35310546	35310546	Missense_Mutation	SNP	G	A	4	141	c.844G>A	c.(844-846)GAA>AAA	p.E282K
Pat_53	Post-Resistance	CCDC107	203260	37	9	35660865	35660865	Missense_Mutation	SNP	C	T	5	509	c.533C>T	c.(532-534)TCG>TTG	p.S178L
Pat_53	Post-Resistance	FBXO10	26267	37	9	37515899	37515899	Splice_Site	SNP	A	C	5	198	c.2696_splice	c.e10+1	p.K899_splice
Pat_53	Post-Resistance	CNTNAP3	79937	37	9	39085766	39085766	Missense_Mutation	SNP	C	T	4	188	c.3409G>A	c.(3409-3411)GCC>ACC	p.A1137T
Pat_53	Post-Resistance	LOC442421	442421	37	9	66499794	66499795	Missense_Mutation	DNP	CG	TA	6	117	c.604_605CG>TA	c.(604-606)CGC>TAC	p.R202Y
Pat_53	Post-Resistance	APBA1	320	37	9	72082836	72082836	Missense_Mutation	SNP	G	A	4	249	c.1385C>T	c.(1384-1386)GCC>GTC	p.A462V
Pat_53	Post-Resistance	ZNF484	83744	37	9	95609456	95609456	Missense_Mutation	SNP	C	T	6	229	c.1613G>A	c.(1612-1614)CGG>CAG	p.R538Q
Pat_53	Post-Resistance	OR13C5	138799	37	9	107361252	107361252	Missense_Mutation	SNP	G	A	4	109	c.443C>T	c.(442-444)TCC>TTC	p.S148F
Pat_53	Post-Resistance	OR13D1	286365	37	9	107457091	107457091	Missense_Mutation	SNP	C	T	4	147	c.389C>T	c.(388-390)GCT>GTT	p.A130V
Pat_53	Post-Resistance	GPR21	2844	37	9	125797566	125797566	Missense_Mutation	SNP	G	A	4	213	c.721G>A	c.(721-723)GAA>AAA	p.E241K
Pat_53	Post-Resistance	MAPKAP1	79109	37	9	128230280	128230280	Missense_Mutation	SNP	G	A	4	179	c.1316C>T	c.(1315-1317)GCC>GTC	p.A439V
Pat_53	Post-Resistance	GARNL3	84253	37	9	130094623	130094623	Missense_Mutation	SNP	G	A	6	222	c.665G>A	c.(664-666)AGC>AAC	p.S222N
Pat_53	Post-Resistance	DNM1	1759	37	9	130980524	130980524	Missense_Mutation	SNP	G	A	6	433	c.176G>A	c.(175-177)CGA>CAA	p.R59Q
Pat_53	Post-Resistance	DNM1	1759	37	9	130984516	130984516	Missense_Mutation	SNP	G	A	4	202	c.890G>A	c.(889-891)CGG>CAG	p.R297Q
Pat_53	Post-Resistance	SPTAN1	6709	37	9	131345061	131345061	Missense_Mutation	SNP	G	A	4	180	c.1739G>A	c.(1738-1740)CGT>CAT	p.R580H
Pat_53	Post-Resistance	USP20	10868	37	9	132630419	132630419	Missense_Mutation	SNP	C	T	4	112	c.826C>T	c.(826-828)CGG>TGG	p.R276W
Pat_53	Post-Resistance	GPR107	57720	37	9	132838709	132838709	Missense_Mutation	SNP	C	T	4	220	c.274C>T	c.(274-276)CGT>TGT	p.R92C
Pat_53	Post-Resistance	BAT2L1	84726	37	9	134334625	134334625	Missense_Mutation	SNP	G	A	4	159	c.1286G>A	c.(1285-1287)CGA>CAA	p.R429Q
Pat_53	Post-Resistance	CSF2RA	1438	37	X	1413250	1413250	Missense_Mutation	SNP	G	A	5	362	c.676G>A	c.(676-678)GTA>ATA	p.V226I
Pat_53	Post-Resistance	ZBED1	9189	37	X	2407302	2407302	Missense_Mutation	SNP	C	T	5	143	c.1459G>A	c.(1459-1461)GCC>ACC	p.A487T
Pat_53	Post-Resistance	FRMPD4	9758	37	X	12632978	12632978	Missense_Mutation	SNP	G	A	35	25	c.400G>A	c.(400-402)GAG>AAG	p.E134K
Pat_53	Post-Resistance	PRPS2	5634	37	X	12840860	12840860	Missense_Mutation	SNP	G	A	5	108	c.902G>A	c.(901-903)CGA>CAA	p.R301Q
Pat_53	Post-Resistance	RPGR	6103	37	X	38146316	38146316	Missense_Mutation	SNP	C	T	4	313	c.1936G>A	c.(1936-1938)GAA>AAA	p.E646K
Pat_53	Post-Resistance	GLA	2717	37	X	100656710	100656710	Missense_Mutation	SNP	C	T	4	166	c.457G>A	c.(457-459)GAC>AAC	p.D153N
Pat_53	Post-Resistance	UTP14A	10813	37	X	129042648	129042648	Missense_Mutation	SNP	G	A	6	673	c.176G>A	c.(175-177)CGG>CAG	p.R59Q
Pat_53	Post-Resistance	NSDHL	50814	37	X	152034456	152034456	Missense_Mutation	SNP	C	T	4	131	c.637C>T	c.(637-639)CCC>TCC	p.P213S
Pat_58	Pre-Treatment	TPRG1L	127262	37	1	3545096	3545096	Missense_Mutation	SNP	G	A	4	39	c.748G>A	c.(748-750)GGA>AGA	p.G250R
Pat_58	Pre-Treatment	ERRFI1	54206	37	1	8073955	8073955	Missense_Mutation	SNP	G	C	3	12	c.704C>G	c.(703-705)CCA>CGA	p.P235R
Pat_58	Pre-Treatment	MTHFR	4524	37	1	11863105	11863105	Missense_Mutation	SNP	A	T	4	21	c.69T>A	c.(67-69)AGT>AGA	p.S23R
Pat_58	Pre-Treatment	KIAA2013	90231	37	1	11983420	11983420	Missense_Mutation	SNP	C	T	4	49	c.1160G>A	c.(1159-1161)CGA>CAA	p.R387Q
Pat_58	Pre-Treatment	SPEN	23013	37	1	16262235	16262235	Missense_Mutation	SNP	C	T	4	61	c.9500C>T	c.(9499-9501)GCT>GTT	p.A3167V
Pat_58	Pre-Treatment	ARHGEF10L	55160	37	1	17965138	17965138	Missense_Mutation	SNP	G	A	3	29	c.2125G>A	c.(2125-2127)GCC>ACC	p.A709T
Pat_58	Pre-Treatment	ASAP3	55616	37	1	23765242	23765242	Missense_Mutation	SNP	G	A	4	48	c.1100C>T	c.(1099-1101)ACC>ATC	p.T367I

Pat_58	Pre-Treatment	RPL11	6135	37	1	24021193	24021193	Missense_Mutation	SNP	G	A	23	63	c.308G>A	c.(307-309)GGA>GAA	p.G103E
Pat_58	Pre-Treatment	SLC30A2	7780	37	1	26369919	26369919	Missense_Mutation	SNP	G	A	4	63	c.395C>T	c.(394-396)ACG>ATG	p.T132M
Pat_58	Pre-Treatment	UBXN11	91544	37	1	26629332	26629332	Missense_Mutation	SNP	G	A	3	34	c.43C>T	c.(43-45)CCC>TCC	p.P15S
Pat_58	Pre-Treatment	GPR3	2827	37	1	27720966	27720966	Missense_Mutation	SNP	C	T	4	62	c.664C>T	c.(664-666)CGC>TGC	p.R222C
Pat_58	Pre-Treatment	GMEB1	10691	37	1	29041259	29041259	Missense_Mutation	SNP	G	A	4	76	c.1696G>A	c.(1696-1698)GTG>ATG	p.V566M
Pat_58	Pre-Treatment	THRAP3	9967	37	1	36769491	36769491	Missense_Mutation	SNP	G	A	4	53	c.2741G>A	c.(2740-2742)CGG>CAG	p.R914Q
Pat_58	Pre-Treatment	PTCH2	8643	37	1	45296653	45296653	Missense_Mutation	SNP	G	A	5	19	c.680C>T	c.(679-681)CCC>CTC	p.P227L
Pat_58	Pre-Treatment	CYP4B1	1580	37	1	47279163	47279163	Missense_Mutation	SNP	G	A	14	40	c.505G>A	c.(505-507)GAA>AAA	p.E169K
Pat_58	Pre-Treatment	C1orf175	374977	37	1	55119789	55119789	Missense_Mutation	SNP	C	A	4	10	c.1190C>A	c.(1189-1191)CCC>CAC	p.P397H
Pat_58	Pre-Treatment	LRRIQ3	127255	37	1	74575152	74575152	Missense_Mutation	SNP	C	T	4	46	c.793G>A	c.(793-795)GAA>AAA	p.E265K
Pat_58	Pre-Treatment	ST6GALNAC5	81849	37	1	77510003	77510003	Missense_Mutation	SNP	G	A	4	71	c.376G>A	c.(376-378)GCC>ACC	p.A126T
Pat_58	Pre-Treatment	ZNF326	284695	37	1	90473211	90473211	Missense_Mutation	SNP	C	T	4	47	c.517C>T	c.(517-519)CGG>TGG	p.R173W
Pat_58	Pre-Treatment	RTCD1	8634	37	1	100740418	100740418	Missense_Mutation	SNP	G	A	4	54	c.512G>A	c.(511-513)CGA>CAA	p.R171Q
Pat_58	Pre-Treatment	SLC6A17	388662	37	1	110740704	110740704	Nonsense_Mutation	SNP	G	T	4	26	c.1822G>T	c.(1822-1824)GAG>TAG	p.E608*
Pat_58	Pre-Treatment	MAGI3	260425	37	1	114133169	114133169	Missense_Mutation	SNP	C	G	3	33	c.827C>G	c.(826-828)ACA>AGA	p.T276R
Pat_58	Pre-Treatment	S100A12	6283	37	1	153347041	153347041	Missense_Mutation	SNP	C	T	37	92	c.28G>A	c.(28-30)GGA>AGA	p.G10R
Pat_58	Pre-Treatment	RAB25	57111	37	1	156038179	156038179	Missense_Mutation	SNP	G	A	4	69	c.358G>A	c.(358-360)GTC>ATC	p.V120I
Pat_58	Pre-Treatment	DUSP27	92235	37	1	167095933	167095933	Missense_Mutation	SNP	G	A	21	69	c.1565G>A	c.(1564-1566)AGC>AAC	p.S522N
Pat_58	Pre-Treatment	TNR	7143	37	1	175375489	175375489	Missense_Mutation	SNP	G	A	28	63	c.362C>T	c.(361-363)CCC>CTC	p.P121L
Pat_58	Pre-Treatment	PAPPA2	60676	37	1	176525627	176525627	Nonsense_Mutation	SNP	C	T	36	26	c.169C>T	c.(169-171)CGA>TGA	p.R57*
Pat_58	Pre-Treatment	ASTN1	460	37	1	176915173	176915173	Missense_Mutation	SNP	C	T	18	46	c.2138G>A	c.(2137-2139)GGG>GAG	p.G713E
Pat_58	Pre-Treatment	CHI3L1	1116	37	1	203150331	203150331	Nonsense_Mutation	SNP	G	A	4	70	c.670C>T	c.(670-672)CGA>TGA	p.R224*
Pat_58	Pre-Treatment	PIGR	5284	37	1	207112655	207112655	Missense_Mutation	SNP	G	A	5	28	c.197C>T	c.(196-198)ACC>ATC	p.T66I
Pat_58	Pre-Treatment	USH2A	7399	37	1	216497021	216497021	Missense_Mutation	SNP	G	A	4	65	c.1345C>T	c.(1345-1347)CGT>TGT	p.R449C
Pat_58	Pre-Treatment	PRSS38	339501	37	1	228005043	228005043	Missense_Mutation	SNP	G	A	4	60	c.445G>A	c.(445-447)GGT>AGT	p.G149S
Pat_58	Pre-Treatment	KIAA1804	84451	37	1	233507802	233507802	Missense_Mutation	SNP	C	T	20	41	c.1571C>T	c.(1570-1572)ACC>ATC	p.T524I
Pat_58	Pre-Treatment	GREM2	64388	37	1	240656324	240656324	Missense_Mutation	SNP	T	C	4	41	c.452A>G	c.(451-453)AAG>AGG	p.K151R
Pat_58	Pre-Treatment	OR2W5	441932	37	1	247654805	247654805	Missense_Mutation	SNP	G	A	4	76	c.376G>A	c.(376-378)GTC>ATC	p.V126I
Pat_58	Pre-Treatment	SPAG6	9576	37	10	22705595	22705595	Missense_Mutation	SNP	G	A	4	74	c.1508G>A	c.(1507-1509)AGC>AAC	p.S503N
Pat_58	Pre-Treatment	PDSS1	23590	37	10	27024423	27024423	Missense_Mutation	SNP	C	T	4	55	c.941C>T	c.(940-942)TCG>TTG	p.S314L
Pat_58	Pre-Treatment	PTCHD3	374308	37	10	27702446	27702446	Missense_Mutation	SNP	T	C	3	28	c.734A>G	c.(733-735)AAG>AGG	p.K245R
Pat_58	Pre-Treatment	RET	5979	37	10	43597792	43597792	Missense_Mutation	SNP	C	T	17	30	c.340C>T	c.(340-342)CGC>TGC	p.R114C
Pat_58	Pre-Treatment	ARHGAP22	58504	37	10	49687709	49687709	Missense_Mutation	SNP	G	A	3	18	c.421C>T	c.(421-423)CGC>TGC	p.R141C
Pat_58	Pre-Treatment	NDST2	8509	37	10	75566525	75566525	Missense_Mutation	SNP	G	A	4	38	c.1138C>T	c.(1138-1140)CGC>TGC	p.R380C
Pat_58	Pre-Treatment	PTEN	5728	37	10	89692899	89692899	Missense_Mutation	SNP	A	C	34	55	c.383A>C	c.(382-384)AAG>ACG	p.K128T
Pat_58	Pre-Treatment	PLCE1	51196	37	10	95791173	95791173	Missense_Mutation	SNP	G	A	12	23	c.370G>A	c.(370-372)GAA>AAA	p.E124K
Pat_58	Pre-Treatment	C10orf12	26148	37	10	98708864	98708864	Missense_Mutation	SNP	G	A	4	55	c.50G>A	c.(49-51)AGC>AAC	p.S17N
Pat_58	Pre-Treatment	GBF1	8729	37	10	104140383	104140383	Missense_Mutation	SNP	C	T	7	248	c.5110C>T	c.(5110-5112)CGC>TGC	p.R1704C
Pat_58	Pre-Treatment	CDHR5	53841	37	11	618994	618994	Missense_Mutation	SNP	G	A	4	57	c.1565C>T	c.(1564-1566)CCG>CTG	p.P522L
Pat_58	Pre-Treatment	MUC2	4583	37	11	1078526	1078526	Missense_Mutation	SNP	C	T	2	1	c.734C>T	c.(733-735)CCG>CTG	p.P245L
Pat_58	Pre-Treatment	KRTAP5-5	439915	37	11	1651483	1651483	Missense_Mutation	SNP	G	C	4	50	c.413G>C	c.(412-414)GGC>GCC	p.G138A
Pat_58	Pre-Treatment	OR52B2	255725	37	11	6191079	6191079	Missense_Mutation	SNP	G	A	12	37	c.478C>T	c.(478-480)CCA>TCA	p.P160S
Pat_58	Pre-Treatment	PAMR1	25891	37	11	35456088	35456088	Missense_Mutation	SNP	C	T	4	80	c.1598G>A	c.(1597-1599)CGG>CAG	p.R533Q
Pat_58	Pre-Treatment	OR5M8	219484	37	11	56258567	56258567	Missense_Mutation	SNP	G	A	32	71	c.280C>T	c.(280-282)CCT>TCT	p.P94S
Pat_58	Pre-Treatment	TNKS1BP1	85456	37	11	57077669	57077669	Missense_Mutation	SNP	G	C	4	71	c.2516C>G	c.(2515-2517)GCA>GGA	p.A839G
Pat_58	Pre-Treatment	P2RX3	5024	37	11	57137436	57137436	Missense_Mutation	SNP	C	T	10	43	c.1160C>T	c.(1159-1161)TCC>TTC	p.S387F
Pat_58	Pre-Treatment	OR9Q2	219957	37	11	57958302	57958302	Missense_Mutation	SNP	C	T	44	85	c.340C>T	c.(340-342)CTT>TTT	p.L114F

Pat_58	Pre-Treatment	OR5A1	219982	37	11	59211486	59211486	Missense_Mutation	SNP	C	T	30	89	c.845C>T	c.(844-846)TCA>TTA	p.S282L
Pat_58	Pre-Treatment	AHNAK	79026	37	11	62295435	62295435	Missense_Mutation	SNP	C	A	7	242	c.6454G>T	c.(6454-6456)GAT>TAT	p.D2152Y
Pat_58	Pre-Treatment	IL18BP	10068	37	11	71711573	71711573	Missense_Mutation	SNP	G	A	4	62	c.205G>A	c.(205-207)GTG>ATG	p.V69M
Pat_58	Pre-Treatment	HTR3A	3359	37	11	113857451	113857451	Missense_Mutation	SNP	G	C	13	56	c.935G>C	c.(934-936)GGT>GCT	p.G312A
Pat_58	Pre-Treatment	TECTA	7007	37	11	121028919	121028919	Missense_Mutation	SNP	C	T	4	71	c.4675C>T	c.(4675-4677)CGG>TGG	p.R1559W
Pat_58	Pre-Treatment	SORL1	6653	37	11	121415957	121415957	Missense_Mutation	SNP	C	T	4	22	c.1870C>T	c.(1870-1872)CCC>TCC	p.P624S
Pat_58	Pre-Treatment	LOH12CR1	118426	37	12	12514232	12514232	Missense_Mutation	SNP	C	T	32	104	c.151C>T	c.(151-153)CCC>TCC	p.P51S
Pat_58	Pre-Treatment	PPFIBP1	8496	37	12	27802985	27802985	Missense_Mutation	SNP	C	A	13	25	c.514C>A	c.(514-516)CTG>ATG	p.L172M
Pat_58	Pre-Treatment	BICD1	636	37	12	32480402	32480402	Missense_Mutation	SNP	G	A	4	67	c.1013G>A	c.(1012-1014)CGG>CAG	p.R338Q
Pat_58	Pre-Treatment	CNTN1	1272	37	12	41410489	41410489	Missense_Mutation	SNP	G	C	7	17	c.2190G>C	c.(2188-2190)TTG>TTC	p.L730F
Pat_58	Pre-Treatment	TMEM117	84216	37	12	44781917	44781917	Missense_Mutation	SNP	C	T	3	17	c.1007C>T	c.(1006-1008)CCG>CTG	p.P336L
Pat_58	Pre-Treatment	CALCOCO1	57658	37	12	54107678	54107678	Missense_Mutation	SNP	G	A	3	18	c.1598C>T	c.(1597-1599)CCG>CTG	p.P533L
Pat_58	Pre-Treatment	ZC3H10	84872	37	12	56515410	56515410	Missense_Mutation	SNP	C	T	4	66	c.1064C>T	c.(1063-1065)CCC>CTC	p.P355L
Pat_58	Pre-Treatment	NUP107	57122	37	12	69107527	69107527	Missense_Mutation	SNP	C	T	13	76	c.908C>T	c.(907-909)ACC>ATC	p.T303I
Pat_58	Pre-Treatment	NAA25	80018	37	12	112486232	112486232	Missense_Mutation	SNP	T	C	19	30	c.1744A>G	c.(1744-1746)ATT>GTT	p.I582V
Pat_58	Pre-Treatment	GCN1L1	10985	37	12	120569047	120569047	Missense_Mutation	SNP	G	A	4	57	c.7505C>T	c.(7504-7506)GCC>GTC	p.A2502V
Pat_58	Pre-Treatment	MLXIP	22877	37	12	122622019	122622019	Missense_Mutation	SNP	G	A	3	25	c.2036G>A	c.(2035-2037)CGG>CAG	p.R679Q
Pat_58	Pre-Treatment	GPR109A	338442	37	12	123187436	123187436	Missense_Mutation	SNP	G	A	7	134	c.395C>T	c.(394-396)CCC>CTC	p.P132L
Pat_58	Pre-Treatment	GPR109B	8843	37	12	123200890	123200890	Missense_Mutation	SNP	G	A	28	79	c.395C>T	c.(394-396)CCC>CTC	p.P132L
Pat_58	Pre-Treatment	EP400	57634	37	12	132504707	132504707	Missense_Mutation	SNP	G	A	5	73	c.4391G>A	c.(4390-4392)GGC>GAC	p.G1464D
Pat_58	Pre-Treatment	TUBA3C	7278	37	13	19753616	19753616	Nonsense_Mutation	SNP	G	A	42	107	c.91C>T	c.(91-93)CAG>TAG	p.Q31*
Pat_58	Pre-Treatment	HS6ST3	266722	37	13	97485361	97485361	Missense_Mutation	SNP	G	A	14	34	c.1325G>A	c.(1324-1326)CGA>CAA	p.R442Q
Pat_58	Pre-Treatment	ARHGEF7	8874	37	13	111767950	111767950	Missense_Mutation	SNP	A	C	4	11	c.77A>C	c.(76-78)GAC>GCC	p.D26A
Pat_58	Pre-Treatment	FSCB	84075	37	14	44974563	44974563	Missense_Mutation	SNP	T	C	4	16	c.1628A>G	c.(1627-1629)CAG>CGG	p.Q543R
Pat_58	Pre-Treatment	PRKCH	5583	37	14	61909931	61909931	Missense_Mutation	SNP	C	T	4	58	c.530C>T	c.(529-531)ACG>ATG	p.T177M
Pat_58	Pre-Treatment	MTHFD1	4522	37	14	64891539	64891539	Missense_Mutation	SNP	G	A	3	19	c.745G>A	c.(745-747)GGG>AGG	p.G249R
Pat_58	Pre-Treatment	PRIMA1	145270	37	14	94245528	94245528	Missense_Mutation	SNP	C	T	4	29	c.223G>A	c.(223-225)GCC>ACC	p.A75T
Pat_58	Pre-Treatment	KIAA0284	283638	37	14	105349564	105349564	Missense_Mutation	SNP	G	A	10	187	c.770G>A	c.(769-771)GGC>GAC	p.G257D
Pat_58	Pre-Treatment	CYFIP1	23191	37	15	22929751	22929751	Missense_Mutation	SNP	G	A	4	41	c.425G>A	c.(424-426)CGC>CAC	p.R142H
Pat_58	Pre-Treatment	C15orf2	23742	37	15	24923547	24923547	Missense_Mutation	SNP	G	A	21	52	c.2533G>A	c.(2533-2535)GAG>AAG	p.E845K
Pat_58	Pre-Treatment	PLA2G4D	283748	37	15	42361057	42361057	Missense_Mutation	SNP	C	T	8	10	c.2313G>A	c.(2311-2313)ATG>ATA	p.M771I
Pat_58	Pre-Treatment	UBR1	197131	37	15	43352305	43352305	Missense_Mutation	SNP	C	T	4	75	c.806G>A	c.(805-807)CGG>CAG	p.R269Q
Pat_58	Pre-Treatment	MAP1A	4130	37	15	43816483	43816483	Missense_Mutation	SNP	G	A	4	37	c.2812G>A	c.(2812-2814)GTG>ATG	p.V938M
Pat_58	Pre-Treatment	CATSPER2	117155	37	15	43939572	43939572	Missense_Mutation	SNP	G	A	4	27	c.239C>T	c.(238-240)GCC>GTC	p.A80V
Pat_58	Pre-Treatment	FRMD5	84978	37	15	44176935	44176935	Missense_Mutation	SNP	C	T	4	32	c.1018G>A	c.(1018-1020)GAA>AAA	p.E340K
Pat_58	Pre-Treatment	SEMA6D	80031	37	15	48057123	48057123	Missense_Mutation	SNP	T	A	4	49	c.1297T>A	c.(1297-1299)TAC>AAC	p.Y433N
Pat_58	Pre-Treatment	IGF1R	3480	37	15	99459313	99459313	Missense_Mutation	SNP	G	A	4	68	c.1949G>A	c.(1948-1950)CGG>CAG	p.R650Q
Pat_58	Pre-Treatment	LINS1	55180	37	15	101109994	101109994	Missense_Mutation	SNP	G	A	3	35	c.1723C>T	c.(1723-1725)CAT>TAT	p.H575Y
Pat_58	Pre-Treatment	PMM2	5373	37	16	8905531	8905531	Missense_Mutation	SNP	C	T	4	65	c.484C>T	c.(484-486)CGG>TGG	p.R162W
Pat_58	Pre-Treatment	ABCC1	4363	37	16	16138401	16138401	Missense_Mutation	SNP	G	A	4	52	c.904G>A	c.(904-906)GTC>ATC	p.V302I
Pat_58	Pre-Treatment	ACSM2B	348158	37	16	20570759	20570759	Missense_Mutation	SNP	C	T	4	14	c.188G>A	c.(187-189)CGA>CAA	p.R63Q
Pat_58	Pre-Treatment	DNAH3	55567	37	16	21053420	21053420	Missense_Mutation	SNP	G	A	9	52	c.4567C>T	c.(4567-4569)CCA>TCA	p.P1523S
Pat_58	Pre-Treatment	RRN3P1	730092	37	16	21809167	21809167	Missense_Mutation	SNP	G	A	4	27	c.533C>T	c.(532-534)CCT>CTT	p.P178L
Pat_58	Pre-Treatment	RABEP2	79874	37	16	28922461	28922461	Missense_Mutation	SNP	C	T	4	63	c.934G>A	c.(934-936)GAG>AAG	p.E312K
Pat_58	Pre-Treatment	SETD1A	9739	37	16	30991353	30991353	Missense_Mutation	SNP	G	A	3	30	c.4246G>A	c.(4246-4248)GAG>AAG	p.E1416K
Pat_58	Pre-Treatment	ZNF267	10308	37	16	31927534	31927534	Missense_Mutation	SNP	C	G	5	128	c.1964C>G	c.(1963-1965)ACT>AGT	p.T655S
Pat_58	Pre-Treatment	SIAH1	6477	37	16	48395954	48395954	Missense_Mutation	SNP	G	A	4	35	c.386C>T	c.(385-387)CCG>CTG	p.P129L

Pat_58	Pre-Treatment	NKD1	85407	37	16	50666209	50666209	Missense_Mutation	SNP	G	A	3	21	c.713G>A	c.(712-714)CGC>CAC	p.R238H
Pat_58	Pre-Treatment	PKD1L2	114780	37	16	81181938	81181938	Missense_Mutation	SNP	T	A	8	22	c.4778A>T	c.(4777-4779)GAG>GTG	p.E1593V
Pat_58	Pre-Treatment	KIAA0513	9764	37	16	85112025	85112025	Missense_Mutation	SNP	G	A	8	32	c.787G>A	c.(787-789)GAC>AAC	p.D263N
Pat_58	Pre-Treatment	SMYD4	114826	37	17	1690763	1690763	Missense_Mutation	SNP	C	T	2	1	c.1673G>A	c.(1672-1674)CGG>CAG	p.R558Q
Pat_58	Pre-Treatment	SMG6	23293	37	17	2203361	2203361	Missense_Mutation	SNP	G	T	4	63	c.686C>A	c.(685-687)ACC>AAC	p.T229N
Pat_58	Pre-Treatment	ZZEF1	23140	37	17	3954131	3954131	Missense_Mutation	SNP	C	T	4	66	c.5807G>A	c.(5806-5808)CGG>CAG	p.R1936Q
Pat_58	Pre-Treatment	SLC2A4	6517	37	17	7187929	7187929	Missense_Mutation	SNP	C	T	4	70	c.853C>T	c.(853-855)CGG>TGG	p.R285W
Pat_58	Pre-Treatment	MYH4	4622	37	17	10348301	10348301	Missense_Mutation	SNP	C	T	14	39	c.5458G>A	c.(5458-5460)GAG>AAG	p.E1820K
Pat_58	Pre-Treatment	MYH2	4620	37	17	10432565	10432565	Missense_Mutation	SNP	C	T	10	25	c.3268G>A	c.(3268-3270)GAG>AAG	p.E1090K
Pat_58	Pre-Treatment	TEKT3	64518	37	17	15231338	15231338	Missense_Mutation	SNP	G	A	16	78	c.634C>T	c.(634-636)CAC>TAC	p.H212Y
Pat_58	Pre-Treatment	ZNF624	57547	37	17	16526195	16526195	Missense_Mutation	SNP	T	C	4	55	c.2005A>G	c.(2005-2007)AAA>GAA	p.K669E
Pat_58	Pre-Treatment	FBXW10	10517	37	17	18647940	18647940	Missense_Mutation	SNP	G	A	5	152	c.383G>A	c.(382-384)AGC>AAC	p.S128N
Pat_58	Pre-Treatment	TAOK1	57551	37	17	27844579	27844579	Nonsense_Mutation	SNP	C	T	5	146	c.1813C>T	c.(1813-1815)CGA>TGA	p.R605*
Pat_58	Pre-Treatment	GPR179	440435	37	17	36485350	36485350	Missense_Mutation	SNP	G	A	4	48	c.4102C>T	c.(4102-4104)CCA>TCA	p.P1368S
Pat_58	Pre-Treatment	PLXDC1	57125	37	17	37224186	37224186	Missense_Mutation	SNP	C	T	10	37	c.1410G>A	c.(1408-1410)ATG>ATA	p.M470I
Pat_58	Pre-Treatment	KRTAP4-4	84616	37	17	39316834	39316834	Missense_Mutation	SNP	C	T	5	144	c.110G>A	c.(109-111)CGC>CAC	p.R37H
Pat_58	Pre-Treatment	CACNA1G	8913	37	17	48669167	48669167	Missense_Mutation	SNP	C	T	4	72	c.2707C>T	c.(2707-2709)CGG>TGG	p.R903W
Pat_58	Pre-Treatment	COIL	8161	37	17	55027593	55027593	Missense_Mutation	SNP	G	A	4	66	c.1010C>T	c.(1009-1011)GCT>GTT	p.A337V
Pat_58	Pre-Treatment	KCNJ2	3759	37	17	68172154	68172154	Missense_Mutation	SNP	G	A	4	45	c.974G>A	c.(973-975)CGC>CAC	p.R325H
Pat_58	Pre-Treatment	SOX9	6662	37	17	70120373	70120373	Missense_Mutation	SNP	G	A	36	110	c.1375G>A	c.(1375-1377)GGC>AGC	p.G459S
Pat_58	Pre-Treatment	GGA3	23163	37	17	73242839	73242839	Missense_Mutation	SNP	C	T	7	30	c.79G>A	c.(79-81)GAA>AAA	p.E27K
Pat_58	Pre-Treatment	KIAA0195	9772	37	17	73489139	73489139	Missense_Mutation	SNP	C	T	6	25	c.2042C>T	c.(2041-2043)CCC>CTC	p.P681L
Pat_58	Pre-Treatment	UNK	85451	37	17	73808245	73808245	Missense_Mutation	SNP	C	T	6	86	c.595C>T	c.(595-597)CGT>TGT	p.R199C
Pat_58	Pre-Treatment	FBF1	85302	37	17	73915951	73915951	Missense_Mutation	SNP	G	A	4	58	c.1891C>T	c.(1891-1893)CGC>TGC	p.R631C
Pat_58	Pre-Treatment	PPP4R1	9989	37	18	9570494	9570494	Missense_Mutation	SNP	A	G	3	47	c.1234T>C	c.(1234-1236)TCA>CCA	p.S412P
Pat_58	Pre-Treatment	ZNF521	25925	37	18	22804770	22804770	Missense_Mutation	SNP	G	A	14	36	c.3112C>T	c.(3112-3114)CAT>TAT	p.H1038Y
Pat_58	Pre-Treatment	DSC3	1825	37	18	28598204	28598204	Missense_Mutation	SNP	C	T	6	21	c.1096G>A	c.(1096-1098)GAA>AAA	p.E366K
Pat_58	Pre-Treatment	DSG3	1830	37	18	29052688	29052688	Missense_Mutation	SNP	G	A	4	16	c.2038G>A	c.(2038-2040)GAA>AAA	p.E680K
Pat_58	Pre-Treatment	ZNF271	10778	37	18	32886791	32886791	Missense_Mutation	SNP	C	T	9	35	c.203C>T	c.(202-204)TCC>TTC	p.S68F
Pat_58	Pre-Treatment	NEDD4L	23327	37	18	56037691	56037691	Missense_Mutation	SNP	G	A	15	35	c.2248G>A	c.(2248-2250)GAA>AAA	p.E750K
Pat_58	Pre-Treatment	CDH20	28316	37	18	59221482	59221482	Missense_Mutation	SNP	G	A	40	110	c.1960G>A	c.(1960-1962)GAC>AAC	p.D654N
Pat_58	Pre-Treatment	ZCCHC2	54877	37	18	60241382	60241382	Missense_Mutation	SNP	C	T	5	98	c.2068C>T	c.(2068-2070)CCT>TCT	p.P690S
Pat_58	Pre-Treatment	CDH7	1005	37	18	63511228	63511228	Missense_Mutation	SNP	G	A	11	61	c.1162G>A	c.(1162-1164)GAA>AAA	p.E388K
Pat_58	Pre-Treatment	ZNF236	7776	37	18	74622104	74622104	Missense_Mutation	SNP	G	A	4	72	c.2626G>A	c.(2626-2628)GAA>AAA	p.E876K
Pat_58	Pre-Treatment	CLPP	8192	37	19	6364549	6364549	Missense_Mutation	SNP	G	A	3	30	c.454G>A	c.(454-456)GCC>ACC	p.A152T
Pat_58	Pre-Treatment	PNPLA6	10908	37	19	7605810	7605810	Missense_Mutation	SNP	G	A	4	40	c.824G>A	c.(823-825)GGT>GAT	p.G275D
Pat_58	Pre-Treatment	MUC16	94025	37	19	9091708	9091708	Missense_Mutation	SNP	C	T	16	21	c.107G>A	c.(106-108)GGA>GAA	p.G36E
Pat_58	Pre-Treatment	QTRT1	81890	37	19	10823637	10823637	Missense_Mutation	SNP	G	A	4	51	c.980G>A	c.(979-981)CGC>CAC	p.R327H
Pat_58	Pre-Treatment	CYP4F12	66002	37	19	15807003	15807003	Missense_Mutation	SNP	C	T	29	62	c.1282C>T	c.(1282-1284)CAT>TAT	p.H428Y
Pat_58	Pre-Treatment	MYO9B	4650	37	19	17283697	17283697	Missense_Mutation	SNP	C	T	4	43	c.2065C>T	c.(2065-2067)CGG>TGG	p.R689W
Pat_58	Pre-Treatment	SLC5A5	6528	37	19	17992993	17992993	Missense_Mutation	SNP	G	A	4	72	c.1207G>A	c.(1207-1209)GCC>ACC	p.A403T
Pat_58	Pre-Treatment	CCDC124	115098	37	19	18054360	18054360	Missense_Mutation	SNP	C	T	3	23	c.508C>T	c.(508-510)CGG>TGG	p.R170W
Pat_58	Pre-Treatment	ZNF431	170959	37	19	21366366	21366366	Missense_Mutation	SNP	G	A	6	166	c.1260G>A	c.(1258-1260)ATG>ATA	p.M420I
Pat_58	Pre-Treatment	ZNF208	7757	37	19	22154522	22154522	Missense_Mutation	SNP	C	T	32	129	c.2930G>A	c.(2929-2931)AGA>AAA	p.R977K
Pat_58	Pre-Treatment	ZNF607	84775	37	19	38189447	38189447	Missense_Mutation	SNP	C	T	5	79	c.1585G>A	c.(1585-1587)GGT>AGT	p.G529S
Pat_58	Pre-Treatment	RYR1	6261	37	19	39039016	39039016	Missense_Mutation	SNP	G	A	4	67	c.12238G>A	c.(12238-12240)GTA>ATA	p.V4080I
Pat_58	Pre-Treatment	IL28B	282617	37	19	39734321	39734321	Missense_Mutation	SNP	A	G	3	12	c.542T>C	c.(541-543)CTC>CCC	p.L181P

Pat_58	Pre-Treatment	CEACAM5	1048	37	19	42224958	42224958	Missense_Mutation	SNP	A	G	30	88	c.1888A>G	c.(1888-1890)AAT>GAT	p.N630D
Pat_58	Pre-Treatment	ERF	2077	37	19	42753111	42753111	Missense_Mutation	SNP	C	T	5	91	c.1153G>A	c.(1153-1155)GGA>AGA	p.G385R
Pat_58	Pre-Treatment	CIC	23152	37	19	42791880	42791880	Splice_Site	SNP	G	A	4	54	c.765_splice	c.e5+1	p.Q255_splice
Pat_58	Pre-Treatment	LIPE	3991	37	19	42911939	42911939	Missense_Mutation	SNP	A	T	3	33	c.1661T>A	c.(1660-1662)CTG>CAG	p.L554Q
Pat_58	Pre-Treatment	PSG6	5675	37	19	43411773	43411773	Nonsense_Mutation	SNP	G	A	6	137	c.940C>T	c.(940-942)CGA>TGA	p.R314*
Pat_58	Pre-Treatment	PSG9	5678	37	19	43771986	43771986	Missense_Mutation	SNP	C	T	35	116	c.380G>A	c.(379-381)CGA>CAA	p.R127Q
Pat_58	Pre-Treatment	NPAS1	4861	37	19	47548577	47548577	Missense_Mutation	SNP	G	A	17	41	c.1441G>A	c.(1441-1443)GAG>AAG	p.E481K
Pat_58	Pre-Treatment	DHDH	27294	37	19	49445771	49445771	Missense_Mutation	SNP	G	A	4	70	c.694G>A	c.(694-696)GTG>ATG	p.V232M
Pat_58	Pre-Treatment	DKKL1	27120	37	19	49868779	49868779	Missense_Mutation	SNP	G	A	4	38	c.197G>A	c.(196-198)CGG>CAG	p.R66Q
Pat_58	Pre-Treatment	KLK15	55554	37	19	51330220	51330220	Missense_Mutation	SNP	G	A	5	24	c.395C>T	c.(394-396)CCC>CTC	p.P132L
Pat_58	Pre-Treatment	TSEN34	79042	37	19	54696042	54696042	Missense_Mutation	SNP	C	G	19	84	c.563C>G	c.(562-564)GCC>GGC	p.A188G
Pat_58	Pre-Treatment	KIR3DX1	90011	37	19	55048172	55048172	Missense_Mutation	SNP	G	A	12	36	c.40G>A	c.(40-42)GAA>AAA	p.E14K
Pat_58	Pre-Treatment	C19orf51	352909	37	19	55677365	55677365	Missense_Mutation	SNP	G	A	5	46	c.89C>T	c.(88-90)CCT>CTT	p.P30L
Pat_58	Pre-Treatment	PEG3	5178	37	19	57325129	57325129	Missense_Mutation	SNP	C	T	12	45	c.4681G>A	c.(4681-4683)GAG>AAG	p.E1561K
Pat_58	Pre-Treatment	MATN3	4148	37	2	20202940	20202940	Missense_Mutation	SNP	C	T	4	64	c.898G>A	c.(898-900)GAC>AAC	p.D300N
Pat_58	Pre-Treatment	GTF3C2	2976	37	2	27560826	27560826	Missense_Mutation	SNP	G	A	81	221	c.917C>T	c.(916-918)CCT>CTT	p.P306L
Pat_58	Pre-Treatment	KCNG3	170850	37	2	42671595	42671595	Missense_Mutation	SNP	G	A	23	64	c.790C>T	c.(790-792)CCG>TCG	p.P264S
Pat_58	Pre-Treatment	SRBD1	55133	37	2	45801772	45801772	Missense_Mutation	SNP	C	T	5	66	c.1163G>A	c.(1162-1164)CGG>CAG	p.R388Q
Pat_58	Pre-Treatment	TET3	200424	37	2	74300721	74300721	Missense_Mutation	SNP	G	A	4	8	c.2135G>A	c.(2134-2136)GGA>GAA	p.G712E
Pat_58	Pre-Treatment	SMYD1	150572	37	2	88383938	88383938	Missense_Mutation	SNP	G	A	16	53	c.241G>A	c.(241-243)GAT>AAT	p.D81N
Pat_58	Pre-Treatment	GCC2	9648	37	2	109124081	109124081	Nonsense_Mutation	SNP	C	T	14	31	c.5050C>T	c.(5050-5052)CGA>TGA	p.R1684*
Pat_58	Pre-Treatment	PAX8	7849	37	2	114000279	114000279	Missense_Mutation	SNP	C	T	5	126	c.466G>A	c.(466-468)GGA>AGA	p.G156R
Pat_58	Pre-Treatment	CNTNAP5	129684	37	2	125547652	125547652	Missense_Mutation	SNP	G	A	8	27	c.2923G>A	c.(2923-2925)GAG>AAG	p.E975K
Pat_58	Pre-Treatment	SCN2A	6326	37	2	166152377	166152377	Missense_Mutation	SNP	G	A	3	27	c.44G>A	c.(43-45)CGC>CAC	p.R15H
Pat_58	Pre-Treatment	TTN	7273	37	2	179554591	179554591	Missense_Mutation	SNP	C	T	19	52	c.28063G>A	c.(28063-28065)GAA>AAA	p.E9355K
Pat_58	Pre-Treatment	TTN	7273	37	2	179611173	179611173	Missense_Mutation	SNP	T	A	8	27	c.15954A>T	c.(15952-15954)GAA>GAT	p.E5318D
Pat_58	Pre-Treatment	TTN	7273	37	2	179611175	179611175	Missense_Mutation	SNP	C	T	8	28	c.15952G>A	c.(15952-15954)GAA>AAA	p.E5318K
Pat_58	Pre-Treatment	TTN	7273	37	2	179616629	179616629	Nonsense_Mutation	SNP	C	A	22	63	c.10498G>T	c.(10498-10500)GAA>TAA	p.E3500*
Pat_58	Pre-Treatment	PDE1A	5136	37	2	183129116	183129116	Missense_Mutation	SNP	C	T	12	37	c.127G>A	c.(127-129)GAA>AAA	p.E43K
Pat_58	Pre-Treatment	MYO1B	4430	37	2	192160877	192160877	Missense_Mutation	SNP	G	A	3	24	c.176G>A	c.(175-177)CGG>CAG	p.R59Q
Pat_58	Pre-Treatment	NRP2	8828	37	2	206617576	206617576	Missense_Mutation	SNP	C	T	4	26	c.1921C>T	c.(1921-1923)CCT>TCT	p.P641S
Pat_58	Pre-Treatment	EPHA4	2043	37	2	222433437	222433437	Splice_Site	SNP	C	G	4	27	c.159_splice	c.e2+1	p.G53_splice
Pat_58	Pre-Treatment	ECEL1	9427	37	2	233349183	233349183	Missense_Mutation	SNP	G	A	6	129	c.1183C>T	c.(1183-1185)CGG>TGG	p.R395W
Pat_58	Pre-Treatment	DNAJB3	414061	37	2	234652194	234652194	Missense_Mutation	SNP	C	G	11	35	c.369G>C	c.(367-369)TTG>TTC	p.L123F
Pat_58	Pre-Treatment	IQCA1	79781	37	2	237406078	237406078	Missense_Mutation	SNP	C	T	5	11	c.64G>A	c.(64-66)GAT>AAT	p.D22N
Pat_58	Pre-Treatment	XRN2	22803	37	20	21309263	21309263	Missense_Mutation	SNP	G	A	4	56	c.382G>A	c.(382-384)GCA>ACA	p.A128T
Pat_58	Pre-Treatment	MYBL2	4605	37	20	42315625	42315625	Nonsense_Mutation	SNP	G	A	3	31	c.413G>A	c.(412-414)TGG>TAG	p.W138*
Pat_58	Pre-Treatment	ARFGAP1	55738	37	20	61919073	61919073	Missense_Mutation	SNP	G	A	3	18	c.1069G>A	c.(1069-1071)GAG>AAG	p.E357K
Pat_58	Pre-Treatment	MX2	4600	37	21	42778797	42778797	Nonsense_Mutation	SNP	C	T	19	49	c.1777C>T	c.(1777-1779)CGA>TGA	p.R593*
Pat_58	Pre-Treatment	RIPK4	54101	37	21	43187175	43187175	Nonsense_Mutation	SNP	C	T	4	5	c.27G>A	c.(25-27)TGG>TGA	p.W9*
Pat_58	Pre-Treatment	PCNT	5116	37	21	47809213	47809213	Missense_Mutation	SNP	G	A	4	67	c.3707G>A	c.(3706-3708)AGC>AAC	p.S1236N
Pat_58	Pre-Treatment	PI4KA	5297	37	22	21119177	21119177	Missense_Mutation	SNP	G	A	24	22	c.2462C>T	c.(2461-2463)TCC>TTC	p.S821F
Pat_58	Pre-Treatment	UPB1	51733	37	22	24919664	24919664	Missense_Mutation	SNP	C	T	4	60	c.994C>T	c.(994-996)CGT>TGT	p.R332C
Pat_58	Pre-Treatment	LARGE	9215	37	22	33673116	33673116	Missense_Mutation	SNP	G	A	4	57	c.2003C>T	c.(2002-2004)CCG>CTG	p.P668L
Pat_58	Pre-Treatment	HMOX1	3162	37	22	35789529	35789529	Nonsense_Mutation	SNP	C	T	42	78	c.805C>T	c.(805-807)CGA>TGA	p.R269*
Pat_58	Pre-Treatment	EFCAB6	64800	37	22	44178131	44178131	Nonsense_Mutation	SNP	G	C	4	41	c.68C>G	c.(67-69)TCA>TGA	p.S23*
Pat_58	Pre-Treatment	CLASP2	23122	37	3	33650098	33650098	Missense_Mutation	SNP	T	C	3	28	c.1409A>G	c.(1408-1410)GAT>GGT	p.D470G

Pat_58	Pre-Treatment	EXOG	9941	37	3	38565470	38565470	Missense_Mutation	SNP	G	A	4	51	c.724G>A	c.(724-726)GAA>AAA	p.E242K
Pat_58	Pre-Treatment	EXOSC7	23016	37	3	45031134	45031134	Missense_Mutation	SNP	C	A	4	23	c.252C>A	c.(250-252)GAC>GAA	p.D84E
Pat_58	Pre-Treatment	SETD2	29072	37	3	47164279	47164279	Missense_Mutation	SNP	G	A	3	22	c.1847C>T	c.(1846-1848)GCT>GTT	p.A616V
Pat_58	Pre-Treatment	COL7A1	1294	37	3	48629118	48629118	Missense_Mutation	SNP	C	T	4	42	c.1495G>A	c.(1495-1497)GTG>ATG	p.V499M
Pat_58	Pre-Treatment	GRM2	2912	37	3	51749930	51749930	Missense_Mutation	SNP	G	A	4	52	c.2141G>A	c.(2140-2142)CGG>CAG	p.R714Q
Pat_58	Pre-Treatment	ERC2	26059	37	3	56330265	56330265	Missense_Mutation	SNP	C	T	41	132	c.856G>A	c.(856-858)GAA>AAA	p.E286K
Pat_58	Pre-Treatment	ADCY5	111	37	3	123019022	123019022	Missense_Mutation	SNP	C	T	4	51	c.2845G>A	c.(2845-2847)GTG>ATG	p.V949M
Pat_58	Pre-Treatment	KALRN	8997	37	3	124165073	124165073	Missense_Mutation	SNP	C	T	4	60	c.3373C>T	c.(3373-3375)CGG>TGG	p.R1125W
Pat_58	Pre-Treatment	TRH	7200	37	3	129695731	129695731	Missense_Mutation	SNP	G	A	6	55	c.401G>A	c.(400-402)CGG>CAG	p.R134Q
Pat_58	Pre-Treatment	PPM1L	151742	37	3	160783314	160783314	Missense_Mutation	SNP	C	T	19	53	c.698C>T	c.(697-699)CCT>CTT	p.P233L
Pat_58	Pre-Treatment	B3GALNT1	8706	37	3	160804396	160804396	Nonsense_Mutation	SNP	C	T	4	58	c.147G>A	c.(145-147)TGG>TGA	p.W49*
Pat_58	Pre-Treatment	MUC4	4585	37	3	195509909	195509909	Missense_Mutation	SNP	G	A	2	0	c.8158C>T	c.(8158-8160)CCT>TCT	p.P2720S
Pat_58	Pre-Treatment	TM4SF19	116211	37	3	196053840	196053840	Missense_Mutation	SNP	C	T	4	40	c.265G>A	c.(265-267)GGG>AGG	p.G89R
Pat_58	Pre-Treatment	ZNF721	170960	37	4	436043	436043	Missense_Mutation	SNP	G	T	10	28	c.2213C>A	c.(2212-2214)ACA>AAA	p.T738K
Pat_58	Pre-Treatment	LETM1	3954	37	4	1818548	1818548	Nonsense_Mutation	SNP	G	A	4	79	c.1837C>T	c.(1837-1839)CAG>TAG	p.Q613*
Pat_58	Pre-Treatment	HTT	3064	37	4	3215820	3215820	Missense_Mutation	SNP	G	A	3	29	c.6916G>A	c.(6916-6918)GCC>ACC	p.A2306T
Pat_58	Pre-Treatment	GPR78	27201	37	4	8588947	8588947	Missense_Mutation	SNP	C	T	18	52	c.949C>T	c.(949-951)CCG>TCG	p.P317S
Pat_58	Pre-Treatment	PI4K2B	55300	37	4	25253996	25253996	Missense_Mutation	SNP	G	A	4	65	c.322G>A	c.(322-324)GAT>AAT	p.D108N
Pat_58	Pre-Treatment	CWH43	80157	37	4	49032922	49032922	Missense_Mutation	SNP	G	A	14	62	c.1453G>A	c.(1453-1455)GAA>AAA	p.E485K
Pat_58	Pre-Treatment	NKX6-1	4825	37	4	85419372	85419372	Missense_Mutation	SNP	C	T	3	16	c.10G>A	c.(10-12)GTG>ATG	p.V4M
Pat_58	Pre-Treatment	EGF	1950	37	4	110932470	110932470	Missense_Mutation	SNP	G	A	15	51	c.3483G>A	c.(3481-3483)ATG>ATA	p.M1161I
Pat_58	Pre-Treatment	BBS7	55212	37	4	122760836	122760836	Missense_Mutation	SNP	G	A	6	23	c.1321C>T	c.(1321-1323)CTT>TTT	p.L441F
Pat_58	Pre-Treatment	SETD7	80854	37	4	140439043	140439043	Missense_Mutation	SNP	C	T	5	96	c.916G>A	c.(916-918)GAT>AAT	p.D306N
Pat_58	Pre-Treatment	TMEM184C	55751	37	4	148555322	148555322	Missense_Mutation	SNP	C	T	3	21	c.1054C>T	c.(1054-1056)CGG>TGG	p.R352W
Pat_58	Pre-Treatment	MAP9	79884	37	4	156278607	156278607	Missense_Mutation	SNP	G	A	12	32	c.1115C>T	c.(1114-1116)TCT>TTT	p.S372F
Pat_58	Pre-Treatment	SPOCK3	50859	37	4	167658743	167658743	Missense_Mutation	SNP	G	A	20	99	c.1016C>T	c.(1015-1017)CCC>CTC	p.P339L
Pat_58	Pre-Treatment	PRDM9	56979	37	5	23527052	23527052	Missense_Mutation	SNP	C	T	5	105	c.1855C>T	c.(1855-1857)CGG>TGG	p.R619W
Pat_58	Pre-Treatment	ITGA2	3673	37	5	52347370	52347370	Missense_Mutation	SNP	G	A	4	77	c.760G>A	c.(760-762)GGA>AGA	p.G254R
Pat_58	Pre-Treatment	DMGDH	29958	37	5	78338173	78338173	Missense_Mutation	SNP	G	A	4	37	c.1126C>T	c.(1126-1128)CCT>TCT	p.P376S
Pat_58	Pre-Treatment	JMY	133746	37	5	78596054	78596054	Nonsense_Mutation	SNP	C	T	29	80	c.1606C>T	c.(1606-1608)CAG>TAG	p.Q536*
Pat_58	Pre-Treatment	SNCAIP	9627	37	5	121780390	121780390	Missense_Mutation	SNP	G	A	4	50	c.1555G>A	c.(1555-1557)GCC>ACC	p.A519T
Pat_58	Pre-Treatment	PCDHA11	56138	37	5	140248752	140248752	Missense_Mutation	SNP	G	A	15	53	c.64G>A	c.(64-66)GAA>AAA	p.E22K
Pat_58	Pre-Treatment	PCDHB4	56131	37	5	140503847	140503847	Missense_Mutation	SNP	G	A	27	77	c.2267G>A	c.(2266-2268)GGA>GAA	p.G756E
Pat_58	Pre-Treatment	PCDHB5	26167	37	5	140515773	140515773	Missense_Mutation	SNP	G	A	60	203	c.757G>A	c.(757-759)GAG>AAG	p.E253K
Pat_58	Pre-Treatment	PCDHB5	26167	37	5	140516739	140516739	Missense_Mutation	SNP	G	A	5	68	c.1723G>A	c.(1723-1725)GTG>ATG	p.V575M
Pat_58	Pre-Treatment	PCDHB7	56129	37	5	140552652	140552652	Missense_Mutation	SNP	C	T	19	53	c.236C>T	c.(235-237)TCG>TTG	p.S79L
Pat_58	Pre-Treatment	CAMK2A	815	37	5	149636182	149636182	Missense_Mutation	SNP	G	A	4	38	c.365C>T	c.(364-366)GCT>GTT	p.A122V
Pat_58	Pre-Treatment	GEMIN5	25929	37	5	154275814	154275815	Missense_Mutation	DNP	GT	AA	3	29	.3434_3435AC>T	c.(3433-3435)TAC>TTT	p.Y1145F
Pat_58	Pre-Treatment	KIF4B	285643	37	5	154394854	154394854	Missense_Mutation	SNP	G	A	24	57	c.1435G>A	c.(1435-1437)GAA>AAA	p.E479K
Pat_58	Pre-Treatment	C5orf40	408263	37	5	156770118	156770118	Missense_Mutation	SNP	G	A	10	28	c.427C>T	c.(427-429)CCG>TCG	p.P143S
Pat_58	Pre-Treatment	ODZ2	57451	37	5	167379679	167379679	Missense_Mutation	SNP	G	A	4	47	c.799G>A	c.(799-801)GCC>ACC	p.A267T
Pat_58	Pre-Treatment	OR2Y1	134083	37	5	180166481	180166481	Missense_Mutation	SNP	C	T	16	50	c.578G>A	c.(577-579)GGA>GAA	p.G193E
Pat_58	Pre-Treatment	SYCP2L	221711	37	6	10935349	10935349	Missense_Mutation	SNP	C	T	9	35	c.1742C>T	c.(1741-1743)CCA>CTA	p.P581L
Pat_58	Pre-Treatment	DHX16	8449	37	6	30633288	30633288	Missense_Mutation	SNP	G	A	19	62	c.889C>T	c.(889-891)CGC>TGC	p.R297C
Pat_58	Pre-Treatment	MUC21	394263	37	6	30954947	30954947	Missense_Mutation	SNP	A	C	12	589	c.995A>C	c.(994-996)AAC>ACC	p.N332T
Pat_58	Pre-Treatment	MICA	4276	37	6	31378439	31378439	Missense_Mutation	SNP	T	C	4	30	c.190T>C	c.(190-192)TGC>CGC	p.C64R
Pat_58	Pre-Treatment	TNXB	7148	37	6	32025954	32025955	Missense_Mutation	DNP	CC	AA	4	50	.7705_7706GG>T	c.(7705-7707)GGG>TTG	p.G2569L

Pat_58	Pre-Treatment	DNAH8	1769	37	6	38840720	38840720	Missense_Mutation	SNP	G	C	10	17	c.6625G>C	c.(6625-6627)GCC>CCC	p.A2209P
Pat_58	Pre-Treatment	TTBK1	84630	37	6	43230630	43230630	Missense_Mutation	SNP	G	A	3	23	c.1528G>A	c.(1528-1530)GGC>AGC	p.G510S
Pat_58	Pre-Treatment	TDRD6	221400	37	6	46657437	46657437	Nonsense_Mutation	SNP	T	A	16	80	c.1572T>A	c.(1570-1572)TAT>TAA	p.Y524*
Pat_58	Pre-Treatment	BCKDHB	594	37	6	80912831	80912831	Nonsense_Mutation	SNP	C	T	4	52	c.853C>T	c.(853-855)CGA>TGA	p.R285*
Pat_58	Pre-Treatment	ZNF292	23036	37	6	87925717	87925717	Nonsense_Mutation	SNP	C	T	10	38	c.265C>T	c.(265-267)CGA>TGA	p.R89*
Pat_58	Pre-Treatment	ZNF292	23036	37	6	87966906	87966906	Missense_Mutation	SNP	G	A	14	28	c.3559G>A	c.(3559-3561)GTC>ATC	p.V1187I
Pat_58	Pre-Treatment	GRIK2	2898	37	6	102124506	102124506	Missense_Mutation	SNP	C	T	6	35	c.550C>T	c.(550-552)CGT>TGT	p.R184C
Pat_58	Pre-Treatment	DCBLD1	285761	37	6	117859900	117859900	Missense_Mutation	SNP	A	G	3	30	c.878A>G	c.(877-879)CAG>CGG	p.Q293R
Pat_58	Pre-Treatment	MYCT1	80177	37	6	153043051	153043051	Missense_Mutation	SNP	G	A	28	67	c.371G>A	c.(370-372)GGA>GAA	p.G124E
Pat_58	Pre-Treatment	MAD1L1	8379	37	7	2054189	2054189	Missense_Mutation	SNP	C	T	4	30	c.1307G>A	c.(1306-1308)CGG>CAG	p.R436Q
Pat_58	Pre-Treatment	CREB5	9586	37	7	28848934	28848934	Missense_Mutation	SNP	G	A	4	53	c.1157G>A	c.(1156-1158)CGG>CAG	p.R386Q
Pat_58	Pre-Treatment	NEUROD6	63974	37	7	31378228	31378228	Missense_Mutation	SNP	G	A	11	32	c.655C>T	c.(655-657)CCC>TCC	p.P219S
Pat_58	Pre-Treatment	PDE1C	5137	37	7	31862845	31862845	Missense_Mutation	SNP	G	A	9	30	c.1424C>T	c.(1423-1425)TCG>TTG	p.S475L
Pat_58	Pre-Treatment	POLR2J4	84820	37	7	44005467	44005467	Missense_Mutation	SNP	C	T	4	32	c.223G>A	c.(223-225)GAG>AAG	p.E75K
Pat_58	Pre-Treatment	PHKG1	5260	37	7	56155446	56155446	Missense_Mutation	SNP	C	T	19	27	c.107G>A	c.(106-108)CGA>CAA	p.R36Q
Pat_58	Pre-Treatment	ZNF727	442319	37	7	63538806	63538806	Missense_Mutation	SNP	C	G	5	75	c.1379C>G	c.(1378-1380)ACC>AGC	p.T460S
Pat_58	Pre-Treatment	ZNF727	442319	37	7	63538824	63538824	Missense_Mutation	SNP	G	A	5	55	c.1397G>A	c.(1396-1398)AGC>AAC	p.S466N
Pat_58	Pre-Treatment	CDK6	1021	37	7	92462448	92462448	Missense_Mutation	SNP	C	T	3	20	c.190G>A	c.(190-192)GTG>ATG	p.V64M
Pat_58	Pre-Treatment	DLX6	1750	37	7	96635571	96635571	Missense_Mutation	SNP	C	G	3	10	c.198C>G	c.(196-198)CAC>CAG	p.H66Q
Pat_58	Pre-Treatment	ASNS	440	37	7	97488576	97488576	Missense_Mutation	SNP	G	A	5	108	c.622C>T	c.(622-624)CGG>TGG	p.R208W
Pat_58	Pre-Treatment	LMTK2	22853	37	7	97821170	97821170	Missense_Mutation	SNP	G	A	4	66	c.1393G>A	c.(1393-1395)GTG>ATG	p.V465M
Pat_58	Pre-Treatment	TRRAP	8295	37	7	98490140	98490140	Missense_Mutation	SNP	C	T	5	92	c.355C>T	c.(355-357)CGC>TGC	p.R119C
Pat_58	Pre-Treatment	C7orf61	402573	37	7	100061137	100061137	Missense_Mutation	SNP	G	A	4	63	c.236C>T	c.(235-237)CCC>CTC	p.P79L
Pat_58	Pre-Treatment	MUC17	140453	37	7	100683647	100683647	Missense_Mutation	SNP	G	A	130	582	c.8950G>A	c.(8950-8952)GAA>AAA	p.E2984K
Pat_58	Pre-Treatment	SND1	27044	37	7	127343369	127343369	Missense_Mutation	SNP	C	T	4	63	c.832C>T	c.(832-834)CTT>TTT	p.L278F
Pat_58	Pre-Treatment	ZC3HAV1	56829	37	7	138764620	138764620	Missense_Mutation	SNP	G	A	5	111	c.1067C>T	c.(1066-1068)GCC>GTC	p.A356V
Pat_58	Pre-Treatment	BRAF	673	37	7	140453136	140453136	Missense_Mutation	SNP	A	T	48	30	c.1799T>A	c.(1798-1800)GTG>GAG	p.V600E
Pat_58	Pre-Treatment	OR9A2	135924	37	7	142723927	142723927	Missense_Mutation	SNP	G	A	10	41	c.293C>T	c.(292-294)TCG>TTG	p.S98L
Pat_58	Pre-Treatment	SSPO	23145	37	7	149523307	149523307	Missense_Mutation	SNP	C	T	4	38	c.14390C>T	c.(14389-14391)GCA>GTA	p.A4797V
Pat_58	Pre-Treatment	DLGAP2	9228	37	8	1616614	1616614	Missense_Mutation	SNP	G	A	3	8	c.1690G>A	c.(1690-1692)GAC>AAC	p.D564N
Pat_58	Pre-Treatment	NAT2	10	37	8	18258201	18258201	Missense_Mutation	SNP	G	A	4	66	c.688G>A	c.(688-690)GGG>AGG	p.G230R
Pat_58	Pre-Treatment	BMP1	649	37	8	22059345	22059345	Missense_Mutation	SNP	G	A	3	30	c.2137G>A	c.(2137-2139)GGC>AGC	p.G713S
Pat_58	Pre-Treatment	EXTL3	2137	37	8	28574136	28574136	Missense_Mutation	SNP	G	A	5	78	c.560G>A	c.(559-561)CGT>CAT	p.R187H
Pat_58	Pre-Treatment	POLB	5423	37	8	42229086	42229086	Missense_Mutation	SNP	G	A	3	17	c.919G>A	c.(919-921)GCA>ACA	p.A307T
Pat_58	Pre-Treatment	TRIM55	84675	37	8	67086715	67086715	Missense_Mutation	SNP	G	A	24	59	c.1534G>A	c.(1534-1536)GAG>AAG	p.E512K
Pat_58	Pre-Treatment	CA1	759	37	8	86253846	86253846	Missense_Mutation	SNP	C	T	12	36	c.19G>A	c.(19-21)GGA>AGA	p.G7R
Pat_58	Pre-Treatment	FBXO10	26267	37	9	37521629	37521629	Missense_Mutation	SNP	C	T	11	19	c.2137G>A	c.(2137-2139)GAC>AAC	p.D713N
Pat_58	Pre-Treatment	TLE1	7088	37	9	84268926	84268926	Missense_Mutation	SNP	G	A	4	45	c.260C>T	c.(259-261)ACG>ATG	p.T87M
Pat_58	Pre-Treatment	SECISBP2	79048	37	9	91940568	91940568	Missense_Mutation	SNP	C	A	4	62	c.409C>A	c.(409-411)CAA>AAA	p.Q137K
Pat_58	Pre-Treatment	IPPK	64768	37	9	95396667	95396667	Splice_Site	SNP	C	A	4	39	c.1170_splice	c.e11+1	p.K390_splice
Pat_58	Pre-Treatment	EPB41L4B	54566	37	9	111954631	111954631	Missense_Mutation	SNP	G	A	8	39	c.2228C>T	c.(2227-2229)CCC>CTC	p.P743L
Pat_58	Pre-Treatment	C9orf84	158401	37	9	114490105	114490105	Missense_Mutation	SNP	C	T	13	25	c.1450G>A	c.(1450-1452)GAT>AAT	p.D484N
Pat_58	Pre-Treatment	PAPPA	5069	37	9	118997788	118997788	Missense_Mutation	SNP	G	T	3	14	c.2604G>T	c.(2602-2604)ATG>ATT	p.M868I
Pat_58	Pre-Treatment	MAPKAP1	79109	37	9	128206856	128206856	Missense_Mutation	SNP	G	A	4	67	c.1367C>T	c.(1366-1368)ACG>ATG	p.T456M
Pat_58	Pre-Treatment	ARSF	416	37	X	3030406	3030406	Missense_Mutation	SNP	G	A	25	58	c.1582G>A	c.(1582-1584)GAT>AAT	p.D528N
Pat_58	Pre-Treatment	MXRA5	25878	37	X	3248289	3248289	Missense_Mutation	SNP	C	T	8	22	c.479G>A	c.(478-480)GGA>GAA	p.G160E
Pat_58	Pre-Treatment	FAM47A	158724	37	X	34150139	34150139	Missense_Mutation	SNP	G	A	17	66	c.257C>T	c.(256-258)CCC>CTC	p.P86L

Pat_58	Pre-Treatment	SUV39H1	6839	37	X	48564896	48564896	Missense_Mutation	SNP	C	T	3	3	c.983C>T	c.(982-984)CCC>CTC	p.P328L
Pat_58	Pre-Treatment	CACNA1F	778	37	X	49076214	49076214	Missense_Mutation	SNP	C	T	3	13	c.2455G>A	c.(2455-2457)GAA>AAA	p.E819K
Pat_58	Pre-Treatment	PAGE3	139793	37	X	55287057	55287057	Missense_Mutation	SNP	G	A	3	39	c.229C>T	c.(229-231)CGG>TGG	p.R77W
Pat_58	Pre-Treatment	OGT	8473	37	X	70781638	70781638	Missense_Mutation	SNP	G	A	4	12	c.1865G>A	c.(1864-1866)GGA>GAA	p.G622E
Pat_58	Pre-Treatment	KIAA2022	340533	37	X	73961331	73961331	Missense_Mutation	SNP	C	T	13	41	c.3061G>A	c.(3061-3063)GAT>AAT	p.D1021N
Pat_58	Pre-Treatment	LPAR4	2846	37	X	78010751	78010751	Missense_Mutation	SNP	C	T	5	69	c.385C>T	c.(385-387)CTC>TTC	p.L129F
Pat_58	Pre-Treatment	CPXCR1	53336	37	X	88009059	88009059	Missense_Mutation	SNP	G	A	7	28	c.644G>A	c.(643-645)GGA>GAA	p.G215E
Pat_58	Pre-Treatment	DOCK11	139818	37	X	117773445	117773445	Missense_Mutation	SNP	C	T	16	78	c.4049C>T	c.(4048-4050)TCG>TTG	p.S1350L
Pat_58	Pre-Treatment	RHOXF2B	727940	37	X	119210996	119210996	Missense_Mutation	SNP	C	T	8	18	c.337G>A	c.(337-339)GAA>AAA	p.E113K
Pat_58	Pre-Treatment	ZBTB33	10009	37	X	119388238	119388238	Missense_Mutation	SNP	G	A	19	84	c.968G>A	c.(967-969)GGA>GAA	p.G323E
Pat_58	Pre-Treatment	ODZ1	10178	37	X	123517777	123517777	Missense_Mutation	SNP	C	T	5	80	c.6983G>A	c.(6982-6984)AGC>AAC	p.S2328N
Pat_58	Pre-Treatment	GABRE	2564	37	X	151123487	151123487	Missense_Mutation	SNP	C	T	7	11	c.1207G>A	c.(1207-1209)GAA>AAA	p.E403K
Pat_58	Pre-Treatment	FAM58A	92002	37	X	152858142	152858142	Missense_Mutation	SNP	C	T	4	28	c.293G>A	c.(292-294)AGC>AAC	p.S98N
Pat_58	Pre-Treatment	NAA10	8260	37	X	153195562	153195562	Missense_Mutation	SNP	C	T	5	77	c.586G>A	c.(586-588)GAG>AAG	p.E196K
Pat_58	Pre-Treatment	MPP1	4354	37	X	154013421	154013421	Missense_Mutation	SNP	C	T	3	22	c.689G>A	c.(688-690)AGT>AAT	p.S230N
Pat_58	Post-Resistance	CA6	765	37	1	9027747	9027747	Missense_Mutation	SNP	G	A	4	318	c.601G>A	c.(601-603)GTT>ATT	p.V201I
Pat_58	Post-Resistance	UBE4B	10277	37	1	10228311	10228311	Nonsense_Mutation	SNP	A	T	27	90	c.3316A>T	c.(3316-3318)AAG>TAG	p.K1106*
Pat_58	Post-Resistance	LOC649330	649330	37	1	12907458	12907458	Missense_Mutation	SNP	T	C	6	224	c.685A>G	c.(685-687)ACG>GCG	p.T229A
Pat_58	Post-Resistance	NBPF1	55672	37	1	16918653	16918653	Splice_Site	SNP	C	T	4	160	c.-35_splice	c.e6+1	
Pat_58	Post-Resistance	MST1P9	11223	37	1	17085872	17085872	Missense_Mutation	SNP	A	G	6	73	c.949T>C	c.(949-951)TGG>CGG	p.W317R
Pat_58	Post-Resistance	CROCC	9696	37	1	17272075	17272075	Missense_Mutation	SNP	G	A	5	31	c.2110G>A	c.(2110-2112)GCC>ACC	p.A704T
Pat_58	Post-Resistance	RPL11	6135	37	1	24021193	24021193	Missense_Mutation	SNP	G	A	93	209	c.308G>A	c.(307-309)GGA>GAA	p.G103E
Pat_58	Post-Resistance	GALE	2582	37	1	24124707	24124707	Missense_Mutation	SNP	G	A	4	158	c.251C>T	c.(250-252)GCG>GTG	p.A84V
Pat_58	Post-Resistance	PTCH2	8643	37	1	45296653	45296653	Missense_Mutation	SNP	G	A	26	50	c.680C>T	c.(679-681)CCC>CTC	p.P227L
Pat_58	Post-Resistance	CYP4B1	1580	37	1	47279163	47279163	Missense_Mutation	SNP	G	A	45	100	c.505G>A	c.(505-507)GAA>AAA	p.E169K
Pat_58	Post-Resistance	S100A12	6283	37	1	153347041	153347041	Missense_Mutation	SNP	C	T	146	337	c.28G>A	c.(28-30)GGA>AGA	p.G10R
Pat_58	Post-Resistance	FDPS	2224	37	1	155282162	155282162	Nonsense_Mutation	SNP	G	A	14	59	c.456G>A	c.(454-456)TGG>TGA	p.W152*
Pat_58	Post-Resistance	VSIG8	391123	37	1	159827563	159827563	Missense_Mutation	SNP	C	G	29	68	c.624G>C	c.(622-624)CAG>CAC	p.Q208H
Pat_58	Post-Resistance	DUSP27	92235	37	1	167095933	167095933	Missense_Mutation	SNP	G	A	95	147	c.1565G>A	c.(1564-1566)AGC>AAC	p.S522N
Pat_58	Post-Resistance	TNR	7143	37	1	175375489	175375489	Missense_Mutation	SNP	G	A	88	211	c.362C>T	c.(361-363)CCC>CTC	p.P121L
Pat_58	Post-Resistance	PAPPA2	60676	37	1	176525627	176525627	Nonsense_Mutation	SNP	C	T	219	80	c.169C>T	c.(169-171)CGA>TGA	p.R57*
Pat_58	Post-Resistance	ASTN1	460	37	1	176915173	176915173	Missense_Mutation	SNP	C	T	78	152	c.2138G>A	c.(2137-2139)GGG>GAG	p.G713E
Pat_58	Post-Resistance	CEP350	9857	37	1	180044327	180044327	Missense_Mutation	SNP	A	T	25	42	c.5738A>T	c.(5737-5739)GAA>GTA	p.E1913V
Pat_58	Post-Resistance	PIGR	5284	37	1	207112655	207112655	Missense_Mutation	SNP	G	A	36	77	c.197C>T	c.(196-198)ACC>ATC	p.T66I
Pat_58	Post-Resistance	HIST3H3	8290	37	1	228612975	228612975	Missense_Mutation	SNP	G	A	6	188	c.52C>T	c.(52-54)CGC>TGC	p.R18C
Pat_58	Post-Resistance	KIAA1804	84451	37	1	233507802	233507802	Missense_Mutation	SNP	C	T	97	176	c.1571C>T	c.(1570-1572)ACC>ATC	p.T524I
Pat_58	Post-Resistance	RET	5979	37	10	43597792	43597792	Missense_Mutation	SNP	C	T	79	48	c.340C>T	c.(340-342)CGC>TGC	p.R114C
Pat_58	Post-Resistance	PSAP	5660	37	10	73587854	73587854	Missense_Mutation	SNP	G	A	4	179	c.637C>T	c.(637-639)CGG>TGG	p.R213W
Pat_58	Post-Resistance	PTEN	5728	37	10	89692899	89692899	Missense_Mutation	SNP	A	C	184	133	c.383A>C	c.(382-384)AAG>ACG	p.K128T
Pat_58	Post-Resistance	PLCE1	51196	37	10	95791173	95791173	Missense_Mutation	SNP	G	A	67	55	c.370G>A	c.(370-372)GAA>AAA	p.E124K
Pat_58	Post-Resistance	OBFC1	79991	37	10	105642449	105642449	Missense_Mutation	SNP	G	A	4	211	c.1100C>T	c.(1099-1101)GCG>GTG	p.A367V
Pat_58	Post-Resistance	OR52E2	119678	37	11	5080082	5080082	Missense_Mutation	SNP	G	A	31	112	c.776C>T	c.(775-777)TCC>TTC	p.S259F
Pat_58	Post-Resistance	TRIM6-TRIM34	445372	37	11	5624931	5624931	Missense_Mutation	SNP	C	T	5	191	c.473C>T	c.(472-474)ACG>ATG	p.T158M
Pat_58	Post-Resistance	OR52B2	255725	37	11	6191079	6191079	Missense_Mutation	SNP	G	A	15	110	c.478C>T	c.(478-480)CCA>TCA	p.P160S
Pat_58	Post-Resistance	OR10A6	390093	37	11	7949500	7949500	Missense_Mutation	SNP	G	A	32	126	c.710C>T	c.(709-711)GCC>GTC	p.A237V
Pat_58	Post-Resistance	OR4A16	81327	37	11	55111552	55111552	Missense_Mutation	SNP	G	A	41	29	c.876G>A	c.(874-876)ATG>ATA	p.M292I
Pat_58	Post-Resistance	OR5M8	219484	37	11	56258567	56258567	Missense_Mutation	SNP	G	A	122	150	c.280C>T	c.(280-282)CCT>TCT	p.P94S

Pat_58	Post-Resistance	P2RX3	5024	37	11	57137436	57137436	Missense_Mutation	SNP	C	T	52	41	c.1160C>T	c.(1159-1161)TCC>TTC	p.S387F
Pat_58	Post-Resistance	OR9Q2	219957	37	11	57958302	57958302	Missense_Mutation	SNP	C	T	81	283	c.340C>T	c.(340-342)CTT>TTT	p.L114F
Pat_58	Post-Resistance	OR5A1	219982	37	11	59211486	59211486	Missense_Mutation	SNP	C	T	193	215	c.845C>T	c.(844-846)TCA>TTA	p.S282L
Pat_58	Post-Resistance	CDC42BPG	55561	37	11	64608092	64608092	Missense_Mutation	SNP	A	C	5	223	c.365T>G	c.(364-366)GTG>GGG	p.V122G
Pat_58	Post-Resistance	KAT5	10524	37	11	65482186	65482186	Missense_Mutation	SNP	G	A	7	696	c.812G>A	c.(811-813)CGT>CAT	p.R271H
Pat_58	Post-Resistance	CLCF1	23529	37	11	67132696	67132696	Missense_Mutation	SNP	G	A	4	126	c.589C>T	c.(589-591)CGC>TGC	p.R197C
Pat_58	Post-Resistance	FOLH1B	219595	37	11	89395322	89395322	Translation_Start_Site	SNP	C	T	4	97	c.-93C>T	c.(-95--91)TACGC>TATGC	
Pat_58	Post-Resistance	CNTN5	53942	37	11	99786792	99786792	Missense_Mutation	SNP	G	A	17	20	c.584G>A	c.(583-585)GGA>GAA	p.G195E
Pat_58	Post-Resistance	CNTN5	53942	37	11	100168359	100168360	Missense_Mutation	DNP	CC	TT	20	40	.2317_2318CC>T	c.(2317-2319)CCG>TTG	p.P773L
Pat_58	Post-Resistance	HTR3A	3359	37	11	113857451	113857451	Missense_Mutation	SNP	G	C	55	157	c.935G>C	c.(934-936)GGT>GCT	p.G312A
Pat_58	Post-Resistance	KCNJ1	3758	37	11	128709244	128709244	Missense_Mutation	SNP	C	T	60	86	c.952G>A	c.(952-954)GAG>AAG	p.E318K
Pat_58	Post-Resistance	CLEC9A	283420	37	12	10217331	10217331	Missense_Mutation	SNP	G	T	120	254	c.472G>T	c.(472-474)GAT>TAT	p.D158Y
Pat_58	Post-Resistance	PRB2	653247	37	12	11546009	11546009	Missense_Mutation	SNP	T	G	5	445	c.1003A>C	c.(1003-1005)AAA>CAA	p.K335Q
Pat_58	Post-Resistance	LOH12CR1	118426	37	12	12514232	12514232	Missense_Mutation	SNP	C	T	141	244	c.151C>T	c.(151-153)CCC>TCC	p.P51S
Pat_58	Post-Resistance	PPFIBP1	8496	37	12	27802985	27802985	Missense_Mutation	SNP	C	A	50	117	c.514C>A	c.(514-516)CTG>ATG	p.L172M
Pat_58	Post-Resistance	CNTN1	1272	37	12	41410489	41410489	Missense_Mutation	SNP	G	C	34	71	c.2190G>C	c.(2188-2190)TTG>TTC	p.L730F
Pat_58	Post-Resistance	NUP107	57122	37	12	69107527	69107527	Missense_Mutation	SNP	C	T	126	208	c.908C>T	c.(907-909)ACC>ATC	p.T303I
Pat_58	Post-Resistance	WSCD2	9671	37	12	108589739	108589739	Missense_Mutation	SNP	G	A	5	357	c.130G>A	c.(130-132)GCT>ACT	p.A44T
Pat_58	Post-Resistance	SVOP	55530	37	12	109316492	109316492	Missense_Mutation	SNP	A	T	4	69	c.1130T>A	c.(1129-1131)CTG>CAG	p.L377Q
Pat_58	Post-Resistance	NAA25	80018	37	12	112486232	112486232	Missense_Mutation	SNP	T	C	104	131	c.1744A>G	c.(1744-1746)ATT>GTT	p.I582V
Pat_58	Post-Resistance	GPR109B	8843	37	12	123200890	123200890	Missense_Mutation	SNP	G	A	86	192	c.395C>T	c.(394-396)CCC>CTC	p.P132L
Pat_58	Post-Resistance	TUBA3C	7278	37	13	19753616	19753616	Nonsense_Mutation	SNP	G	A	173	261	c.91C>T	c.(91-93)CAG>TAG	p.Q31*
Pat_58	Post-Resistance	HS6ST3	266722	37	13	97485361	97485361	Missense_Mutation	SNP	G	A	86	128	c.1325G>A	c.(1324-1326)CGA>CAA	p.R442Q
Pat_58	Post-Resistance	ARHGEF7	8874	37	13	111767950	111767950	Missense_Mutation	SNP	A	C	27	39	c.77A>C	c.(76-78)GAC>GCC	p.D26A
Pat_58	Post-Resistance	GMPR2	51292	37	14	24707523	24707523	Nonsense_Mutation	SNP	G	T	4	141	c.769G>T	c.(769-771)GAG>TAG	p.E257*
Pat_58	Post-Resistance	MAP3K9	4293	37	14	71205096	71205096	Missense_Mutation	SNP	G	T	4	231	c.1710C>A	c.(1708-1710)AGC>AGA	p.S570R
Pat_58	Post-Resistance	CCDC88C	440193	37	14	91779633	91779633	Missense_Mutation	SNP	G	A	5	272	c.2527C>T	c.(2527-2529)CGG>TGG	p.R843W
Pat_58	Post-Resistance	KLC1	3831	37	14	104123952	104123952	Missense_Mutation	SNP	C	T	5	269	c.331C>T	c.(331-333)CGT>TGT	p.R111C
Pat_58	Post-Resistance	C15orf2	23742	37	15	24923547	24923547	Missense_Mutation	SNP	G	A	117	110	c.2533G>A	c.(2533-2535)GAG>AAG	p.E845K
Pat_58	Post-Resistance	OTUD7A	161725	37	15	31776801	31776801	Missense_Mutation	SNP	C	T	14	13	c.1477G>A	c.(1477-1479)GGC>AGC	p.G493S
Pat_58	Post-Resistance	PLA2G4D	283748	37	15	42361057	42361057	Missense_Mutation	SNP	C	T	23	17	c.2313G>A	c.(2311-2313)ATG>ATA	p.M771I
Pat_58	Post-Resistance	CASKIN1	57524	37	16	2239282	2239282	Missense_Mutation	SNP	C	G	12	68	c.443G>C	c.(442-444)GGG>GCG	p.G148A
Pat_58	Post-Resistance	PAQR4	124222	37	16	3021902	3021902	Missense_Mutation	SNP	G	A	4	120	c.775G>A	c.(775-777)GTG>ATG	p.V259M
Pat_58	Post-Resistance	ACSM2A	123876	37	16	20476849	20476849	Missense_Mutation	SNP	G	A	8	114	c.188G>A	c.(187-189)CGA>CAA	p.R63Q
Pat_58	Post-Resistance	ACSM2B	348158	37	16	20570759	20570759	Missense_Mutation	SNP	C	T	23	58	c.188G>A	c.(187-189)CGA>CAA	p.R63Q
Pat_58	Post-Resistance	DNAH3	55567	37	16	21053420	21053420	Missense_Mutation	SNP	G	A	87	154	c.4567C>T	c.(4567-4569)CCA>TCA	p.P1523S
Pat_58	Post-Resistance	RRN3P1	730092	37	16	21809167	21809167	Missense_Mutation	SNP	G	A	5	50	c.533C>T	c.(532-534)CCT>CTT	p.P178L
Pat_58	Post-Resistance	CD19	930	37	16	28948983	28948983	Missense_Mutation	SNP	C	T	4	253	c.1411C>T	c.(1411-1413)CCG>TCG	p.P471S
Pat_58	Post-Resistance	GNAO1	2775	37	16	56362666	56362666	Missense_Mutation	SNP	C	T	4	253	c.427C>T	c.(427-429)CGG>TGG	p.R143W
Pat_58	Post-Resistance	KIAA0895L	653319	37	16	67214167	67214167	Missense_Mutation	SNP	G	A	4	119	c.347C>T	c.(346-348)GCA>GTA	p.A116V
Pat_58	Post-Resistance	PARD6A	50855	37	16	67696424	67696424	Nonsense_Mutation	SNP	G	A	3	84	c.915G>A	c.(913-915)TGG>TGA	p.W305*
Pat_58	Post-Resistance	TSNAXIP1	55815	37	16	67860947	67860947	Missense_Mutation	SNP	G	A	43	179	c.1474G>A	c.(1474-1476)GAG>AAG	p.E492K
Pat_58	Post-Resistance	COG8	84342	37	16	69373451	69373451	Missense_Mutation	SNP	G	A	4	85	c.5C>T	c.(4-6)GCG>GTG	p.A2V
Pat_58	Post-Resistance	CNTNAP4	85445	37	16	76501306	76501306	Missense_Mutation	SNP	G	A	47	51	c.1541G>A	c.(1540-1542)GGA>GAA	p.G514E
Pat_58	Post-Resistance	PKD1L2	114780	37	16	81181938	81181938	Missense_Mutation	SNP	T	A	57	82	c.4778A>T	c.(4777-4779)GAG>GTG	p.E1593V
Pat_58	Post-Resistance	KIAA0513	9764	37	16	85112025	85112025	Missense_Mutation	SNP	G	A	20	52	c.787G>A	c.(787-789)GAC>AAC	p.D263N
Pat_58	Post-Resistance	PITPNM3	83394	37	17	6374648	6374648	Missense_Mutation	SNP	A	G	10	17	c.1457T>C	c.(1456-1458)CTC>CCC	p.L486P

Pat_58	Post-Resistance	MYH4	4622	37	17	10348301	10348301	Missense_Mutation	SNP	C	T	112	195	c.5458G>A	c.(5458-5460)GAG>AAG	p.E1820K
Pat_58	Post-Resistance	MYH2	4620	37	17	10432565	10432565	Missense_Mutation	SNP	C	T	42	121	c.3268G>A	c.(3268-3270)GAG>AAG	p.E1090K
Pat_58	Post-Resistance	TEKT3	64518	37	17	15231338	15231338	Missense_Mutation	SNP	G	A	127	232	c.634C>T	c.(634-636)CAC>TAC	p.H212Y
Pat_58	Post-Resistance	MAPK7	5598	37	17	19284463	19284463	Missense_Mutation	SNP	C	A	4	187	c.941C>A	c.(940-942)CCA>CAA	p.P314Q
Pat_58	Post-Resistance	SLC6A4	6532	37	17	28530357	28530357	Missense_Mutation	SNP	A	G	41	174	c.1651T>C	c.(1651-1653)TTC>CTC	p.F551L
Pat_58	Post-Resistance	PLXDC1	57125	37	17	37224186	37224186	Missense_Mutation	SNP	C	T	71	104	c.1410G>A	c.(1408-1410)ATG>ATA	p.M470I
Pat_58	Post-Resistance	KRTAP4-4	84616	37	17	39316834	39316834	Missense_Mutation	SNP	C	T	6	363	c.110G>A	c.(109-111)CGC>CAC	p.R37H
Pat_58	Post-Resistance	SOX9	6662	37	17	70120373	70120373	Missense_Mutation	SNP	G	A	131	249	c.1375G>A	c.(1375-1377)GGC>AGC	p.G459S
Pat_58	Post-Resistance	GGA3	23163	37	17	73242839	73242839	Missense_Mutation	SNP	C	T	53	101	c.79G>A	c.(79-81)GAA>AAA	p.E27K
Pat_58	Post-Resistance	KIAA0195	9772	37	17	73489139	73489139	Missense_Mutation	SNP	C	T	55	101	c.2042C>T	c.(2041-2043)CCC>CTC	p.P681L
Pat_58	Post-Resistance	CDK3	1018	37	17	73998125	73998125	Missense_Mutation	SNP	G	A	22	115	c.217G>A	c.(217-219)GAG>AAG	p.E73K
Pat_58	Post-Resistance	CBX2	84733	37	17	77758233	77758233	Missense_Mutation	SNP	C	A	3	30	c.991C>A	c.(991-993)CAT>AAT	p.H331N
Pat_58	Post-Resistance	PTPRM	5797	37	18	8380385	8380385	Missense_Mutation	SNP	G	A	4	207	c.3839G>A	c.(3838-3840)TGC>TAC	p.C1280Y
Pat_58	Post-Resistance	POTEC	388468	37	18	14513663	14513663	Missense_Mutation	SNP	C	T	7	371	c.1531G>A	c.(1531-1533)GAG>AAG	p.E511K
Pat_58	Post-Resistance	ZNF521	25925	37	18	22804770	22804770	Missense_Mutation	SNP	G	A	60	87	c.3112C>T	c.(3112-3114)CAT>TAT	p.H1038Y
Pat_58	Post-Resistance	DSC3	1825	37	18	28598204	28598204	Missense_Mutation	SNP	C	T	31	74	c.1096G>A	c.(1096-1098)GAA>AAA	p.E366K
Pat_58	Post-Resistance	DSG3	1830	37	18	29052688	29052688	Missense_Mutation	SNP	G	A	28	59	c.2038G>A	c.(2038-2040)GAA>AAA	p.E680K
Pat_58	Post-Resistance	ZNF271	10778	37	18	32886791	32886791	Missense_Mutation	SNP	C	T	60	131	c.203C>T	c.(202-204)TCC>TTC	p.S68F
Pat_58	Post-Resistance	NEDD4L	23327	37	18	56037691	56037691	Missense_Mutation	SNP	G	A	68	102	c.2248G>A	c.(2248-2250)GAA>AAA	p.E750K
Pat_58	Post-Resistance	CDH20	28316	37	18	59221482	59221482	Missense_Mutation	SNP	G	A	181	354	c.1960G>A	c.(1960-1962)GAC>AAC	p.D654N
Pat_58	Post-Resistance	CDH7	1005	37	18	63511228	63511228	Missense_Mutation	SNP	G	A	139	219	c.1162G>A	c.(1162-1164)GAA>AAA	p.E388K
Pat_58	Post-Resistance	ADAT3	113179	37	19	1912891	1912891	Missense_Mutation	SNP	G	A	4	89	c.797G>A	c.(796-798)CGT>CAT	p.R266H
Pat_58	Post-Resistance	DOT1L	84444	37	19	2217801	2217801	Missense_Mutation	SNP	G	A	3	36	c.2575G>A	c.(2575-2577)GGG>AGG	p.G859R
Pat_58	Post-Resistance	MUC16	94025	37	19	9075612	9075612	Missense_Mutation	SNP	T	G	21	39	c.11834A>C	c.(11833-11835)CAC>CCC	p.H3945P
Pat_58	Post-Resistance	MUC16	94025	37	19	9091708	9091708	Missense_Mutation	SNP	C	T	31	87	c.107G>A	c.(106-108)GGA>GAA	p.G36E
Pat_58	Post-Resistance	OR7D4	125958	37	19	9325014	9325014	Missense_Mutation	SNP	G	A	4	297	c.500C>T	c.(499-501)ACC>ATC	p.T167I
Pat_58	Post-Resistance	CYP4F12	66002	37	19	15807003	15807003	Missense_Mutation	SNP	C	T	113	281	c.1282C>T	c.(1282-1284)CAT>TAT	p.H428Y
Pat_58	Post-Resistance	NXNL1	115861	37	19	17566497	17566497	Missense_Mutation	SNP	C	T	3	13	c.598G>A	c.(598-600)GGA>AGA	p.G200R
Pat_58	Post-Resistance	ZNF90	7643	37	19	20229238	20229238	Missense_Mutation	SNP	G	A	5	282	c.875G>A	c.(874-876)AGA>AAA	p.R292K
Pat_58	Post-Resistance	ZNF737	100129842	37	19	20727870	20727870	Missense_Mutation	SNP	C	G	7	800	c.1139G>C	c.(1138-1140)TGG>TCG	p.W380S
Pat_58	Post-Resistance	ZNF208	7757	37	19	22154522	22154522	Missense_Mutation	SNP	C	T	295	372	c.2930G>A	c.(2929-2931)AGA>AAA	p.R977K
Pat_58	Post-Resistance	CEACAM5	1048	37	19	42224958	42224958	Missense_Mutation	SNP	A	G	236	251	c.1888A>G	c.(1888-1890)AAT>GAT	p.N630D
Pat_58	Post-Resistance	PSG9	5678	37	19	43771986	43771986	Missense_Mutation	SNP	C	T	361	426	c.380G>A	c.(379-381)CGA>CAA	p.R127Q
Pat_58	Post-Resistance	NPAS1	4861	37	19	47548577	47548577	Missense_Mutation	SNP	G	A	52	108	c.1441G>A	c.(1441-1443)GAG>AAG	p.E481K
Pat_58	Post-Resistance	CRX	1406	37	19	48339526	48339526	Missense_Mutation	SNP	C	T	4	194	c.127C>T	c.(127-129)CGC>TGC	p.R43C
Pat_58	Post-Resistance	KLK15	55554	37	19	51330220	51330220	Missense_Mutation	SNP	G	A	26	61	c.395C>T	c.(394-396)CCC>CTC	p.P132L
Pat_58	Post-Resistance	NLRP12	91662	37	19	54299142	54299142	Missense_Mutation	SNP	G	T	4	134	c.3069C>A	c.(3067-3069)AGC>AGA	p.S1023R
Pat_58	Post-Resistance	TSEN34	79042	37	19	54696042	54696042	Missense_Mutation	SNP	C	G	146	186	c.563C>G	c.(562-564)GCC>GGC	p.A188G
Pat_58	Post-Resistance	KIR3DX1	90011	37	19	55048172	55048172	Missense_Mutation	SNP	G	A	48	142	c.40G>A	c.(40-42)GAA>AAA	p.E14K
Pat_58	Post-Resistance	PEG3	5178	37	19	57325129	57325129	Missense_Mutation	SNP	C	T	114	129	c.4681G>A	c.(4681-4683)GAG>AAG	p.E1561K
Pat_58	Post-Resistance	ZNF749	388567	37	19	57955885	57955885	Missense_Mutation	SNP	C	G	5	379	c.1369C>G	c.(1369-1371)CAG>GAG	p.Q457E
Pat_58	Post-Resistance	CYS1	192668	37	2	10206069	10206069	Missense_Mutation	SNP	C	A	4	169	c.333G>T	c.(331-333)CAG>CAT	p.Q111H
Pat_58	Post-Resistance	ASXL2	55252	37	2	26101081	26101081	Missense_Mutation	SNP	T	C	6	608	c.11A>G	c.(10-12)AAG>AGG	p.K4R
Pat_58	Post-Resistance	GTF3C2	2976	37	2	27560826	27560826	Missense_Mutation	SNP	G	A	238	593	c.917C>T	c.(916-918)CCT>CTT	p.P306L
Pat_58	Post-Resistance	QPCT	25797	37	2	37571926	37571926	Missense_Mutation	SNP	C	G	3	55	c.52C>G	c.(52-54)CTG>GTG	p.L18V
Pat_58	Post-Resistance	KCNG3	170850	37	2	42671595	42671595	Missense_Mutation	SNP	G	A	136	231	c.790C>T	c.(790-792)CCG>TCG	p.P264S
Pat_58	Post-Resistance	TET3	200424	37	2	74300721	74300721	Missense_Mutation	SNP	G	A	18	46	c.2135G>A	c.(2134-2136)GGA>GAA	p.G712E

Pat_58	Post-Resistance	C2orf65	130951	37	2	74803695	74803695	Missense_Mutation	SNP	C	A	4	136	c.820G>T	c.(820-822)GCT>TCT	p.A274S
Pat_58	Post-Resistance	SMYD1	150572	37	2	88383938	88383938	Missense_Mutation	SNP	G	A	89	137	c.241G>A	c.(241-243)GAT>AAT	p.D81N
Pat_58	Post-Resistance	SNRNP200	23020	37	2	96943407	96943407	Missense_Mutation	SNP	C	T	4	282	c.5801G>A	c.(5800-5802)GGG>GAG	p.G1934E
Pat_58	Post-Resistance	GCC2	9648	37	2	109124081	109124081	Nonsense_Mutation	SNP	C	T	60	132	c.5050C>T	c.(5050-5052)CGA>TGA	p.R1684*
Pat_58	Post-Resistance	CNTNAP5	129684	37	2	125547652	125547652	Missense_Mutation	SNP	G	A	56	75	c.2923G>A	c.(2923-2925)GAG>AAG	p.E975K
Pat_58	Post-Resistance	LRP1B	53353	37	2	141093183	141093183	Splice_Site	SNP	C	A	26	197	c.12116_splice	c.e78+1	p.G4039_splice
Pat_58	Post-Resistance	TTC21B	79809	37	2	166740494	166740494	Missense_Mutation	SNP	G	A	4	200	c.3494C>T	c.(3493-3495)ACG>ATG	p.T1165M
Pat_58	Post-Resistance	SCN9A	6335	37	2	167133791	167133791	Missense_Mutation	SNP	A	G	64	292	c.2543T>C	c.(2542-2544)ATT>ACT	p.I848T
Pat_58	Post-Resistance	TTN	7273	37	2	179554591	179554591	Missense_Mutation	SNP	C	T	125	225	c.28063G>A	c.(28063-28065)GAA>AAA	p.E9355K
Pat_58	Post-Resistance	TTN	7273	37	2	179611173	179611173	Missense_Mutation	SNP	T	A	29	84	c.15954A>T	c.(15952-15954)GAA>GAT	p.E5318D
Pat_58	Post-Resistance	TTN	7273	37	2	179611175	179611175	Missense_Mutation	SNP	C	T	31	88	c.15952G>A	c.(15952-15954)GAA>AAA	p.E5318K
Pat_58	Post-Resistance	TTN	7273	37	2	179616629	179616629	Nonsense_Mutation	SNP	C	A	150	298	c.10498G>T	c.(10498-10500)GAA>TAA	p.E3500*
Pat_58	Post-Resistance	PDE1A	5136	37	2	183129116	183129116	Missense_Mutation	SNP	C	T	67	112	c.127G>A	c.(127-129)GAA>AAA	p.E43K
Pat_58	Post-Resistance	NIF3L1	60491	37	2	201757983	201757983	Missense_Mutation	SNP	A	T	75	133	c.451A>T	c.(451-453)AGG>TGG	p.R151W
Pat_58	Post-Resistance	NRP2	8828	37	2	206617576	206617576	Missense_Mutation	SNP	C	T	41	72	c.1921C>T	c.(1921-1923)CCT>TCT	p.P641S
Pat_58	Post-Resistance	DNAJB3	414061	37	2	234652194	234652194	Missense_Mutation	SNP	C	G	53	91	c.369G>C	c.(367-369)TTG>TTC	p.L123F
Pat_58	Post-Resistance	IQCA1	79781	37	2	237406078	237406078	Missense_Mutation	SNP	C	T	18	27	c.64G>A	c.(64-66)GAT>AAT	p.D22N
Pat_58	Post-Resistance	SLA2	84174	37	20	35261091	35261091	Nonsense_Mutation	SNP	C	A	3	61	c.289G>T	c.(289-291)GAG>TAG	p.E97*
Pat_58	Post-Resistance	CHD6	84181	37	20	40102126	40102126	Missense_Mutation	SNP	G	A	4	286	c.2500C>T	c.(2500-2502)CGG>TGG	p.R834W
Pat_58	Post-Resistance	CHD6	84181	37	20	40162173	40162173	Missense_Mutation	SNP	A	G	12	157	c.70T>C	c.(70-72)TCT>CCT	p.S24P
Pat_58	Post-Resistance	BAGE2	85319	37	21	11098839	11098839	Translation_Start_Site	SNP	C	T	7	241	c.-121G>A	(-123--119)CCGTG>CCATG	
Pat_58	Post-Resistance	DSCAM	1826	37	21	41450612	41450612	Splice_Site	SNP	A	G	17	96	c.4711_splice	c.e26+1	p.S1571_splice
Pat_58	Post-Resistance	MX2	4600	37	21	42778797	42778797	Nonsense_Mutation	SNP	C	T	89	194	c.1777C>T	c.(1777-1779)CGA>TGA	p.R593*
Pat_58	Post-Resistance	RIPK4	54101	37	21	43187175	43187175	Nonsense_Mutation	SNP	C	T	19	33	c.27G>A	c.(25-27)TGG>TGA	p.W9*
Pat_58	Post-Resistance	HIRA	7290	37	22	19375314	19375314	Missense_Mutation	SNP	C	A	10	70	c.1033G>T	c.(1033-1035)GTA>TTA	p.V345L
Pat_58	Post-Resistance	PI4KA	5297	37	22	21119177	21119177	Missense_Mutation	SNP	G	A	108	43	c.2462C>T	c.(2461-2463)TCC>TTC	p.S821F
Pat_58	Post-Resistance	CABIN1	23523	37	22	24483437	24483437	Missense_Mutation	SNP	G	A	4	161	c.3296G>A	c.(3295-3297)CGG>CAG	p.R1099Q
Pat_58	Post-Resistance	HMOX1	3162	37	22	35789529	35789529	Nonsense_Mutation	SNP	C	T	378	143	c.805C>T	c.(805-807)CGA>TGA	p.R269*
Pat_58	Post-Resistance	APOL2	23780	37	22	36624196	36624196	Missense_Mutation	SNP	T	C	5	369	c.268A>G	c.(268-270)AGG>GGG	p.R90G
Pat_58	Post-Resistance	MKL1	57591	37	22	40816901	40816901	Missense_Mutation	SNP	C	G	9	231	c.831G>C	c.(829-831)CAG>CAC	p.Q277H
Pat_58	Post-Resistance	PRRT3	285368	37	3	9991520	9991520	Missense_Mutation	SNP	G	T	3	79	c.280C>A	c.(280-282)CCA>ACA	p.P94T
Pat_58	Post-Resistance	SLC6A6	6533	37	3	14509693	14509693	Missense_Mutation	SNP	G	A	4	130	c.1069G>A	c.(1069-1071)GTG>ATG	p.V357M
Pat_58	Post-Resistance	HHATL	57467	37	3	42738595	42738595	Missense_Mutation	SNP	G	A	3	75	c.908C>T	c.(907-909)GCG>GTG	p.A303V
Pat_58	Post-Resistance	TDGF1	6997	37	3	46622673	46622673	Missense_Mutation	SNP	C	A	4	118	c.500C>A	c.(499-501)CCA>CAA	p.P167Q
Pat_58	Post-Resistance	ERC2	26059	37	3	56330265	56330265	Missense_Mutation	SNP	C	T	708	240	c.856G>A	c.(856-858)GAA>AAA	p.E286K
Pat_58	Post-Resistance	C3orf63	23272	37	3	56675420	56675420	Missense_Mutation	SNP	G	A	4	283	c.2576C>T	c.(2575-2577)TCT>TTT	p.S859F
Pat_58	Post-Resistance	PPM1L	151742	37	3	160783314	160783314	Missense_Mutation	SNP	C	T	53	152	c.698C>T	c.(697-699)CCT>CTT	p.P233L
Pat_58	Post-Resistance	MAP3K13	9175	37	3	185191197	185191197	Missense_Mutation	SNP	G	A	4	233	c.2078G>A	c.(2077-2079)GGC>GAC	p.G693D
Pat_58	Post-Resistance	ZNF721	170960	37	4	436043	436043	Missense_Mutation	SNP	G	T	26	51	c.2213C>A	c.(2212-2214)ACA>AAA	p.T738K
Pat_58	Post-Resistance	MFSD10	10227	37	4	2934340	2934340	Missense_Mutation	SNP	C	T	4	293	c.518G>A	c.(517-519)CGC>CAC	p.R173H
Pat_58	Post-Resistance	MAN2B2	23324	37	4	6594922	6594922	Missense_Mutation	SNP	G	A	4	126	c.703G>A	c.(703-705)GTG>ATG	p.V235M
Pat_58	Post-Resistance	GRPEL1	80273	37	4	7062744	7062744	Missense_Mutation	SNP	C	T	4	305	c.499G>A	c.(499-501)GGA>AGA	p.G167R
Pat_58	Post-Resistance	GPR78	27201	37	4	8588947	8588947	Missense_Mutation	SNP	C	T	70	136	c.949C>T	c.(949-951)CCG>TCG	p.P317S
Pat_58	Post-Resistance	CWH43	80157	37	4	49032922	49032922	Missense_Mutation	SNP	G	A	118	222	c.1453G>A	c.(1453-1455)GAA>AAA	p.E485K
Pat_58	Post-Resistance	BMP2K	55589	37	4	79792085	79792085	Missense_Mutation	SNP	G	C	7	183	c.1380G>C	c.(1378-1380)CAG>CAC	p.Q460H
Pat_58	Post-Resistance	UNC5C	8633	37	4	96469943	96469943	Missense_Mutation	SNP	C	A	4	276	c.66G>T	c.(64-66)ATG>ATT	p.M22I
Pat_58	Post-Resistance	EGF	1950	37	4	110932470	110932470	Missense_Mutation	SNP	G	A	77	141	c.3483G>A	c.(3481-3483)ATG>ATA	p.M1161I

Pat_58	Post-Resistance	BBS7	55212	37	4	122760836	122760836	Missense_Mutation	SNP	G	A	48	97	c.1321C>T	c.(1321-1323)CTT>TTT	p.L441F
Pat_58	Post-Resistance	MAP9	79884	37	4	156278607	156278607	Missense_Mutation	SNP	G	A	66	119	c.1115C>T	c.(1114-1116)TCT>TTT	p.S372F
Pat_58	Post-Resistance	RAPGEF2	9693	37	4	160259495	160259495	Missense_Mutation	SNP	G	A	4	189	c.1685G>A	c.(1684-1686)AGC>AAC	p.S562N
Pat_58	Post-Resistance	SPOCK3	50859	37	4	167658743	167658743	Missense_Mutation	SNP	G	A	147	260	c.1016C>T	c.(1015-1017)CCC>CTC	p.P339L
Pat_58	Post-Resistance	THBS4	7060	37	5	79336049	79336049	Missense_Mutation	SNP	T	C	3	73	c.238T>C	c.(238-240)TCA>CCA	p.S80P
Pat_58	Post-Resistance	PCDHA11	56138	37	5	140248752	140248752	Missense_Mutation	SNP	G	A	103	48	c.64G>A	c.(64-66)GAA>AAA	p.E22K
Pat_58	Post-Resistance	PCDHB4	56131	37	5	140503847	140503847	Missense_Mutation	SNP	G	A	151	73	c.2267G>A	c.(2266-2268)GGA>GAA	p.G756E
Pat_58	Post-Resistance	PCDHB7	56129	37	5	140552652	140552652	Missense_Mutation	SNP	C	T	107	54	c.236C>T	c.(235-237)TCG>TTG	p.S79L
Pat_58	Post-Resistance	SYNPO	11346	37	5	150028744	150028744	Nonsense_Mutation	SNP	C	T	3	60	c.1639C>T	c.(1639-1641)CGA>TGA	p.R547*
Pat_58	Post-Resistance	KIF4B	285643	37	5	154394854	154394854	Missense_Mutation	SNP	G	A	127	83	c.1435G>A	c.(1435-1437)GAA>AAA	p.E479K
Pat_58	Post-Resistance	C5orf40	408263	37	5	156770118	156770118	Missense_Mutation	SNP	G	A	67	57	c.427C>T	c.(427-429)CCG>TCG	p.P143S
Pat_58	Post-Resistance	OR2Y1	134083	37	5	180166481	180166481	Missense_Mutation	SNP	C	T	89	143	c.578G>A	c.(577-579)GGA>GAA	p.G193E
Pat_58	Post-Resistance	SYCP2L	221711	37	6	10935349	10935349	Missense_Mutation	SNP	C	T	64	84	c.1742C>T	c.(1741-1743)CCA>CTA	p.P581L
Pat_58	Post-Resistance	DHX16	8449	37	6	30633288	30633288	Missense_Mutation	SNP	G	A	89	141	c.889C>T	c.(889-891)CGC>TGC	p.R297C
Pat_58	Post-Resistance	DNAH8	1769	37	6	38840720	38840720	Missense_Mutation	SNP	G	C	51	62	c.6625G>C	c.(6625-6627)GCC>CCC	p.A2209P
Pat_58	Post-Resistance	FOXP4	116113	37	6	41557786	41557786	Missense_Mutation	SNP	C	T	21	115	c.1235C>T	c.(1234-1236)CCG>CTG	p.P412L
Pat_58	Post-Resistance	TDRD6	221400	37	6	46657437	46657437	Nonsense_Mutation	SNP	T	A	121	216	c.1572T>A	c.(1570-1572)TAT>TAA	p.Y524*
Pat_58	Post-Resistance	ZNF292	23036	37	6	87925717	87925717	Nonsense_Mutation	SNP	C	T	19	125	c.265C>T	c.(265-267)CGA>TGA	p.R89*
Pat_58	Post-Resistance	ZNF292	23036	37	6	87966906	87966906	Missense_Mutation	SNP	G	A	29	101	c.3559G>A	c.(3559-3561)GTC>ATC	p.V1187I
Pat_58	Post-Resistance	ZNF292	23036	37	6	87970071	87970071	Missense_Mutation	SNP	G	A	4	222	c.6724G>A	c.(6724-6726)GGG>AGG	p.G2242R
Pat_58	Post-Resistance	GRIK2	2898	37	6	102124506	102124506	Missense_Mutation	SNP	C	T	41	76	c.550C>T	c.(550-552)CGT>TGT	p.R184C
Pat_58	Post-Resistance	MED23	9439	37	6	131944514	131944514	Missense_Mutation	SNP	T	C	81	274	c.373A>G	c.(373-375)ATA>GTA	p.I125V
Pat_58	Post-Resistance	MYCT1	80177	37	6	153043051	153043051	Missense_Mutation	SNP	G	A	140	187	c.371G>A	c.(370-372)GGA>GAA	p.G124E
Pat_58	Post-Resistance	MLLT4	4301	37	6	168316028	168316028	Missense_Mutation	SNP	G	A	4	103	c.2456G>A	c.(2455-2457)CGT>CAT	p.R819H
Pat_58	Post-Resistance	SDK1	221935	37	7	4259872	4259872	Missense_Mutation	SNP	C	A	5	255	c.5671C>A	c.(5671-5673)CAA>AAA	p.Q1891K
Pat_58	Post-Resistance	HOXA6	3203	37	7	27187097	27187097	Missense_Mutation	SNP	G	A	4	129	c.272C>T	c.(271-273)TCG>TTG	p.S91L
Pat_58	Post-Resistance	NEUROD6	63974	37	7	31378228	31378228	Missense_Mutation	SNP	G	A	76	135	c.655C>T	c.(655-657)CCC>TCC	p.P219S
Pat_58	Post-Resistance	PDE1C	5137	37	7	31862845	31862845	Missense_Mutation	SNP	G	A	32	86	c.1424C>T	c.(1423-1425)TCG>TTG	p.S475L
Pat_58	Post-Resistance	TXNDC3	51314	37	7	37936528	37936528	Missense_Mutation	SNP	G	A	4	217	c.1601G>A	c.(1600-1602)CGA>CAA	p.R534Q
Pat_58	Post-Resistance	MRPS24	64951	37	7	43908607	43908607	Missense_Mutation	SNP	G	A	4	245	c.175C>T	c.(175-177)CCG>TCG	p.P59S
Pat_58	Post-Resistance	CDC14C	168448	37	7	48965286	48965286	Missense_Mutation	SNP	G	A	13	294	c.1018G>A	c.(1018-1020)GAA>AAA	p.E340K
Pat_58	Post-Resistance	PHKG1	5260	37	7	56155446	56155446	Missense_Mutation	SNP	C	T	53	114	c.107G>A	c.(106-108)CGA>CAA	p.R36Q
Pat_58	Post-Resistance	ZNF727	442319	37	7	63538806	63538806	Missense_Mutation	SNP	C	G	10	319	c.1379C>G	c.(1378-1380)ACC>AGC	p.T460S
Pat_58	Post-Resistance	ZNF727	442319	37	7	63538824	63538824	Missense_Mutation	SNP	G	A	7	277	c.1397G>A	c.(1396-1398)AGC>AAC	p.S466N
Pat_58	Post-Resistance	DPY19L2P2	349152	37	7	102875158	102875158	Missense_Mutation	SNP	G	A	23	8	c.499C>T	c.(499-501)CCC>TCC	p.P167S
Pat_58	Post-Resistance	PMPCB	9512	37	7	102937911	102937911	Missense_Mutation	SNP	C	T	4	119	c.5C>T	c.(4-6)GCG>GTG	p.A2V
Pat_58	Post-Resistance	CDHR3	222256	37	7	105664915	105664915	Nonsense_Mutation	SNP	T	A	32	141	c.2165T>A	c.(2164-2166)TTG>TAG	p.L722*
Pat_58	Post-Resistance	TMEM209	84928	37	7	129832466	129832466	Missense_Mutation	SNP	C	G	8	129	c.771G>C	c.(769-771)AAG>AAC	p.K257N
Pat_58	Post-Resistance	CPA2	1358	37	7	129917718	129917718	Missense_Mutation	SNP	G	A	4	156	c.749G>A	c.(748-750)GGT>GAT	p.G250D
Pat_58	Post-Resistance	HIPK2	28996	37	7	139299148	139299148	Missense_Mutation	SNP	G	T	4	91	c.1874C>A	c.(1873-1875)GCA>GAA	p.A625E
Pat_58	Post-Resistance	BRAF	673	37	7	140453136	140453136	Missense_Mutation	SNP	A	T	300	55	c.1799T>A	c.(1798-1800)GTG>GAG	p.V600E
Pat_58	Post-Resistance	DLGAP2	9228	37	8	1616614	1616614	Missense_Mutation	SNP	G	A	9	37	c.1690G>A	c.(1690-1692)GAC>AAC	p.D564N
Pat_58	Post-Resistance	TNKS	8658	37	8	9623293	9623293	Missense_Mutation	SNP	G	A	5	261	c.3539G>A	c.(3538-3540)CGC>CAC	p.R1180H
Pat_58	Post-Resistance	TRIM55	84675	37	8	67086715	67086715	Missense_Mutation	SNP	G	A	115	174	c.1534G>A	c.(1534-1536)GAG>AAG	p.E512K
Pat_58	Post-Resistance	CA1	759	37	8	86253846	86253846	Missense_Mutation	SNP	C	T	43	122	c.19G>A	c.(19-21)GGA>AGA	p.G7R
Pat_58	Post-Resistance	NOV	4856	37	8	120430415	120430415	Missense_Mutation	SNP	G	T	4	210	c.428G>T	c.(427-429)CGC>CTC	p.R143L
Pat_58	Post-Resistance	JAK2	3717	37	9	5029852	5029852	Missense_Mutation	SNP	A	G	62	170	c.296A>G	c.(295-297)AAC>AGC	p.N99S

Pat_58	Post-Resistance	FBXO10	26267	37	9	37521629	37521629	Missense_Mutation	SNP	C	T	27	10	c.2137G>A	c.(2137-2139)GAC>AAC	p.D713N
Pat_58	Post-Resistance	C9orf135	138255	37	9	72472877	72472877	Missense_Mutation	SNP	C	T	55	49	c.433C>T	c.(433-435)CCG>TCG	p.P145S
Pat_58	Post-Resistance	EPB41L4B	54566	37	9	111954631	111954631	Missense_Mutation	SNP	G	A	95	63	c.2228C>T	c.(2227-2229)CCC>CTC	p.P743L
Pat_58	Post-Resistance	MUSK	4593	37	9	113563023	113563023	Missense_Mutation	SNP	G	T	4	110	c.2365G>T	c.(2365-2367)GGC>TGC	p.G789C
Pat_58	Post-Resistance	C9orf84	158401	37	9	114490105	114490105	Missense_Mutation	SNP	C	T	104	67	c.1450G>A	c.(1450-1452)GAT>AAT	p.D484N
Pat_58	Post-Resistance	ABL1	25	37	9	133760987	133760987	Missense_Mutation	SNP	G	A	4	80	c.3310G>A	c.(3310-3312)GCA>ACA	p.A1104T
Pat_58	Post-Resistance	FCN1	2219	37	9	137808285	137808285	Missense_Mutation	SNP	C	A	79	194	c.126G>T	c.(124-126)GAG>GAT	p.E42D
Pat_58	Post-Resistance	ABCA2	20	37	9	139912771	139912771	Missense_Mutation	SNP	G	A	4	200	c.1849C>T	c.(1849-1851)CTC>TTC	p.L617F
Pat_58	Post-Resistance	ARSF	416	37	X	3030406	3030406	Missense_Mutation	SNP	G	A	130	201	c.1582G>A	c.(1582-1584)GAT>AAT	p.D528N
Pat_58	Post-Resistance	MXRA5	25878	37	X	3248289	3248289	Missense_Mutation	SNP	C	T	25	50	c.479G>A	c.(478-480)GGA>GAA	p.G160E
Pat_58	Post-Resistance	KAL1	3730	37	X	8504853	8504853	Missense_Mutation	SNP	T	C	3	71	c.1580A>G	c.(1579-1581)AAG>AGG	p.K527R
Pat_58	Post-Resistance	SHROOM2	357	37	X	9900442	9900442	Missense_Mutation	SNP	C	T	14	24	c.3119C>T	c.(3118-3120)CCC>CTC	p.P1040L
Pat_58	Post-Resistance	FAM47A	158724	37	X	34150139	34150139	Missense_Mutation	SNP	G	A	129	227	c.257C>T	c.(256-258)CCC>CTC	p.P86L
Pat_58	Post-Resistance	SUV39H1	6839	37	X	48564896	48564896	Missense_Mutation	SNP	C	T	8	21	c.983C>T	c.(982-984)CCC>CTC	p.P328L
Pat_58	Post-Resistance	CCDC22	28952	37	X	49103295	49103295	Missense_Mutation	SNP	G	A	17	18	c.818G>A	c.(817-819)GGA>GAA	p.G273E
Pat_58	Post-Resistance	CCNB3	85417	37	X	50053963	50053963	Missense_Mutation	SNP	G	A	4	273	c.2794G>A	c.(2794-2796)GCT>ACT	p.A932T
Pat_58	Post-Resistance	AR	367	37	X	66765244	66765244	Missense_Mutation	SNP	C	A	4	33	c.256C>A	c.(256-258)CAG>AAG	p.Q86K
Pat_58	Post-Resistance	OGT	8473	37	X	70781638	70781638	Missense_Mutation	SNP	G	A	28	45	c.1865G>A	c.(1864-1866)GGA>GAA	p.G622E
Pat_58	Post-Resistance	KIAA2022	340533	37	X	73961331	73961331	Missense_Mutation	SNP	C	T	72	119	c.3061G>A	c.(3061-3063)GAT>AAT	p.D1021N
Pat_58	Post-Resistance	CPXCR1	53336	37	X	88009059	88009059	Missense_Mutation	SNP	G	A	33	66	c.644G>A	c.(643-645)GGA>GAA	p.G215E
Pat_58	Post-Resistance	RNF128	79589	37	X	105970196	105970196	Missense_Mutation	SNP	C	T	7	7	c.53C>T	c.(52-54)TCC>TTC	p.S18F
Pat_58	Post-Resistance	DOCK11	139818	37	X	117773445	117773445	Missense_Mutation	SNP	C	T	91	239	c.4049C>T	c.(4048-4050)TCG>TTG	p.S1350L
Pat_58	Post-Resistance	RHOXF2B	727940	37	X	119210996	119210996	Missense_Mutation	SNP	C	T	13	50	c.337G>A	c.(337-339)GAA>AAA	p.E113K
Pat_58	Post-Resistance	ZBTB33	10009	37	X	119388238	119388238	Missense_Mutation	SNP	G	A	145	287	c.968G>A	c.(967-969)GGA>GAA	p.G323E
Pat_58	Post-Resistance	GABRE	2564	37	X	151123487	151123487	Missense_Mutation	SNP	C	T	9	36	c.1207G>A	c.(1207-1209)GAA>AAA	p.E403K
Pat_59	Pre-Treatment	PANK4	55229	37	1	2442805	2442805	Missense_Mutation	SNP	G	A	15	84	c.1805C>T	c.(1804-1806)TCC>TTC	p.S602F
Pat_59	Pre-Treatment	CHD5	26038	37	1	6202505	6202505	Missense_Mutation	SNP	G	A	4	33	c.2204C>T	c.(2203-2205)ACC>ATC	p.T735I
Pat_59	Pre-Treatment	DDI2	84301	37	1	15953236	15953236	Missense_Mutation	SNP	G	A	4	114	c.211G>A	c.(211-213)GTT>ATT	p.V71I
Pat_59	Pre-Treatment	SPEN	23013	37	1	16258763	16258763	Missense_Mutation	SNP	C	T	4	25	c.6028C>T	c.(6028-6030)CGT>TGT	p.R2010C
Pat_59	Pre-Treatment	UBR4	23352	37	1	19455554	19455554	Missense_Mutation	SNP	C	T	3	42	c.8921G>A	c.(8920-8922)CGT>CAT	p.R2974H
Pat_59	Pre-Treatment	SPOCD1	90853	37	1	32256539	32256539	Missense_Mutation	SNP	G	A	3	8	c.3316C>T	c.(3316-3318)CCT>TCT	p.P1106S
Pat_59	Pre-Treatment	YARS	8565	37	1	33248080	33248080	Missense_Mutation	SNP	G	A	21	62	c.967C>T	c.(967-969)CCA>TCA	p.P323S
Pat_59	Pre-Treatment	PHC2	1912	37	1	33797065	33797065	Splice_Site	SNP	T	A	5	140	c.1889_splice	c.e11-1	p.E630_splice
Pat_59	Pre-Treatment	CSMD2	114784	37	1	34164425	34164425	Missense_Mutation	SNP	G	A	4	109	c.3733C>T	c.(3733-3735)CGG>TGG	p.R1245W
Pat_59	Pre-Treatment	CSMD2	114784	37	1	34312515	34312515	Missense_Mutation	SNP	G	A	4	72	c.883C>T	c.(883-885)CGG>TGG	p.R295W
Pat_59	Pre-Treatment	YBX1	4904	37	1	43162924	43162924	Missense_Mutation	SNP	G	A	4	88	c.731G>A	c.(730-732)CGA>CAA	p.R244Q
Pat_59	Pre-Treatment	IPO13	9670	37	1	44432666	44432666	Missense_Mutation	SNP	G	A	4	73	c.2588G>A	c.(2587-2589)CGT>CAT	p.R863H
Pat_59	Pre-Treatment	FAAH	2166	37	1	46871918	46871918	Missense_Mutation	SNP	C	T	4	100	c.829C>T	c.(829-831)CGT>TGT	p.R277C
Pat_59	Pre-Treatment	CYP4A22	284541	37	1	47609541	47609541	Missense_Mutation	SNP	C	T	4	110	c.743C>T	c.(742-744)GCT>GTT	p.A248V
Pat_59	Pre-Treatment	FOXD3	27022	37	1	63789132	63789132	Missense_Mutation	SNP	C	A	4	56	c.403C>A	c.(403-405)CCC>ACC	p.P135T
Pat_59	Pre-Treatment	LEPR	3953	37	1	66036390	66036390	Missense_Mutation	SNP	G	A	4	76	c.275G>A	c.(274-276)CGG>CAG	p.R92Q
Pat_59	Pre-Treatment	SGIP1	84251	37	1	67000047	67000047	Missense_Mutation	SNP	G	T	4	102	c.6G>T	c.(4-6)ATG>ATT	p.M2I
Pat_59	Pre-Treatment	LRRC7	57554	37	1	70493873	70493873	Missense_Mutation	SNP	G	A	4	131	c.1700G>A	c.(1699-1701)CGA>CAA	p.R567Q
Pat_59	Pre-Treatment	C1orf173	127254	37	1	75055719	75055719	Missense_Mutation	SNP	G	A	4	12	c.1772C>T	c.(1771-1773)TCT>TTT	p.S591F
Pat_59	Pre-Treatment	SLC44A5	204962	37	1	75685021	75685021	Missense_Mutation	SNP	G	A	16	80	c.1187C>T	c.(1186-1188)GCG>GTG	p.A396V
Pat_59	Pre-Treatment	ABCA4	24	37	1	94466627	94466627	Missense_Mutation	SNP	C	T	4	91	c.6317G>A	c.(6316-6318)CGC>CAC	p.R2106H
Pat_59	Pre-Treatment	DENND2D	79961	37	1	111738609	111738609	Nonsense_Mutation	SNP	G	A	3	47	c.574C>T	c.(574-576)CGA>TGA	p.R192*

Pat_59	Pre-Treatment	PHTF1	10745	37	1	114248697	114248697	Missense_Mutation	SNP	G	A	18	72	c.1486C>T	c.(1486-1488)CTT>TTT	p.L496F
Pat_59	Pre-Treatment	PTPN22	26191	37	1	114362228	114362228	Nonsense_Mutation	SNP	G	T	4	97	c.2330C>A	c.(2329-2331)TCA>TAA	p.S777*
Pat_59	Pre-Treatment	VTCN1	79679	37	1	117753456	117753456	Missense_Mutation	SNP	G	A	25	70	c.22C>T	c.(22-24)CTC>TTC	p.L8F
Pat_59	Pre-Treatment	HMGCS2	3158	37	1	120302556	120302556	Missense_Mutation	SNP	G	A	4	40	c.616C>T	c.(616-618)CGT>TGT	p.R206C
Pat_59	Pre-Treatment	NOTCH2	4853	37	1	120468172	120468172	Missense_Mutation	SNP	C	T	4	91	c.4267G>A	c.(4267-4269)GCC>ACC	p.A1423T
Pat_59	Pre-Treatment	NBPF9	400818	37	1	144220816	144220816	Missense_Mutation	SNP	A	G	7	277	c.2189A>G	c.(2188-2190)GAG>GGG	p.E730G
Pat_59	Pre-Treatment	CELF3	11189	37	1	151678325	151678325	Nonsense_Mutation	SNP	G	A	3	40	c.1243C>T	c.(1243-1245)CGA>TGA	p.R415*
Pat_59	Pre-Treatment	TCHH	7062	37	1	152079997	152079997	Missense_Mutation	SNP	C	T	4	94	c.5696G>A	c.(5695-5697)GGG>GAG	p.G1899E
Pat_59	Pre-Treatment	RPTN	126638	37	1	152127891	152127891	Missense_Mutation	SNP	T	G	12	766	c.1684A>C	c.(1684-1686)ACA>CCA	p.T562P
Pat_59	Pre-Treatment	SPRR2D	6703	37	1	153012687	153012687	Missense_Mutation	SNP	G	A	50	191	c.136C>T	c.(136-138)CCA>TCA	p.P46S
Pat_59	Pre-Treatment	ASH1L	55870	37	1	155348157	155348157	Missense_Mutation	SNP	G	A	31	82	c.6262C>T	c.(6262-6264)CTT>TTT	p.L2088F
Pat_59	Pre-Treatment	PIGM	93183	37	1	160000565	160000565	Missense_Mutation	SNP	G	A	19	52	c.965C>T	c.(964-966)TCC>TTC	p.S322F
Pat_59	Pre-Treatment	KCNJ9	3765	37	1	160054056	160054056	Nonsense_Mutation	SNP	G	A	6	14	c.236G>A	c.(235-237)TGG>TAG	p.W79*
Pat_59	Pre-Treatment	ITLN2	142683	37	1	160920381	160920381	Missense_Mutation	SNP	G	A	4	137	c.562C>T	c.(562-564)CTC>TTC	p.L188F
Pat_59	Pre-Treatment	C1orf111	284680	37	1	162344248	162344248	Missense_Mutation	SNP	A	C	4	96	c.376T>G	c.(376-378)TGG>GGG	p.W126G
Pat_59	Pre-Treatment	DCAF6	55827	37	1	167906186	167906186	Missense_Mutation	SNP	G	A	4	19	c.37G>A	c.(37-39)GAC>AAC	p.D13N
Pat_59	Pre-Treatment	METTL13	51603	37	1	171751195	171751195	Nonsense_Mutation	SNP	G	T	4	62	c.88G>T	c.(88-90)GAG>TAG	p.E30*
Pat_59	Pre-Treatment	C1orf125	126859	37	1	179462031	179462031	Missense_Mutation	SNP	C	T	4	89	c.2333C>T	c.(2332-2334)TCC>TTC	p.S778F
Pat_59	Pre-Treatment	XPR1	9213	37	1	180805775	180805775	Missense_Mutation	SNP	C	T	4	124	c.1424C>T	c.(1423-1425)CCT>CTT	p.P475L
Pat_59	Pre-Treatment	RNASEL	6041	37	1	182555367	182555367	Missense_Mutation	SNP	C	T	7	44	c.575G>A	c.(574-576)GGG>GAG	p.G192E
Pat_59	Pre-Treatment	GPR25	2848	37	1	200843160	200843160	Missense_Mutation	SNP	G	T	3	23	c.995G>T	c.(994-996)AGG>ATG	p.R332M
Pat_59	Pre-Treatment	CHI3L1	1116	37	1	203154465	203154465	Missense_Mutation	SNP	C	T	4	69	c.104G>A	c.(103-105)CGG>CAG	p.R35Q
Pat_59	Pre-Treatment	USH2A	7399	37	1	215933000	215933001	Splice_Site	DNP	AC	TT	4	75	c.11231_splice	c.e57+1	p.R3744_splice
Pat_59	Pre-Treatment	C1orf65	164127	37	1	223568189	223568189	Missense_Mutation	SNP	C	T	3	32	c.1372C>T	c.(1372-1374)CGG>TGG	p.R458W
Pat_59	Pre-Treatment	ZNF678	339500	37	1	227842427	227842427	Missense_Mutation	SNP	G	A	6	164	c.476G>A	c.(475-477)GGC>GAC	p.G159D
Pat_59	Pre-Treatment	ZNF678	339500	37	1	227842544	227842544	Missense_Mutation	SNP	G	A	6	185	c.593G>A	c.(592-594)AGC>AAC	p.S198N
Pat_59	Pre-Treatment	TAF5L	27097	37	1	229738455	229738455	Missense_Mutation	SNP	G	T	4	97	c.459C>A	c.(457-459)TTC>TTA	p.F153L
Pat_59	Pre-Treatment	LYST	1130	37	1	235940443	235940443	Missense_Mutation	SNP	G	T	4	122	c.5380C>A	c.(5380-5382)CAA>AAA	p.Q1794K
Pat_59	Pre-Treatment	ZP4	57829	37	1	238053450	238053450	Missense_Mutation	SNP	G	T	5	98	c.202C>A	c.(202-204)CAG>AAG	p.Q68K
Pat_59	Pre-Treatment	FH	2271	37	1	241665783	241665783	Missense_Mutation	SNP	C	T	4	48	c.1196G>A	c.(1195-1197)AGC>AAC	p.S399N
Pat_59	Pre-Treatment	KIF26B	55083	37	1	245849094	245849094	Missense_Mutation	SNP	G	A	4	20	c.2809G>A	c.(2809-2811)GAC>AAC	p.D937N
Pat_59	Pre-Treatment	SFMBT2	57713	37	10	7412280	7412280	Missense_Mutation	SNP	G	A	4	127	c.158C>T	c.(157-159)ACA>ATA	p.T53I
Pat_59	Pre-Treatment	USP6NL	9712	37	10	11505381	11505381	Missense_Mutation	SNP	C	T	6	143	c.1546G>A	c.(1546-1548)GCA>ACA	p.A516T
Pat_59	Pre-Treatment	SPAG6	9576	37	10	22657466	22657466	Missense_Mutation	SNP	G	T	4	46	c.331G>T	c.(331-333)GGT>TGT	p.G111C
Pat_59	Pre-Treatment	KIAA1217	56243	37	10	24809159	24809159	Missense_Mutation	SNP	G	A	47	121	c.2285G>A	c.(2284-2286)GGA>GAA	p.G762E
Pat_59	Pre-Treatment	ZWINT	11130	37	10	58118709	58118709	Splice_Site	SNP	C	T	4	64	c.481_splice	c.e6-1	p.E161_splice
Pat_59	Pre-Treatment	UBE2D1	7321	37	10	60121119	60121119	Missense_Mutation	SNP	G	A	4	111	c.46G>A	c.(46-48)GAT>AAT	p.D16N
Pat_59	Pre-Treatment	SLC29A3	55315	37	10	73111447	73111447	Missense_Mutation	SNP	G	A	4	24	c.512G>A	c.(511-513)TGC>TAC	p.C171Y
Pat_59	Pre-Treatment	DLG5	9231	37	10	79581535	79581535	Missense_Mutation	SNP	G	A	2	1	c.2707C>T	c.(2707-2709)CGT>TGT	p.R903C
Pat_59	Pre-Treatment	LRIT2	340745	37	10	85984231	85984231	Nonsense_Mutation	SNP	G	T	4	83	c.750C>A	c.(748-750)TGC>TGA	p.C250*
Pat_59	Pre-Treatment	AGAP11	119385	37	10	88768668	88768668	Missense_Mutation	SNP	G	A	3	50	c.659G>A	c.(658-660)GGT>GAT	p.G220D
Pat_59	Pre-Treatment	IFIT1B	439996	37	10	91143693	91143693	Missense_Mutation	SNP	G	A	6	323	c.623G>A	c.(622-624)CGA>CAA	p.R208Q
Pat_59	Pre-Treatment	PIPSL	266971	37	10	95721032	95721032	Missense_Mutation	SNP	G	A	4	50	c.122C>T	c.(121-123)ACC>ATC	p.T41I
Pat_59	Pre-Treatment	SORBS1	10580	37	10	97194451	97194451	Missense_Mutation	SNP	G	A	4	83	c.100C>T	c.(100-102)CGC>TGC	p.R34C
Pat_59	Pre-Treatment	TLL2	7093	37	10	98188425	98188425	Missense_Mutation	SNP	C	T	19	39	c.601G>A	c.(601-603)GAG>AAG	p.E201K
Pat_59	Pre-Treatment	PPRC1	23082	37	10	103899362	103899362	Missense_Mutation	SNP	G	A	4	117	c.1097G>A	c.(1096-1098)CGA>CAA	p.R366Q
Pat_59	Pre-Treatment	RPL13AP6	644511	37	10	112696573	112696573	Missense_Mutation	SNP	T	C	4	12	c.419A>G	c.(418-420)CAC>CGC	p.H140R

Pat_59	Pre-Treatment	PNLIP	5406	37	10	118321098	118321098	Missense_Mutation	SNP	A	T	4	94	c.1284A>T	c.(1282-1284)TTA>TTT	p.L428F
Pat_59	Pre-Treatment	PNLIPRP1	5407	37	10	118351397	118351397	Missense_Mutation	SNP	G	A	4	134	c.164G>A	c.(163-165)CGC>CAC	p.R55H
Pat_59	Pre-Treatment	SFXN4	119559	37	10	120905783	120905783	Missense_Mutation	SNP	G	A	4	110	c.901C>T	c.(901-903)CCA>TCA	p.P301S
Pat_59	Pre-Treatment	INPP5F	22876	37	10	121571342	121571342	Missense_Mutation	SNP	G	T	4	76	c.1761G>T	c.(1759-1761)TTG>TTT	p.L587F
Pat_59	Pre-Treatment	CPXM2	119587	37	10	125528119	125528119	Missense_Mutation	SNP	C	T	4	81	c.1222G>A	c.(1222-1224)GTC>ATC	p.V408I
Pat_59	Pre-Treatment	PHRF1	57661	37	11	597554	597554	Missense_Mutation	SNP	C	T	3	25	c.878C>T	c.(877-879)ACG>ATG	p.T293M
Pat_59	Pre-Treatment	MUC6	4588	37	11	1026073	1026073	Missense_Mutation	SNP	C	T	2	1	c.2615G>A	c.(2614-2616)GGG>GAG	p.G872E
Pat_59	Pre-Treatment	OR51E2	81285	37	11	4703396	4703396	Missense_Mutation	SNP	A	T	4	71	c.546T>A	c.(544-546)GAT>GAA	p.D182E
Pat_59	Pre-Treatment	CCKBR	887	37	11	6292621	6292621	Missense_Mutation	SNP	C	T	4	94	c.1192C>T	c.(1192-1194)CGC>TGC	p.R398C
Pat_59	Pre-Treatment	NAV2	89797	37	11	20005744	20005744	Missense_Mutation	SNP	C	T	5	65	c.2788C>T	c.(2788-2790)CGG>TGG	p.R930W
Pat_59	Pre-Treatment	LGR4	55366	37	11	27389784	27389784	Missense_Mutation	SNP	G	A	6	334	c.2486C>T	c.(2485-2487)TCC>TTC	p.S829F
Pat_59	Pre-Treatment	NAT10	55226	37	11	34153015	34153015	Missense_Mutation	SNP	G	A	4	108	c.1457G>A	c.(1456-1458)TGC>TAC	p.C486Y
Pat_59	Pre-Treatment	LRP4	4038	37	11	46917450	46917450	Missense_Mutation	SNP	C	T	3	38	c.1168G>A	c.(1168-1170)GGG>AGG	p.G390R
Pat_59	Pre-Treatment	PRG3	10394	37	11	57147199	57147199	Missense_Mutation	SNP	C	T	15	42	c.143G>A	c.(142-144)AGA>AAA	p.R48K
Pat_59	Pre-Treatment	CLP1	10978	37	11	57427043	57427043	Missense_Mutation	SNP	C	T	4	64	c.95C>T	c.(94-96)TCA>TTA	p.S32L
Pat_59	Pre-Treatment	ZP1	22917	37	11	60640871	60640871	Missense_Mutation	SNP	G	T	4	64	c.1264G>T	c.(1264-1266)GGG>TGG	p.G422W
Pat_59	Pre-Treatment	KDM2A	22992	37	11	66999219	66999219	Missense_Mutation	SNP	G	A	3	29	c.1267G>A	c.(1267-1269)GGG>AGG	p.G423R
Pat_59	Pre-Treatment	SHANK2	22941	37	11	70333148	70333148	Missense_Mutation	SNP	C	T	4	49	c.3250G>A	c.(3250-3252)GGA>AGA	p.G1084R
Pat_59	Pre-Treatment	KRTAP5-10	387273	37	11	71276971	71276971	Missense_Mutation	SNP	G	A	6	196	c.338G>A	c.(337-339)GGC>GAC	p.G113D
Pat_59	Pre-Treatment	UVRAG	7405	37	11	75851867	75851867	Nonsense_Mutation	SNP	C	T	4	91	c.1510C>T	c.(1510-1512)CGA>TGA	p.R504*
Pat_59	Pre-Treatment	FOLH1B	219595	37	11	89395322	89395322	Translation_Start_Site	SNP	C	T	5	31	c.-93C>T	c.(-95--91)TACGC>TATGC	
Pat_59	Pre-Treatment	NAALAD2	10003	37	11	89896741	89896741	Missense_Mutation	SNP	G	A	20	110	c.1234G>A	c.(1234-1236)GAT>AAT	p.D412N
Pat_59	Pre-Treatment	PIWIL4	143689	37	11	94326796	94326796	Missense_Mutation	SNP	G	A	4	75	c.1139G>A	c.(1138-1140)TGC>TAC	p.C380Y
Pat_59	Pre-Treatment	MTMR2	8898	37	11	95568474	95568474	Missense_Mutation	SNP	G	A	4	44	c.1912C>T	c.(1912-1914)CCT>TCT	p.P638S
Pat_59	Pre-Treatment	ATM	472	37	11	108164118	108164118	Missense_Mutation	SNP	C	T	4	110	c.4690C>T	c.(4690-4692)CCT>TCT	p.P1564S
Pat_59	Pre-Treatment	PHLDB1	23187	37	11	118498387	118498387	Missense_Mutation	SNP	C	T	4	103	c.848C>T	c.(847-849)CCG>CTG	p.P283L
Pat_59	Pre-Treatment	TRIM29	23650	37	11	119993662	119993662	Missense_Mutation	SNP	C	A	17	55	c.1435G>T	c.(1435-1437)GGT>TGT	p.G479C
Pat_59	Pre-Treatment	SORL1	6653	37	11	121440980	121440980	Splice_Site	SNP	G	A	4	76	c.3337_splice	c.e23+1	p.P1113_splice
Pat_59	Pre-Treatment	ZNF202	7753	37	11	123598943	123598943	Missense_Mutation	SNP	C	T	5	105	c.730G>A	c.(730-732)GTA>ATA	p.V244I
Pat_59	Pre-Treatment	RPUSD4	84881	37	11	126073501	126073501	Missense_Mutation	SNP	G	A	3	40	c.946C>T	c.(946-948)CGC>TGC	p.R316C
Pat_59	Pre-Treatment	APLP2	334	37	11	129999957	129999957	Missense_Mutation	SNP	C	T	5	181	c.1480C>T	c.(1480-1482)CGG>TGG	p.R494W
Pat_59	Pre-Treatment	FGF6	2251	37	12	4554555	4554555	Missense_Mutation	SNP	G	A	4	126	c.182C>T	c.(181-183)TCT>TTT	p.S61F
Pat_59	Pre-Treatment	PHC1	1911	37	12	9091927	9091927	Missense_Mutation	SNP	C	T	4	136	c.2887C>T	c.(2887-2889)CGC>TGC	p.R963C
Pat_59	Pre-Treatment	LRP6	4040	37	12	12397415	12397415	Missense_Mutation	SNP	C	T	4	88	c.230G>A	c.(229-231)CGA>CAA	p.R77Q
Pat_59	Pre-Treatment	ETNK1	55500	37	12	22778224	22778224	Missense_Mutation	SNP	G	C	3	16	c.127G>C	c.(127-129)GCT>CCT	p.A43P
Pat_59	Pre-Treatment	TMTC1	83857	37	12	29908735	29908735	Missense_Mutation	SNP	G	A	6	210	c.314C>T	c.(313-315)ACC>ATC	p.T105I
Pat_59	Pre-Treatment	IPO8	10526	37	12	30783838	30783838	Missense_Mutation	SNP	C	T	5	101	c.3070G>A	c.(3070-3072)GTC>ATC	p.V1024I
Pat_59	Pre-Treatment	HDAC7	51564	37	12	48190835	48190835	Missense_Mutation	SNP	G	A	4	32	c.551C>T	c.(550-552)CCC>CTC	p.P184L
Pat_59	Pre-Treatment	ADCY6	112	37	12	49170283	49170283	Missense_Mutation	SNP	C	T	4	96	c.1463G>A	c.(1462-1464)CGG>CAG	p.R488Q
Pat_59	Pre-Treatment	FMNL3	91010	37	12	50048010	50048010	Missense_Mutation	SNP	C	T	4	41	c.1036G>A	c.(1036-1038)GAG>AAG	p.E346K
Pat_59	Pre-Treatment	METTL7A	25840	37	12	51318910	51318910	Nonsense_Mutation	SNP	G	A	4	123	c.89G>A	c.(88-90)TGG>TAG	p.W30*
Pat_59	Pre-Treatment	KRT74	121391	37	12	52966349	52966349	Nonsense_Mutation	SNP	C	A	4	76	c.574G>T	c.(574-576)GAG>TAG	p.E192*
Pat_59	Pre-Treatment	WIBG	84305	37	12	56295763	56295763	Missense_Mutation	SNP	G	A	6	266	c.508C>T	c.(508-510)CGG>TGG	p.R170W
Pat_59	Pre-Treatment	LRP1	4035	37	12	57552253	57552253	Missense_Mutation	SNP	G	A	4	26	c.1630G>A	c.(1630-1632)GGG>AGG	p.G544R
Pat_59	Pre-Treatment	THAP2	83591	37	12	72068033	72068033	Missense_Mutation	SNP	G	A	4	83	c.122G>A	c.(121-123)CGC>CAC	p.R41H
Pat_59	Pre-Treatment	NR2C1	7181	37	12	95456346	95456346	Missense_Mutation	SNP	C	T	6	19	c.223G>A	c.(223-225)GAT>AAT	p.D75N
Pat_59	Pre-Treatment	NT5DC3	51559	37	12	104208761	104208761	Missense_Mutation	SNP	G	A	6	190	c.347C>T	c.(346-348)ACG>ATG	p.T116M

Pat_59	Pre-Treatment	TCP11L2	255394	37	12	106712125	106712126	Missense_Mutation	DNP	GG	TT	6	168	c.297_298GG>TT	(295-300)TTGGCT>TTTT	.99_100LA>F
Pat_59	Pre-Treatment	UBE3B	89910	37	12	109958962	109958962	Missense_Mutation	SNP	G	A	4	82	c.2086G>A	c.(2086-2088)GAG>AAG	p.E696K
Pat_59	Pre-Treatment	KNTC1	9735	37	12	123055642	123055642	Missense_Mutation	SNP	G	A	4	123	c.1988G>A	c.(1987-1989)GGA>GAA	p.G663E
Pat_59	Pre-Treatment	DNAH10	196385	37	12	124297766	124297766	Missense_Mutation	SNP	A	G	3	53	c.2846A>G	c.(2845-2847)GAG>GGG	p.E949G
Pat_59	Pre-Treatment	PXMP2	5827	37	12	133266955	133266955	Missense_Mutation	SNP	G	A	4	43	c.229G>A	c.(229-231)GTT>ATT	p.V77I
Pat_59	Pre-Treatment	SLC7A1	6541	37	13	30110279	30110279	Missense_Mutation	SNP	C	T	4	115	c.47G>A	c.(46-48)CGG>CAG	p.R16Q
Pat_59	Pre-Treatment	STARD13	90627	37	13	33859634	33859634	Missense_Mutation	SNP	G	T	4	136	c.142C>A	c.(142-144)CAT>AAT	p.H48N
Pat_59	Pre-Treatment	KBTBD7	84078	37	13	41766827	41766827	Missense_Mutation	SNP	C	A	4	82	c.1567G>T	c.(1567-1569)GAT>TAT	p.D523Y
Pat_59	Pre-Treatment	NAA16	79612	37	13	41933006	41933006	Missense_Mutation	SNP	G	A	5	112	c.1318G>A	c.(1318-1320)GCT>ACT	p.A440T
Pat_59	Pre-Treatment	CAB39L	81617	37	13	49885003	49885003	Missense_Mutation	SNP	C	T	5	186	c.961G>A	c.(961-963)GAG>AAG	p.E321K
Pat_59	Pre-Treatment	SETDB2	83852	37	13	50059853	50059853	Missense_Mutation	SNP	G	A	4	110	c.1606G>A	c.(1606-1608)GCA>ACA	p.A536T
Pat_59	Pre-Treatment	GPC6	10082	37	13	95034764	95034764	Missense_Mutation	SNP	T	C	4	177	c.1249T>C	c.(1249-1251)TCC>CCC	p.S417P
Pat_59	Pre-Treatment	LAMP1	3916	37	13	113973906	113973906	Missense_Mutation	SNP	G	A	4	68	c.685G>A	c.(685-687)GGG>AGG	p.G229R
Pat_59	Pre-Treatment	P704P	641455	37	14	20020013	20020013	Missense_Mutation	SNP	G	C	7	325	c.208C>G	c.(208-210)CCC>GCC	p.P70A
Pat_59	Pre-Treatment	SLC39A2	29986	37	14	21468284	21468284	Missense_Mutation	SNP	G	A	4	80	c.256G>A	c.(256-258)GCA>ACA	p.A86T
Pat_59	Pre-Treatment	CDH24	64403	37	14	23524775	23524775	Missense_Mutation	SNP	T	G	3	27	c.168A>C	c.(166-168)GAA>GAC	p.E56D
Pat_59	Pre-Treatment	HOMEZ	57594	37	14	23745910	23745910	Missense_Mutation	SNP	G	A	4	115	c.527C>T	c.(526-528)ACC>ATC	p.T176I
Pat_59	Pre-Treatment	LRRC16B	90668	37	14	24528168	24528168	Missense_Mutation	SNP	T	G	3	50	c.1544T>G	c.(1543-1545)TTG>TGG	p.L515W
Pat_59	Pre-Treatment	IPO4	79711	37	14	24650985	24650985	Missense_Mutation	SNP	G	A	4	62	c.2872C>T	c.(2872-2874)CGT>TGT	p.R958C
Pat_59	Pre-Treatment	SOS2	6655	37	14	50628237	50628237	Nonsense_Mutation	SNP	G	A	4	95	c.1159C>T	c.(1159-1161)CGA>TGA	p.R387*
Pat_59	Pre-Treatment	SYNE2	23224	37	14	64522809	64522809	Nonsense_Mutation	SNP	C	T	4	67	c.9892C>T	c.(9892-9894)CGA>TGA	p.R3298*
Pat_59	Pre-Treatment	SPTB	6710	37	14	65249027	65249027	Missense_Mutation	SNP	C	T	26	143	c.4247G>A	c.(4246-4248)CGG>CAG	p.R1416Q
Pat_59	Pre-Treatment	ZFYVE26	23503	37	14	68233122	68233122	Missense_Mutation	SNP	G	A	4	121	c.5833C>T	c.(5833-5835)CGG>TGG	p.R1945W
Pat_59	Pre-Treatment	PCNX	22990	37	14	71444184	71444184	Missense_Mutation	SNP	G	A	4	136	c.1130G>A	c.(1129-1131)CGG>CAG	p.R377Q
Pat_59	Pre-Treatment	LTBP2	4053	37	14	74975412	74975412	Missense_Mutation	SNP	C	T	6	45	c.3547G>A	c.(3547-3549)GAG>AAG	p.E1183K
Pat_59	Pre-Treatment	LTBP2	4053	37	14	75022207	75022207	Nonsense_Mutation	SNP	C	T	19	146	c.1020G>A	c.(1018-1020)TGG>TGA	p.W340*
Pat_59	Pre-Treatment	EIF2B2	8892	37	14	75475781	75475781	Missense_Mutation	SNP	G	A	6	314	c.946G>A	c.(946-948)GTT>ATT	p.V316I
Pat_59	Pre-Treatment	TTLL5	23093	37	14	76156623	76156623	Missense_Mutation	SNP	C	T	4	117	c.460C>T	c.(460-462)CCC>TCC	p.P154S
Pat_59	Pre-Treatment	TTLL5	23093	37	14	76173393	76173393	Missense_Mutation	SNP	G	T	6	260	c.618G>T	c.(616-618)TTG>TTT	p.L206F
Pat_59	Pre-Treatment	NRXN3	9369	37	14	80164260	80164260	Missense_Mutation	SNP	C	T	41	45	c.2785C>T	c.(2785-2787)CGC>TGC	p.R929C
Pat_59	Pre-Treatment	GTF2A1	2957	37	14	81667978	81667978	Missense_Mutation	SNP	G	A	4	105	c.362C>T	c.(361-363)CCA>CTA	p.P121L
Pat_59	Pre-Treatment	C14orf143	90141	37	14	90398906	90398906	Missense_Mutation	SNP	C	T	25	70	c.283G>A	c.(283-285)GAA>AAA	p.E95K
Pat_59	Pre-Treatment	YY1	7528	37	14	100705725	100705725	Missense_Mutation	SNP	C	G	3	33	c.144C>G	c.(142-144)GAC>GAG	p.D48E
Pat_59	Pre-Treatment	CDCA4	55038	37	14	105477953	105477953	Missense_Mutation	SNP	G	A	3	55	c.314C>T	c.(313-315)GCG>GTG	p.A105V
Pat_59	Pre-Treatment	CYFIP1	23191	37	15	22955212	22955212	Missense_Mutation	SNP	G	A	4	91	c.1606G>A	c.(1606-1608)GAG>AAG	p.E536K
Pat_59	Pre-Treatment	HERC2P2	400322	37	15	23330108	23330108	Missense_Mutation	SNP	C	A	4	54	c.970G>T	c.(970-972)GTC>TTC	p.V324F
Pat_59	Pre-Treatment	RYR3	6263	37	15	34093018	34093018	Missense_Mutation	SNP	G	A	4	117	c.9878G>A	c.(9877-9879)CGC>CAC	p.R3293H
Pat_59	Pre-Treatment	GPR176	11245	37	15	40093401	40093401	Missense_Mutation	SNP	C	T	25	114	c.1480G>A	c.(1480-1482)GTA>ATA	p.V494I
Pat_59	Pre-Treatment	PLCB2	5330	37	15	40584590	40584590	Missense_Mutation	SNP	G	A	3	38	c.2381C>T	c.(2380-2382)GCG>GTG	p.A794V
Pat_59	Pre-Treatment	SLC30A4	7782	37	15	45781209	45781209	Missense_Mutation	SNP	G	A	3	54	c.724C>T	c.(724-726)CGT>TGT	p.R242C
Pat_59	Pre-Treatment	MYO5A	4644	37	15	52646103	52646104	Missense_Mutation	DNP	GG	AA	14	118	.3531_3532CC>T	529-3534)GACCGC>GAT	p.R1178C
Pat_59	Pre-Treatment	VPS13C	54832	37	15	62155710	62155710	Missense_Mutation	SNP	C	A	4	90	c.10881G>T	c.(10879-10881)TTG>TTT	p.L3627F
Pat_59	Pre-Treatment	ZNF609	23060	37	15	64972468	64972468	Missense_Mutation	SNP	G	A	4	110	c.3854G>A	c.(3853-3855)AGC>AAC	p.S1285N
Pat_59	Pre-Treatment	PIAS1	8554	37	15	68434663	68434663	Missense_Mutation	SNP	A	G	4	36	c.590A>G	c.(589-591)CAG>CGG	p.Q197R
Pat_59	Pre-Treatment	THSD4	79875	37	15	72030223	72030223	Missense_Mutation	SNP	G	A	12	67	c.1783G>A	c.(1783-1785)GAC>AAC	p.D595N
Pat_59	Pre-Treatment	GRAMD2	196996	37	15	72460139	72460139	Missense_Mutation	SNP	G	A	4	100	c.310C>T	c.(310-312)CGG>TGG	p.R104W
Pat_59	Pre-Treatment	CSPG4	1464	37	15	75968345	75968345	Missense_Mutation	SNP	C	T	2	2	c.6515G>A	c.(6514-6516)AGC>AAC	p.S2172N

Pat_59	Pre-Treatment	WDR61	80349	37	15	78582055	78582055	Splice_Site	SNP	C	T	4	63	c.469_splice	c.e7-1	p.S157_splice
Pat_59	Pre-Treatment	MORF4L1	10933	37	15	79184656	79184656	Splice_Site	SNP	G	A	4	133	c.657_splice	c.e9+1	p.Q219_splice
Pat_59	Pre-Treatment	MESP2	145873	37	15	90321312	90321312	Missense_Mutation	SNP	C	G	3	39	c.941C>G	c.(940-942)CCA>CGA	p.P314R
Pat_59	Pre-Treatment	PRC1	9055	37	15	91523550	91523550	Nonsense_Mutation	SNP	G	A	4	121	c.892C>T	c.(892-894)CGA>TGA	p.R298*
Pat_59	Pre-Treatment	WDR90	197335	37	16	716591	716591	Missense_Mutation	SNP	C	T	4	22	c.4877C>T	c.(4876-4878)ACC>ATC	p.T1626I
Pat_59	Pre-Treatment	CCDC78	124093	37	16	772979	772979	Nonsense_Mutation	SNP	G	A	4	50	c.1240C>T	c.(1240-1242)CGA>TGA	p.R414*
Pat_59	Pre-Treatment	C16orf91	283951	37	16	1479216	1479216	Nonsense_Mutation	SNP	G	A	4	89	c.130C>T	c.(130-132)CGA>TGA	p.R44*
Pat_59	Pre-Treatment	ZNF174	7727	37	16	3452216	3452216	Missense_Mutation	SNP	G	T	4	60	c.212G>T	c.(211-213)TGC>TTC	p.C71F
Pat_59	Pre-Treatment	ADCY9	115	37	16	4164488	4164488	Missense_Mutation	SNP	T	C	3	107	c.956A>G	c.(955-957)CAC>CGC	p.H319R
Pat_59	Pre-Treatment	KIAA0430	9665	37	16	15716888	15716888	Missense_Mutation	SNP	G	T	4	60	c.2363C>A	c.(2362-2364)GCA>GAA	p.A788E
Pat_59	Pre-Treatment	MYH11	4629	37	16	15844047	15844047	Missense_Mutation	SNP	C	T	4	58	c.2006G>A	c.(2005-2007)CGC>CAC	p.R669H
Pat_59	Pre-Treatment	GGA2	23062	37	16	23499931	23499931	Missense_Mutation	SNP	G	A	35	124	c.575C>T	c.(574-576)TCC>TTC	p.S192F
Pat_59	Pre-Treatment	SEZ6L2	26470	37	16	29899971	29899971	Missense_Mutation	SNP	C	T	4	29	c.929G>A	c.(928-930)GGC>GAC	p.G310D
Pat_59	Pre-Treatment	1-Sep	1731	37	16	30393163	30393163	Missense_Mutation	SNP	C	T	6	273	c.223G>A	c.(223-225)GAG>AAG	p.E75K
Pat_59	Pre-Treatment	SRCAP	10847	37	16	30731568	30731568	Missense_Mutation	SNP	G	A	6	247	c.2903G>A	c.(2902-2904)CGC>CAC	p.R968H
Pat_59	Pre-Treatment	HSD3B7	80270	37	16	30998167	30998167	Missense_Mutation	SNP	G	T	4	66	c.538G>T	c.(538-540)GGG>TGG	p.G180W
Pat_59	Pre-Treatment	ITGAD	3681	37	16	31414878	31414878	Missense_Mutation	SNP	C	T	4	98	c.616C>T	c.(616-618)CGG>TGG	p.R206W
Pat_59	Pre-Treatment	CMTM2	146225	37	16	66614052	66614052	Missense_Mutation	SNP	C	T	4	82	c.409C>T	c.(409-411)CAT>TAT	p.H137Y
Pat_59	Pre-Treatment	CES2	8824	37	16	66975461	66975461	Missense_Mutation	SNP	C	T	4	59	c.1160C>T	c.(1159-1161)CCC>CTC	p.P387L
Pat_59	Pre-Treatment	SLC9A5	6553	37	16	67288998	67288998	Missense_Mutation	SNP	G	A	4	54	c.565G>A	c.(565-567)GTG>ATG	p.V189M
Pat_59	Pre-Treatment	NFATC3	4775	37	16	68160397	68160397	Nonsense_Mutation	SNP	G	T	4	72	c.1285G>T	c.(1285-1287)GGA>TGA	p.G429*
Pat_59	Pre-Treatment	TMED6	146456	37	16	69377432	69377432	Missense_Mutation	SNP	C	T	4	133	c.601G>A	c.(601-603)GTG>ATG	p.V201M
Pat_59	Pre-Treatment	FTSJD1	55783	37	16	71318625	71318625	Missense_Mutation	SNP	G	A	4	39	c.1199C>T	c.(1198-1200)GCT>GTT	p.A400V
Pat_59	Pre-Treatment	ZNF23	7571	37	16	71488051	71488051	Translation_Start_Site	SNP	G	A	4	99	c.-72C>T	c.(-74--70)GACGT>GATGT	
Pat_59	Pre-Treatment	PMFBP1	83449	37	16	72162606	72162606	Missense_Mutation	SNP	G	A	4	55	c.2053C>T	c.(2053-2055)CTC>TTC	p.L685F
Pat_59	Pre-Treatment	ZFP1	162239	37	16	75186852	75186852	Missense_Mutation	SNP	G	A	5	161	c.3G>A	c.(1-3)ATG>ATA	p.M1I
Pat_59	Pre-Treatment	PLCG2	5336	37	16	81925134	81925134	Missense_Mutation	SNP	G	A	4	52	c.925G>A	c.(925-927)GTG>ATG	p.V309M
Pat_59	Pre-Treatment	LRRC50	123872	37	16	84203819	84203819	Missense_Mutation	SNP	A	G	5	88	c.1385A>G	c.(1384-1386)CAA>CGA	p.Q462R
Pat_59	Pre-Treatment	KLHDC4	54758	37	16	87745037	87745037	Missense_Mutation	SNP	C	A	4	30	c.848G>T	c.(847-849)TGG>TTG	p.W283L
Pat_59	Pre-Treatment	CDT1	81620	37	16	88873490	88873490	Missense_Mutation	SNP	G	A	4	123	c.1154G>A	c.(1153-1155)CGC>CAC	p.R385H
Pat_59	Pre-Treatment	ANKRD11	29123	37	16	89351391	89351391	Missense_Mutation	SNP	G	A	4	64	c.1559C>T	c.(1558-1560)GCC>GTC	p.A520V
Pat_59	Pre-Treatment	TUBB3	10381	37	16	90001344	90001344	Missense_Mutation	SNP	G	T	4	114	c.485G>T	c.(484-486)CGC>CTC	p.R162L
Pat_59	Pre-Treatment	PRPF8	10594	37	17	1554459	1554459	Missense_Mutation	SNP	G	A	4	82	c.6796C>T	c.(6796-6798)CGT>TGT	p.R2266C
Pat_59	Pre-Treatment	PAFAH1B1	5048	37	17	2573488	2573488	Missense_Mutation	SNP	G	A	6	269	c.431G>A	c.(430-432)CGA>CAA	p.R144Q
Pat_59	Pre-Treatment	OR3A1	4994	37	17	3195798	3195798	Nonsense_Mutation	SNP	G	A	4	132	c.79C>T	c.(79-81)CAG>TAG	p.Q27*
Pat_59	Pre-Treatment	ZZEF1	23140	37	17	3959530	3959530	Missense_Mutation	SNP	C	T	4	116	c.5275G>A	c.(5275-5277)GAT>AAT	p.D1759N
Pat_59	Pre-Treatment	ARRB2	409	37	17	4619328	4619328	Missense_Mutation	SNP	G	A	4	113	c.115G>A	c.(115-117)GAT>AAT	p.D39N
Pat_59	Pre-Treatment	CAMTA2	23125	37	17	4875601	4875601	Missense_Mutation	SNP	C	A	4	34	c.2734G>T	c.(2734-2736)GCC>TCC	p.A912S
Pat_59	Pre-Treatment	CHRNB1	1140	37	17	7350418	7350418	Missense_Mutation	SNP	G	A	5	82	c.410G>A	c.(409-411)GGC>GAC	p.G137D
Pat_59	Pre-Treatment	TMEM88	92162	37	17	7758835	7758835	Missense_Mutation	SNP	G	A	4	115	c.283G>A	c.(283-285)GGA>AGA	p.G95R
Pat_59	Pre-Treatment	ARHGEF15	22899	37	17	8224273	8224273	Nonsense_Mutation	SNP	G	T	4	109	c.2488G>T	c.(2488-2490)GGA>TGA	p.G830*
Pat_59	Pre-Treatment	DNAH9	1770	37	17	11737985	11737985	Missense_Mutation	SNP	C	A	4	44	c.9277C>A	c.(9277-9279)CAG>AAG	p.Q3093K
Pat_59	Pre-Treatment	TNFRSF13B	23495	37	17	16855777	16855777	Missense_Mutation	SNP	G	A	4	35	c.182C>T	c.(181-183)ACC>ATC	p.T61I
Pat_59	Pre-Treatment	MPRIP	23164	37	17	17062245	17062245	Missense_Mutation	SNP	G	A	3	33	c.1975G>A	c.(1975-1977)GTC>ATC	p.V659I
Pat_59	Pre-Treatment	BLMH	642	37	17	28576167	28576167	Missense_Mutation	SNP	A	T	4	80	c.1236T>A	c.(1234-1236)GAT>GAA	p.D412E
Pat_59	Pre-Treatment	OMG	4974	37	17	29622581	29622581	Missense_Mutation	SNP	G	T	4	82	c.769C>A	c.(769-771)CAA>AAA	p.Q257K
Pat_59	Pre-Treatment	LIG3	3980	37	17	33324765	33324765	Missense_Mutation	SNP	G	A	4	111	c.1832G>A	c.(1831-1833)TGT>TAT	p.C611Y

Pat_59	Pre-Treatment	UNC45B	146862	37	17	33507597	33507597	Missense_Mutation	SNP	A	G	3	68	c.2281A>G	c.(2281-2283)AGG>GGG	p.R761G
Pat_59	Pre-Treatment	ERBB2	2064	37	17	37868249	37868249	Missense_Mutation	SNP	G	A	4	133	c.970G>A	c.(970-972)GCA>ACA	p.A324T
Pat_59	Pre-Treatment	KRT24	192666	37	17	38856585	38856585	Missense_Mutation	SNP	C	T	96	273	c.906G>A	c.(904-906)ATG>ATA	p.M302I
Pat_59	Pre-Treatment	KRT28	162605	37	17	38954550	38954550	Missense_Mutation	SNP	G	C	4	67	c.627C>G	c.(625-627)GAC>GAG	p.D209E
Pat_59	Pre-Treatment	KRTAP4-12	83755	37	17	39280026	39280026	Missense_Mutation	SNP	G	A	4	103	c.349C>T	c.(349-351)CGC>TGC	p.R117C
Pat_59	Pre-Treatment	KRT32	3882	37	17	39623519	39623519	Missense_Mutation	SNP	C	T	3	44	c.59G>A	c.(58-60)CGG>CAG	p.R20Q
Pat_59	Pre-Treatment	JUP	3728	37	17	39919530	39919530	Missense_Mutation	SNP	C	T	4	89	c.1202G>A	c.(1201-1203)AGT>AAT	p.S401N
Pat_59	Pre-Treatment	ACLY	47	37	17	40052894	40052894	Missense_Mutation	SNP	G	A	4	128	c.1438C>T	c.(1438-1440)CCA>TCA	p.P480S
Pat_59	Pre-Treatment	EZH1	2145	37	17	40865352	40865352	Missense_Mutation	SNP	C	T	4	114	c.1079G>A	c.(1078-1080)CGT>CAT	p.R360H
Pat_59	Pre-Treatment	G6PC	2538	37	17	41062969	41062969	Missense_Mutation	SNP	C	A	4	52	c.600C>A	c.(598-600)AGC>AGA	p.S200R
Pat_59	Pre-Treatment	DCAKD	79877	37	17	43111583	43111583	Missense_Mutation	SNP	C	T	4	51	c.288G>A	c.(286-288)ATG>ATA	p.M96I
Pat_59	Pre-Treatment	TBKBP1	9755	37	17	45776832	45776832	Missense_Mutation	SNP	C	A	2	0	c.781C>A	c.(781-783)CTG>ATG	p.L261M
Pat_59	Pre-Treatment	LUC7L3	51747	37	17	48818566	48818566	Missense_Mutation	SNP	C	A	4	53	c.310C>A	c.(310-312)CAT>AAT	p.H104N
Pat_59	Pre-Treatment	C17orf82	388407	37	17	59489494	59489494	Missense_Mutation	SNP	G	A	4	30	c.158G>A	c.(157-159)GGA>GAA	p.G53E
Pat_59	Pre-Treatment	TANC2	26115	37	17	61432525	61432525	Missense_Mutation	SNP	G	A	3	53	c.2134G>A	c.(2134-2136)GTG>ATG	p.V712M
Pat_59	Pre-Treatment	ICAM2	3384	37	17	62081169	62081169	Missense_Mutation	SNP	C	T	3	54	c.484G>A	c.(484-486)GGG>AGG	p.G162R
Pat_59	Pre-Treatment	PLEKHM1P	440456	37	17	62796727	62796727	Missense_Mutation	SNP	G	T	4	29	c.313C>A	c.(313-315)CAG>AAG	p.Q105K
Pat_59	Pre-Treatment	RGS9	8787	37	17	63193265	63193265	Missense_Mutation	SNP	G	A	4	50	c.882G>A	c.(880-882)ATG>ATA	p.M294I
Pat_59	Pre-Treatment	TMEM104	54868	37	17	72832443	72832443	Missense_Mutation	SNP	C	T	26	152	c.1108C>T	c.(1108-1110)CCC>TCC	p.P370S
Pat_59	Pre-Treatment	QRICH2	84074	37	17	74289376	74289376	Missense_Mutation	SNP	G	A	4	71	c.934C>T	c.(934-936)CCT>TCT	p.P312S
Pat_59	Pre-Treatment	TNRC6C	57690	37	17	76046324	76046324	Missense_Mutation	SNP	C	T	3	37	c.1181C>T	c.(1180-1182)ACA>ATA	p.T394I
Pat_59	Pre-Treatment	SYNGR2	9144	37	17	76166904	76166904	Missense_Mutation	SNP	G	A	5	226	c.106G>A	c.(106-108)GCC>ACC	p.A36T
Pat_59	Pre-Treatment	METTL4	64863	37	18	2554890	2554890	Missense_Mutation	SNP	C	T	4	70	c.607G>A	c.(607-609)GAA>AAA	p.E203K
Pat_59	Pre-Treatment	CEP76	79959	37	18	12674535	12674535	Missense_Mutation	SNP	C	T	4	69	c.1841G>A	c.(1840-1842)CGA>CAA	p.R614Q
Pat_59	Pre-Treatment	POTEC	388468	37	18	14543019	14543019	Missense_Mutation	SNP	T	C	7	184	c.127A>G	c.(127-129)ATG>GTG	p.M43V
Pat_59	Pre-Treatment	ZNF396	252884	37	18	32954172	32954172	Missense_Mutation	SNP	C	T	4	50	c.85G>A	c.(85-87)GAG>AAG	p.E29K
Pat_59	Pre-Treatment	KATNAL2	83473	37	18	44585946	44585946	Missense_Mutation	SNP	G	A	5	262	c.254G>A	c.(253-255)CGC>CAC	p.R85H
Pat_59	Pre-Treatment	MEX3C	51320	37	18	48703430	48703430	Missense_Mutation	SNP	G	A	4	42	c.1271C>T	c.(1270-1272)GCG>GTG	p.A424V
Pat_59	Pre-Treatment	DCC	1630	37	18	50432623	50432623	Missense_Mutation	SNP	G	A	16	82	c.622G>A	c.(622-624)GGA>AGA	p.G208R
Pat_59	Pre-Treatment	CDH19	28513	37	18	64235688	64235688	Missense_Mutation	SNP	G	A	34	74	c.455C>T	c.(454-456)CCT>CTT	p.P152L
Pat_59	Pre-Treatment	ZNF407	55628	37	18	72344482	72344482	Nonsense_Mutation	SNP	C	T	8	34	c.1507C>T	c.(1507-1509)CAG>TAG	p.Q503*
Pat_59	Pre-Treatment	SALL3	27164	37	18	76753670	76753670	Missense_Mutation	SNP	C	T	4	8	c.1679C>T	c.(1678-1680)TCC>TTC	p.S560F
Pat_59	Pre-Treatment	SLC39A3	29985	37	19	2737141	2737141	Missense_Mutation	SNP	G	A	4	50	c.115C>T	c.(115-117)CGC>TGC	p.R39C
Pat_59	Pre-Treatment	DPP9	91039	37	19	4704265	4704265	Missense_Mutation	SNP	G	A	4	98	c.478C>T	c.(478-480)CGG>TGG	p.R160W
Pat_59	Pre-Treatment	GTF2F1	2962	37	19	6380596	6380596	Missense_Mutation	SNP	G	A	4	99	c.1337C>T	c.(1336-1338)ACA>ATA	p.T446I
Pat_59	Pre-Treatment	EVI5L	115704	37	19	7914907	7914907	Missense_Mutation	SNP	G	T	3	3	c.652G>T	c.(652-654)GTG>TTG	p.V218L
Pat_59	Pre-Treatment	ICAM1	3383	37	19	10395132	10395132	Missense_Mutation	SNP	G	A	4	108	c.979G>A	c.(979-981)GAG>AAG	p.E327K
Pat_59	Pre-Treatment	ZNF700	90592	37	19	12060645	12060645	Missense_Mutation	SNP	T	A	6	235	c.1806T>A	c.(1804-1806)AGT>AGA	p.S602R
Pat_59	Pre-Treatment	ZNF700	90592	37	19	12060647	12060647	Missense_Mutation	SNP	G	C	6	231	c.1808G>C	c.(1807-1809)TGT>TCT	p.C603S
Pat_59	Pre-Treatment	ZSWIM4	65249	37	19	13919996	13919996	Missense_Mutation	SNP	G	A	4	50	c.974G>A	c.(973-975)GGC>GAC	p.G325D
Pat_59	Pre-Treatment	DCAF15	90379	37	19	14070060	14070060	Missense_Mutation	SNP	C	T	4	42	c.988C>T	c.(988-990)CGG>TGG	p.R330W
Pat_59	Pre-Treatment	EPS15L1	58513	37	19	16524625	16524625	Missense_Mutation	SNP	C	T	3	62	c.1225G>A	c.(1225-1227)GAA>AAA	p.E409K
Pat_59	Pre-Treatment	SLC5A5	6528	37	19	17988895	17988895	Missense_Mutation	SNP	C	A	4	46	c.962C>A	c.(961-963)CCA>CAA	p.P321Q
Pat_59	Pre-Treatment	GMIP	51291	37	19	19747563	19747563	Missense_Mutation	SNP	C	T	4	98	c.1280G>A	c.(1279-1281)GGT>GAT	p.G427D
Pat_59	Pre-Treatment	ZNF93	81931	37	19	20045361	20045361	Missense_Mutation	SNP	A	G	5	124	c.1597A>G	c.(1597-1599)AGA>GGA	p.R533G
Pat_59	Pre-Treatment	ZNF708	7562	37	19	21476519	21476519	Missense_Mutation	SNP	T	C	5	63	c.1249A>G	c.(1249-1251)AAG>GAG	p.K417E
Pat_59	Pre-Treatment	ZNF429	353088	37	19	21720411	21720411	Missense_Mutation	SNP	T	A	6	136	c.1556T>A	c.(1555-1557)ATC>AAC	p.I519N

Pat_59	Pre-Treatment	ZNF257	113835	37	19	22271961	22271961	Missense_Mutation	SNP	A	G	10	120	c.1409A>G	c.(1408-1410)CAG>CGG	p.Q470R
Pat_59	Pre-Treatment	ZNF676	163223	37	19	22362924	22362924	Missense_Mutation	SNP	G	C	5	187	c.1595C>G	c.(1594-1596)CCC>CGC	p.P532R
Pat_59	Pre-Treatment	ZNF99	7652	37	19	22939472	22939472	Missense_Mutation	SNP	A	G	3	73	c.2699T>C	c.(2698-2700)TTC>TCC	p.F900S
Pat_59	Pre-Treatment	ZNF91	7644	37	19	23544867	23544867	Missense_Mutation	SNP	T	C	8	208	c.914A>G	c.(913-915)CAT>CGT	p.H305R
Pat_59	Pre-Treatment	ZNF681	148213	37	19	23926839	23926839	Missense_Mutation	SNP	A	G	4	160	c.1513T>C	c.(1513-1515)TCC>CCC	p.S505P
Pat_59	Pre-Treatment	C19orf2	8725	37	19	30433557	30433557	Missense_Mutation	SNP	G	A	3	18	c.103G>A	c.(103-105)GAG>AAG	p.E35K
Pat_59	Pre-Treatment	TSHZ3	57616	37	19	31768189	31768189	Missense_Mutation	SNP	G	A	4	95	c.2510C>T	c.(2509-2511)TCG>TTG	p.S837L
Pat_59	Pre-Treatment	SLC7A10	56301	37	19	33716540	33716540	Missense_Mutation	SNP	G	A	2	2	c.70C>T	c.(70-72)CCA>TCA	p.P24S
Pat_59	Pre-Treatment	LSM14A	26065	37	19	34699912	34699912	Missense_Mutation	SNP	C	T	4	93	c.494C>T	c.(493-495)GCC>GTC	p.A165V
Pat_59	Pre-Treatment	GRAMD1A	57655	37	19	35512651	35512651	Missense_Mutation	SNP	C	T	3	29	c.1636C>T	c.(1636-1638)CGG>TGG	p.R546W
Pat_59	Pre-Treatment	SIPA1L3	23094	37	19	38572272	38572272	Missense_Mutation	SNP	G	A	4	27	c.67G>A	c.(67-69)GGC>AGC	p.G23S
Pat_59	Pre-Treatment	PSG5	5673	37	19	43688976	43688976	Missense_Mutation	SNP	T	C	10	239	c.388A>G	c.(388-390)AGG>GGG	p.R130G
Pat_59	Pre-Treatment	IRGQ	126298	37	19	44096735	44096735	Missense_Mutation	SNP	G	A	4	34	c.1315C>T	c.(1315-1317)CTC>TTC	p.L439F
Pat_59	Pre-Treatment	C19orf61	56006	37	19	44251899	44251899	Missense_Mutation	SNP	G	A	4	7	c.376C>T	c.(376-378)CCC>TCC	p.P126S
Pat_59	Pre-Treatment	ZNF225	7768	37	19	44636272	44636272	Missense_Mutation	SNP	A	T	4	72	c.1505A>T	c.(1504-1506)CAT>CTT	p.H502L
Pat_59	Pre-Treatment	ZNF234	10780	37	19	44660847	44660847	Missense_Mutation	SNP	C	A	4	121	c.678C>A	c.(676-678)CAC>CAA	p.H226Q
Pat_59	Pre-Treatment	CCDC8	83987	37	19	46915017	46915018	Missense_Mutation	DNP	CC	GG	5	129	.1050_1051GG>C	48-1053)GAGGAG>GAC	350_351EE>D
Pat_59	Pre-Treatment	CRX	1406	37	19	48339604	48339604	Missense_Mutation	SNP	C	T	17	49	c.205C>T	c.(205-207)CGT>TGT	p.R69C
Pat_59	Pre-Treatment	GRIN2D	2906	37	19	48945427	48945427	Missense_Mutation	SNP	C	T	4	116	c.2461C>T	c.(2461-2463)CGG>TGG	p.R821W
Pat_59	Pre-Treatment	FAM83E	54854	37	19	49107049	49107049	Missense_Mutation	SNP	G	A	6	31	c.878C>T	c.(877-879)CCT>CTT	p.P293L
Pat_59	Pre-Treatment	RASIP1	54922	37	19	49227650	49227650	Missense_Mutation	SNP	G	A	4	87	c.2488C>T	c.(2488-2490)CGG>TGG	p.R830W
Pat_59	Pre-Treatment	RUVBL2	10856	37	19	49507652	49507652	Missense_Mutation	SNP	C	T	4	95	c.242C>T	c.(241-243)ACG>ATG	p.T81M
Pat_59	Pre-Treatment	PIH1D1	55011	37	19	49952855	49952855	Missense_Mutation	SNP	A	G	3	95	c.214T>C	c.(214-216)TCC>CCC	p.S72P
Pat_59	Pre-Treatment	SIGLECP3	284367	37	19	51671363	51671363	Missense_Mutation	SNP	G	A	4	58	c.502G>A	c.(502-504)GAC>AAC	p.D168N
Pat_59	Pre-Treatment	ZNF432	9668	37	19	52537431	52537431	Missense_Mutation	SNP	T	A	3	33	c.1501A>T	c.(1501-1503)ATG>TTG	p.M501L
Pat_59	Pre-Treatment	ZNF578	147660	37	19	53014635	53014635	Missense_Mutation	SNP	A	G	7	100	c.1001A>G	c.(1000-1002)CAT>CGT	p.H334R
Pat_59	Pre-Treatment	ZNF845	91664	37	19	53856360	53856360	Missense_Mutation	SNP	A	C	6	121	c.2432A>C	c.(2431-2433)AAC>ACC	p.N811T
Pat_59	Pre-Treatment	ZNF154	7710	37	19	58216322	58216322	Missense_Mutation	SNP	G	A	36	155	c.59C>T	c.(58-60)GCC>GTC	p.A20V
Pat_59	Pre-Treatment	ZNF606	80095	37	19	58499587	58499587	Missense_Mutation	SNP	G	A	4	41	c.388C>T	c.(388-390)CGC>TGC	p.R130C
Pat_59	Pre-Treatment	SNTG2	54221	37	2	1161233	1161233	Splice_Site	SNP	G	A	6	15	c.412_splice	c.e7-1	p.V138_splice
Pat_59	Pre-Treatment	RSAD2	91543	37	2	7018212	7018213	Missense_Mutation	DNP	CC	AA	4	70	c.281_282CC>AA	c.(280-282)GCC>GAA	p.A94E
Pat_59	Pre-Treatment	KLF11	8462	37	2	10187784	10187784	Missense_Mutation	SNP	C	T	4	65	c.320C>T	c.(319-321)ACT>ATT	p.T107I
Pat_59	Pre-Treatment	GREB1	9687	37	2	11738813	11738813	Missense_Mutation	SNP	G	T	6	205	c.2160G>T	c.(2158-2160)TTG>TTT	p.L720F
Pat_59	Pre-Treatment	APOB	338	37	2	21260070	21260070	Missense_Mutation	SNP	C	T	3	38	c.595G>A	c.(595-597)GTG>ATG	p.V199M
Pat_59	Pre-Treatment	C2orf44	80304	37	2	24260988	24260988	Missense_Mutation	SNP	A	T	4	93	c.1377T>A	c.(1375-1377)AAT>AAA	p.N459K
Pat_59	Pre-Treatment	CGREF1	10669	37	2	27324405	27324405	Missense_Mutation	SNP	T	C	7	195	c.694A>G	c.(694-696)AAA>GAA	p.K232E
Pat_59	Pre-Treatment	C2orf16	84226	37	2	27804718	27804718	Missense_Mutation	SNP	G	A	6	284	c.5279G>A	c.(5278-5280)AGT>AAT	p.S1760N
Pat_59	Pre-Treatment	PLB1	151056	37	2	28843826	28843826	Missense_Mutation	SNP	G	A	4	112	c.3508G>A	c.(3508-3510)GCG>ACG	p.A1170T
Pat_59	Pre-Treatment	XDH	7498	37	2	31606627	31606627	Missense_Mutation	SNP	G	A	5	21	c.880C>T	c.(880-882)CCC>TCC	p.P294S
Pat_59	Pre-Treatment	PRKD3	23683	37	2	37516501	37516501	Missense_Mutation	SNP	C	T	4	67	c.715G>A	c.(715-717)GAG>AAG	p.E239K
Pat_59	Pre-Treatment	THADA	63892	37	2	43519999	43519999	Missense_Mutation	SNP	C	T	4	65	c.4792G>A	c.(4792-4794)GAA>AAA	p.E1598K
Pat_59	Pre-Treatment	TSPYL6	388951	37	2	54483191	54483191	Missense_Mutation	SNP	G	T	4	81	c.98C>A	c.(97-99)ACA>AAA	p.T33K
Pat_59	Pre-Treatment	ETAA1	54465	37	2	67631483	67631483	Missense_Mutation	SNP	G	A	4	79	c.1669G>A	c.(1669-1671)GGC>AGC	p.G557S
Pat_59	Pre-Treatment	EXOC6B	23233	37	2	72707789	72707789	Nonsense_Mutation	SNP	C	A	3	4	c.1756G>T	c.(1756-1758)GAG>TAG	p.E586*
Pat_59	Pre-Treatment	C2orf78	388960	37	2	74040645	74040645	Missense_Mutation	SNP	C	T	3	21	c.139C>T	c.(139-141)CGG>TGG	p.R47W
Pat_59	Pre-Treatment	RTKN	6242	37	2	74668867	74668867	Missense_Mutation	SNP	C	T	4	21	c.77G>A	c.(76-78)CGC>CAC	p.R26H
Pat_59	Pre-Treatment	CTNNA2	1496	37	2	80808879	80808879	Missense_Mutation	SNP	G	T	4	91	c.1942G>T	c.(1942-1944)GAT>TAT	p.D648Y

Pat_59	Pre-Treatment	ACTR1B	10120	37	2	98274433	98274433	Missense_Mutation	SNP	G	A	4	110	c.898C>T	c.(898-900)CTC>TTC	p.L300F
Pat_59	Pre-Treatment	LYG2	254773	37	2	99860491	99860491	Missense_Mutation	SNP	G	A	4	105	c.491C>T	c.(490-492)CCC>CTC	p.P164L
Pat_59	Pre-Treatment	SH3RF3	344558	37	2	109964230	109964230	Missense_Mutation	SNP	G	A	3	31	c.674G>A	c.(673-675)CGC>CAC	p.R225H
Pat_59	Pre-Treatment	PSD4	23550	37	2	113942609	113942609	Missense_Mutation	SNP	G	A	4	92	c.1132G>A	c.(1132-1134)GGA>AGA	p.G378R
Pat_59	Pre-Treatment	CLASP1	23332	37	2	122122785	122122785	Missense_Mutation	SNP	C	T	4	21	c.3962G>A	c.(3961-3963)CGG>CAG	p.R1321Q
Pat_59	Pre-Treatment	POTEF	728378	37	2	130877782	130877782	Missense_Mutation	SNP	A	G	5	193	c.307T>C	c.(307-309)TGC>CGC	p.C103R
Pat_59	Pre-Treatment	ACVR1	90	37	2	158595058	158595058	Missense_Mutation	SNP	G	A	4	125	c.1289C>T	c.(1288-1290)CCG>CTG	p.P430L
Pat_59	Pre-Treatment	TTC21B	79809	37	2	166740465	166740465	Nonsense_Mutation	SNP	G	A	4	80	c.3523C>T	c.(3523-3525)CGA>TGA	p.R1175*
Pat_59	Pre-Treatment	SCN9A	6335	37	2	167055671	167055671	Missense_Mutation	SNP	C	T	29	91	c.5445G>A	c.(5443-5445)ATG>ATA	p.M1815I
Pat_59	Pre-Treatment	LRP2	4036	37	2	170011107	170011107	Missense_Mutation	SNP	G	A	4	128	c.12158C>T	c.(12157-12159)TCT>TTT	p.S4053F
Pat_59	Pre-Treatment	LRP2	4036	37	2	170050348	170050348	Missense_Mutation	SNP	C	T	4	113	c.8753G>A	c.(8752-8754)TGC>TAC	p.C2918Y
Pat_59	Pre-Treatment	MYO3B	140469	37	2	171399445	171399445	Missense_Mutation	SNP	G	A	19	117	c.3605G>A	c.(3604-3606)GGG>GAG	p.G1202E
Pat_59	Pre-Treatment	GORASP2	26003	37	2	171811261	171811261	Missense_Mutation	SNP	C	A	3	28	c.668C>A	c.(667-669)CCT>CAT	p.P223H
Pat_59	Pre-Treatment	CCDC141	285025	37	2	179718182	179718182	Missense_Mutation	SNP	G	A	4	108	c.1505C>T	c.(1504-1506)GCT>GTT	p.A502V
Pat_59	Pre-Treatment	CWC22	57703	37	2	180835497	180835497	Missense_Mutation	SNP	G	A	4	83	c.1027C>T	c.(1027-1029)CGG>TGG	p.R343W
Pat_59	Pre-Treatment	NEUROD1	4760	37	2	182542780	182542780	Missense_Mutation	SNP	C	A	5	135	c.808G>T	c.(808-810)GAT>TAT	p.D270Y
Pat_59	Pre-Treatment	PMS1	5378	37	2	190742010	190742010	Missense_Mutation	SNP	C	T	3	54	c.2647C>T	c.(2647-2649)CGT>TGT	p.R883C
Pat_59	Pre-Treatment	HIBCH	26275	37	2	191109629	191109629	Missense_Mutation	SNP	G	A	4	137	c.875C>T	c.(874-876)GCC>GTC	p.A292V
Pat_59	Pre-Treatment	DNAH7	56171	37	2	196740512	196740512	Missense_Mutation	SNP	G	A	4	51	c.6173C>T	c.(6172-6174)CCT>CTT	p.P2058L
Pat_59	Pre-Treatment	HECW2	57520	37	2	197172663	197172663	Missense_Mutation	SNP	G	A	4	115	c.2581C>T	c.(2581-2583)CGG>TGG	p.R861W
Pat_59	Pre-Treatment	COQ10B	80219	37	2	198327295	198327295	Missense_Mutation	SNP	C	T	4	68	c.287C>T	c.(286-288)TCG>TTG	p.S96L
Pat_59	Pre-Treatment	PARD3B	117583	37	2	206480196	206480196	Missense_Mutation	SNP	C	T	17	120	c.3277C>T	c.(3277-3279)CCT>TCT	p.P1093S
Pat_59	Pre-Treatment	TMEM169	92691	37	2	216960853	216960853	Missense_Mutation	SNP	G	A	3	61	c.167G>A	c.(166-168)CGC>CAC	p.R56H
Pat_59	Pre-Treatment	TUBA4A	7277	37	2	220115571	220115571	Missense_Mutation	SNP	C	T	4	76	c.850G>A	c.(850-852)GAG>AAG	p.E284K
Pat_59	Pre-Treatment	KCNE4	23704	37	2	223917622	223917622	Missense_Mutation	SNP	C	T	3	45	c.74C>T	c.(73-75)GCG>GTG	p.A25V
Pat_59	Pre-Treatment	HTR2B	3357	37	2	231973844	231973844	Missense_Mutation	SNP	G	A	4	126	c.833C>T	c.(832-834)CCG>CTG	p.P278L
Pat_59	Pre-Treatment	DIS3L2	129563	37	2	233164770	233164771	Missense_Mutation	DNP	GG	CT	4	52	.1680_1681GG>C	678-1683)CTGGAC>CTC	p.D561Y
Pat_59	Pre-Treatment	CAPN10	11132	37	2	241537456	241537456	Missense_Mutation	SNP	C	T	8	48	c.1895C>T	c.(1894-1896)CCG>CTG	p.P632L
Pat_59	Pre-Treatment	FAM110A	83541	37	20	826310	826310	Missense_Mutation	SNP	G	A	3	47	c.863G>A	c.(862-864)CGG>CAG	p.R288Q
Pat_59	Pre-Treatment	CHGB	1114	37	20	5903172	5903172	Missense_Mutation	SNP	G	A	3	12	c.382G>A	c.(382-384)GGG>AGG	p.G128R
Pat_59	Pre-Treatment	C20orf12	55184	37	20	18445989	18445989	Nonsense_Mutation	SNP	G	T	3	32	c.14C>A	c.(13-15)TCA>TAA	p.S5*
Pat_59	Pre-Treatment	C20orf26	26074	37	20	20258004	20258004	Missense_Mutation	SNP	G	A	12	96	c.2698G>A	c.(2698-2700)GAT>AAT	p.D900N
Pat_59	Pre-Treatment	SUN5	140732	37	20	31573627	31573627	Missense_Mutation	SNP	A	G	3	40	c.812T>C	c.(811-813)CTG>CCG	p.L271P
Pat_59	Pre-Treatment	SUN5	140732	37	20	31584157	31584157	Missense_Mutation	SNP	C	T	4	47	c.398G>A	c.(397-399)AGC>AAC	p.S133N
Pat_59	Pre-Treatment	ITCH	83737	37	20	33069013	33069013	Splice_Site	SNP	T	A	4	86	c.2216_splice	c.e21+2	p.R739_splice
Pat_59	Pre-Treatment	SPAG4	6676	37	20	34207500	34207500	Splice_Site	SNP	G	A	3	53	c.910_splice	c.e10-1	p.P304_splice
Pat_59	Pre-Treatment	CTNNBL1	56259	37	20	36500360	36500360	Missense_Mutation	SNP	C	T	4	107	c.1637C>T	c.(1636-1638)CCG>CTG	p.P546L
Pat_59	Pre-Treatment	KIAA0406	9675	37	20	36640607	36640607	Missense_Mutation	SNP	C	T	4	98	c.1612G>A	c.(1612-1614)GTT>ATT	p.V538I
Pat_59	Pre-Treatment	PLCG1	5335	37	20	39788769	39788769	Missense_Mutation	SNP	C	T	4	60	c.488C>T	c.(487-489)TCA>TTA	p.S163L
Pat_59	Pre-Treatment	PLCG1	5335	37	20	39795392	39795392	Missense_Mutation	SNP	G	A	4	103	c.2194G>A	c.(2194-2196)GAC>AAC	p.D732N
Pat_59	Pre-Treatment	CHD6	84181	37	20	40049366	40049366	Missense_Mutation	SNP	C	T	5	237	c.5909G>A	c.(5908-5910)AGT>AAT	p.S1970N
Pat_59	Pre-Treatment	HNF4A	3172	37	20	43034836	43034836	Missense_Mutation	SNP	G	A	3	49	c.254G>A	c.(253-255)CGG>CAG	p.R85Q
Pat_59	Pre-Treatment	CTSZ	1522	37	20	57581530	57581530	Missense_Mutation	SNP	G	A	4	90	c.154C>T	c.(154-156)CGG>TGG	p.R52W
Pat_59	Pre-Treatment	CDH26	60437	37	20	58559728	58559728	Missense_Mutation	SNP	G	T	4	110	c.576G>T	c.(574-576)TTG>TTT	p.L192F
Pat_59	Pre-Treatment	COL9A3	1299	37	20	61467644	61467644	Missense_Mutation	SNP	G	A	4	70	c.1507G>A	c.(1507-1509)GTC>ATC	p.V503I
Pat_59	Pre-Treatment	DIDO1	11083	37	20	61511181	61511182	Missense_Mutation	DNP	CC	TT	9	12	.6126_6127GG>A	124-6129)GAGGAG>GAA	p.E2043K
Pat_59	Pre-Treatment	MYT1	4661	37	20	62844906	62844906	Missense_Mutation	SNP	G	T	4	93	c.1537G>T	c.(1537-1539)GCT>TCT	p.A513S

Pat_59	Pre-Treatment	ADAMTS1	9510	37	21	28210903	28210903	Missense_Mutation	SNP	A	T	4	58	c.2059T>A	c.(2059-2061)TCC>ACC	p.S687T
Pat_59	Pre-Treatment	ADAMTS1	9510	37	21	28216622	28216622	Missense_Mutation	SNP	C	T	4	10	c.652G>A	c.(652-654)GAA>AAA	p.E218K
Pat_59	Pre-Treatment	LRRC3	81543	37	21	45877068	45877068	Missense_Mutation	SNP	G	T	4	47	c.541G>T	c.(541-543)GTG>TTG	p.V181L
Pat_59	Pre-Treatment	COL6A1	1291	37	21	47404383	47404383	Missense_Mutation	SNP	G	A	3	35	c.428G>A	c.(427-429)GGG>GAG	p.G143E
Pat_59	Pre-Treatment	NEFH	4744	37	22	29885313	29885313	Missense_Mutation	SNP	C	G	5	161	c.1684C>G	c.(1684-1686)CCT>GCT	p.P562A
Pat_59	Pre-Treatment	SEC14L2	23541	37	22	30818389	30818389	Missense_Mutation	SNP	C	T	4	127	c.1205C>T	c.(1204-1206)CCG>CTG	p.P402L
Pat_59	Pre-Treatment	RRP7A	27341	37	22	42908975	42908975	Missense_Mutation	SNP	C	T	4	36	c.784G>A	c.(784-786)GAG>AAG	p.E262K
Pat_59	Pre-Treatment	CELSR1	9620	37	22	46930231	46930231	Missense_Mutation	SNP	G	A	4	60	c.2837C>T	c.(2836-2838)ACG>ATG	p.T946M
Pat_59	Pre-Treatment	TBC1D22A	25771	37	22	47193409	47193409	Missense_Mutation	SNP	G	A	4	79	c.529G>A	c.(529-531)GGT>AGT	p.G177S
Pat_59	Pre-Treatment	TTLL8	164714	37	22	50470341	50470341	Missense_Mutation	SNP	G	A	3	15	c.1481C>T	c.(1480-1482)GCC>GTC	p.A494V
Pat_59	Pre-Treatment	MAPK11	5600	37	22	50705408	50705408	Missense_Mutation	SNP	G	A	4	66	c.565C>T	c.(565-567)CGG>TGG	p.R189W
Pat_59	Pre-Treatment	CPT1B	1375	37	22	51016211	51016211	Missense_Mutation	SNP	C	T	4	60	c.134G>A	c.(133-135)CGC>CAC	p.R45H
Pat_59	Pre-Treatment	TTLL3	26140	37	3	9871045	9871045	Missense_Mutation	SNP	G	A	4	104	c.1520G>A	c.(1519-1521)TGT>TAT	p.C507Y
Pat_59	Pre-Treatment	ATP2B2	491	37	3	10491077	10491077	Missense_Mutation	SNP	C	T	6	19	c.151G>A	c.(151-153)GGG>AGG	p.G51R
Pat_59	Pre-Treatment	NUP210	23225	37	3	13415268	13415268	Missense_Mutation	SNP	C	A	4	34	c.1537G>T	c.(1537-1539)GTG>TTG	p.V513L
Pat_59	Pre-Treatment	NR2C2	7182	37	3	15080734	15080734	Missense_Mutation	SNP	G	A	3	24	c.1616G>A	c.(1615-1617)CGA>CAA	p.R539Q
Pat_59	Pre-Treatment	ZFYVE20	64145	37	3	15131987	15131987	Nonsense_Mutation	SNP	G	A	4	110	c.208C>T	c.(208-210)CGA>TGA	p.R70*
Pat_59	Pre-Treatment	STAC	6769	37	3	36485003	36485003	Missense_Mutation	SNP	C	T	24	37	c.259C>T	c.(259-261)CCT>TCT	p.P87S
Pat_59	Pre-Treatment	ENTPD3	956	37	3	40465357	40465357	Missense_Mutation	SNP	G	A	4	102	c.1256G>A	c.(1255-1257)CGC>CAC	p.R419H
Pat_59	Pre-Treatment	CCDC13	152206	37	3	42777260	42777260	Missense_Mutation	SNP	A	G	22	45	c.1310T>C	c.(1309-1311)GTA>GCA	p.V437A
Pat_59	Pre-Treatment	CYP8B1	1582	37	3	42916093	42916093	Missense_Mutation	SNP	C	T	41	103	c.1216G>A	c.(1216-1218)GAT>AAT	p.D406N
Pat_59	Pre-Treatment	EXOSC7	23016	37	3	45038656	45038656	Missense_Mutation	SNP	G	A	4	109	c.332G>A	c.(331-333)CGG>CAG	p.R111Q
Pat_59	Pre-Treatment	AMT	275	37	3	49455301	49455301	Missense_Mutation	SNP	G	A	3	42	c.983C>T	c.(982-984)GCC>GTC	p.A328V
Pat_59	Pre-Treatment	GRM2	2912	37	3	51743318	51743318	Missense_Mutation	SNP	C	T	3	44	c.319C>T	c.(319-321)CGT>TGT	p.R107C
Pat_59	Pre-Treatment	TNNC1	7134	37	3	52488022	52488022	Missense_Mutation	SNP	T	G	2	1	c.10A>C	c.(10-12)ATC>CTC	p.I4L
Pat_59	Pre-Treatment	ITIH3	3699	37	3	52840374	52840374	Missense_Mutation	SNP	G	A	3	53	c.2008G>A	c.(2008-2010)GAT>AAT	p.D670N
Pat_59	Pre-Treatment	ERC2	26059	37	3	56026137	56026137	Missense_Mutation	SNP	C	T	52	142	c.2203G>A	c.(2203-2205)GAG>AAG	p.E735K
Pat_59	Pre-Treatment	PTPRG	5793	37	3	62257109	62257109	Missense_Mutation	SNP	T	C	3	44	c.3061T>C	c.(3061-3063)TAT>CAT	p.Y1021H
Pat_59	Pre-Treatment	CADPS	8618	37	3	62578418	62578418	Missense_Mutation	SNP	C	A	3	27	c.1331G>T	c.(1330-1332)GGC>GTC	p.G444V
Pat_59	Pre-Treatment	SUCLG2	8801	37	3	67546238	67546238	Missense_Mutation	SNP	A	G	4	73	c.1046T>C	c.(1045-1047)CTC>CCC	p.L349P
Pat_59	Pre-Treatment	FAM86D	692099	37	3	75472158	75472158	Missense_Mutation	SNP	G	A	4	105	c.692C>T	c.(691-693)CCC>CTC	p.P231L
Pat_59	Pre-Treatment	FAM55C	91775	37	3	101520758	101520758	Missense_Mutation	SNP	G	A	4	77	c.773G>A	c.(772-774)AGC>AAC	p.S258N
Pat_59	Pre-Treatment	GSK3B	2932	37	3	119666143	119666143	Missense_Mutation	SNP	C	T	5	152	c.338G>A	c.(337-339)CGT>CAT	p.R113H
Pat_59	Pre-Treatment	OSBPL11	114885	37	3	125271280	125271280	Missense_Mutation	SNP	C	T	4	22	c.1399G>A	c.(1399-1401)GAG>AAG	p.E467K
Pat_59	Pre-Treatment	TRH	7200	37	3	129695650	129695650	Missense_Mutation	SNP	C	A	3	35	c.320C>A	c.(319-321)GCT>GAT	p.A107D
Pat_59	Pre-Treatment	AMOTL2	51421	37	3	134086505	134086505	Missense_Mutation	SNP	G	A	3	19	c.1049C>T	c.(1048-1050)GCT>GTT	p.A350V
Pat_59	Pre-Treatment	XRN1	54464	37	3	142133050	142133050	Missense_Mutation	SNP	G	C	20	52	c.1520C>G	c.(1519-1521)CCT>CGT	p.P507R
Pat_59	Pre-Treatment	ZIC1	7545	37	3	147128782	147128782	Missense_Mutation	SNP	G	A	4	108	c.883G>A	c.(883-885)GTG>ATG	p.V295M
Pat_59	Pre-Treatment	MECOM	2122	37	3	169099202	169099202	Missense_Mutation	SNP	C	T	3	22	c.148G>A	c.(148-150)GCC>ACC	p.A50T
Pat_59	Pre-Treatment	FXR1	8087	37	3	180669215	180669215	Nonsense_Mutation	SNP	G	T	4	66	c.760G>T	c.(760-762)GAG>TAG	p.E254*
Pat_59	Pre-Treatment	CLCN2	1181	37	3	184071570	184071570	Missense_Mutation	SNP	G	A	2	1	c.1735C>T	c.(1735-1737)CGT>TGT	p.R579C
Pat_59	Pre-Treatment	ETV5	2119	37	3	185769911	185769911	Missense_Mutation	SNP	G	A	4	80	c.1219C>T	c.(1219-1221)CGC>TGC	p.R407C
Pat_59	Pre-Treatment	ZNF595	152687	37	4	86222	86222	Missense_Mutation	SNP	A	T	4	120	c.828A>T	c.(826-828)AAA>AAT	p.K276N
Pat_59	Pre-Treatment	ZNF141	7700	37	4	367245	367245	Missense_Mutation	SNP	C	A	5	150	c.1019C>A	c.(1018-1020)ACA>AAA	p.T340K
Pat_59	Pre-Treatment	GAK	2580	37	4	887682	887682	Missense_Mutation	SNP	G	A	5	33	c.857C>T	c.(856-858)ACG>ATG	p.T286M
Pat_59	Pre-Treatment	PPP2R2C	5522	37	4	6374336	6374336	Missense_Mutation	SNP	G	A	22	63	c.539C>T	c.(538-540)TCC>TTC	p.S180F
Pat_59	Pre-Treatment	MAN2B2	23324	37	4	6612825	6612825	Missense_Mutation	SNP	C	T	3	47	c.2383C>T	c.(2383-2385)CGG>TGG	p.R795W

Pat_59	Pre-Treatment	QDPR	5860	37	4	17488827	17488827	Missense_Mutation	SNP	C	T	4	103	c.662G>A	c.(661-663)CGA>CAA	p.R221Q
Pat_59	Pre-Treatment	LGI2	55203	37	4	25028514	25028514	Missense_Mutation	SNP	G	A	4	103	c.317C>T	c.(316-318)GCT>GTT	p.A106V
Pat_59	Pre-Treatment	ANAPC4	29945	37	4	25382008	25382008	Nonsense_Mutation	SNP	C	T	4	79	c.142C>T	c.(142-144)CGA>TGA	p.R48*
Pat_59	Pre-Treatment	GABRG1	2565	37	4	46043129	46043129	Missense_Mutation	SNP	C	T	18	92	c.1274G>A	c.(1273-1275)GGA>GAA	p.G425E
Pat_59	Pre-Treatment	ATP10D	57205	37	4	47560135	47560135	Missense_Mutation	SNP	G	T	4	50	c.2279G>T	c.(2278-2280)GGA>GTA	p.G760V
Pat_59	Pre-Treatment	LRRC66	339977	37	4	52860897	52860897	Missense_Mutation	SNP	C	T	4	73	c.2291G>A	c.(2290-2292)GGG>GAG	p.G764E
Pat_59	Pre-Treatment	GSX2	170825	37	4	54968000	54968000	Missense_Mutation	SNP	G	A	3	45	c.826G>A	c.(826-828)GGG>AGG	p.G276R
Pat_59	Pre-Treatment	ADAMTS3	9508	37	4	73175150	73175150	Missense_Mutation	SNP	C	T	4	116	c.2143G>A	c.(2143-2145)GTG>ATG	p.V715M
Pat_59	Pre-Treatment	FRAS1	80144	37	4	79428649	79428649	Missense_Mutation	SNP	G	C	6	23	c.9391G>C	c.(9391-9393)GTC>CTC	p.V3131L
Pat_59	Pre-Treatment	EMCN	51705	37	4	101342534	101342534	Missense_Mutation	SNP	C	T	19	29	c.569G>A	c.(568-570)AGT>AAT	p.S190N
Pat_59	Pre-Treatment	EMCN	51705	37	4	101386624	101386624	Missense_Mutation	SNP	G	A	4	54	c.332C>T	c.(331-333)ACA>ATA	p.T111I
Pat_59	Pre-Treatment	CCRN4L	25819	37	4	139964386	139964386	Missense_Mutation	SNP	G	A	3	54	c.349G>A	c.(349-351)GTC>ATC	p.V117I
Pat_59	Pre-Treatment	TLR2	7097	37	4	154625222	154625222	Missense_Mutation	SNP	C	T	12	63	c.1163C>T	c.(1162-1164)TCT>TTT	p.S388F
Pat_59	Pre-Treatment	FGB	2244	37	4	155490797	155490797	Missense_Mutation	SNP	G	A	24	52	c.1090G>A	c.(1090-1092)GAA>AAA	p.E364K
Pat_59	Pre-Treatment	RXFP1	59350	37	4	159569854	159569854	Nonsense_Mutation	SNP	C	T	6	30	c.1960C>T	c.(1960-1962)CAG>TAG	p.Q654*
Pat_59	Pre-Treatment	ADAM29	11086	37	4	175898987	175898987	Missense_Mutation	SNP	C	T	5	184	c.2311C>T	c.(2311-2313)CGG>TGG	p.R771W
Pat_59	Pre-Treatment	NSUN2	54888	37	5	6611904	6611904	Missense_Mutation	SNP	C	A	4	39	c.1029G>T	c.(1027-1029)TTG>TTT	p.L343F
Pat_59	Pre-Treatment	TARS	6897	37	5	33467737	33467737	Missense_Mutation	SNP	G	A	4	98	c.2096G>A	c.(2095-2097)CGC>CAC	p.R699H
Pat_59	Pre-Treatment	C5orf42	65250	37	5	37173856	37173856	Splice_Site	SNP	C	T	4	77	c.6171_splice	c.e32+1	p.Q2057_splice
Pat_59	Pre-Treatment	RICTOR	253260	37	5	38947452	38947452	Missense_Mutation	SNP	G	A	4	100	c.4228C>T	c.(4228-4230)CGG>TGG	p.R1410W
Pat_59	Pre-Treatment	RICTOR	253260	37	5	38955743	38955743	Missense_Mutation	SNP	G	A	5	174	c.2563C>T	c.(2563-2565)CGG>TGG	p.R855W
Pat_59	Pre-Treatment	DAB2	1601	37	5	39383049	39383049	Missense_Mutation	SNP	C	T	4	104	c.1012G>A	c.(1012-1014)GGT>AGT	p.G338S
Pat_59	Pre-Treatment	C5orf39	389289	37	5	43039674	43039674	Missense_Mutation	SNP	G	A	4	104	c.475C>T	c.(475-477)CTC>TTC	p.L159F
Pat_59	Pre-Treatment	POC5	134359	37	5	74988292	74988292	Missense_Mutation	SNP	G	T	4	138	c.724C>A	c.(724-726)CAA>AAA	p.Q242K
Pat_59	Pre-Treatment	CMYA5	202333	37	5	79033184	79033184	Missense_Mutation	SNP	G	A	4	89	c.8596G>A	c.(8596-8598)GTT>ATT	p.V2866I
Pat_59	Pre-Treatment	SPZ1	84654	37	5	79616465	79616465	Missense_Mutation	SNP	T	A	4	115	c.431T>A	c.(430-432)ATG>AAG	p.M144K
Pat_59	Pre-Treatment	ATP6AP1L	92270	37	5	81613868	81613868	Missense_Mutation	SNP	G	A	4	62	c.424G>A	c.(424-426)GCC>ACC	p.A142T
Pat_59	Pre-Treatment	HAPLN1	1404	37	5	82940241	82940242	Missense_Mutation	DNP	CC	TT	13	50	c.715_716GG>AA	c.(715-717)GGA>AAA	p.G239K
Pat_59	Pre-Treatment	ARRDC3	57561	37	5	90678845	90678845	Missense_Mutation	SNP	G	A	4	111	c.65C>T	c.(64-66)CCT>CTT	p.P22L
Pat_59	Pre-Treatment	TTC37	9652	37	5	94876500	94876500	Missense_Mutation	SNP	C	T	6	135	c.437G>A	c.(436-438)CGG>CAG	p.R146Q
Pat_59	Pre-Treatment	PCSK1	5122	37	5	95746489	95746489	Missense_Mutation	SNP	C	T	27	61	c.1084G>A	c.(1084-1086)GAC>AAC	p.D362N
Pat_59	Pre-Treatment	SNCAIP	9627	37	5	121759064	121759064	Missense_Mutation	SNP	C	T	4	95	c.632C>T	c.(631-633)TCT>TTT	p.S211F
Pat_59	Pre-Treatment	8-Sep	23176	37	5	132099937	132099937	Missense_Mutation	SNP	T	C	4	45	c.326A>G	c.(325-327)GAT>GGT	p.D109G
Pat_59	Pre-Treatment	LRRTM2	26045	37	5	138209228	138209228	Missense_Mutation	SNP	C	T	16	44	c.1022G>A	c.(1021-1023)AGT>AAT	p.S341N
Pat_59	Pre-Treatment	CTNNA1	1495	37	5	138260295	138260295	Missense_Mutation	SNP	G	A	3	37	c.1643G>A	c.(1642-1644)CGG>CAG	p.R548Q
Pat_59	Pre-Treatment	PCDHB5	26167	37	5	140517195	140517195	Missense_Mutation	SNP	C	T	4	120	c.2179C>T	c.(2179-2181)CCC>TCC	p.P727S
Pat_59	Pre-Treatment	PCDHB16	57717	37	5	140563894	140563894	Missense_Mutation	SNP	C	T	4	133	c.1760C>T	c.(1759-1761)ACC>ATC	p.T587I
Pat_59	Pre-Treatment	PCDHGB1	56104	37	5	140732184	140732184	Missense_Mutation	SNP	G	A	2	1	c.2357G>A	c.(2356-2358)TGT>TAT	p.C786Y
Pat_59	Pre-Treatment	PPARGC1B	133522	37	5	149212865	149212865	Missense_Mutation	SNP	G	A	4	50	c.1229G>A	c.(1228-1230)CGC>CAC	p.R410H
Pat_59	Pre-Treatment	PDE6A	5145	37	5	149323816	149323816	Missense_Mutation	SNP	C	T	4	112	c.421G>A	c.(421-423)GTG>ATG	p.V141M
Pat_59	Pre-Treatment	WWC1	23286	37	5	167882526	167882526	Splice_Site	SNP	G	A	4	77	c.2823_splice	c.e19+1	p.R941_splice
Pat_59	Pre-Treatment	FGF18	8817	37	5	170883681	170883681	Missense_Mutation	SNP	C	T	4	124	c.496C>T	c.(496-498)CGG>TGG	p.R166W
Pat_59	Pre-Treatment	SNCB	6620	37	5	176048231	176048231	Missense_Mutation	SNP	T	A	2	3	c.356A>T	c.(355-357)TAT>TTT	p.Y119F
Pat_59	Pre-Treatment	HK3	3101	37	5	176316669	176316669	Missense_Mutation	SNP	G	A	14	42	c.707C>T	c.(706-708)CCG>CTG	p.P236L
Pat_59	Pre-Treatment	EXOC2	55770	37	6	633105	633105	Missense_Mutation	SNP	C	A	4	66	c.131G>T	c.(130-132)TGT>TTT	p.C44F
Pat_59	Pre-Treatment	LY86	9450	37	6	6626622	6626623	Missense_Mutation	DNP	CC	TT	19	58	c.320_321CC>TT	c.(319-321)CCC>CTT	p.P107L
Pat_59	Pre-Treatment	ATXN1	6310	37	6	16327968	16327968	Missense_Mutation	SNP	C	T	3	22	c.574G>A	c.(574-576)GGA>AGA	p.G192R

Pat_59	Pre-Treatment	CAP2	10486	37	6	17507884	17507884	Missense_Mutation	SNP	G	T	4	119	c.457G>T	c.(457-459)GGT>TGT	p.G153C
Pat_59	Pre-Treatment	KDM1B	221656	37	6	18222197	18222197	Missense_Mutation	SNP	G	A	5	246	c.1834G>A	c.(1834-1836)GAA>AAA	p.E612K
Pat_59	Pre-Treatment	HIST1H2AB	8335	37	6	26033484	26033484	Missense_Mutation	SNP	G	T	4	109	c.313C>A	c.(313-315)CAG>AAG	p.Q105K
Pat_59	Pre-Treatment	BTN2A1	11120	37	6	26465619	26465619	Missense_Mutation	SNP	G	A	4	86	c.919G>A	c.(919-921)GAA>AAA	p.E307K
Pat_59	Pre-Treatment	ZKSCAN3	80317	37	6	28333529	28333529	Missense_Mutation	SNP	A	G	3	62	c.1084A>G	c.(1084-1086)AGA>GGA	p.R362G
Pat_59	Pre-Treatment	SKIV2L	6499	37	6	31936780	31936780	Missense_Mutation	SNP	C	T	3	28	c.3313C>T	c.(3313-3315)CCT>TCT	p.P1105S
Pat_59	Pre-Treatment	TNXB	7148	37	6	32029967	32029967	Missense_Mutation	SNP	G	A	4	43	c.7135C>T	c.(7135-7137)CGT>TGT	p.R2379C
Pat_59	Pre-Treatment	WDR46	9277	37	6	33248598	33248598	Missense_Mutation	SNP	C	T	4	40	c.1282G>A	c.(1282-1284)GGG>AGG	p.G428R
Pat_59	Pre-Treatment	PHF1	5252	37	6	33383066	33383066	Missense_Mutation	SNP	G	A	6	372	c.1294G>A	c.(1294-1296)GGC>AGC	p.G432S
Pat_59	Pre-Treatment	C6orf129	154467	37	6	37451045	37451045	Missense_Mutation	SNP	G	A	4	74	c.211C>T	c.(211-213)CGG>TGG	p.R71W
Pat_59	Pre-Treatment	ZNF318	24149	37	6	43309855	43309855	Missense_Mutation	SNP	G	T	4	80	c.3371C>A	c.(3370-3372)GCA>GAA	p.A1124E
Pat_59	Pre-Treatment	KHDRBS2	202559	37	6	62611258	62611258	Missense_Mutation	SNP	G	A	13	53	c.502C>T	c.(502-504)CGT>TGT	p.R168C
Pat_59	Pre-Treatment	LCA5	167691	37	6	80196800	80196800	Nonsense_Mutation	SNP	A	T	4	73	c.2015T>A	c.(2014-2016)TTA>TAA	p.L672*
Pat_59	Pre-Treatment	DOPEY1	23033	37	6	83818692	83818692	Missense_Mutation	SNP	G	T	4	124	c.384G>T	c.(382-384)TTG>TTT	p.L128F
Pat_59	Pre-Treatment	MDN1	23195	37	6	90420481	90420481	Missense_Mutation	SNP	C	A	4	68	c.7684G>T	c.(7684-7686)GCA>TCA	p.A2562S
Pat_59	Pre-Treatment	BACH2	60468	37	6	90660099	90660099	Missense_Mutation	SNP	G	A	4	70	c.1726C>T	c.(1726-1728)CGG>TGG	p.R576W
Pat_59	Pre-Treatment	C6orf167	253714	37	6	97702558	97702558	Missense_Mutation	SNP	T	C	3	73	c.994A>G	c.(994-996)AGT>GGT	p.S332G
Pat_59	Pre-Treatment	HACE1	57531	37	6	105280946	105280946	Missense_Mutation	SNP	G	A	4	79	c.505C>T	c.(505-507)CAT>TAT	p.H169Y
Pat_59	Pre-Treatment	BEND3	57673	37	6	107390266	107390266	Missense_Mutation	SNP	G	A	4	91	c.2129C>T	c.(2128-2130)TCG>TTG	p.S710L
Pat_59	Pre-Treatment	SMPD2	6610	37	6	109763242	109763242	Missense_Mutation	SNP	T	C	73	158	c.290T>C	c.(289-291)ATC>ACC	p.I97T
Pat_59	Pre-Treatment	TAAR6	319100	37	6	132892037	132892037	Missense_Mutation	SNP	G	A	4	85	c.577G>A	c.(577-579)GTT>ATT	p.V193I
Pat_59	Pre-Treatment	ALDH8A1	64577	37	6	135263615	135263615	Missense_Mutation	SNP	G	A	4	28	c.374C>T	c.(373-375)ACG>ATG	p.T125M
Pat_59	Pre-Treatment	PBOV1	59351	37	6	138539325	138539325	Missense_Mutation	SNP	C	A	4	70	c.208G>T	c.(208-210)GAT>TAT	p.D70Y
Pat_59	Pre-Treatment	ZBTB2	57621	37	6	151687722	151687722	Missense_Mutation	SNP	C	T	4	73	c.479G>A	c.(478-480)CGG>CAG	p.R160Q
Pat_59	Pre-Treatment	ESR1	2099	37	6	152382233	152382233	Missense_Mutation	SNP	T	C	4	65	c.1343T>C	c.(1342-1344)CTC>CCC	p.L448P
Pat_59	Pre-Treatment	FAM120B	84498	37	6	170627722	170627723	Missense_Mutation	DNP	TG	CA	7	361	.1244_1245TG>C	c.(1243-1245)ATG>ACA	p.M415T
Pat_59	Pre-Treatment	MICALL2	79778	37	7	1480281	1480281	Missense_Mutation	SNP	G	A	4	57	c.1751C>T	c.(1750-1752)CCG>CTG	p.P584L
Pat_59	Pre-Treatment	CARD11	84433	37	7	2969705	2969705	Missense_Mutation	SNP	T	C	3	10	c.1574A>G	c.(1573-1575)AAG>AGG	p.K525R
Pat_59	Pre-Treatment	FOXK1	221937	37	7	4794907	4794907	Missense_Mutation	SNP	G	A	4	41	c.943G>A	c.(943-945)GTG>ATG	p.V315M
Pat_59	Pre-Treatment	CYTH3	9265	37	7	6205183	6205183	Missense_Mutation	SNP	C	T	4	95	c.965G>A	c.(964-966)CGG>CAG	p.R322Q
Pat_59	Pre-Treatment	RAC1	5879	37	7	6441553	6441553	Missense_Mutation	SNP	A	G	3	62	c.343A>G	c.(343-345)ACT>GCT	p.T115A
Pat_59	Pre-Treatment	AGR2	10551	37	7	16841300	16841300	Missense_Mutation	SNP	G	A	5	175	c.121C>T	c.(121-123)CCC>TCC	p.P41S
Pat_59	Pre-Treatment	CCDC129	223075	37	7	31617722	31617722	Missense_Mutation	SNP	G	A	4	5	c.844G>A	c.(844-846)GAA>AAA	p.E282K
Pat_59	Pre-Treatment	CCDC129	223075	37	7	31692421	31692421	Missense_Mutation	SNP	A	G	4	99	c.3113A>G	c.(3112-3114)AAG>AGG	p.K1038R
Pat_59	Pre-Treatment	TXNDC3	51314	37	7	37916531	37916531	Missense_Mutation	SNP	G	A	9	26	c.916G>A	c.(916-918)GAT>AAT	p.D306N
Pat_59	Pre-Treatment	AEBP1	165	37	7	44153237	44153237	Missense_Mutation	SNP	C	T	4	126	c.2854C>T	c.(2854-2856)CGC>TGC	p.R952C
Pat_59	Pre-Treatment	ABCA13	154664	37	7	48314320	48314320	Missense_Mutation	SNP	G	A	4	111	c.5057G>A	c.(5056-5058)AGT>AAT	p.S1686N
Pat_59	Pre-Treatment	SPDYE5	442590	37	7	75130942	75130942	Missense_Mutation	SNP	C	T	7	297	c.817C>T	c.(817-819)CGG>TGG	p.R273W
Pat_59	Pre-Treatment	SPDYE5	442590	37	7	75130958	75130958	Missense_Mutation	SNP	G	A	7	237	c.833G>A	c.(832-834)CGT>CAT	p.R278H
Pat_59	Pre-Treatment	DTX2	113878	37	7	76112200	76112200	Missense_Mutation	SNP	G	A	5	196	c.644G>A	c.(643-645)CGC>CAC	p.R215H
Pat_59	Pre-Treatment	SEMA3C	10512	37	7	80374233	80374233	Missense_Mutation	SNP	T	C	4	133	c.2233A>G	c.(2233-2235)AGG>GGG	p.R745G
Pat_59	Pre-Treatment	KIAA1324L	222223	37	7	86542393	86542393	Missense_Mutation	SNP	G	A	18	51	c.1859C>T	c.(1858-1860)CCC>CTC	p.P620L
Pat_59	Pre-Treatment	DBF4	10926	37	7	87507538	87507538	Missense_Mutation	SNP	G	A	4	93	c.217G>A	c.(217-219)GGG>AGG	p.G73R
Pat_59	Pre-Treatment	CYP51A1	1595	37	7	91753148	91753148	Missense_Mutation	SNP	G	A	3	54	c.790C>T	c.(790-792)CGG>TGG	p.R264W
Pat_59	Pre-Treatment	CALCR	799	37	7	93101770	93101770	Missense_Mutation	SNP	C	T	36	130	c.400G>A	c.(400-402)GGT>AGT	p.G134S
Pat_59	Pre-Treatment	COL1A2	1278	37	7	94056318	94056318	Splice_Site	SNP	A	G	3	56	c.3106_splice	c.e47-2	.G1036_splice
Pat_59	Pre-Treatment	ZAN	7455	37	7	100349941	100349941	Missense_Mutation	SNP	C	T	8	256	c.2213C>T	c.(2212-2214)CCC>CTC	p.P738L

Pat_59	Pre-Treatment	MUC17	140453	37	7	100674946	100674946	Missense_Mutation	SNP	G	T	4	74	c.249G>T	c.(247-249)TTG>TTT	p.L83F
Pat_59	Pre-Treatment	LRRC17	10234	37	7	102580006	102580006	Missense_Mutation	SNP	G	A	4	136	c.902G>A	c.(901-903)AGC>AAC	p.S301N
Pat_59	Pre-Treatment	SLC26A5	375611	37	7	103038448	103038448	Missense_Mutation	SNP	G	A	5	153	c.902C>T	c.(901-903)ACT>ATT	p.T301I
Pat_59	Pre-Treatment	CFTR	1080	37	7	117232649	117232650	Missense_Mutation	DNP	AG	GA	14	36	.2428_2429AG>G	c.(2428-2430)AGA>GAA	p.R810E
Pat_59	Pre-Treatment	RBM28	55131	37	7	127953323	127953323	Missense_Mutation	SNP	G	A	5	114	c.2050C>T	c.(2050-2052)CGG>TGG	p.R684W
Pat_59	Pre-Treatment	MEST	4232	37	7	130142537	130142537	Missense_Mutation	SNP	G	A	4	89	c.802G>A	c.(802-804)GCT>ACT	p.A268T
Pat_59	Pre-Treatment	BRAF	673	37	7	140453136	140453136	Missense_Mutation	SNP	A	T	23	83	c.1799T>A	c.(1798-1800)GTG>GAG	p.V600E
Pat_59	Pre-Treatment	GBX1	2636	37	7	150864214	150864214	Missense_Mutation	SNP	C	T	3	17	c.422G>A	c.(421-423)GGC>GAC	p.G141D
Pat_59	Pre-Treatment	NOM1	64434	37	7	156743173	156743173	Missense_Mutation	SNP	G	A	4	91	c.742G>A	c.(742-744)GAA>AAA	p.E248K
Pat_59	Pre-Treatment	DLGAP2	9228	37	8	1645447	1645447	Missense_Mutation	SNP	G	A	4	109	c.2691G>A	c.(2689-2691)ATG>ATA	p.M897I
Pat_59	Pre-Treatment	PHYHIP	9796	37	8	22084462	22084462	Missense_Mutation	SNP	C	T	4	61	c.242G>A	c.(241-243)CGC>CAC	p.R81H
Pat_59	Pre-Treatment	BIN3	55909	37	8	22481537	22481537	Missense_Mutation	SNP	C	T	3	35	c.506G>A	c.(505-507)CGG>CAG	p.R169Q
Pat_59	Pre-Treatment	PTK2B	2185	37	8	27293298	27293298	Nonsense_Mutation	SNP	C	T	5	170	c.1231C>T	c.(1231-1233)CGA>TGA	p.R411*
Pat_59	Pre-Treatment	RB1CC1	9821	37	8	53573822	53573822	Missense_Mutation	SNP	G	A	4	46	c.1378C>T	c.(1378-1380)CTT>TTT	p.L460F
Pat_59	Pre-Treatment	C8orf34	116328	37	8	69688655	69688655	Missense_Mutation	SNP	G	A	5	56	c.1168G>A	c.(1168-1170)GGA>AGA	p.G390R
Pat_59	Pre-Treatment	ZFHX4	79776	37	8	77616870	77616870	Missense_Mutation	SNP	G	T	4	35	c.547G>T	c.(547-549)GCA>TCA	p.A183S
Pat_59	Pre-Treatment	SNTB1	6641	37	8	121823555	121823555	Missense_Mutation	SNP	C	T	5	194	c.529G>A	c.(529-531)GTG>ATG	p.V177M
Pat_59	Pre-Treatment	PHF20L1	51105	37	8	133848943	133848943	Missense_Mutation	SNP	G	A	4	76	c.2068G>A	c.(2068-2070)GAG>AAG	p.E690K
Pat_59	Pre-Treatment	SLC39A4	55630	37	8	145640420	145640420	Missense_Mutation	SNP	C	T	4	42	c.742G>A	c.(742-744)GCC>ACC	p.A248T
Pat_59	Pre-Treatment	PPP1R16A	84988	37	8	145726954	145726954	Missense_Mutation	SNP	C	T	2	0	c.1255C>T	c.(1255-1257)CCA>TCA	p.P419S
Pat_59	Pre-Treatment	RECQL4	9401	37	8	145741409	145741409	Missense_Mutation	SNP	C	T	3	23	c.1094G>A	c.(1093-1095)CGG>CAG	p.R365Q
Pat_59	Pre-Treatment	VLDLR	7436	37	9	2650433	2650433	Missense_Mutation	SNP	C	A	4	57	c.2168C>A	c.(2167-2169)CCA>CAA	p.P723Q
Pat_59	Pre-Treatment	GLIS3	169792	37	9	4117892	4117892	Missense_Mutation	SNP	C	T	4	55	c.1121G>A	c.(1120-1122)CGC>CAC	p.R374H
Pat_59	Pre-Treatment	PTPRD	5789	37	9	8517925	8517925	Missense_Mutation	SNP	G	A	22	62	c.1466C>T	c.(1465-1467)TCT>TTT	p.S489F
Pat_59	Pre-Treatment	ADAMTSL1	92949	37	9	18905865	18905865	Nonsense_Mutation	SNP	C	A	4	15	c.4937C>A	c.(4936-4938)TCA>TAA	p.S1646*
Pat_59	Pre-Treatment	SLC24A2	25769	37	9	19786503	19786503	Missense_Mutation	SNP	G	T	20	55	c.362C>A	c.(361-363)CCG>CAG	p.P121Q
Pat_59	Pre-Treatment	TAF1L	138474	37	9	32632916	32632916	Missense_Mutation	SNP	G	A	5	137	c.2662C>T	c.(2662-2664)CGT>TGT	p.R888C
Pat_59	Pre-Treatment	NFX1	4799	37	9	33318740	33318740	Missense_Mutation	SNP	G	A	5	200	c.1600G>A	c.(1600-1602)GGC>AGC	p.G534S
Pat_59	Pre-Treatment	KIAA1045	23349	37	9	34977113	34977113	Missense_Mutation	SNP	C	T	3	37	c.883C>T	c.(883-885)CGG>TGG	p.R295W
Pat_59	Pre-Treatment	TLN1	7094	37	9	35706812	35706812	Missense_Mutation	SNP	C	T	4	72	c.5041G>A	c.(5041-5043)GCT>ACT	p.A1681T
Pat_59	Pre-Treatment	APBA1	320	37	9	72067109	72067109	Missense_Mutation	SNP	C	A	4	87	c.1897G>T	c.(1897-1899)GAC>TAC	p.D633Y
Pat_59	Pre-Treatment	CDC14B	8555	37	9	99296748	99296748	Missense_Mutation	SNP	C	T	4	48	c.704G>A	c.(703-705)AGA>AAA	p.R235K
Pat_59	Pre-Treatment	SMC2	10592	37	9	106880657	106880657	Splice_Site	SNP	G	A	4	45	c.1996_splice	c.e15+1	p.G666_splice
Pat_59	Pre-Treatment	ACTL7B	10880	37	9	111617958	111617958	Missense_Mutation	SNP	C	T	4	72	c.253G>A	c.(253-255)GAG>AAG	p.E85K
Pat_59	Pre-Treatment	TNC	3371	37	9	117825309	117825309	Missense_Mutation	SNP	C	T	3	20	c.3920G>A	c.(3919-3921)AGC>AAC	p.S1307N
Pat_59	Pre-Treatment	LHX6	26468	37	9	124976570	124976570	Nonsense_Mutation	SNP	G	A	3	18	c.688C>T	c.(688-690)CAG>TAG	p.Q230*
Pat_59	Pre-Treatment	OR1B1	347169	37	9	125391515	125391515	Missense_Mutation	SNP	C	A	3	32	c.300G>T	c.(298-300)TTG>TTT	p.L100F
Pat_59	Pre-Treatment	GTF3C5	9328	37	9	135929329	135929329	Missense_Mutation	SNP	G	A	3	48	c.988G>A	c.(988-990)GGT>AGT	p.G330S
Pat_59	Pre-Treatment	SURF1	6834	37	9	136221717	136221717	Missense_Mutation	SNP	G	A	4	104	c.202C>T	c.(202-204)CTC>TTC	p.L68F
Pat_59	Pre-Treatment	COL5A1	1289	37	9	137658300	137658300	Missense_Mutation	SNP	G	A	10	36	c.2089G>A	c.(2089-2091)GGT>AGT	p.G697S
Pat_59	Pre-Treatment	ZBED1	9189	37	X	2408758	2408758	Missense_Mutation	SNP	C	T	4	116	c.3G>A	c.(1-3)ATG>ATA	p.M1I
Pat_59	Pre-Treatment	SYAP1	94056	37	X	16753433	16753433	Missense_Mutation	SNP	G	A	3	43	c.259G>A	c.(259-261)GTA>ATA	p.V87I
Pat_59	Pre-Treatment	RBBP7	5931	37	X	16870242	16870242	Missense_Mutation	SNP	G	A	4	122	c.967C>T	c.(967-969)CAC>TAC	p.H323Y
Pat_59	Pre-Treatment	ZFX	7543	37	X	24229038	24229038	Missense_Mutation	SNP	G	A	4	66	c.1963G>A	c.(1963-1965)GTT>ATT	p.V655I
Pat_59	Pre-Treatment	FAM48B1	100130302	37	X	24382867	24382867	Missense_Mutation	SNP	C	A	3	35	c.1990C>A	c.(1990-1992)CAG>AAG	p.Q664K
Pat_59	Pre-Treatment	USP11	8237	37	X	47092360	47092360	Missense_Mutation	SNP	G	A	4	69	c.47G>A	c.(46-48)CGG>CAG	p.R16Q
Pat_59	Pre-Treatment	TAF1	6872	37	X	70612758	70612758	Missense_Mutation	SNP	G	A	4	103	c.2962G>A	c.(2962-2964)GTG>ATG	p.V988M

Pat_59	Pre-Treatment	ACRC	93953	37	X	70823930	70823931	Missense_Mutation	DNP	GC	AG	7	97	c.803_804GC>AG	c.(802-804)AGC>AAG	p.S268K
Pat_59	Pre-Treatment	ATRX	546	37	X	76890195	76890196	Splice_Site	DNP	CT	AA	6	126	c.4700_splice	c.e17-1	p.G1567_splice
Pat_59	Pre-Treatment	BTK	695	37	X	100624998	100624998	Missense_Mutation	SNP	G	T	4	46	c.379C>A	c.(379-381)CAG>AAG	p.Q127K
Pat_59	Pre-Treatment	COL4A6	1288	37	X	107462945	107462945	Missense_Mutation	SNP	C	A	4	136	c.310G>T	c.(310-312)GGC>TGC	p.G104C
Pat_59	Pre-Treatment	MAGEC1	9947	37	X	140993747	140993747	Missense_Mutation	SNP	C	T	4	129	c.557C>T	c.(556-558)ACT>ATT	p.T186I
Pat_59	Pre-Treatment	IDS	3423	37	X	148564603	148564603	Nonsense_Mutation	SNP	G	A	4	67	c.1327C>T	c.(1327-1329)CGA>TGA	p.R443*
Pat_59	Pre-Treatment	IDS	3423	37	X	148577978	148577978	Missense_Mutation	SNP	G	A	4	132	c.778C>T	c.(778-780)CCC>TCC	p.P260S
Pat_59	Pre-Treatment	TREX2	11219	37	X	152710323	152710323	Nonsense_Mutation	SNP	G	T	2	0	c.692C>A	c.(691-693)TCA>TAA	p.S231*
Pat_59	Pre-Treatment	OPN1LW	5956	37	X	153418523	153418523	Missense_Mutation	SNP	G	T	4	57	c.520G>T	c.(520-522)GCC>TCC	p.A174S
Pat_59	Pre-Treatment	LAGE3	8270	37	X	153706299	153706299	Missense_Mutation	SNP	G	A	26	30	c.416C>T	c.(415-417)CCC>CTC	p.P139L
Pat_59	Pre-Treatment	ZFY	7544	37	Y	2847907	2847907	Missense_Mutation	SNP	G	A	4	104	c.2279G>A	c.(2278-2280)CGG>CAG	p.R760Q
Pat_59	Post-Resistance	CPSF3L	54973	37	1	1254829	1254829	Missense_Mutation	SNP	C	A	4	66	c.276G>T	c.(274-276)ATG>ATT	p.M92I
Pat_59	Post-Resistance	GNB1	2782	37	1	1721893	1721893	Nonsense_Mutation	SNP	G	A	4	133	c.640C>T	c.(640-642)CGA>TGA	p.R214*
Pat_59	Post-Resistance	PANK4	55229	37	1	2442805	2442805	Missense_Mutation	SNP	G	A	21	32	c.1805C>T	c.(1804-1806)TCC>TTC	p.S602F
Pat_59	Post-Resistance	KIAA0562	9731	37	1	3768955	3768955	Missense_Mutation	SNP	C	T	10	56	c.17G>A	c.(16-18)GGA>GAA	p.G6E
Pat_59	Post-Resistance	ACOT7	11332	37	1	6387452	6387452	Missense_Mutation	SNP	C	T	6	33	c.562G>A	c.(562-564)GAG>AAG	p.E188K
Pat_59	Post-Resistance	H6PD	9563	37	1	9305201	9305201	Missense_Mutation	SNP	C	T	3	26	c.208C>T	c.(208-210)CCC>TCC	p.P70S
Pat_59	Post-Resistance	KIF1B	23095	37	1	10434405	10434405	Missense_Mutation	SNP	C	T	45	214	c.4978C>T	c.(4978-4980)CCC>TCC	p.P1660S
Pat_59	Post-Resistance	CASP9	842	37	1	15844737	15844737	Missense_Mutation	SNP	C	T	13	46	c.286G>A	c.(286-288)GCA>ACA	p.A96T
Pat_59	Post-Resistance	PINK1	65018	37	1	20975090	20975090	Missense_Mutation	SNP	G	A	6	28	c.1216G>A	c.(1216-1218)GAT>AAT	p.D406N
Pat_59	Post-Resistance	USP48	84196	37	1	22021632	22021632	Missense_Mutation	SNP	C	T	4	106	c.2810G>A	c.(2809-2811)CGA>CAA	p.R937Q
Pat_59	Post-Resistance	SRRM1	10250	37	1	24996715	24996715	Missense_Mutation	SNP	C	T	21	217	c.2309C>T	c.(2308-2310)CCC>CTC	p.P770L
Pat_59	Post-Resistance	SYF2	25949	37	1	25555539	25555539	Missense_Mutation	SNP	C	T	16	133	c.208G>A	c.(208-210)GCC>ACC	p.A70T
Pat_59	Post-Resistance	SEPN1	57190	37	1	26135586	26135586	Missense_Mutation	SNP	G	A	14	155	c.817G>A	c.(817-819)GGA>AGA	p.G273R
Pat_59	Post-Resistance	NR0B2	8431	37	1	27238482	27238482	Missense_Mutation	SNP	C	T	5	54	c.628G>A	c.(628-630)GCC>ACC	p.A210T
Pat_59	Post-Resistance	YTHDF2	51441	37	1	29069585	29069585	Missense_Mutation	SNP	C	T	5	168	c.803C>T	c.(802-804)CCG>CTG	p.P268L
Pat_59	Post-Resistance	COL16A1	1307	37	1	32145259	32145259	Missense_Mutation	SNP	C	T	4	82	c.2746G>A	c.(2746-2748)GGC>AGC	p.G916S
Pat_59	Post-Resistance	DCDC2B	149069	37	1	32677721	32677721	Missense_Mutation	SNP	C	T	13	53	c.446C>T	c.(445-447)TCC>TTC	p.S149F
Pat_59	Post-Resistance	KIAA1522	57648	37	1	33236474	33236474	Missense_Mutation	SNP	G	A	5	17	c.1517G>A	c.(1516-1518)GGT>GAT	p.G506D
Pat_59	Post-Resistance	YARS	8565	37	1	33248080	33248080	Missense_Mutation	SNP	G	A	17	69	c.967C>T	c.(967-969)CCA>TCA	p.P323S
Pat_59	Post-Resistance	NCDN	23154	37	1	36030828	36030828	Missense_Mutation	SNP	C	T	4	123	c.1754C>T	c.(1753-1755)GCT>GTT	p.A585V
Pat_59	Post-Resistance	MTF1	4520	37	1	38288344	38288344	Missense_Mutation	SNP	C	T	20	89	c.1216G>A	c.(1216-1218)GAT>AAT	p.D406N
Pat_59	Post-Resistance	RRAGC	64121	37	1	39322712	39322712	Missense_Mutation	SNP	C	T	11	125	c.280G>A	c.(280-282)GAA>AAA	p.E94K
Pat_59	Post-Resistance	MACF1	23499	37	1	39895717	39895717	Missense_Mutation	SNP	C	T	6	56	c.12427C>T	c.(12427-12429)CCC>TCC	p.P4143S
Pat_59	Post-Resistance	TRIT1	54802	37	1	40315926	40315926	Nonsense_Mutation	SNP	G	A	5	43	c.568C>T	c.(568-570)CAA>TAA	p.Q190*
Pat_59	Post-Resistance	HIVEP3	59269	37	1	41978888	41978888	Missense_Mutation	SNP	C	T	5	55	c.6004G>A	c.(6004-6006)GAA>AAA	p.E2002K
Pat_59	Post-Resistance	FOXJ3	22887	37	1	42671440	42671440	Missense_Mutation	SNP	G	A	7	113	c.623C>T	c.(622-624)ACT>ATT	p.T208I
Pat_59	Post-Resistance	PPIH	10465	37	1	43124913	43124913	Missense_Mutation	SNP	G	A	54	399	c.146G>A	c.(145-147)GGA>GAA	p.G49E
Pat_59	Post-Resistance	MAST2	23139	37	1	46473997	46473997	Missense_Mutation	SNP	G	A	10	32	c.932G>A	c.(931-933)AGT>AAT	p.S311N
Pat_59	Post-Resistance	TAL1	6886	37	1	47685450	47685450	Missense_Mutation	SNP	G	A	4	37	c.938C>T	c.(937-939)ACG>ATG	p.T313M
Pat_59	Post-Resistance	NRD1	4898	37	1	52279762	52279762	Splice_Site	SNP	C	T	8	61	c.1824_splice	c.e16-1	p.R608_splice
Pat_59	Post-Resistance	ORC1L	4998	37	1	52838991	52838991	Missense_Mutation	SNP	C	T	11	51	c.2448G>A	c.(2446-2448)ATG>ATA	p.M816I
Pat_59	Post-Resistance	ZCCHC11	23318	37	1	52991465	52991465	Missense_Mutation	SNP	C	T	9	197	c.488G>A	c.(487-489)GGA>GAA	p.G163E
Pat_59	Post-Resistance	CPT2	1376	37	1	53675977	53675977	Missense_Mutation	SNP	C	T	15	92	c.631C>T	c.(631-633)CCC>TCC	p.P211S
Pat_59	Post-Resistance	YIPF1	54432	37	1	54343997	54343997	Missense_Mutation	SNP	C	T	47	323	c.355G>A	c.(355-357)GAT>AAT	p.D119N
Pat_59	Post-Resistance	C1orf177	163747	37	1	55282783	55282783	Missense_Mutation	SNP	A	G	3	40	c.1172A>G	c.(1171-1173)GAC>GGC	p.D391G
Pat_59	Post-Resistance	USP24	23358	37	1	55562632	55562632	Missense_Mutation	SNP	C	T	4	29	c.5449G>A	c.(5449-5451)GAC>AAC	p.D1817N

Pat_59	Post-Resistance	C8B	732	37	1	57399008	57399008	Missense_Mutation	SNP	C	T	9	84	c.1552G>A	c.(1552-1554)GGA>AGA	p.G518R
Pat_59	Post-Resistance	OMA1	115209	37	1	59004511	59004511	Missense_Mutation	SNP	C	T	56	327	c.456G>A	c.(454-456)ATG>ATA	p.M152I
Pat_59	Post-Resistance	ATG4C	84938	37	1	63282440	63282440	Missense_Mutation	SNP	C	T	14	34	c.355C>T	c.(355-357)CTC>TTC	p.L119F
Pat_59	Post-Resistance	ALG6	29929	37	1	63862269	63862269	Splice_Site	SNP	G	A	8	78	c.167_splice	c.e3+1	p.W56_splice
Pat_59	Post-Resistance	C1orf173	127254	37	1	75055719	75055719	Missense_Mutation	SNP	G	A	5	15	c.1772C>T	c.(1771-1773)TCT>TTT	p.S591F
Pat_59	Post-Resistance	LHX8	431707	37	1	75626504	75626504	Missense_Mutation	SNP	C	T	26	195	c.995C>T	c.(994-996)GCT>GTT	p.A332V
Pat_59	Post-Resistance	SLC44A5	204962	37	1	75685021	75685021	Missense_Mutation	SNP	G	A	47	95	c.1187C>T	c.(1186-1188)GCG>GTG	p.A396V
Pat_59	Post-Resistance	LPHN2	23266	37	1	82408751	82408751	Missense_Mutation	SNP	G	A	13	77	c.496G>A	c.(496-498)GCT>ACT	p.A166T
Pat_59	Post-Resistance	ZNF644	84146	37	1	91403293	91403293	Missense_Mutation	SNP	C	T	37	304	c.3437G>A	c.(3436-3438)GGG>GAG	p.G1146E
Pat_59	Post-Resistance	CDC7	8317	37	1	91989627	91989627	Missense_Mutation	SNP	C	T	12	66	c.1360C>T	c.(1360-1362)CCA>TCA	p.P454S
Pat_59	Post-Resistance	TGFBR3	7049	37	1	92193265	92193265	Missense_Mutation	SNP	A	G	9	125	c.836T>C	c.(835-837)GTC>GCC	p.V279A
Pat_59	Post-Resistance	BCAR3	8412	37	1	94054952	94054952	Missense_Mutation	SNP	C	T	6	32	c.511G>A	c.(511-513)GAT>AAT	p.D171N
Pat_59	Post-Resistance	RTCD1	8634	37	1	100736150	100736150	Missense_Mutation	SNP	G	A	36	227	c.328G>A	c.(328-330)GTT>ATT	p.V110I
Pat_59	Post-Resistance	COL11A1	1301	37	1	103354313	103354313	Missense_Mutation	SNP	C	T	11	49	c.4520G>A	c.(4519-4521)GGT>GAT	p.G1507D
Pat_59	Post-Resistance	PHTF1	10745	37	1	114248697	114248697	Missense_Mutation	SNP	G	A	38	75	c.1486C>T	c.(1486-1488)CTT>TTT	p.L496F
Pat_59	Post-Resistance	VTCN1	79679	37	1	117753456	117753456	Missense_Mutation	SNP	G	A	35	46	c.22C>T	c.(22-24)CTC>TTC	p.L8F
Pat_59	Post-Resistance	WARS2	10352	37	1	119619172	119619172	Missense_Mutation	SNP	C	T	41	301	c.149G>A	c.(148-150)GGC>GAC	p.G50D
Pat_59	Post-Resistance	ITGA10	8515	37	1	145532152	145532152	Missense_Mutation	SNP	G	A	14	116	c.796G>A	c.(796-798)GAG>AAG	p.E266K
Pat_59	Post-Resistance	ARNT	405	37	1	150808813	150808813	Missense_Mutation	SNP	G	A	12	112	c.643C>T	c.(643-645)CCA>TCA	p.P215S
Pat_59	Post-Resistance	CELF3	11189	37	1	151681746	151681746	Missense_Mutation	SNP	C	T	19	119	c.356G>A	c.(355-357)GGG>GAG	p.G119E
Pat_59	Post-Resistance	THEM4	117145	37	1	151860798	151860798	Missense_Mutation	SNP	T	C	27	173	c.508A>G	c.(508-510)ATG>GTG	p.M170V
Pat_59	Post-Resistance	SPRR2D	6703	37	1	153012687	153012687	Missense_Mutation	SNP	G	A	50	188	c.136C>T	c.(136-138)CCA>TCA	p.P46S
Pat_59	Post-Resistance	UBAP2L	9898	37	1	154233541	154233541	Missense_Mutation	SNP	C	T	9	50	c.2752C>T	c.(2752-2754)CCG>TCG	p.P918S
Pat_59	Post-Resistance	AQP10	89872	37	1	154296128	154296128	Missense_Mutation	SNP	G	A	12	103	c.553G>A	c.(553-555)GTC>ATC	p.V185I
Pat_59	Post-Resistance	KCNN3	3782	37	1	154680622	154680622	Missense_Mutation	SNP	G	A	4	67	c.2026C>T	c.(2026-2028)CTC>TTC	p.L676F
Pat_59	Post-Resistance	RAG1AP1	55974	37	1	155108460	155108460	Missense_Mutation	SNP	G	A	8	35	c.73G>A	c.(73-75)GCC>ACC	p.A25T
Pat_59	Post-Resistance	ASH1L	55870	37	1	155313444	155313444	Nonsense_Mutation	SNP	G	A	3	77	c.8086C>T	c.(8086-8088)CGA>TGA	p.R2696*
Pat_59	Post-Resistance	ASH1L	55870	37	1	155348157	155348157	Missense_Mutation	SNP	G	A	42	120	c.6262C>T	c.(6262-6264)CTT>TTT	p.L2088F
Pat_59	Post-Resistance	GON4L	54856	37	1	155796738	155796738	Missense_Mutation	SNP	C	T	18	85	c.587G>A	c.(586-588)AGG>AAG	p.R196K
Pat_59	Post-Resistance	SMG5	23381	37	1	156233190	156233190	Missense_Mutation	SNP	G	A	26	139	c.2027C>T	c.(2026-2028)GCG>GTG	p.A676V
Pat_59	Post-Resistance	FCRL3	115352	37	1	157667544	157667544	Missense_Mutation	SNP	G	T	16	147	c.464C>A	c.(463-465)TCC>TAC	p.S155Y
Pat_59	Post-Resistance	DARC	2532	37	1	159175875	159175875	Missense_Mutation	SNP	G	A	4	19	c.646G>A	c.(646-648)GCC>ACC	p.A216T
Pat_59	Post-Resistance	PIGM	93183	37	1	160000565	160000565	Missense_Mutation	SNP	G	A	23	47	c.965C>T	c.(964-966)TCC>TTC	p.S322F
Pat_59	Post-Resistance	KCNJ9	3765	37	1	160054056	160054056	Nonsense_Mutation	SNP	G	A	5	5	c.236G>A	c.(235-237)TGG>TAG	p.W79*
Pat_59	Post-Resistance	VANGL2	57216	37	1	160394935	160394935	Missense_Mutation	SNP	G	A	4	45	c.1333G>A	c.(1333-1335)GGA>AGA	p.G445R
Pat_59	Post-Resistance	ITLN2	142683	37	1	160920963	160920963	Missense_Mutation	SNP	C	T	19	146	c.311G>A	c.(310-312)GGG>GAG	p.G104E
Pat_59	Post-Resistance	KLHDC9	126823	37	1	161069991	161069991	Missense_Mutation	SNP	G	A	34	152	c.1027G>A	c.(1027-1029)GTT>ATT	p.V343I
Pat_59	Post-Resistance	ALDH9A1	223	37	1	165649773	165649773	Missense_Mutation	SNP	G	A	42	237	c.740C>T	c.(739-741)CCC>CTC	p.P247L
Pat_59	Post-Resistance	POGK	57645	37	1	166810212	166810212	Missense_Mutation	SNP	C	T	34	173	c.19C>T	c.(19-21)CCT>TCT	p.P7S
Pat_59	Post-Resistance	F5	2153	37	1	169492544	169492544	Missense_Mutation	SNP	C	T	27	84	c.5939G>A	c.(5938-5940)GGT>GAT	p.G1980D
Pat_59	Post-Resistance	F5	2153	37	1	169495164	169495164	Missense_Mutation	SNP	T	G	44	278	c.5691A>C	c.(5689-5691)CAA>CAC	p.Q1897H
Pat_59	Post-Resistance	FMO3	2328	37	1	171072938	171072938	Missense_Mutation	SNP	G	A	27	232	c.145G>A	c.(145-147)GAG>AAG	p.E49K
Pat_59	Post-Resistance	FMO2	2327	37	1	171173122	171173122	Missense_Mutation	SNP	G	A	5	134	c.746G>A	c.(745-747)CGA>CAA	p.R249Q
Pat_59	Post-Resistance	C1orf9	51430	37	1	172558514	172558514	Missense_Mutation	SNP	G	A	23	188	c.2273G>A	c.(2272-2274)GGA>GAA	p.G758E
Pat_59	Post-Resistance	SLC9A11	284525	37	1	173486836	173486836	Missense_Mutation	SNP	C	T	15	75	c.2747G>A	c.(2746-2748)AGT>AAT	p.S916N
Pat_59	Post-Resistance	RASAL2	9462	37	1	178421618	178421618	Nonsense_Mutation	SNP	C	T	17	161	c.1396C>T	c.(1396-1398)CAA>TAA	p.Q466*
Pat_59	Post-Resistance	CACNA1E	777	37	1	181548282	181548282	Missense_Mutation	SNP	G	T	5	105	c.691G>T	c.(691-693)GCC>TCC	p.A231S

Pat_59	Post-Resistance	RNASEL	6041	37	1	182555367	182555367	Missense_Mutation	SNP	C	T	10	21	c.575G>A	c.(574-576)GGG>GAG	p.G192E
Pat_59	Post-Resistance	NMNAT2	23057	37	1	183253914	183253914	Missense_Mutation	SNP	C	T	5	100	c.460G>A	c.(460-462)GGG>AGG	p.G154R
Pat_59	Post-Resistance	RNF2	6045	37	1	185067424	185067424	Missense_Mutation	SNP	G	A	8	142	c.685G>A	c.(685-687)GTA>ATA	p.V229I
Pat_59	Post-Resistance	PRG4	10216	37	1	186276260	186276260	Missense_Mutation	SNP	C	T	13	64	c.1409C>T	c.(1408-1410)ACC>ATC	p.T470I
Pat_59	Post-Resistance	CFHR4	10877	37	1	196887342	196887342	Missense_Mutation	SNP	C	T	11	25	c.802C>T	c.(802-804)CCA>TCA	p.P268S
Pat_59	Post-Resistance	CFHR5	81494	37	1	196946838	196946838	Missense_Mutation	SNP	C	T	36	226	c.44C>T	c.(43-45)ACT>ATT	p.T15I
Pat_59	Post-Resistance	CRB1	23418	37	1	197398703	197398703	Missense_Mutation	SNP	C	T	15	53	c.2801C>T	c.(2800-2802)CCT>CTT	p.P934L
Pat_59	Post-Resistance	CRB1	23418	37	1	197446894	197446894	Missense_Mutation	SNP	C	G	9	38	c.4106C>G	c.(4105-4107)ACC>AGC	p.T1369S
Pat_59	Post-Resistance	KDM5B	10765	37	1	202702600	202702600	Missense_Mutation	SNP	C	T	4	112	c.3838G>A	c.(3838-3840)GAT>AAT	p.D1280N
Pat_59	Post-Resistance	ELK4	2005	37	1	205585691	205585691	Missense_Mutation	SNP	C	T	10	91	c.1279G>A	c.(1279-1281)GAC>AAC	p.D427N
Pat_59	Post-Resistance	FCAMR	83953	37	1	207139119	207139119	Missense_Mutation	SNP	G	A	4	15	c.254C>T	c.(253-255)GCC>GTC	p.A85V
Pat_59	Post-Resistance	IRF6	3664	37	1	209968653	209968653	Missense_Mutation	SNP	G	A	26	128	c.490C>T	c.(490-492)CCC>TCC	p.P164S
Pat_59	Post-Resistance	TRAF5	7188	37	1	211529764	211529764	Missense_Mutation	SNP	G	A	4	134	c.332G>A	c.(331-333)AGC>AAC	p.S111N
Pat_59	Post-Resistance	PTPN14	5784	37	1	214556719	214556719	Missense_Mutation	SNP	C	T	8	86	c.2479G>A	c.(2479-2481)GAG>AAG	p.E827K
Pat_59	Post-Resistance	USH2A	7399	37	1	216243481	216243481	Missense_Mutation	SNP	G	A	22	122	c.6011C>T	c.(6010-6012)TCT>TTT	p.S2004F
Pat_59	Post-Resistance	USH2A	7399	37	1	216348812	216348812	Missense_Mutation	SNP	A	G	4	54	c.4409T>C	c.(4408-4410)CTG>CCG	p.L1470P
Pat_59	Post-Resistance	RAB3GAP2	25782	37	1	220326699	220326699	Missense_Mutation	SNP	G	A	18	141	c.3695C>T	c.(3694-3696)ACA>ATA	p.T1232I
Pat_59	Post-Resistance	ITPKB	3707	37	1	226923503	226923503	Missense_Mutation	SNP	C	T	5	28	c.1657G>A	c.(1657-1659)GAC>AAC	p.D553N
Pat_59	Post-Resistance	ZNF678	339500	37	1	227842427	227842427	Missense_Mutation	SNP	G	A	6	219	c.476G>A	c.(475-477)GGC>GAC	p.G159D
Pat_59	Post-Resistance	ZNF678	339500	37	1	227842544	227842544	Missense_Mutation	SNP	G	A	9	327	c.593G>A	c.(592-594)AGC>AAC	p.S198N
Pat_59	Post-Resistance	SNAP47	116841	37	1	227946773	227946773	Missense_Mutation	SNP	C	T	21	140	c.710C>T	c.(709-711)CCC>CTC	p.P237L
Pat_59	Post-Resistance	HIST3H3	8290	37	1	228612641	228612641	Missense_Mutation	SNP	C	T	4	121	c.386G>A	c.(385-387)CGC>CAC	p.R129H
Pat_59	Post-Resistance	LYST	1130	37	1	235922785	235922785	Missense_Mutation	SNP	C	T	27	219	c.6368G>A	c.(6367-6369)GGA>GAA	p.G2123E
Pat_59	Post-Resistance	MTR	4548	37	1	236959034	236959034	Missense_Mutation	SNP	C	T	21	105	c.31C>T	c.(31-33)CCC>TCC	p.P11S
Pat_59	Post-Resistance	OR2L2	26246	37	1	248201894	248201894	Missense_Mutation	SNP	G	A	9	87	c.325G>A	c.(325-327)GCA>ACA	p.A109T
Pat_59	Post-Resistance	FRMD4A	55691	37	10	13698668	13698668	Missense_Mutation	SNP	G	A	4	3	c.2921C>T	c.(2920-2922)ACC>ATC	p.T974I
Pat_59	Post-Resistance	RSU1	6251	37	10	16794558	16794558	Missense_Mutation	SNP	G	A	14	73	c.578C>T	c.(577-579)ACC>ATC	p.T193I
Pat_59	Post-Resistance	CUBN	8029	37	10	16975122	16975122	Nonsense_Mutation	SNP	G	A	4	123	c.6088C>T	c.(6088-6090)CGA>TGA	p.R2030*
Pat_59	Post-Resistance	MSRB2	22921	37	10	23399204	23399204	Missense_Mutation	SNP	G	A	40	91	c.253G>A	c.(253-255)GCA>ACA	p.A85T
Pat_59	Post-Resistance	KIAA1217	56243	37	10	24508644	24508644	Missense_Mutation	SNP	G	T	3	22	c.160G>T	c.(160-162)GGT>TGT	p.G54C
Pat_59	Post-Resistance	KIAA1217	56243	37	10	24809159	24809159	Missense_Mutation	SNP	G	A	45	64	c.2285G>A	c.(2284-2286)GGA>GAA	p.G762E
Pat_59	Post-Resistance	KIAA1217	56243	37	10	24820833	24820833	Missense_Mutation	SNP	C	T	4	67	c.3157C>T	c.(3157-3159)CGT>TGT	p.R1053C
Pat_59	Post-Resistance	MTPAP	55149	37	10	30625845	30625845	Missense_Mutation	SNP	G	A	44	144	c.667C>T	c.(667-669)CCA>TCA	p.P223S
Pat_59	Post-Resistance	KIF5B	3799	37	10	32307059	32307059	Missense_Mutation	SNP	G	A	36	64	c.2465C>T	c.(2464-2466)ACC>ATC	p.T822I
Pat_59	Post-Resistance	BMS1	9790	37	10	43289313	43289313	Missense_Mutation	SNP	C	T	30	67	c.1103C>T	c.(1102-1104)CCC>CTC	p.P368L
Pat_59	Post-Resistance	RBP3	5949	37	10	48388900	48388900	Missense_Mutation	SNP	T	C	2	2	c.1978A>G	c.(1978-1980)ACC>GCC	p.T660A
Pat_59	Post-Resistance	ZWINT	11130	37	10	58119898	58119898	Missense_Mutation	SNP	G	A	3	18	c.137C>T	c.(136-138)TCT>TTT	p.S46F
Pat_59	Post-Resistance	RUFY2	55680	37	10	70156634	70156634	Missense_Mutation	SNP	G	A	14	28	c.406C>T	c.(406-408)CCT>TCT	p.P136S
Pat_59	Post-Resistance	C10orf27	219793	37	10	72531206	72531206	Missense_Mutation	SNP	C	T	3	26	c.982G>A	c.(982-984)GAA>AAA	p.E328K
Pat_59	Post-Resistance	HECTD2	143279	37	10	93242749	93242749	Missense_Mutation	SNP	C	T	4	80	c.737C>T	c.(736-738)ACG>ATG	p.T246M
Pat_59	Post-Resistance	PIPSL	266971	37	10	95719566	95719566	Missense_Mutation	SNP	G	A	5	43	c.1588C>T	c.(1588-1590)CCT>TCT	p.P530S
Pat_59	Post-Resistance	TLL2	7093	37	10	98188425	98188425	Missense_Mutation	SNP	C	T	15	36	c.601G>A	c.(601-603)GAG>AAG	p.E201K
Pat_59	Post-Resistance	DHDPSL	112817	37	10	99359537	99359537	Missense_Mutation	SNP	C	T	3	30	c.569C>T	c.(568-570)CCG>CTG	p.P190L
Pat_59	Post-Resistance	C10orf2	56652	37	10	102750720	102750720	Missense_Mutation	SNP	G	A	23	64	c.1687G>A	c.(1687-1689)GAT>AAT	p.D563N
Pat_59	Post-Resistance	POLL	27343	37	10	103347107	103347107	Missense_Mutation	SNP	C	T	13	59	c.11G>A	c.(10-12)AGG>AAG	p.R4K
Pat_59	Post-Resistance	TAF5	6877	37	10	105147086	105147086	Missense_Mutation	SNP	G	T	4	100	c.1984G>T	c.(1984-1986)GTA>TTA	p.V662L
Pat_59	Post-Resistance	CTBP2	1488	37	10	126678107	126678107	Missense_Mutation	SNP	C	T	46	180	c.1318G>A	c.(1318-1320)GAG>AAG	p.E440K

Pat_59	Post-Resistance	DOCK1	1793	37	10	128817004	128817004	Missense_Mutation	SNP	G	A	6	28	c.1169G>A	c.(1168-1170)GGA>GAA	p.G390E
Pat_59	Post-Resistance	FAM196A	642938	37	10	128974017	128974017	Missense_Mutation	SNP	G	A	3	4	c.643C>T	c.(643-645)CCT>TCT	p.P215S
Pat_59	Post-Resistance	INPP5A	3632	37	10	134579283	134579283	Missense_Mutation	SNP	G	A	8	12	c.910G>A	c.(910-912)GAG>AAG	p.E304K
Pat_59	Post-Resistance	AP2A2	161	37	11	988657	988657	Missense_Mutation	SNP	G	A	8	43	c.1237G>A	c.(1237-1239)GAG>AAG	p.E413K
Pat_59	Post-Resistance	MUC5B	727897	37	11	1271471	1271471	Missense_Mutation	SNP	G	C	3	41	c.14780G>C	c.(14779-14781)AGC>ACC	p.S4927T
Pat_59	Post-Resistance	MUC5B	727897	37	11	1271474	1271474	Missense_Mutation	SNP	C	T	10	31	c.14783C>T	c.(14782-14784)ACT>ATT	p.T4928I
Pat_59	Post-Resistance	KRTAP5-4	387267	37	11	1642992	1642992	Missense_Mutation	SNP	C	T	4	53	c.470G>A	c.(469-471)TGT>TAT	p.C157Y
Pat_59	Post-Resistance	TRIM68	55128	37	11	4621621	4621621	Missense_Mutation	SNP	G	A	5	35	c.1343C>T	c.(1342-1344)ACT>ATT	p.T448I
Pat_59	Post-Resistance	OR51L1	119682	37	11	5020900	5020900	Missense_Mutation	SNP	A	G	3	84	c.688A>G	c.(688-690)ATT>GTT	p.I230V
Pat_59	Post-Resistance	OR51Q1	390061	37	11	5443576	5443576	Missense_Mutation	SNP	C	T	31	211	c.146C>T	c.(145-147)ACT>ATT	p.T49I
Pat_59	Post-Resistance	ARNTL	406	37	11	13402785	13402785	Missense_Mutation	SNP	C	T	18	112	c.1601C>T	c.(1600-1602)TCT>TTT	p.S534F
Pat_59	Post-Resistance	BBOX1	8424	37	11	27137043	27137043	Missense_Mutation	SNP	C	T	29	146	c.578C>T	c.(577-579)GCT>GTT	p.A193V
Pat_59	Post-Resistance	CKAP5	9793	37	11	46792348	46792348	Missense_Mutation	SNP	C	T	3	28	c.3176G>A	c.(3175-3177)GGG>GAG	p.G1059E
Pat_59	Post-Resistance	PSMC3	5702	37	11	47444392	47444392	Missense_Mutation	SNP	C	T	6	172	c.724G>A	c.(724-726)GCA>ACA	p.A242T
Pat_59	Post-Resistance	OR4C46	119749	37	11	51515699	51515699	Missense_Mutation	SNP	G	A	21	179	c.418G>A	c.(418-420)GCC>ACC	p.A140T
Pat_59	Post-Resistance	OR4A16	81327	37	11	55110828	55110828	Missense_Mutation	SNP	C	T	14	80	c.152C>T	c.(151-153)CCC>CTC	p.P51L
Pat_59	Post-Resistance	OR8H2	390151	37	11	55873186	55873186	Missense_Mutation	SNP	T	C	4	117	c.668T>C	c.(667-669)TTT>TCT	p.F223S
Pat_59	Post-Resistance	OR5M1	390168	37	11	56380086	56380086	Missense_Mutation	SNP	A	G	36	269	c.893T>C	c.(892-894)ATC>ACC	p.I298T
Pat_59	Post-Resistance	PRG3	10394	37	11	57147199	57147199	Missense_Mutation	SNP	C	T	12	31	c.143G>A	c.(142-144)AGA>AAA	p.R48K
Pat_59	Post-Resistance	SLC43A3	29015	37	11	57182201	57182201	Missense_Mutation	SNP	C	T	43	242	c.947G>A	c.(946-948)AGC>AAC	p.S316N
Pat_59	Post-Resistance	OR5A2	219981	37	11	59189855	59189855	Missense_Mutation	SNP	G	A	10	57	c.572C>T	c.(571-573)TCT>TTT	p.S191F
Pat_59	Post-Resistance	MTA2	9219	37	11	62361511	62361511	Missense_Mutation	SNP	C	T	4	62	c.1843G>A	c.(1843-1845)GCC>ACC	p.A615T
Pat_59	Post-Resistance	MTA2	9219	37	11	62363982	62363982	Missense_Mutation	SNP	C	T	7	32	c.905G>A	c.(904-906)AGC>AAC	p.S302N
Pat_59	Post-Resistance	GANAB	23193	37	11	62397390	62397390	Missense_Mutation	SNP	C	T	4	103	c.1633G>A	c.(1633-1635)GAA>AAA	p.E545K
Pat_59	Post-Resistance	C11orf48	79081	37	11	62435196	62435196	Missense_Mutation	SNP	G	A	31	174	c.337C>T	c.(337-339)CCT>TCT	p.P113S
Pat_59	Post-Resistance	TAF6L	10629	37	11	62554695	62554695	Missense_Mutation	SNP	C	T	3	28	c.1796C>T	c.(1795-1797)CCC>CTC	p.P599L
Pat_59	Post-Resistance	MACROD1	28992	37	11	63919836	63919836	Missense_Mutation	SNP	G	A	4	116	c.328C>T	c.(328-330)CGG>TGG	p.R110W
Pat_59	Post-Resistance	NUDT22	84304	37	11	63994167	63994167	Missense_Mutation	SNP	G	A	3	30	c.43G>A	c.(43-45)GGC>AGC	p.G15S
Pat_59	Post-Resistance	PPP2R5B	5526	37	11	64699040	64699040	Missense_Mutation	SNP	G	A	4	24	c.955G>A	c.(955-957)GGG>AGG	p.G319R
Pat_59	Post-Resistance	SLC25A45	283130	37	11	65144469	65144469	Missense_Mutation	SNP	G	A	5	15	c.418C>T	c.(418-420)CCC>TCC	p.P140S
Pat_59	Post-Resistance	SIPA1	6494	37	11	65413818	65413818	Missense_Mutation	SNP	C	T	8	39	c.1390C>T	c.(1390-1392)CAC>TAC	p.H464Y
Pat_59	Post-Resistance	CFL1	1072	37	11	65622848	65622848	Missense_Mutation	SNP	C	T	9	50	c.460G>A	c.(460-462)GGG>AGG	p.G154R
Pat_59	Post-Resistance	EFEMP2	30008	37	11	65637616	65637616	Missense_Mutation	SNP	C	T	7	19	c.583G>A	c.(583-585)GGG>AGG	p.G195R
Pat_59	Post-Resistance	FOSL1	8061	37	11	65660406	65660406	Missense_Mutation	SNP	C	T	7	35	c.767G>A	c.(766-768)GGA>GAA	p.G256E
Pat_59	Post-Resistance	SPTBN2	6712	37	11	66456591	66456591	Missense_Mutation	SNP	C	T	3	10	c.6010G>A	c.(6010-6012)GAG>AAG	p.E2004K
Pat_59	Post-Resistance	GPR152	390212	37	11	67219036	67219036	Missense_Mutation	SNP	G	A	4	28	c.1160C>T	c.(1159-1161)ACA>ATA	p.T387I
Pat_59	Post-Resistance	C11orf51	25906	37	11	71822279	71822279	Missense_Mutation	SNP	G	A	42	240	c.44C>T	c.(43-45)ACT>ATT	p.T15I
Pat_59	Post-Resistance	PGM2L1	283209	37	11	74085531	74085531	Missense_Mutation	SNP	C	T	4	106	c.208G>A	c.(208-210)GCA>ACA	p.A70T
Pat_59	Post-Resistance	OR2AT4	341152	37	11	74799953	74799953	Missense_Mutation	SNP	G	A	23	75	c.806C>T	c.(805-807)GCT>GTT	p.A269V
Pat_59	Post-Resistance	PICALM	8301	37	11	85779847	85779847	Translation_Start_Site	SNP	C	T	4	18	c.-24G>A	c.(-26--22)GGGTG>GGATG	
Pat_59	Post-Resistance	NAALAD2	10003	37	11	89896741	89896741	Missense_Mutation	SNP	G	A	26	61	c.1234G>A	c.(1234-1236)GAT>AAT	p.D412N
Pat_59	Post-Resistance	PPP2R1B	5519	37	11	111624172	111624172	Missense_Mutation	SNP	C	T	8	61	c.1159G>A	c.(1159-1161)GAT>AAT	p.D387N
Pat_59	Post-Resistance	PHLDB1	23187	37	11	118498446	118498446	Missense_Mutation	SNP	C	T	13	60	c.907C>T	c.(907-909)CCA>TCA	p.P303S
Pat_59	Post-Resistance	TRIM29	23650	37	11	119993662	119993662	Missense_Mutation	SNP	C	A	23	53	c.1435G>T	c.(1435-1437)GGT>TGT	p.G479C
Pat_59	Post-Resistance	OR6X1	390260	37	11	123624496	123624496	Missense_Mutation	SNP	G	A	14	47	c.731C>T	c.(730-732)ACA>ATA	p.T244I
Pat_59	Post-Resistance	OR10G8	219869	37	11	123901131	123901131	Missense_Mutation	SNP	G	A	9	63	c.802G>A	c.(802-804)GAT>AAT	p.D268N
Pat_59	Post-Resistance	CCDC15	80071	37	11	124857828	124857828	Missense_Mutation	SNP	T	A	8	309	c.1706T>A	c.(1705-1707)GTT>GAT	p.V569D

Pat_59	Post-Resistance	ARHGAP32	9743	37	11	129062003	129062003	Missense_Mutation	SNP	C	T	42	246	c.91G>A	c.(91-93)GAG>AAG	p.E31K
Pat_59	Post-Resistance	SNX19	399979	37	11	130748328	130748328	Missense_Mutation	SNP	C	T	4	116	c.2968G>A	c.(2968-2970)GTC>ATC	p.V990I
Pat_59	Post-Resistance	KDM5A	5927	37	12	416913	416913	Missense_Mutation	SNP	G	A	8	47	c.3637C>T	c.(3637-3639)CCT>TCT	p.P1213S
Pat_59	Post-Resistance	WNK1	65125	37	12	995177	995177	Missense_Mutation	SNP	C	T	33	271	c.5207C>T	c.(5206-5208)ACC>ATC	p.T1736I
Pat_59	Post-Resistance	SCNN1A	6337	37	12	6457175	6457175	Missense_Mutation	SNP	G	A	3	2	c.1874C>T	c.(1873-1875)TCC>TTC	p.S625F
Pat_59	Post-Resistance	CD4	920	37	12	6927638	6927638	Missense_Mutation	SNP	G	A	8	37	c.1208G>A	c.(1207-1209)GGG>GAG	p.G403E
Pat_59	Post-Resistance	PEX5	5830	37	12	7354862	7354862	Missense_Mutation	SNP	G	A	14	137	c.668G>A	c.(667-669)GGC>GAC	p.G223D
Pat_59	Post-Resistance	CD163	9332	37	12	7632577	7632577	Missense_Mutation	SNP	G	A	5	49	c.3359C>T	c.(3358-3360)TCA>TTA	p.S1120L
Pat_59	Post-Resistance	CD163	9332	37	12	7639184	7639184	Missense_Mutation	SNP	C	T	21	201	c.2369G>A	c.(2368-2370)GGA>GAA	p.G790E
Pat_59	Post-Resistance	DUSP16	80824	37	12	12633232	12633232	Missense_Mutation	SNP	C	T	26	144	c.740G>A	c.(739-741)GGG>GAG	p.G247E
Pat_59	Post-Resistance	PDE6H	5149	37	12	15131013	15131013	Missense_Mutation	SNP	C	T	5	68	c.67C>T	c.(67-69)CCT>TCT	p.P23S
Pat_59	Post-Resistance	PLEKHA5	54477	37	12	19501339	19501339	Missense_Mutation	SNP	G	A	9	92	c.2407G>A	c.(2407-2409)GAT>AAT	p.D803N
Pat_59	Post-Resistance	IPO8	10526	37	12	30790023	30790023	Missense_Mutation	SNP	G	A	21	155	c.2588C>T	c.(2587-2589)CCC>CTC	p.P863L
Pat_59	Post-Resistance	IPO8	10526	37	12	30815347	30815347	Missense_Mutation	SNP	C	A	4	78	c.1669G>T	c.(1669-1671)GAT>TAT	p.D557Y
Pat_59	Post-Resistance	DDX11	1663	37	12	31256617	31256617	Missense_Mutation	SNP	T	C	3	95	c.2638T>C	c.(2638-2640)TGT>CGT	p.C880R
Pat_59	Post-Resistance	SFRS2IP	9169	37	12	46320935	46320935	Missense_Mutation	SNP	G	A	18	121	c.2549C>T	c.(2548-2550)TCC>TTC	p.S850F
Pat_59	Post-Resistance	PFKM	5213	37	12	48516628	48516628	Missense_Mutation	SNP	G	A	8	56	c.71G>A	c.(70-72)GGT>GAT	p.G24D
Pat_59	Post-Resistance	TROAP	10024	37	12	49724304	49724304	Missense_Mutation	SNP	G	A	7	30	c.1676G>A	c.(1675-1677)TGC>TAC	p.C559Y
Pat_59	Post-Resistance	FMNL3	91010	37	12	50048767	50048767	Missense_Mutation	SNP	C	T	13	92	c.886G>A	c.(886-888)GTA>ATA	p.V296I
Pat_59	Post-Resistance	TMBIM6	7009	37	12	50152016	50152016	Missense_Mutation	SNP	G	A	23	141	c.293G>A	c.(292-294)GGC>GAC	p.G98D
Pat_59	Post-Resistance	SLC4A8	9498	37	12	51890821	51890821	Missense_Mutation	SNP	G	T	13	57	c.2994G>T	c.(2992-2994)AAG>AAT	p.K998N
Pat_59	Post-Resistance	MFSD5	84975	37	12	53647883	53647883	Missense_Mutation	SNP	G	A	7	64	c.1264G>A	c.(1264-1266)GCA>ACA	p.A422T
Pat_59	Post-Resistance	AAAS	8086	37	12	53701392	53701392	Missense_Mutation	SNP	C	T	9	79	c.1522G>A	c.(1522-1524)GGT>AGT	p.G508S
Pat_59	Post-Resistance	KIAA0748	9840	37	12	55356244	55356244	Nonsense_Mutation	SNP	G	A	6	257	c.1438C>T	c.(1438-1440)CAG>TAG	p.Q480*
Pat_59	Post-Resistance	OR6C74	254783	37	12	55641912	55641912	Missense_Mutation	SNP	C	T	16	69	c.841C>T	c.(841-843)CCC>TCC	p.P281S
Pat_59	Post-Resistance	SLC39A5	283375	37	12	56628983	56628983	Missense_Mutation	SNP	C	T	25	128	c.677C>T	c.(676-678)CCT>CTT	p.P226L
Pat_59	Post-Resistance	NXPH4	11247	37	12	57619094	57619094	Missense_Mutation	SNP	G	A	32	166	c.491G>A	c.(490-492)GGA>GAA	p.G164E
Pat_59	Post-Resistance	TSPAN8	7103	37	12	71537987	71537987	Missense_Mutation	SNP	C	A	4	57	c.67G>T	c.(67-69)GGT>TGT	p.G23C
Pat_59	Post-Resistance	E2F7	144455	37	12	77440021	77440021	Nonsense_Mutation	SNP	C	T	4	54	c.626G>A	c.(625-627)TGG>TAG	p.W209*
Pat_59	Post-Resistance	E2F7	144455	37	12	77444361	77444361	Missense_Mutation	SNP	C	A	23	206	c.533G>T	c.(532-534)AGT>ATT	p.S178I
Pat_59	Post-Resistance	NR2C1	7181	37	12	95456346	95456346	Missense_Mutation	SNP	C	T	11	15	c.223G>A	c.(223-225)GAT>AAT	p.D75N
Pat_59	Post-Resistance	NEDD1	121441	37	12	97334304	97334304	Missense_Mutation	SNP	C	T	20	111	c.1235C>T	c.(1234-1236)CCT>CTT	p.P412L
Pat_59	Post-Resistance	UTP20	27340	37	12	101723079	101723079	Missense_Mutation	SNP	C	T	22	147	c.3269C>T	c.(3268-3270)CCT>CTT	p.P1090L
Pat_59	Post-Resistance	STAB2	55576	37	12	104031826	104031826	Missense_Mutation	SNP	C	T	29	215	c.742C>T	c.(742-744)CCT>TCT	p.P248S
Pat_59	Post-Resistance	HSP90B1	7184	37	12	104326111	104326111	Missense_Mutation	SNP	G	A	16	79	c.209G>A	c.(208-210)AGA>AAA	p.R70K
Pat_59	Post-Resistance	SSH1	54434	37	12	109186090	109186090	Missense_Mutation	SNP	C	T	4	73	c.1865G>A	c.(1864-1866)AGC>AAC	p.S622N
Pat_59	Post-Resistance	CUX2	23316	37	12	111758218	111758218	Missense_Mutation	SNP	C	T	6	38	c.2405C>T	c.(2404-2406)TCC>TTC	p.S802F
Pat_59	Post-Resistance	C12orf51	283450	37	12	112699205	112699205	Missense_Mutation	SNP	G	A	21	110	c.1481C>T	c.(1480-1482)GCC>GTC	p.A494V
Pat_59	Post-Resistance	DDX54	79039	37	12	113596795	113596795	Missense_Mutation	SNP	C	T	8	12	c.2533G>A	c.(2533-2535)GGT>AGT	p.G845S
Pat_59	Post-Resistance	TAOK3	51347	37	12	118682769	118682769	Missense_Mutation	SNP	G	A	4	89	c.122C>T	c.(121-123)GCT>GTT	p.A41V
Pat_59	Post-Resistance	DNAH10	196385	37	12	124323225	124323225	Missense_Mutation	SNP	C	T	7	72	c.4771C>T	c.(4771-4773)CAC>TAC	p.H1591Y
Pat_59	Post-Resistance	EP400	57634	37	12	132535158	132535158	Missense_Mutation	SNP	C	T	27	173	c.7352C>T	c.(7351-7353)CCC>CTC	p.P2451L
Pat_59	Post-Resistance	CHFR	55743	37	12	133454140	133454140	Splice_Site	SNP	C	T	8	40	c.233_splice	c.e3+1	p.S78_splice
Pat_59	Post-Resistance	ZMYM2	7750	37	13	20567697	20567697	Missense_Mutation	SNP	G	A	30	140	c.485G>A	c.(484-486)AGA>AAA	p.R162K
Pat_59	Post-Resistance	SACS	26278	37	13	23914203	23914203	Missense_Mutation	SNP	C	T	7	41	c.3812G>A	c.(3811-3813)AGA>AAA	p.R1271K
Pat_59	Post-Resistance	CENPJ	55835	37	13	25458298	25458298	Splice_Site	SNP	C	T	22	59	c.3703_splice	c.e15+1	p.E1235_splice
Pat_59	Post-Resistance	FAM123A	219287	37	13	25744557	25744557	Missense_Mutation	SNP	G	A	8	28	c.1201C>T	c.(1201-1203)CCC>TCC	p.P401S

Pat_59	Post-Resistance	NUPL1	9818	37	13	25882051	25882051	Missense_Mutation	SNP	C	T	30	128	c.215C>T	c.(214-216)CCT>CTT	p.P72L
Pat_59	Post-Resistance	FLT1	2321	37	13	28877458	28877458	Missense_Mutation	SNP	C	T	8	40	c.3863G>A	c.(3862-3864)AGC>AAC	p.S1288N
Pat_59	Post-Resistance	MTUS2	23281	37	13	29933465	29933465	Missense_Mutation	SNP	G	C	4	5	c.3002G>C	c.(3001-3003)CGT>CCT	p.R1001P
Pat_59	Post-Resistance	RXFP2	122042	37	13	32363320	32363320	Missense_Mutation	SNP	C	T	13	59	c.1135C>T	c.(1135-1137)CTT>TTT	p.L379F
Pat_59	Post-Resistance	FRY	10129	37	13	32698760	32698760	Missense_Mutation	SNP	G	A	7	37	c.577G>A	c.(577-579)GAC>AAC	p.D193N
Pat_59	Post-Resistance	FRY	10129	37	13	32759129	32759129	Missense_Mutation	SNP	G	A	39	225	c.3163G>A	c.(3163-3165)GAG>AAG	p.E1055K
Pat_59	Post-Resistance	BRCA2	675	37	13	32912789	32912789	Missense_Mutation	SNP	G	A	12	110	c.4297G>A	c.(4297-4299)GGG>AGG	p.G1433R
Pat_59	Post-Resistance	STARD13	90627	37	13	33704299	33704299	Missense_Mutation	SNP	G	A	3	43	c.515C>T	c.(514-516)CCG>CTG	p.P172L
Pat_59	Post-Resistance	SPG20	23111	37	13	36903605	36903605	Missense_Mutation	SNP	C	T	15	97	c.1058G>A	c.(1057-1059)AGA>AAA	p.R353K
Pat_59	Post-Resistance	LRCH1	23143	37	13	47303045	47303045	Missense_Mutation	SNP	G	A	16	88	c.1828G>A	c.(1828-1830)GTC>ATC	p.V610I
Pat_59	Post-Resistance	HTR2A	3356	37	13	47469692	47469692	Missense_Mutation	SNP	G	A	13	56	c.350C>T	c.(349-351)GCC>GTC	p.A117V
Pat_59	Post-Resistance	WDFY2	115825	37	13	52325544	52325544	Missense_Mutation	SNP	G	A	4	73	c.824G>A	c.(823-825)AGG>AAG	p.R275K
Pat_59	Post-Resistance	ATP7B	540	37	13	52511718	52511718	Missense_Mutation	SNP	C	T	7	43	c.3797G>A	c.(3796-3798)GGG>GAG	p.G1266E
Pat_59	Post-Resistance	PCDH17	27253	37	13	58299207	58299207	Missense_Mutation	SNP	G	A	15	92	c.3259G>A	c.(3259-3261)GAC>AAC	p.D1087N
Pat_59	Post-Resistance	DACH1	1602	37	13	72440354	72440354	Missense_Mutation	SNP	G	A	3	9	c.548C>T	c.(547-549)CCT>CTT	p.P183L
Pat_59	Post-Resistance	SCEL	8796	37	13	78133998	78133998	Missense_Mutation	SNP	G	A	5	246	c.221G>A	c.(220-222)AGG>AAG	p.R74K
Pat_59	Post-Resistance	DOCK9	23348	37	13	99550478	99550478	Missense_Mutation	SNP	C	T	4	15	c.1544G>A	c.(1543-1545)TGC>TAC	p.C515Y
Pat_59	Post-Resistance	COL4A1	1282	37	13	110821984	110821984	Missense_Mutation	SNP	C	T	12	38	c.3868G>A	c.(3868-3870)GGC>AGC	p.G1290S
Pat_59	Post-Resistance	TUBGCP3	10426	37	13	113210420	113210420	Missense_Mutation	SNP	G	A	11	89	c.667C>T	c.(667-669)CCC>TCC	p.P223S
Pat_59	Post-Resistance	RASA3	22821	37	13	114784340	114784340	Missense_Mutation	SNP	C	T	9	30	c.841G>A	c.(841-843)GGC>AGC	p.G281S
Pat_59	Post-Resistance	RASA3	22821	37	13	114817551	114817551	Missense_Mutation	SNP	C	T	3	33	c.253G>A	c.(253-255)GTT>ATT	p.V85I
Pat_59	Post-Resistance	P704P	641455	37	14	20020013	20020013	Missense_Mutation	SNP	G	C	4	218	c.208C>G	c.(208-210)CCC>GCC	p.P70A
Pat_59	Post-Resistance	SLC7A8	23428	37	14	23612350	23612350	Missense_Mutation	SNP	G	A	5	119	c.572C>T	c.(571-573)ACA>ATA	p.T191I
Pat_59	Post-Resistance	MYH6	4624	37	14	23855623	23855623	Missense_Mutation	SNP	C	T	3	35	c.4860G>A	c.(4858-4860)ATG>ATA	p.M1620I
Pat_59	Post-Resistance	TSSK4	283629	37	14	24677242	24677242	Missense_Mutation	SNP	G	A	18	50	c.877G>A	c.(877-879)GTG>ATG	p.V293M
Pat_59	Post-Resistance	G2E3	55632	37	14	31061584	31061584	Missense_Mutation	SNP	G	A	30	112	c.293G>A	c.(292-294)TGT>TAT	p.C98Y
Pat_59	Post-Resistance	CDKL1	8814	37	14	50845006	50845006	Missense_Mutation	SNP	G	A	6	22	c.1243C>T	c.(1243-1245)CCT>TCT	p.P415S
Pat_59	Post-Resistance	ATL1	51062	37	14	51087425	51087425	Missense_Mutation	SNP	G	A	37	152	c.971G>A	c.(970-972)GGT>GAT	p.G324D
Pat_59	Post-Resistance	GPR137C	283554	37	14	53100365	53100365	Nonsense_Mutation	SNP	C	T	5	74	c.985C>T	c.(985-987)CAG>TAG	p.Q329*
Pat_59	Post-Resistance	SAMD4A	23034	37	14	55169263	55169263	Missense_Mutation	SNP	C	T	26	258	c.677C>T	c.(676-678)ACC>ATC	p.T226I
Pat_59	Post-Resistance	WDHD1	11169	37	14	55474076	55474076	Nonsense_Mutation	SNP	C	T	22	163	c.522G>A	c.(520-522)TGG>TGA	p.W174*
Pat_59	Post-Resistance	SGPP1	81537	37	14	64194218	64194218	Missense_Mutation	SNP	G	A	15	110	c.445C>T	c.(445-447)CCC>TCC	p.P149S
Pat_59	Post-Resistance	SYNE2	23224	37	14	64486728	64486728	Missense_Mutation	SNP	G	A	16	135	c.5068G>A	c.(5068-5070)GAA>AAA	p.E1690K
Pat_59	Post-Resistance	PLEKHG3	26030	37	14	65198131	65198131	Missense_Mutation	SNP	G	A	13	89	c.902G>A	c.(901-903)GGG>GAG	p.G301E
Pat_59	Post-Resistance	SPTB	6710	37	14	65249027	65249027	Missense_Mutation	SNP	C	T	25	179	c.4247G>A	c.(4246-4248)CGG>CAG	p.R1416Q
Pat_59	Post-Resistance	PLEKHH1	57475	37	14	68026391	68026391	Missense_Mutation	SNP	A	G	4	19	c.406A>G	c.(406-408)ACA>GCA	p.T136A
Pat_59	Post-Resistance	SLC8A3	6547	37	14	70633821	70633821	Missense_Mutation	SNP	G	A	13	109	c.1319C>T	c.(1318-1320)GCC>GTC	p.A440V
Pat_59	Post-Resistance	ZFYVE1	53349	37	14	73445585	73445585	Missense_Mutation	SNP	C	T	15	130	c.1403G>A	c.(1402-1404)CGA>CAA	p.R468Q
Pat_59	Post-Resistance	LTBP2	4053	37	14	74975412	74975412	Missense_Mutation	SNP	C	T	16	51	c.3547G>A	c.(3547-3549)GAG>AAG	p.E1183K
Pat_59	Post-Resistance	LTBP2	4053	37	14	75022207	75022207	Nonsense_Mutation	SNP	C	T	10	83	c.1020G>A	c.(1018-1020)TGG>TGA	p.W340*
Pat_59	Post-Resistance	KIAA0317	9870	37	14	75138173	75138173	Missense_Mutation	SNP	G	A	5	70	c.1436C>T	c.(1435-1437)ACT>ATT	p.T479I
Pat_59	Post-Resistance	C14orf179	112752	37	14	76525686	76525686	Nonsense_Mutation	SNP	C	T	12	143	c.265C>T	c.(265-267)CAG>TAG	p.Q89*
Pat_59	Post-Resistance	ADCK1	57143	37	14	78392296	78392296	Missense_Mutation	SNP	G	A	4	126	c.1198G>A	c.(1198-1200)GCC>ACC	p.A400T
Pat_59	Post-Resistance	NRXN3	9369	37	14	80164260	80164260	Missense_Mutation	SNP	C	T	54	72	c.2785C>T	c.(2785-2787)CGC>TGC	p.R929C
Pat_59	Post-Resistance	C14orf143	90141	37	14	90398906	90398906	Missense_Mutation	SNP	C	T	54	75	c.283G>A	c.(283-285)GAA>AAA	p.E95K
Pat_59	Post-Resistance	C14orf159	80017	37	14	91655259	91655259	Missense_Mutation	SNP	C	T	3	40	c.925C>T	c.(925-927)CGG>TGG	p.R309W
Pat_59	Post-Resistance	CATSPERB	79820	37	14	92159568	92159568	Missense_Mutation	SNP	C	T	24	153	c.733G>A	c.(733-735)GTG>ATG	p.V245M

Pat_59	Post-Resistance	SLC24A4	123041	37	14	92900255	92900255	Splice_Site	SNP	G	A	18	119	c.191_splice	c.e3-1	p.A64_splice
Pat_59	Post-Resistance	C14orf142	84520	37	14	93673425	93673425	Translation_Start_Site	SNP	C	T	10	31	c.-42G>A	.(-44--40)GGGTG>GGATG	
Pat_59	Post-Resistance	DYNC1H1	1778	37	14	102466357	102466357	Missense_Mutation	SNP	C	T	9	75	c.3836C>T	c.(3835-3837)GCT>GTT	p.A1279V
Pat_59	Post-Resistance	DYNC1H1	1778	37	14	102508839	102508839	Missense_Mutation	SNP	C	T	6	53	c.12394C>T	.(12394-12396)CCC>TCC	p.P4132S
Pat_59	Post-Resistance	ADSSL1	122622	37	14	105204721	105204721	Missense_Mutation	SNP	G	A	11	79	c.304G>A	c.(304-306)GTG>ATG	p.V102M
Pat_59	Post-Resistance	AHNAK2	113146	37	14	105408943	105408943	Missense_Mutation	SNP	C	T	26	265	c.12845G>A	c.(12844-12846)GGT>GAT	p.G4282D
Pat_59	Post-Resistance	AHNAK2	113146	37	14	105412732	105412732	Missense_Mutation	SNP	C	T	10	129	c.9056G>A	c.(9055-9057)GGG>GAG	p.G3019E
Pat_59	Post-Resistance	BTBD6	90135	37	14	105716894	105716894	Missense_Mutation	SNP	G	A	15	165	c.1343G>A	c.(1342-1344)GGG>GAG	p.G448E
Pat_59	Post-Resistance	GPR176	11245	37	15	40093401	40093401	Missense_Mutation	SNP	C	T	26	89	c.1480G>A	c.(1480-1482)GTA>ATA	p.V494I
Pat_59	Post-Resistance	SRP14	6727	37	15	40328590	40328590	Missense_Mutation	SNP	C	T	3	37	c.355G>A	c.(355-357)GCA>ACA	p.A119T
Pat_59	Post-Resistance	RPAP1	26015	37	15	41813218	41813218	Missense_Mutation	SNP	G	A	3	35	c.3166C>T	c.(3166-3168)CGC>TGC	p.R1056C
Pat_59	Post-Resistance	MAPKBP1	23005	37	15	42116238	42116238	Missense_Mutation	SNP	G	A	4	113	c.4210G>A	c.(4210-4212)GCA>ACA	p.A1404T
Pat_59	Post-Resistance	ZSCAN29	146050	37	15	43658361	43658361	Missense_Mutation	SNP	G	A	10	46	c.1169C>T	c.(1168-1170)GCG>GTG	p.A390V
Pat_59	Post-Resistance	PDIA3	2923	37	15	44063358	44063358	Missense_Mutation	SNP	C	T	8	32	c.1460C>T	c.(1459-1461)CCC>CTC	p.P487L
Pat_59	Post-Resistance	C15orf63	25764	37	15	44092830	44092830	Missense_Mutation	SNP	G	A	3	16	c.34G>A	c.(34-36)GAG>AAG	p.E12K
Pat_59	Post-Resistance	DUOX1	53905	37	15	45433199	45433199	Missense_Mutation	SNP	C	T	16	64	c.1496C>T	c.(1495-1497)ACC>ATC	p.T499I
Pat_59	Post-Resistance	MYO5A	4644	37	15	52646103	52646104	Missense_Mutation	DNP	GG	AA	19	138	.3531_3532CC>T	529-3534)GACCGC>GATT	p.R1178C
Pat_59	Post-Resistance	CGNL1	84952	37	15	57820934	57820934	Missense_Mutation	SNP	C	T	14	36	c.3122C>T	c.(3121-3123)ACG>ATG	p.T1041M
Pat_59	Post-Resistance	HSP90AB4P	664618	37	15	58983364	58983364	Missense_Mutation	SNP	C	T	5	19	c.1456G>A	c.(1456-1458)GTG>ATG	p.V486M
Pat_59	Post-Resistance	MYO1E	4643	37	15	59516907	59516907	Missense_Mutation	SNP	C	T	8	50	c.758G>A	c.(757-759)CGG>CAG	p.R253Q
Pat_59	Post-Resistance	TLN2	83660	37	15	63004262	63004262	Missense_Mutation	SNP	G	A	4	32	c.2620G>A	c.(2620-2622)GTG>ATG	p.V874M
Pat_59	Post-Resistance	THSD4	79875	37	15	72030223	72030223	Missense_Mutation	SNP	G	A	19	91	c.1783G>A	c.(1783-1785)GAC>AAC	p.D595N
Pat_59	Post-Resistance	CYP1A1	1543	37	15	75013377	75013377	Missense_Mutation	SNP	C	T	11	39	c.1184G>A	c.(1183-1185)AGT>AAT	p.S395N
Pat_59	Post-Resistance	CHRNA3	1136	37	15	78893612	78893612	Nonsense_Mutation	SNP	G	A	17	76	c.1372C>T	c.(1372-1374)CAA>TAA	p.Q458*
Pat_59	Post-Resistance	AGBL1	123624	37	15	87217645	87217645	Missense_Mutation	SNP	G	A	3	31	c.3061G>A	c.(3061-3063)GCT>ACT	p.A1021T
Pat_59	Post-Resistance	POLG	5428	37	15	89867337	89867337	Splice_Site	SNP	C	T	5	50	c.2070_splice	c.e11+1	p.T690_splice
Pat_59	Post-Resistance	IQGAP1	8826	37	15	90991828	90991828	Missense_Mutation	SNP	G	A	4	75	c.937G>A	c.(937-939)GAC>AAC	p.D313N
Pat_59	Post-Resistance	UNC45A	55898	37	15	91488142	91488142	Missense_Mutation	SNP	G	A	7	26	c.1048G>A	c.(1048-1050)GTG>ATG	p.V350M
Pat_59	Post-Resistance	IGF1R	3480	37	15	99251019	99251019	Missense_Mutation	SNP	G	A	7	12	c.323G>A	c.(322-324)GGC>GAC	p.G108D
Pat_59	Post-Resistance	AXIN1	8312	37	16	396560	396560	Missense_Mutation	SNP	C	T	5	74	c.466G>A	c.(466-468)GTG>ATG	p.V156M
Pat_59	Post-Resistance	NOXO1	124056	37	16	2031176	2031176	Missense_Mutation	SNP	G	A	6	18	c.5C>T	c.(4-6)GCA>GTA	p.A2V
Pat_59	Post-Resistance	PKD1	5310	37	16	2158498	2158498	Missense_Mutation	SNP	G	A	3	29	c.6670C>T	c.(6670-6672)CCT>TCT	p.P2224S
Pat_59	Post-Resistance	CCDC64B	146439	37	16	3080452	3080452	Missense_Mutation	SNP	C	T	5	14	c.760G>A	c.(760-762)GAG>AAG	p.E254K
Pat_59	Post-Resistance	ZNF205	7755	37	16	3170064	3170064	Missense_Mutation	SNP	G	A	4	133	c.1403G>A	c.(1402-1404)CGC>CAC	p.R468H
Pat_59	Post-Resistance	ADCY9	115	37	16	4163814	4163814	Missense_Mutation	SNP	C	T	4	108	c.1630G>A	c.(1630-1632)GAA>AAA	p.E544K
Pat_59	Post-Resistance	ATF7IP2	80063	37	16	10525273	10525273	Missense_Mutation	SNP	G	A	20	81	c.796G>A	c.(796-798)GAC>AAC	p.D266N
Pat_59	Post-Resistance	TNP2	7142	37	16	11362962	11362962	Missense_Mutation	SNP	G	A	17	81	c.158C>T	c.(157-159)CCG>CTG	p.P53L
Pat_59	Post-Resistance	SMG1	23049	37	16	18851019	18851019	Splice_Site	SNP	C	T	33	145	c.6945_splice	c.e42+1	.Q2315_splice
Pat_59	Post-Resistance	GGA2	23062	37	16	23499931	23499931	Missense_Mutation	SNP	G	A	28	77	c.575C>T	c.(574-576)TCC>TTC	p.S192F
Pat_59	Post-Resistance	PALB2	79728	37	16	23635397	23635397	Missense_Mutation	SNP	C	T	16	40	c.2767G>A	c.(2767-2769)GTT>ATT	p.V923I
Pat_59	Post-Resistance	TNRC6A	27327	37	16	24802729	24802729	Nonsense_Mutation	SNP	G	A	12	51	c.2766G>A	c.(2764-2766)TGG>TGA	p.W922*
Pat_59	Post-Resistance	ORAI3	93129	37	16	30964658	30964658	Missense_Mutation	SNP	C	A	5	123	c.381C>A	c.(379-381)AGC>AGA	p.S127R
Pat_59	Post-Resistance	CNOT1	23019	37	16	58562399	58562399	Missense_Mutation	SNP	G	A	24	111	c.6433C>T	c.(6433-6435)CCA>TCA	p.P2145S
Pat_59	Post-Resistance	CNOT1	23019	37	16	58565911	58565911	Missense_Mutation	SNP	G	A	18	76	c.6128C>T	c.(6127-6129)TCC>TTC	p.S2043F
Pat_59	Post-Resistance	ZFP90	146198	37	16	68597523	68597523	Missense_Mutation	SNP	G	A	24	96	c.833G>A	c.(832-834)GGG>GAG	p.G278E
Pat_59	Post-Resistance	PDF	64146	37	16	69362936	69362936	Missense_Mutation	SNP	C	T	29	202	c.721G>A	c.(721-723)GTG>ATG	p.V241M
Pat_59	Post-Resistance	DHX38	9785	37	16	72139037	72139037	Splice_Site	SNP	G	A	3	28	c.2262_splice	c.e16+1	p.E754_splice

Pat_59	Post-Resistance	LRRC50	123872	37	16	84203819	84203819	Missense_Mutation	SNP	A	G	4	38	c.1385A>G	c.(1384-1386)CAA>CGA	p.Q462R
Pat_59	Post-Resistance	KIAA0513	9764	37	16	85111216	85111216	Missense_Mutation	SNP	G	A	3	15	c.760G>A	c.(760-762)GGG>AGG	p.G254R
Pat_59	Post-Resistance	CPNE7	27132	37	16	89645271	89645271	Nonsense_Mutation	SNP	C	T	11	26	c.364C>T	c.(364-366)CAA>TAA	p.Q122*
Pat_59	Post-Resistance	SLC43A2	124935	37	17	1494587	1494587	Missense_Mutation	SNP	C	T	7	64	c.907G>A	c.(907-909)GTG>ATG	p.V303M
Pat_59	Post-Resistance	MNT	4335	37	17	2298284	2298284	Missense_Mutation	SNP	G	A	6	6	c.538C>T	c.(538-540)CCT>TCT	p.P180S
Pat_59	Post-Resistance	GSG2	83903	37	17	3627912	3627912	Missense_Mutation	SNP	C	T	19	71	c.683C>T	c.(682-684)GCC>GTC	p.A228V
Pat_59	Post-Resistance	ANKFY1	51479	37	17	4088208	4088208	Missense_Mutation	SNP	G	A	5	50	c.1604C>T	c.(1603-1605)ACC>ATC	p.T535I
Pat_59	Post-Resistance	MYBBP1A	10514	37	17	4444804	4444804	Missense_Mutation	SNP	G	A	11	123	c.3251C>T	c.(3250-3252)TCC>TTC	p.S1084F
Pat_59	Post-Resistance	POLR2A	5430	37	17	7414585	7414585	Missense_Mutation	SNP	G	A	4	74	c.3865G>A	c.(3865-3867)GAG>AAG	p.E1289K
Pat_59	Post-Resistance	CYB5D1	124637	37	17	7761721	7761721	Missense_Mutation	SNP	G	A	9	45	c.161G>A	c.(160-162)GGG>GAG	p.G54E
Pat_59	Post-Resistance	TRIM16	10626	37	17	15539579	15539579	Missense_Mutation	SNP	G	A	4	81	c.620C>T	c.(619-621)TCG>TTG	p.S207L
Pat_59	Post-Resistance	NCOR1	9611	37	17	15976764	15976764	Missense_Mutation	SNP	G	A	24	131	c.3790C>T	c.(3790-3792)CCT>TCT	p.P1264S
Pat_59	Post-Resistance	MED9	55090	37	17	17394799	17394799	Missense_Mutation	SNP	C	T	3	32	c.431C>T	c.(430-432)CCC>CTC	p.P144L
Pat_59	Post-Resistance	TOP3A	7156	37	17	18196077	18196077	Missense_Mutation	SNP	C	T	15	69	c.1163G>A	c.(1162-1164)CGC>CAC	p.R388H
Pat_59	Post-Resistance	AKAP10	11216	37	17	19866227	19866227	Missense_Mutation	SNP	G	A	18	121	c.245C>T	c.(244-246)TCC>TTC	p.S82F
Pat_59	Post-Resistance	CCDC55	84081	37	17	28512114	28512114	Missense_Mutation	SNP	G	A	7	19	c.1099G>A	c.(1099-1101)GCG>ACG	p.A367T
Pat_59	Post-Resistance	AMAC1	146861	37	17	33520491	33520491	Missense_Mutation	SNP	G	A	8	91	c.836C>T	c.(835-837)CCT>CTT	p.P279L
Pat_59	Post-Resistance	DHRS11	79154	37	17	34955432	34955432	Missense_Mutation	SNP	G	A	22	50	c.535G>A	c.(535-537)GGA>AGA	p.G179R
Pat_59	Post-Resistance	AATF	26574	37	17	35311157	35311157	Missense_Mutation	SNP	C	T	6	78	c.782C>T	c.(781-783)CCA>CTA	p.P261L
Pat_59	Post-Resistance	TBC1D3	729873	37	17	36288264	36288264	Missense_Mutation	SNP	C	T	7	498	c.350C>T	c.(349-351)ACT>ATT	p.T117I
Pat_59	Post-Resistance	MED1	5469	37	17	37564696	37564696	Missense_Mutation	SNP	G	A	9	61	c.3778C>T	c.(3778-3780)CCC>TCC	p.P1260S
Pat_59	Post-Resistance	MED1	5469	37	17	37564779	37564779	Missense_Mutation	SNP	G	A	7	50	c.3695C>T	c.(3694-3696)TCT>TTT	p.S1232F
Pat_59	Post-Resistance	TOP2A	7153	37	17	38557184	38557184	Missense_Mutation	SNP	G	A	88	530	c.2582C>T	c.(2581-2583)TCC>TTC	p.S861F
Pat_59	Post-Resistance	KRT24	192666	37	17	38856585	38856585	Missense_Mutation	SNP	C	T	88	266	c.906G>A	c.(904-906)ATG>ATA	p.M302I
Pat_59	Post-Resistance	ACLY	47	37	17	40028028	40028028	Missense_Mutation	SNP	C	T	5	54	c.2851G>A	c.(2851-2853)GAC>AAC	p.D951N
Pat_59	Post-Resistance	GOSR2	9570	37	17	45012470	45012470	Missense_Mutation	SNP	G	A	31	136	c.412G>A	c.(412-414)GAT>AAT	p.D138N
Pat_59	Post-Resistance	SPAG9	9043	37	17	49064546	49064546	Missense_Mutation	SNP	C	T	15	93	c.2866G>A	c.(2866-2868)GAC>AAC	p.D956N
Pat_59	Post-Resistance	MMD	23531	37	17	53478855	53478855	Missense_Mutation	SNP	G	A	9	71	c.491C>T	c.(490-492)TCT>TTT	p.S164F
Pat_59	Post-Resistance	LOC653653	653653	37	17	58179963	58179963	Missense_Mutation	SNP	G	A	11	66	c.202C>T	c.(202-204)CCA>TCA	p.P68S
Pat_59	Post-Resistance	BCAS3	54828	37	17	58767122	58767122	Missense_Mutation	SNP	G	A	4	66	c.214G>A	c.(214-216)GAT>AAT	p.D72N
Pat_59	Post-Resistance	BCAS3	54828	37	17	58786687	58786687	Splice_Site	SNP	G	A	9	63	c.321_splice	c.e5+1	p.P107_splice
Pat_59	Post-Resistance	MED13	9969	37	17	60030432	60030432	Missense_Mutation	SNP	C	T	13	57	c.6011G>A	c.(6010-6012)GGA>GAA	p.G2004E
Pat_59	Post-Resistance	DCAF7	10238	37	17	61666446	61666446	Missense_Mutation	SNP	G	A	11	77	c.941G>A	c.(940-942)GGA>GAA	p.G314E
Pat_59	Post-Resistance	TMEM104	54868	37	17	72832443	72832443	Missense_Mutation	SNP	C	T	34	93	c.1108C>T	c.(1108-1110)CCC>TCC	p.P370S
Pat_59	Post-Resistance	UBE2O	63893	37	17	74387046	74387046	Missense_Mutation	SNP	G	A	4	113	c.3857C>T	c.(3856-3858)CCG>CTG	p.P1286L
Pat_59	Post-Resistance	EIF4A3	9775	37	17	78111270	78111270	Missense_Mutation	SNP	C	T	4	21	c.898G>A	c.(898-900)GCC>ACC	p.A300T
Pat_59	Post-Resistance	SLC26A11	284129	37	17	78211376	78211376	Missense_Mutation	SNP	C	T	4	6	c.968C>T	c.(967-969)GCG>GTG	p.A323V
Pat_59	Post-Resistance	C17orf62	79415	37	17	80402356	80402356	Missense_Mutation	SNP	G	A	4	38	c.410C>T	c.(409-411)CCC>CTC	p.P137L
Pat_59	Post-Resistance	FN3KRP	79672	37	17	80680740	80680740	Missense_Mutation	SNP	C	T	6	63	c.446C>T	c.(445-447)ACG>ATG	p.T149M
Pat_59	Post-Resistance	EMILIN2	84034	37	18	2891017	2891017	Nonsense_Mutation	SNP	C	T	4	117	c.892C>T	c.(892-894)CAG>TAG	p.Q298*
Pat_59	Post-Resistance	LAMA1	284217	37	18	7013887	7013887	Missense_Mutation	SNP	G	A	3	23	c.3290C>T	c.(3289-3291)ACG>ATG	p.T1097M
Pat_59	Post-Resistance	KIAA0802	23255	37	18	8784078	8784078	Missense_Mutation	SNP	G	A	6	40	c.968G>A	c.(967-969)GGT>GAT	p.G323D
Pat_59	Post-Resistance	TXNDC2	84203	37	18	9887188	9887188	Missense_Mutation	SNP	G	T	6	157	c.712G>T	c.(712-714)GAT>TAT	p.D238Y
Pat_59	Post-Resistance	MPPE1	65258	37	18	11886514	11886514	Missense_Mutation	SNP	C	T	4	125	c.851G>A	c.(850-852)CGG>CAG	p.R284Q
Pat_59	Post-Resistance	AFG3L2	10939	37	18	12329697	12329697	Missense_Mutation	SNP	G	A	15	59	c.2261C>T	c.(2260-2262)TCT>TTT	p.S754F
Pat_59	Post-Resistance	ABHD3	171586	37	18	19231694	19231694	Missense_Mutation	SNP	G	A	16	87	c.1088C>T	c.(1087-1089)CCT>CTT	p.P363L
Pat_59	Post-Resistance	CABYR	26256	37	18	21736775	21736775	Missense_Mutation	SNP	G	A	5	44	c.1310G>A	c.(1309-1311)GGG>GAG	p.G437E

Pat_59	Post-Resistance	OSBPL1A	114876	37	18	21897136	21897136	Missense_Mutation	SNP	G	A	26	149	c.847C>T	c.(847-849)CAC>TAC	p.H283Y
Pat_59	Post-Resistance	TAF4B	6875	37	18	23807205	23807205	Missense_Mutation	SNP	C	T	30	171	c.308C>T	c.(307-309)ACA>ATA	p.T103I
Pat_59	Post-Resistance	DSG1	1828	37	18	28918358	28918358	Missense_Mutation	SNP	C	T	13	155	c.1346C>T	c.(1345-1347)ACC>ATC	p.T449I
Pat_59	Post-Resistance	DSG3	1830	37	18	29054122	29054122	Missense_Mutation	SNP	G	A	22	163	c.2140G>A	c.(2140-2142)GAA>AAA	p.E714K
Pat_59	Post-Resistance	MEP1B	4225	37	18	29793207	29793207	Missense_Mutation	SNP	C	T	7	60	c.1264C>T	c.(1264-1266)CTT>TTT	p.L422F
Pat_59	Post-Resistance	C18orf34	374864	37	18	30806765	30806765	Missense_Mutation	SNP	C	T	13	125	c.1648G>A	c.(1648-1650)GTG>ATG	p.V550M
Pat_59	Post-Resistance	ZNF397OS	100101467	37	18	32833785	32833785	Missense_Mutation	SNP	G	A	6	146	c.1114C>T	c.(1114-1116)CTC>TTC	p.L372F
Pat_59	Post-Resistance	ELP2	55250	37	18	33724961	33724961	Missense_Mutation	SNP	G	A	44	244	c.856G>A	c.(856-858)GTA>ATA	p.V286I
Pat_59	Post-Resistance	DCC	1630	37	18	50432623	50432623	Missense_Mutation	SNP	G	A	40	98	c.622G>A	c.(622-624)GGA>AGA	p.G208R
Pat_59	Post-Resistance	NARS	4677	37	18	55273171	55273171	Missense_Mutation	SNP	C	T	4	78	c.1169G>A	c.(1168-1170)CGG>CAG	p.R390Q
Pat_59	Post-Resistance	CDH20	28316	37	18	59206278	59206278	Missense_Mutation	SNP	G	A	16	129	c.1430G>A	c.(1429-1431)AGT>AAT	p.S477N
Pat_59	Post-Resistance	CDH19	28513	37	18	64235688	64235688	Missense_Mutation	SNP	G	A	50	162	c.455C>T	c.(454-456)CCT>CTT	p.P152L
Pat_59	Post-Resistance	CCDC102B	79839	37	18	66506096	66506096	Missense_Mutation	SNP	G	A	15	109	c.760G>A	c.(760-762)GTA>ATA	p.V254I
Pat_59	Post-Resistance	ZNF407	55628	37	18	72344482	72344482	Nonsense_Mutation	SNP	C	T	10	36	c.1507C>T	c.(1507-1509)CAG>TAG	p.Q503*
Pat_59	Post-Resistance	MBP	4155	37	18	74696756	74696756	Missense_Mutation	SNP	C	T	6	45	c.845G>A	c.(844-846)GGC>GAC	p.G282D
Pat_59	Post-Resistance	HMHA1	23526	37	19	1080267	1080267	Missense_Mutation	SNP	C	T	4	121	c.1717C>T	c.(1717-1719)CGT>TGT	p.R573C
Pat_59	Post-Resistance	ATP8B3	148229	37	19	1807187	1807187	Missense_Mutation	SNP	G	A	18	60	c.595C>T	c.(595-597)CGG>TGG	p.R199W
Pat_59	Post-Resistance	ZNF555	148254	37	19	2853202	2853202	Missense_Mutation	SNP	C	T	4	62	c.1139C>T	c.(1138-1140)CCC>CTC	p.P380L
Pat_59	Post-Resistance	ZNF555	148254	37	19	2853369	2853369	Missense_Mutation	SNP	C	T	12	40	c.1306C>T	c.(1306-1308)CCC>TCC	p.P436S
Pat_59	Post-Resistance	NCLN	56926	37	19	3186212	3186212	Missense_Mutation	SNP	G	A	2	0	c.184G>A	c.(184-186)GGC>AGC	p.G62S
Pat_59	Post-Resistance	TBXA2R	6915	37	19	3600565	3600565	Missense_Mutation	SNP	C	T	3	13	c.68G>A	c.(67-69)CGG>CAG	p.R23Q
Pat_59	Post-Resistance	EEF2	1938	37	19	3984195	3984195	Missense_Mutation	SNP	C	T	26	102	c.157G>A	c.(157-159)GAG>AAG	p.E53K
Pat_59	Post-Resistance	CHAF1A	10036	37	19	4433196	4433196	Missense_Mutation	SNP	C	T	17	83	c.2333C>T	c.(2332-2334)ACC>ATC	p.T778I
Pat_59	Post-Resistance	FEM1A	55527	37	19	4793374	4793374	Missense_Mutation	SNP	A	C	3	99	c.1508A>C	c.(1507-1509)TAC>TCC	p.Y503S
Pat_59	Post-Resistance	ZNF557	79230	37	19	7083178	7083178	Missense_Mutation	SNP	G	A	6	125	c.695G>A	c.(694-696)AGT>AAT	p.S232N
Pat_59	Post-Resistance	CD209	30835	37	19	7810560	7810561	Missense_Mutation	DNP	GG	AA	4	56	c.591_592CC>TT	589-594)ACCCGG>ACTT	p.R198W
Pat_59	Post-Resistance	SNAPC2	6618	37	19	7986659	7986659	Splice_Site	SNP	G	A	3	17	c.372_splice	c.e3+1	p.Q124_splice
Pat_59	Post-Resistance	FBN3	84467	37	19	8175804	8175804	Missense_Mutation	SNP	C	T	8	53	c.4258G>A	c.(4258-4260)GAG>AAG	p.E1420K
Pat_59	Post-Resistance	MUC16	94025	37	19	9089557	9089557	Missense_Mutation	SNP	G	A	8	49	c.2258C>T	c.(2257-2259)ACC>ATC	p.T753I
Pat_59	Post-Resistance	S1PR5	53637	37	19	10625665	10625665	Missense_Mutation	SNP	G	A	3	43	c.23C>T	c.(22-24)CCG>CTG	p.P8L
Pat_59	Post-Resistance	DNM2	1785	37	19	10887845	10887845	Missense_Mutation	SNP	C	T	4	32	c.641C>T	c.(640-642)ACC>ATC	p.T214I
Pat_59	Post-Resistance	ZNF700	90592	37	19	12060645	12060645	Missense_Mutation	SNP	T	A	6	272	c.1806T>A	c.(1804-1806)AGT>AGA	p.S602R
Pat_59	Post-Resistance	ZNF700	90592	37	19	12060647	12060647	Missense_Mutation	SNP	G	C	6	270	c.1808G>C	c.(1807-1809)TGT>TCT	p.C603S
Pat_59	Post-Resistance	ZNF799	90576	37	19	12502214	12502214	Missense_Mutation	SNP	C	T	24	210	c.998G>A	c.(997-999)AGA>AAA	p.R333K
Pat_59	Post-Resistance	ZNF791	163049	37	19	12739470	12739470	Missense_Mutation	SNP	G	A	14	96	c.1127G>A	c.(1126-1128)AGG>AAG	p.R376K
Pat_59	Post-Resistance	RNASEH2A	10535	37	19	12920945	12920945	Missense_Mutation	SNP	C	T	48	85	c.472C>T	c.(472-474)CCC>TCC	p.P158S
Pat_59	Post-Resistance	DNASE2	1777	37	19	12986905	12986905	Missense_Mutation	SNP	C	T	4	55	c.982G>A	c.(982-984)GCC>ACC	p.A328T
Pat_59	Post-Resistance	CD97	976	37	19	14499527	14499527	Nonsense_Mutation	SNP	G	A	31	146	c.87G>A	c.(85-87)TGG>TGA	p.W29*
Pat_59	Post-Resistance	EMR2	30817	37	19	14854549	14854549	Missense_Mutation	SNP	G	A	4	97	c.2231C>T	c.(2230-2232)ACG>ATG	p.T744M
Pat_59	Post-Resistance	EMR2	30817	37	19	14867095	14867095	Missense_Mutation	SNP	C	T	4	113	c.1147G>A	c.(1147-1149)GTG>ATG	p.V383M
Pat_59	Post-Resistance	MED26	9441	37	19	16686939	16686939	Missense_Mutation	SNP	C	T	21	95	c.1702G>A	c.(1702-1704)GAC>AAC	p.D568N
Pat_59	Post-Resistance	GTPBP3	84705	37	19	17452408	17452408	Missense_Mutation	SNP	G	A	6	14	c.1375G>A	c.(1375-1377)GAG>AAG	p.E459K
Pat_59	Post-Resistance	FAM129C	199786	37	19	17641597	17641597	Missense_Mutation	SNP	C	T	4	12	c.182C>T	c.(181-183)CCT>CTT	p.P61L
Pat_59	Post-Resistance	UPF1	5976	37	19	18971213	18971213	Missense_Mutation	SNP	G	A	15	90	c.2299G>A	c.(2299-2301)GAG>AAG	p.E767K
Pat_59	Post-Resistance	KIAA0892	23383	37	19	19454651	19454651	Missense_Mutation	SNP	G	A	31	128	c.979G>A	c.(979-981)GAC>AAC	p.D327N
Pat_59	Post-Resistance	CILP2	148113	37	19	19655636	19655636	Missense_Mutation	SNP	C	T	3	18	c.2282C>T	c.(2281-2283)ACG>ATG	p.T761M
Pat_59	Post-Resistance	ZNF93	81931	37	19	20045254	20045254	Missense_Mutation	SNP	C	T	6	235	c.1490C>T	c.(1489-1491)ACT>ATT	p.T497I

Pat_59	Post-Resistance	ZNF93	81931	37	19	20045361	20045361	Missense_Mutation	SNP	A	G	5	177	c.1597A>G	c.(1597-1599)AGA>GGA	p.R533G
Pat_59	Post-Resistance	ZNF737	100129842	37	19	20727516	20727516	Missense_Mutation	SNP	C	G	5	125	c.1493G>C	c.(1492-1494)AGA>ACA	p.R498T
Pat_59	Post-Resistance	ZNF708	7562	37	19	21476519	21476519	Missense_Mutation	SNP	T	C	8	152	c.1249A>G	c.(1249-1251)AAG>GAG	p.K417E
Pat_59	Post-Resistance	ZNF429	353088	37	19	21720411	21720411	Missense_Mutation	SNP	T	A	6	160	c.1556T>A	c.(1555-1557)ATC>AAC	p.I519N
Pat_59	Post-Resistance	ZNF429	353088	37	19	21720414	21720414	Missense_Mutation	SNP	T	G	6	160	c.1559T>G	c.(1558-1560)CTG>CGG	p.L520R
Pat_59	Post-Resistance	ZNF100	163227	37	19	21909734	21909734	Missense_Mutation	SNP	G	C	11	336	c.1380C>G	c.(1378-1380)GAC>GAG	p.D460E
Pat_59	Post-Resistance	ZNF208	7757	37	19	22155896	22155896	Missense_Mutation	SNP	A	C	8	174	c.1640T>G	c.(1639-1641)ATT>AGT	p.I547S
Pat_59	Post-Resistance	ZNF208	7757	37	19	22157223	22157223	Missense_Mutation	SNP	C	T	13	103	c.613G>A	c.(613-615)GAA>AAA	p.E205K
Pat_59	Post-Resistance	ZNF257	113835	37	19	22271961	22271961	Missense_Mutation	SNP	A	G	21	164	c.1409A>G	c.(1408-1410)CAG>CGG	p.Q470R
Pat_59	Post-Resistance	ZNF676	163223	37	19	22362924	22362924	Missense_Mutation	SNP	G	C	7	266	c.1595C>G	c.(1594-1596)CCC>CGC	p.P532R
Pat_59	Post-Resistance	ZNF99	7652	37	19	22939472	22939472	Missense_Mutation	SNP	A	G	5	148	c.2699T>C	c.(2698-2700)TTC>TCC	p.F900S
Pat_59	Post-Resistance	ZNF91	7644	37	19	23544867	23544867	Missense_Mutation	SNP	T	C	18	301	c.914A>G	c.(913-915)CAT>CGT	p.H305R
Pat_59	Post-Resistance	ZNF507	22847	37	19	32845283	32845283	Missense_Mutation	SNP	G	A	5	59	c.1547G>A	c.(1546-1548)GGG>GAG	p.G516E
Pat_59	Post-Resistance	ZNF507	22847	37	19	32845291	32845291	Nonsense_Mutation	SNP	G	T	4	65	c.1555G>T	c.(1555-1557)GGA>TGA	p.G519*
Pat_59	Post-Resistance	KIAA0355	9710	37	19	34832814	34832814	Missense_Mutation	SNP	G	A	10	83	c.1975G>A	c.(1975-1977)GGC>AGC	p.G659S
Pat_59	Post-Resistance	UBA2	10054	37	19	34943026	34943026	Missense_Mutation	SNP	G	A	25	182	c.1012G>A	c.(1012-1014)GAT>AAT	p.D338N
Pat_59	Post-Resistance	SCN1B	6324	37	19	35524436	35524436	Missense_Mutation	SNP	G	A	24	77	c.241G>A	c.(241-243)GAG>AAG	p.E81K
Pat_59	Post-Resistance	ZNF568	374900	37	19	37488413	37488413	Missense_Mutation	SNP	C	T	8	41	c.1778C>T	c.(1777-1779)ACA>ATA	p.T593I
Pat_59	Post-Resistance	ZNF585A	199704	37	19	37644133	37644133	Missense_Mutation	SNP	A	T	8	36	c.668T>A	c.(667-669)TTC>TAC	p.F223Y
Pat_59	Post-Resistance	SIPA1L3	23094	37	19	38610163	38610163	Missense_Mutation	SNP	C	T	4	25	c.2509C>T	c.(2509-2511)CCC>TCC	p.P837S
Pat_59	Post-Resistance	ZFP36	7538	37	19	39899296	39899296	Missense_Mutation	SNP	C	T	7	97	c.938C>T	c.(937-939)CCC>CTC	p.P313L
Pat_59	Post-Resistance	SHKBP1	92799	37	19	41088274	41088274	Missense_Mutation	SNP	G	A	11	59	c.862G>A	c.(862-864)GTG>ATG	p.V288M
Pat_59	Post-Resistance	CYP2A13	1553	37	19	41599629	41599629	Missense_Mutation	SNP	C	T	6	46	c.926C>T	c.(925-927)ACC>ATC	p.T309I
Pat_59	Post-Resistance	PRR19	284338	37	19	42814570	42814570	Missense_Mutation	SNP	C	T	6	153	c.749C>T	c.(748-750)GCG>GTG	p.A250V
Pat_59	Post-Resistance	PSG5	5673	37	19	43688976	43688976	Missense_Mutation	SNP	T	C	9	331	c.388A>G	c.(388-390)AGG>GGG	p.R130G
Pat_59	Post-Resistance	IRGQ	126298	37	19	44097414	44097414	Nonsense_Mutation	SNP	C	T	3	21	c.636G>A	c.(634-636)TGG>TGA	p.W212*
Pat_59	Post-Resistance	C19orf61	56006	37	19	44251899	44251899	Missense_Mutation	SNP	G	A	3	6	c.376C>T	c.(376-378)CCC>TCC	p.P126S
Pat_59	Post-Resistance	KCNN4	3783	37	19	44280742	44280742	Missense_Mutation	SNP	G	A	6	59	c.206C>T	c.(205-207)ACC>ATC	p.T69I
Pat_59	Post-Resistance	ZNF45	7596	37	19	44417693	44417693	Missense_Mutation	SNP	C	T	7	114	c.1895G>A	c.(1894-1896)AGA>AAA	p.R632K
Pat_59	Post-Resistance	ZNF155	7711	37	19	44500775	44500775	Missense_Mutation	SNP	G	A	5	194	c.766G>A	c.(766-768)GGA>AGA	p.G256R
Pat_59	Post-Resistance	KLC3	147700	37	19	45849946	45849946	Missense_Mutation	SNP	G	A	2	1	c.403G>A	c.(403-405)GAG>AAG	p.E135K
Pat_59	Post-Resistance	SAE1	10055	37	19	47706998	47706998	Splice_Site	SNP	G	A	26	88	c.948_splice	c.e8+1	p.K316_splice
Pat_59	Post-Resistance	CRX	1406	37	19	48339604	48339604	Missense_Mutation	SNP	C	T	10	13	c.205C>T	c.(205-207)CGT>TGT	p.R69C
Pat_59	Post-Resistance	FAM83E	54854	37	19	49107049	49107049	Missense_Mutation	SNP	G	A	5	11	c.878C>T	c.(877-879)CCT>CTT	p.P293L
Pat_59	Post-Resistance	GYS1	2997	37	19	49494602	49494602	Missense_Mutation	SNP	G	A	22	106	c.257C>T	c.(256-258)GCC>GTC	p.A86V
Pat_59	Post-Resistance	LHB	3972	37	19	49519435	49519435	Missense_Mutation	SNP	G	A	16	51	c.316C>T	c.(316-318)CTC>TTC	p.L106F
Pat_59	Post-Resistance	NAPSA	9476	37	19	50865493	50865493	Missense_Mutation	SNP	G	A	8	20	c.161C>T	c.(160-162)CCC>CTC	p.P54L
Pat_59	Post-Resistance	SIGLEC6	946	37	19	52033208	52033208	Missense_Mutation	SNP	G	A	4	18	c.782C>T	c.(781-783)TCC>TTC	p.S261F
Pat_59	Post-Resistance	ZNF534	147658	37	19	52942507	52942507	Missense_Mutation	SNP	A	T	3	16	c.1833A>T	c.(1831-1833)AAA>AAT	p.K611N
Pat_59	Post-Resistance	ZNF578	147660	37	19	53014635	53014635	Missense_Mutation	SNP	A	G	6	193	c.1001A>G	c.(1000-1002)CAT>CGT	p.H334R
Pat_59	Post-Resistance	ZNF611	81856	37	19	53208542	53208542	Missense_Mutation	SNP	C	T	51	398	c.1766G>A	c.(1765-1767)AGT>AAT	p.S589N
Pat_59	Post-Resistance	ZNF415	55786	37	19	53612312	53612312	Missense_Mutation	SNP	G	C	3	81	c.1130C>G	c.(1129-1131)ACA>AGA	p.T377R
Pat_59	Post-Resistance	ZNF845	91664	37	19	53848804	53848804	Missense_Mutation	SNP	G	A	32	135	c.61G>A	c.(61-63)GAG>AAG	p.E21K
Pat_59	Post-Resistance	TTYH1	57348	37	19	54946722	54946722	Missense_Mutation	SNP	G	A	11	34	c.1126G>A	c.(1126-1128)GAC>AAC	p.D376N
Pat_59	Post-Resistance	LILRA2	11027	37	19	55087469	55087469	Missense_Mutation	SNP	G	A	4	79	c.1148G>A	c.(1147-1149)GGT>GAT	p.G383D
Pat_59	Post-Resistance	C19orf51	352909	37	19	55672660	55672660	Splice_Site	SNP	C	T	2	1	c.789_splice	c.e7+1	p.Y263_splice
Pat_59	Post-Resistance	ZNF581	51545	37	19	56156428	56156428	Missense_Mutation	SNP	G	A	30	185	c.491G>A	c.(490-492)AGC>AAC	p.S164N

Pat_59	Post-Resistance	ZNF787	126208	37	19	56600421	56600421	Missense_Mutation	SNP	C	A	2	0	c.120G>T	c.(118-120)TGG>TGT	p.W40C
Pat_59	Post-Resistance	ZNF787	126208	37	19	56600432	56600432	Missense_Mutation	SNP	C	G	2	1	c.109G>C	c.(109-111)GTC>CTC	p.V37L
Pat_59	Post-Resistance	ZNF805	390980	37	19	57765443	57765443	Missense_Mutation	SNP	G	A	3	50	c.1256G>A	c.(1255-1257)CGG>CAG	p.R419Q
Pat_59	Post-Resistance	ZNF549	256051	37	19	58049465	58049465	Missense_Mutation	SNP	G	A	7	75	c.1093G>A	c.(1093-1095)GAA>AAA	p.E365K
Pat_59	Post-Resistance	ZNF154	7710	37	19	58216322	58216322	Missense_Mutation	SNP	G	A	37	113	c.59C>T	c.(58-60)GCC>GTC	p.A20V
Pat_59	Post-Resistance	SNTG2	54221	37	2	1161233	1161233	Splice_Site	SNP	G	A	9	22	c.412_splice	c.e7-1	p.V138_splice
Pat_59	Post-Resistance	SNTG2	54221	37	2	1204796	1204796	Missense_Mutation	SNP	C	T	3	19	c.599C>T	c.(598-600)TCG>TTG	p.S200L
Pat_59	Post-Resistance	LPIN1	23175	37	2	11960601	11960601	Missense_Mutation	SNP	G	A	10	103	c.2474G>A	c.(2473-2475)GGA>GAA	p.G825E
Pat_59	Post-Resistance	WDR35	57539	37	2	20145615	20145615	Missense_Mutation	SNP	C	T	71	333	c.1810G>A	c.(1810-1812)GAT>AAT	p.D604N
Pat_59	Post-Resistance	ITSN2	50618	37	2	24431115	24431115	Missense_Mutation	SNP	C	T	14	57	c.4669G>A	c.(4669-4671)GCT>ACT	p.A1557T
Pat_59	Post-Resistance	ITSN2	50618	37	2	24435559	24435559	Missense_Mutation	SNP	G	A	37	157	c.4049C>T	c.(4048-4050)CCC>CTC	p.P1350L
Pat_59	Post-Resistance	OTOF	9381	37	2	26750740	26750740	Missense_Mutation	SNP	C	T	12	35	c.187G>A	c.(187-189)GAG>AAG	p.E63K
Pat_59	Post-Resistance	XDH	7498	37	2	31606627	31606627	Missense_Mutation	SNP	G	A	10	20	c.880C>T	c.(880-882)CCC>TCC	p.P294S
Pat_59	Post-Resistance	MEMO1	51072	37	2	32094987	32094987	Missense_Mutation	SNP	G	A	6	26	c.692C>T	c.(691-693)TCT>TTT	p.S231F
Pat_59	Post-Resistance	BIRC6	57448	37	2	32725065	32725065	Nonsense_Mutation	SNP	C	T	17	99	c.8920C>T	c.(8920-8922)CAA>TAA	p.Q2974*
Pat_59	Post-Resistance	LTBP1	4052	37	2	33484664	33484664	Missense_Mutation	SNP	C	T	17	110	c.2405C>T	c.(2404-2406)GCA>GTA	p.A802V
Pat_59	Post-Resistance	THADA	63892	37	2	43800132	43800132	Splice_Site	SNP	C	T	16	44	c.1730_splice	c.e12-1	p.G577_splice
Pat_59	Post-Resistance	MSH6	2956	37	2	48027571	48027571	Missense_Mutation	SNP	G	A	4	18	c.2449G>A	c.(2449-2451)GAT>AAT	p.D817N
Pat_59	Post-Resistance	SPTBN1	6711	37	2	54858426	54858426	Missense_Mutation	SNP	C	T	3	33	c.3242C>T	c.(3241-3243)ACC>ATC	p.T1081I
Pat_59	Post-Resistance	RTN4	57142	37	2	55254397	55254397	Missense_Mutation	SNP	C	T	14	120	c.838G>A	c.(838-840)GCA>ACA	p.A280T
Pat_59	Post-Resistance	CCT4	10575	37	2	62099431	62099431	Missense_Mutation	SNP	C	T	7	38	c.1277G>A	c.(1276-1278)GGT>GAT	p.G426D
Pat_59	Post-Resistance	UGP2	7360	37	2	64112875	64112875	Missense_Mutation	SNP	G	A	13	116	c.728G>A	c.(727-729)GGC>GAC	p.G243D
Pat_59	Post-Resistance	SLC1A4	6509	37	2	65231139	65231139	Missense_Mutation	SNP	C	T	4	42	c.623C>T	c.(622-624)ACC>ATC	p.T208I
Pat_59	Post-Resistance	SMYD5	10322	37	2	73452033	73452033	Missense_Mutation	SNP	C	T	16	101	c.980C>T	c.(979-981)CCA>CTA	p.P327L
Pat_59	Post-Resistance	ALMS1	7840	37	2	73653650	73653650	Missense_Mutation	SNP	G	A	4	135	c.1310G>A	c.(1309-1311)TGC>TAC	p.C437Y
Pat_59	Post-Resistance	SLC4A5	57835	37	2	74466532	74466532	Missense_Mutation	SNP	A	G	3	46	c.2249T>C	c.(2248-2250)CTT>CCT	p.L750P
Pat_59	Post-Resistance	POLR1A	25885	37	2	86267551	86267551	Missense_Mutation	SNP	C	T	3	35	c.3704G>A	c.(3703-3705)GGC>GAC	p.G1235D
Pat_59	Post-Resistance	EIF2AK3	9451	37	2	88890467	88890467	Missense_Mutation	SNP	C	T	16	84	c.871G>A	c.(871-873)GAG>AAG	p.E291K
Pat_59	Post-Resistance	PROM2	150696	37	2	95954721	95954721	Missense_Mutation	SNP	C	T	3	59	c.2482C>T	c.(2482-2484)CGG>TGG	p.R828W
Pat_59	Post-Resistance	TMEM131	23505	37	2	98413354	98413354	Missense_Mutation	SNP	G	A	7	62	c.2966C>T	c.(2965-2967)TCC>TTC	p.S989F
Pat_59	Post-Resistance	EIF5B	9669	37	2	99978149	99978149	Missense_Mutation	SNP	G	A	17	106	c.785G>A	c.(784-786)GGT>GAT	p.G262D
Pat_59	Post-Resistance	MFSD9	84804	37	2	103335286	103335286	Missense_Mutation	SNP	C	T	5	60	c.1018G>A	c.(1018-1020)GGG>AGG	p.G340R
Pat_59	Post-Resistance	RGPD3	653489	37	2	107029692	107029692	Missense_Mutation	SNP	A	T	4	131	c.5114T>A	c.(5113-5115)GTG>GAG	p.V1705E
Pat_59	Post-Resistance	GCC2	9648	37	2	109098908	109098908	Splice_Site	SNP	G	A	6	39	c.3345_splice	c.e11+1	p.K1115_splice
Pat_59	Post-Resistance	RANBP2	5903	37	2	109383792	109383792	Missense_Mutation	SNP	G	A	75	472	c.6797G>A	c.(6796-6798)GGA>GAA	p.G2266E
Pat_59	Post-Resistance	MERTK	10461	37	2	112751940	112751940	Missense_Mutation	SNP	G	A	29	190	c.1409G>A	c.(1408-1410)GGG>GAG	p.G470E
Pat_59	Post-Resistance	POLR1B	84172	37	2	113300088	113300088	Missense_Mutation	SNP	G	A	4	112	c.17G>A	c.(16-18)CGG>CAG	p.R6Q
Pat_59	Post-Resistance	POLR1B	84172	37	2	113333260	113333260	Missense_Mutation	SNP	C	T	46	233	c.3362C>T	c.(3361-3363)GCT>GTT	p.A1121V
Pat_59	Post-Resistance	SLC35F5	80255	37	2	114493356	114493356	Missense_Mutation	SNP	G	A	8	58	c.830C>T	c.(829-831)TCC>TTC	p.S277F
Pat_59	Post-Resistance	MARCO	8685	37	2	119750708	119750708	Missense_Mutation	SNP	T	C	13	68	c.1261T>C	c.(1261-1263)TCA>CCA	p.S421P
Pat_59	Post-Resistance	POTEF	728378	37	2	130877782	130877782	Missense_Mutation	SNP	A	G	7	196	c.307T>C	c.(307-309)TGC>CGC	p.C103R
Pat_59	Post-Resistance	ACMSD	130013	37	2	135621025	135621025	Missense_Mutation	SNP	G	A	4	94	c.310G>A	c.(310-312)GTT>ATT	p.V104I
Pat_59	Post-Resistance	LRP1B	53353	37	2	141609326	141609326	Missense_Mutation	SNP	C	A	18	90	c.4606G>T	c.(4606-4608)GGC>TGC	p.G1536C
Pat_59	Post-Resistance	ZEB2	9839	37	2	145155876	145155876	Missense_Mutation	SNP	C	T	5	65	c.2878G>A	c.(2878-2880)GGA>AGA	p.G960R
Pat_59	Post-Resistance	KIF5C	3800	37	2	149798469	149798469	Missense_Mutation	SNP	G	T	4	88	c.466G>T	c.(466-468)GTT>TTT	p.V156F
Pat_59	Post-Resistance	KIF5C	3800	37	2	149835481	149835481	Nonsense_Mutation	SNP	C	T	10	83	c.1339C>T	c.(1339-1341)CAA>TAA	p.Q447*
Pat_59	Post-Resistance	LYPD6	130574	37	2	150327306	150327306	Missense_Mutation	SNP	C	T	16	107	c.458C>T	c.(457-459)CCA>CTA	p.P153L

Pat_59	Post-Resistance	TANC1	85461	37	2	160053131	160053131	Missense_Mutation	SNP	G	A	8	65	c.2992G>A	c.(2992-2994)GAT>AAT	p.D998N
Pat_59	Post-Resistance	TBR1	10716	37	2	162274810	162274810	Missense_Mutation	SNP	G	A	3	45	c.946G>A	c.(946-948)GGA>AGA	p.G316R
Pat_59	Post-Resistance	SCN9A	6335	37	2	167055671	167055671	Missense_Mutation	SNP	C	T	85	118	c.5445G>A	c.(5443-5445)ATG>ATA	p.M1815I
Pat_59	Post-Resistance	XIRP2	129446	37	2	168101965	168101965	Missense_Mutation	SNP	G	A	5	78	c.4063G>A	c.(4063-4065)GAA>AAA	p.E1355K
Pat_59	Post-Resistance	KBTBD10	10324	37	2	170366969	170366969	Missense_Mutation	SNP	G	A	10	101	c.681G>A	c.(679-681)ATG>ATA	p.M227I
Pat_59	Post-Resistance	METTL5	29081	37	2	170678459	170678459	Missense_Mutation	SNP	C	T	16	235	c.218G>A	c.(217-219)GGA>GAA	p.G73E
Pat_59	Post-Resistance	UBR3	130507	37	2	170857821	170857821	Missense_Mutation	SNP	G	A	14	108	c.3926G>A	c.(3925-3927)TGT>TAT	p.C1309Y
Pat_59	Post-Resistance	MYO3B	140469	37	2	171055725	171055725	Missense_Mutation	SNP	C	G	7	85	c.10C>G	c.(10-12)CTG>GTG	p.L4V
Pat_59	Post-Resistance	MYO3B	140469	37	2	171056786	171056786	Missense_Mutation	SNP	G	A	8	49	c.313G>A	c.(313-315)GTC>ATC	p.V105I
Pat_59	Post-Resistance	MYO3B	140469	37	2	171399445	171399445	Missense_Mutation	SNP	G	A	50	157	c.3605G>A	c.(3604-3606)GGG>GAG	p.G1202E
Pat_59	Post-Resistance	SLC25A12	8604	37	2	172671640	172671640	Missense_Mutation	SNP	C	T	28	192	c.1003G>A	c.(1003-1005)GTT>ATT	p.V335I
Pat_59	Post-Resistance	ITGA6	3655	37	2	173355994	173355994	Missense_Mutation	SNP	C	T	10	179	c.2824C>T	c.(2824-2826)CGG>TGG	p.R942W
Pat_59	Post-Resistance	HNRNPA3	220988	37	2	178081499	178081499	Missense_Mutation	SNP	G	A	48	348	c.739G>A	c.(739-741)GGA>AGA	p.G247R
Pat_59	Post-Resistance	TTN	7273	37	2	179560121	179560121	Missense_Mutation	SNP	T	A	10	77	c.27492A>T	c.(27490-27492)AAA>AAT	p.K9164N
Pat_59	Post-Resistance	TTN	7273	37	2	179596038	179596038	Missense_Mutation	SNP	C	T	80	537	c.13723G>A	c.(13723-13725)GTA>ATA	p.V4575I
Pat_59	Post-Resistance	TTN	7273	37	2	179639078	179639078	Missense_Mutation	SNP	C	T	20	158	c.6913G>A	c.(6913-6915)GAG>AAG	p.E2305K
Pat_59	Post-Resistance	DUSP19	142679	37	2	183960196	183960196	Missense_Mutation	SNP	C	T	25	146	c.464C>T	c.(463-465)TCC>TTC	p.S155F
Pat_59	Post-Resistance	STAT1	6772	37	2	191873711	191873711	Missense_Mutation	SNP	C	T	3	41	c.251G>A	c.(250-252)AGG>AAG	p.R84K
Pat_59	Post-Resistance	MPP4	58538	37	2	202510121	202510121	Missense_Mutation	SNP	C	T	6	66	c.1726G>A	c.(1726-1728)GAC>AAC	p.D576N
Pat_59	Post-Resistance	MPP4	58538	37	2	202520939	202520939	Missense_Mutation	SNP	G	A	3	15	c.1282C>T	c.(1282-1284)CGC>TGC	p.R428C
Pat_59	Post-Resistance	PARD3B	117583	37	2	206480196	206480196	Missense_Mutation	SNP	C	T	9	79	c.3277C>T	c.(3277-3279)CCT>TCT	p.P1093S
Pat_59	Post-Resistance	MDH1B	130752	37	2	207604380	207604380	Missense_Mutation	SNP	C	T	7	63	c.1465G>A	c.(1465-1467)GAG>AAG	p.E489K
Pat_59	Post-Resistance	FZD5	7855	37	2	208632587	208632587	Missense_Mutation	SNP	G	A	2	0	c.877C>T	c.(877-879)CAT>TAT	p.H293Y
Pat_59	Post-Resistance	PIKFYVE	200576	37	2	209207373	209207373	Missense_Mutation	SNP	G	A	25	158	c.5027G>A	c.(5026-5028)AGT>AAT	p.S1676N
Pat_59	Post-Resistance	MYL1	4632	37	2	211163201	211163201	Missense_Mutation	SNP	C	A	4	132	c.247G>T	c.(247-249)GGC>TGC	p.G83C
Pat_59	Post-Resistance	VIL1	7429	37	2	219296591	219296591	Nonsense_Mutation	SNP	C	T	5	12	c.1114C>T	c.(1114-1116)CAG>TAG	p.Q372*
Pat_59	Post-Resistance	ALPPL2	251	37	2	233274467	233274467	Missense_Mutation	SNP	T	C	3	11	c.1484T>C	c.(1483-1485)CTG>CCG	p.L495P
Pat_59	Post-Resistance	DGKD	8527	37	2	234343547	234343547	Missense_Mutation	SNP	G	A	24	124	c.586G>A	c.(586-588)GTG>ATG	p.V196M
Pat_59	Post-Resistance	SH3BP4	23677	37	2	235951118	235951118	Missense_Mutation	SNP	G	A	8	41	c.1705G>A	c.(1705-1707)GTG>ATG	p.V569M
Pat_59	Post-Resistance	COPS8	10920	37	2	238005479	238005479	Missense_Mutation	SNP	G	A	9	44	c.517G>A	c.(517-519)GAT>AAT	p.D173N
Pat_59	Post-Resistance	COL6A3	1293	37	2	238253406	238253406	Missense_Mutation	SNP	C	T	4	134	c.7255G>A	c.(7255-7257)GGC>AGC	p.G2419S
Pat_59	Post-Resistance	MLPH	79083	37	2	238434382	238434382	Missense_Mutation	SNP	G	A	5	22	c.814G>A	c.(814-816)GCC>ACC	p.A272T
Pat_59	Post-Resistance	CAPN10	11132	37	2	241537456	241537456	Missense_Mutation	SNP	C	T	15	13	c.1895C>T	c.(1894-1896)CCG>CTG	p.P632L
Pat_59	Post-Resistance	NSFL1C	55968	37	20	1433177	1433177	Missense_Mutation	SNP	G	A	30	126	c.746C>T	c.(745-747)GCC>GTC	p.A249V
Pat_59	Post-Resistance	TMC2	117532	37	20	2593950	2593950	Nonsense_Mutation	SNP	G	A	8	95	c.1854G>A	c.(1852-1854)TGG>TGA	p.W618*
Pat_59	Post-Resistance	SMOX	54498	37	20	4163099	4163099	Missense_Mutation	SNP	G	A	17	90	c.973G>A	c.(973-975)GCG>ACG	p.A325T
Pat_59	Post-Resistance	PRNP	5621	37	20	4680494	4680494	Missense_Mutation	SNP	G	A	12	94	c.628G>A	c.(628-630)GTT>ATT	p.V210I
Pat_59	Post-Resistance	BTBD3	22903	37	20	11899224	11899224	Missense_Mutation	SNP	G	A	30	171	c.301G>A	c.(301-303)GGT>AGT	p.G101S
Pat_59	Post-Resistance	BTBD3	22903	37	20	11903679	11903679	Missense_Mutation	SNP	G	A	15	110	c.934G>A	c.(934-936)GTT>ATT	p.V312I
Pat_59	Post-Resistance	BFSP1	631	37	20	17475036	17475036	Nonsense_Mutation	SNP	C	A	20	103	c.1681G>T	c.(1681-1683)GAG>TAG	p.E561*
Pat_59	Post-Resistance	BFSP1	631	37	20	17475159	17475159	Missense_Mutation	SNP	G	A	4	30	c.1558C>T	c.(1558-1560)CCT>TCT	p.P520S
Pat_59	Post-Resistance	RIN2	54453	37	20	19955744	19955744	Missense_Mutation	SNP	C	T	18	93	c.1075C>T	c.(1075-1077)CCC>TCC	p.P359S
Pat_59	Post-Resistance	C20orf26	26074	37	20	20258004	20258004	Missense_Mutation	SNP	G	A	33	55	c.2698G>A	c.(2698-2700)GAT>AAT	p.D900N
Pat_59	Post-Resistance	TPX2	22974	37	20	30366668	30366668	Missense_Mutation	SNP	G	A	25	149	c.935G>A	c.(934-936)GGA>GAA	p.G312E
Pat_59	Post-Resistance	ASXL1	171023	37	20	31021379	31021379	Missense_Mutation	SNP	G	A	21	105	c.1378G>A	c.(1378-1380)GGG>AGG	p.G460R
Pat_59	Post-Resistance	ZNF341	84905	37	20	32379180	32379180	Missense_Mutation	SNP	G	A	10	34	c.2422G>A	c.(2422-2424)GCG>ACG	p.A808T
Pat_59	Post-Resistance	ITCH	83737	37	20	33059321	33059321	Splice_Site	SNP	G	A	14	77	c.1692_splice	c.e17+1	p.Q564_splice

Pat_59	Post-Resistance	NCOA6	23054	37	20	33330330	33330330	Missense_Mutation	SNP	G	A	24	111	c.3730C>T	c.(3730-3732)CTC>TTC	p.L1244F
Pat_59	Post-Resistance	RALGAPB	57148	37	20	37198592	37198592	Missense_Mutation	SNP	C	T	10	47	c.4016C>T	c.(4015-4017)CCT>CTT	p.P1339L
Pat_59	Post-Resistance	SLC32A1	140679	37	20	37356239	37356239	Missense_Mutation	SNP	G	A	3	25	c.535G>A	c.(535-537)GTG>ATG	p.V179M
Pat_59	Post-Resistance	NCOA3	8202	37	20	46256433	46256433	Missense_Mutation	SNP	T	C	7	84	c.661T>C	c.(661-663)TAT>CAT	p.Y221H
Pat_59	Post-Resistance	SLC9A8	23315	37	20	48503433	48503433	Missense_Mutation	SNP	G	A	6	45	c.1636G>A	c.(1636-1638)GAG>AAG	p.E546K
Pat_59	Post-Resistance	DPM1	8813	37	20	49551698	49551698	Missense_Mutation	SNP	C	T	28	200	c.754G>A	c.(754-756)GGA>AGA	p.G252R
Pat_59	Post-Resistance	TFAP2C	7022	37	20	55212921	55212921	Missense_Mutation	SNP	G	A	31	189	c.1205G>A	c.(1204-1206)AGC>AAC	p.S402N
Pat_59	Post-Resistance	PMEPA1	56937	37	20	56228109	56228109	Missense_Mutation	SNP	A	G	2	8	c.298T>C	c.(298-300)TCA>CCA	p.S100P
Pat_59	Post-Resistance	CDH4	1002	37	20	60427882	60427882	Missense_Mutation	SNP	G	A	10	61	c.805G>A	c.(805-807)GAC>AAC	p.D269N
Pat_59	Post-Resistance	CDH4	1002	37	20	60448813	60448813	Missense_Mutation	SNP	G	A	14	56	c.907G>A	c.(907-909)GAT>AAT	p.D303N
Pat_59	Post-Resistance	TCFL5	10732	37	20	61492833	61492833	Missense_Mutation	SNP	G	T	4	79	c.190C>A	c.(190-192)CAC>AAC	p.H64N
Pat_59	Post-Resistance	DIDO1	11083	37	20	61511181	61511182	Missense_Mutation	DNP	CC	TT	7	17	.6126_6127GG>A	124-6129)GAGGAG>GAA	p.E2043K
Pat_59	Post-Resistance	USP16	10600	37	21	30426414	30426414	Nonsense_Mutation	SNP	G	A	18	109	c.2378G>A	c.(2377-2379)TGG>TAG	p.W793*
Pat_59	Post-Resistance	TIAM1	7074	37	21	32638927	32638927	Missense_Mutation	SNP	G	A	4	55	c.362C>T	c.(361-363)GCC>GTC	p.A121V
Pat_59	Post-Resistance	RCAN1	1827	37	21	35893877	35893877	Missense_Mutation	SNP	G	A	11	22	c.506C>T	c.(505-507)CCA>CTA	p.P169L
Pat_59	Post-Resistance	KCNJ6	3763	37	21	39087081	39087081	Missense_Mutation	SNP	G	A	14	70	c.379C>T	c.(379-381)CCC>TCC	p.P127S
Pat_59	Post-Resistance	DSCAM	1826	37	21	41459109	41459109	Missense_Mutation	SNP	C	G	4	100	c.3956G>C	c.(3955-3957)TGG>TCG	p.W1319S
Pat_59	Post-Resistance	PCNT	5116	37	21	47754392	47754392	Missense_Mutation	SNP	T	C	3	60	c.349T>C	c.(349-351)TGT>CGT	p.C117R
Pat_59	Post-Resistance	IL17RA	23765	37	22	17581362	17581362	Missense_Mutation	SNP	C	T	12	54	c.541C>T	c.(541-543)CTT>TTT	p.L181F
Pat_59	Post-Resistance	MICAL3	57553	37	22	18387536	18387536	Missense_Mutation	SNP	C	T	13	82	c.334G>A	c.(334-336)GTG>ATG	p.V112M
Pat_59	Post-Resistance	MYO18B	84700	37	22	26159261	26159261	Missense_Mutation	SNP	G	A	3	6	c.103G>A	c.(103-105)GGG>AGG	p.G35R
Pat_59	Post-Resistance	NEFH	4744	37	22	29885313	29885313	Missense_Mutation	SNP	C	G	3	65	c.1684C>G	c.(1684-1686)CCT>GCT	p.P562A
Pat_59	Post-Resistance	SEC14L3	266629	37	22	30866231	30866231	Missense_Mutation	SNP	C	T	3	11	c.142G>A	c.(142-144)GAC>AAC	p.D48N
Pat_59	Post-Resistance	LIMK2	3985	37	22	31656000	31656000	Missense_Mutation	SNP	G	A	4	120	c.488G>A	c.(487-489)CGG>CAG	p.R163Q
Pat_59	Post-Resistance	EIF4ENIF1	56478	37	22	31884687	31884687	Missense_Mutation	SNP	C	T	8	31	c.18G>A	c.(16-18)ATG>ATA	p.M6I
Pat_59	Post-Resistance	DEPDC5	9681	37	22	32215053	32215053	Missense_Mutation	SNP	C	T	12	130	c.1712C>T	c.(1711-1713)GCA>GTA	p.A571V
Pat_59	Post-Resistance	ISX	91464	37	22	35478537	35478537	Missense_Mutation	SNP	C	T	31	64	c.256C>T	c.(256-258)CGT>TGT	p.R86C
Pat_59	Post-Resistance	DDX17	10521	37	22	38882386	38882386	Missense_Mutation	SNP	C	T	8	70	c.1750G>A	c.(1750-1752)GAT>AAT	p.D584N
Pat_59	Post-Resistance	SUN2	25777	37	22	39138464	39138464	Missense_Mutation	SNP	G	A	3	16	c.910C>T	c.(910-912)CGG>TGG	p.R304W
Pat_59	Post-Resistance	EP300	2033	37	22	41572507	41572507	Missense_Mutation	SNP	C	T	9	53	c.5036C>T	c.(5035-5037)ACA>ATA	p.T1679I
Pat_59	Post-Resistance	CSDC2	27254	37	22	41970862	41970862	Missense_Mutation	SNP	C	T	4	5	c.425C>T	c.(424-426)CCC>CTC	p.P142L
Pat_59	Post-Resistance	NAGA	4668	37	22	42458969	42458969	Nonsense_Mutation	SNP	C	T	7	26	c.819G>A	c.(817-819)TGG>TGA	p.W273*
Pat_59	Post-Resistance	NDUFA6	4700	37	22	42483096	42483096	Missense_Mutation	SNP	C	T	59	410	c.301G>A	c.(301-303)GAC>AAC	p.D101N
Pat_59	Post-Resistance	EFCAB6	64800	37	22	44027996	44027996	Missense_Mutation	SNP	C	T	7	57	c.2221G>A	c.(2221-2223)GAG>AAG	p.E741K
Pat_59	Post-Resistance	IL17REL	400935	37	22	50435806	50435806	Missense_Mutation	SNP	C	T	3	13	c.917G>A	c.(916-918)AGT>AAT	p.S306N
Pat_59	Post-Resistance	MOV10L1	54456	37	22	50580557	50580557	Missense_Mutation	SNP	G	T	17	67	c.2118G>T	c.(2116-2118)AGG>AGT	p.R706S
Pat_59	Post-Resistance	CNTN4	152330	37	3	2787298	2787298	Missense_Mutation	SNP	C	T	19	73	c.275C>T	c.(274-276)ACC>ATC	p.T92I
Pat_59	Post-Resistance	STAC	6769	37	3	36485003	36485003	Missense_Mutation	SNP	C	T	23	27	c.259C>T	c.(259-261)CCT>TCT	p.P87S
Pat_59	Post-Resistance	TRANK1	9881	37	3	36884166	36884166	Missense_Mutation	SNP	G	A	9	35	c.3445C>T	c.(3445-3447)CCT>TCT	p.P1149S
Pat_59	Post-Resistance	CCDC13	152206	37	3	42777260	42777260	Missense_Mutation	SNP	A	G	32	29	c.1310T>C	c.(1309-1311)GTA>GCA	p.V437A
Pat_59	Post-Resistance	CYP8B1	1582	37	3	42916093	42916093	Missense_Mutation	SNP	C	T	45	54	c.1216G>A	c.(1216-1218)GAT>AAT	p.D406N
Pat_59	Post-Resistance	C3orf71	646450	37	3	48956104	48956104	Missense_Mutation	SNP	G	A	10	23	c.479C>T	c.(478-480)ACT>ATT	p.T160I
Pat_59	Post-Resistance	WDR6	11180	37	3	49050379	49050379	Missense_Mutation	SNP	C	T	11	19	c.1502C>T	c.(1501-1503)CCC>CTC	p.P501L
Pat_59	Post-Resistance	USP4	7375	37	3	49362451	49362451	Missense_Mutation	SNP	C	T	4	84	c.509G>A	c.(508-510)CGG>CAG	p.R170Q
Pat_59	Post-Resistance	RNF123	63891	37	3	49735373	49735373	Splice_Site	SNP	G	A	33	116	c.397_splice	c.e6+1	p.G133_splice
Pat_59	Post-Resistance	MST1R	4486	37	3	49928076	49928076	Missense_Mutation	SNP	C	T	4	28	c.3652G>A	c.(3652-3654)GAG>AAG	p.E1218K
Pat_59	Post-Resistance	ERC2	26059	37	3	56026137	56026137	Missense_Mutation	SNP	C	T	68	79	c.2203G>A	c.(2203-2205)GAG>AAG	p.E735K

Pat_59	Post-Resistance	C3orf67	200844	37	3	58849294	58849294	Missense_Mutation	SNP	C	T	4	13	c.1208G>A	c.(1207-1209)AGC>AAC	p.S403N
Pat_59	Post-Resistance	PTPRG	5793	37	3	62268462	62268462	Missense_Mutation	SNP	C	T	22	129	c.3973C>T	c.(3973-3975)CCC>TCC	p.P1325S
Pat_59	Post-Resistance	GBE1	2632	37	3	81584371	81584371	Nonsense_Mutation	SNP	G	A	3	45	c.1909C>T	c.(1909-1911)CGA>TGA	p.R637*
Pat_59	Post-Resistance	IMPG2	50939	37	3	100949985	100949985	Missense_Mutation	SNP	G	A	5	216	c.3238C>T	c.(3238-3240)CGG>TGG	p.R1080W
Pat_59	Post-Resistance	WDR52	55779	37	3	113152469	113152469	Missense_Mutation	SNP	C	T	25	97	c.43G>A	c.(43-45)GTT>ATT	p.V15I
Pat_59	Post-Resistance	PLA1A	51365	37	3	119325823	119325823	Splice_Site	SNP	G	A	4	54	c.275_splice	c.e2+1	p.R92_splice
Pat_59	Post-Resistance	TXNRD3IT1	645840	37	3	126291268	126291268	Missense_Mutation	SNP	G	A	4	26	c.119C>T	c.(118-120)ACC>ATC	p.T40I
Pat_59	Post-Resistance	RPN1	6184	37	3	128341114	128341114	Missense_Mutation	SNP	G	A	3	31	c.1534C>T	c.(1534-1536)CTC>TTC	p.L512F
Pat_59	Post-Resistance	DNAJC13	23317	37	3	132218155	132218155	Splice_Site	SNP	G	A	11	60	c.4341_splice	c.e37+1	p.E1447_splice
Pat_59	Post-Resistance	AMOTL2	51421	37	3	134080433	134080433	Missense_Mutation	SNP	G	A	3	28	c.1670C>T	c.(1669-1671)GCC>GTC	p.A557V
Pat_59	Post-Resistance	SLC25A36	55186	37	3	140689814	140689814	Missense_Mutation	SNP	C	T	14	50	c.431C>T	c.(430-432)ACT>ATT	p.T144I
Pat_59	Post-Resistance	ZIC1	7545	37	3	147131190	147131190	Missense_Mutation	SNP	C	T	16	45	c.1196C>T	c.(1195-1197)TCT>TTT	p.S399F
Pat_59	Post-Resistance	TIPARP	25976	37	3	156422730	156422730	Missense_Mutation	SNP	G	A	16	76	c.1784G>A	c.(1783-1785)AGA>AAA	p.R595K
Pat_59	Post-Resistance	CHRD	8646	37	3	184100191	184100191	Nonsense_Mutation	SNP	G	A	33	74	c.714G>A	c.(712-714)TGG>TGA	p.W238*
Pat_59	Post-Resistance	HRG	3273	37	3	186394903	186394903	Missense_Mutation	SNP	G	C	4	70	c.809G>C	c.(808-810)CGT>CCT	p.R270P
Pat_59	Post-Resistance	RFC4	5984	37	3	186522423	186522423	Missense_Mutation	SNP	C	T	32	150	c.80G>A	c.(79-81)GGA>GAA	p.G27E
Pat_59	Post-Resistance	MUC4	4585	37	3	195487886	195487886	Missense_Mutation	SNP	G	A	6	24	c.14333C>T	c.(14332-14334)GCT>GTT	p.A4778V
Pat_59	Post-Resistance	MUC4	4585	37	3	195488993	195488993	Missense_Mutation	SNP	G	A	2	2	c.14093C>T	c.(14092-14094)CCG>CTG	p.P4698L
Pat_59	Post-Resistance	DLG1	1739	37	3	196888525	196888525	Missense_Mutation	SNP	G	A	3	27	c.568C>T	c.(568-570)CCC>TCC	p.P190S
Pat_59	Post-Resistance	PIGG	54872	37	4	527682	527682	Missense_Mutation	SNP	G	A	5	18	c.2647G>A	c.(2647-2649)GCC>ACC	p.A883T
Pat_59	Post-Resistance	SLBP	7884	37	4	1701784	1701784	Missense_Mutation	SNP	G	A	12	33	c.295C>T	c.(295-297)CTC>TTC	p.L99F
Pat_59	Post-Resistance	SH3BP2	6452	37	4	2831592	2831592	Missense_Mutation	SNP	C	T	6	64	c.959C>T	c.(958-960)GCT>GTT	p.A320V
Pat_59	Post-Resistance	PPP2R2C	5522	37	4	6374336	6374336	Missense_Mutation	SNP	G	A	26	60	c.539C>T	c.(538-540)TCC>TTC	p.S180F
Pat_59	Post-Resistance	MAN2B2	23324	37	4	6606902	6606902	Missense_Mutation	SNP	G	A	6	20	c.1660G>A	c.(1660-1662)GAG>AAG	p.E554K
Pat_59	Post-Resistance	SH3TC1	54436	37	4	8230054	8230054	Missense_Mutation	SNP	G	A	13	31	c.2633G>A	c.(2632-2634)CGG>CAG	p.R878Q
Pat_59	Post-Resistance	ARAP2	116984	37	4	36121331	36121331	Missense_Mutation	SNP	C	T	28	136	c.3904G>A	c.(3904-3906)GAT>AAT	p.D1302N
Pat_59	Post-Resistance	GABRG1	2565	37	4	46043129	46043129	Missense_Mutation	SNP	C	T	15	86	c.1274G>A	c.(1273-1275)GGA>GAA	p.G425E
Pat_59	Post-Resistance	CWH43	80157	37	4	49034690	49034690	Missense_Mutation	SNP	G	A	13	111	c.1616G>A	c.(1615-1617)GGC>GAC	p.G539D
Pat_59	Post-Resistance	LRRC66	339977	37	4	52861695	52861695	Missense_Mutation	SNP	C	T	9	74	c.1493G>A	c.(1492-1494)GGA>GAA	p.G498E
Pat_59	Post-Resistance	SULT1E1	6783	37	4	70709896	70709896	Missense_Mutation	SNP	G	A	50	204	c.755C>T	c.(754-756)TCG>TTG	p.S252L
Pat_59	Post-Resistance	RUFY3	22902	37	4	71640910	71640910	Missense_Mutation	SNP	G	A	34	145	c.784G>A	c.(784-786)GAC>AAC	p.D262N
Pat_59	Post-Resistance	SLC4A4	8671	37	4	72412246	72412246	Splice_Site	SNP	G	A	3	24	c.2621_splice	c.e19+1	p.R874_splice
Pat_59	Post-Resistance	SHROOM3	57619	37	4	77676326	77676326	Missense_Mutation	SNP	C	T	7	16	c.4690C>T	c.(4690-4692)CCC>TCC	p.P1564S
Pat_59	Post-Resistance	FRAS1	80144	37	4	79428649	79428649	Missense_Mutation	SNP	G	C	12	36	c.9391G>C	c.(9391-9393)GTC>CTC	p.V3131L
Pat_59	Post-Resistance	BMP2K	55589	37	4	79832960	79832960	Missense_Mutation	SNP	G	A	15	56	c.3259G>A	c.(3259-3261)GGC>AGC	p.G1087S
Pat_59	Post-Resistance	ENOPH1	58478	37	4	83369128	83369128	Missense_Mutation	SNP	G	T	4	64	c.140G>T	c.(139-141)TGG>TTG	p.W47L
Pat_59	Post-Resistance	SEC31A	22872	37	4	83791548	83791548	Missense_Mutation	SNP	G	A	36	110	c.812C>T	c.(811-813)GCA>GTA	p.A271V
Pat_59	Post-Resistance	FAM175A	84142	37	4	84383690	84383690	Missense_Mutation	SNP	G	A	40	152	c.1162C>T	c.(1162-1164)CCA>TCA	p.P388S
Pat_59	Post-Resistance	WDFY3	23001	37	4	85612936	85612936	Missense_Mutation	SNP	G	A	3	21	c.9052C>T	c.(9052-9054)CTC>TTC	p.L3018F
Pat_59	Post-Resistance	TSPAN5	10098	37	4	99408002	99408002	Missense_Mutation	SNP	G	A	20	153	c.166C>T	c.(166-168)CTC>TTC	p.L56F
Pat_59	Post-Resistance	EMCN	51705	37	4	101342534	101342534	Missense_Mutation	SNP	C	T	11	79	c.569G>A	c.(568-570)AGT>AAT	p.S190N
Pat_59	Post-Resistance	ANK2	287	37	4	114277533	114277533	Missense_Mutation	SNP	G	A	12	64	c.7759G>A	c.(7759-7761)GAG>AAG	p.E2587K
Pat_59	Post-Resistance	PRSS12	8492	37	4	119256783	119256783	Missense_Mutation	SNP	G	A	29	148	c.665C>T	c.(664-666)ACC>ATC	p.T222I
Pat_59	Post-Resistance	KIAA1109	84162	37	4	123140495	123140495	Missense_Mutation	SNP	G	A	16	70	c.2248G>A	c.(2248-2250)GAA>AAA	p.E750K
Pat_59	Post-Resistance	DCLK2	166614	37	4	151119157	151119157	Missense_Mutation	SNP	G	A	8	30	c.863G>A	c.(862-864)TGT>TAT	p.C288Y
Pat_59	Post-Resistance	KIAA0922	23240	37	4	154502713	154502713	Splice_Site	SNP	G	A	13	58	c.892_splice	c.e9+1	p.D298_splice
Pat_59	Post-Resistance	TLR2	7097	37	4	154625222	154625222	Missense_Mutation	SNP	C	T	17	40	c.1163C>T	c.(1162-1164)TCT>TTT	p.S388F

Pat_59	Post-Resistance	FGB	2244	37	4	155490797	155490797	Missense_Mutation	SNP	G	A	13	47	c.1090G>A	c.(1090-1092)GAA>AAA	p.E364K
Pat_59	Post-Resistance	RXFP1	59350	37	4	159569854	159569854	Nonsense_Mutation	SNP	C	T	6	29	c.1960C>T	c.(1960-1962)CAG>TAG	p.Q654*
Pat_59	Post-Resistance	NAF1	92345	37	4	164085478	164085478	Missense_Mutation	SNP	G	A	7	36	c.431C>T	c.(430-432)TCC>TTC	p.S144F
Pat_59	Post-Resistance	TMEM192	201931	37	4	166009740	166009740	Missense_Mutation	SNP	G	A	3	24	c.454C>T	c.(454-456)CTC>TTC	p.L152F
Pat_59	Post-Resistance	TLL1	7092	37	4	166964438	166964438	Missense_Mutation	SNP	G	A	32	184	c.1391G>A	c.(1390-1392)GGT>GAT	p.G464D
Pat_59	Post-Resistance	WDR17	116966	37	4	177100701	177100701	Missense_Mutation	SNP	G	C	24	131	c.3940G>C	c.(3940-3942)GGG>CGG	p.G1314R
Pat_59	Post-Resistance	KLKB1	3818	37	4	187175919	187175919	Splice_Site	SNP	T	C	6	29	c.1489_splice	c.e12+2	p.E497_splice
Pat_59	Post-Resistance	F11	2160	37	4	187195347	187195347	Missense_Mutation	SNP	G	A	14	83	c.403G>A	c.(403-405)GAA>AAA	p.E135K
Pat_59	Post-Resistance	NIPBL	25836	37	5	37008777	37008777	Missense_Mutation	SNP	C	T	39	150	c.4373C>T	c.(4372-4374)ACT>ATT	p.T1458I
Pat_59	Post-Resistance	PRKAA1	5562	37	5	40764960	40764960	Missense_Mutation	SNP	C	T	12	33	c.1202G>A	c.(1201-1203)GGT>GAT	p.G401D
Pat_59	Post-Resistance	CARD6	84674	37	5	40853842	40853842	Missense_Mutation	SNP	C	T	69	213	c.2408C>T	c.(2407-2409)TCC>TTC	p.S803F
Pat_59	Post-Resistance	TNPO1	3842	37	5	72201170	72201170	Nonsense_Mutation	SNP	G	A	31	103	c.2630G>A	c.(2629-2631)TGG>TAG	p.W877*
Pat_59	Post-Resistance	HMGCR	3156	37	5	74647425	74647425	Missense_Mutation	SNP	G	A	16	49	c.1366G>A	c.(1366-1368)GAG>AAG	p.E456K
Pat_59	Post-Resistance	SPZ1	84654	37	5	79616081	79616081	Missense_Mutation	SNP	C	T	38	141	c.47C>T	c.(46-48)ACC>ATC	p.T16I
Pat_59	Post-Resistance	HAPLN1	1404	37	5	82940241	82940242	Missense_Mutation	DNP	CC	TT	21	39	c.715_716GG>AA	c.(715-717)GGA>AAA	p.G239K
Pat_59	Post-Resistance	PCSK1	5122	37	5	95746489	95746489	Missense_Mutation	SNP	C	T	41	44	c.1084G>A	c.(1084-1086)GAC>AAC	p.D362N
Pat_59	Post-Resistance	GIN1	54826	37	5	102433155	102433155	Nonsense_Mutation	SNP	G	A	4	125	c.871C>T	c.(871-873)CGA>TGA	p.R291*
Pat_59	Post-Resistance	WDR36	134430	37	5	110445948	110445948	Missense_Mutation	SNP	G	A	37	121	c.1555G>A	c.(1555-1557)GAT>AAT	p.D519N
Pat_59	Post-Resistance	CAMK4	814	37	5	110782463	110782463	Missense_Mutation	SNP	C	A	5	114	c.539C>A	c.(538-540)CCA>CAA	p.P180Q
Pat_59	Post-Resistance	APC	324	37	5	112175228	112175228	Missense_Mutation	SNP	A	G	11	27	c.3937A>G	c.(3937-3939)ACT>GCT	p.T1313A
Pat_59	Post-Resistance	CCDC112	153733	37	5	114611031	114611031	Missense_Mutation	SNP	C	T	25	71	c.551G>A	c.(550-552)GGG>GAG	p.G184E
Pat_59	Post-Resistance	COMMD10	51397	37	5	115423238	115423238	Missense_Mutation	SNP	G	A	28	87	c.86G>A	c.(85-87)AGA>AAA	p.R29K
Pat_59	Post-Resistance	SNCAIP	9627	37	5	121759351	121759351	Nonsense_Mutation	SNP	C	T	14	67	c.919C>T	c.(919-921)CAA>TAA	p.Q307*
Pat_59	Post-Resistance	CEP120	153241	37	5	122734882	122734882	Missense_Mutation	SNP	G	A	4	91	c.560C>T	c.(559-561)ACT>ATT	p.T187I
Pat_59	Post-Resistance	ZNF608	57507	37	5	123979209	123979209	Missense_Mutation	SNP	G	A	11	40	c.4291C>T	c.(4291-4293)CCT>TCT	p.P1431S
Pat_59	Post-Resistance	ALDH7A1	501	37	5	125930766	125930766	Missense_Mutation	SNP	A	G	2	5	c.125T>C	c.(124-126)CTG>CCG	p.L42P
Pat_59	Post-Resistance	SEC24A	10802	37	5	134010449	134010449	Missense_Mutation	SNP	C	A	5	35	c.962C>A	c.(961-963)CCA>CAA	p.P321Q
Pat_59	Post-Resistance	HNRNPA0	10949	37	5	137089511	137089511	Missense_Mutation	SNP	G	A	4	76	c.245C>T	c.(244-246)GCG>GTG	p.A82V
Pat_59	Post-Resistance	LRRTM2	26045	37	5	138209228	138209228	Missense_Mutation	SNP	C	T	26	32	c.1022G>A	c.(1021-1023)AGT>AAT	p.S341N
Pat_59	Post-Resistance	PCDHA9	9752	37	5	140229062	140229062	Missense_Mutation	SNP	C	T	4	11	c.982C>T	c.(982-984)CCA>TCA	p.P328S
Pat_59	Post-Resistance	ARAP3	64411	37	5	141041635	141041635	Missense_Mutation	SNP	C	A	4	109	c.2988G>T	c.(2986-2988)TTG>TTT	p.L996F
Pat_59	Post-Resistance	POU4F3	5459	37	5	145719837	145719837	Missense_Mutation	SNP	G	A	3	18	c.847G>A	c.(847-849)GCG>ACG	p.A283T
Pat_59	Post-Resistance	FOXI1	2299	37	5	169533194	169533194	Missense_Mutation	SNP	G	A	2	2	c.233G>A	c.(232-234)GGC>GAC	p.G78D
Pat_59	Post-Resistance	HK3	3101	37	5	176316669	176316669	Missense_Mutation	SNP	G	A	24	43	c.707C>T	c.(706-708)CCG>CTG	p.P236L
Pat_59	Post-Resistance	NSD1	64324	37	5	176722305	176722305	Missense_Mutation	SNP	G	A	15	59	c.7936G>A	c.(7936-7938)GCA>ACA	p.A2646T
Pat_59	Post-Resistance	WRNIP1	56897	37	6	2766533	2766533	Missense_Mutation	SNP	C	T	6	28	c.677C>T	c.(676-678)CCG>CTG	p.P226L
Pat_59	Post-Resistance	RIPK1	8737	37	6	3106127	3106127	Missense_Mutation	SNP	G	A	7	39	c.1418G>A	c.(1417-1419)GGC>GAC	p.G473D
Pat_59	Post-Resistance	TUBB2B	347733	37	6	3225034	3225034	Missense_Mutation	SNP	G	A	5	57	c.1289C>T	c.(1288-1290)GCC>GTC	p.A430V
Pat_59	Post-Resistance	LY86	9450	37	6	6626622	6626623	Missense_Mutation	DNP	CC	TT	10	32	c.320_321CC>TT	c.(319-321)CCC>CTT	p.P107L
Pat_59	Post-Resistance	DSP	1832	37	6	7559602	7559602	Missense_Mutation	SNP	G	A	4	67	c.566G>A	c.(565-567)AGT>AAT	p.S189N
Pat_59	Post-Resistance	SYCP2L	221711	37	6	10959016	10959016	Splice_Site	SNP	G	A	3	46	c.2164_splice	c.e26-1	p.L722_splice
Pat_59	Post-Resistance	PHACTR1	221692	37	6	13206259	13206259	Missense_Mutation	SNP	G	A	4	43	c.877G>A	c.(877-879)GGC>AGC	p.G293S
Pat_59	Post-Resistance	FAM8A1	51439	37	6	17602924	17602924	Missense_Mutation	SNP	G	A	25	121	c.816G>A	c.(814-816)ATG>ATA	p.M272I
Pat_59	Post-Resistance	LRRC16A	55604	37	6	25610371	25610371	Missense_Mutation	SNP	G	A	19	70	c.3941G>A	c.(3940-3942)AGT>AAT	p.S1314N
Pat_59	Post-Resistance	HIST1H2BG	8339	37	6	26216561	26216561	Missense_Mutation	SNP	G	A	57	284	c.311C>T	c.(310-312)CCC>CTC	p.P104L
Pat_59	Post-Resistance	BTN2A3	54718	37	6	26431550	26431550	Missense_Mutation	SNP	G	A	17	51	c.1468G>A	c.(1468-1470)GGG>AGG	p.G490R
Pat_59	Post-Resistance	HIST1H2AJ	8331	37	6	27782454	27782454	Missense_Mutation	SNP	G	A	16	96	c.65C>T	c.(64-66)GCC>GTC	p.A22V

Pat_59	Post-Resistance	MUC21	394263	37	6	30955295	30955295	Missense_Mutation	SNP	G	A	12	93	c.1343G>A	c.(1342-1344)GGA>GAA	p.G448E
Pat_59	Post-Resistance	HLA-DRA	3122	37	6	32411211	32411211	Nonsense_Mutation	SNP	G	A	5	65	c.578G>A	c.(577-579)TGG>TAG	p.W193*
Pat_59	Post-Resistance	BRPF3	27154	37	6	36196724	36196724	Missense_Mutation	SNP	G	A	4	58	c.3325G>A	c.(3325-3327)GTT>ATT	p.V1109I
Pat_59	Post-Resistance	DAAM2	23500	37	6	39869077	39869077	Splice_Site	SNP	G	A	57	237	c.2812_splice	c.e24-1	p.F938_splice
Pat_59	Post-Resistance	TREM1	54210	37	6	41250277	41250277	Missense_Mutation	SNP	C	T	7	36	c.262G>A	c.(262-264)GAA>AAA	p.E88K
Pat_59	Post-Resistance	FRS3	10817	37	6	41738497	41738497	Missense_Mutation	SNP	G	A	16	64	c.1339C>T	c.(1339-1341)CAC>TAC	p.H447Y
Pat_59	Post-Resistance	POLH	5429	37	6	43582212	43582212	Missense_Mutation	SNP	G	A	35	201	c.2060G>A	c.(2059-2061)AGC>AAC	p.S687N
Pat_59	Post-Resistance	TMEM63B	55362	37	6	44116284	44116284	Missense_Mutation	SNP	G	A	11	71	c.1156G>A	c.(1156-1158)GGC>AGC	p.G386S
Pat_59	Post-Resistance	CAPN11	11131	37	6	44147779	44147779	Missense_Mutation	SNP	G	A	20	128	c.1519G>A	c.(1519-1521)GAG>AAG	p.E507K
Pat_59	Post-Resistance	GPR110	266977	37	6	46976856	46976856	Missense_Mutation	SNP	G	A	15	49	c.2315C>T	c.(2314-2316)CCG>CTG	p.P772L
Pat_59	Post-Resistance	GPR110	266977	37	6	46984373	46984373	Missense_Mutation	SNP	G	A	5	60	c.743C>T	c.(742-744)TCT>TTT	p.S248F
Pat_59	Post-Resistance	LRRC1	55227	37	6	53660160	53660160	Missense_Mutation	SNP	C	T	3	42	c.106C>T	c.(106-108)CGG>TGG	p.R36W
Pat_59	Post-Resistance	KHDRBS2	202559	37	6	62611258	62611258	Missense_Mutation	SNP	G	A	32	94	c.502C>T	c.(502-504)CGT>TGT	p.R168C
Pat_59	Post-Resistance	IMPG1	3617	37	6	76713604	76713604	Missense_Mutation	SNP	G	A	13	90	c.1199C>T	c.(1198-1200)GCT>GTT	p.A400V
Pat_59	Post-Resistance	BCKDHB	594	37	6	80912903	80912903	Missense_Mutation	SNP	C	T	20	118	c.925C>T	c.(925-927)CCT>TCT	p.P309S
Pat_59	Post-Resistance	SYNCRIP	10492	37	6	86346837	86346837	Missense_Mutation	SNP	C	T	6	39	c.514G>A	c.(514-516)GAT>AAT	p.D172N
Pat_59	Post-Resistance	ORC3L	23595	37	6	88362837	88362837	Missense_Mutation	SNP	G	A	35	209	c.1386G>A	c.(1384-1386)ATG>ATA	p.M462I
Pat_59	Post-Resistance	USP45	85015	37	6	99885263	99885263	Missense_Mutation	SNP	C	T	6	36	c.2173G>A	c.(2173-2175)GGA>AGA	p.G725R
Pat_59	Post-Resistance	SMPD2	6610	37	6	109763242	109763242	Missense_Mutation	SNP	T	C	98	167	c.290T>C	c.(289-291)ATC>ACC	p.I97T
Pat_59	Post-Resistance	FIG4	9896	37	6	110059614	110059614	Missense_Mutation	SNP	G	A	15	99	c.733G>A	c.(733-735)GAC>AAC	p.D245N
Pat_59	Post-Resistance	NUS1	116150	37	6	118024809	118024809	Missense_Mutation	SNP	G	A	39	203	c.733G>A	c.(733-735)GGT>AGT	p.G245S
Pat_59	Post-Resistance	ASF1A	25842	37	6	119226836	119226836	Missense_Mutation	SNP	G	A	46	295	c.245G>A	c.(244-246)GGA>GAA	p.G82E
Pat_59	Post-Resistance	TRDN	10345	37	6	123673726	123673726	Missense_Mutation	SNP	G	A	8	56	c.1327C>T	c.(1327-1329)CCT>TCT	p.P443S
Pat_59	Post-Resistance	TNFAIP3	7128	37	6	138200429	138200429	Missense_Mutation	SNP	G	A	10	110	c.1847G>A	c.(1846-1848)GGG>GAG	p.G616E
Pat_59	Post-Resistance	TNFAIP3	7128	37	6	138202343	138202343	Missense_Mutation	SNP	C	T	41	135	c.2260C>T	c.(2260-2262)CCC>TCC	p.P754S
Pat_59	Post-Resistance	GPR126	57211	37	6	142724989	142724989	Missense_Mutation	SNP	C	T	15	79	c.2006C>T	c.(2005-2007)ACA>ATA	p.T669I
Pat_59	Post-Resistance	ZBTB2	57621	37	6	151687915	151687915	Missense_Mutation	SNP	C	T	28	107	c.286G>A	c.(286-288)GAA>AAA	p.E96K
Pat_59	Post-Resistance	RBM16	22828	37	6	155153855	155153855	Missense_Mutation	SNP	G	A	10	59	c.3142G>A	c.(3142-3144)GGT>AGT	p.G1048S
Pat_59	Post-Resistance	MLLT4	4301	37	6	168319484	168319484	Missense_Mutation	SNP	G	A	11	70	c.2755G>A	c.(2755-2757)GAA>AAA	p.E919K
Pat_59	Post-Resistance	MLLT4	4301	37	6	168352185	168352185	Missense_Mutation	SNP	G	A	30	197	c.4127G>A	c.(4126-4128)GGT>GAT	p.G1376D
Pat_59	Post-Resistance	DLL1	28514	37	6	170592964	170592964	Missense_Mutation	SNP	G	A	3	17	c.1403C>T	c.(1402-1404)ACC>ATC	p.T468I
Pat_59	Post-Resistance	HEATR2	54919	37	7	794252	794252	Missense_Mutation	SNP	G	A	30	133	c.1051G>A	c.(1051-1053)GAG>AAG	p.E351K
Pat_59	Post-Resistance	C7orf27	221927	37	7	2578169	2578169	Missense_Mutation	SNP	C	T	3	3	c.2000G>A	c.(1999-2001)GGG>GAG	p.G667E
Pat_59	Post-Resistance	PMS2	5395	37	7	6027053	6027053	Missense_Mutation	SNP	C	T	10	36	c.1343G>A	c.(1342-1344)GGA>GAA	p.G448E
Pat_59	Post-Resistance	PMS2	5395	37	7	6043602	6043602	Splice_Site	SNP	C	T	26	195	c.250_splice	c.e3+1	p.T84_splice
Pat_59	Post-Resistance	DAGLB	221955	37	7	6487441	6487441	Nonsense_Mutation	SNP	C	T	4	18	c.33G>A	c.(31-33)TGG>TGA	p.W11*
Pat_59	Post-Resistance	ZNF12	7559	37	7	6732287	6732287	Missense_Mutation	SNP	C	T	28	161	c.286G>A	c.(286-288)GAA>AAA	p.E96K
Pat_59	Post-Resistance	ABCB5	340273	37	7	20725446	20725446	Missense_Mutation	SNP	C	T	7	61	c.662C>T	c.(661-663)ACC>ATC	p.T221I
Pat_59	Post-Resistance	OSBPL3	26031	37	7	24905787	24905787	Missense_Mutation	SNP	C	T	26	93	c.451G>A	c.(451-453)GAA>AAA	p.E151K
Pat_59	Post-Resistance	CCDC129	223075	37	7	31617722	31617722	Missense_Mutation	SNP	G	A	13	14	c.844G>A	c.(844-846)GAA>AAA	p.E282K
Pat_59	Post-Resistance	HERPUD2	64224	37	7	35707173	35707173	Missense_Mutation	SNP	G	A	4	93	c.365C>T	c.(364-366)ACT>ATT	p.T122I
Pat_59	Post-Resistance	ELMO1	9844	37	7	37264560	37264560	Missense_Mutation	SNP	C	T	5	37	c.625G>A	c.(625-627)GTG>ATG	p.V209M
Pat_59	Post-Resistance	TXNDC3	51314	37	7	37916531	37916531	Missense_Mutation	SNP	G	A	10	22	c.916G>A	c.(916-918)GAT>AAT	p.D306N
Pat_59	Post-Resistance	VPS41	27072	37	7	38835078	38835078	Missense_Mutation	SNP	C	T	11	118	c.704G>A	c.(703-705)GGG>GAG	p.G235E
Pat_59	Post-Resistance	TNS3	64759	37	7	47408363	47408363	Missense_Mutation	SNP	G	A	6	27	c.1880C>T	c.(1879-1881)CCC>CTC	p.P627L
Pat_59	Post-Resistance	ABCA13	154664	37	7	48285548	48285548	Missense_Mutation	SNP	G	A	13	51	c.1580G>A	c.(1579-1581)GGT>GAT	p.G527D
Pat_59	Post-Resistance	14-Sep	346288	37	7	55914284	55914284	Missense_Mutation	SNP	C	T	18	120	c.101G>A	c.(100-102)GGT>GAT	p.G34D

Pat_59	Post-Resistance	ZNF479	90827	37	7	57187795	57187795	Missense_Mutation	SNP	C	A	4	127	c.1327G>T	c.(1327-1329)GGC>TGC	p.G443C
Pat_59	Post-Resistance	SPDYE5	442590	37	7	75130942	75130942	Missense_Mutation	SNP	C	T	7	350	c.817C>T	c.(817-819)CGG>TGG	p.R273W
Pat_59	Post-Resistance	SPDYE5	442590	37	7	75130958	75130958	Missense_Mutation	SNP	G	A	9	292	c.833G>A	c.(832-834)CGT>CAT	p.R278H
Pat_59	Post-Resistance	PION	54103	37	7	76940695	76940695	Missense_Mutation	SNP	C	T	5	161	c.2545G>A	c.(2545-2547)GCG>ACG	p.A849T
Pat_59	Post-Resistance	SEMA3C	10512	37	7	80374401	80374401	Missense_Mutation	SNP	G	A	23	174	c.2065C>T	c.(2065-2067)CAC>TAC	p.H689Y
Pat_59	Post-Resistance	PCLO	27445	37	7	82582822	82582822	Missense_Mutation	SNP	G	A	10	73	c.7447C>T	c.(7447-7449)CCT>TCT	p.P2483S
Pat_59	Post-Resistance	KIAA1324L	222223	37	7	86542393	86542393	Missense_Mutation	SNP	G	A	15	64	c.1859C>T	c.(1858-1860)CCC>CTC	p.P620L
Pat_59	Post-Resistance	DBF4	10926	37	7	87537185	87537185	Missense_Mutation	SNP	G	A	15	119	c.1732G>A	c.(1732-1734)GTG>ATG	p.V578M
Pat_59	Post-Resistance	FAM133B	257415	37	7	92210819	92210819	Splice_Site	SNP	C	T	8	72	c.122_splice	c.e2+1	p.W41_splice
Pat_59	Post-Resistance	CALCR	799	37	7	93101770	93101770	Missense_Mutation	SNP	C	T	151	152	c.400G>A	c.(400-402)GGT>AGT	p.G134S
Pat_59	Post-Resistance	COL1A2	1278	37	7	94039582	94039582	Missense_Mutation	SNP	G	A	8	84	c.1064G>A	c.(1063-1065)GGA>GAA	p.G355E
Pat_59	Post-Resistance	BAIAP2L1	55971	37	7	97923410	97923410	Missense_Mutation	SNP	C	T	10	74	c.1436G>A	c.(1435-1437)GGG>GAG	p.G479E
Pat_59	Post-Resistance	TRRAP	8295	37	7	98550857	98550857	Missense_Mutation	SNP	C	T	4	65	c.5510C>T	c.(5509-5511)ACG>ATG	p.T1837M
Pat_59	Post-Resistance	ZKSCAN5	23660	37	7	99128994	99128994	Missense_Mutation	SNP	C	T	5	59	c.1642C>T	c.(1642-1644)CCA>TCA	p.P548S
Pat_59	Post-Resistance	ZAN	7455	37	7	100349941	100349941	Missense_Mutation	SNP	C	T	7	143	c.2213C>T	c.(2212-2214)CCC>CTC	p.P738L
Pat_59	Post-Resistance	SRRT	51593	37	7	100485432	100485432	Missense_Mutation	SNP	C	T	13	93	c.2278C>T	c.(2278-2280)CCA>TCA	p.P760S
Pat_59	Post-Resistance	UFSP1	402682	37	7	100486757	100486757	Missense_Mutation	SNP	C	T	17	74	c.136G>A	c.(136-138)GAG>AAG	p.E46K
Pat_59	Post-Resistance	CUX1	1523	37	7	101845411	101845411	Missense_Mutation	SNP	C	T	17	150	c.2834C>T	c.(2833-2835)ACC>ATC	p.T945I
Pat_59	Post-Resistance	MLL5	55904	37	7	104753005	104753005	Missense_Mutation	SNP	G	A	16	225	c.4802G>A	c.(4801-4803)GGA>GAA	p.G1601E
Pat_59	Post-Resistance	COG5	10466	37	7	107002483	107002483	Missense_Mutation	SNP	C	T	7	23	c.1114G>A	c.(1114-1116)GTT>ATT	p.V372I
Pat_59	Post-Resistance	LAMB4	22798	37	7	107706245	107706245	Missense_Mutation	SNP	C	T	6	236	c.2798G>A	c.(2797-2799)AGC>AAC	p.S933N
Pat_59	Post-Resistance	ASZ1	136991	37	7	117025852	117025852	Missense_Mutation	SNP	G	A	4	108	c.452C>T	c.(451-453)ACC>ATC	p.T151I
Pat_59	Post-Resistance	CFTR	1080	37	7	117232649	117232650	Missense_Mutation	DNP	AG	GA	41	47	.2428_2429AG>G	c.(2428-2430)AGA>GAA	p.R810E
Pat_59	Post-Resistance	CFTR	1080	37	7	117307025	117307025	Missense_Mutation	SNP	C	T	10	36	c.4306C>T	c.(4306-4308)CTC>TTC	p.L1436F
Pat_59	Post-Resistance	GCC1	79571	37	7	127222640	127222640	Missense_Mutation	SNP	G	A	4	33	c.1756C>T	c.(1756-1758)CAC>TAC	p.H586Y
Pat_59	Post-Resistance	SND1	27044	37	7	127334887	127334887	Nonsense_Mutation	SNP	G	A	26	161	c.234G>A	c.(232-234)TGG>TGA	p.W78*
Pat_59	Post-Resistance	FLNC	2318	37	7	128475434	128475434	Missense_Mutation	SNP	C	T	4	116	c.407C>T	c.(406-408)ACG>ATG	p.T136M
Pat_59	Post-Resistance	SMO	6608	37	7	128851597	128851597	Missense_Mutation	SNP	C	T	21	47	c.1922C>T	c.(1921-1923)CCT>CTT	p.P641L
Pat_59	Post-Resistance	CPA5	93979	37	7	130007413	130007413	Splice_Site	SNP	G	A	8	82	c.1038_splice	c.e12+1	p.L346_splice
Pat_59	Post-Resistance	PODXL	5420	37	7	131194182	131194182	Missense_Mutation	SNP	G	A	18	77	c.965C>T	c.(964-966)TCA>TTA	p.S322L
Pat_59	Post-Resistance	CALD1	800	37	7	134617909	134617909	Missense_Mutation	SNP	T	C	4	51	c.389T>C	c.(388-390)CTG>CCG	p.L130P
Pat_59	Post-Resistance	ZC3HAV1	56829	37	7	138732506	138732506	Missense_Mutation	SNP	C	T	21	146	c.2543G>A	c.(2542-2544)GGA>GAA	p.G848E
Pat_59	Post-Resistance	BRAF	673	37	7	140453136	140453136	Missense_Mutation	SNP	A	T	67	84	c.1799T>A	c.(1798-1800)GTG>GAG	p.V600E
Pat_59	Post-Resistance	BRAF	673	37	7	140477794	140477794	Missense_Mutation	SNP	A	T	15	95	c.1514T>A	c.(1513-1515)CTC>CAC	p.L505H
Pat_59	Post-Resistance	AGK	55750	37	7	141296362	141296362	Missense_Mutation	SNP	G	A	10	155	c.142G>A	c.(142-144)GTG>ATG	p.V48M
Pat_59	Post-Resistance	EPHB6	2051	37	7	142568007	142568007	Missense_Mutation	SNP	C	T	45	349	c.2648C>T	c.(2647-2649)CCT>CTT	p.P883L
Pat_59	Post-Resistance	CASP2	835	37	7	142997052	142997052	Missense_Mutation	SNP	C	T	10	76	c.784C>T	c.(784-786)CCT>TCT	p.P262S
Pat_59	Post-Resistance	ZNF746	155061	37	7	149171719	149171719	Missense_Mutation	SNP	C	T	3	20	c.1691G>A	c.(1690-1692)CGG>CAG	p.R564Q
Pat_59	Post-Resistance	AGAP3	116988	37	7	150837123	150837123	Missense_Mutation	SNP	C	T	7	19	c.1724C>T	c.(1723-1725)CCC>CTC	p.P575L
Pat_59	Post-Resistance	CRYGN	155051	37	7	151133333	151133333	Missense_Mutation	SNP	G	A	11	51	c.349C>T	c.(349-351)CCC>TCC	p.P117S
Pat_59	Post-Resistance	MLL3	58508	37	7	151945629	151945629	Missense_Mutation	SNP	C	T	18	118	c.1890G>A	c.(1888-1890)ATG>ATA	p.M630I
Pat_59	Post-Resistance	UBE3C	9690	37	7	157009660	157009660	Missense_Mutation	SNP	G	A	5	77	c.1909G>A	c.(1909-1911)GAT>AAT	p.D637N
Pat_59	Post-Resistance	CSMD1	64478	37	8	3216739	3216739	Missense_Mutation	SNP	G	A	24	98	c.3242C>T	c.(3241-3243)GCC>GTC	p.A1081V
Pat_59	Post-Resistance	PRSS55	203074	37	8	10388830	10388830	Missense_Mutation	SNP	G	A	21	113	c.373G>A	c.(373-375)GGG>AGG	p.G125R
Pat_59	Post-Resistance	XKR6	286046	37	8	11058244	11058244	Missense_Mutation	SNP	C	T	2	0	c.605G>A	c.(604-606)CGG>CAG	p.R202Q
Pat_59	Post-Resistance	MTUS1	57509	37	8	17611888	17611888	Missense_Mutation	SNP	G	A	73	281	c.1429C>T	c.(1429-1431)CCC>TCC	p.P477S
Pat_59	Post-Resistance	KIAA1967	57805	37	8	22471697	22471697	Missense_Mutation	SNP	C	T	10	62	c.797C>T	c.(796-798)GCC>GTC	p.A266V

Pat_59	Post-Resistance	TNFRSF10A	8797	37	8	23054717	23054717	Missense_Mutation	SNP	C	T	12	84	c.1015G>A	c.(1015-1017)GGA>AGA	p.G339R
Pat_59	Post-Resistance	ENTPD4	9583	37	8	23290620	23290620	Missense_Mutation	SNP	C	T	9	46	c.1670G>A	c.(1669-1671)GGC>GAC	p.G557D
Pat_59	Post-Resistance	PBK	55872	37	8	27679862	27679862	Missense_Mutation	SNP	C	T	19	63	c.439G>A	c.(439-441)GCT>ACT	p.A147T
Pat_59	Post-Resistance	TEX15	56154	37	8	30702303	30702303	Missense_Mutation	SNP	C	T	15	122	c.4231G>A	c.(4231-4233)GAT>AAT	p.D1411N
Pat_59	Post-Resistance	ERLIN2	11160	37	8	37597963	37597963	Missense_Mutation	SNP	A	G	39	169	c.188A>G	c.(187-189)CAG>CGG	p.Q63R
Pat_59	Post-Resistance	RAB11FIP1	80223	37	8	37732693	37732693	Missense_Mutation	SNP	C	T	32	225	c.962G>A	c.(961-963)GGG>GAG	p.G321E
Pat_59	Post-Resistance	BAG4	9530	37	8	38050222	38050222	Missense_Mutation	SNP	C	T	11	63	c.287C>T	c.(286-288)CCT>CTT	p.P96L
Pat_59	Post-Resistance	IDO1	3620	37	8	39780144	39780144	Missense_Mutation	SNP	G	A	6	33	c.511G>A	c.(511-513)GAA>AAA	p.E171K
Pat_59	Post-Resistance	ANK1	286	37	8	41573366	41573366	Missense_Mutation	SNP	T	C	3	12	c.1406A>G	c.(1405-1407)GAT>GGT	p.D469G
Pat_59	Post-Resistance	HOOK3	84376	37	8	42868500	42868500	Missense_Mutation	SNP	G	A	17	137	c.1973G>A	c.(1972-1974)AGA>AAA	p.R658K
Pat_59	Post-Resistance	HGSNAT	138050	37	8	43002133	43002133	Missense_Mutation	SNP	C	T	9	50	c.161C>T	c.(160-162)GCT>GTT	p.A54V
Pat_59	Post-Resistance	PRKDC	5591	37	8	48690250	48690250	Nonsense_Mutation	SNP	C	T	22	114	c.12039G>A	c.(12037-12039)TGG>TGA	p.W4013*
Pat_59	Post-Resistance	MCM4	4173	37	8	48878860	48878860	Missense_Mutation	SNP	G	A	37	45	c.946G>A	c.(946-948)GAG>AAG	p.E316K
Pat_59	Post-Resistance	GGH	8836	37	8	63930157	63930157	Missense_Mutation	SNP	G	A	39	166	c.730C>T	c.(730-732)CAT>TAT	p.H244Y
Pat_59	Post-Resistance	SGK3	23678	37	8	67726150	67726150	Missense_Mutation	SNP	G	A	9	91	c.316G>A	c.(316-318)GAA>AAA	p.E106K
Pat_59	Post-Resistance	C8orf34	116328	37	8	69688655	69688655	Missense_Mutation	SNP	G	A	21	46	c.1168G>A	c.(1168-1170)GGA>AGA	p.G390R
Pat_59	Post-Resistance	JPH1	56704	37	8	75227730	75227730	Missense_Mutation	SNP	C	G	2	6	c.505G>C	c.(505-507)GAG>CAG	p.E169Q
Pat_59	Post-Resistance	WWP1	11059	37	8	87410597	87410597	Missense_Mutation	SNP	C	T	18	121	c.361C>T	c.(361-363)CTT>TTT	p.L121F
Pat_59	Post-Resistance	TMEM67	91147	37	8	94776088	94776088	Missense_Mutation	SNP	G	A	16	74	c.425G>A	c.(424-426)GGA>GAA	p.G142E
Pat_59	Post-Resistance	KIAA1429	25962	37	8	95501065	95501065	Missense_Mutation	SNP	G	A	4	84	c.5308C>T	c.(5308-5310)CGT>TGT	p.R1770C
Pat_59	Post-Resistance	TP53INP1	94241	37	8	95952419	95952419	Missense_Mutation	SNP	C	T	9	62	c.142G>A	c.(142-144)GAA>AAA	p.E48K
Pat_59	Post-Resistance	UBR5	51366	37	8	103266598	103266598	Missense_Mutation	SNP	A	G	12	73	c.8332T>C	c.(8332-8334)TCC>CCC	p.S2778P
Pat_59	Post-Resistance	RIMS2	9699	37	8	104897844	104897844	Missense_Mutation	SNP	G	T	4	63	c.351G>T	c.(349-351)TTG>TTT	p.L117F
Pat_59	Post-Resistance	EIF3E	3646	37	8	109240542	109240542	Missense_Mutation	SNP	G	A	54	236	c.676C>T	c.(676-678)CCC>TCC	p.P226S
Pat_59	Post-Resistance	TNFRSF11B	4982	37	8	119945383	119945383	Missense_Mutation	SNP	C	T	7	252	c.187G>A	c.(187-189)GCC>ACC	p.A63T
Pat_59	Post-Resistance	NOV	4856	37	8	120431490	120431490	Missense_Mutation	SNP	G	A	29	164	c.682G>A	c.(682-684)GTC>ATC	p.V228I
Pat_59	Post-Resistance	TAF2	6873	37	8	120816157	120816157	Missense_Mutation	SNP	C	T	32	198	c.521G>A	c.(520-522)GGT>GAT	p.G174D
Pat_59	Post-Resistance	FAM91A1	157769	37	8	124786341	124786341	Missense_Mutation	SNP	G	A	63	296	c.94G>A	c.(94-96)GAA>AAA	p.E32K
Pat_59	Post-Resistance	CPSF1	29894	37	8	145623221	145623221	Missense_Mutation	SNP	G	A	5	29	c.2021C>T	c.(2020-2022)TCC>TTC	p.S674F
Pat_59	Post-Resistance	PTPRD	5789	37	9	8517925	8517925	Missense_Mutation	SNP	G	A	23	30	c.1466C>T	c.(1465-1467)TCT>TTT	p.S489F
Pat_59	Post-Resistance	KIAA1161	57462	37	9	34371053	34371053	Missense_Mutation	SNP	C	T	4	11	c.1889G>A	c.(1888-1890)GGT>GAT	p.G630D
Pat_59	Post-Resistance	TLN1	7094	37	9	35705994	35705994	Missense_Mutation	SNP	C	T	7	46	c.5476G>A	c.(5476-5478)GGC>AGC	p.G1826S
Pat_59	Post-Resistance	ZNF484	83744	37	9	95610681	95610681	Missense_Mutation	SNP	C	T	4	109	c.388G>A	c.(388-390)GAA>AAA	p.E130K
Pat_59	Post-Resistance	WNK2	65268	37	9	96018690	96018690	Missense_Mutation	SNP	C	T	2	0	c.2144C>T	c.(2143-2145)ACC>ATC	p.T715I
Pat_59	Post-Resistance	NIPSNAP3A	25934	37	9	107513363	107513363	Missense_Mutation	SNP	C	T	65	194	c.187C>T	c.(187-189)CGG>TGG	p.R63W
Pat_59	Post-Resistance	C9orf43	257169	37	9	116185685	116185685	Missense_Mutation	SNP	C	T	4	66	c.563C>T	c.(562-564)CCC>CTC	p.P188L
Pat_59	Post-Resistance	TNC	3371	37	9	117848440	117848440	Missense_Mutation	SNP	C	T	3	41	c.1570G>A	c.(1570-1572)GGC>AGC	p.G524S
Pat_59	Post-Resistance	OR1J2	26740	37	9	125273133	125273133	Missense_Mutation	SNP	C	T	31	89	c.53C>T	c.(52-54)CCC>CTC	p.P18L
Pat_59	Post-Resistance	RABGAP1	23637	37	9	125838940	125838940	Missense_Mutation	SNP	G	A	17	68	c.2323G>A	c.(2323-2325)GAC>AAC	p.D775N
Pat_59	Post-Resistance	NUP188	23511	37	9	131761524	131761524	Missense_Mutation	SNP	C	A	4	27	c.3589C>A	c.(3589-3591)CAA>AAA	p.Q1197K
Pat_59	Post-Resistance	CRAT	1384	37	9	131860351	131860351	Missense_Mutation	SNP	G	A	5	116	c.1405C>T	c.(1405-1407)CGC>TGC	p.R469C
Pat_59	Post-Resistance	SETX	23064	37	9	135206812	135206812	Missense_Mutation	SNP	G	A	13	45	c.862C>T	c.(862-864)CCA>TCA	p.P288S
Pat_59	Post-Resistance	COL5A1	1289	37	9	137658300	137658300	Missense_Mutation	SNP	G	A	4	13	c.2089G>A	c.(2089-2091)GGT>AGT	p.G697S
Pat_59	Post-Resistance	LHX3	8022	37	9	139090825	139090825	Missense_Mutation	SNP	A	G	2	3	c.535T>C	c.(535-537)TCG>CCG	p.S179P
Pat_59	Post-Resistance	SNAPC4	6621	37	9	139270839	139270839	Missense_Mutation	SNP	C	T	9	53	c.4379G>A	c.(4378-4380)AGG>AAG	p.R1460K
Pat_59	Post-Resistance	WDR85	92715	37	9	140459568	140459568	Missense_Mutation	SNP	C	T	8	16	c.679G>A	c.(679-681)GTA>ATA	p.V227I
Pat_59	Post-Resistance	EHMT1	79813	37	9	140637972	140637972	Missense_Mutation	SNP	G	A	8	65	c.973G>A	c.(973-975)GGT>AGT	p.G325S

Pat_59	Post-Resistance	PPP2R3B	28227	37	X	322229	322229	Missense_Mutation	SNP	C	T	3	27	c.421G>A	c.(421-423)GTG>ATG	p.V141M
Pat_59	Post-Resistance	MXRA5	25878	37	X	3241189	3241189	Missense_Mutation	SNP	G	A	5	20	c.2537C>T	c.(2536-2538)CCT>CTT	p.P846L
Pat_59	Post-Resistance	KAL1	3730	37	X	8553352	8553352	Missense_Mutation	SNP	G	A	10	12	c.812C>T	c.(811-813)ACT>ATT	p.T271I
Pat_59	Post-Resistance	BMX	660	37	X	15555409	15555409	Nonsense_Mutation	SNP	C	T	4	27	c.1375C>T	c.(1375-1377)CAG>TAG	p.Q459*
Pat_59	Post-Resistance	TXLNG	55787	37	X	16858016	16858016	Missense_Mutation	SNP	G	A	30	90	c.1225G>A	c.(1225-1227)GCA>ACA	p.A409T
Pat_59	Post-Resistance	PTCHD1	139411	37	X	23353248	23353248	Missense_Mutation	SNP	G	A	5	9	c.256G>A	c.(256-258)GAC>AAC	p.D86N
Pat_59	Post-Resistance	FAM47C	442444	37	X	37028134	37028134	Missense_Mutation	SNP	C	T	5	57	c.1651C>T	c.(1651-1653)CCT>TCT	p.P551S
Pat_59	Post-Resistance	CXorf38	159013	37	X	40496279	40496279	Missense_Mutation	SNP	C	T	4	87	c.601G>A	c.(601-603)GTA>ATA	p.V201I
Pat_59	Post-Resistance	KDM6A	7403	37	X	44937658	44937658	Missense_Mutation	SNP	G	T	4	86	c.2846G>T	c.(2845-2847)CGT>CTT	p.R949L
Pat_59	Post-Resistance	PHF16	9767	37	X	46893044	46893044	Missense_Mutation	SNP	G	A	10	19	c.709G>A	c.(709-711)GTC>ATC	p.V237I
Pat_59	Post-Resistance	GPKOW	27238	37	X	48979089	48979089	Missense_Mutation	SNP	G	A	6	9	c.214C>T	c.(214-216)CCT>TCT	p.P72S
Pat_59	Post-Resistance	CACNA1F	778	37	X	49084859	49084859	Missense_Mutation	SNP	G	A	2	2	c.868C>T	c.(868-870)CGT>TGT	p.R290C
Pat_59	Post-Resistance	CCNB3	85417	37	X	50053081	50053081	Missense_Mutation	SNP	G	A	11	5	c.1912G>A	c.(1912-1914)GAA>AAA	p.E638K
Pat_59	Post-Resistance	FAM120C	54954	37	X	54117785	54117785	Missense_Mutation	SNP	G	A	4	38	c.2387C>T	c.(2386-2388)TCT>TTT	p.S796F
Pat_59	Post-Resistance	OPHN1	4983	37	X	67283948	67283948	Missense_Mutation	SNP	G	A	18	65	c.1906C>T	c.(1906-1908)CCC>TCC	p.P636S
Pat_59	Post-Resistance	CHM	1121	37	X	85149271	85149271	Missense_Mutation	SNP	G	A	18	61	c.1432C>T	c.(1432-1434)CCA>TCA	p.P478S
Pat_59	Post-Resistance	PCDH11X	27328	37	X	91091018	91091018	Missense_Mutation	SNP	G	A	25	41	c.515G>A	c.(514-516)GGA>GAA	p.G172E
Pat_59	Post-Resistance	IL1RAPL2	26280	37	X	104984597	104984597	Missense_Mutation	SNP	G	A	21	62	c.961G>A	c.(961-963)GTT>ATT	p.V321I
Pat_59	Post-Resistance	ATG4A	115201	37	X	107369381	107369381	Missense_Mutation	SNP	G	A	10	29	c.85G>A	c.(85-87)GTA>ATA	p.V29I
Pat_59	Post-Resistance	ALG13	79868	37	X	110968271	110968271	Missense_Mutation	SNP	G	A	15	28	c.1711G>A	c.(1711-1713)GGT>AGT	p.G571S
Pat_59	Post-Resistance	AMOT	154796	37	X	112024161	112024161	Missense_Mutation	SNP	G	A	17	39	c.2426C>T	c.(2425-2427)CCC>CTC	p.P809L
Pat_59	Post-Resistance	IL13RA1	3597	37	X	117892047	117892047	Missense_Mutation	SNP	G	A	14	48	c.518G>A	c.(517-519)TGT>TAT	p.C173Y
Pat_59	Post-Resistance	IGSF1	3547	37	X	130409559	130409559	Missense_Mutation	SNP	G	A	14	23	c.3077C>T	c.(3076-3078)ACC>ATC	p.T1026I
Pat_59	Post-Resistance	LAGE3	8270	37	X	153706299	153706299	Missense_Mutation	SNP	G	A	28	9	c.416C>T	c.(415-417)CCC>CTC	p.P139L
Pat_59	Post-Resistance	RAB39B	116442	37	X	154490477	154490477	Missense_Mutation	SNP	C	A	5	197	c.253G>T	c.(253-255)GGT>TGT	p.G85C
Pat_63	Pre-Treatment	HNRNPCL1	343069	37	1	12907456	12907456	Missense_Mutation	SNP	C	T	3	19	c.687G>A	c.(685-687)ATG>ATA	p.M229I
Pat_63	Pre-Treatment	ARHGEF19	128272	37	1	16534505	16534505	Missense_Mutation	SNP	G	A	3	17	c.628C>T	c.(628-630)CGC>TGC	p.R210C
Pat_63	Pre-Treatment	UBR4	23352	37	1	19505624	19505624	Missense_Mutation	SNP	G	A	4	44	c.2275C>T	c.(2275-2277)CGC>TGC	p.R759C
Pat_63	Pre-Treatment	FAM46B	115572	37	1	27332715	27332715	Missense_Mutation	SNP	C	T	3	6	c.998G>A	c.(997-999)GGG>GAG	p.G333E
Pat_63	Pre-Treatment	PTPRU	10076	37	1	29587254	29587254	Missense_Mutation	SNP	G	A	3	18	c.983G>A	c.(982-984)CGC>CAC	p.R328H
Pat_63	Pre-Treatment	MTF1	4520	37	1	38288269	38288269	Missense_Mutation	SNP	G	A	4	19	c.1291C>T	c.(1291-1293)CCC>TCC	p.P431S
Pat_63	Pre-Treatment	PTPRF	5792	37	1	44069142	44069142	Missense_Mutation	SNP	C	T	4	36	c.2396C>T	c.(2395-2397)GCC>GTC	p.A799V
Pat_63	Pre-Treatment	CCDC163P	126661	37	1	45965037	45965037	Missense_Mutation	SNP	A	G	3	27	c.157T>C	c.(157-159)TTC>CTC	p.F53L
Pat_63	Pre-Treatment	RAD54L	8438	37	1	46740370	46740370	Missense_Mutation	SNP	A	C	17	31	c.1850A>C	c.(1849-1851)TAT>TCT	p.Y617S
Pat_63	Pre-Treatment	WLS	79971	37	1	68564415	68564415	Missense_Mutation	SNP	G	A	4	15	c.1532C>T	c.(1531-1533)TCG>TTG	p.S511L
Pat_63	Pre-Treatment	CELSR2	1952	37	1	109803687	109803687	Missense_Mutation	SNP	C	T	5	67	c.3982C>T	c.(3982-3984)CGC>TGC	p.R1328C
Pat_63	Pre-Treatment	CYB561D1	284613	37	1	110038645	110038645	Missense_Mutation	SNP	C	T	3	28	c.454C>T	c.(454-456)CGG>TGG	p.R152W
Pat_63	Pre-Treatment	PTGFRN	5738	37	1	117492182	117492182	Missense_Mutation	SNP	G	A	4	27	c.1201G>A	c.(1201-1203)GTG>ATG	p.V401M
Pat_63	Pre-Treatment	ADAMTSL4	54507	37	1	150530003	150530003	Missense_Mutation	SNP	G	A	4	16	c.2081G>A	c.(2080-2082)CGT>CAT	p.R694H
Pat_63	Pre-Treatment	ZBTB7B	51043	37	1	154987384	154987384	Missense_Mutation	SNP	G	A	4	17	c.248G>A	c.(247-249)GGA>GAA	p.G83E
Pat_63	Pre-Treatment	IGSF8	93185	37	1	160062851	160062851	Missense_Mutation	SNP	C	T	4	28	c.1175G>A	c.(1174-1176)CGG>CAG	p.R392Q
Pat_63	Pre-Treatment	IGFN1	91156	37	1	201195234	201195234	Missense_Mutation	SNP	G	A	3	18	c.2249G>A	c.(2248-2250)TGC>TAC	p.C750Y
Pat_63	Pre-Treatment	RNPEP	6051	37	1	201969032	201969032	Missense_Mutation	SNP	G	A	4	35	c.1093G>A	c.(1093-1095)GCT>ACT	p.A365T
Pat_63	Pre-Treatment	PIK3C2B	5287	37	1	204415126	204415126	Missense_Mutation	SNP	G	A	5	60	c.2636C>T	c.(2635-2637)ACC>ATC	p.T879I
Pat_63	Pre-Treatment	TRIM11	81559	37	1	228582888	228582888	Missense_Mutation	SNP	C	T	2	0	c.925G>A	c.(925-927)GTG>ATG	p.V309M
Pat_63	Pre-Treatment	PGBD5	79605	37	1	230472904	230472904	Missense_Mutation	SNP	G	A	6	39	c.818C>T	c.(817-819)ACG>ATG	p.T273M
Pat_63	Pre-Treatment	C10orf18	54906	37	10	5790629	5790629	Missense_Mutation	SNP	G	A	3	23	c.5245G>A	c.(5245-5247)GTT>ATT	p.V1749I

Pat_63	Pre-Treatment	DNA2	1763	37	10	70225551	70225551	Missense_Mutation	SNP	G	A	3	18	c.718C>T	c.(718-720)CGC>TGC	p.R240C
Pat_63	Pre-Treatment	CDH23	64072	37	10	73453934	73453934	Missense_Mutation	SNP	G	A	4	43	c.2207G>A	c.(2206-2208)CGA>CAA	p.R736Q
Pat_63	Pre-Treatment	HELLS	3070	37	10	96334363	96334363	Missense_Mutation	SNP	G	A	6	94	c.758G>A	c.(757-759)GGT>GAT	p.G253D
Pat_63	Pre-Treatment	SORBS1	10580	37	10	97096979	97096979	Missense_Mutation	SNP	C	T	3	22	c.2938G>A	c.(2938-2940)GAG>AAG	p.E980K
Pat_63	Pre-Treatment	ALDH18A1	5832	37	10	97402832	97402832	Missense_Mutation	SNP	C	T	4	33	c.220G>A	c.(220-222)GTG>ATG	p.V74M
Pat_63	Pre-Treatment	LRRC27	80313	37	10	134161853	134161853	Missense_Mutation	SNP	G	T	8	39	c.919G>T	c.(919-921)GTT>TTT	p.V307F
Pat_63	Pre-Treatment	IRF7	3665	37	11	613827	613827	Missense_Mutation	SNP	G	C	2	3	c.805C>G	c.(805-807)CCG>GCG	p.P269A
Pat_63	Pre-Treatment	MUC2	4583	37	11	1093298	1093298	Missense_Mutation	SNP	C	T	5	2	c.12203C>T	c.(12202-12204)ACG>ATG	p.T4068M
Pat_63	Pre-Treatment	MUC5B	727897	37	11	1271471	1271471	Missense_Mutation	SNP	G	C	3	37	c.14780G>C	c.(14779-14781)AGC>ACC	p.S4927T
Pat_63	Pre-Treatment	OSBPL5	114879	37	11	3141794	3141794	Missense_Mutation	SNP	G	A	5	74	c.463C>T	c.(463-465)CTC>TTC	p.L155F
Pat_63	Pre-Treatment	NAV2	89797	37	11	19970395	19970395	Missense_Mutation	SNP	C	T	4	27	c.2483C>T	c.(2482-2484)CCC>CTC	p.P828L
Pat_63	Pre-Treatment	NAV2	89797	37	11	19970454	19970454	Missense_Mutation	SNP	G	A	5	60	c.2542G>A	c.(2542-2544)GCC>ACC	p.A848T
Pat_63	Pre-Treatment	NAV2	89797	37	11	20065746	20065746	Missense_Mutation	SNP	G	A	3	28	c.3196G>A	c.(3196-3198)GCT>ACT	p.A1066T
Pat_63	Pre-Treatment	ELF5	2001	37	11	34502397	34502397	Missense_Mutation	SNP	G	A	5	75	c.623C>T	c.(622-624)TCG>TTG	p.S208L
Pat_63	Pre-Treatment	NAALADL1	10004	37	11	64820791	64820791	Missense_Mutation	SNP	C	T	2	1	c.1097G>A	c.(1096-1098)GGG>GAG	p.G366E
Pat_63	Pre-Treatment	RELA	5970	37	11	65426287	65426287	Missense_Mutation	SNP	G	A	4	43	c.566C>T	c.(565-567)CCC>CTC	p.P189L
Pat_63	Pre-Treatment	PACS1	55690	37	11	65983993	65983993	Missense_Mutation	SNP	C	T	4	43	c.808C>T	c.(808-810)CGT>TGT	p.R270C
Pat_63	Pre-Treatment	ACTN3	89	37	11	66322644	66322644	Missense_Mutation	SNP	C	T	4	43	c.601C>T	c.(601-603)CGC>TGC	p.R201C
Pat_63	Pre-Treatment	PITPNM1	9600	37	11	67266289	67266289	Missense_Mutation	SNP	G	A	5	22	c.1262C>T	c.(1261-1263)GCT>GTT	p.A421V
Pat_63	Pre-Treatment	PPFIA1	8500	37	11	70184504	70184504	Missense_Mutation	SNP	G	A	5	85	c.1516G>A	c.(1516-1518)GCA>ACA	p.A506T
Pat_63	Pre-Treatment	C2CD3	26005	37	11	73843994	73843994	Missense_Mutation	SNP	C	T	3	35	c.1112G>A	c.(1111-1113)CGG>CAG	p.R371Q
Pat_63	Pre-Treatment	DSCAML1	57453	37	11	117352788	117352788	Missense_Mutation	SNP	G	A	4	33	c.2629C>T	c.(2629-2631)CCC>TCC	p.P877S
Pat_63	Pre-Treatment	BCL9L	283149	37	11	118773233	118773233	Missense_Mutation	SNP	G	A	3	21	c.1219C>T	c.(1219-1221)CGG>TGG	p.R407W
Pat_63	Pre-Treatment	PRDM10	56980	37	11	129814712	129814712	Missense_Mutation	SNP	G	A	3	23	c.716C>T	c.(715-717)CCT>CTT	p.P239L
Pat_63	Pre-Treatment	SPATS2	65244	37	12	49919751	49919751	Missense_Mutation	SNP	G	A	3	33	c.1351G>A	c.(1351-1353)GGA>AGA	p.G451R
Pat_63	Pre-Treatment	DIP2B	57609	37	12	51112597	51112597	Missense_Mutation	SNP	G	A	3	20	c.2957G>A	c.(2956-2958)AGG>AAG	p.R986K
Pat_63	Pre-Treatment	AAAS	8086	37	12	53703435	53703435	Missense_Mutation	SNP	G	A	2	0	c.760C>T	c.(760-762)CCC>TCC	p.P254S
Pat_63	Pre-Treatment	ATF7	11016	37	12	53994775	53994775	Missense_Mutation	SNP	C	T	3	19	c.10G>A	c.(10-12)GAC>AAC	p.D4N
Pat_63	Pre-Treatment	WIBG	84305	37	12	56295898	56295898	Missense_Mutation	SNP	G	A	4	46	c.373C>T	c.(373-375)CCC>TCC	p.P125S
Pat_63	Pre-Treatment	ZFC3H1	196441	37	12	72024472	72024472	Missense_Mutation	SNP	C	T	4	40	c.3632G>A	c.(3631-3633)CGA>CAA	p.R1211Q
Pat_63	Pre-Treatment	OSBPL8	114882	37	12	76793703	76793703	Missense_Mutation	SNP	G	A	4	35	c.418C>T	c.(418-420)CTC>TTC	p.L140F
Pat_63	Pre-Treatment	MYO1H	283446	37	12	109882246	109882246	Missense_Mutation	SNP	G	A	3	29	c.430G>A	c.(430-432)GTT>ATT	p.V144I
Pat_63	Pre-Treatment	PTPN11	5781	37	12	112924333	112924333	Missense_Mutation	SNP	G	A	3	25	c.1279G>A	c.(1279-1281)GGC>AGC	p.G427S
Pat_63	Pre-Treatment	FBXO21	23014	37	12	117628044	117628044	Nonsense_Mutation	SNP	C	T	4	9	c.218G>A	c.(217-219)TGG>TAG	p.W73*
Pat_63	Pre-Treatment	DNAH10	196385	37	12	124419300	124419300	Missense_Mutation	SNP	G	A	3	18	c.13256G>A	c.(13255-13257)CGC>CAC	p.R4419H
Pat_63	Pre-Treatment	POLE	5426	37	12	133219907	133219907	Missense_Mutation	SNP	C	T	4	42	c.4454G>A	c.(4453-4455)CGC>CAC	p.R1485H
Pat_63	Pre-Treatment	LNX2	222484	37	13	28136594	28136594	Missense_Mutation	SNP	C	T	6	104	c.1180G>A	c.(1180-1182)GAC>AAC	p.D394N
Pat_63	Pre-Treatment	FREM2	341640	37	13	39261821	39261821	Missense_Mutation	SNP	G	A	3	10	c.340G>A	c.(340-342)GCA>ACA	p.A114T
Pat_63	Pre-Treatment	THSD1	55901	37	13	52952189	52952189	Missense_Mutation	SNP	G	A	3	17	c.1916C>T	c.(1915-1917)CCG>CTG	p.P639L
Pat_63	Pre-Treatment	RNF113B	140432	37	13	98829075	98829075	Missense_Mutation	SNP	C	T	3	18	c.416G>A	c.(415-417)CGG>CAG	p.R139Q
Pat_63	Pre-Treatment	EFNB2	1948	37	13	107145449	107145449	Missense_Mutation	SNP	G	A	3	23	c.941C>T	c.(940-942)CCG>CTG	p.P314L
Pat_63	Pre-Treatment	TEP1	7011	37	14	20876400	20876400	Missense_Mutation	SNP	A	G	3	35	c.199T>C	c.(199-201)TAT>CAT	p.Y67H
Pat_63	Pre-Treatment	MYH7	4625	37	14	23890202	23890202	Missense_Mutation	SNP	C	T	3	20	c.3301G>A	c.(3301-3303)GGC>AGC	p.G1101S
Pat_63	Pre-Treatment	PSME1	5720	37	14	24607758	24607758	Missense_Mutation	SNP	C	T	4	61	c.658C>T	c.(658-660)CGC>TGC	p.R220C
Pat_63	Pre-Treatment	NKX2-1	7080	37	14	36988240	36988240	Missense_Mutation	SNP	G	A	2	0	c.323C>T	c.(322-324)GCC>GTC	p.A108V
Pat_63	Pre-Treatment	SLC8A3	6547	37	14	70512783	70512783	Missense_Mutation	SNP	C	T	2	1	c.2665G>A	c.(2665-2667)GGG>AGG	p.G889R
Pat_63	Pre-Treatment	C14orf169	79697	37	14	73958995	73958995	Missense_Mutation	SNP	G	A	5	59	c.1274G>A	c.(1273-1275)CGC>CAC	p.R425H

Pat_63	Pre-Treatment	PGF	5228	37	14	75416185	75416185	Missense_Mutation	SNP	C	T	3	18	c.190G>A	c.(190-192)GAG>AAG	p.E64K
Pat_63	Pre-Treatment	WDR25	79446	37	14	100995510	100995510	Missense_Mutation	SNP	C	T	3	21	c.1378C>T	c.(1378-1380)CGG>TGG	p.R460W
Pat_63	Pre-Treatment	RTL1	388015	37	14	101348862	101348862	Missense_Mutation	SNP	C	T	2	0	c.2264G>A	c.(2263-2265)CGC>CAC	p.R755H
Pat_63	Pre-Treatment	JAG2	3714	37	14	105612100	105612100	Missense_Mutation	SNP	T	A	2	0	c.2920A>T	c.(2920-2922)ACC>TCC	p.T974S
Pat_63	Pre-Treatment	JAG2	3714	37	14	105622309	105622309	Nonsense_Mutation	SNP	G	A	3	11	c.493C>T	c.(493-495)CGA>TGA	p.R165*
Pat_63	Pre-Treatment	TRPM1	4308	37	15	31295058	31295058	Missense_Mutation	SNP	C	T	4	50	c.3779G>A	c.(3778-3780)CGG>CAG	p.R1260Q
Pat_63	Pre-Treatment	SLC12A6	9990	37	15	34536188	34536188	Missense_Mutation	SNP	G	A	7	128	c.2029C>T	c.(2029-2031)CGC>TGC	p.R677C
Pat_63	Pre-Treatment	PPIP5K1	9677	37	15	43827510	43827510	Missense_Mutation	SNP	C	T	4	28	c.3664G>A	c.(3664-3666)GCA>ACA	p.A1222T
Pat_63	Pre-Treatment	GABPB1	2553	37	15	50601929	50601929	Missense_Mutation	SNP	G	A	6	131	c.67C>T	c.(67-69)CGT>TGT	p.R23C
Pat_63	Pre-Treatment	ITGA11	22801	37	15	68624780	68624780	Missense_Mutation	SNP	C	G	2	6	c.1462G>C	c.(1462-1464)GAC>CAC	p.D488H
Pat_63	Pre-Treatment	CORO2B	10391	37	15	68937563	68937563	Missense_Mutation	SNP	G	A	4	27	c.80G>A	c.(79-81)CGG>CAG	p.R27Q
Pat_63	Pre-Treatment	MYO9A	4649	37	15	72192220	72192220	Missense_Mutation	SNP	C	T	4	33	c.3278G>A	c.(3277-3279)CGG>CAG	p.R1093Q
Pat_63	Pre-Treatment	MAN2C1	4123	37	15	75648353	75648353	Missense_Mutation	SNP	G	A	2	1	c.3017C>T	c.(3016-3018)CCA>CTA	p.P1006L
Pat_63	Pre-Treatment	MAN2C1	4123	37	15	75656939	75656939	Missense_Mutation	SNP	C	T	3	14	c.490G>A	c.(490-492)GCC>ACC	p.A164T
Pat_63	Pre-Treatment	ASB7	140460	37	15	101169992	101169992	Missense_Mutation	SNP	G	A	3	28	c.562G>A	c.(562-564)GTG>ATG	p.V188M
Pat_63	Pre-Treatment	MSLNL	401827	37	16	830540	830540	Missense_Mutation	SNP	G	A	6	113	c.461C>T	c.(460-462)CCG>CTG	p.P154L
Pat_63	Pre-Treatment	PTX4	390667	37	16	1536044	1536044	Missense_Mutation	SNP	C	T	3	27	c.1318G>A	c.(1318-1320)GGG>AGG	p.G440R
Pat_63	Pre-Treatment	IFT140	9742	37	16	1618271	1618271	Missense_Mutation	SNP	C	T	3	7	c.1717G>A	c.(1717-1719)GCT>ACT	p.A573T
Pat_63	Pre-Treatment	MYH11	4629	37	16	15835393	15835393	Missense_Mutation	SNP	G	A	3	29	c.2786C>T	c.(2785-2787)GCC>GTC	p.A929V
Pat_63	Pre-Treatment	ERN2	10595	37	16	23706364	23706364	Missense_Mutation	SNP	C	G	2	2	c.2020G>C	c.(2020-2022)GCC>CCC	p.A674P
Pat_63	Pre-Treatment	AMFR	267	37	16	56436976	56436976	Missense_Mutation	SNP	G	A	4	44	c.895C>T	c.(895-897)CGT>TGT	p.R299C
Pat_63	Pre-Treatment	CPNE2	221184	37	16	57147257	57147257	Missense_Mutation	SNP	G	A	4	53	c.238G>A	c.(238-240)GTG>ATG	p.V80M
Pat_63	Pre-Treatment	CALB2	794	37	16	71416647	71416647	Missense_Mutation	SNP	G	A	5	92	c.368G>A	c.(367-369)AGG>AAG	p.R123K
Pat_63	Pre-Treatment	DHX38	9785	37	16	72139983	72139983	Missense_Mutation	SNP	G	A	4	51	c.2567G>A	c.(2566-2568)CGA>CAA	p.R856Q
Pat_63	Pre-Treatment	ZNRF1	84937	37	16	75033969	75033969	Missense_Mutation	SNP	C	T	3	17	c.400C>T	c.(400-402)CCC>TCC	p.P134S
Pat_63	Pre-Treatment	HIC1	3090	37	17	1961455	1961455	Missense_Mutation	SNP	G	A	6	13	c.1528G>A	c.(1528-1530)GCG>ACG	p.A510T
Pat_63	Pre-Treatment	SMTNL2	342527	37	17	4496341	4496341	Missense_Mutation	SNP	G	A	4	36	c.605G>A	c.(604-606)CGA>CAA	p.R202Q
Pat_63	Pre-Treatment	DNAH2	146754	37	17	7660485	7660485	Missense_Mutation	SNP	G	A	6	136	c.1981G>A	c.(1981-1983)GTA>ATA	p.V661I
Pat_63	Pre-Treatment	PFAS	5198	37	17	8168720	8168720	Missense_Mutation	SNP	G	A	4	35	c.2395G>A	c.(2395-2397)GTG>ATG	p.V799M
Pat_63	Pre-Treatment	EPN2	22905	37	17	19215459	19215459	Splice_Site	SNP	T	A	4	35	c.972_splice	c.e6+2	p.E324_splice
Pat_63	Pre-Treatment	ABHD15	116236	37	17	27889821	27889821	Missense_Mutation	SNP	C	T	3	23	c.1165G>A	c.(1165-1167)GGA>AGA	p.G389R
Pat_63	Pre-Treatment	KRTAP4-9	100132386	37	17	39261879	39261879	Missense_Mutation	SNP	A	G	6	27	c.239A>G	c.(238-240)TAC>TGC	p.Y80C
Pat_63	Pre-Treatment	KRTAP4-12	83755	37	17	39279809	39279809	Missense_Mutation	SNP	G	C	3	19	c.566C>G	c.(565-567)ACC>AGC	p.T189S
Pat_63	Pre-Treatment	KRT9	3857	37	17	39724804	39724804	Missense_Mutation	SNP	C	T	7	169	c.1126G>A	c.(1126-1128)GGT>AGT	p.G376S
Pat_63	Pre-Treatment	STAT5A	6776	37	17	40456361	40456361	Missense_Mutation	SNP	G	A	4	21	c.1171G>A	c.(1171-1173)GAG>AAG	p.E391K
Pat_63	Pre-Treatment	FZD2	2535	37	17	42635990	42635990	Missense_Mutation	SNP	G	A	3	9	c.934G>A	c.(934-936)GAG>AAG	p.E312K
Pat_63	Pre-Treatment	ABI3	51225	37	17	47299482	47299482	Missense_Mutation	SNP	C	T	5	48	c.832C>T	c.(832-834)CCT>TCT	p.P278S
Pat_63	Pre-Treatment	MSI2	124540	37	17	55478802	55478802	Missense_Mutation	SNP	T	G	36	50	c.375T>G	c.(373-375)GAT>GAG	p.D125E
Pat_63	Pre-Treatment	TRIM37	4591	37	17	57168662	57168662	Missense_Mutation	SNP	G	A	5	91	c.163C>T	c.(163-165)CGT>TGT	p.R55C
Pat_63	Pre-Treatment	ABCA10	10349	37	17	67186498	67186498	Splice_Site	SNP	C	G	5	57	c.2131_splice	c.e19+1	p.D711_splice
Pat_63	Pre-Treatment	ITGB4	3691	37	17	73723311	73723311	Missense_Mutation	SNP	C	T	3	32	c.116C>T	c.(115-117)ACG>ATG	p.T39M
Pat_63	Pre-Treatment	UBE2O	63893	37	17	74387592	74387592	Missense_Mutation	SNP	G	A	4	53	c.3311C>T	c.(3310-3312)GCG>GTG	p.A1104V
Pat_63	Pre-Treatment	GAA	2548	37	17	78092074	78092074	Missense_Mutation	SNP	G	A	4	22	c.2564G>A	c.(2563-2565)GGG>GAG	p.G855E
Pat_63	Pre-Treatment	TXNDC2	84203	37	18	9887452	9887452	Missense_Mutation	SNP	G	A	6	79	c.976G>A	c.(976-978)GAG>AAG	p.E326K
Pat_63	Pre-Treatment	MIB1	57534	37	18	19427017	19427017	Missense_Mutation	SNP	C	T	4	32	c.2324C>T	c.(2323-2325)TCG>TTG	p.S775L
Pat_63	Pre-Treatment	CABYR	26256	37	18	21736603	21736603	Missense_Mutation	SNP	G	A	4	46	c.1138G>A	c.(1138-1140)GAG>AAG	p.E380K
Pat_63	Pre-Treatment	B4GALT6	9331	37	18	29218696	29218696	Missense_Mutation	SNP	G	A	5	62	c.499C>T	c.(499-501)CGC>TGC	p.R167C

Pat_63	Pre-Treatment	FECH	2235	37	18	55222096	55222096	Missense_Mutation	SNP	C	T	4	40	c.893G>A	c.(892-894)CGA>CAA	p.R298Q
Pat_63	Pre-Treatment	FAM69C	125704	37	18	72109259	72109259	Missense_Mutation	SNP	G	C	6	22	c.969C>G	c.(967-969)TTC>TTG	p.F323L
Pat_63	Pre-Treatment	PTBP1	5725	37	19	808413	808413	Missense_Mutation	SNP	G	A	3	7	c.1129G>A	c.(1129-1131)GCC>ACC	p.A377T
Pat_63	Pre-Treatment	REXO1	57455	37	19	1828489	1828489	Missense_Mutation	SNP	C	T	3	12	c.299G>A	c.(298-300)AGT>AAT	p.S100N
Pat_63	Pre-Treatment	ZNF555	148254	37	19	2853202	2853202	Missense_Mutation	SNP	C	T	4	25	c.1139C>T	c.(1138-1140)CCC>CTC	p.P380L
Pat_63	Pre-Treatment	CELF5	60680	37	19	3285958	3285958	Missense_Mutation	SNP	C	T	3	29	c.1121C>T	c.(1120-1122)GCC>GTC	p.A374V
Pat_63	Pre-Treatment	CREB3L3	84699	37	19	4171826	4171826	Missense_Mutation	SNP	G	A	3	13	c.1246G>A	c.(1246-1248)GAG>AAG	p.E416K
Pat_63	Pre-Treatment	KANK3	256949	37	19	8389954	8389954	Nonsense_Mutation	SNP	G	A	4	23	c.1963C>T	c.(1963-1965)CGA>TGA	p.R655*
Pat_63	Pre-Treatment	ACTL9	284382	37	19	8808484	8808484	Missense_Mutation	SNP	G	A	4	30	c.568C>T	c.(568-570)CGT>TGT	p.R190C
Pat_63	Pre-Treatment	KRI1	65095	37	19	10668269	10668269	Missense_Mutation	SNP	G	A	3	33	c.1594C>T	c.(1594-1596)CGC>TGC	p.R532C
Pat_63	Pre-Treatment	ZNF700	90592	37	19	12060645	12060645	Missense_Mutation	SNP	T	A	8	192	c.1806T>A	c.(1804-1806)AGT>AGA	p.S602R
Pat_63	Pre-Treatment	NANOS3	342977	37	19	13988235	13988235	Missense_Mutation	SNP	C	T	3	17	c.173C>T	c.(172-174)CCG>CTG	p.P58L
Pat_63	Pre-Treatment	TECR	9524	37	19	14675918	14675918	Missense_Mutation	SNP	G	A	4	35	c.647G>A	c.(646-648)CGG>CAG	p.R216Q
Pat_63	Pre-Treatment	RASAL3	64926	37	19	15567457	15567457	Missense_Mutation	SNP	C	G	3	8	c.1432G>C	c.(1432-1434)GCG>CCG	p.A478P
Pat_63	Pre-Treatment	AP1M1	8907	37	19	16338969	16338969	Missense_Mutation	SNP	G	A	3	24	c.838G>A	c.(838-840)GAG>AAG	p.E280K
Pat_63	Pre-Treatment	MYO9B	4650	37	19	17322713	17322713	Missense_Mutation	SNP	C	T	4	13	c.6068C>T	c.(6067-6069)GCG>GTG	p.A2023V
Pat_63	Pre-Treatment	ZNF737	100129842	37	19	20728254	20728254	Missense_Mutation	SNP	C	G	5	60	c.755G>C	c.(754-756)AGT>ACT	p.S252T
Pat_63	Pre-Treatment	ZNF708	7562	37	19	21476982	21476982	Missense_Mutation	SNP	G	T	7	137	c.786C>A	c.(784-786)AAC>AAA	p.N262K
Pat_63	Pre-Treatment	ZNF493	284443	37	19	21606960	21606960	Missense_Mutation	SNP	A	G	4	73	c.1115A>G	c.(1114-1116)CAA>CGA	p.Q372R
Pat_63	Pre-Treatment	ZNF429	353088	37	19	21720411	21720411	Missense_Mutation	SNP	T	A	6	62	c.1556T>A	c.(1555-1557)ATC>AAC	p.I519N
Pat_63	Pre-Treatment	ZNF429	353088	37	19	21720414	21720414	Missense_Mutation	SNP	T	G	5	63	c.1559T>G	c.(1558-1560)CTG>CGG	p.L520R
Pat_63	Pre-Treatment	ZNF676	163223	37	19	22363143	22363143	Missense_Mutation	SNP	G	C	6	137	c.1376C>G	c.(1375-1377)ACC>AGC	p.T459S
Pat_63	Pre-Treatment	ZNF492	57615	37	19	22847625	22847625	Missense_Mutation	SNP	G	T	9	84	c.1154G>T	c.(1153-1155)AGA>ATA	p.R385I
Pat_63	Pre-Treatment	ZNF792	126375	37	19	35449270	35449270	Missense_Mutation	SNP	G	A	4	27	c.1489C>T	c.(1489-1491)CGG>TGG	p.R497W
Pat_63	Pre-Treatment	FFAR2	2867	37	19	35941154	35941154	Missense_Mutation	SNP	C	T	7	72	c.538C>T	c.(538-540)CGG>TGG	p.R180W
Pat_63	Pre-Treatment	MLL4	9757	37	19	36212077	36212077	Missense_Mutation	SNP	C	T	3	4	c.1828C>T	c.(1828-1830)CGC>TGC	p.R610C
Pat_63	Pre-Treatment	CD79A	973	37	19	42383300	42383300	Missense_Mutation	SNP	G	A	4	32	c.320G>A	c.(319-321)CGG>CAG	p.R107Q
Pat_63	Pre-Treatment	CNFN	84518	37	19	42893090	42893090	Missense_Mutation	SNP	C	T	5	33	c.100G>A	c.(100-102)GAC>AAC	p.D34N
Pat_63	Pre-Treatment	CCDC8	83987	37	19	46914959	46914959	Missense_Mutation	SNP	T	C	5	77	c.1109A>G	c.(1108-1110)GAG>GGG	p.E370G
Pat_63	Pre-Treatment	SIGLEC10	89790	37	19	51920150	51920150	Missense_Mutation	SNP	G	A	4	41	c.476C>T	c.(475-477)CCG>CTG	p.P159L
Pat_63	Pre-Treatment	ZNF649	65251	37	19	52394652	52394652	Missense_Mutation	SNP	C	T	6	53	c.737G>A	c.(736-738)AGG>AAG	p.R246K
Pat_63	Pre-Treatment	ZNF350	59348	37	19	52469149	52469149	Missense_Mutation	SNP	C	T	5	93	c.557G>A	c.(556-558)AGC>AAC	p.S186N
Pat_63	Pre-Treatment	ZNF28	7576	37	19	53303026	53303026	Missense_Mutation	SNP	T	C	8	216	c.2072A>G	c.(2071-2073)TAC>TGC	p.Y691C
Pat_63	Pre-Treatment	ZNF845	91664	37	19	53856360	53856360	Missense_Mutation	SNP	A	C	5	84	c.2432A>C	c.(2431-2433)AAC>ACC	p.N811T
Pat_63	Pre-Treatment	ZNF761	388561	37	19	53959854	53959854	Missense_Mutation	SNP	A	C	10	117	c.2093A>C	c.(2092-2094)AAC>ACC	p.N698T
Pat_63	Pre-Treatment	ZNF71	58491	37	19	57133527	57133527	Missense_Mutation	SNP	C	T	4	48	c.872C>T	c.(871-873)ACG>ATG	p.T291M
Pat_63	Pre-Treatment	ZSCAN1	284312	37	19	58564806	58564806	Missense_Mutation	SNP	C	T	3	29	c.614C>T	c.(613-615)GCC>GTC	p.A205V
Pat_63	Pre-Treatment	CPSF3	51692	37	2	9597148	9597148	Missense_Mutation	SNP	G	A	3	20	c.1690G>A	c.(1690-1692)GTA>ATA	p.V564I
Pat_63	Pre-Treatment	ITSN2	50618	37	2	24433800	24433800	Missense_Mutation	SNP	G	A	3	26	c.4106C>T	c.(4105-4107)CCG>CTG	p.P1369L
Pat_63	Pre-Treatment	ZNF513	130557	37	2	27601843	27601843	Missense_Mutation	SNP	G	A	5	36	c.290C>T	c.(289-291)GCG>GTG	p.A97V
Pat_63	Pre-Treatment	C2orf16	84226	37	2	27804426	27804426	Missense_Mutation	SNP	C	T	7	139	c.4987C>T	c.(4987-4989)CGC>TGC	p.R1663C
Pat_63	Pre-Treatment	FOSL2	2355	37	2	28631659	28631659	Missense_Mutation	SNP	C	T	3	29	c.388C>T	c.(388-390)CGG>TGG	p.R130W
Pat_63	Pre-Treatment	CYP26B1	56603	37	2	72371194	72371194	Missense_Mutation	SNP	G	A	4	27	c.353C>T	c.(352-354)CCT>CTT	p.P118L
Pat_63	Pre-Treatment	TEKT4	150483	37	2	95539335	95539335	Missense_Mutation	SNP	G	A	3	15	c.569G>A	c.(568-570)CGA>CAA	p.R190Q
Pat_63	Pre-Treatment	WDR33	55339	37	2	128477325	128477325	Missense_Mutation	SNP	G	C	2	2	c.2274C>G	c.(2272-2274)ATC>ATG	p.I758M
Pat_63	Pre-Treatment	UGGT1	56886	37	2	128930154	128930154	Missense_Mutation	SNP	C	T	3	32	c.3112C>T	c.(3112-3114)CGT>TGT	p.R1038C
Pat_63	Pre-Treatment	POTEF	728378	37	2	130877802	130877802	Missense_Mutation	SNP	T	C	6	107	c.287A>G	c.(286-288)AAC>AGC	p.N96S

Pat_63	Pre-Treatment	XIRP2	129446	37	2	168107791	168107791	Missense_Mutation	SNP	C	T	6	142	c.9889C>T	c.(9889-9891)CGC>TGC	p.R3297C
Pat_63	Pre-Treatment	TTN	7273	37	2	179477533	179477533	Missense_Mutation	SNP	G	A	3	22	c.42211C>T	c.(42211-42213)CCC>TCC	p.P14071S
Pat_63	Pre-Treatment	NEU2	4759	37	2	233899565	233899565	Missense_Mutation	SNP	G	A	4	32	c.941G>A	c.(940-942)CGA>CAA	p.R314Q
Pat_63	Pre-Treatment	COL6A3	1293	37	2	238258843	238258843	Missense_Mutation	SNP	C	T	4	22	c.6826G>A	c.(6826-6828)GGA>AGA	p.G2276R
Pat_63	Pre-Treatment	NEU4	129807	37	2	242755688	242755688	Missense_Mutation	SNP	G	A	3	22	c.7G>A	c.(7-9)GTC>ATC	p.V3I
Pat_63	Pre-Treatment	C20orf103	24141	37	20	9496943	9496943	Missense_Mutation	SNP	G	A	4	41	c.410G>A	c.(409-411)AGG>AAG	p.R137K
Pat_63	Pre-Treatment	DTD1	92675	37	20	18724886	18724886	Missense_Mutation	SNP	G	A	3	17	c.620G>A	c.(619-621)CGG>CAG	p.R207Q
Pat_63	Pre-Treatment	LPIN3	64900	37	20	39974625	39974625	Missense_Mutation	SNP	G	A	3	23	c.182G>A	c.(181-183)CGG>CAG	p.R61Q
Pat_63	Pre-Treatment	CHD6	84181	37	20	40033870	40033870	Missense_Mutation	SNP	G	A	3	24	c.7511C>T	c.(7510-7512)ACG>ATG	p.T2504M
Pat_63	Pre-Treatment	TOX2	84969	37	20	42679986	42679986	Missense_Mutation	SNP	C	T	3	14	c.479C>T	c.(478-480)TCG>TTG	p.S160L
Pat_63	Pre-Treatment	ATP9A	10079	37	20	50329565	50329565	Nonsense_Mutation	SNP	G	A	4	10	c.376C>T	c.(376-378)CGA>TGA	p.R126*
Pat_63	Pre-Treatment	C20orf108	116151	37	20	54941182	54941182	Nonsense_Mutation	SNP	C	T	5	36	c.418C>T	c.(418-420)CAG>TAG	p.Q140*
Pat_63	Pre-Treatment	POTED	317754	37	21	14983063	14983063	Missense_Mutation	SNP	G	C	3	36	c.514G>C	c.(514-516)GAA>CAA	p.E172Q
Pat_63	Pre-Treatment	TMPRSS2	7113	37	21	42861441	42861441	Nonsense_Mutation	SNP	C	T	5	27	c.318G>A	c.(316-318)TGG>TGA	p.W106*
Pat_63	Pre-Treatment	PCNT	5116	37	21	47783785	47783785	Missense_Mutation	SNP	G	A	4	30	c.2545G>A	c.(2545-2547)GGG>AGG	p.G849R
Pat_63	Pre-Treatment	MED15	51586	37	22	20938665	20938665	Nonsense_Mutation	SNP	C	T	8	66	c.1756C>T	c.(1756-1758)CAA>TAA	p.Q586*
Pat_63	Pre-Treatment	CCDC116	164592	37	22	21991085	21991085	Missense_Mutation	SNP	C	T	4	32	c.1568C>T	c.(1567-1569)ACA>ATA	p.T523I
Pat_63	Pre-Treatment	LIF	3976	37	22	30639788	30639788	Missense_Mutation	SNP	C	T	3	18	c.461G>A	c.(460-462)CGC>CAC	p.R154H
Pat_63	Pre-Treatment	NCF4	4689	37	22	37263493	37263493	Missense_Mutation	SNP	G	A	3	17	c.331G>A	c.(331-333)GCC>ACC	p.A111T
Pat_63	Pre-Treatment	RIBC2	26150	37	22	45826846	45826846	Missense_Mutation	SNP	G	A	4	16	c.955G>A	c.(955-957)GCC>ACC	p.A319T
Pat_63	Pre-Treatment	CELSR1	9620	37	22	46787620	46787620	Missense_Mutation	SNP	C	T	3	7	c.6058G>A	c.(6058-6060)GGG>AGG	p.G2020R
Pat_63	Pre-Treatment	TUBGCP6	85378	37	22	50659000	50659000	Missense_Mutation	SNP	C	T	4	31	c.3788G>A	c.(3787-3789)CGG>CAG	p.R1263Q
Pat_63	Pre-Treatment	TTLL3	26140	37	3	9870700	9870700	Missense_Mutation	SNP	G	A	3	26	c.1175G>A	c.(1174-1176)CGG>CAG	p.R392Q
Pat_63	Pre-Treatment	TATDN2	9797	37	3	10302032	10302032	Missense_Mutation	SNP	G	A	3	28	c.626G>A	c.(625-627)CGG>CAG	p.R209Q
Pat_63	Pre-Treatment	NR2C2	7182	37	3	15070226	15070226	Missense_Mutation	SNP	G	A	3	22	c.932G>A	c.(931-933)CGG>CAG	p.R311Q
Pat_63	Pre-Treatment	ZBTB47	92999	37	3	42701013	42701013	Missense_Mutation	SNP	G	A	2	0	c.38G>A	c.(37-39)GGT>GAT	p.G13D
Pat_63	Pre-Treatment	FYCO1	79443	37	3	46008656	46008656	Missense_Mutation	SNP	C	T	5	30	c.2170G>A	c.(2170-2172)GAA>AAA	p.E724K
Pat_63	Pre-Treatment	PRKAR2A	5576	37	3	48820418	48820418	Splice_Site	SNP	C	T	3	29	c.542_splice	c.e5+1	p.R181_splice
Pat_63	Pre-Treatment	AMT	275	37	3	49455290	49455290	Missense_Mutation	SNP	C	T	4	49	c.994G>A	c.(994-996)GCA>ACA	p.A332T
Pat_63	Pre-Treatment	APEH	327	37	3	49714393	49714393	Missense_Mutation	SNP	G	A	4	46	c.935G>A	c.(934-936)TGT>TAT	p.C312Y
Pat_63	Pre-Treatment	UBA7	7318	37	3	49849859	49849859	Missense_Mutation	SNP	G	A	4	38	c.676C>T	c.(676-678)CGG>TGG	p.R226W
Pat_63	Pre-Treatment	SLC38A3	10991	37	3	50255803	50255803	Splice_Site	SNP	G	A	4	25	c.1036_splice	c.e12+1	p.N346_splice
Pat_63	Pre-Treatment	COL8A1	1295	37	3	99514900	99514900	Missense_Mutation	SNP	C	T	3	22	c.2155C>T	c.(2155-2157)CCC>TCC	p.P719S
Pat_63	Pre-Treatment	ABTB1	80325	37	3	127396014	127396014	Missense_Mutation	SNP	C	T	3	3	c.647C>T	c.(646-648)GCG>GTG	p.A216V
Pat_63	Pre-Treatment	ASTE1	28990	37	3	130743388	130743388	Nonsense_Mutation	SNP	G	A	4	21	c.763C>T	c.(763-765)CGA>TGA	p.R255*
Pat_63	Pre-Treatment	MRAS	22808	37	3	138091790	138091790	Missense_Mutation	SNP	G	A	4	27	c.65G>A	c.(64-66)GGG>GAG	p.G22E
Pat_63	Pre-Treatment	TRIM42	287015	37	3	140401581	140401581	Missense_Mutation	SNP	G	A	4	33	c.619G>A	c.(619-621)GAG>AAG	p.E207K
Pat_63	Pre-Treatment	B3GALNT1	8706	37	3	160803765	160803765	Missense_Mutation	SNP	C	T	4	36	c.778G>A	c.(778-780)GTA>ATA	p.V260I
Pat_63	Pre-Treatment	EPHB3	2049	37	3	184295757	184295757	Missense_Mutation	SNP	G	A	4	31	c.1711G>A	c.(1711-1713)GTG>ATG	p.V571M
Pat_63	Pre-Treatment	ZNF721	170960	37	4	437235	437235	Missense_Mutation	SNP	T	C	11	126	c.1021A>G	c.(1021-1023)ACC>GCC	p.T341A
Pat_63	Pre-Treatment	ZNF721	170960	37	4	437249	437249	Missense_Mutation	SNP	C	T	8	124	c.1007G>A	c.(1006-1008)GGA>GAA	p.G336E
Pat_63	Pre-Treatment	WHSC1	7468	37	4	1961355	1961355	Missense_Mutation	SNP	C	T	4	46	c.3143C>T	c.(3142-3144)GCG>GTG	p.A1048V
Pat_63	Pre-Treatment	HTT	3064	37	4	3149738	3149738	Missense_Mutation	SNP	C	T	4	13	c.3308C>T	c.(3307-3309)GCT>GTT	p.A1103V
Pat_63	Pre-Treatment	LDB2	9079	37	4	16597493	16597493	Missense_Mutation	SNP	C	T	4	54	c.241G>A	c.(241-243)GGC>AGC	p.G81S
Pat_63	Pre-Treatment	MED28	80306	37	4	17625344	17625344	Missense_Mutation	SNP	G	A	4	16	c.460G>A	c.(460-462)GCC>ACC	p.A154T
Pat_63	Pre-Treatment	SLC34A2	10568	37	4	25665862	25665862	Missense_Mutation	SNP	G	A	4	40	c.289G>A	c.(289-291)GGG>AGG	p.G97R
Pat_63	Pre-Treatment	NFXL1	152518	37	4	47888005	47888005	Missense_Mutation	SNP	G	A	5	94	c.1555C>T	c.(1555-1557)CCC>TCC	p.P519S

Pat_63	Pre-Treatment	FRYL	285527	37	4	48548277	48548277	Missense_Mutation	SNP	C	T	3	25	c.5086G>A	c.(5086-5088)GAT>AAT	p.D1696N
Pat_63	Pre-Treatment	GRID2	2895	37	4	94316843	94316843	Missense_Mutation	SNP	G	A	6	115	c.1331G>A	c.(1330-1332)CGT>CAT	p.R444H
Pat_63	Pre-Treatment	SORBS2	8470	37	4	186545297	186545297	Missense_Mutation	SNP	G	A	3	20	c.1274C>T	c.(1273-1275)CCC>CTC	p.P425L
Pat_63	Pre-Treatment	ADAMTS16	170690	37	5	5209331	5209331	Missense_Mutation	SNP	C	A	21	65	c.1577C>A	c.(1576-1578)GCC>GAC	p.A526D
Pat_63	Pre-Treatment	FBXL7	23194	37	5	15936699	15936699	Missense_Mutation	SNP	G	A	3	22	c.880G>A	c.(880-882)GCG>ACG	p.A294T
Pat_63	Pre-Treatment	C5orf34	375444	37	5	43487184	43487184	Nonsense_Mutation	SNP	G	A	4	34	c.1750C>T	c.(1750-1752)CAG>TAG	p.Q584*
Pat_63	Pre-Treatment	SV2C	22987	37	5	75505613	75505613	Missense_Mutation	SNP	C	T	4	45	c.814C>T	c.(814-816)CGG>TGG	p.R272W
Pat_63	Pre-Treatment	PITX1	5307	37	5	134369492	134369492	Missense_Mutation	SNP	A	G	2	2	c.80T>C	c.(79-81)ATG>ACG	p.M27T
Pat_63	Pre-Treatment	PSD2	84249	37	5	139193880	139193880	Missense_Mutation	SNP	G	A	3	6	c.947G>A	c.(946-948)CGG>CAG	p.R316Q
Pat_63	Pre-Treatment	PCDHB11	56125	37	5	140581277	140581277	Missense_Mutation	SNP	G	A	3	8	c.1930G>A	c.(1930-1932)GTC>ATC	p.V644I
Pat_63	Pre-Treatment	PCDHB12	56124	37	5	140590170	140590170	Missense_Mutation	SNP	C	T	3	14	c.1691C>T	c.(1690-1692)CCG>CTG	p.P564L
Pat_63	Pre-Treatment	PCDHGA3	56112	37	5	140724294	140724294	Missense_Mutation	SNP	G	A	4	25	c.694G>A	c.(694-696)GTC>ATC	p.V232I
Pat_63	Pre-Treatment	C5orf41	153222	37	5	172517654	172517654	Missense_Mutation	SNP	G	A	4	39	c.472G>A	c.(472-474)GAT>AAT	p.D158N
Pat_63	Pre-Treatment	BOD1	91272	37	5	173036279	173036279	Missense_Mutation	SNP	C	A	4	26	c.521G>T	c.(520-522)GGC>GTC	p.G174V
Pat_63	Pre-Treatment	KIAA0319	9856	37	6	24556884	24556884	Nonsense_Mutation	SNP	C	T	4	18	c.2808G>A	c.(2806-2808)TGG>TGA	p.W936*
Pat_63	Pre-Treatment	PBX2	5089	37	6	32156093	32156093	Missense_Mutation	SNP	G	A	6	91	c.484C>T	c.(484-486)CGC>TGC	p.R162C
Pat_63	Pre-Treatment	MOCS1	4337	37	6	39880033	39880033	Missense_Mutation	SNP	C	T	4	45	c.956G>A	c.(955-957)CGA>CAA	p.R319Q
Pat_63	Pre-Treatment	MRPS18A	55168	37	6	43639515	43639515	Missense_Mutation	SNP	C	A	4	35	c.575G>T	c.(574-576)TGG>TTG	p.W192L
Pat_63	Pre-Treatment	COL19A1	1310	37	6	70856581	70856581	Missense_Mutation	SNP	C	T	4	30	c.1801C>T	c.(1801-1803)CCA>TCA	p.P601S
Pat_63	Pre-Treatment	SNAP91	9892	37	6	84270583	84270583	Missense_Mutation	SNP	C	T	4	31	c.2526G>A	c.(2524-2526)ATG>ATA	p.M842I
Pat_63	Pre-Treatment	NT5E	4907	37	6	86200375	86200375	Missense_Mutation	SNP	G	A	4	28	c.1360G>A	c.(1360-1362)GGA>AGA	p.G454R
Pat_63	Pre-Treatment	GABRR1	2569	37	6	89891645	89891645	Missense_Mutation	SNP	C	T	35	37	c.928G>A	c.(928-930)GTG>ATG	p.V310M
Pat_63	Pre-Treatment	SLC16A10	117247	37	6	111498461	111498461	Missense_Mutation	SNP	G	A	4	45	c.535G>A	c.(535-537)GGC>AGC	p.G179S
Pat_63	Pre-Treatment	STXBP5	134957	37	6	147525711	147525711	Missense_Mutation	SNP	G	A	4	31	c.43G>A	c.(43-45)GCC>ACC	p.A15T
Pat_63	Pre-Treatment	ULBP1	80329	37	6	150285193	150285193	Missense_Mutation	SNP	C	T	3	13	c.8C>T	c.(7-9)GCG>GTG	p.A3V
Pat_63	Pre-Treatment	RPS6KA2	6196	37	6	166862280	166862280	Missense_Mutation	SNP	C	T	3	21	c.1264G>A	c.(1264-1266)GGG>AGG	p.G422R
Pat_63	Pre-Treatment	ABCB5	340273	37	7	20782554	20782554	Missense_Mutation	SNP	C	T	3	24	c.1744C>T	c.(1744-1746)CGC>TGC	p.R582C
Pat_63	Pre-Treatment	ZNF479	90827	37	7	57187809	57187809	Missense_Mutation	SNP	T	G	10	43	c.1313A>C	c.(1312-1314)AAA>ACA	p.K438T
Pat_63	Pre-Treatment	GUSB	2990	37	7	65432843	65432843	Missense_Mutation	SNP	C	T	5	56	c.1528G>A	c.(1528-1530)GAC>AAC	p.D510N
Pat_63	Pre-Treatment	WBSCR17	64409	37	7	71130457	71130457	Missense_Mutation	SNP	G	A	4	17	c.1142G>A	c.(1141-1143)CGG>CAG	p.R381Q
Pat_63	Pre-Treatment	SPDYE5	442590	37	7	75130883	75130883	Missense_Mutation	SNP	G	A	31	165	c.758G>A	c.(757-759)CGT>CAT	p.R253H
Pat_63	Pre-Treatment	BRAF	673	37	7	140453136	140453136	Missense_Mutation	SNP	A	T	40	77	c.1799T>A	c.(1798-1800)GTG>GAG	p.V600E
Pat_63	Pre-Treatment	ZNF425	155054	37	7	148801329	148801329	Missense_Mutation	SNP	G	A	3	6	c.1634C>T	c.(1633-1635)ACG>ATG	p.T545M
Pat_63	Pre-Treatment	NUB1	51667	37	7	151065935	151065935	Missense_Mutation	SNP	G	A	3	25	c.1282G>A	c.(1282-1284)GTG>ATG	p.V428M
Pat_63	Pre-Treatment	ZFHX4	79776	37	8	77618490	77618490	Missense_Mutation	SNP	C	T	6	23	c.2167C>T	c.(2167-2169)CAC>TAC	p.H723Y
Pat_63	Pre-Treatment	GRINA	2907	37	8	145066699	145066699	Missense_Mutation	SNP	G	A	3	23	c.889G>A	c.(889-891)GCC>ACC	p.A297T
Pat_63	Pre-Treatment	VPS28	51160	37	8	145650159	145650159	Missense_Mutation	SNP	G	A	4	42	c.344C>T	c.(343-345)CCC>CTC	p.P115L
Pat_63	Pre-Treatment	TMEM215	401498	37	9	32784491	32784491	Missense_Mutation	SNP	G	A	4	29	c.310G>A	c.(310-312)GGC>AGC	p.G104S
Pat_63	Pre-Treatment	TESK1	7016	37	9	35609156	35609156	Missense_Mutation	SNP	G	A	4	34	c.1298G>A	c.(1297-1299)CGC>CAC	p.R433H
Pat_63	Pre-Treatment	PTGS1	5742	37	9	125143686	125143686	Missense_Mutation	SNP	G	A	3	12	c.533G>A	c.(532-534)CGC>CAC	p.R178H
Pat_63	Pre-Treatment	PTGES2	80142	37	9	130886024	130886024	Missense_Mutation	SNP	C	T	6	55	c.643G>A	c.(643-645)GAG>AAG	p.E215K
Pat_63	Pre-Treatment	SPTAN1	6709	37	9	131370209	131370209	Missense_Mutation	SNP	G	A	4	31	c.4225G>A	c.(4225-4227)GGA>AGA	p.G1409R
Pat_63	Pre-Treatment	ZBED1	9189	37	X	2406981	2406981	Missense_Mutation	SNP	G	A	4	37	c.1780C>T	c.(1780-1782)CGC>TGC	p.R594C
Pat_63	Pre-Treatment	SHROOM4	57477	37	X	50350478	50350478	Missense_Mutation	SNP	G	A	4	50	c.3664C>T	c.(3664-3666)CAC>TAC	p.H1222Y
Pat_63	Pre-Treatment	ZCCHC18	644353	37	X	103359558	103359558	Missense_Mutation	SNP	G	C	2	3	c.756G>C	c.(754-756)CAG>CAC	p.Q252H
Pat_63	Pre-Treatment	MAGEC1	9947	37	X	140994583	140994583	Nonsense_Mutation	SNP	A	T	6	90	c.1393A>T	c.(1393-1395)AGA>TGA	p.R465*
Pat_63	Pre-Treatment	MAGEC1	9947	37	X	140994923	140994923	Missense_Mutation	SNP	A	T	8	191	c.1733A>T	c.(1732-1734)CAC>CTC	p.H578L

Pat_63	Post-Resistance	CPSF3L	54973	37	1	1256438	1256438	Missense_Mutation	SNP	C	T	39	236	c.64G>A	c.(64-66)GTC>ATC	p.V22I
Pat_63	Post-Resistance	SSU72	29101	37	1	1480242	1480242	Splice_Site	SNP	C	T	17	96	c.364_splice	c.e3+1	p.D122_splice
Pat_63	Post-Resistance	TNFRSF25	8718	37	1	6522132	6522132	Missense_Mutation	SNP	G	A	13	55	c.847C>T	c.(847-849)CCT>TCT	p.P283S
Pat_63	Post-Resistance	PLEKHG5	57449	37	1	6531547	6531547	Splice_Site	SNP	C	T	8	12	c.1449_splice	c.e13+1	p.M483_splice
Pat_63	Post-Resistance	SLC45A1	50651	37	1	8399720	8399720	Missense_Mutation	SNP	C	T	20	161	c.1942C>T	c.(1942-1944)CCT>TCT	p.P648S
Pat_63	Post-Resistance	CASZ1	54897	37	1	10699867	10699867	Missense_Mutation	SNP	C	T	3	14	c.4412G>A	c.(4411-4413)CGC>CAC	p.R1471H
Pat_63	Post-Resistance	MTOR	2475	37	1	11199652	11199652	Missense_Mutation	SNP	G	A	7	167	c.4936C>T	c.(4936-4938)CCT>TCT	p.P1646S
Pat_63	Post-Resistance	NECAP2	55707	37	1	16767238	16767238	Translation_Start_Site	SNP	G	A	4	42	c.-18G>A	c.(-20--16)CGGTG>CGATG	
Pat_63	Post-Resistance	PADI6	353238	37	1	17715324	17715324	Missense_Mutation	SNP	C	T	6	30	c.911C>T	c.(910-912)CCC>CTC	p.P304L
Pat_63	Post-Resistance	RCC2	55920	37	1	17747291	17747291	Missense_Mutation	SNP	C	T	10	39	c.778G>A	c.(778-780)GCC>ACC	p.A260T
Pat_63	Post-Resistance	PINK1	65018	37	1	20971071	20971071	Missense_Mutation	SNP	C	T	20	102	c.865C>T	c.(865-867)CCA>TCA	p.P289S
Pat_63	Post-Resistance	EPHA8	2046	37	1	22921777	22921777	Missense_Mutation	SNP	G	A	5	17	c.1658G>A	c.(1657-1659)GGC>GAC	p.G553D
Pat_63	Post-Resistance	HNRNPR	10236	37	1	23637215	23637215	Missense_Mutation	SNP	C	T	21	60	c.1634G>A	c.(1633-1635)GGC>GAC	p.G545D
Pat_63	Post-Resistance	NIPAL3	57185	37	1	24785392	24785392	Missense_Mutation	SNP	C	T	9	59	c.788C>T	c.(787-789)GCC>GTC	p.A263V
Pat_63	Post-Resistance	SRRM1	10250	37	1	24989228	24989228	Missense_Mutation	SNP	C	T	4	94	c.1561C>T	c.(1561-1563)CGG>TGG	p.R521W
Pat_63	Post-Resistance	CNKSR1	10256	37	1	26510976	26510976	Missense_Mutation	SNP	G	A	5	8	c.1106G>A	c.(1105-1107)GGG>GAG	p.G369E
Pat_63	Post-Resistance	PIGV	55650	37	1	27120994	27120994	Missense_Mutation	SNP	C	T	7	53	c.469C>T	c.(469-471)CTC>TTC	p.L157F
Pat_63	Post-Resistance	SLC9A1	6548	37	1	27427003	27427003	Missense_Mutation	SNP	G	A	6	248	c.2243C>T	c.(2242-2244)CCT>CTT	p.P748L
Pat_63	Post-Resistance	TINAGL1	64129	37	1	32050631	32050631	Missense_Mutation	SNP	G	A	10	61	c.851G>A	c.(850-852)CGC>CAC	p.R284H
Pat_63	Post-Resistance	YARS	8565	37	1	33256825	33256825	Missense_Mutation	SNP	C	T	42	175	c.622G>A	c.(622-624)GTC>ATC	p.V208I
Pat_63	Post-Resistance	PHC2	1912	37	1	33799821	33799821	Missense_Mutation	SNP	G	A	19	112	c.1628C>T	c.(1627-1629)TCT>TTT	p.S543F
Pat_63	Post-Resistance	ZSCAN20	7579	37	1	33956792	33956792	Missense_Mutation	SNP	T	C	9	47	c.934T>C	c.(934-936)TAC>CAC	p.Y312H
Pat_63	Post-Resistance	CLSPN	63967	37	1	36215390	36215390	Missense_Mutation	SNP	C	T	6	29	c.2051G>A	c.(2050-2052)AGT>AAT	p.S684N
Pat_63	Post-Resistance	AKIRIN1	79647	37	1	39466775	39466775	Missense_Mutation	SNP	G	A	25	122	c.493G>A	c.(493-495)GCA>ACA	p.A165T
Pat_63	Post-Resistance	MACF1	23499	37	1	39798102	39798102	Missense_Mutation	SNP	T	A	5	98	c.1162T>A	c.(1162-1164)TGC>AGC	p.C388S
Pat_63	Post-Resistance	RLF	6018	37	1	40704086	40704086	Missense_Mutation	SNP	A	G	14	61	c.3712A>G	c.(3712-3714)AAC>GAC	p.N1238D
Pat_63	Post-Resistance	KDM4A	9682	37	1	44132742	44132742	Missense_Mutation	SNP	T	C	12	99	c.895T>C	c.(895-897)TAC>CAC	p.Y299H
Pat_63	Post-Resistance	KIF2C	11004	37	1	45232786	45232786	Missense_Mutation	SNP	C	T	4	105	c.2113C>T	c.(2113-2115)CGC>TGC	p.R705C
Pat_63	Post-Resistance	MAST2	23139	37	1	46498314	46498314	Missense_Mutation	SNP	G	A	7	50	c.3461G>A	c.(3460-3462)GGT>GAT	p.G1154D
Pat_63	Post-Resistance	RAD54L	8438	37	1	46740370	46740370	Missense_Mutation	SNP	A	C	46	65	c.1850A>C	c.(1849-1851)TAT>TCT	p.Y617S
Pat_63	Post-Resistance	SPATA6	54558	37	1	48764500	48764500	Missense_Mutation	SNP	G	A	20	111	c.1352C>T	c.(1351-1353)GCC>GTC	p.A451V
Pat_63	Post-Resistance	ORC1L	4998	37	1	52859296	52859296	Missense_Mutation	SNP	G	A	21	80	c.901C>T	c.(901-903)CTC>TTC	p.L301F
Pat_63	Post-Resistance	USP24	23358	37	1	55545272	55545272	Missense_Mutation	SNP	G	A	29	144	c.6659C>T	c.(6658-6660)CCC>CTC	p.P2220L
Pat_63	Post-Resistance	JUN	3725	37	1	59248463	59248463	Missense_Mutation	SNP	G	A	44	270	c.280C>T	c.(280-282)CCC>TCC	p.P94S
Pat_63	Post-Resistance	MIER1	57708	37	1	67423844	67423844	Missense_Mutation	SNP	G	A	26	110	c.442G>A	c.(442-444)GGT>AGT	p.G148S
Pat_63	Post-Resistance	WLS	79971	37	1	68591955	68591955	Missense_Mutation	SNP	C	T	26	97	c.1580G>A	c.(1579-1581)GGA>GAA	p.G527E
Pat_63	Post-Resistance	CLCA1	1179	37	1	86951234	86951234	Missense_Mutation	SNP	G	A	42	191	c.944G>A	c.(943-945)GGA>GAA	p.G315E
Pat_63	Post-Resistance	VCAM1	7412	37	1	101190275	101190275	Missense_Mutation	SNP	G	A	14	24	c.757G>A	c.(757-759)GCT>ACT	p.A253T
Pat_63	Post-Resistance	OLFM3	118427	37	1	102269985	102269985	Missense_Mutation	SNP	C	T	40	199	c.1246G>A	c.(1246-1248)GTG>ATG	p.V416M
Pat_63	Post-Resistance	OLFM3	118427	37	1	102462324	102462324	Missense_Mutation	SNP	C	T	16	114	c.49G>A	c.(49-51)GCC>ACC	p.A17T
Pat_63	Post-Resistance	COL11A1	1301	37	1	103491783	103491783	Missense_Mutation	SNP	C	T	15	116	c.886G>A	c.(886-888)GCA>ACA	p.A296T
Pat_63	Post-Resistance	AMY2B	280	37	1	104122112	104122112	Missense_Mutation	SNP	C	T	20	296	c.1526C>T	c.(1525-1527)TCT>TTT	p.S509F
Pat_63	Post-Resistance	KIAA1324	57535	37	1	109734455	109734455	Nonsense_Mutation	SNP	G	A	39	203	c.1653G>A	c.(1651-1653)TGG>TGA	p.W551*
Pat_63	Post-Resistance	LRIG2	9860	37	1	113650322	113650322	Missense_Mutation	SNP	C	T	23	129	c.1420C>T	c.(1420-1422)CCT>TCT	p.P474S
Pat_63	Post-Resistance	ADAM30	11085	37	1	120437464	120437464	Missense_Mutation	SNP	C	T	6	35	c.1496G>A	c.(1495-1497)GGG>GAG	p.G499E
Pat_63	Post-Resistance	VPS45	11311	37	1	150039942	150039942	Missense_Mutation	SNP	T	C	51	230	c.28T>C	c.(28-30)TAC>CAC	p.Y10H
Pat_63	Post-Resistance	C1orf54	79630	37	1	150249023	150249023	Missense_Mutation	SNP	C	T	20	131	c.283C>T	c.(283-285)CCA>TCA	p.P95S

Pat_63	Post-Resistance	MCL1	4170	37	1	150550844	150550844	Missense_Mutation	SNP	C	T	14	128	c.812G>A	c.(811-813)GGT>GAT	p.G271D
Pat_63	Post-Resistance	CTSK	1513	37	1	150772043	150772043	Missense_Mutation	SNP	G	A	17	108	c.761C>T	c.(760-762)ACC>ATC	p.T254I
Pat_63	Post-Resistance	PRUNE	58497	37	1	150990336	150990336	Missense_Mutation	SNP	G	A	5	99	c.88G>A	c.(88-90)GAC>AAC	p.D30N
Pat_63	Post-Resistance	POGZ	23126	37	1	151413403	151413403	Splice_Site	SNP	C	T	29	170	c.283_splice	c.e3+1	p.A95_splice
Pat_63	Post-Resistance	HRNR	388697	37	1	152191227	152191227	Missense_Mutation	SNP	G	A	10	443	c.2878C>T	c.(2878-2880)CAC>TAC	p.H960Y
Pat_63	Post-Resistance	FLG	2312	37	1	152285655	152285655	Missense_Mutation	SNP	T	A	79	442	c.1707A>T	c.(1705-1707)AGA>AGT	p.R569S
Pat_63	Post-Resistance	ILF2	3608	37	1	153640049	153640049	Missense_Mutation	SNP	G	A	88	683	c.376C>T	c.(376-378)CTC>TTC	p.L126F
Pat_63	Post-Resistance	SLC27A3	11000	37	1	153748460	153748460	Missense_Mutation	SNP	C	T	4	14	c.628C>T	c.(628-630)CCT>TCT	p.P210S
Pat_63	Post-Resistance	PBXIP1	57326	37	1	154923773	154923773	Missense_Mutation	SNP	C	T	4	40	c.344G>A	c.(343-345)GGA>GAA	p.G115E
Pat_63	Post-Resistance	PYGO2	90780	37	1	154931322	154931322	Missense_Mutation	SNP	G	A	19	111	c.1154C>T	c.(1153-1155)ACC>ATC	p.T385I
Pat_63	Post-Resistance	ADAM15	8751	37	1	155030907	155030907	Missense_Mutation	SNP	G	A	15	53	c.1907G>A	c.(1906-1908)GGC>GAC	p.G636D
Pat_63	Post-Resistance	TRIM46	80128	37	1	155156442	155156442	Missense_Mutation	SNP	C	T	10	50	c.2056C>T	c.(2056-2058)CCC>TCC	p.P686S
Pat_63	Post-Resistance	MEF2D	4209	37	1	156437844	156437844	Missense_Mutation	SNP	G	A	18	56	c.1495C>T	c.(1495-1497)CCA>TCA	p.P499S
Pat_63	Post-Resistance	HAPLN2	60484	37	1	156593883	156593883	Missense_Mutation	SNP	G	A	14	50	c.370G>A	c.(370-372)GGC>AGC	p.G124S
Pat_63	Post-Resistance	NES	10763	37	1	156640757	156640757	Missense_Mutation	SNP	C	T	13	66	c.3223G>A	c.(3223-3225)GGT>AGT	p.G1075S
Pat_63	Post-Resistance	FCER1G	2207	37	1	161187838	161187838	Missense_Mutation	SNP	G	A	52	373	c.112G>A	c.(112-114)GTC>ATC	p.V38I
Pat_63	Post-Resistance	C1orf111	284680	37	1	162345157	162345157	Missense_Mutation	SNP	C	T	15	157	c.140G>A	c.(139-141)AGC>AAC	p.S47N
Pat_63	Post-Resistance	LRRC52	440699	37	1	165532853	165532853	Missense_Mutation	SNP	A	G	10	41	c.734A>G	c.(733-735)TAC>TGC	p.Y245C
Pat_63	Post-Resistance	FAM78B	149297	37	1	166039944	166039944	Missense_Mutation	SNP	G	A	10	78	c.320C>T	c.(319-321)TCA>TTA	p.S107L
Pat_63	Post-Resistance	F5	2153	37	1	169498889	169498889	Nonsense_Mutation	SNP	C	T	12	68	c.5376G>A	c.(5374-5376)TGG>TGA	p.W1792*
Pat_63	Post-Resistance	BAT2L2	23215	37	1	171553238	171553238	Missense_Mutation	SNP	C	T	39	426	c.7547C>T	c.(7546-7548)ACT>ATT	p.T2516I
Pat_63	Post-Resistance	KLHL20	27252	37	1	173735353	173735353	Missense_Mutation	SNP	G	A	23	207	c.1220G>A	c.(1219-1221)GGT>GAT	p.G407D
Pat_63	Post-Resistance	CACNA1E	777	37	1	181695261	181695261	Missense_Mutation	SNP	G	A	12	53	c.2203G>A	c.(2203-2205)GTC>ATC	p.V735I
Pat_63	Post-Resistance	CACNA1E	777	37	1	181741281	181741281	Missense_Mutation	SNP	C	T	24	238	c.5053C>T	c.(5053-5055)CCA>TCA	p.P1685S
Pat_63	Post-Resistance	DHX9	1660	37	1	182827344	182827344	Missense_Mutation	SNP	C	T	12	115	c.779C>T	c.(778-780)TCC>TTC	p.S260F
Pat_63	Post-Resistance	HMCN1	83872	37	1	185966567	185966567	Missense_Mutation	SNP	C	T	9	99	c.3785C>T	c.(3784-3786)CCC>CTC	p.P1262L
Pat_63	Post-Resistance	TROVE2	6738	37	1	193046127	193046127	Missense_Mutation	SNP	C	T	7	78	c.1033C>T	c.(1033-1035)CCT>TCT	p.P345S
Pat_63	Post-Resistance	TROVE2	6738	37	1	193051364	193051364	Missense_Mutation	SNP	G	A	19	237	c.1252G>A	c.(1252-1254)GAA>AAA	p.E418K
Pat_63	Post-Resistance	CFH	3075	37	1	196684819	196684819	Missense_Mutation	SNP	G	A	49	500	c.1616G>A	c.(1615-1617)GGT>GAT	p.G539D
Pat_63	Post-Resistance	CFHR5	81494	37	1	196971669	196971669	Missense_Mutation	SNP	C	T	5	137	c.1205C>T	c.(1204-1206)ACA>ATA	p.T402I
Pat_63	Post-Resistance	CRB1	23418	37	1	197391087	197391087	Splice_Site	SNP	G	A	5	58	c.2128_splice	c.e6+1	p.E710_splice
Pat_63	Post-Resistance	CAMSAP1L1	23271	37	1	200813939	200813939	Missense_Mutation	SNP	C	T	15	167	c.1084C>T	c.(1084-1086)CCT>TCT	p.P362S
Pat_63	Post-Resistance	CSRP1	1465	37	1	201454498	201454498	Missense_Mutation	SNP	G	A	8	164	c.418C>T	c.(418-420)CAT>TAT	p.H140Y
Pat_63	Post-Resistance	RNPEP	6051	37	1	201958551	201958551	Nonsense_Mutation	SNP	G	A	13	129	c.629G>A	c.(628-630)TGG>TAG	p.W210*
Pat_63	Post-Resistance	FMOD	2331	37	1	203317046	203317046	Missense_Mutation	SNP	G	A	4	52	c.353C>T	c.(352-354)ACC>ATC	p.T118I
Pat_63	Post-Resistance	PRELP	5549	37	1	203453159	203453159	Missense_Mutation	SNP	C	T	30	216	c.847C>T	c.(847-849)CTC>TTC	p.L283F
Pat_63	Post-Resistance	SOX13	9580	37	1	204082042	204082042	Splice_Site	SNP	G	A	5	55	c.0_splice	c.e2-1	
Pat_63	Post-Resistance	PPP1R15B	84919	37	1	204375346	204375346	Missense_Mutation	SNP	G	T	5	209	c.2016C>A	c.(2014-2016)TTC>TTA	p.F672L
Pat_63	Post-Resistance	PIK3C2B	5287	37	1	204410598	204410598	Splice_Site	SNP	C	T	15	101	c.3249_splice	c.e22+1	p.K1083_splice
Pat_63	Post-Resistance	DSTYK	25778	37	1	205131210	205131210	Missense_Mutation	SNP	G	A	5	89	c.1772C>T	c.(1771-1773)ACT>ATT	p.T591I
Pat_63	Post-Resistance	ELK4	2005	37	1	205589507	205589507	Missense_Mutation	SNP	G	T	5	95	c.667C>A	c.(667-669)CAA>AAA	p.Q223K
Pat_63	Post-Resistance	C1orf186	440712	37	1	206240153	206240153	Missense_Mutation	SNP	C	T	6	302	c.299G>A	c.(298-300)AGT>AAT	p.S100N
Pat_63	Post-Resistance	PIGR	5284	37	1	207112463	207112463	Splice_Site	SNP	C	T	7	62	c.388_splice	c.e3+1	p.G130_splice
Pat_63	Post-Resistance	FCAMR	83953	37	1	207139134	207139134	Missense_Mutation	SNP	C	T	5	37	c.239G>A	c.(238-240)AGG>AAG	p.R80K
Pat_63	Post-Resistance	C4BPA	722	37	1	207317325	207317325	Missense_Mutation	SNP	C	T	9	111	c.1607C>T	c.(1606-1608)CCC>CTC	p.P536L
Pat_63	Post-Resistance	CAMK1G	57172	37	1	209783243	209783243	Missense_Mutation	SNP	T	C	23	197	c.796T>C	c.(796-798)TAC>CAC	p.Y266H
Pat_63	Post-Resistance	RCOR3	55758	37	1	211451577	211451577	Missense_Mutation	SNP	G	A	44	458	c.461G>A	c.(460-462)GGT>GAT	p.G154D

Pat_63	Post-Resistance	LPGAT1	9926	37	1	211956814	211956814	Missense_Mutation	SNP	G	A	14	176	c.484C>T	c.(484-486)CTT>TTT	p.L162F
Pat_63	Post-Resistance	TP53BP2	7159	37	1	223983921	223983921	Missense_Mutation	SNP	G	A	27	222	c.2320C>T	c.(2320-2322)CCA>TCA	p.P774S
Pat_63	Post-Resistance	TMEM63A	9725	37	1	226048620	226048620	Missense_Mutation	SNP	C	T	22	254	c.1163G>A	c.(1162-1164)AGG>AAG	p.R388K
Pat_63	Post-Resistance	ITPKB	3707	37	1	226924475	226924475	Nonsense_Mutation	SNP	G	A	12	154	c.685C>T	c.(685-687)CAG>TAG	p.Q229*
Pat_63	Post-Resistance	ITPKB	3707	37	1	226924849	226924849	Missense_Mutation	SNP	C	T	4	13	c.311G>A	c.(310-312)GGT>GAT	p.G104D
Pat_63	Post-Resistance	OBSCN	84033	37	1	228462389	228462389	Missense_Mutation	SNP	G	A	5	28	c.5800G>A	c.(5800-5802)GAC>AAC	p.D1934N
Pat_63	Post-Resistance	OBSCN	84033	37	1	228494809	228494809	Missense_Mutation	SNP	C	T	5	68	c.12134C>T	.(12133-12135)GCG>GT	p.A4045V
Pat_63	Post-Resistance	SIPA1L2	57568	37	1	232649767	232649767	Missense_Mutation	SNP	C	T	14	206	c.1319G>A	c.(1318-1320)TGC>TAC	p.C440Y
Pat_63	Post-Resistance	IRF2BP2	359948	37	1	234745135	234745135	Missense_Mutation	SNP	C	T	4	115	c.106G>A	c.(106-108)GTC>ATC	p.V36I
Pat_63	Post-Resistance	TBCE	6905	37	1	235605152	235605152	Missense_Mutation	SNP	G	A	10	95	c.1294G>A	c.(1294-1296)GAA>AAA	p.E432K
Pat_63	Post-Resistance	MTR	4548	37	1	237026793	237026793	Missense_Mutation	SNP	G	A	11	140	c.2344G>A	c.(2344-2346)GGC>AGC	p.G782S
Pat_63	Post-Resistance	OPN3	23596	37	1	241761158	241761158	Missense_Mutation	SNP	C	T	8	431	c.835G>A	c.(835-837)GTT>ATT	p.V279I
Pat_63	Post-Resistance	C1orf101	257044	37	1	244627218	244627218	Missense_Mutation	SNP	C	T	38	277	c.74C>T	c.(73-75)ACT>ATT	p.T25I
Pat_63	Post-Resistance	TFB2M	64216	37	1	246707935	246707935	Missense_Mutation	SNP	G	A	4	65	c.907C>T	c.(907-909)CCT>TCT	p.P303S
Pat_63	Post-Resistance	AHCTF1	25909	37	1	247013364	247013364	Missense_Mutation	SNP	G	A	10	141	c.5944C>T	c.(5944-5946)CCA>TCA	p.P1982S
Pat_63	Post-Resistance	OR11L1	391189	37	1	248004661	248004661	Missense_Mutation	SNP	C	T	26	186	c.538G>A	c.(538-540)GAC>AAC	p.D180N
Pat_63	Post-Resistance	OR2L1P	26247	37	1	248154363	248154363	Missense_Mutation	SNP	G	A	30	177	c.551G>A	c.(550-552)CGA>CAA	p.R184Q
Pat_63	Post-Resistance	SH3BP5L	80851	37	1	249110735	249110735	Missense_Mutation	SNP	C	T	14	124	c.373G>A	c.(373-375)GAG>AAG	p.E125K
Pat_63	Post-Resistance	NET1	10276	37	10	5494819	5494819	Splice_Site	SNP	A	G	6	120	c.532_splice	c.e6-2	p.A178_splice
Pat_63	Post-Resistance	PHYH	5264	37	10	13320333	13320333	Nonsense_Mutation	SNP	G	A	17	42	c.985C>T	c.(985-987)CGA>TGA	p.R329*
Pat_63	Post-Resistance	CUBN	8029	37	10	16877012	16877012	Splice_Site	SNP	C	T	12	39	c.10362_splice	c.e64+1	p.E3454_splice
Pat_63	Post-Resistance	TRDMT1	1787	37	10	17210859	17210859	Missense_Mutation	SNP	G	A	13	34	c.232C>T	c.(232-234)CCC>TCC	p.P78S
Pat_63	Post-Resistance	VIM	7431	37	10	17279238	17279238	Missense_Mutation	SNP	G	A	11	32	c.1369G>A	c.(1369-1371)GAA>AAA	p.E457K
Pat_63	Post-Resistance	GPR158	57512	37	10	25464645	25464645	Missense_Mutation	SNP	G	A	16	38	c.296G>A	c.(295-297)TGC>TAC	p.C99Y
Pat_63	Post-Resistance	KIF5B	3799	37	10	32326235	32326235	Missense_Mutation	SNP	C	T	8	51	c.658G>A	c.(658-660)GAA>AAA	p.E220K
Pat_63	Post-Resistance	ANKRD30A	91074	37	10	37430754	37430754	Missense_Mutation	SNP	T	C	5	25	c.761T>C	c.(760-762)GTG>GCG	p.V254A
Pat_63	Post-Resistance	EGR2	1959	37	10	64573491	64573491	Missense_Mutation	SNP	C	T	3	18	c.907G>A	c.(907-909)GCA>ACA	p.A303T
Pat_63	Post-Resistance	PPP3CB	5532	37	10	75255581	75255581	Missense_Mutation	SNP	C	T	12	19	c.67G>A	c.(67-69)GCT>ACT	p.A23T
Pat_63	Post-Resistance	SFTPA2	729238	37	10	81317129	81317129	Missense_Mutation	SNP	G	A	24	93	c.583C>T	c.(583-585)CCT>TCT	p.P195S
Pat_63	Post-Resistance	GHITM	27069	37	10	85912061	85912061	Missense_Mutation	SNP	G	A	8	41	c.995G>A	c.(994-996)CGA>CAA	p.R332Q
Pat_63	Post-Resistance	PI4K2A	55361	37	10	99344579	99344579	Missense_Mutation	SNP	C	T	4	84	c.119C>T	c.(118-120)CCC>CTC	p.P40L
Pat_63	Post-Resistance	SEMA4G	57715	37	10	102739693	102739693	Missense_Mutation	SNP	G	A	33	93	c.1072G>A	c.(1072-1074)GGT>AGT	p.G358S
Pat_63	Post-Resistance	GBF1	8729	37	10	104130485	104130485	Nonsense_Mutation	SNP	G	A	32	140	c.3525G>A	c.(3523-3525)TGG>TGA	p.W1175*
Pat_63	Post-Resistance	NT5C2	22978	37	10	104857092	104857092	Missense_Mutation	SNP	C	T	29	117	c.727G>A	c.(727-729)GGG>AGG	p.G243R
Pat_63	Post-Resistance	MXI1	4601	37	10	111987992	111987992	Missense_Mutation	SNP	C	T	8	115	c.119C>T	c.(118-120)CCC>CTC	p.P40L
Pat_63	Post-Resistance	SMC3	9126	37	10	112337630	112337630	Missense_Mutation	SNP	G	A	5	41	c.308G>A	c.(307-309)GGT>GAT	p.G103D
Pat_63	Post-Resistance	FAM160B1	57700	37	10	116602881	116602881	Missense_Mutation	SNP	A	G	34	90	c.712A>G	c.(712-714)AGC>GGC	p.S238G
Pat_63	Post-Resistance	PRDX3	10935	37	10	120933248	120933248	Splice_Site	SNP	C	T	29	72	c.447_splice	c.e4+1	p.K149_splice
Pat_63	Post-Resistance	SEC23IP	11196	37	10	121663758	121663758	Missense_Mutation	SNP	C	T	5	36	c.1070C>T	c.(1069-1071)CCC>CTC	p.P357L
Pat_63	Post-Resistance	ZRANB1	54764	37	10	126631551	126631551	Nonsense_Mutation	SNP	G	A	12	74	c.489G>A	c.(487-489)TGG>TGA	p.W163*
Pat_63	Post-Resistance	MGMT	4255	37	10	131334559	131334559	Missense_Mutation	SNP	C	T	12	46	c.136C>T	c.(136-138)CCT>TCT	p.P46S
Pat_63	Post-Resistance	LRDD	55367	37	11	799383	799383	Missense_Mutation	SNP	C	T	6	125	c.2657G>A	c.(2656-2658)CGC>CAC	p.R886H
Pat_63	Post-Resistance	LOC338651	338651	37	11	1619077	1619077	Nonsense_Mutation	SNP	G	A	67	347	c.177G>A	c.(175-177)TGG>TGA	p.W59*
Pat_63	Post-Resistance	TSSC4	10078	37	11	2424477	2424477	Missense_Mutation	SNP	C	T	21	102	c.614C>T	c.(613-615)CCC>CTC	p.P205L
Pat_63	Post-Resistance	OSBPL5	114879	37	11	3147774	3147774	Missense_Mutation	SNP	C	T	4	15	c.148G>A	c.(148-150)GAG>AAG	p.E50K
Pat_63	Post-Resistance	OR52I1	390037	37	11	4616214	4616214	Missense_Mutation	SNP	C	T	21	129	c.946C>T	c.(946-948)CTC>TTC	p.L316F
Pat_63	Post-Resistance	OR52E4	390081	37	11	5906196	5906196	Missense_Mutation	SNP	C	T	17	181	c.674C>T	c.(673-675)GCT>GTT	p.A225V

Pat_63	Post-Resistance	OR2D3	120775	37	11	6942752	6942752	Missense_Mutation	SNP	G	A	9	63	c.520G>A	c.(520-522)GTA>ATA	p.V174I
Pat_63	Post-Resistance	NLRP14	338323	37	11	7060086	7060086	Missense_Mutation	SNP	G	A	8	40	c.269G>A	c.(268-270)AGA>AAA	p.R90K
Pat_63	Post-Resistance	SCUBE2	57758	37	11	9051436	9051436	Missense_Mutation	SNP	C	T	26	136	c.2411G>A	c.(2410-2412)TGT>TAT	p.C804Y
Pat_63	Post-Resistance	COPB1	1315	37	11	14480232	14480232	Missense_Mutation	SNP	G	A	18	111	c.2648C>T	c.(2647-2649)GCC>GTC	p.A883V
Pat_63	Post-Resistance	PIK3C2A	5286	37	11	17121459	17121459	Missense_Mutation	SNP	C	T	22	77	c.4066G>A	c.(4066-4068)GAT>AAT	p.D1356N
Pat_63	Post-Resistance	LDHC	3948	37	11	18456416	18456416	Missense_Mutation	SNP	C	T	29	121	c.548C>T	c.(547-549)ACA>ATA	p.T183I
Pat_63	Post-Resistance	DEPDC7	91614	37	11	33047402	33047402	Missense_Mutation	SNP	C	T	22	93	c.271C>T	c.(271-273)CCT>TCT	p.P91S
Pat_63	Post-Resistance	HIPK3	10114	37	11	33375055	33375055	Missense_Mutation	SNP	C	T	52	222	c.3589C>T	c.(3589-3591)CCT>TCT	p.P1197S
Pat_63	Post-Resistance	ABTB2	25841	37	11	34378434	34378434	Missense_Mutation	SNP	C	T	8	20	c.139G>A	c.(139-141)GCC>ACC	p.A47T
Pat_63	Post-Resistance	PRDM11	56981	37	11	45204465	45204465	Missense_Mutation	SNP	C	T	9	57	c.379C>T	c.(379-381)CCG>TCG	p.P127S
Pat_63	Post-Resistance	PRDM11	56981	37	11	45204546	45204546	Missense_Mutation	SNP	G	A	14	47	c.460G>A	c.(460-462)GTC>ATC	p.V154I
Pat_63	Post-Resistance	CRY2	1408	37	11	45892480	45892480	Missense_Mutation	SNP	G	A	3	27	c.1700G>A	c.(1699-1701)AGT>AAT	p.S567N
Pat_63	Post-Resistance	ZNF408	79797	37	11	46726859	46726859	Missense_Mutation	SNP	C	T	12	40	c.1609C>T	c.(1609-1611)CCT>TCT	p.P537S
Pat_63	Post-Resistance	LRP4	4038	37	11	46921498	46921498	Missense_Mutation	SNP	G	A	18	107	c.346C>T	c.(346-348)CCC>TCC	p.P116S
Pat_63	Post-Resistance	ACP2	53	37	11	47269238	47269238	Missense_Mutation	SNP	C	T	20	105	c.251G>A	c.(250-252)CGG>CAG	p.R84Q
Pat_63	Post-Resistance	MADD	8567	37	11	47297562	47297562	Missense_Mutation	SNP	C	T	5	48	c.772C>T	c.(772-774)CCA>TCA	p.P258S
Pat_63	Post-Resistance	P2RX3	5024	37	11	57116162	57116162	Missense_Mutation	SNP	C	T	11	76	c.547C>T	c.(547-549)CTC>TTC	p.L183F
Pat_63	Post-Resistance	SLC43A1	8501	37	11	57263580	57263580	Missense_Mutation	SNP	C	T	16	87	c.616G>A	c.(616-618)GCC>ACC	p.A206T
Pat_63	Post-Resistance	OR5A2	219981	37	11	59189727	59189727	Missense_Mutation	SNP	C	T	20	37	c.700G>A	c.(700-702)GGT>AGT	p.G234S
Pat_63	Post-Resistance	DAK	26007	37	11	61113947	61113947	Missense_Mutation	SNP	G	A	42	166	c.1700G>A	c.(1699-1701)CGG>CAG	p.R567Q
Pat_63	Post-Resistance	UBXN1	51035	37	11	62446073	62446073	Nonsense_Mutation	SNP	C	T	15	67	c.114G>A	c.(112-114)TGG>TGA	p.W38*
Pat_63	Post-Resistance	FLRT1	23769	37	11	63884605	63884605	Missense_Mutation	SNP	C	T	3	21	c.866C>T	c.(865-867)ACG>ATG	p.T289M
Pat_63	Post-Resistance	ATG2A	23130	37	11	64678631	64678631	Missense_Mutation	SNP	G	A	7	44	c.1345C>T	c.(1345-1347)CCT>TCT	p.P449S
Pat_63	Post-Resistance	SIPA1	6494	37	11	65408909	65408909	Missense_Mutation	SNP	G	A	20	64	c.517G>A	c.(517-519)GGT>AGT	p.G173S
Pat_63	Post-Resistance	RELA	5970	37	11	65422003	65422003	Missense_Mutation	SNP	G	A	15	79	c.1502C>T	c.(1501-1503)ACT>ATT	p.T501I
Pat_63	Post-Resistance	TMEM151A	256472	37	11	66062037	66062037	Missense_Mutation	SNP	C	T	14	49	c.320C>T	c.(319-321)TCC>TTC	p.S107F
Pat_63	Post-Resistance	ZDHHC24	254359	37	11	66311411	66311411	Missense_Mutation	SNP	C	T	4	92	c.323G>A	c.(322-324)GGA>GAA	p.G108E
Pat_63	Post-Resistance	LRP5	4041	37	11	68115540	68115540	Missense_Mutation	SNP	G	A	33	121	c.317G>A	c.(316-318)GGC>GAC	p.G106D
Pat_63	Post-Resistance	ANO1	55107	37	11	69933975	69933975	Missense_Mutation	SNP	A	G	3	14	c.226A>G	c.(226-228)AAC>GAC	p.N76D
Pat_63	Post-Resistance	FADD	8772	37	11	70049812	70049812	Missense_Mutation	SNP	G	A	6	22	c.247G>A	c.(247-249)GAG>AAG	p.E83K
Pat_63	Post-Resistance	DEFB108B	245911	37	11	71548594	71548594	Missense_Mutation	SNP	C	T	16	98	c.208C>T	c.(208-210)CCC>TCC	p.P70S
Pat_63	Post-Resistance	SLCO2B1	11309	37	11	74911414	74911414	Missense_Mutation	SNP	C	T	29	167	c.1745C>T	c.(1744-1746)TCC>TTC	p.S582F
Pat_63	Post-Resistance	KLHL35	283212	37	11	75134816	75134816	Missense_Mutation	SNP	C	T	23	204	c.823G>A	c.(823-825)GGG>AGG	p.G275R
Pat_63	Post-Resistance	TAF1D	79101	37	11	93471381	93471381	Missense_Mutation	SNP	G	A	17	120	c.353C>T	c.(352-354)TCA>TTA	p.S118L
Pat_63	Post-Resistance	CASP1	834	37	11	104899988	104899988	Missense_Mutation	SNP	G	C	13	43	c.869C>G	c.(868-870)CCT>CGT	p.P290R
Pat_63	Post-Resistance	ARHGAP20	57569	37	11	110450849	110450849	Missense_Mutation	SNP	G	A	4	102	c.2821C>T	c.(2821-2823)CCA>TCA	p.P941S
Pat_63	Post-Resistance	C11orf53	341032	37	11	111156756	111156756	Missense_Mutation	SNP	T	C	16	66	c.688T>C	c.(688-690)TAT>CAT	p.Y230H
Pat_63	Post-Resistance	DLAT	1737	37	11	111931864	111931864	Missense_Mutation	SNP	G	A	5	69	c.1780G>A	c.(1780-1782)GAG>AAG	p.E594K
Pat_63	Post-Resistance	ZW10	9183	37	11	113644382	113644382	Missense_Mutation	SNP	A	G	16	54	c.7T>C	c.(7-9)TCG>CCG	p.S3P
Pat_63	Post-Resistance	APOA4	337	37	11	116692023	116692023	Missense_Mutation	SNP	C	T	5	25	c.751G>A	c.(751-753)GAG>AAG	p.E251K
Pat_63	Post-Resistance	ABCG4	64137	37	11	119025271	119025271	Missense_Mutation	SNP	G	A	3	15	c.526G>A	c.(526-528)GTG>ATG	p.V176M
Pat_63	Post-Resistance	HSPA8	3312	37	11	122929825	122929825	Missense_Mutation	SNP	G	A	64	277	c.1265C>T	c.(1264-1266)ACC>ATC	p.T422I
Pat_63	Post-Resistance	WNK1	65125	37	12	988814	988814	Missense_Mutation	SNP	C	T	15	258	c.2449C>T	c.(2449-2451)CCA>TCA	p.P817S
Pat_63	Post-Resistance	WNK1	65125	37	12	994754	994754	Missense_Mutation	SNP	C	T	33	504	c.4784C>T	c.(4783-4785)CCC>CTC	p.P1595L
Pat_63	Post-Resistance	WNK1	65125	37	12	1003764	1003764	Missense_Mutation	SNP	G	A	11	219	c.5546G>A	c.(5545-5547)AGT>AAT	p.S1849N
Pat_63	Post-Resistance	ERC1	23085	37	12	1345990	1345990	Missense_Mutation	SNP	G	A	4	71	c.2407G>A	c.(2407-2409)GAA>AAA	p.E803K
Pat_63	Post-Resistance	ITFG2	55846	37	12	2930008	2930008	Missense_Mutation	SNP	C	T	9	138	c.665C>T	c.(664-666)CCT>CTT	p.P222L

Pat_63	Post-Resistance	FOXM1	2305	37	12	2977814	2977814	Missense_Mutation	SNP	C	T	30	412	c.761G>A	c.(760-762)AGG>AAG	p.R254K
Pat_63	Post-Resistance	VWF	7450	37	12	6100984	6100984	Splice_Site	SNP	C	T	7	103	c.6798_splice	c.e38+1	p.Q2266_splice
Pat_63	Post-Resistance	VWF	7450	37	12	6161827	6161827	Missense_Mutation	SNP	G	A	13	139	c.2068C>T	c.(2068-2070)CCC>TCC	p.P690S
Pat_63	Post-Resistance	TAPBPL	55080	37	12	6566703	6566703	Missense_Mutation	SNP	G	A	15	122	c.697G>A	c.(697-699)GGC>AGC	p.G233S
Pat_63	Post-Resistance	ACRBP	84519	37	12	6753756	6753756	Missense_Mutation	SNP	G	A	9	53	c.491C>T	c.(490-492)ACC>ATC	p.T164I
Pat_63	Post-Resistance	ATN1	1822	37	12	7048025	7048025	Missense_Mutation	SNP	G	A	17	73	c.2899G>A	c.(2899-2901)GGC>AGC	p.G967S
Pat_63	Post-Resistance	CD163L1	283316	37	12	7522160	7522160	Missense_Mutation	SNP	C	T	21	135	c.3832G>A	c.(3832-3834)GCC>ACC	p.A1278T
Pat_63	Post-Resistance	MFAP5	8076	37	12	8800727	8800727	Missense_Mutation	SNP	G	A	6	58	c.482C>T	c.(481-483)CCC>CTC	p.P161L
Pat_63	Post-Resistance	A2ML1	144568	37	12	9010549	9010549	Missense_Mutation	SNP	G	A	6	191	c.3115G>A	c.(3115-3117)GCG>ACG	p.A1039T
Pat_63	Post-Resistance	CD69	969	37	12	9907229	9907229	Missense_Mutation	SNP	G	A	54	316	c.445C>T	c.(445-447)CCT>TCT	p.P149S
Pat_63	Post-Resistance	TAS2R31	259290	37	12	11183789	11183789	Missense_Mutation	SNP	G	A	20	167	c.146C>T	c.(145-147)ACT>ATT	p.T49I
Pat_63	Post-Resistance	PRB2	653247	37	12	11546300	11546300	Missense_Mutation	SNP	G	A	32	284	c.712C>T	c.(712-714)CCT>TCT	p.P238S
Pat_63	Post-Resistance	SLCO1C1	53919	37	12	20903666	20903666	Nonsense_Mutation	SNP	G	A	14	100	c.1856G>A	c.(1855-1857)TGG>TAG	p.W619*
Pat_63	Post-Resistance	LDHB	3945	37	12	21788541	21788541	Missense_Mutation	SNP	C	T	11	153	c.940G>A	c.(940-942)GTT>ATT	p.V314I
Pat_63	Post-Resistance	KCNJ8	3764	37	12	21926460	21926460	Missense_Mutation	SNP	G	A	10	41	c.91C>T	c.(91-93)CTC>TTC	p.L31F
Pat_63	Post-Resistance	SOX5	6660	37	12	23728637	23728637	Missense_Mutation	SNP	G	A	25	128	c.1300C>T	c.(1300-1302)CCA>TCA	p.P434S
Pat_63	Post-Resistance	RASSF8	11228	37	12	26220590	26220590	Missense_Mutation	SNP	C	T	4	116	c.1082C>T	c.(1081-1083)ACC>ATC	p.T361I
Pat_63	Post-Resistance	ITPR2	3709	37	12	26540435	26540435	Missense_Mutation	SNP	C	T	5	129	c.7789G>A	c.(7789-7791)GTC>ATC	p.V2597I
Pat_63	Post-Resistance	ITPR2	3709	37	12	26553089	26553089	Missense_Mutation	SNP	C	T	9	394	c.7502G>A	c.(7501-7503)GGG>GAG	p.G2501E
Pat_63	Post-Resistance	C12orf35	55196	37	12	32137253	32137253	Missense_Mutation	SNP	G	A	10	61	c.3364G>A	c.(3364-3366)GAT>AAT	p.D1122N
Pat_63	Post-Resistance	SYT10	341359	37	12	33592329	33592330	Missense_Mutation	DNP	GC	AT	7	97	c.128_129GC>AT	c.(127-129)GGC>GAT	p.G43D
Pat_63	Post-Resistance	PDZRN4	29951	37	12	41966989	41966989	Missense_Mutation	SNP	G	A	37	129	c.1811G>A	c.(1810-1812)AGC>AAC	p.S604N
Pat_63	Post-Resistance	MLL2	8085	37	12	49415914	49415914	Missense_Mutation	SNP	G	A	15	377	c.16433C>T	c.(16432-16434)GCC>GTC	p.A5478V
Pat_63	Post-Resistance	TROAP	10024	37	12	49724535	49724535	Missense_Mutation	SNP	G	A	6	29	c.1907G>A	c.(1906-1908)TGC>TAC	p.C636Y
Pat_63	Post-Resistance	KRT6A	3853	37	12	52881586	52881586	Missense_Mutation	SNP	C	T	8	40	c.1613G>A	c.(1612-1614)GGC>GAC	p.G538D
Pat_63	Post-Resistance	KRT3	3850	37	12	53185132	53185132	Nonsense_Mutation	SNP	G	A	10	36	c.1393C>T	c.(1393-1395)CAA>TAA	p.Q465*
Pat_63	Post-Resistance	SOAT2	8435	37	12	53499774	53499774	Missense_Mutation	SNP	C	T	37	49	c.419C>T	c.(418-420)GCC>GTC	p.A140V
Pat_63	Post-Resistance	AAAS	8086	37	12	53709555	53709555	Missense_Mutation	SNP	C	T	9	18	c.263G>A	c.(262-264)GGC>GAC	p.G88D
Pat_63	Post-Resistance	AMHR2	269	37	12	53819671	53819671	Missense_Mutation	SNP	G	A	6	32	c.820G>A	c.(820-822)GGG>AGG	p.G274R
Pat_63	Post-Resistance	TARBP2	6895	37	12	53899601	53899601	Missense_Mutation	SNP	G	A	18	32	c.910G>A	c.(910-912)GAG>AAG	p.E304K
Pat_63	Post-Resistance	CALCOCO1	57658	37	12	54115369	54115369	Missense_Mutation	SNP	C	T	125	299	c.640G>A	c.(640-642)GAA>AAA	p.E214K
Pat_63	Post-Resistance	HOXC13	3229	37	12	54332778	54332778	Missense_Mutation	SNP	G	A	2	3	c.88G>A	c.(88-90)GGC>AGC	p.G30S
Pat_63	Post-Resistance	ERBB3	2065	37	12	56492545	56492545	Missense_Mutation	SNP	G	A	9	243	c.2695G>A	c.(2695-2697)GTG>ATG	p.V899M
Pat_63	Post-Resistance	MIP	4284	37	12	56846917	56846917	Missense_Mutation	SNP	C	T	17	50	c.545G>A	c.(544-546)GGC>GAC	p.G182D
Pat_63	Post-Resistance	STAC3	246329	37	12	57642515	57642515	Missense_Mutation	SNP	C	T	15	660	c.406G>A	c.(406-408)GAA>AAA	p.E136K
Pat_63	Post-Resistance	C12orf26	84190	37	12	82796774	82796774	Missense_Mutation	SNP	G	A	11	35	c.1144G>A	c.(1144-1146)GTG>ATG	p.V382M
Pat_63	Post-Resistance	APAF1	317	37	12	99119296	99119296	Missense_Mutation	SNP	G	A	28	147	c.3434G>A	c.(3433-3435)GGA>GAA	p.G1145E
Pat_63	Post-Resistance	UTP20	27340	37	12	101750455	101750455	Nonsense_Mutation	SNP	G	T	6	21	c.5518G>T	c.(5518-5520)GAA>TAA	p.E1840*
Pat_63	Post-Resistance	PWP1	11137	37	12	108082571	108082571	Missense_Mutation	SNP	G	A	4	19	c.311G>A	c.(310-312)GGT>GAT	p.G104D
Pat_63	Post-Resistance	SELPLG	6404	37	12	109017693	109017693	Missense_Mutation	SNP	C	T	7	121	c.391G>A	c.(391-393)GCA>ACA	p.A131T
Pat_63	Post-Resistance	RAD9B	144715	37	12	110960110	110960110	Missense_Mutation	SNP	A	T	6	18	c.1019A>T	c.(1018-1020)AAC>ATC	p.N340I
Pat_63	Post-Resistance	PPP1CC	5501	37	12	111159983	111159983	Missense_Mutation	SNP	C	T	11	83	c.839G>A	c.(838-840)GGT>GAT	p.G280D
Pat_63	Post-Resistance	OAS1	4938	37	12	113346593	113346593	Missense_Mutation	SNP	G	A	29	84	c.433G>A	c.(433-435)GTG>ATG	p.V145M
Pat_63	Post-Resistance	CAMKK2	10645	37	12	121698149	121698149	Missense_Mutation	SNP	C	T	3	10	c.769G>A	c.(769-771)GAC>AAC	p.D257N
Pat_63	Post-Resistance	RIMBP2	23504	37	12	130884256	130884256	Nonsense_Mutation	SNP	G	A	4	78	c.3100C>T	c.(3100-3102)CAA>TAA	p.Q1034*
Pat_63	Post-Resistance	RIMBP2	23504	37	12	130929756	130929756	Missense_Mutation	SNP	C	T	9	38	c.589G>A	c.(589-591)GGA>AGA	p.G197R
Pat_63	Post-Resistance	EFHA1	221154	37	13	22141013	22141013	Missense_Mutation	SNP	G	A	4	35	c.281C>T	c.(280-282)TCT>TTT	p.S94F

Pat_63	Post-Resistance	SACS	26278	37	13	23930068	23930068	Missense_Mutation	SNP	C	T	14	58	c.683G>A	c.(682-684)GGC>GAC	p.G228D
Pat_63	Post-Resistance	STARD13	90627	37	13	33692388	33692388	Missense_Mutation	SNP	G	A	21	129	c.2095C>T	c.(2095-2097)CGC>TGC	p.R699C
Pat_63	Post-Resistance	KBTBD7	84078	37	13	41766524	41766524	Missense_Mutation	SNP	C	T	7	261	c.1870G>A	c.(1870-1872)GAA>AAA	p.E624K
Pat_63	Post-Resistance	AKAP11	11215	37	13	42872909	42872909	Missense_Mutation	SNP	G	A	8	100	c.592G>A	c.(592-594)GAG>AAG	p.E198K
Pat_63	Post-Resistance	NUFIP1	26747	37	13	45533675	45533675	Missense_Mutation	SNP	C	T	23	188	c.862G>A	c.(862-864)GCA>ACA	p.A288T
Pat_63	Post-Resistance	ZC3H13	23091	37	13	46544092	46544092	Missense_Mutation	SNP	G	A	4	82	c.2587C>T	c.(2587-2589)CTC>TTC	p.L863F
Pat_63	Post-Resistance	ZC3H13	23091	37	13	46619557	46619557	Missense_Mutation	SNP	C	T	70	389	c.86G>A	c.(85-87)AGG>AAG	p.R29K
Pat_63	Post-Resistance	ITM2B	9445	37	13	48830352	48830352	Missense_Mutation	SNP	G	A	14	80	c.286G>A	c.(286-288)GAT>AAT	p.D96N
Pat_63	Post-Resistance	PIBF1	10464	37	13	73369696	73369696	Splice_Site	SNP	G	A	6	53	c.552_splice	c.e4+1	p.S184_splice
Pat_63	Post-Resistance	MYCBP2	23077	37	13	77671760	77671760	Missense_Mutation	SNP	C	T	14	63	c.9415G>A	c.(9415-9417)GCT>ACT	p.A3139T
Pat_63	Post-Resistance	MYCBP2	23077	37	13	77699555	77699555	Missense_Mutation	SNP	C	T	63	450	c.7819G>A	c.(7819-7821)GTA>ATA	p.V2607I
Pat_63	Post-Resistance	ZIC5	85416	37	13	100617916	100617916	Missense_Mutation	SNP	C	A	7	192	c.1707G>T	c.(1705-1707)AGG>AGT	p.R569S
Pat_63	Post-Resistance	ATP11A	23250	37	13	113473682	113473682	Missense_Mutation	SNP	C	T	32	142	c.635C>T	c.(634-636)GCC>GTC	p.A212V
Pat_63	Post-Resistance	OR11H4	390442	37	14	20711678	20711678	Missense_Mutation	SNP	G	A	42	201	c.728G>A	c.(727-729)GGT>GAT	p.G243D
Pat_63	Post-Resistance	PARP2	10038	37	14	20819205	20819205	Splice_Site	SNP	G	A	6	58	c.461_splice	c.e6-1	p.V154_splice
Pat_63	Post-Resistance	APEX1	328	37	14	20924219	20924219	Missense_Mutation	SNP	G	C	3	106	c.205G>C	c.(205-207)GTG>CTG	p.V69L
Pat_63	Post-Resistance	HNRNPC	3183	37	14	21699216	21699216	Missense_Mutation	SNP	G	A	4	116	c.257C>T	c.(256-258)GCA>GTA	p.A86V
Pat_63	Post-Resistance	MYH7	4625	37	14	23893358	23893358	Missense_Mutation	SNP	C	T	5	37	c.2680G>A	c.(2680-2682)GAA>AAA	p.E894K
Pat_63	Post-Resistance	MYH7	4625	37	14	23898454	23898454	Missense_Mutation	SNP	C	T	41	220	c.1241G>A	c.(1240-1242)GGG>GAG	p.G414E
Pat_63	Post-Resistance	FITM1	161247	37	14	24601766	24601766	Missense_Mutation	SNP	G	A	3	60	c.613G>A	c.(613-615)GCC>ACC	p.A205T
Pat_63	Post-Resistance	PSME2	5721	37	14	24614646	24614646	Missense_Mutation	SNP	G	A	38	198	c.173C>T	c.(172-174)ACT>ATT	p.T58I
Pat_63	Post-Resistance	RNF31	55072	37	14	24621031	24621031	Missense_Mutation	SNP	C	T	48	126	c.1960C>T	c.(1960-1962)CCC>TCC	p.P654S
Pat_63	Post-Resistance	GMPR2	51292	37	14	24706276	24706276	Splice_Site	SNP	G	A	32	174	c.466_splice	c.e6-1	p.A156_splice
Pat_63	Post-Resistance	CIDEB	27141	37	14	24775705	24775705	Missense_Mutation	SNP	C	T	63	246	c.211G>A	c.(211-213)GGA>AGA	p.G71R
Pat_63	Post-Resistance	LTB4R2	56413	37	14	24779980	24779980	Missense_Mutation	SNP	G	A	8	38	c.203G>A	c.(202-204)GGC>GAC	p.G68D
Pat_63	Post-Resistance	SCFD1	23256	37	14	31169402	31169402	Missense_Mutation	SNP	C	T	15	97	c.1348C>T	c.(1348-1350)CCA>TCA	p.P450S
Pat_63	Post-Resistance	HEATR5A	25938	37	14	31782186	31782186	Missense_Mutation	SNP	G	A	6	14	c.3550C>T	c.(3550-3552)CTT>TTT	p.L1184F
Pat_63	Post-Resistance	SEC23A	10484	37	14	39565220	39565220	Missense_Mutation	SNP	C	T	27	199	c.103G>A	c.(103-105)GTT>ATT	p.V35I
Pat_63	Post-Resistance	PNN	5411	37	14	39645283	39645283	Missense_Mutation	SNP	C	T	8	58	c.115C>T	c.(115-117)CCC>TCC	p.P39S
Pat_63	Post-Resistance	FSCB	84075	37	14	44975229	44975229	Missense_Mutation	SNP	G	A	6	28	c.962C>T	c.(961-963)GCT>GTT	p.A321V
Pat_63	Post-Resistance	RPL10L	140801	37	14	47120617	47120617	Missense_Mutation	SNP	G	A	17	81	c.323C>T	c.(322-324)GCT>GTT	p.A108V
Pat_63	Post-Resistance	CDKL1	8814	37	14	50802857	50802857	Missense_Mutation	SNP	C	T	4	26	c.2836G>A	c.(2836-2838)GTA>ATA	p.V946I
Pat_63	Post-Resistance	KTN1	3895	37	14	56146298	56146298	Missense_Mutation	SNP	G	A	8	54	c.3964G>A	c.(3964-3966)GAG>AAG	p.E1322K
Pat_63	Post-Resistance	KIAA0586	9786	37	14	58934459	58934459	Missense_Mutation	SNP	C	T	11	310	c.2033C>T	c.(2032-2034)ACC>ATC	p.T678I
Pat_63	Post-Resistance	DAAM1	23002	37	14	59798636	59798636	Nonsense_Mutation	SNP	C	T	13	85	c.1966C>T	c.(1966-1968)CAG>TAG	p.Q656*
Pat_63	Post-Resistance	PPP2R5E	5529	37	14	63856340	63856340	Missense_Mutation	SNP	G	A	4	41	c.1064C>T	c.(1063-1065)CCC>CTC	p.P355L
Pat_63	Post-Resistance	SYNE2	23224	37	14	64493369	64493369	Missense_Mutation	SNP	G	A	8	26	c.6325G>A	c.(6325-6327)GCC>ACC	p.A2109T
Pat_63	Post-Resistance	SYNE2	23224	37	14	64686082	64686082	Missense_Mutation	SNP	C	T	9	54	c.19745C>T	c.(19744-19746)CCT>CTT	p.P6582L
Pat_63	Post-Resistance	AKAP5	9495	37	14	64935848	64935848	Nonsense_Mutation	SNP	C	T	36	205	c.736C>T	c.(736-738)CAA>TAA	p.Q246*
Pat_63	Post-Resistance	EXD2	55218	37	14	69707693	69707693	Missense_Mutation	SNP	G	A	4	41	c.1367G>A	c.(1366-1368)CGC>CAC	p.R456H
Pat_63	Post-Resistance	ACOT2	10965	37	14	74040241	74040241	Missense_Mutation	SNP	C	T	26	97	c.793C>T	c.(793-795)CTC>TTC	p.L265F
Pat_63	Post-Resistance	ZNF410	57862	37	14	74390131	74390131	Missense_Mutation	SNP	C	T	13	78	c.1304C>T	c.(1303-1305)TCT>TTT	p.S435F
Pat_63	Post-Resistance	FLVCR2	55640	37	14	76091096	76091096	Splice_Site	SNP	G	A	6	51	c.952_splice	c.e3+1	p.G318_splice
Pat_63	Post-Resistance	C14orf118	55668	37	14	76668051	76668051	Nonsense_Mutation	SNP	G	T	21	61	c.1306G>T	c.(1306-1308)GAG>TAG	p.E436*
Pat_63	Post-Resistance	SNW1	22938	37	14	78217816	78217817	Missense_Mutation	DNP	CC	AA	3	27	c.175_176GG>TT	c.(175-177)GGA>TTA	p.G59L
Pat_63	Post-Resistance	ADCK1	57143	37	14	78365567	78365567	Missense_Mutation	SNP	T	C	17	80	c.707T>C	c.(706-708)GTG>GCG	p.V236A
Pat_63	Post-Resistance	NRXN3	9369	37	14	79933620	79933620	Missense_Mutation	SNP	G	A	12	79	c.2200G>A	c.(2200-2202)GCC>ACC	p.A734T

Pat_63	Post-Resistance	C14orf145	145508	37	14	81380683	81380683	Missense_Mutation	SNP	C	T	24	155	c.217G>A	c.(217-219)GCG>ACG	p.A73T
Pat_63	Post-Resistance	FLRT2	23768	37	14	86089009	86089009	Missense_Mutation	SNP	C	T	32	178	c.1151C>T	c.(1150-1152)CCC>CTC	p.P384L
Pat_63	Post-Resistance	GALC	2581	37	14	88414137	88414137	Missense_Mutation	SNP	C	T	19	131	c.1424G>A	c.(1423-1425)GGC>GAC	p.G475D
Pat_63	Post-Resistance	PTPN21	11099	37	14	88946502	88946502	Missense_Mutation	SNP	C	T	6	33	c.1273G>A	c.(1273-1275)GAC>AAC	p.D425N
Pat_63	Post-Resistance	PTPN21	11099	37	14	88963546	88963546	Splice_Site	SNP	C	T	4	45	c.852_splice	c.e9+1	p.T284_splice
Pat_63	Post-Resistance	TTC7B	145567	37	14	91110419	91110419	Missense_Mutation	SNP	G	A	36	256	c.1724C>T	c.(1723-1725)GCC>GTC	p.A575V
Pat_63	Post-Resistance	SERPINA12	145264	37	14	94964729	94964729	Missense_Mutation	SNP	G	T	13	54	c.6C>A	c.(4-6)AAC>AAA	p.N2K
Pat_63	Post-Resistance	AK7	122481	37	14	96953362	96953362	Missense_Mutation	SNP	A	G	14	83	c.2102A>G	c.(2101-2103)AAC>AGC	p.N701S
Pat_63	Post-Resistance	MARK3	4140	37	14	103931956	103931956	Missense_Mutation	SNP	T	A	18	87	c.603T>A	c.(601-603)AAT>AAA	p.N201K
Pat_63	Post-Resistance	KLC1	3831	37	14	104129134	104129134	Missense_Mutation	SNP	T	C	4	19	c.667T>C	c.(667-669)TAC>CAC	p.Y223H
Pat_63	Post-Resistance	CRIP2	1397	37	14	105945540	105945540	Missense_Mutation	SNP	C	T	24	64	c.485C>T	c.(484-486)CCC>CTC	p.P162L
Pat_63	Post-Resistance	NIPA1	123606	37	15	23052593	23052593	Splice_Site	SNP	A	G	9	233	c.478_splice	c.e4+1	p.V160_splice
Pat_63	Post-Resistance	MTMR10	54893	37	15	31283658	31283658	Missense_Mutation	SNP	G	A	13	72	c.52C>T	c.(52-54)CCG>TCG	p.P18S
Pat_63	Post-Resistance	OTUD7A	161725	37	15	31795984	31795984	Missense_Mutation	SNP	C	T	8	71	c.910G>A	c.(910-912)GAA>AAA	p.E304K
Pat_63	Post-Resistance	BAHD1	22893	37	15	40751819	40751819	Missense_Mutation	SNP	G	A	9	100	c.1156G>A	c.(1156-1158)GAG>AAG	p.E386K
Pat_63	Post-Resistance	BAHD1	22893	37	15	40758235	40758235	Missense_Mutation	SNP	G	A	33	297	c.2249G>A	c.(2248-2250)CGC>CAC	p.R750H
Pat_63	Post-Resistance	MGA	23269	37	15	41961589	41961589	Missense_Mutation	SNP	G	A	60	372	c.497G>A	c.(496-498)GGT>GAT	p.G166D
Pat_63	Post-Resistance	EHD4	30844	37	15	42211781	42211781	Missense_Mutation	SNP	C	T	17	147	c.551G>A	c.(550-552)AGG>AAG	p.R184K
Pat_63	Post-Resistance	TRPM7	54822	37	15	50866603	50866603	Missense_Mutation	SNP	C	T	7	45	c.5176G>A	c.(5176-5178)GAA>AAA	p.E1726K
Pat_63	Post-Resistance	CYP19A1	1588	37	15	51519975	51519975	Splice_Site	SNP	C	T	14	79	c.451_splice	c.e5+1	p.A151_splice
Pat_63	Post-Resistance	LEO1	123169	37	15	52245461	52245461	Splice_Site	SNP	C	T	10	72	c.1341_splice	c.e8-1	p.S447_splice
Pat_63	Post-Resistance	FAM63B	54629	37	15	59102428	59102428	Splice_Site	SNP	G	A	24	149	c.964_splice	c.e4-1	p.N322_splice
Pat_63	Post-Resistance	SLTM	79811	37	15	59179448	59179448	Missense_Mutation	SNP	C	T	13	99	c.2667G>A	c.(2665-2667)ATG>ATA	p.M889I
Pat_63	Post-Resistance	MYO1E	4643	37	15	59430537	59430537	Missense_Mutation	SNP	G	A	24	142	c.3110C>T	c.(3109-3111)CCC>CTC	p.P1037L
Pat_63	Post-Resistance	SNX1	6642	37	15	64418401	64418401	Missense_Mutation	SNP	C	T	15	88	c.634C>T	c.(634-636)CCG>TCG	p.P212S
Pat_63	Post-Resistance	CILP	8483	37	15	65490577	65490577	Missense_Mutation	SNP	C	T	21	89	c.2047G>A	c.(2047-2049)GAC>AAC	p.D683N
Pat_63	Post-Resistance	C15orf44	81556	37	15	65892267	65892267	Missense_Mutation	SNP	C	T	15	58	c.331G>A	c.(331-333)GTT>ATT	p.V111I
Pat_63	Post-Resistance	SMAD6	4091	37	15	67073470	67073470	Missense_Mutation	SNP	G	A	7	17	c.1088G>A	c.(1087-1089)GGC>GAC	p.G363D
Pat_63	Post-Resistance	LBXCOR1	390598	37	15	68119394	68119394	Missense_Mutation	SNP	G	A	6	28	c.1096G>A	c.(1096-1098)GAC>AAC	p.D366N
Pat_63	Post-Resistance	FEM1B	10116	37	15	68582046	68582046	Missense_Mutation	SNP	C	T	17	135	c.350C>T	c.(349-351)ACC>ATC	p.T117I
Pat_63	Post-Resistance	MYO9A	4649	37	15	72142435	72142435	Missense_Mutation	SNP	G	A	28	177	c.6655C>T	c.(6655-6657)CGC>TGC	p.R2219C
Pat_63	Post-Resistance	PARP6	56965	37	15	72543552	72543552	Missense_Mutation	SNP	C	T	12	128	c.1304G>A	c.(1303-1305)AGC>AAC	p.S435N
Pat_63	Post-Resistance	CCDC33	80125	37	15	74623340	74623340	Missense_Mutation	SNP	G	A	3	14	c.1564G>A	c.(1564-1566)GAG>AAG	p.E522K
Pat_63	Post-Resistance	ARID3B	10620	37	15	74887991	74887991	Missense_Mutation	SNP	C	T	9	27	c.1562C>T	c.(1561-1563)ACG>ATG	p.T521M
Pat_63	Post-Resistance	EDC3	80153	37	15	74967464	74967464	Missense_Mutation	SNP	A	C	88	470	c.2T>G	c.(1-3)ATG>AGG	p.M1R
Pat_63	Post-Resistance	COX5A	9377	37	15	75216038	75216038	Missense_Mutation	SNP	C	T	7	47	c.413G>A	c.(412-414)GGA>GAA	p.G138E
Pat_63	Post-Resistance	NEIL1	79661	37	15	75647142	75647142	Missense_Mutation	SNP	G	A	4	44	c.1085G>A	c.(1084-1086)GGG>GAG	p.G362E
Pat_63	Post-Resistance	MAN2C1	4123	37	15	75654757	75654757	Missense_Mutation	SNP	C	T	11	56	c.935G>A	c.(934-936)GGC>GAC	p.G312D
Pat_63	Post-Resistance	SCAPER	49855	37	15	76726500	76726500	Missense_Mutation	SNP	G	A	4	85	c.3230C>T	c.(3229-3231)ACC>ATC	p.T1077I
Pat_63	Post-Resistance	CIB2	10518	37	15	78398202	78398202	Missense_Mutation	SNP	C	T	24	89	c.421G>A	c.(421-423)GAT>AAT	p.D141N
Pat_63	Post-Resistance	RASGRF1	5923	37	15	79272981	79272981	Missense_Mutation	SNP	G	A	12	50	c.3523C>T	c.(3523-3525)CTC>TTC	p.L1175F
Pat_63	Post-Resistance	FAH	2184	37	15	80460462	80460462	Missense_Mutation	SNP	G	A	15	58	c.524G>A	c.(523-525)AGG>AAG	p.R175K
Pat_63	Post-Resistance	MESDC2	23184	37	15	81274441	81274441	Missense_Mutation	SNP	C	T	16	140	c.296G>A	c.(295-297)AGC>AAC	p.S99N
Pat_63	Post-Resistance	ZSCAN2	54993	37	15	85164576	85164576	Missense_Mutation	SNP	C	T	36	295	c.1150C>T	c.(1150-1152)CAC>TAC	p.H384Y
Pat_63	Post-Resistance	ALPK3	57538	37	15	85411661	85411661	Missense_Mutation	SNP	G	A	5	23	c.5698G>A	c.(5698-5700)GGC>AGC	p.G1900S
Pat_63	Post-Resistance	SLC28A1	9154	37	15	85478378	85478378	Missense_Mutation	SNP	C	T	16	100	c.1336C>T	c.(1336-1338)CTC>TTC	p.L446F
Pat_63	Post-Resistance	C15orf42	90381	37	15	90126050	90126050	Missense_Mutation	SNP	G	A	36	180	c.788G>A	c.(787-789)GGA>GAA	p.G263E

Pat_63	Post-Resistance	TTLL13	440307	37	15	90794074	90794074	Missense_Mutation	SNP	C	T	28	167	c.212C>T	c.(211-213)ACA>ATA	p.T71I
Pat_63	Post-Resistance	SNRPA1	6627	37	15	101825189	101825189	Missense_Mutation	SNP	C	T	49	489	c.692G>A	c.(691-693)GGC>GAC	p.G231D
Pat_63	Post-Resistance	OR4F4	26682	37	15	102462385	102462385	Missense_Mutation	SNP	C	T	9	668	c.878G>A	c.(877-879)CGG>CAG	p.R293Q
Pat_63	Post-Resistance	RHBDF1	64285	37	16	113745	113745	Nonsense_Mutation	SNP	C	T	12	49	c.302G>A	c.(301-303)TGG>TAG	p.W101*
Pat_63	Post-Resistance	WDR90	197335	37	16	716231	716231	Missense_Mutation	SNP	C	T	22	72	c.4621C>T	c.(4621-4623)CTC>TTC	p.L1541F
Pat_63	Post-Resistance	MSLNL	401827	37	16	824854	824854	Missense_Mutation	SNP	C	T	3	34	c.1718G>A	c.(1717-1719)GGT>GAT	p.G573D
Pat_63	Post-Resistance	MAPK8IP3	23162	37	16	1817641	1817641	Missense_Mutation	SNP	C	T	19	63	c.3311C>T	c.(3310-3312)TCC>TTC	p.S1104F
Pat_63	Post-Resistance	SRRM2	23524	37	16	2817385	2817385	Missense_Mutation	SNP	G	A	32	147	c.6856G>A	c.(6856-6858)GAC>AAC	p.D2286N
Pat_63	Post-Resistance	TNFRSF12A	51330	37	16	3070478	3070478	Missense_Mutation	SNP	G	A	8	53	c.80G>A	c.(79-81)GGG>GAG	p.G27E
Pat_63	Post-Resistance	HMOX2	3163	37	16	4558095	4558095	Nonsense_Mutation	SNP	C	T	3	28	c.586C>T	c.(586-588)CAG>TAG	p.Q196*
Pat_63	Post-Resistance	PPL	5493	37	16	4933859	4933859	Missense_Mutation	SNP	C	T	7	107	c.4797G>A	c.(4795-4797)ATG>ATA	p.M1599I
Pat_63	Post-Resistance	CIITA	4261	37	16	10996560	10996560	Missense_Mutation	SNP	G	A	3	47	c.674G>A	c.(673-675)GGA>GAA	p.G225E
Pat_63	Post-Resistance	MKL2	57496	37	16	14355272	14355272	Missense_Mutation	SNP	C	T	33	136	c.3271C>T	c.(3271-3273)CCA>TCA	p.P1091S
Pat_63	Post-Resistance	KIAA0430	9665	37	16	15692725	15692725	Missense_Mutation	SNP	G	A	6	35	c.4970C>T	c.(4969-4971)CCT>CTT	p.P1657L
Pat_63	Post-Resistance	KIAA0430	9665	37	16	15715746	15715746	Missense_Mutation	SNP	G	A	12	59	c.2483C>T	c.(2482-2484)CCC>CTC	p.P828L
Pat_63	Post-Resistance	KIAA0430	9665	37	16	15718895	15718895	Missense_Mutation	SNP	G	A	31	118	c.2089C>T	c.(2089-2091)CCC>TCC	p.P697S
Pat_63	Post-Resistance	SCNN1G	6340	37	16	23224000	23224000	Missense_Mutation	SNP	G	A	8	82	c.1296G>A	c.(1294-1296)ATG>ATA	p.M432I
Pat_63	Post-Resistance	GGA2	23062	37	16	23478972	23478972	Missense_Mutation	SNP	G	A	9	31	c.1781C>T	c.(1780-1782)CCT>CTT	p.P594L
Pat_63	Post-Resistance	PALB2	79728	37	16	23641289	23641289	Missense_Mutation	SNP	G	A	7	49	c.2186C>T	c.(2185-2187)CCC>CTC	p.P729L
Pat_63	Post-Resistance	TAOK2	9344	37	16	29997130	29997130	Missense_Mutation	SNP	A	G	4	19	c.1940A>G	c.(1939-1941)AAG>AGG	p.K647R
Pat_63	Post-Resistance	HIRIP3	8479	37	16	30005798	30005798	Missense_Mutation	SNP	C	T	5	174	c.668G>A	c.(667-669)AGT>AAT	p.S223N
Pat_63	Post-Resistance	CD2BP2	10421	37	16	30365960	30365960	Missense_Mutation	SNP	C	T	13	443	c.43G>A	c.(43-45)GAG>AAG	p.E15K
Pat_63	Post-Resistance	ITGAL	3683	37	16	30500639	30500639	Missense_Mutation	SNP	C	T	3	44	c.1145C>T	c.(1144-1146)GCA>GTA	p.A382V
Pat_63	Post-Resistance	ZNF668	79759	37	16	31072808	31072808	Missense_Mutation	SNP	C	T	4	111	c.1441G>A	c.(1441-1443)GTG>ATG	p.V481M
Pat_63	Post-Resistance	NOD2	64127	37	16	50756549	50756549	Missense_Mutation	SNP	G	A	67	339	c.2731G>A	c.(2731-2733)GTG>ATG	p.V911M
Pat_63	Post-Resistance	AKTIP	64400	37	16	53532337	53532337	Missense_Mutation	SNP	G	A	35	165	c.214C>T	c.(214-216)CCC>TCC	p.P72S
Pat_63	Post-Resistance	MMP2	4313	37	16	55519659	55519659	Missense_Mutation	SNP	G	A	28	152	c.802G>A	c.(802-804)GAT>AAT	p.D268N
Pat_63	Post-Resistance	CNGB1	1258	37	16	57996948	57996948	Missense_Mutation	SNP	G	A	22	61	c.311C>T	c.(310-312)ACC>ATC	p.T104I
Pat_63	Post-Resistance	TPPP3	51673	37	16	67424473	67424473	Missense_Mutation	SNP	G	A	39	173	c.251C>T	c.(250-252)ACC>ATC	p.T84I
Pat_63	Post-Resistance	LCAT	3931	37	16	67976778	67976778	Missense_Mutation	SNP	C	T	3	88	c.413G>A	c.(412-414)AGC>AAC	p.S138N
Pat_63	Post-Resistance	ESRP2	80004	37	16	68265252	68265252	Nonsense_Mutation	SNP	G	A	13	44	c.1570C>T	c.(1570-1572)CAG>TAG	p.Q524*
Pat_63	Post-Resistance	SMPD3	55512	37	16	68395176	68395176	Missense_Mutation	SNP	G	A	12	28	c.1901C>T	c.(1900-1902)TCC>TTC	p.S634F
Pat_63	Post-Resistance	VPS4A	27183	37	16	69350133	69350133	Missense_Mutation	SNP	G	A	14	63	c.139G>A	c.(139-141)GCC>ACC	p.A47T
Pat_63	Post-Resistance	FUK	197258	37	16	70502848	70502848	Missense_Mutation	SNP	G	T	12	37	c.760G>T	c.(760-762)GAC>TAC	p.D254Y
Pat_63	Post-Resistance	CHST4	10164	37	16	71571554	71571554	Missense_Mutation	SNP	G	A	3	23	c.974G>A	c.(973-975)AGG>AAG	p.R325K
Pat_63	Post-Resistance	DHODH	1723	37	16	72046022	72046022	Missense_Mutation	SNP	G	A	25	131	c.95G>A	c.(94-96)GGA>GAA	p.G32E
Pat_63	Post-Resistance	ZFHX3	463	37	16	72829896	72829896	Missense_Mutation	SNP	G	A	23	78	c.6685C>T	c.(6685-6687)CCT>TCT	p.P2229S
Pat_63	Post-Resistance	CHST6	4166	37	16	75512550	75512550	Missense_Mutation	SNP	G	A	17	54	c.1177C>T	c.(1177-1179)CCC>TCC	p.P393S
Pat_63	Post-Resistance	KLHL36	79786	37	16	84690751	84690751	Missense_Mutation	SNP	G	A	4	47	c.338G>A	c.(337-339)GGC>GAC	p.G113D
Pat_63	Post-Resistance	CDH15	1013	37	16	89258152	89258152	Missense_Mutation	SNP	G	A	5	9	c.1465G>A	c.(1465-1467)GGC>AGC	p.G489S
Pat_63	Post-Resistance	CDH15	1013	37	16	89260199	89260199	Missense_Mutation	SNP	G	A	5	12	c.2029G>A	c.(2029-2031)GCG>ACG	p.A677T
Pat_63	Post-Resistance	OR3A1	4994	37	17	3195759	3195759	Missense_Mutation	SNP	C	T	8	48	c.118G>A	c.(118-120)GTC>ATC	p.V40I
Pat_63	Post-Resistance	MYBBP1A	10514	37	17	4457563	4457563	Missense_Mutation	SNP	G	A	6	48	c.305C>T	c.(304-306)TCT>TTT	p.S102F
Pat_63	Post-Resistance	SMTNL2	342527	37	17	4498522	4498522	Missense_Mutation	SNP	C	T	18	27	c.889C>T	c.(889-891)CGC>TGC	p.R297C
Pat_63	Post-Resistance	SLC13A5	284111	37	17	6606361	6606361	Missense_Mutation	SNP	G	A	8	78	c.644C>T	c.(643-645)GCG>GTG	p.A215V
Pat_63	Post-Resistance	PHF23	79142	37	17	7139108	7139108	Missense_Mutation	SNP	C	T	19	422	c.1049G>A	c.(1048-1050)GGG>GAG	p.G350E
Pat_63	Post-Resistance	EFNB3	1949	37	17	7612602	7612602	Missense_Mutation	SNP	G	A	3	9	c.731G>A	c.(730-732)GGG>GAG	p.G244E

Pat_63	Post-Resistance	CHD3	1107	37	17	7807277	7807277	Missense_Mutation	SNP	G	A	21	67	c.3862G>A	c.(3862-3864)GTG>ATG	p.V1288M
Pat_63	Post-Resistance	C17orf68	80169	37	17	8146340	8146340	Missense_Mutation	SNP	C	T	5	21	c.160G>A	c.(160-162)GGA>AGA	p.G54R
Pat_63	Post-Resistance	ARHGEF15	22899	37	17	8218775	8218775	Missense_Mutation	SNP	C	T	4	67	c.1304C>T	c.(1303-1305)TCC>TTC	p.S435F
Pat_63	Post-Resistance	MYH4	4622	37	17	10366873	10366873	Missense_Mutation	SNP	G	A	11	64	c.736C>T	c.(736-738)CGC>TGC	p.R246C
Pat_63	Post-Resistance	DNAH9	1770	37	17	11835441	11835441	Nonsense_Mutation	SNP	G	A	8	45	c.12216G>A	c.(12214-12216)TGG>TGA	p.W4072*
Pat_63	Post-Resistance	CCDC144A	9720	37	17	16594059	16594059	Splice_Site	SNP	G	A	11	117	c.344_splice	c.e1+1	p.S115_splice
Pat_63	Post-Resistance	TOP3A	7156	37	17	18193994	18193994	Missense_Mutation	SNP	G	A	7	28	c.1474C>T	c.(1474-1476)CCT>TCT	p.P492S
Pat_63	Post-Resistance	FBXW10	10517	37	17	18653160	18653160	Missense_Mutation	SNP	G	A	10	98	c.796G>A	c.(796-798)GAC>AAC	p.D266N
Pat_63	Post-Resistance	FAM18B	51030	37	17	18702245	18702245	Missense_Mutation	SNP	G	A	36	263	c.451G>A	c.(451-453)GTA>ATA	p.V151I
Pat_63	Post-Resistance	WSB1	26118	37	17	25628852	25628852	Missense_Mutation	SNP	G	A	36	204	c.79G>A	c.(79-81)GCT>ACT	p.A27T
Pat_63	Post-Resistance	SLC13A2	9058	37	17	26817804	26817804	Missense_Mutation	SNP	G	A	4	103	c.454G>A	c.(454-456)GCA>ACA	p.A152T
Pat_63	Post-Resistance	C17orf63	55731	37	17	27086229	27086229	Missense_Mutation	SNP	G	A	11	30	c.748C>T	c.(748-750)CCC>TCC	p.P250S
Pat_63	Post-Resistance	ADAP2	55803	37	17	29250074	29250074	Missense_Mutation	SNP	G	A	47	153	c.211G>A	c.(211-213)GAC>AAC	p.D71N
Pat_63	Post-Resistance	UNC45B	146862	37	17	33503031	33503031	Missense_Mutation	SNP	T	C	11	70	c.2009T>C	c.(2008-2010)ATT>ACT	p.I670T
Pat_63	Post-Resistance	SLFN12	55106	37	17	33749797	33749797	Missense_Mutation	SNP	C	T	13	59	c.251G>A	c.(250-252)AGT>AAT	p.S84N
Pat_63	Post-Resistance	GPR179	440435	37	17	36483786	36483786	Missense_Mutation	SNP	G	T	7	98	c.5666C>A	c.(5665-5667)CCC>CAC	p.P1889H
Pat_63	Post-Resistance	PPP1R1B	84152	37	17	37791880	37791880	Missense_Mutation	SNP	G	A	5	124	c.466G>A	c.(466-468)GGC>AGC	p.G156S
Pat_63	Post-Resistance	GSDMA	284110	37	17	38130084	38130084	Splice_Site	SNP	G	A	3	34	c.751_splice	c.e8+1	p.G251_splice
Pat_63	Post-Resistance	MED24	9862	37	17	38185143	38185143	Missense_Mutation	SNP	C	T	9	60	c.1345G>A	c.(1345-1347)GAC>AAC	p.D449N
Pat_63	Post-Resistance	RARA	5914	37	17	38487404	38487404	Translation_Start_Site	SNP	G	A	12	22	c.-66G>A	c.(-68--64)GGGTG>GGATG	
Pat_63	Post-Resistance	SMARCE1	6605	37	17	38785156	38785156	Missense_Mutation	SNP	C	T	6	180	c.1117G>A	c.(1117-1119)GGG>AGG	p.G373R
Pat_63	Post-Resistance	KRT23	25984	37	17	39092786	39092786	Missense_Mutation	SNP	G	A	5	22	c.70C>T	c.(70-72)CGG>TGG	p.R24W
Pat_63	Post-Resistance	KRT39	390792	37	17	39123083	39123083	Missense_Mutation	SNP	G	A	39	206	c.26C>T	c.(25-27)ACC>ATC	p.T9I
Pat_63	Post-Resistance	KRTAP4-7	100132476	37	17	39240729	39240729	Missense_Mutation	SNP	A	G	4	99	c.271A>G	c.(271-273)ATG>GTG	p.M91V
Pat_63	Post-Resistance	KRTAP4-4	84616	37	17	39316834	39316834	Missense_Mutation	SNP	C	T	5	153	c.110G>A	c.(109-111)CGC>CAC	p.R37H
Pat_63	Post-Resistance	PLEKHH3	79990	37	17	40828421	40828421	Missense_Mutation	SNP	C	T	9	60	c.161G>A	c.(160-162)AGG>AAG	p.R54K
Pat_63	Post-Resistance	CNTNAP1	8506	37	17	40842765	40842765	Missense_Mutation	SNP	G	A	43	173	c.1864G>A	c.(1864-1866)GCG>ACG	p.A622T
Pat_63	Post-Resistance	BRCA1	672	37	17	41245156	41245156	Missense_Mutation	SNP	G	A	10	374	c.2392C>T	c.(2392-2394)CCA>TCA	p.P798S
Pat_63	Post-Resistance	DHX8	1659	37	17	41561547	41561547	Missense_Mutation	SNP	G	A	24	158	c.142G>A	c.(142-144)GAC>AAC	p.D48N
Pat_63	Post-Resistance	DHX8	1659	37	17	41585006	41585006	Missense_Mutation	SNP	G	A	42	188	c.2059G>A	c.(2059-2061)GCA>ACA	p.A687T
Pat_63	Post-Resistance	ETV4	2118	37	17	41622343	41622343	Missense_Mutation	SNP	C	T	15	50	c.202G>A	c.(202-204)GCT>ACT	p.A68T
Pat_63	Post-Resistance	C17orf104	284071	37	17	42744625	42744625	Missense_Mutation	SNP	C	T	22	226	c.1346C>T	c.(1345-1347)CCC>CTC	p.P449L
Pat_63	Post-Resistance	C17orf57	124989	37	17	45468892	45468892	Missense_Mutation	SNP	A	G	8	39	c.1672A>G	c.(1672-1674)ATT>GTT	p.I558V
Pat_63	Post-Resistance	KPNB1	3837	37	17	45755759	45755759	Missense_Mutation	SNP	G	A	3	64	c.2333G>A	c.(2332-2334)GGG>GAG	p.G778E
Pat_63	Post-Resistance	XYLT2	64132	37	17	48433566	48433566	Missense_Mutation	SNP	G	A	15	121	c.1426G>A	c.(1426-1428)GAC>AAC	p.D476N
Pat_63	Post-Resistance	MSI2	124540	37	17	55478802	55478802	Missense_Mutation	SNP	T	G	73	95	c.375T>G	c.(373-375)GAT>GAG	p.D125E
Pat_63	Post-Resistance	TEX14	56155	37	17	56694940	56694940	Missense_Mutation	SNP	C	T	25	104	c.595G>A	c.(595-597)GTC>ATC	p.V199I
Pat_63	Post-Resistance	PPM1E	22843	37	17	57058253	57058253	Missense_Mutation	SNP	G	A	10	64	c.2129G>A	c.(2128-2130)AGT>AAT	p.S710N
Pat_63	Post-Resistance	USP32	84669	37	17	58313509	58313509	Missense_Mutation	SNP	T	C	51	270	c.1229A>G	c.(1228-1230)TAT>TGT	p.Y410C
Pat_63	Post-Resistance	MED13	9969	37	17	60088457	60088457	Missense_Mutation	SNP	G	A	10	15	c.1421C>T	c.(1420-1422)ACT>ATT	p.T474I
Pat_63	Post-Resistance	ERN1	2081	37	17	62130186	62130186	Missense_Mutation	SNP	C	T	3	41	c.2207G>A	c.(2206-2208)GGC>GAC	p.G736D
Pat_63	Post-Resistance	HELZ	9931	37	17	65116610	65116610	Missense_Mutation	SNP	G	A	14	66	c.3752C>T	c.(3751-3753)CCT>CTT	p.P1251L
Pat_63	Post-Resistance	KCNJ2	3759	37	17	68171383	68171383	Missense_Mutation	SNP	A	G	13	74	c.203A>G	c.(202-204)TAC>TGC	p.Y68C
Pat_63	Post-Resistance	TTYH2	94015	37	17	72256320	72256320	Missense_Mutation	SNP	G	A	42	163	c.1577G>A	c.(1576-1578)AGG>AAG	p.R526K
Pat_63	Post-Resistance	TMEM104	54868	37	17	72787136	72787136	Missense_Mutation	SNP	G	A	8	50	c.388G>A	c.(388-390)GTG>ATG	p.V130M
Pat_63	Post-Resistance	OTOP2	92736	37	17	72929576	72929576	Missense_Mutation	SNP	C	T	5	72	c.1625C>T	c.(1624-1626)CCT>CTT	p.P542L
Pat_63	Post-Resistance	ATP5H	10476	37	17	73035097	73035097	Missense_Mutation	SNP	G	T	3	58	c.416C>A	c.(415-417)GCT>GAT	p.A139D

Pat_63	Post-Resistance	RECQL5	9400	37	17	73625837	73625837	Missense_Mutation	SNP	G	A	12	72	c.1898C>T	c.(1897-1899)CCC>CTC	p.P633L
Pat_63	Post-Resistance	QRICH2	84074	37	17	74288506	74288506	Nonsense_Mutation	SNP	G	A	8	190	c.1804C>T	c.(1804-1806)CAG>TAG	p.Q602*
Pat_63	Post-Resistance	MGAT5B	146664	37	17	74936506	74936506	Missense_Mutation	SNP	C	T	19	62	c.1634C>T	c.(1633-1635)CCC>CTC	p.P545L
Pat_63	Post-Resistance	SEC14L1	6397	37	17	75192314	75192314	Missense_Mutation	SNP	A	G	12	56	c.740A>G	c.(739-741)TAC>TGC	p.Y247C
Pat_63	Post-Resistance	USP36	57602	37	17	76800019	76800019	Missense_Mutation	SNP	G	A	6	30	c.2258C>T	c.(2257-2259)CCC>CTC	p.P753L
Pat_63	Post-Resistance	CARD14	79092	37	17	78156562	78156562	Missense_Mutation	SNP	C	T	7	36	c.322C>T	c.(322-324)CCT>TCT	p.P108S
Pat_63	Post-Resistance	PDE6G	5148	37	17	79620323	79620323	Missense_Mutation	SNP	G	A	8	26	c.13C>T	c.(13-15)CCG>TCG	p.P5S
Pat_63	Post-Resistance	P4HB	5034	37	17	79803565	79803565	Missense_Mutation	SNP	C	T	5	46	c.1231G>A	c.(1231-1233)GGA>AGA	p.G411R
Pat_63	Post-Resistance	C17orf62	79415	37	17	80403811	80403811	Missense_Mutation	SNP	C	T	7	22	c.227G>A	c.(226-228)GGG>GAG	p.G76E
Pat_63	Post-Resistance	MYOM1	8736	37	18	3173945	3173945	Missense_Mutation	SNP	G	A	6	32	c.1165C>T	c.(1165-1167)CCC>TCC	p.P389S
Pat_63	Post-Resistance	TXNDC2	84203	37	18	9887006	9887006	Missense_Mutation	SNP	G	A	17	161	c.530G>A	c.(529-531)GGT>GAT	p.G177D
Pat_63	Post-Resistance	VAPA	9218	37	18	9954188	9954189	Nonsense_Mutation	DNP	CT	TA	28	185	c.730_731CT>TA	c.(730-732)CTA>TAA	p.L244*
Pat_63	Post-Resistance	LAMA3	3909	37	18	21293981	21293981	Missense_Mutation	SNP	C	T	13	58	c.392C>T	c.(391-393)CCC>CTC	p.P131L
Pat_63	Post-Resistance	LAMA3	3909	37	18	21426373	21426373	Missense_Mutation	SNP	T	C	15	46	c.3832T>C	c.(3832-3834)TGC>CGC	p.C1278R
Pat_63	Post-Resistance	KLHL14	57565	37	18	30350079	30350079	Missense_Mutation	SNP	G	A	7	91	c.476C>T	c.(475-477)TCG>TTG	p.S159L
Pat_63	Post-Resistance	DTNA	1837	37	18	32455318	32455318	Missense_Mutation	SNP	C	T	13	78	c.1778C>T	c.(1777-1779)TCC>TTC	p.S593F
Pat_63	Post-Resistance	NARS	4677	37	18	55283091	55283091	Nonsense_Mutation	SNP	C	T	26	104	c.210G>A	c.(208-210)TGG>TGA	p.W70*
Pat_63	Post-Resistance	ALPK2	115701	37	18	56247520	56247520	Missense_Mutation	SNP	G	A	6	242	c.488C>T	c.(487-489)TCC>TTC	p.S163F
Pat_63	Post-Resistance	ZCCHC2	54877	37	18	60241332	60241332	Missense_Mutation	SNP	C	T	13	44	c.2018C>T	c.(2017-2019)ACT>ATT	p.T673I
Pat_63	Post-Resistance	ZCCHC2	54877	37	18	60242373	60242373	Missense_Mutation	SNP	G	A	7	38	c.3059G>A	c.(3058-3060)AGC>AAC	p.S1020N
Pat_63	Post-Resistance	RTTN	25914	37	18	67812931	67812931	Missense_Mutation	SNP	C	T	14	69	c.2398G>A	c.(2398-2400)GTT>ATT	p.V800I
Pat_63	Post-Resistance	FAM69C	125704	37	18	72109259	72109259	Missense_Mutation	SNP	G	C	18	58	c.969C>G	c.(967-969)TTC>TTG	p.F323L
Pat_63	Post-Resistance	TXNL4A	10907	37	18	77733749	77733749	Missense_Mutation	SNP	C	T	6	189	c.365G>A	c.(364-366)GGG>GAG	p.G122E
Pat_63	Post-Resistance	ADNP2	22850	37	18	77893724	77893724	Missense_Mutation	SNP	G	A	4	75	c.428G>A	c.(427-429)GGT>GAT	p.G143D
Pat_63	Post-Resistance	PTBP1	5725	37	19	804083	804083	Missense_Mutation	SNP	G	A	9	63	c.163G>A	c.(163-165)GGC>AGC	p.G55S
Pat_63	Post-Resistance	TCF3	6929	37	19	1619170	1619170	Missense_Mutation	SNP	C	T	4	55	c.1390G>A	c.(1390-1392)GCC>ACC	p.A464T
Pat_63	Post-Resistance	REXO1	57455	37	19	1820395	1820395	Splice_Site	SNP	C	T	8	49	c.2395_splice	c.e6-1	p.S799_splice
Pat_63	Post-Resistance	THOP1	7064	37	19	2805172	2805172	Missense_Mutation	SNP	G	A	3	20	c.748G>A	c.(748-750)GAG>AAG	p.E250K
Pat_63	Post-Resistance	CELF5	60680	37	19	3281320	3281320	Missense_Mutation	SNP	C	T	8	156	c.727C>T	c.(727-729)CCC>TCC	p.P243S
Pat_63	Post-Resistance	PIP5K1C	23396	37	19	3661915	3661915	Missense_Mutation	SNP	C	T	3	32	c.304G>A	c.(304-306)GTG>ATG	p.V102M
Pat_63	Post-Resistance	MAP2K2	5605	37	19	4110584	4110584	Missense_Mutation	SNP	A	T	7	89	c.373T>A	c.(373-375)TGC>AGC	p.C125S
Pat_63	Post-Resistance	SIRT6	51548	37	19	4175140	4175140	Missense_Mutation	SNP	T	C	3	11	c.623A>G	c.(622-624)GAC>GGC	p.D208G
Pat_63	Post-Resistance	CCDC94	55702	37	19	4251074	4251074	Missense_Mutation	SNP	G	A	4	66	c.176G>A	c.(175-177)CGG>CAG	p.R59Q
Pat_63	Post-Resistance	SHD	56961	37	19	4290454	4290454	Missense_Mutation	SNP	G	A	13	72	c.847G>A	c.(847-849)GGC>AGC	p.G283S
Pat_63	Post-Resistance	STAP2	55620	37	19	4327312	4327312	Splice_Site	SNP	C	T	7	101	c.660_splice	c.e7+1	p.P220_splice
Pat_63	Post-Resistance	TICAM1	148022	37	19	4818206	4818206	Missense_Mutation	SNP	C	T	3	23	c.184G>A	c.(184-186)GAG>AAG	p.E62K
Pat_63	Post-Resistance	DUS3L	56931	37	19	5787710	5787710	Missense_Mutation	SNP	C	T	37	324	c.1102G>A	c.(1102-1104)GGC>AGC	p.G368S
Pat_63	Post-Resistance	C3	718	37	19	6697713	6697713	Missense_Mutation	SNP	C	T	8	58	c.2533G>A	c.(2533-2535)GTG>ATG	p.V845M
Pat_63	Post-Resistance	ZNF557	79230	37	19	7083283	7083283	Missense_Mutation	SNP	G	A	7	208	c.800G>A	c.(799-801)CGC>CAC	p.R267H
Pat_63	Post-Resistance	MCOLN1	57192	37	19	7594599	7594599	Splice_Site	SNP	G	A	7	403	c.1359_splice	c.e11+1	p.K453_splice
Pat_63	Post-Resistance	MCOLN1	57192	37	19	7598655	7598655	Missense_Mutation	SNP	G	A	9	85	c.1717G>A	c.(1717-1719)GAG>AAG	p.E573K
Pat_63	Post-Resistance	HNRNPM	4670	37	19	8536233	8536233	Missense_Mutation	SNP	G	A	4	62	c.919G>A	c.(919-921)GGG>AGG	p.G307R
Pat_63	Post-Resistance	MYO1F	4542	37	19	8601252	8601252	Missense_Mutation	SNP	G	A	3	27	c.1927C>T	c.(1927-1929)CCG>TCG	p.P643S
Pat_63	Post-Resistance	MYO1F	4542	37	19	8619416	8619416	Missense_Mutation	SNP	C	T	21	223	c.271G>A	c.(271-273)GAC>AAC	p.D91N
Pat_63	Post-Resistance	MUC16	94025	37	19	9067711	9067711	Missense_Mutation	SNP	C	T	5	51	c.19735G>A	c.(19735-19737)GAC>AAC	p.D6579N
Pat_63	Post-Resistance	ZNF846	162993	37	19	9868257	9868257	Missense_Mutation	SNP	G	A	15	138	c.1496C>T	c.(1495-1497)ACT>ATT	p.T499I
Pat_63	Post-Resistance	COL5A3	50509	37	19	10080559	10080559	Missense_Mutation	SNP	C	T	11	123	c.3976G>A	c.(3976-3978)GAG>AAG	p.E1326K

Pat_63	Post-Resistance	COL5A3	50509	37	19	10088126	10088126	Missense_Mutation	SNP	G	A	6	30	c.3149C>T	c.(3148-3150)CCC>CTC	p.P1050L
Pat_63	Post-Resistance	RDH8	50700	37	19	10132038	10132038	Missense_Mutation	SNP	A	G	33	154	c.644A>G	c.(643-645)TAC>TGC	p.Y215C
Pat_63	Post-Resistance	ICAM5	7087	37	19	10402201	10402201	Missense_Mutation	SNP	C	T	42	246	c.389C>T	c.(388-390)CCC>CTC	p.P130L
Pat_63	Post-Resistance	CDC37	11140	37	19	10506171	10506171	Missense_Mutation	SNP	C	T	9	594	c.427G>A	c.(427-429)GTG>ATG	p.V143M
Pat_63	Post-Resistance	DNM2	1785	37	19	10886583	10886583	Splice_Site	SNP	G	A	5	32	c.589_splice	c.e4+1	p.G197_splice
Pat_63	Post-Resistance	TMED1	11018	37	19	10945771	10945771	Missense_Mutation	SNP	C	T	31	196	c.304G>A	c.(304-306)GAC>AAC	p.D102N
Pat_63	Post-Resistance	ZNF441	126068	37	19	11891424	11891424	Missense_Mutation	SNP	G	A	13	122	c.785G>A	c.(784-786)AGT>AAT	p.S262N
Pat_63	Post-Resistance	FARSA	2193	37	19	13035584	13035584	Missense_Mutation	SNP	C	T	31	250	c.1064G>A	c.(1063-1065)CGC>CAC	p.R355H
Pat_63	Post-Resistance	PODNL1	79883	37	19	14047243	14047243	Missense_Mutation	SNP	C	T	7	93	c.277G>A	c.(277-279)GAG>AAG	p.E93K
Pat_63	Post-Resistance	PKN1	5585	37	19	14574479	14574479	Missense_Mutation	SNP	G	A	13	81	c.1420G>A	c.(1420-1422)GTC>ATC	p.V474I
Pat_63	Post-Resistance	EMR3	84658	37	19	14749080	14749080	Missense_Mutation	SNP	C	T	13	94	c.1321G>A	c.(1321-1323)GGT>AGT	p.G441S
Pat_63	Post-Resistance	CYP4F12	66002	37	19	15806746	15806746	Nonsense_Mutation	SNP	G	A	11	85	c.1116G>A	c.(1114-1116)TGG>TGA	p.W372*
Pat_63	Post-Resistance	SLC27A1	376497	37	19	17611442	17611442	Splice_Site	SNP	G	A	6	40	c.1471_splice	c.e9+1	p.G491_splice
Pat_63	Post-Resistance	ARRDC2	27106	37	19	18120831	18120831	Missense_Mutation	SNP	G	A	27	180	c.832G>A	c.(832-834)GTG>ATG	p.V278M
Pat_63	Post-Resistance	IL12RB1	3594	37	19	18184374	18184374	Missense_Mutation	SNP	C	T	8	75	c.736G>A	c.(736-738)GAG>AAG	p.E246K
Pat_63	Post-Resistance	ZNF737	100129842	37	19	20728254	20728254	Missense_Mutation	SNP	C	G	8	122	c.755G>C	c.(754-756)AGT>ACT	p.S252T
Pat_63	Post-Resistance	ZNF626	199777	37	19	20807353	20807353	Missense_Mutation	SNP	T	C	6	232	c.1330A>G	c.(1330-1332)AGG>GGG	p.R444G
Pat_63	Post-Resistance	ZNF208	7757	37	19	22155962	22155962	Missense_Mutation	SNP	G	A	6	232	c.1574C>T	c.(1573-1575)ACT>ATT	p.T525I
Pat_63	Post-Resistance	ZNF208	7757	37	19	22156590	22156590	Missense_Mutation	SNP	C	T	6	227	c.1246G>A	c.(1246-1248)GAG>AAG	p.E416K
Pat_63	Post-Resistance	ZNF676	163223	37	19	22364334	22364334	Missense_Mutation	SNP	G	A	7	45	c.185C>T	c.(184-186)TCT>TTT	p.S62F
Pat_63	Post-Resistance	ZNF99	7652	37	19	22939400	22939400	Missense_Mutation	SNP	G	C	4	65	c.2771C>G	c.(2770-2772)GCT>GGT	p.A924G
Pat_63	Post-Resistance	ZNF99	7652	37	19	22941533	22941533	Missense_Mutation	SNP	C	T	18	136	c.905G>A	c.(904-906)GGA>GAA	p.G302E
Pat_63	Post-Resistance	ZNF536	9745	37	19	31040196	31040196	Missense_Mutation	SNP	C	T	8	38	c.3670C>T	c.(3670-3672)CCT>TCT	p.P1224S
Pat_63	Post-Resistance	ZNF507	22847	37	19	32845720	32845720	Missense_Mutation	SNP	G	A	17	175	c.1984G>A	c.(1984-1986)GTC>ATC	p.V662I
Pat_63	Post-Resistance	GPATCH1	55094	37	19	33587204	33587204	Missense_Mutation	SNP	G	A	19	202	c.704G>A	c.(703-705)GGT>GAT	p.G235D
Pat_63	Post-Resistance	ZNF30	90075	37	19	35434639	35434639	Missense_Mutation	SNP	G	A	6	20	c.769G>A	c.(769-771)GAA>AAA	p.E257K
Pat_63	Post-Resistance	ZNF30	90075	37	19	35434793	35434793	Missense_Mutation	SNP	G	C	40	127	c.923G>C	c.(922-924)AGA>ACA	p.R308T
Pat_63	Post-Resistance	MAG	4099	37	19	35801492	35801492	Missense_Mutation	SNP	T	G	5	28	c.1562T>G	c.(1561-1563)GTC>GGC	p.V521G
Pat_63	Post-Resistance	GAPDHS	26330	37	19	36034682	36034682	Missense_Mutation	SNP	G	A	3	13	c.1009G>A	c.(1009-1011)GCA>ACA	p.A337T
Pat_63	Post-Resistance	LRFN3	79414	37	19	36431187	36431187	Missense_Mutation	SNP	G	A	3	11	c.860G>A	c.(859-861)GGC>GAC	p.G287D
Pat_63	Post-Resistance	ZNF829	374899	37	19	37382776	37382776	Missense_Mutation	SNP	G	A	7	83	c.917C>T	c.(916-918)ACT>ATT	p.T306I
Pat_63	Post-Resistance	ZNF573	126231	37	19	38262218	38262218	Missense_Mutation	SNP	T	C	7	67	c.188A>G	c.(187-189)AAC>AGC	p.N63S
Pat_63	Post-Resistance	SIPA1L3	23094	37	19	38573508	38573508	Missense_Mutation	SNP	G	A	3	48	c.1303G>A	c.(1303-1305)GGG>AGG	p.G435R
Pat_63	Post-Resistance	SIPA1L3	23094	37	19	38682823	38682823	Missense_Mutation	SNP	C	T	3	48	c.4469C>T	c.(4468-4470)CCG>CTG	p.P1490L
Pat_63	Post-Resistance	NFKBIB	4793	37	19	39396007	39396007	Missense_Mutation	SNP	C	T	3	14	c.451C>T	c.(451-453)CCC>TCC	p.P151S
Pat_63	Post-Resistance	IL29	282618	37	19	39788715	39788715	Missense_Mutation	SNP	C	A	14	56	c.361C>A	c.(361-363)CTG>ATG	p.L121M
Pat_63	Post-Resistance	SUPT5H	6829	37	19	39936537	39936537	Missense_Mutation	SNP	G	A	14	49	c.7G>A	c.(7-9)GAC>AAC	p.D3N
Pat_63	Post-Resistance	AKT2	208	37	19	40746017	40746017	Missense_Mutation	SNP	C	T	8	343	c.574G>A	c.(574-576)GAT>AAT	p.D192N
Pat_63	Post-Resistance	PRX	57716	37	19	40902800	40902800	Missense_Mutation	SNP	G	A	54	161	c.1459C>T	c.(1459-1461)CCG>TCG	p.P487S
Pat_63	Post-Resistance	LTBP4	8425	37	19	41103210	41103210	Missense_Mutation	SNP	G	A	2	0	c.70G>A	c.(70-72)GCC>ACC	p.A24T
Pat_63	Post-Resistance	ITPKC	80271	37	19	41223735	41223735	Missense_Mutation	SNP	G	A	10	19	c.695G>A	c.(694-696)AGG>AAG	p.R232K
Pat_63	Post-Resistance	MEGF8	1954	37	19	42830535	42830535	Missense_Mutation	SNP	G	A	3	11	c.140G>A	c.(139-141)GGT>GAT	p.G47D
Pat_63	Post-Resistance	ZNF227	7770	37	19	44738971	44738971	Missense_Mutation	SNP	T	C	14	84	c.388T>C	c.(388-390)TGT>CGT	p.C130R
Pat_63	Post-Resistance	CLPTM1	1209	37	19	45480666	45480666	Missense_Mutation	SNP	C	T	24	154	c.535C>T	c.(535-537)CCC>TCC	p.P179S
Pat_63	Post-Resistance	QPCTL	54814	37	19	46206162	46206162	Missense_Mutation	SNP	G	A	6	143	c.1004G>A	c.(1003-1005)GGG>GAG	p.G335E
Pat_63	Post-Resistance	DMWD	1762	37	19	46294251	46294251	Missense_Mutation	SNP	G	A	5	226	c.536C>T	c.(535-537)ACC>ATC	p.T179I
Pat_63	Post-Resistance	ELSPBP1	64100	37	19	48519155	48519155	Missense_Mutation	SNP	C	T	3	38	c.214C>T	c.(214-216)CCA>TCA	p.P72S

Pat_63	Post-Resistance	FUT2	2524	37	19	49206665	49206665	Missense_Mutation	SNP	C	T	24	96	c.452C>T	c.(451-453)CCC>CTC	p.P151L
Pat_63	Post-Resistance	FUZ	80199	37	19	50314928	50314928	Missense_Mutation	SNP	G	A	8	594	c.347C>T	c.(346-348)ACC>ATC	p.T116I
Pat_63	Post-Resistance	IL4I1	259307	37	19	50393094	50393094	Missense_Mutation	SNP	C	T	13	28	c.1537G>A	c.(1537-1539)GAC>AAC	p.D513N
Pat_63	Post-Resistance	KLK6	5653	37	19	51471321	51471321	Missense_Mutation	SNP	C	T	21	91	c.40G>A	c.(40-42)GCC>ACC	p.A14T
Pat_63	Post-Resistance	FPR3	2359	37	19	52327542	52327542	Missense_Mutation	SNP	G	A	35	229	c.541G>A	c.(541-543)GCA>ACA	p.A181T
Pat_63	Post-Resistance	ZNF808	388558	37	19	53058088	53058088	Missense_Mutation	SNP	G	A	4	81	c.1919G>A	c.(1918-1920)CGA>CAA	p.R640Q
Pat_63	Post-Resistance	ZNF600	162966	37	19	53269276	53269276	Missense_Mutation	SNP	C	T	42	281	c.1733G>A	c.(1732-1734)GGA>GAA	p.G578E
Pat_63	Post-Resistance	ZNF468	90333	37	19	53345171	53345171	Missense_Mutation	SNP	G	A	55	201	c.376C>T	c.(376-378)CAT>TAT	p.H126Y
Pat_63	Post-Resistance	LILRB1	10859	37	19	55144064	55144064	Missense_Mutation	SNP	G	A	8	57	c.811G>A	c.(811-813)GCA>ACA	p.A271T
Pat_63	Post-Resistance	NLRP9	338321	37	19	56249610	56249610	Missense_Mutation	SNP	C	A	33	187	c.131G>T	c.(130-132)TGG>TTG	p.W44L
Pat_63	Post-Resistance	ZNF549	256051	37	19	58050030	58050030	Missense_Mutation	SNP	G	A	20	96	c.1658G>A	c.(1657-1659)GGC>GAC	p.G553D
Pat_63	Post-Resistance	ZNF550	162972	37	19	58059242	58059242	Missense_Mutation	SNP	C	T	32	170	c.247G>A	c.(247-249)GGG>AGG	p.G83R
Pat_63	Post-Resistance	ZNF776	284309	37	19	58265876	58265876	Missense_Mutation	SNP	C	T	8	166	c.1378C>T	c.(1378-1380)CAT>TAT	p.H460Y
Pat_63	Post-Resistance	ASAP2	8853	37	2	9490958	9490958	Missense_Mutation	SNP	C	T	14	36	c.1045C>T	c.(1045-1047)CTC>TTC	p.L349F
Pat_63	Post-Resistance	PUM2	23369	37	2	20455102	20455102	Missense_Mutation	SNP	C	T	17	62	c.2623G>A	c.(2623-2625)GTA>ATA	p.V875I
Pat_63	Post-Resistance	GCKR	2646	37	2	27728604	27728604	Missense_Mutation	SNP	C	T	10	40	c.770C>T	c.(769-771)TCC>TTC	p.S257F
Pat_63	Post-Resistance	PLB1	151056	37	2	28748137	28748137	Missense_Mutation	SNP	C	T	3	26	c.247C>T	c.(247-249)CCA>TCA	p.P83S
Pat_63	Post-Resistance	C2orf71	388939	37	2	29293881	29293881	Missense_Mutation	SNP	G	A	5	81	c.3247C>T	c.(3247-3249)CCT>TCT	p.P1083S
Pat_63	Post-Resistance	NLRC4	58484	37	2	32460470	32460470	Missense_Mutation	SNP	C	T	26	81	c.2782G>A	c.(2782-2784)GGT>AGT	p.G928S
Pat_63	Post-Resistance	HEATR5B	54497	37	2	37208682	37208682	Missense_Mutation	SNP	G	A	3	39	c.6167C>T	c.(6166-6168)CCC>CTC	p.P2056L
Pat_63	Post-Resistance	C2orf56	55471	37	2	37468875	37468875	Missense_Mutation	SNP	G	A	19	62	c.563G>A	c.(562-564)GGT>GAT	p.G188D
Pat_63	Post-Resistance	THUMPD2	80745	37	2	39983069	39983069	Missense_Mutation	SNP	C	T	16	61	c.923G>A	c.(922-924)GGA>GAA	p.G308E
Pat_63	Post-Resistance	THADA	63892	37	2	43787403	43787403	Missense_Mutation	SNP	C	T	7	15	c.2433G>A	c.(2431-2433)ATG>ATA	p.M811I
Pat_63	Post-Resistance	LRPPRC	10128	37	2	44117016	44117016	Splice_Site	SNP	C	T	16	56	c.3986_splice	c.e37-1	p.V1329_splice
Pat_63	Post-Resistance	PREPL	9581	37	2	44565611	44565611	Missense_Mutation	SNP	C	T	7	25	c.1034G>A	c.(1033-1035)AGA>AAA	p.R345K
Pat_63	Post-Resistance	MSH6	2956	37	2	48018231	48018231	Nonsense_Mutation	SNP	G	A	6	54	c.426G>A	c.(424-426)TGG>TGA	p.W142*
Pat_63	Post-Resistance	MSH6	2956	37	2	48026684	48026684	Missense_Mutation	SNP	C	T	4	51	c.1562C>T	c.(1561-1563)ACA>ATA	p.T521I
Pat_63	Post-Resistance	MSH6	2956	37	2	48027316	48027316	Nonsense_Mutation	SNP	C	T	17	91	c.2194C>T	c.(2194-2196)CGA>TGA	p.R732*
Pat_63	Post-Resistance	MSH6	2956	37	2	48033352	48033352	Missense_Mutation	SNP	C	T	7	42	c.3656C>T	c.(3655-3657)ACT>ATT	p.T1219I
Pat_63	Post-Resistance	STON1-GTF2A1L	286749	37	2	48808478	48808478	Missense_Mutation	SNP	C	T	29	68	c.706C>T	c.(706-708)CTC>TTC	p.L236F
Pat_63	Post-Resistance	ERLEC1	27248	37	2	54045093	54045093	Missense_Mutation	SNP	C	T	14	30	c.1439C>T	c.(1438-1440)TCT>TTT	p.S480F
Pat_63	Post-Resistance	USP34	9736	37	2	61415817	61415817	Missense_Mutation	SNP	C	T	15	44	c.10061G>A	c.(10060-10062)AGG>AAG	p.R3354K
Pat_63	Post-Resistance	FAM161A	84140	37	2	62067070	62067070	Missense_Mutation	SNP	C	T	22	62	c.1069G>A	c.(1069-1071)GCC>ACC	p.A357T
Pat_63	Post-Resistance	RAB11FIP5	26056	37	2	73315377	73315377	Missense_Mutation	SNP	C	T	21	48	c.1369G>A	c.(1369-1371)GAA>AAA	p.E457K
Pat_63	Post-Resistance	CCT7	10574	37	2	73477537	73477537	Missense_Mutation	SNP	G	T	19	65	c.1174G>T	c.(1174-1176)GCC>TCC	p.A392S
Pat_63	Post-Resistance	GGCX	2677	37	2	85778617	85778617	Missense_Mutation	SNP	C	T	22	115	c.1726G>A	c.(1726-1728)GGA>AGA	p.G576R
Pat_63	Post-Resistance	RNF103	7844	37	2	86831783	86831783	Missense_Mutation	SNP	G	C	3	53	c.1241C>G	c.(1240-1242)TCT>TGT	p.S414C
Pat_63	Post-Resistance	SNRNP200	23020	37	2	96944087	96944087	Missense_Mutation	SNP	C	T	7	66	c.5498G>A	c.(5497-5499)AGC>AAC	p.S1833N
Pat_63	Post-Resistance	CNGA3	1261	37	2	99012353	99012353	Nonsense_Mutation	SNP	G	A	23	141	c.720G>A	c.(718-720)TGG>TGA	p.W240*
Pat_63	Post-Resistance	MRPL30	51263	37	2	99812055	99812055	Missense_Mutation	SNP	C	T	37	279	c.373C>T	c.(373-375)CCA>TCA	p.P125S
Pat_63	Post-Resistance	MAP4K4	9448	37	2	102456309	102456309	Missense_Mutation	SNP	G	A	4	17	c.802G>A	c.(802-804)GGG>AGG	p.G268R
Pat_63	Post-Resistance	PSD4	23550	37	2	113955150	113955150	Missense_Mutation	SNP	G	A	10	45	c.2396G>A	c.(2395-2397)GGC>GAC	p.G799D
Pat_63	Post-Resistance	EPB41L5	57669	37	2	120776803	120776803	Missense_Mutation	SNP	C	T	75	367	c.143C>T	c.(142-144)TCC>TTC	p.S48F
Pat_63	Post-Resistance	LRP1B	53353	37	2	141092120	141092120	Missense_Mutation	SNP	T	C	22	115	c.12125A>G	c.(12124-12126)TAC>TGC	p.Y4042C
Pat_63	Post-Resistance	GALNT5	11227	37	2	158116023	158116023	Missense_Mutation	SNP	G	A	9	86	c.1429G>A	c.(1429-1431)GCC>ACC	p.A477T
Pat_63	Post-Resistance	PKP4	8502	37	2	159519886	159519886	Missense_Mutation	SNP	G	A	4	59	c.2506G>A	c.(2506-2508)GAA>AAA	p.E836K
Pat_63	Post-Resistance	PLA2R1	22925	37	2	160884757	160884757	Nonsense_Mutation	SNP	A	T	13	68	c.1071T>A	c.(1069-1071)TAT>TAA	p.Y357*

Pat_63	Post-Resistance	SCN2A	6326	37	2	166231217	166231217	Missense_Mutation	SNP	G	A	22	123	c.3995G>A	c.(3994-3996)GGA>GAA	p.G1332E
Pat_63	Post-Resistance	STK39	27347	37	2	169020352	169020352	Missense_Mutation	SNP	C	T	13	73	c.469G>A	c.(469-471)GGA>AGA	p.G157R
Pat_63	Post-Resistance	LRP2	4036	37	2	170031804	170031804	Missense_Mutation	SNP	C	T	23	75	c.10667G>A	c.(10666-10668)GGA>GA	p.G3556E
Pat_63	Post-Resistance	LRP2	4036	37	2	170147435	170147435	Missense_Mutation	SNP	G	A	18	46	c.842C>T	c.(841-843)TCC>TTC	p.S281F
Pat_63	Post-Resistance	PHOSPHO2	493911	37	2	170557605	170557605	Missense_Mutation	SNP	G	A	4	89	c.124G>A	c.(124-126)GGA>AGA	p.G42R
Pat_63	Post-Resistance	TTN	7273	37	2	179442563	179442563	Missense_Mutation	SNP	C	T	6	39	c.60886G>A	c.(60886-60888)GAA>AA	p.E20296K
Pat_63	Post-Resistance	TTN	7273	37	2	179480455	179480455	Missense_Mutation	SNP	A	G	19	66	c.40669T>C	c.(40669-40671)TAC>CAC	p.Y13557H
Pat_63	Post-Resistance	TTN	7273	37	2	179611855	179611855	Missense_Mutation	SNP	G	A	15	68	c.15272C>T	c.(15271-15273)ACT>ATT	p.T5091I
Pat_63	Post-Resistance	TTN	7273	37	2	179611942	179611942	Missense_Mutation	SNP	T	C	6	45	c.15185A>G	c.(15184-15186)TAC>TGC	p.Y5062C
Pat_63	Post-Resistance	DNAJC10	54431	37	2	183594666	183594666	Missense_Mutation	SNP	C	T	17	109	c.725C>T	c.(724-726)ACA>ATA	p.T242I
Pat_63	Post-Resistance	ANKAR	150709	37	2	190571704	190571704	Missense_Mutation	SNP	G	A	31	108	c.1738G>A	c.(1738-1740)GCA>ACA	p.A580T
Pat_63	Post-Resistance	PMS1	5378	37	2	190728749	190728749	Nonsense_Mutation	SNP	C	T	4	95	c.2137C>T	c.(2137-2139)CAA>TAA	p.Q713*
Pat_63	Post-Resistance	STAT1	6772	37	2	191849115	191849115	Missense_Mutation	SNP	G	A	5	35	c.1268C>T	c.(1267-1269)CCT>CTT	p.P423L
Pat_63	Post-Resistance	DNAH7	56171	37	2	196729348	196729348	Missense_Mutation	SNP	C	T	11	56	c.7031G>A	c.(7030-7032)GGG>GAG	p.G2344E
Pat_63	Post-Resistance	HSPE1	3336	37	2	198367933	198367933	Missense_Mutation	SNP	G	A	7	135	c.259G>A	c.(259-261)GAT>AAT	p.D87N
Pat_63	Post-Resistance	PPIL3	53938	37	2	201741652	201741652	Missense_Mutation	SNP	C	T	29	117	c.349G>A	c.(349-351)GTA>ATA	p.V117I
Pat_63	Post-Resistance	CASP8	841	37	2	202136343	202136343	Missense_Mutation	SNP	T	A	10	24	c.410T>A	c.(409-411)ATG>AAG	p.M137K
Pat_63	Post-Resistance	CASP8	841	37	2	202141584	202141584	Missense_Mutation	SNP	C	T	9	82	c.695C>T	c.(694-696)CCT>CTT	p.P232L
Pat_63	Post-Resistance	CPS1	1373	37	2	211456650	211456650	Missense_Mutation	SNP	G	A	12	68	c.1043G>A	c.(1042-1044)GGC>GAC	p.G348D
Pat_63	Post-Resistance	SPAG16	79582	37	2	214794858	214794858	Nonsense_Mutation	SNP	G	A	16	73	c.1389G>A	c.(1387-1389)TGG>TGA	p.W463*
Pat_63	Post-Resistance	FN1	2335	37	2	216236937	216236937	Missense_Mutation	SNP	C	T	11	67	c.6409G>A	c.(6409-6411)GTT>ATT	p.V2137I
Pat_63	Post-Resistance	FN1	2335	37	2	216248086	216248086	Missense_Mutation	SNP	C	T	15	81	c.5015G>A	c.(5014-5016)GGA>GAA	p.G1672E
Pat_63	Post-Resistance	FN1	2335	37	2	216262405	216262405	Missense_Mutation	SNP	G	A	5	160	c.3515C>T	c.(3514-3516)ACA>ATA	p.T1172I
Pat_63	Post-Resistance	RNF25	64320	37	2	219529597	219529597	Splice_Site	SNP	C	T	4	25	c.667_splice	c.e9-1	p.E223_splice
Pat_63	Post-Resistance	PRKAG3	53632	37	2	219692297	219692297	Splice_Site	SNP	C	T	18	97	c.875_splice	c.e8+1	p.S292_splice
Pat_63	Post-Resistance	GLB1L	79411	37	2	220102547	220102547	Splice_Site	SNP	C	T	30	97	c.1473_splice	c.e15+1	p.K491_splice
Pat_63	Post-Resistance	TUBA4A	7277	37	2	220116021	220116021	Missense_Mutation	SNP	C	T	11	79	c.400G>A	c.(400-402)GGC>AGC	p.G134S
Pat_63	Post-Resistance	PTPRN	5798	37	2	220166328	220166328	Missense_Mutation	SNP	C	T	7	150	c.1108G>A	c.(1108-1110)GGT>AGT	p.G370S
Pat_63	Post-Resistance	STK11IP	114790	37	2	220476373	220476373	Missense_Mutation	SNP	C	T	47	155	c.2185C>T	c.(2185-2187)CTC>TTC	p.L729F
Pat_63	Post-Resistance	PSMD1	5707	37	2	232028416	232028416	Missense_Mutation	SNP	T	C	22	91	c.2456T>C	c.(2455-2457)GTA>GCA	p.V819A
Pat_63	Post-Resistance	COL6A3	1293	37	2	238274532	238274532	Missense_Mutation	SNP	G	A	20	101	c.5647C>T	c.(5647-5649)CCC>TCC	p.P1883S
Pat_63	Post-Resistance	LRRFIP1	9208	37	2	238671548	238671548	Missense_Mutation	SNP	G	A	19	180	c.1192G>A	c.(1192-1194)GAT>AAT	p.D398N
Pat_63	Post-Resistance	ANKMY1	51281	37	2	241492372	241492372	Missense_Mutation	SNP	C	T	4	97	c.172G>A	c.(172-174)GAA>AAA	p.E58K
Pat_63	Post-Resistance	AGXT	189	37	2	241817455	241817455	Missense_Mutation	SNP	C	T	6	16	c.959C>T	c.(958-960)ACA>ATA	p.T320I
Pat_63	Post-Resistance	PASK	23178	37	2	242066820	242066820	Missense_Mutation	SNP	C	T	15	64	c.1510G>A	c.(1510-1512)GCG>ACG	p.A504T
Pat_63	Post-Resistance	PASK	23178	37	2	242076571	242076571	Missense_Mutation	SNP	C	T	7	36	c.985G>A	c.(985-987)GCG>ACG	p.A329T
Pat_63	Post-Resistance	HDLBP	3069	37	2	242186214	242186214	Missense_Mutation	SNP	T	A	23	113	c.1903A>T	c.(1903-1905)AAC>TAC	p.N635Y
Pat_63	Post-Resistance	C20orf54	113278	37	20	746336	746336	Missense_Mutation	SNP	G	A	9	36	c.83C>T	c.(82-84)CCC>CTC	p.P28L
Pat_63	Post-Resistance	STK35	140901	37	20	2097573	2097573	Missense_Mutation	SNP	G	A	10	53	c.1154G>A	c.(1153-1155)AGC>AAC	p.S385N
Pat_63	Post-Resistance	TMC2	117532	37	20	2596792	2596792	Missense_Mutation	SNP	G	A	8	67	c.1882G>A	c.(1882-1884)GCT>ACT	p.A628T
Pat_63	Post-Resistance	SIGLEC1	6614	37	20	3684715	3684715	Missense_Mutation	SNP	G	A	22	89	c.730C>T	c.(730-732)CTC>TTC	p.L244F
Pat_63	Post-Resistance	CHD6	84181	37	20	40033310	40033310	Missense_Mutation	SNP	G	A	35	133	c.8071C>T	c.(8071-8073)CCT>TCT	p.P2691S
Pat_63	Post-Resistance	CHD6	84181	37	20	40040803	40040803	Missense_Mutation	SNP	G	A	7	42	c.7232C>T	c.(7231-7233)CCC>CTC	p.P2411L
Pat_63	Post-Resistance	TP53TG5	27296	37	20	44004130	44004130	Missense_Mutation	SNP	G	A	10	52	c.317C>T	c.(316-318)TCC>TTC	p.S106F
Pat_63	Post-Resistance	KCNB1	3745	37	20	47989713	47989713	Missense_Mutation	SNP	T	C	32	153	c.2384A>G	c.(2383-2385)AAC>AGC	p.N795S
Pat_63	Post-Resistance	CASS4	57091	37	20	55033445	55033445	Missense_Mutation	SNP	G	A	9	63	c.2003G>A	c.(2002-2004)AGG>AAG	p.R668K
Pat_63	Post-Resistance	BMP7	655	37	20	55777639	55777639	Missense_Mutation	SNP	C	T	16	53	c.652G>A	c.(652-654)GCC>ACC	p.A218T

Pat_63	Post-Resistance	SS18L1	26039	37	20	60738610	60738610	Missense_Mutation	SNP	G	A	3	24	c.653G>A	c.(652-654)GGG>GAG	p.G218E
Pat_63	Post-Resistance	C20orf166	128826	37	20	61167687	61167687	Missense_Mutation	SNP	G	A	3	10	c.157G>A	c.(157-159)GAA>AAA	p.E53K
Pat_63	Post-Resistance	CXADR	1525	37	21	18919438	18919438	Missense_Mutation	SNP	G	A	21	48	c.137G>A	c.(136-138)AGT>AAT	p.S46N
Pat_63	Post-Resistance	CXADR	1525	37	21	18924137	18924137	Missense_Mutation	SNP	C	A	3	60	c.281C>A	c.(280-282)ACG>AAG	p.T94K
Pat_63	Post-Resistance	ADAMTS1	9510	37	21	28214249	28214249	Missense_Mutation	SNP	C	T	22	71	c.1138G>A	c.(1138-1140)GAT>AAT	p.D380N
Pat_63	Post-Resistance	USP16	10600	37	21	30419545	30419545	Nonsense_Mutation	SNP	T	G	46	143	c.1914T>G	c.(1912-1914)TAT>TAG	p.Y638*
Pat_63	Post-Resistance	SOD1	6647	37	21	33040842	33040842	Missense_Mutation	SNP	G	A	15	90	c.416G>A	c.(415-417)GGA>GAA	p.G139E
Pat_63	Post-Resistance	TRAPPC10	7109	37	21	45497586	45497586	Missense_Mutation	SNP	G	A	6	106	c.1390G>A	c.(1390-1392)GCC>ACC	p.A464T
Pat_63	Post-Resistance	CLTCL1	8218	37	22	19223266	19223266	Missense_Mutation	SNP	G	A	13	256	c.922C>T	c.(922-924)CCA>TCA	p.P308S
Pat_63	Post-Resistance	C22orf29	79680	37	22	19838985	19838985	Missense_Mutation	SNP	G	A	7	54	c.800C>T	c.(799-801)CCC>CTC	p.P267L
Pat_63	Post-Resistance	TXNRD2	10587	37	22	19864728	19864728	Missense_Mutation	SNP	C	T	4	114	c.1475G>A	c.(1474-1476)CGG>CAG	p.R492Q
Pat_63	Post-Resistance	DGCR8	54487	37	22	20073988	20073988	Missense_Mutation	SNP	G	A	9	328	c.502G>A	c.(502-504)GTT>ATT	p.V168I
Pat_63	Post-Resistance	TRMT2A	27037	37	22	20103660	20103660	Missense_Mutation	SNP	C	T	5	163	c.500G>A	c.(499-501)CGA>CAA	p.R167Q
Pat_63	Post-Resistance	TRMT2A	27037	37	22	20103990	20103990	Missense_Mutation	SNP	G	A	4	47	c.170C>T	c.(169-171)CCC>CTC	p.P57L
Pat_63	Post-Resistance	ZNF74	7625	37	22	20759874	20759874	Missense_Mutation	SNP	C	T	3	12	c.551C>T	c.(550-552)CCC>CTC	p.P184L
Pat_63	Post-Resistance	SLC7A4	6545	37	22	21384515	21384515	Missense_Mutation	SNP	C	T	6	58	c.1108G>A	c.(1108-1110)GGC>AGC	p.G370S
Pat_63	Post-Resistance	ZNF280A	129025	37	22	22869329	22869329	Missense_Mutation	SNP	G	A	23	204	c.626C>T	c.(625-627)CCC>CTC	p.P209L
Pat_63	Post-Resistance	LOC96610	96610	37	22	23241849	23241849	Splice_Site	SNP	C	T	7	72	c.15463_splice	c.e366+2	
Pat_63	Post-Resistance	GGT5	2687	37	22	24622691	24622691	Missense_Mutation	SNP	C	T	9	92	c.946G>A	c.(946-948)GTG>ATG	p.V316M
Pat_63	Post-Resistance	GGT1	2678	37	22	25019077	25019077	Missense_Mutation	SNP	G	A	10	70	c.737G>A	c.(736-738)GGC>GAC	p.G246D
Pat_63	Post-Resistance	HPS4	89781	37	22	26875274	26875274	Missense_Mutation	SNP	C	T	10	229	c.89G>A	c.(88-90)GGC>GAC	p.G30D
Pat_63	Post-Resistance	TFIP11	24144	37	22	26899709	26899709	Missense_Mutation	SNP	C	T	8	402	c.571G>A	c.(571-573)GGG>AGG	p.G191R
Pat_63	Post-Resistance	SEC14L3	266629	37	22	30864589	30864589	Missense_Mutation	SNP	C	T	14	101	c.329G>A	c.(328-330)GGG>GAG	p.G110E
Pat_63	Post-Resistance	LIMK2	3985	37	22	31674419	31674419	Missense_Mutation	SNP	C	T	25	536	c.1909C>T	c.(1909-1911)CCT>TCT	p.P637S
Pat_63	Post-Resistance	PIK3IP1	113791	37	22	31679107	31679107	Missense_Mutation	SNP	G	A	4	71	c.755C>T	c.(754-756)ACC>ATC	p.T252I
Pat_63	Post-Resistance	PATZ1	23598	37	22	31740613	31740613	Missense_Mutation	SNP	G	A	5	197	c.976C>T	c.(976-978)CTT>TTT	p.L326F
Pat_63	Post-Resistance	FOXRED2	80020	37	22	36900157	36900157	Missense_Mutation	SNP	G	A	10	83	c.1037C>T	c.(1036-1038)TCC>TTC	p.S346F
Pat_63	Post-Resistance	GGA1	26088	37	22	38026050	38026050	Missense_Mutation	SNP	C	T	27	128	c.1204C>T	c.(1204-1206)CCC>TCC	p.P402S
Pat_63	Post-Resistance	TRIOBP	11078	37	22	38131242	38131242	Nonsense_Mutation	SNP	G	A	28	98	c.4899G>A	c.(4897-4899)TGG>TGA	p.W1633*
Pat_63	Post-Resistance	PICK1	9463	37	22	38453850	38453850	Missense_Mutation	SNP	G	A	15	376	c.34G>A	c.(34-36)GAT>AAT	p.D12N
Pat_63	Post-Resistance	CSNK1E	1454	37	22	38695921	38695921	Missense_Mutation	SNP	C	T	22	589	c.715G>A	c.(715-717)GTC>ATC	p.V239I
Pat_63	Post-Resistance	KCNJ4	3761	37	22	38823404	38823404	Missense_Mutation	SNP	C	T	7	241	c.734G>A	c.(733-735)GGC>GAC	p.G245D
Pat_63	Post-Resistance	DDX17	10521	37	22	38882193	38882193	Missense_Mutation	SNP	C	T	17	339	c.1943G>A	c.(1942-1944)GGC>GAC	p.G648D
Pat_63	Post-Resistance	GTPBP1	9567	37	22	39104916	39104916	Missense_Mutation	SNP	G	A	30	185	c.259G>A	c.(259-261)GAC>AAC	p.D87N
Pat_63	Post-Resistance	APOBEC3C	27350	37	22	39413792	39413792	Missense_Mutation	SNP	C	T	47	262	c.196C>T	c.(196-198)CAT>TAT	p.H66Y
Pat_63	Post-Resistance	RPS19BP1	91582	37	22	39928436	39928436	Missense_Mutation	SNP	T	C	14	122	c.145A>G	c.(145-147)AAC>GAC	p.N49D
Pat_63	Post-Resistance	SGSM3	27352	37	22	40801813	40801813	Missense_Mutation	SNP	C	T	16	110	c.779C>T	c.(778-780)CCT>CTT	p.P260L
Pat_63	Post-Resistance	XPNPEP3	63929	37	22	41320405	41320405	Missense_Mutation	SNP	C	T	17	843	c.1276C>T	c.(1276-1278)CTC>TTC	p.L426F
Pat_63	Post-Resistance	EP300	2033	37	22	41513598	41513598	Missense_Mutation	SNP	G	A	14	332	c.502G>A	c.(502-504)GGG>AGG	p.G168R
Pat_63	Post-Resistance	EP300	2033	37	22	41545924	41545924	Missense_Mutation	SNP	C	T	14	192	c.2539C>T	c.(2539-2541)CCA>TCA	p.P847S
Pat_63	Post-Resistance	POLR3H	171568	37	22	41940058	41940058	Nonsense_Mutation	SNP	C	T	9	236	c.48G>A	c.(46-48)TGG>TGA	p.W16*
Pat_63	Post-Resistance	XRCC6	2547	37	22	42046754	42046754	Missense_Mutation	SNP	G	A	15	323	c.988G>A	c.(988-990)GAG>AAG	p.E330K
Pat_63	Post-Resistance	XRCC6	2547	37	22	42054305	42054305	Missense_Mutation	SNP	G	A	18	243	c.1471G>A	c.(1471-1473)GAG>AAG	p.E491K
Pat_63	Post-Resistance	MEI1	150365	37	22	42139163	42139163	Missense_Mutation	SNP	G	A	10	149	c.1411G>A	c.(1411-1413)GAG>AAG	p.E471K
Pat_63	Post-Resistance	TCF20	6942	37	22	42606013	42606013	Missense_Mutation	SNP	C	T	14	359	c.5299G>A	c.(5299-5301)GAG>AAG	p.E1767K
Pat_63	Post-Resistance	TCF20	6942	37	22	42607668	42607668	Missense_Mutation	SNP	G	A	10	209	c.3644C>T	c.(3643-3645)CCC>CTC	p.P1215L
Pat_63	Post-Resistance	TCF20	6942	37	22	42609099	42609099	Missense_Mutation	SNP	C	T	15	633	c.2213G>A	c.(2212-2214)GGC>GAC	p.G738D

Pat_63	Post-Resistance	NFAM1	150372	37	22	42793898	42793898	Missense_Mutation	SNP	C	T	8	317	c.629G>A	c.(628-630)AGC>AAC	p.S210N
Pat_63	Post-Resistance	RRP7A	27341	37	22	42911232	42911232	Missense_Mutation	SNP	C	T	6	172	c.385G>A	c.(385-387)GTG>ATG	p.V129M
Pat_63	Post-Resistance	FAM118A	55007	37	22	45723730	45723730	Missense_Mutation	SNP	G	A	11	459	c.308G>A	c.(307-309)GGC>GAC	p.G103D
Pat_63	Post-Resistance	SMC1B	27127	37	22	45782851	45782851	Missense_Mutation	SNP	G	A	14	716	c.1807C>T	c.(1807-1809)CCT>TCT	p.P603S
Pat_63	Post-Resistance	FBLN1	2192	37	22	45923757	45923757	Missense_Mutation	SNP	G	A	11	514	c.352G>A	c.(352-354)GCG>ACG	p.A118T
Pat_63	Post-Resistance	PKDREJ	10343	37	22	46657298	46657298	Missense_Mutation	SNP	C	T	22	754	c.1922G>A	c.(1921-1923)AGT>AAT	p.S641N
Pat_63	Post-Resistance	SHANK3	85358	37	22	51154142	51154142	Missense_Mutation	SNP	G	A	8	144	c.2359G>A	c.(2359-2361)GGC>AGC	p.G787S
Pat_63	Post-Resistance	ACR	49	37	22	51182491	51182491	Missense_Mutation	SNP	C	T	5	168	c.568C>T	c.(568-570)CCC>TCC	p.P190S
Pat_63	Post-Resistance	CNTN4	152330	37	3	3081863	3081863	Missense_Mutation	SNP	C	T	19	82	c.2306C>T	c.(2305-2307)CCC>CTC	p.P769L
Pat_63	Post-Resistance	EDEM1	9695	37	3	5248941	5248941	Missense_Mutation	SNP	T	C	3	115	c.1321T>C	c.(1321-1323)TTT>CTT	p.F441L
Pat_63	Post-Resistance	SETD5	55209	37	3	9512495	9512495	Missense_Mutation	SNP	C	T	5	27	c.3077C>T	c.(3076-3078)TCC>TTC	p.S1026F
Pat_63	Post-Resistance	TTLL3	26140	37	3	9877103	9877103	Missense_Mutation	SNP	C	T	8	224	c.2249C>T	c.(2248-2250)TCC>TTC	p.S750F
Pat_63	Post-Resistance	IL17RC	84818	37	3	9970108	9970108	Missense_Mutation	SNP	C	T	7	40	c.1210C>T	c.(1210-1212)CCG>TCG	p.P404S
Pat_63	Post-Resistance	IL17RC	84818	37	3	9975138	9975138	Missense_Mutation	SNP	G	A	5	23	c.2237G>A	c.(2236-2238)GGG>GAG	p.G746E
Pat_63	Post-Resistance	TMEM111	55831	37	3	10015370	10015370	Missense_Mutation	SNP	G	A	27	138	c.436C>T	c.(436-438)CTC>TTC	p.L146F
Pat_63	Post-Resistance	ATG7	10533	37	3	11374463	11374463	Missense_Mutation	SNP	C	T	4	16	c.785C>T	c.(784-786)TCT>TTT	p.S262F
Pat_63	Post-Resistance	ZFYVE20	64145	37	3	15115302	15115302	Missense_Mutation	SNP	C	T	13	144	c.2342G>A	c.(2341-2343)GGG>GAG	p.G781E
Pat_63	Post-Resistance	SH3BP5	9467	37	3	15311221	15311221	Missense_Mutation	SNP	C	T	26	185	c.494G>A	c.(493-495)AGG>AAG	p.R165K
Pat_63	Post-Resistance	PLCL2	23228	37	3	17131267	17131267	Missense_Mutation	SNP	G	A	15	114	c.3223G>A	c.(3223-3225)GAG>AAG	p.E1075K
Pat_63	Post-Resistance	OSBPL10	114884	37	3	31725509	31725509	Missense_Mutation	SNP	C	T	23	85	c.1343G>A	c.(1342-1344)GGG>GAG	p.G448E
Pat_63	Post-Resistance	ZNF860	344787	37	3	32031628	32031628	Missense_Mutation	SNP	C	T	14	136	c.1057C>T	c.(1057-1059)CGT>TGT	p.R353C
Pat_63	Post-Resistance	CNOT10	25904	37	3	32746399	32746399	Missense_Mutation	SNP	T	C	18	90	c.214T>C	c.(214-216)TTT>CTT	p.F72L
Pat_63	Post-Resistance	LRRFIP2	9209	37	3	37163148	37163148	Missense_Mutation	SNP	G	A	16	142	c.263C>T	c.(262-264)TCC>TTC	p.S88F
Pat_63	Post-Resistance	GOLGA4	2803	37	3	37367692	37367692	Missense_Mutation	SNP	T	C	14	139	c.4315T>C	c.(4315-4317)TCC>CCC	p.S1439P
Pat_63	Post-Resistance	GOLGA4	2803	37	3	37369306	37369306	Missense_Mutation	SNP	G	A	10	62	c.5929G>A	c.(5929-5931)GAG>AAG	p.E1977K
Pat_63	Post-Resistance	ITGA9	3680	37	3	37860433	37860433	Missense_Mutation	SNP	C	T	7	75	c.3061C>T	c.(3061-3063)CGG>TGG	p.R1021W
Pat_63	Post-Resistance	VILL	50853	37	3	38048063	38048063	Missense_Mutation	SNP	G	A	13	51	c.2329G>A	c.(2329-2331)GCT>ACT	p.A777T
Pat_63	Post-Resistance	ACAA1	30	37	3	38173470	38173470	Missense_Mutation	SNP	G	A	27	142	c.350C>T	c.(349-351)TCC>TTC	p.S117F
Pat_63	Post-Resistance	MYRIP	25924	37	3	40275349	40275349	Splice_Site	SNP	G	A	13	95	c.1906_splice	c.e12-1	p.K636_splice
Pat_63	Post-Resistance	CTNNB1	1499	37	3	41275723	41275723	Missense_Mutation	SNP	C	T	8	191	c.1618C>T	c.(1618-1620)CTT>TTT	p.L540F
Pat_63	Post-Resistance	LRRC2	79442	37	3	46586699	46586699	Missense_Mutation	SNP	C	T	6	52	c.170G>A	c.(169-171)GGC>GAC	p.G57D
Pat_63	Post-Resistance	PTH1R	5745	37	3	46942562	46942562	Missense_Mutation	SNP	C	A	4	18	c.1036C>A	c.(1036-1038)CTG>ATG	p.L346M
Pat_63	Post-Resistance	SETD2	29072	37	3	47125260	47125260	Missense_Mutation	SNP	C	T	26	198	c.6010G>A	c.(6010-6012)GAT>AAT	p.D2004N
Pat_63	Post-Resistance	CSPG5	10675	37	3	47614179	47614179	Missense_Mutation	SNP	G	A	9	108	c.1379C>T	c.(1378-1380)ACC>ATC	p.T460I
Pat_63	Post-Resistance	COL7A1	1294	37	3	48623812	48623812	Missense_Mutation	SNP	G	A	8	290	c.3503C>T	c.(3502-3504)CCC>CTC	p.P1168L
Pat_63	Post-Resistance	IP6K2	51447	37	3	48730580	48730580	Missense_Mutation	SNP	C	T	6	116	c.235G>A	c.(235-237)GAC>AAC	p.D79N
Pat_63	Post-Resistance	AMT	275	37	3	49455124	49455124	Missense_Mutation	SNP	G	A	36	203	c.1061C>T	c.(1060-1062)CCC>CTC	p.P354L
Pat_63	Post-Resistance	CACNA2D2	9254	37	3	50404913	50404913	Nonsense_Mutation	SNP	C	T	8	39	c.2334G>A	c.(2332-2334)TGG>TGA	p.W778*
Pat_63	Post-Resistance	RAD54L2	23132	37	3	51667777	51667777	Splice_Site	SNP	T	C	17	49	c.1008_splice	c.e7+2	p.P336_splice
Pat_63	Post-Resistance	ACY1	95	37	3	52019904	52019904	Missense_Mutation	SNP	G	A	10	62	c.301G>A	c.(301-303)GAT>AAT	p.D101N
Pat_63	Post-Resistance	GLYCTK	132158	37	3	52326454	52326454	Missense_Mutation	SNP	C	T	4	75	c.884C>T	c.(883-885)CCC>CTC	p.P295L
Pat_63	Post-Resistance	SFMBT1	51460	37	3	52950168	52950168	Missense_Mutation	SNP	G	A	11	94	c.1478C>T	c.(1477-1479)TCA>TTA	p.S493L
Pat_63	Post-Resistance	CCDC66	285331	37	3	56601063	56601063	Nonsense_Mutation	SNP	C	T	8	97	c.796C>T	c.(796-798)CAG>TAG	p.Q266*
Pat_63	Post-Resistance	C3orf63	23272	37	3	56680684	56680684	Missense_Mutation	SNP	C	T	12	105	c.2081G>A	c.(2080-2082)AGT>AAT	p.S694N
Pat_63	Post-Resistance	SPATA12	353324	37	3	57108015	57108015	Missense_Mutation	SNP	A	C	4	119	c.293A>C	c.(292-294)CAA>CCA	p.Q98P
Pat_63	Post-Resistance	IL17RD	54756	37	3	57130531	57130531	Missense_Mutation	SNP	C	T	20	90	c.2110G>A	c.(2110-2112)GAG>AAG	p.E704K
Pat_63	Post-Resistance	PRICKLE2	166336	37	3	64133348	64133348	Missense_Mutation	SNP	C	T	20	108	c.818G>A	c.(817-819)GGC>GAC	p.G273D

Pat_63	Post-Resistance	ADAMTS9	56999	37	3	64617589	64617589	Missense_Mutation	SNP	C	T	5	48	c.2188G>A	c.(2188-2190)GAT>AAT	p.D730N
Pat_63	Post-Resistance	FAM19A1	407738	37	3	68055858	68055858	Missense_Mutation	SNP	C	T	23	161	c.89C>T	c.(88-90)ACT>ATT	p.T30I
Pat_63	Post-Resistance	PPP4R2	151987	37	3	73114008	73114008	Missense_Mutation	SNP	C	T	7	132	c.644C>T	c.(643-645)TCT>TTT	p.S215F
Pat_63	Post-Resistance	ROBO1	6091	37	3	78649402	78649402	Missense_Mutation	SNP	G	A	9	96	c.4802C>T	c.(4801-4803)CCC>CTC	p.P1601L
Pat_63	Post-Resistance	ROBO1	6091	37	3	78710408	78710408	Missense_Mutation	SNP	C	T	5	21	c.2092G>A	c.(2092-2094)GAT>AAT	p.D698N
Pat_63	Post-Resistance	EPHA6	285220	37	3	96945179	96945179	Missense_Mutation	SNP	A	T	29	61	c.1186A>T	c.(1186-1188)ACA>TCA	p.T396S
Pat_63	Post-Resistance	TOMM70A	9868	37	3	100105188	100105188	Nonsense_Mutation	SNP	G	A	7	18	c.499C>T	c.(499-501)CAA>TAA	p.Q167*
Pat_63	Post-Resistance	IMPG2	50939	37	3	100972586	100972586	Missense_Mutation	SNP	C	A	8	21	c.1193G>T	c.(1192-1194)TGG>TTG	p.W398L
Pat_63	Post-Resistance	SENP7	57337	37	3	101044800	101044800	Missense_Mutation	SNP	C	T	5	165	c.3140G>A	c.(3139-3141)GGC>GAC	p.G1047D
Pat_63	Post-Resistance	IFT57	55081	37	3	107925531	107925531	Missense_Mutation	SNP	C	T	6	22	c.598G>A	c.(598-600)GAT>AAT	p.D200N
Pat_63	Post-Resistance	KIAA1524	57650	37	3	108279513	108279513	Missense_Mutation	SNP	G	A	29	105	c.1810C>T	c.(1810-1812)CTT>TTT	p.L604F
Pat_63	Post-Resistance	BTLA	151888	37	3	112218193	112218193	Missense_Mutation	SNP	G	A	8	38	c.13C>T	c.(13-15)CCT>TCT	p.P5S
Pat_63	Post-Resistance	CCDC52	152185	37	3	113169336	113169336	Missense_Mutation	SNP	G	A	15	32	c.2170C>T	c.(2170-2172)CCA>TCA	p.P724S
Pat_63	Post-Resistance	GRAMD1C	54762	37	3	113655179	113655179	Missense_Mutation	SNP	G	A	8	59	c.1523G>A	c.(1522-1524)GGC>GAC	p.G508D
Pat_63	Post-Resistance	PARP14	54625	37	3	122418732	122418732	Missense_Mutation	SNP	G	A	19	68	c.1331G>A	c.(1330-1332)AGC>AAC	p.S444N
Pat_63	Post-Resistance	KALRN	8997	37	3	123983478	123983478	Missense_Mutation	SNP	C	T	3	38	c.391C>T	c.(391-393)CCC>TCC	p.P131S
Pat_63	Post-Resistance	ALG1L2	644974	37	3	129814925	129814925	Missense_Mutation	SNP	C	T	3	48	c.458C>T	c.(457-459)TCC>TTC	p.S153F
Pat_63	Post-Resistance	DNAJC13	23317	37	3	132207280	132207280	Missense_Mutation	SNP	G	A	22	50	c.3406G>A	c.(3406-3408)GTG>ATG	p.V1136M
Pat_63	Post-Resistance	TF	7018	37	3	133494435	133494435	Missense_Mutation	SNP	G	A	43	81	c.1846G>A	c.(1846-1848)GTC>ATC	p.V616I
Pat_63	Post-Resistance	PCOLCE2	26577	37	3	142539881	142539881	Missense_Mutation	SNP	G	A	4	79	c.956C>T	c.(955-957)GCC>GTC	p.A319V
Pat_63	Post-Resistance	PLSCR1	5359	37	3	146251283	146251283	Missense_Mutation	SNP	G	A	5	179	c.68C>T	c.(67-69)CCT>CTT	p.P23L
Pat_63	Post-Resistance	IGSF10	285313	37	3	151161004	151161004	Missense_Mutation	SNP	C	T	11	47	c.5731G>A	c.(5731-5733)GAC>AAC	p.D1911N
Pat_63	Post-Resistance	TMEM14E	645843	37	3	152058383	152058383	Missense_Mutation	SNP	C	T	6	123	c.311G>A	c.(310-312)GGA>GAA	p.G104E
Pat_63	Post-Resistance	ZBBX	79740	37	3	167068207	167068207	Splice_Site	SNP	C	T	32	208	c.528_splice	c.e9+1	p.Q176_splice
Pat_63	Post-Resistance	MECOM	2122	37	3	169099115	169099115	Missense_Mutation	SNP	C	T	26	111	c.235G>A	c.(235-237)GAG>AAG	p.E79K
Pat_63	Post-Resistance	LRRIQ4	344657	37	3	169548377	169548377	Missense_Mutation	SNP	A	C	7	20	c.1292A>C	c.(1291-1293)AAT>ACT	p.N431T
Pat_63	Post-Resistance	PIK3CA	5290	37	3	178942525	178942525	Missense_Mutation	SNP	C	T	18	73	c.2332C>T	c.(2332-2334)CCA>TCA	p.P778S
Pat_63	Post-Resistance	EIF2B5	8893	37	3	183860884	183860884	Missense_Mutation	SNP	G	A	10	47	c.1699G>A	c.(1699-1701)GAG>AAG	p.E567K
Pat_63	Post-Resistance	DVL3	1857	37	3	183883938	183883938	Missense_Mutation	SNP	C	T	14	95	c.788C>T	c.(787-789)TCC>TTC	p.S263F
Pat_63	Post-Resistance	LPP	4026	37	3	188327028	188327028	Missense_Mutation	SNP	C	T	73	492	c.509C>T	c.(508-510)CCC>CTC	p.P170L
Pat_63	Post-Resistance	CLDN1	9076	37	3	190026151	190026151	Missense_Mutation	SNP	C	T	10	54	c.551G>A	c.(550-552)TGT>TAT	p.C184Y
Pat_63	Post-Resistance	TFRC	7037	37	3	195794997	195794997	Missense_Mutation	SNP	G	A	3	48	c.806C>T	c.(805-807)GCA>GTA	p.A269V
Pat_63	Post-Resistance	DLG1	1739	37	3	196792287	196792287	Missense_Mutation	SNP	C	T	10	82	c.2266G>A	c.(2266-2268)GAT>AAT	p.D756N
Pat_63	Post-Resistance	ZNF595	152687	37	4	195420	195420	Splice_Site	SNP	G	A	5	13	c.514_splice	c.e5-1	
Pat_63	Post-Resistance	ZNF721	170960	37	4	435649	435649	Missense_Mutation	SNP	T	G	7	173	c.2607A>C	c.(2605-2607)GAA>GAC	p.E869D
Pat_63	Post-Resistance	ZNF721	170960	37	4	436574	436574	Missense_Mutation	SNP	T	A	9	301	c.1682A>T	c.(1681-1683)GAA>GTA	p.E561V
Pat_63	Post-Resistance	SLBP	7884	37	4	1705407	1705407	Missense_Mutation	SNP	G	A	5	199	c.197C>T	c.(196-198)CCT>CTT	p.P66L
Pat_63	Post-Resistance	ADD1	118	37	4	2900208	2900208	Missense_Mutation	SNP	G	A	18	142	c.934G>A	c.(934-936)GAG>AAG	p.E312K
Pat_63	Post-Resistance	HTT	3064	37	4	3142380	3142380	Missense_Mutation	SNP	C	T	19	88	c.2948C>T	c.(2947-2949)ACC>ATC	p.T983I
Pat_63	Post-Resistance	DOK7	285489	37	4	3478120	3478120	Missense_Mutation	SNP	C	T	15	154	c.383C>T	c.(382-384)CCG>CTG	p.P128L
Pat_63	Post-Resistance	EVC	2121	37	4	5806463	5806463	Missense_Mutation	SNP	G	A	7	56	c.2456G>A	c.(2455-2457)AGG>AAG	p.R819K
Pat_63	Post-Resistance	ABLIM2	84448	37	4	8062694	8062694	Missense_Mutation	SNP	C	T	5	16	c.763G>A	c.(763-765)GGT>AGT	p.G255S
Pat_63	Post-Resistance	SH3TC1	54436	37	4	8216266	8216266	Missense_Mutation	SNP	C	T	13	63	c.440C>T	c.(439-441)ACT>ATT	p.T147I
Pat_63	Post-Resistance	SLC2A9	56606	37	4	10022908	10022908	Missense_Mutation	SNP	C	T	17	136	c.146G>A	c.(145-147)AGA>AAA	p.R49K
Pat_63	Post-Resistance	CLNK	116449	37	4	10542163	10542163	Missense_Mutation	SNP	G	A	17	101	c.557C>T	c.(556-558)CCT>CTT	p.P186L
Pat_63	Post-Resistance	CC2D2A	57545	37	4	15538544	15538544	Missense_Mutation	SNP	G	A	5	34	c.1609G>A	c.(1609-1611)GAA>AAA	p.E537K
Pat_63	Post-Resistance	DCAF16	54876	37	4	17805665	17805665	Missense_Mutation	SNP	C	T	12	59	c.100G>A	c.(100-102)GAT>AAT	p.D34N

Pat_63	Post-Resistance	GPR125	166647	37	4	22414900	22414900	Missense_Mutation	SNP	C	T	81	405	c.2137G>A	c.(2137-2139)GGA>AGA	p.G713R
Pat_63	Post-Resistance	DHX15	1665	37	4	24534486	24534486	Splice_Site	SNP	C	T	41	324	c.2100_splice	c.e12+1	p.Q700_splice
Pat_63	Post-Resistance	PGM2	55276	37	4	37848592	37848592	Missense_Mutation	SNP	C	T	8	84	c.1048C>T	c.(1048-1050)CTC>TTC	p.L350F
Pat_63	Post-Resistance	KLF3	51274	37	4	38690239	38690239	Missense_Mutation	SNP	C	T	11	72	c.91C>T	c.(91-93)CCT>TCT	p.P31S
Pat_63	Post-Resistance	TLR10	81793	37	4	38777133	38777133	Missense_Mutation	SNP	C	T	10	77	c.79G>A	c.(79-81)GAA>AAA	p.E27K
Pat_63	Post-Resistance	FRYL	285527	37	4	48581249	48581249	Missense_Mutation	SNP	G	A	12	69	c.2269C>T	c.(2269-2271)CTC>TTC	p.L757F
Pat_63	Post-Resistance	SCFD2	152579	37	4	53740170	53740170	Missense_Mutation	SNP	G	A	18	104	c.2021C>T	c.(2020-2022)GCA>GTA	p.A674V
Pat_63	Post-Resistance	KDR	3791	37	4	55968084	55968084	Missense_Mutation	SNP	T	C	5	48	c.2246A>G	c.(2245-2247)GAG>GGG	p.E749G
Pat_63	Post-Resistance	EXOC1	55763	37	4	56744084	56744084	Missense_Mutation	SNP	G	A	28	80	c.1076G>A	c.(1075-1077)GGT>GAT	p.G359D
Pat_63	Post-Resistance	CEP135	9662	37	4	56878056	56878056	Missense_Mutation	SNP	G	A	8	71	c.2707G>A	c.(2707-2709)GAA>AAA	p.E903K
Pat_63	Post-Resistance	LPHN3	23284	37	4	62813882	62813882	Missense_Mutation	SNP	G	A	7	31	c.2489G>A	c.(2488-2490)GGT>GAT	p.G830D
Pat_63	Post-Resistance	PAQR3	152559	37	4	79841809	79841809	Missense_Mutation	SNP	G	A	18	56	c.820C>T	c.(820-822)CAC>TAC	p.H274Y
Pat_63	Post-Resistance	TMEM150C	441027	37	4	83417348	83417348	Missense_Mutation	SNP	G	A	15	63	c.236C>T	c.(235-237)GCC>GTC	p.A79V
Pat_63	Post-Resistance	COQ2	27235	37	4	84194688	84194688	Missense_Mutation	SNP	G	A	23	67	c.542C>T	c.(541-543)ACC>ATC	p.T181I
Pat_63	Post-Resistance	C4orf36	132989	37	4	87809031	87809031	Missense_Mutation	SNP	C	T	4	42	c.236G>A	c.(235-237)AGG>AAG	p.R79K
Pat_63	Post-Resistance	EMCN	51705	37	4	101331503	101331503	Missense_Mutation	SNP	G	A	12	74	c.761C>T	c.(760-762)TCT>TTT	p.S254F
Pat_63	Post-Resistance	SLC39A8	64116	37	4	103225556	103225556	Missense_Mutation	SNP	C	T	4	101	c.758G>A	c.(757-759)GGT>GAT	p.G253D
Pat_63	Post-Resistance	NUDT6	11162	37	4	123833743	123833743	Missense_Mutation	SNP	C	T	7	46	c.478G>A	c.(478-480)GTT>ATT	p.V160I
Pat_63	Post-Resistance	PCDH10	57575	37	4	134073651	134073651	Missense_Mutation	SNP	G	A	4	10	c.2356G>A	c.(2356-2358)GAC>AAC	p.D786N
Pat_63	Post-Resistance	MAML3	55534	37	4	140811424	140811424	Missense_Mutation	SNP	G	C	27	43	c.1166C>G	c.(1165-1167)TCC>TGC	p.S389C
Pat_63	Post-Resistance	ANAPC10	10393	37	4	146017140	146017140	Missense_Mutation	SNP	G	A	54	221	c.112C>T	c.(112-114)CCA>TCA	p.P38S
Pat_63	Post-Resistance	SH3D19	152503	37	4	152065124	152065124	Missense_Mutation	SNP	C	T	17	105	c.1390G>A	c.(1390-1392)GTT>ATT	p.V464I
Pat_63	Post-Resistance	FNIP2	57600	37	4	159790277	159790277	Missense_Mutation	SNP	G	A	10	42	c.2489G>A	c.(2488-2490)GGA>GAA	p.G830E
Pat_63	Post-Resistance	RAPGEF2	9693	37	4	160253806	160253806	Missense_Mutation	SNP	C	T	13	37	c.1609C>T	c.(1609-1611)CTC>TTC	p.L537F
Pat_63	Post-Resistance	TLL1	7092	37	4	166929191	166929191	Missense_Mutation	SNP	C	T	12	84	c.908C>T	c.(907-909)ACC>ATC	p.T303I
Pat_63	Post-Resistance	TLL1	7092	37	4	166981197	166981197	Missense_Mutation	SNP	C	T	6	36	c.1864C>T	c.(1864-1866)CTT>TTT	p.L622F
Pat_63	Post-Resistance	EXOC3	11336	37	5	466843	466843	Missense_Mutation	SNP	G	A	9	65	c.2068G>A	c.(2068-2070)GAT>AAT	p.D690N
Pat_63	Post-Resistance	ZDHHC11	79844	37	5	819674	819674	Missense_Mutation	SNP	G	A	11	184	c.1112C>T	c.(1111-1113)ACT>ATT	p.T371I
Pat_63	Post-Resistance	ADAMTS16	170690	37	5	5209331	5209331	Missense_Mutation	SNP	C	A	45	148	c.1577C>A	c.(1576-1578)GCC>GAC	p.A526D
Pat_63	Post-Resistance	KIAA0947	23379	37	5	5460861	5460861	Missense_Mutation	SNP	A	G	13	73	c.1414A>G	c.(1414-1416)AGT>GGT	p.S472G
Pat_63	Post-Resistance	ZNF622	90441	37	5	16465657	16465657	Missense_Mutation	SNP	C	T	6	60	c.118G>A	c.(118-120)GCC>ACC	p.A40T
Pat_63	Post-Resistance	RNASEN	29102	37	5	31515175	31515175	Missense_Mutation	SNP	C	T	19	132	c.1210G>A	c.(1210-1212)GAA>AAA	p.E404K
Pat_63	Post-Resistance	RXFP3	51289	37	5	33937023	33937023	Missense_Mutation	SNP	G	A	17	91	c.178G>A	c.(178-180)GCG>ACG	p.A60T
Pat_63	Post-Resistance	SPEF2	79925	37	5	35659175	35659175	Missense_Mutation	SNP	G	A	10	89	c.1033G>A	c.(1033-1035)GAG>AAG	p.E345K
Pat_63	Post-Resistance	NIPBL	25836	37	5	36985446	36985446	Missense_Mutation	SNP	C	T	27	147	c.2164C>T	c.(2164-2166)CCT>TCT	p.P722S
Pat_63	Post-Resistance	NIPBL	25836	37	5	37006491	37006491	Nonsense_Mutation	SNP	G	A	16	135	c.3888G>A	c.(3886-3888)TGG>TGA	p.W1296*
Pat_63	Post-Resistance	C5orf42	65250	37	5	37179515	37179515	Missense_Mutation	SNP	C	T	15	162	c.5768G>A	c.(5767-5769)AGA>AAA	p.R1923K
Pat_63	Post-Resistance	FYB	2533	37	5	39202085	39202085	Nonsense_Mutation	SNP	C	T	10	78	c.978G>A	c.(976-978)TGG>TGA	p.W326*
Pat_63	Post-Resistance	PRKAA1	5562	37	5	40763122	40763122	Missense_Mutation	SNP	C	T	19	79	c.1438G>A	c.(1438-1440)GAA>AAA	p.E480K
Pat_63	Post-Resistance	NNT	23530	37	5	43700235	43700235	Missense_Mutation	SNP	C	A	6	279	c.2891C>A	c.(2890-2892)CCA>CAA	p.P964Q
Pat_63	Post-Resistance	DHX29	54505	37	5	54566436	54566436	Missense_Mutation	SNP	C	T	30	174	c.2963G>A	c.(2962-2964)GGC>GAC	p.G988D
Pat_63	Post-Resistance	PPAP2A	8611	37	5	54721131	54721131	Missense_Mutation	SNP	C	T	7	44	c.758G>A	c.(757-759)AGA>AAA	p.R253K
Pat_63	Post-Resistance	DEPDC1B	55789	37	5	59983011	59983011	Missense_Mutation	SNP	C	T	19	147	c.92G>A	c.(91-93)CGG>CAG	p.R31Q
Pat_63	Post-Resistance	ZNF366	167465	37	5	71740091	71740091	Missense_Mutation	SNP	G	A	16	65	c.1727C>T	c.(1726-1728)GCA>GTA	p.A576V
Pat_63	Post-Resistance	COL4A3BP	10087	37	5	74698883	74698883	Missense_Mutation	SNP	C	T	19	109	c.931G>A	c.(931-933)GAA>AAA	p.E311K
Pat_63	Post-Resistance	MSH3	4437	37	5	80160657	80160657	Missense_Mutation	SNP	C	T	9	94	c.3026C>T	c.(3025-3027)ACC>ATC	p.T1009I
Pat_63	Post-Resistance	ATG10	83734	37	5	81460326	81460326	Missense_Mutation	SNP	C	T	10	99	c.325C>T	c.(325-327)CCT>TCT	p.P109S

Pat_63	Post-Resistance	VCAN	1462	37	5	82836672	82836672	Missense_Mutation	SNP	C	T	14	82	c.7850C>T	c.(7849-7851)ACT>ATT	p.T2617I
Pat_63	Post-Resistance	EDIL3	10085	37	5	83680131	83680131	Missense_Mutation	SNP	C	T	8	90	c.62G>A	c.(61-63)GGC>GAC	p.G21D
Pat_63	Post-Resistance	GPR98	84059	37	5	90049488	90049488	Missense_Mutation	SNP	C	T	27	102	c.11219C>T	c.(11218-11220)ACC>ATC	p.T3740I
Pat_63	Post-Resistance	TTC37	9652	37	5	94852234	94852234	Nonsense_Mutation	SNP	G	A	5	149	c.2572C>T	c.(2572-2574)CAA>TAA	p.Q858*
Pat_63	Post-Resistance	ERAP1	51752	37	5	96117545	96117545	Missense_Mutation	SNP	C	T	12	109	c.2299G>A	c.(2299-2301)GTG>ATG	p.V767M
Pat_63	Post-Resistance	CHD1	1105	37	5	98207772	98207772	Missense_Mutation	SNP	G	A	24	192	c.3844C>T	c.(3844-3846)CTC>TTC	p.L1282F
Pat_63	Post-Resistance	SLCO6A1	133482	37	5	101794120	101794120	Missense_Mutation	SNP	C	T	9	87	c.1097G>A	c.(1096-1098)GGA>GAA	p.G366E
Pat_63	Post-Resistance	PPIP5K2	23262	37	5	102490435	102490435	Missense_Mutation	SNP	C	T	11	61	c.1279C>T	c.(1279-1281)CCA>TCA	p.P427S
Pat_63	Post-Resistance	WDR36	134430	37	5	110445970	110445970	Missense_Mutation	SNP	G	A	30	232	c.1577G>A	c.(1576-1578)GGC>GAC	p.G526D
Pat_63	Post-Resistance	DMXL1	1657	37	5	118513931	118513931	Missense_Mutation	SNP	C	T	20	87	c.7127C>T	c.(7126-7128)ACT>ATT	p.T2376I
Pat_63	Post-Resistance	PPIC	5480	37	5	122359574	122359574	Nonsense_Mutation	SNP	C	T	8	385	c.635G>A	c.(634-636)TGG>TAG	p.W212*
Pat_63	Post-Resistance	CSNK1G3	1456	37	5	122940502	122940502	Missense_Mutation	SNP	G	A	7	59	c.1267G>A	c.(1267-1269)GTA>ATA	p.V423I
Pat_63	Post-Resistance	ZNF608	57507	37	5	124080204	124080204	Missense_Mutation	SNP	C	T	16	88	c.479G>A	c.(478-480)GGC>GAC	p.G160D
Pat_63	Post-Resistance	MEGF10	84466	37	5	126778801	126778801	Missense_Mutation	SNP	G	A	23	128	c.2474G>A	c.(2473-2475)GGA>GAA	p.G825E
Pat_63	Post-Resistance	PRRC1	133619	37	5	126887399	126887399	Missense_Mutation	SNP	G	A	4	88	c.1129G>A	c.(1129-1131)GCT>ACT	p.A377T
Pat_63	Post-Resistance	SLC12A2	6558	37	5	127466804	127466804	Missense_Mutation	SNP	G	A	31	157	c.1094G>A	c.(1093-1095)GGT>GAT	p.G365D
Pat_63	Post-Resistance	P4HA2	8974	37	5	131531158	131531158	Missense_Mutation	SNP	C	T	8	59	c.1387G>A	c.(1387-1389)GCT>ACT	p.A463T
Pat_63	Post-Resistance	ZMAT2	153527	37	5	140081653	140081653	Missense_Mutation	SNP	G	A	28	158	c.175G>A	c.(175-177)GAA>AAA	p.E59K
Pat_63	Post-Resistance	PCDHB5	26167	37	5	140515560	140515560	Missense_Mutation	SNP	A	G	24	166	c.544A>G	c.(544-546)ACG>GCG	p.T182A
Pat_63	Post-Resistance	PCDHGA11	56105	37	5	140801801	140801801	Missense_Mutation	SNP	T	C	3	42	c.1007T>C	c.(1006-1008)ATC>ACC	p.I336T
Pat_63	Post-Resistance	PCDH12	51294	37	5	141336753	141336753	Missense_Mutation	SNP	G	A	17	87	c.664C>T	c.(664-666)CCC>TCC	p.P222S
Pat_63	Post-Resistance	SPINK5	11005	37	5	147480133	147480133	Missense_Mutation	SNP	T	G	44	75	c.1209T>G	c.(1207-1209)TGT>TGG	p.C403W
Pat_63	Post-Resistance	SH3TC2	79628	37	5	148384306	148384306	Missense_Mutation	SNP	G	A	6	40	c.3835C>T	c.(3835-3837)CGG>TGG	p.R1279W
Pat_63	Post-Resistance	SH3TC2	79628	37	5	148384423	148384423	Missense_Mutation	SNP	C	T	16	90	c.3718G>A	c.(3718-3720)GCA>ACA	p.A1240T
Pat_63	Post-Resistance	SLC26A2	1836	37	5	149360196	149360196	Missense_Mutation	SNP	C	T	13	64	c.1040C>T	c.(1039-1041)TCT>TTT	p.S347F
Pat_63	Post-Resistance	CAMK2A	815	37	5	149669130	149669130	Missense_Mutation	SNP	C	T	13	105	c.59G>A	c.(58-60)GGC>GAC	p.G20D
Pat_63	Post-Resistance	TCOF1	6949	37	5	149773019	149773019	Missense_Mutation	SNP	C	T	8	64	c.3685C>T	c.(3685-3687)CCC>TCC	p.P1229S
Pat_63	Post-Resistance	DCTN4	51164	37	5	150110243	150110243	Missense_Mutation	SNP	G	A	10	586	c.784C>T	c.(784-786)CTC>TTC	p.L262F
Pat_63	Post-Resistance	ZNF300	91975	37	5	150275557	150275557	Missense_Mutation	SNP	C	T	6	57	c.1244G>A	c.(1243-1245)GGG>GAG	p.G415E
Pat_63	Post-Resistance	SLC36A2	153201	37	5	150712784	150712784	Splice_Site	SNP	C	T	11	71	c.843_splice	c.e7+1	p.V281_splice
Pat_63	Post-Resistance	FAT2	2196	37	5	150946040	150946040	Missense_Mutation	SNP	G	A	14	79	c.2453C>T	c.(2452-2454)CCC>CTC	p.P818L
Pat_63	Post-Resistance	CYFIP2	26999	37	5	156757803	156757803	Missense_Mutation	SNP	T	C	10	123	c.2210T>C	c.(2209-2211)ATT>ACT	p.I737T
Pat_63	Post-Resistance	PTTG1	9232	37	5	159849859	159849859	Missense_Mutation	SNP	G	A	9	243	c.235G>A	c.(235-237)GGA>AGA	p.G79R
Pat_63	Post-Resistance	SLIT3	6586	37	5	168216587	168216587	Missense_Mutation	SNP	C	A	18	39	c.1057G>T	c.(1057-1059)GGC>TGC	p.G353C
Pat_63	Post-Resistance	DOCK2	1794	37	5	169506061	169506061	Missense_Mutation	SNP	G	A	16	95	c.5077G>A	c.(5077-5079)GTC>ATC	p.V1693I
Pat_63	Post-Resistance	BOD1	91272	37	5	173036279	173036279	Missense_Mutation	SNP	C	A	12	80	c.521G>T	c.(520-522)GGC>GTC	p.G174V
Pat_63	Post-Resistance	CPEB4	80315	37	5	173316758	173316758	Missense_Mutation	SNP	G	A	148	656	c.22G>A	c.(22-24)GTG>ATG	p.V8M
Pat_63	Post-Resistance	GRK6	2870	37	5	176867825	176867825	Missense_Mutation	SNP	C	T	15	121	c.1529C>T	c.(1528-1530)CCC>CTC	p.P510L
Pat_63	Post-Resistance	MAML1	9794	37	5	179201706	179201706	Missense_Mutation	SNP	C	T	5	22	c.2879C>T	c.(2878-2880)GCC>GTC	p.A960V
Pat_63	Post-Resistance	MGAT4B	11282	37	5	179225929	179225929	Missense_Mutation	SNP	G	A	3	50	c.1342C>T	c.(1342-1344)CGG>TGG	p.R448W
Pat_63	Post-Resistance	FARS2	10667	37	6	5431351	5431351	Missense_Mutation	SNP	G	A	17	238	c.850G>A	c.(850-852)GAA>AAA	p.E284K
Pat_63	Post-Resistance	PIP5K1P1	206426	37	6	7987026	7987026	Missense_Mutation	SNP	G	A	29	185	c.257G>A	c.(256-258)AGC>AAC	p.S86N
Pat_63	Post-Resistance	PIP5K1P1	206426	37	6	7987143	7987143	Missense_Mutation	SNP	G	A	15	185	c.374G>A	c.(373-375)CGT>CAT	p.R125H
Pat_63	Post-Resistance	EDN1	1906	37	6	12294193	12294193	Missense_Mutation	SNP	C	T	5	65	c.253C>T	c.(253-255)CTT>TTT	p.L85F
Pat_63	Post-Resistance	SIRT5	23408	37	6	13601162	13601162	Missense_Mutation	SNP	C	T	6	100	c.838C>T	c.(838-840)CCA>TCA	p.P280S
Pat_63	Post-Resistance	RNF182	221687	37	6	13977987	13977987	Missense_Mutation	SNP	G	A	29	235	c.637G>A	c.(637-639)GTC>ATC	p.V213I
Pat_63	Post-Resistance	LRRC16A	55604	37	6	25540227	25540227	Missense_Mutation	SNP	G	A	7	38	c.2249G>A	c.(2248-2250)GGC>GAC	p.G750D

Pat_63	Post-Resistance	HIST1H2BN	8341	37	6	27806783	27806783	Missense_Mutation	SNP	G	A	51	347	c.344G>A	c.(343-345)GGC>GAC	p.G115D
Pat_63	Post-Resistance	HIST1H2BO	8348	37	6	27861284	27861284	Missense_Mutation	SNP	C	T	19	169	c.44C>T	c.(43-45)TCC>TTC	p.S15F
Pat_63	Post-Resistance	OR2B2	81697	37	6	27879509	27879509	Missense_Mutation	SNP	C	T	21	294	c.589G>A	c.(589-591)GCT>ACT	p.A197T
Pat_63	Post-Resistance	SCAND3	114821	37	6	28554209	28554209	Missense_Mutation	SNP	C	T	19	235	c.286G>A	c.(286-288)GTG>ATG	p.V96M
Pat_63	Post-Resistance	MRPS18B	28973	37	6	30590648	30590648	Missense_Mutation	SNP	G	A	22	199	c.394G>A	c.(394-396)GGT>AGT	p.G132S
Pat_63	Post-Resistance	DHX16	8449	37	6	30633255	30633255	Splice_Site	SNP	C	T	13	134	c.921_splice	c.e5+1	p.Q307_splice
Pat_63	Post-Resistance	TUBB	203068	37	6	30692136	30692136	Missense_Mutation	SNP	G	A	18	206	c.1297G>A	c.(1297-1299)GAG>AAG	p.E433K
Pat_63	Post-Resistance	FLOT1	10211	37	6	30709624	30709624	Missense_Mutation	SNP	C	T	18	145	c.64G>A	c.(64-66)GTC>ATC	p.V22I
Pat_63	Post-Resistance	MICA	4276	37	6	31378439	31378439	Missense_Mutation	SNP	T	C	3	46	c.190T>C	c.(190-192)TGC>CGC	p.C64R
Pat_63	Post-Resistance	BAT2	7916	37	6	31591556	31591556	Missense_Mutation	SNP	C	T	14	188	c.160C>T	c.(160-162)CGG>TGG	p.R54W
Pat_63	Post-Resistance	BAT2	7916	37	6	31597360	31597360	Nonsense_Mutation	SNP	G	A	36	323	c.1992G>A	c.(1990-1992)TGG>TGA	p.W664*
Pat_63	Post-Resistance	C6orf27	80737	37	6	31743973	31743973	Missense_Mutation	SNP	G	A	20	203	c.281C>T	c.(280-282)CCT>CTT	p.P94L
Pat_63	Post-Resistance	SKIV2L	6499	37	6	31937457	31937457	Missense_Mutation	SNP	G	A	6	224	c.3706G>A	c.(3706-3708)GAC>AAC	p.D1236N
Pat_63	Post-Resistance	DOM3Z	1797	37	6	31938234	31938234	Nonsense_Mutation	SNP	C	T	5	194	c.834G>A	c.(832-834)TGG>TGA	p.W278*
Pat_63	Post-Resistance	DOM3Z	1797	37	6	31939187	31939187	Missense_Mutation	SNP	G	A	6	94	c.266C>T	c.(265-267)CCG>CTG	p.P89L
Pat_63	Post-Resistance	TNXB	7148	37	6	32021195	32021195	Missense_Mutation	SNP	C	T	6	79	c.8755G>A	c.(8755-8757)GTG>ATG	p.V2919M
Pat_63	Post-Resistance	TNXB	7148	37	6	32023823	32023823	Missense_Mutation	SNP	T	C	5	151	c.8272A>G	c.(8272-8274)ATC>GTC	p.I2758V
Pat_63	Post-Resistance	TNXB	7148	37	6	32053632	32053632	Missense_Mutation	SNP	C	T	7	71	c.3043G>A	c.(3043-3045)GCT>ACT	p.A1015T
Pat_63	Post-Resistance	NOTCH4	4855	37	6	32185774	32185774	Missense_Mutation	SNP	G	A	7	65	c.1622C>T	c.(1621-1623)CCT>CTT	p.P541L
Pat_63	Post-Resistance	HLA-DMB	3109	37	6	32906742	32906742	Missense_Mutation	SNP	C	T	23	317	c.56G>A	c.(55-57)GGT>GAT	p.G19D
Pat_63	Post-Resistance	RING1	6015	37	6	33179637	33179637	Missense_Mutation	SNP	C	T	8	48	c.977C>T	c.(976-978)ACC>ATC	p.T326I
Pat_63	Post-Resistance	DAXX	1616	37	6	33287218	33287218	Missense_Mutation	SNP	G	A	38	339	c.1879C>T	c.(1879-1881)CCC>TCC	p.P627S
Pat_63	Post-Resistance	SYNGAP1	8831	37	6	33403311	33403311	Missense_Mutation	SNP	C	T	11	686	c.683C>T	c.(682-684)ACA>ATA	p.T228I
Pat_63	Post-Resistance	UHRF1BP1	54887	37	6	34823481	34823481	Splice_Site	SNP	G	A	12	117	c.1120_splice	c.e9+1	p.G374_splice
Pat_63	Post-Resistance	MTCH1	23787	37	6	36946333	36946333	Missense_Mutation	SNP	G	A	33	440	c.461C>T	c.(460-462)CCC>CTC	p.P154L
Pat_63	Post-Resistance	PIM1	5292	37	6	37138398	37138398	Missense_Mutation	SNP	C	T	9	158	c.47C>T	c.(46-48)CCC>CTC	p.P16L
Pat_63	Post-Resistance	DNAH8	1769	37	6	38816485	38816485	Missense_Mutation	SNP	G	A	4	102	c.4456G>A	c.(4456-4458)GAT>AAT	p.D1486N
Pat_63	Post-Resistance	DNAH8	1769	37	6	38830213	38830213	Missense_Mutation	SNP	G	A	15	176	c.5638G>A	c.(5638-5640)GGC>AGC	p.G1880S
Pat_63	Post-Resistance	PTCRA	171558	37	6	42890779	42890779	Missense_Mutation	SNP	C	T	19	154	c.73C>T	c.(73-75)CCC>TCC	p.P25S
Pat_63	Post-Resistance	CUL9	23113	37	6	43164471	43164471	Missense_Mutation	SNP	G	A	20	191	c.2674G>A	c.(2674-2676)GAG>AAG	p.E892K
Pat_63	Post-Resistance	XPO5	57510	37	6	43491635	43491635	Missense_Mutation	SNP	C	T	6	236	c.3586G>A	c.(3586-3588)GGT>AGT	p.G1196S
Pat_63	Post-Resistance	POLH	5429	37	6	43571691	43571691	Missense_Mutation	SNP	G	A	17	116	c.827G>A	c.(826-828)GGT>GAT	p.G276D
Pat_63	Post-Resistance	HSP90AB1	3326	37	6	44219940	44219940	Missense_Mutation	SNP	G	A	20	131	c.1667G>A	c.(1666-1668)AGC>AAC	p.S556N
Pat_63	Post-Resistance	PKHD1	5314	37	6	51923135	51923135	Missense_Mutation	SNP	G	A	10	136	c.1498C>T	c.(1498-1500)CTT>TTT	p.L500F
Pat_63	Post-Resistance	PAQR8	85315	37	6	52268097	52268097	Missense_Mutation	SNP	G	A	4	28	c.86G>A	c.(85-87)GGG>GAG	p.G29E
Pat_63	Post-Resistance	EFHC1	114327	37	6	52288858	52288858	Missense_Mutation	SNP	G	A	36	450	c.178G>A	c.(178-180)GCT>ACT	p.A60T
Pat_63	Post-Resistance	COL19A1	1310	37	6	70859743	70859743	Missense_Mutation	SNP	G	A	7	43	c.1930G>A	c.(1930-1932)GGT>AGT	p.G644S
Pat_63	Post-Resistance	IRAK1BP1	134728	37	6	79607677	79607677	Splice_Site	SNP	G	A	18	81	c.512_splice	c.e3+1	p.R171_splice
Pat_63	Post-Resistance	ZNF292	23036	37	6	87966111	87966111	Missense_Mutation	SNP	G	A	14	48	c.2764G>A	c.(2764-2766)GAA>AAA	p.E922K
Pat_63	Post-Resistance	GABRR1	2569	37	6	89891645	89891645	Missense_Mutation	SNP	C	T	21	57	c.928G>A	c.(928-930)GTG>ATG	p.V310M
Pat_63	Post-Resistance	KLHL32	114792	37	6	97489450	97489450	Missense_Mutation	SNP	C	T	28	48	c.287C>T	c.(286-288)GCT>GTT	p.A96V
Pat_63	Post-Resistance	ASCC3	10973	37	6	101054871	101054871	Missense_Mutation	SNP	C	A	24	52	c.4879G>T	c.(4879-4881)GAC>TAC	p.D1627Y
Pat_63	Post-Resistance	ASCC3	10973	37	6	101054918	101054918	Missense_Mutation	SNP	G	A	23	80	c.4832C>T	c.(4831-4833)ACC>ATC	p.T1611I
Pat_63	Post-Resistance	AKD1	221264	37	6	109815288	109815288	Missense_Mutation	SNP	G	A	5	33	c.5429C>T	c.(5428-5430)ACT>ATT	p.T1810I
Pat_63	Post-Resistance	GPR6	2830	37	6	110300722	110300722	Missense_Mutation	SNP	C	T	5	120	c.407C>T	c.(406-408)CCC>CTC	p.P136L
Pat_63	Post-Resistance	TRMT11	60487	37	6	126320759	126320759	Missense_Mutation	SNP	G	A	14	58	c.679G>A	c.(679-681)GGT>AGT	p.G227S
Pat_63	Post-Resistance	ECHDC1	55862	37	6	127611270	127611270	Missense_Mutation	SNP	G	A	21	72	c.668C>T	c.(667-669)GCT>GTT	p.A223V

Pat_63	Post-Resistance	EPB41L2	2037	37	6	131186708	131186708	Missense_Mutation	SNP	C	T	6	157	c.2797G>A	c.(2797-2799)GTG>ATG	p.V933M
Pat_63	Post-Resistance	MAP7	9053	37	6	136667213	136667213	Missense_Mutation	SNP	G	A	8	26	c.2020C>T	c.(2020-2022)CCC>TCC	p.P674S
Pat_63	Post-Resistance	UTRN	7402	37	6	145051492	145051492	Splice_Site	SNP	G	A	6	159	c.7810_splice	c.e53-1	p.A2604_splice
Pat_63	Post-Resistance	LATS1	9113	37	6	150023066	150023066	Missense_Mutation	SNP	C	T	27	104	c.197G>A	c.(196-198)AGA>AAA	p.R66K
Pat_63	Post-Resistance	AKAP12	9590	37	6	151673112	151673112	Missense_Mutation	SNP	G	A	30	75	c.3586G>A	c.(3586-3588)GAG>AAG	p.E1196K
Pat_63	Post-Resistance	TIAM2	26230	37	6	155572097	155572097	Nonsense_Mutation	SNP	G	A	28	86	c.4002G>A	c.(4000-4002)TGG>TGA	p.W1334*
Pat_63	Post-Resistance	MAP3K4	4216	37	6	161505621	161505621	Missense_Mutation	SNP	G	A	14	33	c.2344G>A	c.(2344-2346)GAT>AAT	p.D782N
Pat_63	Post-Resistance	HEATR2	54919	37	7	796510	796510	Missense_Mutation	SNP	C	T	7	56	c.1349C>T	c.(1348-1350)GCC>GTC	p.A450V
Pat_63	Post-Resistance	SUN1	23353	37	7	901071	901071	Missense_Mutation	SNP	G	A	23	172	c.1834G>A	c.(1834-1836)GGG>AGG	p.G612R
Pat_63	Post-Resistance	AMZ1	155185	37	7	2748798	2748798	Missense_Mutation	SNP	G	A	4	10	c.691G>A	c.(691-693)GCA>ACA	p.A231T
Pat_63	Post-Resistance	SKAP2	8935	37	7	26765115	26765115	Missense_Mutation	SNP	G	A	23	118	c.728C>T	c.(727-729)CCT>CTT	p.P243L
Pat_63	Post-Resistance	HOXA10	3206	37	7	27213870	27213870	Missense_Mutation	SNP	G	A	18	171	c.56C>T	c.(55-57)TCA>TTA	p.S19L
Pat_63	Post-Resistance	GHRHR	2692	37	7	31013666	31013666	Missense_Mutation	SNP	G	A	20	152	c.664G>A	c.(664-666)GCA>ACA	p.A222T
Pat_63	Post-Resistance	AVL9	23080	37	7	32582849	32582849	Missense_Mutation	SNP	G	A	24	289	c.190G>A	c.(190-192)GAT>AAT	p.D64N
Pat_63	Post-Resistance	RP9	6100	37	7	33138976	33138976	Missense_Mutation	SNP	G	A	27	144	c.256C>T	c.(256-258)CAT>TAT	p.H86Y
Pat_63	Post-Resistance	BMPER	168667	37	7	33946430	33946430	Missense_Mutation	SNP	G	A	19	117	c.134G>A	c.(133-135)GGT>GAT	p.G45D
Pat_63	Post-Resistance	ANLN	54443	37	7	36446023	36446023	Missense_Mutation	SNP	G	A	16	131	c.721G>A	c.(721-723)GCA>ACA	p.A241T
Pat_63	Post-Resistance	CDK13	8621	37	7	40127849	40127849	Missense_Mutation	SNP	G	A	9	94	c.3154G>A	c.(3154-3156)GAT>AAT	p.D1052N
Pat_63	Post-Resistance	NSUN5P2	260294	37	7	72420385	72420385	Missense_Mutation	SNP	C	T	18	82	c.203G>A	c.(202-204)GGG>GAG	p.G68E
Pat_63	Post-Resistance	MAGI2	9863	37	7	77797274	77797274	Missense_Mutation	SNP	C	T	10	427	c.2555G>A	c.(2554-2556)GGG>GAG	p.G852E
Pat_63	Post-Resistance	AKAP9	10142	37	7	91711873	91711873	Missense_Mutation	SNP	G	A	17	95	c.8057G>A	c.(8056-8058)GGA>GAA	p.G2686E
Pat_63	Post-Resistance	KRIT1	889	37	7	91842696	91842696	Missense_Mutation	SNP	C	T	10	48	c.1838G>A	c.(1837-1839)GGT>GAT	p.G613D
Pat_63	Post-Resistance	ANKIB1	54467	37	7	91981943	91981943	Missense_Mutation	SNP	C	T	43	374	c.1384C>T	c.(1384-1386)CAC>TAC	p.H462Y
Pat_63	Post-Resistance	CALCR	799	37	7	93106879	93106879	Missense_Mutation	SNP	C	T	4	67	c.361G>A	c.(361-363)GAT>AAT	p.D121N
Pat_63	Post-Resistance	AZGP1	563	37	7	99564904	99564904	Missense_Mutation	SNP	G	A	6	14	c.619C>T	c.(619-621)CCC>TCC	p.P207S
Pat_63	Post-Resistance	STAG3	10734	37	7	99778267	99778267	Missense_Mutation	SNP	G	A	6	283	c.88G>A	c.(88-90)GAC>AAC	p.D30N
Pat_63	Post-Resistance	STAG3	10734	37	7	99811421	99811421	Missense_Mutation	SNP	G	A	18	119	c.3661G>A	c.(3661-3663)GAT>AAT	p.D1221N
Pat_63	Post-Resistance	EPHB4	2050	37	7	100404168	100404168	Nonsense_Mutation	SNP	C	T	23	146	c.2358G>A	c.(2356-2358)TGG>TGA	p.W786*
Pat_63	Post-Resistance	MUC17	140453	37	7	100695239	100695239	Missense_Mutation	SNP	T	C	15	117	c.13099T>C	c.(13099-13101)TGC>CGC	p.C4367R
Pat_63	Post-Resistance	MLL5	55904	37	7	104752768	104752768	Missense_Mutation	SNP	C	T	6	182	c.4565C>T	c.(4564-4566)ACA>ATA	p.T1522I
Pat_63	Post-Resistance	PRKAR2B	5577	37	7	106786821	106786821	Missense_Mutation	SNP	G	A	15	171	c.656G>A	c.(655-657)GGG>GAG	p.G219E
Pat_63	Post-Resistance	COG5	10466	37	7	107188753	107188753	Missense_Mutation	SNP	C	T	8	314	c.410G>A	c.(409-411)AGA>AAA	p.R137K
Pat_63	Post-Resistance	THAP5	168451	37	7	108204994	108204994	Missense_Mutation	SNP	G	A	14	126	c.829C>T	c.(829-831)CCT>TCT	p.P277S
Pat_63	Post-Resistance	LRRN3	54674	37	7	110764615	110764615	Missense_Mutation	SNP	C	T	15	59	c.1787C>T	c.(1786-1788)CCC>CTC	p.P596L
Pat_63	Post-Resistance	PPP1R3A	5506	37	7	113518385	113518385	Missense_Mutation	SNP	G	A	25	174	c.2762C>T	c.(2761-2763)ACT>ATT	p.T921I
Pat_63	Post-Resistance	WNT2	7472	37	7	116918397	116918397	Missense_Mutation	SNP	G	A	4	74	c.895C>T	c.(895-897)CGG>TGG	p.R299W
Pat_63	Post-Resistance	PTPRZ1	5803	37	7	121652897	121652897	Missense_Mutation	SNP	G	A	23	138	c.3797G>A	c.(3796-3798)AGT>AAT	p.S1266N
Pat_63	Post-Resistance	WASL	8976	37	7	123332919	123332919	Missense_Mutation	SNP	G	A	20	143	c.829C>T	c.(829-831)CCA>TCA	p.P277S
Pat_63	Post-Resistance	NRF1	4899	37	7	129348961	129348961	Missense_Mutation	SNP	G	A	36	334	c.653G>A	c.(652-654)GGT>GAT	p.G218D
Pat_63	Post-Resistance	TMEM209	84928	37	7	129813752	129813752	Missense_Mutation	SNP	G	A	9	322	c.1372C>T	c.(1372-1374)CTT>TTT	p.L458F
Pat_63	Post-Resistance	EXOC4	60412	37	7	133749105	133749105	Missense_Mutation	SNP	G	A	10	52	c.2749G>A	c.(2749-2751)GGT>AGT	p.G917S
Pat_63	Post-Resistance	NUP205	23165	37	7	135282881	135282881	Missense_Mutation	SNP	C	T	46	365	c.2200C>T	c.(2200-2202)CCT>TCT	p.P734S
Pat_63	Post-Resistance	TBXAS1	6916	37	7	139719873	139719873	Missense_Mutation	SNP	G	A	8	58	c.1717G>A	c.(1717-1719)GTC>ATC	p.V573I
Pat_63	Post-Resistance	BRAF	673	37	7	140453136	140453136	Missense_Mutation	SNP	A	T	51	60	c.1799T>A	c.(1798-1800)GTG>GAG	p.V600E
Pat_63	Post-Resistance	WEE2	494551	37	7	141420800	141420800	Missense_Mutation	SNP	A	G	6	278	c.824A>G	c.(823-825)TAC>TGC	p.Y275C
Pat_63	Post-Resistance	CNTNAP2	26047	37	7	147964124	147964124	Splice_Site	SNP	G	A	19	142	c.3382_splice	c.e21-1	p.L1128_splice
Pat_63	Post-Resistance	SSPO	23145	37	7	149493684	149493684	Missense_Mutation	SNP	G	A	4	23	c.6680G>A	c.(6679-6681)GGG>GAG	p.G2227E

Pat_63	Post-Resistance	MLL3	58508	37	7	151835942	151835942	Missense_Mutation	SNP	G	A	31	241	c.14582C>T	c.(14581-14583)ACT>ATT	p.T4861I
Pat_63	Post-Resistance	MLL3	58508	37	7	151878443	151878443	Missense_Mutation	SNP	G	A	15	109	c.6502C>T	c.(6502-6504)CCT>TCT	p.P2168S
Pat_63	Post-Resistance	MLL3	58508	37	7	151896417	151896417	Missense_Mutation	SNP	G	A	7	64	c.4220C>T	c.(4219-4221)TCC>TTC	p.S1407F
Pat_63	Post-Resistance	RNF32	140545	37	7	156450822	156450822	Missense_Mutation	SNP	G	A	11	73	c.451G>A	c.(451-453)GCA>ACA	p.A151T
Pat_63	Post-Resistance	NOM1	64434	37	7	156759691	156759691	Missense_Mutation	SNP	G	A	12	108	c.2203G>A	c.(2203-2205)GAC>AAC	p.D735N
Pat_63	Post-Resistance	CSMD1	64478	37	8	3565960	3565960	Missense_Mutation	SNP	C	T	4	30	c.985G>A	c.(985-987)GAT>AAT	p.D329N
Pat_63	Post-Resistance	VPS37A	137492	37	8	17132312	17132312	Missense_Mutation	SNP	C	T	9	67	c.487C>T	c.(487-489)CCA>TCA	p.P163S
Pat_63	Post-Resistance	PIWIL2	55124	37	8	22175766	22175766	Missense_Mutation	SNP	G	A	9	56	c.2381G>A	c.(2380-2382)GGC>GAC	p.G794D
Pat_63	Post-Resistance	SLC39A14	23516	37	8	22273459	22273459	Missense_Mutation	SNP	C	T	14	69	c.928C>T	c.(928-930)CTC>TTC	p.L310F
Pat_63	Post-Resistance	SORBS3	10174	37	8	22428736	22428736	Splice_Site	SNP	T	G	6	48	c.1743_splice	c.e18+2	p.Q581_splice
Pat_63	Post-Resistance	NEFM	4741	37	8	24773163	24773163	Missense_Mutation	SNP	G	A	9	70	c.1126G>A	c.(1126-1128)GAA>AAA	p.E376K
Pat_63	Post-Resistance	CHRNA2	1135	37	8	27320857	27320857	Missense_Mutation	SNP	C	T	11	32	c.1103G>A	c.(1102-1104)GGG>GAG	p.G368E
Pat_63	Post-Resistance	TEX15	56154	37	8	30705879	30705879	Missense_Mutation	SNP	C	T	11	41	c.655G>A	c.(655-657)GTT>ATT	p.V219I
Pat_63	Post-Resistance	WHSC1L1	54904	37	8	38133364	38133364	Missense_Mutation	SNP	C	T	9	36	c.4109G>A	c.(4108-4110)TGC>TAC	p.C1370Y
Pat_63	Post-Resistance	AP3M2	10947	37	8	42022650	42022650	Missense_Mutation	SNP	G	A	18	74	c.645G>A	c.(643-645)ATG>ATA	p.M215I
Pat_63	Post-Resistance	POLB	5423	37	8	42227386	42227386	Missense_Mutation	SNP	T	C	3	39	c.793T>C	c.(793-795)TAT>CAT	p.Y265H
Pat_63	Post-Resistance	SLC20A2	6575	37	8	42294934	42294934	Missense_Mutation	SNP	C	T	16	70	c.1096G>A	c.(1096-1098)GGC>AGC	p.G366S
Pat_63	Post-Resistance	MCM4	4173	37	8	48874219	48874219	Missense_Mutation	SNP	C	T	18	45	c.214C>T	c.(214-216)CCT>TCT	p.P72S
Pat_63	Post-Resistance	SNTG1	54212	37	8	51664561	51664561	Missense_Mutation	SNP	G	A	15	329	c.1285G>A	c.(1285-1287)GCT>ACT	p.A429T
Pat_63	Post-Resistance	PXDNL	137902	37	8	52359705	52359705	Missense_Mutation	SNP	C	T	9	397	c.1384G>A	c.(1384-1386)GAA>AAA	p.E462K
Pat_63	Post-Resistance	ARMC1	55156	37	8	66517689	66517689	Missense_Mutation	SNP	C	T	12	442	c.550G>A	c.(550-552)GTG>ATG	p.V184M
Pat_63	Post-Resistance	PDE7A	5150	37	8	66631580	66631580	Missense_Mutation	SNP	T	C	9	594	c.1394A>G	c.(1393-1395)GAT>GGT	p.D465G
Pat_63	Post-Resistance	RRS1	23212	37	8	67341991	67341991	Missense_Mutation	SNP	C	T	9	54	c.625C>T	c.(625-627)CCT>TCT	p.P209S
Pat_63	Post-Resistance	ZFHX4	79776	37	8	77618490	77618490	Missense_Mutation	SNP	C	T	23	76	c.2167C>T	c.(2167-2169)CAC>TAC	p.H723Y
Pat_63	Post-Resistance	ZFHX4	79776	37	8	77618514	77618514	Missense_Mutation	SNP	C	A	12	43	c.2191C>A	c.(2191-2193)CAA>AAA	p.Q731K
Pat_63	Post-Resistance	OSGIN2	734	37	8	90937083	90937083	Missense_Mutation	SNP	G	A	18	110	c.841G>A	c.(841-843)GTG>ATG	p.V281M
Pat_63	Post-Resistance	RAD54B	25788	37	8	95479704	95479704	Missense_Mutation	SNP	G	A	21	80	c.64C>T	c.(64-66)CCT>TCT	p.P22S
Pat_63	Post-Resistance	KIAA1429	25962	37	8	95541537	95541537	Missense_Mutation	SNP	C	T	11	61	c.641G>A	c.(640-642)AGA>AAA	p.R214K
Pat_63	Post-Resistance	UQCRB	7381	37	8	97244030	97244030	Missense_Mutation	SNP	G	A	26	197	c.230C>T	c.(229-231)CCT>CTT	p.P77L
Pat_63	Post-Resistance	MTDH	92140	37	8	98712051	98712051	Missense_Mutation	SNP	C	T	19	219	c.1118C>T	c.(1117-1119)CCC>CTC	p.P373L
Pat_63	Post-Resistance	MTDH	92140	37	8	98731413	98731413	Missense_Mutation	SNP	G	A	14	104	c.1517G>A	c.(1516-1518)AGC>AAC	p.S506N
Pat_63	Post-Resistance	POP1	10940	37	8	99146837	99146837	Missense_Mutation	SNP	C	T	7	184	c.961C>T	c.(961-963)CCT>TCT	p.P321S
Pat_63	Post-Resistance	POP1	10940	37	8	99161211	99161211	Missense_Mutation	SNP	G	A	6	49	c.1879G>A	c.(1879-1881)GGC>AGC	p.G627S
Pat_63	Post-Resistance	FBXO43	286151	37	8	101153317	101153317	Missense_Mutation	SNP	C	T	12	87	c.1165G>A	c.(1165-1167)GAA>AAA	p.E389K
Pat_63	Post-Resistance	ATP6V1C1	528	37	8	104075277	104075277	Splice_Site	SNP	T	C	3	111	c.734_splice	c.e9+2	p.K245_splice
Pat_63	Post-Resistance	RIMS2	9699	37	8	104927751	104927751	Missense_Mutation	SNP	G	A	11	110	c.1175G>A	c.(1174-1176)GGT>GAT	p.G392D
Pat_63	Post-Resistance	PKHD1L1	93035	37	8	110471939	110471939	Missense_Mutation	SNP	C	T	8	76	c.7120C>T	c.(7120-7122)CCT>TCT	p.P2374S
Pat_63	Post-Resistance	ENPP2	5168	37	8	120602792	120602792	Missense_Mutation	SNP	G	A	8	261	c.1160C>T	c.(1159-1161)CCT>CTT	p.P387L
Pat_63	Post-Resistance	TAF2	6873	37	8	120754852	120754852	Missense_Mutation	SNP	G	A	14	328	c.3259C>T	c.(3259-3261)CCC>TCC	p.P1087S
Pat_63	Post-Resistance	MTBP	27085	37	8	121458724	121458724	Missense_Mutation	SNP	C	T	30	750	c.170C>T	c.(169-171)TCA>TTA	p.S57L
Pat_63	Post-Resistance	MTBP	27085	37	8	121502783	121502783	Nonsense_Mutation	SNP	C	T	7	254	c.1420C>T	c.(1420-1422)CAA>TAA	p.Q474*
Pat_63	Post-Resistance	WDR67	93594	37	8	124142446	124142446	Missense_Mutation	SNP	C	T	13	201	c.2279C>T	c.(2278-2280)GCT>GTT	p.A760V
Pat_63	Post-Resistance	ATAD2	29028	37	8	124340756	124340756	Missense_Mutation	SNP	C	T	12	496	c.3542G>A	c.(3541-3543)AGG>AAG	p.R1181K
Pat_63	Post-Resistance	FAM91A1	157769	37	8	124824837	124824837	Missense_Mutation	SNP	G	A	12	489	c.2410G>A	c.(2410-2412)GGT>AGT	p.G804S
Pat_63	Post-Resistance	MTSS1	9788	37	8	125565387	125565387	Missense_Mutation	SNP	G	A	23	829	c.2114C>T	c.(2113-2115)GCC>GTC	p.A705V
Pat_63	Post-Resistance	MYC	4609	37	8	128750635	128750635	Missense_Mutation	SNP	C	T	6	229	c.127C>T	c.(127-129)CCG>TCG	p.P43S
Pat_63	Post-Resistance	TG	7038	37	8	134025851	134025851	Missense_Mutation	SNP	C	T	32	162	c.6404C>T	c.(6403-6405)TCC>TTC	p.S2135F

Pat_63	Post-Resistance	COL22A1	169044	37	8	139603742	139603742	Missense_Mutation	SNP	C	T	5	26	c.4618G>A	c.(4618-4620)GAG>AAG	p.E1540K
Pat_63	Post-Resistance	PTK2	5747	37	8	141874410	141874410	Splice_Site	SNP	C	T	15	424	c.450_splice	c.e5+1	p.Q150_splice
Pat_63	Post-Resistance	PTP4A3	11156	37	8	142437067	142437067	Missense_Mutation	SNP	C	T	23	154	c.227C>T	c.(226-228)CCG>CTG	p.P76L
Pat_63	Post-Resistance	SCRIB	23513	37	8	144891113	144891113	Missense_Mutation	SNP	G	A	9	36	c.1781C>T	c.(1780-1782)ACC>ATC	p.T594I
Pat_63	Post-Resistance	ARHGAP39	80728	37	8	145756120	145756120	Missense_Mutation	SNP	C	T	4	74	c.3023G>A	c.(3022-3024)CGC>CAC	p.R1008H
Pat_63	Post-Resistance	RFX3	5991	37	9	3248135	3248135	Missense_Mutation	SNP	G	A	16	40	c.1865C>T	c.(1864-1866)TCC>TTC	p.S622F
Pat_63	Post-Resistance	SLC24A2	25769	37	9	19622282	19622282	Missense_Mutation	SNP	C	T	5	31	c.946G>A	c.(946-948)GAC>AAC	p.D316N
Pat_63	Post-Resistance	KLHL9	55958	37	9	21333058	21333058	Missense_Mutation	SNP	G	A	10	50	c.1801C>T	c.(1801-1803)CCT>TCT	p.P601S
Pat_63	Post-Resistance	MTAP	4507	37	9	21818104	21818104	Missense_Mutation	SNP	G	A	15	38	c.250G>A	c.(250-252)GAG>AAG	p.E84K
Pat_63	Post-Resistance	BAG1	573	37	9	33264285	33264285	Missense_Mutation	SNP	G	A	3	9	c.388C>T	c.(388-390)CGG>TGG	p.R130W
Pat_63	Post-Resistance	NFX1	4799	37	9	33295050	33295050	Missense_Mutation	SNP	G	A	25	76	c.658G>A	c.(658-660)GAG>AAG	p.E220K
Pat_63	Post-Resistance	NOL6	65083	37	9	33468864	33468864	Missense_Mutation	SNP	C	T	9	172	c.1033G>A	c.(1033-1035)GGT>AGT	p.G345S
Pat_63	Post-Resistance	TLN1	7094	37	9	35711286	35711286	Missense_Mutation	SNP	G	A	6	11	c.3985C>T	c.(3985-3987)CCT>TCT	p.P1329S
Pat_63	Post-Resistance	ZNF658	26149	37	9	40774061	40774061	Missense_Mutation	SNP	G	A	35	179	c.1214C>T	c.(1213-1215)CCC>CTC	p.P405L
Pat_63	Post-Resistance	PIP5K1B	8395	37	9	71606060	71606060	Missense_Mutation	SNP	G	A	12	43	c.1507G>A	c.(1507-1509)GGG>AGG	p.G503R
Pat_63	Post-Resistance	C9orf135	138255	37	9	72435874	72435874	Missense_Mutation	SNP	G	A	14	53	c.79G>A	c.(79-81)GTG>ATG	p.V27M
Pat_63	Post-Resistance	FAM108B1	51104	37	9	74489770	74489770	Missense_Mutation	SNP	C	T	31	159	c.227G>A	c.(226-228)GGC>GAC	p.G76D
Pat_63	Post-Resistance	PCSK5	5125	37	9	78773924	78773924	Missense_Mutation	SNP	C	T	7	299	c.1456C>T	c.(1456-1458)CGC>TGC	p.R486C
Pat_63	Post-Resistance	SECISBP2	79048	37	9	91940421	91940421	Missense_Mutation	SNP	C	G	7	245	c.262C>G	c.(262-264)CAT>GAT	p.H88D
Pat_63	Post-Resistance	SPTLC1	10558	37	9	94809917	94809917	Missense_Mutation	SNP	C	T	9	34	c.962G>A	c.(961-963)AGG>AAG	p.R321K
Pat_63	Post-Resistance	OGN	4969	37	9	95152213	95152213	Missense_Mutation	SNP	G	A	9	70	c.553C>T	c.(553-555)CTT>TTT	p.L185F
Pat_63	Post-Resistance	FGD3	89846	37	9	95778065	95778065	Missense_Mutation	SNP	G	A	22	98	c.1229G>A	c.(1228-1230)GGC>GAC	p.G410D
Pat_63	Post-Resistance	NINJ1	4814	37	9	95887279	95887279	Missense_Mutation	SNP	C	T	14	53	c.370G>A	c.(370-372)GGC>AGC	p.G124S
Pat_63	Post-Resistance	KIAA1529	57653	37	9	100105731	100105731	Missense_Mutation	SNP	A	G	17	48	c.2933A>G	c.(2932-2934)CAT>CGT	p.H978R
Pat_63	Post-Resistance	ABCA1	19	37	9	107594920	107594920	Missense_Mutation	SNP	A	T	8	91	c.1444T>A	c.(1444-1446)TAC>AAC	p.Y482N
Pat_63	Post-Resistance	TXN	7295	37	9	113007065	113007065	Missense_Mutation	SNP	C	T	5	228	c.248G>A	c.(247-249)GGA>GAA	p.G83E
Pat_63	Post-Resistance	CEP110	11064	37	9	123904456	123904456	Missense_Mutation	SNP	G	A	8	30	c.2779G>A	c.(2779-2781)GAG>AAG	p.E927K
Pat_63	Post-Resistance	OLFML2A	169611	37	9	127572430	127572430	Nonsense_Mutation	SNP	G	A	13	40	c.1698G>A	c.(1696-1698)TGG>TGA	p.W566*
Pat_63	Post-Resistance	MAPKAP1	79109	37	9	128322074	128322074	Missense_Mutation	SNP	G	A	4	74	c.686C>T	c.(685-687)GCC>GTC	p.A229V
Pat_63	Post-Resistance	ZBTB43	23099	37	9	129594792	129594792	Missense_Mutation	SNP	G	A	9	30	c.4G>A	c.(4-6)GAG>AAG	p.E2K
Pat_63	Post-Resistance	TRUB2	26995	37	9	131079482	131079482	Missense_Mutation	SNP	G	A	4	19	c.265C>T	c.(265-267)CTC>TTC	p.L89F
Pat_63	Post-Resistance	TOR1B	27348	37	9	132571192	132571192	Missense_Mutation	SNP	G	A	5	72	c.650G>A	c.(649-651)GGC>GAC	p.G217D
Pat_63	Post-Resistance	NUP214	8021	37	9	134003727	134003727	Missense_Mutation	SNP	G	A	17	109	c.250G>A	c.(250-252)GTC>ATC	p.V84I
Pat_63	Post-Resistance	BAT2L1	84726	37	9	134308174	134308174	Missense_Mutation	SNP	C	T	14	50	c.286C>T	c.(286-288)CCA>TCA	p.P96S
Pat_63	Post-Resistance	BAT2L1	84726	37	9	134346214	134346214	Missense_Mutation	SNP	C	T	3	49	c.1951C>T	c.(1951-1953)CCC>TCC	p.P651S
Pat_63	Post-Resistance	GTF3C4	9329	37	9	135553960	135553960	Nonsense_Mutation	SNP	G	A	5	104	c.954G>A	c.(952-954)TGG>TGA	p.W318*
Pat_63	Post-Resistance	UBAC1	10422	37	9	138831520	138831520	Missense_Mutation	SNP	G	A	28	85	c.962C>T	c.(961-963)GCG>GTG	p.A321V
Pat_63	Post-Resistance	WDR85	92715	37	9	140449923	140449923	Missense_Mutation	SNP	G	A	21	114	c.1127C>T	c.(1126-1128)CCC>CTC	p.P376L
Pat_63	Post-Resistance	CACNA1B	774	37	9	140953033	140953033	Missense_Mutation	SNP	G	A	6	33	c.4321G>A	c.(4321-4323)GAC>AAC	p.D1441N
Pat_63	Post-Resistance	CSF2RA	1438	37	X	1422893	1422893	Missense_Mutation	SNP	C	T	20	112	c.1024C>T	c.(1024-1026)CTC>TTC	p.L342F
Pat_63	Post-Resistance	ARSH	347527	37	X	2945417	2945417	Missense_Mutation	SNP	C	T	7	74	c.1100C>T	c.(1099-1101)TCA>TTA	p.S367L
Pat_63	Post-Resistance	PHKA2	5256	37	X	18958136	18958136	Missense_Mutation	SNP	C	T	25	162	c.895G>A	c.(895-897)GAT>AAT	p.D299N
Pat_63	Post-Resistance	CNKSR2	22866	37	X	21450818	21450818	Missense_Mutation	SNP	G	A	5	235	c.317G>A	c.(316-318)AGG>AAG	p.R106K
Pat_63	Post-Resistance	FAM47B	170062	37	X	34961429	34961429	Missense_Mutation	SNP	G	A	4	7	c.481G>A	c.(481-483)GAC>AAC	p.D161N
Pat_63	Post-Resistance	ZNF673	55634	37	X	46322309	46322309	Missense_Mutation	SNP	G	A	15	95	c.142G>A	c.(142-144)GGG>AGG	p.G48R
Pat_63	Post-Resistance	CACNA1F	778	37	X	49062134	49062134	Missense_Mutation	SNP	C	T	10	20	c.5645G>A	c.(5644-5646)GGA>GAA	p.G1882E
Pat_63	Post-Resistance	CACNA1F	778	37	X	49079239	49079239	Missense_Mutation	SNP	C	T	20	59	c.2177G>A	c.(2176-2178)GGC>GAC	p.G726D

Pat_63	Post-Resistance	CACNA1F	778	37	X	49088215	49088215	Missense_Mutation	SNP	C	A	3	48	c.200G>T	c.(199-201)CGG>CTG	p.R67L
Pat_63	Post-Resistance	SHROOM4	57477	37	X	50438894	50438894	Missense_Mutation	SNP	G	A	28	83	c.161C>T	c.(160-162)ACT>ATT	p.T54I
Pat_63	Post-Resistance	FGD1	2245	37	X	54473754	54473754	Missense_Mutation	SNP	C	T	10	22	c.2570G>A	c.(2569-2571)GGA>GAA	p.G857E
Pat_63	Post-Resistance	GNL3L	54552	37	X	54585062	54585062	Missense_Mutation	SNP	A	T	4	4	c.1640A>T	c.(1639-1641)AAT>ATT	p.N547I
Pat_63	Post-Resistance	FAM123B	139285	37	X	63410558	63410558	Missense_Mutation	SNP	G	A	7	11	c.2609C>T	c.(2608-2610)CCT>CTT	p.P870L
Pat_63	Post-Resistance	ZC3H12B	340554	37	X	64722868	64722868	Missense_Mutation	SNP	G	A	4	95	c.2257G>A	c.(2257-2259)GTG>ATG	p.V753M
Pat_63	Post-Resistance	OPHN1	4983	37	X	67283921	67283921	Missense_Mutation	SNP	C	T	12	132	c.1933G>A	c.(1933-1935)GAA>AAA	p.E645K
Pat_63	Post-Resistance	EFNB1	1947	37	X	68060316	68060316	Missense_Mutation	SNP	G	A	3	34	c.860G>A	c.(859-861)AGT>AAT	p.S287N
Pat_63	Post-Resistance	MED12	9968	37	X	70354669	70354669	Missense_Mutation	SNP	G	A	19	65	c.4834G>A	c.(4834-4836)GCA>ACA	p.A1612T
Pat_63	Post-Resistance	PIN4	5303	37	X	71416691	71416691	Missense_Mutation	SNP	A	T	9	44	c.249A>T	c.(247-249)TTA>TTT	p.L83F
Pat_63	Post-Resistance	ATRX	546	37	X	76937029	76937029	Missense_Mutation	SNP	C	T	25	191	c.3719G>A	c.(3718-3720)GGA>GAA	p.G1240E
Pat_63	Post-Resistance	PGAM4	441531	37	X	77224423	77224423	Missense_Mutation	SNP	G	A	22	65	c.713C>T	c.(712-714)ACG>ATG	p.T238M
Pat_63	Post-Resistance	PGK1	5230	37	X	77369261	77369261	Missense_Mutation	SNP	G	A	5	29	c.137G>A	c.(136-138)AGC>AAC	p.S46N
Pat_63	Post-Resistance	HDX	139324	37	X	83581197	83581197	Missense_Mutation	SNP	C	T	13	87	c.1936G>A	c.(1936-1938)GAA>AAA	p.E646K
Pat_63	Post-Resistance	TSC22D3	1831	37	X	106959974	106959974	Missense_Mutation	SNP	G	A	23	87	c.68C>T	c.(67-69)TCC>TTC	p.S23F
Pat_63	Post-Resistance	GUCY2F	2986	37	X	108638689	108638689	Missense_Mutation	SNP	G	A	26	161	c.2305C>T	c.(2305-2307)CCT>TCT	p.P769S
Pat_63	Post-Resistance	PAK3	5063	37	X	110385414	110385414	Missense_Mutation	SNP	G	A	5	168	c.266G>A	c.(265-267)GGG>GAG	p.G89E
Pat_63	Post-Resistance	DOCK11	139818	37	X	117733129	117733129	Missense_Mutation	SNP	C	T	19	117	c.2500C>T	c.(2500-2502)CAT>TAT	p.H834Y
Pat_63	Post-Resistance	RHOXF1	158800	37	X	119249625	119249625	Missense_Mutation	SNP	G	A	6	71	c.148C>T	c.(148-150)CCT>TCT	p.P50S
Pat_63	Post-Resistance	XPNPEP2	7512	37	X	128893157	128893157	Missense_Mutation	SNP	G	A	22	114	c.1369G>A	c.(1369-1371)GAC>AAC	p.D457N
Pat_63	Post-Resistance	XPNPEP2	7512	37	X	128901586	128901586	Missense_Mutation	SNP	G	A	18	91	c.1748G>A	c.(1747-1749)GGG>GAG	p.G583E
Pat_63	Post-Resistance	FRMD7	90167	37	X	131212022	131212022	Missense_Mutation	SNP	C	T	22	81	c.2023G>A	c.(2023-2025)GCC>ACC	p.A675T
Pat_63	Post-Resistance	SLITRK4	139065	37	X	142717099	142717099	Missense_Mutation	SNP	C	T	5	84	c.1826G>A	c.(1825-1827)AGT>AAT	p.S609N
Pat_63	Post-Resistance	SLITRK2	84631	37	X	144904916	144904916	Missense_Mutation	SNP	G	A	20	68	c.973G>A	c.(973-975)GGA>AGA	p.G325R
Pat_63	Post-Resistance	SLITRK2	84631	37	X	144906224	144906224	Missense_Mutation	SNP	G	A	6	235	c.2281G>A	c.(2281-2283)GAG>AAG	p.E761K
Pat_63	Post-Resistance	HCFC1	3054	37	X	153216856	153216856	Missense_Mutation	SNP	G	A	9	356	c.5462C>T	c.(5461-5463)ACC>ATC	p.T1821I
Pat_70	Pre-Treatment	UBE4B	10277	37	1	10228227	10228227	Nonsense_Mutation	SNP	C	T	4	74	c.3232C>T	c.(3232-3234)CAG>TAG	p.Q1078*
Pat_70	Pre-Treatment	NBPF3	84224	37	1	21798107	21798107	Missense_Mutation	SNP	G	C	6	417	c.492G>C	c.(490-492)CAG>CAC	p.Q164H
Pat_70	Pre-Treatment	HSPG2	3339	37	1	22179521	22179521	Missense_Mutation	SNP	G	A	60	94	c.6482C>T	c.(6481-6483)TCA>TTA	p.S2161L
Pat_70	Pre-Treatment	EPHB2	2048	37	1	23191418	23191418	Missense_Mutation	SNP	C	T	66	153	c.1016C>T	c.(1015-1017)TCC>TTC	p.S339F
Pat_70	Pre-Treatment	CSMD2	114784	37	1	34192148	34192148	Missense_Mutation	SNP	C	T	33	79	c.2387G>A	c.(2386-2388)AGA>AAA	p.R796K
Pat_70	Pre-Treatment	HIVEP3	59269	37	1	42041246	42041246	Missense_Mutation	SNP	C	T	134	281	c.5176G>A	c.(5176-5178)GAG>AAG	p.E1726K
Pat_70	Pre-Treatment	CYP4Z1	199974	37	1	47564769	47564769	Missense_Mutation	SNP	G	A	40	107	c.880G>A	c.(880-882)GAA>AAA	p.E294K
Pat_70	Pre-Treatment	C1orf175	374977	37	1	55118930	55118930	Missense_Mutation	SNP	G	A	44	129	c.331G>A	c.(331-333)GAT>AAT	p.D111N
Pat_70	Pre-Treatment	SLC44A5	204962	37	1	75704267	75704267	Missense_Mutation	SNP	C	T	48	104	c.587G>A	c.(586-588)GGA>GAA	p.G196E
Pat_70	Pre-Treatment	CLCA2	9635	37	1	86919106	86919106	Missense_Mutation	SNP	G	A	32	93	c.2210G>A	c.(2209-2211)CGA>CAA	p.R737Q
Pat_70	Pre-Treatment	SLC44A3	126969	37	1	95303356	95303356	Missense_Mutation	SNP	C	T	151	241	c.599C>T	c.(598-600)ACC>ATC	p.T200I
Pat_70	Pre-Treatment	SPAG17	200162	37	1	118548138	118548138	Missense_Mutation	SNP	G	A	28	72	c.4675C>T	c.(4675-4677)CCT>TCT	p.P1559S
Pat_70	Pre-Treatment	HSD3B1	3283	37	1	120057006	120057006	Missense_Mutation	SNP	C	T	35	80	c.860C>T	c.(859-861)CCT>CTT	p.P287L
Pat_70	Pre-Treatment	NBPF9	400818	37	1	144815953	144815953	Missense_Mutation	SNP	A	G	13	372	c.1324A>G	c.(1324-1326)AAT>GAT	p.N442D
Pat_70	Pre-Treatment	NBPF10	100132406	37	1	145360608	145360608	Missense_Mutation	SNP	T	A	30	47	c.9458T>A	c.(9457-9459)CTG>CAG	p.L3153Q
Pat_70	Pre-Treatment	TCHH	7062	37	1	152082320	152082320	Missense_Mutation	SNP	T	C	4	221	c.3373A>G	c.(3373-3375)AGA>GGA	p.R1125G
Pat_70	Pre-Treatment	CRNN	49860	37	1	152382749	152382749	Missense_Mutation	SNP	G	A	6	323	c.809C>T	c.(808-810)ACC>ATC	p.T270I
Pat_70	Pre-Treatment	ATP8B2	57198	37	1	154313359	154313359	Missense_Mutation	SNP	A	T	40	143	c.1163A>T	c.(1162-1164)TAC>TTC	p.Y388F
Pat_70	Pre-Treatment	ADAR	103	37	1	154574460	154574460	Missense_Mutation	SNP	C	A	4	104	c.658G>T	c.(658-660)GCC>TCC	p.A220S
Pat_70	Pre-Treatment	ADAR	103	37	1	154574475	154574475	Missense_Mutation	SNP	C	T	4	111	c.643G>A	c.(643-645)GGT>AGT	p.G215S
Pat_70	Pre-Treatment	DCST2	127579	37	1	154999135	154999135	Missense_Mutation	SNP	G	A	30	81	c.1399C>T	c.(1399-1401)CGT>TGT	p.R467C

Pat_70	Pre-Treatment	OR10K2	391107	37	1	158390397	158390397	Missense_Mutation	SNP	G	A	55	112	c.260C>T	c.(259-261)TCC>TTC	p.S87F
Pat_70	Pre-Treatment	RCSD1	92241	37	1	167654698	167654698	Missense_Mutation	SNP	C	T	39	142	c.149C>T	c.(148-150)TCC>TTC	p.S50F
Pat_70	Pre-Treatment	CACNA1E	777	37	1	181741296	181741296	Missense_Mutation	SNP	G	A	35	156	c.5068G>A	c.(5068-5070)GAG>AAG	p.E1690K
Pat_70	Pre-Treatment	KCNT2	343450	37	1	196436849	196436849	Missense_Mutation	SNP	G	A	17	58	c.527C>T	c.(526-528)GCC>GTC	p.A176V
Pat_70	Pre-Treatment	CFHR2	3080	37	1	196927146	196927146	Missense_Mutation	SNP	G	A	54	165	c.556G>A	c.(556-558)GGT>AGT	p.G186S
Pat_70	Pre-Treatment	CFHR5	81494	37	1	196977679	196977679	Missense_Mutation	SNP	G	A	20	41	c.1576G>A	c.(1576-1578)GAT>AAT	p.D526N
Pat_70	Pre-Treatment	CRB1	23418	37	1	197390318	197390318	Missense_Mutation	SNP	G	A	21	65	c.1360G>A	c.(1360-1362)GGA>AGA	p.G454R
Pat_70	Pre-Treatment	PRELP	5549	37	1	203452937	203452937	Missense_Mutation	SNP	G	A	5	214	c.625G>A	c.(625-627)GAC>AAC	p.D209N
Pat_70	Pre-Treatment	CNST	163882	37	1	246797858	246797858	Missense_Mutation	SNP	C	T	4	211	c.787C>T	c.(787-789)CGG>TGG	p.R263W
Pat_70	Pre-Treatment	MBL2	4153	37	10	54530495	54530495	Missense_Mutation	SNP	C	T	33	22	c.239G>A	c.(238-240)GGA>GAA	p.G80E
Pat_70	Pre-Treatment	CTNNA3	29119	37	10	68535278	68535278	Missense_Mutation	SNP	C	T	47	53	c.1052G>A	c.(1051-1053)GGA>GAA	p.G351E
Pat_70	Pre-Treatment	CTNNA3	29119	37	10	68979585	68979585	Missense_Mutation	SNP	C	T	24	24	c.623G>A	c.(622-624)CGA>CAA	p.R208Q
Pat_70	Pre-Treatment	C10orf27	219793	37	10	72541712	72541712	Missense_Mutation	SNP	A	T	44	53	c.122T>A	c.(121-123)CTG>CAG	p.L41Q
Pat_70	Pre-Treatment	PCGF5	84333	37	10	93008318	93008318	Splice_Site	SNP	G	A	4	95	c.265_splice	c.e4+1	p.Q89_splice
Pat_70	Pre-Treatment	BTBD16	118663	37	10	124045710	124045710	Missense_Mutation	SNP	C	T	36	54	c.332C>T	c.(331-333)GCC>GTC	p.A111V
Pat_70	Pre-Treatment	CDHR5	53841	37	11	618833	618833	Missense_Mutation	SNP	G	C	5	165	c.1726C>G	c.(1726-1728)CCA>GCA	p.P576A
Pat_70	Pre-Treatment	NLRP10	338322	37	11	7981691	7981691	Missense_Mutation	SNP	C	T	30	70	c.1468G>A	c.(1468-1470)GAG>AAG	p.E490K
Pat_70	Pre-Treatment	STK33	65975	37	11	8494797	8494797	Missense_Mutation	SNP	T	G	26	67	c.252A>C	c.(250-252)AGA>AGC	p.R84S
Pat_70	Pre-Treatment	RAG2	5897	37	11	36615559	36615559	Missense_Mutation	SNP	G	A	55	84	c.160C>T	c.(160-162)CAT>TAT	p.H54Y
Pat_70	Pre-Treatment	LRP4	4038	37	11	46911963	46911963	Missense_Mutation	SNP	C	T	22	69	c.1780G>A	c.(1780-1782)GAT>AAT	p.D594N
Pat_70	Pre-Treatment	MYBPC3	4607	37	11	47374188	47374188	Missense_Mutation	SNP	G	A	4	240	c.11C>T	c.(10-12)CCG>CTG	p.P4L
Pat_70	Pre-Treatment	AHNAK	79026	37	11	62295321	62295321	Missense_Mutation	SNP	T	C	8	667	c.6568A>G	c.(6568-6570)AAC>GAC	p.N2190D
Pat_70	Pre-Treatment	AHNAK	79026	37	11	62295516	62295516	Missense_Mutation	SNP	G	T	9	679	c.6373C>A	c.(6373-6375)CAC>AAC	p.H2125N
Pat_70	Pre-Treatment	AHNAK	79026	37	11	62295549	62295549	Missense_Mutation	SNP	C	T	8	582	c.6340G>A	c.(6340-6342)GCC>ACC	p.A2114T
Pat_70	Pre-Treatment	INTS4	92105	37	11	77614645	77614645	Missense_Mutation	SNP	T	G	3	49	c.2038A>C	c.(2038-2040)AAT>CAT	p.N680H
Pat_70	Pre-Treatment	TRPC6	7225	37	11	101375149	101375149	Missense_Mutation	SNP	G	A	4	87	c.551C>T	c.(550-552)CCG>CTG	p.P184L
Pat_70	Pre-Treatment	GRIA4	2893	37	11	105797546	105797546	Missense_Mutation	SNP	G	A	4	213	c.1927G>A	c.(1927-1929)GCT>ACT	p.A643T
Pat_70	Pre-Treatment	OR6T1	219874	37	11	123813604	123813604	Missense_Mutation	SNP	C	T	39	117	c.942G>A	c.(940-942)ATG>ATA	p.M314I
Pat_70	Pre-Treatment	CCDC15	80071	37	11	124857495	124857495	Missense_Mutation	SNP	A	C	5	257	c.1373A>C	c.(1372-1374)CAC>CCC	p.H458P
Pat_70	Pre-Treatment	NCAPD3	23310	37	11	134079064	134079064	Missense_Mutation	SNP	G	A	121	283	c.769C>T	c.(769-771)CAT>TAT	p.H257Y
Pat_70	Pre-Treatment	ERC1	23085	37	12	1553842	1553842	Missense_Mutation	SNP	C	T	82	93	c.3139C>T	c.(3139-3141)CCA>TCA	p.P1047S
Pat_70	Pre-Treatment	CACNA1C	775	37	12	2602410	2602410	Missense_Mutation	SNP	G	A	4	205	c.971G>A	c.(970-972)CGG>CAG	p.R324Q
Pat_70	Pre-Treatment	KLHDC5	57542	37	12	27944688	27944688	Missense_Mutation	SNP	G	A	132	252	c.920G>A	c.(919-921)GGA>GAA	p.G307E
Pat_70	Pre-Treatment	KRT5	3852	37	12	52913539	52913539	Missense_Mutation	SNP	G	A	93	235	c.542C>T	c.(541-543)TCC>TTC	p.S181F
Pat_70	Pre-Treatment	KRT73	319101	37	12	53011993	53011993	Nonsense_Mutation	SNP	G	A	46	148	c.316C>T	c.(316-318)CAG>TAG	p.Q106*
Pat_70	Pre-Treatment	NAV3	89795	37	12	78443859	78443859	Missense_Mutation	SNP	C	T	15	41	c.2110C>T	c.(2110-2112)CGT>TGT	p.R704C
Pat_70	Pre-Treatment	SYT1	6857	37	12	79693212	79693212	Missense_Mutation	SNP	G	A	49	128	c.691G>A	c.(691-693)GAT>AAT	p.D231N
Pat_70	Pre-Treatment	FAM71C	196472	37	12	100042134	100042134	Missense_Mutation	SNP	A	G	48	106	c.182A>G	c.(181-183)GAC>GGC	p.D61G
Pat_70	Pre-Treatment	STAB2	55576	37	12	104100576	104100576	Missense_Mutation	SNP	G	A	18	74	c.4003G>A	c.(4003-4005)GAA>AAA	p.E1335K
Pat_70	Pre-Treatment	PWP1	11137	37	12	108098465	108098465	Nonsense_Mutation	SNP	C	T	4	221	c.1018C>T	c.(1018-1020)CGA>TGA	p.R340*
Pat_70	Pre-Treatment	RPH3A	22895	37	12	113307722	113307722	Missense_Mutation	SNP	G	A	36	99	c.674G>A	c.(673-675)GGG>GAG	p.G225E
Pat_70	Pre-Treatment	RIMBP2	23504	37	12	130926895	130926895	Nonsense_Mutation	SNP	C	T	28	81	c.951G>A	c.(949-951)TGG>TGA	p.W317*
Pat_70	Pre-Treatment	MIPEP	4285	37	13	24453425	24453425	Missense_Mutation	SNP	G	A	109	281	c.521C>T	c.(520-522)TCC>TTC	p.S174F
Pat_70	Pre-Treatment	HS6ST3	266722	37	13	97485024	97485024	Missense_Mutation	SNP	G	A	20	78	c.988G>A	c.(988-990)GAG>AAG	p.E330K
Pat_70	Pre-Treatment	OR4M1	441670	37	14	20249284	20249284	Missense_Mutation	SNP	C	T	41	153	c.803C>T	c.(802-804)TCC>TTC	p.S268F
Pat_70	Pre-Treatment	OR4N2	390429	37	14	20296056	20296056	Missense_Mutation	SNP	T	C	66	275	c.449T>C	c.(448-450)CTT>CCT	p.L150P
Pat_70	Pre-Treatment	C14orf93	60686	37	14	23467809	23467809	Missense_Mutation	SNP	C	T	16	56	c.424G>A	c.(424-426)GAA>AAA	p.E142K

Pat_70	Pre-Treatment	NUBPL	80224	37	14	32068535	32068535	Missense_Mutation	SNP	C	T	34	72	c.332C>T	c.(331-333)CCT>CTT	p.P111L
Pat_70	Pre-Treatment	SOCS4	122809	37	14	55510090	55510090	Missense_Mutation	SNP	C	T	51	118	c.331C>T	c.(331-333)CGG>TGG	p.R111W
Pat_70	Pre-Treatment	MAP3K9	4293	37	14	71216698	71216698	Missense_Mutation	SNP	G	A	29	100	c.1102C>T	c.(1102-1104)CTT>TTT	p.L368F
Pat_70	Pre-Treatment	FOXN3	1112	37	14	89628855	89628855	Missense_Mutation	SNP	G	A	28	79	c.1376C>T	c.(1375-1377)TCC>TTC	p.S459F
Pat_70	Pre-Treatment	OR4N3P	390539	37	15	22413825	22413825	Missense_Mutation	SNP	C	T	73	280	c.124C>T	c.(124-126)CGC>TGC	p.R42C
Pat_70	Pre-Treatment	SPTBN5	51332	37	15	42160775	42160775	Missense_Mutation	SNP	C	T	18	54	c.5773G>A	c.(5773-5775)GCC>ACC	p.A1925T
Pat_70	Pre-Treatment	CKMT1A	548596	37	15	43991226	43991226	Missense_Mutation	SNP	G	A	4	209	c.1193G>A	c.(1192-1194)CGG>CAG	p.R398Q
Pat_70	Pre-Treatment	DTWD1	56986	37	15	49924411	49924411	Missense_Mutation	SNP	C	T	37	76	c.320C>T	c.(319-321)ACT>ATT	p.T107I
Pat_70	Pre-Treatment	SLC27A2	11001	37	15	50515227	50515227	Nonsense_Mutation	SNP	G	A	48	117	c.1038G>A	c.(1036-1038)TGG>TGA	p.W346*
Pat_70	Pre-Treatment	CYP19A1	1588	37	15	51503047	51503047	Missense_Mutation	SNP	C	T	46	129	c.1470G>A	c.(1468-1470)ATG>ATA	p.M490I
Pat_70	Pre-Treatment	HERC1	8925	37	15	63932386	63932386	Nonsense_Mutation	SNP	C	A	47	75	c.11866G>T	c.(11866-11868)GAA>TAA	p.E3956*
Pat_70	Pre-Treatment	AGBL1	123624	37	15	87066090	87066090	Missense_Mutation	SNP	C	T	55	128	c.2467C>T	c.(2467-2469)CCC>TCC	p.P823S
Pat_70	Pre-Treatment	GRIN2A	2903	37	16	9923396	9923396	Missense_Mutation	SNP	C	T	29	67	c.1891G>A	c.(1891-1893)GTA>ATA	p.V631I
Pat_70	Pre-Treatment	SNN	8303	37	16	11770033	11770033	Missense_Mutation	SNP	C	T	3	67	c.118C>T	c.(118-120)CGC>TGC	p.R40C
Pat_70	Pre-Treatment	TMC7	79905	37	16	19041577	19041577	Missense_Mutation	SNP	G	A	18	57	c.743G>A	c.(742-744)GGA>GAA	p.G248E
Pat_70	Pre-Treatment	USP31	57478	37	16	23116791	23116791	Missense_Mutation	SNP	A	T	35	81	c.1060T>A	c.(1060-1062)TCT>ACT	p.S354T
Pat_70	Pre-Treatment	ABCC12	94160	37	16	48119553	48119553	Missense_Mutation	SNP	C	T	53	119	c.3779G>A	c.(3778-3780)GGG>GAG	p.G1260E
Pat_70	Pre-Treatment	GPR114	221188	37	16	57608779	57608779	Missense_Mutation	SNP	G	A	14	73	c.1261G>A	c.(1261-1263)GGC>AGC	p.G421S
Pat_70	Pre-Treatment	ATMIN	23300	37	16	81078133	81078133	Missense_Mutation	SNP	T	C	61	122	c.2030T>C	c.(2029-2031)TTA>TCA	p.L677S
Pat_70	Pre-Treatment	PKD1L2	114780	37	16	81253771	81253771	Missense_Mutation	SNP	C	T	33	75	c.205G>A	c.(205-207)GAA>AAA	p.E69K
Pat_70	Pre-Treatment	KLHL36	79786	37	16	84690846	84690846	Missense_Mutation	SNP	G	A	4	136	c.433G>A	c.(433-435)GAG>AAG	p.E145K
Pat_70	Pre-Treatment	GALNS	2588	37	16	88904094	88904094	Nonsense_Mutation	SNP	C	A	21	95	c.502G>T	c.(502-504)GGA>TGA	p.G168*
Pat_70	Pre-Treatment	TRPV3	162514	37	17	3446887	3446887	Missense_Mutation	SNP	T	C	3	127	c.347A>G	c.(346-348)AAG>AGG	p.K116R
Pat_70	Pre-Treatment	C17orf85	55421	37	17	3717742	3717742	Missense_Mutation	SNP	G	A	15	29	c.1501C>T	c.(1501-1503)CCG>TCG	p.P501S
Pat_70	Pre-Treatment	UBE2G1	7326	37	17	4192683	4192683	Missense_Mutation	SNP	A	G	55	130	c.268T>C	c.(268-270)TGC>CGC	p.C90R
Pat_70	Pre-Treatment	ALOX15	246	37	17	4536765	4536765	Missense_Mutation	SNP	C	T	43	124	c.1192G>A	c.(1192-1194)GAA>AAA	p.E398K
Pat_70	Pre-Treatment	USP6	9098	37	17	5066291	5066291	Nonsense_Mutation	SNP	C	T	63	181	c.3028C>T	c.(3028-3030)CAG>TAG	p.Q1010*
Pat_70	Pre-Treatment	MYH2	4620	37	17	10442646	10442646	Missense_Mutation	SNP	G	A	71	248	c.1292C>T	c.(1291-1293)GCC>GTC	p.A431V
Pat_70	Pre-Treatment	CCDC144A	9720	37	17	16631054	16631054	Missense_Mutation	SNP	G	A	9	29	c.2105G>A	c.(2104-2106)AGA>AAA	p.R702K
Pat_70	Pre-Treatment	RAB11FIP4	84440	37	17	29850600	29850600	Missense_Mutation	SNP	G	A	120	228	c.1000G>A	c.(1000-1002)GAC>AAC	p.D334N
Pat_70	Pre-Treatment	SLFN13	146857	37	17	33769266	33769266	Nonsense_Mutation	SNP	C	T	39	47	c.1238G>A	c.(1237-1239)TGG>TAG	p.W413*
Pat_70	Pre-Treatment	CDK12	51755	37	17	37618868	37618868	Missense_Mutation	SNP	G	A	41	63	c.544G>A	c.(544-546)GAG>AAG	p.E182K
Pat_70	Pre-Treatment	KRTAP4-11	653240	37	17	39274424	39274424	Missense_Mutation	SNP	G	C	14	179	c.144C>G	c.(142-144)AGC>AGG	p.S48R
Pat_70	Pre-Treatment	KRTAP4-12	83755	37	17	39279998	39279998	Missense_Mutation	SNP	C	A	6	244	c.377G>T	c.(376-378)TGC>TTC	p.C126F
Pat_70	Pre-Treatment	SLC26A11	284129	37	17	78226478	78226478	Missense_Mutation	SNP	C	T	25	53	c.1784C>T	c.(1783-1785)TCC>TTC	p.S595F
Pat_70	Pre-Treatment	CLUL1	27098	37	18	618042	618042	Nonsense_Mutation	SNP	G	A	40	103	c.42G>A	c.(40-42)TGG>TGA	p.W14*
Pat_70	Pre-Treatment	TXNDC2	84203	37	18	9887155	9887155	Missense_Mutation	SNP	A	G	5	334	c.679A>G	c.(679-681)ACC>GCC	p.T227A
Pat_70	Pre-Treatment	MEX3C	51320	37	18	48703064	48703064	Missense_Mutation	SNP	G	A	22	77	c.1637C>T	c.(1636-1638)CCT>CTT	p.P546L
Pat_70	Pre-Treatment	DCC	1630	37	18	50832089	50832089	Missense_Mutation	SNP	G	A	32	62	c.2053G>A	c.(2053-2055)GGA>AGA	p.G685R
Pat_70	Pre-Treatment	SERPINB5	5268	37	18	61156661	61156661	Missense_Mutation	SNP	G	A	30	45	c.388G>A	c.(388-390)GGT>AGT	p.G130S
Pat_70	Pre-Treatment	ARRDC5	645432	37	19	4896825	4896825	Missense_Mutation	SNP	G	A	29	98	c.359C>T	c.(358-360)CCT>CTT	p.P120L
Pat_70	Pre-Treatment	C3	718	37	19	6702545	6702545	Missense_Mutation	SNP	C	T	36	95	c.2291G>A	c.(2290-2292)CGA>CAA	p.R764Q
Pat_70	Pre-Treatment	MUC16	94025	37	19	9048764	9048764	Missense_Mutation	SNP	A	G	6	156	c.32867T>C	c.(32866-32868)CTT>CCT	p.L10956P
Pat_70	Pre-Treatment	MUC16	94025	37	19	9048771	9048771	Missense_Mutation	SNP	A	G	6	147	c.32860T>C	c.(32860-32862)TTT>CTT	p.F10954L
Pat_70	Pre-Treatment	MUC16	94025	37	19	9073848	9073848	Missense_Mutation	SNP	G	A	16	75	c.13598C>T	c.(13597-13599)CCT>CTT	p.P4533L
Pat_70	Pre-Treatment	ZNF560	147741	37	19	9577542	9577542	Missense_Mutation	SNP	C	T	51	99	c.2081G>A	c.(2080-2082)CGA>CAA	p.R694Q
Pat_70	Pre-Treatment	ZNF844	284391	37	19	12187307	12187307	Missense_Mutation	SNP	G	C	8	323	c.1372G>C	c.(1372-1374)GAT>CAT	p.D458H

Pat_70	Pre-Treatment	CD97	976	37	19	14499612	14499612	Missense_Mutation	SNP	C	T	93	224	c.172C>T	c.(172-174)CCG>TCG	p.P58S
Pat_70	Pre-Treatment	CYP4F12	66002	37	19	15789078	15789078	Missense_Mutation	SNP	C	T	47	116	c.206C>T	c.(205-207)CCT>CTT	p.P69L
Pat_70	Pre-Treatment	OR10H2	26538	37	19	15839002	15839002	Nonsense_Mutation	SNP	G	A	39	104	c.149G>A	c.(148-150)TGG>TAG	p.W50*
Pat_70	Pre-Treatment	ZNF208	7757	37	19	22154417	22154417	Missense_Mutation	SNP	G	A	5	174	c.3035C>T	c.(3034-3036)CCC>CTC	p.P1012L
Pat_70	Pre-Treatment	ZNF98	148198	37	19	22585641	22585641	Missense_Mutation	SNP	C	T	59	143	c.203G>A	c.(202-204)GGA>GAA	p.G68E
Pat_70	Pre-Treatment	ZNF681	148213	37	19	23926533	23926533	Missense_Mutation	SNP	C	T	4	99	c.1819G>A	c.(1819-1821)GGA>AGA	p.G607R
Pat_70	Pre-Treatment	LSM14A	26065	37	19	34706032	34706032	Missense_Mutation	SNP	G	A	4	113	c.542G>A	c.(541-543)CGC>CAC	p.R181H
Pat_70	Pre-Treatment	KIRREL2	84063	37	19	36349734	36349734	Missense_Mutation	SNP	G	A	29	85	c.490G>A	c.(490-492)GGG>AGG	p.G164R
Pat_70	Pre-Treatment	PRX	57716	37	19	40902620	40902620	Missense_Mutation	SNP	G	C	7	275	c.1639C>G	c.(1639-1641)CAG>GAG	p.Q547E
Pat_70	Pre-Treatment	AXL	558	37	19	41743885	41743885	Missense_Mutation	SNP	G	A	17	79	c.820G>A	c.(820-822)GGA>AGA	p.G274R
Pat_70	Pre-Treatment	MARK4	57787	37	19	45797680	45797680	Missense_Mutation	SNP	C	T	22	54	c.1568C>T	c.(1567-1569)CCG>CTG	p.P523L
Pat_70	Pre-Treatment	ZNF836	162962	37	19	52659056	52659056	Missense_Mutation	SNP	T	A	8	202	c.1880A>T	c.(1879-1881)AAT>ATT	p.N627I
Pat_70	Pre-Treatment	ZNF836	162962	37	19	52659243	52659243	Missense_Mutation	SNP	A	C	5	291	c.1693T>G	c.(1693-1695)TAC>GAC	p.Y565D
Pat_70	Pre-Treatment	ZNF816A	125893	37	19	53453890	53453890	Missense_Mutation	SNP	G	C	6	548	c.1138C>G	c.(1138-1140)CAG>GAG	p.Q380E
Pat_70	Pre-Treatment	ZNF845	91664	37	19	53855197	53855197	Missense_Mutation	SNP	G	A	8	382	c.1269G>A	c.(1267-1269)ATG>ATA	p.M423I
Pat_70	Pre-Treatment	ZNF845	91664	37	19	53856761	53856761	Missense_Mutation	SNP	T	C	5	129	c.2833T>C	c.(2833-2835)TGT>CGT	p.C945R
Pat_70	Pre-Treatment	ZNF761	388561	37	19	53959137	53959137	Missense_Mutation	SNP	G	T	5	262	c.1376G>T	c.(1375-1377)CGT>CTT	p.R459L
Pat_70	Pre-Treatment	ZNF761	388561	37	19	53959151	53959151	Missense_Mutation	SNP	C	A	7	232	c.1390C>A	c.(1390-1392)CAA>AAA	p.Q464K
Pat_70	Pre-Treatment	SBK2	646643	37	19	56041171	56041171	Missense_Mutation	SNP	C	T	11	26	c.976G>A	c.(976-978)GGG>AGG	p.G326R
Pat_70	Pre-Treatment	ZNF776	284309	37	19	58265885	58265885	Missense_Mutation	SNP	G	A	4	213	c.1387G>A	c.(1387-1389)GGA>AGA	p.G463R
Pat_70	Pre-Treatment	ZNF776	284309	37	19	58265928	58265928	Missense_Mutation	SNP	G	A	5	208	c.1430G>A	c.(1429-1431)CGA>CAA	p.R477Q
Pat_70	Pre-Treatment	PXDN	7837	37	2	1651966	1651966	Missense_Mutation	SNP	C	T	87	193	c.3586G>A	c.(3586-3588)GAG>AAG	p.E1196K
Pat_70	Pre-Treatment	NT5C1B	93034	37	2	18768282	18768282	Missense_Mutation	SNP	C	T	53	90	c.278G>A	c.(277-279)GGC>GAC	p.G93D
Pat_70	Pre-Treatment	CGREF1	10669	37	2	27324405	27324405	Missense_Mutation	SNP	T	C	6	243	c.694A>G	c.(694-696)AAA>GAA	p.K232E
Pat_70	Pre-Treatment	C2orf16	84226	37	2	27804634	27804634	Missense_Mutation	SNP	G	A	9	706	c.5195G>A	c.(5194-5196)AGA>AAA	p.R1732K
Pat_70	Pre-Treatment	XDH	7498	37	2	31571779	31571779	Missense_Mutation	SNP	G	A	7	37	c.3037C>T	c.(3037-3039)CCT>TCT	p.P1013S
Pat_70	Pre-Treatment	RPL23AP32	56969	37	2	54756736	54756737	Missense_Mutation	DNP	TT	CC	8	150	c.254_255TT>CC	c.(253-255)TTT>TCC	p.F85S
Pat_70	Pre-Treatment	C2orf86	51057	37	2	63631776	63631776	Missense_Mutation	SNP	C	T	4	188	c.842G>A	c.(841-843)CGC>CAC	p.R281H
Pat_70	Pre-Treatment	STARD7	56910	37	2	96858127	96858127	Missense_Mutation	SNP	G	A	75	178	c.823C>T	c.(823-825)CCC>TCC	p.P275S
Pat_70	Pre-Treatment	SLC9A2	6549	37	2	103324769	103324769	Missense_Mutation	SNP	G	A	70	155	c.2260G>A	c.(2260-2262)GAA>AAA	p.E754K
Pat_70	Pre-Treatment	WASH2P	375260	37	2	114355129	114355129	Missense_Mutation	SNP	G	A	4	56	c.506G>A	c.(505-507)CGC>CAC	p.R169H
Pat_70	Pre-Treatment	CNTNAP5	129684	37	2	125504925	125504925	Nonsense_Mutation	SNP	C	T	97	181	c.2194C>T	c.(2194-2196)CAG>TAG	p.Q732*
Pat_70	Pre-Treatment	CACNB4	785	37	2	152739821	152739821	Missense_Mutation	SNP	C	T	66	186	c.211G>A	c.(211-213)GAA>AAA	p.E71K
Pat_70	Pre-Treatment	GRB14	2888	37	2	165353583	165353583	Nonsense_Mutation	SNP	C	T	18	47	c.1317G>A	c.(1315-1317)TGG>TGA	p.W439*
Pat_70	Pre-Treatment	LRP2	4036	37	2	170028534	170028534	Missense_Mutation	SNP	C	T	53	120	c.11254G>A	c.(11254-11256)GAA>AAA	p.E3752K
Pat_70	Pre-Treatment	TTN	7273	37	2	179613368	179613368	Missense_Mutation	SNP	C	T	45	133	c.13759G>A	c.(13759-13761)GAT>AAT	p.D4587N
Pat_70	Pre-Treatment	COL5A2	1290	37	2	189917518	189917518	Missense_Mutation	SNP	C	T	19	48	c.2672G>A	c.(2671-2673)GGT>GAT	p.G891D
Pat_70	Pre-Treatment	CRYGA	1418	37	2	209027960	209027960	Missense_Mutation	SNP	C	T	35	79	c.220G>A	c.(220-222)GAC>AAC	p.D74N
Pat_70	Pre-Treatment	CPS1	1373	37	2	211457670	211457670	Missense_Mutation	SNP	T	C	5	188	c.1154T>C	c.(1153-1155)ATA>ACA	p.I385T
Pat_70	Pre-Treatment	IKZF2	22807	37	2	213878586	213878586	Missense_Mutation	SNP	C	T	31	91	c.785G>A	c.(784-786)AGA>AAA	p.R262K
Pat_70	Pre-Treatment	IRS1	3667	37	2	227662115	227662115	Missense_Mutation	SNP	G	A	4	195	c.1340C>T	c.(1339-1341)CCG>CTG	p.P447L
Pat_70	Pre-Treatment	HJURP	55355	37	2	234750117	234750117	Nonsense_Mutation	SNP	G	A	70	160	c.1309C>T	c.(1309-1311)CGA>TGA	p.R437*
Pat_70	Pre-Treatment	TRPM8	79054	37	2	234879017	234879017	Missense_Mutation	SNP	G	A	254	345	c.2302G>A	c.(2302-2304)GAG>AAG	p.E768K
Pat_70	Pre-Treatment	COL6A3	1293	37	2	238245090	238245090	Missense_Mutation	SNP	T	G	77	163	c.8653A>C	c.(8653-8655)ACC>CCC	p.T2885P
Pat_70	Pre-Treatment	ZNF343	79175	37	20	2463928	2463928	Missense_Mutation	SNP	C	T	4	200	c.1679G>A	c.(1678-1680)CGG>CAG	p.R560Q
Pat_70	Pre-Treatment	C20orf194	25943	37	20	3305557	3305557	Missense_Mutation	SNP	G	A	55	141	c.1247C>T	c.(1246-1248)CCG>CTG	p.P416L
Pat_70	Pre-Treatment	SIGLEC1	6614	37	20	3673529	3673529	Missense_Mutation	SNP	G	A	17	31	c.3758C>T	c.(3757-3759)TCC>TTC	p.S1253F

Pat_70	Pre-Treatment	MAVS	57506	37	20	3845347	3845347	Missense_Mutation	SNP	G	A	4	232	c.1070G>A	c.(1069-1071)GGC>GAC	p.G357D
Pat_70	Pre-Treatment	PLCB4	5332	37	20	9404500	9404500	Nonsense_Mutation	SNP	C	T	30	47	c.2389C>T	c.(2389-2391)CGA>TGA	p.R797*
Pat_70	Pre-Treatment	FRG1B	284802	37	20	29625934	29625934	Missense_Mutation	SNP	C	T	13	158	c.88C>T	c.(88-90)CAT>TAT	p.H30Y
Pat_70	Pre-Treatment	FRG1B	284802	37	20	29625941	29625941	Missense_Mutation	SNP	A	T	9	180	c.95A>T	c.(94-96)GAT>GTT	p.D32V
Pat_70	Pre-Treatment	FRG1B	284802	37	20	29625947	29625947	Missense_Mutation	SNP	T	C	11	184	c.101T>C	c.(100-102)ATT>ACT	p.I34T
Pat_70	Pre-Treatment	FRG1B	284802	37	20	29625956	29625956	Missense_Mutation	SNP	G	A	7	187	c.110G>A	c.(109-111)AGA>AAA	p.R37K
Pat_70	Pre-Treatment	FRG1B	284802	37	20	29628243	29628243	Missense_Mutation	SNP	T	C	6	286	c.155T>C	c.(154-156)TTG>TCG	p.L52S
Pat_70	Pre-Treatment	FRG1B	284802	37	20	29628245	29628245	Missense_Mutation	SNP	G	A	6	285	c.157G>A	c.(157-159)GCC>ACC	p.A53T
Pat_70	Pre-Treatment	FRG1B	284802	37	20	29628296	29628296	Nonsense_Mutation	SNP	A	T	5	159	c.208A>T	c.(208-210)AAA>TAA	p.K70*
Pat_70	Pre-Treatment	PPP1R16B	26051	37	20	37546839	37546839	Missense_Mutation	SNP	C	T	83	203	c.1234C>T	c.(1234-1236)CCT>TCT	p.P412S
Pat_70	Pre-Treatment	BAGE2	85319	37	21	11049621	11049621	Nonsense_Mutation	SNP	G	A	10	230	c.280C>T	c.(280-282)CGA>TGA	p.R94*
Pat_70	Pre-Treatment	NCAM2	4685	37	21	22656657	22656657	Missense_Mutation	SNP	C	T	22	65	c.274C>T	c.(274-276)CGT>TGT	p.R92C
Pat_70	Pre-Treatment	TRAPPC10	7109	37	21	45518395	45518395	Missense_Mutation	SNP	C	T	39	107	c.3326C>T	c.(3325-3327)TCG>TTG	p.S1109L
Pat_70	Pre-Treatment	CCT8L2	150160	37	22	17071886	17071886	Missense_Mutation	SNP	C	T	41	67	c.1555G>A	c.(1555-1557)GAA>AAA	p.E519K
Pat_70	Pre-Treatment	MED15	51586	37	22	20938666	20938666	Missense_Mutation	SNP	A	C	3	195	c.1757A>C	c.(1756-1758)CAA>CCA	p.Q586P
Pat_70	Pre-Treatment	ZNF280A	129025	37	22	22868747	22868747	Missense_Mutation	SNP	G	A	47	189	c.1208C>T	c.(1207-1209)TCG>TTG	p.S403L
Pat_70	Pre-Treatment	GNAZ	2781	37	22	23465487	23465487	Missense_Mutation	SNP	C	T	27	74	c.937C>T	c.(937-939)CGC>TGC	p.R313C
Pat_70	Pre-Treatment	CHEK2	11200	37	22	29091840	29091841	Missense_Mutation	DNP	TG	CA	9	63	.1116_1117CA>TC	114-1119)TCCAAG>TCTG	p.K373E
Pat_70	Pre-Treatment	SERHL2	253190	37	22	42952530	42952530	Missense_Mutation	SNP	C	T	45	245	c.359C>T	c.(358-360)ACC>ATC	p.T120I
Pat_70	Pre-Treatment	PACSIN2	11252	37	22	43267422	43267422	Missense_Mutation	SNP	G	A	4	207	c.1402C>T	c.(1402-1404)CGC>TGC	p.R468C
Pat_70	Pre-Treatment	ATG7	10533	37	3	11406161	11406161	Missense_Mutation	SNP	G	T	107	212	c.1828G>T	c.(1828-1830)GAT>TAT	p.D610Y
Pat_70	Pre-Treatment	IQSEC1	9922	37	3	12977694	12977694	Missense_Mutation	SNP	C	T	38	122	c.864G>A	c.(862-864)ATG>ATA	p.M288I
Pat_70	Pre-Treatment	SCN11A	11280	37	3	38936214	38936214	Missense_Mutation	SNP	G	A	25	71	c.2645C>T	c.(2644-2646)CCC>CTC	p.P882L
Pat_70	Pre-Treatment	CCR1	1230	37	3	46245516	46245516	Missense_Mutation	SNP	C	T	43	161	c.289G>A	c.(289-291)GAT>AAT	p.D97N
Pat_70	Pre-Treatment	COL7A1	1294	37	3	48610780	48610780	Missense_Mutation	SNP	C	T	27	98	c.6620G>A	c.(6619-6621)GGG>GAG	p.G2207E
Pat_70	Pre-Treatment	ZMYND10	51364	37	3	50378896	50378896	Nonsense_Mutation	SNP	C	T	26	138	c.1268G>A	c.(1267-1269)TGG>TAG	p.W423*
Pat_70	Pre-Treatment	TKT	7086	37	3	53269119	53269119	Missense_Mutation	SNP	G	A	4	237	c.509C>T	c.(508-510)GCC>GTC	p.A170V
Pat_70	Pre-Treatment	ERC2	26059	37	3	55922574	55922574	Missense_Mutation	SNP	C	T	55	98	c.2407G>A	c.(2407-2409)GAG>AAG	p.E803K
Pat_70	Pre-Treatment	THOC7	80145	37	3	63825432	63825432	Missense_Mutation	SNP	G	A	3	49	c.37C>T	c.(37-39)CGT>TGT	p.R13C
Pat_70	Pre-Treatment	ROBO2	6092	37	3	77645802	77645802	Missense_Mutation	SNP	C	T	43	107	c.2755C>T	c.(2755-2757)CCC>TCC	p.P919S
Pat_70	Pre-Treatment	RG9MTD1	54931	37	3	101284175	101284175	Missense_Mutation	SNP	G	A	47	134	c.550G>A	c.(550-552)GAT>AAT	p.D184N
Pat_70	Pre-Treatment	PHLDB2	90102	37	3	111638006	111638006	Missense_Mutation	SNP	G	A	51	129	c.1807G>A	c.(1807-1809)GAA>AAA	p.E603K
Pat_70	Pre-Treatment	FBXO40	51725	37	3	121342006	121342006	Missense_Mutation	SNP	C	T	40	62	c.1730C>T	c.(1729-1731)CCC>CTC	p.P577L
Pat_70	Pre-Treatment	CPNE4	131034	37	3	131261456	131261456	Missense_Mutation	SNP	C	T	31	87	c.1484G>A	c.(1483-1485)GGA>GAA	p.G495E
Pat_70	Pre-Treatment	IGSF10	285313	37	3	151154847	151154847	Missense_Mutation	SNP	C	T	43	90	c.7502G>A	c.(7501-7503)AGA>AAA	p.R2501K
Pat_70	Pre-Treatment	PIK3CA	5290	37	3	178943827	178943827	Nonsense_Mutation	SNP	C	T	3	94	c.2494C>T	c.(2494-2496)CGA>TGA	p.R832*
Pat_70	Pre-Treatment	USP13	8975	37	3	179481949	179481949	Missense_Mutation	SNP	G	A	4	190	c.2252G>A	c.(2251-2253)CGA>CAA	p.R751Q
Pat_70	Pre-Treatment	LIPH	200879	37	3	185251431	185251431	Missense_Mutation	SNP	C	T	48	120	c.454G>A	c.(454-456)GGA>AGA	p.G152R
Pat_70	Pre-Treatment	SDHAP2	727956	37	3	195404650	195404650	Missense_Mutation	SNP	T	A	17	77	c.207T>A	c.(205-207)AAT>AAA	p.N69K
Pat_70	Pre-Treatment	ZNF732	654254	37	4	265307	265307	Missense_Mutation	SNP	T	C	5	129	c.1336A>G	c.(1336-1338)AAA>GAA	p.K446E
Pat_70	Pre-Treatment	DRD5	1816	37	4	9784887	9784887	Missense_Mutation	SNP	C	T	15	84	c.1234C>T	c.(1234-1236)CAC>TAC	p.H412Y
Pat_70	Pre-Treatment	APBB2	323	37	4	40818158	40818158	Missense_Mutation	SNP	G	A	100	208	c.2228C>T	c.(2227-2229)TCC>TTC	p.S743F
Pat_70	Pre-Treatment	AMBN	258	37	4	71468527	71468527	Missense_Mutation	SNP	G	A	22	48	c.583G>A	c.(583-585)GAT>AAT	p.D195N
Pat_70	Pre-Treatment	RASSF6	166824	37	4	74451034	74451034	Missense_Mutation	SNP	C	T	37	78	c.526G>A	c.(526-528)GAA>AAA	p.E176K
Pat_70	Pre-Treatment	GK2	2712	37	4	80329231	80329231	Missense_Mutation	SNP	C	T	43	67	c.124G>A	c.(124-126)GAA>AAA	p.E42K
Pat_70	Pre-Treatment	AFF1	4299	37	4	88048208	88048208	Missense_Mutation	SNP	C	T	51	143	c.2821C>T	c.(2821-2823)CCA>TCA	p.P941S
Pat_70	Pre-Treatment	COL25A1	84570	37	4	109745338	109745338	Missense_Mutation	SNP	C	T	24	96	c.1837G>A	c.(1837-1839)GGA>AGA	p.G613R

Pat_70	Pre-Treatment	PDCD6	10016	37	5	314553	314553	Missense_Mutation	SNP	C	T	4	144	c.499C>T	c.(499-501)CGT>TGT	p.R167C
Pat_70	Pre-Treatment	CMYA5	202333	37	5	79024953	79024953	Missense_Mutation	SNP	C	T	34	91	c.365C>T	c.(364-366)TCC>TTC	p.S122F
Pat_70	Pre-Treatment	FBXL17	64839	37	5	107216866	107216866	Missense_Mutation	SNP	C	A	4	164	c.1837G>T	c.(1837-1839)GGG>TGG	p.G613W
Pat_70	Pre-Treatment	ADAMTS19	171019	37	5	128956432	128956432	Missense_Mutation	SNP	G	A	105	237	c.1582G>A	c.(1582-1584)GAT>AAT	p.D528N
Pat_70	Pre-Treatment	FAM53C	51307	37	5	137680684	137680684	Missense_Mutation	SNP	C	T	51	79	c.307C>T	c.(307-309)CCA>TCA	p.P103S
Pat_70	Pre-Treatment	KDM3B	51780	37	5	137722215	137722215	Missense_Mutation	SNP	T	G	28	69	c.1285T>G	c.(1285-1287)TCC>GCC	p.S429A
Pat_70	Pre-Treatment	PCDHA1	56147	37	5	140166227	140166227	Missense_Mutation	SNP	C	T	31	76	c.352C>T	c.(352-354)CAT>TAT	p.H118Y
Pat_70	Pre-Treatment	SH3RF2	153769	37	5	145393506	145393506	Missense_Mutation	SNP	C	T	77	157	c.941C>T	c.(940-942)TCT>TTT	p.S314F
Pat_70	Pre-Treatment	PPARGC1B	133522	37	5	149215849	149215849	Missense_Mutation	SNP	C	T	96	303	c.1831C>T	c.(1831-1833)CCG>TCG	p.P611S
Pat_70	Pre-Treatment	SLC6A7	6534	37	5	149581944	149581944	Missense_Mutation	SNP	C	T	39	86	c.893C>T	c.(892-894)TCC>TTC	p.S298F
Pat_70	Pre-Treatment	G3BP1	10146	37	5	151183497	151183497	Nonsense_Mutation	SNP	C	T	35	91	c.1246C>T	c.(1246-1248)CGA>TGA	p.R416*
Pat_70	Pre-Treatment	CYFIP2	26999	37	5	156766230	156766230	Missense_Mutation	SNP	C	G	89	167	c.2551C>G	c.(2551-2553)CTC>GTC	p.L851V
Pat_70	Pre-Treatment	COL23A1	91522	37	5	177686748	177686748	Missense_Mutation	SNP	C	T	44	123	c.703G>A	c.(703-705)GGT>AGT	p.G235S
Pat_70	Pre-Treatment	BMP6	654	37	6	7861833	7861833	Splice_Site	SNP	G	A	44	197	c.1006_splice	c.e3+1	p.G336_splice
Pat_70	Pre-Treatment	SYCP2L	221711	37	6	10959052	10959052	Missense_Mutation	SNP	T	G	28	85	c.2199T>G	c.(2197-2199)AAT>AAG	p.N733K
Pat_70	Pre-Treatment	OR2W1	26692	37	6	29012220	29012220	Missense_Mutation	SNP	G	A	88	117	c.733C>T	c.(733-735)CTT>TTT	p.L245F
Pat_70	Pre-Treatment	LRFN2	57497	37	6	40400182	40400182	Missense_Mutation	SNP	G	A	24	54	c.671C>T	c.(670-672)TCG>TTG	p.S224L
Pat_70	Pre-Treatment	TREM1	54210	37	6	41250375	41250375	Nonsense_Mutation	SNP	C	T	56	197	c.164G>A	c.(163-165)TGG>TAG	p.W55*
Pat_70	Pre-Treatment	BMP5	653	37	6	55620459	55620459	Missense_Mutation	SNP	G	T	24	145	c.1237C>A	c.(1237-1239)CAC>AAC	p.H413N
Pat_70	Pre-Treatment	FILIP1	27145	37	6	76063346	76063346	Missense_Mutation	SNP	C	T	4	167	c.538G>A	c.(538-540)GTA>ATA	p.V180I
Pat_70	Pre-Treatment	C6orf182	285753	37	6	109468047	109468047	Missense_Mutation	SNP	C	T	18	58	c.247C>T	c.(247-249)CTT>TTT	p.L83F
Pat_70	Pre-Treatment	LAMA2	3908	37	6	129837370	129837370	Missense_Mutation	SNP	C	T	132	292	c.9247C>T	c.(9247-9249)CCG>TCG	p.P3083S
Pat_70	Pre-Treatment	VNN1	8876	37	6	133013664	133013664	Missense_Mutation	SNP	C	T	20	47	c.886G>A	c.(886-888)GAG>AAG	p.E296K
Pat_70	Pre-Treatment	SYNE1	23345	37	6	152529226	152529226	Missense_Mutation	SNP	T	C	3	184	c.22705A>G	.(22705-22707)AGG>GG	p.R7569G
Pat_70	Pre-Treatment	C6orf118	168090	37	6	165715360	165715360	Missense_Mutation	SNP	C	T	32	65	c.451G>A	c.(451-453)GCT>ACT	p.A151T
Pat_70	Pre-Treatment	TTLL2	83887	37	6	167755036	167755036	Missense_Mutation	SNP	G	A	31	94	c.1648G>A	c.(1648-1650)GAT>AAT	p.D550N
Pat_70	Pre-Treatment	FRMD1	79981	37	6	168464403	168464403	Missense_Mutation	SNP	G	A	3	86	c.682C>T	c.(682-684)CGG>TGG	p.R228W
Pat_70	Pre-Treatment	DNAH11	8701	37	7	21913039	21913039	Missense_Mutation	SNP	G	A	31	62	c.12136G>A	c.(12136-12138)GAA>AA	p.E4046K
Pat_70	Pre-Treatment	STK31	56164	37	7	23808674	23808674	Missense_Mutation	SNP	G	A	38	75	c.1477G>A	c.(1477-1479)GAA>AAA	p.E493K
Pat_70	Pre-Treatment	ADCY1	107	37	7	45717567	45717567	Missense_Mutation	SNP	A	T	49	88	c.1705A>T	c.(1705-1707)ATC>TTC	p.I569F
Pat_70	Pre-Treatment	TNS3	64759	37	7	47333423	47333423	Missense_Mutation	SNP	C	T	49	92	c.3680G>A	c.(3679-3681)GGA>GAA	p.G1227E
Pat_70	Pre-Treatment	ZNF727	442319	37	7	63538758	63538758	Missense_Mutation	SNP	G	A	23	38	c.1331G>A	c.(1330-1332)AGA>AAA	p.R444K
Pat_70	Pre-Treatment	CCL24	6369	37	7	75442699	75442699	Missense_Mutation	SNP	G	A	18	59	c.116C>T	c.(115-117)TCC>TTC	p.S39F
Pat_70	Pre-Treatment	ZAN	7455	37	7	100349878	100349878	Missense_Mutation	SNP	C	T	6	245	c.2150C>T	c.(2149-2151)CCC>CTC	p.P717L
Pat_70	Pre-Treatment	MUC17	140453	37	7	100680525	100680525	Missense_Mutation	SNP	T	C	8	758	c.5828T>C	c.(5827-5829)ATC>ACC	p.I1943T
Pat_70	Pre-Treatment	MUC17	140453	37	7	100682156	100682156	Missense_Mutation	SNP	A	G	7	823	c.7459A>G	c.(7459-7461)ATG>GTG	p.M2487V
Pat_70	Pre-Treatment	CADPS2	93664	37	7	121985672	121985672	Nonsense_Mutation	SNP	G	A	32	59	c.3568C>T	c.(3568-3570)CGA>TGA	p.R1190*
Pat_70	Pre-Treatment	JHDM1D	80853	37	7	139793899	139793899	Missense_Mutation	SNP	G	A	46	134	c.2414C>T	c.(2413-2415)TCC>TTC	p.S805F
Pat_70	Pre-Treatment	BRAF	673	37	7	140453136	140453136	Missense_Mutation	SNP	A	T	39	85	c.1799T>A	c.(1798-1800)GTG>GAG	p.V600E
Pat_70	Pre-Treatment	ZYX	7791	37	7	143085653	143085653	Missense_Mutation	SNP	C	T	33	113	c.1216C>T	c.(1216-1218)CAC>TAC	p.H406Y
Pat_70	Pre-Treatment	GALNTL5	168391	37	7	151711870	151711870	Missense_Mutation	SNP	G	A	29	73	c.1168G>A	c.(1168-1170)GAA>AAA	p.E390K
Pat_70	Pre-Treatment	ADAMDEC1	27299	37	8	24249837	24249837	Missense_Mutation	SNP	C	T	26	52	c.151C>T	c.(151-153)CAC>TAC	p.H51Y
Pat_70	Pre-Treatment	PXDNL	137902	37	8	52384783	52384783	Missense_Mutation	SNP	C	T	51	128	c.776G>A	c.(775-777)GGA>GAA	p.G259E
Pat_70	Pre-Treatment	PCMTD1	115294	37	8	52733185	52733186	Missense_Mutation	DNP	CC	TT	7	234	c.799_800GG>AA	c.(799-801)GGG>AAG	p.G267K
Pat_70	Pre-Treatment	VPS13B	157680	37	8	100733271	100733271	Missense_Mutation	SNP	T	A	5	256	c.7121T>A	c.(7120-7122)CTA>CAA	p.L2374Q
Pat_70	Pre-Treatment	DCAF13	25879	37	8	104452461	104452461	Missense_Mutation	SNP	C	T	5	282	c.1504C>T	c.(1504-1506)CGC>TGC	p.R502C
Pat_70	Pre-Treatment	PKHD1L1	93035	37	8	110520058	110520058	Missense_Mutation	SNP	C	T	50	87	c.11161C>T	c.(11161-11163)CCT>TCT	p.P3721S

Pat_70	Pre-Treatment	FER1L6	654463	37	8	125107259	125107259	Missense_Mutation	SNP	G	A	23	91	c.4675G>A	c.(4675-4677)GAT>AAT	p.D1559N
Pat_70	Pre-Treatment	ST3GAL1	6482	37	8	134472126	134472126	Missense_Mutation	SNP	C	T	144	307	c.904G>A	c.(904-906)GAG>AAG	p.E302K
Pat_70	Pre-Treatment	FAM135B	51059	37	8	139164898	139164898	Missense_Mutation	SNP	G	A	66	146	c.1820C>T	c.(1819-1821)TCA>TTA	p.S607L
Pat_70	Pre-Treatment	MAPK15	225689	37	8	144803941	144803941	Missense_Mutation	SNP	G	A	34	88	c.1349G>A	c.(1348-1350)GGA>GAA	p.G450E
Pat_70	Pre-Treatment	CNTLN	54875	37	9	17330685	17330685	Missense_Mutation	SNP	C	T	92	254	c.1397C>T	c.(1396-1398)TCT>TTT	p.S466F
Pat_70	Pre-Treatment	TAF1L	138474	37	9	32632655	32632655	Missense_Mutation	SNP	G	A	53	129	c.2923C>T	c.(2923-2925)CCC>TCC	p.P975S
Pat_70	Pre-Treatment	RNF20	56254	37	9	104302572	104302572	Missense_Mutation	SNP	C	T	104	184	c.217C>T	c.(217-219)CGT>TGT	p.R73C
Pat_70	Pre-Treatment	OR13F1	138805	37	9	107266613	107266613	Nonsense_Mutation	SNP	C	T	36	67	c.70C>T	c.(70-72)CAG>TAG	p.Q24*
Pat_70	Pre-Treatment	OR13C9	286362	37	9	107380230	107380230	Missense_Mutation	SNP	G	A	25	84	c.256C>T	c.(256-258)CTT>TTT	p.L86F
Pat_70	Pre-Treatment	TXNDC8	255220	37	9	113096507	113096507	Missense_Mutation	SNP	G	A	20	55	c.118C>T	c.(118-120)CCT>TCT	p.P40S
Pat_70	Pre-Treatment	DBC1	1620	37	9	121929721	121929721	Missense_Mutation	SNP	G	A	47	146	c.1927C>T	c.(1927-1929)CCC>TCC	p.P643S
Pat_70	Pre-Treatment	C9orf119	375757	37	9	131038446	131038446	Missense_Mutation	SNP	G	A	32	108	c.22G>A	c.(22-24)GAC>AAC	p.D8N
Pat_70	Pre-Treatment	COL5A1	1289	37	9	137715280	137715280	Missense_Mutation	SNP	G	A	45	119	c.4663G>A	c.(4663-4665)GGT>AGT	p.G1555S
Pat_70	Pre-Treatment	CACNA1B	774	37	9	140948299	140948299	Missense_Mutation	SNP	C	T	179	384	c.3809C>T	c.(3808-3810)GCT>GTT	p.A1270V
Pat_70	Pre-Treatment	NLGN4X	57502	37	X	6069369	6069369	Missense_Mutation	SNP	C	T	34	104	c.139G>A	c.(139-141)GTT>ATT	p.V47I
Pat_70	Pre-Treatment	TBL1X	6907	37	X	9673050	9673050	Missense_Mutation	SNP	G	A	73	181	c.1132G>A	c.(1132-1134)GAC>AAC	p.D378N
Pat_70	Pre-Treatment	FRMPD4	9758	37	X	12734739	12734739	Missense_Mutation	SNP	G	A	90	191	c.2161G>A	c.(2161-2163)GAT>AAT	p.D721N
Pat_70	Pre-Treatment	FANCB	2187	37	X	14882788	14882789	Missense_Mutation	DNP	CC	TT	60	133	c.844_845GG>AA	c.(844-846)GGA>AAA	p.G282K
Pat_70	Pre-Treatment	FANCB	2187	37	X	14883544	14883544	Missense_Mutation	SNP	C	T	52	110	c.89G>A	c.(88-90)GGA>GAA	p.G30E
Pat_70	Pre-Treatment	ASB9	140462	37	X	15262747	15262747	Missense_Mutation	SNP	G	A	39	122	c.766C>T	c.(766-768)CCT>TCT	p.P256S
Pat_70	Pre-Treatment	EIF1AX	1964	37	X	20156735	20156735	Missense_Mutation	SNP	C	T	87	133	c.22G>A	c.(22-24)GGA>AGA	p.G8R
Pat_70	Pre-Treatment	DMD	1756	37	X	32466644	32466644	Missense_Mutation	SNP	C	T	13	74	c.3715G>A	c.(3715-3717)GAA>AAA	p.E1239K
Pat_70	Pre-Treatment	ATP6AP2	10159	37	X	40456507	40456507	Missense_Mutation	SNP	C	T	17	72	c.307C>T	c.(307-309)CCT>TCT	p.P103S
Pat_70	Pre-Treatment	TEX11	56159	37	X	69849480	69849480	Missense_Mutation	SNP	G	A	52	103	c.1634C>T	c.(1633-1635)GCT>GTT	p.A545V
Pat_70	Pre-Treatment	SERPINA7	6906	37	X	105280609	105280609	Missense_Mutation	SNP	C	A	67	186	c.441G>T	c.(439-441)TTG>TTT	p.L147F
Pat_70	Pre-Treatment	RNF128	79589	37	X	106016347	106016347	Missense_Mutation	SNP	C	T	46	80	c.689C>T	c.(688-690)TCT>TTT	p.S230F
Pat_70	Pre-Treatment	ODZ1	10178	37	X	123554529	123554529	Missense_Mutation	SNP	C	T	45	106	c.4593G>A	c.(4591-4593)ATG>ATA	p.M1531I
Pat_70	Pre-Treatment	ODZ1	10178	37	X	124028163	124028163	Nonsense_Mutation	SNP	G	A	49	89	c.517C>T	c.(517-519)CAA>TAA	p.Q173*
Pat_70	Pre-Treatment	BCORL1	63035	37	X	129185837	129185837	Missense_Mutation	SNP	G	A	77	275	c.4699G>A	c.(4699-4701)GAA>AAA	p.E1567K
Pat_70	Pre-Treatment	MCF2	4168	37	X	138708412	138708412	Missense_Mutation	SNP	T	A	34	97	c.627A>T	c.(625-627)AAA>AAT	p.K209N
Pat_70	Pre-Treatment	CNGA2	1260	37	X	150912105	150912105	Missense_Mutation	SNP	A	G	36	80	c.1130A>G	c.(1129-1131)AAC>AGC	p.N377S
Pat_70	Pre-Treatment	GABRE	2564	37	X	151131042	151131042	Missense_Mutation	SNP	G	A	61	147	c.416C>T	c.(415-417)TCT>TTT	p.S139F
Pat_70	Pre-Treatment	CSAG1	158511	37	X	151908796	151908796	Missense_Mutation	SNP	C	T	88	196	c.35C>T	c.(34-36)ACT>ATT	p.T12I
Pat_70	Pre-Treatment	IDH3G	3421	37	X	153052393	153052393	Missense_Mutation	SNP	G	A	4	231	c.787C>T	c.(787-789)CGG>TGG	p.R263W
Pat_70	Post-Resistance	HSPG2	3339	37	1	22179521	22179521	Missense_Mutation	SNP	G	A	26	225	c.6482C>T	c.(6481-6483)TCA>TTA	p.S2161L
Pat_70	Post-Resistance	EPHB2	2048	37	1	23191418	23191418	Missense_Mutation	SNP	C	T	78	438	c.1016C>T	c.(1015-1017)TCC>TTC	p.S339F
Pat_70	Post-Resistance	CSMD2	114784	37	1	34192148	34192148	Missense_Mutation	SNP	C	T	47	264	c.2387G>A	c.(2386-2388)AGA>AAA	p.R796K
Pat_70	Post-Resistance	SLC44A5	204962	37	1	75704267	75704267	Missense_Mutation	SNP	C	T	48	332	c.587G>A	c.(586-588)GGA>GAA	p.G196E
Pat_70	Post-Resistance	CLCA2	9635	37	1	86919106	86919106	Missense_Mutation	SNP	G	A	42	215	c.2210G>A	c.(2209-2211)CGA>CAA	p.R737Q
Pat_70	Post-Resistance	NRAS	4893	37	1	115256528	115256528	Missense_Mutation	SNP	T	G	68	682	c.183A>C	c.(181-183)CAA>CAC	p.Q61H
Pat_70	Post-Resistance	SPAG17	200162	37	1	118548138	118548138	Missense_Mutation	SNP	G	A	36	273	c.4675C>T	c.(4675-4677)CCT>TCT	p.P1559S
Pat_70	Post-Resistance	HSD3B1	3283	37	1	120057006	120057006	Missense_Mutation	SNP	C	T	44	284	c.860C>T	c.(859-861)CCT>CTT	p.P287L
Pat_70	Post-Resistance	NBPF10	100132406	37	1	145359049	145359049	Missense_Mutation	SNP	A	G	4	29	c.9214A>G	c.(9214-9216)AAA>GAA	p.K3072E
Pat_70	Post-Resistance	ATP8B2	57198	37	1	154313359	154313359	Missense_Mutation	SNP	A	T	36	372	c.1163A>T	c.(1162-1164)TAC>TTC	p.Y388F
Pat_70	Post-Resistance	ADAR	103	37	1	154574460	154574460	Missense_Mutation	SNP	C	A	6	262	c.658G>T	c.(658-660)GCC>TCC	p.A220S
Pat_70	Post-Resistance	ADAR	103	37	1	154574475	154574475	Missense_Mutation	SNP	C	T	6	270	c.643G>A	c.(643-645)GGT>AGT	p.G215S
Pat_70	Post-Resistance	DCST2	127579	37	1	154999135	154999135	Missense_Mutation	SNP	G	A	55	189	c.1399C>T	c.(1399-1401)CGT>TGT	p.R467C

Pat_70	Post-Resistance	OR10K2	391107	37	1	158390397	158390397	Missense_Mutation	SNP	G	A	146	500	c.260C>T	c.(259-261)TCC>TTC	p.S87F
Pat_70	Post-Resistance	RCSD1	92241	37	1	167654698	167654698	Missense_Mutation	SNP	C	T	71	309	c.149C>T	c.(148-150)TCC>TTC	p.S50F
Pat_70	Post-Resistance	CACNA1E	777	37	1	181741296	181741296	Missense_Mutation	SNP	G	A	128	527	c.5068G>A	c.(5068-5070)GAG>AAG	p.E1690K
Pat_70	Post-Resistance	SMG7	9887	37	1	183495876	183495876	Missense_Mutation	SNP	A	G	11	790	c.458A>G	c.(457-459)CAC>CGC	p.H153R
Pat_70	Post-Resistance	HMCN1	83872	37	1	185969302	185969302	Missense_Mutation	SNP	G	A	67	416	c.4000G>A	c.(4000-4002)GGG>AGG	p.G1334R
Pat_70	Post-Resistance	KCNT2	343450	37	1	196436849	196436849	Missense_Mutation	SNP	G	A	21	263	c.527C>T	c.(526-528)GCC>GTC	p.A176V
Pat_70	Post-Resistance	CFHR2	3080	37	1	196927146	196927146	Missense_Mutation	SNP	G	A	69	638	c.556G>A	c.(556-558)GGT>AGT	p.G186S
Pat_70	Post-Resistance	CRB1	23418	37	1	197390318	197390318	Missense_Mutation	SNP	G	A	51	203	c.1360G>A	c.(1360-1362)GGA>AGA	p.G454R
Pat_70	Post-Resistance	MBL2	4153	37	10	54530495	54530495	Missense_Mutation	SNP	C	T	31	126	c.239G>A	c.(238-240)GGA>GAA	p.G80E
Pat_70	Post-Resistance	CTNNA3	29119	37	10	68535278	68535278	Missense_Mutation	SNP	C	T	44	325	c.1052G>A	c.(1051-1053)GGA>GAA	p.G351E
Pat_70	Post-Resistance	CTNNA3	29119	37	10	68979585	68979585	Missense_Mutation	SNP	C	T	37	149	c.623G>A	c.(622-624)CGA>CAA	p.R208Q
Pat_70	Post-Resistance	C10orf27	219793	37	10	72541712	72541712	Missense_Mutation	SNP	A	T	51	236	c.122T>A	c.(121-123)CTG>CAG	p.L41Q
Pat_70	Post-Resistance	PTEN	5728	37	10	89717672	89717672	Nonsense_Mutation	SNP	C	T	76	431	c.697C>T	c.(697-699)CGA>TGA	p.R233*
Pat_70	Post-Resistance	C10orf79	80217	37	10	105945872	105945872	Missense_Mutation	SNP	C	T	6	271	c.1870G>A	c.(1870-1872)GGT>AGT	p.G624S
Pat_70	Post-Resistance	BTBD16	118663	37	10	124045710	124045710	Missense_Mutation	SNP	C	T	54	223	c.332C>T	c.(331-333)GCC>GTC	p.A111V
Pat_70	Post-Resistance	CDHR5	53841	37	11	618833	618833	Missense_Mutation	SNP	G	C	8	363	c.1726C>G	c.(1726-1728)CCA>GCA	p.P576A
Pat_70	Post-Resistance	OR10A5	144124	37	11	6867706	6867706	Missense_Mutation	SNP	T	A	100	555	c.793T>A	c.(793-795)TCA>ACA	p.S265T
Pat_70	Post-Resistance	NLRP10	338322	37	11	7981691	7981691	Missense_Mutation	SNP	C	T	45	268	c.1468G>A	c.(1468-1470)GAG>AAG	p.E490K
Pat_70	Post-Resistance	STK33	65975	37	11	8494797	8494797	Missense_Mutation	SNP	T	G	41	271	c.252A>C	c.(250-252)AGA>AGC	p.R84S
Pat_70	Post-Resistance	RAG2	5897	37	11	36615559	36615559	Missense_Mutation	SNP	G	A	33	282	c.160C>T	c.(160-162)CAT>TAT	p.H54Y
Pat_70	Post-Resistance	LRP4	4038	37	11	46911963	46911963	Missense_Mutation	SNP	C	T	20	138	c.1780G>A	c.(1780-1782)GAT>AAT	p.D594N
Pat_70	Post-Resistance	C11orf88	399949	37	11	111386256	111386256	Missense_Mutation	SNP	T	G	24	322	c.247T>G	c.(247-249)TCT>GCT	p.S83A
Pat_70	Post-Resistance	OR6T1	219874	37	11	123813604	123813604	Missense_Mutation	SNP	C	T	43	376	c.942G>A	c.(940-942)ATG>ATA	p.M314I
Pat_70	Post-Resistance	OR10G9	219870	37	11	123893738	123893738	Missense_Mutation	SNP	G	C	10	634	c.19G>C	c.(19-21)GTG>CTG	p.V7L
Pat_70	Post-Resistance	CCDC15	80071	37	11	124857495	124857495	Missense_Mutation	SNP	A	C	7	564	c.1373A>C	c.(1372-1374)CAC>CCC	p.H458P
Pat_70	Post-Resistance	CCDC15	80071	37	11	124857585	124857585	Missense_Mutation	SNP	C	A	8	564	c.1463C>A	c.(1462-1464)CCC>CAC	p.P488H
Pat_70	Post-Resistance	NCAPD3	23310	37	11	134079064	134079064	Missense_Mutation	SNP	G	A	58	508	c.769C>T	c.(769-771)CAT>TAT	p.H257Y
Pat_70	Post-Resistance	ERC1	23085	37	12	1553842	1553842	Missense_Mutation	SNP	C	T	72	422	c.3139C>T	c.(3139-3141)CCA>TCA	p.P1047S
Pat_70	Post-Resistance	KLHDC5	57542	37	12	27944688	27944688	Missense_Mutation	SNP	G	A	126	658	c.920G>A	c.(919-921)GGA>GAA	p.G307E
Pat_70	Post-Resistance	TROAP	10024	37	12	49724313	49724313	Missense_Mutation	SNP	G	T	7	173	c.1685G>T	c.(1684-1686)AGT>ATT	p.S562I
Pat_70	Post-Resistance	KRT5	3852	37	12	52913539	52913539	Missense_Mutation	SNP	G	A	86	661	c.542C>T	c.(541-543)TCC>TTC	p.S181F
Pat_70	Post-Resistance	KRT73	319101	37	12	53011993	53011993	Nonsense_Mutation	SNP	G	A	55	414	c.316C>T	c.(316-318)CAG>TAG	p.Q106*
Pat_70	Post-Resistance	SYT1	6857	37	12	79693212	79693212	Missense_Mutation	SNP	G	A	66	465	c.691G>A	c.(691-693)GAT>AAT	p.D231N
Pat_70	Post-Resistance	FAM71C	196472	37	12	100042134	100042134	Missense_Mutation	SNP	A	G	63	343	c.182A>G	c.(181-183)GAC>GGC	p.D61G
Pat_70	Post-Resistance	STAB2	55576	37	12	104100576	104100576	Missense_Mutation	SNP	G	A	33	271	c.4003G>A	c.(4003-4005)GAA>AAA	p.E1335K
Pat_70	Post-Resistance	RPH3A	22895	37	12	113307722	113307722	Missense_Mutation	SNP	G	A	36	311	c.674G>A	c.(673-675)GGG>GAG	p.G225E
Pat_70	Post-Resistance	RIMBP2	23504	37	12	130926895	130926895	Nonsense_Mutation	SNP	C	T	46	373	c.951G>A	c.(949-951)TGG>TGA	p.W317*
Pat_70	Post-Resistance	MIPEP	4285	37	13	24453425	24453425	Missense_Mutation	SNP	G	A	93	600	c.521C>T	c.(520-522)TCC>TTC	p.S174F
Pat_70	Post-Resistance	HS6ST3	266722	37	13	97485024	97485024	Missense_Mutation	SNP	G	A	38	263	c.988G>A	c.(988-990)GAG>AAG	p.E330K
Pat_70	Post-Resistance	OR4M1	441670	37	14	20249284	20249284	Missense_Mutation	SNP	C	T	49	490	c.803C>T	c.(802-804)TCC>TTC	p.S268F
Pat_70	Post-Resistance	OR4N2	390429	37	14	20296056	20296056	Missense_Mutation	SNP	T	C	61	593	c.449T>C	c.(448-450)CTT>CCT	p.L150P
Pat_70	Post-Resistance	C14orf93	60686	37	14	23467809	23467809	Missense_Mutation	SNP	C	T	21	123	c.424G>A	c.(424-426)GAA>AAA	p.E142K
Pat_70	Post-Resistance	PRKD1	5587	37	14	30095710	30095710	Missense_Mutation	SNP	T	C	44	234	c.1778A>G	c.(1777-1779)CAG>CGG	p.Q593R
Pat_70	Post-Resistance	NUBPL	80224	37	14	32068535	32068535	Missense_Mutation	SNP	C	T	37	300	c.332C>T	c.(331-333)CCT>CTT	p.P111L
Pat_70	Post-Resistance	SOCS4	122809	37	14	55510090	55510090	Missense_Mutation	SNP	C	T	44	296	c.331C>T	c.(331-333)CGG>TGG	p.R111W
Pat_70	Post-Resistance	MAP3K9	4293	37	14	71216698	71216698	Missense_Mutation	SNP	G	A	49	333	c.1102C>T	c.(1102-1104)CTT>TTT	p.L368F
Pat_70	Post-Resistance	FOXN3	1112	37	14	89628855	89628855	Missense_Mutation	SNP	G	A	30	140	c.1376C>T	c.(1375-1377)TCC>TTC	p.S459F

Pat_70	Post-Resistance	KIAA0284	283638	37	14	105349558	105349558	Missense_Mutation	SNP	G	A	15	765	c.764G>A	c.(763-765)GGT>GAT	p.G255D
Pat_70	Post-Resistance	OR4N3P	390539	37	15	22413825	22413825	Missense_Mutation	SNP	C	T	129	645	c.124C>T	c.(124-126)CGC>TGC	p.R42C
Pat_70	Post-Resistance	SPTBN5	51332	37	15	42160775	42160775	Missense_Mutation	SNP	C	T	31	145	c.5773G>A	c.(5773-5775)GCC>ACC	p.A1925T
Pat_70	Post-Resistance	DTWD1	56986	37	15	49924411	49924411	Missense_Mutation	SNP	C	T	31	220	c.320C>T	c.(319-321)ACT>ATT	p.T107I
Pat_70	Post-Resistance	SLC27A2	11001	37	15	50515227	50515227	Nonsense_Mutation	SNP	G	A	45	406	c.1038G>A	c.(1036-1038)TGG>TGA	p.W346*
Pat_70	Post-Resistance	CYP19A1	1588	37	15	51503047	51503047	Missense_Mutation	SNP	C	T	61	479	c.1470G>A	c.(1468-1470)ATG>ATA	p.M490I
Pat_70	Post-Resistance	HERC1	8925	37	15	63932386	63932386	Nonsense_Mutation	SNP	C	A	43	279	c.11866G>T	c.(11866-11868)GAA>TAA	p.E3956*
Pat_70	Post-Resistance	AGBL1	123624	37	15	87066090	87066090	Missense_Mutation	SNP	C	T	44	363	c.2467C>T	c.(2467-2469)CCC>TCC	p.P823S
Pat_70	Post-Resistance	GRIN2A	2903	37	16	9923396	9923396	Missense_Mutation	SNP	C	T	48	281	c.1891G>A	c.(1891-1893)GTA>ATA	p.V631I
Pat_70	Post-Resistance	TMC7	79905	37	16	19041577	19041577	Missense_Mutation	SNP	G	A	33	257	c.743G>A	c.(742-744)GGA>GAA	p.G248E
Pat_70	Post-Resistance	ACSM2A	123876	37	16	20492021	20492021	Missense_Mutation	SNP	G	C	16	91	c.1408G>C	c.(1408-1410)GGG>CGG	p.G470R
Pat_70	Post-Resistance	ACSM2B	348158	37	16	20554458	20554458	Missense_Mutation	SNP	C	G	44	762	c.1408G>C	c.(1408-1410)GGG>CGG	p.G470R
Pat_70	Post-Resistance	USP31	57478	37	16	23116791	23116791	Missense_Mutation	SNP	A	T	36	272	c.1060T>A	c.(1060-1062)TCT>ACT	p.S354T
Pat_70	Post-Resistance	ABCC12	94160	37	16	48119553	48119553	Missense_Mutation	SNP	C	T	60	364	c.3779G>A	c.(3778-3780)GGG>GAG	p.G1260E
Pat_70	Post-Resistance	GPR114	221188	37	16	57608779	57608779	Missense_Mutation	SNP	G	A	20	166	c.1261G>A	c.(1261-1263)GGC>AGC	p.G421S
Pat_70	Post-Resistance	ATMIN	23300	37	16	81078133	81078133	Missense_Mutation	SNP	T	C	97	433	c.2030T>C	c.(2029-2031)TTA>TCA	p.L677S
Pat_70	Post-Resistance	PKD1L2	114780	37	16	81253771	81253771	Missense_Mutation	SNP	C	T	52	305	c.205G>A	c.(205-207)GAA>AAA	p.E69K
Pat_70	Post-Resistance	GALNS	2588	37	16	88904094	88904094	Nonsense_Mutation	SNP	C	A	29	208	c.502G>T	c.(502-504)GGA>TGA	p.G168*
Pat_70	Post-Resistance	C17orf85	55421	37	17	3717742	3717742	Missense_Mutation	SNP	G	A	13	100	c.1501C>T	c.(1501-1503)CCG>TCG	p.P501S
Pat_70	Post-Resistance	UBE2G1	7326	37	17	4192683	4192683	Missense_Mutation	SNP	A	G	62	415	c.268T>C	c.(268-270)TGC>CGC	p.C90R
Pat_70	Post-Resistance	ALOX15	246	37	17	4536765	4536765	Missense_Mutation	SNP	C	T	48	363	c.1192G>A	c.(1192-1194)GAA>AAA	p.E398K
Pat_70	Post-Resistance	USP6	9098	37	17	5066291	5066291	Nonsense_Mutation	SNP	C	T	52	477	c.3028C>T	c.(3028-3030)CAG>TAG	p.Q1010*
Pat_70	Post-Resistance	KDM6B	23135	37	17	7751702	7751702	Missense_Mutation	SNP	T	G	71	629	c.2096T>G	c.(2095-2097)ATG>AGG	p.M699R
Pat_70	Post-Resistance	MYH2	4620	37	17	10442646	10442646	Missense_Mutation	SNP	G	A	100	586	c.1292C>T	c.(1291-1293)GCC>GTC	p.A431V
Pat_70	Post-Resistance	CCDC144A	9720	37	17	16631054	16631054	Missense_Mutation	SNP	G	A	7	58	c.2105G>A	c.(2104-2106)AGA>AAA	p.R702K
Pat_70	Post-Resistance	LGALS9B	284194	37	17	20363690	20363690	Missense_Mutation	SNP	C	T	5	310	c.106G>A	c.(106-108)GCC>ACC	p.A36T
Pat_70	Post-Resistance	SLFN13	146857	37	17	33769266	33769266	Nonsense_Mutation	SNP	C	T	30	168	c.1238G>A	c.(1237-1239)TGG>TAG	p.W413*
Pat_70	Post-Resistance	CDK12	51755	37	17	37618868	37618868	Missense_Mutation	SNP	G	A	20	155	c.544G>A	c.(544-546)GAG>AAG	p.E182K
Pat_70	Post-Resistance	KRTAP4-11	653240	37	17	39274214	39274214	Missense_Mutation	SNP	G	C	19	336	c.354C>G	c.(352-354)AGC>AGG	p.S118R
Pat_70	Post-Resistance	KRTAP4-11	653240	37	17	39274424	39274424	Missense_Mutation	SNP	G	C	24	474	c.144C>G	c.(142-144)AGC>AGG	p.S48R
Pat_70	Post-Resistance	SLC26A11	284129	37	17	78226478	78226478	Missense_Mutation	SNP	C	T	28	174	c.1784C>T	c.(1783-1785)TCC>TTC	p.S595F
Pat_70	Post-Resistance	CLUL1	27098	37	18	618042	618042	Nonsense_Mutation	SNP	G	A	19	303	c.42G>A	c.(40-42)TGG>TGA	p.W14*
Pat_70	Post-Resistance	MEX3C	51320	37	18	48703064	48703064	Missense_Mutation	SNP	G	A	34	205	c.1637C>T	c.(1636-1638)CCT>CTT	p.P546L
Pat_70	Post-Resistance	DCC	1630	37	18	50832089	50832089	Missense_Mutation	SNP	G	A	52	295	c.2053G>A	c.(2053-2055)GGA>AGA	p.G685R
Pat_70	Post-Resistance	SERPINB5	5268	37	18	61156661	61156661	Missense_Mutation	SNP	G	A	17	182	c.388G>A	c.(388-390)GGT>AGT	p.G130S
Pat_70	Post-Resistance	MOBKL2A	126308	37	19	2078392	2078392	Missense_Mutation	SNP	G	T	43	272	c.168C>A	c.(166-168)GAC>GAA	p.D56E
Pat_70	Post-Resistance	ARRDC5	645432	37	19	4896825	4896825	Missense_Mutation	SNP	G	A	23	289	c.359C>T	c.(358-360)CCT>CTT	p.P120L
Pat_70	Post-Resistance	C3	718	37	19	6702545	6702545	Missense_Mutation	SNP	C	T	61	369	c.2291G>A	c.(2290-2292)CGA>CAA	p.R764Q
Pat_70	Post-Resistance	CD209	30835	37	19	7810560	7810560	Missense_Mutation	SNP	G	A	7	310	c.592C>T	c.(592-594)CGG>TGG	p.R198W
Pat_70	Post-Resistance	MUC16	94025	37	19	9073848	9073848	Missense_Mutation	SNP	G	A	28	250	c.13598C>T	c.(13597-13599)CCT>CTT	p.P4533L
Pat_70	Post-Resistance	ZNF560	147741	37	19	9577542	9577542	Missense_Mutation	SNP	C	T	70	435	c.2081G>A	c.(2080-2082)CGA>CAA	p.R694Q
Pat_70	Post-Resistance	ZNF844	284391	37	19	12187443	12187443	Missense_Mutation	SNP	C	G	6	462	c.1508C>G	c.(1507-1509)CCT>CGT	p.P503R
Pat_70	Post-Resistance	CD97	976	37	19	14499612	14499612	Missense_Mutation	SNP	C	T	94	626	c.172C>T	c.(172-174)CCG>TCG	p.P58S
Pat_70	Post-Resistance	CYP4F12	66002	37	19	15789078	15789078	Missense_Mutation	SNP	C	T	59	376	c.206C>T	c.(205-207)CCT>CTT	p.P69L
Pat_70	Post-Resistance	OR10H2	26538	37	19	15839002	15839002	Nonsense_Mutation	SNP	G	A	55	397	c.149G>A	c.(148-150)TGG>TAG	p.W50*
Pat_70	Post-Resistance	ZNF737	100129842	37	19	20728254	20728254	Missense_Mutation	SNP	C	G	6	265	c.755G>C	c.(754-756)AGT>ACT	p.S252T
Pat_70	Post-Resistance	ZNF98	148198	37	19	22585641	22585641	Missense_Mutation	SNP	C	T	60	458	c.203G>A	c.(202-204)GGA>GAA	p.G68E

Pat_70	Post-Resistance	ZNF254	9534	37	19	24309919	24309919	Missense_Mutation	SNP	A	G	11	382	c.1117A>G	c.(1117-1119)ACT>GCT	p.T373A
Pat_70	Post-Resistance	KIRREL2	84063	37	19	36349734	36349734	Missense_Mutation	SNP	G	A	61	351	c.490G>A	c.(490-492)GGG>AGG	p.G164R
Pat_70	Post-Resistance	ZNF573	126231	37	19	38230883	38230884	Missense_Mutation	DNP	TC	AA	39	381	c.507_508GA>TT	(505-510)AAGAAC>AATTA	169_170KN>N
Pat_70	Post-Resistance	AXL	558	37	19	41743885	41743885	Missense_Mutation	SNP	G	A	33	191	c.820G>A	c.(820-822)GGA>AGA	p.G274R
Pat_70	Post-Resistance	MARK4	57787	37	19	45797680	45797680	Missense_Mutation	SNP	C	T	39	233	c.1568C>T	c.(1567-1569)CCG>CTG	p.P523L
Pat_70	Post-Resistance	ZNF649	65251	37	19	52394619	52394619	Missense_Mutation	SNP	T	C	7	355	c.770A>G	c.(769-771)AAA>AGA	p.K257R
Pat_70	Post-Resistance	ZNF845	91664	37	19	53856761	53856761	Missense_Mutation	SNP	T	C	5	261	c.2833T>C	c.(2833-2835)TGT>CGT	p.C945R
Pat_70	Post-Resistance	SBK2	646643	37	19	56041171	56041171	Missense_Mutation	SNP	C	T	16	101	c.976G>A	c.(976-978)GGG>AGG	p.G326R
Pat_70	Post-Resistance	NT5C1B	93034	37	2	18736522	18736522	Missense_Mutation	SNP	T	C	6	491	c.1888A>G	c.(1888-1890)ATG>GTG	p.M630V
Pat_70	Post-Resistance	NT5C1B	93034	37	2	18768282	18768282	Missense_Mutation	SNP	C	T	57	268	c.278G>A	c.(277-279)GGC>GAC	p.G93D
Pat_70	Post-Resistance	RPL23AP32	56969	37	2	54756736	54756737	Missense_Mutation	DNP	TT	CC	8	270	c.254_255TT>CC	c.(253-255)TTT>TCC	p.F85S
Pat_70	Post-Resistance	STARD7	56910	37	2	96858127	96858127	Missense_Mutation	SNP	G	A	56	496	c.823C>T	c.(823-825)CCC>TCC	p.P275S
Pat_70	Post-Resistance	SLC9A2	6549	37	2	103324769	103324769	Missense_Mutation	SNP	G	A	62	505	c.2260G>A	c.(2260-2262)GAA>AAA	p.E754K
Pat_70	Post-Resistance	WASH2P	375260	37	2	114355129	114355129	Missense_Mutation	SNP	G	A	5	136	c.506G>A	c.(505-507)CGC>CAC	p.R169H
Pat_70	Post-Resistance	CLASP1	23332	37	2	122125364	122125364	Missense_Mutation	SNP	C	G	5	172	c.3686G>C	c.(3685-3687)CGG>CCG	p.R1229P
Pat_70	Post-Resistance	CNTNAP5	129684	37	2	125504925	125504925	Nonsense_Mutation	SNP	C	T	80	454	c.2194C>T	c.(2194-2196)CAG>TAG	p.Q732*
Pat_70	Post-Resistance	CACNB4	785	37	2	152739821	152739821	Missense_Mutation	SNP	C	T	89	542	c.211G>A	c.(211-213)GAA>AAA	p.E71K
Pat_70	Post-Resistance	GRB14	2888	37	2	165353583	165353583	Nonsense_Mutation	SNP	C	T	32	199	c.1317G>A	c.(1315-1317)TGG>TGA	p.W439*
Pat_70	Post-Resistance	LRP2	4036	37	2	170028534	170028534	Missense_Mutation	SNP	C	T	61	387	c.11254G>A	c.(11254-11256)GAA>AAA	p.E3752K
Pat_70	Post-Resistance	TTN	7273	37	2	179613368	179613368	Missense_Mutation	SNP	C	T	80	522	c.13759G>A	c.(13759-13761)GAT>AAT	p.D4587N
Pat_70	Post-Resistance	COL5A2	1290	37	2	189917518	189917518	Missense_Mutation	SNP	C	T	35	177	c.2672G>A	c.(2671-2673)GGT>GAT	p.G891D
Pat_70	Post-Resistance	EEF1B2	1933	37	2	207025358	207025358	Missense_Mutation	SNP	A	G	15	542	c.127A>G	c.(127-129)AGC>GGC	p.S43G
Pat_70	Post-Resistance	CRYGA	1418	37	2	209027960	209027960	Missense_Mutation	SNP	C	T	45	374	c.220G>A	c.(220-222)GAC>AAC	p.D74N
Pat_70	Post-Resistance	IKZF2	22807	37	2	213878586	213878586	Missense_Mutation	SNP	C	T	46	226	c.785G>A	c.(784-786)AGA>AAA	p.R262K
Pat_70	Post-Resistance	HJURP	55355	37	2	234750117	234750117	Nonsense_Mutation	SNP	G	A	74	491	c.1309C>T	c.(1309-1311)CGA>TGA	p.R437*
Pat_70	Post-Resistance	TRPM8	79054	37	2	234879017	234879017	Missense_Mutation	SNP	G	A	126	675	c.2302G>A	c.(2302-2304)GAG>AAG	p.E768K
Pat_70	Post-Resistance	COL6A3	1293	37	2	238245090	238245090	Missense_Mutation	SNP	T	G	55	462	c.8653A>C	c.(8653-8655)ACC>CCC	p.T2885P
Pat_70	Post-Resistance	C20orf194	25943	37	20	3305557	3305557	Missense_Mutation	SNP	G	A	47	371	c.1247C>T	c.(1246-1248)CCG>CTG	p.P416L
Pat_70	Post-Resistance	SIGLEC1	6614	37	20	3673529	3673529	Missense_Mutation	SNP	G	A	13	106	c.3758C>T	c.(3757-3759)TCC>TTC	p.S1253F
Pat_70	Post-Resistance	PLCB4	5332	37	20	9404500	9404500	Nonsense_Mutation	SNP	C	T	20	172	c.2389C>T	c.(2389-2391)CGA>TGA	p.R797*
Pat_70	Post-Resistance	FRG1B	284802	37	20	29625934	29625934	Missense_Mutation	SNP	C	T	10	364	c.88C>T	c.(88-90)CAT>TAT	p.H30Y
Pat_70	Post-Resistance	FRG1B	284802	37	20	29625941	29625941	Missense_Mutation	SNP	A	T	17	390	c.95A>T	c.(94-96)GAT>GTT	p.D32V
Pat_70	Post-Resistance	FRG1B	284802	37	20	29625947	29625947	Missense_Mutation	SNP	T	C	13	414	c.101T>C	c.(100-102)ATT>ACT	p.I34T
Pat_70	Post-Resistance	FRG1B	284802	37	20	29628243	29628243	Missense_Mutation	SNP	T	C	13	608	c.155T>C	c.(154-156)TTG>TCG	p.L52S
Pat_70	Post-Resistance	FRG1B	284802	37	20	29628245	29628245	Missense_Mutation	SNP	G	A	13	602	c.157G>A	c.(157-159)GCC>ACC	p.A53T
Pat_70	Post-Resistance	PPP1R16B	26051	37	20	37546839	37546839	Missense_Mutation	SNP	C	T	108	638	c.1234C>T	c.(1234-1236)CCT>TCT	p.P412S
Pat_70	Post-Resistance	BAGE2	85319	37	21	11049621	11049621	Nonsense_Mutation	SNP	G	A	37	663	c.280C>T	c.(280-282)CGA>TGA	p.R94*
Pat_70	Post-Resistance	BAGE2	85319	37	21	11049623	11049623	Splice_Site	SNP	T	C	40	665	c.280_splice	c.e4-1	p.R94_splice
Pat_70	Post-Resistance	BAGE2	85319	37	21	11097573	11097573	Missense_Mutation	SNP	C	T	14	391	c.89G>A	c.(88-90)AGG>AAG	p.R30K
Pat_70	Post-Resistance	NCAM2	4685	37	21	22656657	22656657	Missense_Mutation	SNP	C	T	43	261	c.274C>T	c.(274-276)CGT>TGT	p.R92C
Pat_70	Post-Resistance	TRAPPC10	7109	37	21	45518395	45518395	Missense_Mutation	SNP	C	T	40	289	c.3326C>T	c.(3325-3327)TCG>TTG	p.S1109L
Pat_70	Post-Resistance	GNAZ	2781	37	22	23465487	23465487	Missense_Mutation	SNP	C	T	33	225	c.937C>T	c.(937-939)CGC>TGC	p.R313C
Pat_70	Post-Resistance	CHEK2	11200	37	22	29091840	29091841	Missense_Mutation	DNP	TG	CA	38	176	.1116_1117CA>TC	114-1119)TCCAAG>TCTG	p.K373E
Pat_70	Post-Resistance	SERHL2	253190	37	22	42952530	42952530	Missense_Mutation	SNP	C	T	28	478	c.359C>T	c.(358-360)ACC>ATC	p.T120I
Pat_70	Post-Resistance	ATG7	10533	37	3	11406161	11406161	Missense_Mutation	SNP	G	T	73	589	c.1828G>T	c.(1828-1830)GAT>TAT	p.D610Y
Pat_70	Post-Resistance	IQSEC1	9922	37	3	12977694	12977694	Missense_Mutation	SNP	C	T	40	266	c.864G>A	c.(862-864)ATG>ATA	p.M288I
Pat_70	Post-Resistance	SCN11A	11280	37	3	38936214	38936214	Missense_Mutation	SNP	G	A	43	235	c.2645C>T	c.(2644-2646)CCC>CTC	p.P882L

Pat_70	Post-Resistance	CCR1	1230	37	3	46245516	46245516	Missense_Mutation	SNP	C	T	48	391	c.289G>A	c.(289-291)GAT>AAT	p.D97N
Pat_70	Post-Resistance	COL7A1	1294	37	3	48610780	48610780	Missense_Mutation	SNP	C	T	31	235	c.6620G>A	c.(6619-6621)GGG>GAG	p.G2207E
Pat_70	Post-Resistance	ZMYND10	51364	37	3	50378896	50378896	Nonsense_Mutation	SNP	C	T	33	266	c.1268G>A	c.(1267-1269)TGG>TAG	p.W423*
Pat_70	Post-Resistance	ERC2	26059	37	3	55922574	55922574	Missense_Mutation	SNP	C	T	60	416	c.2407G>A	c.(2407-2409)GAG>AAG	p.E803K
Pat_70	Post-Resistance	ROBO2	6092	37	3	77645802	77645802	Missense_Mutation	SNP	C	T	57	322	c.2755C>T	c.(2755-2757)CCC>TCC	p.P919S
Pat_70	Post-Resistance	RG9MTD1	54931	37	3	101284175	101284175	Missense_Mutation	SNP	G	A	52	318	c.550G>A	c.(550-552)GAT>AAT	p.D184N
Pat_70	Post-Resistance	HHLA2	11148	37	3	108070664	108070664	Missense_Mutation	SNP	A	G	20	142	c.4A>G	c.(4-6)AAG>GAG	p.K2E
Pat_70	Post-Resistance	PHLDB2	90102	37	3	111638006	111638006	Missense_Mutation	SNP	G	A	60	417	c.1807G>A	c.(1807-1809)GAA>AAA	p.E603K
Pat_70	Post-Resistance	BOC	91653	37	3	112991278	112991278	Missense_Mutation	SNP	G	A	8	625	c.689G>A	c.(688-690)CGC>CAC	p.R230H
Pat_70	Post-Resistance	FBXO40	51725	37	3	121342006	121342006	Missense_Mutation	SNP	C	T	31	278	c.1730C>T	c.(1729-1731)CCC>CTC	p.P577L
Pat_70	Post-Resistance	CPNE4	131034	37	3	131261456	131261456	Missense_Mutation	SNP	C	T	22	228	c.1484G>A	c.(1483-1485)GGA>GAA	p.G495E
Pat_70	Post-Resistance	IGSF10	285313	37	3	151154847	151154847	Missense_Mutation	SNP	C	T	35	328	c.7502G>A	c.(7501-7503)AGA>AAA	p.R2501K
Pat_70	Post-Resistance	LIPH	200879	37	3	185251431	185251431	Missense_Mutation	SNP	C	T	41	296	c.454G>A	c.(454-456)GGA>AGA	p.G152R
Pat_70	Post-Resistance	PYDC2	152138	37	3	191179070	191179070	Missense_Mutation	SNP	A	T	37	418	c.119A>T	c.(118-120)CAG>CTG	p.Q40L
Pat_70	Post-Resistance	SDHAP2	727956	37	3	195404650	195404650	Missense_Mutation	SNP	T	A	36	256	c.207T>A	c.(205-207)AAT>AAA	p.N69K
Pat_70	Post-Resistance	DRD5	1816	37	4	9784887	9784887	Missense_Mutation	SNP	C	T	18	218	c.1234C>T	c.(1234-1236)CAC>TAC	p.H412Y
Pat_70	Post-Resistance	APBB2	323	37	4	40818158	40818158	Missense_Mutation	SNP	G	A	83	519	c.2228C>T	c.(2227-2229)TCC>TTC	p.S743F
Pat_70	Post-Resistance	AMBN	258	37	4	71468527	71468527	Missense_Mutation	SNP	G	A	21	123	c.583G>A	c.(583-585)GAT>AAT	p.D195N
Pat_70	Post-Resistance	RASSF6	166824	37	4	74451034	74451034	Missense_Mutation	SNP	C	T	36	272	c.526G>A	c.(526-528)GAA>AAA	p.E176K
Pat_70	Post-Resistance	NAAA	27163	37	4	76842263	76842263	Missense_Mutation	SNP	G	A	4	119	c.680C>T	c.(679-681)TCG>TTG	p.S227L
Pat_70	Post-Resistance	GK2	2712	37	4	80329231	80329231	Missense_Mutation	SNP	C	T	40	337	c.124G>A	c.(124-126)GAA>AAA	p.E42K
Pat_70	Post-Resistance	AFF1	4299	37	4	88048208	88048208	Missense_Mutation	SNP	C	T	58	411	c.2821C>T	c.(2821-2823)CCA>TCA	p.P941S
Pat_70	Post-Resistance	COL25A1	84570	37	4	109745338	109745338	Missense_Mutation	SNP	C	T	49	286	c.1837G>A	c.(1837-1839)GGA>AGA	p.G613R
Pat_70	Post-Resistance	CMYA5	202333	37	5	79024953	79024953	Missense_Mutation	SNP	C	T	76	320	c.365C>T	c.(364-366)TCC>TTC	p.S122F
Pat_70	Post-Resistance	ADAMTS19	171019	37	5	128956432	128956432	Missense_Mutation	SNP	G	A	96	651	c.1582G>A	c.(1582-1584)GAT>AAT	p.D528N
Pat_70	Post-Resistance	FAM53C	51307	37	5	137680684	137680684	Missense_Mutation	SNP	C	T	29	265	c.307C>T	c.(307-309)CCA>TCA	p.P103S
Pat_70	Post-Resistance	KDM3B	51780	37	5	137722215	137722215	Missense_Mutation	SNP	T	G	34	262	c.1285T>G	c.(1285-1287)TCC>GCC	p.S429A
Pat_70	Post-Resistance	PCDHA1	56147	37	5	140166227	140166227	Missense_Mutation	SNP	C	T	44	314	c.352C>T	c.(352-354)CAT>TAT	p.H118Y
Pat_70	Post-Resistance	SH3RF2	153769	37	5	145393506	145393506	Missense_Mutation	SNP	C	T	62	451	c.941C>T	c.(940-942)TCT>TTT	p.S314F
Pat_70	Post-Resistance	PPARGC1B	133522	37	5	149215849	149215849	Missense_Mutation	SNP	C	T	83	602	c.1831C>T	c.(1831-1833)CCG>TCG	p.P611S
Pat_70	Post-Resistance	SLC6A7	6534	37	5	149581944	149581944	Missense_Mutation	SNP	C	T	50	360	c.893C>T	c.(892-894)TCC>TTC	p.S298F
Pat_70	Post-Resistance	G3BP1	10146	37	5	151183497	151183497	Nonsense_Mutation	SNP	C	T	26	269	c.1246C>T	c.(1246-1248)CGA>TGA	p.R416*
Pat_70	Post-Resistance	CYFIP2	26999	37	5	156766230	156766230	Missense_Mutation	SNP	C	G	72	461	c.2551C>G	c.(2551-2553)CTC>GTC	p.L851V
Pat_70	Post-Resistance	COL23A1	91522	37	5	177686748	177686748	Missense_Mutation	SNP	C	T	74	427	c.703G>A	c.(703-705)GGT>AGT	p.G235S
Pat_70	Post-Resistance	BMP6	654	37	6	7861833	7861833	Splice_Site	SNP	G	A	51	393	c.1006_splice	c.e3+1	p.G336_splice
Pat_70	Post-Resistance	SYCP2L	221711	37	6	10959052	10959052	Missense_Mutation	SNP	T	G	29	212	c.2199T>G	c.(2197-2199)AAT>AAG	p.N733K
Pat_70	Post-Resistance	OR2W1	26692	37	6	29012220	29012220	Missense_Mutation	SNP	G	A	152	540	c.733C>T	c.(733-735)CTT>TTT	p.L245F
Pat_70	Post-Resistance	ITPR3	3710	37	6	33643512	33643512	Missense_Mutation	SNP	T	C	5	228	c.3161T>C	c.(3160-3162)ATG>ACG	p.M1054T
Pat_70	Post-Resistance	LRFN2	57497	37	6	40400182	40400182	Missense_Mutation	SNP	G	A	21	147	c.671C>T	c.(670-672)TCG>TTG	p.S224L
Pat_70	Post-Resistance	TREM1	54210	37	6	41250375	41250375	Nonsense_Mutation	SNP	C	T	61	433	c.164G>A	c.(163-165)TGG>TAG	p.W55*
Pat_70	Post-Resistance	BMP5	653	37	6	55620459	55620459	Missense_Mutation	SNP	G	T	56	382	c.1237C>A	c.(1237-1239)CAC>AAC	p.H413N
Pat_70	Post-Resistance	C6orf182	285753	37	6	109468047	109468047	Missense_Mutation	SNP	C	T	19	174	c.247C>T	c.(247-249)CTT>TTT	p.L83F
Pat_70	Post-Resistance	LAMA2	3908	37	6	129837370	129837370	Missense_Mutation	SNP	C	T	78	471	c.9247C>T	c.(9247-9249)CCG>TCG	p.P3083S
Pat_70	Post-Resistance	VNN1	8876	37	6	133013664	133013664	Missense_Mutation	SNP	C	T	19	103	c.886G>A	c.(886-888)GAG>AAG	p.E296K
Pat_70	Post-Resistance	HECA	51696	37	6	139488245	139488245	Missense_Mutation	SNP	G	A	5	259	c.1096G>A	c.(1096-1098)GTG>ATG	p.V366M
Pat_70	Post-Resistance	C6orf118	168090	37	6	165715360	165715360	Missense_Mutation	SNP	C	T	26	228	c.451G>A	c.(451-453)GCT>ACT	p.A151T
Pat_70	Post-Resistance	TTLL2	83887	37	6	167755036	167755036	Missense_Mutation	SNP	G	A	55	278	c.1648G>A	c.(1648-1650)GAT>AAT	p.D550N

Pat_70	Post-Resistance	DNAH11	8701	37	7	21913039	21913039	Missense_Mutation	SNP	G	A	79	199	c.12136G>A	c.(12136-12138)GAA>AAA	p.E4046K
Pat_70	Post-Resistance	STK31	56164	37	7	23808674	23808674	Missense_Mutation	SNP	G	A	34	363	c.1477G>A	c.(1477-1479)GAA>AAA	p.E493K
Pat_70	Post-Resistance	ADCY1	107	37	7	45717567	45717567	Missense_Mutation	SNP	A	T	128	376	c.1705A>T	c.(1705-1707)ATC>TTC	p.I569F
Pat_70	Post-Resistance	TNS3	64759	37	7	47333423	47333423	Missense_Mutation	SNP	C	T	42	284	c.3680G>A	c.(3679-3681)GGA>GAA	p.G1227E
Pat_70	Post-Resistance	ZNF727	442319	37	7	63538758	63538758	Missense_Mutation	SNP	G	A	40	141	c.1331G>A	c.(1330-1332)AGA>AAA	p.R444K
Pat_70	Post-Resistance	CCL24	6369	37	7	75442699	75442699	Missense_Mutation	SNP	G	A	23	230	c.116C>T	c.(115-117)TCC>TTC	p.S39F
Pat_70	Post-Resistance	ZAN	7455	37	7	100349878	100349878	Missense_Mutation	SNP	C	T	6	466	c.2150C>T	c.(2149-2151)CCC>CTC	p.P717L
Pat_70	Post-Resistance	CADPS2	93664	37	7	121985672	121985672	Nonsense_Mutation	SNP	G	A	29	335	c.3568C>T	c.(3568-3570)CGA>TGA	p.R1190*
Pat_70	Post-Resistance	JHDM1D	80853	37	7	139793899	139793899	Missense_Mutation	SNP	G	A	109	442	c.2414C>T	c.(2413-2415)TCC>TTC	p.S805F
Pat_70	Post-Resistance	BRAF	673	37	7	140453136	140453136	Missense_Mutation	SNP	A	T	87	312	c.1799T>A	c.(1798-1800)GTG>GAG	p.V600E
Pat_70	Post-Resistance	ZYX	7791	37	7	143085653	143085653	Missense_Mutation	SNP	C	T	37	305	c.1216C>T	c.(1216-1218)CAC>TAC	p.H406Y
Pat_70	Post-Resistance	GALNTL5	168391	37	7	151711870	151711870	Missense_Mutation	SNP	G	A	33	304	c.1168G>A	c.(1168-1170)GAA>AAA	p.E390K
Pat_70	Post-Resistance	ADAMDEC1	27299	37	8	24249837	24249837	Missense_Mutation	SNP	C	T	31	225	c.151C>T	c.(151-153)CAC>TAC	p.H51Y
Pat_70	Post-Resistance	PXDNL	137902	37	8	52384783	52384783	Missense_Mutation	SNP	C	T	75	446	c.776G>A	c.(775-777)GGA>GAA	p.G259E
Pat_70	Post-Resistance	PCMTD1	115294	37	8	52733185	52733186	Missense_Mutation	DNP	CC	TT	7	535	c.799_800GG>AA	c.(799-801)GGG>AAG	p.G267K
Pat_70	Post-Resistance	PKHD1L1	93035	37	8	110520058	110520058	Missense_Mutation	SNP	C	T	62	363	c.11161C>T	c.(11161-11163)CCT>TCT	p.P3721S
Pat_70	Post-Resistance	CSMD3	114788	37	8	114185984	114185984	Missense_Mutation	SNP	C	T	65	611	c.676G>A	c.(676-678)GCT>ACT	p.A226T
Pat_70	Post-Resistance	FER1L6	654463	37	8	125107259	125107259	Missense_Mutation	SNP	G	A	30	237	c.4675G>A	c.(4675-4677)GAT>AAT	p.D1559N
Pat_70	Post-Resistance	FAM135B	51059	37	8	139164898	139164898	Missense_Mutation	SNP	G	A	60	467	c.1820C>T	c.(1819-1821)TCA>TTA	p.S607L
Pat_70	Post-Resistance	MAPK15	225689	37	8	144803941	144803941	Missense_Mutation	SNP	G	A	18	128	c.1349G>A	c.(1348-1350)GGA>GAA	p.G450E
Pat_70	Post-Resistance	CNTLN	54875	37	9	17330685	17330685	Missense_Mutation	SNP	C	T	79	611	c.1397C>T	c.(1396-1398)TCT>TTT	p.S466F
Pat_70	Post-Resistance	TAF1L	138474	37	9	32632655	32632655	Missense_Mutation	SNP	G	A	58	352	c.2923C>T	c.(2923-2925)CCC>TCC	p.P975S
Pat_70	Post-Resistance	RNF20	56254	37	9	104302572	104302572	Missense_Mutation	SNP	C	T	76	578	c.217C>T	c.(217-219)CGT>TGT	p.R73C
Pat_70	Post-Resistance	OR13F1	138805	37	9	107266613	107266613	Nonsense_Mutation	SNP	C	T	36	238	c.70C>T	c.(70-72)CAG>TAG	p.Q24*
Pat_70	Post-Resistance	OR13C9	286362	37	9	107380230	107380230	Missense_Mutation	SNP	G	A	55	380	c.256C>T	c.(256-258)CTT>TTT	p.L86F
Pat_70	Post-Resistance	TXNDC8	255220	37	9	113096507	113096507	Missense_Mutation	SNP	G	A	32	219	c.118C>T	c.(118-120)CCT>TCT	p.P40S
Pat_70	Post-Resistance	DBC1	1620	37	9	121929721	121929721	Missense_Mutation	SNP	G	A	95	568	c.1927C>T	c.(1927-1929)CCC>TCC	p.P643S
Pat_70	Post-Resistance	C9orf119	375757	37	9	131038446	131038446	Missense_Mutation	SNP	G	A	35	200	c.22G>A	c.(22-24)GAC>AAC	p.D8N
Pat_70	Post-Resistance	COL5A1	1289	37	9	137715280	137715280	Missense_Mutation	SNP	G	A	56	356	c.4663G>A	c.(4663-4665)GGT>AGT	p.G1555S
Pat_70	Post-Resistance	CACNA1B	774	37	9	140948299	140948299	Missense_Mutation	SNP	C	T	113	662	c.3809C>T	c.(3808-3810)GCT>GTT	p.A1270V
Pat_70	Post-Resistance	NLGN4X	57502	37	X	6069369	6069369	Missense_Mutation	SNP	C	T	69	407	c.139G>A	c.(139-141)GTT>ATT	p.V47I
Pat_70	Post-Resistance	TBL1X	6907	37	X	9673050	9673050	Missense_Mutation	SNP	G	A	89	501	c.1132G>A	c.(1132-1134)GAC>AAC	p.D378N
Pat_70	Post-Resistance	FRMPD4	9758	37	X	12734739	12734739	Missense_Mutation	SNP	G	A	71	523	c.2161G>A	c.(2161-2163)GAT>AAT	p.D721N
Pat_70	Post-Resistance	FANCB	2187	37	X	14882788	14882789	Missense_Mutation	DNP	CC	TT	57	333	c.844_845GG>AA	c.(844-846)GGA>AAA	p.G282K
Pat_70	Post-Resistance	FANCB	2187	37	X	14883544	14883544	Missense_Mutation	SNP	C	T	40	273	c.89G>A	c.(88-90)GGA>GAA	p.G30E
Pat_70	Post-Resistance	ASB9	140462	37	X	15262747	15262747	Missense_Mutation	SNP	G	A	50	244	c.766C>T	c.(766-768)CCT>TCT	p.P256S
Pat_70	Post-Resistance	EIF1AX	1964	37	X	20156735	20156735	Missense_Mutation	SNP	C	T	62	357	c.22G>A	c.(22-24)GGA>AGA	p.G8R
Pat_70	Post-Resistance	DMD	1756	37	X	32466644	32466644	Missense_Mutation	SNP	C	T	40	232	c.3715G>A	c.(3715-3717)GAA>AAA	p.E1239K
Pat_70	Post-Resistance	FAM47C	442444	37	X	37028425	37028425	Missense_Mutation	SNP	A	G	9	661	c.1942A>G	c.(1942-1944)AAT>GAT	p.N648D
Pat_70	Post-Resistance	ATP6AP2	10159	37	X	40456507	40456507	Missense_Mutation	SNP	C	T	26	247	c.307C>T	c.(307-309)CCT>TCT	p.P103S
Pat_70	Post-Resistance	TEX11	56159	37	X	69849480	69849480	Missense_Mutation	SNP	G	A	45	453	c.1634C>T	c.(1633-1635)GCT>GTT	p.A545V
Pat_70	Post-Resistance	SERPINA7	6906	37	X	105280609	105280609	Missense_Mutation	SNP	C	A	104	644	c.441G>T	c.(439-441)TTG>TTT	p.L147F
Pat_70	Post-Resistance	RNF128	79589	37	X	106016347	106016347	Missense_Mutation	SNP	C	T	33	196	c.689C>T	c.(688-690)TCT>TTT	p.S230F
Pat_70	Post-Resistance	ODZ1	10178	37	X	123554529	123554529	Missense_Mutation	SNP	C	T	63	349	c.4593G>A	c.(4591-4593)ATG>ATA	p.M1531I
Pat_70	Post-Resistance	ODZ1	10178	37	X	124028163	124028163	Nonsense_Mutation	SNP	G	A	52	362	c.517C>T	c.(517-519)CAA>TAA	p.Q173*
Pat_70	Post-Resistance	BCORL1	63035	37	X	129185837	129185837	Missense_Mutation	SNP	G	A	62	615	c.4699G>A	c.(4699-4701)GAA>AAA	p.E1567K
Pat_70	Post-Resistance	MAGEC1	9947	37	X	140994583	140994583	Nonsense_Mutation	SNP	A	T	9	575	c.1393A>T	c.(1393-1395)AGA>TGA	p.R465*

Pat_70	Post-Resistance	CNGA2	1260	37	X	150912105	150912105	Missense_Mutation	SNP	A	G	42	356	c.1130A>G	c.(1129-1131)AAC>AGC	p.N377S
Pat_70	Post-Resistance	GABRE	2564	37	X	151131042	151131042	Missense_Mutation	SNP	G	A	65	494	c.416C>T	c.(415-417)TCT>TTT	p.S139F
Pat_70	Post-Resistance	CSAG1	158511	37	X	151908796	151908796	Missense_Mutation	SNP	C	T	86	520	c.35C>T	c.(34-36)ACT>ATT	p.T12I
Pat_73	Pre-Treatment	PGD	5226	37	1	10477446	10477446	Missense_Mutation	SNP	C	T	156	265	c.989C>T	c.(988-990)TCC>TTC	p.S330F
Pat_73	Pre-Treatment	CASZ1	54897	37	1	10713493	10713493	Missense_Mutation	SNP	G	A	27	30	c.2621C>T	c.(2620-2622)TCG>TTG	p.S874L
Pat_73	Pre-Treatment	SPEN	23013	37	1	16256981	16256981	Missense_Mutation	SNP	C	T	10	88	c.4246C>T	c.(4246-4248)CGT>TGT	p.R1416C
Pat_73	Pre-Treatment	MRTO4	51154	37	1	19582478	19582478	Missense_Mutation	SNP	A	G	54	69	c.124A>G	c.(124-126)ATC>GTC	p.I42V
Pat_73	Pre-Treatment	RPS6KA1	6195	37	1	26883501	26883501	Missense_Mutation	SNP	C	T	71	113	c.994C>T	c.(994-996)CGT>TGT	p.R332C
Pat_73	Pre-Treatment	HIVEP3	59269	37	1	41976579	41976579	Missense_Mutation	SNP	G	A	4	96	c.6764C>T	c.(6763-6765)TCG>TTG	p.S2255L
Pat_73	Pre-Treatment	KIAA0467	23334	37	1	43911909	43911910	Missense_Mutation	DNP	CC	TT	141	307	.6279_6280CC>T	277-6282)ATCCTC>ATTT	p.L2094F
Pat_73	Pre-Treatment	CYP4X1	260293	37	1	47505108	47505108	Missense_Mutation	SNP	C	T	90	100	c.977C>T	c.(976-978)TCC>TTC	p.S326F
Pat_73	Pre-Treatment	CC2D1B	200014	37	1	52823465	52823465	Missense_Mutation	SNP	G	A	25	23	c.1585C>T	c.(1585-1587)CCG>TCG	p.P529S
Pat_73	Pre-Treatment	C1orf177	163747	37	1	55282732	55282732	Missense_Mutation	SNP	G	A	53	55	c.1121G>A	c.(1120-1122)CGA>CAA	p.R374Q
Pat_73	Pre-Treatment	DHCR24	1718	37	1	55337259	55337259	Missense_Mutation	SNP	C	T	4	104	c.640G>A	c.(640-642)GTA>ATA	p.V214I
Pat_73	Pre-Treatment	RAVER2	55225	37	1	65243395	65243395	Nonsense_Mutation	SNP	C	T	51	91	c.406C>T	c.(406-408)CAG>TAG	p.Q136*
Pat_73	Pre-Treatment	C1orf173	127254	37	1	75038267	75038267	Missense_Mutation	SNP	C	T	88	151	c.3127G>A	c.(3127-3129)GAA>AAA	p.E1043K
Pat_73	Pre-Treatment	BCAR3	8412	37	1	94140384	94140384	Missense_Mutation	SNP	C	T	4	60	c.103G>A	c.(103-105)GCT>ACT	p.A35T
Pat_73	Pre-Treatment	CD53	963	37	1	111440482	111440482	Missense_Mutation	SNP	G	A	77	135	c.556G>A	c.(556-558)GGA>AGA	p.G186R
Pat_73	Pre-Treatment	NBPF9	400818	37	1	144617177	144617177	Missense_Mutation	SNP	G	A	10	580	c.203G>A	c.(202-204)AGA>AAA	p.R68K
Pat_73	Pre-Treatment	NBPF9	400818	37	1	144815953	144815953	Missense_Mutation	SNP	A	G	19	432	c.1324A>G	c.(1324-1326)AAT>GAT	p.N442D
Pat_73	Pre-Treatment	NBPF10	100132406	37	1	145360584	145360584	Missense_Mutation	SNP	G	A	8	53	c.9434G>A	c.(9433-9435)GGG>GAG	p.G3145E
Pat_73	Pre-Treatment	TCHH	7062	37	1	152082710	152082710	Missense_Mutation	SNP	C	G	5	202	c.2983G>C	c.(2983-2985)GAG>CAG	p.E995Q
Pat_73	Pre-Treatment	HRNR	388697	37	1	152188460	152188460	Missense_Mutation	SNP	G	A	73	842	c.5645C>T	c.(5644-5646)TCT>TTT	p.S1882F
Pat_73	Pre-Treatment	FLG	2312	37	1	152279804	152279804	Missense_Mutation	SNP	C	T	304	411	c.7558G>A	c.(7558-7560)GAT>AAT	p.D2520N
Pat_73	Pre-Treatment	CRNN	49860	37	1	152382749	152382749	Missense_Mutation	SNP	G	A	9	520	c.809C>T	c.(808-810)ACC>ATC	p.T270I
Pat_73	Pre-Treatment	ADAR	103	37	1	154574460	154574460	Missense_Mutation	SNP	C	A	4	115	c.658G>T	c.(658-660)GCC>TCC	p.A220S
Pat_73	Pre-Treatment	ADAR	103	37	1	154574475	154574475	Missense_Mutation	SNP	C	T	5	133	c.643G>A	c.(643-645)GGT>AGT	p.G215S
Pat_73	Pre-Treatment	GON4L	54856	37	1	155774924	155774924	Missense_Mutation	SNP	A	C	54	63	c.1461T>G	c.(1459-1461)GAT>GAG	p.D487E
Pat_73	Pre-Treatment	MAEL	84944	37	1	166959004	166959004	Missense_Mutation	SNP	G	A	27	36	c.163G>A	c.(163-165)GCA>ACA	p.A55T
Pat_73	Pre-Treatment	MAEL	84944	37	1	166990989	166990989	Missense_Mutation	SNP	C	T	73	88	c.1202C>T	c.(1201-1203)TCC>TTC	p.S401F
Pat_73	Pre-Treatment	SLC9A11	284525	37	1	173526564	173526564	Missense_Mutation	SNP	C	G	103	172	c.1130G>C	c.(1129-1131)TGG>TCG	p.W377S
Pat_73	Pre-Treatment	RNPEP	6051	37	1	201969084	201969084	Missense_Mutation	SNP	A	G	39	47	c.1145A>G	c.(1144-1146)CAC>CGC	p.H382R
Pat_73	Pre-Treatment	PLXNA2	5362	37	1	208201419	208201419	Missense_Mutation	SNP	C	T	6	398	c.5524G>A	c.(5524-5526)GTG>ATG	p.V1842M
Pat_73	Pre-Treatment	PLXNA2	5362	37	1	208216471	208216471	Missense_Mutation	SNP	G	A	4	163	c.3952C>T	c.(3952-3954)CGT>TGT	p.R1318C
Pat_73	Pre-Treatment	LAMB3	3914	37	1	209804019	209804019	Missense_Mutation	SNP	G	A	36	28	c.884C>T	c.(883-885)CCC>CTC	p.P295L
Pat_73	Pre-Treatment	SUSD4	55061	37	1	223465964	223465964	Missense_Mutation	SNP	G	A	5	127	c.178C>T	c.(178-180)CCC>TCC	p.P60S
Pat_73	Pre-Treatment	OR2M1P	388762	37	1	248285776	248285776	Missense_Mutation	SNP	A	C	5	378	c.339A>C	c.(337-339)TTA>TTC	p.L113F
Pat_73	Pre-Treatment	OR2T10	127069	37	1	248756578	248756578	Missense_Mutation	SNP	C	T	85	8	c.492G>A	c.(490-492)ATG>ATA	p.M164I
Pat_73	Pre-Treatment	DHTKD1	55526	37	10	12129565	12129565	Missense_Mutation	SNP	C	T	4	87	c.554C>T	c.(553-555)TCG>TTG	p.S185L
Pat_73	Pre-Treatment	LYZL1	84569	37	10	29578087	29578087	Nonsense_Mutation	SNP	G	A	39	16	c.41G>A	c.(40-42)TGG>TAG	p.W14*
Pat_73	Pre-Treatment	ZNF248	57209	37	10	38121877	38121877	Missense_Mutation	SNP	G	A	17	4	c.406C>T	c.(406-408)CCC>TCC	p.P136S
Pat_73	Pre-Treatment	SYT15	83849	37	10	46968629	46968629	Missense_Mutation	SNP	G	A	10	5	c.307C>T	c.(307-309)CCC>TCC	p.P103S
Pat_73	Pre-Treatment	ZWINT	11130	37	10	58118208	58118208	Missense_Mutation	SNP	G	T	8	77	c.805C>A	c.(805-807)CAA>AAA	p.Q269K
Pat_73	Pre-Treatment	CYP2C9	1559	37	10	96702071	96702071	Missense_Mutation	SNP	C	T	88	21	c.454C>T	c.(454-456)CTT>TTT	p.L152F
Pat_73	Pre-Treatment	CYP2C8	1558	37	10	96797060	96797060	Missense_Mutation	SNP	C	T	17	9	c.1298G>A	c.(1297-1299)CGA>CAA	p.R433Q
Pat_73	Pre-Treatment	LBX1	10660	37	10	102987272	102987272	Missense_Mutation	SNP	C	T	3	48	c.601G>A	c.(601-603)GGG>AGG	p.G201R
Pat_73	Pre-Treatment	C10orf79	80217	37	10	105920914	105920914	Missense_Mutation	SNP	G	A	25	13	c.3421C>T	c.(3421-3423)CCT>TCT	p.P1141S

Pat_73	Pre-Treatment	HBE1	3046	37	11	5290788	5290788	Missense_Mutation	SNP	A	T	65	109	c.211T>A	c.(211-213)TCC>ACC	p.S71T
Pat_73	Pre-Treatment	CCKBR	887	37	11	6281307	6281307	Missense_Mutation	SNP	G	A	22	31	c.149G>A	c.(148-150)CGA>CAA	p.R50Q
Pat_73	Pre-Treatment	OR4C13	283092	37	11	49974138	49974138	Missense_Mutation	SNP	C	T	249	340	c.164C>T	c.(163-165)TCC>TTC	p.S55F
Pat_73	Pre-Treatment	TMEM109	79073	37	11	60689470	60689470	Missense_Mutation	SNP	C	T	5	135	c.565C>T	c.(565-567)CTC>TTC	p.L189F
Pat_73	Pre-Treatment	AHNAK	79026	37	11	62295522	62295522	Missense_Mutation	SNP	C	T	10	728	c.6367G>A	c.(6367-6369)GAC>AAC	p.D2123N
Pat_73	Pre-Treatment	AHNAK	79026	37	11	62295549	62295549	Missense_Mutation	SNP	C	T	8	625	c.6340G>A	c.(6340-6342)GCC>ACC	p.A2114T
Pat_73	Pre-Treatment	AHNAK	79026	37	11	62296070	62296070	Missense_Mutation	SNP	A	G	11	668	c.5819T>C	c.(5818-5820)GTG>GCG	p.V1940A
Pat_73	Pre-Treatment	AHNAK	79026	37	11	62296147	62296147	Missense_Mutation	SNP	G	C	8	545	c.5742C>G	c.(5740-5742)GAC>GAG	p.D1914E
Pat_73	Pre-Treatment	SF1	7536	37	11	64535657	64535657	Missense_Mutation	SNP	C	T	4	101	c.989G>A	c.(988-990)GGC>GAC	p.G330D
Pat_73	Pre-Treatment	RPS6KB2	6199	37	11	67197022	67197022	Missense_Mutation	SNP	G	A	3	53	c.265G>A	c.(265-267)GGC>AGC	p.G89S
Pat_73	Pre-Treatment	ATM	472	37	11	108218025	108218026	Missense_Mutation	DNP	TG	CT	56	14	.8604_8605TG>C	602-8607)CTTGGT>CTCT	p.G2869C
Pat_73	Pre-Treatment	TMEM25	84866	37	11	118404984	118404984	Missense_Mutation	SNP	T	C	37	45	c.941T>C	c.(940-942)GTG>GCG	p.V314A
Pat_73	Pre-Treatment	SORL1	6653	37	11	121461820	121461820	Nonsense_Mutation	SNP	C	T	4	181	c.4324C>T	c.(4324-4326)CGA>TGA	p.R1442*
Pat_73	Pre-Treatment	ST3GAL4	6484	37	11	126279224	126279224	Missense_Mutation	SNP	G	A	4	176	c.689G>A	c.(688-690)CGG>CAG	p.R230Q
Pat_73	Pre-Treatment	ANO2	57101	37	12	5963247	5963247	Missense_Mutation	SNP	C	T	173	236	c.583G>A	c.(583-585)GAG>AAG	p.E195K
Pat_73	Pre-Treatment	CD163	9332	37	12	7640125	7640125	Missense_Mutation	SNP	C	T	89	103	c.1880G>A	c.(1879-1881)GGA>GAA	p.G627E
Pat_73	Pre-Treatment	CD163	9332	37	12	7640497	7640497	Missense_Mutation	SNP	C	T	58	91	c.1607G>A	c.(1606-1608)GGA>GAA	p.G536E
Pat_73	Pre-Treatment	PLCZ1	89869	37	12	18876451	18876451	Missense_Mutation	SNP	C	T	43	67	c.161G>A	c.(160-162)AGA>AAA	p.R54K
Pat_73	Pre-Treatment	ABCC9	10060	37	12	21954063	21954063	Missense_Mutation	SNP	C	T	51	83	c.4565G>A	c.(4564-4566)GGA>GAA	p.G1522E
Pat_73	Pre-Treatment	FAM113B	91523	37	12	47629931	47629931	Missense_Mutation	SNP	C	T	108	136	c.1085C>T	c.(1084-1086)TCA>TTA	p.S362L
Pat_73	Pre-Treatment	MLL2	8085	37	12	49433006	49433006	Missense_Mutation	SNP	G	A	17	142	c.8365C>T	c.(8365-8367)CGG>TGG	p.R2789W
Pat_73	Pre-Treatment	CPM	1368	37	12	69279577	69279577	Missense_Mutation	SNP	C	T	4	242	c.253G>A	c.(253-255)GAT>AAT	p.D85N
Pat_73	Pre-Treatment	STAB2	55576	37	12	104049246	104049246	Missense_Mutation	SNP	G	A	41	64	c.1621G>A	c.(1621-1623)GGA>AGA	p.G541R
Pat_73	Pre-Treatment	GLT8D2	83468	37	12	104388192	104388192	Missense_Mutation	SNP	C	A	15	87	c.688G>T	c.(688-690)GTG>TTG	p.V230L
Pat_73	Pre-Treatment	POLR3B	55703	37	12	106850963	106850963	Nonsense_Mutation	SNP	C	T	4	177	c.2341C>T	c.(2341-2343)CGA>TGA	p.R781*
Pat_73	Pre-Treatment	C12orf51	283450	37	12	112605243	112605243	Missense_Mutation	SNP	G	A	31	29	c.11146C>T	c.(11146-11148)CCG>TCG	p.P3716S
Pat_73	Pre-Treatment	GCN1L1	10985	37	12	120592781	120592781	Missense_Mutation	SNP	C	T	4	164	c.3694G>A	c.(3694-3696)GAA>AAA	p.E1232K
Pat_73	Pre-Treatment	ACADS	35	37	12	121176225	121176225	Missense_Mutation	SNP	A	G	37	49	c.767A>G	c.(766-768)GAG>GGG	p.E256G
Pat_73	Pre-Treatment	MLXIP	22877	37	12	122614641	122614641	Missense_Mutation	SNP	C	T	19	18	c.892C>T	c.(892-894)CCC>TCC	p.P298S
Pat_73	Pre-Treatment	SACS	26278	37	13	23907979	23907979	Missense_Mutation	SNP	G	A	50	100	c.10036C>T	c.(10036-10038)CCT>TCT	p.P3346S
Pat_73	Pre-Treatment	RNF6	6049	37	13	26788626	26788626	Missense_Mutation	SNP	G	A	4	224	c.1393C>T	c.(1393-1395)CGT>TGT	p.R465C
Pat_73	Pre-Treatment	DZIP1	22873	37	13	96239844	96239844	Missense_Mutation	SNP	C	T	5	402	c.2167G>A	c.(2167-2169)GGG>AGG	p.G723R
Pat_73	Pre-Treatment	RIPK3	11035	37	14	24809028	24809028	Missense_Mutation	SNP	G	A	5	223	c.5C>T	c.(4-6)TCG>TTG	p.S2L
Pat_73	Pre-Treatment	CDKL1	8814	37	14	50845005	50845005	Missense_Mutation	SNP	G	A	23	34	c.1244C>T	c.(1243-1245)CCT>CTT	p.P415L
Pat_73	Pre-Treatment	SNAPC1	6617	37	14	62248986	62248986	Missense_Mutation	SNP	C	T	4	156	c.847C>T	c.(847-849)CGT>TGT	p.R283C
Pat_73	Pre-Treatment	RDH11	51109	37	14	68159310	68159310	Missense_Mutation	SNP	C	T	70	182	c.194G>A	c.(193-195)GGA>GAA	p.G65E
Pat_73	Pre-Treatment	ADAM21P1	145241	37	14	70713206	70713206	Missense_Mutation	SNP	C	T	60	117	c.662G>A	c.(661-663)GGA>GAA	p.G221E
Pat_73	Pre-Treatment	TMEM63C	57156	37	14	77709269	77709269	Missense_Mutation	SNP	T	A	54	57	c.1211T>A	c.(1210-1212)TTC>TAC	p.F404Y
Pat_73	Pre-Treatment	ATXN3	4287	37	14	92548769	92548769	Missense_Mutation	SNP	T	C	75	97	c.650A>G	c.(649-651)GAT>GGT	p.D217G
Pat_73	Pre-Treatment	CPSF2	53981	37	14	92621668	92621668	Splice_Site	SNP	G	A	26	30	c.1442_splice	c.e11+1	p.K481_splice
Pat_73	Pre-Treatment	BRF1	2972	37	14	105693018	105693018	Missense_Mutation	SNP	C	T	4	162	c.868G>A	c.(868-870)GAC>AAC	p.D290N
Pat_73	Pre-Treatment	RYR3	6263	37	15	33945019	33945019	Missense_Mutation	SNP	G	A	4	137	c.4243G>A	c.(4243-4245)GTG>ATG	p.V1415M
Pat_73	Pre-Treatment	FBN1	2200	37	15	48812948	48812948	Missense_Mutation	SNP	G	A	55	53	c.1055C>T	c.(1054-1056)TCC>TTC	p.S352F
Pat_73	Pre-Treatment	TMOD3	29766	37	15	52161474	52161474	Missense_Mutation	SNP	C	T	5	156	c.187C>T	c.(187-189)CCA>TCA	p.P63S
Pat_73	Pre-Treatment	UNC13C	440279	37	15	54847703	54847703	Missense_Mutation	SNP	C	T	4	45	c.5951C>T	c.(5950-5952)ACC>ATC	p.T1984I
Pat_73	Pre-Treatment	FAM81A	145773	37	15	59809020	59809020	Missense_Mutation	SNP	G	A	10	17	c.963G>A	c.(961-963)ATG>ATA	p.M321I
Pat_73	Pre-Treatment	PPIB	5479	37	15	64449091	64449091	Missense_Mutation	SNP	C	G	4	71	c.361G>C	c.(361-363)GAG>CAG	p.E121Q

Pat_73	Pre-Treatment	ACAN	176	37	15	89400834	89400834	Missense_Mutation	SNP	C	T	107	175	c.5018C>T	c.(5017-5019)TCC>TTC	p.S1673F
Pat_73	Pre-Treatment	C15orf58	390637	37	15	90785020	90785020	Missense_Mutation	SNP	G	A	81	113	c.880G>A	c.(880-882)GGA>AGA	p.G294R
Pat_73	Pre-Treatment	SOLH	6650	37	16	601520	601520	Missense_Mutation	SNP	G	A	4	213	c.2201G>A	c.(2200-2202)CGG>CAG	p.R734Q
Pat_73	Pre-Treatment	CCNF	899	37	16	2498959	2498959	Missense_Mutation	SNP	G	A	4	176	c.1198G>A	c.(1198-1200)GCC>ACC	p.A400T
Pat_73	Pre-Treatment	PRSS33	260429	37	16	2836101	2836101	Missense_Mutation	SNP	C	T	23	41	c.68G>A	c.(67-69)AGG>AAG	p.R23K
Pat_73	Pre-Treatment	SYT17	51760	37	16	19236068	19236068	Missense_Mutation	SNP	T	C	54	68	c.1136T>C	c.(1135-1137)TTC>TCC	p.F379S
Pat_73	Pre-Treatment	UMOD	7369	37	16	20360534	20360534	Missense_Mutation	SNP	C	T	17	39	c.89G>A	c.(88-90)AGA>AAA	p.R30K
Pat_73	Pre-Treatment	ACSM1	116285	37	16	20681298	20681298	Missense_Mutation	SNP	G	A	3	42	c.763C>T	c.(763-765)CGG>TGG	p.R255W
Pat_73	Pre-Treatment	OTOA	146183	37	16	21739697	21739697	Missense_Mutation	SNP	G	A	41	83	c.2152G>A	c.(2152-2154)GAC>AAC	p.D718N
Pat_73	Pre-Treatment	GTF3C1	2975	37	16	27472727	27472727	Missense_Mutation	SNP	G	A	4	126	c.6274C>T	c.(6274-6276)CGG>TGG	p.R2092W
Pat_73	Pre-Treatment	RABEP2	79874	37	16	28935769	28935769	Missense_Mutation	SNP	G	A	5	237	c.229C>T	c.(229-231)CGG>TGG	p.R77W
Pat_73	Pre-Treatment	ARMC5	79798	37	16	31473871	31473871	Missense_Mutation	SNP	C	T	3	56	c.1003C>T	c.(1003-1005)CGG>TGG	p.R335W
Pat_73	Pre-Treatment	ZNF267	10308	37	16	31927690	31927690	Missense_Mutation	SNP	G	A	6	200	c.2120G>A	c.(2119-2121)CGG>CAG	p.R707Q
Pat_73	Pre-Treatment	VPS35	55737	37	16	46714582	46714582	Splice_Site	SNP	C	A	13	4	c.506_splice	c.e5+1	p.D169_splice
Pat_73	Pre-Treatment	MMP2	4313	37	16	55516945	55516945	Missense_Mutation	SNP	C	T	121	43	c.278C>T	c.(277-279)ACC>ATC	p.T93I
Pat_73	Pre-Treatment	GOT2	2806	37	16	58752490	58752490	Missense_Mutation	SNP	G	A	4	126	c.538C>T	c.(538-540)CGG>TGG	p.R180W
Pat_73	Pre-Treatment	GLG1	2734	37	16	74502864	74502864	Missense_Mutation	SNP	G	A	45	113	c.2416C>T	c.(2416-2418)CGT>TGT	p.R806C
Pat_73	Pre-Treatment	CHST6	4166	37	16	75513534	75513534	Missense_Mutation	SNP	C	T	4	79	c.193G>A	c.(193-195)GAC>AAC	p.D65N
Pat_73	Pre-Treatment	ANKRD11	29123	37	16	89349010	89349010	Missense_Mutation	SNP	C	T	27	29	c.3940G>A	c.(3940-3942)GAG>AAG	p.E1314K
Pat_73	Pre-Treatment	OR3A2	4995	37	17	3181634	3181634	Missense_Mutation	SNP	G	A	66	91	c.596C>T	c.(595-597)TCC>TTC	p.S199F
Pat_73	Pre-Treatment	NLRP1	22861	37	17	5462968	5462968	Missense_Mutation	SNP	C	T	95	143	c.1048G>A	c.(1048-1050)GCC>ACC	p.A350T
Pat_73	Pre-Treatment	DNAH2	146754	37	17	7679354	7679354	Missense_Mutation	SNP	G	A	6	325	c.4834G>A	c.(4834-4836)GAT>AAT	p.D1612N
Pat_73	Pre-Treatment	C17orf68	80169	37	17	8135746	8135746	Missense_Mutation	SNP	C	T	6	341	c.1993G>A	c.(1993-1995)GTG>ATG	p.V665M
Pat_73	Pre-Treatment	MFSD6L	162387	37	17	8702230	8702230	Missense_Mutation	SNP	G	A	29	39	c.209C>T	c.(208-210)GCC>GTC	p.A70V
Pat_73	Pre-Treatment	MYH2	4620	37	17	10440996	10440996	Missense_Mutation	SNP	C	T	180	277	c.1573G>A	c.(1573-1575)GAG>AAG	p.E525K
Pat_73	Pre-Treatment	DNAH9	1770	37	17	11666863	11666863	Missense_Mutation	SNP	G	A	52	71	c.7102G>A	c.(7102-7104)GAA>AAA	p.E2368K
Pat_73	Pre-Treatment	NCOR1	9611	37	17	16012114	16012114	Missense_Mutation	SNP	G	A	50	66	c.2168C>T	c.(2167-2169)CCA>CTA	p.P723L
Pat_73	Pre-Treatment	CCDC144B	284047	37	17	18528735	18528735	Missense_Mutation	SNP	C	T	5	16	c.26G>A	c.(25-27)CGG>CAG	p.R9Q
Pat_73	Pre-Treatment	NOS2	4843	37	17	26091035	26091035	Missense_Mutation	SNP	T	C	3	51	c.2564A>G	c.(2563-2565)GAG>GGG	p.E855G
Pat_73	Pre-Treatment	MYO18A	399687	37	17	27413553	27413553	Nonsense_Mutation	SNP	G	A	3	26	c.5755C>T	c.(5755-5757)CAG>TAG	p.Q1919*
Pat_73	Pre-Treatment	TAOK1	57551	37	17	27805316	27805316	Missense_Mutation	SNP	G	T	4	199	c.400G>T	c.(400-402)GGT>TGT	p.G134C
Pat_73	Pre-Treatment	CPD	1362	37	17	28789461	28789461	Missense_Mutation	SNP	C	A	4	167	c.3890C>A	c.(3889-3891)CCA>CAA	p.P1297Q
Pat_73	Pre-Treatment	GPR179	440435	37	17	36485284	36485284	Missense_Mutation	SNP	C	T	4	159	c.4168G>A	c.(4168-4170)GAG>AAG	p.E1390K
Pat_73	Pre-Treatment	CNTNAP1	8506	37	17	40837258	40837258	Missense_Mutation	SNP	G	A	4	182	c.535G>A	c.(535-537)GGC>AGC	p.G179S
Pat_73	Pre-Treatment	GPATCH8	23131	37	17	42541860	42541860	Missense_Mutation	SNP	C	T	461	63	c.173G>A	c.(172-174)GGA>GAA	p.G58E
Pat_73	Pre-Treatment	RGS9	8787	37	17	63185416	63185416	Missense_Mutation	SNP	G	A	4	94	c.667G>A	c.(667-669)GTT>ATT	p.V223I
Pat_73	Pre-Treatment	CBLN2	147381	37	18	70205419	70205419	Missense_Mutation	SNP	G	A	41	10	c.667C>T	c.(667-669)CCT>TCT	p.P223S
Pat_73	Pre-Treatment	MIER2	54531	37	19	313536	313536	Missense_Mutation	SNP	C	T	5	227	c.763G>A	c.(763-765)GGG>AGG	p.G255R
Pat_73	Pre-Treatment	TMPRSS9	360200	37	19	2425938	2425938	Missense_Mutation	SNP	G	A	5	116	c.3032G>A	c.(3031-3033)GGA>GAA	p.G1011E
Pat_73	Pre-Treatment	ZNF57	126295	37	19	2917807	2917807	Missense_Mutation	SNP	A	C	7	117	c.1188A>C	c.(1186-1188)CAA>CAC	p.Q396H
Pat_73	Pre-Treatment	ZNF57	126295	37	19	2917842	2917842	Missense_Mutation	SNP	G	A	11	119	c.1223G>A	c.(1222-1224)CGA>CAA	p.R408Q
Pat_73	Pre-Treatment	ZNF57	126295	37	19	2917857	2917857	Missense_Mutation	SNP	C	T	5	116	c.1238C>T	c.(1237-1239)ACG>ATG	p.T413M
Pat_73	Pre-Treatment	STAP2	55620	37	19	4329977	4329977	Missense_Mutation	SNP	G	C	25	49	c.436C>G	c.(436-438)CGT>GGT	p.R146G
Pat_73	Pre-Treatment	FEM1A	55527	37	19	4792725	4792725	Missense_Mutation	SNP	G	A	4	128	c.859G>A	c.(859-861)GAA>AAA	p.E287K
Pat_73	Pre-Treatment	PTPRS	5802	37	19	5212259	5212259	Missense_Mutation	SNP	G	A	4	203	c.4772C>T	c.(4771-4773)GCC>GTC	p.A1591V
Pat_73	Pre-Treatment	SLC25A41	284427	37	19	6427485	6427485	Missense_Mutation	SNP	G	A	3	27	c.652C>T	c.(652-654)CGG>TGG	p.R218W
Pat_73	Pre-Treatment	C3	718	37	19	6678278	6678278	Missense_Mutation	SNP	C	T	40	43	c.4735G>A	c.(4735-4737)GGA>AGA	p.G1579R

Pat_73	Pre-Treatment	EMR1	2015	37	19	6935050	6935050	Missense_Mutation	SNP	C	T	62	107	c.2342C>T	c.(2341-2343)TCC>TTC	p.S781F
Pat_73	Pre-Treatment	MUC16	94025	37	19	9069279	9069279	Missense_Mutation	SNP	G	A	53	93	c.18167C>T	c.(18166-18168)TCA>TTA	p.S6056L
Pat_73	Pre-Treatment	MUC16	94025	37	19	9069999	9069999	Missense_Mutation	SNP	C	T	41	73	c.17447G>A	c.(17446-17448)AGG>AAG	p.R5816K
Pat_73	Pre-Treatment	MUC16	94025	37	19	9083927	9083927	Missense_Mutation	SNP	G	A	19	25	c.7888C>T	c.(7888-7890)CCA>TCA	p.P2630S
Pat_73	Pre-Treatment	LDLR	3949	37	19	11215925	11215925	Missense_Mutation	SNP	C	T	187	247	c.343C>T	c.(343-345)CGC>TGC	p.R115C
Pat_73	Pre-Treatment	ZNF653	115950	37	19	11596534	11596534	Missense_Mutation	SNP	G	A	61	143	c.1507C>T	c.(1507-1509)CCT>TCT	p.P503S
Pat_73	Pre-Treatment	ZNF627	199692	37	19	11728410	11728410	Missense_Mutation	SNP	T	A	5	283	c.1092T>A	c.(1090-1092)GAT>GAA	p.D364E
Pat_73	Pre-Treatment	ZNF844	284391	37	19	12186819	12186819	Missense_Mutation	SNP	C	T	13	26	c.884C>T	c.(883-885)TCC>TTC	p.S295F
Pat_73	Pre-Treatment	ZNF844	284391	37	19	12187443	12187443	Missense_Mutation	SNP	C	G	9	315	c.1508C>G	c.(1507-1509)CCT>CGT	p.P503R
Pat_73	Pre-Treatment	ZNF443	10224	37	19	12541802	12541802	Missense_Mutation	SNP	C	A	146	245	c.1184G>T	c.(1183-1185)TGC>TTC	p.C395F
Pat_73	Pre-Treatment	ZNF564	163050	37	19	12637723	12637723	Missense_Mutation	SNP	C	T	8	420	c.1199G>A	c.(1198-1200)AGA>AAA	p.R400K
Pat_73	Pre-Treatment	MAST1	22983	37	19	12951329	12951330	Missense_Mutation	DNP	CC	TT	36	67	c.153_154CC>TT	151-156)TCCCCG>TCTTC	p.P52S
Pat_73	Pre-Treatment	ZNF333	84449	37	19	14829711	14829711	Missense_Mutation	SNP	C	A	4	187	c.1572C>A	c.(1570-1572)CAC>CAA	p.H524Q
Pat_73	Pre-Treatment	SLC1A6	6511	37	19	15067330	15067331	Missense_Mutation	DNP	CC	TT	10	22	.1126_1127GG>AA	c.(1126-1128)GGC>AAC	p.G376N
Pat_73	Pre-Treatment	PGLYRP2	114770	37	19	15587233	15587233	Missense_Mutation	SNP	G	A	43	35	c.248C>T	c.(247-249)CCC>CTC	p.P83L
Pat_73	Pre-Treatment	CYP4F2	8529	37	19	15996816	15996816	Missense_Mutation	SNP	C	A	6	113	c.1033G>T	c.(1033-1035)GCA>TCA	p.A345S
Pat_73	Pre-Treatment	CYP4F2	8529	37	19	15996840	15996840	Missense_Mutation	SNP	G	A	50	60	c.1009C>T	c.(1009-1011)CTC>TTC	p.L337F
Pat_73	Pre-Treatment	RAB8A	4218	37	19	16232580	16232580	Missense_Mutation	SNP	G	A	8	171	c.206G>A	c.(205-207)CGG>CAG	p.R69Q
Pat_73	Pre-Treatment	SIN3B	23309	37	19	16973254	16973254	Missense_Mutation	SNP	G	A	4	168	c.1150G>A	c.(1150-1152)GGG>AGG	p.G384R
Pat_73	Pre-Treatment	ZNF486	90649	37	19	20308465	20308465	Missense_Mutation	SNP	C	T	36	54	c.946C>T	c.(946-948)CAT>TAT	p.H316Y
Pat_73	Pre-Treatment	ZNF626	199777	37	19	20807353	20807353	Missense_Mutation	SNP	T	C	5	307	c.1330A>G	c.(1330-1332)AGG>GGG	p.R444G
Pat_73	Pre-Treatment	ZNF99	7652	37	19	22939459	22939459	Missense_Mutation	SNP	C	T	71	82	c.2712G>A	c.(2710-2712)ATG>ATA	p.M904I
Pat_73	Pre-Treatment	ZNF99	7652	37	19	22941749	22941749	Missense_Mutation	SNP	G	A	102	186	c.689C>T	c.(688-690)GCT>GTT	p.A230V
Pat_73	Pre-Treatment	LSM14A	26065	37	19	34685419	34685419	Missense_Mutation	SNP	G	A	6	426	c.158G>A	c.(157-159)CGT>CAT	p.R53H
Pat_73	Pre-Treatment	MAP4K1	11184	37	19	39100299	39100299	Missense_Mutation	SNP	G	A	21	23	c.943C>T	c.(943-945)CCT>TCT	p.P315S
Pat_73	Pre-Treatment	CYP2B6	1555	37	19	41512879	41512879	Missense_Mutation	SNP	G	A	33	51	c.554G>A	c.(553-555)GGA>GAA	p.G185E
Pat_73	Pre-Treatment	AXL	558	37	19	41748820	41748820	Missense_Mutation	SNP	C	T	69	110	c.1345C>T	c.(1345-1347)CCC>TCC	p.P449S
Pat_73	Pre-Treatment	ETHE1	23474	37	19	44011031	44011031	Missense_Mutation	SNP	G	A	5	178	c.736C>T	c.(736-738)CGC>TGC	p.R246C
Pat_73	Pre-Treatment	CEACAM20	125931	37	19	45033505	45033505	Missense_Mutation	SNP	G	A	63	50	c.28C>T	c.(28-30)CAC>TAC	p.H10Y
Pat_73	Pre-Treatment	CD3EAP	10849	37	19	45911467	45911467	Nonsense_Mutation	SNP	C	T	6	282	c.241C>T	c.(241-243)CGA>TGA	p.R81*
Pat_73	Pre-Treatment	ERCC1	2067	37	19	45918162	45918162	Missense_Mutation	SNP	G	A	5	92	c.659C>T	c.(658-660)GCG>GTG	p.A220V
Pat_73	Pre-Treatment	ZNF836	162962	37	19	52659224	52659224	Missense_Mutation	SNP	A	T	6	362	c.1712T>A	c.(1711-1713)ATT>AAT	p.I571N
Pat_73	Pre-Treatment	ZNF836	162962	37	19	52659243	52659243	Missense_Mutation	SNP	A	C	8	338	c.1693T>G	c.(1693-1695)TAC>GAC	p.Y565D
Pat_73	Pre-Treatment	ZNF28	7576	37	19	53302985	53302985	Missense_Mutation	SNP	T	A	7	556	c.2113A>T	c.(2113-2115)AAC>TAC	p.N705Y
Pat_73	Pre-Treatment	ZNF816A	125893	37	19	53453890	53453890	Missense_Mutation	SNP	G	C	9	616	c.1138C>G	c.(1138-1140)CAG>GAG	p.Q380E
Pat_73	Pre-Treatment	ZNF761	388561	37	19	53958969	53958969	Missense_Mutation	SNP	T	G	7	563	c.1208T>G	c.(1207-1209)CTT>CGT	p.L403R
Pat_73	Pre-Treatment	ZNF761	388561	37	19	53958983	53958983	Missense_Mutation	SNP	A	C	7	479	c.1222A>C	c.(1222-1224)AAA>CAA	p.K408Q
Pat_73	Pre-Treatment	ZNF761	388561	37	19	53959214	53959214	Missense_Mutation	SNP	A	T	116	153	c.1453A>T	c.(1453-1455)AGG>TGG	p.R485W
Pat_73	Pre-Treatment	NCR1	9437	37	19	55420727	55420727	Missense_Mutation	SNP	G	A	70	86	c.479G>A	c.(478-480)AGA>AAA	p.R160K
Pat_73	Pre-Treatment	NLRP2	55655	37	19	55496441	55496441	Missense_Mutation	SNP	C	T	86	117	c.2057C>T	c.(2056-2058)CCT>CTT	p.P686L
Pat_73	Pre-Treatment	PTPRH	5794	37	19	55713474	55713474	Missense_Mutation	SNP	A	T	76	135	c.1103T>A	c.(1102-1104)GTG>GAG	p.V368E
Pat_73	Pre-Treatment	NLRP11	204801	37	19	56312966	56312966	Missense_Mutation	SNP	C	T	120	150	c.2143G>A	c.(2143-2145)GAG>AAG	p.E715K
Pat_73	Pre-Treatment	ALK	238	37	2	29551311	29551311	Missense_Mutation	SNP	G	A	46	68	c.1319C>T	c.(1318-1320)TCC>TTC	p.S440F
Pat_73	Pre-Treatment	DHX57	90957	37	2	39029964	39029964	Missense_Mutation	SNP	G	A	6	516	c.3910C>T	c.(3910-3912)CCG>TCG	p.P1304S
Pat_73	Pre-Treatment	OXER1	165140	37	2	42990881	42990881	Missense_Mutation	SNP	G	A	3	59	c.439C>T	c.(439-441)CTC>TTC	p.L147F
Pat_73	Pre-Treatment	NRXN1	9378	37	2	50692660	50692660	Missense_Mutation	SNP	T	C	32	43	c.3404A>G	c.(3403-3405)CAA>CGA	p.Q1135R
Pat_73	Pre-Treatment	AFTPH	54812	37	2	64778646	64778646	Missense_Mutation	SNP	C	T	4	240	c.38C>T	c.(37-39)CCA>CTA	p.P13L

Pat_73	Pre-Treatment	TET3	200424	37	2	74275280	74275280	Nonsense_Mutation	SNP	G	T	3	39	c.1831G>T	c.(1831-1833)GAG>TAG	p.E611*
Pat_73	Pre-Treatment	LOXL3	84695	37	2	74762824	74762824	Missense_Mutation	SNP	C	T	40	56	c.1307G>A	c.(1306-1308)GGA>GAA	p.G436E
Pat_73	Pre-Treatment	REG3G	130120	37	2	79255008	79255008	Missense_Mutation	SNP	C	T	99	126	c.409C>T	c.(409-411)CCC>TCC	p.P137S
Pat_73	Pre-Treatment	SH2D6	284948	37	2	85662149	85662149	Missense_Mutation	SNP	A	C	4	13	c.71A>C	c.(70-72)CAC>CCC	p.H24P
Pat_73	Pre-Treatment	TEKT4	150483	37	2	95542459	95542459	Missense_Mutation	SNP	G	A	4	122	c.1253G>A	c.(1252-1254)TGC>TAC	p.C418Y
Pat_73	Pre-Treatment	ANKRD23	200539	37	2	97505471	97505471	Missense_Mutation	SNP	C	T	3	53	c.815G>A	c.(814-816)CGG>CAG	p.R272Q
Pat_73	Pre-Treatment	C2orf55	343990	37	2	99411032	99411032	Missense_Mutation	SNP	G	A	106	117	c.2852C>T	c.(2851-2853)TCT>TTT	p.S951F
Pat_73	Pre-Treatment	IL18RAP	8807	37	2	103040858	103040858	Missense_Mutation	SNP	C	T	4	171	c.563C>T	c.(562-564)GCG>GTG	p.A188V
Pat_73	Pre-Treatment	RGPD4	285190	37	2	108476236	108476236	Missense_Mutation	SNP	G	A	89	104	c.1693G>A	c.(1693-1695)GCC>ACC	p.A565T
Pat_73	Pre-Treatment	MGAT5	4249	37	2	135027998	135027998	Nonsense_Mutation	SNP	C	T	4	155	c.283C>T	c.(283-285)CAG>TAG	p.Q95*
Pat_73	Pre-Treatment	LY75	4065	37	2	160741758	160741758	Missense_Mutation	SNP	C	T	85	149	c.960G>A	c.(958-960)ATG>ATA	p.M320I
Pat_73	Pre-Treatment	DLX1	1745	37	2	172952920	172952920	Missense_Mutation	SNP	C	T	131	224	c.703C>T	c.(703-705)CCC>TCC	p.P235S
Pat_73	Pre-Treatment	TTN	7273	37	2	179430392	179430392	Missense_Mutation	SNP	C	T	103	153	c.72763G>A	c.(72763-72765)GGA>AGA	p.G24255R
Pat_73	Pre-Treatment	TTN	7273	37	2	179445147	179445147	Missense_Mutation	SNP	C	A	4	171	c.59255G>T	c.(59254-59256)CGC>CTC	p.R19752L
Pat_73	Pre-Treatment	TTN	7273	37	2	179480140	179480140	Missense_Mutation	SNP	G	A	163	187	c.40828C>T	c.(40828-40830)CCA>TCA	p.P13610S
Pat_73	Pre-Treatment	TTN	7273	37	2	179614327	179614327	Missense_Mutation	SNP	C	T	40	38	c.12800G>A	c.(12799-12801)GGA>GAA	p.G4267E
Pat_73	Pre-Treatment	BMPR2	659	37	2	203407087	203407087	Missense_Mutation	SNP	C	T	48	65	c.1330C>T	c.(1330-1332)CCC>TCC	p.P444S
Pat_73	Pre-Treatment	EEF1B2	1933	37	2	207025358	207025358	Missense_Mutation	SNP	A	G	12	310	c.127A>G	c.(127-129)AGC>GGC	p.S43G
Pat_73	Pre-Treatment	GIGYF2	26058	37	2	233620981	233620981	Missense_Mutation	SNP	G	A	3	59	c.316G>A	c.(316-318)GGA>AGA	p.G106R
Pat_73	Pre-Treatment	ADAM33	80332	37	20	3654919	3654919	Missense_Mutation	SNP	C	T	4	157	c.613G>A	c.(613-615)GCG>ACG	p.A205T
Pat_73	Pre-Treatment	C20orf27	54976	37	20	3736134	3736134	Missense_Mutation	SNP	C	T	4	107	c.283G>A	c.(283-285)GTG>ATG	p.V95M
Pat_73	Pre-Treatment	GPCPD1	56261	37	20	5560721	5560721	Missense_Mutation	SNP	G	A	4	77	c.406C>T	c.(406-408)CGT>TGT	p.R136C
Pat_73	Pre-Treatment	PLCB4	5332	37	20	9402034	9402034	Missense_Mutation	SNP	G	A	85	79	c.2209G>A	c.(2209-2211)GAA>AAA	p.E737K
Pat_73	Pre-Treatment	MKKS	8195	37	20	10393901	10393901	Missense_Mutation	SNP	A	G	65	86	c.262T>C	c.(262-264)TTC>CTC	p.F88L
Pat_73	Pre-Treatment	BTBD3	22903	37	20	11904102	11904102	Missense_Mutation	SNP	G	A	4	215	c.1357G>A	c.(1357-1359)GTA>ATA	p.V453I
Pat_73	Pre-Treatment	ESF1	51575	37	20	13714427	13714427	Missense_Mutation	SNP	G	A	73	96	c.1891C>T	c.(1891-1893)CCT>TCT	p.P631S
Pat_73	Pre-Treatment	FRG1B	284802	37	20	29625877	29625877	Missense_Mutation	SNP	G	A	6	141	c.31G>A	c.(31-33)GCC>ACC	p.A11T
Pat_73	Pre-Treatment	GDF5	8200	37	20	34021784	34021784	Missense_Mutation	SNP	G	C	56	66	c.1429C>G	c.(1429-1431)CTC>GTC	p.L477V
Pat_73	Pre-Treatment	PHF20	51230	37	20	34526957	34526957	Missense_Mutation	SNP	C	T	62	96	c.2639C>T	c.(2638-2640)TCC>TTC	p.S880F
Pat_73	Pre-Treatment	TGM2	7052	37	20	36779358	36779358	Missense_Mutation	SNP	G	A	127	194	c.535C>T	c.(535-537)CCT>TCT	p.P179S
Pat_73	Pre-Treatment	SLC2A10	81031	37	20	45354042	45354042	Missense_Mutation	SNP	G	A	4	207	c.367G>A	c.(367-369)GTG>ATG	p.V123M
Pat_73	Pre-Treatment	ZMYND8	23613	37	20	45867870	45867870	Missense_Mutation	SNP	G	A	4	216	c.2237C>T	c.(2236-2238)ACT>ATT	p.T746I
Pat_73	Pre-Treatment	NCOA3	8202	37	20	46276009	46276009	Missense_Mutation	SNP	C	T	78	81	c.3445C>T	c.(3445-3447)CCT>TCT	p.P1149S
Pat_73	Pre-Treatment	ARFGAP1	55738	37	20	61919190	61919190	Missense_Mutation	SNP	C	T	3	23	c.1186C>T	c.(1186-1188)CCC>TCC	p.P396S
Pat_73	Pre-Treatment	BTG3	10950	37	21	18966581	18966581	Nonsense_Mutation	SNP	G	A	45	50	c.589C>T	c.(589-591)CGA>TGA	p.R197*
Pat_73	Pre-Treatment	CLIC6	54102	37	21	36079677	36079677	Missense_Mutation	SNP	G	A	31	35	c.1528G>A	c.(1528-1530)GAC>AAC	p.D510N
Pat_73	Pre-Treatment	MX2	4600	37	21	42749759	42749759	Missense_Mutation	SNP	G	A	4	205	c.293G>A	c.(292-294)CGC>CAC	p.R98H
Pat_73	Pre-Treatment	PDE9A	5152	37	21	44192595	44192595	Missense_Mutation	SNP	C	T	19	24	c.1733C>T	c.(1732-1734)TCC>TTC	p.S578F
Pat_73	Pre-Treatment	CCT8L2	150160	37	22	17073380	17073380	Missense_Mutation	SNP	C	T	35	50	c.61G>A	c.(61-63)GAG>AAG	p.E21K
Pat_73	Pre-Treatment	CECR2	27443	37	22	18028128	18028128	Missense_Mutation	SNP	G	A	4	70	c.3085G>A	c.(3085-3087)GCT>ACT	p.A1029T
Pat_73	Pre-Treatment	SLC7A4	6545	37	22	21384097	21384097	Missense_Mutation	SNP	C	T	4	93	c.1526G>A	c.(1525-1527)GGT>GAT	p.G509D
Pat_73	Pre-Treatment	MYO18B	84700	37	22	26423319	26423319	Missense_Mutation	SNP	C	T	90	119	c.7379C>T	c.(7378-7380)TCA>TTA	p.S2460L
Pat_73	Pre-Treatment	PATZ1	23598	37	22	31740540	31740540	Missense_Mutation	SNP	C	T	4	107	c.1049G>A	c.(1048-1050)CGG>CAG	p.R350Q
Pat_73	Pre-Treatment	TMPRSS6	164656	37	22	37462141	37462141	Nonsense_Mutation	SNP	C	T	57	71	c.2415G>A	c.(2413-2415)TGG>TGA	p.W805*
Pat_73	Pre-Treatment	CACNA1I	8911	37	22	40045817	40045817	Missense_Mutation	SNP	C	T	5	62	c.1879C>T	c.(1879-1881)CGG>TGG	p.R627W
Pat_73	Pre-Treatment	TNRC6B	23112	37	22	40662077	40662078	Missense_Mutation	DNP	CC	TT	99	125	c.1843_1844CC>TT	c.(1843-1845)CCC>TTC	p.P615F
Pat_73	Pre-Treatment	WBP2NL	164684	37	22	42423028	42423028	Missense_Mutation	SNP	G	A	276	338	c.773G>A	c.(772-774)GGA>GAA	p.G258E

Pat_73	Pre-Treatment	TBC1D22A	25771	37	22	47433074	47433074	Missense_Mutation	SNP	C	T	5	245	c.1309C>T	c.(1309-1311)CGC>TGC	p.R437C
Pat_73	Pre-Treatment	STAC	6769	37	3	36527634	36527634	Missense_Mutation	SNP	A	G	36	368	c.580A>G	c.(580-582)AAT>GAT	p.N194D
Pat_73	Pre-Treatment	STAC	6769	37	3	36587734	36587734	Missense_Mutation	SNP	G	A	43	73	c.1162G>A	c.(1162-1164)GGA>AGA	p.G388R
Pat_73	Pre-Treatment	SLC22A14	9389	37	3	38358003	38358004	Missense_Mutation	DNP	CC	TT	16	41	.1721_1722CC>T	c.(1720-1722)TCC>TTT	p.S574F
Pat_73	Pre-Treatment	TTC21A	199223	37	3	39156117	39156118	Missense_Mutation	DNP	GG	AA	138	193	c.600_601GG>AA	598-603)CTGGAG>CTAA	p.E201K
Pat_73	Pre-Treatment	CYP8B1	1582	37	3	42916798	42916798	Missense_Mutation	SNP	G	A	55	78	c.511C>T	c.(511-513)CGC>TGC	p.R171C
Pat_73	Pre-Treatment	P4HTM	54681	37	3	49027982	49027982	Missense_Mutation	SNP	G	A	4	36	c.293G>A	c.(292-294)CGT>CAT	p.R98H
Pat_73	Pre-Treatment	RNF123	63891	37	3	49734631	49734631	Missense_Mutation	SNP	G	T	4	67	c.223G>T	c.(223-225)GAC>TAC	p.D75Y
Pat_73	Pre-Treatment	MAGI1	9223	37	3	65364955	65364956	Missense_Mutation	DNP	GG	AA	19	21	.2975_2976CC>T	c.(2974-2976)CCC>CTT	p.P992L
Pat_73	Pre-Treatment	FAM55C	91775	37	3	101520410	101520410	Missense_Mutation	SNP	A	T	46	57	c.425A>T	c.(424-426)GAC>GTC	p.D142V
Pat_73	Pre-Treatment	POLQ	10721	37	3	121238889	121238889	Missense_Mutation	SNP	G	A	61	109	c.1297C>T	c.(1297-1299)CGT>TGT	p.R433C
Pat_73	Pre-Treatment	KALRN	8997	37	3	124281865	124281865	Missense_Mutation	SNP	C	T	79	96	c.5105C>T	c.(5104-5106)CCC>CTC	p.P1702L
Pat_73	Pre-Treatment	SLCO2A1	6578	37	3	133673911	133673911	Missense_Mutation	SNP	A	G	51	67	c.524T>C	c.(523-525)GTT>GCT	p.V175A
Pat_73	Pre-Treatment	B3GALNT1	8706	37	3	160803948	160803948	Missense_Mutation	SNP	G	A	20	33	c.595C>T	c.(595-597)CAC>TAC	p.H199Y
Pat_73	Pre-Treatment	WDR49	151790	37	3	167246950	167246950	Missense_Mutation	SNP	C	T	20	54	c.1240G>A	c.(1240-1242)GAA>AAA	p.E414K
Pat_73	Pre-Treatment	NCEH1	57552	37	3	172351720	172351720	Missense_Mutation	SNP	C	T	6	226	c.892G>A	c.(892-894)GGC>AGC	p.G298S
Pat_73	Pre-Treatment	THPO	7066	37	3	184090780	184090780	Missense_Mutation	SNP	G	A	4	150	c.583C>T	c.(583-585)CTC>TTC	p.L195F
Pat_73	Pre-Treatment	ATP13A4	84239	37	3	193132506	193132506	Missense_Mutation	SNP	G	A	107	64	c.2876C>T	c.(2875-2877)CCT>CTT	p.P959L
Pat_73	Pre-Treatment	MUC4	4585	37	3	195511822	195511822	Missense_Mutation	SNP	G	T	6	25	c.6629C>A	c.(6628-6630)CCT>CAT	p.P2210H
Pat_73	Pre-Treatment	MUC4	4585	37	3	195511937	195511937	Missense_Mutation	SNP	C	T	5	19	c.6514G>A	c.(6514-6516)GGT>AGT	p.G2172S
Pat_73	Pre-Treatment	MUC4	4585	37	3	195513468	195513468	Missense_Mutation	SNP	G	C	3	43	c.4983C>G	c.(4981-4983)CAC>CAG	p.H1661Q
Pat_73	Pre-Treatment	PPARGC1A	10891	37	4	23815677	23815677	Missense_Mutation	SNP	C	T	4	200	c.1429G>A	c.(1429-1431)GAA>AAA	p.E477K
Pat_73	Pre-Treatment	STAP1	26228	37	4	68424640	68424640	Missense_Mutation	SNP	G	A	86	15	c.113G>A	c.(112-114)GGA>GAA	p.G38E
Pat_73	Pre-Treatment	ANKRD17	26057	37	4	73943169	73943169	Missense_Mutation	SNP	T	C	169	50	c.7490A>G	c.(7489-7491)CAT>CGT	p.H2497R
Pat_73	Pre-Treatment	AIMP1	9255	37	4	107258186	107258187	Missense_Mutation	DNP	CT	TG	45	81	c.764_765CT>TG	c.(763-765)GCT>GTG	p.A255V
Pat_73	Pre-Treatment	ENPEP	2028	37	4	111412207	111412207	Missense_Mutation	SNP	G	A	61	79	c.805G>A	c.(805-807)GAT>AAT	p.D269N
Pat_73	Pre-Treatment	KIAA1109	84162	37	4	123161332	123161332	Missense_Mutation	SNP	G	A	4	184	c.4495G>A	c.(4495-4497)GTG>ATG	p.V1499M
Pat_73	Pre-Treatment	ZNF827	152485	37	4	146823374	146823374	Missense_Mutation	SNP	A	G	3	65	c.1037T>C	c.(1036-1038)CTG>CCG	p.L346P
Pat_73	Pre-Treatment	TLL1	7092	37	4	166910623	166910623	Missense_Mutation	SNP	G	A	80	100	c.260G>A	c.(259-261)GGA>GAA	p.G87E
Pat_73	Pre-Treatment	F11	2160	37	4	187201532	187201532	Missense_Mutation	SNP	G	A	4	205	c.1021G>A	c.(1021-1023)GAA>AAA	p.E341K
Pat_73	Pre-Treatment	ADAMTS16	170690	37	5	5242274	5242274	Missense_Mutation	SNP	C	T	4	103	c.2632C>T	c.(2632-2634)CGC>TGC	p.R878C
Pat_73	Pre-Treatment	SPEF2	79925	37	5	35800155	35800155	Missense_Mutation	SNP	C	G	176	293	c.4916C>G	c.(4915-4917)CCA>CGA	p.P1639R
Pat_73	Pre-Treatment	HEATR7B2	133558	37	5	41064585	41064585	Missense_Mutation	SNP	G	A	16	24	c.449C>T	c.(448-450)ACT>ATT	p.T150I
Pat_73	Pre-Treatment	SNX18	112574	37	5	53815644	53815644	Missense_Mutation	SNP	C	T	28	66	c.1862C>T	c.(1861-1863)CCT>CTT	p.P621L
Pat_73	Pre-Treatment	GPBP1	65056	37	5	56531860	56531860	Splice_Site	SNP	G	A	4	86	c.478_splice	c.e6+1	p.E160_splice
Pat_73	Pre-Treatment	FBXL21	26223	37	5	135276266	135276266	Missense_Mutation	SNP	C	T	23	48	c.578C>T	c.(577-579)CCT>CTT	p.P193L
Pat_73	Pre-Treatment	PCDHA1	56147	37	5	140167553	140167553	Missense_Mutation	SNP	G	A	77	119	c.1678G>A	c.(1678-1680)GAC>AAC	p.D560N
Pat_73	Pre-Treatment	PCDHB9	56127	37	5	140568836	140568836	Missense_Mutation	SNP	G	A	5	100	c.1945G>A	c.(1945-1947)GAG>AAG	p.E649K
Pat_73	Pre-Treatment	PCDHB12	56124	37	5	140588687	140588687	Missense_Mutation	SNP	G	A	62	72	c.208G>A	c.(208-210)GAT>AAT	p.D70N
Pat_73	Pre-Treatment	PCDHGB4	8641	37	5	140769667	140769667	Missense_Mutation	SNP	C	T	203	288	c.2216C>T	c.(2215-2217)CCC>CTC	p.P739L
Pat_73	Pre-Treatment	GRM6	2916	37	5	178416382	178416382	Missense_Mutation	SNP	C	T	125	186	c.1037G>A	c.(1036-1038)CGA>CAA	p.R346Q
Pat_73	Pre-Treatment	SYCP2L	221711	37	6	10907857	10907857	Nonsense_Mutation	SNP	G	A	237	158	c.759G>A	c.(757-759)TGG>TGA	p.W253*
Pat_73	Pre-Treatment	EDN1	1906	37	6	12294510	12294510	Missense_Mutation	SNP	G	A	134	92	c.406G>A	c.(406-408)GAG>AAG	p.E136K
Pat_73	Pre-Treatment	MOG	4340	37	6	29635693	29635693	Missense_Mutation	SNP	G	A	5	391	c.584G>A	c.(583-585)CGG>CAG	p.R195Q
Pat_73	Pre-Treatment	VARS2	57176	37	6	30889704	30889704	Missense_Mutation	SNP	C	T	108	303	c.1738C>T	c.(1738-1740)CCT>TCT	p.P580S
Pat_73	Pre-Treatment	CLIC1	1192	37	6	31698735	31698735	Missense_Mutation	SNP	G	A	4	145	c.610C>T	c.(610-612)CGG>TGG	p.R204W
Pat_73	Pre-Treatment	ITPR3	3710	37	6	33650397	33650397	Missense_Mutation	SNP	T	C	4	217	c.4573T>C	c.(4573-4575)TGC>CGC	p.C1525R

Pat_73	Pre-Treatment	C6orf106	64771	37	6	34574375	34574375	Missense_Mutation	SNP	G	A	114	298	c.818C>T	c.(817-819)CCC>CTC	p.P273L
Pat_73	Pre-Treatment	UHRF1BP1	54887	37	6	34826790	34826790	Missense_Mutation	SNP	C	T	84	212	c.2657C>T	c.(2656-2658)CCT>CTT	p.P886L
Pat_73	Pre-Treatment	KCNK5	8645	37	6	39159028	39159028	Missense_Mutation	SNP	C	T	104	65	c.1138G>A	c.(1138-1140)GCC>ACC	p.A380T
Pat_73	Pre-Treatment	PGC	5225	37	6	41710082	41710082	Missense_Mutation	SNP	C	T	257	174	c.593G>A	c.(592-594)GGC>GAC	p.G198D
Pat_73	Pre-Treatment	KLC4	89953	37	6	43029158	43029158	Missense_Mutation	SNP	G	A	100	51	c.85G>A	c.(85-87)GTC>ATC	p.V29I
Pat_73	Pre-Treatment	ZNF318	24149	37	6	43323487	43323487	Missense_Mutation	SNP	G	A	269	613	c.1585C>T	c.(1585-1587)CCC>TCC	p.P529S
Pat_73	Pre-Treatment	MDN1	23195	37	6	90499512	90499512	Missense_Mutation	SNP	G	A	5	164	c.1217C>T	c.(1216-1218)GCC>GTC	p.A406V
Pat_73	Pre-Treatment	OLIG3	167826	37	6	137815225	137815225	Missense_Mutation	SNP	C	T	6	145	c.83G>A	c.(82-84)CGC>CAC	p.R28H
Pat_73	Pre-Treatment	GNA12	2768	37	7	2834734	2834734	Missense_Mutation	SNP	G	A	160	185	c.353C>T	c.(352-354)CCT>CTT	p.P118L
Pat_73	Pre-Treatment	TMEM195	392636	37	7	15584403	15584403	Missense_Mutation	SNP	C	T	117	227	c.403G>A	c.(403-405)GCT>ACT	p.A135T
Pat_73	Pre-Treatment	NPVF	64111	37	7	25266503	25266503	Missense_Mutation	SNP	C	T	110	163	c.281G>A	c.(280-282)AGG>AAG	p.R94K
Pat_73	Pre-Treatment	INHBA	3624	37	7	41729438	41729438	Missense_Mutation	SNP	G	A	83	126	c.1091C>T	c.(1090-1092)TCC>TTC	p.S364F
Pat_73	Pre-Treatment	VWC2	375567	37	7	49842374	49842374	Missense_Mutation	SNP	C	T	94	107	c.764C>T	c.(763-765)CCC>CTC	p.P255L
Pat_73	Pre-Treatment	ZNF713	349075	37	7	55990882	55990882	Missense_Mutation	SNP	G	A	4	187	c.76G>A	c.(76-78)GTG>ATG	p.V26M
Pat_73	Pre-Treatment	ZNF680	340252	37	7	63982110	63982110	Missense_Mutation	SNP	T	A	6	193	c.1022A>T	c.(1021-1023)AAG>ATG	p.K341M
Pat_73	Pre-Treatment	ZNF680	340252	37	7	63982117	63982117	Missense_Mutation	SNP	T	C	4	188	c.1015A>G	c.(1015-1017)AAA>GAA	p.K339E
Pat_73	Pre-Treatment	ZNF498	221785	37	7	99217435	99217435	Missense_Mutation	SNP	G	A	4	184	c.206G>A	c.(205-207)CGG>CAG	p.R69Q
Pat_73	Pre-Treatment	MUC17	140453	37	7	100676537	100676537	Missense_Mutation	SNP	G	C	11	811	c.1840G>C	c.(1840-1842)GCT>CCT	p.A614P
Pat_73	Pre-Treatment	MUC17	140453	37	7	100682124	100682124	Missense_Mutation	SNP	T	A	11	826	c.7427T>A	c.(7426-7428)CTT>CAT	p.L2476H
Pat_73	Pre-Treatment	MUC17	140453	37	7	100684076	100684076	Missense_Mutation	SNP	A	G	8	880	c.9379A>G	c.(9379-9381)ACA>GCA	p.T3127A
Pat_73	Pre-Treatment	MUC17	140453	37	7	100684302	100684302	Missense_Mutation	SNP	C	A	11	817	c.9605C>A	c.(9604-9606)ACT>AAT	p.T3202N
Pat_73	Pre-Treatment	MET	4233	37	7	116380979	116380979	Missense_Mutation	SNP	C	T	288	26	c.1601C>T	c.(1600-1602)CCC>CTC	p.P534L
Pat_73	Pre-Treatment	BRAF	673	37	7	140453136	140453136	Missense_Mutation	SNP	A	T	102	12	c.1799T>A	c.(1798-1800)GTG>GAG	p.V600E
Pat_73	Pre-Treatment	MLL3	58508	37	7	151845580	151845580	Nonsense_Mutation	SNP	G	A	30	189	c.13432C>T	c.(13432-13434)CGA>TGA	p.R4478*
Pat_73	Pre-Treatment	CSMD1	64478	37	8	2976008	2976008	Missense_Mutation	SNP	G	A	80	111	c.6346C>T	c.(6346-6348)CCT>TCT	p.P2116S
Pat_73	Pre-Treatment	SGK223	157285	37	8	8175867	8175867	Missense_Mutation	SNP	C	T	143	169	c.4018G>A	c.(4018-4020)GAG>AAG	p.E1340K
Pat_73	Pre-Treatment	XKR6	286046	37	8	10755518	10755518	Nonsense_Mutation	SNP	G	A	88	124	c.1870C>T	c.(1870-1872)CGA>TGA	p.R624*
Pat_73	Pre-Treatment	AMAC1L2	83650	37	8	11188842	11188842	Missense_Mutation	SNP	G	A	6	340	c.227G>A	c.(226-228)CGA>CAA	p.R76Q
Pat_73	Pre-Treatment	SLC7A2	6542	37	8	17417899	17417899	Missense_Mutation	SNP	C	T	62	64	c.1361C>T	c.(1360-1362)TCG>TTG	p.S454L
Pat_73	Pre-Treatment	REEP4	80346	37	8	21997703	21997703	Missense_Mutation	SNP	G	C	55	80	c.164C>G	c.(163-165)ACA>AGA	p.T55R
Pat_73	Pre-Treatment	ADAMDEC1	27299	37	8	24253266	24253266	Missense_Mutation	SNP	G	A	21	43	c.397G>A	c.(397-399)GAA>AAA	p.E133K
Pat_73	Pre-Treatment	DOCK5	80005	37	8	25149601	25149601	Missense_Mutation	SNP	G	A	3	29	c.383G>A	c.(382-384)CGG>CAG	p.R128Q
Pat_73	Pre-Treatment	NRG1	3084	37	8	32453417	32453417	Missense_Mutation	SNP	G	A	109	147	c.172G>A	c.(172-174)GAA>AAA	p.E58K
Pat_73	Pre-Treatment	ADAM2	2515	37	8	39645680	39645680	Missense_Mutation	SNP	C	T	38	57	c.733G>A	c.(733-735)GAG>AAG	p.E245K
Pat_73	Pre-Treatment	RB1CC1	9821	37	8	53589075	53589075	Missense_Mutation	SNP	A	T	4	136	c.426T>A	c.(424-426)GAT>GAA	p.D142E
Pat_73	Pre-Treatment	PREX2	80243	37	8	68981348	68981348	Missense_Mutation	SNP	G	A	45	44	c.1420G>A	c.(1420-1422)GAG>AAG	p.E474K
Pat_73	Pre-Treatment	HNF4G	3174	37	8	76471119	76471119	Missense_Mutation	SNP	C	T	79	224	c.829C>T	c.(829-831)CGG>TGG	p.R277W
Pat_73	Pre-Treatment	RIMS2	9699	37	8	105263362	105263362	Missense_Mutation	SNP	G	A	14	9	c.3856G>A	c.(3856-3858)GAA>AAA	p.E1286K
Pat_73	Pre-Treatment	ARC	23237	37	8	143695299	143695299	Missense_Mutation	SNP	C	T	16	12	c.334G>A	c.(334-336)GAG>AAG	p.E112K
Pat_73	Pre-Treatment	ZC3H3	23144	37	8	144621256	144621256	Missense_Mutation	SNP	G	A	4	205	c.281C>T	c.(280-282)CCG>CTG	p.P94L
Pat_73	Pre-Treatment	FAM75A6	389730	37	9	43627629	43627629	Missense_Mutation	SNP	T	C	7	213	c.1058A>G	c.(1057-1059)CAA>CGA	p.Q353R
Pat_73	Pre-Treatment	FAM75A6	389730	37	9	43627633	43627633	Missense_Mutation	SNP	T	C	7	212	c.1054A>G	c.(1054-1056)AAT>GAT	p.N352D
Pat_73	Pre-Treatment	WNK2	65268	37	9	95997149	95997149	Missense_Mutation	SNP	G	A	3	49	c.1135G>A	c.(1135-1137)GTC>ATC	p.V379I
Pat_73	Pre-Treatment	KIAA1529	57653	37	9	100093033	100093033	Missense_Mutation	SNP	G	C	3	59	c.2807G>C	c.(2806-2808)AGT>ACT	p.S936T
Pat_73	Pre-Treatment	OR13C8	138802	37	9	107332146	107332146	Missense_Mutation	SNP	G	A	47	50	c.698G>A	c.(697-699)GGA>GAA	p.G233E
Pat_73	Pre-Treatment	OR13C9	286362	37	9	107380371	107380371	Missense_Mutation	SNP	G	A	94	75	c.115C>T	c.(115-117)CTT>TTT	p.L39F
Pat_73	Pre-Treatment	TNC	3371	37	9	117852964	117852964	Missense_Mutation	SNP	C	T	239	585	c.334G>A	c.(334-336)GGC>AGC	p.G112S

Pat_73	Pre-Treatment	GSN	2934	37	9	124094754	124094754	Missense_Mutation	SNP	G	A	5	377	c.2222G>A	c.(2221-2223)CGG>CAG	p.R741Q
Pat_73	Pre-Treatment	SLC27A4	10999	37	9	131117820	131117820	Missense_Mutation	SNP	G	A	6	147	c.1606G>A	c.(1606-1608)GTG>ATG	p.V536M
Pat_73	Pre-Treatment	FAM78A	286336	37	9	134151461	134151461	Missense_Mutation	SNP	C	G	46	7	c.106G>C	c.(106-108)GAA>CAA	p.E36Q
Pat_73	Pre-Treatment	REXO4	57109	37	9	136279788	136279788	Missense_Mutation	SNP	G	C	4	196	c.569C>G	c.(568-570)ACC>AGC	p.T190S
Pat_73	Pre-Treatment	PDHA1	5160	37	X	19371203	19371203	Missense_Mutation	SNP	G	A	4	226	c.422G>A	c.(421-423)CGA>CAA	p.R141Q
Pat_73	Pre-Treatment	YY2	404281	37	X	21861388	21861388	Missense_Mutation	SNP	G	A	4	159	c.176G>A	c.(175-177)CGT>CAT	p.R59H
Pat_73	Pre-Treatment	ZC4H2	55906	37	X	64137703	64137703	Missense_Mutation	SNP	G	A	16	2	c.635C>T	c.(634-636)TCC>TTC	p.S212F
Pat_73	Pre-Treatment	ARR3	407	37	X	69495968	69495968	Missense_Mutation	SNP	G	A	4	90	c.182G>A	c.(181-183)CGT>CAT	p.R61H
Pat_73	Pre-Treatment	ZCCHC5	203430	37	X	77913110	77913110	Missense_Mutation	SNP	G	A	13	0	c.808C>T	c.(808-810)CCC>TCC	p.P270S
Pat_73	Pre-Treatment	GPRASP1	9737	37	X	101909266	101909266	Missense_Mutation	SNP	T	G	94	14	c.425T>G	c.(424-426)GTT>GGT	p.V142G
Pat_73	Pre-Treatment	MAGEA10	4109	37	X	151303681	151303681	Missense_Mutation	SNP	C	T	103	12	c.412G>A	c.(412-414)GTG>ATG	p.V138M
Pat_73	Pre-Treatment	TMEM187	8269	37	X	153247847	153247847	Missense_Mutation	SNP	G	A	2	1	c.334G>A	c.(334-336)GCG>ACG	p.A112T
Pat_73	Post-Resistance	PGD	5226	37	1	10477446	10477446	Missense_Mutation	SNP	C	T	131	167	c.989C>T	c.(988-990)TCC>TTC	p.S330F
Pat_73	Post-Resistance	CASZ1	54897	37	1	10713493	10713493	Missense_Mutation	SNP	G	A	16	21	c.2621C>T	c.(2620-2622)TCG>TTG	p.S874L
Pat_73	Post-Resistance	NBPF1	55672	37	1	16918653	16918653	Splice_Site	SNP	C	T	4	74	c.-35_splice	c.e6+1	
Pat_73	Post-Resistance	MRTO4	51154	37	1	19582478	19582478	Missense_Mutation	SNP	A	G	23	41	c.124A>G	c.(124-126)ATC>GTC	p.I42V
Pat_73	Post-Resistance	RPS6KA1	6195	37	1	26883501	26883501	Missense_Mutation	SNP	C	T	42	64	c.994C>T	c.(994-996)CGT>TGT	p.R332C
Pat_73	Post-Resistance	KIAA0467	23334	37	1	43911909	43911910	Missense_Mutation	DNP	CC	TT	112	149	.6279_6280CC>T	277-6282)ATCCTC>ATTT	p.L2094F
Pat_73	Post-Resistance	CYP4X1	260293	37	1	47505108	47505108	Missense_Mutation	SNP	C	T	37	63	c.977C>T	c.(976-978)TCC>TTC	p.S326F
Pat_73	Post-Resistance	CC2D1B	200014	37	1	52823465	52823465	Missense_Mutation	SNP	G	A	11	16	c.1585C>T	c.(1585-1587)CCG>TCG	p.P529S
Pat_73	Post-Resistance	C1orf177	163747	37	1	55282732	55282732	Missense_Mutation	SNP	G	A	34	14	c.1121G>A	c.(1120-1122)CGA>CAA	p.R374Q
Pat_73	Post-Resistance	RAVER2	55225	37	1	65243395	65243395	Nonsense_Mutation	SNP	C	T	12	79	c.406C>T	c.(406-408)CAG>TAG	p.Q136*
Pat_73	Post-Resistance	C1orf173	127254	37	1	75038267	75038267	Missense_Mutation	SNP	C	T	42	35	c.3127G>A	c.(3127-3129)GAA>AAA	p.E1043K
Pat_73	Post-Resistance	CD53	963	37	1	111440482	111440482	Missense_Mutation	SNP	G	A	27	99	c.556G>A	c.(556-558)GGA>AGA	p.G186R
Pat_73	Post-Resistance	NRAS	4893	37	1	115256529	115256530	Missense_Mutation	DNP	TG	CT	54	146	c.181_182CA>AG	c.(181-183)CAA>AGA	p.Q61R
Pat_73	Post-Resistance	NBPF9	400818	37	1	144615237	144615237	Missense_Mutation	SNP	T	G	8	264	c.107T>G	c.(106-108)GTA>GGA	p.V36G
Pat_73	Post-Resistance	NBPF10	100132406	37	1	145297661	145297661	Missense_Mutation	SNP	C	A	18	479	c.536C>A	c.(535-537)GCT>GAT	p.A179D
Pat_73	Post-Resistance	HRNR	388697	37	1	152188460	152188460	Missense_Mutation	SNP	G	A	80	800	c.5645C>T	c.(5644-5646)TCT>TTT	p.S1882F
Pat_73	Post-Resistance	FLG	2312	37	1	152279804	152279804	Missense_Mutation	SNP	C	T	192	274	c.7558G>A	c.(7558-7560)GAT>AAT	p.D2520N
Pat_73	Post-Resistance	GON4L	54856	37	1	155746233	155746233	Missense_Mutation	SNP	A	G	3	48	c.2131T>C	c.(2131-2133)TGC>CGC	p.C711R
Pat_73	Post-Resistance	GON4L	54856	37	1	155774924	155774924	Missense_Mutation	SNP	A	C	23	39	c.1461T>G	c.(1459-1461)GAT>GAG	p.D487E
Pat_73	Post-Resistance	MAEL	84944	37	1	166959004	166959004	Missense_Mutation	SNP	G	A	11	24	c.163G>A	c.(163-165)GCA>ACA	p.A55T
Pat_73	Post-Resistance	MAEL	84944	37	1	166990989	166990989	Missense_Mutation	SNP	C	T	47	75	c.1202C>T	c.(1201-1203)TCC>TTC	p.S401F
Pat_73	Post-Resistance	SLC9A11	284525	37	1	173526564	173526564	Missense_Mutation	SNP	C	G	67	116	c.1130G>C	c.(1129-1131)TGG>TCG	p.W377S
Pat_73	Post-Resistance	CEP350	9857	37	1	180022975	180022975	Missense_Mutation	SNP	A	G	26	81	c.5080A>G	c.(5080-5082)AGG>GGG	p.R1694G
Pat_73	Post-Resistance	RNPEP	6051	37	1	201969084	201969084	Missense_Mutation	SNP	A	G	21	35	c.1145A>G	c.(1144-1146)CAC>CGC	p.H382R
Pat_73	Post-Resistance	LAMB3	3914	37	1	209804019	209804019	Missense_Mutation	SNP	G	A	23	27	c.884C>T	c.(883-885)CCC>CTC	p.P295L
Pat_73	Post-Resistance	OR2T10	127069	37	1	248756578	248756578	Missense_Mutation	SNP	C	T	69	11	c.492G>A	c.(490-492)ATG>ATA	p.M164I
Pat_73	Post-Resistance	LYZL1	84569	37	10	29578087	29578087	Nonsense_Mutation	SNP	G	A	12	9	c.41G>A	c.(40-42)TGG>TAG	p.W14*
Pat_73	Post-Resistance	ZNF248	57209	37	10	38121877	38121877	Missense_Mutation	SNP	G	A	18	9	c.406C>T	c.(406-408)CCC>TCC	p.P136S
Pat_73	Post-Resistance	CYP2C9	1559	37	10	96702071	96702071	Missense_Mutation	SNP	C	T	48	43	c.454C>T	c.(454-456)CTT>TTT	p.L152F
Pat_73	Post-Resistance	CYP2C8	1558	37	10	96797060	96797060	Missense_Mutation	SNP	C	T	15	6	c.1298G>A	c.(1297-1299)CGA>CAA	p.R433Q
Pat_73	Post-Resistance	C10orf76	79591	37	10	103769782	103769782	Splice_Site	SNP	T	A	3	46	c.832_splice	c.e12-1	p.V278_splice
Pat_73	Post-Resistance	C10orf79	80217	37	10	105920914	105920914	Missense_Mutation	SNP	G	A	13	7	c.3421C>T	c.(3421-3423)CCT>TCT	p.P1141S
Pat_73	Post-Resistance	HBE1	3046	37	11	5290788	5290788	Missense_Mutation	SNP	A	T	37	61	c.211T>A	c.(211-213)TCC>ACC	p.S71T
Pat_73	Post-Resistance	CCKBR	887	37	11	6281307	6281307	Missense_Mutation	SNP	G	A	17	26	c.149G>A	c.(148-150)CGA>CAA	p.R50Q
Pat_73	Post-Resistance	PEX16	9409	37	11	45935923	45935923	Missense_Mutation	SNP	A	G	3	56	c.638T>C	c.(637-639)CTG>CCG	p.L213P

Pat_73	Post-Resistance	OR4C13	283092	37	11	49974138	49974138	Missense_Mutation	SNP	C	T	157	222	c.164C>T	c.(163-165)TCC>TTC	p.S55F
Pat_73	Post-Resistance	ATM	472	37	11	108218025	108218026	Missense_Mutation	DNP	TG	CT	26	15	.8604_8605TG>C	602-8607)CTTGGT>CTCT	p.G2869C
Pat_73	Post-Resistance	ANO2	57101	37	12	5963247	5963247	Missense_Mutation	SNP	C	T	109	142	c.583G>A	c.(583-585)GAG>AAG	p.E195K
Pat_73	Post-Resistance	CD163	9332	37	12	7640125	7640125	Missense_Mutation	SNP	C	T	53	87	c.1880G>A	c.(1879-1881)GGA>GAA	p.G627E
Pat_73	Post-Resistance	CD163	9332	37	12	7640497	7640497	Missense_Mutation	SNP	C	T	37	46	c.1607G>A	c.(1606-1608)GGA>GAA	p.G536E
Pat_73	Post-Resistance	PLCZ1	89869	37	12	18876451	18876451	Missense_Mutation	SNP	C	T	27	51	c.161G>A	c.(160-162)AGA>AAA	p.R54K
Pat_73	Post-Resistance	ABCC9	10060	37	12	21954063	21954063	Missense_Mutation	SNP	C	T	31	48	c.4565G>A	c.(4564-4566)GGA>GAA	p.G1522E
Pat_73	Post-Resistance	FAM113B	91523	37	12	47629931	47629931	Missense_Mutation	SNP	C	T	66	105	c.1085C>T	c.(1084-1086)TCA>TTA	p.S362L
Pat_73	Post-Resistance	STAB2	55576	37	12	104049246	104049246	Missense_Mutation	SNP	G	A	24	35	c.1621G>A	c.(1621-1623)GGA>AGA	p.G541R
Pat_73	Post-Resistance	C12orf34	84915	37	12	110206294	110206294	Missense_Mutation	SNP	G	T	3	53	c.560G>T	c.(559-561)CGG>CTG	p.R187L
Pat_73	Post-Resistance	C12orf51	283450	37	12	112605243	112605243	Missense_Mutation	SNP	G	A	16	29	c.11146C>T	c.(11146-11148)CCG>TCG	p.P3716S
Pat_73	Post-Resistance	ACADS	35	37	12	121176225	121176225	Missense_Mutation	SNP	A	G	10	24	c.767A>G	c.(766-768)GAG>GGG	p.E256G
Pat_73	Post-Resistance	MLXIP	22877	37	12	122614641	122614641	Missense_Mutation	SNP	C	T	5	28	c.892C>T	c.(892-894)CCC>TCC	p.P298S
Pat_73	Post-Resistance	SACS	26278	37	13	23907979	23907979	Missense_Mutation	SNP	G	A	39	97	c.10036C>T	c.(10036-10038)CCT>TCT	p.P3346S
Pat_73	Post-Resistance	HNRNPA1L2	144983	37	13	53217102	53217102	Missense_Mutation	SNP	G	A	17	166	c.475G>A	c.(475-477)GTG>ATG	p.V159M
Pat_73	Post-Resistance	DHRS4	10901	37	14	24424420	24424420	Missense_Mutation	SNP	C	T	3	26	c.305C>T	c.(304-306)ACG>ATG	p.T102M
Pat_73	Post-Resistance	CDKL1	8814	37	14	50845005	50845005	Missense_Mutation	SNP	G	A	13	23	c.1244C>T	c.(1243-1245)CCT>CTT	p.P415L
Pat_73	Post-Resistance	RDH11	51109	37	14	68159310	68159310	Missense_Mutation	SNP	C	T	96	125	c.194G>A	c.(193-195)GGA>GAA	p.G65E
Pat_73	Post-Resistance	ADAM21P1	145241	37	14	70713206	70713206	Missense_Mutation	SNP	C	T	41	74	c.662G>A	c.(661-663)GGA>GAA	p.G221E
Pat_73	Post-Resistance	TMEM63C	57156	37	14	77709269	77709269	Missense_Mutation	SNP	T	A	33	36	c.1211T>A	c.(1210-1212)TTC>TAC	p.F404Y
Pat_73	Post-Resistance	ATXN3	4287	37	14	92548769	92548769	Missense_Mutation	SNP	T	C	38	69	c.650A>G	c.(649-651)GAT>GGT	p.D217G
Pat_73	Post-Resistance	CPSF2	53981	37	14	92621668	92621668	Splice_Site	SNP	G	A	14	26	c.1442_splice	c.e11+1	p.K481_splice
Pat_73	Post-Resistance	ADAM6	8755	37	14	107087201	107087201	Splice_Site	SNP	G	A	9	100	c.5152_splice	c.e111+1	
Pat_73	Post-Resistance	FBN1	2200	37	15	48812948	48812948	Missense_Mutation	SNP	G	A	29	51	c.1055C>T	c.(1054-1056)TCC>TTC	p.S352F
Pat_73	Post-Resistance	ACAN	176	37	15	89400834	89400834	Missense_Mutation	SNP	C	T	79	156	c.5018C>T	c.(5017-5019)TCC>TTC	p.S1673F
Pat_73	Post-Resistance	C15orf58	390637	37	15	90785020	90785020	Missense_Mutation	SNP	G	A	30	85	c.880G>A	c.(880-882)GGA>AGA	p.G294R
Pat_73	Post-Resistance	PRSS33	260429	37	16	2836101	2836101	Missense_Mutation	SNP	C	T	15	14	c.68G>A	c.(67-69)AGG>AAG	p.R23K
Pat_73	Post-Resistance	SYT17	51760	37	16	19236068	19236068	Missense_Mutation	SNP	T	C	42	61	c.1136T>C	c.(1135-1137)TTC>TCC	p.F379S
Pat_73	Post-Resistance	UMOD	7369	37	16	20360534	20360534	Missense_Mutation	SNP	C	T	16	12	c.89G>A	c.(88-90)AGA>AAA	p.R30K
Pat_73	Post-Resistance	OTOA	146183	37	16	21739697	21739697	Missense_Mutation	SNP	G	A	24	57	c.2152G>A	c.(2152-2154)GAC>AAC	p.D718N
Pat_73	Post-Resistance	ZNF646	9726	37	16	31091621	31091621	Missense_Mutation	SNP	T	C	13	29	c.3976T>C	c.(3976-3978)TAC>CAC	p.Y1326H
Pat_73	Post-Resistance	VPS35	55737	37	16	46714582	46714582	Splice_Site	SNP	C	A	17	4	c.506_splice	c.e5+1	p.D169_splice
Pat_73	Post-Resistance	MMP2	4313	37	16	55516945	55516945	Missense_Mutation	SNP	C	T	62	38	c.278C>T	c.(277-279)ACC>ATC	p.T93I
Pat_73	Post-Resistance	CTCF	10664	37	16	67644968	67644968	Missense_Mutation	SNP	T	C	11	105	c.233T>C	c.(232-234)ATG>ACG	p.M78T
Pat_73	Post-Resistance	GLG1	2734	37	16	74502864	74502864	Missense_Mutation	SNP	G	A	20	64	c.2416C>T	c.(2416-2418)CGT>TGT	p.R806C
Pat_73	Post-Resistance	ANKRD11	29123	37	16	89349010	89349010	Missense_Mutation	SNP	C	T	8	20	c.3940G>A	c.(3940-3942)GAG>AAG	p.E1314K
Pat_73	Post-Resistance	OR3A2	4995	37	17	3181634	3181634	Missense_Mutation	SNP	G	A	36	58	c.596C>T	c.(595-597)TCC>TTC	p.S199F
Pat_73	Post-Resistance	NLRP1	22861	37	17	5462968	5462968	Missense_Mutation	SNP	C	T	56	83	c.1048G>A	c.(1048-1050)GCC>ACC	p.A350T
Pat_73	Post-Resistance	MFSD6L	162387	37	17	8702230	8702230	Missense_Mutation	SNP	G	A	12	18	c.209C>T	c.(208-210)GCC>GTC	p.A70V
Pat_73	Post-Resistance	MYH2	4620	37	17	10440996	10440996	Missense_Mutation	SNP	C	T	115	173	c.1573G>A	c.(1573-1575)GAG>AAG	p.E525K
Pat_73	Post-Resistance	DNAH9	1770	37	17	11666863	11666863	Missense_Mutation	SNP	G	A	38	65	c.7102G>A	c.(7102-7104)GAA>AAA	p.E2368K
Pat_73	Post-Resistance	NCOR1	9611	37	17	16012114	16012114	Missense_Mutation	SNP	G	A	30	54	c.2168C>T	c.(2167-2169)CCA>CTA	p.P723L
Pat_73	Post-Resistance	KRTAP4-11	653240	37	17	39274206	39274206	Missense_Mutation	SNP	C	T	5	99	c.362G>A	c.(361-363)AGA>AAA	p.R121K
Pat_73	Post-Resistance	KRTAP4-5	85289	37	17	39305619	39305619	Missense_Mutation	SNP	G	T	5	56	c.401C>A	c.(400-402)TCT>TAT	p.S134Y
Pat_73	Post-Resistance	GPATCH8	23131	37	17	42541860	42541860	Missense_Mutation	SNP	C	T	130	215	c.173G>A	c.(172-174)GGA>GAA	p.G58E
Pat_73	Post-Resistance	EIF4A3	9775	37	17	78115177	78115177	Missense_Mutation	SNP	G	A	25	38	c.313C>T	c.(313-315)CGT>TGT	p.R105C
Pat_73	Post-Resistance	SLC38A10	124565	37	17	79256004	79256005	Missense_Mutation	DNP	GG	AA	29	87	c.485_486CC>TT	c.(484-486)ACC>ATT	p.T162I

Pat_73	Post-Resistance	HGS	9146	37	17	79655770	79655770	Missense_Mutation	SNP	T	A	19	15	c.328T>A	c.(328-330)TAC>AAC	p.Y110N
Pat_73	Post-Resistance	CBLN2	147381	37	18	70205419	70205419	Missense_Mutation	SNP	G	A	29	11	c.667C>T	c.(667-669)CCT>TCT	p.P223S
Pat_73	Post-Resistance	STAP2	55620	37	19	4329977	4329977	Missense_Mutation	SNP	G	C	10	26	c.436C>G	c.(436-438)CGT>GGT	p.R146G
Pat_73	Post-Resistance	C3	718	37	19	6678278	6678278	Missense_Mutation	SNP	C	T	22	29	c.4735G>A	c.(4735-4737)GGA>AGA	p.G1579R
Pat_73	Post-Resistance	EMR1	2015	37	19	6935050	6935050	Missense_Mutation	SNP	C	T	44	61	c.2342C>T	c.(2341-2343)TCC>TTC	p.S781F
Pat_73	Post-Resistance	MUC16	94025	37	19	9069279	9069279	Missense_Mutation	SNP	G	A	48	79	c.18167C>T	c.(18166-18168)TCA>TTA	p.S6056L
Pat_73	Post-Resistance	MUC16	94025	37	19	9069999	9069999	Missense_Mutation	SNP	C	T	42	51	c.17447G>A	c.(17446-17448)AGG>AA	p.R5816K
Pat_73	Post-Resistance	MUC16	94025	37	19	9083927	9083927	Missense_Mutation	SNP	G	A	10	27	c.7888C>T	c.(7888-7890)CCA>TCA	p.P2630S
Pat_73	Post-Resistance	LDLR	3949	37	19	11215925	11215925	Missense_Mutation	SNP	C	T	120	143	c.343C>T	c.(343-345)CGC>TGC	p.R115C
Pat_73	Post-Resistance	ZNF653	115950	37	19	11596534	11596534	Missense_Mutation	SNP	G	A	38	81	c.1507C>T	c.(1507-1509)CCT>TCT	p.P503S
Pat_73	Post-Resistance	ZNF844	284391	37	19	12186819	12186819	Missense_Mutation	SNP	C	T	11	20	c.884C>T	c.(883-885)TCC>TTC	p.S295F
Pat_73	Post-Resistance	ZNF563	147837	37	19	12429554	12429554	Missense_Mutation	SNP	C	T	10	344	c.1285G>A	c.(1285-1287)GCG>ACG	p.A429T
Pat_73	Post-Resistance	ZNF443	10224	37	19	12541802	12541802	Missense_Mutation	SNP	C	A	166	279	c.1184G>T	c.(1183-1185)TGC>TTC	p.C395F
Pat_73	Post-Resistance	MAST1	22983	37	19	12951329	12951330	Missense_Mutation	DNP	CC	TT	10	27	c.153_154CC>TT	151-156)TCCCCG>TCTT	p.P52S
Pat_73	Post-Resistance	SLC1A6	6511	37	19	15067330	15067331	Missense_Mutation	DNP	CC	TT	17	18	.1126_1127GG>A	c.(1126-1128)GGC>AAC	p.G376N
Pat_73	Post-Resistance	PGLYRP2	114770	37	19	15587233	15587233	Missense_Mutation	SNP	G	A	23	32	c.248C>T	c.(247-249)CCC>CTC	p.P83L
Pat_73	Post-Resistance	CYP4F2	8529	37	19	15996840	15996840	Missense_Mutation	SNP	G	A	35	45	c.1009C>T	c.(1009-1011)CTC>TTC	p.L337F
Pat_73	Post-Resistance	ZNF486	90649	37	19	20308465	20308465	Missense_Mutation	SNP	C	T	39	52	c.946C>T	c.(946-948)CAT>TAT	p.H316Y
Pat_73	Post-Resistance	ZNF737	100129842	37	19	20727870	20727870	Missense_Mutation	SNP	C	G	10	251	c.1139G>C	c.(1138-1140)TGG>TCG	p.W380S
Pat_73	Post-Resistance	ZNF208	7757	37	19	22155282	22155282	Missense_Mutation	SNP	T	C	7	170	c.2254A>G	c.(2254-2256)AAG>GAG	p.K752E
Pat_73	Post-Resistance	ZNF99	7652	37	19	22939459	22939459	Missense_Mutation	SNP	C	T	51	71	c.2712G>A	c.(2710-2712)ATG>ATA	p.M904I
Pat_73	Post-Resistance	ZNF99	7652	37	19	22941749	22941749	Missense_Mutation	SNP	G	A	78	132	c.689C>T	c.(688-690)GCT>GTT	p.A230V
Pat_73	Post-Resistance	MAP4K1	11184	37	19	39100299	39100299	Missense_Mutation	SNP	G	A	14	17	c.943C>T	c.(943-945)CCT>TCT	p.P315S
Pat_73	Post-Resistance	CYP2B6	1555	37	19	41512879	41512879	Missense_Mutation	SNP	G	A	32	43	c.554G>A	c.(553-555)GGA>GAA	p.G185E
Pat_73	Post-Resistance	AXL	558	37	19	41748820	41748820	Missense_Mutation	SNP	C	T	33	68	c.1345C>T	c.(1345-1347)CCC>TCC	p.P449S
Pat_73	Post-Resistance	CEACAM20	125931	37	19	45033505	45033505	Missense_Mutation	SNP	G	A	27	18	c.28C>T	c.(28-30)CAC>TAC	p.H10Y
Pat_73	Post-Resistance	ZNF761	388561	37	19	53959214	53959214	Missense_Mutation	SNP	A	T	101	138	c.1453A>T	c.(1453-1455)AGG>TGG	p.R485W
Pat_73	Post-Resistance	NCR1	9437	37	19	55420727	55420727	Missense_Mutation	SNP	G	A	46	68	c.479G>A	c.(478-480)AGA>AAA	p.R160K
Pat_73	Post-Resistance	NLRP2	55655	37	19	55496441	55496441	Missense_Mutation	SNP	C	T	51	74	c.2057C>T	c.(2056-2058)CCT>CTT	p.P686L
Pat_73	Post-Resistance	PTPRH	5794	37	19	55713474	55713474	Missense_Mutation	SNP	A	T	58	89	c.1103T>A	c.(1102-1104)GTG>GAG	p.V368E
Pat_73	Post-Resistance	NLRP11	204801	37	19	56312966	56312966	Missense_Mutation	SNP	C	T	72	87	c.2143G>A	c.(2143-2145)GAG>AAG	p.E715K
Pat_73	Post-Resistance	ZNF749	388567	37	19	57956103	57956104	Missense_Mutation	DNP	TG	CC	6	117	.1587_1588TG>C	585-1590)CATGAG>CAC	p.E530Q
Pat_73	Post-Resistance	ZNF814	730051	37	19	58385546	58385546	Missense_Mutation	SNP	G	T	4	45	c.1212C>A	c.(1210-1212)GAC>GAA	p.D404E
Pat_73	Post-Resistance	ALK	238	37	2	29551311	29551311	Missense_Mutation	SNP	G	A	36	35	c.1319C>T	c.(1318-1320)TCC>TTC	p.S440F
Pat_73	Post-Resistance	NRXN1	9378	37	2	50692660	50692660	Missense_Mutation	SNP	T	C	19	29	c.3404A>G	c.(3403-3405)CAA>CGA	p.Q1135R
Pat_73	Post-Resistance	LOXL3	84695	37	2	74762824	74762824	Missense_Mutation	SNP	C	T	41	30	c.1307G>A	c.(1306-1308)GGA>GAA	p.G436E
Pat_73	Post-Resistance	REG3G	130120	37	2	79255008	79255008	Missense_Mutation	SNP	C	T	65	130	c.409C>T	c.(409-411)CCC>TCC	p.P137S
Pat_73	Post-Resistance	C2orf55	343990	37	2	99411032	99411032	Missense_Mutation	SNP	G	A	38	72	c.2852C>T	c.(2851-2853)TCT>TTT	p.S951F
Pat_73	Post-Resistance	RGPD4	285190	37	2	108476236	108476236	Missense_Mutation	SNP	G	A	76	78	c.1693G>A	c.(1693-1695)GCC>ACC	p.A565T
Pat_73	Post-Resistance	DDX11L2	84771	37	2	114357557	114357557	Nonstop_Mutation	SNP	A	G	4	45	c.382T>C	c.(382-384)TAG>CAG	p.*128Q
Pat_73	Post-Resistance	LY75	4065	37	2	160741758	160741758	Missense_Mutation	SNP	C	T	55	96	c.960G>A	c.(958-960)ATG>ATA	p.M320I
Pat_73	Post-Resistance	DLX1	1745	37	2	172952920	172952920	Missense_Mutation	SNP	C	T	57	82	c.703C>T	c.(703-705)CCC>TCC	p.P235S
Pat_73	Post-Resistance	TTN	7273	37	2	179430392	179430392	Missense_Mutation	SNP	C	T	73	124	c.72763G>A	c.(72763-72765)GGA>AG	p.G24255R
Pat_73	Post-Resistance	TTN	7273	37	2	179480140	179480140	Missense_Mutation	SNP	G	A	83	139	c.40828C>T	c.(40828-40830)CCA>TC	p.P13610S
Pat_73	Post-Resistance	TTN	7273	37	2	179614327	179614327	Missense_Mutation	SNP	C	T	17	30	c.12800G>A	c.(12799-12801)GGA>GA	p.G4267E
Pat_73	Post-Resistance	BMPR2	659	37	2	203407087	203407087	Missense_Mutation	SNP	C	T	28	47	c.1330C>T	c.(1330-1332)CCC>TCC	p.P444S
Pat_73	Post-Resistance	PLCB4	5332	37	20	9402034	9402034	Missense_Mutation	SNP	G	A	33	59	c.2209G>A	c.(2209-2211)GAA>AAA	p.E737K

Pat_73	Post-Resistance	MKKS	8195	37	20	10393901	10393901	Missense_Mutation	SNP	A	G	37	66	c.262T>C	c.(262-264)TTC>CTC	p.F88L
Pat_73	Post-Resistance	ESF1	51575	37	20	13714427	13714427	Missense_Mutation	SNP	G	A	43	67	c.1891C>T	c.(1891-1893)CCT>TCT	p.P631S
Pat_73	Post-Resistance	FRG1B	284802	37	20	29625877	29625877	Missense_Mutation	SNP	G	A	9	144	c.31G>A	c.(31-33)GCC>ACC	p.A11T
Pat_73	Post-Resistance	GDF5	8200	37	20	34021784	34021784	Missense_Mutation	SNP	G	C	21	32	c.1429C>G	c.(1429-1431)CTC>GTC	p.L477V
Pat_73	Post-Resistance	PHF20	51230	37	20	34526957	34526957	Missense_Mutation	SNP	C	T	36	47	c.2639C>T	c.(2638-2640)TCC>TTC	p.S880F
Pat_73	Post-Resistance	TGM2	7052	37	20	36779358	36779358	Missense_Mutation	SNP	G	A	51	89	c.535C>T	c.(535-537)CCT>TCT	p.P179S
Pat_73	Post-Resistance	NCOA3	8202	37	20	46276009	46276009	Missense_Mutation	SNP	C	T	38	66	c.3445C>T	c.(3445-3447)CCT>TCT	p.P1149S
Pat_73	Post-Resistance	BTG3	10950	37	21	18966581	18966581	Nonsense_Mutation	SNP	G	A	38	37	c.589C>T	c.(589-591)CGA>TGA	p.R197*
Pat_73	Post-Resistance	CLIC6	54102	37	21	36079677	36079677	Missense_Mutation	SNP	G	A	18	18	c.1528G>A	c.(1528-1530)GAC>AAC	p.D510N
Pat_73	Post-Resistance	PDE9A	5152	37	21	44192595	44192595	Missense_Mutation	SNP	C	T	9	20	c.1733C>T	c.(1732-1734)TCC>TTC	p.S578F
Pat_73	Post-Resistance	CCT8L2	150160	37	22	17073380	17073380	Missense_Mutation	SNP	C	T	12	24	c.61G>A	c.(61-63)GAG>AAG	p.E21K
Pat_73	Post-Resistance	MYO18B	84700	37	22	26423319	26423319	Missense_Mutation	SNP	C	T	53	86	c.7379C>T	c.(7378-7380)TCA>TTA	p.S2460L
Pat_73	Post-Resistance	TMPRSS6	164656	37	22	37462141	37462141	Nonsense_Mutation	SNP	C	T	26	26	c.2415G>A	c.(2413-2415)TGG>TGA	p.W805*
Pat_73	Post-Resistance	TNRC6B	23112	37	22	40662077	40662078	Missense_Mutation	DNP	CC	TT	54	99	.1843_1844CC>T	c.(1843-1845)CCC>TTC	p.P615F
Pat_73	Post-Resistance	WBP2NL	164684	37	22	42423028	42423028	Missense_Mutation	SNP	G	A	125	186	c.773G>A	c.(772-774)GGA>GAA	p.G258E
Pat_73	Post-Resistance	ITPR1	3708	37	3	4715034	4715034	Missense_Mutation	SNP	C	T	5	101	c.2419C>T	c.(2419-2421)CTC>TTC	p.L807F
Pat_73	Post-Resistance	STAC	6769	37	3	36587734	36587734	Missense_Mutation	SNP	G	A	33	52	c.1162G>A	c.(1162-1164)GGA>AGA	p.G388R
Pat_73	Post-Resistance	SLC22A14	9389	37	3	38358003	38358004	Missense_Mutation	DNP	CC	TT	9	35	.1721_1722CC>T	c.(1720-1722)TCC>TTT	p.S574F
Pat_73	Post-Resistance	TTC21A	199223	37	3	39156117	39156118	Missense_Mutation	DNP	GG	AA	79	154	c.600_601GG>AA	598-603)CTGGAG>CTAA	p.E201K
Pat_73	Post-Resistance	CYP8B1	1582	37	3	42916798	42916798	Missense_Mutation	SNP	G	A	49	65	c.511C>T	c.(511-513)CGC>TGC	p.R171C
Pat_73	Post-Resistance	MAGI1	9223	37	3	65364955	65364956	Missense_Mutation	DNP	GG	AA	7	16	.2975_2976CC>T	c.(2974-2976)CCC>CTT	p.P992L
Pat_73	Post-Resistance	FAM55C	91775	37	3	101520410	101520410	Missense_Mutation	SNP	A	T	20	30	c.425A>T	c.(424-426)GAC>GTC	p.D142V
Pat_73	Post-Resistance	POLQ	10721	37	3	121238889	121238889	Missense_Mutation	SNP	G	A	55	71	c.1297C>T	c.(1297-1299)CGT>TGT	p.R433C
Pat_73	Post-Resistance	KALRN	8997	37	3	124281865	124281865	Missense_Mutation	SNP	C	T	38	59	c.5105C>T	c.(5104-5106)CCC>CTC	p.P1702L
Pat_73	Post-Resistance	SLCO2A1	6578	37	3	133673911	133673911	Missense_Mutation	SNP	A	G	23	22	c.524T>C	c.(523-525)GTT>GCT	p.V175A
Pat_73	Post-Resistance	B3GALNT1	8706	37	3	160803948	160803948	Missense_Mutation	SNP	G	A	19	30	c.595C>T	c.(595-597)CAC>TAC	p.H199Y
Pat_73	Post-Resistance	WDR49	151790	37	3	167246950	167246950	Missense_Mutation	SNP	C	T	15	31	c.1240G>A	c.(1240-1242)GAA>AAA	p.E414K
Pat_73	Post-Resistance	ATP13A4	84239	37	3	193132506	193132506	Missense_Mutation	SNP	G	A	51	39	c.2876C>T	c.(2875-2877)CCT>CTT	p.P959L
Pat_73	Post-Resistance	MUC4	4585	37	3	195511937	195511937	Missense_Mutation	SNP	C	T	7	11	c.6514G>A	c.(6514-6516)GGT>AGT	p.G2172S
Pat_73	Post-Resistance	STAP1	26228	37	4	68424640	68424640	Missense_Mutation	SNP	G	A	51	25	c.113G>A	c.(112-114)GGA>GAA	p.G38E
Pat_73	Post-Resistance	ANKRD17	26057	37	4	73943169	73943169	Missense_Mutation	SNP	T	C	120	65	c.7490A>G	c.(7489-7491)CAT>CGT	p.H2497R
Pat_73	Post-Resistance	AIMP1	9255	37	4	107258186	107258187	Missense_Mutation	DNP	CT	TG	44	67	c.764_765CT>TG	c.(763-765)GCT>GTG	p.A255V
Pat_73	Post-Resistance	ENPEP	2028	37	4	111412207	111412207	Missense_Mutation	SNP	G	A	40	71	c.805G>A	c.(805-807)GAT>AAT	p.D269N
Pat_73	Post-Resistance	TLL1	7092	37	4	166910623	166910623	Missense_Mutation	SNP	G	A	38	56	c.260G>A	c.(259-261)GGA>GAA	p.G87E
Pat_73	Post-Resistance	SPEF2	79925	37	5	35800155	35800155	Missense_Mutation	SNP	C	G	114	174	c.4916C>G	c.(4915-4917)CCA>CGA	p.P1639R
Pat_73	Post-Resistance	HEATR7B2	133558	37	5	41064585	41064585	Missense_Mutation	SNP	G	A	9	25	c.449C>T	c.(448-450)ACT>ATT	p.T150I
Pat_73	Post-Resistance	SNX18	112574	37	5	53815644	53815644	Missense_Mutation	SNP	C	T	19	27	c.1862C>T	c.(1861-1863)CCT>CTT	p.P621L
Pat_73	Post-Resistance	THBS4	7060	37	5	79372734	79372734	Missense_Mutation	SNP	C	T	105	271	c.1949C>T	c.(1948-1950)GCC>GTC	p.A650V
Pat_73	Post-Resistance	FBXL21	26223	37	5	135276266	135276266	Missense_Mutation	SNP	C	T	7	26	c.578C>T	c.(577-579)CCT>CTT	p.P193L
Pat_73	Post-Resistance	PCDHA1	56147	37	5	140167553	140167553	Missense_Mutation	SNP	G	A	48	64	c.1678G>A	c.(1678-1680)GAC>AAC	p.D560N
Pat_73	Post-Resistance	PCDHB12	56124	37	5	140588687	140588687	Missense_Mutation	SNP	G	A	37	69	c.208G>A	c.(208-210)GAT>AAT	p.D70N
Pat_73	Post-Resistance	PCDHGB4	8641	37	5	140769667	140769667	Missense_Mutation	SNP	C	T	109	211	c.2216C>T	c.(2215-2217)CCC>CTC	p.P739L
Pat_73	Post-Resistance	DPYSL3	1809	37	5	146785188	146785188	Nonsense_Mutation	SNP	G	A	29	286	c.796C>T	c.(796-798)CAA>TAA	p.Q266*
Pat_73	Post-Resistance	GRM6	2916	37	5	178416382	178416382	Missense_Mutation	SNP	C	T	59	95	c.1037G>A	c.(1036-1038)CGA>CAA	p.R346Q
Pat_73	Post-Resistance	SYCP2L	221711	37	6	10907857	10907857	Nonsense_Mutation	SNP	G	A	146	57	c.759G>A	c.(757-759)TGG>TGA	p.W253*
Pat_73	Post-Resistance	EDN1	1906	37	6	12294510	12294510	Missense_Mutation	SNP	G	A	99	28	c.406G>A	c.(406-408)GAG>AAG	p.E136K
Pat_73	Post-Resistance	VARS2	57176	37	6	30889704	30889704	Missense_Mutation	SNP	C	T	35	188	c.1738C>T	c.(1738-1740)CCT>TCT	p.P580S

Pat_73	Post-Resistance	C6orf106	64771	37	6	34574375	34574375	Missense_Mutation	SNP	G	A	35	159	c.818C>T	c.(817-819)CCC>CTC	p.P273L
Pat_73	Post-Resistance	UHRF1BP1	54887	37	6	34826790	34826790	Missense_Mutation	SNP	C	T	25	149	c.2657C>T	c.(2656-2658)CCT>CTT	p.P886L
Pat_73	Post-Resistance	KCNK5	8645	37	6	39159028	39159028	Missense_Mutation	SNP	C	T	61	18	c.1138G>A	c.(1138-1140)GCC>ACC	p.A380T
Pat_73	Post-Resistance	PGC	5225	37	6	41710082	41710082	Missense_Mutation	SNP	C	T	124	30	c.593G>A	c.(592-594)GGC>GAC	p.G198D
Pat_73	Post-Resistance	KLC4	89953	37	6	43029158	43029158	Missense_Mutation	SNP	G	A	73	15	c.85G>A	c.(85-87)GTC>ATC	p.V29I
Pat_73	Post-Resistance	ZNF318	24149	37	6	43323487	43323487	Missense_Mutation	SNP	G	A	124	749	c.1585C>T	c.(1585-1587)CCC>TCC	p.P529S
Pat_73	Post-Resistance	GNA12	2768	37	7	2834734	2834734	Missense_Mutation	SNP	G	A	80	133	c.353C>T	c.(352-354)CCT>CTT	p.P118L
Pat_73	Post-Resistance	TMEM195	392636	37	7	15584403	15584403	Missense_Mutation	SNP	C	T	65	123	c.403G>A	c.(403-405)GCT>ACT	p.A135T
Pat_73	Post-Resistance	NPVF	64111	37	7	25266503	25266503	Missense_Mutation	SNP	C	T	69	123	c.281G>A	c.(280-282)AGG>AAG	p.R94K
Pat_73	Post-Resistance	INHBA	3624	37	7	41729438	41729438	Missense_Mutation	SNP	G	A	58	83	c.1091C>T	c.(1090-1092)TCC>TTC	p.S364F
Pat_73	Post-Resistance	VWC2	375567	37	7	49842374	49842374	Missense_Mutation	SNP	C	T	68	85	c.764C>T	c.(763-765)CCC>CTC	p.P255L
Pat_73	Post-Resistance	MET	4233	37	7	116380979	116380979	Missense_Mutation	SNP	C	T	153	39	c.1601C>T	c.(1600-1602)CCC>CTC	p.P534L
Pat_73	Post-Resistance	BRAF	673	37	7	140453136	140453136	Missense_Mutation	SNP	A	T	69	17	c.1799T>A	c.(1798-1800)GTG>GAG	p.V600E
Pat_73	Post-Resistance	CSMD1	64478	37	8	2976008	2976008	Missense_Mutation	SNP	G	A	64	50	c.6346C>T	c.(6346-6348)CCT>TCT	p.P2116S
Pat_73	Post-Resistance	SGK223	157285	37	8	8175867	8175867	Missense_Mutation	SNP	C	T	39	108	c.4018G>A	c.(4018-4020)GAG>AAG	p.E1340K
Pat_73	Post-Resistance	XKR6	286046	37	8	10755518	10755518	Nonsense_Mutation	SNP	G	A	29	58	c.1870C>T	c.(1870-1872)CGA>TGA	p.R624*
Pat_73	Post-Resistance	SLC7A2	6542	37	8	17417899	17417899	Missense_Mutation	SNP	C	T	36	56	c.1361C>T	c.(1360-1362)TCG>TTG	p.S454L
Pat_73	Post-Resistance	REEP4	80346	37	8	21997703	21997703	Missense_Mutation	SNP	G	C	18	55	c.164C>G	c.(163-165)ACA>AGA	p.T55R
Pat_73	Post-Resistance	ADAMDEC1	27299	37	8	24253266	24253266	Missense_Mutation	SNP	G	A	21	27	c.397G>A	c.(397-399)GAA>AAA	p.E133K
Pat_73	Post-Resistance	NRG1	3084	37	8	32453417	32453417	Missense_Mutation	SNP	G	A	77	104	c.172G>A	c.(172-174)GAA>AAA	p.E58K
Pat_73	Post-Resistance	ADAM2	2515	37	8	39645680	39645680	Missense_Mutation	SNP	C	T	41	53	c.733G>A	c.(733-735)GAG>AAG	p.E245K
Pat_73	Post-Resistance	PREX2	80243	37	8	68981348	68981348	Missense_Mutation	SNP	G	A	44	25	c.1420G>A	c.(1420-1422)GAG>AAG	p.E474K
Pat_73	Post-Resistance	HNF4G	3174	37	8	76471119	76471119	Missense_Mutation	SNP	C	T	72	152	c.829C>T	c.(829-831)CGG>TGG	p.R277W
Pat_73	Post-Resistance	RIMS2	9699	37	8	105263362	105263362	Missense_Mutation	SNP	G	A	19	16	c.3856G>A	c.(3856-3858)GAA>AAA	p.E1286K
Pat_73	Post-Resistance	ARC	23237	37	8	143695299	143695299	Missense_Mutation	SNP	C	T	11	4	c.334G>A	c.(334-336)GAG>AAG	p.E112K
Pat_73	Post-Resistance	OR13C8	138802	37	9	107332146	107332146	Missense_Mutation	SNP	G	A	23	49	c.698G>A	c.(697-699)GGA>GAA	p.G233E
Pat_73	Post-Resistance	OR13C9	286362	37	9	107380371	107380371	Missense_Mutation	SNP	G	A	74	96	c.115C>T	c.(115-117)CTT>TTT	p.L39F
Pat_73	Post-Resistance	TNC	3371	37	9	117852964	117852964	Missense_Mutation	SNP	C	T	194	409	c.334G>A	c.(334-336)GGC>AGC	p.G112S
Pat_73	Post-Resistance	USP20	10868	37	9	132641906	132641906	Missense_Mutation	SNP	A	G	8	64	c.2567A>G	c.(2566-2568)CAT>CGT	p.H856R
Pat_73	Post-Resistance	FAM78A	286336	37	9	134151461	134151461	Missense_Mutation	SNP	C	G	31	3	c.106G>C	c.(106-108)GAA>CAA	p.E36Q
Pat_73	Post-Resistance	TUBBP5	643224	37	9	141071420	141071420	Missense_Mutation	SNP	G	A	6	85	c.823G>A	c.(823-825)GAC>AAC	p.D275N
Pat_73	Post-Resistance	ZC4H2	55906	37	X	64137703	64137703	Missense_Mutation	SNP	G	A	8	1	c.635C>T	c.(634-636)TCC>TTC	p.S212F
Pat_73	Post-Resistance	ZCCHC5	203430	37	X	77913110	77913110	Missense_Mutation	SNP	G	A	9	1	c.808C>T	c.(808-810)CCC>TCC	p.P270S
Pat_73	Post-Resistance	GPRASP1	9737	37	X	101909266	101909266	Missense_Mutation	SNP	T	G	64	12	c.425T>G	c.(424-426)GTT>GGT	p.V142G
Pat_73	Post-Resistance	MAGEA10	4109	37	X	151303681	151303681	Missense_Mutation	SNP	C	T	77	17	c.412G>A	c.(412-414)GTG>ATG	p.V138M
Pat_74	Pre-Treatment	CASP9	842	37	1	15844799	15844799	Missense_Mutation	SNP	G	A	33	58	c.224C>T	c.(223-225)TCC>TTC	p.S75F
Pat_74	Pre-Treatment	ATP13A2	23400	37	1	17330867	17330867	Missense_Mutation	SNP	A	G	22	33	c.517T>C	c.(517-519)TAT>CAT	p.Y173H
Pat_74	Pre-Treatment	CSMD2	114784	37	1	34191090	34191090	Missense_Mutation	SNP	C	T	29	49	c.2435G>A	c.(2434-2436)CGG>CAG	p.R812Q
Pat_74	Pre-Treatment	DHCR24	1718	37	1	55337202	55337202	Missense_Mutation	SNP	G	A	37	43	c.697C>T	c.(697-699)CCT>TCT	p.P233S
Pat_74	Pre-Treatment	LEPR	3953	37	1	66058389	66058389	Nonsense_Mutation	SNP	C	T	41	69	c.544C>T	c.(544-546)CAG>TAG	p.Q182*
Pat_74	Pre-Treatment	C1orf173	127254	37	1	75038497	75038497	Missense_Mutation	SNP	C	T	32	39	c.2897G>A	c.(2896-2898)AGA>AAA	p.R966K
Pat_74	Pre-Treatment	AK5	26289	37	1	77949003	77949003	Missense_Mutation	SNP	G	A	24	42	c.1061G>A	c.(1060-1062)GGT>GAT	p.G354D
Pat_74	Pre-Treatment	KIAA1324	57535	37	1	109742693	109742693	Missense_Mutation	SNP	G	T	3	59	c.2641G>T	c.(2641-2643)GTG>TTG	p.V881L
Pat_74	Pre-Treatment	SLC16A1	6566	37	1	113471717	113471717	Missense_Mutation	SNP	C	T	12	27	c.214G>A	c.(214-216)GGA>AGA	p.G72R
Pat_74	Pre-Treatment	NBPF10	100132406	37	1	145327548	145327548	Missense_Mutation	SNP	A	G	3	15	c.4330A>G	c.(4330-4332)AAT>GAT	p.N1444D
Pat_74	Pre-Treatment	NBPF10	100132406	37	1	146398425	146398425	Missense_Mutation	SNP	C	A	6	254	c.1224C>A	c.(1222-1224)GAC>GAA	p.D408E
Pat_74	Pre-Treatment	TCHHL1	126637	37	1	152059823	152059823	Missense_Mutation	SNP	A	C	67	80	c.335T>G	c.(334-336)GTT>GGT	p.V112G

Pat_74	Pre-Treatment	ASH1L	55870	37	1	155313160	155313161	Missense_Mutation	DNP	GG	AA	42	93	.8252_8253CC>T	c.(8251-8253)CCC>CTT	p.P2751L
Pat_74	Pre-Treatment	SPTA1	6708	37	1	158596788	158596788	Missense_Mutation	SNP	C	T	33	58	c.5674G>A	c.(5674-5676)GAG>AAG	p.E1892K
Pat_74	Pre-Treatment	REN	5972	37	1	204128651	204128651	Missense_Mutation	SNP	C	T	4	93	c.565G>A	c.(565-567)GAG>AAG	p.E189K
Pat_74	Pre-Treatment	WDR26	80232	37	1	224592184	224592184	Missense_Mutation	SNP	A	G	67	97	c.806T>C	c.(805-807)CTT>CCT	p.L269P
Pat_74	Pre-Treatment	NEBL	10529	37	10	21134266	21134266	Missense_Mutation	SNP	A	T	21	20	c.1148T>A	c.(1147-1149)ATT>AAT	p.I383N
Pat_74	Pre-Treatment	SGMS1	259230	37	10	52103520	52103520	Missense_Mutation	SNP	G	A	24	23	c.355C>T	c.(355-357)CCC>TCC	p.P119S
Pat_74	Pre-Treatment	LOC729020	729020	37	10	105005787	105005787	Missense_Mutation	SNP	C	T	12	13	c.34C>T	c.(34-36)CTC>TTC	p.L12F
Pat_74	Pre-Treatment	PHRF1	57661	37	11	607875	607875	Nonsense_Mutation	SNP	G	T	16	37	c.2419G>T	c.(2419-2421)GAG>TAG	p.E807*
Pat_74	Pre-Treatment	MUC6	4588	37	11	1017526	1017526	Missense_Mutation	SNP	G	C	9	508	c.5275C>G	c.(5275-5277)CCT>GCT	p.P1759A
Pat_74	Pre-Treatment	MUC5B	727897	37	11	1271468	1271468	Missense_Mutation	SNP	C	T	6	101	c.14777C>T	.(14776-14778)CCG>CT	p.P4926L
Pat_74	Pre-Treatment	OR51G2	81282	37	11	4936406	4936406	Missense_Mutation	SNP	G	A	23	41	c.488C>T	c.(487-489)CCA>CTA	p.P163L
Pat_74	Pre-Treatment	NAV2	89797	37	11	19970400	19970400	Nonsense_Mutation	SNP	C	T	38	53	c.2488C>T	c.(2488-2490)CGA>TGA	p.R830*
Pat_74	Pre-Treatment	DGKZ	8525	37	11	46400602	46400602	Missense_Mutation	SNP	T	C	11	8	c.3044T>C	c.(3043-3045)CTC>CCC	p.L1015P
Pat_74	Pre-Treatment	ANKRD13D	338692	37	11	67067552	67067552	Missense_Mutation	SNP	G	A	4	154	c.770G>A	c.(769-771)CGG>CAG	p.R257Q
Pat_74	Pre-Treatment	BCO2	83875	37	11	112084481	112084481	Missense_Mutation	SNP	G	A	124	202	c.1229G>A	c.(1228-1230)AGG>AAG	p.R410K
Pat_74	Pre-Treatment	KIRREL3	84623	37	11	126294608	126294608	Missense_Mutation	SNP	C	T	4	142	c.2204G>A	c.(2203-2205)GGC>GAC	p.G735D
Pat_74	Pre-Treatment	FLI1	2313	37	11	128680651	128680651	Missense_Mutation	SNP	C	T	49	38	c.1127C>T	c.(1126-1128)TCG>TTG	p.S376L
Pat_74	Pre-Treatment	FOXM1	2305	37	12	2981324	2981324	Missense_Mutation	SNP	G	A	98	172	c.592C>T	c.(592-594)CGC>TGC	p.R198C
Pat_74	Pre-Treatment	PRB2	653247	37	12	11546771	11546771	Missense_Mutation	SNP	G	C	5	242	c.241C>G	c.(241-243)CCA>GCA	p.P81A
Pat_74	Pre-Treatment	PTPRO	5800	37	12	15677831	15677831	Missense_Mutation	SNP	G	A	37	52	c.1975G>A	c.(1975-1977)GAC>AAC	p.D659N
Pat_74	Pre-Treatment	PLCZ1	89869	37	12	18876359	18876359	Missense_Mutation	SNP	T	C	28	37	c.253A>G	c.(253-255)AAA>GAA	p.K85E
Pat_74	Pre-Treatment	SFRS2IP	9169	37	12	46320119	46320119	Missense_Mutation	SNP	G	A	37	98	c.3365C>T	c.(3364-3366)TCC>TTC	p.S1122F
Pat_74	Pre-Treatment	MIP	4284	37	12	56848247	56848247	Missense_Mutation	SNP	C	T	30	64	c.151G>A	c.(151-153)GCC>ACC	p.A51T
Pat_74	Pre-Treatment	GEFT	115557	37	12	58010217	58010217	Missense_Mutation	SNP	C	T	23	33	c.1571C>T	c.(1570-1572)CCC>CTC	p.P524L
Pat_74	Pre-Treatment	ZFC3H1	196441	37	12	72050857	72050857	Missense_Mutation	SNP	C	T	33	69	c.823G>A	c.(823-825)GTC>ATC	p.V275I
Pat_74	Pre-Treatment	POLR3B	55703	37	12	106889920	106889921	Missense_Mutation	DNP	TC	AT	93	133	.2801_2802TC>A	c.(2800-2802)TTC>TAT	p.F934Y
Pat_74	Pre-Treatment	RFX4	5992	37	12	107113748	107113748	Missense_Mutation	SNP	G	C	29	58	c.1149G>C	c.(1147-1149)GAG>GAC	p.E383D
Pat_74	Pre-Treatment	TRPC4	7223	37	13	38225514	38225515	Missense_Mutation	DNP	GG	AA	29	82	.1966_1967CC>T	c.(1966-1968)CCC>TTC	p.P656F
Pat_74	Pre-Treatment	ARHGAP5	394	37	14	32562120	32562120	Missense_Mutation	SNP	G	A	50	82	c.2245G>A	c.(2245-2247)GCT>ACT	p.A749T
Pat_74	Pre-Treatment	AKAP6	9472	37	14	33292789	33292789	Missense_Mutation	SNP	G	A	26	42	c.5770G>A	c.(5770-5772)GGG>AGG	p.G1924R
Pat_74	Pre-Treatment	RTN1	6252	37	14	60213112	60213112	Missense_Mutation	SNP	G	A	25	25	c.329C>T	c.(328-330)TCT>TTT	p.S110F
Pat_74	Pre-Treatment	C14orf43	91748	37	14	74206609	74206609	Missense_Mutation	SNP	G	A	40	59	c.103C>T	c.(103-105)CCC>TCC	p.P35S
Pat_74	Pre-Treatment	C14orf109	26175	37	14	93652819	93652819	Missense_Mutation	SNP	C	T	31	46	c.313C>T	c.(313-315)CCT>TCT	p.P105S
Pat_74	Pre-Treatment	PPP4R4	57718	37	14	94733340	94733340	Missense_Mutation	SNP	G	A	25	33	c.2423G>A	c.(2422-2424)GGA>GAA	p.G808E
Pat_74	Pre-Treatment	EML1	2009	37	14	100344907	100344907	Missense_Mutation	SNP	C	T	69	116	c.469C>T	c.(469-471)CGC>TGC	p.R157C
Pat_74	Pre-Treatment	OR4N4	283694	37	15	22332432	22332432	Translation_Start_Site	SNP	C	T	7	155	c.-742C>T	.(-744--740)AACGT>AATGT	
Pat_74	Pre-Treatment	C15orf2	23742	37	15	24922585	24922585	Missense_Mutation	SNP	C	T	76	163	c.1571C>T	c.(1570-1572)CCT>CTT	p.P524L
Pat_74	Pre-Treatment	VPS39	23339	37	15	42476789	42476789	Missense_Mutation	SNP	G	A	101	220	c.677C>T	c.(676-678)ACC>ATC	p.T226I
Pat_74	Pre-Treatment	CDAN1	146059	37	15	43022848	43022848	Missense_Mutation	SNP	G	A	4	51	c.2122C>T	c.(2122-2124)CCC>TCC	p.P708S
Pat_74	Pre-Treatment	TNFAIP8L3	388121	37	15	51350497	51350497	Missense_Mutation	SNP	C	T	64	102	c.460G>A	c.(460-462)GAG>AAG	p.E154K
Pat_74	Pre-Treatment	UNC13C	440279	37	15	54306599	54306599	Missense_Mutation	SNP	G	A	18	26	c.1499G>A	c.(1498-1500)AGA>AAA	p.R500K
Pat_74	Pre-Treatment	IL21R	50615	37	16	27460591	27460591	Missense_Mutation	SNP	C	T	4	46	c.1604C>T	c.(1603-1605)CCC>CTC	p.P535L
Pat_74	Pre-Treatment	CSNK2A2	1459	37	16	58199491	58199491	Missense_Mutation	SNP	T	C	35	53	c.949A>G	c.(949-951)AAA>GAA	p.K317E
Pat_74	Pre-Treatment	SPNS2	124976	37	17	4428405	4428405	Missense_Mutation	SNP	C	T	4	75	c.490C>T	c.(490-492)CGC>TGC	p.R164C
Pat_74	Pre-Treatment	SMTNL2	342527	37	17	4496274	4496274	Missense_Mutation	SNP	C	T	12	23	c.538C>T	c.(538-540)CCC>TCC	p.P180S
Pat_74	Pre-Treatment	DNAH2	146754	37	17	7636433	7636433	Missense_Mutation	SNP	G	A	4	130	c.428G>A	c.(427-429)CGC>CAC	p.R143H
Pat_74	Pre-Treatment	LLGL1	3996	37	17	18138206	18138206	Missense_Mutation	SNP	G	A	3	43	c.959G>A	c.(958-960)CGC>CAC	p.R320H

Pat_74	Pre-Treatment	TBC1D3	729873	37	17	36288302	36288302	Splice_Site	SNP	G	A	38	309	c.387_splice	c.e6+1	p.Q129_splice
Pat_74	Pre-Treatment	KRTAP1-3	81850	37	17	39190779	39190779	Missense_Mutation	SNP	T	C	5	22	c.295A>G	c.(295-297)AGT>GGT	p.S99G
Pat_74	Pre-Treatment	KRTAP4-8	728224	37	17	39253960	39253960	Missense_Mutation	SNP	C	T	5	14	c.377G>A	c.(376-378)CGC>CAC	p.R126H
Pat_74	Pre-Treatment	EFTUD2	9343	37	17	42936476	42936476	Missense_Mutation	SNP	C	T	4	118	c.1934G>A	c.(1933-1935)CGG>CAG	p.R645Q
Pat_74	Pre-Treatment	WNT9B	7484	37	17	44952593	44952593	Missense_Mutation	SNP	G	A	6	18	c.461G>A	c.(460-462)CGG>CAG	p.R154Q
Pat_74	Pre-Treatment	HLF	3131	37	17	53345135	53345135	Missense_Mutation	SNP	G	A	18	34	c.139G>A	c.(139-141)GAA>AAA	p.E47K
Pat_74	Pre-Treatment	MKS1	54903	37	17	56291149	56291149	Missense_Mutation	SNP	G	T	4	89	c.726C>A	c.(724-726)TTC>TTA	p.F242L
Pat_74	Pre-Treatment	TRIM37	4591	37	17	57153057	57153057	Missense_Mutation	SNP	G	C	26	33	c.635C>G	c.(634-636)ACC>AGC	p.T212S
Pat_74	Pre-Treatment	QRICH2	84074	37	17	74288358	74288358	Missense_Mutation	SNP	A	T	6	254	c.1952T>A	c.(1951-1953)GTT>GAT	p.V651D
Pat_74	Pre-Treatment	CCDC40	55036	37	17	78063636	78063636	Missense_Mutation	SNP	G	A	3	64	c.2785G>A	c.(2785-2787)GGC>AGC	p.G929S
Pat_74	Pre-Treatment	CSNK1D	1453	37	17	80206800	80206800	Missense_Mutation	SNP	G	A	3	9	c.1148C>T	c.(1147-1149)TCG>TTG	p.S383L
Pat_74	Pre-Treatment	TXNDC2	84203	37	18	9887155	9887155	Missense_Mutation	SNP	A	G	5	228	c.679A>G	c.(679-681)ACC>GCC	p.T227A
Pat_74	Pre-Treatment	KLHL14	57565	37	18	30260407	30260407	Missense_Mutation	SNP	G	A	82	133	c.1394C>T	c.(1393-1395)GCG>GTG	p.A465V
Pat_74	Pre-Treatment	ZNF57	126295	37	19	2917793	2917793	Missense_Mutation	SNP	T	C	5	67	c.1174T>C	c.(1174-1176)TAT>CAT	p.Y392H
Pat_74	Pre-Treatment	ZNF57	126295	37	19	2917807	2917807	Missense_Mutation	SNP	A	C	4	61	c.1188A>C	c.(1186-1188)CAA>CAC	p.Q396H
Pat_74	Pre-Treatment	ZNF57	126295	37	19	2917842	2917842	Missense_Mutation	SNP	G	A	4	57	c.1223G>A	c.(1222-1224)CGA>CAA	p.R408Q
Pat_74	Pre-Treatment	ZNF57	126295	37	19	2917857	2917857	Missense_Mutation	SNP	C	T	5	64	c.1238C>T	c.(1237-1239)ACG>ATG	p.T413M
Pat_74	Pre-Treatment	TLE6	79816	37	19	2991857	2991857	Missense_Mutation	SNP	C	T	10	23	c.892C>T	c.(892-894)CCT>TCT	p.P298S
Pat_74	Pre-Treatment	SHD	56961	37	19	4290560	4290560	Missense_Mutation	SNP	C	T	25	70	c.953C>T	c.(952-954)TCA>TTA	p.S318L
Pat_74	Pre-Treatment	ZNF844	284391	37	19	12187307	12187307	Missense_Mutation	SNP	G	C	6	189	c.1372G>C	c.(1372-1374)GAT>CAT	p.D458H
Pat_74	Pre-Treatment	ZNF563	147837	37	19	12429554	12429554	Missense_Mutation	SNP	C	T	8	277	c.1285G>A	c.(1285-1287)GCG>ACG	p.A429T
Pat_74	Pre-Treatment	ZNF563	147837	37	19	12429722	12429722	Missense_Mutation	SNP	T	C	9	317	c.1117A>G	c.(1117-1119)ACG>GCG	p.T373A
Pat_74	Pre-Treatment	ZNF564	163050	37	19	12637723	12637723	Missense_Mutation	SNP	C	T	6	234	c.1199G>A	c.(1198-1200)AGA>AAA	p.R400K
Pat_74	Pre-Treatment	RFX1	5989	37	19	14104424	14104424	Missense_Mutation	SNP	G	A	4	39	c.232C>T	c.(232-234)CTC>TTC	p.L78F
Pat_74	Pre-Treatment	SYDE1	85360	37	19	15224562	15224562	Missense_Mutation	SNP	G	A	58	77	c.1996G>A	c.(1996-1998)GGG>AGG	p.G666R
Pat_74	Pre-Treatment	CYP4F12	66002	37	19	15807289	15807289	Missense_Mutation	SNP	C	T	68	114	c.1364C>T	c.(1363-1365)CCT>CTT	p.P455L
Pat_74	Pre-Treatment	DDX49	54555	37	19	19035761	19035761	Missense_Mutation	SNP	C	A	4	64	c.1000C>A	c.(1000-1002)CAC>AAC	p.H334N
Pat_74	Pre-Treatment	LPAR2	9170	37	19	19737765	19737765	Nonsense_Mutation	SNP	A	T	9	13	c.329T>A	c.(328-330)TTG>TAG	p.L110*
Pat_74	Pre-Treatment	ZNF493	284443	37	19	21606614	21606614	Missense_Mutation	SNP	G	A	5	139	c.769G>A	c.(769-771)GCC>ACC	p.A257T
Pat_74	Pre-Treatment	ZNF208	7757	37	19	22156652	22156652	Missense_Mutation	SNP	T	G	8	117	c.1184A>C	c.(1183-1185)AAA>ACA	p.K395T
Pat_74	Pre-Treatment	ZNF681	148213	37	19	23927307	23927307	Missense_Mutation	SNP	G	T	7	319	c.1045C>A	c.(1045-1047)CAG>AAG	p.Q349K
Pat_74	Pre-Treatment	CD22	933	37	19	35828922	35828922	Missense_Mutation	SNP	A	T	7	11	c.983A>T	c.(982-984)CAG>CTG	p.Q328L
Pat_74	Pre-Treatment	RYR1	6261	37	19	38985160	38985160	Missense_Mutation	SNP	C	T	23	25	c.6443C>T	c.(6442-6444)TCC>TTC	p.S2148F
Pat_74	Pre-Treatment	PRX	57716	37	19	40902620	40902620	Missense_Mutation	SNP	G	C	5	172	c.1639C>G	c.(1639-1641)CAG>GAG	p.Q547E
Pat_74	Pre-Treatment	RPL18	6141	37	19	49119422	49119422	Missense_Mutation	SNP	C	T	4	66	c.335G>A	c.(334-336)CGC>CAC	p.R112H
Pat_74	Pre-Treatment	ZNF845	91664	37	19	53855364	53855364	Missense_Mutation	SNP	C	T	13	234	c.1436C>T	c.(1435-1437)ACA>ATA	p.T479I
Pat_74	Pre-Treatment	LILRA3	11026	37	19	54802527	54802527	Missense_Mutation	SNP	G	A	25	63	c.914C>T	c.(913-915)TCC>TTC	p.S305F
Pat_74	Pre-Treatment	ZIK1	284307	37	19	58102412	58102412	Missense_Mutation	SNP	C	A	4	110	c.1233C>A	c.(1231-1233)GAC>GAA	p.D411E
Pat_74	Pre-Treatment	ZIK1	284307	37	19	58102421	58102421	Missense_Mutation	SNP	A	T	4	101	c.1242A>T	c.(1240-1242)AAA>AAT	p.K414N
Pat_74	Pre-Treatment	C2orf16	84226	37	2	27804634	27804634	Missense_Mutation	SNP	G	A	8	505	c.5195G>A	c.(5194-5196)AGA>AAA	p.R1732K
Pat_74	Pre-Treatment	EXOC6B	23233	37	2	72786608	72786608	Nonsense_Mutation	SNP	G	A	21	34	c.889C>T	c.(889-891)CGA>TGA	p.R297*
Pat_74	Pre-Treatment	TET3	200424	37	2	74320773	74320773	Missense_Mutation	SNP	C	T	27	59	c.2842C>T	c.(2842-2844)CTC>TTC	p.L948F
Pat_74	Pre-Treatment	TGOLN2	10618	37	2	85554362	85554362	Missense_Mutation	SNP	G	T	10	696	c.493C>A	c.(493-495)CCT>ACT	p.P165T
Pat_74	Pre-Treatment	CNNM4	26504	37	2	97464908	97464908	Missense_Mutation	SNP	G	A	4	91	c.1796G>A	c.(1795-1797)CGC>CAC	p.R599H
Pat_74	Pre-Treatment	ANKRD36B	57730	37	2	98201772	98201772	Missense_Mutation	SNP	C	T	3	14	c.251G>A	c.(250-252)CGT>CAT	p.R84H
Pat_74	Pre-Treatment	LY75	4065	37	2	160746866	160746866	Nonsense_Mutation	SNP	C	T	21	48	c.660G>A	c.(658-660)TGG>TGA	p.W220*
Pat_74	Pre-Treatment	XIRP2	129446	37	2	168102458	168102458	Missense_Mutation	SNP	C	T	44	62	c.4556C>T	c.(4555-4557)CCT>CTT	p.P1519L

Pat_74	Pre-Treatment	TTN	7273	37	2	179396519	179396520	Missense_Mutation	DNP	GG	TA	29	47	97118_97119CC>	c.(97117-97119)GCC>GTA	p.A32373V
Pat_74	Pre-Treatment	DNAH7	56171	37	2	196728992	196728992	Missense_Mutation	SNP	C	T	42	83	c.7387G>A	c.(7387-7389)GAT>AAT	p.D2463N
Pat_74	Pre-Treatment	PARD3B	117583	37	2	206050515	206050515	Missense_Mutation	SNP	C	T	66	123	c.1952C>T	c.(1951-1953)GCC>GTC	p.A651V
Pat_74	Pre-Treatment	KIAA1486	57624	37	2	226378119	226378119	Missense_Mutation	SNP	G	A	28	44	c.254G>A	c.(253-255)GGA>GAA	p.G85E
Pat_74	Pre-Treatment	COL4A3	1285	37	2	228128587	228128587	Missense_Mutation	SNP	G	A	13	19	c.1242G>A	c.(1240-1242)ATG>ATA	p.M414I
Pat_74	Pre-Treatment	FRG1B	284802	37	20	29625875	29625875	Missense_Mutation	SNP	T	C	6	86	c.29T>C	c.(28-30)ATC>ACC	p.I10T
Pat_74	Pre-Treatment	RBM12	10137	37	20	34242439	34242439	Missense_Mutation	SNP	T	C	4	87	c.806A>G	c.(805-807)AAC>AGC	p.N269S
Pat_74	Pre-Treatment	TOX2	84969	37	20	42694670	42694670	Missense_Mutation	SNP	C	A	24	20	c.1225C>A	c.(1225-1227)CCC>ACC	p.P409T
Pat_74	Pre-Treatment	RTEL1	51750	37	20	62305428	62305428	Missense_Mutation	SNP	G	A	3	37	c.901G>A	c.(901-903)GCG>ACG	p.A301T
Pat_74	Pre-Treatment	DOPEY2	9980	37	21	37636074	37636074	Missense_Mutation	SNP	C	T	107	184	c.5449C>T	c.(5449-5451)CCC>TCC	p.P1817S
Pat_74	Pre-Treatment	DSCAM	1826	37	21	41452217	41452217	Missense_Mutation	SNP	G	A	21	39	c.4282C>T	c.(4282-4284)CCA>TCA	p.P1428S
Pat_74	Pre-Treatment	TRIOBP	11078	37	22	38086744	38086744	Translation_Start_Site	SNP	C	T	4	144	c.-556C>T	(-558--554)CACGG>CATGG	
Pat_74	Pre-Treatment	TRIOBP	11078	37	22	38120695	38120695	Missense_Mutation	SNP	C	T	41	63	c.2132C>T	c.(2131-2133)CCT>CTT	p.P711L
Pat_74	Pre-Treatment	CCR8	1237	37	3	39374063	39374063	Missense_Mutation	SNP	G	A	80	114	c.241G>A	c.(241-243)GAC>AAC	p.D81N
Pat_74	Pre-Treatment	CSPG5	10675	37	3	47618466	47618466	Missense_Mutation	SNP	C	A	4	47	c.1050G>T	c.(1048-1050)TTG>TTT	p.L350F
Pat_74	Pre-Treatment	ARIH2	10425	37	3	48999097	48999097	Missense_Mutation	SNP	C	T	23	30	c.308C>T	c.(307-309)TCA>TTA	p.S103L
Pat_74	Pre-Treatment	BSN	8927	37	3	49694583	49694583	Missense_Mutation	SNP	C	T	20	23	c.7594C>T	c.(7594-7596)CCC>TCC	p.P2532S
Pat_74	Pre-Treatment	OR5H2	79310	37	3	98002110	98002110	Missense_Mutation	SNP	C	T	35	49	c.379C>T	c.(379-381)CGC>TGC	p.R127C
Pat_74	Pre-Treatment	NIT2	56954	37	3	100058695	100058695	Missense_Mutation	SNP	C	T	14	24	c.163C>T	c.(163-165)CCT>TCT	p.P55S
Pat_74	Pre-Treatment	ARHGAP31	57514	37	3	119112312	119112312	Splice_Site	SNP	A	G	53	76	c.882_splice	c.e8-2	p.K294_splice
Pat_74	Pre-Treatment	ILDR1	286676	37	3	121712140	121712140	Missense_Mutation	SNP	C	T	7	11	c.1456G>A	c.(1456-1458)GAG>AAG	p.E486K
Pat_74	Pre-Treatment	LEKR1	389170	37	3	156742621	156742622	Missense_Mutation	DNP	GA	AC	19	25	c.364_365GA>AC	c.(364-366)GAA>ACA	p.E122T
Pat_74	Pre-Treatment	LRRC34	151827	37	3	169511487	169511487	Missense_Mutation	SNP	C	T	38	61	c.1196G>A	c.(1195-1197)GGA>GAA	p.G399E
Pat_74	Pre-Treatment	SAMD7	344658	37	3	169639115	169639115	Missense_Mutation	SNP	G	T	50	94	c.200G>T	c.(199-201)CGG>CTG	p.R67L
Pat_74	Pre-Treatment	TPRG1	285386	37	3	189038465	189038465	Missense_Mutation	SNP	G	C	19	40	c.684G>C	c.(682-684)AAG>AAC	p.K228N
Pat_74	Pre-Treatment	TP63	8626	37	3	189607246	189607246	Missense_Mutation	SNP	C	T	90	127	c.1625C>T	c.(1624-1626)CCG>CTG	p.P542L
Pat_74	Pre-Treatment	LEPREL1	55214	37	3	189690698	189690698	Missense_Mutation	SNP	G	A	44	71	c.1664C>T	c.(1663-1665)TCC>TTC	p.S555F
Pat_74	Pre-Treatment	UBXN7	26043	37	3	196089400	196089401	Missense_Mutation	DNP	GG	AA	37	71	c.992_993CC>TT	c.(991-993)TCC>TTT	p.S331F
Pat_74	Pre-Treatment	RNF168	165918	37	3	196229915	196229915	Missense_Mutation	SNP	C	T	5	186	c.130G>A	c.(130-132)GTC>ATC	p.V44I
Pat_74	Pre-Treatment	ZNF141	7700	37	4	367026	367026	Missense_Mutation	SNP	T	C	4	101	c.800T>C	c.(799-801)TTC>TCC	p.F267S
Pat_74	Pre-Treatment	CCDC158	339965	37	4	77247121	77247121	Missense_Mutation	SNP	G	A	64	128	c.3046C>T	c.(3046-3048)CCT>TCT	p.P1016S
Pat_74	Pre-Treatment	CFI	3426	37	4	110663728	110663728	Nonsense_Mutation	SNP	G	A	26	50	c.1453C>T	c.(1453-1455)CAG>TAG	p.Q485*
Pat_74	Pre-Treatment	INTU	27152	37	4	128564983	128564983	Missense_Mutation	SNP	G	A	50	56	c.454G>A	c.(454-456)GTC>ATC	p.V152I
Pat_74	Pre-Treatment	PCDH10	57575	37	4	134073358	134073358	Missense_Mutation	SNP	G	T	3	14	c.2063G>T	c.(2062-2064)GGG>GTG	p.G688V
Pat_74	Pre-Treatment	PCDH18	54510	37	4	138451640	138451640	Missense_Mutation	SNP	G	A	45	59	c.1603C>T	c.(1603-1605)CAT>TAT	p.H535Y
Pat_74	Pre-Treatment	MRPL36	64979	37	5	1798790	1798790	Missense_Mutation	SNP	C	T	4	103	c.260G>A	c.(259-261)CGG>CAG	p.R87Q
Pat_74	Pre-Treatment	DNAH5	1767	37	5	13864741	13864741	Missense_Mutation	SNP	C	T	22	40	c.4361G>A	c.(4360-4362)CGA>CAA	p.R1454Q
Pat_74	Pre-Treatment	SPZ1	84654	37	5	79616461	79616461	Missense_Mutation	SNP	G	C	6	146	c.427G>C	c.(427-429)GAG>CAG	p.E143Q
Pat_74	Pre-Treatment	SPZ1	84654	37	5	79616605	79616605	Missense_Mutation	SNP	C	G	3	94	c.571C>G	c.(571-573)CAG>GAG	p.Q191E
Pat_74	Pre-Treatment	MBLAC2	153364	37	5	89757100	89757100	Nonsense_Mutation	SNP	G	A	43	59	c.724C>T	c.(724-726)CGA>TGA	p.R242*
Pat_74	Pre-Treatment	EPB41L4A	64097	37	5	111601990	111601990	Nonsense_Mutation	SNP	G	A	7	12	c.373C>T	c.(373-375)CAG>TAG	p.Q125*
Pat_74	Pre-Treatment	ADAM19	8728	37	5	156924013	156924013	Missense_Mutation	SNP	G	A	19	12	c.1483C>T	c.(1483-1485)CCT>TCT	p.P495S
Pat_74	Pre-Treatment	HIVEP1	3096	37	6	12163562	12163562	Missense_Mutation	SNP	C	T	136	187	c.7025C>T	c.(7024-7026)CCC>CTC	p.P2342L
Pat_74	Pre-Treatment	VARS	7407	37	6	31745399	31745399	Missense_Mutation	SNP	G	A	11	14	c.3767C>T	c.(3766-3768)GCC>GTC	p.A1256V
Pat_74	Pre-Treatment	PKHD1	5314	37	6	51890422	51890422	Missense_Mutation	SNP	G	A	62	85	c.4186C>T	c.(4186-4188)CCA>TCA	p.P1396S
Pat_74	Pre-Treatment	STXBP5	134957	37	6	147646094	147646094	Splice_Site	SNP	G	A	16	33	c.1803_splice	c.e17-1	p.K601_splice
Pat_74	Pre-Treatment	PACRG	135138	37	6	163735909	163735909	Missense_Mutation	SNP	G	T	22	57	c.781G>T	c.(781-783)GGG>TGG	p.G261W

Pat_74	Pre-Treatment	TTLL2	83887	37	6	167754658	167754658	Missense_Mutation	SNP	G	T	26	33	c.1270G>T	c.(1270-1272)GGG>TGG	p.G424W
Pat_74	Pre-Treatment	IL6	3569	37	7	22771151	22771151	Missense_Mutation	SNP	G	A	12	21	c.598G>A	c.(598-600)GAG>AAG	p.E200K
Pat_74	Pre-Treatment	ZNF727	442319	37	7	63538568	63538568	Missense_Mutation	SNP	T	C	4	71	c.1141T>C	c.(1141-1143)TCA>CCA	p.S381P
Pat_74	Pre-Treatment	ZNF727	442319	37	7	63538638	63538638	Missense_Mutation	SNP	G	C	4	104	c.1211G>C	c.(1210-1212)AGC>ACC	p.S404T
Pat_74	Pre-Treatment	ZNF727	442319	37	7	63538736	63538736	Missense_Mutation	SNP	C	T	3	52	c.1309C>T	c.(1309-1311)CCA>TCA	p.P437S
Pat_74	Pre-Treatment	ZNF727	442319	37	7	63538806	63538806	Missense_Mutation	SNP	C	G	4	65	c.1379C>G	c.(1378-1380)ACC>AGC	p.T460S
Pat_74	Pre-Treatment	NSUN5	55695	37	7	72717601	72717601	Missense_Mutation	SNP	G	A	37	51	c.1282C>T	c.(1282-1284)CCA>TCA	p.P428S
Pat_74	Pre-Treatment	ZAN	7455	37	7	100349878	100349878	Missense_Mutation	SNP	C	T	4	142	c.2150C>T	c.(2149-2151)CCC>CTC	p.P717L
Pat_74	Pre-Treatment	ZAN	7455	37	7	100350466	100350466	Missense_Mutation	SNP	C	T	11	182	c.2738C>T	c.(2737-2739)CCC>CTC	p.P913L
Pat_74	Pre-Treatment	ZAN	7455	37	7	100350474	100350474	Missense_Mutation	SNP	T	C	12	184	c.2746T>C	c.(2746-2748)TCC>CCC	p.S916P
Pat_74	Pre-Treatment	MUC17	140453	37	7	100676667	100676667	Missense_Mutation	SNP	A	G	10	791	c.1970A>G	c.(1969-1971)AAC>AGC	p.N657S
Pat_74	Pre-Treatment	MUC17	140453	37	7	100681421	100681421	Missense_Mutation	SNP	G	A	11	756	c.6724G>A	c.(6724-6726)GCA>ACA	p.A2242T
Pat_74	Pre-Treatment	MUC17	140453	37	7	100681455	100681455	Missense_Mutation	SNP	C	A	10	678	c.6758C>A	c.(6757-6759)ACT>AAT	p.T2253N
Pat_74	Pre-Treatment	MUC17	140453	37	7	100682124	100682124	Missense_Mutation	SNP	T	A	10	781	c.7427T>A	c.(7426-7428)CTT>CAT	p.L2476H
Pat_74	Pre-Treatment	MUC17	140453	37	7	100684301	100684302	Missense_Mutation	DNP	AC	CA	10	726	.9604_9605AC>C	c.(9604-9606)ACT>CAT	p.T3202H
Pat_74	Pre-Treatment	C7orf66	154907	37	7	108524203	108524203	Missense_Mutation	SNP	T	C	77	122	c.209A>G	c.(208-210)TAT>TGT	p.Y70C
Pat_74	Pre-Treatment	WNT2	7472	37	7	116960755	116960755	Missense_Mutation	SNP	G	A	4	20	c.176C>T	c.(175-177)CCA>CTA	p.P59L
Pat_74	Pre-Treatment	BRAF	673	37	7	140453136	140453136	Missense_Mutation	SNP	A	T	70	63	c.1799T>A	c.(1798-1800)GTG>GAG	p.V600E
Pat_74	Pre-Treatment	ATG9B	285973	37	7	150720253	150720253	Nonsense_Mutation	SNP	G	A	175	465	c.700C>T	c.(700-702)CGA>TGA	p.R234*
Pat_74	Pre-Treatment	DKK4	27121	37	8	42232353	42232353	Missense_Mutation	SNP	C	T	75	105	c.341G>A	c.(340-342)GGA>GAA	p.G114E
Pat_74	Pre-Treatment	SLCO5A1	81796	37	8	70673984	70673984	Missense_Mutation	SNP	C	T	18	34	c.1034G>A	c.(1033-1035)GGA>GAA	p.G345E
Pat_74	Pre-Treatment	FREM1	158326	37	9	14846015	14846015	Missense_Mutation	SNP	C	A	3	27	c.1336G>T	c.(1336-1338)GGT>TGT	p.G446C
Pat_74	Pre-Treatment	APBA1	320	37	9	72064588	72064588	Missense_Mutation	SNP	C	T	65	79	c.2093G>A	c.(2092-2094)GGG>GAG	p.G698E
Pat_74	Pre-Treatment	OR13D1	286365	37	9	107457507	107457507	Missense_Mutation	SNP	G	A	16	57	c.805G>A	c.(805-807)GCC>ACC	p.A269T
Pat_74	Pre-Treatment	OR13D1	286365	37	9	107457565	107457565	Missense_Mutation	SNP	T	C	3	85	c.863T>C	c.(862-864)CTT>CCT	p.L288P
Pat_74	Pre-Treatment	SLC44A1	23446	37	9	108128643	108128643	Missense_Mutation	SNP	G	A	4	77	c.1427G>A	c.(1426-1428)CGA>CAA	p.R476Q
Pat_74	Pre-Treatment	PTGS1	5742	37	9	125154609	125154609	Missense_Mutation	SNP	C	T	28	37	c.1586C>T	c.(1585-1587)TCC>TTC	p.S529F
Pat_74	Pre-Treatment	WDR34	89891	37	9	131403107	131403107	Missense_Mutation	SNP	G	A	31	32	c.298C>T	c.(298-300)CCG>TCG	p.P100S
Pat_74	Pre-Treatment	SEC16A	9919	37	9	139341390	139341390	Missense_Mutation	SNP	G	A	22	58	c.6709C>T	c.(6709-6711)CCA>TCA	p.P2237S
Pat_74	Pre-Treatment	TUBBP5	643224	37	9	141071195	141071195	Missense_Mutation	SNP	C	T	11	49	c.598C>T	c.(598-600)CCA>TCA	p.P200S
Pat_74	Pre-Treatment	EIF1AX	1964	37	X	20156734	20156734	Missense_Mutation	SNP	C	A	60	14	c.23G>T	c.(22-24)GGA>GTA	p.G8V
Pat_74	Pre-Treatment	UBA1	7317	37	X	47070301	47070301	Missense_Mutation	SNP	T	C	2	6	c.2260T>C	c.(2260-2262)TTT>CTT	p.F754L
Pat_74	Pre-Treatment	FAM123B	139285	37	X	63411254	63411254	Missense_Mutation	SNP	G	A	5	5	c.1913C>T	c.(1912-1914)ACT>ATT	p.T638I
Pat_74	Pre-Treatment	TEX11	56159	37	X	69825286	69825286	Missense_Mutation	SNP	C	T	35	10	c.2077G>A	c.(2077-2079)GAG>AAG	p.E693K
Pat_74	Pre-Treatment	MAGEC1	9947	37	X	140993455	140993455	Missense_Mutation	SNP	G	A	4	51	c.265G>A	c.(265-267)GGC>AGC	p.G89S
Pat_74	Pre-Treatment	MAGEC1	9947	37	X	140993468	140993468	Missense_Mutation	SNP	A	T	4	56	c.278A>T	c.(277-279)CAG>CTG	p.Q93L
Pat_74	Post-Resistance	CASP9	842	37	1	15844799	15844799	Missense_Mutation	SNP	G	A	24	53	c.224C>T	c.(223-225)TCC>TTC	p.S75F
Pat_74	Post-Resistance	ATP13A2	23400	37	1	17330867	17330867	Missense_Mutation	SNP	A	G	16	15	c.517T>C	c.(517-519)TAT>CAT	p.Y173H
Pat_74	Post-Resistance	CSMD2	114784	37	1	34191090	34191090	Missense_Mutation	SNP	C	T	17	30	c.2435G>A	c.(2434-2436)CGG>CAG	p.R812Q
Pat_74	Post-Resistance	DHCR24	1718	37	1	55337202	55337202	Missense_Mutation	SNP	G	A	18	41	c.697C>T	c.(697-699)CCT>TCT	p.P233S
Pat_74	Post-Resistance	LEPR	3953	37	1	66058389	66058389	Nonsense_Mutation	SNP	C	T	44	49	c.544C>T	c.(544-546)CAG>TAG	p.Q182*
Pat_74	Post-Resistance	C1orf173	127254	37	1	75038497	75038497	Missense_Mutation	SNP	C	T	18	40	c.2897G>A	c.(2896-2898)AGA>AAA	p.R966K
Pat_74	Post-Resistance	AK5	26289	37	1	77949003	77949003	Missense_Mutation	SNP	G	A	16	29	c.1061G>A	c.(1060-1062)GGT>GAT	p.G354D
Pat_74	Post-Resistance	SLC16A1	6566	37	1	113471717	113471717	Missense_Mutation	SNP	C	T	12	10	c.214G>A	c.(214-216)GGA>AGA	p.G72R
Pat_74	Post-Resistance	NRAS	4893	37	1	115256529	115256529	Missense_Mutation	SNP	T	C	78	94	c.182A>G	c.(181-183)CAA>CGA	p.Q61R
Pat_74	Post-Resistance	NBPF9	400818	37	1	144619903	144619903	Missense_Mutation	SNP	T	A	5	118	c.587T>A	c.(586-588)GTG>GAG	p.V196E
Pat_74	Post-Resistance	NBPF10	100132406	37	1	145296448	145296448	Missense_Mutation	SNP	T	A	10	296	c.370T>A	c.(370-372)TAT>AAT	p.Y124N

Pat_74	Post-Resistance	NBPF10	100132406	37	1	145303970	145303970	Missense_Mutation	SNP	C	T	73	295	c.1367C>T	c.(1366-1368)TCA>TTA	p.S456L
Pat_74	Post-Resistance	TCHHL1	126637	37	1	152059823	152059823	Missense_Mutation	SNP	A	C	36	46	c.335T>G	c.(334-336)GTT>GGT	p.V112G
Pat_74	Post-Resistance	ASH1L	55870	37	1	155313160	155313161	Missense_Mutation	DNP	GG	AA	31	40	.8252_8253CC>T	c.(8251-8253)CCC>CTT	p.P2751L
Pat_74	Post-Resistance	SPTA1	6708	37	1	158596788	158596788	Missense_Mutation	SNP	C	T	46	61	c.5674G>A	c.(5674-5676)GAG>AAG	p.E1892K
Pat_74	Post-Resistance	WDR26	80232	37	1	224592184	224592184	Missense_Mutation	SNP	A	G	32	52	c.806T>C	c.(805-807)CTT>CCT	p.L269P
Pat_74	Post-Resistance	NEBL	10529	37	10	21134266	21134266	Missense_Mutation	SNP	A	T	12	11	c.1148T>A	c.(1147-1149)ATT>AAT	p.I383N
Pat_74	Post-Resistance	HSD17B7P2	158160	37	10	38654432	38654432	Missense_Mutation	SNP	A	G	3	44	c.524A>G	c.(523-525)AAT>AGT	p.N175S
Pat_74	Post-Resistance	SGMS1	259230	37	10	52103520	52103520	Missense_Mutation	SNP	G	A	25	10	c.355C>T	c.(355-357)CCC>TCC	p.P119S
Pat_74	Post-Resistance	LOC729020	729020	37	10	105005787	105005787	Missense_Mutation	SNP	C	T	22	8	c.34C>T	c.(34-36)CTC>TTC	p.L12F
Pat_74	Post-Resistance	SORCS3	22986	37	10	106982964	106982964	Missense_Mutation	SNP	T	A	78	21	c.2825T>A	c.(2824-2826)CTG>CAG	p.L942Q
Pat_74	Post-Resistance	RPL13AP6	644511	37	10	112696573	112696573	Missense_Mutation	SNP	T	C	2	2	c.419A>G	c.(418-420)CAC>CGC	p.H140R
Pat_74	Post-Resistance	PHRF1	57661	37	11	607875	607875	Nonsense_Mutation	SNP	G	T	29	43	c.2419G>T	c.(2419-2421)GAG>TAG	p.E807*
Pat_74	Post-Resistance	OR51G2	81282	37	11	4936406	4936406	Missense_Mutation	SNP	G	A	12	24	c.488C>T	c.(487-489)CCA>CTA	p.P163L
Pat_74	Post-Resistance	SERGEF	26297	37	11	17809858	17809858	Missense_Mutation	SNP	G	A	9	13	c.1151C>T	c.(1150-1152)TCG>TTG	p.S384L
Pat_74	Post-Resistance	NAV2	89797	37	11	19970400	19970400	Nonsense_Mutation	SNP	C	T	25	37	c.2488C>T	c.(2488-2490)CGA>TGA	p.R830*
Pat_74	Post-Resistance	DGKZ	8525	37	11	46400602	46400602	Missense_Mutation	SNP	T	C	3	4	c.3044T>C	c.(3043-3045)CTC>CCC	p.L1015P
Pat_74	Post-Resistance	BCO2	83875	37	11	112084481	112084481	Missense_Mutation	SNP	G	A	99	148	c.1229G>A	c.(1228-1230)AGG>AAG	p.R410K
Pat_74	Post-Resistance	FLI1	2313	37	11	128680651	128680651	Missense_Mutation	SNP	C	T	17	29	c.1127C>T	c.(1126-1128)TCG>TTG	p.S376L
Pat_74	Post-Resistance	FOXM1	2305	37	12	2981324	2981324	Missense_Mutation	SNP	G	A	87	146	c.592C>T	c.(592-594)CGC>TGC	p.R198C
Pat_74	Post-Resistance	PTPRO	5800	37	12	15677831	15677831	Missense_Mutation	SNP	G	A	28	40	c.1975G>A	c.(1975-1977)GAC>AAC	p.D659N
Pat_74	Post-Resistance	PLCZ1	89869	37	12	18876359	18876359	Missense_Mutation	SNP	T	C	24	30	c.253A>G	c.(253-255)AAA>GAA	p.K85E
Pat_74	Post-Resistance	SFRS2IP	9169	37	12	46320119	46320119	Missense_Mutation	SNP	G	A	30	51	c.3365C>T	c.(3364-3366)TCC>TTC	p.S1122F
Pat_74	Post-Resistance	MIP	4284	37	12	56848247	56848247	Missense_Mutation	SNP	C	T	32	42	c.151G>A	c.(151-153)GCC>ACC	p.A51T
Pat_74	Post-Resistance	GEFT	115557	37	12	58010217	58010217	Missense_Mutation	SNP	C	T	12	31	c.1571C>T	c.(1570-1572)CCC>CTC	p.P524L
Pat_74	Post-Resistance	ZFC3H1	196441	37	12	72050857	72050857	Missense_Mutation	SNP	C	T	21	38	c.823G>A	c.(823-825)GTC>ATC	p.V275I
Pat_74	Post-Resistance	POLR3B	55703	37	12	106889920	106889921	Missense_Mutation	DNP	TC	AT	47	58	.2801_2802TC>A	c.(2800-2802)TTC>TAT	p.F934Y
Pat_74	Post-Resistance	RFX4	5992	37	12	107113748	107113748	Missense_Mutation	SNP	G	C	17	24	c.1149G>C	c.(1147-1149)GAG>GAC	p.E383D
Pat_74	Post-Resistance	TRPC4	7223	37	13	38225514	38225515	Missense_Mutation	DNP	GG	AA	34	44	.1966_1967CC>T	c.(1966-1968)CCC>TTC	p.P656F
Pat_74	Post-Resistance	ARHGAP5	394	37	14	32562120	32562120	Missense_Mutation	SNP	G	A	34	65	c.2245G>A	c.(2245-2247)GCT>ACT	p.A749T
Pat_74	Post-Resistance	AKAP6	9472	37	14	33292789	33292789	Missense_Mutation	SNP	G	A	17	33	c.5770G>A	c.(5770-5772)GGG>AGG	p.G1924R
Pat_74	Post-Resistance	RTN1	6252	37	14	60213112	60213112	Missense_Mutation	SNP	G	A	22	23	c.329C>T	c.(328-330)TCT>TTT	p.S110F
Pat_74	Post-Resistance	C14orf43	91748	37	14	74206609	74206609	Missense_Mutation	SNP	G	A	27	38	c.103C>T	c.(103-105)CCC>TCC	p.P35S
Pat_74	Post-Resistance	C14orf109	26175	37	14	93652819	93652819	Missense_Mutation	SNP	C	T	35	32	c.313C>T	c.(313-315)CCT>TCT	p.P105S
Pat_74	Post-Resistance	PPP4R4	57718	37	14	94733340	94733340	Missense_Mutation	SNP	G	A	15	22	c.2423G>A	c.(2422-2424)GGA>GAA	p.G808E
Pat_74	Post-Resistance	EML1	2009	37	14	100344907	100344907	Missense_Mutation	SNP	C	T	54	63	c.469C>T	c.(469-471)CGC>TGC	p.R157C
Pat_74	Post-Resistance	C15orf2	23742	37	15	24922585	24922585	Missense_Mutation	SNP	C	T	74	122	c.1571C>T	c.(1570-1572)CCT>CTT	p.P524L
Pat_74	Post-Resistance	VPS39	23339	37	15	42476789	42476789	Missense_Mutation	SNP	G	A	64	121	c.677C>T	c.(676-678)ACC>ATC	p.T226I
Pat_74	Post-Resistance	TNFAIP8L3	388121	37	15	51350497	51350497	Missense_Mutation	SNP	C	T	60	88	c.460G>A	c.(460-462)GAG>AAG	p.E154K
Pat_74	Post-Resistance	UNC13C	440279	37	15	54306599	54306599	Missense_Mutation	SNP	G	A	15	29	c.1499G>A	c.(1498-1500)AGA>AAA	p.R500K
Pat_74	Post-Resistance	LOC645752	645752	37	15	78208916	78208916	Missense_Mutation	SNP	C	G	3	52	c.817G>C	c.(817-819)GAA>CAA	p.E273Q
Pat_74	Post-Resistance	CSNK2A2	1459	37	16	58199491	58199491	Missense_Mutation	SNP	T	C	26	26	c.949A>G	c.(949-951)AAA>GAA	p.K317E
Pat_74	Post-Resistance	SMTNL2	342527	37	17	4496274	4496274	Missense_Mutation	SNP	C	T	16	21	c.538C>T	c.(538-540)CCC>TCC	p.P180S
Pat_74	Post-Resistance	TBC1D3	729873	37	17	36288302	36288302	Splice_Site	SNP	G	A	42	306	c.387_splice	c.e6+1	p.Q129_splice
Pat_74	Post-Resistance	KRTAP4-11	653240	37	17	39274150	39274150	Missense_Mutation	SNP	T	A	4	29	c.418A>T	c.(418-420)AGC>TGC	p.S140C
Pat_74	Post-Resistance	WNT9B	7484	37	17	44952593	44952593	Missense_Mutation	SNP	G	A	19	16	c.461G>A	c.(460-462)CGG>CAG	p.R154Q
Pat_74	Post-Resistance	HLF	3131	37	17	53345135	53345135	Missense_Mutation	SNP	G	A	12	32	c.139G>A	c.(139-141)GAA>AAA	p.E47K
Pat_74	Post-Resistance	TRIM37	4591	37	17	57153057	57153057	Missense_Mutation	SNP	G	C	14	27	c.635C>G	c.(634-636)ACC>AGC	p.T212S

Pat_74	Post-Resistance	CSNK1D	1453	37	17	80206800	80206800	Missense_Mutation	SNP	G	A	7	2	c.1148C>T	c.(1147-1149)TCG>TTG	p.S383L
Pat_74	Post-Resistance	KLHL14	57565	37	18	30260407	30260407	Missense_Mutation	SNP	G	A	45	69	c.1394C>T	c.(1393-1395)GCG>GTG	p.A465V
Pat_74	Post-Resistance	TLE6	79816	37	19	2991857	2991857	Missense_Mutation	SNP	C	T	12	21	c.892C>T	c.(892-894)CCT>TCT	p.P298S
Pat_74	Post-Resistance	SHD	56961	37	19	4290560	4290560	Missense_Mutation	SNP	C	T	21	32	c.953C>T	c.(952-954)TCA>TTA	p.S318L
Pat_74	Post-Resistance	SYDE1	85360	37	19	15224562	15224562	Missense_Mutation	SNP	G	A	24	39	c.1996G>A	c.(1996-1998)GGG>AGG	p.G666R
Pat_74	Post-Resistance	CYP4F12	66002	37	19	15807289	15807289	Missense_Mutation	SNP	C	T	63	109	c.1364C>T	c.(1363-1365)CCT>CTT	p.P455L
Pat_74	Post-Resistance	LPAR2	9170	37	19	19737765	19737765	Nonsense_Mutation	SNP	A	T	4	10	c.329T>A	c.(328-330)TTG>TAG	p.L110*
Pat_74	Post-Resistance	CD22	933	37	19	35828922	35828922	Missense_Mutation	SNP	A	T	7	12	c.983A>T	c.(982-984)CAG>CTG	p.Q328L
Pat_74	Post-Resistance	RYR1	6261	37	19	38985160	38985160	Missense_Mutation	SNP	C	T	16	23	c.6443C>T	c.(6442-6444)TCC>TTC	p.S2148F
Pat_74	Post-Resistance	LILRA3	11026	37	19	54802527	54802527	Missense_Mutation	SNP	G	A	13	34	c.914C>T	c.(913-915)TCC>TTC	p.S305F
Pat_74	Post-Resistance	EXOC6B	23233	37	2	72786608	72786608	Nonsense_Mutation	SNP	G	A	14	17	c.889C>T	c.(889-891)CGA>TGA	p.R297*
Pat_74	Post-Resistance	TET3	200424	37	2	74320773	74320773	Missense_Mutation	SNP	C	T	22	24	c.2842C>T	c.(2842-2844)CTC>TTC	p.L948F
Pat_74	Post-Resistance	LY75	4065	37	2	160746866	160746866	Nonsense_Mutation	SNP	C	T	26	31	c.660G>A	c.(658-660)TGG>TGA	p.W220*
Pat_74	Post-Resistance	XIRP2	129446	37	2	168102458	168102458	Missense_Mutation	SNP	C	T	38	49	c.4556C>T	c.(4555-4557)CCT>CTT	p.P1519L
Pat_74	Post-Resistance	DNAH7	56171	37	2	196728992	196728992	Missense_Mutation	SNP	C	T	28	38	c.7387G>A	c.(7387-7389)GAT>AAT	p.D2463N
Pat_74	Post-Resistance	PARD3B	117583	37	2	206050515	206050515	Missense_Mutation	SNP	C	T	30	55	c.1952C>T	c.(1951-1953)GCC>GTC	p.A651V
Pat_74	Post-Resistance	KIAA1486	57624	37	2	226378119	226378119	Missense_Mutation	SNP	G	A	18	26	c.254G>A	c.(253-255)GGA>GAA	p.G85E
Pat_74	Post-Resistance	COL4A3	1285	37	2	228128587	228128587	Missense_Mutation	SNP	G	A	23	15	c.1242G>A	c.(1240-1242)ATG>ATA	p.M414I
Pat_74	Post-Resistance	GGTLC1	92086	37	20	23967157	23967157	Missense_Mutation	SNP	A	G	4	57	c.92T>C	c.(91-93)ATG>ACG	p.M31T
Pat_74	Post-Resistance	FRG1B	284802	37	20	29625875	29625875	Missense_Mutation	SNP	T	C	3	69	c.29T>C	c.(28-30)ATC>ACC	p.I10T
Pat_74	Post-Resistance	TOX2	84969	37	20	42694670	42694670	Missense_Mutation	SNP	C	A	8	21	c.1225C>A	c.(1225-1227)CCC>ACC	p.P409T
Pat_74	Post-Resistance	DOPEY2	9980	37	21	37636074	37636074	Missense_Mutation	SNP	C	T	91	166	c.5449C>T	c.(5449-5451)CCC>TCC	p.P1817S
Pat_74	Post-Resistance	DSCAM	1826	37	21	41452217	41452217	Missense_Mutation	SNP	G	A	27	28	c.4282C>T	c.(4282-4284)CCA>TCA	p.P1428S
Pat_74	Post-Resistance	RIMBP3	85376	37	22	20457350	20457350	Missense_Mutation	SNP	C	T	2	3	c.3952G>A	c.(3952-3954)GGC>AGC	p.G1318S
Pat_74	Post-Resistance	RFPL3	10738	37	22	32756614	32756614	Missense_Mutation	SNP	A	G	3	65	c.749A>G	c.(748-750)GAT>GGT	p.D250G
Pat_74	Post-Resistance	TRIOBP	11078	37	22	38120695	38120695	Missense_Mutation	SNP	C	T	37	65	c.2132C>T	c.(2131-2133)CCT>CTT	p.P711L
Pat_74	Post-Resistance	CCR8	1237	37	3	39374063	39374063	Missense_Mutation	SNP	G	A	49	76	c.241G>A	c.(241-243)GAC>AAC	p.D81N
Pat_74	Post-Resistance	ARIH2	10425	37	3	48999097	48999097	Missense_Mutation	SNP	C	T	20	36	c.308C>T	c.(307-309)TCA>TTA	p.S103L
Pat_74	Post-Resistance	BSN	8927	37	3	49694583	49694583	Missense_Mutation	SNP	C	T	16	20	c.7594C>T	c.(7594-7596)CCC>TCC	p.P2532S
Pat_74	Post-Resistance	OR5H2	79310	37	3	98002110	98002110	Missense_Mutation	SNP	C	T	27	37	c.379C>T	c.(379-381)CGC>TGC	p.R127C
Pat_74	Post-Resistance	NIT2	56954	37	3	100058695	100058695	Missense_Mutation	SNP	C	T	14	24	c.163C>T	c.(163-165)CCT>TCT	p.P55S
Pat_74	Post-Resistance	ARHGAP31	57514	37	3	119112312	119112312	Splice_Site	SNP	A	G	51	58	c.882_splice	c.e8-2	p.K294_splice
Pat_74	Post-Resistance	ILDR1	286676	37	3	121712140	121712140	Missense_Mutation	SNP	C	T	5	10	c.1456G>A	c.(1456-1458)GAG>AAG	p.E486K
Pat_74	Post-Resistance	LEKR1	389170	37	3	156742621	156742622	Missense_Mutation	DNP	GA	AC	21	25	c.364_365GA>AC	c.(364-366)GAA>ACA	p.E122T
Pat_74	Post-Resistance	LRRC34	151827	37	3	169511487	169511487	Missense_Mutation	SNP	C	T	27	49	c.1196G>A	c.(1195-1197)GGA>GAA	p.G399E
Pat_74	Post-Resistance	SAMD7	344658	37	3	169639115	169639115	Missense_Mutation	SNP	G	T	39	32	c.200G>T	c.(199-201)CGG>CTG	p.R67L
Pat_74	Post-Resistance	TPRG1	285386	37	3	189038465	189038465	Missense_Mutation	SNP	G	C	23	19	c.684G>C	c.(682-684)AAG>AAC	p.K228N
Pat_74	Post-Resistance	TP63	8626	37	3	189607246	189607246	Missense_Mutation	SNP	C	T	26	46	c.1625C>T	c.(1624-1626)CCG>CTG	p.P542L
Pat_74	Post-Resistance	LEPREL1	55214	37	3	189690698	189690698	Missense_Mutation	SNP	G	A	30	50	c.1664C>T	c.(1663-1665)TCC>TTC	p.S555F
Pat_74	Post-Resistance	UBXN7	26043	37	3	196089400	196089401	Missense_Mutation	DNP	GG	AA	35	51	c.992_993CC>TT	c.(991-993)TCC>TTT	p.S331F
Pat_74	Post-Resistance	CCDC158	339965	37	4	77247121	77247121	Missense_Mutation	SNP	G	A	62	84	c.3046C>T	c.(3046-3048)CCT>TCT	p.P1016S
Pat_74	Post-Resistance	CFI	3426	37	4	110663728	110663728	Nonsense_Mutation	SNP	G	A	19	23	c.1453C>T	c.(1453-1455)CAG>TAG	p.Q485*
Pat_74	Post-Resistance	INTU	27152	37	4	128564983	128564983	Missense_Mutation	SNP	G	A	35	38	c.454G>A	c.(454-456)GTC>ATC	p.V152I
Pat_74	Post-Resistance	PCDH10	57575	37	4	134073358	134073358	Missense_Mutation	SNP	G	T	11	11	c.2063G>T	c.(2062-2064)GGG>GTG	p.G688V
Pat_74	Post-Resistance	PCDH18	54510	37	4	138451640	138451640	Missense_Mutation	SNP	G	A	34	56	c.1603C>T	c.(1603-1605)CAT>TAT	p.H535Y
Pat_74	Post-Resistance	GYPE	2996	37	4	144826671	144826671	Translation_Start_Site	SNP	C	T	6	48	c.-10G>A	c.(-12--8)TCGTG>TCATG	
Pat_74	Post-Resistance	DNAH5	1767	37	5	13864741	13864741	Missense_Mutation	SNP	C	T	16	23	c.4361G>A	c.(4360-4362)CGA>CAA	p.R1454Q

Pat_74	Post-Resistance	MBLAC2	153364	37	5	89757100	89757100	Nonsense_Mutation	SNP	G	A	26	57	c.724C>T	c.(724-726)CGA>TGA	p.R242*
Pat_74	Post-Resistance	ADAM19	8728	37	5	156924013	156924013	Missense_Mutation	SNP	G	A	4	14	c.1483C>T	c.(1483-1485)CCT>TCT	p.P495S
Pat_74	Post-Resistance	HIVEP1	3096	37	6	12163562	12163562	Missense_Mutation	SNP	C	T	80	130	c.7025C>T	c.(7024-7026)CCC>CTC	p.P2342L
Pat_74	Post-Resistance	VARS	7407	37	6	31745399	31745399	Missense_Mutation	SNP	G	A	11	11	c.3767C>T	c.(3766-3768)GCC>GTC	p.A1256V
Pat_74	Post-Resistance	PKHD1	5314	37	6	51890422	51890422	Missense_Mutation	SNP	G	A	50	74	c.4186C>T	c.(4186-4188)CCA>TCA	p.P1396S
Pat_74	Post-Resistance	COL12A1	1303	37	6	75865396	75865396	Missense_Mutation	SNP	A	G	4	134	c.3425T>C	c.(3424-3426)GTT>GCT	p.V1142A
Pat_74	Post-Resistance	STXBP5	134957	37	6	147646094	147646094	Splice_Site	SNP	G	A	8	30	c.1803_splice	c.e17-1	p.K601_splice
Pat_74	Post-Resistance	PACRG	135138	37	6	163735909	163735909	Missense_Mutation	SNP	G	T	21	33	c.781G>T	c.(781-783)GGG>TGG	p.G261W
Pat_74	Post-Resistance	TTLL2	83887	37	6	167754658	167754658	Missense_Mutation	SNP	G	T	23	20	c.1270G>T	c.(1270-1272)GGG>TGG	p.G424W
Pat_74	Post-Resistance	IL6	3569	37	7	22771151	22771151	Missense_Mutation	SNP	G	A	20	18	c.598G>A	c.(598-600)GAG>AAG	p.E200K
Pat_74	Post-Resistance	NSUN5	55695	37	7	72717601	72717601	Missense_Mutation	SNP	G	A	30	33	c.1282C>T	c.(1282-1284)CCA>TCA	p.P428S
Pat_74	Post-Resistance	C7orf66	154907	37	7	108524203	108524203	Missense_Mutation	SNP	T	C	43	74	c.209A>G	c.(208-210)TAT>TGT	p.Y70C
Pat_74	Post-Resistance	ST7	7982	37	7	116869938	116869938	Missense_Mutation	SNP	A	C	6	23	c.1465A>C	c.(1465-1467)ACC>CCC	p.T489P
Pat_74	Post-Resistance	WNT2	7472	37	7	116960755	116960755	Missense_Mutation	SNP	G	A	15	16	c.176C>T	c.(175-177)CCA>CTA	p.P59L
Pat_74	Post-Resistance	CPA1	1357	37	7	130023310	130023310	Missense_Mutation	SNP	A	G	3	20	c.562A>G	c.(562-564)AGT>GGT	p.S188G
Pat_74	Post-Resistance	BRAF	673	37	7	140453136	140453136	Missense_Mutation	SNP	A	T	61	55	c.1799T>A	c.(1798-1800)GTG>GAG	p.V600E
Pat_74	Post-Resistance	ATG9B	285973	37	7	150720253	150720253	Nonsense_Mutation	SNP	G	A	100	252	c.700C>T	c.(700-702)CGA>TGA	p.R234*
Pat_74	Post-Resistance	DKK4	27121	37	8	42232353	42232353	Missense_Mutation	SNP	C	T	77	90	c.341G>A	c.(340-342)GGA>GAA	p.G114E
Pat_74	Post-Resistance	SLCO5A1	81796	37	8	70673984	70673984	Missense_Mutation	SNP	C	T	16	33	c.1034G>A	c.(1033-1035)GGA>GAA	p.G345E
Pat_74	Post-Resistance	APBA1	320	37	9	72064588	72064588	Missense_Mutation	SNP	C	T	50	62	c.2093G>A	c.(2092-2094)GGG>GAG	p.G698E
Pat_74	Post-Resistance	OR13D1	286365	37	9	107457507	107457507	Missense_Mutation	SNP	G	A	26	37	c.805G>A	c.(805-807)GCC>ACC	p.A269T
Pat_74	Post-Resistance	PTGS1	5742	37	9	125154609	125154609	Missense_Mutation	SNP	C	T	33	39	c.1586C>T	c.(1585-1587)TCC>TTC	p.S529F
Pat_74	Post-Resistance	WDR34	89891	37	9	131403107	131403107	Missense_Mutation	SNP	G	A	13	26	c.298C>T	c.(298-300)CCG>TCG	p.P100S
Pat_74	Post-Resistance	SEC16A	9919	37	9	139341390	139341390	Missense_Mutation	SNP	G	A	20	36	c.6709C>T	c.(6709-6711)CCA>TCA	p.P2237S
Pat_74	Post-Resistance	EIF1AX	1964	37	X	20156734	20156734	Missense_Mutation	SNP	C	A	60	6	c.23G>T	c.(22-24)GGA>GTA	p.G8V
Pat_74	Post-Resistance	FAM123B	139285	37	X	63411254	63411254	Missense_Mutation	SNP	G	A	10	1	c.1913C>T	c.(1912-1914)ACT>ATT	p.T638I
Pat_74	Post-Resistance	TEX11	56159	37	X	69825286	69825286	Missense_Mutation	SNP	C	T	40	5	c.2077G>A	c.(2077-2079)GAG>AAG	p.E693K
Pat_76	Pre-Treatment	AGRN	375790	37	1	984754	984754	Missense_Mutation	SNP	G	C	20	28	c.4437G>C	c.(4435-4437)GAG>GAC	p.E1479D
Pat_76	Pre-Treatment	PUSL1	126789	37	1	1246733	1246733	Missense_Mutation	SNP	G	A	8	8	c.886G>A	c.(886-888)GGG>AGG	p.G296R
Pat_76	Pre-Treatment	CHD5	26038	37	1	6169939	6169939	Missense_Mutation	SNP	C	T	15	31	c.5494G>A	c.(5494-5496)GTG>ATG	p.V1832M
Pat_76	Pre-Treatment	TNFRSF9	3604	37	1	7995073	7995073	Missense_Mutation	SNP	C	T	4	70	c.544G>A	c.(544-546)GGA>AGA	p.G182R
Pat_76	Pre-Treatment	SLC2A7	155184	37	1	9063467	9063467	Missense_Mutation	SNP	T	C	28	34	c.1431A>G	c.(1429-1431)ATA>ATG	p.I477M
Pat_76	Pre-Treatment	KIF1B	23095	37	1	10405979	10405979	Nonsense_Mutation	SNP	G	A	17	32	c.3765G>A	c.(3763-3765)TGG>TGA	p.W1255*
Pat_76	Pre-Treatment	C1orf127	148345	37	1	11017690	11017690	Missense_Mutation	SNP	G	A	7	31	c.229C>T	c.(229-231)CTT>TTT	p.L77F
Pat_76	Pre-Treatment	PTCHD2	57540	37	1	11579548	11579548	Missense_Mutation	SNP	G	A	35	69	c.2026G>A	c.(2026-2028)GAG>AAG	p.E676K
Pat_76	Pre-Treatment	NPPA	4878	37	1	11907322	11907322	Missense_Mutation	SNP	C	T	14	10	c.298G>A	c.(298-300)GGC>AGC	p.G100S
Pat_76	Pre-Treatment	PRAMEF12	390999	37	1	12835290	12835290	Missense_Mutation	SNP	C	T	62	66	c.280C>T	c.(280-282)CGC>TGC	p.R94C
Pat_76	Pre-Treatment	LOC649330	649330	37	1	12907921	12907921	Missense_Mutation	SNP	C	T	10	114	c.222G>A	c.(220-222)ATG>ATA	p.M74I
Pat_76	Pre-Treatment	CELA2A	63036	37	1	15794002	15794002	Missense_Mutation	SNP	G	A	4	109	c.761G>A	c.(760-762)CGG>CAG	p.R254Q
Pat_76	Pre-Treatment	DNAJC16	23341	37	1	15890790	15890790	Nonsense_Mutation	SNP	C	T	43	81	c.1534C>T	c.(1534-1536)CGA>TGA	p.R512*
Pat_76	Pre-Treatment	KLHDC7A	127707	37	1	18807831	18807831	Missense_Mutation	SNP	G	A	16	25	c.356G>A	c.(355-357)AGA>AAA	p.R119K
Pat_76	Pre-Treatment	KLHDC7A	127707	37	1	18808730	18808730	Missense_Mutation	SNP	C	T	19	25	c.1255C>T	c.(1255-1257)CCG>TCG	p.P419S
Pat_76	Pre-Treatment	PLA2G2D	26279	37	1	20442911	20442911	Missense_Mutation	SNP	C	G	13	22	c.100G>C	c.(100-102)GGG>CGG	p.G34R
Pat_76	Pre-Treatment	MUL1	79594	37	1	20827445	20827445	Missense_Mutation	SNP	C	T	3	50	c.797G>A	c.(796-798)CGG>CAG	p.R266Q
Pat_76	Pre-Treatment	ECE1	1889	37	1	21582571	21582571	Nonsense_Mutation	SNP	C	A	29	31	c.889G>T	c.(889-891)GAG>TAG	p.E297*
Pat_76	Pre-Treatment	RAP1GAP	5909	37	1	21936111	21936111	Missense_Mutation	SNP	G	A	32	93	c.1028C>T	c.(1027-1029)CCC>CTC	p.P343L
Pat_76	Pre-Treatment	EPHB2	2048	37	1	23232566	23232566	Missense_Mutation	SNP	A	T	35	32	c.1852A>T	c.(1852-1854)ATC>TTC	p.I618F

Pat_76	Pre-Treatment	GRHL3	57822	37	1	24669215	24669215	Missense_Mutation	SNP	G	A	55	91	c.1253G>A	c.(1252-1254)CGG>CAG	p.R418Q
Pat_76	Pre-Treatment	MAN1C1	57134	37	1	26013027	26013027	Missense_Mutation	SNP	G	A	4	127	c.637G>A	c.(637-639)GGA>AGA	p.G213R
Pat_76	Pre-Treatment	MAP3K6	9064	37	1	27683527	27683527	Missense_Mutation	SNP	G	A	4	139	c.3337C>T	c.(3337-3339)CGG>TGG	p.R1113W
Pat_76	Pre-Treatment	MAP3K6	9064	37	1	27686450	27686450	Missense_Mutation	SNP	G	A	50	82	c.2218C>T	c.(2218-2220)CCC>TCC	p.P740S
Pat_76	Pre-Treatment	CD164L2	388611	37	1	27709119	27709119	Missense_Mutation	SNP	G	A	23	33	c.127C>T	c.(127-129)CGC>TGC	p.R43C
Pat_76	Pre-Treatment	SFRS4	6429	37	1	29475177	29475178	Missense_Mutation	DNP	GG	AA	93	144	.1229_1230CC>T	c.(1228-1230)TCC>TTT	p.S410F
Pat_76	Pre-Treatment	PTPRU	10076	37	1	29652156	29652156	Missense_Mutation	SNP	G	A	51	52	c.4324G>A	c.(4324-4326)GGG>AGG	p.G1442R
Pat_76	Pre-Treatment	SNRNP40	9410	37	1	31769519	31769519	Missense_Mutation	SNP	C	T	4	91	c.80G>A	c.(79-81)GGA>GAA	p.G27E
Pat_76	Pre-Treatment	BAI2	576	37	1	32222263	32222263	Missense_Mutation	SNP	G	A	7	15	c.175C>T	c.(175-177)CCT>TCT	p.P59S
Pat_76	Pre-Treatment	SPOCD1	90853	37	1	32280093	32280093	Missense_Mutation	SNP	C	T	13	11	c.842G>A	c.(841-843)GGG>GAG	p.G281E
Pat_76	Pre-Treatment	LCK	3932	37	1	32751189	32751189	Missense_Mutation	SNP	G	A	37	78	c.1402G>A	c.(1402-1404)GAG>AAG	p.E468K
Pat_76	Pre-Treatment	CSMD2	114784	37	1	34383699	34383699	Missense_Mutation	SNP	G	A	10	24	c.796C>T	c.(796-798)CTC>TTC	p.L266F
Pat_76	Pre-Treatment	CSMD2	114784	37	1	34554741	34554741	Missense_Mutation	SNP	C	T	15	18	c.121G>A	c.(121-123)GGG>AGG	p.G41R
Pat_76	Pre-Treatment	EIF2C1	26523	37	1	36359345	36359345	Missense_Mutation	SNP	G	A	27	52	c.583G>A	c.(583-585)GAG>AAG	p.E195K
Pat_76	Pre-Treatment	C1orf109	54955	37	1	38149083	38149083	Missense_Mutation	SNP	G	A	34	46	c.482C>T	c.(481-483)TCG>TTG	p.S161L
Pat_76	Pre-Treatment	FHL3	2275	37	1	38464940	38464940	Missense_Mutation	SNP	G	T	4	125	c.145C>A	c.(145-147)CAT>AAT	p.H49N
Pat_76	Pre-Treatment	KIAA0754	643314	37	1	39878887	39878887	Missense_Mutation	SNP	C	T	14	16	c.2950C>T	c.(2950-2952)CCA>TCA	p.P984S
Pat_76	Pre-Treatment	NT5C1A	84618	37	1	40131779	40131779	Missense_Mutation	SNP	C	T	25	63	c.265G>A	c.(265-267)GAA>AAA	p.E89K
Pat_76	Pre-Treatment	HPCAL4	51440	37	1	40149802	40149802	Missense_Mutation	SNP	G	A	8	21	c.185C>T	c.(184-186)TCC>TTC	p.S62F
Pat_76	Pre-Treatment	PPIE	10450	37	1	40218614	40218614	Missense_Mutation	SNP	A	G	25	65	c.727A>G	c.(727-729)ACC>GCC	p.T243A
Pat_76	Pre-Treatment	NFYC	4802	37	1	41218908	41218908	Missense_Mutation	SNP	C	T	15	45	c.377C>T	c.(376-378)CCA>CTA	p.P126L
Pat_76	Pre-Treatment	HIVEP3	59269	37	1	42041243	42041243	Missense_Mutation	SNP	G	A	5	224	c.5179C>T	c.(5179-5181)CCG>TCG	p.P1727S
Pat_76	Pre-Treatment	SLC2A1	6513	37	1	43393356	43393356	Missense_Mutation	SNP	G	A	4	62	c.1198C>T	c.(1198-1200)CGT>TGT	p.R400C
Pat_76	Pre-Treatment	TIE1	7075	37	1	43778895	43778895	Missense_Mutation	SNP	C	T	9	17	c.2017C>T	c.(2017-2019)CCA>TCA	p.P673S
Pat_76	Pre-Treatment	PTPRF	5792	37	1	44058256	44058257	Missense_Mutation	DNP	CC	TT	7	19	.1797_1798CC>T	795-1800)GCCCGC>GCT	p.R600C
Pat_76	Pre-Treatment	DMAP1	55929	37	1	44684863	44684863	Missense_Mutation	SNP	C	T	21	43	c.856C>T	c.(856-858)CGC>TGC	p.R286C
Pat_76	Pre-Treatment	RNF220	55182	37	1	45110737	45110737	Missense_Mutation	SNP	C	T	18	29	c.1294C>T	c.(1294-1296)CGG>TGG	p.R432W
Pat_76	Pre-Treatment	IPP	3652	37	1	46211794	46211794	Missense_Mutation	SNP	G	A	4	75	c.290C>T	c.(289-291)ACA>ATA	p.T97I
Pat_76	Pre-Treatment	FAAH	2166	37	1	46871441	46871441	Missense_Mutation	SNP	C	T	10	16	c.760C>T	c.(760-762)CTC>TTC	p.L254F
Pat_76	Pre-Treatment	CYP4A11	1579	37	1	47402978	47402978	Nonsense_Mutation	SNP	C	T	21	29	c.378G>A	c.(376-378)TGG>TGA	p.W126*
Pat_76	Pre-Treatment	SLC5A9	200010	37	1	48697728	48697728	Missense_Mutation	SNP	C	T	59	68	c.802C>T	c.(802-804)CAC>TAC	p.H268Y
Pat_76	Pre-Treatment	SPATA6	54558	37	1	48877245	48877245	Missense_Mutation	SNP	G	A	13	25	c.296C>T	c.(295-297)TCT>TTT	p.S99F
Pat_76	Pre-Treatment	GLIS1	148979	37	1	54060335	54060335	Missense_Mutation	SNP	A	C	13	21	c.241T>G	c.(241-243)TGT>GGT	p.C81G
Pat_76	Pre-Treatment	YIPF1	54432	37	1	54332025	54332025	Missense_Mutation	SNP	G	A	28	23	c.679C>T	c.(679-681)CGT>TGT	p.R227C
Pat_76	Pre-Treatment	PRKAA2	5563	37	1	57159444	57159444	Missense_Mutation	SNP	C	T	34	45	c.482C>T	c.(481-483)TCT>TTT	p.S161F
Pat_76	Pre-Treatment	C1orf168	199920	37	1	57257735	57257735	Missense_Mutation	SNP	C	T	4	142	c.751G>A	c.(751-753)GCC>ACC	p.A251T
Pat_76	Pre-Treatment	C1orf168	199920	37	1	57257821	57257821	Missense_Mutation	SNP	C	T	23	46	c.665G>A	c.(664-666)AGA>AAA	p.R222K
Pat_76	Pre-Treatment	C8A	731	37	1	57341861	57341861	Missense_Mutation	SNP	G	A	13	66	c.443G>A	c.(442-444)GGA>GAA	p.G148E
Pat_76	Pre-Treatment	C8B	732	37	1	57397515	57397515	Missense_Mutation	SNP	T	C	44	48	c.1589A>G	c.(1588-1590)CAA>CGA	p.Q530R
Pat_76	Pre-Treatment	C8B	732	37	1	57425723	57425723	Nonsense_Mutation	SNP	C	T	20	8	c.219G>A	c.(217-219)TGG>TGA	p.W73*
Pat_76	Pre-Treatment	DAB1	1600	37	1	57481054	57481054	Missense_Mutation	SNP	G	A	13	12	c.946C>T	c.(946-948)CTC>TTC	p.L316F
Pat_76	Pre-Treatment	ROR1	4919	37	1	64624732	64624733	Missense_Mutation	DNP	CC	TT	32	57	.1243_1244CC>T	c.(1243-1245)CCC>TTC	p.P415F
Pat_76	Pre-Treatment	ROR1	4919	37	1	64644411	64644411	Missense_Mutation	SNP	G	A	11	24	c.2687G>A	c.(2686-2688)GGA>GAA	p.G896E
Pat_76	Pre-Treatment	LEPR	3953	37	1	66036476	66036476	Nonsense_Mutation	SNP	C	T	7	27	c.361C>T	c.(361-363)CAA>TAA	p.Q121*
Pat_76	Pre-Treatment	PTGFR	5737	37	1	79002109	79002109	Missense_Mutation	SNP	G	A	35	47	c.817G>A	c.(817-819)GGA>AGA	p.G273R
Pat_76	Pre-Treatment	LPHN2	23266	37	1	82417677	82417677	Missense_Mutation	SNP	G	A	32	45	c.1633G>A	c.(1633-1635)GAA>AAA	p.E545K
Pat_76	Pre-Treatment	LPHN2	23266	37	1	82435018	82435018	Missense_Mutation	SNP	C	T	31	47	c.2629C>T	c.(2629-2631)CTT>TTT	p.L877F

Pat_76	Pre-Treatment	COL24A1	255631	37	1	86578285	86578285	Missense_Mutation	SNP	C	T	33	44	c.1564G>A	c.(1564-1566)GGA>AGA	p.G522R
Pat_76	Pre-Treatment	HS2ST1	9653	37	1	87570300	87570300	Missense_Mutation	SNP	C	T	19	35	c.992C>T	c.(991-993)GCC>GTC	p.A331V
Pat_76	Pre-Treatment	RBMXL1	494115	37	1	89448465	89448465	Missense_Mutation	SNP	G	A	131	124	c.1045C>T	c.(1045-1047)CCC>TCC	p.P349S
Pat_76	Pre-Treatment	GBP6	163351	37	1	89834206	89834206	Missense_Mutation	SNP	A	T	37	51	c.96A>T	c.(94-96)GAA>GAT	p.E32D
Pat_76	Pre-Treatment	GBP6	163351	37	1	89835213	89835213	Missense_Mutation	SNP	G	A	29	27	c.299G>A	c.(298-300)GGT>GAT	p.G100D
Pat_76	Pre-Treatment	ZNF644	84146	37	1	91404798	91404798	Missense_Mutation	SNP	G	A	23	38	c.2113C>T	c.(2113-2115)CCT>TCT	p.P705S
Pat_76	Pre-Treatment	CDC7	8317	37	1	91977357	91977357	Missense_Mutation	SNP	C	T	10	11	c.449C>T	c.(448-450)TCC>TTC	p.S150F
Pat_76	Pre-Treatment	EPHX4	253152	37	1	92528636	92528636	Missense_Mutation	SNP	G	A	53	60	c.882G>A	c.(880-882)ATG>ATA	p.M294I
Pat_76	Pre-Treatment	EVI5	7813	37	1	92979352	92979352	Missense_Mutation	SNP	G	A	53	54	c.2294C>T	c.(2293-2295)TCG>TTG	p.S765L
Pat_76	Pre-Treatment	ABCA4	24	37	1	94546093	94546093	Missense_Mutation	SNP	G	A	51	67	c.1040C>T	c.(1039-1041)GCC>GTC	p.A347V
Pat_76	Pre-Treatment	ABCA4	24	37	1	94568678	94568678	Missense_Mutation	SNP	C	T	83	137	c.463G>A	c.(463-465)GAT>AAT	p.D155N
Pat_76	Pre-Treatment	ARHGAP29	9411	37	1	94655515	94655515	Missense_Mutation	SNP	G	C	15	32	c.1406C>G	c.(1405-1407)GCC>GGC	p.A469G
Pat_76	Pre-Treatment	DPYD	1806	37	1	98187170	98187170	Missense_Mutation	SNP	C	T	33	53	c.379G>A	c.(379-381)GGA>AGA	p.G127R
Pat_76	Pre-Treatment	HIAT1	64645	37	1	100534098	100534099	Missense_Mutation	DNP	CC	AT	62	77	c.775_776CC>AT	c.(775-777)CCG>ATG	p.P259M
Pat_76	Pre-Treatment	COL11A1	1301	37	1	103471817	103471817	Splice_Site	SNP	C	T	27	73	c.1737_splice	c.e16+1	p.R579_splice
Pat_76	Pre-Treatment	COL11A1	1301	37	1	103488306	103488306	Missense_Mutation	SNP	C	T	45	68	c.1237G>A	c.(1237-1239)GAA>AAA	p.E413K
Pat_76	Pre-Treatment	GPSM2	29899	37	1	109441582	109441582	Missense_Mutation	SNP	C	T	4	63	c.763C>T	c.(763-765)CTT>TTT	p.L255F
Pat_76	Pre-Treatment	CELSR2	1952	37	1	109793338	109793338	Missense_Mutation	SNP	G	A	5	136	c.637G>A	c.(637-639)GCA>ACA	p.A213T
Pat_76	Pre-Treatment	ATXN7L2	127002	37	1	110033872	110033872	Missense_Mutation	SNP	G	T	27	58	c.1687G>T	c.(1687-1689)GTG>TTG	p.V563L
Pat_76	Pre-Treatment	GPR61	83873	37	1	110086284	110086284	Missense_Mutation	SNP	G	A	4	150	c.640G>A	c.(640-642)GTC>ATC	p.V214I
Pat_76	Pre-Treatment	KCNC4	3749	37	1	110766382	110766382	Missense_Mutation	SNP	G	A	4	120	c.1475G>A	c.(1474-1476)CGG>CAG	p.R492Q
Pat_76	Pre-Treatment	RBM15	64783	37	1	110883778	110883778	Missense_Mutation	SNP	C	T	16	27	c.1751C>T	c.(1750-1752)TCT>TTT	p.S584F
Pat_76	Pre-Treatment	OVGP1	5016	37	1	111957747	111957747	Missense_Mutation	SNP	G	A	26	30	c.1376C>T	c.(1375-1377)TCC>TTC	p.S459F
Pat_76	Pre-Treatment	KCND3	3752	37	1	112525258	112525258	Missense_Mutation	SNP	G	A	7	10	c.91C>T	c.(91-93)CCG>TCG	p.P31S
Pat_76	Pre-Treatment	TSPAN2	10100	37	1	115601575	115601575	Missense_Mutation	SNP	C	T	54	102	c.373G>A	c.(373-375)GAA>AAA	p.E125K
Pat_76	Pre-Treatment	MAN1A2	10905	37	1	118039386	118039386	Missense_Mutation	SNP	C	T	14	29	c.1286C>T	c.(1285-1287)GCT>GTT	p.A429V
Pat_76	Pre-Treatment	GDAP2	54834	37	1	118426126	118426126	Missense_Mutation	SNP	C	T	35	40	c.1231G>A	c.(1231-1233)GAT>AAT	p.D411N
Pat_76	Pre-Treatment	SPAG17	200162	37	1	118598459	118598459	Missense_Mutation	SNP	C	T	16	35	c.2619G>A	c.(2617-2619)ATG>ATA	p.M873I
Pat_76	Pre-Treatment	HAO2	51179	37	1	119929246	119929246	Missense_Mutation	SNP	G	A	21	25	c.563G>A	c.(562-564)GGA>GAA	p.G188E
Pat_76	Pre-Treatment	NBPF9	400818	37	1	144220816	144220816	Missense_Mutation	SNP	A	G	9	495	c.2189A>G	c.(2188-2190)GAG>GGG	p.E730G
Pat_76	Pre-Treatment	BCL9	607	37	1	147096566	147096566	Missense_Mutation	SNP	C	T	29	13	c.4087C>T	c.(4087-4089)CGG>TGG	p.R1363W
Pat_76	Pre-Treatment	NBPF16	728936	37	1	148753328	148753328	Missense_Mutation	SNP	G	A	239	185	c.1345G>A	c.(1345-1347)GAT>AAT	p.D449N
Pat_76	Pre-Treatment	SEMA6C	10500	37	1	151105565	151105566	Missense_Mutation	DNP	CC	TT	12	29	.2187_2188GG>A	185-2190)AAGGAG>AAA	p.E730K
Pat_76	Pre-Treatment	RPTN	126638	37	1	152129435	152129435	Missense_Mutation	SNP	C	T	102	40	c.140G>A	c.(139-141)AGA>AAA	p.R47K
Pat_76	Pre-Treatment	FLG	2312	37	1	152279041	152279041	Missense_Mutation	SNP	G	A	193	627	c.8321C>T	c.(8320-8322)TCC>TTC	p.S2774F
Pat_76	Pre-Treatment	FLG	2312	37	1	152284783	152284783	Missense_Mutation	SNP	G	A	125	555	c.2579C>T	c.(2578-2580)TCG>TTG	p.S860L
Pat_76	Pre-Treatment	FLG2	388698	37	1	152326351	152326351	Missense_Mutation	SNP	C	T	470	234	c.3911G>A	c.(3910-3912)GGA>GAA	p.G1304E
Pat_76	Pre-Treatment	KPRP	448834	37	1	152732181	152732182	Missense_Mutation	DNP	CC	TG	42	168	c.117_118CC>TG	115-120)GCCCCT>GCTG	p.P40A
Pat_76	Pre-Treatment	IVL	3713	37	1	152882308	152882308	Missense_Mutation	SNP	C	T	94	44	c.35C>T	c.(34-36)TCC>TTC	p.S12F
Pat_76	Pre-Treatment	S100A2	6273	37	1	153536245	153536245	Missense_Mutation	SNP	C	T	144	66	c.106G>A	c.(106-108)GAA>AAA	p.E36K
Pat_76	Pre-Treatment	ATP8B2	57198	37	1	154318798	154318798	Missense_Mutation	SNP	G	T	4	139	c.2969G>T	c.(2968-2970)TGC>TTC	p.C990F
Pat_76	Pre-Treatment	KCNN3	3782	37	1	154794606	154794606	Missense_Mutation	SNP	G	A	71	41	c.988C>T	c.(988-990)CTT>TTT	p.L330F
Pat_76	Pre-Treatment	DCST1	149095	37	1	155014087	155014087	Missense_Mutation	SNP	C	G	4	146	c.746C>G	c.(745-747)TCC>TGC	p.S249C
Pat_76	Pre-Treatment	DCST1	149095	37	1	155023142	155023142	Missense_Mutation	SNP	G	A	3	16	c.1919G>A	c.(1918-1920)CGC>CAC	p.R640H
Pat_76	Pre-Treatment	RUSC1	23623	37	1	155297963	155297964	Missense_Mutation	DNP	CC	AT	226	139	.2437_2438CC>A	c.(2437-2439)CCG>ATG	p.P813M
Pat_76	Pre-Treatment	ASH1L	55870	37	1	155448540	155448540	Missense_Mutation	SNP	G	A	19	47	c.4121C>T	c.(4120-4122)TCT>TTT	p.S1374F
Pat_76	Pre-Treatment	PRCC	5546	37	1	156756532	156756532	Missense_Mutation	SNP	C	T	117	64	c.649C>T	c.(649-651)CCC>TCC	p.P217S

Pat_76	Pre-Treatment	NTRK1	4914	37	1	156844761	156844761	Missense_Mutation	SNP	C	T	5	307	c.1315C>T	c.(1315-1317)CTC>TTC	p.L439F
Pat_76	Pre-Treatment	PEAR1	375033	37	1	156883182	156883182	Splice_Site	SNP	G	A	79	41	c.2512_splice	c.e20-1	p.V838_splice
Pat_76	Pre-Treatment	CD1C	911	37	1	158261016	158261016	Missense_Mutation	SNP	G	A	96	66	c.154G>A	c.(154-156)GAG>AAG	p.E52K
Pat_76	Pre-Treatment	OR6K2	81448	37	1	158669934	158669934	Missense_Mutation	SNP	G	A	26	116	c.509C>T	c.(508-510)TCG>TTG	p.S170L
Pat_76	Pre-Treatment	OR6K2	81448	37	1	158670321	158670321	Missense_Mutation	SNP	C	T	87	28	c.122G>A	c.(121-123)GGA>GAA	p.G41E
Pat_76	Pre-Treatment	PYHIN1	149628	37	1	158909027	158909027	Missense_Mutation	SNP	C	T	50	230	c.569C>T	c.(568-570)TCC>TTC	p.S190F
Pat_76	Pre-Treatment	OR10J1	26476	37	1	159409697	159409697	Nonsense_Mutation	SNP	T	G	98	316	c.149T>G	c.(148-150)TTA>TGA	p.L50*
Pat_76	Pre-Treatment	OR10J1	26476	37	1	159410116	159410116	Missense_Mutation	SNP	G	A	56	240	c.568G>A	c.(568-570)GAC>AAC	p.D190N
Pat_76	Pre-Treatment	FCRL6	343413	37	1	159785251	159785251	Splice_Site	SNP	T	G	14	71	c.1179_splice	c.e9+2	p.K393_splice
Pat_76	Pre-Treatment	ATP1A2	477	37	1	160105225	160105225	Missense_Mutation	SNP	G	A	61	50	c.2117G>A	c.(2116-2118)GGA>GAA	p.G706E
Pat_76	Pre-Treatment	ATP1A4	480	37	1	160129209	160129209	Missense_Mutation	SNP	C	T	120	59	c.671C>T	c.(670-672)TCA>TTA	p.S224L
Pat_76	Pre-Treatment	VANGL2	57216	37	1	160388964	160388964	Missense_Mutation	SNP	C	T	4	79	c.365C>T	c.(364-366)ACG>ATG	p.T122M
Pat_76	Pre-Treatment	NDUFS2	4720	37	1	161182173	161182173	Missense_Mutation	SNP	C	T	38	111	c.1019C>T	c.(1018-1020)TCC>TTC	p.S340F
Pat_76	Pre-Treatment	PBX1	5087	37	1	164815831	164815831	Missense_Mutation	SNP	G	A	138	49	c.1211G>A	c.(1210-1212)GGT>GAT	p.G404D
Pat_76	Pre-Treatment	ALDH9A1	223	37	1	165634269	165634269	Missense_Mutation	SNP	C	T	75	25	c.1448G>A	c.(1447-1449)GGA>GAA	p.G483E
Pat_76	Pre-Treatment	ADCY10	55811	37	1	167817683	167817683	Missense_Mutation	SNP	G	A	62	45	c.2353C>T	c.(2353-2355)CAT>TAT	p.H785Y
Pat_76	Pre-Treatment	F5	2153	37	1	169511239	169511239	Missense_Mutation	SNP	C	T	308	154	c.3089G>A	c.(3088-3090)CGA>CAA	p.R1030Q
Pat_76	Pre-Treatment	SELP	6403	37	1	169562902	169562902	Missense_Mutation	SNP	A	C	71	31	c.2348T>G	c.(2347-2349)ATA>AGA	p.I783R
Pat_76	Pre-Treatment	C1orf156	92342	37	1	169762716	169762716	Missense_Mutation	SNP	C	T	230	117	c.121G>A	c.(121-123)GGA>AGA	p.G41R
Pat_76	Pre-Treatment	FMO3	2328	37	1	171079999	171079999	Missense_Mutation	SNP	C	T	82	277	c.688C>T	c.(688-690)CCT>TCT	p.P230S
Pat_76	Pre-Treatment	VAMP4	8674	37	1	171673654	171673654	Missense_Mutation	SNP	G	A	4	69	c.418C>T	c.(418-420)CGT>TGT	p.R140C
Pat_76	Pre-Treatment	TNR	7143	37	1	175372639	175372640	Missense_Mutation	DNP	GG	AA	100	326	c.612_613CC>TT	610-615)TGCCCG>TGTT	p.P205S
Pat_76	Pre-Treatment	TNR	7143	37	1	175375835	175375835	Missense_Mutation	SNP	C	T	121	51	c.16G>A	c.(16-18)GAA>AAA	p.E6K
Pat_76	Pre-Treatment	PAPPA2	60676	37	1	176668460	176668460	Missense_Mutation	SNP	A	G	112	366	c.2971A>G	c.(2971-2973)AAG>GAG	p.K991E
Pat_76	Pre-Treatment	C1orf125	126859	37	1	179460729	179460729	Missense_Mutation	SNP	G	A	33	131	c.2148G>A	c.(2146-2148)ATG>ATA	p.M716I
Pat_76	Pre-Treatment	CEP350	9857	37	1	180023013	180023013	Missense_Mutation	SNP	A	C	99	36	c.5118A>C	c.(5116-5118)GAA>GAC	p.E1706D
Pat_76	Pre-Treatment	XPR1	9213	37	1	180849418	180849418	Missense_Mutation	SNP	C	T	106	82	c.2015C>T	c.(2014-2016)CCT>CTT	p.P672L
Pat_76	Pre-Treatment	CACNA1E	777	37	1	181695216	181695216	Missense_Mutation	SNP	G	A	33	18	c.2158G>A	c.(2158-2160)GAA>AAA	p.E720K
Pat_76	Pre-Treatment	LAMC2	3918	37	1	183192278	183192278	Missense_Mutation	SNP	C	T	63	23	c.772C>T	c.(772-774)CTT>TTT	p.L258F
Pat_76	Pre-Treatment	LAMC2	3918	37	1	183192310	183192310	Missense_Mutation	SNP	C	G	20	86	c.804C>G	c.(802-804)AGC>AGG	p.S268R
Pat_76	Pre-Treatment	APOBEC4	403314	37	1	183616917	183616917	Missense_Mutation	SNP	C	T	131	71	c.1000G>A	c.(1000-1002)GGA>AGA	p.G334R
Pat_76	Pre-Treatment	FAM129A	116496	37	1	184792330	184792330	Nonsense_Mutation	SNP	G	C	49	146	c.956C>G	c.(955-957)TCA>TGA	p.S319*
Pat_76	Pre-Treatment	FAM129A	116496	37	1	184863341	184863341	Splice_Site	SNP	C	T	7	32	c.187_splice	c.e3-1	p.P63_splice
Pat_76	Pre-Treatment	PRG4	10216	37	1	186276274	186276274	Missense_Mutation	SNP	G	T	5	160	c.1423G>T	c.(1423-1425)GCA>TCA	p.A475S
Pat_76	Pre-Treatment	PLA2G4A	5321	37	1	186934540	186934540	Splice_Site	SNP	G	A	18	10	c.1580_splice	c.e15-1	p.D527_splice
Pat_76	Pre-Treatment	FAM5C	339479	37	1	190195350	190195350	Missense_Mutation	SNP	C	T	79	37	c.823G>A	c.(823-825)GAA>AAA	p.E275K
Pat_76	Pre-Treatment	CFH	3075	37	1	196654365	196654365	Missense_Mutation	SNP	C	T	53	247	c.962C>T	c.(961-963)ACC>ATC	p.T321I
Pat_76	Pre-Treatment	CRB1	23418	37	1	197396935	197396935	Missense_Mutation	SNP	G	A	61	27	c.2480G>A	c.(2479-2481)GGA>GAA	p.G827E
Pat_76	Pre-Treatment	KIF14	9928	37	1	200586846	200586846	Missense_Mutation	SNP	G	T	37	150	c.1006C>A	c.(1006-1008)CCC>ACC	p.P336T
Pat_76	Pre-Treatment	KIF14	9928	37	1	200586848	200586848	Missense_Mutation	SNP	A	G	37	151	c.1004T>C	c.(1003-1005)CTT>CCT	p.L335P
Pat_76	Pre-Treatment	CACNA1S	779	37	1	201056982	201056983	Missense_Mutation	DNP	GG	AA	33	41	c.975_976CC>TT	(973-978)ATCCTC>ATTTT	p.L326F
Pat_76	Pre-Treatment	TNNI1	7135	37	1	201383752	201383752	Missense_Mutation	SNP	T	G	23	83	c.83A>C	c.(82-84)GAA>GCA	p.E28A
Pat_76	Pre-Treatment	TNNI1	7135	37	1	201386940	201386940	Translation_Start_Site	SNP	C	T	11	48	c.-18G>A	c.(-20--16)AGGTG>AGATG	
Pat_76	Pre-Treatment	NAV1	89796	37	1	201762969	201762969	Missense_Mutation	SNP	G	A	4	153	c.3371G>A	c.(3370-3372)CGC>CAC	p.R1124H
Pat_76	Pre-Treatment	IPO9	55705	37	1	201843467	201843467	Missense_Mutation	SNP	G	A	4	137	c.2800G>A	c.(2800-2802)GCT>ACT	p.A934T
Pat_76	Pre-Treatment	LGR6	59352	37	1	202283992	202283992	Nonsense_Mutation	SNP	C	T	15	81	c.1630C>T	c.(1630-1632)CAG>TAG	p.Q544*
Pat_76	Pre-Treatment	PPP1R12B	4660	37	1	202464748	202464748	Nonsense_Mutation	SNP	C	T	54	143	c.2386C>T	c.(2386-2388)CGA>TGA	p.R796*

Pat_76	Pre-Treatment	CHI3L1	1116	37	1	203153717	203153717	Missense_Mutation	SNP	A	T	128	57	c.301T>A	c.(301-303)TTT>ATT	p.F101I
Pat_76	Pre-Treatment	ZC3H11A	9877	37	1	203819077	203819077	Missense_Mutation	SNP	A	G	4	145	c.1862A>G	c.(1861-1863)GAG>GGG	p.E621G
Pat_76	Pre-Treatment	TMCC2	9911	37	1	205211131	205211131	Missense_Mutation	SNP	G	A	4	113	c.706G>A	c.(706-708)GTG>ATG	p.V236M
Pat_76	Pre-Treatment	C4BPB	725	37	1	207265145	207265145	Missense_Mutation	SNP	C	T	17	21	c.389C>T	c.(388-390)CCC>CTC	p.P130L
Pat_76	Pre-Treatment	HSD11B1	3290	37	1	209879168	209879168	Missense_Mutation	SNP	G	A	12	84	c.101G>A	c.(100-102)GGA>GAA	p.G34E
Pat_76	Pre-Treatment	KCNH1	3756	37	1	210977434	210977435	Missense_Mutation	DNP	GG	AA	30	16	c.1536_1537CC>TT	1534-1539)TACCAT>TATT	p.H513Y
Pat_76	Pre-Treatment	PTPN14	5784	37	1	214556797	214556797	Missense_Mutation	SNP	C	T	5	246	c.2401G>A	c.(2401-2403)GGG>AGG	p.G801R
Pat_76	Pre-Treatment	USH2A	7399	37	1	215813963	215813963	Missense_Mutation	SNP	C	T	4	108	c.14905G>A	c.(14905-14907)GGA>AGA	p.G4969R
Pat_76	Pre-Treatment	USH2A	7399	37	1	215848169	215848169	Missense_Mutation	SNP	G	A	15	51	c.13084C>T	c.(13084-13086)CCA>TCA	p.P4362S
Pat_76	Pre-Treatment	EPRS	2058	37	1	220152958	220152958	Splice_Site	SNP	C	T	24	53	c.3712_splice	c.e27-1	p.G1238_splice
Pat_76	Pre-Treatment	MIA3	375056	37	1	222801532	222801532	Missense_Mutation	SNP	G	A	91	43	c.970G>A	c.(970-972)GAC>AAC	p.D324N
Pat_76	Pre-Treatment	DISP1	84976	37	1	223177395	223177395	Missense_Mutation	SNP	T	A	37	98	c.2656T>A	c.(2656-2658)TTT>ATT	p.F886I
Pat_76	Pre-Treatment	SUSD4	55061	37	1	223465897	223465897	Missense_Mutation	SNP	C	T	49	185	c.245G>A	c.(244-246)CGA>CAA	p.R82Q
Pat_76	Pre-Treatment	ENAH	55740	37	1	225707053	225707053	Missense_Mutation	SNP	C	T	34	89	c.649G>A	c.(649-651)GAG>AAG	p.E217K
Pat_76	Pre-Treatment	CDC42BPA	8476	37	1	227203785	227203785	Missense_Mutation	SNP	G	A	147	43	c.4748C>T	c.(4747-4749)CCC>CTC	p.P1583L
Pat_76	Pre-Treatment	OBSCN	84033	37	1	228479646	228479646	Missense_Mutation	SNP	G	A	32	23	c.10387G>A	c.(10387-10389)GAA>AAA	p.E3463K
Pat_76	Pre-Treatment	SIPA1L2	57568	37	1	232600998	232600998	Missense_Mutation	SNP	C	T	5	323	c.2408G>A	c.(2407-2409)CGA>CAA	p.R803Q
Pat_76	Pre-Treatment	SIPA1L2	57568	37	1	232601113	232601113	Missense_Mutation	SNP	G	A	52	197	c.2293C>T	c.(2293-2295)CCC>TCC	p.P765S
Pat_76	Pre-Treatment	KIAA1804	84451	37	1	233482322	233482322	Missense_Mutation	SNP	G	A	44	28	c.940G>A	c.(940-942)GAA>AAA	p.E314K
Pat_76	Pre-Treatment	NID1	4811	37	1	236205285	236205285	Missense_Mutation	SNP	G	T	4	82	c.1060C>A	c.(1060-1062)CAG>AAG	p.Q354K
Pat_76	Pre-Treatment	FMN2	56776	37	1	240371077	240371077	Missense_Mutation	SNP	C	T	43	106	c.2965C>T	c.(2965-2967)CCT>TCT	p.P989S
Pat_76	Pre-Treatment	FMN2	56776	37	1	240371209	240371209	Missense_Mutation	SNP	C	T	6	76	c.3097C>T	c.(3097-3099)CCG>TCG	p.P1033S
Pat_76	Pre-Treatment	AKT3	10000	37	1	243777040	243777040	Missense_Mutation	SNP	G	A	23	30	c.629C>T	c.(628-630)TCC>TTC	p.S210F
Pat_76	Pre-Treatment	C1orf100	200159	37	1	244528007	244528007	Missense_Mutation	SNP	C	T	4	85	c.5C>T	c.(4-6)ACT>ATT	p.T2I
Pat_76	Pre-Treatment	ZNF669	79862	37	1	247264023	247264023	Missense_Mutation	SNP	G	A	55	45	c.1048C>T	c.(1048-1050)CGT>TGT	p.R350C
Pat_76	Pre-Treatment	OR2W5	441932	37	1	247655213	247655213	Missense_Mutation	SNP	G	A	41	63	c.784G>A	c.(784-786)GCC>ACC	p.A262T
Pat_76	Pre-Treatment	OR2W3	343171	37	1	248059042	248059042	Missense_Mutation	SNP	G	A	170	247	c.154G>A	c.(154-156)GAC>AAC	p.D52N
Pat_76	Pre-Treatment	OR2L2	26246	37	1	248201597	248201597	Missense_Mutation	SNP	G	A	46	75	c.28G>A	c.(28-30)GAT>AAT	p.D10N
Pat_76	Pre-Treatment	OR2M3	127062	37	1	248366888	248366888	Missense_Mutation	SNP	A	C	119	175	c.519A>C	c.(517-519)GAA>GAC	p.E173D
Pat_76	Pre-Treatment	OR2T33	391195	37	1	248436332	248436332	Missense_Mutation	SNP	G	A	34	40	c.785C>T	c.(784-786)TCC>TTC	p.S262F
Pat_76	Pre-Treatment	OR2T33	391195	37	1	248436951	248436951	Missense_Mutation	SNP	G	A	41	58	c.166C>T	c.(166-168)CCC>TCC	p.P56S
Pat_76	Pre-Treatment	OR14I1	401994	37	1	248845470	248845470	Missense_Mutation	SNP	C	T	8	27	c.136G>A	c.(136-138)GTC>ATC	p.V46I
Pat_76	Pre-Treatment	GTPBP4	23560	37	10	1055472	1055472	Nonsense_Mutation	SNP	C	T	52	82	c.1195C>T	c.(1195-1197)CGA>TGA	p.R399*
Pat_76	Pre-Treatment	NET1	10276	37	10	5468628	5468628	Missense_Mutation	SNP	C	T	4	77	c.139C>T	c.(139-141)CGG>TGG	p.R47W
Pat_76	Pre-Treatment	C10orf18	54906	37	10	5769069	5769069	Missense_Mutation	SNP	G	A	4	137	c.470G>A	c.(469-471)CGT>CAT	p.R157H
Pat_76	Pre-Treatment	C10orf18	54906	37	10	5789058	5789058	Missense_Mutation	SNP	C	T	49	55	c.3674C>T	c.(3673-3675)TCG>TTG	p.S1225L
Pat_76	Pre-Treatment	IL2RA	3559	37	10	6067847	6067847	Missense_Mutation	SNP	C	T	28	51	c.206G>A	c.(205-207)GGA>GAA	p.G69E
Pat_76	Pre-Treatment	ITIH2	3698	37	10	7751024	7751024	Nonsense_Mutation	SNP	C	T	44	103	c.232C>T	c.(232-234)CAG>TAG	p.Q78*
Pat_76	Pre-Treatment	ATP5C1	509	37	10	7842001	7842001	Missense_Mutation	SNP	C	T	20	60	c.584C>T	c.(583-585)TCC>TTC	p.S195F
Pat_76	Pre-Treatment	NMT2	9397	37	10	15154841	15154841	Missense_Mutation	SNP	G	A	4	114	c.1292C>T	c.(1291-1293)ACG>ATG	p.T431M
Pat_76	Pre-Treatment	CUBN	8029	37	10	16962022	16962022	Missense_Mutation	SNP	G	A	37	33	c.6761C>T	c.(6760-6762)CCA>CTA	p.P2254L
Pat_76	Pre-Treatment	PLXDC2	84898	37	10	20432253	20432253	Nonsense_Mutation	SNP	C	T	42	78	c.571C>T	c.(571-573)CGA>TGA	p.R191*
Pat_76	Pre-Treatment	NEBL	10529	37	10	21250695	21250695	Missense_Mutation	SNP	C	G	58	47	c.263G>C	c.(262-264)AGA>ACA	p.R88T
Pat_76	Pre-Treatment	KIAA1217	56243	37	10	24813643	24813643	Missense_Mutation	SNP	A	C	3	61	c.2848A>C	c.(2848-2850)ATT>CTT	p.I950L
Pat_76	Pre-Treatment	KIAA1217	56243	37	10	24834776	24834776	Missense_Mutation	SNP	A	T	38	37	c.5355A>T	c.(5353-5355)AAA>AAT	p.K1785N
Pat_76	Pre-Treatment	ARHGAP21	57584	37	10	24896817	24896817	Missense_Mutation	SNP	G	A	29	50	c.2438C>T	c.(2437-2439)CCT>CTT	p.P813L
Pat_76	Pre-Treatment	THNSL1	79896	37	10	25314107	25314107	Missense_Mutation	SNP	G	A	49	51	c.1955G>A	c.(1954-1956)AGG>AAG	p.R652K

Pat_76	Pre-Treatment	GAD2	2572	37	10	26562608	26562608	Nonsense_Mutation	SNP	G	A	53	57	c.1136G>A	c.(1135-1137)TGG>TAG	p.W379*
Pat_76	Pre-Treatment	GAD2	2572	37	10	26589747	26589747	Missense_Mutation	SNP	G	A	32	75	c.1615G>A	c.(1615-1617)GAG>AAG	p.E539K
Pat_76	Pre-Treatment	PTCHD3	374308	37	10	27702980	27702981	Missense_Mutation	DNP	GG	AA	25	20	c.199_200CC>TT	c.(199-201)CCC>TTC	p.P67F
Pat_76	Pre-Treatment	EPC1	80314	37	10	32576138	32576138	Missense_Mutation	SNP	G	A	4	116	c.1040C>T	c.(1039-1041)TCG>TTG	p.S347L
Pat_76	Pre-Treatment	C10orf68	79741	37	10	33018265	33018266	Missense_Mutation	DNP	CC	TT	30	37	c.706_707CC>TT	c.(706-708)CCT>TTT	p.P236F
Pat_76	Pre-Treatment	ANKRD30A	91074	37	10	37490199	37490199	Missense_Mutation	SNP	G	A	5	111	c.2647G>A	c.(2647-2649)GTA>ATA	p.V883I
Pat_76	Pre-Treatment	ZNF33B	7582	37	10	43088374	43088374	Missense_Mutation	SNP	C	A	39	80	c.2024G>T	c.(2023-2025)TGT>TTT	p.C675F
Pat_76	Pre-Treatment	BMS1	9790	37	10	43316137	43316137	Splice_Site	SNP	G	A	4	62	c.2950_splice	c.e17+1	p.G984_splice
Pat_76	Pre-Treatment	RASGEF1A	221002	37	10	43692445	43692445	Missense_Mutation	SNP	C	T	13	9	c.1327G>A	c.(1327-1329)GCG>ACG	p.A443T
Pat_76	Pre-Treatment	RASGEF1A	221002	37	10	43694453	43694453	Missense_Mutation	SNP	C	T	50	34	c.960G>A	c.(958-960)ATG>ATA	p.M320I
Pat_76	Pre-Treatment	HNRNPF	3185	37	10	43882129	43882129	Missense_Mutation	SNP	C	T	5	179	c.1204G>A	c.(1204-1206)GGG>AGG	p.G402R
Pat_76	Pre-Treatment	ANUBL1	93550	37	10	46121802	46121802	Missense_Mutation	SNP	G	T	4	94	c.1469C>A	c.(1468-1470)CCA>CAA	p.P490Q
Pat_76	Pre-Treatment	SYT15	83849	37	10	46965788	46965789	Missense_Mutation	DNP	GG	AA	4	30	c.748_749CC>TT	c.(748-750)CCC>TTC	p.P250F
Pat_76	Pre-Treatment	FRMPD2	143162	37	10	49395274	49395274	Missense_Mutation	SNP	C	T	13	19	c.2227G>A	c.(2227-2229)GAC>AAC	p.D743N
Pat_76	Pre-Treatment	DRGX	644168	37	10	50574211	50574211	Missense_Mutation	SNP	C	T	21	45	c.757G>A	c.(757-759)GAA>AAA	p.E253K
Pat_76	Pre-Treatment	SLC18A3	6572	37	10	50819762	50819762	Missense_Mutation	SNP	G	A	28	50	c.976G>A	c.(976-978)GAG>AAG	p.E326K
Pat_76	Pre-Treatment	C10orf53	282966	37	10	50902584	50902584	Missense_Mutation	SNP	G	A	18	56	c.218G>A	c.(217-219)GGA>GAA	p.G73E
Pat_76	Pre-Treatment	AGAP6	414189	37	10	51748552	51748552	Missense_Mutation	SNP	C	T	34	54	c.77C>T	c.(76-78)CCC>CTC	p.P26L
Pat_76	Pre-Treatment	ASAH2	56624	37	10	52005142	52005142	Missense_Mutation	SNP	G	A	14	9	c.200C>T	c.(199-201)TCC>TTC	p.S67F
Pat_76	Pre-Treatment	ASAH2	56624	37	10	52005163	52005163	Missense_Mutation	SNP	C	T	7	7	c.179G>A	c.(178-180)GGC>GAC	p.G60D
Pat_76	Pre-Treatment	CSTF2T	23283	37	10	53458427	53458427	Missense_Mutation	SNP	C	T	48	67	c.883G>A	c.(883-885)GTT>ATT	p.V295I
Pat_76	Pre-Treatment	PCDH15	65217	37	10	55626547	55626547	Missense_Mutation	SNP	C	T	33	44	c.3572G>A	c.(3571-3573)GGA>GAA	p.G1191E
Pat_76	Pre-Treatment	ANK3	288	37	10	61941095	61941095	Missense_Mutation	SNP	G	T	69	90	c.2176C>A	c.(2176-2178)CAG>AAG	p.Q726K
Pat_76	Pre-Treatment	ARID5B	84159	37	10	63851357	63851357	Missense_Mutation	SNP	C	T	31	45	c.2135C>T	c.(2134-2136)TCC>TTC	p.S712F
Pat_76	Pre-Treatment	LRRTM3	347731	37	10	68687186	68687186	Missense_Mutation	SNP	C	T	37	55	c.512C>T	c.(511-513)ACC>ATC	p.T171I
Pat_76	Pre-Treatment	CTNNA3	29119	37	10	68940116	68940116	Missense_Mutation	SNP	G	A	35	42	c.1006C>T	c.(1006-1008)CGC>TGC	p.R336C
Pat_76	Pre-Treatment	PBLD	64081	37	10	70056043	70056043	Missense_Mutation	SNP	G	A	4	56	c.263C>T	c.(262-264)GCT>GTT	p.A88V
Pat_76	Pre-Treatment	SLC25A16	8034	37	10	70266454	70266454	Missense_Mutation	SNP	G	A	3	24	c.245C>T	c.(244-246)GCT>GTT	p.A82V
Pat_76	Pre-Treatment	UNC5B	219699	37	10	73046531	73046531	Missense_Mutation	SNP	G	A	5	264	c.638G>A	c.(637-639)CGC>CAC	p.R213H
Pat_76	Pre-Treatment	UNC5B	219699	37	10	73051446	73051446	Missense_Mutation	SNP	G	C	25	25	c.1552G>C	c.(1552-1554)GAC>CAC	p.D518H
Pat_76	Pre-Treatment	CCDC109A	90550	37	10	74644024	74644024	Missense_Mutation	SNP	G	A	29	41	c.862G>A	c.(862-864)GAA>AAA	p.E288K
Pat_76	Pre-Treatment	PLA2G12B	84647	37	10	74714398	74714398	Missense_Mutation	SNP	C	T	20	40	c.46G>A	c.(46-48)GGT>AGT	p.G16S
Pat_76	Pre-Treatment	TTC18	118491	37	10	75038089	75038089	Missense_Mutation	SNP	C	T	8	12	c.2456G>A	c.(2455-2457)GGA>GAA	p.G819E
Pat_76	Pre-Treatment	USP54	159195	37	10	75276315	75276315	Missense_Mutation	SNP	G	A	57	57	c.3869C>T	c.(3868-3870)TCC>TTC	p.S1290F
Pat_76	Pre-Treatment	DLG5	9231	37	10	79589166	79589166	Missense_Mutation	SNP	G	A	54	92	c.2132C>T	c.(2131-2133)TCC>TTC	p.S711F
Pat_76	Pre-Treatment	SFTPD	6441	37	10	81697757	81697757	Missense_Mutation	SNP	G	A	90	111	c.979C>T	c.(979-981)CCC>TCC	p.P327S
Pat_76	Pre-Treatment	MMRN2	79812	37	10	88703241	88703241	Missense_Mutation	SNP	C	T	26	27	c.1300G>A	c.(1300-1302)GAG>AAG	p.E434K
Pat_76	Pre-Treatment	BTAF1	9044	37	10	93711222	93711222	Missense_Mutation	SNP	C	T	17	45	c.463C>T	c.(463-465)CTT>TTT	p.L155F
Pat_76	Pre-Treatment	MYOF	26509	37	10	95119690	95119690	Missense_Mutation	SNP	G	A	66	67	c.3020C>T	c.(3019-3021)TCC>TTC	p.S1007F
Pat_76	Pre-Treatment	CEP55	55165	37	10	95276697	95276697	Missense_Mutation	SNP	C	T	33	36	c.685C>T	c.(685-687)CTT>TTT	p.L229F
Pat_76	Pre-Treatment	LGI1	9211	37	10	95557173	95557173	Missense_Mutation	SNP	G	A	48	63	c.1287G>A	c.(1285-1287)ATG>ATA	p.M429I
Pat_76	Pre-Treatment	PIPSL	266971	37	10	95720163	95720164	Missense_Mutation	DNP	CC	TT	24	25	c.990_991GG>AA	(988-993)ATGGGT>ATAA	.330_331MG>I
Pat_76	Pre-Treatment	ALDH18A1	5832	37	10	97402832	97402832	Missense_Mutation	SNP	C	T	4	75	c.220G>A	c.(220-222)GTG>ATG	p.V74M
Pat_76	Pre-Treatment	TCTN3	26123	37	10	97442505	97442505	Missense_Mutation	SNP	C	T	83	130	c.1355G>A	c.(1354-1356)GGA>GAA	p.G452E
Pat_76	Pre-Treatment	TLL2	7093	37	10	98145849	98145849	Missense_Mutation	SNP	G	A	15	19	c.1976C>T	c.(1975-1977)TCC>TTC	p.S659F
Pat_76	Pre-Treatment	TLL2	7093	37	10	98145910	98145910	Missense_Mutation	SNP	C	T	46	48	c.1915G>A	c.(1915-1917)GAG>AAG	p.E639K
Pat_76	Pre-Treatment	ARHGAP19	84986	37	10	99023320	99023320	Missense_Mutation	SNP	G	A	4	159	c.470C>T	c.(469-471)GCT>GTT	p.A157V

Pat_76	Pre-Treatment	FAM178A	55719	37	10	102672889	102672889	Missense_Mutation	SNP	G	A	4	51	c.22G>A	c.(22-24)GCT>ACT	p.A8T
Pat_76	Pre-Treatment	PSD	5662	37	10	104171563	104171564	Missense_Mutation	DNP	CC	TT	6	9	.1842_1843GG>A	840-1845)AAGGAG>AAA	p.E615K
Pat_76	Pre-Treatment	TRIM8	81603	37	10	104416885	104416885	Missense_Mutation	SNP	C	T	27	40	c.1430C>T	c.(1429-1431)TCC>TTC	p.S477F
Pat_76	Pre-Treatment	SH3PXD2A	9644	37	10	105362751	105362751	Missense_Mutation	SNP	C	A	4	105	c.2140G>T	c.(2140-2142)GCG>TCG	p.A714S
Pat_76	Pre-Treatment	HABP2	3026	37	10	115342983	115342983	Missense_Mutation	SNP	C	T	14	24	c.1103C>T	c.(1102-1104)ACC>ATC	p.T368I
Pat_76	Pre-Treatment	C10orf81	79949	37	10	115526170	115526170	Missense_Mutation	SNP	G	A	12	17	c.11G>A	c.(10-12)GGC>GAC	p.G4D
Pat_76	Pre-Treatment	ATRNL1	26033	37	10	116889240	116889240	Missense_Mutation	SNP	C	T	44	49	c.772C>T	c.(772-774)CAC>TAC	p.H258Y
Pat_76	Pre-Treatment	ATRNL1	26033	37	10	117154237	117154238	Missense_Mutation	DNP	GG	AA	21	61	.3244_3245GG>A	c.(3244-3246)GGA>AAA	p.G1082K
Pat_76	Pre-Treatment	PNLIPRP3	119548	37	10	118236307	118236307	Missense_Mutation	SNP	A	T	21	27	c.1316A>T	c.(1315-1317)AAT>ATT	p.N439I
Pat_76	Pre-Treatment	EIF3A	8661	37	10	120801695	120801695	Missense_Mutation	SNP	A	T	6	228	c.3337T>A	c.(3337-3339)TTG>ATG	p.L1113M
Pat_76	Pre-Treatment	FGFR2	2263	37	10	123325216	123325216	Missense_Mutation	SNP	G	A	4	49	c.112C>T	c.(112-114)CCA>TCA	p.P38S
Pat_76	Pre-Treatment	TACC2	10579	37	10	123989936	123989936	Missense_Mutation	SNP	G	A	4	61	c.8108G>A	c.(8107-8109)CGC>CAC	p.R2703H
Pat_76	Pre-Treatment	DMBT1	1755	37	10	124351944	124351944	Nonsense_Mutation	SNP	G	A	6	244	c.2333G>A	c.(2332-2334)TGG>TAG	p.W778*
Pat_76	Pre-Treatment	DMBT1	1755	37	10	124399555	124399555	Splice_Site	SNP	G	A	12	17	c.6556_splice	c.e52-1	p.A2186_splice
Pat_76	Pre-Treatment	CUZD1	50624	37	10	124593415	124593415	Missense_Mutation	SNP	C	T	24	23	c.1424G>A	c.(1423-1425)GGA>GAA	p.G475E
Pat_76	Pre-Treatment	CHST15	51363	37	10	125798085	125798085	Missense_Mutation	SNP	T	A	23	33	c.1136A>T	c.(1135-1137)CAC>CTC	p.H379L
Pat_76	Pre-Treatment	CHST15	51363	37	10	125805533	125805533	Missense_Mutation	SNP	C	T	30	31	c.196G>A	c.(196-198)GAA>AAA	p.E66K
Pat_76	Pre-Treatment	DOCK1	1793	37	10	128851048	128851048	Missense_Mutation	SNP	T	C	6	11	c.2242T>C	c.(2242-2244)TTC>CTC	p.F748L
Pat_76	Pre-Treatment	DOCK1	1793	37	10	128851054	128851054	Missense_Mutation	SNP	G	A	4	8	c.2248G>A	c.(2248-2250)GTG>ATG	p.V750M
Pat_76	Pre-Treatment	KRTAP5-1	387264	37	11	1606443	1606443	Missense_Mutation	SNP	T	C	4	149	c.37A>G	c.(37-39)AGC>GGC	p.S13G
Pat_76	Pre-Treatment	TNNT3	7140	37	11	1959716	1959716	Nonsense_Mutation	SNP	G	A	14	17	c.771G>A	c.(769-771)TGG>TGA	p.W257*
Pat_76	Pre-Treatment	TSSC4	10078	37	11	2424103	2424104	Missense_Mutation	DNP	CC	TT	20	24	c.240_241CC>TT	.(238-243)TTCCAT>TTTTA	p.H81Y
Pat_76	Pre-Treatment	TRPM5	29850	37	11	2428471	2428471	Missense_Mutation	SNP	T	C	10	18	c.2996A>G	c.(2995-2997)AAC>AGC	p.N999S
Pat_76	Pre-Treatment	ZNF195	7748	37	11	3380508	3380508	Missense_Mutation	SNP	G	A	29	69	c.1730C>T	c.(1729-1731)CCC>CTC	p.P577L
Pat_76	Pre-Treatment	OR52K2	119774	37	11	4471488	4471489	Missense_Mutation	DNP	GG	AA	36	43	c.919_920GG>AA	c.(919-921)GGA>AAA	p.G307K
Pat_76	Pre-Treatment	OR51E1	143503	37	11	4674277	4674277	Missense_Mutation	SNP	C	T	74	118	c.521C>T	c.(520-522)TCC>TTC	p.S174F
Pat_76	Pre-Treatment	OR51E1	143503	37	11	4674409	4674409	Missense_Mutation	SNP	C	T	19	27	c.653C>T	c.(652-654)TCC>TTC	p.S218F
Pat_76	Pre-Treatment	OR51E2	81285	37	11	4703277	4703277	Missense_Mutation	SNP	C	T	21	30	c.665G>A	c.(664-666)CGA>CAA	p.R222Q
Pat_76	Pre-Treatment	OR51E2	81285	37	11	4703632	4703632	Missense_Mutation	SNP	G	A	8	26	c.310C>T	c.(310-312)CAT>TAT	p.H104Y
Pat_76	Pre-Treatment	OR52R1	119695	37	11	4824685	4824685	Missense_Mutation	SNP	C	T	14	33	c.1163G>A	c.(1162-1164)GGA>GAA	p.G388E
Pat_76	Pre-Treatment	OR51F2	119694	37	11	4843021	4843021	Missense_Mutation	SNP	C	T	63	122	c.406C>T	c.(406-408)CGT>TGT	p.R136C
Pat_76	Pre-Treatment	OR52J3	119679	37	11	5068233	5068233	Missense_Mutation	SNP	C	T	20	42	c.478C>T	c.(478-480)CCC>TCC	p.P160S
Pat_76	Pre-Treatment	HBG2	3048	37	11	5275625	5275625	Missense_Mutation	SNP	G	A	25	153	c.212C>T	c.(211-213)TCC>TTC	p.S71F
Pat_76	Pre-Treatment	OR51B5	282763	37	11	5363977	5363977	Missense_Mutation	SNP	G	A	22	33	c.778C>T	c.(778-780)CAT>TAT	p.H260Y
Pat_76	Pre-Treatment	OR52N1	79473	37	11	5809139	5809139	Missense_Mutation	SNP	C	T	4	105	c.908G>A	c.(907-909)CGA>CAA	p.R303Q
Pat_76	Pre-Treatment	OR52N1	79473	37	11	5809289	5809289	Missense_Mutation	SNP	G	A	43	77	c.758C>T	c.(757-759)ACC>ATC	p.T253I
Pat_76	Pre-Treatment	OR52B2	255725	37	11	6190872	6190872	Missense_Mutation	SNP	G	A	21	8	c.685C>T	c.(685-687)CGT>TGT	p.R229C
Pat_76	Pre-Treatment	OR2AG2	338755	37	11	6790164	6790164	Missense_Mutation	SNP	C	T	9	30	c.25G>A	c.(25-27)GGA>AGA	p.G9R
Pat_76	Pre-Treatment	NLRP14	338323	37	11	7079624	7079624	Missense_Mutation	SNP	G	A	58	92	c.2576G>A	c.(2575-2577)GGA>GAA	p.G859E
Pat_76	Pre-Treatment	NLRP14	338323	37	11	7081264	7081264	Missense_Mutation	SNP	C	T	127	147	c.2773C>T	c.(2773-2775)CGG>TGG	p.R925W
Pat_76	Pre-Treatment	PLEKHA7	144100	37	11	16872806	16872806	Missense_Mutation	SNP	G	A	37	50	c.628C>T	c.(628-630)CCC>TCC	p.P210S
Pat_76	Pre-Treatment	KCNJ11	3767	37	11	17409602	17409602	Missense_Mutation	SNP	C	T	4	83	c.37G>A	c.(37-39)GTG>ATG	p.V13M
Pat_76	Pre-Treatment	ABCC8	6833	37	11	17483319	17483319	Missense_Mutation	SNP	T	G	14	16	c.633A>C	c.(631-633)CAA>CAC	p.Q211H
Pat_76	Pre-Treatment	MRGPRX2	117194	37	11	19077339	19077339	Missense_Mutation	SNP	G	A	6	27	c.611C>T	c.(610-612)GCC>GTC	p.A204V
Pat_76	Pre-Treatment	NAV2	89797	37	11	20070338	20070338	Missense_Mutation	SNP	G	A	51	55	c.4036G>A	c.(4036-4038)GTG>ATG	p.V1346M
Pat_76	Pre-Treatment	ANO3	63982	37	11	26620469	26620469	Missense_Mutation	SNP	G	A	20	39	c.1595G>A	c.(1594-1596)GGA>GAA	p.G532E
Pat_76	Pre-Treatment	BDNF	627	37	11	27679666	27679666	Missense_Mutation	SNP	G	A	5	245	c.446C>T	c.(445-447)ACG>ATG	p.T149M

Pat_76	Pre-Treatment	KIF18A	81930	37	11	28058011	28058011	Missense_Mutation	SNP	G	A	37	44	c.2149C>T	c.(2149-2151)CCG>TCG	p.P717S
Pat_76	Pre-Treatment	QSER1	79832	37	11	32953540	32953540	Missense_Mutation	SNP	C	T	5	149	c.349C>T	c.(349-351)CGC>TGC	p.R117C
Pat_76	Pre-Treatment	HIPK3	10114	37	11	33370279	33370279	Missense_Mutation	SNP	G	A	5	133	c.2581G>A	c.(2581-2583)GAC>AAC	p.D861N
Pat_76	Pre-Treatment	ABTB2	25841	37	11	34182562	34182562	Missense_Mutation	SNP	G	A	3	23	c.1727C>T	c.(1726-1728)TCG>TTG	p.S576L
Pat_76	Pre-Treatment	ELF5	2001	37	11	34502425	34502425	Missense_Mutation	SNP	C	T	38	59	c.595G>A	c.(595-597)GAA>AAA	p.E199K
Pat_76	Pre-Treatment	PRR5L	79899	37	11	36484009	36484010	Missense_Mutation	DNP	GG	AA	22	41	c.830_831GG>AA	c.(829-831)GGG>GAA	p.G277E
Pat_76	Pre-Treatment	PRR5L	79899	37	11	36484116	36484116	Missense_Mutation	SNP	G	A	24	18	c.937G>A	c.(937-939)GGG>AGG	p.G313R
Pat_76	Pre-Treatment	RAG1	5896	37	11	36595839	36595839	Missense_Mutation	SNP	C	T	35	31	c.985C>T	c.(985-987)CCC>TCC	p.P329S
Pat_76	Pre-Treatment	TSPAN18	90139	37	11	44950719	44950719	Missense_Mutation	SNP	G	A	40	59	c.737G>A	c.(736-738)GGC>GAC	p.G246D
Pat_76	Pre-Treatment	PRDM11	56981	37	11	45246341	45246341	Missense_Mutation	SNP	C	T	43	34	c.1418C>T	c.(1417-1419)CCC>CTC	p.P473L
Pat_76	Pre-Treatment	SYT13	57586	37	11	45277376	45277376	Missense_Mutation	SNP	C	T	26	34	c.250G>A	c.(250-252)GGA>AGA	p.G84R
Pat_76	Pre-Treatment	GYLTL1B	120071	37	11	45948403	45948403	Missense_Mutation	SNP	G	A	17	26	c.1306G>A	c.(1306-1308)GCC>ACC	p.A436T
Pat_76	Pre-Treatment	MADD	8567	37	11	47303185	47303185	Missense_Mutation	SNP	G	T	4	72	c.1350G>T	c.(1348-1350)GAG>GAT	p.E450D
Pat_76	Pre-Treatment	MADD	8567	37	11	47304035	47304035	Missense_Mutation	SNP	G	A	46	30	c.1573G>A	c.(1573-1575)GCT>ACT	p.A525T
Pat_76	Pre-Treatment	AGBL2	79841	37	11	47707594	47707594	Missense_Mutation	SNP	C	T	14	34	c.1639G>A	c.(1639-1641)GAA>AAA	p.E547K
Pat_76	Pre-Treatment	PTPRJ	5795	37	11	48134319	48134319	Missense_Mutation	SNP	C	T	47	72	c.136C>T	c.(136-138)CCT>TCT	p.P46S
Pat_76	Pre-Treatment	OR4X1	390113	37	11	48285932	48285932	Missense_Mutation	SNP	C	T	16	15	c.520C>T	c.(520-522)CAC>TAC	p.H174Y
Pat_76	Pre-Treatment	OR4C3	256144	37	11	48346737	48346737	Missense_Mutation	SNP	C	T	5	25	c.245C>T	c.(244-246)TCC>TTC	p.S82F
Pat_76	Pre-Treatment	OR4A5	81318	37	11	51412038	51412038	Missense_Mutation	SNP	G	A	51	42	c.358C>T	c.(358-360)CGC>TGC	p.R120C
Pat_76	Pre-Treatment	OR4C46	119749	37	11	51515827	51515827	Missense_Mutation	SNP	G	T	4	119	c.546G>T	c.(544-546)TTG>TTT	p.L182F
Pat_76	Pre-Treatment	OR4C11	219429	37	11	55371006	55371006	Missense_Mutation	SNP	G	A	27	2	c.844C>T	c.(844-846)CCA>TCA	p.P282S
Pat_76	Pre-Treatment	OR5D14	219436	37	11	55563687	55563687	Missense_Mutation	SNP	C	T	85	112	c.656C>T	c.(655-657)TCC>TTC	p.S219F
Pat_76	Pre-Treatment	OR8H2	390151	37	11	55873063	55873063	Missense_Mutation	SNP	C	T	148	248	c.545C>T	c.(544-546)TCC>TTC	p.S182F
Pat_76	Pre-Treatment	OR8H2	390151	37	11	55873104	55873104	Missense_Mutation	SNP	G	A	119	180	c.586G>A	c.(586-588)GAA>AAA	p.E196K
Pat_76	Pre-Treatment	OR8H1	219469	37	11	56057772	56057772	Missense_Mutation	SNP	A	T	14	25	c.767T>A	c.(766-768)TTT>TAT	p.F256Y
Pat_76	Pre-Treatment	OR8K3	219473	37	11	56086579	56086579	Missense_Mutation	SNP	C	T	20	28	c.797C>T	c.(796-798)TCC>TTC	p.S266F
Pat_76	Pre-Treatment	OR5AR1	219493	37	11	56431525	56431525	Missense_Mutation	SNP	C	T	53	80	c.364C>T	c.(364-366)CGT>TGT	p.R122C
Pat_76	Pre-Treatment	SSRP1	6749	37	11	57100229	57100229	Missense_Mutation	SNP	C	T	4	86	c.638G>A	c.(637-639)CGT>CAT	p.R213H
Pat_76	Pre-Treatment	OR1S1	219959	37	11	57983114	57983114	Missense_Mutation	SNP	C	T	58	65	c.898C>T	c.(898-900)CCC>TCC	p.P300S
Pat_76	Pre-Treatment	GLYATL2	219970	37	11	58604580	58604580	Missense_Mutation	SNP	C	T	35	40	c.384G>A	c.(382-384)ATG>ATA	p.M128I
Pat_76	Pre-Treatment	OR4D10	390197	37	11	59245249	59245249	Missense_Mutation	SNP	C	T	3	55	c.347C>T	c.(346-348)TCG>TTG	p.S116L
Pat_76	Pre-Treatment	SCGB2A2	4250	37	11	62037719	62037719	Missense_Mutation	SNP	G	A	4	155	c.31G>A	c.(31-33)GCC>ACC	p.A11T
Pat_76	Pre-Treatment	POLR2G	5436	37	11	62530448	62530448	Missense_Mutation	SNP	C	T	4	119	c.232C>T	c.(232-234)CGG>TGG	p.R78W
Pat_76	Pre-Treatment	CHRM1	1128	37	11	62678196	62678196	Missense_Mutation	SNP	G	A	19	29	c.377C>T	c.(376-378)TCC>TTC	p.S126F
Pat_76	Pre-Treatment	SLC22A9	114571	37	11	63149648	63149648	Missense_Mutation	SNP	G	A	37	62	c.972G>A	c.(970-972)ATG>ATA	p.M324I
Pat_76	Pre-Treatment	SLC22A9	114571	37	11	63176246	63176246	Nonsense_Mutation	SNP	G	A	28	35	c.1496G>A	c.(1495-1497)TGG>TAG	p.W499*
Pat_76	Pre-Treatment	FAU	2197	37	11	64889011	64889011	Missense_Mutation	SNP	C	T	4	90	c.181G>A	c.(181-183)GCC>ACC	p.A61T
Pat_76	Pre-Treatment	CDC42EP2	10435	37	11	65088994	65088994	Missense_Mutation	SNP	C	T	10	25	c.625C>T	c.(625-627)CCC>TCC	p.P209S
Pat_76	Pre-Treatment	MAP3K11	4296	37	11	65374985	65374985	Splice_Site	SNP	C	T	4	56	c.1246_splice	c.e5-1	p.E416_splice
Pat_76	Pre-Treatment	SART1	9092	37	11	65732631	65732631	Missense_Mutation	SNP	G	A	11	21	c.496G>A	c.(496-498)GAG>AAG	p.E166K
Pat_76	Pre-Treatment	SF3B2	10992	37	11	65829443	65829443	Missense_Mutation	SNP	C	T	14	20	c.1951C>T	c.(1951-1953)CCT>TCT	p.P651S
Pat_76	Pre-Treatment	SPTBN2	6712	37	11	66468435	66468436	Missense_Mutation	DNP	GG	AA	17	15	.3134_3135CC>T	c.(3133-3135)ACC>ATT	p.T1045I
Pat_76	Pre-Treatment	TBX10	347853	37	11	67402517	67402517	Nonsense_Mutation	SNP	C	T	18	19	c.225G>A	c.(223-225)TGG>TGA	p.W75*
Pat_76	Pre-Treatment	CPT1A	1374	37	11	68542821	68542822	Missense_Mutation	DNP	GG	AA	30	57	.1537_1538CC>T	c.(1537-1539)CCG>TTG	p.P513L
Pat_76	Pre-Treatment	MRPL21	219927	37	11	68671259	68671259	Missense_Mutation	SNP	G	A	5	115	c.20C>T	c.(19-21)ACG>ATG	p.T7M
Pat_76	Pre-Treatment	KRTAP5-9	3846	37	11	71259749	71259750	Missense_Mutation	DNP	GG	AA	43	74	c.46_47GG>AA	c.(46-48)GGC>AAC	p.G16N
Pat_76	Pre-Treatment	UCP2	7351	37	11	73689327	73689327	Missense_Mutation	SNP	G	A	24	37	c.97C>T	c.(97-99)CCT>TCT	p.P33S

Pat_76	Pre-Treatment	PGM2L1	283209	37	11	74054392	74054392	Missense_Mutation	SNP	G	A	21	34	c.1288C>T	c.(1288-1290)CTT>TTT	p.L430F
Pat_76	Pre-Treatment	KLHL35	283212	37	11	75133763	75133763	Missense_Mutation	SNP	C	T	36	78	c.953G>A	c.(952-954)GGG>GAG	p.G318E
Pat_76	Pre-Treatment	OMP	4975	37	11	76814355	76814356	Missense_Mutation	DNP	CC	TT	15	46	c.470_471CC>TT	c.(469-471)TCC>TTT	p.S157F
Pat_76	Pre-Treatment	PCF11	51585	37	11	82877453	82877453	Missense_Mutation	SNP	G	A	4	109	c.1514G>A	c.(1513-1515)CGA>CAA	p.R505Q
Pat_76	Pre-Treatment	DLG2	1740	37	11	83344290	83344290	Missense_Mutation	SNP	G	A	12	48	c.1589C>T	c.(1588-1590)TCC>TTC	p.S530F
Pat_76	Pre-Treatment	GRM5	2915	37	11	88386431	88386431	Missense_Mutation	SNP	C	T	35	48	c.1052G>A	c.(1051-1053)CGA>CAA	p.R351Q
Pat_76	Pre-Treatment	FAT3	120114	37	11	92085960	92085960	Missense_Mutation	SNP	G	A	55	78	c.682G>A	c.(682-684)GAT>AAT	p.D228N
Pat_76	Pre-Treatment	FAT3	120114	37	11	92086786	92086786	Missense_Mutation	SNP	A	T	15	23	c.1508A>T	c.(1507-1509)GAA>GTA	p.E503V
Pat_76	Pre-Treatment	FAT3	120114	37	11	92569781	92569781	Missense_Mutation	SNP	C	T	51	69	c.10136C>T	c.(10135-10137)TCC>TTC	p.S3379F
Pat_76	Pre-Treatment	CNTN5	53942	37	11	99690347	99690347	Missense_Mutation	SNP	C	T	29	96	c.128C>T	c.(127-129)TCA>TTA	p.S43L
Pat_76	Pre-Treatment	KIAA1377	57562	37	11	101828898	101828898	Splice_Site	SNP	G	A	201	314	c.507_splice	c.e5-1	p.R169_splice
Pat_76	Pre-Treatment	KIAA1377	57562	37	11	101833571	101833571	Missense_Mutation	SNP	G	A	19	33	c.1805G>A	c.(1804-1806)GGA>GAA	p.G602E
Pat_76	Pre-Treatment	MMP1	4312	37	11	102667484	102667484	Missense_Mutation	SNP	C	T	35	46	c.536G>A	c.(535-537)GGA>GAA	p.G179E
Pat_76	Pre-Treatment	MMP13	4322	37	11	102826045	102826045	Missense_Mutation	SNP	C	T	55	87	c.298G>A	c.(298-300)GAT>AAT	p.D100N
Pat_76	Pre-Treatment	DYNC2H1	79659	37	11	103027319	103027319	Missense_Mutation	SNP	C	T	17	10	c.3947C>T	c.(3946-3948)CCT>CTT	p.P1316L
Pat_76	Pre-Treatment	PDGFD	80310	37	11	103780454	103780454	Missense_Mutation	SNP	C	T	43	71	c.1081G>A	c.(1081-1083)GAT>AAT	p.D361N
Pat_76	Pre-Treatment	DDI1	414301	37	11	103907873	103907873	Missense_Mutation	SNP	G	A	4	79	c.323G>A	c.(322-324)CGT>CAT	p.R108H
Pat_76	Pre-Treatment	EXPH5	23086	37	11	108382062	108382062	Missense_Mutation	SNP	C	T	20	40	c.4172G>A	c.(4171-4173)AGT>AAT	p.S1391N
Pat_76	Pre-Treatment	DDX10	1662	37	11	108722931	108722931	Missense_Mutation	SNP	G	A	4	56	c.2299G>A	c.(2299-2301)GCA>ACA	p.A767T
Pat_76	Pre-Treatment	HSPB2	3316	37	11	111784324	111784324	Missense_Mutation	SNP	C	T	51	83	c.254C>T	c.(253-255)CCA>CTA	p.P85L
Pat_76	Pre-Treatment	SIDT2	51092	37	11	117059884	117059884	Splice_Site	SNP	G	C	4	122	c.1279_splice	c.e14-1	p.Q427_splice
Pat_76	Pre-Treatment	RNF214	257160	37	11	117109598	117109598	Missense_Mutation	SNP	C	T	29	31	c.389C>T	c.(388-390)CCA>CTA	p.P130L
Pat_76	Pre-Treatment	DSCAML1	57453	37	11	117301743	117301743	Missense_Mutation	SNP	C	T	36	41	c.5561G>A	c.(5560-5562)GGA>GAA	p.G1854E
Pat_76	Pre-Treatment	TMPRSS4	56649	37	11	117982593	117982593	Missense_Mutation	SNP	C	T	29	59	c.721C>T	c.(721-723)CTC>TTC	p.L241F
Pat_76	Pre-Treatment	MLL	4297	37	11	118352637	118352637	Missense_Mutation	SNP	C	T	42	56	c.3842C>T	c.(3841-3843)CCT>CTT	p.P1281L
Pat_76	Pre-Treatment	PHLDB1	23187	37	11	118498401	118498401	Missense_Mutation	SNP	C	T	39	58	c.862C>T	c.(862-864)CGT>TGT	p.R288C
Pat_76	Pre-Treatment	PHLDB1	23187	37	11	118498923	118498923	Missense_Mutation	SNP	C	T	78	106	c.1384C>T	c.(1384-1386)CCA>TCA	p.P462S
Pat_76	Pre-Treatment	CXCR5	643	37	11	118764491	118764491	Missense_Mutation	SNP	C	T	4	145	c.238C>T	c.(238-240)CGG>TGG	p.R80W
Pat_76	Pre-Treatment	TECTA	7007	37	11	120998886	120998886	Missense_Mutation	SNP	G	A	33	67	c.2200G>A	c.(2200-2202)GAG>AAG	p.E734K
Pat_76	Pre-Treatment	TECTA	7007	37	11	121000408	121000408	Missense_Mutation	SNP	G	A	59	80	c.2429G>A	c.(2428-2430)CGA>CAA	p.R810Q
Pat_76	Pre-Treatment	TECTA	7007	37	11	121036027	121036027	Missense_Mutation	SNP	G	A	4	5	c.5318G>A	c.(5317-5319)CGA>CAA	p.R1773Q
Pat_76	Pre-Treatment	SORL1	6653	37	11	121492874	121492874	Missense_Mutation	SNP	C	T	30	39	c.6068C>T	c.(6067-6069)TCA>TTA	p.S2023L
Pat_76	Pre-Treatment	HSPA8	3312	37	11	122928489	122928489	Missense_Mutation	SNP	G	A	56	68	c.1894C>T	c.(1894-1896)CCC>TCC	p.P632S
Pat_76	Pre-Treatment	GRAMD1B	57476	37	11	123477467	123477467	Missense_Mutation	SNP	C	T	4	22	c.1045C>T	c.(1045-1047)CCC>TCC	p.P349S
Pat_76	Pre-Treatment	OR6X1	390260	37	11	123624328	123624328	Missense_Mutation	SNP	C	T	89	90	c.899G>A	c.(898-900)AGA>AAA	p.R300K
Pat_76	Pre-Treatment	OR4D5	219875	37	11	123810370	123810370	Missense_Mutation	SNP	G	A	44	64	c.47G>A	c.(46-48)GGG>GAG	p.G16E
Pat_76	Pre-Treatment	OR4D5	219875	37	11	123810409	123810409	Missense_Mutation	SNP	C	T	36	47	c.86C>T	c.(85-87)ACT>ATT	p.T29I
Pat_76	Pre-Treatment	VWA5A	4013	37	11	123988246	123988246	Missense_Mutation	SNP	C	T	46	59	c.28C>T	c.(28-30)CTC>TTC	p.L10F
Pat_76	Pre-Treatment	VWA5A	4013	37	11	124016007	124016007	Missense_Mutation	SNP	G	A	22	36	c.2218G>A	c.(2218-2220)GAC>AAC	p.D740N
Pat_76	Pre-Treatment	OR8D1	283159	37	11	124180653	124180653	Missense_Mutation	SNP	C	T	16	48	c.10G>A	c.(10-12)GAA>AAA	p.E4K
Pat_76	Pre-Treatment	OR8B12	219858	37	11	124413016	124413016	Missense_Mutation	SNP	C	A	5	128	c.535G>T	c.(535-537)GAC>TAC	p.D179Y
Pat_76	Pre-Treatment	SPA17	53340	37	11	124564231	124564232	Missense_Mutation	DNP	GG	AA	40	62	c.345_346GG>AA	343-348)GAGGTT>GAAA	p.V116I
Pat_76	Pre-Treatment	SLC37A2	219855	37	11	124954748	124954748	Missense_Mutation	SNP	G	A	14	12	c.1153G>A	c.(1153-1155)GAC>AAC	p.D385N
Pat_76	Pre-Treatment	NTM	50863	37	11	132204942	132204942	Missense_Mutation	SNP	C	T	72	136	c.937C>T	c.(937-939)CCA>TCA	p.P313S
Pat_76	Pre-Treatment	SPATA19	219938	37	11	133715271	133715271	Missense_Mutation	SNP	G	A	26	49	c.71C>T	c.(70-72)ACC>ATC	p.T24I
Pat_76	Pre-Treatment	SLC6A12	6539	37	12	306618	306618	Missense_Mutation	SNP	C	T	30	37	c.1000G>A	c.(1000-1002)GGG>AGG	p.G334R
Pat_76	Pre-Treatment	LRTM2	654429	37	12	1943433	1943434	Missense_Mutation	DNP	GG	AA	15	26	c.659_660GG>AA	c.(658-660)GGG>GAA	p.G220E

Pat_76	Pre-Treatment	CACNA1C	775	37	12	2602383	2602383	Missense_Mutation	SNP	C	T	4	69	c.944C>T	c.(943-945)CCT>CTT	p.P315L
Pat_76	Pre-Treatment	CACNA1C	775	37	12	2614028	2614028	Missense_Mutation	SNP	G	C	6	13	c.1134G>C	c.(1132-1134)AGG>AGC	p.R378S
Pat_76	Pre-Treatment	C12orf32	83695	37	12	2994574	2994575	Missense_Mutation	DNP	CC	TT	28	45	c.42_43CC>TT	(40-45)GCCCCG>GCTTC	p.P15S
Pat_76	Pre-Treatment	DYRK4	8798	37	12	4702179	4702179	Missense_Mutation	SNP	C	T	21	49	c.130C>T	c.(130-132)CTT>TTT	p.L44F
Pat_76	Pre-Treatment	KCNA6	3742	37	12	4919724	4919724	Missense_Mutation	SNP	G	A	18	32	c.517G>A	c.(517-519)GCC>ACC	p.A173T
Pat_76	Pre-Treatment	NTF3	4908	37	12	5603912	5603912	Missense_Mutation	SNP	G	A	30	45	c.532G>A	c.(532-534)GAG>AAG	p.E178K
Pat_76	Pre-Treatment	ANO2	57101	37	12	5708727	5708727	Missense_Mutation	SNP	G	A	51	53	c.2156C>T	c.(2155-2157)TCG>TTG	p.S719L
Pat_76	Pre-Treatment	FAM90A1	55138	37	12	8376706	8376706	Missense_Mutation	SNP	C	T	32	55	c.229G>A	c.(229-231)GAA>AAA	p.E77K
Pat_76	Pre-Treatment	PZP	5858	37	12	9311134	9311134	Missense_Mutation	SNP	C	T	33	30	c.3176G>A	c.(3175-3177)CGA>CAA	p.R1059Q
Pat_76	Pre-Treatment	TAS2R7	50837	37	12	10954661	10954661	Nonsense_Mutation	SNP	C	T	19	21	c.509G>A	c.(508-510)TGG>TAG	p.W170*
Pat_76	Pre-Treatment	PRB1	5542	37	12	11506789	11506789	Missense_Mutation	SNP	T	G	117	171	c.248A>C	c.(247-249)CAA>CCA	p.Q83P
Pat_76	Pre-Treatment	RPL13AP20	387841	37	12	13028826	13028826	Missense_Mutation	SNP	G	A	4	28	c.394G>A	c.(394-396)GCA>ACA	p.A132T
Pat_76	Pre-Treatment	GRIN2B	2904	37	12	13715992	13715992	Missense_Mutation	SNP	C	T	11	29	c.4180G>A	c.(4180-4182)GAC>AAC	p.D1394N
Pat_76	Pre-Treatment	GRIN2B	2904	37	12	13764762	13764762	Nonsense_Mutation	SNP	C	T	34	74	c.1677G>A	c.(1675-1677)TGG>TGA	p.W559*
Pat_76	Pre-Treatment	SLCO1A2	6579	37	12	21428352	21428352	Missense_Mutation	SNP	C	T	5	9	c.1617G>A	c.(1615-1617)ATG>ATA	p.M539I
Pat_76	Pre-Treatment	SLCO1A2	6579	37	12	21457408	21457408	Missense_Mutation	SNP	G	A	32	30	c.542C>T	c.(541-543)TCC>TTC	p.S181F
Pat_76	Pre-Treatment	OVCH1	341350	37	12	29644050	29644050	Missense_Mutation	SNP	C	T	27	55	c.530G>A	c.(529-531)GGA>GAA	p.G177E
Pat_76	Pre-Treatment	CAPRIN2	65981	37	12	30877346	30877346	Missense_Mutation	SNP	G	A	54	58	c.1945C>T	c.(1945-1947)CCA>TCA	p.P649S
Pat_76	Pre-Treatment	ADAMTS20	80070	37	12	43822049	43822049	Missense_Mutation	SNP	C	T	31	48	c.3940G>A	c.(3940-3942)GGA>AGA	p.G1314R
Pat_76	Pre-Treatment	DBX2	440097	37	12	45410133	45410134	Missense_Mutation	DNP	CC	TT	25	31	c.955_956GG>AA	c.(955-957)GGT>AAT	p.G319N
Pat_76	Pre-Treatment	SLC38A1	81539	37	12	46601362	46601362	Missense_Mutation	SNP	G	A	56	70	c.431C>T	c.(430-432)ACC>ATC	p.T144I
Pat_76	Pre-Treatment	FAM113B	91523	37	12	47628868	47628868	Missense_Mutation	SNP	G	A	12	40	c.22G>A	c.(22-24)GAA>AAA	p.E8K
Pat_76	Pre-Treatment	FAM113B	91523	37	12	47629243	47629243	Missense_Mutation	SNP	C	T	45	34	c.397C>T	c.(397-399)CCG>TCG	p.P133S
Pat_76	Pre-Treatment	FAM113B	91523	37	12	47629508	47629508	Missense_Mutation	SNP	C	T	3	29	c.662C>T	c.(661-663)GCG>GTG	p.A221V
Pat_76	Pre-Treatment	RPAP3	79657	37	12	48062776	48062776	Missense_Mutation	SNP	G	C	48	83	c.1636C>G	c.(1636-1638)CCT>GCT	p.P546A
Pat_76	Pre-Treatment	RAPGEF3	10411	37	12	48132959	48132959	Missense_Mutation	SNP	G	A	12	32	c.2302C>T	c.(2302-2304)CCT>TCT	p.P768S
Pat_76	Pre-Treatment	COL2A1	1280	37	12	48367222	48367222	Missense_Mutation	SNP	C	T	49	86	c.4432G>A	c.(4432-4434)GGT>AGT	p.G1478S
Pat_76	Pre-Treatment	ZNF641	121274	37	12	48736968	48736968	Missense_Mutation	SNP	G	A	28	28	c.1105C>T	c.(1105-1107)CCA>TCA	p.P369S
Pat_76	Pre-Treatment	ADCY6	112	37	12	49170953	49170953	Missense_Mutation	SNP	G	A	82	90	c.1310C>T	c.(1309-1311)CCG>CTG	p.P437L
Pat_76	Pre-Treatment	MLL2	8085	37	12	49420129	49420129	Missense_Mutation	SNP	G	A	8	19	c.15620C>T	c.(15619-15621)CCC>CTC	p.P5207L
Pat_76	Pre-Treatment	MLL2	8085	37	12	49420391	49420391	Missense_Mutation	SNP	G	A	4	146	c.15358C>T	c.(15358-15360)CGT>TGT	p.R5120C
Pat_76	Pre-Treatment	MLL2	8085	37	12	49438054	49438054	Missense_Mutation	SNP	G	A	17	31	c.5117C>T	c.(5116-5118)TCC>TTC	p.S1706F
Pat_76	Pre-Treatment	SPATS2	65244	37	12	49890769	49890769	Missense_Mutation	SNP	C	T	23	29	c.680C>T	c.(679-681)CCC>CTC	p.P227L
Pat_76	Pre-Treatment	CSRNP2	81566	37	12	51467709	51467709	Missense_Mutation	SNP	C	G	45	54	c.308G>C	c.(307-309)CGG>CCG	p.R103P
Pat_76	Pre-Treatment	SLC4A8	9498	37	12	51856194	51856194	Nonsense_Mutation	SNP	G	A	34	24	c.1202G>A	c.(1201-1203)TGG>TAG	p.W401*
Pat_76	Pre-Treatment	NR4A1	3164	37	12	52451204	52451204	Missense_Mutation	SNP	G	A	4	102	c.1430G>A	c.(1429-1431)CGT>CAT	p.R477H
Pat_76	Pre-Treatment	KRT84	3890	37	12	52774147	52774147	Missense_Mutation	SNP	C	T	4	61	c.1424G>A	c.(1423-1425)CGG>CAG	p.R475Q
Pat_76	Pre-Treatment	KRT6B	3854	37	12	52844360	52844360	Nonsense_Mutation	SNP	C	T	22	64	c.585G>A	c.(583-585)TGG>TGA	p.W195*
Pat_76	Pre-Treatment	KRT6B	3854	37	12	52845837	52845837	Missense_Mutation	SNP	C	G	10	4	c.26G>C	c.(25-27)AGG>ACG	p.R9T
Pat_76	Pre-Treatment	KRT78	196374	37	12	53239983	53239983	Missense_Mutation	SNP	C	T	14	13	c.754G>A	c.(754-756)GAA>AAA	p.E252K
Pat_76	Pre-Treatment	SOAT2	8435	37	12	53512193	53512193	Missense_Mutation	SNP	C	T	51	65	c.838C>T	c.(838-840)CTC>TTC	p.L280F
Pat_76	Pre-Treatment	NCKAP1L	3071	37	12	54930826	54930826	Missense_Mutation	SNP	G	A	24	49	c.3172G>A	c.(3172-3174)GAA>AAA	p.E1058K
Pat_76	Pre-Treatment	OR6C70	390327	37	12	55863739	55863739	Missense_Mutation	SNP	G	A	26	36	c.184C>T	c.(184-186)CGT>TGT	p.R62C
Pat_76	Pre-Treatment	DNAJC14	85406	37	12	56221745	56221745	Missense_Mutation	SNP	C	T	5	80	c.698G>A	c.(697-699)CGC>CAC	p.R233H
Pat_76	Pre-Treatment	STAT6	6778	37	12	57492287	57492287	Splice_Site	SNP	C	T	4	148	c.2159_splice	c.e19+1	p.E720_splice
Pat_76	Pre-Treatment	ARHGAP9	64333	37	12	57871402	57871402	Missense_Mutation	SNP	C	T	15	37	c.809G>A	c.(808-810)CGC>CAC	p.R270H
Pat_76	Pre-Treatment	DYRK2	8445	37	12	68050955	68050955	Missense_Mutation	SNP	G	C	66	57	c.268G>C	c.(268-270)GTT>CTT	p.V90L

Pat_76	Pre-Treatment	KCNMB4	27345	37	12	70794016	70794016	Missense_Mutation	SNP	G	A	34	60	c.364G>A	c.(364-366)GAA>AAA	p.E122K
Pat_76	Pre-Treatment	CAPS2	84698	37	12	75685579	75685579	Missense_Mutation	SNP	C	A	31	54	c.1242G>T	c.(1240-1242)GAG>GAT	p.E414D
Pat_76	Pre-Treatment	EPYC	1833	37	12	91358003	91358003	Missense_Mutation	SNP	G	A	30	68	c.899C>T	c.(898-900)CCT>CTT	p.P300L
Pat_76	Pre-Treatment	CLLU1OS	574016	37	12	92814859	92814859	Missense_Mutation	SNP	T	C	158	221	c.233A>G	c.(232-234)AAT>AGT	p.N78S
Pat_76	Pre-Treatment	ANKS1B	56899	37	12	100175830	100175830	Missense_Mutation	SNP	C	T	12	6	c.715G>A	c.(715-717)GTG>ATG	p.V239M
Pat_76	Pre-Treatment	UHRF1BP1L	23074	37	12	100444092	100444092	Missense_Mutation	SNP	G	A	16	27	c.3572C>T	c.(3571-3573)TCC>TTC	p.S1191F
Pat_76	Pre-Treatment	KIAA1033	23325	37	12	105546125	105546125	Missense_Mutation	SNP	C	T	26	29	c.2654C>T	c.(2653-2655)CCT>CTT	p.P885L
Pat_76	Pre-Treatment	PRDM4	11108	37	12	108134795	108134795	Missense_Mutation	SNP	G	A	49	68	c.1852C>T	c.(1852-1854)CAC>TAC	p.H618Y
Pat_76	Pre-Treatment	WSCD2	9671	37	12	108604011	108604011	Missense_Mutation	SNP	G	A	4	15	c.611G>A	c.(610-612)GGC>GAC	p.G204D
Pat_76	Pre-Treatment	TMEM119	338773	37	12	108985355	108985355	Missense_Mutation	SNP	G	A	33	38	c.805C>T	c.(805-807)CCC>TCC	p.P269S
Pat_76	Pre-Treatment	MYO1H	283446	37	12	109865367	109865367	Missense_Mutation	SNP	G	A	123	245	c.1877G>A	c.(1876-1878)AGG>AAG	p.R626K
Pat_76	Pre-Treatment	CCDC63	160762	37	12	111336846	111336846	Missense_Mutation	SNP	A	G	27	29	c.1259A>G	c.(1258-1260)AAG>AGG	p.K420R
Pat_76	Pre-Treatment	CUX2	23316	37	12	111749945	111749945	Missense_Mutation	SNP	G	A	20	16	c.1942G>A	c.(1942-1944)GAC>AAC	p.D648N
Pat_76	Pre-Treatment	C12orf51	283450	37	12	112690345	112690346	Missense_Mutation	DNP	GG	AA	23	37	.2168_2169CC>T	c.(2167-2169)TCC>TTT	p.S723F
Pat_76	Pre-Treatment	RPH3A	22895	37	12	113328699	113328699	Missense_Mutation	SNP	G	T	9	14	c.1666G>T	c.(1666-1668)GTC>TTC	p.V556F
Pat_76	Pre-Treatment	TPCN1	53373	37	12	113664698	113664699	Missense_Mutation	DNP	CC	TT	32	36	c.41_42CC>TT	c.(40-42)ACC>ATT	p.T14I
Pat_76	Pre-Treatment	NOS1	4842	37	12	117680432	117680432	Missense_Mutation	SNP	C	T	25	47	c.3041G>A	c.(3040-3042)AGT>AAT	p.S1014N
Pat_76	Pre-Treatment	NOS1	4842	37	12	117768373	117768373	Missense_Mutation	SNP	C	T	26	22	c.502G>A	c.(502-504)GAG>AAG	p.E168K
Pat_76	Pre-Treatment	PITPNM2	57605	37	12	123498444	123498444	Missense_Mutation	SNP	G	A	18	32	c.224C>T	c.(223-225)TCC>TTC	p.S75F
Pat_76	Pre-Treatment	SNRNP35	11066	37	12	123950688	123950688	Nonsense_Mutation	SNP	C	T	4	58	c.601C>T	c.(601-603)CGA>TGA	p.R201*
Pat_76	Pre-Treatment	TCTN2	79867	37	12	124172608	124172608	Nonsense_Mutation	SNP	C	T	72	85	c.775C>T	c.(775-777)CAG>TAG	p.Q259*
Pat_76	Pre-Treatment	DNAH10	196385	37	12	124354974	124354974	Nonsense_Mutation	SNP	G	A	26	13	c.7227G>A	c.(7225-7227)TGG>TGA	p.W2409*
Pat_76	Pre-Treatment	TMEM132D	121256	37	12	130015712	130015712	Missense_Mutation	SNP	C	T	18	26	c.1007G>A	c.(1006-1008)CGA>CAA	p.R336Q
Pat_76	Pre-Treatment	GPR133	283383	37	12	131593273	131593273	Missense_Mutation	SNP	C	T	73	157	c.1892C>T	c.(1891-1893)CCC>CTC	p.P631L
Pat_76	Pre-Treatment	TPTE2	93492	37	13	20025323	20025323	Nonsense_Mutation	SNP	G	A	19	48	c.784C>T	c.(784-786)CGA>TGA	p.R262*
Pat_76	Pre-Treatment	MPHOSPH8	54737	37	13	20221066	20221066	Missense_Mutation	SNP	G	A	5	238	c.853G>A	c.(853-855)GAC>AAC	p.D285N
Pat_76	Pre-Treatment	PARP4	143	37	13	25066708	25066708	Missense_Mutation	SNP	G	A	96	130	c.904C>T	c.(904-906)CTT>TTT	p.L302F
Pat_76	Pre-Treatment	RNF17	56163	37	13	25378548	25378548	Missense_Mutation	SNP	G	A	13	8	c.2072G>A	c.(2071-2073)GGA>GAA	p.G691E
Pat_76	Pre-Treatment	FAM123A	219287	37	13	25744499	25744499	Missense_Mutation	SNP	C	T	15	28	c.1259G>A	c.(1258-1260)GGA>GAA	p.G420E
Pat_76	Pre-Treatment	MTUS2	23281	37	13	29600115	29600115	Missense_Mutation	SNP	C	T	3	22	c.1310C>T	c.(1309-1311)TCC>TTC	p.S437F
Pat_76	Pre-Treatment	RXFP2	122042	37	13	32371390	32371390	Missense_Mutation	SNP	C	A	65	73	c.1839C>A	c.(1837-1839)TTC>TTA	p.F613L
Pat_76	Pre-Treatment	FRY	10129	37	13	32869444	32869444	Nonsense_Mutation	SNP	T	A	39	49	c.8889T>A	c.(8887-8889)TAT>TAA	p.Y2963*
Pat_76	Pre-Treatment	BRCA2	675	37	13	32910983	32910983	Missense_Mutation	SNP	G	A	4	51	c.2491G>A	c.(2491-2493)GTT>ATT	p.V831I
Pat_76	Pre-Treatment	FREM2	341640	37	13	39265494	39265494	Missense_Mutation	SNP	C	T	16	29	c.4013C>T	c.(4012-4014)TCT>TTT	p.S1338F
Pat_76	Pre-Treatment	KIAA0564	23078	37	13	42442530	42442531	Missense_Mutation	DNP	GG	CA	24	59	.1163_1164CC>T	c.(1162-1164)TCC>TTG	p.S388L
Pat_76	Pre-Treatment	SLC25A30	253512	37	13	45980108	45980108	Missense_Mutation	SNP	C	A	4	45	c.217G>T	c.(217-219)GCC>TCC	p.A73S
Pat_76	Pre-Treatment	CYSLTR2	57105	37	13	49281332	49281332	Missense_Mutation	SNP	T	C	74	88	c.379T>C	c.(379-381)TAT>CAT	p.Y127H
Pat_76	Pre-Treatment	ATP7B	540	37	13	52524208	52524209	Missense_Mutation	DNP	GG	AA	39	53	.2664_2665CC>T	662-2667)ACCCAC>ACT	p.H889Y
Pat_76	Pre-Treatment	OLFM4	10562	37	13	53624121	53624121	Missense_Mutation	SNP	G	A	54	53	c.748G>A	c.(748-750)GGT>AGT	p.G250S
Pat_76	Pre-Treatment	DACH1	1602	37	13	72133952	72133952	Missense_Mutation	SNP	G	A	17	28	c.1435C>T	c.(1435-1437)CCG>TCG	p.P479S
Pat_76	Pre-Treatment	DIS3	22894	37	13	73340162	73340162	Missense_Mutation	SNP	G	A	18	27	c.1918C>T	c.(1918-1920)CAC>TAC	p.H640Y
Pat_76	Pre-Treatment	SLITRK1	114798	37	13	84454754	84454754	Missense_Mutation	SNP	C	T	10	17	c.889G>A	c.(889-891)GAT>AAT	p.D297N
Pat_76	Pre-Treatment	SLITRK6	84189	37	13	86368213	86368213	Missense_Mutation	SNP	C	T	26	46	c.2431G>A	c.(2431-2433)GTA>ATA	p.V811I
Pat_76	Pre-Treatment	SLITRK5	26050	37	13	88329952	88329952	Missense_Mutation	SNP	G	A	44	94	c.2309G>A	c.(2308-2310)GGC>GAC	p.G770D
Pat_76	Pre-Treatment	GPC5	2262	37	13	92345753	92345753	Missense_Mutation	SNP	G	A	14	22	c.638G>A	c.(637-639)GGA>GAA	p.G213E
Pat_76	Pre-Treatment	ABCC4	10257	37	13	95830266	95830266	Missense_Mutation	SNP	C	T	56	88	c.1625G>A	c.(1624-1626)CGG>CAG	p.R542Q
Pat_76	Pre-Treatment	PCCA	5095	37	13	100953723	100953723	Missense_Mutation	SNP	C	T	45	57	c.1075C>T	c.(1075-1077)CCT>TCT	p.P359S

Pat_76	Pre-Treatment	COL4A1	1282	37	13	110826832	110826832	Missense_Mutation	SNP	G	A	23	27	c.3367C>T	c.(3367-3369)CCA>TCA	p.P1123S
Pat_76	Pre-Treatment	COL4A2	1284	37	13	111154075	111154075	Missense_Mutation	SNP	C	T	15	27	c.3821C>T	c.(3820-3822)TCC>TTC	p.S1274F
Pat_76	Pre-Treatment	ARHGEF7	8874	37	13	111944497	111944497	Missense_Mutation	SNP	G	A	4	61	c.2230G>A	c.(2230-2232)GTC>ATC	p.V744I
Pat_76	Pre-Treatment	PROZ	8858	37	13	113825991	113825991	Missense_Mutation	SNP	G	A	41	65	c.775G>A	c.(775-777)GAG>AAG	p.E259K
Pat_76	Pre-Treatment	TMCO3	55002	37	13	114203801	114203801	Missense_Mutation	SNP	G	A	18	49	c.1982G>A	c.(1981-1983)AGA>AAA	p.R661K
Pat_76	Pre-Treatment	GAS6	2621	37	13	114541134	114541134	Missense_Mutation	SNP	C	T	4	107	c.497G>A	c.(496-498)GGC>GAC	p.G166D
Pat_76	Pre-Treatment	OR4K5	79317	37	14	20389108	20389108	Missense_Mutation	SNP	C	G	50	137	c.343C>G	c.(343-345)CTT>GTT	p.L115V
Pat_76	Pre-Treatment	OR4K1	79544	37	14	20404475	20404475	Missense_Mutation	SNP	C	T	11	38	c.650C>T	c.(649-651)TCC>TTC	p.S217F
Pat_76	Pre-Treatment	HNRNPC	3183	37	14	21679680	21679680	Missense_Mutation	SNP	G	A	22	36	c.722C>T	c.(721-723)TCC>TTC	p.S241F
Pat_76	Pre-Treatment	OR10G3	26533	37	14	22038638	22038638	Missense_Mutation	SNP	G	A	11	26	c.238C>T	c.(238-240)CCT>TCT	p.P80S
Pat_76	Pre-Treatment	MMP14	4323	37	14	23313059	23313059	Missense_Mutation	SNP	G	A	56	75	c.991G>A	c.(991-993)GGG>AGG	p.G331R
Pat_76	Pre-Treatment	JPH4	84502	37	14	24040266	24040267	Missense_Mutation	DNP	GG	AA	19	28	.1673_1674CC>T	c.(1672-1674)GCC>GTT	p.A558V
Pat_76	Pre-Treatment	FITM1	161247	37	14	24601613	24601613	Missense_Mutation	SNP	G	A	32	26	c.460G>A	c.(460-462)GAG>AAG	p.E154K
Pat_76	Pre-Treatment	RNF31	55072	37	14	24620080	24620080	Missense_Mutation	SNP	C	A	4	101	c.1471C>A	c.(1471-1473)CTA>ATA	p.L491I
Pat_76	Pre-Treatment	GZMH	2999	37	14	25076419	25076419	Missense_Mutation	SNP	C	T	5	315	c.533G>A	c.(532-534)GGC>GAC	p.G178D
Pat_76	Pre-Treatment	GZMB	3002	37	14	25100338	25100338	Missense_Mutation	SNP	C	T	51	95	c.683G>A	c.(682-684)CGA>CAA	p.R228Q
Pat_76	Pre-Treatment	COCH	1690	37	14	31355240	31355240	Missense_Mutation	SNP	C	T	4	70	c.1199C>T	c.(1198-1200)TCG>TTG	p.S400L
Pat_76	Pre-Treatment	ARHGAP5	394	37	14	32621634	32621634	Missense_Mutation	SNP	C	T	15	51	c.4081C>T	c.(4081-4083)CCG>TCG	p.P1361S
Pat_76	Pre-Treatment	AKAP6	9472	37	14	33291332	33291332	Missense_Mutation	SNP	G	A	10	21	c.4313G>A	c.(4312-4314)GGA>GAA	p.G1438E
Pat_76	Pre-Treatment	RALGAPA1	253959	37	14	36041828	36041828	Missense_Mutation	SNP	G	A	14	24	c.5788C>T	c.(5788-5790)CTT>TTT	p.L1930F
Pat_76	Pre-Treatment	LRFN5	145581	37	14	42368131	42368131	Missense_Mutation	SNP	A	C	61	73	c.2110A>C	c.(2110-2112)ACT>CCT	p.T704P
Pat_76	Pre-Treatment	FAM179B	23116	37	14	45481251	45481251	Missense_Mutation	SNP	C	T	31	37	c.3211C>T	c.(3211-3213)CAT>TAT	p.H1071Y
Pat_76	Pre-Treatment	RPL10L	140801	37	14	47120861	47120861	Missense_Mutation	SNP	G	A	63	95	c.79C>T	c.(79-81)CCT>TCT	p.P27S
Pat_76	Pre-Treatment	PYGL	5836	37	14	51378987	51378987	Missense_Mutation	SNP	G	A	6	321	c.1655C>T	c.(1654-1656)ACG>ATG	p.T552M
Pat_76	Pre-Treatment	PTGER2	5732	37	14	52793975	52793975	Missense_Mutation	SNP	G	A	6	22	c.880G>A	c.(880-882)GAA>AAA	p.E294K
Pat_76	Pre-Treatment	EXOC5	10640	37	14	57676775	57676775	Missense_Mutation	SNP	A	T	6	6	c.1618T>A	c.(1618-1620)TTA>ATA	p.L540I
Pat_76	Pre-Treatment	RTN1	6252	37	14	60212705	60212705	Missense_Mutation	SNP	C	T	67	93	c.736G>A	c.(736-738)GAG>AAG	p.E246K
Pat_76	Pre-Treatment	KCNH5	27133	37	14	63175092	63175092	Missense_Mutation	SNP	G	A	61	86	c.2101C>T	c.(2101-2103)CCC>TCC	p.P701S
Pat_76	Pre-Treatment	KCNH5	27133	37	14	63468171	63468171	Missense_Mutation	SNP	G	A	16	39	c.311C>T	c.(310-312)CCT>CTT	p.P104L
Pat_76	Pre-Treatment	SYNE2	23224	37	14	64469684	64469684	Missense_Mutation	SNP	C	T	26	38	c.4033C>T	c.(4033-4035)CTT>TTT	p.L1345F
Pat_76	Pre-Treatment	SYNE2	23224	37	14	64691206	64691206	Missense_Mutation	SNP	G	A	6	223	c.20341G>A	.(20341-20343)GAC>AAC	p.D6781N
Pat_76	Pre-Treatment	MTHFD1	4522	37	14	64892903	64892903	Missense_Mutation	SNP	G	A	5	117	c.1120G>A	c.(1120-1122)GTG>ATG	p.V374M
Pat_76	Pre-Treatment	ZBTB25	7597	37	14	64954009	64954009	Missense_Mutation	SNP	G	A	57	73	c.940C>T	c.(940-942)CGG>TGG	p.R314W
Pat_76	Pre-Treatment	SPTB	6710	37	14	65253757	65253757	Missense_Mutation	SNP	C	T	11	27	c.2926G>A	c.(2926-2928)GTA>ATA	p.V976I
Pat_76	Pre-Treatment	ZFYVE26	23503	37	14	68234443	68234443	Missense_Mutation	SNP	C	T	5	161	c.5768G>A	c.(5767-5769)CGG>CAG	p.R1923Q
Pat_76	Pre-Treatment	SLC8A3	6547	37	14	70633384	70633384	Missense_Mutation	SNP	C	T	16	46	c.1756G>A	c.(1756-1758)GAG>AAG	p.E586K
Pat_76	Pre-Treatment	SYNJ2BP	55333	37	14	70855188	70855188	Missense_Mutation	SNP	G	A	12	20	c.200C>T	c.(199-201)TCG>TTG	p.S67L
Pat_76	Pre-Treatment	PSEN1	5663	37	14	73685912	73685912	Missense_Mutation	SNP	C	T	69	87	c.1319C>T	c.(1318-1320)ACC>ATC	p.T440I
Pat_76	Pre-Treatment	LTBP2	4053	37	14	74970727	74970727	Missense_Mutation	SNP	C	T	9	17	c.4484G>A	c.(4483-4485)GGT>GAT	p.G1495D
Pat_76	Pre-Treatment	YLPM1	56252	37	14	75264383	75264383	Missense_Mutation	SNP	C	T	9	11	c.2383C>T	c.(2383-2385)CCC>TCC	p.P795S
Pat_76	Pre-Treatment	ESRRB	2103	37	14	76905817	76905817	Missense_Mutation	SNP	G	A	3	22	c.121G>A	c.(121-123)GCC>ACC	p.A41T
Pat_76	Pre-Treatment	ISM2	145501	37	14	77948827	77948827	Missense_Mutation	SNP	C	T	13	16	c.811G>A	c.(811-813)GAA>AAA	p.E271K
Pat_76	Pre-Treatment	FLRT2	23768	37	14	86089260	86089260	Missense_Mutation	SNP	G	A	36	69	c.1402G>A	c.(1402-1404)GAG>AAG	p.E468K
Pat_76	Pre-Treatment	EML5	161436	37	14	89082505	89082505	Missense_Mutation	SNP	C	A	6	226	c.5878G>T	c.(5878-5880)GCT>TCT	p.A1960S
Pat_76	Pre-Treatment	CCDC88C	440193	37	14	91773417	91773417	Nonsense_Mutation	SNP	G	A	3	7	c.3160C>T	c.(3160-3162)CGA>TGA	p.R1054*
Pat_76	Pre-Treatment	CCDC88C	440193	37	14	91791263	91791263	Missense_Mutation	SNP	C	A	4	59	c.1202G>T	c.(1201-1203)CGG>CTG	p.R401L
Pat_76	Pre-Treatment	FBLN5	10516	37	14	92343937	92343937	Missense_Mutation	SNP	G	A	22	80	c.1079C>T	c.(1078-1080)TCC>TTC	p.S360F

Pat_76	Pre-Treatment	GOLGA5	9950	37	14	93303772	93303772	Missense_Mutation	SNP	G	A	5	323	c.2093G>A	c.(2092-2094)CGA>CAA	p.R698Q
Pat_76	Pre-Treatment	BTBD7	55727	37	14	93709119	93709119	Missense_Mutation	SNP	G	A	28	52	c.2899C>T	c.(2899-2901)CCT>TCT	p.P967S
Pat_76	Pre-Treatment	KIAA1409	57578	37	14	94158197	94158197	Nonsense_Mutation	SNP	C	T	24	57	c.7027C>T	c.(7027-7029)CAG>TAG	p.Q2343*
Pat_76	Pre-Treatment	DDX24	57062	37	14	94545446	94545446	Missense_Mutation	SNP	G	A	4	154	c.643C>T	c.(643-645)CCC>TCC	p.P215S
Pat_76	Pre-Treatment	SERPINA1	5265	37	14	94844814	94844814	Missense_Mutation	SNP	C	T	28	56	c.1229G>A	c.(1228-1230)GGA>GAA	p.G410E
Pat_76	Pre-Treatment	SERPINA9	327657	37	14	94933701	94933701	Missense_Mutation	SNP	A	C	23	43	c.701T>G	c.(700-702)TTT>TGT	p.F234C
Pat_76	Pre-Treatment	SERPINA3	12	37	14	95088794	95088794	Missense_Mutation	SNP	G	A	16	20	c.1034G>A	c.(1033-1035)GGG>GAG	p.G345E
Pat_76	Pre-Treatment	SERPINA13	388007	37	14	95108179	95108179	Nonsense_Mutation	SNP	G	A	61	104	c.696G>A	c.(694-696)TGG>TGA	p.W232*
Pat_76	Pre-Treatment	DICER1	23405	37	14	95562323	95562323	Missense_Mutation	SNP	G	A	69	110	c.4934C>T	c.(4933-4935)CCA>CTA	p.P1645L
Pat_76	Pre-Treatment	BDKRB2	624	37	14	96707210	96707210	Nonsense_Mutation	SNP	G	A	12	28	c.545G>A	c.(544-546)TGG>TAG	p.W182*
Pat_76	Pre-Treatment	PAPOLA	10914	37	14	97002295	97002295	Missense_Mutation	SNP	C	T	30	42	c.989C>T	c.(988-990)TCC>TTC	p.S330F
Pat_76	Pre-Treatment	SLC25A29	123096	37	14	100759668	100759668	Missense_Mutation	SNP	G	A	4	79	c.125C>T	c.(124-126)ACG>ATG	p.T42M
Pat_76	Pre-Treatment	DYNC1H1	1778	37	14	102482801	102482801	Missense_Mutation	SNP	C	T	4	152	c.7589C>T	c.(7588-7590)CCC>CTC	p.P2530L
Pat_76	Pre-Treatment	CDC42BPB	9578	37	14	103440469	103440469	Nonsense_Mutation	SNP	G	A	19	23	c.1525C>T	c.(1525-1527)CGA>TGA	p.R509*
Pat_76	Pre-Treatment	KIF26A	26153	37	14	104641939	104641940	Missense_Mutation	DNP	GG	AA	8	17	.2814_2815GG>A	812-2817)AAGGCT>AAA	p.A939T
Pat_76	Pre-Treatment	PLD4	122618	37	14	105398187	105398187	Missense_Mutation	SNP	G	A	3	11	c.1021G>A	c.(1021-1023)GAG>AAG	p.E341K
Pat_76	Pre-Treatment	ADAM6	8755	37	14	106350754	106350754	Splice_Site	SNP	G	A	16	30	c.49979_splice	c.e3164-1	
Pat_76	Pre-Treatment	TUBGCP5	114791	37	15	22846940	22846940	Missense_Mutation	SNP	G	A	4	63	c.815G>A	c.(814-816)CGG>CAG	p.R272Q
Pat_76	Pre-Treatment	NIPA1	123606	37	15	23052675	23052675	Missense_Mutation	SNP	G	A	51	129	c.398C>T	c.(397-399)TCC>TTC	p.S133F
Pat_76	Pre-Treatment	C15orf2	23742	37	15	24922816	24922816	Missense_Mutation	SNP	C	A	36	61	c.1802C>A	c.(1801-1803)CCA>CAA	p.P601Q
Pat_76	Pre-Treatment	NDNL2	56160	37	15	29561539	29561539	Missense_Mutation	SNP	G	A	58	166	c.371C>T	c.(370-372)CCC>CTC	p.P124L
Pat_76	Pre-Treatment	TJP1	7082	37	15	30011099	30011099	Missense_Mutation	SNP	G	A	86	57	c.3247C>T	c.(3247-3249)CGC>TGC	p.R1083C
Pat_76	Pre-Treatment	TJP1	7082	37	15	30024841	30024841	Nonsense_Mutation	SNP	G	A	5	168	c.1915C>T	c.(1915-1917)CGA>TGA	p.R639*
Pat_76	Pre-Treatment	CHRFAM7A	89832	37	15	30659708	30659708	Missense_Mutation	SNP	C	T	38	104	c.633G>A	c.(631-633)ATG>ATA	p.M211I
Pat_76	Pre-Treatment	CHRNA7	1139	37	15	32460295	32460295	Missense_Mutation	SNP	G	A	3	23	c.1145G>A	c.(1144-1146)GGG>GAG	p.G382E
Pat_76	Pre-Treatment	CHRM5	1133	37	15	34355031	34355031	Missense_Mutation	SNP	C	T	6	135	c.113C>T	c.(112-114)GCT>GTT	p.A38V
Pat_76	Pre-Treatment	AQR	9716	37	15	35166887	35166887	Missense_Mutation	SNP	G	C	34	110	c.3416C>G	c.(3415-3417)GCC>GGC	p.A1139G
Pat_76	Pre-Treatment	THBS1	7057	37	15	39886338	39886338	Nonsense_Mutation	SNP	G	A	26	21	c.3306G>A	c.(3304-3306)TGG>TGA	p.W1102*
Pat_76	Pre-Treatment	BAHD1	22893	37	15	40754233	40754233	Missense_Mutation	SNP	C	T	19	75	c.1555C>T	c.(1555-1557)CCC>TCC	p.P519S
Pat_76	Pre-Treatment	BAHD1	22893	37	15	40756138	40756138	Missense_Mutation	SNP	G	A	4	133	c.1894G>A	c.(1894-1896)GTC>ATC	p.V632I
Pat_76	Pre-Treatment	RPUSD2	27079	37	15	40866242	40866242	Missense_Mutation	SNP	G	A	71	45	c.1420G>A	c.(1420-1422)GAG>AAG	p.E474K
Pat_76	Pre-Treatment	INO80	54617	37	15	41313319	41313319	Missense_Mutation	SNP	G	A	4	126	c.3053C>T	c.(3052-3054)ACC>ATC	p.T1018I
Pat_76	Pre-Treatment	MAPKBP1	23005	37	15	42105883	42105883	Missense_Mutation	SNP	C	T	98	222	c.902C>T	c.(901-903)ACC>ATC	p.T301I
Pat_76	Pre-Treatment	SPTBN5	51332	37	15	42185575	42185575	Missense_Mutation	SNP	C	T	22	26	c.16G>A	c.(16-18)GAG>AAG	p.E6K
Pat_76	Pre-Treatment	PLA2G4D	283748	37	15	42363971	42363971	Splice_Site	SNP	C	T	66	61	c.1573_splice	c.e15+1	p.A525_splice
Pat_76	Pre-Treatment	ZFP106	64397	37	15	42743482	42743482	Missense_Mutation	SNP	G	A	32	66	c.919C>T	c.(919-921)CCT>TCT	p.P307S
Pat_76	Pre-Treatment	ZFP106	64397	37	15	42743832	42743832	Missense_Mutation	SNP	C	T	88	65	c.569G>A	c.(568-570)GGA>GAA	p.G190E
Pat_76	Pre-Treatment	TTBK2	146057	37	15	43086989	43086989	Missense_Mutation	SNP	G	A	14	7	c.833C>T	c.(832-834)TCC>TTC	p.S278F
Pat_76	Pre-Treatment	TP53BP1	7158	37	15	43748861	43748861	Nonsense_Mutation	SNP	G	A	33	113	c.1930C>T	c.(1930-1932)CAG>TAG	p.Q644*
Pat_76	Pre-Treatment	DUOX1	53905	37	15	45433506	45433506	Missense_Mutation	SNP	G	A	71	51	c.1582G>A	c.(1582-1584)GAG>AAG	p.E528K
Pat_76	Pre-Treatment	SLC28A2	9153	37	15	45545694	45545694	Missense_Mutation	SNP	G	A	21	64	c.146G>A	c.(145-147)GGA>GAA	p.G49E
Pat_76	Pre-Treatment	WDR72	256764	37	15	53908113	53908113	Missense_Mutation	SNP	C	T	27	53	c.2290G>A	c.(2290-2292)GAT>AAT	p.D764N
Pat_76	Pre-Treatment	UNC13C	440279	37	15	54556584	54556584	Missense_Mutation	SNP	A	C	6	19	c.3667A>C	c.(3667-3669)ACC>CCC	p.T1223P
Pat_76	Pre-Treatment	UNC13C	440279	37	15	54919174	54919174	Missense_Mutation	SNP	C	T	32	60	c.6508C>T	c.(6508-6510)CCT>TCT	p.P2170S
Pat_76	Pre-Treatment	MYO1E	4643	37	15	59519723	59519724	Missense_Mutation	DNP	GG	AA	61	51	c.576_577CC>TT	(574-579)TTCCTT>TTTTT	p.L193F
Pat_76	Pre-Treatment	VPS13C	54832	37	15	62160931	62160932	Missense_Mutation	DNP	GG	AA	14	61	10789_10790CC>	c.(10789-10791)CCT>TTT	p.P3597F
Pat_76	Pre-Treatment	USP3	9960	37	15	63796976	63796976	Missense_Mutation	SNP	C	T	4	71	c.38C>T	c.(37-39)GCT>GTT	p.A13V

Pat_76	Pre-Treatment	HERC1	8925	37	15	63984706	63984706	Missense_Mutation	SNP	G	A	9	16	c.5734C>T	c.(5734-5736)CGC>TGC	p.R1912C
Pat_76	Pre-Treatment	ZNF609	23060	37	15	64972957	64972957	Missense_Mutation	SNP	G	A	6	290	c.4058G>A	c.(4057-4059)CGG>CAG	p.R1353Q
Pat_76	Pre-Treatment	CLPX	10845	37	15	65448131	65448132	Missense_Mutation	DNP	GG	AA	56	153	.1209_1210CC>T	207-1212)CTCCGT>CTTT	p.R404C
Pat_76	Pre-Treatment	CILP	8483	37	15	65490345	65490345	Missense_Mutation	SNP	C	T	5	210	c.2279G>A	c.(2278-2280)CGG>CAG	p.R760Q
Pat_76	Pre-Treatment	CILP	8483	37	15	65490642	65490642	Missense_Mutation	SNP	G	A	29	68	c.1982C>T	c.(1981-1983)TCT>TTT	p.S661F
Pat_76	Pre-Treatment	DENND4A	10260	37	15	65983030	65983030	Missense_Mutation	SNP	G	A	15	77	c.3770C>T	c.(3769-3771)CCT>CTT	p.P1257L
Pat_76	Pre-Treatment	MEGF11	84465	37	15	66250017	66250018	Nonsense_Mutation	DNP	CC	TT	37	32	.1154_1155GG>A	c.(1153-1155)TGG>TAA	p.W385*
Pat_76	Pre-Treatment	MAP2K5	5607	37	15	67995693	67995693	Missense_Mutation	SNP	G	A	29	68	c.991G>A	c.(991-993)GAG>AAG	p.E331K
Pat_76	Pre-Treatment	SPESP1	246777	37	15	69238085	69238085	Missense_Mutation	SNP	G	A	29	84	c.212G>A	c.(211-213)GGA>GAA	p.G71E
Pat_76	Pre-Treatment	NOX5	79400	37	15	69347817	69347817	Missense_Mutation	SNP	C	T	4	95	c.2143C>T	c.(2143-2145)CCT>TCT	p.P715S
Pat_76	Pre-Treatment	LRRC49	54839	37	15	71197052	71197052	Missense_Mutation	SNP	C	T	118	237	c.458C>T	c.(457-459)TCG>TTG	p.S153L
Pat_76	Pre-Treatment	ISL2	64843	37	15	76630250	76630250	Missense_Mutation	SNP	G	A	4	153	c.190G>A	c.(190-192)GAG>AAG	p.E64K
Pat_76	Pre-Treatment	TSPAN3	10099	37	15	77348512	77348512	Missense_Mutation	SNP	G	A	4	160	c.149C>T	c.(148-150)ACG>ATG	p.T50M
Pat_76	Pre-Treatment	ACSBG1	23205	37	15	78474348	78474348	Missense_Mutation	SNP	C	T	58	39	c.1034G>A	c.(1033-1035)GGG>GAG	p.G345E
Pat_76	Pre-Treatment	FAH	2184	37	15	80460459	80460459	Missense_Mutation	SNP	G	A	4	70	c.521G>A	c.(520-522)CGA>CAA	p.R174Q
Pat_76	Pre-Treatment	KIAA1199	57214	37	15	81199043	81199043	Missense_Mutation	SNP	G	A	89	74	c.1451G>A	c.(1450-1452)GGC>GAC	p.G484D
Pat_76	Pre-Treatment	C15orf40	123207	37	15	83677352	83677352	Missense_Mutation	SNP	C	T	82	59	c.314G>A	c.(313-315)CGG>CAG	p.R105Q
Pat_76	Pre-Treatment	SLC28A1	9154	37	15	85447408	85447408	Missense_Mutation	SNP	C	T	98	60	c.542C>T	c.(541-543)TCC>TTC	p.S181F
Pat_76	Pre-Treatment	AKAP13	11214	37	15	86122597	86122597	Missense_Mutation	SNP	C	T	41	25	c.1298C>T	c.(1297-1299)CCC>CTC	p.P433L
Pat_76	Pre-Treatment	AKAP13	11214	37	15	86125080	86125080	Missense_Mutation	SNP	G	A	15	44	c.3781G>A	c.(3781-3783)GAA>AAA	p.E1261K
Pat_76	Pre-Treatment	KLHL25	64410	37	15	86311780	86311780	Missense_Mutation	SNP	G	A	40	26	c.1262C>T	c.(1261-1263)GCC>GTC	p.A421V
Pat_76	Pre-Treatment	NTRK3	4916	37	15	88420209	88420209	Missense_Mutation	SNP	G	A	4	103	c.2477C>T	c.(2476-2478)GCT>GTT	p.A826V
Pat_76	Pre-Treatment	DET1	55070	37	15	89073951	89073951	Missense_Mutation	SNP	A	T	5	14	c.986T>A	c.(985-987)CTG>CAG	p.L329Q
Pat_76	Pre-Treatment	C15orf58	390637	37	15	90784313	90784313	Missense_Mutation	SNP	C	T	166	100	c.173C>T	c.(172-174)CCC>CTC	p.P58L
Pat_76	Pre-Treatment	ST8SIA2	8128	37	15	92988160	92988160	Splice_Site	SNP	G	A	48	125	c.842_splice	c.e5+1	p.G281_splice
Pat_76	Pre-Treatment	FAM174B	400451	37	15	93173525	93173525	Missense_Mutation	SNP	G	A	15	27	c.395C>T	c.(394-396)CCA>CTA	p.P132L
Pat_76	Pre-Treatment	SPATA8	145946	37	15	97328244	97328244	Missense_Mutation	SNP	G	A	183	164	c.215G>A	c.(214-216)GGA>GAA	p.G72E
Pat_76	Pre-Treatment	ADAMTS17	170691	37	15	100594150	100594150	Nonsense_Mutation	SNP	C	T	195	353	c.2247G>A	c.(2245-2247)TGG>TGA	p.W749*
Pat_76	Pre-Treatment	LINS1	55180	37	15	101120947	101120947	Missense_Mutation	SNP	G	A	36	34	c.101C>T	c.(100-102)CCA>CTA	p.P34L
Pat_76	Pre-Treatment	PDIA2	64714	37	16	333275	333275	Missense_Mutation	SNP	G	A	5	10	c.106G>A	c.(106-108)GAG>AAG	p.E36K
Pat_76	Pre-Treatment	TMEM8A	58986	37	16	427448	427448	Missense_Mutation	SNP	G	A	14	26	c.437C>T	c.(436-438)TCC>TTC	p.S146F
Pat_76	Pre-Treatment	WDR24	84219	37	16	737222	737222	Missense_Mutation	SNP	C	T	4	111	c.854G>A	c.(853-855)CGG>CAG	p.R285Q
Pat_76	Pre-Treatment	BAIAP3	8938	37	16	1391412	1391412	Missense_Mutation	SNP	C	T	56	82	c.758C>T	c.(757-759)CCC>CTC	p.P253L
Pat_76	Pre-Treatment	HS3ST6	64711	37	16	1961872	1961873	Missense_Mutation	DNP	CC	TT	47	49	c.654_655GG>AA	52-657)GGGGAG>GGAA	p.E219K
Pat_76	Pre-Treatment	PKD1	5310	37	16	2159592	2159592	Missense_Mutation	SNP	G	A	3	17	c.5576C>T	c.(5575-5577)GCT>GTT	p.A1859V
Pat_76	Pre-Treatment	SRRM2	23524	37	16	2809662	2809662	Missense_Mutation	SNP	G	A	4	129	c.833G>A	c.(832-834)CGG>CAG	p.R278Q
Pat_76	Pre-Treatment	SRRM2	23524	37	16	2815330	2815330	Missense_Mutation	SNP	T	C	3	119	c.4801T>C	c.(4801-4803)TCC>CCC	p.S1601P
Pat_76	Pre-Treatment	PRSS22	64063	37	16	2903913	2903913	Missense_Mutation	SNP	C	T	28	44	c.670G>A	c.(670-672)GAC>AAC	p.D224N
Pat_76	Pre-Treatment	CLDN6	9074	37	16	3065689	3065689	Missense_Mutation	SNP	C	T	29	25	c.334G>A	c.(334-336)GAT>AAT	p.D112N
Pat_76	Pre-Treatment	ZSCAN10	84891	37	16	3139460	3139460	Missense_Mutation	SNP	C	T	10	23	c.1810G>A	c.(1810-1812)GAG>AAG	p.E604K
Pat_76	Pre-Treatment	MEFV	4210	37	16	3293401	3293401	Missense_Mutation	SNP	C	T	14	45	c.2086G>A	c.(2086-2088)GAA>AAA	p.E696K
Pat_76	Pre-Treatment	NLRC3	197358	37	16	3607625	3607625	Missense_Mutation	SNP	G	A	15	9	c.2068C>T	c.(2068-2070)CTC>TTC	p.L690F
Pat_76	Pre-Treatment	CREBBP	1387	37	16	3823918	3823919	Missense_Mutation	DNP	GG	AA	27	64	.2296_2297CC>T	c.(2296-2298)CCT>TTT	p.P766F
Pat_76	Pre-Treatment	12-Sep	124404	37	16	4829778	4829778	Missense_Mutation	SNP	G	A	38	42	c.736C>T	c.(736-738)CCT>TCT	p.P246S
Pat_76	Pre-Treatment	PPL	5493	37	16	4934443	4934443	Missense_Mutation	SNP	C	T	4	7	c.4213G>A	c.(4213-4215)GAG>AAG	p.E1405K
Pat_76	Pre-Treatment	PMM2	5373	37	16	8906922	8906922	Missense_Mutation	SNP	G	A	5	238	c.598G>A	c.(598-600)GGT>AGT	p.G200S
Pat_76	Pre-Treatment	GRIN2A	2903	37	16	9858255	9858255	Missense_Mutation	SNP	G	A	39	83	c.3146C>T	c.(3145-3147)CCT>CTT	p.P1049L

Pat_76	Pre-Treatment	GRIN2A	2903	37	16	9923297	9923297	Missense_Mutation	SNP	C	T	37	34	c.1990G>A	c.(1990-1992)GGC>AGC	p.G664S
Pat_76	Pre-Treatment	TNFRSF17	608	37	16	12061606	12061606	Missense_Mutation	SNP	G	A	5	67	c.457G>A	c.(457-459)GCA>ACA	p.A153T
Pat_76	Pre-Treatment	ERCC4	2072	37	16	14029042	14029042	Missense_Mutation	SNP	C	T	45	95	c.1253C>T	c.(1252-1254)TCC>TTC	p.S418F
Pat_76	Pre-Treatment	PDXDC1	23042	37	16	15128324	15128324	Missense_Mutation	SNP	G	A	4	158	c.1916G>A	c.(1915-1917)CGG>CAG	p.R639Q
Pat_76	Pre-Treatment	MYH11	4629	37	16	15813531	15813531	Missense_Mutation	SNP	G	A	4	116	c.4993C>T	c.(4993-4995)CGT>TGT	p.R1665C
Pat_76	Pre-Treatment	C16orf88	400506	37	16	19718383	19718383	Missense_Mutation	SNP	G	A	26	37	c.1226C>T	c.(1225-1227)GCT>GTT	p.A409V
Pat_76	Pre-Treatment	PDILT	204474	37	16	20384348	20384348	Missense_Mutation	SNP	C	T	80	106	c.778G>A	c.(778-780)GAA>AAA	p.E260K
Pat_76	Pre-Treatment	ACSM2B	348158	37	16	20570640	20570641	Missense_Mutation	DNP	GG	CA	10	18	c.306_307CC>TG	304-309)GGCCTG>GGTG	p.L103V
Pat_76	Pre-Treatment	ACSM2B	348158	37	16	20576154	20576154	Missense_Mutation	SNP	C	T	16	35	c.14G>A	c.(13-15)CGA>CAA	p.R5Q
Pat_76	Pre-Treatment	ACSM1	116285	37	16	20648710	20648710	Missense_Mutation	SNP	G	A	27	52	c.1180C>T	c.(1180-1182)CCA>TCA	p.P394S
Pat_76	Pre-Treatment	ACSM1	116285	37	16	20696554	20696554	Missense_Mutation	SNP	G	A	29	72	c.364C>T	c.(364-366)CCT>TCT	p.P122S
Pat_76	Pre-Treatment	DNAH3	55567	37	16	20944667	20944667	Missense_Mutation	SNP	C	A	4	125	c.12160G>T	.(12160-12162)GGG>TG	p.G4054W
Pat_76	Pre-Treatment	OTOA	146183	37	16	21696638	21696638	Missense_Mutation	SNP	C	T	16	18	c.355C>T	c.(355-357)CGC>TGC	p.R119C
Pat_76	Pre-Treatment	VWA3A	146177	37	16	22166979	22166979	Missense_Mutation	SNP	C	T	24	48	c.3497C>T	c.(3496-3498)TCC>TTC	p.S1166F
Pat_76	Pre-Treatment	EEF2K	29904	37	16	22268602	22268602	Missense_Mutation	SNP	C	T	51	66	c.797C>T	c.(796-798)TCC>TTC	p.S266F
Pat_76	Pre-Treatment	RBBP6	5930	37	16	24567014	24567014	Missense_Mutation	SNP	G	A	4	106	c.427G>A	c.(427-429)GAC>AAC	p.D143N
Pat_76	Pre-Treatment	RBBP6	5930	37	16	24578597	24578597	Missense_Mutation	SNP	C	T	83	109	c.1723C>T	c.(1723-1725)CCT>TCT	p.P575S
Pat_76	Pre-Treatment	IL4R	3566	37	16	27363946	27363946	Missense_Mutation	SNP	G	A	5	204	c.599G>A	c.(598-600)CGG>CAG	p.R200Q
Pat_76	Pre-Treatment	XPO6	23214	37	16	28167780	28167780	Missense_Mutation	SNP	G	A	57	104	c.712C>T	c.(712-714)CTT>TTT	p.L238F
Pat_76	Pre-Treatment	SH2B1	25970	37	16	28883678	28883678	Missense_Mutation	SNP	C	T	4	79	c.1681C>T	c.(1681-1683)CGG>TGG	p.R561W
Pat_76	Pre-Treatment	LAT	27040	37	16	28997467	28997467	Missense_Mutation	SNP	C	T	97	148	c.175C>T	c.(175-177)CCC>TCC	p.P59S
Pat_76	Pre-Treatment	KIF22	3835	37	16	29810772	29810772	Missense_Mutation	SNP	C	T	33	67	c.947C>T	c.(946-948)CCT>CTT	p.P316L
Pat_76	Pre-Treatment	C16orf92	146378	37	16	30034984	30034984	Missense_Mutation	SNP	C	T	13	18	c.67C>T	c.(67-69)CCG>TCG	p.P23S
Pat_76	Pre-Treatment	ITGAL	3683	37	16	30500437	30500438	Missense_Mutation	DNP	GG	AA	26	52	.1041_1042GG>A	039-1044)ATGGAG>ATAA	.347_348ME>I
Pat_76	Pre-Treatment	SETD1A	9739	37	16	30991074	30991074	Missense_Mutation	SNP	G	A	3	5	c.3967G>A	c.(3967-3969)GCA>ACA	p.A1323T
Pat_76	Pre-Treatment	STX1B	112755	37	16	31004706	31004706	Missense_Mutation	SNP	C	T	23	38	c.637G>A	c.(637-639)GAT>AAT	p.D213N
Pat_76	Pre-Treatment	STX4	6810	37	16	31046302	31046302	Nonsense_Mutation	SNP	C	T	60	119	c.319C>T	c.(319-321)CAG>TAG	p.Q107*
Pat_76	Pre-Treatment	ZNF668	79759	37	16	31072586	31072586	Missense_Mutation	SNP	C	T	28	46	c.1663G>A	c.(1663-1665)GAC>AAC	p.D555N
Pat_76	Pre-Treatment	PRSS36	146547	37	16	31150517	31150517	Missense_Mutation	SNP	G	A	18	29	c.2510C>T	c.(2509-2511)TCG>TTG	p.S837L
Pat_76	Pre-Treatment	FUS	2521	37	16	31202331	31202331	Nonsense_Mutation	SNP	C	T	32	91	c.1441C>T	c.(1441-1443)CGA>TGA	p.R481*
Pat_76	Pre-Treatment	ITGAX	3687	37	16	31374263	31374263	Missense_Mutation	SNP	C	T	32	44	c.1367C>T	c.(1366-1368)TCC>TTC	p.S456F
Pat_76	Pre-Treatment	ITGAX	3687	37	16	31383723	31383723	Missense_Mutation	SNP	C	T	19	52	c.2185C>T	c.(2185-2187)CCC>TCC	p.P729S
Pat_76	Pre-Treatment	ABCC12	94160	37	16	48138242	48138242	Missense_Mutation	SNP	G	A	47	68	c.2711C>T	c.(2710-2712)CCC>CTC	p.P904L
Pat_76	Pre-Treatment	HEATR3	55027	37	16	50112773	50112773	Missense_Mutation	SNP	G	A	17	27	c.885G>A	c.(883-885)ATG>ATA	p.M295I
Pat_76	Pre-Treatment	TOX3	27324	37	16	52473862	52473862	Missense_Mutation	SNP	C	T	15	8	c.1006G>A	c.(1006-1008)GAA>AAA	p.E336K
Pat_76	Pre-Treatment	CES1	1066	37	16	55857576	55857576	Missense_Mutation	SNP	C	T	14	37	c.422G>A	c.(421-423)GGA>GAA	p.G141E
Pat_76	Pre-Treatment	BBS2	583	37	16	56531684	56531684	Missense_Mutation	SNP	A	T	73	85	c.1768T>A	c.(1768-1770)TTT>ATT	p.F590I
Pat_76	Pre-Treatment	CPNE2	221184	37	16	57153117	57153117	Missense_Mutation	SNP	G	A	28	49	c.518G>A	c.(517-519)GGG>GAG	p.G173E
Pat_76	Pre-Treatment	CSNK2A2	1459	37	16	58199576	58199576	Missense_Mutation	SNP	A	C	24	29	c.864T>G	c.(862-864)AGT>AGG	p.S288R
Pat_76	Pre-Treatment	CDH5	1003	37	16	66413316	66413316	Missense_Mutation	SNP	G	A	46	45	c.76G>A	c.(76-78)GCA>ACA	p.A26T
Pat_76	Pre-Treatment	CA7	766	37	16	66885408	66885408	Missense_Mutation	SNP	G	A	98	151	c.400G>A	c.(400-402)GGG>AGG	p.G134R
Pat_76	Pre-Treatment	HSD11B2	3291	37	16	67470217	67470217	Missense_Mutation	SNP	G	A	67	125	c.730G>A	c.(730-732)GAC>AAC	p.D244N
Pat_76	Pre-Treatment	DPEP3	64180	37	16	68014081	68014081	Missense_Mutation	SNP	C	T	17	26	c.278G>A	c.(277-279)GGC>GAC	p.G93D
Pat_76	Pre-Treatment	ESRP2	80004	37	16	68266371	68266371	Missense_Mutation	SNP	C	T	3	39	c.887G>A	c.(886-888)CGC>CAC	p.R296H
Pat_76	Pre-Treatment	HYDIN	54768	37	16	70871640	70871640	Missense_Mutation	SNP	G	A	19	38	c.13192C>T	c.(13192-13194)CTC>TTC	p.L4398F
Pat_76	Pre-Treatment	HYDIN	54768	37	16	71218881	71218881	Missense_Mutation	SNP	C	T	17	24	c.148G>A	c.(148-150)GAG>AAG	p.E50K
Pat_76	Pre-Treatment	ADAMTS18	170692	37	16	77353954	77353954	Missense_Mutation	SNP	C	T	19	18	c.2324G>A	c.(2323-2325)CGA>CAA	p.R775Q

Pat_76	Pre-Treatment	ADAMTS18	170692	37	16	77355084	77355084	Missense_Mutation	SNP	G	A	24	37	c.2179C>T	c.(2179-2181)CAT>TAT	p.H727Y
Pat_76	Pre-Treatment	VAT1L	57687	37	16	77918574	77918574	Missense_Mutation	SNP	C	T	12	19	c.952C>T	c.(952-954)CTT>TTT	p.L318F
Pat_76	Pre-Treatment	CDYL2	124359	37	16	80718508	80718508	Missense_Mutation	SNP	C	A	4	69	c.543G>T	c.(541-543)TTG>TTT	p.L181F
Pat_76	Pre-Treatment	BCMO1	53630	37	16	81295883	81295883	Missense_Mutation	SNP	G	A	33	28	c.466G>A	c.(466-468)GAG>AAG	p.E156K
Pat_76	Pre-Treatment	GAN	8139	37	16	81391420	81391420	Missense_Mutation	SNP	G	A	6	250	c.857G>A	c.(856-858)CGG>CAG	p.R286Q
Pat_76	Pre-Treatment	PLCG2	5336	37	16	81965224	81965224	Missense_Mutation	SNP	A	T	33	66	c.2704A>T	c.(2704-2706)AGC>TGC	p.S902C
Pat_76	Pre-Treatment	MBTPS1	8720	37	16	84088064	84088064	Missense_Mutation	SNP	G	A	10	19	c.3149C>T	c.(3148-3150)CCT>CTT	p.P1050L
Pat_76	Pre-Treatment	MBTPS1	8720	37	16	84127376	84127376	Missense_Mutation	SNP	G	A	37	39	c.676C>T	c.(676-678)CCC>TCC	p.P226S
Pat_76	Pre-Treatment	ADAD2	161931	37	16	84229876	84229876	Missense_Mutation	SNP	G	A	49	69	c.1426G>A	c.(1426-1428)GAA>AAA	p.E476K
Pat_76	Pre-Treatment	ATP2C2	9914	37	16	84456002	84456002	Missense_Mutation	SNP	G	A	22	25	c.631G>A	c.(631-633)GAC>AAC	p.D211N
Pat_76	Pre-Treatment	KIAA0182	23199	37	16	85688001	85688001	Missense_Mutation	SNP	C	T	42	63	c.544C>T	c.(544-546)CCC>TCC	p.P182S
Pat_76	Pre-Treatment	CDT1	81620	37	16	88873867	88873867	Missense_Mutation	SNP	G	A	4	49	c.1454G>A	c.(1453-1455)AGC>AAC	p.S485N
Pat_76	Pre-Treatment	DPEP1	1800	37	16	89696855	89696855	Missense_Mutation	SNP	G	A	4	82	c.37G>A	c.(37-39)GTC>ATC	p.V13I
Pat_76	Pre-Treatment	NXN	64359	37	17	722732	722733	Missense_Mutation	DNP	GG	AA	37	46	c.766_767CC>TT	c.(766-768)CCC>TTC	p.P256F
Pat_76	Pre-Treatment	MYO1C	4641	37	17	1380826	1380826	Missense_Mutation	SNP	G	A	4	68	c.1547C>T	c.(1546-1548)ACT>ATT	p.T516I
Pat_76	Pre-Treatment	OR1E1	8387	37	17	3300846	3300846	Missense_Mutation	SNP	G	A	54	62	c.859C>T	c.(859-861)CCC>TCC	p.P287S
Pat_76	Pre-Treatment	RABEP1	9135	37	17	5281522	5281522	Missense_Mutation	SNP	G	A	28	59	c.2266G>A	c.(2266-2268)GGA>AGA	p.G756R
Pat_76	Pre-Treatment	ALOX12	239	37	17	6909842	6909842	Missense_Mutation	SNP	G	A	26	63	c.1456G>A	c.(1456-1458)GAT>AAT	p.D486N
Pat_76	Pre-Treatment	C17orf74	201243	37	17	7329674	7329674	Missense_Mutation	SNP	C	T	62	61	c.364C>T	c.(364-366)CGC>TGC	p.R122C
Pat_76	Pre-Treatment	MYH10	4628	37	17	8379226	8379226	Missense_Mutation	SNP	G	A	4	90	c.5827C>T	c.(5827-5829)CGG>TGG	p.R1943W
Pat_76	Pre-Treatment	MYH13	8735	37	17	10248630	10248630	Missense_Mutation	SNP	G	T	88	148	c.1473C>A	c.(1471-1473)TTC>TTA	p.F491L
Pat_76	Pre-Treatment	MYH1	4619	37	17	10398328	10398328	Missense_Mutation	SNP	C	T	52	76	c.5386G>A	c.(5386-5388)GAC>AAC	p.D1796N
Pat_76	Pre-Treatment	MYH2	4620	37	17	10432559	10432559	Missense_Mutation	SNP	C	T	19	33	c.3274G>A	c.(3274-3276)GAA>AAA	p.E1092K
Pat_76	Pre-Treatment	DNAH9	1770	37	17	11572873	11572873	Missense_Mutation	SNP	G	A	36	57	c.3115G>A	c.(3115-3117)GAA>AAA	p.E1039K
Pat_76	Pre-Treatment	TRIM16	10626	37	17	15535907	15535907	Missense_Mutation	SNP	G	A	37	38	c.931C>T	c.(931-933)CGC>TGC	p.R311C
Pat_76	Pre-Treatment	CCDC144A	9720	37	17	16635945	16635945	Missense_Mutation	SNP	G	A	7	7	c.2383G>A	c.(2383-2385)GAA>AAA	p.E795K
Pat_76	Pre-Treatment	MYO15A	51168	37	17	18082167	18082167	Missense_Mutation	SNP	G	A	28	45	c.10576G>A	c.(10576-10578)GAG>AAG	p.E3526K
Pat_76	Pre-Treatment	FAM83G	644815	37	17	18907240	18907240	Missense_Mutation	SNP	C	T	26	24	c.115G>A	c.(115-117)GTG>ATG	p.V39M
Pat_76	Pre-Treatment	RNF112	7732	37	17	19318195	19318195	Missense_Mutation	SNP	C	T	13	19	c.1121C>T	c.(1120-1122)CCT>CTT	p.P374L
Pat_76	Pre-Treatment	LGALS9B	284194	37	17	20363726	20363726	Missense_Mutation	SNP	C	T	40	69	c.70G>A	c.(70-72)GGT>AGT	p.G24S
Pat_76	Pre-Treatment	SUPT6H	6830	37	17	27002156	27002156	Missense_Mutation	SNP	G	A	20	25	c.514G>A	c.(514-516)GAG>AAG	p.E172K
Pat_76	Pre-Treatment	THRA	7067	37	17	38244573	38244573	Missense_Mutation	SNP	G	A	85	5	c.802G>A	c.(802-804)GAC>AAC	p.D268N
Pat_76	Pre-Treatment	KRT39	390792	37	17	39122844	39122844	Missense_Mutation	SNP	C	T	164	17	c.265G>A	c.(265-267)GGT>AGT	p.G89S
Pat_76	Pre-Treatment	KRTAP4-9	100132386	37	17	39261929	39261929	Missense_Mutation	SNP	C	T	4	16	c.289C>T	c.(289-291)CCT>TCT	p.P97S
Pat_76	Pre-Treatment	KRTAP4-4	84616	37	17	39316620	39316621	Missense_Mutation	DNP	GG	AT	69	12	c.323_324CC>AT	c.(322-324)CCC>CAT	p.P108H
Pat_76	Pre-Treatment	KRT13	3860	37	17	39661585	39661585	Missense_Mutation	SNP	T	A	3	23	c.218A>T	c.(217-219)TAT>TTT	p.Y73F
Pat_76	Pre-Treatment	KRT14	3861	37	17	39741234	39741234	Missense_Mutation	SNP	G	A	57	58	c.601C>T	c.(601-603)CGC>TGC	p.R201C
Pat_76	Pre-Treatment	TTC25	83538	37	17	40117275	40117275	Missense_Mutation	SNP	G	A	8	7	c.1793G>A	c.(1792-1794)AGG>AAG	p.R598K
Pat_76	Pre-Treatment	WNK4	65266	37	17	40946862	40946862	Missense_Mutation	SNP	G	A	89	11	c.2423G>A	c.(2422-2424)GGA>GAA	p.G808E
Pat_76	Pre-Treatment	AOC2	314	37	17	41002225	41002225	Missense_Mutation	SNP	C	T	63	99	c.2131C>T	c.(2131-2133)CCC>TCC	p.P711S
Pat_76	Pre-Treatment	TMUB2	79089	37	17	42266818	42266818	Missense_Mutation	SNP	C	G	4	152	c.464C>G	c.(463-465)CCA>CGA	p.P155R
Pat_76	Pre-Treatment	PLEKHM1	9842	37	17	43531155	43531155	Missense_Mutation	SNP	G	A	47	8	c.2063C>T	c.(2062-2064)TCC>TTC	p.S688F
Pat_76	Pre-Treatment	GOSR2	9570	37	17	45009497	45009497	Missense_Mutation	SNP	C	T	114	149	c.268C>T	c.(268-270)CGG>TGG	p.R90W
Pat_76	Pre-Treatment	SCRN2	90507	37	17	45916364	45916364	Missense_Mutation	SNP	G	A	4	83	c.565C>T	c.(565-567)CGC>TGC	p.R189C
Pat_76	Pre-Treatment	HOXB3	3213	37	17	46629484	46629484	Missense_Mutation	SNP	C	T	7	288	c.353G>A	c.(352-354)GGT>GAT	p.G118D
Pat_76	Pre-Treatment	CACNA1G	8913	37	17	48673939	48673939	Missense_Mutation	SNP	C	T	36	10	c.2996C>T	c.(2995-2997)TCC>TTC	p.S999F
Pat_76	Pre-Treatment	ABCC3	8714	37	17	48762122	48762122	Missense_Mutation	SNP	G	A	101	16	c.4166G>A	c.(4165-4167)AGC>AAC	p.S1389N

Pat_76	Pre-Treatment	AKAP1	8165	37	17	55193565	55193565	Missense_Mutation	SNP	G	A	5	89	c.2375G>A	c.(2374-2376)CGA>CAA	p.R792Q
Pat_76	Pre-Treatment	BCAS3	54828	37	17	59112041	59112041	Missense_Mutation	SNP	C	T	4	63	c.1697C>T	c.(1696-1698)CCT>CTT	p.P566L
Pat_76	Pre-Treatment	EFCAB3	146779	37	17	60493646	60493646	Missense_Mutation	SNP	G	A	83	15	c.1273G>A	c.(1273-1275)GGA>AGA	p.G425R
Pat_76	Pre-Treatment	10-Mar	162333	37	17	60814149	60814149	Missense_Mutation	SNP	C	T	71	10	c.1080G>A	c.(1078-1080)ATG>ATA	p.M360I
Pat_76	Pre-Treatment	NOL11	25926	37	17	65734057	65734057	Missense_Mutation	SNP	G	A	80	23	c.1498G>A	c.(1498-1500)GTC>ATC	p.V500I
Pat_76	Pre-Treatment	ABCA9	10350	37	17	67008196	67008196	Missense_Mutation	SNP	C	T	59	16	c.3068G>A	c.(3067-3069)CGA>CAA	p.R1023Q
Pat_76	Pre-Treatment	ABCA9	10350	37	17	67014656	67014656	Nonsense_Mutation	SNP	G	A	300	53	c.2665C>T	c.(2665-2667)CAG>TAG	p.Q889*
Pat_76	Pre-Treatment	ABCA9	10350	37	17	67047281	67047281	Splice_Site	SNP	C	T	34	1	c.-12_splice	c.e2-1	
Pat_76	Pre-Treatment	C17orf80	55028	37	17	71232451	71232451	Missense_Mutation	SNP	C	T	15	3	c.830C>T	c.(829-831)TCC>TTC	p.S277F
Pat_76	Pre-Treatment	GPRC5C	55890	37	17	72436177	72436177	Missense_Mutation	SNP	G	A	18	4	c.262G>A	c.(262-264)GGG>AGG	p.G88R
Pat_76	Pre-Treatment	CD300E	342510	37	17	72610074	72610074	Missense_Mutation	SNP	G	T	3	15	c.487C>A	c.(487-489)CAA>AAA	p.Q163K
Pat_76	Pre-Treatment	NUP85	79902	37	17	73222241	73222241	Missense_Mutation	SNP	C	G	4	96	c.1083C>G	c.(1081-1083)ATC>ATG	p.I361M
Pat_76	Pre-Treatment	SLC38A10	124565	37	17	79226403	79226403	Missense_Mutation	SNP	C	T	73	20	c.1537G>A	c.(1537-1539)GAC>AAC	p.D513N
Pat_76	Pre-Treatment	LRRC45	201255	37	17	79983359	79983360	Missense_Mutation	DNP	CC	TT	40	3	c.637_638CC>TT	c.(637-639)CCT>TTT	p.P213F
Pat_76	Pre-Treatment	LPIN2	9663	37	18	2960660	2960660	Missense_Mutation	SNP	G	A	76	113	c.179C>T	c.(178-180)TCC>TTC	p.S60F
Pat_76	Pre-Treatment	ZFP161	7541	37	18	5291174	5291174	Missense_Mutation	SNP	C	T	25	71	c.1033G>A	c.(1033-1035)GCC>ACC	p.A345T
Pat_76	Pre-Treatment	TMEM200C	645369	37	18	5890387	5890387	Missense_Mutation	SNP	C	T	18	25	c.1676G>A	c.(1675-1677)CGA>CAA	p.R559Q
Pat_76	Pre-Treatment	TXNDC2	84203	37	18	9887689	9887689	Missense_Mutation	SNP	C	T	59	55	c.1213C>T	c.(1213-1215)CCC>TCC	p.P405S
Pat_76	Pre-Treatment	ZNF519	162655	37	18	14106150	14106150	Missense_Mutation	SNP	A	C	12	20	c.389T>G	c.(388-390)TTT>TGT	p.F130C
Pat_76	Pre-Treatment	POTEC	388468	37	18	14542728	14542728	Missense_Mutation	SNP	G	T	4	61	c.418C>A	c.(418-420)CTG>ATG	p.L140M
Pat_76	Pre-Treatment	ANKRD30B	374860	37	18	14851568	14851568	Missense_Mutation	SNP	G	A	13	27	c.3268G>A	c.(3268-3270)GAA>AAA	p.E1090K
Pat_76	Pre-Treatment	LAMA3	3909	37	18	21494505	21494505	Missense_Mutation	SNP	G	A	14	17	c.7461G>A	c.(7459-7461)ATG>ATA	p.M2487I
Pat_76	Pre-Treatment	OSBPL1A	114876	37	18	21946860	21946860	Missense_Mutation	SNP	C	T	4	139	c.278G>A	c.(277-279)CGA>CAA	p.R93Q
Pat_76	Pre-Treatment	ZNF521	25925	37	18	22669428	22669428	Splice_Site	SNP	C	G	25	30	c.3906_splice	c.e7+1	p.Q1302_splice
Pat_76	Pre-Treatment	SS18	6760	37	18	23619273	23619273	Missense_Mutation	SNP	G	A	81	105	c.755C>T	c.(754-756)CCC>CTC	p.P252L
Pat_76	Pre-Treatment	AQP4	361	37	18	24436207	24436207	Missense_Mutation	SNP	C	T	90	119	c.940G>A	c.(940-942)GAC>AAC	p.D314N
Pat_76	Pre-Treatment	CDH2	1000	37	18	25565092	25565092	Missense_Mutation	SNP	G	A	29	27	c.2081C>T	c.(2080-2082)TCC>TTC	p.S694F
Pat_76	Pre-Treatment	DSC1	1823	37	18	28719770	28719770	Missense_Mutation	SNP	C	T	8	16	c.1604G>A	c.(1603-1605)AGA>AAA	p.R535K
Pat_76	Pre-Treatment	MCART2	147407	37	18	29339957	29339957	Missense_Mutation	SNP	G	A	20	46	c.668C>T	c.(667-669)GCC>GTC	p.A223V
Pat_76	Pre-Treatment	ZNF24	7572	37	18	32919934	32919934	Missense_Mutation	SNP	G	A	44	65	c.427C>T	c.(427-429)CTC>TTC	p.L143F
Pat_76	Pre-Treatment	SETBP1	26040	37	18	42529852	42529852	Missense_Mutation	SNP	G	A	9	19	c.547G>A	c.(547-549)GAG>AAG	p.E183K
Pat_76	Pre-Treatment	ZBTB7C	201501	37	18	45566863	45566864	Missense_Mutation	DNP	CC	TT	19	26	c.615_616GG>AA	613-618)AGGGAC>AGAA	p.D206N
Pat_76	Pre-Treatment	MAPK4	5596	37	18	48190519	48190519	Missense_Mutation	SNP	G	A	21	25	c.191G>A	c.(190-192)CGA>CAA	p.R64Q
Pat_76	Pre-Treatment	DCC	1630	37	18	50936948	50936948	Missense_Mutation	SNP	G	A	47	56	c.3062G>A	c.(3061-3063)CGA>CAA	p.R1021Q
Pat_76	Pre-Treatment	ATP8B1	5205	37	18	55335733	55335733	Missense_Mutation	SNP	C	T	38	63	c.2137G>A	c.(2137-2139)GGA>AGA	p.G713R
Pat_76	Pre-Treatment	TNFRSF11A	8792	37	18	60015422	60015422	Missense_Mutation	SNP	C	T	33	46	c.97C>T	c.(97-99)CCA>TCA	p.P33S
Pat_76	Pre-Treatment	SERPINB4	6318	37	18	61324207	61324207	Missense_Mutation	SNP	G	A	7	12	c.626C>T	c.(625-627)TCC>TTC	p.S209F
Pat_76	Pre-Treatment	SERPINB2	5055	37	18	61569055	61569055	Missense_Mutation	SNP	G	A	28	42	c.617G>A	c.(616-618)GGA>GAA	p.G206E
Pat_76	Pre-Treatment	CDH7	1005	37	18	63547911	63547911	Missense_Mutation	SNP	A	T	29	56	c.2139A>T	c.(2137-2139)GAA>GAT	p.E713D
Pat_76	Pre-Treatment	CD226	10666	37	18	67540447	67540447	Missense_Mutation	SNP	C	T	60	106	c.763G>A	c.(763-765)GGA>AGA	p.G255R
Pat_76	Pre-Treatment	CNDP1	84735	37	18	72251769	72251769	Missense_Mutation	SNP	T	C	3	74	c.1495T>C	c.(1495-1497)TTT>CTT	p.F499L
Pat_76	Pre-Treatment	SALL3	27164	37	18	76753711	76753711	Missense_Mutation	SNP	G	A	10	13	c.1720G>A	c.(1720-1722)GAG>AAG	p.E574K
Pat_76	Pre-Treatment	ATP9B	374868	37	18	76856595	76856595	Missense_Mutation	SNP	G	A	12	17	c.239G>A	c.(238-240)AGG>AAG	p.R80K
Pat_76	Pre-Treatment	ADNP2	22850	37	18	77875472	77875472	Missense_Mutation	SNP	G	A	36	52	c.47G>A	c.(46-48)CGA>CAA	p.R16Q
Pat_76	Pre-Treatment	MBD3	53615	37	19	1584657	1584657	Missense_Mutation	SNP	G	A	3	43	c.290C>T	c.(289-291)ACG>ATG	p.T97M
Pat_76	Pre-Treatment	TMPRSS9	360200	37	19	2399117	2399118	Missense_Mutation	DNP	GG	AA	5	2	c.338_339GG>AA	c.(337-339)GGG>GAA	p.G113E
Pat_76	Pre-Treatment	DIRAS1	148252	37	19	2717729	2717729	Missense_Mutation	SNP	G	C	41	55	c.76C>G	c.(76-78)CGC>GGC	p.R26G

Pat_76	Pre-Treatment	PIP5K1C	23396	37	19	3661008	3661008	Missense_Mutation	SNP	G	A	5	233	c.424C>T	c.(424-426)CGC>TGC	p.R142C
Pat_76	Pre-Treatment	PIAS4	51588	37	19	4013123	4013123	Missense_Mutation	SNP	C	T	4	49	c.230C>T	c.(229-231)CCG>CTG	p.P77L
Pat_76	Pre-Treatment	CREB3L3	84699	37	19	4171734	4171734	Missense_Mutation	SNP	G	A	4	114	c.1154G>A	c.(1153-1155)CGA>CAA	p.R385Q
Pat_76	Pre-Treatment	ANKRD24	170961	37	19	4217073	4217073	Missense_Mutation	SNP	G	A	10	20	c.1916G>A	c.(1915-1917)GGG>GAG	p.G639E
Pat_76	Pre-Treatment	ANKRD24	170961	37	19	4219676	4219676	Missense_Mutation	SNP	G	A	4	62	c.3092G>A	c.(3091-3093)CGG>CAG	p.R1031Q
Pat_76	Pre-Treatment	CCDC94	55702	37	19	4249233	4249233	Nonsense_Mutation	SNP	C	A	8	22	c.33C>A	c.(31-33)TAC>TAA	p.Y11*
Pat_76	Pre-Treatment	TMIGD2	126259	37	19	4298151	4298151	Missense_Mutation	SNP	C	T	10	21	c.238G>A	c.(238-240)GTC>ATC	p.V80I
Pat_76	Pre-Treatment	CHAF1A	10036	37	19	4409220	4409221	Missense_Mutation	DNP	CC	TT	74	121	c.424_425CC>TT	c.(424-426)CCC>TTC	p.P142F
Pat_76	Pre-Treatment	TNFSF14	8740	37	19	6665025	6665025	Missense_Mutation	SNP	C	T	21	43	c.635G>A	c.(634-636)GGG>GAG	p.G212E
Pat_76	Pre-Treatment	VAV1	7409	37	19	6854037	6854038	Missense_Mutation	DNP	GG	AA	30	66	.2412_2413GG>A	410-2415)AAGGAG>AAA	p.E805K
Pat_76	Pre-Treatment	EMR1	2015	37	19	6935005	6935005	Missense_Mutation	SNP	C	T	25	79	c.2297C>T	c.(2296-2298)TCC>TTC	p.S766F
Pat_76	Pre-Treatment	ZNF557	79230	37	19	7083192	7083192	Missense_Mutation	SNP	A	T	33	61	c.709A>T	c.(709-711)ACC>TCC	p.T237S
Pat_76	Pre-Treatment	LASS4	79603	37	19	8321133	8321133	Nonsense_Mutation	SNP	G	A	19	15	c.482G>A	c.(481-483)TGG>TAG	p.W161*
Pat_76	Pre-Treatment	2-Mar	51257	37	19	8491561	8491561	Missense_Mutation	SNP	G	A	4	63	c.245G>A	c.(244-246)TGC>TAC	p.C82Y
Pat_76	Pre-Treatment	ZNF414	84330	37	19	8577487	8577487	Splice_Site	SNP	C	T	4	12	c.424_splice	c.e3+1	p.G142_splice
Pat_76	Pre-Treatment	MUC16	94025	37	19	8996484	8996484	Missense_Mutation	SNP	C	G	7	18	c.41088G>C	c.(41086-41088)AAG>AAC	p.K13696N
Pat_76	Pre-Treatment	MUC16	94025	37	19	9020005	9020005	Missense_Mutation	SNP	C	T	141	189	c.37490G>A	c.(37489-37491)AGG>AAG	p.R12497K
Pat_76	Pre-Treatment	MUC16	94025	37	19	9054252	9054252	Missense_Mutation	SNP	G	A	10	14	c.31370C>T	c.(31369-31371)TCG>TTG	p.S10457L
Pat_76	Pre-Treatment	MUC16	94025	37	19	9058282	9058282	Missense_Mutation	SNP	C	T	3	9	c.29164G>A	c.(29164-29166)GAA>AAA	p.E9722K
Pat_76	Pre-Treatment	MUC16	94025	37	19	9061096	9061096	Missense_Mutation	SNP	C	T	26	27	c.26350G>A	c.(26350-26352)GAA>AAA	p.E8784K
Pat_76	Pre-Treatment	MUC16	94025	37	19	9064315	9064315	Missense_Mutation	SNP	G	A	35	45	c.23131C>T	c.(23131-23133)CCC>TCC	p.P7711S
Pat_76	Pre-Treatment	MUC16	94025	37	19	9068557	9068557	Missense_Mutation	SNP	G	A	45	52	c.18889C>T	c.(18889-18891)CCT>TCT	p.P6297S
Pat_76	Pre-Treatment	MUC16	94025	37	19	9076162	9076162	Missense_Mutation	SNP	C	T	20	42	c.11284G>A	c.(11284-11286)GAA>AAA	p.E3762K
Pat_76	Pre-Treatment	MUC16	94025	37	19	9083768	9083768	Missense_Mutation	SNP	C	T	8	12	c.8047G>A	c.(8047-8049)GAG>AAG	p.E2683K
Pat_76	Pre-Treatment	OR1M1	125963	37	19	9204171	9204171	Missense_Mutation	SNP	G	A	4	64	c.251G>A	c.(250-252)AGC>AAC	p.S84N
Pat_76	Pre-Treatment	OR7G1	125962	37	19	9226282	9226282	Missense_Mutation	SNP	G	A	66	102	c.158C>T	c.(157-159)TCC>TTC	p.S53F
Pat_76	Pre-Treatment	OR7D2	162998	37	19	9297226	9297226	Missense_Mutation	SNP	G	A	31	37	c.769G>A	c.(769-771)GGG>AGG	p.G257R
Pat_76	Pre-Treatment	OR7E24	26648	37	19	9362051	9362051	Missense_Mutation	SNP	C	T	23	32	c.332C>T	c.(331-333)TCC>TTC	p.S111F
Pat_76	Pre-Treatment	ZNF560	147741	37	19	9578557	9578557	Missense_Mutation	SNP	C	T	23	49	c.1066G>A	c.(1066-1068)GAT>AAT	p.D356N
Pat_76	Pre-Treatment	ZNF560	147741	37	19	9580356	9580356	Missense_Mutation	SNP	G	A	33	45	c.479C>T	c.(478-480)TCT>TTT	p.S160F
Pat_76	Pre-Treatment	LPPR2	64748	37	19	11472097	11472097	Missense_Mutation	SNP	C	G	13	18	c.596C>G	c.(595-597)GCC>GGC	p.A199G
Pat_76	Pre-Treatment	ZNF442	79973	37	19	12462077	12462077	Missense_Mutation	SNP	C	T	24	47	c.322G>A	c.(322-324)GAA>AAA	p.E108K
Pat_76	Pre-Treatment	FARSA	2193	37	19	13039457	13039457	Missense_Mutation	SNP	G	A	4	1	c.617C>T	c.(616-618)CCC>CTC	p.P206L
Pat_76	Pre-Treatment	DAND5	199699	37	19	13080638	13080638	Missense_Mutation	SNP	C	T	15	18	c.164C>T	c.(163-165)TCT>TTT	p.S55F
Pat_76	Pre-Treatment	CCDC105	126402	37	19	15131365	15131366	Nonsense_Mutation	DNP	GG	AT	14	16	c.768_769GG>AT	766-771)CTGGAG>CTAT	p.E257*
Pat_76	Pre-Treatment	AKAP8L	26993	37	19	15491342	15491342	Missense_Mutation	SNP	C	T	21	30	c.1618G>A	c.(1618-1620)GAG>AAG	p.E540K
Pat_76	Pre-Treatment	CYP4F3	4051	37	19	15752308	15752308	Missense_Mutation	SNP	C	T	21	38	c.83C>T	c.(82-84)TCC>TTC	p.S28F
Pat_76	Pre-Treatment	CYP4F12	66002	37	19	15795640	15795641	Missense_Mutation	DNP	GG	AA	30	68	c.933_934GG>AA	931-936)AAGGCA>AAAA	p.A312T
Pat_76	Pre-Treatment	OR10H2	26538	37	19	15838861	15838861	Missense_Mutation	SNP	G	A	42	77	c.8G>A	c.(7-9)GGG>GAG	p.G3E
Pat_76	Pre-Treatment	CHERP	10523	37	19	16641445	16641445	Missense_Mutation	SNP	G	A	58	96	c.827C>T	c.(826-828)TCC>TTC	p.S276F
Pat_76	Pre-Treatment	TMEM38A	79041	37	19	16799166	16799166	Missense_Mutation	SNP	C	G	8	6	c.884C>G	c.(883-885)GCC>GGC	p.A295G
Pat_76	Pre-Treatment	CPAMD8	27151	37	19	17056424	17056424	Missense_Mutation	SNP	C	T	21	33	c.2869G>A	c.(2869-2871)GAG>AAG	p.E957K
Pat_76	Pre-Treatment	CPAMD8	27151	37	19	17086839	17086839	Missense_Mutation	SNP	C	A	3	21	c.2022G>T	c.(2020-2022)AGG>AGT	p.R674S
Pat_76	Pre-Treatment	CPAMD8	27151	37	19	17107943	17107943	Missense_Mutation	SNP	G	A	3	23	c.1214C>T	c.(1213-1215)CCG>CTG	p.P405L
Pat_76	Pre-Treatment	MYO9B	4650	37	19	17322521	17322521	Missense_Mutation	SNP	C	T	4	88	c.5996C>T	c.(5995-5997)TCG>TTG	p.S1999L
Pat_76	Pre-Treatment	NXNL1	115861	37	19	17571671	17571671	Missense_Mutation	SNP	G	A	21	16	c.8C>T	c.(7-9)TCC>TTC	p.S3F
Pat_76	Pre-Treatment	UNC13A	23025	37	19	17783267	17783267	Missense_Mutation	SNP	C	T	9	23	c.454G>A	c.(454-456)GTG>ATG	p.V152M

Pat_76	Pre-Treatment	COMP	1311	37	19	18899298	18899298	Missense_Mutation	SNP	C	T	7	9	c.788G>A	c.(787-789)GGG>GAG	p.G263E
Pat_76	Pre-Treatment	SFRS14	10147	37	19	19121069	19121069	Nonsense_Mutation	SNP	G	A	5	302	c.1933C>T	c.(1933-1935)CGA>TGA	p.R645*
Pat_76	Pre-Treatment	ZNF14	7561	37	19	19822792	19822792	Missense_Mutation	SNP	G	A	56	78	c.1298C>T	c.(1297-1299)TCC>TTC	p.S433F
Pat_76	Pre-Treatment	ZNF682	91120	37	19	20116872	20116872	Missense_Mutation	SNP	G	A	19	29	c.1439C>T	c.(1438-1440)TCC>TTC	p.S480F
Pat_76	Pre-Treatment	ZNF90	7643	37	19	20216075	20216075	Missense_Mutation	SNP	G	A	77	101	c.176G>A	c.(175-177)GGA>GAA	p.G59E
Pat_76	Pre-Treatment	ZNF90	7643	37	19	20228748	20228748	Missense_Mutation	SNP	G	A	12	15	c.385G>A	c.(385-387)GGT>AGT	p.G129S
Pat_76	Pre-Treatment	ZNF626	199777	37	19	20807233	20807233	Missense_Mutation	SNP	C	T	6	4	c.1450G>A	c.(1450-1452)GAA>AAA	p.E484K
Pat_76	Pre-Treatment	ZNF626	199777	37	19	20807401	20807401	Missense_Mutation	SNP	C	T	54	92	c.1282G>A	c.(1282-1284)GAA>AAA	p.E428K
Pat_76	Pre-Treatment	ZNF676	163223	37	19	22362756	22362756	Missense_Mutation	SNP	G	A	20	25	c.1763C>T	c.(1762-1764)CCC>CTC	p.P588L
Pat_76	Pre-Treatment	ZNF99	7652	37	19	22940472	22940472	Missense_Mutation	SNP	T	G	28	36	c.1966A>C	c.(1966-1968)AAA>CAA	p.K656Q
Pat_76	Pre-Treatment	ZNF536	9745	37	19	31038889	31038889	Missense_Mutation	SNP	G	A	4	108	c.2363G>A	c.(2362-2364)GGC>GAC	p.G788D
Pat_76	Pre-Treatment	ZNF536	9745	37	19	31040082	31040082	Missense_Mutation	SNP	G	A	39	63	c.3556G>A	c.(3556-3558)GAA>AAA	p.E1186K
Pat_76	Pre-Treatment	RHPN2	85415	37	19	33512485	33512485	Missense_Mutation	SNP	C	T	3	45	c.382G>A	c.(382-384)GTC>ATC	p.V128I
Pat_76	Pre-Treatment	RBM42	79171	37	19	36122302	36122302	Missense_Mutation	SNP	G	A	4	76	c.437G>A	c.(436-438)CGG>CAG	p.R146Q
Pat_76	Pre-Treatment	UPK1A	11045	37	19	36164422	36164422	Missense_Mutation	SNP	G	A	3	9	c.443G>A	c.(442-444)CGC>CAC	p.R148H
Pat_76	Pre-Treatment	NPHS1	4868	37	19	36321798	36321798	Missense_Mutation	SNP	C	T	39	46	c.3542G>A	c.(3541-3543)AGA>AAA	p.R1181K
Pat_76	Pre-Treatment	ZNF793	390927	37	19	38028549	38028549	Missense_Mutation	SNP	G	A	12	22	c.989G>A	c.(988-990)CGA>CAA	p.R330Q
Pat_76	Pre-Treatment	ZNF540	163255	37	19	38102515	38102515	Missense_Mutation	SNP	C	T	62	98	c.334C>T	c.(334-336)CGT>TGT	p.R112C
Pat_76	Pre-Treatment	ZNF607	84775	37	19	38189410	38189410	Missense_Mutation	SNP	G	A	24	34	c.1622C>T	c.(1621-1623)TCT>TTT	p.S541F
Pat_76	Pre-Treatment	RYR1	6261	37	19	38995971	38995971	Missense_Mutation	SNP	G	A	4	31	c.8333G>A	c.(8332-8334)GGA>GAA	p.G2778E
Pat_76	Pre-Treatment	RYR1	6261	37	19	39018297	39018297	Missense_Mutation	SNP	C	T	7	15	c.10697C>T	c.(10696-10698)TCC>TTC	p.S3566F
Pat_76	Pre-Treatment	RYR1	6261	37	19	39038941	39038941	Missense_Mutation	SNP	G	A	21	35	c.12163G>A	c.(12163-12165)GAG>AAG	p.E4055K
Pat_76	Pre-Treatment	MRPS12	6183	37	19	39422990	39422990	Missense_Mutation	SNP	C	T	5	101	c.67C>T	c.(67-69)CGG>TGG	p.R23W
Pat_76	Pre-Treatment	FCGBP	8857	37	19	40419983	40419983	Missense_Mutation	SNP	C	T	23	31	c.3011G>A	c.(3010-3012)GGG>GAG	p.G1004E
Pat_76	Pre-Treatment	ZNF780A	284323	37	19	40581648	40581648	Missense_Mutation	SNP	G	A	4	88	c.701C>T	c.(700-702)ACC>ATC	p.T234I
Pat_76	Pre-Treatment	SPTBN4	57731	37	19	41025980	41025981	Missense_Mutation	DNP	GG	AA	12	21	.3576_3577GG>A	574-3579)AGGGAG>AGA	p.E1193K
Pat_76	Pre-Treatment	LTBP4	8425	37	19	41117276	41117276	Nonsense_Mutation	SNP	C	T	4	64	c.2230C>T	c.(2230-2232)CGA>TGA	p.R744*
Pat_76	Pre-Treatment	ERF	2077	37	19	42754607	42754607	Missense_Mutation	SNP	C	T	4	116	c.133G>A	c.(133-135)GTC>ATC	p.V45I
Pat_76	Pre-Treatment	MEGF8	1954	37	19	42880163	42880163	Missense_Mutation	SNP	G	A	4	128	c.7573G>A	c.(7573-7575)GTG>ATG	p.V2525M
Pat_76	Pre-Treatment	PSG3	5671	37	19	43237041	43237041	Missense_Mutation	SNP	G	A	120	219	c.604C>T	c.(604-606)CTC>TTC	p.L202F
Pat_76	Pre-Treatment	PSG8	440533	37	19	43262276	43262276	Missense_Mutation	SNP	G	A	173	210	c.587C>T	c.(586-588)TCT>TTT	p.S196F
Pat_76	Pre-Treatment	PSG1	5669	37	19	43373139	43373140	Missense_Mutation	DNP	CC	TT	110	172	c.756_757GG>AA	754-759)AGGGAG>AGAA	p.E253K
Pat_76	Pre-Treatment	PSG1	5669	37	19	43382107	43382107	Missense_Mutation	SNP	C	T	76	131	c.388G>A	c.(388-390)GGG>AGG	p.G130R
Pat_76	Pre-Treatment	PSG6	5675	37	19	43411960	43411961	Missense_Mutation	DNP	CC	GT	83	195	c.752_753GG>AC	c.(751-753)AGG>AAC	p.R251N
Pat_76	Pre-Treatment	ZNF226	7769	37	19	44681760	44681760	Missense_Mutation	SNP	C	T	8	15	c.2345C>T	c.(2344-2346)TCC>TTC	p.S782F
Pat_76	Pre-Treatment	ZNF285	26974	37	19	44891610	44891610	Missense_Mutation	SNP	C	T	37	43	c.797G>A	c.(796-798)GGA>GAA	p.G266E
Pat_76	Pre-Treatment	ZNF285	26974	37	19	44891787	44891787	Missense_Mutation	SNP	G	A	19	22	c.620C>T	c.(619-621)CCC>CTC	p.P207L
Pat_76	Pre-Treatment	BCAM	4059	37	19	45317445	45317445	Missense_Mutation	SNP	C	T	4	101	c.821C>T	c.(820-822)CCG>CTG	p.P274L
Pat_76	Pre-Treatment	PVRL2	5819	37	19	45389243	45389243	Missense_Mutation	SNP	G	A	51	123	c.1246G>A	c.(1246-1248)GAG>AAG	p.E416K
Pat_76	Pre-Treatment	RELB	5971	37	19	45536001	45536001	Missense_Mutation	SNP	G	A	7	8	c.1201G>A	c.(1201-1203)GAC>AAC	p.D401N
Pat_76	Pre-Treatment	SFRS16	11129	37	19	45556053	45556053	Missense_Mutation	SNP	C	T	28	49	c.202C>T	c.(202-204)CCC>TCC	p.P68S
Pat_76	Pre-Treatment	RTN2	6253	37	19	45998057	45998057	Missense_Mutation	SNP	G	A	7	13	c.286C>T	c.(286-288)CCA>TCA	p.P96S
Pat_76	Pre-Treatment	IGFL2	147920	37	19	46664003	46664003	Missense_Mutation	SNP	C	T	81	149	c.206C>T	c.(205-207)CCC>CTC	p.P69L
Pat_76	Pre-Treatment	PNMAL1	55228	37	19	46973649	46973649	Missense_Mutation	SNP	G	A	17	12	c.644C>T	c.(643-645)CCC>CTC	p.P215L
Pat_76	Pre-Treatment	PTGIR	5739	37	19	47124731	47124731	Missense_Mutation	SNP	G	A	23	37	c.967C>T	c.(967-969)CTT>TTT	p.L323F
Pat_76	Pre-Treatment	GRLF1	2909	37	19	47503857	47503857	Missense_Mutation	SNP	C	T	23	22	c.4412C>T	c.(4411-4413)CCG>CTG	p.P1471L
Pat_76	Pre-Treatment	ZC3H4	23211	37	19	47588399	47588399	Missense_Mutation	SNP	G	A	62	79	c.1021C>T	c.(1021-1023)CGG>TGG	p.R341W

Pat_76	Pre-Treatment	ELSPBP1	64100	37	19	48519260	48519260	Missense_Mutation	SNP	G	A	35	43	c.319G>A	c.(319-321)GAT>AAT	p.D107N
Pat_76	Pre-Treatment	GRIN2D	2906	37	19	48922977	48922977	Missense_Mutation	SNP	C	T	63	133	c.1997C>T	c.(1996-1998)GCC>GTC	p.A666V
Pat_76	Pre-Treatment	LMTK3	114783	37	19	49013354	49013354	Missense_Mutation	SNP	G	A	3	19	c.374C>T	c.(373-375)TCG>TTG	p.S125L
Pat_76	Pre-Treatment	SULT2B1	6820	37	19	49079332	49079333	Missense_Mutation	DNP	CC	TT	50	92	c.206_207CC>TT	c.(205-207)CCC>CTT	p.P69L
Pat_76	Pre-Treatment	FGF21	26291	37	19	49261406	49261406	Missense_Mutation	SNP	G	A	8	21	c.559G>A	c.(559-561)GAT>AAT	p.D187N
Pat_76	Pre-Treatment	CGB2	114336	37	19	49536425	49536425	Missense_Mutation	SNP	C	T	28	44	c.439C>T	c.(439-441)CCA>TCA	p.P147S
Pat_76	Pre-Treatment	SLC6A16	28968	37	19	49813080	49813080	Missense_Mutation	SNP	G	A	22	13	c.704C>T	c.(703-705)CCT>CTT	p.P235L
Pat_76	Pre-Treatment	TBC1D17	79735	37	19	50385521	50385521	Missense_Mutation	SNP	C	T	48	88	c.662C>T	c.(661-663)TCC>TTC	p.S221F
Pat_76	Pre-Treatment	IL4I1	259307	37	19	50399286	50399286	Missense_Mutation	SNP	G	A	8	7	c.38C>T	c.(37-39)CCC>CTC	p.P13L
Pat_76	Pre-Treatment	ZNF473	25888	37	19	50549595	50549595	Missense_Mutation	SNP	C	T	14	31	c.1895C>T	c.(1894-1896)TCC>TTC	p.S632F
Pat_76	Pre-Treatment	C19orf41	126123	37	19	50655885	50655885	Missense_Mutation	SNP	C	T	171	205	c.647G>A	c.(646-648)CGA>CAA	p.R216Q
Pat_76	Pre-Treatment	C19orf41	126123	37	19	50666268	50666268	Missense_Mutation	SNP	C	T	19	38	c.184G>A	c.(184-186)GGG>AGG	p.G62R
Pat_76	Pre-Treatment	MYH14	79784	37	19	50753023	50753023	Missense_Mutation	SNP	G	C	51	51	c.1575G>C	c.(1573-1575)TGG>TGC	p.W525C
Pat_76	Pre-Treatment	MYH14	79784	37	19	50779268	50779268	Missense_Mutation	SNP	C	T	17	16	c.3365C>T	c.(3364-3366)GCC>GTC	p.A1122V
Pat_76	Pre-Treatment	KLK15	55554	37	19	51330397	51330397	Missense_Mutation	SNP	C	T	16	33	c.218G>A	c.(217-219)GGA>GAA	p.G73E
Pat_76	Pre-Treatment	FPR1	2357	37	19	52249742	52249742	Missense_Mutation	SNP	C	T	29	38	c.506G>A	c.(505-507)GGT>GAT	p.G169D
Pat_76	Pre-Treatment	ZNF613	79898	37	19	52448416	52448416	Missense_Mutation	SNP	C	T	19	47	c.1280C>T	c.(1279-1281)CCC>CTC	p.P427L
Pat_76	Pre-Treatment	ZNF701	55762	37	19	53085781	53085781	Missense_Mutation	SNP	G	A	67	71	c.469G>A	c.(469-471)GAA>AAA	p.E157K
Pat_76	Pre-Treatment	ZNF701	55762	37	19	53086538	53086538	Missense_Mutation	SNP	G	C	3	39	c.1226G>C	c.(1225-1227)CGT>CCT	p.R409P
Pat_76	Pre-Treatment	ZNF347	84671	37	19	53644928	53644928	Missense_Mutation	SNP	G	A	54	91	c.1153C>T	c.(1153-1155)CGT>TGT	p.R385C
Pat_76	Pre-Treatment	CACNG8	59283	37	19	54483187	54483187	Missense_Mutation	SNP	G	A	3	19	c.431G>A	c.(430-432)TGC>TAC	p.C144Y
Pat_76	Pre-Treatment	LILRB2	10288	37	19	54783794	54783794	Nonsense_Mutation	SNP	C	T	45	78	c.207G>A	c.(205-207)TGG>TGA	p.W69*
Pat_76	Pre-Treatment	LILRA1	11024	37	19	55107653	55107653	Splice_Site	SNP	G	A	19	35	c.959_splice	c.e7-1	p.G320_splice
Pat_76	Pre-Treatment	LILRB1	10859	37	19	55148297	55148297	Missense_Mutation	SNP	C	T	26	29	c.1921C>T	c.(1921-1923)CCC>TCC	p.P641S
Pat_76	Pre-Treatment	NLRP7	199713	37	19	55450725	55450726	Missense_Mutation	DNP	CC	TT	5	20	.1461_1462GG>A	459-1464)GGGGAG>GGA	p.E488K
Pat_76	Pre-Treatment	SYT5	6861	37	19	55689725	55689725	Missense_Mutation	SNP	C	T	18	14	c.91G>A	c.(91-93)GCC>ACC	p.A31T
Pat_76	Pre-Treatment	PTPRH	5794	37	19	55716882	55716882	Missense_Mutation	SNP	C	T	35	73	c.431G>A	c.(430-432)GGC>GAC	p.G144D
Pat_76	Pre-Treatment	NLRP9	338321	37	19	56244864	56244864	Nonsense_Mutation	SNP	C	T	31	58	c.333G>A	c.(331-333)TGG>TGA	p.W111*
Pat_76	Pre-Treatment	NLRP5	126206	37	19	56530714	56530714	Missense_Mutation	SNP	C	T	33	33	c.572C>T	c.(571-573)TCA>TTA	p.S191L
Pat_76	Pre-Treatment	ZNF543	125919	37	19	57840542	57840542	Missense_Mutation	SNP	C	T	41	42	c.1712C>T	c.(1711-1713)CCT>CTT	p.P571L
Pat_76	Pre-Treatment	ZNF304	57343	37	19	57868658	57868658	Missense_Mutation	SNP	C	T	59	187	c.1421C>T	c.(1420-1422)CCT>CTT	p.P474L
Pat_76	Pre-Treatment	ZSCAN4	201516	37	19	58187859	58187859	Missense_Mutation	SNP	G	A	39	42	c.346G>A	c.(346-348)GAG>AAG	p.E116K
Pat_76	Pre-Treatment	ZSCAN4	201516	37	19	58190127	58190127	Missense_Mutation	SNP	C	T	56	84	c.1156C>T	c.(1156-1158)CAT>TAT	p.H386Y
Pat_76	Pre-Treatment	RPS5	6193	37	19	58904521	58904521	Missense_Mutation	SNP	C	T	22	51	c.287C>T	c.(286-288)GCC>GTC	p.A96V
Pat_76	Pre-Treatment	TSSC1	7260	37	2	3341881	3341881	Missense_Mutation	SNP	T	G	9	24	c.166A>C	c.(166-168)AAT>CAT	p.N56H
Pat_76	Pre-Treatment	ASAP2	8853	37	2	9474929	9474929	Missense_Mutation	SNP	C	T	4	124	c.749C>T	c.(748-750)ACG>ATG	p.T250M
Pat_76	Pre-Treatment	CPSF3	51692	37	2	9613133	9613133	Missense_Mutation	SNP	C	T	5	86	c.2042C>T	c.(2041-2043)ACG>ATG	p.T681M
Pat_76	Pre-Treatment	GREB1	9687	37	2	11752710	11752710	Missense_Mutation	SNP	G	A	4	75	c.3096G>A	c.(3094-3096)ATG>ATA	p.M1032I
Pat_76	Pre-Treatment	PUM2	23369	37	2	20460196	20460196	Missense_Mutation	SNP	G	A	28	43	c.2257C>T	c.(2257-2259)CCA>TCA	p.P753S
Pat_76	Pre-Treatment	APOB	338	37	2	21231860	21231860	Missense_Mutation	SNP	G	A	25	44	c.7880C>T	c.(7879-7881)CCA>CTA	p.P2627L
Pat_76	Pre-Treatment	APOB	338	37	2	21233066	21233066	Missense_Mutation	SNP	G	T	9	17	c.6674C>A	c.(6673-6675)ACA>AAA	p.T2225K
Pat_76	Pre-Treatment	APOB	338	37	2	21235356	21235356	Missense_Mutation	SNP	C	T	15	43	c.4384G>A	c.(4384-4386)GGA>AGA	p.G1462R
Pat_76	Pre-Treatment	DPYSL5	56896	37	2	27167566	27167566	Missense_Mutation	SNP	G	A	38	40	c.1483G>A	c.(1483-1485)GAT>AAT	p.D495N
Pat_76	Pre-Treatment	C2orf53	339779	37	2	27361072	27361072	Missense_Mutation	SNP	C	A	6	4	c.126G>T	c.(124-126)CAG>CAT	p.Q42H
Pat_76	Pre-Treatment	SLC30A3	7781	37	2	27478226	27478226	Missense_Mutation	SNP	G	A	3	47	c.1121C>T	c.(1120-1122)CCG>CTG	p.P374L
Pat_76	Pre-Treatment	PPM1G	5496	37	2	27604584	27604584	Missense_Mutation	SNP	C	T	4	155	c.1523G>A	c.(1522-1524)CGA>CAA	p.R508Q
Pat_76	Pre-Treatment	PLB1	151056	37	2	28812377	28812377	Missense_Mutation	SNP	G	C	57	93	c.1876G>C	c.(1876-1878)GTT>CTT	p.V626L

Pat_76	Pre-Treatment	FAM179A	165186	37	2	29247101	29247101	Missense_Mutation	SNP	G	A	13	21	c.1714G>A	c.(1714-1716)GAG>AAG	p.E572K
Pat_76	Pre-Treatment	ALK	238	37	2	29543713	29543713	Missense_Mutation	SNP	C	T	41	46	c.1450G>A	c.(1450-1452)GAT>AAT	p.D484N
Pat_76	Pre-Treatment	XDH	7498	37	2	31558835	31558835	Missense_Mutation	SNP	C	A	34	64	c.3991G>T	c.(3991-3993)GTG>TTG	p.V1331L
Pat_76	Pre-Treatment	SLC30A6	55676	37	2	32434592	32434592	Nonsense_Mutation	SNP	C	T	4	124	c.847C>T	c.(847-849)CGA>TGA	p.R283*
Pat_76	Pre-Treatment	FAM98A	25940	37	2	33810710	33810710	Missense_Mutation	SNP	G	A	75	112	c.775C>T	c.(775-777)CCT>TCT	p.P259S
Pat_76	Pre-Treatment	MAP4K3	8491	37	2	39487761	39487761	Nonsense_Mutation	SNP	C	T	15	17	c.2294G>A	c.(2293-2295)TGG>TAG	p.W765*
Pat_76	Pre-Treatment	SLC8A1	6546	37	2	40405536	40405536	Missense_Mutation	SNP	C	T	71	112	c.1906G>A	c.(1906-1908)GAG>AAG	p.E636K
Pat_76	Pre-Treatment	ABCG8	64241	37	2	44078738	44078738	Missense_Mutation	SNP	C	T	22	13	c.338C>T	c.(337-339)TCC>TTC	p.S113F
Pat_76	Pre-Treatment	PREPL	9581	37	2	44559788	44559789	Missense_Mutation	DNP	GG	AA	12	18	.1162_1163CC>T	c.(1162-1164)CCT>TTT	p.P388F
Pat_76	Pre-Treatment	FOXN2	3344	37	2	48573793	48573793	Missense_Mutation	SNP	C	T	61	102	c.440C>T	c.(439-441)CCA>CTA	p.P147L
Pat_76	Pre-Treatment	PSME4	23198	37	2	54131220	54131220	Missense_Mutation	SNP	G	A	55	78	c.3017C>T	c.(3016-3018)CCC>CTC	p.P1006L
Pat_76	Pre-Treatment	C2orf63	130162	37	2	55445106	55445106	Missense_Mutation	SNP	G	A	11	37	c.206C>T	c.(205-207)TCC>TTC	p.S69F
Pat_76	Pre-Treatment	EFEMP1	2202	37	2	56094269	56094269	Missense_Mutation	SNP	C	T	47	71	c.1421G>A	c.(1420-1422)GGG>GAG	p.G474E
Pat_76	Pre-Treatment	CCDC85A	114800	37	2	56611435	56611435	Missense_Mutation	SNP	C	T	37	35	c.1607C>T	c.(1606-1608)TCG>TTG	p.S536L
Pat_76	Pre-Treatment	PUS10	150962	37	2	61236063	61236063	Nonsense_Mutation	SNP	G	A	4	15	c.214C>T	c.(214-216)CGA>TGA	p.R72*
Pat_76	Pre-Treatment	PLEK	5341	37	2	68607955	68607955	Missense_Mutation	SNP	T	A	71	93	c.299T>A	c.(298-300)ATT>AAT	p.I100N
Pat_76	Pre-Treatment	FBXO48	554251	37	2	68691389	68691389	Missense_Mutation	SNP	C	T	136	227	c.420G>A	c.(418-420)ATG>ATA	p.M140I
Pat_76	Pre-Treatment	GFPT1	2673	37	2	69597165	69597165	Missense_Mutation	SNP	C	T	39	51	c.191G>A	c.(190-192)GGA>GAA	p.G64E
Pat_76	Pre-Treatment	C2orf42	54980	37	2	70377634	70377634	Missense_Mutation	SNP	G	A	19	39	c.1579C>T	c.(1579-1581)CTT>TTT	p.L527F
Pat_76	Pre-Treatment	PCYOX1	51449	37	2	70502156	70502156	Missense_Mutation	SNP	G	A	42	70	c.560G>A	c.(559-561)GGA>GAA	p.G187E
Pat_76	Pre-Treatment	ATP6V1B1	525	37	2	71191923	71191923	Missense_Mutation	SNP	G	A	12	14	c.1306G>A	c.(1306-1308)GAG>AAG	p.E436K
Pat_76	Pre-Treatment	C2orf78	388960	37	2	74042413	74042413	Missense_Mutation	SNP	G	A	8	8	c.1063G>A	c.(1063-1065)GAA>AAA	p.E355K
Pat_76	Pre-Treatment	SEMA4F	10505	37	2	74906855	74906855	Missense_Mutation	SNP	G	A	3	41	c.1832G>A	c.(1831-1833)CGG>CAG	p.R611Q
Pat_76	Pre-Treatment	HK2	3099	37	2	75108931	75108931	Missense_Mutation	SNP	T	G	23	27	c.1664T>G	c.(1663-1665)ATG>AGG	p.M555R
Pat_76	Pre-Treatment	CTNNA2	1496	37	2	80808840	80808840	Missense_Mutation	SNP	G	A	21	26	c.1903G>A	c.(1903-1905)GAA>AAA	p.E635K
Pat_76	Pre-Treatment	THNSL2	55258	37	2	88484883	88484883	Missense_Mutation	SNP	G	A	29	33	c.1114G>A	c.(1114-1116)GAA>AAA	p.E372K
Pat_76	Pre-Treatment	ZNF2	7549	37	2	95847717	95847717	Missense_Mutation	SNP	C	T	4	137	c.1141C>T	c.(1141-1143)CGG>TGG	p.R381W
Pat_76	Pre-Treatment	TMEM131	23505	37	2	98475846	98475846	Missense_Mutation	SNP	G	A	8	28	c.404C>T	c.(403-405)CCT>CTT	p.P135L
Pat_76	Pre-Treatment	LYG2	254773	37	2	99861748	99861748	Missense_Mutation	SNP	C	T	22	62	c.358G>A	c.(358-360)GGA>AGA	p.G120R
Pat_76	Pre-Treatment	NPAS2	4862	37	2	101565879	101565879	Missense_Mutation	SNP	C	T	21	64	c.535C>T	c.(535-537)CCA>TCA	p.P179S
Pat_76	Pre-Treatment	CREG2	200407	37	2	102000157	102000158	Missense_Mutation	DNP	CC	TT	35	111	c.448_449GG>AA	c.(448-450)GGA>AAA	p.G150K
Pat_76	Pre-Treatment	IL18R1	8809	37	2	103013029	103013029	Missense_Mutation	SNP	C	G	18	58	c.1309C>G	c.(1309-1311)CGA>GGA	p.R437G
Pat_76	Pre-Treatment	TGFBRAP1	9392	37	2	105912941	105912941	Missense_Mutation	SNP	C	T	31	122	c.910G>A	c.(910-912)GGA>AGA	p.G304R
Pat_76	Pre-Treatment	RGPD3	653489	37	2	107049684	107049684	Missense_Mutation	SNP	C	T	143	375	c.2263G>A	c.(2263-2265)GAA>AAA	p.E755K
Pat_76	Pre-Treatment	SULT1C3	442038	37	2	108881461	108881461	Missense_Mutation	SNP	G	A	71	52	c.802G>A	c.(802-804)GGG>AGG	p.G268R
Pat_76	Pre-Treatment	RGPD5	84220	37	2	113147135	113147135	Nonsense_Mutation	SNP	C	T	45	308	c.3387G>A	c.(3385-3387)TGG>TGA	p.W1129*
Pat_76	Pre-Treatment	POLR1B	84172	37	2	113322062	113322062	Missense_Mutation	SNP	C	T	75	97	c.1732C>T	c.(1732-1734)CTT>TTT	p.L578F
Pat_76	Pre-Treatment	IL1F6	27179	37	2	113764178	113764178	Missense_Mutation	SNP	C	T	163	253	c.128C>T	c.(127-129)ACT>ATT	p.T43I
Pat_76	Pre-Treatment	PSD4	23550	37	2	113953840	113953840	Missense_Mutation	SNP	G	A	17	23	c.2342G>A	c.(2341-2343)GGC>GAC	p.G781D
Pat_76	Pre-Treatment	DPP10	57628	37	2	116066815	116066815	Missense_Mutation	SNP	G	A	13	20	c.61G>A	c.(61-63)GAA>AAA	p.E21K
Pat_76	Pre-Treatment	DPP10	57628	37	2	116572369	116572369	Missense_Mutation	SNP	G	A	29	49	c.1701G>A	c.(1699-1701)ATG>ATA	p.M567I
Pat_76	Pre-Treatment	PCDP1	200373	37	2	120373196	120373196	Missense_Mutation	SNP	G	A	8	18	c.463G>A	c.(463-465)GAA>AAA	p.E155K
Pat_76	Pre-Treatment	TMEM177	80775	37	2	120438910	120438911	Nonsense_Mutation	DNP	CT	TA	17	40	c.481_482CT>TA	c.(481-483)CTG>TAG	p.L161*
Pat_76	Pre-Treatment	GLI2	2736	37	2	121748199	121748199	Missense_Mutation	SNP	C	T	40	55	c.4709C>T	c.(4708-4710)TCC>TTC	p.S1570F
Pat_76	Pre-Treatment	TFCP2L1	29842	37	2	121997133	121997133	Splice_Site	SNP	C	T	26	28	c.860_splice	c.e8+1	p.G287_splice
Pat_76	Pre-Treatment	MKI67IP	84365	37	2	122493301	122493301	Missense_Mutation	SNP	G	T	21	35	c.131C>A	c.(130-132)CCT>CAT	p.P44H
Pat_76	Pre-Treatment	CNTNAP5	129684	37	2	125204447	125204447	Missense_Mutation	SNP	C	T	4	137	c.851C>T	c.(850-852)ACG>ATG	p.T284M

Pat_76	Pre-Treatment	MYO7B	4648	37	2	128341852	128341852	Missense_Mutation	SNP	C	T	29	54	c.1499C>T	c.(1498-1500)GCC>GTC	p.A500V
Pat_76	Pre-Treatment	MYO7B	4648	37	2	128346086	128346086	Missense_Mutation	SNP	C	T	24	35	c.1810C>T	c.(1810-1812)CAT>TAT	p.H604Y
Pat_76	Pre-Treatment	LOC401010	401010	37	2	132200417	132200417	Missense_Mutation	SNP	C	T	6	5	c.1585G>A	c.(1585-1587)GAA>AAA	p.E529K
Pat_76	Pre-Treatment	YSK4	80122	37	2	135744766	135744766	Missense_Mutation	SNP	G	A	28	35	c.1676C>T	c.(1675-1677)CCC>CTC	p.P559L
Pat_76	Pre-Treatment	LCT	3938	37	2	136566810	136566810	Missense_Mutation	SNP	G	A	25	33	c.3107C>T	c.(3106-3108)CCT>CTT	p.P1036L
Pat_76	Pre-Treatment	HNMT	3176	37	2	138762777	138762777	Missense_Mutation	SNP	C	T	55	90	c.505C>T	c.(505-507)CTC>TTC	p.L169F
Pat_76	Pre-Treatment	LRP1B	53353	37	2	141232728	141232728	Missense_Mutation	SNP	C	T	30	36	c.9604G>A	c.(9604-9606)GAT>AAT	p.D3202N
Pat_76	Pre-Treatment	LRP1B	53353	37	2	141986902	141986902	Missense_Mutation	SNP	C	T	8	13	c.700G>A	c.(700-702)GAA>AAA	p.E234K
Pat_76	Pre-Treatment	KYNU	8942	37	2	143643012	143643012	Missense_Mutation	SNP	G	A	24	33	c.76G>A	c.(76-78)GAT>AAT	p.D26N
Pat_76	Pre-Treatment	KYNU	8942	37	2	143718310	143718310	Missense_Mutation	SNP	C	T	54	73	c.700C>T	c.(700-702)CCT>TCT	p.P234S
Pat_76	Pre-Treatment	ARHGAP15	55843	37	2	143913139	143913139	Missense_Mutation	SNP	G	A	28	26	c.80G>A	c.(79-81)AGA>AAA	p.R27K
Pat_76	Pre-Treatment	KIF5C	3800	37	2	149864490	149864490	Missense_Mutation	SNP	A	G	31	58	c.2459A>G	c.(2458-2460)GAC>GGC	p.D820G
Pat_76	Pre-Treatment	GALNT5	11227	37	2	158140927	158140927	Missense_Mutation	SNP	G	A	27	34	c.1588G>A	c.(1588-1590)GAG>AAG	p.E530K
Pat_76	Pre-Treatment	SLC4A10	57282	37	2	162807236	162807236	Missense_Mutation	SNP	G	A	2	1	c.2419G>A	c.(2419-2421)GGT>AGT	p.G807S
Pat_76	Pre-Treatment	SCN3A	6328	37	2	165997216	165997216	Missense_Mutation	SNP	G	A	30	68	c.1964C>T	c.(1963-1965)TCC>TTC	p.S655F
Pat_76	Pre-Treatment	SCN9A	6335	37	2	167060726	167060726	Nonsense_Mutation	SNP	G	A	25	25	c.4480C>T	c.(4480-4482)CAA>TAA	p.Q1494*
Pat_76	Pre-Treatment	SCN7A	6332	37	2	167297955	167297955	Missense_Mutation	SNP	G	A	25	39	c.2108C>T	c.(2107-2109)TCC>TTC	p.S703F
Pat_76	Pre-Treatment	XIRP2	129446	37	2	168099884	168099884	Missense_Mutation	SNP	G	A	38	45	c.1982G>A	c.(1981-1983)AGG>AAG	p.R661K
Pat_76	Pre-Treatment	XIRP2	129446	37	2	168106418	168106418	Missense_Mutation	SNP	G	A	32	54	c.8516G>A	c.(8515-8517)AGA>AAA	p.R2839K
Pat_76	Pre-Treatment	ITGA6	3655	37	2	173355997	173355997	Missense_Mutation	SNP	G	A	64	126	c.2827G>A	c.(2827-2829)GGG>AGG	p.G943R
Pat_76	Pre-Treatment	CDCA7	83879	37	2	174232372	174232372	Nonsense_Mutation	SNP	G	T	111	113	c.1096G>T	c.(1096-1098)GAA>TAA	p.E366*
Pat_76	Pre-Treatment	CDCA7	83879	37	2	174232374	174232374	Missense_Mutation	SNP	A	T	112	116	c.1098A>T	c.(1096-1098)GAA>GAT	p.E366D
Pat_76	Pre-Treatment	CHN1	1123	37	2	175666528	175666528	Missense_Mutation	SNP	G	A	4	137	c.1115C>T	c.(1114-1116)CCG>CTG	p.P372L
Pat_76	Pre-Treatment	TTN	7273	37	2	179416869	179416870	Missense_Mutation	DNP	CC	TT	51	83	33053_83054GG>	c.(83053-83055)GGA>AAA	p.G27685K
Pat_76	Pre-Treatment	TTN	7273	37	2	179417904	179417904	Missense_Mutation	SNP	C	T	40	49	c.82019G>A	c.(82018-82020)GGA>GAA	p.G27340E
Pat_76	Pre-Treatment	TTN	7273	37	2	179431781	179431781	Missense_Mutation	SNP	G	A	60	100	c.71374C>T	c.(71374-71376)CGT>TGT	p.R23792C
Pat_76	Pre-Treatment	TTN	7273	37	2	179432002	179432002	Missense_Mutation	SNP	C	T	49	107	c.71153G>A	c.(71152-71154)AGA>AAA	p.R23718K
Pat_76	Pre-Treatment	TTN	7273	37	2	179483389	179483389	Missense_Mutation	SNP	C	T	34	49	c.39184G>A	c.(39184-39186)GGA>AGA	p.G13062R
Pat_76	Pre-Treatment	TTN	7273	37	2	179552911	179552911	Missense_Mutation	SNP	T	G	44	71	c.28506A>C	c.(28504-28506)GAA>GAC	p.E9502D
Pat_76	Pre-Treatment	TTN	7273	37	2	179552940	179552940	Missense_Mutation	SNP	C	T	31	43	c.28477G>A	c.(28477-28479)GAG>AAG	p.E9493K
Pat_76	Pre-Treatment	TTN	7273	37	2	179584053	179584053	Missense_Mutation	SNP	C	T	65	85	c.20332G>A	c.(20332-20334)GGA>AGA	p.G6778R
Pat_76	Pre-Treatment	TTN	7273	37	2	179587255	179587255	Missense_Mutation	SNP	G	A	87	106	c.18527C>T	c.(18526-18528)TCT>TTT	p.S6176F
Pat_76	Pre-Treatment	TTN	7273	37	2	179590750	179590750	Missense_Mutation	SNP	G	A	20	24	c.16567C>T	c.(16567-16569)CCT>TCT	p.P5523S
Pat_76	Pre-Treatment	TTN	7273	37	2	179594203	179594203	Missense_Mutation	SNP	G	A	28	58	c.14948C>T	c.(14947-14949)CCG>CTG	p.P4983L
Pat_76	Pre-Treatment	TTN	7273	37	2	179605785	179605786	Missense_Mutation	DNP	CC	TT	80	99	11661_11662GG>	659-11664)AAGGGT>AAA	p.G3888S
Pat_76	Pre-Treatment	TTN	7273	37	2	179614199	179614199	Nonsense_Mutation	SNP	G	A	18	29	c.12928C>T	c.(12928-12930)CAA>TAA	p.Q4310*
Pat_76	Pre-Treatment	TTN	7273	37	2	179638813	179638813	Missense_Mutation	SNP	C	T	52	77	c.7082G>A	c.(7081-7083)GGA>GAA	p.G2361E
Pat_76	Pre-Treatment	TTN	7273	37	2	179647791	179647791	Missense_Mutation	SNP	C	T	11	15	c.2842G>A	c.(2842-2844)GGC>AGC	p.G948S
Pat_76	Pre-Treatment	CCDC141	285025	37	2	179701823	179701823	Nonsense_Mutation	SNP	G	A	7	20	c.2398C>T	c.(2398-2400)CAA>TAA	p.Q800*
Pat_76	Pre-Treatment	PDE1A	5136	37	2	183070682	183070682	Missense_Mutation	SNP	G	A	14	29	c.935C>T	c.(934-936)TCC>TTC	p.S312F
Pat_76	Pre-Treatment	ZNF804A	91752	37	2	185798352	185798353	Missense_Mutation	DNP	GG	AA	24	49	c.278_279GG>AA	c.(277-279)AGG>AAA	p.R93K
Pat_76	Pre-Treatment	ZNF804A	91752	37	2	185800683	185800683	Missense_Mutation	SNP	C	A	17	27	c.560C>A	c.(559-561)CCA>CAA	p.P187Q
Pat_76	Pre-Treatment	ZSWIM2	151112	37	2	187702046	187702046	Missense_Mutation	SNP	C	T	35	47	c.730G>A	c.(730-732)GGG>AGG	p.G244R
Pat_76	Pre-Treatment	ZSWIM2	151112	37	2	187702277	187702277	Missense_Mutation	SNP	C	T	16	68	c.499G>A	c.(499-501)GGC>AGC	p.G167S
Pat_76	Pre-Treatment	COL3A1	1281	37	2	189854823	189854823	Missense_Mutation	SNP	G	A	31	50	c.692G>A	c.(691-693)GGA>GAA	p.G231E
Pat_76	Pre-Treatment	MYO1B	4430	37	2	192265124	192265124	Missense_Mutation	SNP	G	A	50	106	c.2312G>A	c.(2311-2313)CGG>CAG	p.R771Q
Pat_76	Pre-Treatment	DNAH7	56171	37	2	196723464	196723464	Nonsense_Mutation	SNP	G	A	72	114	c.7801C>T	c.(7801-7803)CAA>TAA	p.Q2601*

Pat_76	Pre-Treatment	DNAH7	56171	37	2	196729497	196729497	Missense_Mutation	SNP	C	T	102	167	c.6882G>A	c.(6880-6882)ATG>ATA	p.M2294I
Pat_76	Pre-Treatment	DNAH7	56171	37	2	196756414	196756414	Missense_Mutation	SNP	G	A	32	76	c.5011C>T	c.(5011-5013)CTT>TTT	p.L1671F
Pat_76	Pre-Treatment	HECW2	57520	37	2	197092934	197092934	Missense_Mutation	SNP	G	A	15	45	c.3809C>T	c.(3808-3810)TCC>TTC	p.S1270F
Pat_76	Pre-Treatment	RAPH1	65059	37	2	204306082	204306082	Missense_Mutation	SNP	G	A	7	15	c.1831C>T	c.(1831-1833)CCG>TCG	p.P611S
Pat_76	Pre-Treatment	ZDBF2	57683	37	2	207173096	207173096	Missense_Mutation	SNP	G	A	9	16	c.3844G>A	c.(3844-3846)GAT>AAT	p.D1282N
Pat_76	Pre-Treatment	PTH2R	5746	37	2	209307123	209307123	Missense_Mutation	SNP	C	T	80	123	c.446C>T	c.(445-447)ACC>ATC	p.T149I
Pat_76	Pre-Treatment	CPS1	1373	37	2	211454911	211454911	Missense_Mutation	SNP	C	T	160	320	c.793C>T	c.(793-795)CCG>TCG	p.P265S
Pat_76	Pre-Treatment	ABCA12	26154	37	2	215843664	215843665	Missense_Mutation	DNP	CC	TT	26	37	.4840_4841GG>A	c.(4840-4842)GGA>AAA	p.G1614K
Pat_76	Pre-Treatment	CXCR1	3577	37	2	219029255	219029255	Missense_Mutation	SNP	C	T	4	143	c.680G>A	c.(679-681)CGT>CAT	p.R227H
Pat_76	Pre-Treatment	SERPINE2	5270	37	2	224842266	224842266	Missense_Mutation	SNP	G	A	47	76	c.1154C>T	c.(1153-1155)CCT>CTT	p.P385L
Pat_76	Pre-Treatment	IRS1	3667	37	2	227662817	227662817	Missense_Mutation	SNP	C	A	4	122	c.638G>T	c.(637-639)CGC>CTC	p.R213L
Pat_76	Pre-Treatment	COL4A4	1286	37	2	227872874	227872874	Missense_Mutation	SNP	C	T	22	23	c.4669G>A	c.(4669-4671)GAG>AAG	p.E1557K
Pat_76	Pre-Treatment	COL4A3	1285	37	2	228155552	228155552	Missense_Mutation	SNP	G	A	22	16	c.3160G>A	c.(3160-3162)GGA>AGA	p.G1054R
Pat_76	Pre-Treatment	SP100	6672	37	2	231404082	231404083	Missense_Mutation	DNP	CC	TT	12	40	.2195_2196CC>T	c.(2194-2196)TCC>TTT	p.S732F
Pat_76	Pre-Treatment	UGT1A6	54578	37	2	234601885	234601885	Missense_Mutation	SNP	C	T	24	44	c.235C>T	c.(235-237)CCA>TCA	p.P79S
Pat_76	Pre-Treatment	ASB18	401036	37	2	237149963	237149963	Missense_Mutation	SNP	C	T	32	44	c.288G>A	c.(286-288)ATG>ATA	p.M96I
Pat_76	Pre-Treatment	RBM44	375316	37	2	238738134	238738134	Missense_Mutation	SNP	C	T	75	106	c.2878C>T	c.(2878-2880)CCT>TCT	p.P960S
Pat_76	Pre-Treatment	HDAC4	9759	37	2	240036829	240036829	Missense_Mutation	SNP	C	T	4	54	c.1696G>A	c.(1696-1698)GAT>AAT	p.D566N
Pat_76	Pre-Treatment	PRR21	643905	37	2	240981477	240981477	Missense_Mutation	SNP	G	A	5	67	c.923C>T	c.(922-924)ACC>ATC	p.T308I
Pat_76	Pre-Treatment	RNPEPL1	57140	37	2	241514551	241514551	Missense_Mutation	SNP	T	A	42	59	c.700T>A	c.(700-702)TTT>ATT	p.F234I
Pat_76	Pre-Treatment	SNED1	25992	37	2	241989314	241989314	Missense_Mutation	SNP	T	C	39	43	c.1699T>C	c.(1699-1701)TGC>CGC	p.C567R
Pat_76	Pre-Treatment	CPXM1	56265	37	20	2774842	2774842	Missense_Mutation	SNP	C	G	58	37	c.2199G>C	c.(2197-2199)AAG>AAC	p.K733N
Pat_76	Pre-Treatment	CPXM1	56265	37	20	2777701	2777701	Missense_Mutation	SNP	G	A	14	28	c.872C>T	c.(871-873)TCC>TTC	p.S291F
Pat_76	Pre-Treatment	SLC4A11	83959	37	20	3209023	3209023	Missense_Mutation	SNP	G	A	59	78	c.2488C>T	c.(2488-2490)CAC>TAC	p.H830Y
Pat_76	Pre-Treatment	SIGLEC1	6614	37	20	3674127	3674127	Missense_Mutation	SNP	G	A	3	51	c.3475C>T	c.(3475-3477)CGC>TGC	p.R1159C
Pat_76	Pre-Treatment	GPCPD1	56261	37	20	5539440	5539440	Missense_Mutation	SNP	G	A	14	32	c.1558C>T	c.(1558-1560)CCG>TCG	p.P520S
Pat_76	Pre-Treatment	PLCB1	23236	37	20	8130959	8130959	Missense_Mutation	SNP	C	T	24	22	c.118C>T	c.(118-120)CCA>TCA	p.P40S
Pat_76	Pre-Treatment	PLCB1	23236	37	20	8626748	8626748	Splice_Site	SNP	G	A	29	42	c.385_splice	c.e5-1	p.E129_splice
Pat_76	Pre-Treatment	C20orf103	24141	37	20	9498795	9498795	Missense_Mutation	SNP	C	T	5	72	c.584C>T	c.(583-585)CCG>CTG	p.P195L
Pat_76	Pre-Treatment	PAK7	57144	37	20	9561234	9561234	Missense_Mutation	SNP	G	A	106	92	c.548C>T	c.(547-549)TCT>TTT	p.S183F
Pat_76	Pre-Treatment	SNAP25	6616	37	20	10256176	10256176	Missense_Mutation	SNP	G	A	21	8	c.37G>A	c.(37-39)GAG>AAG	p.E13K
Pat_76	Pre-Treatment	SEL1L2	80343	37	20	13839970	13839970	Missense_Mutation	SNP	G	A	28	29	c.1756C>T	c.(1756-1758)CAC>TAC	p.H586Y
Pat_76	Pre-Treatment	SEC23B	10483	37	20	18491484	18491484	Missense_Mutation	SNP	C	T	4	75	c.5C>T	c.(4-6)GCG>GTG	p.A2V
Pat_76	Pre-Treatment	C20orf26	26074	37	20	20257987	20257987	Missense_Mutation	SNP	G	A	64	34	c.2681G>A	c.(2680-2682)GGA>GAA	p.G894E
Pat_76	Pre-Treatment	XRN2	22803	37	20	21362668	21362668	Missense_Mutation	SNP	C	T	23	70	c.2621C>T	c.(2620-2622)CCC>CTC	p.P874L
Pat_76	Pre-Treatment	FOXA2	3170	37	20	22563239	22563239	Missense_Mutation	SNP	C	T	36	58	c.623G>A	c.(622-624)CGC>CAC	p.R208H
Pat_76	Pre-Treatment	HM13	81502	37	20	30142599	30142599	Missense_Mutation	SNP	G	T	4	136	c.775G>T	c.(775-777)GCC>TCC	p.A259S
Pat_76	Pre-Treatment	MYLK2	85366	37	20	30409442	30409442	Missense_Mutation	SNP	C	T	118	74	c.674C>T	c.(673-675)TCG>TTG	p.S225L
Pat_76	Pre-Treatment	TTLL9	164395	37	20	30507671	30507671	Missense_Mutation	SNP	C	T	72	61	c.509C>T	c.(508-510)GCC>GTC	p.A170V
Pat_76	Pre-Treatment	HCK	3055	37	20	30674527	30674527	Missense_Mutation	SNP	C	T	3	36	c.932C>T	c.(931-933)ACT>ATT	p.T311I
Pat_76	Pre-Treatment	ZNF341	84905	37	20	32377334	32377334	Missense_Mutation	SNP	G	A	25	93	c.1975G>A	c.(1975-1977)GGC>AGC	p.G659S
Pat_76	Pre-Treatment	AHCY	191	37	20	32878645	32878645	Missense_Mutation	SNP	C	T	4	75	c.658G>A	c.(658-660)GGC>AGC	p.G220S
Pat_76	Pre-Treatment	ITCH	83737	37	20	33059310	33059310	Missense_Mutation	SNP	C	T	49	47	c.1682C>T	c.(1681-1683)TCC>TTC	p.S561F
Pat_76	Pre-Treatment	GSS	2937	37	20	33529540	33529540	Missense_Mutation	SNP	G	A	38	27	c.584C>T	c.(583-585)GCC>GTC	p.A195V
Pat_76	Pre-Treatment	FAM83C	128876	37	20	33875149	33875149	Missense_Mutation	SNP	G	A	25	35	c.1433C>T	c.(1432-1434)CCC>CTC	p.P478L
Pat_76	Pre-Treatment	MANBAL	63905	37	20	35929694	35929694	Missense_Mutation	SNP	C	T	9	15	c.28C>T	c.(28-30)CCG>TCG	p.P10S
Pat_76	Pre-Treatment	TGM2	7052	37	20	36760777	36760777	Missense_Mutation	SNP	C	T	53	113	c.1741G>A	c.(1741-1743)GAC>AAC	p.D581N

Pat_76	Pre-Treatment	TOX2	84969	37	20	42680074	42680074	Missense_Mutation	SNP	G	T	14	20	c.567G>T	c.(565-567)ATG>ATT	p.M189I
Pat_76	Pre-Treatment	JPH2	57158	37	20	42788428	42788428	Missense_Mutation	SNP	G	T	12	32	c.999C>A	c.(997-999)GAC>GAA	p.D333E
Pat_76	Pre-Treatment	JPH2	57158	37	20	42788430	42788430	Missense_Mutation	SNP	C	T	11	31	c.997G>A	c.(997-999)GAC>AAC	p.D333N
Pat_76	Pre-Treatment	HNF4A	3172	37	20	43056995	43056995	Missense_Mutation	SNP	C	T	78	54	c.1150C>T	c.(1150-1152)CAT>TAT	p.H384Y
Pat_76	Pre-Treatment	SEMG2	6407	37	20	43850643	43850643	Missense_Mutation	SNP	C	T	45	25	c.370C>T	c.(370-372)CAC>TAC	p.H124Y
Pat_76	Pre-Treatment	C20orf165	128497	37	20	44516192	44516192	Missense_Mutation	SNP	G	A	4	118	c.38C>T	c.(37-39)CCT>CTT	p.P13L
Pat_76	Pre-Treatment	MMP9	4318	37	20	44641179	44641179	Missense_Mutation	SNP	C	T	50	39	c.1288C>T	c.(1288-1290)CCC>TCC	p.P430S
Pat_76	Pre-Treatment	ZNF334	55713	37	20	45130345	45130345	Missense_Mutation	SNP	C	T	65	134	c.1633G>A	c.(1633-1635)GAA>AAA	p.E545K
Pat_76	Pre-Treatment	ZNF334	55713	37	20	45130930	45130930	Missense_Mutation	SNP	C	T	69	161	c.1048G>A	c.(1048-1050)GAA>AAA	p.E350K
Pat_76	Pre-Treatment	ARFGEF2	10564	37	20	47635499	47635499	Missense_Mutation	SNP	C	T	18	15	c.4588C>T	c.(4588-4590)CCA>TCA	p.P1530S
Pat_76	Pre-Treatment	SALL4	57167	37	20	50408016	50408016	Missense_Mutation	SNP	G	A	17	19	c.1006C>T	c.(1006-1008)CCT>TCT	p.P336S
Pat_76	Pre-Treatment	SALL4	57167	37	20	50408730	50408730	Missense_Mutation	SNP	G	A	31	22	c.292C>T	c.(292-294)CCA>TCA	p.P98S
Pat_76	Pre-Treatment	CBLN4	140689	37	20	54575833	54575833	Missense_Mutation	SNP	C	T	109	100	c.362G>A	c.(361-363)AGT>AAT	p.S121N
Pat_76	Pre-Treatment	MC3R	4159	37	20	54824619	54824620	Missense_Mutation	DNP	GG	AA	31	22	c.720_721GG>AA	718-723)GGGGCA>GGAA	p.A241T
Pat_76	Pre-Treatment	CSTF1	1477	37	20	54974146	54974146	Missense_Mutation	SNP	C	T	123	270	c.769C>T	c.(769-771)CCT>TCT	p.P257S
Pat_76	Pre-Treatment	CASS4	57091	37	20	55027514	55027514	Missense_Mutation	SNP	G	A	12	12	c.1282G>A	c.(1282-1284)GAG>AAG	p.E428K
Pat_76	Pre-Treatment	GNAS	2778	37	20	57484421	57484421	Missense_Mutation	SNP	G	A	24	80	c.2531G>A	c.(2530-2532)CGT>CAT	p.R844H
Pat_76	Pre-Treatment	ZNF831	128611	37	20	57768785	57768785	Missense_Mutation	SNP	C	T	29	25	c.2711C>T	c.(2710-2712)ACC>ATC	p.T904I
Pat_76	Pre-Treatment	ZNF831	128611	37	20	57769723	57769723	Nonsense_Mutation	SNP	C	T	12	10	c.3649C>T	c.(3649-3651)CGA>TGA	p.R1217*
Pat_76	Pre-Treatment	ZNF831	128611	37	20	57770945	57770945	Missense_Mutation	SNP	G	A	89	227	c.3760G>A	c.(3760-3762)GGG>AGG	p.G1254R
Pat_76	Pre-Treatment	SYCP2	10388	37	20	58495521	58495521	Missense_Mutation	SNP	G	A	18	18	c.190C>T	c.(190-192)CAC>TAC	p.H64Y
Pat_76	Pre-Treatment	CDH4	1002	37	20	60448856	60448856	Missense_Mutation	SNP	G	A	4	146	c.950G>A	c.(949-951)CGG>CAG	p.R317Q
Pat_76	Pre-Treatment	DIDO1	11083	37	20	61513427	61513427	Missense_Mutation	SNP	G	A	5	242	c.3881C>T	c.(3880-3882)GCG>GTG	p.A1294V
Pat_76	Pre-Treatment	SRMS	6725	37	20	62178665	62178666	Missense_Mutation	DNP	GG	AA	4	13	c.151_152CC>TT	c.(151-153)CCC>TTC	p.P51F
Pat_76	Pre-Treatment	RTEL1	51750	37	20	62292799	62292799	Missense_Mutation	SNP	G	A	3	43	c.251G>A	c.(250-252)CGG>CAG	p.R84Q
Pat_76	Pre-Treatment	RTEL1	51750	37	20	62320927	62320927	Missense_Mutation	SNP	C	T	4	61	c.1951C>T	c.(1951-1953)CGC>TGC	p.R651C
Pat_76	Pre-Treatment	TPTE	7179	37	21	10908889	10908889	Missense_Mutation	SNP	G	A	6	24	c.1456C>T	c.(1456-1458)CCT>TCT	p.P486S
Pat_76	Pre-Treatment	TPTE	7179	37	21	10920116	10920116	Missense_Mutation	SNP	C	T	24	100	c.1138G>A	c.(1138-1140)GAA>AAA	p.E380K
Pat_76	Pre-Treatment	RBM11	54033	37	21	15599544	15599544	Missense_Mutation	SNP	G	A	4	81	c.776G>A	c.(775-777)AGC>AAC	p.S259N
Pat_76	Pre-Treatment	BTG3	10950	37	21	18966605	18966605	Missense_Mutation	SNP	G	A	45	45	c.565C>T	c.(565-567)CCC>TCC	p.P189S
Pat_76	Pre-Treatment	NCAM2	4685	37	21	22656657	22656657	Missense_Mutation	SNP	C	T	21	51	c.274C>T	c.(274-276)CGT>TGT	p.R92C
Pat_76	Pre-Treatment	JAM2	58494	37	21	27066190	27066190	Missense_Mutation	SNP	G	A	76	117	c.364G>A	c.(364-366)GAA>AAA	p.E122K
Pat_76	Pre-Treatment	HUNK	30811	37	21	33370917	33370917	Missense_Mutation	SNP	C	T	32	61	c.1565C>T	c.(1564-1566)CCC>CTC	p.P522L
Pat_76	Pre-Treatment	C21orf59	56683	37	21	33976521	33976521	Missense_Mutation	SNP	C	T	26	64	c.448G>A	c.(448-450)GTG>ATG	p.V150M
Pat_76	Pre-Treatment	DNAJC28	54943	37	21	34861059	34861059	Missense_Mutation	SNP	T	G	91	107	c.642A>C	c.(640-642)AAA>AAC	p.K214N
Pat_76	Pre-Treatment	SLC5A3	6526	37	21	35467832	35467832	Missense_Mutation	SNP	A	G	76	165	c.335A>G	c.(334-336)TAC>TGC	p.Y112C
Pat_76	Pre-Treatment	SLC5A3	6526	37	21	35467859	35467859	Missense_Mutation	SNP	G	A	99	177	c.362G>A	c.(361-363)AGG>AAG	p.R121K
Pat_76	Pre-Treatment	SETD4	54093	37	21	37420683	37420683	Missense_Mutation	SNP	C	T	105	170	c.219G>A	c.(217-219)ATG>ATA	p.M73I
Pat_76	Pre-Treatment	DOPEY2	9980	37	21	37597961	37597961	Missense_Mutation	SNP	C	T	7	26	c.1469C>T	c.(1468-1470)CCT>CTT	p.P490L
Pat_76	Pre-Treatment	TTC3	7267	37	21	38462544	38462545	Missense_Mutation	DNP	CC	TT	15	35	c.438_439CC>TT	(436-441)TTCCTT>TTTTT	p.L147F
Pat_76	Pre-Treatment	TTC3	7267	37	21	38539906	38539906	Missense_Mutation	SNP	C	T	36	40	c.4451C>T	c.(4450-4452)CCT>CTT	p.P1484L
Pat_76	Pre-Treatment	DSCR4	10281	37	21	39426981	39426981	Missense_Mutation	SNP	C	T	12	47	c.325G>A	c.(325-327)GAC>AAC	p.D109N
Pat_76	Pre-Treatment	DSCAM	1826	37	21	41450781	41450781	Missense_Mutation	SNP	G	A	14	19	c.4544C>T	c.(4543-4545)CCC>CTC	p.P1515L
Pat_76	Pre-Treatment	DSCAM	1826	37	21	41455916	41455916	Missense_Mutation	SNP	G	A	20	32	c.4150C>T	c.(4150-4152)CGG>TGG	p.R1384W
Pat_76	Pre-Treatment	FAM3B	54097	37	21	42694883	42694883	Missense_Mutation	SNP	C	T	26	46	c.53C>T	c.(52-54)TCC>TTC	p.S18F
Pat_76	Pre-Treatment	PRDM15	63977	37	21	43279315	43279315	Missense_Mutation	SNP	C	T	3	63	c.1054G>A	c.(1054-1056)GTG>ATG	p.V352M
Pat_76	Pre-Treatment	PRDM15	63977	37	21	43299455	43299455	Missense_Mutation	SNP	G	A	15	25	c.26C>T	c.(25-27)TCC>TTC	p.S9F

Pat_76	Pre-Treatment	CBS	875	37	21	44483104	44483104	Missense_Mutation	SNP	C	T	4	124	c.913G>A	c.(913-915)GGG>AGG	p.G305R
Pat_76	Pre-Treatment	CRYAA	1409	37	21	44590730	44590730	Missense_Mutation	SNP	G	A	40	50	c.293G>A	c.(292-294)GGA>GAA	p.G98E
Pat_76	Pre-Treatment	SIK1	150094	37	21	44838191	44838191	Missense_Mutation	SNP	G	A	29	28	c.1693C>T	c.(1693-1695)CCT>TCT	p.P565S
Pat_76	Pre-Treatment	RRP1	8568	37	21	45217545	45217546	Missense_Mutation	DNP	CC	TT	41	98	c.586_587CC>TT	c.(586-588)CCC>TTC	p.P196F
Pat_76	Pre-Treatment	C21orf29	54084	37	21	45987779	45987779	Missense_Mutation	SNP	C	T	20	31	c.193G>A	c.(193-195)GCC>ACC	p.A65T
Pat_76	Pre-Treatment	KRTAP10-4	386672	37	21	45994771	45994771	Missense_Mutation	SNP	C	T	33	53	c.1136C>T	c.(1135-1137)TCC>TTC	p.S379F
Pat_76	Pre-Treatment	COL6A1	1291	37	21	47418068	47418069	Missense_Mutation	DNP	GG	AA	11	16	.1558_1559GG>A	c.(1558-1560)GGC>AAC	p.G520N
Pat_76	Pre-Treatment	COL6A1	1291	37	21	47421963	47421963	Missense_Mutation	SNP	G	A	4	15	c.2045G>A	c.(2044-2046)CGG>CAG	p.R682Q
Pat_76	Pre-Treatment	COL6A2	1292	37	21	47532283	47532283	Missense_Mutation	SNP	C	T	8	12	c.506C>T	c.(505-507)CCC>CTC	p.P169L
Pat_76	Pre-Treatment	LSS	4047	37	21	47633739	47633739	Missense_Mutation	SNP	G	A	14	19	c.1022C>T	c.(1021-1023)ACC>ATC	p.T341I
Pat_76	Pre-Treatment	PCNT	5116	37	21	47769597	47769598	Splice_Site	DNP	GG	AA	28	53	c.1208_splice	c.e8-1	p.R403_splice
Pat_76	Pre-Treatment	PCNT	5116	37	21	47817270	47817270	Missense_Mutation	SNP	G	A	11	32	c.4308G>A	c.(4306-4308)ATG>ATA	p.M1436I
Pat_76	Pre-Treatment	DIP2A	23181	37	21	47981665	47981665	Missense_Mutation	SNP	C	T	91	168	c.4036C>T	c.(4036-4038)CGT>TGT	p.R1346C
Pat_76	Pre-Treatment	POTEH	23784	37	22	16267070	16267070	Missense_Mutation	SNP	C	T	48	456	c.1379G>A	c.(1378-1380)GGA>GAA	p.G460E
Pat_76	Pre-Treatment	POTEH	23784	37	22	16279222	16279222	Missense_Mutation	SNP	T	A	50	483	c.1001A>T	c.(1000-1002)AAT>ATT	p.N334I
Pat_76	Pre-Treatment	OR11H1	81061	37	22	16449102	16449102	Missense_Mutation	SNP	G	A	71	111	c.703C>T	c.(703-705)CTT>TTT	p.L235F
Pat_76	Pre-Treatment	RTDR1	27156	37	22	23401774	23401774	Missense_Mutation	SNP	C	T	45	16	c.913G>A	c.(913-915)GGC>AGC	p.G305S
Pat_76	Pre-Treatment	RAB36	9609	37	22	23495309	23495309	Missense_Mutation	SNP	A	T	71	75	c.515A>T	c.(514-516)TAT>TTT	p.Y172F
Pat_76	Pre-Treatment	MMP11	4320	37	22	24124425	24124425	Nonsense_Mutation	SNP	G	A	43	69	c.1088G>A	c.(1087-1089)TGG>TAG	p.W363*
Pat_76	Pre-Treatment	GGT1	2678	37	22	25023398	25023398	Splice_Site	SNP	G	A	25	40	c.1021_splice	c.e12-1	p.V341_splice
Pat_76	Pre-Treatment	MYO18B	84700	37	22	26351183	26351183	Missense_Mutation	SNP	G	A	6	7	c.6009G>A	c.(6007-6009)ATG>ATA	p.M2003I
Pat_76	Pre-Treatment	RFPL1	5988	37	22	29837650	29837650	Missense_Mutation	SNP	G	A	4	104	c.493G>A	c.(493-495)GTG>ATG	p.V165M
Pat_76	Pre-Treatment	CABP7	164633	37	22	30125183	30125183	Missense_Mutation	SNP	C	T	4	4	c.506C>T	c.(505-507)CCC>CTC	p.P169L
Pat_76	Pre-Treatment	SEC14L3	266629	37	22	30863013	30863013	Missense_Mutation	SNP	C	T	53	98	c.475G>A	c.(475-477)GGA>AGA	p.G159R
Pat_76	Pre-Treatment	NCF4	4689	37	22	37261013	37261013	Missense_Mutation	SNP	G	A	24	46	c.170G>A	c.(169-171)CGC>CAC	p.R57H
Pat_76	Pre-Treatment	TMPRSS6	164656	37	22	37499418	37499418	Missense_Mutation	SNP	C	T	43	55	c.67G>A	c.(67-69)GGG>AGG	p.G23R
Pat_76	Pre-Treatment	TRIOBP	11078	37	22	38120224	38120224	Missense_Mutation	SNP	C	T	60	164	c.1661C>T	c.(1660-1662)GCC>GTC	p.A554V
Pat_76	Pre-Treatment	TRIOBP	11078	37	22	38131325	38131326	Missense_Mutation	DNP	CC	TT	10	17	.4982_4983CC>T	c.(4981-4983)TCC>TTT	p.S1661F
Pat_76	Pre-Treatment	TAB1	10454	37	22	39822888	39822888	Missense_Mutation	SNP	C	T	22	33	c.1102C>T	c.(1102-1104)CCG>TCG	p.P368S
Pat_76	Pre-Treatment	CACNA1I	8911	37	22	40069069	40069069	Missense_Mutation	SNP	G	A	44	84	c.4765G>A	c.(4765-4767)GTT>ATT	p.V1589I
Pat_76	Pre-Treatment	EP300	2033	37	22	41556727	41556727	Splice_Site	SNP	G	A	4	62	c.3671_splice	c.e20+1	p.T1224_splice
Pat_76	Pre-Treatment	ACO2	50	37	22	41923334	41923334	Missense_Mutation	SNP	G	A	4	32	c.1996G>A	c.(1996-1998)GGC>AGC	p.G666S
Pat_76	Pre-Treatment	XRCC6	2547	37	22	42053023	42053023	Missense_Mutation	SNP	C	T	8	17	c.1408C>T	c.(1408-1410)CGC>TGC	p.R470C
Pat_76	Pre-Treatment	WNT7B	7477	37	22	46345835	46345835	Missense_Mutation	SNP	C	T	24	27	c.263G>A	c.(262-264)GGC>GAC	p.G88D
Pat_76	Pre-Treatment	SAPS2	9701	37	22	50875947	50875947	Missense_Mutation	SNP	T	C	3	48	c.1696T>C	c.(1696-1698)TAC>CAC	p.Y566H
Pat_76	Pre-Treatment	CNTN4	152330	37	3	3081778	3081778	Missense_Mutation	SNP	C	T	28	65	c.2221C>T	c.(2221-2223)CCC>TCC	p.P741S
Pat_76	Pre-Treatment	IL5RA	3568	37	3	3139668	3139668	Missense_Mutation	SNP	G	A	35	78	c.595C>T	c.(595-597)CCC>TCC	p.P199S
Pat_76	Pre-Treatment	ITPR1	3708	37	3	4735393	4735393	Missense_Mutation	SNP	C	T	11	32	c.4222C>T	c.(4222-4224)CGC>TGC	p.R1408C
Pat_76	Pre-Treatment	EDEM1	9695	37	3	5229995	5229995	Missense_Mutation	SNP	G	A	12	20	c.505G>A	c.(505-507)GAC>AAC	p.D169N
Pat_76	Pre-Treatment	CAMK1	8536	37	3	9803367	9803367	Missense_Mutation	SNP	C	T	64	36	c.504G>A	c.(502-504)ATG>ATA	p.M168I
Pat_76	Pre-Treatment	RPUSD3	285367	37	3	9883915	9883915	Missense_Mutation	SNP	G	A	8	435	c.275C>T	c.(274-276)ACG>ATG	p.T92M
Pat_76	Pre-Treatment	PPARG	5468	37	3	12458228	12458228	Missense_Mutation	SNP	C	T	17	28	c.845C>T	c.(844-846)TCC>TTC	p.S282F
Pat_76	Pre-Treatment	NUP210	23225	37	3	13378363	13378363	Missense_Mutation	SNP	T	C	38	106	c.3608A>G	c.(3607-3609)AAT>AGT	p.N1203S
Pat_76	Pre-Treatment	GRIP2	80852	37	3	14561732	14561732	Missense_Mutation	SNP	C	T	24	10	c.1206G>A	c.(1204-1206)ATG>ATA	p.M402I
Pat_76	Pre-Treatment	FGD5	152273	37	3	14861563	14861563	Missense_Mutation	SNP	C	T	9	61	c.985C>T	c.(985-987)CCT>TCT	p.P329S
Pat_76	Pre-Treatment	PLCL2	23228	37	3	17051292	17051292	Missense_Mutation	SNP	G	A	32	24	c.430G>A	c.(430-432)GTT>ATT	p.V144I
Pat_76	Pre-Treatment	EFHB	151651	37	3	19974997	19974997	Missense_Mutation	SNP	C	T	82	51	c.514G>A	c.(514-516)GAA>AAA	p.E172K

Pat_76	Pre-Treatment	TOP2B	7155	37	3	25639883	25639883	Missense_Mutation	SNP	C	T	4	137	c.4781G>A	c.(4780-4782)CGA>CAA	p.R1594Q
Pat_76	Pre-Treatment	SLC4A7	9497	37	3	27475470	27475470	Missense_Mutation	SNP	G	A	127	104	c.688C>T	c.(688-690)CTT>TTT	p.L230F
Pat_76	Pre-Treatment	OSBPL10	114884	37	3	31725572	31725572	Missense_Mutation	SNP	G	C	41	32	c.1280C>G	c.(1279-1281)TCT>TGT	p.S427C
Pat_76	Pre-Treatment	CNOT10	25904	37	3	32776347	32776347	Missense_Mutation	SNP	C	T	108	299	c.1393C>T	c.(1393-1395)CTC>TTC	p.L465F
Pat_76	Pre-Treatment	GLB1	2720	37	3	33109736	33109736	Missense_Mutation	SNP	C	T	4	140	c.443G>A	c.(442-444)CGC>CAC	p.R148H
Pat_76	Pre-Treatment	ARPP21	10777	37	3	35730819	35730819	Missense_Mutation	SNP	G	A	73	40	c.427G>A	c.(427-429)GAT>AAT	p.D143N
Pat_76	Pre-Treatment	ITGA9	3680	37	3	37783285	37783285	Missense_Mutation	SNP	C	T	17	27	c.2299C>T	c.(2299-2301)CAC>TAC	p.H767Y
Pat_76	Pre-Treatment	DLEC1	9940	37	3	38150967	38150967	Missense_Mutation	SNP	G	A	20	96	c.3174G>A	c.(3172-3174)ATG>ATA	p.M1058I
Pat_76	Pre-Treatment	SCN5A	6331	37	3	38592468	38592468	Missense_Mutation	SNP	C	T	32	18	c.5395G>A	c.(5395-5397)GAG>AAG	p.E1799K
Pat_76	Pre-Treatment	SCN10A	6336	37	3	38739493	38739493	Missense_Mutation	SNP	C	T	55	25	c.5218G>A	c.(5218-5220)GAC>AAC	p.D1740N
Pat_76	Pre-Treatment	CSRNP1	64651	37	3	39185196	39185196	Missense_Mutation	SNP	G	A	13	31	c.1120C>T	c.(1120-1122)CAC>TAC	p.H374Y
Pat_76	Pre-Treatment	CCR8	1237	37	3	39374813	39374813	Missense_Mutation	SNP	C	G	5	115	c.991C>G	c.(991-993)CCT>GCT	p.P331A
Pat_76	Pre-Treatment	LYZL4	131375	37	3	42448635	42448635	Missense_Mutation	SNP	C	T	9	36	c.109G>A	c.(109-111)GAT>AAT	p.D37N
Pat_76	Pre-Treatment	KBTBD5	131377	37	3	42727237	42727237	Missense_Mutation	SNP	G	A	4	63	c.127G>A	c.(127-129)GAG>AAG	p.E43K
Pat_76	Pre-Treatment	HHATL	57467	37	3	42735116	42735116	Missense_Mutation	SNP	C	T	22	8	c.1241G>A	c.(1240-1242)CGA>CAA	p.R414Q
Pat_76	Pre-Treatment	SNRK	54861	37	3	43389492	43389492	Missense_Mutation	SNP	G	A	4	134	c.1741G>A	c.(1741-1743)GGG>AGG	p.G581R
Pat_76	Pre-Treatment	LIMD1	8994	37	3	45636586	45636586	Missense_Mutation	SNP	G	A	3	32	c.215G>A	c.(214-216)AGG>AAG	p.R72K
Pat_76	Pre-Treatment	SACM1L	22908	37	3	45780142	45780142	Missense_Mutation	SNP	C	A	14	43	c.1455C>A	c.(1453-1455)AAC>AAA	p.N485K
Pat_76	Pre-Treatment	SACM1L	22908	37	3	45780147	45780148	Missense_Mutation	DNP	CC	TT	12	43	.1460_1461CC>T	c.(1459-1461)TCC>TTT	p.S487F
Pat_76	Pre-Treatment	LTF	4057	37	3	46485049	46485049	Missense_Mutation	SNP	G	A	6	197	c.1538C>T	c.(1537-1539)GCC>GTC	p.A513V
Pat_76	Pre-Treatment	LRRC2	79442	37	3	46592991	46592991	Missense_Mutation	SNP	C	T	76	58	c.91G>A	c.(91-93)GAG>AAG	p.E31K
Pat_76	Pre-Treatment	PLXNB1	5364	37	3	48456394	48456395	Missense_Mutation	DNP	GG	AA	71	57	.4022_4023CC>T	c.(4021-4023)GCC>GTT	p.A1341V
Pat_76	Pre-Treatment	CCDC51	79714	37	3	48474195	48474195	Missense_Mutation	SNP	C	T	47	125	c.859G>A	c.(859-861)GGT>AGT	p.G287S
Pat_76	Pre-Treatment	CELSR3	1951	37	3	48677662	48677662	Missense_Mutation	SNP	C	T	5	67	c.9356G>A	c.(9355-9357)AGC>AAC	p.S3119N
Pat_76	Pre-Treatment	QARS	5859	37	3	49135820	49135820	Missense_Mutation	SNP	G	A	42	111	c.2050C>T	c.(2050-2052)CCT>TCT	p.P684S
Pat_76	Pre-Treatment	QARS	5859	37	3	49136632	49136632	Missense_Mutation	SNP	C	A	4	97	c.1669G>T	c.(1669-1671)GTG>TTG	p.V557L
Pat_76	Pre-Treatment	BSN	8927	37	3	49698400	49698400	Missense_Mutation	SNP	C	T	4	58	c.9122C>T	c.(9121-9123)GCT>GTT	p.A3041V
Pat_76	Pre-Treatment	UBA7	7318	37	3	49845201	49845201	Missense_Mutation	SNP	G	A	4	67	c.2683C>T	c.(2683-2685)CGC>TGC	p.R895C
Pat_76	Pre-Treatment	DOCK3	1795	37	3	51297699	51297699	Missense_Mutation	SNP	C	T	4	47	c.2297C>T	c.(2296-2298)TCC>TTC	p.S766F
Pat_76	Pre-Treatment	TNNC1	7134	37	3	52485442	52485442	Missense_Mutation	SNP	C	T	42	23	c.419G>A	c.(418-420)GGA>GAA	p.G140E
Pat_76	Pre-Treatment	CACNA1D	776	37	3	53699804	53699804	Missense_Mutation	SNP	G	A	16	37	c.884G>A	c.(883-885)GGA>GAA	p.G295E
Pat_76	Pre-Treatment	CACNA1D	776	37	3	53835242	53835242	Missense_Mutation	SNP	G	A	49	33	c.5198G>A	c.(5197-5199)GGA>GAA	p.G1733E
Pat_76	Pre-Treatment	CACNA2D3	55799	37	3	54925456	54925456	Missense_Mutation	SNP	G	A	4	110	c.2225G>A	c.(2224-2226)GGG>GAG	p.G742E
Pat_76	Pre-Treatment	ERC2	26059	37	3	55768858	55768858	Missense_Mutation	SNP	C	T	11	34	c.2653G>A	c.(2653-2655)GAA>AAA	p.E885K
Pat_76	Pre-Treatment	ERC2	26059	37	3	55984533	55984533	Missense_Mutation	SNP	C	T	16	65	c.2323G>A	c.(2323-2325)GAA>AAA	p.E775K
Pat_76	Pre-Treatment	CCDC66	285331	37	3	56627597	56627597	Nonsense_Mutation	SNP	C	T	32	32	c.1147C>T	c.(1147-1149)CAG>TAG	p.Q383*
Pat_76	Pre-Treatment	HESX1	8820	37	3	57232472	57232472	Missense_Mutation	SNP	C	T	36	35	c.406G>A	c.(406-408)GAT>AAT	p.D136N
Pat_76	Pre-Treatment	FLNB	2317	37	3	58109342	58109342	Missense_Mutation	SNP	C	T	90	47	c.3649C>T	c.(3649-3651)CCC>TCC	p.P1217S
Pat_76	Pre-Treatment	DNASE1L3	1776	37	3	58191217	58191217	Nonsense_Mutation	SNP	G	A	75	77	c.301C>T	c.(301-303)CAA>TAA	p.Q101*
Pat_76	Pre-Treatment	LMOD3	56203	37	3	69168079	69168079	Missense_Mutation	SNP	G	A	4	78	c.1427C>T	c.(1426-1428)CCG>CTG	p.P476L
Pat_76	Pre-Treatment	EPHA3	2042	37	3	89499331	89499331	Missense_Mutation	SNP	T	G	19	41	c.2501T>G	c.(2500-2502)ATT>AGT	p.I834S
Pat_76	Pre-Treatment	PROS1	5627	37	3	93646102	93646102	Missense_Mutation	SNP	G	A	48	120	c.226C>T	c.(226-228)CCG>TCG	p.P76S
Pat_76	Pre-Treatment	OR5H14	403273	37	3	97868560	97868560	Missense_Mutation	SNP	G	A	91	283	c.331G>A	c.(331-333)GAA>AAA	p.E111K
Pat_76	Pre-Treatment	OR5H15	403274	37	3	97888271	97888271	Missense_Mutation	SNP	C	G	46	54	c.728C>G	c.(727-729)GCC>GGC	p.A243G
Pat_76	Pre-Treatment	GPR128	84873	37	3	100349614	100349614	Missense_Mutation	SNP	G	A	52	27	c.295G>A	c.(295-297)GGA>AGA	p.G99R
Pat_76	Pre-Treatment	IMPG2	50939	37	3	101038529	101038529	Missense_Mutation	SNP	C	T	51	148	c.233G>A	c.(232-234)AGA>AAA	p.R78K
Pat_76	Pre-Treatment	ZPLD1	131368	37	3	102187971	102187971	Missense_Mutation	SNP	C	T	66	117	c.925C>T	c.(925-927)CTT>TTT	p.L309F

Pat_76	Pre-Treatment	CCDC54	84692	37	3	107096863	107096864	Missense_Mutation	DNP	GG	AA	49	32	c.429_430GG>AA	427-432)CTGGAA>CTAA	p.E144K
Pat_76	Pre-Treatment	MYH15	22989	37	3	108110641	108110641	Missense_Mutation	SNP	C	T	139	105	c.5456G>A	c.(5455-5457)GGG>GAG	p.G1819E
Pat_76	Pre-Treatment	MYH15	22989	37	3	108149702	108149702	Nonsense_Mutation	SNP	G	A	41	58	c.3349C>T	c.(3349-3351)CAG>TAG	p.Q1117*
Pat_76	Pre-Treatment	MYH15	22989	37	3	108218318	108218318	Nonsense_Mutation	SNP	G	A	42	47	c.568C>T	c.(568-570)CAG>TAG	p.Q190*
Pat_76	Pre-Treatment	CD96	10225	37	3	111263955	111263955	Missense_Mutation	SNP	A	C	56	118	c.124A>C	c.(124-126)AAC>CAC	p.N42H
Pat_76	Pre-Treatment	TMPRSS7	344805	37	3	111793194	111793194	Missense_Mutation	SNP	G	A	110	51	c.1340G>A	c.(1339-1341)AGG>AAG	p.R447K
Pat_76	Pre-Treatment	CCDC80	151887	37	3	112357513	112357513	Missense_Mutation	SNP	G	A	33	94	c.1240C>T	c.(1240-1242)CTT>TTT	p.L414F
Pat_76	Pre-Treatment	ZNF80	7634	37	3	113955513	113955513	Missense_Mutation	SNP	C	T	24	56	c.409G>A	c.(409-411)GAG>AAG	p.E137K
Pat_76	Pre-Treatment	HGD	3081	37	3	120371486	120371486	Missense_Mutation	SNP	G	A	12	28	c.295C>T	c.(295-297)CCA>TCA	p.P99S
Pat_76	Pre-Treatment	RABL3	285282	37	3	120449568	120449568	Missense_Mutation	SNP	G	A	73	72	c.113C>T	c.(112-114)ACT>ATT	p.T38I
Pat_76	Pre-Treatment	GOLGB1	2804	37	3	121409852	121409852	Missense_Mutation	SNP	C	T	24	62	c.8344G>A	c.(8344-8346)GAT>AAT	p.D2782N
Pat_76	Pre-Treatment	PARP15	165631	37	3	122336009	122336009	Missense_Mutation	SNP	C	T	46	126	c.998C>T	c.(997-999)TCA>TTA	p.S333L
Pat_76	Pre-Treatment	MYLK	4638	37	3	123452812	123452812	Missense_Mutation	SNP	G	A	37	82	c.1031C>T	c.(1030-1032)TCC>TTC	p.S344F
Pat_76	Pre-Treatment	KALRN	8997	37	3	124053179	124053179	Missense_Mutation	SNP	C	T	41	138	c.1478C>T	c.(1477-1479)TCC>TTC	p.S493F
Pat_76	Pre-Treatment	SLC12A8	84561	37	3	124909340	124909340	Nonsense_Mutation	SNP	C	T	85	251	c.77G>A	c.(76-78)TGG>TAG	p.W26*
Pat_76	Pre-Treatment	MCM2	4171	37	3	127336204	127336205	Missense_Mutation	DNP	CC	TT	40	21	.1856_1857CC>T	c.(1855-1857)TCC>TTT	p.S619F
Pat_76	Pre-Treatment	DNAJB8	165721	37	3	128181833	128181833	Missense_Mutation	SNP	G	A	19	60	c.256C>T	c.(256-258)CCC>TCC	p.P86S
Pat_76	Pre-Treatment	TOPBP1	11073	37	3	133358805	133358806	Missense_Mutation	DNP	TC	AT	16	60	.2230_2231GA>A	c.(2230-2232)GAA>ATA	p.E744I
Pat_76	Pre-Treatment	KY	339855	37	3	134366318	134366318	Missense_Mutation	SNP	C	T	13	23	c.158G>A	c.(157-159)GGA>GAA	p.G53E
Pat_76	Pre-Treatment	EPHB1	2047	37	3	134670519	134670519	Missense_Mutation	SNP	G	A	49	107	c.430G>A	c.(430-432)GAG>AAG	p.E144K
Pat_76	Pre-Treatment	PPP2R3A	5523	37	3	135720516	135720516	Missense_Mutation	SNP	C	T	25	22	c.176C>T	c.(175-177)CCT>CTT	p.P59L
Pat_76	Pre-Treatment	NCK1	4690	37	3	136664562	136664562	Missense_Mutation	SNP	G	A	135	77	c.364G>A	c.(364-366)GAG>AAG	p.E122K
Pat_76	Pre-Treatment	COPB2	9276	37	3	139097898	139097898	Missense_Mutation	SNP	T	C	57	129	c.346A>G	c.(346-348)ACT>GCT	p.T116A
Pat_76	Pre-Treatment	TRIM42	287015	37	3	140401461	140401461	Missense_Mutation	SNP	G	A	51	139	c.499G>A	c.(499-501)GAG>AAG	p.E167K
Pat_76	Pre-Treatment	TRIM42	287015	37	3	140406746	140406746	Missense_Mutation	SNP	G	A	71	37	c.1222G>A	c.(1222-1224)GAA>AAA	p.E408K
Pat_76	Pre-Treatment	ATR	545	37	3	142254048	142254048	Splice_Site	SNP	C	T	41	24	c.3820_splice	c.e21-1	p.E1274_splice
Pat_76	Pre-Treatment	PLS1	5357	37	3	142388285	142388285	Missense_Mutation	SNP	G	A	52	133	c.124G>A	c.(124-126)GAA>AAA	p.E42K
Pat_76	Pre-Treatment	TRPC1	7220	37	3	142521065	142521065	Missense_Mutation	SNP	C	T	38	41	c.1636C>T	c.(1636-1638)CTT>TTT	p.L546F
Pat_76	Pre-Treatment	MED12L	116931	37	3	151067889	151067889	Missense_Mutation	SNP	C	T	158	398	c.2188C>T	c.(2188-2190)CTC>TTC	p.L730F
Pat_76	Pre-Treatment	IGSF10	285313	37	3	151161477	151161477	Missense_Mutation	SNP	T	G	38	64	c.5258A>C	c.(5257-5259)AAA>ACA	p.K1753T
Pat_76	Pre-Treatment	PLCH1	23007	37	3	155267673	155267673	Missense_Mutation	SNP	C	T	58	41	c.1229G>A	c.(1228-1230)GGA>GAA	p.G410E
Pat_76	Pre-Treatment	C3orf33	285315	37	3	155485353	155485353	Missense_Mutation	SNP	A	T	20	12	c.299T>A	c.(298-300)TTC>TAC	p.F100Y
Pat_76	Pre-Treatment	SLC33A1	9197	37	3	155571045	155571045	Nonsense_Mutation	SNP	G	A	54	30	c.742C>T	c.(742-744)CAG>TAG	p.Q248*
Pat_76	Pre-Treatment	OTOL1	131149	37	3	161221642	161221642	Nonsense_Mutation	SNP	G	A	19	54	c.1346G>A	c.(1345-1347)TGG>TAG	p.W449*
Pat_76	Pre-Treatment	SERPINI2	5276	37	3	167189461	167189461	Missense_Mutation	SNP	C	A	4	82	c.162G>T	c.(160-162)TTG>TTT	p.L54F
Pat_76	Pre-Treatment	MECOM	2122	37	3	168834150	168834150	Missense_Mutation	SNP	G	A	50	46	c.946C>T	c.(946-948)CCT>TCT	p.P316S
Pat_76	Pre-Treatment	MECOM	2122	37	3	168834203	168834203	Missense_Mutation	SNP	C	G	55	42	c.893G>C	c.(892-894)GGA>GCA	p.G298A
Pat_76	Pre-Treatment	MECOM	2122	37	3	169098985	169098985	Missense_Mutation	SNP	T	A	33	36	c.365A>T	c.(364-366)TAT>TTT	p.Y122F
Pat_76	Pre-Treatment	SKIL	6498	37	3	170078829	170078829	Missense_Mutation	SNP	G	A	74	51	c.710G>A	c.(709-711)CGA>CAA	p.R237Q
Pat_76	Pre-Treatment	TNIK	23043	37	3	170912402	170912402	Missense_Mutation	SNP	G	A	6	307	c.329C>T	c.(328-330)GCT>GTT	p.A110V
Pat_76	Pre-Treatment	FNDC3B	64778	37	3	172061986	172061986	Missense_Mutation	SNP	G	A	6	308	c.2188G>A	c.(2188-2190)GTC>ATC	p.V730I
Pat_76	Pre-Treatment	MFN1	55669	37	3	179093044	179093044	Missense_Mutation	SNP	G	A	4	76	c.1012G>A	c.(1012-1014)GAA>AAA	p.E338K
Pat_76	Pre-Treatment	YEATS2	55689	37	3	183469945	183469945	Missense_Mutation	SNP	C	T	128	90	c.1054C>T	c.(1054-1056)CCT>TCT	p.P352S
Pat_76	Pre-Treatment	CLCN2	1181	37	3	184069842	184069842	Missense_Mutation	SNP	G	A	90	243	c.2374C>T	c.(2374-2376)CCT>TCT	p.P792S
Pat_76	Pre-Treatment	MASP1	5648	37	3	186961374	186961374	Missense_Mutation	SNP	C	T	87	60	c.1126G>A	c.(1126-1128)GGG>AGG	p.G376R
Pat_76	Pre-Treatment	LEPREL1	55214	37	3	189706753	189706753	Missense_Mutation	SNP	G	A	71	46	c.898C>T	c.(898-900)CCC>TCC	p.P300S
Pat_76	Pre-Treatment	ATP13A4	84239	37	3	193120506	193120506	Missense_Mutation	SNP	G	A	51	105	c.3526C>T	c.(3526-3528)CCG>TCG	p.P1176S

Pat_76	Pre-Treatment	ATP13A4	84239	37	3	193158390	193158390	Missense_Mutation	SNP	G	A	50	47	c.2476C>T	c.(2476-2478)CCT>TCT	p.P826S
Pat_76	Pre-Treatment	SDHAP1	255812	37	3	195701278	195701278	Missense_Mutation	SNP	C	T	4	79	c.586G>A	c.(586-588)GTG>ATG	p.V196M
Pat_76	Pre-Treatment	OSTalpha	200931	37	3	195943586	195943586	Missense_Mutation	SNP	G	A	9	4	c.3G>A	c.(1-3)ATG>ATA	p.M1I
Pat_76	Pre-Treatment	PDE6B	5158	37	4	654259	654259	Missense_Mutation	SNP	G	A	9	16	c.1471G>A	c.(1471-1473)GAG>AAG	p.E491K
Pat_76	Pre-Treatment	TMEM175	84286	37	4	946167	946167	Missense_Mutation	SNP	G	A	39	74	c.391G>A	c.(391-393)GTG>ATG	p.V131M
Pat_76	Pre-Treatment	WHSC2	7469	37	4	1991456	1991456	Missense_Mutation	SNP	G	A	5	315	c.556C>T	c.(556-558)CGG>TGG	p.R186W
Pat_76	Pre-Treatment	ADD1	118	37	4	2901008	2901008	Missense_Mutation	SNP	G	A	4	97	c.1007G>A	c.(1006-1008)GGA>GAA	p.G336E
Pat_76	Pre-Treatment	OTOP1	133060	37	4	4207848	4207848	Missense_Mutation	SNP	G	A	12	29	c.550C>T	c.(550-552)CTT>TTT	p.L184F
Pat_76	Pre-Treatment	MAN2B2	23324	37	4	6590881	6590881	Missense_Mutation	SNP	C	T	20	39	c.674C>T	c.(673-675)TCC>TTC	p.S225F
Pat_76	Pre-Treatment	AFAP1	60312	37	4	7776536	7776537	Missense_Mutation	DNP	GG	CT	30	25	.1739_1740CC>A	c.(1738-1740)GCC>GAG	p.A580E
Pat_76	Pre-Treatment	BOD1L	259282	37	4	13601911	13601911	Missense_Mutation	SNP	G	A	15	14	c.6613C>T	c.(6613-6615)CTT>TTT	p.L2205F
Pat_76	Pre-Treatment	SLIT2	9353	37	4	20620619	20620619	Missense_Mutation	SNP	G	A	35	55	c.4577G>A	c.(4576-4578)AGG>AAG	p.R1526K
Pat_76	Pre-Treatment	PPARGC1A	10891	37	4	23814447	23814447	Missense_Mutation	SNP	C	T	72	115	c.1942G>A	c.(1942-1944)GAA>AAA	p.E648K
Pat_76	Pre-Treatment	DHX15	1665	37	4	24542469	24542469	Missense_Mutation	SNP	G	A	16	11	c.1588C>T	c.(1588-1590)CCA>TCA	p.P530S
Pat_76	Pre-Treatment	SEL1L3	23231	37	4	25849106	25849106	Nonsense_Mutation	SNP	G	T	4	53	c.543C>A	c.(541-543)TAC>TAA	p.Y181*
Pat_76	Pre-Treatment	ARAP2	116984	37	4	36149359	36149359	Missense_Mutation	SNP	G	A	5	12	c.3010C>T	c.(3010-3012)CCC>TCC	p.P1004S
Pat_76	Pre-Treatment	KLF3	51274	37	4	38690651	38690651	Missense_Mutation	SNP	C	T	4	64	c.503C>T	c.(502-504)TCC>TTC	p.S168F
Pat_76	Pre-Treatment	RBM47	54502	37	4	40439863	40439863	Missense_Mutation	SNP	C	T	19	32	c.1048G>A	c.(1048-1050)GAC>AAC	p.D350N
Pat_76	Pre-Treatment	BEND4	389206	37	4	42119560	42119560	Missense_Mutation	SNP	C	T	4	6	c.1580G>A	c.(1579-1581)AGT>AAT	p.S527N
Pat_76	Pre-Treatment	ATP8A1	10396	37	4	42577653	42577653	Missense_Mutation	SNP	C	T	86	149	c.1192G>A	c.(1192-1194)GAG>AAG	p.E398K
Pat_76	Pre-Treatment	GABRA2	2555	37	4	46314655	46314655	Nonsense_Mutation	SNP	G	A	12	15	c.334C>T	c.(334-336)CGA>TGA	p.R112*
Pat_76	Pre-Treatment	GABRB1	2560	37	4	47405358	47405358	Missense_Mutation	SNP	G	A	24	60	c.568G>A	c.(568-570)GAA>AAA	p.E190K
Pat_76	Pre-Treatment	REST	5978	37	4	57797533	57797533	Missense_Mutation	SNP	C	T	48	80	c.2509C>T	c.(2509-2511)CTT>TTT	p.L837F
Pat_76	Pre-Treatment	UGT2A3	79799	37	4	69796394	69796394	Missense_Mutation	SNP	G	A	41	33	c.1174C>T	c.(1174-1176)CCC>TCC	p.P392S
Pat_76	Pre-Treatment	UGT2B11	10720	37	4	70079869	70079869	Missense_Mutation	SNP	G	A	25	40	c.572C>T	c.(571-573)CCT>CTT	p.P191L
Pat_76	Pre-Treatment	UGT2B11	10720	37	4	70080370	70080370	Missense_Mutation	SNP	C	T	143	255	c.71G>A	c.(70-72)GGA>GAA	p.G24E
Pat_76	Pre-Treatment	UGT2A1	10941	37	4	70455112	70455112	Missense_Mutation	SNP	C	T	7	11	c.1562G>A	c.(1561-1563)GGA>GAA	p.G521E
Pat_76	Pre-Treatment	SLC4A4	8671	37	4	72215790	72215790	Splice_Site	SNP	G	A	4	76	c.550_splice	c.e5+1	p.E184_splice
Pat_76	Pre-Treatment	ADAMTS3	9508	37	4	73414436	73414436	Missense_Mutation	SNP	C	T	23	42	c.263G>A	c.(262-264)GGA>GAA	p.G88E
Pat_76	Pre-Treatment	ANKRD17	26057	37	4	73956389	73956389	Missense_Mutation	SNP	G	A	35	70	c.6956C>T	c.(6955-6957)CCC>CTC	p.P2319L
Pat_76	Pre-Treatment	PPEF2	5470	37	4	76811183	76811183	Missense_Mutation	SNP	G	A	6	176	c.344C>T	c.(343-345)ACG>ATG	p.T115M
Pat_76	Pre-Treatment	RASGEF1B	153020	37	4	82377830	82377830	Missense_Mutation	SNP	G	A	9	10	c.413C>T	c.(412-414)GCT>GTT	p.A138V
Pat_76	Pre-Treatment	AGPAT9	84803	37	4	84502813	84502813	Missense_Mutation	SNP	G	A	42	68	c.307G>A	c.(307-309)GGA>AGA	p.G103R
Pat_76	Pre-Treatment	FAM13A	10144	37	4	89679958	89679958	Missense_Mutation	SNP	G	A	31	40	c.1673C>T	c.(1672-1674)TCC>TTC	p.S558F
Pat_76	Pre-Treatment	MMRN1	22915	37	4	90856152	90856152	Missense_Mutation	SNP	C	A	5	149	c.1321C>A	c.(1321-1323)CAA>AAA	p.Q441K
Pat_76	Pre-Treatment	BMPR1B	658	37	4	96052444	96052444	Missense_Mutation	SNP	C	T	14	21	c.857C>T	c.(856-858)TCC>TTC	p.S286F
Pat_76	Pre-Treatment	UBE2D3	7323	37	4	103720648	103720648	Missense_Mutation	SNP	G	A	31	43	c.314C>T	c.(313-315)TCC>TTC	p.S105F
Pat_76	Pre-Treatment	TET2	54790	37	4	106156166	106156166	Missense_Mutation	SNP	C	T	25	32	c.1067C>T	c.(1066-1068)TCC>TTC	p.S356F
Pat_76	Pre-Treatment	TET2	54790	37	4	106157650	106157650	Missense_Mutation	SNP	C	T	18	22	c.2551C>T	c.(2551-2553)CCT>TCT	p.P851S
Pat_76	Pre-Treatment	NPNT	255743	37	4	106888470	106888470	Missense_Mutation	SNP	G	A	3	16	c.1471G>A	c.(1471-1473)GGG>AGG	p.G491R
Pat_76	Pre-Treatment	AGXT2L1	64850	37	4	109667970	109667970	Missense_Mutation	SNP	C	T	60	99	c.1120G>A	c.(1120-1122)GAC>AAC	p.D374N
Pat_76	Pre-Treatment	ENPEP	2028	37	4	111397920	111397920	Missense_Mutation	SNP	G	A	4	138	c.350G>A	c.(349-351)GGC>GAC	p.G117D
Pat_76	Pre-Treatment	ANK2	287	37	4	114257821	114257821	Missense_Mutation	SNP	G	A	12	52	c.3680G>A	c.(3679-3681)AGA>AAA	p.R1227K
Pat_76	Pre-Treatment	C4orf31	79625	37	4	121957496	121957496	Missense_Mutation	SNP	C	T	57	66	c.1630G>A	c.(1630-1632)GAT>AAT	p.D544N
Pat_76	Pre-Treatment	KIAA1109	84162	37	4	123237921	123237921	Missense_Mutation	SNP	C	T	36	45	c.10574C>T	c.(10573-10575)GCT>GTT	p.A3525V
Pat_76	Pre-Treatment	FAT4	79633	37	4	126240894	126240894	Missense_Mutation	SNP	G	A	55	84	c.3328G>A	c.(3328-3330)GAA>AAA	p.E1110K
Pat_76	Pre-Treatment	FAT4	79633	37	4	126328272	126328272	Missense_Mutation	SNP	G	A	73	104	c.5545G>A	c.(5545-5547)GAC>AAC	p.D1849N

Pat_76	Pre-Treatment	FAT4	79633	37	4	126329641	126329641	Missense_Mutation	SNP	G	A	54	82	c.5612G>A	c.(5611-5613)GGT>GAT	p.G1871D
Pat_76	Pre-Treatment	PLK4	10733	37	4	128814932	128814933	Missense_Mutation	DNP	CC	TT	72	122	.2458_2459CC>T	c.(2458-2460)CCT>TTT	p.P820F
Pat_76	Pre-Treatment	NAA15	80155	37	4	140291541	140291541	Missense_Mutation	SNP	C	T	4	45	c.1930C>T	c.(1930-1932)CCA>TCA	p.P644S
Pat_76	Pre-Treatment	TBC1D9	23158	37	4	141578759	141578759	Missense_Mutation	SNP	G	A	80	120	c.2129C>T	c.(2128-2130)GCC>GTC	p.A710V
Pat_76	Pre-Treatment	HHIP	64399	37	4	145573802	145573802	Missense_Mutation	SNP	G	A	39	68	c.325G>A	c.(325-327)GAA>AAA	p.E109K
Pat_76	Pre-Treatment	C4orf51	646603	37	4	146650373	146650373	Missense_Mutation	SNP	G	A	8	17	c.419G>A	c.(418-420)GGA>GAA	p.G140E
Pat_76	Pre-Treatment	FBXW7	55294	37	4	153245446	153245446	Missense_Mutation	SNP	G	A	3	29	c.1745C>T	c.(1744-1746)TCG>TTG	p.S582L
Pat_76	Pre-Treatment	ARFIP1	27236	37	4	153809337	153809337	Missense_Mutation	SNP	C	T	4	157	c.844C>T	c.(844-846)CGT>TGT	p.R282C
Pat_76	Pre-Treatment	FHDC1	85462	37	4	153897274	153897274	Missense_Mutation	SNP	C	T	6	20	c.2831C>T	c.(2830-2832)TCC>TTC	p.S944F
Pat_76	Pre-Treatment	KIAA0922	23240	37	4	154556617	154556617	Missense_Mutation	SNP	C	T	4	158	c.4448C>T	c.(4447-4449)CCT>CTT	p.P1483L
Pat_76	Pre-Treatment	DCHS2	54798	37	4	155298497	155298497	Missense_Mutation	SNP	C	T	46	38	c.334G>A	c.(334-336)GAC>AAC	p.D112N
Pat_76	Pre-Treatment	GUCY1A3	2982	37	4	156651237	156651237	Missense_Mutation	SNP	C	T	33	76	c.1927C>T	c.(1927-1929)CCA>TCA	p.P643S
Pat_76	Pre-Treatment	GUCY1B3	2983	37	4	156725790	156725791	Missense_Mutation	DNP	GG	AA	31	86	.1600_1601GG>A	c.(1600-1602)GGA>AAA	p.G534K
Pat_76	Pre-Treatment	GLRB	2743	37	4	158041814	158041814	Missense_Mutation	SNP	G	A	24	45	c.229G>A	c.(229-231)GGC>AGC	p.G77S
Pat_76	Pre-Treatment	GLRB	2743	37	4	158057831	158057831	Missense_Mutation	SNP	G	A	48	69	c.508G>A	c.(508-510)GAT>AAT	p.D170N
Pat_76	Pre-Treatment	DDX60	55601	37	4	169146695	169146696	Missense_Mutation	DNP	GG	AA	30	56	.4665_4666CC>T	663-4668)CTCCCA>CTT	p.P1556S
Pat_76	Pre-Treatment	DDX60	55601	37	4	169223519	169223519	Missense_Mutation	SNP	C	T	12	14	c.655G>A	c.(655-657)GAA>AAA	p.E219K
Pat_76	Pre-Treatment	DDX60L	91351	37	4	169348376	169348376	Missense_Mutation	SNP	G	A	8	16	c.1775C>T	c.(1774-1776)TCT>TTT	p.S592F
Pat_76	Pre-Treatment	MORF4	10934	37	4	174537317	174537317	Missense_Mutation	SNP	C	T	87	96	c.478G>A	c.(478-480)GAT>AAT	p.D160N
Pat_76	Pre-Treatment	MORF4	10934	37	4	174537505	174537505	Missense_Mutation	SNP	G	A	103	137	c.290C>T	c.(289-291)CCT>CTT	p.P97L
Pat_76	Pre-Treatment	ADAM29	11086	37	4	175896821	175896821	Missense_Mutation	SNP	C	T	11	26	c.145C>T	c.(145-147)CCA>TCA	p.P49S
Pat_76	Pre-Treatment	ODZ3	55714	37	4	183600893	183600893	Missense_Mutation	SNP	A	T	46	49	c.1401A>T	c.(1399-1401)AGA>AGT	p.R467S
Pat_76	Pre-Treatment	ODZ3	55714	37	4	183714966	183714966	Missense_Mutation	SNP	C	T	12	13	c.7141C>T	c.(7141-7143)CCT>TCT	p.P2381S
Pat_76	Pre-Treatment	ZFP42	132625	37	4	188924469	188924469	Missense_Mutation	SNP	G	A	53	117	c.508G>A	c.(508-510)GAA>AAA	p.E170K
Pat_76	Pre-Treatment	TRIML1	339976	37	4	189061047	189061047	Missense_Mutation	SNP	G	A	11	19	c.335G>A	c.(334-336)GGA>GAA	p.G112E
Pat_76	Pre-Treatment	SDHA	6389	37	5	225600	225600	Missense_Mutation	SNP	G	A	4	88	c.379G>A	c.(379-381)GTG>ATG	p.V127M
Pat_76	Pre-Treatment	BRD9	65980	37	5	865586	865586	Missense_Mutation	SNP	G	A	37	41	c.1636C>T	c.(1636-1638)CCG>TCG	p.P546S
Pat_76	Pre-Treatment	DNAH5	1767	37	5	13719036	13719036	Missense_Mutation	SNP	C	T	31	66	c.12454G>A	c.(12454-12456)GAT>AAT	p.D4152N
Pat_76	Pre-Treatment	DNAH5	1767	37	5	13901602	13901602	Missense_Mutation	SNP	G	A	22	17	c.1811C>T	c.(1810-1812)TCA>TTA	p.S604L
Pat_76	Pre-Treatment	TRIO	7204	37	5	14497016	14497016	Missense_Mutation	SNP	C	T	26	34	c.7909C>T	c.(7909-7911)CGT>TGT	p.R2637C
Pat_76	Pre-Treatment	CDH18	1016	37	5	19838894	19838895	Missense_Mutation	DNP	CC	TT	8	13	c.201_202GG>AA	199-204)ATGGGA>ATAA	p.67_68MG>I
Pat_76	Pre-Treatment	GUSBP1	728411	37	5	21491451	21491451	Missense_Mutation	SNP	C	T	5	83	c.197C>T	c.(196-198)TCC>TTC	p.S66F
Pat_76	Pre-Treatment	CDH6	1004	37	5	31294126	31294126	Missense_Mutation	SNP	G	A	21	41	c.286G>A	c.(286-288)GGA>AGA	p.G96R
Pat_76	Pre-Treatment	RAD1	5810	37	5	34911678	34911678	Missense_Mutation	SNP	G	A	50	79	c.547C>T	c.(547-549)CCT>TCT	p.P183S
Pat_76	Pre-Treatment	PRLR	5618	37	5	35065850	35065850	Missense_Mutation	SNP	G	A	62	98	c.1210C>T	c.(1210-1212)CCC>TCC	p.P404S
Pat_76	Pre-Treatment	PRLR	5618	37	5	35065883	35065883	Missense_Mutation	SNP	C	T	34	36	c.1177G>A	c.(1177-1179)GAC>AAC	p.D393N
Pat_76	Pre-Treatment	SPEF2	79925	37	5	35667216	35667216	Missense_Mutation	SNP	C	T	5	25	c.1210C>T	c.(1210-1212)CTT>TTT	p.L404F
Pat_76	Pre-Treatment	IL7R	3575	37	5	35876456	35876457	Missense_Mutation	DNP	CC	TT	24	45	.1248_1249CC>T	246-1251)CCCCCT>CCT	p.P417S
Pat_76	Pre-Treatment	UGT3A2	167127	37	5	36064452	36064453	Splice_Site	DNP	CC	TT	23	26	c.95_splice	c.e2-1	p.G32_splice
Pat_76	Pre-Treatment	EGFLAM	133584	37	5	38406257	38406257	Missense_Mutation	SNP	G	A	19	30	c.742G>A	c.(742-744)GGA>AGA	p.G248R
Pat_76	Pre-Treatment	PTGER4	5734	37	5	40681235	40681235	Missense_Mutation	SNP	A	T	54	59	c.140A>T	c.(139-141)AAG>ATG	p.K47M
Pat_76	Pre-Treatment	C7	730	37	5	40934512	40934512	Missense_Mutation	SNP	C	T	36	83	c.224C>T	c.(223-225)CCT>CTT	p.P75L
Pat_76	Pre-Treatment	HEATR7B2	133558	37	5	41000395	41000395	Missense_Mutation	SNP	C	T	14	21	c.4409G>A	c.(4408-4410)GGG>GAG	p.G1470E
Pat_76	Pre-Treatment	C6	729	37	5	41149409	41149409	Missense_Mutation	SNP	A	G	65	98	c.2557T>C	c.(2557-2559)TCA>CCA	p.S853P
Pat_76	Pre-Treatment	PARP8	79668	37	5	50090751	50090751	Missense_Mutation	SNP	G	A	26	54	c.928G>A	c.(928-930)GGA>AGA	p.G310R
Pat_76	Pre-Treatment	SNX18	112574	37	5	53815304	53815304	Missense_Mutation	SNP	G	A	4	121	c.1522G>A	c.(1522-1524)GCG>ACG	p.A508T
Pat_76	Pre-Treatment	KIF2A	3796	37	5	61650989	61650989	Missense_Mutation	SNP	G	A	4	66	c.562G>A	c.(562-564)GTT>ATT	p.V188I

Pat_76	Pre-Treatment	ADAMTS6	11174	37	5	64511271	64511271	Nonsense_Mutation	SNP	C	T	18	27	c.2316G>A	c.(2314-2316)TGG>TGA	p.W772*
Pat_76	Pre-Treatment	ADAMTS6	11174	37	5	64522007	64522008	Missense_Mutation	DNP	CC	TT	33	47	.1972_1973GG>A	c.(1972-1974)GGT>AAT	p.G658N
Pat_76	Pre-Treatment	IQGAP2	10788	37	5	75858277	75858277	Missense_Mutation	SNP	G	A	26	43	c.203G>A	c.(202-204)GGG>GAG	p.G68E
Pat_76	Pre-Treatment	GPR98	84059	37	5	89940541	89940541	Missense_Mutation	SNP	G	A	91	134	c.2753G>A	c.(2752-2754)AGA>AAA	p.R918K
Pat_76	Pre-Treatment	GPR98	84059	37	5	90106784	90106784	Missense_Mutation	SNP	G	A	31	39	c.15707G>A	.(15706-15708)GGC>GA	p.G5236D
Pat_76	Pre-Treatment	PCSK1	5122	37	5	95733081	95733081	Missense_Mutation	SNP	C	T	13	28	c.1681G>A	c.(1681-1683)GAG>AAG	p.E561K
Pat_76	Pre-Treatment	RIOK2	55781	37	5	96514819	96514819	Missense_Mutation	SNP	A	T	33	36	c.145T>A	c.(145-147)TGT>AGT	p.C49S
Pat_76	Pre-Treatment	SLCO4C1	353189	37	5	101585427	101585427	Missense_Mutation	SNP	T	A	25	34	c.1535A>T	c.(1534-1536)TAT>TTT	p.Y512F
Pat_76	Pre-Treatment	CAMK4	814	37	5	110818528	110818528	Missense_Mutation	SNP	T	A	76	95	c.874T>A	c.(874-876)TTT>ATT	p.F292I
Pat_76	Pre-Treatment	FEM1C	56929	37	5	114860426	114860426	Missense_Mutation	SNP	C	T	88	87	c.1433G>A	c.(1432-1434)AGG>AAG	p.R478K
Pat_76	Pre-Treatment	FAM170A	340069	37	5	118969718	118969718	Missense_Mutation	SNP	G	A	37	38	c.275G>A	c.(274-276)CGA>CAA	p.R92Q
Pat_76	Pre-Treatment	FTMT	94033	37	5	121188022	121188022	Missense_Mutation	SNP	G	A	11	30	c.364G>A	c.(364-366)GAG>AAG	p.E122K
Pat_76	Pre-Treatment	SNCAIP	9627	37	5	121758806	121758806	Missense_Mutation	SNP	G	A	7	2	c.374G>A	c.(373-375)GGA>GAA	p.G125E
Pat_76	Pre-Treatment	SNCAIP	9627	37	5	121761092	121761092	Missense_Mutation	SNP	G	A	61	93	c.1048G>A	c.(1048-1050)GGA>AGA	p.G350R
Pat_76	Pre-Treatment	SNCAIP	9627	37	5	121761194	121761194	Missense_Mutation	SNP	G	A	26	33	c.1150G>A	c.(1150-1152)GAG>AAG	p.E384K
Pat_76	Pre-Treatment	PRRC1	133619	37	5	126874759	126874759	Missense_Mutation	SNP	C	T	4	144	c.949C>T	c.(949-951)CGT>TGT	p.R317C
Pat_76	Pre-Treatment	FBN2	2201	37	5	127626457	127626457	Missense_Mutation	SNP	C	T	38	58	c.6412G>A	c.(6412-6414)GAC>AAC	p.D2138N
Pat_76	Pre-Treatment	DDX46	9879	37	5	134131837	134131837	Missense_Mutation	SNP	G	A	22	48	c.1951G>A	c.(1951-1953)GGA>AGA	p.G651R
Pat_76	Pre-Treatment	TGFBI	7045	37	5	135388802	135388802	Missense_Mutation	SNP	G	A	7	11	c.1120G>A	c.(1120-1122)GAC>AAC	p.D374N
Pat_76	Pre-Treatment	TGFBI	7045	37	5	135394880	135394881	Missense_Mutation	DNP	GG	AA	3	8	.1780_1781GG>A	c.(1780-1782)GGT>AAT	p.G594N
Pat_76	Pre-Treatment	KLHL3	26249	37	5	137028094	137028094	Missense_Mutation	SNP	G	A	13	28	c.406C>T	c.(406-408)CGG>TGG	p.R136W
Pat_76	Pre-Treatment	LRRTM2	26045	37	5	138209183	138209183	Missense_Mutation	SNP	C	T	12	22	c.1067G>A	c.(1066-1068)GGA>GAA	p.G356E
Pat_76	Pre-Treatment	NRG2	9542	37	5	139260461	139260461	Missense_Mutation	SNP	C	T	4	83	c.971G>A	c.(970-972)GGC>GAC	p.G324D
Pat_76	Pre-Treatment	SLC4A9	83697	37	5	139751845	139751845	Missense_Mutation	SNP	G	A	7	5	c.2761G>A	c.(2761-2763)GTC>ATC	p.V921I
Pat_76	Pre-Treatment	PCDHA4	56144	37	5	140186787	140186788	Nonsense_Mutation	DNP	GG	AA	55	84	c.15_16GG>AA	.(13-18)TGGGGA>TGAAG	p.5_6WG>*R
Pat_76	Pre-Treatment	PCDHA4	56144	37	5	140188520	140188520	Nonsense_Mutation	SNP	G	A	33	40	c.1748G>A	c.(1747-1749)TGG>TAG	p.W583*
Pat_76	Pre-Treatment	PCDHA7	56141	37	5	140214158	140214158	Missense_Mutation	SNP	T	A	100	100	c.190T>A	c.(190-192)TTC>ATC	p.F64I
Pat_76	Pre-Treatment	PCDHA8	56140	37	5	140222893	140222893	Missense_Mutation	SNP	G	A	45	35	c.1987G>A	c.(1987-1989)GCC>ACC	p.A663T
Pat_76	Pre-Treatment	PCDHA10	56139	37	5	140237626	140237626	Missense_Mutation	SNP	C	T	7	11	c.1993C>T	c.(1993-1995)CTT>TTT	p.L665F
Pat_76	Pre-Treatment	PCDHAC2	56134	37	5	140347871	140347871	Missense_Mutation	SNP	C	T	25	38	c.1520C>T	c.(1519-1521)TCC>TTC	p.S507F
Pat_76	Pre-Treatment	PCDHB2	56133	37	5	140474589	140474589	Missense_Mutation	SNP	G	A	26	42	c.215G>A	c.(214-216)GGA>GAA	p.G72E
Pat_76	Pre-Treatment	PCDHB3	56132	37	5	140481729	140481729	Missense_Mutation	SNP	C	T	60	94	c.1496C>T	c.(1495-1497)CCC>CTC	p.P499L
Pat_76	Pre-Treatment	PCDHB6	56130	37	5	140530292	140530292	Missense_Mutation	SNP	C	T	77	149	c.454C>T	c.(454-456)CCT>TCT	p.P152S
Pat_76	Pre-Treatment	PCDHB6	56130	37	5	140532002	140532002	Missense_Mutation	SNP	C	T	91	114	c.2164C>T	c.(2164-2166)CGC>TGC	p.R722C
Pat_76	Pre-Treatment	PCDHB7	56129	37	5	140554046	140554046	Missense_Mutation	SNP	G	A	13	40	c.1630G>A	c.(1630-1632)GAG>AAG	p.E544K
Pat_76	Pre-Treatment	PCDHB16	57717	37	5	140562564	140562564	Missense_Mutation	SNP	G	A	12	18	c.430G>A	c.(430-432)GAA>AAA	p.E144K
Pat_76	Pre-Treatment	PCDHB16	57717	37	5	140562910	140562910	Missense_Mutation	SNP	C	T	20	45	c.776C>T	c.(775-777)TCC>TTC	p.S259F
Pat_76	Pre-Treatment	PCDHB10	56126	37	5	140572462	140572462	Missense_Mutation	SNP	C	T	17	27	c.337C>T	c.(337-339)CCC>TCC	p.P113S
Pat_76	Pre-Treatment	PCDHGA1	56114	37	5	140712307	140712307	Missense_Mutation	SNP	G	A	68	110	c.2056G>A	c.(2056-2058)GAT>AAT	p.D686N
Pat_76	Pre-Treatment	PCDHGA2	56113	37	5	140719019	140719019	Missense_Mutation	SNP	G	A	39	58	c.481G>A	c.(481-483)GAC>AAC	p.D161N
Pat_76	Pre-Treatment	PCDHGA9	56107	37	5	140782892	140782892	Missense_Mutation	SNP	G	A	57	75	c.373G>A	c.(373-375)GAT>AAT	p.D125N
Pat_76	Pre-Treatment	ARAP3	64411	37	5	141041799	141041799	Missense_Mutation	SNP	G	A	4	137	c.2824C>T	c.(2824-2826)CGG>TGG	p.R942W
Pat_76	Pre-Treatment	PPARGC1B	133522	37	5	149212825	149212825	Missense_Mutation	SNP	G	A	4	95	c.1189G>A	c.(1189-1191)GCA>ACA	p.A397T
Pat_76	Pre-Treatment	PDGFRB	5159	37	5	149499118	149499118	Missense_Mutation	SNP	A	C	35	52	c.2710T>G	c.(2710-2712)TAC>GAC	p.Y904D
Pat_76	Pre-Treatment	GLRA1	2741	37	5	151271938	151271938	Missense_Mutation	SNP	C	T	33	36	c.118G>A	c.(118-120)GAT>AAT	p.D40N
Pat_76	Pre-Treatment	KIF4B	285643	37	5	154393439	154393439	Missense_Mutation	SNP	G	A	55	69	c.20G>A	c.(19-21)GGA>GAA	p.G7E
Pat_76	Pre-Treatment	KIF4B	285643	37	5	154396219	154396219	Missense_Mutation	SNP	C	T	9	23	c.2800C>T	c.(2800-2802)CTT>TTT	p.L934F

Pat_76	Pre-Treatment	CYFIP2	26999	37	5	156819926	156819926	Missense_Mutation	SNP	C	T	37	29	c.3680C>T	c.(3679-3681)TCC>TTC	p.S1227F
Pat_76	Pre-Treatment	GABRB2	2561	37	5	160721303	160721303	Missense_Mutation	SNP	G	A	17	17	c.1324C>T	c.(1324-1326)CGG>TGG	p.R442W
Pat_76	Pre-Treatment	ODZ2	57451	37	5	167420012	167420013	Missense_Mutation	DNP	CC	TT	47	89	:.1011_1012CC>T	1009-1014)TACCCT>TATT	p.P338S
Pat_76	Pre-Treatment	CPLX2	10814	37	5	175306947	175306947	Missense_Mutation	SNP	C	T	6	18	c.304C>T	c.(304-306)CCT>TCT	p.P102S
Pat_76	Pre-Treatment	MXD3	83463	37	5	176734669	176734669	Missense_Mutation	SNP	C	T	23	89	c.541G>A	c.(541-543)GGG>AGG	p.G181R
Pat_76	Pre-Treatment	ZNF454	285676	37	5	178392376	178392376	Missense_Mutation	SNP	G	A	20	50	c.971G>A	c.(970-972)GGA>GAA	p.G324E
Pat_76	Pre-Treatment	RUFY1	80230	37	5	179025788	179025788	Missense_Mutation	SNP	G	A	48	104	c.1727G>A	c.(1726-1728)AGG>AAG	p.R576K
Pat_76	Pre-Treatment	TBC1D9B	23061	37	5	179292874	179292874	Missense_Mutation	SNP	C	T	55	72	c.2929G>A	c.(2929-2931)GAA>AAA	p.E977K
Pat_76	Pre-Treatment	RASGEF1C	255426	37	5	179545807	179545807	Missense_Mutation	SNP	C	T	25	39	c.967G>A	c.(967-969)GCC>ACC	p.A323T
Pat_76	Pre-Treatment	DSP	1832	37	6	7558389	7558389	Missense_Mutation	SNP	G	A	4	148	c.314G>A	c.(313-315)CGA>CAA	p.R105Q
Pat_76	Pre-Treatment	DSP	1832	37	6	7569516	7569516	Missense_Mutation	SNP	C	T	39	56	c.1517C>T	c.(1516-1518)CCC>CTC	p.P506L
Pat_76	Pre-Treatment	MAK	4117	37	6	10764812	10764812	Missense_Mutation	SNP	C	T	4	131	c.1745G>A	c.(1744-1746)CGG>CAG	p.R582Q
Pat_76	Pre-Treatment	CAP2	10486	37	6	17556621	17556621	Missense_Mutation	SNP	C	T	4	80	c.1382C>T	c.(1381-1383)ACA>ATA	p.T461I
Pat_76	Pre-Treatment	HDGFL1	154150	37	6	22569943	22569943	Missense_Mutation	SNP	G	A	15	19	c.139G>A	c.(139-141)GAG>AAG	p.E47K
Pat_76	Pre-Treatment	BTN3A3	10384	37	6	26452269	26452269	Missense_Mutation	SNP	G	A	30	58	c.1385G>A	c.(1384-1386)GGG>GAG	p.G462E
Pat_76	Pre-Treatment	SCAND3	114821	37	6	28543719	28543719	Missense_Mutation	SNP	C	T	34	57	c.763G>A	c.(763-765)GAA>AAA	p.E255K
Pat_76	Pre-Treatment	OR2J2	26707	37	6	29142001	29142001	Missense_Mutation	SNP	G	A	17	42	c.589G>A	c.(589-591)GAG>AAG	p.E197K
Pat_76	Pre-Treatment	OR2H1	26716	37	6	29429955	29429955	Missense_Mutation	SNP	C	T	72	121	c.409C>T	c.(409-411)CGC>TGC	p.R137C
Pat_76	Pre-Treatment	HLA-L	3139	37	6	30231076	30231076	Missense_Mutation	SNP	G	A	97	179	c.520G>A	c.(520-522)GGT>AGT	p.G174S
Pat_76	Pre-Treatment	KIAA1949	170954	37	6	30645059	30645059	Missense_Mutation	SNP	G	A	56	68	c.1829C>T	c.(1828-1830)TCC>TTC	p.S610F
Pat_76	Pre-Treatment	C6orf15	29113	37	6	31079874	31079874	Missense_Mutation	SNP	G	A	12	30	c.262C>T	c.(262-264)CCA>TCA	p.P88S
Pat_76	Pre-Treatment	BAT2	7916	37	6	31599967	31599967	Missense_Mutation	SNP	G	C	17	14	c.3517G>C	c.(3517-3519)GGA>CGA	p.G1173R
Pat_76	Pre-Treatment	LY6G6F	259215	37	6	31675497	31675498	Missense_Mutation	DNP	GT	TA	12	22	c.315_316GT>TA	313-318)TGGTGC>TGTA(	105_106WC>(
Pat_76	Pre-Treatment	NEU1	4758	37	6	31827660	31827660	Nonsense_Mutation	SNP	G	A	59	67	c.1084C>T	c.(1084-1086)CAG>TAG	p.Q362*
Pat_76	Pre-Treatment	SKIV2L	6499	37	6	31935813	31935813	Nonsense_Mutation	SNP	G	T	14	22	c.2812G>T	c.(2812-2814)GAG>TAG	p.E938*
Pat_76	Pre-Treatment	C4A	720	37	6	31996291	31996291	Missense_Mutation	SNP	C	T	19	52	c.3212C>T	c.(3211-3213)TCA>TTA	p.S1071L
Pat_76	Pre-Treatment	NOTCH4	4855	37	6	32180981	32180981	Missense_Mutation	SNP	G	A	19	22	c.2369C>T	c.(2368-2370)TCC>TTC	p.S790F
Pat_76	Pre-Treatment	C6orf10	10665	37	6	32260979	32260979	Missense_Mutation	SNP	C	T	43	68	c.1471G>A	c.(1471-1473)GAG>AAG	p.E491K
Pat_76	Pre-Treatment	BTNL2	56244	37	6	32370964	32370965	Missense_Mutation	DNP	CC	TT	5	7	c.456_457GG>AA(	454-459)ATGGAG>ATAAA	.152_153ME>I
Pat_76	Pre-Treatment	HLA-DRB1	3123	37	6	32548562	32548562	Missense_Mutation	SNP	G	A	39	205	c.724C>T	c.(724-726)CTT>TTT	p.L242F
Pat_76	Pre-Treatment	COL11A2	1302	37	6	33138658	33138658	Missense_Mutation	SNP	C	T	36	60	c.3403G>A	c.(3403-3405)GGA>AGA	p.G1135R
Pat_76	Pre-Treatment	DAXX	1616	37	6	33287202	33287202	Missense_Mutation	SNP	G	A	142	224	c.1895C>T	c.(1894-1896)TCT>TTT	p.S632F
Pat_76	Pre-Treatment	ITPR3	3710	37	6	33623635	33623635	Missense_Mutation	SNP	G	A	4	64	c.253G>A	c.(253-255)GCT>ACT	p.A85T
Pat_76	Pre-Treatment	ITPR3	3710	37	6	33656459	33656459	Missense_Mutation	SNP	C	T	3	34	c.6595C>T	c.(6595-6597)CGC>TGC	p.R2199C
Pat_76	Pre-Treatment	TULP1	7287	37	6	35477652	35477652	Missense_Mutation	SNP	C	T	41	63	c.553G>A	c.(553-555)GAA>AAA	p.E185K
Pat_76	Pre-Treatment	DNAH8	1769	37	6	38905837	38905837	Missense_Mutation	SNP	C	A	18	24	c.11000C>A	c.(10999-11001)GCT>GAT	p.A3667D
Pat_76	Pre-Treatment	GLP1R	2740	37	6	39040780	39040780	Missense_Mutation	SNP	C	T	14	37	c.652C>T	c.(652-654)CTC>TTC	p.L218F
Pat_76	Pre-Treatment	TREM2	54209	37	6	41126761	41126762	Missense_Mutation	DNP	GG	AA	4	6	c.525_526CC>TT	(523-528)ATCCTT>ATTTT	p.L176F
Pat_76	Pre-Treatment	TREML2	79865	37	6	41162514	41162514	Missense_Mutation	SNP	C	T	21	38	c.434G>A	c.(433-435)GGA>GAA	p.G145E
Pat_76	Pre-Treatment	PPP2R5D	5528	37	6	42974367	42974367	Missense_Mutation	SNP	G	A	4	107	c.272G>A	c.(271-273)CGC>CAC	p.R91H
Pat_76	Pre-Treatment	C6orf153	88745	37	6	42994986	42994986	Missense_Mutation	SNP	G	A	4	103	c.521G>A	c.(520-522)CGA>CAA	p.R174Q
Pat_76	Pre-Treatment	CUL7	9820	37	6	43019496	43019496	Missense_Mutation	SNP	G	A	5	208	c.586C>T	c.(586-588)CGG>TGG	p.R196W
Pat_76	Pre-Treatment	TTBK1	84630	37	6	43250765	43250765	Missense_Mutation	SNP	G	A	15	13	c.2287G>A	c.(2287-2289)GAG>AAG	p.E763K
Pat_76	Pre-Treatment	ZNF318	24149	37	6	43325084	43325084	Missense_Mutation	SNP	C	T	3	32	c.968G>A	c.(967-969)CGA>CAA	p.R323Q
Pat_76	Pre-Treatment	HSP90AB1	3326	37	6	44218846	44218846	Missense_Mutation	SNP	C	T	84	139	c.1019C>T	c.(1018-1020)CCC>CTC	p.P340L
Pat_76	Pre-Treatment	TCTE1	202500	37	6	44247992	44247992	Missense_Mutation	SNP	G	A	4	92	c.1432C>T	c.(1432-1434)CGC>TGC	p.R478C
Pat_76	Pre-Treatment	RCAN2	10231	37	6	46216620	46216620	Missense_Mutation	SNP	C	T	15	28	c.101G>A	c.(100-102)GGA>GAA	p.G34E

Pat_76	Pre-Treatment	GPR116	221395	37	6	46849828	46849828	Missense_Mutation	SNP	C	T	136	144	c.629G>A	c.(628-630)GGA>GAA	p.G210E
Pat_76	Pre-Treatment	GPR111	222611	37	6	47648023	47648023	Missense_Mutation	SNP	G	A	42	64	c.688G>A	c.(688-690)GAT>AAT	p.D230N
Pat_76	Pre-Treatment	GPR111	222611	37	6	47649928	47649928	Missense_Mutation	SNP	T	G	23	25	c.1633T>G	c.(1633-1635)TAT>GAT	p.Y545D
Pat_76	Pre-Treatment	GPR115	221393	37	6	47684567	47684567	Missense_Mutation	SNP	C	T	43	88	c.1958C>T	c.(1957-1959)ACC>ATC	p.T653I
Pat_76	Pre-Treatment	OPN5	221391	37	6	47754269	47754269	Missense_Mutation	SNP	G	A	19	27	c.149G>A	c.(148-150)GGA>GAA	p.G50E
Pat_76	Pre-Treatment	PKHD1	5314	37	6	51524392	51524393	Missense_Mutation	DNP	CC	TT	12	18	10531_10532GG>	.(10531-10533)GGG>AA	p.G3511K
Pat_76	Pre-Treatment	HMGCLL1	54511	37	6	55406878	55406879	Missense_Mutation	DNP	CC	TT	21	22	c.258_259GG>AA	256-261)AGGGAT>AGAA	p.D87N
Pat_76	Pre-Treatment	COL21A1	81578	37	6	56035908	56035908	Missense_Mutation	SNP	C	T	46	61	c.659G>A	c.(658-660)CGA>CAA	p.R220Q
Pat_76	Pre-Treatment	KIAA1586	57691	37	6	56915578	56915578	Missense_Mutation	SNP	C	T	4	61	c.112C>T	c.(112-114)CCA>TCA	p.P38S
Pat_76	Pre-Treatment	BAI3	577	37	6	69646453	69646453	Missense_Mutation	SNP	C	T	14	18	c.911C>T	c.(910-912)TCG>TTG	p.S304L
Pat_76	Pre-Treatment	BAI3	577	37	6	69723975	69723975	Missense_Mutation	SNP	G	A	17	42	c.1975G>A	c.(1975-1977)GAA>AAA	p.E659K
Pat_76	Pre-Treatment	COL9A1	1297	37	6	70984444	70984444	Missense_Mutation	SNP	G	A	30	28	c.1007C>T	c.(1006-1008)TCC>TTC	p.S336F
Pat_76	Pre-Treatment	IMPG1	3617	37	6	76731904	76731904	Missense_Mutation	SNP	G	A	35	48	c.595C>T	c.(595-597)CTC>TTC	p.L199F
Pat_76	Pre-Treatment	ME1	4199	37	6	83933652	83933652	Missense_Mutation	SNP	C	T	7	22	c.1276G>A	c.(1276-1278)GGA>AGA	p.G426R
Pat_76	Pre-Treatment	TBX18	9096	37	6	85466491	85466492	Missense_Mutation	DNP	CC	TT	20	24	c.695_696GG>AA	c.(694-696)GGG>GAA	p.G232E
Pat_76	Pre-Treatment	NT5E	4907	37	6	86180955	86180955	Missense_Mutation	SNP	G	A	5	15	c.563G>A	c.(562-564)GGG>GAG	p.G188E
Pat_76	Pre-Treatment	EPHA7	2045	37	6	93955105	93955105	Nonsense_Mutation	SNP	C	T	39	53	c.2793G>A	c.(2791-2793)TGG>TGA	p.W931*
Pat_76	Pre-Treatment	EPHA7	2045	37	6	93956552	93956552	Missense_Mutation	SNP	C	T	47	55	c.2684G>A	c.(2683-2685)CGA>CAA	p.R895Q
Pat_76	Pre-Treatment	KIAA0776	23376	37	6	97000533	97000533	Missense_Mutation	SNP	C	T	8	22	c.2161C>T	c.(2161-2163)CCA>TCA	p.P721S
Pat_76	Pre-Treatment	C6orf167	253714	37	6	97676827	97676827	Missense_Mutation	SNP	C	T	4	118	c.1982G>A	c.(1981-1983)CGA>CAA	p.R661Q
Pat_76	Pre-Treatment	GRIK2	2898	37	6	102307279	102307279	Missense_Mutation	SNP	G	A	17	20	c.1435G>A	c.(1435-1437)GAA>AAA	p.E479K
Pat_76	Pre-Treatment	GRIK2	2898	37	6	102372501	102372501	Missense_Mutation	SNP	C	T	52	59	c.1774C>T	c.(1774-1776)CCA>TCA	p.P592S
Pat_76	Pre-Treatment	PRDM1	639	37	6	106547368	106547368	Missense_Mutation	SNP	G	T	4	95	c.605G>T	c.(604-606)CGG>CTG	p.R202L
Pat_76	Pre-Treatment	SOBP	55084	37	6	107827494	107827494	Missense_Mutation	SNP	C	T	63	65	c.284C>T	c.(283-285)CCA>CTA	p.P95L
Pat_76	Pre-Treatment	ARMC2	84071	37	6	109220963	109220963	Missense_Mutation	SNP	G	A	19	28	c.815G>A	c.(814-816)AGG>AAG	p.R272K
Pat_76	Pre-Treatment	FRK	2444	37	6	116263590	116263590	Missense_Mutation	SNP	T	C	35	53	c.1505A>G	c.(1504-1506)AAC>AGC	p.N502S
Pat_76	Pre-Treatment	DSE	29940	37	6	116758336	116758336	Missense_Mutation	SNP	G	A	14	36	c.2705G>A	c.(2704-2706)AGG>AAG	p.R902K
Pat_76	Pre-Treatment	RFX6	222546	37	6	117240459	117240460	Splice_Site	DNP	GG	AA	31	62	c.1182_splice	c.e11+1	p.Q394_splice
Pat_76	Pre-Treatment	RFX6	222546	37	6	117248514	117248514	Missense_Mutation	SNP	G	C	27	44	c.2210G>C	c.(2209-2211)AGA>ACA	p.R737T
Pat_76	Pre-Treatment	MAN1A1	4121	37	6	119623184	119623184	Missense_Mutation	SNP	G	A	13	15	c.785C>T	c.(784-786)TCA>TTA	p.S262L
Pat_76	Pre-Treatment	C6orf170	221322	37	6	121481215	121481215	Missense_Mutation	SNP	G	A	42	69	c.2714C>T	c.(2713-2715)TCA>TTA	p.S905L
Pat_76	Pre-Treatment	C6orf58	352999	37	6	127912754	127912754	Missense_Mutation	SNP	G	A	14	26	c.980G>A	c.(979-981)GGA>GAA	p.G327E
Pat_76	Pre-Treatment	PTPRK	5796	37	6	128304508	128304508	Missense_Mutation	SNP	C	T	67	108	c.3263G>A	c.(3262-3264)CGA>CAA	p.R1088Q
Pat_76	Pre-Treatment	LAMA2	3908	37	6	129802517	129802517	Missense_Mutation	SNP	G	A	80	104	c.7682G>A	c.(7681-7683)GGC>GAC	p.G2561D
Pat_76	Pre-Treatment	C6orf191	253582	37	6	130166939	130166939	Missense_Mutation	SNP	G	A	43	66	c.92C>T	c.(91-93)TCC>TTC	p.S31F
Pat_76	Pre-Treatment	ENPP3	5169	37	6	131973708	131973708	Missense_Mutation	SNP	C	T	101	119	c.304C>T	c.(304-306)CGT>TGT	p.R102C
Pat_76	Pre-Treatment	ENPP3	5169	37	6	131995347	131995347	Missense_Mutation	SNP	G	A	16	18	c.688G>A	c.(688-690)GAT>AAT	p.D230N
Pat_76	Pre-Treatment	TAAR8	83551	37	6	132874774	132874774	Missense_Mutation	SNP	C	T	25	59	c.943C>T	c.(943-945)CCT>TCT	p.P315S
Pat_76	Pre-Treatment	AHI1	54806	37	6	135754272	135754272	Missense_Mutation	SNP	G	A	47	56	c.2159C>T	c.(2158-2160)TCC>TTC	p.S720F
Pat_76	Pre-Treatment	BCLAF1	9774	37	6	136599690	136599690	Missense_Mutation	SNP	G	A	28	170	c.329C>T	c.(328-330)TCA>TTA	p.S110L
Pat_76	Pre-Treatment	MAP7	9053	37	6	136680963	136680963	Missense_Mutation	SNP	C	T	93	152	c.1907G>A	c.(1906-1908)GGA>GAA	p.G636E
Pat_76	Pre-Treatment	MAP7	9053	37	6	136681842	136681842	Missense_Mutation	SNP	C	T	255	352	c.1796G>A	c.(1795-1797)AGA>AAA	p.R599K
Pat_76	Pre-Treatment	KIAA1244	57221	37	6	138619758	138619758	Missense_Mutation	SNP	G	A	10	6	c.3664G>A	c.(3664-3666)GAA>AAA	p.E1222K
Pat_76	Pre-Treatment	HIVEP2	3097	37	6	143081070	143081070	Missense_Mutation	SNP	G	T	3	14	c.6355C>A	c.(6355-6357)CCT>ACT	p.P2119T
Pat_76	Pre-Treatment	PLAGL1	5325	37	6	144263084	144263084	Missense_Mutation	SNP	G	A	16	36	c.869C>T	c.(868-870)TCC>TTC	p.S290F
Pat_76	Pre-Treatment	UTRN	7402	37	6	145156938	145156938	Nonsense_Mutation	SNP	C	T	129	190	c.9688C>T	c.(9688-9690)CAG>TAG	p.Q3230*
Pat_76	Pre-Treatment	FBXL18	80028	37	7	5540167	5540167	Missense_Mutation	SNP	G	A	4	102	c.1733C>T	c.(1732-1734)CCC>CTC	p.P578L

Pat_76	Pre-Treatment	FBXL18	80028	37	7	5540452	5540452	Missense_Mutation	SNP	G	T	17	46	c.1448C>A	c.(1447-1449)CCC>CAC	p.P483H
Pat_76	Pre-Treatment	C7orf26	79034	37	7	6639796	6639796	Missense_Mutation	SNP	C	T	15	15	c.917C>T	c.(916-918)ACC>ATC	p.T306I
Pat_76	Pre-Treatment	COL28A1	340267	37	7	7457519	7457519	Missense_Mutation	SNP	G	A	40	94	c.2107C>T	c.(2107-2109)CCC>TCC	p.P703S
Pat_76	Pre-Treatment	ETV1	2115	37	7	13971333	13971333	Missense_Mutation	SNP	G	A	15	74	c.596C>T	c.(595-597)CCT>CTT	p.P199L
Pat_76	Pre-Treatment	HDAC9	9734	37	7	18975562	18975562	Missense_Mutation	SNP	T	G	72	46	c.2925T>G	c.(2923-2925)AAT>AAG	p.N975K
Pat_76	Pre-Treatment	TWISTNB	221830	37	7	19748518	19748518	Missense_Mutation	SNP	A	C	25	18	c.122T>G	c.(121-123)GTG>GGG	p.V41G
Pat_76	Pre-Treatment	DNAH11	8701	37	7	21639612	21639612	Missense_Mutation	SNP	C	T	12	29	c.2875C>T	c.(2875-2877)CCT>TCT	p.P959S
Pat_76	Pre-Treatment	DNAH11	8701	37	7	21760451	21760451	Missense_Mutation	SNP	G	A	11	26	c.7264G>A	c.(7264-7266)GGA>AGA	p.G2422R
Pat_76	Pre-Treatment	TRA2A	29896	37	7	23556110	23556110	Nonsense_Mutation	SNP	G	A	4	151	c.208C>T	c.(208-210)CGA>TGA	p.R70*
Pat_76	Pre-Treatment	STK31	56164	37	7	23827672	23827672	Missense_Mutation	SNP	C	T	49	114	c.2561C>T	c.(2560-2562)TCA>TTA	p.S854L
Pat_76	Pre-Treatment	BMPER	168667	37	7	34118765	34118765	Missense_Mutation	SNP	G	A	27	110	c.1375G>A	c.(1375-1377)GAT>AAT	p.D459N
Pat_76	Pre-Treatment	POU6F2	11281	37	7	39446295	39446295	Missense_Mutation	SNP	C	T	49	31	c.982C>T	c.(982-984)CTT>TTT	p.L328F
Pat_76	Pre-Treatment	C7orf36	57002	37	7	39612174	39612174	Missense_Mutation	SNP	G	A	46	99	c.550G>A	c.(550-552)GAA>AAA	p.E184K
Pat_76	Pre-Treatment	GLI3	2737	37	7	42065985	42065985	Missense_Mutation	SNP	G	A	14	31	c.1055C>T	c.(1054-1056)TCC>TTC	p.S352F
Pat_76	Pre-Treatment	C7orf44	55744	37	7	43687203	43687203	Missense_Mutation	SNP	C	T	12	105	c.46G>A	c.(46-48)GGA>AGA	p.G16R
Pat_76	Pre-Treatment	PGAM2	5224	37	7	44105164	44105164	Splice_Site	SNP	G	A	52	43	c.-34_splice	c.e1-1	
Pat_76	Pre-Treatment	NPC1L1	29881	37	7	44579071	44579071	Missense_Mutation	SNP	G	A	42	69	c.925C>T	c.(925-927)CCC>TCC	p.P309S
Pat_76	Pre-Treatment	PKD1L1	168507	37	7	47917146	47917146	Missense_Mutation	SNP	G	A	112	74	c.3604C>T	c.(3604-3606)CCC>TCC	p.P1202S
Pat_76	Pre-Treatment	UPP1	7378	37	7	48139273	48139274	Missense_Mutation	DNP	CC	TT	30	65	c.51_52CC>TT	.(49-54)TGCCCC>TGTTC	p.P18S
Pat_76	Pre-Treatment	ABCA13	154664	37	7	48312960	48312960	Missense_Mutation	SNP	G	A	14	37	c.3697G>A	c.(3697-3699)GAT>AAT	p.D1233N
Pat_76	Pre-Treatment	ABCA13	154664	37	7	48338080	48338080	Missense_Mutation	SNP	C	T	16	37	c.9317C>T	c.(9316-9318)TCC>TTC	p.S3106F
Pat_76	Pre-Treatment	ZPBP	11055	37	7	50022979	50022979	Missense_Mutation	SNP	C	T	27	45	c.920G>A	c.(919-921)GGA>GAA	p.G307E
Pat_76	Pre-Treatment	ZNF713	349075	37	7	56007625	56007625	Missense_Mutation	SNP	C	T	49	44	c.1219C>T	c.(1219-1221)CAT>TAT	p.H407Y
Pat_76	Pre-Treatment	ZNF479	90827	37	7	57187752	57187752	Missense_Mutation	SNP	C	T	79	211	c.1370G>A	c.(1369-1371)AGA>AAA	p.R457K
Pat_76	Pre-Treatment	ZNF727	442319	37	7	63538454	63538454	Missense_Mutation	SNP	G	A	27	70	c.1027G>A	c.(1027-1029)GAA>AAA	p.E343K
Pat_76	Pre-Treatment	ZNF107	51427	37	7	64167977	64167977	Missense_Mutation	SNP	A	T	4	102	c.1295A>T	c.(1294-1296)AAA>ATA	p.K432I
Pat_76	Pre-Treatment	CALN1	83698	37	7	71275372	71275372	Missense_Mutation	SNP	C	T	25	85	c.481G>A	c.(481-483)GAA>AAA	p.E161K
Pat_76	Pre-Treatment	POR	5447	37	7	75583414	75583414	Missense_Mutation	SNP	C	T	10	29	c.104C>T	c.(103-105)TCG>TTG	p.S35L
Pat_76	Pre-Treatment	MAGI2	9863	37	7	77885584	77885584	Missense_Mutation	SNP	C	T	8	43	c.1723G>A	c.(1723-1725)GAT>AAT	p.D575N
Pat_76	Pre-Treatment	PCLO	27445	37	7	82451858	82451858	Missense_Mutation	SNP	G	C	76	179	c.14744C>G	.(14743-14745)GCC>GG	p.A4915G
Pat_76	Pre-Treatment	PCLO	27445	37	7	82546104	82546104	Missense_Mutation	SNP	G	A	44	93	c.11198C>T	c.(11197-11199)TCC>TTC	p.S3733F
Pat_76	Pre-Treatment	PCLO	27445	37	7	82586071	82586071	Missense_Mutation	SNP	C	T	6	42	c.4198G>A	c.(4198-4200)GAA>AAA	p.E1400K
Pat_76	Pre-Treatment	PCLO	27445	37	7	82764102	82764102	Missense_Mutation	SNP	T	G	16	34	c.2764A>C	c.(2764-2766)ACT>CCT	p.T922P
Pat_76	Pre-Treatment	PCLO	27445	37	7	82764708	82764708	Missense_Mutation	SNP	C	T	11	45	c.2158G>A	c.(2158-2160)GCC>ACC	p.A720T
Pat_76	Pre-Treatment	PCLO	27445	37	7	82785182	82785182	Nonsense_Mutation	SNP	G	A	25	59	c.775C>T	c.(775-777)CAG>TAG	p.Q259*
Pat_76	Pre-Treatment	ABCB1	5243	37	7	87133609	87133609	Missense_Mutation	SNP	C	T	99	94	c.3793G>A	c.(3793-3795)GGC>AGC	p.G1265S
Pat_76	Pre-Treatment	STEAP4	79689	37	7	87913456	87913456	Nonsense_Mutation	SNP	A	C	27	72	c.129T>G	c.(127-129)TAT>TAG	p.Y43*
Pat_76	Pre-Treatment	SAMD9L	219285	37	7	92762118	92762118	Missense_Mutation	SNP	G	A	26	61	c.3167C>T	c.(3166-3168)TCC>TTC	p.S1056F
Pat_76	Pre-Treatment	COL1A2	1278	37	7	94039582	94039582	Missense_Mutation	SNP	G	A	41	83	c.1064G>A	c.(1063-1065)GGA>GAA	p.G355E
Pat_76	Pre-Treatment	CASD1	64921	37	7	94173748	94173748	Missense_Mutation	SNP	G	A	5	255	c.1382G>A	c.(1381-1383)CGA>CAA	p.R461Q
Pat_76	Pre-Treatment	NPTX2	4885	37	7	98254473	98254473	Missense_Mutation	SNP	G	A	17	46	c.883G>A	c.(883-885)GAC>AAC	p.D295N
Pat_76	Pre-Treatment	CYP3A4	1576	37	7	99359664	99359664	Missense_Mutation	SNP	C	T	73	46	c.1253G>A	c.(1252-1254)AGA>AAA	p.R418K
Pat_76	Pre-Treatment	ZCWPW1	55063	37	7	100017342	100017342	Missense_Mutation	SNP	C	T	9	39	c.193G>A	c.(193-195)GAA>AAA	p.E65K
Pat_76	Pre-Treatment	ZAN	7455	37	7	100348419	100348419	Missense_Mutation	SNP	G	A	7	6	c.1421G>A	c.(1420-1422)GGG>GAG	p.G474E
Pat_76	Pre-Treatment	MUC17	140453	37	7	100678919	100678919	Missense_Mutation	SNP	G	A	228	552	c.4222G>A	c.(4222-4224)GTA>ATA	p.V1408I
Pat_76	Pre-Treatment	MUC17	140453	37	7	100683798	100683798	Missense_Mutation	SNP	C	T	213	537	c.9101C>T	c.(9100-9102)ACC>ATC	p.T3034I
Pat_76	Pre-Treatment	MUC17	140453	37	7	100686761	100686761	Missense_Mutation	SNP	A	C	49	175	c.12064A>C	c.(12064-12066)ACT>CCT	p.T4022P

Pat_76	Pre-Treatment	CUX1	1523	37	7	101918517	101918517	Splice_Site	SNP	G	A	41	107	c.1451_splice	c.e17-1	p.G484_splice
Pat_76	Pre-Treatment	SLC26A5	375611	37	7	103048336	103048336	Missense_Mutation	SNP	C	T	32	69	c.850G>A	c.(850-852)GAG>AAG	p.E284K
Pat_76	Pre-Treatment	RELN	5649	37	7	103185660	103185660	Missense_Mutation	SNP	C	T	57	37	c.6434G>A	c.(6433-6435)GGA>GAA	p.G2145E
Pat_76	Pre-Treatment	RELN	5649	37	7	103294623	103294623	Missense_Mutation	SNP	C	T	28	59	c.1471G>A	c.(1471-1473)GAA>AAA	p.E491K
Pat_76	Pre-Treatment	RELN	5649	37	7	103341421	103341421	Missense_Mutation	SNP	G	A	38	111	c.838C>T	c.(838-840)CCC>TCC	p.P280S
Pat_76	Pre-Treatment	DOCK4	9732	37	7	111423941	111423941	Missense_Mutation	SNP	G	A	7	32	c.3469C>T	c.(3469-3471)CGT>TGT	p.R1157C
Pat_76	Pre-Treatment	IFRD1	3475	37	7	112096120	112096120	Missense_Mutation	SNP	T	G	52	71	c.263T>G	c.(262-264)ATT>AGT	p.I88S
Pat_76	Pre-Treatment	PPP1R3A	5506	37	7	113518127	113518127	Missense_Mutation	SNP	G	A	32	107	c.3020C>T	c.(3019-3021)TCT>TTT	p.S1007F
Pat_76	Pre-Treatment	FOXP2	93986	37	7	114329931	114329931	Missense_Mutation	SNP	G	A	55	192	c.2098G>A	c.(2098-2100)GAA>AAA	p.E700K
Pat_76	Pre-Treatment	MET	4233	37	7	116371883	116371884	Missense_Mutation	DNP	TC	AT	132	51	:.1362_1363TC>A	1360-1365)AATCTT>AAAT	.454_455NL>K
Pat_76	Pre-Treatment	WNT2	7472	37	7	116918241	116918241	Missense_Mutation	SNP	G	A	26	108	c.1051C>T	c.(1051-1053)CCC>TCC	p.P351S
Pat_76	Pre-Treatment	CFTR	1080	37	7	117232163	117232163	Missense_Mutation	SNP	G	A	120	61	c.1942G>A	c.(1942-1944)GAT>AAT	p.D648N
Pat_76	Pre-Treatment	CFTR	1080	37	7	117307052	117307052	Missense_Mutation	SNP	G	A	18	81	c.4333G>A	c.(4333-4335)GAC>AAC	p.D1445N
Pat_76	Pre-Treatment	TSPAN12	23554	37	7	120428929	120428929	Missense_Mutation	SNP	G	A	29	109	c.635C>T	c.(634-636)TCC>TTC	p.S212F
Pat_76	Pre-Treatment	RNF148	378925	37	7	122342384	122342384	Missense_Mutation	SNP	G	A	156	432	c.421C>T	c.(421-423)CCC>TCC	p.P141S
Pat_76	Pre-Treatment	IQUB	154865	37	7	123136870	123136870	Missense_Mutation	SNP	C	T	45	24	c.1114G>A	c.(1114-1116)GAA>AAA	p.E372K
Pat_76	Pre-Treatment	FSCN3	29999	37	7	127236496	127236496	Missense_Mutation	SNP	C	T	153	75	c.956C>T	c.(955-957)TCC>TTC	p.S319F
Pat_76	Pre-Treatment	SND1	27044	37	7	127326763	127326763	Missense_Mutation	SNP	C	T	44	124	c.175C>T	c.(175-177)CTT>TTT	p.L59F
Pat_76	Pre-Treatment	METTL2B	55798	37	7	128119521	128119521	Missense_Mutation	SNP	G	A	16	69	c.512G>A	c.(511-513)TGT>TAT	p.C171Y
Pat_76	Pre-Treatment	FLNC	2318	37	7	128484752	128484752	Missense_Mutation	SNP	G	A	13	79	c.3233G>A	c.(3232-3234)GGC>GAC	p.G1078D
Pat_76	Pre-Treatment	FLNC	2318	37	7	128485144	128485144	Missense_Mutation	SNP	G	A	19	79	c.3625G>A	c.(3625-3627)GAT>AAT	p.D1209N
Pat_76	Pre-Treatment	FLNC	2318	37	7	128493532	128493532	Missense_Mutation	SNP	G	A	39	11	c.6218G>A	c.(6217-6219)GGC>GAC	p.G2073D
Pat_76	Pre-Treatment	PLXNA4	91584	37	7	131831452	131831452	Missense_Mutation	SNP	C	T	50	209	c.4872G>A	c.(4870-4872)ATG>ATA	p.M1624I
Pat_76	Pre-Treatment	PLXNA4	91584	37	7	131853205	131853205	Missense_Mutation	SNP	C	T	19	71	c.4144G>A	c.(4144-4146)GAC>AAC	p.D1382N
Pat_76	Pre-Treatment	PLXNA4	91584	37	7	131853241	131853241	Missense_Mutation	SNP	G	A	12	83	c.4108C>T	c.(4108-4110)CGC>TGC	p.R1370C
Pat_76	Pre-Treatment	PLXNA4	91584	37	7	132192864	132192864	Missense_Mutation	SNP	G	A	35	129	c.589C>T	c.(589-591)CCC>TCC	p.P197S
Pat_76	Pre-Treatment	CHRM2	1129	37	7	136700405	136700405	Missense_Mutation	SNP	G	A	44	60	c.793G>A	c.(793-795)GCC>ACC	p.A265T
Pat_76	Pre-Treatment	DGKI	9162	37	7	137304634	137304634	Missense_Mutation	SNP	G	A	182	91	c.929C>T	c.(928-930)TCC>TTC	p.S310F
Pat_76	Pre-Treatment	KIAA1549	57670	37	7	138552834	138552835	Nonsense_Mutation	DNP	GG	AA	20	22	:.4815_4816CC>T	813-4818)CACCAG>CAT	p.Q1606*
Pat_76	Pre-Treatment	ZC3HAV1	56829	37	7	138758745	138758745	Missense_Mutation	SNP	G	A	5	158	c.1729C>T	c.(1729-1731)CGG>TGG	p.R577W
Pat_76	Pre-Treatment	HIPK2	28996	37	7	139416178	139416178	Missense_Mutation	SNP	C	T	4	146	c.656G>A	c.(655-657)CGG>CAG	p.R219Q
Pat_76	Pre-Treatment	RAB19	401409	37	7	140107597	140107597	Missense_Mutation	SNP	G	A	32	137	c.151G>A	c.(151-153)GGA>AGA	p.G51R
Pat_76	Pre-Treatment	RAB19	401409	37	7	140111792	140111792	Missense_Mutation	SNP	C	T	44	204	c.320C>T	c.(319-321)TCC>TTC	p.S107F
Pat_76	Pre-Treatment	DENND2A	27147	37	7	140301773	140301773	Missense_Mutation	SNP	C	A	54	233	c.425G>T	c.(424-426)GGC>GTC	p.G142V
Pat_76	Pre-Treatment	ADCK2	90956	37	7	140373899	140373899	Missense_Mutation	SNP	C	T	54	26	c.769C>T	c.(769-771)CTT>TTT	p.L257F
Pat_76	Pre-Treatment	BRAF	673	37	7	140453136	140453136	Missense_Mutation	SNP	A	T	114	43	c.1799T>A	c.(1798-1800)GTG>GAG	p.V600E
Pat_76	Pre-Treatment	BRAF	673	37	7	140481408	140481408	Missense_Mutation	SNP	G	A	50	268	c.1400C>T	c.(1399-1401)TCA>TTA	p.S467L
Pat_76	Pre-Treatment	WEE2	494551	37	7	141408728	141408728	Nonsense_Mutation	SNP	G	A	197	99	c.170G>A	c.(169-171)TGG>TAG	p.W57*
Pat_76	Pre-Treatment	MGAM	8972	37	7	141759301	141759301	Missense_Mutation	SNP	G	A	7	8	c.3849G>A	c.(3847-3849)ATG>ATA	p.M1283I
Pat_76	Pre-Treatment	TRPV6	55503	37	7	142574981	142574981	Missense_Mutation	SNP	C	T	30	179	c.401G>A	c.(400-402)CGA>CAA	p.R134Q
Pat_76	Pre-Treatment	TRPV5	56302	37	7	142622769	142622769	Missense_Mutation	SNP	C	T	4	104	c.977G>A	c.(976-978)CGG>CAG	p.R326Q
Pat_76	Pre-Treatment	TRPV5	56302	37	7	142625878	142625878	Missense_Mutation	SNP	C	T	51	136	c.670G>A	c.(670-672)GGA>AGA	p.G224R
Pat_76	Pre-Treatment	TAS2R39	259285	37	7	142880593	142880593	Missense_Mutation	SNP	G	A	8	52	c.82G>A	c.(82-84)GAA>AAA	p.E28K
Pat_76	Pre-Treatment	TAS2R39	259285	37	7	142881212	142881212	Missense_Mutation	SNP	C	T	209	70	c.701C>T	c.(700-702)TCT>TTT	p.S234F
Pat_76	Pre-Treatment	CLCN1	1180	37	7	143044013	143044013	Missense_Mutation	SNP	G	A	38	155	c.2374G>A	c.(2374-2376)GAT>AAT	p.D792N
Pat_76	Pre-Treatment	EPHA1	2041	37	7	143096756	143096756	Missense_Mutation	SNP	C	T	33	181	c.823G>A	c.(823-825)GAA>AAA	p.E275K
Pat_76	Pre-Treatment	TAS2R41	259287	37	7	143175540	143175540	Missense_Mutation	SNP	C	T	36	53	c.575C>T	c.(574-576)CCT>CTT	p.P192L

Pat_76	Pre-Treatment	OR2F1	26211	37	7	143657369	143657369	Missense_Mutation	SNP	T	A	68	219	c.306T>A	c.(304-306)TTT>TTA	p.F102L
Pat_76	Pre-Treatment	OR2A2	442361	37	7	143807452	143807452	Missense_Mutation	SNP	G	A	158	104	c.777G>A	c.(775-777)ATG>ATA	p.M259I
Pat_76	Pre-Treatment	ARHGEF5	7984	37	7	144060324	144060324	Missense_Mutation	SNP	G	A	46	121	c.562G>A	c.(562-564)GAG>AAG	p.E188K
Pat_76	Pre-Treatment	ARHGEF5	7984	37	7	144062290	144062290	Missense_Mutation	SNP	C	T	12	241	c.2528C>T	c.(2527-2529)CCC>CTC	p.P843L
Pat_76	Pre-Treatment	CNTNAP2	26047	37	7	146825794	146825794	Missense_Mutation	SNP	G	A	29	105	c.949G>A	c.(949-951)GGA>AGA	p.G317R
Pat_76	Pre-Treatment	C7orf33	202865	37	7	148311169	148311169	Missense_Mutation	SNP	G	A	91	368	c.240G>A	c.(238-240)ATG>ATA	p.M80I
Pat_76	Pre-Treatment	ZNF786	136051	37	7	148768291	148768292	Missense_Mutation	DNP	GG	AA	26	32	.1572_1573CC>T	570-1575)CTCCGT>CTTT	p.R525C
Pat_76	Pre-Treatment	ZNF398	57541	37	7	148876126	148876126	Missense_Mutation	SNP	A	G	74	254	c.1162A>G	c.(1162-1164)ACC>GCC	p.T388A
Pat_76	Pre-Treatment	ZNF777	27153	37	7	149152767	149152767	Missense_Mutation	SNP	G	A	100	51	c.347C>T	c.(346-348)TCC>TTC	p.S116F
Pat_76	Pre-Treatment	SSPO	23145	37	7	149473161	149473161	Missense_Mutation	SNP	G	A	6	45	c.31G>A	c.(31-33)GCG>ACG	p.A11T
Pat_76	Pre-Treatment	SSPO	23145	37	7	149492413	149492413	Missense_Mutation	SNP	G	A	3	18	c.6302G>A	c.(6301-6303)GGG>GAG	p.G2101E
Pat_76	Pre-Treatment	REPIN1	29803	37	7	150068839	150068839	Missense_Mutation	SNP	C	T	15	90	c.509C>T	c.(508-510)CCC>CTC	p.P170L
Pat_76	Pre-Treatment	GIMAP8	155038	37	7	150174179	150174179	Splice_Site	SNP	G	A	119	67	c.1310_splice	c.e5-1	p.E437_splice
Pat_76	Pre-Treatment	GIMAP8	155038	37	7	150174386	150174386	Missense_Mutation	SNP	G	A	51	37	c.1516G>A	c.(1516-1518)GAC>AAC	p.D506N
Pat_76	Pre-Treatment	TMEM176A	55365	37	7	150499346	150499346	Missense_Mutation	SNP	G	A	27	102	c.218G>A	c.(217-219)GGA>GAA	p.G73E
Pat_76	Pre-Treatment	MLL3	58508	37	7	151945102	151945102	Missense_Mutation	SNP	G	A	31	737	c.2417C>T	c.(2416-2418)TCC>TTC	p.S806F
Pat_76	Pre-Treatment	MLL3	58508	37	7	152027710	152027710	Missense_Mutation	SNP	G	A	56	188	c.365C>T	c.(364-366)TCT>TTT	p.S122F
Pat_76	Pre-Treatment	MLL3	58508	37	7	152027728	152027728	Missense_Mutation	SNP	G	A	5	210	c.347C>T	c.(346-348)TCG>TTG	p.S116L
Pat_76	Pre-Treatment	HTR5A	3361	37	7	154862632	154862632	Missense_Mutation	SNP	C	T	54	278	c.23C>T	c.(22-24)ACC>ATC	p.T8I
Pat_76	Pre-Treatment	HTR5A	3361	37	7	154876022	154876022	Missense_Mutation	SNP	C	T	45	140	c.899C>T	c.(898-900)CCC>CTC	p.P300L
Pat_76	Pre-Treatment	ERICH1	157697	37	8	623397	623398	Missense_Mutation	DNP	CC	TT	81	106	c.954_955GG>AA	52-957)GGGGAG>GGAA	p.E319K
Pat_76	Pre-Treatment	CSMD1	64478	37	8	2806873	2806873	Missense_Mutation	SNP	A	C	19	30	c.10353T>G	c.(10351-10353)TTT>TTG	p.F3451L
Pat_76	Pre-Treatment	SGK223	157285	37	8	8235065	8235065	Missense_Mutation	SNP	G	A	10	4	c.854C>T	c.(853-855)TCA>TTA	p.S285L
Pat_76	Pre-Treatment	RP1L1	94137	37	8	10467667	10467668	Missense_Mutation	DNP	CC	TT	17	37	.3940_3941GG>A	c.(3940-3942)GGG>AAG	p.G1314K
Pat_76	Pre-Treatment	FAM167A	83648	37	8	11281901	11281901	Missense_Mutation	SNP	C	T	49	72	c.626G>A	c.(625-627)CGG>CAG	p.R209Q
Pat_76	Pre-Treatment	SGCZ	137868	37	8	13959889	13959889	Missense_Mutation	SNP	C	T	38	66	c.740G>A	c.(739-741)GGG>GAG	p.G247E
Pat_76	Pre-Treatment	MTMR7	9108	37	8	17159783	17159783	Nonsense_Mutation	SNP	C	T	28	23	c.1500G>A	c.(1498-1500)TGG>TGA	p.W500*
Pat_76	Pre-Treatment	XPO7	23039	37	8	21834014	21834014	Missense_Mutation	SNP	C	T	32	40	c.745C>T	c.(745-747)CCC>TCC	p.P249S
Pat_76	Pre-Treatment	LOXL2	4017	37	8	23225624	23225624	Missense_Mutation	SNP	C	T	23	56	c.241G>A	c.(241-243)GGC>AGC	p.G81S
Pat_76	Pre-Treatment	ADAM28	10863	37	8	24187543	24187543	Missense_Mutation	SNP	G	A	35	55	c.1018G>A	c.(1018-1020)GAA>AAA	p.E340K
Pat_76	Pre-Treatment	ADAM7	8756	37	8	24324376	24324376	Missense_Mutation	SNP	G	C	31	48	c.454G>C	c.(454-456)GAA>CAA	p.E152Q
Pat_76	Pre-Treatment	CDCA2	157313	37	8	25361000	25361000	Missense_Mutation	SNP	G	A	4	132	c.1783G>A	c.(1783-1785)GAG>AAG	p.E595K
Pat_76	Pre-Treatment	EBF2	64641	37	8	25718576	25718576	Missense_Mutation	SNP	C	T	55	81	c.1331G>A	c.(1330-1332)GGA>GAA	p.G444E
Pat_76	Pre-Treatment	DPYSL2	1808	37	8	26513185	26513185	Missense_Mutation	SNP	C	T	56	90	c.1682C>T	c.(1681-1683)CCC>CTC	p.P561L
Pat_76	Pre-Treatment	C8orf80	389643	37	8	27884555	27884555	Missense_Mutation	SNP	C	A	5	141	c.2169G>T	c.(2167-2169)GAG>GAT	p.E723D
Pat_76	Pre-Treatment	C8orf80	389643	37	8	27931885	27931885	Missense_Mutation	SNP	C	T	24	24	c.43G>A	c.(43-45)GTT>ATT	p.V15I
Pat_76	Pre-Treatment	TEX15	56154	37	8	30695198	30695198	Missense_Mutation	SNP	G	A	43	77	c.7453C>T	c.(7453-7455)CCA>TCA	p.P2485S
Pat_76	Pre-Treatment	WRN	7486	37	8	30946405	30946405	Splice_Site	SNP	G	A	6	13	c.1577_splice	c.e13-1	p.D526_splice
Pat_76	Pre-Treatment	WRN	7486	37	8	31015013	31015013	Missense_Mutation	SNP	G	T	4	34	c.3949G>T	c.(3949-3951)GCT>TCT	p.A1317S
Pat_76	Pre-Treatment	ASH2L	9070	37	8	37978665	37978665	Missense_Mutation	SNP	G	A	4	71	c.1163G>A	c.(1162-1164)CGA>CAA	p.R388Q
Pat_76	Pre-Treatment	IDO1	3620	37	8	39771457	39771457	Missense_Mutation	SNP	G	A	3	6	c.16G>A	c.(16-18)GAA>AAA	p.E6K
Pat_76	Pre-Treatment	ZMAT4	79698	37	8	40625228	40625228	Missense_Mutation	SNP	C	T	21	25	c.124G>A	c.(124-126)GTC>ATC	p.V42I
Pat_76	Pre-Treatment	AGPAT6	137964	37	8	41470462	41470463	Missense_Mutation	DNP	CC	TT	27	25	c.894_895CC>TT	892-897)CGCCAC>CGTT	p.H299Y
Pat_76	Pre-Treatment	ANK1	286	37	8	41551487	41551487	Missense_Mutation	SNP	G	A	13	17	c.3461C>T	c.(3460-3462)TCC>TTC	p.S1154F
Pat_76	Pre-Treatment	POTEA	340441	37	8	43152483	43152483	Missense_Mutation	SNP	G	A	43	75	c.469G>A	c.(469-471)GAT>AAT	p.D157N
Pat_76	Pre-Treatment	MCM4	4173	37	8	48882577	48882577	Missense_Mutation	SNP	C	T	58	77	c.1394C>T	c.(1393-1395)GCC>GTC	p.A465V
Pat_76	Pre-Treatment	C8orf22	492307	37	8	49986883	49986883	Missense_Mutation	SNP	C	T	17	31	c.224C>T	c.(223-225)TCT>TTT	p.S75F

Pat_76	Pre-Treatment	PCMTD1	115294	37	8	52733146	52733146	Missense_Mutation	SNP	C	T	6	386	c.839G>A	c.(838-840)AGA>AAA	p.R280K
Pat_76	Pre-Treatment	RP1	6101	37	8	55541492	55541492	Missense_Mutation	SNP	G	A	48	75	c.5050G>A	c.(5050-5052)GAA>AAA	p.E1684K
Pat_76	Pre-Treatment	RP1	6101	37	8	55541652	55541652	Missense_Mutation	SNP	A	G	26	28	c.5210A>G	c.(5209-5211)GAA>GGA	p.E1737G
Pat_76	Pre-Treatment	XKR4	114786	37	8	56436719	56436719	Missense_Mutation	SNP	C	T	23	35	c.1886C>T	c.(1885-1887)CCT>CTT	p.P629L
Pat_76	Pre-Treatment	PLAG1	5324	37	8	57079014	57079014	Missense_Mutation	SNP	G	A	8	19	c.1291C>T	c.(1291-1293)CCC>TCC	p.P431S
Pat_76	Pre-Treatment	CYP7A1	1581	37	8	59409562	59409563	Missense_Mutation	DNP	CC	TT	64	89	c.508_509GG>AA	c.(508-510)GGG>AAG	p.G170K
Pat_76	Pre-Treatment	PREX2	80243	37	8	69028113	69028113	Missense_Mutation	SNP	G	A	73	116	c.3272G>A	c.(3271-3273)GGA>GAA	p.G1091E
Pat_76	Pre-Treatment	C8orf34	116328	37	8	69434163	69434163	Missense_Mutation	SNP	G	T	4	78	c.637G>T	c.(637-639)GAC>TAC	p.D213Y
Pat_76	Pre-Treatment	CRISPLD1	83690	37	8	75925132	75925132	Missense_Mutation	SNP	C	T	30	55	c.385C>T	c.(385-387)CCC>TCC	p.P129S
Pat_76	Pre-Treatment	PAG1	55824	37	8	81899700	81899700	Missense_Mutation	SNP	G	A	36	57	c.179C>T	c.(178-180)CCT>CTT	p.P60L
Pat_76	Pre-Treatment	WWP1	11059	37	8	87393063	87393064	Missense_Mutation	DNP	CT	TC	27	37	c.179_180CT>TC	c.(178-180)TCT>TTC	p.S60F
Pat_76	Pre-Treatment	CNGB3	54714	37	8	87656094	87656094	Nonsense_Mutation	SNP	G	A	27	48	c.1063C>T	c.(1063-1065)CGA>TGA	p.R355*
Pat_76	Pre-Treatment	SLC26A7	115111	37	8	92352666	92352666	Missense_Mutation	SNP	C	T	70	91	c.913C>T	c.(913-915)CTC>TTC	p.L305F
Pat_76	Pre-Treatment	POP1	10940	37	8	99140736	99140736	Missense_Mutation	SNP	C	T	29	29	c.454C>T	c.(454-456)CCC>TCC	p.P152S
Pat_76	Pre-Treatment	POP1	10940	37	8	99161210	99161210	Nonsense_Mutation	SNP	G	A	13	12	c.1878G>A	c.(1876-1878)TGG>TGA	p.W626*
Pat_76	Pre-Treatment	OSR2	116039	37	8	99961245	99961245	Missense_Mutation	SNP	C	T	20	34	c.65C>T	c.(64-66)TCC>TTC	p.S22F
Pat_76	Pre-Treatment	RGS22	26166	37	8	101092508	101092508	Missense_Mutation	SNP	C	T	5	10	c.193G>A	c.(193-195)GAA>AAA	p.E65K
Pat_76	Pre-Treatment	UBR5	51366	37	8	103326127	103326127	Missense_Mutation	SNP	G	A	47	65	c.1912C>T	c.(1912-1914)CCT>TCT	p.P638S
Pat_76	Pre-Treatment	RIMS2	9699	37	8	104778681	104778681	Missense_Mutation	SNP	G	A	19	48	c.614G>A	c.(613-615)CGA>CAA	p.R205Q
Pat_76	Pre-Treatment	RIMS2	9699	37	8	105257255	105257255	Missense_Mutation	SNP	G	A	69	119	c.3500G>A	c.(3499-3501)GGT>GAT	p.G1167D
Pat_76	Pre-Treatment	ZFPM2	23414	37	8	106813565	106813565	Missense_Mutation	SNP	G	A	18	33	c.1255G>A	c.(1255-1257)GAA>AAA	p.E419K
Pat_76	Pre-Treatment	ANGPT1	284	37	8	108306214	108306214	Missense_Mutation	SNP	G	A	80	95	c.988C>T	c.(988-990)CGT>TGT	p.R330C
Pat_76	Pre-Treatment	TRHR	7201	37	8	110131469	110131469	Missense_Mutation	SNP	C	A	124	164	c.982C>A	c.(982-984)CGT>AGT	p.R328S
Pat_76	Pre-Treatment	PKHD1L1	93035	37	8	110457809	110457809	Missense_Mutation	SNP	C	T	4	3	c.5711C>T	c.(5710-5712)CCA>CTA	p.P1904L
Pat_76	Pre-Treatment	PKHD1L1	93035	37	8	110477198	110477198	Missense_Mutation	SNP	C	T	34	43	c.8137C>T	c.(8137-8139)CTT>TTT	p.L2713F
Pat_76	Pre-Treatment	CSMD3	114788	37	8	113243822	113243822	Missense_Mutation	SNP	C	T	65	102	c.10780G>A	c.(10780-10782)GGA>AGA	p.G3594R
Pat_76	Pre-Treatment	CSMD3	114788	37	8	113519002	113519002	Missense_Mutation	SNP	G	A	24	37	c.4813C>T	c.(4813-4815)CCT>TCT	p.P1605S
Pat_76	Pre-Treatment	CSMD3	114788	37	8	113966963	113966963	Missense_Mutation	SNP	C	T	16	28	c.1370G>A	c.(1369-1371)AGA>AAA	p.R457K
Pat_76	Pre-Treatment	ENPP2	5168	37	8	120629774	120629774	Missense_Mutation	SNP	G	A	20	39	c.509C>T	c.(508-510)TCC>TTC	p.S170F
Pat_76	Pre-Treatment	DEPDC6	64798	37	8	120942126	120942126	Missense_Mutation	SNP	C	T	36	63	c.373C>T	c.(373-375)CCA>TCA	p.P125S
Pat_76	Pre-Treatment	FER1L6	654463	37	8	124989687	124989687	Missense_Mutation	SNP	G	A	75	116	c.901G>A	c.(901-903)GAT>AAT	p.D301N
Pat_76	Pre-Treatment	FER1L6	654463	37	8	125083819	125083819	Missense_Mutation	SNP	G	A	14	36	c.4039G>A	c.(4039-4041)GGG>AGG	p.G1347R
Pat_76	Pre-Treatment	FAM135B	51059	37	8	139164961	139164961	Missense_Mutation	SNP	C	T	56	93	c.1757G>A	c.(1756-1758)GGA>GAA	p.G586E
Pat_76	Pre-Treatment	DENND3	22898	37	8	142161766	142161766	Missense_Mutation	SNP	G	A	47	88	c.664G>A	c.(664-666)GAC>AAC	p.D222N
Pat_76	Pre-Treatment	LY6K	54742	37	8	143784711	143784711	Missense_Mutation	SNP	G	A	13	36	c.420G>A	c.(418-420)ATG>ATA	p.M140I
Pat_76	Pre-Treatment	SPATC1	375686	37	8	145095631	145095632	Missense_Mutation	DNP	CC	TT	7	36	c.929_930CC>TT	c.(928-930)CCC>CTT	p.P310L
Pat_76	Pre-Treatment	ERMP1	79956	37	9	5810087	5810087	Missense_Mutation	SNP	G	A	42	87	c.1472C>T	c.(1471-1473)TCC>TTC	p.S491F
Pat_76	Pre-Treatment	PTPRD	5789	37	9	8518132	8518132	Missense_Mutation	SNP	G	A	72	98	c.1259C>T	c.(1258-1260)GCC>GTC	p.A420V
Pat_76	Pre-Treatment	MPDZ	8777	37	9	13188823	13188823	Missense_Mutation	SNP	G	A	6	340	c.2324C>T	c.(2323-2325)CCG>CTG	p.P775L
Pat_76	Pre-Treatment	SH3GL2	6456	37	9	17761434	17761434	Splice_Site	SNP	G	A	28	3	c.115_splice	c.e3-1	p.K39_splice
Pat_76	Pre-Treatment	HAUS6	54801	37	9	19063041	19063041	Missense_Mutation	SNP	G	A	64	127	c.1594C>T	c.(1594-1596)CCA>TCA	p.P532S
Pat_76	Pre-Treatment	DENND4C	55667	37	9	19346035	19346035	Missense_Mutation	SNP	C	T	39	49	c.2413C>T	c.(2413-2415)CCT>TCT	p.P805S
Pat_76	Pre-Treatment	TAF1L	138474	37	9	32630273	32630273	Missense_Mutation	SNP	C	T	60	62	c.5305G>A	c.(5305-5307)GGA>AGA	p.G1769R
Pat_76	Pre-Treatment	DNAI1	27019	37	9	34491492	34491492	Splice_Site	SNP	G	A	20	26	c.622_splice	c.e8-1	p.D208_splice
Pat_76	Pre-Treatment	SHB	6461	37	9	37955901	37955901	Missense_Mutation	SNP	G	A	12	18	c.1205C>T	c.(1204-1206)GCC>GTC	p.A402V
Pat_76	Pre-Treatment	LOC442421	442421	37	9	66499716	66499716	Missense_Mutation	SNP	A	G	10	80	c.526A>G	c.(526-528)AAT>GAT	p.N176D
Pat_76	Pre-Treatment	PGM5	5239	37	9	70993145	70993145	Missense_Mutation	SNP	A	G	4	69	c.292A>G	c.(292-294)ATC>GTC	p.I98V

Pat_76	Pre-Treatment	PIP5K1B	8395	37	9	71509555	71509555	Splice_Site	SNP	G	A	4	149	c.771_splice	c.e8+1	p.R257_splice
Pat_76	Pre-Treatment	PCSK5	5125	37	9	78749077	78749077	Missense_Mutation	SNP	G	T	33	67	c.1261G>T	c.(1261-1263)GCG>TCG	p.A421S
Pat_76	Pre-Treatment	PCSK5	5125	37	9	78804120	78804121	Missense_Mutation	DNP	GG	AA	16	45	.2491_2492GG>A	c.(2491-2493)GGA>AAA	p.G831K
Pat_76	Pre-Treatment	GCNT1	2650	37	9	79118124	79118124	Missense_Mutation	SNP	C	T	28	58	c.827C>T	c.(826-828)CCT>CTT	p.P276L
Pat_76	Pre-Treatment	PRUNE2	158471	37	9	79323229	79323229	Missense_Mutation	SNP	C	T	14	12	c.3961G>A	c.(3961-3963)GAT>AAT	p.D1321N
Pat_76	Pre-Treatment	PRUNE2	158471	37	9	79441589	79441589	Missense_Mutation	SNP	C	T	23	34	c.568G>A	c.(568-570)GAA>AAA	p.E190K
Pat_76	Pre-Treatment	VPS13A	23230	37	9	79827939	79827939	Missense_Mutation	SNP	C	T	24	42	c.610C>T	c.(610-612)CGT>TGT	p.R204C
Pat_76	Pre-Treatment	FRMD3	257019	37	9	85950537	85950537	Missense_Mutation	SNP	C	T	10	15	c.490G>A	c.(490-492)GAT>AAT	p.D164N
Pat_76	Pre-Treatment	UBQLN1	29979	37	9	86280051	86280051	Missense_Mutation	SNP	G	A	4	92	c.1342C>T	c.(1342-1344)CCT>TCT	p.P448S
Pat_76	Pre-Treatment	HNRNPK	3190	37	9	86590392	86590392	Missense_Mutation	SNP	C	T	4	121	c.242G>A	c.(241-243)AGC>AAC	p.S81N
Pat_76	Pre-Treatment	PHF2	5253	37	9	96428104	96428104	Missense_Mutation	SNP	C	T	51	109	c.2074C>T	c.(2074-2076)CCC>TCC	p.P692S
Pat_76	Pre-Treatment	HSD17B3	3293	37	9	99064356	99064356	Missense_Mutation	SNP	G	A	27	36	c.31C>T	c.(31-33)CTC>TTC	p.L11F
Pat_76	Pre-Treatment	CTSL2	1515	37	9	99800270	99800271	Missense_Mutation	DNP	GG	AA	51	63	c.55_56CC>TT	c.(55-57)CCA>TTA	p.P19L
Pat_76	Pre-Treatment	FOXE1	2304	37	9	100616596	100616596	Missense_Mutation	SNP	G	A	25	28	c.400G>A	c.(400-402)GAG>AAG	p.E134K
Pat_76	Pre-Treatment	TRIM14	9830	37	9	100857249	100857250	Missense_Mutation	DNP	GG	AA	18	53	c.599_600CC>TT	c.(598-600)CCC>CTT	p.P200L
Pat_76	Pre-Treatment	LPPR1	54886	37	9	104079716	104079716	Missense_Mutation	SNP	C	T	62	72	c.883C>T	c.(883-885)CGT>TGT	p.R295C
Pat_76	Pre-Treatment	GRIN3A	116443	37	9	104449092	104449092	Missense_Mutation	SNP	C	T	11	32	c.1090G>A	c.(1090-1092)GAA>AAA	p.E364K
Pat_76	Pre-Treatment	CYLC2	1539	37	9	105767050	105767050	Missense_Mutation	SNP	C	T	15	14	c.254C>T	c.(253-255)TCT>TTT	p.S85F
Pat_76	Pre-Treatment	CYLC2	1539	37	9	105767487	105767487	Missense_Mutation	SNP	G	A	11	25	c.574G>A	c.(574-576)GAT>AAT	p.D192N
Pat_76	Pre-Treatment	OR13F1	138805	37	9	107267121	107267121	Missense_Mutation	SNP	C	T	82	130	c.578C>T	c.(577-579)TCC>TTC	p.S193F
Pat_76	Pre-Treatment	OR13C9	286362	37	9	107379644	107379644	Missense_Mutation	SNP	G	A	32	42	c.842C>T	c.(841-843)TCC>TTC	p.S281F
Pat_76	Pre-Treatment	IKBKAP	8518	37	9	111668727	111668727	Missense_Mutation	SNP	G	A	4	109	c.1499C>T	c.(1498-1500)CCG>CTG	p.P500L
Pat_76	Pre-Treatment	TXNDC8	255220	37	9	113096507	113096507	Missense_Mutation	SNP	G	A	24	53	c.118C>T	c.(118-120)CCT>TCT	p.P40S
Pat_76	Pre-Treatment	PTGR1	22949	37	9	114356512	114356512	Missense_Mutation	SNP	G	A	18	24	c.142C>T	c.(142-144)CCC>TCC	p.P48S
Pat_76	Pre-Treatment	ALAD	210	37	9	116154406	116154406	Missense_Mutation	SNP	C	T	3	16	c.157G>A	c.(157-159)GTG>ATG	p.V53M
Pat_76	Pre-Treatment	AKNA	80709	37	9	117118393	117118393	Missense_Mutation	SNP	G	A	27	42	c.2870C>T	c.(2869-2871)CCC>CTC	p.P957L
Pat_76	Pre-Treatment	TNC	3371	37	9	117819506	117819506	Missense_Mutation	SNP	G	A	23	38	c.4505C>T	c.(4504-4506)ACT>ATT	p.T1502I
Pat_76	Pre-Treatment	ASTN2	23245	37	9	119738438	119738438	Missense_Mutation	SNP	C	T	18	20	c.1706G>A	c.(1705-1707)GGC>GAC	p.G569D
Pat_76	Pre-Treatment	TRAF1	7185	37	9	123667467	123667467	Missense_Mutation	SNP	G	A	5	20	c.1082C>T	c.(1081-1083)GCC>GTC	p.A361V
Pat_76	Pre-Treatment	TRAF1	7185	37	9	123675765	123675765	Missense_Mutation	SNP	C	T	18	21	c.546G>A	c.(544-546)ATG>ATA	p.M182I
Pat_76	Pre-Treatment	OR1N1	138883	37	9	125289062	125289063	Missense_Mutation	DNP	CC	TT	17	22	c.510_511GG>AA	508-513)GGGGAA>GGAA	p.E171K
Pat_76	Pre-Treatment	RABGAP1	23637	37	9	125832695	125832695	Missense_Mutation	SNP	C	T	105	130	c.1975C>T	c.(1975-1977)CTT>TTT	p.L659F
Pat_76	Pre-Treatment	LMX1B	4010	37	9	129453221	129453221	Missense_Mutation	SNP	G	A	4	35	c.364G>A	c.(364-366)GTG>ATG	p.V122M
Pat_76	Pre-Treatment	LAMC3	10319	37	9	133901843	133901843	Missense_Mutation	SNP	G	A	9	10	c.545G>A	c.(544-546)GGC>GAC	p.G182D
Pat_76	Pre-Treatment	NTNG2	84628	37	9	135042312	135042312	Missense_Mutation	SNP	C	T	28	37	c.94C>T	c.(94-96)CCC>TCC	p.P32S
Pat_76	Pre-Treatment	SETX	23064	37	9	135204652	135204652	Missense_Mutation	SNP	C	T	27	34	c.2333G>A	c.(2332-2334)CGA>CAA	p.R778Q
Pat_76	Pre-Treatment	ADAMTS13	11093	37	9	136323188	136323189	Missense_Mutation	DNP	CC	TT	8	23	.4049_4050CC>T	c.(4048-4050)ACC>ATT	p.T1350I
Pat_76	Pre-Treatment	DBH	1621	37	9	136518122	136518122	Splice_Site	SNP	G	A	18	31	c.1434_splice	c.e9+1	p.V478_splice
Pat_76	Pre-Treatment	COL5A1	1289	37	9	137688695	137688695	Missense_Mutation	SNP	G	A	14	38	c.2846G>A	c.(2845-2847)GGA>GAA	p.G949E
Pat_76	Pre-Treatment	CAMSAP1	157922	37	9	138707828	138707828	Missense_Mutation	SNP	G	A	11	43	c.4295C>T	c.(4294-4296)CCC>CTC	p.P1432L
Pat_76	Pre-Treatment	SEC16A	9919	37	9	139371934	139371934	Missense_Mutation	SNP	G	A	20	34	c.134C>T	c.(133-135)ACT>ATT	p.T45I
Pat_76	Pre-Treatment	NOTCH1	4851	37	9	139391227	139391227	Missense_Mutation	SNP	G	T	4	96	c.6964C>A	c.(6964-6966)CAA>AAA	p.Q2322K
Pat_76	Pre-Treatment	ANAPC2	29882	37	9	140069793	140069793	Missense_Mutation	SNP	C	T	9	12	c.2152G>A	c.(2152-2154)GAG>AAG	p.E718K
Pat_76	Pre-Treatment	ANAPC2	29882	37	9	140077628	140077628	Missense_Mutation	SNP	G	A	45	116	c.1235C>T	c.(1234-1236)CCT>CTT	p.P412L
Pat_76	Pre-Treatment	NDOR1	27158	37	9	140109131	140109131	Missense_Mutation	SNP	C	T	4	57	c.832C>T	c.(832-834)CCG>TCG	p.P278S
Pat_76	Pre-Treatment	ENTPD8	377841	37	9	140330184	140330184	Missense_Mutation	SNP	C	T	17	21	c.1148G>A	c.(1147-1149)AGG>AAG	p.R383K
Pat_76	Pre-Treatment	SHOX	6473	37	X	591723	591723	Missense_Mutation	SNP	G	A	73	95	c.91G>A	c.(91-93)GAT>AAT	p.D31N

Pat_76	Pre-Treatment	ASMT	438	37	X	1742197	1742197	Missense_Mutation	SNP	G	A	9	16	c.235G>A	c.(235-237)GGA>AGA	p.G79R
Pat_76	Pre-Treatment	ASMT	438	37	X	1748718	1748718	Missense_Mutation	SNP	G	A	71	139	c.448G>A	c.(448-450)GAG>AAG	p.E150K
Pat_76	Pre-Treatment	ARSD	414	37	X	2836227	2836227	Missense_Mutation	SNP	G	A	7	5	c.481C>T	c.(481-483)CAC>TAC	p.H161Y
Pat_76	Pre-Treatment	MXRA5	25878	37	X	3240077	3240077	Missense_Mutation	SNP	C	T	39	40	c.3649G>A	c.(3649-3651)GAA>AAA	p.E1217K
Pat_76	Pre-Treatment	NLGN4X	57502	37	X	6069266	6069266	Missense_Mutation	SNP	G	A	19	31	c.242C>T	c.(241-243)CCC>CTC	p.P81L
Pat_76	Pre-Treatment	VCX	26609	37	X	7811971	7811971	Missense_Mutation	SNP	G	A	130	321	c.535G>A	c.(535-537)GAG>AAG	p.E179K
Pat_76	Pre-Treatment	SHROOM2	357	37	X	9863495	9863495	Missense_Mutation	SNP	C	T	6	7	c.1547C>T	c.(1546-1548)CCA>CTA	p.P516L
Pat_76	Pre-Treatment	TLR8	51311	37	X	12938573	12938573	Missense_Mutation	SNP	C	T	21	64	c.1414C>T	c.(1414-1416)CGT>TGT	p.R472C
Pat_76	Pre-Treatment	TLR8	51311	37	X	12939914	12939914	Missense_Mutation	SNP	G	A	34	48	c.2755G>A	c.(2755-2757)GAG>AAG	p.E919K
Pat_76	Pre-Treatment	EGFL6	25975	37	X	13621532	13621532	Missense_Mutation	SNP	C	T	11	19	c.497C>T	c.(496-498)GCC>GTC	p.A166V
Pat_76	Pre-Treatment	PHEX	5251	37	X	22117199	22117199	Missense_Mutation	SNP	G	A	73	132	c.1009G>A	c.(1009-1011)GAG>AAG	p.E337K
Pat_76	Pre-Treatment	PHEX	5251	37	X	22237170	22237170	Missense_Mutation	SNP	C	T	28	43	c.1718C>T	c.(1717-1719)GCT>GTT	p.A573V
Pat_76	Pre-Treatment	PDK3	5165	37	X	24521608	24521608	Missense_Mutation	SNP	G	A	4	88	c.485G>A	c.(484-486)CGC>CAC	p.R162H
Pat_76	Pre-Treatment	POLA1	5422	37	X	24721395	24721395	Missense_Mutation	SNP	G	A	13	39	c.178G>A	c.(178-180)GAA>AAA	p.E60K
Pat_76	Pre-Treatment	CXorf21	80231	37	X	30578039	30578039	Missense_Mutation	SNP	G	A	14	30	c.434C>T	c.(433-435)CCC>CTC	p.P145L
Pat_76	Pre-Treatment	FAM47A	158724	37	X	34148687	34148687	Missense_Mutation	SNP	G	A	11	23	c.1709C>T	c.(1708-1710)TCG>TTG	p.S570L
Pat_76	Pre-Treatment	CXorf59	286464	37	X	36117969	36117969	Nonsense_Mutation	SNP	G	A	25	68	c.825G>A	c.(823-825)TGG>TGA	p.W275*
Pat_76	Pre-Treatment	SRPX	8406	37	X	38031196	38031196	Missense_Mutation	SNP	C	T	23	68	c.464G>A	c.(463-465)GGG>GAG	p.G155E
Pat_76	Pre-Treatment	RPGR	6103	37	X	38129006	38129006	Missense_Mutation	SNP	G	A	19	41	c.2321C>T	c.(2320-2322)TCC>TTC	p.S774F
Pat_76	Pre-Treatment	MED14	9282	37	X	40551551	40551551	Missense_Mutation	SNP	G	A	16	30	c.1864C>T	c.(1864-1866)CCA>TCA	p.P622S
Pat_76	Pre-Treatment	GPR34	2857	37	X	41555789	41555789	Nonsense_Mutation	SNP	G	A	20	21	c.903G>A	c.(901-903)TGG>TGA	p.W301*
Pat_76	Pre-Treatment	CCDC120	90060	37	X	48925184	48925184	Missense_Mutation	SNP	C	T	7	16	c.1429C>T	c.(1429-1431)CGC>TGC	p.R477C
Pat_76	Pre-Treatment	GPKOW	27238	37	X	48976140	48976140	Missense_Mutation	SNP	C	A	9	27	c.484G>T	c.(484-486)GTC>TTC	p.V162F
Pat_76	Pre-Treatment	PRICKLE3	4007	37	X	49032516	49032516	Missense_Mutation	SNP	C	T	7	19	c.1354G>A	c.(1354-1356)GAG>AAG	p.E452K
Pat_76	Pre-Treatment	DGKK	139189	37	X	50119787	50119787	Nonsense_Mutation	SNP	A	C	18	18	c.3242T>G	c.(3241-3243)TTA>TGA	p.L1081*
Pat_76	Pre-Treatment	PHF8	23133	37	X	54069119	54069119	Missense_Mutation	SNP	C	T	23	52	c.151G>A	c.(151-153)GAT>AAT	p.D51N
Pat_76	Pre-Treatment	FAAH2	158584	37	X	57313331	57313331	Missense_Mutation	SNP	G	A	5	7	c.73G>A	c.(73-75)GGC>AGC	p.G25S
Pat_76	Pre-Treatment	FAAH2	158584	37	X	57405092	57405092	Missense_Mutation	SNP	C	T	4	127	c.751C>T	c.(751-753)CCC>TCC	p.P251S
Pat_76	Pre-Treatment	MTMR8	55613	37	X	63564991	63564991	Missense_Mutation	SNP	G	A	27	45	c.799C>T	c.(799-801)CGC>TGC	p.R267C
Pat_76	Pre-Treatment	ZC4H2	55906	37	X	64137694	64137694	Missense_Mutation	SNP	G	A	10	18	c.644C>T	c.(643-645)CCC>CTC	p.P215L
Pat_76	Pre-Treatment	LAS1L	81887	37	X	64738050	64738050	Missense_Mutation	SNP	C	T	23	43	c.1744G>A	c.(1744-1746)GAG>AAG	p.E582K
Pat_76	Pre-Treatment	MSN	4478	37	X	64936728	64936728	Nonsense_Mutation	SNP	C	T	74	61	c.61C>T	c.(61-63)CAG>TAG	p.Q21*
Pat_76	Pre-Treatment	HEPH	9843	37	X	65476115	65476115	Missense_Mutation	SNP	G	A	40	47	c.2848G>A	c.(2848-2850)GAT>AAT	p.D950N
Pat_76	Pre-Treatment	AR	367	37	X	66905918	66905918	Missense_Mutation	SNP	G	T	25	32	c.1835G>T	c.(1834-1836)TGT>TTT	p.C612F
Pat_76	Pre-Treatment	OTUD6A	139562	37	X	69283186	69283187	Missense_Mutation	DNP	CC	TT	12	9	c.812_813CC>TT	c.(811-813)TCC>TTT	p.S271F
Pat_76	Pre-Treatment	DGAT2L6	347516	37	X	69419701	69419701	Nonsense_Mutation	SNP	G	A	20	32	c.236G>A	c.(235-237)TGG>TAG	p.W79*
Pat_76	Pre-Treatment	P2RY4	5030	37	X	69478907	69478907	Missense_Mutation	SNP	G	A	12	25	c.568C>T	c.(568-570)CGG>TGG	p.R190W
Pat_76	Pre-Treatment	MED12	9968	37	X	70344131	70344131	Missense_Mutation	SNP	G	A	17	30	c.1867G>A	c.(1867-1869)GAC>AAC	p.D623N
Pat_76	Pre-Treatment	MED12	9968	37	X	70345913	70345913	Missense_Mutation	SNP	G	A	6	272	c.2450G>A	c.(2449-2451)CGC>CAC	p.R817H
Pat_76	Pre-Treatment	TAF1	6872	37	X	70586306	70586306	Missense_Mutation	SNP	G	A	5	29	c.142G>A	c.(142-144)GGA>AGA	p.G48R
Pat_76	Pre-Treatment	TAF1	6872	37	X	70597668	70597668	Missense_Mutation	SNP	T	G	15	9	c.927T>G	c.(925-927)GAT>GAG	p.D309E
Pat_76	Pre-Treatment	RGAG4	340526	37	X	71350547	71350547	Missense_Mutation	SNP	C	T	60	113	c.844G>A	c.(844-846)GAA>AAA	p.E282K
Pat_76	Pre-Treatment	PHKA1	5255	37	X	71830949	71830949	Missense_Mutation	SNP	C	T	33	41	c.2455G>A	c.(2455-2457)GAA>AAA	p.E819K
Pat_76	Pre-Treatment	PHKA1	5255	37	X	71838692	71838692	Missense_Mutation	SNP	G	A	36	63	c.2237C>T	c.(2236-2238)TCT>TTT	p.S746F
Pat_76	Pre-Treatment	PHKA1	5255	37	X	71838696	71838696	Missense_Mutation	SNP	G	A	35	61	c.2233C>T	c.(2233-2235)CCC>TCC	p.P745S
Pat_76	Pre-Treatment	CHIC1	53344	37	X	72804260	72804260	Missense_Mutation	SNP	C	A	6	8	c.359C>A	c.(358-360)CCA>CAA	p.P120Q
Pat_76	Pre-Treatment	ZCCHC13	389874	37	X	73524355	73524355	Missense_Mutation	SNP	G	A	35	50	c.254G>A	c.(253-255)CGA>CAA	p.R85Q

Pat_76	Pre-Treatment	ATRX	546	37	X	76939192	76939192	Missense_Mutation	SNP	G	A	161	339	c.1556C>T	c.(1555-1557)TCT>TTT	p.S519F
Pat_76	Pre-Treatment	ATP7A	538	37	X	77254089	77254089	Missense_Mutation	SNP	G	A	44	85	c.1451G>A	c.(1450-1452)GGA>GAA	p.G484E
Pat_76	Pre-Treatment	FAM46D	169966	37	X	79698084	79698084	Missense_Mutation	SNP	A	C	10	27	c.46A>C	c.(46-48)ACA>CCA	p.T16P
Pat_76	Pre-Treatment	BRWD3	254065	37	X	79945476	79945476	Nonsense_Mutation	SNP	G	A	11	35	c.3718C>T	c.(3718-3720)CGA>TGA	p.R1240*
Pat_76	Pre-Treatment	RPS6KA6	27330	37	X	83357077	83357077	Missense_Mutation	SNP	G	A	20	29	c.1744C>T	c.(1744-1746)CCA>TCA	p.P582S
Pat_76	Pre-Treatment	PCDH19	57526	37	X	99663156	99663156	Missense_Mutation	SNP	C	T	5	148	c.440G>A	c.(439-441)CGC>CAC	p.R147H
Pat_76	Pre-Treatment	TSPAN6	7105	37	X	99885830	99885830	Missense_Mutation	SNP	G	A	24	27	c.703C>T	c.(703-705)CGT>TGT	p.R235C
Pat_76	Pre-Treatment	DRP2	1821	37	X	100492690	100492690	Missense_Mutation	SNP	G	A	51	91	c.364G>A	c.(364-366)GAT>AAT	p.D122N
Pat_76	Pre-Treatment	ZMAT1	84460	37	X	101139567	101139567	Missense_Mutation	SNP	G	A	4	97	c.319C>T	c.(319-321)CGG>TGG	p.R107W
Pat_76	Pre-Treatment	NXF2B	728343	37	X	101623758	101623758	Missense_Mutation	SNP	G	A	21	75	c.604C>T	c.(604-606)CCC>TCC	p.P202S
Pat_76	Pre-Treatment	GPRASP1	9737	37	X	101911210	101911210	Missense_Mutation	SNP	G	A	41	84	c.2369G>A	c.(2368-2370)AGA>AAA	p.R790K
Pat_76	Pre-Treatment	GPRASP2	114928	37	X	101971581	101971581	Missense_Mutation	SNP	C	T	29	53	c.1784C>T	c.(1783-1785)TCT>TTT	p.S595F
Pat_76	Pre-Treatment	ESX1	80712	37	X	103499043	103499043	Missense_Mutation	SNP	C	T	22	62	c.298G>A	c.(298-300)GAG>AAG	p.E100K
Pat_76	Pre-Treatment	ESX1	80712	37	X	103499180	103499181	Missense_Mutation	DNP	CC	TT	70	130	c.160_161GG>AA	c.(160-162)GGA>AAA	p.G54K
Pat_76	Pre-Treatment	NRK	203447	37	X	105183928	105183928	Missense_Mutation	SNP	G	A	7	16	c.3862G>A	c.(3862-3864)GAT>AAT	p.D1288N
Pat_76	Pre-Treatment	MUM1L1	139221	37	X	105451179	105451179	Missense_Mutation	SNP	C	T	3	8	c.1754C>T	c.(1753-1755)TCA>TTA	p.S585L
Pat_76	Pre-Treatment	MORC4	79710	37	X	106185285	106185285	Missense_Mutation	SNP	C	T	52	50	c.2543G>A	c.(2542-2544)AGA>AAA	p.R848K
Pat_76	Pre-Treatment	VSIG1	340547	37	X	107315967	107315967	Missense_Mutation	SNP	C	T	83	167	c.473C>T	c.(472-474)TCC>TTC	p.S158F
Pat_76	Pre-Treatment	VSIG1	340547	37	X	107320451	107320451	Missense_Mutation	SNP	G	A	14	6	c.1004G>A	c.(1003-1005)GGA>GAA	p.G335E
Pat_76	Pre-Treatment	COL4A6	1288	37	X	107413919	107413919	Missense_Mutation	SNP	C	T	40	91	c.3416G>A	c.(3415-3417)GGA>GAA	p.G1139E
Pat_76	Pre-Treatment	COL4A6	1288	37	X	107430407	107430407	Missense_Mutation	SNP	C	T	77	83	c.1873G>A	c.(1873-1875)GGA>AGA	p.G625R
Pat_76	Pre-Treatment	COL4A6	1288	37	X	107431160	107431160	Missense_Mutation	SNP	G	A	52	68	c.1688C>T	c.(1687-1689)TCT>TTT	p.S563F
Pat_76	Pre-Treatment	COL4A5	1287	37	X	107814644	107814644	Missense_Mutation	SNP	G	A	47	74	c.386G>A	c.(385-387)GGA>GAA	p.G129E
Pat_76	Pre-Treatment	COL4A5	1287	37	X	107865965	107865965	Nonsense_Mutation	SNP	A	T	22	25	c.2827A>T	c.(2827-2829)AAA>TAA	p.K943*
Pat_76	Pre-Treatment	GUCY2F	2986	37	X	108697082	108697082	Missense_Mutation	SNP	G	A	10	9	c.1039C>T	c.(1039-1041)CCG>TCG	p.P347S
Pat_76	Pre-Treatment	DCX	1641	37	X	110576334	110576335	Missense_Mutation	DNP	GG	AA	16	25	c.995_996CC>TT	c.(994-996)GCC>GTT	p.A332V
Pat_76	Pre-Treatment	KLHL13	90293	37	X	117079486	117079486	Missense_Mutation	SNP	C	T	13	37	c.151G>A	c.(151-153)GAA>AAA	p.E51K
Pat_76	Pre-Treatment	WDR44	54521	37	X	117577623	117577623	Missense_Mutation	SNP	C	T	39	56	c.2485C>T	c.(2485-2487)CGT>TGT	p.R829C
Pat_76	Pre-Treatment	DOCK11	139818	37	X	117676792	117676792	Missense_Mutation	SNP	G	A	61	135	c.207G>A	c.(205-207)ATG>ATA	p.M69I
Pat_76	Pre-Treatment	DOCK11	139818	37	X	117744362	117744362	Missense_Mutation	SNP	G	A	30	40	c.3077G>A	c.(3076-3078)AGT>AAT	p.S1026N
Pat_76	Pre-Treatment	LONRF3	79836	37	X	118123461	118123461	Missense_Mutation	SNP	G	A	18	25	c.1150G>A	c.(1150-1152)GGG>AGG	p.G384R
Pat_76	Pre-Treatment	UPF3B	65109	37	X	118985459	118985459	Missense_Mutation	SNP	T	G	9	30	c.369A>C	c.(367-369)AAA>AAC	p.K123N
Pat_76	Pre-Treatment	ODZ1	10178	37	X	123699255	123699255	Missense_Mutation	SNP	G	A	15	15	c.2233C>T	c.(2233-2235)CCT>TCT	p.P745S
Pat_76	Pre-Treatment	ACTRT1	139741	37	X	127185537	127185537	Missense_Mutation	SNP	C	T	74	93	c.649G>A	c.(649-651)GAG>AAG	p.E217K
Pat_76	Pre-Treatment	OCRL	4952	37	X	128703368	128703368	Missense_Mutation	SNP	C	T	76	130	c.1594C>T	c.(1594-1596)CAT>TAT	p.H532Y
Pat_76	Pre-Treatment	ZDHHC9	51114	37	X	128957792	128957792	Missense_Mutation	SNP	G	A	116	124	c.350C>T	c.(349-351)CCC>CTC	p.P117L
Pat_76	Pre-Treatment	ELF4	2000	37	X	129203363	129203363	Missense_Mutation	SNP	C	T	33	55	c.1099G>A	c.(1099-1101)GGA>AGA	p.G367R
Pat_76	Pre-Treatment	ARHGAP36	158763	37	X	130218339	130218339	Missense_Mutation	SNP	C	T	3	18	c.706C>T	c.(706-708)CCC>TCC	p.P236S
Pat_76	Pre-Treatment	IGSF1	3547	37	X	130409467	130409467	Missense_Mutation	SNP	C	T	55	97	c.3169G>A	c.(3169-3171)GAA>AAA	p.E1057K
Pat_76	Pre-Treatment	MBNL3	55796	37	X	131573612	131573612	Missense_Mutation	SNP	G	A	111	137	c.28C>T	c.(28-30)CGT>TGT	p.R10C
Pat_76	Pre-Treatment	USP26	83844	37	X	132160571	132160571	Missense_Mutation	SNP	G	A	12	28	c.1678C>T	c.(1678-1680)CCC>TCC	p.P560S
Pat_76	Pre-Treatment	MMGT1	93380	37	X	135047268	135047268	Missense_Mutation	SNP	G	A	104	163	c.311C>T	c.(310-312)TCG>TTG	p.S104L
Pat_76	Pre-Treatment	CD40LG	959	37	X	135732446	135732446	Missense_Mutation	SNP	C	G	4	106	c.178C>G	c.(178-180)CAT>GAT	p.H60D
Pat_76	Pre-Treatment	MAGEC1	9947	37	X	140993320	140993320	Missense_Mutation	SNP	A	G	7	141	c.130A>G	c.(130-132)AGC>GGC	p.S44G
Pat_76	Pre-Treatment	MAGEC1	9947	37	X	140993818	140993818	Missense_Mutation	SNP	T	G	54	502	c.628T>G	c.(628-630)TTA>GTA	p.L210V
Pat_76	Pre-Treatment	MAGEC1	9947	37	X	140994421	140994421	Missense_Mutation	SNP	C	T	111	141	c.1231C>T	c.(1231-1233)CCT>TCT	p.P411S
Pat_76	Pre-Treatment	MAGEC1	9947	37	X	140994923	140994923	Missense_Mutation	SNP	A	T	12	470	c.1733A>T	c.(1732-1734)CAC>CTC	p.H578L

Pat_76	Pre-Treatment	MAGEA11	4110	37	X	148797442	148797442	Missense_Mutation	SNP	C	T	48	63	c.296C>T	c.(295-297)CCC>CTC	p.P99L
Pat_76	Pre-Treatment	MAGEA11	4110	37	X	148798372	148798373	Missense_Mutation	DNP	GG	AA	66	74	.1226_1227GG>A	c.(1225-1227)AGG>AAA	p.R409K
Pat_76	Pre-Treatment	GPR50	9248	37	X	150348908	150348908	Missense_Mutation	SNP	T	G	44	69	c.853T>G	c.(853-855)TTC>GTC	p.F285V
Pat_76	Pre-Treatment	MAGEA10	4109	37	X	151303507	151303507	Missense_Mutation	SNP	G	A	27	53	c.586C>T	c.(586-588)CCC>TCC	p.P196S
Pat_76	Pre-Treatment	GABRQ	55879	37	X	151821313	151821314	Missense_Mutation	DNP	GG	AA	76	62	.1468_1469GG>A	c.(1468-1470)GGC>AAC	p.G490N
Pat_76	Pre-Treatment	MAGEA6	4105	37	X	151869683	151869683	Nonsense_Mutation	SNP	C	T	139	83	c.373C>T	c.(373-375)CGA>TGA	p.R125*
Pat_76	Pre-Treatment	MAGEA12	4111	37	X	151900098	151900098	Missense_Mutation	SNP	C	T	103	120	c.703G>A	c.(703-705)GAG>AAG	p.E235K
Pat_76	Pre-Treatment	CETN2	1069	37	X	151996420	151996420	Missense_Mutation	SNP	A	G	40	106	c.484T>C	c.(484-486)TTC>CTC	p.F162L
Pat_76	Pre-Treatment	HAUS7	55559	37	X	152735942	152735942	Missense_Mutation	SNP	G	A	11	13	c.104C>T	c.(103-105)TCC>TTC	p.S35F
Pat_76	Pre-Treatment	HCFC1	3054	37	X	153217050	153217050	Missense_Mutation	SNP	G	A	46	85	c.5369C>T	c.(5368-5370)TCC>TTC	p.S1790F
Pat_76	Pre-Treatment	HCFC1	3054	37	X	153224937	153224937	Missense_Mutation	SNP	G	A	18	16	c.1450C>T	c.(1450-1452)CCT>TCT	p.P484S
Pat_76	Pre-Treatment	FLNA	2316	37	X	153594560	153594560	Nonsense_Mutation	SNP	G	A	20	43	c.1261C>T	c.(1261-1263)CAG>TAG	p.Q421*
Pat_76	Pre-Treatment	PLXNA3	55558	37	X	153691999	153691999	Missense_Mutation	SNP	G	A	12	16	c.1513G>A	c.(1513-1515)GAC>AAC	p.D505N
Pat_76	Pre-Treatment	PLXNA3	55558	37	X	153693191	153693191	Missense_Mutation	SNP	G	A	11	18	c.2023G>A	c.(2023-2025)GGC>AGC	p.G675S
Pat_76	Pre-Treatment	PLXNA3	55558	37	X	153696206	153696206	Missense_Mutation	SNP	G	C	17	40	c.3682G>C	c.(3682-3684)GGT>CGT	p.G1228R
Pat_76	Post-Resistance	AGRN	375790	37	1	984754	984754	Missense_Mutation	SNP	G	C	8	24	c.4437G>C	c.(4435-4437)GAG>GAC	p.E1479D
Pat_76	Post-Resistance	NADK	65220	37	1	1685561	1685561	Missense_Mutation	SNP	T	C	16	94	c.1030A>G	c.(1030-1032)ATG>GTG	p.M344V
Pat_76	Post-Resistance	CHD5	26038	37	1	6169939	6169939	Missense_Mutation	SNP	C	T	14	48	c.5494G>A	c.(5494-5496)GTG>ATG	p.V1832M
Pat_76	Post-Resistance	SLC2A7	155184	37	1	9063467	9063467	Missense_Mutation	SNP	T	C	18	27	c.1431A>G	c.(1429-1431)ATA>ATG	p.I477M
Pat_76	Post-Resistance	KIF1B	23095	37	1	10405979	10405979	Nonsense_Mutation	SNP	G	A	11	24	c.3765G>A	c.(3763-3765)TGG>TGA	p.W1255*
Pat_76	Post-Resistance	C1orf127	148345	37	1	11017690	11017690	Missense_Mutation	SNP	G	A	6	13	c.229C>T	c.(229-231)CTT>TTT	p.L77F
Pat_76	Post-Resistance	PTCHD2	57540	37	1	11579548	11579548	Missense_Mutation	SNP	G	A	31	95	c.2026G>A	c.(2026-2028)GAG>AAG	p.E676K
Pat_76	Post-Resistance	NPPA	4878	37	1	11907322	11907322	Missense_Mutation	SNP	C	T	7	10	c.298G>A	c.(298-300)GGC>AGC	p.G100S
Pat_76	Post-Resistance	PRAMEF12	390999	37	1	12835290	12835290	Missense_Mutation	SNP	C	T	23	49	c.280C>T	c.(280-282)CGC>TGC	p.R94C
Pat_76	Post-Resistance	LOC649330	649330	37	1	12907921	12907921	Missense_Mutation	SNP	C	T	7	68	c.222G>A	c.(220-222)ATG>ATA	p.M74I
Pat_76	Post-Resistance	DNAJC16	23341	37	1	15890790	15890790	Nonsense_Mutation	SNP	C	T	11	36	c.1534C>T	c.(1534-1536)CGA>TGA	p.R512*
Pat_76	Post-Resistance	MST1P9	11223	37	1	17086053	17086053	Missense_Mutation	SNP	G	A	5	19	c.844C>T	c.(844-846)CAC>TAC	p.H282Y
Pat_76	Post-Resistance	KLHDC7A	127707	37	1	18807831	18807831	Missense_Mutation	SNP	G	A	3	8	c.356G>A	c.(355-357)AGA>AAA	p.R119K
Pat_76	Post-Resistance	KLHDC7A	127707	37	1	18808730	18808730	Missense_Mutation	SNP	C	T	17	39	c.1255C>T	c.(1255-1257)CCG>TCG	p.P419S
Pat_76	Post-Resistance	PLA2G2D	26279	37	1	20442911	20442911	Missense_Mutation	SNP	C	G	16	29	c.100G>C	c.(100-102)GGG>CGG	p.G34R
Pat_76	Post-Resistance	ECE1	1889	37	1	21582571	21582571	Nonsense_Mutation	SNP	C	A	12	43	c.889G>T	c.(889-891)GAG>TAG	p.E297*
Pat_76	Post-Resistance	RAP1GAP	5909	37	1	21936111	21936111	Missense_Mutation	SNP	G	A	24	64	c.1028C>T	c.(1027-1029)CCC>CTC	p.P343L
Pat_76	Post-Resistance	EPHB2	2048	37	1	23232566	23232566	Missense_Mutation	SNP	A	T	20	44	c.1852A>T	c.(1852-1854)ATC>TTC	p.I618F
Pat_76	Post-Resistance	GRHL3	57822	37	1	24669215	24669215	Missense_Mutation	SNP	G	A	22	73	c.1253G>A	c.(1252-1254)CGG>CAG	p.R418Q
Pat_76	Post-Resistance	ARID1A	8289	37	1	27106876	27106876	Missense_Mutation	SNP	T	C	8	63	c.6487T>C	c.(6487-6489)TGC>CGC	p.C2163R
Pat_76	Post-Resistance	MAP3K6	9064	37	1	27686450	27686450	Missense_Mutation	SNP	G	A	37	58	c.2218C>T	c.(2218-2220)CCC>TCC	p.P740S
Pat_76	Post-Resistance	CD164L2	388611	37	1	27709119	27709119	Missense_Mutation	SNP	G	A	13	17	c.127C>T	c.(127-129)CGC>TGC	p.R43C
Pat_76	Post-Resistance	SFRS4	6429	37	1	29475177	29475178	Missense_Mutation	DNP	GG	AA	82	133	.1229_1230CC>T	c.(1228-1230)TCC>TTT	p.S410F
Pat_76	Post-Resistance	PTPRU	10076	37	1	29585233	29585233	Missense_Mutation	SNP	G	A	3	33	c.422G>A	c.(421-423)CGT>CAT	p.R141H
Pat_76	Post-Resistance	PTPRU	10076	37	1	29652156	29652156	Missense_Mutation	SNP	G	A	20	70	c.4324G>A	c.(4324-4326)GGG>AGG	p.G1442R
Pat_76	Post-Resistance	SPOCD1	90853	37	1	32280093	32280093	Missense_Mutation	SNP	C	T	8	15	c.842G>A	c.(841-843)GGG>GAG	p.G281E
Pat_76	Post-Resistance	LCK	3932	37	1	32751189	32751189	Missense_Mutation	SNP	G	A	28	36	c.1402G>A	c.(1402-1404)GAG>AAG	p.E468K
Pat_76	Post-Resistance	CSMD2	114784	37	1	34383699	34383699	Missense_Mutation	SNP	G	A	8	15	c.796C>T	c.(796-798)CTC>TTC	p.L266F
Pat_76	Post-Resistance	CSMD2	114784	37	1	34554741	34554741	Missense_Mutation	SNP	C	T	5	15	c.121G>A	c.(121-123)GGG>AGG	p.G41R
Pat_76	Post-Resistance	EIF2C1	26523	37	1	36359345	36359345	Missense_Mutation	SNP	G	A	17	47	c.583G>A	c.(583-585)GAG>AAG	p.E195K
Pat_76	Post-Resistance	C1orf109	54955	37	1	38149083	38149083	Missense_Mutation	SNP	G	A	8	17	c.482C>T	c.(481-483)TCG>TTG	p.S161L
Pat_76	Post-Resistance	KIAA0754	643314	37	1	39878887	39878887	Missense_Mutation	SNP	C	T	4	9	c.2950C>T	c.(2950-2952)CCA>TCA	p.P984S

Pat_76	Post-Resistance	NT5C1A	84618	37	1	40131779	40131779	Missense_Mutation	SNP	C	T	31	65	c.265G>A	c.(265-267)GAA>AAA	p.E89K
Pat_76	Post-Resistance	HPCAL4	51440	37	1	40149802	40149802	Missense_Mutation	SNP	G	A	10	11	c.185C>T	c.(184-186)TCC>TTC	p.S62F
Pat_76	Post-Resistance	PPIE	10450	37	1	40218614	40218614	Missense_Mutation	SNP	A	G	18	52	c.727A>G	c.(727-729)ACC>GCC	p.T243A
Pat_76	Post-Resistance	NFYC	4802	37	1	41218908	41218908	Missense_Mutation	SNP	C	T	5	28	c.377C>T	c.(376-378)CCA>CTA	p.P126L
Pat_76	Post-Resistance	TIE1	7075	37	1	43778895	43778895	Missense_Mutation	SNP	C	T	15	27	c.2017C>T	c.(2017-2019)CCA>TCA	p.P673S
Pat_76	Post-Resistance	PTPRF	5792	37	1	44058256	44058257	Missense_Mutation	DNP	CC	TT	9	15	.1797_1798CC>T	795-1800)GCCCGC>GCT	p.R600C
Pat_76	Post-Resistance	DMAP1	55929	37	1	44684863	44684863	Missense_Mutation	SNP	C	T	13	14	c.856C>T	c.(856-858)CGC>TGC	p.R286C
Pat_76	Post-Resistance	RNF220	55182	37	1	45110737	45110737	Missense_Mutation	SNP	C	T	9	12	c.1294C>T	c.(1294-1296)CGG>TGG	p.R432W
Pat_76	Post-Resistance	FAAH	2166	37	1	46871441	46871441	Missense_Mutation	SNP	C	T	13	13	c.760C>T	c.(760-762)CTC>TTC	p.L254F
Pat_76	Post-Resistance	CYP4A11	1579	37	1	47402978	47402978	Nonsense_Mutation	SNP	C	T	16	20	c.378G>A	c.(376-378)TGG>TGA	p.W126*
Pat_76	Post-Resistance	CYP4Z1	199974	37	1	47548123	47548123	Missense_Mutation	SNP	G	A	7	70	c.482G>A	c.(481-483)CGG>CAG	p.R161Q
Pat_76	Post-Resistance	SLC5A9	200010	37	1	48697728	48697728	Missense_Mutation	SNP	C	T	32	66	c.802C>T	c.(802-804)CAC>TAC	p.H268Y
Pat_76	Post-Resistance	SPATA6	54558	37	1	48877245	48877245	Missense_Mutation	SNP	G	A	5	8	c.296C>T	c.(295-297)TCT>TTT	p.S99F
Pat_76	Post-Resistance	GLIS1	148979	37	1	54060335	54060335	Missense_Mutation	SNP	A	C	6	14	c.241T>G	c.(241-243)TGT>GGT	p.C81G
Pat_76	Post-Resistance	YIPF1	54432	37	1	54332025	54332025	Missense_Mutation	SNP	G	A	8	21	c.679C>T	c.(679-681)CGT>TGT	p.R227C
Pat_76	Post-Resistance	PRKAA2	5563	37	1	57159444	57159444	Missense_Mutation	SNP	C	T	6	18	c.482C>T	c.(481-483)TCT>TTT	p.S161F
Pat_76	Post-Resistance	C1orf168	199920	37	1	57257821	57257821	Missense_Mutation	SNP	C	T	4	24	c.665G>A	c.(664-666)AGA>AAA	p.R222K
Pat_76	Post-Resistance	C8A	731	37	1	57341861	57341861	Missense_Mutation	SNP	G	A	10	28	c.443G>A	c.(442-444)GGA>GAA	p.G148E
Pat_76	Post-Resistance	C8B	732	37	1	57397515	57397515	Missense_Mutation	SNP	T	C	13	31	c.1589A>G	c.(1588-1590)CAA>CGA	p.Q530R
Pat_76	Post-Resistance	C8B	732	37	1	57425723	57425723	Nonsense_Mutation	SNP	C	T	11	11	c.219G>A	c.(217-219)TGG>TGA	p.W73*
Pat_76	Post-Resistance	DAB1	1600	37	1	57481054	57481054	Missense_Mutation	SNP	G	A	6	11	c.946C>T	c.(946-948)CTC>TTC	p.L316F
Pat_76	Post-Resistance	CYP2J2	1573	37	1	60359466	60359466	Missense_Mutation	SNP	T	C	11	131	c.1366A>G	c.(1366-1368)ACT>GCT	p.T456A
Pat_76	Post-Resistance	ROR1	4919	37	1	64624732	64624733	Missense_Mutation	DNP	CC	TT	15	30	.1243_1244CC>T	c.(1243-1245)CCC>TTC	p.P415F
Pat_76	Post-Resistance	ROR1	4919	37	1	64644411	64644411	Missense_Mutation	SNP	G	A	5	16	c.2687G>A	c.(2686-2688)GGA>GAA	p.G896E
Pat_76	Post-Resistance	PTGFR	5737	37	1	79002109	79002109	Missense_Mutation	SNP	G	A	10	33	c.817G>A	c.(817-819)GGA>AGA	p.G273R
Pat_76	Post-Resistance	LPHN2	23266	37	1	82417677	82417677	Missense_Mutation	SNP	G	A	10	24	c.1633G>A	c.(1633-1635)GAA>AAA	p.E545K
Pat_76	Post-Resistance	LPHN2	23266	37	1	82435018	82435018	Missense_Mutation	SNP	C	T	9	26	c.2629C>T	c.(2629-2631)CTT>TTT	p.L877F
Pat_76	Post-Resistance	COL24A1	255631	37	1	86578285	86578285	Missense_Mutation	SNP	C	T	13	30	c.1564G>A	c.(1564-1566)GGA>AGA	p.G522R
Pat_76	Post-Resistance	HS2ST1	9653	37	1	87570300	87570300	Missense_Mutation	SNP	C	T	8	5	c.992C>T	c.(991-993)GCC>GTC	p.A331V
Pat_76	Post-Resistance	RBMXL1	494115	37	1	89448465	89448465	Missense_Mutation	SNP	G	A	30	60	c.1045C>T	c.(1045-1047)CCC>TCC	p.P349S
Pat_76	Post-Resistance	GBP6	163351	37	1	89835213	89835213	Missense_Mutation	SNP	G	A	8	19	c.299G>A	c.(298-300)GGT>GAT	p.G100D
Pat_76	Post-Resistance	ZNF644	84146	37	1	91404798	91404798	Missense_Mutation	SNP	G	A	9	17	c.2113C>T	c.(2113-2115)CCT>TCT	p.P705S
Pat_76	Post-Resistance	CDC7	8317	37	1	91977357	91977357	Missense_Mutation	SNP	C	T	3	10	c.449C>T	c.(448-450)TCC>TTC	p.S150F
Pat_76	Post-Resistance	EPHX4	253152	37	1	92528636	92528636	Missense_Mutation	SNP	G	A	23	53	c.882G>A	c.(880-882)ATG>ATA	p.M294I
Pat_76	Post-Resistance	EVI5	7813	37	1	92979352	92979352	Missense_Mutation	SNP	G	A	6	36	c.2294C>T	c.(2293-2295)TCG>TTG	p.S765L
Pat_76	Post-Resistance	ABCA4	24	37	1	94546093	94546093	Missense_Mutation	SNP	G	A	9	29	c.1040C>T	c.(1039-1041)GCC>GTC	p.A347V
Pat_76	Post-Resistance	ABCA4	24	37	1	94568678	94568678	Missense_Mutation	SNP	C	T	36	89	c.463G>A	c.(463-465)GAT>AAT	p.D155N
Pat_76	Post-Resistance	ARHGAP29	9411	37	1	94655515	94655515	Missense_Mutation	SNP	G	C	3	18	c.1406C>G	c.(1405-1407)GCC>GGC	p.A469G
Pat_76	Post-Resistance	DPYD	1806	37	1	98187170	98187170	Missense_Mutation	SNP	C	T	16	31	c.379G>A	c.(379-381)GGA>AGA	p.G127R
Pat_76	Post-Resistance	HIAT1	64645	37	1	100534098	100534099	Missense_Mutation	DNP	CC	AT	13	34	c.775_776CC>AT	c.(775-777)CCG>ATG	p.P259M
Pat_76	Post-Resistance	COL11A1	1301	37	1	103471817	103471817	Splice_Site	SNP	C	T	9	11	c.1737_splice	c.e16+1	p.R579_splice
Pat_76	Post-Resistance	COL11A1	1301	37	1	103488306	103488306	Missense_Mutation	SNP	C	T	10	25	c.1237G>A	c.(1237-1239)GAA>AAA	p.E413K
Pat_76	Post-Resistance	ATXN7L2	127002	37	1	110033872	110033872	Missense_Mutation	SNP	G	T	9	19	c.1687G>T	c.(1687-1689)GTG>TTG	p.V563L
Pat_76	Post-Resistance	RBM15	64783	37	1	110883778	110883778	Missense_Mutation	SNP	C	T	7	22	c.1751C>T	c.(1750-1752)TCT>TTT	p.S584F
Pat_76	Post-Resistance	OVGP1	5016	37	1	111957747	111957747	Missense_Mutation	SNP	G	A	13	15	c.1376C>T	c.(1375-1377)TCC>TTC	p.S459F
Pat_76	Post-Resistance	KCND3	3752	37	1	112525258	112525258	Missense_Mutation	SNP	G	A	15	23	c.91C>T	c.(91-93)CCG>TCG	p.P31S
Pat_76	Post-Resistance	TSPAN2	10100	37	1	115601575	115601575	Missense_Mutation	SNP	C	T	17	71	c.373G>A	c.(373-375)GAA>AAA	p.E125K

Pat_76	Post-Resistance	MAN1A2	10905	37	1	118039386	118039386	Missense_Mutation	SNP	C	T	3	13	c.1286C>T	c.(1285-1287)GCT>GTT	p.A429V
Pat_76	Post-Resistance	SPAG17	200162	37	1	118598459	118598459	Missense_Mutation	SNP	C	T	4	12	c.2619G>A	c.(2617-2619)ATG>ATA	p.M873I
Pat_76	Post-Resistance	HAO2	51179	37	1	119929246	119929246	Missense_Mutation	SNP	G	A	10	13	c.563G>A	c.(562-564)GGA>GAA	p.G188E
Pat_76	Post-Resistance	BCL9	607	37	1	147096566	147096566	Missense_Mutation	SNP	C	T	33	23	c.4087C>T	c.(4087-4089)CGG>TGG	p.R1363W
Pat_76	Post-Resistance	ACP6	51205	37	1	147126371	147126371	Missense_Mutation	SNP	C	T	8	125	c.718G>A	c.(718-720)GGC>AGC	p.G240S
Pat_76	Post-Resistance	NBPF16	728936	37	1	148753328	148753328	Missense_Mutation	SNP	G	A	89	105	c.1345G>A	c.(1345-1347)GAT>AAT	p.D449N
Pat_76	Post-Resistance	SEMA6C	10500	37	1	151105565	151105566	Missense_Mutation	DNP	CC	TT	6	24	.2187_2188GG>A	185-2190)AAGGAG>AAA	p.E730K
Pat_76	Post-Resistance	RPTN	126638	37	1	152129435	152129435	Missense_Mutation	SNP	C	T	25	30	c.140G>A	c.(139-141)AGA>AAA	p.R47K
Pat_76	Post-Resistance	FLG	2312	37	1	152279041	152279041	Missense_Mutation	SNP	G	A	174	620	c.8321C>T	c.(8320-8322)TCC>TTC	p.S2774F
Pat_76	Post-Resistance	FLG	2312	37	1	152284783	152284783	Missense_Mutation	SNP	G	A	94	586	c.2579C>T	c.(2578-2580)TCG>TTG	p.S860L
Pat_76	Post-Resistance	FLG2	388698	37	1	152326351	152326351	Missense_Mutation	SNP	C	T	251	186	c.3911G>A	c.(3910-3912)GGA>GAA	p.G1304E
Pat_76	Post-Resistance	KPRP	448834	37	1	152732181	152732182	Missense_Mutation	DNP	CC	TG	46	168	c.117_118CC>TG	115-120)GCCCCT>GCTG	p.P40A
Pat_76	Post-Resistance	IVL	3713	37	1	152882308	152882308	Missense_Mutation	SNP	C	T	41	34	c.35C>T	c.(34-36)TCC>TTC	p.S12F
Pat_76	Post-Resistance	S100A2	6273	37	1	153536245	153536245	Missense_Mutation	SNP	C	T	46	37	c.106G>A	c.(106-108)GAA>AAA	p.E36K
Pat_76	Post-Resistance	KCNN3	3782	37	1	154794606	154794606	Missense_Mutation	SNP	G	A	53	34	c.988C>T	c.(988-990)CTT>TTT	p.L330F
Pat_76	Post-Resistance	RUSC1	23623	37	1	155297963	155297964	Missense_Mutation	DNP	CC	AT	133	89	.2437_2438CC>A	c.(2437-2439)CCG>ATG	p.P813M
Pat_76	Post-Resistance	ASH1L	55870	37	1	155448540	155448540	Missense_Mutation	SNP	G	A	8	25	c.4121C>T	c.(4120-4122)TCT>TTT	p.S1374F
Pat_76	Post-Resistance	SYT11	23208	37	1	155838247	155838247	Missense_Mutation	SNP	G	A	7	58	c.526G>A	c.(526-528)GTG>ATG	p.V176M
Pat_76	Post-Resistance	RXFP4	339403	37	1	155912047	155912047	Missense_Mutation	SNP	G	A	17	108	c.547G>A	c.(547-549)GGT>AGT	p.G183S
Pat_76	Post-Resistance	IQGAP3	128239	37	1	156513781	156513781	Missense_Mutation	SNP	C	A	6	162	c.2522G>T	c.(2521-2523)AGG>ATG	p.R841M
Pat_76	Post-Resistance	PRCC	5546	37	1	156756532	156756532	Missense_Mutation	SNP	C	T	80	51	c.649C>T	c.(649-651)CCC>TCC	p.P217S
Pat_76	Post-Resistance	PEAR1	375033	37	1	156883182	156883182	Splice_Site	SNP	G	A	63	43	c.2512_splice	c.e20-1	p.V838_splice
Pat_76	Post-Resistance	FCRL1	115350	37	1	157771783	157771783	Missense_Mutation	SNP	G	A	10	60	c.808C>T	c.(808-810)CAT>TAT	p.H270Y
Pat_76	Post-Resistance	CD1C	911	37	1	158261016	158261016	Missense_Mutation	SNP	G	A	50	36	c.154G>A	c.(154-156)GAG>AAG	p.E52K
Pat_76	Post-Resistance	OR6K2	81448	37	1	158669934	158669934	Missense_Mutation	SNP	G	A	13	94	c.509C>T	c.(508-510)TCG>TTG	p.S170L
Pat_76	Post-Resistance	OR6K2	81448	37	1	158670321	158670321	Missense_Mutation	SNP	C	T	34	18	c.122G>A	c.(121-123)GGA>GAA	p.G41E
Pat_76	Post-Resistance	OR6K6	128371	37	1	158725629	158725630	Missense_Mutation	DNP	GG	AA	15	13	.1024_1025GG>A	c.(1024-1026)GGG>AAG	p.G342K
Pat_76	Post-Resistance	PYHIN1	149628	37	1	158909027	158909027	Missense_Mutation	SNP	C	T	20	80	c.569C>T	c.(568-570)TCC>TTC	p.S190F
Pat_76	Post-Resistance	IFI16	3428	37	1	158986447	158986447	Missense_Mutation	SNP	C	T	8	52	c.506C>T	c.(505-507)CCC>CTC	p.P169L
Pat_76	Post-Resistance	OR10J1	26476	37	1	159409697	159409697	Nonsense_Mutation	SNP	T	G	58	159	c.149T>G	c.(148-150)TTA>TGA	p.L50*
Pat_76	Post-Resistance	OR10J1	26476	37	1	159410116	159410116	Missense_Mutation	SNP	G	A	28	147	c.568G>A	c.(568-570)GAC>AAC	p.D190N
Pat_76	Post-Resistance	FCRL6	343413	37	1	159785251	159785251	Splice_Site	SNP	T	G	8	45	c.1179_splice	c.e9+2	p.K393_splice
Pat_76	Post-Resistance	ATP1A2	477	37	1	160105225	160105225	Missense_Mutation	SNP	G	A	44	45	c.2117G>A	c.(2116-2118)GGA>GAA	p.G706E
Pat_76	Post-Resistance	ATP1A4	480	37	1	160129209	160129209	Missense_Mutation	SNP	C	T	58	48	c.671C>T	c.(670-672)TCA>TTA	p.S224L
Pat_76	Post-Resistance	NDUFS2	4720	37	1	161182173	161182173	Missense_Mutation	SNP	C	T	7	61	c.1019C>T	c.(1018-1020)TCC>TTC	p.S340F
Pat_76	Post-Resistance	PBX1	5087	37	1	164815831	164815831	Missense_Mutation	SNP	G	A	68	59	c.1211G>A	c.(1210-1212)GGT>GAT	p.G404D
Pat_76	Post-Resistance	ALDH9A1	223	37	1	165634269	165634269	Missense_Mutation	SNP	C	T	25	16	c.1448G>A	c.(1447-1449)GGA>GAA	p.G483E
Pat_76	Post-Resistance	POU2F1	5451	37	1	167334719	167334719	Missense_Mutation	SNP	G	A	5	51	c.74G>A	c.(73-75)GGT>GAT	p.G25D
Pat_76	Post-Resistance	ADCY10	55811	37	1	167817683	167817683	Missense_Mutation	SNP	G	A	32	23	c.2353C>T	c.(2353-2355)CAT>TAT	p.H785Y
Pat_76	Post-Resistance	F5	2153	37	1	169511239	169511239	Missense_Mutation	SNP	C	T	44	44	c.3089G>A	c.(3088-3090)CGA>CAA	p.R1030Q
Pat_76	Post-Resistance	SELP	6403	37	1	169562902	169562902	Missense_Mutation	SNP	A	C	10	7	c.2348T>G	c.(2347-2349)ATA>AGA	p.I783R
Pat_76	Post-Resistance	C1orf156	92342	37	1	169762716	169762716	Missense_Mutation	SNP	C	T	50	43	c.121G>A	c.(121-123)GGA>AGA	p.G41R
Pat_76	Post-Resistance	FMO3	2328	37	1	171079999	171079999	Missense_Mutation	SNP	C	T	38	166	c.688C>T	c.(688-690)CCT>TCT	p.P230S
Pat_76	Post-Resistance	TNR	7143	37	1	175372639	175372640	Missense_Mutation	DNP	GG	AA	63	247	c.612_613CC>TT	610-615)TGCCCG>TGTT	p.P205S
Pat_76	Post-Resistance	TNR	7143	37	1	175375835	175375835	Missense_Mutation	SNP	C	T	77	45	c.16G>A	c.(16-18)GAA>AAA	p.E6K
Pat_76	Post-Resistance	PAPPA2	60676	37	1	176668460	176668460	Missense_Mutation	SNP	A	G	58	207	c.2971A>G	c.(2971-2973)AAG>GAG	p.K991E
Pat_76	Post-Resistance	C1orf125	126859	37	1	179460729	179460729	Missense_Mutation	SNP	G	A	7	59	c.2148G>A	c.(2146-2148)ATG>ATA	p.M716I

Pat_76	Post-Resistance	CEP350	9857	37	1	180023013	180023013	Missense_Mutation	SNP	A	C	27	29	c.5118A>C	c.(5116-5118)GAA>GAC	p.E1706D
Pat_76	Post-Resistance	XPR1	9213	37	1	180849418	180849418	Missense_Mutation	SNP	C	T	51	40	c.2015C>T	c.(2014-2016)CCT>CTT	p.P672L
Pat_76	Post-Resistance	CACNA1E	777	37	1	181695216	181695216	Missense_Mutation	SNP	G	A	8	11	c.2158G>A	c.(2158-2160)GAA>AAA	p.E720K
Pat_76	Post-Resistance	LAMC2	3918	37	1	183192278	183192278	Missense_Mutation	SNP	C	T	23	16	c.772C>T	c.(772-774)CTT>TTT	p.L258F
Pat_76	Post-Resistance	LAMC2	3918	37	1	183192310	183192310	Missense_Mutation	SNP	C	G	11	47	c.804C>G	c.(802-804)AGC>AGG	p.S268R
Pat_76	Post-Resistance	APOBEC4	403314	37	1	183616917	183616917	Missense_Mutation	SNP	C	T	39	24	c.1000G>A	c.(1000-1002)GGA>AGA	p.G334R
Pat_76	Post-Resistance	FAM129A	116496	37	1	184792330	184792330	Nonsense_Mutation	SNP	G	C	17	67	c.956C>G	c.(955-957)TCA>TGA	p.S319*
Pat_76	Post-Resistance	FAM129A	116496	37	1	184863341	184863341	Splice_Site	SNP	C	T	5	19	c.187_splice	c.e3-1	p.P63_splice
Pat_76	Post-Resistance	PLA2G4A	5321	37	1	186934540	186934540	Splice_Site	SNP	G	A	3	3	c.1580_splice	c.e15-1	p.D527_splice
Pat_76	Post-Resistance	FAM5C	339479	37	1	190195350	190195350	Missense_Mutation	SNP	C	T	23	33	c.823G>A	c.(823-825)GAA>AAA	p.E275K
Pat_76	Post-Resistance	CFH	3075	37	1	196654365	196654365	Missense_Mutation	SNP	C	T	31	83	c.962C>T	c.(961-963)ACC>ATC	p.T321I
Pat_76	Post-Resistance	CFHR1	3078	37	1	196794779	196794779	Nonsense_Mutation	SNP	G	A	15	84	c.231G>A	c.(229-231)TGG>TGA	p.W77*
Pat_76	Post-Resistance	CRB1	23418	37	1	197396935	197396935	Missense_Mutation	SNP	G	A	16	15	c.2480G>A	c.(2479-2481)GGA>GAA	p.G827E
Pat_76	Post-Resistance	KIF14	9928	37	1	200586846	200586846	Missense_Mutation	SNP	G	T	9	43	c.1006C>A	c.(1006-1008)CCC>ACC	p.P336T
Pat_76	Post-Resistance	KIF14	9928	37	1	200586848	200586848	Missense_Mutation	SNP	A	G	10	39	c.1004T>C	c.(1003-1005)CTT>CCT	p.L335P
Pat_76	Post-Resistance	CACNA1S	779	37	1	201056982	201056983	Missense_Mutation	DNP	GG	AA	20	28	c.975_976CC>TT	(973-978)ATCCTC>ATTTT	p.L326F
Pat_76	Post-Resistance	TNNI1	7135	37	1	201383752	201383752	Missense_Mutation	SNP	T	G	27	65	c.83A>C	c.(82-84)GAA>GCA	p.E28A
Pat_76	Post-Resistance	TNNI1	7135	37	1	201386940	201386940	Translation_Start_Site	SNP	C	T	7	32	c.-18G>A	.(-20--16)AGGTG>AGATG	
Pat_76	Post-Resistance	LGR6	59352	37	1	202283992	202283992	Nonsense_Mutation	SNP	C	T	15	62	c.1630C>T	c.(1630-1632)CAG>TAG	p.Q544*
Pat_76	Post-Resistance	PPP1R12B	4660	37	1	202464748	202464748	Nonsense_Mutation	SNP	C	T	9	37	c.2386C>T	c.(2386-2388)CGA>TGA	p.R796*
Pat_76	Post-Resistance	CHI3L1	1116	37	1	203153717	203153717	Missense_Mutation	SNP	A	T	50	34	c.301T>A	c.(301-303)TTT>ATT	p.F101I
Pat_76	Post-Resistance	PFKFB2	5208	37	1	207252327	207252327	Missense_Mutation	SNP	G	T	22	102	c.1379G>T	c.(1378-1380)AGA>ATA	p.R460I
Pat_76	Post-Resistance	C4BPB	725	37	1	207265145	207265145	Missense_Mutation	SNP	C	T	6	12	c.389C>T	c.(388-390)CCC>CTC	p.P130L
Pat_76	Post-Resistance	HSD11B1	3290	37	1	209879168	209879168	Missense_Mutation	SNP	G	A	10	58	c.101G>A	c.(100-102)GGA>GAA	p.G34E
Pat_76	Post-Resistance	KCNH1	3756	37	1	210977434	210977435	Missense_Mutation	DNP	GG	AA	20	19	.1536_1537CC>T	1534-1539)TACCAT>TATT	p.H513Y
Pat_76	Post-Resistance	KCTD3	51133	37	1	215753284	215753284	Missense_Mutation	SNP	G	A	9	88	c.568G>A	c.(568-570)GTA>ATA	p.V190I
Pat_76	Post-Resistance	USH2A	7399	37	1	215848169	215848169	Missense_Mutation	SNP	G	A	8	26	c.13084C>T	c.(13084-13086)CCA>TCA	p.P4362S
Pat_76	Post-Resistance	EPRS	2058	37	1	220152958	220152958	Splice_Site	SNP	C	T	8	22	c.3712_splice	c.e27-1	.G1238_splice
Pat_76	Post-Resistance	TAF1A	9015	37	1	222743989	222743989	Missense_Mutation	SNP	T	C	10	90	c.623A>G	c.(622-624)TAC>TGC	p.Y208C
Pat_76	Post-Resistance	MIA3	375056	37	1	222801532	222801532	Missense_Mutation	SNP	G	A	19	16	c.970G>A	c.(970-972)GAC>AAC	p.D324N
Pat_76	Post-Resistance	DISP1	84976	37	1	223177395	223177395	Missense_Mutation	SNP	T	A	11	40	c.2656T>A	c.(2656-2658)TTT>ATT	p.F886I
Pat_76	Post-Resistance	SUSD4	55061	37	1	223465897	223465897	Missense_Mutation	SNP	C	T	30	93	c.245G>A	c.(244-246)CGA>CAA	p.R82Q
Pat_76	Post-Resistance	CDC42BPA	8476	37	1	227203785	227203785	Missense_Mutation	SNP	G	A	42	33	c.4748C>T	c.(4747-4749)CCC>CTC	p.P1583L
Pat_76	Post-Resistance	OBSCN	84033	37	1	228479646	228479646	Missense_Mutation	SNP	G	A	20	18	c.10387G>A	c.(10387-10389)GAA>AAA	p.E3463K
Pat_76	Post-Resistance	SIPA1L2	57568	37	1	232601113	232601113	Missense_Mutation	SNP	G	A	9	44	c.2293C>T	c.(2293-2295)CCC>TCC	p.P765S
Pat_76	Post-Resistance	KIAA1804	84451	37	1	233482322	233482322	Missense_Mutation	SNP	G	A	7	13	c.940G>A	c.(940-942)GAA>AAA	p.E314K
Pat_76	Post-Resistance	HEATR1	55127	37	1	236759297	236759297	Missense_Mutation	SNP	T	C	15	37	c.792A>G	c.(790-792)ATA>ATG	p.I264M
Pat_76	Post-Resistance	FMN2	56776	37	1	240371077	240371077	Missense_Mutation	SNP	C	T	77	148	c.2965C>T	c.(2965-2967)CCT>TCT	p.P989S
Pat_76	Post-Resistance	ZNF669	79862	37	1	247264023	247264023	Missense_Mutation	SNP	G	A	20	31	c.1048C>T	c.(1048-1050)CGT>TGT	p.R350C
Pat_76	Post-Resistance	OR2W5	441932	37	1	247655213	247655213	Missense_Mutation	SNP	G	A	19	45	c.784G>A	c.(784-786)GCC>ACC	p.A262T
Pat_76	Post-Resistance	OR2W3	343171	37	1	248059042	248059042	Missense_Mutation	SNP	G	A	99	234	c.154G>A	c.(154-156)GAC>AAC	p.D52N
Pat_76	Post-Resistance	OR2L2	26246	37	1	248201597	248201597	Missense_Mutation	SNP	G	A	15	44	c.28G>A	c.(28-30)GAT>AAT	p.D10N
Pat_76	Post-Resistance	OR2M3	127062	37	1	248366888	248366888	Missense_Mutation	SNP	A	C	50	81	c.519A>C	c.(517-519)GAA>GAC	p.E173D
Pat_76	Post-Resistance	OR2T33	391195	37	1	248436332	248436332	Missense_Mutation	SNP	G	A	17	40	c.785C>T	c.(784-786)TCC>TTC	p.S262F
Pat_76	Post-Resistance	OR2T33	391195	37	1	248436951	248436951	Missense_Mutation	SNP	G	A	18	51	c.166C>T	c.(166-168)CCC>TCC	p.P56S
Pat_76	Post-Resistance	OR14I1	401994	37	1	248845470	248845470	Missense_Mutation	SNP	C	T	3	25	c.136G>A	c.(136-138)GTC>ATC	p.V46I
Pat_76	Post-Resistance	GTPBP4	23560	37	10	1055472	1055472	Nonsense_Mutation	SNP	C	T	13	37	c.1195C>T	c.(1195-1197)CGA>TGA	p.R399*

Pat_76	Post-Resistance	AKR1C2	1646	37	10	5038059	5038059	Splice_Site	SNP	T	C	4	9	c.571_splice	c.e6-1	p.V191_splice
Pat_76	Post-Resistance	C10orf18	54906	37	10	5789058	5789058	Missense_Mutation	SNP	C	T	20	40	c.3674C>T	c.(3673-3675)TCG>TTG	p.S1225L
Pat_76	Post-Resistance	IL2RA	3559	37	10	6067847	6067847	Missense_Mutation	SNP	C	T	6	34	c.206G>A	c.(205-207)GGA>GAA	p.G69E
Pat_76	Post-Resistance	ITIH2	3698	37	10	7751024	7751024	Nonsense_Mutation	SNP	C	T	14	64	c.232C>T	c.(232-234)CAG>TAG	p.Q78*
Pat_76	Post-Resistance	ATP5C1	509	37	10	7842001	7842001	Missense_Mutation	SNP	C	T	8	16	c.584C>T	c.(583-585)TCC>TTC	p.S195F
Pat_76	Post-Resistance	CUBN	8029	37	10	16962022	16962022	Missense_Mutation	SNP	G	A	16	32	c.6761C>T	c.(6760-6762)CCA>CTA	p.P2254L
Pat_76	Post-Resistance	PLXDC2	84898	37	10	20432253	20432253	Nonsense_Mutation	SNP	C	T	27	56	c.571C>T	c.(571-573)CGA>TGA	p.R191*
Pat_76	Post-Resistance	NEBL	10529	37	10	21250695	21250695	Missense_Mutation	SNP	C	G	14	23	c.263G>C	c.(262-264)AGA>ACA	p.R88T
Pat_76	Post-Resistance	KIAA1217	56243	37	10	24834776	24834776	Missense_Mutation	SNP	A	T	17	29	c.5355A>T	c.(5353-5355)AAA>AAT	p.K1785N
Pat_76	Post-Resistance	ARHGAP21	57584	37	10	24896817	24896817	Missense_Mutation	SNP	G	A	7	22	c.2438C>T	c.(2437-2439)CCT>CTT	p.P813L
Pat_76	Post-Resistance	THNSL1	79896	37	10	25314107	25314107	Missense_Mutation	SNP	G	A	11	35	c.1955G>A	c.(1954-1956)AGG>AAG	p.R652K
Pat_76	Post-Resistance	GAD2	2572	37	10	26589747	26589747	Missense_Mutation	SNP	G	A	31	83	c.1615G>A	c.(1615-1617)GAG>AAG	p.E539K
Pat_76	Post-Resistance	PTCHD3	374308	37	10	27702980	27702981	Missense_Mutation	DNP	GG	AA	7	27	c.199_200CC>TT	c.(199-201)CCC>TTC	p.P67F
Pat_76	Post-Resistance	ARMC4	55130	37	10	28149594	28149594	Missense_Mutation	SNP	G	A	6	24	c.2981C>T	c.(2980-2982)GCC>GTC	p.A994V
Pat_76	Post-Resistance	C10orf68	79741	37	10	33018265	33018266	Missense_Mutation	DNP	CC	TT	5	10	c.706_707CC>TT	c.(706-708)CCT>TTT	p.P236F
Pat_76	Post-Resistance	ZNF33A	7581	37	10	38343746	38343746	Missense_Mutation	SNP	G	A	4	29	c.691G>A	c.(691-693)GCA>ACA	p.A231T
Pat_76	Post-Resistance	ZNF33B	7582	37	10	43088374	43088374	Missense_Mutation	SNP	C	A	11	22	c.2024G>T	c.(2023-2025)TGT>TTT	p.C675F
Pat_76	Post-Resistance	RASGEF1A	221002	37	10	43692445	43692445	Missense_Mutation	SNP	C	T	6	10	c.1327G>A	c.(1327-1329)GCG>ACG	p.A443T
Pat_76	Post-Resistance	RASGEF1A	221002	37	10	43694453	43694453	Missense_Mutation	SNP	C	T	28	41	c.960G>A	c.(958-960)ATG>ATA	p.M320I
Pat_76	Post-Resistance	SYT15	83849	37	10	46965788	46965789	Missense_Mutation	DNP	GG	AA	5	8	c.748_749CC>TT	c.(748-750)CCC>TTC	p.P250F
Pat_76	Post-Resistance	FRMPD2	143162	37	10	49395274	49395274	Missense_Mutation	SNP	C	T	8	27	c.2227G>A	c.(2227-2229)GAC>AAC	p.D743N
Pat_76	Post-Resistance	DRGX	644168	37	10	50574211	50574211	Missense_Mutation	SNP	C	T	9	22	c.757G>A	c.(757-759)GAA>AAA	p.E253K
Pat_76	Post-Resistance	SLC18A3	6572	37	10	50819762	50819762	Missense_Mutation	SNP	G	A	32	76	c.976G>A	c.(976-978)GAG>AAG	p.E326K
Pat_76	Post-Resistance	C10orf53	282966	37	10	50902584	50902584	Missense_Mutation	SNP	G	A	12	21	c.218G>A	c.(217-219)GGA>GAA	p.G73E
Pat_76	Post-Resistance	AGAP6	414189	37	10	51748552	51748552	Missense_Mutation	SNP	C	T	26	53	c.77C>T	c.(76-78)CCC>CTC	p.P26L
Pat_76	Post-Resistance	ASAH2	56624	37	10	52005142	52005142	Missense_Mutation	SNP	G	A	7	5	c.200C>T	c.(199-201)TCC>TTC	p.S67F
Pat_76	Post-Resistance	CSTF2T	23283	37	10	53458427	53458427	Missense_Mutation	SNP	C	T	16	45	c.883G>A	c.(883-885)GTT>ATT	p.V295I
Pat_76	Post-Resistance	PCDH15	65217	37	10	55626547	55626547	Missense_Mutation	SNP	C	T	5	23	c.3572G>A	c.(3571-3573)GGA>GAA	p.G1191E
Pat_76	Post-Resistance	ANK3	288	37	10	61941095	61941095	Missense_Mutation	SNP	G	T	19	39	c.2176C>A	c.(2176-2178)CAG>AAG	p.Q726K
Pat_76	Post-Resistance	ARID5B	84159	37	10	63851357	63851357	Missense_Mutation	SNP	C	T	18	40	c.2135C>T	c.(2134-2136)TCC>TTC	p.S712F
Pat_76	Post-Resistance	LRRTM3	347731	37	10	68687186	68687186	Missense_Mutation	SNP	C	T	12	33	c.512C>T	c.(511-513)ACC>ATC	p.T171I
Pat_76	Post-Resistance	CTNNA3	29119	37	10	68940116	68940116	Missense_Mutation	SNP	G	A	13	15	c.1006C>T	c.(1006-1008)CGC>TGC	p.R336C
Pat_76	Post-Resistance	UNC5B	219699	37	10	73051446	73051446	Missense_Mutation	SNP	G	C	12	51	c.1552G>C	c.(1552-1554)GAC>CAC	p.D518H
Pat_76	Post-Resistance	CCDC109A	90550	37	10	74644024	74644024	Missense_Mutation	SNP	G	A	4	12	c.862G>A	c.(862-864)GAA>AAA	p.E288K
Pat_76	Post-Resistance	USP54	159195	37	10	75276315	75276315	Missense_Mutation	SNP	G	A	18	42	c.3869C>T	c.(3868-3870)TCC>TTC	p.S1290F
Pat_76	Post-Resistance	DLG5	9231	37	10	79589166	79589166	Missense_Mutation	SNP	G	A	52	100	c.2132C>T	c.(2131-2133)TCC>TTC	p.S711F
Pat_76	Post-Resistance	SFTPD	6441	37	10	81697757	81697757	Missense_Mutation	SNP	G	A	50	107	c.979C>T	c.(979-981)CCC>TCC	p.P327S
Pat_76	Post-Resistance	MAT1A	4143	37	10	82039945	82039945	Missense_Mutation	SNP	G	A	16	25	c.533C>T	c.(532-534)CCT>CTT	p.P178L
Pat_76	Post-Resistance	C10orf58	84293	37	10	82182205	82182205	Missense_Mutation	SNP	G	A	3	32	c.211G>A	c.(211-213)GAA>AAA	p.E71K
Pat_76	Post-Resistance	MMRN2	79812	37	10	88703241	88703241	Missense_Mutation	SNP	C	T	17	40	c.1300G>A	c.(1300-1302)GAG>AAG	p.E434K
Pat_76	Post-Resistance	BTAF1	9044	37	10	93711222	93711222	Missense_Mutation	SNP	C	T	3	14	c.463C>T	c.(463-465)CTT>TTT	p.L155F
Pat_76	Post-Resistance	MYOF	26509	37	10	95119690	95119690	Missense_Mutation	SNP	G	A	17	52	c.3020C>T	c.(3019-3021)TCC>TTC	p.S1007F
Pat_76	Post-Resistance	CEP55	55165	37	10	95276697	95276697	Missense_Mutation	SNP	C	T	10	14	c.685C>T	c.(685-687)CTT>TTT	p.L229F
Pat_76	Post-Resistance	LGI1	9211	37	10	95557173	95557173	Missense_Mutation	SNP	G	A	27	51	c.1287G>A	c.(1285-1287)ATG>ATA	p.M429I
Pat_76	Post-Resistance	PIPSL	266971	37	10	95720163	95720164	Missense_Mutation	DNP	CC	TT	15	21	c.990_991GG>AA	(988-993)ATGGGT>ATAA	.330_331MG>I
Pat_76	Post-Resistance	TCTN3	26123	37	10	97442505	97442505	Missense_Mutation	SNP	C	T	45	101	c.1355G>A	c.(1354-1356)GGA>GAA	p.G452E
Pat_76	Post-Resistance	TLL2	7093	37	10	98145849	98145849	Missense_Mutation	SNP	G	A	10	22	c.1976C>T	c.(1975-1977)TCC>TTC	p.S659F

Pat_76	Post-Resistance	TLL2	7093	37	10	98145910	98145910	Missense_Mutation	SNP	C	T	19	51	c.1915G>A	c.(1915-1917)GAG>AAG	p.E639K
Pat_76	Post-Resistance	C10orf2	56652	37	10	102750284	102750284	Nonsense_Mutation	SNP	C	T	36	128	c.1576C>T	c.(1576-1578)CAG>TAG	p.Q526*
Pat_76	Post-Resistance	TRIM8	81603	37	10	104416885	104416885	Missense_Mutation	SNP	C	T	26	34	c.1430C>T	c.(1429-1431)TCC>TTC	p.S477F
Pat_76	Post-Resistance	HABP2	3026	37	10	115342983	115342983	Missense_Mutation	SNP	C	T	11	18	c.1103C>T	c.(1102-1104)ACC>ATC	p.T368I
Pat_76	Post-Resistance	ATRNL1	26033	37	10	116889240	116889240	Missense_Mutation	SNP	C	T	18	29	c.772C>T	c.(772-774)CAC>TAC	p.H258Y
Pat_76	Post-Resistance	ATRNL1	26033	37	10	117154237	117154238	Missense_Mutation	DNP	GG	AA	6	16	.3244_3245GG>A	c.(3244-3246)GGA>AAA	p.G1082K
Pat_76	Post-Resistance	PNLIPRP3	119548	37	10	118236307	118236307	Missense_Mutation	SNP	A	T	11	19	c.1316A>T	c.(1315-1317)AAT>ATT	p.N439I
Pat_76	Post-Resistance	TACC2	10579	37	10	123847218	123847218	Missense_Mutation	SNP	G	A	9	8	c.5203G>A	c.(5203-5205)GTT>ATT	p.V1735I
Pat_76	Post-Resistance	DMBT1	1755	37	10	124399555	124399555	Splice_Site	SNP	G	A	12	18	c.6556_splice	c.e52-1	p.A2186_splice
Pat_76	Post-Resistance	CUZD1	50624	37	10	124593415	124593415	Missense_Mutation	SNP	C	T	10	21	c.1424G>A	c.(1423-1425)GGA>GAA	p.G475E
Pat_76	Post-Resistance	CHST15	51363	37	10	125798085	125798085	Missense_Mutation	SNP	T	A	21	36	c.1136A>T	c.(1135-1137)CAC>CTC	p.H379L
Pat_76	Post-Resistance	CHST15	51363	37	10	125805533	125805533	Missense_Mutation	SNP	C	T	12	20	c.196G>A	c.(196-198)GAA>AAA	p.E66K
Pat_76	Post-Resistance	ZNF511	118472	37	10	135123381	135123381	Missense_Mutation	SNP	C	T	14	31	c.329C>T	c.(328-330)TCC>TTC	p.S110F
Pat_76	Post-Resistance	TNNT3	7140	37	11	1959716	1959716	Nonsense_Mutation	SNP	G	A	8	11	c.771G>A	c.(769-771)TGG>TGA	p.W257*
Pat_76	Post-Resistance	TRPM5	29850	37	11	2428471	2428471	Missense_Mutation	SNP	T	C	8	20	c.2996A>G	c.(2995-2997)AAC>AGC	p.N999S
Pat_76	Post-Resistance	ZNF195	7748	37	11	3380508	3380508	Missense_Mutation	SNP	G	A	11	31	c.1730C>T	c.(1729-1731)CCC>CTC	p.P577L
Pat_76	Post-Resistance	TRIM21	6737	37	11	4407081	4407081	Missense_Mutation	SNP	G	A	5	17	c.862C>T	c.(862-864)CAC>TAC	p.H288Y
Pat_76	Post-Resistance	OR52K2	119774	37	11	4471488	4471489	Missense_Mutation	DNP	GG	AA	13	18	c.919_920GG>AA	c.(919-921)GGA>AAA	p.G307K
Pat_76	Post-Resistance	OR51E1	143503	37	11	4674277	4674277	Missense_Mutation	SNP	C	T	43	105	c.521C>T	c.(520-522)TCC>TTC	p.S174F
Pat_76	Post-Resistance	OR51E1	143503	37	11	4674409	4674409	Missense_Mutation	SNP	C	T	6	18	c.653C>T	c.(652-654)TCC>TTC	p.S218F
Pat_76	Post-Resistance	OR51E2	81285	37	11	4703277	4703277	Missense_Mutation	SNP	C	T	7	20	c.665G>A	c.(664-666)CGA>CAA	p.R222Q
Pat_76	Post-Resistance	OR51E2	81285	37	11	4703632	4703632	Missense_Mutation	SNP	G	A	10	16	c.310C>T	c.(310-312)CAT>TAT	p.H104Y
Pat_76	Post-Resistance	OR52R1	119695	37	11	4824685	4824685	Missense_Mutation	SNP	C	T	15	26	c.1163G>A	c.(1162-1164)GGA>GAA	p.G388E
Pat_76	Post-Resistance	OR51F2	119694	37	11	4843021	4843021	Missense_Mutation	SNP	C	T	20	52	c.406C>T	c.(406-408)CGT>TGT	p.R136C
Pat_76	Post-Resistance	OR52J3	119679	37	11	5068233	5068233	Missense_Mutation	SNP	C	T	7	16	c.478C>T	c.(478-480)CCC>TCC	p.P160S
Pat_76	Post-Resistance	HBG2	3048	37	11	5275625	5275625	Missense_Mutation	SNP	G	A	15	96	c.212C>T	c.(211-213)TCC>TTC	p.S71F
Pat_76	Post-Resistance	OR51B5	282763	37	11	5363977	5363977	Missense_Mutation	SNP	G	A	6	22	c.778C>T	c.(778-780)CAT>TAT	p.H260Y
Pat_76	Post-Resistance	OR52N1	79473	37	11	5809289	5809289	Missense_Mutation	SNP	G	A	15	49	c.758C>T	c.(757-759)ACC>ATC	p.T253I
Pat_76	Post-Resistance	OR52B2	255725	37	11	6190872	6190872	Missense_Mutation	SNP	G	A	9	23	c.685C>T	c.(685-687)CGT>TGT	p.R229C
Pat_76	Post-Resistance	OR2AG2	338755	37	11	6790164	6790164	Missense_Mutation	SNP	C	T	9	8	c.25G>A	c.(25-27)GGA>AGA	p.G9R
Pat_76	Post-Resistance	NLRP14	338323	37	11	7079624	7079624	Missense_Mutation	SNP	G	A	28	60	c.2576G>A	c.(2575-2577)GGA>GAA	p.G859E
Pat_76	Post-Resistance	NLRP14	338323	37	11	7081264	7081264	Missense_Mutation	SNP	C	T	33	56	c.2773C>T	c.(2773-2775)CGG>TGG	p.R925W
Pat_76	Post-Resistance	EIF4G2	1982	37	11	10821847	10821847	Missense_Mutation	SNP	G	A	5	39	c.1909C>T	c.(1909-1911)CCT>TCT	p.P637S
Pat_76	Post-Resistance	PLEKHA7	144100	37	11	16872806	16872806	Missense_Mutation	SNP	G	A	8	32	c.628C>T	c.(628-630)CCC>TCC	p.P210S
Pat_76	Post-Resistance	ABCC8	6833	37	11	17483319	17483319	Missense_Mutation	SNP	T	G	16	26	c.633A>C	c.(631-633)CAA>CAC	p.Q211H
Pat_76	Post-Resistance	MRGPRX2	117194	37	11	19077339	19077339	Missense_Mutation	SNP	G	A	12	10	c.611C>T	c.(610-612)GCC>GTC	p.A204V
Pat_76	Post-Resistance	NAV2	89797	37	11	20070338	20070338	Missense_Mutation	SNP	G	A	23	39	c.4036G>A	c.(4036-4038)GTG>ATG	p.V1346M
Pat_76	Post-Resistance	ANO3	63982	37	11	26620469	26620469	Missense_Mutation	SNP	G	A	6	14	c.1595G>A	c.(1594-1596)GGA>GAA	p.G532E
Pat_76	Post-Resistance	ELF5	2001	37	11	34502425	34502425	Missense_Mutation	SNP	C	T	13	27	c.595G>A	c.(595-597)GAA>AAA	p.E199K
Pat_76	Post-Resistance	PRR5L	79899	37	11	36484009	36484010	Missense_Mutation	DNP	GG	AA	18	34	c.830_831GG>AA	c.(829-831)GGG>GAA	p.G277E
Pat_76	Post-Resistance	PRR5L	79899	37	11	36484116	36484116	Missense_Mutation	SNP	G	A	15	18	c.937G>A	c.(937-939)GGG>AGG	p.G313R
Pat_76	Post-Resistance	RAG1	5896	37	11	36595839	36595839	Missense_Mutation	SNP	C	T	13	32	c.985C>T	c.(985-987)CCC>TCC	p.P329S
Pat_76	Post-Resistance	TSPAN18	90139	37	11	44950719	44950719	Missense_Mutation	SNP	G	A	12	37	c.737G>A	c.(736-738)GGC>GAC	p.G246D
Pat_76	Post-Resistance	PRDM11	56981	37	11	45246341	45246341	Missense_Mutation	SNP	C	T	26	48	c.1418C>T	c.(1417-1419)CCC>CTC	p.P473L
Pat_76	Post-Resistance	SYT13	57586	37	11	45277376	45277376	Missense_Mutation	SNP	C	T	18	28	c.250G>A	c.(250-252)GGA>AGA	p.G84R
Pat_76	Post-Resistance	GYLTL1B	120071	37	11	45948403	45948403	Missense_Mutation	SNP	G	A	15	35	c.1306G>A	c.(1306-1308)GCC>ACC	p.A436T
Pat_76	Post-Resistance	MADD	8567	37	11	47304035	47304035	Missense_Mutation	SNP	G	A	11	22	c.1573G>A	c.(1573-1575)GCT>ACT	p.A525T

Pat_76	Post-Resistance	AGBL2	79841	37	11	47681829	47681829	Missense_Mutation	SNP	G	C	5	29	c.2605C>G	c.(2605-2607)CCA>GCA	p.P869A
Pat_76	Post-Resistance	AGBL2	79841	37	11	47707594	47707594	Missense_Mutation	SNP	C	T	10	12	c.1639G>A	c.(1639-1641)GAA>AAA	p.E547K
Pat_76	Post-Resistance	PTPRJ	5795	37	11	48134319	48134319	Missense_Mutation	SNP	C	T	14	48	c.136C>T	c.(136-138)CCT>TCT	p.P46S
Pat_76	Post-Resistance	OR4X1	390113	37	11	48285932	48285932	Missense_Mutation	SNP	C	T	7	25	c.520C>T	c.(520-522)CAC>TAC	p.H174Y
Pat_76	Post-Resistance	OR4A5	81318	37	11	51412038	51412038	Missense_Mutation	SNP	G	A	13	31	c.358C>T	c.(358-360)CGC>TGC	p.R120C
Pat_76	Post-Resistance	OR4C11	219429	37	11	55371006	55371006	Missense_Mutation	SNP	G	A	10	6	c.844C>T	c.(844-846)CCA>TCA	p.P282S
Pat_76	Post-Resistance	OR5D14	219436	37	11	55563687	55563687	Missense_Mutation	SNP	C	T	27	57	c.656C>T	c.(655-657)TCC>TTC	p.S219F
Pat_76	Post-Resistance	OR5AS1	219447	37	11	55798717	55798717	Missense_Mutation	SNP	G	A	3	11	c.823G>A	c.(823-825)GCA>ACA	p.A275T
Pat_76	Post-Resistance	OR8H2	390151	37	11	55873063	55873063	Missense_Mutation	SNP	C	T	41	147	c.545C>T	c.(544-546)TCC>TTC	p.S182F
Pat_76	Post-Resistance	OR8H2	390151	37	11	55873104	55873104	Missense_Mutation	SNP	G	A	31	97	c.586G>A	c.(586-588)GAA>AAA	p.E196K
Pat_76	Post-Resistance	OR8H1	219469	37	11	56057772	56057772	Missense_Mutation	SNP	A	T	6	8	c.767T>A	c.(766-768)TTT>TAT	p.F256Y
Pat_76	Post-Resistance	OR8K3	219473	37	11	56086579	56086579	Missense_Mutation	SNP	C	T	4	18	c.797C>T	c.(796-798)TCC>TTC	p.S266F
Pat_76	Post-Resistance	OR5AR1	219493	37	11	56431525	56431525	Missense_Mutation	SNP	C	T	21	43	c.364C>T	c.(364-366)CGT>TGT	p.R122C
Pat_76	Post-Resistance	OR1S1	219959	37	11	57983114	57983114	Missense_Mutation	SNP	C	T	5	28	c.898C>T	c.(898-900)CCC>TCC	p.P300S
Pat_76	Post-Resistance	GLYATL2	219970	37	11	58604580	58604580	Missense_Mutation	SNP	C	T	5	33	c.384G>A	c.(382-384)ATG>ATA	p.M128I
Pat_76	Post-Resistance	CHRM1	1128	37	11	62678196	62678196	Missense_Mutation	SNP	G	A	12	34	c.377C>T	c.(376-378)TCC>TTC	p.S126F
Pat_76	Post-Resistance	SLC22A9	114571	37	11	63176246	63176246	Nonsense_Mutation	SNP	G	A	13	28	c.1496G>A	c.(1495-1497)TGG>TAG	p.W499*
Pat_76	Post-Resistance	CDC42EP2	10435	37	11	65088994	65088994	Missense_Mutation	SNP	C	T	14	50	c.625C>T	c.(625-627)CCC>TCC	p.P209S
Pat_76	Post-Resistance	SF3B2	10992	37	11	65829443	65829443	Missense_Mutation	SNP	C	T	10	24	c.1951C>T	c.(1951-1953)CCT>TCT	p.P651S
Pat_76	Post-Resistance	SPTBN2	6712	37	11	66468435	66468436	Missense_Mutation	DNP	GG	AA	19	17	.3134_3135CC>T	c.(3133-3135)ACC>ATT	p.T1045I
Pat_76	Post-Resistance	TBX10	347853	37	11	67402517	67402517	Nonsense_Mutation	SNP	C	T	14	38	c.225G>A	c.(223-225)TGG>TGA	p.W75*
Pat_76	Post-Resistance	CPT1A	1374	37	11	68542821	68542822	Missense_Mutation	DNP	GG	AA	34	134	.1537_1538CC>T	c.(1537-1539)CCG>TTG	p.P513L
Pat_76	Post-Resistance	KRTAP5-9	3846	37	11	71259749	71259750	Missense_Mutation	DNP	GG	AA	32	85	c.46_47GG>AA	c.(46-48)GGC>AAC	p.G16N
Pat_76	Post-Resistance	UCP2	7351	37	11	73689327	73689327	Missense_Mutation	SNP	G	A	14	27	c.97C>T	c.(97-99)CCT>TCT	p.P33S
Pat_76	Post-Resistance	PGM2L1	283209	37	11	74054392	74054392	Missense_Mutation	SNP	G	A	7	19	c.1288C>T	c.(1288-1290)CTT>TTT	p.L430F
Pat_76	Post-Resistance	KLHL35	283212	37	11	75133763	75133763	Missense_Mutation	SNP	C	T	24	68	c.953G>A	c.(952-954)GGG>GAG	p.G318E
Pat_76	Post-Resistance	OMP	4975	37	11	76814355	76814356	Missense_Mutation	DNP	CC	TT	19	46	c.470_471CC>TT	c.(469-471)TCC>TTT	p.S157F
Pat_76	Post-Resistance	MYO7A	4647	37	11	76905531	76905531	Missense_Mutation	SNP	G	A	5	9	c.4285G>A	c.(4285-4287)GAG>AAG	p.E1429K
Pat_76	Post-Resistance	DLG2	1740	37	11	83344290	83344290	Missense_Mutation	SNP	G	A	13	21	c.1589C>T	c.(1588-1590)TCC>TTC	p.S530F
Pat_76	Post-Resistance	GRM5	2915	37	11	88386431	88386431	Missense_Mutation	SNP	C	T	6	13	c.1052G>A	c.(1051-1053)CGA>CAA	p.R351Q
Pat_76	Post-Resistance	FAT3	120114	37	11	92085960	92085960	Missense_Mutation	SNP	G	A	14	30	c.682G>A	c.(682-684)GAT>AAT	p.D228N
Pat_76	Post-Resistance	FAT3	120114	37	11	92086786	92086786	Missense_Mutation	SNP	A	T	8	11	c.1508A>T	c.(1507-1509)GAA>GTA	p.E503V
Pat_76	Post-Resistance	FAT3	120114	37	11	92569781	92569781	Missense_Mutation	SNP	C	T	8	32	c.10136C>T	c.(10135-10137)TCC>TTC	p.S3379F
Pat_76	Post-Resistance	CNTN5	53942	37	11	99690347	99690347	Missense_Mutation	SNP	C	T	10	46	c.128C>T	c.(127-129)TCA>TTA	p.S43L
Pat_76	Post-Resistance	KIAA1377	57562	37	11	101828898	101828898	Splice_Site	SNP	G	A	53	132	c.507_splice	c.e5-1	p.R169_splice
Pat_76	Post-Resistance	KIAA1377	57562	37	11	101833571	101833571	Missense_Mutation	SNP	G	A	8	10	c.1805G>A	c.(1804-1806)GGA>GAA	p.G602E
Pat_76	Post-Resistance	MMP1	4312	37	11	102667484	102667484	Missense_Mutation	SNP	C	T	9	16	c.536G>A	c.(535-537)GGA>GAA	p.G179E
Pat_76	Post-Resistance	MMP13	4322	37	11	102826045	102826045	Missense_Mutation	SNP	C	T	25	37	c.298G>A	c.(298-300)GAT>AAT	p.D100N
Pat_76	Post-Resistance	DYNC2H1	79659	37	11	103027319	103027319	Missense_Mutation	SNP	C	T	4	7	c.3947C>T	c.(3946-3948)CCT>CTT	p.P1316L
Pat_76	Post-Resistance	PDGFD	80310	37	11	103780454	103780454	Missense_Mutation	SNP	C	T	34	52	c.1081G>A	c.(1081-1083)GAT>AAT	p.D361N
Pat_76	Post-Resistance	EXPH5	23086	37	11	108382062	108382062	Missense_Mutation	SNP	C	T	8	14	c.4172G>A	c.(4171-4173)AGT>AAT	p.S1391N
Pat_76	Post-Resistance	HSPB2	3316	37	11	111784324	111784324	Missense_Mutation	SNP	C	T	11	60	c.254C>T	c.(253-255)CCA>CTA	p.P85L
Pat_76	Post-Resistance	RNF214	257160	37	11	117109598	117109598	Missense_Mutation	SNP	C	T	7	12	c.389C>T	c.(388-390)CCA>CTA	p.P130L
Pat_76	Post-Resistance	DSCAML1	57453	37	11	117301743	117301743	Missense_Mutation	SNP	C	T	22	49	c.5561G>A	c.(5560-5562)GGA>GAA	p.G1854E
Pat_76	Post-Resistance	TMPRSS4	56649	37	11	117982593	117982593	Missense_Mutation	SNP	C	T	35	51	c.721C>T	c.(721-723)CTC>TTC	p.L241F
Pat_76	Post-Resistance	MLL	4297	37	11	118352637	118352637	Missense_Mutation	SNP	C	T	19	38	c.3842C>T	c.(3841-3843)CCT>CTT	p.P1281L
Pat_76	Post-Resistance	PHLDB1	23187	37	11	118498401	118498401	Missense_Mutation	SNP	C	T	31	52	c.862C>T	c.(862-864)CGT>TGT	p.R288C

Pat_76	Post-Resistance	PHLDB1	23187	37	11	118498923	118498923	Missense_Mutation	SNP	C	T	30	74	c.1384C>T	c.(1384-1386)CCA>TCA	p.P462S
Pat_76	Post-Resistance	TECTA	7007	37	11	120998886	120998886	Missense_Mutation	SNP	G	A	21	43	c.2200G>A	c.(2200-2202)GAG>AAG	p.E734K
Pat_76	Post-Resistance	TECTA	7007	37	11	121000408	121000408	Missense_Mutation	SNP	G	A	21	45	c.2429G>A	c.(2428-2430)CGA>CAA	p.R810Q
Pat_76	Post-Resistance	SORL1	6653	37	11	121492874	121492874	Missense_Mutation	SNP	C	T	4	16	c.6068C>T	c.(6067-6069)TCA>TTA	p.S2023L
Pat_76	Post-Resistance	HSPA8	3312	37	11	122928489	122928489	Missense_Mutation	SNP	G	A	13	34	c.1894C>T	c.(1894-1896)CCC>TCC	p.P632S
Pat_76	Post-Resistance	GRAMD1B	57476	37	11	123477467	123477467	Missense_Mutation	SNP	C	T	7	22	c.1045C>T	c.(1045-1047)CCC>TCC	p.P349S
Pat_76	Post-Resistance	OR6X1	390260	37	11	123624328	123624328	Missense_Mutation	SNP	C	T	16	52	c.899G>A	c.(898-900)AGA>AAA	p.R300K
Pat_76	Post-Resistance	OR4D5	219875	37	11	123810370	123810370	Missense_Mutation	SNP	G	A	17	26	c.47G>A	c.(46-48)GGG>GAG	p.G16E
Pat_76	Post-Resistance	OR4D5	219875	37	11	123810409	123810409	Missense_Mutation	SNP	C	T	6	15	c.86C>T	c.(85-87)ACT>ATT	p.T29I
Pat_76	Post-Resistance	VWA5A	4013	37	11	123988246	123988246	Missense_Mutation	SNP	C	T	14	33	c.28C>T	c.(28-30)CTC>TTC	p.L10F
Pat_76	Post-Resistance	VWA5A	4013	37	11	124016007	124016007	Missense_Mutation	SNP	G	A	8	17	c.2218G>A	c.(2218-2220)GAC>AAC	p.D740N
Pat_76	Post-Resistance	OR8D1	283159	37	11	124180653	124180653	Missense_Mutation	SNP	C	T	15	22	c.10G>A	c.(10-12)GAA>AAA	p.E4K
Pat_76	Post-Resistance	SPA17	53340	37	11	124564231	124564232	Missense_Mutation	DNP	GG	AA	6	28	c.345_346GG>AA	343-348)GAGGTT>GAAA	p.V116I
Pat_76	Post-Resistance	SLC37A2	219855	37	11	124954748	124954748	Missense_Mutation	SNP	G	A	8	22	c.1153G>A	c.(1153-1155)GAC>AAC	p.D385N
Pat_76	Post-Resistance	NTM	50863	37	11	132204942	132204942	Missense_Mutation	SNP	C	T	21	53	c.937C>T	c.(937-939)CCA>TCA	p.P313S
Pat_76	Post-Resistance	SPATA19	219938	37	11	133715271	133715271	Missense_Mutation	SNP	G	A	26	25	c.71C>T	c.(70-72)ACC>ATC	p.T24I
Pat_76	Post-Resistance	SLC6A12	6539	37	12	306618	306618	Missense_Mutation	SNP	C	T	10	21	c.1000G>A	c.(1000-1002)GGG>AGG	p.G334R
Pat_76	Post-Resistance	LRTM2	654429	37	12	1943433	1943434	Missense_Mutation	DNP	GG	AA	4	17	c.659_660GG>AA	c.(658-660)GGG>GAA	p.G220E
Pat_76	Post-Resistance	CACNA1C	775	37	12	2614028	2614028	Missense_Mutation	SNP	G	C	4	10	c.1134G>C	c.(1132-1134)AGG>AGC	p.R378S
Pat_76	Post-Resistance	C12orf32	83695	37	12	2994574	2994575	Missense_Mutation	DNP	CC	TT	6	28	c.42_43CC>TT	(40-45)GCCCCG>GCTTC	p.P15S
Pat_76	Post-Resistance	DYRK4	8798	37	12	4702179	4702179	Missense_Mutation	SNP	C	T	7	27	c.130C>T	c.(130-132)CTT>TTT	p.L44F
Pat_76	Post-Resistance	KCNA6	3742	37	12	4919724	4919724	Missense_Mutation	SNP	G	A	3	18	c.517G>A	c.(517-519)GCC>ACC	p.A173T
Pat_76	Post-Resistance	NTF3	4908	37	12	5603912	5603912	Missense_Mutation	SNP	G	A	17	47	c.532G>A	c.(532-534)GAG>AAG	p.E178K
Pat_76	Post-Resistance	ANO2	57101	37	12	5708727	5708727	Missense_Mutation	SNP	G	A	22	38	c.2156C>T	c.(2155-2157)TCG>TTG	p.S719L
Pat_76	Post-Resistance	GPR162	27239	37	12	6933764	6933764	Missense_Mutation	SNP	G	A	7	32	c.700G>A	c.(700-702)GGT>AGT	p.G234S
Pat_76	Post-Resistance	C1R	715	37	12	7188488	7188488	Missense_Mutation	SNP	C	T	4	5	c.1466G>A	c.(1465-1467)GGG>GAG	p.G489E
Pat_76	Post-Resistance	FAM90A1	55138	37	12	8376706	8376706	Missense_Mutation	SNP	C	T	15	25	c.229G>A	c.(229-231)GAA>AAA	p.E77K
Pat_76	Post-Resistance	PZP	5858	37	12	9311134	9311134	Missense_Mutation	SNP	C	T	15	22	c.3176G>A	c.(3175-3177)CGA>CAA	p.R1059Q
Pat_76	Post-Resistance	TAS2R7	50837	37	12	10954661	10954661	Nonsense_Mutation	SNP	C	T	3	13	c.509G>A	c.(508-510)TGG>TAG	p.W170*
Pat_76	Post-Resistance	PRB3	5544	37	12	11420151	11420151	Missense_Mutation	SNP	G	A	17	49	c.905C>T	c.(904-906)CCT>CTT	p.P302L
Pat_76	Post-Resistance	PRB1	5542	37	12	11506789	11506789	Missense_Mutation	SNP	T	G	29	81	c.248A>C	c.(247-249)CAA>CCA	p.Q83P
Pat_76	Post-Resistance	GPRC5A	9052	37	12	13061589	13061589	Missense_Mutation	SNP	G	A	17	84	c.406G>A	c.(406-408)GGT>AGT	p.G136S
Pat_76	Post-Resistance	GRIN2B	2904	37	12	13715992	13715992	Missense_Mutation	SNP	C	T	9	18	c.4180G>A	c.(4180-4182)GAC>AAC	p.D1394N
Pat_76	Post-Resistance	GRIN2B	2904	37	12	13764762	13764762	Nonsense_Mutation	SNP	C	T	21	70	c.1677G>A	c.(1675-1677)TGG>TGA	p.W559*
Pat_76	Post-Resistance	SLCO1A2	6579	37	12	21457408	21457408	Missense_Mutation	SNP	G	A	8	15	c.542C>T	c.(541-543)TCC>TTC	p.S181F
Pat_76	Post-Resistance	CAPRIN2	65981	37	12	30877346	30877346	Missense_Mutation	SNP	G	A	14	18	c.1945C>T	c.(1945-1947)CCA>TCA	p.P649S
Pat_76	Post-Resistance	DBX2	440097	37	12	45410133	45410134	Missense_Mutation	DNP	CC	TT	30	22	c.955_956GG>AA	c.(955-957)GGT>AAT	p.G319N
Pat_76	Post-Resistance	SLC38A1	81539	37	12	46601362	46601362	Missense_Mutation	SNP	G	A	33	13	c.431C>T	c.(430-432)ACC>ATC	p.T144I
Pat_76	Post-Resistance	FAM113B	91523	37	12	47628868	47628868	Missense_Mutation	SNP	G	A	9	40	c.22G>A	c.(22-24)GAA>AAA	p.E8K
Pat_76	Post-Resistance	FAM113B	91523	37	12	47629243	47629243	Missense_Mutation	SNP	C	T	59	42	c.397C>T	c.(397-399)CCG>TCG	p.P133S
Pat_76	Post-Resistance	RPAP3	79657	37	12	48062776	48062776	Missense_Mutation	SNP	G	C	25	80	c.1636C>G	c.(1636-1638)CCT>GCT	p.P546A
Pat_76	Post-Resistance	RAPGEF3	10411	37	12	48132959	48132959	Missense_Mutation	SNP	G	A	29	15	c.2302C>T	c.(2302-2304)CCT>TCT	p.P768S
Pat_76	Post-Resistance	COL2A1	1280	37	12	48367222	48367222	Missense_Mutation	SNP	C	T	66	68	c.4432G>A	c.(4432-4434)GGT>AGT	p.G1478S
Pat_76	Post-Resistance	ZNF641	121274	37	12	48736968	48736968	Missense_Mutation	SNP	G	A	15	62	c.1105C>T	c.(1105-1107)CCA>TCA	p.P369S
Pat_76	Post-Resistance	ADCY6	112	37	12	49170953	49170953	Missense_Mutation	SNP	G	A	131	91	c.1310C>T	c.(1309-1311)CCG>CTG	p.P437L
Pat_76	Post-Resistance	MLL2	8085	37	12	49420129	49420129	Missense_Mutation	SNP	G	A	25	14	c.15620C>T	.(15619-15621)CCC>CTC	p.P5207L
Pat_76	Post-Resistance	MLL2	8085	37	12	49438054	49438054	Missense_Mutation	SNP	G	A	8	24	c.5117C>T	c.(5116-5118)TCC>TTC	p.S1706F

Pat_76	Post-Resistance	SPATS2	65244	37	12	49890769	49890769	Missense_Mutation	SNP	C	T	30	27	c.680C>T	c.(679-681)CCC>CTC	p.P227L
Pat_76	Post-Resistance	NCKAP5L	57701	37	12	50190132	50190132	Missense_Mutation	SNP	C	T	6	7	c.1511G>A	c.(1510-1512)AGG>AAG	p.R504K
Pat_76	Post-Resistance	CSRNP2	81566	37	12	51467709	51467709	Missense_Mutation	SNP	C	G	46	38	c.308G>C	c.(307-309)CGG>CCG	p.R103P
Pat_76	Post-Resistance	SLC4A8	9498	37	12	51856194	51856194	Nonsense_Mutation	SNP	G	A	39	40	c.1202G>A	c.(1201-1203)TGG>TAG	p.W401*
Pat_76	Post-Resistance	SLC4A8	9498	37	12	51882536	51882536	Nonsense_Mutation	SNP	G	A	14	106	c.2340G>A	c.(2338-2340)TGG>TGA	p.W780*
Pat_76	Post-Resistance	KRT6B	3854	37	12	52844360	52844360	Nonsense_Mutation	SNP	C	T	48	41	c.585G>A	c.(583-585)TGG>TGA	p.W195*
Pat_76	Post-Resistance	KRT6B	3854	37	12	52845837	52845837	Missense_Mutation	SNP	C	G	12	12	c.26G>C	c.(25-27)AGG>ACG	p.R9T
Pat_76	Post-Resistance	KRT76	51350	37	12	53170654	53170654	Missense_Mutation	SNP	C	T	6	3	c.422G>A	c.(421-423)GGT>GAT	p.G141D
Pat_76	Post-Resistance	KRT78	196374	37	12	53239983	53239983	Missense_Mutation	SNP	C	T	15	15	c.754G>A	c.(754-756)GAA>AAA	p.E252K
Pat_76	Post-Resistance	SOAT2	8435	37	12	53512193	53512193	Missense_Mutation	SNP	C	T	36	43	c.838C>T	c.(838-840)CTC>TTC	p.L280F
Pat_76	Post-Resistance	NCKAP1L	3071	37	12	54930826	54930826	Missense_Mutation	SNP	G	A	11	55	c.3172G>A	c.(3172-3174)GAA>AAA	p.E1058K
Pat_76	Post-Resistance	OR6C70	390327	37	12	55863739	55863739	Missense_Mutation	SNP	G	A	27	16	c.184C>T	c.(184-186)CGT>TGT	p.R62C
Pat_76	Post-Resistance	ARHGAP9	64333	37	12	57871402	57871402	Missense_Mutation	SNP	C	T	28	19	c.809G>A	c.(808-810)CGC>CAC	p.R270H
Pat_76	Post-Resistance	IRAK3	11213	37	12	66620573	66620573	Missense_Mutation	SNP	C	T	37	22	c.724C>T	c.(724-726)CCA>TCA	p.P242S
Pat_76	Post-Resistance	DYRK2	8445	37	12	68050955	68050955	Missense_Mutation	SNP	G	C	70	51	c.268G>C	c.(268-270)GTT>CTT	p.V90L
Pat_76	Post-Resistance	LYZ	4069	37	12	69742273	69742273	Missense_Mutation	SNP	A	G	3	52	c.85A>G	c.(85-87)ACT>GCT	p.T29A
Pat_76	Post-Resistance	KCNMB4	27345	37	12	70794016	70794016	Missense_Mutation	SNP	G	A	16	73	c.364G>A	c.(364-366)GAA>AAA	p.E122K
Pat_76	Post-Resistance	CAPS2	84698	37	12	75685579	75685579	Missense_Mutation	SNP	C	A	16	23	c.1242G>T	c.(1240-1242)GAG>GAT	p.E414D
Pat_76	Post-Resistance	EPYC	1833	37	12	91358003	91358003	Missense_Mutation	SNP	G	A	39	18	c.899C>T	c.(898-900)CCT>CTT	p.P300L
Pat_76	Post-Resistance	CLLU1OS	574016	37	12	92814859	92814859	Missense_Mutation	SNP	T	C	118	84	c.233A>G	c.(232-234)AAT>AGT	p.N78S
Pat_76	Post-Resistance	UHRF1BP1L	23074	37	12	100444092	100444092	Missense_Mutation	SNP	G	A	20	16	c.3572C>T	c.(3571-3573)TCC>TTC	p.S1191F
Pat_76	Post-Resistance	KIAA1033	23325	37	12	105546125	105546125	Missense_Mutation	SNP	C	T	4	12	c.2654C>T	c.(2653-2655)CCT>CTT	p.P885L
Pat_76	Post-Resistance	PRDM4	11108	37	12	108134795	108134795	Missense_Mutation	SNP	G	A	58	36	c.1852C>T	c.(1852-1854)CAC>TAC	p.H618Y
Pat_76	Post-Resistance	WSCD2	9671	37	12	108604011	108604011	Missense_Mutation	SNP	G	A	5	22	c.611G>A	c.(610-612)GGC>GAC	p.G204D
Pat_76	Post-Resistance	TMEM119	338773	37	12	108985355	108985355	Missense_Mutation	SNP	G	A	55	31	c.805C>T	c.(805-807)CCC>TCC	p.P269S
Pat_76	Post-Resistance	MYO1H	283446	37	12	109865367	109865367	Missense_Mutation	SNP	G	A	48	276	c.1877G>A	c.(1876-1878)AGG>AAG	p.R626K
Pat_76	Post-Resistance	CCDC63	160762	37	12	111336846	111336846	Missense_Mutation	SNP	A	G	11	38	c.1259A>G	c.(1258-1260)AAG>AGG	p.K420R
Pat_76	Post-Resistance	CUX2	23316	37	12	111749945	111749945	Missense_Mutation	SNP	G	A	30	14	c.1942G>A	c.(1942-1944)GAC>AAC	p.D648N
Pat_76	Post-Resistance	C12orf51	283450	37	12	112690345	112690346	Missense_Mutation	DNP	GG	AA	5	28	.2168_2169CC>T	c.(2167-2169)TCC>TTT	p.S723F
Pat_76	Post-Resistance	TPCN1	53373	37	12	113664698	113664699	Missense_Mutation	DNP	CC	TT	37	28	c.41_42CC>TT	c.(40-42)ACC>ATT	p.T14I
Pat_76	Post-Resistance	NOS1	4842	37	12	117680432	117680432	Missense_Mutation	SNP	C	T	17	23	c.3041G>A	c.(3040-3042)AGT>AAT	p.S1014N
Pat_76	Post-Resistance	NOS1	4842	37	12	117768373	117768373	Missense_Mutation	SNP	C	T	18	50	c.502G>A	c.(502-504)GAG>AAG	p.E168K
Pat_76	Post-Resistance	CIT	11113	37	12	120156650	120156650	Missense_Mutation	SNP	C	T	6	21	c.3731G>A	c.(3730-3732)CGG>CAG	p.R1244Q
Pat_76	Post-Resistance	OGFOD2	79676	37	12	123463861	123463861	Missense_Mutation	SNP	C	T	11	63	c.1021C>T	c.(1021-1023)CCC>TCC	p.P341S
Pat_76	Post-Resistance	PITPNM2	57605	37	12	123498444	123498444	Missense_Mutation	SNP	G	A	10	71	c.224C>T	c.(223-225)TCC>TTC	p.S75F
Pat_76	Post-Resistance	TCTN2	79867	37	12	124172608	124172608	Nonsense_Mutation	SNP	C	T	53	34	c.775C>T	c.(775-777)CAG>TAG	p.Q259*
Pat_76	Post-Resistance	DNAH10	196385	37	12	124354974	124354974	Nonsense_Mutation	SNP	G	A	24	23	c.7227G>A	c.(7225-7227)TGG>TGA	p.W2409*
Pat_76	Post-Resistance	TMEM132D	121256	37	12	130015712	130015712	Missense_Mutation	SNP	C	T	22	46	c.1007G>A	c.(1006-1008)CGA>CAA	p.R336Q
Pat_76	Post-Resistance	GPR133	283383	37	12	131593273	131593273	Missense_Mutation	SNP	C	T	53	348	c.1892C>T	c.(1891-1893)CCC>CTC	p.P631L
Pat_76	Post-Resistance	ZNF268	10795	37	12	133768563	133768563	Missense_Mutation	SNP	C	T	7	114	c.431C>T	c.(430-432)GCC>GTC	p.A144V
Pat_76	Post-Resistance	PARP4	143	37	13	25066708	25066708	Missense_Mutation	SNP	G	A	20	62	c.904C>T	c.(904-906)CTT>TTT	p.L302F
Pat_76	Post-Resistance	FAM123A	219287	37	13	25744499	25744499	Missense_Mutation	SNP	C	T	9	14	c.1259G>A	c.(1258-1260)GGA>GAA	p.G420E
Pat_76	Post-Resistance	MTUS2	23281	37	13	29600115	29600115	Missense_Mutation	SNP	C	T	4	17	c.1310C>T	c.(1309-1311)TCC>TTC	p.S437F
Pat_76	Post-Resistance	RXFP2	122042	37	13	32371390	32371390	Missense_Mutation	SNP	C	A	14	29	c.1839C>A	c.(1837-1839)TTC>TTA	p.F613L
Pat_76	Post-Resistance	FRY	10129	37	13	32869444	32869444	Nonsense_Mutation	SNP	T	A	15	35	c.8889T>A	c.(8887-8889)TAT>TAA	p.Y2963*
Pat_76	Post-Resistance	FREM2	341640	37	13	39265494	39265494	Missense_Mutation	SNP	C	T	9	16	c.4013C>T	c.(4012-4014)TCT>TTT	p.S1338F
Pat_76	Post-Resistance	KIAA0564	23078	37	13	42442530	42442531	Missense_Mutation	DNP	GG	CA	9	26	.1163_1164CC>T	c.(1162-1164)TCC>TTG	p.S388L

Pat_76	Post-Resistance	CYSLTR2	57105	37	13	49281332	49281332	Missense_Mutation	SNP	T	C	52	75	c.379T>C	c.(379-381)TAT>CAT	p.Y127H
Pat_76	Post-Resistance	ATP7B	540	37	13	52524208	52524209	Missense_Mutation	DNP	GG	AA	13	23	.2664_2665CC>T	662-2667)ACCCAC>ACTT	p.H889Y
Pat_76	Post-Resistance	OLFM4	10562	37	13	53624121	53624121	Missense_Mutation	SNP	G	A	8	21	c.748G>A	c.(748-750)GGT>AGT	p.G250S
Pat_76	Post-Resistance	DACH1	1602	37	13	72133952	72133952	Missense_Mutation	SNP	G	A	9	17	c.1435C>T	c.(1435-1437)CCG>TCG	p.P479S
Pat_76	Post-Resistance	DIS3	22894	37	13	73340162	73340162	Missense_Mutation	SNP	G	A	9	3	c.1918C>T	c.(1918-1920)CAC>TAC	p.H640Y
Pat_76	Post-Resistance	SLITRK1	114798	37	13	84454754	84454754	Missense_Mutation	SNP	C	T	8	5	c.889G>A	c.(889-891)GAT>AAT	p.D297N
Pat_76	Post-Resistance	SLITRK6	84189	37	13	86368213	86368213	Missense_Mutation	SNP	C	T	5	23	c.2431G>A	c.(2431-2433)GTA>ATA	p.V811I
Pat_76	Post-Resistance	SLITRK5	26050	37	13	88329952	88329952	Missense_Mutation	SNP	G	A	34	76	c.2309G>A	c.(2308-2310)GGC>GAC	p.G770D
Pat_76	Post-Resistance	GPC5	2262	37	13	92345753	92345753	Missense_Mutation	SNP	G	A	9	19	c.638G>A	c.(637-639)GGA>GAA	p.G213E
Pat_76	Post-Resistance	ABCC4	10257	37	13	95830266	95830266	Missense_Mutation	SNP	C	T	29	71	c.1625G>A	c.(1624-1626)CGG>CAG	p.R542Q
Pat_76	Post-Resistance	DZIP1	22873	37	13	96277078	96277078	Missense_Mutation	SNP	C	T	3	7	c.916G>A	c.(916-918)GAG>AAG	p.E306K
Pat_76	Post-Resistance	PCCA	5095	37	13	100953723	100953723	Missense_Mutation	SNP	C	T	16	50	c.1075C>T	c.(1075-1077)CCT>TCT	p.P359S
Pat_76	Post-Resistance	COL4A1	1282	37	13	110826832	110826832	Missense_Mutation	SNP	G	A	6	14	c.3367C>T	c.(3367-3369)CCA>TCA	p.P1123S
Pat_76	Post-Resistance	PROZ	8858	37	13	113825991	113825991	Missense_Mutation	SNP	G	A	13	58	c.775G>A	c.(775-777)GAG>AAG	p.E259K
Pat_76	Post-Resistance	TMCO3	55002	37	13	114203801	114203801	Missense_Mutation	SNP	G	A	25	35	c.1982G>A	c.(1981-1983)AGA>AAA	p.R661K
Pat_76	Post-Resistance	OR4K5	79317	37	14	20389108	20389108	Missense_Mutation	SNP	C	G	15	80	c.343C>G	c.(343-345)CTT>GTT	p.L115V
Pat_76	Post-Resistance	OR4K1	79544	37	14	20404475	20404475	Missense_Mutation	SNP	C	T	6	11	c.650C>T	c.(649-651)TCC>TTC	p.S217F
Pat_76	Post-Resistance	OR11H4	390442	37	14	20711345	20711345	Missense_Mutation	SNP	G	A	9	25	c.395G>A	c.(394-396)CGA>CAA	p.R132Q
Pat_76	Post-Resistance	HNRNPC	3183	37	14	21679680	21679680	Missense_Mutation	SNP	G	A	10	16	c.722C>T	c.(721-723)TCC>TTC	p.S241F
Pat_76	Post-Resistance	METTL3	56339	37	14	21972004	21972004	Missense_Mutation	SNP	C	T	7	32	c.121G>A	c.(121-123)GCA>ACA	p.A41T
Pat_76	Post-Resistance	OR10G3	26533	37	14	22038638	22038638	Missense_Mutation	SNP	G	A	7	23	c.238C>T	c.(238-240)CCT>TCT	p.P80S
Pat_76	Post-Resistance	MMP14	4323	37	14	23313059	23313059	Missense_Mutation	SNP	G	A	19	43	c.991G>A	c.(991-993)GGG>AGG	p.G331R
Pat_76	Post-Resistance	JPH4	84502	37	14	24040266	24040267	Missense_Mutation	DNP	GG	AA	6	19	.1673_1674CC>T	c.(1672-1674)GCC>GTT	p.A558V
Pat_76	Post-Resistance	FITM1	161247	37	14	24601613	24601613	Missense_Mutation	SNP	G	A	12	28	c.460G>A	c.(460-462)GAG>AAG	p.E154K
Pat_76	Post-Resistance	GMPR2	51292	37	14	24707971	24707971	Missense_Mutation	SNP	G	A	7	40	c.1034G>A	c.(1033-1035)AGT>AAT	p.S345N
Pat_76	Post-Resistance	C14orf21	161424	37	14	24769776	24769776	Missense_Mutation	SNP	C	T	26	185	c.410C>T	c.(409-411)GCC>GTC	p.A137V
Pat_76	Post-Resistance	GZMB	3002	37	14	25100338	25100338	Missense_Mutation	SNP	C	T	10	37	c.683G>A	c.(682-684)CGA>CAA	p.R228Q
Pat_76	Post-Resistance	ARHGAP5	394	37	14	32586491	32586491	Missense_Mutation	SNP	C	T	5	19	c.3863C>T	c.(3862-3864)ACA>ATA	p.T1288I
Pat_76	Post-Resistance	AKAP6	9472	37	14	33291332	33291332	Missense_Mutation	SNP	G	A	4	14	c.4313G>A	c.(4312-4314)GGA>GAA	p.G1438E
Pat_76	Post-Resistance	RALGAPA1	253959	37	14	36041828	36041828	Missense_Mutation	SNP	G	A	5	17	c.5788C>T	c.(5788-5790)CTT>TTT	p.L1930F
Pat_76	Post-Resistance	LRFN5	145581	37	14	42368131	42368131	Missense_Mutation	SNP	A	C	17	38	c.2110A>C	c.(2110-2112)ACT>CCT	p.T704P
Pat_76	Post-Resistance	FAM179B	23116	37	14	45481251	45481251	Missense_Mutation	SNP	C	T	4	8	c.3211C>T	c.(3211-3213)CAT>TAT	p.H1071Y
Pat_76	Post-Resistance	RPL10L	140801	37	14	47120861	47120861	Missense_Mutation	SNP	G	A	16	55	c.79C>T	c.(79-81)CCT>TCT	p.P27S
Pat_76	Post-Resistance	RTN1	6252	37	14	60212705	60212705	Missense_Mutation	SNP	C	T	11	46	c.736G>A	c.(736-738)GAG>AAG	p.E246K
Pat_76	Post-Resistance	KCNH5	27133	37	14	63175092	63175092	Missense_Mutation	SNP	G	A	20	40	c.2101C>T	c.(2101-2103)CCC>TCC	p.P701S
Pat_76	Post-Resistance	KCNH5	27133	37	14	63468171	63468171	Missense_Mutation	SNP	G	A	5	14	c.311C>T	c.(310-312)CCT>CTT	p.P104L
Pat_76	Post-Resistance	SYNE2	23224	37	14	64469684	64469684	Missense_Mutation	SNP	C	T	8	22	c.4033C>T	c.(4033-4035)CTT>TTT	p.L1345F
Pat_76	Post-Resistance	ZBTB25	7597	37	14	64954009	64954009	Missense_Mutation	SNP	G	A	17	29	c.940C>T	c.(940-942)CGG>TGG	p.R314W
Pat_76	Post-Resistance	SPTB	6710	37	14	65253757	65253757	Missense_Mutation	SNP	C	T	5	20	c.2926G>A	c.(2926-2928)GTA>ATA	p.V976I
Pat_76	Post-Resistance	SLC8A3	6547	37	14	70633384	70633384	Missense_Mutation	SNP	C	T	12	27	c.1756G>A	c.(1756-1758)GAG>AAG	p.E586K
Pat_76	Post-Resistance	SYNJ2BP	55333	37	14	70855188	70855188	Missense_Mutation	SNP	G	A	8	13	c.200C>T	c.(199-201)TCG>TTG	p.S67L
Pat_76	Post-Resistance	PSEN1	5663	37	14	73685912	73685912	Missense_Mutation	SNP	C	T	24	57	c.1319C>T	c.(1318-1320)ACC>ATC	p.T440I
Pat_76	Post-Resistance	LTBP2	4053	37	14	74970727	74970727	Missense_Mutation	SNP	C	T	14	21	c.4484G>A	c.(4483-4485)GGT>GAT	p.G1495D
Pat_76	Post-Resistance	YLPM1	56252	37	14	75264383	75264383	Missense_Mutation	SNP	C	T	7	6	c.2383C>T	c.(2383-2385)CCC>TCC	p.P795S
Pat_76	Post-Resistance	ISM2	145501	37	14	77948827	77948827	Missense_Mutation	SNP	C	T	5	9	c.811G>A	c.(811-813)GAA>AAA	p.E271K
Pat_76	Post-Resistance	FLRT2	23768	37	14	86089260	86089260	Missense_Mutation	SNP	G	A	21	43	c.1402G>A	c.(1402-1404)GAG>AAG	p.E468K
Pat_76	Post-Resistance	CCDC88C	440193	37	14	91773417	91773417	Nonsense_Mutation	SNP	G	A	6	6	c.3160C>T	c.(3160-3162)CGA>TGA	p.R1054*

Pat_76	Post-Resistance	FBLN5	10516	37	14	92343937	92343937	Missense_Mutation	SNP	G	A	24	68	c.1079C>T	c.(1078-1080)TCC>TTC	p.S360F
Pat_76	Post-Resistance	UBR7	55148	37	14	93684899	93684899	Missense_Mutation	SNP	G	A	5	36	c.628G>A	c.(628-630)GGA>AGA	p.G210R
Pat_76	Post-Resistance	BTBD7	55727	37	14	93709119	93709119	Missense_Mutation	SNP	G	A	12	28	c.2899C>T	c.(2899-2901)CCT>TCT	p.P967S
Pat_76	Post-Resistance	KIAA1409	57578	37	14	94158197	94158197	Nonsense_Mutation	SNP	C	T	19	46	c.7027C>T	c.(7027-7029)CAG>TAG	p.Q2343*
Pat_76	Post-Resistance	SERPINA1	5265	37	14	94844814	94844814	Missense_Mutation	SNP	C	T	7	21	c.1229G>A	c.(1228-1230)GGA>GAA	p.G410E
Pat_76	Post-Resistance	SERPINA9	327657	37	14	94933701	94933701	Missense_Mutation	SNP	A	C	8	16	c.701T>G	c.(700-702)TTT>TGT	p.F234C
Pat_76	Post-Resistance	SERPINA3	12	37	14	95088794	95088794	Missense_Mutation	SNP	G	A	6	12	c.1034G>A	c.(1033-1035)GGG>GAG	p.G345E
Pat_76	Post-Resistance	SERPINA13	388007	37	14	95108179	95108179	Nonsense_Mutation	SNP	G	A	28	48	c.696G>A	c.(694-696)TGG>TGA	p.W232*
Pat_76	Post-Resistance	DICER1	23405	37	14	95562323	95562323	Missense_Mutation	SNP	G	A	30	57	c.4934C>T	c.(4933-4935)CCA>CTA	p.P1645L
Pat_76	Post-Resistance	BDKRB2	624	37	14	96707210	96707210	Nonsense_Mutation	SNP	G	A	14	41	c.545G>A	c.(544-546)TGG>TAG	p.W182*
Pat_76	Post-Resistance	PAPOLA	10914	37	14	97002295	97002295	Missense_Mutation	SNP	C	T	25	41	c.989C>T	c.(988-990)TCC>TTC	p.S330F
Pat_76	Post-Resistance	CDC42BPB	9578	37	14	103440469	103440469	Nonsense_Mutation	SNP	G	A	7	12	c.1525C>T	c.(1525-1527)CGA>TGA	p.R509*
Pat_76	Post-Resistance	ADAM6	8755	37	14	106350754	106350754	Splice_Site	SNP	G	A	14	33	c.49979_splice	c.e3164-1	
Pat_76	Post-Resistance	NIPA1	123606	37	15	23052675	23052675	Missense_Mutation	SNP	G	A	15	91	c.398C>T	c.(397-399)TCC>TTC	p.S133F
Pat_76	Post-Resistance	C15orf2	23742	37	15	24922816	24922816	Missense_Mutation	SNP	C	A	8	35	c.1802C>A	c.(1801-1803)CCA>CAA	p.P601Q
Pat_76	Post-Resistance	NDNL2	56160	37	15	29561539	29561539	Missense_Mutation	SNP	G	A	22	64	c.371C>T	c.(370-372)CCC>CTC	p.P124L
Pat_76	Post-Resistance	TJP1	7082	37	15	30011099	30011099	Missense_Mutation	SNP	G	A	44	40	c.3247C>T	c.(3247-3249)CGC>TGC	p.R1083C
Pat_76	Post-Resistance	CHRFAM7A	89832	37	15	30659708	30659708	Missense_Mutation	SNP	C	T	34	136	c.633G>A	c.(631-633)ATG>ATA	p.M211I
Pat_76	Post-Resistance	AQR	9716	37	15	35166887	35166887	Missense_Mutation	SNP	G	C	13	34	c.3416C>G	c.(3415-3417)GCC>GGC	p.A1139G
Pat_76	Post-Resistance	THBS1	7057	37	15	39886338	39886338	Nonsense_Mutation	SNP	G	A	8	11	c.3306G>A	c.(3304-3306)TGG>TGA	p.W1102*
Pat_76	Post-Resistance	BAHD1	22893	37	15	40754233	40754233	Missense_Mutation	SNP	C	T	19	44	c.1555C>T	c.(1555-1557)CCC>TCC	p.P519S
Pat_76	Post-Resistance	RPUSD2	27079	37	15	40866242	40866242	Missense_Mutation	SNP	G	A	25	32	c.1420G>A	c.(1420-1422)GAG>AAG	p.E474K
Pat_76	Post-Resistance	MAPKBP1	23005	37	15	42105883	42105883	Missense_Mutation	SNP	C	T	63	210	c.902C>T	c.(901-903)ACC>ATC	p.T301I
Pat_76	Post-Resistance	SPTBN5	51332	37	15	42185575	42185575	Missense_Mutation	SNP	C	T	22	32	c.16G>A	c.(16-18)GAG>AAG	p.E6K
Pat_76	Post-Resistance	PLA2G4D	283748	37	15	42363971	42363971	Splice_Site	SNP	C	T	25	39	c.1573_splice	c.e15+1	p.A525_splice
Pat_76	Post-Resistance	ZFP106	64397	37	15	42743482	42743482	Missense_Mutation	SNP	G	A	6	20	c.919C>T	c.(919-921)CCT>TCT	p.P307S
Pat_76	Post-Resistance	ZFP106	64397	37	15	42743832	42743832	Missense_Mutation	SNP	C	T	40	38	c.569G>A	c.(568-570)GGA>GAA	p.G190E
Pat_76	Post-Resistance	TTBK2	146057	37	15	43086989	43086989	Missense_Mutation	SNP	G	A	10	10	c.833C>T	c.(832-834)TCC>TTC	p.S278F
Pat_76	Post-Resistance	TP53BP1	7158	37	15	43748861	43748861	Nonsense_Mutation	SNP	G	A	19	55	c.1930C>T	c.(1930-1932)CAG>TAG	p.Q644*
Pat_76	Post-Resistance	C15orf43	145645	37	15	45250689	45250689	Missense_Mutation	SNP	C	T	6	3	c.265C>T	c.(265-267)CCT>TCT	p.P89S
Pat_76	Post-Resistance	DUOX1	53905	37	15	45433506	45433506	Missense_Mutation	SNP	G	A	32	49	c.1582G>A	c.(1582-1584)GAG>AAG	p.E528K
Pat_76	Post-Resistance	SLC28A2	9153	37	15	45545694	45545694	Missense_Mutation	SNP	G	A	6	22	c.146G>A	c.(145-147)GGA>GAA	p.G49E
Pat_76	Post-Resistance	HDC	3067	37	15	50535413	50535413	Missense_Mutation	SNP	G	A	3	26	c.1169C>T	c.(1168-1170)TCT>TTT	p.S390F
Pat_76	Post-Resistance	WDR72	256764	37	15	53908113	53908113	Missense_Mutation	SNP	C	T	5	12	c.2290G>A	c.(2290-2292)GAT>AAT	p.D764N
Pat_76	Post-Resistance	UNC13C	440279	37	15	54919174	54919174	Missense_Mutation	SNP	C	T	6	25	c.6508C>T	c.(6508-6510)CCT>TCT	p.P2170S
Pat_76	Post-Resistance	MYO1E	4643	37	15	59519723	59519724	Missense_Mutation	DNP	GG	AA	12	21	c.576_577CC>TT	(574-579)TTCCTT>TTTTT	p.L193F
Pat_76	Post-Resistance	HERC1	8925	37	15	63984706	63984706	Missense_Mutation	SNP	G	A	3	11	c.5734C>T	c.(5734-5736)CGC>TGC	p.R1912C
Pat_76	Post-Resistance	CLPX	10845	37	15	65448131	65448132	Missense_Mutation	DNP	GG	AA	13	50	.1209_1210CC>T	207-1212)CTCCGT>CTTT	p.R404C
Pat_76	Post-Resistance	CILP	8483	37	15	65490642	65490642	Missense_Mutation	SNP	G	A	12	41	c.1982C>T	c.(1981-1983)TCT>TTT	p.S661F
Pat_76	Post-Resistance	DENND4A	10260	37	15	65983030	65983030	Missense_Mutation	SNP	G	A	7	31	c.3770C>T	c.(3769-3771)CCT>CTT	p.P1257L
Pat_76	Post-Resistance	MEGF11	84465	37	15	66250017	66250018	Nonsense_Mutation	DNP	CC	TT	22	29	.1154_1155GG>A	c.(1153-1155)TGG>TAA	p.W385*
Pat_76	Post-Resistance	MAP2K5	5607	37	15	67995693	67995693	Missense_Mutation	SNP	G	A	5	29	c.991G>A	c.(991-993)GAG>AAG	p.E331K
Pat_76	Post-Resistance	LRRC49	54839	37	15	71197052	71197052	Missense_Mutation	SNP	C	T	18	71	c.458C>T	c.(457-459)TCG>TTG	p.S153L
Pat_76	Post-Resistance	CIB2	10518	37	15	78401697	78401697	Missense_Mutation	SNP	C	T	7	37	c.226G>A	c.(226-228)GCG>ACG	p.A76T
Pat_76	Post-Resistance	ACSBG1	23205	37	15	78474348	78474348	Missense_Mutation	SNP	C	T	45	30	c.1034G>A	c.(1033-1035)GGG>GAG	p.G345E
Pat_76	Post-Resistance	KIAA1199	57214	37	15	81199043	81199043	Missense_Mutation	SNP	G	A	42	50	c.1451G>A	c.(1450-1452)GGC>GAC	p.G484D
Pat_76	Post-Resistance	C15orf40	123207	37	15	83677352	83677352	Missense_Mutation	SNP	C	T	22	31	c.314G>A	c.(313-315)CGG>CAG	p.R105Q

Pat_76	Post-Resistance	SLC28A1	9154	37	15	85447408	85447408	Missense_Mutation	SNP	C	T	48	60	c.542C>T	c.(541-543)TCC>TTC	p.S181F
Pat_76	Post-Resistance	AKAP13	11214	37	15	86122597	86122597	Missense_Mutation	SNP	C	T	7	20	c.1298C>T	c.(1297-1299)CCC>CTC	p.P433L
Pat_76	Post-Resistance	KLHL25	64410	37	15	86311780	86311780	Missense_Mutation	SNP	G	A	19	18	c.1262C>T	c.(1261-1263)GCC>GTC	p.A421V
Pat_76	Post-Resistance	DET1	55070	37	15	89073951	89073951	Missense_Mutation	SNP	A	T	5	12	c.986T>A	c.(985-987)CTG>CAG	p.L329Q
Pat_76	Post-Resistance	ACAN	176	37	15	89400288	89400288	Missense_Mutation	SNP	C	T	6	47	c.4472C>T	c.(4471-4473)CCT>CTT	p.P1491L
Pat_76	Post-Resistance	ZNF710	374655	37	15	90610437	90610437	Missense_Mutation	SNP	C	T	5	16	c.68C>T	c.(67-69)GCC>GTC	p.A23V
Pat_76	Post-Resistance	C15orf58	390637	37	15	90784313	90784313	Missense_Mutation	SNP	C	T	122	100	c.173C>T	c.(172-174)CCC>CTC	p.P58L
Pat_76	Post-Resistance	IQGAP1	8826	37	15	91009306	91009306	Missense_Mutation	SNP	C	T	9	66	c.1850C>T	c.(1849-1851)ACC>ATC	p.T617I
Pat_76	Post-Resistance	ST8SIA2	8128	37	15	92988160	92988160	Splice_Site	SNP	G	A	35	108	c.842_splice	c.e5+1	p.G281_splice
Pat_76	Post-Resistance	FAM174B	400451	37	15	93173525	93173525	Missense_Mutation	SNP	G	A	7	18	c.395C>T	c.(394-396)CCA>CTA	p.P132L
Pat_76	Post-Resistance	SPATA8	145946	37	15	97328244	97328244	Missense_Mutation	SNP	G	A	46	54	c.215G>A	c.(214-216)GGA>GAA	p.G72E
Pat_76	Post-Resistance	ADAMTS17	170691	37	15	100594150	100594150	Nonsense_Mutation	SNP	C	T	165	377	c.2247G>A	c.(2245-2247)TGG>TGA	p.W749*
Pat_76	Post-Resistance	LINS1	55180	37	15	101120947	101120947	Missense_Mutation	SNP	G	A	9	11	c.101C>T	c.(100-102)CCA>CTA	p.P34L
Pat_76	Post-Resistance	TMEM8A	58986	37	16	427448	427448	Missense_Mutation	SNP	G	A	14	21	c.437C>T	c.(436-438)TCC>TTC	p.S146F
Pat_76	Post-Resistance	BAIAP3	8938	37	16	1391412	1391412	Missense_Mutation	SNP	C	T	42	79	c.758C>T	c.(757-759)CCC>CTC	p.P253L
Pat_76	Post-Resistance	GNPTG	84572	37	16	1412108	1412109	Missense_Mutation	DNP	CC	TT	3	7	c.387_388CC>TT	385-390)TGCCGT>TGTT	p.R130C
Pat_76	Post-Resistance	EME2	197342	37	16	1825965	1825965	Missense_Mutation	SNP	C	T	6	7	c.1142C>T	c.(1141-1143)CCC>CTC	p.P381L
Pat_76	Post-Resistance	HS3ST6	64711	37	16	1961872	1961873	Missense_Mutation	DNP	CC	TT	29	57	c.654_655GG>AA	52-657)GGGGAG>GGAA	p.E219K
Pat_76	Post-Resistance	PRSS22	64063	37	16	2903913	2903913	Missense_Mutation	SNP	C	T	16	48	c.670G>A	c.(670-672)GAC>AAC	p.D224N
Pat_76	Post-Resistance	CLDN6	9074	37	16	3065689	3065689	Missense_Mutation	SNP	C	T	13	24	c.334G>A	c.(334-336)GAT>AAT	p.D112N
Pat_76	Post-Resistance	ZSCAN10	84891	37	16	3139460	3139460	Missense_Mutation	SNP	C	T	8	18	c.1810G>A	c.(1810-1812)GAG>AAG	p.E604K
Pat_76	Post-Resistance	MEFV	4210	37	16	3293401	3293401	Missense_Mutation	SNP	C	T	13	26	c.2086G>A	c.(2086-2088)GAA>AAA	p.E696K
Pat_76	Post-Resistance	NLRC3	197358	37	16	3607625	3607625	Missense_Mutation	SNP	G	A	5	6	c.2068C>T	c.(2068-2070)CTC>TTC	p.L690F
Pat_76	Post-Resistance	CREBBP	1387	37	16	3823918	3823919	Missense_Mutation	DNP	GG	AA	17	60	.2296_2297CC>T	c.(2296-2298)CCT>TTT	p.P766F
Pat_76	Post-Resistance	12-Sep	124404	37	16	4829778	4829778	Missense_Mutation	SNP	G	A	26	39	c.736C>T	c.(736-738)CCT>TCT	p.P246S
Pat_76	Post-Resistance	PPL	5493	37	16	4934443	4934443	Missense_Mutation	SNP	C	T	6	9	c.4213G>A	c.(4213-4215)GAG>AAG	p.E1405K
Pat_76	Post-Resistance	GRIN2A	2903	37	16	9858255	9858255	Missense_Mutation	SNP	G	A	15	47	c.3146C>T	c.(3145-3147)CCT>CTT	p.P1049L
Pat_76	Post-Resistance	GRIN2A	2903	37	16	9923297	9923297	Missense_Mutation	SNP	C	T	14	26	c.1990G>A	c.(1990-1992)GGC>AGC	p.G664S
Pat_76	Post-Resistance	CIITA	4261	37	16	11001309	11001309	Missense_Mutation	SNP	C	T	3	9	c.1960C>T	c.(1960-1962)CCC>TCC	p.P654S
Pat_76	Post-Resistance	ERCC4	2072	37	16	14029042	14029042	Missense_Mutation	SNP	C	T	15	37	c.1253C>T	c.(1252-1254)TCC>TTC	p.S418F
Pat_76	Post-Resistance	C16orf88	400506	37	16	19718383	19718383	Missense_Mutation	SNP	G	A	15	36	c.1226C>T	c.(1225-1227)GCT>GTT	p.A409V
Pat_76	Post-Resistance	PDILT	204474	37	16	20384348	20384348	Missense_Mutation	SNP	C	T	25	54	c.778G>A	c.(778-780)GAA>AAA	p.E260K
Pat_76	Post-Resistance	ACSM2A	123876	37	16	20476967	20476968	Missense_Mutation	DNP	CC	TG	4	49	c.306_307CC>TG	304-309)GGCCTG>GGTG	p.L103V
Pat_76	Post-Resistance	ACSM2B	348158	37	16	20570640	20570641	Missense_Mutation	DNP	GG	CA	6	16	c.306_307CC>TG	304-309)GGCCTG>GGTG	p.L103V
Pat_76	Post-Resistance	ACSM1	116285	37	16	20648710	20648710	Missense_Mutation	SNP	G	A	29	42	c.1180C>T	c.(1180-1182)CCA>TCA	p.P394S
Pat_76	Post-Resistance	ACSM1	116285	37	16	20696554	20696554	Missense_Mutation	SNP	G	A	24	87	c.364C>T	c.(364-366)CCT>TCT	p.P122S
Pat_76	Post-Resistance	OTOA	146183	37	16	21696638	21696638	Missense_Mutation	SNP	C	T	4	13	c.355C>T	c.(355-357)CGC>TGC	p.R119C
Pat_76	Post-Resistance	VWA3A	146177	37	16	22161253	22161253	Splice_Site	SNP	G	A	33	111	c.3129_splice	c.e29+1	p.L1043_splice
Pat_76	Post-Resistance	VWA3A	146177	37	16	22166979	22166979	Missense_Mutation	SNP	C	T	7	33	c.3497C>T	c.(3496-3498)TCC>TTC	p.S1166F
Pat_76	Post-Resistance	EEF2K	29904	37	16	22268602	22268602	Missense_Mutation	SNP	C	T	29	50	c.797C>T	c.(796-798)TCC>TTC	p.S266F
Pat_76	Post-Resistance	RBBP6	5930	37	16	24578597	24578597	Missense_Mutation	SNP	C	T	37	94	c.1723C>T	c.(1723-1725)CCT>TCT	p.P575S
Pat_76	Post-Resistance	XPO6	23214	37	16	28167780	28167780	Missense_Mutation	SNP	G	A	30	57	c.712C>T	c.(712-714)CTT>TTT	p.L238F
Pat_76	Post-Resistance	LAT	27040	37	16	28997467	28997467	Missense_Mutation	SNP	C	T	70	171	c.175C>T	c.(175-177)CCC>TCC	p.P59S
Pat_76	Post-Resistance	KIF22	3835	37	16	29810772	29810772	Missense_Mutation	SNP	C	T	22	47	c.947C>T	c.(946-948)CCT>CTT	p.P316L
Pat_76	Post-Resistance	ITGAL	3683	37	16	30500437	30500438	Missense_Mutation	DNP	GG	AA	27	65	.1041_1042GG>A	039-1044)ATGGAG>ATAA	.347_348ME>I
Pat_76	Post-Resistance	STX1B	112755	37	16	31004706	31004706	Missense_Mutation	SNP	C	T	13	31	c.637G>A	c.(637-639)GAT>AAT	p.D213N
Pat_76	Post-Resistance	STX4	6810	37	16	31046302	31046302	Nonsense_Mutation	SNP	C	T	19	65	c.319C>T	c.(319-321)CAG>TAG	p.Q107*

Pat_76	Post-Resistance	ZNF668	79759	37	16	31072586	31072586	Missense_Mutation	SNP	C	T	11	34	c.1663G>A	c.(1663-1665)GAC>AAC	p.D555N
Pat_76	Post-Resistance	PRSS36	146547	37	16	31150517	31150517	Missense_Mutation	SNP	G	A	8	19	c.2510C>T	c.(2509-2511)TCG>TTG	p.S837L
Pat_76	Post-Resistance	FUS	2521	37	16	31202331	31202331	Nonsense_Mutation	SNP	C	T	14	25	c.1441C>T	c.(1441-1443)CGA>TGA	p.R481*
Pat_76	Post-Resistance	ITGAX	3687	37	16	31374263	31374263	Missense_Mutation	SNP	C	T	9	42	c.1367C>T	c.(1366-1368)TCC>TTC	p.S456F
Pat_76	Post-Resistance	ITGAX	3687	37	16	31383723	31383723	Missense_Mutation	SNP	C	T	11	49	c.2185C>T	c.(2185-2187)CCC>TCC	p.P729S
Pat_76	Post-Resistance	ABCC12	94160	37	16	48138242	48138242	Missense_Mutation	SNP	G	A	21	65	c.2711C>T	c.(2710-2712)CCC>CTC	p.P904L
Pat_76	Post-Resistance	HEATR3	55027	37	16	50112773	50112773	Missense_Mutation	SNP	G	A	11	13	c.885G>A	c.(883-885)ATG>ATA	p.M295I
Pat_76	Post-Resistance	CES1	1066	37	16	55857576	55857576	Missense_Mutation	SNP	C	T	11	52	c.422G>A	c.(421-423)GGA>GAA	p.G141E
Pat_76	Post-Resistance	CES1	1066	37	16	55862715	55862715	Nonsense_Mutation	SNP	C	T	12	52	c.221G>A	c.(220-222)TGG>TAG	p.W74*
Pat_76	Post-Resistance	BBS2	583	37	16	56531684	56531684	Missense_Mutation	SNP	A	T	17	46	c.1768T>A	c.(1768-1770)TTT>ATT	p.F590I
Pat_76	Post-Resistance	CPNE2	221184	37	16	57153117	57153117	Missense_Mutation	SNP	G	A	21	48	c.518G>A	c.(517-519)GGG>GAG	p.G173E
Pat_76	Post-Resistance	CSNK2A2	1459	37	16	58199576	58199576	Missense_Mutation	SNP	A	C	6	13	c.864T>G	c.(862-864)AGT>AGG	p.S288R
Pat_76	Post-Resistance	CDH5	1003	37	16	66413316	66413316	Missense_Mutation	SNP	G	A	16	39	c.76G>A	c.(76-78)GCA>ACA	p.A26T
Pat_76	Post-Resistance	CA7	766	37	16	66885408	66885408	Missense_Mutation	SNP	G	A	40	90	c.400G>A	c.(400-402)GGG>AGG	p.G134R
Pat_76	Post-Resistance	ZDHHC1	29800	37	16	67432155	67432155	Missense_Mutation	SNP	C	T	25	125	c.887G>A	c.(886-888)AGG>AAG	p.R296K
Pat_76	Post-Resistance	HSD11B2	3291	37	16	67470217	67470217	Missense_Mutation	SNP	G	A	67	147	c.730G>A	c.(730-732)GAC>AAC	p.D244N
Pat_76	Post-Resistance	DPEP3	64180	37	16	68014081	68014081	Missense_Mutation	SNP	C	T	7	17	c.278G>A	c.(277-279)GGC>GAC	p.G93D
Pat_76	Post-Resistance	HYDIN	54768	37	16	70871640	70871640	Missense_Mutation	SNP	G	A	6	31	c.13192C>T	c.(13192-13194)CTC>TTC	p.L4398F
Pat_76	Post-Resistance	HYDIN	54768	37	16	71218881	71218881	Missense_Mutation	SNP	C	T	4	12	c.148G>A	c.(148-150)GAG>AAG	p.E50K
Pat_76	Post-Resistance	ADAMTS18	170692	37	16	77353954	77353954	Missense_Mutation	SNP	C	T	6	17	c.2324G>A	c.(2323-2325)CGA>CAA	p.R775Q
Pat_76	Post-Resistance	VAT1L	57687	37	16	77918574	77918574	Missense_Mutation	SNP	C	T	7	9	c.952C>T	c.(952-954)CTT>TTT	p.L318F
Pat_76	Post-Resistance	BCMO1	53630	37	16	81295883	81295883	Missense_Mutation	SNP	G	A	15	24	c.466G>A	c.(466-468)GAG>AAG	p.E156K
Pat_76	Post-Resistance	PLCG2	5336	37	16	81965224	81965224	Missense_Mutation	SNP	A	T	24	47	c.2704A>T	c.(2704-2706)AGC>TGC	p.S902C
Pat_76	Post-Resistance	MBTPS1	8720	37	16	84088064	84088064	Missense_Mutation	SNP	G	A	4	9	c.3149C>T	c.(3148-3150)CCT>CTT	p.P1050L
Pat_76	Post-Resistance	MBTPS1	8720	37	16	84127376	84127376	Missense_Mutation	SNP	G	A	12	26	c.676C>T	c.(676-678)CCC>TCC	p.P226S
Pat_76	Post-Resistance	ADAD2	161931	37	16	84229876	84229876	Missense_Mutation	SNP	G	A	16	36	c.1426G>A	c.(1426-1428)GAA>AAA	p.E476K
Pat_76	Post-Resistance	ATP2C2	9914	37	16	84456002	84456002	Missense_Mutation	SNP	G	A	20	30	c.631G>A	c.(631-633)GAC>AAC	p.D211N
Pat_76	Post-Resistance	KIAA0182	23199	37	16	85688001	85688001	Missense_Mutation	SNP	C	T	49	108	c.544C>T	c.(544-546)CCC>TCC	p.P182S
Pat_76	Post-Resistance	NXN	64359	37	17	722732	722733	Missense_Mutation	DNP	GG	AA	18	66	c.766_767CC>TT	c.(766-768)CCC>TTC	p.P256F
Pat_76	Post-Resistance	OR1E1	8387	37	17	3300846	3300846	Missense_Mutation	SNP	G	A	20	88	c.859C>T	c.(859-861)CCC>TCC	p.P287S
Pat_76	Post-Resistance	RABEP1	9135	37	17	5281522	5281522	Missense_Mutation	SNP	G	A	6	20	c.2266G>A	c.(2266-2268)GGA>AGA	p.G756R
Pat_76	Post-Resistance	ALOX12	239	37	17	6909842	6909842	Missense_Mutation	SNP	G	A	13	39	c.1456G>A	c.(1456-1458)GAT>AAT	p.D486N
Pat_76	Post-Resistance	NEURL4	84461	37	17	7227274	7227274	Missense_Mutation	SNP	G	A	7	18	c.2120C>T	c.(2119-2121)TCT>TTT	p.S707F
Pat_76	Post-Resistance	C17orf74	201243	37	17	7329674	7329674	Missense_Mutation	SNP	C	T	34	77	c.364C>T	c.(364-366)CGC>TGC	p.R122C
Pat_76	Post-Resistance	PFAS	5198	37	17	8172012	8172012	Missense_Mutation	SNP	G	A	6	17	c.3544G>A	c.(3544-3546)GGC>AGC	p.G1182S
Pat_76	Post-Resistance	MYH13	8735	37	17	10248630	10248630	Missense_Mutation	SNP	G	T	36	133	c.1473C>A	c.(1471-1473)TTC>TTA	p.F491L
Pat_76	Post-Resistance	MYH13	8735	37	17	10265482	10265482	Missense_Mutation	SNP	G	A	19	124	c.458C>T	c.(457-459)CCC>CTC	p.P153L
Pat_76	Post-Resistance	MYH1	4619	37	17	10398328	10398328	Missense_Mutation	SNP	C	T	29	48	c.5386G>A	c.(5386-5388)GAC>AAC	p.D1796N
Pat_76	Post-Resistance	MYH2	4620	37	17	10432559	10432559	Missense_Mutation	SNP	C	T	6	19	c.3274G>A	c.(3274-3276)GAA>AAA	p.E1092K
Pat_76	Post-Resistance	MYH3	4621	37	17	10543521	10543521	Missense_Mutation	SNP	A	G	3	40	c.2474T>C	c.(2473-2475)GTC>GCC	p.V825A
Pat_76	Post-Resistance	DNAH9	1770	37	17	11572873	11572873	Missense_Mutation	SNP	G	A	6	35	c.3115G>A	c.(3115-3117)GAA>AAA	p.E1039K
Pat_76	Post-Resistance	DNAH9	1770	37	17	11593270	11593270	Missense_Mutation	SNP	G	C	5	10	c.4131G>C	c.(4129-4131)CAG>CAC	p.Q1377H
Pat_76	Post-Resistance	TRIM16	10626	37	17	15535907	15535907	Missense_Mutation	SNP	G	A	16	40	c.931C>T	c.(931-933)CGC>TGC	p.R311C
Pat_76	Post-Resistance	MYO15A	51168	37	17	18082167	18082167	Missense_Mutation	SNP	G	A	26	39	c.10576G>A	c.(10576-10578)GAG>AAG	p.E3526K
Pat_76	Post-Resistance	FAM83G	644815	37	17	18907240	18907240	Missense_Mutation	SNP	C	T	12	17	c.115G>A	c.(115-117)GTG>ATG	p.V39M
Pat_76	Post-Resistance	RNF112	7732	37	17	19318195	19318195	Missense_Mutation	SNP	C	T	15	27	c.1121C>T	c.(1120-1122)CCT>CTT	p.P374L
Pat_76	Post-Resistance	LGALS9B	284194	37	17	20363726	20363726	Missense_Mutation	SNP	C	T	23	56	c.70G>A	c.(70-72)GGT>AGT	p.G24S

Pat_76	Post-Resistance	SUPT6H	6830	37	17	27002156	27002156	Missense_Mutation	SNP	G	A	4	17	c.514G>A	c.(514-516)GAG>AAG	p.E172K
Pat_76	Post-Resistance	HNF1B	6928	37	17	36104814	36104814	Missense_Mutation	SNP	A	G	8	43	c.62T>C	c.(61-63)GTC>GCC	p.V21A
Pat_76	Post-Resistance	THRA	7067	37	17	38244573	38244573	Missense_Mutation	SNP	G	A	29	26	c.802G>A	c.(802-804)GAC>AAC	p.D268N
Pat_76	Post-Resistance	KRT39	390792	37	17	39122844	39122844	Missense_Mutation	SNP	C	T	67	35	c.265G>A	c.(265-267)GGT>AGT	p.G89S
Pat_76	Post-Resistance	KRTAP4-4	84616	37	17	39316620	39316621	Missense_Mutation	DNP	GG	AT	74	38	c.323_324CC>AT	c.(322-324)CCC>CAT	p.P108H
Pat_76	Post-Resistance	KRT14	3861	37	17	39741234	39741234	Missense_Mutation	SNP	G	A	51	93	c.601C>T	c.(601-603)CGC>TGC	p.R201C
Pat_76	Post-Resistance	WNK4	65266	37	17	40946862	40946862	Missense_Mutation	SNP	G	A	19	18	c.2423G>A	c.(2422-2424)GGA>GAA	p.G808E
Pat_76	Post-Resistance	AOC2	314	37	17	41002225	41002225	Missense_Mutation	SNP	C	T	39	120	c.2131C>T	c.(2131-2133)CCC>TCC	p.P711S
Pat_76	Post-Resistance	PLEKHM1	9842	37	17	43531155	43531155	Missense_Mutation	SNP	G	A	33	20	c.2063C>T	c.(2062-2064)TCC>TTC	p.S688F
Pat_76	Post-Resistance	GOSR2	9570	37	17	45009497	45009497	Missense_Mutation	SNP	C	T	46	112	c.268C>T	c.(268-270)CGG>TGG	p.R90W
Pat_76	Post-Resistance	CACNA1G	8913	37	17	48673939	48673939	Missense_Mutation	SNP	C	T	42	21	c.2996C>T	c.(2995-2997)TCC>TTC	p.S999F
Pat_76	Post-Resistance	ABCC3	8714	37	17	48762122	48762122	Missense_Mutation	SNP	G	A	59	37	c.4166G>A	c.(4165-4167)AGC>AAC	p.S1389N
Pat_76	Post-Resistance	EFCAB3	146779	37	17	60493646	60493646	Missense_Mutation	SNP	G	A	30	17	c.1273G>A	c.(1273-1275)GGA>AGA	p.G425R
Pat_76	Post-Resistance	10-Mar	162333	37	17	60814149	60814149	Missense_Mutation	SNP	C	T	41	23	c.1080G>A	c.(1078-1080)ATG>ATA	p.M360I
Pat_76	Post-Resistance	NOL11	25926	37	17	65734057	65734057	Missense_Mutation	SNP	G	A	21	15	c.1498G>A	c.(1498-1500)GTC>ATC	p.V500I
Pat_76	Post-Resistance	ABCA9	10350	37	17	67008196	67008196	Missense_Mutation	SNP	C	T	28	18	c.3068G>A	c.(3067-3069)CGA>CAA	p.R1023Q
Pat_76	Post-Resistance	ABCA9	10350	37	17	67014656	67014656	Nonsense_Mutation	SNP	G	A	110	67	c.2665C>T	c.(2665-2667)CAG>TAG	p.Q889*
Pat_76	Post-Resistance	ABCA9	10350	37	17	67047281	67047281	Splice_Site	SNP	C	T	4	6	c.-12_splice	c.e2-1	
Pat_76	Post-Resistance	C17orf80	55028	37	17	71232451	71232451	Missense_Mutation	SNP	C	T	12	5	c.830C>T	c.(829-831)TCC>TTC	p.S277F
Pat_76	Post-Resistance	GPRC5C	55890	37	17	72436177	72436177	Missense_Mutation	SNP	G	A	15	7	c.262G>A	c.(262-264)GGG>AGG	p.G88R
Pat_76	Post-Resistance	SLC38A10	124565	37	17	79226403	79226403	Missense_Mutation	SNP	C	T	23	16	c.1537G>A	c.(1537-1539)GAC>AAC	p.D513N
Pat_76	Post-Resistance	LRRC45	201255	37	17	79983359	79983360	Missense_Mutation	DNP	CC	TT	27	11	c.637_638CC>TT	c.(637-639)CCT>TTT	p.P213F
Pat_76	Post-Resistance	COLEC12	81035	37	18	335059	335059	Missense_Mutation	SNP	C	T	4	6	c.1499G>A	c.(1498-1500)GGA>GAA	p.G500E
Pat_76	Post-Resistance	LPIN2	9663	37	18	2960660	2960660	Missense_Mutation	SNP	G	A	24	37	c.179C>T	c.(178-180)TCC>TTC	p.S60F
Pat_76	Post-Resistance	ZFP161	7541	37	18	5291174	5291174	Missense_Mutation	SNP	C	T	12	22	c.1033G>A	c.(1033-1035)GCC>ACC	p.A345T
Pat_76	Post-Resistance	TMEM200C	645369	37	18	5890387	5890387	Missense_Mutation	SNP	C	T	12	16	c.1676G>A	c.(1675-1677)CGA>CAA	p.R559Q
Pat_76	Post-Resistance	TXNDC2	84203	37	18	9887689	9887689	Missense_Mutation	SNP	C	T	23	59	c.1213C>T	c.(1213-1215)CCC>TCC	p.P405S
Pat_76	Post-Resistance	ZNF519	162655	37	18	14106150	14106150	Missense_Mutation	SNP	A	C	4	11	c.389T>G	c.(388-390)TTT>TGT	p.F130C
Pat_76	Post-Resistance	ANKRD30B	374860	37	18	14851568	14851568	Missense_Mutation	SNP	G	A	4	9	c.3268G>A	c.(3268-3270)GAA>AAA	p.E1090K
Pat_76	Post-Resistance	LAMA3	3909	37	18	21494505	21494505	Missense_Mutation	SNP	G	A	12	18	c.7461G>A	c.(7459-7461)ATG>ATA	p.M2487I
Pat_76	Post-Resistance	ZNF521	25925	37	18	22669428	22669428	Splice_Site	SNP	C	G	6	12	c.3906_splice	c.e7+1	p.Q1302_splice
Pat_76	Post-Resistance	SS18	6760	37	18	23619273	23619273	Missense_Mutation	SNP	G	A	25	58	c.755C>T	c.(754-756)CCC>CTC	p.P252L
Pat_76	Post-Resistance	AQP4	361	37	18	24436207	24436207	Missense_Mutation	SNP	C	T	21	73	c.940G>A	c.(940-942)GAC>AAC	p.D314N
Pat_76	Post-Resistance	CDH2	1000	37	18	25565092	25565092	Missense_Mutation	SNP	G	A	11	23	c.2081C>T	c.(2080-2082)TCC>TTC	p.S694F
Pat_76	Post-Resistance	DSC1	1823	37	18	28719770	28719770	Missense_Mutation	SNP	C	T	3	5	c.1604G>A	c.(1603-1605)AGA>AAA	p.R535K
Pat_76	Post-Resistance	ZNF24	7572	37	18	32919934	32919934	Missense_Mutation	SNP	G	A	6	19	c.427C>T	c.(427-429)CTC>TTC	p.L143F
Pat_76	Post-Resistance	SETBP1	26040	37	18	42529852	42529852	Missense_Mutation	SNP	G	A	4	21	c.547G>A	c.(547-549)GAG>AAG	p.E183K
Pat_76	Post-Resistance	ZBTB7C	201501	37	18	45566863	45566864	Missense_Mutation	DNP	CC	TT	9	24	c.615_616GG>AA	613-618)AGGGAC>AGAA	p.D206N
Pat_76	Post-Resistance	MAPK4	5596	37	18	48190519	48190519	Missense_Mutation	SNP	G	A	11	24	c.191G>A	c.(190-192)CGA>CAA	p.R64Q
Pat_76	Post-Resistance	DCC	1630	37	18	50936948	50936948	Missense_Mutation	SNP	G	A	12	30	c.3062G>A	c.(3061-3063)CGA>CAA	p.R1021Q
Pat_76	Post-Resistance	ATP8B1	5205	37	18	55335733	55335733	Missense_Mutation	SNP	C	T	11	11	c.2137G>A	c.(2137-2139)GGA>AGA	p.G713R
Pat_76	Post-Resistance	TNFRSF11A	8792	37	18	60015422	60015422	Missense_Mutation	SNP	C	T	24	52	c.97C>T	c.(97-99)CCA>TCA	p.P33S
Pat_76	Post-Resistance	SERPINB4	6318	37	18	61324207	61324207	Missense_Mutation	SNP	G	A	3	13	c.626C>T	c.(625-627)TCC>TTC	p.S209F
Pat_76	Post-Resistance	SERPINB2	5055	37	18	61569055	61569055	Missense_Mutation	SNP	G	A	15	14	c.617G>A	c.(616-618)GGA>GAA	p.G206E
Pat_76	Post-Resistance	CDH7	1005	37	18	63547911	63547911	Missense_Mutation	SNP	A	T	8	26	c.2139A>T	c.(2137-2139)GAA>GAT	p.E713D
Pat_76	Post-Resistance	CD226	10666	37	18	67540447	67540447	Missense_Mutation	SNP	C	T	27	51	c.763G>A	c.(763-765)GGA>AGA	p.G255R
Pat_76	Post-Resistance	ADNP2	22850	37	18	77875472	77875472	Missense_Mutation	SNP	G	A	10	15	c.47G>A	c.(46-48)CGA>CAA	p.R16Q

Pat_76	Post-Resistance	DIRAS1	148252	37	19	2717729	2717729	Missense_Mutation	SNP	G	C	28	63	c.76C>G	c.(76-78)CGC>GGC	p.R26G
Pat_76	Post-Resistance	MAP2K2	5605	37	19	4110581	4110581	Missense_Mutation	SNP	T	C	7	60	c.376A>G	c.(376-378)AAC>GAC	p.N126D
Pat_76	Post-Resistance	ANKRD24	170961	37	19	4217073	4217073	Missense_Mutation	SNP	G	A	9	19	c.1916G>A	c.(1915-1917)GGG>GAG	p.G639E
Pat_76	Post-Resistance	CCDC94	55702	37	19	4249233	4249233	Nonsense_Mutation	SNP	C	A	5	20	c.33C>A	c.(31-33)TAC>TAA	p.Y11*
Pat_76	Post-Resistance	TMIGD2	126259	37	19	4298151	4298151	Missense_Mutation	SNP	C	T	10	20	c.238G>A	c.(238-240)GTC>ATC	p.V80I
Pat_76	Post-Resistance	CHAF1A	10036	37	19	4409220	4409221	Missense_Mutation	DNP	CC	TT	37	50	c.424_425CC>TT	c.(424-426)CCC>TTC	p.P142F
Pat_76	Post-Resistance	PTPRS	5802	37	19	5220119	5220119	Missense_Mutation	SNP	G	A	8	12	c.3596C>T	c.(3595-3597)TCG>TTG	p.S1199L
Pat_76	Post-Resistance	SAFB	6294	37	19	5667169	5667169	Missense_Mutation	SNP	C	T	4	7	c.2447C>T	c.(2446-2448)CCC>CTC	p.P816L
Pat_76	Post-Resistance	TNFSF14	8740	37	19	6665025	6665025	Missense_Mutation	SNP	C	T	30	43	c.635G>A	c.(634-636)GGG>GAG	p.G212E
Pat_76	Post-Resistance	VAV1	7409	37	19	6854037	6854038	Missense_Mutation	DNP	GG	AA	23	54	.2412_2413GG>A	410-2415)AAGGAG>AAA	p.E805K
Pat_76	Post-Resistance	EMR1	2015	37	19	6935005	6935005	Missense_Mutation	SNP	C	T	26	52	c.2297C>T	c.(2296-2298)TCC>TTC	p.S766F
Pat_76	Post-Resistance	ZNF557	79230	37	19	7083192	7083192	Missense_Mutation	SNP	A	T	23	44	c.709A>T	c.(709-711)ACC>TCC	p.T237S
Pat_76	Post-Resistance	LASS4	79603	37	19	8321133	8321133	Nonsense_Mutation	SNP	G	A	7	26	c.482G>A	c.(481-483)TGG>TAG	p.W161*
Pat_76	Post-Resistance	MYO1F	4542	37	19	8619449	8619449	Missense_Mutation	SNP	A	G	15	114	c.238T>C	c.(238-240)TAT>CAT	p.Y80H
Pat_76	Post-Resistance	MUC16	94025	37	19	8996484	8996484	Missense_Mutation	SNP	C	G	13	17	c.41088G>C	c.(41086-41088)AAG>AAC	p.K13696N
Pat_76	Post-Resistance	MUC16	94025	37	19	9020005	9020005	Missense_Mutation	SNP	C	T	62	139	c.37490G>A	c.(37489-37491)AGG>AAG	p.R12497K
Pat_76	Post-Resistance	MUC16	94025	37	19	9054252	9054252	Missense_Mutation	SNP	G	A	6	9	c.31370C>T	c.(31369-31371)TCG>TTG	p.S10457L
Pat_76	Post-Resistance	MUC16	94025	37	19	9058282	9058282	Missense_Mutation	SNP	C	T	6	7	c.29164G>A	c.(29164-29166)GAA>AAA	p.E9722K
Pat_76	Post-Resistance	MUC16	94025	37	19	9061096	9061096	Missense_Mutation	SNP	C	T	12	25	c.26350G>A	c.(26350-26352)GAA>AAA	p.E8784K
Pat_76	Post-Resistance	MUC16	94025	37	19	9064315	9064315	Missense_Mutation	SNP	G	A	16	49	c.23131C>T	c.(23131-23133)CCC>TCC	p.P7711S
Pat_76	Post-Resistance	MUC16	94025	37	19	9068557	9068557	Missense_Mutation	SNP	G	A	14	35	c.18889C>T	c.(18889-18891)CCT>TCT	p.P6297S
Pat_76	Post-Resistance	MUC16	94025	37	19	9076162	9076162	Missense_Mutation	SNP	C	T	15	36	c.11284G>A	c.(11284-11286)GAA>AAA	p.E3762K
Pat_76	Post-Resistance	MUC16	94025	37	19	9083768	9083768	Missense_Mutation	SNP	C	T	9	20	c.8047G>A	c.(8047-8049)GAG>AAG	p.E2683K
Pat_76	Post-Resistance	OR7G1	125962	37	19	9226282	9226282	Missense_Mutation	SNP	G	A	31	85	c.158C>T	c.(157-159)TCC>TTC	p.S53F
Pat_76	Post-Resistance	OR7D2	162998	37	19	9297226	9297226	Missense_Mutation	SNP	G	A	10	29	c.769G>A	c.(769-771)GGG>AGG	p.G257R
Pat_76	Post-Resistance	OR7E24	26648	37	19	9362051	9362051	Missense_Mutation	SNP	C	T	10	25	c.332C>T	c.(331-333)TCC>TTC	p.S111F
Pat_76	Post-Resistance	ZNF560	147741	37	19	9578557	9578557	Missense_Mutation	SNP	C	T	12	21	c.1066G>A	c.(1066-1068)GAT>AAT	p.D356N
Pat_76	Post-Resistance	ZNF560	147741	37	19	9580356	9580356	Missense_Mutation	SNP	G	A	16	48	c.479C>T	c.(478-480)TCT>TTT	p.S160F
Pat_76	Post-Resistance	LPPR2	64748	37	19	11472097	11472097	Missense_Mutation	SNP	C	G	8	22	c.596C>G	c.(595-597)GCC>GGC	p.A199G
Pat_76	Post-Resistance	ZNF442	79973	37	19	12462077	12462077	Missense_Mutation	SNP	C	T	12	22	c.322G>A	c.(322-324)GAA>AAA	p.E108K
Pat_76	Post-Resistance	DAND5	199699	37	19	13080638	13080638	Missense_Mutation	SNP	C	T	11	19	c.164C>T	c.(163-165)TCT>TTT	p.S55F
Pat_76	Post-Resistance	MRI1	84245	37	19	13876782	13876782	Missense_Mutation	SNP	C	T	6	77	c.386C>T	c.(385-387)ACC>ATC	p.T129I
Pat_76	Post-Resistance	CCDC105	126402	37	19	15131365	15131366	Nonsense_Mutation	DNP	GG	AT	5	12	c.768_769GG>AT	766-771)CTGGAG>CTAT	p.E257*
Pat_76	Post-Resistance	CYP4F3	4051	37	19	15752308	15752308	Missense_Mutation	SNP	C	T	21	37	c.83C>T	c.(82-84)TCC>TTC	p.S28F
Pat_76	Post-Resistance	CYP4F12	66002	37	19	15795640	15795641	Missense_Mutation	DNP	GG	AA	20	49	c.933_934GG>AA	931-936)AAGGCA>AAAA	p.A312T
Pat_76	Post-Resistance	OR10H2	26538	37	19	15838861	15838861	Missense_Mutation	SNP	G	A	57	75	c.8G>A	c.(7-9)GGG>GAG	p.G3E
Pat_76	Post-Resistance	CHERP	10523	37	19	16641445	16641445	Missense_Mutation	SNP	G	A	22	75	c.827C>T	c.(826-828)TCC>TTC	p.S276F
Pat_76	Post-Resistance	CPAMD8	27151	37	19	17056424	17056424	Missense_Mutation	SNP	C	T	18	52	c.2869G>A	c.(2869-2871)GAG>AAG	p.E957K
Pat_76	Post-Resistance	NXNL1	115861	37	19	17571671	17571671	Missense_Mutation	SNP	G	A	18	28	c.8C>T	c.(7-9)TCC>TTC	p.S3F
Pat_76	Post-Resistance	UNC13A	23025	37	19	17783267	17783267	Missense_Mutation	SNP	C	T	12	45	c.454G>A	c.(454-456)GTG>ATG	p.V152M
Pat_76	Post-Resistance	COMP	1311	37	19	18899298	18899298	Missense_Mutation	SNP	C	T	8	8	c.788G>A	c.(787-789)GGG>GAG	p.G263E
Pat_76	Post-Resistance	SFRS14	10147	37	19	19136391	19136391	Missense_Mutation	SNP	G	A	15	50	c.766C>T	c.(766-768)CCC>TCC	p.P256S
Pat_76	Post-Resistance	ZNF14	7561	37	19	19822792	19822792	Missense_Mutation	SNP	G	A	18	29	c.1298C>T	c.(1297-1299)TCC>TTC	p.S433F
Pat_76	Post-Resistance	ZNF682	91120	37	19	20116872	20116872	Missense_Mutation	SNP	G	A	7	15	c.1439C>T	c.(1438-1440)TCC>TTC	p.S480F
Pat_76	Post-Resistance	ZNF90	7643	37	19	20216075	20216075	Missense_Mutation	SNP	G	A	24	69	c.176G>A	c.(175-177)GGA>GAA	p.G59E
Pat_76	Post-Resistance	ZNF626	199777	37	19	20807233	20807233	Missense_Mutation	SNP	C	T	3	3	c.1450G>A	c.(1450-1452)GAA>AAA	p.E484K
Pat_76	Post-Resistance	ZNF626	199777	37	19	20807401	20807401	Missense_Mutation	SNP	C	T	17	64	c.1282G>A	c.(1282-1284)GAA>AAA	p.E428K

Pat_76	Post-Resistance	ZNF676	163223	37	19	22362756	22362756	Missense_Mutation	SNP	G	A	7	21	c.1763C>T	c.(1762-1764)CCC>CTC	p.P588L
Pat_76	Post-Resistance	ZNF99	7652	37	19	22940472	22940472	Missense_Mutation	SNP	T	G	8	28	c.1966A>C	c.(1966-1968)AAA>CAA	p.K656Q
Pat_76	Post-Resistance	ZNF536	9745	37	19	31040082	31040082	Missense_Mutation	SNP	G	A	21	58	c.3556G>A	c.(3556-3558)GAA>AAA	p.E1186K
Pat_76	Post-Resistance	NPHS1	4868	37	19	36321798	36321798	Missense_Mutation	SNP	C	T	9	47	c.3542G>A	c.(3541-3543)AGA>AAA	p.R1181K
Pat_76	Post-Resistance	ZNF793	390927	37	19	38028549	38028549	Missense_Mutation	SNP	G	A	3	21	c.989G>A	c.(988-990)CGA>CAA	p.R330Q
Pat_76	Post-Resistance	ZNF540	163255	37	19	38102515	38102515	Missense_Mutation	SNP	C	T	15	40	c.334C>T	c.(334-336)CGT>TGT	p.R112C
Pat_76	Post-Resistance	ZNF607	84775	37	19	38189410	38189410	Missense_Mutation	SNP	G	A	9	18	c.1622C>T	c.(1621-1623)TCT>TTT	p.S541F
Pat_76	Post-Resistance	RYR1	6261	37	19	38995971	38995971	Missense_Mutation	SNP	G	A	7	13	c.8333G>A	c.(8332-8334)GGA>GAA	p.G2778E
Pat_76	Post-Resistance	RYR1	6261	37	19	39018297	39018297	Missense_Mutation	SNP	C	T	3	7	c.10697C>T	c.(10696-10698)TCC>TTC	p.S3566F
Pat_76	Post-Resistance	RYR1	6261	37	19	39038941	39038941	Missense_Mutation	SNP	G	A	24	49	c.12163G>A	c.(12163-12165)GAG>AAG	p.E4055K
Pat_76	Post-Resistance	FCGBP	8857	37	19	40419983	40419983	Missense_Mutation	SNP	C	T	16	36	c.3011G>A	c.(3010-3012)GGG>GAG	p.G1004E
Pat_76	Post-Resistance	ADCK4	79934	37	19	41220263	41220263	Missense_Mutation	SNP	C	T	7	49	c.142G>A	c.(142-144)GAT>AAT	p.D48N
Pat_76	Post-Resistance	GRIK5	2901	37	19	42566913	42566913	Missense_Mutation	SNP	C	A	27	39	c.339G>T	c.(337-339)AAG>AAT	p.K113N
Pat_76	Post-Resistance	PSG3	5671	37	19	43237041	43237041	Missense_Mutation	SNP	G	A	44	117	c.604C>T	c.(604-606)CTC>TTC	p.L202F
Pat_76	Post-Resistance	PSG8	440533	37	19	43262276	43262276	Missense_Mutation	SNP	G	A	76	151	c.587C>T	c.(586-588)TCT>TTT	p.S196F
Pat_76	Post-Resistance	PSG1	5669	37	19	43373139	43373140	Missense_Mutation	DNP	CC	TT	29	107	c.756_757GG>AA	754-759)AGGGAG>AGAA	p.E253K
Pat_76	Post-Resistance	PSG1	5669	37	19	43382107	43382107	Missense_Mutation	SNP	C	T	75	163	c.388G>A	c.(388-390)GGG>AGG	p.G130R
Pat_76	Post-Resistance	PSG6	5675	37	19	43411960	43411961	Missense_Mutation	DNP	CC	GT	44	121	c.752_753GG>AC	c.(751-753)AGG>AAC	p.R251N
Pat_76	Post-Resistance	ZNF226	7769	37	19	44681760	44681760	Missense_Mutation	SNP	C	T	8	14	c.2345C>T	c.(2344-2346)TCC>TTC	p.S782F
Pat_76	Post-Resistance	ZNF285	26974	37	19	44891610	44891610	Missense_Mutation	SNP	C	T	11	36	c.797G>A	c.(796-798)GGA>GAA	p.G266E
Pat_76	Post-Resistance	ZNF285	26974	37	19	44891787	44891787	Missense_Mutation	SNP	G	A	7	24	c.620C>T	c.(619-621)CCC>CTC	p.P207L
Pat_76	Post-Resistance	CEACAM20	125931	37	19	45016954	45016954	Missense_Mutation	SNP	C	A	6	20	c.1485G>T	c.(1483-1485)AAG>AAT	p.K495N
Pat_76	Post-Resistance	PVRL2	5819	37	19	45389243	45389243	Missense_Mutation	SNP	G	A	24	55	c.1246G>A	c.(1246-1248)GAG>AAG	p.E416K
Pat_76	Post-Resistance	RELB	5971	37	19	45536001	45536001	Missense_Mutation	SNP	G	A	7	8	c.1201G>A	c.(1201-1203)GAC>AAC	p.D401N
Pat_76	Post-Resistance	SFRS16	11129	37	19	45556053	45556053	Missense_Mutation	SNP	C	T	22	67	c.202C>T	c.(202-204)CCC>TCC	p.P68S
Pat_76	Post-Resistance	IGFL2	147920	37	19	46664003	46664003	Missense_Mutation	SNP	C	T	63	164	c.206C>T	c.(205-207)CCC>CTC	p.P69L
Pat_76	Post-Resistance	PNMAL1	55228	37	19	46973649	46973649	Missense_Mutation	SNP	G	A	6	15	c.644C>T	c.(643-645)CCC>CTC	p.P215L
Pat_76	Post-Resistance	PTGIR	5739	37	19	47124731	47124731	Missense_Mutation	SNP	G	A	12	31	c.967C>T	c.(967-969)CTT>TTT	p.L323F
Pat_76	Post-Resistance	GRLF1	2909	37	19	47503857	47503857	Missense_Mutation	SNP	C	T	14	12	c.4412C>T	c.(4411-4413)CCG>CTG	p.P1471L
Pat_76	Post-Resistance	ZC3H4	23211	37	19	47588399	47588399	Missense_Mutation	SNP	G	A	37	75	c.1021C>T	c.(1021-1023)CGG>TGG	p.R341W
Pat_76	Post-Resistance	ELSPBP1	64100	37	19	48519260	48519260	Missense_Mutation	SNP	G	A	17	60	c.319G>A	c.(319-321)GAT>AAT	p.D107N
Pat_76	Post-Resistance	CABP5	56344	37	19	48537511	48537511	Missense_Mutation	SNP	C	T	8	30	c.457G>A	c.(457-459)GAG>AAG	p.E153K
Pat_76	Post-Resistance	GRIN2D	2906	37	19	48922977	48922977	Missense_Mutation	SNP	C	T	51	140	c.1997C>T	c.(1996-1998)GCC>GTC	p.A666V
Pat_76	Post-Resistance	SULT2B1	6820	37	19	49079332	49079333	Missense_Mutation	DNP	CC	TT	24	98	c.206_207CC>TT	c.(205-207)CCC>CTT	p.P69L
Pat_76	Post-Resistance	CGB2	114336	37	19	49536425	49536425	Missense_Mutation	SNP	C	T	20	35	c.439C>T	c.(439-441)CCA>TCA	p.P147S
Pat_76	Post-Resistance	SLC6A16	28968	37	19	49813080	49813080	Missense_Mutation	SNP	G	A	6	18	c.704C>T	c.(703-705)CCT>CTT	p.P235L
Pat_76	Post-Resistance	TBC1D17	79735	37	19	50385521	50385521	Missense_Mutation	SNP	C	T	19	62	c.662C>T	c.(661-663)TCC>TTC	p.S221F
Pat_76	Post-Resistance	IL4I1	259307	37	19	50399286	50399286	Missense_Mutation	SNP	G	A	12	23	c.38C>T	c.(37-39)CCC>CTC	p.P13L
Pat_76	Post-Resistance	ZNF473	25888	37	19	50549595	50549595	Missense_Mutation	SNP	C	T	11	22	c.1895C>T	c.(1894-1896)TCC>TTC	p.S632F
Pat_76	Post-Resistance	C19orf41	126123	37	19	50655885	50655885	Missense_Mutation	SNP	C	T	39	101	c.647G>A	c.(646-648)CGA>CAA	p.R216Q
Pat_76	Post-Resistance	C19orf41	126123	37	19	50666268	50666268	Missense_Mutation	SNP	C	T	9	41	c.184G>A	c.(184-186)GGG>AGG	p.G62R
Pat_76	Post-Resistance	MYH14	79784	37	19	50753023	50753023	Missense_Mutation	SNP	G	C	35	97	c.1575G>C	c.(1573-1575)TGG>TGC	p.W525C
Pat_76	Post-Resistance	MYH14	79784	37	19	50779268	50779268	Missense_Mutation	SNP	C	T	5	10	c.3365C>T	c.(3364-3366)GCC>GTC	p.A1122V
Pat_76	Post-Resistance	SPIB	6689	37	19	50923210	50923210	Missense_Mutation	SNP	G	C	9	13	c.31G>C	c.(31-33)GGG>CGG	p.G11R
Pat_76	Post-Resistance	KLK15	55554	37	19	51330397	51330397	Missense_Mutation	SNP	C	T	21	56	c.218G>A	c.(217-219)GGA>GAA	p.G73E
Pat_76	Post-Resistance	FPR1	2357	37	19	52249742	52249742	Missense_Mutation	SNP	C	T	18	30	c.506G>A	c.(505-507)GGT>GAT	p.G169D
Pat_76	Post-Resistance	ZNF613	79898	37	19	52448416	52448416	Missense_Mutation	SNP	C	T	8	42	c.1280C>T	c.(1279-1281)CCC>CTC	p.P427L

Pat_76	Post-Resistance	ZNF701	55762	37	19	53085781	53085781	Missense_Mutation	SNP	G	A	22	70	c.469G>A	c.(469-471)GAA>AAA	p.E157K
Pat_76	Post-Resistance	ZNF347	84671	37	19	53644928	53644928	Missense_Mutation	SNP	G	A	20	58	c.1153C>T	c.(1153-1155)CGT>TGT	p.R385C
Pat_76	Post-Resistance	CACNG6	59285	37	19	54503025	54503025	Missense_Mutation	SNP	G	T	6	22	c.544G>T	c.(544-546)GGC>TGC	p.G182C
Pat_76	Post-Resistance	LILRB2	10288	37	19	54783794	54783794	Nonsense_Mutation	SNP	C	T	35	80	c.207G>A	c.(205-207)TGG>TGA	p.W69*
Pat_76	Post-Resistance	LILRA1	11024	37	19	55107653	55107653	Splice_Site	SNP	G	A	8	37	c.959_splice	c.e7-1	p.G320_splice
Pat_76	Post-Resistance	LILRB1	10859	37	19	55148297	55148297	Missense_Mutation	SNP	C	T	23	42	c.1921C>T	c.(1921-1923)CCC>TCC	p.P641S
Pat_76	Post-Resistance	NLRP7	199713	37	19	55450725	55450726	Missense_Mutation	DNP	CC	TT	9	33	.1461_1462GG>A	459-1464)GGGGAG>GGA	p.E488K
Pat_76	Post-Resistance	SYT5	6861	37	19	55689725	55689725	Missense_Mutation	SNP	C	T	7	13	c.91G>A	c.(91-93)GCC>ACC	p.A31T
Pat_76	Post-Resistance	PTPRH	5794	37	19	55716882	55716882	Missense_Mutation	SNP	C	T	18	40	c.431G>A	c.(430-432)GGC>GAC	p.G144D
Pat_76	Post-Resistance	NLRP9	338321	37	19	56244864	56244864	Nonsense_Mutation	SNP	C	T	12	17	c.333G>A	c.(331-333)TGG>TGA	p.W111*
Pat_76	Post-Resistance	NLRP5	126206	37	19	56530714	56530714	Missense_Mutation	SNP	C	T	4	17	c.572C>T	c.(571-573)TCA>TTA	p.S191L
Pat_76	Post-Resistance	PEG3	5178	37	19	57325941	57325941	Missense_Mutation	SNP	G	A	12	20	c.3869C>T	c.(3868-3870)TCT>TTT	p.S1290F
Pat_76	Post-Resistance	ZNF543	125919	37	19	57840542	57840542	Missense_Mutation	SNP	C	T	12	36	c.1712C>T	c.(1711-1713)CCT>CTT	p.P571L
Pat_76	Post-Resistance	ZNF304	57343	37	19	57868658	57868658	Missense_Mutation	SNP	C	T	27	126	c.1421C>T	c.(1420-1422)CCT>CTT	p.P474L
Pat_76	Post-Resistance	ZSCAN4	201516	37	19	58187859	58187859	Missense_Mutation	SNP	G	A	9	22	c.346G>A	c.(346-348)GAG>AAG	p.E116K
Pat_76	Post-Resistance	ZSCAN4	201516	37	19	58190127	58190127	Missense_Mutation	SNP	C	T	33	67	c.1156C>T	c.(1156-1158)CAT>TAT	p.H386Y
Pat_76	Post-Resistance	RPS5	6193	37	19	58904521	58904521	Missense_Mutation	SNP	C	T	23	47	c.287C>T	c.(286-288)GCC>GTC	p.A96V
Pat_76	Post-Resistance	TSSC1	7260	37	2	3341881	3341881	Missense_Mutation	SNP	T	G	3	13	c.166A>C	c.(166-168)AAT>CAT	p.N56H
Pat_76	Post-Resistance	RSAD2	91543	37	2	7035946	7035946	Missense_Mutation	SNP	C	T	6	16	c.959C>T	c.(958-960)CCT>CTT	p.P320L
Pat_76	Post-Resistance	GRHL1	29841	37	2	10104169	10104169	Nonsense_Mutation	SNP	C	T	13	35	c.901C>T	c.(901-903)CGA>TGA	p.R301*
Pat_76	Post-Resistance	RRM2	6241	37	2	10269026	10269026	Missense_Mutation	SNP	C	T	7	29	c.850C>T	c.(850-852)CCA>TCA	p.P284S
Pat_76	Post-Resistance	ATP6V1C2	245973	37	2	10914963	10914963	Nonsense_Mutation	SNP	C	T	23	58	c.688C>T	c.(688-690)CGA>TGA	p.R230*
Pat_76	Post-Resistance	PUM2	23369	37	2	20460196	20460196	Missense_Mutation	SNP	G	A	7	26	c.2257C>T	c.(2257-2259)CCA>TCA	p.P753S
Pat_76	Post-Resistance	APOB	338	37	2	21231860	21231860	Missense_Mutation	SNP	G	A	7	15	c.7880C>T	c.(7879-7881)CCA>CTA	p.P2627L
Pat_76	Post-Resistance	APOB	338	37	2	21235356	21235356	Missense_Mutation	SNP	C	T	12	23	c.4384G>A	c.(4384-4386)GGA>AGA	p.G1462R
Pat_76	Post-Resistance	DPYSL5	56896	37	2	27167566	27167566	Missense_Mutation	SNP	G	A	19	40	c.1483G>A	c.(1483-1485)GAT>AAT	p.D495N
Pat_76	Post-Resistance	ZNF513	130557	37	2	27601169	27601169	Missense_Mutation	SNP	C	T	8	48	c.869G>A	c.(868-870)GGG>GAG	p.G290E
Pat_76	Post-Resistance	PLB1	151056	37	2	28812377	28812377	Missense_Mutation	SNP	G	C	22	47	c.1876G>C	c.(1876-1878)GTT>CTT	p.V626L
Pat_76	Post-Resistance	FAM179A	165186	37	2	29247101	29247101	Missense_Mutation	SNP	G	A	5	11	c.1714G>A	c.(1714-1716)GAG>AAG	p.E572K
Pat_76	Post-Resistance	ALK	238	37	2	29543713	29543713	Missense_Mutation	SNP	C	T	21	44	c.1450G>A	c.(1450-1452)GAT>AAT	p.D484N
Pat_76	Post-Resistance	XDH	7498	37	2	31558835	31558835	Missense_Mutation	SNP	C	A	14	32	c.3991G>T	c.(3991-3993)GTG>TTG	p.V1331L
Pat_76	Post-Resistance	FAM98A	25940	37	2	33810710	33810710	Missense_Mutation	SNP	G	A	7	38	c.775C>T	c.(775-777)CCT>TCT	p.P259S
Pat_76	Post-Resistance	MAP4K3	8491	37	2	39487761	39487761	Nonsense_Mutation	SNP	C	T	3	14	c.2294G>A	c.(2293-2295)TGG>TAG	p.W765*
Pat_76	Post-Resistance	SLC8A1	6546	37	2	40405536	40405536	Missense_Mutation	SNP	C	T	30	59	c.1906G>A	c.(1906-1908)GAG>AAG	p.E636K
Pat_76	Post-Resistance	LOC728819	728819	37	2	43903146	43903146	Missense_Mutation	SNP	C	T	5	26	c.316G>A	c.(316-318)GAT>AAT	p.D106N
Pat_76	Post-Resistance	ABCG8	64241	37	2	44078738	44078738	Missense_Mutation	SNP	C	T	14	27	c.338C>T	c.(337-339)TCC>TTC	p.S113F
Pat_76	Post-Resistance	PREPL	9581	37	2	44559788	44559789	Missense_Mutation	DNP	GG	AA	4	11	.1162_1163CC>T	c.(1162-1164)CCT>TTT	p.P388F
Pat_76	Post-Resistance	FOXN2	3344	37	2	48573793	48573793	Missense_Mutation	SNP	C	T	14	27	c.440C>T	c.(439-441)CCA>CTA	p.P147L
Pat_76	Post-Resistance	PSME4	23198	37	2	54131220	54131220	Missense_Mutation	SNP	G	A	5	33	c.3017C>T	c.(3016-3018)CCC>CTC	p.P1006L
Pat_76	Post-Resistance	C2orf63	130162	37	2	55445106	55445106	Missense_Mutation	SNP	G	A	6	10	c.206C>T	c.(205-207)TCC>TTC	p.S69F
Pat_76	Post-Resistance	EFEMP1	2202	37	2	56094269	56094269	Missense_Mutation	SNP	C	T	22	20	c.1421G>A	c.(1420-1422)GGG>GAG	p.G474E
Pat_76	Post-Resistance	CCDC85A	114800	37	2	56611435	56611435	Missense_Mutation	SNP	C	T	8	22	c.1607C>T	c.(1606-1608)TCG>TTG	p.S536L
Pat_76	Post-Resistance	PLEK	5341	37	2	68607955	68607955	Missense_Mutation	SNP	T	A	32	56	c.299T>A	c.(298-300)ATT>AAT	p.I100N
Pat_76	Post-Resistance	FBXO48	554251	37	2	68691389	68691389	Missense_Mutation	SNP	C	T	42	89	c.420G>A	c.(418-420)ATG>ATA	p.M140I
Pat_76	Post-Resistance	GFPT1	2673	37	2	69597165	69597165	Missense_Mutation	SNP	C	T	3	12	c.191G>A	c.(190-192)GGA>GAA	p.G64E
Pat_76	Post-Resistance	C2orf42	54980	37	2	70377634	70377634	Missense_Mutation	SNP	G	A	8	30	c.1579C>T	c.(1579-1581)CTT>TTT	p.L527F
Pat_76	Post-Resistance	PCYOX1	51449	37	2	70502156	70502156	Missense_Mutation	SNP	G	A	14	38	c.560G>A	c.(559-561)GGA>GAA	p.G187E

Pat_76	Post-Resistance	ATP6V1B1	525	37	2	71191923	71191923	Missense_Mutation	SNP	G	A	8	23	c.1306G>A	c.(1306-1308)GAG>AAG	p.E436K
Pat_76	Post-Resistance	C2orf78	388960	37	2	74043815	74043815	Missense_Mutation	SNP	C	T	3	23	c.2465C>T	c.(2464-2466)TCT>TTT	p.S822F
Pat_76	Post-Resistance	DOK1	1796	37	2	74782764	74782765	Missense_Mutation	DNP	GG	AC	9	14	c.423_424GG>AC	421-426)CTGGAG>CTAC	p.E142Q
Pat_76	Post-Resistance	DOK1	1796	37	2	74783648	74783648	Missense_Mutation	SNP	C	T	11	39	c.853C>T	c.(853-855)CCC>TCC	p.P285S
Pat_76	Post-Resistance	HK2	3099	37	2	75108931	75108931	Missense_Mutation	SNP	T	G	16	27	c.1664T>G	c.(1663-1665)ATG>AGG	p.M555R
Pat_76	Post-Resistance	CTNNA2	1496	37	2	80808840	80808840	Missense_Mutation	SNP	G	A	6	22	c.1903G>A	c.(1903-1905)GAA>AAA	p.E635K
Pat_76	Post-Resistance	THNSL2	55258	37	2	88484883	88484883	Missense_Mutation	SNP	G	A	20	34	c.1114G>A	c.(1114-1116)GAA>AAA	p.E372K
Pat_76	Post-Resistance	TMEM131	23505	37	2	98475846	98475846	Missense_Mutation	SNP	G	A	6	13	c.404C>T	c.(403-405)CCT>CTT	p.P135L
Pat_76	Post-Resistance	MRPL30	51263	37	2	99812220	99812220	Splice_Site	SNP	G	A	6	10	c.537_splice	c.e6+1	
Pat_76	Post-Resistance	LYG2	254773	37	2	99861748	99861748	Missense_Mutation	SNP	C	T	14	64	c.358G>A	c.(358-360)GGA>AGA	p.G120R
Pat_76	Post-Resistance	NPAS2	4862	37	2	101565879	101565879	Missense_Mutation	SNP	C	T	10	25	c.535C>T	c.(535-537)CCA>TCA	p.P179S
Pat_76	Post-Resistance	CREG2	200407	37	2	102000157	102000158	Missense_Mutation	DNP	CC	TT	5	49	c.448_449GG>AA	c.(448-450)GGA>AAA	p.G150K
Pat_76	Post-Resistance	IL18R1	8809	37	2	103013029	103013029	Missense_Mutation	SNP	C	G	7	20	c.1309C>G	c.(1309-1311)CGA>GGA	p.R437G
Pat_76	Post-Resistance	TGFBRAP1	9392	37	2	105912941	105912941	Missense_Mutation	SNP	C	T	4	29	c.910G>A	c.(910-912)GGA>AGA	p.G304R
Pat_76	Post-Resistance	RGPD3	653489	37	2	107049684	107049684	Missense_Mutation	SNP	C	T	42	132	c.2263G>A	c.(2263-2265)GAA>AAA	p.E755K
Pat_76	Post-Resistance	SULT1C3	442038	37	2	108881461	108881461	Missense_Mutation	SNP	G	A	24	31	c.802G>A	c.(802-804)GGG>AGG	p.G268R
Pat_76	Post-Resistance	RGPD5	84220	37	2	113147135	113147135	Nonsense_Mutation	SNP	C	T	27	166	c.3387G>A	c.(3385-3387)TGG>TGA	p.W1129*
Pat_76	Post-Resistance	POLR1B	84172	37	2	113322062	113322062	Missense_Mutation	SNP	C	T	15	33	c.1732C>T	c.(1732-1734)CTT>TTT	p.L578F
Pat_76	Post-Resistance	IL1F6	27179	37	2	113764178	113764178	Missense_Mutation	SNP	C	T	99	211	c.128C>T	c.(127-129)ACT>ATT	p.T43I
Pat_76	Post-Resistance	PSD4	23550	37	2	113953840	113953840	Missense_Mutation	SNP	G	A	17	14	c.2342G>A	c.(2341-2343)GGC>GAC	p.G781D
Pat_76	Post-Resistance	DPP10	57628	37	2	116066815	116066815	Missense_Mutation	SNP	G	A	5	7	c.61G>A	c.(61-63)GAA>AAA	p.E21K
Pat_76	Post-Resistance	DPP10	57628	37	2	116572369	116572369	Missense_Mutation	SNP	G	A	12	17	c.1701G>A	c.(1699-1701)ATG>ATA	p.M567I
Pat_76	Post-Resistance	GLI2	2736	37	2	121748199	121748199	Missense_Mutation	SNP	C	T	28	69	c.4709C>T	c.(4708-4710)TCC>TTC	p.S1570F
Pat_76	Post-Resistance	TFCP2L1	29842	37	2	121992851	121992851	Missense_Mutation	SNP	A	G	6	72	c.1040T>C	c.(1039-1041)GTC>GCC	p.V347A
Pat_76	Post-Resistance	TFCP2L1	29842	37	2	121997133	121997133	Splice_Site	SNP	C	T	6	21	c.860_splice	c.e8+1	p.G287_splice
Pat_76	Post-Resistance	MKI67IP	84365	37	2	122493301	122493301	Missense_Mutation	SNP	G	T	11	12	c.131C>A	c.(130-132)CCT>CAT	p.P44H
Pat_76	Post-Resistance	MYO7B	4648	37	2	128341852	128341852	Missense_Mutation	SNP	C	T	24	65	c.1499C>T	c.(1498-1500)GCC>GTC	p.A500V
Pat_76	Post-Resistance	MYO7B	4648	37	2	128346086	128346086	Missense_Mutation	SNP	C	T	10	29	c.1810C>T	c.(1810-1812)CAT>TAT	p.H604Y
Pat_76	Post-Resistance	YSK4	80122	37	2	135744766	135744766	Missense_Mutation	SNP	G	A	9	12	c.1676C>T	c.(1675-1677)CCC>CTC	p.P559L
Pat_76	Post-Resistance	LCT	3938	37	2	136566810	136566810	Missense_Mutation	SNP	G	A	11	27	c.3107C>T	c.(3106-3108)CCT>CTT	p.P1036L
Pat_76	Post-Resistance	HNMT	3176	37	2	138762777	138762777	Missense_Mutation	SNP	C	T	13	34	c.505C>T	c.(505-507)CTC>TTC	p.L169F
Pat_76	Post-Resistance	LRP1B	53353	37	2	141232728	141232728	Missense_Mutation	SNP	C	T	15	29	c.9604G>A	c.(9604-9606)GAT>AAT	p.D3202N
Pat_76	Post-Resistance	KYNU	8942	37	2	143643012	143643012	Missense_Mutation	SNP	G	A	10	20	c.76G>A	c.(76-78)GAT>AAT	p.D26N
Pat_76	Post-Resistance	KYNU	8942	37	2	143718310	143718310	Missense_Mutation	SNP	C	T	23	37	c.700C>T	c.(700-702)CCT>TCT	p.P234S
Pat_76	Post-Resistance	ARHGAP15	55843	37	2	143913139	143913139	Missense_Mutation	SNP	G	A	5	19	c.80G>A	c.(79-81)AGA>AAA	p.R27K
Pat_76	Post-Resistance	KIF5C	3800	37	2	149864490	149864490	Missense_Mutation	SNP	A	G	22	47	c.2459A>G	c.(2458-2460)GAC>GGC	p.D820G
Pat_76	Post-Resistance	GALNT5	11227	37	2	158140927	158140927	Missense_Mutation	SNP	G	A	5	14	c.1588G>A	c.(1588-1590)GAG>AAG	p.E530K
Pat_76	Post-Resistance	RBMS1	5937	37	2	161349804	161349804	Missense_Mutation	SNP	G	A	7	19	c.71C>T	c.(70-72)GCC>GTC	p.A24V
Pat_76	Post-Resistance	SCN3A	6328	37	2	165997216	165997216	Missense_Mutation	SNP	G	A	13	51	c.1964C>T	c.(1963-1965)TCC>TTC	p.S655F
Pat_76	Post-Resistance	SCN2A	6326	37	2	166188065	166188065	Missense_Mutation	SNP	C	T	4	15	c.2375C>T	c.(2374-2376)TCT>TTT	p.S792F
Pat_76	Post-Resistance	SCN9A	6335	37	2	167060726	167060726	Nonsense_Mutation	SNP	G	A	6	9	c.4480C>T	c.(4480-4482)CAA>TAA	p.Q1494*
Pat_76	Post-Resistance	SCN9A	6335	37	2	167134772	167134772	Missense_Mutation	SNP	C	T	3	12	c.2362G>A	c.(2362-2364)GAT>AAT	p.D788N
Pat_76	Post-Resistance	SCN7A	6332	37	2	167297955	167297955	Missense_Mutation	SNP	G	A	10	25	c.2108C>T	c.(2107-2109)TCC>TTC	p.S703F
Pat_76	Post-Resistance	XIRP2	129446	37	2	168099884	168099884	Missense_Mutation	SNP	G	A	12	30	c.1982G>A	c.(1981-1983)AGG>AAG	p.R661K
Pat_76	Post-Resistance	XIRP2	129446	37	2	168106418	168106418	Missense_Mutation	SNP	G	A	8	25	c.8516G>A	c.(8515-8517)AGA>AAA	p.R2839K
Pat_76	Post-Resistance	ITGA6	3655	37	2	173355997	173355997	Missense_Mutation	SNP	G	A	29	53	c.2827G>A	c.(2827-2829)GGG>AGG	p.G943R
Pat_76	Post-Resistance	CDCA7	83879	37	2	174232372	174232372	Nonsense_Mutation	SNP	G	T	19	49	c.1096G>T	c.(1096-1098)GAA>TAA	p.E366*

Pat_76	Post-Resistance	CDCA7	83879	37	2	174232374	174232374	Missense_Mutation	SNP	A	T	18	49	c.1098A>T	c.(1096-1098)GAA>GAT	p.E366D
Pat_76	Post-Resistance	TTN	7273	37	2	179416869	179416870	Missense_Mutation	DNP	CC	TT	17	72	83053_83054GG>A	c.(83053-83055)GGA>AAA	p.G27685K
Pat_76	Post-Resistance	TTN	7273	37	2	179417904	179417904	Missense_Mutation	SNP	C	T	14	29	c.82019G>A	c.(82018-82020)GGA>GAA	p.G27340E
Pat_76	Post-Resistance	TTN	7273	37	2	179431781	179431781	Missense_Mutation	SNP	G	A	12	51	c.71374C>T	c.(71374-71376)CGT>TGT	p.R23792C
Pat_76	Post-Resistance	TTN	7273	37	2	179432002	179432002	Missense_Mutation	SNP	C	T	19	54	c.71153G>A	c.(71152-71154)AGA>AAA	p.R23718K
Pat_76	Post-Resistance	TTN	7273	37	2	179483389	179483389	Missense_Mutation	SNP	C	T	9	25	c.39184G>A	c.(39184-39186)GGA>AGA	p.G13062R
Pat_76	Post-Resistance	TTN	7273	37	2	179552940	179552940	Missense_Mutation	SNP	C	T	4	24	c.28477G>A	c.(28477-28479)GAG>AAG	p.E9493K
Pat_76	Post-Resistance	TTN	7273	37	2	179584053	179584053	Missense_Mutation	SNP	C	T	30	87	c.20332G>A	c.(20332-20334)GGA>AGA	p.G6778R
Pat_76	Post-Resistance	TTN	7273	37	2	179587255	179587255	Missense_Mutation	SNP	G	A	12	40	c.18527C>T	c.(18526-18528)TCT>TTT	p.S6176F
Pat_76	Post-Resistance	TTN	7273	37	2	179590750	179590750	Missense_Mutation	SNP	G	A	4	9	c.16567C>T	c.(16567-16569)CCT>TCT	p.P5523S
Pat_76	Post-Resistance	TTN	7273	37	2	179594203	179594203	Missense_Mutation	SNP	G	A	18	41	c.14948C>T	c.(14947-14949)CCG>CTG	p.P4983L
Pat_76	Post-Resistance	TTN	7273	37	2	179605785	179605786	Missense_Mutation	DNP	CC	TT	26	52	11661_11662GG>A	659-11664)AAGGGT>AAA	p.G3888S
Pat_76	Post-Resistance	TTN	7273	37	2	179614199	179614199	Nonsense_Mutation	SNP	G	A	4	15	c.12928C>T	c.(12928-12930)CAA>TAA	p.Q4310*
Pat_76	Post-Resistance	TTN	7273	37	2	179638813	179638813	Missense_Mutation	SNP	C	T	11	30	c.7082G>A	c.(7081-7083)GGA>GAA	p.G2361E
Pat_76	Post-Resistance	CCDC141	285025	37	2	179701823	179701823	Nonsense_Mutation	SNP	G	A	4	8	c.2398C>T	c.(2398-2400)CAA>TAA	p.Q800*
Pat_76	Post-Resistance	ZNF804A	91752	37	2	185798352	185798353	Missense_Mutation	DNP	GG	AA	6	12	c.278_279GG>AA	c.(277-279)AGG>AAA	p.R93K
Pat_76	Post-Resistance	ZSWIM2	151112	37	2	187702046	187702046	Missense_Mutation	SNP	C	T	7	24	c.730G>A	c.(730-732)GGG>AGG	p.G244R
Pat_76	Post-Resistance	ZSWIM2	151112	37	2	187702277	187702277	Missense_Mutation	SNP	C	T	8	25	c.499G>A	c.(499-501)GGC>AGC	p.G167S
Pat_76	Post-Resistance	COL3A1	1281	37	2	189854823	189854823	Missense_Mutation	SNP	G	A	9	16	c.692G>A	c.(691-693)GGA>GAA	p.G231E
Pat_76	Post-Resistance	MYO1B	4430	37	2	192265124	192265124	Missense_Mutation	SNP	G	A	25	63	c.2312G>A	c.(2311-2313)CGG>CAG	p.R771Q
Pat_76	Post-Resistance	DNAH7	56171	37	2	196723464	196723464	Nonsense_Mutation	SNP	G	A	14	40	c.7801C>T	c.(7801-7803)CAA>TAA	p.Q2601*
Pat_76	Post-Resistance	DNAH7	56171	37	2	196729497	196729497	Missense_Mutation	SNP	C	T	21	61	c.6882G>A	c.(6880-6882)ATG>ATA	p.M2294I
Pat_76	Post-Resistance	DNAH7	56171	37	2	196756414	196756414	Missense_Mutation	SNP	G	A	13	29	c.5011C>T	c.(5011-5013)CTT>TTT	p.L1671F
Pat_76	Post-Resistance	HECW2	57520	37	2	197092934	197092934	Missense_Mutation	SNP	G	A	6	14	c.3809C>T	c.(3808-3810)TCC>TTC	p.S1270F
Pat_76	Post-Resistance	SPATS2L	26010	37	2	201342632	201342632	Missense_Mutation	SNP	G	A	9	6	c.1555G>A	c.(1555-1557)GAG>AAG	p.E519K
Pat_76	Post-Resistance	RAPH1	65059	37	2	204306082	204306083	Missense_Mutation	DNP	GG	AA	4	29	.1830_1831CC>T	828-1833)TCCCCG>TCTT	p.P611S
Pat_76	Post-Resistance	ZDBF2	57683	37	2	207173096	207173096	Missense_Mutation	SNP	G	A	4	12	c.3844G>A	c.(3844-3846)GAT>AAT	p.D1282N
Pat_76	Post-Resistance	PTH2R	5746	37	2	209307123	209307123	Missense_Mutation	SNP	C	T	24	56	c.446C>T	c.(445-447)ACC>ATC	p.T149I
Pat_76	Post-Resistance	CPS1	1373	37	2	211454911	211454911	Missense_Mutation	SNP	C	T	60	172	c.793C>T	c.(793-795)CCG>TCG	p.P265S
Pat_76	Post-Resistance	ABCA12	26154	37	2	215843664	215843665	Missense_Mutation	DNP	CC	TT	10	18	.4840_4841GG>A	c.(4840-4842)GGA>AAA	p.G1614K
Pat_76	Post-Resistance	SERPINE2	5270	37	2	224842266	224842266	Missense_Mutation	SNP	G	A	14	42	c.1154C>T	c.(1153-1155)CCT>CTT	p.P385L
Pat_76	Post-Resistance	COL4A4	1286	37	2	227872874	227872874	Missense_Mutation	SNP	C	T	7	17	c.4669G>A	c.(4669-4671)GAG>AAG	p.E1557K
Pat_76	Post-Resistance	COL4A3	1285	37	2	228155552	228155552	Missense_Mutation	SNP	G	A	3	8	c.3160G>A	c.(3160-3162)GGA>AGA	p.G1054R
Pat_76	Post-Resistance	SP100	6672	37	2	231404082	231404082	Missense_Mutation	SNP	C	T	19	22	c.2195C>T	c.(2194-2196)TCC>TTC	p.S732F
Pat_76	Post-Resistance	UGT1A6	54578	37	2	234601885	234601885	Missense_Mutation	SNP	C	T	10	23	c.235C>T	c.(235-237)CCA>TCA	p.P79S
Pat_76	Post-Resistance	ASB18	401036	37	2	237149963	237149963	Missense_Mutation	SNP	C	T	24	33	c.288G>A	c.(286-288)ATG>ATA	p.M96I
Pat_76	Post-Resistance	RBM44	375316	37	2	238738134	238738134	Missense_Mutation	SNP	C	T	16	54	c.2878C>T	c.(2878-2880)CCT>TCT	p.P960S
Pat_76	Post-Resistance	RNPEPL1	57140	37	2	241514551	241514551	Missense_Mutation	SNP	T	A	33	54	c.700T>A	c.(700-702)TTT>ATT	p.F234I
Pat_76	Post-Resistance	SNED1	25992	37	2	241989314	241989314	Missense_Mutation	SNP	T	C	13	38	c.1699T>C	c.(1699-1701)TGC>CGC	p.C567R
Pat_76	Post-Resistance	CPXM1	56265	37	20	2774842	2774842	Missense_Mutation	SNP	C	G	16	32	c.2199G>C	c.(2197-2199)AAG>AAC	p.K733N
Pat_76	Post-Resistance	CPXM1	56265	37	20	2777701	2777701	Missense_Mutation	SNP	G	A	4	15	c.872C>T	c.(871-873)TCC>TTC	p.S291F
Pat_76	Post-Resistance	SLC4A11	83959	37	20	3209023	3209023	Missense_Mutation	SNP	G	A	29	83	c.2488C>T	c.(2488-2490)CAC>TAC	p.H830Y
Pat_76	Post-Resistance	GPCPD1	56261	37	20	5539440	5539440	Missense_Mutation	SNP	G	A	3	13	c.1558C>T	c.(1558-1560)CCG>TCG	p.P520S
Pat_76	Post-Resistance	PLCB1	23236	37	20	8130959	8130959	Missense_Mutation	SNP	C	T	4	5	c.118C>T	c.(118-120)CCA>TCA	p.P40S
Pat_76	Post-Resistance	PLCB1	23236	37	20	8626748	8626748	Splice_Site	SNP	G	A	5	21	c.385_splice	c.e5-1	p.E129_splice
Pat_76	Post-Resistance	PAK7	57144	37	20	9561234	9561234	Missense_Mutation	SNP	G	A	19	37	c.548C>T	c.(547-549)TCT>TTT	p.S183F
Pat_76	Post-Resistance	SNAP25	6616	37	20	10256176	10256176	Missense_Mutation	SNP	G	A	4	13	c.37G>A	c.(37-39)GAG>AAG	p.E13K

Pat_76	Post-Resistance	SEL1L2	80343	37	20	13839970	13839970	Missense_Mutation	SNP	G	A	9	23	c.1756C>T	c.(1756-1758)CAC>TAC	p.H586Y
Pat_76	Post-Resistance	KIF16B	55614	37	20	16360462	16360462	Missense_Mutation	SNP	C	T	5	28	c.2185G>A	c.(2185-2187)GAA>AAA	p.E729K
Pat_76	Post-Resistance	C20orf26	26074	37	20	20257987	20257987	Missense_Mutation	SNP	G	A	29	29	c.2681G>A	c.(2680-2682)GGA>GAA	p.G894E
Pat_76	Post-Resistance	INSM1	3642	37	20	20350319	20350319	Missense_Mutation	SNP	C	T	7	20	c.1408C>T	c.(1408-1410)CCC>TCC	p.P470S
Pat_76	Post-Resistance	XRN2	22803	37	20	21362668	21362668	Missense_Mutation	SNP	C	T	3	18	c.2621C>T	c.(2620-2622)CCC>CTC	p.P874L
Pat_76	Post-Resistance	FOXA2	3170	37	20	22563239	22563239	Missense_Mutation	SNP	C	T	33	39	c.623G>A	c.(622-624)CGC>CAC	p.R208H
Pat_76	Post-Resistance	MYLK2	85366	37	20	30409442	30409442	Missense_Mutation	SNP	C	T	77	87	c.674C>T	c.(673-675)TCG>TTG	p.S225L
Pat_76	Post-Resistance	TTLL9	164395	37	20	30507671	30507671	Missense_Mutation	SNP	C	T	35	35	c.509C>T	c.(508-510)GCC>GTC	p.A170V
Pat_76	Post-Resistance	ZNF341	84905	37	20	32377334	32377334	Missense_Mutation	SNP	G	A	20	82	c.1975G>A	c.(1975-1977)GGC>AGC	p.G659S
Pat_76	Post-Resistance	ITCH	83737	37	20	33059310	33059310	Missense_Mutation	SNP	C	T	18	16	c.1682C>T	c.(1681-1683)TCC>TTC	p.S561F
Pat_76	Post-Resistance	GSS	2937	37	20	33529540	33529540	Missense_Mutation	SNP	G	A	17	16	c.584C>T	c.(583-585)GCC>GTC	p.A195V
Pat_76	Post-Resistance	FAM83C	128876	37	20	33875149	33875149	Missense_Mutation	SNP	G	A	3	15	c.1433C>T	c.(1432-1434)CCC>CTC	p.P478L
Pat_76	Post-Resistance	MANBAL	63905	37	20	35929694	35929694	Missense_Mutation	SNP	C	T	3	7	c.28C>T	c.(28-30)CCG>TCG	p.P10S
Pat_76	Post-Resistance	TGM2	7052	37	20	36760777	36760777	Missense_Mutation	SNP	C	T	29	90	c.1741G>A	c.(1741-1743)GAC>AAC	p.D581N
Pat_76	Post-Resistance	L3MBTL	26013	37	20	42143326	42143326	Missense_Mutation	SNP	C	T	3	8	c.346C>T	c.(346-348)CCG>TCG	p.P116S
Pat_76	Post-Resistance	TOX2	84969	37	20	42680074	42680074	Missense_Mutation	SNP	G	T	16	15	c.567G>T	c.(565-567)ATG>ATT	p.M189I
Pat_76	Post-Resistance	JPH2	57158	37	20	42788428	42788428	Missense_Mutation	SNP	G	T	15	52	c.999C>A	c.(997-999)GAC>GAA	p.D333E
Pat_76	Post-Resistance	JPH2	57158	37	20	42788430	42788430	Missense_Mutation	SNP	C	T	15	51	c.997G>A	c.(997-999)GAC>AAC	p.D333N
Pat_76	Post-Resistance	HNF4A	3172	37	20	43056995	43056995	Missense_Mutation	SNP	C	T	48	62	c.1150C>T	c.(1150-1152)CAT>TAT	p.H384Y
Pat_76	Post-Resistance	SEMG2	6407	37	20	43850643	43850643	Missense_Mutation	SNP	C	T	19	16	c.370C>T	c.(370-372)CAC>TAC	p.H124Y
Pat_76	Post-Resistance	MMP9	4318	37	20	44641179	44641179	Missense_Mutation	SNP	C	T	27	24	c.1288C>T	c.(1288-1290)CCC>TCC	p.P430S
Pat_76	Post-Resistance	ZNF334	55713	37	20	45130345	45130345	Missense_Mutation	SNP	C	T	37	90	c.1633G>A	c.(1633-1635)GAA>AAA	p.E545K
Pat_76	Post-Resistance	ZNF334	55713	37	20	45130930	45130930	Missense_Mutation	SNP	C	T	23	129	c.1048G>A	c.(1048-1050)GAA>AAA	p.E350K
Pat_76	Post-Resistance	ARFGEF2	10564	37	20	47635499	47635499	Missense_Mutation	SNP	C	T	8	8	c.4588C>T	c.(4588-4590)CCA>TCA	p.P1530S
Pat_76	Post-Resistance	SALL4	57167	37	20	50408016	50408016	Missense_Mutation	SNP	G	A	6	10	c.1006C>T	c.(1006-1008)CCT>TCT	p.P336S
Pat_76	Post-Resistance	SALL4	57167	37	20	50408730	50408730	Missense_Mutation	SNP	G	A	19	20	c.292C>T	c.(292-294)CCA>TCA	p.P98S
Pat_76	Post-Resistance	CBLN4	140689	37	20	54575833	54575833	Missense_Mutation	SNP	C	T	25	38	c.362G>A	c.(361-363)AGT>AAT	p.S121N
Pat_76	Post-Resistance	MC3R	4159	37	20	54824619	54824620	Missense_Mutation	DNP	GG	AA	23	21	c.720_721GG>AA	718-723)GGGGCA>GGAA	p.A241T
Pat_76	Post-Resistance	CSTF1	1477	37	20	54974146	54974146	Missense_Mutation	SNP	C	T	40	135	c.769C>T	c.(769-771)CCT>TCT	p.P257S
Pat_76	Post-Resistance	CASS4	57091	37	20	55027514	55027514	Missense_Mutation	SNP	G	A	11	10	c.1282G>A	c.(1282-1284)GAG>AAG	p.E428K
Pat_76	Post-Resistance	GNAS	2778	37	20	57484421	57484421	Missense_Mutation	SNP	G	A	7	25	c.2531G>A	c.(2530-2532)CGT>CAT	p.R844H
Pat_76	Post-Resistance	ZNF831	128611	37	20	57768785	57768785	Missense_Mutation	SNP	C	T	28	16	c.2711C>T	c.(2710-2712)ACC>ATC	p.T904I
Pat_76	Post-Resistance	ZNF831	128611	37	20	57769723	57769723	Nonsense_Mutation	SNP	C	T	5	13	c.3649C>T	c.(3649-3651)CGA>TGA	p.R1217*
Pat_76	Post-Resistance	ZNF831	128611	37	20	57770945	57770945	Missense_Mutation	SNP	G	A	48	167	c.3760G>A	c.(3760-3762)GGG>AGG	p.G1254R
Pat_76	Post-Resistance	SYCP2	10388	37	20	58495521	58495521	Missense_Mutation	SNP	G	A	9	6	c.190C>T	c.(190-192)CAC>TAC	p.H64Y
Pat_76	Post-Resistance	SRMS	6725	37	20	62178665	62178666	Missense_Mutation	DNP	GG	AA	4	13	c.151_152CC>TT	c.(151-153)CCC>TTC	p.P51F
Pat_76	Post-Resistance	NCAM2	4685	37	21	22656657	22656657	Missense_Mutation	SNP	C	T	7	21	c.274C>T	c.(274-276)CGT>TGT	p.R92C
Pat_76	Post-Resistance	JAM2	58494	37	21	27066190	27066190	Missense_Mutation	SNP	G	A	50	85	c.364G>A	c.(364-366)GAA>AAA	p.E122K
Pat_76	Post-Resistance	SFRS15	57466	37	21	33067289	33067289	Missense_Mutation	SNP	G	A	8	11	c.1073C>T	c.(1072-1074)CCA>CTA	p.P358L
Pat_76	Post-Resistance	HUNK	30811	37	21	33370917	33370917	Missense_Mutation	SNP	C	T	15	31	c.1565C>T	c.(1564-1566)CCC>CTC	p.P522L
Pat_76	Post-Resistance	C21orf59	56683	37	21	33976521	33976521	Missense_Mutation	SNP	C	T	14	42	c.448G>A	c.(448-450)GTG>ATG	p.V150M
Pat_76	Post-Resistance	DNAJC28	54943	37	21	34861059	34861059	Missense_Mutation	SNP	T	G	19	24	c.642A>C	c.(640-642)AAA>AAC	p.K214N
Pat_76	Post-Resistance	SLC5A3	6526	37	21	35467832	35467832	Missense_Mutation	SNP	A	G	38	86	c.335A>G	c.(334-336)TAC>TGC	p.Y112C
Pat_76	Post-Resistance	SLC5A3	6526	37	21	35467859	35467859	Missense_Mutation	SNP	G	A	39	83	c.362G>A	c.(361-363)AGG>AAG	p.R121K
Pat_76	Post-Resistance	SETD4	54093	37	21	37420683	37420683	Missense_Mutation	SNP	C	T	68	158	c.219G>A	c.(217-219)ATG>ATA	p.M73I
Pat_76	Post-Resistance	DOPEY2	9980	37	21	37597961	37597961	Missense_Mutation	SNP	C	T	8	13	c.1469C>T	c.(1468-1470)CCT>CTT	p.P490L
Pat_76	Post-Resistance	TTC3	7267	37	21	38462544	38462545	Missense_Mutation	DNP	CC	TT	4	24	c.438_439CC>TT	(436-441)TTCCTT>TTTTT	p.L147F

Pat_76	Post-Resistance	TTC3	7267	37	21	38539906	38539906	Missense_Mutation	SNP	C	T	6	10	c.4451C>T	c.(4450-4452)CCT>CTT	p.P1484L
Pat_76	Post-Resistance	DSCR4	10281	37	21	39426981	39426981	Missense_Mutation	SNP	C	T	6	27	c.325G>A	c.(325-327)GAC>AAC	p.D109N
Pat_76	Post-Resistance	DSCAM	1826	37	21	41450781	41450781	Missense_Mutation	SNP	G	A	5	11	c.4544C>T	c.(4543-4545)CCC>CTC	p.P1515L
Pat_76	Post-Resistance	DSCAM	1826	37	21	41455916	41455916	Missense_Mutation	SNP	G	A	5	15	c.4150C>T	c.(4150-4152)CGG>TGG	p.R1384W
Pat_76	Post-Resistance	FAM3B	54097	37	21	42694883	42694883	Missense_Mutation	SNP	C	T	16	35	c.53C>T	c.(52-54)TCC>TTC	p.S18F
Pat_76	Post-Resistance	PRDM15	63977	37	21	43299455	43299455	Missense_Mutation	SNP	G	A	6	15	c.26C>T	c.(25-27)TCC>TTC	p.S9F
Pat_76	Post-Resistance	CRYAA	1409	37	21	44590730	44590730	Missense_Mutation	SNP	G	A	11	25	c.293G>A	c.(292-294)GGA>GAA	p.G98E
Pat_76	Post-Resistance	SIK1	150094	37	21	44838191	44838191	Missense_Mutation	SNP	G	A	9	29	c.1693C>T	c.(1693-1695)CCT>TCT	p.P565S
Pat_76	Post-Resistance	RRP1	8568	37	21	45217545	45217546	Missense_Mutation	DNP	CC	TT	18	79	c.586_587CC>TT	c.(586-588)CCC>TTC	p.P196F
Pat_76	Post-Resistance	C21orf29	54084	37	21	45987779	45987779	Missense_Mutation	SNP	C	T	10	25	c.193G>A	c.(193-195)GCC>ACC	p.A65T
Pat_76	Post-Resistance	KRTAP10-4	386672	37	21	45994771	45994771	Missense_Mutation	SNP	C	T	49	96	c.1136C>T	c.(1135-1137)TCC>TTC	p.S379F
Pat_76	Post-Resistance	COL6A1	1291	37	21	47418068	47418069	Missense_Mutation	DNP	GG	AA	7	11	.1558_1559GG>A	c.(1558-1560)GGC>AAC	p.G520N
Pat_76	Post-Resistance	COL6A2	1292	37	21	47532283	47532283	Missense_Mutation	SNP	C	T	4	4	c.506C>T	c.(505-507)CCC>CTC	p.P169L
Pat_76	Post-Resistance	LSS	4047	37	21	47633739	47633739	Missense_Mutation	SNP	G	A	9	25	c.1022C>T	c.(1021-1023)ACC>ATC	p.T341I
Pat_76	Post-Resistance	PCNT	5116	37	21	47769597	47769598	Splice_Site	DNP	GG	AA	11	31	c.1208_splice	c.e8-1	p.R403_splice
Pat_76	Post-Resistance	PCNT	5116	37	21	47817270	47817270	Missense_Mutation	SNP	G	A	10	17	c.4308G>A	c.(4306-4308)ATG>ATA	p.M1436I
Pat_76	Post-Resistance	DIP2A	23181	37	21	47981665	47981665	Missense_Mutation	SNP	C	T	34	67	c.4036C>T	c.(4036-4038)CGT>TGT	p.R1346C
Pat_76	Post-Resistance	POTEH	23784	37	22	16267070	16267070	Missense_Mutation	SNP	C	T	15	202	c.1379G>A	c.(1378-1380)GGA>GAA	p.G460E
Pat_76	Post-Resistance	POTEH	23784	37	22	16279222	16279222	Missense_Mutation	SNP	T	A	13	182	c.1001A>T	c.(1000-1002)AAT>ATT	p.N334I
Pat_76	Post-Resistance	OR11H1	81061	37	22	16449102	16449102	Missense_Mutation	SNP	G	A	34	36	c.703C>T	c.(703-705)CTT>TTT	p.L235F
Pat_76	Post-Resistance	RTDR1	27156	37	22	23401774	23401774	Missense_Mutation	SNP	C	T	23	22	c.913G>A	c.(913-915)GGC>AGC	p.G305S
Pat_76	Post-Resistance	RAB36	9609	37	22	23495309	23495309	Missense_Mutation	SNP	A	T	32	49	c.515A>T	c.(514-516)TAT>TTT	p.Y172F
Pat_76	Post-Resistance	MMP11	4320	37	22	24124425	24124425	Nonsense_Mutation	SNP	G	A	33	68	c.1088G>A	c.(1087-1089)TGG>TAG	p.W363*
Pat_76	Post-Resistance	CABIN1	23523	37	22	24481098	24481099	Missense_Mutation	DNP	CC	TT	8	27	.3257_3258CC>T	c.(3256-3258)CCC>CTT	p.P1086L
Pat_76	Post-Resistance	GGT1	2678	37	22	25023398	25023398	Splice_Site	SNP	G	A	25	44	c.1021_splice	c.e12-1	p.V341_splice
Pat_76	Post-Resistance	MYO18B	84700	37	22	26351183	26351183	Missense_Mutation	SNP	G	A	4	14	c.6009G>A	c.(6007-6009)ATG>ATA	p.M2003I
Pat_76	Post-Resistance	CABP7	164633	37	22	30125183	30125183	Missense_Mutation	SNP	C	T	4	12	c.506C>T	c.(505-507)CCC>CTC	p.P169L
Pat_76	Post-Resistance	SEC14L3	266629	37	22	30863013	30863013	Missense_Mutation	SNP	C	T	32	60	c.475G>A	c.(475-477)GGA>AGA	p.G159R
Pat_76	Post-Resistance	NCF4	4689	37	22	37261013	37261013	Missense_Mutation	SNP	G	A	27	44	c.170G>A	c.(169-171)CGC>CAC	p.R57H
Pat_76	Post-Resistance	TMPRSS6	164656	37	22	37499418	37499418	Missense_Mutation	SNP	C	T	32	52	c.67G>A	c.(67-69)GGG>AGG	p.G23R
Pat_76	Post-Resistance	TRIOBP	11078	37	22	38120224	38120224	Missense_Mutation	SNP	C	T	51	157	c.1661C>T	c.(1660-1662)GCC>GTC	p.A554V
Pat_76	Post-Resistance	TRIOBP	11078	37	22	38131325	38131326	Missense_Mutation	DNP	CC	TT	6	17	.4982_4983CC>T	c.(4981-4983)TCC>TTT	p.S1661F
Pat_76	Post-Resistance	TAB1	10454	37	22	39822888	39822888	Missense_Mutation	SNP	C	T	23	57	c.1102C>T	c.(1102-1104)CCG>TCG	p.P368S
Pat_76	Post-Resistance	CACNA1I	8911	37	22	40069069	40069069	Missense_Mutation	SNP	G	A	60	108	c.4765G>A	c.(4765-4767)GTT>ATT	p.V1589I
Pat_76	Post-Resistance	XRCC6	2547	37	22	42053023	42053023	Missense_Mutation	SNP	C	T	7	16	c.1408C>T	c.(1408-1410)CGC>TGC	p.R470C
Pat_76	Post-Resistance	WNT7B	7477	37	22	46345835	46345835	Missense_Mutation	SNP	C	T	14	38	c.263G>A	c.(262-264)GGC>GAC	p.G88D
Pat_76	Post-Resistance	CNTN4	152330	37	3	3081778	3081778	Missense_Mutation	SNP	C	T	12	19	c.2221C>T	c.(2221-2223)CCC>TCC	p.P741S
Pat_76	Post-Resistance	IL5RA	3568	37	3	3139668	3139668	Missense_Mutation	SNP	G	A	22	32	c.595C>T	c.(595-597)CCC>TCC	p.P199S
Pat_76	Post-Resistance	ITPR1	3708	37	3	4735393	4735393	Missense_Mutation	SNP	C	T	11	10	c.4222C>T	c.(4222-4224)CGC>TGC	p.R1408C
Pat_76	Post-Resistance	C3orf31	132001	37	3	11871271	11871271	Missense_Mutation	SNP	G	A	10	38	c.479C>T	c.(478-480)GCT>GTT	p.A160V
Pat_76	Post-Resistance	PPARG	5468	37	3	12458228	12458228	Missense_Mutation	SNP	C	T	9	13	c.845C>T	c.(844-846)TCC>TTC	p.S282F
Pat_76	Post-Resistance	NUP210	23225	37	3	13378363	13378363	Missense_Mutation	SNP	T	C	25	64	c.3608A>G	c.(3607-3609)AAT>AGT	p.N1203S
Pat_76	Post-Resistance	GRIP2	80852	37	3	14561732	14561732	Missense_Mutation	SNP	C	T	16	19	c.1206G>A	c.(1204-1206)ATG>ATA	p.M402I
Pat_76	Post-Resistance	FGD5	152273	37	3	14861563	14861563	Missense_Mutation	SNP	C	T	9	20	c.985C>T	c.(985-987)CCT>TCT	p.P329S
Pat_76	Post-Resistance	PLCL2	23228	37	3	17051292	17051292	Missense_Mutation	SNP	G	A	4	14	c.430G>A	c.(430-432)GTT>ATT	p.V144I
Pat_76	Post-Resistance	EFHB	151651	37	3	19974997	19974997	Missense_Mutation	SNP	C	T	11	23	c.514G>A	c.(514-516)GAA>AAA	p.E172K
Pat_76	Post-Resistance	SLC4A7	9497	37	3	27475470	27475470	Missense_Mutation	SNP	G	A	16	21	c.688C>T	c.(688-690)CTT>TTT	p.L230F

Pat_76	Post-Resistance	OSBPL10	114884	37	3	31725572	31725572	Missense_Mutation	SNP	G	C	16	31	c.1280C>G	c.(1279-1281)TCT>TGT	p.S427C
Pat_76	Post-Resistance	CNOT10	25904	37	3	32776347	32776347	Missense_Mutation	SNP	C	T	42	122	c.1393C>T	c.(1393-1395)CTC>TTC	p.L465F
Pat_76	Post-Resistance	ARPP21	10777	37	3	35730819	35730819	Missense_Mutation	SNP	G	A	14	36	c.427G>A	c.(427-429)GAT>AAT	p.D143N
Pat_76	Post-Resistance	ITGA9	3680	37	3	37783285	37783285	Missense_Mutation	SNP	C	T	7	23	c.2299C>T	c.(2299-2301)CAC>TAC	p.H767Y
Pat_76	Post-Resistance	DLEC1	9940	37	3	38150967	38150967	Missense_Mutation	SNP	G	A	18	29	c.3174G>A	c.(3172-3174)ATG>ATA	p.M1058I
Pat_76	Post-Resistance	SCN5A	6331	37	3	38592468	38592468	Missense_Mutation	SNP	C	T	10	19	c.5395G>A	c.(5395-5397)GAG>AAG	p.E1799K
Pat_76	Post-Resistance	SCN10A	6336	37	3	38739493	38739493	Missense_Mutation	SNP	C	T	17	44	c.5218G>A	c.(5218-5220)GAC>AAC	p.D1740N
Pat_76	Post-Resistance	CSRNP1	64651	37	3	39185196	39185196	Missense_Mutation	SNP	G	A	13	14	c.1120C>T	c.(1120-1122)CAC>TAC	p.H374Y
Pat_76	Post-Resistance	SACM1L	22908	37	3	45780142	45780142	Missense_Mutation	SNP	C	A	3	18	c.1455C>A	c.(1453-1455)AAC>AAA	p.N485K
Pat_76	Post-Resistance	SACM1L	22908	37	3	45780147	45780148	Missense_Mutation	DNP	CC	TT	3	18	.1460_1461CC>T	c.(1459-1461)TCC>TTT	p.S487F
Pat_76	Post-Resistance	LRRC2	79442	37	3	46592991	46592991	Missense_Mutation	SNP	C	T	10	39	c.91G>A	c.(91-93)GAG>AAG	p.E31K
Pat_76	Post-Resistance	PLXNB1	5364	37	3	48456394	48456395	Missense_Mutation	DNP	GG	AA	21	48	.4022_4023CC>T	c.(4021-4023)GCC>GTT	p.A1341V
Pat_76	Post-Resistance	CCDC51	79714	37	3	48474195	48474195	Missense_Mutation	SNP	C	T	15	49	c.859G>A	c.(859-861)GGT>AGT	p.G287S
Pat_76	Post-Resistance	QARS	5859	37	3	49135820	49135820	Missense_Mutation	SNP	G	A	21	48	c.2050C>T	c.(2050-2052)CCT>TCT	p.P684S
Pat_76	Post-Resistance	TNNC1	7134	37	3	52485442	52485442	Missense_Mutation	SNP	C	T	8	18	c.419G>A	c.(418-420)GGA>GAA	p.G140E
Pat_76	Post-Resistance	PBRM1	55193	37	3	52682442	52682442	Missense_Mutation	SNP	C	T	3	16	c.731G>A	c.(730-732)AGT>AAT	p.S244N
Pat_76	Post-Resistance	CACNA1D	776	37	3	53835242	53835242	Missense_Mutation	SNP	G	A	13	33	c.5198G>A	c.(5197-5199)GGA>GAA	p.G1733E
Pat_76	Post-Resistance	ERC2	26059	37	3	55984533	55984533	Missense_Mutation	SNP	C	T	3	19	c.2323G>A	c.(2323-2325)GAA>AAA	p.E775K
Pat_76	Post-Resistance	CCDC66	285331	37	3	56627597	56627597	Nonsense_Mutation	SNP	C	T	13	18	c.1147C>T	c.(1147-1149)CAG>TAG	p.Q383*
Pat_76	Post-Resistance	FLNB	2317	37	3	58109342	58109342	Missense_Mutation	SNP	C	T	20	54	c.3649C>T	c.(3649-3651)CCC>TCC	p.P1217S
Pat_76	Post-Resistance	DNASE1L3	1776	37	3	58191217	58191217	Nonsense_Mutation	SNP	G	A	23	49	c.301C>T	c.(301-303)CAA>TAA	p.Q101*
Pat_76	Post-Resistance	ROBO1	6091	37	3	78683100	78683100	Missense_Mutation	SNP	C	T	5	39	c.3466G>A	c.(3466-3468)GGC>AGC	p.G1156S
Pat_76	Post-Resistance	EPHA3	2042	37	3	89499331	89499331	Missense_Mutation	SNP	T	G	6	20	c.2501T>G	c.(2500-2502)ATT>AGT	p.I834S
Pat_76	Post-Resistance	PROS1	5627	37	3	93646102	93646102	Missense_Mutation	SNP	G	A	13	18	c.226C>T	c.(226-228)CCG>TCG	p.P76S
Pat_76	Post-Resistance	OR5H14	403273	37	3	97868560	97868560	Missense_Mutation	SNP	G	A	29	76	c.331G>A	c.(331-333)GAA>AAA	p.E111K
Pat_76	Post-Resistance	OR5H15	403274	37	3	97888271	97888271	Missense_Mutation	SNP	C	G	3	18	c.728C>G	c.(727-729)GCC>GGC	p.A243G
Pat_76	Post-Resistance	GPR128	84873	37	3	100349614	100349614	Missense_Mutation	SNP	G	A	12	26	c.295G>A	c.(295-297)GGA>AGA	p.G99R
Pat_76	Post-Resistance	IMPG2	50939	37	3	101038529	101038529	Missense_Mutation	SNP	C	T	10	27	c.233G>A	c.(232-234)AGA>AAA	p.R78K
Pat_76	Post-Resistance	ZPLD1	131368	37	3	102187971	102187971	Missense_Mutation	SNP	C	T	14	39	c.925C>T	c.(925-927)CTT>TTT	p.L309F
Pat_76	Post-Resistance	CCDC54	84692	37	3	107096863	107096864	Missense_Mutation	DNP	GG	AA	6	13	c.429_430GG>AA	427-432)CTGGAA>CTAA	p.E144K
Pat_76	Post-Resistance	MYH15	22989	37	3	108110641	108110641	Missense_Mutation	SNP	C	T	13	44	c.5456G>A	c.(5455-5457)GGG>GAG	p.G1819E
Pat_76	Post-Resistance	MYH15	22989	37	3	108149702	108149702	Nonsense_Mutation	SNP	G	A	4	8	c.3349C>T	c.(3349-3351)CAG>TAG	p.Q1117*
Pat_76	Post-Resistance	MYH15	22989	37	3	108218318	108218318	Nonsense_Mutation	SNP	G	A	9	9	c.568C>T	c.(568-570)CAG>TAG	p.Q190*
Pat_76	Post-Resistance	CD96	10225	37	3	111263955	111263955	Missense_Mutation	SNP	A	C	16	44	c.124A>C	c.(124-126)AAC>CAC	p.N42H
Pat_76	Post-Resistance	TMPRSS7	344805	37	3	111793194	111793194	Missense_Mutation	SNP	G	A	13	25	c.1340G>A	c.(1339-1341)AGG>AAG	p.R447K
Pat_76	Post-Resistance	CCDC80	151887	37	3	112357513	112357513	Missense_Mutation	SNP	G	A	11	20	c.1240C>T	c.(1240-1242)CTT>TTT	p.L414F
Pat_76	Post-Resistance	ZNF80	7634	37	3	113955513	113955513	Missense_Mutation	SNP	C	T	16	44	c.409G>A	c.(409-411)GAG>AAG	p.E137K
Pat_76	Post-Resistance	RABL3	285282	37	3	120449568	120449568	Missense_Mutation	SNP	G	A	14	37	c.113C>T	c.(112-114)ACT>ATT	p.T38I
Pat_76	Post-Resistance	GOLGB1	2804	37	3	121409852	121409852	Missense_Mutation	SNP	C	T	12	13	c.8344G>A	c.(8344-8346)GAT>AAT	p.D2782N
Pat_76	Post-Resistance	PARP15	165631	37	3	122336009	122336009	Missense_Mutation	SNP	C	T	13	33	c.998C>T	c.(997-999)TCA>TTA	p.S333L
Pat_76	Post-Resistance	MYLK	4638	37	3	123452812	123452812	Missense_Mutation	SNP	G	A	18	33	c.1031C>T	c.(1030-1032)TCC>TTC	p.S344F
Pat_76	Post-Resistance	KALRN	8997	37	3	124053179	124053179	Missense_Mutation	SNP	C	T	24	69	c.1478C>T	c.(1477-1479)TCC>TTC	p.S493F
Pat_76	Post-Resistance	SLC12A8	84561	37	3	124909340	124909340	Nonsense_Mutation	SNP	C	T	48	91	c.77G>A	c.(76-78)TGG>TAG	p.W26*
Pat_76	Post-Resistance	MCM2	4171	37	3	127336204	127336205	Missense_Mutation	DNP	CC	TT	5	25	.1856_1857CC>T	c.(1855-1857)TCC>TTT	p.S619F
Pat_76	Post-Resistance	DNAJB8	165721	37	3	128181833	128181833	Missense_Mutation	SNP	G	A	19	39	c.256C>T	c.(256-258)CCC>TCC	p.P86S
Pat_76	Post-Resistance	TOPBP1	11073	37	3	133358805	133358806	Missense_Mutation	DNP	TC	AT	5	8	.2230_2231GA>A	c.(2230-2232)GAA>ATA	p.E744I
Pat_76	Post-Resistance	KY	339855	37	3	134366318	134366318	Missense_Mutation	SNP	C	T	5	6	c.158G>A	c.(157-159)GGA>GAA	p.G53E

Pat_76	Post-Resistance	EPHB1	2047	37	3	134670519	134670519	Missense_Mutation	SNP	G	A	15	54	c.430G>A	c.(430-432)GAG>AAG	p.E144K
Pat_76	Post-Resistance	PPP2R3A	5523	37	3	135720516	135720516	Missense_Mutation	SNP	C	T	10	16	c.176C>T	c.(175-177)CCT>CTT	p.P59L
Pat_76	Post-Resistance	NCK1	4690	37	3	136664562	136664562	Missense_Mutation	SNP	G	A	22	38	c.364G>A	c.(364-366)GAG>AAG	p.E122K
Pat_76	Post-Resistance	COPB2	9276	37	3	139097898	139097898	Missense_Mutation	SNP	T	C	12	23	c.346A>G	c.(346-348)ACT>GCT	p.T116A
Pat_76	Post-Resistance	TRIM42	287015	37	3	140401461	140401461	Missense_Mutation	SNP	G	A	21	59	c.499G>A	c.(499-501)GAG>AAG	p.E167K
Pat_76	Post-Resistance	TRIM42	287015	37	3	140406746	140406746	Missense_Mutation	SNP	G	A	6	16	c.1222G>A	c.(1222-1224)GAA>AAA	p.E408K
Pat_76	Post-Resistance	PLS1	5357	37	3	142388285	142388285	Missense_Mutation	SNP	G	A	25	47	c.124G>A	c.(124-126)GAA>AAA	p.E42K
Pat_76	Post-Resistance	TRPC1	7220	37	3	142521065	142521065	Missense_Mutation	SNP	C	T	6	16	c.1636C>T	c.(1636-1638)CTT>TTT	p.L546F
Pat_76	Post-Resistance	MED12L	116931	37	3	151067889	151067889	Missense_Mutation	SNP	C	T	69	163	c.2188C>T	c.(2188-2190)CTC>TTC	p.L730F
Pat_76	Post-Resistance	IGSF10	285313	37	3	151161477	151161477	Missense_Mutation	SNP	T	G	11	34	c.5258A>C	c.(5257-5259)AAA>ACA	p.K1753T
Pat_76	Post-Resistance	PLCH1	23007	37	3	155267673	155267673	Missense_Mutation	SNP	C	T	12	28	c.1229G>A	c.(1228-1230)GGA>GAA	p.G410E
Pat_76	Post-Resistance	SLC33A1	9197	37	3	155571045	155571045	Nonsense_Mutation	SNP	G	A	9	15	c.742C>T	c.(742-744)CAG>TAG	p.Q248*
Pat_76	Post-Resistance	OTOL1	131149	37	3	161221642	161221642	Nonsense_Mutation	SNP	G	A	4	15	c.1346G>A	c.(1345-1347)TGG>TAG	p.W449*
Pat_76	Post-Resistance	MECOM	2122	37	3	168834150	168834150	Missense_Mutation	SNP	G	A	7	20	c.946C>T	c.(946-948)CCT>TCT	p.P316S
Pat_76	Post-Resistance	MECOM	2122	37	3	168834203	168834203	Missense_Mutation	SNP	C	G	5	26	c.893G>C	c.(892-894)GGA>GCA	p.G298A
Pat_76	Post-Resistance	MECOM	2122	37	3	169098985	169098985	Missense_Mutation	SNP	T	A	9	15	c.365A>T	c.(364-366)TAT>TTT	p.Y122F
Pat_76	Post-Resistance	SKIL	6498	37	3	170078829	170078829	Missense_Mutation	SNP	G	A	17	32	c.710G>A	c.(709-711)CGA>CAA	p.R237Q
Pat_76	Post-Resistance	YEATS2	55689	37	3	183469945	183469945	Missense_Mutation	SNP	C	T	20	53	c.1054C>T	c.(1054-1056)CCT>TCT	p.P352S
Pat_76	Post-Resistance	CLCN2	1181	37	3	184069842	184069842	Missense_Mutation	SNP	G	A	58	97	c.2374C>T	c.(2374-2376)CCT>TCT	p.P792S
Pat_76	Post-Resistance	MASP1	5648	37	3	186961374	186961374	Missense_Mutation	SNP	C	T	14	44	c.1126G>A	c.(1126-1128)GGG>AGG	p.G376R
Pat_76	Post-Resistance	LEPREL1	55214	37	3	189706753	189706753	Missense_Mutation	SNP	G	A	9	37	c.898C>T	c.(898-900)CCC>TCC	p.P300S
Pat_76	Post-Resistance	ATP13A4	84239	37	3	193120506	193120506	Missense_Mutation	SNP	G	A	33	54	c.3526C>T	c.(3526-3528)CCG>TCG	p.P1176S
Pat_76	Post-Resistance	ATP13A4	84239	37	3	193158390	193158390	Missense_Mutation	SNP	G	A	7	28	c.2476C>T	c.(2476-2478)CCT>TCT	p.P826S
Pat_76	Post-Resistance	PDE6B	5158	37	4	654259	654259	Missense_Mutation	SNP	G	A	3	26	c.1471G>A	c.(1471-1473)GAG>AAG	p.E491K
Pat_76	Post-Resistance	TMEM175	84286	37	4	946167	946167	Missense_Mutation	SNP	G	A	21	35	c.391G>A	c.(391-393)GTG>ATG	p.V131M
Pat_76	Post-Resistance	OTOP1	133060	37	4	4207848	4207848	Missense_Mutation	SNP	G	A	4	13	c.550C>T	c.(550-552)CTT>TTT	p.L184F
Pat_76	Post-Resistance	MAN2B2	23324	37	4	6590881	6590881	Missense_Mutation	SNP	C	T	23	43	c.674C>T	c.(673-675)TCC>TTC	p.S225F
Pat_76	Post-Resistance	AFAP1	60312	37	4	7776536	7776537	Missense_Mutation	DNP	GG	CT	12	22	.1739_1740CC>A	c.(1738-1740)GCC>GAG	p.A580E
Pat_76	Post-Resistance	BOD1L	259282	37	4	13601911	13601911	Missense_Mutation	SNP	G	A	4	17	c.6613C>T	c.(6613-6615)CTT>TTT	p.L2205F
Pat_76	Post-Resistance	SLIT2	9353	37	4	20620619	20620619	Missense_Mutation	SNP	G	A	6	22	c.4577G>A	c.(4576-4578)AGG>AAG	p.R1526K
Pat_76	Post-Resistance	PPARGC1A	10891	37	4	23814447	23814447	Missense_Mutation	SNP	C	T	19	69	c.1942G>A	c.(1942-1944)GAA>AAA	p.E648K
Pat_76	Post-Resistance	ARAP2	116984	37	4	36149359	36149359	Missense_Mutation	SNP	G	A	3	7	c.3010C>T	c.(3010-3012)CCC>TCC	p.P1004S
Pat_76	Post-Resistance	PGM2	55276	37	4	37846170	37846170	Missense_Mutation	SNP	T	C	8	18	c.905T>C	c.(904-906)GTC>GCC	p.V302A
Pat_76	Post-Resistance	RBM47	54502	37	4	40439863	40439863	Missense_Mutation	SNP	C	T	12	27	c.1048G>A	c.(1048-1050)GAC>AAC	p.D350N
Pat_76	Post-Resistance	BEND4	389206	37	4	42119560	42119560	Missense_Mutation	SNP	C	T	3	5	c.1580G>A	c.(1579-1581)AGT>AAT	p.S527N
Pat_76	Post-Resistance	GABRA2	2555	37	4	46314655	46314655	Nonsense_Mutation	SNP	G	A	4	14	c.334C>T	c.(334-336)CGA>TGA	p.R112*
Pat_76	Post-Resistance	GABRB1	2560	37	4	47405358	47405358	Missense_Mutation	SNP	G	A	8	23	c.568G>A	c.(568-570)GAA>AAA	p.E190K
Pat_76	Post-Resistance	REST	5978	37	4	57797533	57797533	Missense_Mutation	SNP	C	T	16	69	c.2509C>T	c.(2509-2511)CTT>TTT	p.L837F
Pat_76	Post-Resistance	UGT2A3	79799	37	4	69796394	69796394	Missense_Mutation	SNP	G	A	8	24	c.1174C>T	c.(1174-1176)CCC>TCC	p.P392S
Pat_76	Post-Resistance	UGT2B11	10720	37	4	70079869	70079869	Missense_Mutation	SNP	G	A	11	26	c.572C>T	c.(571-573)CCT>CTT	p.P191L
Pat_76	Post-Resistance	UGT2B11	10720	37	4	70080370	70080370	Missense_Mutation	SNP	C	T	66	145	c.71G>A	c.(70-72)GGA>GAA	p.G24E
Pat_76	Post-Resistance	UGT2A1	10941	37	4	70455112	70455112	Missense_Mutation	SNP	C	T	7	8	c.1562G>A	c.(1561-1563)GGA>GAA	p.G521E
Pat_76	Post-Resistance	ADAMTS3	9508	37	4	73414436	73414436	Missense_Mutation	SNP	C	T	8	16	c.263G>A	c.(262-264)GGA>GAA	p.G88E
Pat_76	Post-Resistance	ANKRD17	26057	37	4	73956389	73956389	Missense_Mutation	SNP	G	A	3	19	c.6956C>T	c.(6955-6957)CCC>CTC	p.P2319L
Pat_76	Post-Resistance	RASGEF1B	153020	37	4	82377830	82377830	Missense_Mutation	SNP	G	A	7	13	c.413C>T	c.(412-414)GCT>GTT	p.A138V
Pat_76	Post-Resistance	AGPAT9	84803	37	4	84502813	84502813	Missense_Mutation	SNP	G	A	11	41	c.307G>A	c.(307-309)GGA>AGA	p.G103R
Pat_76	Post-Resistance	FAM13A	10144	37	4	89679958	89679958	Missense_Mutation	SNP	G	A	16	29	c.1673C>T	c.(1672-1674)TCC>TTC	p.S558F

Pat_76	Post-Resistance	BMPR1B	658	37	4	96052444	96052444	Missense_Mutation	SNP	C	T	5	21	c.857C>T	c.(856-858)TCC>TTC	p.S286F
Pat_76	Post-Resistance	UBE2D3	7323	37	4	103720648	103720648	Missense_Mutation	SNP	G	A	9	18	c.314C>T	c.(313-315)TCC>TTC	p.S105F
Pat_76	Post-Resistance	TET2	54790	37	4	106156166	106156166	Missense_Mutation	SNP	C	T	10	12	c.1067C>T	c.(1066-1068)TCC>TTC	p.S356F
Pat_76	Post-Resistance	TET2	54790	37	4	106157650	106157650	Missense_Mutation	SNP	C	T	15	16	c.2551C>T	c.(2551-2553)CCT>TCT	p.P851S
Pat_76	Post-Resistance	NPNT	255743	37	4	106888470	106888470	Missense_Mutation	SNP	G	A	9	9	c.1471G>A	c.(1471-1473)GGG>AGG	p.G491R
Pat_76	Post-Resistance	AGXT2L1	64850	37	4	109667970	109667970	Missense_Mutation	SNP	C	T	14	56	c.1120G>A	c.(1120-1122)GAC>AAC	p.D374N
Pat_76	Post-Resistance	ANK2	287	37	4	114257821	114257821	Missense_Mutation	SNP	G	A	10	16	c.3680G>A	c.(3679-3681)AGA>AAA	p.R1227K
Pat_76	Post-Resistance	C4orf31	79625	37	4	121957496	121957496	Missense_Mutation	SNP	C	T	22	24	c.1630G>A	c.(1630-1632)GAT>AAT	p.D544N
Pat_76	Post-Resistance	KIAA1109	84162	37	4	123237921	123237921	Missense_Mutation	SNP	C	T	8	30	c.10574C>T	c.(10573-10575)GCT>GTT	p.A3525V
Pat_76	Post-Resistance	FAT4	79633	37	4	126240894	126240894	Missense_Mutation	SNP	G	A	15	22	c.3328G>A	c.(3328-3330)GAA>AAA	p.E1110K
Pat_76	Post-Resistance	FAT4	79633	37	4	126328272	126328272	Missense_Mutation	SNP	G	A	21	50	c.5545G>A	c.(5545-5547)GAC>AAC	p.D1849N
Pat_76	Post-Resistance	FAT4	79633	37	4	126329641	126329641	Missense_Mutation	SNP	G	A	19	40	c.5612G>A	c.(5611-5613)GGT>GAT	p.G1871D
Pat_76	Post-Resistance	PLK4	10733	37	4	128814932	128814933	Missense_Mutation	DNP	CC	TT	23	71	.2458_2459CC>T	c.(2458-2460)CCT>TTT	p.P820F
Pat_76	Post-Resistance	TBC1D9	23158	37	4	141578759	141578759	Missense_Mutation	SNP	G	A	41	107	c.2129C>T	c.(2128-2130)GCC>GTC	p.A710V
Pat_76	Post-Resistance	HHIP	64399	37	4	145573802	145573802	Missense_Mutation	SNP	G	A	14	31	c.325G>A	c.(325-327)GAA>AAA	p.E109K
Pat_76	Post-Resistance	FHDC1	85462	37	4	153897274	153897274	Missense_Mutation	SNP	C	T	5	15	c.2831C>T	c.(2830-2832)TCC>TTC	p.S944F
Pat_76	Post-Resistance	DCHS2	54798	37	4	155298497	155298497	Missense_Mutation	SNP	C	T	14	26	c.334G>A	c.(334-336)GAC>AAC	p.D112N
Pat_76	Post-Resistance	GUCY1A3	2982	37	4	156651237	156651237	Missense_Mutation	SNP	C	T	9	41	c.1927C>T	c.(1927-1929)CCA>TCA	p.P643S
Pat_76	Post-Resistance	GUCY1B3	2983	37	4	156725790	156725791	Missense_Mutation	DNP	GG	AA	12	23	.1600_1601GG>A	c.(1600-1602)GGA>AAA	p.G534K
Pat_76	Post-Resistance	GLRB	2743	37	4	158041814	158041814	Missense_Mutation	SNP	G	A	7	15	c.229G>A	c.(229-231)GGC>AGC	p.G77S
Pat_76	Post-Resistance	GLRB	2743	37	4	158057831	158057831	Missense_Mutation	SNP	G	A	8	23	c.508G>A	c.(508-510)GAT>AAT	p.D170N
Pat_76	Post-Resistance	DDX60	55601	37	4	169146695	169146696	Missense_Mutation	DNP	GG	AA	5	20	.4665_4666CC>T	663-4668)CTCCCA>CTTT	p.P1556S
Pat_76	Post-Resistance	MORF4	10934	37	4	174537317	174537317	Missense_Mutation	SNP	C	T	31	70	c.478G>A	c.(478-480)GAT>AAT	p.D160N
Pat_76	Post-Resistance	MORF4	10934	37	4	174537505	174537505	Missense_Mutation	SNP	G	A	28	73	c.290C>T	c.(289-291)CCT>CTT	p.P97L
Pat_76	Post-Resistance	ADAM29	11086	37	4	175896821	175896821	Missense_Mutation	SNP	C	T	5	17	c.145C>T	c.(145-147)CCA>TCA	p.P49S
Pat_76	Post-Resistance	ODZ3	55714	37	4	183600893	183600893	Missense_Mutation	SNP	A	T	17	18	c.1401A>T	c.(1399-1401)AGA>AGT	p.R467S
Pat_76	Post-Resistance	ODZ3	55714	37	4	183714966	183714966	Missense_Mutation	SNP	C	T	5	7	c.7141C>T	c.(7141-7143)CCT>TCT	p.P2381S
Pat_76	Post-Resistance	C4orf41	60684	37	4	184600505	184600505	Splice_Site	SNP	G	A	8	13	c.832_splice	c.e9-1	p.I278_splice
Pat_76	Post-Resistance	ZFP42	132625	37	4	188924469	188924469	Missense_Mutation	SNP	G	A	13	58	c.508G>A	c.(508-510)GAA>AAA	p.E170K
Pat_76	Post-Resistance	TRIML1	339976	37	4	189061047	189061047	Missense_Mutation	SNP	G	A	8	15	c.335G>A	c.(334-336)GGA>GAA	p.G112E
Pat_76	Post-Resistance	PLEKHG4B	153478	37	5	151653	151653	Missense_Mutation	SNP	G	A	7	25	c.863G>A	c.(862-864)AGT>AAT	p.S288N
Pat_76	Post-Resistance	BRD9	65980	37	5	865586	865586	Missense_Mutation	SNP	G	A	15	34	c.1636C>T	c.(1636-1638)CCG>TCG	p.P546S
Pat_76	Post-Resistance	DNAH5	1767	37	5	13719036	13719036	Missense_Mutation	SNP	C	T	15	48	c.12454G>A	c.(12454-12456)GAT>AAT	p.D4152N
Pat_76	Post-Resistance	DNAH5	1767	37	5	13901602	13901602	Missense_Mutation	SNP	G	A	6	8	c.1811C>T	c.(1810-1812)TCA>TTA	p.S604L
Pat_76	Post-Resistance	TRIO	7204	37	5	14497016	14497016	Missense_Mutation	SNP	C	T	17	28	c.7909C>T	c.(7909-7911)CGT>TGT	p.R2637C
Pat_76	Post-Resistance	CDH6	1004	37	5	31294126	31294126	Missense_Mutation	SNP	G	A	5	12	c.286G>A	c.(286-288)GGA>AGA	p.G96R
Pat_76	Post-Resistance	RAD1	5810	37	5	34911678	34911678	Missense_Mutation	SNP	G	A	19	41	c.547C>T	c.(547-549)CCT>TCT	p.P183S
Pat_76	Post-Resistance	PRLR	5618	37	5	35065850	35065850	Missense_Mutation	SNP	G	A	19	58	c.1210C>T	c.(1210-1212)CCC>TCC	p.P404S
Pat_76	Post-Resistance	PRLR	5618	37	5	35065883	35065883	Missense_Mutation	SNP	C	T	16	28	c.1177G>A	c.(1177-1179)GAC>AAC	p.D393N
Pat_76	Post-Resistance	SPEF2	79925	37	5	35667216	35667216	Missense_Mutation	SNP	C	T	7	7	c.1210C>T	c.(1210-1212)CTT>TTT	p.L404F
Pat_76	Post-Resistance	IL7R	3575	37	5	35876456	35876457	Missense_Mutation	DNP	CC	TT	9	22	.1248_1249CC>T	246-1251)CCCCCT>CCTT	p.P417S
Pat_76	Post-Resistance	UGT3A2	167127	37	5	36064452	36064453	Splice_Site	DNP	CC	TT	4	14	c.95_splice	c.e2-1	p.G32_splice
Pat_76	Post-Resistance	EGFLAM	133584	37	5	38406257	38406257	Missense_Mutation	SNP	G	A	12	13	c.742G>A	c.(742-744)GGA>AGA	p.G248R
Pat_76	Post-Resistance	PTGER4	5734	37	5	40681235	40681235	Missense_Mutation	SNP	A	T	24	45	c.140A>T	c.(139-141)AAG>ATG	p.K47M
Pat_76	Post-Resistance	C7	730	37	5	40934512	40934512	Missense_Mutation	SNP	C	T	14	49	c.224C>T	c.(223-225)CCT>CTT	p.P75L
Pat_76	Post-Resistance	HEATR7B2	133558	37	5	41000395	41000395	Missense_Mutation	SNP	C	T	9	17	c.4409G>A	c.(4408-4410)GGG>GAG	p.G1470E
Pat_76	Post-Resistance	C6	729	37	5	41149409	41149409	Missense_Mutation	SNP	A	G	27	59	c.2557T>C	c.(2557-2559)TCA>CCA	p.S853P

Pat_76	Post-Resistance	PARP8	79668	37	5	50090751	50090751	Missense_Mutation	SNP	G	A	13	24	c.928G>A	c.(928-930)GGA>AGA	p.G310R
Pat_76	Post-Resistance	ADAMTS6	11174	37	5	64511271	64511271	Nonsense_Mutation	SNP	C	T	9	14	c.2316G>A	c.(2314-2316)TGG>TGA	p.W772*
Pat_76	Post-Resistance	ADAMTS6	11174	37	5	64522007	64522008	Missense_Mutation	DNP	CC	TT	10	29	.1972_1973GG>A	c.(1972-1974)GGT>AAT	p.G658N
Pat_76	Post-Resistance	IQGAP2	10788	37	5	75858277	75858277	Missense_Mutation	SNP	G	A	9	28	c.203G>A	c.(202-204)GGG>GAG	p.G68E
Pat_76	Post-Resistance	GPR98	84059	37	5	90106784	90106784	Missense_Mutation	SNP	G	A	15	14	c.15707G>A	.(15706-15708)GGC>GA	p.G5236D
Pat_76	Post-Resistance	PCSK1	5122	37	5	95733081	95733081	Missense_Mutation	SNP	C	T	3	18	c.1681G>A	c.(1681-1683)GAG>AAG	p.E561K
Pat_76	Post-Resistance	RIOK2	55781	37	5	96514819	96514819	Missense_Mutation	SNP	A	T	8	11	c.145T>A	c.(145-147)TGT>AGT	p.C49S
Pat_76	Post-Resistance	SLCO4C1	353189	37	5	101585427	101585427	Missense_Mutation	SNP	T	A	9	22	c.1535A>T	c.(1534-1536)TAT>TTT	p.Y512F
Pat_76	Post-Resistance	CAMK4	814	37	5	110818528	110818528	Missense_Mutation	SNP	T	A	19	26	c.874T>A	c.(874-876)TTT>ATT	p.F292I
Pat_76	Post-Resistance	FEM1C	56929	37	5	114860426	114860426	Missense_Mutation	SNP	C	T	15	40	c.1433G>A	c.(1432-1434)AGG>AAG	p.R478K
Pat_76	Post-Resistance	SEMA6A	57556	37	5	115783483	115783483	Missense_Mutation	SNP	T	G	3	10	c.1919A>C	c.(1918-1920)AAA>ACA	p.K640T
Pat_76	Post-Resistance	FAM170A	340069	37	5	118969718	118969718	Missense_Mutation	SNP	G	A	10	28	c.275G>A	c.(274-276)CGA>CAA	p.R92Q
Pat_76	Post-Resistance	FTMT	94033	37	5	121188022	121188022	Missense_Mutation	SNP	G	A	4	16	c.364G>A	c.(364-366)GAG>AAG	p.E122K
Pat_76	Post-Resistance	SNCAIP	9627	37	5	121758806	121758806	Missense_Mutation	SNP	G	A	4	6	c.374G>A	c.(373-375)GGA>GAA	p.G125E
Pat_76	Post-Resistance	SNCAIP	9627	37	5	121761092	121761092	Missense_Mutation	SNP	G	A	20	48	c.1048G>A	c.(1048-1050)GGA>AGA	p.G350R
Pat_76	Post-Resistance	SNCAIP	9627	37	5	121761194	121761194	Missense_Mutation	SNP	G	A	18	39	c.1150G>A	c.(1150-1152)GAG>AAG	p.E384K
Pat_76	Post-Resistance	FBN2	2201	37	5	127626457	127626457	Missense_Mutation	SNP	C	T	17	36	c.6412G>A	c.(6412-6414)GAC>AAC	p.D2138N
Pat_76	Post-Resistance	DDX46	9879	37	5	134131837	134131837	Missense_Mutation	SNP	G	A	4	17	c.1951G>A	c.(1951-1953)GGA>AGA	p.G651R
Pat_76	Post-Resistance	TGFBI	7045	37	5	135388802	135388802	Missense_Mutation	SNP	G	A	6	15	c.1120G>A	c.(1120-1122)GAC>AAC	p.D374N
Pat_76	Post-Resistance	KLHL3	26249	37	5	137028094	137028094	Missense_Mutation	SNP	G	A	14	26	c.406C>T	c.(406-408)CGG>TGG	p.R136W
Pat_76	Post-Resistance	LRRTM2	26045	37	5	138209183	138209183	Missense_Mutation	SNP	C	T	10	24	c.1067G>A	c.(1066-1068)GGA>GAA	p.G356E
Pat_76	Post-Resistance	IK	3550	37	5	140032614	140032614	Missense_Mutation	SNP	G	A	9	27	c.289G>A	c.(289-291)GAG>AAG	p.E97K
Pat_76	Post-Resistance	PCDHA4	56144	37	5	140186787	140186788	Nonsense_Mutation	DNP	GG	AA	11	45	c.15_16GG>AA	.(13-18)TGGGGA>TGAAG	p.5_6WG>*R
Pat_76	Post-Resistance	PCDHA4	56144	37	5	140188520	140188520	Nonsense_Mutation	SNP	G	A	17	35	c.1748G>A	c.(1747-1749)TGG>TAG	p.W583*
Pat_76	Post-Resistance	PCDHA7	56141	37	5	140214158	140214158	Missense_Mutation	SNP	T	A	56	123	c.190T>A	c.(190-192)TTC>ATC	p.F64I
Pat_76	Post-Resistance	PCDHA8	56140	37	5	140222893	140222893	Missense_Mutation	SNP	G	A	30	57	c.1987G>A	c.(1987-1989)GCC>ACC	p.A663T
Pat_76	Post-Resistance	PCDHA10	56139	37	5	140237626	140237626	Missense_Mutation	SNP	C	T	9	17	c.1993C>T	c.(1993-1995)CTT>TTT	p.L665F
Pat_76	Post-Resistance	PCDHAC2	56134	37	5	140347871	140347871	Missense_Mutation	SNP	C	T	26	31	c.1520C>T	c.(1519-1521)TCC>TTC	p.S507F
Pat_76	Post-Resistance	PCDHB1	29930	37	5	140431731	140431731	Missense_Mutation	SNP	G	A	3	3	c.676G>A	c.(676-678)GCT>ACT	p.A226T
Pat_76	Post-Resistance	PCDHB1	29930	37	5	140432475	140432475	Missense_Mutation	SNP	G	A	5	26	c.1420G>A	c.(1420-1422)GTC>ATC	p.V474I
Pat_76	Post-Resistance	PCDHB2	56133	37	5	140474589	140474589	Missense_Mutation	SNP	G	A	10	16	c.215G>A	c.(214-216)GGA>GAA	p.G72E
Pat_76	Post-Resistance	PCDHB3	56132	37	5	140481729	140481729	Missense_Mutation	SNP	C	T	23	83	c.1496C>T	c.(1495-1497)CCC>CTC	p.P499L
Pat_76	Post-Resistance	PCDHB6	56130	37	5	140530292	140530292	Missense_Mutation	SNP	C	T	44	100	c.454C>T	c.(454-456)CCT>TCT	p.P152S
Pat_76	Post-Resistance	PCDHB6	56130	37	5	140532002	140532002	Missense_Mutation	SNP	C	T	43	95	c.2164C>T	c.(2164-2166)CGC>TGC	p.R722C
Pat_76	Post-Resistance	PCDHB7	56129	37	5	140554046	140554046	Missense_Mutation	SNP	G	A	10	21	c.1630G>A	c.(1630-1632)GAG>AAG	p.E544K
Pat_76	Post-Resistance	PCDHB16	57717	37	5	140562564	140562564	Missense_Mutation	SNP	G	A	7	9	c.430G>A	c.(430-432)GAA>AAA	p.E144K
Pat_76	Post-Resistance	PCDHB16	57717	37	5	140562910	140562910	Missense_Mutation	SNP	C	T	19	29	c.776C>T	c.(775-777)TCC>TTC	p.S259F
Pat_76	Post-Resistance	PCDHB9	56127	37	5	140567229	140567229	Missense_Mutation	SNP	C	T	3	31	c.337C>T	c.(337-339)CCC>TCC	p.P113S
Pat_76	Post-Resistance	PCDHB9	56127	37	5	140568021	140568021	Missense_Mutation	SNP	G	A	5	2	c.1129G>A	c.(1129-1131)GAA>AAA	p.E377K
Pat_76	Post-Resistance	PCDHB10	56126	37	5	140572462	140572462	Missense_Mutation	SNP	C	T	8	23	c.337C>T	c.(337-339)CCC>TCC	p.P113S
Pat_76	Post-Resistance	PCDHGA1	56114	37	5	140712307	140712307	Missense_Mutation	SNP	G	A	44	78	c.2056G>A	c.(2056-2058)GAT>AAT	p.D686N
Pat_76	Post-Resistance	PCDHGA2	56113	37	5	140719019	140719019	Missense_Mutation	SNP	G	A	28	41	c.481G>A	c.(481-483)GAC>AAC	p.D161N
Pat_76	Post-Resistance	PCDHGA9	56107	37	5	140782892	140782892	Missense_Mutation	SNP	G	A	14	42	c.373G>A	c.(373-375)GAT>AAT	p.D125N
Pat_76	Post-Resistance	SH3RF2	153769	37	5	145379890	145379890	Missense_Mutation	SNP	G	T	3	13	c.648G>T	c.(646-648)AAG>AAT	p.K216N
Pat_76	Post-Resistance	PDGFRB	5159	37	5	149499118	149499118	Missense_Mutation	SNP	A	C	25	44	c.2710T>G	c.(2710-2712)TAC>GAC	p.Y904D
Pat_76	Post-Resistance	GLRA1	2741	37	5	151271938	151271938	Missense_Mutation	SNP	C	T	8	21	c.118G>A	c.(118-120)GAT>AAT	p.D40N
Pat_76	Post-Resistance	GALNT10	55568	37	5	153709295	153709295	Nonsense_Mutation	SNP	C	T	5	20	c.565C>T	c.(565-567)CGA>TGA	p.R189*

Pat_76	Post-Resistance	KIF4B	285643	37	5	154393439	154393439	Missense_Mutation	SNP	G	A	25	78	c.20G>A	c.(19-21)GGA>GAA	p.G7E
Pat_76	Post-Resistance	KIF4B	285643	37	5	154396219	154396219	Missense_Mutation	SNP	C	T	10	26	c.2800C>T	c.(2800-2802)CTT>TTT	p.L934F
Pat_76	Post-Resistance	CYFIP2	26999	37	5	156819926	156819926	Missense_Mutation	SNP	C	T	29	44	c.3680C>T	c.(3679-3681)TCC>TTC	p.S1227F
Pat_76	Post-Resistance	GABRB2	2561	37	5	160721303	160721303	Missense_Mutation	SNP	G	A	11	19	c.1324C>T	c.(1324-1326)CGG>TGG	p.R442W
Pat_76	Post-Resistance	ODZ2	57451	37	5	167420012	167420013	Missense_Mutation	DNP	CC	TT	28	49	.1011_1012CC>T	1009-1014)TACCCT>TATT	p.P338S
Pat_76	Post-Resistance	CPLX2	10814	37	5	175306947	175306947	Missense_Mutation	SNP	C	T	11	13	c.304C>T	c.(304-306)CCT>TCT	p.P102S
Pat_76	Post-Resistance	MXD3	83463	37	5	176734669	176734669	Missense_Mutation	SNP	C	T	25	44	c.541G>A	c.(541-543)GGG>AGG	p.G181R
Pat_76	Post-Resistance	ZNF454	285676	37	5	178392376	178392376	Missense_Mutation	SNP	G	A	4	22	c.971G>A	c.(970-972)GGA>GAA	p.G324E
Pat_76	Post-Resistance	RUFY1	80230	37	5	179025788	179025788	Missense_Mutation	SNP	G	A	28	79	c.1727G>A	c.(1726-1728)AGG>AAG	p.R576K
Pat_76	Post-Resistance	TBC1D9B	23061	37	5	179292874	179292874	Missense_Mutation	SNP	C	T	25	41	c.2929G>A	c.(2929-2931)GAA>AAA	p.E977K
Pat_76	Post-Resistance	RASGEF1C	255426	37	5	179545807	179545807	Missense_Mutation	SNP	C	T	10	27	c.967G>A	c.(967-969)GCC>ACC	p.A323T
Pat_76	Post-Resistance	DSP	1832	37	6	7569516	7569516	Missense_Mutation	SNP	C	T	25	45	c.1517C>T	c.(1516-1518)CCC>CTC	p.P506L
Pat_76	Post-Resistance	HDGFL1	154150	37	6	22569943	22569943	Missense_Mutation	SNP	G	A	9	35	c.139G>A	c.(139-141)GAG>AAG	p.E47K
Pat_76	Post-Resistance	HIST1H1D	3007	37	6	26234911	26234911	Missense_Mutation	SNP	C	T	7	36	c.251G>A	c.(250-252)GGC>GAC	p.G84D
Pat_76	Post-Resistance	BTN3A3	10384	37	6	26452269	26452269	Missense_Mutation	SNP	G	A	11	26	c.1385G>A	c.(1384-1386)GGG>GAG	p.G462E
Pat_76	Post-Resistance	SCAND3	114821	37	6	28543719	28543719	Missense_Mutation	SNP	C	T	4	20	c.763G>A	c.(763-765)GAA>AAA	p.E255K
Pat_76	Post-Resistance	OR2J2	26707	37	6	29142001	29142001	Missense_Mutation	SNP	G	A	18	28	c.589G>A	c.(589-591)GAG>AAG	p.E197K
Pat_76	Post-Resistance	OR2H1	26716	37	6	29429955	29429955	Missense_Mutation	SNP	C	T	52	144	c.409C>T	c.(409-411)CGC>TGC	p.R137C
Pat_76	Post-Resistance	HLA-L	3139	37	6	30231076	30231076	Missense_Mutation	SNP	G	A	29	89	c.520G>A	c.(520-522)GGT>AGT	p.G174S
Pat_76	Post-Resistance	KIAA1949	170954	37	6	30645059	30645059	Missense_Mutation	SNP	G	A	25	48	c.1829C>T	c.(1828-1830)TCC>TTC	p.S610F
Pat_76	Post-Resistance	C6orf15	29113	37	6	31079874	31079874	Missense_Mutation	SNP	G	A	7	17	c.262C>T	c.(262-264)CCA>TCA	p.P88S
Pat_76	Post-Resistance	LY6G6F	259215	37	6	31675497	31675498	Missense_Mutation	DNP	GT	TA	4	18	c.315_316GT>TA	313-318)TGGTGC>TGTA	105_106WC>
Pat_76	Post-Resistance	NEU1	4758	37	6	31827660	31827660	Nonsense_Mutation	SNP	G	A	43	80	c.1084C>T	c.(1084-1086)CAG>TAG	p.Q362*
Pat_76	Post-Resistance	SKIV2L	6499	37	6	31935813	31935813	Nonsense_Mutation	SNP	G	T	3	18	c.2812G>T	c.(2812-2814)GAG>TAG	p.E938*
Pat_76	Post-Resistance	C4A	720	37	6	31996291	31996291	Missense_Mutation	SNP	C	T	28	68	c.3212C>T	c.(3211-3213)TCA>TTA	p.S1071L
Pat_76	Post-Resistance	NOTCH4	4855	37	6	32180981	32180981	Missense_Mutation	SNP	G	A	9	14	c.2369C>T	c.(2368-2370)TCC>TTC	p.S790F
Pat_76	Post-Resistance	C6orf10	10665	37	6	32260979	32260979	Missense_Mutation	SNP	C	T	13	25	c.1471G>A	c.(1471-1473)GAG>AAG	p.E491K
Pat_76	Post-Resistance	C6orf10	10665	37	6	32261012	32261012	Missense_Mutation	SNP	C	T	13	60	c.1438G>A	c.(1438-1440)GTA>ATA	p.V480I
Pat_76	Post-Resistance	C6orf10	10665	37	6	32261248	32261248	Missense_Mutation	SNP	C	T	10	37	c.1202G>A	c.(1201-1203)AGG>AAG	p.R401K
Pat_76	Post-Resistance	HLA-DRB1	3123	37	6	32548562	32548562	Missense_Mutation	SNP	G	A	9	59	c.724C>T	c.(724-726)CTT>TTT	p.L242F
Pat_76	Post-Resistance	COL11A2	1302	37	6	33138658	33138658	Missense_Mutation	SNP	C	T	22	35	c.3403G>A	c.(3403-3405)GGA>AGA	p.G1135R
Pat_76	Post-Resistance	DAXX	1616	37	6	33287202	33287202	Missense_Mutation	SNP	G	A	28	65	c.1895C>T	c.(1894-1896)TCT>TTT	p.S632F
Pat_76	Post-Resistance	TULP1	7287	37	6	35477652	35477652	Missense_Mutation	SNP	C	T	17	31	c.553G>A	c.(553-555)GAA>AAA	p.E185K
Pat_76	Post-Resistance	DNAH8	1769	37	6	38905837	38905837	Missense_Mutation	SNP	C	A	12	23	c.11000C>A	c.(10999-11001)GCT>GAT	p.A3667D
Pat_76	Post-Resistance	DNAH8	1769	37	6	38906638	38906638	Missense_Mutation	SNP	G	A	3	12	c.11230G>A	c.(11230-11232)GTT>ATT	p.V3744I
Pat_76	Post-Resistance	DNAH8	1769	37	6	38998080	38998080	Missense_Mutation	SNP	C	T	12	46	c.13385C>T	c.(13384-13386)ACC>ATC	p.T4462I
Pat_76	Post-Resistance	GLP1R	2740	37	6	39040780	39040780	Missense_Mutation	SNP	C	T	12	32	c.652C>T	c.(652-654)CTC>TTC	p.L218F
Pat_76	Post-Resistance	TREM2	54209	37	6	41126761	41126762	Missense_Mutation	DNP	GG	AA	5	6	c.525_526CC>TT	(523-528)ATCCTT>ATTTT	p.L176F
Pat_76	Post-Resistance	TREML2	79865	37	6	41162514	41162514	Missense_Mutation	SNP	C	T	10	30	c.434G>A	c.(433-435)GGA>GAA	p.G145E
Pat_76	Post-Resistance	TTBK1	84630	37	6	43250765	43250765	Missense_Mutation	SNP	G	A	3	9	c.2287G>A	c.(2287-2289)GAG>AAG	p.E763K
Pat_76	Post-Resistance	HSP90AB1	3326	37	6	44218846	44218846	Missense_Mutation	SNP	C	T	20	49	c.1019C>T	c.(1018-1020)CCC>CTC	p.P340L
Pat_76	Post-Resistance	GPR116	221395	37	6	46849828	46849828	Missense_Mutation	SNP	C	T	22	59	c.629G>A	c.(628-630)GGA>GAA	p.G210E
Pat_76	Post-Resistance	GPR111	222611	37	6	47648023	47648023	Missense_Mutation	SNP	G	A	22	49	c.688G>A	c.(688-690)GAT>AAT	p.D230N
Pat_76	Post-Resistance	GPR111	222611	37	6	47649928	47649928	Missense_Mutation	SNP	T	G	5	10	c.1633T>G	c.(1633-1635)TAT>GAT	p.Y545D
Pat_76	Post-Resistance	GPR115	221393	37	6	47684567	47684567	Missense_Mutation	SNP	C	T	6	29	c.1958C>T	c.(1957-1959)ACC>ATC	p.T653I
Pat_76	Post-Resistance	PKHD1	5314	37	6	51524392	51524393	Missense_Mutation	DNP	CC	TT	6	13	10531_10532GG>	c.(10531-10533)GGG>AA	p.G3511K
Pat_76	Post-Resistance	BAI3	577	37	6	69646453	69646453	Missense_Mutation	SNP	C	T	4	17	c.911C>T	c.(910-912)TCG>TTG	p.S304L

Pat_76	Post-Resistance	COL9A1	1297	37	6	70984444	70984444	Missense_Mutation	SNP	G	A	9	14	c.1007C>T	c.(1006-1008)TCC>TTC	p.S336F
Pat_76	Post-Resistance	COL9A1	1297	37	6	70991139	70991139	Missense_Mutation	SNP	G	A	3	12	c.830C>T	c.(829-831)CCC>CTC	p.P277L
Pat_76	Post-Resistance	IMPG1	3617	37	6	76731904	76731904	Missense_Mutation	SNP	G	A	5	25	c.595C>T	c.(595-597)CTC>TTC	p.L199F
Pat_76	Post-Resistance	HTR1B	3351	37	6	78173077	78173077	Missense_Mutation	SNP	C	T	6	28	c.44G>A	c.(43-45)GGC>GAC	p.G15D
Pat_76	Post-Resistance	ME1	4199	37	6	83933652	83933652	Missense_Mutation	SNP	C	T	5	16	c.1276G>A	c.(1276-1278)GGA>AGA	p.G426R
Pat_76	Post-Resistance	TBX18	9096	37	6	85466491	85466492	Missense_Mutation	DNP	CC	TT	6	30	c.695_696GG>AA	c.(694-696)GGG>GAA	p.G232E
Pat_76	Post-Resistance	NT5E	4907	37	6	86180955	86180955	Missense_Mutation	SNP	G	A	3	4	c.563G>A	c.(562-564)GGG>GAG	p.G188E
Pat_76	Post-Resistance	EPHA7	2045	37	6	93955105	93955105	Nonsense_Mutation	SNP	C	T	8	18	c.2793G>A	c.(2791-2793)TGG>TGA	p.W931*
Pat_76	Post-Resistance	EPHA7	2045	37	6	93956552	93956552	Missense_Mutation	SNP	C	T	9	22	c.2684G>A	c.(2683-2685)CGA>CAA	p.R895Q
Pat_76	Post-Resistance	KIAA0776	23376	37	6	97000533	97000533	Missense_Mutation	SNP	C	T	4	12	c.2161C>T	c.(2161-2163)CCA>TCA	p.P721S
Pat_76	Post-Resistance	GRIK2	2898	37	6	102307279	102307279	Missense_Mutation	SNP	G	A	3	19	c.1435G>A	c.(1435-1437)GAA>AAA	p.E479K
Pat_76	Post-Resistance	GRIK2	2898	37	6	102372501	102372501	Missense_Mutation	SNP	C	T	17	30	c.1774C>T	c.(1774-1776)CCA>TCA	p.P592S
Pat_76	Post-Resistance	SOBP	55084	37	6	107827494	107827494	Missense_Mutation	SNP	C	T	22	70	c.284C>T	c.(283-285)CCA>CTA	p.P95L
Pat_76	Post-Resistance	SEC63	11231	37	6	108279182	108279182	Missense_Mutation	SNP	C	T	27	115	c.32G>A	c.(31-33)AGT>AAT	p.S11N
Pat_76	Post-Resistance	ARMC2	84071	37	6	109220963	109220963	Missense_Mutation	SNP	G	A	4	14	c.815G>A	c.(814-816)AGG>AAG	p.R272K
Pat_76	Post-Resistance	HDAC2	3066	37	6	114274532	114274532	Missense_Mutation	SNP	C	T	4	26	c.830G>A	c.(829-831)GGT>GAT	p.G277D
Pat_76	Post-Resistance	FRK	2444	37	6	116263590	116263590	Missense_Mutation	SNP	T	C	13	23	c.1505A>G	c.(1504-1506)AAC>AGC	p.N502S
Pat_76	Post-Resistance	DSE	29940	37	6	116758336	116758336	Missense_Mutation	SNP	G	A	3	28	c.2705G>A	c.(2704-2706)AGG>AAG	p.R902K
Pat_76	Post-Resistance	RFX6	222546	37	6	117240459	117240460	Splice_Site	DNP	GG	AA	11	17	c.1182_splice	c.e11+1	p.Q394_splice
Pat_76	Post-Resistance	RFX6	222546	37	6	117248514	117248514	Missense_Mutation	SNP	G	C	7	30	c.2210G>C	c.(2209-2211)AGA>ACA	p.R737T
Pat_76	Post-Resistance	C6orf170	221322	37	6	121481215	121481215	Missense_Mutation	SNP	G	A	14	32	c.2714C>T	c.(2713-2715)TCA>TTA	p.S905L
Pat_76	Post-Resistance	C6orf58	352999	37	6	127898569	127898569	Missense_Mutation	SNP	C	T	8	72	c.239C>T	c.(238-240)CCA>CTA	p.P80L
Pat_76	Post-Resistance	PTPRK	5796	37	6	128304508	128304508	Missense_Mutation	SNP	C	T	16	37	c.3263G>A	c.(3262-3264)CGA>CAA	p.R1088Q
Pat_76	Post-Resistance	LAMA2	3908	37	6	129802517	129802517	Missense_Mutation	SNP	G	A	26	58	c.7682G>A	c.(7681-7683)GGC>GAC	p.G2561D
Pat_76	Post-Resistance	C6orf191	253582	37	6	130166939	130166939	Missense_Mutation	SNP	G	A	22	53	c.92C>T	c.(91-93)TCC>TTC	p.S31F
Pat_76	Post-Resistance	ENPP3	5169	37	6	131973708	131973708	Missense_Mutation	SNP	C	T	31	67	c.304C>T	c.(304-306)CGT>TGT	p.R102C
Pat_76	Post-Resistance	ENPP3	5169	37	6	131995347	131995347	Missense_Mutation	SNP	G	A	13	12	c.688G>A	c.(688-690)GAT>AAT	p.D230N
Pat_76	Post-Resistance	TAAR8	83551	37	6	132874774	132874774	Missense_Mutation	SNP	C	T	6	25	c.943C>T	c.(943-945)CCT>TCT	p.P315S
Pat_76	Post-Resistance	AHI1	54806	37	6	135754272	135754272	Missense_Mutation	SNP	G	A	17	31	c.2159C>T	c.(2158-2160)TCC>TTC	p.S720F
Pat_76	Post-Resistance	BCLAF1	9774	37	6	136599690	136599690	Missense_Mutation	SNP	G	A	7	45	c.329C>T	c.(328-330)TCA>TTA	p.S110L
Pat_76	Post-Resistance	MAP7	9053	37	6	136680963	136680963	Missense_Mutation	SNP	C	T	26	66	c.1907G>A	c.(1906-1908)GGA>GAA	p.G636E
Pat_76	Post-Resistance	MAP7	9053	37	6	136681842	136681842	Missense_Mutation	SNP	C	T	64	125	c.1796G>A	c.(1795-1797)AGA>AAA	p.R599K
Pat_76	Post-Resistance	KIAA1244	57221	37	6	138619758	138619758	Missense_Mutation	SNP	G	A	7	7	c.3664G>A	c.(3664-3666)GAA>AAA	p.E1222K
Pat_76	Post-Resistance	PLAGL1	5325	37	6	144263084	144263084	Missense_Mutation	SNP	G	A	11	27	c.869C>T	c.(868-870)TCC>TTC	p.S290F
Pat_76	Post-Resistance	UTRN	7402	37	6	145156938	145156938	Nonsense_Mutation	SNP	C	T	52	134	c.9688C>T	c.(9688-9690)CAG>TAG	p.Q3230*
Pat_76	Post-Resistance	FBXL18	80028	37	7	5540452	5540452	Missense_Mutation	SNP	G	T	9	33	c.1448C>A	c.(1447-1449)CCC>CAC	p.P483H
Pat_76	Post-Resistance	C7orf26	79034	37	7	6639796	6639796	Missense_Mutation	SNP	C	T	13	16	c.917C>T	c.(916-918)ACC>ATC	p.T306I
Pat_76	Post-Resistance	COL28A1	340267	37	7	7457519	7457519	Missense_Mutation	SNP	G	A	22	34	c.2107C>T	c.(2107-2109)CCC>TCC	p.P703S
Pat_76	Post-Resistance	ETV1	2115	37	7	13971333	13971333	Missense_Mutation	SNP	G	A	9	21	c.596C>T	c.(595-597)CCT>CTT	p.P199L
Pat_76	Post-Resistance	AHR	196	37	7	17349748	17349748	Splice_Site	SNP	G	A	3	16	c.253_splice	c.e2+1	p.V85_splice
Pat_76	Post-Resistance	HDAC9	9734	37	7	18975562	18975562	Missense_Mutation	SNP	T	G	23	21	c.2925T>G	c.(2923-2925)AAT>AAG	p.N975K
Pat_76	Post-Resistance	TWISTNB	221830	37	7	19748518	19748518	Missense_Mutation	SNP	A	C	15	13	c.122T>G	c.(121-123)GTG>GGG	p.V41G
Pat_76	Post-Resistance	DNAH11	8701	37	7	21639612	21639612	Missense_Mutation	SNP	C	T	3	19	c.2875C>T	c.(2875-2877)CCT>TCT	p.P959S
Pat_76	Post-Resistance	STK31	56164	37	7	23827672	23827672	Missense_Mutation	SNP	C	T	16	54	c.2561C>T	c.(2560-2562)TCA>TTA	p.S854L
Pat_76	Post-Resistance	GARS	2617	37	7	30656730	30656730	Missense_Mutation	SNP	G	A	10	89	c.1195G>A	c.(1195-1197)GGT>AGT	p.G399S
Pat_76	Post-Resistance	BMPER	168667	37	7	34118765	34118765	Missense_Mutation	SNP	G	A	22	94	c.1375G>A	c.(1375-1377)GAT>AAT	p.D459N
Pat_76	Post-Resistance	POU6F2	11281	37	7	39446295	39446295	Missense_Mutation	SNP	C	T	23	25	c.982C>T	c.(982-984)CTT>TTT	p.L328F

Pat_76	Post-Resistance	C7orf36	57002	37	7	39612174	39612174	Missense_Mutation	SNP	G	A	13	55	c.550G>A	c.(550-552)GAA>AAA	p.E184K
Pat_76	Post-Resistance	GLI3	2737	37	7	42065985	42065985	Missense_Mutation	SNP	G	A	5	20	c.1055C>T	c.(1054-1056)TCC>TTC	p.S352F
Pat_76	Post-Resistance	C7orf44	55744	37	7	43687203	43687203	Missense_Mutation	SNP	C	T	7	34	c.46G>A	c.(46-48)GGA>AGA	p.G16R
Pat_76	Post-Resistance	PGAM2	5224	37	7	44105164	44105164	Splice_Site	SNP	G	A	30	26	c.-34_splice	c.e1-1	
Pat_76	Post-Resistance	NPC1L1	29881	37	7	44579071	44579071	Missense_Mutation	SNP	G	A	28	76	c.925C>T	c.(925-927)CCC>TCC	p.P309S
Pat_76	Post-Resistance	PKD1L1	168507	37	7	47917146	47917146	Missense_Mutation	SNP	G	A	79	78	c.3604C>T	c.(3604-3606)CCC>TCC	p.P1202S
Pat_76	Post-Resistance	UPP1	7378	37	7	48139273	48139274	Missense_Mutation	DNP	CC	TT	10	21	c.51_52CC>TT	.(49-54)TGCCCC>TGTTC	p.P18S
Pat_76	Post-Resistance	ABCA13	154664	37	7	48311987	48311987	Missense_Mutation	SNP	G	T	7	24	c.2724G>T	c.(2722-2724)TTG>TTT	p.L908F
Pat_76	Post-Resistance	ABCA13	154664	37	7	48338080	48338080	Missense_Mutation	SNP	C	T	8	20	c.9317C>T	c.(9316-9318)TCC>TTC	p.S3106F
Pat_76	Post-Resistance	ZPBP	11055	37	7	50022979	50022979	Missense_Mutation	SNP	C	T	8	29	c.920G>A	c.(919-921)GGA>GAA	p.G307E
Pat_76	Post-Resistance	ZNF713	349075	37	7	56007625	56007625	Missense_Mutation	SNP	C	T	21	33	c.1219C>T	c.(1219-1221)CAT>TAT	p.H407Y
Pat_76	Post-Resistance	ZNF479	90827	37	7	57187752	57187752	Missense_Mutation	SNP	C	T	23	113	c.1370G>A	c.(1369-1371)AGA>AAA	p.R457K
Pat_76	Post-Resistance	ZNF727	442319	37	7	63538454	63538454	Missense_Mutation	SNP	G	A	9	43	c.1027G>A	c.(1027-1029)GAA>AAA	p.E343K
Pat_76	Post-Resistance	CALN1	83698	37	7	71275372	71275372	Missense_Mutation	SNP	C	T	14	63	c.481G>A	c.(481-483)GAA>AAA	p.E161K
Pat_76	Post-Resistance	POR	5447	37	7	75583414	75583414	Missense_Mutation	SNP	C	T	5	14	c.104C>T	c.(103-105)TCG>TTG	p.S35L
Pat_76	Post-Resistance	MAGI2	9863	37	7	77885584	77885584	Missense_Mutation	SNP	C	T	10	51	c.1723G>A	c.(1723-1725)GAT>AAT	p.D575N
Pat_76	Post-Resistance	PCLO	27445	37	7	82451858	82451858	Missense_Mutation	SNP	G	C	31	85	c.14744C>G	.(14743-14745)GCC>GGC	p.A4915G
Pat_76	Post-Resistance	PCLO	27445	37	7	82546104	82546104	Missense_Mutation	SNP	G	A	15	28	c.11198C>T	c.(11197-11199)TCC>TTC	p.S3733F
Pat_76	Post-Resistance	PCLO	27445	37	7	82764102	82764102	Missense_Mutation	SNP	T	G	4	9	c.2764A>C	c.(2764-2766)ACT>CCT	p.T922P
Pat_76	Post-Resistance	PCLO	27445	37	7	82764708	82764708	Missense_Mutation	SNP	C	T	5	15	c.2158G>A	c.(2158-2160)GCC>ACC	p.A720T
Pat_76	Post-Resistance	PCLO	27445	37	7	82785182	82785182	Nonsense_Mutation	SNP	G	A	4	16	c.775C>T	c.(775-777)CAG>TAG	p.Q259*
Pat_76	Post-Resistance	SEMA3A	10371	37	7	83636707	83636707	Missense_Mutation	SNP	G	A	7	52	c.1102C>T	c.(1102-1104)CCT>TCT	p.P368S
Pat_76	Post-Resistance	ABCB1	5243	37	7	87133609	87133609	Missense_Mutation	SNP	C	T	42	49	c.3793G>A	c.(3793-3795)GGC>AGC	p.G1265S
Pat_76	Post-Resistance	RUNDC3B	154661	37	7	87407136	87407136	Missense_Mutation	SNP	G	A	5	14	c.872G>A	c.(871-873)CGA>CAA	p.R291Q
Pat_76	Post-Resistance	STEAP4	79689	37	7	87913456	87913456	Nonsense_Mutation	SNP	A	C	13	38	c.129T>G	c.(127-129)TAT>TAG	p.Y43*
Pat_76	Post-Resistance	PEX1	5189	37	7	92119180	92119180	Missense_Mutation	SNP	G	A	3	26	c.3484C>T	c.(3484-3486)CCT>TCT	p.P1162S
Pat_76	Post-Resistance	SAMD9L	219285	37	7	92762118	92762118	Missense_Mutation	SNP	G	A	10	48	c.3167C>T	c.(3166-3168)TCC>TTC	p.S1056F
Pat_76	Post-Resistance	COL1A2	1278	37	7	94039582	94039582	Missense_Mutation	SNP	G	A	9	29	c.1064G>A	c.(1063-1065)GGA>GAA	p.G355E
Pat_76	Post-Resistance	NPTX2	4885	37	7	98254473	98254473	Missense_Mutation	SNP	G	A	15	76	c.883G>A	c.(883-885)GAC>AAC	p.D295N
Pat_76	Post-Resistance	CYP3A4	1576	37	7	99359664	99359664	Missense_Mutation	SNP	C	T	32	43	c.1253G>A	c.(1252-1254)AGA>AAA	p.R418K
Pat_76	Post-Resistance	ZAN	7455	37	7	100348419	100348419	Missense_Mutation	SNP	G	A	8	10	c.1421G>A	c.(1420-1422)GGG>GAG	p.G474E
Pat_76	Post-Resistance	MUC17	140453	37	7	100678919	100678919	Missense_Mutation	SNP	G	A	258	544	c.4222G>A	c.(4222-4224)GTA>ATA	p.V1408I
Pat_76	Post-Resistance	MUC17	140453	37	7	100683798	100683798	Missense_Mutation	SNP	C	T	188	594	c.9101C>T	c.(9100-9102)ACC>ATC	p.T3034I
Pat_76	Post-Resistance	MUC17	140453	37	7	100686761	100686761	Missense_Mutation	SNP	A	C	41	127	c.12064A>C	c.(12064-12066)ACT>CCT	p.T4022P
Pat_76	Post-Resistance	ZNHIT1	10467	37	7	100867093	100867093	Missense_Mutation	SNP	T	C	22	110	c.413T>C	c.(412-414)GTG>GCG	p.V138A
Pat_76	Post-Resistance	CUX1	1523	37	7	101918517	101918517	Splice_Site	SNP	G	A	38	83	c.1451_splice	c.e17-1	p.G484_splice
Pat_76	Post-Resistance	SLC26A5	375611	37	7	103048336	103048336	Missense_Mutation	SNP	C	T	6	34	c.850G>A	c.(850-852)GAG>AAG	p.E284K
Pat_76	Post-Resistance	RELN	5649	37	7	103185660	103185660	Missense_Mutation	SNP	C	T	37	32	c.6434G>A	c.(6433-6435)GGA>GAA	p.G2145E
Pat_76	Post-Resistance	RELN	5649	37	7	103294623	103294623	Missense_Mutation	SNP	C	T	8	27	c.1471G>A	c.(1471-1473)GAA>AAA	p.E491K
Pat_76	Post-Resistance	RELN	5649	37	7	103341421	103341421	Missense_Mutation	SNP	G	A	32	61	c.838C>T	c.(838-840)CCC>TCC	p.P280S
Pat_76	Post-Resistance	IFRD1	3475	37	7	112096120	112096120	Missense_Mutation	SNP	T	G	15	11	c.263T>G	c.(262-264)ATT>AGT	p.I88S
Pat_76	Post-Resistance	PPP1R3A	5506	37	7	113518127	113518127	Missense_Mutation	SNP	G	A	10	38	c.3020C>T	c.(3019-3021)TCT>TTT	p.S1007F
Pat_76	Post-Resistance	PPP1R3A	5506	37	7	113558273	113558273	Missense_Mutation	SNP	G	A	8	35	c.779C>T	c.(778-780)TCA>TTA	p.S260L
Pat_76	Post-Resistance	FOXP2	93986	37	7	114329931	114329931	Missense_Mutation	SNP	G	A	13	53	c.2098G>A	c.(2098-2100)GAA>AAA	p.E700K
Pat_76	Post-Resistance	MET	4233	37	7	116371883	116371884	Missense_Mutation	DNP	TC	AT	24	15	.1362_1363TC>A	1360-1365)AATCTT>AAAT	.454_455NL>K
Pat_76	Post-Resistance	WNT2	7472	37	7	116918241	116918241	Missense_Mutation	SNP	G	A	19	80	c.1051C>T	c.(1051-1053)CCC>TCC	p.P351S
Pat_76	Post-Resistance	CFTR	1080	37	7	117232163	117232163	Missense_Mutation	SNP	G	A	26	18	c.1942G>A	c.(1942-1944)GAT>AAT	p.D648N

Pat_76	Post-Resistance	CFTR	1080	37	7	117307052	117307052	Missense_Mutation	SNP	G	A	7	51	c.4333G>A	c.(4333-4335)GAC>AAC	p.D1445N
Pat_76	Post-Resistance	TSPAN12	23554	37	7	120428929	120428929	Missense_Mutation	SNP	G	A	5	30	c.635C>T	c.(634-636)TCC>TTC	p.S212F
Pat_76	Post-Resistance	RNF148	378925	37	7	122342384	122342384	Missense_Mutation	SNP	G	A	64	310	c.421C>T	c.(421-423)CCC>TCC	p.P141S
Pat_76	Post-Resistance	IQUB	154865	37	7	123136870	123136870	Missense_Mutation	SNP	C	T	19	11	c.1114G>A	c.(1114-1116)GAA>AAA	p.E372K
Pat_76	Post-Resistance	FSCN3	29999	37	7	127236496	127236496	Missense_Mutation	SNP	C	T	123	50	c.956C>T	c.(955-957)TCC>TTC	p.S319F
Pat_76	Post-Resistance	SND1	27044	37	7	127326763	127326763	Missense_Mutation	SNP	C	T	16	116	c.175C>T	c.(175-177)CTT>TTT	p.L59F
Pat_76	Post-Resistance	FLNC	2318	37	7	128484752	128484752	Missense_Mutation	SNP	G	A	15	73	c.3233G>A	c.(3232-3234)GGC>GAC	p.G1078D
Pat_76	Post-Resistance	FLNC	2318	37	7	128485144	128485144	Missense_Mutation	SNP	G	A	55	186	c.3625G>A	c.(3625-3627)GAT>AAT	p.D1209N
Pat_76	Post-Resistance	FLNC	2318	37	7	128493532	128493532	Missense_Mutation	SNP	G	A	29	15	c.6218G>A	c.(6217-6219)GGC>GAC	p.G2073D
Pat_76	Post-Resistance	PLXNA4	91584	37	7	131831452	131831452	Missense_Mutation	SNP	C	T	39	149	c.4872G>A	c.(4870-4872)ATG>ATA	p.M1624I
Pat_76	Post-Resistance	PLXNA4	91584	37	7	131853205	131853205	Missense_Mutation	SNP	C	T	30	79	c.4144G>A	c.(4144-4146)GAC>AAC	p.D1382N
Pat_76	Post-Resistance	PLXNA4	91584	37	7	131853241	131853241	Missense_Mutation	SNP	G	A	21	89	c.4108C>T	c.(4108-4110)CGC>TGC	p.R1370C
Pat_76	Post-Resistance	PLXNA4	91584	37	7	132192864	132192864	Missense_Mutation	SNP	G	A	31	128	c.589C>T	c.(589-591)CCC>TCC	p.P197S
Pat_76	Post-Resistance	CHRM2	1129	37	7	136700405	136700405	Missense_Mutation	SNP	G	A	15	27	c.793G>A	c.(793-795)GCC>ACC	p.A265T
Pat_76	Post-Resistance	DGKI	9162	37	7	137304634	137304634	Missense_Mutation	SNP	G	A	73	40	c.929C>T	c.(928-930)TCC>TTC	p.S310F
Pat_76	Post-Resistance	KIAA1549	57670	37	7	138552834	138552835	Nonsense_Mutation	DNP	GG	AA	6	18	.4815_4816CC>T	813-4818)CACCAG>CATT	p.Q1606*
Pat_76	Post-Resistance	RAB19	401409	37	7	140107597	140107597	Missense_Mutation	SNP	G	A	10	79	c.151G>A	c.(151-153)GGA>AGA	p.G51R
Pat_76	Post-Resistance	RAB19	401409	37	7	140111792	140111792	Missense_Mutation	SNP	C	T	34	164	c.320C>T	c.(319-321)TCC>TTC	p.S107F
Pat_76	Post-Resistance	DENND2A	27147	37	7	140301773	140301773	Missense_Mutation	SNP	C	A	43	161	c.425G>T	c.(424-426)GGC>GTC	p.G142V
Pat_76	Post-Resistance	ADCK2	90956	37	7	140373899	140373899	Missense_Mutation	SNP	C	T	39	25	c.769C>T	c.(769-771)CTT>TTT	p.L257F
Pat_76	Post-Resistance	BRAF	673	37	7	140453136	140453136	Missense_Mutation	SNP	A	T	28	23	c.1799T>A	c.(1798-1800)GTG>GAG	p.V600E
Pat_76	Post-Resistance	BRAF	673	37	7	140481408	140481408	Missense_Mutation	SNP	G	A	27	184	c.1400C>T	c.(1399-1401)TCA>TTA	p.S467L
Pat_76	Post-Resistance	WEE2	494551	37	7	141408728	141408728	Nonsense_Mutation	SNP	G	A	124	66	c.170G>A	c.(169-171)TGG>TAG	p.W57*
Pat_76	Post-Resistance	MGAM	8972	37	7	141759301	141759301	Missense_Mutation	SNP	G	A	7	9	c.3849G>A	c.(3847-3849)ATG>ATA	p.M1283I
Pat_76	Post-Resistance	TRPV6	55503	37	7	142574981	142574981	Missense_Mutation	SNP	C	T	40	141	c.401G>A	c.(400-402)CGA>CAA	p.R134Q
Pat_76	Post-Resistance	TRPV5	56302	37	7	142625878	142625878	Missense_Mutation	SNP	C	T	19	83	c.670G>A	c.(670-672)GGA>AGA	p.G224R
Pat_76	Post-Resistance	TAS2R39	259285	37	7	142880593	142880593	Missense_Mutation	SNP	G	A	8	25	c.82G>A	c.(82-84)GAA>AAA	p.E28K
Pat_76	Post-Resistance	TAS2R39	259285	37	7	142881212	142881212	Missense_Mutation	SNP	C	T	106	61	c.701C>T	c.(700-702)TCT>TTT	p.S234F
Pat_76	Post-Resistance	CLCN1	1180	37	7	143044013	143044013	Missense_Mutation	SNP	G	A	17	58	c.2374G>A	c.(2374-2376)GAT>AAT	p.D792N
Pat_76	Post-Resistance	EPHA1	2041	37	7	143096756	143096756	Missense_Mutation	SNP	C	T	60	190	c.823G>A	c.(823-825)GAA>AAA	p.E275K
Pat_76	Post-Resistance	TAS2R41	259287	37	7	143175540	143175540	Missense_Mutation	SNP	C	T	8	23	c.575C>T	c.(574-576)CCT>CTT	p.P192L
Pat_76	Post-Resistance	OR2F1	26211	37	7	143657369	143657369	Missense_Mutation	SNP	T	A	35	90	c.306T>A	c.(304-306)TTT>TTA	p.F102L
Pat_76	Post-Resistance	OR2A2	442361	37	7	143807452	143807452	Missense_Mutation	SNP	G	A	102	91	c.777G>A	c.(775-777)ATG>ATA	p.M259I
Pat_76	Post-Resistance	ARHGEF5	7984	37	7	144060324	144060324	Missense_Mutation	SNP	G	A	31	96	c.562G>A	c.(562-564)GAG>AAG	p.E188K
Pat_76	Post-Resistance	ARHGEF5	7984	37	7	144062290	144062290	Missense_Mutation	SNP	C	T	8	137	c.2528C>T	c.(2527-2529)CCC>CTC	p.P843L
Pat_76	Post-Resistance	ARHGEF5	7984	37	7	144068336	144068336	Missense_Mutation	SNP	C	T	6	150	c.3614C>T	c.(3613-3615)TCA>TTA	p.S1205L
Pat_76	Post-Resistance	CNTNAP2	26047	37	7	146825794	146825794	Missense_Mutation	SNP	G	A	7	46	c.949G>A	c.(949-951)GGA>AGA	p.G317R
Pat_76	Post-Resistance	C7orf33	202865	37	7	148311169	148311169	Missense_Mutation	SNP	G	A	43	133	c.240G>A	c.(238-240)ATG>ATA	p.M80I
Pat_76	Post-Resistance	ZNF786	136051	37	7	148768291	148768292	Missense_Mutation	DNP	GG	AA	18	22	.1572_1573CC>T	570-1575)CTCCGT>CTTT	p.R525C
Pat_76	Post-Resistance	ZNF398	57541	37	7	148876126	148876126	Missense_Mutation	SNP	A	G	27	192	c.1162A>G	c.(1162-1164)ACC>GCC	p.T388A
Pat_76	Post-Resistance	ZNF777	27153	37	7	149152767	149152767	Missense_Mutation	SNP	G	A	45	22	c.347C>T	c.(346-348)TCC>TTC	p.S116F
Pat_76	Post-Resistance	KRBA1	84626	37	7	149422535	149422535	Missense_Mutation	SNP	G	A	3	29	c.1256G>A	c.(1255-1257)AGG>AAG	p.R419K
Pat_76	Post-Resistance	SSPO	23145	37	7	149473161	149473161	Missense_Mutation	SNP	G	A	5	31	c.31G>A	c.(31-33)GCG>ACG	p.A11T
Pat_76	Post-Resistance	SSPO	23145	37	7	149492413	149492413	Missense_Mutation	SNP	G	A	9	34	c.6302G>A	c.(6301-6303)GGG>GAG	p.G2101E
Pat_76	Post-Resistance	REPIN1	29803	37	7	150068839	150068839	Missense_Mutation	SNP	C	T	6	42	c.509C>T	c.(508-510)CCC>CTC	p.P170L
Pat_76	Post-Resistance	GIMAP8	155038	37	7	150174179	150174179	Splice_Site	SNP	G	A	46	43	c.1310_splice	c.e5-1	p.E437_splice
Pat_76	Post-Resistance	GIMAP8	155038	37	7	150174386	150174386	Missense_Mutation	SNP	G	A	28	22	c.1516G>A	c.(1516-1518)GAC>AAC	p.D506N

Pat_76	Post-Resistance	TMEM176A	55365	37	7	150499346	150499346	Missense_Mutation	SNP	G	A	17	81	c.218G>A	c.(217-219)GGA>GAA	p.G73E
Pat_76	Post-Resistance	NOS3	4846	37	7	150696324	150696324	Missense_Mutation	SNP	G	A	20	144	c.1003G>A	c.(1003-1005)GCA>ACA	p.A335T
Pat_76	Post-Resistance	MLL3	58508	37	7	152027710	152027710	Missense_Mutation	SNP	G	A	17	94	c.365C>T	c.(364-366)TCT>TTT	p.S122F
Pat_76	Post-Resistance	HTR5A	3361	37	7	154862632	154862632	Missense_Mutation	SNP	C	T	33	197	c.23C>T	c.(22-24)ACC>ATC	p.T8I
Pat_76	Post-Resistance	HTR5A	3361	37	7	154876022	154876022	Missense_Mutation	SNP	C	T	22	97	c.899C>T	c.(898-900)CCC>CTC	p.P300L
Pat_76	Post-Resistance	RNF32	140545	37	7	156437211	156437211	Missense_Mutation	SNP	G	A	3	38	c.34G>A	c.(34-36)GAT>AAT	p.D12N
Pat_76	Post-Resistance	ERICH1	157697	37	8	623397	623398	Missense_Mutation	DNP	CC	TT	30	82	c.954_955GG>AA	952-957)GGGGAG>GGAA	p.E319K
Pat_76	Post-Resistance	CSMD1	64478	37	8	2806873	2806873	Missense_Mutation	SNP	A	C	4	7	c.10353T>G	c.(10351-10353)TTT>TTG	p.F3451L
Pat_76	Post-Resistance	CSMD1	64478	37	8	3253899	3253899	Nonsense_Mutation	SNP	G	A	3	5	c.2413C>T	c.(2413-2415)CAG>TAG	p.Q805*
Pat_76	Post-Resistance	SGK223	157285	37	8	8235065	8235065	Missense_Mutation	SNP	G	A	10	18	c.854C>T	c.(853-855)TCA>TTA	p.S285L
Pat_76	Post-Resistance	FAM167A	83648	37	8	11281901	11281901	Missense_Mutation	SNP	C	T	19	48	c.626G>A	c.(625-627)CGG>CAG	p.R209Q
Pat_76	Post-Resistance	SGCZ	137868	37	8	13959889	13959889	Missense_Mutation	SNP	C	T	8	28	c.740G>A	c.(739-741)GGG>GAG	p.G247E
Pat_76	Post-Resistance	TUSC3	7991	37	8	15531307	15531307	Missense_Mutation	SNP	C	T	10	32	c.760C>T	c.(760-762)CCT>TCT	p.P254S
Pat_76	Post-Resistance	MTMR7	9108	37	8	17159783	17159783	Nonsense_Mutation	SNP	C	T	9	26	c.1500G>A	c.(1498-1500)TGG>TGA	p.W500*
Pat_76	Post-Resistance	XPO7	23039	37	8	21834014	21834014	Missense_Mutation	SNP	C	T	20	36	c.745C>T	c.(745-747)CCC>TCC	p.P249S
Pat_76	Post-Resistance	LOXL2	4017	37	8	23225624	23225624	Missense_Mutation	SNP	C	T	22	49	c.241G>A	c.(241-243)GGC>AGC	p.G81S
Pat_76	Post-Resistance	ADAM28	10863	37	8	24187543	24187543	Missense_Mutation	SNP	G	A	13	25	c.1018G>A	c.(1018-1020)GAA>AAA	p.E340K
Pat_76	Post-Resistance	ADAM7	8756	37	8	24324376	24324376	Missense_Mutation	SNP	G	C	21	31	c.454G>C	c.(454-456)GAA>CAA	p.E152Q
Pat_76	Post-Resistance	EBF2	64641	37	8	25718576	25718576	Missense_Mutation	SNP	C	T	15	46	c.1331G>A	c.(1330-1332)GGA>GAA	p.G444E
Pat_76	Post-Resistance	DPYSL2	1808	37	8	26513185	26513185	Missense_Mutation	SNP	C	T	27	99	c.1682C>T	c.(1681-1683)CCC>CTC	p.P561L
Pat_76	Post-Resistance	C8orf80	389643	37	8	27931885	27931885	Missense_Mutation	SNP	C	T	5	12	c.43G>A	c.(43-45)GTT>ATT	p.V15I
Pat_76	Post-Resistance	TEX15	56154	37	8	30695198	30695198	Missense_Mutation	SNP	G	A	10	25	c.7453C>T	c.(7453-7455)CCA>TCA	p.P2485S
Pat_76	Post-Resistance	ZMAT4	79698	37	8	40625228	40625228	Missense_Mutation	SNP	C	T	5	17	c.124G>A	c.(124-126)GTC>ATC	p.V42I
Pat_76	Post-Resistance	AGPAT6	137964	37	8	41470462	41470463	Missense_Mutation	DNP	CC	TT	12	31	c.894_895CC>TT	892-897)CGCCAC>CGTT	p.H299Y
Pat_76	Post-Resistance	ANK1	286	37	8	41551487	41551487	Missense_Mutation	SNP	G	A	7	16	c.3461C>T	c.(3460-3462)TCC>TTC	p.S1154F
Pat_76	Post-Resistance	POTEA	340441	37	8	43152483	43152483	Missense_Mutation	SNP	G	A	32	78	c.469G>A	c.(469-471)GAT>AAT	p.D157N
Pat_76	Post-Resistance	MCM4	4173	37	8	48882577	48882577	Missense_Mutation	SNP	C	T	12	37	c.1394C>T	c.(1393-1395)GCC>GTC	p.A465V
Pat_76	Post-Resistance	C8orf22	492307	37	8	49986883	49986883	Missense_Mutation	SNP	C	T	4	14	c.224C>T	c.(223-225)TCT>TTT	p.S75F
Pat_76	Post-Resistance	RP1	6101	37	8	55541492	55541492	Missense_Mutation	SNP	G	A	15	34	c.5050G>A	c.(5050-5052)GAA>AAA	p.E1684K
Pat_76	Post-Resistance	RP1	6101	37	8	55541652	55541652	Missense_Mutation	SNP	A	G	8	22	c.5210A>G	c.(5209-5211)GAA>GGA	p.E1737G
Pat_76	Post-Resistance	XKR4	114786	37	8	56436719	56436719	Missense_Mutation	SNP	C	T	15	23	c.1886C>T	c.(1885-1887)CCT>CTT	p.P629L
Pat_76	Post-Resistance	PLAG1	5324	37	8	57079014	57079014	Missense_Mutation	SNP	G	A	4	11	c.1291C>T	c.(1291-1293)CCC>TCC	p.P431S
Pat_76	Post-Resistance	CYP7A1	1581	37	8	59409562	59409563	Missense_Mutation	DNP	CC	TT	14	53	c.508_509GG>AA	c.(508-510)GGG>AAG	p.G170K
Pat_76	Post-Resistance	PREX2	80243	37	8	69028113	69028113	Missense_Mutation	SNP	G	A	23	44	c.3272G>A	c.(3271-3273)GGA>GAA	p.G1091E
Pat_76	Post-Resistance	CRISPLD1	83690	37	8	75925132	75925132	Missense_Mutation	SNP	C	T	11	13	c.385C>T	c.(385-387)CCC>TCC	p.P129S
Pat_76	Post-Resistance	ZFHX4	79776	37	8	77763658	77763658	Missense_Mutation	SNP	C	T	3	22	c.4366C>T	c.(4366-4368)CCT>TCT	p.P1456S
Pat_76	Post-Resistance	PAG1	55824	37	8	81899700	81899700	Missense_Mutation	SNP	G	A	16	32	c.179C>T	c.(178-180)CCT>CTT	p.P60L
Pat_76	Post-Resistance	WWP1	11059	37	8	87393063	87393064	Missense_Mutation	DNP	CT	TC	10	8	c.179_180CT>TC	c.(178-180)TCT>TTC	p.S60F
Pat_76	Post-Resistance	CNGB3	54714	37	8	87656094	87656094	Nonsense_Mutation	SNP	G	A	9	33	c.1063C>T	c.(1063-1065)CGA>TGA	p.R355*
Pat_76	Post-Resistance	SLC26A7	115111	37	8	92352666	92352666	Missense_Mutation	SNP	C	T	22	40	c.913C>T	c.(913-915)CTC>TTC	p.L305F
Pat_76	Post-Resistance	POP1	10940	37	8	99140736	99140736	Missense_Mutation	SNP	C	T	7	11	c.454C>T	c.(454-456)CCC>TCC	p.P152S
Pat_76	Post-Resistance	POP1	10940	37	8	99161210	99161210	Nonsense_Mutation	SNP	G	A	6	6	c.1878G>A	c.(1876-1878)TGG>TGA	p.W626*
Pat_76	Post-Resistance	OSR2	116039	37	8	99961245	99961245	Missense_Mutation	SNP	C	T	17	32	c.65C>T	c.(64-66)TCC>TTC	p.S22F
Pat_76	Post-Resistance	UBR5	51366	37	8	103326127	103326127	Missense_Mutation	SNP	G	A	8	21	c.1912C>T	c.(1912-1914)CCT>TCT	p.P638S
Pat_76	Post-Resistance	RIMS2	9699	37	8	104778681	104778681	Missense_Mutation	SNP	G	A	10	20	c.614G>A	c.(613-615)CGA>CAA	p.R205Q
Pat_76	Post-Resistance	RIMS2	9699	37	8	105257255	105257255	Missense_Mutation	SNP	G	A	37	70	c.3500G>A	c.(3499-3501)GGT>GAT	p.G1167D
Pat_76	Post-Resistance	ZFPM2	23414	37	8	106813565	106813565	Missense_Mutation	SNP	G	A	6	28	c.1255G>A	c.(1255-1257)GAA>AAA	p.E419K

Pat_76	Post-Resistance	ANGPT1	284	37	8	108306214	108306214	Missense_Mutation	SNP	G	A	26	45	c.988C>T	c.(988-990)CGT>TGT	p.R330C
Pat_76	Post-Resistance	TRHR	7201	37	8	110131469	110131469	Missense_Mutation	SNP	C	A	33	78	c.982C>A	c.(982-984)CGT>AGT	p.R328S
Pat_76	Post-Resistance	PKHD1L1	93035	37	8	110477198	110477198	Missense_Mutation	SNP	C	T	16	41	c.8137C>T	c.(8137-8139)CTT>TTT	p.L2713F
Pat_76	Post-Resistance	CSMD3	114788	37	8	113243822	113243822	Missense_Mutation	SNP	C	T	18	18	c.10780G>A	.(10780-10782)GGA>AG	p.G3594R
Pat_76	Post-Resistance	CSMD3	114788	37	8	113519002	113519002	Missense_Mutation	SNP	G	A	7	25	c.4813C>T	c.(4813-4815)CCT>TCT	p.P1605S
Pat_76	Post-Resistance	CSMD3	114788	37	8	113966963	113966963	Missense_Mutation	SNP	C	T	4	10	c.1370G>A	c.(1369-1371)AGA>AAA	p.R457K
Pat_76	Post-Resistance	ENPP2	5168	37	8	120629774	120629774	Missense_Mutation	SNP	G	A	3	14	c.509C>T	c.(508-510)TCC>TTC	p.S170F
Pat_76	Post-Resistance	DEPDC6	64798	37	8	120942126	120942126	Missense_Mutation	SNP	C	T	14	30	c.373C>T	c.(373-375)CCA>TCA	p.P125S
Pat_76	Post-Resistance	FER1L6	654463	37	8	124989687	124989687	Missense_Mutation	SNP	G	A	41	107	c.901G>A	c.(901-903)GAT>AAT	p.D301N
Pat_76	Post-Resistance	FER1L6	654463	37	8	125083819	125083819	Missense_Mutation	SNP	G	A	14	49	c.4039G>A	c.(4039-4041)GGG>AGG	p.G1347R
Pat_76	Post-Resistance	FAM135B	51059	37	8	139164961	139164961	Missense_Mutation	SNP	C	T	21	59	c.1757G>A	c.(1756-1758)GGA>GAA	p.G586E
Pat_76	Post-Resistance	DENND3	22898	37	8	142161766	142161766	Missense_Mutation	SNP	G	A	25	68	c.664G>A	c.(664-666)GAC>AAC	p.D222N
Pat_76	Post-Resistance	LY6K	54742	37	8	143784711	143784711	Missense_Mutation	SNP	G	A	11	24	c.420G>A	c.(418-420)ATG>ATA	p.M140I
Pat_76	Post-Resistance	SPATC1	375686	37	8	145095631	145095632	Missense_Mutation	DNP	CC	TT	16	28	c.929_930CC>TT	c.(928-930)CCC>CTT	p.P310L
Pat_76	Post-Resistance	ERMP1	79956	37	9	5810087	5810087	Missense_Mutation	SNP	G	A	17	28	c.1472C>T	c.(1471-1473)TCC>TTC	p.S491F
Pat_76	Post-Resistance	PTPRD	5789	37	9	8518132	8518132	Missense_Mutation	SNP	G	A	26	73	c.1259C>T	c.(1258-1260)GCC>GTC	p.A420V
Pat_76	Post-Resistance	BNC2	54796	37	9	16436831	16436831	Missense_Mutation	SNP	C	T	12	39	c.1361G>A	c.(1360-1362)GGT>GAT	p.G454D
Pat_76	Post-Resistance	SH3GL2	6456	37	9	17761434	17761434	Splice_Site	SNP	G	A	10	9	c.115_splice	c.e3-1	p.K39_splice
Pat_76	Post-Resistance	HAUS6	54801	37	9	19063041	19063041	Missense_Mutation	SNP	G	A	17	41	c.1594C>T	c.(1594-1596)CCA>TCA	p.P532S
Pat_76	Post-Resistance	DENND4C	55667	37	9	19346035	19346035	Missense_Mutation	SNP	C	T	9	19	c.2413C>T	c.(2413-2415)CCT>TCT	p.P805S
Pat_76	Post-Resistance	TAF1L	138474	37	9	32630273	32630273	Missense_Mutation	SNP	C	T	17	40	c.5305G>A	c.(5305-5307)GGA>AGA	p.G1769R
Pat_76	Post-Resistance	DNAI1	27019	37	9	34491492	34491492	Splice_Site	SNP	G	A	15	18	c.622_splice	c.e8-1	p.D208_splice
Pat_76	Post-Resistance	SHB	6461	37	9	37955901	37955901	Missense_Mutation	SNP	G	A	3	7	c.1205C>T	c.(1204-1206)GCC>GTC	p.A402V
Pat_76	Post-Resistance	LOC442421	442421	37	9	66499716	66499716	Missense_Mutation	SNP	A	G	9	43	c.526A>G	c.(526-528)AAT>GAT	p.N176D
Pat_76	Post-Resistance	PCSK5	5125	37	9	78749077	78749077	Missense_Mutation	SNP	G	T	16	45	c.1261G>T	c.(1261-1263)GCG>TCG	p.A421S
Pat_76	Post-Resistance	PCSK5	5125	37	9	78790033	78790033	Missense_Mutation	SNP	G	A	3	32	c.1888G>A	c.(1888-1890)GAG>AAG	p.E630K
Pat_76	Post-Resistance	PCSK5	5125	37	9	78804120	78804121	Missense_Mutation	DNP	GG	AA	9	27	.2491_2492GG>A	c.(2491-2493)GGA>AAA	p.G831K
Pat_76	Post-Resistance	GCNT1	2650	37	9	79118124	79118124	Missense_Mutation	SNP	C	T	11	26	c.827C>T	c.(826-828)CCT>CTT	p.P276L
Pat_76	Post-Resistance	PRUNE2	158471	37	9	79323229	79323229	Missense_Mutation	SNP	C	T	9	14	c.3961G>A	c.(3961-3963)GAT>AAT	p.D1321N
Pat_76	Post-Resistance	PRUNE2	158471	37	9	79441589	79441589	Missense_Mutation	SNP	C	T	12	18	c.568G>A	c.(568-570)GAA>AAA	p.E190K
Pat_76	Post-Resistance	VPS13A	23230	37	9	79827939	79827939	Missense_Mutation	SNP	C	T	6	13	c.610C>T	c.(610-612)CGT>TGT	p.R204C
Pat_76	Post-Resistance	FRMD3	257019	37	9	85950537	85950537	Missense_Mutation	SNP	C	T	10	17	c.490G>A	c.(490-492)GAT>AAT	p.D164N
Pat_76	Post-Resistance	KIF27	55582	37	9	86518174	86518174	Missense_Mutation	SNP	G	A	4	20	c.1259C>T	c.(1258-1260)ACC>ATC	p.T420I
Pat_76	Post-Resistance	PHF2	5253	37	9	96428104	96428104	Missense_Mutation	SNP	C	T	39	98	c.2074C>T	c.(2074-2076)CCC>TCC	p.P692S
Pat_76	Post-Resistance	HSD17B3	3293	37	9	99064356	99064356	Missense_Mutation	SNP	G	A	16	45	c.31C>T	c.(31-33)CTC>TTC	p.L11F
Pat_76	Post-Resistance	CTSL2	1515	37	9	99800270	99800271	Missense_Mutation	DNP	GG	AA	8	37	c.55_56CC>TT	c.(55-57)CCA>TTA	p.P19L
Pat_76	Post-Resistance	FOXE1	2304	37	9	100616596	100616596	Missense_Mutation	SNP	G	A	14	28	c.400G>A	c.(400-402)GAG>AAG	p.E134K
Pat_76	Post-Resistance	TRIM14	9830	37	9	100857249	100857250	Missense_Mutation	DNP	GG	AA	12	36	c.599_600CC>TT	c.(598-600)CCC>CTT	p.P200L
Pat_76	Post-Resistance	LPPR1	54886	37	9	104079716	104079716	Missense_Mutation	SNP	C	T	15	43	c.883C>T	c.(883-885)CGT>TGT	p.R295C
Pat_76	Post-Resistance	GRIN3A	116443	37	9	104449092	104449092	Missense_Mutation	SNP	C	T	7	21	c.1090G>A	c.(1090-1092)GAA>AAA	p.E364K
Pat_76	Post-Resistance	CYLC2	1539	37	9	105767050	105767050	Missense_Mutation	SNP	C	T	5	6	c.254C>T	c.(253-255)TCT>TTT	p.S85F
Pat_76	Post-Resistance	OR13F1	138805	37	9	107267121	107267121	Missense_Mutation	SNP	C	T	51	105	c.578C>T	c.(577-579)TCC>TTC	p.S193F
Pat_76	Post-Resistance	OR13C9	286362	37	9	107379644	107379644	Missense_Mutation	SNP	G	A	11	30	c.842C>T	c.(841-843)TCC>TTC	p.S281F
Pat_76	Post-Resistance	TXNDC8	255220	37	9	113096507	113096507	Missense_Mutation	SNP	G	A	6	20	c.118C>T	c.(118-120)CCT>TCT	p.P40S
Pat_76	Post-Resistance	ZNF618	114991	37	9	116795009	116795009	Splice_Site	SNP	G	A	18	107	c.1168_splice	c.e12+1	p.E390_splice
Pat_76	Post-Resistance	AKNA	80709	37	9	117118393	117118393	Missense_Mutation	SNP	G	A	7	25	c.2870C>T	c.(2869-2871)CCC>CTC	p.P957L
Pat_76	Post-Resistance	TNC	3371	37	9	117819506	117819506	Missense_Mutation	SNP	G	A	11	35	c.4505C>T	c.(4504-4506)ACT>ATT	p.T1502I

Pat_76	Post-Resistance	ASTN2	23245	37	9	119738438	119738438	Missense_Mutation	SNP	C	T	13	14	c.1706G>A	c.(1705-1707)GGC>GAC	p.G569D
Pat_76	Post-Resistance	TRAF1	7185	37	9	123667467	123667467	Missense_Mutation	SNP	G	A	5	15	c.1082C>T	c.(1081-1083)GCC>GTC	p.A361V
Pat_76	Post-Resistance	TRAF1	7185	37	9	123675765	123675765	Missense_Mutation	SNP	C	T	5	20	c.546G>A	c.(544-546)ATG>ATA	p.M182I
Pat_76	Post-Resistance	OR1N1	138883	37	9	125289062	125289063	Missense_Mutation	DNP	CC	TT	6	15	c.510_511GG>AA	508-513)GGGGAA>GGAA	p.E171K
Pat_76	Post-Resistance	RABGAP1	23637	37	9	125832695	125832695	Missense_Mutation	SNP	C	T	22	47	c.1975C>T	c.(1975-1977)CTT>TTT	p.L659F
Pat_76	Post-Resistance	SPTAN1	6709	37	9	131394511	131394511	Missense_Mutation	SNP	C	T	4	18	c.6853C>T	c.(6853-6855)CAC>TAC	p.H2285Y
Pat_76	Post-Resistance	LAMC3	10319	37	9	133901843	133901843	Missense_Mutation	SNP	G	A	8	13	c.545G>A	c.(544-546)GGC>GAC	p.G182D
Pat_76	Post-Resistance	NTNG2	84628	37	9	135042312	135042312	Missense_Mutation	SNP	C	T	20	31	c.94C>T	c.(94-96)CCC>TCC	p.P32S
Pat_76	Post-Resistance	SETX	23064	37	9	135204652	135204652	Missense_Mutation	SNP	C	T	5	20	c.2333G>A	c.(2332-2334)CGA>CAA	p.R778Q
Pat_76	Post-Resistance	ADAMTS13	11093	37	9	136323188	136323189	Missense_Mutation	DNP	CC	TT	4	7	.4049_4050CC>T	c.(4048-4050)ACC>ATT	p.T1350I
Pat_76	Post-Resistance	DBH	1621	37	9	136518122	136518122	Splice_Site	SNP	G	A	16	52	c.1434_splice	c.e9+1	p.V478_splice
Pat_76	Post-Resistance	CAMSAP1	157922	37	9	138707828	138707828	Missense_Mutation	SNP	G	A	17	36	c.4295C>T	c.(4294-4296)CCC>CTC	p.P1432L
Pat_76	Post-Resistance	SEC16A	9919	37	9	139371934	139371934	Missense_Mutation	SNP	G	A	6	24	c.134C>T	c.(133-135)ACT>ATT	p.T45I
Pat_76	Post-Resistance	ANAPC2	29882	37	9	140069793	140069793	Missense_Mutation	SNP	C	T	8	10	c.2152G>A	c.(2152-2154)GAG>AAG	p.E718K
Pat_76	Post-Resistance	ANAPC2	29882	37	9	140077628	140077628	Missense_Mutation	SNP	G	A	45	83	c.1235C>T	c.(1234-1236)CCT>CTT	p.P412L
Pat_76	Post-Resistance	ENTPD8	377841	37	9	140330184	140330184	Missense_Mutation	SNP	C	T	12	10	c.1148G>A	c.(1147-1149)AGG>AAG	p.R383K
Pat_76	Post-Resistance	SHOX	6473	37	X	591723	591723	Missense_Mutation	SNP	G	A	41	75	c.91G>A	c.(91-93)GAT>AAT	p.D31N
Pat_76	Post-Resistance	ASMT	438	37	X	1742197	1742197	Missense_Mutation	SNP	G	A	6	14	c.235G>A	c.(235-237)GGA>AGA	p.G79R
Pat_76	Post-Resistance	ASMT	438	37	X	1748718	1748718	Missense_Mutation	SNP	G	A	47	133	c.448G>A	c.(448-450)GAG>AAG	p.E150K
Pat_76	Post-Resistance	ARSD	414	37	X	2836227	2836227	Missense_Mutation	SNP	G	A	3	10	c.481C>T	c.(481-483)CAC>TAC	p.H161Y
Pat_76	Post-Resistance	MXRA5	25878	37	X	3240077	3240077	Missense_Mutation	SNP	C	T	11	20	c.3649G>A	c.(3649-3651)GAA>AAA	p.E1217K
Pat_76	Post-Resistance	NLGN4X	57502	37	X	6069266	6069266	Missense_Mutation	SNP	G	A	17	22	c.242C>T	c.(241-243)CCC>CTC	p.P81L
Pat_76	Post-Resistance	VCX	26609	37	X	7811971	7811971	Missense_Mutation	SNP	G	A	75	248	c.535G>A	c.(535-537)GAG>AAG	p.E179K
Pat_76	Post-Resistance	SHROOM2	357	37	X	9863495	9863495	Missense_Mutation	SNP	C	T	4	12	c.1547C>T	c.(1546-1548)CCA>CTA	p.P516L
Pat_76	Post-Resistance	TLR8	51311	37	X	12938573	12938573	Missense_Mutation	SNP	C	T	11	33	c.1414C>T	c.(1414-1416)CGT>TGT	p.R472C
Pat_76	Post-Resistance	TLR8	51311	37	X	12939914	12939914	Missense_Mutation	SNP	G	A	11	34	c.2755G>A	c.(2755-2757)GAG>AAG	p.E919K
Pat_76	Post-Resistance	EGFL6	25975	37	X	13621532	13621532	Missense_Mutation	SNP	C	T	10	28	c.497C>T	c.(496-498)GCC>GTC	p.A166V
Pat_76	Post-Resistance	PHEX	5251	37	X	22117199	22117199	Missense_Mutation	SNP	G	A	37	57	c.1009G>A	c.(1009-1011)GAG>AAG	p.E337K
Pat_76	Post-Resistance	PHEX	5251	37	X	22237170	22237170	Missense_Mutation	SNP	C	T	13	43	c.1718C>T	c.(1717-1719)GCT>GTT	p.A573V
Pat_76	Post-Resistance	POLA1	5422	37	X	24721395	24721395	Missense_Mutation	SNP	G	A	11	10	c.178G>A	c.(178-180)GAA>AAA	p.E60K
Pat_76	Post-Resistance	CXorf21	80231	37	X	30578039	30578039	Missense_Mutation	SNP	G	A	7	27	c.434C>T	c.(433-435)CCC>CTC	p.P145L
Pat_76	Post-Resistance	FAM47A	158724	37	X	34148687	34148687	Missense_Mutation	SNP	G	A	5	12	c.1709C>T	c.(1708-1710)TCG>TTG	p.S570L
Pat_76	Post-Resistance	CXorf59	286464	37	X	36117969	36117969	Nonsense_Mutation	SNP	G	A	14	24	c.825G>A	c.(823-825)TGG>TGA	p.W275*
Pat_76	Post-Resistance	SRPX	8406	37	X	38031196	38031196	Missense_Mutation	SNP	C	T	19	35	c.464G>A	c.(463-465)GGG>GAG	p.G155E
Pat_76	Post-Resistance	RPGR	6103	37	X	38129006	38129006	Missense_Mutation	SNP	G	A	7	21	c.2321C>T	c.(2320-2322)TCC>TTC	p.S774F
Pat_76	Post-Resistance	GPR34	2857	37	X	41555789	41555789	Nonsense_Mutation	SNP	G	A	7	18	c.903G>A	c.(901-903)TGG>TGA	p.W301*
Pat_76	Post-Resistance	GRIPAP1	56850	37	X	48844287	48844287	Missense_Mutation	SNP	G	A	3	9	c.953C>T	c.(952-954)TCC>TTC	p.S318F
Pat_76	Post-Resistance	TFE3	7030	37	X	48895543	48895543	Missense_Mutation	SNP	G	A	3	10	c.877C>T	c.(877-879)CCC>TCC	p.P293S
Pat_76	Post-Resistance	CCDC120	90060	37	X	48925184	48925184	Missense_Mutation	SNP	C	T	10	20	c.1429C>T	c.(1429-1431)CGC>TGC	p.R477C
Pat_76	Post-Resistance	GPKOW	27238	37	X	48976140	48976140	Missense_Mutation	SNP	C	A	6	15	c.484G>T	c.(484-486)GTC>TTC	p.V162F
Pat_76	Post-Resistance	PRICKLE3	4007	37	X	49032516	49032516	Missense_Mutation	SNP	C	T	3	6	c.1354G>A	c.(1354-1356)GAG>AAG	p.E452K
Pat_76	Post-Resistance	DGKK	139189	37	X	50119787	50119787	Nonsense_Mutation	SNP	A	C	10	19	c.3242T>G	c.(3241-3243)TTA>TGA	p.L1081*
Pat_76	Post-Resistance	PHF8	23133	37	X	54069119	54069119	Missense_Mutation	SNP	C	T	27	51	c.151G>A	c.(151-153)GAT>AAT	p.D51N
Pat_76	Post-Resistance	FAAH2	158584	37	X	57313331	57313331	Missense_Mutation	SNP	G	A	4	5	c.73G>A	c.(73-75)GGC>AGC	p.G25S
Pat_76	Post-Resistance	MTMR8	55613	37	X	63564991	63564991	Missense_Mutation	SNP	G	A	15	42	c.799C>T	c.(799-801)CGC>TGC	p.R267C
Pat_76	Post-Resistance	LAS1L	81887	37	X	64738050	64738050	Missense_Mutation	SNP	C	T	13	26	c.1744G>A	c.(1744-1746)GAG>AAG	p.E582K
Pat_76	Post-Resistance	MSN	4478	37	X	64936728	64936728	Nonsense_Mutation	SNP	C	T	26	61	c.61C>T	c.(61-63)CAG>TAG	p.Q21*

Pat_76	Post-Resistance	HEPH	9843	37	X	65476115	65476115	Missense_Mutation	SNP	G	A	13	23	c.2848G>A	c.(2848-2850)GAT>AAT	p.D950N
Pat_76	Post-Resistance	AR	367	37	X	66905918	66905918	Missense_Mutation	SNP	G	T	4	15	c.1835G>T	c.(1834-1836)TGT>TTT	p.C612F
Pat_76	Post-Resistance	OTUD6A	139562	37	X	69283186	69283187	Missense_Mutation	DNP	CC	TT	5	22	c.812_813CC>TT	c.(811-813)TCC>TTT	p.S271F
Pat_76	Post-Resistance	DGAT2L6	347516	37	X	69419701	69419701	Nonsense_Mutation	SNP	G	A	9	20	c.236G>A	c.(235-237)TGG>TAG	p.W79*
Pat_76	Post-Resistance	P2RY4	5030	37	X	69478907	69478907	Missense_Mutation	SNP	G	A	9	27	c.568C>T	c.(568-570)CGG>TGG	p.R190W
Pat_76	Post-Resistance	MED12	9968	37	X	70344131	70344131	Missense_Mutation	SNP	G	A	11	24	c.1867G>A	c.(1867-1869)GAC>AAC	p.D623N
Pat_76	Post-Resistance	TAF1	6872	37	X	70586306	70586306	Missense_Mutation	SNP	G	A	4	14	c.142G>A	c.(142-144)GGA>AGA	p.G48R
Pat_76	Post-Resistance	TAF1	6872	37	X	70597668	70597668	Missense_Mutation	SNP	T	G	5	23	c.927T>G	c.(925-927)GAT>GAG	p.D309E
Pat_76	Post-Resistance	ACRC	93953	37	X	70823696	70823696	Missense_Mutation	SNP	A	G	88	353	c.569A>G	c.(568-570)GAC>GGC	p.D190G
Pat_76	Post-Resistance	RGAG4	340526	37	X	71350547	71350547	Missense_Mutation	SNP	C	T	28	72	c.844G>A	c.(844-846)GAA>AAA	p.E282K
Pat_76	Post-Resistance	PHKA1	5255	37	X	71830949	71830949	Missense_Mutation	SNP	C	T	11	22	c.2455G>A	c.(2455-2457)GAA>AAA	p.E819K
Pat_76	Post-Resistance	PHKA1	5255	37	X	71838692	71838692	Missense_Mutation	SNP	G	A	7	29	c.2237C>T	c.(2236-2238)TCT>TTT	p.S746F
Pat_76	Post-Resistance	PHKA1	5255	37	X	71838696	71838696	Missense_Mutation	SNP	G	A	7	29	c.2233C>T	c.(2233-2235)CCC>TCC	p.P745S
Pat_76	Post-Resistance	ZCCHC13	389874	37	X	73524355	73524355	Missense_Mutation	SNP	G	A	11	36	c.254G>A	c.(253-255)CGA>CAA	p.R85Q
Pat_76	Post-Resistance	ATRX	546	37	X	76939192	76939192	Missense_Mutation	SNP	G	A	37	92	c.1556C>T	c.(1555-1557)TCT>TTT	p.S519F
Pat_76	Post-Resistance	ATP7A	538	37	X	77254089	77254089	Missense_Mutation	SNP	G	A	19	72	c.1451G>A	c.(1450-1452)GGA>GAA	p.G484E
Pat_76	Post-Resistance	FAM46D	169966	37	X	79698084	79698084	Missense_Mutation	SNP	A	C	6	12	c.46A>C	c.(46-48)ACA>CCA	p.T16P
Pat_76	Post-Resistance	RPS6KA6	27330	37	X	83357077	83357077	Missense_Mutation	SNP	G	A	4	21	c.1744C>T	c.(1744-1746)CCA>TCA	p.P582S
Pat_76	Post-Resistance	TSPAN6	7105	37	X	99885830	99885830	Missense_Mutation	SNP	G	A	7	26	c.703C>T	c.(703-705)CGT>TGT	p.R235C
Pat_76	Post-Resistance	DRP2	1821	37	X	100492690	100492690	Missense_Mutation	SNP	G	A	22	78	c.364G>A	c.(364-366)GAT>AAT	p.D122N
Pat_76	Post-Resistance	NXF2B	728343	37	X	101623758	101623758	Missense_Mutation	SNP	G	A	10	54	c.604C>T	c.(604-606)CCC>TCC	p.P202S
Pat_76	Post-Resistance	GPRASP1	9737	37	X	101911210	101911210	Missense_Mutation	SNP	G	A	22	42	c.2369G>A	c.(2368-2370)AGA>AAA	p.R790K
Pat_76	Post-Resistance	GPRASP2	114928	37	X	101971581	101971581	Missense_Mutation	SNP	C	T	11	34	c.1784C>T	c.(1783-1785)TCT>TTT	p.S595F
Pat_76	Post-Resistance	RAB40AL	282808	37	X	102192944	102192944	Missense_Mutation	SNP	C	T	25	102	c.698C>T	c.(697-699)GCC>GTC	p.A233V
Pat_76	Post-Resistance	ESX1	80712	37	X	103499043	103499043	Missense_Mutation	SNP	C	T	22	28	c.298G>A	c.(298-300)GAG>AAG	p.E100K
Pat_76	Post-Resistance	ESX1	80712	37	X	103499180	103499181	Missense_Mutation	DNP	CC	TT	54	163	c.160_161GG>AA	c.(160-162)GGA>AAA	p.G54K
Pat_76	Post-Resistance	MORC4	79710	37	X	106185285	106185285	Missense_Mutation	SNP	C	T	8	25	c.2543G>A	c.(2542-2544)AGA>AAA	p.R848K
Pat_76	Post-Resistance	VSIG1	340547	37	X	107315967	107315967	Missense_Mutation	SNP	C	T	35	66	c.473C>T	c.(472-474)TCC>TTC	p.S158F
Pat_76	Post-Resistance	VSIG1	340547	37	X	107320451	107320451	Missense_Mutation	SNP	G	A	4	13	c.1004G>A	c.(1003-1005)GGA>GAA	p.G335E
Pat_76	Post-Resistance	COL4A6	1288	37	X	107413919	107413919	Missense_Mutation	SNP	C	T	36	52	c.3416G>A	c.(3415-3417)GGA>GAA	p.G1139E
Pat_76	Post-Resistance	COL4A6	1288	37	X	107430407	107430407	Missense_Mutation	SNP	C	T	52	99	c.1873G>A	c.(1873-1875)GGA>AGA	p.G625R
Pat_76	Post-Resistance	COL4A6	1288	37	X	107431160	107431160	Missense_Mutation	SNP	G	A	29	54	c.1688C>T	c.(1687-1689)TCT>TTT	p.S563F
Pat_76	Post-Resistance	COL4A5	1287	37	X	107814644	107814644	Missense_Mutation	SNP	G	A	11	35	c.386G>A	c.(385-387)GGA>GAA	p.G129E
Pat_76	Post-Resistance	COL4A5	1287	37	X	107865965	107865965	Nonsense_Mutation	SNP	A	T	12	21	c.2827A>T	c.(2827-2829)AAA>TAA	p.K943*
Pat_76	Post-Resistance	GUCY2F	2986	37	X	108697082	108697082	Missense_Mutation	SNP	G	A	5	7	c.1039C>T	c.(1039-1041)CCG>TCG	p.P347S
Pat_76	Post-Resistance	DCX	1641	37	X	110576334	110576335	Missense_Mutation	DNP	GG	AA	6	19	c.995_996CC>TT	c.(994-996)GCC>GTT	p.A332V
Pat_76	Post-Resistance	SLC6A14	11254	37	X	115590014	115590014	Missense_Mutation	SNP	C	A	6	49	c.1822C>A	c.(1822-1824)CCA>ACA	p.P608T
Pat_76	Post-Resistance	KLHL13	90293	37	X	117079486	117079486	Missense_Mutation	SNP	C	T	7	23	c.151G>A	c.(151-153)GAA>AAA	p.E51K
Pat_76	Post-Resistance	WDR44	54521	37	X	117577623	117577623	Missense_Mutation	SNP	C	T	22	32	c.2485C>T	c.(2485-2487)CGT>TGT	p.R829C
Pat_76	Post-Resistance	DOCK11	139818	37	X	117676792	117676792	Missense_Mutation	SNP	G	A	23	54	c.207G>A	c.(205-207)ATG>ATA	p.M69I
Pat_76	Post-Resistance	DOCK11	139818	37	X	117744362	117744362	Missense_Mutation	SNP	G	A	10	32	c.3077G>A	c.(3076-3078)AGT>AAT	p.S1026N
Pat_76	Post-Resistance	LONRF3	79836	37	X	118123461	118123461	Missense_Mutation	SNP	G	A	7	28	c.1150G>A	c.(1150-1152)GGG>AGG	p.G384R
Pat_76	Post-Resistance	UPF3B	65109	37	X	118985459	118985459	Missense_Mutation	SNP	T	G	4	15	c.369A>C	c.(367-369)AAA>AAC	p.K123N
Pat_76	Post-Resistance	AKAP14	158798	37	X	119037548	119037548	Missense_Mutation	SNP	C	T	5	12	c.260C>T	c.(259-261)TCG>TTG	p.S87L
Pat_76	Post-Resistance	ODZ1	10178	37	X	123699255	123699255	Missense_Mutation	SNP	G	A	21	28	c.2233C>T	c.(2233-2235)CCT>TCT	p.P745S
Pat_76	Post-Resistance	ACTRT1	139741	37	X	127185537	127185537	Missense_Mutation	SNP	C	T	27	65	c.649G>A	c.(649-651)GAG>AAG	p.E217K
Pat_76	Post-Resistance	OCRL	4952	37	X	128703368	128703368	Missense_Mutation	SNP	C	T	16	79	c.1594C>T	c.(1594-1596)CAT>TAT	p.H532Y

Pat_76	Post-Resistance	ZDHHC9	51114	37	X	128957792	128957792	Missense_Mutation	SNP	G	A	27	46	c.350C>T	c.(349-351)CCC>CTC	p.P117L
Pat_76	Post-Resistance	ELF4	2000	37	X	129203363	129203363	Missense_Mutation	SNP	C	T	24	86	c.1099G>A	c.(1099-1101)GGA>AGA	p.G367R
Pat_76	Post-Resistance	ARHGAP36	158763	37	X	130218339	130218339	Missense_Mutation	SNP	C	T	10	21	c.706C>T	c.(706-708)CCC>TCC	p.P236S
Pat_76	Post-Resistance	IGSF1	3547	37	X	130409467	130409467	Missense_Mutation	SNP	C	T	30	80	c.3169G>A	c.(3169-3171)GAA>AAA	p.E1057K
Pat_76	Post-Resistance	MBNL3	55796	37	X	131573612	131573612	Missense_Mutation	SNP	G	A	49	116	c.28C>T	c.(28-30)CGT>TGT	p.R10C
Pat_76	Post-Resistance	USP26	83844	37	X	132160571	132160571	Missense_Mutation	SNP	G	A	3	18	c.1678C>T	c.(1678-1680)CCC>TCC	p.P560S
Pat_76	Post-Resistance	MMGT1	93380	37	X	135047268	135047268	Missense_Mutation	SNP	G	A	42	93	c.311C>T	c.(310-312)TCG>TTG	p.S104L
Pat_76	Post-Resistance	GPR112	139378	37	X	135431671	135431671	Missense_Mutation	SNP	G	A	7	37	c.5806G>A	c.(5806-5808)GCA>ACA	p.A1936T
Pat_76	Post-Resistance	MAGEC1	9947	37	X	140993818	140993818	Missense_Mutation	SNP	T	G	18	196	c.628T>G	c.(628-630)TTA>GTA	p.L210V
Pat_76	Post-Resistance	MAGEC1	9947	37	X	140994421	140994421	Missense_Mutation	SNP	C	T	35	61	c.1231C>T	c.(1231-1233)CCT>TCT	p.P411S
Pat_76	Post-Resistance	MAGEA11	4110	37	X	148797442	148797442	Missense_Mutation	SNP	C	T	23	58	c.296C>T	c.(295-297)CCC>CTC	p.P99L
Pat_76	Post-Resistance	MAGEA11	4110	37	X	148798372	148798373	Missense_Mutation	DNP	GG	AA	45	78	.1226_1227GG>A	c.(1225-1227)AGG>AAA	p.R409K
Pat_76	Post-Resistance	GPR50	9248	37	X	150348908	150348908	Missense_Mutation	SNP	T	G	30	52	c.853T>G	c.(853-855)TTC>GTC	p.F285V
Pat_76	Post-Resistance	MAGEA10	4109	37	X	151303507	151303507	Missense_Mutation	SNP	G	A	16	37	c.586C>T	c.(586-588)CCC>TCC	p.P196S
Pat_76	Post-Resistance	GABRQ	55879	37	X	151821313	151821314	Missense_Mutation	DNP	GG	AA	20	55	.1468_1469GG>A	c.(1468-1470)GGC>AAC	p.G490N
Pat_76	Post-Resistance	MAGEA6	4105	37	X	151869683	151869683	Nonsense_Mutation	SNP	C	T	76	90	c.373C>T	c.(373-375)CGA>TGA	p.R125*
Pat_76	Post-Resistance	MAGEA12	4111	37	X	151900098	151900098	Missense_Mutation	SNP	C	T	42	110	c.703G>A	c.(703-705)GAG>AAG	p.E235K
Pat_76	Post-Resistance	CETN2	1069	37	X	151996420	151996420	Missense_Mutation	SNP	A	G	13	57	c.484T>C	c.(484-486)TTC>CTC	p.F162L
Pat_76	Post-Resistance	HCFC1	3054	37	X	153217050	153217050	Missense_Mutation	SNP	G	A	33	62	c.5369C>T	c.(5368-5370)TCC>TTC	p.S1790F
Pat_76	Post-Resistance	HCFC1	3054	37	X	153224937	153224937	Missense_Mutation	SNP	G	A	10	22	c.1450C>T	c.(1450-1452)CCT>TCT	p.P484S
Pat_76	Post-Resistance	FLNA	2316	37	X	153594560	153594560	Nonsense_Mutation	SNP	G	A	26	34	c.1261C>T	c.(1261-1263)CAG>TAG	p.Q421*
Pat_76	Post-Resistance	PLXNA3	55558	37	X	153691999	153691999	Missense_Mutation	SNP	G	A	4	14	c.1513G>A	c.(1513-1515)GAC>AAC	p.D505N
Pat_76	Post-Resistance	PLXNA3	55558	37	X	153693191	153693191	Missense_Mutation	SNP	G	A	11	14	c.2023G>A	c.(2023-2025)GGC>AGC	p.G675S
Pat_76	Post-Resistance	PLXNA3	55558	37	X	153696206	153696206	Missense_Mutation	SNP	G	C	23	33	c.3682G>C	c.(3682-3684)GGT>CGT	p.G1228R
Pat_01	Pre-Treatment	RERE	473	37	1	8557555	8557555	Frame_Shift_Del	DEL	G	-	8	585	c.914delC	c.(913-915)CCAfs	p.P305fs
Pat_01	Pre-Treatment	PABPC4	8761	37	1	40028016	40028016	Frame_Shift_Del	DEL	G	-	7	491	c.1693delC	c.(1693-1695)CAGfs	p.Q565fs
Pat_01	Pre-Treatment	TMCO2	127391	37	1	40713708	40713709	Frame_Shift_Del	DEL	TC	-	14	732	c.43_44delTC	c.(43-45)TCTfs	p.S15fs
Pat_01	Pre-Treatment	SV2A	9900	37	1	149885223	149885225	In_Frame_Del	DEL	TCA	-	7	429	c.168_170delTGA	c.(166-171)GATGAC>GAC	p.56_57DD>D
Pat_01	Pre-Treatment	LCE1F	353137	37	1	152749003	152749008	In_Frame_Del	DEL	TGGCTC	-	8	305	156_161delTGGC	154-162)TGTGGCTCC>T	p.GS53del
Pat_01	Pre-Treatment	CCT3	7203	37	1	156290648	156290648	Frame_Shift_Del	DEL	T	-	9	706	c.591delA	c.(589-591)AAAfs	p.K197fs
Pat_01	Pre-Treatment	OR10Z1	128368	37	1	158576487	158576487	Frame_Shift_Del	DEL	G	-	9	1448	c.259delG	c.(259-261)GGGfs	p.G87fs
Pat_01	Pre-Treatment	NOS1AP	9722	37	1	162326888	162326890	In_Frame_Del	DEL	CAG	-	8	112	c.901_903delCAG	c.(901-903)CAGdel	p.Q306del
Pat_01	Pre-Treatment	LOC642587	642587	37	1	209605637	209605648	In_Frame_Del	DEL	CAGCAGCA	-	13	60	263delAGCAGCA	264)GTAGCAGCAGCAGC	p.AAAA93del
Pat_01	Pre-Treatment	DIP2C	22982	37	10	412274	412275	Frame_Shift_Del	DEL	CA	-	9	171	c.2208_2209delTG	c.(2206-2211)TGTGCAfs	p.C736fs
Pat_01	Pre-Treatment	NUP98	4928	37	11	3720389	3720389	Frame_Shift_Del	DEL	T	-	7	756	c.3932delA	c.(3931-3933)AACfs	p.N1311fs
Pat_01	Pre-Treatment	DENND5A	23258	37	11	9199797	9199799	In_Frame_Del	DEL	ATC	-	8	430	.1786_1788delGA	c.(1786-1788)GATdel	p.D596del
Pat_01	Pre-Treatment	AMPD3	272	37	11	10508911	10508915	Splice_Site	DEL	GGTGC	-	118	473	c.939_splice	c.e6+1	p.K313_splice
Pat_01	Pre-Treatment	NDUFV1	4723	37	11	67376193	67376194	Splice_Site	INS	-	GT	8	493	c.326_splice	c.e3+1	p.R109_splice
Pat_01	Pre-Treatment	PAK1	5058	37	11	77069990	77069992	In_Frame_Del	DEL	CAT	-	8	691	c.548_550delATG	c.(547-552)GATGCT>GCT	p.D183del
Pat_01	Pre-Treatment	CHD4	1108	37	12	6711207	6711209	In_Frame_Del	DEL	CTT	-	7	62	c.355_357delAAG	c.(355-357)AAGdel	p.K119del
Pat_01	Pre-Treatment	SFRS2IP	9169	37	12	46318575	46318577	In_Frame_Del	DEL	GGT	-	7	938	.3840_3842delAC	(3838-3843)CCACCC>CC	1280_1281PP>
Pat_01	Pre-Treatment	C12orf42	374470	37	12	103695960	103695960	Frame_Shift_Del	DEL	G	-	7	694	c.1009delC	c.(1009-1011)CGCfs	p.R337fs
Pat_01	Pre-Treatment	KIAA1704	55425	37	13	45580365	45580367	In_Frame_Del	DEL	GAT	-	18	1000	c.250_252delGAT	c.(250-252)GATdel	p.D88del
Pat_01	Pre-Treatment	ZC3H13	23091	37	13	46542016	46542017	Frame_Shift_Del	DEL	CT	-	8	300	c.3943_3944delAG	c.(3943-3945)AGGfs	p.R1315fs
Pat_01	Pre-Treatment	DZIP1	22873	37	13	96237096	96237096	Frame_Shift_Del	DEL	T	-	8	196	c.2418delA	c.(2416-2418)AAAfs	p.K806fs
Pat_01	Pre-Treatment	KIAA0391	9692	37	14	35592700	35592700	Frame_Shift_Del	DEL	T	-	9	197	c.249delT	c.(247-249)CATfs	p.H83fs
Pat_01	Pre-Treatment	ARID4A	5926	37	14	58831996	58831997	Frame_Shift_Del	DEL	AG	-	9	354	c.3189_3190delAG	c.(3187-3192)CAAGAGfs	p.Q1063fs

Pat_01	Pre-Treatment	AMN	81693	37	14	103396993	103396994	In_Frame_Ins	INS	-	GCCGGG	12	26	38_1339insGCCG	c.(1336-1341)insGCCGG	.448_449insA
Pat_01	Pre-Treatment	WDR72	256764	37	15	53992038	53992038	Frame_Shift_Del	DEL	A	-	12	1076	c.1674delT	c.(1672-1674)TTTfs	p.F558fs
Pat_01	Pre-Treatment	FEM1B	10116	37	15	68583340	68583340	Frame_Shift_Del	DEL	T	-	8	851	c.1644delT	c.(1642-1644)GATfs	p.D548fs
Pat_01	Pre-Treatment	CPLX3	594855	37	15	75122558	75122560	In_Frame_Del	DEL	GAG	-	7	564	c.340_342delGAG	c.(340-342)GAGdel	p.E118del
Pat_01	Pre-Treatment	UBN1	29855	37	16	4910691	4910693	In_Frame_Del	DEL	AGA	-	11	1032	c.698_700delAGA	.(697-702)GAGAAG>GA	p.K238del
Pat_01	Pre-Treatment	C16orf70	80262	37	16	67180989	67180989	Frame_Shift_Del	DEL	C	-	7	915	c.1224delC	c.(1222-1224)GGCfs	p.G408fs
Pat_01	Pre-Treatment	FANCA	2175	37	16	89869675	89869675	Frame_Shift_Del	DEL	T	-	7	448	c.784delA	c.(784-786)ATGfs	p.M262fs
Pat_01	Pre-Treatment	FXR2	9513	37	17	7495872	7495874	In_Frame_Del	DEL	CGG	-	14	1160	.1773_1775delCC	(1771-1776)CGCCGT>CG	.591_592RR>
Pat_01	Pre-Treatment	MYOCD	93649	37	17	12647692	12647694	In_Frame_Del	DEL	CAG	-	7	131	c.910_912delCAG	c.(910-912)CAGdel	p.Q310del
Pat_01	Pre-Treatment	CXXC1	30827	37	18	47812275	47812277	In_Frame_Del	DEL	CTG	-	7	170	c.481_483delCAG	c.(481-483)CAGdel	p.Q161del
Pat_01	Pre-Treatment	CRTC1	23373	37	19	18887993	18887993	Frame_Shift_Del	DEL	C	-	7	371	c.1706delC	c.(1705-1707)TCCfs	p.S569fs
Pat_01	Pre-Treatment	FFAR2	2867	37	19	35940788	35940790	In_Frame_Del	DEL	CTG	-	8	175	c.172_174delCTG	c.(172-174)CTGdel	p.L62del
Pat_01	Pre-Treatment	CCDC97	90324	37	19	41825698	41825700	In_Frame_Del	DEL	AGG	-	7	92	c.722_724delAGG	.(721-726)CAGGAG>CA	p.E245del
Pat_01	Pre-Treatment	FLT3LG	2323	37	19	49978960	49978962	In_Frame_Del	DEL	CTG	-	8	450	c.46_48delCTG	c.(46-48)CTGdel	p.L20del
Pat_01	Pre-Treatment	HS1BP3	64342	37	2	20840864	20840864	Frame_Shift_Del	DEL	G	-	9	1311	c.275delC	c.(274-276)CCAfs	p.P92fs
Pat_01	Pre-Treatment	AGBL5	60509	37	2	27278900	27278901	Frame_Shift_Ins	INS	-	C	8	1065	c.1259_1260insC	c.(1258-1260)ATCfs	p.I420fs
Pat_01	Pre-Treatment	ZNF831	128611	37	20	57766219	57766220	Frame_Shift_Ins	INS	-	C	10	163	c.145_146insC	c.(145-147)GCCfs	p.A49fs
Pat_01	Pre-Treatment	CCT8	10694	37	21	30445903	30445903	Frame_Shift_Del	DEL	A	-	83	282	c.9delT	c.(7-9)CTTfs	p.L3fs
Pat_01	Pre-Treatment	KRTAP10-6	386674	37	21	46012219	46012220	In_Frame_Ins	INS	-	CGCAGC	11	227	7insCAGCTGCTG	)CCG>CCCAGCTGCTGC	9_49P>PSCC
Pat_01	Pre-Treatment	TCF20	6942	37	22	42610948	42610948	Frame_Shift_Del	DEL	G	-	7	590	c.364delC	c.(364-366)CAGfs	p.Q122fs
Pat_01	Pre-Treatment	ATRIP	84126	37	3	48501288	48501288	Frame_Shift_Del	DEL	C	-	9	803	c.1028delC	c.(1027-1029)ACCfs	p.T343fs
Pat_01	Pre-Treatment	FOXP1	27086	37	3	71247357	71247359	In_Frame_Del	DEL	TGC	-	9	494	c.174_176delGCA	c.(172-177)CAGCAA>CAA	p.58_59QQ>Q
Pat_01	Pre-Treatment	VEPH1	79674	37	3	157081226	157081227	Frame_Shift_Ins	INS	-	T	9	334	c.1661_1662insA	c.(1660-1662)AACfs	p.N554fs
Pat_01	Pre-Treatment	EIF4A2	1974	37	3	186504426	186504427	Frame_Shift_Del	DEL	GA	-	131	285	c.763_764delGA	c.(763-765)GAGfs	p.E255fs
Pat_01	Pre-Treatment	FGFRL1	53834	37	4	1019055	1019056	Frame_Shift_Del	DEL	CA	-	9	47	c.1435_1436delC	c.(1435-1437)CACfs	p.H479fs
Pat_01	Pre-Treatment	FGF5	2250	37	4	81187992	81187994	In_Frame_Del	DEL	TCC	-	9	324	c.14_16delTCC	c.(13-18)TTCCTC>TTC	p.L9del
Pat_01	Pre-Treatment	ZFR	51663	37	5	32419951	32419953	In_Frame_Del	DEL	GGT	-	8	930	c.393_395delACC	.(391-396)CCACCC>CC	.131_132PP>
Pat_01	Pre-Treatment	THBS4	7060	37	5	79372774	79372776	In_Frame_Del	DEL	TGA	-	7	1219	.1989_1991delTG	.(1987-1992)TGTGAT>TG	p.D668del
Pat_01	Pre-Treatment	H2AFY	9555	37	5	134724672	134724673	Frame_Shift_Ins	INS	-	G	107	216	c.111_112insC	c.(109-114)CCCAAGfs	p.P37fs
Pat_01	Pre-Treatment	IK	3550	37	5	140032593	140032594	Frame_Shift_Del	DEL	GA	-	8	153	c.268_269delGA	c.(268-270)GAGfs	p.E90fs
Pat_01	Pre-Treatment	NUP153	9972	37	6	17633077	17633078	Splice_Site	INS	-	AA	10	54	c.2465_splice	c.e17-1	p.G822_splice
Pat_01	Pre-Treatment	BTN2A2	10385	37	6	26384091	26384093	In_Frame_Del	DEL	CCT	-	17	850	c.42_44delCCT	c.(40-45)TCCCTC>TCC	p.L24del
Pat_01	Pre-Treatment	PBX2	5089	37	6	32156158	32156160	In_Frame_Del	DEL	GCT	-	8	468	c.417_419delAGC	.(415-420)GCAGCT>GCT	.139_140AA>
Pat_01	Pre-Treatment	FOXP4	116113	37	6	41555085	41555085	Frame_Shift_Del	DEL	C	-	7	931	c.707delC	c.(706-708)GCCfs	p.A236fs
Pat_01	Pre-Treatment	OLIG3	167826	37	6	137815210	137815212	In_Frame_Del	DEL	TGG	-	7	277	c.96_98delCCA	c.(94-99)CACCAG>CAG	p.H32del
Pat_01	Pre-Treatment	PARK2	5071	37	6	161781122	161781122	Frame_Shift_Del	DEL	T	-	8	660	c.1283delA	c.(1282-1284)AATfs	p.N428fs
Pat_01	Pre-Treatment	CCDC126	90693	37	7	23651156	23651156	Frame_Shift_Del	DEL	T	-	308	363	c.222delT	c.(220-222)GCTfs	p.A74fs
Pat_01	Pre-Treatment	HOXA10	3206	37	7	27213229	27213231	In_Frame_Del	DEL	CGC	-	2	4	c.695_697delGCG	.(694-699)GGCGCG>GC	p.G232del
Pat_01	Pre-Treatment	INHBA	3624	37	7	41729741	41729743	In_Frame_Del	DEL	TTC	-	8	115	c.786_788delGAA	c.(784-789)AAGAAA>AAA	.262_263KK>
Pat_01	Pre-Treatment	PEX1	5189	37	7	92146721	92146721	Frame_Shift_Del	DEL	T	-	7	254	c.1108delA	c.(1108-1110)ATTfs	p.I370fs
Pat_01	Pre-Treatment	KIAA1147	57189	37	7	141365101	141365103	In_Frame_Del	DEL	AGC	-	7	329	c.836_838delGCT	c.(835-840)TGCTTG>TTG	p.C279del
Pat_01	Pre-Treatment	OR9A4	130075	37	7	141619203	141619203	Frame_Shift_Del	DEL	T	-	12	1014	c.528delT	c.(526-528)AATfs	p.N176fs
Pat_01	Pre-Treatment	EPHA1	2041	37	7	143095836	143095836	Frame_Shift_Del	DEL	C	-	7	460	c.1194delG	c.(1192-1194)GGGfs	p.G398fs
Pat_01	Pre-Treatment	ZNF777	27153	37	7	149152747	149152747	Frame_Shift_Del	DEL	G	-	7	943	c.367delC	c.(367-369)CACfs	p.H123fs
Pat_01	Pre-Treatment	ABCA1	19	37	9	107593323	107593323	Frame_Shift_Del	DEL	C	-	7	296	c.1775delG	c.(1774-1776)GGCfs	p.G592fs
Pat_01	Pre-Treatment	ENG	2022	37	9	130587583	130587584	Frame_Shift_Ins	INS	-	A	25	231	c.742_743insT	c.(742-744)GATfs	p.D248fs
Pat_01	Pre-Treatment	ARMCX3	51566	37	X	100880152	100880154	In_Frame_Del	DEL	TGA	-	7	699	c.183_185delTGA	c.(181-186)TCTGAT>TCT	p.D66del

Pat_01	Post-Resistance	ZBTB8A	653121	37	1	33065979	33065981	In_Frame_Del	DEL	GAA	-	7	369	.1285_1287delGA	c.(1285-1287)GAAdel	p.E433del
Pat_01	Post-Resistance	RHBDL2	54933	37	1	39384834	39384834	Frame_Shift_Del	DEL	C	-	7	356	c.51delG	c.(49-51)GGGfs	p.G17fs
Pat_01	Post-Resistance	MFSD2A	84879	37	1	40424435	40424435	Frame_Shift_Del	DEL	C	-	7	968	c.330delC	c.(328-330)GACfs	p.D110fs
Pat_01	Post-Resistance	TMCO2	127391	37	1	40713708	40713709	Frame_Shift_Del	DEL	TC	-	7	809	c.43_44delTC	c.(43-45)TCTfs	p.S15fs
Pat_01	Post-Resistance	KDM4A	9682	37	1	44157180	44157180	Frame_Shift_Del	DEL	C	-	7	642	c.2256delC	c.(2254-2256)GTCfs	p.V752fs
Pat_01	Post-Resistance	MAST2	23139	37	1	46494559	46494559	Frame_Shift_Del	DEL	T	-	8	793	c.2172delT	c.(2170-2172)CCTfs	p.P724fs
Pat_01	Post-Resistance	DOCK7	85440	37	1	63128738	63128738	Frame_Shift_Del	DEL	G	-	7	1409	c.102delC	c.(100-102)CTCfs	p.L34fs
Pat_01	Post-Resistance	WDR78	79819	37	1	67390426	67390426	Frame_Shift_Del	DEL	T	-	7	597	c.89delA	c.(88-90)AAGfs	p.K30fs
Pat_01	Post-Resistance	LPAR3	23566	37	1	85331664	85331665	Frame_Shift_Ins	INS	-	A	8	288	c.139_140insT	c.(139-141)TCTfs	p.S47fs
Pat_01	Post-Resistance	TCHH	7062	37	1	152082211	152082213	In_Frame_Del	DEL	CTC	-	10	209	.3480_3482delGA	.(3478-3483)AAGAGA>AA	p.R1163del
Pat_01	Post-Resistance	TCHH	7062	37	1	152084580	152084582	In_Frame_Del	DEL	CTC	-	12	188	.1111_1113delGA	c.(1111-1113)GAGdel	p.E371del
Pat_01	Post-Resistance	PRCC	5546	37	1	156761535	156761536	Frame_Shift_Ins	INS	-	C	14	765	c.1130_1131insC	c.(1129-1131)GTCfs	p.V377fs
Pat_01	Post-Resistance	NOS1AP	9722	37	1	162326758	162326758	Frame_Shift_Del	DEL	C	-	9	1331	c.771delC	c.(769-771)CACfs	p.H257fs
Pat_01	Post-Resistance	TNR	7143	37	1	175372615	175372615	Frame_Shift_Del	DEL	C	-	10	1438	c.637delG	c.(637-639)GTGfs	p.V213fs
Pat_01	Post-Resistance	DHX9	1660	37	1	182845333	182845333	Frame_Shift_Del	DEL	T	-	7	1233	c.1964delT	c.(1963-1965)GTTfs	p.V655fs
Pat_01	Post-Resistance	CFH	3075	37	1	196646766	196646766	Frame_Shift_Del	DEL	T	-	8	1559	c.588delT	c.(586-588)GGTfs	p.G196fs
Pat_01	Post-Resistance	LOC642587	642587	37	1	209605637	209605648	In_Frame_Del	DEL	CAGCAGCA	-	11	55	263delAGCAGCA	264)GTAGCAGCAGCAGC	p.AAAA93del
Pat_01	Post-Resistance	TMEM206	55248	37	1	212548597	212548597	Frame_Shift_Del	DEL	T	-	7	870	c.829delA	c.(829-831)AGTfs	p.S277fs
Pat_01	Post-Resistance	PTPN14	5784	37	1	214588042	214588042	Frame_Shift_Del	DEL	T	-	9	1572	c.372delA	c.(370-372)AAAfs	p.K124fs
Pat_01	Post-Resistance	OBSCN	84033	37	1	228467013	228467013	Frame_Shift_Del	DEL	G	-	7	656	c.7264delG	c.(7264-7266)GGGfs	p.G2422fs
Pat_01	Post-Resistance	SLC16A9	220963	37	10	61414180	61414180	Frame_Shift_Del	DEL	T	-	8	278	c.604delA	c.(604-606)ATAfs	p.I202fs
Pat_01	Post-Resistance	ANAPC16	119504	37	10	73983786	73983786	Frame_Shift_Del	DEL	C	-	7	557	c.114delC	c.(112-114)TACfs	p.Y38fs
Pat_01	Post-Resistance	APBB1	322	37	11	6423808	6423808	Frame_Shift_Del	DEL	C	-	9	504	c.1252delG	c.(1252-1254)GAAfs	p.E418fs
Pat_01	Post-Resistance	AMPD3	272	37	11	10508911	10508915	Splice_Site	DEL	GGTGC	-	49	644	c.939_splice	c.e6+1	p.K313_splice
Pat_01	Post-Resistance	PSMA1	5682	37	11	14529252	14529254	In_Frame_Del	DEL	CAT	-	8	681	c.683_685delATG	c.(682-687)GATGTG>GTG	p.D228del
Pat_01	Post-Resistance	C11orf46	120534	37	11	30352754	30352754	Frame_Shift_Del	DEL	A	-	17	635	c.259delA	c.(259-261)AAAfs	p.K87fs
Pat_01	Post-Resistance	PRRG4	79056	37	11	32874997	32874999	In_Frame_Del	DEL	CAC	-	9	685	c.605_607delCAC	c.(604-609)TCACCA>TCA	p.P206del
Pat_01	Post-Resistance	OR8H3	390152	37	11	55890089	55890089	Frame_Shift_Del	DEL	A	-	7	1904	c.241delA	c.(241-243)AAAfs	p.K81fs
Pat_01	Post-Resistance	FADS2	9415	37	11	61615748	61615748	Frame_Shift_Del	DEL	C	-	7	699	c.736delC	c.(736-738)CCCfs	p.P246fs
Pat_01	Post-Resistance	RARRES3	5920	37	11	63313709	63313709	Frame_Shift_Del	DEL	A	-	9	297	c.476delA	c.(475-477)CAAfs	p.Q159fs
Pat_01	Post-Resistance	DRAP1	10589	37	11	65688853	65688853	Frame_Shift_Del	DEL	C	-	8	797	c.565delC	c.(565-567)CCCfs	p.P189fs
Pat_01	Post-Resistance	PRDM10	56980	37	11	129772249	129772251	In_Frame_Del	DEL	TGG	-	8	1025	.3440_3442delCC	.(3439-3444)ACCAAC>AA	p.T1147del
Pat_01	Post-Resistance	ZCRB1	85437	37	12	42706971	42706971	Frame_Shift_Del	DEL	T	-	7	111	c.552delA	c.(550-552)AAAfs	p.K184fs
Pat_01	Post-Resistance	SFRS2IP	9169	37	12	46318575	46318577	In_Frame_Del	DEL	GGT	-	10	1216	.3840_3842delAC	(3838-3843)CCACCC>CC	1280_1281PP
Pat_01	Post-Resistance	MLL2	8085	37	12	49442512	49442514	In_Frame_Del	DEL	TCC	-	7	1216	.4059_4061delGG	(4057-4062)GAGGAA>GA	1353_1354EE
Pat_01	Post-Resistance	PRPF40B	25766	37	12	50025258	50025258	Frame_Shift_Del	DEL	C	-	10	676	c.93delC	c.(91-93)ATCfs	p.I31fs
Pat_01	Post-Resistance	SUOX	6821	37	12	56397930	56397930	Frame_Shift_Del	DEL	T	-	7	616	c.757delT	c.(757-759)TTTfs	p.F253fs
Pat_01	Post-Resistance	ACACB	32	37	12	109604774	109604775	Frame_Shift_Ins	INS	-	G	7	474	c.762_763insG	c.(760-765)TTTGGGfs	p.F254fs
Pat_01	Post-Resistance	KIAA1704	55425	37	13	45580365	45580367	In_Frame_Del	DEL	GAT	-	13	1122	c.250_252delGAT	c.(250-252)GATdel	p.D88del
Pat_01	Post-Resistance	LRCH1	23143	37	13	47243183	47243186	Frame_Shift_Del	DEL	CCTG	-	16	1460	.471_474delCCT	c.(469-474)GCCCTGfs	p.A157fs
Pat_01	Post-Resistance	IRF9	10379	37	14	24633132	24633134	In_Frame_Del	DEL	AGC	-	10	270	c.541_543delAGC	c.(541-543)AGCdel	p.S187del
Pat_01	Post-Resistance	IPO4	79711	37	14	24655611	24655611	Frame_Shift_Del	DEL	A	-	7	748	c.887delT	c.(886-888)TTCfs	p.F296fs
Pat_01	Post-Resistance	KIAA0391	9692	37	14	35592700	35592700	Frame_Shift_Del	DEL	T	-	8	234	c.249delT	c.(247-249)CATfs	p.H83fs
Pat_01	Post-Resistance	ARID4A	5926	37	14	58831996	58831997	Frame_Shift_Del	DEL	AG	-	10	392	.3189_3190delA	c.(3187-3192)CAAGAGfs	p.Q1063fs
Pat_01	Post-Resistance	DDX24	57062	37	14	94545821	94545823	In_Frame_Del	DEL	CCT	-	16	549	c.266_268delAGG	.(265-270)GAGGGA>GG	p.E89del
Pat_01	Post-Resistance	HSP90AA1	3320	37	14	102552130	102552130	Frame_Shift_Del	DEL	G	-	8	743	c.494delC	c.(493-495)TCAfs	p.S165fs
Pat_01	Post-Resistance	AMN	81693	37	14	103396993	103396994	In_Frame_Ins	INS	-	GCCGGG	14	12	38_1339insGCCG	c.(1336-1341)insGCCGGG	.448_449insA

Pat_01	Post-Resistance	NIPA1	123606	37	15	23086365	23086367	In_Frame_Del	DEL	GCC	-	4	9	c.45_47delGGC	c.(43-48)GCGGCC>GCC	p.15_16AA>A
Pat_01	Post-Resistance	PIGB	9488	37	15	55621922	55621922	Frame_Shift_Del	DEL	T	-	8	914	c.523delT	c.(523-525)TTTfs	p.F175fs
Pat_01	Post-Resistance	RNF111	54778	37	15	59359142	59359144	In_Frame_Del	DEL	CAC	-	7	974	.1546_1548delCA	c.(1546-1548)CACdel	p.H520del
Pat_01	Post-Resistance	PPIB	5479	37	15	64454280	64454280	Frame_Shift_Del	DEL	G	-	10	2889	c.209delC	c.(208-210)CCAfs	p.P70fs
Pat_01	Post-Resistance	KIAA1199	57214	37	15	81173394	81173394	Frame_Shift_Del	DEL	T	-	7	580	c.534delT	c.(532-534)TATfs	p.Y178fs
Pat_01	Post-Resistance	MKL2	57496	37	16	14334253	14334255	In_Frame_Del	DEL	CAG	-	10	686	c.991_993delCAG	c.(991-993)CAGdel	p.Q334del
Pat_01	Post-Resistance	IL4R	3566	37	16	27373787	27373789	In_Frame_Del	DEL	GAG	-	9	115	.1114_1116delGA	c.(1114-1116)GAGdel	p.E376del
Pat_01	Post-Resistance	IL21R	50615	37	16	27460530	27460530	Frame_Shift_Del	DEL	C	-	8	293	c.1543delC	c.(1543-1545)CCCfs	p.P515fs
Pat_01	Post-Resistance	CD2BP2	10421	37	16	30365545	30365545	Frame_Shift_Del	DEL	C	-	8	1078	c.177delG	c.(175-177)GGGfs	p.G59fs
Pat_01	Post-Resistance	LRRC36	55282	37	16	67409201	67409201	Frame_Shift_Del	DEL	C	-	7	1807	c.1546delC	c.(1546-1548)CCCfs	p.P516fs
Pat_01	Post-Resistance	WWP2	11060	37	16	69959337	69959338	Frame_Shift_Ins	INS	-	T	8	2315	c.1184_1185insT	c.(1183-1185)TCGfs	p.S395fs
Pat_01	Post-Resistance	FXR2	9513	37	17	7495872	7495874	In_Frame_Del	DEL	CGG	-	19	1162	.1773_1775delCC	(1771-1776)CGCCGT>CG	.591_592RR>
Pat_01	Post-Resistance	KDM6B	23135	37	17	7750576	7750576	Frame_Shift_Del	DEL	C	-	7	805	c.1063delC	c.(1063-1065)CCCfs	p.P355fs
Pat_01	Post-Resistance	MYH10	4628	37	17	8415820	8415822	In_Frame_Del	DEL	TTC	-	11	101	.2806_2808delGA	c.(2806-2808)GAAdel	p.E936del
Pat_01	Post-Resistance	NUFIP2	57532	37	17	27620932	27620934	In_Frame_Del	DEL	TGG	-	13	858	c.144_146delCCA	c.(142-147)CACCAT>CAT	p.48_49HH>H
Pat_01	Post-Resistance	TTLL6	284076	37	17	46863643	46863643	Frame_Shift_Del	DEL	C	-	7	1537	c.1644delG	c.(1642-1644)AAGfs	p.K548fs
Pat_01	Post-Resistance	VEZF1	7716	37	17	56056605	56056607	In_Frame_Del	DEL	TGC	-	7	813	.1044_1046delGC	.(1042-1047)CAGCAA>CA	.348_349QQ>
Pat_01	Post-Resistance	TEX2	55852	37	17	62291438	62291440	In_Frame_Del	DEL	TCC	-	7	216	c.138_140delGGA	.(136-141)GAGGAA>GA	p.46_47EE>E
Pat_01	Post-Resistance	C18orf19	125228	37	18	13681751	13681751	Frame_Shift_Del	DEL	T	-	7	603	c.326delA	c.(325-327)AAGfs	p.K109fs
Pat_01	Post-Resistance	C18orf8	29919	37	18	21110531	21110531	Frame_Shift_Del	DEL	G	-	7	507	c.1849delG	c.(1849-1851)GAAfs	p.E617fs
Pat_01	Post-Resistance	CXXC1	30827	37	18	47812275	47812277	In_Frame_Del	DEL	CTG	-	10	147	c.481_483delCAG	c.(481-483)CAGdel	p.Q161del
Pat_01	Post-Resistance	STK11	6794	37	19	1207156	1207156	Frame_Shift_Del	DEL	A	-	11	22	c.244delA	c.(244-246)AAGfs	p.K82fs
Pat_01	Post-Resistance	FFAR2	2867	37	19	35940788	35940790	In_Frame_Del	DEL	CTG	-	7	161	c.172_174delCTG	c.(172-174)CTGdel	p.L62del
Pat_01	Post-Resistance	PLEKHG2	64857	37	19	39913725	39913725	Frame_Shift_Del	DEL	C	-	7	952	c.2031delC	c.(2029-2031)GTCfs	p.V677fs
Pat_01	Post-Resistance	CD3EAP	10849	37	19	45910372	45910372	Frame_Shift_Del	DEL	C	-	8	896	c.43delC	c.(43-45)CCCfs	p.P15fs
Pat_01	Post-Resistance	PLEKHA4	57664	37	19	49340723	49340723	Frame_Shift_Del	DEL	G	-	7	575	c.2163delC	c.(2161-2163)CCCfs	p.P721fs
Pat_01	Post-Resistance	ZNF816A	125893	37	19	53454172	53454173	Frame_Shift_Del	DEL	TG	-	11	618	c.855_856delCA	c.(853-858)TACAAGfs	p.Y285fs
Pat_01	Post-Resistance	SMC6	79677	37	2	17898126	17898126	Frame_Shift_Del	DEL	T	-	7	101	c.1228delA	c.(1228-1230)ATAfs	p.I410fs
Pat_01	Post-Resistance	FOXN2	3344	37	2	48573666	48573667	Frame_Shift_Ins	INS	-	A	7	401	c.313_314insA	c.(313-315)GAAfs	p.E105fs
Pat_01	Post-Resistance	EHBP1	23301	37	2	63101604	63101604	Frame_Shift_Del	DEL	A	-	7	653	c.1227delA	c.(1225-1227)CCAfs	p.P409fs
Pat_01	Post-Resistance	AFTPH	54812	37	2	64778672	64778674	In_Frame_Del	DEL	GAT	-	9	900	c.64_66delGAT	c.(64-66)GATdel	p.D26del
Pat_01	Post-Resistance	REV1	51455	37	2	100055102	100055102	Frame_Shift_Del	DEL	T	-	8	537	c.1174delA	c.(1174-1176)ATGfs	p.M392fs
Pat_01	Post-Resistance	SULT1C3	442038	37	2	108863685	108863685	Frame_Shift_Del	DEL	A	-	7	361	c.35delA	c.(34-36)GAAfs	p.E12fs
Pat_01	Post-Resistance	TNFAIP6	7130	37	2	152226673	152226673	Frame_Shift_Del	DEL	A	-	7	814	c.534delA	c.(532-534)TTAfs	p.L178fs
Pat_01	Post-Resistance	WIPF1	7456	37	2	175436671	175436673	In_Frame_Del	DEL	GAG	-	7	141	c.860_862delCTC	.(859-864)CCTCAG>CAG	p.P287del
Pat_01	Post-Resistance	PPP1R1C	151242	37	2	182852619	182852619	Frame_Shift_Del	DEL	C	-	7	1341	c.135delC	c.(133-135)AACfs	p.N45fs
Pat_01	Post-Resistance	SGOL2	151246	37	2	201437003	201437004	Frame_Shift_Ins	INS	-	T	8	347	c.1934_1935insT	c.(1933-1935)AATfs	p.N645fs
Pat_01	Post-Resistance	C2orf67	151050	37	2	210887680	210887680	Frame_Shift_Del	DEL	T	-	8	123	c.2957delA	c.(2956-2958)AATfs	p.N986fs
Pat_01	Post-Resistance	RQCD1	9125	37	2	219449364	219449364	Frame_Shift_Del	DEL	T	-	9	1803	c.350delT	c.(349-351)CTTfs	p.L117fs
Pat_01	Post-Resistance	GIGYF2	26058	37	2	233676006	233676008	In_Frame_Del	DEL	CAG	-	10	648	.1951_1953delCA	c.(1951-1953)CAGdel	p.Q655del
Pat_01	Post-Resistance	HDLBP	3069	37	2	242186208	242186208	Frame_Shift_Del	DEL	C	-	8	561	c.1909delG	c.(1909-1911)GAAfs	p.E637fs
Pat_01	Post-Resistance	CST4	1472	37	20	23667825	23667826	Frame_Shift_Ins	INS	-	C	7	851	c.241_242insG	c.(241-243)GTGfs	p.V81fs
Pat_01	Post-Resistance	CCT8	10694	37	21	30445903	30445903	Frame_Shift_Del	DEL	A	-	88	427	c.9delT	c.(7-9)CTTfs	p.L3fs
Pat_01	Post-Resistance	PWP2	5822	37	21	45535692	45535694	In_Frame_Del	DEL	GAG	-	7	99	c.727_729delGAG	c.(727-729)GAGdel	p.E247del
Pat_01	Post-Resistance	TBC1D10A	83874	37	22	30691732	30691732	Frame_Shift_Del	DEL	C	-	8	292	c.518delG	c.(517-519)GGCfs	p.G173fs
Pat_01	Post-Resistance	CDC42EP1	11135	37	22	37964409	37964429	In_Frame_Del	DEL	CTGCTGCA	-	7	152	AGCGCCTGCTG	AGCGCCTGCTGCAAAC	APAANPS254
Pat_01	Post-Resistance	GRM7	2917	37	3	7621013	7621013	Frame_Shift_Del	DEL	T	-	7	158	c.2420delT	c.(2419-2421)ATTfs	p.I807fs

Pat_01	Post-Resistance	MAGI1	9223	37	3	65342666	65342666	Frame_Shift_Del	DEL	T	-	7	1008	c.3776delA	c.(3775-3777)AAGfs	p.K1259fs
Pat_01	Post-Resistance	LRIG1	26018	37	3	66436625	66436627	In_Frame_Del	DEL	GCT	-	10	1499	.1567_1569delAG	c.(1567-1569)AGCdel	p.S524del
Pat_01	Post-Resistance	FOXP1	27086	37	3	71247357	71247359	In_Frame_Del	DEL	TGC	-	16	457	c.174_176delGCA	c.(172-177)CAGCAA>CAA	p.58_59QQ>Q
Pat_01	Post-Resistance	CCDC80	151887	37	3	112326049	112326049	Frame_Shift_Del	DEL	C	-	8	597	c.2480delG	c.(2479-2481)GGAfs	p.G827fs
Pat_01	Post-Resistance	KALRN	8997	37	3	123946891	123946891	Frame_Shift_Del	DEL	A	-	8	726	c.122delA	c.(121-123)GAAfs	p.E41fs
Pat_01	Post-Resistance	TMEM108	66000	37	3	133098606	133098606	Frame_Shift_Del	DEL	G	-	8	1430	c.51delG	c.(49-51)CTGfs	p.L17fs
Pat_01	Post-Resistance	VEPH1	79674	37	3	157081227	157081227	Frame_Shift_Del	DEL	T	-	8	440	c.1661delA	c.(1660-1662)AACfs	p.N554fs
Pat_01	Post-Resistance	PSMD2	5708	37	3	184024574	184024574	Frame_Shift_Del	DEL	G	-	7	1137	c.1986delG	c.(1984-1986)ATGfs	p.M662fs
Pat_01	Post-Resistance	MUC4	4585	37	3	195517485	195517486	Frame_Shift_Del	DEL	AG	-	7	556	c.965_966delCT	c.(964-966)TCTfs	p.S322fs
Pat_01	Post-Resistance	UBXN7	26043	37	3	196088753	196088753	Frame_Shift_Del	DEL	T	-	7	423	c.1270delA	c.(1270-1272)AGGfs	p.R424fs
Pat_01	Post-Resistance	PDE6B	5158	37	4	661763	661765	In_Frame_Del	DEL	AGG	-	9	324	.2471_2473delAG	(2470-2475)AAGGAG>AA	p.E828del
Pat_01	Post-Resistance	CRIPAK	285464	37	4	1389057	1389058	Frame_Shift_Ins	INS	-	AT	7	1017	c.758_759insAT	c.(757-759)ACGfs	p.T253fs
Pat_01	Post-Resistance	CRIPAK	285464	37	4	1389287	1389287	Frame_Shift_Del	DEL	C	-	7	1193	c.988delC	c.(988-990)CCCfs	p.P330fs
Pat_01	Post-Resistance	GRPEL1	80273	37	4	7062606	7062606	Frame_Shift_Del	DEL	C	-	8	1743	c.637delG	c.(637-639)GTGfs	p.V213fs
Pat_01	Post-Resistance	FRYL	285527	37	4	48622661	48622662	Frame_Shift_Del	DEL	AG	-	7	1270	c.308_309delCT	c.(307-309)TCTfs	p.S103fs
Pat_01	Post-Resistance	PKD2	5311	37	4	88986559	88986559	Frame_Shift_Del	DEL	A	-	9	422	c.2152delA	c.(2152-2154)AAAfs	p.K718fs
Pat_01	Post-Resistance	ANK2	287	37	4	114214679	114214681	In_Frame_Del	DEL	CAC	-	8	381	.2460_2462delCA	(2458-2463)GTCACC>GT	p.T826del
Pat_01	Post-Resistance	INTU	27152	37	4	128608872	128608872	Frame_Shift_Del	DEL	T	-	7	699	c.1299delT	c.(1297-1299)CATfs	p.H433fs
Pat_01	Post-Resistance	ODZ3	55714	37	4	183652245	183652245	Frame_Shift_Del	DEL	T	-	7	234	c.2920delT	c.(2920-2922)TTTfs	p.F974fs
Pat_01	Post-Resistance	MYO10	4651	37	5	16694605	16694606	Frame_Shift_Ins	INS	-	C	8	411	c.3674_3675insG	c.(3673-3675)GGCfs	p.G1225fs
Pat_01	Post-Resistance	NIPBL	25836	37	5	37063925	37063927	In_Frame_Del	DEL	GAA	-	8	134	.7894_7896delGA	c.(7894-7896)GAAdel	p.E2636del
Pat_01	Post-Resistance	GZMK	3003	37	5	54326347	54326347	Frame_Shift_Del	DEL	A	-	7	358	c.298delA	c.(298-300)AAAfs	p.K100fs
Pat_01	Post-Resistance	BDP1	55814	37	5	70797445	70797446	Frame_Shift_Del	DEL	AG	-	7	542	c.2013_2014delAG	c.(2011-2016)ACAGAGfs	p.T671fs
Pat_01	Post-Resistance	THBS4	7060	37	5	79372774	79372776	In_Frame_Del	DEL	TGA	-	15	1138	.1989_1991delTG	.(1987-1992)TGTGAT>TG	p.D668del
Pat_01	Post-Resistance	H2AFY	9555	37	5	134724672	134724673	Frame_Shift_Ins	INS	-	G	52	268	c.111_112insC	c.(109-114)CCCAAGfs	p.P37fs
Pat_01	Post-Resistance	CDC25C	995	37	5	137627690	137627690	Frame_Shift_Del	DEL	T	-	7	299	c.731delA	c.(730-732)AAGfs	p.K244fs
Pat_01	Post-Resistance	BTN2A2	10385	37	6	26384091	26384093	In_Frame_Del	DEL	CCT	-	38	1097	c.42_44delCCT	c.(40-45)TCCCTC>TCC	p.L24del
Pat_01	Post-Resistance	MAS1L	116511	37	6	29455156	29455157	Frame_Shift_Del	DEL	AC	-	7	553	c.523_524delGT	c.(523-525)GTCfs	p.V175fs
Pat_01	Post-Resistance	PPP1R10	5514	37	6	30569334	30569334	Frame_Shift_Del	DEL	G	-	8	440	c.2815delC	c.(2815-2817)CTGfs	p.L939fs
Pat_01	Post-Resistance	TUBB	203068	37	6	30688336	30688336	Frame_Shift_Del	DEL	C	-	7	857	c.53delC	c.(52-54)GCCfs	p.A18fs
Pat_01	Post-Resistance	BAT3	7917	37	6	31612806	31612806	Frame_Shift_Del	DEL	G	-	7	734	c.1304delC	c.(1303-1305)CCGfs	p.P435fs
Pat_01	Post-Resistance	PHF3	23469	37	6	64422954	64422954	Frame_Shift_Del	DEL	C	-	8	1165	c.5470delC	c.(5470-5472)CCCfs	p.P1824fs
Pat_01	Post-Resistance	CCDC126	90693	37	7	23651156	23651156	Frame_Shift_Del	DEL	T	-	252	557	c.222delT	c.(220-222)GCTfs	p.A74fs
Pat_01	Post-Resistance	NRF1	4899	37	7	129311286	129311288	In_Frame_Del	DEL	GCT	-	8	302	c.241_243delGCT	c.(241-243)GCTdel	p.A84del
Pat_01	Post-Resistance	ATG9B	285973	37	7	150721484	150721484	Frame_Shift_Del	DEL	C	-	10	61	c.27delG	c.(25-27)GGGfs	p.G9fs
Pat_01	Post-Resistance	ADAM9	8754	37	8	38880792	38880793	Frame_Shift_Ins	INS	-	G	9	788	c.862_863insG	c.(862-864)CGGfs	p.R288fs
Pat_01	Post-Resistance	PREX2	80243	37	8	68942851	68942852	Frame_Shift_Del	DEL	AG	-	9	668	c.663_664delAG	c.(661-666)TTAGAAfs	p.L221fs
Pat_01	Post-Resistance	HNF4G	3174	37	8	76471135	76471135	Frame_Shift_Del	DEL	G	-	7	921	c.845delG	c.(844-846)CGGfs	p.R282fs
Pat_01	Post-Resistance	PDP1	54704	37	8	94934712	94934712	Frame_Shift_Del	DEL	T	-	7	546	c.425delT	c.(424-426)GTTfs	p.V142fs
Pat_01	Post-Resistance	RANBP6	26953	37	9	6012690	6012690	Frame_Shift_Del	DEL	T	-	7	258	c.2918delA	c.(2917-2919)AATfs	p.N973fs
Pat_01	Post-Resistance	HNRNPK	3190	37	9	86586806	86586808	In_Frame_Del	DEL	GGT	-	9	463	c.942_944delACC	c.(940-945)CCACCT>CCT	.314_315PP>
Pat_01	Post-Resistance	KIAA1529	57653	37	9	100137790	100137790	Frame_Shift_Del	DEL	C	-	9	413	c.5310delC	c.(5308-5310)CTCfs	p.L1770fs
Pat_01	Post-Resistance	CRB2	286204	37	9	126139182	126139184	In_Frame_Del	DEL	CCT	-	11	45	.3699_3701delCC	.(3697-3702)TGCCTC>TG	p.L1239del
Pat_01	Post-Resistance	DDX3X	1654	37	X	41205517	41205517	Frame_Shift_Del	DEL	A	-	7	612	c.1351delA	c.(1351-1353)AAAfs	p.K451fs
Pat_01	Post-Resistance	ARMCX3	51566	37	X	100880152	100880154	In_Frame_Del	DEL	TGA	-	8	746	c.183_185delTGA	c.(181-186)TCTGAT>TCT	p.D66del
Pat_01	Post-Resistance	MAP7D3	79649	37	X	135314194	135314194	Frame_Shift_Del	DEL	G	-	9	751	c.922delC	c.(922-924)CAGfs	p.Q308fs
Pat_01	Post-Resistance	ZNF185	7739	37	X	152087570	152087572	In_Frame_Del	DEL	GAG	-	9	92	c.475_477delGAG	c.(475-477)GAGdel	p.E165del

Pat_02	Post-Resistance	FAM43B	163933	37	1	20880268	20880270	In_Frame_Del	DEL	GAG	-	4	5	c.802_804delGAG	c.(802-804)GAGdel	p.E272del
Pat_02	Post-Resistance	ANKRD13C	81573	37	1	70740447	70740448	Frame_Shift_Del	DEL	TT	-	7	237	c.1349_1350delAA	c.(1348-1350)AAAfs	p.K450fs
Pat_02	Post-Resistance	TNNI3K	51086	37	1	74957824	74957826	In_Frame_Del	DEL	CTT	-	12	449	.2225_2227delCT	.(2224-2229)CCTTCT>CC	p.S746del
Pat_02	Post-Resistance	NOTCH2	4853	37	1	120468185	120468185	Frame_Shift_Del	DEL	G	-	8	291	c.4254delC	c.(4252-4254)CCCfs	p.P1418fs
Pat_02	Post-Resistance	PRG4	10216	37	1	186276524	186276526	In_Frame_Del	DEL	AGG	-	7	217	.1673_1675delAG	(1672-1677)AAGGAG>AA	p.E559del
Pat_02	Post-Resistance	SFMBT2	57713	37	10	7212995	7212997	In_Frame_Del	DEL	CTC	-	9	436	.2437_2439delGA	c.(2437-2439)GAGdel	p.E813del
Pat_02	Post-Resistance	SMARCC2	6601	37	12	56559113	56559113	Frame_Shift_Del	DEL	G	-	8	245	c.3128delC	c.(3127-3129)CCTfs	p.P1043fs
Pat_02	Post-Resistance	SFRS8	6433	37	12	132281734	132281736	In_Frame_Del	DEL	AGA	-	7	266	.2546_2548delAG	.(2545-2550)GAGAAG>GA	p.K853del
Pat_02	Post-Resistance	LRCH1	23143	37	13	47243183	47243186	Frame_Shift_Del	DEL	CCTG	-	16	682	c.471_474delCCT	c.(469-474)GCCCTGfs	p.A157fs
Pat_02	Post-Resistance	LMO7	4008	37	13	76415307	76415308	Frame_Shift_Del	DEL	AG	-	7	289	c.2946_2947delAG	c.(2944-2949)GCAGAGfs	p.A982fs
Pat_02	Post-Resistance	C15orf24	56851	37	15	34393991	34393993	In_Frame_Del	DEL	AGC	-	13	332	c.48_50delGCT	c.(46-51)CTGCTA>CTA	p.16_17LL>L
Pat_02	Post-Resistance	B2M	567	37	15	45003781	45003782	Frame_Shift_Del	DEL	CT	-	78	105	c.37_38delCT	c.(37-39)CTCfs	p.L13fs
Pat_02	Post-Resistance	ZNF609	23060	37	15	64972995	64972997	In_Frame_Del	DEL	CAC	-	8	531	.4096_4098delCA	c.(4096-4098)CACdel	p.H1371del
Pat_02	Post-Resistance	PPL	5493	37	16	4934835	4934835	Frame_Shift_Del	DEL	T	-	7	313	c.3821delA	c.(3820-3822)AAGfs	p.K1274fs
Pat_02	Post-Resistance	MKS1	54903	37	17	56290367	56290369	In_Frame_Del	DEL	CTC	-	7	374	c.832_834delGAG	c.(832-834)GAGdel	p.E278del
Pat_02	Post-Resistance	TMPRSS9	360200	37	19	2422242	2422242	Frame_Shift_Del	DEL	C	-	10	280	c.2443delC	c.(2443-2445)CCAfs	p.P815fs
Pat_02	Post-Resistance	ECSIT	51295	37	19	11618821	11618821	Frame_Shift_Del	DEL	G	-	7	334	c.781delC	c.(781-783)CAGfs	p.Q261fs
Pat_02	Post-Resistance	GRAMD1A	57655	37	19	35510312	35510312	Frame_Shift_Del	DEL	C	-	7	264	c.1350delC	c.(1348-1350)GGCfs	p.G450fs
Pat_02	Post-Resistance	RYR1	6261	37	19	38948159	38948160	Frame_Shift_Del	DEL	TG	-	9	498	c.1814_1815delTG	c.(1813-1815)CTGfs	p.L605fs
Pat_02	Post-Resistance	ANKRD23	200539	37	2	97507821	97507821	Frame_Shift_Del	DEL	G	-	7	268	c.276delC	c.(274-276)CCCfs	p.P92fs
Pat_02	Post-Resistance	GZF1	64412	37	20	23345921	23345923	In_Frame_Del	DEL	GAG	-	8	186	c.901_903delGAG	c.(901-903)GAGdel	p.E306del
Pat_02	Post-Resistance	GINS1	9837	37	20	25422397	25422397	Frame_Shift_Del	DEL	A	-	8	146	c.507delA	c.(505-507)TTAfs	p.L169fs
Pat_02	Post-Resistance	NCOA6	23054	37	20	33330968	33330970	In_Frame_Del	DEL	TGC	-	12	333	.3090_3092delGC	.(3088-3093)CAGCAA>CA	030_1031QQ
Pat_02	Post-Resistance	LAMA5	3911	37	20	60889865	60889866	Frame_Shift_Ins	INS	-	C	7	361	c.8185_8186insG	c.(8185-8187)GCTfs	p.A2729fs
Pat_02	Post-Resistance	C22orf32	91689	37	22	42478046	42478048	In_Frame_Del	DEL	GAT	-	9	392	c.304_306delGAT	c.(304-306)GATdel	p.D107del
Pat_02	Post-Resistance	SHANK3	85358	37	22	51159909	51159909	Frame_Shift_Del	DEL	C	-	2	4	c.3696delC	c.(3694-3696)AGCfs	p.S1232fs
Pat_02	Post-Resistance	WWTR1	25937	37	3	149260194	149260196	In_Frame_Del	DEL	CTG	-	7	142	c.697_699delCAG	c.(697-699)CAGdel	p.Q233del
Pat_02	Post-Resistance	CRIPAK	285464	37	4	1389147	1389148	Frame_Shift_Del	DEL	AT	-	8	536	c.848_849delAT	c.(847-849)CATfs	p.H283fs
Pat_02	Post-Resistance	YTHDC1	91746	37	4	69202891	69202893	In_Frame_Del	DEL	TCC	-	8	80	c.735_737delGGA	c.(733-738)GAGGAA>GA	.245_246EE>
Pat_02	Post-Resistance	BMP2K	55589	37	4	79792164	79792166	In_Frame_Del	DEL	CAC	-	7	59	.1459_1461delCA	c.(1459-1461)CACdel	p.H494del
Pat_02	Post-Resistance	ZNF827	152485	37	4	146823381	146823383	In_Frame_Del	DEL	GTG	-	7	184	.1028_1030delCA	.(1027-1032)CCACAA>CA	p.P343del
Pat_02	Post-Resistance	SH3D19	152503	37	4	152095944	152095944	Frame_Shift_Del	DEL	G	-	7	1808	c.572delC	c.(571-573)CCAfs	p.P191fs
Pat_02	Post-Resistance	SH3RF1	57630	37	4	170043324	170043326	In_Frame_Del	DEL	CAG	-	10	279	.1271_1273delCT	(1270-1275)GCTGGA>GG	p.A424del
Pat_02	Post-Resistance	PLEKHG4B	153478	37	5	163098	163098	Frame_Shift_Del	DEL	G	-	3	3	c.1843delG	c.(1843-1845)GCCfs	p.A615fs
Pat_02	Post-Resistance	C5orf51	285636	37	5	41909932	41909939	Frame_Shift_Del	DEL	GAGCTGAT	-	18	18	92_299delGAGCT	c.(292-300)GAGCTGATTfs	p.E98fs
Pat_02	Post-Resistance	NNT	23530	37	5	43651893	43651893	Frame_Shift_Del	DEL	C	-	7	490	c.1770delC	c.(1768-1770)GACfs	p.D590fs
Pat_02	Post-Resistance	SLC12A2	6558	37	5	127420207	127420209	In_Frame_Del	DEL	CGG	-	7	94	c.561_563delCGG	c.(559-564)TCCGGC>TCC	p.G192del
Pat_02	Post-Resistance	STK19	8859	37	6	31939829	31939830	Frame_Shift_Ins	INS	-	A	12	624	c.56_57insA	c.(55-57)GCAfs	p.A19fs
Pat_02	Post-Resistance	DAXX	1616	37	6	33287898	33287900	In_Frame_Del	DEL	TCC	-	8	151	.1353_1355delGG	(1351-1356)GAGGAA>GA	.451_452EE>
Pat_02	Post-Resistance	UHRF1BP1	54887	37	6	34839369	34839369	Frame_Shift_Del	DEL	C	-	11	439	c.3990delC	c.(3988-3990)ATCfs	p.I1330fs
Pat_02	Post-Resistance	ZNF318	24149	37	6	43323502	43323502	Frame_Shift_Del	DEL	T	-	13	722	c.1570delA	c.(1570-1572)AGGfs	p.R524fs
Pat_02	Post-Resistance	DST	667	37	6	56501426	56501426	Frame_Shift_Del	DEL	G	-	197	421	c.2890delC	c.(2890-2892)CAGfs	p.Q964fs
Pat_02	Post-Resistance	IFNGR1	3459	37	6	137519505	137519506	Frame_Shift_Del	DEL	CT	-	7	281	c.1132_1133delAG	c.(1132-1134)AGTfs	p.S378fs
Pat_02	Post-Resistance	TMEM60	85025	37	7	77423460	77423460	Frame_Shift_Del	DEL	T	-	7	257	c.231delA	c.(229-231)AAAfs	p.K77fs
Pat_02	Post-Resistance	DYNC1I1	1780	37	7	95614249	95614249	Frame_Shift_Del	DEL	T	-	9	476	c.754delT	c.(754-756)TTTfs	p.F252fs
Pat_02	Post-Resistance	ZKSCAN5	23660	37	7	99103706	99103706	Frame_Shift_Del	DEL	C	-	7	692	c.39delC	c.(37-39)GACfs	p.D13fs
Pat_02	Post-Resistance	WNT2	7472	37	7	116955171	116955175	Frame_Shift_Del	DEL	TCCTT	-	7	316	538_542delAAGG	c.(538-543)AAGGATfs	p.K180fs

Pat_02	Post-Resistance	TNPO3	23534	37	7	128610259	128610259	Frame_Shift_Del	DEL	G	-	10	1212	c.2541delC	c.(2539-2541)CCCfs	p.P847fs
Pat_02	Post-Resistance	ZNF398	57541	37	7	148876153	148876153	Frame_Shift_Del	DEL	C	-	7	697	c.1189delC	c.(1189-1191)CCCfs	p.P397fs
Pat_02	Post-Resistance	NOM1	64434	37	7	156743209	156743211	In_Frame_Del	DEL	GAG	-	7	164	c.778_780delGAG	c.(778-780)GAGdel	p.E264del
Pat_02	Post-Resistance	RAB11FIP1	80223	37	8	37732235	37732235	Frame_Shift_Del	DEL	C	-	9	601	c.1420delG	c.(1420-1422)GAGfs	p.E474fs
Pat_02	Post-Resistance	ESRP1	54845	37	8	95686610	95686611	Frame_Shift_Ins	INS	-	A	7	268	c.1527_1528insA	c.(1525-1530)CATAAAfs	p.H509fs
Pat_02	Post-Resistance	CSMD3	114788	37	8	114448928	114448928	Frame_Shift_Del	DEL	T	-	9	870	c.156delA	c.(154-156)TTAfs	p.L52fs
Pat_02	Post-Resistance	MYC	4609	37	8	128750605	128750607	In_Frame_Del	DEL	CAG	-	9	382	c.97_99delCAG	c.(97-99)CAGdel	p.Q37del
Pat_02	Post-Resistance	FOXB2	442425	37	9	79635081	79635083	In_Frame_Del	DEL	CCG	-	7	38	c.511_513delCCG	c.(511-513)CCGdel	p.P174del
Pat_02	Post-Resistance	AKNA	80709	37	9	117124014	117124014	Frame_Shift_Del	DEL	G	-	7	830	c.2094delC	c.(2092-2094)CCCfs	p.P698fs
Pat_02	Post-Resistance	TNC	3371	37	9	117797539	117797539	Frame_Shift_Del	DEL	G	-	8	437	c.5731delC	c.(5731-5733)CGGfs	p.R1911fs
Pat_02	Post-Resistance	FAM157B	100132403	37	9	141107536	141107537	In_Frame_Ins	INS	-	GCA	5	10	c.218_219insGCA	.(217-219)CGG>CGGCA	p.85_86insQ
Pat_02	Post-Resistance	ARMCX3	51566	37	X	100880152	100880154	In_Frame_Del	DEL	TGA	-	8	511	c.183_185delTGA	c.(181-186)TCTGAT>TCT	p.D66del
Pat_02	Post-Resistance	MAMLD1	10046	37	X	149639633	149639635	In_Frame_Del	DEL	GCA	-	10	243	.1788_1790delGC	.(1786-1791)CTGCAG>CT	p.Q606del
Pat_02	Post-Resistance	CD99L2	83692	37	X	149984524	149984526	In_Frame_Del	DEL	GTG	-	10	466	c.156_158delCAC	c.(154-159)ACCACA>ACA	p.52_53TT>T
Pat_05	Pre-Treatment	TNFRSF9	3604	37	1	7980912	7980914	In_Frame_Del	DEL	CTT	-	10	506	c.749_751delAAG	.(748-753)GAAGGA>GG	p.E250del
Pat_05	Pre-Treatment	C1orf201	90529	37	1	24696167	24696168	Frame_Shift_Del	DEL	AA	-	32	192	c.733_734delTT	c.(733-735)TTCfs	p.F245fs
Pat_05	Pre-Treatment	EYA3	2140	37	1	28343685	28343687	In_Frame_Del	DEL	CTG	-	7	1393	c.563_565delCAG	c.(562-567)GCAGTA>GTA	p.A188del
Pat_05	Pre-Treatment	DLGAP3	58512	37	1	35370281	35370283	In_Frame_Del	DEL	TGG	-	8	260	c.702_704delCCA	.(700-705)CACCAG>CA	p.H234del
Pat_05	Pre-Treatment	HIAT1	64645	37	1	100534121	100534122	Frame_Shift_Ins	INS	-	T	9	290	c.798_799insT	c.(796-801)AGCTTTfs	p.S266fs
Pat_05	Pre-Treatment	BCL9	607	37	1	147091501	147091501	Frame_Shift_Del	DEL	C	-	13	585	c.1540delC	c.(1540-1542)CCCfs	p.P514fs
Pat_05	Pre-Treatment	BCL9	607	37	1	147092681	147092681	Frame_Shift_Del	DEL	C	-	8	845	c.2720delC	c.(2719-2721)TCCfs	p.S907fs
Pat_05	Pre-Treatment	PBXIP1	57326	37	1	154917508	154917510	In_Frame_Del	DEL	GGT	-	9	512	.2186_2188delAC	(2185-2190)CACCGG>CG	p.H729del
Pat_05	Pre-Treatment	ISG20L2	81875	37	1	156694023	156694023	Frame_Shift_Del	DEL	G	-	11	712	c.865delC	c.(865-867)CTCfs	p.L289fs
Pat_05	Pre-Treatment	PVRL4	81607	37	1	161059028	161059030	In_Frame_Del	DEL	AGC	-	8	710	c.57_59delGCT	c.(55-60)CTGCTA>CTA	p.19_20LL>L
Pat_05	Pre-Treatment	APOBEC4	403314	37	1	183616826	183616828	In_Frame_Del	DEL	TTC	-	8	806	.1089_1091delGA	.(1087-1092)AAGAAA>AA	.363_364KK>
Pat_05	Pre-Treatment	REN	5972	37	1	204135375	204135377	In_Frame_Del	DEL	AGC	-	7	593	c.45_47delGCT	c.(43-48)CTGCTC>CTC	p.15_16LL>L
Pat_05	Pre-Treatment	PPP1R15B	84919	37	1	204380466	204380466	Frame_Shift_Del	DEL	A	-	7	486	c.74delT	c.(73-75)TTCfs	p.F25fs
Pat_05	Pre-Treatment	TMEM206	55248	37	1	212583815	212583815	Frame_Shift_Del	DEL	C	-	7	2185	c.85delG	c.(85-87)GAGfs	p.E29fs
Pat_05	Pre-Treatment	HEATR1	55127	37	1	236719429	236719429	Frame_Shift_Del	DEL	T	-	9	775	c.5485delA	c.(5485-5487)ACTfs	p.T1829fs
Pat_05	Pre-Treatment	JMJD1C	221037	37	10	64952699	64952699	Frame_Shift_Del	DEL	T	-	10	336	c.6075delA	c.(6073-6075)AAAfs	p.K2025fs
Pat_05	Pre-Treatment	IDE	3416	37	10	94274688	94274689	Frame_Shift_Del	DEL	AC	-	90	210	c.772_773delGT	c.(772-774)GTTfs	p.V258fs
Pat_05	Pre-Treatment	HPSE2	60495	37	10	100401606	100401607	Frame_Shift_Del	DEL	TC	-	8	998	c.1095_1096delG	c.(1093-1098)CAGAAAfs	p.Q365fs
Pat_05	Pre-Treatment	CNNM2	54805	37	10	104678768	104678768	Frame_Shift_Del	DEL	C	-	8	810	c.531delC	c.(529-531)ATCfs	p.I177fs
Pat_05	Pre-Treatment	SORCS3	22986	37	10	107005314	107005314	Frame_Shift_Del	DEL	G	-	8	606	c.2883delG	c.(2881-2883)TTGfs	p.L961fs
Pat_05	Pre-Treatment	FAM45A	404636	37	10	120871369	120871369	Frame_Shift_Del	DEL	T	-	7	474	c.261delT	c.(259-261)CATfs	p.H87fs
Pat_05	Pre-Treatment	EML3	256364	37	11	62369967	62369967	Frame_Shift_Del	DEL	C	-	4	2	c.2671delG	c.(2671-2673)GCCfs	p.A891fs
Pat_05	Pre-Treatment	PTS	5805	37	11	112101391	112101391	Frame_Shift_Del	DEL	A	-	7	500	c.229delA	c.(229-231)AAAfs	p.K77fs
Pat_05	Pre-Treatment	PRDM10	56980	37	11	129772249	129772251	In_Frame_Del	DEL	TGG	-	10	912	.3440_3442delCC	.(3439-3444)ACCAAC>AA	p.T1147del
Pat_05	Pre-Treatment	PRB2	653247	37	12	11546788	11546790	In_Frame_Del	DEL	GGA	-	7	323	c.222_224delTCC	c.(220-225)CCTCCA>CCA	p.74_75PP>P
Pat_05	Pre-Treatment	NR4A1	3164	37	12	52448766	52448766	Frame_Shift_Del	DEL	G	-	8	1039	c.654delG	c.(652-654)CTGfs	p.L218fs
Pat_05	Pre-Treatment	OR6C75	390323	37	12	55759486	55759486	Frame_Shift_Del	DEL	T	-	7	264	c.592delT	c.(592-594)TTTfs	p.F198fs
Pat_05	Pre-Treatment	RFC3	5983	37	13	34398062	34398063	Frame_Shift_Ins	INS	-	A	8	133	c.234_235insA	c.(232-237)TCTAAAfs	p.S78fs
Pat_05	Pre-Treatment	ZC3H13	23091	37	13	46542016	46542017	Frame_Shift_Del	DEL	CT	-	10	237	c.3943_3944delA	c.(3943-3945)AGGfs	p.R1315fs
Pat_05	Pre-Treatment	SLAIN1	122060	37	13	78320722	78320722	Frame_Shift_Del	DEL	A	-	8	222	c.498delA	c.(496-498)GGAfs	p.G166fs
Pat_05	Pre-Treatment	LIG4	3981	37	13	108861736	108861737	Frame_Shift_Ins	INS	-	T	7	199	c.1880_1881insA	c.(1879-1881)AAGfs	p.K627fs
Pat_05	Pre-Treatment	COL4A1	1282	37	13	110857850	110857850	Frame_Shift_Del	DEL	T	-	7	705	c.894delA	c.(892-894)AAAfs	p.K298fs
Pat_05	Pre-Treatment	ACIN1	22985	37	14	23528607	23528609	In_Frame_Del	DEL	TCT	-	9	135	.3774_3776delAG	.(3772-3777)GAAGAG>GA	1258_1259EE

Pat_05	Pre-Treatment	RGS6	9628	37	14	73002904	73002905	Frame_Shift_Del	DEL	AC	-	8	534	c.1289_1290delAC	c.(1288-1290)TACfs	p.Y430fs
Pat_05	Pre-Treatment	MGA	23269	37	15	42003383	42003385	In_Frame_Del	DEL	CAG	-	9	366	.2920_2922delCA	c.(2920-2922)CAGdel	p.Q981del
Pat_05	Pre-Treatment	C15orf17	57184	37	15	75197009	75197011	In_Frame_Del	DEL	GCA	-	7	1131	c.423_425delTGC	c.(421-426)TCTGCA>TCA	p.A142del
Pat_05	Pre-Treatment	SLC5A11	115584	37	16	24921737	24921739	In_Frame_Del	DEL	CAG	-	8	111	.1761_1763delCA	(1759-1764)GCCAGC>GC	p.S592del
Pat_05	Pre-Treatment	CTNS	1497	37	17	3543532	3543532	Frame_Shift_Del	DEL	T	-	7	885	c.32delT	c.(31-33)CTTfs	p.L11fs
Pat_05	Pre-Treatment	ZNF207	7756	37	17	30677314	30677316	In_Frame_Del	DEL	AAG	-	9	1245	c.10_12delAAG	c.(10-12)AAGdel	p.K7del
Pat_05	Pre-Treatment	GADD45GIP1	90480	37	19	13065273	13065275	In_Frame_Del	DEL	GCT	-	8	484	c.416_418delAGC	.(415-420)CAGCGG>CG	p.Q139del
Pat_05	Pre-Treatment	LSM14A	26065	37	19	34710340	34710340	Frame_Shift_Del	DEL	C	-	8	722	c.826delC	c.(826-828)CGGfs	p.R276fs
Pat_05	Pre-Treatment	CAPNS1	826	37	19	36632024	36632025	In_Frame_Ins	INS	-	GGC	5	11	c.111_112insGGC	c.(109-114)insGGC	p.56_57insG
Pat_05	Pre-Treatment	KIF3C	3797	37	2	26203790	26203791	Frame_Shift_Ins	INS	-	C	7	191	c.996_997insG	c.(994-999)GGGAATfs	p.G332fs
Pat_05	Pre-Treatment	ZNF514	84874	37	2	95815034	95815035	Frame_Shift_Ins	INS	-	T	11	309	c.1195_1196insA	c.(1195-1197)ACCfs	p.T399fs
Pat_05	Pre-Treatment	AAMP	14	37	2	219134766	219134766	Frame_Shift_Del	DEL	G	-	10	1446	c.44delC	c.(43-45)CCAfs	p.P15fs
Pat_05	Pre-Treatment	DOCK10	55619	37	2	225750871	225750871	Frame_Shift_Del	DEL	C	-	7	984	c.521delG	c.(520-522)GGTfs	p.G174fs
Pat_05	Pre-Treatment	CHRNG	1146	37	2	233404488	233404490	In_Frame_Del	DEL	CTG	-	7	552	c.31_33delCTG	c.(31-33)CTGdel	p.L14del
Pat_05	Pre-Treatment	GIGYF2	26058	37	2	233676006	233676008	In_Frame_Del	DEL	CAG	-	8	509	.1951_1953delCA	c.(1951-1953)CAGdel	p.Q655del
Pat_05	Pre-Treatment	TP53RK	112858	37	20	45315634	45315634	Frame_Shift_Del	DEL	G	-	7	729	c.520delC	c.(520-522)CTGfs	p.L174fs
Pat_05	Pre-Treatment	TFIP11	24144	37	22	26906183	26906185	In_Frame_Del	DEL	TCA	-	8	424	c.54_56delTGA	c.(52-57)GATGAC>GAC	p.18_19DD>D
Pat_05	Pre-Treatment	DDX17	10521	37	22	38881965	38881967	In_Frame_Del	DEL	GGA	-	11	744	.2169_2171delTC	(2167-2172)CCTCCC>CC	.723_724PP>
Pat_05	Pre-Treatment	TNRC6B	23112	37	22	40708591	40708591	Frame_Shift_Del	DEL	G	-	9	1192	c.4518delG	c.(4516-4518)CTGfs	p.L1506fs
Pat_05	Pre-Treatment	KCTD6	200845	37	3	58486772	58486772	Frame_Shift_Del	DEL	G	-	11	684	c.127delG	c.(127-129)GGGfs	p.G43fs
Pat_05	Pre-Treatment	LRIG1	26018	37	3	66436625	66436627	In_Frame_Del	DEL	GCT	-	12	1043	.1567_1569delAG	c.(1567-1569)AGCdel	p.S524del
Pat_05	Pre-Treatment	CPOX	1371	37	3	98304319	98304319	Frame_Shift_Del	DEL	G	-	7	1856	c.1138delC	c.(1138-1140)CAGfs	p.Q380fs
Pat_05	Pre-Treatment	LNP1	348801	37	3	100148586	100148588	In_Frame_Del	DEL	GAT	-	9	1320	c.13_15delGAT	c.(13-15)GATdel	p.D10del
Pat_05	Pre-Treatment	BBX	56987	37	3	107497244	107497244	Frame_Shift_Del	DEL	A	-	8	502	c.2081delA	c.(2080-2082)GAAfs	p.E694fs
Pat_05	Pre-Treatment	ACAD11	84129	37	3	132297681	132297681	Frame_Shift_Del	DEL	C	-	8	748	c.1733delG	c.(1732-1734)GGAfs	p.G578fs
Pat_05	Pre-Treatment	XRN1	54464	37	3	142144319	142144319	Frame_Shift_Del	DEL	G	-	7	221	c.468delC	c.(466-468)TCCfs	p.S156fs
Pat_05	Pre-Treatment	THPO	7066	37	3	184093760	184093761	Frame_Shift_Ins	INS	-	GTTA	17	163	c.56_57insTAAC	c.(55-57)ACGfs	p.T19fs
Pat_05	Pre-Treatment	UTP3	57050	37	4	71554620	71554622	In_Frame_Del	DEL	GAG	-	7	165	c.226_228delGAG	c.(226-228)GAGdel	p.E81del
Pat_05	Pre-Treatment	CDKL2	8999	37	4	76539579	76539580	Frame_Shift_Ins	INS	-	T	7	164	c.222_223insA	c.(220-225)AAACGAfs	p.K74fs
Pat_05	Pre-Treatment	PTPN13	5783	37	4	87622849	87622849	Frame_Shift_Del	DEL	C	-	9	450	c.1090delC	c.(1090-1092)CACfs	p.H364fs
Pat_05	Pre-Treatment	EXOSC9	5393	37	4	122723894	122723894	Frame_Shift_Del	DEL	T	-	15	514	c.227delT	c.(226-228)CTTfs	p.L76fs
Pat_05	Pre-Treatment	SCLT1	132320	37	4	129864163	129864163	Frame_Shift_Del	DEL	T	-	7	336	c.1620delA	c.(1618-1620)AAAfs	p.K540fs
Pat_05	Pre-Treatment	CDH10	1008	37	5	24492973	24492973	Frame_Shift_Del	DEL	A	-	7	822	c.1577delT	c.(1576-1578)TTCfs	p.F526fs
Pat_05	Pre-Treatment	ISOC1	51015	37	5	128440739	128440739	Frame_Shift_Del	DEL	G	-	7	837	c.400delG	c.(400-402)GGGfs	p.G134fs
Pat_05	Pre-Treatment	SLC22A4	6583	37	5	131676327	131676327	Frame_Shift_Del	DEL	T	-	12	605	c.1514delT	c.(1513-1515)CTTfs	p.L505fs
Pat_05	Pre-Treatment	CTNNA1	1495	37	5	138160447	138160449	In_Frame_Del	DEL	GGA	-	7	970	c.817_819delGGA	c.(817-819)GGAdel	p.G276del
Pat_05	Pre-Treatment	TMEM14C	51522	37	6	10725219	10725219	Frame_Shift_Del	DEL	G	-	7	2443	c.46delG	c.(46-48)GGCfs	p.G16fs
Pat_05	Pre-Treatment	RANBP9	10048	37	6	13632610	13632610	Frame_Shift_Del	DEL	T	-	8	820	c.1939delA	c.(1939-1941)ATGfs	p.M647fs
Pat_05	Pre-Treatment	FAM65B	9750	37	6	24873931	24873931	Frame_Shift_Del	DEL	G	-	8	293	c.198delC	c.(196-198)CCCfs	p.P66fs
Pat_05	Pre-Treatment	HIST1H2BJ	8970	37	6	27100400	27100401	Frame_Shift_Del	DEL	TG	-	7	2128	c.129_130delCA	c.(127-132)TACAAGfs	p.Y43fs
Pat_05	Pre-Treatment	NFKBIL1	4795	37	6	31525882	31525884	In_Frame_Del	DEL	CAG	-	9	205	c.640_642delCAG	c.(640-642)CAGdel	p.Q217del
Pat_05	Pre-Treatment	KIAA1009	22832	37	6	84896233	84896233	Frame_Shift_Del	DEL	A	-	7	237	c.1218delT	c.(1216-1218)TTTfs	p.F406fs
Pat_05	Pre-Treatment	NOX3	50508	37	6	155743925	155743926	Frame_Shift_Del	DEL	CA	-	8	739	c.1210_1211delTG	c.(1210-1212)TGCfs	p.C404fs
Pat_05	Pre-Treatment	TWISTNB	221830	37	7	19738111	19738113	In_Frame_Del	DEL	TTC	-	9	1498	c.843_845delGAA	c.(841-846)AAGAAA>AAA	.281_282KK>
Pat_05	Pre-Treatment	ITGB8	3696	37	7	20444381	20444382	Frame_Shift_Del	DEL	GT	-	10	900	c.1818_1819delGT	c.(1816-1821)ACGTGTfs	p.T606fs
Pat_05	Pre-Treatment	ZNRF2	223082	37	7	30395358	30395359	Frame_Shift_Del	DEL	AA	-	8	880	c.580_581delAA	c.(580-582)AAAfs	p.K194fs
Pat_05	Pre-Treatment	PSPH	5723	37	7	56082719	56082721	In_Frame_Del	DEL	AGG	-	35	441	c.565_567delCCT	c.(565-567)CCTdel	p.P189del

Pat_05	Pre-Treatment	STX1A	6804	37	7	73123425	73123427	In_Frame_Del	DEL	CAT	-	12	808	c.56_58delATG	c.(55-60)GATGTC>GTC	p.D19del
Pat_05	Pre-Treatment	GPC2	221914	37	7	99771554	99771554	Frame_Shift_Del	DEL	C	-	10	713	c.796delG	c.(796-798)GTCfs	p.V266fs
Pat_05	Pre-Treatment	SRRT	51593	37	7	100479332	100479332	Frame_Shift_Del	DEL	G	-	12	251	c.304delG	c.(304-306)GGGfs	p.G102fs
Pat_05	Pre-Treatment	RAB11FIP1	80223	37	8	37728963	37728966	Frame_Shift_Del	DEL	GTGA	-	102	374	3354_3357delTCA	c.(3352-3357)ACTCACfs	p.T1118fs
Pat_05	Pre-Treatment	NSMAF	8439	37	8	59510031	59510031	Frame_Shift_Del	DEL	C	-	9	1728	c.1707delG	c.(1705-1707)GTGfs	p.V569fs
Pat_05	Pre-Treatment	TOX	9760	37	8	59750796	59750798	In_Frame_Del	DEL	CTT	-	11	669	c.766_768delAAG	c.(766-768)AAGdel	p.K256del
Pat_05	Pre-Treatment	COPS5	10987	37	8	67974094	67974095	Frame_Shift_Del	DEL	AG	-	7	1274	c.137_138delCT	c.(136-138)ACTfs	p.T46fs
Pat_05	Pre-Treatment	SULF1	23213	37	8	70514026	70514026	Frame_Shift_Del	DEL	T	-	11	1341	c.1023delT	c.(1021-1023)CCTfs	p.P341fs
Pat_05	Pre-Treatment	EIF2C2	27161	37	8	141554344	141554345	Frame_Shift_Ins	INS	-	G	7	1015	c.1806_1807insC	c.(1804-1809)CCCGCCfs	p.P602fs
Pat_05	Pre-Treatment	PUF60	22827	37	8	144906520	144906522	In_Frame_Del	DEL	GCC	-	10	302	c.72_74delGGC	c.(70-75)GCGGCA>GCA	p.24_25AA>A
Pat_05	Pre-Treatment	C9orf98	158067	37	9	135753607	135753607	Frame_Shift_Del	DEL	G	-	9	214	c.36delC	c.(34-36)CCCfs	p.P12fs
Pat_05	Pre-Treatment	TXLNG	55787	37	X	16850849	16850850	Frame_Shift_Del	DEL	AG	-	9	163	c.968_969delAG	c.(967-969)CAGfs	p.Q323fs
Pat_05	Pre-Treatment	CNKSR2	22866	37	X	21627678	21627680	In_Frame_Del	DEL	GAG	-	8	126	.2635_2637delGA	c.(2635-2637)GAGdel	p.E886del
Pat_05	Post-Resistance	BCL9	607	37	1	147091501	147091501	Frame_Shift_Del	DEL	C	-	17	792	c.1540delC	c.(1540-1542)CCCfs	p.P514fs
Pat_05	Post-Resistance	TCHH	7062	37	1	152082211	152082213	In_Frame_Del	DEL	CTC	-	8	231	.3480_3482delGA	.(3478-3483)AAGAGA>AA	p.R1163del
Pat_05	Post-Resistance	KPRP	448834	37	1	152732678	152732678	Frame_Shift_Del	DEL	C	-	8	1055	c.614delC	c.(613-615)ACCfs	p.T205fs
Pat_05	Post-Resistance	GON4L	54856	37	1	155735138	155735141	Frame_Shift_Del	DEL	CTGT	-	27	1052	4123_4126delACA	c.(4123-4128)ACAGTCfs	p.T1375fs
Pat_05	Post-Resistance	ISG20L2	81875	37	1	156694023	156694023	Frame_Shift_Del	DEL	G	-	15	713	c.865delC	c.(865-867)CTCfs	p.L289fs
Pat_05	Post-Resistance	CALCOCO1	57658	37	12	54115378	54115378	Frame_Shift_Del	DEL	C	-	8	1470	c.631delG	c.(631-633)GAGfs	p.E211fs
Pat_05	Post-Resistance	LRP1	4035	37	12	57605740	57605742	In_Frame_Del	DEL	TGC	-	7	742	13289_13291delT	13288-13293)TTGCTG>T	4430_4431LL
Pat_05	Post-Resistance	GLI1	2735	37	12	57865177	57865177	Frame_Shift_Del	DEL	C	-	8	564	c.2654delC	c.(2653-2655)TCCfs	p.S885fs
Pat_05	Post-Resistance	NCOR2	9612	37	12	124848228	124848228	Frame_Shift_Del	DEL	G	-	7	964	c.2925delC	c.(2923-2925)CCCfs	p.P975fs
Pat_05	Post-Resistance	TPSD1	23430	37	16	1306312	1306314	In_Frame_Del	DEL	CTG	-	7	413	c.31_33delCTG	c.(31-33)CTGdel	p.L14del
Pat_05	Post-Resistance	SETD1A	9739	37	16	30982809	30982811	In_Frame_Del	DEL	TCC	-	7	152	.3127_3129delTC	c.(3127-3129)TCCdel	p.S1058del
Pat_05	Post-Resistance	KDM6B	23135	37	17	7751859	7751861	In_Frame_Del	DEL	CAC	-	7	94	.2253_2255delCA	.(2251-2256)GTCACC>GT	p.T762del
Pat_05	Post-Resistance	NEK8	284086	37	17	27064841	27064841	Frame_Shift_Del	DEL	C	-	8	1384	c.894delC	c.(892-894)ATCfs	p.I298fs
Pat_05	Post-Resistance	AP2B1	163	37	17	33953803	33953803	Frame_Shift_Del	DEL	G	-	8	1360	c.880delG	c.(880-882)GGGfs	p.G294fs
Pat_05	Post-Resistance	RAB11FIP5	26056	37	2	73315337	73315339	In_Frame_Del	DEL	TGG	-	7	449	.1407_1409delCC	.(1405-1410)CACCAA>CA	p.H469del
Pat_05	Post-Resistance	GINS1	9837	37	20	25422397	25422397	Frame_Shift_Del	DEL	A	-	7	136	c.507delA	c.(505-507)TTAfs	p.L169fs
Pat_05	Post-Resistance	DIDO1	11083	37	20	61512380	61512381	Frame_Shift_Ins	INS	-	G	12	141	c.4927_4928insC	c.(4927-4929)CGCfs	p.R1643fs
Pat_05	Post-Resistance	CCDC116	164592	37	22	21990728	21990730	In_Frame_Del	DEL	GCA	-	10	196	.1211_1213delGC	.(1210-1215)TGCAGC>TG	p.S407del
Pat_05	Post-Resistance	C22orf43	51233	37	22	23959767	23959769	In_Frame_Del	DEL	CAT	-	14	276	c.512_514delATG	c.(511-516)GATGCC>GCC	p.D171del
Pat_05	Post-Resistance	MYH9	4627	37	22	36689419	36689421	In_Frame_Del	DEL	CCT	-	10	427	.4049_4051delAG	(4048-4053)GAGGCC>GC	p.E1350del
Pat_05	Post-Resistance	LIMD1	8994	37	3	45636543	45636545	In_Frame_Del	DEL	CAG	-	9	80	c.172_174delCAG	c.(172-174)CAGdel	p.Q63del
Pat_05	Post-Resistance	QRICH1	54870	37	3	49094314	49094316	In_Frame_Del	DEL	TGC	-	8	203	.1317_1319delGC	.(1315-1320)CAGCAA>CA	.439_440QQ>
Pat_05	Post-Resistance	LNP1	348801	37	3	100148586	100148588	In_Frame_Del	DEL	GAT	-	7	1303	c.13_15delGAT	c.(13-15)GATdel	p.D10del
Pat_05	Post-Resistance	GOLGB1	2804	37	3	121413503	121413503	Frame_Shift_Del	DEL	T	-	7	435	c.5852delA	c.(5851-5853)AATfs	p.N1951fs
Pat_05	Post-Resistance	UTP3	57050	37	4	71554620	71554622	In_Frame_Del	DEL	GAG	-	8	152	c.226_228delGAG	c.(226-228)GAGdel	p.E81del
Pat_05	Post-Resistance	SLC1A3	6507	37	5	36679799	36679799	Frame_Shift_Del	DEL	G	-	8	1552	c.931delG	c.(931-933)GGGfs	p.G311fs
Pat_05	Post-Resistance	LARP1	23367	37	5	154181822	154181822	Frame_Shift_Del	DEL	G	-	7	357	c.1972delG	c.(1972-1974)GGGfs	p.G658fs
Pat_05	Post-Resistance	TULP1	7287	37	6	35478775	35478777	In_Frame_Del	DEL	TCC	-	7	360	c.360_362delGGA	.(358-363)GAGGAA>GAA	.120_121EE>
Pat_05	Post-Resistance	KIAA1009	22832	37	6	84896233	84896233	Frame_Shift_Del	DEL	A	-	7	171	c.1218delT	c.(1216-1218)TTTfs	p.F406fs
Pat_05	Post-Resistance	ABCB4	5244	37	7	87053264	87053264	Frame_Shift_Del	DEL	C	-	7	906	c.2169delG	c.(2167-2169)GGGfs	p.G723fs
Pat_05	Post-Resistance	TAF6	6878	37	7	99705124	99705124	Frame_Shift_Del	DEL	G	-	8	1360	c.1779delC	c.(1777-1779)CCCfs	p.P593fs
Pat_05	Post-Resistance	SLC12A9	56996	37	7	100463628	100463628	Frame_Shift_Del	DEL	G	-	7	877	c.2146delG	c.(2146-2148)GGGfs	p.G716fs
Pat_05	Post-Resistance	WNT16	51384	37	7	120971879	120971879	Frame_Shift_Del	DEL	G	-	9	569	c.494delG	c.(493-495)TGGfs	p.W165fs
Pat_05	Post-Resistance	RAB11FIP1	80223	37	8	37728963	37728966	Frame_Shift_Del	DEL	GTGA	-	104	258	3354_3357delTCA	c.(3352-3357)ACTCACfs	p.T1118fs

Pat_05	Post-Resistance	BHLHE22	27319	37	8	65493617	65493618	In_Frame_Ins	INS	-	GGC	10	16	c.270_271insGGC	c.(268-273)insGGC	p.97_98insG
Pat_05	Post-Resistance	IKBKAP	8518	37	9	111693425	111693427	Translation_Start_Site	DEL	ATG	-	48	192			
Pat_06	Pre-Treatment	CAMTA1	23261	37	1	7811329	7811329	Frame_Shift_Del	DEL	A	-	7	1129	c.4760delA	c.(4759-4761)CAAfs	p.Q1587fs
Pat_06	Pre-Treatment	CLSTN1	22883	37	1	9790640	9790642	In_Frame_Del	DEL	CCT	-	7	499	.2870_2872delAG	(2869-2874)GAGGGG>GG	p.E957del
Pat_06	Pre-Treatment	FBLIM1	54751	37	1	16103673	16103673	Frame_Shift_Del	DEL	C	-	7	1304	c.899delC	c.(898-900)GCCfs	p.A300fs
Pat_06	Pre-Treatment	MST1P9	11223	37	1	17086003	17086003	Frame_Shift_Del	DEL	G	-	7	1135	c.894delC	c.(892-894)GGCfs	p.G298fs
Pat_06	Pre-Treatment	TSSK3	81629	37	1	32828389	32828390	Frame_Shift_Ins	INS	-	A	8	1113	c.87_88insA	c.(85-90)TCCAAAfs	p.S29fs
Pat_06	Pre-Treatment	EIF2C4	192670	37	1	36307305	36307305	Frame_Shift_Del	DEL	A	-	11	1084	c.2129delA	c.(2128-2130)CAAfs	p.Q710fs
Pat_06	Pre-Treatment	MACF1	23499	37	1	39788668	39788670	In_Frame_Del	DEL	GGA	-	8	986	.4239_4241delGG	(4237-4242)CTGGAG>CT	p.E1417del
Pat_06	Pre-Treatment	MPL	4352	37	1	43814993	43814995	In_Frame_Del	DEL	CTG	-	8	893	.1528_1530delCT	c.(1528-1530)CTGdel	p.L513del
Pat_06	Pre-Treatment	IPO13	9670	37	1	44425920	44425922	Splice_Site	DEL	GGT	-	10	2459	c.2029_splice	c.e12-1	p.V677_splice
Pat_06	Pre-Treatment	EIF2B3	8891	37	1	45407182	45407182	Frame_Shift_Del	DEL	T	-	21	626	c.450delA	c.(448-450)AAAfs	p.K150fs
Pat_06	Pre-Treatment	MAST2	23139	37	1	46494559	46494559	Frame_Shift_Del	DEL	T	-	9	1448	c.2172delT	c.(2170-2172)CCTfs	p.P724fs
Pat_06	Pre-Treatment	PCSK9	255738	37	1	55505552	55505553	In_Frame_Ins	INS	-	CTG	5	9	c.42_43insCTG	c.(40-45)insCTG	p.23_24insL
Pat_06	Pre-Treatment	JUN	3725	37	1	59248443	59248443	Frame_Shift_Del	DEL	G	-	8	1536	c.300delC	c.(298-300)CCCfs	p.P100fs
Pat_06	Pre-Treatment	SGIP1	84251	37	1	67147814	67147814	Frame_Shift_Del	DEL	C	-	7	1129	c.1077delC	c.(1075-1077)GGCfs	p.G359fs
Pat_06	Pre-Treatment	WDR78	79819	37	1	67390426	67390426	Frame_Shift_Del	DEL	T	-	9	754	c.89delA	c.(88-90)AAGfs	p.K30fs
Pat_06	Pre-Treatment	LRRIQ3	127255	37	1	74575212	74575213	Frame_Shift_Ins	INS	-	T	27	573	c.732_733insA	c.(730-735)AAACAGfs	p.K244fs
Pat_06	Pre-Treatment	LRRIQ3	127255	37	1	74648381	74648381	Frame_Shift_Del	DEL	T	-	8	1269	c.414delA	c.(412-414)AAAfs	p.K138fs
Pat_06	Pre-Treatment	TNNI3K	51086	37	1	74957824	74957826	In_Frame_Del	DEL	CTT	-	36	1808	.2225_2227delCT	.(2224-2229)CCTTCT>CC	p.S746del
Pat_06	Pre-Treatment	CDC7	8317	37	1	91967356	91967357	Frame_Shift_Ins	INS	-	A	17	497	c.83_84insA	c.(82-84)TTAfs	p.L28fs
Pat_06	Pre-Treatment	SLC44A3	126969	37	1	95357932	95357932	Frame_Shift_Del	DEL	T	-	8	933	c.1716delT	c.(1714-1716)GCTfs	p.A572fs
Pat_06	Pre-Treatment	AMY2B	280	37	1	104115838	104115838	Frame_Shift_Del	DEL	A	-	9	2770	c.469delA	c.(469-471)AAAfs	p.K157fs
Pat_06	Pre-Treatment	WNT2B	7482	37	1	113052023	113052025	In_Frame_Del	DEL	CTG	-	12	303	c.139_141delCTG	c.(139-141)CTGdel	p.L50del
Pat_06	Pre-Treatment	TSPAN2	10100	37	1	115601537	115601537	Frame_Shift_Del	DEL	T	-	7	1456	c.411delA	c.(409-411)AAAfs	p.K137fs
Pat_06	Pre-Treatment	PSMB4	5692	37	1	151372073	151372073	Frame_Shift_Del	DEL	T	-	7	682	c.10delT	c.(10-12)TTTfs	p.F4fs
Pat_06	Pre-Treatment	SPRR4	163778	37	1	152944376	152944378	In_Frame_Del	DEL	CAG	-	7	660	c.10_12delCAG	c.(10-12)CAGdel	p.Q7del
Pat_06	Pre-Treatment	SPRR2G	6706	37	1	153122566	153122568	In_Frame_Del	DEL	CTG	-	12	1072	c.19_21delCAG	c.(19-21)CAGdel	p.Q7del
Pat_06	Pre-Treatment	S100A8	6279	37	1	153362715	153362715	Frame_Shift_Del	DEL	T	-	7	1013	c.146delA	c.(145-147)AAGfs	p.K49fs
Pat_06	Pre-Treatment	KCNN3	3782	37	1	154842331	154842333	In_Frame_Del	DEL	TGC	-	14	74	c.108_110delGCA	c.(106-111)CAGCAA>CAA	p.36_37QQ>Q
Pat_06	Pre-Treatment	GPATCH4	54865	37	1	156565504	156565504	Frame_Shift_Del	DEL	T	-	8	265	c.629delA	c.(628-630)AAGfs	p.K210fs
Pat_06	Pre-Treatment	NES	10763	37	1	156642804	156642804	Frame_Shift_Del	DEL	G	-	20	1720	c.1176delC	c.(1174-1176)CCCfs	p.P392fs
Pat_06	Pre-Treatment	PVRL4	81607	37	1	161044057	161044059	In_Frame_Del	DEL	CAC	-	13	723	.1105_1107delGT	c.(1105-1107)GTGdel	p.V369del
Pat_06	Pre-Treatment	PCP4L1	654790	37	1	161254154	161254156	In_Frame_Del	DEL	GGA	-	11	740	c.90_92delGGA	c.(88-93)GCGGAG>GCG	p.E35del
Pat_06	Pre-Treatment	SLC9A11	284525	37	1	173552687	173552688	Frame_Shift_Ins	INS	-	A	7	399	c.597_598insT	c.(595-600)TTTGGAfs	p.F199fs
Pat_06	Pre-Treatment	DHX9	1660	37	1	182845333	182845333	Frame_Shift_Del	DEL	T	-	11	1493	c.1964delT	c.(1963-1965)GTTfs	p.V655fs
Pat_06	Pre-Treatment	IPO9	55705	37	1	201843998	201844000	In_Frame_Del	DEL	GAG	-	12	542	.2872_2874delGA	c.(2872-2874)GAGdel	p.E962del
Pat_06	Pre-Treatment	ZC3H11A	9877	37	1	203786224	203786225	Frame_Shift_Ins	INS	-	T	25	640	c.26_27insT	c.(25-27)TATfs	p.Y9fs
Pat_06	Pre-Treatment	PIK3C2B	5287	37	1	204434363	204434363	Frame_Shift_Del	DEL	A	-	7	1515	c.1018delT	c.(1018-1020)TGCfs	p.C340fs
Pat_06	Pre-Treatment	CR1L	1379	37	1	207867814	207867814	Frame_Shift_Del	DEL	A	-	7	1447	c.580delA	c.(580-582)AAAfs	p.K194fs
Pat_06	Pre-Treatment	KCTD3	51133	37	1	215747171	215747171	Frame_Shift_Del	DEL	T	-	7	799	c.126delT	c.(124-126)TCTfs	p.S42fs
Pat_06	Pre-Treatment	TP53BP2	7159	37	1	223991931	223991931	Frame_Shift_Del	DEL	T	-	7	1343	c.594delA	c.(592-594)AAAfs	p.K198fs
Pat_06	Pre-Treatment	OBSCN	84033	37	1	228467013	228467013	Frame_Shift_Del	DEL	G	-	7	885	c.7264delG	c.(7264-7266)GGGfs	p.G2422fs
Pat_06	Pre-Treatment	RHOU	58480	37	1	228879414	228879414	Frame_Shift_Del	DEL	C	-	7	651	c.704delC	c.(703-705)TCTfs	p.S235fs
Pat_06	Pre-Treatment	C10orf18	54906	37	10	5788554	5788554	Frame_Shift_Del	DEL	A	-	8	566	c.3170delA	c.(3169-3171)GAAfs	p.E1057fs
Pat_06	Pre-Treatment	ITIH2	3698	37	10	7791225	7791225	Frame_Shift_Del	DEL	A	-	9	1605	c.2769delA	c.(2767-2769)GGAfs	p.G923fs
Pat_06	Pre-Treatment	NEBL	10529	37	10	21124517	21124517	Frame_Shift_Del	DEL	T	-	9	1578	c.1374delA	c.(1372-1374)AAAfs	p.K458fs

Pat_06	Pre-Treatment	MPP7	143098	37	10	28347455	28347455	Frame_Shift_Del	DEL	T	-	9	2255	c.1376delA	c.(1375-1377)AACfs	p.N459fs
Pat_06	Pre-Treatment	FRMPD2	143162	37	10	49409420	49409420	Frame_Shift_Del	DEL	T	-	7	2068	c.1805delA	c.(1804-1806)AAGfs	p.K602fs
Pat_06	Pre-Treatment	A1CF	29974	37	10	52569667	52569669	In_Frame_Del	DEL	AGC	-	9	528	.1618_1620delGC	c.(1618-1620)GCTdel	p.A540del
Pat_06	Pre-Treatment	ARID5B	84159	37	10	63852298	63852298	Frame_Shift_Del	DEL	A	-	7	728	c.3076delA	c.(3076-3078)AAAfs	p.K1026fs
Pat_06	Pre-Treatment	ZMIZ1	57178	37	10	81050829	81050831	In_Frame_Del	DEL	GCA	-	9	895	c.654_656delGCA	.(652-657)GGGCAG>GG	p.Q222del
Pat_06	Pre-Treatment	ZMIZ1	57178	37	10	81066062	81066062	Frame_Shift_Del	DEL	C	-	8	546	c.2629delC	c.(2629-2631)CCCfs	p.P877fs
Pat_06	Pre-Treatment	STAMBPL1	57559	37	10	90682146	90682146	Frame_Shift_Del	DEL	A	-	17	539	c.1207delA	c.(1207-1209)AAAfs	p.K403fs
Pat_06	Pre-Treatment	FAS	355	37	10	90768708	90768708	Frame_Shift_Del	DEL	T	-	7	4111	c.397delT	c.(397-399)TTTfs	p.F133fs
Pat_06	Pre-Treatment	HECTD2	143279	37	10	93247481	93247481	Frame_Shift_Del	DEL	A	-	7	1115	c.1137delA	c.(1135-1137)GCAfs	p.A379fs
Pat_06	Pre-Treatment	TACC2	10579	37	10	123970380	123970380	Frame_Shift_Del	DEL	C	-	9	876	c.6440delC	c.(6439-6441)ACCfs	p.T2147fs
Pat_06	Pre-Treatment	DMBT1	1755	37	10	124345598	124345599	Frame_Shift_Del	DEL	GA	-	7	2750	.1482_1483delG	c.(1480-1485)CTGAGGfs	p.L494fs
Pat_06	Pre-Treatment	DOCK1	1793	37	10	129231579	129231579	Frame_Shift_Del	DEL	C	-	7	1232	c.4884delC	c.(4882-4884)CGCfs	p.R1628fs
Pat_06	Pre-Treatment	PHRF1	57661	37	11	592586	592588	In_Frame_Del	DEL	GAG	-	8	1189	c.532_534delGAG	c.(532-534)GAGdel	p.E181del
Pat_06	Pre-Treatment	OR51B6	390058	37	11	5373220	5373220	Frame_Shift_Del	DEL	A	-	7	1251	c.483delA	c.(481-483)CTAfs	p.L161fs
Pat_06	Pre-Treatment	PSMA1	5682	37	11	14529252	14529254	In_Frame_Del	DEL	CAT	-	8	904	c.683_685delATG	c.(682-687)GATGTG>GTG	p.D228del
Pat_06	Pre-Treatment	PAMR1	25891	37	11	35513670	35513670	Frame_Shift_Del	DEL	C	-	7	1999	c.302delG	c.(301-303)GGTfs	p.G101fs
Pat_06	Pre-Treatment	ARHGAP1	392	37	11	46702224	46702224	Frame_Shift_Del	DEL	G	-	8	848	c.709delC	c.(709-711)CTGfs	p.L237fs
Pat_06	Pre-Treatment	FNBP4	23360	37	11	47744589	47744591	In_Frame_Del	DEL	GGA	-	8	33	.2742_2744delTC	.(2740-2745)CCTCCA>CC	.914_915PP>
Pat_06	Pre-Treatment	FNBP4	23360	37	11	47746087	47746087	Frame_Shift_Del	DEL	G	-	8	1730	c.2252delC	c.(2251-2253)CCTfs	p.P751fs
Pat_06	Pre-Treatment	SERPING1	710	37	11	57365774	57365776	In_Frame_Del	DEL	CTG	-	14	66	c.31_33delCTG	c.(31-33)CTGdel	p.L15del
Pat_06	Pre-Treatment	UBXN1	51035	37	11	62444384	62444384	Frame_Shift_Del	DEL	C	-	7	826	c.745delG	c.(745-747)GAGfs	p.E249fs
Pat_06	Pre-Treatment	SF1	7536	37	11	64534435	64534437	In_Frame_Del	DEL	GCT	-	10	1552	.1517_1519delAG	.(1516-1521)CAGCCT>CC	p.Q506del
Pat_06	Pre-Treatment	EHBP1L1	254102	37	11	65351726	65351726	Frame_Shift_Del	DEL	G	-	8	1520	c.3108delG	c.(3106-3108)CTGfs	p.L1036fs
Pat_06	Pre-Treatment	SNX32	254122	37	11	65617623	65617623	Frame_Shift_Del	DEL	C	-	10	812	c.255delC	c.(253-255)ATCfs	p.I85fs
Pat_06	Pre-Treatment	NUMA1	4926	37	11	71724190	71724190	Frame_Shift_Del	DEL	C	-	7	1146	c.4359delG	c.(4357-4359)GGGfs	p.G1453fs
Pat_06	Pre-Treatment	DGAT2	84649	37	11	75509300	75509300	Frame_Shift_Del	DEL	G	-	7	1490	c.838delG	c.(838-840)GGAfs	p.G280fs
Pat_06	Pre-Treatment	PAK1	5058	37	11	77069990	77069992	In_Frame_Del	DEL	CAT	-	9	632	c.548_550delATG	c.(547-552)GATGCT>GCT	p.D183del
Pat_06	Pre-Treatment	USP35	57558	37	11	77920720	77920722	In_Frame_Del	DEL	CGC	-	7	687	.1819_1821delCG	c.(1819-1821)CGCdel	p.R610del
Pat_06	Pre-Treatment	FAT3	120114	37	11	92531072	92531074	In_Frame_Del	DEL	GAC	-	9	1070	.4893_4895delGA	.(4891-4896)ATGACG>AT	p.T1633del
Pat_06	Pre-Treatment	C11orf54	28970	37	11	93494710	93494710	Frame_Shift_Del	DEL	T	-	9	1672	c.804delT	c.(802-804)CATfs	p.H268fs
Pat_06	Pre-Treatment	MRE11A	4361	37	11	94153333	94153335	In_Frame_Del	DEL	ATC	-	8	514	.2083_2085delGA	c.(2083-2085)GATdel	p.D695del
Pat_06	Pre-Treatment	BARX2	8538	37	11	129246064	129246064	Frame_Shift_Del	DEL	A	-	8	1086	c.134delA	c.(133-135)TACfs	p.Y45fs
Pat_06	Pre-Treatment	GUCY2C	2984	37	12	14766135	14766135	Frame_Shift_Del	DEL	T	-	8	1653	c.3138delA	c.(3136-3138)AAAfs	p.K1046fs
Pat_06	Pre-Treatment	NELL2	4753	37	12	44917102	44917102	Frame_Shift_Del	DEL	T	-	7	1866	c.1970delA	c.(1969-1971)AATfs	p.N657fs
Pat_06	Pre-Treatment	SFRS2IP	9169	37	12	46318575	46318577	In_Frame_Del	DEL	GGT	-	26	1702	.3840_3842delAC	(3838-3843)CCACCC>CC	1280_1281PP>
Pat_06	Pre-Treatment	SFRS2IP	9169	37	12	46320707	46320708	Frame_Shift_Del	DEL	TC	-	10	970	.2776_2777delG	c.(2776-2778)GAAfs	p.E926fs
Pat_06	Pre-Treatment	PRPF40B	25766	37	12	50025258	50025258	Frame_Shift_Del	DEL	C	-	7	1108	c.93delC	c.(91-93)ATCfs	p.I31fs
Pat_06	Pre-Treatment	OR6C75	390323	37	12	55759192	55759192	Frame_Shift_Del	DEL	T	-	13	836	c.298delT	c.(298-300)TTTfs	p.F100fs
Pat_06	Pre-Treatment	ESYT1	23344	37	12	56537395	56537395	Frame_Shift_Del	DEL	C	-	9	1528	c.3257delC	c.(3256-3258)TCCfs	p.S1086fs
Pat_06	Pre-Treatment	KIF5A	3798	37	12	57972048	57972048	Frame_Shift_Del	DEL	G	-	7	943	c.2461delG	c.(2461-2463)GGGfs	p.G821fs
Pat_06	Pre-Treatment	B4GALNT1	2583	37	12	58025102	58025103	Frame_Shift_Ins	INS	-	C	10	737	c.263_264insG	c.(262-264)GGCfs	p.G88fs
Pat_06	Pre-Treatment	CEP290	80184	37	12	88524078	88524079	Frame_Shift_Ins	INS	-	T	15	1077	c.635_636insA	c.(634-636)AACfs	p.N212fs
Pat_06	Pre-Treatment	CCDC63	160762	37	12	111311658	111311659	Frame_Shift_Ins	INS	-	A	11	337	c.382_383insA	c.(382-384)GAAfs	p.E128fs
Pat_06	Pre-Treatment	C12orf51	283450	37	12	112605648	112605650	In_Frame_Del	DEL	CAG	-	13	541	11014_11016delC	c.(11014-11016)CTGdel	p.L3672del
Pat_06	Pre-Treatment	KSR2	283455	37	12	117977605	117977605	Frame_Shift_Del	DEL	G	-	11	638	c.1519delC	c.(1519-1521)CTCfs	p.L507fs
Pat_06	Pre-Treatment	MLEC	9761	37	12	121134166	121134168	In_Frame_Del	DEL	GAA	-	8	542	c.697_699delGAA	c.(697-699)GAAdel	p.E238del
Pat_06	Pre-Treatment	WASF3	10810	37	13	27250862	27250863	Splice_Site	DEL	GT	-	7	949	c.716_splice	c.e7+1	p.R239_splice

Pat_06	Pre-Treatment	WASF3	10810	37	13	27259836	27259836	Frame_Shift_Del	DEL	A	-	8	685	c.1363delA	c.(1363-1365)AAAfs	p.K455fs
Pat_06	Pre-Treatment	CKAP2	26586	37	13	53049034	53049034	Frame_Shift_Del	DEL	A	-	7	233	c.1810delA	c.(1810-1812)AAAfs	p.K604fs
Pat_06	Pre-Treatment	FBXL3	26224	37	13	77581683	77581683	Frame_Shift_Del	DEL	A	-	8	306	c.884delT	c.(883-885)TTAfs	p.L295fs
Pat_06	Pre-Treatment	MYCBP2	23077	37	13	77748553	77748553	Frame_Shift_Del	DEL	G	-	7	951	c.5430delC	c.(5428-5430)ACCfs	p.T1810fs
Pat_06	Pre-Treatment	SLITRK5	26050	37	13	88328374	88328375	Frame_Shift_Del	DEL	TC	-	7	1061	c.731_732delTC	c.(730-732)ATCfs	p.I244fs
Pat_06	Pre-Treatment	UBAC2	337867	37	13	99966405	99966405	Frame_Shift_Del	DEL	C	-	7	1206	c.444delC	c.(442-444)GTCfs	p.V148fs
Pat_06	Pre-Treatment	SALL2	6297	37	14	21991334	21991336	In_Frame_Del	DEL	GGT	-	11	551	.2526_2528delAC	.(2524-2529)CCACCT>CC	.842_843PP>
Pat_06	Pre-Treatment	RBM23	55147	37	14	23371030	23371030	Frame_Shift_Del	DEL	G	-	9	1133	c.1309delC	c.(1309-1311)CAGfs	p.Q437fs
Pat_06	Pre-Treatment	CPNE6	9362	37	14	24545608	24545608	Frame_Shift_Del	DEL	C	-	7	1081	c.1098delC	c.(1096-1098)ATCfs	p.I366fs
Pat_06	Pre-Treatment	TINF2	26277	37	14	24710268	24710268	Frame_Shift_Del	DEL	C	-	7	2120	c.562delG	c.(562-564)GCCfs	p.A188fs
Pat_06	Pre-Treatment	FERMT2	10979	37	14	53360081	53360082	Frame_Shift_Ins	INS	-	T	9	267	c.455_456insA	c.(454-456)AAGfs	p.K152fs
Pat_06	Pre-Treatment	C14orf39	317761	37	14	60903565	60903565	Frame_Shift_Del	DEL	A	-	14	581	c.1762delT	c.(1762-1764)TGAfs	p.*588fs
Pat_06	Pre-Treatment	ZBTB1	22890	37	14	64989787	64989787	Frame_Shift_Del	DEL	A	-	7	1373	c.1565delA	c.(1564-1566)CAAfs	p.Q522fs
Pat_06	Pre-Treatment	C14orf115	55237	37	14	74824463	74824463	Frame_Shift_Del	DEL	G	-	14	903	c.977delG	c.(976-978)CGGfs	p.R326fs
Pat_06	Pre-Treatment	GALC	2581	37	14	88406276	88406276	Frame_Shift_Del	DEL	T	-	10	2322	c.1884delA	c.(1882-1884)AAAfs	p.K628fs
Pat_06	Pre-Treatment	ATXN3	4287	37	14	92537355	92537357	In_Frame_Del	DEL	CTG	-	7	517	c.913_915delCAG	c.(913-915)CAGdel	p.Q305del
Pat_06	Pre-Treatment	RIN3	79890	37	14	93125641	93125643	In_Frame_Del	DEL	CCA	-	7	537	.2162_2164delCC	.(2161-2166)GCCACC>GC	p.T725del
Pat_06	Pre-Treatment	CHGA	1113	37	14	93398009	93398009	Frame_Shift_Del	DEL	A	-	8	696	c.770delA	c.(769-771)CACfs	p.H257fs
Pat_06	Pre-Treatment	BTBD7	55727	37	14	93720048	93720048	Frame_Shift_Del	DEL	T	-	9	1323	c.1697delA	c.(1696-1698)AATfs	p.N566fs
Pat_06	Pre-Treatment	DICER1	23405	37	14	95562455	95562455	Frame_Shift_Del	DEL	T	-	10	2394	c.4802delA	c.(4801-4803)AAGfs	p.K1601fs
Pat_06	Pre-Treatment	DYNC1H1	1778	37	14	102476702	102476703	Frame_Shift_Del	DEL	AG	-	8	481	c.6311_6312delAG	c.(6310-6312)AAGfs	p.K2104fs
Pat_06	Pre-Treatment	EIF5	1983	37	14	103803136	103803137	Frame_Shift_Ins	INS	-	T	9	725	c.277_278insT	c.(277-279)ATTfs	p.I93fs
Pat_06	Pre-Treatment	AKT1	207	37	14	105242073	105242075	In_Frame_Del	DEL	CTC	-	13	532	c.349_351delGAG	c.(349-351)GAGdel	p.E117del
Pat_06	Pre-Treatment	ATP10A	57194	37	15	25963499	25963501	In_Frame_Del	DEL	CCT	-	8	106	.1409_1411delAG	(1408-1413)GAGGTG>GT	p.E470del
Pat_06	Pre-Treatment	MTMR10	54893	37	15	31239358	31239358	Frame_Shift_Del	DEL	G	-	7	2035	c.1523delC	c.(1522-1524)CCTfs	p.P508fs
Pat_06	Pre-Treatment	SLC12A6	9990	37	15	34628626	34628626	Frame_Shift_Del	DEL	G	-	7	556	c.256delC	c.(256-258)CAGfs	p.Q86fs
Pat_06	Pre-Treatment	PAK6	56924	37	15	40566360	40566360	Frame_Shift_Del	DEL	G	-	8	796	c.1761delG	c.(1759-1761)CTGfs	p.L587fs
Pat_06	Pre-Treatment	TP53BP1	7158	37	15	43748493	43748494	Frame_Shift_Del	DEL	GG	-	7	297	c.2297_2298delCC	c.(2296-2298)CCCfs	p.P766fs
Pat_06	Pre-Treatment	TRIM69	140691	37	15	45059455	45059455	Frame_Shift_Del	DEL	A	-	7	778	c.988delA	c.(988-990)AAAfs	p.K330fs
Pat_06	Pre-Treatment	SLC28A2	9153	37	15	45567679	45567680	Frame_Shift_Del	DEL	TG	-	7	2237	c.1945_1946delTG	c.(1945-1947)TGTfs	p.C649fs
Pat_06	Pre-Treatment	ONECUT1	3175	37	15	53049972	53049972	Frame_Shift_Del	DEL	G	-	8	1414	c.1178delC	c.(1177-1179)ACAfs	p.T393fs
Pat_06	Pre-Treatment	ZNF280D	54816	37	15	56970872	56970873	Frame_Shift_Ins	INS	-	T	7	1070	c.1151_1152insA	c.(1150-1152)CATfs	p.H384fs
Pat_06	Pre-Treatment	SNAPC5	10302	37	15	66786799	66786801	In_Frame_Del	DEL	TCC	-	7	721	c.270_272delGGA	.(268-273)GAGGAA>GA	p.90_91EE>E
Pat_06	Pre-Treatment	SPESP1	246777	37	15	69238674	69238676	In_Frame_Del	DEL	AGC	-	9	467	c.801_803delAGC	c.(799-804)CTAGCA>CTA	p.A271del
Pat_06	Pre-Treatment	IQGAP1	8826	37	15	91019925	91019925	Frame_Shift_Del	DEL	A	-	7	563	c.2815delA	c.(2815-2817)AAAfs	p.K939fs
Pat_06	Pre-Treatment	BLM	641	37	15	91304286	91304288	In_Frame_Del	DEL	TGA	-	8	649	.1683_1685delTG	.(1681-1686)TTTGAT>TT	p.D566del
Pat_06	Pre-Treatment	VPS33B	26276	37	15	91550236	91550238	In_Frame_Del	DEL	TCC	-	15	1581	c.642_644delGGA	c.(640-645)GAGGAT>GAT	p.E214del
Pat_06	Pre-Treatment	TPSD1	23430	37	16	1306312	1306314	In_Frame_Del	DEL	CTG	-	9	805	c.31_33delCTG	c.(31-33)CTGdel	p.L14del
Pat_06	Pre-Treatment	ABCA3	21	37	16	2373622	2373622	Frame_Shift_Del	DEL	A	-	7	2325	c.515delT	c.(514-516)TTCfs	p.F172fs
Pat_06	Pre-Treatment	TIGD7	91151	37	16	3350471	3350472	Frame_Shift_Ins	INS	-	T	7	477	c.143_144insA	c.(142-144)AATfs	p.N48fs
Pat_06	Pre-Treatment	C16orf62	57020	37	16	19580800	19580802	In_Frame_Del	DEL	TCC	-	14	566	c.172_174delTCC	c.(172-174)TCCdel	p.S64del
Pat_06	Pre-Treatment	ATXN2L	11273	37	16	28847350	28847350	Frame_Shift_Del	DEL	G	-	7	684	c.2992delG	c.(2992-2994)GGGfs	p.G998fs
Pat_06	Pre-Treatment	SRCAP	10847	37	16	30724910	30724910	Frame_Shift_Del	DEL	T	-	7	1006	c.2371delT	c.(2371-2373)TTTfs	p.F791fs
Pat_06	Pre-Treatment	RSPRY1	89970	37	16	57255221	57255222	Frame_Shift_Del	DEL	GC	-	7	1198	c.1055_1056delGC	c.(1054-1056)TGCfs	p.C352fs
Pat_06	Pre-Treatment	FHOD1	29109	37	16	67267852	67267852	Frame_Shift_Del	DEL	G	-	8	329	c.1754delC	c.(1753-1755)CCTfs	p.P585fs
Pat_06	Pre-Treatment	ACD	65057	37	16	67693646	67693648	In_Frame_Del	DEL	GCA	-	13	1230	c.551_553delTGC	.(550-555)CTGCAG>CA	p.L184del
Pat_06	Pre-Treatment	EDC4	23644	37	16	67913767	67913769	In_Frame_Del	DEL	CAG	-	7	241	.1836_1838delCA	(1834-1839)CCCAGC>CC	p.S617del

Pat_06	Pre-Treatment	CDH3	1001	37	16	68718504	68718504	Frame_Shift_Del	DEL	A	-	7	1486	c.1201delA	c.(1201-1203)AAAfs	p.K401fs
Pat_06	Pre-Treatment	TERF2IP	54386	37	16	75690204	75690206	In_Frame_Del	DEL	GAA	-	9	237	c.895_897delGAA	c.(895-897)GAAdel	p.E304del
Pat_06	Pre-Treatment	CNTNAP4	85445	37	16	76389351	76389351	Frame_Shift_Del	DEL	G	-	7	1214	c.333delG	c.(331-333)CTGfs	p.L111fs
Pat_06	Pre-Treatment	MNT	4335	37	17	2290831	2290831	Frame_Shift_Del	DEL	G	-	12	1592	c.1113delC	c.(1111-1113)CCCfs	p.P371fs
Pat_06	Pre-Treatment	ZNF232	7775	37	17	5012755	5012756	Frame_Shift_Del	DEL	AG	-	7	1556	c.350_351delCT	c.(349-351)CCTfs	p.P117fs
Pat_06	Pre-Treatment	DHX33	56919	37	17	5372037	5372039	In_Frame_Del	DEL	CCT	-	8	245	c.141_143delAGG	.(139-144)GGAGGC>GG	p.47_48GG>G
Pat_06	Pre-Treatment	BCL6B	255877	37	17	6927858	6927858	Frame_Shift_Del	DEL	C	-	7	1159	c.540delC	c.(538-540)GGCfs	p.G180fs
Pat_06	Pre-Treatment	PLSCR3	57048	37	17	7294059	7294059	Frame_Shift_Del	DEL	C	-	8	1323	c.725delG	c.(724-726)GGCfs	p.G242fs
Pat_06	Pre-Treatment	PER1	5187	37	17	8049759	8049761	In_Frame_Del	DEL	AGG	-	8	311	.1967_1969delCC	.(1966-1971)TCCTAT>TA	p.S656del
Pat_06	Pre-Treatment	NDEL1	81565	37	17	8370271	8370273	In_Frame_Del	DEL	CTC	-	10	927	c.968_970delCTC	c.(967-972)GCTCCT>GCT	p.P327del
Pat_06	Pre-Treatment	USP43	124739	37	17	9578264	9578265	Frame_Shift_Del	DEL	TG	-	7	2721	c.797_798delTG	c.(796-798)CTGfs	p.L266fs
Pat_06	Pre-Treatment	SUPT6H	6830	37	17	27002006	27002006	Frame_Shift_Del	DEL	A	-	9	323	c.364delA	c.(364-366)AAAfs	p.K122fs
Pat_06	Pre-Treatment	RHOT1	55288	37	17	30525994	30525994	Frame_Shift_Del	DEL	G	-	7	1108	c.898delG	c.(898-900)GAAfs	p.E300fs
Pat_06	Pre-Treatment	ZNF207	7756	37	17	30677314	30677316	In_Frame_Del	DEL	AAG	-	9	1413	c.10_12delAAG	c.(10-12)AAGdel	p.K7del
Pat_06	Pre-Treatment	CCL23	6368	37	17	34340806	34340806	Frame_Shift_Del	DEL	C	-	8	615	c.229delG	c.(229-231)GAGfs	p.E77fs
Pat_06	Pre-Treatment	STARD3	10948	37	17	37815015	37815015	Frame_Shift_Del	DEL	G	-	7	1280	c.588delG	c.(586-588)CTGfs	p.L196fs
Pat_06	Pre-Treatment	STAT5A	6776	37	17	40453398	40453399	Frame_Shift_Ins	INS	-	C	7	419	c.1095_1096insC	c.(1093-1098)AATCCCfs	p.N365fs
Pat_06	Pre-Treatment	HDAC5	10014	37	17	42157800	42157801	Frame_Shift_Ins	INS	-	G	7	598	c.2793_2794insC	c.(2791-2796)CCCATTfs	p.P931fs
Pat_06	Pre-Treatment	CCDC103	388389	37	17	42980014	42980015	Frame_Shift_Del	DEL	AG	-	10	328	c.558_559delAG	c.(556-561)GCAGAGfs	p.A186fs
Pat_06	Pre-Treatment	BRIP1	83990	37	17	59878722	59878722	Frame_Shift_Del	DEL	C	-	8	1226	c.1032delG	c.(1030-1032)GGGfs	p.G344fs
Pat_06	Pre-Treatment	DCAF7	10238	37	17	61661029	61661029	Frame_Shift_Del	DEL	C	-	8	445	c.694delC	c.(694-696)CAGfs	p.Q232fs
Pat_06	Pre-Treatment	FTSJ3	117246	37	17	61901516	61901518	In_Frame_Del	DEL	TCC	-	8	1232	.1080_1082delGG	(1078-1083)GAGGAA>GA	.360_361EE>
Pat_06	Pre-Treatment	COG1	9382	37	17	71204457	71204458	Frame_Shift_Ins	INS	-	C	7	682	c.2810_2811insC	c.(2809-2811)GTCfs	p.V937fs
Pat_06	Pre-Treatment	SLC26A11	284129	37	17	78201649	78201651	In_Frame_Del	DEL	TGC	-	14	1016	c.626_628delTGC	c.(625-630)ATGCTG>ATG	p.L213del
Pat_06	Pre-Treatment	FAM38B	63895	37	18	10689722	10689723	Frame_Shift_Del	DEL	GG	-	7	787	c.959_960delCC	c.(958-960)TCCfs	p.S320fs
Pat_06	Pre-Treatment	ESCO1	114799	37	18	19153983	19153984	Frame_Shift_Del	DEL	TG	-	8	1212	c.821_822delCA	c.(820-822)ACAfs	p.T274fs
Pat_06	Pre-Treatment	HAUS1	115106	37	18	43685174	43685174	Frame_Shift_Del	DEL	A	-	9	241	c.45delA	c.(43-45)TTAfs	p.L15fs
Pat_06	Pre-Treatment	MBD2	8932	37	18	51750459	51750459	Frame_Shift_Del	DEL	G	-	7	405	c.471delC	c.(469-471)CCCfs	p.P157fs
Pat_06	Pre-Treatment	WDR7	23335	37	18	54358513	54358513	Frame_Shift_Del	DEL	G	-	11	980	c.784delG	c.(784-786)GGGfs	p.G262fs
Pat_06	Pre-Treatment	DSEL	92126	37	18	65180521	65180521	Frame_Shift_Del	DEL	C	-	7	712	c.1355delG	c.(1354-1356)GGAfs	p.G452fs
Pat_06	Pre-Treatment	GTF2F1	2962	37	19	6381791	6381793	In_Frame_Del	DEL	CTT	-	7	129	c.751_753delAAG	c.(751-753)AAGdel	p.K251del
Pat_06	Pre-Treatment	ZNF442	79973	37	19	12461740	12461741	Frame_Shift_Ins	INS	-	A	7	638	c.658_659insT	c.(658-660)TGGfs	p.W220fs
Pat_06	Pre-Treatment	NWD1	284434	37	19	16908642	16908642	Frame_Shift_Del	DEL	T	-	9	1920	c.3404delT	c.(3403-3405)GTTfs	p.V1135fs
Pat_06	Pre-Treatment	ZNF43	7594	37	19	22002025	22002026	Splice_Site	INS	-	A	7	459	c.4_splice	c.e2-1	p.G2_splice
Pat_06	Pre-Treatment	WDR88	126248	37	19	33666419	33666421	In_Frame_Del	DEL	TCA	-	16	865	.1360_1362delTC	c.(1360-1362)TCAdel	p.S458del
Pat_06	Pre-Treatment	FFAR2	2867	37	19	35940788	35940790	In_Frame_Del	DEL	CTG	-	7	335	c.172_174delCTG	c.(172-174)CTGdel	p.L62del
Pat_06	Pre-Treatment	CAPN12	147968	37	19	39224369	39224371	In_Frame_Del	DEL	TCG	-	7	472	.1929_1931delCG	.(1927-1932)TACGAG>TA	.643_644YE>
Pat_06	Pre-Treatment	CAPN12	147968	37	19	39228931	39228931	Frame_Shift_Del	DEL	T	-	12	517	c.947delA	c.(946-948)AAGfs	p.K316fs
Pat_06	Pre-Treatment	PAF1	54623	37	19	39879780	39879780	Frame_Shift_Del	DEL	T	-	9	1503	c.520delA	c.(520-522)AGCfs	p.S174fs
Pat_06	Pre-Treatment	CEACAM5	1048	37	19	42224866	42224866	Frame_Shift_Del	DEL	C	-	7	1910	c.1796delC	c.(1795-1797)TCCfs	p.S599fs
Pat_06	Pre-Treatment	CD3EAP	10849	37	19	45911859	45911861	In_Frame_Del	DEL	GAA	-	7	441	c.633_635delGAA	.(631-636)CGGAAG>CG	p.K217del
Pat_06	Pre-Treatment	SAE1	10055	37	19	47712448	47712450	In_Frame_Del	DEL	CTT	-	7	877	c.981_983delCTT	c.(979-984)AACTTC>AAC	p.F331del
Pat_06	Pre-Treatment	TEAD2	8463	37	19	49850472	49850473	Frame_Shift_Ins	INS	-	G	14	1369	c.883_884insC	c.(883-885)CATfs	p.H295fs
Pat_06	Pre-Treatment	FUZ	80199	37	19	50310483	50310485	In_Frame_Del	DEL	CAG	-	15	398	.1180_1182delCT	c.(1180-1182)CTGdel	p.L394del
Pat_06	Pre-Treatment	ATF5	22809	37	19	50435750	50435750	Frame_Shift_Del	DEL	C	-	7	667	c.250delC	c.(250-252)CCCfs	p.P84fs
Pat_06	Pre-Treatment	ZNF649	65251	37	19	52393999	52393999	Frame_Shift_Del	DEL	C	-	8	2696	c.1390delG	c.(1390-1392)GAAfs	p.E464fs
Pat_06	Pre-Treatment	LENG1	79165	37	19	54660660	54660660	Frame_Shift_Del	DEL	C	-	7	645	c.416delG	c.(415-417)GGCfs	p.G139fs

Pat_06	Pre-Treatment	SOX11	6664	37	2	5833526	5833528	In_Frame_Del	DEL	GAC	-	10	181	c.673_675delGAC	c.(673-675)GACdel	p.D233del
Pat_06	Pre-Treatment	GREB1	9687	37	2	11738052	11738053	Frame_Shift_Ins	INS	-	C	7	2274	c.2100_2101insC	c.(2098-2103)ATTCCCfs	p.I700fs
Pat_06	Pre-Treatment	GREB1	9687	37	2	11750934	11750934	Frame_Shift_Del	DEL	G	-	9	430	c.2787delG	c.(2785-2787)CTGfs	p.L929fs
Pat_06	Pre-Treatment	PUM2	23369	37	2	20482977	20482979	In_Frame_Del	DEL	GCT	-	10	801	.1449_1451delAG	(1447-1452)GCAGCT>GC	.483_484AA>
Pat_06	Pre-Treatment	OTOF	9381	37	2	26693554	26693556	In_Frame_Del	DEL	CTT	-	7	340	.3928_3930delAA	c.(3928-3930)AAGdel	p.K1310del
Pat_06	Pre-Treatment	RTN4	57142	37	2	55253745	55253746	Frame_Shift_Ins	INS	-	T	11	269	c.1489_1490insA	c.(1489-1491)ATAfs	p.I497fs
Pat_06	Pre-Treatment	AFTPH	54812	37	2	64778672	64778674	In_Frame_Del	DEL	GAT	-	13	1383	c.64_66delGAT	c.(64-66)GATdel	p.D26del
Pat_06	Pre-Treatment	HK2	3099	37	2	75104378	75104378	Frame_Shift_Del	DEL	G	-	7	1466	c.961delG	c.(961-963)GGGfs	p.G321fs
Pat_06	Pre-Treatment	GGCX	2677	37	2	85778065	85778065	Frame_Shift_Del	DEL	T	-	8	1375	c.1871delA	c.(1870-1872)AAGfs	p.K624fs
Pat_06	Pre-Treatment	SLC9A4	389015	37	2	103124586	103124587	Frame_Shift_Del	DEL	TC	-	7	1348	c.1247_1248delTC	c.(1246-1248)TTCfs	p.F416fs
Pat_06	Pre-Treatment	MRPS9	64965	37	2	105708963	105708963	Frame_Shift_Del	DEL	A	-	7	915	c.756delA	c.(754-756)TCAfs	p.S252fs
Pat_06	Pre-Treatment	SULT1C4	27233	37	2	108998938	108998938	Frame_Shift_Del	DEL	G	-	8	902	c.393delG	c.(391-393)AAGfs	p.K131fs
Pat_06	Pre-Treatment	GCC2	9648	37	2	109087883	109087884	Frame_Shift_Ins	INS	-	A	11	999	c.2098_2099insA	c.(2098-2100)GAAfs	p.E700fs
Pat_06	Pre-Treatment	POLR1B	84172	37	2	113331367	113331367	Frame_Shift_Del	DEL	G	-	8	1265	c.2500delG	c.(2500-2502)GGGfs	p.G834fs
Pat_06	Pre-Treatment	SCN9A	6335	37	2	167141131	167141131	Frame_Shift_Del	DEL	G	-	8	794	c.1806delC	c.(1804-1806)ATCfs	p.I602fs
Pat_06	Pre-Treatment	LRP2	4036	37	2	170012800	170012800	Frame_Shift_Del	DEL	T	-	8	1351	c.12135delA	c.(12133-12135)AAAfs	p.K4045fs
Pat_06	Pre-Treatment	CDCA7	83879	37	2	174229648	174229650	In_Frame_Del	DEL	GGA	-	10	347	c.588_590delGGA	c.(586-591)ATGGAG>ATG	p.E202del
Pat_06	Pre-Treatment	TTN	7273	37	2	179422872	179422872	Frame_Shift_Del	DEL	C	-	8	459	c.79505delG	c.(79504-79506)GGAfs	p.G26502fs
Pat_06	Pre-Treatment	ALS2CR11	151254	37	2	202352352	202352352	Frame_Shift_Del	DEL	T	-	7	290	c.1855delA	c.(1855-1857)ATTfs	p.I619fs
Pat_06	Pre-Treatment	ATIC	471	37	2	216214333	216214333	Frame_Shift_Del	DEL	G	-	7	1187	c.1734delG	c.(1732-1734)CTGfs	p.L578fs
Pat_06	Pre-Treatment	ALPI	248	37	2	233320926	233320928	In_Frame_Del	DEL	TGC	-	10	225	c.17_19delTGC	c.(16-21)GTGCTG>GTG	p.L10del
Pat_06	Pre-Treatment	DEFB118	117285	37	20	29960672	29960672	Frame_Shift_Del	DEL	A	-	7	179	c.71delA	c.(70-72)GAAfs	p.E24fs
Pat_06	Pre-Treatment	ROMO1	140823	37	20	34287672	34287672	Frame_Shift_Del	DEL	T	-	9	1140	c.118delT	c.(118-120)TTTfs	p.F40fs
Pat_06	Pre-Treatment	SFRS6	6431	37	20	42089162	42089163	Frame_Shift_Del	DEL	TC	-	7	848	c.598_599delTC	c.(598-600)TCTfs	p.S200fs
Pat_06	Pre-Treatment	SLC9A8	23315	37	20	48466159	48466159	Frame_Shift_Del	DEL	T	-	8	557	c.476delT	c.(475-477)GTTfs	p.V159fs
Pat_06	Pre-Treatment	SALL4	57167	37	20	50408526	50408526	Frame_Shift_Del	DEL	G	-	7	1330	c.496delC	c.(496-498)CAGfs	p.Q166fs
Pat_06	Pre-Treatment	SYCP2	10388	37	20	58452518	58452519	Frame_Shift_Ins	INS	-	T	9	270	c.3071_3072insA	c.(3070-3072)AACfs	p.N1024fs
Pat_06	Pre-Treatment	RTEL1	51750	37	20	62292822	62292824	In_Frame_Del	DEL	GCT	-	9	218	c.274_276delGCT	c.(274-276)GCTdel	p.A96del
Pat_06	Pre-Treatment	LCA5L	150082	37	21	40794907	40794907	Frame_Shift_Del	DEL	T	-	7	691	c.832delA	c.(832-834)ATAfs	p.I278fs
Pat_06	Pre-Treatment	ZNF295	49854	37	21	43412376	43412376	Frame_Shift_Del	DEL	G	-	9	1056	c.1829delC	c.(1828-1830)TCAfs	p.S610fs
Pat_06	Pre-Treatment	PKNOX1	5316	37	21	44450072	44450072	Frame_Shift_Del	DEL	C	-	7	1174	c.1172delC	c.(1171-1173)GCCfs	p.A391fs
Pat_06	Pre-Treatment	MED15	51586	37	22	20918916	20918918	In_Frame_Del	DEL	CAG	-	36	439	c.631_633delCAG	c.(631-633)CAGdel	p.Q218del
Pat_06	Pre-Treatment	MED15	51586	37	22	20922855	20922857	In_Frame_Del	DEL	GCA	-	12	1334	.1089_1091delGC	(1087-1092)GTGCAG>GT	p.Q367del
Pat_06	Pre-Treatment	RAB36	9609	37	22	23494663	23494665	In_Frame_Del	DEL	GGT	-	10	1105	c.375_377delGGT	c.(373-378)AAGGTG>AAG	p.V129del
Pat_06	Pre-Treatment	SF3A1	10291	37	22	30742328	30742330	In_Frame_Del	DEL	CTG	-	26	884	c.364_366delCAG	c.(364-366)CAGdel	p.Q122del
Pat_06	Pre-Treatment	SMCR7L	54471	37	22	39910089	39910090	Frame_Shift_Del	DEL	CT	-	9	555	c.1153_1154delCT	c.(1153-1155)CTAfs	p.L385fs
Pat_06	Pre-Treatment	NAGA	4668	37	22	42463133	42463133	Frame_Shift_Del	DEL	G	-	7	2154	c.486delC	c.(484-486)CCCfs	p.P162fs
Pat_06	Pre-Treatment	FANCD2	2177	37	3	10116273	10116274	Frame_Shift_Del	DEL	CC	-	9	416	c.2775_2776delCC	c.(2773-2778)TTCCGAfs	p.F925fs
Pat_06	Pre-Treatment	DYNC1LI1	51143	37	3	32571050	32571050	Frame_Shift_Del	DEL	T	-	7	212	c.1288delA	c.(1288-1290)ATTfs	p.I430fs
Pat_06	Pre-Treatment	DLEC1	9940	37	3	38127767	38127767	Frame_Shift_Del	DEL	G	-	7	1412	c.1471delG	c.(1471-1473)GGGfs	p.G491fs
Pat_06	Pre-Treatment	NKTR	4820	37	3	42680269	42680271	In_Frame_Del	DEL	GAG	-	10	596	.3073_3075delGA	c.(3073-3075)GAGdel	p.E1029del
Pat_06	Pre-Treatment	HHATL	57467	37	3	42740315	42740317	In_Frame_Del	DEL	AGC	-	9	398	c.366_368delGCT	c.(364-369)CTGCTT>CTT	p.122_123LL>L
Pat_06	Pre-Treatment	ZNF167	55888	37	3	44612159	44612159	Frame_Shift_Del	DEL	T	-	7	1272	c.1557delT	c.(1555-1557)GGTfs	p.G519fs
Pat_06	Pre-Treatment	CACNA2D2	9254	37	3	50418529	50418529	Frame_Shift_Del	DEL	C	-	8	2041	c.681delG	c.(679-681)TGGfs	p.W227fs
Pat_06	Pre-Treatment	NT5DC2	64943	37	3	52568595	52568595	Frame_Shift_Del	DEL	G	-	8	1136	c.75delC	c.(73-75)ACCfs	p.T25fs
Pat_06	Pre-Treatment	ROBO2	6092	37	3	77657038	77657038	Frame_Shift_Del	DEL	C	-	9	654	c.3226delC	c.(3226-3228)CCCfs	p.P1076fs
Pat_06	Pre-Treatment	DPPA4	55211	37	3	109049606	109049606	Frame_Shift_Del	DEL	T	-	9	467	c.444delA	c.(442-444)AAAfs	p.K148fs

Pat_06	Pre-Treatment	KIAA2018	205717	37	3	113380090	113380090	Frame_Shift_Del	DEL	T	-	19	463	c.439delA	c.(439-441)ATTfs	p.I147fs
Pat_06	Pre-Treatment	DIRC2	84925	37	3	122514097	122514097	Frame_Shift_Del	DEL	G	-	2	4	c.58delG	c.(58-60)GGGfs	p.G20fs
Pat_06	Pre-Treatment	ABTB1	80325	37	3	127393289	127393290	Frame_Shift_Ins	INS	-	C	9	269	c.112_113insC	c.(112-114)ACCfs	p.T38fs
Pat_06	Pre-Treatment	NEK11	79858	37	3	130748696	130748696	Frame_Shift_Del	DEL	C	-	7	819	c.144delC	c.(142-144)GACfs	p.D48fs
Pat_06	Pre-Treatment	EIF2A	83939	37	3	150280427	150280427	Frame_Shift_Del	DEL	C	-	9	249	c.272delC	c.(271-273)GCAfs	p.A91fs
Pat_06	Pre-Treatment	ATP11B	23200	37	3	182602674	182602674	Frame_Shift_Del	DEL	T	-	8	305	c.2643delT	c.(2641-2643)TATfs	p.Y881fs
Pat_06	Pre-Treatment	EIF4G1	1981	37	3	184039744	184039746	In_Frame_Del	DEL	GAA	-	11	304	.1372_1374delGA	c.(1372-1374)GAAdel	p.E465del
Pat_06	Pre-Treatment	TRA2B	6434	37	3	185637260	185637262	In_Frame_Del	DEL	TCC	-	9	585	c.745_747delGGA	c.(745-747)GGAdel	p.G249del
Pat_06	Pre-Treatment	KLF3	51274	37	4	38690460	38690460	Frame_Shift_Del	DEL	A	-	7	945	c.312delA	c.(310-312)ATAfs	p.I104fs
Pat_06	Pre-Treatment	GABRG1	2565	37	4	46060358	46060358	Frame_Shift_Del	DEL	A	-	17	563	c.792delT	c.(790-792)TTTfs	p.F264fs
Pat_06	Pre-Treatment	CSN3	1448	37	4	71114987	71114987	Frame_Shift_Del	DEL	C	-	7	1269	c.360delC	c.(358-360)ATCfs	p.I120fs
Pat_06	Pre-Treatment	NUP54	53371	37	4	77065307	77065309	In_Frame_Del	DEL	TGC	-	8	1781	c.288_290delGCA	c.(286-291)CAGCAA>CAA	p.96_97QQ>Q
Pat_06	Pre-Treatment	PRDM8	56978	37	4	81123250	81123252	In_Frame_Del	DEL	CAG	-	8	132	c.634_636delCAG	c.(634-636)CAGdel	p.Q217del
Pat_06	Pre-Treatment	SEC31A	22872	37	4	83785675	83785677	In_Frame_Del	DEL	TGC	-	7	906	.1272_1274delGC	.(1270-1275)CAGCAC>CA	p.Q424del
Pat_06	Pre-Treatment	CDS1	1040	37	4	85556475	85556475	Frame_Shift_Del	DEL	T	-	30	534	c.781delT	c.(781-783)TTTfs	p.F261fs
Pat_06	Pre-Treatment	SPARCL1	8404	37	4	88403670	88403671	Frame_Shift_Del	DEL	AG	-	9	548	c.1573_1574delCT	c.(1573-1575)CTAfs	p.L525fs
Pat_06	Pre-Treatment	NAP1L5	266812	37	4	89618484	89618486	In_Frame_Del	DEL	TCC	-	9	305	c.420_422delGGA	.(418-423)GAGGAA>GAA	.140_141EE>
Pat_06	Pre-Treatment	NPNT	255743	37	4	106863682	106863684	In_Frame_Del	DEL	CCA	-	13	594	c.982_984delCCA	c.(982-984)CCAdel	p.P333del
Pat_06	Pre-Treatment	SEC24B	10427	37	4	110402913	110402915	In_Frame_Del	DEL	GAG	-	9	1342	.1141_1143delGA	c.(1141-1143)GAGdel	p.E384del
Pat_06	Pre-Treatment	KIAA1109	84162	37	4	123178593	123178593	Frame_Shift_Del	DEL	G	-	7	1926	c.6562delG	c.(6562-6564)GGGfs	p.G2188fs
Pat_06	Pre-Treatment	POU4F2	5458	37	4	147560457	147560458	In_Frame_Ins	INS	-	GGC	26	33	c.165_166insGGC	c.(163-168)insGGC	p.68_69insG
Pat_06	Pre-Treatment	LRBA	987	37	4	151842374	151842374	Frame_Shift_Del	DEL	A	-	7	1478	c.621delT	c.(619-621)TTTfs	p.F207fs
Pat_06	Pre-Treatment	CPE	1363	37	4	166405613	166405613	Frame_Shift_Del	DEL	T	-	7	2322	c.830delT	c.(829-831)ATTfs	p.I277fs
Pat_06	Pre-Treatment	DNAH5	1767	37	5	13919383	13919383	Frame_Shift_Del	DEL	T	-	15	1377	c.877delA	c.(877-879)AGAfs	p.R293fs
Pat_06	Pre-Treatment	PDZD2	23037	37	5	31799656	31799657	Frame_Shift_Ins	INS	-	G	7	625	c.301_302insG	c.(301-303)AGGfs	p.R101fs
Pat_06	Pre-Treatment	NIPBL	25836	37	5	37063925	37063927	In_Frame_Del	DEL	GAA	-	7	237	.7894_7896delGA	c.(7894-7896)GAAdel	p.E2636del
Pat_06	Pre-Treatment	EMB	133418	37	5	49707099	49707099	Frame_Shift_Del	DEL	T	-	7	1018	c.315delA	c.(313-315)AAAfs	p.K105fs
Pat_06	Pre-Treatment	ADAMTS6	11174	37	5	64569175	64569175	Frame_Shift_Del	DEL	C	-	9	2410	c.1612delG	c.(1612-1614)GAAfs	p.E538fs
Pat_06	Pre-Treatment	THBS4	7060	37	5	79355567	79355567	Frame_Shift_Del	DEL	C	-	7	1706	c.826delC	c.(826-828)CCCfs	p.P276fs
Pat_06	Pre-Treatment	VCAN	1462	37	5	82816057	82816057	Frame_Shift_Del	DEL	T	-	7	1261	c.1932delT	c.(1930-1932)CCTfs	p.P644fs
Pat_06	Pre-Treatment	PAM	5066	37	5	102296908	102296910	In_Frame_Del	DEL	AGA	-	8	1183	.1137_1139delAG	.(1135-1140)CGAGAA>CG	p.E383del
Pat_06	Pre-Treatment	AP3S1	1176	37	5	115202418	115202421	Frame_Shift_Del	DEL	AAGA	-	16	634	.121_124delAAG	c.(121-126)AAGAGAfs	p.K41fs
Pat_06	Pre-Treatment	ZNF608	57507	37	5	124079813	124079815	In_Frame_Del	DEL	CTC	-	11	1431	c.868_870delGAG	c.(868-870)GAGdel	p.E290del
Pat_06	Pre-Treatment	LMNB1	4001	37	5	126168434	126168436	In_Frame_Del	DEL	GAG	-	7	882	.1660_1662delGA	c.(1660-1662)GAGdel	p.E559del
Pat_06	Pre-Treatment	RAD50	10111	37	5	131944382	131944382	Frame_Shift_Del	DEL	A	-	7	141	c.2794delA	c.(2794-2796)AAAfs	p.K932fs
Pat_06	Pre-Treatment	IL9	3578	37	5	135229787	135229787	Frame_Shift_Del	DEL	G	-	10	518	c.237delC	c.(235-237)ACCfs	p.T79fs
Pat_06	Pre-Treatment	ANKHD1-EIF4EBP	404734	37	5	139885350	139885350	Frame_Shift_Del	DEL	G	-	12	1529	c.3304delG	c.(3304-3306)GGAfs	p.G1102fs
Pat_06	Pre-Treatment	PCDHA2	56146	37	5	140176837	140176838	Frame_Shift_Ins	INS	-	C	8	467	c.2288_2289insC	c.(2287-2289)GACfs	p.D763fs
Pat_06	Pre-Treatment	PCDHB10	56126	37	5	140574324	140574324	Frame_Shift_Del	DEL	T	-	7	955	c.2199delT	c.(2197-2199)CCTfs	p.P733fs
Pat_06	Pre-Treatment	PCDHGC3	5098	37	5	140857742	140857742	Frame_Shift_Del	DEL	A	-	9	940	c.2059delA	c.(2059-2061)AAAfs	p.K687fs
Pat_06	Pre-Treatment	DIAPH1	1729	37	5	140953309	140953309	Frame_Shift_Del	DEL	G	-	7	149	c.2108delC	c.(2107-2109)CCAfs	p.P703fs
Pat_06	Pre-Treatment	LARP1	23367	37	5	154181822	154181822	Frame_Shift_Del	DEL	G	-	11	882	c.1972delG	c.(1972-1974)GGGfs	p.G658fs
Pat_06	Pre-Treatment	RNF145	153830	37	5	158603761	158603761	Frame_Shift_Del	DEL	G	-	9	394	c.500delC	c.(499-501)ACAfs	p.T167fs
Pat_06	Pre-Treatment	HNRNPH1	3187	37	5	179050112	179050112	Frame_Shift_Del	DEL	C	-	9	713	c.23delG	c.(22-24)GGAfs	p.G8fs
Pat_06	Pre-Treatment	TUBB2A	7280	37	6	3154114	3154116	In_Frame_Del	DEL	CCT	-	7	846	.1319_1321delAG	(1318-1323)GAGGGC>GG	p.E440del
Pat_06	Pre-Treatment	CDYL	9425	37	6	4892244	4892244	Frame_Shift_Del	DEL	A	-	8	806	c.484delA	c.(484-486)AAAfs	p.K162fs
Pat_06	Pre-Treatment	RANBP9	10048	37	6	13632610	13632610	Frame_Shift_Del	DEL	T	-	7	1283	c.1939delA	c.(1939-1941)ATGfs	p.M647fs

Pat_06	Pre-Treatment	KIF13A	63971	37	6	17780984	17780984	Frame_Shift_Del	DEL	C	-	7	611	c.3823delG	c.(3823-3825)GCAfs	p.A1275fs
Pat_06	Pre-Treatment	KDM1B	221656	37	6	18213941	18213941	Frame_Shift_Del	DEL	T	-	7	2021	c.1429delT	c.(1429-1431)TTTfs	p.F477fs
Pat_06	Pre-Treatment	SLC17A1	6568	37	6	25830753	25830753	Frame_Shift_Del	DEL	T	-	7	1710	c.33delA	c.(31-33)AAAfs	p.K11fs
Pat_06	Pre-Treatment	GABBR1	2550	37	6	29599254	29599254	Frame_Shift_Del	DEL	C	-	10	1706	c.208delG	c.(208-210)GAGfs	p.E70fs
Pat_06	Pre-Treatment	TRIM26	7726	37	6	30157254	30157254	Frame_Shift_Del	DEL	T	-	17	1006	c.845delA	c.(844-846)AAGfs	p.K282fs
Pat_06	Pre-Treatment	PPP1R10	5514	37	6	30569334	30569334	Frame_Shift_Del	DEL	G	-	8	570	c.2815delC	c.(2815-2817)CTGfs	p.L939fs
Pat_06	Pre-Treatment	PPP1R10	5514	37	6	30570264	30570266	In_Frame_Del	DEL	GGA	-	7	202	.2160_2162delTC	.(2158-2163)CCTCCA>CC	.720_721PP>
Pat_06	Pre-Treatment	DDR1	780	37	6	30863251	30863251	Frame_Shift_Del	DEL	C	-	7	2055	c.1584delC	c.(1582-1584)GGCfs	p.G528fs
Pat_06	Pre-Treatment	BAT1	7919	37	6	31504446	31504446	Frame_Shift_Del	DEL	A	-	10	494	c.447delT	c.(445-447)TTTfs	p.F149fs
Pat_06	Pre-Treatment	BAT3	7917	37	6	31608162	31608163	Frame_Shift_Ins	INS	-	G	8	1860	c.3047_3048insC	c.(3046-3048)CCAfs	p.P1016fs
Pat_06	Pre-Treatment	HSPA1L	3305	37	6	31778562	31778564	In_Frame_Del	DEL	CAG	-	8	920	.1186_1188delCT	c.(1186-1188)CTGdel	p.L396del
Pat_06	Pre-Treatment	SCUBE3	222663	37	6	35205699	35205699	Frame_Shift_Del	DEL	G	-	8	1306	c.733delG	c.(733-735)GGGfs	p.G245fs
Pat_06	Pre-Treatment	ZNF318	24149	37	6	43323502	43323502	Frame_Shift_Del	DEL	T	-	9	1140	c.1570delA	c.(1570-1572)AGGfs	p.R524fs
Pat_06	Pre-Treatment	MUT	4594	37	6	49409649	49409649	Frame_Shift_Del	DEL	T	-	7	1944	c.1712delA	c.(1711-1713)AAGfs	p.K571fs
Pat_06	Pre-Treatment	HCRTR2	3062	37	6	55039411	55039411	Frame_Shift_Del	DEL	C	-	11	696	c.26delC	c.(25-27)TCCfs	p.S9fs
Pat_06	Pre-Treatment	DST	667	37	6	56362804	56362804	Frame_Shift_Del	DEL	A	-	7	1028	c.13587delT	c.(13585-13587)GTTfs	p.V4529fs
Pat_06	Pre-Treatment	PHF3	23469	37	6	64408371	64408371	Frame_Shift_Del	DEL	A	-	10	1635	c.2858delA	c.(2857-2859)GAAfs	p.E953fs
Pat_06	Pre-Treatment	PHF3	23469	37	6	64415953	64415953	Frame_Shift_Del	DEL	A	-	11	1784	c.3402delA	c.(3400-3402)CCAfs	p.P1134fs
Pat_06	Pre-Treatment	MAP3K7	6885	37	6	91296568	91296570	In_Frame_Del	DEL	GAG	-	15	214	c.33_35delCTC	c.(31-36)TCCTCG>TCG	p.11_12SS>S
Pat_06	Pre-Treatment	MARCKS	4082	37	6	114181209	114181210	Frame_Shift_Ins	INS	-	A	10	48	c.453_454insA	c.(451-456)CCGAAAfs	p.P151fs
Pat_06	Pre-Treatment	SLC2A12	154091	37	6	134350115	134350115	Frame_Shift_Del	DEL	A	-	8	479	c.848delT	c.(847-849)CTAfs	p.L283fs
Pat_06	Pre-Treatment	IFNGR1	3459	37	6	137519505	137519506	Frame_Shift_Del	DEL	CT	-	12	926	c.1132_1133delAG	c.(1132-1134)AGTfs	p.S378fs
Pat_06	Pre-Treatment	REPS1	85021	37	6	139266690	139266690	Frame_Shift_Del	DEL	T	-	15	1625	c.422delA	c.(421-423)AAGfs	p.K141fs
Pat_06	Pre-Treatment	TIAM2	26230	37	6	155450474	155450474	Frame_Shift_Del	DEL	G	-	7	405	c.117delG	c.(115-117)GAGfs	p.E39fs
Pat_06	Pre-Treatment	PRKAR1B	5575	37	7	720281	720281	Frame_Shift_Del	DEL	G	-	12	639	c.260delC	c.(259-261)CCGfs	p.P87fs
Pat_06	Pre-Treatment	PHF14	9678	37	7	11075380	11075381	Frame_Shift_Del	DEL	AG	-	16	1542	c.1569_1570delAG	c.(1567-1572)CAAGAGfs	p.Q523fs
Pat_06	Pre-Treatment	TWISTNB	221830	37	7	19738111	19738113	In_Frame_Del	DEL	TTC	-	9	2401	c.843_845delGAA	c.(841-846)AAGAAA>AAA	.281_282KK>
Pat_06	Pre-Treatment	POU6F2	11281	37	7	39379288	39379290	In_Frame_Del	DEL	CAG	-	9	237	c.559_561delCAG	c.(559-561)CAGdel	p.Q196del
Pat_06	Pre-Treatment	H2AFV	94239	37	7	44874102	44874102	Frame_Shift_Del	DEL	A	-	8	431	c.385delT	c.(385-387)TAGfs	p.*129fs
Pat_06	Pre-Treatment	EGFR	1956	37	7	55240694	55240695	Frame_Shift_Del	DEL	CG	-	7	829	c.1938_1939delCG	c.(1936-1941)ATCGCCfs	p.I646fs
Pat_06	Pre-Treatment	STX1A	6804	37	7	73123425	73123427	In_Frame_Del	DEL	CAT	-	7	958	c.56_58delATG	c.(55-60)GATGTC>GTC	p.D19del
Pat_06	Pre-Treatment	TMEM60	85025	37	7	77423460	77423460	Frame_Shift_Del	DEL	T	-	14	574	c.231delA	c.(229-231)AAAfs	p.K77fs
Pat_06	Pre-Treatment	PHTF2	57157	37	7	77569580	77569581	Frame_Shift_Ins	INS	-	T	8	776	c.1701_1702insT	c.(1699-1704)TTCTTTfs	p.F567fs
Pat_06	Pre-Treatment	PCLO	27445	37	7	82390055	82390055	Frame_Shift_Del	DEL	T	-	7	156	c.15188delA	c.(15187-15189)AAGfs	p.K5063fs
Pat_06	Pre-Treatment	PCLO	27445	37	7	82578907	82578907	Frame_Shift_Del	DEL	G	-	7	1546	c.10997delC	c.(10996-10998)CCAfs	p.P3666fs
Pat_06	Pre-Treatment	AKAP9	10142	37	7	91671392	91671393	Frame_Shift_Del	DEL	AG	-	8	304	c.4950_4951delAG	c.(4948-4953)TCAGAGfs	p.S1650fs
Pat_06	Pre-Treatment	TAF6	6878	37	7	99705124	99705124	Frame_Shift_Del	DEL	G	-	8	1473	c.1779delC	c.(1777-1779)CCCfs	p.P593fs
Pat_06	Pre-Treatment	ACHE	43	37	7	100491788	100491790	In_Frame_Del	DEL	GAG	-	8	108	c.64_66delCTC	c.(64-66)CTCdel	p.L22del
Pat_06	Pre-Treatment	RELN	5649	37	7	103270544	103270545	Frame_Shift_Del	DEL	GG	-	8	1501	c.2544_2545delCC	c.(2542-2547)TCCCAGfs	p.S848fs
Pat_06	Pre-Treatment	EXOC4	60412	37	7	133682285	133682285	Frame_Shift_Del	DEL	C	-	7	779	c.2247delC	c.(2245-2247)CTCfs	p.L749fs
Pat_06	Pre-Treatment	MLL3	58508	37	7	151856009	151856009	Frame_Shift_Del	DEL	T	-	8	1439	c.11609delA	c.(11608-11610)AAGfs	p.K3870fs
Pat_06	Pre-Treatment	XRCC2	7516	37	7	152346220	152346220	Frame_Shift_Del	DEL	A	-	17	604	c.350delT	c.(349-351)TTGfs	p.L117fs
Pat_06	Pre-Treatment	C8orf42	157695	37	8	494659	494664	In_Frame_Del	DEL	GGCGGC	-	12	30	.94_99delGCCGC	c.(94-99)GCCGCCdel	p.AA32del
Pat_06	Pre-Treatment	SFTPC	6440	37	8	22020159	22020161	In_Frame_Del	DEL	GTG	-	20	818	c.115_117delGTG	c.(115-117)GTGdel	p.V44del
Pat_06	Pre-Treatment	WRN	7486	37	8	30945377	30945379	In_Frame_Del	DEL	AAG	-	15	336	.1517_1519delAA	.(1516-1521)AAAGAA>AA	p.E510del
Pat_06	Pre-Treatment	UNC5D	137970	37	8	35608248	35608248	Frame_Shift_Del	DEL	T	-	12	1572	c.2084delT	c.(2083-2085)GTTfs	p.V695fs
Pat_06	Pre-Treatment	MYST3	7994	37	8	41798420	41798422	In_Frame_Del	DEL	CTC	-	10	711	.2977_2979delGA	c.(2977-2979)GAGdel	p.E993del

Pat_06	Pre-Treatment	TOX	9760	37	8	59750796	59750798	In_Frame_Del	DEL	CTT	-	8	699	c.766_768delAAG	c.(766-768)AAGdel	p.K256del
Pat_06	Pre-Treatment	MYBL1	4603	37	8	67488452	67488453	Frame_Shift_Ins	INS	-	T	7	1127	c.1259_1260insA	c.(1258-1260)AACfs	p.N420fs
Pat_06	Pre-Treatment	ARFGEF1	10565	37	8	68128855	68128856	Frame_Shift_Ins	INS	-	G	7	805	c.4655_4656insC	c.(4654-4656)CCAfs	p.P1552fs
Pat_06	Pre-Treatment	LRRCC1	85444	37	8	86038947	86038948	Frame_Shift_Del	DEL	AG	-	10	374	c.1296_1297delAG	c.(1294-1299)CAAGAGfs	p.Q432fs
Pat_06	Pre-Treatment	MMP16	4325	37	8	89086959	89086959	Frame_Shift_Del	DEL	A	-	8	1634	c.1096delT	c.(1096-1098)TGGfs	p.W366fs
Pat_06	Pre-Treatment	MMP16	4325	37	8	89128860	89128860	Frame_Shift_Del	DEL	T	-	7	1829	c.959delA	c.(958-960)AATfs	p.N320fs
Pat_06	Pre-Treatment	NBN	4683	37	8	90965666	90965666	Frame_Shift_Del	DEL	T	-	12	1073	c.1651delA	c.(1651-1653)AGGfs	p.R551fs
Pat_06	Pre-Treatment	RUNX1T1	862	37	8	92998419	92998419	Frame_Shift_Del	DEL	T	-	8	839	c.1212delA	c.(1210-1212)AAAfs	p.K404fs
Pat_06	Pre-Treatment	UBR5	51366	37	8	103289348	103289349	Frame_Shift_Ins	INS	-	T	8	729	c.6360_6361insA	c.(6358-6363)AAAGAAfs	p.K2120fs
Pat_06	Pre-Treatment	LRP12	29967	37	8	105503633	105503633	Frame_Shift_Del	DEL	C	-	7	609	c.1848delG	c.(1846-1848)GGGfs	p.G616fs
Pat_06	Pre-Treatment	TSNARE1	203062	37	8	143310866	143310868	In_Frame_Del	DEL	GAT	-	11	705	c.1519_1521delAT	c.(1519-1521)ATCdel	p.I507del
Pat_06	Pre-Treatment	ZC3H3	23144	37	8	144621235	144621235	Frame_Shift_Del	DEL	C	-	7	536	c.302delG	c.(301-303)GGCfs	p.G101fs
Pat_06	Pre-Treatment	ZNF251	90987	37	8	145947867	145947867	Frame_Shift_Del	DEL	A	-	7	890	c.1178delT	c.(1177-1179)TTCfs	p.F393fs
Pat_06	Pre-Treatment	KIAA0020	9933	37	9	2837296	2837296	Frame_Shift_Del	DEL	T	-	10	1106	c.188delA	c.(187-189)AAGfs	p.K63fs
Pat_06	Pre-Treatment	C9orf46	55848	37	9	5361787	5361787	Frame_Shift_Del	DEL	A	-	7	341	c.183delT	c.(181-183)TTTfs	p.F61fs
Pat_06	Pre-Treatment	KIAA1045	23349	37	9	34977582	34977584	In_Frame_Del	DEL	CAG	-	7	175	.1050_1052delCA	(1048-1053)GCCAGC>GC	p.S354del
Pat_06	Pre-Treatment	VCP	7415	37	9	35062983	35062985	In_Frame_Del	DEL	AAG	-	13	988	c.801_803delCTT	c.(799-804)TTCTTG>TTG	p.F267del
Pat_06	Pre-Treatment	KLF9	687	37	9	73002714	73002714	Frame_Shift_Del	DEL	T	-	8	700	c.713delA	c.(712-714)AAGfs	p.K238fs
Pat_06	Pre-Treatment	GOLGA2	2801	37	9	131019390	131019390	Frame_Shift_Del	DEL	A	-	12	754	c.2965delT	c.(2965-2967)TACfs	p.Y989fs
Pat_06	Pre-Treatment	CEL	1056	37	9	135941982	135941982	Frame_Shift_Del	DEL	G	-	12	1121	c.613delG	c.(613-615)GGGfs	p.G205fs
Pat_06	Pre-Treatment	RALGDS	5900	37	9	135975698	135975700	In_Frame_Del	DEL	CTC	-	7	2126	.2524_2526delGA	c.(2524-2526)GAGdel	p.E842del
Pat_06	Pre-Treatment	WDR5	11091	37	9	137019598	137019598	Frame_Shift_Del	DEL	C	-	12	2800	c.642delC	c.(640-642)AACfs	p.N214fs
Pat_06	Pre-Treatment	YY2	404281	37	X	21857869	21857871	In_Frame_Del	DEL	TGG	-	7	124	c.17_19delTGG	c.(16-21)CTGGTG>CTG	p.V11del
Pat_06	Pre-Treatment	GNL3L	54552	37	X	54578339	54578341	In_Frame_Del	DEL	GAA	-	9	351	c.1113_1115delGA	(1111-1116)GGGAAG>GG	p.K375del
Pat_06	Pre-Treatment	TAF1	6872	37	X	70603000	70603000	Frame_Shift_Del	DEL	A	-	7	439	c.1930delA	c.(1930-1932)AAAfs	p.K644fs
Pat_06	Pre-Treatment	KIAA2022	340533	37	X	73960934	73960934	Frame_Shift_Del	DEL	T	-	7	1158	c.3458delA	c.(3457-3459)AACfs	p.N1153fs
Pat_06	Pre-Treatment	BRWD3	254065	37	X	79932487	79932487	Frame_Shift_Del	DEL	C	-	8	2050	c.5030delG	c.(5029-5031)GGAfs	p.G1677fs
Pat_06	Pre-Treatment	TAF7L	54457	37	X	100536709	100536709	Frame_Shift_Del	DEL	T	-	9	1119	c.719delA	c.(718-720)AAGfs	p.K240fs
Pat_06	Pre-Treatment	FAM199X	139231	37	X	103432837	103432839	In_Frame_Del	DEL	CAG	-	8	998	c.846_848delCAG	.(844-849)GCCAGC>GCC	p.S286del
Pat_06	Pre-Treatment	PAK3	5063	37	X	110406206	110406208	In_Frame_Del	DEL	GAA	-	10	596	c.577_579delGAA	c.(577-579)GAAdel	p.E197del
Pat_06	Pre-Treatment	SLC6A14	11254	37	X	115584256	115584256	Frame_Shift_Del	DEL	T	-	8	529	c.1234delT	c.(1234-1236)TTTfs	p.F412fs
Pat_06	Pre-Treatment	NKAP	79576	37	X	119072752	119072753	Frame_Shift_Del	DEL	TC	-	11	973	c.407_408delGA	c.(406-408)AGAfs	p.R136fs
Pat_06	Pre-Treatment	PLAC1	10761	37	X	133700524	133700525	Frame_Shift_Ins	INS	-	G	8	1803	c.188_189insC	c.(187-189)CCAfs	p.P63fs
Pat_06	Pre-Treatment	SLC9A6	10479	37	X	135106581	135106581	Frame_Shift_Del	DEL	T	-	7	1820	c.1459delT	c.(1459-1461)TTTfs	p.F487fs
Pat_06	Pre-Treatment	BRS3	680	37	X	135574250	135574250	Frame_Shift_Del	DEL	G	-	8	3201	c.916delG	c.(916-918)GCCfs	p.A306fs
Pat_06	Pre-Treatment	HTATSF1	27336	37	X	135585048	135585050	In_Frame_Del	DEL	AAG	-	21	737	c.682_684delAAG	c.(682-684)AAGdel	p.K232del
Pat_06	Pre-Treatment	CD99L2	83692	37	X	149937526	149937528	In_Frame_Del	DEL	GGC	-	13	1668	c.768_770delGCC	.(766-771)CCGCCC>CCC	.256_257PP>I
Pat_06	Post-Resistance	CLSTN1	22883	37	1	9790640	9790642	In_Frame_Del	DEL	CCT	-	11	509	.2870_2872delAG	(2869-2874)GAGGGG>GG	p.E957del
Pat_06	Post-Resistance	EXOSC10	5394	37	1	11128120	11128120	Frame_Shift_Del	DEL	T	-	7	453	c.2572delA	c.(2572-2574)ATTfs	p.I858fs
Pat_06	Post-Resistance	SPEN	23013	37	1	16262680	16262680	Frame_Shift_Del	DEL	C	-	10	1174	c.9945delC	c.(9943-9945)CACfs	p.H3315fs
Pat_06	Post-Resistance	MST1P9	11223	37	1	17086003	17086003	Frame_Shift_Del	DEL	G	-	11	1323	c.894delC	c.(892-894)GGCfs	p.G298fs
Pat_06	Post-Resistance	IGSF21	84966	37	1	18554420	18554420	Frame_Shift_Del	DEL	C	-	12	1242	c.99delC	c.(97-99)CTCfs	p.L33fs
Pat_06	Post-Resistance	USP48	84196	37	1	22083040	22083040	Frame_Shift_Del	DEL	T	-	7	1307	c.411delA	c.(409-411)AAAfs	p.K137fs
Pat_06	Post-Resistance	PEF1	553115	37	1	32100885	32100885	Frame_Shift_Del	DEL	C	-	7	491	c.263delG	c.(262-264)GGCfs	p.G88fs
Pat_06	Post-Resistance	PHC2	1912	37	1	33799792	33799792	Frame_Shift_Del	DEL	G	-	7	1565	c.1657delC	c.(1657-1659)CAGfs	p.Q553fs
Pat_06	Post-Resistance	EIF2B3	8891	37	1	45407182	45407182	Frame_Shift_Del	DEL	T	-	12	339	c.450delA	c.(448-450)AAAfs	p.K150fs
Pat_06	Post-Resistance	PCSK9	255738	37	1	55505552	55505553	In_Frame_Ins	INS	-	CTG	10	18	c.42_43insCTG	c.(40-45)insCTG	p.23_24insL

Pat_06	Post-Resistance	FGGY	55277	37	1	59812017	59812017	Frame_Shift_Del	DEL	G	-	8	540	c.412delG	c.(412-414)GGGfs	p.G138fs
Pat_06	Post-Resistance	LRRIQ3	127255	37	1	74575212	74575213	Frame_Shift_Ins	INS	-	T	20	410	c.732_733insA	c.(730-735)AAACAGfs	p.K244fs
Pat_06	Post-Resistance	TNNI3K	51086	37	1	74957824	74957826	In_Frame_Del	DEL	CTT	-	20	1936	.2225_2227delCT	.(2224-2229)CCTTCT>CC	p.S746del
Pat_06	Post-Resistance	TRIM33	51592	37	1	114968116	114968118	In_Frame_Del	DEL	TGT	-	10	2370	.1648_1650delAC	c.(1648-1650)ACAdel	p.T550del
Pat_06	Post-Resistance	PTGFRN	5738	37	1	117527425	117527426	Frame_Shift_Del	DEL	GC	-	7	1086	c.2291_2292delG	c.(2290-2292)AGCfs	p.S764fs
Pat_06	Post-Resistance	FMO5	2330	37	1	146684955	146684955	Frame_Shift_Del	DEL	T	-	8	2762	c.407delA	c.(406-408)AAGfs	p.K136fs
Pat_06	Post-Resistance	RFX5	5993	37	1	151318741	151318741	Frame_Shift_Del	DEL	G	-	7	756	c.56delC	c.(55-57)CCAfs	p.P19fs
Pat_06	Post-Resistance	TCHH	7062	37	1	152082211	152082213	In_Frame_Del	DEL	CTC	-	13	313	.3480_3482delGA	.(3478-3483)AAGAGA>AA	p.R1163del
Pat_06	Post-Resistance	TCHH	7062	37	1	152084657	152084658	In_Frame_Ins	INS	-	CTC	9	614	.1035_1036insGA	c.(1033-1038)insGAG	p.345_346insE
Pat_06	Post-Resistance	ILF2	3608	37	1	153640096	153640096	Frame_Shift_Del	DEL	T	-	7	1876	c.329delA	c.(328-330)AAGfs	p.K110fs
Pat_06	Post-Resistance	KCNN3	3782	37	1	154842331	154842333	In_Frame_Del	DEL	TGC	-	10	105	c.108_110delGCA	c.(106-111)CAGCAA>CAA	p.36_37QQ>Q
Pat_06	Post-Resistance	NES	10763	37	1	156642804	156642804	Frame_Shift_Del	DEL	G	-	18	1915	c.1176delC	c.(1174-1176)CCCfs	p.P392fs
Pat_06	Post-Resistance	PVRL4	81607	37	1	161044057	161044059	In_Frame_Del	DEL	CAC	-	8	714	.1105_1107delGT	c.(1105-1107)GTGdel	p.V369del
Pat_06	Post-Resistance	PCP4L1	654790	37	1	161254154	161254156	In_Frame_Del	DEL	GGA	-	10	830	c.90_92delGGA	c.(88-93)GCGGAG>GCG	p.E35del
Pat_06	Post-Resistance	CACNA1S	779	37	1	201046178	201046180	In_Frame_Del	DEL	AGC	-	7	1026	.1695_1697delGC	.(1693-1698)CTGCTC>CT	.565_566LL>
Pat_06	Post-Resistance	IPO9	55705	37	1	201843998	201844000	In_Frame_Del	DEL	GAG	-	12	549	.2872_2874delGA	c.(2872-2874)GAGdel	p.E962del
Pat_06	Post-Resistance	GPR37L1	9283	37	1	202097525	202097527	In_Frame_Del	DEL	CTG	-	8	88	.1287_1289delCT	(1285-1290)GACTGC>GA	p.C436del
Pat_06	Post-Resistance	ZC3H11A	9877	37	1	203786225	203786225	Frame_Shift_Del	DEL	T	-	13	364	c.27delT	c.(25-27)TATfs	p.Y9fs
Pat_06	Post-Resistance	AVPR1B	553	37	1	206225073	206225075	In_Frame_Del	DEL	GGT	-	7	833	c.633_635delGGT	.(631-636)CCGGTG>CC	p.V212del
Pat_06	Post-Resistance	DYRK3	8444	37	1	206821441	206821441	Frame_Shift_Del	DEL	A	-	9	600	c.898delA	c.(898-900)AAAfs	p.K300fs
Pat_06	Post-Resistance	MOSC2	54996	37	1	220955170	220955170	Frame_Shift_Del	DEL	T	-	7	993	c.935delT	c.(934-936)CTTfs	p.L312fs
Pat_06	Post-Resistance	OR2W5	441932	37	1	247654684	247654684	Frame_Shift_Del	DEL	G	-	7	702	c.255delG	c.(253-255)CTGfs	p.L85fs
Pat_06	Post-Resistance	OR2T33	391195	37	1	248436882	248436882	Frame_Shift_Del	DEL	T	-	7	2732	c.235delA	c.(235-237)ATGfs	p.M79fs
Pat_06	Post-Resistance	NET1	10276	37	10	5497067	5497070	Frame_Shift_Del	DEL	AGCA	-	7	768	1183_1186delAG	c.(1183-1188)AGCAAGfs	p.S395fs
Pat_06	Post-Resistance	NCOA4	8031	37	10	51585146	51585147	Frame_Shift_Del	DEL	GT	-	7	320	.1245_1246delGT	c.(1243-1248)GAGTGTfs	p.E415fs
Pat_06	Post-Resistance	SLC16A12	387700	37	10	91203597	91203598	Frame_Shift_Ins	INS	-	A	11	389	c.129_130insT	c.(127-132)TTTGTGfs	p.F43fs
Pat_06	Post-Resistance	TNKS2	80351	37	10	93601945	93601946	Frame_Shift_Ins	INS	-	A	11	291	c.1856_1857insA	c.(1855-1857)ACAfs	p.T619fs
Pat_06	Post-Resistance	PAX2	5076	37	10	102584452	102584452	Frame_Shift_Del	DEL	C	-	8	1691	c.1036delC	c.(1036-1038)CCCfs	p.P346fs
Pat_06	Post-Resistance	ATRNL1	26033	37	10	117486826	117486826	Frame_Shift_Del	DEL	G	-	7	378	c.3864delG	c.(3862-3864)GTGfs	p.V1288fs
Pat_06	Post-Resistance	RAB11FIP2	22841	37	10	119798647	119798647	Frame_Shift_Del	DEL	T	-	7	1027	c.1101delA	c.(1099-1101)AAAfs	p.K367fs
Pat_06	Post-Resistance	CUZD1	50624	37	10	124593215	124593215	Frame_Shift_Del	DEL	T	-	8	1210	c.1624delA	c.(1624-1626)AGGfs	p.R542fs
Pat_06	Post-Resistance	PTPRE	5791	37	10	129876002	129876004	In_Frame_Del	DEL	AGC	-	8	742	.1847_1849delAG	(1846-1851)AAGCAG>AA	p.Q620del
Pat_06	Post-Resistance	PHRF1	57661	37	11	592586	592588	In_Frame_Del	DEL	GAG	-	8	1106	c.532_534delGAG	c.(532-534)GAGdel	p.E181del
Pat_06	Post-Resistance	BRSK2	9024	37	11	1471060	1471060	Frame_Shift_Del	DEL	C	-	8	1128	c.1281delC	c.(1279-1281)AGCfs	p.S427fs
Pat_06	Post-Resistance	DENND5A	23258	37	11	9182390	9182390	Frame_Shift_Del	DEL	T	-	8	1271	c.2306delA	c.(2305-2307)AAGfs	p.K769fs
Pat_06	Post-Resistance	PAX6	5080	37	11	31812317	31812317	Frame_Shift_Del	DEL	G	-	7	714	c.1124delC	c.(1123-1125)CCAfs	p.P375fs
Pat_06	Post-Resistance	PAMR1	25891	37	11	35513670	35513670	Frame_Shift_Del	DEL	C	-	8	2309	c.302delG	c.(301-303)GGTfs	p.G101fs
Pat_06	Post-Resistance	DGKZ	8525	37	11	46400752	46400753	Splice_Site	INS	-	C	10	932	c.3104_splice	c.e30-1	p.A1035_splice
Pat_06	Post-Resistance	CHRM4	1132	37	11	46406723	46406723	Frame_Shift_Del	DEL	T	-	7	353	c.1385delA	c.(1384-1386)AAGfs	p.K462fs
Pat_06	Post-Resistance	CPSF7	79869	37	11	61183765	61183767	In_Frame_Del	DEL	AGG	-	8	305	c.775_777delCCT	c.(775-777)CCTdel	p.P259del
Pat_06	Post-Resistance	SLC22A12	116085	37	11	64367266	64367268	In_Frame_Del	DEL	CTG	-	10	750	.1189_1191delCT	c.(1189-1191)CTGdel	p.L400del
Pat_06	Post-Resistance	TM7SF2	7108	37	11	64880874	64880874	Frame_Shift_Del	DEL	G	-	7	594	c.487delG	c.(487-489)GGGfs	p.G163fs
Pat_06	Post-Resistance	LRFN4	78999	37	11	66625231	66625233	In_Frame_Del	DEL	CTG	-	11	200	c.16_18delCTG	c.(16-18)CTGdel	p.L10del
Pat_06	Post-Resistance	UVRAG	7405	37	11	75727924	75727924	Frame_Shift_Del	DEL	T	-	7	1016	c.1126delT	c.(1126-1128)TTTfs	p.F376fs
Pat_06	Post-Resistance	NCAPD3	23310	37	11	134048586	134048586	Frame_Shift_Del	DEL	G	-	7	778	c.2725delC	c.(2725-2727)CAGfs	p.Q909fs
Pat_06	Post-Resistance	PRMT8	56341	37	12	3649780	3649780	Frame_Shift_Del	DEL	C	-	7	927	c.84delC	c.(82-84)AGCfs	p.S28fs
Pat_06	Post-Resistance	TAS2R50	259296	37	12	11139432	11139432	Frame_Shift_Del	DEL	A	-	7	186	c.28delT	c.(28-30)TCAfs	p.S10fs

Pat_06	Post-Resistance	ITPR2	3709	37	12	26589238	26589239	Frame_Shift_Del	DEL	AG	-	8	763	c.6684_6685delCT	c.(6682-6687)CTCTGGfs	p.L2228fs
Pat_06	Post-Resistance	PKP2	5318	37	12	32955396	32955396	Frame_Shift_Del	DEL	T	-	7	1541	c.2240delA	c.(2239-2241)AAGfs	p.K747fs
Pat_06	Post-Resistance	SFRS2IP	9169	37	12	46318575	46318577	In_Frame_Del	DEL	GGT	-	23	1840	.3840_3842delAC	(3838-3843)CCACCC>CC	1280_1281PP>
Pat_06	Post-Resistance	SFRS2IP	9169	37	12	46320707	46320708	Frame_Shift_Del	DEL	TC	-	14	983	c.2776_2777delGA	c.(2776-2778)GAAfs	p.E926fs
Pat_06	Post-Resistance	PRPF40B	25766	37	12	50025258	50025258	Frame_Shift_Del	DEL	C	-	10	1377	c.93delC	c.(91-93)ATCfs	p.I31fs
Pat_06	Post-Resistance	ACCN2	41	37	12	50452565	50452567	In_Frame_Del	DEL	GAG	-	7	744	c.16_18delGAG	c.(16-18)GAGdel	p.E9del
Pat_06	Post-Resistance	KRT77	374454	37	12	53097076	53097078	In_Frame_Del	DEL	CCA	-	8	645	c.141_143delTGG	.(139-144)GGTGGA>GG	p.47_48GG>G
Pat_06	Post-Resistance	B4GALNT1	2583	37	12	58025102	58025103	Frame_Shift_Ins	INS	-	C	8	820	c.263_264insG	c.(262-264)GGCfs	p.G88fs
Pat_06	Post-Resistance	CAND1	55832	37	12	67699692	67699692	Frame_Shift_Del	DEL	G	-	7	985	c.2244delG	c.(2242-2244)CAGfs	p.Q748fs
Pat_06	Post-Resistance	ZDHHC17	23390	37	12	77203639	77203640	Splice_Site	INS	-	A	7	194	c.543_splice	c.e5+2	p.Q181_splice
Pat_06	Post-Resistance	CEP290	80184	37	12	88524078	88524079	Frame_Shift_Ins	INS	-	T	11	967	c.635_636insA	c.(634-636)AACfs	p.N212fs
Pat_06	Post-Resistance	UTP20	27340	37	12	101680157	101680157	Frame_Shift_Del	DEL	T	-	13	1117	c.385delT	c.(385-387)TTTfs	p.F129fs
Pat_06	Post-Resistance	SPIC	121599	37	12	101876674	101876674	Frame_Shift_Del	DEL	A	-	7	501	c.315delA	c.(313-315)GGAfs	p.G105fs
Pat_06	Post-Resistance	CUX2	23316	37	12	111758235	111758237	In_Frame_Del	DEL	TCC	-	7	345	.2422_2424delTC	c.(2422-2424)TCCdel	p.S813del
Pat_06	Post-Resistance	C12orf51	283450	37	12	112605648	112605650	In_Frame_Del	DEL	CAG	-	7	590	11014_11016delCT	c.(11014-11016)CTGdel	p.L3672del
Pat_06	Post-Resistance	WASF3	10810	37	13	27250862	27250863	Splice_Site	DEL	GT	-	15	728	c.716_splice	c.e7+1	p.R239_splice
Pat_06	Post-Resistance	WASF3	10810	37	13	27259836	27259836	Frame_Shift_Del	DEL	A	-	10	779	c.1363delA	c.(1363-1365)AAAfs	p.K455fs
Pat_06	Post-Resistance	ATP7B	540	37	13	52549201	52549201	Frame_Shift_Del	DEL	C	-	85	281	c.155delG	c.(154-156)GGCfs	p.G52fs
Pat_06	Post-Resistance	FBXL3	26224	37	13	77581683	77581683	Frame_Shift_Del	DEL	A	-	14	275	c.884delT	c.(883-885)TTAfs	p.L295fs
Pat_06	Post-Resistance	GPR18	2841	37	13	99907540	99907540	Frame_Shift_Del	DEL	A	-	8	508	c.587delT	c.(586-588)TTCfs	p.F196fs
Pat_06	Post-Resistance	OR4L1	122742	37	14	20528881	20528881	Frame_Shift_Del	DEL	A	-	7	1006	c.678delA	c.(676-678)CCAfs	p.P226fs
Pat_06	Post-Resistance	TEP1	7011	37	14	20854270	20854270	Frame_Shift_Del	DEL	G	-	8	998	c.2946delC	c.(2944-2946)CCCfs	p.P982fs
Pat_06	Post-Resistance	ACIN1	22985	37	14	23528502	23528503	Frame_Shift_Del	DEL	TC	-	10	276	c.3880_3881delGA	c.(3880-3882)GAAfs	p.E1294fs
Pat_06	Post-Resistance	PCK2	5106	37	14	24572757	24572757	Frame_Shift_Del	DEL	T	-	7	923	c.1507delT	c.(1507-1509)TTTfs	p.F503fs
Pat_06	Post-Resistance	KLHDC2	23588	37	14	50241333	50241334	Frame_Shift_Del	DEL	TG	-	7	1251	c.288_289delTG	c.(286-291)GCTGTGfs	p.A96fs
Pat_06	Post-Resistance	ARID4A	5926	37	14	58831995	58831996	Frame_Shift_Ins	INS	-	AG	8	512	c.3188_3189insAG	c.(3187-3189)CAAfs	p.Q1063fs
Pat_06	Post-Resistance	KCNH5	27133	37	14	63174303	63174303	Frame_Shift_Del	DEL	G	-	9	2261	c.2890delC	c.(2890-2892)CAGfs	p.Q964fs
Pat_06	Post-Resistance	RBM25	58517	37	14	73563781	73563783	In_Frame_Del	DEL	GAA	-	11	480	c.702_704delGAA	.(700-705)AGGAAG>AGG	p.K238del
Pat_06	Post-Resistance	PNMA1	9240	37	14	74179325	74179327	In_Frame_Del	DEL	CCT	-	7	97	.1016_1018delAG	(1015-1020)GAGGCT>GC	p.E339del
Pat_06	Post-Resistance	GALC	2581	37	14	88406276	88406276	Frame_Shift_Del	DEL	T	-	9	2157	c.1884delA	c.(1882-1884)AAAfs	p.K628fs
Pat_06	Post-Resistance	FOXN3	1112	37	14	89629149	89629151	In_Frame_Del	DEL	GAG	-	20	290	.1080_1082delCT	.(1078-1083)TCCTCA>TC	.360_361SS>S
Pat_06	Post-Resistance	AKT1	207	37	14	105242073	105242075	In_Frame_Del	DEL	CTC	-	10	689	c.349_351delGAG	c.(349-351)GAGdel	p.E117del
Pat_06	Post-Resistance	ZFP106	64397	37	15	42734498	42734498	Frame_Shift_Del	DEL	A	-	9	433	c.3467delT	c.(3466-3468)TTCfs	p.F1156fs
Pat_06	Post-Resistance	TTBK2	146057	37	15	43038031	43038031	Frame_Shift_Del	DEL	G	-	7	1929	c.3697delC	c.(3697-3699)CAAfs	p.Q1233fs
Pat_06	Post-Resistance	MNS1	55329	37	15	56736847	56736847	Frame_Shift_Del	DEL	T	-	8	1363	c.481delA	c.(481-483)ACCfs	p.T161fs
Pat_06	Post-Resistance	ALPK3	57538	37	15	85400267	85400267	Frame_Shift_Del	DEL	A	-	8	585	c.2904delA	c.(2902-2904)CCAfs	p.P968fs
Pat_06	Post-Resistance	FURIN	5045	37	15	91422039	91422039	Frame_Shift_Del	DEL	G	-	8	665	c.886delG	c.(886-888)GGGfs	p.G296fs
Pat_06	Post-Resistance	TFAP4	7023	37	16	4308219	4308219	Frame_Shift_Del	DEL	T	-	8	371	c.854delA	c.(853-855)AAGfs	p.K285fs
Pat_06	Post-Resistance	CLEC16A	23274	37	16	11141159	11141159	Frame_Shift_Del	DEL	T	-	7	188	c.1826delT	c.(1825-1827)ATTfs	p.I609fs
Pat_06	Post-Resistance	CLEC16A	23274	37	16	11272415	11272415	Frame_Shift_Del	DEL	C	-	7	658	c.3030delC	c.(3028-3030)GTCfs	p.V1010fs
Pat_06	Post-Resistance	NTAN1	123803	37	16	15131931	15131931	Frame_Shift_Del	DEL	T	-	8	480	c.890delA	c.(889-891)AATfs	p.N297fs
Pat_06	Post-Resistance	SRCAP	10847	37	16	30731611	30731611	Frame_Shift_Del	DEL	C	-	7	1911	c.2946delC	c.(2944-2946)GACfs	p.D982fs
Pat_06	Post-Resistance	ITGAD	3681	37	16	31435495	31435495	Frame_Shift_Del	DEL	C	-	7	464	c.3232delC	c.(3232-3234)CCAfs	p.P1078fs
Pat_06	Post-Resistance	GPT2	84706	37	16	46956286	46956286	Frame_Shift_Del	DEL	C	-	13	921	c.1170delC	c.(1168-1170)AACfs	p.N390fs
Pat_06	Post-Resistance	NUDT21	11051	37	16	56485066	56485066	Frame_Shift_Del	DEL	C	-	7	1640	c.49delG	c.(49-51)GTCfs	p.V17fs
Pat_06	Post-Resistance	CCDC135	84229	37	16	57731885	57731887	In_Frame_Del	DEL	GGA	-	8	320	c.24_26delGGA	c.(22-27)GTGGAG>GTG	p.E13del
Pat_06	Post-Resistance	ACD	65057	37	16	67693646	67693648	In_Frame_Del	DEL	GCA	-	11	1229	c.551_553delTGC	.(550-555)CTGCAG>CAG	p.L184del

Pat_06	Post-Resistance	TSNAXIP1	55815	37	16	67859576	67859576	Frame_Shift_Del	DEL	G	-	7	1192	c.659delG	c.(658-660)TGGfs	p.W220fs
Pat_06	Post-Resistance	DHX38	9785	37	16	72138457	72138457	Frame_Shift_Del	DEL	T	-	7	791	c.2083delT	c.(2083-2085)TTTfs	p.F695fs
Pat_06	Post-Resistance	MYO18A	399687	37	17	27493058	27493058	Frame_Shift_Del	DEL	C	-	9	1323	c.901delG	c.(901-903)GACfs	p.D301fs
Pat_06	Post-Resistance	NUFIP2	57532	37	17	27614342	27614342	Frame_Shift_Del	DEL	T	-	8	756	c.670delA	c.(670-672)AGGfs	p.R224fs
Pat_06	Post-Resistance	GAS2L2	246176	37	17	34074257	34074257	Frame_Shift_Del	DEL	G	-	10	2200	c.863delC	c.(862-864)CCGfs	p.P288fs
Pat_06	Post-Resistance	CDK12	51755	37	17	37686962	37686962	Frame_Shift_Del	DEL	C	-	7	1352	c.3866delC	c.(3865-3867)GCCfs	p.A1289fs
Pat_06	Post-Resistance	FAM134C	162427	37	17	40737147	40737148	Frame_Shift_Del	DEL	TC	-	7	465	c.722_723delGA	c.(721-723)AGAfs	p.R241fs
Pat_06	Post-Resistance	MPP3	4356	37	17	41888206	41888206	Frame_Shift_Del	DEL	T	-	8	1639	c.1427delA	c.(1426-1428)AACfs	p.N476fs
Pat_06	Post-Resistance	CCDC43	124808	37	17	42756253	42756253	Frame_Shift_Del	DEL	T	-	8	165	c.646delA	c.(646-648)AGGfs	p.R216fs
Pat_06	Post-Resistance	CCDC103	388389	37	17	42980014	42980015	Frame_Shift_Del	DEL	AG	-	13	304	c.558_559delAG	c.(556-561)GCAGAGfs	p.A186fs
Pat_06	Post-Resistance	HOXB7	3217	37	17	46685277	46685277	Frame_Shift_Del	DEL	T	-	8	2779	c.581delA	c.(580-582)AAGfs	p.K194fs
Pat_06	Post-Resistance	ANKRD40	91369	37	17	48777070	48777071	Frame_Shift_Ins	INS	-	G	7	690	c.467_468insC	c.(466-468)CCTfs	p.P156fs
Pat_06	Post-Resistance	MKS1	54903	37	17	56290367	56290369	In_Frame_Del	DEL	CTC	-	8	1744	c.832_834delGAG	c.(832-834)GAGdel	p.E278del
Pat_06	Post-Resistance	ACE	1636	37	17	61560495	61560495	Frame_Shift_Del	DEL	C	-	8	2126	c.1448delC	c.(1447-1449)ACCfs	p.T483fs
Pat_06	Post-Resistance	GNA13	10672	37	17	63052468	63052469	Frame_Shift_Del	DEL	CG	-	9	560	c.243_244delCG	c.(241-246)CGCGAGfs	p.R81fs
Pat_06	Post-Resistance	SLC16A6	9120	37	17	66267124	66267125	Frame_Shift_Ins	INS	-	A	7	1102	c.1176_1177insT	c.(1174-1179)TTTGGGfs	p.F392fs
Pat_06	Post-Resistance	KIAA0195	9772	37	17	73482037	73482039	In_Frame_Del	DEL	TGC	-	7	442	c.230_232delTGC	.(229-234)GTGCTG>GTG	p.L81del
Pat_06	Post-Resistance	KIAA0195	9772	37	17	73491063	73491063	Frame_Shift_Del	DEL	C	-	7	1553	c.2676delC	c.(2674-2676)ATCfs	p.I892fs
Pat_06	Post-Resistance	DNAH17	8632	37	17	76425217	76425217	Frame_Shift_Del	DEL	G	-	9	1400	c.3390delC	c.(3388-3390)CCCfs	p.P1130fs
Pat_06	Post-Resistance	MPND	84954	37	19	4352936	4352938	In_Frame_Del	DEL	GAG	-	8	270	c.574_576delGAG	c.(574-576)GAGdel	p.E195del
Pat_06	Post-Resistance	GTF2F1	2962	37	19	6381410	6381412	In_Frame_Del	DEL	CTC	-	7	82	c.976_978delGAG	c.(976-978)GAGdel	p.E326del
Pat_06	Post-Resistance	SLC25A41	284427	37	19	6433605	6433605	Frame_Shift_Del	DEL	G	-	8	467	c.100delC	c.(100-102)CAAfs	p.Q34fs
Pat_06	Post-Resistance	CD209	30835	37	19	7808004	7808004	Frame_Shift_Del	DEL	T	-	7	1123	c.1136delA	c.(1135-1137)AAGfs	p.K379fs
Pat_06	Post-Resistance	FBXL12	54850	37	19	9922225	9922228	Frame_Shift_Del	DEL	GCAG	-	7	829	.325_328delCTG	c.(325-330)CTGCACfs	p.L109fs
Pat_06	Post-Resistance	RFX1	5989	37	19	14083694	14083696	In_Frame_Del	DEL	CCG	-	7	46	.1173_1175delCG	(1171-1176)GGCGGG>GG	.391_392GG>
Pat_06	Post-Resistance	F2RL3	9002	37	19	17000408	17000408	Frame_Shift_Del	DEL	C	-	8	1412	c.134delC	c.(133-135)GCCfs	p.A45fs
Pat_06	Post-Resistance	ZNF43	7594	37	19	22002025	22002026	Splice_Site	INS	-	A	11	416	c.4_splice	c.e2-1	p.G2_splice
Pat_06	Post-Resistance	FFAR2	2867	37	19	35940788	35940790	In_Frame_Del	DEL	CTG	-	9	266	c.172_174delCTG	c.(172-174)CTGdel	p.L62del
Pat_06	Post-Resistance	TEAD2	8463	37	19	49850472	49850473	Frame_Shift_Ins	INS	-	G	28	1519	c.883_884insC	c.(883-885)CATfs	p.H295fs
Pat_06	Post-Resistance	FUZ	80199	37	19	50310483	50310485	In_Frame_Del	DEL	CAG	-	13	400	.1180_1182delCT	c.(1180-1182)CTGdel	p.L394del
Pat_06	Post-Resistance	PTOV1	53635	37	19	50363527	50363527	Frame_Shift_Del	DEL	G	-	7	249	c.1242delG	c.(1240-1242)ATGfs	p.M414fs
Pat_06	Post-Resistance	ZNF416	55659	37	19	58084579	58084579	Frame_Shift_Del	DEL	A	-	8	1541	c.693delT	c.(691-693)TTTfs	p.F231fs
Pat_06	Post-Resistance	ZIK1	284307	37	19	58101799	58101799	Frame_Shift_Del	DEL	A	-	7	755	c.620delA	c.(619-621)CAAfs	p.Q207fs
Pat_06	Post-Resistance	PUM2	23369	37	2	20482977	20482979	In_Frame_Del	DEL	GCT	-	7	606	.1449_1451delAG	(1447-1452)GCAGCT>GC	.483_484AA>
Pat_06	Post-Resistance	HS1BP3	64342	37	2	20840864	20840864	Frame_Shift_Del	DEL	G	-	7	2425	c.275delC	c.(274-276)CCAfs	p.P92fs
Pat_06	Post-Resistance	GTF3C2	2976	37	2	27549710	27549710	Frame_Shift_Del	DEL	C	-	7	469	c.2568delG	c.(2566-2568)GGGfs	p.G856fs
Pat_06	Post-Resistance	CRIM1	51232	37	2	36583501	36583503	In_Frame_Del	DEL	GCT	-	8	125	c.66_68delGCT	c.(64-69)GGGCTG>GGG	p.L27del
Pat_06	Post-Resistance	AFTPH	54812	37	2	64778672	64778674	In_Frame_Del	DEL	GAT	-	7	1194	c.64_66delGAT	c.(64-66)GATdel	p.D26del
Pat_06	Post-Resistance	MOGS	7841	37	2	74691815	74691815	Frame_Shift_Del	DEL	C	-	8	515	c.387delG	c.(385-387)GGGfs	p.G129fs
Pat_06	Post-Resistance	SEMA4F	10505	37	2	74900583	74900583	Splice_Site	DEL	G	-	14	1098	c.551_splice	c.e6-1	p.G184_splice
Pat_06	Post-Resistance	VPS24	51652	37	2	86732976	86732978	In_Frame_Del	DEL	TCC	-	9	418	c.618_620delGGA	.(616-621)GAGGAA>GAA	.206_207EE>
Pat_06	Post-Resistance	GCC2	9648	37	2	109087883	109087884	Frame_Shift_Ins	INS	-	A	10	773	c.2098_2099insA	c.(2098-2100)GAAfs	p.E700fs
Pat_06	Post-Resistance	ZC3H6	376940	37	2	113088959	113088961	In_Frame_Del	DEL	GAT	-	8	669	.2464_2466delGA	c.(2464-2466)GATdel	p.D825del
Pat_06	Post-Resistance	CDCA7	83879	37	2	174229648	174229650	In_Frame_Del	DEL	GGA	-	14	352	c.588_590delGGA	c.(586-591)ATGGAG>ATG	p.E202del
Pat_06	Post-Resistance	NEUROD1	4760	37	2	182542972	182542972	Frame_Shift_Del	DEL	G	-	11	793	c.616delC	c.(616-618)CACfs	p.H206fs
Pat_06	Post-Resistance	HTR2B	3357	37	2	231973838	231973838	Frame_Shift_Del	DEL	T	-	12	1285	c.839delA	c.(838-840)AAGfs	p.K280fs
Pat_06	Post-Resistance	DGKD	8527	37	2	234346026	234346026	Frame_Shift_Del	DEL	C	-	7	490	c.823delC	c.(823-825)CACfs	p.H275fs

Pat_06	Post-Resistance	ADAM33	80332	37	20	3652888	3652888	Frame_Shift_Del	DEL	G	-	9	1100	c.1490delC	c.(1489-1491)CCAfs	p.P497fs
Pat_06	Post-Resistance	RRBP1	6238	37	20	17617358	17617358	Frame_Shift_Del	DEL	T	-	10	1072	c.902delA	c.(901-903)AAGfs	p.K301fs
Pat_06	Post-Resistance	PLAC4	191585	37	21	42551432	42551432	Frame_Shift_Del	DEL	T	-	7	338	c.124delA	c.(124-126)AGAfs	p.R42fs
Pat_06	Post-Resistance	SLC19A1	6573	37	21	46951916	46951918	In_Frame_Del	DEL	CAG	-	16	192	c.334_336delCTG	c.(334-336)CTGdel	p.L112del
Pat_06	Post-Resistance	LSS	4047	37	21	47641824	47641824	Frame_Shift_Del	DEL	C	-	9	874	c.494delG	c.(493-495)GGTfs	p.G165fs
Pat_06	Post-Resistance	MED15	51586	37	22	20918793	20918795	In_Frame_Del	DEL	CAG	-	10	313	c.508_510delCAG	c.(508-510)CAGdel	p.Q174del
Pat_06	Post-Resistance	MED15	51586	37	22	20918916	20918918	In_Frame_Del	DEL	CAG	-	29	372	c.631_633delCAG	c.(631-633)CAGdel	p.Q218del
Pat_06	Post-Resistance	ASCC2	84164	37	22	30218355	30218355	Frame_Shift_Del	DEL	T	-	7	1082	c.510delA	c.(508-510)AAAfs	p.K170fs
Pat_06	Post-Resistance	TBC1D10A	83874	37	22	30688545	30688545	Frame_Shift_Del	DEL	G	-	8	1130	c.1346delC	c.(1345-1347)CCAfs	p.P449fs
Pat_06	Post-Resistance	SF3A1	10291	37	22	30742328	30742330	In_Frame_Del	DEL	CTG	-	17	873	c.364_366delCAG	c.(364-366)CAGdel	p.Q122del
Pat_06	Post-Resistance	SFI1	9814	37	22	32002366	32002366	Frame_Shift_Del	DEL	A	-	8	454	c.2107delA	c.(2107-2109)AAAfs	p.K703fs
Pat_06	Post-Resistance	SH3BP1	23616	37	22	38039752	38039754	In_Frame_Del	DEL	AGG	-	9	692	c.575_577delAGG	c.(574-579)AAGGAG>AAG	p.E197del
Pat_06	Post-Resistance	CYP2D6	1565	37	22	42524213	42524214	Frame_Shift_Ins	INS	-	G	8	196	c.805_806insC	c.(805-807)CGAfs	p.R269fs
Pat_06	Post-Resistance	TCF20	6942	37	22	42605990	42605992	In_Frame_Del	DEL	CTG	-	9	380	.5320_5322delCA	c.(5320-5322)CAGdel	p.Q1774del
Pat_06	Post-Resistance	SRGAP3	9901	37	3	9027284	9027286	In_Frame_Del	DEL	GCT	-	9	456	.3217_3219delAG	c.(3217-3219)AGCdel	p.S1074del
Pat_06	Post-Resistance	GRIP2	80852	37	3	14552763	14552763	Frame_Shift_Del	DEL	C	-	7	339	c.2137delG	c.(2137-2139)GACfs	p.D713fs
Pat_06	Post-Resistance	TRANK1	9881	37	3	36897261	36897261	Frame_Shift_Del	DEL	G	-	8	1766	c.2170delC	c.(2170-2172)CGGfs	p.R724fs
Pat_06	Post-Resistance	LTF	4057	37	3	46479445	46479445	Frame_Shift_Del	DEL	T	-	7	1942	c.2084delA	c.(2083-2085)AAGfs	p.K695fs
Pat_06	Post-Resistance	SCAP	22937	37	3	47456383	47456383	Frame_Shift_Del	DEL	T	-	8	685	c.3240delA	c.(3238-3240)AAAfs	p.K1080fs
Pat_06	Post-Resistance	KLHDC8B	200942	37	3	49211690	49211691	Frame_Shift_Ins	INS	-	G	8	946	c.395_396insG	c.(394-396)CTGfs	p.L132fs
Pat_06	Post-Resistance	ROBO2	6092	37	3	77657038	77657038	Frame_Shift_Del	DEL	C	-	16	664	c.3226delC	c.(3226-3228)CCCfs	p.P1076fs
Pat_06	Post-Resistance	KIAA2018	205717	37	3	113380090	113380090	Frame_Shift_Del	DEL	T	-	12	406	c.439delA	c.(439-441)ATTfs	p.I147fs
Pat_06	Post-Resistance	ATP6V1A	523	37	3	113505224	113505224	Frame_Shift_Del	DEL	T	-	7	1307	c.710delT	c.(709-711)CTTfs	p.L237fs
Pat_06	Post-Resistance	NR1I2	8856	37	3	119531660	119531660	Frame_Shift_Del	DEL	G	-	7	769	c.647delG	c.(646-648)CGGfs	p.R216fs
Pat_06	Post-Resistance	PARP15	165631	37	3	122340370	122340370	Frame_Shift_Del	DEL	A	-	7	609	c.1143delA	c.(1141-1143)GGAfs	p.G381fs
Pat_06	Post-Resistance	EIF4G1	1981	37	3	184039744	184039746	In_Frame_Del	DEL	GAA	-	10	280	.1372_1374delGA	c.(1372-1374)GAAdel	p.E465del
Pat_06	Post-Resistance	CLCN2	1181	37	3	184070896	184070896	Frame_Shift_Del	DEL	C	-	9	917	c.2068delG	c.(2068-2070)GAGfs	p.E690fs
Pat_06	Post-Resistance	SLC2A9	56606	37	4	9828133	9828133	Frame_Shift_Del	DEL	T	-	11	856	c.1511delA	c.(1510-1512)AACfs	p.N504fs
Pat_06	Post-Resistance	ANAPC4	29945	37	4	25390191	25390191	Frame_Shift_Del	DEL	A	-	8	1112	c.438delA	c.(436-438)CCAfs	p.P146fs
Pat_06	Post-Resistance	GABRG1	2565	37	4	46060358	46060358	Frame_Shift_Del	DEL	A	-	15	572	c.792delT	c.(790-792)TTTfs	p.F264fs
Pat_06	Post-Resistance	CLOCK	9575	37	4	56304530	56304532	In_Frame_Del	DEL	CTG	-	11	322	.2278_2280delCA	c.(2278-2280)CAGdel	p.Q760del
Pat_06	Post-Resistance	PRDM8	56978	37	4	81123250	81123252	In_Frame_Del	DEL	CAG	-	7	161	c.634_636delCAG	c.(634-636)CAGdel	p.Q217del
Pat_06	Post-Resistance	CDS1	1040	37	4	85556475	85556475	Frame_Shift_Del	DEL	T	-	13	431	c.781delT	c.(781-783)TTTfs	p.F261fs
Pat_06	Post-Resistance	NAP1L5	266812	37	4	89618484	89618486	In_Frame_Del	DEL	TCC	-	16	344	c.420_422delGGA	c.(418-423)GAGGAA>GAA	p.140_141EE>
Pat_06	Post-Resistance	NPNT	255743	37	4	106863682	106863684	In_Frame_Del	DEL	CCA	-	22	735	c.982_984delCCA	c.(982-984)CCAdel	p.P333del
Pat_06	Post-Resistance	KIAA1109	84162	37	4	123178593	123178593	Frame_Shift_Del	DEL	G	-	8	1870	c.6562delG	c.(6562-6564)GGGfs	p.G2188fs
Pat_06	Post-Resistance	ANKRD50	57182	37	4	125591169	125591169	Frame_Shift_Del	DEL	T	-	8	501	c.3263delA	c.(3262-3264)AATfs	p.N1088fs
Pat_06	Post-Resistance	POU4F2	5458	37	4	147560457	147560458	In_Frame_Ins	INS	-	GGC	22	38	c.165_166insGGC	c.(163-168)insGGC	p.68_69insG
Pat_06	Post-Resistance	LRBA	987	37	4	151842374	151842374	Frame_Shift_Del	DEL	A	-	11	1238	c.621delT	c.(619-621)TTTfs	p.F207fs
Pat_06	Post-Resistance	FHDC1	85462	37	4	153889130	153889130	Splice_Site	DEL	A	-	7	1485	c.1101_splice	c.e9-2	p.R367_splice
Pat_06	Post-Resistance	TLL1	7092	37	4	167020619	167020619	Frame_Shift_Del	DEL	G	-	8	1634	c.2847delG	c.(2845-2847)GTGfs	p.V949fs
Pat_06	Post-Resistance	CLPTM1L	81037	37	5	1331941	1331943	In_Frame_Del	DEL	TCT	-	7	526	c.947_949delAGA	c.(946-951)AAGAGC>AGC	p.K316del
Pat_06	Post-Resistance	NIPBL	25836	37	5	37063925	37063927	In_Frame_Del	DEL	GAA	-	7	174	.7894_7896delGA	c.(7894-7896)GAAdel	p.E2636del
Pat_06	Post-Resistance	FGF10	2255	37	5	44388715	44388717	In_Frame_Del	DEL	AGC	-	7	814	c.68_70delGCT	c.(67-72)TGCTTT>TTT	p.C23del
Pat_06	Post-Resistance	FAM172A	83989	37	5	93111877	93111877	Frame_Shift_Del	DEL	G	-	7	1387	c.1096delC	c.(1096-1098)CGGfs	p.R366fs
Pat_06	Post-Resistance	AP3S1	1176	37	5	115202418	115202421	Frame_Shift_Del	DEL	AAGA	-	16	601	c.121_124delAAG	c.(121-126)AAGAGAfs	p.K41fs
Pat_06	Post-Resistance	FBN2	2201	37	5	127648337	127648337	Frame_Shift_Del	DEL	G	-	7	2504	c.4868delC	c.(4867-4869)CCTfs	p.P1623fs

Pat_06	Post-Resistance	EGR1	1958	37	5	137801633	137801635	In_Frame_Del	DEL	CAG	-	7	129	c.183_185delCAG	c.(181-186)AACAGC>AAC	p.S67del
Pat_06	Post-Resistance	JAKMIP2	9832	37	5	147040890	147040890	Frame_Shift_Del	DEL	T	-	8	1125	c.248delA	c.(247-249)AAGfs	p.K83fs
Pat_06	Post-Resistance	FAT2	2196	37	5	150885487	150885488	Frame_Shift_Ins	INS	-	G	7	1810	c.12688_12689ins	c.(12688-12690)CTGfs	p.L4230fs
Pat_06	Post-Resistance	CPLX2	10814	37	5	175306965	175306967	In_Frame_Del	DEL	GAG	-	8	285	c.322_324delGAG	c.(322-324)GAGdel	p.E114del
Pat_06	Post-Resistance	HIVEP1	3096	37	6	12089463	12089463	Frame_Shift_Del	DEL	A	-	7	556	c.87delA	c.(85-87)TCAfs	p.S29fs
Pat_06	Post-Resistance	HLA-G	3135	37	6	29797195	29797196	Frame_Shift_Ins	INS	-	C	8	2152	c.620_621insC	c.(619-621)GACfs	p.D207fs
Pat_06	Post-Resistance	TRIM26	7726	37	6	30157254	30157254	Frame_Shift_Del	DEL	T	-	10	797	c.845delA	c.(844-846)AAGfs	p.K282fs
Pat_06	Post-Resistance	GTF2H4	2968	37	6	30877804	30877804	Frame_Shift_Del	DEL	T	-	8	1563	c.338delT	c.(337-339)ATTfs	p.I113fs
Pat_06	Post-Resistance	CFB	629	37	6	31905102	31905102	Frame_Shift_Del	DEL	A	-	7	994	c.536delA	c.(535-537)GAAfs	p.E179fs
Pat_06	Post-Resistance	FANCE	2178	37	6	35425714	35425715	Frame_Shift_Ins	INS	-	C	7	807	c.922_923insC	c.(922-924)GCCfs	p.A308fs
Pat_06	Post-Resistance	MAPK13	5603	37	6	36099144	36099146	In_Frame_Del	DEL	GCT	-	7	1218	c.216_218delGCT	c.(214-219)GAGCTG>GAG	p.L76del
Pat_06	Post-Resistance	KHDRBS2	202559	37	6	62604602	62604602	Frame_Shift_Del	DEL	C	-	9	2668	c.748delG	c.(748-750)GCAfs	p.A250fs
Pat_06	Post-Resistance	MAP3K7	6885	37	6	91296568	91296570	In_Frame_Del	DEL	GAG	-	15	288	c.33_35delCTC	c.(31-36)TCCTCG>TCG	p.11_12SS>S
Pat_06	Post-Resistance	FYN	2534	37	6	111983042	111983042	Frame_Shift_Del	DEL	T	-	7	1242	c.1514delA	c.(1513-1515)AAGfs	p.K505fs
Pat_06	Post-Resistance	SASH1	23328	37	6	148848658	148848658	Frame_Shift_Del	DEL	A	-	10	1839	c.1354delA	c.(1354-1356)AAAfs	p.K452fs
Pat_06	Post-Resistance	CARD11	84433	37	7	2968323	2968323	Frame_Shift_Del	DEL	G	-	7	1007	c.1663delC	c.(1663-1665)CGGfs	p.R555fs
Pat_06	Post-Resistance	ICA1	3382	37	7	8198251	8198251	Frame_Shift_Del	DEL	T	-	8	342	c.611delA	c.(610-612)AACfs	p.N204fs
Pat_06	Post-Resistance	PHF14	9678	37	7	11075380	11075381	Frame_Shift_Del	DEL	AG	-	9	1577	c.1569_1570delAG	c.(1567-1572)CAAGAGfs	p.Q523fs
Pat_06	Post-Resistance	ETV1	2115	37	7	13975473	13975473	Frame_Shift_Del	DEL	G	-	8	996	c.414delC	c.(412-414)CCCfs	p.P138fs
Pat_06	Post-Resistance	AGR2	10551	37	7	16841329	16841329	Frame_Shift_Del	DEL	T	-	8	1019	c.92delA	c.(91-93)AAGfs	p.K31fs
Pat_06	Post-Resistance	OSBPL3	26031	37	7	24910452	24910453	Frame_Shift_Del	DEL	TC	-	13	669	c.279_280delGA	c.(277-282)GAGAAGfs	p.E93fs
Pat_06	Post-Resistance	HOXA1	3198	37	7	27135314	27135316	In_Frame_Del	DEL	CGA	-	11	449	c.216_218delTCG	c.(214-219)CATCAC>CAC	p.72_73HH>H
Pat_06	Post-Resistance	JAZF1	221895	37	7	27872456	27872456	Frame_Shift_Del	DEL	G	-	13	2181	c.695delC	c.(694-696)CCGfs	p.P232fs
Pat_06	Post-Resistance	GARS	2617	37	7	30634583	30634585	In_Frame_Del	DEL	CTG	-	10	323	c.46_48delCTG	c.(46-48)CTGdel	p.L20del
Pat_06	Post-Resistance	POU6F2	11281	37	7	39379288	39379290	In_Frame_Del	DEL	CAG	-	21	266	c.559_561delCAG	c.(559-561)CAGdel	p.Q196del
Pat_06	Post-Resistance	ABCA13	154664	37	7	48318519	48318519	Frame_Shift_Del	DEL	A	-	7	448	c.7728delA	c.(7726-7728)TTAfs	p.L2576fs
Pat_06	Post-Resistance	STX1A	6804	37	7	73123425	73123427	In_Frame_Del	DEL	CAT	-	8	1316	c.56_58delATG	c.(55-60)GATGTC>GTC	p.D19del
Pat_06	Post-Resistance	HIP1	3092	37	7	75168684	75168684	Frame_Shift_Del	DEL	T	-	7	2508	c.3020delA	c.(3019-3021)AAGfs	p.K1007fs
Pat_06	Post-Resistance	TMEM60	85025	37	7	77423460	77423460	Frame_Shift_Del	DEL	T	-	15	508	c.231delA	c.(229-231)AAAfs	p.K77fs
Pat_06	Post-Resistance	PHTF2	57157	37	7	77569581	77569581	Frame_Shift_Del	DEL	T	-	10	585	c.1702delT	c.(1702-1704)TTTfs	p.F568fs
Pat_06	Post-Resistance	AKAP9	10142	37	7	91671392	91671393	Frame_Shift_Del	DEL	AG	-	9	254	c.4950_4951delAG	c.(4948-4953)TCAGAGfs	p.S1650fs
Pat_06	Post-Resistance	CYP51A1	1595	37	7	91752494	91752494	Frame_Shift_Del	DEL	T	-	8	844	c.1026delA	c.(1024-1026)AAAfs	p.K342fs
Pat_06	Post-Resistance	MLL5	55904	37	7	104749488	104749488	Frame_Shift_Del	DEL	G	-	7	814	c.3568delG	c.(3568-3570)GGAfs	p.G1190fs
Pat_06	Post-Resistance	NUP205	23165	37	7	135301911	135301911	Frame_Shift_Del	DEL	T	-	7	687	c.3606delT	c.(3604-3606)GATfs	p.D1202fs
Pat_06	Post-Resistance	GSTK1	373156	37	7	142961764	142961764	Frame_Shift_Del	DEL	A	-	9	1910	c.278delA	c.(277-279)GAAfs	p.E93fs
Pat_06	Post-Resistance	CHPF2	54480	37	7	150932283	150932283	Frame_Shift_Del	DEL	G	-	7	1379	c.413delG	c.(412-414)CGGfs	p.R138fs
Pat_06	Post-Resistance	MLL3	58508	37	7	151874013	151874013	Frame_Shift_Del	DEL	T	-	7	846	c.8525delA	c.(8524-8526)AATfs	p.N2842fs
Pat_06	Post-Resistance	XRCC2	7516	37	7	152346220	152346220	Frame_Shift_Del	DEL	A	-	8	569	c.350delT	c.(349-351)TTGfs	p.L117fs
Pat_06	Post-Resistance	WDR60	55112	37	7	158704352	158704353	Frame_Shift_Ins	INS	-	A	10	727	c.1572_1573insA	c.(1570-1575)GGGAAAfs	p.G524fs
Pat_06	Post-Resistance	SFTPC	6440	37	8	22020159	22020161	In_Frame_Del	DEL	GTG	-	11	1007	c.115_117delGTG	c.(115-117)GTGdel	p.V44del
Pat_06	Post-Resistance	WRN	7486	37	8	30945377	30945379	In_Frame_Del	DEL	AAG	-	7	269	.1517_1519delAA	.(1516-1521)AAAGAA>AA	p.E510del
Pat_06	Post-Resistance	ZFHX4	79776	37	8	77765755	77765755	Frame_Shift_Del	DEL	A	-	7	1497	c.6463delA	c.(6463-6465)ATAfs	p.I2155fs
Pat_06	Post-Resistance	LRRCC1	85444	37	8	86038947	86038948	Frame_Shift_Del	DEL	AG	-	7	371	c.1296_1297delAG	c.(1294-1299)CAAGAGfs	p.Q432fs
Pat_06	Post-Resistance	CA2	760	37	8	86386588	86386588	Frame_Shift_Del	DEL	T	-	8	1774	c.387delT	c.(385-387)GATfs	p.D129fs
Pat_06	Post-Resistance	TMEM55A	55529	37	8	92032481	92032481	Frame_Shift_Del	DEL	T	-	10	738	c.266delA	c.(265-267)AACfs	p.N89fs
Pat_06	Post-Resistance	RUNX1T1	862	37	8	92998419	92998419	Frame_Shift_Del	DEL	T	-	9	824	c.1212delA	c.(1210-1212)AAAfs	p.K404fs
Pat_06	Post-Resistance	CCNE2	9134	37	8	95902737	95902737	Frame_Shift_Del	DEL	T	-	7	1605	c.359delA	c.(358-360)AAGfs	p.K120fs

Pat_06	Post-Resistance	VPS13B	157680	37	8	100887781	100887781	Frame_Shift_Del	DEL	C	-	10	883	c.11956delC	c.(11956-11958)CCCfs	p.P3986fs
Pat_06	Post-Resistance	DCAF13	25879	37	8	104442912	104442912	Frame_Shift_Del	DEL	A	-	8	1055	c.1153delA	c.(1153-1155)AAAfs	p.K385fs
Pat_06	Post-Resistance	ENPP2	5168	37	8	120592369	120592369	Frame_Shift_Del	DEL	T	-	7	2390	c.1767delA	c.(1765-1767)AAAfs	p.K589fs
Pat_06	Post-Resistance	ZNF572	137209	37	8	125987892	125987893	Frame_Shift_Ins	INS	-	A	7	583	c.10_11insA	c.(10-12)GAAfs	p.E4fs
Pat_06	Post-Resistance	FAM135B	51059	37	8	139149485	139149485	Frame_Shift_Del	DEL	T	-	10	898	c.3920delA	c.(3919-3921)AACfs	p.N1307fs
Pat_06	Post-Resistance	TSNARE1	203062	37	8	143310866	143310868	In_Frame_Del	DEL	GAT	-	12	873	.1519_1521delAT	c.(1519-1521)ATCdel	p.I507del
Pat_06	Post-Resistance	PAX5	5079	37	9	37020764	37020764	Frame_Shift_Del	DEL	A	-	8	1383	c.81delT	c.(79-81)TTTfs	p.F27fs
Pat_06	Post-Resistance	FBP1	2203	37	9	97380075	97380075	Frame_Shift_Del	DEL	C	-	7	395	c.401delG	c.(400-402)GGAfs	p.G134fs
Pat_06	Post-Resistance	TMEM38B	55151	37	9	108456999	108456999	Frame_Shift_Del	DEL	T	-	7	840	c.58delT	c.(58-60)TTTfs	p.F20fs
Pat_06	Post-Resistance	TNC	3371	37	9	117797539	117797539	Frame_Shift_Del	DEL	G	-	16	1423	c.5731delC	c.(5731-5733)CGGfs	p.R1911fs
Pat_06	Post-Resistance	CRB2	286204	37	9	126139182	126139184	In_Frame_Del	DEL	CCT	-	9	112	.3699_3701delCC	.(3697-3702)TGCCTC>TG	p.L1239del
Pat_06	Post-Resistance	FAM129B	64855	37	9	130270778	130270778	Frame_Shift_Del	DEL	G	-	7	1482	c.1357delC	c.(1357-1359)CACfs	p.H453fs
Pat_06	Post-Resistance	GOLGA2	2801	37	9	131019390	131019390	Frame_Shift_Del	DEL	A	-	11	810	c.2965delT	c.(2965-2967)TACfs	p.Y989fs
Pat_06	Post-Resistance	CEL	1056	37	9	135941982	135941982	Frame_Shift_Del	DEL	G	-	18	1462	c.613delG	c.(613-615)GGGfs	p.G205fs
Pat_06	Post-Resistance	C9orf86	55684	37	9	139734218	139734218	Frame_Shift_Del	DEL	C	-	8	671	c.1831delC	c.(1831-1833)CCCfs	p.P611fs
Pat_06	Post-Resistance	CDKL5	6792	37	X	18622143	18622144	Frame_Shift_Ins	INS	-	T	7	1519	c.1099_1100insT	c.(1099-1101)CTAfs	p.L367fs
Pat_06	Post-Resistance	DMD	1756	37	X	32717353	32717353	Frame_Shift_Del	DEL	A	-	7	1124	c.707delT	c.(706-708)TTCfs	p.F236fs
Pat_06	Post-Resistance	PCDH19	57526	37	X	99663560	99663562	In_Frame_Del	DEL	CAG	-	7	126	c.34_36delCTG	c.(34-36)CTGdel	p.L12del
Pat_06	Post-Resistance	IRS4	8471	37	X	107975867	107975869	In_Frame_Del	DEL	GTC	-	7	1834	.3706_3708delGA	c.(3706-3708)GACdel	p.D1236del
Pat_06	Post-Resistance	NKAP	79576	37	X	119072752	119072753	Frame_Shift_Del	DEL	TC	-	7	865	c.407_408delGA	c.(406-408)AGAfs	p.R136fs
Pat_06	Post-Resistance	BCORL1	63035	37	X	129147360	129147361	Frame_Shift_Ins	INS	-	C	7	1405	c.612_613insC	c.(610-615)TGTCCCfs	p.C204fs
Pat_06	Post-Resistance	BCORL1	63035	37	X	129190011	129190011	Frame_Shift_Del	DEL	C	-	7	420	c.5036delC	c.(5035-5037)TCCfs	p.S1679fs
Pat_06	Post-Resistance	CD99L2	83692	37	X	149937526	149937528	In_Frame_Del	DEL	GGC	-	11	1875	c.768_770delGCC	.(766-771)CCGCCC>CC	.256_257PP>
Pat_08	Pre-Treatment	ARID1A	8289	37	1	27057930	27057931	Frame_Shift_Ins	INS	-	C	9	679	c.1638_1639insC	c.(1636-1641)CAGAGCfs	p.Q546fs
Pat_08	Pre-Treatment	MUTYH	4595	37	1	45795066	45795066	Frame_Shift_Del	DEL	T	-	7	1007	c.1553delA	c.(1552-1554)AAGfs	p.K518fs
Pat_08	Pre-Treatment	NUDT17	200035	37	1	145586936	145586938	In_Frame_Del	DEL	TCC	-	10	323	c.750_752delGGA	c.(748-753)GAGGAT>GAT	p.E250del
Pat_08	Pre-Treatment	TYSND1	219743	37	10	71905929	71905931	In_Frame_Del	DEL	CAG	-	2	4	c.412_414delCTG	c.(412-414)CTGdel	p.L138del
Pat_08	Pre-Treatment	TSPAN4	7106	37	11	864443	864445	In_Frame_Del	DEL	CTG	-	13	337	c.262_264delCTG	c.(262-264)CTGdel	p.L92del
Pat_08	Pre-Treatment	FAM111A	63901	37	11	58920855	58920857	In_Frame_Del	DEL	ATT	-	8	306	.1714_1716delAT	c.(1714-1716)ATTdel	p.I572del
Pat_08	Pre-Treatment	PRB1	5542	37	12	11506815	11506816	In_Frame_Ins	INS	-	GGA	12	399	c.221_222insTCC	c.(220-222)CCA>CCTCC	p.74_74P>PP
Pat_08	Pre-Treatment	PRB2	653247	37	12	11546233	11546235	In_Frame_Del	DEL	GGA	-	7	151	c.777_779delTCC	c.(775-780)CCTCCA>CC	.259_260PP>
Pat_08	Pre-Treatment	DHX37	57647	37	12	125465270	125465272	In_Frame_Del	DEL	CTC	-	3	3	c.502_504delGAG	c.(502-504)GAGdel	p.E168del
Pat_08	Pre-Treatment	PIWIL1	9271	37	12	130845801	130845801	Frame_Shift_Del	DEL	C	-	64	85	c.1742delC	c.(1741-1743)ACCfs	p.T581fs
Pat_08	Pre-Treatment	MSLNL	401827	37	16	830829	830831	In_Frame_Del	DEL	AAG	-	7	506	c.170_172delCTT	c.(169-174)GCTTTC>GTC	p.57_58AF>V
Pat_08	Pre-Treatment	ZFHX3	463	37	16	72821468	72821469	Frame_Shift_Del	DEL	AG	-	14	777	10706_10707delC	c.(10705-10707)CCTfs	p.P3569fs
Pat_08	Pre-Treatment	ITGAE	3682	37	17	3638140	3638141	Frame_Shift_Ins	INS	-	G	13	432	c.2625_2626insC	c.(2623-2628)CCCAGAfs	p.P875fs
Pat_08	Pre-Treatment	BPTF	2186	37	17	65850118	65850118	Frame_Shift_Del	DEL	C	-	67	243	c.676delC	c.(676-678)CCCfs	p.P226fs
Pat_08	Pre-Treatment	SERTAD1	29950	37	19	40929409	40929411	In_Frame_Del	DEL	CTC	-	9	377	c.43_45delGAG	c.(43-45)GAGdel	p.E15del
Pat_08	Pre-Treatment	ZC3H4	23211	37	19	47572401	47572403	In_Frame_Del	DEL	CTC	-	8	246	.2344_2346delGA	c.(2344-2346)GAGdel	p.E782del
Pat_08	Pre-Treatment	RAB11FIP5	26056	37	2	73315337	73315339	In_Frame_Del	DEL	TGG	-	7	278	.1407_1409delCC	.(1405-1410)CACCAA>CA	p.H469del
Pat_08	Pre-Treatment	RALGAPA2	57186	37	20	20527432	20527433	Frame_Shift_Ins	INS	-	A	21	50	c.3200_3201insT	c.(3199-3201)TTCfs	p.F1067fs
Pat_08	Pre-Treatment	ULK4	54986	37	3	41860985	41860985	Frame_Shift_Del	DEL	T	-	8	74	c.1778delA	c.(1777-1779)AAGfs	p.K593fs
Pat_08	Pre-Treatment	CRIPAK	285464	37	4	1388714	1388715	Frame_Shift_Del	DEL	CA	-	10	448	c.415_416delCA	c.(415-417)CACfs	p.H139fs
Pat_08	Pre-Treatment	CRIPAK	285464	37	4	1388993	1388994	Frame_Shift_Del	DEL	CA	-	12	795	c.694_695delCA	c.(694-696)CACfs	p.H232fs
Pat_08	Pre-Treatment	ENPEP	2028	37	4	111470502	111470503	In_Frame_Ins	INS	-	AATACT	8	89	152_2153insAATA	152-2154)GAA>GAATAC	.718_719insY
Pat_08	Pre-Treatment	TPBG	7162	37	6	83074809	83074810	Frame_Shift_Del	DEL	CG	-	3	5	c.131_132delCG	c.(130-132)TCGfs	p.S44fs
Pat_08	Pre-Treatment	ANK1	286	37	8	41543694	41543695	Frame_Shift_Del	DEL	TG	-	42	98	.4365_4366delC	c.(4363-4368)GTCATCfs	p.V1455fs

Pat_08	Pre-Treatment	DENND3	22898	37	8	142161936	142161937	Splice_Site	INS	-	GTTA	7	209	c.834_splice	c.e7+1	p.K278_splice
Pat_08	Pre-Treatment	CT45A5	441521	37	X	134948047	134948047	Frame_Shift_Del	DEL	G	-	25	567	c.278delC	c.(277-279)CCTfs	p.P93fs
Pat_08	Pre-Treatment	RBMX	27316	37	X	135956571	135956572	Frame_Shift_Ins	INS	-	GG	15	336	c.905_906insCC	c.(904-906)CCAfs	p.P302fs
Pat_08	Post-Resistance	TMEM52	339456	37	1	1850628	1850636	In_Frame_Del	DEL	GCGGCAG	-	3	4	9_77delCCTGCC	7-78)CTCCTGCCGCTG>	.23_26LLPL>
Pat_08	Post-Resistance	MMEL1	79258	37	1	2560819	2560821	In_Frame_Del	DEL	CAG	-	7	54	c.103_105delCTG	c.(103-105)CTGdel	p.L35del
Pat_08	Post-Resistance	MST1P9	11223	37	1	17085995	17085996	Frame_Shift_Ins	INS	-	C	7	218	c.901_902insG	c.(901-903)GCGfs	p.A301fs
Pat_08	Post-Resistance	C1orf173	127254	37	1	75037803	75037803	Frame_Shift_Del	DEL	G	-	7	792	c.3591delC	c.(3589-3591)TCCfs	p.S1197fs
Pat_08	Post-Resistance	GBP4	115361	37	1	89662859	89662861	In_Frame_Del	DEL	CCA	-	8	447	c.167_169delTGG	.(166-171)GTGGCC>GC	p.V56del
Pat_08	Post-Resistance	KIAA1324	57535	37	1	109727724	109727725	Frame_Shift_Del	DEL	AC	-	9	791	c.1010_1011delAC	c.(1009-1011)TACfs	p.Y337fs
Pat_08	Post-Resistance	LYZL2	119180	37	10	30900902	30900902	Frame_Shift_Del	DEL	T	-	7	1631	c.567delA	c.(565-567)AAAfs	p.K189fs
Pat_08	Post-Resistance	POLL	27343	37	10	103345131	103345133	In_Frame_Del	DEL	GGA	-	7	103	c.513_515delTCC	c.(511-516)CCTCCC>CC	.171_172PP>
Pat_08	Post-Resistance	TSPAN4	7106	37	11	864443	864445	In_Frame_Del	DEL	CTG	-	10	400	c.262_264delCTG	c.(262-264)CTGdel	p.L92del
Pat_08	Post-Resistance	OR4D11	219986	37	11	59271848	59271848	Frame_Shift_Del	DEL	C	-	8	1523	c.800delC	c.(799-801)ACAfs	p.T267fs
Pat_08	Post-Resistance	TIGD3	220359	37	11	65123714	65123714	Frame_Shift_Del	DEL	C	-	7	355	c.435delC	c.(433-435)TTCfs	p.F145fs
Pat_08	Post-Resistance	PRB2	653247	37	12	11546506	11546508	In_Frame_Del	DEL	TTG	-	7	1060	c.504_506delCAA	c.(502-507)AACAAG>AA	p.N168del
Pat_08	Post-Resistance	NEUROD4	58158	37	12	55421128	55421128	Frame_Shift_Del	DEL	C	-	8	3752	c.905delC	c.(904-906)ACCfs	p.T302fs
Pat_08	Post-Resistance	CUX2	23316	37	12	111760230	111760231	Frame_Shift_Del	DEL	GG	-	4	8	.2772_2773delG	c.(2770-2775)CTGGGCfs	p.L924fs
Pat_08	Post-Resistance	BRAP	8315	37	12	112121081	112121081	Frame_Shift_Del	DEL	T	-	7	522	c.113delA	c.(112-114)AAGfs	p.K38fs
Pat_08	Post-Resistance	PIWIL1	9271	37	12	130845801	130845801	Frame_Shift_Del	DEL	C	-	107	193	c.1742delC	c.(1741-1743)ACCfs	p.T581fs
Pat_08	Post-Resistance	C14orf39	317761	37	14	60903565	60903565	Frame_Shift_Del	DEL	A	-	7	228	c.1762delT	c.(1762-1764)TGAfs	p.*588fs
Pat_08	Post-Resistance	EML1	2009	37	14	100367334	100367334	Frame_Shift_Del	DEL	T	-	7	669	c.966delT	c.(964-966)GGTfs	p.G322fs
Pat_08	Post-Resistance	ADAM6	8755	37	14	106774086	106774087	Splice_Site	INS	-	ATACACG	8	25	c.15674_splice	c.e430+1	
Pat_08	Post-Resistance	CLPX	10845	37	15	65450094	65450094	Frame_Shift_Del	DEL	T	-	7	863	c.1047delA	c.(1045-1047)AAAfs	p.K349fs
Pat_08	Post-Resistance	NUDT21	11051	37	16	56485066	56485066	Frame_Shift_Del	DEL	C	-	7	794	c.49delG	c.(49-51)GTCfs	p.V17fs
Pat_08	Post-Resistance	ACD	65057	37	16	67693646	67693648	In_Frame_Del	DEL	GCA	-	7	633	c.551_553delTGC	.(550-555)CTGCAG>CA	p.L184del
Pat_08	Post-Resistance	RANBP10	57610	37	16	67763279	67763281	In_Frame_Del	DEL	GAG	-	8	101	.1254_1256delCT	.(1252-1257)TCCTCG>TC	.418_419SS>
Pat_08	Post-Resistance	MYOCD	93649	37	17	12647692	12647694	In_Frame_Del	DEL	CAG	-	9	114	c.910_912delCAG	c.(910-912)CAGdel	p.Q310del
Pat_08	Post-Resistance	BPTF	2186	37	17	65850118	65850118	Frame_Shift_Del	DEL	C	-	158	336	c.676delC	c.(676-678)CCCfs	p.P226fs
Pat_08	Post-Resistance	OR7E24	26648	37	19	9362007	9362007	Frame_Shift_Del	DEL	C	-	8	421	c.288delC	c.(286-288)GTCfs	p.V96fs
Pat_08	Post-Resistance	ZNF224	7767	37	19	44611162	44611162	Frame_Shift_Del	DEL	G	-	7	745	c.849delG	c.(847-849)ACGfs	p.T283fs
Pat_08	Post-Resistance	ZC3H4	23211	37	19	47572401	47572403	In_Frame_Del	DEL	CTC	-	9	458	.2344_2346delGA	c.(2344-2346)GAGdel	p.E782del
Pat_08	Post-Resistance	CPT1C	126129	37	19	50203964	50203964	Frame_Shift_Del	DEL	G	-	7	281	c.305delG	c.(304-306)CGGfs	p.R102fs
Pat_08	Post-Resistance	SLC30A3	7781	37	2	27479380	27479380	Frame_Shift_Del	DEL	G	-	7	536	c.892delC	c.(892-894)CGCfs	p.R298fs
Pat_08	Post-Resistance	ZDBF2	57683	37	2	207174869	207174869	Frame_Shift_Del	DEL	A	-	9	77	c.5617delA	c.(5617-5619)AAAfs	p.K1873fs
Pat_08	Post-Resistance	RALGAPA2	57186	37	20	20527432	20527433	Frame_Shift_Ins	INS	-	A	36	94	c.3200_3201insT	c.(3199-3201)TTCfs	p.F1067fs
Pat_08	Post-Resistance	SFRS15	57466	37	21	33043971	33043972	Frame_Shift_Del	DEL	TC	-	9	388	.3184_3185delG	c.(3184-3186)GATfs	p.D1062fs
Pat_08	Post-Resistance	MN1	4330	37	22	28195625	28195627	In_Frame_Del	DEL	GCT	-	8	40	c.905_907delAGC	.(904-909)CAGCCC>CC	p.Q302del
Pat_08	Post-Resistance	SATB1	6304	37	3	18391133	18391135	In_Frame_Del	DEL	CTG	-	11	118	.1819_1821delCA	c.(1819-1821)CAGdel	p.Q607del
Pat_08	Post-Resistance	PRKCD	5580	37	3	53220653	53220653	Frame_Shift_Del	DEL	G	-	7	1794	c.1294delG	c.(1294-1296)GGGfs	p.G432fs
Pat_08	Post-Resistance	MYLK	4638	37	3	123368043	123368044	Splice_Site	INS	-	G	8	340	c.4289_splice	c.e25-1	p.E1430_splic
Pat_08	Post-Resistance	TRIM59	286827	37	3	160156367	160156368	Frame_Shift_Ins	INS	-	T	8	92	c.604_605insA	c.(604-606)AGTfs	p.S202fs
Pat_08	Post-Resistance	SAMD7	344658	37	3	169646268	169646268	Frame_Shift_Del	DEL	G	-	8	685	c.943delG	c.(943-945)GGGfs	p.G315fs
Pat_08	Post-Resistance	FXR1	8087	37	3	180666228	180666228	Frame_Shift_Del	DEL	A	-	9	252	c.364delA	c.(364-366)AAAfs	p.K122fs
Pat_08	Post-Resistance	CRIPAK	285464	37	4	1388714	1388715	Frame_Shift_Del	DEL	CA	-	8	968	c.415_416delCA	c.(415-417)CACfs	p.H139fs
Pat_08	Post-Resistance	LIMCH1	22998	37	4	41648508	41648509	Frame_Shift_Del	DEL	GA	-	7	291	.1263_1264delG	c.(1261-1266)CGGAGAfs	p.R421fs
Pat_08	Post-Resistance	ENPEP	2028	37	4	111470502	111470503	In_Frame_Ins	INS	-	AATACT	16	179	152_2153insAATA	152-2154)GAA>GAATAC	.718_719insY
Pat_08	Post-Resistance	ITGA1	3672	37	5	52157315	52157315	Frame_Shift_Del	DEL	A	-	9	422	c.217delA	c.(217-219)AAAfs	p.K73fs

Pat_08	Post-Resistance	KCNN2	3781	37	5	113698631	113698632	In_Frame_Ins	INS	-	GCC	8	20	c.159_160insGCC	c.(157-162)insGCC	p.58_59insA
Pat_08	Post-Resistance	PCDHB12	56124	37	5	140589279	140589279	Frame_Shift_Del	DEL	G	-	7	933	c.800delG	c.(799-801)TGGfs	p.W267fs
Pat_08	Post-Resistance	DEK	7913	37	6	18264079	18264081	In_Frame_Del	DEL	TCC	-	8	339	c.138_140delGGA	c.(136-141)GAGGAA>GA	p.46_47EE>E
Pat_08	Post-Resistance	ZBTB22	9278	37	6	33283522	33283522	Frame_Shift_Del	DEL	C	-	7	1632	c.1172delG	c.(1171-1173)GGTfs	p.G391fs
Pat_08	Post-Resistance	DAXX	1616	37	6	33287898	33287900	In_Frame_Del	DEL	TCC	-	7	210	.1353_1355delGG	(1351-1356)GAGGAA>GA	.451_452EE>
Pat_08	Post-Resistance	SLC26A8	116369	37	6	35980013	35980013	Frame_Shift_Del	DEL	G	-	7	1932	c.325delC	c.(325-327)CAAfs	p.Q109fs
Pat_08	Post-Resistance	CUL9	23113	37	6	43173022	43173022	Frame_Shift_Del	DEL	T	-	7	1570	c.4654delT	c.(4654-4656)TACfs	p.Y1552fs
Pat_08	Post-Resistance	MEP1A	4224	37	6	46787424	46787424	Frame_Shift_Del	DEL	G	-	8	1917	c.539delG	c.(538-540)TGGfs	p.W180fs
Pat_08	Post-Resistance	GLCCI1	113263	37	7	8008992	8008994	In_Frame_Del	DEL	CCT	-	8	129	c.11_13delCCT	c.(10-15)GCCTCC>GCC	p.S13del
Pat_08	Post-Resistance	STX1A	6804	37	7	73123425	73123427	In_Frame_Del	DEL	CAT	-	10	999	c.56_58delATG	c.(55-60)GATGTC>GTC	p.D19del
Pat_08	Post-Resistance	LIMK1	3984	37	7	73535323	73535323	Frame_Shift_Del	DEL	C	-	7	1982	c.1725delC	c.(1723-1725)TGCfs	p.C575fs
Pat_08	Post-Resistance	ZKSCAN5	23660	37	7	99103706	99103706	Frame_Shift_Del	DEL	C	-	7	895	c.39delC	c.(37-39)GACfs	p.D13fs
Pat_08	Post-Resistance	MLL5	55904	37	7	104750923	104750923	Splice_Site	DEL	G	-	8	2137	c.3845_splice	c.e25-1	.G1282_splice
Pat_08	Post-Resistance	SSPO	23145	37	7	149474083	149474083	Frame_Shift_Del	DEL	G	-	9	982	c.293delG	c.(292-294)TGGfs	p.W98fs
Pat_08	Post-Resistance	ANK1	286	37	8	41543694	41543695	Frame_Shift_Del	DEL	TG	-	99	243	.4365_4366delC	c.(4363-4368)GTCATCfs	p.V1455fs
Pat_08	Post-Resistance	HAS2	3037	37	8	122627104	122627104	Frame_Shift_Del	DEL	G	-	8	1372	c.904delC	c.(904-906)CAAfs	p.Q302fs
Pat_08	Post-Resistance	RLN2	6019	37	9	5304560	5304561	Frame_Shift_Ins	INS	-	A	7	358	c.20_21insT	c.(19-21)TTCfs	p.F7fs
Pat_08	Post-Resistance	NOL6	65083	37	9	33466939	33466939	Frame_Shift_Del	DEL	G	-	12	1560	c.1921delC	c.(1921-1923)CTGfs	p.L641fs
Pat_08	Post-Resistance	TPRN	286262	37	9	140087025	140087027	In_Frame_Del	DEL	TCC	-	11	83	.1659_1661delGG	(1657-1662)GAGGAA>GA	.553_554EE>
Pat_08	Post-Resistance	FRMPD4	9758	37	X	12734864	12734864	Frame_Shift_Del	DEL	G	-	7	816	c.2286delG	c.(2284-2286)GTGfs	p.V762fs
Pat_08	Post-Resistance	HUWE1	10075	37	X	53589091	53589093	In_Frame_Del	DEL	TCC	-	9	277	.7317_7319delGG	(7315-7320)GAGGAA>GA	2439_2440EE
Pat_08	Post-Resistance	ATRX	546	37	X	76907782	76907784	In_Frame_Del	DEL	TCC	-	7	285	.4377_4379delGG	(4375-4380)GAGGAA>GA	1459_1460EE
Pat_11	Pre-Treatment	MFN2	9927	37	1	12052736	12052736	Frame_Shift_Del	DEL	T	-	8	670	c.300delT	c.(298-300)GCTfs	p.A100fs
Pat_11	Pre-Treatment	PTPRF	5792	37	1	44071946	44071948	In_Frame_Del	DEL	GCG	-	8	323	.3519_3521delGC	(3517-3522)CAGCGG>CA	p.R1178del
Pat_11	Pre-Treatment	SNX7	51375	37	1	99167423	99167424	Frame_Shift_Del	DEL	TG	-	7	386	.1089_1090delT	c.(1087-1092)GTTGAAfs	p.V363fs
Pat_11	Pre-Treatment	SLC22A15	55356	37	1	116605457	116605457	Frame_Shift_Del	DEL	A	-	8	745	c.1246delA	c.(1246-1248)AACfs	p.N416fs
Pat_11	Pre-Treatment	ECM1	1893	37	1	150482151	150482151	Frame_Shift_Del	DEL	C	-	9	965	c.136delC	c.(136-138)CCCfs	p.P46fs
Pat_11	Pre-Treatment	LCE2A	353139	37	1	152671425	152671425	Frame_Shift_Del	DEL	C	-	8	908	c.48delC	c.(46-48)TGCfs	p.C16fs
Pat_11	Pre-Treatment	NPR1	4881	37	1	153659175	153659175	Frame_Shift_Del	DEL	C	-	8	780	c.1812delC	c.(1810-1812)GACfs	p.D604fs
Pat_11	Pre-Treatment	BCAN	63827	37	1	156626160	156626160	Frame_Shift_Del	DEL	G	-	9	873	c.2029delG	c.(2029-2031)GGGfs	p.G677fs
Pat_11	Pre-Treatment	TAGLN2	8407	37	1	159888725	159888725	Frame_Shift_Del	DEL	G	-	7	419	c.465delC	c.(463-465)TCCfs	p.S155fs
Pat_11	Pre-Treatment	PRG4	10216	37	1	186276127	186276128	In_Frame_Ins	INS	-	AGG	11	258	.1276_1277insAG	(1276-1278)AAG>AAGGA	p.426_427insE
Pat_11	Pre-Treatment	SRGAP2	23380	37	1	206603573	206603574	Splice_Site	DEL	GT	-	7	685	c.1294_splice	c.e11+1	p.G432_splice
Pat_11	Pre-Treatment	RGS7	6000	37	1	240976980	240976980	Frame_Shift_Del	DEL	C	-	7	287	c.894delG	c.(892-894)TTGfs	p.L298fs
Pat_11	Pre-Treatment	SYT15	83849	37	10	46969401	46969403	In_Frame_Del	DEL	CAG	-	9	94	c.58_60delCTG	c.(58-60)CTGdel	p.L21del
Pat_11	Pre-Treatment	MKI67	4288	37	10	129902204	129902205	Frame_Shift_Del	DEL	TG	-	7	122	.7899_7900delC	c.(7897-7902)CACAAAfs	p.H2633fs
Pat_11	Pre-Treatment	NAT10	55226	37	11	34154601	34154601	Frame_Shift_Del	DEL	C	-	8	626	c.1646delC	c.(1645-1647)TCCfs	p.S549fs
Pat_11	Pre-Treatment	MYBPC3	4607	37	11	47372804	47372806	In_Frame_Del	DEL	TTG	-	2	4	c.276_278delCAA	c.(274-279)CTCAAG>CTG	p.K93del
Pat_11	Pre-Treatment	OR10Q1	219960	37	11	57996280	57996280	Frame_Shift_Del	DEL	G	-	7	525	c.68delC	c.(67-69)ACAfs	p.T23fs
Pat_11	Pre-Treatment	GANAB	23193	37	11	62393580	62393581	Frame_Shift_Del	DEL	TA	-	10	1162	c.2681_2682delTA	c.(2680-2682)ATAfs	p.I894fs
Pat_11	Pre-Treatment	SIK2	23235	37	11	111594527	111594529	In_Frame_Del	DEL	CAG	-	7	352	.2455_2457delCA	c.(2455-2457)CAGdel	p.Q822del
Pat_11	Pre-Treatment	ZNF202	7753	37	11	123601205	123601205	Frame_Shift_Del	DEL	G	-	8	857	c.392delC	c.(391-393)CCAfs	p.P131fs
Pat_11	Pre-Treatment	PRB1	5542	37	12	11506632	11506633	In_Frame_Ins	INS	-	GGA	16	1063	c.404_405insTCC	c.(403-405)CCA>CCTCCA	.135_135P>P
Pat_11	Pre-Treatment	PRB2	653247	37	12	11546544	11546545	In_Frame_Ins	INS	-	GGA	7	767	c.467_468insTCC	c.(466-468)CCA>CCTCCA	.156_156P>P
Pat_11	Pre-Treatment	SLC4A8	9498	37	12	51865070	51865070	Splice_Site	DEL	G	-	8	617	c.1659_splice	c.e14-1	p.K553_splice
Pat_11	Pre-Treatment	HOXC11	3227	37	12	54367179	54367180	Frame_Shift_Del	DEL	CC	-	7	576	c.154_155delCC	c.(154-156)CCCfs	p.P52fs
Pat_11	Pre-Treatment	SLC39A5	283375	37	12	56628997	56628999	In_Frame_Del	DEL	CTG	-	12	544	c.691_693delCTG	c.(691-693)CTGdel	p.L234del

Pat_11	Pre-Treatment	TSPAN31	6302	37	12	58140401	58140402	Frame_Shift_Del	DEL	CA	-	8	279	c.342_343delCA	c.(340-345)GTCATGfs	p.V114fs
Pat_11	Pre-Treatment	OLFM4	10562	37	13	53624374	53624376	In_Frame_Del	DEL	ACA	-	7	305	.1001_1003delAC	.(1000-1005)TACAAC>TA	p.N337del
Pat_11	Pre-Treatment	LMO7	4008	37	13	76415307	76415308	Frame_Shift_Del	DEL	AG	-	9	283	c.2946_2947delAG	c.(2944-2949)GCAGAGfs	p.A982fs
Pat_11	Pre-Treatment	ABCC4	10257	37	13	95887054	95887055	Frame_Shift_Del	DEL	CC	-	2	4	c.340_341delGG	c.(340-342)GGAfs	p.G114fs
Pat_11	Pre-Treatment	ZIC5	85416	37	13	100617727	100617727	Frame_Shift_Del	DEL	G	-	7	486	c.1896delC	c.(1894-1896)CCCfs	p.P632fs
Pat_11	Pre-Treatment	ZIC2	7546	37	13	100635008	100635010	In_Frame_Del	DEL	CCA	-	8	126	c.690_692delCCA	.(688-693)GCCCAC>GCC	p.H239del
Pat_11	Pre-Treatment	COL4A2	1284	37	13	111156234	111156234	Frame_Shift_Del	DEL	C	-	7	219	c.4179delC	c.(4177-4179)ATCfs	p.I1393fs
Pat_11	Pre-Treatment	PABPN1	8106	37	14	23790952	23790953	Frame_Shift_Ins	INS	-	C	2	4	c.274_275insC	c.(274-276)GCCfs	p.A92fs
Pat_11	Pre-Treatment	DHRS4L2	317749	37	14	24464310	24464311	Frame_Shift_Del	DEL	CT	-	7	914	c.376_377delCT	c.(376-378)CTAfs	p.L126fs
Pat_11	Pre-Treatment	FMN1	342184	37	15	33149283	33149285	In_Frame_Del	DEL	CAC	-	8	571	.3190_3192delGT	c.(3190-3192)GTGdel	p.V1064del
Pat_11	Pre-Treatment	JMJD7-PLA2G4B	8681	37	15	42138399	42138400	Splice_Site	DEL	AG	-	8	258	c.1601_splice	c.e17-1	p.D534_splice
Pat_11	Pre-Treatment	NOX5	79400	37	15	69331226	69331226	Frame_Shift_Del	DEL	T	-	7	357	c.1401delT	c.(1399-1401)CCTfs	p.P467fs
Pat_11	Pre-Treatment	EFTUD1	79631	37	15	82450051	82450052	Splice_Site	DEL	AA	-	7	468	c.2030_splice	c.e17+1	p.R677_splice
Pat_11	Pre-Treatment	NAGPA	51172	37	16	5083678	5083679	Frame_Shift_Del	DEL	GC	-	10	105	c.137_138delGC	c.(136-138)CGCfs	p.R46fs
Pat_11	Pre-Treatment	C16orf62	57020	37	16	19580800	19580802	In_Frame_Del	DEL	TCC	-	7	294	c.172_174delTCC	c.(172-174)TCCdel	p.S64del
Pat_11	Pre-Treatment	VPS35	55737	37	16	46695735	46695735	Frame_Shift_Del	DEL	T	-	10	260	c.2106delA	c.(2104-2106)AAAfs	p.K702fs
Pat_11	Pre-Treatment	PLD2	5338	37	17	4720001	4720002	Frame_Shift_Del	DEL	TA	-	7	845	c.1542_1543delTA	c.(1540-1545)CTTATCfs	p.L514fs
Pat_11	Pre-Treatment	KDM6B	23135	37	17	7751859	7751861	In_Frame_Del	DEL	CAC	-	7	143	.2253_2255delCA	(2251-2256)GTCACC>GT	p.T762del
Pat_11	Pre-Treatment	CHD3	1107	37	17	7788146	7788148	In_Frame_Del	DEL	GAG	-	4	5	c.22_24delGAG	c.(22-24)GAGdel	p.E14del
Pat_11	Pre-Treatment	TEKT3	64518	37	17	15234734	15234735	Frame_Shift_Del	DEL	TG	-	10	134	c.168_169delCA	c.(166-171)TACAAAfs	p.Y56fs
Pat_11	Pre-Treatment	SLC5A10	125206	37	17	18863872	18863872	Frame_Shift_Del	DEL	A	-	8	806	c.360delA	c.(358-360)TTAfs	p.L120fs
Pat_11	Pre-Treatment	ZNRF4	148066	37	19	5455868	5455868	Frame_Shift_Del	DEL	C	-	9	441	c.366delC	c.(364-366)GTCfs	p.V122fs
Pat_11	Pre-Treatment	ATP4A	495	37	19	36054349	36054351	In_Frame_Del	DEL	CTT	-	9	1058	c.91_93delAAG	c.(91-93)AAGdel	p.K31del
Pat_11	Pre-Treatment	DMRTC2	63946	37	19	42353044	42353045	Splice_Site	DEL	GT	-	7	348	c.628_splice	c.e5+1	p.G210_splice
Pat_11	Pre-Treatment	LHB	3972	37	19	49519948	49519950	In_Frame_Del	DEL	CAG	-	7	390	c.37_39delCTG	c.(37-39)CTGdel	p.L13del
Pat_11	Pre-Treatment	SHANK1	50944	37	19	51171736	51171738	In_Frame_Del	DEL	TGA	-	7	389	.3479_3481delTC	.(3478-3483)ATCAAG>AA	p.I1160del
Pat_11	Pre-Treatment	ZNF814	730051	37	19	58385404	58385404	Frame_Shift_Del	DEL	T	-	2	4	c.1354delA	c.(1354-1356)AGGfs	p.R452fs
Pat_11	Pre-Treatment	KIF3C	3797	37	2	26203464	26203466	In_Frame_Del	DEL	GTT	-	7	556	.1321_1323delAA	c.(1321-1323)AACdel	p.N441del
Pat_11	Pre-Treatment	RAB11FIP5	26056	37	2	73303133	73303133	Frame_Shift_Del	DEL	G	-	7	816	c.1746delC	c.(1744-1746)ACCfs	p.T582fs
Pat_11	Pre-Treatment	WBP1	23559	37	2	74687543	74687543	Frame_Shift_Del	DEL	C	-	7	330	c.545delC	c.(544-546)GCCfs	p.A182fs
Pat_11	Pre-Treatment	ITPRIPL1	150771	37	2	96992793	96992795	In_Frame_Del	DEL	GAG	-	13	195	c.424_426delGAG	c.(424-426)GAGdel	p.E147del
Pat_11	Pre-Treatment	HOXD9	3235	37	2	176988002	176988002	Frame_Shift_Del	DEL	C	-	2	4	c.506delC	c.(505-507)GCCfs	p.A169fs
Pat_11	Pre-Treatment	SPHKAP	80309	37	2	228883847	228883848	Frame_Shift_Del	DEL	CA	-	8	520	c.1722_1723delTG	c.(1720-1725)GGTGAAfs	p.G574fs
Pat_11	Pre-Treatment	C20orf96	140680	37	20	257710	257712	In_Frame_Del	DEL	TTC	-	7	734	c.798_800delGAA	c.(796-801)AAGAAA>AAA	.266_267KK>
Pat_11	Pre-Treatment	IL10RB	3588	37	21	34668489	34668489	Frame_Shift_Del	DEL	T	-	9	761	c.805delT	c.(805-807)TTTfs	p.F269fs
Pat_11	Pre-Treatment	C21orf58	54058	37	21	47721986	47721988	In_Frame_Del	DEL	TGG	-	4	9	c.894_896delCCA	c.(892-897)CACCAT>CAT	.298_299HH>
Pat_11	Pre-Treatment	MYH9	4627	37	22	36682821	36682821	Frame_Shift_Del	DEL	G	-	8	544	c.5004delC	c.(5002-5004)GCCfs	p.A1668fs
Pat_11	Pre-Treatment	TNRC6B	23112	37	22	40708591	40708591	Frame_Shift_Del	DEL	G	-	8	565	c.4518delG	c.(4516-4518)CTGfs	p.L1506fs
Pat_11	Pre-Treatment	MLC1	23209	37	22	50502593	50502595	In_Frame_Del	DEL	AGC	-	7	125	c.927_929delGCT	c.(925-930)CTGCTA>CTA	.309_310LL>
Pat_11	Pre-Treatment	TMEM40	55287	37	3	12778265	12778265	Frame_Shift_Del	DEL	G	-	8	377	c.542delC	c.(541-543)GCAfs	p.A181fs
Pat_11	Pre-Treatment	ZNF662	389114	37	3	42950290	42950290	Frame_Shift_Del	DEL	T	-	8	636	c.40delT	c.(40-42)TTTfs	p.F14fs
Pat_11	Pre-Treatment	FBXW12	285231	37	3	48420887	48420888	Splice_Site	DEL	CA	-	7	746	c.616_splice	c.e7-2	p.V206_splice
Pat_11	Pre-Treatment	SEMA3F	6405	37	3	50214214	50214214	Frame_Shift_Del	DEL	A	-	8	547	c.563delA	c.(562-564)TACfs	p.Y188fs
Pat_11	Pre-Treatment	C3orf63	23272	37	3	56667435	56667436	Frame_Shift_Del	DEL	GA	-	8	218	c.3200_3201delTC	c.(3199-3201)TTCfs	p.F1067fs
Pat_11	Pre-Treatment	ROBO2	6092	37	3	77657038	77657038	Frame_Shift_Del	DEL	C	-	7	269	c.3226delC	c.(3226-3228)CCCfs	p.P1076fs
Pat_11	Pre-Treatment	GPR149	344758	37	3	154055553	154055553	Frame_Shift_Del	DEL	G	-	7	605	c.2131delC	c.(2131-2133)CAGfs	p.Q711fs
Pat_11	Pre-Treatment	PDE6B	5158	37	4	661763	661765	In_Frame_Del	DEL	AGG	-	7	394	.2471_2473delAG	(2470-2475)AAGGAG>AA	p.E828del

Pat_11	Pre-Treatment	CRIPAK	285464	37	4	1389147	1389148	Frame_Shift_Del	DEL	AT	-	17	701	c.848_849delAT	c.(847-849)CATfs	p.H283fs
Pat_11	Pre-Treatment	SLC34A2	10568	37	4	25673248	25673249	Frame_Shift_Del	DEL	CG	-	8	1192	c.953_954delCG	c.(952-954)TCGfs	p.S318fs
Pat_11	Pre-Treatment	PRDM5	11107	37	4	121738071	121738072	Frame_Shift_Del	DEL	TG	-	8	353	c.658_659delCA	c.(658-660)CAGfs	p.Q220fs
Pat_11	Pre-Treatment	BRD8	10902	37	5	137488268	137488269	Frame_Shift_Del	DEL	TC	-	10	692	c.2758_2759delG	c.(2758-2760)GAAfs	p.E920fs
Pat_11	Pre-Treatment	HSPA9	3313	37	5	137902690	137902691	Frame_Shift_Del	DEL	CT	-	7	393	c.878_879delAG	c.(877-879)GAGfs	p.E293fs
Pat_11	Pre-Treatment	ATXN1	6310	37	6	16327864	16327865	In_Frame_Ins	INS	-	TGC	11	22	c.677_678insGCA	c.(676-678)CAC>CAGCAC	p.225_226ins
Pat_11	Pre-Treatment	MAP3K5	4217	37	6	136913692	136913694	In_Frame_Del	DEL	CTG	-	8	292	.2937_2939delCA	.(2935-2940)AGCAGT>AG	.979_980SS>
Pat_11	Pre-Treatment	ARID1B	57492	37	6	157517438	157517438	Frame_Shift_Del	DEL	T	-	8	438	c.3948delT	c.(3946-3948)AGTfs	p.S1316fs
Pat_11	Pre-Treatment	TULP4	56995	37	6	158923337	158923337	Frame_Shift_Del	DEL	C	-	10	675	c.2642delC	c.(2641-2643)ACCfs	p.T881fs
Pat_11	Pre-Treatment	LIMK1	3984	37	7	73513509	73513509	Frame_Shift_Del	DEL	C	-	10	1608	c.549delC	c.(547-549)GACfs	p.D183fs
Pat_11	Pre-Treatment	GPC2	221914	37	7	99771554	99771554	Frame_Shift_Del	DEL	C	-	7	548	c.796delG	c.(796-798)GTCfs	p.V266fs
Pat_11	Pre-Treatment	AP1S1	1174	37	7	100802405	100802405	Frame_Shift_Del	DEL	G	-	7	145	c.357delG	c.(355-357)ATGfs	p.M119fs
Pat_11	Pre-Treatment	MOGAT3	346606	37	7	100842086	100842086	Frame_Shift_Del	DEL	G	-	7	634	c.314delC	c.(313-315)CCGfs	p.P105fs
Pat_11	Pre-Treatment	CUX1	1523	37	7	101845358	101845358	Frame_Shift_Del	DEL	C	-	8	956	c.2781delC	c.(2779-2781)GTCfs	p.V927fs
Pat_11	Pre-Treatment	SPDYE6	729597	37	7	101991235	101991236	Frame_Shift_Del	DEL	TG	-	8	1233	c.687_688delCA	c.(685-690)GTCATAfs	p.V229fs
Pat_11	Pre-Treatment	CTTNBP2	83992	37	7	117450827	117450827	Frame_Shift_Del	DEL	G	-	7	1269	c.406delC	c.(406-408)CAAfs	p.Q136fs
Pat_11	Pre-Treatment	GBX1	2636	37	7	150845991	150845991	Frame_Shift_Del	DEL	C	-	7	463	c.777delG	c.(775-777)GGGfs	p.G259fs
Pat_11	Pre-Treatment	XRCC2	7516	37	7	152346220	152346220	Frame_Shift_Del	DEL	A	-	7	262	c.350delT	c.(349-351)TTGfs	p.L117fs
Pat_11	Pre-Treatment	KIAA1967	57805	37	8	22472975	22472975	Frame_Shift_Del	DEL	C	-	7	403	c.1243delC	c.(1243-1245)CCCfs	p.P415fs
Pat_11	Pre-Treatment	PALM2-AKAP2	445815	37	9	112899247	112899247	Frame_Shift_Del	DEL	C	-	53	82	c.2119delC	c.(2119-2121)CCCfs	p.P707fs
Pat_11	Pre-Treatment	GRIN1	2902	37	9	140056884	140056886	In_Frame_Del	DEL	GAG	-	9	113	.1780_1782delGA	c.(1780-1782)GAGdel	p.E598del
Pat_11	Pre-Treatment	GPR34	2857	37	X	41555610	41555610	Frame_Shift_Del	DEL	G	-	2	4	c.724delG	c.(724-726)GGGfs	p.G242fs
Pat_11	Pre-Treatment	GDI1	2664	37	X	153668286	153668287	Splice_Site	DEL	AG	-	7	469	c.389_splice	c.e5-1	p.N130_splice
Pat_11	Pre-Treatment	PLXNA3	55558	37	X	153699572	153699572	Frame_Shift_Del	DEL	A	-	8	504	c.5281delA	c.(5281-5283)ACAfs	p.T1761fs
Pat_11	Post-Resistance	RERE	473	37	1	8716109	8716109	Frame_Shift_Del	DEL	T	-	7	831	c.248delA	c.(247-249)AAGfs	p.K83fs
Pat_11	Post-Resistance	MFN2	9927	37	1	12052736	12052736	Frame_Shift_Del	DEL	T	-	8	887	c.300delT	c.(298-300)GCTfs	p.A100fs
Pat_11	Post-Resistance	ZMYM4	9202	37	1	35846959	35846960	Frame_Shift_Ins	INS	-	A	7	279	c.1281_1282insA	c.(1279-1284)CTGAAAfs	p.L427fs
Pat_11	Post-Resistance	SNIP1	79753	37	1	38003368	38003370	In_Frame_Del	DEL	TCC	-	8	628	.1170_1172delGG	.(1168-1173)GAGGAA>GA	.390_391EE>
Pat_11	Post-Resistance	DAB1	1600	37	1	57537235	57537235	Frame_Shift_Del	DEL	T	-	8	335	c.518delA	c.(517-519)AAGfs	p.K173fs
Pat_11	Post-Resistance	PGM1	5236	37	1	64095210	64095210	Frame_Shift_Del	DEL	G	-	7	821	c.361delG	c.(361-363)GGGfs	p.G121fs
Pat_11	Post-Resistance	VANGL1	81839	37	1	116206586	116206586	Frame_Shift_Del	DEL	T	-	8	350	c.509delT	c.(508-510)CTTfs	p.L170fs
Pat_11	Post-Resistance	ZNF687	57592	37	1	151263487	151263487	Frame_Shift_Del	DEL	G	-	9	685	c.3516delG	c.(3514-3516)CTGfs	p.L1172fs
Pat_11	Post-Resistance	PSMB4	5692	37	1	151374040	151374040	Frame_Shift_Del	DEL	A	-	7	1735	c.716delA	c.(715-717)GAAfs	p.E239fs
Pat_11	Post-Resistance	SCAMP3	10067	37	1	155230129	155230129	Frame_Shift_Del	DEL	C	-	8	918	c.380delG	c.(379-381)GGCfs	p.G127fs
Pat_11	Post-Resistance	C1orf107	27042	37	1	210014267	210014267	Frame_Shift_Del	DEL	C	-	8	780	c.1352delC	c.(1351-1353)TCCfs	p.S451fs
Pat_11	Post-Resistance	MYO3A	53904	37	10	26417378	26417378	Frame_Shift_Del	DEL	A	-	10	175	c.2173delA	c.(2173-2175)AAAfs	p.K725fs
Pat_11	Post-Resistance	SLK	9748	37	10	105727547	105727549	In_Frame_Del	DEL	AGA	-	10	316	c.44_46delAGA	c.(43-48)GAGAAG>GAG	p.K19del
Pat_11	Post-Resistance	ADD3	120	37	10	111890224	111890225	Frame_Shift_Del	DEL	GT	-	28	290	c.1712_1713delGT	c.(1711-1713)CGTfs	p.R571fs
Pat_11	Post-Resistance	MYBPC3	4607	37	11	47359101	47359103	In_Frame_Del	DEL	TCT	-	14	263	.2441_2443delAG	.(2440-2445)AAGAGC>AG	p.K814del
Pat_11	Post-Resistance	OR4D9	390199	37	11	59282479	59282479	Frame_Shift_Del	DEL	T	-	7	664	c.94delT	c.(94-96)TTTfs	p.F32fs
Pat_11	Post-Resistance	NOX4	50507	37	11	89106662	89106663	Splice_Site	INS	-	A	22	611	c.1075_splice	c.e12-1	p.C359_splice
Pat_11	Post-Resistance	C11orf54	28970	37	11	93494710	93494710	Frame_Shift_Del	DEL	T	-	7	983	c.804delT	c.(802-804)CATfs	p.H268fs
Pat_11	Post-Resistance	BUD13	84811	37	11	116628987	116628987	Frame_Shift_Del	DEL	T	-	10	1201	c.1497delA	c.(1495-1497)AAAfs	p.K499fs
Pat_11	Post-Resistance	SIDT2	51092	37	11	117054525	117054527	In_Frame_Del	DEL	GTG	-	10	571	c.733_735delGTG	c.(733-735)GTGdel	p.V249del
Pat_11	Post-Resistance	BCL9L	283149	37	11	118773004	118773004	Frame_Shift_Del	DEL	G	-	7	1028	c.1448delC	c.(1447-1449)CCGfs	p.P483fs
Pat_11	Post-Resistance	CCDC153	283152	37	11	119061043	119061043	Frame_Shift_Del	DEL	G	-	7	520	c.599delC	c.(598-600)CCTfs	p.P200fs
Pat_11	Post-Resistance	VWF	7450	37	12	6128360	6128362	In_Frame_Del	DEL	CTT	-	8	442	.4222_4224delAA	c.(4222-4224)AAGdel	p.K1408del

Pat_11	Post-Resistance	PRPF40B	25766	37	12	50025258	50025258	Frame_Shift_Del	DEL	C	-	9	923	c.93delC	c.(91-93)ATCfs	p.I31fs
Pat_11	Post-Resistance	SMARCC2	6601	37	12	56559113	56559113	Frame_Shift_Del	DEL	G	-	11	546	c.3128delC	c.(3127-3129)CCTfs	p.P1043fs
Pat_11	Post-Resistance	SLC39A5	283375	37	12	56628997	56628999	In_Frame_Del	DEL	CTG	-	11	856	c.691_693delCTG	c.(691-693)CTGdel	p.L234del
Pat_11	Post-Resistance	EP400	57634	37	12	132445252	132445253	Frame_Shift_Ins	INS	-	C	8	134	c.88_89insC	c.(88-90)GCCfs	p.A30fs
Pat_11	Post-Resistance	ZC3H13	23091	37	13	46553948	46553949	Frame_Shift_Del	DEL	CT	-	11	1056	c.1911_1912delAG	c.(1909-1914)AGAGATfs	p.R637fs
Pat_11	Post-Resistance	LRCH1	23143	37	13	47243183	47243186	Frame_Shift_Del	DEL	CCTG	-	16	1353	c.471_474delCCT	c.(469-474)GCCCTGfs	p.A157fs
Pat_11	Post-Resistance	CYSLTR2	57105	37	13	49281593	49281593	Frame_Shift_Del	DEL	T	-	8	1173	c.640delT	c.(640-642)TTTfs	p.F214fs
Pat_11	Post-Resistance	EBPL	84650	37	13	50235208	50235209	Frame_Shift_Ins	INS	-	A	8	182	c.516_517insT	c.(514-519)TTTAACfs	p.F172fs
Pat_11	Post-Resistance	DIS3	22894	37	13	73337684	73337684	Frame_Shift_Del	DEL	T	-	10	405	c.2032delA	c.(2032-2034)ATTfs	p.I678fs
Pat_11	Post-Resistance	LMO7	4008	37	13	76415307	76415308	Frame_Shift_Del	DEL	AG	-	9	504	c.2946_2947delAG	c.(2944-2949)GCAGAGfs	p.A982fs
Pat_11	Post-Resistance	ZIC2	7546	37	13	100635008	100635010	In_Frame_Del	DEL	CCA	-	7	156	c.690_692delCCA	c.(688-693)GCCCAC>GCC	p.H239del
Pat_11	Post-Resistance	FANCM	57697	37	14	45645955	45645955	Frame_Shift_Del	DEL	A	-	7	164	c.3998delA	c.(3997-3999)CAAfs	p.Q1333fs
Pat_11	Post-Resistance	ABHD12B	145447	37	14	51347190	51347190	Frame_Shift_Del	DEL	G	-	8	553	c.356delG	c.(355-357)CGGfs	p.R119fs
Pat_11	Post-Resistance	PTPN21	11099	37	14	88940113	88940113	Frame_Shift_Del	DEL	T	-	10	421	c.2545delA	c.(2545-2547)ATTfs	p.I849fs
Pat_11	Post-Resistance	BTBD7	55727	37	14	93761193	93761193	Frame_Shift_Del	DEL	T	-	7	433	c.173delA	c.(172-174)AAGfs	p.K58fs
Pat_11	Post-Resistance	CCNK	8812	37	14	99969244	99969246	In_Frame_Del	DEL	CAG	-	10	650	c.934_936delCAG	c.(934-936)CAGdel	p.Q315del
Pat_11	Post-Resistance	IREB2	3658	37	15	78755395	78755395	Frame_Shift_Del	DEL	T	-	7	887	c.238delT	c.(238-240)TTTfs	p.F80fs
Pat_11	Post-Resistance	CHRNA3	1136	37	15	78913068	78913070	In_Frame_Del	DEL	CAG	-	3	3	c.67_69delCTG	c.(67-69)CTGdel	p.L23del
Pat_11	Post-Resistance	TIGD7	91151	37	16	3350471	3350472	Frame_Shift_Ins	INS	-	T	10	335	c.143_144insA	c.(142-144)AATfs	p.N48fs
Pat_11	Post-Resistance	C16orf62	57020	37	16	19580800	19580802	In_Frame_Del	DEL	TCC	-	8	310	c.172_174delTCC	c.(172-174)TCCdel	p.S64del
Pat_11	Post-Resistance	CD2BP2	10421	37	16	30365550	30365552	In_Frame_Del	DEL	CAT	-	11	1686	c.170_172delATG	c.(169-174)GATGGG>GG	p.D57del
Pat_11	Post-Resistance	CHD3	1107	37	17	7798765	7798765	Frame_Shift_Del	DEL	C	-	8	677	c.1612delC	c.(1612-1614)CCCfs	p.P538fs
Pat_11	Post-Resistance	GAS2L2	246176	37	17	34074257	34074257	Frame_Shift_Del	DEL	G	-	8	1342	c.863delC	c.(862-864)CCGfs	p.P288fs
Pat_11	Post-Resistance	C18orf34	374864	37	18	30913143	30913143	Frame_Shift_Del	DEL	T	-	10	105	c.874delA	c.(874-876)ATGfs	p.M292fs
Pat_11	Post-Resistance	SNAPC2	6618	37	19	7986967	7986968	Frame_Shift_Ins	INS	-	C	7	1080	c.420_421insC	c.(418-423)AAGCCCfs	p.K140fs
Pat_11	Post-Resistance	NUDT19	390916	37	19	33200189	33200190	Frame_Shift_Del	DEL	CT	-	11	751	c.813_814delCT	c.(811-816)GCCTCTfs	p.A271fs
Pat_11	Post-Resistance	ATP4A	495	37	19	36054349	36054351	In_Frame_Del	DEL	CTT	-	11	1734	c.91_93delAAG	c.(91-93)AAGdel	p.K31del
Pat_11	Post-Resistance	ZNF566	84924	37	19	36940726	36940726	Frame_Shift_Del	DEL	C	-	7	1490	c.410delG	c.(409-411)GGAfs	p.G137fs
Pat_11	Post-Resistance	U2AF2	11338	37	19	56171899	56171901	In_Frame_Del	DEL	AGA	-	7	241	c.248_250delAGA	c.(247-252)GAGAAG>GA	p.K87del
Pat_11	Post-Resistance	DHX57	90957	37	2	39095411	39095413	In_Frame_Del	DEL	CCA	-	7	410	c.135_137delTGG	c.(133-138)GGTGGA>GG	p.45_46GG>G
Pat_11	Post-Resistance	TMEM127	55654	37	2	96919781	96919783	In_Frame_Del	DEL	TGC	-	9	444	c.480_482delGCA	c.(478-483)CAGCAT>CAT	p.Q160del
Pat_11	Post-Resistance	ITPRIPL1	150771	37	2	96992793	96992795	In_Frame_Del	DEL	GAG	-	10	262	c.424_426delGAG	c.(424-426)GAGdel	p.E147del
Pat_11	Post-Resistance	RIF1	55183	37	2	152320541	152320541	Frame_Shift_Del	DEL	A	-	7	249	c.4507delA	c.(4507-4509)AAAfs	p.K1503fs
Pat_11	Post-Resistance	HOXD8	3234	37	2	176995458	176995458	Frame_Shift_Del	DEL	C	-	7	1018	c.364delC	c.(364-366)CCCfs	p.P122fs
Pat_11	Post-Resistance	DNAH7	56171	37	2	196801374	196801374	Frame_Shift_Del	DEL	A	-	8	226	c.3221delT	c.(3220-3222)TTGfs	p.L1074fs
Pat_11	Post-Resistance	ALS2CR11	151254	37	2	202352352	202352352	Frame_Shift_Del	DEL	T	-	7	203	c.1855delA	c.(1855-1857)ATTfs	p.I619fs
Pat_11	Post-Resistance	CRYGA	1418	37	2	209025577	209025577	Frame_Shift_Del	DEL	C	-	11	810	c.476delG	c.(475-477)GGTfs	p.G159fs
Pat_11	Post-Resistance	PRDM15	63977	37	21	43221415	43221417	In_Frame_Del	DEL	CTG	-	9	570	.4507_4509delCA	c.(4507-4509)CAGdel	p.Q1503del
Pat_11	Post-Resistance	CECR6	27439	37	22	17601300	17601302	In_Frame_Del	DEL	CCA	-	10	253	c.716_718delTGG	c.(715-720)GTGGGC>GG	p.V239del
Pat_11	Post-Resistance	MICAL3	57553	37	22	18314825	18314827	In_Frame_Del	DEL	CTC	-	7	98	.2848_2850delGA	c.(2848-2850)GAGdel	p.E950del
Pat_11	Post-Resistance	SREBF2	6721	37	22	42271637	42271637	Frame_Shift_Del	DEL	C	-	7	605	c.1295delC	c.(1294-1296)TCCfs	p.S432fs
Pat_11	Post-Resistance	BIK	638	37	22	43525245	43525247	In_Frame_Del	DEL	GCT	-	9	181	c.417_419delGCT	c.(415-420)GCGCTG>GC	p.L144del
Pat_11	Post-Resistance	CLASP2	23122	37	3	33602361	33602361	Frame_Shift_Del	DEL	T	-	12	718	c.2869delA	c.(2869-2871)ATGfs	p.M957fs
Pat_11	Post-Resistance	XIRP1	165904	37	3	39228955	39228958	Frame_Shift_Del	DEL	TGTC	-	9	249	1979_1982delGA	c.(1978-1983)AGACACfs	p.R660fs
Pat_11	Post-Resistance	DOCK3	1795	37	3	51417604	51417604	Frame_Shift_Del	DEL	C	-	7	312	c.5549delC	c.(5548-5550)ACCfs	p.T1850fs
Pat_11	Post-Resistance	VPRBP	9730	37	3	51457448	51457448	Frame_Shift_Del	DEL	T	-	7	1450	c.2976delA	c.(2974-2976)AAAfs	p.K992fs
Pat_11	Post-Resistance	FILIP1L	11259	37	3	99568272	99568273	Frame_Shift_Ins	INS	-	T	13	397	c.2247_2248insA	c.(2245-2250)AAACTAfs	p.K749fs

Pat_11	Post-Resistance	WWTR1	25937	37	3	149260194	149260196	In_Frame_Del	DEL	CTG	-	10	281	c.697_699delCAG	c.(697-699)CAGdel	p.Q233del
Pat_11	Post-Resistance	ATP13A3	79572	37	3	194147849	194147850	Frame_Shift_Ins	INS	-	A	11	308	c.3079_3080insT	c.(3079-3081)TGGfs	p.W1027fs
Pat_11	Post-Resistance	PDE6B	5158	37	4	661763	661765	In_Frame_Del	DEL	AGG	-	12	535	.2471_2473delAG	(2470-2475)AAGGAG>AA	p.E828del
Pat_11	Post-Resistance	CRIPAK	285464	37	4	1388930	1388931	Frame_Shift_Ins	INS	-	CA	9	42	c.631_632insCA	c.(631-633)TCAfs	p.S211fs
Pat_11	Post-Resistance	FAM193A	8603	37	4	2698177	2698177	Frame_Shift_Del	DEL	A	-	8	241	c.2491delA	c.(2491-2493)AAAfs	p.K831fs
Pat_11	Post-Resistance	TBC1D1	23216	37	4	38020014	38020014	Frame_Shift_Del	DEL	A	-	7	409	c.922delA	c.(922-924)AAAfs	p.K308fs
Pat_11	Post-Resistance	WDFY3	23001	37	4	85611708	85611709	Frame_Shift_Del	DEL	CA	-	12	511	.9313_9314delT	c.(9313-9315)TGGfs	p.W3105fs
Pat_11	Post-Resistance	NAP1L5	266812	37	4	89618484	89618486	In_Frame_Del	DEL	TCC	-	7	257	c.420_422delGGA	.(418-423)GAGGAA>GA	.140_141EE>
Pat_11	Post-Resistance	NPNT	255743	37	4	106863682	106863684	In_Frame_Del	DEL	CCA	-	7	466	c.982_984delCCA	c.(982-984)CCAdel	p.P333del
Pat_11	Post-Resistance	EXOSC9	5393	37	4	122723894	122723894	Frame_Shift_Del	DEL	T	-	9	397	c.227delT	c.(226-228)CTTfs	p.L76fs
Pat_11	Post-Resistance	FRG1	2483	37	4	190876218	190876219	Frame_Shift_Ins	INS	-	AT	8	628	c.344_345insAT	c.(343-345)AAAfs	p.K115fs
Pat_11	Post-Resistance	C5orf23	79614	37	5	32789822	32789823	Frame_Shift_Del	DEL	GT	-	9	289	c.315_316delGT	c.(313-318)GGGTGTfs	p.G105fs
Pat_11	Post-Resistance	C9	735	37	5	39341300	39341301	Frame_Shift_Ins	INS	-	G	7	389	c.423_424insC	c.(421-426)CCCTGCfs	p.P141fs
Pat_11	Post-Resistance	ADAMTS6	11174	37	5	64569170	64569170	Frame_Shift_Del	DEL	T	-	10	835	c.1617delA	c.(1615-1617)AAAfs	p.K539fs
Pat_11	Post-Resistance	TAF9	6880	37	5	68660786	68660788	In_Frame_Del	DEL	TCA	-	7	273	c.777_779delTGA	.(775-780)GATGAC>GA	.259_260DD>
Pat_11	Post-Resistance	ATXN1	6310	37	6	16327864	16327865	In_Frame_Ins	INS	-	TGC	8	39	c.677_678insGCA	.(676-678)CAC>CAGCAC	p.225_226ins
Pat_11	Post-Resistance	BAT1	7919	37	6	31504446	31504446	Frame_Shift_Del	DEL	A	-	7	246	c.447delT	c.(445-447)TTTfs	p.F149fs
Pat_11	Post-Resistance	BAT4	7918	37	6	31631854	31631854	Frame_Shift_Del	DEL	C	-	7	487	c.402delG	c.(400-402)GGGfs	p.G134fs
Pat_11	Post-Resistance	ZNF318	24149	37	6	43323502	43323502	Frame_Shift_Del	DEL	T	-	10	1393	c.1570delA	c.(1570-1572)AGGfs	p.R524fs
Pat_11	Post-Resistance	TMEM63B	55362	37	6	44122157	44122159	In_Frame_Del	DEL	CTG	-	7	486	.2282_2284delCT	.(2281-2286)ACTGCT>AC	p.A764del
Pat_11	Post-Resistance	DST	667	37	6	56510689	56510690	Frame_Shift_Del	DEL	TC	-	7	542	.1653_1654delG	c.(1651-1656)GAGAAGfs	p.E551fs
Pat_11	Post-Resistance	TTK	7272	37	6	80751896	80751897	Frame_Shift_Ins	INS	-	A	9	366	c.2551_2552insA	c.(2551-2553)GAAfs	p.E851fs
Pat_11	Post-Resistance	TPBG	7162	37	6	83075190	83075190	Frame_Shift_Del	DEL	C	-	7	1066	c.512delC	c.(511-513)GCCfs	p.A171fs
Pat_11	Post-Resistance	SEC63	11231	37	6	108214774	108214774	Frame_Shift_Del	DEL	T	-	7	126	c.1586delA	c.(1585-1587)AAGfs	p.K529fs
Pat_11	Post-Resistance	HOXA1	3198	37	7	27135314	27135316	In_Frame_Del	DEL	CGA	-	11	332	c.216_218delTCG	c.(214-219)CATCAC>CAC	p.72_73HH>H
Pat_11	Post-Resistance	PKD1L1	168507	37	7	47852764	47852764	Frame_Shift_Del	DEL	C	-	10	1057	c.7301delG	c.(7300-7302)GGCfs	p.G2434fs
Pat_11	Post-Resistance	STX1A	6804	37	7	73123425	73123427	In_Frame_Del	DEL	CAT	-	11	1019	c.56_58delATG	c.(55-60)GATGTC>GTC	p.D19del
Pat_11	Post-Resistance	EPHB4	2050	37	7	100410591	100410591	Frame_Shift_Del	DEL	C	-	7	1255	c.1896delG	c.(1894-1896)GGGfs	p.G632fs
Pat_11	Post-Resistance	MOGAT3	346606	37	7	100841562	100841562	Frame_Shift_Del	DEL	C	-	8	440	c.578delG	c.(577-579)GGTfs	p.G193fs
Pat_11	Post-Resistance	SLC26A3	1811	37	7	107432325	107432325	Frame_Shift_Del	DEL	A	-	8	640	c.332delT	c.(331-333)TTCfs	p.F111fs
Pat_11	Post-Resistance	LAMB4	22798	37	7	107763584	107763584	Frame_Shift_Del	DEL	A	-	7	787	c.26delT	c.(25-27)TTGfs	p.L9fs
Pat_11	Post-Resistance	WASL	8976	37	7	123332839	123332841	In_Frame_Del	DEL	AGG	-	9	314	c.907_909delCCT	c.(907-909)CCTdel	p.P303del
Pat_11	Post-Resistance	SLC13A4	26266	37	7	135378949	135378951	In_Frame_Del	DEL	TCT	-	8	709	.1052_1054delAG	.(1051-1056)AAGACC>AC	p.K351del
Pat_11	Post-Resistance	SVOPL	136306	37	7	138312996	138312996	Frame_Shift_Del	DEL	C	-	7	745	c.976delG	c.(976-978)GACfs	p.D326fs
Pat_11	Post-Resistance	ZC3HAV1	56829	37	7	138732539	138732539	Frame_Shift_Del	DEL	T	-	7	925	c.2510delA	c.(2509-2511)AACfs	p.N837fs
Pat_11	Post-Resistance	EPHA1	2041	37	7	143104714	143104714	Frame_Shift_Del	DEL	G	-	7	4115	c.140delC	c.(139-141)CCAfs	p.P47fs
Pat_11	Post-Resistance	BNIP3L	665	37	8	26240684	26240686	In_Frame_Del	DEL	ACA	-	9	282	c.38_40delACA	c.(37-42)CACAAC>CAC	p.N18del
Pat_11	Post-Resistance	PBK	55872	37	8	27668477	27668479	In_Frame_Del	DEL	TCA	-	7	317	c.768_770delTGA	c.(766-771)GATGAA>GAA	p.D256del
Pat_11	Post-Resistance	BHLHE22	27319	37	8	65493617	65493618	In_Frame_Ins	INS	-	GGC	3	3	c.270_271insGGC	c.(268-273)insGGC	p.97_98insG
Pat_11	Post-Resistance	SULF1	23213	37	8	70514026	70514026	Frame_Shift_Del	DEL	T	-	10	1137	c.1023delT	c.(1021-1023)CCTfs	p.P341fs
Pat_11	Post-Resistance	LRRCC1	85444	37	8	86038947	86038948	Frame_Shift_Del	DEL	AG	-	7	263	.1296_1297delA	c.(1294-1299)CAAGAGfs	p.Q432fs
Pat_11	Post-Resistance	CYP11B2	1585	37	8	143993951	143993953	In_Frame_Del	DEL	GCA	-	9	224	.1391_1393delTG	(1390-1395)CTGCAC>CA	p.L464del
Pat_11	Post-Resistance	PALM2-AKAP2	445815	37	9	112899247	112899247	Frame_Shift_Del	DEL	C	-	54	62	c.2119delC	c.(2119-2121)CCCfs	p.P707fs
Pat_11	Post-Resistance	SNAPC4	6621	37	9	139277995	139277997	In_Frame_Del	DEL	GCT	-	8	10	.1624_1626delAG	c.(1624-1626)AGCdel	p.S542del
Pat_11	Post-Resistance	CNKSR2	22866	37	X	21627678	21627680	In_Frame_Del	DEL	GAG	-	14	144	.2635_2637delGA	c.(2635-2637)GAGdel	p.E886del
Pat_11	Post-Resistance	ATRX	546	37	X	76931742	76931744	In_Frame_Del	DEL	TCA	-	7	328	.3786_3788delTG	.(3784-3789)GATGAC>GA	1262_1263DD
Pat_11	Post-Resistance	ARMCX3	51566	37	X	100880152	100880154	In_Frame_Del	DEL	TGA	-	13	810	c.183_185delTGA	c.(181-186)TCTGAT>TCT	p.D66del

Pat_11	Post-Resistance	ZNF185	7739	37	X	152087570	152087572	In_Frame_Del	DEL	GAG	-	10	97	c.475_477delGAG	c.(475-477)GAGdel	p.E165del
Pat_11	Post-Resistance	F8	2157	37	X	154157686	154157686	Frame_Shift_Del	DEL	T	-	10	224	c.4379delA	c.(4378-4380)AATfs	p.N1460fs
Pat_16	Post-Resistance	CLSTN1	22883	37	1	9790726	9790728	In_Frame_Del	DEL	TCC	-	10	142	.2784_2786delGG	(2782-2787)GAGGAA>GA	.928_929EE>
Pat_16	Post-Resistance	AADACL3	126767	37	1	12785494	12785494	Frame_Shift_Del	DEL	G	-	8	322	c.584delG	c.(583-585)TGTfs	p.C195fs
Pat_16	Post-Resistance	ATP13A2	23400	37	1	17313000	17313002	In_Frame_Del	DEL	CAG	-	8	252	.3361_3363delCT	c.(3361-3363)CTGdel	p.L1121del
Pat_16	Post-Resistance	PADI4	23569	37	1	17672605	17672606	Frame_Shift_Ins	INS	-	A	8	350	c.1018_1019insA	c.(1018-1020)GAGfs	p.E340fs
Pat_16	Post-Resistance	UBXN11	91544	37	1	26608843	26608844	In_Frame_Ins	INS	-	GGGACA	8	68	509_1510insTGTC	c.(1507-1512)insTGTCCC	.503_504insC
Pat_16	Post-Resistance	ARID1A	8289	37	1	27100182	27100184	In_Frame_Del	DEL	GCA	-	7	290	.3978_3980delGC	.(3976-3981)CCGCAG>CC	p.Q1334del
Pat_16	Post-Resistance	TMCO2	127391	37	1	40713708	40713709	Frame_Shift_Del	DEL	TC	-	22	469	c.43_44delTC	c.(43-45)TCTfs	p.S15fs
Pat_16	Post-Resistance	PTPRF	5792	37	1	44071946	44071948	In_Frame_Del	DEL	GCG	-	10	264	.3519_3521delGC	(3517-3522)CAGCGG>CA	p.R1178del
Pat_16	Post-Resistance	FOXD2	2306	37	1	47904370	47904371	Frame_Shift_Ins	INS	-	C	7	1449	c.563_564insC	c.(562-564)ATCfs	p.I188fs
Pat_16	Post-Resistance	TCHH	7062	37	1	152083818	152083820	In_Frame_Del	DEL	CGG	-	9	139	.1873_1875delCC	c.(1873-1875)CCGdel	p.P625del
Pat_16	Post-Resistance	CACNA1E	777	37	1	181680102	181680103	Frame_Shift_Del	DEL	AG	-	9	311	c.1068_1069delAG	c.(1066-1071)AAAGAGfs	p.K356fs
Pat_16	Post-Resistance	CDC73	79577	37	1	193111146	193111147	Frame_Shift_Del	DEL	AG	-	7	283	c.679_680delAG	c.(679-681)AGAfs	p.R227fs
Pat_16	Post-Resistance	EPHX1	2052	37	1	226026384	226026384	Frame_Shift_Del	DEL	C	-	12	1087	c.394delC	c.(394-396)CCCfs	p.P132fs
Pat_16	Post-Resistance	SFMBT2	57713	37	10	7212995	7212997	In_Frame_Del	DEL	CTC	-	9	697	.2437_2439delGA	c.(2437-2439)GAGdel	p.E813del
Pat_16	Post-Resistance	KIAA1462	57608	37	10	30318585	30318585	Frame_Shift_Del	DEL	C	-	8	798	c.492delG	c.(490-492)ATGfs	p.M164fs
Pat_16	Post-Resistance	NFKB2	4791	37	10	104158163	104158163	Frame_Shift_Del	DEL	C	-	8	1210	c.874delC	c.(874-876)CCCfs	p.P292fs
Pat_16	Post-Resistance	ADAM12	8038	37	10	127737897	127737897	Frame_Shift_Del	DEL	C	-	8	652	c.1851delG	c.(1849-1851)GGGfs	p.G617fs
Pat_16	Post-Resistance	KRTAP5-5	439915	37	11	1651199	1651200	In_Frame_Ins	INS	-	CTGTGGCT	92	89	130insGGCTGTG	27-132)insGGCTGTGGCT	.43_44insGCG
Pat_16	Post-Resistance	UBQLN3	50613	37	11	5529918	5529920	In_Frame_Del	DEL	TGG	-	10	459	c.869_871delCCA	c.(868-873)ACCAGC>AGC	p.T290del
Pat_16	Post-Resistance	OR10A2	341276	37	11	6891253	6891255	In_Frame_Del	DEL	TTC	-	10	252	c.268_270delTTC	c.(268-270)TTCdel	p.F94del
Pat_16	Post-Resistance	PRB2	653247	37	12	11546544	11546545	In_Frame_Ins	INS	-	GGA	12	477	c.467_468insTCC	c.(466-468)CCA>CCTCCA	.156_156P>P
Pat_16	Post-Resistance	SFRS2IP	9169	37	12	46318575	46318577	In_Frame_Del	DEL	GGT	-	7	683	.3840_3842delAC	(3838-3843)CCACCC>CC	1280_1281PP>
Pat_16	Post-Resistance	ESPL1	9700	37	12	53683876	53683877	Frame_Shift_Del	DEL	TG	-	7	219	c.5121_5122delTG	c.(5119-5124)ACTGTGfs	p.T1707fs
Pat_16	Post-Resistance	GPR182	11318	37	12	57389063	57389063	Frame_Shift_Del	DEL	G	-	7	423	c.70delG	c.(70-72)GGAfs	p.G24fs
Pat_16	Post-Resistance	NCOR2	9612	37	12	124848228	124848228	Frame_Shift_Del	DEL	G	-	8	553	c.2925delC	c.(2923-2925)CCCfs	p.P975fs
Pat_16	Post-Resistance	PABPC3	5042	37	13	25671804	25671806	In_Frame_Del	DEL	GCT	-	10	183	.1468_1470delGC	c.(1468-1470)GCTdel	p.A496del
Pat_16	Post-Resistance	WASF3	10810	37	13	27257023	27257023	Frame_Shift_Del	DEL	C	-	7	795	c.1263delC	c.(1261-1263)GGCfs	p.G421fs
Pat_16	Post-Resistance	B3GALTL	145173	37	13	31803392	31803392	Frame_Shift_Del	DEL	A	-	9	256	c.231delA	c.(229-231)TTAfs	p.L77fs
Pat_16	Post-Resistance	C14orf4	64207	37	14	77493792	77493794	In_Frame_Del	DEL	TGT	-	8	65	c.342_344delACA	c.(340-345)CAACAG>CAG	.114_115QQ>
Pat_16	Post-Resistance	RIN3	79890	37	14	93118772	93118772	Frame_Shift_Del	DEL	C	-	8	373	c.1378delC	c.(1378-1380)CCCfs	p.P460fs
Pat_16	Post-Resistance	SPG11	80208	37	15	44876678	44876679	Frame_Shift_Ins	INS	-	T	16	82	c.5199_5200insA	c.(5197-5202)AAATGCfs	p.K1733fs
Pat_16	Post-Resistance	SLC24A1	9187	37	15	65918177	65918179	In_Frame_Del	DEL	CTG	-	10	272	.1759_1761delCT	c.(1759-1761)CTGdel	p.L591del
Pat_16	Post-Resistance	IL32	9235	37	16	3119304	3119305	Frame_Shift_Ins	INS	-	G	8	771	c.653_654insG	c.(652-654)GACfs	p.D218fs
Pat_16	Post-Resistance	C16orf71	146562	37	16	4796953	4796955	In_Frame_Del	DEL	GAG	-	10	53	.1207_1209delGA	c.(1207-1209)GAGdel	p.E409del
Pat_16	Post-Resistance	SLC5A11	115584	37	16	24921737	24921739	In_Frame_Del	DEL	CAG	-	10	366	.1761_1763delCA	(1759-1764)GCCAGC>GC	p.S592del
Pat_16	Post-Resistance	ADCY7	113	37	16	50324522	50324522	Frame_Shift_Del	DEL	A	-	8	293	c.326delA	c.(325-327)TATfs	p.Y109fs
Pat_16	Post-Resistance	HSD11B2	3291	37	16	67470245	67470245	Frame_Shift_Del	DEL	G	-	8	1012	c.758delG	c.(757-759)TGGfs	p.W253fs
Pat_16	Post-Resistance	EDC4	23644	37	16	67913786	67913788	In_Frame_Del	DEL	AGC	-	11	191	.1855_1857delAG	c.(1855-1857)AGCdel	p.S629del
Pat_16	Post-Resistance	ZFHX3	463	37	16	72821594	72821596	In_Frame_Del	DEL	GCC	-	7	321	0579_10581delG	c.(10579-10581)GGCdel	p.G3527del
Pat_16	Post-Resistance	CMIP	80790	37	16	81735318	81735319	Frame_Shift_Del	DEL	GC	-	8	1847	c.1809_1810delG	c.(1807-1812)CTGCAGfs	p.L603fs
Pat_16	Post-Resistance	SMCR7	125170	37	17	18167778	18167780	In_Frame_Del	DEL	GCT	-	8	152	.1065_1067delGC	(1063-1068)CGGCTG>CG	p.L360del
Pat_16	Post-Resistance	FBXO47	494188	37	17	37101376	37101376	Frame_Shift_Del	DEL	T	-	56	179	c.630delA	c.(628-630)AAAfs	p.K210fs
Pat_16	Post-Resistance	FKBP10	60681	37	17	39975559	39975559	Frame_Shift_Del	DEL	C	-	7	200	c.825delC	c.(823-825)CTCfs	p.L275fs
Pat_16	Post-Resistance	EFTUD2	9343	37	17	42928700	42928701	Frame_Shift_Ins	INS	-	A	8	870	c.2860_2861insT	c.(2860-2862)GATfs	p.D954fs
Pat_16	Post-Resistance	SP2	6668	37	17	45993612	45993612	Frame_Shift_Del	DEL	C	-	7	1330	c.175delC	c.(175-177)CCCfs	p.P59fs

Pat_16	Post-Resistance	KIAA0195	9772	37	17	73491062	73491063	Frame_Shift_Ins	INS	-	C	7	566	c.2675_2676insC	c.(2674-2676)ATCfs	p.I892fs
Pat_16	Post-Resistance	EVI5L	115704	37	19	7917989	7917989	Frame_Shift_Del	DEL	C	-	7	2010	c.1005delC	c.(1003-1005)ATCfs	p.I335fs
Pat_16	Post-Resistance	CARM1	10498	37	19	11022887	11022887	Frame_Shift_Del	DEL	G	-	8	1775	c.586delG	c.(586-588)GGGfs	p.G196fs
Pat_16	Post-Resistance	OR7A5	26659	37	19	14938205	14938205	Frame_Shift_Del	DEL	G	-	7	515	c.849delC	c.(847-849)CCCfs	p.P283fs
Pat_16	Post-Resistance	DMKN	93099	37	19	36002362	36002412	In_Frame_Del	DEL	CACTGCTC	-	29	40	GGCGGCAGCAGT	GGCGGCAGCAGTGGC(	GSSSGGSSG
Pat_16	Post-Resistance	SBSN	374897	37	19	36019046	36019047	Frame_Shift_Del	DEL	CT	-	7	933	c.137_138delAG	c.(136-138)GAGfs	p.E46fs
Pat_16	Post-Resistance	C19orf55	148137	37	19	36255947	36255949	In_Frame_Del	DEL	CTC	-	25	1505	c.639_641delCTC	c.(637-642)ATCTCC>ATC	p.S218del
Pat_16	Post-Resistance	CADM4	199731	37	19	44127492	44127492	Frame_Shift_Del	DEL	A	-	162	258	c.1157delT	c.(1156-1158)TTCfs	p.F386fs
Pat_16	Post-Resistance	NUCB1	4924	37	19	49425109	49425111	In_Frame_Del	DEL	AGC	-	8	291	.1199_1201delAG	(1198-1203)AAGCAG>AA	p.Q407del
Pat_16	Post-Resistance	U2AF2	11338	37	19	56171899	56171901	In_Frame_Del	DEL	AGA	-	9	401	c.248_250delAGA	.(247-252)GAGAAG>GAG	p.K87del
Pat_16	Post-Resistance	DHX57	90957	37	2	39095411	39095413	In_Frame_Del	DEL	CCA	-	7	183	c.135_137delTGG	.(133-138)GGTGGA>GG	p.45_46GG>G
Pat_16	Post-Resistance	OTX1	5013	37	2	63283259	63283261	In_Frame_Del	DEL	CCA	-	7	435	c.873_875delCCA	.(871-876)GGCCAC>GGC	p.H301del
Pat_16	Post-Resistance	TGOLN2	10618	37	2	85554289	85554289	Frame_Shift_Del	DEL	G	-	8	1425	c.566delC	c.(565-567)CCAfs	p.P189fs
Pat_16	Post-Resistance	DNAH7	56171	37	2	196788374	196788374	Frame_Shift_Del	DEL	T	-	11	146	c.3770delA	c.(3769-3771)AATfs	p.N1257fs
Pat_16	Post-Resistance	CCNYL1	151195	37	2	208611842	208611843	Frame_Shift_Del	DEL	GG	-	7	297	c.558_559delGG	c.(556-561)CTGGGAfs	p.L186fs
Pat_16	Post-Resistance	CRYGA	1418	37	2	209025577	209025577	Frame_Shift_Del	DEL	C	-	12	572	c.476delG	c.(475-477)GGTfs	p.G159fs
Pat_16	Post-Resistance	ABCB6	10058	37	2	220078193	220078194	Frame_Shift_Del	DEL	TC	-	7	1266	c.1686_1687delGA	c.(1684-1689)GAGAACfs	p.E562fs
Pat_16	Post-Resistance	GINS1	9837	37	20	25422397	25422397	Frame_Shift_Del	DEL	A	-	7	143	c.507delA	c.(505-507)TTAfs	p.L169fs
Pat_16	Post-Resistance	LPIN3	64900	37	20	39977799	39977799	Frame_Shift_Del	DEL	C	-	7	711	c.625delC	c.(625-627)CCCfs	p.P209fs
Pat_16	Post-Resistance	SLC19A1	6573	37	21	46951916	46951918	In_Frame_Del	DEL	CAG	-	7	119	c.334_336delCTG	c.(334-336)CTGdel	p.L112del
Pat_16	Post-Resistance	TFIP11	24144	37	22	26906183	26906185	In_Frame_Del	DEL	TCA	-	8	379	c.54_56delTGA	c.(52-57)GATGAC>GAC	p.18_19DD>D
Pat_16	Post-Resistance	NEFH	4744	37	22	29885859	29885876	In_Frame_Del	DEL	GTCCCCAG	-	135	241	delGCTAAGTCCC	247)GCTAAGTCCCCAGA	.AKSPEK750d
Pat_16	Post-Resistance	SREBF2	6721	37	22	42262949	42262951	In_Frame_Del	DEL	GCA	-	7	168	c.203_205delGCA	.(202-207)GGCAGC>GGC	p.S74del
Pat_16	Post-Resistance	CACNA1D	776	37	3	53529193	53529195	Translation_Start_Site	DEL	GAT	-	11	363			
Pat_16	Post-Resistance	PCOLCE2	26577	37	3	142542392	142542392	Frame_Shift_Del	DEL	A	-	281	157	c.931delT	c.(931-933)TATfs	p.Y311fs
Pat_16	Post-Resistance	PDE6B	5158	37	4	661763	661765	In_Frame_Del	DEL	AGG	-	10	348	.2471_2473delAG	(2470-2475)AAGGAG>AA	p.E828del
Pat_16	Post-Resistance	MMRN1	22915	37	4	90844391	90844393	In_Frame_Del	DEL	AGC	-	10	1861	c.923_925delAGC	.(922-927)GAGCAG>GAG	p.Q313del
Pat_16	Post-Resistance	PAPD7	11044	37	5	6755013	6755014	Frame_Shift_Del	DEL	AC	-	17	277	c.1584_1585delAC	c.(1582-1587)AAACACfs	p.K528fs
Pat_16	Post-Resistance	TIMD4	91937	37	5	156378745	156378747	In_Frame_Del	DEL	TTG	-	8	1011	c.455_457delCAA	c.(454-459)ACAAGC>AGC	p.T152del
Pat_16	Post-Resistance	FKBPL	63943	37	6	32097086	32097086	Frame_Shift_Del	DEL	C	-	7	1657	c.472delG	c.(472-474)GAGfs	p.E158fs
Pat_16	Post-Resistance	FOXP4	116113	37	6	41557781	41557781	Frame_Shift_Del	DEL	C	-	7	314	c.1230delC	c.(1228-1230)CACfs	p.H410fs
Pat_16	Post-Resistance	CUL7	9820	37	6	43011212	43011212	Frame_Shift_Del	DEL	G	-	9	475	c.3329delC	c.(3328-3330)CCTfs	p.P1110fs
Pat_16	Post-Resistance	SNAP91	9892	37	6	84285768	84285768	Frame_Shift_Del	DEL	A	-	2	4	c.2304delT	c.(2302-2304)CTTfs	p.L768fs
Pat_16	Post-Resistance	FOXK1	221937	37	7	4798771	4798771	Frame_Shift_Del	DEL	C	-	7	1249	c.1334delC	c.(1333-1335)TCCfs	p.S445fs
Pat_16	Post-Resistance	GLCCI1	113263	37	7	8126097	8126099	In_Frame_Del	DEL	CAG	-	8	1232	.1573_1575delCA	c.(1573-1575)CAGdel	p.Q528del
Pat_16	Post-Resistance	DFNA5	1687	37	7	24749939	24749940	Frame_Shift_Del	DEL	CC	-	7	416	c.765_766delGG	c.(763-768)CTGGACfs	p.L255fs
Pat_16	Post-Resistance	POU6F2	11281	37	7	39379288	39379290	In_Frame_Del	DEL	CAG	-	10	175	c.559_561delCAG	c.(559-561)CAGdel	p.Q196del
Pat_16	Post-Resistance	POLM	27434	37	7	44120414	44120414	Frame_Shift_Del	DEL	G	-	7	433	c.290delC	c.(289-291)CCAfs	p.P97fs
Pat_16	Post-Resistance	KRIT1	889	37	7	91864157	91864157	Frame_Shift_Del	DEL	T	-	8	477	c.810delA	c.(808-810)AAAfs	p.K270fs
Pat_16	Post-Resistance	TAF6	6878	37	7	99705124	99705124	Frame_Shift_Del	DEL	G	-	7	1072	c.1779delC	c.(1777-1779)CCCfs	p.P593fs
Pat_16	Post-Resistance	PUS7	54517	37	7	105122810	105122810	Frame_Shift_Del	DEL	T	-	7	959	c.998delA	c.(997-999)AACfs	p.N333fs
Pat_16	Post-Resistance	MDFIC	29969	37	7	114562639	114562641	In_Frame_Del	DEL	GAG	-	13	82	c.168_170delGAG	.(166-171)AAGAGG>AAG	p.R62del
Pat_16	Post-Resistance	OR9A4	130075	37	7	141619203	141619203	Frame_Shift_Del	DEL	T	-	7	830	c.528delT	c.(526-528)AATfs	p.N176fs
Pat_16	Post-Resistance	BNIP3L	665	37	8	26240684	26240686	In_Frame_Del	DEL	ACA	-	7	392	c.38_40delACA	c.(37-42)CACAAC>CAC	p.N18del
Pat_16	Post-Resistance	ST18	9705	37	8	53062481	53062482	Frame_Shift_Ins	INS	-	T	7	247	c.1862_1863insA	c.(1861-1863)AATfs	p.N621fs
Pat_16	Post-Resistance	PABPC1	26986	37	8	101724994	101724995	Frame_Shift_Ins	INS	-	A	7	120	c.761_762insT	c.(760-762)AAGfs	p.K254fs
Pat_16	Post-Resistance	ZC3H3	23144	37	8	144522387	144522389	In_Frame_Del	DEL	GAG	-	8	65	.2637_2639delCT	(2635-2640)TCCTCA>TC	.879_880SS>

Pat_16	Post-Resistance	CNKSR2	22866	37	X	21627678	21627680	In_Frame_Del	DEL	GAG	-	9	162	.2635_2637delGA	c.(2635-2637)GAGdel	p.E886del
Pat_16	Post-Resistance	RBM10	8241	37	X	47030467	47030469	In_Frame_Del	DEL	GGC	-	7	145	c.242_244delGGC	.(241-246)AGGCGG>AG	p.81_82RR>R
Pat_16	Post-Resistance	NUDT11	55190	37	X	51239296	51239309	Translation_Start_Site	DEL	TCGAGGCA	-	13	29			
Pat_16	Pre-Treatment	CAMTA1	23261	37	1	7811329	7811329	Frame_Shift_Del	DEL	A	-	7	781	c.4760delA	c.(4759-4761)CAAfs	p.Q1587fs
Pat_16	Pre-Treatment	TMCO2	127391	37	1	40713708	40713709	Frame_Shift_Del	DEL	TC	-	9	600	c.43_44delTC	c.(43-45)TCTfs	p.S15fs
Pat_16	Pre-Treatment	WDR78	79819	37	1	67390426	67390426	Frame_Shift_Del	DEL	T	-	8	539	c.89delA	c.(88-90)AAGfs	p.K30fs
Pat_16	Pre-Treatment	TYW3	127253	37	1	75229742	75229744	In_Frame_Del	DEL	ATG	-	7	421	c.725_727delATG	c.(724-729)AATGAT>AAT	p.D247del
Pat_16	Pre-Treatment	CLCA4	22802	37	1	87029432	87029432	Frame_Shift_Del	DEL	A	-	8	322	c.537delA	c.(535-537)TCAfs	p.S179fs
Pat_16	Pre-Treatment	GBP5	115362	37	1	89735095	89735096	Frame_Shift_Del	DEL	GC	-	7	1057	c.143_144delGC	c.(142-144)CGCfs	p.R48fs
Pat_16	Pre-Treatment	SLC16A1	6566	37	1	113471890	113471890	Frame_Shift_Del	DEL	G	-	7	367	c.41delC	c.(40-42)CCAfs	p.P14fs
Pat_16	Pre-Treatment	BCAN	63827	37	1	156626160	156626160	Frame_Shift_Del	DEL	G	-	8	771	c.2029delG	c.(2029-2031)GGGfs	p.G677fs
Pat_16	Pre-Treatment	PEAR1	375033	37	1	156884483	156884483	Frame_Shift_Del	DEL	C	-	7	278	c.3007delC	c.(3007-3009)CCCfs	p.P1003fs
Pat_16	Pre-Treatment	OR10Z1	128368	37	1	158576487	158576487	Frame_Shift_Del	DEL	G	-	7	957	c.259delG	c.(259-261)GGGfs	p.G87fs
Pat_16	Pre-Treatment	SMG7	9887	37	1	183515266	183515267	Frame_Shift_Ins	INS	-	A	8	164	c.2536_2537insA	c.(2536-2538)GAAfs	p.E846fs
Pat_16	Pre-Treatment	APOBEC4	403314	37	1	183616826	183616828	In_Frame_Del	DEL	TTC	-	12	592	.1089_1091delGA	.(1087-1092)AAGAAA>AA	.363_364KK>
Pat_16	Pre-Treatment	RAB7L1	8934	37	1	205741633	205741633	Frame_Shift_Del	DEL	C	-	7	1484	c.187delG	c.(187-189)GATfs	p.D63fs
Pat_16	Pre-Treatment	OR10A2	341276	37	11	6891253	6891255	In_Frame_Del	DEL	TTC	-	11	215	c.268_270delTTC	c.(268-270)TTCdel	p.F94del
Pat_16	Pre-Treatment	C11orf46	120534	37	11	30352754	30352754	Frame_Shift_Del	DEL	A	-	7	398	c.259delA	c.(259-261)AAAfs	p.K87fs
Pat_16	Pre-Treatment	ENO2	2026	37	12	7031245	7031245	Frame_Shift_Del	DEL	G	-	7	1029	c.1094delG	c.(1093-1095)TGGfs	p.W365fs
Pat_16	Pre-Treatment	CLEC4A	50856	37	12	8281937	8281937	Frame_Shift_Del	DEL	A	-	11	150	c.277delA	c.(277-279)AAAfs	p.K93fs
Pat_16	Pre-Treatment	CAND1	55832	37	12	67699692	67699692	Frame_Shift_Del	DEL	G	-	8	488	c.2244delG	c.(2242-2244)CAGfs	p.Q748fs
Pat_16	Pre-Treatment	EP400	57634	37	12	132491394	132491394	Frame_Shift_Del	DEL	T	-	7	253	c.3276delT	c.(3274-3276)GCTfs	p.A1092fs
Pat_16	Pre-Treatment	TSC22D1	8848	37	13	45148706	45148708	In_Frame_Del	DEL	TGC	-	7	591	.1503_1505delGC	.(1501-1506)CAGCAA>CA	.501_502QQ>
Pat_16	Pre-Treatment	FBXL3	26224	37	13	77581683	77581683	Frame_Shift_Del	DEL	A	-	7	244	c.884delT	c.(883-885)TTAfs	p.L295fs
Pat_16	Pre-Treatment	MYCBP2	23077	37	13	77641917	77641917	Frame_Shift_Del	DEL	G	-	8	903	c.12140delC	c.(12139-12141)CCAfs	p.P4047fs
Pat_16	Pre-Treatment	ERCC5	2073	37	13	103524612	103524612	Frame_Shift_Del	DEL	A	-	12	236	c.2743delA	c.(2743-2745)AAAfs	p.K915fs
Pat_16	Pre-Treatment	SPG11	80208	37	15	44876678	44876679	Frame_Shift_Ins	INS	-	T	14	100	c.5199_5200insA	c.(5197-5202)AAATGCfs	p.K1733fs
Pat_16	Pre-Treatment	DMXL2	23312	37	15	51758424	51758424	Frame_Shift_Del	DEL	A	-	7	486	c.7474delT	c.(7474-7476)TCAfs	p.S2492fs
Pat_16	Pre-Treatment	RNF111	54778	37	15	59359142	59359144	In_Frame_Del	DEL	CAC	-	7	568	.1546_1548delCA	c.(1546-1548)CACdel	p.H520del
Pat_16	Pre-Treatment	SLC24A1	9187	37	15	65918177	65918179	In_Frame_Del	DEL	CTG	-	8	252	.1759_1761delCT	c.(1759-1761)CTGdel	p.L591del
Pat_16	Pre-Treatment	POLG	5428	37	15	89876828	89876833	In_Frame_Del	DEL	TGCTGC	-	8	52	53_158delGCAG	(151-159)CAGCAGCAA>C	.51_53QQQ>
Pat_16	Pre-Treatment	IL27	246778	37	16	28511176	28511178	In_Frame_Del	DEL	CTC	-	5	3	c.526_528delGAG	c.(526-528)GAGdel	p.E176del
Pat_16	Pre-Treatment	EDC4	23644	37	16	67913767	67913769	In_Frame_Del	DEL	CAG	-	8	160	.1836_1838delCA	(1834-1839)CCCAGC>CC	p.S617del
Pat_16	Pre-Treatment	TRIM16	10626	37	17	15554725	15554725	Frame_Shift_Del	DEL	C	-	7	1027	c.199delG	c.(199-201)GATfs	p.D67fs
Pat_16	Pre-Treatment	FBXO47	494188	37	17	37101376	37101376	Frame_Shift_Del	DEL	T	-	63	211	c.630delA	c.(628-630)AAAfs	p.K210fs
Pat_16	Pre-Treatment	HOXB2	3212	37	17	46622130	46622132	In_Frame_Del	DEL	AGG	-	10	514	c.142_144delCCT	c.(142-144)CCTdel	p.P48del
Pat_16	Pre-Treatment	PIP5K1C	23396	37	19	3633460	3633460	Frame_Shift_Del	DEL	G	-	7	75	c.1979delC	c.(1978-1980)CCGfs	p.P660fs
Pat_16	Pre-Treatment	LGI4	163175	37	19	35625552	35625554	In_Frame_Del	DEL	CAG	-	9	191	c.31_33delCTG	c.(31-33)CTGdel	p.L11del
Pat_16	Pre-Treatment	DMKN	93099	37	19	36002362	36002412	In_Frame_Del	DEL	CCACTGCT	-	14	12	GGCGGCAGCAGT	GGCGGCAGCAGTGGC	GSSSGGSSG
Pat_16	Pre-Treatment	CADM4	199731	37	19	44127492	44127492	Frame_Shift_Del	DEL	A	-	209	301	c.1157delT	c.(1156-1158)TTCfs	p.F386fs
Pat_16	Pre-Treatment	ZC3H4	23211	37	19	47572401	47572403	In_Frame_Del	DEL	CTC	-	8	473	.2344_2346delGA	c.(2344-2346)GAGdel	p.E782del
Pat_16	Pre-Treatment	ZNF649	65251	37	19	52394014	52394014	Frame_Shift_Del	DEL	C	-	7	1235	c.1375delG	c.(1375-1377)GATfs	p.D459fs
Pat_16	Pre-Treatment	PUM2	23369	37	2	20482977	20482979	In_Frame_Del	DEL	GCT	-	8	399	.1449_1451delAG	(1447-1452)GCAGCT>GC	.483_484AA>
Pat_16	Pre-Treatment	HS1BP3	64342	37	2	20840864	20840864	Frame_Shift_Del	DEL	G	-	10	1025	c.275delC	c.(274-276)CCAfs	p.P92fs
Pat_16	Pre-Treatment	GPR113	165082	37	2	26534413	26534413	Frame_Shift_Del	DEL	C	-	7	309	c.2183delG	c.(2182-2184)GGTfs	p.G728fs
Pat_16	Pre-Treatment	DHX57	90957	37	2	39095411	39095413	In_Frame_Del	DEL	CCA	-	9	246	c.135_137delTGG	.(133-138)GGTGGA>GG	p.45_46GG>G
Pat_16	Pre-Treatment	CDCA7	83879	37	2	174229648	174229650	In_Frame_Del	DEL	GGA	-	7	187	c.588_590delGGA	c.(586-591)ATGGAG>ATG	p.E202del

Pat_16	Pre-Treatment	PTPRA	5786	37	20	3016542	3016544	In_Frame_Del	DEL	AGC	-	8	695	.2186_2188delAG	(2185-2190)AAGCAG>AA	p.Q733del
Pat_16	Pre-Treatment	PTPN1	5770	37	20	49196293	49196293	Frame_Shift_Del	DEL	C	-	11	409	c.918delC	c.(916-918)ATCfs	p.I306fs
Pat_16	Pre-Treatment	COL6A6	131873	37	3	130318621	130318621	Frame_Shift_Del	DEL	C	-	7	212	c.4620delC	c.(4618-4620)GGCfs	p.G1540fs
Pat_16	Pre-Treatment	PCOLCE2	26577	37	3	142542392	142542392	Frame_Shift_Del	DEL	A	-	205	154	c.931delT	c.(931-933)TATfs	p.Y311fs
Pat_16	Pre-Treatment	SMC4	10051	37	3	160143940	160143940	Frame_Shift_Del	DEL	A	-	8	786	c.2557delA	c.(2557-2559)AAAfs	p.K853fs
Pat_16	Pre-Treatment	ATP13A3	79572	37	3	194181471	194181473	In_Frame_Del	DEL	GAG	-	10	527	c.139_141delCTC	c.(139-141)CTCdel	p.L47del
Pat_16	Pre-Treatment	ANKRD17	26057	37	4	73956601	73956601	Frame_Shift_Del	DEL	G	-	8	1042	c.6744delC	c.(6742-6744)CCCfs	p.P2248fs
Pat_16	Pre-Treatment	NUP54	53371	37	4	77065307	77065309	In_Frame_Del	DEL	TGC	-	7	1036	c.288_290delGCA	c.(286-291)CAGCAA>CAA	p.96_97QQ>Q
Pat_16	Pre-Treatment	MMRN1	22915	37	4	90844391	90844393	In_Frame_Del	DEL	AGC	-	12	1517	c.923_925delAGC	.(922-927)GAGCAG>GAG	p.Q313del
Pat_16	Pre-Treatment	SCLT1	132320	37	4	129864163	129864163	Frame_Shift_Del	DEL	T	-	10	376	c.1620delA	c.(1618-1620)AAAfs	p.K540fs
Pat_16	Pre-Treatment	FGG	2266	37	4	155526059	155526059	Frame_Shift_Del	DEL	C	-	7	1185	c.1289delG	c.(1288-1290)GGAfs	p.G430fs
Pat_16	Pre-Treatment	SORBS2	8470	37	4	186515044	186515044	Frame_Shift_Del	DEL	C	-	7	806	c.3130delG	c.(3130-3132)GAAfs	p.E1044fs
Pat_16	Pre-Treatment	ADAMTS6	11174	37	5	64569170	64569170	Frame_Shift_Del	DEL	T	-	7	1003	c.1617delA	c.(1615-1617)AAAfs	p.K539fs
Pat_16	Pre-Treatment	SLC22A4	6583	37	5	131676327	131676327	Frame_Shift_Del	DEL	T	-	7	704	c.1514delT	c.(1513-1515)CTTfs	p.L505fs
Pat_16	Pre-Treatment	HIVEP1	3096	37	6	12089463	12089463	Frame_Shift_Del	DEL	A	-	10	322	c.87delA	c.(85-87)TCAfs	p.S29fs
Pat_16	Pre-Treatment	BTN1A1	696	37	6	26509321	26509321	Frame_Shift_Del	DEL	G	-	8	679	c.1500delG	c.(1498-1500)ATGfs	p.M500fs
Pat_16	Pre-Treatment	CDSN	1041	37	6	31084620	31084622	In_Frame_Del	DEL	CCA	-	7	253	c.770_772delTGG	.(769-774)GTGGAC>GAC	p.V257del
Pat_16	Pre-Treatment	CDK19	23097	37	6	110943300	110943300	Frame_Shift_Del	DEL	T	-	8	932	c.1101delA	c.(1099-1101)AAAfs	p.K367fs
Pat_16	Pre-Treatment	GLCCI1	113263	37	7	8126097	8126099	In_Frame_Del	DEL	CAG	-	9	1141	.1573_1575delCA	c.(1573-1575)CAGdel	p.Q528del
Pat_16	Pre-Treatment	DYNC1I1	1780	37	7	95614249	95614249	Frame_Shift_Del	DEL	T	-	8	1582	c.754delT	c.(754-756)TTTfs	p.F252fs
Pat_16	Pre-Treatment	NAPEPLD	222236	37	7	102769241	102769242	Splice_Site	INS	-	A	8	553	c.-15_splice	c.e2-1	
Pat_16	Pre-Treatment	LAMB4	22798	37	7	107763584	107763584	Frame_Shift_Del	DEL	A	-	7	662	c.26delT	c.(25-27)TTGfs	p.L9fs
Pat_16	Pre-Treatment	SGK223	157285	37	8	8176387	8176388	In_Frame_Ins	INS	-	GGGGCG	23	22	497_3498insCGCC	96-3498)CCG>CCCGCC	166_1166P>P
Pat_16	Pre-Treatment	CDCA2	157313	37	8	25340934	25340936	In_Frame_Del	DEL	ATG	-	7	651	.1052_1054delAT	c.(1051-1056)TATGAT>TAT	p.D354del
Pat_16	Pre-Treatment	WRN	7486	37	8	30945377	30945379	In_Frame_Del	DEL	AAG	-	10	254	.1517_1519delAA	.(1516-1521)AAAGAA>AA	p.E510del
Pat_16	Pre-Treatment	WHSC1L1	54904	37	8	38205092	38205092	Frame_Shift_Del	DEL	T	-	9	759	c.598delA	c.(598-600)AGCfs	p.S200fs
Pat_16	Pre-Treatment	UBR5	51366	37	8	103289348	103289349	Frame_Shift_Ins	INS	-	T	8	584	c.6360_6361insA	c.(6358-6363)AAAGAAfs	p.K2120fs
Pat_16	Pre-Treatment	CNKSR2	22866	37	X	21627678	21627680	In_Frame_Del	DEL	GAG	-	7	130	.2635_2637delGA	c.(2635-2637)GAGdel	p.E886del
Pat_16	Pre-Treatment	HTATSF1	27336	37	X	135585048	135585050	In_Frame_Del	DEL	AAG	-	15	305	c.682_684delAAG	c.(682-684)AAGdel	p.K232del
Pat_21	Post-Resistance	FRAS1	80144	37	4	78979223	78979223	Frame_Shift_Del	DEL	G	-	10	364	c.60delG	c.(58-60)TTGfs	p.L20fs
Pat_22	Pre-Treatment	GRRP1	79927	37	1	26487798	26487798	Frame_Shift_Del	DEL	C	-	2	4	c.16delC	c.(16-18)CCCfs	p.P6fs
Pat_22	Pre-Treatment	SASS6	163786	37	1	100584675	100584676	Frame_Shift_Ins	INS	-	T	2	4	c.567_568insA	c.(565-570)AAACAAfs	p.K189fs
Pat_22	Pre-Treatment	TCL6	27004	37	14	96136897	96136897	Frame_Shift_Del	DEL	G	-	2	4	c.377delG	c.(376-378)TGGfs	p.W126fs
Pat_22	Pre-Treatment	LINGO1	84894	37	15	77908217	77908217	Frame_Shift_Del	DEL	C	-	2	4	c.32delG	c.(31-33)GGCfs	p.G11fs
Pat_22	Pre-Treatment	ICAM4	3386	37	19	10397719	10397719	Frame_Shift_Del	DEL	T	-	3	4	c.31delT	c.(31-33)TTTfs	p.F11fs
Pat_22	Pre-Treatment	CNOT3	4849	37	19	54649671	54649671	Frame_Shift_Del	DEL	T	-	10	125	c.729delT	c.(727-729)CCCfs	p.P243fs
Pat_22	Pre-Treatment	NLRP13	126204	37	19	56424279	56424279	Frame_Shift_Del	DEL	G	-	2	4	c.904delC	c.(904-906)CAAfs	p.Q302fs
Pat_22	Pre-Treatment	KRTAP10-7	386675	37	21	46021199	46021200	Frame_Shift_Ins	INS	-	T	47	174	c.663_664insT	c.(661-666)TCCTCCfs	p.S221fs
Pat_22	Pre-Treatment	GARS	2617	37	7	30634677	30634679	In_Frame_Del	DEL	CCG	-	4	7	c.140_142delCCG	.(139-144)CCCGCC>CCC	p.A50del
Pat_22	Pre-Treatment	PCLO	27445	37	7	82763982	82763982	Frame_Shift_Del	DEL	C	-	2	4	c.2884delG	c.(2884-2886)GCCfs	p.A962fs
Pat_22	Pre-Treatment	NCBP1	4686	37	9	100410326	100410326	Frame_Shift_Del	DEL	A	-	2	4	c.718delA	c.(718-720)AAAfs	p.K240fs
Pat_22	Pre-Treatment	FGD1	2245	37	X	54472756	54472756	Frame_Shift_Del	DEL	T	-	2	4	c.2672delA	c.(2671-2673)AAGfs	p.K891fs
Pat_22	Pre-Treatment	MAP7D3	79649	37	X	135314194	135314194	Frame_Shift_Del	DEL	G	-	8	236	c.922delC	c.(922-924)CAGfs	p.Q308fs
Pat_22	Post-Resistance	CLSTN1	22883	37	1	9790640	9790642	In_Frame_Del	DEL	CCT	-	7	145	.2870_2872delAG	(2869-2874)GAGGGG>GG	p.E957del
Pat_22	Post-Resistance	SPEN	23013	37	1	16203144	16203146	In_Frame_Del	DEL	CAG	-	8	807	c.852_854delCAG	c.(850-855)ATCAGC>ATC	p.S289del
Pat_22	Post-Resistance	TYW3	127253	37	1	75229742	75229744	In_Frame_Del	DEL	ATG	-	7	263	c.725_727delATG	c.(724-729)AATGAT>AAT	p.D247del
Pat_22	Post-Resistance	ARHGAP29	9411	37	1	94639896	94639896	Frame_Shift_Del	DEL	T	-	9	695	c.3315delA	c.(3313-3315)AAAfs	p.K1105fs

Pat_22	Post-Resistance	BCL9	607	37	1	147092681	147092681	Frame_Shift_Del	DEL	C	-	12	1437	c.2720delC	c.(2719-2721)TCCfs	p.S907fs
Pat_22	Post-Resistance	ARNT	405	37	1	150789283	150789283	Frame_Shift_Del	DEL	G	-	10	558	c.1783delC	c.(1783-1785)CGGfs	p.R595fs
Pat_22	Post-Resistance	TCHH	7062	37	1	152082957	152082959	In_Frame_Del	DEL	CTC	-	13	348	.2734_2736delGA	c.(2734-2736)GAGdel	p.E912del
Pat_22	Post-Resistance	HRNR	388697	37	1	152186039	152186040	Frame_Shift_Del	DEL	CC	-	9	377	.8065_8066delG	c.(8065-8067)GGTfs	p.G2689fs
Pat_22	Post-Resistance	SLC27A3	11000	37	1	153751860	153751860	Frame_Shift_Del	DEL	C	-	9	685	c.1927delC	c.(1927-1929)CCCfs	p.P643fs
Pat_22	Post-Resistance	TDRD10	126668	37	1	154493908	154493908	Frame_Shift_Del	DEL	C	-	7	971	c.322delC	c.(322-324)CCCfs	p.P108fs
Pat_22	Post-Resistance	F5	2153	37	1	169510711	169510712	Frame_Shift_Del	DEL	GG	-	9	1135	.3616_3617delC	c.(3616-3618)CCAfs	p.P1206fs
Pat_22	Post-Resistance	PLA2G4A	5321	37	1	186925445	186925447	In_Frame_Del	DEL	TGA	-	9	1387	.1548_1550delTG	.(1546-1551)TTTGAT>TT	p.D519del
Pat_22	Post-Resistance	PTPN14	5784	37	1	214557049	214557051	In_Frame_Del	DEL	CCT	-	13	198	.2147_2149delAG	(2146-2151)GAGGCT>GC	p.E716del
Pat_22	Post-Resistance	MTR	4548	37	1	237024474	237024474	Frame_Shift_Del	DEL	A	-	8	125	c.2093delA	c.(2092-2094)CAAfs	p.Q698fs
Pat_22	Post-Resistance	PARD3	56288	37	10	34671501	34671501	Frame_Shift_Del	DEL	T	-	8	420	c.1366delA	c.(1366-1368)ATAfs	p.I456fs
Pat_22	Post-Resistance	ARID5B	84159	37	10	63852298	63852298	Frame_Shift_Del	DEL	A	-	7	369	c.3076delA	c.(3076-3078)AAAfs	p.K1026fs
Pat_22	Post-Resistance	FGFR2	2263	37	10	123239466	123239466	Frame_Shift_Del	DEL	A	-	42	141	c.2371delT	c.(2371-2373)TCTfs	p.S791fs
Pat_22	Post-Resistance	DNHD1	144132	37	11	6578614	6578616	In_Frame_Del	DEL	GAG	-	8	35	.8089_8091delGA	c.(8089-8091)GAGdel	p.E2703del
Pat_22	Post-Resistance	OR10A2	341276	37	11	6891253	6891255	In_Frame_Del	DEL	TTC	-	9	361	c.268_270delTTC	c.(268-270)TTCdel	p.F94del
Pat_22	Post-Resistance	PAMR1	25891	37	11	35513670	35513670	Frame_Shift_Del	DEL	C	-	9	1687	c.302delG	c.(301-303)GGTfs	p.G101fs
Pat_22	Post-Resistance	LRP4	4038	37	11	46880748	46880748	Frame_Shift_Del	DEL	C	-	7	341	c.5504delG	c.(5503-5505)GGCfs	p.G1835fs
Pat_22	Post-Resistance	MYBPC3	4607	37	11	47359101	47359103	In_Frame_Del	DEL	TCT	-	7	201	.2441_2443delAG	(2440-2445)AAGAGC>AG	p.K814del
Pat_22	Post-Resistance	NEU3	10825	37	11	74705655	74705655	Frame_Shift_Del	DEL	C	-	7	1449	c.196delC	c.(196-198)CCCfs	p.P66fs
Pat_22	Post-Resistance	TSKU	25987	37	11	76506673	76506675	In_Frame_Del	DEL	CTG	-	13	231	c.13_15delCTG	c.(13-15)CTGdel	p.L9del
Pat_22	Post-Resistance	DDX10	1662	37	11	108788635	108788637	In_Frame_Del	DEL	TGA	-	10	91	.2340_2342delTG	(2338-2343)AGTGAT>AG	p.D788del
Pat_22	Post-Resistance	CHD4	1108	37	12	6711546	6711546	Frame_Shift_Del	DEL	T	-	7	633	c.218delA	c.(217-219)AAGfs	p.K73fs
Pat_22	Post-Resistance	PRB1	5542	37	12	11506632	11506633	In_Frame_Ins	INS	-	GGA	14	887	c.404_405insTCC	c.(403-405)CCA>CCTCCA	.135_135P>P
Pat_22	Post-Resistance	ITGA7	3679	37	12	56092271	56092271	Frame_Shift_Del	DEL	C	-	9	406	c.1100delG	c.(1099-1101)GGTfs	p.G367fs
Pat_22	Post-Resistance	ATXN2	6311	37	12	111893853	111893853	Frame_Shift_Del	DEL	G	-	7	887	c.3724delC	c.(3724-3726)CACfs	p.H1242fs
Pat_22	Post-Resistance	VPS33A	65082	37	12	122748169	122748169	Frame_Shift_Del	DEL	A	-	7	126	c.246delT	c.(244-246)TTTfs	p.F82fs
Pat_22	Post-Resistance	SFRS8	6433	37	12	132281734	132281736	In_Frame_Del	DEL	AGA	-	10	546	.2546_2548delAG	(2545-2550)GAGAAG>GA	p.K853del
Pat_22	Post-Resistance	RXFP2	122042	37	13	32376429	32376429	Frame_Shift_Del	DEL	A	-	15	202	c.2152delA	c.(2152-2154)AAAfs	p.K718fs
Pat_22	Post-Resistance	C13orf34	79866	37	13	73320117	73320117	Frame_Shift_Del	DEL	A	-	8	401	c.774delA	c.(772-774)GCAfs	p.A258fs
Pat_22	Post-Resistance	NIN	51199	37	14	51288635	51288635	Frame_Shift_Del	DEL	G	-	7	1728	c.140delC	c.(139-141)CCAfs	p.P47fs
Pat_22	Post-Resistance	C14orf115	55237	37	14	74824463	74824463	Frame_Shift_Del	DEL	G	-	8	477	c.977delG	c.(976-978)CGGfs	p.R326fs
Pat_22	Post-Resistance	VPS13C	54832	37	15	62270851	62270851	Frame_Shift_Del	DEL	T	-	7	376	c.2264delA	c.(2263-2265)AATfs	p.N755fs
Pat_22	Post-Resistance	MPG	4350	37	16	133163	133163	Frame_Shift_Del	DEL	C	-	7	735	c.428delC	c.(427-429)ACCfs	p.T143fs
Pat_22	Post-Resistance	EME2	197342	37	16	1824298	1824300	In_Frame_Del	DEL	TGC	-	7	327	c.422_424delTGC	c.(421-426)TTGCTG>TTG	.141_142LL>
Pat_22	Post-Resistance	C16orf88	400506	37	16	19725705	19725706	Frame_Shift_Ins	INS	-	T	8	90	c.652_653insA	c.(652-654)ATCfs	p.I218fs
Pat_22	Post-Resistance	ATP2A1	487	37	16	28913640	28913640	Frame_Shift_Del	DEL	C	-	12	404	c.2457delC	c.(2455-2457)CGCfs	p.R819fs
Pat_22	Post-Resistance	ITGAL	3683	37	16	30531249	30531251	In_Frame_Del	DEL	GCT	-	7	928	.3300_3302delGC	(3298-3303)GGGCTG>GG	p.L1106del
Pat_22	Post-Resistance	IRF8	3394	37	16	85936681	85936681	Frame_Shift_Del	DEL	T	-	8	876	c.60delT	c.(58-60)AGTfs	p.S20fs
Pat_22	Post-Resistance	SMCR7	125170	37	17	18167868	18167868	Frame_Shift_Del	DEL	G	-	9	760	c.1155delG	c.(1153-1155)CTGfs	p.L385fs
Pat_22	Post-Resistance	GAS2L2	246176	37	17	34071994	34071996	In_Frame_Del	DEL	TCC	-	9	137	.2520_2522delGG	(2518-2523)GAGGAA>GA	.840_841EE>
Pat_22	Post-Resistance	TNS4	84951	37	17	38643307	38643307	Frame_Shift_Del	DEL	G	-	8	2643	c.1269delC	c.(1267-1269)CCCfs	p.P423fs
Pat_22	Post-Resistance	OTOP2	92736	37	17	72926595	72926595	Frame_Shift_Del	DEL	T	-	9	288	c.865delT	c.(865-867)TTTfs	p.F289fs
Pat_22	Post-Resistance	FN3K	64122	37	17	80708466	80708466	Frame_Shift_Del	DEL	C	-	7	697	c.765delC	c.(763-765)TTCfs	p.F255fs
Pat_22	Post-Resistance	STXBP2	6813	37	19	7706923	7706923	Frame_Shift_Del	DEL	C	-	8	1090	c.582delC	c.(580-582)GGCfs	p.G194fs
Pat_22	Post-Resistance	CD209	30835	37	19	7807935	7807935	Frame_Shift_Del	DEL	G	-	7	260	c.1205delC	c.(1204-1206)CCTfs	p.P402fs
Pat_22	Post-Resistance	TRMT1	55621	37	19	13226516	13226516	Frame_Shift_Del	DEL	T	-	7	1045	c.377delA	c.(376-378)AAGfs	p.K126fs
Pat_22	Post-Resistance	SIGLEC8	27181	37	19	51961617	51961619	In_Frame_Del	DEL	GCA	-	7	357	c.23_25delTGC	c.(22-27)CTGCCC>CCC	p.L8del

Pat_22	Post-Resistance	ZNF552	79818	37	19	58319468	58319468	Frame_Shift_Del	DEL	T	-	7	539	c.1164delA	c.(1162-1164)AAAfs	p.K388fs
Pat_22	Post-Resistance	C2orf71	388939	37	2	29295647	29295649	In_Frame_Del	DEL	TCC	-	8	550	.1479_1481delGG	(1477-1482)GAGGAA>GA	.493_494EE>I
Pat_22	Post-Resistance	GCC2	9648	37	2	109087883	109087884	Frame_Shift_Ins	INS	-	A	8	701	c.2098_2099insA	c.(2098-2100)GAAfs	p.E700fs
Pat_22	Post-Resistance	AMMECR1L	83607	37	2	128627077	128627077	Frame_Shift_Del	DEL	T	-	8	459	c.675delA	c.(673-675)AAAfs	p.K225fs
Pat_22	Post-Resistance	CIR1	9541	37	2	175260285	175260286	Frame_Shift_Del	DEL	GA	-	9	754	c.65_66delTC	c.(64-66)ATCfs	p.I22fs
Pat_22	Post-Resistance	DNAH7	56171	37	2	196788374	196788374	Frame_Shift_Del	DEL	T	-	7	216	c.3770delA	c.(3769-3771)AATfs	p.N1257fs
Pat_22	Post-Resistance	IGFBP2	3485	37	2	217498290	217498291	Splice_Site	INS	-	CCGCTGC	6	5	c.14_splice	c.e1+1	p.P5_splice
Pat_22	Post-Resistance	CD93	22918	37	20	23065992	23065992	Frame_Shift_Del	DEL	C	-	7	766	c.838delG	c.(838-840)GATfs	p.D280fs
Pat_22	Post-Resistance	TMEM90B	79953	37	20	24524183	24524185	In_Frame_Del	DEL	GGA	-	10	663	c.450_452delGGA	.(448-453)GTGGAG>GTG	p.E155del
Pat_22	Post-Resistance	SPINLW1	57119	37	20	44174297	44174297	Frame_Shift_Del	DEL	T	-	7	1164	c.204delA	c.(202-204)AAAfs	p.K68fs
Pat_22	Post-Resistance	C20orf85	128602	37	20	56735727	56735727	Frame_Shift_Del	DEL	C	-	7	237	c.263delC	c.(262-264)TCCfs	p.S88fs
Pat_22	Post-Resistance	SYCP2	10388	37	20	58467046	58467047	Frame_Shift_Ins	INS	-	T	8	144	c.2362_2363insA	c.(2362-2364)ATGfs	p.M788fs
Pat_22	Post-Resistance	CDH4	1002	37	20	60485488	60485498	Frame_Shift_Del	DEL	GGTCCCCG	-	17	136	_1209delAGGTCC	98-1209)GAGGTCCCCG	p.E400fs
Pat_22	Post-Resistance	IFNGR2	3460	37	21	34799292	34799292	Frame_Shift_Del	DEL	T	-	7	990	c.514delT	c.(514-516)TTTfs	p.F172fs
Pat_22	Post-Resistance	KRTAP10-7	386675	37	21	46021199	46021200	Frame_Shift_Ins	INS	-	T	132	519	c.663_664insT	c.(661-666)TCCTCCfs	p.S221fs
Pat_22	Post-Resistance	DIP2A	23181	37	21	47987309	47987311	In_Frame_Del	DEL	TGG	-	8	561	.4490_4492delTG	(4489-4494)CTGGTG>CT	p.V1501del
Pat_22	Post-Resistance	ARVCF	421	37	22	19969169	19969169	Frame_Shift_Del	DEL	G	-	7	340	c.461delC	c.(460-462)CCAfs	p.P154fs
Pat_22	Post-Resistance	PICK1	9463	37	22	38471034	38471036	In_Frame_Del	DEL	GGA	-	7	222	.1143_1145delGG	(1141-1146)GGGGAG>GG	p.E388del
Pat_22	Post-Resistance	BIK	638	37	22	43525245	43525247	In_Frame_Del	DEL	GCT	-	12	399	c.417_419delGCT	.(415-420)GCGCTG>GCG	p.L144del
Pat_22	Post-Resistance	SCUBE1	80274	37	22	43619184	43619184	Frame_Shift_Del	DEL	G	-	8	1135	c.1246delC	c.(1246-1248)CGGfs	p.R416fs
Pat_22	Post-Resistance	NKTR	4820	37	3	42679035	42679036	Frame_Shift_Ins	INS	-	C	13	1170	c.1839_1840insC	c.(1837-1842)AGTCCCfs	p.S613fs
Pat_22	Post-Resistance	ATP13A3	79572	37	3	194147850	194147850	Frame_Shift_Del	DEL	A	-	10	288	c.3079delT	c.(3079-3081)TGGfs	p.W1027fs
Pat_22	Post-Resistance	RNF168	165918	37	3	196214338	196214338	Frame_Shift_Del	DEL	T	-	9	931	c.490delA	c.(490-492)AGGfs	p.R164fs
Pat_22	Post-Resistance	OTOP1	133060	37	4	4228274	4228282	In_Frame_Del	DEL	CCACAGCAC	-	7	49	_318delCTGCTG	.(310-318)CTGCTGTGGde	p.LLW104del
Pat_22	Post-Resistance	CCDC158	339965	37	4	77305357	77305357	Frame_Shift_Del	DEL	T	-	8	267	c.610delA	c.(610-612)ATAfs	p.I204fs
Pat_22	Post-Resistance	PCDH10	57575	37	4	134073569	134073571	In_Frame_Del	DEL	CTG	-	7	98	.2274_2276delCT	.(2272-2277)CTCTGC>CT	p.C763del
Pat_22	Post-Resistance	LRAT	9227	37	4	155670198	155670198	Frame_Shift_Del	DEL	G	-	7	334	c.603delG	c.(601-603)TTGfs	p.L201fs
Pat_22	Post-Resistance	TLL1	7092	37	4	166964485	166964485	Frame_Shift_Del	DEL	G	-	8	741	c.1438delG	c.(1438-1440)GATfs	p.D480fs
Pat_22	Post-Resistance	NNT	23530	37	5	43704415	43704416	Frame_Shift_Del	DEL	TC	-	7	461	c.3170_3171delTC	c.(3169-3171)TTCfs	p.F1057fs
Pat_22	Post-Resistance	RGNEF	64283	37	5	73072464	73072464	Frame_Shift_Del	DEL	G	-	7	1260	c.783delG	c.(781-783)TTGfs	p.L261fs
Pat_22	Post-Resistance	SSBP2	23635	37	5	80809493	80809493	Frame_Shift_Del	DEL	G	-	8	654	c.326delC	c.(325-327)CCAfs	p.P109fs
Pat_22	Post-Resistance	KCNN2	3781	37	5	113698631	113698632	In_Frame_Ins	INS	-	GCC	8	23	c.159_160insGCC	c.(157-162)insGCC	p.58_59insA
Pat_22	Post-Resistance	LMNB1	4001	37	5	126154700	126154701	Frame_Shift_Del	DEL	AG	-	8	434	c.1026_1027delAG	c.(1024-1029)AAAGAGfs	p.K342fs
Pat_22	Post-Resistance	TNXB	7148	37	6	32037508	32037508	Frame_Shift_Del	DEL	A	-	18	75	c.5409delT	c.(5407-5409)TTTfs	p.F1803fs
Pat_22	Post-Resistance	TNXB	7148	37	6	32063945	32063945	Frame_Shift_Del	DEL	C	-	4	7	c.1685delG	c.(1684-1686)GGCfs	p.G562fs
Pat_22	Post-Resistance	PHF1	5252	37	6	33380050	33380050	Frame_Shift_Del	DEL	C	-	7	241	c.10delC	c.(10-12)CCCfs	p.P4fs
Pat_22	Post-Resistance	DNAH8	1769	37	6	38749053	38749053	Frame_Shift_Del	DEL	C	-	7	655	c.1512delC	c.(1510-1512)GACfs	p.D504fs
Pat_22	Post-Resistance	ZNF318	24149	37	6	43323502	43323502	Frame_Shift_Del	DEL	T	-	8	1407	c.1570delA	c.(1570-1572)AGGfs	p.R524fs
Pat_22	Post-Resistance	MYO6	4646	37	6	76599857	76599858	Frame_Shift_Ins	INS	-	A	14	152	c.2742_2743insA	c.(2740-2745)CAGAAAfs	p.Q914fs
Pat_22	Post-Resistance	GABRR1	2569	37	6	89891719	89891721	In_Frame_Del	DEL	AAG	-	7	333	c.852_854delCTT	c.(850-855)TTCTTG>TTG	p.F284del
Pat_22	Post-Resistance	GLCCI1	113263	37	7	8008992	8008994	In_Frame_Del	DEL	CCT	-	8	83	c.11_13delCCT	c.(10-15)GCCTCC>GCC	p.S13del
Pat_22	Post-Resistance	DTX2	113878	37	7	76112249	76112249	Frame_Shift_Del	DEL	A	-	10	1428	c.693delA	c.(691-693)CCAfs	p.P231fs
Pat_22	Post-Resistance	PTCD1	26024	37	7	99032605	99032607	In_Frame_Del	DEL	CTC	-	10	387	c.259_261delGAG	c.(259-261)GAGdel	p.E87del
Pat_22	Post-Resistance	LUC7L2	51631	37	7	139094365	139094366	Frame_Shift_Del	DEL	AG	-	8	121	c.744_745delAG	c.(742-747)GAAGAGfs	p.E248fs
Pat_22	Post-Resistance	HIPK2	28996	37	7	139416310	139416310	Frame_Shift_Del	DEL	T	-	8	761	c.524delA	c.(523-525)AACfs	p.N175fs
Pat_22	Post-Resistance	SSPO	23145	37	7	149474083	149474083	Frame_Shift_Del	DEL	G	-	8	455	c.293delG	c.(292-294)TGGfs	p.W98fs
Pat_22	Post-Resistance	PRKDC	5591	37	8	48746799	48746799	Frame_Shift_Del	DEL	T	-	13	821	c.8110delA	c.(8110-8112)AGGfs	p.R2704fs

Pat_22	Post-Resistance	STAU2	27067	37	8	74507471	74507471	Frame_Shift_Del	DEL	T	-	10	339	c.1091delA	c.(1090-1092)AATfs	p.N364fs
Pat_22	Post-Resistance	ESRP1	54845	37	8	95686610	95686611	Frame_Shift_Ins	INS	-	A	8	380	c.1527_1528insA	c.(1525-1530)CATAAAfs	p.H509fs
Pat_22	Post-Resistance	KANK1	23189	37	9	712491	712491	Frame_Shift_Del	DEL	G	-	9	758	c.1725delG	c.(1723-1725)GTGfs	p.V575fs
Pat_22	Post-Resistance	CLIC3	9022	37	9	139889553	139889553	Frame_Shift_Del	DEL	C	-	2	4	c.381delG	c.(379-381)CTGfs	p.L127fs
Pat_22	Post-Resistance	PRKX	5613	37	X	3539313	3539314	Frame_Shift_Del	DEL	AA	-	8	197	c.859_860delTT	c.(859-861)TTAfs	p.L287fs
Pat_22	Post-Resistance	MSL3	10943	37	X	11790307	11790307	Frame_Shift_Del	DEL	C	-	7	938	c.1314delC	c.(1312-1314)TACfs	p.Y438fs
Pat_22	Post-Resistance	FAM47C	442444	37	X	37027594	37027594	Frame_Shift_Del	DEL	C	-	8	477	c.1111delC	c.(1111-1113)CCCfs	p.P371fs
Pat_22	Post-Resistance	BTK	695	37	X	100611894	100611894	Frame_Shift_Del	DEL	C	-	7	1650	c.1227delG	c.(1225-1227)GGGfs	p.G409fs
Pat_22	Post-Resistance	TEX13A	56157	37	X	104463676	104463676	Frame_Shift_Del	DEL	C	-	8	1241	c.1200delG	c.(1198-1200)GGGfs	p.G400fs
Pat_22	Post-Resistance	MAP7D3	79649	37	X	135314194	135314194	Frame_Shift_Del	DEL	G	-	7	980	c.922delC	c.(922-924)CAGfs	p.Q308fs
Pat_22	Post-Resistance	HTATSF1	27336	37	X	135585048	135585050	In_Frame_Del	DEL	AAG	-	7	436	c.682_684delAAG	c.(682-684)AAGdel	p.K232del
Pat_22	Post-Resistance	MAGEC1	9947	37	X	140995035	140995037	In_Frame_Del	DEL	TCT	-	10	661	.1845_1847delTC	.(1843-1848)CCTCTT>CC	p.L616del
Pat_22	Post-Resistance	SPANXN3	139067	37	X	142605149	142605149	Frame_Shift_Del	DEL	T	-	13	382	c.71delA	c.(70-72)AATfs	p.N24fs
Pat_24	Pre-Treatment	TP73	7161	37	1	3645986	3645988	In_Frame_Del	DEL	GCA	-	7	135	.1170_1172delGC	(1168-1173)CGGCAG>CG	p.Q394del
Pat_24	Pre-Treatment	ERRFI1	54206	37	1	8073804	8073804	Frame_Shift_Del	DEL	G	-	7	311	c.855delC	c.(853-855)CCCfs	p.P285fs
Pat_24	Pre-Treatment	EIF4G3	8672	37	1	21177856	21177856	Frame_Shift_Del	DEL	C	-	8	380	c.3499delG	c.(3499-3501)GAAfs	p.E1167fs
Pat_24	Pre-Treatment	ZBTB40	9923	37	1	22838561	22838563	In_Frame_Del	DEL	AAG	-	11	176	.2395_2397delAA	c.(2395-2397)AAGdel	p.K803del
Pat_24	Pre-Treatment	HTR1D	3352	37	1	23520195	23520195	Frame_Shift_Del	DEL	G	-	8	270	c.518delC	c.(517-519)CCGfs	p.P173fs
Pat_24	Pre-Treatment	RPS6KA1	6195	37	1	26873740	26873741	Frame_Shift_Del	DEL	CT	-	7	158	c.286_287delCT	c.(286-288)CTGfs	p.L96fs
Pat_24	Pre-Treatment	ZSCAN20	7579	37	1	33959126	33959126	Frame_Shift_Del	DEL	C	-	8	565	c.1784delC	c.(1783-1785)GCTfs	p.A595fs
Pat_24	Pre-Treatment	PIAS3	10401	37	1	145579285	145579285	Frame_Shift_Del	DEL	C	-	7	1183	c.622delC	c.(622-624)CCCfs	p.P208fs
Pat_24	Pre-Treatment	MCL1	4170	37	1	150551952	150551952	Frame_Shift_Del	DEL	C	-	7	166	c.55delG	c.(55-57)GCCfs	p.A19fs
Pat_24	Pre-Treatment	TCHH	7062	37	1	152084580	152084582	In_Frame_Del	DEL	CTC	-	9	221	.1111_1113delGA	c.(1111-1113)GAGdel	p.E371del
Pat_24	Pre-Treatment	FLG	2312	37	1	152275760	152275761	Frame_Shift_Del	DEL	CA	-	8	723	.11601_11602delT	.(11599-11604)AGTGACfs	p.S3867fs
Pat_24	Pre-Treatment	UBAP2L	9898	37	1	154224054	154224054	Frame_Shift_Del	DEL	C	-	7	538	c.1589delC	c.(1588-1590)TCTfs	p.S530fs
Pat_24	Pre-Treatment	CCT3	7203	37	1	156290648	156290648	Frame_Shift_Del	DEL	T	-	7	731	c.591delA	c.(589-591)AAAfs	p.K197fs
Pat_24	Pre-Treatment	FCRL5	83416	37	1	157491062	157491062	Frame_Shift_Del	DEL	G	-	9	242	c.2260delC	c.(2260-2262)CTCfs	p.L754fs
Pat_24	Pre-Treatment	CCDC19	25790	37	1	159854336	159854336	Frame_Shift_Del	DEL	C	-	8	941	c.787delG	c.(787-789)GAAfs	p.E263fs
Pat_24	Pre-Treatment	TEDDM1	127670	37	1	182369245	182369245	Frame_Shift_Del	DEL	C	-	7	635	c.376delG	c.(376-378)GAGfs	p.E126fs
Pat_24	Pre-Treatment	HMCN1	83872	37	1	185958660	185958660	Frame_Shift_Del	DEL	C	-	8	443	c.3089delC	c.(3088-3090)GCAfs	p.A1030fs
Pat_24	Pre-Treatment	CD55	1604	37	1	207510731	207510732	Frame_Shift_Del	DEL	AT	-	7	359	c.1037_1038delAT	c.(1036-1038)AATfs	p.N346fs
Pat_24	Pre-Treatment	ITPKB	3707	37	1	226836425	226836425	Frame_Shift_Del	DEL	G	-	7	674	c.1980delC	c.(1978-1980)TTCfs	p.F660fs
Pat_24	Pre-Treatment	TTC13	79573	37	1	231067586	231067586	Frame_Shift_Del	DEL	G	-	7	427	c.1021delC	c.(1021-1023)CAAfs	p.Q341fs
Pat_24	Pre-Treatment	TTC13	79573	37	1	231114543	231114545	In_Frame_Del	DEL	AGC	-	5	6	c.32_34delGCT	c.(31-36)TGCTTC>TTC	p.C11del
Pat_24	Pre-Treatment	RPP38	10557	37	10	15146145	15146145	Frame_Shift_Del	DEL	A	-	7	80	c.832delA	c.(832-834)AAAfs	p.K278fs
Pat_24	Pre-Treatment	TRIM8	81603	37	10	104416541	104416541	Frame_Shift_Del	DEL	C	-	8	690	c.1086delC	c.(1084-1086)GTCfs	p.V362fs
Pat_24	Pre-Treatment	SLK	9748	37	10	105767938	105767938	Frame_Shift_Del	DEL	A	-	8	579	c.2608delA	c.(2608-2610)AAAfs	p.K870fs
Pat_24	Pre-Treatment	APBB1	322	37	11	6422218	6422218	Splice_Site	DEL	C	-	7	1006	c.1672_splice	c.e11+1	p.G558_splice
Pat_24	Pre-Treatment	PLEKHA7	144100	37	11	16822574	16822574	Frame_Shift_Del	DEL	C	-	8	669	c.2356delG	c.(2356-2358)GAAfs	p.E786fs
Pat_24	Pre-Treatment	TMEM132A	54972	37	11	60695118	60695118	Frame_Shift_Del	DEL	C	-	7	857	c.321delC	c.(319-321)GTCfs	p.V107fs
Pat_24	Pre-Treatment	AHNAK	79026	37	11	62296087	62296087	Frame_Shift_Del	DEL	G	-	8	1049	c.5802delC	c.(5800-5802)CCCfs	p.P1934fs
Pat_24	Pre-Treatment	MRGPRF	116535	37	11	68772804	68772804	Frame_Shift_Del	DEL	C	-	4	4	c.974delG	c.(973-975)GGCfs	p.G325fs
Pat_24	Pre-Treatment	CHRDL2	25884	37	11	74413900	74413901	Frame_Shift_Del	DEL	GC	-	7	359	c.1058_1059delGC	c.(1057-1059)CGCfs	p.R353fs
Pat_24	Pre-Treatment	DYNC2H1	79659	37	11	103124106	103124106	Frame_Shift_Del	DEL	A	-	7	255	c.10135delA	c.(10135-10137)ATTfs	p.I3379fs
Pat_24	Pre-Treatment	TREH	11181	37	11	118529635	118529635	Frame_Shift_Del	DEL	C	-	14	637	c.1524delG	c.(1522-1524)CAGfs	p.Q508fs
Pat_24	Pre-Treatment	UBASH3B	84959	37	11	122659833	122659833	Frame_Shift_Del	DEL	C	-	8	874	c.797delC	c.(796-798)ACCfs	p.T266fs
Pat_24	Pre-Treatment	PARP11	57097	37	12	3935352	3935352	Frame_Shift_Del	DEL	T	-	9	341	c.295delA	c.(295-297)AGAfs	p.R99fs

Pat_24	Pre-Treatment	DYRK4	8798	37	12	4719362	4719362	Frame_Shift_Del	DEL	A	-	9	112	c.1057delA	c.(1057-1059)AAAfs	p.K353fs
Pat_24	Pre-Treatment	LRRC23	10233	37	12	7014818	7014819	Frame_Shift_Del	DEL	AG	-	7	257	c.21_22delAG	c.(19-24)CTAGAAfs	p.L7fs
Pat_24	Pre-Treatment	ETV6	2120	37	12	12022502	12022502	Frame_Shift_Del	DEL	C	-	9	997	c.608delC	c.(607-609)TCCfs	p.S203fs
Pat_24	Pre-Treatment	PPFIBP1	8496	37	12	27829484	27829485	Frame_Shift_Del	DEL	TT	-	7	260	c.1585_1586delTT	c.(1585-1587)TTTfs	p.F529fs
Pat_24	Pre-Treatment	SMARCC2	6601	37	12	56575490	56575490	Frame_Shift_Del	DEL	C	-	8	711	c.838delG	c.(838-840)GAGfs	p.E280fs
Pat_24	Pre-Treatment	STAT2	6773	37	12	56750268	56750270	In_Frame_Del	DEL	CCA	-	8	276	c.86_88delTGG	c.(85-90)GTGGAC>GAC	p.V29del
Pat_24	Pre-Treatment	PPTC7	160760	37	12	111020740	111020742	In_Frame_Del	DEL	CGC	-	8	4	c.95_97delGCG	c.(94-99)GGCGAC>GAC	p.G32del
Pat_24	Pre-Treatment	NAA25	80018	37	12	112481653	112481654	Frame_Shift_Del	DEL	TA	-	8	127	c.2025_2026delTA	c.(2023-2028)CATAAGfs	p.H675fs
Pat_24	Pre-Treatment	COQ5	84274	37	12	120954405	120954406	Frame_Shift_Del	DEL	CC	-	7	1364	c.538_539delGG	c.(538-540)GGAfs	p.G180fs
Pat_24	Pre-Treatment	P2RX7	5027	37	12	121598747	121598747	Frame_Shift_Del	DEL	A	-	7	842	c.406delA	c.(406-408)AAAfs	p.K136fs
Pat_24	Pre-Treatment	CDK2AP1	8099	37	12	123746312	123746312	Frame_Shift_Del	DEL	C	-	10	783	c.319delG	c.(319-321)GCAfs	p.A107fs
Pat_24	Pre-Treatment	ZNF664	144348	37	12	124497356	124497357	Frame_Shift_Ins	INS	-	AA	10	585	c.665_666insAA	c.(664-666)ACAfs	p.T222fs
Pat_24	Pre-Treatment	IL25	64806	37	14	23845057	23845058	Frame_Shift_Del	DEL	TG	-	7	390	c.502_503delTG	c.(502-504)TGTfs	p.C168fs
Pat_24	Pre-Treatment	ZFP36L1	677	37	14	69259613	69259613	Frame_Shift_Del	DEL	C	-	8	956	c.43delG	c.(43-45)GAAfs	p.E15fs
Pat_24	Pre-Treatment	PAPLN	89932	37	14	73731388	73731388	Frame_Shift_Del	DEL	G	-	8	454	c.3079delG	c.(3079-3081)GGGfs	p.G1027fs
Pat_24	Pre-Treatment	NEK9	91754	37	14	75580056	75580057	Frame_Shift_Del	DEL	GA	-	7	394	c.923_924delTC	c.(922-924)CTCfs	p.L308fs
Pat_24	Pre-Treatment	BAG5	9529	37	14	104026871	104026871	Frame_Shift_Del	DEL	C	-	8	410	c.631delG	c.(631-633)GAGfs	p.E211fs
Pat_24	Pre-Treatment	C15orf55	256646	37	15	34647879	34647880	Frame_Shift_Del	DEL	CA	-	8	311	c.1586_1587delCA	c.(1585-1587)TCAfs	p.S529fs
Pat_24	Pre-Treatment	WDR72	256764	37	15	53992038	53992038	Frame_Shift_Del	DEL	A	-	7	774	c.1674delT	c.(1672-1674)TTTfs	p.F558fs
Pat_24	Pre-Treatment	NAGPA	51172	37	16	5083678	5083679	Frame_Shift_Del	DEL	GC	-	8	93	c.137_138delGC	c.(136-138)CGCfs	p.R46fs
Pat_24	Pre-Treatment	TMC7	79905	37	16	19058466	19058467	Frame_Shift_Del	DEL	GG	-	8	858	c.1635_1636delGC	c.(1633-1638)CTGGGGfs	p.L545fs
Pat_24	Pre-Treatment	KIAA0556	23247	37	16	27786300	27786300	Frame_Shift_Del	DEL	G	-	7	343	c.4344delG	c.(4342-4344)CTGfs	p.L1448fs
Pat_24	Pre-Treatment	ARMC5	79798	37	16	31471010	31471010	Frame_Shift_Del	DEL	G	-	8	73	c.165delG	c.(163-165)GCGfs	p.A55fs
Pat_24	Pre-Treatment	SALL1	6299	37	16	51175949	51175950	Frame_Shift_Del	DEL	TG	-	10	377	c.183_184delCA	c.(181-186)CACAAGfs	p.H61fs
Pat_24	Pre-Treatment	TCF25	22980	37	16	89951019	89951020	Frame_Shift_Ins	INS	-	A	9	161	c.384_385insA	c.(382-387)AAGAAAfs	p.K128fs
Pat_24	Pre-Treatment	PLD2	5338	37	17	4719974	4719974	Frame_Shift_Del	DEL	C	-	8	814	c.1515delC	c.(1513-1515)TTCfs	p.F505fs
Pat_24	Pre-Treatment	SHBG	6462	37	17	7535237	7535237	Frame_Shift_Del	DEL	G	-	8	643	c.756delG	c.(754-756)TTGfs	p.L252fs
Pat_24	Pre-Treatment	DNAH2	146754	37	17	7702024	7702025	Frame_Shift_Del	DEL	TG	-	8	460	c.8547_8548delTG	c.(8545-8550)GATGAAfs	p.D2849fs
Pat_24	Pre-Treatment	MYH8	4626	37	17	10303940	10303941	Frame_Shift_Del	DEL	TG	-	7	585	c.3501_3502delCA	c.(3499-3504)AACAAGfs	p.N1167fs
Pat_24	Pre-Treatment	MYH2	4620	37	17	10433227	10433228	Frame_Shift_Del	DEL	TG	-	2	4	c.2861_2862delCA	c.(2860-2862)TCAfs	p.S954fs
Pat_24	Pre-Treatment	MYH3	4621	37	17	10535988	10535988	Frame_Shift_Del	DEL	C	-	9	577	c.4761delG	c.(4759-4761)CTGfs	p.L1587fs
Pat_24	Pre-Treatment	ALDOC	230	37	17	26900923	26900923	Frame_Shift_Del	DEL	C	-	8	389	c.829delG	c.(829-831)GAAfs	p.E277fs
Pat_24	Pre-Treatment	SEZ6	124925	37	17	27296913	27296914	Frame_Shift_Ins	INS	-	C	8	100	c.915_916insG	c.(913-918)GGGCCTfs	p.G305fs
Pat_24	Pre-Treatment	KRT25	147183	37	17	38906647	38906647	Frame_Shift_Del	DEL	A	-	8	410	c.1160delT	c.(1159-1161)ATAfs	p.I387fs
Pat_24	Pre-Treatment	CNTNAP1	8506	37	17	40843873	40843873	Frame_Shift_Del	DEL	C	-	9	988	c.2394delC	c.(2392-2394)TTCfs	p.F798fs
Pat_24	Pre-Treatment	AARSD1	80755	37	17	41131190	41131190	Frame_Shift_Del	DEL	G	-	8	1339	c.414delC	c.(412-414)ATCfs	p.I138fs
Pat_24	Pre-Treatment	HEXIM2	124790	37	17	43246388	43246388	Frame_Shift_Del	DEL	G	-	9	1707	c.73delG	c.(73-75)GGTfs	p.G25fs
Pat_24	Pre-Treatment	NFE2L1	4779	37	17	46134729	46134729	Frame_Shift_Del	DEL	A	-	8	536	c.837delA	c.(835-837)ATAfs	p.I279fs
Pat_24	Pre-Treatment	MED13	9969	37	17	60112873	60112874	Frame_Shift_Del	DEL	GA	-	8	290	c.566_567delTC	c.(565-567)CTCfs	p.L189fs
Pat_24	Pre-Treatment	UBE2O	63893	37	17	74394955	74394957	In_Frame_Del	DEL	GTT	-	7	869	.1744_1746delAA	c.(1744-1746)AACdel	p.N582del
Pat_24	Pre-Treatment	FASN	2194	37	17	80046409	80046409	Frame_Shift_Del	DEL	G	-	8	85	c.2450delC	c.(2449-2451)CCAfs	p.P817fs
Pat_24	Pre-Treatment	DSG1	1828	37	18	28923960	28923960	Splice_Site	DEL	T	-	7	154	c.1891_splice	c.e13+2	p.G631_splice
Pat_24	Pre-Treatment	ZBTB7C	201501	37	18	45566519	45566519	Frame_Shift_Del	DEL	C	-	7	161	c.960delG	c.(958-960)GGGfs	p.G320fs
Pat_24	Pre-Treatment	SPTBN4	57731	37	19	41076369	41076369	Frame_Shift_Del	DEL	C	-	8	296	c.7054delC	c.(7054-7056)CCCfs	p.P2352fs
Pat_24	Pre-Treatment	HNRNPUL1	11100	37	19	41811694	41811695	Frame_Shift_Ins	INS	-	A	10	443	c.2376_2377insA	c.(2374-2379)TACAACfs	p.Y792fs
Pat_24	Pre-Treatment	CNOT3	4849	37	19	54656711	54656713	In_Frame_Del	DEL	TCT	-	8	1098	.2012_2014delTC	.(2011-2016)CTCTTC>CT	p.F673del
Pat_24	Pre-Treatment	LILRB1	10859	37	19	55146148	55146150	In_Frame_Del	DEL	CTC	-	10	112	.1417_1419delCT	c.(1417-1419)CTCdel	p.L479del

Pat_24	Pre-Treatment	TMEM18	129787	37	2	675512	675513	Frame_Shift_Del	DEL	AG	-	9	401	c.175_176delCT	c.(175-177)CTAfs	p.L59fs
Pat_24	Pre-Treatment	CRIM1	51232	37	2	36668399	36668400	Splice_Site	DEL	AG	-	7	209	c.506_splice	c.e3-1	p.E169_splice
Pat_24	Pre-Treatment	LHCGR	3973	37	2	48914899	48914901	In_Frame_Del	DEL	CTT	-	8	450	.2035_2037delAA	c.(2035-2037)AAGdel	p.K679del
Pat_24	Pre-Treatment	ANKRD57	65124	37	2	110373559	110373559	Frame_Shift_Del	DEL	G	-	7	456	c.1493delG	c.(1492-1494)AGGfs	p.R498fs
Pat_24	Pre-Treatment	GLI2	2736	37	2	121743888	121743888	Frame_Shift_Del	DEL	G	-	7	207	c.1991delG	c.(1990-1992)TGCfs	p.C664fs
Pat_24	Pre-Treatment	GPR155	151556	37	2	175326340	175326341	Frame_Shift_Del	DEL	CC	-	7	425	c.1444_1445delGG	c.(1444-1446)GGAfs	p.G482fs
Pat_24	Pre-Treatment	PDE11A	50940	37	2	178762800	178762801	Frame_Shift_Del	DEL	CT	-	8	453	c.1286_1287delAG	c.(1285-1287)GAGfs	p.E429fs
Pat_24	Pre-Treatment	COL3A1	1281	37	2	189873846	189873846	Frame_Shift_Del	DEL	T	-	121	123	c.3722delT	c.(3721-3723)GTTfs	p.V1241fs
Pat_24	Pre-Treatment	CASP10	843	37	2	202093774	202093774	Frame_Shift_Del	DEL	C	-	10	1024	c.1534delC	c.(1534-1536)CCCfs	p.P512fs
Pat_24	Pre-Treatment	NBEAL1	65065	37	2	204058567	204058567	Frame_Shift_Del	DEL	C	-	7	461	c.6884delC	c.(6883-6885)ACCfs	p.T2295fs
Pat_24	Pre-Treatment	FN1	2335	37	2	216296605	216296606	Frame_Shift_Del	DEL	CT	-	8	671	c.497_498delAG	c.(496-498)GAGfs	p.E166fs
Pat_24	Pre-Treatment	DES	1674	37	2	220283700	220283701	Frame_Shift_Del	DEL	GC	-	3	6	c.516_517delGC	c.(514-519)CAGCGCfs	p.Q172fs
Pat_24	Pre-Treatment	DEFB119	245932	37	20	29965168	29965168	Frame_Shift_Del	DEL	A	-	8	753	c.136delT	c.(136-138)TACfs	p.Y46fs
Pat_24	Pre-Treatment	SUN5	140732	37	20	31571699	31571699	Frame_Shift_Del	DEL	C	-	8	991	c.1041delG	c.(1039-1041)GGGfs	p.G347fs
Pat_24	Pre-Treatment	ZHX3	23051	37	20	39831558	39831559	Frame_Shift_Ins	INS	-	T	7	980	c.1998_1999insA	c.(1996-2001)AAAGTGfs	p.K666fs
Pat_24	Pre-Treatment	SYS1-DBNDD2	767557	37	20	44037564	44037564	Frame_Shift_Del	DEL	C	-	8	730	c.263delC	c.(262-264)ACCfs	p.T88fs
Pat_24	Pre-Treatment	SNX21	90203	37	20	44469908	44469908	Frame_Shift_Del	DEL	C	-	9	1030	c.1078delC	c.(1078-1080)CCCfs	p.P360fs
Pat_24	Pre-Treatment	PWP2	5822	37	21	45542213	45542214	Frame_Shift_Del	DEL	AC	-	8	369	c.1792_1793delAC	c.(1792-1794)ACAfs	p.T598fs
Pat_24	Pre-Treatment	MICAL3	57553	37	22	18314652	18314654	In_Frame_Del	DEL	TCC	-	7	47	.3021_3023delGG	(3019-3024)GAGGAC>GA	p.E1007del
Pat_24	Pre-Treatment	DGCR14	8220	37	22	19124913	19124913	Frame_Shift_Del	DEL	C	-	7	760	c.958delG	c.(958-960)GAGfs	p.E320fs
Pat_24	Pre-Treatment	GCAT	23464	37	22	38211707	38211707	Frame_Shift_Del	DEL	G	-	7	494	c.852delG	c.(850-852)CTGfs	p.L284fs
Pat_24	Pre-Treatment	TMEM40	55287	37	3	12790198	12790200	In_Frame_Del	DEL	GAG	-	8	319	c.165_167delCTC	c.(163-168)TCCTCT>TCT	p.55_56SS>S
Pat_24	Pre-Treatment	ANKRD28	23243	37	3	15720817	15720817	Frame_Shift_Del	DEL	G	-	8	561	c.2462delC	c.(2461-2463)TCAfs	p.S821fs
Pat_24	Pre-Treatment	EXOG	9941	37	3	38537920	38537920	Frame_Shift_Del	DEL	T	-	37	68	c.62delT	c.(61-63)GTGfs	p.V21fs
Pat_24	Pre-Treatment	COL7A1	1294	37	3	48631059	48631060	Frame_Shift_Del	DEL	TG	-	10	877	c.336_337delCA	c.(334-339)TACAAGfs	p.Y112fs
Pat_24	Pre-Treatment	DOCK3	1795	37	3	51399987	51399988	Frame_Shift_Del	DEL	CT	-	8	259	c.5175_5176delCT	c.(5173-5178)GGCTCAfs	p.G1725fs
Pat_24	Pre-Treatment	CPOX	1371	37	3	98304365	98304366	Frame_Shift_Del	DEL	AG	-	7	611	c.1091_1092delCT	c.(1090-1092)TCTfs	p.S364fs
Pat_24	Pre-Treatment	MYH15	22989	37	3	108102443	108102443	Frame_Shift_Del	DEL	T	-	7	424	c.5825delA	c.(5824-5826)AAGfs	p.K1942fs
Pat_24	Pre-Treatment	GRK7	131890	37	3	141535708	141535708	Frame_Shift_Del	DEL	G	-	8	733	c.1478delG	c.(1477-1479)CGGfs	p.R493fs
Pat_24	Pre-Treatment	P2RY13	53829	37	3	151046039	151046039	Frame_Shift_Del	DEL	C	-	8	377	c.805delG	c.(805-807)GCTfs	p.A269fs
Pat_24	Pre-Treatment	AP2M1	1173	37	3	183901278	183901279	Frame_Shift_Del	DEL	CG	-	8	352	c.1182_1183delCG	c.(1180-1185)TTCGCGfs	p.F394fs
Pat_24	Pre-Treatment	FAM193A	8603	37	4	2695447	2695447	Frame_Shift_Del	DEL	G	-	9	596	c.2065delG	c.(2065-2067)GCCfs	p.A689fs
Pat_24	Pre-Treatment	TBC1D14	57533	37	4	7011611	7011612	Frame_Shift_Ins	INS	-	AT	209	440	c.1454_1455insAT	c.(1453-1455)CCAfs	p.P485fs
Pat_24	Pre-Treatment	UGT2B11	10720	37	4	70079993	70079993	Frame_Shift_Del	DEL	C	-	8	356	c.448delG	c.(448-450)GCAfs	p.A150fs
Pat_24	Pre-Treatment	NAAA	27163	37	4	76862043	76862045	In_Frame_Del	DEL	CAG	-	4	4	c.58_60delCTG	c.(58-60)CTGdel	p.L20del
Pat_24	Pre-Treatment	MAML3	55534	37	4	140810639	140810641	In_Frame_Del	DEL	GCT	-	10	78	.1937_1939delAG	(1936-1941)CAGCCG>CC	p.Q646del
Pat_24	Pre-Treatment	FASTKD3	79072	37	5	7867769	7867769	Frame_Shift_Del	DEL	T	-	8	241	c.428delA	c.(427-429)AAGfs	p.K143fs
Pat_24	Pre-Treatment	ROPN1L	83853	37	5	10442412	10442413	Splice_Site	DEL	TA	-	8	312	c.131_splice	c.e1+2	p.G44_splice
Pat_24	Pre-Treatment	SLC45A2	51151	37	5	33947305	33947305	Frame_Shift_Del	DEL	T	-	8	1057	c.1331delA	c.(1330-1332)AACfs	p.N444fs
Pat_24	Pre-Treatment	BDP1	55814	37	5	70786918	70786918	Frame_Shift_Del	DEL	G	-	8	257	c.1600delG	c.(1600-1602)GAAfs	p.E534fs
Pat_24	Pre-Treatment	JAKMIP2	9832	37	5	147040607	147040607	Frame_Shift_Del	DEL	A	-	10	554	c.531delT	c.(529-531)GATfs	p.D177fs
Pat_24	Pre-Treatment	DCTN4	51164	37	5	150090860	150090860	Frame_Shift_Del	DEL	C	-	8	283	c.1234delG	c.(1234-1236)GAGfs	p.E412fs
Pat_24	Pre-Treatment	LARP1	23367	37	5	154181822	154181822	Frame_Shift_Del	DEL	G	-	11	422	c.1972delG	c.(1972-1974)GGGfs	p.G658fs
Pat_24	Pre-Treatment	WWC1	23286	37	5	167882494	167882494	Frame_Shift_Del	DEL	C	-	8	439	c.2792delC	c.(2791-2793)TCCfs	p.S931fs
Pat_24	Pre-Treatment	FLT4	2324	37	5	180047630	180047632	In_Frame_Del	DEL	GAG	-	8	130	.2383_2385delCT	c.(2383-2385)CTCdel	p.L795del
Pat_24	Pre-Treatment	HDGFL1	154150	37	6	22570346	22570347	In_Frame_Ins	INS	-	GGC	9	14	c.542_543insGGC	.(541-543)AGG>AGGGC	p.188_189insA
Pat_24	Pre-Treatment	ITPR3	3710	37	6	33657874	33657875	Frame_Shift_Del	DEL	TA	-	8	361	c.6931_6932delTA	c.(6931-6933)TATfs	p.Y2311fs

Pat_24	Pre-Treatment	FTSJD2	23070	37	6	37414140	37414140	Frame_Shift_Del	DEL	C	-	8	1104	c.359delC	c.(358-360)TCCfs	p.S120fs
Pat_24	Pre-Treatment	KIF6	221458	37	6	39580993	39580993	Frame_Shift_Del	DEL	A	-	8	253	c.611delT	c.(610-612)TTAfs	p.L204fs
Pat_24	Pre-Treatment	UBR2	23304	37	6	42657355	42657355	Frame_Shift_Del	DEL	T	-	7	1630	c.5073delT	c.(5071-5073)TGTfs	p.C1691fs
Pat_24	Pre-Treatment	SRF	6722	37	6	43146551	43146551	Frame_Shift_Del	DEL	C	-	7	1430	c.1362delC	c.(1360-1362)GTCfs	p.V454fs
Pat_24	Pre-Treatment	GSTA3	2940	37	6	52770601	52770602	Frame_Shift_Ins	INS	-	A	8	306	c.31_32insT	c.(31-33)AATfs	p.N11fs
Pat_24	Pre-Treatment	CNR1	1268	37	6	88853620	88853621	Frame_Shift_Ins	INS	-	T	8	975	c.1373_1374insA	c.(1372-1374)AAGfs	p.K458fs
Pat_24	Pre-Treatment	HS3ST5	222537	37	6	114378467	114378467	Frame_Shift_Del	DEL	T	-	8	212	c.995delA	c.(994-996)AATfs	p.N332fs
Pat_24	Pre-Treatment	HBS1L	10767	37	6	135314919	135314932	Frame_Shift_Del	DEL	GAATGAAG	-	8	98	060delGGACTTC	1062)AAGGACTTCATTC	p.K349fs
Pat_24	Pre-Treatment	PRKAR1B	5575	37	7	720281	720281	Frame_Shift_Del	DEL	G	-	7	364	c.260delC	c.(259-261)CCGfs	p.P87fs
Pat_24	Pre-Treatment	HOXA11	3207	37	7	27222461	27222462	Frame_Shift_Ins	INS	-	T	7	648	c.895_896insA	c.(895-897)ATTfs	p.I299fs
Pat_24	Pre-Treatment	EGFR	1956	37	7	55229326	55229326	Splice_Site	DEL	T	-	8	516	c.1631_splice	c.e13+2	p.G544_splice
Pat_24	Pre-Treatment	FKBP9L	360132	37	7	55766777	55766778	Frame_Shift_Del	DEL	CA	-	8	418	c.6_7delTG	c.(4-9)GATGAAfs	p.D2fs
Pat_24	Pre-Treatment	PCLO	27445	37	7	82585325	82585325	Frame_Shift_Del	DEL	A	-	7	318	c.4944delT	c.(4942-4944)ACTfs	p.T1648fs
Pat_24	Pre-Treatment	CLDN12	9069	37	7	90042244	90042246	In_Frame_Del	DEL	TCC	-	8	1116	c.254_256delTCC	c.(253-258)GTCCTC>GTC	p.L86del
Pat_24	Pre-Treatment	PTCD1	26024	37	7	99032605	99032607	In_Frame_Del	DEL	CTC	-	8	507	c.259_261delGAG	c.(259-261)GAGdel	p.E87del
Pat_24	Pre-Treatment	CYP3A43	64816	37	7	99457609	99457610	Frame_Shift_Del	DEL	AT	-	8	232	c.1022_1023delAT	c.(1021-1023)AATfs	p.N341fs
Pat_24	Pre-Treatment	ZCWPW1	55063	37	7	100000151	100000151	Frame_Shift_Del	DEL	T	-	10	2168	c.1459delA	c.(1459-1461)ACCfs	p.T487fs
Pat_24	Pre-Treatment	SLC26A5	375611	37	7	102993339	102993339	Frame_Shift_Del	DEL	A	-	8	1273	c.1549delT	c.(1549-1551)TAGfs	p.*517fs
Pat_24	Pre-Treatment	MET	4233	37	7	116403141	116403141	Frame_Shift_Del	DEL	G	-	7	656	c.2402delG	c.(2401-2403)TGTfs	p.C801fs
Pat_24	Pre-Treatment	OR2A25	392138	37	7	143771315	143771315	Frame_Shift_Del	DEL	G	-	8	439	c.3delG	c.(1-3)ATGfs	p.M1fs
Pat_24	Pre-Treatment	PDIA4	9601	37	7	148702234	148702234	Frame_Shift_Del	DEL	T	-	7	949	c.1521delA	c.(1519-1521)AAAfs	p.K507fs
Pat_24	Pre-Treatment	NOM1	64434	37	7	156743209	156743211	In_Frame_Del	DEL	GAG	-	7	108	c.778_780delGAG	c.(778-780)GAGdel	p.E264del
Pat_24	Pre-Treatment	ADRB3	155	37	8	37823104	37823105	Frame_Shift_Del	DEL	CC	-	2	4	c.883_884delGG	c.(883-885)GGTfs	p.G295fs
Pat_24	Pre-Treatment	PTDSS1	9791	37	8	97318739	97318739	Frame_Shift_Del	DEL	G	-	8	490	c.962delG	c.(961-963)TGGfs	p.W321fs
Pat_24	Pre-Treatment	WISP1	8840	37	8	134225137	134225137	Frame_Shift_Del	DEL	T	-	8	138	c.100delT	c.(100-102)TTTfs	p.F34fs
Pat_24	Pre-Treatment	NAPRT1	93100	37	8	144659876	144659876	Frame_Shift_Del	DEL	C	-	4	5	c.388delG	c.(388-390)GTGfs	p.V130fs
Pat_24	Pre-Treatment	TDRD7	23424	37	9	100235846	100235847	Frame_Shift_Del	DEL	TG	-	8	248	.2017_2018delT	c.(2017-2019)TGTfs	p.C673fs
Pat_24	Pre-Treatment	HEMGN	55363	37	9	100692776	100692777	Frame_Shift_Del	DEL	TT	-	8	292	c.900_901delAA	c.(898-903)AAAATAfs	p.K300fs
Pat_24	Pre-Treatment	OR1N2	138882	37	9	125315457	125315457	Frame_Shift_Del	DEL	T	-	7	324	c.9delT	c.(7-9)GGTfs	p.G3fs
Pat_24	Pre-Treatment	PTGES2	80142	37	9	130889794	130889794	Frame_Shift_Del	DEL	C	-	4	9	c.203delG	c.(202-204)GGAfs	p.G68fs
Pat_24	Pre-Treatment	RAPGEF1	2889	37	9	134504038	134504039	Frame_Shift_Del	DEL	GG	-	8	403	c.863_864delCC	c.(862-864)CCCfs	p.P288fs
Pat_24	Pre-Treatment	IQSEC2	23096	37	X	53264131	53264133	In_Frame_Del	DEL	TGG	-	4	9	.3735_3737delCC	.(3733-3738)CACCAT>CA	1245_1246HH
Pat_24	Post-Resistance	PIAS3	10401	37	1	145583934	145583935	Frame_Shift_Del	DEL	AG	-	8	499	.1165_1166delA	c.(1165-1167)AGTfs	p.S389fs
Pat_24	Post-Resistance	HIST2H2AB	317772	37	1	149859168	149859168	Frame_Shift_Del	DEL	C	-	7	1193	c.299delG	c.(298-300)GGTfs	p.G100fs
Pat_24	Post-Resistance	KPRP	448834	37	1	152732678	152732678	Frame_Shift_Del	DEL	C	-	7	425	c.614delC	c.(613-615)ACCfs	p.T205fs
Pat_24	Post-Resistance	PBXIP1	57326	37	1	154917508	154917510	In_Frame_Del	DEL	GGT	-	8	255	.2186_2188delAC	(2185-2190)CACCGG>CG	p.H729del
Pat_24	Post-Resistance	NFASC	23114	37	1	204924033	204924033	Frame_Shift_Del	DEL	C	-	7	595	c.489delC	c.(487-489)AACfs	p.N163fs
Pat_24	Post-Resistance	GPR44	11251	37	11	60620166	60620167	In_Frame_Ins	INS	-	GCG	12	12	.1029_1030insCG	c.(1027-1032)insCGC	p.343_344ins
Pat_24	Post-Resistance	C11orf95	65998	37	11	63533335	63533337	In_Frame_Del	DEL	TCC	-	7	50	c.579_581delGGA	.(577-582)GAGGAA>GAA	.193_194EE>
Pat_24	Post-Resistance	LTBP3	4054	37	11	65325326	65325328	In_Frame_Del	DEL	CAG	-	7	38	c.103_105delCTG	c.(103-105)CTGdel	p.L35del
Pat_24	Post-Resistance	ATG16L2	89849	37	11	72528863	72528865	In_Frame_Del	DEL	AGG	-	9	274	c.281_283delAGG	.(280-285)CAGGAG>CA	p.E98del
Pat_24	Post-Resistance	USPL1	10208	37	13	31227343	31227343	Frame_Shift_Del	DEL	C	-	7	614	c.1297delC	c.(1297-1299)CACfs	p.H433fs
Pat_24	Post-Resistance	SLC24A1	9187	37	15	65938021	65938021	Frame_Shift_Del	DEL	A	-	4	4	c.2212delA	c.(2212-2214)AAGfs	p.K738fs
Pat_24	Post-Resistance	CIRH1A	84916	37	16	69167515	69167515	Frame_Shift_Del	DEL	G	-	7	271	c.153delG	c.(151-153)CAGfs	p.Q51fs
Pat_24	Post-Resistance	ZC3H18	124245	37	16	88694417	88694417	Frame_Shift_Del	DEL	G	-	10	504	c.2359delG	c.(2359-2361)GGGfs	p.G787fs
Pat_24	Post-Resistance	PRPF8	10594	37	17	1562781	1562781	Frame_Shift_Del	DEL	C	-	8	434	c.5008delG	c.(5008-5010)GACfs	p.D1670fs
Pat_24	Post-Resistance	ITGAE	3682	37	17	3638187	3638188	Frame_Shift_Del	DEL	TT	-	7	788	.2578_2579delA	c.(2578-2580)AACfs	p.N860fs

Pat_24	Post-Resistance	EIF5A	1984	37	17	7213020	7213021	Frame_Shift_Del	DEL	CT	-	8	503	c.66_67delCT	c.(64-69)TGCTCAfs	p.C22fs
Pat_24	Post-Resistance	ENGASE	64772	37	17	77075668	77075668	Frame_Shift_Del	DEL	C	-	7	738	c.514delC	c.(514-516)CCCfs	p.P172fs
Pat_24	Post-Resistance	HAUS1	115106	37	18	43685174	43685174	Frame_Shift_Del	DEL	A	-	10	71	c.45delA	c.(43-45)TTAfs	p.L15fs
Pat_24	Post-Resistance	SEMA6B	10501	37	19	4552597	4552597	Frame_Shift_Del	DEL	G	-	7	189	c.826delC	c.(826-828)CGCfs	p.R276fs
Pat_24	Post-Resistance	HNRNPUL1	11100	37	19	41811694	41811695	Frame_Shift_Ins	INS	-	A	9	511	c.2376_2377insA	c.(2374-2379)TACAACfs	p.Y792fs
Pat_24	Post-Resistance	PSG5	5673	37	19	43689036	43689036	Frame_Shift_Del	DEL	G	-	9	875	c.328delC	c.(328-330)CAGfs	p.Q110fs
Pat_24	Post-Resistance	SNRNP70	6625	37	19	49589712	49589712	Frame_Shift_Del	DEL	C	-	10	2050	c.41delC	c.(40-42)GCCfs	p.A14fs
Pat_24	Post-Resistance	HRC	3270	37	19	49656769	49656771	In_Frame_Del	DEL	CCT	-	10	100	.1724_1726delAG	(1723-1728)GAGGGG>GG	p.E575del
Pat_24	Post-Resistance	LILRB1	10859	37	19	55146148	55146150	In_Frame_Del	DEL	CTC	-	10	126	.1417_1419delCT	c.(1417-1419)CTCdel	p.L479del
Pat_24	Post-Resistance	HS1BP3	64342	37	2	20840864	20840864	Frame_Shift_Del	DEL	G	-	8	778	c.275delC	c.(274-276)CCAfs	p.P92fs
Pat_24	Post-Resistance	LRP1B	53353	37	2	141607895	141607896	Frame_Shift_Ins	INS	-	T	2	4	c.4714_4715insA	c.(4714-4716)ATGfs	p.M1572fs
Pat_24	Post-Resistance	COL3A1	1281	37	2	189873846	189873846	Frame_Shift_Del	DEL	T	-	36	140	c.3722delT	c.(3721-3723)GTTfs	p.V1241fs
Pat_24	Post-Resistance	CCDC108	255101	37	2	219886541	219886541	Frame_Shift_Del	DEL	C	-	8	474	c.3091delG	c.(3091-3093)GAGfs	p.E1031fs
Pat_24	Post-Resistance	NCOA3	8202	37	20	46268539	46268539	Frame_Shift_Del	DEL	C	-	17	226	c.2926delC	c.(2926-2928)CAAfs	p.Q976fs
Pat_24	Post-Resistance	CELSR1	9620	37	22	46929720	46929721	Frame_Shift_Del	DEL	GG	-	7	679	c.3347_3348delCC	c.(3346-3348)TCCfs	p.S1116fs
Pat_24	Post-Resistance	TBC1D5	9779	37	3	17446189	17446189	Frame_Shift_Del	DEL	T	-	8	1029	c.438delA	c.(436-438)GAAfs	p.E146fs
Pat_24	Post-Resistance	EXOG	9941	37	3	38537920	38537920	Frame_Shift_Del	DEL	T	-	16	78	c.62delT	c.(61-63)GTGfs	p.V21fs
Pat_24	Post-Resistance	CRIPAK	285464	37	4	1388714	1388715	Frame_Shift_Del	DEL	CA	-	7	615	c.415_416delCA	c.(415-417)CACfs	p.H139fs
Pat_24	Post-Resistance	TBC1D14	57533	37	4	7011611	7011612	Frame_Shift_Ins	INS	-	AT	128	538	c.1454_1455insAT	c.(1453-1455)CCAfs	p.P485fs
Pat_24	Post-Resistance	RASGEF1B	153020	37	4	82363492	82363492	Frame_Shift_Del	DEL	T	-	7	78	c.967delA	c.(967-969)ACTfs	p.T323fs
Pat_24	Post-Resistance	FAT1	2195	37	4	187510184	187510184	Frame_Shift_Del	DEL	G	-	7	655	c.13329delC	c.(13327-13329)CCCfs	p.P4443fs
Pat_24	Post-Resistance	PAIP1	10605	37	5	43555989	43555990	Frame_Shift_Del	DEL	AG	-	8	667	c.377_378delCT	c.(376-378)TCTfs	p.S126fs
Pat_24	Post-Resistance	BAT2	7916	37	6	31604005	31604005	Frame_Shift_Del	DEL	C	-	10	849	c.5644delC	c.(5644-5646)CCCfs	p.P1882fs
Pat_24	Post-Resistance	TFAP2B	7021	37	6	50796386	50796386	Frame_Shift_Del	DEL	A	-	8	412	c.595delA	c.(595-597)AAAfs	p.K199fs
Pat_24	Post-Resistance	DLX6	1750	37	7	96635545	96635547	In_Frame_Del	DEL	CAC	-	7	63	c.172_174delCAC	c.(172-174)CACdel	p.H63del
Pat_24	Post-Resistance	CNPY4	245812	37	7	99717402	99717402	Frame_Shift_Del	DEL	T	-	11	273	c.35delT	c.(34-36)CTTfs	p.L12fs
Pat_24	Post-Resistance	TMEM139	135932	37	7	142983583	142983583	Frame_Shift_Del	DEL	C	-	7	861	c.312delC	c.(310-312)CGCfs	p.R104fs
Pat_24	Post-Resistance	PAXIP1	22976	37	7	154760267	154760269	In_Frame_Del	DEL	CTG	-	7	51	.1642_1644delCA	c.(1642-1644)CAGdel	p.Q548del
Pat_24	Post-Resistance	KIAA0196	9897	37	8	126090986	126090986	Frame_Shift_Del	DEL	G	-	8	209	c.705delC	c.(703-705)TACfs	p.Y235fs
Pat_24	Post-Resistance	C9orf142	286257	37	9	139887414	139887414	Frame_Shift_Del	DEL	C	-	8	498	c.218delC	c.(217-219)ACCfs	p.T73fs
Pat_24	Post-Resistance	ENTPD2	954	37	9	139943111	139943112	Frame_Shift_Del	DEL	AA	-	4	7	c.1485_1486delTT	c.(1483-1488)ATTTAGfs	p.I495fs
Pat_24	Post-Resistance	TPRN	286262	37	9	140087025	140087027	In_Frame_Del	DEL	TCC	-	13	57	.1659_1661delGG	(1657-1662)GAGGAA>GA	.553_554EE>
Pat_24	Post-Resistance	NLGN4X	57502	37	X	5821444	5821445	Frame_Shift_Del	DEL	TG	-	4	9	c.1274_1275delCA	c.(1273-1275)ACAfs	p.T425fs
Pat_24	Post-Resistance	SYN1	6853	37	X	47434113	47434113	Frame_Shift_Del	DEL	G	-	4	5	c.1367delC	c.(1366-1368)CCGfs	p.P456fs
Pat_24	Post-Resistance	TSPY4	728395	37	Y	9197004	9197004	Frame_Shift_Del	DEL	G	-	2	4	c.717delG	c.(715-717)CTGfs	p.L239fs
Pat_27	Post-Resistance	PABPC4	8761	37	1	40028016	40028016	Frame_Shift_Del	DEL	G	-	10	428	c.1693delC	c.(1693-1695)CAGfs	p.Q565fs
Pat_27	Post-Resistance	GBP2	2634	37	1	89587526	89587528	In_Frame_Del	DEL	CCA	-	7	650	c.122_124delTGG	.(121-126)GTGGCG>GCC	p.V41del
Pat_27	Post-Resistance	TCHH	7062	37	1	152082957	152082959	In_Frame_Del	DEL	CTC	-	12	557	.2734_2736delGA	c.(2734-2736)GAGdel	p.E912del
Pat_27	Post-Resistance	PAPPA2	60676	37	1	176525710	176525710	Frame_Shift_Del	DEL	G	-	7	1162	c.252delG	c.(250-252)GTGfs	p.V84fs
Pat_27	Post-Resistance	FAM129A	116496	37	1	184764538	184764538	Frame_Shift_Del	DEL	C	-	7	1270	c.2360delG	c.(2359-2361)GGAfs	p.G787fs
Pat_27	Post-Resistance	AGT	183	37	1	230839055	230839055	Frame_Shift_Del	DEL	A	-	7	302	c.1290delT	c.(1288-1290)TTTfs	p.F430fs
Pat_27	Post-Resistance	CEP164	22897	37	11	117280451	117280453	In_Frame_Del	DEL	CGC	-	7	1356	.3866_3868delCG	(3865-3870)TCGCCG>TC	p.P1292del
Pat_27	Post-Resistance	GPR19	2842	37	12	12814274	12814274	Frame_Shift_Del	DEL	T	-	13	519	c.1109delA	c.(1108-1110)AACfs	p.N370fs
Pat_27	Post-Resistance	TENC1	23371	37	12	53452903	53452903	Frame_Shift_Del	DEL	C	-	9	454	c.1478delC	c.(1477-1479)ACCfs	p.T493fs
Pat_27	Post-Resistance	RBM19	9904	37	12	114395612	114395612	Frame_Shift_Del	DEL	T	-	7	536	c.815delA	c.(814-816)AAGfs	p.K272fs
Pat_27	Post-Resistance	INTS6	26512	37	13	51948408	51948408	Frame_Shift_Del	DEL	T	-	8	1034	c.2040delA	c.(2038-2040)AAAfs	p.K680fs
Pat_27	Post-Resistance	APBA2	321	37	15	29346361	29346363	In_Frame_Del	DEL	GAG	-	7	863	c.274_276delGAG	c.(274-276)GAGdel	p.E95del

Pat_27	Post-Resistance	MEF2A	4205	37	15	100252710	100252715	In_Frame_Del	DEL	CAGCAG	-	12	31	258_1263delCAGC	c.(1258-1263)CAGCAGdel	p.QQ428del
Pat_27	Post-Resistance	NFAT5	10725	37	16	69726420	69726422	In_Frame_Del	DEL	CAG	-	7	159	.2638_2640delCA	c.(2638-2640)CAGdel	p.Q888del
Pat_27	Post-Resistance	CHRNB1	1140	37	17	7357666	7357668	In_Frame_Del	DEL	CTG	-	9	574	c.871_873delCTG	c.(871-873)CTGdel	p.L294del
Pat_27	Post-Resistance	SLC16A6	9120	37	17	66267125	66267125	Frame_Shift_Del	DEL	A	-	7	483	c.1176delT	c.(1174-1176)TTTfs	p.F392fs
Pat_27	Post-Resistance	KIAA0195	9772	37	17	73491063	73491063	Frame_Shift_Del	DEL	C	-	7	641	c.2676delC	c.(2674-2676)ATCfs	p.I892fs
Pat_27	Post-Resistance	ICAM1	3383	37	19	10394740	10394740	Frame_Shift_Del	DEL	C	-	7	487	c.669delC	c.(667-669)AGCfs	p.S223fs
Pat_27	Post-Resistance	SLC44A2	57153	37	19	10748914	10748916	In_Frame_Del	DEL	TTC	-	8	241	.1852_1854delTT	c.(1852-1854)TTCdel	p.F621del
Pat_27	Post-Resistance	KIR2DL4	3805	37	19	55324675	55324675	Splice_Site	DEL	A	-	7	92	c.801_splice	c.e6+1	p.S267_splice
Pat_27	Post-Resistance	PSME4	23198	37	2	54167139	54167140	Splice_Site	INS	-	G	8	400	c.501_splice	c.e4-1	p.N167_splice
Pat_27	Post-Resistance	OTX1	5013	37	2	63283275	63283277	In_Frame_Del	DEL	CAC	-	8	424	c.889_891delCAC	c.(889-891)CACdel	p.H301del
Pat_27	Post-Resistance	TEKT4	150483	37	2	95539829	95539830	Frame_Shift_Ins	INS	-	G	8	379	c.689_690insG	c.(688-690)CCGfs	p.P230fs
Pat_27	Post-Resistance	PLA2R1	22925	37	2	160801442	160801442	Frame_Shift_Del	DEL	T	-	8	446	c.4119delA	c.(4117-4119)AAAfs	p.K1373fs
Pat_27	Post-Resistance	CERKL	375298	37	2	182403897	182403899	In_Frame_Del	DEL	TCC	-	7	571	.1536_1538delGG	.(1534-1539)GAGGAT>GA	p.E512del
Pat_27	Post-Resistance	CLTCL1	8218	37	22	19220690	19220690	Frame_Shift_Del	DEL	T	-	8	1191	c.1520delA	c.(1519-1521)AAGfs	p.K507fs
Pat_27	Post-Resistance	CCDC116	164592	37	22	21990728	21990730	In_Frame_Del	DEL	GCA	-	7	171	.1211_1213delGC	.(1210-1215)TGCAGC>TG	p.S407del
Pat_27	Post-Resistance	CNTN6	27255	37	3	1371501	1371501	Frame_Shift_Del	DEL	A	-	8	298	c.1246delA	c.(1246-1248)AAAfs	p.K416fs
Pat_27	Post-Resistance	SGOL1	151648	37	3	20216050	20216050	Frame_Shift_Del	DEL	T	-	10	74	c.973delA	c.(973-975)ATGfs	p.M325fs
Pat_27	Post-Resistance	XIRP1	165904	37	3	39228955	39228958	Frame_Shift_Del	DEL	TGTC	-	7	171	1979_1982delGA	c.(1978-1983)AGACACfs	p.R660fs
Pat_27	Post-Resistance	HHATL	57467	37	3	42739670	42739672	In_Frame_Del	DEL	GAA	-	13	393	c.655_657delTTC	c.(655-657)TTCdel	p.F219del
Pat_27	Post-Resistance	CELSR3	1951	37	3	48685385	48685385	Frame_Shift_Del	DEL	C	-	7	955	c.7018delG	c.(7018-7020)GCCfs	p.A2340fs
Pat_27	Post-Resistance	VGLL3	389136	37	3	87027685	87027685	Frame_Shift_Del	DEL	G	-	8	584	c.394delC	c.(394-396)CTAfs	p.L132fs
Pat_27	Post-Resistance	FILIP1L	11259	37	3	99569346	99569346	Frame_Shift_Del	DEL	T	-	7	573	c.1174delA	c.(1174-1176)ATGfs	p.M392fs
Pat_27	Post-Resistance	TMEM22	80723	37	3	136573486	136573486	Frame_Shift_Del	DEL	A	-	7	217	c.184delA	c.(184-186)AAAfs	p.K62fs
Pat_27	Post-Resistance	SULT1B1	27284	37	4	70599153	70599153	Frame_Shift_Del	DEL	A	-	7	858	c.575delT	c.(574-576)TTGfs	p.L192fs
Pat_27	Post-Resistance	FGF5	2250	37	4	81187992	81187994	In_Frame_Del	DEL	TCC	-	7	445	c.14_16delTCC	c.(13-18)TTCCTC>TTC	p.L9del
Pat_27	Post-Resistance	WDFY3	23001	37	4	85611708	85611709	Frame_Shift_Del	DEL	CA	-	7	390	c.9313_9314delTG	c.(9313-9315)TGGfs	p.W3105fs
Pat_27	Post-Resistance	BTNL8	79908	37	5	180338421	180338421	Frame_Shift_Del	DEL	C	-	7	1234	c.480delC	c.(478-480)TTCfs	p.F160fs
Pat_27	Post-Resistance	FOXF2	2295	37	6	1390277	1390279	In_Frame_Del	DEL	CCG	-	10	6	c.95_97delCCG	c.(94-99)CCCGCC>CCC	p.A41del
Pat_27	Post-Resistance	HSP90AB1	3326	37	6	44221052	44221052	Frame_Shift_Del	DEL	T	-	7	2628	c.2002delT	c.(2002-2004)TTTfs	p.F668fs
Pat_27	Post-Resistance	TBX18	9096	37	6	85446744	85446744	Frame_Shift_Del	DEL	G	-	7	958	c.1483delC	c.(1483-1485)CAGfs	p.Q495fs
Pat_27	Post-Resistance	ARID1B	57492	37	6	157100024	157100026	In_Frame_Del	DEL	GGA	-	7	57	c.787_789delGGA	c.(787-789)GGAdel	p.G270del
Pat_27	Post-Resistance	TTYH3	80727	37	7	2687612	2687614	In_Frame_Del	DEL	CTG	-	7	402	c.646_648delCTG	c.(646-648)CTGdel	p.L219del
Pat_27	Post-Resistance	SDK1	221935	37	7	4008947	4008947	Frame_Shift_Del	DEL	G	-	8	1753	c.1605delG	c.(1603-1605)TCGfs	p.S535fs
Pat_27	Post-Resistance	PURB	5814	37	7	44924044	44924046	In_Frame_Del	DEL	CGC	-	7	611	c.902_904delGCG	.(901-906)GGCGAA>GA	p.G301del
Pat_27	Post-Resistance	AKAP9	10142	37	7	91603085	91603085	Frame_Shift_Del	DEL	A	-	8	161	c.109delA	c.(109-111)AAAfs	p.K37fs
Pat_27	Post-Resistance	MLL3	58508	37	7	151856009	151856009	Frame_Shift_Del	DEL	T	-	8	1214	c.11609delA	c.(11608-11610)AAGfs	p.K3870fs
Pat_27	Post-Resistance	PSD3	23362	37	8	18413785	18413785	Frame_Shift_Del	DEL	G	-	7	845	c.2862delC	c.(2860-2862)CCCfs	p.P954fs
Pat_27	Post-Resistance	EPB49	2039	37	8	21927773	21927773	Frame_Shift_Del	DEL	C	-	7	440	c.532delC	c.(532-534)CCCfs	p.P178fs
Pat_27	Post-Resistance	PTPLAD2	401494	37	9	21007046	21007046	Frame_Shift_Del	DEL	T	-	9	280	c.689delA	c.(688-690)AAGfs	p.K230fs
Pat_27	Post-Resistance	HUWE1	10075	37	X	53589091	53589093	In_Frame_Del	DEL	TCC	-	7	168	.7317_7319delGG	(7315-7320)GAGGAA>GA	2439_2440EE
Pat_27	Post-Resistance	ATRX	546	37	X	76931742	76931744	In_Frame_Del	DEL	TCA	-	7	249	.3786_3788delTG	.(3784-3789)GATGAC>GA	1262_1263DD
Pat_28	Post-Resistance	RBBP5	5929	37	1	205074198	205074198	Frame_Shift_Del	DEL	A	-	31	120	c.317delT	c.(316-318)TTCfs	p.F106fs
Pat_28	Post-Resistance	CR2	1380	37	1	207642044	207642044	Frame_Shift_Del	DEL	C	-	7	677	c.618delC	c.(616-618)GTCfs	p.V206fs
Pat_28	Post-Resistance	PITRM1	10531	37	10	3187863	3187863	Frame_Shift_Del	DEL	T	-	2	4	c.2088delA	c.(2086-2088)AAAfs	p.K696fs
Pat_28	Post-Resistance	PTEN	5728	37	10	89693002	89693003	Frame_Shift_Ins	INS	-	A	41	19	c.486_487insA	c.(484-489)GACAAAfs	p.D162fs
Pat_28	Post-Resistance	CAPN5	726	37	11	76830082	76830082	Frame_Shift_Del	DEL	T	-	17	19	c.1174delT	c.(1174-1176)TTCfs	p.F392fs
Pat_28	Post-Resistance	FGFR1OP2	26127	37	12	27109491	27109492	Frame_Shift_Ins	INS	-	AA	59	245	c.151_152insAA	c.(151-153)CAAfs	p.Q51fs

Pat_28	Post-Resistance	LRCH1	23143	37	13	47243183	47243186	Frame_Shift_Del	DEL	CCTG	-	11	659	.471_474delCCT	c.(469-474)GCCCTGfs	p.A157fs
Pat_28	Post-Resistance	MAP3K9	4293	37	14	71275774	71275776	In_Frame_Del	DEL	CCT	-	4	3	c.113_115delAGG	.(112-117)GAGGCG>GC	p.E38del
Pat_28	Post-Resistance	ITGA11	22801	37	15	68624270	68624271	Frame_Shift_Ins	INS	-	G	8	20	c.1696_1697insC	c.(1696-1698)CTGfs	p.L566fs
Pat_28	Post-Resistance	NKTR	4820	37	3	42680269	42680271	In_Frame_Del	DEL	GAG	-	7	249	.3073_3075delGA	c.(3073-3075)GAGdel	p.E1029del
Pat_28	Post-Resistance	NAP1L5	266812	37	4	89618484	89618486	In_Frame_Del	DEL	TCC	-	7	135	c.420_422delGGA	.(418-423)GAGGAA>GAA	.140_141EE>
Pat_28	Post-Resistance	MMRN1	22915	37	4	90844391	90844393	In_Frame_Del	DEL	AGC	-	7	991	c.923_925delAGC	.(922-927)GAGCAG>GA	p.Q313del
Pat_28	Post-Resistance	BMP6	654	37	6	7880531	7880532	Frame_Shift_Ins	INS	-	A	61	335	c.1497_1498insA	c.(1495-1500)CTGAAAfs	p.L499fs
Pat_28	Post-Resistance	TRERF1	55809	37	6	42222620	42222620	Frame_Shift_Del	DEL	T	-	222	86	c.2625delA	c.(2623-2625)AAAfs	p.K875fs
Pat_28	Post-Resistance	TARP	445347	37	7	38313227	38313227	Frame_Shift_Del	DEL	T	-	7	522	c.388delA	c.(388-390)ATCfs	p.I130fs
Pat_30	Pre-Treatment	MMEL1	79258	37	1	2560819	2560821	In_Frame_Del	DEL	CAG	-	11	40	c.103_105delCTG	c.(103-105)CTGdel	p.L35del
Pat_30	Pre-Treatment	ESPNP	284729	37	1	17026043	17026044	In_Frame_Ins	INS	-	GCA	3	6	.1291_1292insTG	(1291-1293)CCG>CTGCC	p.430_431insL
Pat_30	Pre-Treatment	MST1P9	11223	37	1	17085590	17085595	In_Frame_Del	DEL	GCGCTG	-	9	340	26_1131delCAGC	c.(1126-1131)CAGCGCdel	p.QR376del
Pat_30	Pre-Treatment	NFIA	4774	37	1	61848988	61848989	Frame_Shift_Del	DEL	GG	-	9	1268	.1026_1027delG	c.(1024-1029)CTGGGAfs	p.L342fs
Pat_30	Pre-Treatment	SLC27A3	11000	37	1	153751860	153751860	Frame_Shift_Del	DEL	C	-	7	591	c.1927delC	c.(1927-1929)CCCfs	p.P643fs
Pat_30	Pre-Treatment	HAX1	10456	37	1	154246391	154246391	Frame_Shift_Del	DEL	C	-	8	514	c.458delC	c.(457-459)TCCfs	p.S153fs
Pat_30	Pre-Treatment	TNR	7143	37	1	175372615	175372615	Frame_Shift_Del	DEL	C	-	8	1386	c.637delG	c.(637-639)GTGfs	p.V213fs
Pat_30	Pre-Treatment	PRG4	10216	37	1	186277340	186277340	Frame_Shift_Del	DEL	C	-	7	1140	c.2489delC	c.(2488-2490)ACCfs	p.T830fs
Pat_30	Pre-Treatment	ACBD3	64746	37	1	226352490	226352491	Frame_Shift_Ins	INS	-	T	10	251	c.568_569insA	c.(568-570)AGGfs	p.R190fs
Pat_30	Pre-Treatment	PSD	5662	37	10	104173620	104173622	In_Frame_Del	DEL	CCT	-	8	155	.1457_1459delAG	(1456-1461)GAGGCA>GC	p.E486del
Pat_30	Pre-Treatment	APBB1	322	37	11	6432090	6432092	In_Frame_Del	DEL	TCC	-	7	42	c.486_488delGGA	c.(484-489)GAGGAT>GAT	p.E162del
Pat_30	Pre-Treatment	OR10A2	341276	37	11	6891253	6891255	In_Frame_Del	DEL	TTC	-	8	445	c.268_270delTTC	c.(268-270)TTCdel	p.F94del
Pat_30	Pre-Treatment	PLEKHA7	144100	37	11	16847710	16847710	Frame_Shift_Del	DEL	G	-	7	1731	c.1300delC	c.(1300-1302)CAGfs	p.Q434fs
Pat_30	Pre-Treatment	USH1C	10083	37	11	17542501	17542501	Frame_Shift_Del	DEL	C	-	7	1983	c.1126delG	c.(1126-1128)GAAfs	p.E376fs
Pat_30	Pre-Treatment	OR9G4	283189	37	11	56510933	56510933	Frame_Shift_Del	DEL	A	-	7	606	c.355delT	c.(355-357)TCCfs	p.S119fs
Pat_30	Pre-Treatment	EML3	256364	37	11	62376055	62376055	Frame_Shift_Del	DEL	C	-	7	1054	c.1069delG	c.(1069-1071)GCCfs	p.A357fs
Pat_30	Pre-Treatment	USP35	57558	37	11	77920720	77920722	In_Frame_Del	DEL	CGC	-	7	442	.1819_1821delCG	c.(1819-1821)CGCdel	p.R610del
Pat_30	Pre-Treatment	MED17	9440	37	11	93528167	93528167	Frame_Shift_Del	DEL	T	-	97	243	c.953delT	c.(952-954)ATTfs	p.I318fs
Pat_30	Pre-Treatment	IGSF9B	22997	37	11	133807827	133807827	Frame_Shift_Del	DEL	G	-	7	96	c.439delC	c.(439-441)CAGfs	p.Q147fs
Pat_30	Pre-Treatment	PRB2	653247	37	12	11546233	11546235	In_Frame_Del	DEL	GGA	-	7	361	c.777_779delTCC	c.(775-780)CCTCCA>CCA	.259_260PP>
Pat_30	Pre-Treatment	LRP1	4035	37	12	57605948	57605948	Frame_Shift_Del	DEL	G	-	7	210	c.13398delG	c.(13396-13398)GTGfs	p.V4466fs
Pat_30	Pre-Treatment	PIP4K2C	79837	37	12	57988949	57988949	Frame_Shift_Del	DEL	C	-	7	1078	c.313delC	c.(313-315)CCCfs	p.P105fs
Pat_30	Pre-Treatment	SIRT4	23409	37	12	120750293	120750294	Frame_Shift_Ins	INS	-	G	7	340	c.532_533insG	c.(532-534)CGGfs	p.R178fs
Pat_30	Pre-Treatment	DNAH10	196385	37	12	124274524	124274524	Frame_Shift_Del	DEL	G	-	7	585	c.1488delG	c.(1486-1488)ACGfs	p.T496fs
Pat_30	Pre-Treatment	EP400	57634	37	12	132547156	132547158	In_Frame_Del	DEL	GAC	-	9	314	.8244_8246delGA	(8242-8247)CAGACG>CA	p.T2752del
Pat_30	Pre-Treatment	TEP1	7011	37	14	20852647	20852647	Frame_Shift_Del	DEL	C	-	12	1255	c.3242delG	c.(3241-3243)GGTfs	p.G1081fs
Pat_30	Pre-Treatment	SAMD4A	23034	37	14	55226890	55226890	Frame_Shift_Del	DEL	G	-	7	1484	c.1185delG	c.(1183-1185)GAGfs	p.E395fs
Pat_30	Pre-Treatment	HERC1	8925	37	15	63928179	63928180	Frame_Shift_Del	DEL	TG	-	8	1894	12394_12395delC	c.(12394-12396)CAAfs	p.Q4132fs
Pat_30	Pre-Treatment	DNAH3	55567	37	16	21132130	21132132	In_Frame_Del	DEL	CAG	-	8	219	.1628_1630delCT	.(1627-1632)GCTGAT>GA	p.A543del
Pat_30	Pre-Treatment	POLDIP2	26073	37	17	26684394	26684395	Splice_Site	INS	-	G	7	6	c.78_splice	c.e2+1	p.W26_splice
Pat_30	Pre-Treatment	GAS2L2	246176	37	17	34074257	34074257	Frame_Shift_Del	DEL	G	-	7	922	c.863delC	c.(862-864)CCGfs	p.P288fs
Pat_30	Pre-Treatment	RAMP2	10266	37	17	40913329	40913329	Frame_Shift_Del	DEL	C	-	2	4	c.50delC	c.(49-51)ACCfs	p.T17fs
Pat_30	Pre-Treatment	CA10	56934	37	17	50008357	50008357	Frame_Shift_Del	DEL	C	-	8	1682	c.272delG	c.(271-273)GGCfs	p.G91fs
Pat_30	Pre-Treatment	TIMP2	7077	37	17	76869979	76869982	Frame_Shift_Del	DEL	ACTG	-	59	369	.150_153delCAG	c.(148-153)GTCAGTfs	p.V50fs
Pat_30	Pre-Treatment	ASXL3	80816	37	18	31325784	31325784	Frame_Shift_Del	DEL	C	-	8	883	c.5972delC	c.(5971-5973)TCCfs	p.S1991fs
Pat_30	Pre-Treatment	ZNF490	57474	37	19	12692378	12692378	Frame_Shift_Del	DEL	G	-	7	714	c.511delC	c.(511-513)CTTfs	p.L171fs
Pat_30	Pre-Treatment	ATP4A	495	37	19	36054349	36054351	In_Frame_Del	DEL	CTT	-	11	1373	c.91_93delAAG	c.(91-93)AAGdel	p.K31del
Pat_30	Pre-Treatment	KLC3	147700	37	19	45850756	45850758	In_Frame_Del	DEL	GAG	-	7	486	c.541_543delGAG	c.(541-543)GAGdel	p.E184del

Pat_30	Pre-Treatment	TSKS	60385	37	19	50243088	50243088	Frame_Shift_Del	DEL	C	-	8	352	c.1724delG	c.(1723-1725)GGAfs	p.G575fs
Pat_30	Pre-Treatment	ACPT	93650	37	19	51298106	51298106	Frame_Shift_Del	DEL	C	-	10	1393	c.1050delC	c.(1048-1050)CTCfs	p.L350fs
Pat_30	Pre-Treatment	ZNF432	9668	37	19	52537288	52537288	Frame_Shift_Del	DEL	T	-	7	538	c.1644delA	c.(1642-1644)AAAfs	p.K548fs
Pat_30	Pre-Treatment	NLRP9	338321	37	19	56249563	56249563	Frame_Shift_Del	DEL	C	-	10	1762	c.178delG	c.(178-180)GACfs	p.D60fs
Pat_30	Pre-Treatment	PUM2	23369	37	2	20494235	20494235	Frame_Shift_Del	DEL	C	-	8	977	c.1054delG	c.(1054-1056)GTGfs	p.V352fs
Pat_30	Pre-Treatment	CAD	790	37	2	27464020	27464020	Frame_Shift_Del	DEL	C	-	8	1261	c.5733delC	c.(5731-5733)CACfs	p.H1911fs
Pat_30	Pre-Treatment	KIF3B	9371	37	20	30898763	30898765	In_Frame_Del	DEL	GAG	-	8	127	.1183_1185delGA	c.(1183-1185)GAGdel	p.E399del
Pat_30	Pre-Treatment	CECR6	27439	37	22	17601300	17601302	In_Frame_Del	DEL	CCA	-	8	100	c.716_718delTGG	.(715-720)GTGGGC>GG	p.V239del
Pat_30	Pre-Treatment	MN1	4330	37	22	28194933	28194934	In_Frame_Ins	INS	-	TGC	11	46	.1598_1599insGC	.(1597-1599)CAA>CAGCA	.533_533Q>Q
Pat_30	Pre-Treatment	MTMR3	8897	37	22	30408494	30408494	Frame_Shift_Del	DEL	C	-	8	1893	c.1259delC	c.(1258-1260)ACCfs	p.T420fs
Pat_30	Pre-Treatment	TAB1	10454	37	22	39772049	39772049	Frame_Shift_Del	DEL	C	-	7	689	c.108delC	c.(106-108)GACfs	p.D36fs
Pat_30	Pre-Treatment	MKL1	57591	37	22	40816887	40816889	In_Frame_Del	DEL	TGC	-	12	343	c.843_845delGCA	.(841-846)CAGCAC>CAC	p.Q281del
Pat_30	Pre-Treatment	SGOL1	151648	37	3	20216050	20216050	Frame_Shift_Del	DEL	T	-	7	89	c.973delA	c.(973-975)ATGfs	p.M325fs
Pat_30	Pre-Treatment	XYLB	9942	37	3	38454444	38454444	Frame_Shift_Del	DEL	C	-	7	493	c.1551delC	c.(1549-1551)CTCfs	p.L517fs
Pat_30	Pre-Treatment	TM4SF4	7104	37	3	149192694	149192694	Frame_Shift_Del	DEL	G	-	9	170	c.30delG	c.(28-30)CTGfs	p.L10fs
Pat_30	Pre-Treatment	MED12L	116931	37	3	151148114	151148116	In_Frame_Del	DEL	CAG	-	15	374	.6331_6333delCA	c.(6331-6333)CAGdel	p.Q2115del
Pat_30	Pre-Treatment	FGF5	2250	37	4	81187992	81187994	In_Frame_Del	DEL	TCC	-	7	385	c.14_16delTCC	c.(13-18)TTCCTC>TTC	p.L9del
Pat_30	Pre-Treatment	CFI	3426	37	4	110662159	110662159	Frame_Shift_Del	DEL	C	-	7	1416	c.1642delG	c.(1642-1644)GAAfs	p.E548fs
Pat_30	Pre-Treatment	RASGRF2	5924	37	5	80409566	80409568	In_Frame_Del	DEL	CCA	-	11	466	.2297_2299delCC	(2296-2301)CCCACC>CC	p.T770del
Pat_30	Pre-Treatment	PCDHGB4	8641	37	5	140767492	140767497	In_Frame_Del	DEL	TGCCAG	-	2	4	.41_46delTGCCA	(40-48)CTGCCAGTG>CT	p.PV15del
Pat_30	Pre-Treatment	SPRY4	81848	37	5	141694154	141694154	Frame_Shift_Del	DEL	G	-	8	666	c.520delC	c.(520-522)CGGfs	p.R174fs
Pat_30	Pre-Treatment	C6orf223	221416	37	6	43970503	43970504	In_Frame_Ins	INS	-	GCG	10	34	c.369_370insGCG	c.(367-372)insGCG	p.132_133insA
Pat_30	Pre-Treatment	COL12A1	1303	37	6	75887504	75887504	Frame_Shift_Del	DEL	G	-	8	1469	c.2312delC	c.(2311-2313)CCAfs	p.P771fs
Pat_30	Pre-Treatment	WBSCR17	64409	37	7	71142212	71142212	Frame_Shift_Del	DEL	C	-	7	1623	c.1421delC	c.(1420-1422)GCAfs	p.A474fs
Pat_30	Pre-Treatment	C7orf51	222950	37	7	100086313	100086313	Frame_Shift_Del	DEL	C	-	7	781	c.969delC	c.(967-969)ATCfs	p.I323fs
Pat_30	Pre-Treatment	SRRT	51593	37	7	100482040	100482042	In_Frame_Del	DEL	AGG	-	7	78	c.809_811delAGG	.(808-813)CAGGAG>CA	p.E275del
Pat_30	Pre-Treatment	FOXP2	93986	37	7	114271580	114271582	Splice_Site	DEL	CAG	-	7	66	c.598_splice	c.e6-1	p.Q200_splice
Pat_30	Pre-Treatment	CCNE2	9134	37	8	95902737	95902737	Frame_Shift_Del	DEL	T	-	7	1288	c.359delA	c.(358-360)AAGfs	p.K120fs
Pat_30	Pre-Treatment	KIAA2026	158358	37	9	5968044	5968044	Frame_Shift_Del	DEL	T	-	4	6	c.2187delA	c.(2185-2187)AAAfs	p.K729fs
Pat_30	Pre-Treatment	RUSC2	9853	37	9	35555452	35555452	Frame_Shift_Del	DEL	C	-	7	623	c.2410delC	c.(2410-2412)CCCfs	p.P804fs
Pat_30	Pre-Treatment	FRMPD4	9758	37	X	12734864	12734864	Frame_Shift_Del	DEL	G	-	7	777	c.2286delG	c.(2284-2286)GTGfs	p.V762fs
Pat_30	Post-Resistance	EXTL1	2134	37	1	26349533	26349535	In_Frame_Del	DEL	CCT	-	7	187	c.396_398delCCT	c.(394-399)TGCCTC>TGC	p.L137del
Pat_30	Post-Resistance	RPS6KA1	6195	37	1	26885311	26885311	Frame_Shift_Del	DEL	C	-	7	321	c.1098delC	c.(1096-1098)ATCfs	p.I366fs
Pat_30	Post-Resistance	KIAA0467	23334	37	1	43898257	43898257	Frame_Shift_Del	DEL	C	-	7	318	c.2815delC	c.(2815-2817)CCCfs	p.P939fs
Pat_30	Post-Resistance	LCE2A	353139	37	1	152671425	152671425	Frame_Shift_Del	DEL	C	-	14	1173	c.48delC	c.(46-48)TGCfs	p.C16fs
Pat_30	Post-Resistance	GATAD2B	57459	37	1	153784567	153784567	Frame_Shift_Del	DEL	G	-	7	533	c.1461delC	c.(1459-1461)CCCfs	p.P487fs
Pat_30	Post-Resistance	SHC1	6464	37	1	154938468	154938468	Frame_Shift_Del	DEL	G	-	7	511	c.1338delC	c.(1336-1338)CCCfs	p.P446fs
Pat_30	Post-Resistance	GON4L	54856	37	1	155774769	155774769	Frame_Shift_Del	DEL	C	-	7	766	c.1616delG	c.(1615-1617)GGAfs	p.G539fs
Pat_30	Post-Resistance	EFCAB2	84288	37	1	245133550	245133551	Frame_Shift_Del	DEL	GC	-	5	4	c.126_127delGC	c.(124-129)GGGCGCfs	p.G42fs
Pat_30	Post-Resistance	PTEN	5728	37	10	89623858	89623861	Splice_Site	DEL	GGCT	-	4	4	c.-365_splice	c.e1+1	
Pat_30	Post-Resistance	B4GALNT4	338707	37	11	369845	369847	In_Frame_Del	DEL	GCT	-	4	8	c.42_44delGCT	c.(40-45)AAGCTG>AAG	p.L22del
Pat_30	Post-Resistance	C11orf95	65998	37	11	63531514	63531516	In_Frame_Del	DEL	CTC	-	7	55	.1579_1581delGA	c.(1579-1581)GAGdel	p.E527del
Pat_30	Post-Resistance	GPR137	56834	37	11	64055631	64055631	Frame_Shift_Del	DEL	C	-	7	716	c.728delC	c.(727-729)GCCfs	p.A243fs
Pat_30	Post-Resistance	CTSF	8722	37	11	66335859	66335859	Frame_Shift_Del	DEL	C	-	2	4	c.99delG	c.(97-99)GGGfs	p.G33fs
Pat_30	Post-Resistance	KRTAP5-8	57830	37	11	71249125	71249126	In_Frame_Ins	INS	-	GCTCCGG	10	586	CTGTGGCTCC	nsGGCTGTGGCTCCGGC	_23insGCGS
Pat_30	Post-Resistance	MED17	9440	37	11	93528167	93528167	Frame_Shift_Del	DEL	T	-	58	83	c.953delT	c.(952-954)ATTfs	p.I318fs
Pat_30	Post-Resistance	EFS	10278	37	14	23829997	23829997	Frame_Shift_Del	DEL	G	-	7	282	c.64delC	c.(64-66)CAGfs	p.Q22fs

Pat_30	Post-Resistance	NYNRIN	57523	37	14	24886571	24886571	Frame_Shift_Del	DEL	G	-	2	4	c.5616delG	c.(5614-5616)CTGfs	p.L1872fs
Pat_30	Post-Resistance	AKT1	207	37	14	105242073	105242075	In_Frame_Del	DEL	CTC	-	8	283	c.349_351delGAG	c.(349-351)GAGdel	p.E117del
Pat_30	Post-Resistance	NUDT21	11051	37	16	56485066	56485066	Frame_Shift_Del	DEL	C	-	10	872	c.49delG	c.(49-51)GTCfs	p.V17fs
Pat_30	Post-Resistance	CAMTA2	23125	37	17	4883038	4883038	Frame_Shift_Del	DEL	G	-	7	407	c.1579delC	c.(1579-1581)CAGfs	p.Q527fs
Pat_30	Post-Resistance	WNK4	65266	37	17	40932962	40932962	Frame_Shift_Del	DEL	C	-	8	248	c.246delC	c.(244-246)GACfs	p.D82fs
Pat_30	Post-Resistance	TIMP2	7077	37	17	76869979	76869982	Frame_Shift_Del	DEL	ACTG	-	102	187	c.150_153delCAGT	c.(148-153)GTCAGTfs	p.V50fs
Pat_30	Post-Resistance	ZNF700	90592	37	19	12060595	12060596	Frame_Shift_Del	DEL	CA	-	78	233	c.1756_1757delCA	c.(1756-1758)CACfs	p.H586fs
Pat_30	Post-Resistance	GLTSCR1	29998	37	19	48197567	48197568	Frame_Shift_Ins	INS	-	C	7	54	c.2479_2480insC	c.(2479-2481)GCCfs	p.A827fs
Pat_30	Post-Resistance	PMEPA1	56937	37	20	56284593	56284595	In_Frame_Del	DEL	CGG	-	6	10	c.44_46delCCG	c.(43-48)GCCGGG>GGG	p.A15del
Pat_30	Post-Resistance	MN1	4330	37	22	28194933	28194934	In_Frame_Ins	INS	-	TGC	12	66	.1598_1599insGC	.(1597-1599)CAA>CAGCA	.533_533Q>Q
Pat_30	Post-Resistance	HSCB	150274	37	22	29140667	29140667	Frame_Shift_Del	DEL	C	-	7	300	c.398delC	c.(397-399)GCCfs	p.A133fs
Pat_30	Post-Resistance	MTMR3	8897	37	22	30408494	30408494	Frame_Shift_Del	DEL	C	-	7	1546	c.1259delC	c.(1258-1260)ACCfs	p.T420fs
Pat_30	Post-Resistance	C22orf30	253143	37	22	32099549	32099549	Frame_Shift_Del	DEL	G	-	7	574	c.5987delC	c.(5986-5988)CCAfs	p.P1996fs
Pat_30	Post-Resistance	MKL1	57591	37	22	40816887	40816889	In_Frame_Del	DEL	TGC	-	16	275	c.843_845delGCA	c.(841-846)CAGCAC>CAC	p.Q281del
Pat_30	Post-Resistance	ADCY5	111	37	3	123167191	123167193	In_Frame_Del	DEL	GCT	-	4	4	c.200_202delAGC	.(199-204)CAGCGC>CGC	p.Q67del
Pat_30	Post-Resistance	CXCL5	6374	37	4	74864215	74864217	In_Frame_Del	DEL	CAG	-	2	4	c.82_84delCTG	c.(82-84)CTGdel	p.L28del
Pat_30	Post-Resistance	STK19	8859	37	6	31939829	31939830	Frame_Shift_Ins	INS	-	A	10	832	c.56_57insA	c.(55-57)GCAfs	p.A19fs
Pat_30	Post-Resistance	SCUBE3	222663	37	6	35210453	35210453	Frame_Shift_Del	DEL	C	-	8	670	c.1589delC	c.(1588-1590)TCCfs	p.S530fs
Pat_30	Post-Resistance	BYSL	705	37	6	41900405	41900405	Frame_Shift_Del	DEL	C	-	8	656	c.1275delC	c.(1273-1275)GTCfs	p.V425fs
Pat_30	Post-Resistance	CNPY3	10695	37	6	42897358	42897360	In_Frame_Del	DEL	TGC	-	9	73	c.50_52delTGC	c.(49-54)TTGCTG>TTG	p.17_18LL>L
Pat_30	Post-Resistance	C6orf223	221416	37	6	43970503	43970504	In_Frame_Ins	INS	-	GCG	11	77	c.369_370insGCG	c.(367-372)insGCG	p.132_133insA
Pat_30	Post-Resistance	TNFRSF21	27242	37	6	47253989	47253989	Frame_Shift_Del	DEL	G	-	8	1536	c.439delC	c.(439-441)CATfs	p.H147fs
Pat_30	Post-Resistance	GARS	2617	37	7	30671998	30671998	Frame_Shift_Del	DEL	C	-	7	389	c.2039delC	c.(2038-2040)ACCfs	p.T680fs
Pat_30	Post-Resistance	AGFG2	3268	37	7	100161550	100161551	Frame_Shift_Ins	INS	-	C	8	1285	c.1265_1266insC	c.(1264-1266)TTCfs	p.F422fs
Pat_30	Post-Resistance	SRRT	51593	37	7	100482040	100482042	In_Frame_Del	DEL	AGG	-	7	67	c.809_811delAGG	.(808-813)CAGGAG>CAG	p.E275del
Pat_30	Post-Resistance	FLNC	2318	37	7	128480704	128480704	Frame_Shift_Del	DEL	G	-	9	1330	c.1652delG	c.(1651-1653)TGGfs	p.W551fs
Pat_30	Post-Resistance	ARHGEF5	7984	37	7	144075858	144075858	Frame_Shift_Del	DEL	C	-	11	1561	c.4535delC	c.(4534-4536)TCCfs	p.S1512fs
Pat_30	Post-Resistance	ZNF398	57541	37	7	148876153	148876153	Frame_Shift_Del	DEL	C	-	10	1166	c.1189delC	c.(1189-1191)CCCfs	p.P397fs
Pat_30	Post-Resistance	NOS3	4846	37	7	150696157	150696157	Frame_Shift_Del	DEL	C	-	8	1303	c.940delC	c.(940-942)CCCfs	p.P314fs
Pat_30	Post-Resistance	CDK5	1020	37	7	150754217	150754217	Frame_Shift_Del	DEL	T	-	9	1308	c.68delA	c.(67-69)AACfs	p.N23fs
Pat_30	Post-Resistance	LSM1	27257	37	8	38027393	38027393	Frame_Shift_Del	DEL	C	-	8	1110	c.158delG	c.(157-159)GGCfs	p.G53fs
Pat_30	Post-Resistance	TPD52	7163	37	8	80965625	80965625	Frame_Shift_Del	DEL	G	-	7	203	c.296delC	c.(295-297)GCAfs	p.A99fs
Pat_30	Post-Resistance	DDX58	23586	37	9	32466441	32466443	Splice_Site	DEL	TAT	-	2	4	c.2186_splice	c.e16-1	p.G729_splice
Pat_30	Post-Resistance	TFE3	7030	37	X	48887806	48887808	In_Frame_Del	DEL	CCT	-	7	233	.1589_1591delAG	(1588-1593)GAGGGG>GG	p.E530del
Pat_31	Pre-Treatment	CAMTA1	23261	37	1	7811329	7811329	Frame_Shift_Del	DEL	A	-	9	765	c.4760delA	c.(4759-4761)CAAfs	p.Q1587fs
Pat_31	Pre-Treatment	BEND5	79656	37	1	49201967	49201967	Frame_Shift_Del	DEL	T	-	7	255	c.1052delA	c.(1051-1053)AAGfs	p.K351fs
Pat_31	Pre-Treatment	ST6GALNAC5	81849	37	1	77334292	77334293	In_Frame_Ins	INS	-	CAGCAA	29	25	126_127insCAGC	c.(124-129)insCAGCAA	p.48_49insQQ
Pat_31	Pre-Treatment	BCL9	607	37	1	147091501	147091501	Frame_Shift_Del	DEL	C	-	8	422	c.1540delC	c.(1540-1542)CCCfs	p.P514fs
Pat_31	Pre-Treatment	PSMB4	5692	37	1	151374040	151374040	Frame_Shift_Del	DEL	A	-	12	1434	c.716delA	c.(715-717)GAAfs	p.E239fs
Pat_31	Pre-Treatment	TCHH	7062	37	1	152082301	152082303	In_Frame_Del	DEL	CTC	-	10	868	.3390_3392delGA	.(3388-3393)AAGAGA>AA	p.R1133del
Pat_31	Pre-Treatment	TCHH	7062	37	1	152084580	152084582	In_Frame_Del	DEL	CTC	-	10	265	.1111_1113delGA	c.(1111-1113)GAGdel	p.E371del
Pat_31	Pre-Treatment	FLG2	388698	37	1	152324558	152324559	Frame_Shift_Del	DEL	TG	-	11	1623	c.5703_5704delCA	c.(5701-5706)CACAGCfs	p.H1901fs
Pat_31	Pre-Treatment	KCNN3	3782	37	1	154680586	154680588	In_Frame_Del	DEL	GCT	-	7	208	.2060_2062delAG	.(2059-2064)CAGCTC>CT	p.Q687del
Pat_31	Pre-Treatment	KCNN3	3782	37	1	154842331	154842333	In_Frame_Del	DEL	TGC	-	8	81	c.108_110delGCA	c.(106-111)CAGCAA>CAA	p.36_37QQ>Q
Pat_31	Pre-Treatment	PBXIP1	57326	37	1	154917508	154917510	In_Frame_Del	DEL	GGT	-	7	260	.2186_2188delAC	(2185-2190)CACCGG>CG	p.H729del
Pat_31	Pre-Treatment	SHC1	6464	37	1	154942910	154942911	Frame_Shift_Ins	INS	-	G	7	236	c.92_93insC	c.(91-93)CCGfs	p.P31fs
Pat_31	Pre-Treatment	BCAN	63827	37	1	156626160	156626160	Frame_Shift_Del	DEL	G	-	7	656	c.2029delG	c.(2029-2031)GGGfs	p.G677fs

Pat_31	Pre-Treatment	NES	10763	37	1	156642804	156642804	Frame_Shift_Del	DEL	G	-	15	902	c.1176delC	c.(1174-1176)CCCfs	p.P392fs
Pat_31	Pre-Treatment	OR10Z1	128368	37	1	158576487	158576487	Frame_Shift_Del	DEL	G	-	10	1048	c.259delG	c.(259-261)GGGfs	p.G87fs
Pat_31	Pre-Treatment	PVRL4	81607	37	1	161044104	161044106	In_Frame_Del	DEL	CCA	-	7	562	.1058_1060delTG	(1057-1062)GTGGGT>GG	p.V353del
Pat_31	Pre-Treatment	PCP4L1	654790	37	1	161254154	161254156	In_Frame_Del	DEL	GGA	-	13	492	c.90_92delGGA	c.(88-93)GCGGAG>GCG	p.E35del
Pat_31	Pre-Treatment	PAPPA2	60676	37	1	176762724	176762724	Frame_Shift_Del	DEL	C	-	9	575	c.5049delC	c.(5047-5049)ATCfs	p.I1683fs
Pat_31	Pre-Treatment	CACNA1E	777	37	1	181680102	181680103	Frame_Shift_Del	DEL	AG	-	17	359	c.1068_1069delAG	c.(1066-1071)AAAGAGfs	p.K356fs
Pat_31	Pre-Treatment	PRG4	10216	37	1	186276643	186276645	In_Frame_Del	DEL	AAG	-	7	774	.1792_1794delAA	c.(1792-1794)AAGdel	p.K599del
Pat_31	Pre-Treatment	PPP1R15B	84919	37	1	204379335	204379335	Frame_Shift_Del	DEL	C	-	10	187	c.1205delG	c.(1204-1206)AGTfs	p.S402fs
Pat_31	Pre-Treatment	LOC642587	642587	37	1	209605637	209605648	In_Frame_Del	DEL	CAGCAGCA	-	21	39	263delAGCAGCA	264)GTAGCAGCAGCAGC	p.AAAA93del
Pat_31	Pre-Treatment	PTPN14	5784	37	1	214557049	214557051	In_Frame_Del	DEL	CCT	-	10	221	.2147_2149delAG	(2146-2151)GAGGCT>GC	p.E716del
Pat_31	Pre-Treatment	MIA3	375056	37	1	222838784	222838785	Frame_Shift_Del	DEL	CC	-	7	1664	c.5547_5548delCC	c.(5545-5550)GGCCCAfs	p.G1849fs
Pat_31	Pre-Treatment	AGT	183	37	1	230839055	230839055	Frame_Shift_Del	DEL	A	-	9	362	c.1290delT	c.(1288-1290)TTTfs	p.F430fs
Pat_31	Pre-Treatment	LZTS2	84445	37	10	102763415	102763417	In_Frame_Del	DEL	CCT	-	18	675	c.560_562delCCT	c.(559-564)GCCTCC>GCC	p.S197del
Pat_31	Pre-Treatment	FRG2B	441581	37	10	135438960	135438960	Frame_Shift_Del	DEL	C	-	18	680	c.480delG	c.(478-480)AGGfs	p.R160fs
Pat_31	Pre-Treatment	LOC653544	653544	37	10	135491013	135491014	Frame_Shift_Ins	INS	-	T	11	775	c.624_625insT	c.(622-627)GCCAGGfs	p.A208fs
Pat_31	Pre-Treatment	FADS2	9415	37	11	61607885	61607887	In_Frame_Del	DEL	TCC	-	12	620	c.398_400delTCC	c.(397-402)TTCCTC>TTC	p.L137del
Pat_31	Pre-Treatment	UVRAG	7405	37	11	75694430	75694431	Splice_Site	INS	-	A	14	125	c.700_splice	c.e8-1	p.K234_splice
Pat_31	Pre-Treatment	CADM1	23705	37	11	115080312	115080314	In_Frame_Del	DEL	TGG	-	7	212	.1058_1060delCC	.(1057-1062)ACCATC>AT	p.T353del
Pat_31	Pre-Treatment	H2AFX	3014	37	11	118965823	118965823	Frame_Shift_Del	DEL	G	-	8	751	c.282delC	c.(280-282)CTCfs	p.L94fs
Pat_31	Pre-Treatment	PRB2	653247	37	12	11546506	11546508	In_Frame_Del	DEL	TTG	-	30	991	c.504_506delCAA	c.(502-507)AACAAG>AAG	p.N168del
Pat_31	Pre-Treatment	PRB2	653247	37	12	11546732	11546733	In_Frame_Ins	INS	-	AGA	12	1080	c.279_280insTCT	c.(277-282)insTCT	p.93_94insS
Pat_31	Pre-Treatment	GPR19	2842	37	12	12814274	12814274	Frame_Shift_Del	DEL	T	-	8	535	c.1109delA	c.(1108-1110)AACfs	p.N370fs
Pat_31	Pre-Treatment	R3HDM2	22864	37	12	57674205	57674207	In_Frame_Del	DEL	TGC	-	11	245	.1236_1238delGC	.(1234-1239)CAGCAA>CA	.412_413QQ>
Pat_31	Pre-Treatment	EP400	57634	37	12	132446446	132446448	In_Frame_Del	DEL	GAG	-	9	306	.1282_1284delGA	c.(1282-1284)GAGdel	p.E437del
Pat_31	Pre-Treatment	EP400	57634	37	12	132547138	132547139	In_Frame_Ins	INS	-	CAA	8	295	.8226_8227insCA	c.(8224-8229)insCAA	.2748_2749ins
Pat_31	Pre-Treatment	KBTBD7	84078	37	13	41768293	41768293	Frame_Shift_Del	DEL	A	-	7	529	c.101delT	c.(100-102)TTCfs	p.F34fs
Pat_31	Pre-Treatment	TSC22D1	8848	37	13	45148706	45148708	In_Frame_Del	DEL	TGC	-	21	336	.1503_1505delGC	.(1501-1506)CAGCAA>CA	.501_502QQ>
Pat_31	Pre-Treatment	FARP1	10160	37	13	99092237	99092237	Frame_Shift_Del	DEL	G	-	10	1272	c.2456delG	c.(2455-2457)TGGfs	p.W819fs
Pat_31	Pre-Treatment	FAM155A	728215	37	13	108518338	108518338	Frame_Shift_Del	DEL	C	-	11	696	c.607delG	c.(607-609)GACfs	p.D203fs
Pat_31	Pre-Treatment	FAM155A	728215	37	13	108518687	108518689	In_Frame_Del	DEL	CTG	-	10	119	c.256_258delCAG	c.(256-258)CAGdel	p.Q86del
Pat_31	Pre-Treatment	APEX1	328	37	14	20923820	20923820	Frame_Shift_Del	DEL	A	-	9	256	c.16delA	c.(16-18)AAAfs	p.K6fs
Pat_31	Pre-Treatment	EXOC5	10640	37	14	57714403	57714403	Frame_Shift_Del	DEL	C	-	4	7	c.55delG	c.(55-57)GAAfs	p.E19fs
Pat_31	Pre-Treatment	PTPN21	11099	37	14	88945628	88945630	In_Frame_Del	DEL	TCC	-	10	161	.2145_2147delGG	(2143-2148)GAGGAC>GA	p.E715del
Pat_31	Pre-Treatment	BTBD7	55727	37	14	93720048	93720048	Frame_Shift_Del	DEL	T	-	7	409	c.1697delA	c.(1696-1698)AATfs	p.N566fs
Pat_31	Pre-Treatment	MEIS2	4212	37	15	37385874	37385874	Frame_Shift_Del	DEL	T	-	7	944	c.547delA	c.(547-549)ATGfs	p.M183fs
Pat_31	Pre-Treatment	HERC1	8925	37	15	63922683	63922683	Frame_Shift_Del	DEL	C	-	7	1682	c.12948delG	c.(12946-12948)GGGfs	p.G4316fs
Pat_31	Pre-Treatment	KIAA0430	9665	37	16	15729982	15729984	In_Frame_Del	DEL	CCA	-	7	475	c.360_362delTGG	c.(358-363)GGTGGC>GG	.120_121GG>
Pat_31	Pre-Treatment	C16orf88	400506	37	16	19725706	19725706	Frame_Shift_Del	DEL	T	-	8	217	c.652delA	c.(652-654)ATCfs	p.I218fs
Pat_31	Pre-Treatment	LOC100132247	100132247	37	16	22545744	22545755	In_Frame_Del	DEL	CACCCTCA	-	14	77	1451delTCCACC	1452)CTTCCACCCTCAG	p.PPSA485del
Pat_31	Pre-Treatment	SETD1A	9739	37	16	30982809	30982811	In_Frame_Del	DEL	TCC	-	9	289	.3127_3129delTC	c.(3127-3129)TCCdel	p.S1058del
Pat_31	Pre-Treatment	CCDC135	84229	37	16	57731885	57731887	In_Frame_Del	DEL	GGA	-	7	260	c.24_26delGGA	c.(22-27)GTGGAG>GTG	p.E13del
Pat_31	Pre-Treatment	ACD	65057	37	16	67693646	67693648	In_Frame_Del	DEL	GCA	-	11	783	c.551_553delTGC	c.(550-555)CTGCAG>CAG	p.L184del
Pat_31	Pre-Treatment	ADAMTS18	170692	37	16	77356311	77356311	Frame_Shift_Del	DEL	A	-	16	313	c.2085delT	c.(2083-2085)TTTfs	p.F695fs
Pat_31	Pre-Treatment	KIAA0182	23199	37	16	85682290	85682290	Frame_Shift_Del	DEL	C	-	17	439	c.359delC	c.(358-360)ACCfs	p.T120fs
Pat_31	Pre-Treatment	YBX2	51087	37	17	7193599	7193599	Frame_Shift_Del	DEL	G	-	7	681	c.715delC	c.(715-717)CGGfs	p.R239fs
Pat_31	Pre-Treatment	CHRNB1	1140	37	17	7357666	7357668	In_Frame_Del	DEL	CTG	-	9	547	c.871_873delCTG	c.(871-873)CTGdel	p.L294del
Pat_31	Pre-Treatment	KDM6B	23135	37	17	7751859	7751861	In_Frame_Del	DEL	CAC	-	7	142	.2253_2255delCA	(2251-2256)GTCACC>GT	p.T762del

Pat_31	Pre-Treatment	CHD3	1107	37	17	7798765	7798765	Frame_Shift_Del	DEL	C	-	9	443	c.1612delC	c.(1612-1614)CCCfs	p.P538fs
Pat_31	Pre-Treatment	PRR11	55771	37	17	57247171	57247171	Frame_Shift_Del	DEL	A	-	11	218	c.58delA	c.(58-60)AAAfs	p.K20fs
Pat_31	Pre-Treatment	USP36	57602	37	17	76795074	76795074	Frame_Shift_Del	DEL	G	-	8	931	c.3156delC	c.(3154-3156)GTCfs	p.V1052fs
Pat_31	Pre-Treatment	PIAS4	51588	37	19	4037775	4037777	In_Frame_Del	DEL	GAG	-	9	47	.1435_1437delGA	c.(1435-1437)GAGdel	p.E487del
Pat_31	Pre-Treatment	MLLT1	4298	37	19	6222272	6222274	In_Frame_Del	DEL	AGG	-	8	127	c.968_970delCCT	c.(967-972)TCCTTC>TTC	p.S323del
Pat_31	Pre-Treatment	GADD45GIP1	90480	37	19	13065273	13065275	In_Frame_Del	DEL	GCT	-	8	306	c.416_418delAGC	.(415-420)CAGCGG>CG	p.Q139del
Pat_31	Pre-Treatment	SFRS14	10147	37	19	19136394	19136394	Frame_Shift_Del	DEL	T	-	8	342	c.763delA	c.(763-765)ATAfs	p.I255fs
Pat_31	Pre-Treatment	ATP4A	495	37	19	36054349	36054351	In_Frame_Del	DEL	CTT	-	12	1307	c.91_93delAAG	c.(91-93)AAGdel	p.K31del
Pat_31	Pre-Treatment	HAUS5	23354	37	19	36108990	36108990	Frame_Shift_Del	DEL	C	-	7	882	c.714delC	c.(712-714)CACfs	p.H238fs
Pat_31	Pre-Treatment	PSG1	5669	37	19	43382402	43382402	Frame_Shift_Del	DEL	G	-	8	795	c.93delC	c.(91-93)CCCfs	p.P31fs
Pat_31	Pre-Treatment	TEAD2	8463	37	19	49850472	49850473	Frame_Shift_Ins	INS	-	G	10	761	c.883_884insC	c.(883-885)CATfs	p.H295fs
Pat_31	Pre-Treatment	LILRB1	10859	37	19	55146148	55146150	In_Frame_Del	DEL	CTC	-	9	181	.1417_1419delCT	c.(1417-1419)CTCdel	p.L479del
Pat_31	Pre-Treatment	RPL23AP32	56969	37	2	54756588	54756588	Frame_Shift_Del	DEL	A	-	8	499	c.106delA	c.(106-108)AAAfs	p.K36fs
Pat_31	Pre-Treatment	TMEM127	55654	37	2	96919781	96919783	In_Frame_Del	DEL	TGC	-	9	357	c.480_482delGCA	c.(478-483)CAGCAT>CAT	p.Q160del
Pat_31	Pre-Treatment	ANKRD36	375248	37	2	97808574	97808575	Splice_Site	INS	-	A	27	63	c.901_splice	c.e8+2	p.V301_splice
Pat_31	Pre-Treatment	MRPS9	64965	37	2	105713707	105713707	Frame_Shift_Del	DEL	G	-	7	251	c.1024delG	c.(1024-1026)GGAfs	p.G342fs
Pat_31	Pre-Treatment	CYP20A1	57404	37	2	204150380	204150380	Frame_Shift_Del	DEL	A	-	9	235	c.896delA	c.(895-897)CAAfs	p.Q299fs
Pat_31	Pre-Treatment	ALPP	250	37	2	233243529	233243531	In_Frame_Del	DEL	TGC	-	7	125	c.17_19delTGC	c.(16-21)ATGCTG>ATG	p.L13del
Pat_31	Pre-Treatment	GAL3ST2	64090	37	2	242738494	242738496	In_Frame_Del	DEL	TCC	-	9	432	c.44_46delTCC	c.(43-48)ATCCTC>ATC	p.L20del
Pat_31	Pre-Treatment	ZMYND8	23613	37	20	45875072	45875072	Frame_Shift_Del	DEL	T	-	7	589	c.1904delA	c.(1903-1905)AAGfs	p.K635fs
Pat_31	Pre-Treatment	CTCFL	140690	37	20	56099187	56099187	Frame_Shift_Del	DEL	T	-	9	1575	c.75delA	c.(73-75)AAAfs	p.K25fs
Pat_31	Pre-Treatment	TPTE	7179	37	21	10944697	10944697	Frame_Shift_Del	DEL	A	-	19	725	c.537delT	c.(535-537)TTTfs	p.F179fs
Pat_31	Pre-Treatment	IFNGR2	3460	37	21	34799292	34799292	Frame_Shift_Del	DEL	T	-	9	1239	c.514delT	c.(514-516)TTTfs	p.F172fs
Pat_31	Pre-Treatment	DNAJC28	54943	37	21	34860940	34860940	Frame_Shift_Del	DEL	G	-	11	948	c.761delC	c.(760-762)CCAfs	p.P254fs
Pat_31	Pre-Treatment	PLAC4	191585	37	21	42551313	42551313	Frame_Shift_Del	DEL	C	-	10	86	c.243delG	c.(241-243)TGGfs	p.W81fs
Pat_31	Pre-Treatment	DGCR14	8220	37	22	19124913	19124913	Frame_Shift_Del	DEL	C	-	7	940	c.958delG	c.(958-960)GAGfs	p.E320fs
Pat_31	Pre-Treatment	MYH9	4627	37	22	36689419	36689421	In_Frame_Del	DEL	CCT	-	9	369	.4049_4051delAG	(4048-4053)GAGGCC>GC	p.E1350del
Pat_31	Pre-Treatment	TCF20	6942	37	22	42605990	42605992	In_Frame_Del	DEL	CTG	-	8	323	.5320_5322delCA	c.(5320-5322)CAGdel	p.Q1774del
Pat_31	Pre-Treatment	CCR3	1232	37	3	46306948	46306948	Frame_Shift_Del	DEL	T	-	7	703	c.299delT	c.(298-300)GTTfs	p.V100fs
Pat_31	Pre-Treatment	BSN	8927	37	3	49698670	49698670	Frame_Shift_Del	DEL	T	-	7	249	c.9392delT	c.(9391-9393)CTTfs	p.L3131fs
Pat_31	Pre-Treatment	SLCO2A1	6578	37	3	133670082	133670083	Frame_Shift_Ins	INS	-	A	7	198	c.830_831insT	c.(829-831)TTCfs	p.F277fs
Pat_31	Pre-Treatment	PDE6B	5158	37	4	661763	661765	In_Frame_Del	DEL	AGG	-	9	358	.2471_2473delAG	(2470-2475)AAGGAG>AA	p.E828del
Pat_31	Pre-Treatment	SCLT1	132320	37	4	129864163	129864163	Frame_Shift_Del	DEL	T	-	9	377	c.1620delA	c.(1618-1620)AAAfs	p.K540fs
Pat_31	Pre-Treatment	FRG1	2483	37	4	190878555	190878556	Frame_Shift_Ins	INS	-	A	9	119	c.435_436insA	c.(433-438)GGGAAAfs	p.G145fs
Pat_31	Pre-Treatment	MED10	84246	37	5	6374471	6374471	Frame_Shift_Del	DEL	T	-	7	352	c.275delA	c.(274-276)AATfs	p.N92fs
Pat_31	Pre-Treatment	C6	729	37	5	41160299	41160300	Frame_Shift_Del	DEL	AC	-	8	491	c.1628_1629delG	c.(1627-1629)TGTfs	p.C543fs
Pat_31	Pre-Treatment	HAPLN1	1404	37	5	82937358	82937358	Frame_Shift_Del	DEL	T	-	9	571	c.1022delA	c.(1021-1023)AAGfs	p.K341fs
Pat_31	Pre-Treatment	MCC	4163	37	5	112824048	112824049	In_Frame_Ins	INS	-	GCC	9	30	c.63_64insGGC	c.(61-66)insGGC	p.21_22insG
Pat_31	Pre-Treatment	KCTD16	57528	37	5	143853531	143853531	Frame_Shift_Del	DEL	A	-	7	227	c.1141delA	c.(1141-1143)AAAfs	p.K381fs
Pat_31	Pre-Treatment	ATXN1	6310	37	6	16327864	16327865	In_Frame_Ins	INS	-	TGC	27	41	c.677_678insGCA	c.(676-678)CAC>CAGCAC	p.225_226ins
Pat_31	Pre-Treatment	BAT2	7916	37	6	31597338	31597340	In_Frame_Del	DEL	AGC	-	8	915	.1970_1972delAG	(1969-1974)AAGCAG>AA	p.Q661del
Pat_31	Pre-Treatment	CYP21A2	1589	37	6	31975223	31975224	Frame_Shift_Ins	INS	-	T	8	403	c.916_917insT	c.(916-918)GTTfs	p.V306fs
Pat_31	Pre-Treatment	PHACTR2	9749	37	6	144086414	144086414	Frame_Shift_Del	DEL	A	-	7	401	c.678delA	c.(676-678)TCAfs	p.S226fs
Pat_31	Pre-Treatment	NOX3	50508	37	6	155743925	155743926	Frame_Shift_Del	DEL	CA	-	7	880	c.1210_1211delTG	c.(1210-1212)TGCfs	p.C404fs
Pat_31	Pre-Treatment	TWISTNB	221830	37	7	19738111	19738113	In_Frame_Del	DEL	TTC	-	7	1597	c.843_845delGAA	c.(841-846)AAGAAA>AAA	.281_282KK>
Pat_31	Pre-Treatment	POM121	9883	37	7	72413723	72413724	In_Frame_Ins	INS	-	CTC	13	201	.3191_3192insCT	.(3190-3192)TTC>TTCTC	.1064_1065ins
Pat_31	Pre-Treatment	PTCD1	26024	37	7	99032605	99032607	In_Frame_Del	DEL	CTC	-	9	498	c.259_261delGAG	c.(259-261)GAGdel	p.E87del

Pat_31	Pre-Treatment	GPC2	221914	37	7	99771554	99771554	Frame_Shift_Del	DEL	C	-	8	794	c.796delG	c.(796-798)GTCfs	p.V266fs
Pat_31	Pre-Treatment	FOXP2	93986	37	7	114271580	114271582	Splice_Site	DEL	CAG	-	9	56	c.598_splice	c.e6-1	p.Q200_splice
Pat_31	Pre-Treatment	WASL	8976	37	7	123332839	123332841	In_Frame_Del	DEL	AGG	-	7	179	c.907_909delCCT	c.(907-909)CCTdel	p.P303del
Pat_31	Pre-Treatment	LUC7L2	51631	37	7	139094365	139094366	Frame_Shift_Del	DEL	AG	-	8	120	c.744_745delAG	c.(742-747)GAAGAGfs	p.E248fs
Pat_31	Pre-Treatment	OR9A4	130075	37	7	141619203	141619203	Frame_Shift_Del	DEL	T	-	7	956	c.528delT	c.(526-528)AATfs	p.N176fs
Pat_31	Pre-Treatment	CDK5	1020	37	7	150754217	150754217	Frame_Shift_Del	DEL	T	-	8	1275	c.68delA	c.(67-69)AACfs	p.N23fs
Pat_31	Pre-Treatment	EPB49	2039	37	8	21926552	21926552	Frame_Shift_Del	DEL	C	-	10	989	c.275delC	c.(274-276)TCCfs	p.S92fs
Pat_31	Pre-Treatment	SFTPC	6440	37	8	22020159	22020161	In_Frame_Del	DEL	GTG	-	10	330	c.115_117delGTG	c.(115-117)GTGdel	p.V44del
Pat_31	Pre-Treatment	KIAA1967	57805	37	8	22473324	22473324	Frame_Shift_Del	DEL	C	-	7	486	c.1507delC	c.(1507-1509)CCCfs	p.P503fs
Pat_31	Pre-Treatment	CHD7	55636	37	8	61769038	61769040	In_Frame_Del	DEL	GGA	-	10	118	.7199_7201delGG	(7198-7203)CGGAGG>CG	2400_2401RR>
Pat_31	Pre-Treatment	KCNB2	9312	37	8	73479985	73479985	Frame_Shift_Del	DEL	C	-	7	610	c.16delC	c.(16-18)CCCfs	p.P6fs
Pat_31	Pre-Treatment	TSNARE1	203062	37	8	143310866	143310868	In_Frame_Del	DEL	GAT	-	9	361	.1519_1521delAT	c.(1519-1521)ATCdel	p.I507del
Pat_31	Pre-Treatment	TPRN	286262	37	9	140087025	140087027	In_Frame_Del	DEL	TCC	-	7	41	.1659_1661delGG	(1657-1662)GAGGAA>GA	.553_554EE>I
Pat_31	Pre-Treatment	MAP7D3	79649	37	X	135314194	135314194	Frame_Shift_Del	DEL	G	-	7	603	c.922delC	c.(922-924)CAGfs	p.Q308fs
Pat_31	Pre-Treatment	MAGEC1	9947	37	X	140994639	140994641	In_Frame_Del	DEL	CTC	-	7	756	.1449_1451delCT	(1447-1452)AGCTCC>AG	.483_484SS>
Pat_31	Pre-Treatment	MAGEC1	9947	37	X	140995035	140995037	In_Frame_Del	DEL	TCT	-	7	696	.1845_1847delTC	.(1843-1848)CCTCTT>CC	p.L616del
Pat_31	Post-Resistance	SPEN	23013	37	1	16262465	16262466	Frame_Shift_Ins	INS	-	C	7	98	c.9730_9731insC	c.(9730-9732)ACCfs	p.T3244fs
Pat_31	Post-Resistance	NBPF1	55672	37	1	16918438	16918438	Frame_Shift_Del	DEL	G	-	8	1302	c.79delC	c.(79-81)CAGfs	p.Q27fs
Pat_31	Post-Resistance	PABPC4	8761	37	1	40028016	40028016	Frame_Shift_Del	DEL	G	-	8	301	c.1693delC	c.(1693-1695)CAGfs	p.Q565fs
Pat_31	Post-Resistance	ST6GALNAC5	81849	37	1	77334292	77334293	In_Frame_Ins	INS	-	CAGCAA	23	22	126_127insCAGC	c.(124-129)insCAGCAA	p.48_49insQQ
Pat_31	Post-Resistance	SPAG17	200162	37	1	118642274	118642274	Frame_Shift_Del	DEL	G	-	7	605	c.784delC	c.(784-786)CTGfs	p.L262fs
Pat_31	Post-Resistance	NOTCH2	4853	37	1	120458346	120458347	Frame_Shift_Del	DEL	CG	-	17	813	.6998_6999delC	c.(6997-6999)GCGfs	p.A2333fs
Pat_31	Post-Resistance	ECM1	1893	37	1	150483467	150483467	Frame_Shift_Del	DEL	C	-	9	873	c.501delC	c.(499-501)TTCfs	p.F167fs
Pat_31	Post-Resistance	NUP210L	91181	37	1	154026862	154026862	Frame_Shift_Del	DEL	G	-	7	219	c.3325delC	c.(3325-3327)CAGfs	p.Q1109fs
Pat_31	Post-Resistance	KCNN3	3782	37	1	154842331	154842333	In_Frame_Del	DEL	TGC	-	17	199	c.108_110delGCA	c.(106-111)CAGCAA>CAA	p.36_37QQ>Q
Pat_31	Post-Resistance	OR10Z1	128368	37	1	158576487	158576487	Frame_Shift_Del	DEL	G	-	7	702	c.259delG	c.(259-261)GGGfs	p.G87fs
Pat_31	Post-Resistance	KCNJ9	3765	37	1	160054230	160054232	In_Frame_Del	DEL	TGC	-	8	213	c.410_412delTGC	.(409-414)GTGCTG>GTG	p.L141del
Pat_31	Post-Resistance	HMCN1	83872	37	1	186050426	186050426	Frame_Shift_Del	DEL	C	-	8	987	c.8687delC	c.(8686-8688)TCCfs	p.S2896fs
Pat_31	Post-Resistance	LOC642587	642587	37	1	209605637	209605648	In_Frame_Del	DEL	CAGCAGCA	-	11	31	263delAGCAGCA	264)GTAGCAGCAGCAGC	p.AAAA93del
Pat_31	Post-Resistance	URB2	9816	37	1	229771782	229771782	Frame_Shift_Del	DEL	G	-	8	1101	c.1422delG	c.(1420-1422)TTGfs	p.L474fs
Pat_31	Post-Resistance	CHRM3	1131	37	1	240072444	240072444	Frame_Shift_Del	DEL	A	-	10	132	c.1693delA	c.(1693-1695)AAAfs	p.K565fs
Pat_31	Post-Resistance	OR2M2	391194	37	1	248343440	248343441	Frame_Shift_Del	DEL	GG	-	8	1323	c.153_154delGG	c.(151-156)CTGGACfs	p.L51fs
Pat_31	Post-Resistance	SFMBT2	57713	37	10	7212995	7212997	In_Frame_Del	DEL	CTC	-	8	560	.2437_2439delGA	c.(2437-2439)GAGdel	p.E813del
Pat_31	Post-Resistance	MTPAP	55149	37	10	30653930	30653932	In_Frame_Del	DEL	TCC	-	8	135	c.250_252delGGA	c.(250-252)GGAdel	p.G84del
Pat_31	Post-Resistance	CHST15	51363	37	10	125804296	125804296	Frame_Shift_Del	DEL	A	-	4	8	c.686delT	c.(685-687)TTCfs	p.F229fs
Pat_31	Post-Resistance	C11orf95	65998	37	11	63533335	63533337	In_Frame_Del	DEL	TCC	-	8	41	c.579_581delGGA	.(577-582)GAGGAA>GA	.193_194EE>I
Pat_31	Post-Resistance	TSKU	25987	37	11	76506673	76506675	In_Frame_Del	DEL	CTG	-	10	155	c.13_15delCTG	c.(13-15)CTGdel	p.L9del
Pat_31	Post-Resistance	PRDM10	56980	37	11	129827738	129827738	Frame_Shift_Del	DEL	G	-	7	1265	c.137delC	c.(136-138)CCAfs	p.P46fs
Pat_31	Post-Resistance	PRPF40B	25766	37	12	50027673	50027675	In_Frame_Del	DEL	CAG	-	7	392	c.544_546delCAG	c.(544-546)CAGdel	p.Q185del
Pat_31	Post-Resistance	GEFT	115557	37	12	58005763	58005763	Frame_Shift_Del	DEL	G	-	8	196	c.86delG	c.(85-87)CGGfs	p.R29fs
Pat_31	Post-Resistance	CUX2	23316	37	12	111758235	111758237	In_Frame_Del	DEL	TCC	-	10	207	.2422_2424delTC	c.(2422-2424)TCCdel	p.S813del
Pat_31	Post-Resistance	PTPN21	11099	37	14	88945628	88945630	In_Frame_Del	DEL	TCC	-	8	136	.2145_2147delGG	(2143-2148)GAGGAC>GA	p.E715del
Pat_31	Post-Resistance	HERC2	8924	37	15	28518115	28518115	Frame_Shift_Del	DEL	C	-	19	239	c.836delG	c.(835-837)GGAfs	p.G279fs
Pat_31	Post-Resistance	THBS1	7057	37	15	39881489	39881489	Frame_Shift_Del	DEL	C	-	8	749	c.1860delC	c.(1858-1860)TGCfs	p.C620fs
Pat_31	Post-Resistance	SHC4	399694	37	15	49254948	49254948	Frame_Shift_Del	DEL	G	-	10	401	c.265delC	c.(265-267)CGCfs	p.R89fs
Pat_31	Post-Resistance	CPEB1	64506	37	15	83224645	83224646	Frame_Shift_Del	DEL	CT	-	7	183	c.1013_1014delAG	c.(1012-1014)GAGfs	p.E338fs
Pat_31	Post-Resistance	C16orf79	283870	37	16	2260586	2260588	In_Frame_Del	DEL	CAG	-	7	44	c.115_117delCTG	c.(115-117)CTGdel	p.L39del

Pat_31	Post-Resistance	RABEP2	79874	37	16	28931200	28931202	In_Frame_Del	DEL	CTG	-	11	92	c.337_339delCAG	c.(337-339)CAGdel	p.Q113del
Pat_31	Post-Resistance	LRRC36	55282	37	16	67409220	67409220	Frame_Shift_Del	DEL	C	-	8	1339	c.1565delC	c.(1564-1566)ACCfs	p.T522fs
Pat_31	Post-Resistance	ACD	65057	37	16	67693646	67693648	In_Frame_Del	DEL	GCA	-	10	1012	c.551_553delTGC	.(550-555)CTGCAG>CAG	p.L184del
Pat_31	Post-Resistance	KIAA0182	23199	37	16	85682290	85682290	Frame_Shift_Del	DEL	C	-	14	358	c.359delC	c.(358-360)ACCfs	p.T120fs
Pat_31	Post-Resistance	PELP1	27043	37	17	4575894	4575894	Frame_Shift_Del	DEL	G	-	9	154	c.2392delC	c.(2392-2394)CTGfs	p.L798fs
Pat_31	Post-Resistance	PELP1	27043	37	17	4607293	4607295	In_Frame_Del	DEL	CAG	-	12	862	c.112_114delCTG	c.(112-114)CTGdel	p.L38del
Pat_31	Post-Resistance	DHX33	56919	37	17	5372037	5372039	In_Frame_Del	DEL	CCT	-	7	228	c.141_143delAGG	.(139-144)GGAGGC>GG	p.47_48GG>G
Pat_31	Post-Resistance	PLSCR3	57048	37	17	7294059	7294059	Frame_Shift_Del	DEL	C	-	9	770	c.725delG	c.(724-726)GGCfs	p.G242fs
Pat_31	Post-Resistance	CHD3	1107	37	17	7788146	7788148	In_Frame_Del	DEL	GAG	-	10	87	c.22_24delGAG	c.(22-24)GAGdel	p.E14del
Pat_31	Post-Resistance	NUFIP2	57532	37	17	27620932	27620934	In_Frame_Del	DEL	TGG	-	7	582	c.144_146delCCA	c.(142-147)CACCAT>CAT	p.48_49HH>H
Pat_31	Post-Resistance	KCNH4	23415	37	17	40328259	40328259	Frame_Shift_Del	DEL	C	-	10	393	c.642delG	c.(640-642)GGGfs	p.G214fs
Pat_31	Post-Resistance	KIAA0195	9772	37	17	73482037	73482039	In_Frame_Del	DEL	TGC	-	7	313	c.230_232delTGC	.(229-234)GTGCTG>GTG	p.L81del
Pat_31	Post-Resistance	CBX4	8535	37	17	77808241	77808243	In_Frame_Del	DEL	GTG	-	11	103	.1198_1200delCA	c.(1198-1200)CACdel	p.H400del
Pat_31	Post-Resistance	LRG1	116844	37	19	4538890	4538890	Frame_Shift_Del	DEL	C	-	7	276	c.106delG	c.(106-108)GTCfs	p.V36fs
Pat_31	Post-Resistance	SLC25A41	284427	37	19	6433605	6433605	Frame_Shift_Del	DEL	G	-	8	173	c.100delC	c.(100-102)CAAfs	p.Q34fs
Pat_31	Post-Resistance	MCOLN1	57192	37	19	7592423	7592423	Frame_Shift_Del	DEL	C	-	8	914	c.589delC	c.(589-591)CCCfs	p.P197fs
Pat_31	Post-Resistance	MYO1F	4542	37	19	8595361	8595361	Frame_Shift_Del	DEL	C	-	7	1167	c.2140delG	c.(2140-2142)GAGfs	p.E714fs
Pat_31	Post-Resistance	SBSN	374897	37	19	36019046	36019047	Frame_Shift_Del	DEL	CT	-	8	449	c.137_138delAG	c.(136-138)GAGfs	p.E46fs
Pat_31	Post-Resistance	BCL3	602	37	19	45262726	45262726	Frame_Shift_Del	DEL	C	-	7	1428	c.1219delC	c.(1219-1221)CCCfs	p.P407fs
Pat_31	Post-Resistance	RELB	5971	37	19	45540824	45540824	Frame_Shift_Del	DEL	C	-	4	7	c.1516delC	c.(1516-1518)CCCfs	p.P506fs
Pat_31	Post-Resistance	HRC	3270	37	19	49656769	49656771	In_Frame_Del	DEL	CCT	-	7	58	.1724_1726delAG	(1723-1728)GAGGGG>GG	p.E575del
Pat_31	Post-Resistance	TBC1D17	79735	37	19	50385312	50385312	Frame_Shift_Del	DEL	C	-	7	2268	c.542delC	c.(541-543)TCCfs	p.S181fs
Pat_31	Post-Resistance	SIGLEC9	27180	37	19	51628233	51628235	In_Frame_Del	DEL	TGC	-	7	114	c.2_4delTGC	c.(1-6)ATGCTG>ATG	p.L6del
Pat_31	Post-Resistance	BRE	9577	37	2	28521301	28521301	Frame_Shift_Del	DEL	A	-	7	350	c.1031delA	c.(1030-1032)CAAfs	p.Q344fs
Pat_31	Post-Resistance	HK2	3099	37	2	75061739	75061740	Frame_Shift_Del	DEL	TC	-	11	816	c.32_33delTC	c.(31-33)TTCfs	p.F11fs
Pat_31	Post-Resistance	GAL3ST2	64090	37	2	242738494	242738496	In_Frame_Del	DEL	TCC	-	17	471	c.44_46delTCC	c.(43-48)ATCCTC>ATC	p.L20del
Pat_31	Post-Resistance	MED15	51586	37	22	20918793	20918795	In_Frame_Del	DEL	CAG	-	8	183	c.508_510delCAG	c.(508-510)CAGdel	p.Q174del
Pat_31	Post-Resistance	PI4KA	5297	37	22	21064242	21064242	Frame_Shift_Del	DEL	C	-	8	373	c.5953delG	c.(5953-5955)GACfs	p.D1985fs
Pat_31	Post-Resistance	TFIP11	24144	37	22	26906183	26906185	In_Frame_Del	DEL	TCA	-	11	380	c.54_56delTGA	c.(52-57)GATGAC>GAC	p.18_19DD>D
Pat_31	Post-Resistance	POLR2F	5435	37	22	38363691	38363691	Frame_Shift_Del	DEL	G	-	7	891	c.353delG	c.(352-354)TGGfs	p.W118fs
Pat_31	Post-Resistance	PRKCD	5580	37	3	53220653	53220653	Frame_Shift_Del	DEL	G	-	7	1087	c.1294delG	c.(1294-1296)GGGfs	p.G432fs
Pat_31	Post-Resistance	PDE6B	5158	37	4	661763	661765	In_Frame_Del	DEL	AGG	-	10	199	.2471_2473delAG	(2470-2475)AAGGAG>AA	p.E828del
Pat_31	Post-Resistance	CRIPAK	285464	37	4	1388530	1388531	Frame_Shift_Ins	INS	-	CA	12	1495	c.231_232insCA	c.(229-234)GCTCATfs	p.A77fs
Pat_31	Post-Resistance	CRIPAK	285464	37	4	1388993	1388994	Frame_Shift_Del	DEL	CA	-	14	1562	c.694_695delCA	c.(694-696)CACfs	p.H232fs
Pat_31	Post-Resistance	GABRG1	2565	37	4	46060358	46060358	Frame_Shift_Del	DEL	A	-	8	95	c.792delT	c.(790-792)TTTfs	p.F264fs
Pat_31	Post-Resistance	SPRY1	10252	37	4	124322763	124322763	Frame_Shift_Del	DEL	A	-	8	843	c.17delA	c.(16-18)CAAfs	p.Q6fs
Pat_31	Post-Resistance	RGS14	10636	37	5	176798525	176798525	Frame_Shift_Del	DEL	C	-	9	904	c.1433delC	c.(1432-1434)TCCfs	p.S478fs
Pat_31	Post-Resistance	ATXN1	6310	37	6	16327864	16327865	In_Frame_Ins	INS	-	TGC	30	57	c.677_678insGCA	.(676-678)CAC>CAGCAC	p.225_226insC
Pat_31	Post-Resistance	REPS1	85021	37	6	139266690	139266690	Frame_Shift_Del	DEL	T	-	9	787	c.422delA	c.(421-423)AAGfs	p.K141fs
Pat_31	Post-Resistance	GRM1	2911	37	6	146755399	146755401	In_Frame_Del	DEL	CAG	-	7	600	.3052_3054delCA	c.(3052-3054)CAGdel	p.Q1022del
Pat_31	Post-Resistance	STK31	56164	37	7	23809306	23809306	Frame_Shift_Del	DEL	G	-	7	303	c.1644delG	c.(1642-1644)ATGfs	p.M548fs
Pat_31	Post-Resistance	HOXA1	3198	37	7	27135314	27135316	In_Frame_Del	DEL	CGA	-	10	355	c.216_218delTCG	c.(214-219)CATCAC>CAC	p.72_73HH>H
Pat_31	Post-Resistance	MEPCE	56257	37	7	100028067	100028068	Frame_Shift_Ins	INS	-	G	7	114	c.426_427insG	c.(424-429)CCTGGGfs	p.P142fs
Pat_31	Post-Resistance	FOXP2	93986	37	7	114271580	114271582	Splice_Site	DEL	CAG	-	10	52	c.598_splice	c.e6-1	p.Q200_splice
Pat_31	Post-Resistance	RBM28	55131	37	7	127964714	127964715	Frame_Shift_Del	DEL	TG	-	8	1595	c.1236_1237delCA	c.(1234-1239)CTCAAGfs	p.L412fs
Pat_31	Post-Resistance	OR9A4	130075	37	7	141619203	141619203	Frame_Shift_Del	DEL	T	-	14	482	c.528delT	c.(526-528)AATfs	p.N176fs
Pat_31	Post-Resistance	PAXIP1	22976	37	7	154760670	154760672	In_Frame_Del	DEL	TGC	-	8	49	.1239_1241delGC	.(1237-1242)CAGCAC>CA	p.Q413del

Pat_31	Post-Resistance	RBM33	155435	37	7	155531073	155531074	Frame_Shift_Del	DEL	CA	-	10	498	c.1713_1714delC	c.(1711-1716)CCCACAfs	p.P571fs
Pat_31	Post-Resistance	NEFM	4741	37	8	24771483	24771483	Frame_Shift_Del	DEL	G	-	7	502	c.177delG	c.(175-177)CCGfs	p.P59fs
Pat_31	Post-Resistance	GOT1L1	137362	37	8	37791958	37791958	Frame_Shift_Del	DEL	G	-	8	1097	c.1119delC	c.(1117-1119)CCCfs	p.P373fs
Pat_31	Post-Resistance	SDCBP	6386	37	8	59484810	59484811	Frame_Shift_Del	DEL	GA	-	8	834	c.177_178delGA	c.(175-180)CTGAGTfs	p.L59fs
Pat_31	Post-Resistance	CHD7	55636	37	8	61769038	61769040	In_Frame_Del	DEL	GGA	-	8	97	.7199_7201delGG	(7198-7203)CGGAGG>CG	2400_2401RR
Pat_31	Post-Resistance	ZFHX4	79776	37	8	77775449	77775451	In_Frame_Del	DEL	CCT	-	8	68	.9364_9366delCC	c.(9364-9366)CCTdel	p.P3128del
Pat_31	Post-Resistance	TSNARE1	203062	37	8	143310866	143310868	In_Frame_Del	DEL	GAT	-	8	393	.1519_1521delAT	c.(1519-1521)ATCdel	p.I507del
Pat_31	Post-Resistance	ZC3H3	23144	37	8	144522387	144522389	In_Frame_Del	DEL	GAG	-	7	94	.2637_2639delCT	.(2635-2640)TCCTCA>TC	.879_880SS>
Pat_31	Post-Resistance	CYC1	1537	37	8	145151068	145151068	Frame_Shift_Del	DEL	C	-	7	1144	c.368delC	c.(367-369)TCCfs	p.S123fs
Pat_31	Post-Resistance	FAM75A6	389730	37	9	43625017	43625017	Frame_Shift_Del	DEL	G	-	11	719	c.3670delC	c.(3670-3672)CATfs	p.H1224fs
Pat_31	Post-Resistance	NR4A3	8013	37	9	102590616	102590618	In_Frame_Del	DEL	CAC	-	15	94	c.292_294delCAC	c.(292-294)CACdel	p.H108del
Pat_31	Post-Resistance	MAP7D3	79649	37	X	135314194	135314194	Frame_Shift_Del	DEL	G	-	9	441	c.922delC	c.(922-924)CAGfs	p.Q308fs
Pat_32	Pre-Treatment	NBPF1	55672	37	1	16892147	16892147	Frame_Shift_Del	DEL	G	-	11	1848	c.3270delC	c.(3268-3270)GGCfs	p.G1090fs
Pat_32	Pre-Treatment	EXTL1	2134	37	1	26349533	26349535	In_Frame_Del	DEL	CCT	-	8	189	c.396_398delCCT	c.(394-399)TGCCTC>TGC	p.L137del
Pat_32	Pre-Treatment	SDC3	9672	37	1	31347370	31347370	Frame_Shift_Del	DEL	C	-	7	553	c.936delG	c.(934-936)GGGfs	p.G312fs
Pat_32	Pre-Treatment	MAP7D1	55700	37	1	36636587	36636587	Frame_Shift_Del	DEL	C	-	8	307	c.62delC	c.(61-63)ACCfs	p.T21fs
Pat_32	Pre-Treatment	HIAT1	64645	37	1	100534122	100534122	Frame_Shift_Del	DEL	T	-	7	137	c.799delT	c.(799-801)TTTfs	p.F267fs
Pat_32	Pre-Treatment	C1orf189	388701	37	1	154171938	154171939	Frame_Shift_Del	DEL	GA	-	7	529	c.270_271delTC	c.(268-273)AATCAGfs	p.N90fs
Pat_32	Pre-Treatment	ISG20L2	81875	37	1	156694023	156694023	Frame_Shift_Del	DEL	G	-	8	196	c.865delC	c.(865-867)CTCfs	p.L289fs
Pat_32	Pre-Treatment	HMCN1	83872	37	1	186151356	186151356	Frame_Shift_Del	DEL	G	-	8	240	c.16351delG	c.(16351-16353)GGAfs	p.G5451fs
Pat_32	Pre-Treatment	CDC42BPA	8476	37	1	227257519	227257519	Frame_Shift_Del	DEL	C	-	8	174	c.2863delG	c.(2863-2865)GCAfs	p.A955fs
Pat_32	Pre-Treatment	ARID5B	84159	37	10	63852298	63852298	Frame_Shift_Del	DEL	A	-	9	249	c.3076delA	c.(3076-3078)AAAfs	p.K1026fs
Pat_32	Pre-Treatment	LDB3	11155	37	10	88439241	88439242	Frame_Shift_Del	DEL	TC	-	40	75	c.211_212delTC	c.(211-213)TCTfs	p.S71fs
Pat_32	Pre-Treatment	PDE3B	5140	37	11	14666110	14666110	Frame_Shift_Del	DEL	G	-	6	13	c.489delG	c.(487-489)CTGfs	p.L163fs
Pat_32	Pre-Treatment	C11orf9	745	37	11	61539013	61539013	Frame_Shift_Del	DEL	C	-	7	216	c.782delC	c.(781-783)TCCfs	p.S261fs
Pat_32	Pre-Treatment	SLC25A45	283130	37	11	65146856	65146856	Frame_Shift_Del	DEL	C	-	7	331	c.330delG	c.(328-330)GGGfs	p.G110fs
Pat_32	Pre-Treatment	NDUFV1	4723	37	11	67377888	67377889	Frame_Shift_Del	DEL	GG	-	7	459	c.547_548delGG	c.(547-549)GGCfs	p.G183fs
Pat_32	Pre-Treatment	C15orf52	388115	37	15	40631782	40631782	Frame_Shift_Del	DEL	C	-	7	549	c.294delG	c.(292-294)GGGfs	p.G98fs
Pat_32	Pre-Treatment	SPTBN5	51332	37	15	42159187	42159187	Frame_Shift_Del	DEL	C	-	4	4	c.6345delG	c.(6343-6345)CTGfs	p.L2115fs
Pat_32	Pre-Treatment	BLM	641	37	15	91304286	91304288	In_Frame_Del	DEL	TGA	-	11	306	.1683_1685delTG	.(1681-1686)TTTGAT>TT	p.D566del
Pat_32	Pre-Treatment	DHX33	56919	37	17	5365825	5365825	Frame_Shift_Del	DEL	G	-	8	428	c.492delC	c.(490-492)GACfs	p.D164fs
Pat_32	Pre-Treatment	NUFIP2	57532	37	17	27620990	27620992	In_Frame_Del	DEL	GCT	-	7	91	c.86_88delAGC	c.(85-90)CAGCCG>CCG	p.Q29del
Pat_32	Pre-Treatment	STXBP4	252983	37	17	53068301	53068301	Frame_Shift_Del	DEL	G	-	45	120	c.163delG	c.(163-165)GGAfs	p.G55fs
Pat_32	Pre-Treatment	ELAC1	55520	37	18	48510487	48510488	Frame_Shift_Ins	INS	-	CA	31	74	c.179_180insCA	c.(178-180)ATCfs	p.I60fs
Pat_32	Pre-Treatment	SMAD4	4089	37	18	48584514	48584514	Frame_Shift_Del	DEL	G	-	8	107	c.687delG	c.(685-687)CTGfs	p.L229fs
Pat_32	Pre-Treatment	DOHH	83475	37	19	3492277	3492278	Frame_Shift_Del	DEL	GC	-	4	9	c.571_572delGC	c.(571-573)GCCfs	p.A191fs
Pat_32	Pre-Treatment	CHERP	10523	37	19	16640581	16640583	In_Frame_Del	DEL	TGC	-	13	89	.1005_1007delGC	.(1003-1008)CAGCAA>CA	.335_336QQ>
Pat_32	Pre-Treatment	SPTBN4	57731	37	19	41060321	41060322	Frame_Shift_Del	DEL	AC	-	2	4	c.4943_4944delAC	c.(4942-4944)GACfs	p.D1648fs
Pat_32	Pre-Treatment	ZNF579	163033	37	19	56089908	56089909	In_Frame_Ins	INS	-	CCG	5	9	.1097_1098insCG	(1096-1098)GGG>GGCGG	.366_366G>G
Pat_32	Pre-Treatment	AGBL5	60509	37	2	27278901	27278901	Frame_Shift_Del	DEL	C	-	9	647	c.1260delC	c.(1258-1260)ATCfs	p.I420fs
Pat_32	Pre-Treatment	GTF3C2	2976	37	2	27559092	27559092	Frame_Shift_Del	DEL	C	-	8	250	c.1328delG	c.(1327-1329)GGCfs	p.G443fs
Pat_32	Pre-Treatment	GCC2	9648	37	2	109087832	109087832	Frame_Shift_Del	DEL	T	-	7	254	c.2047delT	c.(2047-2049)TTGfs	p.L683fs
Pat_32	Pre-Treatment	CCDC150	284992	37	2	197596853	197596853	Frame_Shift_Del	DEL	G	-	9	133	c.3166delG	c.(3166-3168)GGGfs	p.G1056fs
Pat_32	Pre-Treatment	TRPM8	79054	37	2	234879010	234879010	Frame_Shift_Del	DEL	C	-	10	978	c.2295delC	c.(2293-2295)CACfs	p.H765fs
Pat_32	Pre-Treatment	SNX21	90203	37	20	44469908	44469908	Frame_Shift_Del	DEL	C	-	8	897	c.1078delC	c.(1078-1080)CCCfs	p.P360fs
Pat_32	Pre-Treatment	CEBPB	1051	37	20	48807612	48807614	In_Frame_Del	DEL	GCC	-	8	277	c.42_44delGCC	c.(40-45)CTGCCG>CTG	p.P19del
Pat_32	Pre-Treatment	SLMO2	51012	37	20	57613630	57613630	Frame_Shift_Del	DEL	G	-	8	1184	c.92delC	c.(91-93)CCAfs	p.P31fs

Pat_32	Pre-Treatment	SLC17A9	63910	37	20	61594045	61594045	Frame_Shift_Del	DEL	C	-	7	441	c.567delC	c.(565-567)TTCfs	p.F189fs
Pat_32	Pre-Treatment	KCNE2	9992	37	21	35742893	35742893	Frame_Shift_Del	DEL	C	-	7	456	c.116delC	c.(115-117)GCCfs	p.A39fs
Pat_32	Pre-Treatment	PTTG1IP	754	37	21	46276194	46276196	In_Frame_Del	DEL	GCA	-	8	173	c.361_363delTGC	c.(361-363)TGCdel	p.C121del
Pat_32	Pre-Treatment	C22orf32	91689	37	22	42478046	42478048	In_Frame_Del	DEL	GAT	-	8	461	c.304_306delGAT	c.(304-306)GATdel	p.D107del
Pat_32	Pre-Treatment	MCAT	27349	37	22	43537228	43537230	In_Frame_Del	DEL	CAG	-	7	576	c.449_451delCTG	.(448-453)GCTGGA>GGA	p.A150del
Pat_32	Pre-Treatment	CELSR3	1951	37	3	48698223	48698224	Frame_Shift_Del	DEL	CT	-	8	53	c.1844_1845delAG	c.(1843-1845)GAGfs	p.E615fs
Pat_32	Pre-Treatment	GSK3B	2932	37	3	119624606	119624606	Frame_Shift_Del	DEL	A	-	10	638	c.809delT	c.(808-810)ATCfs	p.I270fs
Pat_32	Pre-Treatment	TMCC1	23023	37	3	129370576	129370578	In_Frame_Del	DEL	CTG	-	10	198	.1708_1710delCA	c.(1708-1710)CAGdel	p.Q570del
Pat_32	Pre-Treatment	FGFRL1	53834	37	4	1019055	1019056	Frame_Shift_Del	DEL	CA	-	8	9	c.1435_1436delCA	c.(1435-1437)CACfs	p.H479fs
Pat_32	Pre-Treatment	CRIPAK	285464	37	4	1389330	1389331	Frame_Shift_Del	DEL	CA	-	8	831	c.1031_1032delCA	c.(1030-1032)TCAfs	p.S344fs
Pat_32	Pre-Treatment	PROM1	8842	37	4	15995680	15995680	Frame_Shift_Del	DEL	T	-	8	225	c.1697delA	c.(1696-1698)AATfs	p.N566fs
Pat_32	Pre-Treatment	EPHA5	2044	37	4	66213776	66213777	Frame_Shift_Del	DEL	TG	-	8	425	c.2653_2654delCA	c.(2653-2655)CAAfs	p.Q885fs
Pat_32	Pre-Treatment	C5orf35	133383	37	5	56208946	56208946	Frame_Shift_Del	DEL	C	-	7	308	c.575delC	c.(574-576)TCAfs	p.S192fs
Pat_32	Pre-Treatment	IK	3550	37	5	140032593	140032594	Frame_Shift_Del	DEL	GA	-	8	73	c.268_269delGA	c.(268-270)GAGfs	p.E90fs
Pat_32	Pre-Treatment	PCDHB4	56131	37	5	140502607	140502607	Frame_Shift_Del	DEL	C	-	8	316	c.1027delC	c.(1027-1029)CCCfs	p.P343fs
Pat_32	Pre-Treatment	SPRY4	81848	37	5	141694361	141694363	In_Frame_Del	DEL	TGC	-	9	416	c.311_313delGCA	c.(310-315)AGCACA>ACA	p.S104del
Pat_32	Pre-Treatment	RBM27	54439	37	5	145647319	145647320	Frame_Shift_Ins	INS	-	A	7	74	c.2439_2440insA	c.(2437-2442)CTTAAAfs	p.L813fs
Pat_32	Pre-Treatment	C6orf134	79969	37	6	30610757	30610757	Frame_Shift_Del	DEL	G	-	7	462	c.937delG	c.(937-939)GGGfs	p.G313fs
Pat_32	Pre-Treatment	DAXX	1616	37	6	33288519	33288520	Frame_Shift_Del	DEL	TA	-	8	452	c.1032_1033delTA	c.(1030-1035)TATAGGfs	p.Y344fs
Pat_32	Pre-Treatment	SRPK1	6732	37	6	35888274	35888274	Frame_Shift_Del	DEL	G	-	8	446	c.45delC	c.(43-45)ACCfs	p.T15fs
Pat_32	Pre-Treatment	TNRC18	84629	37	7	5352831	5352833	In_Frame_Del	DEL	CTG	-	5	6	.7689_7691delCA	.(7687-7692)AGCAGT>AG	2563_2564SS
Pat_32	Pre-Treatment	NEUROD6	63974	37	7	31378634	31378635	Frame_Shift_Ins	INS	-	T	10	301	c.248_249insA	c.(247-249)AAGfs	p.K83fs
Pat_32	Pre-Treatment	LIMK1	3984	37	7	73510992	73510993	Frame_Shift_Del	DEL	GA	-	8	311	c.193_194delGA	c.(193-195)GAGfs	p.E65fs
Pat_32	Pre-Treatment	PRKRIP1	79706	37	7	102065517	102065519	In_Frame_Del	DEL	GAG	-	8	209	c.514_516delGAG	c.(514-516)GAGdel	p.E176del
Pat_32	Pre-Treatment	TNPO3	23534	37	7	128610259	128610259	Frame_Shift_Del	DEL	G	-	8	815	c.2541delC	c.(2539-2541)CCCfs	p.P847fs
Pat_32	Pre-Treatment	PRKDC	5591	37	8	48746799	48746799	Frame_Shift_Del	DEL	T	-	8	422	c.8110delA	c.(8110-8112)AGGfs	p.R2704fs
Pat_32	Pre-Treatment	EIF2C2	27161	37	8	141554345	141554345	Frame_Shift_Del	DEL	G	-	8	378	c.1806delC	c.(1804-1806)CCCfs	p.P602fs
Pat_32	Pre-Treatment	TSTA3	7264	37	8	144696820	144696820	Frame_Shift_Del	DEL	G	-	8	288	c.438delC	c.(436-438)GCCfs	p.A146fs
Pat_32	Pre-Treatment	HABP4	22927	37	9	99212888	99212889	Frame_Shift_Ins	INS	-	G	4	2	c.327_328insG	c.(325-330)CCCGGGfs	p.P109fs
Pat_32	Pre-Treatment	NUP188	23511	37	9	131742947	131742949	In_Frame_Del	DEL	CTC	-	7	211	.1332_1334delCT	.(1330-1335)CTCTCC>CT	p.S445del
Pat_32	Pre-Treatment	HTATSF1	27336	37	X	135585048	135585050	In_Frame_Del	DEL	AAG	-	7	321	c.682_684delAAG	c.(682-684)AAGdel	p.K232del
Pat_32	Pre-Treatment	HCFC1	3054	37	X	153228755	153228755	Frame_Shift_Del	DEL	T	-	7	622	c.633delA	c.(631-633)AAAfs	p.K211fs
Pat_32	Post-Resistance	TNFRSF9	3604	37	1	7980912	7980914	In_Frame_Del	DEL	CTT	-	8	576	c.749_751delAAG	.(748-753)GAAGGA>GGA	p.E250del
Pat_32	Post-Resistance	SPEN	23013	37	1	16255142	16255143	Frame_Shift_Del	DEL	GA	-	7	281	c.2407_2408delGA	c.(2407-2409)GAGfs	p.E803fs
Pat_32	Post-Resistance	FUCA1	2517	37	1	24192052	24192053	Frame_Shift_Del	DEL	CC	-	8	369	c.452_453delGG	c.(451-453)TGGfs	p.W151fs
Pat_32	Post-Resistance	EXTL1	2134	37	1	26349533	26349535	In_Frame_Del	DEL	CCT	-	11	261	c.396_398delCCT	c.(394-399)TGCCTC>TGC	p.L137del
Pat_32	Post-Resistance	MACF1	23499	37	1	39788668	39788670	In_Frame_Del	DEL	GGA	-	9	742	.4239_4241delGG	(4237-4242)CTGGAG>CT	p.E1417del
Pat_32	Post-Resistance	MAST2	23139	37	1	46494559	46494559	Frame_Shift_Del	DEL	T	-	10	683	c.2172delT	c.(2170-2172)CCTfs	p.P724fs
Pat_32	Post-Resistance	WDR78	79819	37	1	67390426	67390426	Frame_Shift_Del	DEL	T	-	7	417	c.89delA	c.(88-90)AAGfs	p.K30fs
Pat_32	Post-Resistance	ZRANB2	9406	37	1	71536533	71536533	Frame_Shift_Del	DEL	G	-	8	1363	c.660delC	c.(658-660)CCCfs	p.P220fs
Pat_32	Post-Resistance	TCHH	7062	37	1	152083818	152083820	In_Frame_Del	DEL	CGG	-	7	113	.1873_1875delCC	c.(1873-1875)CCGdel	p.P625del
Pat_32	Post-Resistance	RPTN	126638	37	1	152128709	152128712	Frame_Shift_Del	DEL	TGTC	-	9	2069	c.863_866delGACA	c.(862-867)AGACAAfs	p.R288fs
Pat_32	Post-Resistance	FLG2	388698	37	1	152324558	152324559	Frame_Shift_Del	DEL	TG	-	7	1240	c.5703_5704delCA	c.(5701-5706)CACAGCfs	p.H1901fs
Pat_32	Post-Resistance	ISG20L2	81875	37	1	156694023	156694023	Frame_Shift_Del	DEL	G	-	12	364	c.865delC	c.(865-867)CTCfs	p.L289fs
Pat_32	Post-Resistance	OR10R2	343406	37	1	158450570	158450571	Frame_Shift_Del	DEL	CA	-	7	539	c.903_904delCA	c.(901-906)GTCACTfs	p.V301fs
Pat_32	Post-Resistance	PCP4L1	654790	37	1	161254154	161254156	In_Frame_Del	DEL	GGA	-	7	523	c.90_92delGGA	c.(88-93)GCGGAG>GCG	p.E35del
Pat_32	Post-Resistance	PRG4	10216	37	1	186276374	186276376	In_Frame_Del	DEL	CCA	-	15	290	.1523_1525delCC	.(1522-1527)CCCACC>CC	p.T511del

Pat_32	Post-Resistance	PCDH15	65217	37	10	55587198	55587200	In_Frame_Del	DEL	GGC	-	9	159	.4320_4322delGC	.(4318-4323)CCGCCT>CC	1440_1441PP>
Pat_32	Post-Resistance	LDB3	11155	37	10	88439241	88439242	Frame_Shift_Del	DEL	TC	-	42	105	c.211_212delTC	c.(211-213)TCTfs	p.S71fs
Pat_32	Post-Resistance	HELLS	3070	37	10	96331163	96331163	Frame_Shift_Del	DEL	A	-	7	148	c.454delA	c.(454-456)AAAfs	p.K152fs
Pat_32	Post-Resistance	LOC653544	653544	37	10	135491036	135491036	Frame_Shift_Del	DEL	G	-	8	325	c.647delG	c.(646-648)AGGfs	p.R216fs
Pat_32	Post-Resistance	OR10A2	341276	37	11	6891253	6891255	In_Frame_Del	DEL	TTC	-	7	308	c.268_270delTTC	c.(268-270)TTCdel	p.F94del
Pat_32	Post-Resistance	TMEM132A	54972	37	11	60695118	60695118	Frame_Shift_Del	DEL	C	-	8	450	c.321delC	c.(319-321)GTCfs	p.V107fs
Pat_32	Post-Resistance	STX5	6811	37	11	62598584	62598585	Frame_Shift_Ins	INS	-	G	7	35	c.131_132insC	c.(130-132)CCAfs	p.P44fs
Pat_32	Post-Resistance	KDM2A	22992	37	11	67018079	67018081	In_Frame_Del	DEL	GAG	-	7	48	.2578_2580delGA	c.(2578-2580)GAGdel	p.E866del
Pat_32	Post-Resistance	PRB2	653247	37	12	11546419	11546421	In_Frame_Del	DEL	GGA	-	9	189	c.591_593delTCC	c.(589-594)CCTCCA>CCA	.197_198PP>
Pat_32	Post-Resistance	PRB2	653247	37	12	11546727	11546728	In_Frame_Ins	INS	-	GGA	16	609	c.284_285insTCC	c.(283-285)CCA>CCTCCA	p.95_95P>PP
Pat_32	Post-Resistance	PRB2	653247	37	12	11546732	11546733	In_Frame_Ins	INS	-	AGA	9	551	c.279_280insTCT	c.(277-282)insTCT	p.93_94insS
Pat_32	Post-Resistance	PRB2	653247	37	12	11546856	11546858	In_Frame_Del	DEL	AGA	-	10	420	c.154_156delTCT	c.(154-156)TCTdel	p.S52del
Pat_32	Post-Resistance	LGR5	8549	37	12	71960435	71960436	Frame_Shift_Ins	INS	-	A	8	542	c.953_954insA	c.(952-954)ATAfs	p.I318fs
Pat_32	Post-Resistance	DCLK1	9201	37	13	36367554	36367554	Frame_Shift_Del	DEL	G	-	8	441	c.2007delC	c.(2005-2007)TTCfs	p.F669fs
Pat_32	Post-Resistance	FAM155A	728215	37	13	108518687	108518689	In_Frame_Del	DEL	CTG	-	7	41	c.256_258delCAG	c.(256-258)CAGdel	p.Q86del
Pat_32	Post-Resistance	NAA30	122830	37	14	57858199	57858201	In_Frame_Del	DEL	AGG	-	4	9	c.524_526delAGG	.(523-528)CAGGAG>CA	p.E180del
Pat_32	Post-Resistance	BEGAIN	57596	37	14	101005271	101005273	In_Frame_Del	DEL	CCT	-	7	34	c.815_817delAGG	.(814-819)GAGGCC>GC	p.E272del
Pat_32	Post-Resistance	CPLX3	594855	37	15	75122558	75122560	In_Frame_Del	DEL	GAG	-	7	221	c.340_342delGAG	c.(340-342)GAGdel	p.E118del
Pat_32	Post-Resistance	NAGPA	51172	37	16	5083678	5083679	Frame_Shift_Del	DEL	GC	-	7	49	c.137_138delGC	c.(136-138)CGCfs	p.R46fs
Pat_32	Post-Resistance	KIAA0182	23199	37	16	85682290	85682290	Frame_Shift_Del	DEL	C	-	10	221	c.359delC	c.(358-360)ACCfs	p.T120fs
Pat_32	Post-Resistance	STXBP4	252983	37	17	53068301	53068301	Frame_Shift_Del	DEL	G	-	106	57	c.163delG	c.(163-165)GGAfs	p.G55fs
Pat_32	Post-Resistance	CHERP	10523	37	19	16640581	16640583	In_Frame_Del	DEL	TGC	-	18	99	.1005_1007delGC	.(1003-1008)CAGCAA>CA	.335_336QQ>
Pat_32	Post-Resistance	TEAD2	8463	37	19	49850472	49850473	Frame_Shift_Ins	INS	-	G	13	528	c.883_884insC	c.(883-885)CATfs	p.H295fs
Pat_32	Post-Resistance	ZNF579	163033	37	19	56089908	56089909	In_Frame_Ins	INS	-	CCG	5	4	.1097_1098insCG	(1096-1098)GGG>GGCG	.366_366G>G
Pat_32	Post-Resistance	GIGYF2	26058	37	2	233676006	233676008	In_Frame_Del	DEL	CAG	-	8	244	.1951_1953delCA	c.(1951-1953)CAGdel	p.Q655del
Pat_32	Post-Resistance	SNX21	90203	37	20	44469908	44469908	Frame_Shift_Del	DEL	C	-	8	1385	c.1078delC	c.(1078-1080)CCCfs	p.P360fs
Pat_32	Post-Resistance	PREX1	57580	37	20	47361666	47361667	Frame_Shift_Del	DEL	CG	-	8	2053	c.309_310delCG	c.(307-312)ATCGAAfs	p.I103fs
Pat_32	Post-Resistance	DDX27	55661	37	20	47858504	47858504	Frame_Shift_Del	DEL	A	-	7	285	c.2065delA	c.(2065-2067)AAAfs	p.K689fs
Pat_32	Post-Resistance	SLMO2	51012	37	20	57613630	57613630	Frame_Shift_Del	DEL	G	-	11	1889	c.92delC	c.(91-93)CCAfs	p.P31fs
Pat_32	Post-Resistance	TIAM1	7074	37	21	32595809	32595809	Frame_Shift_Del	DEL	G	-	7	417	c.1908delC	c.(1906-1908)CCCfs	p.P636fs
Pat_32	Post-Resistance	PTTG1IP	754	37	21	46276194	46276196	In_Frame_Del	DEL	GCA	-	10	252	c.361_363delTGC	c.(361-363)TGCdel	p.C121del
Pat_32	Post-Resistance	DIP2A	23181	37	21	47987309	47987311	In_Frame_Del	DEL	TGG	-	7	546	.4490_4492delTG	(4489-4494)CTGGTG>CT	p.V1501del
Pat_32	Post-Resistance	MED15	51586	37	22	20918916	20918918	In_Frame_Del	DEL	CAG	-	8	38	c.631_633delCAG	c.(631-633)CAGdel	p.Q218del
Pat_32	Post-Resistance	TFIP11	24144	37	22	26906183	26906185	In_Frame_Del	DEL	TCA	-	8	344	c.54_56delTGA	c.(52-57)GATGAC>GAC	p.18_19DD>D
Pat_32	Post-Resistance	C22orf32	91689	37	22	42478046	42478048	In_Frame_Del	DEL	GAT	-	9	492	c.304_306delGAT	c.(304-306)GATdel	p.D107del
Pat_32	Post-Resistance	WDR6	11180	37	3	49051381	49051382	Frame_Shift_Ins	INS	-	G	9	132	c.2504_2505insG	c.(2503-2505)GCGfs	p.A835fs
Pat_32	Post-Resistance	BBX	56987	37	3	107497243	107497244	Frame_Shift_Ins	INS	-	A	7	245	c.2080_2081insA	c.(2080-2082)GAAfs	p.E694fs
Pat_32	Post-Resistance	TMCC1	23023	37	3	129370576	129370578	In_Frame_Del	DEL	CTG	-	10	211	.1708_1710delCA	c.(1708-1710)CAGdel	p.Q570del
Pat_32	Post-Resistance	PDE6B	5158	37	4	661763	661765	In_Frame_Del	DEL	AGG	-	7	318	.2471_2473delAG	(2470-2475)AAGGAG>AA	p.E828del
Pat_32	Post-Resistance	TMEM175	84286	37	4	946206	946207	Frame_Shift_Del	DEL	TG	-	9	426	c.430_431delTG	c.(430-432)TGTfs	p.C144fs
Pat_32	Post-Resistance	CRIPAK	285464	37	4	1389057	1389058	Frame_Shift_Ins	INS	-	AT	7	1180	c.758_759insAT	c.(757-759)ACGfs	p.T253fs
Pat_32	Post-Resistance	CRIPAK	285464	37	4	1389330	1389331	Frame_Shift_Del	DEL	CA	-	12	1319	c.1031_1032delCA	c.(1030-1032)TCAfs	p.S344fs
Pat_32	Post-Resistance	C4orf23	152992	37	4	8470022	8470022	Frame_Shift_Del	DEL	T	-	8	451	c.1189delT	c.(1189-1191)TTAfs	p.L397fs
Pat_32	Post-Resistance	BOD1L	259282	37	4	13603546	13603547	Frame_Shift_Del	DEL	CA	-	7	1117	c.4977_4978delTG	c.(4975-4980)TCTGAAfs	p.S1659fs
Pat_32	Post-Resistance	CPEB2	132864	37	4	15067858	15067858	Frame_Shift_Del	DEL	T	-	10	840	c.1624delT	c.(1624-1626)TTTfs	p.F542fs
Pat_32	Post-Resistance	KLF3	51274	37	4	38691496	38691496	Frame_Shift_Del	DEL	C	-	7	1001	c.691delC	c.(691-693)CAAfs	p.Q231fs
Pat_32	Post-Resistance	MTHFD2L	441024	37	4	75167509	75167509	Frame_Shift_Del	DEL	A	-	7	268	c.1027delA	c.(1027-1029)AAAfs	p.K343fs

Pat_32	Post-Resistance	MMRN1	22915	37	4	90844391	90844393	In_Frame_Del	DEL	AGC	-	8	1729	c.923_925delAGC	.(922-927)GAGCAG>GA	p.Q313del
Pat_32	Post-Resistance	EXOSC9	5393	37	4	122723894	122723894	Frame_Shift_Del	DEL	T	-	8	503	c.227delT	c.(226-228)CTTfs	p.L76fs
Pat_32	Post-Resistance	PCDH10	57575	37	4	134073569	134073571	In_Frame_Del	DEL	CTG	-	11	161	.2274_2276delCT	.(2272-2277)CTCTGC>CT	p.C763del
Pat_32	Post-Resistance	POU4F2	5458	37	4	147561241	147561243	In_Frame_Del	DEL	CAC	-	11	85	c.511_513delCAC	c.(511-513)CACdel	p.H182del
Pat_32	Post-Resistance	SLC22A4	6583	37	5	131676327	131676327	Frame_Shift_Del	DEL	T	-	9	472	c.1514delT	c.(1513-1515)CTTfs	p.L505fs
Pat_32	Post-Resistance	SYNJ2	8871	37	6	158508009	158508009	Frame_Shift_Del	DEL	C	-	7	135	c.3331delC	c.(3331-3333)CCCfs	p.P1111fs
Pat_32	Post-Resistance	SUN1	23353	37	7	883110	883110	Frame_Shift_Del	DEL	C	-	7	1346	c.611delC	c.(610-612)GCCfs	p.A204fs
Pat_32	Post-Resistance	GLCCI1	113263	37	7	8126097	8126099	In_Frame_Del	DEL	CAG	-	7	1184	.1573_1575delCA	c.(1573-1575)CAGdel	p.Q528del
Pat_32	Post-Resistance	HOXA1	3198	37	7	27135314	27135316	In_Frame_Del	DEL	CGA	-	7	145	c.216_218delTCG	c.(214-219)CATCAC>CAC	p.72_73HH>H
Pat_32	Post-Resistance	POU6F2	11281	37	7	39379288	39379290	In_Frame_Del	DEL	CAG	-	7	171	c.559_561delCAG	c.(559-561)CAGdel	p.Q196del
Pat_32	Post-Resistance	AKAP9	10142	37	7	91671392	91671393	Frame_Shift_Del	DEL	AG	-	11	201	.4950_4951delA	c.(4948-4953)TCAGAGfs	p.S1650fs
Pat_32	Post-Resistance	SAMD9L	219285	37	7	92761061	92761061	Frame_Shift_Del	DEL	T	-	10	918	c.4224delA	c.(4222-4224)AAAfs	p.K1408fs
Pat_32	Post-Resistance	CCDC132	55610	37	7	92923947	92923948	Frame_Shift_Ins	INS	-	G	7	507	c.1166_1167insG	c.(1165-1167)CAGfs	p.Q389fs
Pat_32	Post-Resistance	GPC2	221914	37	7	99771554	99771554	Frame_Shift_Del	DEL	C	-	8	870	c.796delG	c.(796-798)GTCfs	p.V266fs
Pat_32	Post-Resistance	PRKRIP1	79706	37	7	102065517	102065519	In_Frame_Del	DEL	GAG	-	9	305	c.514_516delGAG	c.(514-516)GAGdel	p.E176del
Pat_32	Post-Resistance	PAXIP1	22976	37	7	154760670	154760672	In_Frame_Del	DEL	TGC	-	9	44	.1239_1241delGC	.(1237-1242)CAGCAC>CA	p.Q413del
Pat_32	Post-Resistance	DLC1	10395	37	8	12957611	12957613	In_Frame_Del	DEL	GCT	-	10	124	.2233_2235delAG	c.(2233-2235)AGCdel	p.S745del
Pat_32	Post-Resistance	PRKDC	5591	37	8	48746799	48746799	Frame_Shift_Del	DEL	T	-	7	689	c.8110delA	c.(8110-8112)AGGfs	p.R2704fs
Pat_32	Post-Resistance	ROR2	4920	37	9	94486026	94486028	In_Frame_Del	DEL	TCC	-	7	152	.2748_2750delGG	(2746-2751)GAGGAA>GA	.916_917EE>
Pat_32	Post-Resistance	PRDM12	59335	37	9	133543701	133543702	Splice_Site	DEL	GT	-	22	175	c.570_splice	c.e3+1	p.E190_splice
Pat_32	Post-Resistance	ABL1	25	37	9	133759490	133759492	In_Frame_Del	DEL	AAG	-	11	186	.1813_1815delAA	c.(1813-1815)AAGdel	p.K609del
Pat_32	Post-Resistance	NHS	4810	37	X	17742525	17742525	Frame_Shift_Del	DEL	C	-	8	688	c.1152delC	c.(1150-1152)ATCfs	p.I384fs
Pat_32	Post-Resistance	ACOT9	23597	37	X	23754034	23754034	Splice_Site	DEL	G	-	7	1066	c.118_splice	c.e2+1	p.V40_splice
Pat_32	Post-Resistance	DUSP21	63904	37	X	44703633	44703634	Frame_Shift_Del	DEL	TG	-	20	519	c.255_256delTG	c.(253-258)TTTGACfs	p.F85fs
Pat_32	Post-Resistance	ZNF630	57232	37	X	47920326	47920327	Splice_Site	DEL	TA	-	8	716	c.16_splice	c.e3-1	p.E6_splice
Pat_32	Post-Resistance	NUDT11	55190	37	X	51239296	51239309	Translation_Start_Site	DEL	TCGAGGCA	-	12	43			
Pat_32	Post-Resistance	HUWE1	10075	37	X	53589091	53589093	In_Frame_Del	DEL	TCC	-	7	274	.7317_7319delGG	(7315-7320)GAGGAA>GA	2439_2440EE
Pat_32	Post-Resistance	HEPH	9843	37	X	65390435	65390435	Frame_Shift_Del	DEL	G	-	25	175	c.32delG	c.(31-33)TGGfs	p.W11fs
Pat_32	Post-Resistance	TAF1	6872	37	X	70603000	70603000	Frame_Shift_Del	DEL	A	-	9	332	c.1930delA	c.(1930-1932)AAAfs	p.K644fs
Pat_32	Post-Resistance	ARMCX3	51566	37	X	100880152	100880154	In_Frame_Del	DEL	TGA	-	8	896	c.183_185delTGA	c.(181-186)TCTGAT>TCT	p.D66del
Pat_32	Post-Resistance	BHLHB9	80823	37	X	102004419	102004421	In_Frame_Del	DEL	GAG	-	19	623	c.496_498delGAG	c.(496-498)GAGdel	p.E171del
Pat_32	Post-Resistance	FRMD7	90167	37	X	131231343	131231343	Frame_Shift_Del	DEL	C	-	8	1556	c.235delG	c.(235-237)GTGfs	p.V79fs
Pat_32	Post-Resistance	HTATSF1	27336	37	X	135585048	135585050	In_Frame_Del	DEL	AAG	-	10	644	c.682_684delAAG	c.(682-684)AAGdel	p.K232del
Pat_36	Post-Resistance	PLEKHG5	57449	37	1	6536011	6536013	In_Frame_Del	DEL	CTC	-	7	309	c.295_297delGAG	c.(295-297)GAGdel	p.E99del
Pat_36	Post-Resistance	DNAJC11	55735	37	1	6727803	6727804	Frame_Shift_Del	DEL	TC	-	7	45	c.343_344delGA	c.(343-345)GAAfs	p.E115fs
Pat_36	Post-Resistance	VAMP3	9341	37	1	7838212	7838214	In_Frame_Del	DEL	TCA	-	8	468	c.266_268delTCA	c.(265-270)TTCATC>TTC	p.I94del
Pat_36	Post-Resistance	GRIK3	2899	37	1	37324835	37324835	Frame_Shift_Del	DEL	C	-	7	355	c.978delG	c.(976-978)CTGfs	p.L326fs
Pat_36	Post-Resistance	EIF2B3	8891	37	1	45407181	45407182	Frame_Shift_Ins	INS	-	T	7	233	c.450_451insA	c.(448-453)AAAGCAfs	p.K150fs
Pat_36	Post-Resistance	MIER1	57708	37	1	67447526	67447526	Frame_Shift_Del	DEL	C	-	7	512	c.1294delC	c.(1294-1296)CCCfs	p.P432fs
Pat_36	Post-Resistance	LRRIQ3	127255	37	1	74575212	74575213	Frame_Shift_Ins	INS	-	T	12	196	c.732_733insA	c.(730-735)AAACAGfs	p.K244fs
Pat_36	Post-Resistance	TNNI3K	51086	37	1	74957824	74957826	In_Frame_Del	DEL	CTT	-	11	676	.2225_2227delCT	.(2224-2229)CCTTCT>CC	p.S746del
Pat_36	Post-Resistance	BCL10	8915	37	1	85736511	85736511	Frame_Shift_Del	DEL	T	-	8	257	c.136delA	c.(136-138)ATAfs	p.I46fs
Pat_36	Post-Resistance	ZNF326	284695	37	1	90470782	90470784	In_Frame_Del	DEL	GTG	-	14	532	c.188_190delGTG	c.(187-192)AGTGGT>AGT	p.G68del
Pat_36	Post-Resistance	EVI5	7813	37	1	93159366	93159366	Frame_Shift_Del	DEL	T	-	7	230	c.1222delA	c.(1222-1224)ATGfs	p.M408fs
Pat_36	Post-Resistance	COL11A1	1301	37	1	103348792	103348792	Frame_Shift_Del	DEL	C	-	7	473	c.4934delG	c.(4933-4935)GGTfs	p.G1645fs
Pat_36	Post-Resistance	SLC16A4	9122	37	1	110906427	110906427	Frame_Shift_Del	DEL	A	-	8	163	c.1425delT	c.(1423-1425)TTTfs	p.F475fs
Pat_36	Post-Resistance	SYCP1	6847	37	1	115537600	115537601	Frame_Shift_Ins	INS	-	A	19	141	c.2891_2892insA	c.(2890-2892)AGAfs	p.R964fs

Pat_36	Post-Resistance	HFE2	148738	37	1	145415369	145415371	In_Frame_Del	DEL	GAG	-	8	174	c.188_190delGAG	.(187-192)CGAGGA>CGA	p.G69del
Pat_36	Post-Resistance	ADAMTSL4	54507	37	1	150526141	150526141	Frame_Shift_Del	DEL	C	-	7	429	c.674delC	c.(673-675)TCCfs	p.S225fs
Pat_36	Post-Resistance	MCL1	4170	37	1	150551492	150551494	In_Frame_Del	DEL	TCC	-	7	252	c.513_515delGGA	.(511-516)GAGGAC>GAC	p.E171del
Pat_36	Post-Resistance	TCHH	7062	37	1	152084580	152084582	In_Frame_Del	DEL	CTC	-	9	80	.1111_1113delGA	c.(1111-1113)GAGdel	p.E371del
Pat_36	Post-Resistance	SPRR2B	6701	37	1	153043134	153043134	Frame_Shift_Del	DEL	G	-	8	593	c.182delC	c.(181-183)CCAfs	p.P61fs
Pat_36	Post-Resistance	ADAR	103	37	1	154574333	154574333	Frame_Shift_Del	DEL	G	-	8	477	c.785delC	c.(784-786)CCAfs	p.P262fs
Pat_36	Post-Resistance	NES	10763	37	1	156642804	156642804	Frame_Shift_Del	DEL	G	-	10	424	c.1176delC	c.(1174-1176)CCCfs	p.P392fs
Pat_36	Post-Resistance	PCP4L1	654790	37	1	161254154	161254156	In_Frame_Del	DEL	GGA	-	7	287	c.90_92delGGA	c.(88-93)GCGGAG>GCG	p.E35del
Pat_36	Post-Resistance	POU2F1	5451	37	1	167385016	167385018	In_Frame_Del	DEL	CCA	-	8	548	.2201_2203delCC	.(2200-2205)TCCACC>TC	p.T738del
Pat_36	Post-Resistance	PRG4	10216	37	1	186276524	186276526	In_Frame_Del	DEL	AGG	-	9	320	.1673_1675delAG	(1672-1677)AAGGAG>AA	p.E559del
Pat_36	Post-Resistance	PKP1	5317	37	1	201292157	201292157	Frame_Shift_Del	DEL	G	-	8	808	c.1583delG	c.(1582-1584)TGCfs	p.C528fs
Pat_36	Post-Resistance	REN	5972	37	1	204135375	204135377	In_Frame_Del	DEL	AGC	-	9	464	c.45_47delGCT	c.(43-48)CTGCTC>CTC	p.15_16LL>L
Pat_36	Post-Resistance	TMEM81	388730	37	1	205052694	205052694	Frame_Shift_Del	DEL	C	-	7	624	c.755delG	c.(754-756)GGCfs	p.G252fs
Pat_36	Post-Resistance	LOC642587	642587	37	1	209605637	209605648	In_Frame_Del	DEL	CAGCAGCA	-	11	49	263delAGCAGCA	264)GTAGCAGCAGCAGC	p.AAAA93del
Pat_36	Post-Resistance	KCTD3	51133	37	1	215747171	215747171	Frame_Shift_Del	DEL	T	-	7	835	c.126delT	c.(124-126)TCTfs	p.S42fs
Pat_36	Post-Resistance	MIA3	375056	37	1	222803699	222803700	Frame_Shift_Del	DEL	CT	-	15	1414	.3137_3138delCT	c.(3136-3138)CCTfs	p.P1046fs
Pat_36	Post-Resistance	FAM177B	400823	37	1	222920005	222920007	In_Frame_Del	DEL	GAG	-	8	226	c.118_120delGAG	c.(118-120)GAGdel	p.E46del
Pat_36	Post-Resistance	FBXO28	23219	37	1	224345075	224345075	Frame_Shift_Del	DEL	T	-	7	969	c.734delT	c.(733-735)CTAfs	p.L245fs
Pat_36	Post-Resistance	OBSCN	84033	37	1	228467013	228467013	Frame_Shift_Del	DEL	G	-	7	351	c.7264delG	c.(7264-7266)GGGfs	p.G2422fs
Pat_36	Post-Resistance	EXOC8	149371	37	1	231471559	231471560	Frame_Shift_Del	DEL	CC	-	8	840	.1932_1933delG	c.(1930-1935)TTGGAGfs	p.L644fs
Pat_36	Post-Resistance	SLC35F3	148641	37	1	234444927	234444927	Frame_Shift_Del	DEL	G	-	8	513	c.482delG	c.(481-483)TGGfs	p.W161fs
Pat_36	Post-Resistance	MTR	4548	37	1	237024474	237024474	Frame_Shift_Del	DEL	A	-	8	188	c.2093delA	c.(2092-2094)CAAfs	p.Q698fs
Pat_36	Post-Resistance	RYR2	6262	37	1	237969494	237969494	Frame_Shift_Del	DEL	T	-	7	198	c.14209delT	c.(14209-14211)TTTfs	p.F4737fs
Pat_36	Post-Resistance	OR2W3	343171	37	1	248059041	248059042	Frame_Shift_Del	DEL	GG	-	8	1982	c.153_154delGG	c.(151-156)CTGGACfs	p.L51fs
Pat_36	Post-Resistance	OR2L2	26246	37	1	248201719	248201719	Frame_Shift_Del	DEL	G	-	7	1799	c.150delG	c.(148-150)TTGfs	p.L50fs
Pat_36	Post-Resistance	OR2L3	391192	37	1	248224578	248224578	Frame_Shift_Del	DEL	T	-	7	1140	c.595delT	c.(595-597)TTTfs	p.F199fs
Pat_36	Post-Resistance	OR2T10	127069	37	1	248756363	248756363	Frame_Shift_Del	DEL	T	-	7	452	c.707delA	c.(706-708)AAGfs	p.K236fs
Pat_36	Post-Resistance	TSPAN4	7106	37	11	864443	864445	In_Frame_Del	DEL	CTG	-	8	299	c.262_264delCTG	c.(262-264)CTGdel	p.L92del
Pat_36	Post-Resistance	NUP98	4928	37	11	3720389	3720389	Frame_Shift_Del	DEL	T	-	8	587	c.3932delA	c.(3931-3933)AACfs	p.N1311fs
Pat_36	Post-Resistance	OR52E8	390079	37	11	5878504	5878504	Frame_Shift_Del	DEL	G	-	7	1712	c.429delC	c.(427-429)ACCfs	p.T143fs
Pat_36	Post-Resistance	OR10A5	144124	37	11	6867223	6867225	In_Frame_Del	DEL	TTC	-	8	293	c.310_312delTTC	c.(310-312)TTCdel	p.F108del
Pat_36	Post-Resistance	PARVA	55742	37	11	12534902	12534902	Frame_Shift_Del	DEL	A	-	9	940	c.793delA	c.(793-795)AAAfs	p.K265fs
Pat_36	Post-Resistance	OR8I2	120586	37	11	55861308	55861308	Frame_Shift_Del	DEL	T	-	8	640	c.525delT	c.(523-525)CATfs	p.H175fs
Pat_36	Post-Resistance	PGA3	643834	37	11	60971045	60971047	In_Frame_Del	DEL	GCT	-	8	493	c.9_11delGCT	c.(7-12)TGGCTG>TGG	p.L7del
Pat_36	Post-Resistance	FADS2	9415	37	11	61607885	61607887	In_Frame_Del	DEL	TCC	-	8	747	c.398_400delTCC	c.(397-402)TTCCTC>TTC	p.L137del
Pat_36	Post-Resistance	TSKU	25987	37	11	76506673	76506675	In_Frame_Del	DEL	CTG	-	9	201	c.13_15delCTG	c.(13-15)CTGdel	p.L9del
Pat_36	Post-Resistance	NDUFC2	4718	37	11	77784147	77784147	Frame_Shift_Del	DEL	A	-	15	327	c.207delT	c.(205-207)TTTfs	p.F69fs
Pat_36	Post-Resistance	CASP5	838	37	11	104879687	104879687	Frame_Shift_Del	DEL	T	-	19	265	c.28delA	c.(28-30)AGGfs	p.R10fs
Pat_36	Post-Resistance	CADM1	23705	37	11	115080312	115080314	In_Frame_Del	DEL	TGG	-	8	292	.1058_1060delCC	.(1057-1062)ACCATC>AT	p.T353del
Pat_36	Post-Resistance	IFT46	56912	37	11	118427645	118427647	In_Frame_Del	DEL	TCA	-	8	511	c.159_161delTGA	c.(157-162)GATGAA>GAA	p.D53del
Pat_36	Post-Resistance	CBL	867	37	11	119149356	119149358	In_Frame_Del	DEL	ATG	-	10	218	.1364_1366delAT	c.(1363-1368)TATGAT>TAT	p.D460del
Pat_36	Post-Resistance	CBL	867	37	11	119170435	119170435	Frame_Shift_Del	DEL	A	-	7	2569	c.2665delA	c.(2665-2667)AAAfs	p.K889fs
Pat_36	Post-Resistance	PRB2	653247	37	12	11546727	11546728	In_Frame_Ins	INS	-	GGA	11	679	c.284_285insTCC	c.(283-285)CCA>CCTCCA	p.95_95P>PP
Pat_36	Post-Resistance	PRB2	653247	37	12	11546732	11546733	In_Frame_Ins	INS	-	AGA	11	641	c.279_280insTCT	c.(277-282)insTCT	p.93_94insS
Pat_36	Post-Resistance	KIF21A	55605	37	12	39727052	39727052	Frame_Shift_Del	DEL	T	-	8	465	c.2449delA	c.(2449-2451)AGAfs	p.R817fs
Pat_36	Post-Resistance	RPAP3	79657	37	12	48084302	48084302	Frame_Shift_Del	DEL	T	-	8	547	c.666delA	c.(664-666)AAAfs	p.K222fs
Pat_36	Post-Resistance	PRPF40B	25766	37	12	50027729	50027729	Frame_Shift_Del	DEL	C	-	7	396	c.600delC	c.(598-600)GACfs	p.D200fs

Pat_36	Post-Resistance	DIP2B	57609	37	12	51034605	51034606	Frame_Shift_Del	DEL	GG	-	8	202	c.271_272delGG	c.(271-273)GGGfs	p.G91fs
Pat_36	Post-Resistance	KRT73	319101	37	12	53012151	53012151	Frame_Shift_Del	DEL	C	-	10	337	c.158delG	c.(157-159)GGTfs	p.G53fs
Pat_36	Post-Resistance	OR6C75	390323	37	12	55759192	55759192	Frame_Shift_Del	DEL	T	-	8	276	c.298delT	c.(298-300)TTTfs	p.F100fs
Pat_36	Post-Resistance	RAP1B	5908	37	12	69047987	69047988	Frame_Shift_Del	DEL	AC	-	8	1019	c.279_280delAC	c.(277-282)TTACAAfs	p.L93fs
Pat_36	Post-Resistance	SBNO1	55206	37	12	123794283	123794283	Frame_Shift_Del	DEL	T	-	12	418	c.3416delA	c.(3415-3417)AATfs	p.N1139fs
Pat_36	Post-Resistance	TPTE2	93492	37	13	20041394	20041394	Frame_Shift_Del	DEL	A	-	7	214	c.483delT	c.(481-483)TTTfs	p.F161fs
Pat_36	Post-Resistance	DIAPH3	81624	37	13	60582733	60582734	Frame_Shift_Ins	INS	-	T	10	370	c.958_959insA	c.(958-960)ATTfs	p.I320fs
Pat_36	Post-Resistance	LMO7	4008	37	13	76415307	76415308	Frame_Shift_Del	DEL	AG	-	8	211	c.2946_2947delAG	c.(2944-2949)GCAGAGfs	p.A982fs
Pat_36	Post-Resistance	RBM26	64062	37	13	79918806	79918807	Frame_Shift_Ins	INS	-	T	7	96	c.2187_2188insA	c.(2185-2190)AAACAGfs	p.K729fs
Pat_36	Post-Resistance	SIPA1L1	26037	37	14	72190482	72190484	In_Frame_Del	DEL	TCC	-	11	417	.4390_4392delTC	c.(4390-4392)TCCdel	p.S1468del
Pat_36	Post-Resistance	ZSCAN10	84891	37	16	3142237	3142237	Frame_Shift_Del	DEL	G	-	7	151	c.312delC	c.(310-312)CCCfs	p.P104fs
Pat_36	Post-Resistance	MEFV	4210	37	16	3294471	3294471	Splice_Site	DEL	A	-	8	470	c.1726_splice	c.e7+1	p.E576_splice
Pat_36	Post-Resistance	UBN1	29855	37	16	4910691	4910693	In_Frame_Del	DEL	AGA	-	13	663	c.698_700delAGA	.(697-702)GAGAAG>GAG	p.K238del
Pat_36	Post-Resistance	DNAH3	55567	37	16	21132130	21132132	In_Frame_Del	DEL	CAG	-	7	195	.1628_1630delCT	.(1627-1632)GCTGAT>GA	p.A543del
Pat_36	Post-Resistance	TNRC6A	27327	37	16	24807240	24807240	Frame_Shift_Del	DEL	A	-	8	724	c.3541delA	c.(3541-3543)AAAfs	p.K1181fs
Pat_36	Post-Resistance	SRCAP	10847	37	16	30736314	30736314	Frame_Shift_Del	DEL	C	-	8	798	c.5569delC	c.(5569-5571)CCCfs	p.P1857fs
Pat_36	Post-Resistance	SETD1A	9739	37	16	30982809	30982811	In_Frame_Del	DEL	TCC	-	10	169	.3127_3129delTC	c.(3127-3129)TCCdel	p.S1058del
Pat_36	Post-Resistance	COQ9	57017	37	16	57486732	57486734	In_Frame_Del	DEL	GAG	-	10	365	c.262_264delGAG	c.(262-264)GAGdel	p.E91del
Pat_36	Post-Resistance	CNGB1	1258	37	16	57983275	57983277	In_Frame_Del	DEL	TCC	-	10	119	.1101_1103delGG	(1099-1104)GAGGAA>GA	.367_368EE>
Pat_36	Post-Resistance	EXOC3L	283849	37	16	67220950	67220951	Frame_Shift_Del	DEL	CC	-	7	349	c.1131_1132delGG	c.(1129-1134)CTGGAGfs	p.L377fs
Pat_36	Post-Resistance	SLC9A5	6553	37	16	67300017	67300019	In_Frame_Del	DEL	GAG	-	8	197	.2107_2109delGA	c.(2107-2109)GAGdel	p.E708del
Pat_36	Post-Resistance	KIAA0182	23199	37	16	85682290	85682290	Frame_Shift_Del	DEL	C	-	11	223	c.359delC	c.(358-360)ACCfs	p.T120fs
Pat_36	Post-Resistance	C17orf85	55421	37	17	3721809	3721811	In_Frame_Del	DEL	TCC	-	8	279	.1056_1058delGG	(1054-1059)GAGGAA>GA	.352_353EE>
Pat_36	Post-Resistance	MYOCD	93649	37	17	12639482	12639482	Frame_Shift_Del	DEL	C	-	7	472	c.420delC	c.(418-420)AACfs	p.N140fs
Pat_36	Post-Resistance	SLC13A2	9058	37	17	26821446	26821446	Frame_Shift_Del	DEL	C	-	8	168	c.1224delC	c.(1222-1224)CTCfs	p.L408fs
Pat_36	Post-Resistance	SUPT6H	6830	37	17	27001303	27001305	In_Frame_Del	DEL	GAG	-	8	166	c.112_114delGAG	c.(112-114)GAGdel	p.E43del
Pat_36	Post-Resistance	SUPT6H	6830	37	17	27027202	27027204	In_Frame_Del	DEL	AGC	-	13	778	.4573_4575delAG	c.(4573-4575)AGCdel	p.S1528del
Pat_36	Post-Resistance	KRTAP4-8	728224	37	17	39254335	39254336	Frame_Shift_Ins	INS	-	T	38	60	c.1_2insA	c.(1-3)ATGfs	p.M1fs
Pat_36	Post-Resistance	COIL	8161	37	17	55028117	55028118	Frame_Shift_Ins	INS	-	T	7	309	c.485_486insA	c.(484-486)AACfs	p.N162fs
Pat_36	Post-Resistance	USP32	84669	37	17	58257949	58257949	Frame_Shift_Del	DEL	T	-	7	583	c.4598delA	c.(4597-4599)AACfs	p.N1533fs
Pat_36	Post-Resistance	ZNF236	7776	37	18	74593429	74593430	Frame_Shift_Ins	INS	-	A	7	209	c.1372_1373insA	c.(1372-1374)GAAfs	p.E458fs
Pat_36	Post-Resistance	HAUS8	93323	37	19	17160706	17160707	Frame_Shift_Del	DEL	GA	-	10	635	c.1209_1210delTC	c.(1207-1212)TCTCGTfs	p.S403fs
Pat_36	Post-Resistance	RYR1	6261	37	19	38948159	38948160	Frame_Shift_Del	DEL	TG	-	7	801	c.1814_1815delTG	c.(1813-1815)CTGfs	p.L605fs
Pat_36	Post-Resistance	PSG1	5669	37	19	43371298	43371298	Frame_Shift_Del	DEL	C	-	7	196	c.1248delG	c.(1246-1248)TGGfs	p.W416fs
Pat_36	Post-Resistance	CCDC8	83987	37	19	46915034	46915034	Frame_Shift_Del	DEL	G	-	10	328	c.1034delC	c.(1033-1035)GCAfs	p.A345fs
Pat_36	Post-Resistance	SLC8A2	6543	37	19	47935681	47935683	In_Frame_Del	DEL	TCC	-	21	374	.2130_2132delGG	(2128-2133)GAGGAC>GA	p.E710del
Pat_36	Post-Resistance	MAMSTR	284358	37	19	49218105	49218106	Frame_Shift_Ins	INS	-	G	8	224	c.485_486insC	c.(484-486)CCAfs	p.P162fs
Pat_36	Post-Resistance	CNOT3	4849	37	19	54649671	54649671	Frame_Shift_Del	DEL	T	-	10	319	c.729delT	c.(727-729)CCCfs	p.P243fs
Pat_36	Post-Resistance	TMC4	147798	37	19	54675747	54675749	In_Frame_Del	DEL	TCC	-	12	227	c.201_203delGGA	c.(199-204)GAGGAT>GAT	p.E67del
Pat_36	Post-Resistance	ATP6V1C2	245973	37	2	10917819	10917820	Frame_Shift_Del	DEL	AG	-	19	244	c.934_935delAG	c.(934-936)AGAfs	p.R312fs
Pat_36	Post-Resistance	RASGRP3	25780	37	2	33749070	33749070	Frame_Shift_Del	DEL	C	-	9	917	c.641delC	c.(640-642)ACCfs	p.T214fs
Pat_36	Post-Resistance	PSME4	23198	37	2	54167139	54167140	Splice_Site	INS	-	G	8	382	c.501_splice	c.e4-1	p.N167_splice
Pat_36	Post-Resistance	AFTPH	54812	37	2	64778672	64778674	In_Frame_Del	DEL	GAT	-	8	706	c.64_66delGAT	c.(64-66)GATdel	p.D26del
Pat_36	Post-Resistance	ZNF514	84874	37	2	95815944	95815945	Frame_Shift_Del	DEL	GG	-	7	854	c.285_286delCC	c.(283-288)TTCCAGfs	p.F95fs
Pat_36	Post-Resistance	ANKRD36	375248	37	2	97808574	97808575	Splice_Site	INS	-	A	14	40	c.901_splice	c.e8+2	p.V301_splice
Pat_36	Post-Resistance	RBM45	129831	37	2	178988920	178988920	Frame_Shift_Del	DEL	A	-	15	255	c.1135delA	c.(1135-1137)AAAfs	p.K379fs
Pat_36	Post-Resistance	NCKAP1	10787	37	2	183888543	183888544	Frame_Shift_Del	DEL	GC	-	7	455	c.209_210delGC	c.(208-210)CGCfs	p.R70fs

Pat_36	Post-Resistance	SGOL2	151246	37	2	201436992	201436992	Frame_Shift_Del	DEL	A	-	7	332	c.1923delA	c.(1921-1923)CTAfs	p.L641fs
Pat_36	Post-Resistance	TRPM8	79054	37	2	234879009	234879010	Frame_Shift_Ins	INS	-	C	8	991	c.2294_2295insC	c.(2293-2295)CACfs	p.H765fs
Pat_36	Post-Resistance	GAL3ST2	64090	37	2	242738494	242738496	In_Frame_Del	DEL	TCC	-	11	323	c.44_46delTCC	c.(43-48)ATCCTC>ATC	p.L20del
Pat_36	Post-Resistance	SEL1L2	80343	37	20	13850192	13850192	Frame_Shift_Del	DEL	T	-	7	234	c.1212delA	c.(1210-1212)AAAfs	p.K404fs
Pat_36	Post-Resistance	MYBL2	4605	37	20	42338611	42338611	Frame_Shift_Del	DEL	C	-	7	1146	c.1514delC	c.(1513-1515)ACCfs	p.T505fs
Pat_36	Post-Resistance	NCOA3	8202	37	20	46279864	46279866	In_Frame_Del	DEL	CAA	-	10	84	.3790_3792delCA	c.(3790-3792)CAAdel	p.Q1276del
Pat_36	Post-Resistance	CTCFL	140690	37	20	56099187	56099187	Frame_Shift_Del	DEL	T	-	7	901	c.75delA	c.(73-75)AAAfs	p.K25fs
Pat_36	Post-Resistance	TPTE	7179	37	21	10944697	10944697	Frame_Shift_Del	DEL	A	-	9	480	c.537delT	c.(535-537)TTTfs	p.F179fs
Pat_36	Post-Resistance	ADAMTS5	11096	37	21	28302327	28302327	Frame_Shift_Del	DEL	C	-	8	1369	c.2103delG	c.(2101-2103)GGGfs	p.G701fs
Pat_36	Post-Resistance	TFIP11	24144	37	22	26906183	26906185	In_Frame_Del	DEL	TCA	-	9	331	c.54_56delTGA	c.(52-57)GATGAC>GAC	p.18_19DD>D
Pat_36	Post-Resistance	MN1	4330	37	22	28194933	28194934	In_Frame_Ins	INS	-	TGC	20	63	.1598_1599insGC	.(1597-1599)CAA>CAGCA	.533_533Q>Q
Pat_36	Post-Resistance	SELM	140606	37	22	31503422	31503422	Frame_Shift_Del	DEL	C	-	4	6	c.70delG	c.(70-72)GCCfs	p.A24fs
Pat_36	Post-Resistance	SH3BP1	23616	37	22	38039752	38039754	In_Frame_Del	DEL	AGG	-	7	227	c.575_577delAGG	.(574-579)AAGGAG>AAG	p.E197del
Pat_36	Post-Resistance	TRIOBP	11078	37	22	38120245	38120253	In_Frame_Del	DEL	CTCCAGA	-	7	498	2_1690delCCTCC	1-1692)GCCTCCAGAACC	p.SRT562del
Pat_36	Post-Resistance	TAB1	10454	37	22	39772009	39772009	Frame_Shift_Del	DEL	C	-	7	463	c.68delC	c.(67-69)TCCfs	p.S23fs
Pat_36	Post-Resistance	ATP2B2	491	37	3	10443796	10443796	Frame_Shift_Del	DEL	C	-	7	611	c.634delG	c.(634-636)GACfs	p.D212fs
Pat_36	Post-Resistance	SYN2	6854	37	3	12046124	12046126	In_Frame_Del	DEL	AGC	-	2	4	c.99_101delAGC	c.(97-102)CAACCG>CAG	p.P40del
Pat_36	Post-Resistance	XPC	7508	37	3	14219966	14219968	In_Frame_Del	DEL	CCT	-	9	107	c.101_103delAGG	c.(100-105)GAGGAT>GAT	p.E34del
Pat_36	Post-Resistance	ULK4	54986	37	3	41860984	41860985	Frame_Shift_Ins	INS	-	T	8	82	c.1778_1779insA	c.(1777-1779)AAGfs	p.K593fs
Pat_36	Post-Resistance	NKTR	4820	37	3	42679035	42679036	Frame_Shift_Ins	INS	-	C	8	823	c.1839_1840insC	c.(1837-1842)AGTCCCfs	p.S613fs
Pat_36	Post-Resistance	DNAH1	25981	37	3	52430786	52430786	Frame_Shift_Del	DEL	G	-	8	701	c.11583delG	c.(11581-11583)CTGfs	p.L3861fs
Pat_36	Post-Resistance	PRKCD	5580	37	3	53220653	53220653	Frame_Shift_Del	DEL	G	-	10	1044	c.1294delG	c.(1294-1296)GGGfs	p.G432fs
Pat_36	Post-Resistance	ERC2	26059	37	3	55733470	55733472	In_Frame_Del	DEL	TGG	-	13	836	.2781_2783delCC	.(2779-2784)CACCAT>CA	.927_928HH>I
Pat_36	Post-Resistance	LRIG1	26018	37	3	66436625	66436627	In_Frame_Del	DEL	GCT	-	9	712	.1567_1569delAG	c.(1567-1569)AGCdel	p.S524del
Pat_36	Post-Resistance	ZNF717	100131827	37	3	75790810	75790811	Frame_Shift_Ins	INS	-	T	7	153	c.134_135insA	c.(133-135)ACCfs	p.T45fs
Pat_36	Post-Resistance	TMCC1	23023	37	3	129370576	129370578	In_Frame_Del	DEL	CTG	-	11	275	.1708_1710delCA	c.(1708-1710)CAGdel	p.Q570del
Pat_36	Post-Resistance	ASTE1	28990	37	3	130733047	130733047	Frame_Shift_Del	DEL	T	-	12	64	c.1894delA	c.(1894-1896)AGGfs	p.R632fs
Pat_36	Post-Resistance	GRK7	131890	37	3	141535708	141535708	Frame_Shift_Del	DEL	G	-	7	754	c.1478delG	c.(1477-1479)CGGfs	p.R493fs
Pat_36	Post-Resistance	PARL	55486	37	3	183560119	183560119	Frame_Shift_Del	DEL	G	-	8	885	c.724delC	c.(724-726)CAAfs	p.Q242fs
Pat_36	Post-Resistance	CRIPAK	285464	37	4	1389054	1389055	Frame_Shift_Ins	INS	-	CA	12	1266	c.755_756insCA	c.(754-756)CTCfs	p.L252fs
Pat_36	Post-Resistance	CRIPAK	285464	37	4	1389057	1389058	Frame_Shift_Ins	INS	-	AT	10	1312	c.758_759insAT	c.(757-759)ACGfs	p.T253fs
Pat_36	Post-Resistance	CRIPAK	285464	37	4	1389330	1389331	Frame_Shift_Del	DEL	CA	-	13	1459	c.1031_1032delCA	c.(1030-1032)TCAfs	p.S344fs
Pat_36	Post-Resistance	CCKAR	886	37	4	26483672	26483674	In_Frame_Del	DEL	CTG	-	7	188	c.873_875delCAG	.(871-876)AGCAGG>AGC	p.S291del
Pat_36	Post-Resistance	CLOCK	9575	37	4	56336953	56336954	Frame_Shift_Ins	INS	-	A	10	279	c.368_369insT	c.(367-369)TTAfs	p.L123fs
Pat_36	Post-Resistance	MMRN1	22915	37	4	90844391	90844393	In_Frame_Del	DEL	AGC	-	12	1286	c.923_925delAGC	.(922-927)GAGCAG>GAG	p.Q313del
Pat_36	Post-Resistance	ANK2	287	37	4	114214679	114214681	In_Frame_Del	DEL	CAC	-	10	226	.2460_2462delCA	.(2458-2463)GTCACC>GT	p.T826del
Pat_36	Post-Resistance	ANK2	287	37	4	114260460	114260460	Frame_Shift_Del	DEL	C	-	7	530	c.3875delC	c.(3874-3876)ACAfs	p.T1292fs
Pat_36	Post-Resistance	OTUD4	54726	37	4	146063356	146063356	Frame_Shift_Del	DEL	C	-	8	665	c.1619delG	c.(1618-1620)GGAfs	p.G540fs
Pat_36	Post-Resistance	LRBA	987	37	4	151842374	151842374	Frame_Shift_Del	DEL	A	-	8	441	c.621delT	c.(619-621)TTTfs	p.F207fs
Pat_36	Post-Resistance	DDX4	54514	37	5	55076947	55076948	Frame_Shift_Del	DEL	TC	-	8	221	c.550_551delTC	c.(550-552)TCTfs	p.S184fs
Pat_36	Post-Resistance	TAF9	6880	37	5	68660786	68660788	In_Frame_Del	DEL	TCA	-	7	366	c.777_779delTGA	c.(775-780)GATGAC>GAC	.259_260DD>I
Pat_36	Post-Resistance	THBS4	7060	37	5	79372774	79372776	In_Frame_Del	DEL	TGA	-	13	806	.1989_1991delTG	.(1987-1992)TGTGAT>TG	p.D668del
Pat_36	Post-Resistance	HAVCR2	84868	37	5	156535948	156535950	In_Frame_Del	DEL	AGC	-	7	180	c.45_47delGCT	c.(43-48)CTGCTA>CTA	p.15_16LL>L
Pat_36	Post-Resistance	NSD1	64324	37	5	176683996	176683996	Frame_Shift_Del	DEL	A	-	7	357	c.4810delA	c.(4810-4812)AAAfs	p.K1604fs
Pat_36	Post-Resistance	CANX	821	37	5	179149920	179149920	Frame_Shift_Del	DEL	T	-	41	1847	c.1298delT	c.(1297-1299)ATTfs	p.I433fs
Pat_36	Post-Resistance	RASGEF1C	255426	37	5	179564993	179564993	Frame_Shift_Del	DEL	G	-	12	1016	c.60delC	c.(58-60)CCCfs	p.P20fs
Pat_36	Post-Resistance	RPP40	10799	37	6	4995370	4995371	Frame_Shift_Del	DEL	TT	-	8	542	c.1033_1034delAA	c.(1033-1035)AATfs	p.N345fs

Pat_36	Post-Resistance	ATXN1	6310	37	6	16327900	16327901	In_Frame_Ins	INS	-	TGC	11	81	c.641_642insGCA	c.(640-642)CAG>CAGCAG	.214_214Q>Q
Pat_36	Post-Resistance	ATXN1	6310	37	6	16327907	16327909	In_Frame_Del	DEL	TGA	-	10	77	c.633_635delTCA	c.(631-636)CATCAG>CAG	p.H211del
Pat_36	Post-Resistance	SLC17A2	10246	37	6	25921520	25921520	Frame_Shift_Del	DEL	T	-	8	472	c.361delA	c.(361-363)ATGfs	p.M121fs
Pat_36	Post-Resistance	GABBR1	2550	37	6	29599254	29599254	Frame_Shift_Del	DEL	C	-	7	920	c.208delG	c.(208-210)GAGfs	p.E70fs
Pat_36	Post-Resistance	HLA-F	3134	37	6	29694802	29694803	Frame_Shift_Ins	INS	-	T	13	998	c.1179_1180insT	c.(1177-1182)TTGTTTfs	p.L393fs
Pat_36	Post-Resistance	HLA-L	3139	37	6	30231140	30231140	Frame_Shift_Del	DEL	T	-	8	701	c.584delT	c.(583-585)ATTfs	p.I195fs
Pat_36	Post-Resistance	RING1	6015	37	6	33178989	33178990	Frame_Shift_Ins	INS	-	G	7	1107	c.510_511insG	c.(508-513)AGTGGGfs	p.S170fs
Pat_36	Post-Resistance	UHRF1BP1	54887	37	6	34804004	34804006	In_Frame_Del	DEL	CAG	-	9	866	c.912_914delCAG	c.(910-915)AACAGC>AAC	p.S308del
Pat_36	Post-Resistance	CUL9	23113	37	6	43167713	43167714	Frame_Shift_Del	DEL	AT	-	9	441	c.3203_3204delAT	c.(3202-3204)CATfs	p.H1068fs
Pat_36	Post-Resistance	MEP1A	4224	37	6	46761166	46761166	Frame_Shift_Del	DEL	T	-	8	1332	c.31delT	c.(31-33)TTTfs	p.F11fs
Pat_36	Post-Resistance	TMEM14A	28978	37	6	52541950	52541950	Frame_Shift_Del	DEL	T	-	7	1116	c.50delT	c.(49-51)ATTfs	p.I17fs
Pat_36	Post-Resistance	GSTA1	2938	37	6	52658948	52658948	Frame_Shift_Del	DEL	T	-	10	1656	c.389delA	c.(388-390)AATfs	p.N130fs
Pat_36	Post-Resistance	KLHL31	401265	37	6	53519759	53519759	Frame_Shift_Del	DEL	T	-	11	746	c.312delA	c.(310-312)AAAfs	p.K104fs
Pat_36	Post-Resistance	MYO6	4646	37	6	76599857	76599858	Frame_Shift_Ins	INS	-	A	9	204	c.2742_2743insA	c.(2740-2745)CAGAAAfs	p.Q914fs
Pat_36	Post-Resistance	RARS2	57038	37	6	88229955	88229955	Frame_Shift_Del	DEL	T	-	7	618	c.1055delA	c.(1054-1056)AAGfs	p.K352fs
Pat_36	Post-Resistance	GRM1	2911	37	6	146755399	146755401	In_Frame_Del	DEL	CAG	-	9	492	.3052_3054delCA	c.(3052-3054)CAGdel	p.Q1022del
Pat_36	Post-Resistance	IQCE	23288	37	7	2623881	2623881	Frame_Shift_Del	DEL	C	-	7	587	c.786delC	c.(784-786)CTCfs	p.L262fs
Pat_36	Post-Resistance	ZDHHC4	55146	37	7	6621848	6621849	Frame_Shift_Ins	INS	-	T	7	776	c.336_337insT	c.(334-339)CTGTTTfs	p.L112fs
Pat_36	Post-Resistance	PHF14	9678	37	7	11075380	11075381	Frame_Shift_Del	DEL	AG	-	9	982	c.1569_1570delA	c.(1567-1572)CAAGAGfs	p.Q523fs
Pat_36	Post-Resistance	MPP6	51678	37	7	24705666	24705666	Frame_Shift_Del	DEL	A	-	9	468	c.910delA	c.(910-912)AAAfs	p.K304fs
Pat_36	Post-Resistance	OSBPL3	26031	37	7	24846521	24846522	Splice_Site	DEL	TC	-	8	522	c.2318_splice	c.e21-1	p.N773_splice
Pat_36	Post-Resistance	GARS	2617	37	7	30634583	30634585	In_Frame_Del	DEL	CTG	-	7	97	c.46_48delCTG	c.(46-48)CTGdel	p.L20del
Pat_36	Post-Resistance	C7orf16	10842	37	7	31735179	31735179	Frame_Shift_Del	DEL	A	-	13	751	c.179delA	c.(178-180)CAAfs	p.Q60fs
Pat_36	Post-Resistance	FKBP9	11328	37	7	33014804	33014804	Frame_Shift_Del	DEL	C	-	7	438	c.378delC	c.(376-378)ATCfs	p.I126fs
Pat_36	Post-Resistance	OGDH	4967	37	7	44684936	44684936	Frame_Shift_Del	DEL	T	-	13	399	c.233delT	c.(232-234)ATTfs	p.I78fs
Pat_36	Post-Resistance	ABCA13	154664	37	7	48318279	48318280	Frame_Shift_Del	DEL	AG	-	7	1006	c.7488_7489delA	c.(7486-7491)TTAGAAfs	p.L2496fs
Pat_36	Post-Resistance	MRPS17	51373	37	7	56022659	56022659	Frame_Shift_Del	DEL	G	-	7	1700	c.181delG	c.(181-183)GGGfs	p.G61fs
Pat_36	Post-Resistance	DTX2	113878	37	7	76112249	76112249	Frame_Shift_Del	DEL	A	-	17	1426	c.693delA	c.(691-693)CCAfs	p.P231fs
Pat_36	Post-Resistance	ABCB4	5244	37	7	87074281	87074282	Frame_Shift_Ins	INS	-	A	7	98	c.1015_1016insT	c.(1015-1017)TCAfs	p.S339fs
Pat_36	Post-Resistance	PEX1	5189	37	7	92146721	92146721	Frame_Shift_Del	DEL	T	-	23	386	c.1108delA	c.(1108-1110)ATTfs	p.I370fs
Pat_36	Post-Resistance	ZCWPW1	55063	37	7	100000151	100000151	Frame_Shift_Del	DEL	T	-	7	2574	c.1459delA	c.(1459-1461)ACCfs	p.T487fs
Pat_36	Post-Resistance	ZCWPW1	55063	37	7	100004397	100004398	Frame_Shift_Ins	INS	-	A	7	239	c.1089_1090insT	c.(1087-1092)TTTGGAfs	p.F363fs
Pat_36	Post-Resistance	SRRT	51593	37	7	100482040	100482042	In_Frame_Del	DEL	AGG	-	9	57	c.809_811delAGG	.(808-813)CAGGAG>CAG	p.E275del
Pat_36	Post-Resistance	RINT1	60561	37	7	105204285	105204285	Frame_Shift_Del	DEL	G	-	7	226	c.1777delG	c.(1777-1779)GATfs	p.D593fs
Pat_36	Post-Resistance	TNPO3	23534	37	7	128610259	128610259	Frame_Shift_Del	DEL	G	-	8	1114	c.2541delC	c.(2539-2541)CCCfs	p.P847fs
Pat_36	Post-Resistance	RBM33	155435	37	7	155531073	155531074	Frame_Shift_Del	DEL	CA	-	10	523	c.1713_1714delC	c.(1711-1716)CCCACAfs	p.P571fs
Pat_36	Post-Resistance	C8orf80	389643	37	8	27888776	27888776	Frame_Shift_Del	DEL	T	-	15	652	c.1892delA	c.(1891-1893)AATfs	p.N631fs
Pat_36	Post-Resistance	TMEM66	51669	37	8	29931442	29931442	Frame_Shift_Del	DEL	G	-	7	1473	c.233delC	c.(232-234)CCAfs	p.P78fs
Pat_36	Post-Resistance	MYST3	7994	37	8	41798420	41798422	In_Frame_Del	DEL	CTC	-	7	496	.2977_2979delGA	c.(2977-2979)GAGdel	p.E993del
Pat_36	Post-Resistance	MYST3	7994	37	8	41836184	41836184	Frame_Shift_Del	DEL	T	-	11	1400	c.1019delA	c.(1018-1020)AACfs	p.N340fs
Pat_36	Post-Resistance	POP1	10940	37	8	99158810	99158811	Frame_Shift_Del	DEL	AG	-	7	485	c.1609_1610delA	c.(1609-1611)AGAfs	p.R537fs
Pat_36	Post-Resistance	DPYS	1807	37	8	105440214	105440214	Frame_Shift_Del	DEL	T	-	8	1461	c.1086delA	c.(1084-1086)AAAfs	p.K362fs
Pat_36	Post-Resistance	NDUFB9	4715	37	8	125559305	125559306	Frame_Shift_Del	DEL	CC	-	8	1225	c.359_360delCC	c.(358-360)GCCfs	p.A120fs
Pat_36	Post-Resistance	KCNQ3	3786	37	8	133142050	133142050	Frame_Shift_Del	DEL	G	-	8	306	c.2078delC	c.(2077-2079)CCGfs	p.P693fs
Pat_36	Post-Resistance	SMARCA2	6595	37	9	2104067	2104068	Frame_Shift_Del	DEL	GC	-	8	388	c.3190_3191delG	c.(3190-3192)GCGfs	p.A1064fs
Pat_36	Post-Resistance	GRIN1	2902	37	9	140056884	140056886	In_Frame_Del	DEL	GAG	-	7	141	.1780_1782delGA	c.(1780-1782)GAGdel	p.E598del
Pat_36	Post-Resistance	ARHGAP6	395	37	X	11200196	11200196	Frame_Shift_Del	DEL	T	-	8	1912	c.1316delA	c.(1315-1317)AAGfs	p.K439fs

Pat_36	Post-Resistance	OFD1	8481	37	X	13764946	13764946	Frame_Shift_Del	DEL	A	-	10	241	c.702delA	c.(700-702)GCAfs	p.A234fs
Pat_36	Post-Resistance	OFD1	8481	37	X	13778677	13778677	Frame_Shift_Del	DEL	G	-	8	763	c.2098delG	c.(2098-2100)GAGfs	p.E700fs
Pat_36	Post-Resistance	FAM48B1	100130302	37	X	24382374	24382376	In_Frame_Del	DEL	TGC	-	11	37	.1497_1499delTG	.(1495-1500)ATTGCT>AT	p.A517del
Pat_36	Post-Resistance	PHF8	23133	37	X	54011405	54011407	In_Frame_Del	DEL	CTC	-	37	537	.2491_2493delGA	c.(2491-2493)GAGdel	p.E831del
Pat_36	Post-Resistance	ARMCX3	51566	37	X	100880152	100880154	In_Frame_Del	DEL	TGA	-	10	973	c.183_185delTGA	c.(181-186)TCTGAT>TCT	p.D66del
Pat_36	Post-Resistance	RAB9B	51209	37	X	103080347	103080348	Frame_Shift_Del	DEL	CC	-	7	1613	c.367_368delGG	c.(367-369)GGTfs	p.G123fs
Pat_36	Post-Resistance	IRS4	8471	37	X	107977802	107977803	Frame_Shift_Ins	INS	-	C	26	1011	c.1772_1773insG	c.(1771-1773)GGCfs	p.G591fs
Pat_36	Post-Resistance	CXorf56	63932	37	X	118694316	118694316	Frame_Shift_Del	DEL	G	-	7	826	c.157delC	c.(157-159)CGGfs	p.R53fs
Pat_36	Post-Resistance	AIFM1	9131	37	X	129267377	129267378	Frame_Shift_Del	DEL	CT	-	7	3116	c.1358_1359delAG	c.(1357-1359)GAGfs	p.E453fs
Pat_36	Post-Resistance	SPANXN3	139067	37	X	142605149	142605149	Frame_Shift_Del	DEL	T	-	10	476	c.71delA	c.(70-72)AATfs	p.N24fs
Pat_36	Post-Resistance	SPANXN2	494119	37	X	142803692	142803692	Frame_Shift_Del	DEL	T	-	11	464	c.71delA	c.(70-72)AATfs	p.N24fs
Pat_36	Post-Resistance	MAMLD1	10046	37	X	149639325	149639327	In_Frame_Del	DEL	CAG	-	11	240	.1480_1482delCA	c.(1480-1482)CAGdel	p.Q502del
Pat_36	Post-Resistance	MAMLD1	10046	37	X	149639633	149639635	In_Frame_Del	DEL	GCA	-	7	211	.1788_1790delGC	.(1786-1791)CTGCAG>CT	p.Q606del
Pat_36	Post-Resistance	HMGB3	3149	37	X	150156358	150156360	In_Frame_Del	DEL	GAG	-	10	143	c.574_576delGAG	c.(574-576)GAGdel	p.E198del
Pat_36	Post-Resistance	PASD1	139135	37	X	150817142	150817144	In_Frame_Del	DEL	GCT	-	11	858	c.685_687delGCT	c.(685-687)GCTdel	p.A236del
Pat_36	Post-Resistance	F8	2157	37	X	154157686	154157686	Frame_Shift_Del	DEL	T	-	11	252	c.4379delA	c.(4378-4380)AATfs	p.N1460fs
Pat_37	Post-Resistance	UBR4	23352	37	1	19488943	19488943	Frame_Shift_Del	DEL	C	-	7	577	c.4927delG	c.(4927-4929)GAAfs	p.E1643fs
Pat_37	Post-Resistance	MTPAP	55149	37	10	30653930	30653932	In_Frame_Del	DEL	TCC	-	11	399	c.250_252delGGA	c.(250-252)GGAdel	p.G84del
Pat_37	Post-Resistance	NLRP6	171389	37	11	281553	281555	In_Frame_Del	DEL	GAG	-	13	300	.1819_1821delGA	c.(1819-1821)GAGdel	p.E611del
Pat_37	Post-Resistance	UBQLN3	50613	37	11	5529918	5529920	In_Frame_Del	DEL	TGG	-	9	663	c.869_871delCCA	.(868-873)ACCAGC>AGC	p.T290del
Pat_37	Post-Resistance	SPON1	10418	37	11	14276276	14276277	Splice_Site	DEL	GT	-	63	174	c.1092_splice	c.e9+1	p.E364_splice
Pat_37	Post-Resistance	RIN1	9610	37	11	66103474	66103474	Frame_Shift_Del	DEL	T	-	6	9	c.242delA	c.(241-243)CACfs	p.H81fs
Pat_37	Post-Resistance	MMP1	4312	37	11	102668791	102668793	In_Frame_Del	DEL	CAG	-	13	298	c.31_33delCTG	c.(31-33)CTGdel	p.L11del
Pat_37	Post-Resistance	TMPRSS13	84000	37	11	117789346	117789360	In_Frame_Del	DEL	GAGATGCCC	-	10	102	9delGCCGGGCATI	)GGCCGGGCATCTCCAC	p.GRASP72de
Pat_37	Post-Resistance	RERG	85004	37	12	15262412	15262412	Frame_Shift_Del	DEL	C	-	12	2794	c.232delG	c.(232-234)GAAfs	p.E78fs
Pat_37	Post-Resistance	ESPL1	9700	37	12	53683876	53683877	Frame_Shift_Del	DEL	TG	-	8	286	c.5121_5122delTG	c.(5119-5124)ACTGTGfs	p.T1707fs
Pat_37	Post-Resistance	OR6C65	403282	37	12	55794610	55794610	Frame_Shift_Del	DEL	T	-	7	289	c.298delT	c.(298-300)TTTfs	p.F100fs
Pat_37	Post-Resistance	R3HDM2	22864	37	12	57651794	57651794	Frame_Shift_Del	DEL	G	-	7	349	c.2386delC	c.(2386-2388)CGGfs	p.R796fs
Pat_37	Post-Resistance	C12orf56	115749	37	12	64784307	64784307	Frame_Shift_Del	DEL	C	-	7	18	c.39delG	c.(37-39)AGGfs	p.R13fs
Pat_37	Post-Resistance	UTP20	27340	37	12	101736770	101736770	Frame_Shift_Del	DEL	T	-	9	601	c.4348delT	c.(4348-4350)TTTfs	p.F1450fs
Pat_37	Post-Resistance	IFT81	28981	37	12	110618365	110618367	In_Frame_Del	DEL	CAA	-	15	281	.1327_1329delCA	c.(1327-1329)CAAdel	p.Q445del
Pat_37	Post-Resistance	WASF3	10810	37	13	27250862	27250863	Splice_Site	DEL	GT	-	8	440	c.716_splice	c.e7+1	p.R239_splice
Pat_37	Post-Resistance	MLH3	27030	37	14	75514338	75514338	Frame_Shift_Del	DEL	T	-	7	248	c.2021delA	c.(2020-2022)AATfs	p.N674fs
Pat_37	Post-Resistance	ASPG	374569	37	14	104571684	104571684	Frame_Shift_Del	DEL	G	-	7	147	c.1070delG	c.(1069-1071)CGGfs	p.R357fs
Pat_37	Post-Resistance	MGA	23269	37	15	42003383	42003385	In_Frame_Del	DEL	CAG	-	12	323	.2920_2922delCA	c.(2920-2922)CAGdel	p.Q981del
Pat_37	Post-Resistance	ZNF592	9640	37	15	85327539	85327539	Frame_Shift_Del	DEL	A	-	7	194	c.1633delA	c.(1633-1635)AAAfs	p.K545fs
Pat_37	Post-Resistance	SRCAP	10847	37	16	30731611	30731611	Frame_Shift_Del	DEL	C	-	8	1480	c.2946delC	c.(2944-2946)GACfs	p.D982fs
Pat_37	Post-Resistance	RNF167	26001	37	17	4845690	4845690	Frame_Shift_Del	DEL	C	-	8	688	c.220delC	c.(220-222)CCCfs	p.P74fs
Pat_37	Post-Resistance	CNTROB	116840	37	17	7843518	7843519	Frame_Shift_Del	DEL	GA	-	12	448	c.1269_1270delGA	c.(1267-1272)CGGAGAfs	p.R423fs
Pat_37	Post-Resistance	TRIM16	10626	37	17	15554874	15554886	Frame_Shift_Del	DEL	AGTGGCCC	-	9	54	0delCCAGGGCCA	7-51)CCCAGGGCCACTG	p.P13fs
Pat_37	Post-Resistance	ZNF207	7756	37	17	30677314	30677316	In_Frame_Del	DEL	AAG	-	8	1090	c.10_12delAAG	c.(10-12)AAGdel	p.K7del
Pat_37	Post-Resistance	BZRAP1	9256	37	17	56387404	56387406	In_Frame_Del	DEL	TCC	-	8	209	.3813_3815delGG	.(3811-3816)GAGGAA>GA	1271_1272EE
Pat_37	Post-Resistance	FTSJ3	117246	37	17	61899155	61899157	In_Frame_Del	DEL	CTC	-	10	640	.1522_1524delGA	c.(1522-1524)GAGdel	p.E508del
Pat_37	Post-Resistance	C18orf10	25941	37	18	34376822	34376842	In_Frame_Del	DEL	ACCGGAGG	-	11	70	TCAGGACCCTCC	)TCAGGACCCTCCGGTC	GPSGPS277
Pat_37	Post-Resistance	TMEFF2	23671	37	2	193059175	193059177	In_Frame_Del	DEL	GCA	-	9	176	c.74_76delTGC	c.(73-78)CTGCCC>CCC	p.L25del
Pat_37	Post-Resistance	GBX2	2637	37	2	237076427	237076429	In_Frame_Del	DEL	GGC	-	4	9	c.186_188delGCC	.(184-189)CCGCCC>CCC	p.62_63PP>P
Pat_37	Post-Resistance	KIF3B	9371	37	20	30898763	30898765	In_Frame_Del	DEL	GAG	-	7	147	.1183_1185delGA	c.(1183-1185)GAGdel	p.E399del

Pat_37	Post-Resistance	MICAL3	57553	37	22	18314825	18314827	In_Frame_Del	DEL	CTC	-	7	171	.2848_2850delGA	c.(2848-2850)GAGdel	p.E950del
Pat_37	Post-Resistance	CRYBB2	1415	37	22	25627664	25627664	Frame_Shift_Del	DEL	C	-	7	540	c.543delC	c.(541-543)CACfs	p.H181fs
Pat_37	Post-Resistance	SF3A1	10291	37	22	30742328	30742330	In_Frame_Del	DEL	CTG	-	14	474	c.364_366delCAG	c.(364-366)CAGdel	p.Q122del
Pat_37	Post-Resistance	PICK1	9463	37	22	38471034	38471036	In_Frame_Del	DEL	GGA	-	7	133	.1143_1145delGG	(1141-1146)GGGGAG>GG	p.E388del
Pat_37	Post-Resistance	MAPK8IP2	23542	37	22	51041769	51041771	In_Frame_Del	DEL	GAG	-	7	37	c.289_291delGAG	c.(289-291)GAGdel	p.E103del
Pat_37	Post-Resistance	GRM7	2917	37	3	7621013	7621013	Frame_Shift_Del	DEL	T	-	7	105	c.2420delT	c.(2419-2421)ATTfs	p.I807fs
Pat_37	Post-Resistance	XPC	7508	37	3	14219966	14219968	In_Frame_Del	DEL	CCT	-	13	198	c.101_103delAGG	c.(100-105)GAGGAT>GAT	p.E34del
Pat_37	Post-Resistance	MLH1	4292	37	3	37070349	37070349	Frame_Shift_Del	DEL	C	-	8	1768	c.1484delC	c.(1483-1485)ACCfs	p.T495fs
Pat_37	Post-Resistance	SLC25A38	54977	37	3	39437924	39437924	Frame_Shift_Del	DEL	C	-	7	1105	c.828delC	c.(826-828)ATCfs	p.I276fs
Pat_37	Post-Resistance	HHATL	57467	37	3	42740315	42740317	In_Frame_Del	DEL	AGC	-	9	265	c.366_368delGCT	c.(364-369)CTGCTT>CTT	.122_123LL>L
Pat_37	Post-Resistance	LIMD1	8994	37	3	45636543	45636545	In_Frame_Del	DEL	CAG	-	8	112	c.172_174delCAG	c.(172-174)CAGdel	p.Q63del
Pat_37	Post-Resistance	ALS2CL	259173	37	3	46729622	46729624	In_Frame_Del	DEL	GCA	-	11	267	c.266_268delTGC	.(265-270)CTGCGA>CGA	p.L89del
Pat_37	Post-Resistance	VPRBP	9730	37	3	51457448	51457448	Frame_Shift_Del	DEL	T	-	8	1050	c.2976delA	c.(2974-2976)AAAfs	p.K992fs
Pat_37	Post-Resistance	CPEB2	132864	37	4	15067858	15067858	Frame_Shift_Del	DEL	T	-	7	911	c.1624delT	c.(1624-1626)TTTfs	p.F542fs
Pat_37	Post-Resistance	GABRG1	2565	37	4	46060358	46060358	Frame_Shift_Del	DEL	A	-	12	270	c.792delT	c.(790-792)TTTfs	p.F264fs
Pat_37	Post-Resistance	SEC31A	22872	37	4	83745800	83745800	Frame_Shift_Del	DEL	T	-	8	115	c.3319delA	c.(3319-3321)ATTfs	p.I1107fs
Pat_37	Post-Resistance	KIAA1109	84162	37	4	123188069	123188078	Frame_Shift_Del	DEL	GATTCAGA	-	57	277	_7458delGGATTC	447-7458)GTGGATTCAGA	p.V2483fs
Pat_37	Post-Resistance	PDZD2	23037	37	5	31799541	31799541	Frame_Shift_Del	DEL	C	-	7	837	c.186delC	c.(184-186)AGCfs	p.S62fs
Pat_37	Post-Resistance	JARID2	3720	37	6	15501164	15501164	Frame_Shift_Del	DEL	T	-	8	1311	c.1972delT	c.(1972-1974)TTTfs	p.F658fs
Pat_37	Post-Resistance	ATXN1	6310	37	6	16328093	16328093	Frame_Shift_Del	DEL	G	-	8	720	c.449delC	c.(448-450)CCAfs	p.P150fs
Pat_37	Post-Resistance	HLA-DPB1	3115	37	6	33052934	33052934	Frame_Shift_Del	DEL	C	-	7	808	c.572delC	c.(571-573)ACCfs	p.T191fs
Pat_37	Post-Resistance	PHF1	5252	37	6	33383637	33383637	Frame_Shift_Del	DEL	C	-	7	1097	c.1466delC	c.(1465-1467)GCCfs	p.A489fs
Pat_37	Post-Resistance	PHACTR2	9749	37	6	144086414	144086414	Frame_Shift_Del	DEL	A	-	8	256	c.678delA	c.(676-678)TCAfs	p.S226fs
Pat_37	Post-Resistance	GRM1	2911	37	6	146755399	146755401	In_Frame_Del	DEL	CAG	-	9	958	.3052_3054delCA	c.(3052-3054)CAGdel	p.Q1022del
Pat_37	Post-Resistance	GLCCI1	113263	37	7	8126097	8126099	In_Frame_Del	DEL	CAG	-	7	1014	.1573_1575delCA	c.(1573-1575)CAGdel	p.Q528del
Pat_37	Post-Resistance	PHF14	9678	37	7	11075380	11075381	Frame_Shift_Del	DEL	AG	-	9	971	.1569_1570delAG	c.(1567-1572)CAAGAGfs	p.Q523fs
Pat_37	Post-Resistance	LIMK1	3984	37	7	73535311	73535311	Frame_Shift_Del	DEL	C	-	7	1466	c.1713delC	c.(1711-1713)TGCfs	p.C571fs
Pat_37	Post-Resistance	KIAA0020	9933	37	9	2837296	2837296	Frame_Shift_Del	DEL	T	-	7	1086	c.188delA	c.(187-189)AAGfs	p.K63fs
Pat_37	Post-Resistance	KIAA2026	158358	37	9	5968043	5968044	Frame_Shift_Ins	INS	-	T	5	8	c.2187_2188insA	c.(2185-2190)AAAGCAfs	p.K729fs
Pat_40	Pre-Treatment	TNFRSF9	3604	37	1	7998254	7998254	Frame_Shift_Del	DEL	T	-	8	324	c.345delA	c.(343-345)AAAfs	p.K115fs
Pat_40	Pre-Treatment	RERE	473	37	1	8716284	8716285	Frame_Shift_Del	DEL	TC	-	9	196	c.72_73delGA	c.(70-75)GAGAAAfs	p.E24fs
Pat_40	Pre-Treatment	FABP3	2170	37	1	31842256	31842257	Frame_Shift_Del	DEL	TG	-	8	869	c.221_222delCA	c.(220-222)ACAfs	p.T74fs
Pat_40	Pre-Treatment	JAK1	3716	37	1	65332708	65332708	Frame_Shift_Del	DEL	C	-	8	461	c.831delG	c.(829-831)TTGfs	p.L277fs
Pat_40	Pre-Treatment	FNDC7	163479	37	1	109276138	109276138	Frame_Shift_Del	DEL	A	-	7	133	c.2124delA	c.(2122-2124)CCAfs	p.P708fs
Pat_40	Pre-Treatment	TCHH	7062	37	1	152082211	152082213	In_Frame_Del	DEL	CTC	-	7	113	.3480_3482delGA	.(3478-3483)AAGAGA>AA	p.R1163del
Pat_40	Pre-Treatment	TCHH	7062	37	1	152084489	152084490	In_Frame_Ins	INS	-	CTC	3	3	.1203_1204insGA	c.(1201-1206)insGAG	p.401_402insE
Pat_40	Pre-Treatment	RPTN	126638	37	1	152127845	152127848	Frame_Shift_Del	DEL	TGTC	-	8	1303	1727_1730delGA	c.(1726-1731)AGACAAfs	p.R576fs
Pat_40	Pre-Treatment	POU2F1	5451	37	1	167385016	167385018	In_Frame_Del	DEL	CCA	-	8	448	.2201_2203delCC	.(2200-2205)TCCACC>TC	p.T738del
Pat_40	Pre-Treatment	PAPPA2	60676	37	1	176709182	176709182	Frame_Shift_Del	DEL	T	-	7	432	c.4001delT	c.(4000-4002)CTTfs	p.L1334fs
Pat_40	Pre-Treatment	PRG4	10216	37	1	186276374	186276376	In_Frame_Del	DEL	CCA	-	7	376	.1523_1525delCC	(1522-1527)CCCACC>CC	p.T511del
Pat_40	Pre-Treatment	OR14I1	401994	37	1	248844831	248844832	Frame_Shift_Del	DEL	CT	-	8	299	c.774_775delAG	c.(772-777)TTAGGAfs	p.L258fs
Pat_40	Pre-Treatment	JMJD1C	221037	37	10	64966802	64966802	Frame_Shift_Del	DEL	G	-	7	157	c.4627delC	c.(4627-4629)CAAfs	p.Q1543fs
Pat_40	Pre-Treatment	KCNMA1	3778	37	10	78729786	78729786	Frame_Shift_Del	DEL	T	-	11	163	c.2306delA	c.(2305-2307)AAGfs	p.K769fs
Pat_40	Pre-Treatment	ZMIZ1	57178	37	10	81072446	81072446	Frame_Shift_Del	DEL	C	-	12	388	c.3144delC	c.(3142-3144)GACfs	p.D1048fs
Pat_40	Pre-Treatment	CPXM2	119587	37	10	125528165	125528167	In_Frame_Del	DEL	CAG	-	8	348	.1174_1176delCT	c.(1174-1176)CTGdel	p.L392del
Pat_40	Pre-Treatment	FTH1	2495	37	11	61732517	61732517	Frame_Shift_Del	DEL	T	-	11	611	c.329delA	c.(328-330)AATfs	p.N110fs
Pat_40	Pre-Treatment	SF3B2	10992	37	11	65836146	65836146	Frame_Shift_Del	DEL	A	-	9	108	c.2618delA	c.(2617-2619)CAAfs	p.Q873fs

Pat_40	Pre-Treatment	CCS	9973	37	11	66372993	66372994	Frame_Shift_Del	DEL	GA	-	7	116	c.601_602delGA	c.(601-603)GATfs	p.D201fs
Pat_40	Pre-Treatment	MMP12	4321	37	11	102738795	102738796	Frame_Shift_Ins	INS	-	T	34	1	c.629_630insA	c.(628-630)ACCfs	p.T210fs
Pat_40	Pre-Treatment	TAS2R31	259290	37	12	11183679	11183680	Frame_Shift_Del	DEL	TA	-	8	348	c.255_256delTA	c.(253-258)TATAATfs	p.Y85fs
Pat_40	Pre-Treatment	PRB1	5542	37	12	11506815	11506816	In_Frame_Ins	INS	-	GGA	7	153	c.221_222insTCC	c.(220-222)CCA>CCTCCA	p.74_74P>PP
Pat_40	Pre-Treatment	PRB2	653247	37	12	11546544	11546545	In_Frame_Ins	INS	-	GGA	7	255	c.467_468insTCC	c.(466-468)CCA>CCTCCA	.156_156P>P
Pat_40	Pre-Treatment	GPR19	2842	37	12	12814274	12814274	Frame_Shift_Del	DEL	T	-	7	369	c.1109delA	c.(1108-1110)AACfs	p.N370fs
Pat_40	Pre-Treatment	KIAA0528	9847	37	12	22646202	22646202	Frame_Shift_Del	DEL	A	-	9	706	c.1217delT	c.(1216-1218)TTAfs	p.L406fs
Pat_40	Pre-Treatment	MARS	4141	37	12	57883053	57883053	Frame_Shift_Del	DEL	T	-	7	56	c.204delT	c.(202-204)TATfs	p.Y68fs
Pat_40	Pre-Treatment	MDM1	56890	37	12	68689067	68689067	Frame_Shift_Del	DEL	C	-	8	207	c.2112delG	c.(2110-2112)AAGfs	p.K704fs
Pat_40	Pre-Treatment	SART3	9733	37	12	108917255	108917255	Frame_Shift_Del	DEL	G	-	8	478	c.2871delC	c.(2869-2871)GCCfs	p.A957fs
Pat_40	Pre-Treatment	TPCN1	53373	37	12	113704096	113704098	In_Frame_Del	DEL	CTG	-	26	743	c.349_351delCTG	c.(349-351)CTGdel	p.L122del
Pat_40	Pre-Treatment	SFRS8	6433	37	12	132281734	132281736	In_Frame_Del	DEL	AGA	-	7	362	.2546_2548delAG	(2545-2550)GAGAAG>GA	p.K853del
Pat_40	Pre-Treatment	POLE	5426	37	12	133220099	133220100	Frame_Shift_Del	DEL	CA	-	11	489	c.4337_4338delTG	c.(4336-4338)GTGfs	p.V1446fs
Pat_40	Pre-Treatment	NUFIP1	26747	37	13	45563293	45563293	Frame_Shift_Del	DEL	G	-	4	7	c.279delC	c.(277-279)TTCfs	p.F93fs
Pat_40	Pre-Treatment	ZC3H13	23091	37	13	46549613	46549614	Frame_Shift_Del	DEL	CT	-	4	9	c.2272_2273delAG	c.(2272-2274)AGGfs	p.R758fs
Pat_40	Pre-Treatment	DIAPH3	81624	37	13	60582733	60582734	Frame_Shift_Ins	INS	-	T	10	250	c.958_959insA	c.(958-960)ATTfs	p.I320fs
Pat_40	Pre-Treatment	C14orf43	91748	37	14	74205926	74205928	In_Frame_Del	DEL	CTG	-	10	34	c.784_786delCAG	c.(784-786)CAGdel	p.Q262del
Pat_40	Pre-Treatment	DMXL2	23312	37	15	51773148	51773149	Frame_Shift_Del	DEL	AT	-	7	210	c.6154_6155delAT	c.(6154-6156)ATGfs	p.M2052fs
Pat_40	Pre-Treatment	ZNF609	23060	37	15	64972995	64972997	In_Frame_Del	DEL	CAC	-	9	450	.4096_4098delCA	c.(4096-4098)CACdel	p.H1371del
Pat_40	Pre-Treatment	DIS3L	115752	37	15	66607405	66607405	Frame_Shift_Del	DEL	G	-	8	299	c.846delG	c.(844-846)ATGfs	p.M282fs
Pat_40	Pre-Treatment	PKM2	5315	37	15	72502122	72502123	Frame_Shift_Del	DEL	CA	-	8	549	c.456_457delTG	c.(454-459)TGTGACfs	p.C152fs
Pat_40	Pre-Treatment	CYP1A2	1544	37	15	75044574	75044575	Frame_Shift_Del	DEL	CA	-	8	596	c.1152_1153delCA	c.(1150-1155)TTCACCfs	p.F384fs
Pat_40	Pre-Treatment	CPLX3	594855	37	15	75122558	75122560	In_Frame_Del	DEL	GAG	-	7	155	c.340_342delGAG	c.(340-342)GAGdel	p.E118del
Pat_40	Pre-Treatment	ADCY9	115	37	16	4016132	4016132	Frame_Shift_Del	DEL	G	-	8	186	c.3706delC	c.(3706-3708)CAGfs	p.Q1236fs
Pat_40	Pre-Treatment	GLYR1	84656	37	16	4895089	4895089	Frame_Shift_Del	DEL	A	-	7	309	c.141delT	c.(139-141)TTTfs	p.F47fs
Pat_40	Pre-Treatment	ARHGAP17	55114	37	16	24942118	24942119	Frame_Shift_Del	DEL	GG	-	7	717	c.2501_2502delCC	c.(2500-2502)TCCfs	p.S834fs
Pat_40	Pre-Treatment	APOB48R	55911	37	16	28509543	28509543	Frame_Shift_Del	DEL	A	-	2	4	c.3070delA	c.(3070-3072)AACfs	p.N1024fs
Pat_40	Pre-Treatment	SETD1A	9739	37	16	30982809	30982811	In_Frame_Del	DEL	TCC	-	11	96	.3127_3129delTC	c.(3127-3129)TCCdel	p.S1058del
Pat_40	Pre-Treatment	TRPV2	51393	37	17	16335490	16335492	In_Frame_Del	DEL	TGC	-	8	110	.1865_1867delTG	(1864-1869)GTGCTG>GT	p.L627del
Pat_40	Pre-Treatment	MYO1D	4642	37	17	31092016	31092017	Frame_Shift_Del	DEL	AG	-	9	124	c.914_915delCT	c.(913-915)TCTfs	p.S305fs
Pat_40	Pre-Treatment	MMP28	79148	37	17	34105964	34105964	Frame_Shift_Del	DEL	C	-	8	239	c.307delG	c.(307-309)GCTfs	p.A103fs
Pat_40	Pre-Treatment	KLHL10	317719	37	17	39998235	39998235	Frame_Shift_Del	DEL	T	-	7	190	c.355delT	c.(355-357)TTTfs	p.F119fs
Pat_40	Pre-Treatment	BPTF	2186	37	17	65940454	65940456	In_Frame_Del	DEL	CAC	-	9	410	.6666_6668delCA	(6664-6669)AGCACC>AG	p.T2227del
Pat_40	Pre-Treatment	KPNA2	3838	37	17	66040578	66040579	Frame_Shift_Ins	INS	-	T	7	682	c.1306_1307insT	c.(1306-1308)ATTfs	p.I436fs
Pat_40	Pre-Treatment	DOK6	220164	37	18	67406306	67406307	Frame_Shift_Ins	INS	-	T	43	262	c.705_706insT	c.(703-708)GAAAGAfs	p.E235fs
Pat_40	Pre-Treatment	DMKN	93099	37	19	36002362	36002412	In_Frame_Del	DEL	CCACTGCT	-	7	17	GGCGGCAGCAGT	GGCGGCAGCAGTGGC	GSSSGGSSG
Pat_40	Pre-Treatment	ZFP112	7771	37	19	44832512	44832512	Frame_Shift_Del	DEL	C	-	8	522	c.1816delG	c.(1816-1818)GAAfs	p.E606fs
Pat_40	Pre-Treatment	NPAS1	4861	37	19	47542363	47542364	Frame_Shift_Del	DEL	CC	-	8	105	c.758_759delCC	c.(757-759)TCCfs	p.S253fs
Pat_40	Pre-Treatment	FLT3LG	2323	37	19	49978960	49978962	In_Frame_Del	DEL	CTG	-	7	178	c.46_48delCTG	c.(46-48)CTGdel	p.L20del
Pat_40	Pre-Treatment	ZNF160	90338	37	19	53572481	53572482	Frame_Shift_Del	DEL	AC	-	7	267	c.1305_1306delGT	c.(1303-1308)AGGTACfs	p.R435fs
Pat_40	Pre-Treatment	TMC4	147798	37	19	54672280	54672280	Frame_Shift_Del	DEL	G	-	4	9	c.587delC	c.(586-588)CCAfs	p.P196fs
Pat_40	Pre-Treatment	HS1BP3	64342	37	2	20840864	20840864	Frame_Shift_Del	DEL	G	-	7	424	c.275delC	c.(274-276)CCAfs	p.P92fs
Pat_40	Pre-Treatment	USP34	9736	37	2	61447530	61447530	Frame_Shift_Del	DEL	T	-	7	1116	c.7962delA	c.(7960-7962)AAAfs	p.K2654fs
Pat_40	Pre-Treatment	SLC9A4	389015	37	2	103120126	103120127	Frame_Shift_Del	DEL	TA	-	8	257	c.940_941delTA	c.(940-942)TACfs	p.Y314fs
Pat_40	Pre-Treatment	XIRP2	129446	37	2	168099958	168099958	Frame_Shift_Del	DEL	G	-	7	248	c.2056delG	c.(2056-2058)GGGfs	p.G686fs
Pat_40	Pre-Treatment	SAMHD1	25939	37	20	35526234	35526234	Frame_Shift_Del	DEL	G	-	8	395	c.1737delC	c.(1735-1737)ACCfs	p.T579fs
Pat_40	Pre-Treatment	TPTE	7179	37	21	10944697	10944697	Frame_Shift_Del	DEL	A	-	15	300	c.537delT	c.(535-537)TTTfs	p.F179fs

Pat_40	Pre-Treatment	MN1	4330	37	22	28195603	28195605	In_Frame_Del	DEL	TGC	-	3	5	c.927_929delGCA	c.(925-930)CAGCAT>CAT	p.Q309del
Pat_40	Pre-Treatment	MTMR3	8897	37	22	30408494	30408494	Frame_Shift_Del	DEL	C	-	7	954	c.1259delC	c.(1258-1260)ACCfs	p.T420fs
Pat_40	Pre-Treatment	TRIOBP	11078	37	22	38120245	38120253	In_Frame_Del	DEL	CCTCCAGA	-	9	316	2_1690delCCTCC	1-1692)GCCTCCAGAACC	p.SRT562del
Pat_40	Pre-Treatment	GRIP2	80852	37	3	14555863	14555864	Frame_Shift_Del	DEL	GC	-	4	8	c.1723_1724delGC	c.(1723-1725)GCCfs	p.A575fs
Pat_40	Pre-Treatment	GTF2E1	2960	37	3	120489634	120489634	Frame_Shift_Del	DEL	A	-	7	442	c.508delA	c.(508-510)AAAfs	p.K170fs
Pat_40	Pre-Treatment	CRIPAK	285464	37	4	1388345	1388346	Frame_Shift_Del	DEL	CA	-	7	551	c.46_47delCA	c.(46-48)CACfs	p.H16fs
Pat_40	Pre-Treatment	CRIPAK	285464	37	4	1389147	1389148	Frame_Shift_Del	DEL	AT	-	12	415	c.848_849delAT	c.(847-849)CATfs	p.H283fs
Pat_40	Pre-Treatment	CRIPAK	285464	37	4	1389175	1389176	Frame_Shift_Del	DEL	CA	-	10	471	c.876_877delCA	c.(874-879)CTCACAfs	p.L292fs
Pat_40	Pre-Treatment	CRIPAK	285464	37	4	1389236	1389237	Frame_Shift_Ins	INS	-	CA	7	616	c.937_938insCA	c.(937-939)TCAfs	p.S313fs
Pat_40	Pre-Treatment	CRIPAK	285464	37	4	1389425	1389426	Frame_Shift_Del	DEL	CA	-	15	715	c.1126_1127delCA	c.(1126-1128)CACfs	p.H376fs
Pat_40	Pre-Treatment	HTT	3064	37	4	3076604	3076606	In_Frame_Del	DEL	CAG	-	8	18	c.58_60delCAG	c.(58-60)CAGdel	p.Q40del
Pat_40	Pre-Treatment	SMAD1	4086	37	4	146436139	146436139	Frame_Shift_Del	DEL	A	-	9	462	c.374delA	c.(373-375)TACfs	p.Y125fs
Pat_40	Pre-Treatment	HAND2	9464	37	4	174450345	174450347	In_Frame_Del	DEL	GGC	-	2	4	c.94_96delGCC	c.(94-96)GCCdel	p.A32del
Pat_40	Pre-Treatment	TNPO1	3842	37	5	72195897	72195898	Frame_Shift_Del	DEL	TA	-	8	320	c.2403_2404delTA	c.(2401-2406)TTTATAfs	p.F801fs
Pat_40	Pre-Treatment	GPR98	84059	37	5	89948207	89948207	Frame_Shift_Del	DEL	G	-	7	367	c.3461delG	c.(3460-3462)TGGfs	p.W1154fs
Pat_40	Pre-Treatment	SRP19	6728	37	5	112227328	112227328	Frame_Shift_Del	DEL	G	-	2	4	c.67delG	c.(67-69)GCTfs	p.A23fs
Pat_40	Pre-Treatment	SLC22A4	6583	37	5	131676327	131676327	Frame_Shift_Del	DEL	T	-	11	385	c.1514delT	c.(1513-1515)CTTfs	p.L505fs
Pat_40	Pre-Treatment	KIF3A	11127	37	5	132070092	132070093	Frame_Shift_Del	DEL	TC	-	8	539	c.84_85delGA	c.(82-87)GAGAAAfs	p.E28fs
Pat_40	Pre-Treatment	RREB1	6239	37	6	7230034	7230034	Frame_Shift_Del	DEL	G	-	4	9	c.1702delG	c.(1702-1704)GGGfs	p.G568fs
Pat_40	Pre-Treatment	PHF14	9678	37	7	11075380	11075381	Frame_Shift_Del	DEL	AG	-	9	542	c.1569_1570delAG	c.(1567-1572)CAAGAGfs	p.Q523fs
Pat_40	Pre-Treatment	ZNF716	441234	37	7	57529007	57529008	In_Frame_Ins	INS	-	TCT	8	174	c.840_841insTCT	c.(838-843)insTCT	p.281_282insS
Pat_40	Pre-Treatment	ZNF716	441234	37	7	57529089	57529091	In_Frame_Del	DEL	TCT	-	7	338	c.922_924delTCT	c.(922-924)TCTdel	p.S309del
Pat_40	Pre-Treatment	TNPO3	23534	37	7	128610259	128610259	Frame_Shift_Del	DEL	G	-	7	582	c.2541delC	c.(2539-2541)CCCfs	p.P847fs
Pat_40	Pre-Treatment	OR9A4	130075	37	7	141619203	141619203	Frame_Shift_Del	DEL	T	-	15	531	c.528delT	c.(526-528)AATfs	p.N176fs
Pat_40	Pre-Treatment	KCNU1	157855	37	8	36766827	36766828	Splice_Site	DEL	AG	-	7	334	c.2107_splice	c.e21-1	p.K703_splice
Pat_40	Pre-Treatment	SULF1	23213	37	8	70514026	70514026	Frame_Shift_Del	DEL	T	-	9	885	c.1023delT	c.(1021-1023)CCTfs	p.P341fs
Pat_40	Pre-Treatment	ZNF704	619279	37	8	81733778	81733778	Frame_Shift_Del	DEL	T	-	8	1134	c.52delA	c.(52-54)ATGfs	p.M18fs
Pat_40	Pre-Treatment	NBN	4683	37	8	90967512	90967512	Frame_Shift_Del	DEL	T	-	10	363	c.1396delA	c.(1396-1398)AGGfs	p.R466fs
Pat_40	Pre-Treatment	CCNE2	9134	37	8	95895082	95895083	Frame_Shift_Del	DEL	CT	-	8	512	c.869_870delAG	c.(868-870)GAGfs	p.E290fs
Pat_40	Pre-Treatment	TP53INP1	94241	37	8	95952409	95952411	In_Frame_Del	DEL	TCT	-	7	185	c.150_152delAGA	c.(148-153)GAAGAG>GAG	p.50_51EE>E
Pat_40	Pre-Treatment	RNF19A	25897	37	8	101299727	101299727	Splice_Site	DEL	A	-	10	498	c.674_splice	c.e3+1	p.G225_splice
Pat_40	Pre-Treatment	DPYS	1807	37	8	105440214	105440214	Frame_Shift_Del	DEL	T	-	12	1004	c.1086delA	c.(1084-1086)AAAfs	p.K362fs
Pat_40	Pre-Treatment	HEATR7A	727957	37	8	145255353	145255353	Frame_Shift_Del	DEL	A	-	4	3	c.1050delA	c.(1048-1050)CTAfs	p.L350fs
Pat_40	Pre-Treatment	SMARCA2	6595	37	9	2039777	2039779	In_Frame_Del	DEL	CAG	-	14	10	c.667_669delCAG	c.(667-669)CAGdel	p.Q238del
Pat_40	Pre-Treatment	MLLT3	4300	37	9	20414377	20414379	In_Frame_Del	DEL	CTG	-	7	55	c.465_467delCAG	c.(463-468)AGCAGT>AGT	.155_156SS>S
Pat_40	Pre-Treatment	ZNF367	195828	37	9	99160470	99160470	Frame_Shift_Del	DEL	G	-	7	488	c.547delC	c.(547-549)CAGfs	p.Q183fs
Pat_40	Pre-Treatment	KIAA1529	57653	37	9	100082418	100082418	Frame_Shift_Del	DEL	C	-	7	679	c.1639delC	c.(1639-1641)CCCfs	p.P547fs
Pat_40	Pre-Treatment	SVEP1	79987	37	9	113166648	113166649	Frame_Shift_Ins	INS	-	T	7	549	c.9624_9625insA	c.(9622-9627)GCAGAAfs	p.A3208fs
Pat_40	Pre-Treatment	NUP214	8021	37	9	134007993	134007993	Frame_Shift_Del	DEL	A	-	8	157	c.674delA	c.(673-675)GAAfs	p.E225fs
Pat_40	Pre-Treatment	MED12	9968	37	X	70360589	70360591	In_Frame_Del	DEL	AGC	-	10	195	.6149_6151delAG	(6148-6153)GAGCAG>GA	p.Q2076del
Pat_40	Pre-Treatment	ALG13	79868	37	X	110928220	110928220	Frame_Shift_Del	DEL	A	-	7	483	c.272delA	c.(271-273)GAAfs	p.E91fs
Pat_40	Pre-Treatment	CUL4B	8450	37	X	119694117	119694119	In_Frame_Del	DEL	GAG	-	8	77	c.429_431delCTC	c.(427-432)TCCTCA>TCA	.143_144SS>S
Pat_40	Pre-Treatment	CDR1	1038	37	X	139865995	139865995	Frame_Shift_Del	DEL	C	-	8	428	c.537delG	c.(535-537)TGGfs	p.W179fs
Pat_40	Post-Resistance	VAMP3	9341	37	1	7838212	7838214	In_Frame_Del	DEL	TCA	-	14	928	c.266_268delTCA	c.(265-270)TTCATC>TTC	p.I94del
Pat_40	Post-Resistance	RERE	473	37	1	8716284	8716285	Frame_Shift_Del	DEL	TC	-	15	263	c.72_73delGA	c.(70-75)GAGAAAfs	p.E24fs
Pat_40	Post-Resistance	AADACL3	126767	37	1	12785494	12785494	Frame_Shift_Del	DEL	G	-	8	304	c.584delG	c.(583-585)TGTfs	p.C195fs
Pat_40	Post-Resistance	ZNF362	149076	37	1	33745818	33745820	In_Frame_Del	DEL	CCA	-	8	738	c.443_445delCCA	c.(442-447)CCCACC>CCC	p.T151del

Pat_40	Post-Resistance	MACF1	23499	37	1	39788668	39788670	In_Frame_Del	DEL	GGA	-	8	675	.4239_4241delGG	(4237-4242)CTGGAG>CT	p.E1417del
Pat_40	Post-Resistance	ROR1	4919	37	1	64608186	64608187	Frame_Shift_Del	DEL	CA	-	7	519	c.1027_1028delCA	c.(1027-1029)CACfs	p.H343fs
Pat_40	Post-Resistance	CDC7	8317	37	1	91967356	91967357	Frame_Shift_Ins	INS	-	A	12	179	c.83_84insA	c.(82-84)TTAfs	p.L28fs
Pat_40	Post-Resistance	BRDT	676	37	1	92447228	92447230	In_Frame_Del	DEL	AGC	-	8	599	.1918_1920delAG	c.(1918-1920)AGCdel	p.S648del
Pat_40	Post-Resistance	COL11A1	1301	37	1	103355065	103355065	Frame_Shift_Del	DEL	T	-	8	423	c.4410delA	c.(4408-4410)AAAfs	p.K1470fs
Pat_40	Post-Resistance	FLG2	388698	37	1	152324558	152324559	Frame_Shift_Del	DEL	TG	-	7	1252	c.5703_5704delCA	c.(5701-5706)CACAGCfs	p.H1901fs
Pat_40	Post-Resistance	LCE2A	353139	37	1	152671425	152671425	Frame_Shift_Del	DEL	C	-	7	1127	c.48delC	c.(46-48)TGCfs	p.C16fs
Pat_40	Post-Resistance	PVRL4	81607	37	1	161044057	161044059	In_Frame_Del	DEL	CAC	-	8	398	.1105_1107delGT	c.(1105-1107)GTGdel	p.V369del
Pat_40	Post-Resistance	PVRL4	81607	37	1	161044104	161044106	In_Frame_Del	DEL	CCA	-	7	527	.1058_1060delTG	(1057-1062)GTGGGT>GG	p.V353del
Pat_40	Post-Resistance	POU2F1	5451	37	1	167385016	167385018	In_Frame_Del	DEL	CCA	-	10	867	.2201_2203delCC	.(2200-2205)TCCACC>TC	p.T738del
Pat_40	Post-Resistance	RCSD1	92241	37	1	167654710	167654711	Frame_Shift_Ins	INS	-	C	7	642	c.161_162insC	c.(160-162)TTCfs	p.F54fs
Pat_40	Post-Resistance	GLUL	2752	37	1	182355463	182355463	Frame_Shift_Del	DEL	G	-	7	810	c.403delC	c.(403-405)CAGfs	p.Q135fs
Pat_40	Post-Resistance	PRG4	10216	37	1	186276127	186276128	In_Frame_Ins	INS	-	AGG	10	277	.1276_1277insAG	(1276-1278)AAG>AAGGA	p.426_427insE
Pat_40	Post-Resistance	PRG4	10216	37	1	186276374	186276376	In_Frame_Del	DEL	CCA	-	10	386	.1523_1525delCC	(1522-1527)CCCACC>CC	p.T511del
Pat_40	Post-Resistance	PRG4	10216	37	1	186276386	186276388	In_Frame_Del	DEL	AGG	-	7	418	.1535_1537delAG	(1534-1539)AAGGAG>AA	p.E513del
Pat_40	Post-Resistance	SYT2	127833	37	1	202573647	202573649	In_Frame_Del	DEL	TTC	-	8	250	c.279_281delGAA	c.(277-282)AAGAAC>AAC	p.K93del
Pat_40	Post-Resistance	WNT9A	7483	37	1	228111954	228111954	Frame_Shift_Del	DEL	C	-	7	336	c.500delG	c.(499-501)GGCfs	p.G167fs
Pat_40	Post-Resistance	CDH23	64072	37	10	73337735	73337736	Frame_Shift_Del	DEL	AC	-	4	7	c.818_819delAC	c.(817-819)TACfs	p.Y273fs
Pat_40	Post-Resistance	HECTD2	143279	37	10	93247481	93247481	Frame_Shift_Del	DEL	A	-	9	425	c.1137delA	c.(1135-1137)GCAfs	p.A379fs
Pat_40	Post-Resistance	CTR9	9646	37	11	10789947	10789947	Frame_Shift_Del	DEL	T	-	7	527	c.2018delT	c.(2017-2019)GTAfs	p.V673fs
Pat_40	Post-Resistance	BTBD10	84280	37	11	13441232	13441232	Frame_Shift_Del	DEL	G	-	8	1155	c.359delC	c.(358-360)CCAfs	p.P120fs
Pat_40	Post-Resistance	MMP12	4321	37	11	102738795	102738796	Frame_Shift_Ins	INS	-	T	23	3	c.629_630insA	c.(628-630)ACCfs	p.T210fs
Pat_40	Post-Resistance	CBL	867	37	11	119149356	119149358	In_Frame_Del	DEL	ATG	-	7	98	.1364_1366delAT	c.(1363-1368)TATGAT>TAT	p.D460del
Pat_40	Post-Resistance	GPR19	2842	37	12	12814274	12814274	Frame_Shift_Del	DEL	T	-	7	629	c.1109delA	c.(1108-1110)AACfs	p.N370fs
Pat_40	Post-Resistance	PLBD1	79887	37	12	14664498	14664499	Frame_Shift_Del	DEL	AT	-	7	852	c.991_992delAT	c.(991-993)ATGfs	p.M331fs
Pat_40	Post-Resistance	SFRS2IP	9169	37	12	46318575	46318577	In_Frame_Del	DEL	GGT	-	10	810	.3840_3842delAC	(3838-3843)CCACCC>CC	1280_1281PP>
Pat_40	Post-Resistance	MARS	4141	37	12	57883053	57883053	Frame_Shift_Del	DEL	T	-	7	123	c.204delT	c.(202-204)TATfs	p.Y68fs
Pat_40	Post-Resistance	TPCN1	53373	37	12	113704096	113704098	In_Frame_Del	DEL	CTG	-	19	831	c.349_351delCTG	c.(349-351)CTGdel	p.L122del
Pat_40	Post-Resistance	SFRS8	6433	37	12	132281734	132281736	In_Frame_Del	DEL	AGA	-	10	461	.2546_2548delAG	.(2545-2550)GAGAAG>GA	p.K853del
Pat_40	Post-Resistance	POLE	5426	37	12	133220099	133220100	Frame_Shift_Del	DEL	CA	-	18	774	c.4337_4338delTG	c.(4336-4338)GTGfs	p.V1446fs
Pat_40	Post-Resistance	ABCC4	10257	37	13	95768189	95768190	Frame_Shift_Del	DEL	AA	-	8	647	c.2521_2522delTT	c.(2521-2523)TTAfs	p.L841fs
Pat_40	Post-Resistance	RNASE7	84659	37	14	21511560	21511561	Frame_Shift_Del	DEL	CC	-	7	343	c.409_410delCC	c.(409-411)CCCfs	p.P137fs
Pat_40	Post-Resistance	RBM23	55147	37	14	23378776	23378776	Frame_Shift_Del	DEL	T	-	7	978	c.95delA	c.(94-96)AAGfs	p.K32fs
Pat_40	Post-Resistance	FANCM	57697	37	14	45642288	45642289	Frame_Shift_Del	DEL	CT	-	12	525	c.2191_2192delCT	c.(2191-2193)CTCfs	p.L731fs
Pat_40	Post-Resistance	FAM63B	54629	37	15	59064201	59064203	In_Frame_Del	DEL	GAG	-	7	201	c.607_609delGAG	c.(607-609)GAGdel	p.E206del
Pat_40	Post-Resistance	ZNF609	23060	37	15	64972995	64972997	In_Frame_Del	DEL	CAC	-	9	671	.4096_4098delCA	c.(4096-4098)CACdel	p.H1371del
Pat_40	Post-Resistance	ZNF609	23060	37	15	64973567	64973567	Frame_Shift_Del	DEL	C	-	10	509	c.4222delC	c.(4222-4224)CCCfs	p.P1408fs
Pat_40	Post-Resistance	CLPX	10845	37	15	65456384	65456384	Frame_Shift_Del	DEL	G	-	8	951	c.656delC	c.(655-657)ACAfs	p.T219fs
Pat_40	Post-Resistance	PARP16	54956	37	15	65551806	65551808	In_Frame_Del	DEL	AGC	-	7	347	c.906_908delGCT	c.(904-909)CTGCTC>CTC	.302_303LL>L
Pat_40	Post-Resistance	DNAH3	55567	37	16	21132130	21132132	In_Frame_Del	DEL	CAG	-	9	254	.1628_1630delCT	.(1627-1632)GCTGAT>GA	p.A543del
Pat_40	Post-Resistance	TNRC6A	27327	37	16	24788376	24788378	In_Frame_Del	DEL	CAG	-	9	150	c.286_288delCAG	c.(286-288)CAGdel	p.Q103del
Pat_40	Post-Resistance	RABEP2	79874	37	16	28916779	28916779	Frame_Shift_Del	DEL	G	-	4	9	c.1547delC	c.(1546-1548)GCAfs	p.A516fs
Pat_40	Post-Resistance	STX4	6810	37	16	31046299	31046299	Frame_Shift_Del	DEL	C	-	7	680	c.316delC	c.(316-318)CCCfs	p.P106fs
Pat_40	Post-Resistance	IRX6	79190	37	16	55362674	55362676	In_Frame_Del	DEL	GAG	-	8	106	c.784_786delGAG	c.(784-786)GAGdel	p.E268del
Pat_40	Post-Resistance	TRPV2	51393	37	17	16335490	16335492	In_Frame_Del	DEL	TGC	-	11	179	.1865_1867delTG	(1864-1869)GTGCTG>GT	p.L627del
Pat_40	Post-Resistance	TUBG1	7283	37	17	40764472	40764472	Frame_Shift_Del	DEL	G	-	7	793	c.427delG	c.(427-429)GGGfs	p.G143fs
Pat_40	Post-Resistance	PNPO	55163	37	17	46022008	46022010	In_Frame_Del	DEL	TGC	-	8	835	c.290_292delTGC	c.(289-294)TTGCTG>TTG	p.97_98LL>L

Pat_40	Post-Resistance	COIL	8161	37	17	55027262	55027263	Frame_Shift_Del	DEL	AG	-	7	391	c.1340_1341delCT	c.(1339-1341)TCTfs	p.S447fs
Pat_40	Post-Resistance	GALR2	8811	37	17	74073334	74073334	Frame_Shift_Del	DEL	C	-	2	4	c.986delC	c.(985-987)ACCfs	p.T329fs
Pat_40	Post-Resistance	ROCK1	6093	37	18	18564364	18564367	Frame_Shift_Del	DEL	TATT	-	8	261	2434_2437delAAT	c.(2434-2439)AATACTfs	p.N812fs
Pat_40	Post-Resistance	DOK6	220164	37	18	67406306	67406307	Frame_Shift_Ins	INS	-	T	69	334	c.705_706insT	c.(703-708)GAAAGAfs	p.E235fs
Pat_40	Post-Resistance	MAST1	22983	37	19	12978651	12978651	Frame_Shift_Del	DEL	C	-	2	4	c.2426delC	c.(2425-2427)GCCfs	p.A809fs
Pat_40	Post-Resistance	SERTAD1	29950	37	19	40929409	40929411	In_Frame_Del	DEL	CTC	-	8	202	c.43_45delGAG	c.(43-45)GAGdel	p.E15del
Pat_40	Post-Resistance	ZFP112	7771	37	19	44832512	44832512	Frame_Shift_Del	DEL	C	-	7	739	c.1816delG	c.(1816-1818)GAAfs	p.E606fs
Pat_40	Post-Resistance	TEAD2	8463	37	19	49850472	49850473	Frame_Shift_Ins	INS	-	G	8	530	c.883_884insC	c.(883-885)CATfs	p.H295fs
Pat_40	Post-Resistance	FLT3LG	2323	37	19	49978960	49978962	In_Frame_Del	DEL	CTG	-	8	235	c.46_48delCTG	c.(46-48)CTGdel	p.L20del
Pat_40	Post-Resistance	TMC4	147798	37	19	54675747	54675749	In_Frame_Del	DEL	TCC	-	11	147	c.201_203delGGA	c.(199-204)GAGGAT>GAT	p.E67del
Pat_40	Post-Resistance	RNASEH1	246243	37	2	3595620	3595620	Frame_Shift_Del	DEL	C	-	8	1134	c.675delG	c.(673-675)TGGfs	p.W225fs
Pat_40	Post-Resistance	DHX57	90957	37	2	39095411	39095413	In_Frame_Del	DEL	CCA	-	9	268	c.135_137delTGG	.(133-138)GGTGGA>GG	p.45_46GG>G
Pat_40	Post-Resistance	ST3GAL5	8869	37	2	86075199	86075200	Frame_Shift_Del	DEL	GG	-	8	1168	c.446_447delCC	c.(445-447)CCCfs	p.P149fs
Pat_40	Post-Resistance	MYO7B	4648	37	2	128367225	128367226	Frame_Shift_Del	DEL	CA	-	8	454	c.2959_2960delCA	c.(2959-2961)CACfs	p.H987fs
Pat_40	Post-Resistance	XIRP2	129446	37	2	168099958	168099958	Frame_Shift_Del	DEL	G	-	7	437	c.2056delG	c.(2056-2058)GGGfs	p.G686fs
Pat_40	Post-Resistance	TTN	7273	37	2	179481647	179481647	Frame_Shift_Del	DEL	G	-	9	475	c.40265delC	c.(40264-40266)CCAfs	p.P13422fs
Pat_40	Post-Resistance	SATB2	23314	37	2	200213559	200213559	Frame_Shift_Del	DEL	G	-	7	411	c.1038delC	c.(1036-1038)CCCfs	p.P346fs
Pat_40	Post-Resistance	ABI2	10152	37	2	204193211	204193213	Translation_Start_Site	DEL	GAG	-	4	9	c.-26_-24delGAG	.(-28--22)ATGAGGA>ATGA	
Pat_40	Post-Resistance	JAG1	182	37	20	10639255	10639256	Frame_Shift_Del	DEL	CA	-	28	444	c.554_555delTG	c.(553-555)GTGfs	p.V185fs
Pat_40	Post-Resistance	NCOA6	23054	37	20	33330968	33330970	In_Frame_Del	DEL	TGC	-	12	324	.3090_3092delGC	.(3088-3093)CAGCAA>CA	030_1031QQ
Pat_40	Post-Resistance	YTHDF1	54915	37	20	61833650	61833652	In_Frame_Del	DEL	CCT	-	10	496	.1640_1642delAG	(1639-1644)GAGGTG>GT	p.E547del
Pat_40	Post-Resistance	TPTE	7179	37	21	10944697	10944697	Frame_Shift_Del	DEL	A	-	18	520	c.537delT	c.(535-537)TTTfs	p.F179fs
Pat_40	Post-Resistance	KRTAP19-4	337971	37	21	31869379	31869381	In_Frame_Del	DEL	CCT	-	7	890	c.48_50delAGG	c.(46-51)GGAGGC>GGC	p.16_17GG>G
Pat_40	Post-Resistance	IFNGR2	3460	37	21	34799292	34799292	Frame_Shift_Del	DEL	T	-	8	858	c.514delT	c.(514-516)TTTfs	p.F172fs
Pat_40	Post-Resistance	DYRK1A	1859	37	21	38884370	38884372	In_Frame_Del	DEL	CAC	-	10	228	.1828_1830delCA	c.(1828-1830)CACdel	p.H619del
Pat_40	Post-Resistance	ZNF70	7621	37	22	24087314	24087314	Frame_Shift_Del	DEL	G	-	7	320	c.14delC	c.(13-15)CCAfs	p.P5fs
Pat_40	Post-Resistance	TRIOBP	11078	37	22	38120245	38120253	In_Frame_Del	DEL	CCTCCAGA	-	8	355	2_1690delCCTCC	1-1692)GCCTCCAGAACC	p.SRT562del
Pat_40	Post-Resistance	RANGAP1	5905	37	22	41650469	41650471	In_Frame_Del	DEL	TCC	-	41	302	.1101_1103delGG	(1099-1104)GAGGAA>GA	.367_368EE>
Pat_40	Post-Resistance	CACNA1D	776	37	3	53529193	53529195	Translation_Start_Site	DEL	GAT	-	8	148			
Pat_40	Post-Resistance	ADAMTS9	56999	37	3	64518879	64518880	Frame_Shift_Del	DEL	TG	-	7	1380	c.5680_5681delCA	c.(5680-5682)CAAfs	p.Q1894fs
Pat_40	Post-Resistance	ADAMTS9	56999	37	3	64644422	64644422	Frame_Shift_Del	DEL	C	-	7	2484	c.725delG	c.(724-726)AGAfs	p.R242fs
Pat_40	Post-Resistance	MITF	4286	37	3	70014329	70014329	Frame_Shift_Del	DEL	C	-	7	1501	c.1493delC	c.(1492-1494)TCCfs	p.S498fs
Pat_40	Post-Resistance	VGLL3	389136	37	3	87027857	87027859	In_Frame_Del	DEL	CTC	-	12	199	c.220_222delGAG	c.(220-222)GAGdel	p.E74del
Pat_40	Post-Resistance	TMCC1	23023	37	3	129370576	129370578	In_Frame_Del	DEL	CTG	-	11	253	.1708_1710delCA	c.(1708-1710)CAGdel	p.Q570del
Pat_40	Post-Resistance	CRIPAK	285464	37	4	1389114	1389115	Frame_Shift_Ins	INS	-	CA	18	604	c.815_816insCA	c.(814-816)CTCfs	p.L272fs
Pat_40	Post-Resistance	CRIPAK	285464	37	4	1389147	1389148	Frame_Shift_Del	DEL	AT	-	7	576	c.848_849delAT	c.(847-849)CATfs	p.H283fs
Pat_40	Post-Resistance	CRIPAK	285464	37	4	1389236	1389237	Frame_Shift_Ins	INS	-	CA	7	780	c.937_938insCA	c.(937-939)TCAfs	p.S313fs
Pat_40	Post-Resistance	CRIPAK	285464	37	4	1389425	1389426	Frame_Shift_Del	DEL	CA	-	9	817	c.1126_1127delCA	c.(1126-1128)CACfs	p.H376fs
Pat_40	Post-Resistance	RUFY3	22902	37	4	71628327	71628327	Frame_Shift_Del	DEL	G	-	7	508	c.270delG	c.(268-270)CTGfs	p.L90fs
Pat_40	Post-Resistance	MMRN1	22915	37	4	90844391	90844393	In_Frame_Del	DEL	AGC	-	11	1361	c.923_925delAGC	.(922-927)GAGCAG>GAG	p.Q313del
Pat_40	Post-Resistance	POU4F2	5458	37	4	147560457	147560458	In_Frame_Ins	INS	-	GGC	4	8	c.165_166insGGC	c.(163-168)insGGC	p.68_69insG
Pat_40	Post-Resistance	LRBA	987	37	4	151509211	151509211	Frame_Shift_Del	DEL	T	-	8	783	c.6352delA	c.(6352-6354)ATCfs	p.I2118fs
Pat_40	Post-Resistance	DDX60	55601	37	4	169229302	169229302	Frame_Shift_Del	DEL	A	-	8	98	c.119delT	c.(118-120)TTGfs	p.L40fs
Pat_40	Post-Resistance	CDH10	1008	37	5	24492973	24492973	Frame_Shift_Del	DEL	A	-	9	833	c.1577delT	c.(1576-1578)TTCfs	p.F526fs
Pat_40	Post-Resistance	TIMD4	91937	37	5	156378745	156378747	In_Frame_Del	DEL	TTG	-	7	631	c.455_457delCAA	c.(454-459)ACAAGC>AGC	p.T152del
Pat_40	Post-Resistance	TBC1D7	51256	37	6	13321262	13321263	Frame_Shift_Del	DEL	CC	-	8	1506	c.258_259delGG	c.(256-261)TTGGATfs	p.L86fs
Pat_40	Post-Resistance	NUP153	9972	37	6	17675499	17675499	Frame_Shift_Del	DEL	T	-	11	727	c.684delA	c.(682-684)AAAfs	p.K228fs

Pat_40	Post-Resistance	BTN2A2	10385	37	6	26384091	26384093	In_Frame_Del	DEL	CCT	-	8	478	c.42_44delCCT	c.(40-45)TCCCTC>TCC	p.L24del
Pat_40	Post-Resistance	ANKS1A	23294	37	6	34951143	34951143	Frame_Shift_Del	DEL	C	-	7	520	c.953delC	c.(952-954)ACCfs	p.T318fs
Pat_40	Post-Resistance	TREML2	79865	37	6	41168714	41168716	In_Frame_Del	DEL	CAG	-	9	121	c.31_33delCTG	c.(31-33)CTGdel	p.L11del
Pat_40	Post-Resistance	MDFI	4188	37	6	41621169	41621171	In_Frame_Del	DEL	CTG	-	7	208	c.597_599delCTG	c.(595-600)CTCTGC>CTC	p.C204del
Pat_40	Post-Resistance	TTK	7272	37	6	80751896	80751897	Frame_Shift_Ins	INS	-	A	9	301	c.2551_2552insA	c.(2551-2553)GAAfs	p.E851fs
Pat_40	Post-Resistance	KIAA1009	22832	37	6	84896233	84896233	Frame_Shift_Del	DEL	A	-	12	422	c.1218delT	c.(1216-1218)TTTfs	p.F406fs
Pat_40	Post-Resistance	SUN1	23353	37	7	883110	883110	Frame_Shift_Del	DEL	C	-	7	1067	c.611delC	c.(610-612)GCCfs	p.A204fs
Pat_40	Post-Resistance	SDK1	221935	37	7	4119173	4119173	Frame_Shift_Del	DEL	A	-	7	210	c.3281delA	c.(3280-3282)TATfs	p.Y1094fs
Pat_40	Post-Resistance	USP42	84132	37	7	6155014	6155015	Frame_Shift_Del	DEL	TT	-	8	418	c.302_303delTT	c.(301-303)CTTfs	p.L101fs
Pat_40	Post-Resistance	HOXA11	3207	37	7	27222461	27222462	Frame_Shift_Ins	INS	-	T	7	328	c.895_896insA	c.(895-897)ATTfs	p.I299fs
Pat_40	Post-Resistance	ZNF716	441234	37	7	57529007	57529008	In_Frame_Ins	INS	-	TCT	11	243	c.840_841insTCT	c.(838-843)insTCT	p.281_282insS
Pat_40	Post-Resistance	STAG3	10734	37	7	99780446	99780446	Frame_Shift_Del	DEL	C	-	7	1864	c.320delC	c.(319-321)GCCfs	p.A107fs
Pat_40	Post-Resistance	TNPO3	23534	37	7	128610259	128610259	Frame_Shift_Del	DEL	G	-	9	1107	c.2541delC	c.(2539-2541)CCCfs	p.P847fs
Pat_40	Post-Resistance	LUZP6	767558	37	7	135635394	135635394	Frame_Shift_Del	DEL	C	-	7	1039	c.223delG	c.(223-225)GCTfs	p.A75fs
Pat_40	Post-Resistance	OR9A4	130075	37	7	141619203	141619203	Frame_Shift_Del	DEL	T	-	19	889	c.528delT	c.(526-528)AATfs	p.N176fs
Pat_40	Post-Resistance	PRKDC	5591	37	8	48746799	48746799	Frame_Shift_Del	DEL	T	-	9	1201	c.8110delA	c.(8110-8112)AGGfs	p.R2704fs
Pat_40	Post-Resistance	ST18	9705	37	8	53062481	53062482	Frame_Shift_Ins	INS	-	T	10	509	c.1862_1863insA	c.(1861-1863)AATfs	p.N621fs
Pat_40	Post-Resistance	MYBL1	4603	37	8	67488452	67488453	Frame_Shift_Ins	INS	-	T	11	1093	c.1259_1260insA	c.(1258-1260)AACfs	p.N420fs
Pat_40	Post-Resistance	SULF1	23213	37	8	70514026	70514026	Frame_Shift_Del	DEL	T	-	9	1917	c.1023delT	c.(1021-1023)CCTfs	p.P341fs
Pat_40	Post-Resistance	KCNB2	9312	37	8	73479985	73479985	Frame_Shift_Del	DEL	C	-	8	671	c.16delC	c.(16-18)CCCfs	p.P6fs
Pat_40	Post-Resistance	NBN	4683	37	8	90967512	90967512	Frame_Shift_Del	DEL	T	-	8	584	c.1396delA	c.(1396-1398)AGGfs	p.R466fs
Pat_40	Post-Resistance	DECR1	1666	37	8	91057151	91057151	Frame_Shift_Del	DEL	G	-	10	939	c.813delG	c.(811-813)CTGfs	p.L271fs
Pat_40	Post-Resistance	RUNX1T1	862	37	8	93088215	93088215	Frame_Shift_Del	DEL	T	-	11	956	c.66delA	c.(64-66)AAAfs	p.K22fs
Pat_40	Post-Resistance	TP53INP1	94241	37	8	95952409	95952411	In_Frame_Del	DEL	TCT	-	10	353	c.150_152delAGA	.(148-153)GAAGAG>GA	p.50_51EE>E
Pat_40	Post-Resistance	ZFPM2	23414	37	8	106813775	106813776	Frame_Shift_Del	DEL	GG	-	7	482	.1465_1466delG	c.(1465-1467)GGGfs	p.G489fs
Pat_40	Post-Resistance	COL14A1	7373	37	8	121279110	121279110	Frame_Shift_Del	DEL	C	-	7	1286	c.3061delC	c.(3061-3063)CCAfs	p.P1021fs
Pat_40	Post-Resistance	MYC	4609	37	8	128750605	128750607	In_Frame_Del	DEL	CAG	-	7	205	c.97_99delCAG	c.(97-99)CAGdel	p.Q37del
Pat_40	Post-Resistance	PLEC	5339	37	8	145000951	145000953	Splice_Site	DEL	CCT	-	9	501	c.4455_splice	c.e30+1	p.E1485_splice
Pat_40	Post-Resistance	KANK1	23189	37	9	732475	732477	In_Frame_Del	DEL	GAG	-	14	422	.3103_3105delGA	c.(3103-3105)GAGdel	p.E1039del
Pat_40	Post-Resistance	SMARCA2	6595	37	9	2039777	2039779	In_Frame_Del	DEL	CAG	-	13	41	c.667_669delCAG	c.(667-669)CAGdel	p.Q238del
Pat_40	Post-Resistance	KIAA1432	57589	37	9	5774148	5774148	Frame_Shift_Del	DEL	G	-	7	222	c.3937delG	c.(3937-3939)GGAfs	p.G1313fs
Pat_40	Post-Resistance	MLLT3	4300	37	9	20414377	20414379	In_Frame_Del	DEL	CTG	-	7	41	c.465_467delCAG	c.(463-468)AGCAGT>AGT	.155_156SS>
Pat_40	Post-Resistance	FAM157B	100132403	37	9	141107536	141107537	In_Frame_Ins	INS	-	GCA	12	20	c.218_219insGCA	.(217-219)CGG>CGGCA	p.85_86insQ
Pat_40	Post-Resistance	CNKSR2	22866	37	X	21627678	21627680	In_Frame_Del	DEL	GAG	-	8	177	.2635_2637delGA	c.(2635-2637)GAGdel	p.E886del
Pat_40	Post-Resistance	PHF8	23133	37	X	54011405	54011407	In_Frame_Del	DEL	CTC	-	7	306	.2491_2493delGA	c.(2491-2493)GAGdel	p.E831del
Pat_40	Post-Resistance	ATRX	546	37	X	76778785	76778787	In_Frame_Del	DEL	TCT	-	7	462	.6792_6794delAG	.(6790-6795)GAAGAG>GA	2264_2265EE
Pat_40	Post-Resistance	ALG13	79868	37	X	110987997	110987999	In_Frame_Del	DEL	CCT	-	10	90	.2797_2799delCC	c.(2797-2799)CCTdel	p.P945del
Pat_40	Post-Resistance	ODZ1	10178	37	X	123540196	123540196	Frame_Shift_Del	DEL	G	-	7	502	c.5105delC	c.(5104-5106)GCAfs	p.A1702fs
Pat_40	Post-Resistance	MAP7D3	79649	37	X	135314194	135314194	Frame_Shift_Del	DEL	G	-	7	651	c.922delC	c.(922-924)CAGfs	p.Q308fs
Pat_40	Post-Resistance	HTATSF1	27336	37	X	135585048	135585050	In_Frame_Del	DEL	AAG	-	15	342	c.682_684delAAG	c.(682-684)AAGdel	p.K232del
Pat_40	Post-Resistance	SPANXN2	494119	37	X	142803692	142803692	Frame_Shift_Del	DEL	T	-	16	339	c.71delA	c.(70-72)AATfs	p.N24fs
Pat_40	Post-Resistance	PLXNA3	55558	37	X	153688565	153688565	Frame_Shift_Del	DEL	G	-	8	104	c.42delG	c.(40-42)GTGfs	p.V14fs
Pat_41	Pre-Treatment	MST1P9	11223	37	1	17086085	17086086	Frame_Shift_Ins	INS	-	C	12	44	c.811_812insG	c.(811-813)GCGfs	p.A271fs
Pat_41	Pre-Treatment	TNNI3K	51086	37	1	74957824	74957826	In_Frame_Del	DEL	CTT	-	7	707	.2225_2227delCT	.(2224-2229)CCTTCT>CC	p.S746del
Pat_41	Pre-Treatment	TRIM33	51592	37	1	114968116	114968118	In_Frame_Del	DEL	TGT	-	9	804	.1648_1650delAC	c.(1648-1650)ACAdel	p.T550del
Pat_41	Pre-Treatment	ADAM30	11085	37	1	120436591	120436591	Frame_Shift_Del	DEL	T	-	7	943	c.2369delA	c.(2368-2370)AAGfs	p.K790fs
Pat_41	Pre-Treatment	TCHH	7062	37	1	152082957	152082959	In_Frame_Del	DEL	CTC	-	11	364	.2734_2736delGA	c.(2734-2736)GAGdel	p.E912del

Pat_41	Pre-Treatment	PRCC	5546	37	1	156761535	156761536	Frame_Shift_Ins	INS	-	C	14	415	c.1130_1131insC	c.(1129-1131)GTCfs	p.V377fs
Pat_41	Pre-Treatment	IGSF9	57549	37	1	159900128	159900128	Frame_Shift_Del	DEL	C	-	7	312	c.1915delG	c.(1915-1917)GTAfs	p.V639fs
Pat_41	Pre-Treatment	NR1I3	9970	37	1	161202999	161203000	Frame_Shift_Ins	INS	-	G	8	862	c.367_368insC	c.(367-369)CGCfs	p.R123fs
Pat_41	Pre-Treatment	CACNA1E	777	37	1	181680102	181680103	Frame_Shift_Del	DEL	AG	-	8	239	c.1068_1069delAG	c.(1066-1071)AAAGAGfs	p.K356fs
Pat_41	Pre-Treatment	ASPM	259266	37	1	197065253	197065253	Frame_Shift_Del	DEL	T	-	7	684	c.8862delA	c.(8860-8862)AAAfs	p.K2954fs
Pat_41	Pre-Treatment	AGT	183	37	1	230839055	230839055	Frame_Shift_Del	DEL	A	-	8	184	c.1290delT	c.(1288-1290)TTTfs	p.F430fs
Pat_41	Pre-Treatment	MYO3A	53904	37	10	26462760	26462760	Frame_Shift_Del	DEL	A	-	9	159	c.3567delA	c.(3565-3567)CCAfs	p.P1189fs
Pat_41	Pre-Treatment	PCDH15	65217	37	10	55587198	55587200	In_Frame_Del	DEL	GGC	-	9	233	.4320_4322delGC	(4318-4323)CCGCCT>CC	1440_1441PP>
Pat_41	Pre-Treatment	FAS	355	37	10	90768708	90768708	Frame_Shift_Del	DEL	T	-	11	2497	c.397delT	c.(397-399)TTTfs	p.F133fs
Pat_41	Pre-Treatment	ABCC2	1244	37	10	101559000	101559000	Frame_Shift_Del	DEL	A	-	9	524	c.904delA	c.(904-906)AAAfs	p.K302fs
Pat_41	Pre-Treatment	PTPRE	5791	37	10	129876002	129876004	In_Frame_Del	DEL	AGC	-	8	321	.1847_1849delAG	(1846-1851)AAGCAG>AA	p.Q620del
Pat_41	Pre-Treatment	LOC338651	338651	37	11	1619173	1619202	In_Frame_Del	DEL	GCCACAGC	-	84	448	ACAGGAGCCAC	ACAGGAGCCACAGCCC	RSHSPPWS1
Pat_41	Pre-Treatment	DDX10	1662	37	11	108577464	108577464	Splice_Site	DEL	A	-	7	691	c.1224_splice	c.e10-2	p.R408_splice
Pat_41	Pre-Treatment	CBL	867	37	11	119170435	119170435	Frame_Shift_Del	DEL	A	-	8	2278	c.2665delA	c.(2665-2667)AAAfs	p.K889fs
Pat_41	Pre-Treatment	PRB2	653247	37	12	11546506	11546508	In_Frame_Del	DEL	TTG	-	20	836	c.504_506delCAA	c.(502-507)AACAAG>AAG	p.N168del
Pat_41	Pre-Treatment	LRP1	4035	37	12	57605740	57605742	In_Frame_Del	DEL	TGC	-	7	344	13289_13291delT	13288-13293)TTGCTG>T	4430_4431LL>
Pat_41	Pre-Treatment	GLI1	2735	37	12	57860075	57860075	Frame_Shift_Del	DEL	G	-	9	714	c.815delG	c.(814-816)TGGfs	p.W272fs
Pat_41	Pre-Treatment	SFRS8	6433	37	12	132281734	132281736	In_Frame_Del	DEL	AGA	-	17	672	.2546_2548delAG	(2545-2550)GAGAAG>GA	p.K853del
Pat_41	Pre-Treatment	EP400	57634	37	12	132445252	132445253	Frame_Shift_Ins	INS	-	C	9	74	c.88_89insC	c.(88-90)GCCfs	p.A30fs
Pat_41	Pre-Treatment	POLE	5426	37	12	133220099	133220100	Frame_Shift_Del	DEL	CA	-	13	1002	c.4337_4338delTG	c.(4336-4338)GTGfs	p.V1446fs
Pat_41	Pre-Treatment	FAM155A	728215	37	13	108518338	108518338	Frame_Shift_Del	DEL	C	-	16	486	c.607delG	c.(607-609)GACfs	p.D203fs
Pat_41	Pre-Treatment	LRP10	26020	37	14	23341527	23341529	In_Frame_Del	DEL	CCT	-	17	294	c.15_17delCCT	c.(13-18)ACCCTC>ACC	p.L11del
Pat_41	Pre-Treatment	C14orf39	317761	37	14	60903565	60903565	Frame_Shift_Del	DEL	A	-	8	314	c.1762delT	c.(1762-1764)TGAfs	p.*588fs
Pat_41	Pre-Treatment	C14orf43	91748	37	14	74205926	74205928	In_Frame_Del	DEL	CTG	-	8	57	c.784_786delCAG	c.(784-786)CAGdel	p.Q262del
Pat_41	Pre-Treatment	BEGAIN	57596	37	14	101005271	101005273	In_Frame_Del	DEL	CCT	-	8	43	c.815_817delAGG	.(814-819)GAGGCC>GCC	p.E272del
Pat_41	Pre-Treatment	ZNF609	23060	37	15	64967246	64967247	Frame_Shift_Ins	INS	-	A	8	482	c.2193_2194insA	c.(2191-2196)GACAAAfs	p.D731fs
Pat_41	Pre-Treatment	SLC24A1	9187	37	15	65943128	65943130	In_Frame_Del	DEL	GAG	-	7	55	.2641_2643delGA	c.(2641-2643)GAGdel	p.E890del
Pat_41	Pre-Treatment	IL32	9235	37	16	3119304	3119305	Frame_Shift_Ins	INS	-	G	11	631	c.653_654insG	c.(652-654)GACfs	p.D218fs
Pat_41	Pre-Treatment	NFAT5	10725	37	16	69726420	69726422	In_Frame_Del	DEL	CAG	-	7	132	.2638_2640delCA	c.(2638-2640)CAGdel	p.Q888del
Pat_41	Pre-Treatment	ZFHX3	463	37	16	72822564	72822566	In_Frame_Del	DEL	TGC	-	9	257	.9609_9611delGC	.(9607-9612)CAGCAA>CA	203_3204QQ>
Pat_41	Pre-Treatment	ANKRD11	29123	37	16	89349641	89349641	Frame_Shift_Del	DEL	T	-	7	287	c.3309delA	c.(3307-3309)AAAfs	p.K1103fs
Pat_41	Pre-Treatment	C17orf85	55421	37	17	3721809	3721811	In_Frame_Del	DEL	TCC	-	17	281	.1056_1058delGG	(1054-1059)GAGGAA>GA	.352_353EE>
Pat_41	Pre-Treatment	KDM6B	23135	37	17	7751859	7751861	In_Frame_Del	DEL	CAC	-	8	110	.2253_2255delCA	(2251-2256)GTCACC>GT	p.T762del
Pat_41	Pre-Treatment	SUPT6H	6830	37	17	27027202	27027204	In_Frame_Del	DEL	AGC	-	16	917	.4573_4575delAG	c.(4573-4575)AGCdel	p.S1528del
Pat_41	Pre-Treatment	KRTAP4-1	85285	37	17	39340796	39340852	Splice_Site	DEL	TGGGGTG	-	13	265	c.246_splice	c.e2-1	p.S82_splice
Pat_41	Pre-Treatment	ETV4	2118	37	17	41610701	41610701	Frame_Shift_Del	DEL	G	-	7	79	c.399delC	c.(397-399)CCCfs	p.P133fs
Pat_41	Pre-Treatment	ITGB1BP3	27231	37	19	3941094	3941094	Frame_Shift_Del	DEL	C	-	7	449	c.421delC	c.(421-423)CCCfs	p.P141fs
Pat_41	Pre-Treatment	HAUS8	93323	37	19	17160706	17160707	Frame_Shift_Del	DEL	GA	-	8	723	c.1209_1210delTC	c.(1207-1212)TCTCGTfs	p.S403fs
Pat_41	Pre-Treatment	ZNF43	7594	37	19	22002025	22002026	Splice_Site	INS	-	A	8	482	c.4_splice	c.e2-1	p.G2_splice
Pat_41	Pre-Treatment	PRX	57716	37	19	40900180	40900182	In_Frame_Del	DEL	TCC	-	7	44	.4077_4079delGG	(4075-4080)GAGGAA>GA	1359_1360EE>
Pat_41	Pre-Treatment	ATP6V1C2	245973	37	2	10917819	10917820	Frame_Shift_Del	DEL	AG	-	15	321	c.934_935delAG	c.(934-936)AGAfs	p.R312fs
Pat_41	Pre-Treatment	SLC9A2	6549	37	2	103324746	103324746	Frame_Shift_Del	DEL	C	-	7	608	c.2237delC	c.(2236-2238)ACCfs	p.T746fs
Pat_41	Pre-Treatment	DCAF17	80067	37	2	172334537	172334538	Frame_Shift_Ins	INS	-	A	8	192	c.1223_1224insA	c.(1222-1224)GTAfs	p.V408fs
Pat_41	Pre-Treatment	FKBP7	51661	37	2	179343217	179343217	Frame_Shift_Del	DEL	T	-	10	1180	c.10delA	c.(10-12)ACCfs	p.T4fs
Pat_41	Pre-Treatment	TTN	7273	37	2	179596076	179596076	Frame_Shift_Del	DEL	T	-	8	1407	c.13685delA	c.(13684-13686)AATfs	p.N4562fs
Pat_41	Pre-Treatment	USP40	55230	37	2	234394236	234394237	Frame_Shift_Ins	INS	-	T	8	122	c.3477_3478insA	c.(3475-3480)AAACAAfs	p.K1159fs
Pat_41	Pre-Treatment	GAL3ST2	64090	37	2	242738494	242738496	In_Frame_Del	DEL	TCC	-	15	312	c.44_46delTCC	c.(43-48)ATCCTC>ATC	p.L20del

Pat_41	Pre-Treatment	OSBPL2	9885	37	20	60854258	60854258	Frame_Shift_Del	DEL	C	-	7	354	c.537delC	c.(535-537)CACfs	p.H179fs
Pat_41	Pre-Treatment	IFNGR2	3460	37	21	34799292	34799292	Frame_Shift_Del	DEL	T	-	10	1249	c.514delT	c.(514-516)TTTfs	p.F172fs
Pat_41	Pre-Treatment	MYH9	4627	37	22	36696948	36696950	In_Frame_Del	DEL	CTC	-	10	350	.2785_2787delGA	c.(2785-2787)GAGdel	p.E929del
Pat_41	Pre-Treatment	MKL1	57591	37	22	40816887	40816889	In_Frame_Del	DEL	TGC	-	9	224	c.843_845delGCA	c.(841-846)CAGCAC>CAC	p.Q281del
Pat_41	Pre-Treatment	SREBF2	6721	37	22	42262949	42262951	In_Frame_Del	DEL	GCA	-	7	211	c.203_205delGCA	.(202-207)GGCAGC>GG	p.S74del
Pat_41	Pre-Treatment	BIK	638	37	22	43525245	43525247	In_Frame_Del	DEL	GCT	-	11	177	c.417_419delGCT	.(415-420)GCGCTG>GC	p.L144del
Pat_41	Pre-Treatment	ULK4	54986	37	3	41860985	41860985	Frame_Shift_Del	DEL	T	-	9	117	c.1778delA	c.(1777-1779)AAGfs	p.K593fs
Pat_41	Pre-Treatment	PRKCD	5580	37	3	53220653	53220653	Frame_Shift_Del	DEL	G	-	9	1161	c.1294delG	c.(1294-1296)GGGfs	p.G432fs
Pat_41	Pre-Treatment	DPPA4	55211	37	3	109049606	109049606	Frame_Shift_Del	DEL	T	-	10	333	c.444delA	c.(442-444)AAAfs	p.K148fs
Pat_41	Pre-Treatment	KTELC1	56983	37	3	119205753	119205753	Frame_Shift_Del	DEL	A	-	7	541	c.712delA	c.(712-714)AAAfs	p.K238fs
Pat_41	Pre-Treatment	GRK7	131890	37	3	141535708	141535708	Frame_Shift_Del	DEL	G	-	7	728	c.1478delG	c.(1477-1479)CGGfs	p.R493fs
Pat_41	Pre-Treatment	MED12L	116931	37	3	151095826	151095828	In_Frame_Del	DEL	TGG	-	9	329	.4238_4240delTG	.(4237-4242)TTGGTG>TT	p.V1414del
Pat_41	Pre-Treatment	HGFAC	3083	37	4	3443784	3443786	In_Frame_Del	DEL	TCC	-	7	87	c.56_58delTCC	c.(55-60)TTCCTC>TTC	p.L29del
Pat_41	Pre-Treatment	ADH1A	124	37	4	100208033	100208033	Frame_Shift_Del	DEL	C	-	8	1004	c.233delG	c.(232-234)GGAfs	p.G78fs
Pat_41	Pre-Treatment	INTS12	57117	37	4	106621122	106621122	Frame_Shift_Del	DEL	A	-	9	881	c.41delT	c.(40-42)TTGfs	p.L14fs
Pat_41	Pre-Treatment	RRH	10692	37	4	110756541	110756541	Frame_Shift_Del	DEL	T	-	12	236	c.317delT	c.(316-318)ATTfs	p.I106fs
Pat_41	Pre-Treatment	TRAM1L1	133022	37	4	118005517	118005517	Frame_Shift_Del	DEL	T	-	7	642	c.1033delA	c.(1033-1035)AGAfs	p.R345fs
Pat_41	Pre-Treatment	ZNF827	152485	37	4	146823381	146823383	In_Frame_Del	DEL	GTG	-	7	98	.1028_1030delCA	.(1027-1032)CCACAA>CA	p.P343del
Pat_41	Pre-Treatment	FRG1	2483	37	4	190878555	190878556	Frame_Shift_Ins	INS	-	A	7	79	c.435_436insA	c.(433-438)GGGAAAfs	p.G145fs
Pat_41	Pre-Treatment	DNAH5	1767	37	5	13919383	13919383	Frame_Shift_Del	DEL	T	-	8	1057	c.877delA	c.(877-879)AGAfs	p.R293fs
Pat_41	Pre-Treatment	EGR1	1958	37	5	137801633	137801635	In_Frame_Del	DEL	CAG	-	9	118	c.183_185delCAG	c.(181-186)AACAGC>AAC	p.S67del
Pat_41	Pre-Treatment	ANKHD1-EIF4EBP	404734	37	5	139905676	139905676	Frame_Shift_Del	DEL	A	-	9	986	c.4588delA	c.(4588-4590)AAAfs	p.K1530fs
Pat_41	Pre-Treatment	LARP1	23367	37	5	154181822	154181822	Frame_Shift_Del	DEL	G	-	7	352	c.1972delG	c.(1972-1974)GGGfs	p.G658fs
Pat_41	Pre-Treatment	TRIM52	84851	37	5	180687612	180687614	In_Frame_Del	DEL	TCC	-	9	250	c.201_203delGGA	.(199-204)GAGGAC>GAC	p.E67del
Pat_41	Pre-Treatment	MAS1L	116511	37	6	29455156	29455157	Frame_Shift_Del	DEL	AC	-	11	203	c.523_524delGT	c.(523-525)GTCfs	p.V175fs
Pat_41	Pre-Treatment	BAT2	7916	37	6	31593814	31593815	Frame_Shift_Ins	INS	-	G	13	189	c.857_858insG	c.(856-858)GCGfs	p.A286fs
Pat_41	Pre-Treatment	RUNX2	860	37	6	45390467	45390469	In_Frame_Del	DEL	CAG	-	10	92	c.196_198delCAG	c.(196-198)CAGdel	p.Q71del
Pat_41	Pre-Treatment	GRIK2	2898	37	6	102503432	102503432	Frame_Shift_Del	DEL	A	-	7	318	c.2539delA	c.(2539-2541)AAAfs	p.K847fs
Pat_41	Pre-Treatment	VWC2	375567	37	7	49815163	49815163	Frame_Shift_Del	DEL	C	-	3	6	c.132delC	c.(130-132)GGCfs	p.G44fs
Pat_41	Pre-Treatment	CYP51A1	1595	37	7	91752494	91752494	Frame_Shift_Del	DEL	T	-	7	570	c.1026delA	c.(1024-1026)AAAfs	p.K342fs
Pat_41	Pre-Treatment	GIGYF1	64599	37	7	100283635	100283637	In_Frame_Del	DEL	TCC	-	8	161	.1014_1016delGG	(1012-1017)GAGGAA>GA	.338_339EE>I
Pat_41	Pre-Treatment	SRRT	51593	37	7	100482040	100482042	In_Frame_Del	DEL	AGG	-	7	62	c.809_811delAGG	.(808-813)CAGGAG>CA	p.E275del
Pat_41	Pre-Treatment	OR9A4	130075	37	7	141619203	141619203	Frame_Shift_Del	DEL	T	-	7	774	c.528delT	c.(526-528)AATfs	p.N176fs
Pat_41	Pre-Treatment	TRY6	154754	37	7	142468305	142468306	Splice_Site	INS	-	AG	10	312	c.46_splice	c.e1+2	
Pat_41	Pre-Treatment	PRKDC	5591	37	8	48746799	48746799	Frame_Shift_Del	DEL	T	-	7	1048	c.8110delA	c.(8110-8112)AGGfs	p.R2704fs
Pat_41	Pre-Treatment	ZHX2	22882	37	8	123963963	123963964	Frame_Shift_Ins	INS	-	A	11	92	c.213_214insA	c.(211-216)TCCAAAfs	p.S71fs
Pat_41	Pre-Treatment	AMELX	265	37	X	11316787	11316787	Frame_Shift_Del	DEL	G	-	7	921	c.264delG	c.(262-264)GTGfs	p.V88fs
Pat_41	Pre-Treatment	PHF8	23133	37	X	54011405	54011407	In_Frame_Del	DEL	CTC	-	21	455	.2491_2493delGA	c.(2491-2493)GAGdel	p.E831del
Pat_41	Pre-Treatment	TAF1	6872	37	X	70603000	70603000	Frame_Shift_Del	DEL	A	-	8	172	c.1930delA	c.(1930-1932)AAAfs	p.K644fs
Pat_41	Pre-Treatment	ATRX	546	37	X	76907782	76907784	In_Frame_Del	DEL	TCC	-	7	352	.4377_4379delGG	(4375-4380)GAGGAA>GA	1459_1460EE
Pat_41	Pre-Treatment	IRS4	8471	37	X	107977802	107977803	Frame_Shift_Ins	INS	-	C	10	864	c.1772_1773insG	c.(1771-1773)GGCfs	p.G591fs
Pat_41	Pre-Treatment	IGSF1	3547	37	X	130411036	130411036	Frame_Shift_Del	DEL	C	-	10	1628	c.2485delG	c.(2485-2487)GCCfs	p.A829fs
Pat_41	Pre-Treatment	PLAC1	10761	37	X	133700354	133700354	Frame_Shift_Del	DEL	T	-	7	260	c.359delA	c.(358-360)AAGfs	p.K120fs
Pat_41	Pre-Treatment	SPANXN3	139067	37	X	142605149	142605149	Frame_Shift_Del	DEL	T	-	10	464	c.71delA	c.(70-72)AATfs	p.N24fs
Pat_41	Pre-Treatment	MAMLD1	10046	37	X	149639633	149639635	In_Frame_Del	DEL	GCA	-	7	174	.1788_1790delGC	.(1786-1791)CTGCAG>CT	p.Q606del
Pat_41	Post-Resistance	TNFRSF9	3604	37	1	7980912	7980914	In_Frame_Del	DEL	CTT	-	7	503	c.749_751delAAG	.(748-753)GAAGGA>GG	p.E250del
Pat_41	Post-Resistance	MFN2	9927	37	1	12061824	12061825	Splice_Site	INS	-	G	31	933	c.971_splice	c.e10-1	p.G324_splice

Pat_41	Post-Resistance	SPEN	23013	37	1	16262680	16262680	Frame_Shift_Del	DEL	C	-	7	484	c.9945delC	c.(9943-9945)CACfs	p.H3315fs
Pat_41	Post-Resistance	PAFAH2	5051	37	1	26310537	26310537	Frame_Shift_Del	DEL	G	-	9	1119	c.452delC	c.(451-453)CCAfs	p.P151fs
Pat_41	Post-Resistance	RPS6KA1	6195	37	1	26885311	26885311	Frame_Shift_Del	DEL	C	-	8	388	c.1098delC	c.(1096-1098)ATCfs	p.I366fs
Pat_41	Post-Resistance	ARID1A	8289	37	1	27106254	27106255	Frame_Shift_Del	DEL	AG	-	7	712	c.5865_5866delAG	c.(5863-5868)CTAGAGfs	p.L1955fs
Pat_41	Post-Resistance	ZMYM6	9204	37	1	35476363	35476364	Frame_Shift_Ins	INS	-	A	17	265	c.1336_1337insT	c.(1336-1338)TACfs	p.Y446fs
Pat_41	Post-Resistance	ST3GAL3	6487	37	1	44360095	44360096	Frame_Shift_Del	DEL	CG	-	7	616	c.343_344delCG	c.(343-345)CGCfs	p.R115fs
Pat_41	Post-Resistance	SPATA1	64173	37	1	85018771	85018772	Frame_Shift_Ins	INS	-	A	2	4	c.1344_1345insA	c.(1342-1347)CAGAAAfs	p.Q448fs
Pat_41	Post-Resistance	ZNF326	284695	37	1	90470782	90470784	In_Frame_Del	DEL	GTG	-	10	658	c.188_190delGTG	c.(187-192)AGTGGT>AGT	p.G68del
Pat_41	Post-Resistance	PRPF38B	55119	37	1	109242456	109242456	Frame_Shift_Del	DEL	A	-	23	280	c.1455delA	c.(1453-1455)TCAfs	p.S485fs
Pat_41	Post-Resistance	MAGI3	260425	37	1	114225919	114225919	Frame_Shift_Del	DEL	A	-	11	239	c.3729delA	c.(3727-3729)CTAfs	p.L1243fs
Pat_41	Post-Resistance	TRIM33	51592	37	1	114968116	114968118	In_Frame_Del	DEL	TGT	-	7	1152	.1648_1650delAC	c.(1648-1650)ACAdel	p.T550del
Pat_41	Post-Resistance	GDAP2	54834	37	1	118454625	118454626	Frame_Shift_Del	DEL	TG	-	14	403	c.549_550delCA	c.(547-552)CACATAfs	p.H183fs
Pat_41	Post-Resistance	BCL9	607	37	1	147091501	147091501	Frame_Shift_Del	DEL	C	-	14	406	c.1540delC	c.(1540-1542)CCCfs	p.P514fs
Pat_41	Post-Resistance	TCHH	7062	37	1	152081327	152081328	In_Frame_Ins	INS	-	GCT	9	142	.4365_4366insAG	c.(4363-4368)insAGC	.1455_1456ins
Pat_41	Post-Resistance	TCHH	7062	37	1	152084657	152084658	In_Frame_Ins	INS	-	CTC	7	135	.1035_1036insGA	c.(1033-1038)insGAG	p.345_346insE
Pat_41	Post-Resistance	PRCC	5546	37	1	156761535	156761536	Frame_Shift_Ins	INS	-	C	7	507	c.1130_1131insC	c.(1129-1131)GTCfs	p.V377fs
Pat_41	Post-Resistance	CACNA1E	777	37	1	181680102	181680103	Frame_Shift_Del	DEL	AG	-	11	181	c.1068_1069delAG	c.(1066-1071)AAAGAGfs	p.K356fs
Pat_41	Post-Resistance	SMG7	9887	37	1	183502435	183502436	Frame_Shift_Ins	INS	-	T	96	1218	c.980_981insT	c.(979-981)TGTfs	p.C327fs
Pat_41	Post-Resistance	EDEM3	80267	37	1	184680896	184680896	Frame_Shift_Del	DEL	T	-	34	507	c.1652delA	c.(1651-1653)AATfs	p.N551fs
Pat_41	Post-Resistance	PRG4	10216	37	1	186276056	186276058	In_Frame_Del	DEL	AGG	-	9	189	.1205_1207delAG	(1204-1209)AAGGAG>AA	p.E403del
Pat_41	Post-Resistance	PRG4	10216	37	1	186276127	186276128	In_Frame_Ins	INS	-	AGG	9	327	.1276_1277insAG	(1276-1278)AAG>AAGGA	p.426_427insE
Pat_41	Post-Resistance	PRG4	10216	37	1	186276433	186276434	In_Frame_Ins	INS	-	AGG	11	344	.1582_1583insAG	(1582-1584)AAG>AAGGA	p.528_529insE
Pat_41	Post-Resistance	PLXNA2	5362	37	1	208391176	208391176	Frame_Shift_Del	DEL	G	-	18	252	c.92delC	c.(91-93)CCAfs	p.P31fs
Pat_41	Post-Resistance	KCTD3	51133	37	1	215793922	215793922	Frame_Shift_Del	DEL	A	-	21	339	c.2410delA	c.(2410-2412)AAAfs	p.K804fs
Pat_41	Post-Resistance	USH2A	7399	37	1	215901396	215901396	Frame_Shift_Del	DEL	A	-	8	800	c.12042delT	c.(12040-12042)CCTfs	p.P4014fs
Pat_41	Post-Resistance	EPHX1	2052	37	1	226026384	226026384	Frame_Shift_Del	DEL	C	-	7	621	c.394delC	c.(394-396)CCCfs	p.P132fs
Pat_41	Post-Resistance	ZNF678	339500	37	1	227842489	227842489	Frame_Shift_Del	DEL	C	-	15	551	c.538delC	c.(538-540)CCCfs	p.P180fs
Pat_41	Post-Resistance	RGS7	6000	37	1	241032080	241032081	Frame_Shift_Ins	INS	-	T	52	928	c.522_523insA	c.(520-525)CAAGCAfs	p.Q174fs
Pat_41	Post-Resistance	CHML	1122	37	1	241798554	241798554	Frame_Shift_Del	DEL	A	-	8	951	c.515delT	c.(514-516)GTAfs	p.V172fs
Pat_41	Post-Resistance	CSTF2T	23283	37	10	53457748	53457748	Frame_Shift_Del	DEL	G	-	2	4	c.1562delC	c.(1561-1563)GCAfs	p.A521fs
Pat_41	Post-Resistance	USP54	159195	37	10	75258890	75258891	Frame_Shift_Del	DEL	GG	-	8	545	c.4551_4552delCC	c.(4549-4554)TCCCAAfs	p.S1517fs
Pat_41	Post-Resistance	CYP2C8	1558	37	10	96818090	96818090	Splice_Site	DEL	A	-	7	236	c.819_splice	c.e5+1	p.Q273_splice
Pat_41	Post-Resistance	CPXM2	119587	37	10	125528165	125528167	In_Frame_Del	DEL	CAG	-	7	525	.1174_1176delCT	c.(1174-1176)CTGdel	p.L392del
Pat_41	Post-Resistance	PKP3	11187	37	11	403623	403623	Frame_Shift_Del	DEL	G	-	8	59	c.1929delG	c.(1927-1929)GCGfs	p.A643fs
Pat_41	Post-Resistance	LOC338651	338651	37	11	1619173	1619202	In_Frame_Del	DEL	GCCACAGC	-	66	307	ACAGGAGCCACA	CACAGGAGCCACAGCCC	RSHSPPWS1
Pat_41	Post-Resistance	OR52A5	390054	37	11	5153679	5153679	Frame_Shift_Del	DEL	A	-	7	224	c.194delT	c.(193-195)TTGfs	p.L65fs
Pat_41	Post-Resistance	FAM160A2	84067	37	11	6244097	6244097	Frame_Shift_Del	DEL	C	-	7	535	c.967delG	c.(967-969)GTTfs	p.V323fs
Pat_41	Post-Resistance	LIN7C	55327	37	11	27520904	27520906	Splice_Site	DEL	ACC	-	7	161	c.438_splice	c.e4+1	p.V146_splice
Pat_41	Post-Resistance	CPSF7	79869	37	11	61183649	61183649	Frame_Shift_Del	DEL	G	-	15	173	c.893delC	c.(892-894)CCAfs	p.P298fs
Pat_41	Post-Resistance	VEGFB	7423	37	11	64004663	64004663	Frame_Shift_Del	DEL	A	-	7	283	c.379delA	c.(379-381)AAAfs	p.K127fs
Pat_41	Post-Resistance	TPCN2	219931	37	11	68846258	68846258	Frame_Shift_Del	DEL	G	-	7	242	c.1407delG	c.(1405-1407)CTGfs	p.L469fs
Pat_41	Post-Resistance	FUT4	2526	37	11	94277537	94277537	Frame_Shift_Del	DEL	G	-	2	4	c.238delG	c.(238-240)GGGfs	p.G80fs
Pat_41	Post-Resistance	MMP12	4321	37	11	102738795	102738796	Frame_Shift_Ins	INS	-	T	10	24	c.629_630insA	c.(628-630)ACCfs	p.T210fs
Pat_41	Post-Resistance	RAD51AP1	10635	37	12	4653063	4653063	Frame_Shift_Del	DEL	A	-	10	112	c.202delA	c.(202-204)AAAfs	p.K68fs
Pat_41	Post-Resistance	ATN1	1822	37	12	7046235	7046236	Frame_Shift_Del	DEL	CA	-	7	294	c.1805_1806delCA	c.(1804-1806)CCAfs	p.P602fs
Pat_41	Post-Resistance	TAS2R10	50839	37	12	10978836	10978836	Frame_Shift_Del	DEL	A	-	9	444	c.33delT	c.(31-33)TTTfs	p.F11fs
Pat_41	Post-Resistance	PRB1	5542	37	12	11506632	11506633	In_Frame_Ins	INS	-	GGA	12	440	c.404_405insTCC	c.(403-405)CCA>CCTCCA	.135_135P>P

Pat_41	Post-Resistance	PRB1	5542	37	12	11506815	11506816	In_Frame_Ins	INS	-	GGA	11	361	c.221_222insTCC	c.(220-222)CCA>CCTCCA	p.74_74P>PP
Pat_41	Post-Resistance	PRB2	653247	37	12	11546544	11546545	In_Frame_Ins	INS	-	GGA	16	351	c.467_468insTCC	c.(466-468)CCA>CCTCCA	.156_156P>P
Pat_41	Post-Resistance	PRB2	653247	37	12	11546788	11546790	In_Frame_Del	DEL	GGA	-	11	160	c.222_224delTCC	c.(220-225)CCTCCA>CCA	p.74_75PP>P
Pat_41	Post-Resistance	EPS8	2059	37	12	15822389	15822389	Frame_Shift_Del	DEL	C	-	8	281	c.448delG	c.(448-450)GCAfs	p.A150fs
Pat_41	Post-Resistance	FAR2	55711	37	12	29450110	29450110	Frame_Shift_Del	DEL	A	-	7	472	c.522delA	c.(520-522)CCAfs	p.P174fs
Pat_41	Post-Resistance	LRRK2	120892	37	12	40704376	40704377	Frame_Shift_Del	DEL	TG	-	7	1255	c.4461_4462delTG	c.(4459-4464)TTTGTGfs	p.F1487fs
Pat_41	Post-Resistance	CCT2	10576	37	12	69987371	69987372	Frame_Shift_Del	DEL	GG	-	8	412	c.960_961delGG	c.(958-963)GTGGAAfs	p.V320fs
Pat_41	Post-Resistance	TMTC3	160418	37	12	88566417	88566417	Frame_Shift_Del	DEL	T	-	13	358	c.1094delT	c.(1093-1095)CTTfs	p.L365fs
Pat_41	Post-Resistance	KIAA1033	23325	37	12	105534127	105534128	Frame_Shift_Del	DEL	AT	-	8	739	c.1508_1509delAT	c.(1507-1509)CATfs	p.H503fs
Pat_41	Post-Resistance	ARPC3	10094	37	12	110878130	110878130	Frame_Shift_Del	DEL	T	-	9	100	c.170delA	c.(169-171)AACfs	p.N57fs
Pat_41	Post-Resistance	POLE	5426	37	12	133220099	133220100	Frame_Shift_Del	DEL	CA	-	21	663	c.4337_4338delTG	c.(4336-4338)GTGfs	p.V1446fs
Pat_41	Post-Resistance	TRPC4	7223	37	13	38357110	38357111	Frame_Shift_Ins	INS	-	T	18	310	c.360_361insA	c.(358-363)AAACCTfs	p.K120fs
Pat_41	Post-Resistance	CKAP2	26586	37	13	53049034	53049034	Frame_Shift_Del	DEL	A	-	14	142	c.1810delA	c.(1810-1812)AAAfs	p.K604fs
Pat_41	Post-Resistance	LMO7	4008	37	13	76415307	76415308	Frame_Shift_Del	DEL	AG	-	15	307	c.2946_2947delAG	c.(2944-2949)GCAGAGfs	p.A982fs
Pat_41	Post-Resistance	MYCBP2	23077	37	13	77670520	77670521	Frame_Shift_Ins	INS	-	A	8	702	c.9766_9767insT	c.(9766-9768)AGCfs	p.S3256fs
Pat_41	Post-Resistance	RNF113B	140432	37	13	98828697	98828697	Frame_Shift_Del	DEL	T	-	26	565	c.794delA	c.(793-795)AACfs	p.N265fs
Pat_41	Post-Resistance	FAM155A	728215	37	13	108518338	108518338	Frame_Shift_Del	DEL	C	-	12	539	c.607delG	c.(607-609)GACfs	p.D203fs
Pat_41	Post-Resistance	OR4Q3	441669	37	14	20215682	20215683	Frame_Shift_Ins	INS	-	T	7	367	c.96_97insT	c.(94-99)TTGTTTfs	p.L32fs
Pat_41	Post-Resistance	LRP10	26020	37	14	23341527	23341529	In_Frame_Del	DEL	CCT	-	15	307	c.15_17delCCT	c.(13-18)ACCCTC>ACC	p.L11del
Pat_41	Post-Resistance	PPP2R3C	55012	37	14	35585934	35585935	Frame_Shift_Ins	INS	-	T	9	106	c.67_68insA	c.(67-69)AGTfs	p.S23fs
Pat_41	Post-Resistance	MAP3K9	4293	37	14	71205006	71205006	Frame_Shift_Del	DEL	C	-	8	198	c.1800delG	c.(1798-1800)GGGfs	p.G600fs
Pat_41	Post-Resistance	PCNX	22990	37	14	71489915	71489916	Splice_Site	DEL	AG	-	7	569	c.3151_splice	c.e13-1	p.S1051_splice
Pat_41	Post-Resistance	DCAF4	26094	37	14	73422362	73422363	Frame_Shift_Del	DEL	CC	-	8	878	c.1137_1138delCC	c.(1135-1140)CTCCAAfs	p.L379fs
Pat_41	Post-Resistance	C14orf174	161394	37	14	77844468	77844468	Frame_Shift_Del	DEL	C	-	7	280	c.707delC	c.(706-708)ACCfs	p.T236fs
Pat_41	Post-Resistance	SEL1L	6400	37	14	81970641	81970643	In_Frame_Del	DEL	TCT	-	7	363	c.516_518delAGA	.(514-519)GAAGAG>GAG	.172_173EE>
Pat_41	Post-Resistance	PLA2G4E	123745	37	15	42302330	42302331	Frame_Shift_Ins	INS	-	C	7	102	c.115_116insG	c.(115-117)GCCfs	p.A39fs
Pat_41	Post-Resistance	ZFP106	64397	37	15	42742957	42742957	Frame_Shift_Del	DEL	A	-	8	590	c.1444delT	c.(1444-1446)TCCfs	p.S482fs
Pat_41	Post-Resistance	AP4E1	23431	37	15	51242051	51242053	In_Frame_Del	DEL	CAG	-	7	512	.1345_1347delCA	c.(1345-1347)CAGdel	p.Q449del
Pat_41	Post-Resistance	GLCE	26035	37	15	69553629	69553629	Frame_Shift_Del	DEL	A	-	8	715	c.790delA	c.(790-792)AAGfs	p.K264fs
Pat_41	Post-Resistance	PML	5371	37	15	74337151	74337151	Frame_Shift_Del	DEL	G	-	13	143	c.2451delG	c.(2449-2451)CAGfs	p.Q817fs
Pat_41	Post-Resistance	NRG4	145957	37	15	76301581	76301582	Frame_Shift_Ins	INS	-	C	34	516	c.63_64insG	c.(61-66)GGGCTTfs	p.G21fs
Pat_41	Post-Resistance	AGPHD1	123688	37	15	78825826	78825826	Frame_Shift_Del	DEL	T	-	9	204	c.936delT	c.(934-936)CGTfs	p.R312fs
Pat_41	Post-Resistance	IL32	9235	37	16	3119304	3119305	Frame_Shift_Ins	INS	-	G	20	533	c.653_654insG	c.(652-654)GACfs	p.D218fs
Pat_41	Post-Resistance	AGRP	181	37	16	67516932	67516932	Frame_Shift_Del	DEL	G	-	8	572	c.212delC	c.(211-213)GCAfs	p.A71fs
Pat_41	Post-Resistance	ZFHX3	463	37	16	72822564	72822566	In_Frame_Del	DEL	TGC	-	12	217	.9609_9611delGC	.(9607-9612)CAGCAA>CA	3203_3204QQ
Pat_41	Post-Resistance	ADAMTS18	170692	37	16	77356311	77356311	Frame_Shift_Del	DEL	A	-	26	267	c.2085delT	c.(2083-2085)TTTfs	p.F695fs
Pat_41	Post-Resistance	EFNB3	1949	37	17	7611373	7611373	Frame_Shift_Del	DEL	C	-	7	91	c.220delC	c.(220-222)CCTfs	p.P74fs
Pat_41	Post-Resistance	MYH13	8735	37	17	10210253	10210254	Splice_Site	DEL	CA	-	28	109	c.5295_splice	c.e36+1	p.D1765_splice
Pat_41	Post-Resistance	SUPT6H	6830	37	17	27027202	27027204	In_Frame_Del	DEL	AGC	-	8	569	.4573_4575delAG	c.(4573-4575)AGCdel	p.S1528del
Pat_41	Post-Resistance	KRTAP4-1	85285	37	17	39340796	39340852	Splice_Site	DEL	TGGGGTGC	-	65	224	c.246_splice	c.e2-1	p.S82_splice
Pat_41	Post-Resistance	GHDC	84514	37	17	40345560	40345562	In_Frame_Del	DEL	GCA	-	3	4	c.38_40delTGC	c.(37-42)CTGCCA>CCA	p.L13del
Pat_41	Post-Resistance	ZNF652	22834	37	17	47394579	47394579	Frame_Shift_Del	DEL	C	-	7	231	c.509delG	c.(508-510)GGAfs	p.G170fs
Pat_41	Post-Resistance	KIAA0195	9772	37	17	73482037	73482039	In_Frame_Del	DEL	TGC	-	7	209	c.230_232delTGC	.(229-234)GTGCTG>GTG	p.L81del
Pat_41	Post-Resistance	ALPK2	115701	37	18	56246440	56246440	Frame_Shift_Del	DEL	T	-	9	1000	c.1568delA	c.(1567-1569)AAGfs	p.K523fs
Pat_41	Post-Resistance	BSG	682	37	19	579603	579603	Frame_Shift_Del	DEL	G	-	21	111	c.519delG	c.(517-519)AAGfs	p.K173fs
Pat_41	Post-Resistance	ILF3	3609	37	19	10789308	10789308	Frame_Shift_Del	DEL	C	-	19	189	c.579delC	c.(577-579)GACfs	p.D193fs
Pat_41	Post-Resistance	ZNF90	7643	37	19	20216076	20216076	Frame_Shift_Del	DEL	A	-	35	590	c.177delA	c.(175-177)GGAfs	p.G59fs

Pat_41	Post-Resistance	ZNF714	148206	37	19	21300549	21300550	Frame_Shift_Del	DEL	TG	-	11	490	c.1082_1083delTG	c.(1081-1083)ATGfs	p.M361fs
Pat_41	Post-Resistance	GPATCH1	55094	37	19	33585147	33585148	Frame_Shift_Del	DEL	AA	-	20	211	c.525_526delAA	c.(523-528)GTAAAGfs	p.V175fs
Pat_41	Post-Resistance	DMKN	93099	37	19	36002394	36002405	In_Frame_Del	DEL	CACTGCTG	-	7	49	337delAGCAGCA	26-837)AGCAGCAGTGG	p.SSSG276del
Pat_41	Post-Resistance	C19orf55	148137	37	19	36255947	36255949	In_Frame_Del	DEL	CTC	-	7	665	c.639_641delCTC	c.(637-642)ATCTCC>ATC	p.S218del
Pat_41	Post-Resistance	RYR1	6261	37	19	38948159	38948160	Frame_Shift_Del	DEL	TG	-	12	731	c.1814_1815delTG	c.(1813-1815)CTGfs	p.L605fs
Pat_41	Post-Resistance	ZNF283	284349	37	19	44351735	44351735	Frame_Shift_Del	DEL	T	-	7	72	c.982delT	c.(982-984)TTTfs	p.F328fs
Pat_41	Post-Resistance	LIG1	3978	37	19	48664673	48664674	Frame_Shift_Del	DEL	CG	-	8	455	c.198_199delCG	c.(196-201)AGCGAAfs	p.S66fs
Pat_41	Post-Resistance	FCGRT	2217	37	19	50017191	50017191	Frame_Shift_Del	DEL	G	-	7	498	c.126delG	c.(124-126)CCGfs	p.P42fs
Pat_41	Post-Resistance	ZNF808	388558	37	19	53046598	53046598	Frame_Shift_Del	DEL	C	-	7	657	c.61delC	c.(61-63)CAGfs	p.Q21fs
Pat_41	Post-Resistance	ATP6V1C2	245973	37	2	10917819	10917820	Frame_Shift_Del	DEL	AG	-	20	261	c.934_935delAG	c.(934-936)AGAfs	p.R312fs
Pat_41	Post-Resistance	C2orf71	388939	37	2	29295647	29295649	In_Frame_Del	DEL	TCC	-	8	481	.1479_1481delGG	(1477-1482)GAGGAA>GA	.493_494EE>
Pat_41	Post-Resistance	SLC9A2	6549	37	2	103324746	103324746	Frame_Shift_Del	DEL	C	-	34	512	c.2237delC	c.(2236-2238)ACCfs	p.T746fs
Pat_41	Post-Resistance	DGKD	8527	37	2	234365952	234365952	Frame_Shift_Del	DEL	G	-	22	280	c.2558delG	c.(2557-2559)TGGfs	p.W853fs
Pat_41	Post-Resistance	TGM6	343641	37	20	2384126	2384126	Frame_Shift_Del	DEL	C	-	14	180	c.1073delC	c.(1072-1074)ACCfs	p.T358fs
Pat_41	Post-Resistance	ATRN	8455	37	20	3542970	3542970	Frame_Shift_Del	DEL	G	-	55	927	c.1495delG	c.(1495-1497)GGGfs	p.G499fs
Pat_41	Post-Resistance	RALGAPB	57148	37	20	37203485	37203485	Frame_Shift_Del	DEL	C	-	24	295	c.4360delC	c.(4360-4362)CCCfs	p.P1454fs
Pat_41	Post-Resistance	FAM83D	81610	37	20	37555322	37555323	In_Frame_Ins	INS	-	GCG	4	4	c.327_328insGCG	c.(325-330)insGCG	p.116_117insA
Pat_41	Post-Resistance	PREX1	57580	37	20	47317371	47317372	Frame_Shift_Del	DEL	TA	-	8	1074	c.836_837delTA	c.(835-837)TTAfs	p.L279fs
Pat_41	Post-Resistance	KCNB1	3745	37	20	47989771	47989772	Frame_Shift_Ins	INS	-	G	7	1562	c.2325_2326insC	c.(2323-2328)CCCAAAfs	p.P775fs
Pat_41	Post-Resistance	TAF4	6874	37	20	60574086	60574087	Frame_Shift_Del	DEL	GC	-	8	1410	c.2865_2866delGC	c.(2863-2868)AAGCAGfs	p.K955fs
Pat_41	Post-Resistance	KCNJ15	3772	37	21	39671215	39671215	Frame_Shift_Del	DEL	C	-	7	232	c.32delC	c.(31-33)ACCfs	p.T11fs
Pat_41	Post-Resistance	BRWD1	54014	37	21	40558989	40558989	Frame_Shift_Del	DEL	A	-	15	319	c.6926delT	c.(6925-6927)TTAfs	p.L2309fs
Pat_41	Post-Resistance	DIP2A	23181	37	21	47918510	47918510	Frame_Shift_Del	DEL	C	-	7	745	c.419delC	c.(418-420)TCAfs	p.S140fs
Pat_41	Post-Resistance	CRKL	1399	37	22	21288130	21288130	Frame_Shift_Del	DEL	G	-	8	536	c.375delG	c.(373-375)CTGfs	p.L125fs
Pat_41	Post-Resistance	C22orf43	51233	37	22	23959767	23959769	In_Frame_Del	DEL	CAT	-	9	281	c.512_514delATG	c.(511-516)GATGCC>GCC	p.D171del
Pat_41	Post-Resistance	NF2	4771	37	22	30057196	30057197	Frame_Shift_Ins	INS	-	A	7	371	c.678_679insA	c.(676-681)AATAAAfs	p.N226fs
Pat_41	Post-Resistance	MYH9	4627	37	22	36691101	36691102	Frame_Shift_Del	DEL	CA	-	7	401	c.3506_3507delTG	c.(3505-3507)GTGfs	p.V1169fs
Pat_41	Post-Resistance	MYH9	4627	37	22	36696948	36696950	In_Frame_Del	DEL	CTC	-	10	291	.2785_2787delGA	c.(2785-2787)GAGdel	p.E929del
Pat_41	Post-Resistance	EIF3L	51386	37	22	38247385	38247385	Frame_Shift_Del	DEL	A	-	21	193	c.181delA	c.(181-183)AAAfs	p.K61fs
Pat_41	Post-Resistance	C22orf32	91689	37	22	42478046	42478048	In_Frame_Del	DEL	GAT	-	8	484	c.304_306delGAT	c.(304-306)GATdel	p.D107del
Pat_41	Post-Resistance	TCF20	6942	37	22	42610573	42610575	In_Frame_Del	DEL	AGG	-	12	243	c.737_739delCCT	c.(736-741)TCCTTC>TTC	p.S246del
Pat_41	Post-Resistance	POLDIP3	84271	37	22	42988072	42988073	Frame_Shift_Del	DEL	CA	-	7	659	c.909_910delTG	c.(907-912)TGTGGGfs	p.C303fs
Pat_41	Post-Resistance	BHLHE40	8553	37	3	5023155	5023157	In_Frame_Del	DEL	CAG	-	8	1446	c.337_339delCAG	c.(337-339)CAGdel	p.Q116del
Pat_41	Post-Resistance	CAPN7	23473	37	3	15283742	15283742	Frame_Shift_Del	DEL	A	-	21	143	c.1846delA	c.(1846-1848)AAAfs	p.K616fs
Pat_41	Post-Resistance	ERC2	26059	37	3	55733470	55733472	In_Frame_Del	DEL	TGG	-	9	882	.2781_2783delCC	.(2779-2784)CACCAT>CA	.927_928HH>
Pat_41	Post-Resistance	POLQ	10721	37	3	121207671	121207673	In_Frame_Del	DEL	CTT	-	7	359	.4105_4107delAA	c.(4105-4107)AAGdel	p.K1369del
Pat_41	Post-Resistance	PARP14	54625	37	3	122418640	122418640	Frame_Shift_Del	DEL	A	-	7	579	c.1239delA	c.(1237-1239)ATAfs	p.I413fs
Pat_41	Post-Resistance	MBD4	8930	37	3	129155872	129155873	Frame_Shift_Del	DEL	AG	-	28	516	c.614_615delCT	c.(613-615)TCTfs	p.S205fs
Pat_41	Post-Resistance	CEP63	80254	37	3	134267969	134267970	Frame_Shift_Del	DEL	TG	-	8	313	c.1133_1134delTG	c.(1132-1134)CTGfs	p.L378fs
Pat_41	Post-Resistance	MED12L	116931	37	3	151095826	151095828	In_Frame_Del	DEL	TGG	-	109	309	.4238_4240delTG	.(4237-4242)TTGGTG>TT	p.V1414del
Pat_41	Post-Resistance	SKIL	6498	37	3	170078207	170078207	Frame_Shift_Del	DEL	A	-	9	57	c.88delA	c.(88-90)AAAfs	p.K30fs
Pat_41	Post-Resistance	MUC4	4585	37	3	195513582	195513582	Frame_Shift_Del	DEL	G	-	3	6	c.4869delC	c.(4867-4869)TCCfs	p.S1623fs
Pat_41	Post-Resistance	CRIPAK	285464	37	4	1388345	1388346	Frame_Shift_Del	DEL	CA	-	10	1216	c.46_47delCA	c.(46-48)CACfs	p.H16fs
Pat_41	Post-Resistance	CRIPAK	285464	37	4	1388441	1388442	Frame_Shift_Ins	INS	-	CG	8	1660	c.142_143insCG	c.(142-144)ATGfs	p.M48fs
Pat_41	Post-Resistance	CRIPAK	285464	37	4	1388683	1388684	Frame_Shift_Del	DEL	CA	-	11	1260	c.384_385delCA	c.(382-387)CTCACAfs	p.L128fs
Pat_41	Post-Resistance	CRIPAK	285464	37	4	1389392	1389393	Frame_Shift_Del	DEL	CA	-	10	1602	c.1093_1094delCA	c.(1093-1095)CACfs	p.H365fs
Pat_41	Post-Resistance	TBC1D1	23216	37	4	38119764	38119765	Frame_Shift_Del	DEL	CA	-	7	690	c.2913_2914delCA	c.(2911-2916)CTCACCfs	p.L971fs

Pat_41	Post-Resistance	CSN2	1447	37	4	70823289	70823289	Frame_Shift_Del	DEL	A	-	11	125	c.378delT	c.(376-378)TTTfs	p.F126fs
Pat_41	Post-Resistance	MMRN1	22915	37	4	90844391	90844393	In_Frame_Del	DEL	AGC	-	10	1403	c.923_925delAGC	.(922-927)GAGCAG>GA	p.Q313del
Pat_41	Post-Resistance	MAML3	55534	37	4	140811064	140811072	Splice_Site	DEL	TGCTGCTG	-	13	213	c.1513_splice	c.e3-1	p.Q505_splice
Pat_41	Post-Resistance	THBS4	7060	37	5	79372774	79372776	In_Frame_Del	DEL	TGA	-	12	863	.1989_1991delTG	.(1987-1992)TGTGAT>TG	p.D668del
Pat_41	Post-Resistance	MSH3	4437	37	5	79966113	79966114	Frame_Shift_Ins	INS	-	G	16	212	c.777_778insG	c.(775-780)TTTGGGfs	p.F259fs
Pat_41	Post-Resistance	RASGRF2	5924	37	5	80409566	80409568	In_Frame_Del	DEL	CCA	-	7	375	.2297_2299delCC	(2296-2301)CCCACC>CC	p.T770del
Pat_41	Post-Resistance	WDR36	134430	37	5	110459863	110459865	In_Frame_Del	DEL	GAA	-	19	424	.2494_2496delGA	c.(2494-2496)GAAdel	p.E833del
Pat_41	Post-Resistance	CTNNA1	1495	37	5	138160447	138160449	In_Frame_Del	DEL	GGA	-	8	721	c.817_819delGGA	c.(817-819)GGAdel	p.G276del
Pat_41	Post-Resistance	LARP1	23367	37	5	154173390	154173390	Frame_Shift_Del	DEL	C	-	18	1116	c.899delC	c.(898-900)GCCfs	p.A300fs
Pat_41	Post-Resistance	UBLCP1	134510	37	5	158697424	158697425	Frame_Shift_Del	DEL	TG	-	7	485	c.303_304delTG	c.(301-306)ATTGAAfs	p.I101fs
Pat_41	Post-Resistance	FGF18	8817	37	5	170883644	170883644	Frame_Shift_Del	DEL	C	-	8	542	c.459delC	c.(457-459)TTCfs	p.F153fs
Pat_41	Post-Resistance	NSD1	64324	37	5	176637122	176637122	Frame_Shift_Del	DEL	A	-	20	151	c.1722delA	c.(1720-1722)GGAfs	p.G574fs
Pat_41	Post-Resistance	TUBB2B	347733	37	6	3225002	3225004	In_Frame_Del	DEL	CCT	-	9	340	.1319_1321delAG	(1318-1323)GAGGGC>GG	p.E440del
Pat_41	Post-Resistance	DST	667	37	6	56510689	56510690	Frame_Shift_Del	DEL	TC	-	7	391	c.1653_1654delG	c.(1651-1656)GAGAAGfs	p.E551fs
Pat_41	Post-Resistance	FRK	2444	37	6	116325059	116325059	Frame_Shift_Del	DEL	T	-	19	87	c.447delA	c.(445-447)AAAfs	p.K149fs
Pat_41	Post-Resistance	SHPRH	257218	37	6	146275964	146275964	Frame_Shift_Del	DEL	T	-	8	65	c.495delA	c.(493-495)AAAfs	p.K165fs
Pat_41	Post-Resistance	MTHFD1L	25902	37	6	151358163	151358164	Frame_Shift_Ins	INS	-	A	8	184	c.2757_2758insA	c.(2755-2760)GACAAAfs	p.D919fs
Pat_41	Post-Resistance	PHF10	55274	37	6	170104147	170104148	Frame_Shift_Ins	INS	-	G	24	263	c.1448_1449insC	c.(1447-1449)CCAfs	p.P483fs
Pat_41	Post-Resistance	GPER	2852	37	7	1132270	1132270	Frame_Shift_Del	DEL	C	-	11	222	c.906delC	c.(904-906)CACfs	p.H302fs
Pat_41	Post-Resistance	PHF14	9678	37	7	11075380	11075381	Frame_Shift_Del	DEL	AG	-	10	687	c.1569_1570delA	c.(1567-1572)CAAGAGfs	p.Q523fs
Pat_41	Post-Resistance	TRA2A	29896	37	7	23552546	23552546	Frame_Shift_Del	DEL	A	-	14	378	c.492delT	c.(490-492)TTTfs	p.F164fs
Pat_41	Post-Resistance	OGDH	4967	37	7	44684936	44684936	Frame_Shift_Del	DEL	T	-	10	465	c.233delT	c.(232-234)ATTfs	p.I78fs
Pat_41	Post-Resistance	ZNF716	441234	37	7	57529007	57529008	In_Frame_Ins	INS	-	TCT	12	190	c.840_841insTCT	c.(838-843)insTCT	p.281_282ins
Pat_41	Post-Resistance	ZNF716	441234	37	7	57529089	57529091	In_Frame_Del	DEL	TCT	-	10	366	c.922_924delTCT	c.(922-924)TCTdel	p.S309del
Pat_41	Post-Resistance	CYP51A1	1595	37	7	91752494	91752494	Frame_Shift_Del	DEL	T	-	7	555	c.1026delA	c.(1024-1026)AAAfs	p.K342fs
Pat_41	Post-Resistance	PEX1	5189	37	7	92120786	92120786	Frame_Shift_Del	DEL	T	-	8	458	c.3238delA	c.(3238-3240)AGTfs	p.S1080fs
Pat_41	Post-Resistance	TRRAP	8295	37	7	98609744	98609745	Frame_Shift_Ins	INS	-	A	11	169	c.11346_11347ins	c.(11344-11349)CACAAAf	p.H3782fs
Pat_41	Post-Resistance	PTCD1	26024	37	7	99032605	99032607	In_Frame_Del	DEL	CTC	-	7	437	c.259_261delGAG	c.(259-261)GAGdel	p.E87del
Pat_41	Post-Resistance	MCM7	4176	37	7	99691822	99691822	Frame_Shift_Del	DEL	C	-	8	1018	c.1822delG	c.(1822-1824)GCTfs	p.A608fs
Pat_41	Post-Resistance	MEPCE	56257	37	7	100028452	100028454	In_Frame_Del	DEL	CAG	-	9	1204	c.811_813delCAG	c.(811-813)CAGdel	p.Q274del
Pat_41	Post-Resistance	AP1S1	1174	37	7	100802405	100802405	Frame_Shift_Del	DEL	G	-	22	207	c.357delG	c.(355-357)ATGfs	p.M119fs
Pat_41	Post-Resistance	CBLL1	79872	37	7	107395909	107395909	Frame_Shift_Del	DEL	A	-	7	1059	c.413delA	c.(412-414)GAAfs	p.E138fs
Pat_41	Post-Resistance	CTTNBP2	83992	37	7	117431783	117431784	Frame_Shift_Del	DEL	CC	-	7	1572	c.1466_1467delG	c.(1465-1467)CGGfs	p.R489fs
Pat_41	Post-Resistance	CHRM2	1129	37	7	136700150	136700150	Frame_Shift_Del	DEL	T	-	10	536	c.538delT	c.(538-540)TTTfs	p.F180fs
Pat_41	Post-Resistance	BRAF	673	37	7	140482927	140482927	Frame_Shift_Del	DEL	G	-	8	260	c.1208delC	c.(1207-1209)CCTfs	p.P403fs
Pat_41	Post-Resistance	OR9A4	130075	37	7	141619203	141619203	Frame_Shift_Del	DEL	T	-	18	1002	c.528delT	c.(526-528)AATfs	p.N176fs
Pat_41	Post-Resistance	DLC1	10395	37	8	12957611	12957613	In_Frame_Del	DEL	GCT	-	9	175	.2233_2235delAG	c.(2233-2235)AGCdel	p.S745del
Pat_41	Post-Resistance	PRKDC	5591	37	8	48746799	48746799	Frame_Shift_Del	DEL	T	-	11	962	c.8110delA	c.(8110-8112)AGGfs	p.R2704fs
Pat_41	Post-Resistance	LACTB2	51110	37	8	71556428	71556429	Frame_Shift_Del	DEL	TC	-	7	1159	c.463_464delGA	c.(463-465)GAAfs	p.E155fs
Pat_41	Post-Resistance	ZNF704	619279	37	8	81733778	81733778	Frame_Shift_Del	DEL	T	-	9	1386	c.52delA	c.(52-54)ATGfs	p.M18fs
Pat_41	Post-Resistance	TMEM55A	55529	37	8	92021005	92021006	Frame_Shift_Del	DEL	TG	-	8	512	c.504_505delCA	c.(502-507)TTCAACfs	p.F168fs
Pat_41	Post-Resistance	ESRP1	54845	37	8	95686611	95686611	Frame_Shift_Del	DEL	A	-	10	210	c.1528delA	c.(1528-1530)AAAfs	p.K510fs
Pat_41	Post-Resistance	UBR5	51366	37	8	103298813	103298813	Frame_Shift_Del	DEL	C	-	16	128	c.4990delG	c.(4990-4992)GATfs	p.D1664fs
Pat_41	Post-Resistance	CSMD3	114788	37	8	113303887	113303887	Frame_Shift_Del	DEL	A	-	8	555	c.8826delT	c.(8824-8826)TCTfs	p.S2942fs
Pat_41	Post-Resistance	ZHX2	22882	37	8	123963963	123963964	Frame_Shift_Ins	INS	-	A	15	60	c.213_214insA	c.(211-216)TCCAAAfs	p.S71fs
Pat_41	Post-Resistance	ATAD2	29028	37	8	124368685	124368685	Frame_Shift_Del	DEL	A	-	10	262	c.1590delT	c.(1588-1590)TTTfs	p.F530fs
Pat_41	Post-Resistance	FER1L6	654463	37	8	125022956	125022956	Splice_Site	DEL	T	-	7	793	c.1821_splice	c.e14+2	p.L607_splice

Pat_41	Post-Resistance	PLEC	5339	37	8	144995120	144995122	In_Frame_Del	DEL	TGA	-	8	194	.9278_9280delTC	.(9277-9282)ATCAAG>AA	p.I3093del
Pat_41	Post-Resistance	TFE3	7030	37	X	48887952	48887952	Frame_Shift_Del	DEL	C	-	21	294	c.1445delG	c.(1444-1446)GGAfs	p.G482fs
Pat_41	Post-Resistance	PHF8	23133	37	X	54011405	54011407	In_Frame_Del	DEL	CTC	-	13	493	.2491_2493delGA	c.(2491-2493)GAGdel	p.E831del
Pat_41	Post-Resistance	FAM155B	27112	37	X	68725672	68725672	Frame_Shift_Del	DEL	A	-	7	70	c.547delA	c.(547-549)AAAfs	p.K183fs
Pat_41	Post-Resistance	OGT	8473	37	X	70782825	70782825	Frame_Shift_Del	DEL	T	-	10	352	c.2106delT	c.(2104-2106)ACTfs	p.T702fs
Pat_41	Post-Resistance	TCEAL6	158931	37	X	101396101	101396101	Frame_Shift_Del	DEL	T	-	14	293	c.203delA	c.(202-204)AAGfs	p.K68fs
Pat_41	Post-Resistance	RGAG1	57529	37	X	109694602	109694603	Frame_Shift_Del	DEL	GG	-	7	369	c.757_758delGG	c.(757-759)GGAfs	p.G253fs
Pat_41	Post-Resistance	STAG2	10735	37	X	123159727	123159727	Frame_Shift_Del	DEL	G	-	8	892	c.82delG	c.(82-84)GAAfs	p.E28fs
Pat_41	Post-Resistance	GPR112	139378	37	X	135455156	135455156	Frame_Shift_Del	DEL	G	-	8	1340	c.7709delG	c.(7708-7710)CGGfs	p.R2570fs
Pat_41	Post-Resistance	MAGEC1	9947	37	X	140994114	140994116	In_Frame_Del	DEL	CTC	-	7	542	c.924_926delCTC	c.(922-927)AGCTCC>AGC	.308_309SS>
Pat_41	Post-Resistance	ZNF185	7739	37	X	152087570	152087572	In_Frame_Del	DEL	GAG	-	9	81	c.475_477delGAG	c.(475-477)GAGdel	p.E165del
Pat_41	Post-Resistance	L1CAM	3897	37	X	153130092	153130092	Frame_Shift_Del	DEL	G	-	7	410	c.3114delC	c.(3112-3114)CCCfs	p.P1038fs
Pat_41	Post-Resistance	F8	2157	37	X	154158427	154158428	Frame_Shift_Ins	INS	-	T	3	4	c.3637_3638insA	c.(3637-3639)ATTfs	p.I1213fs
Pat_44	Pre-Treatment	ARID1A	8289	37	1	27057991	27057991	Frame_Shift_Del	DEL	C	-	10	459	c.1699delC	c.(1699-1701)CAGfs	p.Q567fs
Pat_44	Pre-Treatment	RIT1	6016	37	1	155874584	155874585	Frame_Shift_Del	DEL	TA	-	7	66	c.174_175delTA	c.(172-177)TATAAGfs	p.Y58fs
Pat_44	Pre-Treatment	MBD6	114785	37	12	57918829	57918830	Frame_Shift_Ins	INS	-	T	24	135	c.310_311insT	c.(310-312)CGGfs	p.R104fs
Pat_44	Pre-Treatment	CEP290	80184	37	12	88473975	88473975	Frame_Shift_Del	DEL	T	-	2	4	c.5210delA	c.(5209-5211)AAGfs	p.K1737fs
Pat_44	Pre-Treatment	IPO4	79711	37	14	24656873	24656874	Frame_Shift_Del	DEL	CT	-	8	129	c.407_408delAG	c.(406-408)GAGfs	p.E136fs
Pat_44	Pre-Treatment	BCL11B	64919	37	14	99641544	99641546	In_Frame_Del	DEL	CTC	-	5	7	.1627_1629delGA	c.(1627-1629)GAGdel	p.E543del
Pat_44	Pre-Treatment	PDE8A	5151	37	15	85658713	85658713	Frame_Shift_Del	DEL	C	-	2	4	c.1394delC	c.(1393-1395)ACAfs	p.T465fs
Pat_44	Pre-Treatment	TSC2	7249	37	16	2112527	2112527	Frame_Shift_Del	DEL	T	-	2	4	c.1287delT	c.(1285-1287)TATfs	p.Y429fs
Pat_44	Pre-Treatment	CMIP	80790	37	16	81691378	81691379	Splice_Site	DEL	AG	-	3	4	c.640_splice	c.e5-1	p.N214_splice
Pat_44	Pre-Treatment	ATP6V0A1	535	37	17	40639289	40639289	Frame_Shift_Del	DEL	G	-	7	192	c.927delG	c.(925-927)CTGfs	p.L309fs
Pat_44	Pre-Treatment	BAHCC1	57597	37	17	79409922	79409922	Frame_Shift_Del	DEL	C	-	2	4	c.1547delC	c.(1546-1548)GCCfs	p.A516fs
Pat_44	Pre-Treatment	C19orf35	374872	37	19	2275696	2275696	Frame_Shift_Del	DEL	C	-	4	9	c.1405delG	c.(1405-1407)GCGfs	p.A469fs
Pat_44	Pre-Treatment	STAP2	55620	37	19	4324499	4324500	Frame_Shift_Del	DEL	CC	-	4	5	c.1099_1100delGG	c.(1099-1101)GGCfs	p.G367fs
Pat_44	Pre-Treatment	UNC13A	23025	37	19	17766924	17766926	In_Frame_Del	DEL	CCT	-	2	4	.1313_1315delAG	(1312-1317)GAGGTG>GT	p.E438del
Pat_44	Pre-Treatment	KIRREL2	84063	37	19	36352837	36352838	Frame_Shift_Del	DEL	CC	-	3	5	c.1421_1422delCC	c.(1420-1422)ACCfs	p.T474fs
Pat_44	Pre-Treatment	SIPA1L3	23094	37	19	38684299	38684299	Frame_Shift_Del	DEL	C	-	4	9	c.4719delC	c.(4717-4719)TTCfs	p.F1573fs
Pat_44	Pre-Treatment	GTF3C3	9330	37	2	197649613	197649614	Frame_Shift_Ins	INS	-	T	2	4	c.1081_1082insA	c.(1081-1083)ACTfs	p.T361fs
Pat_44	Pre-Treatment	CADPS	8618	37	3	62464070	62464070	Frame_Shift_Del	DEL	T	-	2	4	c.3195delA	c.(3193-3195)GAAfs	p.E1065fs
Pat_44	Pre-Treatment	PRDM13	59336	37	6	100061624	100061625	In_Frame_Ins	INS	-	CCG	11	4	.1113_1114insCC	c.(1111-1116)insCCG	p.378_379insP
Pat_44	Pre-Treatment	FAM83H	286077	37	8	144811169	144811170	Frame_Shift_Ins	INS	-	GT	7	268	c.704_705insAC	c.(703-705)GTGfs	p.V235fs
Pat_44	Pre-Treatment	CCDC22	28952	37	X	49105637	49105637	Frame_Shift_Del	DEL	G	-	2	4	c.1549delG	c.(1549-1551)GATfs	p.D517fs
Pat_44	Post-Resistance	ATAD3B	83858	37	1	1420436	1420437	Frame_Shift_Del	DEL	CC	-	4	7	c.791_792delCC	c.(790-792)GCCfs	p.A264fs
Pat_44	Post-Resistance	LHX4	89884	37	1	180243506	180243506	Frame_Shift_Del	DEL	C	-	7	519	c.965delC	c.(964-966)TCCfs	p.S322fs
Pat_44	Post-Resistance	PGBD2	267002	37	1	249211274	249211274	Frame_Shift_Del	DEL	A	-	8	305	c.491delA	c.(490-492)TATfs	p.Y164fs
Pat_44	Post-Resistance	CHAT	1103	37	10	50872887	50872887	Frame_Shift_Del	DEL	G	-	8	799	c.2042delG	c.(2041-2043)TGCfs	p.C681fs
Pat_44	Post-Resistance	ZMIZ1	57178	37	10	81067245	81067245	Frame_Shift_Del	DEL	C	-	7	185	c.2752delC	c.(2752-2754)CCCfs	p.P918fs
Pat_44	Post-Resistance	FBXL15	79176	37	10	104181190	104181190	Frame_Shift_Del	DEL	C	-	2	4	c.133delC	c.(133-135)CAGfs	p.Q45fs
Pat_44	Post-Resistance	UBQLN3	50613	37	11	5529918	5529920	In_Frame_Del	DEL	TGG	-	7	460	c.869_871delCCA	.(868-873)ACCAGC>AGC	p.T290del
Pat_44	Post-Resistance	AMBRA1	55626	37	11	46564695	46564696	Frame_Shift_Del	DEL	CG	-	4	4	c.871_872delCG	c.(871-873)CGAfs	p.R291fs
Pat_44	Post-Resistance	CKAP5	9793	37	11	46789159	46789159	Frame_Shift_Del	DEL	T	-	7	329	c.3377delA	c.(3376-3378)AAGfs	p.K1126fs
Pat_44	Post-Resistance	RARRES3	5920	37	11	63313709	63313709	Frame_Shift_Del	DEL	A	-	8	184	c.476delA	c.(475-477)CAAfs	p.Q159fs
Pat_44	Post-Resistance	VEGFB	7423	37	11	64004663	64004663	Frame_Shift_Del	DEL	A	-	7	218	c.379delA	c.(379-381)AAAfs	p.K127fs
Pat_44	Post-Resistance	ODZ4	26011	37	11	78387242	78387242	Frame_Shift_Del	DEL	T	-	2	4	c.5451delA	c.(5449-5451)AAAfs	p.K1817fs
Pat_44	Post-Resistance	ADAMTS8	11095	37	11	130298118	130298120	In_Frame_Del	DEL	GCA	-	7	1	c.62_64delTGC	c.(61-66)CTGCCG>CCG	p.L21del

Pat_44	Post-Resistance	RAD52	5893	37	12	1023096	1023097	Frame_Shift_Del	DEL	CC	-	7	140	c.1158_1159delGG	c.(1156-1161)TGGGACfs	p.W386fs
Pat_44	Post-Resistance	XPO4	64328	37	13	21436912	21436912	Frame_Shift_Del	DEL	T	-	7	869	c.261delA	c.(259-261)AAAfs	p.K87fs
Pat_44	Post-Resistance	RNASE8	122665	37	14	21526082	21526084	In_Frame_Del	DEL	CTG	-	7	118	c.31_33delCTG	c.(31-33)CTGdel	p.L16del
Pat_44	Post-Resistance	KCNH5	27133	37	14	63174357	63174357	Frame_Shift_Del	DEL	T	-	8	323	c.2836delA	c.(2836-2838)AGCfs	p.S946fs
Pat_44	Post-Resistance	ZFYVE26	23503	37	14	68222747	68222747	Frame_Shift_Del	DEL	C	-	10	1189	c.6704delG	c.(6703-6705)GGAfs	p.G2235fs
Pat_44	Post-Resistance	TRIP11	9321	37	14	92436027	92436027	Frame_Shift_Del	DEL	A	-	8	318	c.5930delT	c.(5929-5931)TTAfs	p.L1977fs
Pat_44	Post-Resistance	BCL11B	64919	37	14	99641544	99641546	In_Frame_Del	DEL	CTC	-	5	11	.1627_1629delGA	c.(1627-1629)GAGdel	p.E543del
Pat_44	Post-Resistance	SPINT1	6692	37	15	41149075	41149077	In_Frame_Del	DEL	CAC	-	7	724	.1492_1494delCA	c.(1492-1494)CACdel	p.H501del
Pat_44	Post-Resistance	FBN1	2200	37	15	48704838	48704839	Frame_Shift_Del	DEL	AC	-	9	472	c.8153_8154delGT	c.(8152-8154)TGTfs	p.C2718fs
Pat_44	Post-Resistance	SCAPER	49855	37	15	77046232	77046233	Frame_Shift_Del	DEL	CC	-	8	595	c.1782_1783delG	c.(1780-1785)ATGGAAfs	p.M594fs
Pat_44	Post-Resistance	POLR3E	55718	37	16	22339834	22339834	Frame_Shift_Del	DEL	C	-	8	261	c.1870delC	c.(1870-1872)CCCfs	p.P624fs
Pat_44	Post-Resistance	NUTF2	10204	37	16	67902402	67902403	Splice_Site	DEL	AG	-	8	964	c.172_splice	c.e4-1	p.S58_splice
Pat_44	Post-Resistance	PLSCR3	57048	37	17	7294059	7294059	Frame_Shift_Del	DEL	C	-	7	471	c.725delG	c.(724-726)GGCfs	p.G242fs
Pat_44	Post-Resistance	SPAG9	9043	37	17	49077041	49077041	Frame_Shift_Del	DEL	T	-	10	152	c.1645delA	c.(1645-1647)AGGfs	p.R549fs
Pat_44	Post-Resistance	ZNF442	79973	37	19	12461637	12461638	Frame_Shift_Del	DEL	TC	-	7	651	c.761_762delGA	c.(760-762)AGAfs	p.R254fs
Pat_44	Post-Resistance	MAP3K10	4294	37	19	40697953	40697953	Frame_Shift_Del	DEL	G	-	2	4	c.15delG	c.(13-15)GAGfs	p.E5fs
Pat_44	Post-Resistance	ZNF649	65251	37	19	52394014	52394014	Frame_Shift_Del	DEL	C	-	8	713	c.1375delG	c.(1375-1377)GATfs	p.D459fs
Pat_44	Post-Resistance	MYT1L	23040	37	2	1921068	1921068	Frame_Shift_Del	DEL	G	-	8	309	c.1527delC	c.(1525-1527)CCCfs	p.P509fs
Pat_44	Post-Resistance	NTSR2	23620	37	2	11800201	11800201	Frame_Shift_Del	DEL	C	-	8	318	c.957delG	c.(955-957)ATGfs	p.M319fs
Pat_44	Post-Resistance	MITD1	129531	37	2	99787009	99787009	Frame_Shift_Del	DEL	C	-	9	397	c.584delG	c.(583-585)CGAfs	p.R195fs
Pat_44	Post-Resistance	EPHA4	2043	37	2	222301266	222301266	Frame_Shift_Del	DEL	C	-	7	585	c.2199delG	c.(2197-2199)GGGfs	p.G733fs
Pat_44	Post-Resistance	CLIC6	54102	37	21	36042463	36042492	In_Frame_Del	DEL	GGGTCCC	-	4	5	GAAGCGGGGGT	AAGCGGGGGTCCCGGC	AGVPAGDS2
Pat_44	Post-Resistance	TRIOBP	11078	37	22	38120392	38120400	In_Frame_Del	DEL	CTCCAGA	-	7	420	9_1837delCCTCC	8-1839)GCCTCCAGAACC	p.SRT611del
Pat_44	Post-Resistance	CLASP2	23122	37	3	33602361	33602361	Frame_Shift_Del	DEL	T	-	21	481	c.2869delA	c.(2869-2871)ATGfs	p.M957fs
Pat_44	Post-Resistance	DLEC1	9940	37	3	38151740	38151740	Frame_Shift_Del	DEL	C	-	8	497	c.3411delC	c.(3409-3411)AGCfs	p.S1137fs
Pat_44	Post-Resistance	CADPS	8618	37	3	62478091	62478091	Frame_Shift_Del	DEL	C	-	8	1527	c.2758delG	c.(2758-2760)GAGfs	p.E920fs
Pat_44	Post-Resistance	CRIPAK	285464	37	4	1389147	1389148	Frame_Shift_Del	DEL	AT	-	11	854	c.848_849delAT	c.(847-849)CATfs	p.H283fs
Pat_44	Post-Resistance	TTC23L	153657	37	5	34850347	34850347	Frame_Shift_Del	DEL	G	-	7	474	c.313delG	c.(313-315)GGGfs	p.G105fs
Pat_44	Post-Resistance	SLCO6A1	133482	37	5	101794149	101794149	Frame_Shift_Del	DEL	A	-	7	204	c.1068delT	c.(1066-1068)TTTfs	p.F356fs
Pat_44	Post-Resistance	DMXL1	1657	37	5	118533562	118533563	Frame_Shift_Del	DEL	CG	-	7	588	c.7656_7657delC	c.(7654-7659)ATCGCAfs	p.I2552fs
Pat_44	Post-Resistance	LRRC1	55227	37	6	53787534	53787535	Frame_Shift_Del	DEL	GG	-	7	1416	c.1518_1519delG	c.(1516-1521)CTGGACfs	p.L506fs
Pat_44	Post-Resistance	PRDM13	59336	37	6	100061624	100061625	In_Frame_Ins	INS	-	CCG	6	4	c.1113_1114insCC	c.(1111-1116)insCCG	p.378_379insP
Pat_44	Post-Resistance	IFNGR1	3459	37	6	137519505	137519506	Frame_Shift_Del	DEL	CT	-	10	376	c.1132_1133delAG	c.(1132-1134)AGTfs	p.S378fs
Pat_44	Post-Resistance	PHACTR2	9749	37	6	144086414	144086414	Frame_Shift_Del	DEL	A	-	8	150	c.678delA	c.(676-678)TCAfs	p.S226fs
Pat_44	Post-Resistance	UNC93A	54346	37	6	167728864	167728865	Frame_Shift_Del	DEL	CC	-	8	876	c.1298_1299delC	c.(1297-1299)TCCfs	p.S433fs
Pat_44	Post-Resistance	PHTF2	57157	37	7	77569580	77569581	Frame_Shift_Ins	INS	-	T	8	269	c.1701_1702insT	c.(1699-1704)TTCTTTfs	p.F567fs
Pat_44	Post-Resistance	PIK3CG	5294	37	7	106509566	106509566	Frame_Shift_Del	DEL	G	-	7	385	c.1560delG	c.(1558-1560)CTGfs	p.L520fs
Pat_44	Post-Resistance	FOXP2	93986	37	7	114271580	114271582	Splice_Site	DEL	CAG	-	7	54	c.598_splice	c.e6-1	p.Q200_splice
Pat_44	Post-Resistance	ELP3	55140	37	8	27987174	27987174	Frame_Shift_Del	DEL	C	-	7	405	c.773delC	c.(772-774)ACCfs	p.T258fs
Pat_44	Post-Resistance	STAU2	27067	37	8	74507471	74507471	Frame_Shift_Del	DEL	T	-	7	172	c.1091delA	c.(1090-1092)AATfs	p.N364fs
Pat_44	Post-Resistance	TNFRSF11B	4982	37	8	119936812	119936812	Frame_Shift_Del	DEL	T	-	8	366	c.1007delA	c.(1006-1008)AATfs	p.N336fs
Pat_44	Post-Resistance	DMRT2	10655	37	9	1056908	1056908	Frame_Shift_Del	DEL	G	-	8	523	c.1321delG	c.(1321-1323)GACfs	p.D441fs
Pat_44	Post-Resistance	ZNF462	58499	37	9	109736498	109736498	Frame_Shift_Del	DEL	G	-	8	1338	c.6776delG	c.(6775-6777)TGCfs	p.C2259fs
Pat_44	Post-Resistance	C9orf173	441476	37	9	140147214	140147214	Frame_Shift_Del	DEL	C	-	2	4	c.590delC	c.(589-591)ACCfs	p.T197fs
Pat_44	Post-Resistance	KAL1	3730	37	X	8565091	8565091	Frame_Shift_Del	DEL	G	-	8	126	c.525delC	c.(523-525)CCCfs	p.P175fs
Pat_45	Pre-Treatment	SNRNP40	9410	37	1	31742030	31742031	Frame_Shift_Del	DEL	TG	-	7	498	c.832_833delCA	c.(832-834)CAAfs	p.Q278fs
Pat_45	Pre-Treatment	LDLRAD1	388633	37	1	54480002	54480002	Frame_Shift_Del	DEL	C	-	2	4	c.109delG	c.(109-111)GCCfs	p.A37fs

Pat_45	Pre-Treatment	CDC7	8317	37	1	91967356	91967357	Frame_Shift_Ins	INS	-	A	9	252	c.83_84insA	c.(82-84)TTAfs	p.L28fs
Pat_45	Pre-Treatment	CELSR2	1952	37	1	109815643	109815644	Frame_Shift_Del	DEL	CC	-	4	7	c.8332_8333delCC	c.(8332-8334)CCCfs	p.P2778fs
Pat_45	Pre-Treatment	FAM40A	85369	37	1	110585707	110585708	Splice_Site	INS	-	T	4	9	c.886_splice	c.e9-2	p.C296_splice
Pat_45	Pre-Treatment	APOBEC4	403314	37	1	183616826	183616828	In_Frame_Del	DEL	TTC	-	7	555	.1089_1091delGA	.(1087-1092)AAGAAA>AA	.363_364KK>I
Pat_45	Pre-Treatment	HEATR1	55127	37	1	236719429	236719429	Frame_Shift_Del	DEL	T	-	7	360	c.5485delA	c.(5485-5487)ACTfs	p.T1829fs
Pat_45	Pre-Treatment	FOLH1	2346	37	11	49179535	49179535	Frame_Shift_Del	DEL	T	-	8	192	c.1501delA	c.(1501-1503)AGTfs	p.S501fs
Pat_45	Pre-Treatment	PGA5	5222	37	11	61015898	61015899	Frame_Shift_Ins	INS	-	AG	8	629	c.664_665insAG	c.(664-666)AAGfs	p.K222fs
Pat_45	Pre-Treatment	PDE2A	5138	37	11	72353321	72353323	In_Frame_Del	DEL	GCG	-	4	4	c.119_121delCGC	c.(118-123)CCGCAG>CAG	p.P40del
Pat_45	Pre-Treatment	MLL2	8085	37	12	49426661	49426669	In_Frame_Del	DEL	GTTGTTGAA	-	2	4	9_11827delTTCAA	8-11829)CTTCAACAACA	p.LQQ3940del
Pat_45	Pre-Treatment	ACAD10	80724	37	12	112130539	112130539	Frame_Shift_Del	DEL	C	-	8	138	c.26delC	c.(25-27)TCCfs	p.S9fs
Pat_45	Pre-Treatment	RFC3	5983	37	13	34398062	34398063	Frame_Shift_Ins	INS	-	A	10	126	c.234_235insA	c.(232-237)TCTAAAfs	p.S78fs
Pat_45	Pre-Treatment	ARID4A	5926	37	14	58831996	58831997	Frame_Shift_Del	DEL	AG	-	10	138	c.3189_3190delAG	c.(3187-3192)CAAGAGfs	p.Q1063fs
Pat_45	Pre-Treatment	TMEM30B	161291	37	14	61747546	61747546	Frame_Shift_Del	DEL	G	-	4	2	c.320delC	c.(319-321)CCAfs	p.P107fs
Pat_45	Pre-Treatment	PLA2G4D	283748	37	15	42363022	42363022	Frame_Shift_Del	DEL	C	-	4	5	c.1936delG	c.(1936-1938)GTGfs	p.V646fs
Pat_45	Pre-Treatment	TLE3	7090	37	15	70358548	70358550	In_Frame_Del	DEL	GCT	-	2	4	c.380_382delAGC	c.(379-384)CAGCTC>CTC	p.Q127del
Pat_45	Pre-Treatment	GSPT1	2935	37	16	12009531	12009533	In_Frame_Del	DEL	CCG	-	3	5	c.45_47delCGG	c.(43-48)GGCGGG>GGG	p.15_16GG>G
Pat_45	Pre-Treatment	TRIM72	493829	37	16	31230512	31230513	Splice_Site	DEL	GT	-	4	7	c.486_splice	c.e3+1	p.E162_splice
Pat_45	Pre-Treatment	CDK10	8558	37	16	89761176	89761177	Frame_Shift_Del	DEL	CC	-	4	5	c.772_773delCC	c.(772-774)CCCfs	p.P258fs
Pat_45	Pre-Treatment	PRDM7	11105	37	16	90126961	90126962	Frame_Shift_Del	DEL	AG	-	7	96	c.1020_1021delCT	c.(1018-1023)TTCTATfs	p.F340fs
Pat_45	Pre-Treatment	TP53	7157	37	17	7579378	7579379	Frame_Shift_Ins	INS	-	T	19	36	c.308_309insA	c.(307-309)TACfs	p.Y103fs
Pat_45	Pre-Treatment	MYH10	4628	37	17	8526401	8526401	Frame_Shift_Del	DEL	C	-	7	792	c.164delG	c.(163-165)GGAfs	p.G55fs
Pat_45	Pre-Treatment	AKAP10	11216	37	17	19880956	19880956	Frame_Shift_Del	DEL	G	-	2	4	c.37delC	c.(37-39)CGCfs	p.R13fs
Pat_45	Pre-Treatment	TP53I13	90313	37	17	27896102	27896102	Frame_Shift_Del	DEL	C	-	4	6	c.139delC	c.(139-141)CAGfs	p.Q47fs
Pat_45	Pre-Treatment	KLHL14	57565	37	18	30350355	30350355	Frame_Shift_Del	DEL	G	-	4	5	c.200delC	c.(199-201)CCTfs	p.P67fs
Pat_45	Pre-Treatment	LMAN1	3998	37	18	57013285	57013285	Splice_Site	DEL	T	-	10	161	c.823_splice	c.e8-1	p.P275_splice
Pat_45	Pre-Treatment	SERPINB12	89777	37	18	61233923	61233923	Frame_Shift_Del	DEL	C	-	9	408	c.897delC	c.(895-897)TTCfs	p.F299fs
Pat_45	Pre-Treatment	CRTC1	23373	37	19	18794544	18794545	Frame_Shift_Del	DEL	GC	-	4	5	c.32_33delGC	c.(31-33)AGCfs	p.S11fs
Pat_45	Pre-Treatment	C19orf47	126526	37	19	40834399	40834399	Frame_Shift_Del	DEL	G	-	10	184	c.471delC	c.(469-471)CCCfs	p.P157fs
Pat_45	Pre-Treatment	SMC6	79677	37	2	17898356	17898356	Frame_Shift_Del	DEL	T	-	7	248	c.1180delA	c.(1180-1182)AGTfs	p.S394fs
Pat_45	Pre-Treatment	ALMS1	7840	37	2	73786106	73786108	In_Frame_Del	DEL	TGC	-	8	93	10224_10226delT	(10222-10227)AGTGCT>A	p.A3413del
Pat_45	Pre-Treatment	EIF2AK3	9451	37	2	88926730	88926732	In_Frame_Del	DEL	CAG	-	4	5	c.61_63delCTG	c.(61-63)CTGdel	p.L21del
Pat_45	Pre-Treatment	XIRP2	129446	37	2	168104998	168105000	In_Frame_Del	DEL	CCT	-	8	202	.7096_7098delCC	c.(7096-7098)CCTdel	p.P2370del
Pat_45	Pre-Treatment	CYP20A1	57404	37	2	204150380	204150380	Frame_Shift_Del	DEL	A	-	11	229	c.896delA	c.(895-897)CAAfs	p.Q299fs
Pat_45	Pre-Treatment	DSTN	11034	37	20	17581679	17581680	Frame_Shift_Ins	INS	-	T	7	350	c.300_301insT	c.(298-303)ATGTTTfs	p.M100fs
Pat_45	Pre-Treatment	TMEM90B	79953	37	20	24524183	24524185	In_Frame_Del	DEL	GGA	-	10	318	c.450_452delGGA	c.(448-453)GTGGAG>GTG	p.E155del
Pat_45	Pre-Treatment	SH3BGR	6450	37	21	40823995	40823995	Frame_Shift_Del	DEL	G	-	7	523	c.162delG	c.(160-162)TTGfs	p.L54fs
Pat_45	Pre-Treatment	COL18A1	80781	37	21	46925143	46925143	Frame_Shift_Del	DEL	C	-	2	4	c.4200delC	c.(4198-4200)GGCfs	p.G1400fs
Pat_45	Pre-Treatment	ITPR1	3708	37	3	4753512	4753512	Frame_Shift_Del	DEL	T	-	2	4	c.5036delT	c.(5035-5037)CTGfs	p.L1679fs
Pat_45	Pre-Treatment	NCKIPSD	51517	37	3	48723233	48723233	Frame_Shift_Del	DEL	C	-	4	8	c.8delG	c.(7-9)CGCfs	p.R3fs
Pat_45	Pre-Treatment	UROC1	131669	37	3	126236513	126236513	Frame_Shift_Del	DEL	G	-	4	2	c.50delC	c.(49-51)CCAfs	p.P17fs
Pat_45	Pre-Treatment	MRAS	22808	37	3	138121035	138121037	In_Frame_Del	DEL	AGA	-	12	809	c.551_553delAGA	c.(550-555)CAGAAG>CAG	p.K189del
Pat_45	Pre-Treatment	ATR	545	37	3	142254993	142254994	Frame_Shift_Del	DEL	GG	-	8	259	c.3775_3776delCC	c.(3775-3777)CCAfs	p.P1259fs
Pat_45	Pre-Treatment	PCOLCE2	26577	37	3	142548586	142548586	Frame_Shift_Del	DEL	T	-	8	508	c.813delA	c.(811-813)AAAfs	p.K271fs
Pat_45	Pre-Treatment	CYP4V2	285440	37	4	187118244	187118245	Frame_Shift_Ins	INS	-	T	15	409	c.564_565insT	c.(562-567)TGCTTTfs	p.C188fs
Pat_45	Pre-Treatment	LRRC14B	389257	37	5	191802	191803	Frame_Shift_Del	DEL	CG	-	4	2	c.149_150delCG	c.(148-150)ACGfs	p.T50fs
Pat_45	Pre-Treatment	ZFR	51663	37	5	32419951	32419953	In_Frame_Del	DEL	GGT	-	8	375	c.393_395delACC	c.(391-396)CCACCC>CCC	.131_132PP>I
Pat_45	Pre-Treatment	MCC	4163	37	5	112824048	112824049	In_Frame_Ins	INS	-	GCC	3	5	c.63_64insGGC	c.(61-66)insGGC	p.21_22insG

Pat_45	Pre-Treatment	ZNF608	57507	37	5	124079813	124079815	In_Frame_Del	DEL	CTC	-	9	423	c.868_870delGAG	c.(868-870)GAGdel	p.E290del
Pat_45	Pre-Treatment	ZNF354A	6940	37	5	178140336	178140336	Frame_Shift_Del	DEL	G	-	8	325	c.543delC	c.(541-543)CCCfs	p.P181fs
Pat_45	Pre-Treatment	TULP1	7287	37	6	35479547	35479547	Frame_Shift_Del	DEL	G	-	4	2	c.227delC	c.(226-228)CCAfs	p.P76fs
Pat_45	Pre-Treatment	SEC63	11231	37	6	108214774	108214774	Frame_Shift_Del	DEL	T	-	8	95	c.1586delA	c.(1585-1587)AAGfs	p.K529fs
Pat_45	Pre-Treatment	RSPH4A	345895	37	6	116951612	116951612	Frame_Shift_Del	DEL	C	-	7	397	c.1813delC	c.(1813-1815)CCCfs	p.P605fs
Pat_45	Pre-Treatment	ELFN1	392617	37	7	1784529	1784529	Frame_Shift_Del	DEL	C	-	2	4	c.297delC	c.(295-297)ATCfs	p.I99fs
Pat_45	Pre-Treatment	PEX1	5189	37	7	92146721	92146721	Frame_Shift_Del	DEL	T	-	13	310	c.1108delA	c.(1108-1110)ATTfs	p.I370fs
Pat_45	Pre-Treatment	LUC7L2	51631	37	7	139094365	139094366	Frame_Shift_Del	DEL	AG	-	7	137	c.744_745delAG	c.(742-747)GAAGAGfs	p.E248fs
Pat_45	Pre-Treatment	MLL3	58508	37	7	151874148	151874148	Frame_Shift_Del	DEL	T	-	13	221	c.8390delA	c.(8389-8391)AAGfs	p.K2797fs
Pat_45	Pre-Treatment	ADAM28	10863	37	8	24167472	24167473	Frame_Shift_Ins	INS	-	A	8	314	c.216_217insA	c.(214-219)TTGAAAfs	p.L72fs
Pat_45	Pre-Treatment	TP53INP1	94241	37	8	95952409	95952411	In_Frame_Del	DEL	TCT	-	7	139	c.150_152delAGA	.(148-153)GAAGAG>GA	p.50_51EE>E
Pat_45	Post-Resistance	CPSF3L	54973	37	1	1256424	1256424	Frame_Shift_Del	DEL	G	-	8	524	c.78delC	c.(76-78)GGCfs	p.G26fs
Pat_45	Post-Resistance	FOXJ3	22887	37	1	42744103	42744104	Frame_Shift_Del	DEL	GG	-	7	112	c.284_285delCC	c.(283-285)CCCfs	p.P95fs
Pat_45	Post-Resistance	PTCH2	8643	37	1	45288194	45288194	Frame_Shift_Del	DEL	G	-	8	89	c.3505delC	c.(3505-3507)CTGfs	p.L1169fs
Pat_45	Post-Resistance	AGL	178	37	1	100378028	100378028	Frame_Shift_Del	DEL	A	-	10	148	c.3904delA	c.(3904-3906)AAAfs	p.K1302fs
Pat_45	Post-Resistance	TCHHL1	126637	37	1	152058653	152058654	Frame_Shift_Del	DEL	AA	-	7	520	c.1504_1505delTT	c.(1504-1506)TTAfs	p.L502fs
Pat_45	Post-Resistance	RPTN	126638	37	1	152127312	152127313	Frame_Shift_Del	DEL	GA	-	11	890	c.2262_2263delTC	c.(2260-2265)CATCAGfs	p.H754fs
Pat_45	Post-Resistance	EDEM3	80267	37	1	184692951	184692951	Frame_Shift_Del	DEL	T	-	7	333	c.787delA	c.(787-789)AGAfs	p.R263fs
Pat_45	Post-Resistance	PRG4	10216	37	1	186276433	186276434	In_Frame_Ins	INS	-	AGG	8	586	.1582_1583insAG	(1582-1584)AAG>AAGGA	p.528_529insE
Pat_45	Post-Resistance	IPO9	55705	37	1	201843998	201844000	In_Frame_Del	DEL	GAG	-	11	151	.2872_2874delGA	c.(2872-2874)GAGdel	p.E962del
Pat_45	Post-Resistance	TBCE	6905	37	1	235543449	235543449	Frame_Shift_Del	DEL	G	-	8	537	c.85delG	c.(85-87)GTCfs	p.V29fs
Pat_45	Post-Resistance	HEATR1	55127	37	1	236739561	236739562	Frame_Shift_Del	DEL	TA	-	7	311	c.3041_3042delTA	c.(3040-3042)ATAfs	p.I1014fs
Pat_45	Post-Resistance	KIAA1217	56243	37	10	24833923	24833923	Frame_Shift_Del	DEL	C	-	8	526	c.5225delC	c.(5224-5226)GCCfs	p.A1742fs
Pat_45	Post-Resistance	NANOS1	340719	37	10	120789523	120789525	In_Frame_Del	DEL	CGG	-	4	5	c.210_212delCGG	c.(208-213)AACGGC>AAC	p.G74del
Pat_45	Post-Resistance	APBB1	322	37	11	6423808	6423808	Frame_Shift_Del	DEL	C	-	8	224	c.1252delG	c.(1252-1254)GAAfs	p.E418fs
Pat_45	Post-Resistance	KBTBD4	55709	37	11	47594883	47594883	Frame_Shift_Del	DEL	C	-	9	271	c.1156delG	c.(1156-1158)GAGfs	p.E386fs
Pat_45	Post-Resistance	FNBP4	23360	37	11	47744589	47744591	In_Frame_Del	DEL	GGA	-	5	11	.2742_2744delTC	.(2740-2745)CCTCCA>CC	.914_915PP>
Pat_45	Post-Resistance	FNBP4	23360	37	11	47788664	47788669	In_Frame_Del	DEL	GGTGGT	-	4	4	172_177delACCA	c.(172-177)ACCACCdel	p.TT58del
Pat_45	Post-Resistance	PRB2	653247	37	12	11546788	11546790	In_Frame_Del	DEL	GGA	-	11	204	c.222_224delTCC	c.(220-225)CCTCCA>CCA	p.74_75PP>P
Pat_45	Post-Resistance	GRIP1	23426	37	12	66771014	66771014	Frame_Shift_Del	DEL	C	-	7	642	c.2517delG	c.(2515-2517)TGGfs	p.W839fs
Pat_45	Post-Resistance	DUSP6	1848	37	12	89744437	89744438	Frame_Shift_Del	DEL	TG	-	8	471	c.765_766delCA	c.(763-768)TACAAGfs	p.Y255fs
Pat_45	Post-Resistance	OLFM4	10562	37	13	53624374	53624376	In_Frame_Del	DEL	ACA	-	7	194	.1001_1003delAC	.(1000-1005)TACAAC>TA	p.N337del
Pat_45	Post-Resistance	TEP1	7011	37	14	20852647	20852647	Frame_Shift_Del	DEL	C	-	12	770	c.3242delG	c.(3241-3243)GGTfs	p.G1081fs
Pat_45	Post-Resistance	OR4E2	26686	37	14	22133534	22133535	Frame_Shift_Del	DEL	AA	-	8	474	c.238_239delAA	c.(238-240)AAGfs	p.K80fs
Pat_45	Post-Resistance	MAP4K5	11183	37	14	50952892	50952892	Frame_Shift_Del	DEL	G	-	2	4	c.187delC	c.(187-189)CAAfs	p.Q63fs
Pat_45	Post-Resistance	BTBD7	55727	37	14	93717858	93717858	Frame_Shift_Del	DEL	G	-	7	662	c.1893delC	c.(1891-1893)ATCfs	p.I631fs
Pat_45	Post-Resistance	TNFAIP2	7127	37	14	103599784	103599786	In_Frame_Del	DEL	AGC	-	8	236	.1631_1633delAG	(1630-1635)GAGCAG>GA	p.Q548del
Pat_45	Post-Resistance	MGA	23269	37	15	42003383	42003385	In_Frame_Del	DEL	CAG	-	10	172	.2920_2922delCA	c.(2920-2922)CAGdel	p.Q981del
Pat_45	Post-Resistance	CHRNA5	1138	37	15	78879004	78879005	Frame_Shift_Del	DEL	AA	-	7	429	c.276_277delAA	c.(274-279)TTAATGfs	p.L92fs
Pat_45	Post-Resistance	CHD2	1106	37	15	93480819	93480819	Frame_Shift_Del	DEL	A	-	9	127	c.515delA	c.(514-516)CAAfs	p.Q172fs
Pat_45	Post-Resistance	SCARF1	8578	37	17	1542127	1542129	In_Frame_Del	DEL	CAG	-	8	93	.1335_1337delCT	(1333-1338)TGCTGG>TG	p.C445del
Pat_45	Post-Resistance	PELP1	27043	37	17	4575894	4575894	Frame_Shift_Del	DEL	G	-	8	117	c.2392delC	c.(2392-2394)CTGfs	p.L798fs
Pat_45	Post-Resistance	ENO3	2027	37	17	4859894	4859894	Frame_Shift_Del	DEL	G	-	10	419	c.1094delG	c.(1093-1095)TGGfs	p.W365fs
Pat_45	Post-Resistance	TP53	7157	37	17	7579378	7579379	Frame_Shift_Ins	INS	-	T	16	53	c.308_309insA	c.(307-309)TACfs	p.Y103fs
Pat_45	Post-Resistance	KDM6B	23135	37	17	7751859	7751861	In_Frame_Del	DEL	CAC	-	7	101	.2253_2255delCA	(2251-2256)GTCACC>GT	p.T762del
Pat_45	Post-Resistance	KLHL11	55175	37	17	40021586	40021588	In_Frame_Del	DEL	GCC	-	2	4	c.36_38delGGC	c.(34-39)GCGGCC>GCC	p.12_13AA>A
Pat_45	Post-Resistance	PLCD3	113026	37	17	43192760	43192762	In_Frame_Del	DEL	TCC	-	9	51	.1509_1511delGG	.(1507-1512)GAGGAT>GA	p.E503del

Pat_45	Post-Resistance	BRIP1	83990	37	17	59876512	59876512	Frame_Shift_Del	DEL	A	-	9	182	c.1289delT	c.(1288-1290)ATAfs	p.I430fs
Pat_45	Post-Resistance	TANC2	26115	37	17	61278171	61278174	Frame_Shift_Del	DEL	CTGA	-	8	941	.400_403delCTG	c.(400-405)CTGACTfs	p.L134fs
Pat_45	Post-Resistance	ACE	1636	37	17	61560474	61560474	Frame_Shift_Del	DEL	G	-	8	877	c.1427delG	c.(1426-1428)TGGfs	p.W476fs
Pat_45	Post-Resistance	DNAH17	8632	37	17	76425217	76425217	Frame_Shift_Del	DEL	G	-	7	439	c.3390delC	c.(3388-3390)CCCfs	p.P1130fs
Pat_45	Post-Resistance	USP36	57602	37	17	76799858	76799859	Frame_Shift_Ins	INS	-	C	16	230	c.2418_2419insG	c.(2416-2421)CAGAGCfs	p.Q806fs
Pat_45	Post-Resistance	DOT1L	84444	37	19	2191199	2191199	Frame_Shift_Del	DEL	C	-	7	452	c.453delC	c.(451-453)ATCfs	p.I151fs
Pat_45	Post-Resistance	SLC5A5	6528	37	19	18001737	18001737	Frame_Shift_Del	DEL	G	-	7	745	c.1694delG	c.(1693-1695)TGGfs	p.W565fs
Pat_45	Post-Resistance	ZFP36	7538	37	19	39898948	39898950	In_Frame_Del	DEL	CAC	-	8	474	c.590_592delCAC	c.(589-594)TCACCA>TCA	p.P201del
Pat_45	Post-Resistance	ZNF780B	163131	37	19	40540840	40540842	In_Frame_Del	DEL	TTT	-	7	364	.1924_1926delAA	c.(1924-1926)AAAdel	p.K642del
Pat_45	Post-Resistance	TBC1D17	79735	37	19	50385607	50385607	Frame_Shift_Del	DEL	C	-	8	384	c.748delC	c.(748-750)CCCfs	p.P250fs
Pat_45	Post-Resistance	PTPRH	5794	37	19	55718055	55718055	Splice_Site	DEL	A	-	8	339	c.352_splice	c.e3+1	p.A118_splice
Pat_45	Post-Resistance	SLC9A4	389015	37	2	103149137	103149137	Frame_Shift_Del	DEL	A	-	11	151	c.2387delA	c.(2386-2388)CAAfs	p.Q796fs
Pat_45	Post-Resistance	GTF3C3	9330	37	2	197641204	197641204	Frame_Shift_Del	DEL	C	-	9	231	c.1540delG	c.(1540-1542)GAAfs	p.E514fs
Pat_45	Post-Resistance	TNP1	7141	37	2	217724625	217724626	Frame_Shift_Del	DEL	CG	-	7	505	c.132_133delCG	c.(130-135)GGCGATfs	p.G44fs
Pat_45	Post-Resistance	DGCR8	54487	37	22	20074025	20074026	Frame_Shift_Del	DEL	AT	-	7	279	c.539_540delAT	c.(538-540)GATfs	p.D180fs
Pat_45	Post-Resistance	TBC1D10A	83874	37	22	30691732	30691732	Frame_Shift_Del	DEL	C	-	7	187	c.518delG	c.(517-519)GGCfs	p.G173fs
Pat_45	Post-Resistance	SCUBE1	80274	37	22	43619184	43619184	Frame_Shift_Del	DEL	G	-	8	558	c.1246delC	c.(1246-1248)CGGfs	p.R416fs
Pat_45	Post-Resistance	ABHD6	57406	37	3	58260511	58260511	Frame_Shift_Del	DEL	G	-	7	400	c.650delG	c.(649-651)TGCfs	p.C217fs
Pat_45	Post-Resistance	CPOX	1371	37	3	98304296	98304297	Frame_Shift_Del	DEL	GA	-	8	745	c.1160_1161delTC	c.(1159-1161)CTCfs	p.L387fs
Pat_45	Post-Resistance	MYH15	22989	37	3	108139933	108139933	Splice_Site	DEL	A	-	8	256	c.3889_splice	c.e29+1	.G1297_splice
Pat_45	Post-Resistance	MRAS	22808	37	3	138121035	138121037	In_Frame_Del	DEL	AGA	-	7	386	c.551_553delAGA	.(550-555)CAGAAG>CA	p.K189del
Pat_45	Post-Resistance	PKD2	5311	37	4	88929174	88929176	In_Frame_Del	DEL	GAG	-	6	3	c.289_291delGAG	c.(289-291)GAGdel	p.E102del
Pat_45	Post-Resistance	CXXC4	80319	37	4	105412094	105412096	In_Frame_Del	DEL	GAG	-	8	95	c.357_359delCTC	c.(355-360)TCCTCG>TCG	.119_120SS>
Pat_45	Post-Resistance	SCLT1	132320	37	4	129864163	129864163	Frame_Shift_Del	DEL	T	-	8	188	c.1620delA	c.(1618-1620)AAAfs	p.K540fs
Pat_45	Post-Resistance	PDLIM4	8572	37	5	131606779	131606779	Frame_Shift_Del	DEL	C	-	8	440	c.499delC	c.(499-501)CCCfs	p.P167fs
Pat_45	Post-Resistance	TXNDC15	79770	37	5	134231988	134231989	Frame_Shift_Del	DEL	TC	-	7	121	c.760_761delTC	c.(760-762)TCTfs	p.S254fs
Pat_45	Post-Resistance	PCDHA6	56142	37	5	140208053	140208053	Frame_Shift_Del	DEL	T	-	8	476	c.377delT	c.(376-378)ATTfs	p.I126fs
Pat_45	Post-Resistance	VARS2	57176	37	6	30883771	30883771	Frame_Shift_Del	DEL	G	-	7	1285	c.520delG	c.(520-522)GGGfs	p.G174fs
Pat_45	Post-Resistance	COL9A1	1297	37	6	70964878	70964878	Frame_Shift_Del	DEL	C	-	8	383	c.1586delG	c.(1585-1587)GGTfs	p.G529fs
Pat_45	Post-Resistance	MDN1	23195	37	6	90374221	90374221	Frame_Shift_Del	DEL	C	-	8	466	c.14221delG	c.(14221-14223)GAGfs	p.E4741fs
Pat_45	Post-Resistance	SUN1	23353	37	7	883110	883110	Frame_Shift_Del	DEL	C	-	8	1502	c.611delC	c.(610-612)GCCfs	p.A204fs
Pat_45	Post-Resistance	MNX1	3110	37	7	156802730	156802732	In_Frame_Del	DEL	GCC	-	4	8	c.313_315delGGC	c.(313-315)GGCdel	p.G105del
Pat_45	Post-Resistance	TP53INP1	94241	37	8	95952409	95952411	In_Frame_Del	DEL	TCT	-	10	125	c.150_152delAGA	.(148-153)GAAGAG>GA	p.50_51EE>E
Pat_45	Post-Resistance	CYC1	1537	37	8	145152139	145152141	In_Frame_Del	DEL	TGA	-	8	114	c.878_880delTGA	c.(877-882)TTGATG>TTG	p.M296del
Pat_45	Post-Resistance	ELAVL2	1993	37	9	23701410	23701410	Frame_Shift_Del	DEL	G	-	9	1190	c.680delC	c.(679-681)CCAfs	p.P227fs
Pat_45	Post-Resistance	PIGO	84720	37	9	35091693	35091693	Frame_Shift_Del	DEL	G	-	9	181	c.2191delC	c.(2191-2193)CGTfs	p.R731fs
Pat_45	Post-Resistance	GPR144	347088	37	9	127239329	127239331	In_Frame_Del	DEL	CTG	-	4	3	.2842_2844delCT	c.(2842-2844)CTGdel	p.L948del
Pat_45	Post-Resistance	ANGPTL2	23452	37	9	129870357	129870357	Frame_Shift_Del	DEL	G	-	7	87	c.654delC	c.(652-654)CCCfs	p.P218fs
Pat_45	Post-Resistance	C9orf69	90120	37	9	139008444	139008446	In_Frame_Del	DEL	CAG	-	8	77	c.375_377delCTG	.(373-378)TGCTGG>TG	p.C125del
Pat_45	Post-Resistance	GYG2	8908	37	X	2799201	2799202	Frame_Shift_Ins	INS	-	GGAA	4	7	1453_1454insGG	c.(1453-1455)GGGfs	p.G485fs
Pat_51	Pre-Treatment	TARS2	80222	37	1	150460373	150460374	Frame_Shift_Ins	INS	-	T	7	125	c.106_107insT	c.(106-108)CTTfs	p.L36fs
Pat_51	Pre-Treatment	FAM5B	57795	37	1	177250096	177250097	Frame_Shift_Ins	INS	-	C	7	45	c.1784_1785insC	c.(1783-1785)GGCfs	p.G595fs
Pat_51	Pre-Treatment	TSPAN4	7106	37	11	864443	864445	In_Frame_Del	DEL	CTG	-	9	102	c.262_264delCTG	c.(262-264)CTGdel	p.L92del
Pat_51	Pre-Treatment	TSPAN10	83882	37	17	79614933	79614936	Splice_Site	DEL	TAAC	-	9	17	c.681_splice	c.e3-1	p.F227_splice
Pat_51	Pre-Treatment	EPN1	29924	37	19	56190126	56190150	Frame_Shift_Del	DEL	TACAACG	-	11	34	CCTCACCTACAA	CCTCACCTACAACGTTG	p.D45fs
Pat_51	Pre-Treatment	BLCAP	10904	37	20	36147480	36147480	Frame_Shift_Del	DEL	G	-	15	33	c.97delC	c.(97-99)CTGfs	p.L33fs
Pat_51	Pre-Treatment	BAP1	8314	37	3	52442559	52442562	Frame_Shift_Del	DEL	GACC	-	14	1	.183_186delGGT	c.(181-186)AAGGTCfs	p.K61fs

Pat_51	Pre-Treatment	HLA-A	3105	37	6	29911319	29911319	Frame_Shift_Del	DEL	G	-	7	52	c.618delG	c.(616-618)ACGfs	p.T206fs
Pat_51	Pre-Treatment	PRSS35	167681	37	6	84233673	84233702	In_Frame_Del	DEL	AGGACTAT	-	9	75	ATGGAAAGGACT	GATGGAAAGGACTATGT	GKDYVKGS1
Pat_51	Pre-Treatment	ZAN	7455	37	7	100385562	100385596	Frame_Shift_Del	DEL	CTTGCAAG	-	8	28	GCTACCGCTTGC	AGCTACCGCTTGCAAG	p.G2344fs
Pat_53	Pre-Treatment	PLEKHG5	57449	37	1	6536011	6536013	In_Frame_Del	DEL	CTC	-	10	330	c.295_297delGAG	c.(295-297)GAGdel	p.E99del
Pat_53	Pre-Treatment	CAMTA1	23261	37	1	7811329	7811329	Frame_Shift_Del	DEL	A	-	11	995	c.4760delA	c.(4759-4761)CAAfs	p.Q1587fs
Pat_53	Pre-Treatment	PRDM2	7799	37	1	14108749	14108749	Frame_Shift_Del	DEL	A	-	29	1122	c.4459delA	c.(4459-4461)AAAfs	p.K1487fs
Pat_53	Pre-Treatment	MST1P9	11223	37	1	17085995	17085996	Frame_Shift_Ins	INS	-	C	9	175	c.901_902insG	c.(901-903)GCGfs	p.A301fs
Pat_53	Pre-Treatment	MST1P9	11223	37	1	17086085	17086086	Frame_Shift_Ins	INS	-	C	13	28	c.811_812insG	c.(811-813)GCGfs	p.A271fs
Pat_53	Pre-Treatment	ZBTB40	9923	37	1	22838561	22838563	In_Frame_Del	DEL	AAG	-	9	171	.2395_2397delAA	c.(2395-2397)AAGdel	p.K803del
Pat_53	Pre-Treatment	ARID1A	8289	37	1	27100182	27100184	In_Frame_Del	DEL	GCA	-	9	214	.3978_3980delGC	.(3976-3981)CCGCAG>CC	p.Q1334del
Pat_53	Pre-Treatment	SFRS4	6429	37	1	29475219	29475221	In_Frame_Del	DEL	CTT	-	7	241	.1186_1188delAA	c.(1186-1188)AAGdel	p.K396del
Pat_53	Pre-Treatment	TMCO2	127391	37	1	40713708	40713709	Frame_Shift_Del	DEL	TC	-	8	562	c.43_44delTC	c.(43-45)TCTfs	p.S15fs
Pat_53	Pre-Treatment	CCDC30	728621	37	1	43002200	43002201	Frame_Shift_Del	DEL	AG	-	37	269	c.45_46delAG	c.(43-48)AAAGAGfs	p.K15fs
Pat_53	Pre-Treatment	EIF2B3	8891	37	1	45407182	45407182	Frame_Shift_Del	DEL	T	-	10	341	c.450delA	c.(448-450)AAAfs	p.K150fs
Pat_53	Pre-Treatment	IPP	3652	37	1	46184897	46184898	Frame_Shift_Del	DEL	AC	-	15	438	c.1163_1164delGT	c.(1162-1164)TGTfs	p.C388fs
Pat_53	Pre-Treatment	IPP	3652	37	1	46193446	46193446	Frame_Shift_Del	DEL	C	-	9	694	c.905delG	c.(904-906)GGTfs	p.G302fs
Pat_53	Pre-Treatment	LRRC41	10489	37	1	46752129	46752129	Frame_Shift_Del	DEL	A	-	9	234	c.400delT	c.(400-402)TCCfs	p.S134fs
Pat_53	Pre-Treatment	BEND5	79656	37	1	49201966	49201967	Frame_Shift_Ins	INS	-	T	11	238	c.1052_1053insA	c.(1051-1053)AAGfs	p.K351fs
Pat_53	Pre-Treatment	LRRIQ3	127255	37	1	74575212	74575213	Frame_Shift_Ins	INS	-	T	15	307	c.732_733insA	c.(730-735)AAACAGfs	p.K244fs
Pat_53	Pre-Treatment	TNNI3K	51086	37	1	74957824	74957826	In_Frame_Del	DEL	CTT	-	10	577	.2225_2227delCT	.(2224-2229)CCTTCT>CC	p.S746del
Pat_53	Pre-Treatment	RBMXL1	494115	37	1	89448604	89448605	Frame_Shift_Ins	INS	-	GG	26	787	c.905_906insCC	c.(904-906)CCAfs	p.P302fs
Pat_53	Pre-Treatment	RBMXL1	494115	37	1	89449509	89449509	Frame_Shift_Del	DEL	T	-	74	537	c.1delA	c.(1-3)ATGfs	p.M1fs
Pat_53	Pre-Treatment	EVI5	7813	37	1	93159366	93159366	Frame_Shift_Del	DEL	T	-	7	365	c.1222delA	c.(1222-1224)ATGfs	p.M408fs
Pat_53	Pre-Treatment	KIAA1324	57535	37	1	109727724	109727725	Frame_Shift_Del	DEL	AC	-	9	629	c.1010_1011delAC	c.(1009-1011)TACfs	p.Y337fs
Pat_53	Pre-Treatment	GSTM3	2947	37	1	110280279	110280279	Frame_Shift_Del	DEL	T	-	8	623	c.467delA	c.(466-468)AAGfs	p.K156fs
Pat_53	Pre-Treatment	RPTN	126638	37	1	152127881	152127884	Frame_Shift_Del	DEL	TGTC	-	9	2980	1691_1694delGAC	c.(1690-1695)AGACAAfs	p.R564fs
Pat_53	Pre-Treatment	ASH1L	55870	37	1	155307999	155308000	Frame_Shift_Ins	INS	-	T	10	306	c.8698_8699insA	c.(8698-8700)ACAfs	p.T2900fs
Pat_53	Pre-Treatment	KIAA0907	22889	37	1	155886422	155886423	Frame_Shift_Del	DEL	CT	-	21	550	.1546_1547delAG	c.(1546-1548)AGGfs	p.R516fs
Pat_53	Pre-Treatment	SLAMF1	6504	37	1	160589601	160589601	Frame_Shift_Del	DEL	T	-	19	869	c.829delA	c.(829-831)AGCfs	p.S277fs
Pat_53	Pre-Treatment	PVRL4	81607	37	1	161044057	161044059	In_Frame_Del	DEL	CAC	-	8	312	.1105_1107delGT	c.(1105-1107)GTGdel	p.V369del
Pat_53	Pre-Treatment	POU2F1	5451	37	1	167385016	167385018	In_Frame_Del	DEL	CCA	-	10	583	.2201_2203delCC	.(2200-2205)TCCACC>TC	p.T738del
Pat_53	Pre-Treatment	CACNA1E	777	37	1	181680102	181680103	Frame_Shift_Del	DEL	AG	-	14	263	.1068_1069delAG	c.(1066-1071)AAAGAGfs	p.K356fs
Pat_53	Pre-Treatment	APOBEC4	403314	37	1	183616826	183616828	In_Frame_Del	DEL	TTC	-	11	662	.1089_1091delGA	.(1087-1092)AAGAAA>AA	.363_364KK>
Pat_53	Pre-Treatment	PRG4	10216	37	1	186276524	186276526	In_Frame_Del	DEL	AGG	-	7	491	.1673_1675delAG	(1672-1677)AAGGAG>AA	p.E559del
Pat_53	Pre-Treatment	IPO9	55705	37	1	201843998	201844000	In_Frame_Del	DEL	GAG	-	7	209	.2872_2874delGA	c.(2872-2874)GAGdel	p.E962del
Pat_53	Pre-Treatment	TMEM63A	9725	37	1	226034840	226034842	In_Frame_Del	DEL	CTG	-	12	414	.2323_2325delCA	c.(2323-2325)CAGdel	p.Q775del
Pat_53	Pre-Treatment	PCDH15	65217	37	10	55587198	55587200	In_Frame_Del	DEL	GGC	-	11	215	.4320_4322delGC	.(4318-4323)CCGCCT>CC	1440_1441PP>
Pat_53	Pre-Treatment	ANK3	288	37	10	61828745	61828747	In_Frame_Del	DEL	GTG	-	7	161	11892_11894delC	11890-11895)ACCACT>A	3964_3965TT>
Pat_53	Pre-Treatment	FAS	355	37	10	90768708	90768708	Frame_Shift_Del	DEL	T	-	10	3598	c.397delT	c.(397-399)TTTfs	p.F133fs
Pat_53	Pre-Treatment	TM9SF3	56889	37	10	98336475	98336475	Frame_Shift_Del	DEL	T	-	8	481	c.214delA	c.(214-216)AGTfs	p.S72fs
Pat_53	Pre-Treatment	C10orf62	414157	37	10	99350236	99350237	Frame_Shift_Ins	INS	-	CA	9	278	c.582_583insCA	c.(580-585)AATCACfs	p.N194fs
Pat_53	Pre-Treatment	LOC653544	653544	37	10	135491013	135491014	Frame_Shift_Ins	INS	-	T	8	266	c.624_625insT	c.(622-627)GCCAGGfs	p.A208fs
Pat_53	Pre-Treatment	LOC653544	653544	37	10	135491036	135491036	Frame_Shift_Del	DEL	G	-	14	268	c.647delG	c.(646-648)AGGfs	p.R216fs
Pat_53	Pre-Treatment	TSPAN4	7106	37	11	864443	864445	In_Frame_Del	DEL	CTG	-	10	226	c.262_264delCTG	c.(262-264)CTGdel	p.L92del
Pat_53	Pre-Treatment	OR10A5	144124	37	11	6867223	6867225	In_Frame_Del	DEL	TTC	-	10	212	c.310_312delTTC	c.(310-312)TTCdel	p.F108del
Pat_53	Pre-Treatment	RARRES3	5920	37	11	63313709	63313709	Frame_Shift_Del	DEL	A	-	11	526	c.476delA	c.(475-477)CAAfs	p.Q159fs
Pat_53	Pre-Treatment	VEGFB	7423	37	11	64004663	64004663	Frame_Shift_Del	DEL	A	-	14	595	c.379delA	c.(379-381)AAAfs	p.K127fs

Pat_53	Pre-Treatment	UVRAG	7405	37	11	75727924	75727924	Frame_Shift_Del	DEL	T	-	7	515	c.1126delT	c.(1126-1128)TTTfs	p.F376fs
Pat_53	Pre-Treatment	CD3G	917	37	11	118220583	118220583	Frame_Shift_Del	DEL	A	-	16	225	c.205delA	c.(205-207)AAAfs	p.K69fs
Pat_53	Pre-Treatment	MLL	4297	37	11	118344185	118344186	Frame_Shift_Ins	INS	-	C	7	690	c.2311_2312insC	c.(2311-2313)ACCfs	p.T771fs
Pat_53	Pre-Treatment	CHEK1	1111	37	11	125505377	125505378	Frame_Shift_Ins	INS	-	A	27	827	c.667_668insA	c.(667-669)GAAfs	p.E223fs
Pat_53	Pre-Treatment	SRPR	6734	37	11	126137087	126137087	Frame_Shift_Del	DEL	T	-	26	1121	c.509delA	c.(508-510)AAGfs	p.K170fs
Pat_53	Pre-Treatment	PRDM10	56980	37	11	129772249	129772251	In_Frame_Del	DEL	TGG	-	8	651	.3440_3442delCC	.(3439-3444)ACCAAC>AA	p.T1147del
Pat_53	Pre-Treatment	GLB1L3	112937	37	11	134181005	134181005	Frame_Shift_Del	DEL	C	-	7	1271	c.1228delC	c.(1228-1230)CCCfs	p.P410fs
Pat_53	Pre-Treatment	LRRC23	10233	37	12	7015719	7015719	Frame_Shift_Del	DEL	C	-	10	2402	c.383delC	c.(382-384)GCCfs	p.A128fs
Pat_53	Pre-Treatment	PRB2	653247	37	12	11546506	11546508	In_Frame_Del	DEL	TTG	-	10	695	c.504_506delCAA	c.(502-507)AACAAG>AAG	p.N168del
Pat_53	Pre-Treatment	CASC1	55259	37	12	25314066	25314068	In_Frame_Del	DEL	CTC	-	7	864	c.67_69delGAG	c.(67-69)GAGdel	p.E23del
Pat_53	Pre-Treatment	SFRS2IP	9169	37	12	46320707	46320708	Frame_Shift_Del	DEL	TC	-	8	397	c.2776_2777delGA	c.(2776-2778)GAAfs	p.E926fs
Pat_53	Pre-Treatment	CCNT1	904	37	12	49087434	49087436	In_Frame_Del	DEL	ATG	-	47	1644	.1561_1563delCA	c.(1561-1563)CATdel	p.H521del
Pat_53	Pre-Treatment	OR10A7	121364	37	12	55615114	55615116	In_Frame_Del	DEL	CTT	-	10	455	c.306_308delCTT	c.(304-309)TACTTC>TAC	p.F107del
Pat_53	Pre-Treatment	IKZF4	64375	37	12	56428977	56428978	Frame_Shift_Del	DEL	GG	-	7	1087	c.1620_1621delGG	c.(1618-1623)CTGGACfs	p.L540fs
Pat_53	Pre-Treatment	B4GALNT1	2583	37	12	58025102	58025103	Frame_Shift_Ins	INS	-	C	8	228	c.263_264insG	c.(262-264)GGCfs	p.G88fs
Pat_53	Pre-Treatment	MSI1	4440	37	12	120800902	120800903	Frame_Shift_Ins	INS	-	C	7	722	c.345_346insG	c.(343-348)GGGCTGfs	p.G115fs
Pat_53	Pre-Treatment	POP5	51367	37	12	121017154	121017156	In_Frame_Del	DEL	CTC	-	7	364	c.457_459delGAG	c.(457-459)GAGdel	p.E153del
Pat_53	Pre-Treatment	SBNO1	55206	37	12	123794283	123794283	Frame_Shift_Del	DEL	T	-	19	422	c.3416delA	c.(3415-3417)AATfs	p.N1139fs
Pat_53	Pre-Treatment	POLE	5426	37	12	133220099	133220100	Frame_Shift_Del	DEL	CA	-	14	762	c.4337_4338delTG	c.(4336-4338)GTGfs	p.V1446fs
Pat_53	Pre-Treatment	TSC22D1	8848	37	13	45148706	45148708	In_Frame_Del	DEL	TGC	-	7	250	.1503_1505delGC	.(1501-1506)CAGCAA>CA	.501_502QQ>
Pat_53	Pre-Treatment	ZC3H13	23091	37	13	46553948	46553949	Frame_Shift_Del	DEL	CT	-	7	576	c.1911_1912delAG	c.(1909-1914)AGAGATfs	p.R637fs
Pat_53	Pre-Treatment	LRCH1	23143	37	13	47243183	47243186	Frame_Shift_Del	DEL	CCTG	-	8	1045	.471_474delCCT	c.(469-474)GCCCTGfs	p.A157fs
Pat_53	Pre-Treatment	ZIC2	7546	37	13	100635008	100635010	In_Frame_Del	DEL	CCA	-	13	96	c.690_692delCCA	.(688-693)GCCCAC>GC	p.H239del
Pat_53	Pre-Treatment	LRP10	26020	37	14	23341527	23341529	In_Frame_Del	DEL	CCT	-	14	266	c.15_17delCCT	c.(13-18)ACCCTC>ACC	p.L11del
Pat_53	Pre-Treatment	JPH4	84502	37	14	24040436	24040436	Frame_Shift_Del	DEL	C	-	23	388	c.1504delG	c.(1504-1506)GCAfs	p.A502fs
Pat_53	Pre-Treatment	PSMA6	5687	37	14	35782216	35782216	Frame_Shift_Del	DEL	A	-	11	835	c.539delA	c.(538-540)GAAfs	p.E180fs
Pat_53	Pre-Treatment	C14orf106	55320	37	14	45693722	45693722	Frame_Shift_Del	DEL	T	-	14	304	c.2068delA	c.(2068-2070)AGTfs	p.S690fs
Pat_53	Pre-Treatment	MGAT2	4247	37	14	50088327	50088327	Frame_Shift_Del	DEL	C	-	7	399	c.341delC	c.(340-342)GCCfs	p.A114fs
Pat_53	Pre-Treatment	PRKCH	5583	37	14	62014535	62014535	Frame_Shift_Del	DEL	T	-	7	1033	c.1836delT	c.(1834-1836)CCTfs	p.P612fs
Pat_53	Pre-Treatment	SIPA1L1	26037	37	14	72190482	72190484	In_Frame_Del	DEL	TCC	-	10	347	.4390_4392delTC	c.(4390-4392)TCCdel	p.S1468del
Pat_53	Pre-Treatment	C15orf24	56851	37	15	34393991	34393993	In_Frame_Del	DEL	AGC	-	14	679	c.48_50delGCT	c.(46-51)CTGCTA>CTA	p.16_17LL>L
Pat_53	Pre-Treatment	C15orf52	388115	37	15	40631782	40631782	Frame_Shift_Del	DEL	C	-	8	435	c.294delG	c.(292-294)GGGfs	p.G98fs
Pat_53	Pre-Treatment	SLTM	79811	37	15	59182564	59182565	Frame_Shift_Del	DEL	CT	-	32	519	c.1994_1995delAG	c.(1993-1995)GAGfs	p.E665fs
Pat_53	Pre-Treatment	RNF111	54778	37	15	59359142	59359144	In_Frame_Del	DEL	CAC	-	7	387	.1546_1548delCA	c.(1546-1548)CACdel	p.H520del
Pat_53	Pre-Treatment	ZNF609	23060	37	15	64972995	64972997	In_Frame_Del	DEL	CAC	-	9	632	.4096_4098delCA	c.(4096-4098)CACdel	p.H1371del
Pat_53	Pre-Treatment	SLC24A1	9187	37	15	65918177	65918179	In_Frame_Del	DEL	CTG	-	9	227	.1759_1761delCT	c.(1759-1761)CTGdel	p.L591del
Pat_53	Pre-Treatment	CPLX3	594855	37	15	75122558	75122560	In_Frame_Del	DEL	GAG	-	7	146	c.340_342delGAG	c.(340-342)GAGdel	p.E118del
Pat_53	Pre-Treatment	UBN1	29855	37	16	4910691	4910693	In_Frame_Del	DEL	AGA	-	8	932	c.698_700delAGA	.(697-702)GAGAAG>GA	p.K238del
Pat_53	Pre-Treatment	KIAA0430	9665	37	16	15729982	15729984	In_Frame_Del	DEL	CCA	-	10	509	c.360_362delTGG	.(358-363)GGTGGC>GG	.120_121GG>
Pat_53	Pre-Treatment	EIF3CL	728689	37	16	28734579	28734581	In_Frame_Del	DEL	GAG	-	12	2259	c.871_873delGAG	c.(871-873)GAGdel	p.E295del
Pat_53	Pre-Treatment	ITGAL	3683	37	16	30531249	30531251	In_Frame_Del	DEL	GCT	-	8	732	.3300_3302delGC	(3298-3303)GGGCTG>GG	p.L1106del
Pat_53	Pre-Treatment	SRCAP	10847	37	16	30736370	30736371	Frame_Shift_Ins	INS	-	C	13	486	c.5625_5626insC	c.(5623-5628)CAGCCCfs	p.Q1875fs
Pat_53	Pre-Treatment	BRD7	29117	37	16	50368678	50368679	Frame_Shift_Del	DEL	CT	-	54	778	c.830_831delAG	c.(829-831)GAGfs	p.E277fs
Pat_53	Pre-Treatment	COQ9	57017	37	16	57486732	57486734	In_Frame_Del	DEL	GAG	-	9	371	c.262_264delGAG	c.(262-264)GAGdel	p.E91del
Pat_53	Pre-Treatment	CKLF	51192	37	16	66592117	66592117	Frame_Shift_Del	DEL	T	-	7	766	c.103delT	c.(103-105)TTTfs	p.F35fs
Pat_53	Pre-Treatment	ZFP90	146198	37	16	68598462	68598463	Frame_Shift_Ins	INS	-	A	9	653	c.1772_1773insA	c.(1771-1773)CGAfs	p.R591fs
Pat_53	Pre-Treatment	NOB1	28987	37	16	69782978	69782980	In_Frame_Del	DEL	TCC	-	10	322	c.567_569delGGA	.(565-570)GAGGAA>GA	.189_190EE>

Pat_53	Pre-Treatment	ADAMTS18	170692	37	16	77356311	77356311	Frame_Shift_Del	DEL	A	-	7	305	c.2085delT	c.(2083-2085)TTTfs	p.F695fs
Pat_53	Pre-Treatment	NUP88	4927	37	17	5290964	5290964	Frame_Shift_Del	DEL	T	-	7	845	c.1796delA	c.(1795-1797)AAGfs	p.K599fs
Pat_53	Pre-Treatment	FXR2	9513	37	17	7495872	7495874	In_Frame_Del	DEL	CGG	-	12	1022	.1773_1775delCC	(1771-1776)CGCCGT>CG	.591_592RR>
Pat_53	Pre-Treatment	SUPT6H	6830	37	17	27027202	27027204	In_Frame_Del	DEL	AGC	-	19	830	.4573_4575delAG	c.(4573-4575)AGCdel	p.S1528del
Pat_53	Pre-Treatment	SUPT6H	6830	37	17	27028487	27028487	Frame_Shift_Del	DEL	A	-	7	266	c.5025delA	c.(5023-5025)GGAfs	p.G1675fs
Pat_53	Pre-Treatment	CDC27	996	37	17	45219355	45219355	Frame_Shift_Del	DEL	C	-	7	701	c.1415delG	c.(1414-1416)GGTfs	p.G472fs
Pat_53	Pre-Treatment	SPAG9	9043	37	17	49077041	49077041	Frame_Shift_Del	DEL	T	-	8	210	c.1645delA	c.(1645-1647)AGGfs	p.R549fs
Pat_53	Pre-Treatment	BZRAP1	9256	37	17	56387404	56387406	In_Frame_Del	DEL	TCC	-	7	138	.3813_3815delGG	(3811-3816)GAGGAA>GA	1271_1272EE
Pat_53	Pre-Treatment	FTSJ3	117246	37	17	61899155	61899157	In_Frame_Del	DEL	CTC	-	8	503	.1522_1524delGA	c.(1522-1524)GAGdel	p.E508del
Pat_53	Pre-Treatment	BPTF	2186	37	17	65940454	65940456	In_Frame_Del	DEL	CAC	-	7	578	.6666_6668delCA	(6664-6669)AGCACC>AG	p.T2227del
Pat_53	Pre-Treatment	ZNF236	7776	37	18	74593429	74593430	Frame_Shift_Ins	INS	-	A	7	300	c.1372_1373insA	c.(1372-1374)GAAfs	p.E458fs
Pat_53	Pre-Treatment	C19orf29	58509	37	19	3613226	3613227	In_Frame_Ins	INS	-	CCTCGC	14	86	15_1616insGCGA	15-1617)GCG>GGCGAG	.538_539insG
Pat_53	Pre-Treatment	DNM2	1785	37	19	10940986	10940986	Frame_Shift_Del	DEL	C	-	10	505	c.2475delC	c.(2473-2475)TTCfs	p.F825fs
Pat_53	Pre-Treatment	ZNF563	147837	37	19	12430217	12430217	Frame_Shift_Del	DEL	A	-	10	505	c.622delT	c.(622-624)TGGfs	p.W208fs
Pat_53	Pre-Treatment	CHERP	10523	37	19	16640581	16640583	In_Frame_Del	DEL	TGC	-	9	65	.1005_1007delGC	.(1003-1008)CAGCAA>CA	.335_336QQ>
Pat_53	Pre-Treatment	HAMP	57817	37	19	35773520	35773522	In_Frame_Del	DEL	CTC	-	9	479	c.40_42delCTC	c.(40-42)CTCdel	p.L18del
Pat_53	Pre-Treatment	C19orf55	148137	37	19	36255947	36255949	In_Frame_Del	DEL	CTC	-	8	624	c.639_641delCTC	c.(637-642)ATCTCC>ATC	p.S218del
Pat_53	Pre-Treatment	LYPD3	27076	37	19	43969653	43969655	In_Frame_Del	DEL	AGC	-	7	671	c.69_71delGCT	c.(67-72)CTGCTT>CTT	p.23_24LL>L
Pat_53	Pre-Treatment	RSPH6A	81492	37	19	46299147	46299149	In_Frame_Del	DEL	CCT	-	7	193	.2132_2134delAG	(2131-2136)GAGGGC>GG	p.E711del
Pat_53	Pre-Treatment	RSPH6A	81492	37	19	46299165	46299167	In_Frame_Del	DEL	CCT	-	16	222	.2114_2116delAG	(2113-2118)GAGGGC>GG	p.E705del
Pat_53	Pre-Treatment	SLC8A2	6543	37	19	47935681	47935683	In_Frame_Del	DEL	TCC	-	10	291	.2130_2132delGG	(2128-2133)GAGGAC>GA	p.E710del
Pat_53	Pre-Treatment	ASXL2	55252	37	2	26022304	26022306	In_Frame_Del	DEL	CTG	-	15	685	c.351_353delCAG	c.(349-354)AGCAGT>AGT	.117_118SS>
Pat_53	Pre-Treatment	DHX57	90957	37	2	39095411	39095413	In_Frame_Del	DEL	CCA	-	12	253	c.135_137delTGG	.(133-138)GGTGGA>GG	p.45_46GG>G
Pat_53	Pre-Treatment	PSME4	23198	37	2	54167139	54167140	Splice_Site	INS	-	G	8	637	c.501_splice	c.e4-1	p.N167_splice
Pat_53	Pre-Treatment	MTIF2	4528	37	2	55464461	55464461	Frame_Shift_Del	DEL	T	-	7	267	c.1974delA	c.(1972-1974)AAAfs	p.K658fs
Pat_53	Pre-Treatment	UGP2	7360	37	2	64084969	64084969	Frame_Shift_Del	DEL	A	-	9	1913	c.154delA	c.(154-156)AAAfs	p.K52fs
Pat_53	Pre-Treatment	TMEM127	55654	37	2	96919781	96919783	In_Frame_Del	DEL	TGC	-	11	348	c.480_482delGCA	c.(478-483)CAGCAT>CAT	p.Q160del
Pat_53	Pre-Treatment	ITPRIPL1	150771	37	2	96992793	96992795	In_Frame_Del	DEL	GAG	-	14	147	c.424_426delGAG	c.(424-426)GAGdel	p.E147del
Pat_53	Pre-Treatment	IL1F6	27179	37	2	113764196	113764198	In_Frame_Del	DEL	GCC	-	7	1273	c.146_148delGCC	c.(145-150)TGCCGA>TGA	p.49_50CR>*
Pat_53	Pre-Treatment	MKI67IP	84365	37	2	122485323	122485323	Frame_Shift_Del	DEL	T	-	7	548	c.859delA	c.(859-861)AGAfs	p.R287fs
Pat_53	Pre-Treatment	PLA2R1	22925	37	2	160801441	160801442	Frame_Shift_Ins	INS	-	T	8	660	c.4119_4120insA	c.(4117-4122)AAAGGCfs	p.K1373fs
Pat_53	Pre-Treatment	MYO3B	140469	37	2	171240259	171240259	Frame_Shift_Del	DEL	C	-	7	356	c.1225delC	c.(1225-1227)CCCfs	p.P409fs
Pat_53	Pre-Treatment	RBM45	129831	37	2	178988920	178988920	Frame_Shift_Del	DEL	A	-	20	321	c.1135delA	c.(1135-1137)AAAfs	p.K379fs
Pat_53	Pre-Treatment	ITGAV	3685	37	2	187521084	187521085	Frame_Shift_Ins	INS	-	G	8	1043	c.1675_1676insG	c.(1675-1677)AGGfs	p.R559fs
Pat_53	Pre-Treatment	SLC11A1	6556	37	2	219252307	219252307	Frame_Shift_Del	DEL	T	-	14	1437	c.591delT	c.(589-591)GCTfs	p.A197fs
Pat_53	Pre-Treatment	GIGYF2	26058	37	2	233676006	233676008	In_Frame_Del	DEL	CAG	-	11	343	.1951_1953delCA	c.(1951-1953)CAGdel	p.Q655del
Pat_53	Pre-Treatment	GAL3ST2	64090	37	2	242738494	242738496	In_Frame_Del	DEL	TCC	-	7	267	c.44_46delTCC	c.(43-48)ATCCTC>ATC	p.L20del
Pat_53	Pre-Treatment	FRG1B	284802	37	20	29628229	29628230	Frame_Shift_Ins	INS	-	A	61	695	c.141_142insA	c.(139-144)GGGAAAfs	p.G47fs
Pat_53	Pre-Treatment	NCOA6	23054	37	20	33330968	33330970	In_Frame_Del	DEL	TGC	-	7	223	.3090_3092delGC	.(3088-3093)CAGCAA>CA	030_1031QQ
Pat_53	Pre-Treatment	KCNB1	3745	37	20	47989771	47989772	Frame_Shift_Ins	INS	-	G	7	1044	c.2325_2326insC	c.(2323-2328)CCCAAAfs	p.P775fs
Pat_53	Pre-Treatment	YTHDF1	54915	37	20	61833650	61833652	In_Frame_Del	DEL	CCT	-	10	428	.1640_1642delAG	(1639-1644)GAGGTG>GT	p.E547del
Pat_53	Pre-Treatment	TPTE	7179	37	21	10944697	10944697	Frame_Shift_Del	DEL	A	-	16	605	c.537delT	c.(535-537)TTTfs	p.F179fs
Pat_53	Pre-Treatment	C21orf91	54149	37	21	19169352	19169352	Frame_Shift_Del	DEL	G	-	7	325	c.211delC	c.(211-213)CAGfs	p.Q71fs
Pat_53	Pre-Treatment	SFRS15	57466	37	21	33044257	33044259	In_Frame_Del	DEL	GCT	-	10	348	.2897_2899delAG	(2896-2901)CAGCCA>CC	p.Q966del
Pat_53	Pre-Treatment	SF3A1	10291	37	22	30742328	30742330	In_Frame_Del	DEL	CTG	-	9	252	c.364_366delCAG	c.(364-366)CAGdel	p.Q122del
Pat_53	Pre-Treatment	MYH9	4627	37	22	36689419	36689421	In_Frame_Del	DEL	CCT	-	7	157	.4049_4051delAG	(4048-4053)GAGGCC>GC	p.E1350del
Pat_53	Pre-Treatment	CDC42EP1	11135	37	22	37964409	37964429	In_Frame_Del	DEL	TGCTGCA	-	37	87	AGCGCCTGCTG	AGCGCCTGCTGCAAAC	APAANPS254

Pat_53	Pre-Treatment	DNAJB7	150353	37	22	41257114	41257115	Frame_Shift_Ins	INS	-	T	8	404	c.884_885insA	c.(883-885)AAGfs	p.K295fs
Pat_53	Pre-Treatment	RANGAP1	5905	37	22	41650469	41650471	In_Frame_Del	DEL	TCC	-	23	304	.1101_1103delGG	(1099-1104)GAGGAA>GA	.367_368EE>
Pat_53	Pre-Treatment	SREBF2	6721	37	22	42262949	42262951	In_Frame_Del	DEL	GCA	-	7	159	c.203_205delGCA	.(202-207)GGCAGC>GG	p.S74del
Pat_53	Pre-Treatment	ARFGAP3	26286	37	22	43213780	43213780	Frame_Shift_Del	DEL	T	-	16	787	c.896delA	c.(895-897)AATfs	p.N299fs
Pat_53	Pre-Treatment	TATDN2	9797	37	3	10291121	10291123	In_Frame_Del	DEL	CTC	-	8	742	c.237_239delCTC	c.(235-240)AACTCC>AAC	p.S83del
Pat_53	Pre-Treatment	NKTR	4820	37	3	42679764	42679764	Frame_Shift_Del	DEL	A	-	8	234	c.2568delA	c.(2566-2568)TCAfs	p.S856fs
Pat_53	Pre-Treatment	ANO10	55129	37	3	43647213	43647213	Frame_Shift_Del	DEL	T	-	12	299	c.132delA	c.(130-132)AAAfs	p.K44fs
Pat_53	Pre-Treatment	MAP4	4134	37	3	47957524	47957525	Frame_Shift_Del	DEL	TG	-	7	679	c.1792_1793delC	c.(1792-1794)CAAfs	p.Q598fs
Pat_53	Pre-Treatment	ALAS1	211	37	3	52246368	52246368	Frame_Shift_Del	DEL	G	-	8	1999	c.1694delG	c.(1693-1695)CGGfs	p.R565fs
Pat_53	Pre-Treatment	LNP1	348801	37	3	100148586	100148588	In_Frame_Del	DEL	GAT	-	13	987	c.13_15delGAT	c.(13-15)GATdel	p.D10del
Pat_53	Pre-Treatment	EAF2	55840	37	3	121573658	121573659	Frame_Shift_Ins	INS	-	A	7	478	c.326_327insA	c.(325-327)GTAfs	p.V109fs
Pat_53	Pre-Treatment	MED12L	116931	37	3	151148114	151148116	In_Frame_Del	DEL	CAG	-	12	305	.6331_6333delCA	c.(6331-6333)CAGdel	p.Q2115del
Pat_53	Pre-Treatment	PHC3	80012	37	3	169896635	169896637	In_Frame_Del	DEL	TGG	-	15	1587	c.68_70delCCA	c.(67-72)ACCATC>ATC	p.T23del
Pat_53	Pre-Treatment	FETUB	26998	37	3	186362544	186362544	Frame_Shift_Del	DEL	A	-	10	383	c.429delA	c.(427-429)TCAfs	p.S143fs
Pat_53	Pre-Treatment	RNF168	165918	37	3	196214338	196214338	Frame_Shift_Del	DEL	T	-	12	1197	c.490delA	c.(490-492)AGGfs	p.R164fs
Pat_53	Pre-Treatment	CRIPAK	285464	37	4	1388498	1388499	Frame_Shift_Del	DEL	CA	-	8	1203	c.199_200delCA	c.(199-201)CACfs	p.H67fs
Pat_53	Pre-Treatment	CRIPAK	285464	37	4	1388622	1388623	Frame_Shift_Ins	INS	-	CA	10	1005	c.323_324insCA	c.(322-324)CTCfs	p.L108fs
Pat_53	Pre-Treatment	PROM1	8842	37	4	15995680	15995680	Frame_Shift_Del	DEL	T	-	8	327	c.1697delA	c.(1696-1698)AATfs	p.N566fs
Pat_53	Pre-Treatment	KLF3	51274	37	4	38691476	38691476	Frame_Shift_Del	DEL	C	-	7	938	c.671delC	c.(670-672)TCCfs	p.S224fs
Pat_53	Pre-Treatment	FIP1L1	81608	37	4	54319248	54319249	Frame_Shift_Del	DEL	AG	-	26	207	c.1447_1448delA	c.(1447-1449)AGAfs	p.R483fs
Pat_53	Pre-Treatment	AASDH	132949	37	4	57220269	57220269	Frame_Shift_Del	DEL	A	-	25	268	c.1319delT	c.(1318-1320)TTGfs	p.L440fs
Pat_53	Pre-Treatment	MMRN1	22915	37	4	90844391	90844393	In_Frame_Del	DEL	AGC	-	8	1289	c.923_925delAGC	.(922-927)GAGCAG>GA	p.Q313del
Pat_53	Pre-Treatment	EXOSC9	5393	37	4	122723894	122723894	Frame_Shift_Del	DEL	T	-	9	441	c.227delT	c.(226-228)CTTfs	p.L76fs
Pat_53	Pre-Treatment	OTUD4	54726	37	4	146077123	146077125	In_Frame_Del	DEL	CAG	-	7	327	c.458_460delCTG	c.(457-462)GCTGAT>GAT	p.A153del
Pat_53	Pre-Treatment	LRBA	987	37	4	151509211	151509211	Frame_Shift_Del	DEL	T	-	10	1102	c.6352delA	c.(6352-6354)ATCfs	p.I2118fs
Pat_53	Pre-Treatment	PAPD7	11044	37	5	6755013	6755014	Frame_Shift_Del	DEL	AC	-	9	177	c.1584_1585delA	c.(1582-1587)AAACACfs	p.K528fs
Pat_53	Pre-Treatment	CTNND2	1501	37	5	11110989	11110991	In_Frame_Del	DEL	TTC	-	43	1126	.2442_2444delGA	.(2440-2445)AAGAAA>AA	.814_815KK>
Pat_53	Pre-Treatment	DNAH5	1767	37	5	13701426	13701426	Frame_Shift_Del	DEL	A	-	7	385	c.13458delT	c.(13456-13458)TTTfs	p.F4486fs
Pat_53	Pre-Treatment	CDH10	1008	37	5	24492973	24492973	Frame_Shift_Del	DEL	A	-	7	965	c.1577delT	c.(1576-1578)TTCfs	p.F526fs
Pat_53	Pre-Treatment	C6	729	37	5	41160299	41160300	Frame_Shift_Del	DEL	AC	-	9	581	c.1628_1629delG	c.(1627-1629)TGTfs	p.C543fs
Pat_53	Pre-Treatment	TAF9	6880	37	5	68660786	68660788	In_Frame_Del	DEL	TCA	-	8	354	c.777_779delTGA	c.(775-780)GATGAC>GA	.259_260DD>
Pat_53	Pre-Treatment	THBS4	7060	37	5	79372774	79372776	In_Frame_Del	DEL	TGA	-	9	838	.1989_1991delTG	.(1987-1992)TGTGAT>TG	p.D668del
Pat_53	Pre-Treatment	MSH3	4437	37	5	79970915	79970915	Frame_Shift_Del	DEL	A	-	12	828	c.1141delA	c.(1141-1143)AAAfs	p.K381fs
Pat_53	Pre-Treatment	AP3S1	1176	37	5	115202418	115202421	Frame_Shift_Del	DEL	AAGA	-	7	277	c.121_124delAAG	c.(121-126)AAGAGAfs	p.K41fs
Pat_53	Pre-Treatment	PCDHB3	56132	37	5	140481964	140481976	Frame_Shift_Del	DEL	GGCGGCT	-	7	112	743delCCGGGCG	-1743)CCCCGGGCGGC	p.P577fs
Pat_53	Pre-Treatment	TIMD4	91937	37	5	156378745	156378747	In_Frame_Del	DEL	TTG	-	9	716	c.455_457delCAA	c.(454-459)ACAAGC>AG	p.T152del
Pat_53	Pre-Treatment	RNF145	153830	37	5	158621763	158621763	Frame_Shift_Del	DEL	A	-	7	924	c.254delT	c.(253-255)TTGfs	p.L85fs
Pat_53	Pre-Treatment	CANX	821	37	5	179149920	179149920	Frame_Shift_Del	DEL	T	-	8	376	c.1298delT	c.(1297-1299)ATTfs	p.I433fs
Pat_53	Pre-Treatment	DSP	1832	37	6	7575664	7575664	Frame_Shift_Del	DEL	A	-	8	990	c.2573delA	c.(2572-2574)GAAfs	p.E858fs
Pat_53	Pre-Treatment	BTN2A2	10385	37	6	26384091	26384093	In_Frame_Del	DEL	CCT	-	10	526	c.42_44delCCT	c.(40-45)TCCCTC>TCC	p.L24del
Pat_53	Pre-Treatment	BTN2A3	54718	37	6	26422388	26422390	In_Frame_Del	DEL	CCT	-	31	837	c.42_44delCCT	c.(40-45)TCCCTC>TCC	p.L19del
Pat_53	Pre-Treatment	HLA-A	3105	37	6	29911319	29911319	Frame_Shift_Del	DEL	G	-	24	169	c.618delG	c.(616-618)ACGfs	p.T206fs
Pat_53	Pre-Treatment	BAT2	7916	37	6	31604005	31604005	Frame_Shift_Del	DEL	C	-	8	1619	c.5644delC	c.(5644-5646)CCCfs	p.P1882fs
Pat_53	Pre-Treatment	BAT3	7917	37	6	31617055	31617055	Frame_Shift_Del	DEL	G	-	7	413	c.344delC	c.(343-345)CCTfs	p.P115fs
Pat_53	Pre-Treatment	FKBPL	63943	37	6	32097086	32097086	Frame_Shift_Del	DEL	C	-	7	1472	c.472delG	c.(472-474)GAGfs	p.E158fs
Pat_53	Pre-Treatment	FKBP5	2289	37	6	35610515	35610515	Frame_Shift_Del	DEL	T	-	7	658	c.87delA	c.(85-87)AAAfs	p.K29fs
Pat_53	Pre-Treatment	ZNF318	24149	37	6	43323502	43323502	Frame_Shift_Del	DEL	T	-	9	1684	c.1570delA	c.(1570-1572)AGGfs	p.R524fs

Pat_53	Pre-Treatment	CD2AP	23607	37	6	47576961	47576961	Frame_Shift_Del	DEL	A	-	7	393	c.1735delA	c.(1735-1737)AAAfs	p.K579fs
Pat_53	Pre-Treatment	KIAA1009	22832	37	6	84896233	84896233	Frame_Shift_Del	DEL	A	-	11	463	c.1218delT	c.(1216-1218)TTTfs	p.F406fs
Pat_53	Pre-Treatment	GRM1	2911	37	6	146755399	146755401	In_Frame_Del	DEL	CAG	-	9	339	.3052_3054delCA	c.(3052-3054)CAGdel	p.Q1022del
Pat_53	Pre-Treatment	COX19	90639	37	7	1009017	1009017	Frame_Shift_Del	DEL	T	-	7	1627	c.270delA	c.(268-270)AAAfs	p.K90fs
Pat_53	Pre-Treatment	C7orf16	10842	37	7	31735179	31735179	Frame_Shift_Del	DEL	A	-	12	671	c.179delA	c.(178-180)CAAfs	p.Q60fs
Pat_53	Pre-Treatment	POU6F2	11281	37	7	39379288	39379290	In_Frame_Del	DEL	CAG	-	7	85	c.559_561delCAG	c.(559-561)CAGdel	p.Q196del
Pat_53	Pre-Treatment	OGDH	4967	37	7	44684936	44684936	Frame_Shift_Del	DEL	T	-	15	609	c.233delT	c.(232-234)ATTfs	p.I78fs
Pat_53	Pre-Treatment	DTX2	113878	37	7	76112249	76112249	Frame_Shift_Del	DEL	A	-	11	1281	c.693delA	c.(691-693)CCAfs	p.P231fs
Pat_53	Pre-Treatment	CYP51A1	1595	37	7	91752494	91752494	Frame_Shift_Del	DEL	T	-	10	663	c.1026delA	c.(1024-1026)AAAfs	p.K342fs
Pat_53	Pre-Treatment	XRCC2	7516	37	7	152346220	152346220	Frame_Shift_Del	DEL	A	-	7	287	c.350delT	c.(349-351)TTGfs	p.L117fs
Pat_53	Pre-Treatment	SFTPC	6440	37	8	22020159	22020161	In_Frame_Del	DEL	GTG	-	8	251	c.115_117delGTG	c.(115-117)GTGdel	p.V44del
Pat_53	Pre-Treatment	C8orf80	389643	37	8	27888776	27888776	Frame_Shift_Del	DEL	T	-	7	576	c.1892delA	c.(1891-1893)AATfs	p.N631fs
Pat_53	Pre-Treatment	MYST3	7994	37	8	41798420	41798422	In_Frame_Del	DEL	CTC	-	17	519	.2977_2979delGA	c.(2977-2979)GAGdel	p.E993del
Pat_53	Pre-Treatment	PABPC1	26986	37	8	101730036	101730037	Frame_Shift_Ins	INS	-	C	24	276	c.467_468insG	c.(466-468)GAAfs	p.E156fs
Pat_53	Pre-Treatment	C8orf76	84933	37	8	124250059	124250063	Frame_Shift_Del	DEL	CGCCT	-	28	138	332_336delAGGC	c.(331-336)GAGGCGfs	p.E111fs
Pat_53	Pre-Treatment	ANXA13	312	37	8	124707761	124707762	Frame_Shift_Ins	INS	-	T	13	772	c.451_452insA	c.(451-453)ATCfs	p.I151fs
Pat_53	Pre-Treatment	PLEC	5339	37	8	145000951	145000953	Splice_Site	DEL	CCT	-	7	494	c.4455_splice	c.e30+1	p.E1485_splice
Pat_53	Pre-Treatment	MLLT3	4300	37	9	20414377	20414379	In_Frame_Del	DEL	CTG	-	13	97	c.465_467delCAG	c.(463-468)AGCAGT>AGT	.155_156SS>
Pat_53	Pre-Treatment	TAF1L	138474	37	9	32633584	32633584	Frame_Shift_Del	DEL	T	-	10	255	c.1994delA	c.(1993-1995)AAGfs	p.K665fs
Pat_53	Pre-Treatment	VCP	7415	37	9	35059646	35059647	Frame_Shift_Ins	INS	-	T	10	234	c.1847_1848insA	c.(1846-1848)AATfs	p.N616fs
Pat_53	Pre-Treatment	TLN1	7094	37	9	35720430	35720430	Frame_Shift_Del	DEL	T	-	7	801	c.1283delA	c.(1282-1284)AAGfs	p.K428fs
Pat_53	Pre-Treatment	C9orf114	51490	37	9	131591119	131591120	Frame_Shift_Ins	INS	-	T	11	253	c.102_103insA	c.(100-105)AAATGGfs	p.K34fs
Pat_53	Pre-Treatment	NUP188	23511	37	9	131750436	131750436	Frame_Shift_Del	DEL	C	-	9	679	c.2504delC	c.(2503-2505)TCCfs	p.S835fs
Pat_53	Pre-Treatment	PRRG1	5638	37	X	37312611	37312611	Frame_Shift_Del	DEL	C	-	15	355	c.394delC	c.(394-396)CCCfs	p.P132fs
Pat_53	Pre-Treatment	PHF8	23133	37	X	54011405	54011407	In_Frame_Del	DEL	CTC	-	10	242	.2491_2493delGA	c.(2491-2493)GAGdel	p.E831del
Pat_53	Pre-Treatment	IRS4	8471	37	X	107977802	107977803	Frame_Shift_Ins	INS	-	C	10	367	c.1772_1773insG	c.(1771-1773)GGCfs	p.G591fs
Pat_53	Pre-Treatment	SLC25A5	292	37	X	118603706	118603707	Frame_Shift_Ins	INS	-	G	56	590	c.194_195insG	c.(193-195)CAGfs	p.Q65fs
Pat_53	Pre-Treatment	MAGEC1	9947	37	X	140994639	140994641	In_Frame_Del	DEL	CTC	-	7	470	.1449_1451delCT	(1447-1452)AGCTCC>AG	.483_484SS>
Pat_53	Pre-Treatment	SPANXN3	139067	37	X	142605149	142605149	Frame_Shift_Del	DEL	T	-	12	233	c.71delA	c.(70-72)AATfs	p.N24fs
Pat_53	Post-Resistance	CAMTA1	23261	37	1	7811329	7811329	Frame_Shift_Del	DEL	A	-	8	622	c.4760delA	c.(4759-4761)CAAfs	p.Q1587fs
Pat_53	Post-Resistance	TNFRSF9	3604	37	1	7998254	7998254	Frame_Shift_Del	DEL	T	-	8	643	c.345delA	c.(343-345)AAAfs	p.K115fs
Pat_53	Post-Resistance	PRDM2	7799	37	1	14108749	14108749	Frame_Shift_Del	DEL	A	-	48	794	c.4459delA	c.(4459-4461)AAAfs	p.K1487fs
Pat_53	Post-Resistance	MST1P9	11223	37	1	17086085	17086086	Frame_Shift_Ins	INS	-	C	7	9	c.811_812insG	c.(811-813)GCGfs	p.A271fs
Pat_53	Post-Resistance	ZBTB40	9923	37	1	22838561	22838563	In_Frame_Del	DEL	AAG	-	7	187	.2395_2397delAA	c.(2395-2397)AAGdel	p.K803del
Pat_53	Post-Resistance	CCDC30	728621	37	1	43002200	43002201	Frame_Shift_Del	DEL	AG	-	24	139	c.45_46delAG	c.(43-48)AAAGAGfs	p.K15fs
Pat_53	Post-Resistance	LRRIQ3	127255	37	1	74575212	74575213	Frame_Shift_Ins	INS	-	T	20	398	c.732_733insA	c.(730-735)AAACAGfs	p.K244fs
Pat_53	Post-Resistance	BCL10	8915	37	1	85736511	85736511	Frame_Shift_Del	DEL	T	-	9	305	c.136delA	c.(136-138)ATAfs	p.I46fs
Pat_53	Post-Resistance	GBP3	2635	37	1	89473441	89473442	Frame_Shift_Ins	INS	-	T	23	504	c.1753_1754insA	c.(1753-1755)ACCfs	p.T585fs
Pat_53	Post-Resistance	EVI5	7813	37	1	93159366	93159366	Frame_Shift_Del	DEL	T	-	7	299	c.1222delA	c.(1222-1224)ATGfs	p.M408fs
Pat_53	Post-Resistance	TRIM33	51592	37	1	114968116	114968118	In_Frame_Del	DEL	TGT	-	9	620	.1648_1650delAC	c.(1648-1650)ACAdel	p.T550del
Pat_53	Post-Resistance	CD160	11126	37	1	145704034	145704034	Frame_Shift_Del	DEL	A	-	7	501	c.383delT	c.(382-384)TTCfs	p.F128fs
Pat_53	Post-Resistance	BCL9	607	37	1	147091501	147091501	Frame_Shift_Del	DEL	C	-	12	251	c.1540delC	c.(1540-1542)CCCfs	p.P514fs
Pat_53	Post-Resistance	ADAMTSL4	54507	37	1	150530506	150530506	Frame_Shift_Del	DEL	G	-	12	207	c.2263delG	c.(2263-2265)GGGfs	p.G755fs
Pat_53	Post-Resistance	RPTN	126638	37	1	152127845	152127848	Frame_Shift_Del	DEL	TGTC	-	8	1574	1727_1730delGAC	c.(1726-1731)AGACAAfs	p.R576fs
Pat_53	Post-Resistance	RPTN	126638	37	1	152127881	152127884	Frame_Shift_Del	DEL	TGTC	-	13	2210	1691_1694delGAC	c.(1690-1695)AGACAAfs	p.R564fs
Pat_53	Post-Resistance	RPTN	126638	37	1	152127917	152127920	Frame_Shift_Del	DEL	TGTC	-	14	2404	1655_1658delGAC	c.(1654-1659)AGACAAfs	p.R552fs
Pat_53	Post-Resistance	NPR1	4881	37	1	153659175	153659175	Frame_Shift_Del	DEL	C	-	12	231	c.1812delC	c.(1810-1812)GACfs	p.D604fs

Pat_53	Post-Resistance	KIAA0907	22889	37	1	155886422	155886423	Frame_Shift_Del	DEL	CT	-	22	506	c.1546_1547delAG	c.(1546-1548)AGGfs	p.R516fs
Pat_53	Post-Resistance	SLAMF1	6504	37	1	160589601	160589601	Frame_Shift_Del	DEL	T	-	12	820	c.829delA	c.(829-831)AGCfs	p.S277fs
Pat_53	Post-Resistance	PVRL4	81607	37	1	161044057	161044059	In_Frame_Del	DEL	CAC	-	7	218	.1105_1107delGT	c.(1105-1107)GTGdel	p.V369del
Pat_53	Post-Resistance	PCP4L1	654790	37	1	161254154	161254156	In_Frame_Del	DEL	GGA	-	9	299	c.90_92delGGA	c.(88-93)GCGGAG>GCG	p.E35del
Pat_53	Post-Resistance	ABL2	27	37	1	179078404	179078404	Frame_Shift_Del	DEL	G	-	8	662	c.1998delC	c.(1996-1998)CCCfs	p.P666fs
Pat_53	Post-Resistance	APOBEC4	403314	37	1	183616826	183616828	In_Frame_Del	DEL	TTC	-	10	448	.1089_1091delGA	.(1087-1092)AAGAAA>AA	.363_364KK>
Pat_53	Post-Resistance	PRG4	10216	37	1	186276374	186276376	In_Frame_Del	DEL	CCA	-	7	370	.1523_1525delCC	.(1522-1527)CCCACC>CC	p.T511del
Pat_53	Post-Resistance	TP53BP2	7159	37	1	223991931	223991931	Frame_Shift_Del	DEL	T	-	7	640	c.594delA	c.(592-594)AAAfs	p.K198fs
Pat_53	Post-Resistance	CUBN	8029	37	10	17113554	17113554	Frame_Shift_Del	DEL	A	-	7	339	c.2496delT	c.(2494-2496)TTTfs	p.F832fs
Pat_53	Post-Resistance	FRMPD2	143162	37	10	49409419	49409420	Frame_Shift_Ins	INS	-	T	8	350	c.1805_1806insA	c.(1804-1806)AAGfs	p.K602fs
Pat_53	Post-Resistance	BICC1	80114	37	10	60380663	60380663	Splice_Site	DEL	T	-	7	249	c.237_splice	c.e2+2	p.K79_splice
Pat_53	Post-Resistance	RUFY2	55680	37	10	70156583	70156583	Frame_Shift_Del	DEL	T	-	12	195	c.457delA	c.(457-459)ATGfs	p.M153fs
Pat_53	Post-Resistance	TM9SF3	56889	37	10	98336475	98336475	Frame_Shift_Del	DEL	T	-	9	294	c.214delA	c.(214-216)AGTfs	p.S72fs
Pat_53	Post-Resistance	LZTS2	84445	37	10	102763415	102763417	In_Frame_Del	DEL	CCT	-	8	308	c.560_562delCCT	c.(559-564)GCCTCC>GCC	p.S197del
Pat_53	Post-Resistance	UBQLN3	50613	37	11	5529918	5529920	In_Frame_Del	DEL	TGG	-	8	146	c.869_871delCCA	c.(868-873)ACCAGC>AGC	p.T290del
Pat_53	Post-Resistance	TSG101	7251	37	11	18505466	18505466	Frame_Shift_Del	DEL	T	-	8	669	c.794delA	c.(793-795)AAGfs	p.K265fs
Pat_53	Post-Resistance	APIP	51074	37	11	34910341	34910341	Frame_Shift_Del	DEL	T	-	7	190	c.283delA	c.(283-285)AGCfs	p.S95fs
Pat_53	Post-Resistance	PAMR1	25891	37	11	35513670	35513670	Frame_Shift_Del	DEL	C	-	11	558	c.302delG	c.(301-303)GGTfs	p.G101fs
Pat_53	Post-Resistance	ACCS	84680	37	11	44098856	44098856	Frame_Shift_Del	DEL	A	-	8	457	c.584delA	c.(583-585)TATfs	p.Y195fs
Pat_53	Post-Resistance	TSKU	25987	37	11	76506673	76506675	In_Frame_Del	DEL	CTG	-	9	121	c.13_15delCTG	c.(13-15)CTGdel	p.L9del
Pat_53	Post-Resistance	TAF1D	79101	37	11	93471453	93471453	Frame_Shift_Del	DEL	T	-	7	533	c.281delA	c.(280-282)AAGfs	p.K94fs
Pat_53	Post-Resistance	CD3G	917	37	11	118220583	118220583	Frame_Shift_Del	DEL	A	-	10	143	c.205delA	c.(205-207)AAAfs	p.K69fs
Pat_53	Post-Resistance	CBL	867	37	11	119149356	119149358	In_Frame_Del	DEL	ATG	-	7	102	c.1364_1366delAT	c.(1363-1368)TATGAT>TA	p.D460del
Pat_53	Post-Resistance	C11orf61	79684	37	11	124637350	124637350	Frame_Shift_Del	DEL	C	-	7	280	c.1402delG	c.(1402-1404)GAAfs	p.E468fs
Pat_53	Post-Resistance	CHEK1	1111	37	11	125505377	125505378	Frame_Shift_Ins	INS	-	A	12	489	c.667_668insA	c.(667-669)GAAfs	p.E223fs
Pat_53	Post-Resistance	SRPR	6734	37	11	126137087	126137087	Frame_Shift_Del	DEL	T	-	35	1096	c.509delA	c.(508-510)AAGfs	p.K170fs
Pat_53	Post-Resistance	PRB1	5542	37	12	11506815	11506816	In_Frame_Ins	INS	-	GGA	9	354	c.221_222insTCC	c.(220-222)CCA>CCTCCA	p.74_74P>PP
Pat_53	Post-Resistance	SFRS2IP	9169	37	12	46320707	46320708	Frame_Shift_Del	DEL	TC	-	7	232	c.2776_2777delGA	c.(2776-2778)GAAfs	p.E926fs
Pat_53	Post-Resistance	CCNT1	904	37	12	49087434	49087436	In_Frame_Del	DEL	ATG	-	35	867	c.1561_1563delCA	c.(1561-1563)CATdel	p.H521del
Pat_53	Post-Resistance	KRT1	3848	37	12	53069189	53069190	In_Frame_Ins	INS	-	GCC	2	4	.1722_1723insGG	c.(1720-1725)insGGC	p.574_575insG
Pat_53	Post-Resistance	OR10A7	121364	37	12	55615114	55615116	In_Frame_Del	DEL	CTT	-	11	307	c.306_308delCTT	c.(304-309)TACTTC>TAC	p.F107del
Pat_53	Post-Resistance	ESYT1	23344	37	12	56525070	56525070	Frame_Shift_Del	DEL	T	-	7	309	c.684delT	c.(682-684)TATfs	p.Y228fs
Pat_53	Post-Resistance	UHRF1BP1L	23074	37	12	100466559	100466559	Frame_Shift_Del	DEL	G	-	7	257	c.1440delC	c.(1438-1440)CCCfs	p.P480fs
Pat_53	Post-Resistance	SBNO1	55206	37	12	123794283	123794283	Frame_Shift_Del	DEL	T	-	10	189	c.3416delA	c.(3415-3417)AATfs	p.N1139fs
Pat_53	Post-Resistance	POLE	5426	37	12	133220099	133220100	Frame_Shift_Del	DEL	CA	-	13	328	c.4337_4338delTG	c.(4336-4338)GTGfs	p.V1446fs
Pat_53	Post-Resistance	SACS	26278	37	13	23914687	23914687	Frame_Shift_Del	DEL	T	-	27	853	c.3328delA	c.(3328-3330)ATTfs	p.I1110fs
Pat_53	Post-Resistance	LRCH1	23143	37	13	47243183	47243186	Frame_Shift_Del	DEL	CCTG	-	7	864	c.471_474delCCT	c.(469-474)GCCCTGfs	p.A157fs
Pat_53	Post-Resistance	ABCC4	10257	37	13	95696016	95696016	Frame_Shift_Del	DEL	T	-	11	276	c.3655delA	c.(3655-3657)ATCfs	p.I1219fs
Pat_53	Post-Resistance	LRP10	26020	37	14	23341527	23341529	In_Frame_Del	DEL	CCT	-	14	206	c.15_17delCCT	c.(13-18)ACCCTC>ACC	p.L11del
Pat_53	Post-Resistance	C14orf106	55320	37	14	45693722	45693722	Frame_Shift_Del	DEL	T	-	15	199	c.2068delA	c.(2068-2070)AGTfs	p.S690fs
Pat_53	Post-Resistance	MGAT2	4247	37	14	50088327	50088327	Frame_Shift_Del	DEL	C	-	7	355	c.341delC	c.(340-342)GCCfs	p.A114fs
Pat_53	Post-Resistance	C15orf24	56851	37	15	34393991	34393993	In_Frame_Del	DEL	AGC	-	21	611	c.48_50delGCT	c.(46-51)CTGCTA>CTA	p.16_17LL>L
Pat_53	Post-Resistance	SLTM	79811	37	15	59182564	59182565	Frame_Shift_Del	DEL	CT	-	22	405	c.1994_1995delAG	c.(1993-1995)GAGfs	p.E665fs
Pat_53	Post-Resistance	CPLX3	594855	37	15	75122558	75122560	In_Frame_Del	DEL	GAG	-	7	175	c.340_342delGAG	c.(340-342)GAGdel	p.E118del
Pat_53	Post-Resistance	TIGD7	91151	37	16	3350472	3350472	Frame_Shift_Del	DEL	T	-	8	281	c.143delA	c.(142-144)AATfs	p.N48fs
Pat_53	Post-Resistance	C16orf88	400506	37	16	19722723	19722724	Frame_Shift_Ins	INS	-	T	7	250	c.957_958insA	c.(955-960)AAAGGCfs	p.K319fs
Pat_53	Post-Resistance	EIF3CL	728689	37	16	28734579	28734581	In_Frame_Del	DEL	GAG	-	16	2050	c.871_873delGAG	c.(871-873)GAGdel	p.E295del

Pat_53	Post-Resistance	ITGAL	3683	37	16	30531249	30531251	In_Frame_Del	DEL	GCT	-	9	484	.3300_3302delGC	(3298-3303)GGGCTG>GG	p.L1106del
Pat_53	Post-Resistance	SRCAP	10847	37	16	30736370	30736371	Frame_Shift_Ins	INS	-	C	14	564	c.5625_5626insC	c.(5623-5628)CAGCCCfs	p.Q1875fs
Pat_53	Post-Resistance	BRD7	29117	37	16	50368678	50368679	Frame_Shift_Del	DEL	CT	-	44	726	c.830_831delAG	c.(829-831)GAGfs	p.E277fs
Pat_53	Post-Resistance	IRX6	79190	37	16	55362674	55362676	In_Frame_Del	DEL	GAG	-	12	82	c.784_786delGAG	c.(784-786)GAGdel	p.E268del
Pat_53	Post-Resistance	CPNE2	221184	37	16	57153143	57153144	Frame_Shift_Del	DEL	TA	-	8	356	c.544_545delTA	c.(544-546)TATfs	p.Y182fs
Pat_53	Post-Resistance	CIAPIN1	57019	37	16	57473182	57473182	Frame_Shift_Del	DEL	C	-	7	690	c.222delG	c.(220-222)CTGfs	p.L74fs
Pat_53	Post-Resistance	COQ9	57017	37	16	57486732	57486734	In_Frame_Del	DEL	GAG	-	10	305	c.262_264delGAG	c.(262-264)GAGdel	p.E91del
Pat_53	Post-Resistance	SLC9A5	6553	37	16	67300017	67300019	In_Frame_Del	DEL	GAG	-	8	118	.2107_2109delGA	c.(2107-2109)GAGdel	p.E708del
Pat_53	Post-Resistance	KIAA0182	23199	37	16	85682290	85682290	Frame_Shift_Del	DEL	C	-	8	177	c.359delC	c.(358-360)ACCfs	p.T120fs
Pat_53	Post-Resistance	FXR2	9513	37	17	7495872	7495874	In_Frame_Del	DEL	CGG	-	19	1016	.1773_1775delCC	(1771-1776)CGCCGT>CG	.591_592RR>
Pat_53	Post-Resistance	CNTROB	116840	37	17	7843518	7843519	Frame_Shift_Del	DEL	GA	-	10	271	c.1269_1270delG	c.(1267-1272)CGGAGAfs	p.R423fs
Pat_53	Post-Resistance	CYTSB	92521	37	17	20135087	20135087	Frame_Shift_Del	DEL	G	-	8	414	c.2088delG	c.(2086-2088)CTGfs	p.L696fs
Pat_53	Post-Resistance	SUPT6H	6830	37	17	27027202	27027204	In_Frame_Del	DEL	AGC	-	12	637	.4573_4575delAG	c.(4573-4575)AGCdel	p.S1528del
Pat_53	Post-Resistance	SSH2	85464	37	17	27959375	27959375	Frame_Shift_Del	DEL	G	-	9	744	c.2756delC	c.(2755-2757)CCAfs	p.P919fs
Pat_53	Post-Resistance	GPATCH8	23131	37	17	42477345	42477346	Frame_Shift_Del	DEL	AG	-	10	1073	c.2099_2100delCT	c.(2098-2100)TCTfs	p.S700fs
Pat_53	Post-Resistance	CCDC43	124808	37	17	42756253	42756253	Frame_Shift_Del	DEL	T	-	8	78	c.646delA	c.(646-648)AGGfs	p.R216fs
Pat_53	Post-Resistance	MYL4	4635	37	17	45299094	45299095	Frame_Shift_Del	DEL	GC	-	8	284	c.360_361delGC	c.(358-363)CTGCAGfs	p.L120fs
Pat_53	Post-Resistance	COX11	1353	37	17	53040139	53040139	Frame_Shift_Del	DEL	A	-	8	183	c.786delT	c.(784-786)TTTfs	p.F262fs
Pat_53	Post-Resistance	SLC9A3R1	9368	37	17	72764624	72764624	Frame_Shift_Del	DEL	C	-	8	604	c.906delC	c.(904-906)AGCfs	p.S302fs
Pat_53	Post-Resistance	CHERP	10523	37	19	16640581	16640583	In_Frame_Del	DEL	TGC	-	7	29	.1005_1007delGC	.(1003-1008)CAGCAA>CA	.335_336QQ>
Pat_53	Post-Resistance	LSM14A	26065	37	19	34710340	34710340	Frame_Shift_Del	DEL	C	-	8	401	c.826delC	c.(826-828)CGGfs	p.R276fs
Pat_53	Post-Resistance	HAMP	57817	37	19	35773520	35773522	In_Frame_Del	DEL	CTC	-	11	291	c.40_42delCTC	c.(40-42)CTCdel	p.L18del
Pat_53	Post-Resistance	LYPD3	27076	37	19	43969653	43969655	In_Frame_Del	DEL	AGC	-	10	401	c.69_71delGCT	c.(67-72)CTGCTT>CTT	p.23_24LL>L
Pat_53	Post-Resistance	PNMAL1	55228	37	19	46973195	46973197	In_Frame_Del	DEL	CTT	-	8	336	.1096_1098delAA	c.(1096-1098)AAGdel	p.K366del
Pat_53	Post-Resistance	ASXL2	55252	37	2	26022304	26022306	In_Frame_Del	DEL	CTG	-	11	454	c.351_353delCAG	c.(349-354)AGCAGT>AGT	.117_118SS>
Pat_53	Post-Resistance	USP34	9736	37	2	61575023	61575025	In_Frame_Del	DEL	TGG	-	9	114	.2265_2267delCC	.(2263-2268)CACCAT>CA	.755_756HH>
Pat_53	Post-Resistance	DYSF	8291	37	2	71801420	71801422	In_Frame_Del	DEL	CCG	-	8	332	.3267_3269delCC	.(3265-3270)TTCCGC>TT	p.R1093del
Pat_53	Post-Resistance	ITPRIPL1	150771	37	2	96992793	96992795	In_Frame_Del	DEL	GAG	-	9	82	c.424_426delGAG	c.(424-426)GAGdel	p.E147del
Pat_53	Post-Resistance	7-Mar	64844	37	2	160604680	160604680	Frame_Shift_Del	DEL	T	-	9	133	c.879delT	c.(877-879)ACTfs	p.T293fs
Pat_53	Post-Resistance	GRB14	2888	37	2	165365288	165365288	Frame_Shift_Del	DEL	T	-	16	369	c.891delA	c.(889-891)AAAfs	p.K297fs
Pat_53	Post-Resistance	RBM45	129831	37	2	178988920	178988920	Frame_Shift_Del	DEL	A	-	8	234	c.1135delA	c.(1135-1137)AAAfs	p.K379fs
Pat_53	Post-Resistance	ASNSD1	54529	37	2	190531266	190531266	Frame_Shift_Del	DEL	T	-	7	398	c.408delT	c.(406-408)GATfs	p.D136fs
Pat_53	Post-Resistance	CYP20A1	57404	37	2	204150380	204150380	Frame_Shift_Del	DEL	A	-	8	234	c.896delA	c.(895-897)CAAfs	p.Q299fs
Pat_53	Post-Resistance	RQCD1	9125	37	2	219449364	219449364	Frame_Shift_Del	DEL	T	-	13	885	c.350delT	c.(349-351)CTTfs	p.L117fs
Pat_53	Post-Resistance	DSTN	11034	37	20	17581488	17581489	Frame_Shift_Ins	INS	-	T	12	349	c.109_110insT	c.(109-111)ATTfs	p.I37fs
Pat_53	Post-Resistance	FRG1B	284802	37	20	29628229	29628230	Frame_Shift_Ins	INS	-	A	36	581	c.141_142insA	c.(139-144)GGGAAAfs	p.G47fs
Pat_53	Post-Resistance	BCL2L1	598	37	20	30309591	30309591	Frame_Shift_Del	DEL	A	-	7	1960	c.431delT	c.(430-432)TTCfs	p.F144fs
Pat_53	Post-Resistance	MYLK2	85366	37	20	30407987	30407987	Frame_Shift_Del	DEL	C	-	8	272	c.111delC	c.(109-111)GGCfs	p.G37fs
Pat_53	Post-Resistance	SYCP2	10388	37	20	58490593	58490593	Frame_Shift_Del	DEL	T	-	7	483	c.526delA	c.(526-528)ATGfs	p.M176fs
Pat_53	Post-Resistance	SFRS15	57466	37	21	33044257	33044259	In_Frame_Del	DEL	GCT	-	13	314	.2897_2899delAG	(2896-2901)CAGCCA>CC	p.Q966del
Pat_53	Post-Resistance	TCP10L	140290	37	21	33949091	33949091	Frame_Shift_Del	DEL	C	-	7	554	c.641delG	c.(640-642)GGTfs	p.G214fs
Pat_53	Post-Resistance	IFNGR2	3460	37	21	34799292	34799292	Frame_Shift_Del	DEL	T	-	13	1666	c.514delT	c.(514-516)TTTfs	p.F172fs
Pat_53	Post-Resistance	TTC3	7267	37	21	38538054	38538054	Frame_Shift_Del	DEL	A	-	8	714	c.3538delA	c.(3538-3540)AAAfs	p.K1180fs
Pat_53	Post-Resistance	SF3A1	10291	37	22	30742328	30742330	In_Frame_Del	DEL	CTG	-	8	216	c.364_366delCAG	c.(364-366)CAGdel	p.Q122del
Pat_53	Post-Resistance	CDC42EP1	11135	37	22	37964409	37964429	In_Frame_Del	DEL	TGCTGCA	-	31	80	AGCGCCTGCTG	AGCGCCTGCTGCAAAC	APAANPS254
Pat_53	Post-Resistance	RANGAP1	5905	37	22	41650469	41650471	In_Frame_Del	DEL	TCC	-	25	252	.1101_1103delGG	(1099-1104)GAGGAA>GA	.367_368EE>
Pat_53	Post-Resistance	ARFGAP3	26286	37	22	43213780	43213780	Frame_Shift_Del	DEL	T	-	13	730	c.896delA	c.(895-897)AATfs	p.N299fs

Pat_53	Post-Resistance	TUBGCP6	85378	37	22	50664481	50664481	Frame_Shift_Del	DEL	G	-	7	195	c.1831delC	c.(1831-1833)CGGfs	p.R611fs
Pat_53	Post-Resistance	CNTN6	27255	37	3	1371501	1371501	Frame_Shift_Del	DEL	A	-	7	337	c.1246delA	c.(1246-1248)AAAfs	p.K416fs
Pat_53	Post-Resistance	NKTR	4820	37	3	42679035	42679036	Frame_Shift_Ins	INS	-	C	14	827	c.1839_1840insC	c.(1837-1842)AGTCCCfs	p.S613fs
Pat_53	Post-Resistance	ANO10	55129	37	3	43647213	43647213	Frame_Shift_Del	DEL	T	-	8	251	c.132delA	c.(130-132)AAAfs	p.K44fs
Pat_53	Post-Resistance	ABHD5	51099	37	3	43756534	43756534	Frame_Shift_Del	DEL	A	-	10	379	c.757delA	c.(757-759)AATfs	p.N253fs
Pat_53	Post-Resistance	MYLK	4638	37	3	123368043	123368044	Splice_Site	INS	-	G	7	131	c.4289_splice	c.e25-1	p.E1430_splice
Pat_53	Post-Resistance	TOPBP1	11073	37	3	133329880	133329880	Frame_Shift_Del	DEL	T	-	7	559	c.4141delA	c.(4141-4143)ATCfs	p.I1381fs
Pat_53	Post-Resistance	DBR1	51163	37	3	137880741	137880743	In_Frame_Del	DEL	TCG	-	8	142	.1623_1625delCG	.(1621-1626)GATGAT>GA	.541_542DD>
Pat_53	Post-Resistance	MED12L	116931	37	3	151148114	151148116	In_Frame_Del	DEL	CAG	-	13	257	.6331_6333delCA	c.(6331-6333)CAGdel	p.Q2115del
Pat_53	Post-Resistance	PHC3	80012	37	3	169896635	169896637	In_Frame_Del	DEL	TGG	-	14	959	c.68_70delCCA	c.(67-72)ACCATC>ATC	p.T23del
Pat_53	Post-Resistance	PARL	55486	37	3	183585678	183585678	Frame_Shift_Del	DEL	A	-	7	316	c.296delT	c.(295-297)ATAfs	p.I99fs
Pat_53	Post-Resistance	FETUB	26998	37	3	186362544	186362544	Frame_Shift_Del	DEL	A	-	8	242	c.429delA	c.(427-429)TCAfs	p.S143fs
Pat_53	Post-Resistance	PROM1	8842	37	4	15995680	15995680	Frame_Shift_Del	DEL	T	-	11	253	c.1697delA	c.(1696-1698)AATfs	p.N566fs
Pat_53	Post-Resistance	FIP1L1	81608	37	4	54319248	54319249	Frame_Shift_Del	DEL	AG	-	34	150	c.1447_1448delAG	c.(1447-1449)AGAfs	p.R483fs
Pat_53	Post-Resistance	CFI	3426	37	4	110670394	110670394	Frame_Shift_Del	DEL	C	-	8	1093	c.1128delG	c.(1126-1128)CTGfs	p.L376fs
Pat_53	Post-Resistance	EXOSC9	5393	37	4	122728764	122728764	Frame_Shift_Del	DEL	T	-	7	359	c.592delT	c.(592-594)TTTfs	p.F198fs
Pat_53	Post-Resistance	CLGN	1047	37	4	141313402	141313402	Frame_Shift_Del	DEL	T	-	7	749	c.1622delA	c.(1621-1623)AAGfs	p.K541fs
Pat_53	Post-Resistance	OTUD4	54726	37	4	146077123	146077125	In_Frame_Del	DEL	CAG	-	11	287	c.458_460delCTG	c.(457-462)GCTGAT>GAT	p.A153del
Pat_53	Post-Resistance	HMGB2	3148	37	4	174253277	174253279	In_Frame_Del	DEL	TCC	-	14	267	c.582_584delGGA	c.(580-585)GAGGAA>GAA	.194_195EE>
Pat_53	Post-Resistance	CTNND2	1501	37	5	11110989	11110991	In_Frame_Del	DEL	TTC	-	27	844	.2442_2444delGA	.(2440-2445)AAGAAA>AA	.814_815KK>
Pat_53	Post-Resistance	MYO10	4651	37	5	16694605	16694606	Frame_Shift_Ins	INS	-	C	7	299	c.3674_3675insG	c.(3673-3675)GGCfs	p.G1225fs
Pat_53	Post-Resistance	CDH10	1008	37	5	24492973	24492973	Frame_Shift_Del	DEL	A	-	8	871	c.1577delT	c.(1576-1578)TTCfs	p.F526fs
Pat_53	Post-Resistance	THBS4	7060	37	5	79372774	79372776	In_Frame_Del	DEL	TGA	-	11	470	.1989_1991delTG	.(1987-1992)TGTGAT>TG	p.D668del
Pat_53	Post-Resistance	MSH3	4437	37	5	79970915	79970915	Frame_Shift_Del	DEL	A	-	18	941	c.1141delA	c.(1141-1143)AAAfs	p.K381fs
Pat_53	Post-Resistance	AP3S1	1176	37	5	115202418	115202421	Frame_Shift_Del	DEL	AAGA	-	7	259	c.121_124delAAGA	c.(121-126)AAGAGAfs	p.K41fs
Pat_53	Post-Resistance	ZNF608	57507	37	5	124079813	124079815	In_Frame_Del	DEL	CTC	-	14	585	c.868_870delGAG	c.(868-870)GAGdel	p.E290del
Pat_53	Post-Resistance	RAPGEF6	51735	37	5	130782332	130782332	Frame_Shift_Del	DEL	T	-	7	422	c.3265delA	c.(3265-3267)AGGfs	p.R1089fs
Pat_53	Post-Resistance	SLC22A4	6583	37	5	131676327	131676327	Frame_Shift_Del	DEL	T	-	7	524	c.1514delT	c.(1513-1515)CTTfs	p.L505fs
Pat_53	Post-Resistance	IK	3550	37	5	140032593	140032594	Frame_Shift_Del	DEL	GA	-	10	190	c.268_269delGA	c.(268-270)GAGfs	p.E90fs
Pat_53	Post-Resistance	PCDH1	5097	37	5	141244442	141244442	Frame_Shift_Del	DEL	G	-	9	392	c.1454delC	c.(1453-1455)CCAfs	p.P485fs
Pat_53	Post-Resistance	LARP1	23367	37	5	154173389	154173390	Frame_Shift_Ins	INS	-	C	13	762	c.898_899insC	c.(898-900)GCCfs	p.A300fs
Pat_53	Post-Resistance	MRPL22	29093	37	5	154336746	154336746	Frame_Shift_Del	DEL	A	-	8	412	c.313delA	c.(313-315)AAAfs	p.K105fs
Pat_53	Post-Resistance	BTN2A2	10385	37	6	26384091	26384093	In_Frame_Del	DEL	CCT	-	9	321	c.42_44delCCT	c.(40-45)TCCCTC>TCC	p.L24del
Pat_53	Post-Resistance	BTN2A3	54718	37	6	26422388	26422390	In_Frame_Del	DEL	CCT	-	18	489	c.42_44delCCT	c.(40-45)TCCCTC>TCC	p.L19del
Pat_53	Post-Resistance	HLA-A	3105	37	6	29911319	29911319	Frame_Shift_Del	DEL	G	-	22	166	c.618delG	c.(616-618)ACGfs	p.T206fs
Pat_53	Post-Resistance	BAT2	7916	37	6	31604005	31604005	Frame_Shift_Del	DEL	C	-	9	1126	c.5644delC	c.(5644-5646)CCCfs	p.P1882fs
Pat_53	Post-Resistance	BAT3	7917	37	6	31608571	31608571	Frame_Shift_Del	DEL	G	-	7	221	c.2842delC	c.(2842-2844)CAGfs	p.Q948fs
Pat_53	Post-Resistance	KIFC1	3833	37	6	33372838	33372838	Frame_Shift_Del	DEL	G	-	7	261	c.966delG	c.(964-966)CCGfs	p.P322fs
Pat_53	Post-Resistance	ZNF318	24149	37	6	43323502	43323502	Frame_Shift_Del	DEL	T	-	7	1062	c.1570delA	c.(1570-1572)AGGfs	p.R524fs
Pat_53	Post-Resistance	C6orf165	154313	37	6	88144700	88144700	Frame_Shift_Del	DEL	A	-	11	191	c.1423delA	c.(1423-1425)AAAfs	p.K475fs
Pat_53	Post-Resistance	ARID1B	57492	37	6	157510806	157510806	Frame_Shift_Del	DEL	C	-	7	502	c.3527delC	c.(3526-3528)ACCfs	p.T1176fs
Pat_53	Post-Resistance	QKI	9444	37	6	163899920	163899920	Frame_Shift_Del	DEL	A	-	7	255	c.394delA	c.(394-396)AAAfs	p.K132fs
Pat_53	Post-Resistance	COX19	90639	37	7	1009017	1009017	Frame_Shift_Del	DEL	T	-	8	1450	c.270delA	c.(268-270)AAAfs	p.K90fs
Pat_53	Post-Resistance	GLCCI1	113263	37	7	8126097	8126099	In_Frame_Del	DEL	CAG	-	7	776	.1573_1575delCA	c.(1573-1575)CAGdel	p.Q528del
Pat_53	Post-Resistance	C7orf16	10842	37	7	31735179	31735179	Frame_Shift_Del	DEL	A	-	10	482	c.179delA	c.(178-180)CAAfs	p.Q60fs
Pat_53	Post-Resistance	OGDH	4967	37	7	44684936	44684936	Frame_Shift_Del	DEL	T	-	9	629	c.233delT	c.(232-234)ATTfs	p.I78fs
Pat_53	Post-Resistance	DTX2	113878	37	7	76112249	76112249	Frame_Shift_Del	DEL	A	-	10	950	c.693delA	c.(691-693)CCAfs	p.P231fs

Pat_53	Post-Resistance	TMEM60	85025	37	7	77423460	77423460	Frame_Shift_Del	DEL	T	-	9	466	c.231delA	c.(229-231)AAAfs	p.K77fs
Pat_53	Post-Resistance	PHTF2	57157	37	7	77569581	77569581	Frame_Shift_Del	DEL	T	-	14	735	c.1702delT	c.(1702-1704)TTTfs	p.F568fs
Pat_53	Post-Resistance	PCLO	27445	37	7	82784451	82784451	Frame_Shift_Del	DEL	T	-	10	418	c.1506delA	c.(1504-1506)CAAfs	p.Q502fs
Pat_53	Post-Resistance	SLC25A40	55972	37	7	87483549	87483549	Frame_Shift_Del	DEL	A	-	8	481	c.234delT	c.(232-234)TATfs	p.Y78fs
Pat_53	Post-Resistance	CYP51A1	1595	37	7	91752494	91752494	Frame_Shift_Del	DEL	T	-	12	530	c.1026delA	c.(1024-1026)AAAfs	p.K342fs
Pat_53	Post-Resistance	CCDC132	55610	37	7	92923947	92923948	Frame_Shift_Ins	INS	-	G	9	419	c.1166_1167insG	c.(1165-1167)CAGfs	p.Q389fs
Pat_53	Post-Resistance	PTCD1	26024	37	7	99032605	99032607	In_Frame_Del	DEL	CTC	-	7	275	c.259_261delGAG	c.(259-261)GAGdel	p.E87del
Pat_53	Post-Resistance	GPC2	221914	37	7	99771554	99771554	Frame_Shift_Del	DEL	C	-	10	500	c.796delG	c.(796-798)GTCfs	p.V266fs
Pat_53	Post-Resistance	DNAJC2	27000	37	7	102964992	102964992	Frame_Shift_Del	DEL	T	-	7	367	c.590delA	c.(589-591)AATfs	p.N197fs
Pat_53	Post-Resistance	LAMB4	22798	37	7	107763584	107763584	Frame_Shift_Del	DEL	A	-	7	503	c.26delT	c.(25-27)TTGfs	p.L9fs
Pat_53	Post-Resistance	OR9A4	130075	37	7	141619203	141619203	Frame_Shift_Del	DEL	T	-	10	460	c.528delT	c.(526-528)AATfs	p.N176fs
Pat_53	Post-Resistance	CNPY1	285888	37	7	155299760	155299760	Frame_Shift_Del	DEL	G	-	8	143	c.196delC	c.(196-198)CAGfs	p.Q66fs
Pat_53	Post-Resistance	RP1L1	94137	37	8	10467706	10467707	In_Frame_Ins	INS	-	CCC	23	347	.3901_3902insGG	(3901-3903)GTG>GGGGT	.1300_1301ins
Pat_53	Post-Resistance	MTMR7	9108	37	8	17169103	17169103	Frame_Shift_Del	DEL	C	-	8	1209	c.1018delG	c.(1018-1020)GATfs	p.D340fs
Pat_53	Post-Resistance	C8orf80	389643	37	8	27888776	27888776	Frame_Shift_Del	DEL	T	-	7	417	c.1892delA	c.(1891-1893)AATfs	p.N631fs
Pat_53	Post-Resistance	GOT1L1	137362	37	8	37791833	37791834	Frame_Shift_Ins	INS	-	T	9	219	c.1243_1244insA	c.(1243-1245)ACAfs	p.T415fs
Pat_53	Post-Resistance	ADAM9	8754	37	8	38880792	38880793	Frame_Shift_Ins	INS	-	G	8	338	c.862_863insG	c.(862-864)CGGfs	p.R288fs
Pat_53	Post-Resistance	PRKDC	5591	37	8	48746799	48746799	Frame_Shift_Del	DEL	T	-	7	832	c.8110delA	c.(8110-8112)AGGfs	p.R2704fs
Pat_53	Post-Resistance	CA2	760	37	8	86386635	86386635	Frame_Shift_Del	DEL	T	-	10	454	c.434delT	c.(433-435)ATTfs	p.I145fs
Pat_53	Post-Resistance	TP53INP1	94241	37	8	95952409	95952411	In_Frame_Del	DEL	TCT	-	7	148	c.150_152delAGA	.(148-153)GAAGAG>GA	p.50_51EE>E
Pat_53	Post-Resistance	PABPC1	26986	37	8	101721933	101721933	Frame_Shift_Del	DEL	T	-	9	139	c.999delA	c.(997-999)AAAfs	p.K333fs
Pat_53	Post-Resistance	C8orf76	84933	37	8	124250059	124250063	Frame_Shift_Del	DEL	CGCCT	-	11	137	332_336delAGGC	c.(331-336)GAGGCGfs	p.E111fs
Pat_53	Post-Resistance	TSNARE1	203062	37	8	143310866	143310868	In_Frame_Del	DEL	GAT	-	7	124	.1519_1521delAT	c.(1519-1521)ATCdel	p.I507del
Pat_53	Post-Resistance	MLLT3	4300	37	9	20414377	20414379	In_Frame_Del	DEL	CTG	-	9	36	c.465_467delCAG	c.(463-468)AGCAGT>AGT	.155_156SS>
Pat_53	Post-Resistance	NFIL3	4783	37	9	94172779	94172779	Frame_Shift_Del	DEL	T	-	8	610	c.238delA	c.(238-240)AGGfs	p.R80fs
Pat_53	Post-Resistance	ECM2	1842	37	9	95277146	95277148	In_Frame_Del	DEL	TCC	-	9	140	c.819_821delGGA	c.(817-822)GAGGAT>GAT	p.E273del
Pat_53	Post-Resistance	C9orf114	51490	37	9	131591119	131591120	Frame_Shift_Ins	INS	-	T	7	173	c.102_103insA	c.(100-105)AAATGGfs	p.K34fs
Pat_53	Post-Resistance	TXLNG	55787	37	X	16850849	16850850	Frame_Shift_Del	DEL	AG	-	8	90	c.968_969delAG	c.(967-969)CAGfs	p.Q323fs
Pat_53	Post-Resistance	PRRG1	5638	37	X	37312611	37312611	Frame_Shift_Del	DEL	C	-	9	312	c.394delC	c.(394-396)CCCfs	p.P132fs
Pat_53	Post-Resistance	PHF8	23133	37	X	54011405	54011407	In_Frame_Del	DEL	CTC	-	12	209	.2491_2493delGA	c.(2491-2493)GAGdel	p.E831del
Pat_53	Post-Resistance	OPHN1	4983	37	X	67454384	67454384	Frame_Shift_Del	DEL	A	-	7	220	c.431delT	c.(430-432)TTAfs	p.L144fs
Pat_53	Post-Resistance	BRWD3	254065	37	X	79938006	79938007	Frame_Shift_Del	DEL	AG	-	8	550	.4354_4355delCT	c.(4354-4356)CTAfs	p.L1452fs
Pat_53	Post-Resistance	ARMCX3	51566	37	X	100880152	100880154	In_Frame_Del	DEL	TGA	-	16	255	c.183_185delTGA	c.(181-186)TCTGAT>TCT	p.D66del
Pat_53	Post-Resistance	PSMD10	5716	37	X	107331258	107331258	Frame_Shift_Del	DEL	T	-	8	340	c.285delA	c.(283-285)AAAfs	p.K95fs
Pat_53	Post-Resistance	SLC25A5	292	37	X	118603706	118603707	Frame_Shift_Ins	INS	-	G	46	503	c.194_195insG	c.(193-195)CAGfs	p.Q65fs
Pat_53	Post-Resistance	HTATSF1	27336	37	X	135585048	135585050	In_Frame_Del	DEL	AAG	-	10	256	c.682_684delAAG	c.(682-684)AAGdel	p.K232del
Pat_53	Post-Resistance	MAGEC1	9947	37	X	140994114	140994116	In_Frame_Del	DEL	CTC	-	13	388	c.924_926delCTC	.(922-927)AGCTCC>AGC	.308_309SS>
Pat_58	Pre-Treatment	TCHH	7062	37	1	152084580	152084582	In_Frame_Del	DEL	CTC	-	8	39	.1111_1113delGA	c.(1111-1113)GAGdel	p.E371del
Pat_58	Pre-Treatment	BUB1B	701	37	15	40477506	40477506	Frame_Shift_Del	DEL	C	-	7	159	c.892delC	c.(892-894)CCCfs	p.P298fs
Pat_58	Pre-Treatment	RAI1	10743	37	17	17699359	17699359	Frame_Shift_Del	DEL	C	-	3	5	c.3097delC	c.(3097-3099)CCCfs	p.P1033fs
Pat_58	Pre-Treatment	POLDIP2	26073	37	17	26684394	26684395	Splice_Site	INS	-	G	3	5	c.78_splice	c.e2+1	p.W26_splice
Pat_58	Pre-Treatment	SEMA6B	10501	37	19	4544182	4544182	Frame_Shift_Del	DEL	G	-	2	4	c.2098delC	c.(2098-2100)CACfs	p.H700fs
Pat_58	Pre-Treatment	INHBA	3624	37	7	41729741	41729743	In_Frame_Del	DEL	TTC	-	8	21	c.786_788delGAA	c.(784-789)AAGAAA>AAA	.262_263KK>
Pat_58	Pre-Treatment	AUTS2	26053	37	7	70231241	70231242	Frame_Shift_Ins	INS	-	C	8	138	c.1610_1611insC	c.(1609-1611)CACfs	p.H537fs
Pat_58	Pre-Treatment	POMT1	10585	37	9	134393867	134393879	Frame_Shift_Del	DEL	AGACCATC	-	33	150	386delGAAGACC	2-1386)TGGAAGACCATC	p.W458fs
Pat_58	Pre-Treatment	TPRN	286262	37	9	140087025	140087027	In_Frame_Del	DEL	TCC	-	3	5	.1659_1661delGG	(1657-1662)GAGGAA>GA	.553_554EE>
Pat_58	Post-Resistance	DLGAP3	58512	37	1	35370281	35370283	In_Frame_Del	DEL	TGG	-	7	371	c.702_704delCCA	.(700-705)CACCAG>CAG	p.H234del

Pat_58	Post-Resistance	SNIP1	79753	37	1	38003363	38003365	In_Frame_Del	DEL	CTT	-	9	423	.1175_1177delAA	(1174-1179)GAAGTG>GT	p.E392del
Pat_58	Post-Resistance	BCL10	8915	37	1	85736511	85736511	Frame_Shift_Del	DEL	T	-	11	373	c.136delA	c.(136-138)ATAfs	p.I46fs
Pat_58	Post-Resistance	EVI5	7813	37	1	93159366	93159366	Frame_Shift_Del	DEL	T	-	7	327	c.1222delA	c.(1222-1224)ATGfs	p.M408fs
Pat_58	Post-Resistance	COL11A1	1301	37	1	103355065	103355065	Frame_Shift_Del	DEL	T	-	9	325	c.4410delA	c.(4408-4410)AAAfs	p.K1470fs
Pat_58	Post-Resistance	HAX1	10456	37	1	154245864	154245866	In_Frame_Del	DEL	GAA	-	7	230	c.106_108delGAA	c.(106-108)GAAdel	p.E40del
Pat_58	Post-Resistance	EPHX1	2052	37	1	226026384	226026384	Frame_Shift_Del	DEL	C	-	8	751	c.394delC	c.(394-396)CCCfs	p.P132fs
Pat_58	Post-Resistance	UBQLN3	50613	37	11	5529918	5529920	In_Frame_Del	DEL	TGG	-	8	364	c.869_871delCCA	.(868-873)ACCAGC>AGC	p.T290del
Pat_58	Post-Resistance	IFT46	56912	37	11	118427683	118427685	In_Frame_Del	DEL	ATC	-	9	282	c.121_123delGAT	c.(121-123)GATdel	p.D41del
Pat_58	Post-Resistance	SFRS2IP	9169	37	12	46320707	46320708	Frame_Shift_Del	DEL	TC	-	7	403	.2776_2777delG	c.(2776-2778)GAAfs	p.E926fs
Pat_58	Post-Resistance	SLC39A5	283375	37	12	56628997	56628999	In_Frame_Del	DEL	CTG	-	8	586	c.691_693delCTG	c.(691-693)CTGdel	p.L234del
Pat_58	Post-Resistance	TMTC3	160418	37	12	88566417	88566417	Frame_Shift_Del	DEL	T	-	7	392	c.1094delT	c.(1093-1095)CTTfs	p.L365fs
Pat_58	Post-Resistance	RXFP2	122042	37	13	32376429	32376429	Frame_Shift_Del	DEL	A	-	32	451	c.2152delA	c.(2152-2154)AAAfs	p.K718fs
Pat_58	Post-Resistance	LRCH1	23143	37	13	47127609	47127611	In_Frame_Del	DEL	CCA	-	3	6	c.78_80delCCA	c.(76-81)CCCCAC>CCC	p.H33del
Pat_58	Post-Resistance	LRCH1	23143	37	13	47243183	47243186	Frame_Shift_Del	DEL	CCTG	-	13	792	.471_474delCCT	c.(469-474)GCCCTGfs	p.A157fs
Pat_58	Post-Resistance	SIPA1L1	26037	37	14	72190482	72190484	In_Frame_Del	DEL	TCC	-	13	439	.4390_4392delTC	c.(4390-4392)TCCdel	p.S1468del
Pat_58	Post-Resistance	C14orf43	91748	37	14	74205926	74205928	In_Frame_Del	DEL	CTG	-	7	55	c.784_786delCAG	c.(784-786)CAGdel	p.Q262del
Pat_58	Post-Resistance	BTBD7	55727	37	14	93761193	93761193	Frame_Shift_Del	DEL	T	-	7	439	c.173delA	c.(172-174)AAGfs	p.K58fs
Pat_58	Post-Resistance	VPS33B	26276	37	15	91550236	91550238	In_Frame_Del	DEL	TCC	-	8	508	c.642_644delGGA	c.(640-645)GAGGAT>GAT	p.E214del
Pat_58	Post-Resistance	SETD1A	9739	37	16	30982809	30982811	In_Frame_Del	DEL	TCC	-	11	329	.3127_3129delTC	c.(3127-3129)TCCdel	p.S1058del
Pat_58	Post-Resistance	C17orf85	55421	37	17	3721809	3721811	In_Frame_Del	DEL	TCC	-	7	303	.1056_1058delGG	(1054-1059)GAGGAA>GA	.352_353EE>
Pat_58	Post-Resistance	SDF2	6388	37	17	26988863	26988863	Frame_Shift_Del	DEL	C	-	7	975	c.32delG	c.(31-33)GGTfs	p.G11fs
Pat_58	Post-Resistance	ZNF207	7756	37	17	30677314	30677316	In_Frame_Del	DEL	AAG	-	8	883	c.10_12delAAG	c.(10-12)AAGdel	p.K7del
Pat_58	Post-Resistance	FAM134C	162427	37	17	40737147	40737148	Frame_Shift_Del	DEL	TC	-	8	277	c.722_723delGA	c.(721-723)AGAfs	p.R241fs
Pat_58	Post-Resistance	PLCD3	113026	37	17	43192760	43192762	In_Frame_Del	DEL	TCC	-	7	100	.1509_1511delGG	.(1507-1512)GAGGAT>GA	p.E503del
Pat_58	Post-Resistance	TNFSF9	8744	37	19	6531149	6531151	In_Frame_Del	DEL	GCT	-	7	193	c.102_104delGCT	.(100-105)GGGCTG>GG	p.L41del
Pat_58	Post-Resistance	CYP4F3	4051	37	19	15769322	15769322	Frame_Shift_Del	DEL	T	-	9	1204	c.1271delT	c.(1270-1272)GTTfs	p.V424fs
Pat_58	Post-Resistance	NWD1	284434	37	19	16908642	16908642	Frame_Shift_Del	DEL	T	-	10	1393	c.3404delT	c.(3403-3405)GTTfs	p.V1135fs
Pat_58	Post-Resistance	FFAR2	2867	37	19	35940788	35940790	In_Frame_Del	DEL	CTG	-	7	166	c.172_174delCTG	c.(172-174)CTGdel	p.L62del
Pat_58	Post-Resistance	USP34	9736	37	2	61575023	61575025	In_Frame_Del	DEL	TGG	-	13	264	.2265_2267delCC	.(2263-2268)CACCAT>CA	.755_756HH>
Pat_58	Post-Resistance	ZMYND8	23613	37	20	45875072	45875072	Frame_Shift_Del	DEL	T	-	10	706	c.1904delA	c.(1903-1905)AAGfs	p.K635fs
Pat_58	Post-Resistance	SYCP2	10388	37	20	58452518	58452519	Frame_Shift_Ins	INS	-	T	7	153	c.3071_3072insA	c.(3070-3072)AACfs	p.N1024fs
Pat_58	Post-Resistance	C22orf43	51233	37	22	23959767	23959769	In_Frame_Del	DEL	CAT	-	8	288	c.512_514delATG	c.(511-516)GATGCC>GCC	p.D171del
Pat_58	Post-Resistance	APPL1	26060	37	3	57276921	57276921	Frame_Shift_Del	DEL	A	-	8	321	c.453delA	c.(451-453)TCAfs	p.S151fs
Pat_58	Post-Resistance	ETV5	2119	37	3	185783667	185783667	Frame_Shift_Del	DEL	G	-	7	383	c.845delC	c.(844-846)CCAfs	p.P282fs
Pat_58	Post-Resistance	ATP13A3	79572	37	3	194181471	194181473	In_Frame_Del	DEL	GAG	-	9	462	c.139_141delCTC	c.(139-141)CTCdel	p.L47del
Pat_58	Post-Resistance	CPEB2	132864	37	4	15067858	15067858	Frame_Shift_Del	DEL	T	-	8	567	c.1624delT	c.(1624-1626)TTTfs	p.F542fs
Pat_58	Post-Resistance	SORBS2	8470	37	4	186544620	186544622	In_Frame_Del	DEL	GGT	-	10	170	.1949_1951delAC	(1948-1953)CACCGC>CG	p.H650del
Pat_58	Post-Resistance	PAPD7	11044	37	5	6755013	6755014	Frame_Shift_Del	DEL	AC	-	7	105	.1584_1585delAC	c.(1582-1587)AAACACfs	p.K528fs
Pat_58	Post-Resistance	NIPBL	25836	37	5	36985083	36985083	Frame_Shift_Del	DEL	A	-	7	166	c.1801delA	c.(1801-1803)AAAfs	p.K601fs
Pat_58	Post-Resistance	DEK	7913	37	6	18264079	18264081	In_Frame_Del	DEL	TCC	-	7	331	c.138_140delGGA	.(136-141)GAGGAA>GA	p.46_47EE>E
Pat_58	Post-Resistance	CYP21A2	1589	37	6	31975223	31975224	Frame_Shift_Ins	INS	-	T	7	414	c.916_917insT	c.(916-918)GTTfs	p.V306fs
Pat_58	Post-Resistance	SLC17A5	26503	37	6	74351590	74351590	Frame_Shift_Del	DEL	A	-	10	529	c.349delT	c.(349-351)TATfs	p.Y117fs
Pat_58	Post-Resistance	ARHGAP18	93663	37	6	129959602	129959603	Frame_Shift_Ins	INS	-	T	7	724	c.488_489insA	c.(487-489)AACfs	p.N163fs
Pat_58	Post-Resistance	SDK1	221935	37	7	4008947	4008947	Frame_Shift_Del	DEL	G	-	16	1579	c.1605delG	c.(1603-1605)TCGfs	p.S535fs
Pat_58	Post-Resistance	NEUROD6	63974	37	7	31378634	31378635	Frame_Shift_Ins	INS	-	T	10	624	c.248_249insA	c.(247-249)AAGfs	p.K83fs
Pat_58	Post-Resistance	INHBA	3624	37	7	41729741	41729743	In_Frame_Del	DEL	TTC	-	7	127	c.786_788delGAA	c.(784-789)AAGAAA>AAA	.262_263KK>
Pat_58	Post-Resistance	WBSCR17	64409	37	7	71142234	71142234	Frame_Shift_Del	DEL	G	-	10	1838	c.1443delG	c.(1441-1443)CAGfs	p.Q481fs

Pat_58	Post-Resistance	STX1A	6804	37	7	73123425	73123427	In_Frame_Del	DEL	CAT	-	14	1048	c.56_58delATG	c.(55-60)GATGTC>GTC	p.D19del
Pat_58	Post-Resistance	MEPCE	56257	37	7	100028823	100028825	In_Frame_Del	DEL	CCA	-	7	285	.1182_1184delCC	(1180-1185)CGCCAC>CG	p.H399del
Pat_58	Post-Resistance	SRRT	51593	37	7	100482040	100482042	In_Frame_Del	DEL	AGG	-	9	115	c.809_811delAGG	.(808-813)CAGGAG>CA	p.E275del
Pat_58	Post-Resistance	LRRC17	10234	37	7	102584992	102584993	Frame_Shift_Ins	INS	-	A	7	442	c.1264_1265insA	c.(1264-1266)GAAfs	p.E422fs
Pat_58	Post-Resistance	WNT2	7472	37	7	116955171	116955175	Frame_Shift_Del	DEL	TCCTT	-	7	481	538_542delAAGG	c.(538-543)AAGGATfs	p.K180fs
Pat_58	Post-Resistance	ZNF398	57541	37	7	148876153	148876153	Frame_Shift_Del	DEL	C	-	7	782	c.1189delC	c.(1189-1191)CCCfs	p.P397fs
Pat_58	Post-Resistance	CDK5	1020	37	7	150754217	150754217	Frame_Shift_Del	DEL	T	-	7	1117	c.68delA	c.(67-69)AACfs	p.N23fs
Pat_58	Post-Resistance	NOM1	64434	37	7	156743209	156743211	In_Frame_Del	DEL	GAG	-	9	206	c.778_780delGAG	c.(778-780)GAGdel	p.E264del
Pat_58	Post-Resistance	WDR60	55112	37	7	158704353	158704353	Frame_Shift_Del	DEL	A	-	7	468	c.1573delA	c.(1573-1575)AAAfs	p.K525fs
Pat_58	Post-Resistance	MYST3	7994	37	8	41798420	41798422	In_Frame_Del	DEL	CTC	-	11	638	.2977_2979delGA	c.(2977-2979)GAGdel	p.E993del
Pat_58	Post-Resistance	SULF1	23213	37	8	70514026	70514026	Frame_Shift_Del	DEL	T	-	8	910	c.1023delT	c.(1021-1023)CCTfs	p.P341fs
Pat_58	Post-Resistance	INTS8	55656	37	8	95892420	95892421	Frame_Shift_Ins	INS	-	A	7	256	c.2946_2947insA	c.(2944-2949)AGGAAAfs	p.R982fs
Pat_58	Post-Resistance	C9orf131	138724	37	9	35043650	35043650	Frame_Shift_Del	DEL	C	-	8	1214	c.1024delC	c.(1024-1026)CCCfs	p.P342fs
Pat_58	Post-Resistance	NFIL3	4783	37	9	94172779	94172779	Frame_Shift_Del	DEL	T	-	8	552	c.238delA	c.(238-240)AGGfs	p.R80fs
Pat_58	Post-Resistance	POMT1	10585	37	9	134393867	134393879	Frame_Shift_Del	DEL	AGACCATC	-	211	288	386delGAAGACC	2-1386)TGGAAGACCATC	p.W458fs
Pat_58	Post-Resistance	LRCH2	57631	37	X	114468474	114468476	In_Frame_Del	DEL	CCG	-	3	6	c.129_131delCGG	.(127-132)GGCGGG>GG	p.43_44GG>G
Pat_58	Post-Resistance	NKAP	79576	37	X	119072752	119072753	Frame_Shift_Del	DEL	TC	-	11	425	c.407_408delGA	c.(406-408)AGAfs	p.R136fs
Pat_58	Post-Resistance	AFF2	2334	37	X	147733548	147733548	Frame_Shift_Del	DEL	A	-	7	828	c.76delA	c.(76-78)AAAfs	p.K26fs
Pat_59	Pre-Treatment	SNIP1	79753	37	1	38003368	38003370	In_Frame_Del	DEL	TCC	-	7	191	.1170_1172delGG	.(1168-1173)GAGGAA>GA	.390_391EE>
Pat_59	Pre-Treatment	CDC14A	8556	37	1	100843107	100843107	Frame_Shift_Del	DEL	A	-	7	152	c.146delA	c.(145-147)TATfs	p.Y49fs
Pat_59	Pre-Treatment	FMO5	2330	37	1	146684955	146684955	Frame_Shift_Del	DEL	T	-	7	468	c.407delA	c.(406-408)AAGfs	p.K136fs
Pat_59	Pre-Treatment	TCHH	7062	37	1	152081323	152081324	In_Frame_Ins	INS	-	GGC	7	172	.4369_4370insGC	(4369-4371)CAG>CGCCA	.1456_1457ins
Pat_59	Pre-Treatment	TCHH	7062	37	1	152082211	152082213	In_Frame_Del	DEL	CTC	-	8	85	.3480_3482delGA	.(3478-3483)AAGAGA>AA	p.R1163del
Pat_59	Pre-Treatment	PAPPA2	60676	37	1	176762724	176762724	Frame_Shift_Del	DEL	C	-	8	220	c.5049delC	c.(5047-5049)ATCfs	p.I1683fs
Pat_59	Pre-Treatment	FAM5B	57795	37	1	177247719	177247719	Frame_Shift_Del	DEL	A	-	7	594	c.1033delA	c.(1033-1035)AAAfs	p.K345fs
Pat_59	Pre-Treatment	ETNK2	55224	37	1	204120939	204120939	Frame_Shift_Del	DEL	A	-	2	4	c.42delT	c.(40-42)TTTfs	p.F14fs
Pat_59	Pre-Treatment	PARP1	142	37	1	226558192	226558192	Frame_Shift_Del	DEL	C	-	8	194	c.2097delG	c.(2095-2097)GGGfs	p.G699fs
Pat_59	Pre-Treatment	OR2L2	26246	37	1	248201881	248201881	Frame_Shift_Del	DEL	G	-	7	143	c.312delG	c.(310-312)TTGfs	p.L104fs
Pat_59	Pre-Treatment	ZNF365	22891	37	10	64159366	64159366	Frame_Shift_Del	DEL	A	-	9	384	c.1087delA	c.(1087-1089)AAAfs	p.K363fs
Pat_59	Pre-Treatment	FAM53B	9679	37	10	126370292	126370292	Frame_Shift_Del	DEL	A	-	2	4	c.790delT	c.(790-792)TCCfs	p.S264fs
Pat_59	Pre-Treatment	NUP98	4928	37	11	3720389	3720389	Frame_Shift_Del	DEL	T	-	8	335	c.3932delA	c.(3931-3933)AACfs	p.N1311fs
Pat_59	Pre-Treatment	DCHS1	8642	37	11	6662763	6662764	In_Frame_Ins	INS	-	CAA	4	9	c.81_82insTTG	c.(79-84)insTTG	p.33_34insL
Pat_59	Pre-Treatment	C11orf80	79703	37	11	66512290	66512291	In_Frame_Ins	INS	-	GGC	8	4	c.77_78insGGC	c.(76-78)GGG>GGGGCG	p.34_35insA
Pat_59	Pre-Treatment	C11orf54	28970	37	11	93486914	93486914	Frame_Shift_Del	DEL	A	-	9	97	c.221delA	c.(220-222)CAAfs	p.Q74fs
Pat_59	Pre-Treatment	KDM4D	55693	37	11	94730807	94730807	Frame_Shift_Del	DEL	A	-	7	147	c.271delA	c.(271-273)AAAfs	p.K91fs
Pat_59	Pre-Treatment	NPAT	4863	37	11	108032189	108032192	Frame_Shift_Del	DEL	GGTC	-	7	622	3621_3624delGAC	c.(3619-3624)ATGACCfs	p.M1207fs
Pat_59	Pre-Treatment	TMPRSS5	80975	37	11	113561583	113561583	Frame_Shift_Del	DEL	C	-	2	4	c.1043delG	c.(1042-1044)GGCfs	p.G348fs
Pat_59	Pre-Treatment	PRB1	5542	37	12	11506327	11506329	In_Frame_Del	DEL	GGA	-	10	251	c.708_710delTCC	c.(706-711)CCTCCA>CCA	.236_237PP>
Pat_59	Pre-Treatment	PRB1	5542	37	12	11506510	11506512	In_Frame_Del	DEL	GGA	-	42	707	c.525_527delTCC	c.(523-528)CCTCCA>CCA	.175_176PP>
Pat_59	Pre-Treatment	PRB1	5542	37	12	11506632	11506633	In_Frame_Ins	INS	-	GGA	13	1007	c.404_405insTCC	c.(403-405)CCA>CCTCCA	.135_135P>P
Pat_59	Pre-Treatment	PRB2	653247	37	12	11546419	11546421	In_Frame_Del	DEL	GGA	-	7	183	c.591_593delTCC	c.(589-594)CCTCCA>CCA	.197_198PP>
Pat_59	Pre-Treatment	CASC1	55259	37	12	25314066	25314068	In_Frame_Del	DEL	CTC	-	7	599	c.67_69delGAG	c.(67-69)GAGdel	p.E23del
Pat_59	Pre-Treatment	NCKAP5L	57701	37	12	50188584	50188586	In_Frame_Del	DEL	TGG	-	2	4	.3057_3059delCC	.(3055-3060)TACCAA>TA	1019_1020YQ
Pat_59	Pre-Treatment	OR6C75	390323	37	12	55759192	55759192	Frame_Shift_Del	DEL	T	-	7	263	c.298delT	c.(298-300)TTTfs	p.F100fs
Pat_59	Pre-Treatment	MARS	4141	37	12	57883053	57883053	Frame_Shift_Del	DEL	T	-	11	99	c.204delT	c.(202-204)TATfs	p.Y68fs
Pat_59	Pre-Treatment	GNPTAB	79158	37	12	102158002	102158002	Frame_Shift_Del	DEL	T	-	10	312	c.2693delA	c.(2692-2694)AAGfs	p.K898fs
Pat_59	Pre-Treatment	TMEM116	89894	37	12	112374986	112374986	Frame_Shift_Del	DEL	G	-	8	84	c.151delC	c.(151-153)CAAfs	p.Q51fs

Pat_59	Pre-Treatment	TPTE2	93492	37	13	20041394	20041394	Frame_Shift_Del	DEL	A	-	7	114	c.483delT	c.(481-483)TTTfs	p.F161fs
Pat_59	Pre-Treatment	RXFP2	122042	37	13	32376428	32376429	Frame_Shift_Ins	INS	-	A	9	154	c.2151_2152insA	c.(2149-2154)ATTAAAfs	p.I717fs
Pat_59	Pre-Treatment	NBEA	26960	37	13	35517069	35517069	Frame_Shift_Del	DEL	G	-	2	4	c.112delG	c.(112-114)GGGfs	p.G38fs
Pat_59	Pre-Treatment	ABCC4	10257	37	13	95696016	95696016	Frame_Shift_Del	DEL	T	-	12	240	c.3655delA	c.(3655-3657)ATCfs	p.I1219fs
Pat_59	Pre-Treatment	ERCC5	2073	37	13	103459866	103459866	Frame_Shift_Del	DEL	T	-	8	170	c.249delT	c.(247-249)TATfs	p.Y83fs
Pat_59	Pre-Treatment	HEATR5A	25938	37	14	31856337	31856337	Frame_Shift_Del	DEL	T	-	7	285	c.299delA	c.(298-300)AAGfs	p.K100fs
Pat_59	Pre-Treatment	KIAA0391	9692	37	14	35592700	35592700	Frame_Shift_Del	DEL	T	-	7	49	c.249delT	c.(247-249)CATfs	p.H83fs
Pat_59	Pre-Treatment	CREBBP	1387	37	16	3817721	3817721	Frame_Shift_Del	DEL	T	-	7	242	c.3250delA	c.(3250-3252)ATCfs	p.I1084fs
Pat_59	Pre-Treatment	UBN1	29855	37	16	4910691	4910693	In_Frame_Del	DEL	AGA	-	9	504	c.698_700delAGA	c.(697-702)GAGAAG>GAG	p.K238del
Pat_59	Pre-Treatment	1-Sep	1731	37	16	30392716	30392717	Frame_Shift_Ins	INS	-	T	7	163	c.383_384insA	c.(382-384)AACfs	p.N128fs
Pat_59	Pre-Treatment	COQ9	57017	37	16	57486732	57486734	In_Frame_Del	DEL	GAG	-	10	184	c.262_264delGAG	c.(262-264)GAGdel	p.E91del
Pat_59	Pre-Treatment	LGALS9	3965	37	17	25973579	25973579	Frame_Shift_Del	DEL	G	-	7	751	c.634delG	c.(634-636)GCCfs	p.A212fs
Pat_59	Pre-Treatment	SPAG9	9043	37	17	49077041	49077041	Frame_Shift_Del	DEL	T	-	11	218	c.1645delA	c.(1645-1647)AGGfs	p.R549fs
Pat_59	Pre-Treatment	PPM1D	8493	37	17	58677987	58677987	Frame_Shift_Del	DEL	C	-	4	9	c.212delC	c.(211-213)GCAfs	p.A71fs
Pat_59	Pre-Treatment	BPTF	2186	37	17	65822234	65822236	In_Frame_Del	DEL	GAG	-	6	13	c.394_396delGAG	c.(394-396)GAGdel	p.E138del
Pat_59	Pre-Treatment	AZI1	22994	37	17	79166370	79166370	Frame_Shift_Del	DEL	A	-	4	9	c.2462delT	c.(2461-2463)CTGfs	p.L821fs
Pat_59	Pre-Treatment	LMAN1	3998	37	18	57013285	57013285	Splice_Site	DEL	T	-	9	314	c.823_splice	c.e8-1	p.P275_splice
Pat_59	Pre-Treatment	ISYNA1	51477	37	19	18547527	18547528	Frame_Shift_Del	DEL	CG	-	2	4	c.575_576delCG	c.(574-576)GCGfs	p.A192fs
Pat_59	Pre-Treatment	C19orf47	126526	37	19	40834399	40834399	Frame_Shift_Del	DEL	G	-	7	236	c.471delC	c.(469-471)CCCfs	p.P157fs
Pat_59	Pre-Treatment	NOVA2	4858	37	19	46476609	46476610	Translation_Start_Site	INS	-	G	4	7			
Pat_59	Pre-Treatment	FPR3	2359	37	19	52327875	52327875	Frame_Shift_Del	DEL	T	-	13	451	c.874delT	c.(874-876)TTTfs	p.F292fs
Pat_59	Pre-Treatment	ROCK2	9475	37	2	11332379	11332379	Frame_Shift_Del	DEL	G	-	7	707	c.4058delC	c.(4057-4059)CCAfs	p.P1353fs
Pat_59	Pre-Treatment	HNRPLL	92906	37	2	38818670	38818670	Splice_Site	DEL	A	-	7	332	c.308_splice	c.e2+1	p.C103_splice
Pat_59	Pre-Treatment	TET3	200424	37	2	74273651	74273651	Frame_Shift_Del	DEL	T	-	4	9	c.202delT	c.(202-204)TTTfs	p.F68fs
Pat_59	Pre-Treatment	LOXL3	84695	37	2	74779723	74779723	Frame_Shift_Del	DEL	C	-	4	6	c.39delG	c.(37-39)GGGfs	p.G13fs
Pat_59	Pre-Treatment	SCN9A	6335	37	2	167055992	167055992	Frame_Shift_Del	DEL	T	-	7	636	c.5124delA	c.(5122-5124)AAAfs	p.K1708fs
Pat_59	Pre-Treatment	DNAJC10	54431	37	2	183594603	183594605	In_Frame_Del	DEL	CAA	-	7	298	c.662_664delCAA	c.(661-666)TCAAAG>TAG	.221_222SK>
Pat_59	Pre-Treatment	NINL	22981	37	20	25485706	25485708	In_Frame_Del	DEL	GCA	-	4	9	c.524_526delTGC	c.(523-528)CTGCAG>CAG	p.L175del
Pat_59	Pre-Treatment	RBL1	5933	37	20	35663913	35663914	Splice_Site	INS	-	A	4	9	c.1904_splice	c.e15-1	p.D635_splice
Pat_59	Pre-Treatment	FAM83D	81610	37	20	37555322	37555323	In_Frame_Ins	INS	-	GCG	8	12	c.327_328insGCG	c.(325-330)insGCG	p.116_117insA
Pat_59	Pre-Treatment	CNOT10	25904	37	3	32805950	32805950	Frame_Shift_Del	DEL	C	-	8	289	c.1844delC	c.(1843-1845)TCAfs	p.S615fs
Pat_59	Pre-Treatment	NKTR	4820	37	3	42680269	42680271	In_Frame_Del	DEL	GAG	-	7	148	.3073_3075delGA	c.(3073-3075)GAGdel	p.E1029del
Pat_59	Pre-Treatment	VGLL3	389136	37	3	87027857	87027859	In_Frame_Del	DEL	CTC	-	7	49	c.220_222delGAG	c.(220-222)GAGdel	p.E74del
Pat_59	Pre-Treatment	WDR49	151790	37	3	167293789	167293789	Frame_Shift_Del	DEL	C	-	8	252	c.403delG	c.(403-405)GCAfs	p.A135fs
Pat_59	Pre-Treatment	MUC4	4585	37	3	195513456	195513456	Frame_Shift_Del	DEL	A	-	6	4	c.4995delT	c.(4993-4995)CTTfs	p.L1665fs
Pat_59	Pre-Treatment	MUC4	4585	37	3	195516779	195516779	Frame_Shift_Del	DEL	T	-	10	262	c.1672delA	c.(1672-1674)ACAfs	p.T558fs
Pat_59	Pre-Treatment	RNF168	165918	37	3	196214338	196214338	Frame_Shift_Del	DEL	T	-	9	583	c.490delA	c.(490-492)AGGfs	p.R164fs
Pat_59	Pre-Treatment	UGT2B11	10720	37	4	70078331	70078332	Frame_Shift_Del	DEL	AC	-	7	730	c.829_830delGT	c.(829-831)GTTfs	p.V277fs
Pat_59	Pre-Treatment	AFM	173	37	4	74347532	74347532	Frame_Shift_Del	DEL	T	-	7	188	c.40delT	c.(40-42)TTTfs	p.F14fs
Pat_59	Pre-Treatment	ADAMTS16	170690	37	5	5186212	5186213	Frame_Shift_Del	DEL	TA	-	7	170	c.811_812delTA	c.(811-813)TATfs	p.Y271fs
Pat_59	Pre-Treatment	PAM	5066	37	5	102296908	102296910	In_Frame_Del	DEL	AGA	-	7	330	.1137_1139delAG	(1135-1140)CGAGAA>CG	p.E383del
Pat_59	Pre-Treatment	MGC29506	51237	37	5	138725510	138725512	In_Frame_Del	DEL	CAG	-	3	6	c.34_36delCTG	c.(34-36)CTGdel	p.L12del
Pat_59	Pre-Treatment	TRIM26	7726	37	6	30157254	30157254	Frame_Shift_Del	DEL	T	-	9	242	c.845delA	c.(844-846)AAGfs	p.K282fs
Pat_59	Pre-Treatment	STK19	8859	37	6	31939829	31939830	Frame_Shift_Ins	INS	-	A	7	304	c.56_57insA	c.(55-57)GCAfs	p.A19fs
Pat_59	Pre-Treatment	DAXX	1616	37	6	33287898	33287900	In_Frame_Del	DEL	TCC	-	11	82	.1353_1355delGG	(1351-1356)GAGGAA>GA	.451_452EE>
Pat_59	Pre-Treatment	MAP3K7	6885	37	6	91296568	91296570	In_Frame_Del	DEL	GAG	-	9	58	c.33_35delCTC	c.(31-36)TCCTCG>TCG	p.11_12SS>S
Pat_59	Pre-Treatment	PRDM1	639	37	6	106536280	106536280	Frame_Shift_Del	DEL	T	-	7	351	c.247delT	c.(247-249)TTAfs	p.L83fs

Pat_59	Pre-Treatment	C7orf16	10842	37	7	31735179	31735179	Frame_Shift_Del	DEL	A	-	8	327	c.179delA	c.(178-180)CAAfs	p.Q60fs
Pat_59	Pre-Treatment	POLM	27434	37	7	44120414	44120414	Frame_Shift_Del	DEL	G	-	8	98	c.290delC	c.(289-291)CCAfs	p.P97fs
Pat_59	Pre-Treatment	TMEM60	85025	37	7	77423460	77423460	Frame_Shift_Del	DEL	T	-	11	207	c.231delA	c.(229-231)AAAfs	p.K77fs
Pat_59	Pre-Treatment	PCLO	27445	37	7	82545386	82545386	Frame_Shift_Del	DEL	G	-	8	437	c.11916delC	c.(11914-11916)CCCfs	p.P3972fs
Pat_59	Pre-Treatment	SERPINE1	5054	37	7	100773817	100773817	Frame_Shift_Del	DEL	C	-	8	553	c.387delC	c.(385-387)GTCfs	p.V129fs
Pat_59	Pre-Treatment	TNPO3	23534	37	7	128610259	128610259	Frame_Shift_Del	DEL	G	-	7	504	c.2541delC	c.(2539-2541)CCCfs	p.P847fs
Pat_59	Pre-Treatment	SGK223	157285	37	8	8175804	8175806	In_Frame_Del	DEL	TCA	-	8	299	.4079_4081delTG	.(4078-4083)ATGAAG>AA	p.M1360del
Pat_59	Pre-Treatment	ADAM28	10863	37	8	24167472	24167473	Frame_Shift_Ins	INS	-	A	10	134	c.216_217insA	c.(214-219)TTGAAAfs	p.L72fs
Pat_59	Pre-Treatment	SLC26A7	115111	37	8	92406218	92406218	Frame_Shift_Del	DEL	T	-	7	163	c.1886delT	c.(1885-1887)ATTfs	p.I629fs
Pat_59	Pre-Treatment	RGS22	26166	37	8	100990177	100990178	Frame_Shift_Ins	INS	-	T	7	150	c.3486_3487insA	c.(3484-3489)AAATTGfs	p.K1162fs
Pat_59	Pre-Treatment	CRAT	1384	37	9	131864813	131864814	Frame_Shift_Ins	INS	-	C	7	305	c.495_496insG	c.(493-498)GGGAAGfs	p.G165fs
Pat_59	Pre-Treatment	PPP2R4	5524	37	9	131890273	131890273	Frame_Shift_Del	DEL	C	-	2	4	c.247delC	c.(247-249)CAGfs	p.Q83fs
Pat_59	Pre-Treatment	NHS	4810	37	X	17394330	17394330	Frame_Shift_Del	DEL	C	-	2	4	c.450delC	c.(448-450)TTCfs	p.F150fs
Pat_59	Pre-Treatment	NAP1L3	4675	37	X	92928035	92928036	Frame_Shift_Ins	INS	-	C	9	42	c.268_269insG	c.(268-270)GCCfs	p.A90fs
Pat_59	Pre-Treatment	BHLHB9	80823	37	X	102004419	102004421	In_Frame_Del	DEL	GAG	-	8	102	c.496_498delGAG	c.(496-498)GAGdel	p.E171del
Pat_59	Pre-Treatment	TCEAL4	79921	37	X	102841867	102841868	Frame_Shift_Del	DEL	AG	-	2	4	c.264_265delAG	c.(262-267)TCAGAGfs	p.S88fs
Pat_59	Post-Resistance	SCNN1D	6339	37	1	1226736	1226736	Frame_Shift_Del	DEL	G	-	2	4	c.1663delG	c.(1663-1665)GCCfs	p.A555fs
Pat_59	Post-Resistance	HSPG2	3339	37	1	22202765	22202766	Frame_Shift_Del	DEL	CC	-	2	4	c.2959_2960delG	c.(2959-2961)GGAfs	p.G987fs
Pat_59	Post-Resistance	SASS6	163786	37	1	100550947	100550947	Frame_Shift_Del	DEL	G	-	10	788	c.1911delC	c.(1909-1911)TCCfs	p.S637fs
Pat_59	Post-Resistance	FNDC7	163479	37	1	109276138	109276138	Frame_Shift_Del	DEL	A	-	7	155	c.2124delA	c.(2122-2124)CCAfs	p.P708fs
Pat_59	Post-Resistance	PRG4	10216	37	1	186276524	186276526	In_Frame_Del	DEL	AGG	-	11	237	.1673_1675delAG	(1672-1677)AAGGAG>AA	p.E559del
Pat_59	Post-Resistance	PIH1D2	120379	37	11	111941931	111941932	Frame_Shift_Ins	INS	-	T	10	380	c.377_378insA	c.(376-378)AATfs	p.N126fs
Pat_59	Post-Resistance	SNX19	399979	37	11	130775872	130775872	Frame_Shift_Del	DEL	G	-	7	161	c.2419delC	c.(2419-2421)CAAfs	p.Q807fs
Pat_59	Post-Resistance	DDX12	440081	37	12	9574061	9574061	Frame_Shift_Del	DEL	G	-	7	368	c.1975delC	c.(1975-1977)CTGfs	p.L659fs
Pat_59	Post-Resistance	PRB1	5542	37	12	11506327	11506329	In_Frame_Del	DEL	GGA	-	8	133	c.708_710delTCC	c.(706-711)CCTCCA>CCA	.236_237PP>
Pat_59	Post-Resistance	PRB1	5542	37	12	11506632	11506633	In_Frame_Ins	INS	-	GGA	7	405	c.404_405insTCC	c.(403-405)CCA>CCTCCA	.135_135P>P
Pat_59	Post-Resistance	RERG	85004	37	12	15262412	15262412	Frame_Shift_Del	DEL	C	-	8	956	c.232delG	c.(232-234)GAAfs	p.E78fs
Pat_59	Post-Resistance	PPM1A	5494	37	14	60752371	60752371	Frame_Shift_Del	DEL	G	-	7	452	c.864delG	c.(862-864)TTGfs	p.L288fs
Pat_59	Post-Resistance	KIAA0317	9870	37	14	75151191	75151191	Frame_Shift_Del	DEL	T	-	7	133	c.209delA	c.(208-210)TATfs	p.Y70fs
Pat_59	Post-Resistance	C14orf174	161394	37	14	77844868	77844869	Frame_Shift_Ins	INS	-	A	7	344	c.1107_1108insA	c.(1105-1110)GAGAAAfs	p.E369fs
Pat_59	Post-Resistance	TTC8	123016	37	14	89338724	89338726	In_Frame_Del	DEL	CAA	-	7	323	.1323_1325delCA	.(1321-1326)GTCAAC>GT	p.N445del
Pat_59	Post-Resistance	C14orf102	55051	37	14	90798215	90798215	Frame_Shift_Del	DEL	C	-	7	287	c.34delG	c.(34-36)GAGfs	p.E12fs
Pat_59	Post-Resistance	NFAT5	10725	37	16	69693775	69693775	Frame_Shift_Del	DEL	C	-	8	229	c.1288delC	c.(1288-1290)CAAfs	p.Q430fs
Pat_59	Post-Resistance	STXBP4	252983	37	17	53077006	53077007	Frame_Shift_Del	DEL	TG	-	7	158	c.301_302delTG	c.(301-303)TGGfs	p.W101fs
Pat_59	Post-Resistance	EXOC7	23265	37	17	74097358	74097358	Frame_Shift_Del	DEL	G	-	7	225	c.411delC	c.(409-411)AACfs	p.N137fs
Pat_59	Post-Resistance	CEBPZ	10153	37	2	37454908	37454908	Frame_Shift_Del	DEL	T	-	8	54	c.1428delA	c.(1426-1428)AAAfs	p.K476fs
Pat_59	Post-Resistance	IFIH1	64135	37	2	163134716	163134716	Frame_Shift_Del	DEL	T	-	7	140	c.1764delA	c.(1762-1764)AAAfs	p.K588fs
Pat_59	Post-Resistance	OSBPL6	114880	37	2	179248813	179248813	Frame_Shift_Del	DEL	C	-	9	652	c.1923delC	c.(1921-1923)TTCfs	p.F641fs
Pat_59	Post-Resistance	TNS1	7145	37	2	218712998	218712998	Frame_Shift_Del	DEL	A	-	8	88	c.1867delT	c.(1867-1869)TCGfs	p.S623fs
Pat_59	Post-Resistance	RQCD1	9125	37	2	219449364	219449364	Frame_Shift_Del	DEL	T	-	7	445	c.350delT	c.(349-351)CTTfs	p.L117fs
Pat_59	Post-Resistance	C20orf194	25943	37	20	3355680	3355681	Frame_Shift_Del	DEL	GG	-	8	819	c.501_502delCC	c.(499-504)TCCCAAfs	p.S167fs
Pat_59	Post-Resistance	XPNPEP3	63929	37	22	41318413	41318413	Frame_Shift_Del	DEL	G	-	7	715	c.1132delG	c.(1132-1134)GGGfs	p.G378fs
Pat_59	Post-Resistance	TUBGCP6	85378	37	22	50666360	50666360	Frame_Shift_Del	DEL	A	-	4	2	c.1388delT	c.(1387-1389)TTCfs	p.F463fs
Pat_59	Post-Resistance	CRIPAK	285464	37	4	1389236	1389237	Frame_Shift_Ins	INS	-	CA	8	361	c.937_938insCA	c.(937-939)TCAfs	p.S313fs
Pat_59	Post-Resistance	CRIPAK	285464	37	4	1389297	1389298	Frame_Shift_Del	DEL	CA	-	10	461	c.998_999delCA	c.(997-999)TCAfs	p.S333fs
Pat_59	Post-Resistance	GABRG1	2565	37	4	46060358	46060358	Frame_Shift_Del	DEL	A	-	7	137	c.792delT	c.(790-792)TTTfs	p.F264fs
Pat_59	Post-Resistance	KIAA0947	23379	37	5	5447608	5447609	Frame_Shift_Del	DEL	TT	-	2	4	c.493_494delTT	c.(493-495)TTTfs	p.F165fs

Pat_59	Post-Resistance	HNRNPA0	10949	37	5	137089109	137089111	In_Frame_Del	DEL	CCG	-	2	4	c.645_647delCGG	.(643-648)GGCGGT>GG	.215_216GG>
Pat_59	Post-Resistance	BTN2A2	10385	37	6	26384091	26384093	In_Frame_Del	DEL	CCT	-	15	241	c.42_44delCCT	c.(40-45)TCCCTC>TCC	p.L24del
Pat_59	Post-Resistance	RRAGD	58528	37	6	90121645	90121647	In_Frame_Del	DEL	TCC	-	6	7	c.66_68delGGA	c.(64-69)GAGGAT>GAT	p.E22del
Pat_59	Post-Resistance	PMPCB	9512	37	7	102952294	102952295	Frame_Shift_Del	DEL	TA	-	7	245	c.1280_1281delT	c.(1279-1281)TTAfs	p.L427fs
Pat_59	Post-Resistance	RBM33	155435	37	7	155531073	155531074	Frame_Shift_Del	DEL	CA	-	9	258	.1713_1714delC	c.(1711-1716)CCCACAfs	p.P571fs
Pat_59	Post-Resistance	RANBP6	26953	37	9	6013873	6013873	Frame_Shift_Del	DEL	C	-	8	308	c.1735delG	c.(1735-1737)GAAfs	p.E579fs
Pat_63	Pre-Treatment	MAP3K6	9064	37	1	27687695	27687696	Frame_Shift_Ins	INS	-	G	4	6	c.1784_1785insC	c.(1783-1785)CCGfs	p.P595fs
Pat_63	Pre-Treatment	HDAC1	3065	37	1	32782289	32782289	Frame_Shift_Del	DEL	G	-	7	245	c.186delG	c.(184-186)GAGfs	p.E62fs
Pat_63	Pre-Treatment	AMY2B	280	37	1	104118151	104118151	Frame_Shift_Del	DEL	C	-	7	517	c.1090delC	c.(1090-1092)CAAfs	p.Q364fs
Pat_63	Pre-Treatment	FAM102B	284611	37	1	109172239	109172240	Frame_Shift_Del	DEL	GG	-	8	155	.1000_1001delG	c.(1000-1002)GGGfs	p.G334fs
Pat_63	Pre-Treatment	ANP32E	81611	37	1	150201420	150201420	Frame_Shift_Del	DEL	C	-	7	238	c.478delG	c.(478-480)GAGfs	p.E160fs
Pat_63	Pre-Treatment	ILF2	3608	37	1	153635185	153635185	Frame_Shift_Del	DEL	G	-	7	457	c.1008delC	c.(1006-1008)GCCfs	p.A336fs
Pat_63	Pre-Treatment	PLA2G4A	5321	37	1	186925445	186925447	In_Frame_Del	DEL	TGA	-	14	255	.1548_1550delTG	.(1546-1551)TTTGAT>TT	p.D519del
Pat_63	Pre-Treatment	LAMB3	3914	37	1	209795971	209795971	Frame_Shift_Del	DEL	C	-	7	225	c.2611delG	c.(2611-2613)GAGfs	p.E871fs
Pat_63	Pre-Treatment	RUFY2	55680	37	10	70156583	70156583	Frame_Shift_Del	DEL	T	-	10	50	c.457delA	c.(457-459)ATGfs	p.M153fs
Pat_63	Pre-Treatment	DGKZ	8525	37	11	46391529	46391529	Frame_Shift_Del	DEL	C	-	7	138	c.1104delC	c.(1102-1104)CGCfs	p.R368fs
Pat_63	Pre-Treatment	MMP1	4312	37	11	102668791	102668793	In_Frame_Del	DEL	CAG	-	7	93	c.31_33delCTG	c.(31-33)CTGdel	p.L11del
Pat_63	Pre-Treatment	PAN3	255967	37	13	28713064	28713064	Frame_Shift_Del	DEL	G	-	4	7	c.270delG	c.(268-270)CTGfs	p.L90fs
Pat_63	Pre-Treatment	ITM2B	9445	37	13	48807583	48807583	Frame_Shift_Del	DEL	C	-	3	4	c.87delC	c.(85-87)ATCfs	p.I29fs
Pat_63	Pre-Treatment	FOXN3	1112	37	14	89629149	89629151	In_Frame_Del	DEL	GAG	-	5	5	.1080_1082delCT	.(1078-1083)TCCTCA>TC	.360_361SS>
Pat_63	Pre-Treatment	BTBD7	55727	37	14	93720048	93720048	Frame_Shift_Del	DEL	T	-	7	141	c.1697delA	c.(1696-1698)AATfs	p.N566fs
Pat_63	Pre-Treatment	SEPHS2	22928	37	16	30456879	30456879	Frame_Shift_Del	DEL	A	-	4	7	c.170delT	c.(169-171)ATGfs	p.M57fs
Pat_63	Pre-Treatment	WSCD1	23302	37	17	5984072	5984074	In_Frame_Del	DEL	CTG	-	4	6	c.94_96delCTG	c.(94-96)CTGdel	p.L35del
Pat_63	Pre-Treatment	FMNL1	752	37	17	43319435	43319437	In_Frame_Del	DEL	CCG	-	2	4	.1807_1809delCC	c.(1807-1809)CCGdel	p.P612del
Pat_63	Pre-Treatment	MAP3K14	9020	37	17	43344473	43344473	Frame_Shift_Del	DEL	C	-	4	4	c.2419delG	c.(2419-2421)GATfs	p.D807fs
Pat_63	Pre-Treatment	ACE	1636	37	17	61574550	61574550	Frame_Shift_Del	DEL	G	-	3	4	c.3744delG	c.(3742-3744)CTGfs	p.L1248fs
Pat_63	Pre-Treatment	SPOPL	339745	37	2	139326585	139326586	Frame_Shift_Del	DEL	CG	-	7	554	c.1114_1115delCG	c.(1114-1116)CGAfs	p.R372fs
Pat_63	Pre-Treatment	THBD	7056	37	20	23029278	23029279	Frame_Shift_Del	DEL	GC	-	4	8	c.863_864delGC	c.(862-864)TGCfs	p.C288fs
Pat_63	Pre-Treatment	DOK5	55816	37	20	53260114	53260114	Frame_Shift_Del	DEL	C	-	4	5	c.853delC	c.(853-855)CAAfs	p.Q285fs
Pat_63	Pre-Treatment	PCNT	5116	37	21	47831343	47831343	Frame_Shift_Del	DEL	C	-	4	5	c.5356delC	c.(5356-5358)CAGfs	p.Q1786fs
Pat_63	Pre-Treatment	TRIOBP	11078	37	22	38120098	38120109	In_Frame_Del	DEL	TCCAGAAC	-	7	61	1546delCCTCCA	1548)GCCTCCAGAACCT	p.SRTS513del
Pat_63	Pre-Treatment	TRIOBP	11078	37	22	38120245	38120253	In_Frame_Del	DEL	CTCCAGA	-	8	155	2_1690delCCTCC	1-1692)GCCTCCAGAACC	p.SRT562del
Pat_63	Pre-Treatment	ARFGAP3	26286	37	22	43213780	43213780	Frame_Shift_Del	DEL	T	-	18	1303	c.896delA	c.(895-897)AATfs	p.N299fs
Pat_63	Pre-Treatment	TMCC1	23023	37	3	129546725	129546725	Frame_Shift_Del	DEL	G	-	4	8	c.497delC	c.(496-498)TCTfs	p.S166fs
Pat_63	Pre-Treatment	LMLN	89782	37	3	197687255	197687255	Frame_Shift_Del	DEL	C	-	7	201	c.163delC	c.(163-165)CCCfs	p.P55fs
Pat_63	Pre-Treatment	CRIPAK	285464	37	4	1389236	1389237	Frame_Shift_Ins	INS	-	CA	13	325	c.937_938insCA	c.(937-939)TCAfs	p.S313fs
Pat_63	Pre-Treatment	WFS1	7466	37	4	6293083	6293084	Frame_Shift_Del	DEL	TC	-	3	6	c.620_621delTC	c.(619-621)GTCfs	p.V207fs
Pat_63	Pre-Treatment	CCNA2	890	37	4	122740016	122740017	Frame_Shift_Ins	INS	-	A	7	121	c.1054_1055insT	c.(1054-1056)CCAfs	p.P352fs
Pat_63	Pre-Treatment	DIAPH1	1729	37	5	140953387	140953387	Frame_Shift_Del	DEL	G	-	4	5	c.2030delC	c.(2029-2031)CCAfs	p.P677fs
Pat_63	Pre-Treatment	KLHDC3	116138	37	6	42986216	42986216	Frame_Shift_Del	DEL	T	-	8	180	c.655delT	c.(655-657)TTTfs	p.F219fs
Pat_63	Pre-Treatment	ATG5	9474	37	6	106764043	106764043	Frame_Shift_Del	DEL	C	-	7	420	c.41delG	c.(40-42)GGAfs	p.G14fs
Pat_63	Pre-Treatment	BCL7B	9275	37	7	72957887	72957888	Frame_Shift_Del	DEL	CA	-	8	477	c.255_256delTG	c.(253-258)CTTGAAfs	p.L85fs
Pat_63	Pre-Treatment	SEMA3C	10512	37	7	80546049	80546051	In_Frame_Del	DEL	TAG	-	7	331	c.47_49delCTA	c.(46-51)TCTATC>TTC	p.16_17SI>F
Pat_63	Pre-Treatment	DOCK4	9732	37	7	111407097	111407097	Frame_Shift_Del	DEL	G	-	7	196	c.3879delC	c.(3877-3879)AGCfs	p.S1293fs
Pat_63	Pre-Treatment	MET	4233	37	7	116339595	116339595	Frame_Shift_Del	DEL	G	-	7	576	c.457delG	c.(457-459)GACfs	p.D153fs
Pat_63	Pre-Treatment	IDO2	169355	37	8	39836691	39836692	Frame_Shift_Del	DEL	GC	-	4	4	c.340_341delGC	c.(340-342)GCGfs	p.A114fs
Pat_63	Pre-Treatment	SULF1	23213	37	8	70514026	70514026	Frame_Shift_Del	DEL	T	-	10	1278	c.1023delT	c.(1021-1023)CCTfs	p.P341fs

Pat_63	Pre-Treatment	ATAD2	29028	37	8	124368685	124368685	Frame_Shift_Del	DEL	A	-	9	251	c.1590delT	c.(1588-1590)TTTfs	p.F530fs
Pat_63	Pre-Treatment	ANXA13	312	37	8	124724928	124724928	Frame_Shift_Del	DEL	G	-	8	860	c.81delC	c.(79-81)TGCfs	p.C27fs
Pat_63	Pre-Treatment	MYC	4609	37	8	128750605	128750607	In_Frame_Del	DEL	CAG	-	7	264	c.97_99delCAG	c.(97-99)CAGdel	p.Q37del
Pat_63	Pre-Treatment	KIF24	347240	37	9	34256285	34256285	Frame_Shift_Del	DEL	G	-	4	9	c.3320delC	c.(3319-3321)TCAfs	p.S1107fs
Pat_63	Pre-Treatment	ALDH1A1	216	37	9	75531976	75531976	Frame_Shift_Del	DEL	G	-	8	398	c.895delC	c.(895-897)CAGfs	p.Q299fs
Pat_63	Pre-Treatment	TPRN	286262	37	9	140087025	140087027	In_Frame_Del	DEL	TCC	-	4	8	.1659_1661delGG	(1657-1662)GAGGAA>GA	.553_554EE>
Pat_63	Pre-Treatment	CDKL5	6792	37	X	18631336	18631336	Frame_Shift_Del	DEL	A	-	8	141	c.2217delA	c.(2215-2217)CTAfs	p.L739fs
Pat_63	Pre-Treatment	ZBTB33	10009	37	X	119388255	119388257	In_Frame_Del	DEL	GAG	-	7	180	c.985_987delGAG	c.(985-987)GAGdel	p.E333del
Pat_63	Pre-Treatment	PRRG3	79057	37	X	150869296	150869297	Frame_Shift_Ins	INS	-	G	4	8	c.487_488insG	c.(487-489)CGGfs	p.R163fs
Pat_63	Post-Resistance	PHACTR4	65979	37	1	28785729	28785730	Frame_Shift_Ins	INS	-	A	9	74	c.150_151insA	c.(148-153)AGGAAAfs	p.R50fs
Pat_63	Post-Resistance	ROR1	4919	37	1	64608186	64608187	Frame_Shift_Del	DEL	CA	-	7	324	c.1027_1028delCA	c.(1027-1029)CACfs	p.H343fs
Pat_63	Post-Resistance	FNDC7	163479	37	1	109276138	109276138	Frame_Shift_Del	DEL	A	-	7	93	c.2124delA	c.(2122-2124)CCAfs	p.P708fs
Pat_63	Post-Resistance	S100A1	6271	37	1	153604197	153604197	Frame_Shift_Del	DEL	G	-	7	1554	c.165delG	c.(163-165)GTGfs	p.V55fs
Pat_63	Post-Resistance	SLAMF1	6504	37	1	160589601	160589601	Frame_Shift_Del	DEL	T	-	9	292	c.829delA	c.(829-831)AGCfs	p.S277fs
Pat_63	Post-Resistance	PRG4	10216	37	1	186276548	186276550	In_Frame_Del	DEL	AGG	-	12	307	.1697_1699delAG	(1696-1701)AAGGAG>AA	p.E567del
Pat_63	Post-Resistance	CTSE	1510	37	1	206325294	206325294	Frame_Shift_Del	DEL	C	-	8	400	c.519delC	c.(517-519)GGCfs	p.G173fs
Pat_63	Post-Resistance	RUFY2	55680	37	10	70156583	70156583	Frame_Shift_Del	DEL	T	-	8	60	c.457delA	c.(457-459)ATGfs	p.M153fs
Pat_63	Post-Resistance	SAAL1	113174	37	11	18127531	18127533	In_Frame_Del	DEL	CCT	-	7	44	c.56_58delAGG	c.(55-60)GAGGTG>GTG	p.E19del
Pat_63	Post-Resistance	FADS2	9415	37	11	61607885	61607887	In_Frame_Del	DEL	TCC	-	7	421	c.398_400delTCC	c.(397-402)TTCCTC>TTC	p.L137del
Pat_63	Post-Resistance	IFFO1	25900	37	12	6649704	6649706	In_Frame_Del	DEL	GGC	-	8	220	.1623_1625delGC	(1621-1626)CCGCCA>CC	.541_542PP>
Pat_63	Post-Resistance	DHX37	57647	37	12	125473494	125473494	Frame_Shift_Del	DEL	G	-	7	85	c.75delC	c.(73-75)CCCfs	p.P25fs
Pat_63	Post-Resistance	LIG4	3981	37	13	108862104	108862105	Frame_Shift_Del	DEL	GA	-	7	387	c.1512_1513delTC	c.(1510-1515)TCTCGTfs	p.S504fs
Pat_63	Post-Resistance	VPS18	57617	37	15	41188208	41188208	Frame_Shift_Del	DEL	A	-	108	690	c.164delA	c.(163-165)GAGfs	p.E55fs
Pat_63	Post-Resistance	FAM174B	400451	37	15	93198679	93198684	In_Frame_Del	DEL	TGGAGC	-	4	5	206_211delGCTC	(205-213)AGCTCCAAC>A	p.SS69del
Pat_63	Post-Resistance	AFTPH	54812	37	2	64778672	64778674	In_Frame_Del	DEL	GAT	-	9	345	c.64_66delGAT	c.(64-66)GATdel	p.D26del
Pat_63	Post-Resistance	LRP2	4036	37	2	170136098	170136099	Frame_Shift_Ins	INS	-	A	8	29	c.1348_1349insT	c.(1348-1350)TCAfs	p.S450fs
Pat_63	Post-Resistance	PRKAG3	53632	37	2	219692729	219692729	Frame_Shift_Del	DEL	G	-	4	9	c.772delC	c.(772-774)CTGfs	p.L258fs
Pat_63	Post-Resistance	OLIG1	116448	37	21	34442677	34442679	In_Frame_Del	DEL	CCT	-	6	12	c.125_127delCCT	c.(124-129)CCCTCC>CCC	p.S48del
Pat_63	Post-Resistance	DNAJB7	150353	37	22	41257114	41257115	Frame_Shift_Ins	INS	-	T	10	952	c.884_885insA	c.(883-885)AAGfs	p.K295fs
Pat_63	Post-Resistance	SREBF2	6721	37	22	42271637	42271637	Frame_Shift_Del	DEL	C	-	7	608	c.1295delC	c.(1294-1296)TCCfs	p.S432fs
Pat_63	Post-Resistance	TCF20	6942	37	22	42610776	42610778	In_Frame_Del	DEL	TGC	-	13	337	c.534_536delGCA	c.(532-537)CAGCAA>CAA	.178_179QQ>
Pat_63	Post-Resistance	ARFGAP3	26286	37	22	43213780	43213780	Frame_Shift_Del	DEL	T	-	19	1761	c.896delA	c.(895-897)AATfs	p.N299fs
Pat_63	Post-Resistance	NCEH1	57552	37	3	172365826	172365826	Frame_Shift_Del	DEL	T	-	8	100	c.313delA	c.(313-315)AGCfs	p.S105fs
Pat_63	Post-Resistance	AASDH	132949	37	4	57220269	57220269	Frame_Shift_Del	DEL	A	-	9	111	c.1319delT	c.(1318-1320)TTGfs	p.L440fs
Pat_63	Post-Resistance	CCNO	10309	37	5	54529340	54529340	Frame_Shift_Del	DEL	G	-	6	8	c.12delC	c.(10-12)CCCfs	p.P4fs
Pat_63	Post-Resistance	DEPDC1B	55789	37	5	59938636	59938637	Splice_Site	INS	-	A	13	70	c.757_splice	c.e6+1	p.W253_splice
Pat_63	Post-Resistance	MSH3	4437	37	5	79970915	79970915	Frame_Shift_Del	DEL	A	-	10	387	c.1141delA	c.(1141-1143)AAAfs	p.K381fs
Pat_63	Post-Resistance	LARP1	23367	37	5	154173389	154173390	Frame_Shift_Ins	INS	-	C	9	659	c.898_899insC	c.(898-900)GCCfs	p.A300fs
Pat_63	Post-Resistance	RDBP	7936	37	6	31926206	31926206	Frame_Shift_Del	DEL	G	-	7	366	c.18delC	c.(16-18)CCCfs	p.P6fs
Pat_63	Post-Resistance	SLC35F1	222553	37	6	118606435	118606435	Frame_Shift_Del	DEL	C	-	8	749	c.936delC	c.(934-936)GTCfs	p.V312fs
Pat_63	Post-Resistance	DNAH11	8701	37	7	21698641	21698641	Frame_Shift_Del	DEL	A	-	2	4	c.5335delA	c.(5335-5337)AAAfs	p.K1779fs
Pat_63	Post-Resistance	EGFR	1956	37	7	55221748	55221748	Frame_Shift_Del	DEL	C	-	7	332	c.792delC	c.(790-792)TGCfs	p.C264fs
Pat_63	Post-Resistance	PEX1	5189	37	7	92146721	92146721	Frame_Shift_Del	DEL	T	-	7	171	c.1108delA	c.(1108-1110)ATTfs	p.I370fs
Pat_63	Post-Resistance	PXDNL	137902	37	8	52359603	52359603	Frame_Shift_Del	DEL	C	-	7	2188	c.1486delG	c.(1486-1488)GTGfs	p.V496fs
Pat_63	Post-Resistance	SULF1	23213	37	8	70514026	70514026	Frame_Shift_Del	DEL	T	-	21	2547	c.1023delT	c.(1021-1023)CCTfs	p.P341fs
Pat_63	Post-Resistance	ZNF704	619279	37	8	81733778	81733778	Frame_Shift_Del	DEL	T	-	9	765	c.52delA	c.(52-54)ATGfs	p.M18fs
Pat_63	Post-Resistance	ZHX1	11244	37	8	124266775	124266775	Frame_Shift_Del	DEL	T	-	10	1528	c.1412delA	c.(1411-1413)AAGfs	p.K471fs

Pat_63	Post-Resistance	ATAD2	29028	37	8	124368685	124368685	Frame_Shift_Del	DEL	A	-	8	313	c.1590delT	c.(1588-1590)TTTfs	p.F530fs
Pat_63	Post-Resistance	MYC	4609	37	8	128750605	128750607	In_Frame_Del	DEL	CAG	-	7	471	c.97_99delCAG	c.(97-99)CAGdel	p.Q37del
Pat_63	Post-Resistance	CNKSR2	22866	37	X	21627678	21627680	In_Frame_Del	DEL	GAG	-	12	101	.2635_2637delGA	c.(2635-2637)GAGdel	p.E886del
Pat_63	Post-Resistance	ZFP92	139735	37	X	152686591	152686591	Frame_Shift_Del	DEL	G	-	2	4	c.756delG	c.(754-756)CTGfs	p.L252fs
Pat_70	Pre-Treatment	PLEKHG5	57449	37	1	6536011	6536013	In_Frame_Del	DEL	CTC	-	18	458	c.295_297delGAG	c.(295-297)GAGdel	p.E99del
Pat_70	Pre-Treatment	MST1P9	11223	37	1	17085995	17085996	Frame_Shift_Ins	INS	-	C	11	232	c.901_902insG	c.(901-903)GCGfs	p.A301fs
Pat_70	Pre-Treatment	SFRS4	6429	37	1	29475219	29475221	In_Frame_Del	DEL	CTT	-	12	156	.1186_1188delAA	c.(1186-1188)AAGdel	p.K396del
Pat_70	Pre-Treatment	TMCO2	127391	37	1	40713708	40713709	Frame_Shift_Del	DEL	TC	-	10	341	c.43_44delTC	c.(43-45)TCTfs	p.S15fs
Pat_70	Pre-Treatment	CPT2	1376	37	1	53676267	53676284	In_Frame_Del	DEL	GTGGCAAT	-	23	173	elGAGTAGTGGC	ATGAGTAGTGGCAATGA	SSGNEE308d
Pat_70	Pre-Treatment	USP24	23358	37	1	55620379	55620380	Frame_Shift_Ins	INS	-	TGAA	52	115	.1182_1183insTTC	c.(1180-1185)TCAGATfs	p.S394fs
Pat_70	Pre-Treatment	TCHH	7062	37	1	152083818	152083820	In_Frame_Del	DEL	CGG	-	9	81	.1873_1875delCC	c.(1873-1875)CCGdel	p.P625del
Pat_70	Pre-Treatment	KCNN3	3782	37	1	154842331	154842333	In_Frame_Del	DEL	TGC	-	7	84	c.108_110delGCA	c.(106-111)CAGCAA>CAA	p.36_37QQ>Q
Pat_70	Pre-Treatment	KIAA0907	22889	37	1	155886422	155886423	Frame_Shift_Del	DEL	CT	-	9	379	.1546_1547delAG	c.(1546-1548)AGGfs	p.R516fs
Pat_70	Pre-Treatment	LOC642587	642587	37	1	209605637	209605648	In_Frame_Del	DEL	CAGCAGCA	-	7	36	263delAGCAGCA	264)GTAGCAGCAGCAGC	p.AAAA93del
Pat_70	Pre-Treatment	TMEM63A	9725	37	1	226034840	226034842	In_Frame_Del	DEL	CTG	-	13	392	.2323_2325delCA	c.(2323-2325)CAGdel	p.Q775del
Pat_70	Pre-Treatment	AGT	183	37	1	230839055	230839055	Frame_Shift_Del	DEL	A	-	7	104	c.1290delT	c.(1288-1290)TTTfs	p.F430fs
Pat_70	Pre-Treatment	CPXM2	119587	37	10	125528165	125528167	In_Frame_Del	DEL	CAG	-	8	447	.1174_1176delCT	c.(1174-1176)CTGdel	p.L392del
Pat_70	Pre-Treatment	PAMR1	25891	37	11	35513670	35513670	Frame_Shift_Del	DEL	C	-	13	976	c.302delG	c.(301-303)GGTfs	p.G101fs
Pat_70	Pre-Treatment	KBTBD4	55709	37	11	47599139	47599139	Frame_Shift_Del	DEL	A	-	8	1015	c.413delT	c.(412-414)TTGfs	p.L138fs
Pat_70	Pre-Treatment	STX5	6811	37	11	62598584	62598585	Frame_Shift_Ins	INS	-	G	9	28	c.131_132insC	c.(130-132)CCAfs	p.P44fs
Pat_70	Pre-Treatment	DDX6	1656	37	11	118629613	118629614	Splice_Site	INS	-	G	12	401	c.865_splice	c.e9-1	p.N289_splice
Pat_70	Pre-Treatment	CHEK1	1111	37	11	125505377	125505378	Frame_Shift_Ins	INS	-	A	12	420	c.667_668insA	c.(667-669)GAAfs	p.E223fs
Pat_70	Pre-Treatment	PRB2	653247	37	12	11546506	11546508	In_Frame_Del	DEL	TTG	-	16	443	c.504_506delCAA	c.(502-507)AACAAG>AAG	p.N168del
Pat_70	Pre-Treatment	SFRS2IP	9169	37	12	46318575	46318577	In_Frame_Del	DEL	GGT	-	8	492	.3840_3842delAC	(3838-3843)CCACCC>CC	1280_1281PP
Pat_70	Pre-Treatment	SYCP3	50511	37	12	102122901	102122901	Frame_Shift_Del	DEL	T	-	7	58	c.643delA	c.(643-645)ATTfs	p.I215fs
Pat_70	Pre-Treatment	POLE	5426	37	12	133220099	133220100	Frame_Shift_Del	DEL	CA	-	16	659	.4337_4338delTG	c.(4336-4338)GTGfs	p.V1446fs
Pat_70	Pre-Treatment	PABPC3	5042	37	13	25671804	25671806	In_Frame_Del	DEL	GCT	-	8	82	.1468_1470delGC	c.(1468-1470)GCTdel	p.A496del
Pat_70	Pre-Treatment	TEP1	7011	37	14	20852647	20852647	Frame_Shift_Del	DEL	C	-	10	650	c.3242delG	c.(3241-3243)GGTfs	p.G1081fs
Pat_70	Pre-Treatment	APEX1	328	37	14	20923820	20923820	Frame_Shift_Del	DEL	A	-	9	303	c.16delA	c.(16-18)AAAfs	p.K6fs
Pat_70	Pre-Treatment	LRP10	26020	37	14	23341527	23341529	In_Frame_Del	DEL	CCT	-	23	301	c.15_17delCCT	c.(13-18)ACCCTC>ACC	p.L11del
Pat_70	Pre-Treatment	PSMA6	5687	37	14	35782215	35782216	Frame_Shift_Ins	INS	-	A	7	382	c.538_539insA	c.(538-540)GAAfs	p.E180fs
Pat_70	Pre-Treatment	C14orf106	55320	37	14	45693722	45693722	Frame_Shift_Del	DEL	T	-	8	151	c.2068delA	c.(2068-2070)AGTfs	p.S690fs
Pat_70	Pre-Treatment	ZNF609	23060	37	15	64972995	64972997	In_Frame_Del	DEL	CAC	-	10	630	.4096_4098delCA	c.(4096-4098)CACdel	p.H1371del
Pat_70	Pre-Treatment	SLC24A1	9187	37	15	65918177	65918179	In_Frame_Del	DEL	CTG	-	13	178	.1759_1761delCT	c.(1759-1761)CTGdel	p.L591del
Pat_70	Pre-Treatment	APOB48R	55911	37	16	28507398	28507424	Splice_Site	DEL	CAGGAGG	-	15	31	c.1043_splice	c.e2+1	p.A348_splice
Pat_70	Pre-Treatment	EIF3CL	728689	37	16	28734579	28734581	In_Frame_Del	DEL	GAG	-	9	1502	c.871_873delGAG	c.(871-873)GAGdel	p.E295del
Pat_70	Pre-Treatment	SETD1A	9739	37	16	30982809	30982811	In_Frame_Del	DEL	TCC	-	8	174	.3127_3129delTC	c.(3127-3129)TCCdel	p.S1058del
Pat_70	Pre-Treatment	SLC9A5	6553	37	16	67300017	67300019	In_Frame_Del	DEL	GAG	-	12	173	.2107_2109delGA	c.(2107-2109)GAGdel	p.E708del
Pat_70	Pre-Treatment	ENO3	2027	37	17	4859894	4859894	Frame_Shift_Del	DEL	G	-	7	511	c.1094delG	c.(1093-1095)TGGfs	p.W365fs
Pat_70	Pre-Treatment	KDM6B	23135	37	17	7751859	7751864	In_Frame_Del	DEL	CACCAC	-	16	142	253_2258delCACC	251-2259)GTCACCACC>	p.TT760del
Pat_70	Pre-Treatment	TRPV2	51393	37	17	16335490	16335492	In_Frame_Del	DEL	TGC	-	9	217	.1865_1867delTG	(1864-1869)GTGCTG>GT	p.L627del
Pat_70	Pre-Treatment	CDK12	51755	37	17	37686901	37686901	Frame_Shift_Del	DEL	C	-	7	895	c.3805delC	c.(3805-3807)CCCfs	p.P1269fs
Pat_70	Pre-Treatment	KRT10	3858	37	17	38978766	38978768	In_Frame_Del	DEL	TCC	-	8	79	c.70_72delGGA	c.(70-72)GGAdel	p.G24del
Pat_70	Pre-Treatment	KRTAP4-5	85289	37	17	39305775	39305776	In_Frame_Ins	INS	-	GCAGCTG	22	101	5insGCCCCAGCT	)CAG>CGCCCCAGCTG	81_82insRPS
Pat_70	Pre-Treatment	FMNL1	752	37	17	43319434	43319435	In_Frame_Ins	INS	-	CCG	7	6	.1806_1807insCC	c.(1804-1809)insCCG	p.612_613insP
Pat_70	Pre-Treatment	NPEPPS	9520	37	17	45669428	45669429	Splice_Site	INS	-	A	13	28	c.1365_splice	c.e11+2	p.K455_splice
Pat_70	Pre-Treatment	CXXC1	30827	37	18	47812275	47812277	In_Frame_Del	DEL	CTG	-	12	174	c.481_483delCAG	c.(481-483)CAGdel	p.Q161del

Pat_70	Pre-Treatment	LDLR	3949	37	19	11216065	11216065	Frame_Shift_Del	DEL	C	-	8	446	c.483delC	c.(481-483)ATCfs	p.I161fs
Pat_70	Pre-Treatment	HAMP	57817	37	19	35773520	35773522	In_Frame_Del	DEL	CTC	-	14	421	c.40_42delCTC	c.(40-42)CTCdel	p.L18del
Pat_70	Pre-Treatment	ZFP36	7538	37	19	39898948	39898950	In_Frame_Del	DEL	CAC	-	8	764	c.590_592delCAC	c.(589-594)TCACCA>TCA	p.P201del
Pat_70	Pre-Treatment	LYPD3	27076	37	19	43969653	43969655	In_Frame_Del	DEL	AGC	-	17	799	c.69_71delGCT	c.(67-72)CTGCTT>CTT	p.23_24LL>L
Pat_70	Pre-Treatment	SLC8A2	6543	37	19	47935681	47935683	In_Frame_Del	DEL	TCC	-	19	361	.2130_2132delGG	(2128-2133)GAGGAC>GA	p.E710del
Pat_70	Pre-Treatment	TMC4	147798	37	19	54675747	54675749	In_Frame_Del	DEL	TCC	-	8	147	c.201_203delGGA	c.(199-204)GAGGAT>GAT	p.E67del
Pat_70	Pre-Treatment	LILRB2	10288	37	19	54780707	54780709	In_Frame_Del	DEL	GAG	-	7	281	.1435_1437delCT	c.(1435-1437)CTCdel	p.L479del
Pat_70	Pre-Treatment	LILRB1	10859	37	19	55146148	55146150	In_Frame_Del	DEL	CTC	-	7	74	.1417_1419delCT	c.(1417-1419)CTCdel	p.L479del
Pat_70	Pre-Treatment	ZNF579	163033	37	19	56089908	56089909	In_Frame_Ins	INS	-	CCG	7	10	.1097_1098insCG	(1096-1098)GGG>GGCGG	.366_366G>G
Pat_70	Pre-Treatment	C2orf71	388939	37	2	29295647	29295649	In_Frame_Del	DEL	TCC	-	9	387	.1479_1481delGG	(1477-1482)GAGGAA>GA	.493_494EE>
Pat_70	Pre-Treatment	ITPRIPL1	150771	37	2	96992793	96992795	In_Frame_Del	DEL	GAG	-	12	158	c.424_426delGAG	c.(424-426)GAGdel	p.E147del
Pat_70	Pre-Treatment	SLC20A1	6574	37	2	113416607	113416608	Frame_Shift_Del	DEL	AG	-	7	85	c.984_985delAG	c.(982-987)CCAGAGfs	p.P328fs
Pat_70	Pre-Treatment	UGGT1	56886	37	2	128938648	128938649	Splice_Site	INS	-	GGCCCTT	7	168	c.4083_splice	c.e36+2	.Q1361_splice
Pat_70	Pre-Treatment	NCOA6	23054	37	20	33330968	33330970	In_Frame_Del	DEL	TGC	-	11	209	.3090_3092delGC	.(3088-3093)CAGCAA>CA	030_1031QQ
Pat_70	Pre-Treatment	SFRS15	57466	37	21	33044257	33044259	In_Frame_Del	DEL	GCT	-	7	311	.2897_2899delAG	(2896-2901)CAGCCA>CC	p.Q966del
Pat_70	Pre-Treatment	TRIOBP	11078	37	22	38120029	38120031	In_Frame_Del	DEL	CCT	-	12	310	.1466_1468delCC	(1465-1470)GCCTCC>GC	p.S491del
Pat_70	Pre-Treatment	TRIOBP	11078	37	22	38120323	38120325	In_Frame_Del	DEL	CCT	-	11	644	.1760_1762delCC	(1759-1764)GCCTCC>GC	p.S589del
Pat_70	Pre-Treatment	RANGAP1	5905	37	22	41650469	41650471	In_Frame_Del	DEL	TCC	-	15	215	.1101_1103delGG	(1099-1104)GAGGAA>GA	.367_368EE>
Pat_70	Pre-Treatment	XPC	7508	37	3	14219966	14219968	In_Frame_Del	DEL	CCT	-	9	163	c.101_103delAGG	c.(100-105)GAGGAT>GAT	p.E34del
Pat_70	Pre-Treatment	QRICH1	54870	37	3	49094313	49094314	In_Frame_Ins	INS	-	TGC	36	73	.1319_1320insGC	.(1318-1320)CAA>CAGCA	.440_440Q>Q
Pat_70	Pre-Treatment	ROBO2	6092	37	3	77657038	77657038	Frame_Shift_Del	DEL	C	-	7	139	c.3226delC	c.(3226-3228)CCCfs	p.P1076fs
Pat_70	Pre-Treatment	LNP1	348801	37	3	100148586	100148588	In_Frame_Del	DEL	GAT	-	9	1040	c.13_15delGAT	c.(13-15)GATdel	p.D10del
Pat_70	Pre-Treatment	CRIPAK	285464	37	4	1388900	1388901	Frame_Shift_Del	DEL	CA	-	13	686	c.601_602delCA	c.(601-603)CACfs	p.H201fs
Pat_70	Pre-Treatment	CRIPAK	285464	37	4	1389392	1389393	Frame_Shift_Del	DEL	CA	-	12	1369	c.1093_1094delC	c.(1093-1095)CACfs	p.H365fs
Pat_70	Pre-Treatment	PROM1	8842	37	4	15995680	15995680	Frame_Shift_Del	DEL	T	-	7	170	c.1697delA	c.(1696-1698)AATfs	p.N566fs
Pat_70	Pre-Treatment	MMRN1	22915	37	4	90844391	90844393	In_Frame_Del	DEL	AGC	-	9	1178	c.923_925delAGC	.(922-927)GAGCAG>GA	p.Q313del
Pat_70	Pre-Treatment	RRH	10692	37	4	110756541	110756541	Frame_Shift_Del	DEL	T	-	7	182	c.317delT	c.(316-318)ATTfs	p.I106fs
Pat_70	Pre-Treatment	SDHA	6389	37	5	256484	256485	Frame_Shift_Del	DEL	TT	-	23	389	c.1944_1945delTT	c.(1942-1947)ACTTTGfs	p.T648fs
Pat_70	Pre-Treatment	HLA-F	3134	37	6	29694802	29694803	Frame_Shift_Ins	INS	-	T	15	715	c.1179_1180insT	c.(1177-1182)TTGTTTfs	p.L393fs
Pat_70	Pre-Treatment	KIAA1949	170954	37	6	30653494	30653496	In_Frame_Del	DEL	TGC	-	7	114	c.300_302delGCA	c.(298-303)CAGCAA>CAA	.100_101QQ>
Pat_70	Pre-Treatment	ZBTB22	9278	37	6	33283253	33283254	Frame_Shift_Del	DEL	CC	-	8	1203	c.1440_1441delG	c.(1438-1443)GGGGACfs	p.G480fs
Pat_70	Pre-Treatment	MDN1	23195	37	6	90432674	90432675	Frame_Shift_Ins	INS	-	T	8	413	c.5966_5967insA	c.(5965-5967)AAGfs	p.K1989fs
Pat_70	Pre-Treatment	MAP3K7	6885	37	6	91296568	91296570	In_Frame_Del	DEL	GAG	-	8	99	c.33_35delCTC	c.(31-36)TCCTCG>TCG	p.11_12SS>S
Pat_70	Pre-Treatment	HOXA1	3198	37	7	27135314	27135316	In_Frame_Del	DEL	CGA	-	7	134	c.216_218delTCG	c.(214-219)CATCAC>CAC	p.72_73HH>H
Pat_70	Pre-Treatment	GARS	2617	37	7	30634583	30634585	In_Frame_Del	DEL	CTG	-	7	130	c.46_48delCTG	c.(46-48)CTGdel	p.L20del
Pat_70	Pre-Treatment	DTX2	113878	37	7	76112249	76112249	Frame_Shift_Del	DEL	A	-	22	1228	c.693delA	c.(691-693)CCAfs	p.P231fs
Pat_70	Pre-Treatment	RSBN1L	222194	37	7	77326220	77326222	In_Frame_Del	DEL	CCG	-	10	140	c.434_436delCCG	.(433-438)CCCGCC>CC	p.A151del
Pat_70	Pre-Treatment	MCM7	4176	37	7	99695272	99695272	Frame_Shift_Del	DEL	C	-	7	1266	c.1082delG	c.(1081-1083)GGTfs	p.G361fs
Pat_70	Pre-Treatment	MUC17	140453	37	7	100684131	100684133	In_Frame_Del	DEL	CTC	-	36	1591	.9434_9436delCT	.(9433-9438)TCTCCT>TC	p.P3146del
Pat_70	Pre-Treatment	MUC17	140453	37	7	100684307	100684308	In_Frame_Ins	INS	-	CTC	61	1466	.9610_9611insCT	.(9610-9612)TCT>TCTCC	.3204_3205ins
Pat_70	Pre-Treatment	SCRIB	23513	37	8	144890900	144890902	In_Frame_Del	DEL	TCC	-	8	45	.1992_1994delGG	(1990-1995)GAGGAA>GA	.664_665EE>
Pat_70	Pre-Treatment	KANK1	23189	37	9	732475	732477	In_Frame_Del	DEL	GAG	-	10	365	.3103_3105delGA	c.(3103-3105)GAGdel	p.E1039del
Pat_70	Pre-Treatment	TAF1L	138474	37	9	32633584	32633584	Frame_Shift_Del	DEL	T	-	7	165	c.1994delA	c.(1993-1995)AAGfs	p.K665fs
Pat_70	Pre-Treatment	NR4A3	8013	37	9	102590616	102590618	In_Frame_Del	DEL	CAC	-	10	72	c.292_294delCAC	c.(292-294)CACdel	p.H108del
Pat_70	Pre-Treatment	PRDM12	59335	37	9	133543701	133543702	Splice_Site	DEL	GT	-	16	192	c.570_splice	c.e3+1	p.E190_splice
Pat_70	Pre-Treatment	CEL	1056	37	9	135941982	135941982	Frame_Shift_Del	DEL	G	-	7	408	c.613delG	c.(613-615)GGGfs	p.G205fs
Pat_70	Pre-Treatment	TSPAN7	7102	37	X	38530682	38530682	Frame_Shift_Del	DEL	C	-	7	761	c.323delC	c.(322-324)TCAfs	p.S108fs

Pat_70	Pre-Treatment	PHF8	23133	37	X	54011405	54011407	In_Frame_Del	DEL	CTC	-	13	368	.2491_2493delGA	c.(2491-2493)GAGdel	p.E831del
Pat_70	Pre-Treatment	BHLHB9	80823	37	X	102004419	102004421	In_Frame_Del	DEL	GAG	-	7	311	c.496_498delGAG	c.(496-498)GAGdel	p.E171del
Pat_70	Pre-Treatment	FAM199X	139231	37	X	103432837	103432839	In_Frame_Del	DEL	CAG	-	7	330	c.846_848delCAG	.(844-849)GCCAGC>GCC	p.S286del
Pat_70	Pre-Treatment	SLC25A5	292	37	X	118603706	118603707	Frame_Shift_Ins	INS	-	G	33	745	c.194_195insG	c.(193-195)CAGfs	p.Q65fs
Pat_70	Pre-Treatment	CD99L2	83692	37	X	149984524	149984526	In_Frame_Del	DEL	GTG	-	7	466	c.156_158delCAC	c.(154-159)ACCACA>ACA	p.52_53TT>T
Pat_70	Pre-Treatment	BCAP31	10134	37	X	152981034	152981043	Frame_Shift_Del	DEL	CCTCTGGG	-	35	239	_304delGCCCAG	295-306)GCCCAGAGGAA	p.A99fs
Pat_70	Post-Resistance	RPL22	6146	37	1	6257785	6257785	Frame_Shift_Del	DEL	T	-	7	253	c.44delA	c.(43-45)AAGfs	p.K15fs
Pat_70	Post-Resistance	PLEKHG5	57449	37	1	6536011	6536013	In_Frame_Del	DEL	CTC	-	29	618	c.295_297delGAG	c.(295-297)GAGdel	p.E99del
Pat_70	Post-Resistance	AADACL3	126767	37	1	12785494	12785494	Frame_Shift_Del	DEL	G	-	17	724	c.584delG	c.(583-585)TGTfs	p.C195fs
Pat_70	Post-Resistance	MST1P9	11223	37	1	17085995	17085996	Frame_Shift_Ins	INS	-	C	18	358	c.901_902insG	c.(901-903)GCGfs	p.A301fs
Pat_70	Post-Resistance	RPS6KA1	6195	37	1	26885311	26885311	Frame_Shift_Del	DEL	C	-	9	496	c.1098delC	c.(1096-1098)ATCfs	p.I366fs
Pat_70	Post-Resistance	XKR8	55113	37	1	28293145	28293147	In_Frame_Del	DEL	CTG	-	9	611	c.622_624delCTG	c.(622-624)CTGdel	p.L211del
Pat_70	Post-Resistance	SFRS4	6429	37	1	29475219	29475221	In_Frame_Del	DEL	CTT	-	17	348	.1186_1188delAA	c.(1186-1188)AAGdel	p.K396del
Pat_70	Post-Resistance	SFRS4	6429	37	1	29475575	29475575	Frame_Shift_Del	DEL	G	-	8	1472	c.832delC	c.(832-834)CAAfs	p.Q278fs
Pat_70	Post-Resistance	ZMYM6	9204	37	1	35485090	35485090	Frame_Shift_Del	DEL	T	-	8	426	c.292delA	c.(292-294)ATGfs	p.M98fs
Pat_70	Post-Resistance	ZMYM4	9202	37	1	35846959	35846960	Frame_Shift_Ins	INS	-	A	9	272	c.1281_1282insA	c.(1279-1284)CTGAAAfs	p.L427fs
Pat_70	Post-Resistance	INPP5B	3633	37	1	38411495	38411495	Frame_Shift_Del	DEL	C	-	7	319	c.85delG	c.(85-87)GACfs	p.D29fs
Pat_70	Post-Resistance	TMCO2	127391	37	1	40713708	40713709	Frame_Shift_Del	DEL	TC	-	13	879	c.43_44delTC	c.(43-45)TCTfs	p.S15fs
Pat_70	Post-Resistance	STIL	6491	37	1	47767947	47767947	Frame_Shift_Del	DEL	T	-	7	420	c.224delA	c.(223-225)AATfs	p.N75fs
Pat_70	Post-Resistance	CPT2	1376	37	1	53676267	53676284	In_Frame_Del	DEL	GTGGCAAT	-	10	399	elGAGTAGTGGC	ATGAGTAGTGGCAATGA	SSGNEE308d
Pat_70	Post-Resistance	USP24	23358	37	1	55620379	55620380	Frame_Shift_Ins	INS	-	TGAA	55	389	.1182_1183insTTC	c.(1180-1185)TCAGATfs	p.S394fs
Pat_70	Post-Resistance	TNNI3K	51086	37	1	74957824	74957826	In_Frame_Del	DEL	CTT	-	13	1099	.2225_2227delCT	.(2224-2229)CCTTCT>CC	p.S746del
Pat_70	Post-Resistance	BCL10	8915	37	1	85736511	85736511	Frame_Shift_Del	DEL	T	-	16	450	c.136delA	c.(136-138)ATAfs	p.I46fs
Pat_70	Post-Resistance	CDC7	8317	37	1	91967356	91967357	Frame_Shift_Ins	INS	-	A	10	286	c.83_84insA	c.(82-84)TTAfs	p.L28fs
Pat_70	Post-Resistance	IGSF3	3321	37	1	117122270	117122272	In_Frame_Del	DEL	GTC	-	7	60	.3076_3078delGA	c.(3076-3078)GACdel	p.D1026del
Pat_70	Post-Resistance	ADAM30	11085	37	1	120436591	120436591	Frame_Shift_Del	DEL	T	-	8	1059	c.2369delA	c.(2368-2370)AAGfs	p.K790fs
Pat_70	Post-Resistance	NBPF9	400818	37	1	144615246	144615247	Splice_Site	INS	-	AG	8	135	c.114_splice	c.e3+2	p.L38_splice
Pat_70	Post-Resistance	HFE2	148738	37	1	145415369	145415371	In_Frame_Del	DEL	GAG	-	8	464	c.188_190delGAG	.(187-192)CGAGGA>CGA	p.G69del
Pat_70	Post-Resistance	ADAMTSL4	54507	37	1	150530506	150530506	Frame_Shift_Del	DEL	G	-	8	546	c.2263delG	c.(2263-2265)GGGfs	p.G755fs
Pat_70	Post-Resistance	MCL1	4170	37	1	150551492	150551494	In_Frame_Del	DEL	TCC	-	14	591	c.513_515delGGA	.(511-516)GAGGAC>GAC	p.E171del
Pat_70	Post-Resistance	TCHH	7062	37	1	152082957	152082959	In_Frame_Del	DEL	CTC	-	12	399	.2734_2736delGA	c.(2734-2736)GAGdel	p.E912del
Pat_70	Post-Resistance	LCE4A	199834	37	1	152681693	152681698	In_Frame_Del	DEL	TGTGGT	-	12	389	142_147delTGTG	c.(142-147)TGTGGTdel	p.CG48del
Pat_70	Post-Resistance	SLC27A3	11000	37	1	153751859	153751860	Frame_Shift_Ins	INS	-	C	7	740	c.1926_1927insC	c.(1924-1929)CGTCCCfs	p.R642fs
Pat_70	Post-Resistance	KIAA0907	22889	37	1	155886422	155886423	Frame_Shift_Del	DEL	CT	-	25	917	.1546_1547delAG	c.(1546-1548)AGGfs	p.R516fs
Pat_70	Post-Resistance	ISG20L2	81875	37	1	156694023	156694023	Frame_Shift_Del	DEL	G	-	14	573	c.865delC	c.(865-867)CTCfs	p.L289fs
Pat_70	Post-Resistance	ARHGAP30	257106	37	1	161039361	161039361	Frame_Shift_Del	DEL	A	-	7	501	c.54delT	c.(52-54)TTTfs	p.F18fs
Pat_70	Post-Resistance	PVRL4	81607	37	1	161044057	161044059	In_Frame_Del	DEL	CAC	-	7	581	.1105_1107delGT	c.(1105-1107)GTGdel	p.V369del
Pat_70	Post-Resistance	PVRL4	81607	37	1	161044104	161044106	In_Frame_Del	DEL	CCA	-	9	736	.1058_1060delTG	(1057-1062)GTGGGT>GG	p.V353del
Pat_70	Post-Resistance	GPA33	10223	37	1	167024257	167024259	In_Frame_Del	DEL	GCA	-	8	642	c.781_783delTGC	c.(781-783)TGCdel	p.C261del
Pat_70	Post-Resistance	C1orf114	57821	37	1	169366580	169366580	Frame_Shift_Del	DEL	T	-	7	159	c.1265delA	c.(1264-1266)AAGfs	p.K422fs
Pat_70	Post-Resistance	PAPPA2	60676	37	1	176762724	176762724	Frame_Shift_Del	DEL	C	-	11	872	c.5049delC	c.(5047-5049)ATCfs	p.I1683fs
Pat_70	Post-Resistance	CACNA1E	777	37	1	181680102	181680103	Frame_Shift_Del	DEL	AG	-	33	674	.1068_1069delAG	c.(1066-1071)AAAGAGfs	p.K356fs
Pat_70	Post-Resistance	APOBEC4	403314	37	1	183616826	183616828	In_Frame_Del	DEL	TTC	-	10	787	.1089_1091delGA	.(1087-1092)AAGAAA>AA	.363_364KK>
Pat_70	Post-Resistance	CAMSAP1L1	23271	37	1	200822549	200822549	Frame_Shift_Del	DEL	A	-	9	341	c.3782delA	c.(3781-3783)CAAfs	p.Q1261fs
Pat_70	Post-Resistance	IPO9	55705	37	1	201843998	201844000	In_Frame_Del	DEL	GAG	-	12	473	.2872_2874delGA	c.(2872-2874)GAGdel	p.E962del
Pat_70	Post-Resistance	LOC642587	642587	37	1	209605637	209605648	In_Frame_Del	DEL	CAGCAGCA	-	10	82	263delAGCAGCA	264)GTAGCAGCAGCAGC	p.AAAA93del
Pat_70	Post-Resistance	INTS7	25896	37	1	212115191	212115193	In_Frame_Del	DEL	TGC	-	7	917	.2862_2864delGC	.(2860-2865)CAGCAA>CA	.954_955QQ>

Pat_70	Post-Resistance	TMEM63A	9725	37	1	226034840	226034842	In_Frame_Del	DEL	CTG	-	37	766	.2323_2325delCA	c.(2323-2325)CAGdel	p.Q775del
Pat_70	Post-Resistance	AGT	183	37	1	230839055	230839055	Frame_Shift_Del	DEL	A	-	8	309	c.1290delT	c.(1288-1290)TTTfs	p.F430fs
Pat_70	Post-Resistance	KMO	8564	37	1	241753511	241753511	Frame_Shift_Del	DEL	T	-	8	682	c.1206delT	c.(1204-1206)ACTfs	p.T402fs
Pat_70	Post-Resistance	ANK3	288	37	10	61828727	61828729	In_Frame_Del	DEL	GTG	-	10	264	11910_11912delC	11908-11913)ACCACT>A	3970_3971TT
Pat_70	Post-Resistance	ZMIZ1	57178	37	10	81072446	81072446	Frame_Shift_Del	DEL	C	-	8	1241	c.3144delC	c.(3142-3144)GACfs	p.D1048fs
Pat_70	Post-Resistance	PANK1	53354	37	10	91359120	91359120	Frame_Shift_Del	DEL	T	-	7	1206	c.1199delA	c.(1198-1200)AAGfs	p.K400fs
Pat_70	Post-Resistance	SEMA4G	57715	37	10	102743836	102743836	Frame_Shift_Del	DEL	A	-	7	538	c.2480delA	c.(2479-2481)GAAfs	p.E827fs
Pat_70	Post-Resistance	LZTS2	84445	37	10	102763415	102763417	In_Frame_Del	DEL	CCT	-	16	648	c.560_562delCCT	.(559-564)GCCTCC>GCC	p.S197del
Pat_70	Post-Resistance	TACC2	10579	37	10	123970380	123970380	Frame_Shift_Del	DEL	C	-	10	625	c.6440delC	c.(6439-6441)ACCfs	p.T2147fs
Pat_70	Post-Resistance	CPXM2	119587	37	10	125528165	125528167	In_Frame_Del	DEL	CAG	-	12	1142	.1174_1176delCT	c.(1174-1176)CTGdel	p.L392del
Pat_70	Post-Resistance	LOC653544	653544	37	10	135491013	135491014	Frame_Shift_Ins	INS	-	T	9	548	c.624_625insT	c.(622-627)GCCAGGfs	p.A208fs
Pat_70	Post-Resistance	TSPAN4	7106	37	11	864443	864445	In_Frame_Del	DEL	CTG	-	15	403	c.262_264delCTG	c.(262-264)CTGdel	p.L92del
Pat_70	Post-Resistance	OR10A5	144124	37	11	6867223	6867225	In_Frame_Del	DEL	TTC	-	13	409	c.310_312delTTC	c.(310-312)TTCdel	p.F108del
Pat_70	Post-Resistance	OR10A2	341276	37	11	6891253	6891255	In_Frame_Del	DEL	TTC	-	15	558	c.268_270delTTC	c.(268-270)TTCdel	p.F94del
Pat_70	Post-Resistance	C11orf46	120534	37	11	30352754	30352754	Frame_Shift_Del	DEL	A	-	18	610	c.259delA	c.(259-261)AAAfs	p.K87fs
Pat_70	Post-Resistance	OR8I2	120586	37	11	55861308	55861308	Frame_Shift_Del	DEL	T	-	15	1003	c.525delT	c.(523-525)CATfs	p.H175fs
Pat_70	Post-Resistance	FADS2	9415	37	11	61607885	61607887	In_Frame_Del	DEL	TCC	-	11	888	c.398_400delTCC	c.(397-402)TTCCTC>TTC	p.L137del
Pat_70	Post-Resistance	RARRES3	5920	37	11	63313708	63313709	Frame_Shift_Ins	INS	-	A	11	618	c.475_476insA	c.(475-477)CAAfs	p.Q159fs
Pat_70	Post-Resistance	FAU	2197	37	11	64888248	64888250	In_Frame_Del	DEL	TCT	-	7	340	c.305_307delAGA	c.(304-309)AAGACA>ACA	p.K102del
Pat_70	Post-Resistance	KDM2A	22992	37	11	67018079	67018081	In_Frame_Del	DEL	GAG	-	9	134	.2578_2580delGA	c.(2578-2580)GAGdel	p.E866del
Pat_70	Post-Resistance	ATG16L2	89849	37	11	72528863	72528865	In_Frame_Del	DEL	AGG	-	9	300	c.281_283delAGG	.(280-285)CAGGAG>CAG	p.E98del
Pat_70	Post-Resistance	C11orf30	56946	37	11	76207304	76207304	Frame_Shift_Del	DEL	C	-	9	858	c.1154delC	c.(1153-1155)TCCfs	p.S385fs
Pat_70	Post-Resistance	MMP12	4321	37	11	102738793	102738794	Splice_Site	INS	-	T	11	49	c.630_splice	c.e5+1	p.T210_splice
Pat_70	Post-Resistance	DDX10	1662	37	11	108788635	108788637	In_Frame_Del	DEL	TGA	-	7	182	.2340_2342delTG	.(2338-2343)AGTGAT>AG	p.D788del
Pat_70	Post-Resistance	CHEK1	1111	37	11	125505377	125505378	Frame_Shift_Ins	INS	-	A	22	872	c.667_668insA	c.(667-669)GAAfs	p.E223fs
Pat_70	Post-Resistance	PRDM10	56980	37	11	129772249	129772251	In_Frame_Del	DEL	TGG	-	9	1039	.3440_3442delCC	.(3439-3444)ACCAAC>AA	p.T1147del
Pat_70	Post-Resistance	KLHDC5	57542	37	12	27950769	27950769	Frame_Shift_Del	DEL	G	-	8	423	c.1188delG	c.(1186-1188)GTGfs	p.V396fs
Pat_70	Post-Resistance	FAR2	55711	37	12	29450110	29450110	Frame_Shift_Del	DEL	A	-	7	686	c.522delA	c.(520-522)CCAfs	p.P174fs
Pat_70	Post-Resistance	C12orf35	55196	37	12	32134718	32134720	In_Frame_Del	DEL	CCT	-	7	520	c.829_831delCCT	c.(829-831)CCTdel	p.P281del
Pat_70	Post-Resistance	KIF21A	55605	37	12	39735366	39735368	In_Frame_Del	DEL	TCC	-	12	258	.1860_1862delGG	(1858-1863)GAGGAA>GA	.620_621EE>
Pat_70	Post-Resistance	ANO6	196527	37	12	45610140	45610142	In_Frame_Del	DEL	GGA	-	9	134	c.36_38delGGA	c.(34-39)ATGGAG>ATG	p.E16del
Pat_70	Post-Resistance	SFRS2IP	9169	37	12	46318575	46318577	In_Frame_Del	DEL	GGT	-	9	781	.3840_3842delAC	(3838-3843)CCACCC>CC	1280_1281PP
Pat_70	Post-Resistance	SFRS2IP	9169	37	12	46320707	46320708	Frame_Shift_Del	DEL	TC	-	14	596	.2776_2777delG	c.(2776-2778)GAAfs	p.E926fs
Pat_70	Post-Resistance	PRPF40B	25766	37	12	50025258	50025258	Frame_Shift_Del	DEL	C	-	7	697	c.93delC	c.(91-93)ATCfs	p.I31fs
Pat_70	Post-Resistance	TENC1	23371	37	12	53451561	53451561	Frame_Shift_Del	DEL	C	-	7	1102	c.963delC	c.(961-963)TTCfs	p.F321fs
Pat_70	Post-Resistance	AMHR2	269	37	12	53818999	53819001	In_Frame_Del	DEL	CTG	-	7	566	c.475_477delCTG	c.(475-477)CTGdel	p.L162del
Pat_70	Post-Resistance	OR10A7	121364	37	12	55615114	55615116	In_Frame_Del	DEL	CTT	-	7	774	c.306_308delCTT	c.(304-309)TACTTC>TAC	p.F107del
Pat_70	Post-Resistance	SLC39A5	283375	37	12	56628997	56628999	In_Frame_Del	DEL	CTG	-	7	662	c.691_693delCTG	c.(691-693)CTGdel	p.L234del
Pat_70	Post-Resistance	GOLGA2B	55592	37	12	100551828	100551830	In_Frame_Del	DEL	CCT	-	12	162	c.23_25delAGG	c.(22-27)GAGGTG>GTG	p.E8del
Pat_70	Post-Resistance	CUX2	23316	37	12	111758235	111758237	In_Frame_Del	DEL	TCC	-	7	230	.2422_2424delTC	c.(2422-2424)TCCdel	p.S813del
Pat_70	Post-Resistance	GCN1L1	10985	37	12	120595737	120595739	In_Frame_Del	DEL	CTC	-	9	270	.3001_3003delGA	c.(3001-3003)GAGdel	p.E1001del
Pat_70	Post-Resistance	SBNO1	55206	37	12	123794283	123794283	Frame_Shift_Del	DEL	T	-	14	573	c.3416delA	c.(3415-3417)AATfs	p.N1139fs
Pat_70	Post-Resistance	NCOR2	9612	37	12	124848228	124848228	Frame_Shift_Del	DEL	G	-	7	778	c.2925delC	c.(2923-2925)CCCfs	p.P975fs
Pat_70	Post-Resistance	EP400	57634	37	12	132547138	132547139	In_Frame_Ins	INS	-	CAG	14	320	.8226_8227insCA	c.(8224-8229)insCAG	.2748_2749ins
Pat_70	Post-Resistance	POLE	5426	37	12	133220099	133220100	Frame_Shift_Del	DEL	CA	-	38	1337	.4337_4338delTG	c.(4336-4338)GTGfs	p.V1446fs
Pat_70	Post-Resistance	TPTE2	93492	37	13	20041394	20041394	Frame_Shift_Del	DEL	A	-	9	347	c.483delT	c.(481-483)TTTfs	p.F161fs
Pat_70	Post-Resistance	PABPC3	5042	37	13	25671804	25671806	In_Frame_Del	DEL	GCT	-	7	224	.1468_1470delGC	c.(1468-1470)GCTdel	p.A496del

Pat_70	Post-Resistance	CDK8	1024	37	13	26975609	26975611	In_Frame_Del	DEL	CAG	-	7	266	.1117_1119delCA	c.(1117-1119)CAGdel	p.Q377del
Pat_70	Post-Resistance	WASF3	10810	37	13	27250862	27250863	Splice_Site	DEL	GT	-	12	559	c.716_splice	c.e7+1	p.R239_splice
Pat_70	Post-Resistance	RXFP2	122042	37	13	32376429	32376429	Frame_Shift_Del	DEL	A	-	15	261	c.2152delA	c.(2152-2154)AAAfs	p.K718fs
Pat_70	Post-Resistance	ZC3H13	23091	37	13	46542016	46542017	Frame_Shift_Del	DEL	CT	-	12	396	.3943_3944delA	c.(3943-3945)AGGfs	p.R1315fs
Pat_70	Post-Resistance	LRCH1	23143	37	13	47243183	47243186	Frame_Shift_Del	DEL	CCTG	-	17	1386	.471_474delCCT	c.(469-474)GCCCTGfs	p.A157fs
Pat_70	Post-Resistance	RBM26	64062	37	13	79918806	79918807	Frame_Shift_Ins	INS	-	T	11	182	c.2187_2188insA	c.(2185-2190)AAACAGfs	p.K729fs
Pat_70	Post-Resistance	TOX4	9878	37	14	21961060	21961062	In_Frame_Del	DEL	GCT	-	18	404	.1285_1287delGC	c.(1285-1287)GCTdel	p.A434del
Pat_70	Post-Resistance	LRP10	26020	37	14	23341527	23341529	In_Frame_Del	DEL	CCT	-	17	562	c.15_17delCCT	c.(13-18)ACCCTC>ACC	p.L11del
Pat_70	Post-Resistance	IRF9	10379	37	14	24633132	24633134	In_Frame_Del	DEL	AGC	-	7	303	c.541_543delAGC	c.(541-543)AGCdel	p.S187del
Pat_70	Post-Resistance	G2E3	55632	37	14	31074771	31074772	Frame_Shift_Ins	INS	-	A	7	76	c.1071_1072insA	c.(1069-1074)ATTAAAfs	p.I357fs
Pat_70	Post-Resistance	CTAGE5	4253	37	14	39746243	39746243	Frame_Shift_Del	DEL	T	-	7	374	c.169delT	c.(169-171)TTTfs	p.F57fs
Pat_70	Post-Resistance	C14orf106	55320	37	14	45693722	45693722	Frame_Shift_Del	DEL	T	-	18	365	c.2068delA	c.(2068-2070)AGTfs	p.S690fs
Pat_70	Post-Resistance	PLEKHG3	26030	37	14	65207900	65207900	Frame_Shift_Del	DEL	C	-	8	716	c.1665delC	c.(1663-1665)GACfs	p.D555fs
Pat_70	Post-Resistance	C14orf43	91748	37	14	74205926	74205928	In_Frame_Del	DEL	CTG	-	12	133	c.784_786delCAG	c.(784-786)CAGdel	p.Q262del
Pat_70	Post-Resistance	C14orf115	55237	37	14	74824463	74824463	Frame_Shift_Del	DEL	G	-	7	631	c.977delG	c.(976-978)CGGfs	p.R326fs
Pat_70	Post-Resistance	MLH3	27030	37	14	75514604	75514604	Frame_Shift_Del	DEL	T	-	9	241	c.1755delA	c.(1753-1755)AAAfs	p.K585fs
Pat_70	Post-Resistance	PTPN21	11099	37	14	88945628	88945630	In_Frame_Del	DEL	TCC	-	7	308	.2145_2147delGG	(2143-2148)GAGGAC>GA	p.E715del
Pat_70	Post-Resistance	TTC8	123016	37	14	89338724	89338726	In_Frame_Del	DEL	CAA	-	7	648	.1323_1325delCA	.(1321-1326)GTCAAC>GT	p.N445del
Pat_70	Post-Resistance	ATXN3	4287	37	14	92537355	92537357	In_Frame_Del	DEL	CTG	-	8	374	c.913_915delCAG	c.(913-915)CAGdel	p.Q305del
Pat_70	Post-Resistance	YY1	7528	37	14	100705708	100705710	In_Frame_Del	DEL	GAG	-	10	123	c.127_129delGAG	c.(127-129)GAGdel	p.E47del
Pat_70	Post-Resistance	C15orf52	388115	37	15	40631782	40631782	Frame_Shift_Del	DEL	C	-	7	585	c.294delG	c.(292-294)GGGfs	p.G98fs
Pat_70	Post-Resistance	ZFP106	64397	37	15	42742957	42742957	Frame_Shift_Del	DEL	A	-	7	1046	c.1444delT	c.(1444-1446)TCCfs	p.S482fs
Pat_70	Post-Resistance	ADAL	161823	37	15	43641115	43641115	Frame_Shift_Del	DEL	A	-	10	423	c.563delA	c.(562-564)CAAfs	p.Q188fs
Pat_70	Post-Resistance	TUBGCP4	27229	37	15	43687855	43687855	Frame_Shift_Del	DEL	G	-	7	2064	c.1140delG	c.(1138-1140)TTGfs	p.L380fs
Pat_70	Post-Resistance	SPG11	80208	37	15	44905698	44905698	Frame_Shift_Del	DEL	T	-	10	378	c.3075delA	c.(3073-3075)AAAfs	p.K1025fs
Pat_70	Post-Resistance	ZNF609	23060	37	15	64972995	64972997	In_Frame_Del	DEL	CAC	-	11	877	.4096_4098delCA	c.(4096-4098)CACdel	p.H1371del
Pat_70	Post-Resistance	SPG21	51324	37	15	65262526	65262526	Frame_Shift_Del	DEL	T	-	8	876	c.487delA	c.(487-489)ATAfs	p.I163fs
Pat_70	Post-Resistance	SLC24A1	9187	37	15	65918177	65918179	In_Frame_Del	DEL	CTG	-	21	370	.1759_1761delCT	c.(1759-1761)CTGdel	p.L591del
Pat_70	Post-Resistance	NOX5	79400	37	15	69328208	69328210	In_Frame_Del	DEL	CTG	-	11	857	.1120_1122delCT	c.(1120-1122)CTGdel	p.L380del
Pat_70	Post-Resistance	KIF7	374654	37	15	90189153	90189155	In_Frame_Del	DEL	CTC	-	8	207	.1891_1893delGA	c.(1891-1893)GAGdel	p.E631del
Pat_70	Post-Resistance	RAB40C	57799	37	16	677579	677580	Frame_Shift_Ins	INS	-	C	13	337	c.803_804insC	c.(802-804)AGCfs	p.S268fs
Pat_70	Post-Resistance	NTAN1	123803	37	16	15131931	15131931	Frame_Shift_Del	DEL	T	-	8	579	c.890delA	c.(889-891)AATfs	p.N297fs
Pat_70	Post-Resistance	C16orf62	57020	37	16	19580800	19580802	In_Frame_Del	DEL	TCC	-	9	374	c.172_174delTCC	c.(172-174)TCCdel	p.S64del
Pat_70	Post-Resistance	C16orf88	400506	37	16	19725705	19725706	Frame_Shift_Ins	INS	-	T	11	191	c.652_653insA	c.(652-654)ATCfs	p.I218fs
Pat_70	Post-Resistance	DNAH3	55567	37	16	21132130	21132132	In_Frame_Del	DEL	CAG	-	8	287	.1628_1630delCT	.(1627-1632)GCTGAT>GA	p.A543del
Pat_70	Post-Resistance	IL4R	3566	37	16	27373787	27373789	In_Frame_Del	DEL	GAG	-	10	169	.1114_1116delGA	c.(1114-1116)GAGdel	p.E376del
Pat_70	Post-Resistance	EIF3CL	728689	37	16	28734579	28734581	In_Frame_Del	DEL	GAG	-	11	2604	c.871_873delGAG	c.(871-873)GAGdel	p.E295del
Pat_70	Post-Resistance	ATP2A1	487	37	16	28913640	28913640	Frame_Shift_Del	DEL	C	-	11	525	c.2457delC	c.(2455-2457)CGCfs	p.R819fs
Pat_70	Post-Resistance	ITGAL	3683	37	16	30531249	30531251	In_Frame_Del	DEL	GCT	-	7	1252	.3300_3302delGC	(3298-3303)GGGCTG>GG	p.L1106del
Pat_70	Post-Resistance	SETD1A	9739	37	16	30982809	30982811	In_Frame_Del	DEL	TCC	-	8	300	.3127_3129delTC	c.(3127-3129)TCCdel	p.S1058del
Pat_70	Post-Resistance	SALL1	6299	37	16	51175413	51175415	In_Frame_Del	DEL	CTG	-	7	444	c.718_720delCAG	c.(718-720)CAGdel	p.Q240del
Pat_70	Post-Resistance	COQ9	57017	37	16	57486732	57486734	In_Frame_Del	DEL	GAG	-	8	738	c.262_264delGAG	c.(262-264)GAGdel	p.E91del
Pat_70	Post-Resistance	SLC9A5	6553	37	16	67300017	67300019	In_Frame_Del	DEL	GAG	-	15	284	.2107_2109delGA	c.(2107-2109)GAGdel	p.E708del
Pat_70	Post-Resistance	MARVELD3	91862	37	16	71668442	71668442	Frame_Shift_Del	DEL	G	-	7	338	c.942delG	c.(940-942)GCGfs	p.A314fs
Pat_70	Post-Resistance	ZFHX3	463	37	16	72822564	72822566	In_Frame_Del	DEL	TGC	-	14	387	.9609_9611delGC	.(9607-9612)CAGCAA>CA	203_3204QQ
Pat_70	Post-Resistance	KDM6B	23135	37	17	7751859	7751864	In_Frame_Del	DEL	CACCAC	-	18	104	253_2258delCAC	251-2259)GTCACCACC>	p.TT760del
Pat_70	Post-Resistance	CHD3	1107	37	17	7801857	7801859	In_Frame_Del	DEL	AAG	-	10	244	.2095_2097delAA	c.(2095-2097)AAGdel	p.K703del

Pat_70	Post-Resistance	TRPV2	51393	37	17	16335490	16335492	In_Frame_Del	DEL	TGC	-	17	381	.1865_1867delTG	(1864-1869)GTGCTG>GT	p.L627del
Pat_70	Post-Resistance	MED9	55090	37	17	17394705	17394707	In_Frame_Del	DEL	CAG	-	9	587	c.337_339delCAG	c.(337-339)CAGdel	p.Q117del
Pat_70	Post-Resistance	NUFIP2	57532	37	17	27620932	27620934	In_Frame_Del	DEL	TGG	-	7	655	c.144_146delCCA	c.(142-147)CACCAT>CAT	p.48_49HH>H
Pat_70	Post-Resistance	CDK12	51755	37	17	37686901	37686901	Frame_Shift_Del	DEL	C	-	8	1658	c.3805delC	c.(3805-3807)CCCfs	p.P1269fs
Pat_70	Post-Resistance	KRT10	3858	37	17	38978766	38978768	In_Frame_Del	DEL	TCC	-	16	130	c.70_72delGGA	c.(70-72)GGAdel	p.G24del
Pat_70	Post-Resistance	KRTAP4-5	85289	37	17	39305775	39305776	In_Frame_Ins	INS	-	GCAGCTG	104	345	5insGCCCCAGCT	)CAG>CGCCCCAGCTG	81_82insRPS
Pat_70	Post-Resistance	STAT5B	6777	37	17	40370236	40370236	Frame_Shift_Del	DEL	G	-	12	283	c.1102delC	c.(1102-1104)CAGfs	p.Q368fs
Pat_70	Post-Resistance	CDC27	996	37	17	45219355	45219355	Frame_Shift_Del	DEL	C	-	9	742	c.1415delG	c.(1414-1416)GGTfs	p.G472fs
Pat_70	Post-Resistance	NPEPPS	9520	37	17	45669428	45669429	Splice_Site	INS	-	A	14	54	c.1365_splice	c.e11+2	p.K455_splice
Pat_70	Post-Resistance	HOXB2	3212	37	17	46622130	46622132	In_Frame_Del	DEL	AGG	-	9	373	c.142_144delCCT	c.(142-144)CCTdel	p.P48del
Pat_70	Post-Resistance	BZRAP1	9256	37	17	56387404	56387406	In_Frame_Del	DEL	TCC	-	9	270	.3813_3815delGG	(3811-3816)GAGGAA>GA	1271_1272EE
Pat_70	Post-Resistance	GGA3	23163	37	17	73239175	73239175	Frame_Shift_Del	DEL	T	-	7	695	c.497delA	c.(496-498)AACfs	p.N166fs
Pat_70	Post-Resistance	NEDD4L	23327	37	18	55992284	55992286	In_Frame_Del	DEL	TCC	-	16	943	c.570_572delTCC	c.(568-573)CTTCCT>CTT	p.P194del
Pat_70	Post-Resistance	MLLT1	4298	37	19	6222272	6222274	In_Frame_Del	DEL	AGG	-	10	152	c.968_970delCCT	c.(967-972)TCCTTC>TTC	p.S323del
Pat_70	Post-Resistance	HAUS8	93323	37	19	17160706	17160707	Frame_Shift_Del	DEL	GA	-	11	1102	c.1209_1210delTC	c.(1207-1212)TCTCGTfs	p.S403fs
Pat_70	Post-Resistance	ANO8	57719	37	19	17439422	17439424	In_Frame_Del	DEL	TCC	-	7	82	.1773_1775delGG	(1771-1776)GAGGAC>GA	p.E591del
Pat_70	Post-Resistance	IL12RB1	3594	37	19	18194264	18194265	Frame_Shift_Ins	INS	-	G	8	850	c.101_102insC	c.(100-102)CCGfs	p.P34fs
Pat_70	Post-Resistance	LSM14A	26065	37	19	34710340	34710340	Frame_Shift_Del	DEL	C	-	11	708	c.826delC	c.(826-828)CGGfs	p.R276fs
Pat_70	Post-Resistance	HAMP	57817	37	19	35773520	35773522	In_Frame_Del	DEL	CTC	-	25	853	c.40_42delCTC	c.(40-42)CTCdel	p.L18del
Pat_70	Post-Resistance	ZNF569	148266	37	19	37916813	37916815	In_Frame_Del	DEL	TTC	-	7	2209	c.193_195delGAA	c.(193-195)GAAdel	p.E65del
Pat_70	Post-Resistance	FAM98C	147965	37	19	38899502	38899504	In_Frame_Del	DEL	AAG	-	16	178	.1030_1032delAA	c.(1030-1032)AAGdel	p.K349del
Pat_70	Post-Resistance	ZFP36	7538	37	19	39898948	39898950	In_Frame_Del	DEL	CAC	-	9	976	c.590_592delCAC	c.(589-594)TCACCA>TCA	p.P201del
Pat_70	Post-Resistance	SERTAD1	29950	37	19	40929409	40929411	In_Frame_Del	DEL	CTC	-	7	353	c.43_45delGAG	c.(43-45)GAGdel	p.E15del
Pat_70	Post-Resistance	LYPD3	27076	37	19	43969653	43969655	In_Frame_Del	DEL	AGC	-	16	1004	c.69_71delGCT	c.(67-72)CTGCTT>CTT	p.23_24LL>L
Pat_70	Post-Resistance	MARK4	57787	37	19	45805664	45805664	Frame_Shift_Del	DEL	C	-	7	1703	c.1955delC	c.(1954-1956)GCCfs	p.A652fs
Pat_70	Post-Resistance	RSPH6A	81492	37	19	46299165	46299167	In_Frame_Del	DEL	CCT	-	9	437	.2114_2116delAG	(2113-2118)GAGGGC>GG	p.E705del
Pat_70	Post-Resistance	PNMAL1	55228	37	19	46973195	46973197	In_Frame_Del	DEL	CTT	-	7	585	.1096_1098delAA	c.(1096-1098)AAGdel	p.K366del
Pat_70	Post-Resistance	SLC8A2	6543	37	19	47935681	47935683	In_Frame_Del	DEL	TCC	-	40	605	.2130_2132delGG	(2128-2133)GAGGAC>GA	p.E710del
Pat_70	Post-Resistance	TMC4	147798	37	19	54675747	54675749	In_Frame_Del	DEL	TCC	-	18	392	c.201_203delGGA	c.(199-204)GAGGAT>GAT	p.E67del
Pat_70	Post-Resistance	LILRB2	10288	37	19	54780707	54780709	In_Frame_Del	DEL	GAG	-	22	582	.1435_1437delCT	c.(1435-1437)CTCdel	p.L479del
Pat_70	Post-Resistance	LILRB1	10859	37	19	55146148	55146150	In_Frame_Del	DEL	CTC	-	9	201	.1417_1419delCT	c.(1417-1419)CTCdel	p.L479del
Pat_70	Post-Resistance	C2orf71	388939	37	2	29295647	29295649	In_Frame_Del	DEL	TCC	-	17	728	.1479_1481delGG	(1477-1482)GAGGAA>GA	.493_494EE>
Pat_70	Post-Resistance	DHX57	90957	37	2	39095411	39095413	In_Frame_Del	DEL	CCA	-	11	285	c.135_137delTGG	.(133-138)GGTGGA>GG	p.45_46GG>G
Pat_70	Post-Resistance	USP34	9736	37	2	61577526	61577527	Splice_Site	INS	-	A	7	489	c.1378_splice	c.e12-1	p.T460_splice
Pat_70	Post-Resistance	AFTPH	54812	37	2	64778672	64778674	In_Frame_Del	DEL	GAT	-	11	758	c.64_66delGAT	c.(64-66)GATdel	p.D26del
Pat_70	Post-Resistance	RAB11FIP5	26056	37	2	73315337	73315339	In_Frame_Del	DEL	TGG	-	7	407	.1407_1409delCC	.(1405-1410)CACCAA>CA	p.H469del
Pat_70	Post-Resistance	ALMS1	7840	37	2	73613032	73613037	In_Frame_Del	DEL	GGAGGA	-	7	25	.36_41delGGAGG	(34-42)CTGGAGGAG>CT	p.EE27del
Pat_70	Post-Resistance	TMEM127	55654	37	2	96919781	96919783	In_Frame_Del	DEL	TGC	-	13	511	c.480_482delGCA	c.(478-483)CAGCAT>CAT	p.Q160del
Pat_70	Post-Resistance	ITPRIPL1	150771	37	2	96992793	96992795	In_Frame_Del	DEL	GAG	-	12	203	c.424_426delGAG	c.(424-426)GAGdel	p.E147del
Pat_70	Post-Resistance	REV1	51455	37	2	100055102	100055102	Frame_Shift_Del	DEL	T	-	7	555	c.1174delA	c.(1174-1176)ATGfs	p.M392fs
Pat_70	Post-Resistance	GCC2	9648	37	2	109087883	109087884	Frame_Shift_Ins	INS	-	A	11	994	c.2098_2099insA	c.(2098-2100)GAAfs	p.E700fs
Pat_70	Post-Resistance	NPHP1	4867	37	2	110922711	110922713	In_Frame_Del	DEL	CTT	-	7	650	c.644_646delAAG	.(643-648)GAAGGC>GG	p.E215del
Pat_70	Post-Resistance	SLC20A1	6574	37	2	113416607	113416608	Frame_Shift_Del	DEL	AG	-	8	241	c.984_985delAG	c.(982-987)CCAGAGfs	p.P328fs
Pat_70	Post-Resistance	UGGT1	56886	37	2	128938648	128938649	Splice_Site	INS	-	GCCCTT	20	359	c.4083_splice	c.e36+2	.Q1361_splice
Pat_70	Post-Resistance	RIF1	55183	37	2	152293790	152293790	Frame_Shift_Del	DEL	T	-	7	797	c.1408delT	c.(1408-1410)TTTfs	p.F470fs
Pat_70	Post-Resistance	PLA2R1	22925	37	2	160801441	160801442	Frame_Shift_Ins	INS	-	T	12	709	c.4119_4120insA	c.(4117-4122)AAAGGCfs	p.K1373fs
Pat_70	Post-Resistance	PPP1R1C	151242	37	2	182852619	182852619	Frame_Shift_Del	DEL	C	-	8	1336	c.135delC	c.(133-135)AACfs	p.N45fs

Pat_70	Post-Resistance	SLC11A1	6556	37	2	219252307	219252307	Frame_Shift_Del	DEL	T	-	10	1368	c.591delT	c.(589-591)GCTfs	p.A197fs
Pat_70	Post-Resistance	DOCK10	55619	37	2	225729790	225729790	Frame_Shift_Del	DEL	A	-	9	544	c.1272delT	c.(1270-1272)TTTfs	p.F424fs
Pat_70	Post-Resistance	USP40	55230	37	2	234394236	234394237	Frame_Shift_Ins	INS	-	T	8	184	c.3477_3478insA	c.(3475-3480)AAACAAfs	p.K1159fs
Pat_70	Post-Resistance	GAL3ST2	64090	37	2	242738494	242738496	In_Frame_Del	DEL	TCC	-	17	503	c.44_46delTCC	c.(43-48)ATCCTC>ATC	p.L20del
Pat_70	Post-Resistance	FRG1B	284802	37	20	29625899	29625900	Frame_Shift_Ins	INS	-	AT	20	404	c.53_54insAT	c.(52-54)AAAfs	p.K18fs
Pat_70	Post-Resistance	NCOA6	23054	37	20	33330968	33330970	In_Frame_Del	DEL	TGC	-	14	508	.3090_3092delGC	.(3088-3093)CAGCAA>CA	030_1031QQ
Pat_70	Post-Resistance	KCNB1	3745	37	20	47989771	47989772	Frame_Shift_Ins	INS	-	G	7	2126	c.2325_2326insC	c.(2323-2328)CCCAAAfs	p.P775fs
Pat_70	Post-Resistance	CTCFL	140690	37	20	56099187	56099187	Frame_Shift_Del	DEL	T	-	13	1891	c.75delA	c.(73-75)AAAfs	p.K25fs
Pat_70	Post-Resistance	COL9A3	1299	37	20	61468444	61468444	Frame_Shift_Del	DEL	C	-	7	2144	c.1613delC	c.(1612-1614)GCAfs	p.A538fs
Pat_70	Post-Resistance	SFRS15	57466	37	21	33044257	33044259	In_Frame_Del	DEL	GCT	-	29	637	.2897_2899delAG	(2896-2901)CAGCCA>CC	p.Q966del
Pat_70	Post-Resistance	KRTAP10-6	386674	37	21	46012219	46012220	In_Frame_Ins	INS	-	CGCAGCA	8	160	7insCAGCTGCTG	)CCG>CCCAGCTGCTGC	9_49P>PSCC
Pat_70	Post-Resistance	MCM3AP	8888	37	21	47663397	47663397	Frame_Shift_Del	DEL	G	-	7	592	c.5278delC	c.(5278-5280)CGGfs	p.R1760fs
Pat_70	Post-Resistance	C22orf43	51233	37	22	23959767	23959769	In_Frame_Del	DEL	CAT	-	8	375	c.512_514delATG	c.(511-516)GATGCC>GCC	p.D171del
Pat_70	Post-Resistance	MYH9	4627	37	22	36689419	36689421	In_Frame_Del	DEL	CCT	-	7	427	.4049_4051delAG	(4048-4053)GAGGCC>GC	p.E1350del
Pat_70	Post-Resistance	TRIOBP	11078	37	22	38120323	38120325	In_Frame_Del	DEL	CCT	-	8	1133	.1760_1762delCC	(1759-1764)GCCTCC>GC	p.S589del
Pat_70	Post-Resistance	MKL1	57591	37	22	40807831	40807831	Frame_Shift_Del	DEL	G	-	9	687	c.2359delC	c.(2359-2361)CTGfs	p.L787fs
Pat_70	Post-Resistance	RANGAP1	5905	37	22	41650469	41650471	In_Frame_Del	DEL	TCC	-	44	427	.1101_1103delGG	.(1099-1104)GAGGAA>GA	.367_368EE>
Pat_70	Post-Resistance	TCF20	6942	37	22	42610573	42610575	In_Frame_Del	DEL	AGG	-	21	384	c.737_739delCCT	c.(736-741)TCCTTC>TTC	p.S246del
Pat_70	Post-Resistance	TCF20	6942	37	22	42610776	42610778	In_Frame_Del	DEL	TGC	-	8	320	c.534_536delGCA	c.(532-537)CAGCAA>CAA	.178_179QQ>
Pat_70	Post-Resistance	BIK	638	37	22	43525245	43525247	In_Frame_Del	DEL	GCT	-	10	332	c.417_419delGCT	.(415-420)GCGCTG>GCC	p.L144del
Pat_70	Post-Resistance	GRM7	2917	37	3	7621013	7621013	Frame_Shift_Del	DEL	T	-	7	137	c.2420delT	c.(2419-2421)ATTfs	p.I807fs
Pat_70	Post-Resistance	XPC	7508	37	3	14219966	14219968	In_Frame_Del	DEL	CCT	-	9	236	c.101_103delAGG	c.(100-105)GAGGAT>GAT	p.E34del
Pat_70	Post-Resistance	KAT2B	8850	37	3	20113879	20113879	Frame_Shift_Del	DEL	C	-	8	822	c.358delC	c.(358-360)CCCfs	p.P120fs
Pat_70	Post-Resistance	CLASP2	23122	37	3	33602361	33602361	Frame_Shift_Del	DEL	T	-	11	827	c.2869delA	c.(2869-2871)ATGfs	p.M957fs
Pat_70	Post-Resistance	PDCD6IP	10015	37	3	33866811	33866811	Frame_Shift_Del	DEL	T	-	8	328	c.595delT	c.(595-597)TTTfs	p.F199fs
Pat_70	Post-Resistance	MLH1	4292	37	3	37070349	37070349	Frame_Shift_Del	DEL	C	-	9	1766	c.1484delC	c.(1483-1485)ACCfs	p.T495fs
Pat_70	Post-Resistance	HHATL	57467	37	3	42739670	42739672	In_Frame_Del	DEL	GAA	-	7	472	c.655_657delTTC	c.(655-657)TTCdel	p.F219del
Pat_70	Post-Resistance	CDC25A	993	37	3	48200922	48200923	Frame_Shift_Del	DEL	TC	-	15	454	.1345_1346delG	c.(1345-1347)GATfs	p.D449fs
Pat_70	Post-Resistance	QRICH1	54870	37	3	49094313	49094314	In_Frame_Ins	INS	-	TGC	68	169	.1319_1320insGC	.(1318-1320)CAA>CAGCA	.440_440Q>Q
Pat_70	Post-Resistance	USP4	7375	37	3	49321969	49321971	In_Frame_Del	DEL	TCT	-	10	550	.2318_2320delAG	.(2317-2322)AAGACC>AC	p.K773del
Pat_70	Post-Resistance	DAG1	1605	37	3	49569266	49569268	In_Frame_Del	DEL	CCA	-	11	640	.1322_1324delCC	.(1321-1326)TCCACC>TC	p.T446del
Pat_70	Post-Resistance	FOXP1	27086	37	3	71027087	71027087	Frame_Shift_Del	DEL	G	-	9	731	c.1240delC	c.(1240-1242)CTGfs	p.L414fs
Pat_70	Post-Resistance	FOXP1	27086	37	3	71247357	71247359	In_Frame_Del	DEL	TGC	-	9	419	c.174_176delGCA	c.(172-177)CAGCAA>CA	p.58_59QQ>Q
Pat_70	Post-Resistance	VGLL3	389136	37	3	87027857	87027859	In_Frame_Del	DEL	CTC	-	29	246	c.220_222delGAG	c.(220-222)GAGdel	p.E74del
Pat_70	Post-Resistance	TBC1D23	55773	37	3	100039736	100039736	Frame_Shift_Del	DEL	A	-	8	246	c.1939delA	c.(1939-1941)AAAfs	p.K647fs
Pat_70	Post-Resistance	LNP1	348801	37	3	100148586	100148588	In_Frame_Del	DEL	GAT	-	7	1420	c.13_15delGAT	c.(13-15)GATdel	p.D10del
Pat_70	Post-Resistance	SLC9A10	285335	37	3	111981842	111981845	Frame_Shift_Del	DEL	GCAT	-	8	337	1123_1126delATG	c.(1123-1128)ATGCCTfs	p.M375fs
Pat_70	Post-Resistance	KIAA2018	205717	37	3	113380090	113380090	Frame_Shift_Del	DEL	T	-	9	281	c.439delA	c.(439-441)ATTfs	p.I147fs
Pat_70	Post-Resistance	GPR156	165829	37	3	119885960	119885960	Frame_Shift_Del	DEL	C	-	9	1485	c.2364delG	c.(2362-2364)GGGfs	p.G788fs
Pat_70	Post-Resistance	PARP14	54625	37	3	122433232	122433232	Frame_Shift_Del	DEL	A	-	10	203	c.3956delA	c.(3955-3957)GAAfs	p.E1319fs
Pat_70	Post-Resistance	ZXDC	79364	37	3	126178522	126178522	Frame_Shift_Del	DEL	T	-	11	2630	c.2186delA	c.(2185-2187)AAGfs	p.K729fs
Pat_70	Post-Resistance	TMCC1	23023	37	3	129546680	129546682	In_Frame_Del	DEL	GCA	-	9	317	c.540_542delTGC	.(538-543)GCTGCA>GCA	.180_181AA>
Pat_70	Post-Resistance	DBR1	51163	37	3	137880741	137880743	In_Frame_Del	DEL	TCG	-	11	417	.1623_1625delCG	.(1621-1626)GATGAT>GA	.541_542DD>
Pat_70	Post-Resistance	FXR1	8087	37	3	180666228	180666228	Frame_Shift_Del	DEL	A	-	8	410	c.364delA	c.(364-366)AAAfs	p.K122fs
Pat_70	Post-Resistance	ATP13A3	79572	37	3	194181471	194181473	In_Frame_Del	DEL	GAG	-	8	737	c.139_141delCTC	c.(139-141)CTCdel	p.L47del
Pat_70	Post-Resistance	TNK2	10188	37	3	195595229	195595229	Frame_Shift_Del	DEL	G	-	12	310	c.1895delC	c.(1894-1896)CCGfs	p.P632fs
Pat_70	Post-Resistance	CRIPAK	285464	37	4	1388900	1388901	Frame_Shift_Del	DEL	CA	-	9	1300	c.601_602delCA	c.(601-603)CACfs	p.H201fs

Pat_70	Post-Resistance	CRIPAK	285464	37	4	1389456	1389457	Frame_Shift_Del	DEL	CA	-	13	843	c.1157_1158delCA	c.(1156-1158)TCAfs	p.S386fs
Pat_70	Post-Resistance	GRK4	2868	37	4	3015470	3015470	Frame_Shift_Del	DEL	A	-	11	397	c.656delA	c.(655-657)CAAfs	p.Q219fs
Pat_70	Post-Resistance	OTOP1	133060	37	4	4228274	4228282	In_Frame_Del	DEL	CACAGCAC	-	7	115	_318delCTGCTG	.(310-318)CTGCTGTGGde	p.LLW104del
Pat_70	Post-Resistance	LYAR	55646	37	4	4276167	4276169	In_Frame_Del	DEL	CTT	-	7	1332	c.757_759delAAG	c.(757-759)AAGdel	p.K253del
Pat_70	Post-Resistance	PROM1	8842	37	4	15995680	15995680	Frame_Shift_Del	DEL	T	-	24	492	c.1697delA	c.(1696-1698)AATfs	p.N566fs
Pat_70	Post-Resistance	GABRG1	2565	37	4	46060358	46060358	Frame_Shift_Del	DEL	A	-	8	284	c.792delT	c.(790-792)TTTfs	p.F264fs
Pat_70	Post-Resistance	KIAA1211	57482	37	4	57182265	57182267	In_Frame_Del	DEL	AGA	-	9	185	.2597_2599delAG	(2596-2601)CAGAAG>CA	p.K870del
Pat_70	Post-Resistance	UTP3	57050	37	4	71554620	71554622	In_Frame_Del	DEL	GAG	-	8	220	c.226_228delGAG	c.(226-228)GAGdel	p.E81del
Pat_70	Post-Resistance	SEC31A	22872	37	4	83745800	83745800	Frame_Shift_Del	DEL	T	-	9	223	c.3319delA	c.(3319-3321)ATTfs	p.I1107fs
Pat_70	Post-Resistance	SEC31A	22872	37	4	83785565	83785565	Frame_Shift_Del	DEL	T	-	13	267	c.1384delA	c.(1384-1386)ATTfs	p.I462fs
Pat_70	Post-Resistance	WDFY3	23001	37	4	85611708	85611709	Frame_Shift_Del	DEL	CA	-	15	602	c.9313_9314delTG	c.(9313-9315)TGGfs	p.W3105fs
Pat_70	Post-Resistance	NAP1L5	266812	37	4	89618431	89618433	In_Frame_Del	DEL	CCT	-	8	446	c.473_475delAGG	c.(472-477)GAGGCT>GCT	p.E158del
Pat_70	Post-Resistance	RRH	10692	37	4	110756541	110756541	Frame_Shift_Del	DEL	T	-	7	382	c.317delT	c.(316-318)ATTfs	p.I106fs
Pat_70	Post-Resistance	GAB1	2549	37	4	144390234	144390236	In_Frame_Del	DEL	TGT	-	7	473	.1977_1979delTG	c.(1975-1980)TATGTT>TAT	p.V662del
Pat_70	Post-Resistance	OTUD4	54726	37	4	146077123	146077125	In_Frame_Del	DEL	CAG	-	16	479	c.458_460delCTG	c.(457-462)GCTGAT>GAT	p.A153del
Pat_70	Post-Resistance	SDHA	6389	37	5	256484	256485	Frame_Shift_Del	DEL	TT	-	55	811	c.1944_1945delTT	c.(1942-1947)ACTTTGfs	p.T648fs
Pat_70	Post-Resistance	PAPD7	11044	37	5	6755013	6755014	Frame_Shift_Del	DEL	AC	-	16	362	c.1584_1585delAC	c.(1582-1587)AAACACfs	p.K528fs
Pat_70	Post-Resistance	NNT	23530	37	5	43651893	43651893	Frame_Shift_Del	DEL	C	-	7	1392	c.1770delC	c.(1768-1770)GACfs	p.D590fs
Pat_70	Post-Resistance	AP3B1	8546	37	5	77536741	77536741	Frame_Shift_Del	DEL	T	-	8	1167	c.224delA	c.(223-225)AATfs	p.N75fs
Pat_70	Post-Resistance	TNFAIP8	25816	37	5	118728991	118728992	Frame_Shift_Del	DEL	TG	-	7	694	c.512_513delTG	c.(511-513)TTGfs	p.L171fs
Pat_70	Post-Resistance	ALDH7A1	501	37	5	125891661	125891661	Frame_Shift_Del	DEL	T	-	8	299	c.1055delA	c.(1054-1056)AAGfs	p.K352fs
Pat_70	Post-Resistance	SLC12A2	6558	37	5	127420207	127420209	In_Frame_Del	DEL	CGG	-	8	172	c.561_563delCGG	c.(559-564)TCCGGC>TCC	p.G192del
Pat_70	Post-Resistance	RAPGEF6	51735	37	5	130782332	130782332	Frame_Shift_Del	DEL	T	-	7	716	c.3265delA	c.(3265-3267)AGGfs	p.R1089fs
Pat_70	Post-Resistance	RAPGEF6	51735	37	5	130815368	130815369	Frame_Shift_Ins	INS	-	T	8	648	c.1918_1919insA	c.(1918-1920)AGTfs	p.S640fs
Pat_70	Post-Resistance	SLC22A4	6583	37	5	131676327	131676327	Frame_Shift_Del	DEL	T	-	12	902	c.1514delT	c.(1513-1515)CTTfs	p.L505fs
Pat_70	Post-Resistance	IK	3550	37	5	140032593	140032594	Frame_Shift_Del	DEL	GA	-	10	289	c.268_269delGA	c.(268-270)GAGfs	p.E90fs
Pat_70	Post-Resistance	KCTD16	57528	37	5	143853531	143853531	Frame_Shift_Del	DEL	A	-	8	195	c.1141delA	c.(1141-1143)AAAfs	p.K381fs
Pat_70	Post-Resistance	LARS	51520	37	5	145523014	145523014	Frame_Shift_Del	DEL	C	-	7	1847	c.1838delG	c.(1837-1839)GGTfs	p.G613fs
Pat_70	Post-Resistance	HAVCR2	84868	37	5	156535948	156535950	In_Frame_Del	DEL	AGC	-	10	550	c.45_47delGCT	c.(43-48)CTGCTA>CTA	p.15_16LL>L
Pat_70	Post-Resistance	RIOK1	83732	37	6	7393450	7393452	In_Frame_Del	DEL	GAC	-	8	343	c.190_192delGAC	c.(190-192)GACdel	p.D69del
Pat_70	Post-Resistance	JARID2	3720	37	6	15501164	15501164	Frame_Shift_Del	DEL	T	-	8	1199	c.1972delT	c.(1972-1974)TTTfs	p.F658fs
Pat_70	Post-Resistance	HSPA1L	3305	37	6	31778562	31778564	In_Frame_Del	DEL	CAG	-	8	532	.1186_1188delCT	c.(1186-1188)CTGdel	p.L396del
Pat_70	Post-Resistance	STK19	8859	37	6	31939829	31939830	Frame_Shift_Ins	INS	-	A	13	856	c.56_57insA	c.(55-57)GCAfs	p.A19fs
Pat_70	Post-Resistance	SYNGAP1	8831	37	6	33411201	33411203	In_Frame_Del	DEL	CAC	-	7	329	.2872_2874delCA	c.(2872-2874)CACdel	p.H966del
Pat_70	Post-Resistance	TULP1	7287	37	6	35478775	35478777	In_Frame_Del	DEL	TCC	-	7	363	c.360_362delGGA	.(358-363)GAGGAA>GAA	.120_121EE>
Pat_70	Post-Resistance	MDFI	4188	37	6	41621169	41621171	In_Frame_Del	DEL	CTG	-	10	444	c.597_599delCTG	c.(595-600)CTCTGC>CTC	p.C204del
Pat_70	Post-Resistance	GABRR1	2569	37	6	89891719	89891721	In_Frame_Del	DEL	AAG	-	11	598	c.852_854delCTT	c.(850-855)TTCTTG>TTG	p.F284del
Pat_70	Post-Resistance	GABRR2	2570	37	6	89975427	89975429	In_Frame_Del	DEL	AAG	-	7	564	c.867_869delCTT	c.(865-870)TTCTTG>TTG	p.F289del
Pat_70	Post-Resistance	REV3L	5980	37	6	111693904	111693904	Frame_Shift_Del	DEL	G	-	7	963	c.5654delC	c.(5653-5655)CCAfs	p.P1885fs
Pat_70	Post-Resistance	CCDC28A	25901	37	6	139097330	139097330	Frame_Shift_Del	DEL	A	-	10	517	c.343delA	c.(343-345)AAAfs	p.K115fs
Pat_70	Post-Resistance	MTHFD1L	25902	37	6	151358163	151358164	Frame_Shift_Ins	INS	-	A	8	428	c.2757_2758insA	c.(2755-2760)GACAAAfs	p.D919fs
Pat_70	Post-Resistance	QKI	9444	37	6	163899920	163899920	Frame_Shift_Del	DEL	A	-	8	404	c.394delA	c.(394-396)AAAfs	p.K132fs
Pat_70	Post-Resistance	CARD11	84433	37	7	2963941	2963943	In_Frame_Del	DEL	GGA	-	8	351	.1864_1866delTC	c.(1864-1866)TCCdel	p.S622del
Pat_70	Post-Resistance	PHF14	9678	37	7	11075380	11075381	Frame_Shift_Del	DEL	AG	-	11	1375	c.1569_1570delAG	c.(1567-1572)CAAGAGfs	p.Q523fs
Pat_70	Post-Resistance	HOXA1	3198	37	7	27135314	27135316	In_Frame_Del	DEL	CGA	-	8	280	c.216_218delTCG	c.(214-219)CATCAC>CAC	p.72_73HH>H
Pat_70	Post-Resistance	NEUROD6	63974	37	7	31378635	31378635	Frame_Shift_Del	DEL	T	-	7	1030	c.248delA	c.(247-249)AAGfs	p.K83fs
Pat_70	Post-Resistance	POU6F2	11281	37	7	39379288	39379290	In_Frame_Del	DEL	CAG	-	11	221	c.559_561delCAG	c.(559-561)CAGdel	p.Q196del

Pat_70	Post-Resistance	AEBP1	165	37	7	44153778	44153780	In_Frame_Del	DEL	AGA	-	7	265	.3395_3397delAG	.(3394-3399)GAGAAA>GA	p.K1133del
Pat_70	Post-Resistance	STX1A	6804	37	7	73123425	73123427	In_Frame_Del	DEL	CAT	-	7	923	c.56_58delATG	c.(55-60)GATGTC>GTC	p.D19del
Pat_70	Post-Resistance	LIMK1	3984	37	7	73513509	73513509	Frame_Shift_Del	DEL	C	-	7	1429	c.549delC	c.(547-549)GACfs	p.D183fs
Pat_70	Post-Resistance	DTX2	113878	37	7	76112249	76112249	Frame_Shift_Del	DEL	A	-	46	2230	c.693delA	c.(691-693)CCAfs	p.P231fs
Pat_70	Post-Resistance	TMEM60	85025	37	7	77423460	77423460	Frame_Shift_Del	DEL	T	-	7	359	c.231delA	c.(229-231)AAAfs	p.K77fs
Pat_70	Post-Resistance	SEMA3D	223117	37	7	84651801	84651801	Frame_Shift_Del	DEL	G	-	7	1892	c.1320delC	c.(1318-1320)TTCfs	p.F440fs
Pat_70	Post-Resistance	AKAP9	10142	37	7	91671392	91671393	Frame_Shift_Del	DEL	AG	-	10	179	c.4950_4951delAG	c.(4948-4953)TCAGAGfs	p.S1650fs
Pat_70	Post-Resistance	AKAP9	10142	37	7	91732039	91732039	Frame_Shift_Del	DEL	G	-	8	1491	c.11229delG	c.(11227-11229)ATGfs	p.M3743fs
Pat_70	Post-Resistance	CNPY4	245812	37	7	99717401	99717402	Frame_Shift_Ins	INS	-	T	7	321	c.34_35insT	c.(34-36)CTTfs	p.L12fs
Pat_70	Post-Resistance	AGFG2	3268	37	7	100150976	100150976	Frame_Shift_Del	DEL	C	-	7	713	c.438delC	c.(436-438)GTCfs	p.V146fs
Pat_70	Post-Resistance	KCND2	3751	37	7	119915596	119915597	Frame_Shift_Ins	INS	-	C	24	154	c.910_911insC	c.(910-912)TCCfs	p.S304fs
Pat_70	Post-Resistance	TNPO3	23534	37	7	128610259	128610259	Frame_Shift_Del	DEL	G	-	11	1543	c.2541delC	c.(2539-2541)CCCfs	p.P847fs
Pat_70	Post-Resistance	OR9A4	130075	37	7	141619203	141619203	Frame_Shift_Del	DEL	T	-	10	950	c.528delT	c.(526-528)AATfs	p.N176fs
Pat_70	Post-Resistance	SGK223	157285	37	8	8175804	8175806	In_Frame_Del	DEL	TCA	-	7	1234	.4079_4081delTG	.(4078-4083)ATGAAG>AA	p.M1360del
Pat_70	Post-Resistance	DLC1	10395	37	8	12957997	12957997	Frame_Shift_Del	DEL	G	-	8	446	c.1849delC	c.(1849-1851)CGGfs	p.R617fs
Pat_70	Post-Resistance	TUSC3	7991	37	8	15601076	15601078	In_Frame_Del	DEL	CTA	-	8	1357	c.892_894delCTA	c.(892-894)CTAdel	p.L298del
Pat_70	Post-Resistance	C8orf80	389643	37	8	27888776	27888776	Frame_Shift_Del	DEL	T	-	7	937	c.1892delA	c.(1891-1893)AATfs	p.N631fs
Pat_70	Post-Resistance	MYST3	7994	37	8	41798420	41798422	In_Frame_Del	DEL	CTC	-	8	668	.2977_2979delGA	c.(2977-2979)GAGdel	p.E993del
Pat_70	Post-Resistance	PRKDC	5591	37	8	48746799	48746799	Frame_Shift_Del	DEL	T	-	12	1442	c.8110delA	c.(8110-8112)AGGfs	p.R2704fs
Pat_70	Post-Resistance	MYBL1	4603	37	8	67488452	67488453	Frame_Shift_Ins	INS	-	T	7	923	c.1259_1260insA	c.(1258-1260)AACfs	p.N420fs
Pat_70	Post-Resistance	SULF1	23213	37	8	70514026	70514026	Frame_Shift_Del	DEL	T	-	11	1441	c.1023delT	c.(1021-1023)CCTfs	p.P341fs
Pat_70	Post-Resistance	NBN	4683	37	8	90967512	90967512	Frame_Shift_Del	DEL	T	-	8	537	c.1396delA	c.(1396-1398)AGGfs	p.R466fs
Pat_70	Post-Resistance	DPYS	1807	37	8	105440214	105440214	Frame_Shift_Del	DEL	T	-	11	1576	c.1086delA	c.(1084-1086)AAAfs	p.K362fs
Pat_70	Post-Resistance	WDR67	93594	37	8	124140520	124140521	Splice_Site	INS	-	T	9	192	c.1885_splice	c.e14-1	p.F629_splice
Pat_70	Post-Resistance	ATAD2	29028	37	8	124368685	124368685	Frame_Shift_Del	DEL	A	-	9	261	c.1590delT	c.(1588-1590)TTTfs	p.F530fs
Pat_70	Post-Resistance	EIF2C2	27161	37	8	141554345	141554345	Frame_Shift_Del	DEL	G	-	8	827	c.1806delC	c.(1804-1806)CCCfs	p.P602fs
Pat_70	Post-Resistance	TSNARE1	203062	37	8	143310866	143310868	In_Frame_Del	DEL	GAT	-	11	488	.1519_1521delAT	c.(1519-1521)ATCdel	p.I507del
Pat_70	Post-Resistance	KANK1	23189	37	9	732475	732477	In_Frame_Del	DEL	GAG	-	12	623	.3103_3105delGA	c.(3103-3105)GAGdel	p.E1039del
Pat_70	Post-Resistance	RANBP6	26953	37	9	6012690	6012690	Frame_Shift_Del	DEL	T	-	8	531	c.2918delA	c.(2917-2919)AATfs	p.N973fs
Pat_70	Post-Resistance	TAF1L	138474	37	9	32633584	32633584	Frame_Shift_Del	DEL	T	-	14	530	c.1994delA	c.(1993-1995)AAGfs	p.K665fs
Pat_70	Post-Resistance	KIF24	347240	37	9	34257623	34257623	Frame_Shift_Del	DEL	T	-	7	230	c.1982delA	c.(1981-1983)AAGfs	p.K661fs
Pat_70	Post-Resistance	HRCT1	646962	37	9	35906605	35906607	In_Frame_Del	DEL	CCG	-	9	78	c.321_323delCCG	.(319-324)CACCGC>CAC	p.R108del
Pat_70	Post-Resistance	ROR2	4920	37	9	94486026	94486028	In_Frame_Del	DEL	TCC	-	7	405	.2748_2750delGG	(2746-2751)GAGGAA>GA	.916_917EE>I
Pat_70	Post-Resistance	XPA	7507	37	9	100455962	100455964	In_Frame_Del	DEL	TTC	-	9	302	c.250_252delGAA	c.(250-252)GAAdel	p.E84del
Pat_70	Post-Resistance	NR4A3	8013	37	9	102590616	102590618	In_Frame_Del	DEL	CAC	-	9	175	c.292_294delCAC	c.(292-294)CACdel	p.H108del
Pat_70	Post-Resistance	TNC	3371	37	9	117797539	117797539	Frame_Shift_Del	DEL	G	-	11	875	c.5731delC	c.(5731-5733)CGGfs	p.R1911fs
Pat_70	Post-Resistance	ASTN2	23245	37	9	119976989	119976991	In_Frame_Del	DEL	CAG	-	13	294	c.661_663delCTG	c.(661-663)CTGdel	p.L221del
Pat_70	Post-Resistance	RAB14	51552	37	9	123954449	123954450	Frame_Shift_Ins	INS	-	T	7	475	c.105_106insA	c.(103-108)AAATTTfs	p.K35fs
Pat_70	Post-Resistance	DAB2IP	153090	37	9	124522389	124522391	In_Frame_Del	DEL	AAG	-	12	355	c.757_759delAAG	c.(757-759)AAGdel	p.K257del
Pat_70	Post-Resistance	PRDM12	59335	37	9	133543701	133543702	Splice_Site	DEL	GT	-	33	447	c.570_splice	c.e3+1	p.E190_splice
Pat_70	Post-Resistance	GRIN1	2902	37	9	140056884	140056886	In_Frame_Del	DEL	GAG	-	13	201	.1780_1782delGA	c.(1780-1782)GAGdel	p.E598del
Pat_70	Post-Resistance	IQSEC2	23096	37	X	53285045	53285047	In_Frame_Del	DEL	CTC	-	7	152	c.934_936delGAG	c.(934-936)GAGdel	p.E312del
Pat_70	Post-Resistance	PHF8	23133	37	X	54011405	54011407	In_Frame_Del	DEL	CTC	-	36	867	.2491_2493delGA	c.(2491-2493)GAGdel	p.E831del
Pat_70	Post-Resistance	NAP1L2	4674	37	X	72433664	72433666	In_Frame_Del	DEL	TCC	-	8	165	c.663_665delGGA	.(661-666)GAGGAC>GAC	p.E221del
Pat_70	Post-Resistance	ARMCX3	51566	37	X	100880152	100880154	In_Frame_Del	DEL	TGA	-	14	1187	c.183_185delTGA	c.(181-186)TCTGAT>TCT	p.D66del
Pat_70	Post-Resistance	BHLHB9	80823	37	X	102004419	102004421	In_Frame_Del	DEL	GAG	-	20	809	c.496_498delGAG	c.(496-498)GAGdel	p.E171del
Pat_70	Post-Resistance	SLC6A14	11254	37	X	115584255	115584256	Frame_Shift_Ins	INS	-	T	7	360	c.1233_1234insT	c.(1231-1236)TTATTTfs	p.L411fs

Pat_70	Post-Resistance	SLC25A5	292	37	X	118603706	118603707	Frame_Shift_Ins	INS	-	G	74	1071	c.194_195insG	c.(193-195)CAGfs	p.Q65fs
Pat_70	Post-Resistance	ZBTB33	10009	37	X	119387381	119387382	Frame_Shift_Del	DEL	TG	-	7	1884	c.111_112delTG	c.(109-114)ATTGTGfs	p.I37fs
Pat_70	Post-Resistance	CUL4B	8450	37	X	119694117	119694119	In_Frame_Del	DEL	GAG	-	11	194	c.429_431delCTC	c.(427-432)TCCTCA>TCA	.143_144SS>
Pat_70	Post-Resistance	USP26	83844	37	X	132160788	132160788	Frame_Shift_Del	DEL	A	-	13	696	c.1461delT	c.(1459-1461)TTTfs	p.F487fs
Pat_70	Post-Resistance	PLAC1	10761	37	X	133700525	133700525	Frame_Shift_Del	DEL	G	-	7	1281	c.188delC	c.(187-189)CCAfs	p.P63fs
Pat_70	Post-Resistance	MAGEC1	9947	37	X	140994114	140994116	In_Frame_Del	DEL	CTC	-	8	1124	c.924_926delCTC	.(922-927)AGCTCC>AGC	.308_309SS>
Pat_70	Post-Resistance	MAMLD1	10046	37	X	149639325	149639327	In_Frame_Del	DEL	CAG	-	10	285	.1480_1482delCA	c.(1480-1482)CAGdel	p.Q502del
Pat_70	Post-Resistance	CD99L2	83692	37	X	149984524	149984526	In_Frame_Del	DEL	GTG	-	13	1064	c.156_158delCAC	c.(154-159)ACCACA>ACA	p.52_53TT>T
Pat_70	Post-Resistance	ZNF185	7739	37	X	152087570	152087572	In_Frame_Del	DEL	GAG	-	10	119	c.475_477delGAG	c.(475-477)GAGdel	p.E165del
Pat_70	Post-Resistance	BCAP31	10134	37	X	152981034	152981043	Frame_Shift_Del	DEL	CCTCTGGG	-	27	513	_304delGCCCAG	295-306)GCCCAGAGGAA	p.A99fs
Pat_70	Post-Resistance	F8	2157	37	X	154157686	154157686	Frame_Shift_Del	DEL	T	-	12	329	c.4379delA	c.(4378-4380)AATfs	p.N1460fs
Pat_73	Pre-Treatment	AHDC1	27245	37	1	27875353	27875355	In_Frame_Del	DEL	AGG	-	11	126	.3272_3274delCC	.(3271-3276)TCCTTC>TT	p.S1091del
Pat_73	Pre-Treatment	THRAP3	9967	37	1	36752261	36752262	Frame_Shift_Del	DEL	AG	-	8	578	c.430_431delAG	c.(430-432)AGAfs	p.R144fs
Pat_73	Pre-Treatment	ROR1	4919	37	1	64608186	64608187	Frame_Shift_Del	DEL	CA	-	7	450	c.1027_1028delCA	c.(1027-1029)CACfs	p.H343fs
Pat_73	Pre-Treatment	PRG4	10216	37	1	186276143	186276145	In_Frame_Del	DEL	CTC	-	25	446	.1292_1294delCT	.(1291-1296)ACTCCC>AC	p.P432del
Pat_73	Pre-Treatment	INTS7	25896	37	1	212115191	212115193	In_Frame_Del	DEL	TGC	-	8	382	.2862_2864delGC	.(2860-2865)CAGCAA>CA	.954_955QQ>
Pat_73	Pre-Treatment	FLVCR1	28982	37	1	213037113	213037114	Frame_Shift_Del	DEL	AC	-	7	265	c.785_786delAC	c.(784-786)AACfs	p.N262fs
Pat_73	Pre-Treatment	LZTS2	84445	37	10	102763415	102763417	In_Frame_Del	DEL	CCT	-	10	336	c.560_562delCCT	.(559-564)GCCTCC>GCC	p.S197del
Pat_73	Pre-Treatment	LOC653544	653544	37	10	135491036	135491036	Frame_Shift_Del	DEL	G	-	17	421	c.647delG	c.(646-648)AGGfs	p.R216fs
Pat_73	Pre-Treatment	FADS2	9415	37	11	61615748	61615748	Frame_Shift_Del	DEL	C	-	8	852	c.736delC	c.(736-738)CCCfs	p.P246fs
Pat_73	Pre-Treatment	KLHL35	283212	37	11	75134762	75134762	Frame_Shift_Del	DEL	C	-	7	657	c.877delG	c.(877-879)GAGfs	p.E293fs
Pat_73	Pre-Treatment	PRB2	653247	37	12	11546506	11546508	In_Frame_Del	DEL	TTG	-	25	726	c.504_506delCAA	c.(502-507)AACAAG>AAG	p.N168del
Pat_73	Pre-Treatment	DACH1	1602	37	13	72440659	72440664	Splice_Site	DEL	GCCGCC	-	4	7	c.242_splice	c.e2-1	p.G81_splice
Pat_73	Pre-Treatment	SNX6	58533	37	14	35099154	35099154	Frame_Shift_Del	DEL	G	-	2	4	c.49delC	c.(49-51)CTGfs	p.L17fs
Pat_73	Pre-Treatment	FANCM	57697	37	14	45642288	45642289	Frame_Shift_Del	DEL	CT	-	7	172	c.2191_2192delCT	c.(2191-2193)CTCfs	p.L731fs
Pat_73	Pre-Treatment	C14orf39	317761	37	14	60903565	60903565	Frame_Shift_Del	DEL	A	-	7	168	c.1762delT	c.(1762-1764)TGAfs	p.*588fs
Pat_73	Pre-Treatment	EIF3CL	728689	37	16	28734579	28734581	In_Frame_Del	DEL	GAG	-	7	2395	c.871_873delGAG	c.(871-873)GAGdel	p.E295del
Pat_73	Pre-Treatment	CD2BP2	10421	37	16	30365550	30365552	In_Frame_Del	DEL	CAT	-	11	1107	c.170_172delATG	.(169-174)GATGGG>GG	p.D57del
Pat_73	Pre-Treatment	PSTPIP2	9050	37	18	43591185	43591185	Frame_Shift_Del	DEL	C	-	7	530	c.316delG	c.(316-318)GAAfs	p.E106fs
Pat_73	Pre-Treatment	SPPL2B	56928	37	19	2340953	2340953	Frame_Shift_Del	DEL	C	-	7	129	c.897delC	c.(895-897)CTCfs	p.L299fs
Pat_73	Pre-Treatment	USE1	55850	37	19	17330180	17330181	Frame_Shift_Del	DEL	TC	-	4	2	c.581_582delTC	c.(580-582)ATCfs	p.I194fs
Pat_73	Pre-Treatment	C2orf71	388939	37	2	29295647	29295649	In_Frame_Del	DEL	TCC	-	7	418	.1479_1481delGG	(1477-1482)GAGGAA>GA	.493_494EE>
Pat_73	Pre-Treatment	ARHGAP25	9938	37	2	69002410	69002410	Frame_Shift_Del	DEL	C	-	7	1250	c.119delC	c.(118-120)ACCfs	p.T40fs
Pat_73	Pre-Treatment	ANKRD36	375248	37	2	97808574	97808575	Splice_Site	INS	-	A	19	49	c.901_splice	c.e8+2	p.V301_splice
Pat_73	Pre-Treatment	CD28	940	37	2	204591576	204591576	Frame_Shift_Del	DEL	C	-	7	305	c.273delC	c.(271-273)GGCfs	p.G91fs
Pat_73	Pre-Treatment	PLAC4	191585	37	21	42551313	42551313	Frame_Shift_Del	DEL	C	-	13	87	c.243delG	c.(241-243)TGGfs	p.W81fs
Pat_73	Pre-Treatment	RNF215	200312	37	22	30783221	30783223	In_Frame_Del	DEL	GCA	-	6	4	c.80_82delTGC	c.(79-84)CTGCCC>CCC	p.L27del
Pat_73	Pre-Treatment	MST1R	4486	37	3	49940112	49940112	Frame_Shift_Del	DEL	C	-	7	302	c.931delG	c.(931-933)GCCfs	p.A311fs
Pat_73	Pre-Treatment	LNP1	348801	37	3	100148586	100148588	In_Frame_Del	DEL	GAT	-	7	944	c.13_15delGAT	c.(13-15)GATdel	p.D10del
Pat_73	Pre-Treatment	ACTL6A	86	37	3	179301188	179301188	Frame_Shift_Del	DEL	G	-	215	180	c.1074delG	c.(1072-1074)CAGfs	p.Q358fs
Pat_73	Pre-Treatment	CRIPAK	285464	37	4	1388441	1388442	Frame_Shift_Ins	INS	-	CG	18	2494	c.142_143insCG	c.(142-144)ATGfs	p.M48fs
Pat_73	Pre-Treatment	CRIPAK	285464	37	4	1389143	1389144	Frame_Shift_Ins	INS	-	CA	7	1287	c.844_845insCA	c.(844-846)TCAfs	p.S282fs
Pat_73	Pre-Treatment	SH3TC2	79628	37	5	148386620	148386620	Frame_Shift_Del	DEL	C	-	7	265	c.3499delG	c.(3499-3501)GTGfs	p.V1167fs
Pat_73	Pre-Treatment	SLIT3	6586	37	5	168137990	168137991	Frame_Shift_Del	DEL	TG	-	4	8	c.2628_2629delCA	c.(2626-2631)TACAAGfs	p.Y876fs
Pat_73	Pre-Treatment	FOXC1	2296	37	6	1612017	1612018	In_Frame_Ins	INS	-	CGG	21	42	.1337_1338insCG	(1336-1338)CAC>CACGG	p.456_457insG
Pat_73	Pre-Treatment	RIOK1	83732	37	6	7393450	7393452	In_Frame_Del	DEL	GAC	-	9	357	c.190_192delGAC	c.(190-192)GACdel	p.D69del
Pat_73	Pre-Treatment	ATXN1	6310	37	6	16327900	16327901	In_Frame_Ins	INS	-	TGC	7	202	c.641_642insGCA	.(640-642)CAG>CAGCAG	.214_214Q>Q

Pat_73	Pre-Treatment	ATXN1	6310	37	6	16327907	16327909	In_Frame_Del	DEL	TGA	-	8	199	c.633_635delTCA	c.(631-636)CATCAG>CAG	p.H211del
Pat_73	Pre-Treatment	PPP1R10	5514	37	6	30570264	30570266	In_Frame_Del	DEL	GGA	-	7	218	.2160_2162delTC	(2158-2163)CCTCCA>CC	.720_721PP>
Pat_73	Pre-Treatment	DDR1	780	37	6	30863251	30863251	Frame_Shift_Del	DEL	C	-	8	1757	c.1584delC	c.(1582-1584)GGCfs	p.G528fs
Pat_73	Pre-Treatment	CFB	629	37	6	31895549	31895549	Frame_Shift_Del	DEL	T	-	7	2402	c.20delT	c.(19-21)CTTfs	p.L7fs
Pat_73	Pre-Treatment	TULP1	7287	37	6	35478775	35478777	In_Frame_Del	DEL	TCC	-	10	454	c.360_362delGGA	.(358-363)GAGGAA>GAA	.120_121EE>
Pat_73	Pre-Treatment	FTSJD2	23070	37	6	37447821	37447821	Frame_Shift_Del	DEL	G	-	9	955	c.2408delG	c.(2407-2409)TGGfs	p.W803fs
Pat_73	Pre-Treatment	MDFI	4188	37	6	41621169	41621171	In_Frame_Del	DEL	CTG	-	21	773	c.597_599delCTG	c.(595-600)CTCTGC>CTC	p.C204del
Pat_73	Pre-Treatment	TTBK1	84630	37	6	43250681	43250683	In_Frame_Del	DEL	GAG	-	11	210	.2203_2205delGA	c.(2203-2205)GAGdel	p.E740del
Pat_73	Pre-Treatment	TNFRSF21	27242	37	6	47200623	47200624	Frame_Shift_Del	DEL	CA	-	8	1338	.1845_1846delTG	c.(1843-1848)ATTGAAfs	p.I615fs
Pat_73	Pre-Treatment	KCNB2	9312	37	8	73480397	73480397	Frame_Shift_Del	DEL	A	-	8	393	c.428delA	c.(427-429)CAAfs	p.Q143fs
Pat_73	Pre-Treatment	C9orf43	257169	37	9	116187646	116187648	In_Frame_Del	DEL	GCA	-	7	154	c.888_890delGCA	.(886-891)CGGCAG>CGC	p.Q304del
Pat_73	Pre-Treatment	TNC	3371	37	9	117848734	117848735	Frame_Shift_Del	DEL	CA	-	8	704	.1275_1276delTG	c.(1273-1278)TGTGATfs	p.C425fs
Pat_73	Post-Resistance	DPH2	1802	37	1	44436809	44436809	Frame_Shift_Del	DEL	C	-	2	4	c.432delC	c.(430-432)GACfs	p.D144fs
Pat_73	Post-Resistance	LOC653544	653544	37	10	135491036	135491036	Frame_Shift_Del	DEL	G	-	14	238	c.647delG	c.(646-648)AGGfs	p.R216fs
Pat_73	Post-Resistance	PRB2	653247	37	12	11546506	11546508	In_Frame_Del	DEL	TTG	-	8	425	c.504_506delCAA	c.(502-507)AACAAG>AAG	p.N168del
Pat_73	Post-Resistance	LRP1	4035	37	12	57605740	57605742	In_Frame_Del	DEL	TGC	-	8	150	13289_13291delT	13288-13293)TTGCTG>T	4430_4431LL>
Pat_73	Post-Resistance	C14orf4	64207	37	14	77493648	77493650	In_Frame_Del	DEL	GCG	-	4	9	c.486_488delCGC	.(484-489)GCCGCT>GCT	.162_163AA>
Pat_73	Post-Resistance	DYX1C1	161582	37	15	55759242	55759242	Frame_Shift_Del	DEL	T	-	2	4	c.523delA	c.(523-525)ATTfs	p.I175fs
Pat_73	Post-Resistance	CHRNA3	1136	37	15	78913068	78913070	In_Frame_Del	DEL	CAG	-	6	3	c.67_69delCTG	c.(67-69)CTGdel	p.L23del
Pat_73	Post-Resistance	CCDC144B	284047	37	17	18498059	18498060	Splice_Site	INS	-	A	7	41	c.1867_splice	c.e9-1	p.E623_splice
Pat_73	Post-Resistance	ITPRIPL1	150771	37	2	96992793	96992795	In_Frame_Del	DEL	GAG	-	9	78	c.424_426delGAG	c.(424-426)GAGdel	p.E147del
Pat_73	Post-Resistance	MFF	56947	37	2	228197214	228197214	Frame_Shift_Del	DEL	G	-	7	775	c.339delG	c.(337-339)CTGfs	p.L113fs
Pat_73	Post-Resistance	MKL1	57591	37	22	40816887	40816889	In_Frame_Del	DEL	TGC	-	7	122	c.843_845delGCA	.(841-846)CAGCAC>CAC	p.Q281del
Pat_73	Post-Resistance	C22orf26	55267	37	22	46449890	46449890	Frame_Shift_Del	DEL	G	-	4	4	c.84delC	c.(82-84)CCCfs	p.P28fs
Pat_73	Post-Resistance	LNP1	348801	37	3	100148586	100148588	In_Frame_Del	DEL	GAT	-	7	480	c.13_15delGAT	c.(13-15)GATdel	p.D10del
Pat_73	Post-Resistance	ACTL6A	86	37	3	179301188	179301188	Frame_Shift_Del	DEL	G	-	107	129	c.1074delG	c.(1072-1074)CAGfs	p.Q358fs
Pat_73	Post-Resistance	CRIPAK	285464	37	4	1388441	1388442	Frame_Shift_Ins	INS	-	CG	25	1243	c.142_143insCG	c.(142-144)ATGfs	p.M48fs
Pat_73	Post-Resistance	FOXC1	2296	37	6	1612017	1612018	In_Frame_Ins	INS	-	CGG	4	6	.1337_1338insCG	(1336-1338)CAC>CACGG	p.456_457insG
Pat_73	Post-Resistance	RIOK1	83732	37	6	7393450	7393452	In_Frame_Del	DEL	GAC	-	8	225	c.190_192delGAC	c.(190-192)GACdel	p.D69del
Pat_73	Post-Resistance	MDFI	4188	37	6	41621169	41621171	In_Frame_Del	DEL	CTG	-	7	337	c.597_599delCTG	c.(595-600)CTCTGC>CTC	p.C204del
Pat_74	Pre-Treatment	ZBTB40	9923	37	1	22838561	22838563	In_Frame_Del	DEL	AAG	-	9	77	.2395_2397delAA	c.(2395-2397)AAGdel	p.K803del
Pat_74	Pre-Treatment	PHACTR4	65979	37	1	28785730	28785730	Frame_Shift_Del	DEL	A	-	7	96	c.151delA	c.(151-153)AAAfs	p.K51fs
Pat_74	Pre-Treatment	HFE2	148738	37	1	145415369	145415371	In_Frame_Del	DEL	GAG	-	9	86	c.188_190delGAG	.(187-192)CGAGGA>CGA	p.G69del
Pat_74	Pre-Treatment	DARC	2532	37	1	159176167	159176167	Frame_Shift_Del	DEL	G	-	7	732	c.938delG	c.(937-939)CGCfs	p.R313fs
Pat_74	Pre-Treatment	RNF141	50862	37	11	10536563	10536563	Frame_Shift_Del	DEL	G	-	7	300	c.593delC	c.(592-594)GCAfs	p.A198fs
Pat_74	Pre-Treatment	RNF121	55298	37	11	71705825	71705825	Frame_Shift_Del	DEL	G	-	7	439	c.688delG	c.(688-690)GGGfs	p.G230fs
Pat_74	Pre-Treatment	PRB2	653247	37	12	11546506	11546508	In_Frame_Del	DEL	TTG	-	8	355	c.504_506delCAA	c.(502-507)AACAAG>AAG	p.N168del
Pat_74	Pre-Treatment	C15orf24	56851	37	15	34393991	34393993	In_Frame_Del	DEL	AGC	-	7	451	c.48_50delGCT	c.(46-51)CTGCTA>CTA	p.16_17LL>L
Pat_74	Pre-Treatment	CHD2	1106	37	15	93480819	93480819	Frame_Shift_Del	DEL	A	-	7	179	c.515delA	c.(514-516)CAAfs	p.Q172fs
Pat_74	Pre-Treatment	CXXC1	30827	37	18	47812275	47812277	In_Frame_Del	DEL	CTG	-	7	75	c.481_483delCAG	c.(481-483)CAGdel	p.Q161del
Pat_74	Pre-Treatment	LRP2	4036	37	2	170009348	170009349	Frame_Shift_Del	DEL	AC	-	7	646	12421_12422delG	c.(12421-12423)GTAfs	p.V4141fs
Pat_74	Pre-Treatment	C20orf85	128602	37	20	56735727	56735727	Frame_Shift_Del	DEL	C	-	8	112	c.263delC	c.(262-264)TCCfs	p.S88fs
Pat_74	Pre-Treatment	PLAC4	191585	37	21	42551313	42551313	Frame_Shift_Del	DEL	C	-	7	39	c.243delG	c.(241-243)TGGfs	p.W81fs
Pat_74	Pre-Treatment	TRIOBP	11078	37	22	38120029	38120031	In_Frame_Del	DEL	CCT	-	18	261	.1466_1468delCC	(1465-1470)GCCTCC>GC	p.S491del
Pat_74	Pre-Treatment	CTNNB1	1499	37	3	41266134	41266136	In_Frame_Del	DEL	CTT	-	35	58	c.131_133delCTT	c.(130-135)CCTTCT>CCT	p.S45del
Pat_74	Pre-Treatment	CRIPAK	285464	37	4	1388900	1388901	Frame_Shift_Del	DEL	CA	-	9	428	c.601_602delCA	c.(601-603)CACfs	p.H201fs
Pat_74	Pre-Treatment	TMEM154	201799	37	4	153562130	153562137	Frame_Shift_Del	DEL	AAAGTCGG	-	8	98	79_486delCCGAC	c.(478-486)GCCGACTTTf	p.A160fs

Pat_74	Pre-Treatment	PHF3	23469	37	6	64394097	64394097	Frame_Shift_Del	DEL	A	-	9	672	c.474delA	c.(472-474)ACAfs	p.T158fs
Pat_74	Pre-Treatment	CDCA7L	55536	37	7	21956486	21956486	Frame_Shift_Del	DEL	A	-	7	331	c.51delT	c.(49-51)TTTfs	p.F17fs
Pat_74	Pre-Treatment	MUC17	140453	37	7	100684131	100684133	In_Frame_Del	DEL	CTC	-	29	830	.9434_9436delCT	.(9433-9438)TCTCCT>TC	p.P3146del
Pat_74	Pre-Treatment	CSGALNACT1	55790	37	8	19315974	19315974	Frame_Shift_Del	DEL	T	-	7	1461	c.814delA	c.(814-816)AGGfs	p.R272fs
Pat_74	Pre-Treatment	MYST3	7994	37	8	41798420	41798422	In_Frame_Del	DEL	CTC	-	7	253	.2977_2979delGA	c.(2977-2979)GAGdel	p.E993del
Pat_74	Post-Resistance	ZBTB40	9923	37	1	22838561	22838563	In_Frame_Del	DEL	AAG	-	8	59	.2395_2397delAA	c.(2395-2397)AAGdel	p.K803del
Pat_74	Post-Resistance	XPOT	11260	37	12	64812755	64812755	Frame_Shift_Del	DEL	T	-	8	100	c.370delT	c.(370-372)TTTfs	p.F124fs
Pat_74	Post-Resistance	RTN4	57142	37	2	55253746	55253746	Frame_Shift_Del	DEL	T	-	7	64	c.1489delA	c.(1489-1491)ATAfs	p.I497fs
Pat_74	Post-Resistance	RNF160	26046	37	21	30339206	30339206	Frame_Shift_Del	DEL	T	-	7	44	c.1745delA	c.(1744-1746)AATfs	p.N582fs
Pat_74	Post-Resistance	PLAC4	191585	37	21	42551313	42551313	Frame_Shift_Del	DEL	C	-	5	8	c.243delG	c.(241-243)TGGfs	p.W81fs
Pat_74	Post-Resistance	MYH9	4627	37	22	36689419	36689421	In_Frame_Del	DEL	CCT	-	7	62	.4049_4051delAG	(4048-4053)GAGGCC>GC	p.E1350del
Pat_74	Post-Resistance	TRIOBP	11078	37	22	38120029	38120031	In_Frame_Del	DEL	CCT	-	14	186	.1466_1468delCC	(1465-1470)GCCTCC>GC	p.S491del
Pat_74	Post-Resistance	CTNNB1	1499	37	3	41266134	41266136	In_Frame_Del	DEL	CTT	-	26	36	c.131_133delCTT	c.(130-135)CCTTCT>CCT	p.S45del
Pat_74	Post-Resistance	TMEM154	201799	37	4	153562130	153562137	Frame_Shift_Del	DEL	AAAGTCGG	-	12	60	79_486delCCGAC	c.(478-486)GCCGACTTTf	p.A160fs
Pat_74	Post-Resistance	MPP6	51678	37	7	24705665	24705666	Frame_Shift_Ins	INS	-	A	7	168	c.909_910insA	c.(907-912)AGCAAAfs	p.S303fs
Pat_74	Post-Resistance	MUC17	140453	37	7	100684131	100684133	In_Frame_Del	DEL	CTC	-	9	487	.9434_9436delCT	.(9433-9438)TCTCCT>TC	p.P3146del
Pat_76	Pre-Treatment	LRRC47	57470	37	1	3712520	3712520	Frame_Shift_Del	DEL	C	-	4	8	c.521delG	c.(520-522)CGCfs	p.R174fs
Pat_76	Pre-Treatment	DNAJC11	55735	37	1	6727803	6727804	Frame_Shift_Del	DEL	TC	-	9	81	c.343_344delGA	c.(343-345)GAAfs	p.E115fs
Pat_76	Pre-Treatment	HFE2	148738	37	1	145415369	145415371	In_Frame_Del	DEL	GAG	-	7	230	c.188_190delGAG	.(187-192)CGAGGA>CG	p.G69del
Pat_76	Pre-Treatment	POLR3C	10623	37	1	145608575	145608575	Frame_Shift_Del	DEL	G	-	7	444	c.232delC	c.(232-234)CAGfs	p.Q78fs
Pat_76	Pre-Treatment	PEAR1	375033	37	1	156877507	156877507	Frame_Shift_Del	DEL	C	-	8	511	c.750delC	c.(748-750)TGCfs	p.C250fs
Pat_76	Pre-Treatment	PVRL4	81607	37	1	161044104	161044106	In_Frame_Del	DEL	CCA	-	8	373	.1058_1060delTG	(1057-1062)GTGGGT>GG	p.V353del
Pat_76	Pre-Treatment	PCP4L1	654790	37	1	161254154	161254156	In_Frame_Del	DEL	GGA	-	10	316	c.90_92delGGA	c.(88-93)GCGGAG>GCG	p.E35del
Pat_76	Pre-Treatment	POU2F1	5451	37	1	167385016	167385018	In_Frame_Del	DEL	CCA	-	12	784	.2201_2203delCC	.(2200-2205)TCCACC>TC	p.T738del
Pat_76	Pre-Treatment	SCYL3	57147	37	1	169825006	169825006	Frame_Shift_Del	DEL	A	-	113	75	c.1405delT	c.(1405-1407)TCTfs	p.S469fs
Pat_76	Pre-Treatment	KLHL20	27252	37	1	173744859	173744859	Frame_Shift_Del	DEL	C	-	8	317	c.1516delC	c.(1516-1518)CAGfs	p.Q506fs
Pat_76	Pre-Treatment	PAPPA2	60676	37	1	176809369	176809369	Frame_Shift_Del	DEL	G	-	7	615	c.5263delG	c.(5263-5265)GGGfs	p.G1755fs
Pat_76	Pre-Treatment	GPR25	2848	37	1	200842776	200842778	In_Frame_Del	DEL	TGC	-	7	36	c.611_613delTGC	c.(610-615)TTGCTG>TTG	.204_205LL>
Pat_76	Pre-Treatment	PPP2R5A	5525	37	1	212534111	212534111	Frame_Shift_Del	DEL	A	-	8	57	c.1460delA	c.(1459-1461)TAAfs	p.*487fs
Pat_76	Pre-Treatment	PANK1	53354	37	10	91359120	91359120	Frame_Shift_Del	DEL	T	-	7	536	c.1199delA	c.(1198-1200)AAGfs	p.K400fs
Pat_76	Pre-Treatment	MKI67	4288	37	10	129905725	129905725	Frame_Shift_Del	DEL	T	-	7	289	c.4379delA	c.(4378-4380)AAGfs	p.K1460fs
Pat_76	Pre-Treatment	SYT8	90019	37	11	1858552	1858552	Frame_Shift_Del	DEL	C	-	2	4	c.1097delC	c.(1096-1098)GCCfs	p.A366fs
Pat_76	Pre-Treatment	ACCSL	390110	37	11	44074222	44074222	Frame_Shift_Del	DEL	G	-	7	624	c.783delG	c.(781-783)CTGfs	p.L261fs
Pat_76	Pre-Treatment	RAD9A	5883	37	11	67164978	67164978	Frame_Shift_Del	DEL	C	-	7	108	c.1124delC	c.(1123-1125)TCCfs	p.S375fs
Pat_76	Pre-Treatment	TCIRG1	10312	37	11	67811611	67811612	Frame_Shift_Del	DEL	AC	-	4	3	c.820_821delAC	c.(820-822)ACAfs	p.T274fs
Pat_76	Pre-Treatment	CCDC15	80071	37	11	124857232	124857252	In_Frame_Del	DEL	GAAGGCC	-	28	142	TGAGCCAGAAG	CTGAGCCAGAAGGCCA	EPEGQAI371
Pat_76	Pre-Treatment	SFRS8	6433	37	12	132281734	132281736	In_Frame_Del	DEL	AGA	-	12	545	.2546_2548delAG	(2545-2550)GAGAAG>GA	p.K853del
Pat_76	Pre-Treatment	IPO4	79711	37	14	24656873	24656874	Frame_Shift_Del	DEL	CT	-	7	197	c.407_408delAG	c.(406-408)GAGfs	p.E136fs
Pat_76	Pre-Treatment	TMED10	10972	37	14	75614382	75614383	Frame_Shift_Del	DEL	CG	-	7	1036	c.395_396delCG	c.(394-396)GCGfs	p.A132fs
Pat_76	Pre-Treatment	DMXL2	23312	37	15	51780185	51780185	Frame_Shift_Del	DEL	A	-	7	661	c.5183delT	c.(5182-5184)TTCfs	p.F1728fs
Pat_76	Pre-Treatment	MCTP2	55784	37	15	94841579	94841579	Frame_Shift_Del	DEL	A	-	7	514	c.85delA	c.(85-87)AAAfs	p.K29fs
Pat_76	Pre-Treatment	IGFALS	3483	37	16	1841122	1841123	Frame_Shift_Ins	INS	-	C	4	7	c.1296_1297insG	c.(1294-1299)GGGCTGfs	p.G432fs
Pat_76	Pre-Treatment	ABCA3	21	37	16	2373583	2373583	Frame_Shift_Del	DEL	A	-	8	627	c.554delT	c.(553-555)TTCfs	p.F185fs
Pat_76	Pre-Treatment	KIF1C	10749	37	17	4906945	4906945	Frame_Shift_Del	DEL	G	-	20	34	c.759delG	c.(757-759)GAGfs	p.E253fs
Pat_76	Pre-Treatment	MYOCD	93649	37	17	12647692	12647694	In_Frame_Del	DEL	CAG	-	7	20	c.910_912delCAG	c.(910-912)CAGdel	p.Q310del
Pat_76	Pre-Treatment	TOP3A	7156	37	17	18188461	18188462	Frame_Shift_Del	DEL	TG	-	7	271	.1871_1872delC	c.(1870-1872)GCAfs	p.A624fs
Pat_76	Pre-Treatment	ADAM11	4185	37	17	42851673	42851673	Frame_Shift_Del	DEL	T	-	4	6	c.1003delT	c.(1003-1005)TTCfs	p.F335fs

Pat_76	Pre-Treatment	ABCA6	23460	37	17	67125767	67125767	Frame_Shift_Del	DEL	A	-	8	117	c.917delT	c.(916-918)TTAfs	p.L306fs
Pat_76	Pre-Treatment	GRIN2C	2905	37	17	72839130	72839131	In_Frame_Ins	INS	-	CTCCGGG	2	4	5_3146insCCCCG	5-3147)CTG>CCCCCGGA	048_1049insP
Pat_76	Pre-Treatment	DHPS	1725	37	19	12791042	12791042	Frame_Shift_Del	DEL	C	-	8	472	c.305delG	c.(304-306)GGAfs	p.G102fs
Pat_76	Pre-Treatment	OR10H1	26539	37	19	15918794	15918795	Frame_Shift_Del	DEL	AG	-	115	137	c.53_54delCT	c.(52-54)TCTfs	p.S18fs
Pat_76	Pre-Treatment	PSG9	5678	37	19	43772052	43772053	Frame_Shift_Ins	INS	-	C	213	362	c.313_314insG	c.(313-315)GCAfs	p.A105fs
Pat_76	Pre-Treatment	LILRB5	10990	37	19	54760181	54760181	Frame_Shift_Del	DEL	A	-	48	62	c.380delT	c.(379-381)TTAfs	p.L127fs
Pat_76	Pre-Treatment	RAB11FIP5	26056	37	2	73315337	73315339	In_Frame_Del	DEL	TGG	-	7	216	.1407_1409delCC	.(1405-1410)CACCAA>CA	p.H469del
Pat_76	Pre-Treatment	RBM45	129831	37	2	178988920	178988920	Frame_Shift_Del	DEL	A	-	8	105	c.1135delA	c.(1135-1137)AAAfs	p.K379fs
Pat_76	Pre-Treatment	ABI2	10152	37	2	204193211	204193213	Translation_Start_Site	DEL	GAG	-	3	3	c.-26_-24delGAG	.(-28--22)ATGAGGA>ATGA	
Pat_76	Pre-Treatment	NINL	22981	37	20	25442165	25442166	Frame_Shift_Del	DEL	TG	-	8	167	c.3688_3689delCA	c.(3688-3690)CAAfs	p.Q1230fs
Pat_76	Pre-Treatment	SYCP2	10388	37	20	58467047	58467047	Frame_Shift_Del	DEL	T	-	8	95	c.2362delA	c.(2362-2364)ATGfs	p.M788fs
Pat_76	Pre-Treatment	SFRS15	57466	37	21	33043971	33043972	Frame_Shift_Del	DEL	TC	-	9	206	c.3184_3185delGA	c.(3184-3186)GATfs	p.D1062fs
Pat_76	Pre-Treatment	HMGXB4	10042	37	22	35661543	35661544	Frame_Shift_Ins	INS	-	A	8	47	c.1162_1163insA	c.(1162-1164)GAAfs	p.E388fs
Pat_76	Pre-Treatment	COLQ	8292	37	3	15518644	15518645	Frame_Shift_Del	DEL	CA	-	4	5	c.453_454delTG	c.(451-456)CCTGAAfs	p.P151fs
Pat_76	Pre-Treatment	KIAA2018	205717	37	3	113380090	113380090	Frame_Shift_Del	DEL	T	-	8	133	c.439delA	c.(439-441)ATTfs	p.I147fs
Pat_76	Pre-Treatment	GPR156	165829	37	3	119885960	119885960	Frame_Shift_Del	DEL	C	-	8	1157	c.2364delG	c.(2362-2364)GGGfs	p.G788fs
Pat_76	Pre-Treatment	DIRC2	84925	37	3	122598119	122598119	Frame_Shift_Del	DEL	G	-	9	666	c.1331delG	c.(1330-1332)TGGfs	p.W444fs
Pat_76	Pre-Treatment	FAM194A	131831	37	3	150421591	150421593	In_Frame_Del	DEL	TCC	-	7	29	c.93_95delGGA	c.(91-96)GAGGAA>GAA	p.31_32EE>E
Pat_76	Pre-Treatment	PHC3	80012	37	3	169896635	169896637	In_Frame_Del	DEL	TGG	-	13	918	c.68_70delCCA	c.(67-72)ACCATC>ATC	p.T23del
Pat_76	Pre-Treatment	EMCN	51705	37	4	101439033	101439033	Frame_Shift_Del	DEL	G	-	7	486	c.39delC	c.(37-39)CCCfs	p.P13fs
Pat_76	Pre-Treatment	RRH	10692	37	4	110756541	110756541	Frame_Shift_Del	DEL	T	-	7	117	c.317delT	c.(316-318)ATTfs	p.I106fs
Pat_76	Pre-Treatment	RBM27	54439	37	5	145641118	145641118	Frame_Shift_Del	DEL	A	-	8	137	c.1939delA	c.(1939-1941)ACCfs	p.T647fs
Pat_76	Pre-Treatment	PPP2R2B	5521	37	5	145969651	145969652	Frame_Shift_Ins	INS	-	C	8	387	c.1190_1191insG	c.(1189-1191)GGCfs	p.G397fs
Pat_76	Pre-Treatment	KIF13A	63971	37	6	17764958	17764958	Frame_Shift_Del	DEL	A	-	4	8	c.4801delT	c.(4801-4803)TCCfs	p.S1601fs
Pat_76	Pre-Treatment	HLA-F	3134	37	6	29694802	29694803	Frame_Shift_Ins	INS	-	T	7	426	c.1179_1180insT	c.(1177-1182)TTGTTTfs	p.L393fs
Pat_76	Pre-Treatment	CCHCR1	54535	37	6	31122281	31122281	Frame_Shift_Del	DEL	G	-	7	951	c.526delC	c.(526-528)CAAfs	p.Q176fs
Pat_76	Pre-Treatment	HSPA1L	3305	37	6	31778150	31778151	Frame_Shift_Del	DEL	GG	-	7	558	c.1599_1600delCC	c.(1597-1602)GTCCAGfs	p.V533fs
Pat_76	Pre-Treatment	RNF5	6048	37	6	32147672	32147672	Frame_Shift_Del	DEL	C	-	7	397	c.291delC	c.(289-291)CGCfs	p.R97fs
Pat_76	Pre-Treatment	PKHD1	5314	37	6	51523814	51523815	Frame_Shift_Del	DEL	TC	-	7	294	.11109_11110delG	c.(11107-11112)GAGAATfs	p.E3703fs
Pat_76	Pre-Treatment	ICK	22858	37	6	52883129	52883129	Frame_Shift_Del	DEL	T	-	7	455	c.662delA	c.(661-663)AAGfs	p.K221fs
Pat_76	Pre-Treatment	GLCCI1	113263	37	7	8126097	8126099	In_Frame_Del	DEL	CAG	-	9	683	.1573_1575delCA	c.(1573-1575)CAGdel	p.Q528del
Pat_76	Pre-Treatment	POU6F2	11281	37	7	39379288	39379290	In_Frame_Del	DEL	CAG	-	7	105	c.559_561delCAG	c.(559-561)CAGdel	p.Q196del
Pat_76	Pre-Treatment	LIMK1	3984	37	7	73535323	73535323	Frame_Shift_Del	DEL	C	-	7	768	c.1725delC	c.(1723-1725)TGCfs	p.C575fs
Pat_76	Pre-Treatment	GIGYF1	64599	37	7	100280978	100280980	In_Frame_Del	DEL	CTG	-	7	306	.2140_2142delCA	c.(2140-2142)CAGdel	p.Q714del
Pat_76	Pre-Treatment	EPHB4	2050	37	7	100410591	100410591	Frame_Shift_Del	DEL	C	-	7	514	c.1896delG	c.(1894-1896)GGGfs	p.G632fs
Pat_76	Pre-Treatment	PPP1R3A	5506	37	7	113519082	113519082	Frame_Shift_Del	DEL	T	-	7	1411	c.2065delA	c.(2065-2067)AGAfs	p.R689fs
Pat_76	Pre-Treatment	LUC7L2	51631	37	7	139094365	139094366	Frame_Shift_Del	DEL	AG	-	15	163	c.744_745delAG	c.(742-747)GAAGAGfs	p.E248fs
Pat_76	Pre-Treatment	OR9A4	130075	37	7	141619203	141619203	Frame_Shift_Del	DEL	T	-	10	492	c.528delT	c.(526-528)AATfs	p.N176fs
Pat_76	Pre-Treatment	CNTNAP2	26047	37	7	146829358	146829358	Frame_Shift_Del	DEL	G	-	8	410	c.1105delG	c.(1105-1107)GTGfs	p.V369fs
Pat_76	Pre-Treatment	SSPO	23145	37	7	149501110	149501110	Frame_Shift_Del	DEL	G	-	4	9	c.8246delG	c.(8245-8247)TGGfs	p.W2749fs
Pat_76	Pre-Treatment	ANXA13	312	37	8	124707761	124707762	Frame_Shift_Ins	INS	-	T	7	468	c.451_452insA	c.(451-453)ATCfs	p.I151fs
Pat_76	Pre-Treatment	FLJ43860	389690	37	8	142505021	142505022	Frame_Shift_Ins	INS	-	TGTG	10	27	c.424_425insCAC	c.(424-426)AAGfs	p.K142fs
Pat_76	Pre-Treatment	OFD1	8481	37	X	13786842	13786842	Frame_Shift_Del	DEL	A	-	7	519	c.2934delA	c.(2932-2934)TCAfs	p.S978fs
Pat_76	Pre-Treatment	FGD1	2245	37	X	54497147	54497148	Frame_Shift_Ins	INS	-	G	3	4	c.527_528insC	c.(526-528)CCAfs	p.P176fs
Pat_76	Pre-Treatment	NXF5	55998	37	X	101097764	101097764	Frame_Shift_Del	DEL	T	-	8	374	c.1delA	c.(1-3)ATGfs	p.M1fs
Pat_76	Pre-Treatment	CXorf66	347487	37	X	139038599	139038599	Frame_Shift_Del	DEL	T	-	9	302	c.542delA	c.(541-543)AAGfs	p.K181fs
Pat_76	Post-Resistance	PVRL4	81607	37	1	161044057	161044059	In_Frame_Del	DEL	CAC	-	7	256	.1105_1107delGT	c.(1105-1107)GTGdel	p.V369del

Pat_76	Post-Resistance	SCYL3	57147	37	1	169825006	169825006	Frame_Shift_Del	DEL	A	-	38	16	c.1405delT	c.(1405-1407)TCTfs	p.S469fs
Pat_76	Post-Resistance	CCDC15	80071	37	11	124857232	124857252	In_Frame_Del	DEL	GAAGGCC	-	11	52	TGAGCCAGAAG	CTGAGCCAGAAGGCCA	EPEGQAI371
Pat_76	Post-Resistance	SFRS8	6433	37	12	132281734	132281736	In_Frame_Del	DEL	AGA	-	10	252	.2546_2548delAG	(2545-2550)GAGAAG>GA	p.K853del
Pat_76	Post-Resistance	RAP1GAP2	23108	37	17	2894618	2894618	Frame_Shift_Del	DEL	A	-	2	4	c.841delA	c.(841-843)AATfs	p.N281fs
Pat_76	Post-Resistance	OR10H1	26539	37	19	15918794	15918795	Frame_Shift_Del	DEL	AG	-	62	187	c.53_54delCT	c.(52-54)TCTfs	p.S18fs
Pat_76	Post-Resistance	LGI4	163175	37	19	35625454	35625454	Frame_Shift_Del	DEL	G	-	2	4	c.131delC	c.(130-132)CCGfs	p.P44fs
Pat_76	Post-Resistance	SBSN	374897	37	19	36019046	36019047	Frame_Shift_Del	DEL	CT	-	7	260	c.137_138delAG	c.(136-138)GAGfs	p.E46fs
Pat_76	Post-Resistance	PSG9	5678	37	19	43772052	43772053	Frame_Shift_Ins	INS	-	C	75	217	c.313_314insG	c.(313-315)GCAfs	p.A105fs
Pat_76	Post-Resistance	LILRB5	10990	37	19	54760181	54760181	Frame_Shift_Del	DEL	A	-	48	66	c.380delT	c.(379-381)TTAfs	p.L127fs
Pat_76	Post-Resistance	PHC3	80012	37	3	169896635	169896637	In_Frame_Del	DEL	TGG	-	12	426	c.68_70delCCA	c.(67-72)ACCATC>ATC	p.T23del
Pat_76	Post-Resistance	THEMIS	387357	37	6	128134540	128134540	Frame_Shift_Del	DEL	T	-	13	27	c.1246delA	c.(1246-1248)ATCfs	p.I416fs

Strand	Exon	Transcript Position	Other Transcripts	Refseq mRNA_Id	Refseq prot_Id	SwissProt acc Id	SwissProt entry Id	UniProt Region	COSMIC overlapping mutations	COSMIC total alterations in gene	ref context	gc content	dbSNP RS
-	3	486	IAA0562_uc001ak	NM_014704	NP_055519	O60308	CE104_HUMAN			0	TTGTGGAAACTG	0.368	
+	2	716	pv.2_Missense_Mu	NM_025106	NP_079382	Q96BD6	SPSB1_HUMAN	B30.2/SPRY.		0	TGCACTCTGTCG	0.647	
+	4	493	SF8_uc010obc.1_	NM_001243	NP_001234	P28908	TNR8_HUMAN	(Potential).|TNFR-Cys 2.		5	TAGACGACCTC	0.597	
+	21	4982	p.S1614F|VPS13D	NM_015378	NP_056193	Q5THJ4	VP13D_HUMAN			5	TCAAATCCTTTAC	0.438	
-	3	438	MEF5_uc001aur.2_	NM_001010889	NP_001010889	Q5VXH4	PRAM6_HUMAN			0	TAGCTTCAGACC	0.493	
+	4	364	e_Mutation_p.S95	NM_004070	NP_004061	P51800	CLCKA_HUMAN			1	ATCTTTCCTGGA	0.627	
+	3	1201		NM_030812	NP_110439	Q9H568	ACTL8_HUMAN			4	TCTGGGAGGGT	0.577	rs115420942
-	2	1083	K2N1_uc001bdg.2	NM_018584	NP_061054	Q7Z7J9	CK2N1_HUMAN			0	CACCAGGAGGT	0.438	
-	10	1263	xm.1_Missense_M	NM_052896	NP_443128	Q7Z408	CSMD2_HUMAN	xtracellular (Potential).		12	CGAGGGGCCTC	0.537	
-	3	1224	Q_uc001byr.2_5'F	NM_005066	NP_005057	P23246	SFPQ_HUMAN	RRM 2.		8	TGAAAGATTACG	0.448	
-	6	819	ion_p.S214F|CSF3	NM_000760	NP_000751	Q99062	CSF3R_HUMAN	III 1.|Extracellular (Potentia		3	GTGGGGACATG	0.507	
-	11	1858	a.1_Missense_Mu	NM_000831	NP_000822	Q13003	GRIK3_HUMAN	ical; (Potential).		7	GACCCCCAGGT	0.562	
+	1	24	P1_uc010oid.1_5'I	NM_003462	NP_003453	O14645	IDLC_HUMAN			2	GGCAAACAAGG	0.647	
+	2	161	ALI1_uc010oie.1_	NM_003462	NP_003453	O14645	IDLC_HUMAN			2	AGGCTCGGCTA	0.577	
+	10	1509	p.W419*|CYP4X1_	NM_178033	NP_828847	Q8N118	CP4X1_HUMAN			2	TGTCTGGAAAA	0.418	
+	6	869	DN_uc010onr.1_M	NM_153703	NP_714914	Q7Z5L7	PODN_HUMAN	LRR 7.		2	CTGCCCTGTAC	0.662	rs138853761
+	7	1189	wk.1_Missense_M	NM_052940	NP_443172	Q9Y546	LRC42_HUMAN			0	GGAGCCTAGAG	0.458	
-	3	383	_p.E44K|C8B_uc	NM_000066	NP_000057	P07358	CO8B_HUMAN	TSP type-1 1.		4	GACTTCCTTGTC	0.498	
+	2	353		NM_152489	NP_689702	Q5VVX9	UBE2U_HUMAN			0	AATGGGAAGTT	0.294	
-	7	1152	dy.2_Missense_M	NM_001018067	NP_001018077	Q8NC51	PAIRB_HUMAN			1	TAACCGAATCTTC	0.403	
-	13	1448		NM_000329	NP_000320	Q16518	RPE65_HUMAN			1	GGTATGAATCAG	0.393	
-	7	1327	IQ3_uc001dfz.3_	NM_001105659	NP_001099129	A6PVS8	LRIQ3_HUMAN			2	TGCAGGAAAAA	0.353	
-	14	3835		NM_001002912	NP_001002912	Q5RHP9	CA173_HUMAN	Glu-rich.		5	CCCTTCCTTCAC	0.592	
-	14	2596		NM_001002912	NP_001002912	Q5RHP9	CA173_HUMAN	Glu-rich.		5	CTCCCCTTTTC	0.522	
-	22	2078	p.S603F|SLC44A5	NM_152697	NP_689910	Q8NCS7	CTL5_HUMAN	cellular (Potential).		4	TTAAAGATGCTG	0.284	
+	7	944	lib.3_Missense_Mu	NM_144573	NP_653174	Q0ZGT2	NEXN_HUMAN	Glu-rich.		2	ACAACGACCAT	0.318	
+	11	1739	_p.I417S|NEXN_	NM_144573	NP_653174	Q0ZGT2	NEXN_HUMAN	Glu-rich.		2	TTGAAATTAAAGA	0.294	
+	2	253	2_5'UTR|CLCA4_	NM_012128	NP_036260	Q14CN2	CLCA4_HUMAN			2	AAAAAAGATTTTT	0.333	
+	2	248	sw.1_Nonsense_M	NM_003503	NP_003494	O00311	CDC7_HUMAN			5	GCTCTTTAAAAA	0.403	
+	2	360	se_Mutation_p.S64	NM_020190	NP_064575	Q9NRN5	OLFL3_HUMAN	Potential.		0	CATCTCCGGGA	0.587	
+	3	557	se_Mutation_p.W1	NM_001767	NP_001758	P06729	CD2_HUMAN	Potential).|Ig-like C2-type.		1	AAGTGGACCAC	0.502	
+	4	725_726	hw.2_Missense_M	NM_000862	NP_000853	P14060	3BHS1_HUMAN			2	GGAAGGAAGC	0.5	
+	34	4366_4367	10_uc010oyl.1_Int	NM_001039703	NP_001034792	A6NDV3	A6NDV3_HUMAN			0	ACTGAATAGATG	0.48	
+	3	387	CM1_uc001euu.2_	NM_004425	NP_004416	Q16610	ECM1_HUMAN			3	CTCCTCTCAGC	0.587	
-	3	1199		NM_001009931	NP_001009931	Q86YZ3	HORN_HUMAN	4		3	TTGTCCCTGGC	0.562	
-	3	7754		NM_002016	NP_002007	P20930	FILA_HUMAN	ich.|Filaggrin 15.		16	CCTGACTGTCA	0.587	
-	2	177		NM_001014291	NP_001014313	Q9BYE4	SPR2G_HUMAN			0	GCGTGGGGCAC	0.582	
+	5	1602	_Mutation_p.G140	NM_000906	NP_000897	P16066	ANPRA_HUMAN	cellular (Potential).		7	TGACAGGATACC	0.483	
-	16	2372	UP210L_uc010pe	NM_207308	NP_997191	Q5VU65	P210L_HUMAN			11	TATACTGGAGTTA	0.493	
-	9	1463	|PKLR_uc001fka.3	NM_000298	NP_000289	P30613	KPYR_HUMAN	ic activator binding.		5	TTGTGGTCAGC	0.617	
-	5	549	_p.S54F|PAQR6_	NM_198406	NP_940798	Q6TCH4	PAQR6_HUMAN	ical; (Potential).		0	GGAAGGAGTTG	0.677	
-	17	2005		NM_178229	NP_839943	Q86VI3	IQGA3_HUMAN			6	GTCGGGAACTA	0.607	
+	1	364		NM_001004473	NP_001004473	Q8NGX5	O10K1_HUMAN	lasmic (Potential).		1	TATGATCGCTATA	0.527	

+	1	751		NM_001004478	NP_001004478	Q8NGY1	O10Z1_HUMAN	Name=6; (Potential).		2	ATTATTCATTATG	0.517	
+	4	403		NM_002001	NP_001992	P12319	FCERA_HUMAN	ar (Potential).|Ig-like 1.		5	AGAGTGAACCT	0.408	
+	5	601		NM_002001	NP_001992	P12319	FCERA_HUMAN	xtracellular	p.V168F(1)	5	CCACAGTTGAA	0.438	
+	2	724		NM_001639	NP_001630	P02743	SAMP_HUMAN	Pentaxin.		2	ACTATGAAATCA	0.488	
+	5	761	sz.1_Missense_M	NM_001004310	NP_001004310	Q6DN72	FCRL6_HUMAN	3.|Extracell	p.S240F(1)	3	TGTATTCCTTCTA	0.592	rs140713881
-	1	130	on_p.P5S|SLAMF	NM_033438	NP_254273	Q96A28	SLAF9_HUMAN			1	CCAAGGAAAGG	0.587	
-	1	410	AMF1_uc010pjm.1	NM_003037	NP_003028	Q13291	SLAF1_HUMAN	ellular (Potential).		2	GTAGCTTGCCC	0.557	
-	2	435		NM_199351	NP_955383	Q71H61	ILDR2_HUMAN			1	TTATTACCATGAA	0.455	
-	14	1860	plj.1_Missense_M	NM_018417	NP_060887	Q96PN6	ADCYA_HUMAN			3	CTTTTTCCATATC	0.378	
-	18	5745		NM_000130	NP_000121	P12259	FA5_HUMAN			6	TGAACCTAAAAT	0.368	
+	9	1572	_Mutation_p.G47	NM_002021	NP_002012	Q01740	FMO1_HUMAN			1	CCCAGGAAAAT	0.507	
+	3	557	_uc009wwd.2_Intr	NM_014283	NP_055098	Q9UBS9	OSPT_HUMAN			2	CTATTTCTCCAA	0.308	
+	12	4826	PA2_uc009www.2_	NM_020318	NP_064714	Q9BXP8	PAPP2_HUMAN			16	CACATCATACC	0.423	
-	6	1931	LGPS2_uc010pnb	NM_004673	NP_004664	O95841	ANGL1_HUMAN	ogen C-terminal.		0	ATCATCATCTG	0.403	
+	6	1071	uc001gof.1_Intron	NM_033343	NP_203129	Q969G2	LHX4_HUMAN			1	AGGCGGACAGT	0.502	
-	8	1063	wyh.1_Missense_	NM_052966	NP_443198	Q9BZQ8	NIBAN_HUMAN			4	CTTAATCCTTCT	0.468	
-	8	1221	yo.2_Missense_M	NM_000963	NP_000954	P35354	PGH2_HUMAN			2	CAATACGATTTT	0.378	
-	2	271	S2_uc009wyo.2_5	NM_000963	NP_000954	P35354	PGH2_HUMAN	EGF-like.		2	TCCGGGTACAA	0.438	
+	21	3605		NM_000186	NP_000177	P08603	CFAH_HUMAN	Sushi 19.		6	TTACTTCATTCC	0.403	
+	3	418		NM_030787	NP_110414	Q9BXR6	FHR5_HUMAN	Sushi 2.		2	TCATTCTGAAT	0.318	
-	2	124		NM_001994	NP_001985	P05160	F13B_HUMAN	Sushi 1.		3	GAGGAAAACCA	0.303	
-	1	961	z.1_RNA|CRB1_u	NM_194314	NP_919290	Q5SVQ8	ZBT41_HUMAN			2	TCCAGGGTCCT	0.388	
+	18	2123	p.G487E|PTPRC_	NM_002838	NP_002829	P08575	PTPRC_HUMAN	lasmic (Potential).		12	TGAAGGAAGAC	0.338	
+	10	1454	_Mutation_p.P38	NM_203459	NP_982284	Q08AD1	CAMP2_HUMAN			4	ATTTGCCTTCTA	0.343	
+	7	1145	1hel.1_Missense_	NM_032960	NP_116584	P49137	MAPK2_HUMAN	rotein kinase.		0	AATTTCCCAACC	0.468	
+	4	622		NM_000715	NP_000706	P04003	C4BPA_HUMAN			3	GAAGGGTGAGT	0.318	
-	8	1234	34_uc001hgx.1_3'	NM_001025109	NP_001020280	P28906	CD34_HUMAN	lasmic (Potential).		1	GTCTTCGCCCT	0.517	
-	20	2923	_p.R816C|INTS7_	NM_015434	NP_056249	Q9NVH2	INT7_HUMAN	Gln-rich.		0	TAAGCGAATTTG	0.463	
+	13	5959		NM_016343	NP_057427	P49454	CENPF_HUMAN	Potential.		13	TAGTTCAAACA	0.418	
+	13	6500		NM_016343	NP_057427	P49454	CENPF_HUMAN	tion with NDE1 and NDEL		13	GAGCTCAACAC	0.512	
+	13	6803		NM_016343	NP_057427	P49454	CENPF_HUMAN	n repeats.|Interaction with		13	TAAGGTCTGAAA	0.353	
-	63	12935		NM_206933	NP_996816	O75445	USH2A_HUMAN	ential).|Fibronectin type-III		26	TTTTTCCATTTG	0.473	
-	63	12712		NM_206933	NP_996816	O75445	USH2A_HUMAN	II 26.|Extracellular (Potenti		26	GTACTCCAGGA	0.483	
+	1	1415		NM_152610	NP_689823	Q8N715	CA065_HUMAN	Potential.		2	TCATGGACTGC	0.602	
-	3	581	_Mutation_p.P27	NM_020997	NP_066277	O75610	LFTY1_HUMAN			0	CTCGTGGACGG	0.716	
-	19	3631	.D1044N|NID1_u	NM_002508	NP_002499	P14543	NID1_HUMAN			2	AAGATCGAGAG	0.502	
-	7	762	1LB_uc010pxt.1_	NM_019891	NP_063944	Q86YB8	ERO1B_HUMAN			0	TCTCATCTGAAC	0.398	
+	4	262	1hxv.1_Missense_	NM_145861	NP_665860	Q8WWZ3	EDAD_HUMAN			0	CCCACGAAATT	0.249	
+	5	2869	e.1_Missense_Mu	NM_020066	NP_064450	Q9NZ56	FMN2_HUMAN	ro-rich.|FH1.		12	CTCCCCCTCTC	0.602	
+	5	2023	_p.E629K|NLRP3_	NM_001079821	NP_001073289	Q96P20	NALP3_HUMAN			26	CAGCTGGAATTG	0.468	
+	1	544		NM_001004689	NP_001004689	Q8NG83	OR2M3_HUMAN	ellular (Potential).		2	ACTTCCCCTCC	0.418	
-	5	633	n_p.E126K|AKR1	NM_205845	NP_995317	P52895	AK1C2_HUMAN			0	CTTCTCCATGG	0.458	
-	6	647	p.R224Q|PRKCQ_	NM_006257	NP_006248	Q04759	KPCT_HUMAN	l-ester/DAG-type 1.		6	TACGTCGGCAC	0.378	
-	4	584		NM_001010924	NP_001010924	Q5VUB5	F1711_HUMAN	ellular (Potential).		4	AATTACCTGTTC	0.463	
-	6	691	AM188A_uc001iof	NM_024948	NP_079224	Q9H8M7	F188A_HUMAN			1	TGAACGATCTT	0.289	
-	10	1302	j.2_RNA|NEBL_uc	NM_006393	NP_006384	O76041	NEBL_HUMAN	Nebulin 8.		2	TATTCTCGCTAAA	0.373	
+	3	358	ct.1_Missense_Mu	NM_012443	NP_036575	O75602	SPAG6_HUMAN			1	TTATAATGATGAC	0.408	

+	2	621	AA1217_uc010qcy	NM_019590	NP_062536	Q5T5P2	SKT_HUMAN		7	GGCCCCGAAGTT	0.517	
-	18	2748	qdt.1_Missense_M	NM_018076	NP_060546	Q5T2S8	ARMC4_HUMAN	ARM 7.	6	TAAGTTCCAAACC	0.338	
+	7	1054		NM_052997	NP_443723	Q9BXX3	AN30A_HUMAN		9	CGTGGCCAGCAA	0.423	
+	13	1718		NM_052997	NP_443723	Q9BXX3	AN30A_HUMAN		9	TAAATGGAAAATT	0.323	
-	3	1715	np.2_Missense_Mu	NM_004962	NP_004953	P55107	BMP3B_HUMAN		2	TGGTTGGATGGA	0.587	
+	3	1246		NM_199459	NP_955629	Q711Q0	CJ071_HUMAN		0	AAAGCTCCCAAG	0.542	
-	21	2867	ggt.1_Missense_Mu	NM_018245	NP_060715	Q9ULD0	OGDHL_HUMAN		1	CTTTCTCCTCCA	0.632	
-	33	5659	ation_p.P1715L|P	NM_033056	NP_149045	Q96QU1	PCD15_HUMAN	lasmic (Potential).	13	agaaggaggagaaat	0.129	
-	33	4986	ation_p.E1491K|P	NM_033056	NP_149045	Q96QU1	PCD15_HUMAN	lasmic (Potential).	13	TGTTTTCCTTATA	0.368	
+	17	2318	kj.1_Missense_Mu	NM_001080512	NP_001073981	Q9H694	BICC1_HUMAN		4	CTATCAAGGAGT	0.448	
-	8	903	qie.1_Missense_M	NM_198215	NP_937858	Q8NE31	FA13C_HUMAN		2	ATGGGGCTGACT	0.443	
-	37	5419	K3_uc010qih.1_In	NM_020987	NP_066267	Q12955	ANK3_HUMAN	Ser-rich.	19	TTTTTTCCTGTAA	0.418	
-	37	4976	K3_uc010qih.1_In	NM_020987	NP_066267	Q12955	ANK3_HUMAN	Ser-rich.	19	CCAGAGGAAACT	0.473	
+	17	2573	01jrg.2_Missense_	NM_080722	NP_542453	Q8WXS8	ATS14_HUMAN	TSP type-1 2.	6	GGCCCCCTGCA	0.617	
+	8	1020	:.1_Missense_Muta	NM_004190	NP_004181	P07098	LIPG_HUMAN		0	CAGCAGGAACTT	0.348	
+	7	1345	p.P365S|CYP26A1	NM_000783	NP_000774	O43174	CP26A_HUMAN		3	TTCATTCCATTTG	0.458	
+	2	631	gnu.1_Missense_M	NM_181745	NP_859529	Q5NUL3	O3FA1_HUMAN	cellular (Potential).	0	AAATTTCGATTTG	0.438	
+	2	618	98R|CYP2C19_uc	NM_000772	NP_000763	P33260	CP2CI_HUMAN		5	GGAAGAGGAAGT	0.448	
-	7	1068	nse_Mutation_p.E2	NM_000770	NP_000761	P10632	CP2C8_HUMAN		0	TCTCTTCCTGGA	0.423	
+	3	1371		NM_032727	NP_116116	Q16352	AINX_HUMAN	Tail.	2	TCTCATCCACTGC	0.473	
-	5	739	k.2_RNA|PCGF6_	NM_001011663	NP_001011663	Q9BYE7	PCGF6_HUMAN		1	TTACCAGGTTTAG	0.289	
+	10	2058	q.1_Missense_Mu	NM_006951	NP_008882	Q15542	TAF5_HUMAN	WD 5.	2	TTTTCTCCCAATG	0.373	
+	13	2097		NM_001008723	NP_001008723	Q5T655	CC147_HUMAN	Potential.	5	AGAATCCTCAGA	0.453	
-	6	785	_p.Q215*|AFAP1L	NM_001001936	NP_001001936	Q8N4X5	AF1L2_HUMAN		2	GCCACTGGTAAG	0.647	
+	2	632		NM_002775	NP_002766	Q92743	HTRA1_HUMAN		0	GCCATAAATATAA	0.453	rs35089212
+	7	543	T1_uc009xzz.1_M	NM_007329	NP_015568	Q9UGM3	DMBT1_HUMAN	SRCR 1.	7	GTTGTGGCTGGG	0.602	
+	20	2283	zz.1_Missense_Mu	NM_007329	NP_015568	Q9UGM3	DMBT1_HUMAN		7	CTGTAGGATCTG	0.537	
+	26	3362	3T1_uc009xzz.1_M	NM_007329	NP_015568	Q9UGM3	DMBT1_HUMAN	SRCR 8.	7	CATAGTGAAGAC	0.532	
-	3	595		NM_001010912	NP_001010912	Q5SQS8	CJ120_HUMAN		1	GTAAACCTTTCA	0.478	
-	13	8936	v.1_Missense_Muta	NM_002417	NP_002408	P46013	KI67_HUMAN	approximate repeats.|16.	7	CCAGGGGTTGG	0.527	
-	13	1861	9ycc.2_Missense_	NM_021924	NP_068743	Q9HBB8	CDHR5_HUMAN	dem repeats.|2.|Extracellula	0	TCCCATACTGGC	0.672	
+	11	1256		NM_017511	NP_059981	Q9HC84	MUC5B_HUMAN	TIL 1.	0	CTGCAGGGACGG	0.667	
+	11	1355		NM_017511	NP_059981	Q9HC84	MUC5B_HUMAN		0	CCTACTCCACAG	0.662	
+	1	905		NM_001005172	NP_001005172	Q8NGK3	O52K2_HUMAN	lasmic (Potential).	2	AAATCCGTGAGA	0.493	rs138594066
+	1	175		NM_001005171	NP_001005171	Q8NGK4	O52K1_HUMAN	Name=2; (Potential).	0	CTCCATGAACCC	0.498	
-	2	692		NM_030774	NP_110401	Q9H255	O51E2_HUMAN	Name=4; (Potential).	5	ATCCGCGGACCA	0.557	
-	1	972	.1_Intron|HBE1_uc	NM_033180	NP_149420	Q9Y5P1	O51B2_HUMAN	lasmic (Potential).	3	TGTTTAGATAAAA	0.368	
-	16	6858		NM_003737	NP_003728	Q96JQ0	PCD16_HUMAN	.|Extracellular (Potential).	5	AGGCTCCTCCAC	0.592	
+	1	589		NM_207186	NP_997069	Q9H209	O10A4_HUMAN	cellular (Potential).	1	GTGTTTGAACTGC	0.498	
-	1	906		NM_001004461	NP_001004461	Q8NH74	O10A6_HUMAN	lasmic (Potential).	2	TAATTTCATCAAA	0.383	
-	1	499		NM_001004461	NP_001004461	Q8NH74	O10A6_HUMAN	cellular (Potential).	2	AAAAGGGAAAAC	0.323	
-	2	940		NM_176821	NP_789791	Q86W26	NAL10_HUMAN	NACHT.	9	ACATGACGTGCT	0.532	
-	2	633	IO1_uc001mgh.1_	NM_002315	NP_002306	P25800	RBTN1_HUMAN	I zinc-binding 1.	0	AGTCTTCGTGCC	0.607	
+	12	2121	yic.2_Missense_M	NM_004211	NP_004202	Q9Y345	SC6A5_HUMAN	Name=9; (Potential).	4	CATCATGGGTTTT	0.522	
+	9	1067	_p.R333Q|NELL1_	NM_006157	NP_006148	Q92832	NELL1_HUMAN	VWFC 1.	3	AATGCCGAAGGA	0.517	
-	6	1166	ku.1_Missense_Mu	NM_020826	NP_065877	Q7L8C5	SYT13_HUMAN	toplasmic (Potential).	1	TTAGCTCGTTTA	0.547	
-	5	736	ykx.2_Missense_M	NM_001101802	NP_001095272	Q96BD5	PF21A_HUMAN	Gln-rich.	2	GTTCATGAAGCT	0.373	

-	28	4284		NM_002334	NP_002325	O75096	LRP4_HUMAN	ellular (Potential).	4	AACAGGGACAT	0.527	
+	2	561	9ymb.2_Missense	NR_027044					0	GTGTGGGGCAG	0.517	
+	3	806	ik.1_Nonsense_M	NM_001004704	NP_001004704	Q8NH72	OR4C6_HUMAN	ellular (Potential).	2	TTGTTTCAGTTG	0.433	
+	1	294		NM_001004739	NP_001004739	Q8NGL0	OR5L2_HUMAN	ellular (Potential).	1	TGCATGGTGCA	0.468	
+	1	626		NM_001005202	NP_001005202	Q8NH51	OR8K3_HUMAN	Name=5; (Potential).	4	TGATTTCATCTC	0.378	
-	1	647		NM_001005282	NP_001005282	Q8NGP6	OR5M8_HUMAN	Name=5; (Potential).	1	AGGTAGGAAATA	0.413	
-	1	91		NM_001002925	NP_001002925	Q8NGF4	O5AP2_HUMAN	ellular (Potential).	4	GACTCCTTGTA	0.408	
+	5	1059	G1_uc001nkr.1_	NM_000062	NP_000053	P05155	IC1_HUMAN		1	TCCTCCTCAAT	0.552	
+	1	775	Q1_uc001nmj.2_I	NM_001005186	NP_001005186	Q8NGQ2	OR6Q1_HUMAN	Name=6; (Potential).	1	GCACTCTTTTC	0.522	
+	1	809		NM_001004729	NP_001004729	Q8NGI8	O5AN1_HUMAN	ellular (Potential).	1	TTCAAGCTTTG	0.388	
+	1	509		NM_001004706	NP_001004706	Q8NGI4	OR4DB_HUMAN	ellular (Potential).	2	TCTGTGGACCCA	0.507	
+	3	292		NM_006552	NP_006543	O95968	SG1D1_HUMAN	p.G82R(1)	1	TTCAGGGAAAAA	0.413	
-	5	912	L3_uc001ntt.1_Mi	NM_153265	NP_694997	Q32P44	EMAL3_HUMAN		1	TCCAGGGCCCC	0.577	
+	2	631	ux.2_Missense_M	NM_173810	NP_776171	Q8N5M4	TTC9C_HUMAN	TPR 2.	2	AGCCCGTGAAC	0.512	
-	9	1607	2A25_uc009yoq.1	NM_199352	NP_955384	Q6T423	S22AP_HUMAN	lasmic (Potential).	4	AGGCTATTTACT	0.507	
+	4	745	pc.1_Missense_M	NM_178864	NP_849195	Q8IUM7	NPAS4_HUMAN		0	TCACAGCTTTCT	0.627	
+	7	2194	c.1_Missense_M	NM_178864	NP_849195	Q8IUM7	NPAS4_HUMAN		0	CCTGTCCCTGT	0.607	
+	11	1211	TN3_uc010rpi.1_R	NM_001104	NP_001095	Q08043	ACTN3_HUMAN	Spectrin 1.	0	TGCTCTCGGAGA	0.652	
-	1	660	lank|CABP4_uc00	NM_206997	NP_996880	Q8TDT2	GP152_HUMAN	lasmic (Potential).	0	ACAGGCTGTGG	0.677	
-	21	4822	1opz.2_Missense_	NM_012309	NP_036441	Q9UPX8	SHAN2_HUMAN		5	ggcgggggagcggg	0.413	
-	15	2168	09ysn.1_Intron|SH	NM_012309	NP_036441	Q9UPX8	SHAN2_HUMAN	PDZ.	5	TGTGGCCGACT	0.587	
+	14	5006		NM_014786	NP_055601	Q96PE2	ARHGH_HUMAN		0	TCTCCTCCAGCT	0.642	
+	8	1060	fz.2_Missense_M	NM_014361	NP_055176	O94779	CNTN5_HUMAN	like C2-type 2.	8	TGGCGGAAGAC	0.398	
-	2	317		NM_002427	NP_002418	P45452	MMP13_HUMAN	switch (By similarity).	3	AACCCCGCATC	0.418	
+	1	1390	.2_Intron|PDGFD_	NM_001001711	NP_001001711	Q8WTU0	DDI1_HUMAN		5	ACAAGGAAATT	0.468	rs35182086
-	7	895	9yyb.1_Missense_	NM_020809	NP_065860	Q9P2F6	RHG20_HUMAN	s-associating.	5	AATGTCCTTGG	0.413	
-	13	1729	rwj.1_Missense_M	NM_002716	NP_002707	P30154	2AAB_HUMAN	HEAT 14.	0	TGAAGCGAACAT	0.363	
+	4	745	O2_uc010rwt.1_	NM_031938	NP_114144	Q9BYV7	BCDO2_HUMAN		0	AAAACAGAAAAG	0.308	
+	12	1766		NM_001076682	NP_001070150	P13591	NCAM1_HUMAN	5.|Extracellular (Potential).	1	TGGTTTCGGGAT	0.552	
+	8	1687	3A_uc009yyx.2_	NM_213621	NP_998786	P46098	5HT3A_HUMAN	Cytoplasmic (Potential).	0	TGGGCTCCGTGC	0.602	
-	3	723		NM_000482	NP_000473				0	TGAATTCGTCAG	0.622	rs145184607
+	3	208	.1_5'UTR|POU2F3	NM_014352	NP_055167	Q9UKI9	PO2F3_HUMAN		2	AATGATCGAAAT	0.378	
+	18	2535		NM_003105	NP_003096	Q92673	SORL_HUMAN	ntial).|LDL-receptor class	15	TTGAATGGAAGC	0.453	
+	1	454		NM_001007249	NP_001007250	Q15614	OR8G2_HUMAN		0	TCCTATCACCAC	0.448	
-	1	20		NM_012378	NP_036510	Q15620	OR8B8_HUMAN	ellular (Potential).	1	CGAAGGAGGAA	0.502	
+	5	420	qce.2_Missense_M	NM_152713	NP_689926	P46977	STT3A_HUMAN	enal (Potential).	0	GTACTCCATTTTT	0.448	
+	2	1064	_p.V134I|NTM_u	NM_016522	NP_057606	Q9P121	NTRI_HUMAN		6	TGCAAGGTAGG	0.552	
+	6	616	fq.1_Missense_Mu	NM_001975	NP_001966	P09104	ENOG_HUMAN		0	TGTATCGCCAC	0.627	
-	3	159	sge.1_Missense_	NM_174941	NP_777601	Q9NR16	C163B_HUMAN	ellular (Potential).	11	CAAATCTGTTC	0.448	
-	14	3352	.R1075Q|CD163_	NM_004244	NP_004235	Q86VB7	C163A_HUMAN	lasmic (Potential).	8	TGTCTTCGCTTT	0.433	
-	3	449	DA_uc001quq.1_M	NM_020661	NP_065712	Q9GZX7	AICDA_HUMAN		2	CCCCTCGGGCT	0.652	
+	25	3543	se_Mutation_p.P1	NM_004570	NP_004561	O75747	P3C2G_HUMAN	PI3K/PI4K.	21	TTCGTCCACAA	0.408	
+	3	1041		NM_000921	NP_000912	Q14432	PDE3A_HUMAN		4	TTCAGGAACCA	0.483	
+	2	138	.2_Intron|SLCO1A	NM_000415	NP_000406	P10997	IAPP_HUMAN		0	TTTGCAGAAAATT	0.338	
-	11	1563		NM_016551	NP_057635	Q9NS93	TM7S3_HUMAN	ical; (Potential).	2	CCACCGAATAG	0.428	
+	14	1865	_Mutation_p.V78	NM_152641	NP_689854	Q68CP9	ARID2_HUMAN		10	TGTTGTTCGTG	0.378	
+	1	854		NM_001005203	NP_001005203	Q8NH09	OR8S1_HUMAN	Name=7; (Potential).	1	TGAATTCCCTCA	0.408	

+	13	2215	ATS2_uc001ruf.2_	NM_023071	NP_075559	Q86XZ4	SPAS2_HUMAN	Ser-rich.	1	CCTCTCCTCCCA	0.537	
-	5	2359	smk.1_Missense_M	NM_032130	NP_115506	Q8IYM0	F186B_HUMAN		1	ACATGGTTGATCC	0.488	
+	12	1586_1587	p.P432S|SMARCD	NM_003076	NP_003067	Q96GM5	SMRD1_HUMAN	R/NR3C1 interaction with tl	1	GGTAACCCAGAG	0.535	
+	6	724	a.2_Missense_Mu	NM_005276	NP_005267	P21695	GPDA_HUMAN		0	GGCTGGGACTC	0.577	
+	24	3023	lt.2_Missense_Mu	NM_173602	NP_775873	Q9P265	DIP2B_HUMAN		6	CTGCTTCCGTGA	0.458	
-	1	241		NM_175068	NP_778238	Q86Y46	K2C73_HUMAN	lead.|Gly-rich.	6	AGCCTCCTGCCC	0.652	
-	2	794		NM_015848	NP_056932	Q01546	K22O_HUMAN	Coil 1B.|Rod.	2	AGAAGTGAATCTA	0.542	
-	10	1691_1692	Missense_Mutatio	NM_000966	NP_000957	P13631	RARG_HUMAN	gand-binding.	4	AATCTCCATCTT	0.55	
-	2	388_389	_p.P76L|SP7_uc	NM_152860	NP_690599	Q8TDD2	SP7_HUMAN		0	GAAAAGGGAGG	0.579	
-	1	202		NM_001005493	NP_001005493	A6NF89	OR6C6_HUMAN	Name=2; (Potential).	2	TACTTCCAAAAA	0.378	
+	1	184		NM_001005497	NP_001005497	A6NL08	O6C75_HUMAN	lasmic (Potential).	3	TCCTTCGGAAC	0.433	
-	1	243		NM_014770	NP_055585	Q99490	AGAP2_HUMAN		5	ACCTCGAATGC	0.527	rs143760313
-	7	825	L_uc001sqk.1_5'F	NM_006576	NP_006567	O75366	AVIL_HUMAN	e 3.|Core (By similarity).	1	CTACCTCTGTGA	0.493	
-	3	859	zql.2_Missense_M	NM_152440	NP_689653	Q96MD2	CL066_HUMAN		1	ACTTGGCAAGA	0.458	
-	6	773	tl.1_Missense_Mut	NM_021150	NP_066973	Q9Y3R0	GRIP1_HUMAN	PDZ 2.	2	CTGGACGAGATT	0.383	
+	3	1196		NM_013381	NP_037513	Q9UKU6	TRHDE_HUMAN	cellular (Potential).	3	CCTATTCCTTGC	0.378	
-	4	2288	.2_Missense_Muta	NM_139137	NP_631875	Q96PR1	KCNC2_HUMAN	lasmic (Potential).	6	TGTAATCACCTG	0.463	
+	16	4358_4359	V3_uc010sub.1_M	NM_014903	NP_055718	Q8IVL0	NAV3_HUMAN	Ser-rich.	17	CACGAGGTCCA	0.55	
+	17	3739	ab.1_Missense_Mu	NM_001079910	NP_001073379	Q96JM4	LRIQ1_HUMAN		6	AGTACTGAATACC	0.363	
-	2	795	di.2_Missense_Mu	NM_020698	NP_065749	Q9ULS5	TMCC3_HUMAN		2	TCTAAGGAATTT	0.498	
+	5	935_936	.2_Intron|TMPO_u	NM_001032283	NP_001027454	P42167	LAP2B_HUMAN	otential).|NAKAP95-binding	2	TGAATGGACAA	0.396	
+	22	2587	811F|MYBPC1_uc	NM_206820	NP_996556	Q00872	MYPC1_HUMAN		4	CCCATTCTCGTG	0.423	
+	53	5785	AB2_uc009zug.2_F	NM_017564	NP_060034	Q8WWQ8	STAB2_HUMAN	lar (Potential).|FAS1 6.	14	CGGGAGCTCTTG	0.428	
-	2	245	_p.E29K|SELPLG_	NM_003006	NP_002997	Q14242	SELPL_HUMAN	cellular (Potential).	0	CTTTCTCGGCTT	0.572	
+	7	816	_p.T186I|MAPKA	NM_139078	NP_620777	Q8IW41	MAPK5_HUMAN	rotein kinase.	3	AGTTCACCCCTT	0.453	
-	16	3180	wn.1_Missense_M	NM_000620	NP_000611	P29475	NOS1_HUMAN	avodoxin-like.	7	TCATTTCCATCA	0.498	
+	20	3327		NM_144668	NP_653269	Q8TBY9	WDR66_HUMAN		2	CAAAGGGAAAA	0.468	
-	16	2589	uek.1_Missense_M	NM_020845	NP_065896	Q9BZ72	PITM2_HUMAN	DDHD.	3	AGGGGGCGCCA	0.667	
+	7	1647	1uhf.1_Missense_	NM_052907	NP_443139	Q14DG7	T132B_HUMAN	cellular (Potential).	19	CCCGGGAAAGC	0.537	
+	8	2004	1uhf.1_Missense_	NM_052907	NP_443139	Q14DG7	T132B_HUMAN	cellular (Potential).	19	CTCGTAGCTGGC	0.597	
+	5	1623	p.R215Q|ZNF140_	NM_003440	NP_003431	P52738	ZN140_HUMAN	C2H2-type 6.	0	TTACTCGACATCA	0.418	
-	3	606	n_p.T18I|GJB6_uc	NM_006783	NP_006774	O95452	CXB6_HUMAN	lasmic (Potential).	1	ATGCTGGTGGAG	0.512	
+	3	1566	.1_Missense_Muta	NM_004795	NP_004786	Q9UEF7	KLOT_HUMAN	e-1 2.|Extracellular (Potenti	3	ACATTTCCCTGT	0.438	
-	5	1174	uwz.2_Missense_M	NM_025138	NP_079414	Q86XN7	CM023_HUMAN		5	AGGACGAGAAT	0.338	
-	34	4179		NM_015058	NP_055873	A3KMH1	K0564_HUMAN		6	CCAACAACTATT	0.358	
-	6	1772	.1_Intron|DACH1_	NM_080759	NP_542937	Q9UI36	DACH1_HUMAN		1	GGCCTTCTCCCC	0.567	
+	1	167	a.1_RNA|POTEG_	NM_001005356	NP_001005356	Q6S5H5	POTEG_HUMAN		1	GGAGCGGCAAG	0.592	
+	1	698		NM_001005501	NP_001005501	Q8NGD2	OR4K2_HUMAN	lasmic (Potential).	4	GAGGATCATCTA	0.388	
+	1	313		NM_001004063	NP_001004063	Q8NGD4	OR4K1_HUMAN	Name=3; (Potential).	3	GTTCTTCACAGT	0.428	
-	1	694_695		NM_001004714	NP_001004714	Q8NH42	OR4KD_HUMAN	lasmic (Potential).	2	AGGATCGACTAG	0.495	
-	1	289		NM_001005465	NP_001005465	Q8NGC4	O10G3_HUMAN	cellular (Potential).	2	CACAGCCACCAA	0.483	
+	1	266		NM_001001912	NP_001001912	Q8NGC2	OR4E2_HUMAN	cellular (Potential).	4	AGAAAGAAAGA	0.443	
+	13	4653		NM_004274	NP_004265	Q13023	AKAP6_HUMAN		21	CATGTGGAGGAT	0.368	
+	13	5941		NM_004274	NP_004265	Q13023	AKAP6_HUMAN		21	CACATGGGAAAG	0.383	
-	10	1538	p.L383F|RALGAP	NM_014990	NP_055805	Q6GYQ0	RGPA1_HUMAN		4	ACAGAGACTAGA	0.378	rs145415708
+	3	1657	R1_uc010amu.1_I	NM_001049	NP_001040	P30872	SSR1_HUMAN	lasmic (Potential).	5	CGCCGCGGAGG	0.587	
-	4	686	lwuv.1_Splice_Site	NM_001079537	NP_001073005	Q86SZ2	TPC6B_HUMAN		0	TAAATACCTTAGA	0.333	

-	5	702	_Mutation_p.D98N	NM_018168	NP_060638	Q9NVL8	CN105_HUMAN			0	TATGGTCCCTTG	0.413	
-	2	469	:dd.2_Missense_M	NM_001001872	NP_001001872	Q86TY3	CN037_HUMAN	cellular (Potential).		0	TGAGGGGACAC	0.488	
+	1	173		NM_003813	NP_003804	Q9UKJ8	ADA21_HUMAN			2	GGCTCCTGGAT	0.542	
+	14	1644	_p.S375F|DCAF4_	NM_015604	NP_056419	Q8WV16	DCAF4_HUMAN			3	GGGCTCCCGGG	0.637	
-	2	530	se_Mutation_p.S10	NM_001040108	NP_001035197	Q9UHC1	MLH3_HUMAN			2	CAGCACTGGCC	0.438	
+	9	1812	RXN3_uc010asv.1_	NM_004796	NP_004787	Q9Y4C0	NRX3A_HUMAN	4.|Extracellular (Potential).		10	AACATTGAAACG	0.433	
-	11	1172	ense_Mutation_p.S	NM_152446	NP_689659	Q6ZU80	CE128_HUMAN	Potential.		0	TGCTTGGAAATCT	0.403	
-	11	1595	ALC_uc010tvy.1_M	NM_000153	NP_000144	P54803	GALC_HUMAN			0	TAAGGAAGAAATG	0.289	
-	20	3465		NM_018036	NP_060506	Q96BY7	ATG2B_HUMAN			3	GAGAACGATAGTT	0.358	
+	8	891		NM_152327	NP_689540	Q96M32	KAD7_HUMAN	Potential.		1	TCTGTTCATACC	0.368	
+	4	672		NM_182560	NP_872366	Q52M58	CN177_HUMAN			0	AGACATGAAGAA	0.453	
+	7	1519	|OR4N4_uc010tzv	NM_001005241	NP_001005241	Q8N0Y3	OR4N4_HUMAN	cellular (Potential).		5	TTCTGTGATGTC	0.532	
-	10	1070	Splice_Site_p.V58_	NM_001012423	NP_001012423					0	GCAAACCTGCCC	0.547	
-	1	706		NM_019066	NP_061939					0	GCAGAGGGGCCT	0.577	
-	1	105		NM_002487	NP_002478	Q99608	NECD_HUMAN			0	TCAGATCCTTACT	0.647	
-	6	801	zba.2_Nonsense_M	NM_000814	NP_000805	P28472	GBRB3_HUMAN	cellular (Probable).		5	TCCTCGAGACC	0.557	
-	1	226	RA5_uc001zbd.1_	NM_021912	NP_068712	P28472	GBRB3_HUMAN			5	GCAAATCCAGAG	0.577	
-	26	3632_3633	e_Mutation_p.E10	NM_002420	NP_002411	Q7Z4N2	TRPM1_HUMAN	lasmic (Potential).		4	CTTCTCCCGGAA	0.609	
-	4	1645		NM_001103184	NP_001096654	Q68DA7	FMN1_HUMAN	ction with alpha-catenin (By		1	CTAGCTCGTGTTT	0.468	rs144234543
+	3	1205	zhl.1_Missense_Mu	NM_012125	NP_036257	P08912	ACM5_HUMAN	llular (By similarity).		2	ACAGTTCCACTG	0.542	
+	2	315		NM_207444	NP_997327	Q8NAA6	CO053_HUMAN			0	TCCAAGGAAATG	0.498	
+	16	1669	_p.W754*|JMJD7-P	NM_001114633	NP_001108105	P0C869	PA24B_HUMAN	PLA2c.		1	GTTCTGGGACC	0.642	
-	13	2735		NM_016642	NP_057726	Q9NRC6	SPTN5_HUMAN			2	TCCAGGGCCCT	0.622	
-	2	843	zpx.2_Intron|ZFP1(	NM_022473	NP_071918	Q9H2Y7	ZF106_HUMAN			3	GGAGCCTCCTG	0.448	
-	10	1659	p.D208N|TGM5_u	NM_201631	NP_963925	O43548	TGM5_HUMAN			1	TGCCATCGTGCA	0.537	
+	2	334	e_Mutation_p.P32S	NM_014444	NP_055259	Q9UGJ1	GCP4_HUMAN			3	GACTTCCCTTTC	0.527	
-	11	1569		NM_000138	NP_000129	P35555	FBN1_HUMAN	Pro-rich.		3	GAACAGGGAGA	0.507	
-	4	1184		NM_203349	NP_976224	Q6S5L8	SHC4_HUMAN	PID.		5	TTACTTTTGCCAA	0.323	
-	23	3485	ew.1_Missense_Mu	NM_017672	NP_060142	Q96QT4	TRPM7_HUMAN	cellular (Potential).		10	GAAATGGAGTC	0.313	
+	3	538	agd.2_Missense_M	NM_004751	NP_004742	O95395	GCNT3_HUMAN	nenal (Potential).		2	AACTTTCTTTCAG	0.473	
+	4	3241		NM_015042	NP_055857	O15014	ZN609_HUMAN			3	ATCATTCCCAAG	0.572	
+	3	845	ujp.1_Missense_M	NM_002755	NP_002746	Q02750	MP2K1_HUMAN	rotein kinase.		0	AACTCTCCGTAC	0.507	
+	9	2651_2652		NM_001031807	NP_001026977	P84550	SKOR1_HUMAN			0	CTATGCCATCCA	0.574	
-	7	620	se_Mutation_p.W78	NM_022369	NP_071764	Q9BX79	STRA6_HUMAN	cellular (Potential).		1	TATCTTCCAGGC	0.612	
-	3	278	G4_uc010bkn.2_F	NM_138573	NP_612640	Q8WWG1	NRG4_HUMAN	ar (Potential).|EGF-like.		0	AAATGGGCTGG	0.393	
-	25	3213	bx.2_Missense_M	NM_020843	NP_065894	Q9BY12	SCAPE_HUMAN			3	GAAGTCCAGTTG	0.388	
-	5	691	32_uc010uoj.1_Mis	NM_004644	NP_004635	Q13367	AP3B2_HUMAN			5	TGTAGAGTTTAG	0.567	
+	14	1750	p.R509H|ADAMTS	NM_207517	NP_997400	P82987	ATL3_HUMAN	TSP type-1 3	p.R509R(1)	27	CCACCGCGGAG	0.458	
-	7	1667	nr.3_Missense_Mu	NM_002693	NP_002684	P54098	DPOG1_HUMAN			2	ATCAACGACTTC	0.602	
+	6	1301	DIA2_uc002cgo.1_	NM_006849	NP_006840	Q13087	PDIA2_HUMAN	Thioredoxin 1.		2	CTGGTGGAATTC	0.692	
-	10	1441	clz.2_Missense_M	NM_014714	NP_055529	Q96RY7	IF140_HUMAN	WD 5.		5	CGGGGCTGCCC	0.582	
-	4	592	S22_uc002crz.1_I	NM_022119	NP_071402	Q9GZN4	BSSP4_HUMAN	Peptidase S1.		1	GATCCAGCAGT	0.607	
+	3	619	rf68_uc002cza.2_	NM_024109	NP_077014	Q9BUU2	MET22_HUMAN			0	GAAGCTCAGCTG	0.592	
-	30	4167	YH11_uc010bvg.2_	NM_002474	NP_002465	P35749	MYH11_HUMAN	Potential.		15	CTCCTCGTCCA	0.592	
+	8	1249		NM_017888	NP_060358	Q6NUN0	ACSM5_HUMAN	P (By similarity).		2	CTGTACGAAGGC	0.617	
+	10	1452		NM_017888	NP_060358	Q6NUN0	ACSM5_HUMAN			2	TTGCTATTTGGTA	0.363	
-	4	532	p.R108C|ACSM2E	NM_182617	NP_872423	Q68CK6	ACS2B_HUMAN		p.R108C(1)	5	CCACACGATCCC	0.562	rs148136861

+	12	1932	gc.1_Missense_M	NM_001114	NP_001105	P51828	ADCY7_HUMAN	lasmic (Potential).		1	TGAGGGGCTCA	0.602	
-	2	2411	_Mutation_p.P69	NM_002968	NP_002959	Q9NSC2	SALL1_HUMAN			8	TGTTGGGGATCT	0.527	
+	6	1187	kl.2_Missense_M	NM_032206	NP_115582	Q86WI3	NLRC5_HUMAN	NACHT.		7	TGGCCCAGGCC	0.562	
+	15	1631	_Missense_Mutati	NM_024712	NP_078988	Q96BJ8	ELMO3_HUMAN	ELMO.		0	TGGCCCGCACT	0.662	
-	6	973		NM_000229	NP_000220	P04180	LCAT_HUMAN			0	TCACGTGACTGC	0.577	
-	5	1220	KL_uc002fdc.2_In	NM_152649	NP_689862	Q8NB16	MLKL_HUMAN	rotein kinase.		2	ATGTTGGGAGAT	0.353	
-	4	571	TL1_uc010chk.2_	NM_021149	NP_066972	Q14019	COTL1_HUMAN			1	TACTCCGTCTGG	0.612	
+	5	350	z.2_Missense_M	NM_001012759	NP_001012777	Q2VPK5	CTU2_HUMAN			1	ATTCTGCCAAAA	0.562	
+	10	1524	vqr.1_Missense_	NM_000934	NP_000925	P08697	A2AP_HUMAN			0	AGGAGGATTAC	0.602	
-	1	935		NM_003555	NP_003546	P47890	OR1G1_HUMAN	lasmic (Potential).		0	TAAGGGGAATGA	0.423	
+	7	958	u.2_Missense_M	NM_182538	NP_872344	Q6ZMD2	SPNS3_HUMAN			1	CAGCAACCCCG	0.642	
-	2	362	GR2_uc002ger.3_	NM_001181	NP_001172	P07307	ASGR2_HUMAN	lasmic (Potential).		1	TCCTGGGATTCA	0.517	
+	9	1649_1650	_5'Flank|EIF4A1_	NM_015670	NP_056485	Q9H4L4	SENP3_HUMAN	Protease.		2	AATCCCCATCCA	0.505	
-	21	3310_3311	rf68_uc010cnv.2_	NM_025099	NP_079375	Q2NKJ3	CTC1_HUMAN			0	ACCACGGCTTCG	0.579	
+	21	2759_2760	_Mutation_p.S44	NM_012393	NP_036525	O15067	PUR4_HUMAN			5	CTTCTCCCAGCT	0.649	
+	9	1394	va.1_Missense_M	NM_153210	NP_694942	Q70EL4	UBP43_HUMAN			5	ACTCTCTGTGG	0.502	
-	3	144	uc002gml.1_Intron	NM_002472	NP_002463	P13535	MYH8_HUMAN	osin head-like.		11	GTAGGGAGCAG	0.498	
-	5	525	uc002gml.1_Intron	NM_005963	NP_005954	P12882	MYH1_HUMAN	osin head-like.		21	TGCCTCGGTAG	0.512	
-	27	3757	_Missense_Mutati	NM_001100112	NP_001093582	Q9UKX2	MYH2_HUMAN	Potential.		14	GCTCCCCAAGC	0.532	
-	21	2506	_Missense_Mutati	NM_001100112	NP_001093582	Q9UKX2	MYH2_HUMAN	IQ.		14	TGGGTTCGGGTA	0.473	
-	15	1897		NM_002470	NP_002461	P11055	MYH3_HUMAN	osin head-like.		7	GCCCAACCACA	0.552	
+	52	10310	oo.2_Splice_Site_	NM_001372	NP_001363	Q9NYC9	DYH9_HUMAN			20	TGAAAGTACGT	0.348	
+	7	871	E182K|RICH2_uc	NM_014859	NP_055674	Q17R89	RHG44_HUMAN	BAR.		0	GGGAAGAAATG	0.547	
+	14	2031	_p.V659I|MPRIP_	NM_201274	NP_958431	Q6WCQ1	MPRIP_HUMAN	ction with RHOA.		0	CCCCCGTCCAC	0.602	
-	12	1551	P3A_uc002gsw.1	NM_004618	NP_004609	Q13472	TOP3A_HUMAN			3	CCAGGAAATGG	0.537	
+	11	2082	.P253L|EPN2_uc	NM_014964	NP_055779	O95208	EPN2_HUMAN	E]-P-W.|3 X 3 AA repeats o		1	TGCTCCCGCCA	0.517	
-	3	524		NM_173624	NP_775895					0	GCTTCCAGTTC	0.542	
-	14	3151	bb.1_Missense_M	NM_001033561	NP_001028733	Q96QT6	PHF12_HUMAN			1	TTCTCCGAGAAG	0.507	
-	2	1746	IP2_uc002hdx.3_	NM_020772	NP_065823	Q7Z417	NUFP2_HUMAN			4	TGAGGGAATTA	0.453	
-	4	668	_p.D76N|SLFN11_	NM_001104588	NP_001098058	Q7Z7L1	SLN11_HUMAN			3	TAAATCCAGTC	0.438	
-	4	2584	_p.P752S|SLFN13_	NM_144682	NP_653283	Q68D06	SLN13_HUMAN			2	TTGGAGGATTTT	0.393	
-	5	2251		NM_001145027	NP_001138499					1	CACATATTAATTG	0.418	
+	7	1091	_p.P266S|CASC3_	NM_007359	NP_031385	O15234	CASC3_HUMAN	and localization in nucleu		1	GGAGTCCTCCA	0.368	
-	7	1735	2_RNA|TMEM99_	NM_000421	NP_000412	P13645	K1C10_HUMAN	ich.|Gly-rich.|Tail.		0	CGGAAGAGGAG	0.313	rs112018671
-	5	967		NM_021013	NP_066293	O76011	KRT34_HUMAN	Rod.|Coil 2.		1	TGTGCGTCTCA	0.582	
-	12	1798	P1_uc002hxo.1_	NM_177977	NP_817084	P54257	HAP1_HUMAN	Glu-rich.		2	CAGTTCCACCT	0.622	
+	3	516	_Mutation_p.G15	NM_145273	NP_660316	Q6UXG3	CLM9_HUMAN	ellular (Potential).		0	CCCCAGGATTG	0.572	
+	4	551	R56C|CRHR1_uc	NM_001145146	NP_001138618	P34998	CRFR1_HUMAN	ellular (Pot	p.R96S(1)	3	CCGCCCGCGT	0.642	
+	6	903	PT_uc002ijx.3_In	NM_016835	NP_058519	P10636	TAU_HUMAN			1	TAGGAGACCTG	0.682	
+	10	1551	B3_uc010wkr.1_	NM_000212	NP_000203	P05106	ITB3_HUMAN	ial).|Cysteine-rich tandem		6	AGGACGAATGC	0.627	rs150951945
-	2	762	B3_uc010dbf.2_5'	NM_002147	NP_002138	P09067	HXB5_HUMAN	Homeobox.		0	GCGCTCGGACA	0.577	
+	13	3274	c002irv.1_Nonsen	NM_018896	NP_061496	O43497	CAC1G_HUMAN	lasmic (Potential).		1	GCTTCCAGGCG	0.587	
+	12	1696	k.3_Nonsense_M	NM_003786	NP_003777	O15438	MRP3_HUMAN	ilarity).|ABC transmembra		4	CACCTGGATGT	0.662	
+	3	130		NM_153228	NP_694960	Q8N957	ANKF1_HUMAN			2	ACAGAGGCTGA	0.433	
+	8	1631	_p.S530F|TBX4_u	NM_018488	NP_060958	P57082	TBX4_HUMAN			2	AATCTTCCTTAC	0.532	
-	9	1740	p.2_Missense_M	NM_005121	NP_005112	Q9UHV7	MED13_HUMAN			2	CTGAGGAGTTG	0.458	
+	9	1466	'Flank|ACE_uc010	NM_000789	NP_000780	P12821	ACE_HUMAN	otential).|Peptidase M2 1.		4	GTGGGCGTACC	0.552	

-	19	3844	ig.2_Nonsense_Mu	NM_018672	NP_061142	Q8WWZ7	ABCA5_HUMAN	ical; (Potential).	4	AATCTGAACTGT	0.308
-	19	2478	p.D179N|C17orf28	NM_030630	NP_085133	Q8IV36	CQ028_HUMAN		0	GGTGTCGTACC	0.622
-	1	186_187	2jnf.2_Missense_M	NM_006937	NP_008868	P61956	SUMO2_HUMAN		0	ACCTTGGGCTTT	0.698
+	7	698	CR1_uc002kcz.2_	NM_024083	NP_076988	Q9BZE9	ASPC1_HUMAN		162	CACTTCCCTTG	0.662
-	22	3143	zj.1_Missense_Mu	NM_005559	NP_005550	P25391	LAMA1_HUMAN	inin EGF-like 11.	21	AGGGGGGCAGA	0.552
-	1	1671		NM_172241	NP_758441	Q96RT6	CTGE2_HUMAN		1	TCCTCCCCGTG	0.512
+	21	2559	ur.2_Missense_Mu	NM_198129	NP_937762	Q16787	LAMA3_HUMAN	IV 1 (domain IV B).	11	AGGAGCCAGCC	0.433
-	16	3078	2_uc002kwk.3_3'U	NM_024422	NP_077740	Q02487	DSC2_HUMAN	lasmic (Potential).	3	CTTGTCGTTCAC	0.413
+	13	2118	3_uc002kwt.2_5'F	NM_001944	NP_001935	P32926	DSG3_HUMAN	lasmic (Potential).	9	GTGGGGAATTG	0.428
+	5	654		NM_001943	NP_001934	Q14126	DSG2_HUMAN	r (Potential).|Cadherin 1.	9	ACAACGAACCA	0.373
+	12	5081	q.2_Missense_Mu	NM_030632	NP_085135	Q9C0F0	ASXL3_HUMAN		3	AAGCAGACAAG	0.473
+	8	1436_1437	lh.1_Missense_Mu	NM_006033	NP_006024	Q9Y5X9	LIPE_HUMAN	PLAT.	2	TGCCACCAACAC	0.559
+	8	1183	p.H346Y|CTDP1_u	NM_004715	NP_004706	Q9Y5B0	CTDP1_HUMAN		0	TAAATCATTCTC	0.493
-	12	1305	ndz.2_Nonsense_	NM_007322	NP_015561	Q9H6Z4	RANB3_HUMAN		1	CTCCTGGGACG	0.572
+	15	1811	NPLA6_uc002mgr.	NM_006702	NP_006693	Q8IY17	PLPL6_HUMAN	ytoplasmic (Potential).	3	CATCATTGCCC	0.612
+	11	2508	_Mutation_p.D830	NM_020902	NP_065953	Q9P1Y5	CAMP3_HUMAN	Pro-rich.	1	CCCACGACGTA	0.716
-	4	521	q.2_Missense_Mu	NM_021155	NP_066978	Q9NNX6	CD209_HUMAN	|7 X approximate tandem r	1	CAGCCAGGTCA	0.557
-	81	43373	wj.2_Missense_Mu	NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).	57	GGGAGTCCACC	0.517
-	3	31148		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	ch.|Extracellular (Potential).	57	GAGTAGCATCC	0.532
-	3	14344		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).	57	AAACCCCTCAG	0.498
-	3	11893		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).	57	TGGTAACCTCCT	0.453
-	1	5870		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	ch.|Extracellular (Potential).	57	TGTTTCCCATA	0.502
+	6	893	ARM1_uc002mqa.	NM_199141	NP_954592	Q86X55	CARM1_HUMAN		0	CATCTCGGAGC	0.597
+	3	2106		NR_027049					0	CCTACGAACAC	0.438
-	4	1707	_p.R487*|ZNF20_u	NM_021143	NP_066966	P17024	ZNF20_HUMAN	2H2-type 15.	0	TTCTCGACATG	0.398
-	5	787	i.2_Missense_Mu	NM_002918	NP_002909	P22670	RFX1_HUMAN		2	GAAGAGCCTGG	0.527
-	14	1703	p.L169F|ILVBL_uc	NM_006844	NP_006835	A1L0T0	ILVBL_HUMAN	sphate binding (By similari	2	GATGAGGCTGT	0.577
-	15	2656	p.S197F|RASAL3	NM_022904	NP_075055	Q86YV0	RASL3_HUMAN		0	AGGCGGAGTCC	0.716
+	1	432_433		NM_013939	NP_039227	O60403	O10H2_HUMAN	lasmic (Potential).	3	GAGCCCACGGG	0.634
-	8	1263	BP1_uc002nft.1_R	NM_031941	NP_114147	Q8N6Y0	USBP1_HUMAN		1	ATGCTTCCTTTT	0.597
+	9	845_846	SBP4_uc002niz.2_	NM_032627	NP_116016	Q9BWG4	SSBP4_HUMAN	Pro-rich.	0	CGCCTCCTCGT	0.678
-	4	818	mc.2_Missense_M	NM_023002	NP_075378	Q86UW8	HPLN4_HUMAN	Link 1.	1	TATGGCGATACC	0.701
+	8	1279_1280	w.3_Missense_Mu	NM_153221	NP_694953	Q8IUL8	CILP2_HUMAN		1	CCTGAGGACTGT	0.683
-	18	2104	p.P637S|GMIP_uc	NM_016573	NP_057657	Q9P107	GMIP_HUMAN	Rho-GAP.	1	GCTGGGGCTGG	0.617
-	5	1656	208_uc002nqo.1_	NM_007153	NP_009084				7	CAGTATGAATTC	0.358
-	2	277	se_Mutation_p.L4	NM_007153	NP_009084				7	CACCCAGGAAG	0.308
+	4	494	ecy.2_Missense_M	NM_033468	NP_258429	Q9Y2Q1	ZN257_HUMAN		0	AACATGAGAAT	0.363
+	2	968	edd.1_Missense_M	NM_014717	NP_055532	O15090	ZN536_HUMAN	2H2-type 3.	11	CTGTACCTTCT	0.667
+	15	4353		NM_015073	NP_055888	O60292	SI1L3_HUMAN		2	GCAGCCACAGC	0.602
-	2	2165		NM_020862	NP_065913	Q9P244	LRFN1_HUMAN	lasmic (Potential).	2	GGGCGCGGCGC	0.741
+	2	261	2omf.2_Missense_	NM_020129	NP_064514	Q8TCE9	PPL13_HUMAN	Galectin.	2	CTGTTTCCTTGC	0.522
-	31	14265		NM_003890	NP_003881	Q9Y6R7	FCGBP_HUMAN	TIL 11.	9	CACAGGGCAGG	0.637
+	5	901	EACAM21_uc002o	NM_001098506	NP_001091976	Q3KPI0	CEA21_HUMAN	lasmic (Potential).	1	CCAGCGATCAG	0.532
-	2	421	g.1_Intron|PSG3_	NM_021016	NP_066296	Q16557	PSG3_HUMAN	g-like V-type.	2	TCGTCCACTGT	0.453
-	3	498	ovi.2_Missense_M	NM_002782	NP_002773	Q00889	PSG6_HUMAN	like C2-type 1.	2	AGATGGAGGGC	0.507
-	10	1083		NM_138568	NP_612635	Q2M3D2	EX3L2_HUMAN		1	TCCCTCCTCAG	0.672
+	2	972	lc.1_Nonsense_M	NM_014681	NP_055496	Q14147	DHX34_HUMAN	ase ATP-binding.	5	GCACCCAGCCC	0.637

+	2	257	_p.G18R|CPT1C_	NM_152359	NP_689572	Q8TCG5	CPT1C_HUMAN	lasmic (Potential).		3	CGGACGGGGCT	0.587
-	7	876	Y|KLK6_uc010ycn	NM_001012964	NP_001012982	Q92876	KLK6_HUMAN	Peptidase S1.		0	GAGGTGGTCTC	0.383
-	6	603	qar.3_Missense_M	NM_001102603	NP_001096073	Q9HCG1	ZN160_HUMAN	KRAB.		1	CTTTCCCTTCCT	0.458
-	1	1411		NM_033341	NP_203127	Q96P09	BIRC8_HUMAN	BIR.		1	CCAAGGATCTT	0.433
+	7	2752	eqr.1_Missense_M	NM_018555	NP_061025	Q9NQX6	ZN331_HUMAN	C2H2-type 12.		6	TCCTACGAATGT	0.468
+	7	1034	_p.S251F|PRKCG_	NM_002739	NP_002730	P05129	KPCG_HUMAN	C2.		9	GACCTCCCGCA	0.677
+	1	124	Dera.1_Missense_	NM_031896	NP_114102	P62955	CCG7_HUMAN			1	TACATGGAAGAA	0.627
-	7	1489	LRB2_uc002qfc.2_	NM_005874	NP_005865	Q8N423	LIRB2_HUMAN	Potential).|Ig-like C2-type 4.		1	GGTGAGACAGC	0.632
-	2	1440		NM_176820	NP_789790	Q7RTR0	NALP9_HUMAN			7	ATGCTTCCAATG	0.468
+	3	1038	NF776_uc002qqa.	NM_173632	NP_775903	Q68DI1	ZN776_HUMAN	C2H2-type 3.		1	ATGAATCATTTT	0.388
-	4	1328	s.1_Intron|CMPK2	NM_207315	NP_997198	Q5EBM0	CMPK2_HUMAN	Potential.		0	TTGACGAAACA	0.542
+	14	1580	ja.1_Missense_Mu	NM_005680	NP_005671	Q53T94	TAF1B_HUMAN			3	CACAGCCTTCAG	0.418
-	26	9693		NM_000384	NP_000375	P04114	APOB_HUMAN	eparin-binding.		27	CCAAAGGATTTG	0.348
-	26	7164		NM_000384	NP_000375	P04114	APOB_HUMAN			27	ACCTCTCGATTA	0.373
-	26	5229		NM_000384	NP_000375	P04114	APOB_HUMAN			27	CTTTCCCATCCA	0.473
-	5	537		NM_000384	NP_000375	P04114	APOB_HUMAN	Vitellogenin.		27	TCCCTTCTGGAA	0.512
+	1	2225		NM_032266	NP_115642	Q68DN1	CB016_HUMAN			1	AGTAGGGACTG	0.428
+	14	1631_1632	512_uc010ylx.1_	NM_032434	NP_115810	Q96ME7	ZN512_HUMAN			1	GCTTCCCGAGAC	0.535
-	16	1740		NM_000379	NP_000370	P47989	XDH_HUMAN			8	CTGGGGGGTCT	0.498
+	13	1696	se_Mutation_p.L4	NM_017735	NP_060205	Q6P3X3	TTC27_HUMAN	TPR 2.		1	GAAATCCTTAGA	0.373
-	15	2455	j.3_Missense_Mut	NM_005633	NP_005624	Q07889	SOS1_HUMAN	Ras-GEF.		10	CTTCCAACTAAT	0.333
-	6	923		NM_018079	NP_060549	Q8N5C6	SRBD1_HUMAN	Potential.		1	TTTTCTGGATTG	0.343
+	9	1415	.3_Intron|LHCGR_	NM_172196	NP_751946	Q9UNN4	TF2AY_HUMAN			0	GGACATCGTTTA	0.244
-	2	153		NM_015717	NP_056532	Q9UJ71	CLC4K_HUMAN	lasmic (Potential).		2	CCCCGGGACCA	0.552
-	24	3231	_Missense_Mutatio	NM_021196	NP_067019	Q9BY07	S4A5_HUMAN	cellular (Potential).		9	TTTTTTCCTTCTC	0.527
+	12	1851	_p.V616M|CTNNA2	NM_004389	NP_004380	P26232	CTNA2_HUMAN			9	CGCCTGGTGTAT	0.522
+	5	1039	Intron|TEKT4_uc0	NM_144705	NP_653306	Q8WW24	TEKT4_HUMAN	Potential.		3	CTGCGGGAAATC	0.607
+	16	2548	10yvi.1_Nonsense_	NM_144992	NP_659429	Q502W6	VWA3B_HUMAN			6	AGGTTCAGAAA	0.413
-	23	3753	.2_Missense_Muta	NM_002285	NP_002276	P51826	AFF3_HUMAN			6	AGTAGTCGTAGC	0.547
+	2	218		NM_024065	NP_076970	Q9H2J4	PDCL3_HUMAN			0	GAAGAGGAGCAG	0.522
+	4	531_532	SH2P_uc002tkd.2_	NM_182905	NP_878908					0	CCCCTCCGGTG	0.574
+	24	4205	flu.2_Missense_M	NM_130773	NP_570129	Q8WYK1	CNTP5_HUMAN	lasmic (Potential).		10	TATCCAGAAAATT	0.433
+	5	1363		NM_080386	NP_525125	Q13748	TBA3C_HUMAN			0	AGTTCTCTGAGG	0.582
+	4	1148	HSD7B_uc002tvb.	NM_001080427	NP_001073896				p.S414F(1)	7	AAGTCTCTCTCC	0.493
+	25	3063_3064	.2_Missense_Mut	NM_018151	NP_060621	Q5UIP0	RIF1_HUMAN			15	GGAATCCAGTGG	0.337
-	66	9669		NM_004543	NP_004534	P20929	NEBU_HUMAN	Nebulin 86.		20	CCACATCCATAG	0.463
-	41	5059		NM_004543	NP_004534	P20929	NEBU_HUMAN			20	TACTTGGTCTTG	0.468
+	5	2203	.NT5_uc010zci.1_	NM_014568	NP_055383	Q7Z7M9	GALT5_HUMAN	ienal (Potential).		4	ACAATTCCTCCA	0.343
-	39	5530	pa.2_Missense_Mu	NM_002349	NP_002340	O60449	LY75_HUMAN			0	AAATTACCGTGC	0.368
-	15	1844	b.2_Missense_Mu	NM_001935	NP_001926	P27487	DPP4_HUMAN	cellular (Potential).		3	TTCCTTCCTCCT	0.303
-	17	3471	uc002udp.2_Intron	NM_002977	NP_002968	Q15858	SCN9A_HUMAN			13	CTTTTTCCTTGAG	0.393
+	8	1516	udy.2_Missense_	NM_152381	NP_689594	A4UGR9	XIRP2_HUMAN			14	TTAAACCGTTTA	0.373
+	8	2992	udy.2_Missense_	NM_152381	NP_689594	A4UGR9	XIRP2_HUMAN			14	GCCATTCAAGAT	0.393
+	19	2307	3B_uc002ufz.2_Mi	NM_138995	NP_620482	Q8WXR4	MYO3B_HUMAN	yosin head-like.		19	ATCTTGGATATC	0.403
+	3	837		NM_006898	NP_008829	P31249	HXD3_HUMAN	Homeobox.		0	TGTGCCGGCCG	0.592
-	7	985	A_uc002ume.2_M	NM_003690	NP_003681	O75569	PRKRA_HUMAN	ıssociation and interaction		2	TCATACCTATATC	0.294
-	78	19870	TN_uc010zfj.1_Intr	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN			153	GAGGTTCTGATG	0.428

-	31	7428	TN_uc010zfj.1_Mi	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN			153	AATGTGAACCC	0.463	
-	42	3123	frx.2_Missense_M	NM_000393	NP_000384	P05997	CO5A2_HUMAN			2	CCCATGAGAGC	0.612	
-	39	2883	rx.2_Missense_M	NM_000393	NP_000384	P05997	CO5A2_HUMAN			2	ATCTCCCTTCT	0.443	
-	7	1244		NM_014585	NP_055400	Q9NP59	S40A1_HUMAN			1	CCCATCCATCT	0.512	
+	26	2972	p.K513N|AOX1_u	NM_001159	NP_001150	Q06278	ADO_HUMAN			6	TACAAGGAAAT	0.368	
+	12	1737	nse_Mutation_p.H	NM_015040	NP_055855	Q9Y2I7	FYV1_HUMAN			10	AACTTCCATATC	0.532	
+	42	6363		NM_015040	NP_055855	Q9Y2I7	FYV1_HUMAN	atalytic.|PIPK.		10	TGTCTCCGGAG	0.433	
+	7	1261	.1_Intron|MAP2_u	NM_002374	NP_002365	P11137	MAP2_HUMAN			17	AACATCGCCCT	0.438	rs144486691
-	5	824		NM_001608	NP_001599	P28330	ACADL_HUMAN			0	TTGCTTCCATTG	0.323	
-	1	169		NM_079420	NP_524144	P05976	MYL1_HUMAN			1	CGCAGCCGCAG	0.313	
+	32	4036	.P1308S|CPS1_u	NM_001875	NP_001866	P31327	CPSM_HUMAN			13	ATAATTCCTGCT	0.343	
+	1	41_42	62_uc002vhs.2_5'	NM_198559	NP_940961	Q7Z7H3	CB062_HUMAN			0	TCCAAGGTTTAC	0.574	
+	3	1058		NM_025216	NP_079492	Q9GZT5	WN10A_HUMAN			2	CCCTGCCCACA	0.657	
-	27	4489		NM_194302	NP_919278	Q6ZU64	CC108_HUMAN			4	TTCCTCGTTCTT	0.532	
+	25	2570	.1_Intron|SP100_	NM_003113	NP_003104	P23497	SP100_HUMAN	HMG box 2.		5	TAACACCGCTG	0.289	
+	11	1666	PP_uc002vsr.2_R	NM_001632	NP_001623	P05187	PPB1_HUMAN			1	CGCCCCCCGCC	0.736	
+	1	153	up.2_Intron|UGT1	NM_019075	NP_061948	Q9HAW8	UD110_HUMAN			3	TGGGAGTCACT	0.567	
+	1	389	up.2_Intron|UGT1	NM_019075	NP_061948	Q9HAW8	UD110_HUMAN			3	CCAGTGGTTTT	0.378	
+	9	1037	_p.E193K|LRRFIP	NM_001137552	NP_001131024	Q32MZ4	LRRF1_HUMAN	Potential.		3	TGCTCGAGGTA	0.368	
+	3	367		NM_001080504	NP_001073973	Q6ZP01	RBM44_HUMAN			4	TTATTAGAGCCA	0.338	
-	13	2479	_p.E117K|FERMT	NM_017671	NP_060141	Q9BQL6	FERM1_HUMAN	FERM.		3	AAACTCAGGCA	0.547	
-	5	1114	nj.2_Missense_M	NM_020341	NP_065074	Q9P286	PAK7_HUMAN	Linker.		23	AAATCGGATTTC	0.473	
-	2	176	0zrl.1_Missense_	NM_025229	NP_079505	Q5TEA6	SE1L2_HUMAN	ellular (Potential).		2	TTCTTTCCTTTT	0.254	
+	6	706		NM_020689	NP_065740	Q9HC58	NCKX3_HUMAN	(Potential).|Alpha-1.		1	TTCAGGGGTCT	0.522	
+	3	1280	.1_Intron|GZF1_u	NM_022482	NP_071927	Q9H116	GZF1_HUMAN	2H2-type 2.		1	GCGCCACGTGC	0.652	
-	22	3892	_p.A924V|NINL_uc	NM_025176	NP_079452	Q9Y2I6	NINL_HUMAN	Potential.		5	TCCTGGCCTGC	0.677	
+	6	639	xb.1_RNA|TTLL9_	NM_001008409	NP_001008409	Q3SXZ7	TTLL9_HUMAN	TTL.		2	GGCAGGAAAGC	0.552	
+	16	2750		NM_016436	NP_057520	Q9BVI0	PHF20_HUMAN			1	CCTTTCCCCGC	0.607	
-	24	3005	xgk.2_Missense_	NM_152503	NP_689716	Q9H579	CT132_HUMAN			0	GATGGGAAGTT	0.373	
+	3	360	n_p.P64S|TOX2_u	NM_001098798	NP_001092268	Q96NM4	TOX2_HUMAN			1	TGCTCCCTGCC	0.647	
+	8	1128_1129	_RNA|PABPC1L_	NM_001124756	NP_001118228	Q4VXU2	PAP1L_HUMAN	RRM 4.		1	AAAGGCCGTGA	0.564	
+	2	1637	_p.S527F|SEMG2_	NM_003008	NP_002999	Q02383	SEMG2_HUMAN	at-rich region.|3-2.		1	AAAGTCTGGTC	0.378	
+	2	176	ATN4_uc010zwr.	NM_014276	NP_055091	Q9UBG7	RBPJL_HUMAN			1	CGACAGGCGGA	0.652	
-	13	1752	gho.1_Nonsense_	NM_022829	NP_073740	Q8WWT9	S13A3_HUMAN	ellular (Potential).		1	CAGCTGGAAGA	0.557	
-	21	3040	zyt.1_Missense_M	NM_080829	NP_543019	Q96MK2	FA65C_HUMAN			2	GGTTTCCCGGG	0.602	
+	7	2222	ze.1_Missense_M	NM_001164116	NP_001157588	Q9NQ75	CASS4_HUMAN			3	GACTCCTGAGA	0.527	
-	7	980		NM_198996	NP_945347	Q6XZB0	LIPI_HUMAN			2	GGCTTGATAAC	0.323	
+	18	2749	cb.1_Missense_M	NM_004540	NP_004531	O15394	NCAM2_HUMAN	lasmic (Potential).		4	AAGACGACAGC	0.358	
-	1	210		NM_181621	NP_853652	Q52LG2	KR132_HUMAN	approximate repeats.|2.		0	GGGCTCCCAGC	0.607	
-	5	2362	yuj.3_Missense_	NM_001001890	NP_001001890	Q01196	RUNX1_HUMAN	o/Ser/Thr-ri	p.Q262*(1)	387	GGATCCCAGGT	0.517	
-	3	457	wo.2_Missense_M	NM_002240	NP_002231	P48051	IRK6_HUMAN	llular (By similarity).		1	TTGAGGTTGGTA	0.478	
-	16	3442	CAM_uc002yyr.1_	NM_001389	NP_001380	O60469	DSCAM_HUMAN	III 2.|Extracellular (Potentia		11	TGAGATGATATA	0.517	
-	14	1940	yzp.2_Missense_	NM_022115	NP_071398	P57071	PRD15_HUMAN			0	CCCGGGGTGTG	0.562	
-	2	273		NM_003225	NP_003216	P04155	TFF1_HUMAN			0	CTTCTGGAGGG	0.483	
+	9	1280	_p.S356L|TRPM2_	NM_003307	NP_003298	O94759	TRPM2_HUMAN	lasmic (Potential).		3	GGGCTCGGGCC	0.642	rs138507862
-	5	739	gpv.1_Missense_	NM_144991	NP_659428	Q8WU66	TSEAR_HUMAN			0	GGTGGCGTCTG	0.672	rs146216896
+	2	466	IR1306_hsa-mir-	NM_022720	NP_073557	Q8WYQ5	DGCR8_HUMAN	d retention.|Necessary for		0	ACCTCCCCTGC	0.637	

+	2	198	2zuz.1_Missense_	NM_003347	NP_003338	P68036	UB2L3_HUMAN		0	ATTGTTCCTGTG	0.413	
-	7	714		NM_016449	NP_057533	Q6PGQ1	CV043_HUMAN		1	AGAACCTGGAA	0.398	
+	14	1869	p.G531E|CABIN1_	NM_012295	NP_036427	Q9Y6J0	CABIN_HUMAN		5	GATTTGGACCTG	0.537	
+	4	530	_p.E69K|UPB1_u	NM_016327	NP_057411	Q9UBR1	BUP1_HUMAN	N hydrolase.	2	TGGACAGAATTT	0.502	
-	6	685	nse_Mutation_p.P	NM_014303	NP_055118	O00541	PESC_HUMAN	r nucleolar localization.	0	CATAGGGAGTG	0.567	
+	13	1728	alz.1_Missense_M	NM_000343	NP_000334	P13866	SC5A1_HUMAN	ical; (Potential).	1	TTTCACGTATGA	0.478	
-	15	1442	c010gwo.2_Misse	NM_174932	NP_777592	Q8NFQ6	BPIL2_HUMAN		2	TTTGAGGATGTT	0.473	
+	10	1115	4_uc003apz.3_3'	NM_000631	NP_000622	Q15080	NCF4_HUMAN		1	AGGCTCGTGGC	0.597	
+	8	1085	aqc.3_Missense_	NM_000395	NP_000386	P32927	IL3RB_HUMAN	ellular (Potential).	3	AGTGCTCCCCA	0.667	
-	3	724	OX10_uc003auo.	NM_006941	NP_008872	P56693	SOX10_HUMAN	HMG box.	0	CGCTTGTCACTT	0.627	
+	2	1203	xy.2_Missense_M	NM_002409	NP_002400	Q09327	MGAT3_HUMAN	enal (Potential).	0	AGATCCCGGCC	0.632	
+	4	474	M50_uc011aqd.1_	NM_015380	NP_056195	Q9Y512	SAM50_HUMAN		1	TCCGTCTTGGA	0.363	
-	24	5787	CP6_uc010har.1_	NM_020461	NP_065194	Q96RT7	GCP6_HUMAN		4	CCCAGGGGGCC	0.612	
-	22	3605	brg.1_Missense_	NM_014850	NP_055665	O43295	SRGP2_HUMAN	Potential.	9	GAGTTCCCGCA	0.647	
-	2	572	va.1_Missense_M	NM_173472	NP_775743	Q96PS1	CC024_HUMAN		0	AAGTCCCGGTC	0.517	
-	23	3932	120N|ATP2B2_uc	NM_001001331	NP_001001331	Q01814	AT2B2_HUMAN	lasmic (Potential).	6	GTTATGGATGG	0.537	
+	1	230	3bvy.1_Missense_	NM_014229	NP_055044	P48066	S6A11_HUMAN	Name=1; (Potential).	4	CCGGGGAGATC	0.552	
+	7	1336	NH8_uc010hex.1_	NM_144633	NP_653234	Q96L42	KCNH8_HUMAN	ellular (Potential).	5	AAATGGAGAGG	0.408	
+	4	575	_p.S51L|RARB_uc	NM_016152	NP_057236	P10826	RARB_HUMAN	Hinge.	3	GACTTCGAAGC	0.502	
-	19	1779	10_uc003cds.1_5'	NM_199347	NP_955379	Q6ZWH5	NEK10_HUMAN	Potential.	13	TCAATATTTTCAG	0.348	
+	6	736	AC_uc011aya.1_	NM_003149	NP_003140	Q99469	STAC_HUMAN		4	CAGATCTTGTG	0.478	
-	12	2016	.D608N|SCN5A_	NM_198056	NP_932173	Q14524	SCN5A_HUMAN		9	TGGGTCGCCTG	0.647	
-	10	1672		NM_014139	NP_054858	Q9UI33	SCNBA_HUMAN		9	ACTTACCTTTTT	0.358	
-	2	3150	_Mutation_p.D97	NM_194293	NP_919269	Q702N8	XIRP1_HUMAN		8	GGGGTCCAGTG	0.672	
-	1	997_998	mg.2_Intron|CYP8	NM_004391	NP_004382	Q9UNU6	CP8B1_HUMAN		2	CACTCCCGGGG	0.559	
-	10	1733	_p.Q187*|SLC6A2	NM_020208	NP_064593	Q9NP91	S6A20_HUMAN	ellular (Potential).	2	GGCTTGATACTT	0.572	
-	4	471	al.1_Missense_M	NM_024513	NP_078789	Q9BQS8	FYCO1_HUMAN	RUN.	1	AAAGCGGATCC	0.507	rs141476300
-	14	1484	bbd.1_Missense_	NM_003074	NP_003065	Q92922	SMRC1_HUMAN	SWIRM.	3	ACCATGATGCAT	0.433	
+	11	2069_2070	n_p.P509L|MIR12	NM_138615	NP_619520	Q7L2E3	DHX30_HUMAN	ase ATP-binding.	4	AACCCCAGCCT	0.624	
-	48	11609_1161	cuk.2_Missense_	NM_001407	NP_001398	Q9NYQ7	CELR3_HUMAN		11	AGAGGGAGCG	0.668	
+	31	3249		NM_004947	NP_004938	Q8IZD9	DOCK3_HUMAN		0	CCTATGAACTG	0.428	
+	21	3843	BO2_uc011bgk.1_	NM_002942	NP_002933	Q9HCK4	ROBO2_HUMAN	lasmic (Potential).	11	TGGATCCACTT	0.438	
+	1	460		NM_001005338	NP_001005338	A6NKK0	OR5H1_HUMAN	Name=4; (Potential).	2	GGTATTCTTCAT	0.373	
+	1	340		NM_001005514	NP_001005514	A6NHG9	O5H14_HUMAN	Name=3; (Potential).	1	TGTTTTCTCTTG	0.398	
-	8	1007	p.S266F|SENP7_	NM_020654	NP_065705	Q9BQF6	SENP7_HUMAN		5	TTCCTGGAAATC	0.363	
-	27	2713	hn.1_Nonsense_	NM_014429	NP_055244	Q86VD1	MORC1_HUMAN		8	ATATTGGACCAT	0.279	
+	4	714	96_uc003dxx.2_In	NM_198196	NP_937839	P40200	TACT_HUMAN	Potential).|Ig-like V-type 2.	3	CTTAGGAAAAC	0.428	
+	13	1432	bji.1_Missense_M	NM_014980	NP_055795	Q9Y2K9	STB5L_HUMAN	WD 8.	9	TGTATTCTATAGG	0.308	
+	23	2575	bji.1_Missense_M	NM_014980	NP_055795	Q9Y2K9	STB5L_HUMAN		9	AAAATTCCTATA	0.284	
+	25	3246	bji.1_Missense_M	NM_014980	NP_055795	Q9Y2K9	STB5L_HUMAN	WD 14.	9	CCAATGAAGGA	0.403	
-	13	5830	.Q1868*|GOLGB1	NM_004487	NP_004478	Q14789	GOGB1_HUMAN	ic (Potential).|Potential.	10	TTCTTGGATTT	0.368	
-	14	2264	MA5B_uc003egb.	NM_001031702	NP_001026872	Q9P283	SEM5B_HUMAN	ellular (Potential).	7	GGCTGGCCCCA	0.607	
-	7	788	_Mutation_p.R16	NM_053025	NP_444253	Q15746	MYLK_HUMAN	like C2-type 2.	9	CAACTCGGCCC	0.562	
+	12	2534	_uc003epw.1_Intr	NM_001063	NP_001054	P02787	TRFE_HUMAN	ansferrin-like 1.	2	TCATACCGTCGT	0.587	
+	3	1795		NM_152616	NP_689829	Q8IWZ5	TRI42_HUMAN		7	CCAGCGAAGCT	0.592	
+	16	2003	p.T615R|PLS1_uc	NM_001145319	NP_001138791	Q14651	PLSI_HUMAN	.|Actin-binding 2.	1	TTATGACGGTGT	0.388	rs149708405
+	10	1491	yn.2_Missense_M	NM_053002	NP_443728	Q86YW9	MD12L_HUMAN		7	CTTTATCATAAG	0.343	

-	7	1040	_p.I66F|IFT80_uc	NM_020800	NP_065851	Q9P2H3	IFT80_HUMAN	WD 4.	1	ATAAAATAAGAT	0.269	
+	13	1511	CI_uc003fgt.2_5'	NM_002740	NP_002731	P41743	KPCI_HUMAN	rotein kinase.	5	AAATTTTAAGAG	0.343	
+	6	770	e_Mutation_p.T24	NM_033540	NP_284941	Q8IWA4	MFN1_HUMAN	lasmic (Potential).	3	TGAATACGGTAG	0.358	
-	2	86	1D1_uc011bqn.1_	NM_020640	NP_065691	Q96GG9	DCNL1_HUMAN	UBA-like.	1	CTGACGAACTT	0.308	
-	5	1231		NM_014398	NP_055213	Q9UQV4	LAMP3_HUMAN	enal (Potential).	3	TGAAGGAATGC	0.473	
-	7	971	brs.1_Missense_	NM_001966	NP_001957	Q08426	ECHP_HUMAN	yl-CoA dehydrogenase.	3	CAAAAGAAATG	0.418	
-	7	699	y.2_Missense_Mu	NM_004454	NP_004445	P41161	ETV5_HUMAN		5	GTGGGGGAAAT	0.612	
+	10	2044	G1_uc003fqr.2_Int	NM_001102416	NP_001095886	P01042	KNG1_HUMAN		1	GACCTCCCCAA	0.433	
-	2	2996	p.2_Intron|MUC4_	NM_018406	NP_060876	Q99102	MUC4_HUMAN	Ser-rich.	0	CAATTCGGTTG	0.552	
+	15	2196_2197	.2_3'UTR|ADD1_	NM_001119	NP_001110	P35611	ADDA_HUMAN		1	AAGCCCCACTG	0.649	
-	6	767	md.2_Missense_	NM_020041	NP_064425	Q9NRM0	GTR9_HUMAN	Name=6; (Potential).	3	CACTCCAAACA	0.587	
-	2	197	_Site_p.D30_splic	NM_147182	NP_671711	Q6PIL6	KCIP4_HUMAN		0	GCTGTCTGTGG	0.498	
+	3	307	C4_uc003grp.2_5	NM_013367	NP_037499	Q9UJX5	APC4_HUMAN		5	TTTCCACCAAAT	0.333	
-	47	6901	gyi.1_Splice_Site_	NM_015030	NP_055845	O94915	FRYL_HUMAN		1	AAAGCCTATCA	0.313	
+	5	1208	cam.1_Missense_	NM_001075	NP_001066	P36537	UDB10_HUMAN		5	CCATTGTTTTTG	0.453	
+	10	1410	j.1_Missense_Mu	NM_000253	NP_000244	P55157	MTP_HUMAN	Vitellogenin.	4	TGACAGCAGCA	0.433	
+	1	643		NM_001977	NP_001968	Q07075	AMPE_HUMAN	ellular (Potential).	5	CAGTCCACTAC	0.612	
+	1	665		NM_001977	NP_001968	Q07075	AMPE_HUMAN	ellular (Potential).	5	GAAGCCCCTGT	0.612	
+	8	7244	e_Mutation_p.G71	NM_024582	NP_078858	Q6V0I7	FAT4_HUMAN	|Extracellular (Potential).	18	GACAGGACAAA	0.413	
-	4	3379	p.D209N|PCDH18	NM_019035	NP_061908	Q9HCL0	PCD18_HUMAN	y similarity).|Cytoplasmic (	5	TGGTATCCCCAG	0.512	
-	9	982	0A7_uc010ipa.2_	NM_001029998	NP_001025169	Q0GE19	NTCP7_HUMAN	ical; (Potential).	0	TGGATAGAAAAT	0.284	
-	10	1213		NM_004564	NP_004555	O75879	GATB_HUMAN		0	CGACTTCGTTCT	0.403	
-	25	7132		NM_017639	NP_060109	Q6V1P9	PCD23_HUMAN	Cadherin 21.	4	AATATCCCCTG	0.413	
-	5	1326_1327	e_Mutation_p.G42	NM_000508	NP_000499	P02671	FIBA_HUMAN	By similarity.	3	CTTGTCCCTGG	0.5	
-	5	1108	RF1_uc010irc.1_5	NM_020870	NP_065921	Q7Z6J0	SH3R1_HUMAN	SH3 2.	3	CAGCCGAGTTA	0.453	
-	13	2114	1ckv.1_Missense_	NM_021069	NP_066547	O94875	SRBS2_HUMAN		1	CCATGGGGCAG	0.602	
-	3	544		NM_024830	NP_079106	Q8NF37	PCAT1_HUMAN	enal (Potential).	2	CACAGGGATGG	0.657	
-	18	3126		NM_003966	NP_003957	Q13591	SEM5A_HUMAN	.|Extracellular (Potential).	2	GGTTCCGAATG	0.587	rs143717547
-	77	13511	fc.2_Missense_Mu	NM_001369	NP_001360	Q8TE73	DYH5_HUMAN		31	AAAATCCCTGG	0.408	
-	75	13123	fc.2_Missense_Mu	NM_001369	NP_001360	Q8TE73	DYH5_HUMAN		31	ATCATCAGCCAG	0.577	
-	23	3544		NM_001369	NP_001360	Q8TE73	DYH5_HUMAN	n (By similarity).	31	AAATTCAGAAA	0.403	
+	53	8315	IO_uc003jfg.2_R	NM_007118	NP_009049	O75962	TRIO_HUMAN	-like C2-type.	18	CTCATCGTCGG	0.572	
-	8	1716	.D447N|CDH18_	NM_004934	NP_004925	Q13634	CAD18_HUMAN	(Potential).|Cadherin 4.	7	TCTGTCGAGAA	0.363	rs145743816
-	5	915	g.2_Missense_Mu	NM_016279	NP_057363	Q9ULB4	CADH9_HUMAN	(Potential).|Cadherin 2.	9	TTCCAGAAAGG	0.448	
-	12	1292	p.E58K|AGXT2_u	NM_031900	NP_114106	Q9BYV1	AGT2_HUMAN		4	TGTTTTCCTGTA	0.398	
-	4	492		NM_001737	NP_001728	P02748	CO9_HUMAN	receptor class A.	0	CACTTTCACAAT	0.478	
-	21	2627	3jmi.3_Missense_	NM_173489	NP_775760	Q7Z745	HTRB2_HUMAN		8	CTTGGGAGCAT	0.498	
-	7	1686		NM_021072	NP_066550	O60741	HCN1_HUMAN	toplasmic (Potential).	1	CAGCTCGAACA	0.413	
+	10	1351	p.S397F|IL31RA_	NM_139017	NP_620586	Q8NI17	IL31R_HUMAN	tential).|Fibronectin type-III	1	CATCTCTGTGTA	0.428	
+	10	1704	_p.L481I|BDP1_u	NM_018429	NP_060899	A6H8Y1	BDP1_HUMAN		2	AATCTTTTAGAA	0.378	
+	5	5248_5249	x.1_Missense_Mu	NM_005909	NP_005900	P46821	MAP1B_HUMAN		5	GATCACCCTACA	0.465	
-	8	911	_p.E230K|FAM169	NM_015566	NP_056381	Q9Y6X4	F169A_HUMAN		0	TTGCTTCGTATTC	0.338	
+	18	2013	p.D601E|PDE8B_	NM_003719	NP_003710	O95263	PDE8B_HUMAN	ytic (By similarity).	0	CATGACGTGGA	0.552	
+	14	10296	.R1560C|VCAN_	NM_004385	NP_004376	P13611	CSPG2_HUMAN	Sushi.	16	AAACCTCGTTAT	0.423	
+	15	10540	p.R1641K|VCAN_	NM_004385	NP_004376	P13611	CSPG2_HUMAN		16	GTCGAGGCGCT	0.408	
+	20	4132	98_uc003kjt.2_5'	NM_032119	NP_115495	Q8WXG9	GPR98_HUMAN	ellular (Potential).	16	ACCATCCCTCC	0.448	
+	3	208	Intron|CAST_uc01	NM_001042443	NP_001035908	P20810	ICAL_HUMAN		5	AGATGGAAGGA	0.388	

+	22	1693	439F|CAST_uc00	NM_001042443	NP_001035908	P20810	ICAL_HUMAN		5	ACTTCCTTCTG	0.378	
-	35	5048	n.2_Missense_Mu	NM_001270	NP_001261	O14646	CHD1_HUMAN	repeats of H-S-D-H-R.	5	TGAGTGAGAAC	0.408	
+	21	4184		NM_002372	NP_002363	Q16706	MA2A1_HUMAN	enal (Potential).	3	AAAAGGGTTTG	0.453	
-	4	316	TARD4_uc003kpi.	NM_139164	NP_631903	Q96DR4	STAR4_HUMAN	START.	1	CCAATCCAAAC	0.393	
-	6	1953	3kxy.1_Missense_	NM_133456	NP_597713	Q2M3G4	SHRM1_HUMAN		1	GGGAGGGGAGC	0.587	rs142835485
+	1	1576	p.E526K|PCDHA1	NM_018900	NP_061723	Q9Y5I3	PCDA1_HUMAN	|Extracellular (Potential).	1	ACCACGAGGAG	0.677	
+	1	1940	03lhc.1_Nonsense	NM_018905	NP_061728	Q9Y5H9	PCDA2_HUMAN	|Extracellular (Potential).	4	AGCTTCAGCTG	0.647	
+	1	217	lhd.2_Intron|PCD	NM_018906	NP_061729	Q9Y5H8	PCDA3_HUMAN	|Extracellular (Potential).	8	ACGGGGACCTT	0.622	
+	1	642	03lhf.2_Intron|PC	NM_018907	NP_061730	Q9UN74	PCDA4_HUMAN	(Potential).|Cadherin 2.	6	CTCTGGAAAAA	0.478	
+	1	204	003lhi.2_Intron|P	NM_018908	NP_061731	Q9Y5H7	PCDA5_HUMAN	(Potential). p.Q49fs*50(1)	3	TCCAAGGGCCG	0.642	
+	1	392	hh.1_Intron|PCDH	NM_018910	NP_061733	Q9UN72	PCDA7_HUMAN	|Extracellular (Potential).	4	CCCTCCGGTGT	0.587	
+	1	812		NM_018938	NP_061761	Q9Y5E5	PCDB4_HUMAN	|Extracellular (Potential).	3	TGCTGGAAACTT	0.418	
+	1	797	ah.1_Missense_	NM_018939	NP_061762	Q9Y5E3	PCDB6_HUMAN	|Extracellular (Potential).	1	AGCCAGAGATT	0.483	
+	1	1608	B16_uc010jfw.1_	NM_020957	NP_066008	Q9NRJ7	PCDBG_HUMAN	(Potential).|Cadherin 2.	2	ACTGAGTTCCC	0.398	
+	1	2311	dan.1_Missense_	NM_018912	NP_061735	Q9Y5H4	PCDG1_HUMAN	lasmic (Potential).	3	TTTTCCCCCAG	0.547	
+	1	1766	010jfx.1_Missens	NM_018916	NP_061739	Q9Y5H0	PCDG3_HUMAN	(Potential).|Cadherin 6.	1	GGTGACCAAGG	0.682	
+	1	1889	10jfx.1_Missense_	NM_018916	NP_061739	Q9Y5H0	PCDG3_HUMAN	(Potential).|Cadherin 6.	1	GGCGCGAGCCC	0.706	
+	5	1139	p.R367C|TCERG1	NM_006706	NP_006697	O14776	TCRG1_HUMAN	Pro-rich.	2	CGTTTCGTGTT	0.468	
-	9	1682	loh.3_Missense_	NM_004576	NP_004567	Q00005	2ABB_HUMAN		2	GGATAGCCCGG	0.502	
-	6	1451	sense_Mutation_	NM_014790	NP_055605	Q96AA8	JKIP2_HUMAN	Potential.	2	ATTTTCCTTGG	0.408	
+	9	1563	IA1_uc011dcx.1_	NM_001114183	NP_001107655	P42261	GRIA1_HUMAN	ellular (Potential).	6	GGGGCGATAAT	0.478	
-	5	691	NJL_uc003lyc.1_	NM_024565	NP_078841	Q8IV13	CCNJL_HUMAN	clin N-terminal.	0	TTCCCGATCCT	0.557	
+	5	1030	_p.V223I|ODZ2_u	NM_001122679	NP_001116151				10	GAACGGTTTAC	0.567	
-	20	2617	.2_Missense_Mu	NM_003062	NP_003053	O75094	SLIT3_HUMAN	LRRNT 4.	4	TGTCTCCATAC	0.632	
+	2	713	I1_uc003maj.3_I	NM_012188	NP_036320	Q12951	FOXI1_HUMAN		4	TGTTTCCTCTA	0.512	
+	8	1138	17_uc003meu.2_	NM_001099408	NP_001092878	A6NMX2	I4E1B_HUMAN	ning mRNA cap binding (B	0	CAAGGGGGACA	0.622	
+	5	657	_p.E50K|ZFP2_uc	NM_030613	NP_085116	Q6ZN57	ZFP2_HUMAN		3	GGTAATGAATTT	0.413	
+	1	936	.2_5'UTR|DCDC2_	NM_181337	NP_851854	Q9UBP8	KAAG1_HUMAN		0	GCGCGGGATCG	0.657	
-	1	534		NM_001005226	NP_001005226				1	CAGCACTGAGT	0.498	
-	3	528	p.G121D|HLA-DO	NM_002119	NP_002110	P06340	DOA_HUMAN	ntial).|Alpha-2.|Ig-like C1-t	0	TTTGGCCGTTG	0.587	
+	2	1543	tj.1_RNA|BRPF3_	NM_015695	NP_056510	Q9ULD4	BRPF3_HUMAN		2	TGGCTCCCTCA	0.448	
-	7	831	on_p.G231D|YIPF	NM_015388	NP_056203	Q9GZM5	YIPF3_HUMAN	ical; (Potential).	0	AGAGGCCATAG	0.547	
+	6	421	ense_Mutation_p.	NM_005588	NP_005579	Q16819	MEP1A_HUMAN	otential).|Metalloprotease.	3	TTTGATGGGTTG	0.313	
-	9	851	.G199R|CRISP2_	NM_001142408	NP_001135880	P16562	CRIS2_HUMAN		1	TAGTCCTTTGT	0.323	
-	1	194		NM_138733	NP_620061	P07205	PGK2_HUMAN		1	TTCTTCATGGG	0.418	
+	2	249		NM_001010872	NP_001010872	Q5T0W9	FA83B_HUMAN		6	TACCAAGAATTT	0.383	
-	6	1821	P5_uc011dxf.1_In	NM_021073	NP_066551	P22003	BMP5_HUMAN		2	ATAATCCAGTCC	0.254	
+	4	947	di.3_Missense_M	NM_152731	NP_689944	Q5SZJ8	BEND6_HUMAN		0	TTAAGGGTGGG	0.438	
+	10	3331	n.2_Missense_Mu	NM_015153	NP_055968	Q92576	PHF3_HUMAN		5	CTATGTCTAAAG	0.363	
-	10	1091	OL9A1_uc003pff.	NM_001851	NP_001842	P20849	CO9A1_HUMAN	lical region (COL3).	4	GCTTTCCCGGT	0.622	
+	14	2670	at.2_Missense_M	NM_019842	NP_062816	Q9NR82	KCNQ5_HUMAN		7	TTACAGGAAAGC	0.522	
+	1	1171		NM_032602	NP_115991	Q969M2	CXA10_HUMAN	lasmic (Potential).	0	CCCAGGACCCA	0.522	
-	10	1362	p.R140C|C6orf167	NM_198468	NP_940870	Q6ZRQ5	MMS22_HUMAN		0	ATGGCGATCAA	0.328	
-	10	1411	u.2_Missense_Mu	NM_005068	NP_005059	P81133	SIM1_HUMAN	minded C-terminal.	4	TGTCATGATCAG	0.532	
-	14	6325	3L_uc003puz.3_	NM_002912	NP_002903	O60673	DPOLZ_HUMAN		6	GACTTGGGGCA	0.433	
-	29	4979	1_Intron|GOPC_u	NM_002944	NP_002935	P08922	ROS_HUMAN	III 7.|Extracellular (Potentia	25	CAACTGATAAC	0.443	
-	8	1572		NM_005907	NP_005898	P33908	MA1A1_HUMAN	enal (Potential).	4	ACTGTTCGAATA	0.343	

-	22	3581	c.2_Missense_Mut	NM_002844	NP_002835	Q15262	PTPRK_HUMAN	phatase 1.|Cytoplasmic (Po	8	TGGGAGGGTTTG	0.483	
-	101	19489	.R820K|SYNE1_uc	NM_182961	NP_892006	Q8NF91	SYNE1_HUMAN	lasmic (Potential).	45	TTCATTCTCATCT	0.378	
-	55	9090	pu.3_Missense_Mu	NM_182961	NP_892006	Q8NF91	SYNE1_HUMAN	lasmic (Potential).	45	TTTTTTCCTAGTA	0.398	
+	2	387	'CT1_uc003qpc.3_	NM_025107	NP_079383	Q8N699	MYCT1_HUMAN		1	TTTTACCGCCACA	0.517	rs17852097
-	20	3097		NM_005577	NP_005568	P08519	APOA_HUMAN	Kringle 31.	6	CAGGATCTGGAT	0.453	
+	5	837	p.V205M|PACRG_	NM_152410	NP_689623	Q96M98	PACRG_HUMAN		0	ATGAATGGTGAGT	0.428	
+	5	751		NM_001145121	NP_001138593	B9ZVM9	B9ZVM9_HUMAN		0	CGACTCCCGGTG	0.522	
-	4	441	n.1_Missense_Mut	NM_001013836	NP_001013858	Q9Y6D9	MD1L1_HUMAN	Potential. p.R59G(1)	2	TCGAACGGATCT	0.562	rs121908982
-	3	566	p.R177H|ACTB_u	NM_001101	NP_001092	P60709	ACTB_HUMAN		0	TCCAGACGCAGG	0.642	
+	36	6042		NM_003777	NP_003768	Q96DT5	DYH11_HUMAN	1 (By similarity).	15	TGAACCCGGGTTA	0.398	
+	61	9794		NM_003777	NP_003768	Q96DT5	DYH11_HUMAN	k (By similarity).	15	TTGCAGGTTGAT	0.338	
+	22	2712	p.R882Q|STK31_u	NM_031414	NP_113602	Q9BXU1	STK31_HUMAN	rotein kinase.	9	GTCAGCGAGCCT	0.383	
-	2	772	bw.1_Missense_M	NM_013389	NP_037521	Q9UHC9	NPCL1_HUMAN	cellular (Potential).	5	GCAACCCCCTCA	0.632	
+	8	1313	3tvz.2_Missense_M	NM_022479	NP_071924	Q6IS24	GLTL3_HUMAN	nenal (Potential).	7	CATTAAGGAAAA	0.448	
-	14	3887_3888		NM_032408	NP_115784	Q9UIG0	BAZ1B_HUMAN		7	TCTGCGGACATA	0.431	rs148299208
-	19	3585	p.P1097S|MAGI2_	NM_012301	NP_036433	Q86UL8	MAGI2_HUMAN	Pro-rich.	11	CAAGGGTGGGG	0.612	
-	8	13625	v.2_Missense_Mut	NM_033026	NP_149015	Q9Y6V0	PCLO_HUMAN		7	GTTTATCAAACCA	0.463	
-	7	12686	p.R4133C|PCLO_u	NM_033026	NP_149015	Q9Y6V0	PCLO_HUMAN		7	CTCTACGAAATT	0.408	
-	6	11237	p.D3650N|PCLO_u	NM_033026	NP_149015	Q9Y6V0	PCLO_HUMAN		7	TTATATCATCAGG	0.468	
-	6	9714	p.S3142L|PCLO_u	NM_033026	NP_149015	Q9Y6V0	PCLO_HUMAN		7	AAATATGATCTAG	0.428	
-	5	8217	_Mutation_p.G264	NM_033026	NP_149015	Q9Y6V0	PCLO_HUMAN		7	AAAGCTCCAGAG	0.433	
-	3	2357	nv.2_Missense_Mu	NM_033026	NP_149015	Q9Y6V0	PCLO_HUMAN	Pro-rich.	7	GTTTTGGTGCAG	0.532	
-	16	2180	nc.1_Missense_Mu	NM_000927	NP_000918	P08183	MDR1_HUMAN	r 1.|Cytoplasmic (Potential)	7	ACAAACGATGAG	0.393	
+	33	8809	p.Q2485*|AKAP9_	NM_005751	NP_005742	Q99996	AKAP9_HUMAN		26	GCCGTTCAGTTA	0.373	
-	5	1117	10lff.2_Missense_	NM_001039372	NP_001034461	A8MVW5	HECA2_HUMAN	ical; (Potential).	5	CACATGGATATA	0.289	
-	3	577	10lff.2_Missense_	NM_001039372	NP_001034461	A8MVW5	HECA2_HUMAN	1.|Extracellular (Potential).	5	CTCCCATTTTTTA	0.507	
+	3	228	RPC1B_uc003uqb.	NM_005720	NP_005711	O15143	ARC1B_HUMAN		0	GTGCACGAGCTC	0.577	
-	7	1349	_p.R381C|TRIM4_	NM_033017	NP_148977	Q9C037	TRIM4_HUMAN	B30.2/SPRY.	2	TTGAACGATCAG	0.512	
+	8	969	_p.P60S|STAG3_u	NM_012447	NP_036579	Q9UJ98	STAG3_HUMAN		8	AGGGGCCAGGG	0.522	
-	2	433		NM_001004323	NP_001004323	Q8IZ16	CG061_HUMAN		0	CTTTTGGGAGCT	0.542	
-	4	497		NM_138403	NP_612412	Q9BUA6	MYL10_HUMAN	nd 1.|1 (Potential).	2	AGTCCTCTTTGT	0.622	
-	66	10533	.2_Missense_Muta	NM_005045	NP_005036	P78509	RELN_HUMAN	rg-rich (basic).	19	GGGTATCGCCTAA	0.328	
-	44	7031	z.2_Missense_Muta	NM_005045	NP_005036	P78509	RELN_HUMAN		19	AGCGAAGGCGAG	0.498	
-	1	371	z.2_Missense_Mu	NM_005045	NP_005036	P78509	RELN_HUMAN	Reelin.	19	TTGTCCCGGAA	0.637	
+	8	1033	P29_uc011klz.1_In	NM_018844	NP_061332	Q9UHQ4	BAP29_HUMAN	lasmic (Potential).	2	CAGGATCGTTTAG	0.299	
-	4	492	e_Mutation_p.G74E	NM_012252	NP_036384	O14948	TFEC_HUMAN	anscriptional transactivation	1	GAAATTCCTTGTT	0.333	
+	2	755	h.1_Missense_Mu	NM_000245	NP_000236	P08581	MET_HUMAN	ular (Potential).|Sema.	159	GTAAAGGACCGG	0.463	
+	6	809	pa.1_Missense_Mu	NM_005011	NP_005002	Q16656	NRF1_HUMAN		1	GCAAGCCCATCT	0.542	
+	11	1529	a.1_Missense_Mu	NM_005011	NP_005002	Q16656	NRF1_HUMAN	transcriptional activation.	1	GCAACGGACCAG	0.602	
+	5	568	e_Mutation_p.G78	NM_001868	NP_001859	P15085	CBPA1_HUMAN		1	CGGGGGGCAGT	0.622	
+	6	717	qf.2_Missense_Mu	NM_002402	NP_002393	Q5EB52	MEST_HUMAN		2	CTGGTCGGCTTA	0.468	rs142718124
-	2	497	n_p.E90K|PLXNA4_	NM_020911	NP_065962	Q9HCM2	PLXA4_HUMAN	ular (Potential).|Sema.	1	TGTCCTCGTCCG	0.547	
-	11	1848	3vtv.2_Missense_M	NM_194071	NP_919047	Q70SY1	CR3L2_HUMAN	nenal (Potential).	160	ACTTCTCCAGGCT	0.547	
+	2	253	0lnb.2_Missense_	NM_001085429	NP_001078898	A2RRL7	TM213_HUMAN	cellular (Potential).	0	ACCCTGGAGCAG	0.562	
+	13	1788	AS1_uc003vvi.2_M	NM_001130966	NP_001124438	P24557	THAS_HUMAN	lasmic (Potential).	3	CTGCTCCACGTG	0.692	
-	15	1859_1860		NM_004333	NP_004324	P15056	BRAF_HUMAN	rotein kinase_R603>I(2)|p.T	18290	GATTTCACTGTAG	0.366	rs121913378
-	1	553		NM_176817	NP_789787	P59533	T2R38_HUMAN	Name=4; (Potential).	2	ACAGAGGACAGT	0.453	

+	1	595		NM_176881	NP_795362	P59534	T2R39_HUMAN	cellular (Potential).		1	AAGAAAACATACT	0.438	
-	6	2601	wcu.3_Nonsense_	NM_014690	NP_055505	Q86XD5	F131B_HUMAN			0	CTTCTCGTGGGG	0.597	
-	4	1978	ense_Mutation_p.W	NM_014690	NP_055505	Q86XD5	F131B_HUMAN			0	TCCCCCAGCCCT	0.612	
+	1	364		NM_012365	NP_036497	Q96R48	OR2A5_HUMAN	lasmic (Potential).		3	TACGATCGGTACA	0.468	rs139541008
+	70	9759_9760		NM_198455	NP_940857	A2VEC9	SSPO_HUMAN	SP type-1 12.		0	GCTGGGGGATGC	0.703	
+	4	479	362_uc003wgm.2_	NM_001099220	NP_001092690	O60290	ZN862_HUMAN			1	AGGTCCCACCAC	0.517	
+	2	903	3_uc003wip.2_Spli	NM_004769	NP_004760	Q9UHC3	ACCN3_HUMAN			2	GCCCCAGATCTTC	0.572	
-	2	848		NM_001098834	NP_001092304	Q14549	GBX1_HUMAN			0	CCTCTTCCTCCTC	0.592	
-	60	9821	p.W2473*|CSMD1_	NM_033225	NP_150094	Q96PZ7	CSMD1_HUMAN	Extracellular (Potential).		25	CCTTTCCACACCC	0.557	
-	4	6182		NM_178857	NP_849188	Q8IWN7	RP1L1_HUMAN			8	GGGTCTCCACTTC	0.597	
-	9	1336	e_Mutation_p.E398	NM_138715	NP_619729	P21757	MSRE_HUMAN	xtracellular (Potential).		1	GCACTTCCCAGC	0.542	
+	2	967		NM_000015	NP_000006	P11245	ARY2_HUMAN			2	ATGGATCCCTTAC	0.274	
-	8	1225	e_Mutation_p.E25	NM_001135691	NP_001129163	P54219	VMAT1_HUMAN	l, vesicle (Potential).		2	CAAACTCGTACAT	0.522	rs144299315
-	4	941	xbj.3_Missense_M	NM_001099335	NP_001092805	Q92561	PHYIP_HUMAN	onectin type-III.		0	GTACTCCGTGCC	0.642	
+	22	2820	nse_Mutation_p.L8	NM_018068	NP_060538	Q8TC59	PIWL2_HUMAN	Piwi.		1	TCTATCTTCTTGC	0.398	
+	14	1545	se_Mutation_p.D25	NM_014265	NP_055080	Q9UKQ2	ADA28_HUMAN	Extracellular (Potential).		5	CCTGATGATAGAT	0.502	
+	16	1917	ec.2_Missense_Mu	NM_003817	NP_003808	Q9H2U9	ADAM7_HUMAN	ar (Potential).|Cys-rich.		5	GACATTGGCCTGC	0.373	
-	15	1704	xek.2_Intron|EBF2_	NM_022659	NP_073150	Q9HAK2	COE2_HUMAN		p.G563R(1)	4	TGAATCCATTTCC	0.493	rs144787348
-	13	1182	.2_Intron|EBF2_uc	NM_022659	NP_073150	Q9HAK2	COE2_HUMAN			4	ATGTCCTACAAAA	0.488	
-	1	4630		NM_031271	NP_112561	Q9BXT5	TEX15_HUMAN			7	TAATTTCCCCCTT	0.378	
-	30	3653	IK1_uc003xoj.2_M	NM_020476	NP_065209	P16157	ANK1_HUMAN			9	GTGGTTCCTGTTA	0.537	
-	17	2740	DNL_uc003xqt.3_F	NM_144651	NP_653252	A1KZ92	PXDNL_HUMAN			2	TAGACTGAATCCA	0.662	
-	17	2622	DNL_uc003xqt.3_F	NM_144651	NP_653252	A1KZ92	PXDNL_HUMAN			2	AACAAGGAGGGT	0.692	
-	6	1173	n_p.R278*|PCMTD	NM_052937	NP_443169	Q96MG8	PCMD1_HUMAN			0	TCTTTCTTTTCCT	0.363	
+	4	3384	P1_uc011ldy.1_Intr	NM_006269	NP_006260	P56715	RP1_HUMAN			12	AAACTCCAAAAGA	0.418	
+	1	130		NM_052898	NP_443130	Q5GH76	XKR4_HUMAN			2	TGCAGGGATTGG	0.443	
+	8	962	n.1_RNA|CSPP1_u	NM_001077204	NP_001070672	Q1MSJ5	CSPP1_HUMAN			5	GAGGATCGTGTTT	0.373	rs114953032
+	3	270	lyy.1_Missense_M	NM_052958	NP_443190	Q49A92	CH034_HUMAN			1	CAGAATCCAAAGC	0.308	
+	6	557	p.E170K|C8orf34_	NM_052958	NP_443190	Q49A92	CH034_HUMAN			1	CTTCAGGAAACAC	0.388	
+	3	2833		NM_004770	NP_004761	Q92953	KCNB2_HUMAN	lasmic (Pote	p.P749S(1)	7	ACTACCCCGCAG	0.562	rs143326877
+	2	2353	au.1_Nonsense_Mu	NM_024721	NP_078997	Q86UP3	ZFHX4_HUMAN	C2H2-type 2.		15	AAATATCAGCAGA	0.517	
-	2	564	_p.R41K|TPD52_u	NM_001025252	NP_001020423	P55327	TPD52_HUMAN	Potential.	p.R81del(1)	1	AGTTCTCTTCTTA	0.428	
-	2	199	P2_uc010lzv.1_Int	NM_002677	NP_002668	P02689	MYP2_HUMAN			0	AAATTTCCCAGT	0.398	
-	8	1474	c.1_Missense_Muta	NM_015668	NP_056483	Q8NE09	RGS22_HUMAN			7	TCTCTCCCAATGT	0.343	
-	5	545	hb.1_Missense_M	NM_152628	NP_689841	Q8N9S9	SNX31_HUMAN			0	ATAATTTCGATTCT	0.368	
-	57	9295	nt.2_Missense_Mu	NM_198123	NP_937756	Q7Z407	CSMD3_HUMAN	Extracellular (Potential).		63	AATGAGGTTGTGA	0.393	
+	3	1420		NM_014943	NP_055758	Q9Y6X8	ZHX2_HUMAN	omodimerization.|Required		2	AAGTTTCCTTACC	0.502	
+	2	2310	n_p.S99F|FAM83A	NM_032899	NP_116288	Q86UY5	FA83A_HUMAN			4	CCAGCTCCCTACA	0.662	
-	1	1098	nds.2_Missense_M	NM_001115	NP_001106	P40145	ADCY8_HUMAN	ical; (Potential).		6	TGTAGGTGGCGA	0.672	
-	5	1213		NM_152888	NP_690848	Q8NFW1	COMA1_HUMAN	SP N-terminal.		13	AGATTTCCTTCAC	0.453	
-	4	710	eu.2_Missense_Mu	NM_001029976	NP_001025147	P17020	ZNF16_HUMAN			5	CTGTAGGGATTTC	0.537	
+	22	3629	_p.Q762*|KDM4C_	NM_015061	NP_055876	Q9H3R0	KDM4C_HUMAN			1	ATTATCCAAGGGC	0.448	
-	10	2409	EM1_uc010mic.2_F	NM_144966	NP_659403	Q5H8C1	FREM1_HUMAN	CSPG 3.		5	AATCTTCAAAGAT	0.373	
-	2	384	KN2A_uc010miu.2	NM_000077	NP_000068	P42771	CD2A1_HUMAN	ANK 2.	)|p.V28_V51de	3678	CCACTCGGGCGC	0.677	rs121913387
+	1	783		NM_004039	NP_004030					0	GCATCAGGAAAGA	0.478	
-	4	965_966		NM_001145196	NP_001138668	Q5VVP1	F75A6_HUMAN			0	AGCTTCCATCTGA	0.525	
-	1	1026		NM_001126334	NP_001119806	Q5VV16	FX4L5_HUMAN			0	CCCCGCCCCACC	0.547	

-	2	937		NM_001163	NP_001154	Q02410	APBA1_HUMAN		1	CTCGTCGCGCT	0.726	
+	11	2141	RNA|uc004aho.1_	NM_153267	NP_694999	Q7Z304	MAMC2_HUMAN	MAM 4.	2	GGAGAGTGTAC	0.483	
-	16	2390	ahy.2_Missense_M	NM_001007471	NP_001007472	Q9HCF6	TRPM3_HUMAN	lasmic (Potential).	9	CTGTTCGTCCT	0.567	
+	22	2748	_uc004ajc.1_Splice	NM_138691	NP_619636	Q8TDI8	TMC1_HUMAN		1	AAAATGGTATGA	0.303	
+	3	923	e_Mutation_p.P12	NM_006200	NP_006191	Q92824	PCSK5_HUMAN	Catalytic.	3	ATGATCCCAAGT	0.478	
+	19	2928	SK5_uc004akb.2	NM_006200	NP_006191	Q92824	PCSK5_HUMAN	(Cys-rich motif).	3	AGGAGCTGATG	0.458	
-	8	4931		NM_015225	NP_056040	Q8WUY3	PRUN2_HUMAN		0	TTTTCTCTAAATC	0.368	
-	8	1175		NM_015225	NP_056040	Q8WUY3	PRUN2_HUMAN		0	GACTTCCTTGA	0.552	
-	2	1658	bq.1_Missense_M	NM_133445	NP_597702	Q8TCU5	NMD3A_HUMAN	ellular (Potential).	7	CCAACGAAGTT	0.512	
+	1	200		NM_001004485	NP_001004485	Q8NGS4	O13F1_HUMAN	Name=2; (Potential).	3	TCTCTCCTTTCT	0.483	
-	7	983	bea.2_Missense_M	NM_019114	NP_061987	Q9H329	E41LB_HUMAN	FERM.	3	GAACCGAAACT	0.443	
+	14	2478	ez.1_Missense_Mu	NM_005592	NP_005583	O15146	MUSK_HUMAN	e.|Cytoplasmic (Potential).	6	CTCTGGGAGATC	0.527	
-	7	824	rf84_uc004bfq.2_	NM_173521	NP_775792	Q5VXU9	CI084_HUMAN		2	TCAATTCCATGC	0.353	
+	1	442		NM_001004457	NP_001004457	Q8NGR9	OR1N2_HUMAN	lasmic (Potential).	4	CACTCCATTAC	0.522	
-	11	2007	p.P535L|CIZ1_uc	NM_001131016	NP_001124488	Q9ULV3	CIZ1_HUMAN		4	GCTGAGGCTCC	0.667	
+	4	550	1mbx.1_Missense	NM_001136557	NP_001130029	Q5VW38	GP107_HUMAN		1	TGAATTACTGTA	0.363	
+	11	1096	p.S228F|ASS1_uc	NM_000050	NP_000041	P00966	ASSY_HUMAN		1	GACCTCCTTGG	0.652	
+	15	2213	e_Mutation_p.P13	NM_005085	NP_005076	P35658	NU214_HUMAN	approximate repeats.	16	AGATCCTGTAAT	0.448	
+	24	3598	_Missense_Mutat	NM_139025	NP_620594	Q76LX8	ATS13_HUMAN	SP type-1 7.	6	TGGACGAGGCG	0.667	
+	7	1473		NM_000093	NP_000084	P20908	CO5A1_HUMAN	nhelical region.	11	GAACCCCGACC	0.592	
+	44	3896		NM_000093	NP_000084	P20908	CO5A1_HUMAN	le-helical region.	11	AGGGGGACAAA	0.617	
-	11	1852	p.G508R|CAMSA	NM_015447	NP_056262	Q5T5Y3	CAMP1_HUMAN		3	TCTCCCTTCCC	0.532	
-	10	1607	H1_uc004cia.1_5	NM_017617	NP_060087	P46531	NOTC1_HUMAN	GF-like 14; calcium-binding	856	TGCAGGGGGTG	0.647	
-	3	281	u.1_Missense_Mu	NM_003792	NP_003783	O60869	EDF1_HUMAN	ype.|Interaction with NR5A	0	CTGCCGACCTT	0.632	
+	2	324	|NDOR1_uc011m	NM_014434	NP_055249	Q9UHB4	NDOR1_HUMAN		0	TGAAGGTAAGG	0.512	
-	4	809		NM_015419	NP_056234	Q9NR99	MXRA5_HUMAN	LRRCT.	8	TCCACGGATTTC	0.478	
+	16	3294	mij.1_Missense_M	NM_014728	NP_055543	Q14CM0	FRPD4_HUMAN		13	AGTCAGAAAAC	0.547	
+	10	953		NM_005089	NP_005080	Q15696	U2AFM_HUMAN	RRM.	3	CTGCCCCGTGA	0.428	
-	5	1007	fb.2_Missense_Mu	NM_153346	NP_699177	Q8NDZ0	BEND2_HUMAN		5	CATTTTCATTTTC	0.433	
-	3	496	4czl.2_Missense_	NM_031892	NP_114098	Q96B97	SH3K1_HUMAN		0	TTTCTTCATCTC	0.393	
+	3	296	mjn.1_Missense_	NM_014927	NP_055742	Q8WXI2	CNKR2_HUMAN	CRIC.	2	TAAAAACCCTTTC	0.303	
+	9	2561	se_Mutation_p.S8	NM_003410	NP_003401	P17010	ZFX_HUMAN	2H2-type 12.	2	TTATTTCCATTCA	0.433	
+	4	1809	4dni.2_Missense_	NM_033215	NP_149992	Q6ZSY5	PPR3F_HUMAN	ellular (Potential).	3	GGAATCGCCTC	0.612	rs148829919
-	1	488		NM_138703	NP_619648	Q8TD90	MAGE2_HUMAN	MAGE 1.	2	GCTTTTCATTCTC	0.537	
+	1	1071	4efm.1_Nonsense	NM_032968	NP_116750	Q9BZA7	PC11X_HUMAN	(Potential).|Cadherin 1.	2	CTGATTCGAATT	0.443	
-	3	438		NM_018476	NP_060946	Q9HBH7	BEX1_HUMAN		1	ATGCATCATATCC	0.517	rs1045082
+	19	3503	.1_Missense_Mut	NM_198465	NP_940867	Q7Z2Y5	NRK_HUMAN		14	TCGTTCGAACCA	0.493	
-	3	1385	m.1_Missense_M	NM_012471	NP_036603	Q9UL62	TRPC5_HUMAN	nic (Potential).|ANK 4.	1	TGATTTCGTAGTT	0.512	
+	3	1024		NM_001004308	NP_001004308	Q6ZR62	ZCH16_HUMAN		1	AGGATGAAGAG	0.473	
+	3	367	e_Mutation_p.P62	NM_018990	NP_061863	O75995	SASH3_HUMAN		3	CACCCCAGAAG	0.547	
-	8	1610	_p.E447K|IGSF1_	NM_001555	NP_001546	Q8N6C5	IGSF1_HUMAN	otential).|Ig-like C2-type 5.	5	ATGTTTCTCTTTC	0.463	
+	6	659	e_Mutation_p.M13	NM_018666	NP_061136	Q9NXZ1	SAGE1_HUMAN		3	AGAATGGAAAA	0.463	
+	6	2218	p.D438N|GPR112	NM_153834	NP_722576	Q8IZF6	GP112_HUMAN	ellular (Potential).	12	CAACTGATGAA	0.498	
-	1	848	uc004fbf.1_RNA	NM_004065	NP_004056	P51861	CDR1_HUMAN		0	CAAATCCAGGT	0.438	
-	7	881	RE_uc011myd.1_	NM_004961	NP_004952	P78334	GBRE_HUMAN		2	CAAACCGCCTG	0.493	
-	5	625	4ffl.2_Missense_	NM_001011543	NP_001011543	P43363	MAGAA_HUMAN		0	AACCTCCTCTG	0.383	
+	3	1002	_Mutation_p.E270	NM_005363	NP_005354	P43360	MAGA6_HUMAN	MAGE.	0	TGCTATGAGTTC	0.527	

+	15	2743	P9Y_uc010nwu.1_I	NM_004654	NP_004645	O00507	USP9Y_HUMAN		0	TTTTATCGCCATG	0.348	
+	2	161	ALI1_uc010oie.1_F	NM_003462	NP_003453	O14645	IDLC_HUMAN		2	AGGCTCGGCTA	0.577	
-	1	130	on_p.P5S|SLAMF	NM_033438	NP_254273	Q96A28	SLAF9_HUMAN		1	CCAAGGAAAGG	0.587	
-	1	410	AMF1_uc010pjm.1	NM_003037	NP_003028	Q13291	SLAF1_HUMAN	cellular (Potential).	2	CGTAGCTTGCCC	0.557	
+	10	1454	e_Mutation_p.P38	NM_203459	NP_982284	Q08AD1	CAMP2_HUMAN		4	ATTTGCCTTCTAC	0.343	
+	13	6500		NM_016343	NP_057427	P49454	CENPF_HUMAN	ction with NDE1 and NDEL	13	TGAGCTCAACAC	0.512	
+	17	2318	kj.1_Missense_Mu	NM_001080512	NP_001073981	Q9H694	BICC1_HUMAN		4	CTATCAAGGAGT	0.448	
+	1	589		NM_207186	NP_997069	Q9H209	O10A4_HUMAN	cellular (Potential).	1	GTGTTTGAACTG	0.498	
+	1	509		NM_001004706	NP_001004706	Q8NGI4	OR4DB_HUMAN	cellular (Potential).	2	TCTGTGGACCCA	0.507	
+	8	1722		NM_025004	NP_079280	Q0P6D6	CCD15_HUMAN		2	TCTCCCCAAAG	0.403	rs112861775
+	14	1644	_p.S375F|DCAF4_	NM_015604	NP_056419	Q8WV16	DCAF4_HUMAN		3	GGGCTCCCGGG	0.637	
+	2	334	e_Mutation_p.P32	NM_014444	NP_055259	Q9UGJ1	GCP4_HUMAN		3	GACTTCCCTTTC	0.527	
-	4	532	p.R108C|ACSM2E	NM_182617	NP_872423	Q68CK6	ACS2B_HUMAN	p.R108C(1)	5	CACACGATCCC	0.562	rs148136861
+	9	1649_1650	_5'Flank|EIF4A1_u	NM_015670	NP_056485	Q9H4L4	SENP3_HUMAN	Protease.	2	AATCCCCATCCA	0.505	
-	12	1798	P1_uc002hxo.1_M	NM_177977	NP_817084	P54257	HAP1_HUMAN	Glu-rich.	2	CCAGTTCCACCT	0.622	
+	6	903	APT_uc002ijx.3_In	NM_016835	NP_058519	P10636	TAU_HUMAN		1	CTAGGAGACCTG	0.682	
+	10	1551	GB3_uc010wkr.1_R	NM_000212	NP_000203	P05106	ITB3_HUMAN	ial).|Cysteine-rich tandem r	6	CAGGACGAATGC	0.627	rs150951945
-	2	762	B3_uc010dbf.2_5'	NM_002147	NP_002138	P09067	HXB5_HUMAN	Homeobox.	0	GCGCTCGGACA	0.577	
-	9	1740	zp.2_Missense_Mu	NM_005121	NP_005112	Q9UHV7	MED13_HUMAN		2	TCTGAGGAGTTG	0.458	
-	26	7164		NM_000384	NP_000375	P04114	APOB_HUMAN		27	ACCTCTCGATTAA	0.373	
-	24	3231	Missense_Mutatio	NM_021196	NP_067019	Q9BY07	S4A5_HUMAN	cellular (Potential).	9	TTTTTTCCTTCTC	0.527	
+	3	367		NM_001080504	NP_001073973	Q6ZP01	RBM44_HUMAN		4	TTATTAGAGCCA	0.338	
+	2	444		NM_022358	NP_071753	Q9H427	KCNKF_HUMAN	ical; (Potential).	0	CCAGAGCCTGG	0.672	
+	2	1629	zxg.1_Missense_M	NM_080752	NP_542790	Q96MP5	ZSWM3_HUMAN		2	CAGACGCACAG	0.577	rs139419541
-	13	1752	gho.1_Nonsense_	NM_022829	NP_073740	Q8WWT9	S13A3_HUMAN	cellular (Potential).	1	CCAGCTGGAAGA	0.557	
-	12	2016	p.D608N|SCN5A_u	NM_198056	NP_932173	Q14524	SCN5A_HUMAN		9	TGGGTCGCCTG	0.647	
-	13	5830	p.Q1868*|GOLGB1	NM_004487	NP_004478	Q14789	GOGB1_HUMAN	ic (Potential).|Potential.	10	CTTCTTGGATTTG	0.368	
-	9	1116	dx.1_Missense_Mu	NM_024007	NP_076870	Q9UH73	COE1_HUMAN	IPT/TIG.	5	TCCATCCTTCACT	0.468	
-	3	528	p.G121D|HLA-DO	NM_002119	NP_002110	P06340	DOA_HUMAN	ntial).|Alpha-2.|Ig-like C1-ty	0	GTTTGGCCGTTG	0.587	
+	6	421	ense_Mutation_p.C	NM_005588	NP_005579	Q16819	MEP1A_HUMAN	Potential).|Metalloprotease.	3	TTTGATGGGTTG	0.313	
-	22	3581	c.2_Missense_Mu	NM_002844	NP_002835	Q15262	PTPRK_HUMAN	phatase 1.|Cytoplasmic (Po	8	TGGGAGGGTTTG	0.483	
-	2	772	bw.1_Missense_M	NM_013389	NP_037521	Q9UHC9	NPCL1_HUMAN	cellular (Potential).	5	GCAACCCCCTCA	0.632	
-	14	3887_3888		NM_032408	NP_115784	Q9UIG0	BAZ1B_HUMAN		7	TCTGCGGACATA	0.431	rs148299208
+	8	969	_p.P60S|STAG3_u	NM_012447	NP_036579	Q9UJ98	STAG3_HUMAN		8	AGGGGCCAGGG	0.522	
-	4	492	e_Mutation_p.G74E	NM_012252	NP_036384	O14948	TFEC_HUMAN	anscriptional transactivatio	1	GAAATTCCTTGTT	0.333	
+	1	595		NM_176881	NP_795362	P59534	T2R39_HUMAN	cellular (Potential).	1	AAGAAAACATACT	0.438	
+	16	1917	ec.2_Missense_Mu	NM_003817	NP_003808	Q9H2U9	ADAM7_HUMAN	ar (Potential).|Cys-rich.	5	ACATTGGCCTG	0.373	
-	30	3653	IK1_uc003xoj.2_M	NM_020476	NP_065209	P16157	ANK1_HUMAN		9	GTGGTTCCTGTT	0.537	
+	10	953		NM_005089	NP_005080	Q15696	U2AFM_HUMAN	RRM.	3	CTGCCCCGTGA	0.428	
+	19	3503	c.1_Missense_Mut	NM_198465	NP_940867	Q7Z2Y5	NRK_HUMAN		14	TCGTTCGAACCA	0.493	
+	3	1002	e_Mutation_p.E270	NM_005363	NP_005354	P43360	MAGA6_HUMAN	MAGE.	0	TGCTATGAGTTC	0.527	
-	20	1882	p.R557C|CDK11B_	NM_033486	NP_277021	P21127	CD11B_HUMAN	rotein kinase.	1	GGCGCGGTACC	0.687	
-	10	1474	ATA21_uc010occ.	NM_198546	NP_940948	Q7Z572	SPT21_HUMAN		3	TGATTTCCTCTAA	0.542	
-	2	554		NM_152365	NP_689578	Q8NAX2	CA172_HUMAN		2	GCTGCCCATGGT	0.642	
-	8	1333	IA7_uc001cux.2_5	NM_006671	NP_006662	O00341	EAA5_HUMAN	ical; (Potential).	3	GATGGCGGCCA	0.627	
-	13	1443	R11_uc010pbm.1_	NM_001145862	NP_001139334	A4FU01	MTMRB_HUMAN	ularin phosphatase.	1	TGTTCGGGCTT	0.562	
-	2	1066	ie.1_Missense_Mu	NM_007113	NP_009044	Q07283	TRHY_HUMAN	eats of R-R-E-Q-E-E- E-R-	5	tctcctcctcctgctcgcg	0	

-	3	1023		NM_001122965	NP_001116437	Q6XPR3	RPTN_HUMAN	Gln-rich.	0	CTGACTGTAGT	0.507	rs12117644
-	18	3154	uc001fdc.1_RNA	NM_014856	NP_055671	O75064	DEN4B_HUMAN	Gln-rich.	1	CTGCCTCTTGA	0.453	
-	2	1266	c010plt.1_5'Flank|	NM_033418	NP_219486	O95568	MET18_HUMAN		0	ACCTACACCAA	0.348	rs1801567
-	6	1408	kv.2_Missense_M	NM_206933	NP_996816	O75445	USH2A_HUMAN	nal.|Extracellular (Potential	26	GAGAGGATGGG	0.443	
+	34	9203	p.I3053M|OBSCN	NM_001098623	NP_001092093	Q5VST9	OBSCN_HUMAN	Ig-like 30.	28	GAGATCGATGC	0.657	
-	1	1019	KG1_uc001jjn.2_I	NM_015235	NP_056050	Q9H0L4	CSTFT_HUMAN	Gly-rich.	1	AGGAGGCAGAC	0.572	
+	4	1231		NM_000314	NP_000305	P60484	PTEN_HUMAN	hatase tensi7_Y68insY(1)|	2334	ACAAGATATACAA	0.279	
-	6	810	h.1_Missense_Mu	NM_002334	NP_002325	O75096	LRP4_HUMAN	ential).|LDL-receptor class	4	AGACTCGTCTG	0.622	
-	1	292		NM_006637	NP_006628	Q13606	OR5I1_HUMAN	ellular (Potential).	1	CACACCCATAAT	0.428	
-	1	617		NM_001004740	NP_001004740	Q8NGP8	OR5M1_HUMAN	Name=5; (Potential).	1	AGAGATTAAAG	0.443	
-	13	1912	CE_uc001nrb.2_F	NM_152718	NP_689931	Q96DN2	VWCE_HUMAN	VWFC 3.	1	TTCTCGGGGGC	0.672	
-	8	2614	p.S614L|TRPC6_	NM_004621	NP_004612	Q9Y210	TRPC6_HUMAN	lasmic (Potential).	4	TGGAATGAACTG	0.328	
-	3	318	_uc001pmu.2_5'Fl	NM_138789	NP_620144	Q8WWB5	PIHD2_HUMAN		1	ATTGGGGAGCT	0.363	
+	13	1942	e_Mutation_p.Y59	NM_005480	NP_005471	Q12815	TROAP_HUMAN	approximate tandem repea	1	AGTCCTACTGTA	0.617	
+	1	255	KC5_uc001set.2_I	NM_004503	NP_004494	P09630	HXC6_HUMAN		3	AGAACCGGATCT	0.562	
-	17	2082	p.P410S|R3HDM2	NM_014925	NP_055740	Q9Y2K5	R3HD2_HUMAN	Gln-rich.	2	AGAGGGAGACT	0.547	
+	26	3147	x.2_Missense_Mu	NM_178826	NP_849148	Q32M45	ANO4_HUMAN	lasmic (Potential).	6	GATACCGGGACT	0.408	
+	8	905		NM_017564	NP_060034	Q8WWQ8	STAB2_HUMAN	r (Potential).|EGF-like 4.	14	TCAATCCATGTT	0.483	
+	2	360		NM_007076	NP_009007	Q9BVA6	FICD_HUMAN		0	ATGCCGCCACC	0.662	
+	2	876	_p.E82K|GPC6_u	NM_005708	NP_005699	Q9Y625	GPC6_HUMAN		0	AAACTCGAATTT	0.413	
-	1	461		NM_001001968	NP_001001968	Q8NH40	OR6S1_HUMAN	Name=4; (Potential).	2	CGAGTCCCCCC	0.607	
+	3	307	HD4_uc010tna.1_	NM_022060	NP_071343	Q8TB40	ABHD4_HUMAN		1	GGGGCGGCGTG	0.577	
-	8	1465	C35F4_uc010apa.	NM_001080455	NP_001073924				2	TCTTTTCCTTCAG	0.522	
+	15	1725	qv.2_Missense_Mu	NM_015197	NP_056012	Q86VP3	PACS2_HUMAN		1	GGTGTGCACGT	0.632	
+	15	2318	_Mutation_p.R39	NM_006122	NP_006113	P49641	MA2A2_HUMAN	enal (Potential).	3	TCTGTGCGCATC	0.672	
-	24	2048	ze.1_Missense_Mu	NM_002582	NP_002573	O95453	PARN_HUMAN		2	GTCAGGAACTT	0.527	
-	16	2723	_p.T663I|KCTD1	NM_001100915	NP_001094385	Q17RG1	KCD19_HUMAN		1	GCAGTGTAAGC	0.552	
-	4	669	.2_5'UTR|KCTD1	NM_001100915	NP_001094385	Q17RG1	KCD19_HUMAN		1	CACTCGCACTC	0.612	
-	34	5280		NM_032821	NP_116210	Q4G0P3	HYDIN_HUMAN		2	AGTTTCCACCA	0.488	
+	14	2519	vof.1_Missense_M	NM_005153	NP_005144	Q14694	UBP10_HUMAN		0	ATTACCGCCGA	0.572	
-	12	2633	CHC14_uc002fkb.	NM_015144	NP_055959	Q8WYQ9	ZCH14_HUMAN		2	CAAACGTGGAC	0.632	
-	4	568	|TP53_uc010cni.1	NM_001126112	NP_001119584	P04637	P53_HUMAN	with HIPK1 (G105_T125del	22245	TGACCGTGCAA	0.542	
-	31	4319		NM_003802	NP_003793	Q9UKX3	MYH13_HUMAN	Potential.	6	TCGCCGTCTCC	0.532	
-	29	4074		NM_002470	NP_002461	P11055	MYH3_HUMAN	Potential.	7	CAGGGCGTGCG	0.552	
+	4	400		NM_002795	NP_002786	P49720	PSB3_HUMAN		0	AGCCAGTCATT	0.517	
-	2	875	_5'Flank|PLEKHH	NM_016602	NP_057686	P46092	CCR10_HUMAN	Name=7; (Potential).	0	CAGTGCGACAT	0.677	
-	18	2941	w.1_Missense_Mu	NM_004104	NP_004095	P49327	FAS_HUMAN		1	GGCACGGGAGG	0.687	
+	1	718		NM_005913	NP_005904	P33032	MC5R_HUMAN	Name=6; (Potential).	6	TCACCGTCACC	0.617	
+	4	1429	YR_uc002kva.2_	NM_012189	NP_036321	O75952	CABYR_HUMAN		0	TTCAATAGTCTC	0.502	rs142770673
-	9	1375		NM_152769	NP_689982	Q8N350	DOS_HUMAN		0	AGGGGCGGGGG	0.692	
-	2	642	N5_uc002mat.1_In	NM_052972	NP_443204	P02750	A2GL_HUMAN		1	CAGCGGACCCC	0.577	
-	4	452	vq.2_Missense_M	NM_021155	NP_066978	Q9NNX6	CD209_HUMAN	|2.|7 X approximate tanden	1	CAGCCGGGTCA	0.567	rs146082308
+	1	85		NM_017682	NP_060152	Q8NFU1	BEST2_HUMAN	ical; (Potential).	2	AGCATCTACAAA	0.547	
+	2	751		NM_173482	NP_775753	Q8IYK2	CC105_HUMAN	Potential.	1	GATATGGAAAAAT	0.498	
-	4	1447	p.K353E|ZNF708_	NM_021269	NP_067092	P17019	ZN708_HUMAN		6	GTTTCTTTCCAG	0.343	
+	29	5900		NM_014727	NP_055542	Q9UMN6	MLL4_HUMAN	Poly-Pro.	11	ATCTCCACCAC	0.657	
+	29	6004		NM_014727	NP_055542	Q9UMN6	MLL4_HUMAN		11	ACTGAGCCCTTC	0.667	

+	29	6164		NM_014727	NP_055542	Q9UMN6	MLL4_HUMAN		11	TGGAGCCCCCC	0.697	
+	98	14321	.2_Missense_Mut	NM_000540	NP_000531	P21817	RYR1_HUMAN		12	ATGGGGACATC	0.612	
+	100	14561	.2_Missense_Mut	NM_000540	NP_000531	P21817	RYR1_HUMAN		12	TTCTTTGCTGCC	0.587	
-	12	2175	se_Mutation_p.A	NM_001081563	NP_001075032	Q09013	DMPK_HUMAN	p.T544M(1)	3	TGACAGCTGGA	0.662	
+	3	296	_p.A75V|NUCB1_	NM_006184	NP_006175	Q02818	NUCB1_HUMAN		0	GGCTGCCAATG	0.582	
+	5	3725		NM_020719	NP_065770	Q9ULL5	PRR12_HUMAN	Pro-rich.	2	CTCATCGGGTG	0.622	
+	2	96	eti.2_Missense_M	NM_033106	NP_149097	Q9UBC7	GALP_HUMAN		0	TCCCTCCGTCC	0.642	
+	4	655	p.R173Q|ZNF324	NM_207395	NP_997278	Q6AW86	Z324B_HUMAN		1	GTACCGGGTGC	0.677	
+	14	1746	512_uc010ylx.1_	NM_032434	NP_115810	Q96ME7	ZN512_HUMAN		1	TTCCAGAAAGT	0.488	
-	1	760	sd.3_Missense_M	NM_021097	NP_066920	P32418	NAC1_HUMAN	ical; (Potential).	4	CACAACACAGA	0.443	
-	9	1458	1_uc010ypn.1_Mi	NM_003400	NP_003391	O14980	XPO1_HUMAN	ex-mediated mRNA export	4	TTTGGTCTCAA	0.348	
-	7	932		NM_005735	NP_005726	P42025	ACTY_HUMAN		1	CAACGTGTACT	0.642	
+	6	596	0zbl.1_Missense_	NM_018460	NP_060930	Q53QZ3	RHG15_HUMAN	PH.	2	CCAAGGAAAAA	0.358	
-	282	81666	843*|TTN_uc010z	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	ACCCTGTCCAG	0.423	
+	3	339		NM_080628	NP_542195	A0PJX2	CT118_HUMAN	TLD.	0	GGGACCAGGAC	0.677	
-	4	598	se_Mutation_p.G1	NM_198433	NP_940835	O14965	AURKA_HUMAN		8	CAGGTCCTGAA	0.383	
-	1	326	GP_uc002yvx.1_	NM_153681	NP_710148	P57054	PIGP_HUMAN		0	TAAATCGCTCTTT	0.478	
-	1	5912	E2_uc002yyx.2_I	NM_182832	NP_878252	Q8WY50	PLAC4_HUMAN		0	tgtccagggtgaggag	0.04	
-	28	6150	i.2_Missense_Mut	NM_198056	NP_932173	Q14524	SCN5A_HUMAN		9	GTTATCGCTGG	0.607	
-	23	4417	G1408E|SCN5A_	NM_198056	NP_932173	Q14524	SCN5A_HUMAN		9	GGTACCCGGCC	0.542	
-	2	310	m.1_Missense_M	NM_000581	NP_000572	P07203	GPX1_HUMAN		1	TGCACGGGAAG	0.617	
-	17	2101	.R523C|ITIH4_uc	NM_002218	NP_002209	Q14624	ITIH4_HUMAN		3	CAGACGGCGGA	0.622	
+	18	1678	p.E450K|CACNA2	NM_018398	NP_060868	Q8IZS8	CA2D3_HUMAN	lar (Potential).|Cache.	7	AGTACGAAGAA	0.443	
-	5	506		NM_018338	NP_060808	Q96MT7	WDR52_HUMAN		1	TACTGTCGTCCA	0.423	
-	5	916	ln.2_RNA|PAQR3	NM_001040202	NP_001035292	Q6TCH7	PAQR3_HUMAN	enal (Potential).	0	ACGGGGTGCAA	0.353	
+	10	1421	e_Mutation_p.K19	NM_005983	NP_005974	Q13309	SKP2_HUMAN		4	CATCAAATGCCG	0.453	
+	1	672	uc011ctk.1_Intron	NM_032567	NP_115956	Q9BXG8	SPZ1_HUMAN		1	AAACAGGAGATG	0.358	
+	8	3268	e_Mutation_p.N98	NM_001105251	NP_001098721	Q7Z3T8	ZFY16_HUMAN		0	ACAGCAATTTAC	0.353	
+	20	4090	98_uc003kjt.2_5'	NM_032119	NP_115495	Q8WXG9	GPR98_HUMAN	ellular (Potential).	16	TTACCGGACTAG	0.443	
+	10	1820		NM_133369	NP_588610	Q6ZN44	UNC5A_HUMAN	toplasmic (Potential).	1	GGGCAGCTGGG	0.667	
+	5	723	11dme.1_Intron|HLA-J_uc003nou.3_RNA|HLA-J_uc003nov.3_RNA						0	CTGAGAGGCAA	0.438	rs113017032
+	56	7970	y.2_Missense_Mu	NM_002224	NP_002215	Q14573	ITPR3_HUMAN	lasmic (Potential).	19	CTACACGGGCC	0.537	
+	12	1398	vn.1_Missense_M	NM_007058	NP_008989	Q9UMQ6	CAN11_HUMAN	Domain III.	2	ACTGGCGGCAT	0.612	
-	2	976		NM_001003760	NP_001003760	Q9H511	KLH31_HUMAN		1	TTGCATCATTCT	0.408	
-	12	1237	nse_Mutation_p.F	NM_014841	NP_055656	O60641	AP180_HUMAN		1	TGGCTGGAGAA	0.453	
-	3	414	q.2_Missense_Mu	NM_001080453	NP_001073922	Q8N201	INT1_HUMAN		0	CGACGGAGAAAT	0.577	
+	8	902	k.2_Missense_Mu	NM_001159767	NP_001153239	Q9Y6E2	BZW2_HUMAN		2	AGGAGCTTTCC	0.488	
+	35	5930		NM_003777	NP_003768	Q96DT5	DYH11_HUMAN	1 (By similarity).	15	TGGCAGTACAA	0.438	
+	9	1413	_5'Flank|AEBP1_	NM_001129	NP_001120	Q8IUX7	AEBP1_HUMAN		0	GAAAGGCGAG	0.647	
+	16	2096	n_p.V570I|DYNC1	NM_004411	NP_004402	O14576	DC1I1_HUMAN	WD 7.	4	ATGACGTTGGA	0.473	rs145694237
+	17	3762	Mutation_p.S493F	NM_022742	NP_073579	Q96JN2	CC136_HUMAN	ical; (Potential).	2	TCTTCTCCTTGC	0.532	
-	15	1860		NM_004333	NP_004324	P15056	BRAF_HUMAN	rotein kinas_R603>I(2)|p.T	18290	GATTTCACTGTA	0.368	
+	8	1601		NM_014141	NP_054860	Q9UHC6	CNTP2_HUMAN	1.|Extracellular (Potential).	11	ACAGGGAAATTT	0.433	
+	2	890		NM_024012	NP_076917	P47898	5HT5A_HUMAN	smic (By similarity).	3	CGTGGCGGGAG	0.607	
-	14	1457	ck.1_Missense_M	NM_001464	NP_001455	Q99965	ADAM2_HUMAN	r (Potential).|Disintegrin.	2	CAGATGATCCA	0.408	
+	10	988	pc.2_Missense_M	NM_005662	NP_005653	Q9Y277	VDAC3_HUMAN	nded; (By similarity).	1	ACTGGAAGCTT	0.398	
+	4	4659		NM_001001670	NP_001001670	Q6ZQQ2	F75D1_HUMAN		0	GCCTGGTGTGT	0.517	

-	5	1131		NM_017561	NP_060031	A1L443	FA22F_HUMAN	Pro-rich.	0	GTGGGCGTTGGT	0.692	
-	18	3549	ua.1_Missense_Mu	NM_153366	NP_699197	Q4LDE5	SVEP1_HUMAN		7	GGACACGATTCA	0.423	
-	26	2318	_p.N394I|TEX11_u	NM_001003811	NP_001003811	Q8IYF3	TEX11_HUMAN		5	ATGTCATTGCATC	0.388	
-	10	1474	ATA21_uc010occ.1	NM_198546	NP_940948	Q7Z572	SPT21_HUMAN		3	TGATTTCCTCTAA	0.542	
-	2	554		NM_152365	NP_689578	Q8NAX2	CA172_HUMAN		2	GCTGCCCATGGT	0.642	
+	8	1012	ciy.2_Missense_Mu	NM_001255	NP_001246	Q12834	CDC20_HUMAN		0	GGCCACACTGA	0.562	
-	6	1408	kv.2_Missense_Mu	NM_206933	NP_996816	O75445	USH2A_HUMAN	nal.|Extracellular (Potential	26	AGAGAGGATGGG	0.443	
+	4	1231		NM_000314	NP_000305	P60484	PTEN_HUMAN	hatase tensi7_Y68insY(1)|	2334	ACAAGATATACAA	0.279	
-	4	531	_Mutation_p.D144	NM_199292	NP_954986	P07101	TY3H_HUMAN		0	GCCAGGTCCCCT	0.697	
-	1	292		NM_006637	NP_006628	Q13606	OR5I1_HUMAN	cellular (Potential).	1	CACACCCATAATA	0.428	
-	8	2614	_p.S614L|TRPC6_	NM_004621	NP_004612	Q9Y210	TRPC6_HUMAN	lasmic (Potential).	4	TGGAATGAACTG	0.328	
+	29	6083	Flank|PFDN5_uc0	NM_012291	NP_036423	Q14674	ESPL1_HUMAN		3	GATTTGTATATGT	0.547	
-	7	795		NM_024057	NP_076962	Q8NFH4	NUP37_HUMAN		1	TATTTTGAGGATA	0.353	
+	8	905		NM_017564	NP_060034	Q8WWQ8	STAB2_HUMAN	r (Potential).|EGF-like 4.	14	TCAATCCATGTTT	0.483	
+	2	876	_p.E82K|GPC6_u	NM_005708	NP_005699	Q9Y625	GPC6_HUMAN		0	AAACTCGAATTT	0.413	
+	4	1054	ml.2_Missense_Mu	NM_004274	NP_004265	Q13023	AKAP6_HUMAN		21	AGGTATCTCAAG	0.468	
-	8	1465	C35F4_uc010apa.	NM_001080455	NP_001073924				2	TCTTTTCCTTCAG	0.522	
+	8	902	IP_uc002dcx.3_R	NM_006985	NP_008916	Q9UND3	NPIP_HUMAN	Pro-rich.	0	CCTCAGCGGATG	0.557	
-	2	1257	uc002dyl.1_5'Flank	NM_024671	NP_078947	Q9H5H4	ZN768_HUMAN	C2H2-type 4.	0	TCGCAGGAGGTA	0.632	
-	34	5280		NM_032821	NP_116210	Q4G0P3	HYDIN_HUMAN		2	AGTTTCCACCAG	0.488	
-	4	568	R|TP53_uc010cni.1	NM_001126112	NP_001119584	P04637	P53_HUMAN	with HIPK1 (G105_T125del	22245	CTGACCGTGCAA	0.542	
-	7	554	3_Intron|PIK3R5_u	NM_014308	NP_055123	Q8WYR1	PI3R5_HUMAN		5	CAGCACGGTGC	0.642	rs149885535
+	19	2544	_p.E479G|KSR1_u	NM_014238	NP_055053	Q8IVT5	KSR1_HUMAN	rotein kinase.	4	GCGGGGAAGGAA	0.572	
-	18	2941	w.1_Missense_Mu	NM_004104	NP_004095	P49327	FAS_HUMAN		1	GGCACGGGAGG	0.687	
-	1	757	TEC_uc010xaj.1_F	NM_001137671	NP_001131143	B2RU33	POTEC_HUMAN		3	ACAGCACCACTT	0.622	
+	4	1429	BYR_uc002kva.2_	NM_012189	NP_036321	O75952	CABYR_HUMAN		0	CTTCAATAGTCTC	0.502	rs142770673
-	37	5246	p.C223Y|MYO5B_	NM_001080467	NP_001073936	Q9ULV0	MYO5B_HUMAN	Dilute.	5	TCCAGGCAGTAT	0.522	
-	2	642	N5_uc002mat.1_In	NM_052972	NP_443204	P02750	A2GL_HUMAN		1	CAGCGGACCCC	0.577	
-	8	1939	nkc.2_Missense_M	NM_032152	NP_115528	Q96QH2	PRAM_HUMAN	SH3.	0	GTTCTGGGCACG	0.701	
+	2	751		NM_173482	NP_775753	Q8IYK2	CC105_HUMAN	Potential.	1	GATATGGAAAAAT	0.498	
+	29	6004		NM_014727	NP_055542	Q9UMN6	MLL4_HUMAN		11	ACTGAGCCCTTC	0.667	
+	29	6164		NM_014727	NP_055542	Q9UMN6	MLL4_HUMAN		11	CTGGAGCCCCCC	0.697	
+	98	14321	u.2_Missense_Mut	NM_000540	NP_000531	P21817	RYR1_HUMAN		12	CATGGGGACATC	0.612	
+	100	14561	u.2_Missense_Mut	NM_000540	NP_000531	P21817	RYR1_HUMAN		12	TTCTTTGCTGCC	0.587	
-	5	1308	uj.3_Missense_Mu	NM_182707	NP_874366	Q9UQ74	PSG8_HUMAN	-like C2-type 3.	0	AGCTTTCCTTGC	0.468	
+	3	273	880_uc002pzb.3_	NM_001145434	NP_001138906	Q6PDB4	ZN880_HUMAN	KRAB.	0	AAATAGCAAACA	0.423	
+	11	1400	_p.V391I|BRSK1_	NM_032430	NP_115806	Q8TDC3	BRSK1_HUMAN		6	AATGATGTTGGT	0.393	
+	3	1505		NM_021216	NP_067039	Q9NQZ8	ZNF71_HUMAN	C2H2-type 11.	1	CAGAGCGCCTAC	0.642	
+	3	1069	c002sma.1_Silent_	NM_016170	NP_057254	O43763	TLX2_HUMAN		0	TGCCCCCGGACC	0.726	
-	7	932		NM_005735	NP_005726	P42025	ACTY_HUMAN		1	GCAACGTGTACT	0.642	
-	3	687		NM_001099771	NP_001093241	A5A3E0	POTEF_HUMAN		5	ATCTTGTTCCTGA	0.607	
+	6	596	0zbl.1_Missense_	NM_018460	NP_060930	Q53QZ3	RHG15_HUMAN	PH.	2	GCCAAGGAAAAA	0.358	
-	4	848	f.2_Missense_Mut	NM_003111	NP_003102	Q02447	SP3_HUMAN	ation domain (Gln-rich).	6	CTGTGGTATGAG	0.453	
-	282	81666	843*|TTN_uc010z	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	ACCCTGTCCAG	0.423	
-	4	598	se_Mutation_p.G1	NM_198433	NP_940835	O14965	AURKA_HUMAN		8	CAGGTCCTGAA	0.383	
-	1	326	GP_uc002yvx.1_M	NM_153681	NP_710148	P57054	PIGP_HUMAN		0	TAAATCGCTCTTT	0.478	
-	28	6150	i.2_Missense_Mut	NM_198056	NP_932173	Q14524	SCN5A_HUMAN		9	GGTTATCGCTGG	0.607	

+	18	1678	p.E450K|CACNA2	NM_018398	NP_060868	Q8IZS8	CA2D3_HUMAN	lar (Potential).|Cache.	7	TAGTACGAAGAA	0.443	
+	13	3836	p.A355T|PPP2R3	NM_002718	NP_002709	Q06190	P2R3A_HUMAN		7	TTTGCCGCTGAG	0.448	
-	5	485	r.1_Intron|PHC3_u	NM_024947	NP_079223	Q8NDX5	PHC3_HUMAN	Ser-rich.	2	GGGAACGGCTTA	0.453	
-	13	1384	se_Mutation_p.A42	NM_001313	NP_001304	Q14194	DPYL1_HUMAN		2	CCACCGCCTGC	0.458	
+	10	1421	e_Mutation_p.K19	NM_005983	NP_005974	Q13309	SKP2_HUMAN		4	CATCAAATGCCG	0.453	
+	8	3268	e_Mutation_p.N98	NM_001105251	NP_001098721	Q7Z3T8	ZFY16_HUMAN		0	ACAGCAATTTAC	0.353	
+	1	645		NR_024356					0	GCTCATCGGGAT	0.662	
-	2	976		NM_001003760	NP_001003760	Q9H511	KLH31_HUMAN		1	CTTGCATCATTCT	0.408	
-	3	414	xq.2_Missense_Mu	NM_001080453	NP_001073922	Q8N201	INT1_HUMAN		0	CGACGGAGAAAT	0.577	
+	8	902	k.2_Missense_Mut	NM_001159767	NP_001153239	Q9Y6E2	BZW2_HUMAN		2	AGGAGCTTTCC	0.488	
+	16	2039	e.1_Missense_Mu	NM_031414	NP_113602	Q9BXU1	STK31_HUMAN		9	TCAGATGATCCT	0.308	
+	13	1662	ldp.2_Missense_M	NM_020879	NP_065930	Q8IYE0	CC146_HUMAN		2	GACTGAGAGAGT	0.313	
+	16	2096	n_p.V570I|DYNC1	NM_004411	NP_004402	O14576	DC1I1_HUMAN	WD 7.	4	TATGACGTTGGA	0.473	rs145694237
+	17	3762	Mutation_p.S493F	NM_022742	NP_073579	Q96JN2	CC136_HUMAN	ical; (Potential).	2	TCTTCTCCTTGC	0.532	
-	15	1860		NM_004333	NP_004324	P15056	BRAF_HUMAN	rotein kinas_R603>I(2)|p.T	18290	GATTTCACTGTA	0.368	
+	8	1601		NM_014141	NP_054860	Q9UHC6	CNTP2_HUMAN	1.|Extracellular (Potential).	11	ACAGGGAAATTT	0.433	
-	14	1457	ck.1_Missense_M	NM_001464	NP_001455	Q99965	ADAM2_HUMAN	r (Potential).|Disintegrin.	2	GCAGATGATCCAT	0.408	
+	10	988	pc.2_Missense_Mu	NM_005662	NP_005653	Q9Y277	VDAC3_HUMAN	nded; (By similarity).	1	AACTGGAAGCTT	0.398	
-	14	2175		NM_031415	NP_113603	Q9BYG8	GSDMC_HUMAN		3	GATGCTCCTTAC	0.468	
+	6	1697		NM_001702	NP_001693	O14514	BAI1_HUMAN	(Potential).|TSP type-1 4.	8	GTGCCAGGGCC	0.697	
+	21	3206	_p.F338L|RGS3_u	NM_144488	NP_652759	P49796	RGS3_HUMAN		3	CCTCTTCTTCACA	0.607	
-	6	637	p.R123H|PRICKLI	NM_006150	NP_006141	O43900	PRIC3_HUMAN	l zinc-binding 1.	1	CCTGCACGGCTG	0.562	
-	12	1474	_p.P402L|FOXP3_	NM_014009	NP_054728	Q9BZS1	FOXP3_HUMAN		0	GGCCAGGTGTA	0.622	
-	26	2318	_p.N394I|TEX11_u	NM_001003811	NP_001003811	Q8IYF3	TEX11_HUMAN		5	ATGTCATTGCAT	0.388	
-	18	2892	ID5_uc001amc.1_	NM_015557	NP_056372	Q8TDI0	CHD5_HUMAN		12	TGAGCCGCCTG	0.592	
-	6	1389	nx.2_Missense_M	NM_001079843	NP_001073312	Q86V15	CASZ1_HUMAN		1	GTCGGGGCTGC	0.632	
+	5	738	M1_uc001axg.1_M	NM_017556	NP_060026	Q8WUP2	FBLI1_HUMAN	Pro-rich.	1	GTGCTTCCTGAC	0.652	
-	3	1243	_p.S231L|HSPB7_	NM_014424	NP_055239	Q9UBY9	HSPB7_HUMAN		0	GAGCCGAGGTC	0.642	
-	2	66	G2D_uc009vpo.2_	NM_012400	NP_036532	Q9UNK4	PA2GD_HUMAN		0	GGATTGGAATCA	0.577	
-	5	536	p.P94S|EIF4G3_u	NM_003760	NP_003751	O43432	IF4G3_HUMAN		1	AAAAGGACCTG	0.423	
+	4	534	se_Mutation_p.P3	NM_000478	NP_000469	P05186	PPBT_HUMAN		5	AAGTTCCCCTTC	0.473	
-	65	8508	qd.2_Missense_Mu	NM_005529	NP_005520	P98160	PGBM_HUMAN	ike C2-type 13.	9	CACCTGGGGCT	0.677	
+	4	383	_p.H108N|GRHL3_	NM_021180	NP_067003	Q8TE85	GRHL3_HUMAN		1	CCCACACACCTC	0.522	
+	8	1610	C21_uc010ofa.1_M	NM_022778	NP_073615	Q6P2H3	CEP85_HUMAN	Potential.	0	CCATCAGAAGCA	0.542	
+	7	807	os.2_Missense_M	NM_152660	NP_689873	Q8TAV0	FA76A_HUMAN	Potential.	0	TCAAAAGGATCA	0.448	
-	4	3698	se_Mutation_p.P82	NM_024503	NP_078779	Q5T1R4	ZEP3_HUMAN	TRAF-dependent NF-Kapp	6	GTGATGGGAACT	0.552	rs144929442
-	4	1479	se_Mutation_p.S8	NM_024503	NP_078779	Q5T1R4	ZEP3_HUMAN		6	TGGACGGATGCT	0.607	
+	12	1672	nse_Mutation_p.Q	NM_001017922	NP_001017922	Q96PL5	ERMAP_HUMAN	lasmic (Potential).	1	GCCCTTCAGGAG	0.562	
+	14	2321	_p.Q704K|TIE1_uc	NM_005424	NP_005415	P35590	TIE1_HUMAN	cellular (Potential).	7	CCAGTCCAAGAG	0.642	
+	20	4028	wt.2_Missense_M	NM_002840	NP_002831	P10586	PTPRF_HUMAN	cellular (Potential).	10	TGAAGGAACCC	0.592	
-	28	4910	ctz.2_Missense_M	NM_015269	NP_056084	Q5TAX3	TUT4_HUMAN	Pro-rich.	3	CCAGGGAATTT	0.463	
-	5	1273	e_Mutation_p.P347	NM_015269	NP_056084	Q5TAX3	TUT4_HUMAN		3	GGAAGGAGGTG	0.328	
-	3	1480		NM_201546	NP_963840	Q5VXM1	CDCP2_HUMAN	CUB 2.	1	GGGTGGGGCCA	0.632	
-	4	696	yr.1_Nonsense_M	NM_021080	NP_066566	O75553	DAB1_HUMAN		3	CTACTTGAAGTT	0.453	
+	8	1092	j.3_Nonsense_Mu	NM_018291	NP_060761	Q96C11	FGGY_HUMAN		1	ATCTGTGGAACG	0.572	
-	3	402		NM_152377	NP_689590	Q8N0U7	CA087_HUMAN		2	TTGCCCCTGTTA	0.368	
+	7	1276_1277	K7_uc001dap.2_I	NM_014495	NP_055310	Q9Y5C1	ANGL3_HUMAN	nogen C-terminal.	0	AGTGTGGAGAAA	0.391	

-	11	1820	73_uc001dgi.3_Mi	NM_001002912	NP_001002912	Q5RHP9	CA173_HUMAN	Glu-rich.	5	TCTTTTTTATCAT	0.403	
+	6	716	HN2_uc001div.2_	NM_012302	NP_036434	O95490	LPHN2_HUMAN	otential).|Olfactomedin-like	9	CCCTATCGTACC	0.398	
+	13	2645	E822K|LPHN2_uc	NM_012302	NP_036434	O95490	LPHN2_HUMAN	ular (Potential).|GPS.	9	CACAGGGAAATT	0.428	
+	16	3119	HN2_uc009wcd.2_	NM_012302	NP_036434	O95490	LPHN2_HUMAN	Name=5; (Potential).	9	ATATGGAGCTTCA	0.358	
-	8	1905	e_Mutation_p.E25	NM_152763	NP_689976	Q5T1N1	AKND1_HUMAN		3	GCTCCTCGTTGG	0.662	
-	11	1958	p.E568*|NOTCH2_	NM_024408	NP_077719	Q04721	NOTC2_HUMAN	ng (Potential).|Extracellular	27	TCTCCTCACACA	0.463	
-	3	1227	h.2_Missense_Mu	NM_014849	NP_055664	Q7L0J3	SV2A_HUMAN	ical; (Potential).	7	AGAAGGCGAAGA	0.532	
-	5	909	eto.2_Missense_M	NM_020205	NP_064590	Q6GQQ9	OTU7B_HUMAN	|OTU.|TRAF-binding.	3	CCAAAGGAAGCA	0.517	
-	3	2451		NM_001009931	NP_001009931	Q86YZ3	HORN_HUMAN	8	3	TGTTGGCCGTGG	0.597	
-	3	1020		NM_016190	NP_057274	Q9UBG3	CRNN_HUMAN	Gln-rich.	3	GTGTCTGGGTGC	0.602	
-	3	326	RL4_uc010phy.1_F	NM_031282	NP_112572	Q96PJ5	FCRL4_HUMAN	otential).|Ig-like C2-type 1.	4	TTTCTCCCCAGT	0.517	
-	8	1547	sn.2_RNA|FCRL3_	NM_052939	NP_443171	Q96P31	FCRL3_HUMAN	5.|Extracellular (Potential).	4	CCTCATGATAAA	0.582	
-	1	367		NM_001004475	NP_001004475	Q8NGX3	O10T2_HUMAN	lasmic (Potential).	3	CATAGCGATCAT	0.478	
-	4	665		NM_003126	NP_003117	P02549	SPTA1_HUMAN	Spectrin 2.	8	GGCCCGCAGCA	0.527	
-	1	772		NM_001005279	NP_001005279	Q8NGY2	OR6K2_HUMAN	Name=6; (Potential).	1	ACATGAGAGTCA	0.468	
-	12	2129	p.G441S|ARHGA	NM_001025598	NP_001020769	Q7Z6I6	RHG30_HUMAN		3	GGGGCCAGCGG	0.567	
-	7	1089	se_Mutation_p.P9	NM_001025598	NP_001020769	Q7Z6I6	RHG30_HUMAN		3	GCAGTGGCCTG	0.587	
-	6	1308	_p.E16K|PVRL4_	NM_030916	NP_112178	Q96NY8	PVRL4_HUMAN	cellular (Potential).	2	AGTCTTCCTGGG	0.602	
-	3	209	p.W12C|DEDD_u	NM_001039712	NP_001034801	O75618	DEDD_HUMAN		0	TTCTGGCCACAC	0.592	
+	1	576		NR_024151					0	ACAAGACGTTCT	0.637	
+	3	478	cr.1_Nonsense_M	NM_145697	NP_663735	Q9BZD4	NUF2_HUMAN	the N-terminus of NDC80.	4	GGAATTCGACTG	0.348	
-	2	304		NM_199351	NP_955383	Q71H61	ILDR2_HUMAN	.|Extracellular (Potential).	1	AGGTTTCTCTTG	0.537	
-	14	1981	te_p.S78_splice|S	NM_178527	NP_848622	Q5TAH2	S9A11_HUMAN		2	GCTACTCTAAAC	0.333	
-	15	1952	glh.1_Missense_M	NM_033127	NP_149118	Q96JE7	SC16B_HUMAN		4	ATGAAGGATTTG	0.498	
+	3	245	rf49_uc001glv.1_F	NM_032126	NP_115502	Q5T0J7	CA049_HUMAN	Potential.	0	TTTACCAAAGCA	0.418	
+	6	1811	pb.1_Missense_M	NM_201253	NP_957705	P82279	CRUM1_HUMAN	otential).|Laminin G-like 1.	9	TCATTTCCCACA	0.458	
+	5	1140	_Mutation_p.R297	NM_000299	NP_000290	Q13835	PKP1_HUMAN	ARM 2.	2	CTCCTCCGCAGC	0.617	
+	13	2534_2535	p.V873S|CR2_uc	NM_001877	NP_001868	P20023	CR2_HUMAN	xtracellular (Potential).	8	GTGTATGTTGACT	0.441	
-	9	1466	_p.M306I|IRF6_u	NM_006147	NP_006138	O14896	IRF6_HUMAN		2	GTAGATCATCCG	0.453	
+	7	1275	xcu.1_Missense_	NM_014388	NP_055203	Q68CQ4	DIEXF_HUMAN		0	CAGATCCCGAGG	0.468	
-	5	717	ic.2_Missense_M	NM_172362	NP_758872	O95259	KCNH1_HUMAN	lasmic (Potential).	5	CAGGCGGGAGT	0.517	
-	21	4948	v.2_Missense_Mu	NM_206933	NP_996816	O75445	USH2A_HUMAN	1.|Extracellular (Potential).	26	TGAAACGGATTC	0.433	
+	2	276	hoi.2_Missense_M	NM_144780	NP_659004	O15121	DEGS1_HUMAN	ical; (Potential).	0	CCAGTTGGGTGC	0.383	
+	27	7217	SCN_uc001hsp.1_	NM_001098623	NP_001092093	Q5VST9	OBSCN_HUMAN		28	AGTGATGGAGCC	0.632	
+	41	11140	.G3699E|OBSCN_	NM_001098623	NP_001092093	Q5VST9	OBSCN_HUMAN	Ig-like 37.	28	GTGCGGGAAGG	0.622	
+	2	234		NM_173508	NP_775779	Q8IY50	S35F3_HUMAN		2	CCCGGAGACTGT	0.647	
+	7	704	BCE_uc010pxr.1_	NM_003193	NP_003184	Q15813	TBCE_HUMAN	LRR 2.	0	AATTTCCCTCCG	0.333	
+	8	1124	n_p.R234L|MTR_u	NM_000254	NP_000245	Q99707	METH_HUMAN	Hcy-binding.	3	GTGGGCGGACTC	0.393	
+	41	6485		NM_001035	NP_001026	Q92736	RYR2_HUMAN	ilarity).|4 X approximate re	33	TGGCATCCCTTG	0.502	
-	2	770		NM_022469	NP_071914	Q9H772	GREM2_HUMAN		0	CCGAGTCGCTCA	0.517	
+	6	770	.1_Intron|SDCCA	NM_006642	NP_006633	Q86SQ7	SDCG8_HUMAN		0	AAAGACCATTTT	0.413	
+	11	2817	_p.Q411*|KIF26B_	NM_018012	NP_060482	Q2KJY2	KI26B_HUMAN		3	ACCATCCAGATT	0.607	
+	1	276		NM_001001915	NP_001001915	Q8NGZ5	OR2G2_HUMAN	cellular (Potential).	0	ACCCATGAAAAC	0.522	
+	1	26		NM_001004696	NP_001004696	Q8NH00	OR2T4_HUMAN	cellular (Potential).	1	TGGCCAGCCACA	0.483	rs140989725
+	1	55		NM_001004696	NP_001004696	Q8NH00	OR2T4_HUMAN	cellular (Potential).	1	ATCCTGATGGGA	0.488	
-	13	1525	p.S95F|PITRM1_uc001igu.1_Missense_Mutation_p.S5			E7ES23	E7ES23_HUMAN		1	CGGGGGACAGA	0.557	
+	8	1072	p.D274N|AKR1C3	NM_003739	NP_003730	P42330	AK1C3_HUMAN		1	GCCATAGATGGC	0.358	

-	9	1472	ND7_uc001iml.2_F	NM_152751	NP_689964	Q8N7W2	BEND7_HUMAN		2	TGTCCCTTTTCTT	0.557	
-	3	340	e_Mutation_p.R10	NM_001029954	NP_001025125	Q49AH0	CDNF_HUMAN		0	TTGGGCGAGTG	0.438	
+	3	992	DC2_uc001iqh.1_I	NM_032812	NP_116201	Q6UX71	PXDC2_HUMAN	cellular (Potential).	4	ATATCTCGAATAT	0.333	
-	28	3287	BL_uc001iqk.2_Mi	NM_006393	NP_006384	O76041	NEBL_HUMAN	SH3.	2	TGTAATCGTACAT	0.502	
+	6	1989	e_Mutation_p.G37	NM_019590	NP_062536	Q5T5P2	SKT_HUMAN		7	CTGCAGGATTAT	0.552	
-	16	2397	qdt.1_Missense_M	NM_018076	NP_060546	Q5T2S8	ARMC4_HUMAN	ARM 5.	6	GCTGATCTGTTA	0.428	
+	7	2588	_p.A624E|ZEB1_u	NM_030751	NP_110378	P37275	ZEB1_HUMAN		5	AGGTGGCATACA	0.488	
-	1	736	_p.G94R|GDF10_	NM_004962	NP_004953	P55107	BMP3B_HUMAN		2	CCCTCCCGGCC	0.662	
-	4	382	_p.R73Q|A1CF_uc	NM_138932	NP_620310	Q9NQ94	A1CF_HUMAN	RRM 1.	1	GGTCTCGGGGA	0.393	
-	25	3711	se_Mutation_p.R1	NM_033056	NP_149045	Q96QU1	PCD15_HUMAN	.|Extracellular (Potential).	13	GGACTCGAAGTA	0.373	
-	19	2776	CDH15_uc010qhw.	NM_033056	NP_149045	Q96QU1	PCD15_HUMAN	(Potential).|Cadherin 7.	13	ACTGCTCCATCT	0.423	rs146468805
-	40	12746	p.S750T|ANK3_uc	NM_020987	NP_066267	Q12955	ANK3_HUMAN		19	GCAAAACTTCTG	0.328	
-	1	235	IK3_uc001jkz.3_In	NM_020987	NP_066267	Q12955	ANK3_HUMAN		19	TGATTTCTAAATC	0.408	
+	10	2638		NM_032199	NP_115575	Q14865	ARI5B_HUMAN		4	CTTTTCCTTCCC	0.483	
+	2	1010	mx.3_Intron|CTNN	NM_178011	NP_821079	Q86VH5	LRRT3_HUMAN	lar (Potential).|LRR 4.	3	AGTTTCGGGGC	0.448	
+	6	1371	e_Mutation_p.P39	NM_032578	NP_115967	Q86TC9	MYPN_HUMAN	action with CARP.	5	ATTCCTCCAGCA	0.458	
-	2	256		NM_020999	NP_066279	Q9Y4Z2	NGN3_HUMAN		0	CGGACGTGGG	0.716	
+	6	1031	LC29A3_uc001jrt.	NM_018344	NP_060814	Q9BZD2	S29A3_HUMAN	ical; (Potential).	0	CCCCGCCATCT	0.562	
+	2	949	G3_uc001kcp.2_M	NM_001010848	NP_001010848	P56975	NRG3_HUMAN	Extracellular (Potential).	6	TGATCGAAACC	0.557	
+	7	1252	mk.1_Missense_M	NM_033282	NP_150598	Q9UHM6	OPN4_HUMAN	Name=7; (Potential).	1	GGCCTCTGCAA	0.602	
+	3	125		NM_019054	NP_061927	Q86V20	FA35A_HUMAN		4	TGGAGGATCTC	0.338	
+	20	2455_2456		NM_006204	NP_006195	P51160	PDE6C_HUMAN		4	AATTACCTAAAC	0.277	
-	4	620	uv.2_Missense_M	NM_020992	NP_066272	O00151	PDLI1_HUMAN		0	CACCCCGCTGG	0.572	
-	11	1822	_p.P478L|CRTAC1	NM_018058	NP_060528	Q9NQ79	CRAC1_HUMAN		5	CCACGGGCTCC	0.607	
+	26	3678		NM_014978	NP_055793	Q9UPU3	SORC3_HUMAN	lasmic (Potential).	10	AAAATCCCTTGG	0.488	
+	7	447	u.1_RNA|PNLIPR	NM_005396	NP_005387	P54317	LIPR2_HUMAN		1	ACATTCGGGTT	0.562	
-	7	1375	orf46_uc010qst.1_	NM_153810	NP_722517	Q86Y37	CJ046_HUMAN		0	TGAACCCACTC	0.348	
+	10	1295		NM_014937	NP_055752	Q9Y2H2	SAC2_HUMAN	SAC.	2	TTAACTTGGTAG	0.338	
+	3	440	lw.2_Missense_M	NM_001083909	NP_001077378	Q86SQ6	GP123_HUMAN	cellular (Potential).	0	CTCAGGATCTG	0.657	
-	13	1964	p.G652E|TRPM5_	NM_014555	NP_055370	Q9NZQ8	TRPM5_HUMAN	ical; (Potential).	4	AGGCTCCTAGC	0.647	
-	2	365		NM_001039165	NP_001034254	Q86SM8	MRGRE_HUMAN	cellular (Potential).	2	CACATCCTCCT	0.667	
-	1	865	G2_uc001mak.1_Ir	NM_145053	NP_659490	Q8IYU4	UBQLN_HUMAN		3	AATGAACTGCC	0.473	
-	1	911	G2_uc001mak.1_Ir	NM_001005289	NP_001005289	Q8NGJ2	O52H1_HUMAN	lasmic (Potential).	2	GCTTGGTCTTC	0.408	
-	8	1224	5_uc001mbn.2_In	NM_033034	NP_149023	Q9C035	TRIM5_HUMAN	B30.2/SPRY.	1	TTTCGGAGAGC	0.413	
-	1	926		NM_001005173	NP_001005173	Q8NGH7	O52L1_HUMAN	cellular (Potential).	2	AACATGGACAT	0.502	
+	7	1852	_p.C430S|DNHD1_	NM_144666	NP_653267	Q96M86	DNHD1_HUMAN		2	ATCGGTGCTAT	0.552	
-	12	2308	cw.1_Missense_M	NM_002645	NP_002636	O00443	P3C2A_HUMAN		10	GATAGGAAAAA	0.308	
-	1	532		NM_147199	NP_671732	Q96LB2	MRGX1_HUMAN	Name=3; (Potential).	3	AAGTAGGAAAAC	0.547	
+	7	810	qj.2_Missense_Mu	NM_213599	NP_998764	Q75V66	ANO5_HUMAN	lasmic (Potential).	4	CACACTCCTATA	0.463	
+	18	2283	qj.2_Missense_Mu	NM_213599	NP_998764	Q75V66	ANO5_HUMAN	cellular (Potential).	4	GATGGGAGCAG	0.403	
-	7	803	o.1_Missense_Mu	NM_015957	NP_057041	Q96GX9	MTNB_HUMAN		0	GCTGTGAAGGA	0.313	
-	2	412	1_5'Flank|C11orf7	NM_000536	NP_000527	P55895	RAG2_HUMAN		5	TGGCTGGGTAG	0.433	
+	7	843	2_uc001ndg.3_RN	NM_000506	NP_000497	P00734	THRB_HUMAN	Kringle 2.	3	AGACGGGGATG	0.632	
-	12	1585	_p.L427F|FOLH1_	NM_004476	NP_004467	Q04609	FOLH1_HUMAN	.|Extracellular (Probable).	3	CTTGAAGGAGTC	0.368	
-	1	899		NM_001005270	NP_001005270	Q96R67	OR4CC_HUMAN	lasmic (Potential).	3	TTCTCCAAAGCT	0.348	
+	1	272		NM_001004701	NP_001004701	Q8NGL9	OR4CG_HUMAN	cellular (Potential).	2	CTATCTCCTTCAG	0.448	
+	1	857		NM_001004735	NP_001004735	Q8NGL3	OR5DE_HUMAN	Name=7; (Potential).	3	ACCCCATGCTGA	0.428	

-	1	547		NM_001004058	NP_001004058	Q8NH50	OR8K5_HUMAN	ellular (Potential).	4	CAAAGGAACAT	0.353	
+	1	374_375		NM_001004745	NP_001004745	Q8NG75	OR5T1_HUMAN	Name=3; (Potential).	3	ATGCTTTCTCTT	0.411	
-	6	940	LS5_uc010rmq.1	NM_054108	NP_473449	Q96KN8	HRSL5_HUMAN		1	TCCTTCCATCA	0.512	
+	3	540	X5_uc001nzw.2_	NM_012094	NP_036226	P30044	PRDX5_HUMAN	Thioredoxin.	1	GAGCCCACAAG	0.577	
-	5	1522	v.1_Missense_Mu	NM_006795	NP_006786	Q9H4M9	EHD1_HUMAN		0	GTGCCCGAACG	0.667	
-	3	906	e.1_Missense_M	NM_138456	NP_612465	Q8N1L9	BATF2_HUMAN		1	AGGGTGAGGGC	0.612	
+	5	357		NM_001008778	NP_001008778	Q5MJ68	SPDYC_HUMAN	ired for CDK- binding (By	0	GCAAACGACAT	0.562	
+	15	2758	_5'Flank|PCNXL3	NM_032223	NP_115599	Q9H6A9	PCX3_HUMAN	ical; (Potential).	0	GCCTCCTGCCC	0.632	
+	4	696	S4_uc010rpc.1_5'	NM_178864	NP_849195	Q8IUM7	NPAS4_HUMAN		0	GATTCCATGCT	0.612	
+	10	1190	D13D_uc001okg.	NM_207354	NP_997237	Q6ZTN6	AN13D_HUMAN		1	ACACCGGGGTG	0.687	rs144238691
-	6	1157	lice_Site_p.G323_	NM_004910	NP_004901	O00562	PITM1_HUMAN		3	AGCCCCTGCCG	0.632	
+	1	238		NM_003251	NP_003242	Q92748	THRSP_HUMAN		1	ACCATGGGCTG	0.632	
-	5	951	S2_uc010rsq.1_5'	NM_024678	NP_078954	Q96I59	SYNM_HUMAN		2	GTTCTCCAGCT	0.343	
-	26	4517		NM_001098816	NP_001092286	Q6N022	TEN4_HUMAN	lar (Potential).|NHL 3.	4	CTTACCCCTGG	0.443	
+	11	1687	rtq.1_Missense_	NM_001156474	NP_001149946	Q6ZN84	CCD81_HUMAN		1	TGCGCTTAATG	0.373	
-	1	940	w.1_RNA|PGR_u	NM_000926	NP_000917	P06401	PRGR_HUMAN	lating, Pro-Rich.	4	CCTGTCCCTGG	0.637	
+	5	494	*|C11orf70_uc001	NM_032930	NP_116319	Q9BRQ4	CK070_HUMAN		1	AAATATGAAATAT	0.343	
-	5	809		NM_002425	NP_002416	P09238	MMP10_HUMAN		4	CTCACCGTAGA	0.458	
-	10	1316		NM_002426	NP_002417	P39900	MMP12_HUMAN	mopexin-like 3.	0	CGATTCCTTGG	0.393	
-	5	807	xg.1_Missense_M	NM_001225	NP_001216	P49662	CASP4_HUMAN		4	TCAGACTGAGG	0.473	
-	5	1697	p.R457Q|GUCY1	NM_000855	NP_000846	P33402	GCYA2_HUMAN		8	GCCCTCGGCCC	0.463	
+	3	515	.R60Q|LAYN_uc0	NM_178834	NP_849156	Q6UX15	LAYN_HUMAN	.|Extracellular (Potential).	0	TTCTCGAAGAC	0.463	
+	14	2088		NM_001076682	NP_001070150	P13591	NCAM1_HUMAN	tential).|Fibronectin type-III	1	GCATTCCAAGT	0.532	
+	5	917	s.1_Missense_M	NM_006169	NP_006160	P40261	NNMT_HUMAN		1	GGGCCGGGAG	0.542	
+	3	343	4_uc010rxr.1_5'U	NM_019894	NP_063947	Q9NRS4	TMPS4_HUMAN	lasmic (Potential).	2	TCAAACCCCTG	0.552	
+	19	2644	_p.G786E|GRIK4_	NM_014619	NP_055434	Q16099	GRIK4_HUMAN	ellular (Potential).	3	GGAAGGAGGGA	0.567	
+	45	6228	_p.E896K|SORL1_	NM_003105	NP_003096	Q92673	SORL_HUMAN	tential).|Fibronectin type-III	15	TTAAAGGAAAAG	0.343	
+	1	597		NM_001001965	NP_001001965	Q8NGN0	OR4D5_HUMAN	Name=5; (Potential).	1	TTTAATGGTGTC	0.502	
-	1	71		NM_001004474	NP_001004474	Q8NGN2	O10S1_HUMAN	ellular (Potential).	2	AGAAGTGGCTC	0.502	
+	2	268		NM_052959	NP_443191	Q96QZ0	PANX3_HUMAN	ellular (Potential).	0	TGCTTCACCAT	0.562	
-	2	1158	_p.M350I|KCNJ1_	NM_000220	NP_000211	P48048	IRK1_HUMAN	smic (By similarity).	4	TCTCTTCATCCT	0.428	
-	4	649	e_Mutation_p.R36	NM_003044	NP_003035	P48065	S6A12_HUMAN	lasmic (Potential).	1	GCCCCGATCCT	0.577	
+	20	3060	_uc001qkn.2_Miss	NM_199460	NP_955630	Q13936	CAC1C_HUMAN	1 of repeat III; (Potential).|	11	CATTTCCCTGG	0.582	
-	1	348		NM_020996	NP_066276	P10767	FGF6_HUMAN		3	GTCGGGGAGCA	0.632	
+	11	1959		NM_017417	NP_059113	Q9NY28	GALT8_HUMAN	ectin.|Lumenal (Potential).	4	TGTGGGAAATC	0.512	
-	17	2517	F_uc010set.1_Int	NM_000552	NP_000543	P04275	VWF_HUMAN		12	ACAGGGGACTG	0.557	
+	6	783	l.2_Missense_Mu	NM_201442	NP_958850	P09871	C1S_HUMAN	CUB 1.	1	ATGGGGAGATC	0.483	
-	10	1897		NM_001733	NP_001724	P00736	C1R_HUMAN	eptidase S1.	0	CTACGGGCAGA	0.517	
+	1	143		NM_001007033	NP_001007034	Q6EIG7	CLC6A_HUMAN	lasmic (Potential).	1	TCAAAGTACAG	0.458	
+	2	98	D1_uc009zhh.2_5'	NM_001114396	NP_001107868	Q13241	KLRD1_HUMAN		0	CTTTCAGATTCT	0.328	
-	1	298		NM_023919	NP_076408	Q9NYW3	TA2R7_HUMAN	ellular (Potential).	1	TCATTTCTTTACC	0.358	
-	3	700	B4_uc001qzf.1_In	NM_006249	NP_006240	Q04118	PRB3_HUMAN	G-[PQS]-P-[PS]-Q-[GE]-G-	1	CGGACGAGGT	0.622	rs113884749
-	3	1119		NM_006248	NP_006239				0	TGGAGGAGATC	0.612	
-	10	1545		NM_024829	NP_079105	Q6P4A8	PLBL1_HUMAN		0	AAGGATCCTTCT	0.448	
-	3	279	rdr.2_Missense_	NM_024730	NP_079006	Q9H628	RERGL_HUMAN	all GTPase-like.	0	AATGAATCGCT	0.333	
-	3	277	rdr.2_Missense_M	NM_024730	NP_079006	Q9H628	RERGL_HUMAN	all GTPase-like.	0	TGAATCGCTTA	0.338	rs138852095
+	27	3807	se_Mutation_p.E1	NM_004570	NP_004561	O75747	P3C2G_HUMAN	PX.	21	ACAACGAAACA	0.418	

+	29	4063	se_Mutation_p.S1	NM_004570	NP_004561	O75747	P3C2G_HUMAN		21	AAGAATCATCAC	0.284	
+	27	3157	ria.2_Missense_M	NM_003622	NP_003613	Q86W92	LIPB1_HUMAN		5	TTGTCCAATGG	0.383	
+	14	1765	nn.1_Missense_M	NM_001843	NP_001834	Q12860	CNTN1_HUMAN	-like C2-type 6.	9	TTAACAAAGAGA	0.393	
-	25	3619	_p.P325T|ADAMTS	NM_025003	NP_079279	P59510	ATS20_HUMAN	TSP type-1 8.	19	ACAAGGGGTAA	0.373	
-	10	941	_p.C228F|SLC38A	NM_030674	NP_109599	Q9H2H9	S38A1_HUMAN	ical; (Potential).	5	CCATACAGCTC	0.269	
+	4	1828	rpq.2_Missense_M	NM_138371	NP_612380	Q96HM7	F113B_HUMAN	Pro-rich.	5	ATGCAGGTTTCT	0.527	
-	34	2465	DL2A1_uc001rqv.2	NM_001844	NP_001835	P02458	CO2A1_HUMAN	le-helical region.	2	GGGCCCAGCGA	0.627	
-	10	1541		NM_003482	NP_003473	O14686	MLL2_HUMAN	of S/P-P-P-E/P-E/A.|Pro-ri	41	CCAGTGGAGAA	0.622	
-	11	1140	001rxh.1_Missense	NM_000617	NP_000608	P49281	NRAM2_HUMAN	cellular (Potential).	1	GAGTTATCTTTAG	0.408	
-	5	900	sns.1_Nonsense_M	NM_001146225	NP_001139697	Q14CN4	K2C72_HUMAN	inker 12.|Rod.	6	GGACTGGATCT	0.572	
-	1	194	_p.S59A|KRT8_uc	NM_002273	NP_002264	P05787	K2C8_HUMAN	ead.|Ser-rich.	2	GCGGGAACCGG	0.662	
+	7	915	p.Y237H|EIF4B_u	NM_001417	NP_001408	P23588	IF4B_HUMAN	g-rich.|Asp-rich.	2	gggatgggtatcgggat	0.388	
+	3	738	eq.2_Missense_M	NM_006897	NP_008828	P31274	HXC9_HUMAN	Homeobox.	3	CTCTTCAATATG	0.537	
+	8	781	G173C|DGKA_uc0	NM_001345	NP_001336	P23743	DGKA_HUMAN	nd 2.|2 (Probable).	4	GCAGTGGCTCT	0.547	
-	10	1105		NM_173595	NP_775866	Q8NB46	ANR52_HUMAN	ANK 11.	2	TGTTCCCAAATT	0.577	
-	22	2521	_p.R598*|MYO1A_	NM_005379	NP_005370	Q9UBC5	MYO1A_HUMAN	IQ 3.	7	CTTTCGGGCCTG	0.443	rs147166068
-	10	1123	p.R132C|MYO1A_	NM_005379	NP_005370	Q9UBC5	MYO1A_HUMAN	yosin head-like.	7	ATCACGGATGC	0.527	
+	6	1248	.2_RNA|SLC26A1	NM_133489	NP_597996	Q8NG04	S2610_HUMAN		2	CCAACCAGGTG	0.537	
-	10	1585	1svf.2_Missense_M	NM_032735	NP_116124	Q8N1M1	BEST3_HUMAN	lasmic (Potential).	0	AAGCAGGATTTC	0.592	
+	2	949		NM_013381	NP_037513	Q9UKU6	TRHDE_HUMAN	cellular (Potential).	3	CAGTGGAAACT	0.403	
-	3	263	ltan.2_Missense_M	NM_152589	NP_689802	Q8NA57	CL050_HUMAN		3	TTCGAGGTTTG	0.378	
-	3	1553	az.2_Missense_M	NM_001946	NP_001937	Q16828	DUS6_HUMAN	-protein phosphatase.	0	GTGCTGGAACC	0.507	
-	4	698	CN_uc001tbr.2_Int	NM_133503	NP_598010	P07585	PGS2_HUMAN	LRR 6.	4	GGAGAGCTTCT	0.398	
-	9	926		NM_003566	NP_003557	Q15075	EEA1_HUMAN	Potential.	3	CATCTTCTATACC	0.333	
-	2	532	e_Mutation_p.S28	NM_021229	NP_067052	Q9HB63	NET4_HUMAN		2	AGCGGGAACTC	0.512	
-	13	2732	tgk.2_Missense_M	NM_152788	NP_690001	Q7Z6G8	ANS1B_HUMAN		0	GGTGTTCTTTCA	0.423	
+	1	399	9ztx.2_Missense_M	NM_139319	NP_647480	Q8NDX2	VGLU3_HUMAN	lasmic (Potential).	3	ATTCTTTGGGAA	0.383	
-	13	2187		NM_024312	NP_077288	Q3T906	GNPTA_HUMAN		2	CTTTGGGAATATC	0.423	
+	5	1429	_Mutation_p.G22	NM_014653	NP_055468	Q2TBF2	WSCD2_HUMAN		3	CAGATGGAAGT	0.458	
+	2	702		NM_004416	NP_004407	Q86Y01	DTX1_HUMAN	WWE 2.	4	CTACGATATGGA	0.622	
-	2	854		NM_022363	NP_071758	Q9H2C1	LHX5_HUMAN	I zinc-binding 2.	0	ACACACCATGC	0.582	
-	5	1857	u.1_Missense_Mu	NM_016569	NP_057653	O15119	TBX3_HUMAN	ox; second part.	3	CAAAAGGGTTG	0.353	
-	1	1020	_p.P19L|TBX3_uc	NM_016569	NP_057653	O15119	TBX3_HUMAN		3	GGAACGGATGG	0.687	
+	16	2059	iij.1_Missense_Mu	NM_004764	NP_004755	Q96J94	PIWL1_HUMAN	ng (By similarity).|Piwi.	2	TGACCCGGTGA	0.507	
-	3	636	4L_uc001ujz.1_5'	NM_175066	NP_778236	Q8N8A6	DDX51_HUMAN		2	GTCCTCGATAGG	0.587	
-	9	1152		NM_005932	NP_005923	Q99797	MIPEP_HUMAN		1	CTTACGGAATTTT	0.308	
+	1	876		NM_001033602	NP_001028774	Q5JR59	MTUS2_HUMAN		0	AGTGGGGGCAC	0.512	
+	1	1965		NM_001033602	NP_001028774	Q5JR59	MTUS2_HUMAN		0	GGAGAGGACAG	0.542	
+	4	840	RY_uc010tdw.1_R	NM_023037	NP_075463	Q5TBA9	FRY_HUMAN		7	GAGCTCCCTTT	0.408	
+	35	5165	RY_uc010tdw.1_R	NM_023037	NP_075463	Q5TBA9	FRY_HUMAN		7	TTGAAAGAATCT	0.383	
+	11	1345	S5B_uc010abg.2_	NM_015032	NP_055847	Q9NTI5	PDS5B_HUMAN	HEAT.	4	GAGAGAGAACAT	0.249	
-	11	1823	uwz.2_Missense_M	NM_025138	NP_079414	Q86XN7	CM023_HUMAN	Pro-rich.	5	GCCCTGGGAAC	0.512	
-	9	2102	p.H553Y|ELF1_uc	NM_172373	NP_758961	P32519	ELF1_HUMAN		1	TCAAATGATCTTC	0.418	
-	7	2226	7B_uc010tgu.1_Mi	NM_000053	NP_000044	P35670	ATP7B_HUMAN	cellular (Potential).	3	AGTCCTGGAATG	0.483	
-	2	1673	RK6_uc010afe.1_	NM_032229	NP_115605	Q9H5Y7	SLIK6_HUMAN	lar (Potential).|LRR 7.	3	ACGATCCTTCTT	0.343	
-	31	4066	p.S107L|ABCC4_u	NM_005845	NP_005836	O15439	MRP4_HUMAN		4	AGGTCGAGGGC	0.383	
-	12	1430	OCK9_uc010tis.1_	NM_015296	NP_056111	Q9BZ29	DOCK9_HUMAN		1	GCTTCGGATACT	0.532	

-	11	1143	RS2_uc010tjm.1_F	NM_024537	NP_078813	Q9HA77	SYCM_HUMAN		0	GCCCCAGGAGC	0.637	
+	1	305		NM_002929	NP_002920	Q15835	RK_HUMAN	GS.|N-terminal.	2	GCAGCCCATCG	0.582	
+	1	423		NM_001004724	NP_001004724	Q8IXE1	OR4N5_HUMAN	Name=4; (Potential).	1	AGCCTGCTATGC	0.517	
-	2	908	akj.2_Nonsense_	NM_012244	NP_036376	Q9UHI5	LAT2_HUMAN		1	TTGGCGAGACA	0.547	rs142012722
+	2	129	34L1_uc010tnu.1_	NM_001082488	NP_001075957	P0CG22	DR4L1_HUMAN		0	TCACAGGATCG	0.418	
+	9	4699		NM_025081	NP_079357	Q9P2P1	NYNRI_HUMAN		3	CAAAGGATGTG	0.607	
-	3	291		NM_001911	NP_001902	P08311	CATG_HUMAN	eptidase S1.	2	GCTGGGTGTTT	0.532	rs34281853
+	10	1156	_p.P220S|SRP54_	NM_003136	NP_003127	P61011	SRP54_HUMAN	G-domain.	1	AAAAGTCCGATT	0.373	
+	10	1867	CM_uc010anf.2_	NM_020937	NP_065988	Q8IYD8	FANCM_HUMAN	case C-terminal.	7	TCCTTTCTGAAG	0.398	
-	2	396	v.2_5'UTR|PYGL_	NM_002863	NP_002854	P06737	PYGL_HUMAN		1	ATGTAAAATTCC	0.403	
-	6	1007	O34_uc001xbv.2_	NM_199047	NP_950248	Q6SJ96	TBPL2_HUMAN		0	ACAATTCGTGGT	0.333	
-	4	352	B_uc010tsm.1_Int	NM_198686	NP_941959	P59190	RAB15_HUMAN		1	CGCTGCTAATGT	0.537	
+	10	1118_1119	_p.R342L|GALNTL	NM_020692	NP_065743	Q8N428	GLTL1_HUMAN	main B.|Lumenal (Potential	2	CAGCCGGGTGG	0.525	
+	16	4819	xmv.2_Missense_	NM_015556	NP_056371	O43166	SI1L1_HUMAN		4	AACCCGAAGGA	0.393	
-	10	2469	_p.S195F|ZFYVE1	NM_021260	NP_067083	Q9HBF4	ZFYV1_HUMAN	YVE-type 1.	1	TAAAGGACGTC	0.527	
+	6	347	p.D105N|C14orf17	NM_001102564	NP_001096034	Q96FT9	IFT43_HUMAN		0	TTCCGGATCTG	0.483	
+	1	1486	_5'Flank|TMED8_	NM_001010860	NP_001010860	Q9P1V8	SAM15_HUMAN		0	TACTCAGATCCC	0.398	rs151304084
-	6	739	o.3_Missense_Mu	NM_005065	NP_005056	Q9UBV2	SE1L1_HUMAN	with ERLEC1, OS9 and SY	1	GATACCGATATG	0.348	
-	15	2023		NM_001080414	NP_001073883	Q9P219	DAPLE_HUMAN	Potential.	3	CTCCTCCTGGA	0.632	
-	28	5808	v.2_Missense_Mut	NM_030621	NP_085124	Q9UPY3	DICER_HUMAN	DRBM.	5	CCTTCCCGTCGT	0.428	
+	7	858	gg.3_Missense_Mu	NM_001099402	NP_001092872	O75909	CCNK_HUMAN		0	TGTCCCGGTCG	0.473	
+	25	2699	on.3_Missense_M	NM_153046	NP_694591	Q8NDG6	TDRD9_HUMAN		3	ATCAGACAGGT	0.358	
+	18	2838	2_uc001ypc.2_No	NM_022489	NP_071934	Q27J81	INF2_HUMAN	otential.|FH2.	0	TGTGTGAGGAC	0.657	
+	24	2896	p.E959G|CYFIP1_	NM_014608	NP_055423	Q7L576	CYFP1_HUMAN		9	CATGGAGGAGC	0.572	
-	81	12620		NM_004667	NP_004658	O95714	HERC2_HUMAN	RCC1 17.	13	GTCCCCGTCCC	0.627	
+	2	1093		NM_015995	NP_057079	Q9Y2Y9	KLF13_HUMAN		0	TCCACCCGGGA	0.701	
+	35	5006	r.2_Missense_Mut	NM_001036	NP_001027	Q15413	RYR3_HUMAN	eats.|Cytoplasmic (By simil	10	CGGACGAGTCC	0.567	
-	10	1645	se_Mutation_p.P4	NM_133647	NP_598408	Q9UHW9	S12A6_HUMAN	ical; (Potential).	7	CAGAGGGAAAG	0.438	
-	2	368	uc001zit.1_5'Flank	NM_020660	NP_065711	Q9UKL4	CXD2_HUMAN	lasmic (Potential).	0	CTATGGACTCAG	0.557	
-	3	503	1zkd.3_Missense_	NM_005739	NP_005730	O95267	GRP1_HUMAN	ansforming activity (By sim	2	GATATAGGGTGA	0.393	
+	4	2402		NM_020857	NP_065908	Q9P253	VPS18_HUMAN	Clathrin.	3	TGGGGCCAGCC	0.637	
+	2	225	_p.P62Q|JMJD7-P	NM_005090	NP_005081	P0C869	PA24B_HUMAN		1	CTGGCCGGCCC	0.622	
-	13	2151	_p.Y372N|TGM5_u	NM_201631	NP_963925	O43548	TGM5_HUMAN		1	CTACATAAACATT	0.433	
-	11	1216	wh.3_5'Flank|MYE	NM_016132	NP_057216	Q9P2K5	MYEF2_HUMAN	Gly-rich.	3	CATTCCCATACC	0.289	
-	8	1114	ew.1_Missense_M	NM_017672	NP_060142	Q96QT4	TRPM7_HUMAN	lasmic (Potential).	10	CACAGGGACAC	0.408	
-	30	7625	y.1_Missense_Mu	NM_015263	NP_056078	Q8TDJ6	DMXL2_HUMAN		9	ACAAAGGAAGA	0.219	
+	1	617		NM_001080534	NP_001074003	Q8NB66	UN13C_HUMAN		7	AAAATCCTGGG	0.438	
+	1	2500		NM_001080534	NP_001074003	Q8NB66	UN13C_HUMAN		7	AGATTTCGGACA	0.438	
-	27	5153	api.2_Missense_M	NM_005848	NP_005839	Q7Z401	MYCPP_HUMAN		4	AGGGGCCAGAA	0.403	
+	10	1545	se_Mutation_p.R4	NM_024505	NP_078781	Q96PH1	NOX5_HUMAN	smic (Potential).|C-terminal	2	CACATTCGGTCC	0.567	
-	11	1020_1021	p.R333C|GRAMD	NM_001012642	NP_001012660	Q8IUY3	GRAM2_HUMAN		0	AATACGGAACGC	0.475	rs144563180
-	14	1441	A6_uc002axl.2_N	NM_022369	NP_071764	Q9BX79	STRA6_HUMAN	cellular (Potential).	1	CTCATCCAACAG	0.622	
-	3	636	.2_RNA|MESDC2_	NM_015154	NP_055969	Q14696	MESD_HUMAN	omain (By similarity).	0	TACACCTGGCCC	0.493	
+	3	1246	e_Mutation_p.P37	NM_001008226	NP_001008227	Q658L1	F154B_HUMAN		2	ATTATTCCTGCA	0.358	
+	11	1414	p.S397N|ADAMTS	NM_207517	NP_997400	P82987	ATL3_HUMAN		27	ATGCAGCATGG	0.418	
+	15	1875	p.K551E|ADAMTS	NM_207517	NP_997400	P82987	ATL3_HUMAN		27	GGCTGAAACAA	0.388	
+	15	1691	LC28A1_uc010upf	NM_004213	NP_004204	O00337	S28A1_HUMAN		3	TGAACGAGTTT	0.597	

+	22	4215	_p.S998F|BLM_uc	NM_000057	NP_000048	P54132	BLM_HUMAN			6	GAAATCCTCCA	0.398
+	6	1404	2B_uc010uqv.1_M	NM_014848	NP_055663	Q7L1I2	SV2B_HUMAN	lasmic (Potential).		8	GGTTTCCAACA	0.368
+	2	579	p.E177K|IGF1R_u	NM_000875	NP_000866	P08069	IGF1R_HUMAN			8	CAAAGGAATGT	0.522
+	7	938	uwc.1_Missense_	NM_015944	NP_057028	Q9Y303	NAGA_HUMAN			4	GGATCGCCCAC	0.672
-	2	756		NM_000243	NP_000234	O15553	MEFV_HUMAN			6	TAGGTCGCATC	0.617
-	4	931		NM_152457	NP_689670	Q96LX8	ZN597_HUMAN	2H2-type 4.		0	CCACATAAAACC	0.443
+	3	355	AT15_uc010uxc.1	NM_001083601	NP_001077070	Q9H7X0	NAT15_HUMAN	etyltransferase.		0	CCATCGAGTAA	0.657
-	31	7354	vw.2_Missense_M	NM_004380	NP_004371	Q92793	CBP_HUMAN			127	GGGGTGGGGG	0.647
-	7	1237		NM_003223	NP_003214	Q01664	TFAP4_HUMAN			1	CCTCCCGGCTC	0.706
-	13	4425	1293N|GRIN2A_	NM_001134407	NP_001127879	Q12879	NMDE1_HUMAN	lasmic (Potential).		45	GTTATCGTAGG	0.527
-	3	553	.3_Intron|CPPED	NM_018340	NP_060810	Q9BRF8	CPPED_HUMAN			0	GTCATCTCCCC	0.607
+	14	2028	p.P633Q|TMC7_u	NM_024847	NP_079123	Q7Z402	TMC7_HUMAN	ellular (Potential).		3	TGGGCCGTTCA	0.607
-	43	6364		NM_017539	NP_060009	Q8TD57	DYH3_HUMAN	3 (By similarity).		18	TCGTCGATCCA	0.517
-	5	1511_1512	p.R165*|ZKSCAN	NM_001012981	NP_001012999	Q63HK3	ZKSC2_HUMAN			4	TTTCGGGGACA	0.455
+	3	735	223S|JMJD5_uc	NM_024773	NP_079049	Q8N371	KDM8_HUMAN			3	CAGTCCCCCGG	0.512
+	3	286	_p.W18*|IL21R_u	NM_181078	NP_851564	Q9HBE5	IL21R_HUMAN			4	AGGCTGGGGCT	0.632
+	19	2925	Mutation_p.N914S	NM_173201	NP_775293	O14983	AT2A1_HUMAN	ame=8; (By similarity).		4	ACTGAACAGGT	0.632
+	6	722	uc002dsc.2_Intron	NM_014387	NP_055202	O43561	LAT_HUMAN	lasmic (Potential).		0	AGGCTGGGTGG	0.607
+	13	1623	_Mutation_p.P40	NM_002209	NP_002200	P20701	ITAL_HUMAN	Extracellular (Potential).		10	GTGCCCCACTG	0.597
-	11	1636	fg.1_Missense_M	NM_173502	NP_775773	Q5K4E3	POLS2_HUMAN	ptidase S1 2.		1	TGATTCCAGCC	0.567
+	7	716	p.1_Missense_Mu	NM_005353	NP_005344	Q13349	ITAD_HUMAN	lar (Potential).|VWFA.		1	TGAAAGGCCTG	0.597
+	16	1888	cap.1_Splice_Site_	NM_005353	NP_005344	Q13349	ITAD_HUMAN			1	CCTCAGGAGTC	0.632
-	9	1226	ep.2_Missense_	NM_005880	NP_005871	O60884	DNJA2_HUMAN			1	GTTAGGAACTTC	0.403
+	4	1903	c010cbm.1_Misse	NM_022162	NP_071445	Q9HC29	NOD2_HUMAN	NACHT.		4	CCCCTGGAATTC	0.567
+	4	2179	a.1_Missense_M	NM_025134	NP_079410	Q3L8U1	CHD9_HUMAN			7	TTTACCTGGTG	0.308
-	9	1162	m.1_Missense_Mu	NM_002080	NP_002071	P00505	AATM_HUMAN			2	GATGCGGTCAG	0.488
-	5	965	oh.2_Missense_	NM_001796	NP_001787	P55286	CADH8_HUMAN	(Potential).|Cadherin 2.		9	TACTCCTCCTTG	0.448
+	11	1843		NM_001795	NP_001786	P33151	CADH5_HUMAN	|Extracellular (Potential).		6	GGATGCCAAGT	0.592
-	1	528	vjt.1_Missense_M	NM_001082486	NP_001075955	Q96AP0	ACD_HUMAN			1	CTTTCCTCGGA	0.746
-	84	14757	DIN_uc010cfy.2_R	NM_032821	NP_116210	Q4G0P3	HYDIN_HUMAN			2	AAACTGGGAGG	0.622
-	56	9492		NM_032821	NP_116210	Q4G0P3	HYDIN_HUMAN			2	TGCATGGAAGA	0.468
-	25	3961		NM_032821	NP_116210	Q4G0P3	HYDIN_HUMAN			2	GTTTTTCTTAGTT	0.463
-	18	3148	_p.S498F|ADAMT	NM_199355	NP_955387	Q8TE60	ATS18_HUMAN			18	ATGAGGAATTG	0.388
+	2	406	utation_p.R63K|B	NM_017429	NP_059125	Q9HAY6	BCDO1_HUMAN			0	CATCAGAGACG	0.358
+	7	1865	ense_Mutation_p.	NM_013370	NP_037502	Q9UJX0	OSGI1_HUMAN			0	GCTGACTTTGC	0.647
+	5	764	C50_uc010chi.1_	NM_178452	NP_848547	Q8NEP3	DAAF1_HUMAN	LRR 4.		0	GCCTCCCAGTC	0.388
-	16	2404_2405	sf.1_Missense_M	NM_014389	NP_055204	Q8IZL8	PELP1_HUMAN	Pro-rich.		2	TCAGGGCCAG	0.629
-	8	1232	R1_uc010vur.1_	NM_002616	NP_002607	O15534	PER1_HUMAN			9	TGCAGGGGCCC	0.642
-	6	864		NM_001128076	NP_001121548	A6NLX3	SPDE4_HUMAN			0	CGGGCCCACAC	0.592
-	36	5338_5339	uc002gml.1_Intron	NM_017533	NP_060003	Q9Y623	MYH4_HUMAN	Potential.		13	TCTCTCCCTGGA	0.446
-	3	304	uc002gml.1_Intron	NM_017533	NP_060003	Q9Y623	MYH4_HUMAN	osin head-like.		13	AGCTTCGGTCT	0.458
+	51	10107	o.2_Missense_M	NM_001372	NP_001363	Q9NYC9	DYH9_HUMAN			20	TCTCCCTTGCC	0.502
+	4	506	0vvi.1_Missense_	NM_003010	NP_003001	P45985	MP2K4_HUMAN	rotein kinas	p.?(1)	58	AACTTCTTATGG	0.353
+	13	1118	_uc002gsj.1_3'UT	NM_001388	NP_001379	P55039	DRG2_HUMAN			1	TGGAGCATGAG	0.662
+	1	50		NM_002986	NP_002977	P51671	CCL11_HUMAN			0	ATAAAAGGCAG	0.557
-	4	1148	_p.F283L|HNF1B_	NM_000458	NP_000449	P35680	HNF1B_HUMAN	obox; HNF1-type.		3	TGCCGGAATGC	0.622
+	5	913	2_uc002hui.1_Mi	NM_133264	NP_573571	Q8TF74	WIPF2_HUMAN			3	GACCTCCTGCT	0.607

-	1	520		NM_033059	NP_149048	Q9BYQ6	KR411_HUMAN	C-[GIKRQVHEL]- [SPTR]-[	0	GACGCAGGcagc	0.323	rs141357429
-	4	859	vfr.1_Missense_Mu	NM_153490	NP_705694	P13646	K1C13_HUMAN	inker 12.|Rod.	5	GCCTGGGGTGG	0.577	
-	2	157		NM_024320	NP_077296	Q9BU68	PR15L_HUMAN		1	TTTCCGGAGGA	0.567	
-	7	1743	.3_Missense_Mut	NM_020178	NP_064563	Q9NS85	CAH10_HUMAN		2	TGTTCATTATGAT	0.393	
+	11	1346	issense_Mutation_	NM_030938	NP_112200	Q96GC9	VMP1_HUMAN	lasmic (Potential).	0	CACACCACAGG	0.488	
+	16	2355	_uc010wpj.1_Mis	NM_000789	NP_000780	P12821	ACE_HUMAN	otential).|Peptidase M2 2.	4	CGTCCCGGAAAT	0.532	
+	9	2140	pm.1_Missense_	NM_030779	NP_110406	Q9H252	KCNH6_HUMAN	toplasmic (Potential).	1	CCAGCGGGCAG	0.607	
-	32	4606	se_Mutation_p.A2	NM_080282	NP_525021	Q8WWZ4	ABCAA_HUMAN	ntial).|ABC transporter 2.	4	ACCAGCTCCATT	0.358	
-	2	617	_p.A157V|CDC42	NM_012121	NP_036253	Q9H3Q1	BORG4_HUMAN		0	TGCCCGCCTCC	0.662	
-	4	378	r.2_Missense_Mut	NM_015654	NP_056469	Q9BTE0	NAT9_HUMAN	cetyltransferase.	0	CAAGGTGAGGT	0.592	
-	5	628	1_Missense_Muta	NM_014984	NP_055799	Q9UPN4	AZI1_HUMAN		4	AACTCCGGGCA	0.637	
+	3	1396	.F208L|TGIF1_uc	NM_170695	NP_733796	Q15583	TGIF1_HUMAN		1	AAAACTTCACA	0.488	
+	3	844		NM_153000	NP_694545	Q8J025	APCD1_HUMAN	ellular (Potential).	0	AGCTCGGCCAG	0.667	
+	5	2973	_p.S807F|ZNF532	NM_018181	NP_060651	Q9HCE3	ZN532_HUMAN		2	ACAAATCTCCCT	0.512	
-	1	628		NM_005912	NP_005903	P32245	MC4R_HUMAN	lasmic (Potential).	1	TTCTTGGCTATT	0.453	
+	9	1243	_p.E234K|SERPI	NM_001143818	NP_001137290	P05120	PAI2_HUMAN		2	AAGATGAAGTT	0.368	
+	2	628		NM_012283	NP_036415	Q9UJ96	KCNG2_HUMAN		0	AGGGCGAGTGC	0.701	
+	5	658	se_Mutation_p.S1	NM_024100	NP_077005	Q9BV38	WDR18_HUMAN	WD 4.	1	TGCTCTCCGTCC	0.652	
+	8	1867		NM_177401	NP_796375	Q504T8	MIDN_HUMAN		0	GGACTCCGTGT	0.682	
+	2	1084	2_Intron|SCAMP4_	NM_138422	NP_612431	Q96EY9	ADAT3_HUMAN		2	TGTACGTGACC	0.731	
-	10	1606		NM_005934	NP_005925	Q03111	ENL_HUMAN		1	CAGGCTTGCTG	0.667	
-	5	877	xjg.1_Missense_M	NM_005490	NP_005481	Q9BRG2	SH23A_HUMAN		2	TCGGGGGACGT	0.667	
-	4	665_666	320_uc002mjl.1_	NM_016579	NP_057663	Q9NPF0	CD320_HUMAN	ellular (Potential).	0	AGGGGGCCCCA	0.609	
-	5	34481		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).	57	CACCAGAAGAA	0.458	
-	3	26315		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	h.|Extracellular (Potential)	57	GGGAGGAAGTT	0.493	
-	3	24798		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	h.|Extracellular (Potential)	57	ATCATCATTTCT	0.483	
-	3	23674		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	h.|Extracellular (Potential)	57	TAGCTCTGTCT	0.547	
-	1	8465		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	h.|Extracellular (Potential)	57	TAGTTCCCGCA	0.493	
-	1	575		NM_001005191	NP_001005191	Q8NG98	OR7D4_HUMAN	ellular (Potential).	4	GGAGGGTGTTA	0.502	
-	4	595	YK2_uc002mod.2_	NM_003331	NP_003322	P29597	TYK2_HUMAN	FERM.	9	AAAGAGATTGA	0.527	
-	4	719	_p.M127I|CCDC15	NM_145045	NP_659482	A5D8V7	CC151_HUMAN	Potential.	1	TCCGCCATCTC	0.667	
-	4	814	_p.P48S|ZNF823_	NM_001080493	NP_001073962	P16415	ZN823_HUMAN	2H2-type 3.	2	AAAAGGAAAGG	0.413	
-	20	3624	nwy.3_Missense_	NM_001127221	NP_001120693	O00555	CAC1A_HUMAN	lasmic (Potential).	2	GTTCCCCGGGT	0.652	
-	14	2065	mwy.3_Missense_	NM_001127221	NP_001120693	O00555	CAC1A_HUMAN	smic (Potential).|II.	2	TTCATGGAGTTG	0.577	
+	1	705		NM_001004713	NP_001004713	O60431	OR1I1_HUMAN	lasmic (Potential).	3	AAGTGGAAAGC	0.537	
+	7	874	F3_uc010xom.1_	NM_000896	NP_000887	Q08477	CP4F3_HUMAN		3	GCGGCGCCGCA	0.572	
+	1	97		NM_013938	NP_039226	O60404	O10H3_HUMAN	Name=1; (Potential).	0	TGTACCTCCTG	0.498	
-	3	117	9orf42_uc002neo.	NM_024104	NP_077009	Q9BQ49	CS042_HUMAN	ellular (Potential).	0	TCTTTTTCCTACA	0.502	
-	13	1527		NM_015692	NP_056507	Q8IZJ3	CPMD8_HUMAN		13	GCACTGGCTGG	0.592	
-	4	589_590	nse_Mutation_p.S	NM_031941	NP_114147	Q8N6Y0	USBP1_HUMAN		1	CAAGGGAACCT	0.683	
-	1	159	_5'Flank|uc002ngr	NM_004335	NP_004326	Q10589	BST2_HUMAN	ellular (Potential).	3	GCCTCGCTGTT	0.562	
+	2	465	_p.S190L|ZNF493	NM_175910	NP_787106	Q6ZR52	ZN493_HUMAN	2H2-type 2.	1	GCAAATCATTTT	0.299	
+	2	903	_p.P336L|ZNF493_	NM_175910	NP_787106	Q6ZR52	ZN493_HUMAN	ype 7; degenerate.	1	AACCCCTACTA	0.348	rs142651314
+	2	260	257_uc010ecy.2_5	NM_033468	NP_258429	Q9Y2Q1	ZN257_HUMAN	KRAB.	0	ATAGGGATGTG	0.403	
-	3	1051		NM_001001411	NP_001001411	Q8N7Q3	ZN676_HUMAN	2H2-type 3.	0	GAATTATCTTAT	0.363	
+	4	1759	rk.1_Missense_M	NM_203282	NP_975011	O75437	ZN254_HUMAN		0	TACTGAAGAGA	0.353	
+	4	1782	rk.1_Missense_M	NM_203282	NP_975011	O75437	ZN254_HUMAN	2H2-type 13.	0	GTGAAAAATGT	0.358	

-	11	1248	C123_uc010edg.2_	NM_032816	NP_116205	Q96ST8	CEP89_HUMAN	Potential.		0	CTTGAGGGTGG	0.383	
-	1	307_308	ad.1_Missense_Mu	NM_198538	NP_940940	Q6UWP8	SBSN_HUMAN	a/Gly/His-rich.		1	CTTGCCGGTGTG	0.554	
+	3	449		NM_014727	NP_055542	Q9UMN6	MLL4_HUMAN			11	GCCCCGAGGTC	0.527	
+	3	1484		NM_014727	NP_055542	Q9UMN6	MLL4_HUMAN	Pro-rich.		11	CTCCTCCCACTC	0.672	
-	5	676	uc002oev.1_Intron	NM_206894	NP_996777	Q6PG37	ZN790_HUMAN			2	TGTTGAGTATGAT	0.353	
-	6	854	gx.1_Missense_M	NM_014898	NP_055713	Q9Y2G7	ZFP30_HUMAN			0	CAAGTCCACAG	0.358	
+	13	1556	iu.2_Missense_Mu	NM_000540	NP_000531	P21817	RYR1_HUMAN	Cytoplasmic.		12	AGAGCCTCTTC	0.701	
-	13	1058	oiy.1_Missense_M	NM_007181	NP_009112	Q92918	M4K1_HUMAN			8	TGATCCGCCGA	0.607	
-	4	461		NM_001828	NP_001819	Q05315	LPPL_HUMAN	Galectin.		0	AGATATCTCTCC	0.418	
-	7	2178	e_Mutation_p.P49	NM_181882	NP_870998	Q9BXM0	PRAX_HUMAN	L]-[LIVMAP]- [AQKHRPE];		2	CTCAGGGAGTT	0.577	
-	4	541	K4_uc002oos.2_	NM_024876	NP_079152	Q96D53	ADCK4_HUMAN			0	GTTCTCGAGAG	0.592	
+	3	706		NM_002483	NP_002474	P40199	CEAM6_HUMAN	like C2-type	p.P186P(1)	1	CCTCCCGGTCA	0.527	
-	11	1478	_p.W53*|GRIK5_u	NM_002088	NP_002079	Q16478	GRIK5_HUMAN	ellular (Potential).		0	CCCGTCCAGGA	0.697	
-	5	1040	2ozb.3_Missense_	NM_004234	NP_004225	Q14590	ZN235_HUMAN			3	AGTACGAACAC	0.438	rs144837895
+	3	368	e_Mutation_p.P11	NM_015710	NP_056525	Q9NZM5	GSCR2_HUMAN			1	GAAACCCCTTC	0.527	
-	4	257	lutation_p.R75L|S	NM_000979	NP_000970	Q07020	RL18_HUMAN			0	TTTCCCGGCCA	0.582	
-	2	492	se_Mutation_p.D2	NM_053003	NP_443729	Q96PQ1	SIG12_HUMAN	2.|Extracellular (Potential).		5	TAGGTCCTGGG	0.587	
+	4	2668	dw.1_Missense_M	NM_138374	NP_612383	Q96IR2	ZN845_HUMAN	2H2-type 23.		0	ATAAGGCAATT	0.383	
+	4	2891	dw.1_Missense_M	NM_138374	NP_612383	Q96IR2	ZN845_HUMAN	2H2-type 26.		0	CTTCCGTCACA	0.363	rs150688663
-	11	1685	A6_uc002qel.1_Mi	NM_006864	NP_006855	O75022	LIRB3_HUMAN	lasmic (Potential).		3	CCACCCTGTCC	0.423	
+	4	931	gr.2_Missense_M	NM_006847	NP_006838	Q8NHJ6	LIRB4_HUMAN	2.|Extracellular (Potential).		3	GCACGGGGGGA	0.607	
+	5	727	10esf.2_Missense_	NM_013289	NP_037421	P43629	KI3L1_HUMAN	ellular (Potential).		5	CATATGAGAAA	0.552	
-	2	1670		NM_176820	NP_789790	Q7RTR0	NALP9_HUMAN			7	CAAACCAATGA	0.338	
-	1	610	2qnt.2_Missense_	NM_001146186	NP_001139658	Q9GZU2	PEG3_HUMAN	SCAN box.		12	GAGCTCGATGA	0.537	
-	5	1533		NM_052882	NP_443114	Q96PE6	ZIM3_HUMAN	2H2-type 8.		2	GGATTTTTTTATG	0.383	
+	3	702	NF776_uc002qqa.	NM_173632	NP_775903	Q68DI1	ZN776_HUMAN			1	TATGTCACATGA	0.403	
-	3	1016	_p.C230G|ZNF417	NM_152475	NP_689688	Q8TAU3	ZN417_HUMAN	2H2-type 3.		0	CCCACACTCTC	0.433	
-	4	2172	IF418_uc010yho.1	NM_133460	NP_597717	Q8TF45	ZN418_HUMAN	2H2-type 15.		0	CAAAGGATTTC	0.433	
+	5	1285	nse_Mutation_p.H	NM_003436	NP_003427	B4DHH9	B4DHH9_HUMAN			1	AGTGCCATGAG	0.542	
-	17	2414		NM_012293	NP_036425	Q92626	PXDN_HUMAN			8	TCGGTGGGGGT	0.652	
-	14	2761	se_Mutation_p.S64	NM_015025	NP_055840	Q9UL68	MYT1L_HUMAN			6	CAAACGAGGTC	0.483	
-	10	1760_1761	lutation_p.311_31	NM_015025	NP_055840	Q9UL68	MYT1L_HUMAN			6	CTTTTCCATGAG	0.475	
+	3	896	c.1_Missense_Mu	NM_003597	NP_003588	O14901	KLF11_HUMAN			2	CACTGACAAAG	0.527	
-	51	6853	AS_uc010exl.1_Mi	NM_015909	NP_056993	A2RRP1	NBAS_HUMAN			4	CTGCCGTGATT	0.418	rs144615326
+	3	557	uc002rvb.2_Intron	NM_012249	NP_036381	P17081	RHOQ_HUMAN			2	ACCCAATGACC	0.393	
-	40	4636	ense_Mutation_p.	NM_014614	NP_055429	Q14997	PSME4_HUMAN			5	GAGGCGATATG	0.383	
-	3	257	se_Mutation_p.P66	NM_144709	NP_653310	Q3MIT2	PUS10_HUMAN	Potential.	p.P66R(1)	4	GAGGTGGGTTC	0.353	
+	5	541		NM_019617	NP_062563	Q9NS71	GKN1_HUMAN	BRICHOS.		1	GGATTCCAACA	0.507	
+	3	563	se_Mutation_p.G4	NM_001298	NP_001289	Q16281	CNGA3_HUMAN			6	GCCGGGGATCG	0.587	
-	7	1415		NM_207362	NP_997245	Q6NV74	CB055_HUMAN	Pro-rich.		0	GCGCCTCCCCA	0.756	
-	10	1873_1874	_p.A596V|TBC1D8	NM_001102426	NP_001095896	O95759	TBCD8_HUMAN	ab-GAP TBC.		3	GGTGGGCATAG	0.569	
+	21	5084	e_Mutation_p.H85	NM_182588	NP_872394	Q7Z3J3	RGPD4_HUMAN			2	CAGATCACTTA	0.453	
+	9	1823	fjj.2_Missense_Mu	NM_021815	NP_068587	Q9GZV3	SC5A7_HUMAN	lasmic (Potential).		4	TGATGCTGTTGT	0.358	
+	24	2608		NM_001029996	NP_001025167	Q4G0U5	PCDP1_HUMAN			0	AAGTGGAATTC	0.383	
+	2	525	0flu.2_Missense_	NM_130773	NP_570129	Q8WYK1	CNTP5_HUMAN	|Extracellular (Potential).		10	TCACAGCCCAG	0.478	
+	12	2217	flu.2_Missense_M	NM_130773	NP_570129	Q8WYK1	CNTP5_HUMAN	ential).|Fibrinogen C-termi		10	TCTCCAGGTGT	0.532	
-	2	585		NM_004807	NP_004798	O60243	H6ST1_HUMAN	enal (Potential).		1	TCTCGTAGCAGG	0.622	

+	6	562		NM_033416	NP_219484	Q96G21	IMP4_HUMAN	Brix.	2	GGAGGCCAAGC	0.642	
-	1	1002		NR_002826					0	GGACGGGGCCA	0.577	rs112041013
-	14	3070	AP5_uc002ttq.2_I	NM_207363	NP_997246	O14513	NCKP5_HUMAN		0	TGGCAGGCCTT	0.632	
+	2	175	.1_RNA|THSD7B_	NM_001080427	NP_001073896				7	CAAAGGAAAGA	0.537	
+	2	608	HSD7B_uc002tvb.	NM_001080427	NP_001073896				7	TCCTCTTGGGG	0.463	
+	25	4413	D7B_uc010zbj.1_	NM_001080427	NP_001073896				7	GATAATGAAATC	0.378	
-	72	12103		NM_018557	NP_061027	Q9NZR2	LRP1B_HUMAN		50	GCCATACCACAC	0.438	
-	55	9712		NM_018557	NP_061027	Q9NZR2	LRP1B_HUMAN	ntial).|LDL-receptor class A	50	AGTCATCCTTATT	0.398	
-	7	1830	1B_uc010fnl.1_In	NM_018557	NP_061027	Q9NZR2	LRP1B_HUMAN	ntial).|LDL-receptor class	50	CATTTGTTGCAC	0.403	
+	10	1004	p.E292K|KYNU_u	NM_003937	NP_003928	Q16719	KYNU_HUMAN		2	TTCATGAAAAG	0.308	
-	71	10581		NM_004543	NP_004534	P20929	NEBU_HUMAN	Nebulin 95.	20	TGACATGAATAG	0.348	
+	8	1100		NM_052905	NP_443137	Q96PY5	FMNL2_HUMAN	GBD/FH3.	3	CTCATCCACAC	0.378	
+	3	1489	J3_uc010zce.1_3'	NM_002239	NP_002230	P48549	IRK3_HUMAN	smic (By similarity).	2	TTGGGAGACTTG	0.413	
+	4	550	o.2_Missense_Mu	NM_173355	NP_775491	O95045	UPP2_HUMAN		0	CATCCCCTCCA	0.408	
+	10	1311	C4A10_uc002uby.	NM_022058	NP_071341	Q6U841	S4A10_HUMAN	lasmic (Potential).	5	TCTGGGACCCC	0.333	
-	8	2104	ci.2_Missense_M	NM_033272	NP_150375	Q9NS40	KCNH7_HUMAN	y filter (By similarity).	5	CATTCCCGAAT	0.383	
-	17	3783	zcx.1_Missense_	NM_014900	NP_055715	Q53SF7	COBL1_HUMAN		3	TGAGTCTTGAC	0.428	
-	28	5539	y.2_Missense_Mut	NM_006922	NP_008853	Q9NY46	SCN3A_HUMAN		10	AGCTTCCTTTTT	0.453	
+	7	1186	_p.S299L|SCN2A_	NM_001040142	NP_001035232	Q99250	SCN2A_HUMAN	I.	8	CAATTCATTGGA	0.333	
-	6	981	.R85*|SCN9A_uc	NM_002977	NP_002968	Q15858	SCN9A_HUMAN	r; Name=S p.R214*(1)	13	AGTTCGAAGAG	0.338	
-	20	3098	f.1_Missense_Mu	NM_004525	NP_004516	P98164	LRP2_HUMAN	ellular (Potential).	29	TCATACGATTTC	0.398	
-	185	36159	.1_Missense_Mut	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	TCCCTTCGTCTT	0.433	
-	61	15111	_uc010zfj.1_Intro	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	CACAGGCTTCA	0.463	
-	58	14493	_uc010zfj.1_Intro	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	TGCATTGGTTGT	0.388	
-	52	12562	N_uc010zfj.1_Intr	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	AAAATGGAGCA	0.463	
-	46	15286	N_uc010zfi.1_Intr	NM_133379	NP_596870	Q8WZ42	TITIN_HUMAN		153	TCACCTCCTGAA	0.393	
-	46	11904	N_uc010zfi.1_Intr	NM_133379	NP_596870	Q8WZ42	TITIN_HUMAN		153	CTATTTCTTCAC	0.358	
-	46	10905	N_uc010zfi.1_Intr	NM_133379	NP_596870	Q8WZ42	TITIN_HUMAN		153	AAGAGTGATGGT	0.418	
-	28	5598	TN_uc010zfj.1_Mi	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	AATAAGGGTAG	0.413	
+	12	1208	qn.1_Missense_M	NM_032168	NP_115544	Q8IWA0	WDR75_HUMAN		2	TGATTATGGTCT	0.333	
+	6	944	y.2_RNA|OBFC2	NM_001031716	NP_001026886	Q96AH0	SOSB2_HUMAN		0	CACTGGCCCTG	0.388	
-	43	8022		NM_018897	NP_061720	Q8WXX0	DYH7_HUMAN	k (By similarity).	12	TTTTTTCAGTTTT	0.418	
-	9	848		NM_018897	NP_061720	Q8WXX0	DYH7_HUMAN	n (By similarity).	12	AATTTCCATTCT	0.294	
-	1	261	se_Mutation_p.Q4	NM_024989	NP_079265	Q75T13	PGAP1_HUMAN	enal (Potential).	4	CTTACCTGATA	0.562	
+	42	6732	zs.3_Missense_M	NM_001114132	NP_001107604	Q6ZS30	NBEL1_HUMAN	BEACH.	2	TCGACAGTTCCA	0.338	
+	5	1937		NM_020923	NP_065974	Q9HCK1	ZDBF2_HUMAN		3	AACTTCGGAAG	0.438	
-	7	617		NM_001099334	NP_001092804	Q0P641	CB080_HUMAN		1	TTTGCGGGCGT	0.463	
-	21	2712	zji.1_Missense_M	NM_005235	NP_005226	Q15303	ERBB4_HUMAN	.|Cytoplasm p.E872K(1)	33	CTTTTTCATCTCC	0.378	
-	17	2886	_p.P830S|TNS1_	NM_022648	NP_072174	Q9HBL0	TENS1_HUMAN		4	CCCTGGAGGGC	0.602	
-	16	1379	vj.1_Nonsense_M	NM_022648	NP_072174	Q9HBL0	TENS1_HUMAN		4	GGTGTTATAGTC	0.607	
-	15	1689	x.1_Missense_Mu	NM_024506	NP_078782	Q6UWU2	GLB1L_HUMAN		0	AGACCCAAAGC	0.453	
+	4	246	se_Mutation_p.Q6	NM_013335	NP_037467	Q96IJ6	GMPPA_HUMAN		0	TTCTACCAACCT	0.532	
+	5	1539	p.K528*|ACCN4_	NM_182847	NP_878267	Q96FT7	ACCN4_HUMAN	ellular (Potential).	2	CGAGGAAGTAC	0.443	
-	7	4371	.E1442K|SPHKA	NM_001142644	NP_001136116	Q2M3C7	SPKAP_HUMAN		10	AGGTTCCCCAG	0.498	
-	2	446	R55_uc010fxs.1_	NM_005683	NP_005674	Q9Y2T6	GPR55_HUMAN	ellular (Potential).	1	TACCTGGGACA	0.562	
+	5	736	mp.1_Missense_M	NM_001017915	NP_001017915	Q92835	SHIP1_HUMAN		2	CCCAGGACTCT	0.473	
+	2	187		NM_153325	NP_697020	Q8N687	DB125_HUMAN		3	TCACATGAATATA	0.368	

-	6	725	20orf27_uc002wjh.	NM_001039140	NP_001034229	Q9GZN8	CT027_HUMAN		0	TGTGCTCTGAGT	0.662	
+	2	241	_p.P14T|SMOX_u	NM_175839	NP_787033	Q9NWM0	SMOX_HUMAN		1	GATGACCCTCTC	0.617	
-	6	1798	nj.2_Missense_Mu	NM_020341	NP_065074	Q9P286	PAK7_HUMAN	Linker.	23	AGGAGGAGCCC	0.652	
+	1	344		NM_001052	NP_001043	P31391	SSR4_HUMAN	Name=2; (Potential).	1	GCCGACGAGCTC	0.662	
+	2	63	tj.1_RNA|FRG1B_uc010gdr.1_RNA|FRG1B_uc010ztk.1_Intron						0	AGAATCGCCCTG	0.353	rs7266938
-	5	953	11_splice|COMMD	NM_053041	NP_444269	Q86VX2	COMD7_HUMAN		1	AATTATACCTTTT	0.274	
+	33	4352		NM_020884	NP_065935	A7E2Y1	MYH7B_HUMAN	Potential.	2	CAGTGGAGGAG	0.627	
-	28	4302		NM_032221	NP_115597	Q8TD26	CHD6_HUMAN		14	CTGCCCGGCTG	0.408	
-	16	2573	e_Mutation_p.E81	NM_007050	NP_008981	O14522	PTPRT_HUMAN	lasmic (Potential).	20	CCATCTCCCTCT	0.557	
+	14	2221	wj.1_Missense_Mu	NM_002466	NP_002457	P10244	MYBB_HUMAN		5	CTGCGGGGGGA	0.617	
+	3	231	_p.N21Y|TOX2_u	NM_001098798	NP_001092268	Q96NM4	TOX2_HUMAN		1	GCGAGAACAAC	0.507	
+	2	427	G2_uc010ggz.2_I	NM_003007	NP_002998	P04279	SEMG1_HUMAN		2	CATTTTCACAGG	0.418	
-	4	389	ws.1_Missense_M	NM_002999	NP_002990	P31431	SDC4_HUMAN	cellular (Potential).	0	GGGTGAGATTC	0.527	
+	11	1246	9A8_uc010gic.2_	NM_015266	NP_056081	Q9Y2E8	SL9A8_HUMAN		1	CAGATCCTCATG	0.552	
+	6	2087	e_Mutation_p.S62	NM_001164116	NP_001157588	Q9NQ75	CASS4_HUMAN		3	CTGAATCACACC	0.408	
-	9	2426		NM_003185	NP_003176	O00268	TAF4_HUMAN		3	GTGCCGAGACA	0.512	
+	13	1481	p.E415*|OSBPL2_	NM_144498	NP_653081	Q9H1P3	OSBL2_HUMAN		2	GGCTGGAGGAG	0.622	
-	5	1126_1127	p.S342F|EEF1A2_	NM_001958	NP_001949	Q05639	EF1A2_HUMAN		0	ACCTGGGAGGT	0.678	
-	3	606		NM_080823	NP_543013	Q9H3Y6	SRMS_HUMAN	SH2.	2	CAGGCCGGGAA	0.637	
-	21	1714	TE_uc002yir.1_Mi	NM_199261	NP_954870	P56180	TPTE_HUMAN	2 tensin-type.	5	CATTTTCCTAAT	0.318	
+	1	509		NM_174981	NP_778146	Q86YR6	POTED_HUMAN		6	AAGTCCCCAGA	0.567	
+	19	2577	P25_uc002yjz.1_M	NM_013396	NP_037528	Q9UHP3	UBP25_HUMAN		5	ATGCAAGGTTGG	0.343	
-	4	714	YR1_uc002yme.2_	NM_052954	NP_443186	Q96J86	CYYR1_HUMAN	lasmic (Potential).	0	GAGTATGGAGGA	0.527	
-	9	1715	on_p.K417N|GRIK	NM_000830	NP_000821	P39086	GRIK1_HUMAN	cellular (Potential).	3	ACAAACCTTCTT	0.438	
+	2	268		NM_172201	NP_751951	Q9Y6J6	KCNE2_HUMAN		0	TTGATGCTGAGA	0.458	
+	12	1582		NM_005441	NP_005432	Q13112	CAF1B_HUMAN		2	CATCCCGGAGG	0.532	
-	2	251		NM_003225	NP_003216	P04155	TFF1_HUMAN	P-type.	0	TATTAGGATAGAA	0.468	
-	2	250		NM_080860	NP_543136	Q8WYR4	RSPH1_HUMAN	MORN 2.	1	GAATTCGTAGCT	0.502	
+	1	96	.1_Intron|C21orf2	NM_198689	NP_941962	P60409	KR107_HUMAN		0	CTGGTTCCTGTG	0.662	
+	1	632	.1_Intron|C21orf2	NM_198699	NP_941972	P60413	KR10C_HUMAN	repeats of C-C-X(3).	0	CCGCCCTGTGT	0.716	
+	3	718	e_Mutation_p.P86	NM_006031	NP_006022	O95613	PCNT_HUMAN		8	CCACCCAGCAG	0.438	
-	7	829	p.N135K|SLC25A	NM_005984	NP_005975	P53007	TXTP_HUMAN	e=5; (Potential).|Solcar 3.	0	GGAGTGTTTCC	0.612	
+	5	1643		NM_152612	NP_689825	Q8IYX3	CC116_HUMAN		2	CACCTCCCACT	0.662	
-	8	1305	_5'UTR|HPS4_uc	NM_022081	NP_071364	Q9NQG7	HPS4_HUMAN		0	TCGGTGAAGCA	0.562	
+	4	2181	H_uc003afp.2_5'	NM_021076	NP_066554	P12036	NFH_HUMAN	S-P-[AEPV]-[EAK]- [AEVK]	0	CAAAGTCCCCT	0.557	
-	21	2755	h.1_Missense_Mu	NM_002473	NP_002464	P35579	MYH9_HUMAN	Potential.	11	CTGCCGGCTCA	0.617	
-	8	1045	_p.V302I|TMPRSS	NM_153609	NP_705837	Q8IU80	TMPS6_HUMAN	xtracellular (Potential).	6	CCAGACGACCG	0.667	
+	4	570	us.2_Missense_M	NM_012407	NP_036539	Q9NRD5	PICK1_HUMAN	PDZ.	0	GCCTTGGACGG	0.547	
-	13	2130	xp.2_Missense_M	NM_001098504	NP_001091974	Q92841	DDX17_HUMAN		4	CTAGAGCTCTGT	0.532	
+	4	536	RAP2_uc011aoo.	NM_004810	NP_004801	O75791	GRAP2_HUMAN	SH2.	2	GGGGACTTCTC	0.562	
-	2	222	dr.1_Missense_M	NM_015140	NP_055955	Q14166	TTL12_HUMAN		1	TTCCCCAGCGT	0.642	
-	20	3449	XNB2_uc003bku.1	NM_012401	NP_036533	O15031	PLXB2_HUMAN	cellular (Potential).	6	CACCCGGGCGT	0.642	
+	18	2440	p.P653S|CNTN6_	NM_014461	NP_055276	Q9UQ52	CNTN6_HUMAN	nectin type-III 2.	8	TCAATTCCAGAA	0.388	
+	24	3235	pf.2_Missense_M	NM_175607	NP_783200	Q8IWV2	CNTN4_HUMAN		7	CCACTTCGAATG	0.468	
+	42	5755	R1_uc011asu.1_I	NM_001099952	NP_001093422	Q14643	ITPR1_HUMAN	lasmic (Potential).	21	CACTCCTTTTTCT	0.428	
-	16	2027	RIP2_uc011avh.1_	NM_001080423	NP_001073892	Q9C0E4	GRIP2_HUMAN	PDZ 5.	1	CTCGTTTCCTG	0.483	
-	10	1351	y.3_Missense_Mu	NM_001128176	NP_001121648	P10828	THB_HUMAN	g.|Interaction with NR2F6.	3	CACTGCCATTTC	0.527	

+	7	2062	cen.2_Missense_M	NM_003242	NP_003233	P37173	TGFR2_HUMAN	lasmic (Potential).	26	GAAGACGGCTC	0.592	
-	15	1510		NM_207359	NP_997242	Q6ZQY3	GADL1_HUMAN		0	CCTTTCCCCGG	0.562	
+	2	1361		NM_001137674	NP_001131146	A6NHJ4	ZN860_HUMAN	C2H2-type 2.	1	GAAGCGATACC	0.368	
+	6	552	P21_uc011axy.1_M	NM_016300	NP_057384	Q9UBL0	ARP21_HUMAN		3	TTCCAGTTTTTC	0.363	
-	9	3829		NM_014831	NP_055646	O15050	TRNK1_HUMAN	TPR 3.	2	AATGCACCTCCT	0.478	
+	21	6812	GA4_uc010hgs.2_	NM_002078	NP_002069	Q13439	GOGA4_HUMAN	RIP.|Potential.	4	CTCTTTGGAGAA	0.363	
+	3	424	003cja.2_Missense	NM_145755	NP_665698	Q8NDW8	TT21A_HUMAN		1	TATGCTCACAAA	0.542	
+	5	797	kz.3_Missense_M	NM_001042646	NP_001036111	Q9UPV9	TRAK1_HUMAN	al.|HAP1 N-terminal.	1	CAACCCCGTAAG	0.577	
+	6	2604	IF167_uc003cnj.2_	NM_018651	NP_061121	Q9P0L1	ZN167_HUMAN	C2H2-type 13.	2	ACCAGCGAACTC	0.458	rs151170690
+	1	944		NM_014240	NP_055055	Q9UGP4	LIMD1_HUMAN		1	TGTCAGCACCC	0.622	
+	2	1312	_p.E355K|CCRL2_	NM_003965	NP_003956	O00421	CCRL2_HUMAN	lasmic (Potential).	1	CCACCGAAGTG	0.423	
-	26	3041	pz.1_Nonsense_M	NM_147129	NP_667340	Q60I27	AL2CL_HUMAN		5	GAGCTCCCTGG	0.607	
-	54	5048	a-mir-711|MI0012	NM_000094	NP_000085	Q02388	CO7A1_HUMAN	le-helical region.	11	CATTTCGTCCAT	0.567	
-	5	428		NM_000884	NP_000875	P12268	IMDH2_HUMAN		1	GAATCCCTGTTC	0.512	
-	5	1033	mw.2_Missense_M	NM_003392	NP_003383	P41221	WNT5A_HUMAN		0	GCACTTGCAGG	0.552	
-	13	2537	lm.2_Missense_M	NM_003716	NP_003707	Q9ULU8	CAPS1_HUMAN		3	GATGTCGGTGA	0.512	
-	23	3441	3dmh.1_Missense_	NM_182920	NP_891550	Q9P2N4	ATS9_HUMAN	TSP type-1 6.	4	AGTCCCAATGAT	0.413	
-	2	612	x.1_Missense_Mu	NM_007114	NP_009045	P82094	TMF1_HUMAN		0	CGTTGTGATTTG	0.428	
-	2	1677	lnt.2_Missense_M	NM_198271	NP_938012	Q0VAK6	LMOD3_HUMAN		1	CTTCAGCTTCAC	0.532	
-	3	1206		NM_016206	NP_057290	A8MV65	VGLL3_HUMAN		0	TCTGTCTTTGTG	0.542	
+	4	1237	lrp.1_Missense_M	NM_001080448	NP_001073917	Q9UF33	EPHA6_HUMAN	cellular (Potential).	16	ATACATGGAAGC	0.383	
+	5	942	x.2_Missense_Mu	NM_198196	NP_937839	P40200	TACT_HUMAN	cellular (Potential).	3	TCTTGAGGAGC	0.498	
+	3	659	dyn.2_Missense_M	NM_001008272	NP_001008273	Q9UI15	TAGL3_HUMAN	CH.	0	AAATCTCCCAGT	0.488	
+	8	968	bjd.1_Missense_M	NM_033364	NP_203528	Q7Z4T9	AAT1_HUMAN	Potential.	3	TCTAAAAGAGCT	0.443	
+	10	1045	bji.1_Missense_M	NM_014980	NP_055795	Q9Y2K9	STB5L_HUMAN		9	GAAAATCTGAAT	0.254	
+	1	161	1bjn.1_Missense_	NM_021082	NP_066568	Q16348	S15A2_HUMAN		1	TGAATCCTTTCC	0.493	
-	9	1494	hrt.2_Missense_M	NM_022757	NP_073594	Q49A88	CCD14_HUMAN		0	CTGTTGGAAGT	0.353	
-	7	877	003eht.3_Missense	NM_024628	NP_078904	A0AV02	S12A8_HUMAN		0	GAGGTCGCCCC	0.637	
+	4	787	SEC_uc003ekj.2_	NM_021937	NP_068756	P57772	SELB_HUMAN		1	GCTCCATCAGCC	0.582	
-	18	3673_3674		NM_015103	NP_055918	Q9Y4D7	PLXD1_HUMAN	cellular (Potential).	1	CTCCCCGGGGT	0.668	
+	4	1367	_Mutation_p.D365	NM_023943	NP_076432	Q6UXF1	TM108_HUMAN	cellular (Potential).	4	GCCTTCGATACC	0.592	rs79118437
-	5	685	plu.1_Nonsense_M	NM_016577	NP_057661	Q9NRW1	RAB6B_HUMAN		1	TCTGTTGGAAGG	0.547	
-	13	2017		NM_173543	NP_775814	Q8IYY4	DZI1L_HUMAN		2	TGGCTGGGCCT	0.577	
-	2	1219		NM_005067	NP_005058	O43255	SIAH2_HUMAN	SBD.	2	CTGAAGGGTGG	0.537	
-	4	4475		NM_178822	NP_849144	Q6WRI0	IGS10_HUMAN		13	TGGGAGTCGCC	0.493	
-	1	293	_p.E89K|SERPIN	NM_006217	NP_006208	O75830	SPI2_HUMAN		3	AGGTTTCCTGTT	0.358	
+	7	1388	hwy.1_Missense_	NM_207015	NP_996898	Q58DX5	NADL2_HUMAN	cellular (Potential).	1	TTGTTGGATTTG	0.299	
-	6	827	C39_uc003fkn.2_	NM_181426	NP_852091	Q9UFE4	CCD39_HUMAN	Potential.	4	CTCCATCCCTCT	0.348	
+	33	4874	c003fnv.3_Missens	NM_198241	NP_937884	Q04637	IF4G1_HUMAN	.|EIF4A-binding.	7	AGGATGCCTTCT	0.577	
-	2	892		NM_001025266	NP_001020437	A6NLC5	CC070_HUMAN		0	AGGGGGAGAGA	0.537	
+	1	108		NM_153708	NP_714919	P59025	RTP1_HUMAN	lasmic (Potential).	3	AGGTGGAAATT	0.527	
-	2	442	ASP1_uc003frk.1_	NM_001879	NP_001870	P48740	MASP1_HUMAN	MBL2.|Homodimerization	4	AGTCTGGATAAC	0.483	
-	2	1027		NM_001004312	NP_001004312	Q5QGT7	RTP2_HUMAN	ical; (Potential).	0	CCAGCGAAGAG	0.587	
-	3	1118	3fsg.2_Missense_M	NM_018192	NP_060662	Q8IVL5	P3H2_HUMAN		4	CTGTATCTTCAAC	0.418	
-	19	2227		NM_198505	NP_940907	Q4VNC0	AT135_HUMAN		11	CAATGATCACTTG	0.468	
-	2	2438	p.2_Intron|MUC4_	NM_018406	NP_060876	Q99102	MUC4_HUMAN		0	GGTGTCAGTCAT	0.562	
+	9	987	p.R322Q|LMLN_u	NM_033029	NP_149018	Q96KR4	LMLN_HUMAN		1	AGTTCGAAAAGT	0.308	

+	3	305	.P50L|ZNF595_uc	NM_182524	NP_872330	Q7Z3I0	Q7Z3I0_HUMAN		0	TAACCCAGACC	0.398	
+	2	666	ao.3_Missense_M	NM_000283	NP_000274	P35913	PDE6B_HUMAN	GAF 1.	0	GCGAAGACGAA	0.403	
+	7	1459	gcg.2_Missense_M	NM_021923	NP_068742	Q8N441	FGRL1_HUMAN	lasmic (Potential).	0	ACCTTCCCTCGT	0.736	
-	8	831	lk.1_Missense_Mu	NM_006527	NP_006518	Q14493	SLBP_HUMAN		0	TGGTGGGTGTG	0.493	
+	11	1380	se_Mutation_p.E3	NM_018986	NP_061859	Q8TE82	S3TC1_HUMAN		3	CGCAGGAAAAA	0.577	
+	13	2581	.R781S|STIM2_uc	NM_020860	NP_065911	Q9P246	STIM2_HUMAN	lasmic (Potential).	2	AACCTCGCCAC	0.483	rs142749005
-	2	557	n_p.L60I|TLR10_u	NM_030956	NP_112218	Q9BXR5	TLR10_HUMAN	lar (Potential).|LRR 2.	2	AAAAAGGAGGT	0.423	
+	8	3224	zz.1_Missense_M	NM_020722	NP_065773	Q6ZU35	K1211_HUMAN	Pro-rich.	2	CCCCGGCTCCG	0.652	
-	5	458		NM_182502	NP_872308	Q86T26	TM11B_HUMAN	racellular (Potential).	1	TGAACCATTGG	0.328	
-	9	1264		NM_001042784	NP_001036249	Q5M9N0	CD158_HUMAN	Potential.	6	AGATTCCTGAC	0.368	
+	3	226		NM_006419	NP_006410	O43927	CXL13_HUMAN		0	ATTGATCGAATT	0.393	
-	2	827_828		NM_006168	NP_006159	P78426	NKX61_HUMAN	Homeobox.	0	GTCATCCCCAAC	0.54	
+	4	1156	n.2_Missense_Mu	NM_020203	NP_064588	Q9NQ76	MEPE_HUMAN		3	AGTTTCATTAC	0.438	
-	5	982	_p.R163S|ABCG2	NM_004827	NP_004818	Q9UNQ0	ABCG2_HUMAN	er.|Cytoplasmic (Potential).	1	ATGACCCTGTT	0.438	
+	3	1691	190A_uc010ikv.2_	NM_001145065	NP_001138537	Q9C0I3	F190A_HUMAN		2	CATTTCGTGAA	0.363	
+	6	2267	M190A_uc003hsw.	NM_001145065	NP_001138537	Q9C0I3	F190A_HUMAN		2	GTTCTTCAAGAG	0.313	
-	6	911	_uc011ced.1_Mis	NM_000670	NP_000661	P08319	ADH4_HUMAN		2	GGTTTCAGATC	0.378	
+	29	3407	_p.D279N|ANK2_u	NM_001148	NP_001139	Q01484	ANK2_HUMAN	raction with SPTBN1.	14	ATGGGGACAGC	0.468	
-	21	2688	utation_p.G803S|	NM_001083	NP_001074	O76074	PDE5A_HUMAN	ytic (By similarity).	0	GCAGCCATCTA	0.517	
-	3	515	_p.P89S|PRDM5_	NM_018699	NP_061169	Q9NQX1	PRDM5_HUMAN	SET.	2	AGATGGTGCCT	0.448	
+	1	106		NM_024582	NP_078858	Q6V0I7	FAT4_HUMAN		18	TTCCGGGGCAG	0.632	
+	1	783	P_uc003ijr.1_Miss	NM_022475	NP_071920	Q96QV1	HHIP_HUMAN	Arg-rich.	6	TGGGAACCCCC	0.592	
-	18	4567		NM_017639	NP_060109	Q6V1P9	PCD23_HUMAN	Cadherin 13.	4	TGCACCAGAAG	0.483	
-	5	962	e_Mutation_p.P30	NM_000508	NP_000499	P02671	FIBA_HUMAN	By similarity.	3	TCCAGGTCCAG	0.572	
+	10	1555	_p.S391F|GUCY1	NM_000857	NP_000848	Q02153	GCYB1_HUMAN	anylate cyclase.	0	TGATTCCCGGA	0.488	
-	5	684		NM_001334	NP_001325	P43234	CATO_HUMAN		0	ATCCAGAATGT	0.294	
+	8	1434	L3_uc010irs.2_3'	NM_018248	NP_060718	Q8TAT5	NEIL3_HUMAN		4	AAACGATATAACT	0.373	
-	4	458	PDLIM3_uc003ixy.	NM_014476	NP_055291	Q53GG5	PDLI3_HUMAN		2	GTTCCCGTCCT	0.473	
-	13	3274	ckv.1_Missense_	NM_021069	NP_066547	O94875	SRBS2_HUMAN		1	TTCTCCCGCAGT	0.607	
-	3	390	.1_5'UTR|CTNND	NM_001332	NP_001323	Q9UQB3	CTND2_HUMAN	Potential.	8	TTGCATCGCTCC	0.522	
-	53	8891		NM_001369	NP_001360	Q8TE73	DYH5_HUMAN	4 (By similarity).	31	CATTTCCCTGA	0.438	
+	3	433		NM_138348	NP_612357	Q96BN8	F105B_HUMAN		2	CAAAAAAGAAT	0.323	
+	9	1098		NM_020227	NP_064612	Q9NQV7	PRDM9_HUMAN	SET.	6	TATGTGGATGGA	0.423	
+	27	4021	_Mutation_p.E79	NM_024867	NP_079143	Q9C093	SPEF2_HUMAN		4	AAAAGGAGCCA	0.403	
-	1	296	.2_Missense_Mut	NM_199335	NP_955367	O15117	FYB_HUMAN		2	GGGTTCCTTGT	0.552	
-	18	2276	jmi.3_Nonsense_	NM_173489	NP_775760	Q7Z745	HTRB2_HUMAN	HEAT 7.	8	ATCCTGAGTCA	0.388	
-	4	659		NM_000436	NP_000427	P55809	SCOT1_HUMAN		3	CCATGCGTTTTAT	0.423	
+	5	431	R_uc011cpq.1_5'	NM_000163	NP_000154	P10912	GHR_HUMAN	ellular (Potential).	6	AGCTAACTAGC	0.333	
+	9	1203	_p.S348T|IL31RA_	NM_139017	NP_620586	Q8NI17	IL31R_HUMAN	tential).|Fibronectin type-III	1	AAAGCTCTGCT	0.522	
-	2	294	kin.2_Missense_	NM_001884	NP_001875	P10915	HPLN1_HUMAN	g-like V-type.	5	TTTTATGGATTCC	0.428	
+	4	658	se_Mutation_p.R8	NM_198150	NP_937793	Q6UWY0	ARSK_HUMAN		1	TAACAGGACTA	0.413	
+	16	3357	y.3_Missense_Mu	NM_001127511	NP_001120983	P25054	APC_HUMAN	through a l1(1)|p.K993fs*	2515	AAAGTAAGTTTT	0.348	
+	3	1252		NM_175856	NP_787052	Q70JA7	CHSS3_HUMAN	enal (Potential).	3	AACTTCGCTAC	0.488	
-	3	462	n_p.S107F|FNIP1_	NM_133372	NP_588613	Q8TF40	FNIP1_HUMAN		2	CAGAAGATGAA	0.308	
+	3	345		NM_002188	NP_002179	P35225	IL13_HUMAN		2	CAGCTGGGGTA	0.612	
+	21	3055		NM_014829	NP_055644	Q7L014	DDX46_HUMAN		1	ACTCTGAAGCC	0.418	
-	5	1429	se_Mutation_p.G	NM_020389	NP_065122	Q9HCX4	TRPC7_HUMAN	ical; (Potential).	0	CATCCCGAAAT	0.572	

-	3	661	LHL3_uc010jem.1_	NM_017415	NP_059111	Q9UH77	KLHL3_HUMAN	BTB.		0	GTAGGGGCTGC	0.542
+	1	1384	hh.1_Intron|PCDH	NM_018910	NP_061733	Q9UN72	PCDA7_HUMAN	|Extracellular (Potential).		4	TATACGGTGTTC	0.667
+	1	1132		NM_018940	NP_061763	Q9Y5E2	PCDB7_HUMAN	r (Potential).|Cadherin 3.		6	CTATTCAGGCC	0.418
-	3	1004	jgh.2_Missense_M	NM_005471	NP_005462	P46926	GNPI1_HUMAN			0	TCTCCGGGTGG	0.542
-	2	194		NM_003122	NP_003113	P00995	ISK1_HUMAN			0	CCAGGGAGTCA	0.373
-	2	470	on_p.G92E|CSF1	NM_005211	NP_005202	P07333	CSF1R_HUMAN	1.|Extracellular (Potential).		54	TGCCTCCCAGG	0.597
-	5	842	MD4_uc010jii.2_Int	NM_138379	NP_612388	Q96H15	TIMD4_HUMAN	xtracellular (Potential).		2	ATGTTGATGGG	0.398
+	26	5531	.3_Missense_Mut	NM_001122679	NP_001116151					10	ATGATCGAAATAT	0.507
+	3	748		NM_003862	NP_003853	O76093	FGF18_HUMAN			0	TGGGCCGCAGG	0.592
+	4	1395	mcf.2_Missense_M	NM_153607	NP_705835	Q8IUR6	CE041_HUMAN	Glu-rich.		0	ggaggatgttgatgatg	0.139
+	2	179		NM_015980	NP_057064	Q9Y328	NSG2_HUMAN	lasmic (Potential).		1	AGAAGGGAACC	0.532
+	13	2239		NM_133369	NP_588610	Q6ZN44	UNC5A_HUMAN	lasmic (Potential).		1	GGAATGGCACG	0.622
-	4	580		NM_001012418	NP_001012418	Q86YV6	MYLK4_HUMAN			4	CTTGGCTGTCA	0.463
-	7	1709	orf146_uc003mvy.	NM_173563	NP_775834	Q8IXS0	CF146_HUMAN			1	TTTCTTCCTTCT	0.388
+	16	2482	q.1_Missense_Mu	NM_004415	NP_004406	P15924	DESP_HUMAN	Globular 1.		9	TTCAGAGGTTCT	0.363
+	9	7846	EP1_uc011diq.1_	NM_002114	NP_002105	P15822	ZEP1_HUMAN			6	TAATCCCCTCAG	0.532
+	3	692	p.W120G|EDN1_u	NM_001955	NP_001946	P05305	EDN1_HUMAN	ndothelin-like.		1	AGTGCTGGAAT	0.443
+	3	534	dkk.1_Missense_	NM_007048	NP_008979	O00481	BT3A1_HUMAN	1.|Extracellular (Potential).		2	TGTTCCCGACC	0.572
+	3	275	1_5'UTR|PRSS16_	NM_005865	NP_005856	Q9NQE7	TSSP_HUMAN			5	ACATTGGGTTG	0.488
-	3	2488		NM_052923	NP_443155	Q6R2W3	SCND3_HUMAN			1	TTGCATGGATATT	0.413
-	1	906		NM_030876	NP_110503	Q9UGF6	OR5V1_HUMAN	Name=7; (Potential).		4	ACACTGAAACC	0.423
+	4	641	c003nuj.2_Silent_	NM_000594	NP_000585	P01375	TNFA_HUMAN	ellular (Potential).		3	TCAGCCGCATC	0.632
-	28	3543	tion_p.S976*|EHM	NM_006709	NP_006700	Q96KQ7	EHMT2_HUMAN	Post-SET.		1	CGGCTGAGTGC	0.582
-	19	6917		NM_019105	NP_061978	P22105	TENX_HUMAN	nectin type-III 15.		0	CACCCGCACCG	0.632
-	5	1239	sq.1_Missense_M	NM_012391	NP_036523	O95238	SPDEF_HUMAN	ETS.		5	CCTTCTCCTTG	0.637
-	8	1581		NM_001010903	NP_001010903	P0C671	CF222_HUMAN			4	TGGGTCGTCGG	0.607
+	25	3473		NM_001371	NP_001362					21	TTTCAGGATCTT	0.333
+	27	3854		NM_001371	NP_001362				p.R1085Q(2)	21	TCTGTCGATATCT	0.328
+	58	8884		NM_001371	NP_001362					21	ATATATGAATTG	0.378
+	32	6398	9_uc010jyk.2_Mis	NM_015089	NP_055904	Q8IWT3	CUL9_HUMAN	RING-type 1.		12	AGCAGAACCTTG	0.592
-	2	680	_p.P33S|CLIC5_u	NM_001114086	NP_001107558	Q9NZA1	CLIC5_HUMAN			2	GAAAGGACAGT	0.478
+	1	4054	e.2_Missense_Mu	NM_001010870	NP_001010870	O60522	TDRD6_HUMAN	Tudor 6.		6	GTCCACCTTTG	0.373
+	6	994	p.H303Y|GPR115_	NM_153838	NP_722580	Q8IZF3	GP115_HUMAN	ellular (Potential).		8	GGTTTCACATC	0.393
-	1	403		NM_138733	NP_620061	P07205	PGK2_HUMAN			1	CTACACAGTCC	0.537
-	3	334	wu.1_Missense_M	NM_002388	NP_002379	P25205	MCM3_HUMAN			3	GGAAGGCAACC	0.468
+	10	1423	AG_uc010jzt.2_R	NM_014464	NP_055279	Q9UJW2	TINAG_HUMAN			4	ACAAGGGCAGA	0.363
+	5	1186		NM_001010872	NP_001010872	Q5T0W9	FA83B_HUMAN			6	TCACGGATACA	0.328
+	6	933		NM_207410	NP_997293	Q6UXV0	GFRAL_HUMAN	ellular (Potential).		2	ATATCCTTGGG	0.413
-	3	436	MGCLL1_uc011dx	NM_019036	NP_061909	Q8TB92	HMGC2_HUMAN			4	CTACCTTTTCATT	0.308
-	7	1931	f.1_Missense_Mu	NM_021073	NP_066551	P22003	BMP5_HUMAN			2	CAGATGAACCT	0.333
-	23	2334	OL21A1_uc011dx	NM_030820	NP_110447	Q96P44	COLA1_HUMAN	ollagen-like 4.		2	TGATTTCCTTTGT	0.299
-	10	1607	se_Mutation_p.D	NM_030820	NP_110447	Q96P44	COLA1_HUMAN	ollagen-like 1.		2	AGGGTCACCCT	0.458
-	4	891	se_Mutation_p.R	NM_030820	NP_110447	Q96P44	COLA1_HUMAN			2	GAATTCGTGTT	0.323
+	3	1070	k.2_Missense_Mut	NM_001704	NP_001695	O60242	BAI3_HUMAN	ellular (Potential).		50	GGATCGACGAC	0.493
+	6	538_539	kam.1_Missense_	NM_001858	NP_001849	Q14993	COJA1_HUMAN	P N-terminal.		4	AGAAGGTGGTG	0.332
-	10	1746	L12A1_uc003phu	NM_004370	NP_004361	Q99715	COCA1_HUMAN	VWFA 2.		9	TCTCTCTGACAT	0.378
-	13	1697		NM_001563	NP_001554	Q17R60	IMPG1_HUMAN			3	ACAGATCCATTT	0.498

+	17	2793	p.Q836K|DOPEY1	NM_015018	NP_055833	Q5JWR5	DOP1_HUMAN			4	CAAACCAGGGA	0.463	
-	3	895		NM_198568	NP_940970	Q6PEY0	CXB7_HUMAN	ical; (Potential).		0	ATGACCAAGAA	0.388	
+	16	1980_1981	e_Mutation_p.G48	NM_014942	NP_055757	Q9Y2G4	ANKR6_HUMAN			3	CTGCAGGTCCA	0.53	
-	3	1299	u.2_Missense_Mu	NM_001143957	NP_001137429	Q9BZJ6	GPR63_HUMAN	lasmic (Potential).		2	TCCTCAAGGCA	0.463	
+	5	867	SP3_uc003pvo.2_	NM_003880	NP_003871	O95389	WISP3_HUMAN	TSP type-1.		0	CTTGCGACAGC	0.338	rs140750750
-	27	3886	.P1186S|LAMA4_	NM_001105206	NP_001098676	Q16363	LAMA4_HUMAN	minin G-like 2.		9	TAGGGGAAGGT	0.458	
-	3	234		NM_001010876	NP_001010876	Q5VVB8	CF191_HUMAN			1	GAAATCAAATG	0.338	
-	9	1442	3qci.2_Missense_	NM_001431	NP_001422	O43491	E41L2_HUMAN	FERM.		2	CCCAGCTTGAT	0.413	
+	7	1097	el.2_Missense_Mu	NM_004865	NP_004856	P62380	TBPL1_HUMAN			0	GTGTTTGAAAG	0.388	
+	4	559	B_uc003qgr.2_Mis	NM_018945	NP_061818	Q9NP56	PDE7B_HUMAN			1	CTGCTTCGTGGA	0.468	
+	2	185	n_p.Q3K|TAB2_uc	NM_015093	NP_055908	Q9NYJ8	TAB2_HUMAN			0	TGGCCCAAGGA	0.423	
-	45	7290	u.3_Missense_Mu	NM_182961	NP_892006	Q8NF91	SYNE1_HUMAN	ytoplasmic (Potential).		45	GAGGTGGTTAT	0.413	
+	2	173	n_p.M1L|VIP_uc0	NM_003381	NP_003372	P01282	VIP_HUMAN			0	CAGAAATGGAC	0.478	
-	3	493		NM_018452	NP_060922	Q9NWH2	CF035_HUMAN			0	CAAGGGAAGAC	0.493	
+	10	1307_1308	YNJ2_uc011efn.1	NM_003898	NP_003889	O15056	SYNJ2_HUMAN	SAC.	p.T411T(1)	1	AAGACCCTGG	0.564	rs150778836
+	9	1583	2A1_uc003qtd.2_	NM_003057	NP_003048	O15245	S22A1_HUMAN	ical; (Potential).		0	GCAAGCCTTGC	0.498	
-	18	2804		NM_005577	NP_005568	P08519	APOA_HUMAN	Kringle 30.		6	TACTCCCACCTG	0.512	rs35765299
+	3	566	_5'Flank|TTYH3_	NM_025250	NP_079526	Q9C0H2	TTYH3_HUMAN	ellular (Potential).		0	CCAACCGCACG	0.711	
-	17	1646	a.2_Missense_Mu	NM_004080	NP_004071	Q9Y6T7	DGKB_HUMAN	DAGKc.		12	GTCAGGAACAT	0.373	
-	5	596	p.D137N|DGKB_u	NM_004080	NP_004071	Q9Y6T7	DGKB_HUMAN			12	AATGTCCTTCA	0.433	
+	6	949	uh.2_Missense_M	NM_178559	NP_848654	Q2M3G0	ABCB5_HUMAN	r 1.|Extracellular (Potential)		6	TGGTAGCACAC	0.403	
+	16	2425	h.2_Missense_Mu	NM_178559	NP_848654	Q2M3G0	ABCB5_HUMAN	tential).|ABC transporter 2		6	TGCAAGGACAA	0.483	
+	19	2983	uh.2_Nonstop_Mu	NM_178559	NP_848654	Q2M3G0	ABCB5_HUMAN			6	TGCAGTGATGC	0.368	
+	3	676	kwc.1_RNA|INMT_	NM_006774	NP_006765	O95050	INMT_HUMAN			0	GAGGAGGTGGA	0.582	
+	9	817	_p.L224P|AVL9_u	NM_015060	NP_055875	Q8NBF6	AVL9_HUMAN	ical; (Potential).		0	TATCCCTTTTTCC	0.328	
+	7	1355	kal.1_Missense_M	NM_007270	NP_009201	O95302	FKBP9_HUMAN	se FKBP-type 4.		14	GATTACCTCAAA	0.527	
+	8	1345	e_Mutation_p.R27	NM_198428	NP_940820	Q3SYG4	PTHB1_HUMAN			5	CAAATTCGATTC	0.378	
-	5	1323	tes.3_Missense_	NM_022373	NP_071768	Q9BSE4	HERP2_HUMAN			3	CTTGCCCAGGA	0.408	
+	7	1198	3tvz.2_Missense_	NM_022479	NP_071924	Q6IS24	GLTL3_HUMAN	enal (Potential).		7	CTCTTCGCGTT	0.537	
+	10	1116		NM_000265	NP_000256	P14598	NCF1_HUMAN	-rich (highly basic).		1	GAGCCCGCTCG	0.517	
-	6	10908	.R3540Q|PCLO_	NM_033026	NP_149015	Q9Y6V0	PCLO_HUMAN			7	GTGCCCGTATG	0.443	
-	5	8183	_Mutation_p.P263	NM_033026	NP_149015	Q9Y6V0	PCLO_HUMAN			7	AAATTGGAATTT	0.458	
-	3	2934	v.2_Missense_Mu	NM_033026	NP_149015	Q9Y6V0	PCLO_HUMAN	Pro-rich.		7	TAGGTCGTGGG	0.517	
+	3	1009		NM_002523	NP_002514	P47972	NPTX2_HUMAN	Pentaxin.		3	CCAACGAGATC	0.637	
+	18	2374	p.S722F|TRRAP_	NM_003496	NP_003487	Q9Y4A5	TRRAP_HUMAN		p.S722F(10)	37	TGTCTCCCTCT	0.413	rs147405090
+	52	8015_8016	.R2585*|TRRAP_	NM_003496	NP_003487	Q9Y4A5	TRRAP_HUMAN			37	ACTCTCCGAGA	0.475	
-	15	1882	TAF6_uc011kji.1_	NM_139315	NP_647476	P49848	TAF6_HUMAN			2	ACTCCCAGGAC	0.652	
+	14	2890	AN_uc003uwl.2_	NM_003386	NP_003377	Q9Y493	ZAN_HUMAN	ate) (mucin-like domain).|E		11	CCATCTCCCCA	0.502	
+	14	2893	AN_uc003uwl.2_	NM_003386	NP_003377	Q9Y493	ZAN_HUMAN	ate) (mucin-like domain).|E		11	TCTCCCCAGAA	0.498	
+	4	485		NM_001283	NP_001274	P61966	AP1S1_HUMAN			0	CAGGACACCTC	0.577	
-	3	173	vey.2_Missense_M	NM_007356	NP_031382	A4D0S4	LAMB4_HUMAN	inin N-terminal.		8	TGGTGGGATGA	0.517	
+	10	1479	D1_uc011kmo.1_	NM_001007245	NP_001007246	O00458	IFRD1_HUMAN			2	GGGCAGTGGAG	0.433	
-	4	1731		NM_033427	NP_219499	Q8WZ74	CTTB2_HUMAN	Pro-rich.		5	TTTTTGGAGGGA	0.537	
-	4	1212		NM_033427	NP_219499	Q8WZ74	CTTB2_HUMAN	Pro-rich.		5	AGGTGGGAAAG	0.547	
+	12	3361	.2_Intron|PTPRZ1_	NM_002851	NP_002842	P23471	PTPRZ_HUMAN	ellular (Potential).		9	TCATGCCCTCT	0.453	
-	23	2788	b.2_Missense_Mu	NM_005763	NP_005754	Q9UDR5	AASS_HUMAN	pine dehydrogenase.		2	AAAGGGCCCCA	0.368	
-	5	1124	_p.E21K|CADPS2_	NM_017954	NP_060424	Q86UW7	CAPS2_HUMAN			2	ACTTTCCAAAT	0.343	

+	3	1086	_p.T182I|BPGM_	NM_199186	NP_954655	P07738	PMGE_HUMAN		0	GCAAAACCATTC	0.443	
-	1	663	NND2A_uc003vvw	NM_015689	NP_056504	Q9ULE3	DEN2A_HUMAN		4	CCGACCCATCC	0.597	
-	15	1860		NM_004333	NP_004324	P15056	BRAF_HUMAN	rotein kinas_R603>I(2)|p.T	18290	ATTTCACTGTA	0.368	
+	1	595		NM_001001656	NP_001001656	Q8NGU2	OR9A4_HUMAN	Name=5; (Potential).	1	TTTATCCTCTTC	0.403	
+	14	1639		NM_004668	NP_004659	O43451	MGA_HUMAN	(Potential).|Maltase.	2	TTGTAGGATATG	0.353	
-	15	1885		NM_000420	NP_000411	P23276	KELL_HUMAN	cellular (Potential).	4	TGGGGGTTGGA	0.542	
-	1	454		NM_001001658	NP_001001658	Q8NGT5	OR9A2_HUMAN	Name=4; (Potential).	1	AGATTTCAGAAA	0.413	
+	1	19		NM_001001667	NP_001001667	Q8N148	OR6V1_HUMAN	cellular (Potential).	1	GCCAGCCCTCC	0.393	
-	4	584	jo.1_Missense_M	NM_007189	NP_009120	Q9UG63	ABCF2_HUMAN	C transporter 1.	1	GCAAGGGTGTC	0.562	
-	12	1443	_p.E435*|SMARC	NM_001003801	NP_001003801	Q6STE5	SMRD3_HUMAN		2	GAACTCAGCCC	0.637	
+	13	2623	vv.1_Missense_M	NM_053043	NP_444271	Q96EV2	RBM33_HUMAN		1	CAGAAGCTCAC	0.552	
+	10	1160_1161	M2_uc011kwi.1_I	NM_003970	NP_003961	P54296	MYOM2_HUMAN	like C2-type 2.	6	CCTGTCCTTCAG	0.569	
+	29	3705	kwi.1_Splice_Site	NM_003970	NP_003961	P54296	MYOM2_HUMAN		6	CAAAGGTATCA	0.418	
-	52	8407	_Mutation_p.E20	NM_033225	NP_150094	Q96PZ7	CSMD1_HUMAN	r (Potential).|Sushi 17.	25	AGTTTCGCTGC	0.458	
-	25	4282	p.P690S|CSMD1_	NM_033225	NP_150094	Q96PZ7	CSMD1_HUMAN	lar (Potential).|CUB 8.	25	ATACGGAGCTG	0.468	
-	2	307		NM_001926	NP_001917	Q01524	DEF6_HUMAN		0	TGACAGTGCAG	0.438	
+	5	836		NM_016353	NP_057437	Q9UIJ5	ZDHC2_HUMAN	DHHC-type.	0	TCTGTGATAAG	0.388	
-	12	1564	e_Mutation_p.R36	NM_001135691	NP_001129163	P54219	VMAT1_HUMAN	lasmic (Potential).	2	ATACCGACCCA	0.498	rs138845247
+	4	1100	10ltz.2_RNA|SLC	NM_016612	NP_057696	Q9NYZ2	MFRN1_HUMAN	ical; Name=6; (Potential).	0	CCATTTCTTGGT	0.512	
+	16	1905	AM28_uc010lua.2	NM_014265	NP_055080	Q9UKQ2	ADA28_HUMAN	ar (Potential).|Cys-rich.	5	GTGGCGATAAC	0.408	
+	9	953	ec.2_Missense_M	NM_003817	NP_003808	Q9H2U9	ADAM7_HUMAN	B.|Extracellular (Potential).	5	CTTAAAACACG	0.299	
-	6	1148	_p.E364K|CLU_uc	NM_203339	NP_976084	P10909	CLUS_HUMAN		2	CTGCTCGTTCA	0.572	
+	13	1595	r.1_Missense_Mu	NM_018091	NP_060561	Q9H9T3	ELP3_HUMAN	cetyltransferase.	0	TGGTCCCTGTG	0.428	
+	4	678	qa.1_Missense_M	NM_001005365	NP_001005365	Q6S8J7	POTEA_HUMAN	ANK 4.	1	ACAGCGAATGG	0.303	rs148181653
-	6	1168	_p.R276K|PCMT	NM_052937	NP_443169	Q96MG8	PCMD1_HUMAN		0	TTTTCCTTTTGG	0.373	
-	15	2681	xrf.3_Missense_M	NM_014781	NP_055596	Q8TDY2	RBCC1_HUMAN		11	TGTTTGGATGG	0.363	rs34016926
+	1	339		NM_052898	NP_443130	Q5GH76	XKR4_HUMAN		2	GCAGGGAGCAG	0.463	
+	3	928	xui.2_RNA|CLVS1	NM_173519	NP_775790	Q8IUQ0	CLVS1_HUMAN	CRAL-TRIO.	5	TCAATCCTTAAAC	0.378	
-	2	365		NM_004820	NP_004811	O75881	CP7B1_HUMAN		3	GATAAGGAAGC	0.373	
+	2	838		NM_004770	NP_004761	Q92953	KCNB2_HUMAN	lasmic (Potential).	7	TGAACGAGAAC	0.512	
-	10	1618	_p.S485G|RUNX1	NM_175634	NP_783552	Q06455	MTG8_HUMAN		16	CTCGCTTGAAT	0.483	
-	6	975	se_Mutation_p.V1	NM_012415	NP_036547	O95073	FSBP_HUMAN		4	ATATACAAGGTA	0.358	
+	14	2536	.1_Missense_Muta	NM_002380	NP_002371	O00339	MATN2_HUMAN	VWFA 2.	2	CCGACGGACGG	0.557	
+	1	409		NM_024410	NP_077721	Q14990	ODFP1_HUMAN		2	AAGATGAGAAG	0.363	
+	3	1185		NM_030788	NP_110415	Q9H295	TM7S4_HUMAN	ical; (Potential).	4	GGTTCCTCTCA	0.398	
+	50	8637		NM_177531	NP_803875	Q86WI1	PKHL1_HUMAN	cellular (Potential).	14	AGCTTTCACCGT	0.443	
-	62	10049	nt.2_Missense_M	NM_198123	NP_937756	Q7Z407	CSMD3_HUMAN	r (Potential).|Sushi 26.	63	GGGCAGGTATA	0.383	
-	22	2211	tion_p.Y601H|PTK	NM_153831	NP_722560	Q05397	FAK1_HUMAN	rotein kinase.	6	GTCATAGGCCC	0.522	
-	7	1375	1_5'Flank|LRRC14	NM_004260	NP_004251	O94761	RECQ4_HUMAN		4	CGGTGGGGTCC	0.627	
+	33	4322	gv.2_Missense_M	NM_203447	NP_982272	Q8NF50	DOCK8_HUMAN	DHR-2.	6	AGACACATTGG	0.403	
-	38	5360	.V1143A|PTPRD_	NM_002839	NP_002830	P23468	PTPRD_HUMAN	).|Tyrosine-protein phosph	22	GCACAACCATC	0.468	
-	1	254		NM_001017363	NP_001017363	A6NKF2	ARI3C_HUMAN		1	AAGGCGAGCTG	0.413	rs143589793
-	15	2604	NAP3_uc011lqr.1_	NM_033655	NP_387504	Q9BZ76	CNTP3_HUMAN	inal.|Extracellular (Potenti	1	CTTACGATCTCC	0.448	rs148747631
-	7	1311	4aia.2_Missense_	NM_001007471	NP_001007472	Q9HCF6	TRPM3_HUMAN	lasmic (Potential).	9	GCACGGGAGGG	0.537	
-	8	6452	_5'Flank|PRUNE2	NM_015225	NP_056040	Q8WUY3	PRUN2_HUMAN		0	CAGAATCGTGAC	0.488	
-	8	3341		NM_015225	NP_056040	Q8WUY3	PRUN2_HUMAN		0	GCTTTCCCCGA	0.468	
+	1	203		NM_001013735	NP_001013757	Q5VYV0	FOXB2_HUMAN	Fork-head.	0	CTTCAACGACT	0.617	

-	18	2172	.N614H|SLC28A3	NM_022127	NP_071410	Q9HAS3	S28A3_HUMAN	ellular (Potential).	4	GCAGTTAAAGG	0.438	
-	2	454		NM_017594	NP_060064	Q96HU8	DIRA2_HUMAN		0	GATGGGGATGC	0.582	
-	1	963	04atq.3_5'Flank|F	NM_198841	NP_942138	Q5T036	F120S_HUMAN		0	GGACACTTGAG	0.657	
-	5	1131		NM_017561	NP_060031	A1L443	FA22F_HUMAN	Pro-rich.	0	TGGGCGTTGGT	0.692	
-	6	1050		NM_005458	NP_005449	O75899	GABR2_HUMAN	ellular (Potential).	4	GATGAGTTGGC	0.542	
+	3	895	ag.1_Missense_	NM_006981	NP_008912	Q92570	NR4A3_HUMAN		173	CCCTGCCCAGC	0.572	
+	6	689	x.2_RNA|STX17_	NM_017919	NP_060389	P56962	STX17_HUMAN	omology.|Cytoplasmic (Pot	1	GCCAACTGGTC	0.343	
-	1	420	N3A_uc004bbq.1_	NM_147180	NP_671709	Q96LZ3	CANB2_HUMAN	EF-hand 3.	2	CACCTGGAAGA	0.532	
-	1	190	3A_uc004bbq.1_	NM_147180	NP_671709	Q96LZ3	CANB2_HUMAN	F-hand 1.|1.	2	TCAGAGACCCT	0.557	
+	1	814		NM_001004483	NP_001004483	Q8NGS7	O13C8_HUMAN	ellular (Potential).	2	CAGGTAATGAA	0.453	
-	1	709		NM_001001956	NP_001001956	Q8NGT0	O13C9_HUMAN	lasmic (Potential).	0	GAAAGCTTTGC	0.408	
-	6	1754	_p.E473K|SVEP1_	NM_153366	NP_699197	Q4LDE5	SVEP1_HUMAN	Sushi 2.	7	TGCCTTCTAGTC	0.473	
-	6	1704	_p.M456T|SVEP1_	NM_153366	NP_699197	Q4LDE5	SVEP1_HUMAN	Sushi 2.	7	TATAACATTTCCC	0.428	
+	6	1983	483_uc004bfg.2_I	NM_133464	NP_597721	Q8TF39	ZN483_HUMAN	2H2-type 6.	1	GAAAAGCCTTT	0.398	
+	8	3209	p.G638E|PAPPA_	NM_002581	NP_002572	Q13219	PAPP1_HUMAN		9	CCATGGAAGTG	0.438	
-	8	1645	b.1_Nonsense_M	NM_001080497	NP_001073966	Q9H1U4	MEGF9_HUMAN	ellular (Potential).	0	TAAATTGGGTCC	0.403	
+	3	457	_p.S68L|LRRC8A	NM_019594	NP_062540	Q8IWT6	LRC8A_HUMAN		0	TGATTCGTTCC	0.612	rs147311433
-	10	1608	PGEF1_uc010mz	NM_005312	NP_005303	Q13905	RPGF1_HUMAN		7	TCTGCAGGTCC	0.627	
+	43	3836		NM_000093	NP_000084	P20908	CO5A1_HUMAN	le-helical region.	11	GTCCCCCTGGA	0.632	
-	5	881		NM_182974	NP_892019	Q7Z4J2	GL6D1_HUMAN	enal (Potential).	1	CTCCTCTCATA	0.522	
+	3	342	Mutation_p.E113K	NM_015160	NP_055975	Q10713	MPPA_HUMAN		0	TTTTTGGAAAAT	0.303	
-	2	1463	A2_uc004ckl.1_5'	NM_004479	NP_004470	Q11130	FUT7_HUMAN	enal (Potential).	0	CATTGGCACGG	0.647	
+	8	1073	es.1_Missense_	NM_014434	NP_055249	Q9UHB4	NDOR1_HUMAN	-binding FR-type.	0	TCTATCCCTCC	0.632	
-	2	464	25A6_uc004cpu.2_	NM_001636	NP_001627	P12236	ADT3_HUMAN	al; Name=3; (By similarity).	0	CGCCGGCCGCA	0.642	
+	6	500	.2_Missense_Mut	NM_175569	NP_780778	P55808	XG_HUMAN	ellular (Potential).	1	ACCGTGATGAC	0.627	
+	8	1032	_p.M64I|GYG2_u	NM_003918	NP_003909	O15488	GLYG2_HUMAN		2	TCCATGAAACC	0.507	
+	4	550		NM_001011719	NP_001011719	Q5FYA8	ARSH_HUMAN	ical; (Potential).	1	TCATTCCCAAG	0.517	
-	6	6504		NM_015419	NP_056234	Q9NR99	MXRA5_HUMAN	like C2-type 5.	8	CGCTGTCCTTG	0.662	
-	5	4379		NM_015419	NP_056234	Q9NR99	MXRA5_HUMAN		8	AAGGGGAGGGT	0.507	
-	6	2360	ndi.2_Missense_	NM_181332	NP_851849	Q8N0W4	NLGNX_HUMAN	ellular (Potential).	4	GAAATGATGTC	0.498	
-	4	1265	ndi.2_Missense_	NM_181332	NP_851849	Q8N0W4	NLGNX_HUMAN	ellular (Potential).	4	CCCCAGCCCCC	0.572	
-	4	1235	ndi.2_Missense_	NM_181332	NP_851849	Q8N0W4	NLGNX_HUMAN	ellular (Potential).	4	TCTTGGGGTCC	0.582	
+	3	553		NM_013452	NP_038480	Q9H320	VCX1_HUMAN	ts of L-S-Q-E-S- [EQ]-V-E-	0	TGGAGGAACCA	0.647	
+	19	2870	e_Mutation_p.R5	NM_015691	NP_056506	Q9ULE0	WWC3_HUMAN		4	CAGCCGCCGGG	0.557	
+	4	579	p.E105K|HCCS_u	NM_005333	NP_005324	P53701	CCHL_HUMAN		0	TCAGAGAAGAG	0.398	
+	6	861	p.R199C|HCCS_u	NM_005333	NP_005324	P53701	CCHL_HUMAN		0	GAATTCGTTCC	0.463	
+	3	493	e_Mutation_p.R5	NM_001118885	NP_001112357	P23416	GLRA2_HUMAN	ellular (Probable).	2	GGGAAGGACAT	0.403	
+	9	960	cwj.2_Missense_	NM_152581	NP_689794	Q8NHP6	MSPD2_HUMAN		1	CTCTTCTTAAAA	0.199	
+	6	777	cyd.2_Missense_	NM_001037540	NP_001032629	Q9UN30	SCML1_HUMAN		3	TTCCCCGAGCA	0.507	
-	20	1830	se_Mutation_p.L5	NM_001079858	NP_001073327	Q8IZP9	GPR64_HUMAN	ellular (Potential).	0	CTTTAATGTGA	0.512	
+	5	567	A1_uc011mjd.1_	NM_000284	NP_000275	P08559	ODPA_HUMAN		1	AGGACGAAAAG	0.488	
-	16	2053	4czj.1_Missense_	NM_001001671	NP_001001671	Q6ZN16	M3K15_HUMAN	milarity).|Protein kinase.	7	CAATCCCATACG	0.468	
-	15	2161_2162	_p.L663F|MAP7D	NM_152780	NP_689993	Q96T17	MA7D2_HUMAN		3	GATAAGGTTTTT	0.426	
+	1	314		NM_152577	NP_689790	Q8N7E2	ZN645_HUMAN	RING-type.	2	AAGTCGGATAT	0.403	
+	2	289	e_Mutation_p.E32	NM_002970	NP_002961	P21673	SAT1_HUMAN	cetyltransferase.	0	GGAAGAACAAG	0.517	
+	4	651	h.2_Missense_Mu	NM_005391	NP_005382	Q15120	PDK3_HUMAN	stidine kinase.	6	TTGATCCTTTCA	0.373	
+	9	712	_p.G236D|POLA1_	NM_016937	NP_058633	P09884	DPOLA_HUMAN		3	TACAGGCGATG	0.358	

+	2	479		NM_173699	NP_775970	Q96M61	MAGBI_HUMAN		1	CAAGGGAAGCT	0.463	
+	3	970	nse_Mutation_p.L2	NM_001097579	NP_001091048	Q9UPC5	GPR34_HUMAN	Name=5; (Potential).	1	TCTGGCTAATTTT	0.328	
+	3	990	nse_Mutation_p.L2	NM_001097579	NP_001091048	Q9UPC5	GPR34_HUMAN	Name=5; (Potential).	1	ATAATCCTTTCAT	0.328	
-	6	775	_p.S184L|MAOB_	NM_000898	NP_000889	P27338	AOFB_HUMAN	Cytoplasmic.	2	GTTGTCGAGATG	0.463	rs12850496
+	15	2171	hq.2_Missense_M	NM_004651	NP_004642	P51784	UBP11_HUMAN		3	TGAACTCCAATG	0.597	
-	4	2073	w.3_Missense_Mu	NM_153380	NP_700359	P51814	ZNF41_HUMAN	C2H2-type 13.	3	TGGATTCTATGAT	0.468	
+	4	1542_1543	4dni.2_Missense_	NM_033215	NP_149992	Q6ZSY5	PPR3F_HUMAN	cellular (Potential).	3	GGCAGGGGGTG	0.668	
-	25	3432		NM_001013742	NP_001013764	Q5KSL6	DGKK_HUMAN		2	CCACTGTCTTG	0.443	
-	3	257		NM_173358	NP_775494	Q7RTT5	SSX7_HUMAN	KRAB-related.	1	TTCTTAGAGAAG	0.388	
+	1	335	e_Mutation_p.P68	NM_022117	NP_071400	Q9H2G4	TSYL2_HUMAN	Pro-rich.	0	GGGCCCCGCGC	0.692	
-	9	3182		NM_198510	NP_940912	Q6UXX5	ITH5L_HUMAN		6	CAGCTCCTCCC	0.483	
+	3	567	Q154K|TRO_uc00	NM_001039705	NP_001034794	Q12816	TROP_HUMAN		1	GGCTCCCAATCC	0.502	
+	5	716	IEPH_uc010nkr.2_	NM_138737	NP_620074	Q9BQS7	HEPH_HUMAN	cellular (Potential).	9	ACTCCCCTCCTC	0.478	
-	2	1979	g.2_Missense_Mu	NM_145119	NP_660095	Q8NG27	PJA1_HUMAN		0	GATTGGCCACCT	0.567	
+	3	297		NM_198512	NP_940914	Q6ZPD8	DG2L6_HUMAN		1	AGGTGGCAGGC	0.557	
+	6	902	TAF1_uc004dzt.3_	NM_138923	NP_620278	P21675	TAF1_HUMAN	otein kinase 1.	17	TAGAATCAGAAG	0.512	
-	1	1191	nqj.1_Missense_M	NM_021963	NP_068798	Q9ULW6	NP1L2_HUMAN		1	CGCCAGGATCTG	0.363	
+	5	792	fz.2_Missense_Mu	NM_022144	NP_071427	Q9H2S6	TNMD_HUMAN	cellular (Potential).	1	ATCCCACTCTAAT	0.378	
+	8	1271	rh.1_Missense_Mu	NM_001939	NP_001930	Q13474	DRP2_HUMAN	Spectrin 2.	2	TTGCCATTTCTG	0.488	
+	4	969	ehw.2_Missense_	NM_016608	NP_057692	Q9P291	ARMX1_HUMAN	ARM 1.	4	ATTGATGATATTC	0.468	
+	4	1511	ehw.2_Missense_	NM_016608	NP_057692	Q9P291	ARMX1_HUMAN	ARM 3.	4	AAAGAATGGGAT	0.333	
+	5	1633	eib.1_Missense_	NM_016607	NP_057691	Q9UH62	ARMX3_HUMAN		2	CATGGCCAAAC	0.239	
-	2	4238	n.2_Missense_Mu	NM_032441	NP_115817	Q5H9K5	ZMAT1_HUMAN		1	CTATCTCCTATC	0.408	
+	5	4093	.Q1098*|GPRASP	NM_014710	NP_055525	Q5JY77	GASP1_HUMAN	PRD1-binding.	2	GAAGATCAGGAA	0.468	
+	11	1204	K_uc010npc.1_5'U	NM_198465	NP_940867	Q7Z2Y5	NRK_HUMAN	rotein kinase.	14	CTGTTTCGTCCT	0.363	
-	2	663	_p.P216L|SERPIN	NM_000354	NP_000345	P05543	THBG_HUMAN		0	TGGATGGATCA	0.403	
-	1	564	p.G183E|SERPIN	NM_000354	NP_000345	P05543	THBG_HUMAN		0	ACTTTCCCTTTG	0.408	
-	11	1508	nse_Mutation_p.P	NM_024657	NP_078933	Q8TE76	MORC4_HUMAN	CW-type.	1	GGTCAGGAACC	0.403	
+	12	1141	1_Missense_Muta	NM_052936	NP_443168	Q8WYN0	ATG4A_HUMAN		1	CCCCAGGAAATT	0.428	
+	46	4311	_p.P1367L|COL4A	NM_033380	NP_203699	P29400	CO4A5_HUMAN	le-helical region.	4	TGGTCCTTCAG	0.483	
+	51	5102	p.P1631S|COL4A	NM_033380	NP_203699	P29400	CO4A5_HUMAN	llagen IV NC1.	4	TCAGCTCCCTTC	0.488	
+	3	1689	nsr.1_Missense_M	NM_020769	NP_065820	Q8NET4	RGAG1_HUMAN		4	CTCTATGAAAGC	0.512	
+	4	852	_p.D42N|HTR2C_	NM_000868	NP_000859	P28335	5HT2C_HUMAN	llular (By similarity).	3	CCTCCGATGGT	0.423	rs143566182
+	4	541	A14_uc011mtm.1_	NM_007231	NP_009162	Q9UN76	S6A14_HUMAN	cellular (Potential).	3	TTGCTTCTTTTCA	0.343	
-	11	1219	p.R317Q|THOC2_	NM_001081550	NP_001075019	Q8NI27	THOC2_HUMAN		3	ACCTTCGGTAGA	0.343	
+	3	404	MST4_uc010nrj.1_	NM_016542	NP_057626	Q9P289	MST4_HUMAN	nilarity).|Protein kinase.	9	GGCTCATTTGGG	0.398	
-	3	849	vh.1_Missense_M	NM_004484	NP_004475	P51654	GPC3_HUMAN		5	GACTTGGAAACC	0.468	
+	10	1558	26B_uc004eyx.3_	NM_182540	NP_872346	Q5JSJ4	DX26B_HUMAN		0	ACAGATGACTTG	0.343	
-	8	1247	wc.1_Missense_	NM_024597	NP_078873	Q8IWC1	MA7D3_HUMAN		4	CCTCCGGGGATG	0.597	
-	2	311		NM_145665	NP_663698	Q8TAD1	SPNXE_HUMAN		0	TCTTTCGGGCG	0.428	
+	9	1069	R1_uc004fck.3_Mi	NM_002024	NP_002015	Q06787	FMR1_HUMAN	KH 2.	3	TTAGTAGGTAAG	0.328	
+	11	1199	_p.S337F|FMR1_	NM_002024	NP_002015	Q06787	FMR1_HUMAN		3	CAAATTCCCTTC	0.259	
+	3	537		NM_152578	NP_689791	Q8N0W7	FMR1N_HUMAN	xtracellular (Potential).	1	GAGAGTGAATGT	0.368	
+	14	1595	TM1_uc011mxz.1_	NM_000252	NP_000243	Q13496	MTM1_HUMAN	ularin phosphatase.	3	AATAAAGAAAAAT	0.363	
+	14	1714	TM1_uc011mxz.1_	NM_000252	NP_000243	Q13496	MTM1_HUMAN		3	GATCAAGCAACA	0.358	
+	5	622	MGB3_uc004fer.2_	NM_005342	NP_005333	O15347	HMGB3_HUMAN		0	TTGCCCGGAAA	0.289	
-	10	996	04fir.2_Missense_	NM_004135	NP_004126	P51553	IDH3G_HUMAN		0	CATCACCATGAC	0.617	

-	41	6961	ı.1_Missense_Muta	NM_001110556	NP_001104026	P21333	FLNA_HUMAN	Filamin 21.	6	GTGGGCTCCCC	0.667	
+	2	210		NM_004699	NP_004690	Q14320	FA50A_HUMAN		1	CCGCAGGAGAAC	0.577	
-	4	492	.2_uc001afk.2_5'Fl	NM_017971	NP_060441	Q9BYC9	RM20_HUMAN		0	TCCCCCAAGGC	0.498	
-	3	843	SLC35E2_uc001ah	NM_182838	NP_878258	P0CK97	S35E2_HUMAN	ical; (Potential).	1	TCATAAGGAAGTT	0.468	
+	13	3076	p.R998Q|PRDM16	NM_022114	NP_071397	Q9HAZ2	PRD16_HUMAN	f TGF-beta signaling.|Intera	7	ACGTCCGGAACA	0.617	
+	10	1476	p.L423R|PIK3CD_	NM_005026	NP_005017	O00329	PK3CD_HUMAN		7	CCAACCTCATGC	0.652	
-	4	732	tb.1_Missense_Mu	NM_005957	NP_005948	P42898	MTHR_HUMAN		0	TCACTTCGGATG	0.567	
+	36	8173	atx.2_Missense_M	NM_015378	NP_056193	Q5THJ4	VP13D_HUMAN		5	ATGCGGAACCT	0.502	
+	5	958		NM_001013641	NP_001013663	A0PJX8	TMM82_HUMAN	.|Helical; (Potential).	2	ATGGGCGGCCTC	0.682	
-	13	2154	_p.L26F|ARHGEF	NM_153213	NP_694945	Q8IW93	ARHGJ_HUMAN	PH.	3	GTGGAGGAGCT	0.647	
-	4	1468		NM_152232	NP_689418	Q8TE23	TS1R2_HUMAN		4	GGCTGACCGTGT	0.637	
-	22	2954	m.1_Missense_Mu	NM_020765	NP_065816	Q5T4S7	UBR4_HUMAN		25	TTCTCCTAACTG	0.438	
-	16	2136	G463R|TMCO4_u	NM_181719	NP_859070	Q5TGY1	TMCO4_HUMAN		0	CAGCCCCGTGC	0.642	
-	7	1370	_p.R398C|ZNF683	NM_173574	NP_775845	Q8IZ20	ZN683_HUMAN	type 3; degenerate.	0	CAGGCGCAGGT	0.637	
-	1	422		NM_018066	NP_060536	Q9H9Y4	GPN2_HUMAN		0	TGGCCGGGTCC	0.731	
-	6	435_436	p.P91S|EYA3_uc	NM_001990	NP_001981	Q99504	EYA3_HUMAN		3	TCCAGGGTAAG	0.416	
-	5	1025	1_uc001bsa.1_Mi	NM_002379	NP_002370	P21941	MATN1_HUMAN	VWFA 2.	1	GAAGCGACCCA	0.567	
+	7	1159	p.W172*|HCRTR1_	NM_001525	NP_001516	O43613	OX1R_HUMAN	lasmic (Potential).	1	AACTGGAAGCG	0.647	
+	3	283	SP_uc001coj.1_M	NM_002482	NP_002473	P49321	NASP_HUMAN	TPR 1.	1	ATTCCAGCAGCT	0.348	
+	20	3395	R_uc009waq.2_3'	NM_002303	NP_002294	P48357	LEPR_HUMAN	lasmic (Potential).	1	TGGAGGGAAAT	0.373	
+	17	1725	_p.A103V|SGIP1_	NM_032291	NP_115667	Q9BQI5	SGIP1_HUMAN		3	GCGGGCTGAAA	0.458	
-	5	1879	se_Mutation_p.S4	NM_015534	NP_056349	Q8IYH5	ZZZ3_HUMAN		5	TGGCAGATGGC	0.393	
+	4	447	se_Mutation_p.R8	NM_001081472	NP_001074941				1	GGAGCGTCTTG	0.308	
-	10	1391	LN2_uc001dkn.2_	NM_153259	NP_694991	Q8IZK6	MCLN2_HUMAN	ical; (Potential).	4	TAGAGGTTCCAA	0.408	
-	6	1125	_p.F321L|GFI1_uc	NM_001127215	NP_001120687	Q99684	GFI1_HUMAN	C2H2-type 3.	1	TCTTGAAGCTCT	0.428	
-	8	731	e|WDR77_uc010o	NM_024102	NP_077007	Q9BQA1	MEP50_HUMAN		0	CATCACCTGTAGA	0.313	
+	5	1193	vgy.1_Missense_M	NM_138959	NP_620409	Q8TAA9	VANG1_HUMAN	lasmic (Potential).	1	TGGCCGGGCTG	0.463	
-	4	532	_p.A31V|REG4_u	NM_001159352	NP_001152824	Q9BYZ8	REG4_HUMAN		1	CAGGAGCACAG	0.373	
-	2	317	Z_uc010pdc.1_Mi	NM_015100	NP_055915	Q7Z3K3	POGZ_HUMAN		3	GGTCGGTGTCC	0.388	
-	3	1807		NM_001122965	NP_001116437	Q6XPR3	RPTN_HUMAN	Gln-rich.	0	AGTGGGAACTCT	0.463	
-	23	3281	P210L_uc010peh	NM_207308	NP_997191	Q5VU65	P210L_HUMAN		11	TATTTTCTTCCC	0.378	
-	9	1006	_p.P328L|THBS3_	NM_007112	NP_009043	P49746	TSP3_HUMAN	alcium-binding (Potential).	5	AGCCCGGGAAA	0.617	
-	9	1016	j.1_Nonsense_Mu	NM_005998	NP_005989	P49368	TCPG_HUMAN		2	AATTCGGGTGA	0.468	
-	5	1048	DCAF8_uc010pjb.	NM_015726	NP_056541	Q5TAQ9	DCAF8_HUMAN	WD 2.	2	TGTTAGGAAGAA	0.428	
-	5	842	_p.R212Q|SLAMF	NM_052931	NP_443163	Q96DU3	SLAF6_HUMAN	lasmic (Potential).	2	TGTGTTCGCTGA	0.483	rs149372302
-	8	2418		NM_005099	NP_005090	O75173	ATS4_HUMAN	Cys-rich.	5	TGATGCGATCAC	0.547	
-	7	696	e_Mutation_p.P99	NM_019026	NP_061899	Q9UM00	TMCO1_HUMAN	Poly-Pro.	1	AGAAGGAGGTG	0.473	
-	5	769	.2_Missense_Mut	NM_153832	NP_722561	Q8N6U8	GP161_HUMAN	Name=4; (Potential).	0	TGAAGCCAGATG	0.552	
+	9	1633	_Mutation_p.I499	NM_002021	NP_002012	Q01740	FMO1_HUMAN		1	GGTCATCAAAGC	0.458	
-	3	927	|ANGPTL1_uc00	NM_004673	NP_004664	O95841	ANGL1_HUMAN	Potential.	0	GGAAAGTTCAA	0.398	
+	70	11078		NM_031935	NP_114141	Q96RW7	HMCN1_HUMAN		23	AGAGTGCATGGT	0.388	
+	7	1615	_Mutation_p.P429	NM_005807	NP_005798	Q92954	PRG4_HUMAN	ats of K-X-P-X-P-T-T-X.|23	1	AGGAGCCTGCA	0.637	
-	46	6775		NM_003292	NP_003283	P12270	TPR_HUMAN		7	GACACCAGCAA	0.393	
+	4	554		NM_133494	NP_598001	Q8TDX7	NEK7_HUMAN	rotein kinase.	4	AAGCACGTGCTG	0.279	
+	13	2359	p.A682V|PKP1_uc	NM_000299	NP_000290	Q13835	PKP1_HUMAN	ARM 9.	2	CAGAAGCTGCCC	0.577	
+	15	1970	bi.2_Missense_M	NM_001005388	NP_001005388	O94856	NFASC_HUMAN	otential).|Ig-like C2-type 6.	6	AAGCACGACCCC	0.597	
+	4	871	_p.A272T|RASSF	NM_182663	NP_872604	Q8WWW0	RASF5_HUMAN		1	CTGGCGGCTACC	0.587	

+	4	860	.1_RNA|CD55_uc(	NM_000574	NP_000565	P08174	DAF_HUMAN	Sushi 3.	1	CCTTCTCATGTAA	0.378	
-	5	1015	e_Mutation_p.G16	NM_144567	NP_653168	Q5VTE6	ANGE2_HUMAN		0	ACTAATCCAACAT	0.418	
-	6	1688		NM_024746	NP_079022	Q6UWX4	HIPL2_HUMAN		1	AAAGATCCTGCT	0.438	
+	12	1583		NM_016002	NP_057086	Q8NBX0	SCPDH_HUMAN		1	GATTGACAGACT(	0.418	
+	6	857	iln.2_Missense_M	NM_153498	NP_705718	Q8IU85	KCC1D_HUMAN	rotein kinase.	2	TCCATCGGAGTG	0.408	
-	1	3215		NR_003525					0	TAGGTGGACCTG	0.498	
-	1	1979		NR_003525					0	GGGTCTCCTGCT(	0.552	
+	12	1598		NM_052997	NP_443723	Q9BXX3	AN30A_HUMAN		9	CAGAATCCAAAC/	0.279	
-	23	3507	se_Mutation_p.E1	NM_033056	NP_149045	Q96QU1	PCD15_HUMAN	.|Extracellular (Potential).	13	ATTCCTCCTGTGT	0.413	
+	2	813	1jmx.3_Intron|CTN	NM_178011	NP_821079	Q86VH5	LRRT3_HUMAN	lar (Potential).|LRR 2.	3	AGCTCACCTGGC	0.383	
-	8	1938	ıu.3_Missense_Mu	NM_001144000	NP_001137472	A6NIR3	AGAP5_HUMAN	ANK 1.	0	CTTGCGGCAGG(	0.662	
+	13	2746	AA0913_uc001jvi.2	NM_015037	NP_055852	A7E2V4	K0913_HUMAN		1	GTGCCGGGCAG	0.572	
+	8	1187	GI1_uc001kjd.3_Int	NM_005097	NP_005088	O95970	LGI1_HUMAN	EAR 2.	4	CCACTGTAGTATG	0.458	
-	5	762	kuv.2_Missense_M	NM_020992	NP_066272	O00151	PDLI1_HUMAN		0	TGCAAAACCAAG/	0.458	
-	11	1163	9L1_uc001kqt.1_M	NM_018294	NP_060764	Q69YN2	C19L1_HUMAN		0	TCATCAGATAAG(	0.488	
-	1	441	C2_uc009xxx.2_Ir	NR_026715					0	GCCAGGTGCCCC	0.537	
+	4	456		NM_058222	NP_478129	Q96PL2	TECTB_HUMAN	ZP.	0	ATTTGAGAGCCA/	0.498	
+	9	939		NM_000936	NP_000927	P16233	LIPP_HUMAN		3	TTGCTGGATTCC(	0.448	rs146995349
-	2	606	b.1_Missense_Mut	NM_001112704	NP_001106175	Q5SQQ9	VAX1_HUMAN	Homeobox.	2	GCAGCGCTGGA	0.657	
-	5	923	›.P216S|SIRT3_uc	NM_012239	NP_036371	Q9NTG7	SIRT3_HUMAN	tylase sirtuin-type.	1	GCAGCGGCTCCC	0.587	
-	15	2518	qwh.1_5'Flank|CDI	NM_021924	NP_068743	Q9HBB8	CDHR5_HUMAN	lasmic (Potential).	0	TGAGAACGACCA	0.706	
-	2	258		NM_016564	NP_057648	Q8N111	CEND_HUMAN	lasmic (Potential).	0	CGGGGGTACCT	0.692	
+	51	14351	:b.2_Missense_Mu	NM_017511	NP_059981	Q9HC84	MUC5B_HUMAN	em repeats, Ser/Thr- rich.|	0	CCACCCCGTCCT(	0.642	
-	1	71	x.1_Intron|LOC338	NM_001005922	NP_001005922	Q6L8H4	KRA51_HUMAN		0	CACAGCTGGAGC	0.672	
-	22	3313	p.E1008K|NUP98_	NM_016320	NP_057404	P52948	NUP98_HUMAN		12	AGATTTCTTGAG/	0.418	
+	1	496		NM_001005170	NP_001005170	Q8NH67	O52I2_HUMAN	lasmic (Potential).	1	AGAATTCTCACG(	0.498	
-	4	1132	.1_Intron|MUC15_	NM_145650	NP_663625	Q8N387	MUC15_HUMAN	lasmic (Potential).	3	GGTTCCGGTGCA	0.378	
+	11	1850	_p.V427I|PDHX_u	NM_003477	NP_003468	O00330	ODPX_HUMAN		1	TGGCGGTTGGG/	0.498	
-	10	1430	ew.1_Missense_M	NM_001001991	NP_001001991	Q6UXH9	PAMR1_HUMAN	Peptidase S1.	2	GCCACGGCCAGC	0.547	
+	4	321	yd.2_Missense_M	NM_002231	NP_002222	P27701	CD82_HUMAN	ical; (Potential).	1	CTGGGCGCAGTG	0.617	
+	15	1879	Incz.2_Missense_I	NM_001142673	NP_001136145	O75143	ATG13_HUMAN		0	TTTGCTCCCAAG.	0.512	
+	6	1068	3_uc001nej.2_Intro	NM_005693	NP_005684	Q13133	NR1H3_HUMAN	-binding (Potential).	3	CTCAGCCGGGAG	0.582	
+	1	385		NM_001004739	NP_001004739	Q8NGL0	OR5L2_HUMAN	lasmic (Potential).	1	TGTAACCCCCTG(	0.532	
+	11	2586	_p.A799V|TMEM13	NM_178031	NP_821174	Q24JP5	T132A_HUMAN	lization similar to full-length	1	AGGTGGCAGGCA	0.612	
+	3	291_292	1_Intron|DAK_uc0	NM_015533	NP_056348	Q3LXA3	DHAK_HUMAN	DhaK.	0	TGGCTGGCTGT(	0.624	
+	1	629	2A9_uc001nwx.2_	NM_080866	NP_543142	Q8IVM8	S22A9_HUMAN	cellular (Potential).	3	GGCTGGGTGTAT(	0.512	
-	20	3284	9ypw.2_5'Flank|R/	NM_005609	NP_005600	P11217	PYGM_HUMAN		2	TCTCCCGGGCAT/	0.617	
+	8	1504	.2_RNA|KDM2A_u	NM_012308	NP_036440	Q9Y2K7	KDM2A_HUMAN	JmjC.	9	CATGTGGACTTTG	0.433	
+	23	4900	g.2_Missense_Mut	NM_002335	NP_002326	O75197	LRP5_HUMAN	nic (Potential).|PPPSP mot	7	CCTCCGTCCCCC	0.582	
+	4	485	_p.W116*|FOLR1_	NM_016724	NP_057936	P15328	FOLR1_HUMAN		1	GGCCCTGGATCC/	0.572	
+	19	2287	osg.2_Missense_M	NM_001567	NP_001558	O15357	SHIP2_HUMAN		4	GACATCGTCACC/	0.552	
-	7	829	e_Mutation_p.P17	NM_015159	NP_055974	Q92567	F168A_HUMAN		0	CAACAGGTGCTG	0.602	
-	9	3007	m.2_Missense_Mu	NM_016578	NP_057662	Q96T23	RSF1_HUMAN	Potential.	4	CGGCACGCTCTT	0.338	
+	10	2986	sp.1_Missense_Mu	NM_020798	NP_065849	Q9P2H5	UBP35_HUMAN		3	TTCTTCCCTAAG(	0.587	
+	2	224	PRSS23_uc010rts.	NM_007173	NP_009104	O95084	PRS23_HUMAN		2	GGCAGGGATTC(	0.552	
+	2	1369		NM_015036	NP_055851	O94919	ENDD1_HUMAN		0	CCTGTCCGTGTC(	0.547	
+	12	1323	_p.R299C|ELMOD	NM_018712	NP_061182	Q8N336	ELMD1_HUMAN	ELMO.	0	AAATTCCGCAAG/	0.463	rs140465562

+	1	229		NM_017516	NP_059986	Q14964	RB39A_HUMAN	(By similarity).	0	CGGCGGGACAG	0.741	
+	8	1453	JL5_uc001pju.2_R	NM_003478	NP_003469	Q93034	CUL5_HUMAN		1	CTCATGGAATG	0.328	
+	21	2037	e_Mutation_p.R68	NM_001040455	NP_001035545	Q8NBJ9	SIDT2_HUMAN	ellular (Potential).	0	ATCTTCCGCCGC	0.642	
-	9	1712	_p.R319W|SLC37	NM_001164277	NP_001157749	O43826	G6PT1_HUMAN	ical; (Potential).	1	TACCCGGAAGA	0.567	
+	6	1422	.R403C|NLRX1_	NM_024618	NP_078894	Q86UT6	NLRX1_HUMAN	raction with MAVS.|NACH	2	TTCCTGCGCCTC	0.592	
+	25	3555	rzp.1_Missense_M	NM_003105	NP_003096	Q92673	SORL_HUMAN	ential).|LDL-receptor class	15	AGTGCCGGAGT	0.517	
+	1	569		NM_001005197	NP_001005197	Q8NGM9	OR8D4_HUMAN	ellular (Potential).	1	CTGCTCCAGCA	0.373	
-	2	244	09zcl.2_Missense_	NM_145013	NP_659450	Q8TAV5	CK045_HUMAN		0	cagggcggagaGGT	0.124	
+	6	715	78_uc010sde.1_Missense_Mutation_p.S54G|LOC100288778_uc010sdf.1_Missense_Mutation_p.S54G|LOC100288						0	TGCCCAGCATT	0.587	
+	8	1455	.1_Missense_Muta	NM_000616	NP_000607	P01730	CD4_HUMAN	ical; (Potential).	0	TGGGGGGCGTC	0.627	
+	2	375	_p.P43L|CLEC4A	NM_016184	NP_057268	Q9UMR7	CLC4A_HUMAN	lasmic (Potential).	0	ATTCCCCAAGC	0.398	
-	2	203		NM_014358	NP_055173	Q9ULY5	CLC4E_HUMAN		1	TCTCTCTGTAG	0.408	
+	22	2854	p.C499Y|A2ML1_	NM_144670	NP_653271	A8K2U0	A2ML1_HUMAN		3	GCTGTGCCCAA	0.418	
-	12	1431	k.1_Missense_Mut	NM_000014	NP_000005	P01023	A2MG_HUMAN		5	GTGTTCTTCTG	0.418	
-	3	700	B4_uc001qzf.1_Int	NM_006249	NP_006240	Q04118	PRB3_HUMAN	G-[PQS]-P-[PS]-Q-[GE]-G-	1	CGGACGAGGT	0.622	rs113884749
-	3	257	zt.2_Missense_Mu	NM_002723	NP_002714	P10163	PRB4_HUMAN	R]-[PR]-P-Q-G-G-N-Q-[PS	1	TCCTGGAGGAG	0.607	
+	6	645		NM_006446	NP_006437	Q9Y6L6	SO1B1_HUMAN	Name=4; (Potential).	8	TGCTTCGTGGA	0.348	rs138965366
+	4	865		NM_018169	NP_060639	Q9HCM1	CL035_HUMAN		2	TGCCGGCACTA	0.418	
-	19	2689	nse_Mutation_p.V	NM_017641	NP_060111	Q7Z4S6	KI21A_HUMAN		7	GAGTAACTTTC	0.483	
+	4	1135_1136	_p.S15F|FAM113B	NM_138371	NP_612380	Q96HM7	F113B_HUMAN		5	GAACTCCTGGA	0.604	
-	9	1585	|CCNT1_uc009zk	NM_001240	NP_001231	O60563	CCNT1_HUMAN	Potential.	6	GGGCAGCATAT	0.463	
-	19	2501	ut.1_Missense_Mu	NM_175736	NP_783863	Q8IVF7	FMNL3_HUMAN	FH2.	4	TGACGGAAGCG	0.552	
-	1	194	_p.S59A|KRT8_uc	NM_002273	NP_002264	P05787	K2C8_HUMAN	ead.|Ser-rich.	2	GCGGGAACCGG	0.662	
-	8	896	nse_Mutation_p.T2	NM_001130059	NP_001123531	P17544	ATF7_HUMAN	activation domain.	2	TGGCAGTACCC	0.537	
+	3	351	NP_uc001sht.2_5'	NM_014182	NP_054901	Q53FV1	ORML2_HUMAN		0	ACTGGGAGCAA	0.517	
-	27	5409	.P545S|BAZ2A_	NM_013449	NP_038477	Q9UIF9	BAZ2A_HUMAN		0	CTTTGGGAAAC	0.542	
-	9	1569	_5'Flank|BAZ2A_	NM_001686	NP_001677	P06576	ATPB_HUMAN		1	TCCTTTGATGGT	0.468	
-	5	608	_uc001soc.2_Miss	NM_032496	NP_115885	Q9BRR9	RHG09_HUMAN	SH3.	1	AGCTTCTAGGC	0.552	
+	18	2579	se_Mutation_p.S8	NM_003667	NP_003658	O75473	LGR5_HUMAN	lasmic (Potential).	9	AAGATCAAAAC	0.448	
+	4	680	vy.2_Missense_Mu	NM_173353	NP_775489	Q8IWU9	TPH2_HUMAN		4	CCACCCAGTAA	0.468	
-	9	926	rf50_uc001tan.2_	NM_152589	NP_689802	Q8NA57	CL050_HUMAN		3	CATGCGTTGTAG	0.358	rs112656239
+	15	1831		NM_017564	NP_060034	Q8WWQ8	STAB2_HUMAN	lar (Potential).|FAS1 2.	14	ATGGAGTTGGT	0.403	
+	8	823	FX4_uc001tlt.2_M	NM_213594	NP_998759	Q33E94	RFX4_HUMAN		1	TTGTCGGCGTG	0.542	
+	9	1264	E3B_uc001too.1_	NM_130466	NP_569733	Q7Z3V4	UBE3B_HUMAN		4	GACCCCGTCCT	0.398	
+	5	789	1tzs.2_Missense_	NM_002560	NP_002551	Q99571	P2RX4_HUMAN	ellular (Potential).	0	GGTGGCGGCCT	0.522	
-	10	1394	_p.Q26H|ANAPC	NM_016237	NP_057321	Q9UJX4	APC5_HUMAN		6	GTTTTCTGTGC	0.552	
-	2	564	ci.1_Missense_Mu	NM_002956	NP_002947	P30622	CLIP1_HUMAN	Ser-rich.	3	TGGCCGTAGAA	0.557	
-	8	1690	15A4_uc001uhv.2_	NM_145648	NP_663623	Q8N697	S15A4_HUMAN	ical; (Potential).	0	GGAGGGTAGCT	0.468	
-	5	1682		NM_133448	NP_597705	Q14C87	T132D_HUMAN	ellular (Potential).	14	TTTCACCGGGA	0.562	
-	2	450		NM_133448	NP_597705	Q14C87	T132D_HUMAN	ellular (Potential).	14	AGCAAGGAAAAC	0.527	
+	18	2209	ij.1_Missense_Mu	NM_004764	NP_004755	Q96J94	PIWL1_HUMAN	Piwi.	2	GAGACGGCCAG	0.478	
+	3	573	RS8_uc001ujb.1_5	NM_004592	NP_004583	Q12872	SFSWA_HUMAN		0	ATGGGAGCTAC	0.453	
-	25	3134		NM_006437	NP_006428	Q9UKK3	PARP4_HUMAN	VWFA.	4	GTGACGATTTG	0.333	
+	33	4828	RY_uc010tdw.1_R	NM_023037	NP_075463	Q5TBA9	FRY_HUMAN		7	GCCAACAATGA	0.448	
-	1	442		NM_145203	NP_660204	Q8N752	KC1AL_HUMAN		1	CACAACGAGTT	0.587	
-	17	2165	zc.3_Missense_M	NM_001127615	NP_001121087	Q8TC92	ENOX1_HUMAN		2	CACCCGTGAAT	0.433	
-	38	3394	4A1_uc010agl.2_	NM_001845	NP_001836	P02462	CO4A1_HUMAN	le-helical region.	6	GCATTCCTGGG	0.527	

-	5	728	vsf.2_Missense_M	NM_006322	NP_006313	Q96CW5	GCP3_HUMAN		1	TGGGAGGAGAG	0.577	
+	8	830	1vxb.1_Splice_Site	NM_005484	NP_005475	Q9UGN5	PARP2_HUMAN		2	ACTTGGTAGGAC	0.353	
-	20	2981	EP1_uc010tlf.1_R	NM_007110	NP_009041	Q99973	TEP1_HUMAN		5	GGGGGGAATGT	0.557	
-	31	4745	Mutation_p.R1447	NM_020920	NP_065971	Q9HCK8	CHD8_HUMAN		10	AGTGCGGAAGC	0.493	
+	4	678	OX4_uc010tlu.1_	NM_014828	NP_055643	O94842	TOX4_HUMAN		1	ATTTCCGGAGGG	0.488	
-	9	2687	IN1_uc001wir.3_M	NM_014977	NP_055792	Q9UKV3	ACINU_HUMAN		4	GAGGTTCTGGAA	0.537	
-	14	1479	PO4_uc001wmy.1_	NM_024658	NP_078934	Q8TEX9	IPO4_HUMAN	HEAT 3.	1	GTGTCCAAGAG	0.577	
-	5	1813	.R475W|NOVA1_	NM_002515	NP_002506	P51513	NOVA1_HUMAN		5	CAGCCCGAACTC	0.448	
-	5	720	tqb.1_Missense_M	NM_006364	NP_006355	Q15436	SC23A_HUMAN		5	GTAATAAGTCCA	0.383	
+	4	807	y.1_Missense_Mu	NM_054024	NP_473365	Q96PC5	MIA2_HUMAN		2	AGTATGGAACAG	0.443	
-	1	866		NM_032135	NP_115511	Q5H9T9	FSCB_HUMAN		9	CCCGACGATTTA	0.373	
-	11	1560	xbt.2_Missense_M	NM_014750	NP_055565	Q15398	DLGP5_HUMAN		2	TCGAAGCAATGT	0.338	
+	4	951	dx.2_Missense_Mu	NM_016651	NP_057735	Q9NYF0	DACT1_HUMAN		5	AAAACGGGAAT	0.493	
-	1	1432	1_Intron|TMEM30	NM_001017970	NP_001017970	Q3MIR4	CC50B_HUMAN		0	GCCGCCGTGCGC	0.687	
-	9	1669	_p.L540V|KCNH5_	NM_139318	NP_647479	Q8NCM2	KCNH5_HUMAN	lasmic (Potential).	9	GGTTTAGATGAA	0.483	
+	62	12420	NE2_uc010apx.1_	NM_015180	NP_055995	Q8WXH0	SYNE2_HUMAN	Cytoplasmic (Potential).	14	GCCACCGTACTA	0.458	rs144164967
-	2	1674		NM_003814	NP_003805	O43506	ADA20_HUMAN	Extracellular (Potential).	1	ACTGCCGTATGG	0.443	rs147557544
-	11	3145	vo.1_Missense_Mu	NM_001002860	NP_001002860	Q9P203	BTBD7_HUMAN		1	TATTCCTGTGGA	0.478	
+	3	1081	gl.1_Missense_M	NM_001127258	NP_001120730	Q96JK4	HIPL1_HUMAN		2	GAGACCCCTTTG	0.527	
-	1	400		NR_024387					0	TCGTTACATTTAT	0.373	
+	4	1390		NM_020857	NP_065908	Q9P253	VPS18_HUMAN		3	TGACCGGGCAG	0.632	
+	10	2280		NM_019074	NP_061947	Q9NR61	DLL4_HUMAN	lasmic (Potential).	2	GAGTGTCGGATA	0.562	
-	13	1854		NM_015540	NP_056355	Q9BWH6	RPAP1_HUMAN		1	GATTCCAGGGAA	0.597	
+	7	855	_Mutation_p.S19	NM_001128608	NP_001122080	O60336	MABP1_HUMAN	WD 3.	10	ATTGCAGCTACT	0.517	
-	17	2017	lk.1_Missense_Mu	NM_174916	NP_777576	Q8IWV7	UBR1_HUMAN		1	GACAACGTAAAG	0.393	
+	13	1837		NM_024908	NP_079184	Q9H967	WDR76_HUMAN	WD 7.	0	CAACTCGGTATA	0.418	rs140407429
+	10	1278	e_Mutation_p.A37	NM_002044	NP_002035	Q01415	GALK2_HUMAN		1	TTGGGGCTCAA	0.438	
+	6	1484	_p.P365S|SLC27A	NM_003645	NP_003636	O14975	S27A2_HUMAN	lasmic (Potential).	2	AGAGTTCCCAAA	0.353	
-	6	745	_p.A165V|CYP19A	NM_031226	NP_112503	P11511	CP19A_HUMAN		3	GATTCAGCACAG	0.537	
-	6	804		NM_003613	NP_003604	O75339	CILP1_HUMAN		7	CCATTGGGCAG	0.537	
-	8	3321		NM_005477	NP_005468	Q9Y3Q4	HCN4_HUMAN	lasmic (Potential).	6	ATCAGCGGGGTC	0.687	
-	5	1233	n_p.F107L|CYP1A	NM_000499	NP_000490	P04798	CP1A1_HUMAN		5	GGATGAAGGCCT	0.577	
-	5	753_754	2azg.2_Splice_Site	NM_020447	NP_065180	Q5XKK7	CO017_HUMAN		0	GTTCACCTGCTA	0.53	rs143038267
+	12	2270	_uc002bgg.2_Mis	NM_172217	NP_757366	Q14005	IL16_HUMAN		4	CCACCTGTGGC	0.512	
-	2	835		NM_032246	NP_115622	Q6ZN04	MEX3B_HUMAN	KH 2.	2	CACGAGCCCCA	0.662	
-	14	1683	gu.1_Missense_M	NM_024580	NP_078856	Q7Z2Z2	ETUD1_HUMAN		1	GCAATAAAAGAC	0.433	rs142283736
+	7	3091	13_uc002blu.1_Mi	NM_007200	NP_009131	Q12802	AKP13_HUMAN		9	GTGCCAAGGACA	0.463	
+	12	6954	_Mutation_p.D21	NM_013227	NP_037359	E7EX88	E7EX88_HUMAN		3	CTGGAGACAGG	0.612	
+	14	1847		NM_002569	NP_002560	P09958	FURIN_HUMAN		7	ATCCCTCTGGCG	0.572	
-	10	1551	2bvx.1_Missense_	NM_139057	NP_620688	Q8TE56	ATS17_HUMAN	Disintegrin.	3	CTTACCTCCATG	0.572	
-	11	1633	clz.2_Missense_M	NM_014714	NP_055529	Q96RY7	IF140_HUMAN		5	GACTCGGGGAG	0.617	
+	5	1113	yv.1_Missense_Mu	NM_018723	NP_061193	Q9NWB1	RFOX1_HUMAN		0	AATACACGGCCC	0.637	rs146499343
-	10	1588	x.2_Missense_Mu	NM_001007240	NP_001007241	P55259	GP2_HUMAN		4	CTCTCCGAGTG	0.527	
-	19	2353	_p.P278S|ARHGA	NM_001006634	NP_001006635	Q68EM7	RHG17_HUMAN	g (Potential).|Pro-rich.	0	GGGAGGGGTGT	0.622	
-	4	562	issense_Mutation	NM_000086	NP_000077	Q13286	CLN3_HUMAN		0	ATCGGCGTTGGG	0.483	
+	5	1403	22S|SH2B1_uc002	NM_001145795	NP_001139267	Q9NRF2	SH2B1_HUMAN	dependent of JAK2 phosp	2	AGCATCCCCTGC	0.542	
+	3	456	t_Site|FBXL19_uc	NM_001099784	NP_001093254	Q6PCT2	FXL19_HUMAN	PHD-type.	4	ACACGGTGGAG	0.602	

+	3	341	eag.2_Missense_M	NM_025193	NP_079469	Q9H2F3	3BHS7_HUMAN		0	TGGCCGGAGCC	0.647	
-	4	617	XDC2_uc002eyb.2_RNA|PDXDC2_uc002eyc.2_RNA						0	TTTGGCGGTCT	0.373	rs139165288
+	16	2493	p.G630E|CNTNAP	NM_033401	NP_207837	Q9C0A0	CNTP4_HUMAN	ential).|Fibrinogen C-termin	2	GGGTAGGAAGAA	0.408	
+	8	1132	vnt.1_Missense_Mu	NM_001257	NP_001248	P55290	CAD13_HUMAN	Cadherin 2.	1	TGGCTGGACTG	0.418	
-	6	1179	se_Mutation_p.G3	NM_020947	NP_065998	Q6P9B6	K1609_HUMAN	TLD.	2	CAGTCCGTTCG	0.597	
-	4	1556	p.G334E|NLRP1_	NM_033004	NP_127497	Q9C000	NALP1_HUMAN	IT.|ATP (Potential).	9	GCAGCCCCCTGC	0.532	
-	6	1191	PL1_uc010clk.2_M	NM_014336	NP_055151	Q9NZN9	AIPL1_HUMAN		0	gcagggggccctgcgg	0.264	
-	3	400	se_Mutation_p.R8	NM_014336	NP_055151	Q9NZN9	AIPL1_HUMAN	ase FKBP-type.	0	GGCTCCGGGAT	0.632	
-	28	4367	URL4_uc002gfy.1_	NM_032442	NP_115818	Q96JN8	NEUL4_HUMAN		2	CCCCAGGTTCTC	0.612	
+	3	459	F11_uc010vtw.1_In	NM_175734	NP_783861	Q0P670	CQ074_HUMAN	Arg-rich.	0	ccgccgccgccgccac	0.413	
+	75	11602	nm.1_Missense_M	NM_020877	NP_065928	Q9P225	DYH2_HUMAN	6 (By similarity).	13	CCAGCGCTTCC	0.657	
+	25	4151	Missense_Mutation	NM_001005273	NP_001005273	Q12873	CHD3_HUMAN		1	ACCTAGCCCGGA	0.527	
+	16	3097		NM_000180	NP_000171	Q02846	GUC2D_HUMAN	ase.|Cytoplasmic (Potential)	1	CCTCGCGCATGG	0.697	
-	18	2179	n.1_Missense_Mut	NM_002018	NP_002009	Q13045	FLII_HUMAN	ction with ACTL6A.	2	AGAGGGCTCCC	0.592	
+	2	179	S9C_uc010vyb.1_	NM_001040078	NP_001035167	Q6DKI2	LEG9C_HUMAN	Galectin 1.	1	GGGCCGTTCTC	0.562	
-	2	171	se_Mutation_p.A3	NM_001042685	NP_001036150	Q3B8N2	LEG9B_HUMAN	Galectin 1.	1	GAACGGCCCCAT	0.562	rs144269928
-	11	2310	cry.1_Missense_Mu	NM_178860	NP_849191	Q53EL9	SEZ6_HUMAN	cellular (Potential).	2	CATTGCGGGGCA	0.612	
+	10	2747		NM_207313	NP_997196	Q6IEE7	T132E_HUMAN	ical; (Potential).	1	CTGGGCGTCTTC	0.637	
-	1	520		NM_033059	NP_149048	Q9BYQ6	KR411_HUMAN	C-[GIKRQVHEL]- [SPTR]-[	0	GACGCAGGcagc	0.323	rs141357429
+	17	2897	NAP1_uc010wgs.1_	NM_003632	NP_003623	P78357	CNTP1_HUMAN	3.|Extracellular (Potential).	8	TCACCGGCCCT	0.567	
-	11	3171	_p.C973R|PLEKHI	NM_014798	NP_055613	Q9Y4G2	PKHM1_HUMAN	ol-ester/DAG-type.	0	CTGGCAGATGA	0.582	
+	6	885	e_Mutation_p.R18	NM_006310	NP_006301	P55786	PSA_HUMAN		0	TGACCGGAAAC	0.343	
+	2	339	n_p.Q8*|B4GALNT	NM_153446	NP_703147	Q8NHY0	B4GN2_HUMAN	nenal (Potential).	2	TTCCTTCAAGCA	0.502	
-	1	649	p.S205F|TOB1_uc	NM_005749	NP_005740	P50616	TOB1_HUMAN		1	TGGGAGAAGTA	0.473	
-	16	2161	itf.2_Missense_Mu	NM_001130528	NP_001124000	O60271	JIP4_HUMAN		5	TCTGAGGCAGA	0.483	
+	4	461	p.R46W|PCTP_uc	NM_021213	NP_067036	Q9UKL6	PPCT_HUMAN	START.	1	ACCTTCGGCAG	0.572	rs151142834
-	6	1458		NM_007146	NP_009077	Q14119	VEZF1_HUMAN	ts of P-[LV]-T-[IL]-T-[ST]- P.	2	TCATTGGGCTGG	0.488	
-	22	4862	nse_Mutation_p.S1	NM_004758	NP_004749	O95153	RIMB1_HUMAN		3	GATGCTAAAGAG	0.463	
-	3	307	2jde.2_Missense_M	NM_022579	NP_072101	Q14406	CSHL_HUMAN		0	AGAAGGAGGTC	0.527	
-	4	565	_p.S141F|ABCA9_	NM_080283	NP_525022	Q8IUA7	ABCA9_HUMAN		6	CCCCAAGAAAAC	0.368	
-	18	2762	vsc.1_Missense_M	NM_020753	NP_065804	Q8WXE0	CSKI2_HUMAN	Pro-rich.	1	GGGCCGCTCTG	0.657	
-	18	1927	n_p.T516I|UNC13D	NM_199242	NP_954712	Q70J99	UN13D_HUMAN	ction with RAB27A.	2	TGAGGGTACTG	0.622	
+	9	1258	p.W331R|SEC14L	NM_003003	NP_002994	Q92503	S14L1_HUMAN	CRAL-TRIO.	2	GGAGGCTGGCAT	0.498	
+	3	417	vub.1_Missense_M	NM_017950	NP_060420	Q4G0X9	CCD40_HUMAN		3	ATACGATAGTGTT	0.562	
+	8	4802	IA|RNF213_uc010	NM_020914	NP_065965	Q9HCF4	ALO17_HUMAN		21	GTTTCTGATGTGA	0.602	
+	9	2032	T|FOXK2_uc002kf	NM_004514	NP_004505	Q01167	FOXK2_HUMAN		0	CACAACGGTGAC	0.627	
+	5	1526		NM_153000	NP_694545	Q8J025	APCD1_HUMAN	cellular (Potential).	0	GTGCGGGGCCG	0.587	
-	16	2026	PIRE1_uc010wzx.1	NM_001128626	NP_001122098	Q08AE8	SPIR1_HUMAN		0	GGGCAGTGGAG	0.517	
-	5	1696	xxk.1_Missense_M	NM_022751	NP_073588	Q9H706	FA59A_HUMAN	Pro-rich.	2	TGGAGGGACTG	0.577	
+	12	4163	q.2_Missense_Mu	NM_030632	NP_085135	Q9C0F0	ASXL3_HUMAN		3	AGATTTCCTTCTG	0.498	
+	7	962	e_Mutation_p.R13	NM_020776	NP_065827	Q86T90	K1328_HUMAN		1	GCAGATCGTGTT	0.458	
+	4	1209	wn.3_Missense_Mu	NM_152791	NP_690004	Q8NEP9	ZN555_HUMAN	C2H2-type 8.	1	CAGTGTGGGAAG	0.448	
+	9	696	E6_uc010dtg.2_Mis	NM_024760	NP_079036	Q9H808	TLE6_HUMAN		1	CTGAGGGTTCCC	0.652	
+	10	1291	p.G362R|TJP3_uc	NM_014428	NP_055243	O95049	ZO3_HUMAN	PDZ 3.	3	CTGGCAGGGGGC	0.672	
-	2	334	_p.R27*|UBXN6_u	NM_025241	NP_079517	Q9BZV1	UBXN6_HUMAN		0	GGTTTCGGATGG	0.657	
-	3	1676	I4_uc010dub.1_5'F	NM_001080400	NP_001073869	Q96Q06	PLIN4_HUMAN	roximate tandem repeat.|15	0	CCCCCGTGAGC	0.612	
+	6	768	S4_uc002mji.2_5'U	NM_024552	NP_078828	Q9HA82	CERS4_HUMAN	Helical; (Potential).	1	TGGGCGGCCTC	0.617	

-	22	2888	p.L359M|ADAMTS	NM_030957	NP_112219	Q9H324	ATS10_HUMAN	TSP type-1 2.	4	GGGCAGCTTGC	0.672	
+	4	1683	ym.1_Missense_M	NM_001136501	NP_001129973	Q08AG5	ZN844_HUMAN		0	CTTCACATCTG	0.408	
-	4	1523		NM_145276	NP_660319	Q8TA94	ZN563_HUMAN	2H2-type 11.	0	ATAACGCTTTCC	0.428	
-	1	71	um.1_Missense_M	NM_032301	NP_115677	Q5XUX1	FBXW9_HUMAN		1	GGTCTGTCTCT	0.687	
-	22	3677	ao.1_Missense_M	NM_000435	NP_000426	Q9UM47	NOTC3_HUMAN	GF-like 30; calcium-binding	21	GCAGCGCAAAC	0.652	
-	5	705	HERP_uc002nej.2_	NM_006387	NP_006378	Q8IWX8	CHERP_HUMAN	CID.	2	CAGCCGCAGCT	0.642	
+	31	5190	l_Missense_Mutat	NM_004145	NP_004136	Q13459	MYO9B_HUMAN	rbol-ester/DAG-type.	1	CAGAGCCACTGC	0.577	
+	4	1706		NM_031218	NP_112495	P35789	ZNF93_HUMAN		1	TTCATACTAGAGA	0.358	
+	2	903	_p.P336L|ZNF493_	NM_175910	NP_787106	Q6ZR52	ZN493_HUMAN	ype 7; degenerate.	1	CAACCCCTACTA	0.348	rs142651314
-	6	2953	208_uc002nqo.1_I	NM_007153	NP_009084				7	GCTTTGCCACAT	0.453	
+	4	1483		NM_020855	NP_065906	Q9P255	ZN492_HUMAN	2H2-type 10.	0	TAAGATAATTCAT	0.363	
+	4	1759	rk.1_Missense_M	NM_203282	NP_975011	O75437	ZN254_HUMAN		0	TACTGAAGAGA	0.353	
+	4	1782	rk.1_Missense_M	NM_203282	NP_975011	O75437	ZN254_HUMAN	2H2-type 13.	0	GTGAAAAATGT	0.358	
-	4	1973	dm.1_Missense_M	NM_001007248	NP_001007249	Q96NL3	ZN599_HUMAN	2H2-type 12.	2	CAGTGTGGATCC	0.423	
-	1	386		NM_152481	NP_689694	Q17R55	F187B_HUMAN	ellular (Potential).	2	GGGTGGTGACA	0.532	
+	6	735	ap.2_Missense_Mu	NM_024321	NP_077297	Q9BTD8	RBM42_HUMAN	Pro-rich.	0	GGGCTCCATGG	0.677	
+	17	5043		NM_015073	NP_055888	O60292	SI1L3_HUMAN		2	ATCGAGGATGAC	0.582	
+	5	632		NM_001001414	NP_001001414	Q6ZVX7	NCRP1_HUMAN	FBA.	1	CCGACCGCCGC	0.682	
+	18	2264	AXL_uc010ehk.2_	NM_021913	NP_068713	P30530	UFO_HUMAN	Potential).|Protein kinase.	13	GACTTCGGGCTC	0.552	
-	2	518	tion_p.G127E|PSG	NM_006905	NP_008836	P11464	PSG1_HUMAN	g-like V-type.	2	TCATCTCCCTTT	0.502	
+	2	764	0ekb.1_Missense_	NM_006732	NP_006723	P53539	FOSB_HUMAN		3	CCACGGTCACC	0.517	
-	3	467	.E145G|STRN4_	NM_013403	NP_037535	Q9NRL3	STRN4_HUMAN		0	TTCTTCTCCCCC	0.493	
-	10	1290	H4_uc002pgb.1_I	NM_015168	NP_055983	Q9UPT8	ZC3H4_HUMAN		6	TGGGAGTTCGA	0.453	
+	5	479		NM_004533	NP_004524	Q14324	MYPC2_HUMAN	like C2-type 1.	1	GGACACCTGTG	0.602	
+	4	1385	dw.1_Missense_M	NM_138374	NP_612383	Q96IR2	ZN845_HUMAN	C2H2-type 8.	0	GTCAGATGTCAT	0.408	
+	11	1796	se_Mutation_p.R4	NM_006669	NP_006660	Q8NHL6	LIRB1_HUMAN	lasmic (Potential).	3	ACATCGACGTC	0.473	
+	2	336	20H2_uc002qkk.1_	NM_032701	NP_116090	Q86Y97	SV422_HUMAN		0	GGTTTCCGCACC	0.687	
+	22	4156	bp.1_Missense_M	NM_014668	NP_055483	Q4ZG55	GREB1_HUMAN		1	TGCCCTCCCCC	0.647	
-	3	226	2rfu.1_RNA|DNA	NM_016544	NP_057628	Q9NZQ0	DJC27_HUMAN		1	GACGTGTACCC	0.343	
-	7	575	_p.T154I|IFT172_	NM_015662	NP_056477	Q9UG01	IF172_HUMAN	WD 4.	2	ACGATGGTACCA	0.358	
+	3	557	uc002rvb.2_Intron	NM_012249	NP_036381	P17081	RHOQ_HUMAN		2	ACCCAATGACC	0.393	
+	10	1486	p.S300F|EHBP1_	NM_015252	NP_056067	Q8NDI1	EHBP1_HUMAN		2	GGATTCTCCTCC	0.373	
+	45	5270	YSF_uc010fej.2_M	NM_003494	NP_003485	O75923	DYSF_HUMAN	mic (Potential).|C2 5.	7	ATGTTCGAGCTG	0.572	
+	3	790		NM_003124	NP_003115	P35270	SPRE_HUMAN		2	GGAAAAGGACG	0.512	
-	2	875	2sit.3_Missense_	NM_015470	NP_056285	Q9BXF6	RFIP5_HUMAN		0	TGGGAGGATGG	0.552	
-	9	1678	nc.2_Missense_M	NM_133637	NP_598376	Q8TE96	DQX1_HUMAN		2	AGGACGGGTAA	0.527	
+	5	852	2_5'Flank|TMEM1	NM_004804	NP_004795	O76071	CIAO1_HUMAN	WD 5.	0	ATGACCGTACTG	0.542	rs142522111
+	3	512	.2_Missense_Mut	NM_002881	NP_002872	P11234	RALB_HUMAN		3	GAATTCAGGTAT	0.443	
+	6	1178	0flu.2_Missense_	NM_130773	NP_570129	Q8WYK1	CNTP5_HUMAN	1.|Extracellular (Potential).	10	CACTCGGTCCTC	0.607	
-	4	618		NM_005915	NP_005906	Q14566	MCM6_HUMAN		0	GATTTCGGCAG	0.398	
+	2	361	HSD7B_uc002tvb.	NM_001080427	NP_001073896				7	ACCGAACTGTG	0.532	
-	63	10964		NM_018557	NP_061027	Q9NZR2	LRP1B_HUMAN	ntial).|LDL-receptor class A	50	CAGAATGGAATA	0.328	
-	9	1274	0fnn.2_Missense_	NM_001006636	NP_001006637	Q4AE62	GTDC1_HUMAN		1	GCCTCTGAAAAA	0.358	
-	129	17979	.Q2353K|NEB_uc	NM_004543	NP_004534	P20929	NEBU_HUMAN	Nebulin 162.	20	GCATCTGCTGAG	0.448	
-	40	4879		NM_004543	NP_004534	P20929	NEBU_HUMAN	Nebulin 40.	20	TTGCAGCAACA	0.303	
+	8	7058	se_Mutation_p.P2	NM_152381	NP_689594	A4UGR9	XIRP2_HUMAN	Pro-rich.	14	CTCTTCCTCCAC	0.458	
+	4	669	gh.2_Missense_M	NM_000817	NP_000808	Q99259	DCE1_HUMAN		1	ACAGCGACCGG	0.552	

-	287	84469	77V|TTN_uc010z	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN			153	TGGGAGCACAA	0.448	
-	17	3046	_p.T895I|TTN_uc0	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN			153	GTGGAGTAACA	0.353	
+	4	2591		NM_194250	NP_919226	Q7Z570	Z804A_HUMAN			11	CATATCCTTAA	0.318	
-	3	192	rv.2_Missense_M	NM_014362	NP_055177	Q6NVY1	HIBCH_HUMAN			0	CACCTCTTCTG	0.358	
-	41	7471		NM_018897	NP_061720	Q8WXX0	DYH7_HUMAN	4 (By similarity).		12	TGAAAAGGGCT	0.458	
-	12	1603	p.G446V|FAM126	NM_173822	NP_776183	Q8IXS8	F126B_HUMAN			1	CAGTGCCAACC	0.453	
-	3	587	_p.W67*|GPR1_u	NM_005279	NP_005270	P46091	GPR1_HUMAN	lasmic (Potential).		0	TTCTTCCACTT	0.458	
+	11	1612	iv.2_Missense_Mu	NM_015690	NP_056505	Q9NRP7	STK36_HUMAN			11	CCAGCGCATCC	0.507	
+	5	426	e_Mutation_p.D12	NM_013335	NP_037467	Q96IJ6	GMPPA_HUMAN			0	GCTCCGACTTC	0.597	
-	4	1389	h.1_Missense_Mu	NM_024536	NP_078812	Q8IZ52	CHSS2_HUMAN	enal (Potential).		0	AAAGCGGGAGG	0.657	
+	7	536	se_Mutation_p.F67	NM_015575	NP_056390	Q6Y7W6	PERQ2_HUMAN			7	AAAGAATTTCTG	0.418	
+	7	1413	10_uc002vzn.1_M	NM_023083	NP_075571	Q9HC96	CAN10_HUMAN	Domain III 1	p.A410A(1)	6	CCCAGCGAGCA	0.657	
-	3	1147	_Mutation_p.A326	NM_014948	NP_055763	O94941	RNF37_HUMAN	U-box.		2	TCCGGGCCTTG	0.602	
-	7	782_783	ci.1_Missense_Mu	NM_024704	NP_078980	Q96L93	KI16B_HUMAN	inesin-motor.		8	GGTCCGGTTGA	0.48	
+	2	435	130264_uc010zsd	NM_020689	NP_065740	Q9HC58	NCKX3_HUMAN	ellular (Potential).		1	ATGCCGGACTC	0.547	
-	5	635	wtu.2_Missense_	NM_178312	NP_842564	Q9BX51	GGTL1_HUMAN			1	CGTGACGTTGG	0.622	
+	2	63	tj.1_RNA|FRG1B_uc010gdr.1_RNA|FRG1B_uc010ztk.1_Intron							0	GAATCGCCCTG	0.353	rs7266938
+	8	1220	2wxg.2_Missense_	NM_080625	NP_542192	Q9NUG4	CT160_HUMAN			4	GCGGAGTAAGC	0.607	
+	12	2260	eb.2_Missense_Mu	NM_015338	NP_056153	Q8IXJ9	ASXL1_HUMAN		p.Q592fs*5(1)	248	GCGCCAGGACC	0.637	
+	11	2022	sense_Mutation_p.	NM_020336	NP_065069	Q86X10	RLGPB_HUMAN			2	CAGCTCTTGAA	0.438	
+	15	1847_1848	uc002xjn.1_Intron	NM_003286	NP_003277	P11387	TOP1_HUMAN			7	GGACTCCATCA	0.455	
-	5	896	tron|SYS1-DBND	NM_014477	NP_055292	Q9Y2B4	T53G5_HUMAN			1	GCGATCTCCAC	0.557	
-	14	1466	_Mutation_p.E35	NM_006045	NP_006036	O75110	ATP9A_HUMAN	lasmic (Potential).		4	AGTCTTCGTAC	0.597	
+	17	1772	_Mutation_p.L501	NM_016434	NP_057518	Q9NZ71	RTEL1_HUMAN			0	TCATCCTTACCA	0.677	
-	14	2312		NM_020713	NP_065764	Q96KM6	Z512B_HUMAN	-type 6; atypical.		0	CGTTGGGACAG	0.622	
-	1	130		NM_181609	NP_853640	Q7Z4W3	KR193_HUMAN			0	TCCGTAGCCTC	0.567	
+	3	204	_p.P30S|PPIL2_u	NM_148175	NP_680480	Q13356	PPIL2_HUMAN			2	ATCTCCCACAA	0.353	
+	19	3912	p.D1062N|BCR_u	NM_004327	NP_004318	P11274	BCR_HUMAN	Rho-GAP.		12	CCTTCGACGTC	0.632	
+	5	730		NM_019601	NP_062547	Q9UGT4	SUSD2_HUMAN	ellular (Potential).		1	CGGCTCTTTCA	0.552	
-	13	1968	p.P595L|AP1B1_	NM_001127	NP_001118	Q10567	AP1B1_HUMAN	ich (stalk region).		2	TGCGAGGTGGC	0.637	
+	4	2181	H_uc003afp.2_5'	NM_021076	NP_066554	P12036	NFH_HUMAN	S-P-[AEPV]-[EAK]- [AEVK]		0	CAAAGTCCCCT	0.557	
-	3	961		NM_052906	NP_443138	Q5R3F8	LRFN6_HUMAN	tracellular (Potential).		2	CAGGTCGTGCA	0.592	
+	6	795	atq.1_Missense_M	NM_001039141	NP_001034230	Q9H2D6	TARA_HUMAN			1	GATCCCGAGGA	0.627	
-	4	458	o.2_Missense_Mu	NM_152221	NP_689407	P49674	KC1E_HUMAN	rotein kinase.		3	TGGACGGGATC	0.647	
+	3	344	ion_p.G6D|L3MBT	NM_031488	NP_113676	Q969R5	LMBL2_HUMAN	FCS-type.		3	CGTGGGTACAA	0.512	
+	14	1795	H7B_uc010gyl.1_I	NM_017590	NP_060060	Q9UGR2	Z3H7B_HUMAN			1	TCTTCGACCCG	0.622	
+	22	2806	H7B_uc010gyl.1_I	NM_017590	NP_060060	Q9UGR2	Z3H7B_HUMAN	C2H2-type.		1	AGTCCGAGAAG	0.622	
+	13	1258	nse_Mutation_p.R	NM_016300	NP_057384	Q9UBL0	ARP21_HUMAN			3	TCTTTCGGTTG	0.303	
+	9	1026	c.2_Missense_Mu	NM_002207	NP_002198	Q13797	ITA9_HUMAN	r (Potential).|FG-GAP 5.		6	TGGGGGCCCC	0.542	
+	4	697	C22A13_uc011ay	NM_004256	NP_004247	Q9Y226	S22AD_HUMAN	ical; (Potential).		1	TGACAGAATGG	0.622	
-	14	2344	p.P717L|SCN5A_	NM_198056	NP_932173	Q14524	SCN5A_HUMAN	S1 of repeat II; (Potential).		9	TAAACGGGTCC	0.547	
+	5	608	sense_Mutation_p	NM_001904	NP_001895	P35222	CTNB1_HUMAN	ARM 1.	del(1)|p.A20_	3166	CACACGTGCAA	0.433	
+	14	2032	p.G606S|TRAK1_	NM_001042646	NP_001036111	Q9UPV9	TRAK1_HUMAN			1	GGCCCGGTGTG	0.512	
+	14	2053	p.R613W|TRAK1_	NM_001042646	NP_001036111	Q9UPV9	TRAK1_HUMAN			1	GCTTCCGGACG	0.582	
+	10	1065	it.1_Missense_Mu	NM_015340	NP_056155	Q15031	SYLM_HUMAN			2	CGGGCGAAAAG	0.557	
+	3	449	10hiv.1_Missense	NM_031200	NP_112477	P51686	CCR9_HUMAN	Name=2; (Potential).		3	CTCTTTCTTGTC	0.473	
+	2	820	al.1_Intron|CXCR	NM_006564	NP_006555	O00574	CXCR6_HUMAN	Name=6; (Potential).		1	ATGCCCTTCAAC	0.493	

-	4	514		NM_000258	NP_000249	P08590	MYL3_HUMAN	EF-hand 2.	0	CTTGTCGAAGA	0.587
-	3	578	_p.L44F|CCDC51_	NM_024661	NP_078937	Q96ER9	CCD51_HUMAN	Potential.	0	CTCGAGAGTAG	0.612
-	2	4427	uf.1_Missense_M	NM_001407	NP_001398	Q9NYQ7	CELR3_HUMAN	ial).|EGF-like 1; calcium-bi	11	CAGGGCTCTCG	0.662
-	20	4283	dc.1_Missense_M	NM_002447	NP_002438	Q04912	RON_HUMAN	Potential).|Protein kinase.	6	CCACCTCCCCC	0.557
+	43	4447		NM_004947	NP_004938	Q8IZD9	DOCK3_HUMAN	DHR-2.	0	CCTGTGGATTG	0.537
+	3	645	_p.G79R|ABHD6_	NM_020676	NP_065727	Q9BV23	ABHD6_HUMAN	lasmic (Potential).	2	TCCACGGATTC	0.448
-	7	2117		NM_198859	NP_942559	Q7Z3G6	PRIC2_HUMAN		5	GCCCCCTTCCT	0.547
-	12	1332	.D106N|LRIG1_u	NM_015541	NP_056356	Q96JA1	LRIG1_HUMAN	lar (Potential).|LRRCT.	5	GCTGTCGCTGC	0.562
+	6	1612	e_Mutation_p.P46	NM_005233	NP_005224	P29320	EPHA3_HUMAN	tential).|Fibronectin type-III	33	AACATCCTAATG	0.453
+	4	1217	rp.1_Missense_M	NM_001080448	NP_001073917	Q9UF33	EPHA6_HUMAN	ellular (Potential).	16	GTCCTCCACAC	0.373
+	12	1861	T1_uc011big.1_Mi	NM_017699	NP_060169	Q9NXL6	SIDT1_HUMAN	lasmic (Potential).	5	AGAGCGACTTC	0.552
-	5	807	bb.1_Splice_Site_	NM_000796	NP_000787	P35462	DRD3_HUMAN		4	TGTACCTGAAAA	0.498
+	6	643_644	p.P105L|UPK1B_	NM_006952	NP_008883	O75841	UPK1B_HUMAN	ellular (Potential).	0	CTATCCCTGGCC	0.46
-	2	418	39A_uc003ecl.1_	NM_018266	NP_060736	Q9NV64	TM39A_HUMAN		2	AGAAGGTAAAG	0.483
-	17	4112_4113	.A203T|HEG1_uc	NM_020733	NP_065784	Q9ULI3	HEG1_HUMAN	lasmic (Potential).	2	GTAGGCCGGGT	0.431
-	5	1016	oy.2_Missense_M	NM_032169	NP_115545	Q709F0	ACD11_HUMAN		1	TTGTCATTATCG	0.403
+	5	1030		NM_003571	NP_003562	Q13515	BFSP2_HUMAN		0	CCACAGCAACA	0.572
-	14	1829	eyh.2_Missense_	NM_152394	NP_689607	Q7L0X2	F194A_HUMAN		3	TCATCTCCACTT	0.453
+	16	2076	M1_uc003fcg.2_M	NM_024996	NP_079272	Q96RP9	EFGM_HUMAN		4	GTAGCTCCAAAT	0.383
-	13	2749	p.S827F|MECOM_	NM_005241	NP_005232	Q03112	EVI1_HUMAN		14	GTTCAGAATGA	0.408
-	16	2449	_p.T290A|ABCC5_	NM_005688	NP_005679	O15440	MRP5_HUMAN	C transporter 1.	4	TTTCCGTAATACA	0.428
-	16	1883	13A4_uc011bsr.1_	NM_032279	NP_115655	Q4VNC1	AT134_HUMAN	ellular (Potential).	2	CAATTCCTTCC	0.473
+	6	1442	1bus.1_Missense_	NM_182524	NP_872330	Q7Z3I0	Q7Z3I0_HUMAN		0	AGAATGTGGCA	0.383
-	3	1986		NM_053042	NP_444270	Q9C0D4	Z518B_HUMAN		4	ATGCAGCTCCA	0.378
+	27	3029	s.1_Missense_Mu	NM_004787	NP_004778	O94813	SLIT2_HUMAN	EGF-like 1.	11	TTTACCGATGCA	0.398
-	13	1259		NM_003215	NP_003206	P42680	TEC_HUMAN	rotein kinase.	9	GGCTCGCCATT	0.453
+	5	1220	yb.1_Missense_	NM_020846	NP_065897	Q9P270	SLAI2_HUMAN		0	ACCCAGAAATT	0.478
-	10	1921	k.1_RNA|CENPC	NM_001812	NP_001803	Q03188	CENPC_HUMAN		2	TCTGCCTTTTAA	0.343
-	1	1475		NM_033214	NP_149991	Q14410	GLPK2_HUMAN		4	TCAAATCGTTCC	0.507
+	45	7493	a.2_Missense_M	NM_080683	NP_542414	Q12923	PTN13_HUMAN	protein phosphatase.	6	ACTTCGACTGG	0.448
+	5	782	6_splice|HSPA4L_	NM_014278	NP_055093	O95757	HS74L_HUMAN		4	TGCAGGTGAGC	0.328
+	9	1367	_p.V331I|HSPA4L_	NM_014278	NP_055093	O95757	HS74L_HUMAN		4	AAGCTGTTGCA	0.338
-	17	1613	jz.3_Missense_M	NM_001102653	NP_001096123	Q01804	OTUD4_HUMAN		3	CAGGAGAAGGG	0.353
-	7	1613	me.2_Nonsense_	NM_001009555	NP_001009555	Q5HYK7	SH319_HUMAN	Pro-rich.	2	GGCTTGTGATG	0.552
-	7	1368	ime.2_Missense_	NM_001009555	NP_001009555	Q5HYK7	SH319_HUMAN	Pro-rich.	2	TTCCCGCTTCT	0.537
+	3	364_365	B_uc010ipv.2_Intr	NM_005141	NP_005132	P02675	FIBB_HUMAN		3	CTACAGGATGTC	0.401
-	3	1339	sn.3_Nonsense_	NM_021647	NP_067679	O75121	MFA3L_HUMAN	lasmic (Potential).	1	TCCAGGTAAGC	0.483
-	4	809		NM_153343	NP_699174	Q6UWR7	ENPP6_HUMAN	ellular (Potential).	1	GATCCACTTGG	0.547
+	3	470	v.1_RNA|C5orf22_	NM_018356	NP_060826	Q49AR2	CE022_HUMAN		2	ACTTTTTAGTA	0.378
-	20	4256	iuq.1_Missense_	NM_030955	NP_112217	P58397	ATS12_HUMAN	SP type-1 5.	9	AGCACAGGGAC	0.557
-	6	1038		NM_001007527	NP_001007528	Q68DH5	LMBD2_HUMAN	lasmic (Potential).	0	GAATTTCCACC	0.423
-	12	1984	1_Missense_Muta	NM_000065	NP_000056	P13671	CO6_HUMAN	SP type-1 3.	7	GGCAGGATTAT	0.502
-	1	633	4_uc003jng.2_5'F	NM_001014279	NP_001014301	Q3ZCQ2	AX2R_HUMAN		0	GGGTTCCTCTG	0.607
+	21	3298	.2_Missense_Muta	NM_012343	NP_036475	Q13423	NNTM_HUMAN	chondrial matrix.	3	ATTCAGCAGCT	0.343
+	10	2324		NM_005921	NP_005912	Q13233	M3K1_HUMAN		2	TGGGGGCAGCA	0.577
+	13	1990	.G542R|POLK_uc	NM_016218	NP_057302	Q9UBT6	POLK_HUMAN	UBZ-type 1.	4	CTCAAGGGTGC	0.368
+	2	10147		NM_153610	NP_705838	Q8N3K9	CMYA5_HUMAN		9	GTCACGGTAAT	0.483

-	8	1129	SK1_uc010jbi.1_In	NM_000439	NP_000430	P29120	NEC1_HUMAN	Catalytic.		2	CGTTTCCCGAA	0.512	
-	2	1198	j.1_Missense_Mut	NM_005260	NP_005251	O60383	GDF9_HUMAN			1	GTGACGGTGAT	0.512	
-	2	962	1_RNA|TRPC7_uc	NM_020389	NP_065122	Q9HCX4	TRPC7_HUMAN	lasmic (Potential).		0	CTTACCTTCTTG	0.493	
+	20	4926_4927	p.P1232F|KDM3B_	NM_016604	NP_057688	Q7LBC6	KDM3B_HUMAN	JmjC.		11	GGATTCCCATCG	0.421	
+	1	1887	.2_Intron|PCDHA6	NM_018903	NP_061726	Q9UN75	PCDAC_HUMAN	|Extracellular (Potential).		0	GGGTGCGGGCC	0.682	
+	1	1848	HA7_uc003lhq.2_In	NM_018898	NP_061721	Q9H158	PCDC1_HUMAN	cellular (Pote	p.P558S(1)	5	TGTTTCCCTTGC	0.493	rs140626189
+	1	802		NM_018940	NP_061763	Q9Y5E2	PCDB7_HUMAN	r (Potential).|Cadherin 2.		6	TTCAGTTTAACC	0.498	
+	1	964	DHGA4_uc003ljq.1	NM_018919	NP_061742	Q9Y5G7	PCDG6_HUMAN	|Extracellular (Potential).		1	AAGCCCGGGAT	0.413	
+	11	2285	p.R542Q|LARP1_	NM_033551	NP_291029	Q6PKG0	LARP1_HUMAN			4	TGGGCGGAAGA	0.502	
-	2	1043		NM_130899	NP_570969	Q8TC56	FA71B_HUMAN	Ala-rich.		6	TGCTCCCGCCA	0.532	
+	19	2120	61_splice|CYFIP2_	NM_001037333	NP_001032410	Q96F07	CYFP2_HUMAN			0	ATGGAGTAAGA	0.522	
+	2	495		NM_000811	NP_000802	Q16445	GBRA6_HUMAN			12	TGGAGGTAAGA	0.453	
+	8	1317	lyy.3_Missense_M	NM_000816	NP_000807	P18507	GBRG2_HUMAN	ical; (Probable).		5	CAGCACCATTG	0.463	
+	10	1903	lissense_Mutation_	NM_001122679	NP_001116151					10	GCGACGTGCCC	0.577	
+	11	1648	leq.1_Missense_M	NM_017785	NP_060255	Q96EA4	SPDLY_HUMAN			2	GTGCTCCCTGTG	0.448	
+	3	342	ick.3_Missense_M	NM_001205	NP_001196	Q12981	SEC20_HUMAN	Cytoplasmic (Potential).		1	TCCAGGAAGTG	0.473	
-	10	1399	T2L2_uc003mja.2_	NM_153373	NP_699204	Q8IUZ5	AT2L2_HUMAN			1	CCTCTTCAGTTG	0.512	
-	7	1576	ense_Mutation_p.A	NM_000843	NP_000834	O15303	GRM6_HUMAN	cellular (Potential).		8	CCGGGCGCATCT	0.642	
+	1	326	q.1_Missense_Mu	NM_004415	NP_004406	P15924	DESP_HUMAN	plakophilin 1 and junction p		9	GGGCCGCATGA	0.697	
-	23	2971	ch.3_Missense_M	NM_022113	NP_071396	Q9H1H9	KI13A_HUMAN			4	ACCGGTGGCCCC	0.473	
+	7	1298	e_Mutation_p.R27	NM_006355	NP_006346	O00635	TRI38_HUMAN	B30.2/SPRY.		0	TGTTAAGGAGTC	0.438	
+	7	1253	c011dly.1_RNA|LC	NM_001098479	NP_001091949	P30511	HLAF_HUMAN			0	GCCTCCGGAGT	0.512	
-	4	1107	39_uc003npd.2_In	NM_025236	NP_079512	Q9H2S5	RNF39_HUMAN	B30.2/SPRY.		0	GGGTGCCGTGA	0.756	
-	13	6352	rf.3_Missense_Mu	NM_014641	NP_055456	Q14676	MDC1_HUMAN	uclear localization (NLS2).		4	GGTCGGTCACC	0.547	
-	10	4203	C1_uc011dmp.1_	NM_014641	NP_055456	Q14676	MDC1_HUMAN	on with the PRKDC comple		4	TGTGGAGGTGG	0.532	
+	2	229	CA_uc003rxz.1_5'UTR							0	CAGAAATGCAGG	0.552	rs17200172
-	2	821	2_5'Flank|ATF6B_	NM_022110	NP_071393	Q9UIM3	FKBPL_HUMAN			0	CTGACAGGAGGT	0.587	
-	3	737	_Mutation_p.E219	NM_002123	NP_002114	P01920	DQB1_HUMAN	ential).|Beta-2.|Ig-like C1-ty		0	CCACTCCACGG	0.537	
-	3	592	fb.2_Missense_Mu	NM_001142883	NP_001136355	Q96PC2	IP6K3_HUMAN			0	AGGGCTCCAGC	0.622	
-	10	4907	318_uc003ouw.2_I	NM_014345	NP_055160	Q5VUA4	ZN318_HUMAN			7	GTGTCTGAACTT	0.502	
-	3	221		NM_032111	NP_115487	Q6P1L8	RM14_HUMAN			1	GAATCGCACTC	0.532	
-	2	585	bx.2_Missense_Mu	NM_001498	NP_001489	P48506	GSH1_HUMAN			2	ACCAACCGGACT	0.378	rs148272922
+	1	818		NM_032602	NP_115991	Q969M2	CXA10_HUMAN	lasmic (Potential).		0	TGATTTGCTCTT	0.423	
-	4	830	qi.1_Missense_M	NM_001040179	NP_001035269	Q969V1	MCHR2_HUMAN	Name=4; (Potential).		8	ACCTTCGAGTAG	0.443	rs145638548
-	27	3384	at.1_Missense_Mu	NM_001145128	NP_001138600	Q5TCS8	AKD1_HUMAN			1	CTTCAAGAATTTC	0.303	rs144036651
+	2	567_568		NM_175057	NP_778227	Q96RI9	TAAR9_HUMAN	cellular (Potential).		0	TAGGAGGCTGCC	0.406	
-	2	277	fr.1_Missense_Mu	NM_001033080	NP_001028252	Q9P1P5	TAAR2_HUMAN	Name=2; (Potential).		1	GAATCCCAGGA	0.423	
+	12	1592	ense_Mutation_p.A	NM_015440	NP_056255	Q6UB35	C1TM_HUMAN	hydrofolate synthetase.		4	CTGACCGCACAC	0.502	
-	82	16305	ou.3_Missense_M	NM_182961	NP_892006	Q8NF91	SYNE1_HUMAN	lasmic (Potential).		45	TTCCAGGTAACT	0.398	
-	29	4657		NM_005577	NP_005568	P08519	APOA_HUMAN	Kringle 36.		6	AGGATATGCCTC	0.448	
+	9	1153		NM_000301	NP_000292	P00747	PLMN_HUMAN			4	TGGCTCCCACA	0.488	
-	3	421		NM_182924	NP_891554	Q8IY33	MILK2_HUMAN	CH.		1	CAGCCGGTCAG	0.657	rs150995341
-	9	1183	sh.1_Missense_M	NM_001013836	NP_001013858	Q9Y6D9	MD1L1_HUMAN	Potential.		2	TCGTTCTCCAGC	0.637	
+	3	873	p.S125L|FOXK1_	NM_001037165	NP_001032242	P85037	FOXK1_HUMAN			2	CGCGTCGGAGC	0.657	
+	7	964	.S268N|SLC29A4_	NM_153247	NP_694979	Q7RTT9	S29A4_HUMAN	lasmic (Potential).		1	TGACAGCCACC	0.662	
-	8	1320		NM_001077653	NP_001071121	Q9UMR3	TBX20_HUMAN			1	AATGGCGTAGTC	0.498	
+	48	13316	CA13_uc010kyt.1_	NM_152701	NP_689914	Q86UQ4	ABCAD_HUMAN			10	CAATACGGTAAT	0.358	

+	10	1116		NM_000265	NP_000256	P14598	NCF1_HUMAN	-rich (highly basic).	1	GAGCCCGCTCG	0.517	
-	11	1659		NM_012431	NP_036563	O15041	SEM3E_HUMAN	Sema.	3	TCATCAGGATAG	0.393	
-	3	337		NM_006304	NP_006295	P60896	DSS1_HUMAN		0	CATACGGGGTT	0.363	
+	1	1411	.1_5'Flank|ZCWP	NM_019606	NP_062552	Q7L2J0	MEPCE_HUMAN	in3-type SAM.	1	TGGGCGCCTTC	0.562	
+	4	734	p.G181S|SERPIN	NM_000602	NP_000593	P05121	PAI1_HUMAN		3	TCAACGGCCAG	0.562	
-	7	718		NM_138403	NP_612412	Q9BUA6	MYL10_HUMAN	EF-hand 2.	2	TTTTTCTTTGATG	0.562	
-	22	3342	v.2_Missense_Mu	NM_002291	NP_002282	P07942	LAMB1_HUMAN	inin EGF-like 10.	8	CGTGTGGTACA	0.532	
-	3	330	3A1_uc010lks.2_	NM_022444	NP_071889	Q9BZW2	S13A1_HUMAN		2	AAATTCCATTTT	0.378	
-	12	2684	JB_uc003vko.2_M	NM_178827	NP_849149	Q8NA54	IQUB_HUMAN		4	GGATTTATTCC	0.468	
-	4	393	PDH1_uc011kon.	NM_001142573	NP_001136045	P20839	IMDH1_HUMAN		4	CTGGGGTGCAG	0.612	
+	9	1728	_p.A525T|ZYX_uc	NM_001010972	NP_001010972	Q15942	ZYX_HUMAN	zinc-binding 3.	0	TGGTCGCCCTG	0.607	
+	44	6434		NM_198455	NP_940857	A2VEC9	SSPO_HUMAN	F5/8 type C.	0	CTCCTCCAACG	0.617	
-	5	995	p.R232C|KCNH2_	NM_000238	NP_000229	Q12809	KCNH2_HUMAN	lasmic (Potential).	4	GGTGCGGTAGC	0.617	
+	24	3030	_p.P913L|ARHGE	NM_014629	NP_055444	O15013	ARHGA_HUMAN		1	ACCCCCGGACC	0.592	
-	1	101	.1_Intron|FAM66D	NM_201402	NP_958804	Q6R6M4	U17L2_HUMAN		3	AAGTCCGCTGG	0.522	
-	18	6054	.I1837T|MYST3_	NM_001099412	NP_001092882	Q92794	MYST3_HUMAN		7	TGCCAATGTTG	0.562	
+	8	801	pc.2_Missense_Mu	NM_005662	NP_005653	Q9Y277	VDAC3_HUMAN	nded; (By similarity).	1	GTTTTGGCATT	0.423	
+	2	243		NM_000749	NP_000740	Q05901	ACHB3_HUMAN	ellular (Potential).	1	TCCAAGGTTAT	0.423	
+	3	461	qa.1_Missense_M	NM_001005365	NP_001005365	Q6S8J7	POTEA_HUMAN	ANK 2.	1	AGGCCGTACAA	0.373	
+	5	482	TG1_uc010lxz.1_	NM_018967	NP_061840	Q9NSN8	SNTG1_HUMAN		5	TTGATGATCCA	0.383	
+	1	420		NM_022454	NP_071899	Q9H6I2	SOX17_HUMAN	HMG box.	1	CCGATGAACG	0.677	
-	22	3851	nt.2_Missense_Mu	NM_198123	NP_937756	Q7Z407	CSMD3_HUMAN	xtracellular (Potential).	63	GTGCACTCCAC	0.507	
-	7	2645	i.2_RNA|ZFAT_uc	NM_020863	NP_065914	Q9P243	ZFAT_HUMAN		1	CAGTGCTGTGT	0.478	
-	4	684	_p.S158L|ZFAT_uc	NM_020863	NP_065914	Q9P243	ZFAT_HUMAN		1	TTTTCGAGGCT	0.438	
-	3	552	c003yxj.2_Missens	NM_000497	NP_000488	P15538	C11B1_HUMAN		3	GGCTCCCCCGG	0.632	
+	18	2474	3zjl.3_Missense_	NM_020829	NP_065880	Q4ADV7	RIC1_HUMAN		0	AGAAGCTACCT	0.542	
-	1	2961	_p.I632L|RANBP6	NM_012416	NP_036548	O60518	RNBP6_HUMAN	HEAT 7.	3	TCCCTATTGCTG	0.363	
+	21	2593	zoh.1_Missense_	NM_017794	NP_060264	Q5VW36	K1797_HUMAN		10	ATGACGATGAA	0.378	
+	1	490	42421_uc004aed.1_RNA						0	TTAACCCCTTCC	0.582	
+	7	613	_RNA|TMC1_uc0	NM_138691	NP_619636	Q8TDI8	TMC1_HUMAN	rg/Asp/Glu/Lys-rich (highly	1	AAGAGGAAGAG	0.413	
-	5	1128		NM_004297	NP_004288	O95837	GNA14_HUMAN	(By similarity).	2	CACCAACATCC	0.428	
+	13	2217	lsz.1_Missense_	NM_001018064	NP_001018074	Q16620	NTRK2_HUMAN	ellular (Potential).	16	AAACCGGTCGG	0.458	rs142393662
-	5	1131		NM_017561	NP_060031	A1L443	FA22F_HUMAN	Pro-rich.	0	TGGGCGTTGGT	0.692	
+	10	7136	ssense_Mutation_p	NM_021224	NP_067047	Q96JM2	ZN462_HUMAN		5	GTTGTCCCCATT	0.428	
+	5	692	.1_Intron|SLC31A	NM_001859	NP_001850	O15431	COPT1_HUMAN	ical; (Potential).	0	GGCCGGTACAG	0.502	
+	3	883	L27A1_uc010mvd.	NM_032888	NP_116277	Q8IZC6	CORA1_HUMAN	Pro-rich.	4	CACCCGCCACG	0.672	rs145824150
-	12	3883	f.2_Missense_Mut	NM_002160	NP_002151	P24821	TENA_HUMAN	nectin type-III 7.	7	CCTCGGCCACC	0.502	
-	2	558	_p.A153T|ASTN2_	NM_198187	NP_937830	O75129	ASTN2_HUMAN	ellular (Potential).	9	CGCTGCTGTGC	0.607	
-	10	4055	p.K910R|SETX_uc	NM_015046	NP_055861	Q7Z333	SETX_HUMAN		3	GACCCTTTTTC	0.438	
-	1	105		NM_001080483	NP_001073952	A6NI61	TMM8C_HUMAN	ical; (Potential).	0	TAGACCATGGC	0.647	
-	9	1460		NM_017617	NP_060087	P46531	NOTC1_HUMAN	GF-like 12; calcium-binding	856	CCTCGCAGTGC	0.652	
+	10	1733	.R468Q|GRIN1_uc	NM_007327	NP_015566	Q05586	NMDZ1_HUMAN	ellular (Potential).	1	GGCACGGACCA	0.632	
+	3	531	_p.P165L|EHMT1_	NM_024757	NP_079033	Q9H9B1	EHMT1_HUMAN		3	GACTCCAAGCG	0.657	
-	5	687	.2_Missense_Mut	NM_003662	NP_003653	O00625	PIR_HUMAN		1	TGACAGCAACT	0.473	
+	4	938		NM_014271	NP_055086	Q9NZN1	IRPL1_HUMAN	2.|Extracellular (Potential).	5	CTCTGCTATAATT	0.393	
-	6	1982	_p.T440I|TAB3_uc	NM_152787	NP_690000	Q8N5C8	TAB3_HUMAN	Pro-rich.	1	ATGGAGTACAA	0.393	
-	16	2197	D_uc004ddb.1_N	NM_004006	NP_003997	P11532	DMD_HUMAN	Spectrin 3.	6	TTATCCCAACAC	0.388	

+	1	1665		NM_001013736	NP_001013758	Q5HY64	FA47C_HUMAN		3	AGCCTCCTGAG	0.617	
+	4	742	hh.2_Missense_M	NM_005676	NP_005667	P98175	RBM10_HUMAN	Poly-Glu.	5	aggatgaggaggagg	0.522	
+	8	1202	p.S352N|WDR13_	NM_017883	NP_060353	Q9H1Z4	WDR13_HUMAN		2	GGGGAGCCCTG	0.627	
-	19	1766	p.R210K|TEX11_u	NM_001003811	NP_001003811	Q8IYF3	TEX11_HUMAN		5	AACCTCTCTCT	0.328	
-	3	1571_1572		NM_001008537	NP_001008537	Q5QGS0	K2022_HUMAN		15	ATTGTCCTGAAA	0.416	
+	6	1814	w.2_Missense_Mu	NM_000052	NP_000043	Q04656	ATP7A_HUMAN	ytoplasmic (Potential).	0	GATTTGGAGCC	0.388	
+	4	249	_p.L45F|ARL13A_	NM_001012990	NP_001013008	Q5H913	AR13A_HUMAN		1	CAGTACTTCCC	0.428	
+	10	1465	h.1_Missense_Mu	NM_001939	NP_001930	Q13474	DRP2_HUMAN	WW.	2	CCAATAAAGTT	0.502	
-	16	2789	ense_Mutation_p.	NM_024657	NP_078933	Q8TE76	MORC4_HUMAN	Potential.	1	CTTTGGTTCTTT	0.488	
-	1	3026		NM_003604	NP_003595	O14654	IRS4_HUMAN		10	GGGGAGGAAGT	0.488	
-	4	1187	_p.R258C|DCX_uc	NM_000555	NP_000546	O43602	DCX_HUMAN	oublecortin 2.	4	CATAGCGAAATT	0.388	
-	6	2388	m.1_Missense_M	NM_012471	NP_036603	Q9UL62	TRPC5_HUMAN	ical; (Potential).	1	GCAACGAACTT	0.463	
-	2	137	A69_uc004ery.1_	NM_001000	NP_000991	P62891	RL39_HUMAN		0	CTGGGGAATGG	0.408	
+	1	310		NM_182540	NP_872346	Q5JSJ4	DX26B_HUMAN		0	CGGCAGTGAGG	0.557	
-	8	1196	nwc.1_Missense_	NM_024597	NP_078873	Q8IWC1	MA7D3_HUMAN		4	CGGGAGTGCTT	0.582	
+	5	943	.2_Intron|MAGEA	NM_005366	NP_005357	P43364	MAGAB_HUMAN	MAGE.	2	TGAAGGAAGTG	0.473	
+	12	1615	eh.1_Missense_M	NM_003828	NP_003819	Q13613	MTMR1_HUMAN	ularin phosphatase.	1	ATGCGGATGCT	0.378	
+	2	1208	3202-2|MI0014253	NM_003492	NP_003483	Q14656	TM187_HUMAN		0	CACAGGCCACT	0.552	
-	6	631	se_Mutation_p.K1	NM_002436	NP_002427	Q00013	EM55_HUMAN	SH3.	3	TCCTTTTTGGG	0.463	
-	5	887	.R241W|TMLHE_	NM_018196	NP_060666	Q9NVH6	TMLH_HUMAN		1	GTGCCGATCCA	0.418	rs146027951
-	21	2902	RSF25_uc001ani.	NM_001042663	NP_001036128	O94827	PKHG5_HUMAN		1	CCTCGGACTTA	0.697	
-	2	262		NM_001009611	NP_001009611	O60810	PRAM4_HUMAN		1	GGCGGCGGAAG	0.602	
-	2	227	_p.P13S|ATP13A	NM_022089	NP_071372	Q9NQ11	AT132_HUMAN	ical; (Potential).	4	GGTGGGCGTGC	0.527	
+	1	2328	C7A_uc009vpg.2_	NM_152375	NP_689588	Q5VTJ3	KLD7A_HUMAN		3	GGGCACCCTCC	0.647	
+	3	435	_p.Q90*|SYTL1_	NM_032872	NP_116261	Q8IYJ3	SYTL1_HUMAN		1	GCTCCCAGCGG	0.642	
-	6	1017	K2_uc010olo.1_Mi	NM_007170	NP_009101	Q96S53	TESK2_HUMAN	rotein kinase.	5	CATCGGGGATC	0.542	
+	8	1233	nr.1_Missense_Mu	NM_153703	NP_714914	Q7Z5L7	PODN_HUMAN	LRR 12.	2	GCGGTTGCACA	0.662	
-	3	385		NM_022159	NP_071442	Q9HBW9	ELTD1_HUMAN	GF-like 2; calcium-binding	2	TGTGTTAGTGC	0.343	
+	6	978	_p.D75N|CLCA4_u	NM_012128	NP_036260	Q14CN2	CLCA4_HUMAN	VWFA.	2	TTCTTGATAAGT	0.423	
-	2	714	P6_uc009wjj.1_Int	NM_016361	NP_057445	Q9NPH0	PPA6_HUMAN		4	GGGTGGGACCT	0.418	
+	14	1688	vkt.1_Missense_M	NM_001102663	NP_001096133				0	CTCAGCAGGGA	0.478	
+	3	814	.2_Intron|CD1E_u	NM_030893	NP_112155	P15812	CD1E_HUMAN	Ig-like.	3	CCCTCGATTTC	0.507	
+	1	586		NM_001004478	NP_001004478	Q8NGY1	O10Z1_HUMAN	ellular (Potential).	2	CGAGTGAGCTG	0.498	
+	10	1447	wb.2_Missense_M	NM_015569	NP_056384	Q9UQ16	DYN3_HUMAN		1	GCCTTCCTTGA	0.398	
-	6	1040	A11_uc010pmq.1_	NM_178527	NP_848622	Q5TAH2	S9A11_HUMAN		2	GGATTCTGTTG	0.274	
-	7	1507_1508	_Mutation_p.G432	NM_004319	NP_004310	O14525	ASTN1_HUMAN		15	TGGCTCCCCTC	0.589	
+	3	355	R3_uc010poy.1_M	NM_021023	NP_066303	Q02985	FHR3_HUMAN	Sushi 2.	0	TATTTTCCTTATT	0.299	
+	3	391		NM_030787	NP_110414	Q9BXR6	FHR5_HUMAN	Sushi 2.	2	TGTGTTCCTTTC	0.308	
-	6	981		NM_001994	NP_001985	P05160	F13B_HUMAN	Sushi 5.	3	TATTTCTGCTG	0.363	
-	30	4297	gh.1_Missense_	NM_018072	NP_060542	Q9H583	HEAT1_HUMAN		3	GCTCCGGGACG	0.443	
-	4	531		NM_001010924	NP_001010924	Q5VUB5	F1711_HUMAN	ellular (Potential).	4	CCGAAGGGGAG	0.517	
-	8	919		NM_001031746	NP_001026916	Q8IW00	CJ072_HUMAN	lasmic (Potential).	0	GGTGGGGTTTG	0.488	
+	3	2053		NM_199459	NP_955629	Q711Q0	CJ071_HUMAN		0	TCAATCCCCAG	0.542	
-	6	1624	hv.1_Missense_M	NM_014912	NP_055727	Q8NE35	CPEB3_HUMAN	RRM 1.	0	TTACCTTTAGGA	0.413	
+	22	2606	.P710L|HELLS_u	NM_018063	NP_060533	Q9NRZ9	HELLS_HUMAN		2	CAGTCCTGAAT	0.323	
+	3	807	C19_uc009xus.1_	NM_000772	NP_000763	P33260	CP2CI_HUMAN		5	CCAATGGTGGG	0.323	
+	4	962	212*|CYP2C19_u	NM_000772	NP_000763	P33260	CP2CI_HUMAN		5	CCATGGATCCA	0.294	

-	9	1393	P2C8_uc010qob.1	NM_000770	NP_000761	P10632	CP2C8_HUMAN		0	CAAATTCGTTTTC	0.363	
+	1	386	y.2_Intron|DHDPS	NM_001009997	NP_001009997	Q5T681	CJ062_HUMAN		0	GCTCCACGGTTC	0.582	
-	20	2209	ise_Mutation_p.Q6	NM_198060	NP_932326	Q86VF7	NRAP_HUMAN	Nebulin 16.	10	TTGTACTGCAGC	0.502	
-	1	488		NM_001005238	NP_001005238	Q8NGK0	O51G2_HUMAN	Name=4; (Potential).	2	GGTAATGGAAAA	0.473	
+	7	1301	ax.1_5'UTR|ZNF21	NM_013250	NP_037382	Q9UL58	ZN215_HUMAN		0	CTTTAGACATGAA	0.403	
-	3	366		NM_000315	NP_000306	P01270	PTHY_HUMAN		1	TCCTTTTTTCGGG	0.458	
-	13	2124	q.1_Missense_Mu	NM_024783	NP_079059	Q5U5Z8	CBPC2_HUMAN		2	AGACACTGAGTGA	0.259	
+	1	922		NM_001004739	NP_001004739	Q8NGL0	OR5L2_HUMAN	lasmic (Potential).	1	GGCTCCAAAATTC	0.463	
+	1	151		NM_001005201	NP_001005201	Q8N146	OR8H3_HUMAN	lasmic (Potential).	2	ATAATCCGCCTGC	0.438	
+	1	298		NM_001004747	NP_001004747	Q8NGG3	OR5T3_HUMAN	Name=2; (Potential).	0	TTCTTGGATGCTT	0.383	
+	1	29		NM_001013358	NP_001013376	P0C7N8	OR9G9_HUMAN	cellular (Potential).	0	TGACTGAGTTTAT	0.478	
+	2	1105	ır.2_Missense_Mu	NM_015177	NP_055992	Q9Y2E6	DTX4_HUMAN		3	CAGCAAGACCGC	0.632	
-	10	1516	ss.2_Missense_M	NM_001040118	NP_001035207	Q96P48	ARAP1_HUMAN	PH 2.	1	AGCGCGGTCAG	0.622	rs138364636
+	6	820	e_Mutation_p.E19	NM_018480	NP_060950	Q8IUX1	T126B_HUMAN		0	GTATTTGAAGAGA	0.333	
+	1	1190		NM_001161630	NP_001155102	B2RXH2	KD4DL_HUMAN	JmjC.	0	CACGATGGATTG	0.512	
+	16	2258	e_Mutation_p.I64	NM_014361	NP_055176	O94779	CNTN5_HUMAN	-like C2-type 6.	8	GGAACATCCTTCT	0.463	
-	3	2639	R_uc009yww.1_RN	NM_000926	NP_000917	P06401	PRGR_HUMAN	uclear receptor.	4	AGGACCATGCCA	0.368	
-	4	1441	_p.R351*|GUCY1A	NM_000855	NP_000846	P33402	GCYA2_HUMAN		8	CACATCGAAGCTC	0.473	
+	1	299		NM_000486	NP_000477	P41181	AQP2_HUMAN	nic (Potential).|NPA 1.	2	CCCTGCCGTGAC	0.662	
-	3	776		NM_004693	NP_004684	O95678	K2C75_HUMAN	Coil 1B.|Rod.	0	CAAATTCATTCTC	0.478	
+	21	2435		NM_017564	NP_060034	Q8WWQ8	STAB2_HUMAN	r (Potential).|EGF-like 6.	14	GCTCAGGAAATGC	0.413	
+	5	1112		NM_001080533	NP_001074002	A6NIH7	U119B_HUMAN		1	AAAATCCTTACGA	0.443	
+	63	10837_10838		NM_207437	NP_997320	Q8IVF4	DYH10_HUMAN	|AAA 5 (By similarity).	6	TCCACGGGGAAC	0.594	
-	1	2778		NM_052910	NP_443142	Q96PX8	SLIK1_HUMAN	ical; (Potential).	5	AGGCGGAGGTG	0.592	
-	45	5042	p.P306S|DOCK9_u	NM_015296	NP_056111	Q9BZ29	DOCK9_HUMAN	DHR-2.	1	GTGGGGGAGAA	0.592	
+	1	158	a.1_RNA|POTEG_	NM_001005356	NP_001005356	Q6S5H5	POTEG_HUMAN		1	GGTGCAGGGGG	0.592	
-	1	127	xvo.3_Missense_M	NM_005065	NP_005056	Q9UBV2	SE1L1_HUMAN		1	CTATCCGGACCC	0.706	
+	14	1474	_p.P465S|SLC24A	NM_153646	NP_705932	Q8NFF2	NCKX4_HUMAN	ic (Potential).|Alpha-2.	3	AGTGTTCCAGAC	0.542	
+	6	523	_p.I147R|KIAA14	NM_020818	NP_065869	Q9P2D8	UNC79_HUMAN		17	TGTGTATAGACCC	0.418	
+	3	846	ujp.1_Missense_M	NM_002755	NP_002746	Q02750	MP2K1_HUMAN	rotein kinase.	0	ACTCTCCGTACAT	0.512	
-	9	713	_p.P230L|GRAMD	NM_001012642	NP_001012660	Q8IUY3	GRAM2_HUMAN		0	GATGATGGAGGG	0.537	
+	2	2715	_p.P799S|C15orf3	NM_015492	NP_056307	Q6ZRI6	CO039_HUMAN		0	CTGGGCCCTGG	0.642	
-	13	1918	_p.T617N|ACSBG	NM_015162	NP_055977	Q96GR2	ACBG1_HUMAN		1	TCAGAGGTGTCTC	0.527	
+	1	318	9M|SLCO3A1_uc	NM_013272	NP_037404	Q9UIG8	SO3A1_HUMAN	lasmic (Potential).	1	CAACATCAAGATC	0.662	
-	12	3745		NM_032444	NP_115820	Q8IY92	SLX4_HUMAN	PLK1 and TERF2-TERF2I	0	CCTGGGGAGGCC	0.662	
+	13	1422	RN1_uc002cxb.2_	NM_001142290	NP_001135762	O60291	MGRN1_HUMAN		2	GCTGTCCCCTCGC	0.662	
-	14	2043		NM_153603	NP_705831	P83436	COG7_HUMAN		0	GACTAAAGGCGGC	0.517	
+	2	1755		NM_006040	NP_006031	Q9Y661	HS3S4_HUMAN	ienal (Potential).	2	GAGGGTGATAAAT	0.468	
+	2	232	D2_uc010cbk.1_Mi	NM_022162	NP_071445	Q9HC29	NOD2_HUMAN	CARD 1.	4	CTGGTCGAGCTG	0.602	
-	2	391	p.W81*|CES7_uc	NM_001143685	NP_001137157	Q6NT32	EST5A_HUMAN		0	TTATCCCAGGGCC	0.592	
-	4	729	nse_Mutation_p.P	NM_017853	NP_060323	Q9NX01	TXN4B_HUMAN		1	ATTTGGGAATATT	0.383	
-	5	802	8B_uc010vmu.1_	NM_001011880	NP_001011880	Q6UXF7	CL18B_HUMAN		0	CAGGCACCCTTC	0.607	
+	2	120	|TRAPPC2L_uc00	NM_016209	NP_057293	Q9UL33	TPC2L_HUMAN		0	CCTACGGAGAACC	0.552	
-	9	1486	2fnc.1_Missense_	NM_013275	NP_037407	Q6UB99	ANR11_HUMAN		6	TGACGGGGGCC	0.547	
-	1	697		NM_002551	NP_002542	P47893	OR3A2_HUMAN	Name=5; (Potential).	1	GAACCAAAGGTGT	0.562	
-	10	1218	TP53_uc002gii.1_	NM_001126112	NP_001119584	P04637	P53_HUMAN	teraction wit3)|p.R342Q(2)|	22245	GCTCTCGGAACAT	0.498	
-	45	7282	om.2_Missense_M	NM_006311	NP_006302	O75376	NCOR1_HUMAN	with C1D (By similarity).	5	GCCGTTCCGTTC	0.502	

-	4	2350	p.R674C|SLFN13_	NM_144682	NP_653283	Q68D06	SLN13_HUMAN		2	AGTACGGAAAT	0.433	
-	6	1756		NM_139285	NP_644814	Q8NHY3	GA2L2_HUMAN		2	AGGTCCCAGG	0.612	
-	3	372_373	nse_Mutation_p.G	NM_152349	NP_689562	Q8N1A0	KT222_HUMAN	Potential.	2	CTAGTCCTTCAA	0.46	
-	16	2488	.2_Intron|TTLL6_	NM_001130918	NP_001124390	Q8N841	TTLL6_HUMAN		0	CAGAGCTGTCA	0.547	
+	1	120	.1_Intron|B4GALN	NM_153446	NP_703147	Q8NHY0	B4GN2_HUMAN	lasmic (Potential).	2	GCCGGGAATGT	0.667	
+	9	1125		NM_153228	NP_694960	Q8N957	ANKF1_HUMAN	onectin type-III.	2	CACCGGCATGT	0.502	
+	12	2517	pm.1_Missense_	NM_030779	NP_110406	Q9H252	KCNH6_HUMAN	lasmic (Potential).	1	CTCAGGAAGAC	0.622	
-	24	5443		NM_000334	NP_000325	P35499	SCN4A_HUMAN		3	TTGGCGAGCTG	0.667	
+	5	1028	jip.2_Missense_M	NM_018658	NP_061128	Q9NPI9	IRK16_HUMAN	smic (By similarity).	3	CCCAAACCATTC	0.463	
-	2	609		NM_006678	NP_006669	Q08708	CLM6_HUMAN	(Potential).|Ig-like V-type.	0	TGATGGACACT	0.547	
+	12	1755	jth.2_Missense_M	NM_198955	NP_945193	Q3V5L5	MGT5B_HUMAN	enal (Potential).	3	CGCCCCCCTGG	0.657	
-	5	1264		NM_002522	NP_002513	Q15818	NPTX1_HUMAN	Pentaxin.	0	CCTGGGTGGCA	0.622	
-	10	1602	m.2_Missense_M	NM_024421	NP_077739	Q08554	DSC1_HUMAN	(Potential).|Cadherin 3.	4	GTGAGCTCGCT	0.408	
+	15	2641	p.1_Missense_M	NM_001942	NP_001933	Q02413	DSG1_HUMAN	lasmic (Potential).	7	TAATTTCTGAGA	0.517	
+	8	1055	.R268Q|RNF165_	NM_152470	NP_689683	Q6ZSG1	RN165_HUMAN	G-type; atypical.	0	CTGCCGAGTGG	0.577	
+	2	168	02ljj.3_5'UTR|SE	NM_080475	NP_536723	Q96P15	SPB11_HUMAN		1	AGTCTGCTTTAT	0.443	
-	3	208		NM_017550	NP_060020	Q8N344	MIER2_HUMAN		0	GTCTGGGCACC	0.597	
+	4	708	.2_Intron|MADCA	NM_130760	NP_570116	Q13477	MADCA_HUMAN	T- T-S-[QP]-E.|Extracellular	0	GCCTCCCGACA	0.592	
-	29	3841	_uc002mfl.2_5'U	NM_000064	NP_000055	P01024	CO3_HUMAN		5	TAGTATCTCTGT	0.577	
+	11	1150	a.1_Missense_Mu	NM_005428	NP_005419	P15498	VAV_HUMAN	DH.	16	GCGATGGAGAA	0.627	
-	48	6181	l3_uc002mje.2_5'	NM_032447	NP_115823	Q75N90	FBN3_HUMAN	TB 8.	11	CAGTTCGCAGG	0.612	rs149936210
-	3	19097		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).	57	TTTATAGAAGGA	0.448	
-	1	6782		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	h.|Extracellular (Potential)	57	TAAAGGAAACC	0.468	
-	1	2516		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).	57	TGGAGGAAAGA	0.502	
-	10	1717	wr.1_Missense_M	NM_152476	NP_689689	Q96MR9	ZN560_HUMAN	2H2-type 6.	6	AAAAAGAGATG	0.413	
+	6	1372	vq.1_Missense_M	NM_018443	NP_060913	Q9NR11	ZN302_HUMAN	2H2-type 5.	0	TAGTTCGTCTC	0.413	
-	5	449	e_Mutation_p.P11	NM_000234	NP_000225	P18858	DNLI1_HUMAN		3	CCATGGGAGAG	0.557	
+	32	4599	.1_Missense_Mut	NM_024729	NP_079005	Q7Z406	MYH14_HUMAN	Potential.	1	GTGAGGAGCTG	0.706	
-	4	340	n_p.T41I|KLK5_uc	NM_001077491	NP_001070959	Q9Y337	KLK5_HUMAN		0	GCACGGTGTTA	0.627	
+	7	2419	p.R600K|ZNF761_	NM_001008401	NP_001008401	Q86XN6	ZN761_HUMAN	2H2-type 16.	1	ATAGGAGAATTC	0.398	
+	6	1933	470_uc010etn.2_I	NM_001001668	NP_001001668	Q6ECI4	ZN470_HUMAN	2H2-type 7.	2	ACTCATACTGG	0.413	
-	1	554	qnt.2_Missense_	NM_001146186	NP_001139658	Q9GZU2	PEG3_HUMAN	SCAN box.	12	GGTTTCGGAGT	0.502	
+	3	2079	47_uc002qpm.3_	NM_001023561	NP_001018855	O43361	ZN749_HUMAN		0	CTGGAGAAAAG	0.388	
+	4	2168	ud.1_Intron|ZNF5	NM_153263	NP_694995	Q6P9A3	ZN549_HUMAN		1	AGAGCCCTAGC	0.428	
+	1	439		NM_001105569	NP_001099039	A6NI15	MSGN1_HUMAN	-loop-helix motif.	1	ACACCCTCCGG	0.572	
-	4	854	.2_3'UTR|TMEM17	NM_198276	NP_938017	Q86X19	TMM17_HUMAN		0	GAAACGAACTG	0.428	
-	12	2083	p.R615W|LOXL3_	NM_032603	NP_115992	P58215	LOXL3_HUMAN	yl-oxidase like.	0	ATGCCGGTAGA	0.517	
-	4	1138		NM_000575	NP_000566	P01583	IL1A_HUMAN		1	TTTAGAGGTTT	0.453	
+	2	108	|THSD7B_uc002t	NM_001080427	NP_001073896				7	AGTGTGGTGTTT	0.507	
-	17	3485	p.P1036L|SCN1A_	NM_006920	NP_008851	P35498	SCN1A_HUMAN		13	CTACGGGCTGT	0.418	
-	29	5058		NM_004525	NP_004516	P98164	LRP2_HUMAN	B 13.|Extracellular (Poten	29	GAGTCCATGAA	0.478	
-	4	1537	.2_Missense_Mut	NM_003111	NP_003102	Q02447	SP3_HUMAN	ation domain (Gln-rich).	6	GTCCAGAAGGG	0.433	
+	14	1735	fe.1_Nonsense_M	NM_032523	NP_115912	Q9BZF3	OSBL6_HUMAN		1	GTGATCAGGTT	0.328	
-	226	45691	_uc010zfi.1_Miss	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	TGGTTCCAACG	0.443	
-	46	15390	N_uc010zfi.1_Intr	NM_133379	NP_596870	Q8WZ42	TITIN_HUMAN		153	CTCCCCTGGGG	0.498	
-	17	2224		NM_018897	NP_061720	Q8WXX0	DYH7_HUMAN	similarity).|Potential.	12	CCAAATGAATAA	0.328	
-	15	1632	hj.1_Missense_M	NM_006190	NP_006181	Q13416	ORC2_HUMAN		0	ATAGGAGGTTT	0.433	

+	17	2525	e_Mutation_p.R77	NM_152526	NP_689739	Q8TEW8	PAR3L_HUMAN			4	GGTTCGAGGCC	0.517	
-	10	1922_1923	we.1_Missense_M	NM_005689	NP_005680	Q9NP58	ABCB6_HUMAN	.|ABC transmembrane typ		2	AGTAGGTGCCA	0.51	
+	1	760	mv.1_Missense_	NM_019076	NP_061949	Q9HAW9	UD18_HUMAN			2	CCTCTGAAATT	0.418	
-	1	143	zpn.1_Missense_	NM_015985	NP_057069	Q9Y264	ANGP4_HUMAN			2	CACAAGGAGGA	0.592	
-	1	238	PROKR2_uc010z	NM_144773	NP_658986	Q8NFJ6	PKR2_HUMAN	lasmic (Potential).		5	ATAGCGGGTGA	0.552	
+	5	794	P1_uc010zri.1_In	NM_080826	NP_543016	B1AKI9	ISM1_HUMAN			0	TGTTTAGGAATT	0.398	
-	9	885	L1L2_uc010zrl.1_	NM_025229	NP_079505	Q5TEA6	SE1L2_HUMAN	ellular (Potential).		2	GTCTTTCCGTT	0.368	
+	2	162		NM_153324	NP_697019	Q8N688	DB123_HUMAN			0	CCAAAGATGCT	0.423	
+	14	1760	e_Mutation_p.R42	NM_012156	NP_036288	Q9H4G0	E41L1_HUMAN	trin--actin-binding.		3	GGATCGAGACT	0.607	
+	1	371	.2_Intron|SGK2_u	NM_016276	NP_057360	Q9HBY8	SGK2_HUMAN			6	TGTCCCCCCAG	0.617	
+	5	733	p.R20W|NCAM2_	NM_004540	NP_004531	O15394	NCAM2_HUMAN	2.|Extracellular (Potential).		4	CAGATCGGTTC	0.403	
-	3	575	_p.P33L|RCAN1_u	NM_004414	NP_004405	P53805	RCAN1_HUMAN			0	CTGGCGGAGAG	0.542	
-	2	671	p.G177S|CLDN14	NM_012130	NP_036262	O95500	CLD14_HUMAN	ical; (Potential).		0	GCCACCAATGA	0.637	
-	12	1399	p.D273N|TMPRS	NM_024022	NP_076927	P57727	TMPS3_HUMAN	.|Extracellular (Potential).		3	GCTGTCCCCCT	0.597	
+	13	2837	L_uc011akd.1_Mi	NM_021115	NP_066938	Q9BYH1	SE6L1_HUMAN	xtracellular (Potential).		6	GCCAGGAGAGT	0.567	
+	7	3572	tq.1_Missense_M	NM_001039141	NP_001034230	Q9H2D6	TARA_HUMAN			1	AGTCCCCCCAA	0.667	
+	2	1635	xy.2_Missense_M	NM_002409	NP_002400	Q09327	MGAT3_HUMAN	enal (Potential).		0	GGTTCGACGGC	0.637	
+	11	1815	e_Mutation_p.P55	NM_018995	NP_061868	Q9BXT6	M10L1_HUMAN			3	GGAGGCCTTCT	0.473	
-	2	934	hfn.2_Missense_	NM_005442	NP_005433	O95936	EOMES_HUMAN	T-box.		4	GTAGTGGGCAG	0.502	
-	7	970	_p.F259S|SCN5A_	NM_198056	NP_932173	Q14524	SCN5A_HUMAN	=S5 of repeat I; (Potential).		9	GGCAGAAGACT	0.592	
-	2	389		NM_006514	NP_006505	Q9Y5Y9	SCNAA_HUMAN	S1 of repeat I; (Potential).|		10	GATATGAGTGG	0.483	
-	14	2453	1A_uc010hhn.1_5	NM_014139	NP_054858	Q9UI33	SCNBA_HUMAN	II.		9	ATCCCCCATGT	0.498	
-	2	885_886	tron|NAT6_uc003	NM_012191	NP_036323	Q93015	NAT6_HUMAN			1	AAGGGGGCCCT	0.579	
+	31	5284		NM_015512	NP_056327	Q9P2D7	DYH1_HUMAN	.1 (By similarity).		3	TGGTGCCATCC	0.612	
+	5	784		NM_022072	NP_071355	Q9H649	NSUN3_HUMAN			1	TGTTTTCTTCTG	0.398	
+	1	644		NM_001005515	NP_001005515	A6NDH6	O5H15_HUMAN	Name=5; (Potential).		2	CTATTCTTATAT	0.348	
+	1	848		NM_001004736	NP_001004736	Q8NHB7	OR5K1_HUMAN	Name=7; (Potential).		1	TAGTTCCCTTAC	0.308	
-	2	1379	.2_Intron|CD96_u	NM_024508	NP_078784	Q9BTP6	ZBED2_HUMAN			1	CTGCCCTTTCC	0.602	
-	5	557	2018_uc003eal.2_	NM_001009899	NP_001009899	Q68DE3	K2018_HUMAN	-loop-helix motif.		3	GGGCAGGAGAA	0.368	
+	4	505		NM_017554	NP_060024	Q460N5	PAR14_HUMAN			6	TTCCTCTTTGGT	0.378	
+	5	2003		NM_001102608	NP_001096078	A6NMZ7	CO6A6_HUMAN	cal region.|VWFA 4.		8	CAGATCGGGTG	0.418	
+	4	873	_Mutation_p.R200	NM_023943	NP_076432	Q6UXF1	TM108_HUMAN	ellular (Pote	p.R200Q(1)	4	AGGACGAAATC	0.592	rs140878635
-	1	469		NM_001134659	NP_001128131	A6NEV1	PR23A_HUMAN			0	CTCCTCGTAGG	0.632	
-	8	847	5_uc010hus.1_R	NM_001039547	NP_001034636	Q6ZS86	GLPK5_HUMAN			0	GGTATCGAAATT	0.348	
-	2	401	_uc003ewz.2_Mis	NM_000096	NP_000087	P00450	CERU_HUMAN	1.|Plastocyanin-like 1.		1	ATGTTCCCTGC	0.328	
-	11	1028	_p.M235I|ZBBX_u	NM_024687	NP_078963	A8MT70	ZBBX_HUMAN			2	TCTTTTCATCGT	0.328	
-	7	2080	fk.2_Missense_Mu	NM_005241	NP_005232	Q03112	EVI1_HUMAN			14	TTTTTTCGAGGC	0.512	
+	13	1768	se_Mutation_p.S4	NM_003722	NP_003713	Q9H3D4	P63_HUMAN	SAM.		12	TTCATCATGTC	0.448	
-	4	455	LG1_uc010ial.2_	NM_001098424	NP_001091894	Q12959	DLG1_HUMAN			3	AGAGCTTGGAA	0.408	
-	2	178		NM_001001290	NP_001001290	Q9NRM0	GTR9_HUMAN			3	TCGGTCCTTTT	0.388	
-	3	3405		NM_053042	NP_444270	Q9C0D4	Z518B_HUMAN			4	AAACAACTTTGA	0.443	
+	13	1672	_p.S292F|FAM114	NM_138389	NP_612398	Q8IWE2	NXP20_HUMAN			1	TGGCCTCTTTAT	0.323	
-	6	785		NM_182592	NP_872398	Q8N8F6	YIPF7_HUMAN			0	CCTTCCATGTG	0.453	
+	9	1541_1542	se_Mutation_p.E	NM_145263	NP_660306	Q8TC71	MIEAP_HUMAN			4	ATCCAGGAGATA	0.426	
-	11	1834		NM_001042784	NP_001036249	Q5M9N0	CD158_HUMAN	Potential.		6	CTTGTCCTTCT	0.478	
-	10	1812	p.S358F|LEF1_uc	NM_016269	NP_057353	Q9UJU2	LEF1_HUMAN			1	ATGCAGATTCC	0.433	
+	38	9920	K2_uc003ibh.3_I	NM_001148	NP_001139	Q01484	ANK2_HUMAN			14	ATTCTCCCGAT	0.443	

+	3	617	e_Mutation_p.P14	NM_001128933	NP_001122405	Q9UMS6	SYNP2_HUMAN		2	GAAGTTCCCCTA	0.547
+	6	940	R17_uc003ium.3_	NM_170710	NP_733828	Q8IZU2	WDR17_HUMAN		6	ACAACATTTAATC	0.433
-	2	138_139	AM173B_uc010itr.	NM_199133	NP_954584	Q6P4H8	F173B_HUMAN		2	AGAACCCCCAGT	0.475
-	14	2020		NM_001369	NP_001360	Q8TE73	DYH5_HUMAN	n (By similarity).	31	TGCGAATTATAG	0.532
-	3	374	.1_Intron|TTC33_	NM_012382	NP_036514	Q6PID6	TTC33_HUMAN	TPR 1.	1	CTCCCGATATCT	0.284
-	6	1463		NM_021072	NP_066550	O60741	HCN1_HUMAN	toplasmic (Potential).	1	TAGGATCCGCATT	0.383
+	5	1551	486K|MARVELD2_	NM_001038603	NP_001033692	Q8N4S9	MALD2_HUMAN	lasmic (Potential).	0	ATTCGGAAAGC	0.408
+	30	6646	p.T2128I|BDP1_u	NM_018429	NP_060899	A6H8Y1	BDP1_HUMAN		2	TGTAACCAAAG	0.338
+	2	578		NM_153610	NP_705838	Q8N3K9	CMYA5_HUMAN		9	GCAGTCCTTTAA	0.383
+	70	14320	.E2448K|GPR98_	NM_032119	NP_115495	Q8WXG9	GPR98_HUMAN	ellular (Potential).	16	GGAGCCGAACTG	0.438
-	8	1706	w.1_Missense_Mu	NM_004883	NP_004874	O14511	NRG2_HUMAN	lasmic (Potential).	6	TCCCAGAGAAG	0.542
+	1	323	HB2_uc003lim.1_	NM_018936	NP_061759	Q9Y5E7	PCDB2_HUMAN	(Potential).|Cadherin 1.	6	ACTTGCTGTGA	0.502
+	1	2443	_5'Flank|PCDHB1	NM_019120	NP_061993	Q9UN66	PCDB8_HUMAN	lasmic (Potential).	4	AGTACGAGGTGT	0.577
+	1	1418	DHGA5_uc003lju.1	NM_018925	NP_061748	Q9Y5G0	PCDGH_HUMAN	(Potential).|Cadherin 5.	0	CGCCTCGGACC	0.587
-	2	439	FIP2_uc003lwr.2_	NM_001001343	NP_001001343	Q8TBE3	FNDC9_HUMAN	onectin type-III.	0	TGTAAGGGAAG	0.567
+	3	380	ED9_uc010jko.2_	NM_017510	NP_059980	Q9BVK6	TMED9_HUMAN	Lumenal (Potential).	0	CAATTCCACCA	0.562
-	7	2280	.R705W|NEDD9_	NM_006403	NP_006394	Q14511	CASL_HUMAN		0	CTGCCGATCCT	0.517
-	3	577	1dip.1_Splice_Site	NM_032744	NP_116133	Q96IZ2	CF105_HUMAN		0	TACAAACTGGAA	0.363
+	4	2526	EP1_uc011diq.1_	NM_002114	NP_002105	P15822	ZEP1_HUMAN		6	GATTCCCCCAAA	0.433
+	4	1052	p.K313Q|ZNF193_	NM_006299	NP_006290	O15535	ZN193_HUMAN	C2H2-type 3.	0	ACTGCAAGGAG	0.458
-	1	7		NM_030959	NP_112221	Q9UGF7	O12D3_HUMAN	ellular (Potential).	3	ATTCTCCATTGCT	0.343
+	3	1230	_p.P263S|OR2H1_	NM_030883	NP_112145	Q9GZK4	OR2H1_HUMAN	ellular (Potential).	0	AAAAATCCGTAT	0.517
-	2	284	R1_uc003nmp.3_	NM_006398	NP_006389	O15205	UBD_HUMAN	Ubiquitin 1.	0	AAAGGTCATTAA	0.488
+	15	2234		NM_001371	NP_001362				21	AAGTCCGGACG	0.368
+	14	3331		NM_032538	NP_115927	Q5TCY1	TTBK1_HUMAN		9	ATGGCCCGGCC	0.667
-	13	2123	yp.3_Missense_M	NM_001098518	NP_001091988	Q8IZF2	GP116_HUMAN	ellular (Potential).	2	TCTTACCAGCAG	0.393
-	3	1538	f.1_Missense_Mu	NM_021073	NP_066551	P22003	BMP5_HUMAN		2	ATCCCCTGTTT	0.348
-	64	0851_10852		NM_014611	NP_055426	Q9NU22	MDN1_HUMAN		10	GCAGGGGGAAC	0.495
-	9	3120	nw.2_Missense_M	NM_021813	NP_068585	Q9BYV9	BACH2_HUMAN		6	TGGCTCCAAGC	0.642
-	5	1325	p.D362N|EPHA7_	NM_004440	NP_004431	Q15375	EPHA7_HUMAN	tential).|Fibronectin type-III	28	TCACATCGTTTC	0.498
+	17	2033		NM_173560	NP_775831	Q8HWS3	RFX6_HUMAN		3	TCATTAACCAAG	0.527
+	12	2039		NM_020340	NP_065073	Q5TH69	BIG3_HUMAN	SEC7.	2	GTCCCTGGAAG	0.572
+	2	1234		NM_016217	NP_057301	Q9UBI9	HDC_HUMAN		0	CATGTGTTCAGA	0.607
-	9	6741		NM_006734	NP_006725	P31629	ZEP2_HUMAN		6	ATAGCCTCTGGT	0.438
+	16	4238	qf.2_Missense_Mu	NM_012454	NP_036586	Q8IVF5	TIAM2_HUMAN		4	GACAGTGACCTG	0.532
+	5	919	22A3_uc011efx.1_	NM_021977	NP_068812	O75751	S22A3_HUMAN		4	ATTACTCGGAAG	0.428
+	13	1733	e.1_Missense_Mu	NM_031414	NP_113602	Q9BXU1	STK31_HUMAN		9	ATCCTAGAGAAG	0.378
+	4	434	_p.E71K|ADCYAP	NM_001118	NP_001109	P41586	PACR_HUMAN	ellular (Potential).	1	TGGGTGAGATG	0.562
+	14	1562		NM_016616	NP_057700	Q8N427	TXND3_HUMAN	NDK 2.	3	AATACTGGAAAC	0.403
-	5	1673		NM_033273	NP_150376	Q96JC4	ZN479_HUMAN	C2H2-type 11.	4	ATTCTTCACATG	0.428
-	9	1623	dy.1_Missense_Mu	NM_012301	NP_036433	Q86UL8	MAGI2_HUMAN	PDZ 2.	11	CATCCGGAATCA	0.428
-	5	366	uix.1_Missense_M	NM_018849	NP_061337	P21439	MDR3_HUMAN	rity).|ABC transmembrane	6	GGAAAAGTTCAC	0.244
+	4	1908		NM_181646	NP_857597	A4D1E1	Z804B_HUMAN		11	TCAATGGCCTA	0.418
+	4	2384		NM_181646	NP_857597	A4D1E1	Z804B_HUMAN		11	AGAAAGGCAGTT	0.388
+	68	10894	p.T3533I|TRRAP_	NM_003496	NP_003487	Q9Y4A5	TRRAP_HUMAN	PI3K/PI4K.	37	GGAGACCACCA	0.582
-	50	8277	.2_Missense_Mut	NM_005045	NP_005036	P78509	RELN_HUMAN		19	TTACCTGAAGTTT	0.483
-	3	619	T2_uc003vja.2_In	NM_003391	NP_003382	P09544	WNT2_HUMAN	p.E107E(1)	7	CAGATTCCCGAC	0.398

-	15	1860		NM_004333	NP_004324	P15056	BRAF_HUMAN	rotein kinas_R603>I(2)|p.T	18290	GATTTCACTGTAC	0.368	
+	7	2428	ɔ.1_Intron|uc011kt	NM_001130025	NP_001123497	A6NFQ2	F115C_HUMAN		0	ACCTTTGGTCAG	0.617	
+	1	533		NM_001004685	NP_001004685	O95006	OR2F2_HUMAN	ellular (Potential).	4	ACATATCCTGTGA	0.498	
+	5	1198		NM_014141	NP_054860	Q9UHC6	CNTP2_HUMAN	1.|Extracellular (Potential).	11	TGCACGGAGAA	0.388	
+	4	1084		NM_175571	NP_783161	Q8ND71	GIMA8_HUMAN		7	GTCCTCCTTGTG	0.562	
+	11	1683	_p.E463K|NOS3_u	NM_000603	NP_000594	P29474	NOS3_HUMAN	ction with NOSIP.	8	CATCAGGAGATG	0.627	
-	5	416	vs.1_Missense_M	NM_007349	NP_031375	Q6ZW49	PAXI1_HUMAN	tion with PA1 (By similarity	5	CTCCCCCATAGA	0.443	
-	2	232	ı_p.S22L|SPAG11	NM_016512	NP_057596	Q08648	SG11B_HUMAN		0	TGAGACGATCCT	0.582	
-	3	660		NM_003155	NP_003146	P52823	STC1_HUMAN		4	ACTCTTCCTGCA	0.537	
+	4	557	ı_p.E34K|ADAMD	NM_014479	NP_055294	O15204	ADEC1_HUMAN		2	GGAGAGGAAATT	0.453	
+	16	1766	DAM18_uc010lwx.	NM_014237	NP_055052	Q9Y3Q7	ADA18_HUMAN	xtracellular (Potential).	6	TGAGATCAGATG	0.368	
-	1	272		NM_152418	NP_689631	Q8NA75	DC4L2_HUMAN		1	TCTGGACCTTTT	0.502	
-	5	407		NM_005836	NP_005827	P52758	UK114_HUMAN		1	TAGCAGGAAAAT	0.274	
+	10	1639		NM_024915	NP_079191	Q6ISB3	GRHL2_HUMAN		3	AGAAAGGGAAA	0.468	
-	13	3201	M135B_uc003yva	NM_015912	NP_056996	Q49AJ0	F135B_HUMAN		9	GGACCCCATGAT	0.512	
-	2	759		NM_001163	NP_001154	Q02410	APBA1_HUMAN		1	CGCATTCATGGC	0.677	
+	3	923_924	e_Mutation_p.P12	NM_006200	NP_006191	Q92824	PCSK5_HUMAN	Catalytic.	3	ATGATCCCAAGT	0.475	
+	1	894		NM_001005235	NP_001005235	Q8NGR5	OR1L4_HUMAN	lasmic (Potential).	0	AGATATGAAAAG	0.398	
-	1	876		NM_203434	NP_982258	Q5T953	IER5L_HUMAN	Ala-rich.	0	gcgggcggagaagcg	0.353	
+	3	832		NM_006059	NP_006050	Q9Y6N6	LAMC3_HUMAN	ninin N-terminal.	3	GTTTGGGGACG	0.592	
+	10	1238	nd.1_Missense_M	NM_002183	NP_002174	P26951	IL3RA_HUMAN	ellular (Potential).	3	AGGAGGAGGGC	0.667	
-	5	3341		NM_015419	NP_056234	Q9NR99	MXRA5_HUMAN		8	ACATCTCTTTCAT	0.458	
-	6	526	M9B_uc004csh.2_	NM_205849	NP_995321	Q8IZU0	FAM9B_HUMAN		0	CTAACACTTCTAT	0.318	
+	4	983	_p.W221*|MAGEB	NM_002363	NP_002354	P43366	MAGB1_HUMAN	MAGE.	0	GATCTGGAAATT	0.483	
-	5	370	z.1_Missense_Mu	NM_175723	NP_783729	O60225	SSX5_HUMAN		0	AAGATTCCCTGG	0.423	
+	5	652	_5'UTR|TBC1D25_	NM_002536	NP_002527	Q3MII6	TBC25_HUMAN		1	AGGTCCAACAA	0.582	
-	23	3169		NM_001013742	NP_001013764	Q5KSL6	DGKK_HUMAN		2	TTACCCGATCTC	0.438	
+	2	1132		NM_005448	NP_005439	O95972	BMP15_HUMAN		2	ATTTTGTACAAG	0.463	
-	1	1		NM_001009616	NP_001009616	Q5MJ07	SPXN5_HUMAN		0	TTCCATGATTCTG	0.448	
+	6	2479	_p.D461N|NHSL2_	NM_001013627	NP_001013649	Q5HYW2	NHSL2_HUMAN		0	AGTCCGACCTA	0.512	
-	22	2196	p.M707V|RPS6KA	NM_014496	NP_055311	Q9UK32	KS6A6_HUMAN		8	CAACCATTGCTC	0.403	rs145715341
+	13	2218	ntr.1_Missense_M	NM_019045	NP_061918	Q5JSH3	WDR44_HUMAN		5	GCAACGGCCAT	0.343	
+	2	105	e_Mutation_p.Y26	NM_006649	NP_006640	Q9BVJ6	UT14A_HUMAN		2	AAAAgactacctcttg	0.259	
+	6	744		NM_016024	NP_057108	Q9Y388	RBMX2_HUMAN	Lys-rich.	4	CAAATCCAGGA	0.557	
-	8	1820_1821	_p.P567*|GPC3_u	NM_004484	NP_004475	P51654	GPC3_HUMAN		5	CCTTCGGAGTTG	0.495	
+	2	768		NM_001727	NP_001718	P32247	BRS3_HUMAN	ellular (Potential).	1	TCTTATCCTGTCT	0.348	
-	5	1312	ɔ.R227Q|FGF13_u	NM_004114	NP_004105	Q92913	FGF13_HUMAN		3	CAGATCGGGAG	0.517	
-	3	582		NM_005362	NP_005353	P43357	MAGA3_HUMAN	MAGE.	0	TGGCTCGATACT	0.532	
+	2	993	RY3_uc010nvl.1_In	NM_005840	NP_005831	O43610	SPY3_HUMAN	PR.|Cys-rich.	0	CTGAGAGCCTCC	0.582	
+	2	1001	RY3_uc010nvl.1_In	NM_005840	NP_005831	O43610	SPY3_HUMAN	PR.|Cys-rich.	0	CTCCTCGATTATG	0.592	
+	2	241		NM_000815	NP_000806	O14764	GBRD_HUMAN	ellular (Probable).	3	TGATAGCCGGCT	0.677	
-	21	2902	RSF25_uc001ani.	NM_001042663	NP_001036128	O94827	PKHG5_HUMAN		1	GCCTCGGACTTA	0.697	
-	2	262		NM_001009611	NP_001009611	O60810	PRAM4_HUMAN		1	GGCGGCGGAAG	0.602	
+	3	526	on_p.A3P|TMEM51	NM_001136216	NP_001129688	Q9NW97	TMM51_HUMAN		0	ATGATGGCCCAG	0.557	
-	7	1702		NM_004431	NP_004422	P29317	EPHA2_HUMAN	tential).|Fibronectin type-III	10	AATTCGTGCACC	0.617	
-	2	227	ı_p.P13S|ATP13A	NM_022089	NP_071372	Q9NQ11	AT132_HUMAN	ical; (Potential).	4	GGTGGGCGTGC	0.527	
+	1	2328	C7A_uc009vpg.2_	NM_152375	NP_689588	Q5VTJ3	KLD7A_HUMAN		3	GGGCACCCTCC	0.647	

-	85	12608	2_5'Flank|UBR4_u	NM_020765	NP_065816	Q5T4S7	UBR4_HUMAN		25	CCGAGCTGCCA	0.537	
+	12	1741	b.2_Missense_Mu	NM_032264	NP_115640	Q9H094	NBPF3_HUMAN	NBPF 4.	2	GAAAAAGGACC	0.468	
+	16	2953		NM_020526	NP_065387	P29322	EPHA8_HUMAN	mic (Potential).|SAM.	13	CATCCGCATGG	0.692	
+	5	589	se_Mutation_p.V1	NM_198137	NP_937770	Q7RTX7	CTSR4_HUMAN	=Segment S4; (Potential).	1	TGGCGGTGGAG	0.627	
+	3	435	_p.Q90*|SYTL1_	NM_032872	NP_116261	Q8IYJ3	SYTL1_HUMAN		1	GCTCCCAGCGG	0.642	
+	7	969	_p.D146Y|EIF3I_u	NM_003757	NP_003748	Q13347	EIF3I_HUMAN	WD 3.	1	TGCAATGACTCT	0.532	
+	15	2243		NM_017629	NP_060099	Q9HCK5	AGO4_HUMAN	Piwi.	1	GGCCAGAACTA	0.393	
+	2	214	ciy.2_Missense_M	NM_001255	NP_001246	Q12834	CDC20_HUMAN		0	AGGCCCGGCCC	0.672	
-	6	1017	K2_uc010olo.1_Mi	NM_007170	NP_009101	Q96S53	TESK2_HUMAN	rotein kinase.	5	CATCGGGGATC	0.542	
+	15	1648	.S512G|RAD54L_	NM_001142548	NP_001136020	Q92698	RAD54_HUMAN	case C-terminal.	3	GCCGTAGCAGT	0.547	
-	8	952	p.P263S|SPATA6_	NM_019073	NP_061946	Q9NWH7	SPAT6_HUMAN		1	TGGGGGATCAA	0.418	
+	8	1233	nr.1_Missense_Mu	NM_153703	NP_714914	Q7Z5L7	PODN_HUMAN	LRR 12.	2	GCGGTTGCACA	0.662	
-	2	1413		NM_152268	NP_689481	Q7L3T8	SYPM_HUMAN		2	TGCAGGGTCCT	0.512	
+	19	1835	K1_uc001czp.2_I	NM_015888	NP_056972	Q9UJC3	HOOK1_HUMAN	Potential.	2	CAGATATAAATC	0.353	
+	2	188	D1_uc001dbp.1_	NM_020925	NP_065976	Q5VU97	CAHD1_HUMAN	ellular (Potential).	2	AATCTCAAATG	0.378	
-	3	385		NM_022159	NP_071442	Q9HBW9	ELTD1_HUMAN	GF-like 2; calcium-binding	2	TGTGTTAGTGC	0.343	
+	6	978	_p.D75N|CLCA4_u	NM_012128	NP_036260	Q14CN2	CLCA4_HUMAN	VWFA.	2	TTCTTGATAAGT	0.423	
-	1	264	e_Mutation_p.A3V	NM_024408	NP_077719	Q04721	NOTC2_HUMAN		27	GCAGGGCGGG	0.647	rs150390977
-	2	714	P6_uc009wjj.1_Int	NM_016361	NP_057445	Q9NPH0	PPA6_HUMAN		4	GGGTGGGACCT	0.418	
-	3	3611	uc001ezv.2_Intron	NM_001014342	NP_001014364	Q5D862	FILA2_HUMAN	Ser-rich.	17	CTGTCCAAAAC	0.493	
+	3	814	.2_Intron|CD1E_u	NM_030893	NP_112155	P15812	CD1E_HUMAN	Ig-like.	3	CCCTCGATTTC	0.507	
+	1	586		NM_001004478	NP_001004478	Q8NGY1	O10Z1_HUMAN	ellular (Potential).	2	CGAGTGAGCTG	0.498	
+	1	931		NM_001005184	NP_001005184	Q8NGW6	OR6K6_HUMAN	Name=7; (Potential).	1	CTCCCTTTTTC	0.438	
+	3	275	_p.R85H|FCRL6_u	NM_001004310	NP_001004310	Q6DN72	FCRL6_HUMAN	1.|Extracellular (Potential).	3	GAGCCGTGGCC	0.488	rs147917646
-	10	1448	_p.A214T|ARHGA	NM_001025598	NP_001020769	Q7Z6I6	RHG30_HUMAN		3	CTCTGCTGCCT	0.632	
+	10	1447	wb.2_Missense_M	NM_015569	NP_056384	Q9UQ16	DYN3_HUMAN		1	GCCTTCCTTGA	0.398	
-	6	1040	A11_uc010pmq.1_	NM_178527	NP_848622	Q5TAH2	S9A11_HUMAN		2	GGATTCTGTTG	0.274	
-	7	1507_1508	_Mutation_p.G432	NM_004319	NP_004310	O14525	ASTN1_HUMAN		15	TGGCTCCCCTC	0.589	
+	7	2159	_Mutation_p.E610	NM_005807	NP_005798	Q92954	PRG4_HUMAN	-X-P-X-P-T-T-X.|42; appro	1	TAAGGAGACTG	0.592	
+	3	355	R3_uc010poy.1_M	NM_021023	NP_066303	Q02985	FHR3_HUMAN	Sushi 2.	0	TATTTTCCTTATT	0.299	
+	3	391		NM_030787	NP_110414	Q9BXR6	FHR5_HUMAN	Sushi 2.	2	TGTGTTCCTTTC	0.308	
-	6	981		NM_001994	NP_001985	P05160	F13B_HUMAN	Sushi 5.	3	TATTTCTGCTG	0.363	
-	1	347_348	e_Mutation_p.E31	NM_018136	NP_060606	Q8IZT6	ASPM_HUMAN		6	gcctcctcctcggccg	0.277	
+	3	757	YRK3_uc001hei.2_	NM_003582	NP_003573	O43781	DYRK3_HUMAN		3	GGGCCTATATT	0.428	
-	2	1179	ha.3_Missense_M	NM_025179	NP_079455	O75051	PLXA2_HUMAN	lar (Potential).|Sema.	3	CAGCCGCAGCA	0.572	
+	10	1269	_p.T323M|HHAT_	NM_001122834	NP_001116306	Q5VTY9	HHAT_HUMAN	ical; (Potential).	2	TTCCACGGCGA	0.557	
-	48	9761		NM_206933	NP_996816	O75445	USH2A_HUMAN	ential).|Fibronectin type-III	26	GAAGAGATCTG	0.358	
-	15	2157	RS_uc001hlz.1_M	NM_004446	NP_004437	P07814	SYEP_HUMAN	yl-tRNA synthetase.	2	TGTGATCAAGTG	0.393	
+	4	1739		NM_021958	NP_068777	Q14774	HLX_HUMAN	Ser-rich.	2	gagcagcggcggcgg	0.224	
-	30	4297	gh.1_Missense_	NM_018072	NP_060542	Q9H583	HEAT1_HUMAN		3	GCTCCGGGACG	0.443	
+	7	726	|GTPBP4_uc010q	NM_012341	NP_036473	Q9BZE4	NOG1_HUMAN		2	TGTTAGGTTGT	0.557	
-	3	245		NM_145314	NP_660357	Q8WVF2	UCMA_HUMAN		0	TCTTGAGGAAAT	0.577	
-	4	531		NM_001010924	NP_001010924	Q5VUB5	F1711_HUMAN	ellular (Potential).	4	CCGAAGGGGAG	0.517	
+	5	599	1izo.1_RNA|HSD17B7P2_uc001izp.1_Missense_Mutation_p.N173S						0	TCGCAATGCAA	0.453	rs2257765
-	8	919		NM_001031746	NP_001026916	Q8IW00	CJ072_HUMAN	lasmic (Potential).	0	GGTGGGGTTTG	0.488	
+	3	2053		NM_199459	NP_955629	Q711Q0	CJ071_HUMAN		0	TCAATCCCCAG	0.542	
-	9	1349	_p.K409R|CTNNA	NM_001127384	NP_001120856	Q9UI47	CTNA3_HUMAN		8	TTTCCTTTTCCC	0.438	

-	6	1624	hv.1_Missense_Mu	NM_014912	NP_055727	Q8NE35	CPEB3_HUMAN	RRM 1.	0	TTACCTTTAGGA	0.413	
-	23	2908	_p.L389F|IDE_uc0	NM_004969	NP_004960	P14735	IDE_HUMAN		3	ACTGCCAACAT	0.428	
+	19	5153	.E1491K|PLCE1_	NM_016341	NP_057425	Q9P212	PLCE1_HUMAN	I-PLC X-box.	3	TTGGAGAAAAG	0.303	
+	22	2606	.P710L|HELLS_u	NM_018063	NP_060533	Q9NRZ9	HELLS_HUMAN		2	CAGTCCTGAAT	0.323	
+	3	807	C19_uc009xus.1_	NM_000772	NP_000763	P33260	CP2CI_HUMAN		5	CCAATGGTGGG	0.323	
+	4	962	V212*|CYP2C19_u	NM_000772	NP_000763	P33260	CP2CI_HUMAN		5	CCATGGATCCA	0.294	
-	9	1393	P2C8_uc010qob.1	NM_000770	NP_000761	P10632	CP2C8_HUMAN		0	CAAATTCGTTTT	0.363	
+	1	386	y.2_Intron|DHDPS	NM_001009997	NP_001009997	Q5T681	CJ062_HUMAN		0	GCTCCACGGTTC	0.582	
-	14	2391	ense_Mutation_p.R	NM_014631	NP_055446	Q5TCZ1	SPD2A_HUMAN		0	GCGCCGTAAAG	0.647	
-	1	341	C2_uc009xxx.2_Ir	NR_026715					0	GATGCAGTCAA	0.592	
-	20	2209	se_Mutation_p.Q	NM_198060	NP_932326	Q86VF7	NRAP_HUMAN	Nebulin 16.	10	TTGTACTGCAGC	0.502	
+	10	2035	RC2_uc001lay.1_	NM_198514	NP_940916	Q8NBF2	NHLC2_HUMAN		1	GACTGCGTGTG	0.463	rs150975627
+	5	723		NM_198075	NP_932341	Q8IYG6	LRC56_HUMAN		1	GAGGACGCTGG	0.647	
-	1	488		NM_001005238	NP_001005238	Q8NGK0	O51G2_HUMAN	Name=4; (Potential).	2	GTAATGGAAAA	0.473	
-	2	619	2_uc001mak.1_Ir	NM_017481	NP_059509	Q9H347	UBQL3_HUMAN		3	GACCCGGGATG	0.552	
-	21	3000	Mutation_p.Y557	NM_001100167	NP_001093637	Q9Y6F6	MRVI1_HUMAN	ical; (Potential).	3	ATTGTAGAGCCC	0.532	
-	3	366		NM_000315	NP_000306	P01270	PTHY_HUMAN		1	CCTTTTTTCGG	0.458	
-	5	416	RFGAP2_uc010rh	NM_032389	NP_115765	Q8N6H7	ARFG2_HUMAN	interaction with coatomer.	1	TCTATCCAAAGC	0.502	
-	13	2124	q.1_Missense_Mu	NM_024783	NP_079059	Q5U5Z8	CBPC2_HUMAN		2	GACACTGAGTG	0.259	
+	1	922		NM_001004739	NP_001004739	Q8NGL0	OR5L2_HUMAN	lasmic (Potential).	1	GCTCCAAAATT	0.463	
+	1	151		NM_001005201	NP_001005201	Q8N146	OR8H3_HUMAN	lasmic (Potential).	2	TAATCCGCCTG	0.438	
+	1	298		NM_001004747	NP_001004747	Q8NGG3	OR5T3_HUMAN	Name=2; (Potential).	0	TCTTGGATGCT	0.383	
+	1	29		NM_001013358	NP_001013376	P0C7N8	OR9G9_HUMAN	ellular (Potential).	0	TGACTGAGTTTA	0.478	
+	2	1105	r.2_Missense_Mu	NM_015177	NP_055992	Q9Y2E6	DTX4_HUMAN		3	CAGCAAGACCG	0.632	
-	4	849	225C|CYBASC3_	NM_001161452	NP_001154924	Q8NBI2	CYAC3_HUMAN		0	TGGGCGCTTCC	0.607	
-	2	906	er.2_Missense_Mu	NM_033347	NP_203133	Q9Y2U2	KCNK7_HUMAN		0	ACGGGGTGCA	0.652	
+	10	1054	rm.1_Missense_M	NM_001619	NP_001610	P25098	ARBK1_HUMAN	rotein kinase.	1	CCACACGCCAG	0.662	
+	23	4900	.2_Missense_Mut	NM_002335	NP_002326	O75197	LRP5_HUMAN	nic (Potential).|PPPSP mot	7	CTCCGTCCCCC	0.582	
-	10	1516	ss.2_Missense_M	NM_001040118	NP_001035207	Q96P48	ARAP1_HUMAN	PH 2.	1	AGCGCGGTCAG	0.622	rs138364636
+	1	1652		NM_014786	NP_055601	Q96PE2	ARHGH_HUMAN		0	GAGAGCAAAGT	0.642	
+	6	820	_Mutation_p.E19	NM_018480	NP_060950	Q8IUX1	T126B_HUMAN		0	TATTTGAAGAG	0.333	
-	1	683	_p.L161F|GRM5_	NM_001143831	NP_001137303	P41594	GRM5_HUMAN	ellular (Potential).	9	TGGAGCAAATT	0.498	
+	1	1190		NM_001161630	NP_001155102	B2RXH2	KD4DL_HUMAN	JmjC.	0	CACGATGGATTG	0.512	
+	16	2258	e_Mutation_p.I64	NM_014361	NP_055176	O94779	CNTN5_HUMAN	like C2-type 6.	8	GAACATCCTTC	0.463	
-	3	2639	_uc009yww.1_R	NM_000926	NP_000917	P06401	PRGR_HUMAN	clear receptor.	4	AGGACCATGCC	0.368	
-	4	1441	_p.R351*|GUCY1A	NM_000855	NP_000846	P33402	GCYA2_HUMAN		8	ACATCGAAGCT	0.473	
-	11	1321	_Mutation_p.H31	NM_020809	NP_065860	Q9P2F6	RHG20_HUMAN		5	CAGGTGAGTGC	0.428	
+	4	653	EM25_uc001pti.2_	NM_032780	NP_116169	Q86YD3	TMM25_HUMAN	ellular (Potential).	0	CCCGCCGGCCA	0.617	
+	16	2001	w.1_Nonsense_M	NM_014619	NP_055434	Q16099	GRIK4_HUMAN	lasmic (Potential).	3	CCTACGAGTGG	0.438	
+	8	1632		NM_025004	NP_079280	Q0P6D6	CCD15_HUMAN		2	TCTCCACAAAG	0.418	rs113451248
-	1	198	ds.1_Missense_M	NM_016533	NP_057617	Q9NZG7	NINJ2_HUMAN		2	GCACCGGGTGC	0.597	
+	9	1375	se_Mutation_p.R2	NM_201442	NP_958850	P09871	C1S_HUMAN	CUB 2.	1	CTTGCGGAGAG	0.468	rs147341600
-	3	370	124G|PRH1_uc00	NM_007244	NP_009175	Q16378	PROL4_HUMAN		0	CAGGCTGACAG	0.532	
+	1	287		NM_001310	NP_001301	O60519	CRBL2_HUMAN		0	TGACAGTAAGG	0.677	
+	21	2442	MP_uc001rgi.2_R	NM_006152	NP_006143	Q12912	LRMP_HUMAN	enal (Potential).	2	ATGCCGCTCCC	0.502	
-	11	2773	_p.K514R|SFRS2I	NM_004719	NP_004710	Q99590	SCAFB_HUMAN		0	GAGACTTCCTG	0.473	
-	9	1530	|CCNT1_uc009zk	NM_001240	NP_001231	O60563	CCNT1_HUMAN	Potential.	6	CTTCTGGGCAG	0.438	

+	1	299		NM_000486	NP_000477	P41181	AQP2_HUMAN	nic (Potential).|NPA 1.	2	CCCTGCCGTGA	0.662
-	6	546	n_p.W150L|SLC1	NM_000617	NP_000608	P49281	NRAM2_HUMAN	lasmic (Potential).	1	TCAGCCACAGG	0.428
-	3	776		NM_004693	NP_004684	O95678	K2C75_HUMAN	oil 1B.|Rod.	0	AAATTCATTCTC	0.478
-	2	1328	r.3_Missense_Mut	NM_006163	NP_006154	Q16621	NFE2_HUMAN	Basic motif.	0	TGCCCCGTCGT	0.567
+	3	538	RDH5_uc010spu.	NM_002905	NP_002896	Q92781	RDH1_HUMAN		1	TCATCGGACCC	0.587
-	2	408	_Mutation_p.Q20	NM_001113201	NP_001106672	Q13765	NACA_HUMAN		1	CAGCCTGGGGC	0.483
-	1	446		NM_145913	NP_666018	Q8N695	SC5A8_HUMAN	ical; (Potential).	0	TGCCCGCGAAC	0.682
+	22	2783		NM_014503	NP_055318	O75691	UTP20_HUMAN		4	GGTGGCAGAGG	0.498
+	21	2435		NM_017564	NP_060034	Q8WWQ8	STAB2_HUMAN	r (Potential).|EGF-like 6.	14	CTCAGGAAATG	0.413
+	6	871	_p.V264I|TPCN1_	NM_017901	NP_060371	Q9ULQ1	TPC1_HUMAN	=S3 of repeat I; (Potential).	3	TGTTGGTACGG	0.652
+	7	851	h.2_Missense_Mu	NM_138432	NP_612441	Q96GA7	SDSL_HUMAN		0	AGCCGGCAAGC	0.622
+	5	1112		NM_001080533	NP_001074002	A6NIH7	U119B_HUMAN		1	AAATCCTTACGA	0.443
-	3	328	S33A_uc001uce.	NM_022916	NP_075067	Q96AX1	VP33A_HUMAN		1	CTGCCGGCAAA	0.373
-	5	1715	se_Mutation_p.P4	NM_183044	NP_898865	Q9Y252	RNF6_HUMAN		2	ATGATGGCTCA	0.448
-	1	1414	uzo.1_Missense_	NM_183422	NP_904358	Q15714	T22D1_HUMAN		0	TGCCAGTAACA	0.388
+	2	1640	14C_uc001vgc.2_	NM_021645	NP_067677	Q5TAP6	UT14C_HUMAN		5	TGGACGGACCG	0.547
-	1	2778		NM_052910	NP_443142	Q96PX8	SLIK1_HUMAN	ical; (Potential).	5	AGGCGGAGGTG	0.592
-	45	5042	.P306S|DOCK9_	NM_015296	NP_056111	Q9BZ29	DOCK9_HUMAN	DHR-2.	1	GTGGGGGAGAA	0.592
-	5	1033	p.Q215K|NOVA1_	NM_002515	NP_002506	P51513	NOVA1_HUMAN		5	TCTTCTGGATGA	0.458
+	25	3115	e_Mutation_p.K98	NM_014992	NP_055807	Q9Y4D1	DAAM1_HUMAN	FH2.	1	GAAAAAGGAGG	0.418
-	23	3911		NM_000428	NP_000419	Q14767	LTBP2_HUMAN	m-binding (Potential).|Cys-	2	CACCCTCACAC	0.647
-	1	127	vo.3_Missense_M	NM_005065	NP_005056	Q9UBV2	SE1L1_HUMAN		1	TATCCGGACCC	0.706
+	14	1474	p.P465S|SLC24A	NM_153646	NP_705932	Q8NFF2	NCKX4_HUMAN	ic (Potential).|Alpha-2.	3	AGTGTTCCAGAC	0.542
+	6	523	_p.I147R|KIAA14	NM_020818	NP_065869	Q9P2D8	UNC79_HUMAN		17	TGTGTATAGACC	0.418
-	3	845		NM_001080451	NP_001073920	Q86U17	SPA11_HUMAN		1	GGACGGTGCAA	0.532
-	4	407	K2_uc001ypx.2_	NM_138420	NP_612429	Q8IVF2	AHNK2_HUMAN		1	ATGTCCGTGAG	0.592
-	1	1786		NM_019066	NP_061939				0	TACTCTAGGTAC	0.488
-	9	1274	zba.2_Missense_	NM_000814	NP_000805	P28472	GBRB3_HUMAN	lasmic (Probable).	5	CATTCATTTCATT	0.453
+	2	410	_p.T14M|GREM1_	NM_013372	NP_037504	O60565	GREM1_HUMAN		0	TGTGACGGAGC	0.642
-	3	522	.2_Intron|BMF_uc	NM_033503	NP_277038	Q96LC9	BMF_HUMAN	BH3.	1	AAGCCGGTGGA	0.602
-	6	1279		NM_139265	NP_644670	Q9H223	EHD4_HUMAN		2	CGTGCTCGTCT	0.637
-	12	3139	AA1370_uc002acf	NM_019600	NP_062546	Q32MH5	K1370_HUMAN		0	AGGTACAGAAA	0.368
-	9	3382	X7_uc002adn.1_	NM_022841	NP_073752	Q2KHR2	RFX7_HUMAN		0	ATGCTGCACAG	0.458
-	20	3000	p.P953L|SLTM_uc	NM_024755	NP_079031	Q9NWH9	SLTM_HUMAN		1	AGGGTGGACCA	0.507
+	6	1741	fu.2_Missense_M	NM_017610	NP_060080	Q6ZNA4	RN111_HUMAN		2	CATGTGGAGGG	0.498
-	61	8256	.R2728C|VPS13	NM_020821	NP_065872	Q709C8	VP13C_HUMAN		2	TATGCGGAAAT	0.448
+	2	472	c002amk.2_5'Flan	NM_203373	NP_976307	Q6P050	FXL22_HUMAN		0	CGACTTGCGCT	0.746
+	4	1235		NM_015042	NP_055857	O15014	ZN609_HUMAN		3	TCGGGGCAGCC	0.547
+	3	846	ujp.1_Missense_M	NM_002755	NP_002746	Q02750	MP2K1_HUMAN	rotein kinase.	0	CTCTCCGTACA	0.512
-	9	713	_p.P230L|GRAMD	NM_001012642	NP_001012660	Q8IUY3	GRAM2_HUMAN		0	GATGATGGAGGG	0.537
+	5	1129	299K|CD276_uc	NM_001024736	NP_001019907	Q5ZPR3	CD276_HUMAN	2.|Extracellular (Potential).	1	TCACCGAAGGC	0.647
-	9	983	_p.T165I|UBL7_uc	NM_032907	NP_116296	Q96S82	UBL7_HUMAN		1	AGGCGGTGGCC	0.682
+	2	2715	_p.P799S|C15orf3	NM_015492	NP_056307	Q6ZRI6	CO039_HUMAN		0	CTGGGCCCTGG	0.642
+	3	247	_p.D16H|HMG20	NM_018200	NP_060670	Q9NP66	HM20A_HUMAN		3	TTGCAGATGAA	0.418
-	13	1918	_p.T617N|ACSBG	NM_015162	NP_055977	Q96GR2	ACBG1_HUMAN		1	CAGAGGTGTCT	0.527
+	2	1796	unk.1_Missense_	NM_015206	NP_056021	Q9UPX6	K1024_HUMAN		4	CAACAGCAAGG	0.517
+	20	3282	b.1_RNA|LRRK1_	NM_024652	NP_078928	Q38SD2	LRRK1_HUMAN		12	TGACAGGTGAG	0.582

+	38	4934	_uc002cio.1_Misse	NM_145294	NP_660337	Q96KV7	WDR90_HUMAN		1	CACCACGGAGG	0.652	
-	13	5309		NM_032444	NP_115820	Q8IY92	SLX4_HUMAN	raction with PLK1 and TEF	0	TCGGCGTTATG	0.502	
-	12	3745		NM_032444	NP_115820	Q8IY92	SLX4_HUMAN	PLK1 and TERF2-TERF2I	0	CTGGGGAGGC	0.662	
+	13	1422	N1_uc002cxb.2_	NM_001142290	NP_001135762	O60291	MGRN1_HUMAN		2	CTGTCCCCTCG	0.662	
-	27	3907	2_RNA|ABCC6_u	NM_001171	NP_001162	O95255	MRP6_HUMAN	similarity).|ABC transporter	3	CCTGCGTGGAT	0.597	
-	14	2043		NM_153603	NP_705831	P83436	COG7_HUMAN		0	ACTAAAGGCGG	0.517	
+	2	1755		NM_006040	NP_006031	Q9Y661	HS3S4_HUMAN	enal (Potential).	2	AGGGTGATAAA	0.468	
-	3	824		NM_001080417	NP_001073886	Q9UEG4	ZN629_HUMAN	2H2-type 3.	0	CTTGTAGGGCT	0.657	
-	3	713	efb.1_RNA|ABCC	NM_033226	NP_150229	Q96J65	MRP9_HUMAN	smembrane type-1 1.	3	CAACACGCGTG	0.572	
+	2	232	2_uc010cbk.1_Mi	NM_022162	NP_071445	Q9HC29	NOD2_HUMAN	CARD 1.	4	TGGTCGAGCTG	0.602	
-	2	391	p.W81*|CES7_uc	NM_001143685	NP_001137157	Q6NT32	EST5A_HUMAN		0	TATCCCAGGGC	0.592	
+	16	1794		NM_005886	NP_005877	Q9BVA0	KTNB1_HUMAN	NA1 and NDEL1 (By simila	0	AGGCCGTGAAG	0.637	
+	2	221	se_Mutation_p.V5	NM_024922	NP_079198	Q6UWW8	EST3_HUMAN		5	TGGGCGTGAAG	0.632	rs149175900
-	18	2924	OD1_uc010ced.2	NM_013241	NP_037373	Q9Y613	FHOD1_HUMAN	FH2.	3	ACGGCGGGCAC	0.662	
-	3	633		NM_032178	NP_115554	Q96CW6	S7A6O_HUMAN		1	TGGCCGTCTCC	0.542	rs139184366
-	4	729	nse_Mutation_p.P	NM_017853	NP_060323	Q9NX01	TXN4B_HUMAN		1	TTTGGGAATATT	0.383	
-	5	802	8B_uc010vmu.1_	NM_001011880	NP_001011880	Q6UXF7	CL18B_HUMAN		0	AGGCACCCTTC	0.607	
+	2	120	|TRAPPC2L_uc00	NM_016209	NP_057293	Q9UL33	TPC2L_HUMAN		0	CTACGGAGAAC	0.552	
-	9	1486	fnc.1_Missense_	NM_013275	NP_037407	Q6UB99	ANR11_HUMAN		6	TGACGGGGGCC	0.547	
+	2	147	n|CDK10_uc002fc	NM_052988	NP_443714	Q15131	CDK10_HUMAN		1	CCGGAGTGTGA	0.522	
-	1	697		NM_002551	NP_002542	P47893	OR3A2_HUMAN	Name=5; (Potential).	1	AACCAAAGGTG	0.562	
-	1	617		NM_003554	NP_003545	P47887	OR1E2_HUMAN	Name=5; (Potential).	1	TCACCCATTCA	0.473	
+	1	64	|VMO1_uc010vsi.	NM_001014985	NP_001014985				0	AGTGGCGGCGC	0.672	
+	23	3033		NM_006612	NP_006603	O43896	KIF1C_HUMAN		2	AGGCAGCCCCC	0.647	
-	10	1218	TP53_uc002gii.1_	NM_001126112	NP_001119584	P04637	P53_HUMAN	teraction wit3)|p.R342Q(2)|	22245	CTCTCGGAACA	0.498	
-	4	760	uc010cnq.1_RNA	NM_001139	NP_001130	O75342	LX12B_HUMAN	ipoxygenase.	0	CCTCCGCACCG	0.657	
-	39	5629	.R1876C|MYH10_	NM_005964	NP_005955	P35580	MYH10_HUMAN	Potential.	2	GCGACGGACTA	0.448	
-	2	337	glo.2_Missense_	NM_144681	NP_653282	Q96M95	CCD42_HUMAN		1	ACTCCGACGCC	0.542	
+	13	2060	p.S682N|USP43_	NM_153210	NP_694942	Q70EL4	UBP43_HUMAN		5	TGACAGCACGG	0.542	
-	30	4146		NM_003802	NP_003793	Q9UKX3	MYH13_HUMAN	Potential.	6	CTCCTCCTCATA	0.612	
-	45	7282	m.2_Missense_M	NM_006311	NP_006302	O75376	NCOR1_HUMAN	with C1D (By similarity).	5	CCGTTCCGTTC	0.502	
+	2	370	B_uc010vwe.1_Int	NM_018955	NP_061828	P0CG47	UBB_HUMAN	biquitin-like 2.	3	GGTATGCAGATC	0.537	
+	7	1129	bj.2_Missense_Mu	NM_003593	NP_003584	O15353	FOXN1_HUMAN	Fork-head.	1	AGACAGCACCC	0.557	
+	5	727	37B2_uc010wbq.1_RNA|LRRC37B2_uc010csi.2_RNA						0	CCAGGATATGAC	0.249	
-	4	2350	p.R674C|SLFN13_	NM_144682	NP_653283	Q68D06	SLN13_HUMAN		2	AGTACGGAAAT	0.433	
-	6	1756		NM_139285	NP_644814	Q8NHY3	GA2L2_HUMAN		2	AGGTCCCAGGA	0.612	
+	3	512	cwb.2_Missense_	NM_004448	NP_004439	P04626	ERBB2_HUMAN	ellular (Pote p.R92G(1)	143	AAGTGAGGCAG	0.597	
-	5	492	_p.R144C|IKZF3_	NM_012481	NP_036613	Q9UKT9	IKZF3_HUMAN		6	TGGGCGTTCAC	0.428	
-	3	372_373	nse_Mutation_p.G	NM_152349	NP_689562	Q8N1A0	KT222_HUMAN	Potential.	2	CTAGTCCTTCAA	0.46	
-	1	355		NM_031960	NP_114166	Q9BYQ9	KRA48_HUMAN	IKRQVHEC]- [SPRT]-[STC	0	gctggacacacagcag	0.204	
-	2	2008		NM_018143	NP_060613	Q9NVR0	KLH11_HUMAN		0	TGTGCCATGCA	0.527	
-	5	486	N1_uc010whc.1_I	NM_003766	NP_003757	Q14457	BECN1_HUMAN		1	GACTTGCCTTCA	0.582	
-	5	371	n_p.V25I|GPATCH	NM_001002909	NP_001002909	Q9UKJ3	GPTC8_HUMAN	Potential.	4	TTTCTACTTCTAG	0.393	
-	16	2488	.2_Intron|TTLL6_u	NM_001130918	NP_001124390	Q8N841	TTLL6_HUMAN		0	CAGAGCTGTCA	0.547	
+	1	120	.1_Intron|B4GALN	NM_153446	NP_703147	Q8NHY0	B4GN2_HUMAN	lasmic (Potential).	2	GCCGGGAATGT	0.667	
+	9	1125		NM_153228	NP_694960	Q8N957	ANKF1_HUMAN	onectin type-III.	2	CACCGGCATGT	0.502	
+	12	2517	pm.1_Missense_	NM_030779	NP_110406	Q9H252	KCNH6_HUMAN	lasmic (Potential).	1	CTCAGGAAGAC	0.622	

-	22	3126		NM_080284	NP_525023	Q8N139	ABCA6_HUMAN		7	AGTAGCCCATTG	0.299	
+	5	1028	jip.2_Missense_M	NM_018658	NP_061128	Q9NPI9	IRK16_HUMAN	smic (By similarity).	3	CCCAAACCATTC	0.463	
-	2	609		NM_006678	NP_006669	Q08708	CLM6_HUMAN	(Potential).|Ig-like V-type.	0	TGATGGACACTC	0.547	
+	4	577	_p.R106L|NUP85_	NM_024844	NP_079120	Q9BW27	NUP85_HUMAN		1	ACTACCGATCAG	0.199	
+	12	1755	jth.2_Missense_M	NM_198955	NP_945193	Q3V5L5	MGT5B_HUMAN	enal (Potential).	3	CGCCCCCCTGG	0.657	
-	11	1379	02jwb.1_Translati	NM_025090	NP_079366	Q9P275	UBP36_HUMAN		5	CGGACGTATGTT	0.433	
+	7	906	jyd.1_Missense_M	NM_173626	NP_775897	Q86WA9	S2611_HUMAN	ical; (Potential).	0	TGCTGCTGGTG	0.682	
-	5	1264		NM_002522	NP_002513	Q15818	NPTX1_HUMAN	Pentaxin.	0	CCTGGGTGGCA	0.622	
-	4	842	e_Mutation_p.G27	NM_001614	NP_001605	P63261	ACTG_HUMAN		2	GATGCCGCAAG	0.537	
-	6	921	IRE1_uc010wzx.1	NM_001128626	NP_001122098	Q08AE8	SPIR1_HUMAN		0	CTGCCGCTCTTC	0.443	
-	10	1602	m.2_Missense_Mu	NM_024421	NP_077739	Q08554	DSC1_HUMAN	r (Potential).|Cadherin 3.	4	GTGAGCTCGCT	0.408	
+	15	2641	p.1_Missense_Mu	NM_001942	NP_001933	Q02413	DSG1_HUMAN	lasmic (Potential).	7	TAATTTCTGAGAC	0.517	
+	11	1920	xq.2_Missense_Mu	NM_030632	NP_085135	Q9C0F0	ASXL3_HUMAN	Ser-rich.	3	GAGCCTGTACCA	0.488	
+	8	1055	.R268Q|RNF165_	NM_152470	NP_689683	Q6ZSG1	RN165_HUMAN	G-type; atypical.	0	CTGCCGAGTGG	0.577	
+	3	644	p.Y131C|LIPG_uc	NM_006033	NP_006024	Q9Y5X9	LIPE_HUMAN		2	AGCTTTACACGG	0.557	
+	2	168	02ljj.3_5'UTR|SEI	NM_080475	NP_536723	Q96P15	SPB11_HUMAN		1	AGTCTGCTTTATC	0.443	
-	3	208		NM_017550	NP_060020	Q8N344	MIER2_HUMAN		0	GTCTGGGCACC	0.597	
+	4	708	.2_Intron|MADCAN	NM_130760	NP_570116	Q13477	MADCA_HUMAN	T- T-S-[QP]-E.|Extracellular	0	AGCCTCCCGACA	0.592	
-	4	434	ED16_uc010xfw.1_	NM_005481	NP_005472	Q9Y2X0	MED16_HUMAN	WD 1.	0	GAGCCGGGAGC	0.642	
+	4	1228	wn.3_Missense_M	NM_152791	NP_690004	Q8NEP9	ZN555_HUMAN	2H2-type 8.	1	TTTATCCCCAGTC	0.463	
+	4	1336	a.1_Missense_Mu	NM_173480	NP_775751	Q68EA5	ZNF57_HUMAN	2H2-type 9.	3	GAACAATGTGGC	0.428	
+	4	1430	a.1_Missense_Mu	NM_173480	NP_775751	Q68EA5	ZNF57_HUMAN	2H2-type 10.	3	GAAAAACCTTCA	0.453	
+	1	79		NM_003811	NP_003802	P41273	TNFL9_HUMAN	lasmic (Potential).	1	AGCCCCGTGGC	0.572	
-	29	3841	3_uc002mfl.2_5'U	NM_000064	NP_000055	P01024	CO3_HUMAN		5	TAGTATCTCTGT	0.577	
+	11	1150	a.1_Missense_Mu	NM_005428	NP_005419	P15498	VAV_HUMAN	DH.	16	GCGATGGAGAA	0.627	
-	48	6181	l3_uc002mje.2_5'F	NM_032447	NP_115823	Q75N90	FBN3_HUMAN	TB 8.	11	CAGTTCGCAGG	0.612	rs149936210
-	20	2204		NM_012335	NP_036467	O00160	MYO1F_HUMAN	IQ.	3	TTCGGGCAAAG	0.662	
-	27	38206		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	ellular (Potential).	57	GGTGGGCACAG	0.537	
-	3	19097		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).	57	TTTATAGAAGGAT	0.448	
-	1	6782		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	ch.|Extracellular (Potential).	57	TAAAGGAAACC	0.468	
-	1	2516		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).	57	TGGAGGAAAGA	0.502	
-	10	1717	wr.1_Missense_M	NM_152476	NP_689689	Q96MR9	ZN560_HUMAN	2H2-type 6.	6	AAAAAGAGATG	0.413	
-	1	211	T1_uc002mnh.2_5	NM_001379	NP_001370	P26358	DNMT1_HUMAN	.|Interaction with the PRC2	6	TGTGGGCACCC	0.736	
+	4	1515	ym.1_Missense_M	NM_001136501	NP_001129973	Q08AG5	ZN844_HUMAN		0	CTTCAGATCTGC	0.423	
-	11	1417	_Missense_Mutati	NM_013447	NP_038475	Q9UHX3	EMR2_HUMAN	ellular (Potential).	4	GGGCAGGGTCT	0.607	
-	2	454		NM_024527	NP_078803	Q96I13	ABHD8_HUMAN		0	GGAGAGGTCCC	0.692	
+	2	903	_p.P336L|ZNF493_	NM_175910	NP_787106	Q6ZR52	ZN493_HUMAN	ype 7; degenerate.	1	AACCCCTACTA	0.348	rs142651314
-	4	1395	1_Intron|ZNF208_	NM_007153	NP_009084				7	TGACCTCATGTT	0.368	
+	4	1512		NM_020855	NP_065906	Q9P255	ZN492_HUMAN	2H2-type 11.	0	ACAAATGTGAAG	0.373	
-	4	1567		NM_138330	NP_612203	Q8TD23	ZN675_HUMAN	2H2-type 12.	2	GATTGGATAAAC	0.368	
+	6	1372	vq.1_Missense_M	NM_018443	NP_060913	Q9NR11	ZN302_HUMAN	2H2-type 5.	0	ATAGTTCGTCTC	0.413	
+	25	2614	_Mutation_p.S81	NM_001111020	NP_001104490	O00267	SPT5H_HUMAN	m repeats of G- S-[QR]-T-I	4	TGGCAGCCGCA	0.632	
-	4	581	RB_uc010egw.1_I	NM_000713	NP_000704	P30043	BLVRB_HUMAN		0	TGGCGGCATCA	0.547	
-	5	602		NM_145296	NP_660339	Q8NFZ8	CADM4_HUMAN	otential).|Ig-like C2-type 1.	0	GAAACCGTACTG	0.597	
+	10	1302	F3A_uc002pek.2_I	NM_152795	NP_690008	Q9Y2N7	HIF3A_HUMAN		3	ATGGGGCTTCA	0.672	
-	14	2373	H4_uc002pgb.1_Ir	NM_015168	NP_055983	Q9UPT8	ZC3H4_HUMAN	Potential.	6	CTCCTCCTGCT	0.701	
-	5	449	e_Mutation_p.P11	NM_000234	NP_000225	P18858	DNLI1_HUMAN		3	CCATGGGAGAG	0.557	

+	2	1765		NM_014330	NP_055145	O75807	PR15A_HUMAN	eraction with MLL.|4 X 34	1	GGACTGGGGAG	0.627	
+	32	4599	.1_Missense_Mut	NM_024729	NP_079005	Q7Z406	MYH14_HUMAN	Potential.	1	GTGAGGAGCTG	0.706	
-	4	340	n_p.T41I|KLK5_uc	NM_001077491	NP_001070959	Q9Y337	KLK5_HUMAN		0	GCACGGTGTTA	0.627	
-	5	2086	ydj.1_Missense_M	NM_001102657	NP_001096127	Q6ZNA1	ZN836_HUMAN	2H2-type 13.	0	TTATGAATTGAAA	0.383	
-	5	2067	dj.1_Missense_M	NM_001102657	NP_001096127	Q6ZNA1	ZN836_HUMAN	2H2-type 13.	0	ACTGTAATTGAA	0.388	
+	4	1385_1386	dw.1_Missense_M	NM_138374	NP_612383	Q96IR2	ZN845_HUMAN	C2H2-type 8.	0	TCAGATGTCATC	0.411	
+	7	2419	_p.R600K|ZNF761_	NM_001008401	NP_001008401	Q86XN6	ZN761_HUMAN	2H2-type 16.	1	ATAGGAGAATTC	0.398	
+	4	292	_p.R79Q|RPS9_u	NM_001013	NP_001004	P46781	RS9_HUMAN		1	GCTGCGGCGGC	0.433	
-	3	294	ne.2_Missense_M	NM_022103	NP_071386	Q5HYK9	ZN667_HUMAN	KRAB.	1	ATTCTCCAACAT	0.443	
+	6	1933	470_uc010etn.2_I	NM_001001668	NP_001001668	Q6ECI4	ZN470_HUMAN	C2H2-type 7.	2	ACTCATACTGG	0.413	
-	1	554	qnt.2_Missense_M	NM_001146186	NP_001139658	Q9GZU2	PEG3_HUMAN	SCAN box.	12	AGGTTTCGGAGT	0.502	
+	3	2079	47_uc002qpm.3_	NM_001023561	NP_001018855	O43361	ZN749_HUMAN		0	CTGGAGAAAAG	0.388	
+	5	1461	nse_Mutation_p.F	NM_024691	NP_078967	Q96HQ0	ZN419_HUMAN	C2H2-type 8.	0	GAGATTCTTTAG	0.423	
+	4	2168	ud.1_Intron|ZNF5	NM_153263	NP_694995	Q6P9A3	ZN549_HUMAN		1	AGAGCCCTAGC	0.428	
-	3	1987		NM_003433	NP_003424	P52740	ZN132_HUMAN	2H2-type 12.	2	TCAGGCTGGAG	0.498	
+	1	439		NM_001105569	NP_001099039	A6NI15	MSGN1_HUMAN	-loop-helix motif.	1	ACACCCTCCGG	0.572	
+	3	1112	w.2_Missense_M	NM_002252	NP_002243	Q9BQ31	KCNS3_HUMAN	=Segment S2; (Potential).	4	ATCCGGTGCTG	0.577	
-	6	1404	p.R13L|ADCY3_u	NM_004036	NP_004027	O60266	ADCY3_HUMAN	lasmic (Potential).	4	TTCTCCCGCACA	0.642	
-	1	1055	3C_uc010ykr.1_M	NM_002254	NP_002245	O14782	KIF3C_HUMAN	inesin-motor.	4	GGGAGCGGGAG	0.597	
+	12	1842	002rkr.2_Missense	NM_013392	NP_037524	Q9UHY1	NRBP_HUMAN		3	CCTTGCGGCCC	0.522	
+	1	5338	1_5'Flank|ZNF512_	NM_032266	NP_115642	Q68DN1	CB016_HUMAN	m repeat of P-S-E-R-S-H-	1	CCTCTGAGAGA	0.527	
+	4	556	_p.P103S|SPTBN	NM_003128	NP_003119	Q01082	SPTB2_HUMAN	1.|Actin-binding.	8	CTAAACCCACC	0.512	
-	4	854	.2_3'UTR|TMEM1	NM_198276	NP_938017	Q86X19	TMM17_HUMAN		0	GAAACGAACTG	0.428	
-	3	842	_p.A23V|TGFBRA	NM_004257	NP_004248	Q8WUH2	TGFA1_HUMAN	CNH.	2	CAGCCGCCCCA	0.532	
-	4	1138		NM_000575	NP_000566	P01583	IL1A_HUMAN		1	TTTTAGAGGTTTC	0.453	
-	8	1412	_p.I375M|ERCC3_	NM_000122	NP_000113	P19447	ERCC3_HUMAN	ase ATP-binding.	7	TCCAGGATCATG	0.552	
+	2	108	|THSD7B_uc002t	NM_001080427	NP_001073896				7	AGTGTGGTGTTT	0.507	
-	17	3485	p.P1036L|SCN1A_	NM_006920	NP_008851	P35498	SCN1A_HUMAN		13	CTACGGGCTGT	0.418	
+	8	9514	dy.2_Missense_M	NM_152381	NP_689594	A4UGR9	XIRP2_HUMAN		14	AAATTCACAGA	0.473	
-	29	5058		NM_004525	NP_004516	P98164	LRP2_HUMAN	B 13.|Extracellular (Poten	29	GAGTCCATGAA	0.478	
-	4	1537	.2_Missense_Mut	NM_003111	NP_003102	Q02447	SP3_HUMAN	ation domain (Gln-rich).	6	GTCCAGAAGGG	0.433	
-	4	1003	.2_Missense_Mut	NM_003111	NP_003102	Q02447	SP3_HUMAN		6	TGCCCGAGAGT	0.443	
+	14	1735	fe.1_Nonsense_M	NM_032523	NP_115912	Q9BZF3	OSBL6_HUMAN		1	GTGATCAGGTTG	0.328	
-	226	45691	_uc010zfi.1_Miss	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	TGGTTCCAACG	0.443	
-	88	22894	_uc010zfj.1_Intro	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	TGGCTGGTTCC	0.403	
-	46	15390	N_uc010zfi.1_Intr	NM_133379	NP_596870	Q8WZ42	TITIN_HUMAN		153	CTCCCCTGGGG	0.498	
+	4	1819		NM_019048	NP_061921	Q9NWL6	ASND1_HUMAN	agine synthetase.	3	TGGCTGTGCAG	0.403	
-	17	2224		NM_018897	NP_061720	Q8WXX0	DYH7_HUMAN	similarity).|Potential.	12	CCAAATGAATAA	0.328	
-	15	1632	hj.1_Missense_M	NM_006190	NP_006181	Q13416	ORC2_HUMAN		0	ATAGGAGGTTT	0.433	
+	17	2525	_Mutation_p.R77	NM_152526	NP_689739	Q8TEW8	PAR3L_HUMAN		4	GGTTCGAGGCC	0.517	
-	4	471	jv.2_Missense_Mu	NM_015680	NP_056495	Q9BV87	CNPD1_HUMAN		0	GTGCCGGAGCC	0.522	rs148051282
-	10	1922_1923	e.1_Missense_M	NM_005689	NP_005680	Q9NP58	ABCB6_HUMAN	.|ABC transmembrane typ	2	AGTAGGTGCCAA	0.51	
+	1	760	mv.1_Missense_M	NM_019076	NP_061949	Q9HAW9	UD18_HUMAN		2	CCTCTGAAATT	0.418	
-	1	143	zpn.1_Missense_	NM_015985	NP_057069	Q9Y264	ANGP4_HUMAN		2	CACAAGGAGGA	0.592	
-	1	238	PROKR2_uc010z	NM_144773	NP_658986	Q8NFJ6	PKR2_HUMAN	lasmic (Potential).	5	ATAGCGGGTGA	0.552	
-	12	1270	wmd.3_Splice_Sit	NM_019593	NP_062539	Q9NPB8	GPCP1_HUMAN		0	GCACCCTGACA	0.383	
+	3	1542		NM_001200	NP_001191	P12643	BMP2_HUMAN		2	ACCAAGATGAA	0.483	

+	5	794	P1_uc010zri.1_In	NM_080826	NP_543016	B1AKI9	ISM1_HUMAN		0	TGTTTAGGAATT	0.398	
-	9	885	L1L2_uc010zrl.1_	NM_025229	NP_079505	Q5TEA6	SE1L2_HUMAN	ellular (Potential).	2	GTCTTTCCGTT	0.368	
+	2	162		NM_153324	NP_697019	Q8N688	DB123_HUMAN		0	CCAAAGATGCT	0.423	
+	14	1760	e_Mutation_p.R42	NM_012156	NP_036288	Q9H4G0	E41L1_HUMAN	trin--actin-binding.	3	GGATCGAGACT	0.607	
+	1	371	.2_Intron|SGK2_u	NM_016276	NP_057360	Q9HBY8	SGK2_HUMAN		6	TGTCCCCCCAG	0.617	
+	11	1610	.2_Missense_Mu	NM_181659	NP_858045	Q9Y6Q9	NCOA3_HUMAN		5	CACATGGGAGT	0.498	
+	2	516	4A1_uc002ydc.1_	NM_016354	NP_057438	Q96BD0	SO4A1_HUMAN	Name=1; (Potential).	1	CAAGGGCATCC	0.647	
-	4	724		NM_080823	NP_543013	Q9H3Y6	SRMS_HUMAN		2	ATTCGGAGTGT	0.667	
-	1	598	02ygf.2_Missense_	NM_003224	NP_003215	Q13795	ARFRP_HUMAN		2	CATGTACTTGT	0.517	
+	5	733	p.R20W|NCAM2_	NM_004540	NP_004531	O15394	NCAM2_HUMAN	2.|Extracellular (Potential).	4	CAGATCGGTTC	0.403	
-	3	575	_p.P33L|RCAN1_u	NM_004414	NP_004405	P53805	RCAN1_HUMAN		0	CTGGCGGAGAG	0.542	
-	2	671	p.G177S|CLDN14	NM_012130	NP_036262	O95500	CLD14_HUMAN	ical; (Potential).	0	GCCACCAATGA	0.637	
-	12	1399	p.D273N|TMPRS	NM_024022	NP_076927	P57727	TMPS3_HUMAN	.|Extracellular (Potential).	3	GCTGTCCCCCT	0.597	
-	5	618	g.1_Missense_M	NM_033661	NP_387510	P57081	WDR4_HUMAN	WD 2.	1	AGAAGGACTCG	0.612	
-	20	1968	.2_Missense_Mut	NM_001001438	NP_001001438	P48449	ERG7_HUMAN	PFTB 4.	0	CCTCCCCCCAG	0.612	
+	13	2837	L_uc011akd.1_Mi	NM_021115	NP_066938	Q9BYH1	SE6L1_HUMAN	xtracellular (Potential).	6	GCCAGGAGAGT	0.567	
+	7	3572	tq.1_Missense_M	NM_001039141	NP_001034230	Q9H2D6	TARA_HUMAN		1	AGTCCCCCCAA	0.667	
+	2	1635	xy.2_Missense_M	NM_002409	NP_002400	Q09327	MGAT3_HUMAN	enal (Potential).	0	GGTTCGACGGC	0.637	
-	2	485	.1_Missense_Mut	NM_032311	NP_115687	Q9BY77	PDIP3_HUMAN		0	AGGCAGCAGGG	0.552	
+	11	1815	e_Mutation_p.P55	NM_018995	NP_061868	Q9BXT6	M10L1_HUMAN		3	GGAGGCCTTCT	0.473	
+	2	356	|CAV3_uc003brb.	NM_001234	NP_001225	P56539	CAV3_HUMAN	r interaction with DAG1.	2	TCTCCTTCTGC	0.577	
+	2	911	sg.2_Missense_M	NM_004634	NP_004625	P55201	BRPF1_HUMAN	ith MYST3 and MYST4.	3	TGCGAGCACCA	0.562	
-	13	2394	p.P571T|XPC_uc	NM_004628	NP_004619	Q01831	XPC_HUMAN	in involved in damage reco	3	GCTGGGCAGGA	0.597	
-	2	934	hfn.2_Missense_	NM_005442	NP_005433	O95936	EOMES_HUMAN	T-box.	4	GTAGTGGGCAG	0.502	
-	7	970	_p.F259S|SCN5A_	NM_198056	NP_932173	Q14524	SCN5A_HUMAN	=S5 of repeat I; (Potential).	9	GGCAGAAGACT	0.592	
-	2	389		NM_006514	NP_006505	Q9Y5Y9	SCNAA_HUMAN	S1 of repeat I; (Potential).|	10	GATATGAGTGG	0.483	
-	14	2453	1A_uc010hhn.1_5	NM_014139	NP_054858	Q9UI33	SCNBA_HUMAN	II.	9	ATCCCCCATGT	0.498	
+	3	777	0hiv.1_Missense_	NM_031200	NP_112477	P51686	CCR9_HUMAN	ellular (Potential).	3	TGAGAGCACCA	0.493	
-	5	618	se_Mutation_p.P1	NM_016479	NP_057563	Q8N114	SHSA5_HUMAN	ic (Potential).|Pro-rich.	0	TGGAGGCTGAG	0.602	rs151337676
-	21	2794		NM_003335	NP_003326	P41226	UBA7_HUMAN		2	CCGTGGCCCAC	0.577	
-	2	885_886	tron|NAT6_uc003	NM_012191	NP_036323	Q93015	NAT6_HUMAN		1	AAGGGGGCCCT	0.579	
+	5	2740	e_Mutation_p.R21	NM_000839	NP_000830	Q14416	GRM2_HUMAN	lasmic (Potential).	1	CAGCCGCTTTG	0.637	
+	4	706	dn.2_Intron|GLYC	NM_145262	NP_660305	Q8IVS8	GLCTK_HUMAN		0	TGGCAGCCCGT	0.622	
+	8	1363	ldt.1_Missense_M	NM_015512	NP_056327	Q9P2D7	DYH1_HUMAN	(By similarity).	3	AGGACCCTTGC	0.602	
+	31	5284		NM_015512	NP_056327	Q9P2D7	DYH1_HUMAN	1 (By similarity).	3	TGGTGCCATCC	0.612	
-	13	1556	1_uc010hmg.2_R	NM_004656	NP_004647	Q92560	BAP1_HUMAN		65	CGAGTGTGTGG	0.602	
+	58	6334	ion_p.R102H|STA	NM_015136	NP_055951	Q9NY15	STAB1_HUMAN	|Extracellular (Potential).	9	TGGCCGTGTGT	0.642	
+	2	1183	EF3_uc003dih.2_	NM_181727	NP_859078	Q7Z6I5	SPT12_HUMAN		0	TTACTGAGGGC	0.299	
+	5	784		NM_022072	NP_071355	Q9H649	NSUN3_HUMAN		1	TGTTTTCTTCTG	0.398	
+	1	644		NM_001005515	NP_001005515	A6NDH6	O5H15_HUMAN	Name=5; (Potential).	2	CTATTCTTATAT	0.348	
+	1	848		NM_001004736	NP_001004736	Q8NHB7	OR5K1_HUMAN	Name=7; (Potential).	1	TAGTTCCCTTAC	0.308	
+	12	1994	77_splice|GPR12	NM_032787	NP_116176	Q96K78	GP128_HUMAN		4	ATGGGGTAAGT	0.308	
-	2	1379	.2_Intron|CD96_u	NM_024508	NP_078784	Q9BTP6	ZBED2_HUMAN		1	CTGCCCTTTCC	0.602	
-	5	557	2018_uc003eal.2_	NM_001009899	NP_001009899	Q68DE3	K2018_HUMAN	-loop-helix motif.	3	GGGCAGGAGAA	0.368	
+	13	1432	bji.1_Missense_M	NM_014980	NP_055795	Q9Y2K9	STB5L_HUMAN	WD 8.	9	TGTATTCTATAGG	0.308	
+	4	505		NM_017554	NP_060024	Q460N5	PAR14_HUMAN		6	TTCCTCTTTGGT	0.378	
+	5	2003		NM_001102608	NP_001096078	A6NMZ7	CO6A6_HUMAN	cal region.|VWFA 4.	8	CAGATCGGGTG	0.418	

+	4	873	_Mutation_p.R200	NM_023943	NP_076432	Q6UXF1	TM108_HUMAN	ellular (Pote	p.R200Q(1)	4	AGGACGAAATC	0.592	rs140878635
+	11	3585	.R271Q|PPP2R3	NM_002718	NP_002709	Q06190	P2R3A_HUMAN	EF-hand 2.		7	TGAACGGATGG	0.493	rs149384978
-	1	469		NM_001134659	NP_001128131	A6NEV1	PR23A_HUMAN			0	CTCCTCGTAGG	0.632	
-	8	847	5_uc010hus.1_R	NM_001039547	NP_001034636	Q6ZS86	GLPK5_HUMAN			0	GGTATCGAAATT	0.348	
+	2	1611		NM_004267	NP_004258	Q9Y4C5	CHST2_HUMAN	enal (Potential).		3	CGGGGGGCGC	0.667	
-	2	401	_uc003ewz.2_Mis	NM_000096	NP_000087	P00450	CERU_HUMAN	1.|Plastocyanin-like 1.		1	AATGTTCCCTGC	0.328	
-	11	1028	_p.M235I|ZBBX_u	NM_024687	NP_078963	A8MT70	ZBBX_HUMAN			2	TCTTTTCATCGT	0.328	
-	7	2080	fk.2_Missense_Mu	NM_005241	NP_005232	Q03112	EVI1_HUMAN			14	TTTTTTCGAGGC	0.512	
+	24	3707	_Mutation_p.R117	NM_198241	NP_937884	Q04637	IF4G1_HUMAN			7	GGACCGTGGGG	0.627	
+	7	1084	.A280T|CHRD_uc	NM_003741	NP_003732	Q9H2X0	CHRD_HUMAN	CHRD 2.		3	TGGCTGCAGGT	0.617	
+	13	1768	e_Mutation_p.S4	NM_003722	NP_003713	Q9H3D4	P63_HUMAN	SAM.		12	GTTCATCATGTC	0.448	
-	8	13589	tion_p.L69F|MUC	NM_018406	NP_060876	Q99102	MUC4_HUMAN	NIDO.		0	CATGAGCACCG	0.622	
+	5	1146	141_uc003gab.2_	NM_003441	NP_003432	Q15928	ZN141_HUMAN	2H2-type 6.		0	TAGGTCCACAA	0.378	
+	5	1178	141_uc003gab.2_	NM_003441	NP_003432	Q15928	ZN141_HUMAN			0	ATTCATACTGGA	0.398	
-	5	1288		NM_177998	NP_819056	Q7RTM1	OTOP1_HUMAN			3	GTAGCGGGGGT	0.572	
-	2	178		NM_001001290	NP_001001290	Q9NRM0	GTR9_HUMAN			3	TCGGTCCTTTT	0.388	
-	3	3405		NM_053042	NP_444270	Q9C0D4	Z518B_HUMAN			4	AAACAACTTTGA	0.443	
+	28	3112	s.1_Missense_Mu	NM_004787	NP_004778	O94813	SLIT2_HUMAN	EGF-like 2.		11	ATGGAGGAACT	0.448	
+	13	1672	_p.S292F|FAM114	NM_138389	NP_612398	Q8IWE2	NXP20_HUMAN			1	TGGCCTCTTTAT	0.323	
-	6	785		NM_182592	NP_872398	Q8N8F6	YIPF7_HUMAN			0	TCCTTCCATGTG	0.453	
+	9	1541_1542	se_Mutation_p.E	NM_145263	NP_660306	Q8TC71	MIEAP_HUMAN			4	ATCCAGGAGATA	0.426	
-	16	2661	.1_Missense_Mut	NM_002253	NP_002244	P35968	VGFR2_HUMAN	ical; (Potential).		33	GGTCCGTAGGA	0.433	rs1139774
+	9	3142		NM_031889	NP_114095	Q9NRM1	ENAM_HUMAN			3	GAGGAGGAACA	0.443	
-	11	1834		NM_001042784	NP_001036249	Q5M9N0	CD158_HUMAN	Potential.		6	CTTGTCCTTCT	0.478	
+	11	1546	.2_Missense_Mut	NM_198892	NP_942595	Q9NSY1	BMP2K_HUMAN	Gln/His-rich.		1	CTCACcagcagcag	0.254	
+	4	452	APP1_uc010ilh.2_	NM_014395	NP_055210	Q9UN19	DAPP1_HUMAN	SH2.		0	AGGCACTCTGA	0.418	
-	10	1812	p.S358F|LEF1_uc	NM_016269	NP_057353	Q9UJU2	LEF1_HUMAN			1	ATGCAGATTCC	0.433	
+	38	9920	K2_uc003ibh.3_I	NM_001148	NP_001139	Q01484	ANK2_HUMAN			14	ATTCTCCCGAT	0.443	
+	3	617	e_Mutation_p.P14	NM_001128933	NP_001122405	Q9UMS6	SYNP2_HUMAN			2	AAGTTCCCCTA	0.547	
+	32	4282	.W1411*|KIAA092	NM_015196	NP_056011	A2VDJ0	T131L_HUMAN	lasmic (Potential).		2	CTGTGGCCCAC	0.567	
+	6	1377		NM_001034845	NP_001030017	Q49A17	GLTL6_HUMAN	main A.|Lumenal (Potential		4	TCATCCGGACCC	0.517	rs146548110
+	6	940	17_uc003ium.3_	NM_170710	NP_733828	Q8IZU2	WDR17_HUMAN			6	ACAACATTTAATC	0.433	
+	1	502		NM_178556	NP_848651	Q8N9V2	TRIML_HUMAN			4	TCCAGCGAGGC	0.577	rs138508820
-	2	138_139	AM173B_uc010itr.	NM_199133	NP_954584	Q6P4H8	F173B_HUMAN			2	AGAACCCCCAGT	0.475	
-	14	2020		NM_001369	NP_001360	Q8TE73	DYH5_HUMAN	n (By similarity).		31	TGCGAATTATAG	0.532	
-	26	5351	rf42_uc011coz.1_	NM_023073	NP_075561	E9PH94	E9PH94_HUMAN			7	GAGTCCAAAAA	0.323	
-	3	374	.1_Intron|TTC33_	NM_012382	NP_036514	Q6PID6	TTC33_HUMAN	TPR 1.		1	CTCCCGATATCT	0.284	
-	6	1463		NM_021072	NP_066550	O60741	HCN1_HUMAN	toplasmic (Potential).		1	AGGATCCGCAT	0.383	
+	5	1551	486K|MARVELD2_	NM_001038603	NP_001033692	Q8N4S9	MALD2_HUMAN	lasmic (Potential).		0	ATTCGGAAAGC	0.408	
+	30	6646	p.T2128I|BDP1_u	NM_018429	NP_060899	A6H8Y1	BDP1_HUMAN			2	TGTAACCAAAG	0.338	
-	2	2246	s.1_Missense_Mu	NM_003633	NP_003624	O14682	ENC1_HUMAN	Kelch 2.		3	TGGGGGCAGCC	0.602	
+	2	1269		NM_005242	NP_005233	P55085	PAR2_HUMAN	lasmic (Potential).		1	TGTCCGCACTG	0.448	rs149001132
+	2	578		NM_153610	NP_705838	Q8N3K9	CMYA5_HUMAN			9	GCAGTCCTTTAA	0.383	
+	1	1158	uc011ctk.1_RNA	NM_032567	NP_115956	Q9BXG8	SPZ1_HUMAN	eucine-zipper.		1	TGGAGGAACAG	0.423	
+	70	14320	.E2448K|GPR98_	NM_032119	NP_115495	Q8WXG9	GPR98_HUMAN	ellular (Potential).		16	GAGCCGAACTG	0.438	
+	1	424	c003kni.2_5'Flan	NM_198507	NP_940909	Q8TBP5	F174A_HUMAN	ellular (Potential).		0	CCGGGGAAGGC	0.701	
-	16	2395	m.1_Missense_M	NM_015082	NP_055897	Q6MZW2	FSTL4_HUMAN			2	GGTCATACAGG	0.582	

-	8	1706	w.1_Missense_Mu	NM_004883	NP_004874	O14511	NRG2_HUMAN	lasmic (Potential).	6	TCCCAGAGAAG	0.542
+	1	323	HB2_uc003lim.1_	NM_018936	NP_061759	Q9Y5E7	PCDB2_HUMAN	(Potential).|Cadherin 1.	6	ACTTGCTGTGA	0.502
+	1	2443	_5'Flank|PCDHB1	NM_019120	NP_061993	Q9UN66	PCDB8_HUMAN	lasmic (Potential).	4	AGTACGAGGTG	0.577
+	1	1418	HGA5_uc003lju.1	NM_018925	NP_061748	Q9Y5G0	PCDGH_HUMAN	(Potential).|Cadherin 5.	0	CGCCTCGGACC	0.587
-	3	562	e_Mutation_p.G41	NM_001024947	NP_001020118	Q969M3	YIPF5_HUMAN	lasmic (Potential).	2	ATAGCCAGCAT	0.403
+	2	162	_Missense_Mutat	NM_024028	NP_076933	Q8NBM8	PCYXL_HUMAN		1	TTGGGGCTGGG	0.587
-	21	3341	jhd.2_Missense_	NM_002609	NP_002600	P09619	PGFRB_HUMAN	Potential).|Protein kinase.	17	CTCGAGAAGCA	0.557
-	2	439	IP2_uc003lwr.2_	NM_001001343	NP_001001343	Q8TBE3	FNDC9_HUMAN	onectin type-III.	0	TGTAAGGGAAG	0.567
+	39	4038	CK2_uc010jjm.2_	NM_004946	NP_004937	Q92608	DOCK2_HUMAN	teraction with CRKL.	7	TCAGCCAGAAC	0.587
+	4	685	2_splice|TSPAN1	NM_012171	NP_036303	Q96FV3	TSN17_HUMAN		0	AATACGTGAGT	0.547
+	3	380	ED9_uc010jko.2_	NM_017510	NP_059980	Q9BVK6	TMED9_HUMAN	Lumenal (Potential).	0	CAATTCCACCA	0.562
+	5	1766	kz.1_Missense_M	NM_182594	NP_872400	Q8N9F8	ZN454_HUMAN	2H2-type 12.	3	AATGTAATAAAT	0.388
-	2	1013	h.3_Missense_M	NM_002406	NP_002397	P26572	MGAT1_HUMAN	enal (Potential).	1	CCGGCGGCACC	0.701
+	5	1950	e_Mutation_p.R41	NM_033549	NP_291027	Q8WV44	TRI41_HUMAN	30.2/SPRY.	0	CGTGAGGAAAA	0.582
+	3	447	P2L_uc011dim.1_	NM_001040274	NP_001035364	Q5T4T6	SYC2L_HUMAN		2	AGAAAGAGAGC	0.323
-	7	2280	.R705W|NEDD9_	NM_006403	NP_006394	Q14511	CASL_HUMAN		0	CTGCCGATCCT	0.517
-	3	577	1dip.1_Splice_Sit	NM_032744	NP_116133	Q96IZ2	CF105_HUMAN		0	TACAAACTGGAA	0.363
+	4	2526	EP1_uc011diq.1_	NM_002114	NP_002105	P15822	ZEP1_HUMAN		6	ATTCCCCCAAA	0.433
-	1	7		NM_030959	NP_112221	Q9UGF7	O12D3_HUMAN	ellular (Potential).	3	TTCTCCATTGCT	0.343
+	3	1230	_p.P263S|OR2H1_	NM_030883	NP_112145	Q9GZK4	OR2H1_HUMAN	ellular (Potential).	0	AAAAATCCGTAT	0.517
-	2	284	R1_uc003nmp.3_	NM_006398	NP_006389	O15205	UBD_HUMAN	Ubiquitin 1.	0	AAAGGTCATTAA	0.488
-	10	4339	C1_uc011dmp.1_	NM_014641	NP_055456	Q14676	MDC1_HUMAN	on with the PRKDC compl	4	TGACAGGTCGG	0.572
-	10	1351	_p.R463C|CCHCR	NM_019052	NP_061925	Q8TD31	CCHCR_HUMAN	Potential.	1	AGCACGGCTCA	0.652
-	8	919	_uc010juo.1_RN	NM_005452	NP_005443	O15213	WDR46_HUMAN	WD 3.	0	CAGCTGTAGCC	0.562
+	2	200	e_Mutation_p.G65	NM_152753	NP_689966	Q8IX30	SCUB3_HUMAN	lcium-binding (Potential).	1	GGACGGCAAAC	0.572
+	8	1639	_p.R414T|RNF8_u	NM_003958	NP_003949	O76064	RNF8_HUMAN		1	GCAAAGAGATT	0.373
+	15	2234		NM_001371	NP_001362				21	AAGTCCGGACG	0.368
+	14	3331		NM_032538	NP_115927	Q5TCY1	TTBK1_HUMAN		9	ATGGCCCGGCC	0.667
-	13	2123	yp.3_Missense_	NM_001098518	NP_001091988	Q8IZF2	GP116_HUMAN	ellular (Potential).	2	CTTACCAGCAG	0.393
+	7	652	_p.R191*|FBXO9_	NM_012347	NP_036479	Q9UK97	FBX9_HUMAN	F-box.	1	TCTTCCGATGG	0.453
-	3	1538	f.1_Missense_Mu	NM_021073	NP_066551	P22003	BMP5_HUMAN		2	ATCCCCTGTTT	0.348
-	59	8708	ht.2_Missense_M	NM_004370	NP_004361	Q99715	COCA1_HUMAN	n (COL2) with 1 imperfecti	9	TGCACCGTCTT	0.458
-	64	0851_10852		NM_014611	NP_055426	Q9NU22	MDN1_HUMAN		10	CAGGGGGAAC	0.495
-	9	3120	w.2_Missense_M	NM_021813	NP_068585	Q9BYV9	BACH2_HUMAN		6	TGGCTCCAAGC	0.642
-	5	1325	p.D362N|EPHA7_	NM_004440	NP_004431	Q15375	EPHA7_HUMAN	tential).|Fibronectin type-III	28	TCACATCGTTTC	0.498
-	9	1825	_p.A401V|ASCC3_	NM_006828	NP_006819	Q8N3C0	HELC1_HUMAN	binding 1.|ATP (Potential).	6	TAGGGGCACAA	0.398
-	10	2150	tx.1_Missense_M	NM_003931	NP_003922	Q92558	WASF1_HUMAN		0	ATGGTCGAATG	0.562
+	17	2033		NM_173560	NP_775831	Q8HWS3	RFX6_HUMAN		3	TCATTAACCAAG	0.527
+	12	2039		NM_020340	NP_065073	Q5TH69	BIG3_HUMAN	SEC7.	2	GTCCCTGGAAG	0.572
+	2	1234		NM_016217	NP_057301	Q9UBI9	HDC_HUMAN		0	CATGTGTTCAGA	0.607
+	16	4238	qf.2_Missense_Mu	NM_012454	NP_036586	Q8IVF5	TIAM2_HUMAN		4	ACAGTGACCTG	0.532
+	5	919	22A3_uc011efx.1_	NM_021977	NP_068812	O75751	S22A3_HUMAN		4	TTACTCGGAAG	0.428
+	13	1733	e.1_Missense_Mu	NM_031414	NP_113602	Q9BXU1	STK31_HUMAN		9	TCCTAGAGAAG	0.378
+	4	434	_p.E71K|ADCYAP	NM_001118	NP_001109	P41586	PACR_HUMAN	ellular (Potential).	1	TGGGTGAGATG	0.562
+	14	1562		NM_016616	NP_057700	Q8N427	TXND3_HUMAN	NDK 2.	3	AATACTGGAAAC	0.403
+	5	911	xo.2_Missense_M	NM_007252	NP_009183	P78424	PO6F2_HUMAN	-rich.|Gln-rich.	1	TCACGCCACCCA	0.468
+	2	846		NM_018697	NP_061167	Q9NS86	LANC2_HUMAN		2	TGGAAGAAGGG	0.398

-	5	1673		NM_033273	NP_150376	Q96JC4	ZN479_HUMAN	C2H2-type 11.	4	ATTCTTCACATGT	0.428	
+	4	1390		NM_001159522	NP_001152994	A8MUV8	ZN727_HUMAN	C2H2-type 9.	0	GCAAAAGCTTTAC	0.388	
+	5	983		NM_153363	NP_699194	Q8IYX0	ZN679_HUMAN		1	AGAGAAACCCTAC	0.408	
-	9	1623	dy.1_Missense_Mu	NM_012301	NP_036433	Q86UL8	MAGI2_HUMAN	PDZ 2.	11	CATCCGGAATCA	0.428	
-	5	366	uix.1_Missense_M	NM_018849	NP_061337	P21439	MDR3_HUMAN	rity).|ABC transmembrane t	6	GGAAAAGTTCAC	0.244	
+	4	1908		NM_181646	NP_857597	A4D1E1	Z804B_HUMAN		11	TTCAATGGCCTAC	0.418	
+	4	2384		NM_181646	NP_857597	A4D1E1	Z804B_HUMAN		11	AGAAAGGCAGTT	0.388	
+	68	10894	p.T3533I|TRRAP_	NM_003496	NP_003487	Q9Y4A5	TRRAP_HUMAN	PI3K/PI4K.	37	GGAGACCACCA	0.582	
+	14	2798	ZAN_uc003uwl.2_F	NM_003386	NP_003377	Q9Y493	ZAN_HUMAN	ate) (mucin-like domain).|E	11	AAAAACTCACCAT	0.502	
+	3	10033	C17_uc010lho.1_F	NM_001040105	NP_001035194	Q685J3	MUC17_HUMAN	9 X approximate tandem re	27	CTGACGGTACTAC	0.493	
-	20	3239	pg.3_RNA|DPY19L	NR_003561					0	CTTGACACTTGC	0.373	
-	50	8277	.2_Missense_Muta	NM_005045	NP_005036	P78509	RELN_HUMAN		19	TTACCTGAAGTTT	0.483	
-	29	3981	ykg.3_Missense_M	NM_017954	NP_060424	Q86UW7	CAPS2_HUMAN		2	GAGGCTGTGGCC	0.458	
-	2	2081		NM_005302	NP_005293	O15354	GPR37_HUMAN	lasmic (Potential).	3	CCTCGGGTACAG	0.433	
+	40	6802	a.3_Missense_Mut	NM_001458	NP_001449	Q14315	FLNC_HUMAN	adomain insert.	12	GCGGGGCGGGG	0.682	
-	15	1860		NM_004333	NP_004324	P15056	BRAF_HUMAN	rotein kinas_R603>I(2)|p.T	18290	GATTTCACTGTAC	0.368	
+	7	2428	p.1_Intron|uc011kt	NM_001130025	NP_001123497	A6NFQ2	F115C_HUMAN		0	ACCTTTGGTCAGT	0.617	
+	1	533		NM_001004685	NP_001004685	O95006	OR2F2_HUMAN	cellular (Potential).	4	ACATATCCTGTGA	0.498	
+	5	1198		NM_014141	NP_054860	Q9UHC6	CNTP2_HUMAN	1.|Extracellular (Potential).	11	TGCACGGAGAAC	0.388	
+	4	1084		NM_175571	NP_783161	Q8ND71	GIMA8_HUMAN		7	GTCCTCCTTGTGC	0.562	
+	11	1683	p.E463K|NOS3_u	NM_000603	NP_000594	P29474	NOS3_HUMAN	ction with NOSIP.	8	CATCAGGAGATGC	0.627	
-	5	416	xvs.1_Missense_M	NM_007349	NP_031375	Q6ZW49	PAXI1_HUMAN	ction with PA1 (By similarity	5	CTCCCCCATAGA	0.443	
-	2	232	n_p.S22L|SPAG11	NM_016512	NP_057596	Q08648	SG11B_HUMAN		0	TGAGACGATCCT	0.582	
-	3	660		NM_003155	NP_003146	P52823	STC1_HUMAN		4	ACTCTTCCTGCAC	0.537	
+	4	557	n_p.E34K|ADAMDE	NM_014479	NP_055294	O15204	ADEC1_HUMAN		2	GGAGAGGAAATT	0.453	
+	2	1839		NM_025069	NP_079345	Q9H7S9	ZN703_HUMAN		2	CACCCCTATGGC	0.517	
+	16	1766	DAM18_uc010lwx.2	NM_014237	NP_055052	Q9Y3Q7	ADA18_HUMAN	Extracellular (Potential).	6	TGAGATCAGATGC	0.368	
+	4	374		NM_032237	NP_115613	Q9H5K3	SG196_HUMAN	ical; (Potential).	0	TGCCTCGACCAC	0.572	
-	31	2907	ee.1_Missense_Mu	NM_003580	NP_003571	Q92636	FAN_HUMAN	WD 6.	1	CTGCTACACTGT	0.378	
-	1	272		NM_152418	NP_689631	Q8NA75	DC4L2_HUMAN		1	TCTGGACCTTTTT	0.502	
+	5	544		NM_022351	NP_071746	Q8N987	NECA1_HUMAN		1	GCAAAACAAAGA	0.308	
-	5	407		NM_005836	NP_005827	P52758	UK114_HUMAN		1	TAGCAGGAAAAT	0.274	
+	10	1639		NM_024915	NP_079191	Q6ISB3	GRHL2_HUMAN		3	AGAAAGGGAAA	0.468	
-	1	390	ype.2_Missense_M	NM_021021	NP_066301	Q13884	SNTB1_HUMAN	PH 1.	5	ACGCCGCAGCG	0.458	
-	13	3201	AM135B_uc003yva	NM_015912	NP_056996	Q49AJ0	F135B_HUMAN		9	GGACCCCATGATC	0.512	
+	20	3322		NM_001702	NP_001693	O14514	BAI1_HUMAN	lasmic (Potential).	8	CGGAACCGCCTC	0.657	
-	6	1253	nse_Mutation_p.R	NM_021061	NP_066405	P15622	ZN250_HUMAN	C2H2-type 7.	0	ACTGAGCGGTCG	0.577	
+	1	860	SK1B_uc011lrq.1_I	NM_138333	NP_612206	Q96E09	F122A_HUMAN		0	GAAACAGCAGCA	0.498	
-	2	759		NM_001163	NP_001154	Q02410	APBA1_HUMAN		1	CGCATTCATGGC	0.677	
+	3	923_924	e_Mutation_p.P12	NM_006200	NP_006191	Q92824	PCSK5_HUMAN	Catalytic.	3	ATGATCCCAAGTC	0.475	
-	6	545	nsf.2_Missense_M	NM_007001	NP_008932	Q76EJ3	S35D2_HUMAN	ical; (Potential).	0	AAGCCCCGAGAA	0.408	rs149450685
+	1	894		NM_001005235	NP_001005235	Q8NGR5	OR1L4_HUMAN	lasmic (Potential).	0	AGATATGAAAAGC	0.398	
+	13	1126	se_Mutation_p.E26	NM_001005373	NP_001005373	Q6UWE0	LRSM1_HUMAN	Potential.	0	TGCAGGAACAG	0.587	
-	1	876		NM_203434	NP_982258	Q5T953	IER5L_HUMAN	Ala-rich.	0	gcgggcggagaagcg	0.353	
+	3	832		NM_006059	NP_006050	Q9Y6N6	LAMC3_HUMAN	inin N-terminal.	3	CGTTTGGGGACG	0.592	
+	43	3786		NM_000093	NP_000084	P20908	CO5A1_HUMAN	le-helical region.	11	GAGACGGTCTCC	0.622	
-	16	1746	mez.1_Missense_	NM_001130969	NP_001124441	Q6X4W1	NELF_HUMAN		0	AAGTACGTCTCG	0.672	

+	10	1238	d.1_Missense_Mu	NM_002183	NP_002174	P26951	IL3RA_HUMAN	ellular (Potential).	3	AGGAGGAGGGC	0.667	
-	5	3341		NM_015419	NP_056234	Q9NR99	MXRA5_HUMAN		8	ACATCTCTTTCAT	0.458	
-	6	526	M9B_uc004csh.2_	NM_205849	NP_995321	Q8IZU0	FAM9B_HUMAN		0	CTAACACTTCTAT	0.318	
+	4	983	_p.W221*|MAGEB	NM_002363	NP_002354	P43366	MAGB1_HUMAN	MAGE.	0	GATCTGGAAATT	0.483	
-	15	1951	.D595N|RPGR_uc	NM_001034853	NP_001030025	Q92834	RPGR_HUMAN	Glu-rich.	1	cttttgaatcctctgctcc	0.179	
+	5	815	lhh.2_Missense_M	NM_005676	NP_005667	P98175	RBM10_HUMAN	RRM 1.	5	AGATCCGTGGC	0.607	
-	5	370	z.1_Missense_Mut	NM_175723	NP_783729	O60225	SSX5_HUMAN		0	AGATTCCCTGG	0.423	
+	5	652	_5'UTR|TBC1D25_	NM_002536	NP_002527	Q3MII6	TBC25_HUMAN		1	AGGTCCAACAA	0.582	
+	7	564	1_Missense_Muta	NM_006044	NP_006035	Q9UBN7	HDAC6_HUMAN	ne deacetylase 1.	4	ACAACCCAGTAC	0.502	
-	4	601	_p.T138I|FOXP3_	NM_014009	NP_054728	Q9BZS1	FOXP3_HUMAN		0	CCCCAGTGGCG	0.662	
-	23	3169		NM_001013742	NP_001013764	Q5KSL6	DGKK_HUMAN		2	TTACCCGATCTC	0.438	
+	2	1132		NM_005448	NP_005439	O95972	BMP15_HUMAN		2	ATTTTGTACAAG	0.463	
-	1	1		NM_001009616	NP_001009616	Q5MJ07	SPXN5_HUMAN		0	TTCCATGATTCTG	0.448	
-	5	2051	lsc.2_Missense_M	NM_001111125	NP_001104595	Q5JU85	IQEC2_HUMAN	Pro-rich.	3	GCTGGCGGTGG	0.632	
+	6	2479	_p.D461N|NHSL2_	NM_001013627	NP_001013649	Q5HYW2	NHSL2_HUMAN		0	AGTCCGACCTA	0.512	
-	22	2196	p.M707V|RPS6KA	NM_014496	NP_055311	Q9UK32	KS6A6_HUMAN		8	CAACCATTGCTC	0.403	rs145715341
-	7	759	o.2_Missense_Mu	NM_000061	NP_000052	Q06187	BTK_HUMAN		6	TTGGGGGAAGA	0.478	
-	4	1735	_p.S168*|MORF4L	NM_012286	NP_036418	Q15014	MO4L2_HUMAN		0	CCTGCGATTTCT	0.413	
-	5	1127	tron|TEX13A_uc0	NM_031274	NP_112564	Q9BXU3	TX13A_HUMAN		2	ATCAAAGGCCT	0.547	
+	11	1149	_uc010npc.1_Splic	NM_198465	NP_940867	Q7Z2Y5	NRK_HUMAN		14	TTTTTTAGGTCCC	0.413	
+	2	874	LDN2_uc004emt.	NM_020384	NP_065117	P57739	CLD2_HUMAN	ical; (Potential).	1	TGGCGGTAGCA	0.537	
+	13	2218	ntr.1_Missense_M	NM_019045	NP_061918	Q5JSH3	WDR44_HUMAN		5	GCAACGGCCAT	0.343	
+	5	401	P14_uc004esf.2_I	NM_178813	NP_848928	Q86UN6	AKA28_HUMAN		0	ACAGAAGTGTG	0.333	
+	2	105	e_Mutation_p.Y26	NM_006649	NP_006640	Q9BVJ6	UT14A_HUMAN		2	AAAAgactacctcttg	0.259	
+	6	744		NM_016024	NP_057108	Q9Y388	RBMX2_HUMAN	Lys-rich.	4	CAAATCCAGGA	0.557	
-	3	459	_Mutation_p.P77L|	NM_018388	NP_060858	Q9NUK0	MBNL3_HUMAN	Pro-rich.	0	TGGGAGGATTA	0.418	
-	8	1820_1821	_p.P567*|GPC3_u	NM_004484	NP_004475	P51654	GPC3_HUMAN		5	CCTTCGGAGTTG	0.495	
+	2	768		NM_001727	NP_001718	P32247	BRS3_HUMAN	ellular (Potential).	1	TCTTATCCTGTCT	0.348	
-	5	1312	.R227Q|FGF13_	NM_004114	NP_004105	Q92913	FGF13_HUMAN		3	CAGATCGGGAG	0.517	
-	3	582		NM_005362	NP_005353	P43357	MAGA3_HUMAN	MAGE.	0	GGCTCGATACTT	0.532	
+	2	993	Y3_uc010nvl.1_In	NM_005840	NP_005831	O43610	SPY3_HUMAN	PR.|Cys-rich.	0	TGAGAGCCTCC	0.582	
+	2	1001	Y3_uc010nvl.1_In	NM_005840	NP_005831	O43610	SPY3_HUMAN	PR.|Cys-rich.	0	CTCCTCGATTATG	0.592	
-	6	781	1_Missense_Muta	NM_030937	NP_112199	Q96S94	CCNL2_HUMAN	Cyclin-like 2.	3	GCGTCCGGGCA	0.478	
-	5	566	ie.2_Missense_Mu	NM_023018	NP_075394	O95544	NADK_HUMAN		0	GCTGGCGATGG	0.522	
-	9	1430	5_uc001amc.1_5'	NM_015557	NP_056372	Q8TDI0	CHD5_HUMAN	PHD-type 2.	12	CGGGTTGAGGC	0.517	
-	3	255	me.2_Missense_	NM_000983	NP_000974	P35268	RL22_HUMAN		0	ACGGTGATCTTG	0.542	
-	8	1859	.G357D|CLSTN1_	NM_001009566	NP_001009566	O94985	CSTN1_HUMAN	ellular (Potential).	1	GGGTGCCGTTG	0.622	
+	18	1954	_p.P330L|CLCN6_	NM_001286	NP_001277	P51797	CLCN6_HUMAN	c (By similarity).|CBS 1.	0	CTACCCGCACA	0.627	
+	1	151		NM_001080830	NP_001074299	O95522	PRA12_HUMAN		3	TTCATGGAGGCC	0.597	
+	1	1735		NM_006511	NP_006502	Q92681	RSCA1_HUMAN	UBA.	1	ATTGACCGCATT	0.468	
+	3	307	LCNKB_uc001ax	NM_000085	NP_000076	P51801	CLCKB_HUMAN		1	GGTCCGAGGTA	0.632	rs139676842
+	19	2044	ense_Mutation_p.	NM_000085	NP_000076	P51801	CLCKB_HUMAN	CBS 2.	1	TTCATTCCCTCT	0.602	rs144513133
+	2	1201		NM_000871	NP_000862	P50406	5HT6R_HUMAN	smic (By similarity).	1	ACGCCCAGGGG	0.537	
-	23	2147	GAP_uc001bew.2_	NM_002885	NP_002876	P47736	RPGP1_HUMAN		3	GTGATCGAGAG	0.692	
-	73	9777	d.2_Missense_Mu	NM_005529	NP_005520	P98160	PGBM_HUMAN	ike C2-type 18.	9	GCTTGGACCAG	0.632	
-	27	3512	d.2_Missense_Mu	NM_005529	NP_005520	P98160	PGBM_HUMAN	GF-like 5; second part.	9	TGCAGCGTTCAC	0.637	
-	14	1773	qd.2_Missense_M	NM_005529	NP_005520	P98160	PGBM_HUMAN	inin IV type A 1.	9	ACTCGTGCAGG	0.652	

+	13	1857	TC1_uc001bnp.1_	NM_015023	NP_055838	Q8N5D0	WDTC1_HUMAN		2	GGCCCGCTGC	0.582	
-	5	1040	_Mutation_p.R256	NM_004672	NP_004663	O95382	M3K6_HUMAN		9	GTCTCCGCTGC	0.562	
+	5	573	_p.W135*|GMEB1_	NM_006582	NP_006573	Q9Y692	GMEB1_HUMAN	SAND.	0	GACTGGAAGAG	0.428	
+	7	841	_p.A225T|GMEB1_	NM_006582	NP_006573	Q9Y692	GMEB1_HUMAN		0	TCACCGCTGCT	0.502	
+	5	1632	A_uc001bvm.2_I	NM_001040441	NP_001035531	Q96BR9	ZBT8A_HUMAN		0	TGGAAGCTGAA	0.463	
+	1	4075	.1_Intron|MACF1_	NM_015038	NP_055853	O94854	K0754_HUMAN	Ala-rich.|8.	0	AGCCCACCTCC	0.726	rs783822
-	13	2894		NM_020883	NP_065934	Q9P217	ZSWM5_HUMAN		0	ACCATCGTACC	0.542	
-	11	2610		NM_020883	NP_065934	Q9P217	ZSWM5_HUMAN		0	GTGAACCAGCG	0.527	
-	8	1123	_Mutation_p.G35	NM_000778	NP_000769	Q02928	CP4AB_HUMAN		4	GGCTCCATCAC	0.617	
-	2	708	se_Mutation_p.A4	NM_003189	NP_003180	P17542	TAL1_HUMAN		1	CGGCCGCGCGG	0.527	
-	5	669_670	5RL_uc001cwx.3_	NM_001031672	NP_001026842	Q6IPT4	NB5R5_HUMAN	-binding FR-type.	0	CTATCCCTCTGA	0.347	
-	3	2008_2009	_Intron|KANK4_u	NM_181712	NP_859063	Q5T7N3	KANK4_HUMAN		6	TCCTTCCCTGG	0.619	
+	13	2076	PR_uc009waq.2_I	NM_002303	NP_002294	P48357	LEPR_HUMAN	Fibronectin type-III 2.|WSX	1	TAATTGGAGCA	0.423	
-	12	2141	73_uc001dgi.3_Mi	NM_001002912	NP_001002912	Q5RHP9	CA173_HUMAN	Glu-rich.	5	TCAATTTCTAAGG	0.413	
+	3	382	2_5'UTR|CLCA4_	NM_012128	NP_036260	Q14CN2	CLCA4_HUMAN		2	AGGTAGAGATG	0.363	
-	9	1173	_p.P232S|CCBL2_	NM_001008661	NP_001008661	Q6YP21	KAT3_HUMAN		1	ACCTGGAAAAG	0.308	
-	1	76_77	T_uc010oug.1_5'U	NM_001918	NP_001909	P11182	ODB2_HUMAN		1	GCTTCCCCGCAT	0.579	
-	8	1552	_p.T424A|COL11A	NM_001854	NP_001845	P12107	COBA1_HUMAN	nhelical region.	12	TTTCTGTAATATC	0.338	
-	7	662	fm.1_Missense_M	NM_133181	NP_573444	Q8TE67	ES8L3_HUMAN	Pro-rich.	3	CCTTTCCATAG	0.597	
+	11	1190	t.2_Missense_Mut	NM_201653	NP_970615	Q9BZP6	CHIA_HUMAN		1	CCATTGATCTG	0.498	
-	5	1313		NM_001047980	NP_001041445	P0C2Y1	NBPF7_HUMAN	NBPF 1.	2	TTGAATAAGTGA	0.468	
+	2	302	1orf51_uc001euj.2	NM_144697	NP_653298	Q8N365	CA051_HUMAN		0	GTTCACGGCCC	0.602	
+	16	3230	.A1014T|SETDB1_	NM_001145415	NP_001138887	Q15047	SETB1_HUMAN	SET.	3	GCCGGGCTGGG	0.542	
-	3	1246		NM_001008536	NP_001008536	Q5QJ38	TCHL1_HUMAN		2	CTCTCCTCTCT	0.473	
-	2	1147_1148	e.1_Missense_M	NM_007113	NP_009044	Q07283	TRHY_HUMAN	repeats of R-R-E-Q-Q-L.|2	5	gcgcctcagctgctgc	0	
-	3	5990_5991		NM_001009931	NP_001009931	Q86YZ3	HORN_HUMAN	22	3	ACCACCCTGAG	0.604	
+	2	506		NM_005547	NP_005538	P07476	INVO_HUMAN	QEK]-[PLSQE]-[EQDV]- [	3	TGTTGGAGCTC	0.259	
-	2	754	SHC1_uc001ffx.2_	NM_183001	NP_892113	P29353	SHC1_HUMAN	PID.	2	CCAGGGCACGC	0.602	
-	6	947	|PKLR_uc001fka.3	NM_000298	NP_000289	P30613	KPYR_HUMAN		5	CTTCCGGACCC	0.602	
-	1	91	23E|ROBLD3_uc	NM_020131	NP_064516	Q9NRR5	UBQL4_HUMAN	biquitin-like.	2	CTCCTTGTCCTT	0.438	
+	3	1046	.2_Missense_Mut	NM_014655	NP_055470	Q96H78	S2544_HUMAN	Solcar 3.	1	CCAATCCCATG	0.562	
-	12	1319	sb.1_Missense_M	NM_178229	NP_839943	Q86VI3	IQGA3_HUMAN		6	TAGACGATGCAA	0.597	
+	1	194		NM_001004473	NP_001004473	Q8NGX5	O10K1_HUMAN	Name=2; (Potential).	1	TTGCCATCCTTT	0.488	
-	15	2193		NM_003126	NP_003117	P02549	SPTA1_HUMAN	Spectrin 7.	8	TGGCAACTTCA	0.443	
-	3	560	.2_Intron|SLAMF	NM_033438	NP_254273	Q96A28	SLAF9_HUMAN	.|Extracellular (Potential).	1	AGGCACCTTCC	0.527	
+	8	1624	lg.2_Missense_M	NM_021165	NP_066988	Q9C0B6	FAM5B_HUMAN		6	TCCTGGAACAG	0.587	
+	13	1532	pos.1_Missense_	NM_024420	NP_077734	P47712	PA24A_HUMAN	PLA2c.	3	CACACGAACCC	0.393	
-	2	1784	73_uc001gtb.2_I	NM_003783	NP_003774	O43825	B3GT2_HUMAN	enal (Potential).	1	AGGGGGTACAG	0.428	
-	7	2682	_Mutation_p.R80	NM_018136	NP_060606	Q8IZT6	ASPM_HUMAN		6	CTGACGTTCTC	0.328	
-	14	2305	_5'Flank|PLEKHA	NM_014935	NP_055750	Q9Y2H5	PKHA6_HUMAN		4	TCTTCCTCAGC	0.597	
-	3	1057	_p.M223I|LRRN2_	NM_006338	NP_006329	O75325	LRRN2_HUMAN	tracellular (Potential).	2	AGGTTCATGCC	0.607	
-	2	402	_p.V65M|LGTN_u	NM_006893	NP_008824	P41214	EIF2D_HUMAN		0	ACTCACGTACA	0.458	
+	4	827	2_uc009xch.2_Mis	NM_001877	NP_001868	P20023	CR2_HUMAN	xtracellular (Potential).	8	ATGAAGGGTGA	0.453	
-	11	2562	ic.2_Missense_M	NM_172362	NP_758872	O95259	KCNH1_HUMAN	lasmic (Potential).	5	GGATACGGGCG	0.662	
-	17	3849	kv.2_Missense_M	NM_206933	NP_996816	O75445	USH2A_HUMAN	tential).|Fibronectin type-III	26	TAACTTAAAGTC	0.423	
+	12	1666		NM_018060	NP_060530	Q9NSE4	SYIM_HUMAN		4	TTGGTGTATATC	0.363	
-	12	2057	BP2_uc010puz.1_	NM_001031685	NP_001026855	Q13625	ASPP2_HUMAN		3	GGCCGGACGG	0.532	

-	4	1384	9xes.2_Missense_	NM_003607	NP_003598	Q5VT25	MRCKA_HUMAN	rotein kinase.	11	GTTATTGTCATCC	0.294	
+	2	897		NM_020435	NP_065168	Q5T442	CXG2_HUMAN	cellular (Potential).	0	TGCGACCGTTCT	0.642	
+	89	19968	sr.1_Missense_Mu	NM_001098623	NP_001092093	Q5VST9	OBSCN_HUMAN	otein kinase 1.	28	GTGAGCGAAGCC	0.612	
+	92	20169	sr.1_Missense_Mu	NM_001098623	NP_001092093	Q5VST9	OBSCN_HUMAN	otein kinase 1.	28	GGGCCCGGCCT	0.701	
+	13	1678	_p.R492*|ACTN2_u	NM_001103	NP_001094	P35609	ACTN2_HUMAN	Spectrin 2.	5	GGGACCGACTG	0.383	
+	5	2683	ve.1_Missense_Mu	NM_020066	NP_064450	Q9NZ56	FMN2_HUMAN	Pro-rich.|FH1.	12	GGTCTGCTGGG	0.532	
+	9	1700	o.3_Missense_Mu	NM_152609	NP_689822	Q6PJW8	CNST_HUMAN		0	GTGACCGTATAC	0.502	
-	4	658	_p.P183A|TUBB8_	NM_177987	NP_817124	Q3ZCM7	TBB8_HUMAN		1	GGTGGGTGTGG	0.537	
-	3	520	_p.L121F|IL2RA_	NM_000417	NP_000408	P01589	IL2RA_HUMAN	cellular (Potential).	2	TGGAAGGCTCG	0.507	
+	3	423	gav.1_Missense_M	NM_032905	NP_116294	Q96I25	SPF45_HUMAN		0	ATGACCGGCAAA	0.512	
-	13	2540	o.2_Nonsense_Mu	NM_030569	NP_085046	Q86UX2	ITIH5_HUMAN		4	GTGTCGCTGGA	0.592	
+	6	1692	e_Mutation_p.R28	NM_019590	NP_062536	Q5T5P2	SKT_HUMAN		7	CATCCGGTCAG	0.498	
+	16	3759	n_p.S1084F|KIAA	NM_019590	NP_062536	Q5T5P2	SKT_HUMAN		7	CCTCCTCCTCAA	0.542	
+	4	1325		NM_020752	NP_065803	Q5T848	GP158_HUMAN	Name=1; (Potential).	8	TCATCTCCTTCC	0.522	
-	2	976	ense_Mutation_p.G	NM_020848	NP_065899	Q9P266	K1462_HUMAN	Pro-rich.	4	GCTCCTCCCCTA	0.597	
-	9	1286	tion_p.G385E|PAR	NM_019619	NP_062565	Q8TEW0	PARD3_HUMAN		1	GTTTTCCCGAG	0.517	
+	7	794		NM_052997	NP_443723	Q9BXX3	AN30A_HUMAN		9	CCTTGGCGGAAA	0.423	
+	7	1016		NM_052997	NP_443723	Q9BXX3	AN30A_HUMAN		9	AAATTACGAGTC	0.433	
-	6	2139	NF248_uc001izc.2	NM_021045	NP_066383	Q8NDW4	ZN248_HUMAN		1	TCATACGGCTTC	0.443	
-	1	2221		NM_002900	NP_002891	P10745	RET3_HUMAN	mate tandem repeats.|3.	2	GGCTGTGGAACA	0.627	
-	1	1687		NM_002900	NP_002891	P10745	RET3_HUMAN	mate tandem repeats.|2.	2	GGAGCTCCATGT	0.652	
-	1	1235		NM_002900	NP_002891	P10745	RET3_HUMAN	mate tandem repeats.|2.	2	GGCCGGCATTG	0.647	
-	24	2863	.1_Missense_Mut	NM_020987	NP_066267	Q12955	ANK3_HUMAN		19	CCAATTCCTTAAG	0.483	
-	18	2317	_p.R703*|ANK3_u	NM_020987	NP_066267	Q12955	ANK3_HUMAN	ANK 20.	19	TCACTCGATCTT	0.522	
-	8	1915	jlk.2_Missense_M	NM_014836	NP_055651	O94844	RHBT1_HUMAN	BTB 2.	1	CTCCATCGTCCA	0.527	rs139669589
+	2	1515_1516	jmx.3_Intron|CTNN	NM_178011	NP_821079	Q86VH5	LRRT3_HUMAN	lar (Potential).|LRRCT.	3	TTGCTCCCTTGT	0.401	
+	3	957	oy.2_Intron|STOX1	NM_001130161	NP_001123633	Q6ZVD7	STOX1_HUMAN		2	GGAGCACCACAT	0.458	
+	6	786	_Mutation_p.Q203	NM_004922	NP_004913	P53992	SC24C_HUMAN		3	ACTCCCCAGCGA	0.607	
-	6	1634	_p.V146I|MMRN2	NM_024756	NP_079032	Q9H8L6	MMRN2_HUMAN		1	GGATGACGTCCA	0.647	
+	4	1721	35A_uc001kej.3_5	NM_019054	NP_061927	Q86V20	FA35A_HUMAN		4	TTGGGAGTTATT	0.328	
-	1	2137		NR_002319					0	CATTATCCAGTG	0.537	
+	29	6876	jm.2_Missense_Mu	NM_016341	NP_057425	Q9P212	PLCE1_HUMAN	s-associating 1.	3	CATTCCAGAGAG	0.373	
+	8	1228	qny.1_Missense_M	NM_000769	NP_000760	P33261	CP2CJ_HUMAN		6	GACCCTCGTCAC	0.393	rs17879685
-	9	1491		NM_032211	NP_115587	Q96JB6	LOXL4_HUMAN	SRCR 4.	5	CGCTCCCCCAG	0.637	
+	19	2623	_p.A795T|GBF1_uc	NM_004193	NP_004184	Q92538	GBF1_HUMAN	SEC7.	2	GGGGAAGCACCA	0.547	
+	2	337	se_Mutation_p.T47	NM_017787	NP_060257	Q9NX94	OPA1L_HUMAN		1	TGACACAGGAC	0.438	rs79433636
-	38	4955	xxq.2_Missense_M	NM_025145	NP_079421	Q8NDM7	WDR96_HUMAN		0	AGTCAGTTTAGA	0.328	
-	9	1212	_p.A357V|AFAP1L	NM_001001936	NP_001001936	Q8N4X5	AF1L2_HUMAN		2	CTGAAGCCGAC	0.527	
+	1	157		NM_181840	NP_862823	Q7Z418	KCNKI_HUMAN		1	GTGGCAGCAGAT	0.567	
+	15	8353	ACC2_uc001lfz.2_	NM_206862	NP_996744	O95359	TACC2_HUMAN		10	GAGCCCGACTTA	0.542	
+	18	2223	T1_uc009xzz.1_M	NM_007329	NP_015568	Q9UGM3	DMBT1_HUMAN		7	CCAGTCCCGGT	0.522	
-	6	1322	ZD1_uc010qty.1_	NM_022034	NP_071317	Q86UP6	CUZD1_HUMAN	llular (Potential).|ZP.	2	CTTTACCTTTCTG	0.299	
-	3	497	_p.E223*|C10orf9	NM_001004298	NP_001004298	Q96M02	CJ090_HUMAN		2	CTCCTCTTTGG	0.647	
+	2	376	ybe.2_Missense_	NM_138499	NP_612508	Q6NUJ5	PWP2B_HUMAN	Pro-rich.	0	GCCCCCGTACC	0.751	
+	15	2817	_p.S874F|KNDC1_	NM_152643	NP_689856	Q76NI1	VKIND_HUMAN		2	CCATTTCCGAGA	0.537	
-	10	1034	_p.S367N|ADAM8_uc009ybi.2_Missense_Mutation_p.S			P78325	ADAM8_HUMAN		3	CCAATGCTGCCC	0.682	
-	9	655	YCE1_uc009ybn.2_	NM_001143764	NP_001137236	Q8N0S2	SYCE1_HUMAN	Potential.	1	AAATCTCCTTTG	0.522	

-	8	867	_p.A169T|OSBPL	NM_020896	NP_065947	Q9H0X9	OSBL5_HUMAN	PH.	3	CAGGGCGTCCA	0.701	
+	1	766	_uc001mam.1_Int	NM_001004757	NP_001004757	Q8NH59	O51Q1_HUMAN	Name=6; (Potential).	1	TACATTCCCATG	0.517	
-	1	737		NM_001146033	NP_001139505	P0C7T3	O56A5_HUMAN	lasmic (Potential).	0	AGTGGGAACCA	0.473	
-	1	155		NM_001005173	NP_001005173	Q8NGH7	O52L1_HUMAN	ellular (Potential).	2	AATCCCTACCA	0.463	
-	3	1568	p.G422D|ZNF214_	NM_013249	NP_037381	Q9UL59	ZN214_HUMAN	2H2-type 6.	1	GTAAAGCCTTTA	0.413	
+	1	1004		NM_014469	NP_055284	O75526	HNRGT_HUMAN	g/Gly/Pro-rich.	0	GGGATCATCTG	0.662	
-	4	650	P3_uc010rbu.1_In	NM_020645	NP_065696	Q9NQ35	NRIP3_HUMAN		0	CCAGGCGGAGG	0.542	
-	19	2545	e_Mutation_p.S79	NM_020974	NP_066025	Q9NQ36	SCUB2_HUMAN	CUB.	2	TTTGGGGATTCA	0.547	
-	3	541	se_Mutation_p.G9	NM_015213	NP_056028	Q6IQ26	DEN5A_HUMAN	UDENN.	1	CCATTCCTACTG	0.393	
-	1	1274	TL4_uc001mjo.2_	NM_177559	NP_808227				0	GCTGACGGGCG	0.567	rs74507390
+	3	1667		NM_032867	NP_116256	Q6ZW33	MICLK_HUMAN	Poly-Pro.	1	ctcctcctcctcctcc	0.458	
+	15	1698_1699	.2_Missense_Muta	NM_001178	NP_001169	O00327	BMAL1_HUMAN	PAC.	0	AAGGAAGTAGA	0.361	
+	7	985	HA_uc009yho.2_	NM_005566	NP_005557	P00338	LDHA_HUMAN		3	CAGTGCTTATGA	0.388	
+	16	1714_1715	23LK>F*|PRMT3_	NM_005788	NP_005779	O60678	ANM3_HUMAN		0	GCCTTGAAAGG	0.366	
+	9	1770	ic.2_Nonsense_	NM_004211	NP_004202	Q9Y345	SC6A5_HUMAN		4	TGCTACAGGTA	0.458	
-	4	1753		NM_003654	NP_003645	O43916	CHST1_HUMAN	enal (Potential).	5	GGAAGCGCCA	0.672	
+	7	1680		NM_005456	NP_005447	Q9UQF2	JIP1_HUMAN	SH3.	4	GACACGAAGAC	0.602	
+	12	1716	Site_p.R535_splic	NM_152312	NP_689525	Q8N3Y3	LARG2_HUMAN		3	CCTCAGGGCCT	0.642	
-	17	2182	y.2_Missense_Mu	NM_004476	NP_004467	Q04609	FOLH1_HUMAN	ellular (Probable).	3	CAATTTCTGTAA	0.269	
+	1	785		NM_001005275	NP_001005275	Q8NGL6	O4A15_HUMAN	lasmic (Potential).	2	GAAACGAAAAG	0.438	
+	12	1181		NM_002559	NP_002550	P56373	P2RX3_HUMAN	lasmic (Potential).	0	AAATCGCGGCT	0.547	
+	9	2251	sense_Mutation_p	NM_001085458	NP_001078927	O60716	CTND1_HUMAN	ARM 5.	6	CATTTTCATTGTT	0.453	
-	1	644		NM_001005469	NP_001005469	Q8NH48	OR5B3_HUMAN	Name=5; (Potential).	0	TGTAGGATATC	0.403	
+	3	251	npb.2_Missense_	NM_148975	NP_683876	Q96JQ5	M4A4A_HUMAN	ical; (Potential).	0	GCATGGGAATA	0.428	
+	10	2151	_Mutation_p.R654	NM_178031	NP_821174	Q24JP5	T132A_HUMAN	By similarity).|Extracellular	1	GAGCCGGGGCA	0.662	
+	5	930		NR_002775					0	AGAACGCCATG	0.567	
+	3	665	o.1_Missense_Mu	NM_004265	NP_004256	O95864	FADS2_HUMAN	ical; (Potential).	2	CTCTCAGGTGA	0.567	
+	4	951	nw.1_Missense_M	NM_001040694	NP_001035784	Q9NQS7	INCE_HUMAN		1	CGGGACGGGG	0.622	
-	12	1767	t.1_Missense_Mut	NM_153265	NP_694997	Q32P44	EMAL3_HUMAN	WD 4.	1	GCTCCGCCCCC	0.542	
+	2	340	ense_Mutation_p.	NM_020155	NP_064540	Q96N19	G137A_HUMAN	ellular (Potential).	1	GCCTGCTGCCG	0.622	
-	30	3926		NM_017525	NP_059995	Q6DT37	MRCKG_HUMAN	CNH.	4	GGCCACGAGAC	0.652	
+	6	1348	_p.S394C|SIPA1_	NM_006747	NP_006738	Q96FS4	SIPA1_HUMAN	Rap-GAP.	0	GCACTCCCTCT	0.542	
+	5	835	x.1_Missense_Mu	NM_001134775	NP_001128247	Q9H0B6	KLC2_HUMAN	TPR 1.	0	CCCGGCTCCGC	0.632	
+	7	698	S_uc001ois.2_R	NM_005125	NP_005116	O14618	CCS_HUMAN	xide dismutase-like.	0	TCACAGGGAAC	0.602	
-	2	707		NM_005117	NP_005108	O95750	FGF19_HUMAN		1	CTTGATCTCCA	0.657	
-	22	5329	tation_p.D1156N|u	NM_012309	NP_036441	Q9UPX8	SHAN2_HUMAN		5	TAGATCCCCAG	0.562	
+	25	2918	sg.2_Missense_M	NM_001567	NP_001558	O15357	SHIP2_HUMAN		4	AGAGGCCTCCT	0.632	
-	5	883	_5'UTR|ARAP1_uc	NM_001040118	NP_001035207	Q96P48	ARAP1_HUMAN		1	CTCATCGTAGT	0.657	
+	9	1142	e_Mutation_p.P3	NM_152222	NP_689408	Q969Z4	TR19L_HUMAN	lasmic (Potential).	1	TAACCCGACCA	0.652	
-	19	3660		NM_015531	NP_056346	Q4AC94	C2CD3_HUMAN		7	CTCACGATGCT	0.433	
+	1	278		NM_003251	NP_003242	Q92748	THRSP_HUMAN		1	GGCAGGCAGCG	0.607	
+	23	12341	i.3_Missense_Mut	NM_001008781	NP_001008781	Q8TDW7	FAT3_HUMAN	GF-like 4; calcium-binding	5	TGTGAGAACGG	0.627	
+	4	827		NM_001098672	NP_001092142	Q6MZM0	HPHL1_HUMAN	e 2.|Extracellular (Potential	3	TGGATCGAGAG	0.383	
-	2	691	hp.2_Missense_M	NM_025208	NP_079484	Q9GZP0	PDGFD_HUMAN	CUB.	2	AGATATCATTTTC	0.383	
+	3	627_628	piv.2_Missense_M	NM_000829	NP_000820	P48058	GRIA4_HUMAN	ellular (Potential).	8	AAGCTCCTTTTA	0.391	
-	6	1250	xd.1_Missense_M	NM_152315	NP_689528	Q8N323	FA55A_HUMAN		0	CCCGAGGGATA	0.433	
+	7	1404	2_Missense_Muta	NM_015157	NP_055972	Q86UU1	PHLB1_HUMAN		0	GCCCCCGGCTG	0.657	

-	2	1064	P2_uc001pwn.3_In	NM_004205	NP_004196	O75604	UBP2_HUMAN		4	CATGCCGTCTC	0.647	
+	8	1964		NM_025004	NP_079280	Q0P6D6	CCD15_HUMAN		2	AAGGTGTTCTT	0.423	
+	2	403	_p.R30H|KCNJ5_	NM_000890	NP_000881	P48544	IRK5_HUMAN	smic (By similarity).	1	GGCCCGCGATT	0.577	rs142140011
+	4	1136		NM_052875	NP_443107	Q4G0F5	VP26B_HUMAN		0	TGACACGATAG	0.532	
+	13	1536	1L2_uc009zdg.1_	NM_138342	NP_612351	Q8IW92	GLBL2_HUMAN		3	ATGATCGGGGG	0.542	
-	3	229	_p.R56C|MLF2_u	NM_005439	NP_005430	Q15773	MLF2_HUMAN		1	CCGGCGGCTGG	0.517	
-	1	312	lutation_p.Y34*|E	NM_001144831	NP_001138303	Q99623	PHB2_HUMAN	transcriptional repression.	3	ACACCGTAGGC	0.716	
-	1	271		NM_020634	NP_065685	Q9NR23	GDF3_HUMAN		6	CCCGCGGACGC	0.493	
+	1	81		NM_199286	NP_954980	Q6W0C5	DPPA3_HUMAN		0	CCGATGGACCC	0.493	
-	6	799		NM_014358	NP_055173	Q9ULY5	CLC4E_HUMAN	ellular (Potential).	1	TCAAAGGATTTAT	0.418	
-	4	552	M_uc009zgk.1_5'U	NM_000014	NP_000005	P01023	A2MG_HUMAN		5	CAACACGAAATT	0.393	
+	15	2248	ense_Mutation_p.	NM_004570	NP_004561	O75747	P3C2G_HUMAN		21	TGCATACCATTTT	0.413	
+	9	1157	zip.2_Missense_M	NM_017435	NP_059131	Q9NYB5	SO1C1_HUMAN	ellular (Potential).	7	AAGATCCCCAG	0.388	
-	9	1457		NM_021957	NP_068776	P54840	GYS2_HUMAN		2	TTTTTTCCAAAC	0.294	
+	19	2607	nh.1_Nonsense_M	NM_198578	NP_940980	Q5S007	LRRK2_HUMAN		24	CTAATTTAAGGA	0.318	
-	2	121		NM_025003	NP_079279	P59510	ATS20_HUMAN		19	CTACTTCGTAGG	0.567	
+	4	434	_uc001rny.3_Intro	NM_001114182	NP_001107654	Q9NWZ3	IRAK4_HUMAN	Death.	0	TGCTCCCAGGT	0.393	
-	11	2026	_p.N265I|SFRS2I	NM_004719	NP_004710	Q99590	SCAFB_HUMAN		0	TCTTCATTAACCA	0.353	
-	19	3805	Y6_uc001rsi.3_M	NM_015270	NP_056085	O43306	ADCY6_HUMAN	lasmic (Potential).	0	CCTGATCGTAGG	0.552	
+	13	1896	n_p.V577I|TROAP	NM_005480	NP_005471	Q12815	TROAP_HUMAN	ate tandem repeats.|Cys-ri	1	CTTGAGGTACCT	0.597	
+	2	581	nf.1_Missense_Mu	NM_005556	NP_005547	P08729	K2C7_HUMAN	Rod.|Coil 1B.	0	GGTCAGCTTGAG	0.622	
-	4	860		NM_004693	NP_004684	O95678	K2C75_HUMAN	oil 1B.|Rod.	0	GATCTCCTCGG	0.483	
-	1	408	nh.2_Missense_M	NM_000424	NP_000415	P13647	K2C5_HUMAN	ead.|Gly-rich.	0	CTGAAGCTGCCA	0.348	
-	9	1622		NM_175053	NP_778223	Q7RTS7	K2C74_HUMAN	Tail.	2	GCTTTCCTTGCT	0.627	
-	11	1710	_Mutation_p.R54	NM_000889	NP_000880	P26010	ITB7_HUMAN	epeats.|Extracellular (Pote	8	TGCAGCGTCCAC	0.622	rs61730604
+	2	458		NM_021191	NP_067014	Q9HD90	NDF4_HUMAN		4	GGGCTCCCAAA	0.413	
-	2	228	tion_p.R61H|TME	NM_001130963	NP_001124435	O14524	T194A_HUMAN		0	CTGGCACGCTTT	0.388	
+	8	1693	o.2_Missense_Mu	NM_014903	NP_055718	Q8IVL0	NAV3_HUMAN		17	GATCCCTAAGG	0.423	
+	3	731	zm.1_Missense_M	NM_024560	NP_078836	Q9H6R3	ACSS3_HUMAN		4	GATCATGTAAAG	0.373	
-	48	6972	q.2_Missense_Mu	NM_025114	NP_079390	O15078	CE290_HUMAN	Potential.	7	CTTTACGAAGCC	0.313	
+	12	1994	ztx.2_Missense_M	NM_139319	NP_647480	Q8NDX2	VGLU3_HUMAN	lasmic (Potential).	3	AGAAGGAATGG	0.448	
+	34	4636	l.1_RNA|ACACB_	NM_001093	NP_001084	O00763	ACACB_HUMAN		8	GGATGCGTAACT	0.552	
+	35	4824	l.1_RNA|ACACB_	NM_001093	NP_001084	O00763	ACACB_HUMAN		8	GGCTGCTCCTG	0.607	
-	7	974	TD10_uc001toj.1_	NM_031954	NP_114160	Q9H3F6	BACD3_HUMAN		0	CACGCGCTCGA	0.716	
-	54	8893		NM_001109662	NP_001103132				2	CGATGGCGTCAC	0.687	
-	29	4385		NM_001109662	NP_001103132				2	AGGAGGGGACA	0.567	
-	28	4908		NM_000620	NP_000611	P29475	NOS1_HUMAN		7	TCACTTCGTACG	0.488	
+	12	1684		NM_194286	NP_919262	A7MD48	SRRM4_HUMAN		2	CCTTCAGGGAGC	0.657	
+	74	12798	fu.3_Missense_M	NM_207437	NP_997320	Q8IVF4	DYH10_HUMAN	Potential.	6	TCAAAGGGTGA	0.532	
+	40	7387	.P2450L|EP400_u	NM_015409	NP_056224	Q96L91	EP400_HUMAN		12	TGAATCCCTTTC	0.388	
-	16	1308	_p.G289E|TPTE2_	NM_199254	NP_954863	Q6XPS3	TPTE2_HUMAN	hatase tensin-type.	0	TCTACTCCCTGA	0.368	
-	3	707	vo.2_Missense_M	NM_001142296	NP_001135768	Q8N0X7	SPG20_HUMAN		0	GGAGTTGAGGTG	0.453	
-	11	2938	wz.2_Missense_M	NM_025138	NP_079414	Q86XN7	CM023_HUMAN	Ser-rich.	5	CAATGGGAGTGG	0.438	
-	11	2032	wz.2_Missense_M	NM_025138	NP_079414	Q86XN7	CM023_HUMAN		5	GGACCGTGGTG	0.542	
-	11	1348	Missense_Mutatio	NM_001268	NP_001259	O95199	RCBT2_HUMAN	RCC1 5.	5	CCTGCGTCTTG	0.577	
+	7	731		NM_001846	NP_001837	P08572	CO4A2_HUMAN		6	CACAGGGGCCC	0.672	
+	5	1062	|POTEG_uc010ah	NM_001005356	NP_001005356	Q6S5H5	POTEG_HUMAN		1	ATCTATCTGGAC	0.358	

-	15	2287_2288	p.D628N|CHD8_u	NM_020920	NP_065971	Q9HCK8	CHD8_HUMAN		10	GAGATCCCCAAA	0.421	
-	20	2493		NM_002471	NP_002462	P13533	MYH6_HUMAN	IQ.	4	CACCTGCGTTCC	0.483	
+	3	629		NM_025081	NP_079357	Q9P2P1	NYNRI_HUMAN		3	TCTGCTGGAGCA	0.632	
+	1	240		NM_005249	NP_005240	P55316	FOXG1_HUMAN		4	TGATCCCCAAGT	0.393	
-	11	2785	IH5_uc001xfy.2_3'	NM_139318	NP_647479	Q8NCM2	KCNH5_HUMAN	nbly) (By similarity).|Cytopla	9	TGACTTCCTGCA	0.522	
-	3	887	p.P140L|ESR2_uc	NM_001437	NP_001428	Q92731	ESR2_HUMAN	Modulating.	3	GAACCTGGACCA	0.483	
-	13	1967	s.2_Missense_Mu	NM_000347	NP_000338	P11277	SPTB1_HUMAN	Spectrin 4.	11	CAGAGTCGTTTG	0.557	
+	8	1012_1013		NM_152443	NP_689656	Q96NR8	RDH12_HUMAN		1	TGCACCCAGGC	0.634	rs104894476
+	27	5377	p.P1533L|PCNX_	NM_014982	NP_055797	Q96RV3	PCX1_HUMAN		1	GTGAACCTGGCC	0.453	
+	2	351		NM_006399	NP_006390	Q16520	BATF_HUMAN	Basic motif.	1	AAAAATCGTATTG	0.522	
-	13	2166	wc.1_Missense_M	NM_007039	NP_008970	Q16825	PTN21_HUMAN		4	GCCACGGGCAGG	0.682	
+	37	6039	ybs.1_Missense_M	NM_020818	NP_065869	Q9P2D8	UNC79_HUMAN		17	AAGAATTTACCAG	0.418	
+	2	246	ch.2_Missense_M	NM_023112	NP_075601	Q96DC9	OTUB2_HUMAN		0	TTTACCGGAGGA	0.453	rs144803702
-	3	890		NM_001080451	NP_001073920	Q86U17	SPA11_HUMAN		1	GGAGGACCAGC	0.537	
+	7	1486	AIP2_uc010txz.1_	NM_006291	NP_006282	Q03169	TNAP2_HUMAN		1	GCTGGGCCCCC	0.632	
+	5	508	_Mutation_p.E158	NM_024071	NP_076976	Q9BQ24	ZFY21_HUMAN		0	AATCGAAATTGTA	0.498	
+	1	1169		NM_018958	NP_061831	Q9NZP6	CO002_HUMAN		8	CGAGCTCCTGCT	0.612	
+	3	559	p.G118R|APBA2_	NM_005503	NP_005494	Q99767	APBA2_HUMAN		0	TGCAACGGGGAG	0.652	
-	27	4456	se_Mutation_p.S13	NM_002420	NP_002411	Q7Z4N2	TRPM1_HUMAN	lasmic (Potential).	4	CCCCGGGAATAG	0.453	
+	17	2689	_Mutation_p.S581	NM_001013703	NP_001013725	Q9P2K8	E2AK4_HUMAN	otein kinase 2.	4	CTGACAGCAAAC	0.353	
+	26	7062	bt.1_Missense_Mu	NM_170589	NP_733468	Q8NG31	CASC5_HUMAN	ation and for interaction wit	5	AATCACGTTGGG	0.323	
+	19	2766		NM_006293	NP_006284	Q06418	TYRO3_HUMAN	lasmic (Potential).	6	GACTGTCGGTAC	0.647	
+	3	395	.1_Intron|MGA_uc	NM_001164273	NP_001157745	Q8IWI9	MGAP_HUMAN		12	TCAGTACTGTCA	0.522	
-	15	1744	_p.E54K|PLA2G4	NM_001080490	NP_001073959	Q3MJ16	PA24E_HUMAN	PLA2c.	0	ACCCACCGATGT	0.617	
+	1	556	0udg.1_Intron|CA	NM_000070	NP_000061	P20807	CAN3_HUMAN	alpain catalytic.	1	CCGGATGAGACC	0.478	
+	7	954	3_uc010bfc.1_Spli	NM_014547	NP_055362	Q9NYL9	TMOD3_HUMAN		1	CTACTGTAAGTAA	0.388	
+	1	2164		NM_001080534	NP_001074003	Q8NB66	UN13C_HUMAN	p.P722P(1)	7	TCTTCTCCATGCC	0.408	
+	19	5077		NM_001080534	NP_001074003	Q8NB66	UN13C_HUMAN	MHD1.	7	CCTTTTGTCATG	0.348	
-	9	3907	X7_uc002adn.1_M	NM_022841	NP_073752	Q2KHR2	RFX7_HUMAN		0	TGGAATCGATCA	0.413	
+	3	298	X5_uc010bid.1_M	NM_024505	NP_078781	Q96PH1	NOX5_HUMAN	nal regulatory region; intera	2	ATGGCAGCCCCA	0.552	
-	15	2687	p.L333F|MYO9A_	NM_006901	NP_008832	B2RTY4	MYO9A_HUMAN		3	ACTTTTCAAAATT	0.348	
+	4	1424	jg.2_Missense_Mu	NM_001130136	NP_001123608	Q6UXK2	ISLR2_HUMAN	lar (Potential).|LRRCT.	0	TGCAGGGGGTG	0.731	
+	4	722	C33_uc002axp.2_	NM_025055	NP_079331	Q8N5R6	CCD33_HUMAN	C2.	5	GTGATCCTCAAG	0.448	
+	21	3640	.R1139Q|ADAMTS	NM_207517	NP_997400	P82987	ATL3_HUMAN		27	GTGGCGGGGCA	0.552	rs148037443
-	3	440	10upl.1_Translatio	NM_001012338	NP_001012338	Q16288	NTRK3_HUMAN	cellular (Potential).	281	TTGAGCGTGTGA	0.443	rs147992979
-	9	1516	p.R401Q|PCSK6_	NM_002570	NP_002561	P29122	PCSK6_HUMAN	Catalytic.	2	ATTTTTCGCTCA	0.532	
+	1	780		NM_001001674	NP_001001674	Q8NGB8	O4F15_HUMAN	cellular (Potential).	0	CACATGGCCTTC	0.423	
+	5	955	_Missense_Mutati	NM_002434	NP_002425	P29372	3MG_HUMAN		2	GACCGCGAGCTC	0.637	
-	4	704	M8A_uc002cgv.3_	NM_021259	NP_067082	Q9HCN3	TMM8A_HUMAN	cellular (Potential).	3	ATGATGGAAATC	0.667	
+	2	694	_p.A198T|PIGQ_u	NM_148920	NP_683721	Q9BRB3	PIGQ_HUMAN		1	GTGGAGGCCAG	0.667	
+	12	1451	ge.1_Missense_Mu	NM_001761	NP_001752	P41002	CCNF_HUMAN		2	GCTGCCGCAGCC	0.667	
+	13	8644		NM_016333	NP_057417	Q9UQ35	SRRM2_HUMAN	r-rich.|Arg-rich.	4	GAGCGTCGCCGT	0.642	
+	5	849	MEN2_uc010bsx.2	NM_172229	NP_757384	Q8NCW0	KREM2_HUMAN	ular (Potential).|WSC.	2	TGGCCCGGGGA	0.622	
+	14	1967	p.A327T|A2BP1_	NM_018723	NP_061193	Q9NWB1	RFOX1_HUMAN		0	ACTGCCGCTGCC	0.498	rs139929599
-	11	1355	se_Mutation_p.L28	NM_003470	NP_003461	Q93009	UBP7_HUMAN		3	CCTGTAAGCCATG	0.363	
-	13	3478	uyn.1_Missense_	NM_001134407	NP_001127879	Q12879	NMDE1_HUMAN	lasmic (Potential).	45	ACATAGTTATTGA	0.478	
+	8	1161	ssense_Mutation_	NM_024847	NP_079123	Q7Z402	TMC7_HUMAN	lasmic (Potential).	3	GAATGCGGCAGA	0.398	

+	9	1419	ssense_Mutation_	NM_024847	NP_079123	Q7Z402	TMC7_HUMAN	lasmic (Potential).	3	TCATCCGCTATG	0.343	rs150991752
-	5	1189		NM_001012991	NP_001013009	Q1ED39	CP088_HUMAN	th ZFP106 (By similarity).	0	GGGGCGGCTGA	0.567	
-	9	1238	_p.P343L|ACSM2	NM_182617	NP_872423	Q68CK6	ACS2B_HUMAN		5	TTTCTGGAAGA	0.527	
-	13	2072	31_uc010bxm.2_5	NM_020718	NP_065769	Q70CQ4	UBP31_HUMAN		10	TCCACGGGGAC	0.562	
-	22	3050	p.2_Missense_Mu	NM_033266	NP_150296	Q76MJ5	ERN2_HUMAN	lasmic (Potential).	6	TGAGTCTGGCG	0.642	
+	14	1764	me.2_Missense_M	NM_212535	NP_997700	P05771	KPCB_HUMAN	rotein kinase.	9	CCGTGGATTGG	0.458	
-	32	4932	u.2_Missense_Mu	NM_001520	NP_001511	Q12789	TF3C1_HUMAN		5	TGCTCCGGCGC	0.602	rs142762967
-	6	872	'Flank|RNF40_uc0	NM_001014979	NP_001014979	A1A4V9	CP093_HUMAN		0	AGGCCGCTGTG	0.542	
-	25	3931	C11_uc002efh.1_	NM_033151	NP_149163	Q96J66	ABCCB_HUMAN	r 2.|Cytoplasmic (Potential)	6	CCATGGGCTCC	0.597	
-	15	1679	ge.1_Splice_Site_	NM_013263	NP_037395	Q9NPI1	BRD7_HUMAN		0	ACTTACCTTCA	0.443	
-	2	779_780		NM_024336	NP_077312	P78415	IRX3_HUMAN		0	GTACTGGCCATA	0.678	
-	5	764		NM_013242	NP_037374	Q9Y6A4	CP080_HUMAN		0	CCGTCGGATGC	0.483	
-	2	980	_Missense_Mutati	NM_033309	NP_171608	Q6UX72	B3GN9_HUMAN	enal (Potential).	0	CGTCGGGGCAG	0.577	
-	14	2271	33922_uc010vms.1_RNA						0	ggggaggggagggg	0.498	
-	13	2432	_p.K259N|ADAMT	NM_199355	NP_955387	Q8TE60	ATS18_HUMAN	Cys-rich.	18	TAGGGTTTCCA	0.378	
+	2	404		NM_020927	NP_065978	Q9HCJ6	VAT1L_HUMAN		1	TGCCAGGATTT	0.438	
+	10	1210	RISPLD2_uc002fi	NM_031476	NP_113664	Q9H0B8	CRLD2_HUMAN	LCCL 1.	0	GCCAGTCGTCTA	0.532	
-	2	400		NM_198491	NP_940893	Q6ZTR7	FA92B_HUMAN		1	CTGCCGGTAAT	0.657	
-	7	1167		NM_003486	NP_003477	Q01650	LAT1_HUMAN		0	TGGATCATGGA	0.657	
-	16	1770	_Site_p.E336_splic	NM_021962	NP_068781	Q12979	ABR_HUMAN		1	AACTCCTGGGG	0.562	
+	6	670	_Mutation_p.G78S|	NM_001383	NP_001374	Q9BZG8	DPH1_HUMAN		1	TCCTGGGCTGC	0.582	
-	16	3789	v.1_Missense_Mu	NM_017575	NP_060045	Q86US8	EST1A_HUMAN		4	AACAAAGGTCTG	0.582	
-	5	744	_Mutation_p.R13	NM_002561	NP_002552	Q93086	P2RX5_HUMAN	ellular (Potential).	0	TCTCCGCAGGC	0.662	
-	15	2462	_p.E771K|ATP2A3	NM_174955	NP_777615	Q93084	AT2A3_HUMAN	ame=5; (By similarity).	5	GACCTCGCCAA	0.602	
-	15	2112	_Mutation_p.R684	NM_014520	NP_055335	Q9BQG0	MBB1A_HUMAN		2	GGCACGCGGGG	0.647	
+	25	2718	.2_Missense_Mut	NM_002663	NP_002654	O14939	PLD2_HUMAN		5	CCCTGCGGACT	0.647	
-	7	532	141I|CAMTA2_uc	NM_015099	NP_055914	O94983	CMTA2_HUMAN	CG-1.	1	AAGGACGATGT	0.572	rs149046611
+	4	445		NM_006612	NP_006603	O43896	KIF1C_HUMAN	inesin-motor.	2	CAATCCTAAACA	0.542	
-	4	1847	hd.3_Missense_M	NM_001128833	NP_001122305	Q9P1Z0	ZBTB4_HUMAN	Pro-rich.	4	GGTGGGTGTGG	0.662	
+	2	812	A_uc002ghe.2_5'	NM_001102614	NP_001096084	P0C7Q6	AMCL3_HUMAN	ical; (Potential).	0	TGCTGGGCTCT	0.627	
-	16	2366	p.E822K|ALOXE3	NM_021628	NP_067641	Q9BYJ1	LOXE3_HUMAN	ipoxygenase.	5	GGCCTCCTCTG	0.617	
+	8	1629	p.P503L|ARHGEF	NM_173728	NP_776089	O94989	ARHGF_HUMAN	DH.	3	GGGGCCTTTCT	0.587	
-	13	1321	uc002gml.1_Intron	NM_002472	NP_002463	P13535	MYH8_HUMAN	osin head-like.	11	TGCCAACCTTG	0.507	
-	23	3037	uc002gml.1_Intron	NM_017533	NP_060003	Q9Y623	MYH4_HUMAN	Potential.	13	TGTTCTCTGTGG	0.343	
-	23	2786	uc002gml.1_Intron	NM_005963	NP_005954	P12882	MYH1_HUMAN	Potential.	21	AGCTTCCTGAG	0.358	
+	20	4064_4065	_Missense_Mutati	NM_001372	NP_001363	Q9NYC9	DYH9_HUMAN	.|Stem (By similarity).	20	GCCATGGAGTTG	0.559	
+	8	1132_1133	CD_uc002gnp.1_	NM_153604	NP_705832	Q8IZQ8	MYCD_HUMAN		5	GAAGTCCCCTC	0.485	
-	1	235	16_uc002gor.1_I	NM_006382	NP_006373	O95170	CDRT1_HUMAN		0	ACAACGAAAATA	0.493	
+	6	1033_1034	wa.1_Missense_	NM_001130842	NP_001124314	Q9HBT8	Z286A_HUMAN		1	CCAAAGGATCTT	0.337	
+	8	1090	p.R345Q|MPRIP_	NM_201274	NP_958431	Q6WCQ1	MPRIP_HUMAN	ith F-actin (By similarity).	0	GAAGCGGGTGA	0.667	
+	6	1016		NM_024052	NP_076957	Q8IVV7	CQ039_HUMAN		1	ATCAGTCCCTCA	0.468	
-	20	2398	.1_Missense_Mut	NM_002018	NP_002009	Q13045	FLII_HUMAN	h ACTL6A.|Gelsolin-like 3.	2	CACGTCGGACC	0.672	
-	5	716	_uc010vxs.1_Mis	NM_004618	NP_004609	Q13472	TOP3A_HUMAN	Toprim.	3	TACACACGTGGA	0.468	
+	1	275	gul.2_Missense_	NM_031456	NP_113644	Q5XX13	FBW10_HUMAN		1	TATTTTCGTTGT	0.493	
-	5	441	AP4_uc002gvs.2_	NM_002404	NP_002395	P55083	MFAP4_HUMAN	ogen C-terminal.	0	TAGGCCGTGTTG	0.587	
-	3	260	_Splice_Site_p.K69_splice|IFT20_uc010wae.1_Intron|T			Q8IY31	IFT20_HUMAN		0	CAATTTCTTTTA	0.393	
-	4	1151	ht.2_Missense_M	NM_001094	NP_001085	Q16515	ACCN1_HUMAN	llular (By similarity).	4	CCATCTCTGAGG	0.547	

+	6	700	tron|ACACA_uc00	NM_173625	NP_775896	Q8N4C9	CQ078_HUMAN		0	AGGAGCCAGGA	0.493	
-	15	3139	p.G844S|SRCIN1_	NM_025248	NP_079524	Q9C0H9	SRCN1_HUMAN	Pro-rich.	0	CTGGCCGTGGG	0.692	
-	3	791	_p.R104*|PIP4K2	NM_003559	NP_003550	P78356	PI42B_HUMAN	PIPK.	1	GGTTTCGGAACA	0.498	
-	9	1166	vt.2_Missense_Mu	NM_198993	NP_945344	Q6ZMT1	STAC2_HUMAN	SH3.	1	GATCTCCAGGC	0.627	
-	4	1019	P_uc010wfs.1_Intr	NM_005557	NP_005548	P08779	K1C16_HUMAN	Rod.|Coil 2.	1	TCTGCTCGTACT	0.617	
+	3	1391	p.A411T|KLHL10_	NM_152467	NP_689680	Q6JEL2	KLH10_HUMAN	Kelch 3.	4	CTCATCGCCCCC	0.498	
+	11	1457	BG2_uc002ias.2_	NM_016437	NP_057521	Q9NRH3	TBG2_HUMAN		1	GGAAGCGGGAT	0.498	
+	7	1181	AP1_uc010wgs.1_	NM_003632	NP_003623	P78357	CNTP1_HUMAN	1.|Extracellular (Potential).	8	CCGCGGCTGCA	0.632	
-	11	1405	gg.3_Missense_M	NM_000342	NP_000333	P02730	B3AT_HUMAN	.|Membrane (anion exchan	3	ATGGCGGGTGAC	0.582	
-	6	879	.R260W|KIF18B_	NM_001080443	NP_001073912				2	ATGCCCGCTCTG	0.627	
-	4	815	p.R187C|DCAKD_	NM_024819	NP_079095	Q8WVC6	DCAKD_HUMAN	DPCK.	0	CTGGCGTTTGG	0.642	rs138288180
-	6	844	se_Mutation_p.P1	NM_199282	NP_954976	Q6ZUM4	RHG27_HUMAN		0	TCTGCTGGGACC	0.612	
+	2	134	iky.2_Missense_M	NM_004287	NP_004278	O14653	GOSR2_HUMAN	lasmic (Potential).	2	TGGGACGCCTG	0.517	
-	1	185		NM_000088	NP_000079	P02452	CO1A1_HUMAN		382	CGTGCGTCAGG	0.572	
+	3	881	T2_uc010dbo.2_	NM_022167	NP_071450	Q9H1B5	XYLT2_HUMAN	enal (Potential).	1	ATCACGAGCAG	0.592	
-	1	657	mn.1_Intron|ACSF	NM_001267	NP_001258	O15335	CHAD_HUMAN	LRR 6.	3	GTCCACGTGGA	0.632	
+	5	460	n_p.E8K|STXBP4_	NM_178509	NP_848604	Q6ZWJ1	STXB4_HUMAN	PDZ.	1	TTGAAGAAGCA	0.358	
-	7	1018_1019	198L|SEPT4_uc0	NM_004574	NP_004565	O43236	SEPT4_HUMAN	(By similarity).	0	ACTTCGGGAGGT	0.574	rs148239346
+	7	726	4_uc010wou.1_R	NM_000717	NP_000708	P22748	CAH4_HUMAN		0	CAAGGAGGAGA	0.587	
-	25	5812		NM_005121	NP_005112	Q9UHV7	MED13_HUMAN		2	AGCAAGCACTG	0.403	
+	20	2987	E_uc010wpj.1_Mi	NM_000789	NP_000780	P12821	ACE_HUMAN	otential).|Peptidase M2 2.	4	CACCACGAAATG	0.572	
+	7	685	_p.S136F|PSMC5_	NM_002805	NP_002796	P62195	PRS8_HUMAN		1	GTGTCTCTGGCT	0.522	
-	17	3288		NM_000334	NP_000325	P35499	SCN4A_HUMAN	=S2 of repeat III; (Potentia	3	GAAGACCTTGT	0.557	
-	25	2989	C46_uc010dep.2	NM_145036	NP_659473	Q8N8E3	CE112_HUMAN	Potential.	0	TGTCTTCAAGTT	0.328	
-	32	4204	z.2_Missense_Mu	NM_080283	NP_525022	Q8IUA7	ABCA9_HUMAN	C transporter 2.	6	CCGCTCCCTTTC	0.507	
+	3	538	rq.1_Nonsense_M	NM_178233	NP_839947	Q7RTS5	OTOP3_HUMAN		1	ATCTTCCGAGTG	0.607	
-	23	2744	p.R815W|FBF1_u	NM_001080542	NP_001074011	Q8TES7	FBF1_HUMAN		0	CACCCGCCAGC	0.652	
-	4	1059	2_Missense_Muta	NM_001159772	NP_001153244	Q8WVQ1	CANT1_HUMAN	enal (Potential).	0	CCACGGTGCCG	0.582	
-	5	2039	orf70_uc010wuq.1_	NM_001109760	NP_001103230	Q0VG06	FP100_HUMAN		2	TGTGTGTGGCG	0.682	
-	4	819	168H|CSNK1D_u	NM_001893	NP_001884	P48730	KC1D_HUMAN	rotein kinase.	2	TTCTCACGATAG	0.617	
-	37	5441	zj.1_Missense_Mu	NM_005559	NP_005550	P25391	LAMA1_HUMAN	n II and I.|Potential.	21	CATGAGCAGCA	0.463	
+	70	9361	s.3_Missense_Mu	NM_198129	NP_937762	Q16787	LAMA3_HUMAN	minin G-like 4.	11	GGAGGGAAGTT	0.493	
+	6	5037		NM_015559	NP_056374	Q9Y6X0	SETBP_HUMAN		3	GTGAAAGCCAAA	0.662	
+	7	869	p.R206Q|RNF165_	NM_152470	NP_689683	Q6ZSG1	RN165_HUMAN		0	ATAGCGAAGACC	0.522	
-	3	230		NM_139171	NP_631910	P59095	STAR6_HUMAN	START.	1	TGCAATGATTTAT	0.328	
+	2	324	nc.2_Missense_Mu	NM_001144967	NP_001138439	Q96PU5	NED4L_HUMAN	C2.	4	ACAGGGAGAGT	0.373	
-	7	839	2A|CCBE1_uc002	NM_133459	NP_597716	Q6UXH8	CCBE1_HUMAN	ollagen-like 1.	3	GGGAGGGCCCT	0.577	
+	7	716	F|SERPINB10_uc	NM_002575	NP_002566	P05120	PAI2_HUMAN		2	GGTTTCCTCAAT	0.333	
+	27	3040	_Missense_Mutatic	NM_198531	NP_940933	O43861	ATP9B_HUMAN	lasmic (Potential).	3	CTTGTCCTTCA	0.433	
+	2	1223	_p.S257F|NFATC1	NM_006162	NP_006153	O95644	NFAC1_HUMAN	X SP repeats.	2	CTCCTCCAGAC	0.726	
-	12	1588	CSK4_uc002lta.2_	NM_017573	NP_060043	Q6UW60	PCSK4_HUMAN		0	GTGAGCGAGATC	0.692	
-	8	993	a.2_Missense_Mu	NM_017573	NP_060043	Q6UW60	PCSK4_HUMAN	ytic (By similarity).	0	GCCGTCGCAGT	0.692	
+	14	1434	lvr.2_Missense_Mu	NM_152988	NP_694533	Q8TCT7	PSL1_HUMAN	ical; (Potential).	0	ACCATCGGTAAG	0.537	
+	4	1228	wn.3_Missense_M	NM_152791	NP_690004	Q8NEP9	ZN555_HUMAN	2H2-type 8.	1	TTTATCCCCAGTC	0.463	
+	7	986	.D260G|TJP3_uc	NM_014428	NP_055243	O95049	ZO3_HUMAN		3	CTCGGACCTCG	0.612	
+	17	2150	f.2_RNA|UHRF1_	NM_001048201	NP_001041666	Q96T88	UHRF1_HUMAN		2	CGGGTCCCCGC	0.687	
-	8	1080	c.2_Missense_Mu	NM_000635	NP_000626	P48378	RFX2_HUMAN	type winged-helix.	6	TCAGACGAATCC	0.577	

-	10	1116		NM_000064	NP_000055	P01024	CO3_HUMAN		5	GTAGGGAGAGG	0.602
+	26	3233	.A6_uc002mgr.1_M	NM_006702	NP_006693	Q8IY17	PLPL6_HUMAN	asmic (Potential).|GXSXG.	3	GCGGCACGTCCA	0.672
-	3	220		NM_005001	NP_004992	O95182	NDUA7_HUMAN		0	GATTCCCGGCGG	0.582
-	39	39322	C16_uc010dwj.2_5	NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	ılar (Potential).|SEA 7.	57	CCCTCTCTGTGG	0.562
-	3	15725		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).	57	TCAGAGGAACCA	0.498
-	5	1214		NM_198535	NP_940937	Q32M78	ZN699_HUMAN	C2H2-type 8.	0	TTAAGGAGGAG	0.433
-	12	1133	RI1_uc002mox.1_I	NM_023008	NP_075384	Q8N9T8	KRI1_HUMAN	Glu-rich.	1	ACTTTCCGCAGC	0.587
+	23	3453	057_splice|SMAR	NM_003072	NP_003063	P51532	SMCA4_HUMAN	p.?(1)	67	CTTGCAGGAGTC	0.632
-	4	381	dyn.1_RNA|ZNF62	NM_145233	NP_660276	Q96I27	ZN625_HUMAN		0	GATGATCTTTCTT	0.398
-	3	572		NM_024038	NP_076943	Q9BQ61	CS043_HUMAN		0	GGGGCCGAGTTT	0.532
-	15	1970	vk.2_Missense_Mu	NM_017722	NP_060192	Q9NXH9	TRM1_HUMAN		2	AGCTTCGTCGG	0.637
-	6	1326	sense_Mutation_p.	NM_001008701	NP_001008701	O94910	LPHN1_HUMAN	ke.|Extracellular (Potential)	5	GTCCACGCGGT	0.602
-	8	1337	nao.1_Missense_M	NM_000435	NP_000426	Q9UM47	NOTC3_HUMAN	GF-like 10; calcium-binding	21	GCCACGACCGC	0.657
-	14	1402	S15L1_uc002nea.	NM_021235	NP_067058	Q9UBC2	EP15R_HUMAN		5	CCGGACGTCGC	0.627
+	6	2190	_p.R455*|NWD1_uc002nev.3_Nonsense_Mutation_p.R3			Q149M9	NWD1_HUMAN	NACHT.	7	TCTTCCCGGTAA	0.378
+	12	1126		NM_015016	NP_055831	O60307	MAST3_HUMAN	nilarity).|Protein kinase.	5	GCAACGGAGCC	0.597
+	14	1441		NM_015016	NP_055831	O60307	MAST3_HUMAN	rotein kinase.	5	GAGTACCTGCAT	0.652
+	2	151	EP1_uc002nit.1_5'U	NM_017712	NP_060182	Q9NXJ5	PGPI_HUMAN		0	GTGAACGCCAGT	0.542
-	3	405	:.1_Intron|PBX4_u	NM_025245	NP_079521	Q9BYU1	PBX4_HUMAN		2	ATCTGTCGGATCT	0.512
-	4	694	nop.2_Missense_M	NM_033196	NP_149973	O95780	ZN682_HUMAN	C2H2-type 1.	2	TCTTATGATAAGA	0.333
-	3	1610		NM_001001411	NP_001001411	Q8N7Q3	ZN676_HUMAN	C2H2-type 10.	0	GACCAGCTGAAG	0.448
-	4	1399		NM_001098626	NP_001092096	A6NK75	ZNF98_HUMAN	C2H2-type 9.	2	TGAATTCTCTTAT	0.373
+	4	3095	edd.1_Missense_M	NM_014717	NP_055532	O15090	ZN536_HUMAN		11	CGCCTCCCTCC	0.572
-	2	1423		NM_020856	NP_065907	Q63HK5	TSH3_HUMAN		8	GGGGACGTGAAG	0.552
+	13	2088	CH1_uc002nuh.1_	NM_018025	NP_060495	Q9BRR8	GPTC1_HUMAN		1	GATGTCGGGGAT	0.448
+	6	1276	_p.L352F|ZNF567_	NM_152603	NP_689816	Q8N184	ZN567_HUMAN	C2H2-type 5.	0	TCACACCTCATT	0.478
+	10	3427		NM_015073	NP_055888	O60292	SI1L3_HUMAN	PDZ.	2	GAACGGGCTCG	0.667
+	3	294	F1B_uc002oia.2_3	NM_033520	NP_277055	Q9GZP8	IMUP_HUMAN		0	ACGGATGTGAAG	0.687
-	4	424	n_p.R55H|SIRT2_u	NM_012237	NP_036369	Q8IXJ6	SIRT2_HUMAN	etylase sirtuin-type.	0	TCACAGCGTTCG	0.572
+	6	817	:.1_RNA|TIMM50_	NM_001001563	NP_001001563	Q3ZCQ8	TIM50_HUMAN	intermembrane (Potential).	1	ACAGATGATCAT	0.607
-	26	12093		NM_003890	NP_003881	Q9Y6R7	FCGBP_HUMAN	Cys-rich.	9	CTGCCCCGGCT	0.537
-	17	8396		NM_003890	NP_003881	Q9Y6R7	FCGBP_HUMAN		9	GTTCCTACCTCA	0.532
+	2	2010	sk.3_Missense_M	NM_022752	NP_073589	Q6ZN55	ZN574_HUMAN	C2H2-type 14.	0	GCCCCCGCTCCT	0.652
+	3	656		NM_133444	NP_597701	Q8TF50	ZN526_HUMAN		0	CTGCTACGGTAG	0.597
+	10	2639		NM_015125	NP_055940	Q96RK0	CIC_HUMAN	Pro-rich.	11	CCCTCCCACCG	0.682
-	5	626		NM_145296	NP_660339	Q8NFZ8	CADM4_HUMAN	Potential).|Ig-like C2-type 1.	0	CACCGTCGTCCT	0.597
+	6	1199	226_uc010ejg.2_3	NM_001032373	NP_001027545	Q9NYT6	ZN226_HUMAN	C2H2-type 4.	0	TTAATGTTCATTG	0.478
+	8	1258	t.2_Missense_Mut	NM_012116	NP_036248	Q9ULV8	CBLC_HUMAN		6	GAGGCCGTGAGT	0.642
+	3	1146_1147	ocf.2_Missense_M	NM_001080401	NP_001073870	Q8N819	PPM1N_HUMAN		0	CTGGGGGAGG	0.46
+	6	1224	ekn.2_Splice_Site_	NM_017659	NP_060129	Q9NXS2	QPCTL_HUMAN		1	GCAGAGGTACCA	0.592
-	1	1961		NM_032040	NP_114429	Q9H0W5	CCDC8_HUMAN		3	GGGGCCTCTGCC	0.607
+	6	617	p.G148E|CCDC15	NM_144688	NP_653289	Q8N6L0	CC155_HUMAN		2	GCTTCGGAGGCG	0.562
+	15	2148	Dyas.1_Missense_I	NM_153329	NP_699160	Q8IZ83	A16A1_HUMAN		1	GCCTTCGTGTCC	0.692
+	25	3052		NM_004533	NP_004524	Q14324	MYPC2_HUMAN	onectin type-III 3.	1	GGCAATGAATAC	0.537
-	3	300_301	K1_uc010ycg.1_R	NM_002257	NP_002248	P06870	KLK1_HUMAN	Peptidase S1.	0	AAACTGGGCTGT	0.55
-	6	814	71F|KLK8_uc002p	NM_007196	NP_009127	O60259	KLK8_HUMAN	Peptidase S1.	1	CCTCCAGAATCG	0.557
-	2	232	w.1_RNA|KLK9_uc	NM_012315	NP_036447	Q9UKQ9	KLK9_HUMAN	Peptidase S1.	1	TCGCCCCACAGA	0.677

-	5	740	97V|KLK12_uc01	NM_145894	NP_665901	Q9UKR0	KLK12_HUMAN	eptidase S1.	1	CTCCCCCACAC	0.542	
-	7	1874	ycy.1_Missense_	NM_033130	NP_149121	Q96LC7	SIG10_HUMAN	3.|Extracellular (Potential).	1	TCCTTCGTGCT	0.667	
-	2	79	_uc002qae.2_Spl	NM_001008801	NP_001008801	Q5VIY5	ZN468_HUMAN		2	TCAATCCTGAAT	0.433	
+	3	580		NM_001012728	NP_001012746	A6NFQ7	DPRX_HUMAN		0	GCTTCCATTCT	0.398	
-	5	1742	n.1_Missense_Mu	NM_003180	NP_003171	O00445	SYT5_HUMAN	lasmic (Potential).	0	CAGCTCCCGCC	0.701	
+	7	1656	mi.2_Missense_M	NM_153447	NP_703148	P59047	NALP5_HUMAN	NACHT.	7	CTCATGGTTCA	0.527	
+	5	956	p.G264E|ZNF583_	NM_001159860	NP_001153332	Q96ND8	ZN583_HUMAN		1	TACTGGAGAGA	0.438	
+	3	809		NM_152677	NP_689890	Q8NAM6	ZSCA4_HUMAN		1	AAGAAGGGATT	0.388	
+	5	809	qrf.2_Missense_M	NM_003436	NP_003427	B4DHH9	B4DHH9_HUMAN		1	TCACAGCTCAG	0.468	
-	6	859	se_Mutation_p.R1	NM_015025	NP_055840	Q9UL68	MYT1L_HUMAN		6	GCGTGCGATGC	0.617	
-	3	205	AS_uc002rcd.1_R	NM_015909	NP_056993	A2RRP1	NBAS_HUMAN		4	AATAATAAACGAT	0.274	
+	24	2234		NM_004939	NP_004930	Q92499	DDX1_HUMAN	essary for interaction with	4	AGGCTGTACCA	0.338	
-	25	4290		NM_000384	NP_000375	P04114	APOB_HUMAN		27	GTAACGAGCCC	0.527	
+	10	1331	hv.3_Missense_M	NM_020134	NP_064519	Q9BPU6	DPYL5_HUMAN		2	CGCAAGGGCCG	0.537	
+	6	980	10yli.1_Missense_	NM_173650	NP_775921	Q8N7S2	DNJ5G_HUMAN		1	GAAGATGATTTT	0.338	
-	4	1293	_Mutation_p.M34	NM_021209	NP_067032	Q9NPP4	NLRC4_HUMAN	NACHT.	6	TTCACCCATCTG	0.438	
-	8	1492	nd.1_Missense_	NM_015475	NP_056290	Q8NCA5	FA98A_HUMAN	Gly-rich.	1	GCCTGcacgacca	0.373	
+	15	1770	.2_Missense_Mut	NM_053276	NP_444506	Q6UXI7	VITRN_HUMAN	VWFA 2.	2	TCGACGGCTCC	0.602	
-	7	1111	_p.T185M|EIF2AK	NM_002759	NP_002750	P19525	E2AK2_HUMAN		5	TCACACGTAGTA	0.368	
-	9	1119	_p.A254V|LRPPR	NM_133259	NP_573566	P42704	LPPRC_HUMAN		3	GCAACGCTACA	0.353	rs119466000
+	8	3829	i.1_Missense_Mut	NM_000179	NP_000170	P52701	MSH6_HUMAN		168	GACGGCAATAG	0.303	
-	1	356	P2_uc002rxq.3_I	NM_001003937	NP_001003937	Q8N831	TSYL6_HUMAN		0	ACTGCGACCCG	0.647	
-	4	994	10ypj.1_Missense_	NM_022893	NP_075044	Q9H165	BC11A_HUMAN		13	CCCTTCTGCCA	0.572	
-	8	1092		NM_014709	NP_055524	Q70CQ2	UBP34_HUMAN		19	TTTCTGTGTCC	0.249	
+	29	3413	F_uc010fek.2_Mi	NM_003494	NP_003485	O75923	DYSF_HUMAN	lasmic (Potential).	7	GCTGGGAGTAT	0.617	
+	30	3660	2_Missense_Muta	NM_003494	NP_003485	O75923	DYSF_HUMAN	ic (Potential).|Arg-rich.	7	CTGGCGCCGTC	0.662	
-	9	1069	se_Mutation_p.S3	NM_021196	NP_067019	Q9BY07	S4A5_HUMAN	lasmic (Potential).	9	TTGTAGGATTTTG	0.328	
-	25	3225	n_p.R838W|DCT	NM_004082	NP_004073	Q14203	DCTN1_HUMAN	Potential.	5	CAGCCGCACAT	0.572	
+	2	754	c002sma.1_Silent_	NM_016170	NP_057254	O43763	TLX2_HUMAN		0	GCGCCGCATAG	0.667	
-	4	635	1_uc002smc.2_5'	NM_133637	NP_598376	Q8TE96	DQX1_HUMAN	ase ATP-binding.	2	GGGTCGAGGCC	0.607	
+	3	2159		NM_000189	NP_000180	P52789	HXK2_HUMAN	Regulatory.	2	ACACGGAGAGT	0.488	
+	1	432	C285033_uc002s	NM_001037228	NP_001032305	Q3KRF4	Q3KRF4_HUMAN		0	TGCTTCCTTCC	0.547	
+	9	1094	_Mutation_p.S31	NM_015341	NP_056156	Q15003	CND2_HUMAN		2	TGTGTCGGCCC	0.488	
-	18	2664	szi.3_Missense_	NM_182911	NP_878915	Q9BZW7	TSG10_HUMAN	ith HIF1A (By similarity).	2	GAGATCGATGG	0.383	
-	7	1512	c.2_Nonsense_Mu	NM_016316	NP_057400	Q9UBZ9	REV1_HUMAN	UmuC.	2	TATTTCGTATACC	0.308	
-	2	735	.R206W|ST6GAL	NM_001142351	NP_001135823	Q96JF0	SIAT2_HUMAN	enal (Potential).	11	GAGCCGGTACA	0.617	
-	2	151	_p.R11Q|ST6GAL	NM_001142351	NP_001135823	Q96JF0	SIAT2_HUMAN	lasmic (Potential).	11	AGCATTCGTTGT	0.507	
+	20	3830	_Mutation_p.D43	NM_182588	NP_872394	Q7Z3J3	RGPD4_HUMAN		2	AATGGGATAACT	0.443	
+	9	1404	fjj.2_Missense_Mu	NM_021815	NP_068587	Q9GZV3	SC5A7_HUMAN	ellular (Potential).	4	AAAGAAATCGT	0.433	
+	6	971	dx.2_Nonsense_M	NM_001056	NP_001047	O00338	ST1C2_HUMAN		1	TTCCTGGTTTG	0.438	
+	4	829	r.1_RNA|SULT1C	NM_006588	NP_006579	O75897	ST1C4_HUMAN		0	AGAATGAATAA	0.423	
-	14	4388_4389	AP5_uc002ttq.2_I	NM_207363	NP_997246	O14513	NCKP5_HUMAN		0	CCTCCCAACACT	0.614	
-	8	3256		NM_002299	NP_002290	P09848	LPH_HUMAN	ential).|4 X approximate re	13	TCACCCCTGGG	0.512	
+	4	1168	SD7B_uc002tvb.	NM_001080427	NP_001073896				7	AGCAGGATCCC	0.542	
-	45	8435		NM_018557	NP_061027	Q9NZR2	LRP1B_HUMAN	ellular (Potential).	50	GAACAATTCACT	0.408	
-	77	11578		NM_004543	NP_004534	P20929	NEBU_HUMAN	Nebulin 104.	20	ATTTTTCCTGCAT	0.423	
+	22	3941	om.1_Missense_	NM_033394	NP_203752	Q9C0D5	TANC1_HUMAN	ANK 10.	3	ATGGCGATGCC	0.552	

-	7	1400	e_Mutation_p.D20	NM_004490	NP_004481	Q14449	GRB14_HUMAN	PH.	7	AAATATCACTATT	0.333	
-	3	554	_p.S21F|SCN3A_	NM_006922	NP_008853	Q9NY46	SCN3A_HUMAN		10	GCAAGAGATTCT	0.438	
-	8	1021	lf.1_Missense_Mut	NM_004525	NP_004516	P98164	LRP2_HUMAN	s A 7.|Extracellular (Potenti	29	ACCATTCTCTTGG	0.448	
-	284	83316	393K|TTN_uc010z	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	AAGTTTCCCGCT	0.413	
-	275	76341	068K|TTN_uc010z	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	CCTTTTCGTTAAC	0.418	
-	275	73362	075R|TTN_uc010z	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	ATTTTCCAAAGT	0.418	
-	255	56146	36Q|TTN_uc010z	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	ACTTTTCGCCAA	0.478	rs148684589
-	223	44670	_uc010zfi.1_Misse	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	CTGAGGTCTTTC	0.393	
-	100	25998	N_uc010zfj.1_Intro	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	TATTTTTCATATTC	0.368	
+	39	2843		NM_000090	NP_000081	P02461	CO3A1_HUMAN	le-helical region.	13	CTGCGGGTAACA	0.557	
-	46	3582	frx.2_Missense_M	NM_000393	NP_000384	P05997	CO5A2_HUMAN		2	TTACCGGATCTC	0.537	
-	18	1417	.5A2_uc010frx.2_I	NM_000393	NP_000384	P05997	CO5A2_HUMAN		2	GGATTTCCTGGA	0.328	
-	8	2033		NM_014585	NP_055400	Q9NP59	S40A1_HUMAN		1	TCCTTCCTAACTT	0.393	
+	19	3488	uqx.1_Splice_Site	NM_144708	NP_653309	Q7Z5J8	ANKAR_HUMAN		4	TTTATAGGGAATT	0.343	
+	8	1795	p.P407L|NAB1_uc	NM_005966	NP_005957	Q13506	NAB1_HUMAN		0	ACAGTCCTAACG	0.483	
-	2	817		NM_004657	NP_004648	O95810	SDPR_HUMAN		2	CATTTTCCTCCTG	0.468	
-	9	1302		NM_016192	NP_057276	Q9UIK5	TEFF2_HUMAN	lding.|Extracellular (Potenti	5	TAGTCCTTTTTTT	0.398	
+	2	235	_uc010zgq.1_Intr	NM_001080539	NP_001074008	Q8NCX0	CC150_HUMAN		0	CTTCAGCAAAGG	0.403	
-	7	802	NKRD44_uc002uul	NM_153697	NP_710181	Q8N8A2	ANR44_HUMAN	ANK 7.	5	GCTGCAGCATGC	0.468	
+	28	3304	_p.S624L|AOX1_u	NM_001159	NP_001150	Q06278	ADO_HUMAN		6	CAATGTCGAATG	0.453	
-	6	598	_p.T145I|ICA1L_u	NM_138468	NP_612477	Q8NDH6	ICA1L_HUMAN	AH.	0	ATCAAGGTATCA	0.463	
+	5	625	r.2_Missense_Mut	NM_001875	NP_001866	P31327	CPSM_HUMAN	horibosyltransferase homo	13	GAGTGGACACA	0.299	
+	2	327	zjl.1_Missense_M	NM_001080500	NP_001073969	B2RUY7	VWC2L_HUMAN	VWFC 1.	0	GAGAACGATTTT	0.458	
-	5	1492	jm.1_Missense_M	NM_000465	NP_000456	Q99728	BARD1_HUMAN	ANK 1.	2	TTGGATCACTTC	0.323	
+	3	362	_p.G4E|ATIC_uc0	NM_004044	NP_004035	P31939	PUR9_HUMAN		29	GGGGGGACGTG	0.398	
+	16	1909	_p.L304P|VIL1_uc	NM_007127	NP_009058	P09327	VILI_HUMAN	Core.	1	AAAACCTGGTCA	0.507	
+	3	1005	_p.S47F|TTLL4_u	NM_014640	NP_055455	Q14679	TTLL4_HUMAN		3	CTTCCTCCTATAA	0.537	
+	2	563		NM_080671	NP_542402	Q8WWG9	KCNE4_HUMAN	lasmic (Potential).	1	CACCTCACCATT	0.637	
+	5	529		NM_031313	NP_112603	P10696	PPBN_HUMAN		1	CCTCAGGAAAGT	0.617	
+	24	2935	se_Mutation_p.E93	NM_152879	NP_690618	Q16760	DGKD_HUMAN		5	TGTCCGAGGAG	0.627	
-	2	290	nw.1_Missense_M	NM_022817	NP_073728	O15055	PER2_HUMAN		2	TCCACGGGCTCC	0.607	
+	6	789		NM_001001891	NP_001001891	Q6IWH7	ANO7_HUMAN	lasmic (Potential).	3	ACTACTCCTGCC	0.632	
+	15	1766		NM_001001891	NP_001001891	Q6IWH7	ANO7_HUMAN	ical; (Potential).	3	AACCTCGTCTTC	0.657	rs149170904
+	13	1349	FARP2_uc010zor.	NM_014808	NP_055623	O94887	FARP2_HUMAN		3	TCTCTCCCTCCA	0.542	
+	12	1990		NM_003245	NP_003236	Q08188	TGM3_HUMAN		9	GCTGATGGTGGA	0.647	
+	8	865	ow.1_Missense_M	NM_080751	NP_542789	Q8TDI7	TMC2_HUMAN	ical; (Potential).	3	GGCATGCCCTATG	0.443	
+	2	537		NM_012409	NP_036541	Q9UKY0	PRND_HUMAN		0	GGACTTCGGGTC	0.597	
+	4	472	e_Mutation_p.E14	NM_018993	NP_061866	Q8WYP3	RIN2_HUMAN	SH2.	5	CTCAAGGAATTT	0.493	
+	4	886		NM_014012	NP_054731	O75628	REM1_HUMAN		4	GGCCCGCTGCC	0.612	
+	3	1706		NM_001011718	NP_001011718	Q5GH72	XKR7_HUMAN		3	CACACCAGTGG	0.657	
+	7	808	p.R192G|HCK_uc	NM_002110	NP_002101	P08631	HCK_HUMAN	SH2.	9	CCCCCCGAAGC	0.587	rs144393224
+	3	197	se_Mutation_p.S2	NM_031483	NP_113671	Q96J02	ITCH_HUMAN		6	GTATGTCTGACA	0.388	
-	3	902	xdk.2_Intron|CPNE	NM_152838	NP_690051	Q9NTZ6	RBM12_HUMAN	Pro-rich.	3	CGGGGGCACAG	0.602	
+	9	2477	_Intron|DLGAP4_u	NM_014902	NP_055717	Q9Y2H0	DLGP4_HUMAN		3	CCTCTCGGAGG	0.468	
-	2	614	ICOA5_uc002xre.2	NM_020967	NP_066018	Q9HCD5	NCOA5_HUMAN	harge).|Transcription repre	2	ATTGGGGATCGA	0.537	
-	8	1235	_p.P194L|STAU1_	NM_017453	NP_059347	O95793	STAU1_HUMAN		5	GTCTGTGGCTGA	0.488	
-	2	1037	yx.1_Missense_M	NM_173091	NP_775114	Q13469	NFAC2_HUMAN	SP repeats.|3; approximat	2	GCTCCGGGAGC	0.726	

-	77	10670		NM_005560	NP_005551	O15230	LAMA5_HUMAN	minin G-like 5.		3	TGGGAGGTCTG	0.687	rs141478116
-	7	1139		NM_005560	NP_005551	O15230	LAMA5_HUMAN			3	ACTCACACTGG	0.687	
-	13	1442	L1_uc011abm.1_	NM_017859	NP_060329	Q9NWZ5	UCKL1_HUMAN			0	CACGCGCACTG	0.637	
+	5	1116	_uc010gks.2_Spl	NM_003195	NP_003186	Q15560	TCEA2_HUMAN			0	GGACCGTGAGT	0.682	
+	3	3383	ON_uc002ysd.2_	NM_138927	NP_620305	P18583	SON_HUMAN	repeats of [ED]-R-S-M-M-		6	CTGACCGATCT	0.453	
-	7	2111		NM_003906	NP_003897	O60318	MCM3A_HUMAN			5	AGGGCCGCAGC	0.612	
-	11	1322	e_Mutation_p.E36	NM_003325	NP_003316	P54198	HIRA_HUMAN			1	CTCCTCGCTCA	0.557	
+	5	546	_p.R157H|CDC45_	NM_003504	NP_003495	O75419	CDC45_HUMAN			1	GAAGCGCACAC	0.517	
-	3	771	.R186W|TRMT2A_	NM_182984	NP_892029	Q8IZ69	TRM2A_HUMAN	Potential.		1	CTTCCGCTCAA	0.632	
-	1	4573		NM_015672	NP_056487					0	GCTGGGGAGGT	0.572	
+	17	1567	e_Mutation_p.R36	NM_005160	NP_005151	P35626	ARBK2_HUMAN	kinase C-terminal.		7	CTCCCCGGGGA	0.428	
+	4	549	p.3_Missense_M	NM_001013694	NP_001013716	Q9UH36	SRR1L_HUMAN			0	TGACCCTCTGT	0.448	
+	6	632	eo.2_Missense_M	NM_133455	NP_597712	Q96A84	EMID1_HUMAN	ollagen-like.		0	GGGCAGCCCCG	0.493	
+	7	2163	2L1_uc003afc.1_	NM_152236	NP_689422	Q99501	GA2L1_HUMAN			0	CCGCCGCCCCT	0.667	
-	4	633	aii.1_Missense_M	NM_004861	NP_004852	Q99999	G3ST1_HUMAN	enal (Potential).		0	GGGGTCGCGGA	0.647	
+	3	527	e_Mutation_p.K11	NM_000355	NP_000346	P20062	TCO2_HUMAN			1	CACAAGGGGGA	0.617	
+	11	1705	issense_Mutation	NM_006932	NP_008863	P53814	SMTN_HUMAN			3	GCCCCCGACCC	0.622	
+	20	2447	I1_uc011alp.1_Mi	NM_001007467	NP_001007468	A8K8P3	SFI1_HUMAN			1	GCTGCGGTGAG	0.637	
+	7	1626	atq.1_Missense_M	NM_001039141	NP_001034230	Q9H2D6	TARA_HUMAN			1	CCCCACAACAT	0.597	
+	7	2145	atq.1_Missense_M	NM_001039141	NP_001034230	Q9H2D6	TARA_HUMAN			1	CCCCAGAACAT	0.592	
+	15	5931	174H|TRIOBP_uc	NM_001039141	NP_001034230	Q9H2D6	TARA_HUMAN	PH.		1	CGTACGTCCAA	0.572	
-	7	1038	e.1_Missense_M	NM_020831	NP_065882	Q969V6	MKL1_HUMAN	Gln-rich.		5	TGCTGCTGGTT	0.657	
+	7	1956_1957		NM_001429	NP_001420	Q09472	EP300_HUMAN			64	GTGTAGGAGTTC	0.366	
-	6	1011	e_Mutation_p.M1I|	NM_000106	NP_000097	Q6NWU0	Q6NWU0_HUMAN			2	GTCACCATCCC	0.612	
-	5	916	10gyv.2_5'UTR|CY	NR_002570						0	GTCTCGGGGTG	0.612	
-	2	282		NM_022766	NP_073603	Q8TCT0	CERK1_HUMAN	o sulfatide and phosphoino		1	AACGGCGATGA	0.443	
-	33	5300	p.R524C|PLXNB2_	NM_012401	NP_036533	O15031	PLXB2_HUMAN	lasmic (Potential).		6	CACGCGGCTCA	0.617	
+	14	1867	blc.2_Missense_M	NM_014678	NP_055493	O75170	PP6R2_HUMAN			0	CACACGGATCG	0.667	
+	15	2004	blc.2_Missense_M	NM_014678	NP_055493	O75170	PP6R2_HUMAN			0	CGAACCGCAGG	0.692	
+	6	753	w.1_Missense_M	NM_006614	NP_006605	O00533	CHL1_HUMAN	2.|Extracellular (Potential).		12	TCCCACCTTTAC	0.398	
+	49	6965	R1_uc011asu.1_In	NM_001099952	NP_001093422	Q14643	ITPR1_HUMAN	lasmic (Potential).		21	TCTGCGGTCTG	0.423	
-	8	790	G204R|C3orf32_u	NM_015931	NP_057015	Q9Y2M2	CC032_HUMAN	Cys-rich.	p.G182E(1)	1	GGCTCCGCAGC	0.662	
+	14	1747	_p.P544S|ATG7_u	NM_006395	NP_006386	O95352	ATG7_HUMAN			1	ACATCCCTGGT	0.493	
-	5	1795	_p.E474K|IQSEC1_	NM_014869	NP_055684	Q6DN90	IQEC1_HUMAN	SEC7.		1	CATCTCGTCCA	0.612	
-	4	692	385D_uc010hfb.1_	NM_024697	NP_078973	Q9H6B1	Z385D_HUMAN	atrin-type 1.		5	CCGCAGCCTGG	0.443	
+	19	2326	_p.G689R|ARPP21	NM_016300	NP_057384	Q9UBL0	ARP21_HUMAN	Gln-rich.		3	AACAGGGATTC	0.468	
+	1	203	LC22A13_uc011ay	NM_004256	NP_004247	Q9Y226	S22AD_HUMAN	ellular (Potential).		1	CCACTGTGCAG	0.532	
+	12	1074	_p.C185F|XYLB_u	NM_005108	NP_005099	O75191	XYLB_HUMAN			1	CTTCTGCAACC	0.607	
-	11	1751		NM_014139	NP_054858	Q9UI33	SCNBA_HUMAN			9	CCTTTGGAGAG	0.498	
-	10	1662		NM_014139	NP_054858	Q9UI33	SCNBA_HUMAN			9	TTTTGGCAATCTT	0.378	
+	4	1315	ab.1_Missense_M	NM_001134440	NP_001127912	Q8TBZ5	ZN502_HUMAN	2H2-type 8.		0	AATGTAAAGAAT	0.388	
-	9	2519		NM_022842	NP_073753	Q9H5V8	CDCP1_HUMAN	lasmic (Potential).		3	AGCGAGGAGGT	0.587	
-	3	542	n.2_Missense_M	NM_022842	NP_073753	Q9H5V8	CDCP1_HUMAN	ellular (Potential).		3	TCTAAACCGATG	0.552	
+	2	905	_p.S219L|CCRL2_	NM_003965	NP_003956	O00421	CCRL2_HUMAN	Name=5; (Potential).		1	ACATTTCGGTTC	0.393	
-	6	1135	qf.1_Missense_M	NM_013270	NP_037402	Q9UI38	TSP50_HUMAN			0	CCTGCCCGTTG	0.657	
-	22	7632	R3_uc010hkf.2_5	NM_001407	NP_001398	Q9NYQ7	CELR3_HUMAN	ellular (Potential).		11	GCGTCCGTGGA	0.597	rs118038433
+	5	7862		NM_003458	NP_003449	Q9UPA5	BSN_HUMAN			8	CGACAGCAGCG	0.637	

-	2	941	3HD14B_uc003dc	NM_032750	NP_116139	Q96IU4	ABHEB_HUMAN		0	AGAGGGCCTGG	0.632	
-	3	1034		NM_001947	NP_001938	Q16829	DUS7_HUMAN	protein phosphatase.	1	GGCTTCGTCTG	0.607	
+	2	103	CTK_uc003ddn.2_	NM_145262	NP_660305	Q8IVS8	GLCTK_HUMAN		0	ATGGCTGCAGCC	0.657	
-	13	1599	1_uc010hmg.2_R	NM_004656	NP_004647	Q92560	BAP1_HUMAN		65	AGGCCGTGTCT	0.647	
-	3	666	_p.N36S|FAM107	NM_007177	NP_009108	O95990	F107A_HUMAN		0	CGGGGTTCAGC	0.622	
-	5	456_457	hob.2_Missense_	NM_003848	NP_003839	Q96I99	SUCB2_HUMAN	ATP-grasp.	2	GCTTCAGCAAC	0.485	
+	17	3210	.1_RNA|ROBO2_	NM_002942	NP_002933	Q9HCK4	ROBO2_HUMAN	cellular (Potential).	11	TGTGGTGAAGC	0.393	
+	1	599		NM_153605	NP_705833				0	CCCTTCTCCAGT	0.458	
-	6	1095	se_Mutation_p.P25	NM_170662	NP_733762	Q13191	CBLB_HUMAN	-PTB.|SH2-like.	9	TAACCTGGATGT	0.333	
-	1	183	dxk.2_Missense_	NM_005459	NP_005450	O95843	GUC1C_HUMAN	EF-hand 1.	0	TAAATTCATGTAG	0.388	
-	16	1645	hn.1_Missense_M	NM_014429	NP_055244	Q86VD1	MORC1_HUMAN	CW-type.	8	GTTTTCCAAGC	0.274	
-	3	207		NM_018338	NP_060808	Q96MT7	WDR52_HUMAN		1	CTTCCCCTTTG	0.323	
-	5	793		NM_199420	NP_955452	O75417	DPOLQ_HUMAN	ase ATP-binding.	11	AGTCTCCCAGCA	0.383	
+	15	1487	bjn.1_Missense_	NM_021082	NP_066568	Q16348	S15A2_HUMAN		1	TCAAATCCTTTCA	0.323	
-	7	753_754	e_Mutation_p.E15	NM_053025	NP_444253	Q15746	MYLK_HUMAN		9	GCACTCCCCCC	0.55	
+	5	857	hf.1_Missense_M	NM_001024660	NP_001019831	O60229	KALRN_HUMAN	Spectrin 1.	6	TGGAGGAGCTG	0.627	
+	1	215	uc011bkc.1_5'UT	NM_000373	NP_000364	P11172	UMPS_HUMAN	OPRTase.	1	CCCATCTACATC	0.602	
+	11	1353	on_p.V337A|SEC6	NM_013336	NP_037468	P61619	S61A1_HUMAN	lasmic (Potential).	1	GCAGGTTGCAA	0.562	
+	15	4413	6A6_uc003eni.3_5	NM_001102608	NP_001096078	A6NMZ7	CO6A6_HUMAN	le-helical region.	8	AGTTGGGGAAA	0.373	
+	19	1865	no.2_Missense_M	NM_014382	NP_055197	P98194	AT2C1_HUMAN	smic (By similarity).	1	TCCACCTAGAA	0.418	
+	6	567	htq.1_Missense_	NM_015268	NP_056083	O75165	DJC13_HUMAN		2	AAGGAGGATTT	0.328	
-	2	529	_p.Q80*|AMOTL2	NM_016201	NP_057285	Q9Y2J4	AMOL2_HUMAN		1	GCCCTGGTGCT	0.672	
+	7	814	mc.1_Splice_Site_	NM_000532	NP_000523	P05166	PCCB_HUMAN		0	GTCAGGTGAGA	0.473	
+	10	1909	_Mutation_p.R425	NM_032383	NP_115759	Q969F9	HPS3_HUMAN		6	GGCCCGCACGG	0.398	rs145158238
-	6	1083	ns.1_Missense_M	NM_015472	NP_056287	Q9GZV5	WWTR1_HUMAN		4	GGAAACGGGTC	0.413	
+	2	1200	33GNT5_uc003fll.	NM_032047	NP_114436	Q9BYG0	B3GN5_HUMAN	enal (Potential).	1	GTGTTCATCGT	0.438	
+	18	2597	003flz.2_Translatic	NM_018023	NP_060493	Q9ULM3	YETS2_HUMAN	Gly-rich.	4	TGGGAGTGGTG	0.224	
+	13	1512	t.2_Missense_Mu	NM_004423	NP_004414	Q92997	DVL3_HUMAN	DEP.	3	AAGGCTTCACG	0.582	
+	3	2238	ense_Mutation_p.	NM_144635	NP_653236	Q6UXB0	F131A_HUMAN		1	AGCCAGCCCCC	0.662	
+	1	1377		NM_153690	NP_710157	Q8N2R8	FA43A_HUMAN		1	CGCGCGGCTGC	0.706	
+	5	607	_p.E20K|OSTalph	NM_152672	NP_689885	Q86UW1	OSTA_HUMAN	ical; (Potential).	1	TGGTGGAAGGC	0.507	
-	27	4028	AK_uc010ibi.2_Mi	NM_005255	NP_005246	O14976	GAK_HUMAN	J.	4	CTTGTCGGGGT	0.532	
+	6	772	EA_uc003gdd.2_	NM_001017405	NP_001017405	Q7L5Y9	MAEA_HUMAN		2	CGCCCGACACG	0.602	
-	8	1229	bvl.1_Missense_M	NM_020972	NP_066023	Q9HCC9	LST2_HUMAN		3	GGCAGCGGGTC	0.657	
+	8	3378	_p.S177F|RGS12_	NM_198229	NP_937872	O14924	RGS12_HUMAN	RGS.	1	GAAGTCCCCGC	0.587	
-	4	949	p.E225K|JAKMIP1	NM_144720	NP_653321	Q96N16	JKIP1_HUMAN	association with microtub	4	AAGTTCCTTCT	0.542	
+	3	404	A3_uc011bxo.1_	NM_020973	NP_066024	Q9H227	GBA3_HUMAN		0	ATCATCGATGAT	0.363	
+	19	2512	p.E660K|LIMCH1_	NM_014988	NP_055803	Q9UPQ0	LIMC1_HUMAN	Glu-rich.	4	ATGAGGAGGTA	0.478	
+	8	1293	ze.1_Missense_	NM_000812	NP_000803	P18505	GBRB1_HUMAN	ical; (Probable).	2	GCGATTGATATT	0.453	
-	3	465	_p.G55R|KDR_uc	NM_002253	NP_002244	P35968	VGFR2_HUMAN	1.|Extracellular (Potential).	33	TCTGTCCCCTGA	0.428	
+	10	1396	_p.Q396*|PAICS_u	NM_006452	NP_006443	P22234	PUR6_HUMAN	R carboxylase.	0	CTGCTCAGATAT	0.413	
-	12	2270	ah.1_Missense_M	NM_004439	NP_004430	P54756	EPHA5_HUMAN	Potential).|Protein kinase.	24	TCAAACGTCCAC	0.358	
-	1	1833	GNRHR_uc003hd	NM_000406	NP_000397	P30968	GNRHR_HUMAN	cellular (Potential).	1	GGGGAGGTTGC	0.463	
-	7	713		NM_182502	NP_872308	Q86T26	TM11B_HUMAN	.|Extracellular (Potential).	1	CCCCTCCAGGG	0.502	
+	1	331	ihr.2_Missense_	NM_053039	NP_444267	Q9BY64	UDB28_HUMAN		1	TTTTTCACAAGA	0.294	
+	2	778	ihr.2_Missense_M	NM_053039	NP_444267	Q9BY64	UDB28_HUMAN		1	TTATGCGAAACT	0.398	
+	13	917		NM_016519	NP_057603	Q9NP70	AMBN_HUMAN		4	TCCAGGATTTGG	0.507	

+	27	4724	ite_p.G1396_splic	NM_080683	NP_542414	Q12923	PTN13_HUMAN			6	TTTTAGGTGATC	0.383	
+	4	467	_Mutation_p.D101	NM_014606	NP_055421	Q15034	HERC3_HUMAN	RCC1 2.		4	TCAGTGACCGA	0.512	
+	8	1097	j.1_Missense_Mu	NM_000253	NP_000244	P55157	MTP_HUMAN	Vitellogenin.		4	GCAGTTGATTCA	0.463	
-	40	6518	xc.1_Missense_Mu	NM_001813	NP_001804	Q02224	CENPE_HUMAN	inding domain.|Potential.		9	GAAGTGAGAGG	0.363	
+	12	1960_1961	p.G543K|GSTCD_	NM_001031720	NP_001026890	Q8NEC7	GSTCD_HUMAN			2	TTGTGGGAGTCC	0.45	
+	9	962	_p.R288*|ANK2_uc	NM_001148	NP_001139	Q01484	ANK2_HUMAN	ANK 8.	p.R288*(1)	14	TGGATCGAGGC	0.428	rs146907003
+	2	1719		NM_152618	NP_689831	Q6ZW61	BBS12_HUMAN			2	AGTTACTGCAC	0.413	
+	9	10450	_p.D1782N|FAT4_	NM_024582	NP_078858	Q6V0I7	FAT4_HUMAN	|Extracellula	p.D3484N(2)	18	CTGTTGATTCAG	0.458	rs143981594
+	13	12422	p.G2404E|FAT4_u	NM_024582	NP_078858	Q6V0I7	FAT4_HUMAN	1.|Extracellular (Potential).		18	TCAATGGAAGGC	0.413	
+	2	292_293	on_p.P6F|ARFIP1_	NM_001025595	NP_001020766	P53367	ARFP1_HUMAN			1	AATCTCCCAAAA	0.347	
-	7	1324	tz.1_Missense_Mu	NM_006529	NP_006520	O75311	GLRA3_HUMAN	ical; (Probable).		3	AGAATGAAACC	0.478	
-	2	273	_5'Flank|AGA_uc	NM_000027	NP_000018	P20933	ASPG_HUMAN			0	AGAGCCGTCAC	0.507	
-	7	860		NM_024830	NP_079106	Q8NF37	PCAT1_HUMAN	enal (Potential).		2	GCCACGTCCAT	0.617	
-	4	532	4_uc011cmf.1_5'U	NM_016358	NP_057442	P78413	IRX4_HUMAN			0	TGGTTCCATAC	0.677	
-	4	441		NM_032286	NP_115662	Q9BTT4	MED10_HUMAN			1	AAGGCGGGTGA	0.517	
-	19	3314	D2_uc011cmz.1_	NM_001332	NP_001323	Q9UQB3	CTND2_HUMAN			8	GGAGGGCGTGC	0.577	
-	56	9455	H5_uc003jfc.2_5'F	NM_001369	NP_001360	Q8TE73	DYH5_HUMAN	4 (By similarity).		31	CCAAACTGCAG	0.413	
-	3	1083	0itw.1_Missense_	NM_001102562	NP_001096032	A6NNE9	MARHB_HUMAN	ical; (Potential).		0	TAGATCCATAAA	0.448	
-	4	930	.D185N|CDH18_	NM_004934	NP_004925	Q13634	CAD18_HUMAN	(Potential).|Cadherin 2.		7	TGCATCAGTAG	0.433	
-	2	380	n_p.M1I|CDH18_	NM_004934	NP_004925	Q13634	CAD18_HUMAN			7	AATTTTCATTGTA	0.428	
+	3	321		NM_020227	NP_064612	Q9NQV7	PRDM9_HUMAN	RAB-related.		6	ACTGGGAGAAA	0.428	
-	12	2476	10_uc011cnu.1_	NM_006727	NP_006718	Q9Y6N8	CAD10_HUMAN	lasmic (Potential).		12	CTTTCATTAATG	0.463	
-	30	3957	p.A1163T|RNASE	NM_013235	NP_037367	Q9NRR4	RNC_HUMAN	8 and pri-miRNA processin		0	TTATGGCGTACT	0.527	
+	9	2135	_p.V583I|PDZD2_	NM_178140	NP_835260	O15018	PDZD2_HUMAN			9	CCATCCGTCATC	0.463	
+	20	4268	m.2_Missense_Mu	NM_178140	NP_835260	O15018	PDZD2_HUMAN			9	CGGGGGAGAAA	0.657	
+	20	5993	m.2_Missense_Mu	NM_178140	NP_835260	O15018	PDZD2_HUMAN			9	GTCCGGCAGAA	0.512	
-	34	6808	rf42_uc011coz.1_	NM_023073	NP_075561	E9PH94	E9PH94_HUMAN			7	ATTTCCAGCAG	0.433	
-	22	2202	26_splice|RICTOR	NM_152756	NP_689969	Q6R327	RICTR_HUMAN			10	TACTCACATCA	0.318	
-	6	857	1_Missense_Muta	NM_000065	NP_000056	P13671	CO6_HUMAN	MACPF.		7	ATATTCCTCCA	0.423	
+	28	2855	iwr.2_Missense_M	NM_016338	NP_057422	Q9UI26	IPO11_HUMAN			4	AAACAGGAACT	0.333	
+	4	1287	ELD2_uc003jwr.1_	NM_001038603	NP_001033692	Q8N4S9	MALD2_HUMAN	lasmic (Potential).		0	AAGTTAATTTC	0.423	
-	2	2573	s.1_Missense_Mu	NM_003633	NP_003624	O14682	ENC1_HUMAN	Kelch 4.		3	GCCAGGGCTGG	0.507	
+	18	1958	p.G583E|PDE8B_	NM_003719	NP_003710	O95263	PDE8B_HUMAN	tic (By similarity).		0	CCAGGGAAGCC	0.567	
-	4	1551	_p.P401S|ANKRD	NM_001004441	NP_001004441	A5PLL1	AN34B_HUMAN			1	GGAAGGAGATG	0.488	
+	1	271		NR_003719						0	TGTTTGGGTTT	0.443	
+	11	2122	98_uc003kjt.2_5'	NM_032119	NP_115495	Q8WXG9	GPR98_HUMAN	ellular (Potential).		16	TACATTCCCTTA	0.363	
+	49	10328	.A1117V|GPR98_	NM_032119	NP_115495	Q8WXG9	GPR98_HUMAN	tracellular (Potential).		16	CGTGGCCTTGT	0.473	
+	75	16226	G3083E|GPR98_	NM_032119	NP_115495	Q8WXG9	GPR98_HUMAN	ellular (Potential).		16	GAGTGGACTAG	0.388	
+	20	2646	_Mutation_p.G75	NM_000919	NP_000910	P19021	AMD_HUMAN	idating lyase (By similarity)		0	TACAAGGATTTG	0.398	
+	2	1436		NM_207317	NP_997200	Q6S9Z5	ZN474_HUMAN			0	AAGACGCATTA	0.478	rs76983161
+	3	324	NCAIP_uc010jcu.	NM_005460	NP_005451	Q9Y6H5	SNCAP_HUMAN			2	AAAACGAAGAC	0.478	
+	1	541	p.D181N|PCDHA1	NM_018900	NP_061723	Q9Y5I3	PCDA1_HUMAN	|Extracellular (Potential).		1	CTTTGGATGTAG	0.423	
+	1	1853	lhd.2_Intron|PCDH	NM_018906	NP_061729	Q9Y5H8	PCDA3_HUMAN	|Extracellular (Potential).		8	CGGTGCGCGCA	0.677	
+	1	1789	03lhf.2_Intron|PCD	NM_018907	NP_061730	Q9UN74	PCDA4_HUMAN	|Extracellular (Potential).		6	CGCGCCAGCAC	0.677	
+	1	2140	.1_Intron|PCDHG	NM_018924	NP_061747	Q9Y5G1	PCDGF_HUMAN	lasmic (Potential).		0	CCCTGCGCCTG	0.582	
-	23	12656	AT2_uc003lud.3_	NM_001447	NP_001438	Q9NYQ8	FAT2_HUMAN	lasmic (Potential).		6	CATCACGACTG	0.622	
-	11	9177	2A_uc011dcs.1_In	NM_001447	NP_001438	Q9NYQ8	FAT2_HUMAN	(Potential).|Cadherin 27.		6	CATGCGCCCCA	0.463	

-	4	579	_p.D98N|GLRA1_	NM_001146040	NP_001139512	P23415	GLRA1_HUMAN	ellular (Probable).	2	GGGGTCGTTCC	0.517	
+	3	907	_Mutation_p.R131	NM_001135037	NP_001128509	P55082	MFAP3_HUMAN	.|Extracellular (Potential).	0	CCAATTCGTGCC	0.443	
+	6	1477	IPAL4_uc011ddq.	NM_001099287	NP_001092757	Q0D2K0	NIPA4_HUMAN	lasmic (Potential).	0	CCTCATCACCAG	0.478	
-	10	1392	r.1_Intron|GABRB	NM_021911	NP_068711	P47870	GBRB2_HUMAN	lasmic (Probable).	0	GAGAAATCGTaat	0.184	rs150956270
+	35	3574	CK2_uc010jjm.2_	NM_004946	NP_004937	Q92608	DOCK2_HUMAN	nteraction with CRKL.	7	GCACCCAACCA	0.587	
-	4	839	mkq.2_Missense_	NM_014275	NP_055090	Q9UQ53	MGT4B_HUMAN	enal (Potential).	0	GGTACGAGTGC	0.682	
+	7	1592	wr.2_Missense_M	NM_006567	NP_006558	O95363	SYFM_HUMAN	FDX-ACB.	0	GTACCGCCACA	0.592	
+	10	3560	p.P1057L|RREB1_	NM_001003698	NP_001003698	Q92766	RREB1_HUMAN	Pro-rich.	11	GCCCCCCGTGA	0.657	
+	5	723	ag.1_Missense_M	NM_030948	NP_112210	Q9C0D0	PHAR1_HUMAN		0	AAAGCGAAAAG	0.438	
-	2	119	C1D7_uc003nao.	NM_016495	NP_057579	Q9P0N9	TBCD7_HUMAN		1	TGAACGAAAGT	0.388	
+	1	275	AN4_uc011dlb.1_	NM_001007531	NP_001007532	Q5M9Q1	NKAPL_HUMAN		2	GGCGGCTCCC	0.617	
-	4	3842		NM_052923	NP_443155	Q6R2W3	SCND3_HUMAN		1	agttcatttcgtatttcaa	0	
+	5	561	_Mutation_p.G119	NM_013993	NP_054699	Q08345	DDR1_HUMAN	(Potential).|F5/8 type C.	9	GGTGGGCACCC	0.672	
-	2	626	S1C1_uc010jsj.1_	NM_014069	NP_054788	Q9UIG4	PS1C2_HUMAN		0	CCGGCCAAGGG	0.667	
+	6	761	se_Mutation_p.P1	NM_080686	NP_542417	P48634	PRC2A_HUMAN	AA type A repeats.	0	ATTTCCGACCC	0.577	
+	9	1100	.3_Missense_Mut	NM_080686	NP_542417	P48634	PRC2A_HUMAN	7 AA type A repeats.	0	TCCCCGTGTGG	0.493	
+	16	2984	T2_uc003nvc.3_	NM_080686	NP_542417	P48634	PRC2A_HUMAN	AA type A repeats.	0	CCAGGGCCCCC	0.692	
+	25	3229	1_Missense_Muta	NM_007293	NP_009224	P0C0L4	CO4A_HUMAN		0	AGTTTCGGAAG	0.612	
-	15	5777		NM_019105	NP_061978	P22105	TENX_HUMAN		0	GGCGACGGCCG	0.642	
-	3	589	BP_uc003odz.2_	NM_003190	NP_003181	O15533	TPSN_HUMAN	enal (Potential).	1	TGGTCGCAAGA	0.602	
+	31	4219		NM_002224	NP_002215	Q14573	ITPR3_HUMAN	lasmic (Potential).	19	TGGTCGTGTTC	0.612	
-	2	425	dsq.1_Missense_	NM_012391	NP_036523	O95238	SPDEF_HUMAN		5	GCTGGCGCTGC	0.667	
+	62	9419	uc003oof.1_Intron	NM_001371	NP_001362				21	TCATTTCAAGATC	0.358	
+	10	1062	h.2_RNA|GLP1R_	NM_002062	NP_002053	P43220	GLP1R_HUMAN	lasmic (Potential).	5	TCCAAACTGAA	0.547	
-	2	1327		NM_020737	NP_065788	Q9ULH4	LRFN2_HUMAN	xtracellular (Potential).	3	AGGCGGCTCGC	0.622	
+	8	1336	_p.S291F|FOXP4_	NM_001012426	NP_001012426	Q8IVH2	FOXP4_HUMAN		1	CTCTTCCCACG	0.632	
+	12	2933	p.R953Q|CUL9_u	NM_015089	NP_055904	Q8IWT3	CUL9_HUMAN		12	GATTCGATCCC	0.597	
+	1	361	_p.A88T|SLC22A7	NM_153320	NP_696961	Q9Y694	S22A7_HUMAN		0	CCCAGGCTCTC	0.637	
-	7	1041	p.R247Q|GTPBP2	NM_019096	NP_061969	Q9BX10	GTPB2_HUMAN		2	GGACCCGCTCC	0.597	
+	16	1568	se_Mutation_p.E4	NM_018426	NP_060896	Q5T3F8	TM63B_HUMAN		3	TTCTTTGAAGCC	0.597	
+	7	1184	p.R325Q|RUNX2_	NM_001024630	NP_001019801	Q13950	RUNX2_HUMAN	o/Ser/Thr-rich.	3	CACACGGGGCA	0.592	
-	22	2282	lutation_p.E69K|C	NM_030820	NP_110447	Q96P44	COLA1_HUMAN	ollagen-like 4.	2	TGGTTCTCCTG	0.418	
+	30	4688	14_splice|BAI3_u	NM_001704	NP_001695	O60242	BAI3_HUMAN		50	TTACAGAGAAG	0.234	
-	9	1057	OL9A1_uc003pff.	NM_001851	NP_001842	P20849	CO9A1_HUMAN	elical region (COL3).	4	CGGGGGGCCC	0.577	
-	3	590	ou.2_Missense_M	NM_001143957	NP_001137429	Q9BZJ6	GPR63_HUMAN	ellular (Potential).	2	GTCAGGATGCT	0.473	
+	6	1091	SP3_uc003pvo.2_	NM_003880	NP_003871	O95389	WISP3_HUMAN	CTCK.	0	AAATGGAAGAT	0.373	
+	8	882	_p.P255S|NT5DC1	NM_152729	NP_689942	Q5TFE4	NT5D1_HUMAN		0	AGAGACCTTTC	0.398	
-	32	5474	.1_RNA|GOPC_u	NM_002944	NP_002935	P08922	ROS_HUMAN	III 9.|Extracellular (Potentia	25	TTTGGGAATGC	0.338	
+	2	662	e_Mutation_p.G3	NM_000165	NP_000156	P17302	CXA1_HUMAN	lasmic (Potential).	2	AGTACGGTATT	0.443	
+	14	2737	qai.2_Missense_	NM_181782	NP_861447	Q8NI08	NCOA7_HUMAN		3	CATGCAGCTACT	0.507	
+	3	279	1_uc010kfm.1_Mi	NM_000045	NP_000036	P05089	ARGI1_HUMAN		1	TGTGGGAAAAG	0.483	
-	1	931	P3_uc010kfq.2_I	NM_001145659	NP_001139131	A4FU28	CTGE9_HUMAN		0	TTTCGGAGGAT	0.368	
-	2	524	RA_uc003qhk.2_	NM_014432	NP_055247	Q9UHF4	I20RA_HUMAN	ellular (Potential).	4	ACAGGGAACTG	0.353	
-	6	3204	p.R781*|LATS1_u	NM_004690	NP_004681	O95835	LATS1_HUMAN	rotein kinase.	6	ACATCGACAGC	0.473	
+	2	521		NM_030949	NP_112211	Q8TAE6	PP14C_HUMAN		0	GAGCTTCAAAAT	0.443	
-	43	6870	u.3_Missense_M	NM_182961	NP_892006	Q8NF91	SYNE1_HUMAN	ic (Potential).|Potential.	45	GATATTCTCTCAT	0.368	
-	5	1302	p.R275Q|RSPH3_	NM_031924	NP_114130	Q86UC2	RSPH3_HUMAN	Potential.	2	CTTCTCGGTGT	0.388	

-	6	728	_p.E215K|PHF10_	NM_018288	NP_060758	Q8WUB8	PHF10_HUMAN	SAY.	1	GCGTTCCCGGT	0.368
+	2	436	md.2_Missense_M	NM_018641	NP_061111	Q9NRB3	CHSTC_HUMAN	enal (Potential).	1	AGAGCGTGAGA	0.687
-	4	1024	RADIL_uc011jwc.1	NM_018059	NP_060529	Q96JH8	RADIL_HUMAN		7	TGCTGGGCTTG	0.682
+	13	1897	p.V592M|USP42_	NM_032172	NP_115548	Q9H9J4	UBP42_HUMAN		5	AGCCCGTGATG	0.537
+	15	3238	wq.1_Missense_M	NM_032172	NP_115548	Q9H9J4	UBP42_HUMAN	Arg-rich.	5	ACACCGAGGGC	0.692
+	2	326	w.2_Missense_M	NM_006908	NP_008839	P63000	RAC1_HUMAN		2	CATTTCCTGGA	0.353
-	7	2138		NM_015204	NP_056019	Q9UPZ6	THS7A_HUMAN	ellular (Potential).	3	ATGGGGCATCA	0.522
+	3	517	_p.T27_splice|KL	NM_001031710	NP_001026880	Q8IXQ5	KLHL7_HUMAN		0	TTGTAGCTAAC	0.383
-	2	140	kut.1_Intron|DFNA	NM_001127453	NP_001120925	O60443	DFNA5_HUMAN		1	CAGGTCACCAT	0.373
+	3	1630	_Mutation_p.L200	NM_001989	NP_001980	P49640	EVX1_HUMAN		1	TCCTTCCTCACC	0.726
+	16	1488	ADCYAP1R1_uc0	NM_001118	NP_001109	P41586	PACR_HUMAN	lasmic (Potential).	1	TGAACCGTTACT	0.587
+	12	1680	lp.2_Missense_M	NM_002541	NP_002532	Q02218	ODO1_HUMAN		2	GCAGCCGCTCA	0.572
+	15	2542		NM_021116	NP_066939	Q08828	ADCY1_HUMAN	lasmic (Potential).	6	TCCTGCCGGCC	0.607
-	22	3234	w.2_Missense_Mu	NM_022748	NP_073585	Q68CZ2	TENS3_HUMAN		4	CCATGGGCTTG	0.602
-	45	6761	1_Intron|PKD1L1_	NM_138295	NP_612152	Q8TDX9	PK1L1_HUMAN	lasmic (Potential).	11	GGTGGCGAGCT	0.657
-	26	4149		NM_138295	NP_612152	Q8TDX9	PK1L1_HUMAN		11	ACTTACCTTATT	0.338
+	26	9800	_p.D333N|ABCA1	NM_152701	NP_689914	Q86UQ4	ABCAD_HUMAN		10	CTTAGCGATTCT	0.368
+	4	329	e_Mutation_p.A87	NM_000265	NP_000256	P14598	NCF1_HUMAN	PX.	1	GGGCCGCCGAG	0.652
+	12	2240	fj.3_Missense_Mut	NM_020892	NP_065943	Q86UW9	DTX2_HUMAN		2	TCATCTTCACA	0.463
-	3	2846	v.2_Missense_Mu	NM_033026	NP_149015	Q9Y6V0	PCLO_HUMAN	Pro-rich.	7	GTTCTTCCTTCT	0.483
-	16	2063		NM_006080	NP_006071	Q14563	SEM3A_HUMAN	-like C2-type.	4	TGATTCTCTCTT	0.408
+	3	1246	.G285S|STEAP2_	NM_152999	NP_694544	Q8NFT2	STEA2_HUMAN	oxidoreductase.	2	ATTACGGCACC	0.408
-	3	3481_3482	g.2_Missense_M	NM_017654	NP_060124	Q5K651	SAMD9_HUMAN		7	CCGATGGATACT	0.381
+	44	3376	1A2_uc011kib.1_I	NM_000089	NP_000080	P08123	CO1A2_HUMAN		9	GCCCCGTGGGT	0.537
+	6	711	_p.V208I|ARPC1	NM_005720	NP_005711	O15143	ARC1B_HUMAN		0	ATGGCGTCTGT	0.637
+	3	773	AN1_uc003usl.1_	NM_003439	NP_003430	P17029	ZKSC1_HUMAN		3	GTCTCGGAAAC	0.532
+	15	1678	3_uc011kjk.1_Mi	NM_012447	NP_036579	Q9UJ98	STAG3_HUMAN		8	GGCTCGGCTGA	0.562
-	12	2599	_p.S610F|EPHB4	NM_004444	NP_004435	P54760	EPHB4_HUMAN	Potential).|Protein kinase.	15	GGAAGGAGTCC	0.607
+	8	1007	liv.2_Missense_M	NM_004279	NP_004270	O75439	MPPB_HUMAN		4	GGGATCGCTCT	0.403
+	17	2528	e_Mutation_p.R66	NM_182931	NP_891847	Q8IZD2	MLL5_HUMAN		3	GCAGCGTCGGA	0.398
-	9	1107	cv.2_Missense_M	NM_182691	NP_872633	P78362	SRPK2_HUMAN	rotein kinase.	6	CTGAGGTGATG	0.473
-	4	1488		NM_002711	NP_002702	Q16821	PPR3A_HUMAN		34	TCTCTTCGTAAA	0.363
+	10	1472	w.1_Missense_M	NM_080928	NP_563616	Q8WXK1	ASB15_HUMAN	ANK 8.	3	ATTATGAAATTG	0.428
-	4	673	g.1_Missense_Mu	NM_006193	NP_006184	O43316	PAX4_HUMAN		1	GGGTACCCCGG	0.572
-	4	750		NM_001708	NP_001699	P03999	OPSB_HUMAN	Name=6; (Potential).	0	ACCACCATGCG	0.567
+	2	368	rc.1_Missense_M	NM_001008749	NP_001008749	A4D1S5	RAB19_HUMAN		0	CGTGCGTTCCC	0.438
-	1	608	NND2A_uc003vvw	NM_015689	NP_056504	Q9ULE3	DEN2A_HUMAN		4	GGGATCGTTCT	0.602
-	15	1860		NM_004333	NP_004324	P15056	BRAF_HUMAN	rotein kinas_R603>I(2)|p.T	18290	ATTTCACTGTA	0.368
+	13	1565		NM_004668	NP_004659	O43451	MGA_HUMAN	(Potential).|Maltase.	2	CAATCCCAACTG	0.363
+	1	240		NM_178829	NP_849151	Q96L11	CG034_HUMAN		0	AAACGCCCTCT	0.547
+	1	698		NM_001004685	NP_001004685	O95006	OR2F2_HUMAN	lasmic (Potential).	4	AGAAGGAAGAA	0.512
-	7	1413		NM_004911	NP_004902	P13667	PDIA4_HUMAN		6	GCTTACCTGGA	0.562
+	12	1459	PO_uc010lpl.1_Int	NM_198455	NP_940857	A2VEC9	SSPO_HUMAN	TIL 1.	0	GCTGCGAGGCG	0.672
+	3	836	lpu.2_Missense_M	NM_018384	NP_060854	Q96F15	GIMA5_HUMAN	lasmic (Potential).	2	CCCTGGATGAC	0.552
-	6	1403	_p.I368F|KCNH2_	NM_000238	NP_000229	Q12809	KCNH2_HUMAN	=Segment S2; (Potential).	4	CACAATGAACA	0.607
-	3	406	x.2_RNA|VIPR2_	NM_003382	NP_003373	P41587	VIPR2_HUMAN	ellular (Potential).	2	GCAGGGCACCG	0.567
-	32	5419	.D1069N|CSMD1_	NM_033225	NP_150094	Q96PZ7	CSMD1_HUMAN	ar (Potential).|CUB 10.	25	CAAATCATTCAG	0.423

+	3	621	AT5_uc011kwm.1_	NM_018361	NP_060831	Q9NUQ2	PLCE_HUMAN		0	GCTGACATCTTG	0.473	
+	4	805	tz.2_Missense_Mu	NM_001715	NP_001706	P51451	BLK_HUMAN	SH3.	3	TGATCGGGACC	0.567	
+	19	3399	_p.V993I|PCM1_u	NM_006197	NP_006188	Q15154	PCM1_HUMAN		36	TCTTACGTAGAA	0.413	
-	5	680	SAH1_uc003wyn.2_	NM_177924	NP_808592	Q13510	ASAH1_HUMAN		0	ATATCAGTAACAG	0.323	
-	13	1577	se_Mutation_p.S3	NM_001135691	NP_001129163	P54219	VMAT1_HUMAN	ical; (Potential).	2	ATTAGGGAACAC	0.468	
+	14	1774	p.R567C|XPO7_u	NM_015024	NP_055839	Q9UIA9	XPO7_HUMAN		5	CAGTTTCGTAAG	0.483	
+	4	530	_p.E25K|ADAMD	NM_014479	NP_055294	O15204	ADEC1_HUMAN		2	TACACTGAAACA	0.468	
+	2	235	xea.1_Missense_M	NM_003817	NP_003808	Q9H2U9	ADAM7_HUMAN	cellular (Potential).	5	GAAGCGAGATA	0.403	
+	9	906	xec.2_Missense_M	NM_003817	NP_003808	Q9H2U9	ADAM7_HUMAN	2B.|Extracellular (Potential).	5	AATATAGAAACTA	0.318	
+	3	443	nse_Mutation_p.D	NM_004331	NP_004322	O60238	BNI3L_HUMAN		0	ATGTTTGATGTG	0.398	
+	3	445	nse_Mutation_p.D	NM_004331	NP_004322	O60238	BNI3L_HUMAN		0	GTTTGATGTGGA	0.398	
+	5	1324	xgb.1_Missense_M	NM_016240	NP_057324	Q6AZY7	SCAR3_HUMAN	cellular (Potential).	4	GCCGAGGAGCTC	0.602	
-	2	175	ense_Mutation_p.N	NM_172366	NP_758954	Q8IX29	FBX16_HUMAN		1	GATGGTTTAGG	0.373	
+	9	1048	p.L275P|ADAM32_	NM_145004	NP_659441	Q8TC27	ADA32_HUMAN	2B.|Extracellular (Potential).	3	TAACCTAAGGC	0.303	
+	8	850	CM4_uc011ldi.1_M	NM_182746	NP_877423	P33991	MCM4_HUMAN		4	CTGACTCAATCT	0.328	
+	14	2076	_p.R661C|MCM4_	NM_182746	NP_877423	P33991	MCM4_HUMAN	MCM.	4	ACAGGCGTCTG	0.463	rs144738849
-	17	2692	DNL_uc003xqt.3_F	NM_144651	NP_653252	A1KZ92	PXDNL_HUMAN		2	TGGAGCGCGCG	0.662	
+	5	1047		NM_147189	NP_671722	Q8TC76	F110B_HUMAN		1	GGAGGCCGACA	0.677	
-	22	2009	ee.1_Missense_Mu	NM_003580	NP_003571	Q92636	FAN_HUMAN		1	CTCTTCACCTG	0.363	
+	5	1781	_p.A433S|YTHDF3	NM_152758	NP_689971	Q7Z739	YTHD3_HUMAN	YTH.	0	CGTATGCTGGT	0.418	
-	16	2734	3xxl.1_Missense_M	NM_006421	NP_006412	Q9Y6D6	BIG1_HUMAN	SEC7.	8	CATACGAAGGG	0.398	
-	10	3078	R736W|SLCO5A1_	NM_030958	NP_112220	Q9H2Y9	SO5A1_HUMAN	lasmic (Potential).	4	AGTCCGGGCAT	0.572	
-	3	219	ense_Mutation_p.	NM_001738	NP_001729	P00915	CAH1_HUMAN		2	CATATCCCCAGT	0.328	
+	4	623	S8_uc011lgq.1_RN	NM_017864	NP_060334	Q75QN2	INT8_HUMAN		0	CAAAACCCGGAC	0.353	
+	42	7898	iw.2_Missense_Mu	NM_017890	NP_060360	Q7Z7G8	VP13B_HUMAN		20	TTGATTCTGTATT	0.443	rs145208175
-	22	2984	s.1_Missense_Mu	NM_015902	NP_056986	O95071	UBR5_HUMAN	Poly-Ser.	28	TACCTTCGGCTA	0.413	
+	2	1099		NM_003301	NP_003292	P34981	TRFR_HUMAN	lasmic (Potential).	3	GTCAGACCATTT	0.473	
+	1	250	_Translation_Start	NM_173851	NP_776250	Q8IWU4	ZNT8_HUMAN	lasmic (Potential).	4	AAAGAACGTATC	0.428	
-	2	193	se_Mutation_p.E2	NM_207506	NP_997389	Q8N8I0	SAM12_HUMAN		1	ACCTTCAGCATG	0.418	
+	7	960	2_5'UTR|COL14A	NM_021110	NP_066933	Q05707	COEA1_HUMAN	VWFA 1.	12	ATAAAGGAGGAA	0.363	
-	9	2444	Y8_uc010mds.2_I	NM_001115	NP_001106	P40145	ADCY8_HUMAN	ical; (Potential).	6	AACTTTGTATTG	0.353	
+	10	2265		NM_003235	NP_003226	P01266	THYG_HUMAN	globulin type-1 7.	15	GGACGGTGCAG	0.527	rs145363255
-	11	1988		NM_152888	NP_690848	Q8NFW1	COMA1_HUMAN	ke 1.|Pro-rich.|Gly-rich.	13	TTCTCTCCCTTA	0.587	
-	6	1294		NM_152888	NP_690848	Q8NFW1	COMA1_HUMAN	SP N-terminal.	13	ACACATCCCTGG	0.522	rs145554134
+	13	1399		NM_139021	NP_620590	Q8TD08	MK15_HUMAN		2	CTGCGCCCTCCC	0.687	
-	1	4908		NM_031308	NP_112598	P58107	EPIPL_HUMAN	Plectin 27.	2	AACATTCCTGCT	0.627	
+	9	1275		NM_003801	NP_003792	O43292	GPAA1_HUMAN		0	GGCTACGCTCT	0.637	
-	6	1275	RPIN_uc003zbb.2_	NM_030974	NP_112236	Q9H0F6	SHRPN_HUMAN	tion with SHANK1 (By simi	1	CTGGCGGGAAA	0.652	
-	25	2779		NM_013291	NP_037423	Q10570	CPSF1_HUMAN	lization signal (Potential).	1	CTCACGGAAGT	0.642	
+	12	4202	10mgx.1_Splice_S	NM_015158	NP_055973	Q14678	KANK1_HUMAN		4	TGCCGGTATGTT	0.522	
+	3	659	LR_uc003zhm.1_F	NM_003383	NP_003374	P98155	VLDLR_HUMAN	ential).|LDL-receptor class	3	CCAGCCGATGG	0.453	
+	27	5048	_p.G342S|ADAMT	NM_001040272	NP_001035362	Q8N6G6	ATL1_HUMAN		5	CGGGATGGCATC	0.527	
-	2	553	TR|CDKN2A_uc01	NM_000077	NP_000068	P42771	CD2A1_HUMAN	ANK 4. I83fs*2(2)|p.P1	3678	CCACGGGCAGA	0.731	rs121913386
-	1	1687	uc003zrh.1_RNA	NM_153809	NP_722516	Q8IZX4	TAF1L_HUMAN		26	CATCAGGAATTT	0.483	
+	36	4421	wr.2_Missense_M	NM_006377	NP_006368	O14795	UN13B_HUMAN	MHD2.	5	AAAACCTTCCTG	0.512	
-	6	994	u.3_Missense_Mu	NM_006289	NP_006280	Q9Y490	TLN1_HUMAN	FERM.	13	CAGGAGGTTCA	0.577	
+	1	287		NM_001039792	NP_001034881	Q6UXD1	HRCT1_HUMAN		0	GCGGCGGGGCC	0.542	

+	18	2026	.1_Missense_Mut	NM_014791	NP_055606	Q14680	MELK_HUMAN	KA1.	6	GGCAGCGGCTT	0.453	
-	3	1430		NM_003028	NP_003019	Q15464	SHB_HUMAN	with LAT, FAK1, JAK1 and	3	GGACCGGACAC	0.512	
+	2	146		NM_000692	NP_000683	P30837	AL1B1_HUMAN		1	TTAGCCTCCAG	0.602	
-	8	3852_3853		NM_015225	NP_056040	Q8WUY3	PRUN2_HUMAN		0	TGCTCTGAATCT	0.45	
-	4	999		NM_016848	NP_058544	Q92529	SHC3_HUMAN	PID.	4	TGGCCGTGGAG	0.547	
-	23	4108	q.2_Missense_Mu	NM_000264	NP_000255	Q13635	PTC1_HUMAN	lasmic (Potential).	379	CTCTGGGGGGG	0.657	
-	38	7118	ty.2_Missense_M	NM_153366	NP_699197	Q4LDE5	SVEP1_HUMAN	Sushi 14.	7	GAGAGGAACAC	0.483	
-	5	1510		NM_001101338	NP_001094808	P0CG24	ZN883_HUMAN	2H2-type 3.	0	AGTATGGACTC	0.363	
-	7	705	_p.S151L|ALAD_u	NM_000031	NP_000022	P13716	HEM2_HUMAN		0	TGTCCGACGGG	0.627	
+	18	4798	q.1_Missense_M	NM_002581	NP_002572	Q13219	PAPP1_HUMAN	Sushi 4.	9	GCCAGGAGATG	0.537	
-	24	2990		NM_001735	NP_001726	P01031	CO5_HUMAN		2	ACAAGATCTCA	0.428	
+	3	315	e_Mutation_p.D8	NM_198469	NP_940871	Q5VZ52	MORN5_HUMAN		0	ACTGCGACGGC	0.507	
+	2	191	wa.2_Missense_	NM_138777	NP_620132	Q96E11	RRFM_HUMAN		3	GACCCGTTTCA	0.463	rs140821991
+	7	1774	w.1_Missense_M	NM_173689	NP_775960	Q5IJ48	CRUM2_HUMAN	otential).|Laminin G-like 1.	1	AACTCCGCTGC	0.682	
+	6	627	vj.2_Missense_Mu	NM_014397	NP_055212	Q9HC98	NEK6_HUMAN	rotein kinase.	3	GCGCCGTGGAG	0.607	
+	7	819	zo.1_Missense_M	NM_001045476	NP_001038941	Q5JTN6	WDR38_HUMAN	WD 6.	0	TATTCCCGCATG	0.612	
-	5	1145	3_5'UTR|SH2D3C	NM_170600	NP_733745	Q8N5H7	SH2D3_HUMAN		1	CTGTCCCAGGC	0.657	
+	11	1480	.R465W|DNM1_u	NM_004408	NP_004399	Q05193	DYN1_HUMAN		2	ACATCCGGGAG	0.697	
-	6	1271	B6_uc011mbt.1_	NM_017873	NP_060343	Q9NWX5	ASB6_HUMAN	SOCS box.	0	GCTCTCCAGCT	0.607	
+	33	6032	_Mutation_p.P14	NM_005085	NP_005076	P35658	NU214_HUMAN	1 X 5 AA approximate repe	16	TGCTCCAGTGT	0.537	
-	11	2639	F1_uc004cbm.2_	NM_007344	NP_031370	Q15361	TTF1_HUMAN		4	GTCTCGAAATG	0.313	
-	4	990	11mdf.1_Missens	NM_020385	NP_065118	Q9GZR2	REXO4_HUMAN	xonuclease.	0	CACACGGGCGG	0.557	
+	7	1470		NM_000093	NP_000084	P20908	CO5A1_HUMAN	nhelical region.	11	GGAGAACCCCG	0.592	
-	17	2635	ia.1_Missense_M	NM_017617	NP_060087	P46531	NOTC1_HUMAN	GF-like 23; calcium-binding	856	GTGCCGGCACG	0.701	
-	21	3308	_Mutation_p.D98	NM_001606	NP_001597	Q9BZC7	ABCA2_HUMAN	C transporter 1.	0	GATGTCGTGCC	0.632	
+	7	1269	p.G411D|EHMT1_	NM_024757	NP_079033	Q9H9B1	EHMT1_HUMAN		3	AGGCGGTGACG	0.587	
-	2	1285		NM_178129	NP_835230	Q86VZ1	P2RY8_HUMAN	lasmic (Potential).	5	TGGCTCCCTCC	0.706	
-	7	764	se_Mutation_p.H2	NM_006089	NP_006080	Q9UQR0	SCML2_HUMAN	MBT 2.	0	TGATATGAACTT	0.428	
-	6	574	.2_Intron|CDKL5_	NM_000330	NP_000321	O15537	XLRS1_HUMAN	F5/8 type C.	2	GGTCCGAGTTG	0.587	
-	1	404		NM_001017930	NP_001017930	A6NGE4	DC8L1_HUMAN	Glu-rich.	4	TGTCTCCTCTC	0.368	
-	4	597	p.R102Q|BCOR_u	NM_001123385	NP_001116857	Q6W2J9	BCOR_HUMAN		4	CCTCCCGACCT	0.562	
+	5	812	_p.L203F|EBP_uc	NM_006579	NP_006570	Q15125	EBP_HUMAN	ical; (Potential).	1	GAGTCCTTGTG	0.562	
-	6	2988	OM4_uc004dpd.3	NM_020717	NP_065768	Q9ULL8	SHRM4_HUMAN		1	AGCCATTTCCC	0.269	
-	12	1449	R8_uc011mou.1_	NM_017677	NP_060147	Q96EF0	MTMR8_HUMAN	ularin phosphatase.	4	GAAAGGCCACA	0.398	
+	2	660	GJB1_uc004dzg.3	NM_001097642	NP_001091111	P08034	CXB1_HUMAN	ellular (Probable).	1	AAAACCGTCTTC	0.617	
+	8	1294	N1_uc011mpt.1_	NM_052957	NP_443189	Q96QF7	ACRC_HUMAN	sp/Ser-rich.	3	AAGCTCCCGAC	0.557	
-	31	3651	qi.1_Missense_M	NM_002637	NP_002628	P46020	KPB1_HUMAN		4	GTACACGATTC	0.448	rs143802511
-	34	4071	Splice_Site_p.D94	NM_153252	NP_694984	Q6RI45	BRWD3_HUMAN		4	TGTATCCTTAATT	0.328	
-	17	1945	_p.Y231F|BRWD3_	NM_153252	NP_694984	Q6RI45	BRWD3_HUMAN		4	GACGATAATCC	0.383	
+	6	1474	fa.2_Missense_M	NM_019117	NP_061990	Q9C0H6	KLHL4_HUMAN	Kelch 1.	5	GGGCACTTTATG	0.403	
-	1	121	L_uc004ehc.1_5'	NM_024885	NP_079161	Q5H9L4	TAF7L_HUMAN		1	CCCACGGTCGA	0.527	
-	14	1526	_p.E15K|BTK_uc0	NM_000061	NP_000052	Q06187	BTK_HUMAN	rotein kinase.	6	GGCTTCTTCAA	0.428	
+	15	2701	c.1_Missense_Mut	NM_198465	NP_940867	Q7Z2Y5	NRK_HUMAN		14	CACATCATGTC	0.294	
+	7	1266	sk.1_Nonsense_M	NM_182607	NP_872413	Q86XK7	VSIG1_HUMAN	lasmic (Potential).	2	gagtcagagccTGG	0.408	
+	30	2652	p.G817E|COL4A5	NM_033380	NP_203699	P29400	CO4A5_HUMAN	le-helical region.	4	TGCCAGGAATAG	0.438	
+	44	4151	_Mutation_p.P131	NM_033380	NP_203699	P29400	CO4A5_HUMAN	le-helical region.	4	GTAATCCTGGC	0.383	
-	1	1622		NM_003604	NP_003595	O14654	IRS4_HUMAN		10	CACCTCGGGAT	0.632	

+	7	1114	164_uc010npq.2_M	NM_032227	NP_115603	Q5U3C3	TM164_HUMAN	ical; (Potential).	3	ACCATGACCCAC	0.522	
+	8	1044		NM_007231	NP_009162	Q9UN76	S6A14_HUMAN		3	GGAAAGATGCTC	0.259	
-	2	2416	r.2_Missense_Mut	NM_017544	NP_060014	O15226	NKRF_HUMAN	G-patch.	2	CTTCCCGCTTAT	0.493	
+	22	2581	e_Mutation_p.E79	NM_000276	NP_000267	Q01968	OCRL_HUMAN	Rho-GAP.	4	TGTTACGAGCTG	0.517	
-	15	3065	_p.I937F|IGSF1_	NM_001555	NP_001546	Q8N6C5	IGSF1_HUMAN	otential).|Ig-like C2-type 9.	5	GTAGATACAGCT	0.517	
+	6	1844	_p.P313L|GPR112_	NM_153834	NP_722576	Q8IZF6	GP112_HUMAN	ellular (Potential).	12	CACACCTGCCC	0.428	
+	3	1264		NM_001727	NP_001718	P32247	BRS3_HUMAN	lasmic (Potential).	1	GGTCCCGGGCA	0.512	
+	4	876	EC1_uc010nsl.1_	NM_005462	NP_005453	O60732	MAGC1_HUMAN		4	GTCTCCACTCC	0.498	
+	4	1679	EC1_uc010nsl.1_	NM_005462	NP_005453	O60732	MAGC1_HUMAN		4	CTGAGAGAACTC	0.478	
+	4	1681	EC1_uc010nsl.1_	NM_005462	NP_005453	O60732	MAGC1_HUMAN		4	TGAGAGAACTCA	0.483	
+	4	2369	EC1_uc010nsl.1_	NM_005462	NP_005453	O60732	MAGC1_HUMAN		4	AAATTCCTCAGA	0.562	
-	13	2122	u.1_Missense_Mu	NM_001110556	NP_001104026	P21333	FLNA_HUMAN	Filamin 4.	6	CTTGTCGTCAC	0.632	
+	16	1851	_p.P538S|ATAD3B_	NM_031921	NP_114127	Q5T9A4	ATD3B_HUMAN		0	AGCACCCCCTAT	0.647	
-	9	1430	5_uc001amc.1_5'	NM_015557	NP_056372	Q8TDI0	CHD5_HUMAN	PHD-type 2.	12	CGGGTTGAGGC	0.517	
-	3	255	me.2_Missense_M	NM_000983	NP_000974	P35268	RL22_HUMAN		0	CGGTGATCTTG	0.542	
-	8	1859	.G357D|CLSTN1_	NM_001009566	NP_001009566	O94985	CSTN1_HUMAN	ellular (Potential).	1	GGGTGCCGTTG	0.622	
+	1	151		NM_001080830	NP_001074299	O95522	PRA12_HUMAN		3	TTCATGGAGGCC	0.597	
+	3	319		NM_001013641	NP_001013663	A0PJX8	TMM82_HUMAN	Leu-rich.	2	GACCCGAAAAG	0.697	
+	19	2044	ense_Mutation_p.	NM_000085	NP_000076	P51801	CLCKB_HUMAN	CBS 2.	1	TTCATTCCCTCT	0.602	rs144513133
-	73	9777	d.2_Missense_Mu	NM_005529	NP_005520	P98160	PGBM_HUMAN	ike C2-type 18.	9	GCTTGGACCAG	0.632	
+	5	573	_p.W135*|GMEB1_	NM_006582	NP_006573	Q9Y692	GMEB1_HUMAN	SAND.	0	GACTGGAAGAG	0.428	
-	11	2056		NM_005955	NP_005946	Q14872	MTF1_HUMAN		2	GTCCCGGCATG	0.607	
-	11	2610		NM_020883	NP_065934	Q9P217	ZSWM5_HUMAN		0	GTGAACCAGCG	0.527	
-	5	669_670	5RL_uc001cwx.3_	NM_001031672	NP_001026842	Q6IPT4	NB5R5_HUMAN	-binding FR-type.	0	CTATCCCTCTGA	0.347	
-	12	2141	73_uc001dgi.3_Mi	NM_001002912	NP_001002912	Q5RHP9	CA173_HUMAN	Glu-rich.	5	TCAATTTCTAAG	0.413	
+	3	382	2_5'UTR|CLCA4_	NM_012128	NP_036260	Q14CN2	CLCA4_HUMAN		2	AGGTAGAGATG	0.363	
-	9	1173	_p.P232S|CCBL2_	NM_001008661	NP_001008661	Q6YP21	KAT3_HUMAN		1	ACCTGGAAAAG	0.308	
-	1	76_77	T_uc010oug.1_5'U	NM_001918	NP_001909	P11182	ODB2_HUMAN		1	GCTTCCCCGCAT	0.579	
-	8	1552	_p.T424A|COL11A	NM_001854	NP_001845	P12107	COBA1_HUMAN	nhelical region.	12	TTTCTGTAATATC	0.338	
-	7	662	fm.1_Missense_M	NM_133181	NP_573444	Q8TE67	ES8L3_HUMAN	Pro-rich.	3	CCTTTCCATAG	0.597	
+	78	9679	BPF10_uc010oyl.1	NM_001039703	NP_001034792	A6NDV3	A6NDV3_HUMAN		0	GGAGCTGCTGG	0.468	
-	3	1246		NM_001008536	NP_001008536	Q5QJ38	TCHL1_HUMAN		2	CTCTCCTCTCT	0.473	
-	3	5990_5991		NM_001009931	NP_001009931	Q86YZ3	HORN_HUMAN	22	3	ACCACCCTGAG	0.604	
+	2	506		NM_005547	NP_005538	P07476	INVO_HUMAN	QEK]-[PLSQE]-[EQDV]- [	3	TGTTGGAGCTC	0.259	
-	1	91	23E|ROBLD3_uc	NM_020131	NP_064516	Q9NRR5	UBQL4_HUMAN	biquitin-like.	2	CTCCTTGTCCTT	0.438	
-	12	1319	sb.1_Missense_M	NM_178229	NP_839943	Q86VI3	IQGA3_HUMAN		6	TAGACGATGCA	0.597	
+	1	194		NM_001004473	NP_001004473	Q8NGX5	O10K1_HUMAN	Name=2; (Potential).	1	TTGCCATCCTTT	0.488	
-	3	560	.2_Intron|SLAMF	NM_033438	NP_254273	Q96A28	SLAF9_HUMAN	.|Extracellular (Potential).	1	AGGCACCTTCC	0.527	
+	8	1624	lg.2_Missense_M	NM_021165	NP_066988	Q9C0B6	FAM5B_HUMAN		6	TCCTGGAACAG	0.587	
-	8	2173	pj.1_Missense_M	NM_014875	NP_055690	Q15058	KIF14_HUMAN	inesin-motor.	7	TGGGTCATCAC	0.388	rs144936292
-	14	2305	_5'Flank|PLEKHA	NM_014935	NP_055750	Q9Y2H5	PKHA6_HUMAN		4	TTCTTCCTCAGC	0.597	
-	3	1057	_p.M223I|LRRN2_	NM_006338	NP_006329	O75325	LRRN2_HUMAN	tracellular (Potential).	2	AGGTTCATGCC	0.607	
+	4	827	2_uc009xch.2_Mis	NM_001877	NP_001868	P20023	CR2_HUMAN	xtracellular (Potential).	8	ATGAAGGGTGA	0.453	
+	12	1666		NM_018060	NP_060530	Q9NSE4	SYIM_HUMAN		4	TTGGTGTATATC	0.363	
-	22	4088	u.2_Intron|PCNXL	NM_014801	NP_055616	A6NKB5	PCX2_HUMAN	ical; (Potential).	2	CTTGTGAAGCA	0.448	
+	13	1678	_p.R492*|ACTN2_	NM_001103	NP_001094	P35609	ACTN2_HUMAN	Spectrin 2.	5	GGGACCGACTG	0.383	
+	2	598	pxx.1_Missense_M	NM_000254	NP_000245	Q99707	METH_HUMAN	Hcy-binding.	3	AAGATCATGCCA	0.458	

-	3	520	_p.L121F|IL2RA_	NM_000417	NP_000408	P01589	IL2RA_HUMAN	cellular (Potential).	2	TGGAAGGCTCG	0.507	
+	16	3759	n_p.S1084F|KIAA	NM_019590	NP_062536	Q5T5P2	SKT_HUMAN		7	CCTCCTCCTCAA	0.542	
+	4	1325		NM_020752	NP_065803	Q5T848	GP158_HUMAN	Name=1; (Potential).	8	TCATCTCCTTCC	0.522	
+	9	1103	O3A_uc009xkp.1_	NM_017433	NP_059129	Q8NEV4	MYO3A_HUMAN	rotein kinase.	18	ACCCCCAAAAC	0.388	
-	2	976	nse_Mutation_p.G	NM_020848	NP_065899	Q9P266	K1462_HUMAN	Pro-rich.	4	GCTCCTCCCCTA	0.597	
-	6	2139	NF248_uc001izc.2	NM_021045	NP_066383	Q8NDW4	ZN248_HUMAN		1	TCATACGGCTTC	0.443	
-	1	1687		NM_002900	NP_002891	P10745	RET3_HUMAN	mate tandem repeats.|2.	2	GGAGCTCCATGT	0.652	
-	1	1235		NM_002900	NP_002891	P10745	RET3_HUMAN	mate tandem repeats.|2.	2	GGCCGGCATTG	0.647	
-	24	2863	.1_Missense_Mut	NM_020987	NP_066267	Q12955	ANK3_HUMAN		19	CCAATTCCTTAAG	0.483	
-	18	2317	_p.R703*|ANK3_	NM_020987	NP_066267	Q12955	ANK3_HUMAN	ANK 20.	19	TCACTCGATCTT	0.522	
+	2	1515_1516	jmx.3_Intron|CTN	NM_178011	NP_821079	Q86VH5	LRRT3_HUMAN	lar (Potential).|LRRCT.	3	TTGCTCCCTTGT	0.401	
+	3	957	y.2_Intron|STOX1	NM_001130161	NP_001123633	Q6ZVD7	STOX1_HUMAN		2	GGAGCACCACAT	0.458	
+	6	786	_Mutation_p.Q203	NM_004922	NP_004913	P53992	SC24C_HUMAN		3	ACTCCCCAGCGA	0.607	
-	1	2137		NR_002319					0	CATTATCCAGTG	0.537	
+	8	1228	qny.1_Missense_	NM_000769	NP_000760	P33261	CP2CJ_HUMAN		6	GACCCTCGTCAC	0.393	rs17879685
-	38	4955	xxq.2_Missense_	NM_025145	NP_079421	Q8NDM7	WDR96_HUMAN		0	AGTCAGTTTAGA	0.328	
+	8	1332	.1_Intron|WDR11_	NM_018117	NP_060587	Q9BZH6	WDR11_HUMAN	WD 3.	0	GCTGTCCTGTCA	0.483	
+	15	8353	ACC2_uc001lfz.2_	NM_206862	NP_996744	O95359	TACC2_HUMAN		10	GAGCCCGACTTA	0.542	
+	18	2223	T1_uc009xzz.1_M	NM_007329	NP_015568	Q9UGM3	DMBT1_HUMAN		7	CCAGTCCCGGT	0.522	
-	6	1322	ZD1_uc010qty.1_	NM_022034	NP_071317	Q86UP6	CUZD1_HUMAN	llular (Potential).|ZP.	2	CTTTACCTTTCTG	0.299	
-	3	497	_p.E223*|C10orf9	NM_001004298	NP_001004298	Q96M02	CJ090_HUMAN		2	CTCCTCTTTGG	0.647	
+	15	2817	_p.S874F|KNDC1_	NM_152643	NP_689856	Q76NI1	VKIND_HUMAN		2	CCATTTCCGAGA	0.537	
-	9	655	YCE1_uc009ybn.2_	NM_001143764	NP_001137236	Q8N0S2	SYCE1_HUMAN	Potential.	1	AAATCTCCTTTG	0.522	
+	1	766	_uc001mam.1_Int	NM_001004757	NP_001004757	Q8NH59	O51Q1_HUMAN	Name=6; (Potential).	1	TACATTCCCATG	0.517	
+	1	281	.1_Intron|TRIM22_	NM_001005175	NP_001005175	Q8NGI2	O52N4_HUMAN	cellular (Potential).	2	GCTCTAGTACAAT	0.463	
+	1	1004		NM_014469	NP_055284	O75526	HNRGT_HUMAN	g/Gly/Pro-rich.	0	GGGATCATCTG	0.662	
+	15	1698_1699	.2_Missense_Mut	NM_001178	NP_001169	O00327	BMAL1_HUMAN	PAC.	0	CAAGGAAGTAGA	0.361	
+	8	1511		NM_020229	NP_064614	Q9NQV5	PRD11_HUMAN		1	CTTCATCATTCA	0.562	
+	12	1716	Site_p.R535_splic	NM_152312	NP_689525	Q8N3Y3	LARG2_HUMAN		3	CCTCAGGGCCT	0.642	
-	17	2182	ly.2_Missense_Mu	NM_004476	NP_004467	Q04609	FOLH1_HUMAN	cellular (Probable).	3	CAATTTCTGTAA	0.269	
+	1	785		NM_001005275	NP_001005275	Q8NGL6	O4A15_HUMAN	lasmic (Potential).	2	GGAAACGAAAAG	0.438	
+	4	1602	se_Mutation_p.R6	NM_015457	NP_056272	Q9C0B5	ZDHC5_HUMAN	DHHC-type.	1	CCCCCTCGATGT	0.507	
-	1	644		NM_001005469	NP_001005469	Q8NH48	OR5B3_HUMAN	Name=5; (Potential).	0	GTGTAGGATATC	0.403	
+	3	251	npb.2_Missense_	NM_148975	NP_683876	Q96JQ5	M4A4A_HUMAN	ical; (Potential).	0	AGCATGGGAATA	0.428	
+	3	665	o.1_Missense_Mu	NM_004265	NP_004256	O95864	FADS2_HUMAN	ical; (Potential).	2	CTCTCAGGTGA	0.567	
-	6	1318_1319	wj.2_Missense_M	NM_004790	NP_004781	Q4U2R8	S22A6_HUMAN	ical; (Potential).	0	GAAGAGGTGGCG	0.624	
+	6	1348	_p.S394C|SIPA1_	NM_006747	NP_006738	Q96FS4	SIPA1_HUMAN	Rap-GAP.	0	CGCACTCCCTCT	0.542	
+	5	835	x.1_Missense_Mu	NM_001134775	NP_001128247	Q9H0B6	KLC2_HUMAN	TPR 1.	0	GCCCGGCTCCGC	0.632	
+	7	698	CS_uc001ois.2_R	NM_005125	NP_005116	O14618	CCS_HUMAN	xide dismutase-like.	0	TCACAGGGAAC	0.602	
-	2	707		NM_005117	NP_005108	O95750	FGF19_HUMAN		1	CCTTGATCTCCA	0.657	
+	25	2918	sg.2_Missense_M	NM_001567	NP_001558	O15357	SHIP2_HUMAN		4	AGAGGCCTCCT	0.632	
+	9	1142	se_Mutation_p.P3	NM_152222	NP_689408	Q969Z4	TR19L_HUMAN	lasmic (Potential).	1	CTAACCCGACCA	0.652	
+	4	827		NM_001098672	NP_001092142	Q6MZM0	HPHL1_HUMAN	e 2.|Extracellular (Potential	3	GTGGATCGAGAG	0.383	
+	3	627_628	piv.2_Missense_M	NM_000829	NP_000820	P48058	GRIA4_HUMAN	cellular (Potential).	8	GAAGCTCCTTTT	0.391	
+	10	1589		NM_015191	NP_056006	Q9H0K1	SIK2_HUMAN		3	ACCAATCAACTG	0.552	
-	8	1237	gy.1_Missense_M	NM_014987	NP_055802	Q9UPX0	TUTLB_HUMAN	ar (Potential).|Ig-like 4.	0	CGGGCACGTAAA	0.517	
-	3	229	_p.R56C|MLF2_u	NM_005439	NP_005430	Q15773	MLF2_HUMAN		1	CCGGCGGCTGG	0.517	

-	6	799		NM_014358	NP_055173	Q9ULY5	CLC4E_HUMAN	cellular (Potential).	1	TCAAAGGATTTAT	0.418	
-	4	552	M_uc009zgk.1_5'U	NM_000014	NP_000005	P01023	A2MG_HUMAN		5	CAACACGAAATT	0.393	
-	3	176	zt.2_Missense_Mu	NM_002723	NP_002714	P10163	PRB4_HUMAN	R]-[PR]-P-Q-G-G-N-Q-[PS	1	GACGTTGGGGCT	0.572	
+	15	2248	ense_Mutation_p.T	NM_004570	NP_004561	O75747	P3C2G_HUMAN		21	TGCATACCATTTT	0.413	
+	9	1157	zip.2_Missense_M	NM_017435	NP_059131	Q9NYB5	SO1C1_HUMAN	cellular (Potential).	7	AAGATCCCCAG	0.388	
+	19	2607	nh.1_Nonsense_M	NM_198578	NP_940980	Q5S007	LRRK2_HUMAN		24	CTAATTTAAGGA	0.318	
+	4	434	_uc001rny.3_Intro	NM_001114182	NP_001107654	Q9NWZ3	IRAK4_HUMAN	Death.	0	TGCTCCCAGGT	0.393	
-	4	860		NM_004693	NP_004684	O95678	K2C75_HUMAN	Coil 1B.|Rod.	0	GATCTCCTCGG	0.483	
-	9	1622		NM_175053	NP_778223	Q7RTS7	K2C74_HUMAN	Tail.	2	GCTTTCCTTGCT	0.627	
+	8	1693	o.2_Missense_Mu	NM_014903	NP_055718	Q8IVL0	NAV3_HUMAN		17	GATCCCTAAGG	0.423	
-	29	4385		NM_001109662	NP_001103132				2	AGGAGGGGACA	0.567	
-	28	4908		NM_000620	NP_000611	P29475	NOS1_HUMAN		7	TCACTTCGTACG	0.488	
+	12	1684		NM_194286	NP_919262	A7MD48	SRRM4_HUMAN		2	CCTTCAGGGAGC	0.657	
+	74	12798	ufu.3_Missense_M	NM_207437	NP_997320	Q8IVF4	DYH10_HUMAN	Potential.	6	TCAAAGGGTGA	0.532	
+	40	7387	.P2450L|EP400_u	NM_015409	NP_056224	Q96L91	EP400_HUMAN		12	TGAATCCCTTTC	0.388	
-	16	1308	_p.G289E|TPTE2_	NM_199254	NP_954863	Q6XPS3	TPTE2_HUMAN	hatase tensin-type.	0	TCTACTCCCTGA	0.368	
-	7	2930	.2_RNA|CENPJ_u	NM_018451	NP_060921	Q9HC77	CENPJ_HUMAN		2	GGTCTTGACTTA	0.348	
-	3	707	vo.2_Missense_M	NM_001142296	NP_001135768	Q8N0X7	SPG20_HUMAN		0	GAGTTGAGGTG	0.453	
-	1	457		NM_025113	NP_079389	Q9H714	CM018_HUMAN		0	ACTACACGCATC	0.453	
-	15	2287_2288	p.D628N|CHD8_u	NM_020920	NP_065971	Q9HCK8	CHD8_HUMAN		10	GAGATCCCCAAA	0.421	
-	2	1292	200Q|SALL2_uc0	NM_005407	NP_005398	Q9Y467	SALL2_HUMAN		3	GGCCTCGGGCT	0.607	
-	8	1172	_p.W75L|ADCY4_	NM_139247	NP_640340	Q8NFM4	ADCY4_HUMAN	lasmic (Potential).	3	GTGACCAAACG	0.602	
+	3	629		NM_025081	NP_079357	Q9P2P1	NYNRI_HUMAN		3	CTGCTGGAGCA	0.632	
+	3	356		NM_016039	NP_057123	Q9Y224	CN166_HUMAN		0	AAGATCGACAA	0.368	
-	11	2785	IH5_uc001xfy.2_3'	NM_139318	NP_647479	Q8NCM2	KCNH5_HUMAN	bly) (By similarity).|Cytopla	9	GACTTCCTGCA	0.522	
-	3	887	p.P140L|ESR2_uc	NM_001437	NP_001428	Q92731	ESR2_HUMAN	Modulating.	3	AACCTGGACCA	0.483	
+	8	1012_1013		NM_152443	NP_689656	Q96NR8	RDH12_HUMAN		1	TGCACCCAGGC	0.634	rs104894476
+	2	351		NM_006399	NP_006390	Q16520	BATF_HUMAN	Basic motif.	1	AAAAATCGTATTG	0.522	
-	13	2166	wc.1_Missense_M	NM_007039	NP_008970	Q16825	PTN21_HUMAN		4	CCACGGGCAGG	0.682	
+	37	6039	ybs.1_Missense_M	NM_020818	NP_065869	Q9P2D8	UNC79_HUMAN		17	AGAATTTACCAG	0.418	
-	3	890		NM_001080451	NP_001073920	Q86U17	SPA11_HUMAN		1	GGAGGACCAGC	0.537	
+	7	1486	AIP2_uc010txz.1_	NM_006291	NP_006282	Q03169	TNAP2_HUMAN		1	GCTGGGCCCCC	0.632	
+	5	508	_Mutation_p.E158	NM_024071	NP_076976	Q9BQ24	ZFY21_HUMAN		0	AATCGAAATTGTA	0.498	
+	12	2306		NM_015656	NP_056471	Q9ULI4	KI26A_HUMAN		1	CCGCACGCCTC	0.721	
+	11	3534	ne.2_Missense_Mu	NM_170589	NP_733468	Q8NG31	CASC5_HUMAN	A approximate repeats.	5	ATAACGAAAGTG	0.378	
+	1	556	0udg.1_Intron|CA	NM_000070	NP_000061	P20807	CAN3_HUMAN	alpain catalytic.	1	CGGATGAGACC	0.478	
-	9	1516	p.R401Q|PCSK6_	NM_002570	NP_002561	P29122	PCSK6_HUMAN	Catalytic.	2	ATTTTTCGCTCA	0.532	
+	1	780		NM_001001674	NP_001001674	Q8NGB8	O4F15_HUMAN	cellular (Potential).	0	ACATGGCCTTC	0.423	
-	4	704	M8A_uc002cgv.3_	NM_021259	NP_067082	Q9HCN3	TMM8A_HUMAN	cellular (Potential).	3	ATGATGGAAATC	0.667	
+	2	694	_p.A198T|PIGQ_u	NM_148920	NP_683721	Q9BRB3	PIGQ_HUMAN		1	TGGAGGCCAGC	0.667	
+	2	976	24_uc002cqm.2_	NM_020705	NP_065756	Q9ULP9	TBC24_HUMAN		0	GAAGACGGTGT	0.602	
-	13	3478	uyn.1_Missense_	NM_001134407	NP_001127879	Q12879	NMDE1_HUMAN	lasmic (Potential).	45	ACATAGTTATTGA	0.478	
-	1	655	_5'Flank|CLEC16	NM_014015	NP_054734	O95424	DEXI_HUMAN		0	CGTCGAGCTCC	0.637	
+	8	1161	ssense_Mutation_	NM_024847	NP_079123	Q7Z402	TMC7_HUMAN	lasmic (Potential).	3	GAATGCGGCAGA	0.398	
-	9	1238	_p.P343L|ACSM2	NM_182617	NP_872423	Q68CK6	ACS2B_HUMAN		5	TTTCTGGAAGA	0.527	
-	13	1450	n.1_Missense_Mut	NM_003460	NP_003451	Q05996	ZP2_HUMAN	llular (Potential).|ZP.	3	CACTGGAGGAG	0.428	
+	2	444		NM_000336	NP_000327	P51168	SCNNB_HUMAN	llular (By similarity).	7	AGACCATGGAC	0.602	rs150466803

+	14	1764	me.2_Missense_M	NM_212535	NP_997700	P05771	KPCB_HUMAN	rotein kinase.		9	CCGTGGATTGG	0.458	
-	25	3931	C11_uc002efh.1_	NM_033151	NP_149163	Q96J66	ABCCB_HUMAN	r 2.|Cytoplasmic (Potential)		6	CCATGGGCTCC	0.597	
+	9	1361	efx.2_Missense_M	NM_182922	NP_891552	Q7Z4Q2	HEAT3_HUMAN			2	GAATTCCTTCA	0.502	
+	1	1169	H3_uc010vli.1_5'U	NM_001793	NP_001784	P22223	CADH3_HUMAN		p.?(1)	5	TCCTCCTTCTC	0.731	
-	13	2432	_p.K259N|ADAMT	NM_199355	NP_955387	Q8TE60	ATS18_HUMAN	Cys-rich.		18	TAGGGTTTCCA	0.378	
+	2	404		NM_020927	NP_065978	Q9HCJ6	VAT1L_HUMAN			1	TGCCAGGATTT	0.438	
-	2	404	fhu.1_Missense_M	NM_172347	NP_758857	Q8TDN1	KCNG4_HUMAN	lasmic (Potential).		3	CTCCTCGTAGC	0.622	
+	10	1210	RISPLD2_uc002fi	NM_031476	NP_113664	Q9H0B8	CRLD2_HUMAN	LCCL 1.		0	CCAGTCGTCTA	0.532	
-	16	1770	_Site_p.E336_splic	NM_021962	NP_068781	Q12979	ABR_HUMAN			1	AACTCCTGGGG	0.562	
-	16	3789	qv.1_Missense_Mu	NM_017575	NP_060045	Q86US8	EST1A_HUMAN			4	AACAAAGGTCTG	0.582	
+	2	812	A_uc002ghe.2_5'F	NM_001102614	NP_001096084	P0C7Q6	AMCL3_HUMAN	ical; (Potential).		0	TGCTGGGCTCT	0.627	
-	13	1321	uc002gml.1_Intron	NM_002472	NP_002463	P13535	MYH8_HUMAN	osin head-like.		11	TGCCAACCTTG	0.507	
-	23	3037	uc002gml.1_Intron	NM_017533	NP_060003	Q9Y623	MYH4_HUMAN	Potential.		13	GTTCTCTGTGG	0.343	
-	23	2786	uc002gml.1_Intron	NM_005963	NP_005954	P12882	MYH1_HUMAN	Potential.		21	AGCTTCCTGAG	0.358	
-	34	4909	_Missense_Mutati	NM_001100112	NP_001093582	Q9UKX2	MYH2_HUMAN	Potential.		14	GGTTTCTCTTC	0.468	
-	1	235	16_uc002gor.1_I	NM_006382	NP_006373	O95170	CDRT1_HUMAN			0	ACAACGAAAATA	0.493	
+	6	1016		NM_024052	NP_076957	Q8IVV7	CQ039_HUMAN			1	ATCAGTCCCTCA	0.468	
+	1	275	gul.2_Missense_M	NM_031456	NP_113644	Q5XX13	FBW10_HUMAN			1	TATTTTCGTTGTG	0.493	
-	3	260	_Splice_Site_p.K69_splice|IFT20_uc010wae.1_Intron|T			Q8IY31	IFT20_HUMAN			0	CAATTTCTTTTAG	0.393	
-	4	1151	ht.2_Missense_M	NM_001094	NP_001085	Q16515	ACCN1_HUMAN	llular (By similarity).		4	CATCTCTGAGG	0.547	
-	15	3139	p.G844S|SRCIN1_	NM_025248	NP_079524	Q9C0H9	SRCN1_HUMAN	Pro-rich.		0	CTGGCCGTGGG	0.692	
-	9	1166	vt.2_Missense_Mu	NM_198993	NP_945344	Q6ZMT1	STAC2_HUMAN	SH3.		1	GATCTCCAGGC	0.627	
-	4	1019	P_uc010wfs.1_Int	NM_005557	NP_005548	P08779	K1C16_HUMAN	Rod.|Coil 2.		1	CTGCTCGTACT	0.617	
-	7	1018_1019	198L|SEPT4_uc0	NM_004574	NP_004565	O43236	SEPT4_HUMAN	(By similarity).		0	ACTTCGGGAGG	0.574	rs148239346
+	7	726	4_uc010wou.1_R	NM_000717	NP_000708	P22748	CAH4_HUMAN			0	CAAGGAGGAGA	0.587	
+	20	2987	E_uc010wpj.1_Mi	NM_000789	NP_000780	P12821	ACE_HUMAN	otential).|Peptidase M2 2.		4	ACCACGAAATG	0.572	
+	7	685	_p.S136F|PSMC5_	NM_002805	NP_002796	P62195	PRS8_HUMAN			1	TGTCTCTGGCT	0.522	
-	4	2190	p.R673C|TEX2_u	NM_018469	NP_060939	Q8IWB9	TEX2_HUMAN			1	AGGGCGGGGTG	0.483	
-	25	2989	C46_uc010dep.2	NM_145036	NP_659473	Q8N8E3	CE112_HUMAN	Potential.		0	TGTCTTCAAGTT	0.328	
-	4	1059	2_Missense_Muta	NM_001159772	NP_001153244	Q8WVQ1	CANT1_HUMAN	enal (Potential).		0	CCACGGTGCCG	0.582	
+	2	867	XNDC2_uc002koh	NM_001098529	NP_001091999	Q86VQ3	TXND2_HUMAN	repeat of Q-P-K-X-G-D-I-P		2	TCAGAAAAAGCC	0.547	rs146821851
-	1	720	TEC_uc010xaj.1_	NM_001137671	NP_001131143	B2RU33	POTEC_HUMAN			3	TAAAGGAGTTG	0.607	
-	15	2532		NM_005406	NP_005397	Q13464	ROCK1_HUMAN	h FHOD1.|Potential.|REM.		5	AATTCTGACTGA	0.294	
+	70	9361	s.3_Missense_Mu	NM_198129	NP_937762	Q16787	LAMA3_HUMAN	minin G-like 4.		11	GGAGGGAAGTT	0.493	
+	6	5037		NM_015559	NP_056374	Q9Y6X0	SETBP_HUMAN			3	TGAAAGCCAAA	0.662	
+	7	869	p.R206Q|RNF165_	NM_152470	NP_689683	Q6ZSG1	RN165_HUMAN			0	ATAGCGAAGAC	0.522	
-	3	230		NM_139171	NP_631910	P59095	STAR6_HUMAN	START.		1	TGCAATGATTTAT	0.328	
-	7	839	2A|CCBE1_uc002	NM_133459	NP_597716	Q6UXH8	CCBE1_HUMAN	ollagen-like 1.		3	GGGAGGGCCCT	0.577	
+	7	716	F|SERPINB10_uc	NM_002575	NP_002566	P05120	PAI2_HUMAN			2	GGTTTCCTCAAT	0.333	
+	27	3040	_Missense_Mutatic	NM_198531	NP_940933	O43861	ATP9B_HUMAN	lasmic (Potential).		3	CTTGTCCTTCA	0.433	
+	2	1223	_p.S257F|NFATC1	NM_006162	NP_006153	O95644	NFAC1_HUMAN	X SP repeats.		2	CTCCTCCAGAC	0.726	
+	2	157	JP3_uc010xhu.1_	NM_014428	NP_055243	O95049	ZO3_HUMAN	PDZ 1.		3	GGCCCGGTGG	0.642	
+	7	986	.D260G|TJP3_uc	NM_014428	NP_055243	O95049	ZO3_HUMAN			3	CTCGGACCTCG	0.612	
-	5	667	R2_uc010xhx.1_R	NM_015174	NP_055989	Q9UPR6	ZFR2_HUMAN	Pro-rich.		2	TGGAGGATAGA	0.677	
-	8	1080	c.2_Missense_Mu	NM_000635	NP_000626	P48378	RFX2_HUMAN	type winged-helix.		6	TCAGACGAATCC	0.577	
-	10	1116		NM_000064	NP_000055	P01024	CO3_HUMAN			5	GTAGGGAGAGG	0.602	
-	3	15725		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).		57	CAGAGGAACCA	0.498	

-	5	1214		NM_198535	NP_940937	Q32M78	ZN699_HUMAN	C2H2-type 8.		0	TTAAGGAGGAG	0.433	
+	23	3453	057_splice|SMAR	NM_003072	NP_003063	P51532	SMCA4_HUMAN		p.?(1)	67	CTTGCAGGAGTC	0.632	
-	2	160	on_p.T5M|ACP5_u	NM_001611	NP_001602	P13686	PPA5_HUMAN			1	AGCGCCGTCCAC	0.647	
-	4	381	dyn.1_RNA|ZNF62	NM_145233	NP_660276	Q96I27	ZN625_HUMAN			0	GATGATCTTTCTT	0.398	
-	15	1970	vk.2_Missense_Mu	NM_017722	NP_060192	Q9NXH9	TRM1_HUMAN			2	AGCTTCGTCGG	0.637	
-	6	1335	sense_Mutation_p.	NM_001008701	NP_001008701	O94910	LPHN1_HUMAN	ke.|Extracellular (Potential)		5	TGAAGGCATAGT	0.597	
-	5	559	_p.R106W|ELL_uc	NM_006532	NP_006523	P55199	ELL_HUMAN			1	GTTTCCGAAACT	0.602	
-	3	405	.1_Intron|PBX4_u	NM_025245	NP_079521	Q9BYU1	PBX4_HUMAN			2	ATCTGTCGGATCT	0.512	
+	4	3095	dd.1_Missense_M	NM_014717	NP_055532	O15090	ZN536_HUMAN			11	CGCCTCCCTCC	0.572	
-	2	1423		NM_020856	NP_065907	Q63HK5	TSH3_HUMAN			8	GGGACGTGAAG	0.552	
+	10	3427		NM_015073	NP_055888	O60292	SI1L3_HUMAN	PDZ.		2	GAACGGGCTCG	0.667	
+	13	4095		NM_015073	NP_055888	O60292	SI1L3_HUMAN			2	GCCACGATGGG	0.632	
+	6	817	.1_RNA|TIMM50_	NM_001001563	NP_001001563	Q3ZCQ8	TIM50_HUMAN	intermembrane (Potential).		1	ACAGATGATCAT	0.607	
-	26	12093		NM_003890	NP_003881	Q9Y6R7	FCGBP_HUMAN	Cys-rich.		9	CTGCCCCGGCT	0.537	
-	3	383	e.1_5'UTR|CYP2A	NM_000762	NP_000753	P11509	CP2A6_HUMAN			2	CGCTCCCCGTTG	0.706	
+	10	2639		NM_015125	NP_055940	Q96RK0	CIC_HUMAN	Pro-rich.		11	CCCTCCCACCG	0.682	
+	3	1146_1147	ocf.2_Missense_M	NM_001080401	NP_001073870	Q8N819	PPM1N_HUMAN			0	CTGGGGGAGG	0.46	
+	6	617	p.G148E|CCDC15	NM_144688	NP_653289	Q8N6L0	CC155_HUMAN			2	CTTCGGAGGCG	0.562	
+	6	599_600		NM_021228	NP_067051	Q9H7N4	SFR19_HUMAN			0	GCAAAACGGGT	0.614	
+	25	3052		NM_004533	NP_004524	Q14324	MYPC2_HUMAN	onectin type-III 3.		1	GGCAATGAATAC	0.537	
-	3	300_301	K1_uc010ycg.1_R	NM_002257	NP_002248	P06870	KLK1_HUMAN	Peptidase S1.		0	AAACTGGGCTG	0.55	
-	6	814	71F|KLK8_uc002p	NM_007196	NP_009127	O60259	KLK8_HUMAN	Peptidase S1.		1	CCTCCAGAATCG	0.557	
-	7	1874	0ycy.1_Missense_	NM_033130	NP_149121	Q96LC7	SIG10_HUMAN	3.|Extracellular (Potential).		1	CTCCTTCGTGCT	0.667	
-	5	1664		NM_014650	NP_055465	O94892	ZN432_HUMAN	C2H2-type 9.		3	TGAGTTCGCTGA	0.423	
+	6	1236		NM_001099694	NP_001093164	Q96N58	ZN578_HUMAN	C2H2-type 4.		0	CCCTTACATGCC	0.423	
+	3	809		NM_152677	NP_689890	Q8NAM6	ZSCA4_HUMAN			1	GAAGAAGGGATT	0.388	
-	3	205	AS_uc002rcd.1_R	NM_015909	NP_056993	A2RRP1	NBAS_HUMAN			4	AATAATAAACGAT	0.274	
-	25	4290		NM_000384	NP_000375	P04114	APOB_HUMAN			27	GTAACGAGCCC	0.527	
+	10	1331	hv.3_Missense_M	NM_020134	NP_064519	Q9BPU6	DPYL5_HUMAN			2	CGCAAGGGCCG	0.537	
+	6	980	010yli.1_Missense_	NM_173650	NP_775921	Q8N7S2	DNJ5G_HUMAN			1	GAAGATGATTTT	0.338	
-	7	651	p.A147T|RBKS_uc	NM_022128	NP_071411	Q9H477	RBSK_HUMAN			2	TGCAGCGCTGC	0.498	rs144415591
-	11	1117		NM_000379	NP_000370	P47989	XDH_HUMAN			8	ACTCACCGCCA	0.52	
+	5	861		NM_005400	NP_005391	Q02156	KPCE_HUMAN			10	TGTGCTGGGTTA	0.542	
-	4	994	10ypj.1_Missense_	NM_022893	NP_075044	Q9H165	BC11A_HUMAN			13	CCCTTCTGCCA	0.572	
-	8	1092		NM_014709	NP_055524	Q70CQ2	UBP34_HUMAN			19	GTTTCTGTGTCC	0.249	
+	29	3413	F_uc010fek.2_Mis	NM_003494	NP_003485	O75923	DYSF_HUMAN	lasmic (Potential).		7	GGCTGGGAGTAT	0.617	
-	9	1069	se_Mutation_p.S3	NM_021196	NP_067019	Q9BY07	S4A5_HUMAN	lasmic (Potential).		9	TTGTAGGATTTTG	0.328	
+	2	261		NM_138800	NP_620155	Q96BQ3	TRI43_HUMAN	RING-type.		1	CCTTTCGTGGG	0.502	
+	1	432	C285033_uc002s	NM_001037228	NP_001032305	Q3KRF4	Q3KRF4_HUMAN			0	CTGCTTCCTTCC	0.547	
-	18	2664	szi.3_Missense_M	NM_182911	NP_878915	Q9BZW7	TSG10_HUMAN	ith HIF1A (By similarity).		2	GAGATCGATGG	0.383	
-	2	151	_p.R11Q|ST6GAL	NM_001142351	NP_001135823	Q96JF0	SIAT2_HUMAN	lasmic (Potential).		11	AGCATTCGTTGT	0.507	
+	20	3830	e_Mutation_p.D43	NM_182588	NP_872394	Q7Z3J3	RGPD4_HUMAN			2	AATGGGATAACT	0.443	
+	9	1404	0fjj.2_Missense_Mu	NM_021815	NP_068587	Q9GZV3	SC5A7_HUMAN	cellular (Potential).		4	CAAAGAAATCGT	0.433	
+	6	971	dx.2_Nonsense_M	NM_001056	NP_001047	O00338	ST1C2_HUMAN			1	GTTCCTGGTTTG	0.438	
+	4	829	r.1_RNA|SULT1C4	NM_006588	NP_006579	O75897	ST1C4_HUMAN			0	AAGAATGAATAAA	0.423	
+	14	2645	2_Missense_Mutat	NM_012455	NP_036587	Q8NDX1	PSD4_HUMAN	PH.		2	GCAGGGAGAAG	0.622	
+	4	683	l.2_Missense_Mut	NM_002881	NP_002872	P11234	RALB_HUMAN			3	GCCAACGTGGAC	0.547	

-	45	8435		NM_018557	NP_061027	Q9NZR2	LRP1B_HUMAN	ellular (Potential).	50	AACAATTCACT	0.408	
-	42	7772		NM_018557	NP_061027	Q9NZR2	LRP1B_HUMAN		50	CACATCTAGTG	0.398	
-	77	11578		NM_004543	NP_004534	P20929	NEBU_HUMAN	Nebulin 104.	20	ATTTTTCCTGCA	0.423	
-	7	1400	_Mutation_p.D20	NM_004490	NP_004481	Q14449	GRB14_HUMAN	PH.	7	AATATCACTATT	0.333	
-	3	554	_p.S21F|SCN3A_	NM_006922	NP_008853	Q9NY46	SCN3A_HUMAN		10	CAAGAGATTCT	0.438	
+	1	242	po.2_Missense_M	NM_152381	NP_689594	A4UGR9	XIRP2_HUMAN		14	GAAGCCGGAAG	0.512	
-	8	1021	f.1_Missense_Mu	NM_004525	NP_004516	P98164	LRP2_HUMAN	s A 7.|Extracellular (Potenti	29	CCATTCTCTTG	0.448	
-	284	83316	93K|TTN_uc010z	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	AGTTTCCCGCT	0.413	
-	275	76341	68K|TTN_uc010z	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	CTTTTCGTTAA	0.418	
-	275	73362	75R|TTN_uc010z	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	ATTTTCCAAAGT	0.418	
-	100	25998	_uc010zfj.1_Intro	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	ATTTTTCATATTC	0.368	
+	5	974	upr.1_Missense_	NM_177454	NP_803237	Q6P995	F171B_HUMAN	ellular (Potential).	10	GGGATCGCATA	0.358	rs149646688
-	46	3582	frx.2_Missense_M	NM_000393	NP_000384	P05997	CO5A2_HUMAN		2	TACCGGATCTC	0.537	
+	19	3488	uqx.1_Splice_Site	NM_144708	NP_653309	Q7Z5J8	ANKAR_HUMAN		4	TTTATAGGGAATT	0.343	
+	8	1795	p.P407L|NAB1_uc	NM_005966	NP_005957	Q13506	NAB1_HUMAN		0	CAGTCCTAACG	0.483	
-	6	598	_p.T145I|ICA1L_u	NM_138468	NP_612477	Q8NDH6	ICA1L_HUMAN	AH.	0	TCAAGGTATCA	0.463	
+	5	625	r.2_Missense_Mut	NM_001875	NP_001866	P31327	CPSM_HUMAN	horibosyltransferase homo	13	GAGTGGACACA	0.299	
+	3	362	_p.G4E|ATIC_uc	NM_004044	NP_004035	P31939	PUR9_HUMAN		29	GGGGGGACGTG	0.398	
+	16	1909	_p.L304P|VIL1_uc	NM_007127	NP_009058	P09327	VILI_HUMAN	Core.	1	AAACCTGGTCA	0.507	
+	3	1005	_p.S47F|TTLL4_u	NM_014640	NP_055455	Q14679	TTLL4_HUMAN		3	TTCCTCCTATAA	0.537	
+	4	563	zlp.1_Missense_M	NM_152386	NP_689599	Q8IWX5	SGPP2_HUMAN	ical; (Potential).	2	AGTATCCATTTG	0.458	
+	5	529		NM_031313	NP_112603	P10696	PPBN_HUMAN		1	CTCAGGAAAGT	0.617	
-	2	290	nw.1_Missense_M	NM_022817	NP_073728	O15055	PER2_HUMAN		2	CCACGGGCTCC	0.607	
+	6	789		NM_001001891	NP_001001891	Q6IWH7	ANO7_HUMAN	lasmic (Potential).	3	CTACTCCTGCC	0.632	
+	13	1349	FARP2_uc010zor.	NM_014808	NP_055623	O94887	FARP2_HUMAN		3	CTCTCCCTCCA	0.542	
+	9	1458	DH_uc002wcg.1_	NM_152783	NP_689996	Q8N465	D2HDH_HUMAN		0	AGCACGTGGTG	0.587	
+	8	865	w.1_Missense_M	NM_080751	NP_542789	Q8TDI7	TMC2_HUMAN	ical; (Potential).	3	GCATGCCCTAT	0.443	
-	16	1509	.L337R|SEL1L2_u	NM_025229	NP_079505	Q5TEA6	SE1L2_HUMAN	r (Potential).|Sel1-like 9.	2	GGCCTAGTTCA	0.438	
+	3	1706		NM_001011718	NP_001011718	Q5GH72	XKR7_HUMAN		3	CACACCAGTGG	0.657	
+	3	197	se_Mutation_p.S2	NM_031483	NP_113671	Q96J02	ITCH_HUMAN		6	TATGTCTGACA	0.388	
-	8	1235	_p.P194L|STAU1_	NM_017453	NP_059347	O95793	STAU1_HUMAN		5	TCTGTGGCTGA	0.488	
+	18	2229		NM_017895	NP_060365	Q96GQ7	DDX27_HUMAN		2	CAAGCGGGCCC	0.567	
+	4	549	p.3_Missense_M	NM_001013694	NP_001013716	Q9UH36	SRR1L_HUMAN		0	TGACCCTCTGT	0.448	
-	4	633	aii.1_Missense_M	NM_004861	NP_004852	Q99999	G3ST1_HUMAN	enal (Potential).	0	GGGGTCGCGGA	0.647	
+	3	527	e_Mutation_p.K11	NM_000355	NP_000346	P20062	TCO2_HUMAN		1	CACAAGGGGGA	0.617	
+	11	1705	issense_Mutation	NM_006932	NP_008863	P53814	SMTN_HUMAN		3	GCCCCCGACCC	0.622	
+	4	588	1_uc003axr.2_Int	NM_004711	NP_004702	O43759	SNG1_HUMAN		0	TTGGCGCCGAC	0.687	
+	7	1956_1957		NM_001429	NP_001420	Q09472	EP300_HUMAN		64	GTGTAGGAGTTC	0.366	
-	6	1011	e_Mutation_p.M1I|	NM_000106	NP_000097	Q6NWU0	6NWU0_HUMAN		2	GTCACCATCCC	0.612	
+	15	2004	blc.2_Missense_M	NM_014678	NP_055493	O75170	PP6R2_HUMAN		0	CGAACCGCAGG	0.692	
-	41	5872	.2_Missense_Mut	NM_002972	NP_002963	O95248	MTMR5_HUMAN		0	TCAGGCGTCCG	0.682	
+	6	753	w.1_Missense_M	NM_006614	NP_006605	O00533	CHL1_HUMAN	2.|Extracellular (Potential).	12	TCCCACCTTTAC	0.398	
-	4	692	85D_uc010hfb.1_	NM_024697	NP_078973	Q9H6B1	Z385D_HUMAN	atrin-type 1.	5	CCGCAGCCTGG	0.443	
+	19	2326	p.G689R|ARPP21	NM_016300	NP_057384	Q9UBL0	ARP21_HUMAN	Gln-rich.	3	AACAGGGATTC	0.468	
-	11	1751		NM_014139	NP_054858	Q9UI33	SCNBA_HUMAN		9	CCTTTGGAGAG	0.498	
-	10	1662		NM_014139	NP_054858	Q9UI33	SCNBA_HUMAN		9	TTTTGGCAATCTT	0.378	
+	13	1355	_p.V201I|VIPR1_	NM_004624	NP_004615	P32241	VIPR1_HUMAN	lasmic (Potential).	1	AGGGCGTCCTG	0.687	

-	3	542	on.2_Missense_Mu	NM_022842	NP_073753	Q9H5V8	CDCP1_HUMAN	cellular (Potential).	3	TCTAAACCGATG	0.552	
-	6	1095	se_Mutation_p.P25	NM_170662	NP_733762	Q13191	CBLB_HUMAN	-PTB.|SH2-like.	9	TAACCTGGATGT	0.333	
-	1	183	dxk.2_Missense_	NM_005459	NP_005450	O95843	GUC1C_HUMAN	EF-hand 1.	0	TAAATTCATGTAG	0.388	
-	3	207		NM_018338	NP_060808	Q96MT7	WDR52_HUMAN		1	CCTTCCCCTTTG	0.323	
-	5	793		NM_199420	NP_955452	O75417	DPOLQ_HUMAN	ase ATP-binding.	11	AGTCTCCCAGCA	0.383	
+	15	1487	bjn.1_Missense_M	NM_021082	NP_066568	Q16348	S15A2_HUMAN		1	TCAAATCCTTTCA	0.323	
-	7	753_754	e_Mutation_p.E15	NM_053025	NP_444253	Q15746	MYLK_HUMAN		9	GCACTCCCCCC	0.55	
+	11	1353	on_p.V337A|SEC6	NM_013336	NP_037468	P61619	S61A1_HUMAN	lasmic (Potential).	1	GCAGGTTGCAA	0.562	
+	15	4413	6A6_uc003eni.3_5	NM_001102608	NP_001096078	A6NMZ7	CO6A6_HUMAN	le-helical region.	8	AAGTTGGGGAAA	0.373	
+	19	1865	no.2_Missense_Mu	NM_014382	NP_055197	P98194	AT2C1_HUMAN	smic (By similarity).	1	ATCCACCTAGAA	0.418	
+	6	567	htq.1_Missense_M	NM_015268	NP_056083	O75165	DJC13_HUMAN		2	CAAGGAGGATTT	0.328	
-	2	529	_p.Q80*|AMOTL2	NM_016201	NP_057285	Q9Y2J4	AMOL2_HUMAN		1	GCCCTGGTGCT	0.672	
+	2	1200	33GNT5_uc003fll.	NM_032047	NP_114436	Q9BYG0	B3GN5_HUMAN	enal (Potential).	1	CGTGTTCATCGT	0.438	
+	13	1512	nt.2_Missense_Mu	NM_004423	NP_004414	Q92997	DVL3_HUMAN	DEP.	3	AAGGCTTCACG	0.582	
+	5	607	_p.E20K|OSTalph	NM_152672	NP_689885	Q86UW1	OSTA_HUMAN	ical; (Potential).	1	ATGGTGGAAGGC	0.507	
+	8	3378	_p.S177F|RGS12_	NM_198229	NP_937872	O14924	RGS12_HUMAN	RGS.	1	GAAGTCCCCGC	0.587	
+	3	404	3A3_uc011bxo.1_	NM_020973	NP_066024	Q9H227	GBA3_HUMAN		0	ATCATCGATGAT	0.363	
+	8	1293	oze.1_Missense_M	NM_000812	NP_000803	P18505	GBRB1_HUMAN	ical; (Probable).	2	GCGATTGATATT	0.453	
-	3	465	_p.G55R|KDR_uc	NM_002253	NP_002244	P35968	VGFR2_HUMAN	1.|Extracellular (Potential).	33	TCTGTCCCCTGA	0.428	
+	1	331	Dihr.2_Missense_M	NM_053039	NP_444267	Q9BY64	UDB28_HUMAN		1	ATTTTTCACAAGA	0.294	
+	2	778	Dihr.2_Missense_M	NM_053039	NP_444267	Q9BY64	UDB28_HUMAN		1	TTATGCGAAACT	0.398	
-	40	6518	xc.1_Missense_Mu	NM_001813	NP_001804	Q02224	CENPE_HUMAN	binding domain.|Potential.	9	GAAGTGAGAGG	0.363	
+	12	1960_1961	p.G543K|GSTCD_	NM_001031720	NP_001026890	Q8NEC7	GSTCD_HUMAN		2	TTGTGGGAGTCC	0.45	
+	9	10450	p.D1782N|FAT4_u	NM_024582	NP_078858	Q6V0I7	FAT4_HUMAN	|Extracellula p.D3484N(2)	18	GCTGTTGATTCAG	0.458	rs143981594
+	13	12422	p.G2404E|FAT4_u	NM_024582	NP_078858	Q6V0I7	FAT4_HUMAN	1.|Extracellular (Potential).	18	TCAATGGAAGGC	0.413	
+	2	293	on_p.P6L|ARFIP1_	NM_001025595	NP_001020766	P53367	ARFP1_HUMAN		1	AATCTCCCAAAA	0.343	
-	7	1324	tz.1_Missense_Mu	NM_006529	NP_006520	O75311	GLRA3_HUMAN	ical; (Probable).	3	CAGAATGAAACC	0.478	
-	19	3314	ND2_uc011cmz.1_	NM_001332	NP_001323	Q9UQB3	CTND2_HUMAN		8	GGAGGGCGTGC	0.577	
+	3	764		NM_012304	NP_036436	Q9UJT9	FBXL7_HUMAN		3	CCGACCCGCCTC	0.647	
-	4	930	p.D185N|CDH18_u	NM_004934	NP_004925	Q13634	CAD18_HUMAN	r (Potential).|Cadherin 2.	7	CTGCATCAGTAG	0.433	
-	2	380	on_p.M1I|CDH18_u	NM_004934	NP_004925	Q13634	CAD18_HUMAN		7	AATTTTCATTGTA	0.428	
+	3	321		NM_020227	NP_064612	Q9NQV7	PRDM9_HUMAN	KRAB-related.	6	GACTGGGAGAAA	0.428	
-	12	2476	H10_uc011cnu.1_	NM_006727	NP_006718	Q9Y6N8	CAD10_HUMAN	lasmic (Potential).	12	CTTTCATTAATGA	0.463	
+	20	4268	m.2_Missense_Mu	NM_178140	NP_835260	O15018	PDZD2_HUMAN		9	CGGGGGAGAAA	0.657	
-	8	1241		NM_001007527	NP_001007528	Q68DH5	LMBD2_HUMAN	lasmic (Potential).	0	CTGTAGGGCACt	0.224	
+	4	1287	ELD2_uc003jwr.1_	NM_001038603	NP_001033692	Q8N4S9	MALD2_HUMAN	lasmic (Potential).	0	GAAGTTAATTTCA	0.423	
-	2	2573	ss.1_Missense_Mu	NM_003633	NP_003624	O14682	ENC1_HUMAN	Kelch 4.	3	GCCAGGGCTGG	0.507	
+	1	816	uc011ctk.1_RNA	NM_032567	NP_115956	Q9BXG8	SPZ1_HUMAN	notif (By similarity).	1	AAACAGCAGATG	0.353	
-	4	1551	_p.P401S|ANKRD	NM_001004441	NP_001004441	A5PLL1	AN34B_HUMAN		1	GGAAGGAGATG	0.488	
+	32	7174	e_Mutation_p.R66	NM_032119	NP_115495	Q8WXG9	GPR98_HUMAN	cellular (Potential).	16	GTTTATCGTGTT	0.418	
+	49	10328	p.A1117V|GPR98_	NM_032119	NP_115495	Q8WXG9	GPR98_HUMAN	xtracellular (Potential).	16	CCGTGGCCTTGT	0.473	
+	75	16226	.G3083E|GPR98_	NM_032119	NP_115495	Q8WXG9	GPR98_HUMAN	cellular (Potential).	16	AGAGTGGACTAG	0.388	
+	20	2646	e_Mutation_p.G75	NM_000919	NP_000910	P19021	AMD_HUMAN	idating lyase (By similarity)	0	TACAAGGATTTG	0.398	
+	3	324	SNCAIP_uc010jcu.	NM_005460	NP_005451	Q9Y6H5	SNCAP_HUMAN		2	CAAAACGAAGAC	0.478	
-	7	1046	xf.1_Missense_Mu	NM_007054	NP_008985	Q9Y496	KIF3A_HUMAN	Kinesin-motor.	1	AGTTACGATAAG	0.383	
+	1	541	p.D181N|PCDHA1	NM_018900	NP_061723	Q9Y5I3	PCDA1_HUMAN	|Extracellular (Potential).	1	CTTTGGATGTAG	0.423	
+	1	2140	q.1_Intron|PCDHG	NM_018924	NP_061747	Q9Y5G1	PCDGF_HUMAN	lasmic (Potential).	0	CCCTGCGCCTG	0.582	

+	5	1306	p.R383W|PPARG	NM_133263	NP_573570	Q86YN6	PRGC2_HUMAN		0	TCCGCCGGCCT	0.448	
+	3	907	_Mutation_p.R131	NM_001135037	NP_001128509	P55082	MFAP3_HUMAN	.|Extracellular (Potential).	0	CAATTCGTGCC	0.443	
-	2	579	ense_Mutation_p.	NM_024007	NP_076870	Q9UH73	COE1_HUMAN		5	CTCCACGAACC	0.632	
-	10	1392	r.1_Intron|GABRB	NM_021911	NP_068711	P47870	GBRB2_HUMAN	lasmic (Probable).	0	GAGAAATCGTaat	0.184	rs150956270
-	4	3842		NM_052923	NP_443155	Q6R2W3	SCND3_HUMAN		1	agttcatttcgtatttcaa	0	
-	3	582	IM26_uc003npt.2_	NM_003449	NP_003440	Q12899	TRI26_HUMAN	B box-type.	3	CTCCCGGCACA	0.657	
+	25	3229	1_Missense_Muta	NM_007293	NP_009224	P0C0L4	CO4A_HUMAN		0	AGTTTCGGAAG	0.612	
+	62	9419	uc003oof.1_Intron	NM_001371	NP_001362				21	TCATTTCAAGATC	0.358	
+	10	1062	h.2_RNA|GLP1R_	NM_002062	NP_002053	P43220	GLP1R_HUMAN	lasmic (Potential).	5	TCCAAACTGAA	0.547	
+	1	361	_p.A88T|SLC22A7	NM_153320	NP_696961	Q9Y694	S22A7_HUMAN		0	CCCAGGCTCTC	0.637	
+	11	1337	wh.1_Missense_M	NM_005588	NP_005579	Q16819	MEP1A_HUMAN	lar (Potential).|MAM.	3	CTGCCCCACAG	0.517	
-	11	2069	lwl.1_Missense_M	NM_153840	NP_722582	Q5T601	GP110_HUMAN	lasmic (Potential).	3	AATACGACGTG	0.468	rs138895375
-	22	2282	lutation_p.E69K|C	NM_030820	NP_110447	Q96P44	COLA1_HUMAN	ollagen-like 4.	2	TGGTTCTCCTG	0.418	
+	30	4688	14_splice|BAI3_u	NM_001704	NP_001695	O60242	BAI3_HUMAN		50	TTACAGAGAAG	0.234	
+	6	1091	SP3_uc003pvo.2_	NM_003880	NP_003871	O95389	WISP3_HUMAN	CTCK.	0	AAATGGAAGAT	0.373	
+	8	882	_p.P255S|NT5DC1	NM_152729	NP_689942	Q5TFE4	NT5D1_HUMAN		0	AGAGACCTTTC	0.398	
+	3	279	1_uc010kfm.1_Mi	NM_000045	NP_000036	P05089	ARGI1_HUMAN		1	TGTGGGAAAAG	0.483	
-	1	931	P3_uc010kfq.2_Ir	NM_001145659	NP_001139131	A4FU28	CTGE9_HUMAN		0	TTTCGGAGGAT	0.368	
-	6	3204	p.R781*|LATS1_u	NM_004690	NP_004681	O95835	LATS1_HUMAN	rotein kinase.	6	ACATCGACAGC	0.473	
-	43	6870	u.3_Missense_Mu	NM_182961	NP_892006	Q8NF91	SYNE1_HUMAN	ic (Potential).|Potential.	45	GATATTCTCTCAT	0.368	
-	6	728	_p.E215K|PHF10_	NM_018288	NP_060758	Q8WUB8	PHF10_HUMAN	SAY.	1	GCGTTCCCGGT	0.368	
-	9	2112		NM_005618	NP_005609	O00548	DLL1_HUMAN	ical; (Potential).	5	GCACACGGCCA	0.701	
-	4	1024	RADIL_uc011jwc.1	NM_018059	NP_060529	Q96JH8	RADIL_HUMAN		7	TGCTGGGCTTG	0.682	
+	2	326	w.2_Missense_M	NM_006908	NP_008839	P63000	RAC1_HUMAN		2	CATTTCCTGGA	0.353	
-	2	140	kut.1_Intron|DFNA	NM_001127453	NP_001120925	O60443	DFNA5_HUMAN		1	CAGGTCACCAT	0.373	
+	12	1680	lp.2_Missense_Mu	NM_002541	NP_002532	Q02218	ODO1_HUMAN		2	GCAGCCGCTCA	0.572	
-	22	3234	w.2_Missense_Mu	NM_022748	NP_073585	Q68CZ2	TENS3_HUMAN		4	CCATGGCTTG	0.602	
+	26	9800	_p.D333N|ABCA1	NM_152701	NP_689914	Q86UQ4	ABCAD_HUMAN		10	CTTAGCGATTCT	0.368	
+	19	4407	.P1198T|AUTS2_	NM_015570	NP_056385	Q8WXX7	AUTS2_HUMAN		3	CTCCCCCGCTC	0.662	
+	12	2240	fj.3_Missense_Mu	NM_020892	NP_065943	Q86UW9	DTX2_HUMAN		2	CTCATCTTCACA	0.463	
+	8	2568	gm.2_Missense_M	NM_198467	NP_940869	Q6PCB5	RSBNL_HUMAN		1	AAGACGATGAC	0.308	
-	3	2846	v.2_Missense_Mu	NM_033026	NP_149015	Q9Y6V0	PCLO_HUMAN	Pro-rich.	7	GTTCTTCCTTCT	0.483	
-	16	2063		NM_006080	NP_006071	Q14563	SEM3A_HUMAN	-like C2-type.	4	TGATTCTCTCTT	0.408	
-	12	2599	_p.S610F|EPHB4	NM_004444	NP_004435	P54760	EPHB4_HUMAN	Potential).|Protein kinase.	15	GGAAGGAGTCC	0.607	
-	6	1205	zb.2_Missense_M	NM_001146210	NP_001139682	P0CI01	SPDE6_HUMAN		0	CTCGTCGTCCT	0.552	
-	9	1107	cv.2_Missense_M	NM_182691	NP_872633	P78362	SRPK2_HUMAN	rotein kinase.	6	CTGAGGTGATG	0.473	
+	13	1565		NM_004668	NP_004659	O43451	MGA_HUMAN	(Potential).|Maltase.	2	CAATCCCAACTG	0.363	
+	1	698		NM_001004685	NP_001004685	O95006	OR2F2_HUMAN	lasmic (Potential).	4	AGAAGGAAGAA	0.512	
+	3	836	lpu.2_Missense_M	NM_018384	NP_060854	Q96F15	GIMA5_HUMAN	lasmic (Potential).	2	GCCCTGGATGAC	0.552	
-	3	406	x.2_RNA|VIPR2_	NM_003382	NP_003373	P41587	VIPR2_HUMAN	ellular (Potential).	2	GCAGGGCACCG	0.567	
-	32	5419	.D1069N|CSMD1_	NM_033225	NP_150094	Q96PZ7	CSMD1_HUMAN	ar (Potential).|CUB 10.	25	CAAATCATTCAG	0.423	
-	13	1577	se_Mutation_p.S3	NM_001135691	NP_001129163	P54219	VMAT1_HUMAN	ical; (Potential).	2	TTAGGGAACAC	0.468	
-	16	3801_3802	2_Missense_Muta	NM_005144	NP_005135	O43593	HAIR_HUMAN	JmjC.	2	TGCCCGGAGAC	0.658	
+	4	530	_p.E25K|ADAMD	NM_014479	NP_055294	O15204	ADEC1_HUMAN		2	TACACTGAAACA	0.468	
+	9	906	ec.2_Missense_M	NM_003817	NP_003808	Q9H2U9	ADAM7_HUMAN	B.|Extracellular (Potential).	5	AATATAGAAACTA	0.318	
+	3	443	nse_Mutation_p.D	NM_004331	NP_004322	O60238	BNI3L_HUMAN		0	TGTTTGATGTG	0.398	
+	3	445	nse_Mutation_p.D	NM_004331	NP_004322	O60238	BNI3L_HUMAN		0	TTTGATGTGGA	0.398	

+	5	1324	xgb.1_Missense_M	NM_016240	NP_057324	Q6AZY7	SCAR3_HUMAN	cellular (Potential).	4	GCCGAGGAGCTC	0.602	
-	2	175	ense_Mutation_p.N	NM_172366	NP_758954	Q8IX29	FBX16_HUMAN		1	TGATGGTTTAGG	0.373	
+	8	850	CM4_uc011ldi.1_M	NM_182746	NP_877423	P33991	MCM4_HUMAN		4	CTGACTCAATCTT	0.328	
+	5	1047		NM_147189	NP_671722	Q8TC76	F110B_HUMAN		1	GGAGGCCGACA	0.677	
-	22	2009	ee.1_Missense_Mu	NM_003580	NP_003571	Q92636	FAN_HUMAN		1	ACTCTTCACCTG	0.363	
-	16	2734	3xxl.1_Missense_M	NM_006421	NP_006412	Q9Y6D6	BIG1_HUMAN	SEC7.	8	ACATACGAAGGG	0.398	
-	3	219	ense_Mutation_p.(	NM_001738	NP_001729	P00915	CAH1_HUMAN		2	CATATCCCCAGTC	0.328	
+	4	623	S8_uc011lgq.1_RN	NM_017864	NP_060334	Q75QN2	INT8_HUMAN		0	CAAAACCCGGAC	0.353	
+	42	7898	iw.2_Missense_Mu	NM_017890	NP_060360	Q7Z7G8	VP13B_HUMAN		20	TTGATTCTGTATT	0.443	rs145208175
+	2	1099		NM_003301	NP_003292	P34981	TRFR_HUMAN	lasmic (Potential).	3	GTCAGACCATTT	0.473	
+	7	960	2_5'UTR|COL14A	NM_021110	NP_066933	Q05707	COEA1_HUMAN	VWFA 1.	12	ATAAAGGAGGAA	0.363	
-	9	2444	Y8_uc010mds.2_I	NM_001115	NP_001106	P40145	ADCY8_HUMAN	ical; (Potential).	6	AACTTTGTATTGC	0.353	
-	30	2939	ljo.1_Missense_M	NM_152888	NP_690848	Q8NFW1	COMA1_HUMAN	ly-rich.|Collagen-like 6.	13	TCAGTCCTGGA	0.383	
-	11	1988		NM_152888	NP_690848	Q8NFW1	COMA1_HUMAN	ke 1.|Pro-rich.|Gly-rich.	13	TTCTCTCCCTTAG	0.587	
+	13	1399		NM_139021	NP_620590	Q8TD08	MK15_HUMAN		2	CTGCGCCCTCCC	0.687	
-	1	4908		NM_031308	NP_112598	P58107	EPIPL_HUMAN	Plectin 27.	2	AACATTCCTGCT	0.627	
-	25	2779		NM_013291	NP_037423	Q10570	CPSF1_HUMAN	lization signal (Potential).	1	CTCACGGAAGT	0.642	
-	1	2961	_p.I632L|RANBP6	NM_012416	NP_036548	O60518	RNBP6_HUMAN	HEAT 7.	3	TCCCTATTGCTGA	0.363	
-	24	3077		NM_000170	NP_000161	P23378	GCSP_HUMAN		2	AGGCCGGTCCC	0.557	
-	2	553	TR|CDKN2A_uc01	NM_000077	NP_000068	P42771	CD2A1_HUMAN	ANK 4. I83fs*2(2)|p.P1	3678	CCACGGGCAGA	0.731	rs121913386
+	36	4421	wr.2_Missense_M	NM_006377	NP_006368	O14795	UN13B_HUMAN	MHD2.	5	AAAACCTTCCTG	0.512	
+	2	146		NM_000692	NP_000683	P30837	AL1B1_HUMAN		1	CTTAGCCTCCAG	0.602	
-	5	1131		NM_017561	NP_060031	A1L443	FA22F_HUMAN	Pro-rich.	0	GTGGGCGTTGGT	0.692	
+	18	2329		NM_001855	NP_001846	P39059	COFA1_HUMAN	lical region 2 (COL2).	6	GGAAAAAGGGAC	0.617	
-	38	7118	nty.2_Missense_Mu	NM_153366	NP_699197	Q4LDE5	SVEP1_HUMAN	Sushi 14.	7	CGAGAGGAACAC	0.483	
-	5	1510		NM_001101338	NP_001094808	P0CG24	ZN883_HUMAN	C2H2-type 3.	0	CAGTATGGACTC	0.363	
+	7	1774	aw.1_Missense_Mu	NM_173689	NP_775960	Q5IJ48	CRUM2_HUMAN	Potential).|Laminin G-like 1.	1	CAACTCCGCTGC	0.682	
+	4	541	_uc004bxn.1_Intro	NM_178001	NP_821068	Q15257	PTPA_HUMAN		3	TCCTGCGATGAA	0.154	
-	6	1271	SB6_uc011mbt.1_	NM_017873	NP_060343	Q9NWX5	ASB6_HUMAN	SOCS box.	0	AGCTCTCCAGCT	0.607	
-	11	2639	F1_uc004cbm.2_	NM_007344	NP_031370	Q15361	TTF1_HUMAN		4	TGTCTCGAAATG	0.313	
-	4	990	11mdf.1_Missense	NM_020385	NP_065118	Q9GZR2	REXO4_HUMAN	Exonuclease.	0	CACACGGGCGG	0.557	
+	1	1462	T1_uc011mei.1_5'	NM_001080482	NP_001073951	C9J069	CI172_HUMAN		0	AAGGCCGGCGC	0.751	
-	7	764	se_Mutation_p.H2	NM_006089	NP_006080	Q9UQR0	SCML2_HUMAN	MBT 2.	0	TGATATGAACTTC	0.428	
-	1	404		NM_001017930	NP_001017930	A6NGE4	DC8L1_HUMAN	Glu-rich.	4	CTGTCTCCTCTC	0.368	
-	34	4071	Splice_Site_p.D94	NM_153252	NP_694984	Q6RI45	BRWD3_HUMAN		4	TGTATCCTTAATT	0.328	
+	15	2701	c.1_Missense_Mut	NM_198465	NP_940867	Q7Z2Y5	NRK_HUMAN		14	GCACATCATGTC	0.294	
+	7	1266	sk.1_Nonsense_M	NM_182607	NP_872413	Q86XK7	VSIG1_HUMAN	lasmic (Potential).	2	gagtcagagccTGG	0.408	
+	30	2652	p.G817E|COL4A5	NM_033380	NP_203699	P29400	CO4A5_HUMAN	le-helical region.	4	TGCCAGGAATAG	0.438	
+	44	4151	_Mutation_p.P131	NM_033380	NP_203699	P29400	CO4A5_HUMAN	le-helical region.	4	GGTAATCCTGGC	0.383	
-	15	3065	_p.I937F|IGSF1_	NM_001555	NP_001546	Q8N6C5	IGSF1_HUMAN	Potential).|Ig-like C2-type 9.	5	AGTAGATACAGC	0.517	
+	4	2369	EC1_uc010nsl.1_I	NM_005462	NP_005453	O60732	MAGC1_HUMAN		4	CAAATTCCTCAGA	0.562	
+	3	1144		NM_000314	NP_000305	P60484	PTEN_HUMAN	hatase tensi7_N212>Y(2)|p	2334	GATTTCCTGCAGA	0.289	
+	14	1708		NM_001012423	NP_001012423				1	GCCGAGTGTCC	0.607	
-	11	1435	o.1_Missense_Mu	NM_005374	NP_005365	Q14168	MPP2_HUMAN	ylate kinase-like.	0	GTAGCGCCCAG	0.627	rs149328604
-	4	1916	799_uc002mts.3_I	NM_001080821	NP_001074290	Q96GE5	ZN799_HUMAN	C2H2-type 17.	6	TTACATTCATACG	0.413	
-	16	3123	uc002udp.2_Intron	NM_002977	NP_002968	Q15858	SCN9A_HUMAN	II.	13	GACCAGCGACCT	0.478	
-	8	1212	yi.1_Missense_Mu	NM_000961	NP_000952	Q16647	PTGIS_HUMAN		3	AAGGGGAAGAG	0.562	

-	13	1491	C10_uc003bkh.2_	NM_032019	NP_114408	Q969S8	HDA10_HUMAN			0	CTGGGGAGTGG	0.657	
-	1	572	_p.H16N|MAGI1_	NM_001033057	NP_001028229	Q96QZ7	MAGI1_HUMAN			6	TTCGTGAACCC	0.602	
+	8	1480	.L7R|PIK3R1_uc0	NM_181523	NP_852664	P27986	P85A_HUMAN		p.?(1)	101	AGCACTGCCTC	0.353	
+	10	1748	1dur.2_Missense_	NM_020978	NP_066188	P19961	AMY2B_HUMAN			0	CCAAATAATAAT	0.363	rs144066229
+	12	1400	_RNA|NBPF9_uc	NM_001037675	NP_001032764	Q3BBV1	NBPFK_HUMAN	NBPF 2.		0	ATGACAATGAA	0.423	
+	7	1252	_Mutation_p.T308	NM_005807	NP_005798	Q92954	PRG4_HUMAN	ats of K-X-P-X-P-T-T-X.|7.		1	CCACCACCAAG	0.642	
+	3	1144		NM_000314	NP_000305	P60484	PTEN_HUMAN	hatase tensi7_N212>Y(2)|		2334	ATTTCCTGCAG	0.289	
+	1	2080		NR_003268						0	TAGACGCTCTG	0.418	
+	14	1708		NM_001012423	NP_001012423					1	GCCGAGTGTCC	0.607	
-	13	2057	b.2_Missense_M	NM_015092	NP_055907	Q96Q15	SMG1_HUMAN	with SMG8 and SMG9.		16	ACTTATAGGCA	0.398	
-	9	1179	cjf.2_Intron|PRDM	NM_001098173	NP_001091643	Q9NQW5	PRDM7_HUMAN			1	CCCCATACCAG	0.522	
-	11	1435	o.1_Missense_Mu	NM_005374	NP_005365	Q14168	MPP2_HUMAN	ylate kinase-like.		0	GTAGCGCCCAG	0.627	rs149328604
-	4	508	ra.2_Missense_M	NM_052916	NP_443148	Q96PX1	RN157_HUMAN			1	CCTGGCAATAC	0.483	
-	6	2022	ense_Mutation_p.	NM_001010880	NP_001010880	O75290	Z780A_HUMAN	2H2-type 16.		0	AATAAGTTGCAT	0.403	
-	5	1005	77_uc010ydf.1_5'	NM_023074	NP_075562	Q9BS31	ZN649_HUMAN	2H2-type 3.		3	CTGTACCTCTTG	0.502	
+	6	1175		NM_001099694	NP_001093164	Q96N58	ZN578_HUMAN			0	ACACTGGTGAG	0.418	
-	16	3123	uc002udp.2_Intron	NM_002977	NP_002968	Q15858	SCN9A_HUMAN	II.		13	ACCAGCGACCT	0.478	
-	5	635	wtu.2_Missense_	NM_178312	NP_842564	Q9BX51	GGTL1_HUMAN			1	CGTGACGTTGG	0.622	
+	2	127	tj.1_RNA|FRG1B_uc010gdr.1_RNA|FRG1B_uc010ztk.1_Intron							0	ATTCAGATGCAA	0.333	
-	8	1212	yi.1_Missense_M	NM_000961	NP_000952	Q16647	PTGIS_HUMAN			3	AAGGGGAAGAG	0.562	
-	4	356	nc.2_Missense_M	NM_006585	NP_006576	P50990	TCPQ_HUMAN			0	ATTACAATCATTT	0.368	
+	3	591	e_Mutation_p.S44	NM_006031	NP_006022	O95613	PCNT_HUMAN			8	CAGTCAGTGAC	0.552	
-	3	3294	ron|ABCA11P_uc0	NM_133474	NP_597731	D9N162	D9N162_HUMAN			1	CATTCTCCACAT	0.418	
+	8	1480	.L7R|PIK3R1_uc0	NM_181523	NP_852664	P27986	P85A_HUMAN		p.?(1)	101	AGCACTGCCTC	0.353	
-	4	272		NM_138493	NP_612502	Q9P0B6	CF129_HUMAN	Potential.		0	TTGCCGAAGAA	0.542	
+	2	269	F25_uc003qwl.1_	NM_030615	NP_085118	Q9UIL4	KIF25_HUMAN	inesin-moto	p.W3C(1)	2	TGACATGGACC	0.602	
-	5	698	U_uc003ynm.3_M	NM_001099754	NP_001093224	Q9NX95	SYBU_HUMAN	raction with KIF5B.|Ser-ric		1	AGGACCTCGAC	0.473	
-	9	870	nse_Mutation_p.L	NM_017871	NP_060341	Q5TA45	INT11_HUMAN			0	CGGTCAGCCCC	0.577	
+	2	401		NM_152228	NP_689414	Q7RTX0	TS1R3_HUMAN	ellular (Potential).		0	GCAGTACCAGC	0.642	
+	3	857	nv.2_Intron|TAS1	NM_138697	NP_619642	Q7RTX1	TS1R1_HUMAN	ellular (Potential).		3	CGAGTCCGTGG	0.642	
-	4	1598_1599	HL21_uc009vme.	NM_014851	NP_055666	Q9UJP4	KLH21_HUMAN	Kelch 6.		1	CAGAGACGTAC	0.629	
+	18	4676	aoj.2_Missense_	NM_015215	NP_056030	Q9Y6Y1	CMTA1_HUMAN			9	CCTTCCCTCCG	0.488	
-	12	1399		NM_207420	NP_997303	Q6PXP3	GTR7_HUMAN	lasmic (Potential).		0	CTCCGGAATAA	0.478	
+	4	1478	asi.1_Missense_M	NM_020780	NP_065831	Q9P2K9	PTHD2_HUMAN	ellular (Potential).		7	TGGGGGGACAG	0.512	
-	1	306		NM_001089591	NP_001083060					0	AAAGAGTTTGT	0.428	
+	1	536	C7A_uc009vpg.2_	NM_152375	NP_689588	Q5VTJ3	KLD7A_HUMAN			3	GCTTGGGCAGC	0.632	
+	8	1985	p.G461S|PAX7_u	NM_002584	NP_002575	P23759	PAX7_HUMAN			203	AGTACGGCCAG	0.642	rs140323790
-	11	1562	fc.2_Missense_M	NM_032236	NP_115612	Q86UV5	UBP48_HUMAN			2	ATCCCGATCTAC	0.363	
-	4	621	.2_Intron|RHCE_	NM_020485	NP_065231	P18577	RHCE_HUMAN	ical; (Potential).		0	CCCAAAATAGG	0.542	
-	25	3671	sw.1_Missense_M	NM_004672	NP_004663	O95382	M3K6_HUMAN			9	GCTGGGAGTCC	0.647	
+	4	1171	xt.2_Missense_M	NM_032884	NP_116273	Q6P1W5	CA094_HUMAN			0	ACTTTCCTACA	0.512	
-	2	437	122_uc001ccb.1_	NM_024640	NP_078916	Q86U90	YRDC_HUMAN	YrdC-like.		0	GTCTTTCAGGA	0.478	
-	2	149	oix.1_Missense_	NM_016257	NP_057341	Q9UM19	HPCL4_HUMAN		p.P10H(1)	1	CCTCGGGGGCC	0.632	
-	6	1390_1391	.2_Intron|PPIE_uc	NM_001720	NP_001711	P34820	BMP8B_HUMAN			0	GAGTCCAGTGG	0.639	
+	12	1444	se_Mutation_p.R3	NM_001017922	NP_001017922	Q96PL5	ERMAP_HUMAN	(Potential).|B30.2/SPRY.		1	CCCCTTCGCCCT	0.448	
-	9	1249	_Mutation_p.P40	NM_000778	NP_000769	Q02928	CP4AB_HUMAN			4	ATCAGGGAAGG	0.577	
-	9	1244	e_Mutation_p.T39	NM_000778	NP_000769	Q02928	CP4AB_HUMAN			4	GGAAGGTGACG	0.582	

-	17	2295	rf168_uc001cyl.2_	NM_001004303	NP_001004303	Q5VWT5	CA168_HUMAN		5	TTCTAGGAGAG	0.323	
-	1	342_343		NM_032027	NP_114416	Q9BX74	TM2D1_HUMAN		1	ACGGCCTCCG	0.673	
-	3	2055	3_Intron|KANK4_u	NM_181712	NP_859063	Q5T7N3	KANK4_HUMAN		6	CCCAATAGTGG	0.617	
-	4	377		NM_018841	NP_061329	Q9UBI6	GBG12_HUMAN		0	TGAAAGGGTTT	0.453	
-	11	1931	P2_uc001dmy.1_R	NM_004120	NP_004111	P32456	GBP2_HUMAN		1	CTGTTCCTAAA	0.408	
-	12	1667	_p.M202L|HFM1_u	NM_001017975	NP_001017975	A2PYH4	HFM1_HUMAN	case C-terminal.	0	AGTACATTTGTA	0.328	
-	18	2341	RHGAP29_uc001d	NM_004815	NP_004806	Q52LW3	RHG29_HUMAN		11	ATGACCACAAA	0.328	
-	2	265	PYD_uc001drw.2_	NM_000110	NP_000101	Q12882	DPYD_HUMAN		8	GATTTCTTTTC	0.383	
-	40	3424	.G1048R|COL11A	NM_001854	NP_001845	P12107	COBA1_HUMAN	le-helical region.	12	AGCTCCAGGAA	0.383	
+	7	1186	va.1_Missense_M	NM_001144937	NP_001138409	Q5VTL7	FNDC7_HUMAN	nectin type-III 5.	2	CTGTCCGTGGT	0.512	
+	2	370	_p.G114E|CD2_uc	NM_001767	NP_001758	P06729	CD2_HUMAN	-3 (CD58) binding region 2.	1	AAAAGGAAAAA	0.308	
+	76	9459	BPF10_uc010oyl.1	NM_001039703	NP_001034792	A6NDV3	A6NDV3_HUMAN		0	TGCTGGATGAG	0.483	
+	10	1004	IKRD35_uc010oyx	NM_144698	NP_653299	Q8N283	ANR35_HUMAN	Potential.	5	GTGGAGGTGG	0.557	
-	3	4818	uc001ezv.2_Intron	NM_001014342	NP_001014364	Q5D862	FILA2_HUMAN		17	CTTCACTGTCA	0.507	
+	2	1035		NM_001025231	NP_001020402	Q5T749	KPRP_HUMAN	Pro-rich.	5	GTGCCGAATCG	0.617	
+	3	589	o.2_Missense_M	NM_021948	NP_068767	Q96GW7	PGCB_HUMAN	g-like V-type.	2	CCGGGGCCGG	0.711	
-	1	815		NM_001005278	NP_001005278	Q8NGY6	OR6N2_HUMAN	Name=7; (Potential).	0	GTGTTCGGTCA	0.433	
-	7	816		NM_017625	NP_060095	Q8WWA0	ITLN1_HUMAN	nogen C-terminal.	7	AAATCCCGCAG	0.488	
+	10	1625		NM_002022	NP_002013	P31512	FMO4_HUMAN		3	CTTATCAGTACC	0.498	
-	3	263		NM_005092	NP_005083	Q9UNG2	TNF18_HUMAN	cellular (Potential).	1	TGAGGGTAATG	0.333	
+	12	2886		NM_022093	NP_071376	Q9UQP3	TENN_HUMAN	nectin type-III 8.	9	ACGGAGAGACC	0.607	
-	12	3066	g.3_Missense_Mu	NM_007314	NP_009298	P42684	ABL2_HUMAN	g (By similarity).|Pro-rich.	14	GTTGTGAGTGG	0.572	
+	34	8228	_p.K750N|CEP350	NM_014810	NP_055625	Q5VT06	CE350_HUMAN		4	GAGAAATCCCT	0.363	
+	4	366	qh.2_Missense_M	NM_173156	NP_775179	Q92540	SMG7_HUMAN		3	CAAATCCGAAT	0.423	
+	7	1183	_Mutation_p.P285	NM_005807	NP_005798	Q92954	PRG4_HUMAN	K-X-P-X-P-T-T-X.|4; appro	1	CCACCCCCAAG	0.637	
+	7	1369	_Mutation_p.P347	NM_005807	NP_005798	Q92954	PRG4_HUMAN	ats of K-X-P-X-P-T-T-X.|12	1	CCACCCCCAAG	0.652	
-	8	1763	ot.1_Missense_M	NM_199051	NP_950252	Q76B58	FAM5C_HUMAN		5	TGGCATGGACTT	0.468	
+	6	922	_p.G531R|CFHR4_	NM_006684	NP_006675	Q92496	FHR4_HUMAN	Sushi 5.	3	TTAAAAGGAAAA	0.279	
+	3	511		NM_030787	NP_110414	Q9BXR6	FHR5_HUMAN	Sushi 2.	2	ACATTTCGTGTG	0.378	
-	8	2163	pj.1_Missense_M	NM_014875	NP_055690	Q15058	KIF14_HUMAN	inesin-motor.	7	CCAGGGTGAAA	0.373	
-	42	5436		NM_000069	NP_000060	Q13698	CAC1S_HUMAN	lasmic (Potential).	5	AGGAGGTGCCT	0.597	
-	2	103	_Mutation_p.E12K|	NM_000364	NP_000355	P45379	TNNT2_HUMAN		0	CTCCTCGTACT	0.567	
-	18	3275	_p.L962S|LAMB3_	NM_001017402	NP_001017402	Q13751	LAMB3_HUMAN	nain I.|Potential.	6	CCTGCAACCGG	0.602	
-	7	2070	_p.I479N|SUSD4_	NM_017982	NP_060452	Q5VX71	SUSD4_HUMAN	lasmic (Potential).	0	CTGCAATGTCG	0.617	
+	1	214		NM_019090	NP_061963	Q9P2G4	K1383_HUMAN		1	ATATTCCTCAGG	0.408	
-	4	479	M20_uc009xfx.1_	NM_014765	NP_055580	Q15388	TOM20_HUMAN	lasmic (Potential).	0	ATATTCACCTGT	0.408	
-	3	490	nse_Mutation_p.P	NM_002924	NP_002915	P49802	RGS7_HUMAN	DEP.	7	GCTAGGTATCT	0.378	
+	1	619		NM_001004698	NP_001004698	A6NFC9	OR2W5_HUMAN		3	GCTCTCCTCCT	0.567	rs141044958
-	1	906		NM_001004691	NP_001004691	Q8NG81	OR2M7_HUMAN	lasmic (Potential).	2	GATTTTCATTAAT	0.403	
-	5	791	mo.3_Missense_M	NM_152751	NP_689964	Q8N7W2	BEND7_HUMAN	Poly-Lys.	2	TTCTTTTTATTTC	0.433	
-	23	2739	j.2_RNA|NEBL_uc	NM_006393	NP_006384	O76041	NEBL_HUMAN	Nebulin 22.	2	ACCATTGAAATA	0.383	
+	15	3515	A1217_uc010qda	NM_019590	NP_062536	Q5T5P2	SKT_HUMAN		7	ACTTGGAAAAG	0.502	
+	20	2543	.S728F|MYO3A_u	NM_017433	NP_059129	Q8NEV4	MYO3A_HUMAN	osin head-like.	18	AAATTCCTTCG	0.333	
-	9	1207	1ito.2_Missense_	NM_145698	NP_663736	Q5T8D3	ACBD5_HUMAN		0	AATCCAGAATTT	0.413	
-	2	2401	nse_Mutation_p.R	NM_020848	NP_065899	Q9P266	K1462_HUMAN		4	TGACTTCGGCCT	0.617	
+	5	1842	33A_uc010qev.1_	NM_006974	NP_008905	Q06730	ZN33A_HUMAN	2H2-type 9.	3	ATGTCCCGAATG	0.423	
+	5	599	1izo.1_RNA|HSD17B7P2_uc001izp.1_Missense_Mutation_p.N173S						0	TCGCAATGCAA	0.453	rs2257765

-	12	1599	TKN2_uc001jlv.2_	NM_145307	NP_660350	Q8IZC4	RTKN2_HUMAN		0	TGTCTCTTTTTC	0.418	
-	10	1468	_p.A449T|CTNNA	NM_001127384	NP_001120856	Q9UI47	CTNA3_HUMAN		8	ATTGGCTGCAA	0.289	
-	27	3320	.2_Missense_Mut	NM_015179	NP_055994	Q5JTH9	RRP12_HUMAN	Glu-rich.	3	cctcctcctcctcctcct	0.547	
-	2	661	c001kvi.1_Missen	NM_002779	NP_002770	A5PKW4	PSD1_HUMAN	Pro-rich.	3	GCAAGGAGCCT	0.692	
-	26	2226	a-mir-936|MI0005	NM_000494	NP_000485	Q9UMD9	COHA1_HUMAN	tential).|Triple-helical regio	5	GGAGCCCTTGG	0.498	
-	13	1831	9ycc.2_Missense_	NM_021924	NP_068743	Q9HBB8	CDHR5_HUMAN	dem repeats.|2.|Extracellul	0	TCCTGGCTCTG	0.667	rs139058512
-	1	1006		NM_001005177	NP_001005177	Q8NGF1	O52R1_HUMAN	Name=6; (Potential).	1	GGCTGGGATAT	0.483	
+	3	411		NM_021801	NP_068573	Q9NRE1	MMP26_HUMAN		0	ATCTGGAGCAA	0.408	
+	1	80	2_uc001mak.1_I	NM_001005162	NP_001005162	Q8NGF0	O52B6_HUMAN	ellular (Potential).	1	TGACACTCGCA	0.502	
+	1	890		NM_001003443	NP_001003443	Q8NH54	O56A3_HUMAN	Name=7; (Potential).	0	TTACGGGGTGA	0.443	
-	1	887		NM_001001917	NP_001001917	Q8NGH5	O56A1_HUMAN	Name=7; (Potential).	3	CAATAGGGTTC	0.458	
-	3	982	_p.P208L|FAM160	NM_001098794	NP_001092264	Q8N612	F16A2_HUMAN		2	GACGGGGAGCG	0.582	
-	1	262		NM_001004461	NP_001004461	Q8NH74	O10A6_HUMAN	ellular (Potential).	2	TTTTTCAGTAGA	0.438	
-	1	1095	p.R59K|STK33_uc	NM_030906	NP_112168	Q9BYT3	STK33_HUMAN		7	TTTTTCTCTCCA	0.378	
-	2	199	NF141_uc001mit.	NM_016422	NP_057506	Q8WVD5	RN141_HUMAN		0	TGGTAACTTGT	0.378	
+	17	1901	ds.1_Missense_M	NM_031418	NP_113606	Q9BYT9	ANO3_HUMAN	ellular (Potential).	4	TGGAATTTCATC	0.388	
-	3	581	n_p.S154F|MPPE	NM_001584	NP_001575	Q15777	MPPD2_HUMAN		1	GGAGGGACTGA	0.413	
-	6	703	.1_Missense_Mut	NM_002334	NP_002325	O75096	LRP4_HUMAN	ellular (Potential).	4	CTGGCACTGCT	0.632	
+	1	31		NM_001004727	NP_001004727	Q8NGF9	OR4X2_HUMAN	ellular (Potential).	0	TTTCTCCCAAC	0.433	
+	1	116		NM_001004059	NP_001004059	Q8NH73	OR4S2_HUMAN	Name=1; (Potential).	3	TCTGGGAAATC	0.388	
+	1	636		NM_001004738	NP_001004738	Q8NGL2	OR5L1_HUMAN	Name=5; (Potential).	5	ATCATGATCATC	0.502	
+	1	898		NM_001001952	NP_001001952	Q8NGL1	OR5DI_HUMAN	lasmic (Potential).	3	TCAAGGATACA	0.413	
+	1	474_475		NM_001005492	NP_001005492	Q8NH18	OR5J2_HUMAN	Name=4; (Potential).	4	TTAATCCACACA	0.441	
-	1	563		NM_001004471	NP_001004471	Q8NGQ4	O10Q1_HUMAN	ellular (Potential).	2	GGACGGGAGG	0.622	
+	1	800		NM_001004728	NP_001004728	Q8NGJ0	OR5A1_HUMAN	ellular (Potential).	2	CAGCTCCAGCT	0.522	
+	1	553		NM_001004708	NP_001004708	Q8NGJ1	OR4D6_HUMAN	ellular (Potential).	1	AGGTGGTAAAA	0.507	
+	1	689	oaj.2_Nonsense_	NM_018484	NP_060954	Q9NSA0	S22AB_HUMAN	ellular (Potential).	2	AGCTGGAGCGA	0.682	
-	4	846	_p.S258L|MEN1_u	NM_130800	NP_570712	O00255	MEN1_HUMAN	tion with FA3L(1)|p.D252fs	238	CCAGCGAGTCG	0.308	
+	5	678	v.1_RNA|TSGA10	NM_152762	NP_689975	Q3SY00	T10IP_HUMAN		0	AGGTCCAGCTG	0.647	
-	7	894	_p.L242F|CPT1A_	NM_001876	NP_001867	P50416	CPT1A_HUMAN	lasmic (Potential).	2	TCGGAGGTAGA	0.657	
+	10	1915	35_uc010rsp.1_5	NM_020798	NP_065849	Q9P2H5	UBP35_HUMAN		3	CCGAGGAGCCC	0.587	
+	4	813	DC83_uc001pbi.1_	NM_173556	NP_775827	Q8IWF9	CCD83_HUMAN	Potential.	1	ATGAAGGAAAA	0.383	
-	6	3114	_Mutation_p.E689	NM_000926	NP_000917	P06401	PRGR_HUMAN	teroid-binding.	4	ATGATTCTTTCAT	0.378	
-	2	391		NM_002422	NP_002413	P08254	MMP3_HUMAN		2	TTCCTCCACTTC	0.468	
-	10	1365		NM_002427	NP_002418	P45452	MMP13_HUMAN	mopexin-like 4.	3	TGGGTCCGTTG	0.308	
-	2	200		NM_002427	NP_002418	P45452	MMP13_HUMAN		3	CATTCTCCTTCA	0.448	
-	2	162		NM_002427	NP_002418	P45452	MMP13_HUMAN		3	TAGTATGATCTC	0.458	
-	6	875	_p.V212F|CASP4_	NM_001225	NP_001216	P49662	CASP4_HUMAN		4	TCTGACCCACA	0.498	
-	3	474	issense_Mutatio	NM_052968	NP_443200	Q6Q788	APOA5_HUMAN	Potential.	0	GTCTTCCCCCA	0.657	
+	8	1722		NM_025004	NP_079280	Q0P6D6	CCD15_HUMAN		2	TCTCCCCAAAG	0.403	rs112861775
-	11	1603	gy.1_Missense_M	NM_014987	NP_055802	Q9UPX0	TUTLB_HUMAN	ar (Potential).|Ig-like 5.	0	CTTCCCTACCT	0.632	
-	7	774	dl.1_Missense_M	NM_016615	NP_057699	Q9NSD5	S6A13_HUMAN	Name=5; (Potential).	0	GTAAGGAAATG	0.453	
+	14	1496	_p.F402C|B4GAL	NM_173593	NP_775864	Q6L9W6	B4GN3_HUMAN	enal (Potential).	2	GTCCTTCCCAG	0.622	
+	11	1431	X47_uc001rax.2_	NM_016355	NP_057439	Q9H0S4	DDX47_HUMAN	case C-terminal.	0	CCAGAGAACAG	0.423	
-	2	441	2A1_uc001rqv.2_I	NM_001844	NP_001835	P02458	CO2A1_HUMAN	VWFC.	2	AGATGGGGCAG	0.488	
-	3	336	lr.1_Missense_Mu	NM_024095	NP_077000	Q9H765	ASB8_HUMAN	ANK 1.	1	GCAAGGGCTTC	0.483	
-	3	404	_p.P66L|ZNF641_	NM_152320	NP_689533	Q96N77	ZN641_HUMAN		2	CCCAGGGAGCA	0.537	

-	7	1199		NM_002282	NP_002273	P78385	KRT83_HUMAN	Rod.|Coil 2.		1	GCAGGGCGCCC	0.627	
-	7	1269		NM_033448	NP_258259	Q3SY84	K2C71_HUMAN	Coil 2.|Rod.		2	GCAGGGCGCCC	0.652	
+	9	970	T2_uc009zms.2_I	NM_003578	NP_003569	O75908	SOAT2_HUMAN			1	AGGTGGAATTAT	0.547	
+	1	209	KC5_uc001set.2_I	NM_004503	NP_004494	P09630	HXC6_HUMAN			3	TATGATCCAGTG	0.562	
-	2	463		NM_020370	NP_065103	Q9NQS5	GPR84_HUMAN	lasmic (Potential).		2	CTTAGGGTGGG	0.567	
+	1	259		NM_001005182	NP_001005182	Q96RD1	OR6C1_HUMAN	ellular (Potential).		2	CAGGAGATAAA	0.383	
+	1	940		NM_001005519	NP_001005519	A6NDL8	O6C68_HUMAN	lasmic (Potential).		1	GCATTTCGTTTA	0.279	
+	17	2175	c.1_Missense_Mut	NM_001982	NP_001973	P21860	ERBB3_HUMAN	ical; (Potential).		8	GGGCGGCACTT	0.448	
-	1	369		NM_012064	NP_036196	P30301	MIP_HUMAN	llular (By similarity).		1	TCCTCGGACAG	0.597	
-	11	1165	PS2_uc001sxi.3_I	NM_032606	NP_115995	Q9BXY5	CAYP2_HUMAN			2	TAAGGGATTGG	0.343	
+	13	1785	_p.R564K|ACSS3_	NM_024560	NP_078836	Q9H6R3	ACSS3_HUMAN			4	GTCACAGAATTT	0.398	
-	1	1123		NM_152638	NP_689851	Q8TC90	CL012_HUMAN			2	CGGAGGATCTG	0.632	
-	5	1898	p.R585Q|USP44_	NM_001042403	NP_001035862	Q9H0E7	UBP44_HUMAN			3	TTCTCTCGGTTAT	0.423	
+	11	1707	ztx.2_Missense_M	NM_139319	NP_647480	Q8NDX2	VGLU3_HUMAN	ical; (Potential).		3	TCTGTCCCCTCAT	0.493	
+	6	515	.G138E|MYBPC1_	NM_206820	NP_996556	Q00872	MYPC1_HUMAN	like C2-type 1.		4	TGCAGGAAATTA	0.383	
+	2	272		NM_017564	NP_060034	Q8WWQ8	STAB2_HUMAN	ellular (Potential).		14	GGCAAGAAGAT	0.423	
-	7	2885		NM_014840	NP_055655	O60285	NUAK1_HUMAN			2	GGGAGGGGATG	0.582	
-	22	5039		NM_015335	NP_056150	Q71F56	MD13L_HUMAN			8	CCGTGGGAATTC	0.473	
-	27	3168		NM_006836	NP_006827	Q92616	GCN1L_HUMAN			4	GAGGCGAGCCC	0.567	
+	31	5409		NM_207437	NP_997320	Q8IVF4	DYH10_HUMAN	1 (By similarity).		6	CTACGGCTACG	0.597	
-	9	3011	1uia.2_Missense_	NM_133448	NP_597705	Q14C87	T132D_HUMAN	ellular (Potential).		14	TCTGGGGAGGT	0.527	
+	29	4921	bi.2_Missense_Mu	NM_015678	NP_056493	Q8NFP9	NBEA_HUMAN			11	TCATTTCGGTTCT	0.373	
+	1	2788		NM_207361	NP_997244	Q5SZK8	FREM2_HUMAN	xtracellular (Potential).		11	TGGACAACCAG	0.547	
-	26	3235		NM_052867	NP_443099	Q8IZF0	NALCN_HUMAN	S5 of repeat III; (Potential)		16	AATTTCCTTGAA	0.438	
-	26	2019	4A1_uc010agl.2_I	NM_001845	NP_001836	P02462	CO4A1_HUMAN	le-helical region.		6	CTCACCTGGCA	0.622	
-	13	1711	p.E255K|ADCY4_	NM_139247	NP_640340	Q8NFM4	ADCY4_HUMAN	lasmic (Potential).		3	CTTCTCTCTGA	0.562	
+	9	2663	FATC4_uc010tot.1	NM_004554	NP_004545	Q14934	NFAC4_HUMAN	Pro-rich.		3	CAGTTTCCTTCC	0.657	
-	4	700	se_Mutation_p.P1	NM_001083893	NP_001077362	Q13033	STRN3_HUMAN			0	TGTGGGAGCCT	0.353	
+	13	5916		NM_004274	NP_004265	Q13023	AKAP6_HUMAN			21	TCAAAGGTATCA	0.363	
+	3	423	_p.G90D|NPAS3_	NM_173159	NP_071406	Q8IXF0	NPAS3_HUMAN			2	GGAAGGCCCTC	0.448	
-	13	1961	s.2_Missense_Mu	NM_000347	NP_000338	P11277	SPTB1_HUMAN	Spectrin 4.		11	GTTTGGACTGC	0.557	
-	2	1590	e_Mutation_p.G27	NM_183002	NP_892114	P57103	NAC3_HUMAN	lasmic (Potential).		7	TGGTCACCCTCT	0.483	
-	2	595		NM_001105579	NP_001099049	A6NDD5	SYN1L_HUMAN			0	TGGATGGTGACA	0.577	
-	2	960	zh.2_Missense_Mu	NM_003485	NP_003476	Q15743	OGR1_HUMAN	lasmic (Potential).		1	GATGCCCTGGT	0.657	
-	27	3393	aub.1_Missense_	NM_024764	NP_079040	Q9H7T0	CTSRB_HUMAN			5	TCCACGGATGGA	0.428	
+	3	811	_p.D286N|SERPIN	NM_006215	NP_006206	P29622	KAIN_HUMAN			4	TGCAGGACCAG	0.493	
-	7	802	_p.A197V|DICER1_	NM_030621	NP_085124	Q9UPY3	DICER_HUMAN	ase ATP-binding.		5	TGGAAGCAGTTA	0.358	
+	14	1696		NM_001012423	NP_001012423					1	ACCTCGGCCCA	0.607	
+	11	2017	at.1_Missense_Mu	NM_005503	NP_005494	Q99767	APBA2_HUMAN	PDZ 1.		0	ATGGCGGCCCG	0.662	rs1046394
-	27	4363	e_Mutation_p.S13	NM_002420	NP_002411	Q7Z4N2	TRPM1_HUMAN	lasmic (Potential).		4	GGATAGGAAATA	0.398	
+	5	1335	_p.E422K|C15orf55	NM_175741	NP_786883	Q86Y26	NUT_HUMAN			30	AAGAGGAAGAA	0.517	
+	11	1843	bi.2_Missense_M	NM_003246	NP_003237	P07996	TSP1_HUMAN	EGF-like 1.		6	CAATCCCTGCT	0.517	
+	12	1383	_Intron|GCOM1_u	NM_001018100	NP_001018110	P0CAP1	GCOM1_HUMAN			1	AAGTGGAAACC	0.363	
+	4	777	e_Mutation_p.E57	NM_000236	NP_000227	P11150	LIPC_HUMAN			1	TTTGGAGAAACC	0.478	
+	13	1932	.1_Intron|IQCH_u	NM_001031715	NP_001026885	Q86VS3	IQCH_HUMAN			4	AATATATGATATTT	0.433	
-	13	2759	bla.2_Missense_M	NM_144572	NP_653173	Q9UPU7	TBD2B_HUMAN		p.D903N(1)	3	CGCGTCGGTTC	0.617	rs117285325
+	2	1781	unk.1_Missense_M	NM_015206	NP_056021	Q9UPX6	K1024_HUMAN			4	TGCCAATGGGG	0.532	

+	12	1753	unn.1_Missense_	NM_018689	NP_061159	Q8WUJ3	K1199_HUMAN		3	GGAACATCATAG	0.532	
-	5	2991	s.1_Missense_Mu	NM_001717	NP_001708	Q01954	BNC1_HUMAN	2H2-type 6.	3	ACAGACGAAAAC	0.498	
+	7	756	p.R15*|LRRC28_u	NM_144598	NP_653199	Q86X40	LRC28_HUMAN	LRR 8.	0	TAGGTCGATCTC	0.348	
+	25	4872	_p.V248F|CACNA	NM_021098	NP_066921	O95180	CAC1H_HUMAN	6 of repeat III; (Potential).|	2	CTCATCGTCAGC	0.647	
-	1	227		NM_000243	NP_000234	O15553	MEFV_HUMAN	DAPIN.	6	ACTCTTCCCCAT	0.642	
-	13	3523	uyn.1_Missense_	NM_001134407	NP_001127879	Q12879	NMDE1_HUMAN	lasmic (Potential).	45	TTAGGGTTGGAC	0.493	
-	13	3418	uyn.1_Missense_	NM_001134407	NP_001127879	Q12879	NMDE1_HUMAN	lasmic (Potential).	45	TTGTCTCCAAAA	0.433	
-	53	9011	bd.1_Missense_M	NM_017539	NP_060009	Q8TD57	DYH3_HUMAN		18	CAGTTCCTGAG	0.532	
+	1	1355		NM_006539	NP_006530	O60359	CCG3_HUMAN		0	CAGCAGGAAGA	0.443	
+	3	201		NM_013292	NP_037424	Q96A32	MLRS_HUMAN	|EF-hand 1.	0	AGGAGGACCTT	0.542	
+	34	9656	CAP_uc002dzg.1_	NM_006662	NP_006653	Q6ZRS2	SRCAP_HUMAN		4	GTAATTCAGGAT	0.617	
+	3	456	75Q|TSNAXIP1_uc	NM_018430	NP_060900	Q2TAA8	TXIP1_HUMAN		0	AAATCGAAAAC	0.582	
-	5	1044	se_Mutation_p.E2	NM_020947	NP_065998	Q6P9B6	K1609_HUMAN	TLD.	2	CACCTCCCAAG	0.582	
-	30	4839		NM_006445	NP_006436	Q6P2Q9	PRP8_HUMAN		6	GAAGATCTGGAT	0.512	
-	10	1551	fux.1_Missense_	NM_015229	NP_056044	O75153	K0664_HUMAN		2	GCCGGGGATGA	0.662	
+	14	1872	NASEK_uc002gea	NM_000697	NP_000688	P18054	LOX12_HUMAN	ipoxygenase.	1	TGCCTCTGGGG	0.468	
-	9	1087	d.1_Missense_Mu	NM_004860	NP_004851	P51116	FXR2_HUMAN		0	GGTAGCTTCGG	0.418	
+	14	2631	oo.2_Missense_M	NM_001372	NP_001363	Q9NYC9	DYH9_HUMAN	n (By similarity).	20	ATCAAGGAATCTG	0.418	
+	1	331		NR_002211					0	GGATTCGAGACC	0.607	
+	15	5208		NM_016239	NP_057323	Q9UKN7	MYO15_HUMAN	osin head-like.	9	AGGAGGAGCAG	0.498	
-	19	3680		NM_014680	NP_055495	Q14667	K0100_HUMAN		4	CACTTAGAGGCT	0.537	
+	2	362	_uc002hcz.1_RNA	NM_005702	NP_005693	O75616	ERAL1_HUMAN		1	TGGTCCTCCTG	0.522	
-	4	1027	F12_uc002hdj.1_	NM_001033561	NP_001028733	Q96QT6	PHF12_HUMAN	ction with SIN3A.	1	TGGGTGTGCCA	0.562	
-	1	229	sense_Mutation_	NM_001042471	NP_001035936	Q8TAX9	GSDMB_HUMAN		2	GCCCAGAATCC	0.502	
-	1	310		NM_031957	NP_114163	Q9BYS1	KRA15_HUMAN	-C-[QEPVRC]- [TPIVLE]-[	0	AGCTGATCTGG	0.632	
-	1	329		NM_030966	NP_112228	Q8IUG1	KRA13_HUMAN		0	TCCACTGCTGC	0.652	
-	1	335		NM_002279	NP_002270	Q14525	KT33B_HUMAN	inker 1.|Rod.	0	GCAAGGGCTCC	0.602	
+	1	573	2A_uc002hyx.2_5'	NM_033194	NP_149971	Q9BQS6	HSPB9_HUMAN		0	TCTAAGGCTTCC	0.627	
+	10	1304	p.P197S|TUBG2_	NM_016437	NP_057521	Q9NRH3	TBG2_HUMAN		1	TCATCCCGTGG	0.657	
+	1	1206		NM_001466	NP_001457	Q14332	FZD2_HUMAN	lasmic (Potential).	3	GGCATGAAGTG	0.627	
+	10	1978	_p.P512L|CLTC_u	NM_004859	NP_004850	Q00610	CLH1_HUMAN	lexible linker.	48	ACACTCCAGATT	0.363	
+	13	2731	pm.1_Missense_	NM_030779	NP_110406	Q9H252	KCNH6_HUMAN	lasmic (Potential).	1	GAGTCCAGGGC	0.637	
-	2	708_709	wro.1_Missense_	NM_173477	NP_775748	Q495M9	USH1G_HUMAN		2	GCTGAGGGTGT	0.708	
+	3	204	knq.2_Missense_	NM_015210	NP_056025	Q9Y4B5	CC165_HUMAN	Potential.	0	TCGGCGAGAAC	0.488	rs149471544
-	1	809	TEC_uc010xaj.1_	NM_001137671	NP_001131143	B2RU33	POTEC_HUMAN		3	CCAAGCGCCCA	0.597	
+	9	1244		NM_001944	NP_001935	P32926	DSG3_HUMAN	|Extracellular (Potential).	9	TAAGAGAAGGA	0.383	
+	2	673_674	lbx.2_Missense_	NM_145055	NP_659492	Q96B23	CR025_HUMAN		2	CCTTCCTCTAGT	0.505	
+	6	1719	_p.Q226*|DCC_uc	NM_005215	NP_005206	P43146	DCC_HUMAN	otential).|Ig-like C2-type 4.	17	TATTTTCAGATAG	0.308	
+	8	1169	p.S343F|SERPIN	NM_012397	NP_036529	Q9UIV8	SPB13_HUMAN		1	ACAGTTCCTTTG	0.567	
-	3	20955		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).	57	GGTATCCATTGG	0.463	
-	1	3628		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).	57	CAGGATCAGGAG	0.458	
+	3	434		NM_152356	NP_689569	Q8N8L2	ZN491_HUMAN	ype 1; degenerate.	2	GATATTCATCCT	0.393	
+	1	130	ZNF763_uc010xm	NM_144566	NP_653167	Q9H0M5	ZN700_HUMAN		0	GCTATGCCCTGC	0.647	
-	4	866	799_uc002mts.3_	NM_001080821	NP_001074290	Q96GE5	ZN799_HUMAN	2H2-type 4.	6	GATAGGAACTG	0.368	
-	4	914		NM_005815	NP_005806	Q9Y2A4	ZN443_HUMAN	2H2-type 4.	1	GATAGGAACTG	0.358	
+	8	1454		NM_004843	NP_004834	Q6UWB1	I27RA_HUMAN	tential).|Fibronectin type-III	0	ACCGGGGCCTG	0.637	
+	13	1610		NM_023944	NP_076433				7	GGGTGGAGCCC	0.567	

-	3	757	_p.L181F|KIAA168	NM_025249	NP_079525	Q9H0B3	K1683_HUMAN		2	ACAGAAGGCGGT	0.607	
-	3	590	_p.S125F|KIAA16	NM_025249	NP_079525	Q9H0B3	K1683_HUMAN	IQ 1.	2	ATCTGGGAAATC	0.572	
-	4	1282	op.2_Missense_M	NM_033196	NP_149973	O95780	ZN682_HUMAN	2H2-type 8.	2	TCTTGTGTTTAGT	0.358	
-	5	1987	208_uc002nqo.1_I	NM_007153	NP_009084				7	TGAATTCTCTTAT	0.368	
-	5	580	nto.1_Missense_M	NM_032139	NP_115515	Q96NW4	ANR27_HUMAN		5	ACTCTCTCACAT	0.498	
+	22	2699	dd.2_Nonsense_M	NM_173636	NP_775907	O43379	WDR62_HUMAN		0	CCGGCCAAGAG	0.602	
+	14	1476	oe.2_Missense_M	NM_138392	NP_612401	Q8TBC3	SHKB1_HUMAN		2	TCGCTTCCTTTA	0.617	
+	6	798	zt.1_Missense_Mu	NM_005581	NP_005572	P50895	BCAM_HUMAN	Potential).|Ig-like V-type 2.	1	GCCTGGACAGC	0.677	
-	3	479	e_Mutation_p.E14	NM_017509	NP_059979	Q9H2R5	KLK15_HUMAN	eptidase S1.	2	AGGCTCGTTGT	0.687	
-	7	1841	0ycy.1_Missense_	NM_033130	NP_149121	Q96LC7	SIG10_HUMAN	3.|Extracellular (Potential).	1	CAGGACCCCGG	0.667	
-	5	1930	NF614_uc010epj.2	NM_025040	NP_079316	Q8N883	ZN614_HUMAN		5	CATAAGGTTTCT	0.433	
+	6	1175		NM_001099694	NP_001093164	Q96N58	ZN578_HUMAN		0	ACACTGGTGAG	0.418	
-	6	1052	gfi.2_Missense_Mu	NM_012276	NP_036408	P59901	LIRA4_HUMAN	4.|Extracellular (Potential).	2	CCGTGGGGCCC	0.612	
+	7	785	d.2_Nonsense_Mu	NM_004829	NP_004820	O76036	NCTR1_HUMAN	ellular (Potential).	2	CTCTGGGATCA	0.468	
-	4	1400	p.E442K|NLRP7_u	NM_206828	NP_996611	Q8WX94	NALP7_HUMAN	NACHT.	3	GGACTCCTGCA	0.652	
+	15	2027	p.P600S|BRSK1_	NM_032430	NP_115806	Q8TDC3	BRSK1_HUMAN		6	TGACGCCAGAG	0.607	
+	4	2178	tg.2_Missense_Mu	NM_176811	NP_789781	Q86W28	NALP8_HUMAN		13	ACGAATGATAAG	0.512	
+	5	1133	p.P323L|ZNF583_	NM_001159860	NP_001153332	Q96ND8	ZN583_HUMAN		1	AGAGACCTTTCG	0.403	
+	6	2209	470_uc010etn.2_I	NM_001001668	NP_001001668	Q6ECI4	ZN470_HUMAN	2H2-type 11.	2	GAATGTAAGGA	0.438	
+	5	1616		NM_152677	NP_689890	Q8NAM6	ZSCA4_HUMAN		1	TCCCATGGAGTC	0.463	
+	4	315	nse_Mutation_p.S	NM_000547	NP_000538	P07202	PERT_HUMAN	ellular (Potential).	20	TTCTGTCTTTTTC	0.388	
-	10	1753	e_Mutation_p.G3	NM_015025	NP_055840	Q9UL68	MYT1L_HUMAN		6	ATGAGTCCGTTG	0.478	
+	4	677	ense_Mutation_p.	NM_198182	NP_937825	Q9NZI5	GRHL1_HUMAN		2	TGTGGGAATCC	0.552	
-	11	1427	gt.1_Missense_Mu	NM_018263	NP_060733	Q76L83	ASXL2_HUMAN		1	GGTTTTCTTTAC	0.413	
+	3	428		NM_001105519	NP_001098989	A6NJV1	CB070_HUMAN		1	CGTGAGGGAGC	0.592	
-	1	1709_1710		NM_001029883	NP_001025054	A6NGG8	CB071_HUMAN		1	GTCCTCCCCTCC	0.589	
-	10	2732	Mutation_p.S890F|	NM_021097	NP_066920	P32418	NAC1_HUMAN	lasmic (Potential).	4	CAGGGGACACT	0.557	
+	1	684	GTF2A1L_uc002r	NM_006873	NP_006864	B7ZL16	B7ZL16_HUMAN		5	AACAAGGAGATG	0.413	
-	11	1103	2A1L_uc002rwt.2_	NM_000233	NP_000224	P22888	LSHR_HUMAN	ellular (Potential).	8	TTCAGGAGCAC	0.423	
-	10	1009	p.S250F|FSHR_u	NM_000145	NP_000136	P23945	FSHR_HUMAN	ellular (Potential).	8	GAGAGGATCTC	0.408	
+	10	3436	jg.2_Nonsense_M	NM_015120	NP_055935	Q8TCU4	ALMS1_HUMAN	roximate tandem repeat.|1	9	TCTACCAACAG	0.488	
+	8	2423	_p.V651G|CNGA3	NM_001298	NP_001289	Q16281	CNGA3_HUMAN		6	CCAGGTGAAGG	0.562	
+	6	941	R1_uc002tbw.3_I	NM_016232	NP_057316	Q01638	ILRL1_HUMAN	otential).|Ig-like C2-type 3.	4	ATAAAGGAAGTG	0.373	
+	6	2790	d.2_Missense_Mu	NM_181453	NP_852118	Q8IWJ2	GCC2_HUMAN	Potential.	1	ATCTTTTAATTCA	0.313	
+	1	293_294	_uc010yxw.1_5'U	NM_172003	NP_742000	Q8IUF1	CBWD2_HUMAN		0	GCCTCGGCGCC	0.54	
-	8	3835		NM_002299	NP_002290	P09848	LPH_HUMAN	ential).|4 X approximate rep	13	CCACTCCGTTT	0.507	
-	8	2251	e_Mutation_p.P56	NM_014795	NP_055610	O60315	ZEB2_HUMAN		9	GCCAGGAAAAC	0.418	
+	8	9488	dy.2_Missense_M	NM_152381	NP_689594	A4UGR9	XIRP2_HUMAN		14	AAGAAGGCCCA	0.468	
-	2	459	KL_uc002uod.1_I	NM_002500	NP_002491	Q13562	NDF1_HUMAN	lu.|Glu-rich (acidic).	1	GTCAtcctcctcttcc	0.383	
-	2	139	n_p.L19F|PDE1A_	NM_001003683	NP_001003683	P54750	PDE1A_HUMAN		3	CTGTAAGATACT	0.403	
+	4	797	p.S174L|ITGAV_u	NM_002210	NP_002201	P06756	ITAV_HUMAN	Extracellular (Potential).	4	GTAGATCACGTA	0.353	
-	53	4515	frx.2_Missense_M	NM_000393	NP_000384	P05997	CO5A2_HUMAN	lar collagen NC1.	2	TTGATCGTCCA	0.383	rs139229616
-	48	9100		NM_018897	NP_061720	Q8WXX0	DYH7_HUMAN	5 (By similarity).	12	TTGATCCATTTAT	0.408	
+	3	285	10ziu.1_5'Flank|E	NM_001037663	NP_001032752	P24534	EF1B_HUMAN	ST C-terminal.	0	TGTCCAGCCCA	0.468	
-	1	166		NM_079420	NP_524144	P05976	MYL1_HUMAN		1	AGCCGCAGCCA	0.318	rs143705321
+	11	1576	iv.2_Missense_Mu	NM_015690	NP_056505	Q9NRP7	STK36_HUMAN		11	GGCTCCTCTCA	0.557	
+	2	473	G_uc010fwh.1_5'U	NM_005876	NP_005867	Q15772	SPEG_HUMAN		14	CACCCCCACGG	0.607	

+	36	8650		NM_005876	NP_005867	Q15772	SPEG_HUMAN	Pro-rich.	14	CGATCCCAGCC	0.627	
+	2	745		NM_002191	NP_002182	P05111	INHA_HUMAN		1	GCTGTCCCCTC	0.682	
-	3	226	zlm.1_Missense_	NM_004438	NP_004429	P54764	EPHA4_HUMAN	ellular (Potential).	12	TTTTTTCATCCAT	0.428	
-	30	3248		NM_000092	NP_000083	P53420	CO4A4_HUMAN	le-helical reg p.P865S(1)	11	CAGCTGGCCCG	0.622	
-	24	2443		NM_000092	NP_000083	P53420	CO4A4_HUMAN	le-helical region.	11	CTGGATCCCCTT	0.463	
+	2	315	_Mutation_p.M65	NM_030926	NP_112188	Q9NQX7	ITM2C_HUMAN	type II membrane protein;	0	GGCATGGTCGT	0.622	
-	3	1088		NM_006056	NP_006047	Q9HB89	NMUR1_HUMAN	ellular (Potential).	5	TCTGTCCACTG	0.622	
-	2	552_553	20orf26_uc002wr	NM_016652	NP_057736	Q9BZJ0	CRNL1_HUMAN		3	CTTTGGGAATCC	0.653	
+	3	428	xew.2_Missense_	NM_012156	NP_036288	Q9H4G0	E41L1_HUMAN		3	GAAATCGCCCC	0.567	
+	12	1285		NM_004139	NP_004130	P18428	LBP_HUMAN		2	AAGTTGGACTAT	0.358	
+	10	1360	ggc.2_Missense_	NM_015568	NP_056383	Q96T49	PP16B_HUMAN		3	CCAGGACAGAC	0.602	
-	3	1440	|CTCFL_uc010gj	NM_080618	NP_542185	Q8NI51	CTCFL_HUMAN	2H2-type 1.	4	GACATCACAGT	0.388	
+	8	2816	.R127H|GNAS_uc	NM_080425	NP_536350	P63092	GNAS2_HUMAN	(By similar7)|p.R201L(1)|	292	CTGCCGTGTCC	0.423	rs121913495
-	32	3282		NM_014258	NP_055073	Q9BX26	SYCP2_HUMAN		5	TTTACTGGTATG	0.264	
-	5	743	_Mutation_p.E13	NM_005975	NP_005966	Q13882	PTK6_HUMAN	rotein kinase.	2	GATCTCCGACT	0.652	
+	7	846	qt.2_Missense_M	NM_014339	NP_055154	Q96F46	I17RA_HUMAN	ellular (Potential).	2	TTTTCCGCACA	0.552	
-	9	985	n.1_Missense_Mu	NM_014303	NP_055118	O00541	PESC_HUMAN		0	TCACCCCATCG	0.597	
-	3	534_535	26EF>DI|SYN3_u	NM_003490	NP_003481	O14994	SYN3_HUMAN	and synaptic-vesicle bindin	1	TGAGAATTCAGC	0.441	
+	3	1108		NM_030642	NP_085145	Q9BWW9	APOL5_HUMAN		0	GATCCCGTGTG	0.607	
-	14	1677	AB6_uc010gzi.1_	NM_022785	NP_073622	Q5THR3	EFCB6_HUMAN		7	CAGGAGGAAAG	0.368	
+	10	1166	ak.2_Missense_M	NM_024324	NP_077300	Q6UXH1	CREL2_HUMAN		0	AAGCCCGACAC	0.552	
-	3	702		NM_012401	NP_036533	O15031	PLXB2_HUMAN	lar (Potential).|Sema.	6	TGTAGGCTTCA	0.607	
+	26	3620	.E1133K|CHL1_u	NM_006614	NP_006605	O00533	CHL1_HUMAN	lasmic (Potential).	12	AAAAGGAAGAT	0.224	
-	3	1039	AP3_uc003bri.1_	NM_014850	NP_055665	O43295	SRGP2_HUMAN		9	ATTGTTCATGAA	0.542	
-	9	1330	e_Mutation_p.S23	NM_022340	NP_071735	Q9H1K0	RBNS5_HUMAN	ry for the correct targeting	2	GGACCGAGCTG	0.592	
-	6	1181		NM_024697	NP_078973	Q9H6B1	Z385D_HUMAN		5	GTGTTTCCTTTA	0.438	
+	12	1880	Mutation_p.R620	NM_007335	NP_031361	Q9Y238	DLEC1_HUMAN		9	TCATACGATTTG	0.488	
+	15	2323	.1_Missense_Mut	NM_007335	NP_031361	Q9Y238	DLEC1_HUMAN		9	CAGGGGAGAAC	0.488	
-	28	5098	i.2_Missense_Mut	NM_198056	NP_932173	Q14524	SCN5A_HUMAN	; Name=S4 of repeat IV; (P	9	TCAGTCTGAGG	0.597	
-	26	4631		NM_014139	NP_054858	Q9UI33	SCNBA_HUMAN	; Name=S4 of repeat IV; (B	9	AGCCCGGACAA	0.473	
-	19	2330	z.1_Nonsense_M	NM_147129	NP_667340	Q60I27	AL2CL_HUMAN		5	CTCCTGGGCCA	0.627	
-	2	260	ntron|NAT6_uc00	NM_012191	NP_036323	Q93015	NAT6_HUMAN		1	AGCTGGGGTCT	0.597	
+	1	1859		NM_013286	NP_037418	Q8NDT2	RB15B_HUMAN		0	GTTTGCCCAAG	0.597	
+	72	11768	dv.2_Missense_M	NM_015512	NP_056327	Q9P2D7	DYH1_HUMAN	6 (By similarity).	3	TGGGCCCCTGG	0.562	
+	74	12217	dv.2_Missense_M	NM_015512	NP_056327	Q9P2D7	DYH1_HUMAN		3	GGGAGGAGGTG	0.617	
-	9	788	1_uc010hmg.2_5'	NM_004656	NP_004647	Q92560	BAP1_HUMAN		65	GATGTCGTGGT	0.632	
+	8	1434	z.2_Nonsense_M	NM_016483	NP_057567	Q9BWX1	PHF7_HUMAN		1	ACAATCGAAAA	0.438	
+	13	1536	ei.1_Missense_M	NM_015136	NP_055951	Q9NY15	STAB1_HUMAN	lar (Potential).|FAS1 1.	9	TCTTCCACGTG	0.582	
-	3	1130		NM_015576	NP_056391	O15083	ERC2_HUMAN	Potential.	2	CGTTTCAATTCT	0.468	
-	2	363	3dmh.1_5'UTR|AD	NM_182920	NP_891550	Q9P2N4	ATS9_HUMAN		4	GATTAAATAGAA	0.488	
-	15	3011	I1_uc003dmp.2_	NM_001033057	NP_001028229	Q96QZ7	MAGI1_HUMAN	PDZ 4.	6	TCCACCCAGAA	0.438	
+	3	934	e_Mutation_p.E23	NM_005233	NP_005224	P29320	EPHA3_HUMAN	ar (Potential p.E237K(1)	33	AGGAGGAAGAT	0.473	rs139652107
+	1	272_273		NM_001004737	NP_001004737	Q8NHB8	OR5K2_HUMAN	ellular (Potential).	2	CAAAAGGATTTC	0.446	
-	12	1120		NM_014981	NP_055796	Q9Y2K3	MYH15_HUMAN	osin head-like.	7	ATCAGGAAGAA	0.448	
+	5	370	px.1_Missense_M	NM_016388	NP_057472	Q6PIZ9	TRAT1_HUMAN	lasmic (Potential).	1	ATGGATGAAAAT	0.343	
+	4	1420	w.3_Missense_M	NM_000388	NP_000379	P41180	CASR_HUMAN	ellular (Potential).	7	CCAAGGAGTTTT	0.507	
+	3	716		NM_015720	NP_056535	Q9NZ53	PDXL2_HUMAN	ellular (Potential).	2	CTCATCAGGTG	0.622	

+	5	1751_1752	D12_uc010hsq.2_	NM_207335	NP_997218	Q3ZCT8	KBTBC_HUMAN	Kelch 4.	1	CCAGTGGAATGT	0.475	
-	14	3699		NM_014602	NP_055417	Q99570	PI3R4_HUMAN	WD 2.	12	CAATTCGGCTGT	0.403	
-	3	243	j.2_RNA|ANAPC1	NM_015391	NP_056206	Q9BS18	APC13_HUMAN		1	TGACAGATTCTG	0.423	rs11544840
-	36	4287		NM_001041	NP_001032	P14410	SUIS_HUMAN	crase.|Lumenal.	14	TGCATTGATTAGT	0.254	
-	25	2953		NM_001041	NP_001032	P14410	SUIS_HUMAN	|P-type 2.|Isomaltase.	14	ATTACCGTTCTCC	0.299	
-	5	1014	_p.G329E|SERPIN	NM_006217	NP_006208	O75830	SPI2_HUMAN		3	GTTATTCCAGAA	0.303	
+	27	3308	1_Missense_Mutat	NM_014616	NP_055431	Q9Y2G3	AT11B_HUMAN	ical; (Potential).	3	TAGATGGCTCTG	0.294	
+	15	2062	_p.P557L|ECE2_u	NM_014693	NP_055508	O60344	ECE2_HUMAN	dothelin-converting enzyme	4	GACCCCCCAGA	0.612	
+	15	2457	e_Mutation_p.G60	NM_006206	NP_006197	P16234	PGFRA_HUMAN	e.|Cytoplasmic (Potential).	674	CTTTGGATTGAA	0.443	
-	11	2615	_p.S721F|AASDH_	NM_181806	NP_861522	Q4L235	ACSF4_HUMAN		4	CACTTAGATACA	0.368	
-	5	722	EF2_uc003hiz.1_	NM_006239	NP_006230	O14830	PPE2_HUMAN		4	GGAGTGGGAAG	0.527	
+	56	8643		NM_025074	NP_079350	Q86XX4	FRAS1_HUMAN	(Potential).|Calx-beta 2.	5	CTAGAGGGATGT	0.468	
-	21	3698		NM_014991	NP_055806	Q8IZQ1	WDFY3_HUMAN		3	CGGAGGGAGGA	0.343	
-	4	357	.P96S|ADH1A_uc	NM_000667	NP_000658	P07327	ADH1A_HUMAN		2	ACTGAGGAATAG	0.393	
+	4	1977	e_Mutation_p.G59	NM_001128933	NP_001122405	Q9UMS6	SYNP2_HUMAN	Pro-rich.	2	CCCAGGGTCTG	0.542	
-	6	847_848	e_Mutation_p.P11	NM_144643	NP_653244	Q96NL6	SCLT1_HUMAN	Potential.	5	CCCAGGGGAAA	0.386	
-	14	3568		NM_017639	NP_060109	Q6V1P9	PCD23_HUMAN	Cadherin 10.	4	CTGGATCGTGAG	0.453	
-	14	3031		NM_017639	NP_060109	Q6V1P9	PCD23_HUMAN	Cadherin 8.	4	CAAGTTCCTTAGA	0.363	
+	6	773		NM_000824	NP_000815	P48167	GLRB_HUMAN	cellular (Probable).	2	TTGTTTCCCATG	0.348	
+	8	717	p.R131Q|RXFP1_	NM_021634	NP_067647	Q9HBX9	RXFP1_HUMAN	xtracellular (Potential).	0	TCAGTCGAATTT	0.294	
+	8	1130	HL2_uc003irc.2_M	NM_007246	NP_009177	O95198	KLHL2_HUMAN		0	CGTATATTAATGA	0.443	
+	21	3689	_p.*1037Y|TLL1_u	NM_012464	NP_036596	O43897	TLL1_HUMAN		7	AAAATAACACCA	0.308	
-	6	533	s.1_Nonsense_Mu	NM_016950	NP_058646	Q9BQ16	TICN3_HUMAN		3	CCCCTCCACTGC	0.388	
-	2	623		NM_005429	NP_005420	P49767	VEGFC_HUMAN		5	TACACTGGACA	0.423	
-	19	2358	.P529S|NSUN2_	NM_017755	NP_060225	Q08J23	NSUN2_HUMAN		1	GGGTGGATGGA	0.627	
-	3	690	.D105N|CDH18_	NM_004934	NP_004925	Q13634	CAD18_HUMAN	(Potential).|Cadherin 1.	7	TGGTATCGTCAA	0.438	
-	3	262	jju.1_Missense_M	NM_001042625	NP_001036090	Q8WWF8	CAPSL_HUMAN	nd 1.|1 (Potential).	1	GTTCGATTATTAT	0.303	
-	3	550		NM_004465	NP_004456	O15520	FGF10_HUMAN		3	GAGCTCCTTTTC	0.438	
+	4	504		NM_138453	NP_612462	Q96E17	RAB3C_HUMAN		2	ACAATGCCCAAG	0.413	
+	11	1983	d.2_Nonsense_M	NM_181523	NP_852664	P27986	P85A_HUMAN	(2)|p.Q475_E476>VLQ(1)|	101	ACATCCCAGGTG	0.284	
+	6	691	0A5_uc003jvk.2_	NM_022902	NP_075053	Q8TAD4	ZNT5_HUMAN	ical; (Potential).	1	TGTTTATTGCTTT	0.363	
-	13	1651	_p.L397S|WDR41_	NM_018268	NP_060738	Q9HAD4	WDR41_HUMAN		0	AGGTATAAGTCA	0.348	
+	7	4311	.2_Missense_Mut	NM_004385	NP_004376	P13611	CSPG2_HUMAN	minoglycan attachment do	16	AAATTTCACCCT	0.443	
-	6	1038	p.1_Missense_Mu	NM_005711	NP_005702	O43854	EDIL3_HUMAN	5/8 type C 1.	2	TGCAGCTGTCC	0.398	
+	23	2999	.2_Intron|PAM_uc	NM_000919	NP_000910	P19021	AMD_HUMAN	ical; (Potential).	0	GTTATTCCGGTG	0.483	
+	17	2443_2444	ui.3_Nonsense_M	NM_032446	NP_115822	Q96KG7	MEG10_HUMAN	P2M1, self-assembly and f	4	CGGTTGGATTGG	0.416	
+	3	562	uj.3_Missense_Mu	NM_130809	NP_570721	Q96M27	PRRC1_HUMAN	Pro-rich.	0	TCGGGTCCTCCT	0.502	
+	1	2048	hh.1_Intron|PCDH	NM_018910	NP_061733	Q9UN72	PCDA7_HUMAN	cellular (Potential).	4	GGCATCGTTGG	0.632	
+	1	1916	HA6_uc003lhn.2_I	NM_018902	NP_061725	Q9Y5I1	PCDAB_HUMAN	|Extracellula p.S353S(1)	1	TGACTTCCTTGT	0.572	
+	1	1805		NM_018938	NP_061761	Q9Y5E5	PCDB4_HUMAN	|Extracellular (Potential).	3	GCTGTCGTACC	0.731	
+	1	716	B16_uc003liv.2_5	NM_019120	NP_061993	Q9UN66	PCDB8_HUMAN	|Extracellular (Potential).	4	CCAACTCCTATT	0.502	
-	2	399	sense_Mutation_p	NM_014790	NP_055605	Q96AA8	JKIP2_HUMAN		2	TTATTTCGCCCT	0.458	
+	2	459	RIA1_uc011dcx.1_	NM_001114183	NP_001107655	P42261	GRIA1_HUMAN	cellular (Potential).	6	TTATTTCCAAAC	0.453	
-	5	932	bl.1_Nonsense_M	NM_012300	NP_036432	Q9UKB1	FBW1B_HUMAN	p.N260_I262(1	2	CTGATCCCTGGC	0.328	
-	9	1636	_p.D279N|RNF44_	NM_014901	NP_055716	Q7L0R7	RNF44_HUMAN		0	GCTGTCCGGGT	0.657	
+	14	2512		NM_133369	NP_588610	Q6ZN44	UNC5A_HUMAN	toplasmic (Potential).	1	GGCGGGGTGCC	0.672	
+	4	2386	EP1_uc011diq.1_	NM_002114	NP_002105	P15822	ZEP1_HUMAN		6	AGATGCGCCCAC	0.507	

+	3	628		NM_001076781	NP_001070249	Q9UJN7	ZN391_HUMAN		3	AATCCTCTTTGA	0.423	
+	1	886		NM_012367	NP_036499	P58173	OR2B6_HUMAN	lasmic (Potential).	1	ACAAGGAGGTA	0.383	
-	3	1726		NM_052923	NP_443155	Q6R2W3	SCND3_HUMAN	grase catalytic.	1	TAACTTCCTTAAT	0.343	
+	1	503		NM_030946	NP_112208	Q9UGF5	O14J1_HUMAN	cellular (Potential).	1	CTGTGGGAAGA	0.483	
+	2	360	uc010jsz.1_Missen	NM_001320	NP_001311	P67870	CSK2B_HUMAN		0	GGAGGTGTCCT	0.502	
+	20	1904_1905	.1_Missense_Muta	NM_172166	NP_751898	O43196	MSH5_HUMAN		3	TGATCACATTCA	0.554	
-	18	2255	issense_Mutation_	NM_006709	NP_006700	Q96KQ7	EHMT2_HUMAN		1	GTCCTCCTCCT	0.647	
-	3	582	3obz.2_Missense_	NR_003937		Q5SR06	Q5SR06_HUMAN		0	ACCGGCTGTCT	0.542	
-	10	843_844	kw.3_Missense_Mu	NM_003322	NP_003313	O00294	TULP1_HUMAN		3	CTCCTCCTTCTG	0.723	
-	4	512	_p.S134L|SLC26A	NM_052961	NP_443193	Q96RN1	S26A8_HUMAN	ical; (Potential).	2	ATTACCGAAGAA	0.393	
+	73	11127_1112	8oog.1_5'UTR|uc0	NM_001371	NP_001362				21	TTGGGCCGACC	0.411	
+	6	812		NM_032538	NP_115927	Q5TCY1	TTBK1_HUMAN	rotein kinase.	9	CTTCGGGCTGG	0.647	
-	10	6683	318_uc003ouw.2_I	NM_014345	NP_055160	Q5VUA4	ZN318_HUMAN		7	TCCAGGGAACTA	0.473	
+	4	771	PATS1_uc010jzb.2	NM_145026	NP_659463	Q496A3	SPAS1_HUMAN		1	GGCATCGTCCT	0.478	rs145942181
+	1	550	P2D_uc011dwt.1_	NM_172238	NP_758438	Q7Z6R9	AP2D_HUMAN		7	ATGCCGAGGTAT	0.333	
+	9	1246		NM_207410	NP_997293	Q6UXV0	GFRAL_HUMAN	lasmic (Potential).	2	CTTCATCGATCC	0.264	
+	24	3584	x.1_Missense_Mu	NM_001704	NP_001695	O60242	BAI3_HUMAN	lasmic (Potential).	50	TTTAATAAACTTG	0.388	
+	29	4361	p.E1305K|BAI3_uc	NM_001704	NP_001695	O60242	BAI3_HUMAN	lasmic (Potential).	50	ATGATGGAAAGT	0.388	
+	19	2230	.3_Missense_Muta	NM_003318	NP_003309	P33981	TTK_HUMAN	rotein kinase.	11	TTTGGTCCTTAG	0.254	
+	3	467		NM_001010905	NP_001010905	Q6P5S2	CF058_HUMAN		0	GGATATCATCAG	0.398	
-	15	2283	ense_Mutation_p.D	NM_001431	NP_001422	O43491	E41L2_HUMAN		2	TTTCGTCTTTCC	0.423	
-	4	1074	.S272F|BCLAF1_u	NM_014739	NP_055554	Q9NYF8	BCLF1_HUMAN		1	GAACCAGACCCA	0.448	
+	2	179	2L_uc011edq.1_5'	NM_001077706	NP_001071174	Q008S8	ECT2L_HUMAN		0	TTCAGGAAAGA	0.378	
+	2	326	ow.2_Missense_Mu	NM_006908	NP_008839	P63000	RAC1_HUMAN		2	GCATTTCCTGGA	0.353	
+	13	2655	_p.P614S|AUTS2_	NM_015570	NP_056385	Q8WXX7	AUTS2_HUMAN		3	ACAGATCCTTTCA	0.368	
-	16	1792	_p.R383G|TYW1B_	NM_001145440	NP_001138912	Q6NUM6	TYW1B_HUMAN		0	TTTCTCTGCAGTA	0.418	
-	7	834	ense_Mutation_p.F	NM_032158	NP_115534				0	CCTGGCGGGGG	0.622	
+	2	471	SCR28_uc003tzl.2	NM_182504	NP_872310	Q6UE05	WBS28_HUMAN	ical; (Potential).	1	GCTCTTGGTGGTA	0.602	
-	21	1767	2_5'Flank|PION_uc	NM_017439	NP_059135	A4D1B5	GSAP_HUMAN		1	GACCTTCTTTTTC	0.368	
-	17	2519		NM_012431	NP_036563	O15041	SEM3E_HUMAN		3	CATCGTCCTTGTT	0.483	
+	16	1797	u.2_Missense_Mu	NM_021151	NP_066974	Q9UKG9	OCTC_HUMAN		3	GAGGAAGGTCTT	0.373	
-	2	323	10lff.2_Missense_	NM_001039372	NP_001034461	A8MVW5	HECA2_HUMAN	cellular (Potential).	5	TGGCATCATGGT	0.453	
+	15	3450	ZAN_uc003uwl.2_	NM_003386	NP_003377	Q9Y493	ZAN_HUMAN	cellular (Potential).	11	CAATTGCTTCTAC	0.572	
-	17	2143	ey.2_Missense_Mu	NM_007356	NP_031382	A4D0S4	LAMB4_HUMAN	minin IV type B.	8	AGACATCTATGGA	0.408	
+	14	1921	nq.1_Missense_M	NM_000492	NP_000483	P13569	CFTR_HUMAN	otential).|ABC transporter 1	5	ATGGCTAACAAA	0.269	
-	10	1125	lks.2_Missense_M	NM_022444	NP_071889	Q9BZW2	S13A1_HUMAN	ical; (Potential).	2	ACAAATCCGGGG	0.428	
-	15	1859_1860		NM_004333	NP_004324	P15056	BRAF_HUMAN	rotein kinas_R603>I(2)|p.T	18290	GATTTCACTGTAG	0.366	rs121913378
+	4	426_427		NM_002652	NP_002643	P12273	PIP_HUMAN		1	GTAATCCCCATC	0.436	
-	14	2431		NM_005232	NP_005223	P21709	EPHA1_HUMAN	e.|Cytoplasmic (Potential).	5	GGGTTTCGTATGT	0.483	
+	19	2756	ol.1_Missense_Mu	NM_198455	NP_940857	A2VEC9	SSPO_HUMAN	VWFC 1.	0	GCCCTTCACAGG	0.612	
-	14	2410	kwj.1_Missense_M	NM_033225	NP_150094	Q96PZ7	CSMD1_HUMAN	lar (Potential).|CUB 4.	25	GAAATTCCAAGC	0.468	
+	2	392_393		NM_000015	NP_000006	P11245	ARY2_HUMAN		2	TACATCCCTCCA	0.5	
+	5	904	_p.R145C|SH2D4A	NM_022071	NP_071354	Q9H788	SH24A_HUMAN		0	ATCAATCGTATGA	0.398	
-	2	598		NM_002318	NP_002309	Q9Y4K0	LOXL2_HUMAN	SRCR 1.	3	AGAAGTCGTCAT	0.637	rs144452398
-	6	1453	kgk.2_Missense_M	NM_173833	NP_776194	Q6ZMJ2	SCAR5_HUMAN	.|Extracellular (Potential).	2	GTACCTCTCTCC	0.582	
-	3	7628		NM_031271	NP_112561	Q9BXT5	TEX15_HUMAN		7	ATAGATGAATTTA	0.353	
-	19	2155	ck.1_Missense_Mu	NM_001464	NP_001455	Q99965	ADAM2_HUMAN	ical; (Potential).	2	AGAAAGGAATGA	0.318	

-	5	629	cw.1_Missense_M	NM_004198	NP_004189	Q15825	ACHA6_HUMAN	Extracellular.		0	TATCCACTTTTGA	0.353	
+	2	346	/S1_uc003xui.2_Ir	NM_173519	NP_775790	Q8IUQ0	CLVS1_HUMAN			5	CTTCTTCCAAAAT	0.478	
+	5	1166	i.2_RNA|CLVS1_u	NM_173519	NP_775790	Q8IUQ0	CLVS1_HUMAN			5	CATGGGAACTTG	0.448	
-	15	1990	1_Intron|uc003xyy	NM_007332	NP_015628	O75762	TRPA1_HUMAN	ytoplasmic (Potential).		6	TTCATCCCATCTC	0.338	
-	1	5171		NM_031308	NP_112598	P58107	EPIPL_HUMAN	Plectin 30.		2	GGGGTCCGCCA	0.667	
-	27	3608	3zkl.2_Missense_M	NM_002839	NP_002830	P23468	PTPRD_HUMAN	III 7.|Extracellular (Potentia		22	TCGGGAGAAGG	0.468	
-	9	2295	EM1_uc010mic.2_F	NM_144966	NP_659403	Q5H8C1	FREM1_HUMAN	CSPG 3.		5	GATCTCCCCAGC	0.483	
-	1	2210	uc003zrh.1_RNA	NM_153809	NP_722516	Q8IZX4	TAF1L_HUMAN			26	AGGGTCCATTTT	0.433	
+	8	660	se_Mutation_p.P1	NM_021111	NP_066934	O95980	RECK_HUMAN	ot repeats.|Knot 3.		3	ATTAGTCCACAAT	0.373	
-	4	1058	mw.2_Missense_M	NM_013438	NP_038466	Q9UMX0	UBQL1_HUMAN			0	CAAACCCAAGCT	0.403	
+	2	247	e_Mutation_p.S12	NM_014425	NP_055240	Q9Y283	INVS_HUMAN			2	CTGGTTCATCATT	0.453	
-	12	1713		NM_005502	NP_005493	O95477	ABCA1_HUMAN	Extracellular.		17	TGGCCAAAAACC	0.517	
+	1	32	fh.1_Missense_M	NM_004108	NP_004099	Q15485	FCN2_HUMAN			1	CTGTGGGGGTC	0.607	
+	6	995		NM_000718	NP_000709	Q00975	CAC1B_HUMAN	cellular (Potential).		6	AGTGCCGGGAG	0.592	
-	1	926		NM_001135995	NP_001129467	Q9H3M9	ATX3L_HUMAN	Josephin.		6	GTAATCGAGCCA	0.393	
-	8	1215	b.2_Nonsense_Mu	NM_021804	NP_068576	Q9BYF1	ACE2_HUMAN	ellular (Potential).		3	AGGTCCCAAGCT	0.463	
+	4	624	rf22_uc010ngv.2_I	NM_152632	NP_689845	Q6ZTR5	CX022_HUMAN			3	ATTTTTCCAACTA	0.398	
+	14	2421	rf22_uc010ngv.2_I	NM_152632	NP_689845	Q6ZTR5	CX022_HUMAN			3	GATACTGATTTAG	0.343	
-	17	2140		NM_032591	NP_115980	Q96T83	SL9A7_HUMAN			2	CGGCTCGAAACC	0.632	
-	11	1232	pg.1_Missense_M	NM_002547	NP_002538	O60890	OPHN1_HUMAN	PH.		2	CCAAGGGCCCC	0.423	
-	12	1624	MT2B_uc004egt.2	NM_024917	NP_079193	Q96GJ1	TRM2_HUMAN			1	GGATGGCCCTG	0.363	
+	6	1793	e_Mutation_p.W35	NM_000868	NP_000859	P28335	5HT2C_HUMAN	ame=7; (By similarity).		3	TGTTTGGATTGGC	0.383	
+	5	680	p.E149K|MST4_uc	NM_016542	NP_057626	Q9P289	MST4_HUMAN	rotein kinase.		9	CTAAAGGAAATTT	0.358	
-	3	521		NM_016249	NP_057333	Q9UBF1	MAGC2_HUMAN	Ser-rich.		2	AAGAGGATGTGC	0.468	
-	10	1481		NM_000808	NP_000799	P34903	GBRA3_HUMAN	lasmic (Probable).		1	ATGGTGGAAAAT	0.547	
+	27	4795		NM_198576	NP_940978	O00468	AGRIN_HUMAN			3	ATCCAGGACCA	0.726	
+	1	338		NM_080431	NP_536356	Q8TDY3	ACTT2_HUMAN			0	AATTCCAGGCTC	0.597	
+	9	2380		NM_015215	NP_056030	Q9Y6Y1	CMTA1_HUMAN			9	ACCAACGGGGTA	0.677	
-	10	1717	zx.1_Missense_Mu	NM_012102	NP_036234	Q9P2R6	RERE_HUMAN	ELM2.		2	AGAAGGAAATGC	0.443	
+	1	136		NM_001080830	NP_001074299	O95522	PRA12_HUMAN			3	CTCTTTCCCCCA	0.627	
-	4	1316		NM_001146344	NP_001139816	O60813	PRA11_HUMAN			0	GGCAGGATACA	0.498	
+	4	1056		NM_001012276	NP_001012276	Q5VWM4	PRAM8_HUMAN	LRR 1.		0	AGCTGGACCTGA	0.582	
-	3	1200		NM_001099850	NP_001093320	Q5VWM3	PRA18_HUMAN			0	GCCGTGAAAGCA	0.567	
-	16	1792	co.1_Missense_M	NM_181719	NP_859070	Q5TGY1	TMCO4_HUMAN			0	CCACGGCCTTCA	0.677	
-	12	2780	_p.E166K|KIF17_u	NM_020816	NP_065867	Q9P2E2	KIF17_HUMAN		p.E888K(1)	4	TATCTTCGTCCCA	0.577	rs141985868
-	22	3629	.T845P|EIF4G3_u	NM_003760	NP_003751	O43432	IF4G3_HUMAN			1	TAAGGTCCTTCG	0.502	
+	2	326	.L42F|TMEM57_u	NM_018202	NP_060672	Q8N5G2	MACOI_HUMAN	ical; (Potential).		0	CTTGTCCTCCTAC	0.368	
-	2	180		NM_152365	NP_689578	Q8NAX2	CA172_HUMAN	Pro-rich.		2	GTTTATCATATGT	0.637	
-	21	3380	_p.S651F|BAI2_uc	NM_001703	NP_001694	O60241	BAI2_HUMAN	Name=3; (Potential).		13	AGGAGGAGAGA	0.647	
-	31	1902	cfi.1_Missense_Mu	NM_001852	NP_001843	Q14055	CO9A2_HUMAN	lical region 2 (COL2).		2	TGCCCCCGTCCC	0.512	
+	11	1631	q.2_Missense_Mu	NM_005424	NP_005415	P35590	TIE1_HUMAN	tential).|Fibronectin type-III		7	GTGTTCGTGTGC	0.602	
-	14	1748	lg.1_Missense_M	NM_003738	NP_003729	Q9Y6C5	PTC2_HUMAN	lasmic (Potential).		18	GGCAGGATCTGA	0.592	
+	2	291		NM_006252	NP_006243	P54646	AAPK2_HUMAN	rotein kinase.		6	CGTCATCCTCATA	0.254	
-	3	1307	orf168_uc009vzv.	NM_001004303	NP_001004303	Q5VWT5	CA168_HUMAN			5	CTTGGGAACAGC	0.607	
+	4	574		NM_000562	NP_000553	P07357	CO8A_HUMAN	MACPF.		3	ATTCCAGGATCAC	0.498	
+	6	922		NM_000562	NP_000553	P07357	CO8A_HUMAN	MACPF.		3	TGGTGGGTGTAC	0.408	
+	10	1660		NM_000562	NP_000553	P07357	CO8A_HUMAN	EGF-like.		3	CCATCCTCGAGC	0.617	

-	5	638	_p.L129F|C8B_uc	NM_000066	NP_000057	P07358	CO8B_HUMAN	MACPF.	4	GATCAAGAACTG	0.458	
+	2	775_776	s.1_Nonsense_M	NM_001134673	NP_001128145	Q12857	NFIA_HUMAN	CTF/NF-I.	2	ACAGGGAAAAA	0.48	
+	6	983	K7_uc001dap.2_I	NM_014495	NP_055310	Q9Y5C1	ANGL3_HUMAN	ogen C-terminal.	0	TTTCAGGAGAATT	0.318	
-	4	554_555	se_Mutation_p.S9	NM_002227	NP_002218	P23458	JAK1_HUMAN	FERM.	61	CGGAGGGACAT	0.554	rs67657858
-	6	677	173_uc001dgi.3_5	NM_001002912	NP_001002912	Q5RHP9	CA173_HUMAN		5	GTATATGGTCGAG	0.403	
-	15	2127		NM_001013660	NP_001013682	Q6ZNA5	FRRS1_HUMAN	(Potential).|Cytochrome b5	1	AATCAGGAAGATT	0.448	
+	3	669	l.1_Missense_Mut	NM_000642	NP_000633	P35573	GDE_HUMAN	-glucanotransferase.	3	CTGGTTCATTTCA	0.308	
+	5	357	vu.1_Missense_M	NM_000851	NP_000842	P46439	GSTM5_HUMAN	ST C-terminal.	6	AAGATTCGTGTG	0.542	
-	7	763	e_Mutation_p.P19	NM_002557	NP_002548	Q12889	OVGP1_HUMAN		5	GATTTGGGGTCTT	0.483	
-	2	332	98F|ATP5F1_uc00	NM_024102	NP_077007	Q9BQA1	MEP50_HUMAN	WD 1.	0	GAATCGGAGGCC	0.582	
-	2	995	BN1_uc001edr.2_	NM_018364	NP_060834	Q5VWQ0	RSBN1_HUMAN		1	AAATTTAATCGG	0.393	
-	4	586	n_p.R77*|VTCN1_	NM_024626	NP_078902	Q7Z7D3	VTCN1_HUMAN	Potential).|Ig-like V-type 2.	0	ACCATCGGGGAG	0.552	
-	26	3783		NM_206996	NP_996879	Q6Q759	SPG17_HUMAN		6	CTTGTCCAATGAA	0.448	
-	2	261	RS2_uc010oxg.1_	NM_015836	NP_056651	Q9UGM6	SYWM_HUMAN		0	GTAATGGAGTGGA	0.502	
+	11	1337	GA10_uc009wiw.	NM_003637	NP_003628	O75578	ITA10_HUMAN	r (Potential).|FG-GAP 4.	8	GAGTTCCCCCCT	0.592	
+	10	1187	KRD35_uc010oy	NM_144698	NP_653299	Q8N283	ANR35_HUMAN		5	AGGCTCTAGTCT	0.592	
+	7	948	sense_Mutation_p.	NM_004425	NP_004416	Q16610	ECM1_HUMAN	roximate repeats.|1.	3	AGTTCTCGGTCA	0.632	
-	3	1598		NM_001009931	NP_001009931	Q86YZ3	HORN_HUMAN	5	3	TAGATCCTTGTC	0.562	
-	3	428		NM_001009931	NP_001009931	Q86YZ3	HORN_HUMAN	1	3	TCTCCTCTTTTTC	0.418	
-	3	6625		NM_002016	NP_002007	P20930	FILA_HUMAN	Ser-rich.	16	ATTGTTCCTTGT	0.547	
-	3	682	uc001ezv.2_Intron	NM_002016	NP_002007	P20930	FILA_HUMAN	Potential.	16	CATAATCATATAC	0.353	
-	3	726		NM_016190	NP_057274	Q9UBG3	CRNN_HUMAN	Gln-rich.	3	CTCTGTCCTGTT	0.582	
+	2	348		NM_178353	NP_848130	Q5T753	LCE1E_HUMAN	Cys-rich.	0	GCCAGCCCTCA	0.657	
-	9	1699	1fjn.2_Missense_	NM_006589	NP_006580	P81408	F189B_HUMAN		2	GGAGCGAAAGA	0.701	
+	1	308		NM_001004473	NP_001004473	Q8NGX5	O10K1_HUMAN	Name=3; (Potential).	1	TGTTTTCCTTCCT	0.498	
-	8	1197		NM_003126	NP_003117	P02549	SPTA1_HUMAN	Spectrin 4.	8	GGATGGGAAAGT	0.478	
-	1	85		NM_001004467	NP_001004467	Q5JRS4	O10J3_HUMAN	Name=1; (Potential).	2	CAACAAAGAAGA	0.448	
-	2	388		NM_030916	NP_112178	Q96NY8	PVRL4_HUMAN		2	CCGCGGGGCAC	0.632	
-	6	2161		NM_005099	NP_005090	O75173	ATS4_HUMAN	Cys-rich.	5	TCACCTGAGCCA	0.627	
-	13	2279		NM_000130	NP_000121	P12259	FA5_HUMAN	B.	6	CTAAACGATCAT	0.403	
-	7	1088	f112_uc001ggj.2_	NM_000450	NP_000441	P16581	LYAM2_HUMAN	ar (Potential).|Sushi 3.	5	CATTCTGAGGCT	0.512	
+	14	5246	PA2_uc009www.2_	NM_020318	NP_064714	Q9BXP8	PAPP2_HUMAN		16	CATCCTCCCGCA	0.517	
-	23	3997	N1_uc001glb.1_I	NM_004319	NP_004310	O14525	ASTN1_HUMAN		15	TCAAGTCCGTAG	0.567	
+	38	5309	1gox.1_Missense_	NM_000721	NP_000712	Q15878	CAC1E_HUMAN	Name=S6 of repeat IV.	6	AGATGCTCAACC	0.547	
+	45	7370		NM_031935	NP_114141	Q96RW7	HMCN1_HUMAN		23	AGTGTCCATGGTA	0.408	
+	7	1183	_Mutation_p.P285	NM_005807	NP_005798	Q92954	PRG4_HUMAN	K-X-P-X-P-T-T-X.|4; appro	1	CCACCCCCAAG	0.637	
+	5	617		NM_001039152	NP_001034241	Q2M5E4	RGS21_HUMAN		2	AAAAATGGCTCC	0.333	
+	9	3670	.D1067N|CRB1_	NM_201253	NP_957705	P82279	CRUM1_HUMAN	ng (Potential).|Extracellular	9	AACATCGATGAAT	0.483	
-	8	2173	pj.1_Missense_M	NM_014875	NP_055690	Q15058	KIF14_HUMAN	inesin-motor.	7	CTGGGTCATCAC	0.388	rs144936292
+	4	241	RPE_uc010pqn.1_	NM_003094	NP_003085	P62304	RUXE_HUMAN		0	GAGATTCATTCTA	0.313	
+	6	727		NM_000715	NP_000706	P04003	C4BPA_HUMAN	Sushi 3.	3	AGCCTCCTCCAGA	0.448	
+	27	4537	.G1016E|CR1_uc	NM_000573	NP_000564	P17927	CR1_HUMAN	ar (Potential).|Sushi 23.	3	TCAATGGAATGGT	0.378	
-	64	14398		NM_206933	NP_996816	O75445	USH2A_HUMAN	II 32.|Extracellular (Potenti	26	ATAATTCGTAATA	0.418	
+	30	8209	CN_uc001hsp.1_	NM_001098623	NP_001092093	Q5VST9	OBSCN_HUMAN	Ig-like 26.	28	GGGCTCCGAGG	0.692	
+	2	464	hvy.1_Missense_	NM_173508	NP_775779	Q8IY50	S35F3_HUMAN	ical; (Potential).	2	CTCCTCGTGGG	0.637	
+	37	5303		NM_001035	NP_001026	Q92736	RYR2_HUMAN	ilarity).|4 X approximate re	33	TGTCCCCATGAC	0.557	
+	1	668	e.1_Missense_Mu	NM_020066	NP_064450	Q9NZ56	FMN2_HUMAN		12	GTCCTGGGCCTG	0.682	

+	5	3164	e.1_Missense_Mu	NM_020066	NP_064450	Q9NZ56	FMN2_HUMAN	ro-rich.|FH1.		12	ACCCCCTCTAC	0.711
+	3	1175		NM_175911	NP_787107	Q8N349	OR2LD_HUMAN	Name=7; (Potential).		4	CCATCCTTACC	0.468
-	4	855	ihz.2_Missense_	NM_024803	NP_079079	A6NHL2	TBAL3_HUMAN			1	AAATGTATTCTC	0.512
+	6	672	LAH_uc001int.2_	NM_001039702	NP_001034791	Q9NV23	SAST_HUMAN			0	TGGCATCGCATT	0.393
-	8	2105		NM_001010924	NP_001010924	Q5VUB5	F1711_HUMAN	lasmic (Potential).		4	CGGCTTCCCAC	0.572
-	27	2827	b.1_Missense_Mu	NM_003638	NP_003629	P53708	ITA8_HUMAN	ellular (Potential).		6	GCTTTCTCCTC	0.478
-	20	2044	b.1_Missense_Mu	NM_003638	NP_003629	P53708	ITA8_HUMAN	ellular (Potential).		6	TGCTCCTTCCCC	0.363
-	16	2001	BL_uc001iqk.2_Int	NM_006393	NP_006384	O76041	NEBL_HUMAN	Nebulin 15.		2	TGCATTCCTTTC	0.368
-	2	419		NM_005028	NP_005019	P48426	PI42A_HUMAN	PIPK.		2	ACAGGGATTTG	0.353
-	1	344		NM_001034842	NP_001030014	Q3KNS1	PTHD3_HUMAN			4	CCGGGGGGGT	0.721
-	13	1342	_p.S313F|MPP7_u	NM_173496	NP_775767	Q5T2T1	MPP7_HUMAN			1	TGTTGGAAACT	0.408
+	31	2789		NM_052997	NP_443723	Q9BXX3	AN30A_HUMAN			9	TAAGTGGAAAAT	0.328
+	8	1780	.H321Y|ZNF37A_	NM_001007094	NP_001007095	P17032	ZN37A_HUMAN	2H2-type 4.		1	GAATTCATACAG	0.418
+	12	1711	_p.E506K|ALOX5_	NM_000698	NP_000689	P09917	LOX5_HUMAN	ipoxygenase.		2	TGTCGGAGTAC	0.711
-	12	1524	_p.L442F|FRMPD	NM_001018071	NP_001018081	Q68DX3	FRPD2_HUMAN	FERM.		1	GGCAAGGACCC	0.537
-	11	1535	p.D408N|OGDHL_	NM_018245	NP_060715	Q9ULD0	OGDHL_HUMAN			1	GTCATCGGCAT	0.562
+	2	309	.1_Missense_Mut	NM_001145263	NP_001138735	Q13772	NCOA4_HUMAN			2	TTCTCCGGGCT	0.493
-	11	1515	p.P374S|PCDH15	NM_033056	NP_149045	Q96QU1	PCD15_HUMAN	|Extracellular (Potential).		13	AAGAGGATGAC	0.348
-	37	11398	K3_uc010qih.1_In	NM_020987	NP_066267	Q12955	ANK3_HUMAN			19	GGCCTTCTTTCT	0.418
-	14	2017	mw.2_Missense_	NM_001127384	NP_001120856	Q9UI47	CTNA3_HUMAN			8	CAGTTCCTCTG	0.299
+	37	2599	e_Mutation_p.G62	NM_005203	NP_005194	Q5TAT6	CODA1_HUMAN	l).|Triple-helical region 3 (		1	TAAAGGGGATA	0.428
+	2	468	T3_uc009xqs.1_R	NM_152635	NP_689848	Q8WWZ8	OIT3_HUMAN			2	CCCACGCACCT	0.567
-	4	370	0qkx.1_5'UTR|PL	NM_001001791	NP_001001791	Q5SWW7	CJ055_HUMAN			0	CCAGCGAACTG	0.562
+	6	492	PA1_uc010qlt.1_	NM_005411	NP_005402	Q8IWL2	SFTA1_HUMAN			0	TCTCAGCCCTC	0.557
+	2	845	tt.2_Missense_Mu	NM_001548	NP_001539	P09914	IFIT1_HUMAN	TPR 5.		0	GACAGGAAGCT	0.453
+	2	562	9E|CYP2C19_uc	NM_000772	NP_000763	P33260	CP2CI_HUMAN		p.G79V(1)	5	TGCATGGATATG	0.423
+	9	6856	1lfz.2_Missense_	NM_206862	NP_996744	O95359	TACC2_HUMAN			10	CCAGTGGGGAG	0.562
+	2	766		NM_153442	NP_703143	Q8NDV2	GPR26_HUMAN	lasmic (Potential).		1	ACAGCGAGCCA	0.572
-	9	1464	XM2_uc001lhj.2_	NM_198148	NP_937791	Q8N436	CPXM2_HUMAN			2	CATTGCCGTGG	0.597
+	13	1962	_p.P523S|C10orf1	NM_015608	NP_056423	Q3B7T1	EDRF1_HUMAN			10	TCTGATCCATCA	0.373
-	12	1578	_p.P389S|ADAM1	NM_003474	NP_003465	O43184	ADA12_HUMAN	otential).|Peptidase M12B.		9	CATGGGAAATG	0.547
-	3	969	_p.P380R|C10orf9	NM_001004298	NP_001004298	Q96M02	CJ090_HUMAN			2	TTTTGGGGCTG	0.498
-	1	748		NM_001005164	NP_001005164	Q8NGJ4	O52E2_HUMAN	Name=6; (Potential).		3	GGCAAGGATTA	0.453
-	1	643	5_uc001mbq.1_I	NM_001005168	NP_001005168	Q6IFG1	O52E8_HUMAN	Name=5; (Potential).		2	TAACATCCAGTA	0.478
-	1	380		NM_001005173	NP_001005173	Q8NGH7	O52L1_HUMAN	ellular (Potential).		2	AATCTCGTGGG	0.537
+	4	820	GA4_uc001mcn.	NM_001037329	NP_001032406	Q8IV77	CNGA4_HUMAN	ellular (Potential).		1	GCCGCCAGCCA	0.582
-	2	735		NM_003737	NP_003728	Q96JQ0	PCD16_HUMAN	|Extracellular (Potential).		5	CTCACGGTCCA	0.597
+	1	697_698		NM_001004489	NP_001004489	Q9H205	O2AG1_HUMAN	lasmic (Potential).		1	TGAGGGGAGG	0.49
+	6	1275	ax.1_Intron|ZNF21	NM_013250	NP_037382	Q9UL58	ZN215_HUMAN	KRAB.		0	GAGAAAGAAAT	0.358
+	4	1110		NM_176822	NP_789792	Q86W24	NAL14_HUMAN	NACHT.		8	TTCGATGAACTG	0.453
+	4	1327		NM_176822	NP_789792	Q86W24	NAL14_HUMAN	NACHT.		8	TGCAAGAGAGG	0.388
+	11	3457		NM_176822	NP_789792	Q86W24	NAL14_HUMAN			8	GTAAACTACAAG	0.398
-	3	1348	e_Mutation_p.P38	NM_213618	NP_998783	P78524	ST5_HUMAN	Pro-rich.		1	TTTGGGGACAG	0.587
-	18	3002	22_uc001mpa.2_	NM_173588	NP_775859	Q8N9C0	IGS22_HUMAN	nectin type-III 2.		7	TCATCTCAAGGA	0.562
+	3	532	S2_uc001mqn.2_	NM_001143830	NP_001137302	O43903	GAS2_HUMAN	CH.		2	TGCAGGAGAAA	0.388
-	9	791	1L1_uc001muf.1_	NM_001326	NP_001317	Q12996	CSTF3_HUMAN			0	TACTCCGATCTT	0.239
-	2	807	1_5'Flank|C11orf7	NM_000536	NP_000527	P55895	RAG2_HUMAN			5	GACATGAAAAG	0.423

-	9	1472_1473	_p.P284L|PHF21A	NM_001101802	NP_001095272	Q96BD5	PF21A_HUMAN		2	GGACGGGGTG	0.584	
+	3	485	go.3_Missense_M	NM_002843	NP_002834	Q12913	PTPRJ_HUMAN	cellular (Potential).	8	CAATTCCTGAC	0.418	
+	1	227		NM_001005512	NP_001005512	Q6IF82	O4A47_HUMAN	Name=2; (Potential).	2	CATTTCCCCCA	0.423	
+	2	402		NM_024114	NP_077019	Q8IWZ4	TRI48_HUMAN	B box-type.	0	TCTGAGGAGCAA	0.483	
+	3	224	C6_uc010rik.1_5'F	NM_001004704	NP_001004704	Q8NH72	OR4C6_HUMAN		2	TATTTAGGATTCT	0.368	
+	1	221		NM_001004739	NP_001004739	Q8NGL0	OR5L2_HUMAN	Name=2; (Potential).	1	GCTACTCCTCAAT	0.463	
+	1	932		NM_001001921	NP_001001921	Q8N127	O5AS1_HUMAN	lasmic (Potential).	5	GATATTCAAATGA	0.284	
+	1	740		NM_001005200	NP_001005200	Q8N162	OR8H2_HUMAN	Name=6; (Potential).	2	TCTTGGGAGTCA	0.353	
+	1	692		NM_001005205	NP_001005205	Q8NGP2	OR8J1_HUMAN	lasmic (Potential).	2	TTCATCAGAAGG	0.343	
-	1	465	NR_uc001njn.3_F	NM_005161	NP_005152	P35414	APJ_HUMAN	cellular (Potential).	6	AAAATCACCAC	0.562	
-	7	1048		NM_003146	NP_003137	Q08945	SSRP1_HUMAN		2	TGGGGGATCCA	0.458	
+	5	925	no.2_Missense_M	NM_001142521	NP_001135993	Q96PZ2	F111A_HUMAN		3	TTCTTTCCTTTCT	0.408	
+	1	326		NM_001004706	NP_001004706	Q8NGI4	OR4DB_HUMAN	Name=3; (Potential).	2	TTGGTGGGGCAG	0.468	
+	1	694		NM_001004711	NP_001004711	Q8NGE8	OR4D9_HUMAN	lasmic (Potential).	0	GGGAAGGCAGG	0.502	
+	6	677	A2_uc009ymu.2_3	NM_000139	NP_000130	Q01362	FCERB_HUMAN	ical; (Potential).	1	TTCTGGGACTTG	0.403	
+	3	432	1_Intron|DAK_uc0	NM_015533	NP_056348	Q3LXA3	DHAK_HUMAN	acetone binding (By similari	0	TCTGGCCATGAG	0.637	
-	4	655	A2_uc010rlx.1_5'U	NM_004739	NP_004730	O94776	MTA2_HUMAN	BAH.	2	ATTGCCGAGAAA	0.522	
-	7	1209	q.1_RNA|SLC22A	NM_199352	NP_955384	Q6T423	S22AP_HUMAN	lasmic (Potential).	4	ACGGCTCATGTG	0.502	
+	1	213	A10_uc001nwu.3_	NM_001039752	NP_001034841	Q63ZE4	S22AA_HUMAN	lasmic (Potential).	2	AATGGCCTTTGA	0.398	
+	9	1712	2A10_uc001nwu.3_	NM_001039752	NP_001034841	Q63ZE4	S22AA_HUMAN	ical; (Potential).	2	ATTTATGGAATCT	0.443	
+	1	1087	yps.1_Missense_M	NM_144585	NP_653186	Q96S37	S22AC_HUMAN		1	GACACGGAGCCG	0.667	
-	7	754		NM_017525	NP_059995	Q6DT37	MRCKG_HUMAN	rotein kinase.	4	CGTAGTGGCCCT	0.592	
+	10	1382	ense_Mutation_p.	NM_003273	NP_003264	O76062	ERG24_HUMAN		1	CTTACCGCATCAT	0.652	
-	7	753	_p.M160I|CABP2_	NM_016366	NP_057450	Q9NPB3	CABP2_HUMAN	EF-hand 4.	1	AGACATCATTCG	0.572	
+	16	2306	.R703Q|PPFIA1_u	NM_003626	NP_003617	Q13136	LIPA1_HUMAN		3	CCCACGAAGGA	0.602	
-	32	6434	p.D216N|ODZ4_u	NM_001098816	NP_001092286	Q6N022	TEN4_HUMAN	ular (Potential).|YD 8.	4	TGAAGTCCTGTAT	0.557	
-	8	1079	e_Mutation_p.P26	NM_007166	NP_009097	Q13492	PICAL_HUMAN		2	GGTCTGGTATAT	0.279	
+	2	975		NM_005959	NP_005950	P49286	MTR1B_HUMAN	Name=7; (Potential).	2	TATTTGTCACTA	0.512	
+	9	1662	uc001pen.1_Intron	NM_001098672	NP_001092142	Q6MZM0	HPHL1_HUMAN	e 3.|Extracellular (Potential	3	CTCAGGATTTGT	0.473	
-	9	2662	p.R630K|TRPC6_	NM_004621	NP_004612	Q9Y210	TRPC6_HUMAN	lasmic (Potential).	4	TTGGCCCTTGCA	0.428	
+	2	325	R3A_uc009yyx.2_	NM_213621	NP_998786	P46098	5HT3A_HUMAN	cellular (Potential).	0	CAGGAGGAGCC	0.562	
-	3	723		NM_000482	NP_000473				0	TGAATTCGTCAG	0.622	rs145184607
+	16	5318		NM_005422	NP_005413	O75443	TECTA_HUMAN		10	CAACCGAACTT	0.542	
+	5	530		NM_017425	NP_059121	Q15506	SP17_HUMAN	IQ.	0	CCAGAGAGGAG	0.403	
-	7	836	dy.1_Missense_Mu	NM_152640	NP_689853	Q8IZD4	DCP1B_HUMAN	Poly-Gln.	1	ctgctgctgGTGGA	0.458	
-	24	2994	_p.N3Y|A2M_uc0	NM_000014	NP_000005	P01023	A2MG_HUMAN		5	GTGTGTTTTGCAT	0.393	
-	31	4104	.2_Missense_Muta	NM_002864	NP_002855				5	GTCCATCGCAAG	0.433	
-	3	532		NM_006248	NP_006239				0	TGTCTCCTTGTG	0.607	
+	25	3540	se_Mutation_p.R1	NM_004570	NP_004561	O75747	P3C2G_HUMAN	PI3K/PI4K.	21	ATCTTCGTCCAC	0.403	
+	29	4033	se_Mutation_p.S1	NM_004570	NP_004561	O75747	P3C2G_HUMAN	PX.	21	CCTCTCTGAGG	0.289	
-	14	1824	se_Mutation_p.H2	NM_033123	NP_149114	Q86YW0	PLCZ1_HUMAN	C2.	3	GGACATGAATAA	0.308	
+	1	813	Z1_uc001rdw.3_5'	NM_033328	NP_201585	Q96KX2	CAZA3_HUMAN		2	ACCAAGCTCAA	0.408	
-	25	3156	.G1046S|ABCC9_	NM_005691	NP_005682	O60706	ABCC9_HUMAN	ntial).|ABC transmembrane	6	AATGCCTGCTC	0.413	
-	23	2759		NM_183378	NP_899234	Q7RTY7	OVCH1_HUMAN	CUB 3.	10	TGTAATCCACCTA	0.363	
+	2	297	_p.P30S|C12orf72	NM_001135864	NP_001129336	Q8IXQ9	MET20_HUMAN		0	TGTTTCCCTGTG	0.537	
-	5	1331	_p.V406I|PKP2_uc	NM_004572	NP_004563	Q99959	PKP2_HUMAN	ARM 2.	2	CTGAACTTTTAG	0.438	
+	13	1972	rf40_uc009zjv.1_	NM_001031748	NP_001026918	Q86WS4	CL040_HUMAN		6	GTGAATCTGTAAT	0.398	

+	4	517	e_Mutation_p.G93F	NM_000725	NP_000716	P54284	CACB3_HUMAN	SH3.		0	GGATCGGGCGG	0.627	
-	2	656	nse_Mutation_p.A1	NM_007210	NP_009141	Q8NCL4	GALT6_HUMAN	nenal (Potential).		2	GCAAAGGCATTG	0.567	
-	7	1297		NM_005555	NP_005546	P04259	K2C6B_HUMAN	Rod.|Coil 2.		2	CCATCTCCCCAC	0.562	
+	12	2574	p.C503Y|ESPL1_	NM_012291	NP_036423	Q14674	ESPL1_HUMAN			3	TCGGCTGTCCCA	0.602	
+	16	3041	p.L659F|ESPL1_u	NM_012291	NP_036423	Q14674	ESPL1_HUMAN			3	CAGGTTCTTTCAC	0.527	
+	1	49		NM_001005183	NP_001005183	A6NM76	O6C76_HUMAN	cellular (Potential).		0	CTGACGGATAAT	0.388	
+	8	1092	RBB3_uc010sqc.1_	NM_001982	NP_001973	P21860	ERBB3_HUMAN	cellular (Potential).		8	AACATCCTGTGT	0.507	
+	25	3155	RBB3_uc009zok.2	NM_001982	NP_001973	P21860	ERBB3_HUMAN	lasmic (Potential).		8	TAGCCCCTGGG	0.502	
+	3	293	sqh.2_Missense_M	NM_005726	NP_005717	P43897	EFTS_HUMAN			0	ATCTGGCTCCAC	0.473	
+	11	1561	ssense_Mutation_p	NM_002392	NP_002383	Q00987	MDM2_HUMAN	or interaction with USP2.		3	AAGAAACCCAAG	0.393	
+	9	1371	u.2_Missense_Mut	NM_001135805	NP_001129277	P21579	SYT1_HUMAN	Phospholipid binding (Proba		6	TTTGATCGTTTCT	0.393	
+	2	455	zm.1_Missense_M	NM_024560	NP_078836	Q9H6R3	ACSS3_HUMAN			4	CATATTGAAAATG	0.338	
-	31	3826	sui.1_RNA|PPFIA2	NM_003625	NP_003616	B7Z663	B7Z663_HUMAN			6	CTAAATCCAGCTC	0.443	
+	4	465	CYL2_uc001thm.1_	NM_017988	NP_060458	Q6P3W7	SCYL2_HUMAN	rotein kinase.		6	CCTTCCCCTATAT	0.328	
-	15	2162		NM_145913	NP_666018	Q8N695	SC5A8_HUMAN	lasmic (Potential).		0	TTGAAAGCAGGA	0.383	
+	6	1283	e_Mutation_p.R36	NM_016816	NP_058132	P00973	OAS1_HUMAN			2	CAGAAGAGGAC	0.373	
+	3	766	uc001txf.2_Intron	NM_178499	NP_848594	Q8IWA6	CCD60_HUMAN			3	CCAGCCGAAAAG	0.423	
-	6	1297	SL_uc001tzk.1_3'U	NM_003733	NP_003724	Q15646	OASL_HUMAN	biquitin-like 1.		1	GGAGGGGATGG	0.542	
+	12	1752	p.R118Q|DNAH10	NM_207437	NP_997320	Q8IVF4	DYH10_HUMAN	n (By similarity).		6	GGAACGATCTCT	0.418	
-	8	1348	_p.S303F|RIMBP2	NM_015347	NP_056162	O15034	RIMB2_HUMAN	onectin type-III 2.		11	GGTGGGAGGGG	0.637	
-	2	469		NM_004004	NP_003995	P29033	CXB2_HUMAN	ical; (Potential).		0	GCGTGGACACG	0.552	
+	13	1611	y.2_Nonsense_Mu	NM_175854	NP_787050	Q58A45	PAN3_HUMAN	se.|Interaction with PAN2.		1	TGGCCCAGTACC	0.299	
+	10	916	ba.2_Missense_M	NM_130806	NP_570718	Q8WXD0	RXFP2_HUMAN	xtracellular (Potential).		0	GCGATTCGCTCAC	0.323	rs144275111
-	5	727	D13_uc001uux.2_	NM_178006	NP_821074	Q9Y3M8	STA13_HUMAN			4	TGCTTTCGCTGT	0.627	
-	4	1156	vo.2_Missense_Mu	NM_001142296	NP_001135768	Q8N0X7	SPG20_HUMAN			0	TATCAGGAAACAT	0.448	
+	7	861	s.1_RNA|RB1_uc0	NM_000321	NP_000312	P06400	RB_HUMAN		p.?(5)	358	CACCTCCCATGTT	0.249	
-	4	514	e_Mutation_p.A13	NM_007015	NP_008946	O75829	LECT1_HUMAN	BRICHOS.		2	CTTGCGCTTTAAT	0.448	
+	3	218	n_p.M16I|SCEL_uc	NM_144777	NP_659001	O95171	SCEL_HUMAN			5	GAGATGAAGAG	0.443	
-	19	2851	nse_Mutation_p.P1	NM_198968	NP_945319	Q86YF9	DZIP1_HUMAN			2	GAAAAGGATCTT	0.269	
+	19	2304	11A_uc001vsm.1_M	NM_015205	NP_056020	P98196	AT11A_HUMAN	lasmic (Potential).		4	CAGCGGGAGCC	0.657	
+	1	902		NM_172194	NP_751944	Q8NH05	OR4Q3_HUMAN	lasmic (Potential).		3	GAAGAAGCTGA	0.388	
+	1	178		NM_001005503	NP_001005503	Q8NGC1	O11G2_HUMAN	cellular (Potential).		2	CCAGGGAGGGG	0.527	
-	3	186_187	kp.1_Missense_M	NM_002471	NP_002462	P13533	MYH6_HUMAN	yosin head-like.		4	TCATCGGGCACG	0.579	
+	3	305	e_Mutation_p.P51	NM_173159	NP_071406	Q8IXF0	NPAS3_HUMAN	x-loop-helix motif.		2	CCTCTTCCTGCA	0.488	
+	11	1384	IPOL1_uc010ams.	NM_138731	NP_620059	Q8TD10	MIPO1_HUMAN	Potential.		2	AGACTTCAGCAA	0.433	
-	1	663		NM_080746	NP_542784	Q96L21	RL10L_HUMAN			1	CATCAGGGATGA	0.517	
+	2	976		NM_000953	NP_000944	Q13258	PD2R_HUMAN	cellular (Potential).		4	TTTAAGGATGTCA	0.398	
+	4	502	pt.1_Missense_Mu	NM_017799	NP_060269	Q9NX78	CN101_HUMAN			2	TGCTGCGGGGG	0.418	
+	3	694	xex.3_Nonsense_	NM_021003	NP_066283	P35813	PPM1A_HUMAN			1	AATGTAAAGAAT	0.418	
+	4	1285_1286	xex.3_Missense_M	NM_021003	NP_066283	P35813	PPM1A_HUMAN			1	ATGCACCCAAAG	0.376	
-	12	1359	wc.1_Missense_M	NM_007039	NP_008970	Q16825	PTN21_HUMAN	Poly-Pro.		4	ACTGCGGTGGG	0.413	
+	8	1183	_splice|TDP1_uc0	NM_018319	NP_060789	Q9NUW8	TYDP1_HUMAN			2	AAGGGTTCGTAC	0.428	
-	14	1389	PERB_uc010aub.1_	NM_024764	NP_079040	Q9H7T0	CTSRB_HUMAN			5	GGGGATGAAATA	0.408	
-	8	801		NM_024764	NP_079040	Q9H7T0	CTSRB_HUMAN			5	TGGTATCATAATC	0.378	
+	1	135	n_p.E18K|KIAA140	NM_020818	NP_065869	Q9P2D8	UNC79_HUMAN			17	ATCATTGAATATC	0.338	
-	3	242	MA1_uc001ybx.1_	NM_178013	NP_821092	Q86XR5	PRIMA_HUMAN	xtracellular (Potential).		2	gaggtggcgggggtgg	0.353	
+	2	170	n_p.S72F|SERPIN	NM_006215	NP_006206	P29622	KAIN_HUMAN			4	CAGCTCCCACCA	0.557	

+	3	610		NM_182560	NP_872366	Q52M58	CN177_HUMAN			0	GGCCAGGTGCT	0.473	
+	9	1684_1685	e_Mutation_p.G51	NM_014844	NP_055659	O15040	TCPR2_HUMAN			3	GTCCTGGGCAGT	0.54	
+	9	2088	e_Mutation_p.S64	NM_014844	NP_055659	O15040	TCPR2_HUMAN			3	TGAACTCACTCA	0.602	
-	15	2293		NM_006035	NP_006026	Q9Y5S2	MRCKB_HUMAN	Potential.		11	CTCGGATTTGAT	0.463	
-	8	1240	.2_Missense_Muta	NM_005163	NP_005154	P31749	AKT1_HUMAN	rotein kinase.		134	TTGGCGTACTCC	0.687	
-	12	1913	q.2_Missense_Mut	NM_003257	NP_003248	Q07157	ZO1_HUMAN	PDZ 3.		6	CTTCTCTTATGAT	0.368	
+	2	259		NM_001211	NP_001202	O60566	BUB1B_HUMAN			4	CATGTCCCTGG	0.413	
-	15	2095_2096	P1_uc001zoc.2_5'l	NM_015540	NP_056355	Q9BWH6	RPAP1_HUMAN			1	TTCTTGGGGAG	0.599	
+	8	1291		NM_006293	NP_006284	Q06418	TYRO3_HUMAN	III 2.|Extracellular (Potentia		6	CCCTGGGACCCT	0.567	
+	17	2359		NM_198141	NP_937784	Q8TET4	GANC_HUMAN			2	GGTATTCTCTGTT	0.512	
-	7	3802_3803	pv.2_Missense_M	NM_022473	NP_071918	Q9H2Y7	ZF106_HUMAN			3	AGTGGGAAAAG	0.525	
+	1	561		NM_001080534	NP_001074003	Q8NB66	UN13C_HUMAN			7	AAAATGGAAAAA	0.458	
+	2	701	p.P141L|RNF111_	NM_017610	NP_060080	Q6ZNA4	RN111_HUMAN			2	CTTCTCCTTCAT	0.383	
+	3	240	uha.1_Missense_M	NM_152450	NP_689663	Q8TBF8	FA81A_HUMAN			1	GCCAGTCCCTGA	0.522	
-	3	400	02apj.3_Missense_	NM_005848	NP_005839	Q7Z401	MYCPP_HUMAN			4	AACACGAGGCC	0.363	
+	15	1985	ukf.1_Missense_M	NM_017691	NP_060161	Q8IUZ0	LRC49_HUMAN			1	TCCAAAGGAAAA	0.308	
-	9	1150	o.2_RNA|PARP6_u	NM_020214	NP_064599	Q2NL67	PARP6_HUMAN			0	CTGGGGGCTGG	0.597	
-	8	3320		NM_005477	NP_005468	Q9Y3Q4	HCN4_HUMAN	lasmic (Potential).		6	CAGCGGGGTCC	0.687	rs148714049
-	8	1566	se_Mutation_p.E3	NM_000781	NP_000772	P05108	CP11A_HUMAN			2	TCATCTCTAGCT	0.562	
-	26	3021	79F|MAN2C1_uc0	NM_006715	NP_006706	Q9NTJ4	MA2C1_HUMAN			0	CAAGAGATCGC	0.622	
-	16	2717	RF1_uc002ber.3_	NM_002891	NP_002882	Q13972	RGRF1_HUMAN			6	GTGTAGCCATTG	0.597	
+	13	1864	unn.1_Missense_M	NM_018689	NP_061159	Q8WUJ3	K1199_HUMAN			3	GATTTAAGGCAG	0.542	
-	16	1834	C3_uc002bgp.2_N	NM_001080532	NP_001074001	Q7Z5M5	TMC3_HUMAN	lasmic (Potential).		2	AGGCTCGAAATA	0.473	
-	3	477	os.1_Missense_Mu	NM_001717	NP_001708	Q01954	BNC1_HUMAN			3	TCCAAGGCATGG	0.493	
+	6	3070		NM_020778	NP_065829	Q96L96	ALPK3_HUMAN			12	GTTTCCCAAAAA	0.537	
+	7	1643	O3A1_uc010boc.1_	NM_013272	NP_037404	Q9UIG8	SO3A1_HUMAN	r (Potential).|Kazal-like.		1	CCGATTCCTTCA	0.468	
+	7	1691	p.S155F|RAB11FI	NM_014700	NP_055515	O75154	RFIP3_HUMAN			0	ACCCTTCCCCCG	0.592	
+	35	4388	_uc002cio.1_Misse	NM_145294	NP_660337	Q96KV7	WDR90_HUMAN	WD 17.		1	CAGCCCCGGGG	0.632	
+	1	1373		NM_020982	NP_066192	O95484	CLD9_HUMAN	cellular (Potential).		0	AGGCCCTCAAG	0.697	
-	5	884	ense_Mutation_p.G	NM_032805	NP_116194	Q96SZ4	ZSC10_HUMAN			1	GGACCCATCTT	0.637	
-	12	4921		NM_032444	NP_115820	Q8IY92	SLX4_HUMAN	raction with PLK1 and TEF		0	AGAGGGGCTCCA	0.647	
-	11	2253	dbg.1_Nonsense_	NM_015914	NP_056998	Q6PKC3	TXD11_HUMAN	Thioredoxin 2.		0	CTAGCTGGATGA	0.522	
-	15	1905	dx.2_Missense_Mu	NM_002474	NP_002465	P35749	MYH11_HUMAN	yosin head-like.		15	TGTCATTCAGCG	0.542	
+	29	4317	vl.2_Missense_Mut	NM_004996	NP_004987	P33527	MRP1_HUMAN	sporter 2.|Cytoplasmic.		4	TGTTTTCGGGTT	0.562	
-	5	920	wb.2_Missense_M	NM_015092	NP_055907	Q96Q15	SMG1_HUMAN	with SMG8 and SMG9.		16	TGTTTAACTAGTA	0.274	
+	5	619	fs.2_Missense_Mu	NM_016138	NP_057222	Q99807	COQ7_HUMAN	oximate tandem repeats.		1	GCCTCGACCAT	0.468	
+	13	1747		NM_017888	NP_060358	Q6NUN0	ACSM5_HUMAN			2	CTAACGCGGGAA	0.483	rs138362252
-	1	469_470	_uc002dja.2_RNA	NR_002594						0	CTTGAGGAAGGC	0.639	
+	2	1468		NM_006539	NP_006530	O60359	CCG3_HUMAN			0	ACTACGAACAG	0.562	
-	7	1030_1031	xz.1_Missense_M	NM_001109763	NP_001103233	Q6UXU4	GSG1L_HUMAN			1	TGCTTCCTGTGC	0.649	
+	8	1144	2IP_uc002drv.2_Mi	NM_032815	NP_116204	Q8NCF5	NF2IP_HUMAN	Ubiquitin-like.		1	ATGTCCCACTATG	0.547	
-	9	1639_1640	P397F|SEZ6L2_uc	NM_201575	NP_963869	Q6UXD5	SE6L2_HUMAN	xtracellular (Potential).		2	GGAAGGGGGCGA	0.564	
+	7	1615		NM_014712	NP_055527	O15047	SET1A_HUMAN	Ser-rich.	p.S310F(1)	3	CCTTTTCCCGCC	0.522	rs146035438
+	13	1965	gc.1_Missense_M	NM_001114	NP_001105	P51828	ADCY7_HUMAN	lasmic (Potential).		1	CCAAGTCCGATG	0.662	
-	2	3320	_Mutation_p.P100	NM_002968	NP_002959	Q9NSC2	SALL1_HUMAN			8	CCTGAGGAGAAA	0.572	
+	10	2618	ekl.2_Missense_Mu	NM_032206	NP_115582	Q86WI3	NLRC5_HUMAN			7	CGTGTCCTACCGT	0.547	
-	21	3136	NOT1_uc002enx.2	NM_016284	NP_057368	A5YKK6	CNOT1_HUMAN			6	ATTTTGGATCCAA	0.418	

-	1	125	5_uc002esm.2_5'I	NM_013241	NP_037373	Q9Y613	FHOD1_HUMAN			3	GTCTTCCCCGC	0.677	
-	72	12396	DIN_uc010cfy.2_R	NM_032821	NP_116210	Q4G0P3	HYDIN_HUMAN			2	GTTGAGGTGTG	0.493	
-	2	185	ı_p.S29F|TAT_uc(	NM_000353	NP_000344	P17735	ATTY_HUMAN			2	GCACAGAGCTT	0.527	
-	10	1415	ep.1_Missense_Mu	NM_012091	NP_036223	Q9BUB4	ADAT1_HUMAN	to I editase.		2	TGAAGAGTTCC	0.413	
-	2	329		NM_152342	NP_689555	Q8N8U2	CDYL2_HUMAN			1	GCTTGGAGGTA	0.527	
+	3	376	e_Mutation_p.N13	NM_001257	NP_001248	P55290	CAD13_HUMAN			1	TGAGAAACATA	0.527	
-	9	1090	cjf.2_Intron|PRDM	NM_001098173	NP_001091643	Q9NQW5	PRDM7_HUMAN	SET.		1	CCCCAGACCAG	0.532	
-	12	1879	PV3_uc010vrl.1_M	NM_145068	NP_659505	Q8NET8	TRPV3_HUMAN	lasmic (Potential).		4	CAGGCATCCGA	0.567	
-	6	918	th.1_Missense_Mu	NM_053285	NP_444515	Q969V4	TEKT1_HUMAN	Potential.		2	TTGTATCCTTCAG	0.537	
+	6	972	se_Mutation_p.H2	NM_001143990	NP_001137462	Q9BUR4	WAP53_HUMAN	WD 3.		0	TACAACCACCTG	0.602	
+	3	873	2gld.2_Missense_	NM_173728	NP_776089	O94989	ARHGF_HUMAN			3	CCGCCCCCACC	0.677	
+	15	2462	_p.S816F|USP43_	NM_153210	NP_694942	Q70EL4	UBP43_HUMAN			5	TGGATCCAAGG	0.577	rs76912039
-	34	4976	uc002gml.1_Intron	NM_005963	NP_005954	P12882	MYH1_HUMAN	Potential.		21	CATTTCATTGAG	0.498	
-	27	3495	_Missense_Mutati	NM_001100112	NP_001093582	Q9UKX2	MYH2_HUMAN	Potential.		14	CAGCTCCTCAAT	0.552	
+	10	1132	s.3_Missense_Mut	NM_014859	NP_055674	Q17R89	RHG44_HUMAN	Rho-GAP.		0	GAGATCGCCTTC	0.637	
-	16	3118		NM_014680	NP_055495	Q14667	K0100_HUMAN			4	TGACAAGATCTA	0.507	rs114130011
-	5	1332	F12_uc002hdj.1_M	NM_001033561	NP_001028733	Q96QT6	PHF12_HUMAN	action with SIN3A.		1	GTAAGGGAACGA	0.388	
+	50	7681	o.2_Nonsense_Mu	NM_001042492	NP_001035957	P21359	NF1_HUMAN		p.R2450*(1)	330	GAAGTTCGAAGT	0.363	
-	6	1470	ıht.2_Missense_Mu	NM_001094	NP_001085	Q16515	ACCN1_HUMAN	llular (By similarity).		4	ACTTACGAGATAT	0.438	
-	2	972	ht.2_Missense_Mu	NM_001094	NP_001085	Q16515	ACCN1_HUMAN	llular (By similarity).		4	TCTCTCCCCAG	0.612	
+	9	1214	hjc.2_Missense_M	NM_173167	NP_775259	Q8IWX7	UN45B_HUMAN			6	GAGCGCGATCAC	0.468	rs148057044
-	5	2416		NM_001145027	NP_001138499					1	TAAACTCCTCATC	0.423	
-	6	1268		NM_002278	NP_002269	Q14532	K1H2_HUMAN	Coil 2.|Rod.		0	GTCCTCGTTCTC	0.617	rs70964671
-	1	448	P_uc010wfs.1_Int	NM_000226	NP_000217	P35527	K1C9_HUMAN	Head.		3	cccactcccatagcca	0.09	
-	1	441	T14_uc010cxp.1_M	NM_000526	NP_000517	P02533	K1C14_HUMAN	Coil 1A.|Rod.		1	AGGAGGCCAGG	0.458	
+	1	265	.1_5'UTR|WNK4_u	NM_032387	NP_115763	Q96J92	WNK4_HUMAN			7	CTCCGGACCCC	0.716	
-	3	697	K|MEOX1_uc002i	NM_004527	NP_004518	P50221	MEOX1_HUMAN	Homeobox.		0	TTCATCCTTCGG	0.582	
-	1	107	101_uc010wis.1_	NM_032376	NP_115752	Q96IK0	TM101_HUMAN	ical; (Potential).		2	CCAAAAGGGGC	0.622	
-	1	486	ikd.2_Missense_M	NM_015443	NP_056258	Q7Z3B3	K1267_HUMAN			2	CTAAGGAAAACT	0.438	
+	3	296	jgl.2_Missense_M	NM_002266	NP_002257	P52292	IMA2_HUMAN	IBB.		2	TAAGCTCATTTC	0.413	
-	4	640	17orf28_uc002jmk.	NM_030630	NP_085133	Q8IV36	CQ028_HUMAN			0	TCCTCCGGTGG	0.662	
-	2	901	ense_Mutation_p.G	NM_001454	NP_001445	Q92949	FOXJ1_HUMAN			1	ATGCCCCAGCC	0.736	
+	3	275	.P32L|SEPT9_uc0	NM_001113491	NP_001106963	Q9UHD8	SEPT9_HUMAN			3	GACTCCCCTAC	0.567	
-	6	927	ı_p.L56F|LGALS3	NM_005567	NP_005558	Q08380	LG3BP_HUMAN			4	GAGGAGGATGG	0.612	
+	32	4292	lk.3_RNA|SMCHD	NM_015295	NP_056110	A6NHR9	SMHD1_HUMAN			0	AAAAACCCGTTC	0.353	
+	2	1157	NDC2_uc002koh.	NM_001098529	NP_001091999	Q86VQ3	TXND2_HUMAN	repeat of Q-P-K-X-G-D-I-P		2	CAAGGAGAGTGA	0.562	
+	21	2215	D30B_uc010xak.1	NM_001145029	NP_001138501	Q9BXX2	AN30B_HUMAN			2	GAGTCTCCTGATA	0.289	
-	9	1728	_p.L286*|NPC1_u	NM_000271	NP_000262	O15118	NPC1_HUMAN			2	TAATTTAACACA	0.463	
-	9	1709	p.C280S|NPC1_u	NM_000271	NP_000262	O15118	NPC1_HUMAN			2	GGTGCAGTTCG	0.448	
+	53	6901	us.3_Missense_M	NM_198129	NP_937762	Q16787	LAMA3_HUMAN	omain II and I.		11	GAGATGGTCTTC	0.423	
-	10	1810	n.1_Missense_Mu	NM_001792	NP_001783	P19022	CADH2_HUMAN	r (Potential).|Cadherin 3.		4	AAAGTCGATTG	0.393	
-	13	2062	wi.3_Missense_Mu	NM_001941	NP_001932	Q14574	DSC3_HUMAN	r (Potential).|Cadherin 5.		4	GATATGAAAGAC	0.333	
-	3	728	n_p.R92*|DSC2_u	NM_024422	NP_077740	Q02487	DSC2_HUMAN			3	ACTTCTCTTCTC	0.338	
-	12	2022_2023	m.2_Missense_M	NM_024421	NP_077739	Q08554	DSC1_HUMAN	r (Potential).|Cadherin 5.		4	TCCTCATTATTC	0.391	
-	12	2073	1012_uc002kxd.3_	NM_014939	NP_055754	Q9Y2L5	TPPC8_HUMAN			0	TAAATCGATGGC	0.333	
-	1	202	nf.2_Missense_Mu	NM_002930	NP_002921	Q99578	RIT2_HUMAN			1	CCGGGGAGCAG	0.537	rs140593847
+	9	1131	LC14A1_uc002lbh	NM_001146036	NP_001139508	Q13336	UT1_HUMAN			2	TAACAGGACTCA	0.512	

-	13	1037	_uc002lbq.3_Silen	NM_024430	NP_077748	Q9H939	PPIP2_HUMAN			1	CTTTTAGGAATTG	0.249	
-	1	1626	AL2_uc002lco.2_	NM_016427	NP_057511	Q8IYF1	ELOA2_HUMAN			4	CCGAATCCCAGGA	0.547	
-	1	817	AL2_uc002lco.2_	NM_016427	NP_057511	Q8IYF1	ELOA2_HUMAN			4	CACTTTCTCTCA	0.662	
+	3	1014	C_uc010xdr.1_5'U	NM_005215	NP_005206	P43146	DCC_HUMAN	otential).|Ig-like C2-type 2.		17	AGGTTCCTTTCA	0.388	
+	12	2494	_p.S484L|DCC_uc	NM_005215	NP_005206	P43146	DCC_HUMAN	tential).|Fibronectin type-III		17	TCAATTCAAGAGT	0.408	
-	4	1859		NM_052947	NP_443179	Q86TB3	ALPK2_HUMAN			14	CATTCGGCTTCTT	0.512	
+	6	632	xet.1_Missense_M	NM_001040147	NP_001035237	O75635	SPB7_HUMAN			3	CAAAGGCAAGT	0.393	
+	12	2390	b.2_Missense_Mu	NM_033646	NP_387450	Q9ULB5	CADH7_HUMAN	lasmic (Potential).		4	ACTCCAGAAATT	0.483	
-	3	2151	e.2_RNA|ZNF516_	NM_014643	NP_055458	Q92618	ZN516_HUMAN			1	TCGCCGGTGTCT	0.542	
+	2	1550	ra.2_Missense_Mu	NM_171999	NP_741996	Q9BXA9	SALL3_HUMAN			4	GCAAGCCCGTGC	0.716	
+	7	2014		NM_001194	NP_001185	Q9UL51	HCN2_HUMAN	ytoplasmic (Potential).		0	TCGAGACGGTGG	0.701	
+	7	1253	b.1_Missense_Mu	NM_004368	NP_004359	Q99439	CNN2_HUMAN			0	AGGTCCCTGAAT	0.637	
+	4	1073	wq.2_Missense_M	NM_024967	NP_079243	Q9HAH1	ZN556_HUMAN	C2H2-type 7	p.S329F(1)	3	CCTCATCCTTACA	0.522	rs142040650
-	5	428	_p.P124L|PIP5K1	NM_012398	NP_036530	O60331	PI51C_HUMAN	PIPK.		4	GGGCGGGGGTG	0.622	
+	8	1096	_p.N211S|ZNF557_	NM_001044388	NP_001037853	Q8N988	ZN557_HUMAN	C2H2-type 3.		2	AATGCAATGACTG	0.453	
-	5	36001		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).		57	AAAATTCTGGGG	0.493	
-	5	35987		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).		57	CCAACTGAAGTTA	0.493	
-	3	18701		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).		57	CCAAGAGATGTCA	0.488	
-	4	1916	799_uc002mts.3_I	NM_001080821	NP_001074290	Q96GE5	ZN799_HUMAN	C2H2-type 17.		6	TTACATTCATACG	0.413	
+	8	852		NM_173483	NP_775754	Q6NT55	CP4FN_HUMAN			2	AGTGATTATATCT	0.557	
+	1	255		NM_013939	NP_039227	O60403	O10H2_HUMAN	cellular (Potential).		3	ATCATCCCGCGC	0.627	
-	9	1513	P1_uc002nft.1_R	NM_031941	NP_114147	Q8N6Y0	USBP1_HUMAN			1	TGGGTCCCCAGA	0.607	
+	4	1529		NM_031218	NP_112495	P35789	ZNF93_HUMAN	C2H2-type 12.		1	ATAAGAAAATTCA	0.368	
+	4	1613		NM_031218	NP_112495	P35789	ZNF93_HUMAN	C2H2-type 13.		1	ATAAGAAAATTCA	0.348	
-	4	1190	pc.1_Missense_M	NM_001076675	NP_001070143	Q68DY1	ZN626_HUMAN	C2H2-type 7.		1	GCTTTGCCACATT	0.383	
-	4	827	pc.1_Missense_M	NM_001076675	NP_001070143	Q68DY1	ZN626_HUMAN			1	GGTTTCTCTCCA	0.393	
-	4	743	pc.1_Missense_M	NM_001076675	NP_001070143	Q68DY1	ZN626_HUMAN			1	GGTTTCCCTCCA	0.363	
+	4	1124	cy.2_Missense_M	NM_033468	NP_258429	Q9Y2Q1	ZN257_HUMAN	C2H2-type 6.		0	AAATGTGAAGAGT	0.423	
-	3	1834		NM_001001411	NP_001001411	Q8N7Q3	ZN676_HUMAN	C2H2-type 13.		0	CACATTTGTAGCC	0.388	
-	3	1829		NM_001001411	NP_001001411	Q8N7Q3	ZN676_HUMAN			0	TTGTAGCGTTTCT	0.388	
-	4	1530		NM_001098626	NP_001092096	A6NK75	ZNF98_HUMAN	C2H2-type 11.		2	TAAAAGCTTTGC	0.373	
-	7	2771		NM_001080409	NP_001073878					2	TTAAAAGCTTTG	0.368	
-	4	326		NM_001080409	NP_001073878					2	CTCTGATCTGGC	0.289	
+	4	475	1_5'UTR|LRP3_uc	NM_002333	NP_002324	O75074	LRP3_HUMAN	lar (Potential).|CUB 1.		3	CCTGCCTTCATCT	0.662	
+	15	2245	cd.3_Missense_M	NM_199180	NP_954649	Q6UWL6	KIRR2_HUMAN	cytoplasmic (Potential).		3	CCACATCCTTTGG	0.617	
-	5	1009	p.H236Y|ZNF565_	NM_152477	NP_689690	Q8N9K5	ZN565_HUMAN	C2H2-type 5.		2	CTGTGTGGATTCT	0.507	
+	8	1979	p.R402C|ZNF383_	NM_152604	NP_689817	Q8NA42	ZN383_HUMAN	C2H2-type 11.		2	CTCATTCGTCATC	0.378	
+	8	1821	L3_uc002olw.2_Int	NM_016941	NP_058637	Q9NYJ7	DLL3_HUMAN	lasmic (Potential).		3	AGGTAGCGACGC	0.562	
-	3	232_233		NM_001828	NP_001819	Q05315	LPPL_HUMAN	Galectin.		0	GAAATGGAAGAC	0.505	
+	9	738	2ooe.2_Missense_	NM_138392	NP_612401	Q8TBC3	SHKB1_HUMAN			2	TGTTTTCCAGCC	0.627	
+	2	375	2orj.1_Missense_	NM_004363	NP_004354	P06731	CEAM5_HUMAN	Ig-like 1.		2	TAATAGGAACTCA	0.468	
-	14	1750	p.W144*|GRIK5_u	NM_002088	NP_002079	Q16478	GRIK5_HUMAN	lasmic (Potential).		0	TTATACCACTCAT	0.607	
-	3	750	_Mutation_p.E96K	NM_182707	NP_874366	Q9UQ74	PSG8_HUMAN	-like C2-type 1.		0	GTATTTCACATTC	0.512	
-	3	571	10eio.1_Missense_	NM_006905	NP_008836	P11464	PSG1_HUMAN		p.E145G(1)	2	GAGTCTCCACTGT	0.517	
-	5	1261	wf.3_Missense_Mu	NM_002784	NP_002775	Q00887	PSG9_HUMAN	-like C2-type 3.		2	CGCTATGATTTCT	0.443	
+	5	1076	eji.2_Intron|ZNF23	NM_181756	NP_861421	A6NK53	ZN233_HUMAN	type 2; degenerate.		2	GGAATGGTGACA	0.507	
+	6	853	en.2_Missense_M	NM_006247	NP_006238	P53041	PPP5_HUMAN	Catalytic.		2	ACCAACCCCTAT	0.557	

+	2	416	)2_uc010xyu.1_In	NM_014601	NP_055416	Q9NZN4	EHD2_HUMAN		2	;ACTTCGACGGC.	0.677	
+	5	2330	ıc002pxc.1_5'Flan	NM_007147	NP_009078	Q9Y473	ZN175_HUMAN	:2H2-type 14.	0	;GAAATCGTTCA(	0.438	rs145951696
-	5	1020		NM_003830	NP_003821	O15389	SIGL5_HUMAN	'otential).|Ig-like C2-type 2.	4	;TATTGGAGATG(	0.622	
+	2	710	p.G222E|FPR2_u(	NM_001005738	NP_001005738	P25090	FPR2_HUMAN	Name=5; (Potential).	4	;CTATGGGCTCAT	0.502	
+	2	496		NM_002030	NP_002021	P25089	FPR3_HUMAN	Name=3; (Potential).	6	TGTTATGATAGA(	0.468	
-	7	964	p.S147L|ZNF611_	NM_030972	NP_112234	Q8N823	ZN611_HUMAN		1	AGTAATGAAGAA'	0.378	
-	7	1008	-15_uc002qau.2_M	NR_028343		Q09FC8	ZN415_HUMAN		1	;AGGAACCATGG'	0.383	
+	5	623	L1_uc002qhl.3_Int	NM_012314	NP_036446	P43632	KI2S4_HUMAN	'otential).|Ig-like C2-type 2.	0	,CCCACGGAGGG	0.592	
+	9	2952	tg.2_Missense_Mu	NM_176811	NP_789781	Q86W28	NALP8_HUMAN		13	,GGCTGGAAAAC'	0.512	
+	8	1918	uc002qnk.1_Intron	NM_020828	NP_065879	Q8NHY6	ZFP28_HUMAN		1	AGAAGCCTTTTG	0.428	
-	4	322	F329_uc002qro.1_I	NM_024620	NP_078896	Q86UD4	ZN329_HUMAN		1	,GCAGGGAACTT	0.463	
+	4	800	IF8_uc002qrz.2_R	NM_021089	NP_066575	P17098	ZNF8_HUMAN		1	;GCTCCCCAGGA	0.473	
-	12	1501	:b.1_Missense_Mu	NM_012293	NP_036425	Q92626	PXDN_HUMAN	-like C2-type 3.	8	;ACCAGGTGCCG	0.602	
-	9	1162		NM_000384	NP_000375	P04114	APOB_HUMAN	Vitellogenin.	27	AGATTAGCTCTC'	0.458	
-	16	2240	\\|ATAD2B_uc002re	NM_017552	NP_060022	Q9ULI0	ATD2B_HUMAN		1	'GGGCACTAAGC.	0.502	
-	1	1370	F3C_uc010ykr.1_M	NM_002254	NP_002245	O14782	KIF3C_HUMAN	:inesin-motor.	4	:CCACTCGGATG'	0.607	
-	12	1641	ɜyv.1_Missense_M	NM_021095	NP_066918	Q9Y289	SC5A6_HUMAN		2	'GGGAGGAAATAT	0.468	
+	1	5312	1_5'Flank|ZNF512	NM_032266	NP_115642	Q68DN1	CB016_HUMAN	m repeat of P-S-E-R-S-H-I-	1	;TCCCTCTGAGA(	0.557	
+	5	910	ımm.1_Missense_I	NM_199280	NP_954974	Q6ZUX3	F179A_HUMAN		4	:CTGAGGCCAGC(	0.637	
-	1	1027		NM_001029883	NP_001025054	A6NGG8	CB071_HUMAN		1	GGGGAGACCCT(	0.587	
-	33	5500	p.P115S|HEATR5	NM_019024	NP_061897	Q9P2D3	HTR5B_HUMAN		8	;TGGAGGAACCT	0.408	
-	2	1120		NM_005760	NP_005751	Q03701	CEBPZ_HUMAN		1	;GGCTCGAGTTT'	0.413	
-	1	676	(HH2_uc002rtf.3_I	NM_001101330	NP_001094800				0	:TGCATATTTCA(	0.378	
-	10	2016	p.E586K|FSHR_u	NM_000145	NP_000136	P23945	FSHR_HUMAN	lasmic (Potential).	8	;CATTTCATAGCA	0.483	
+	5	1560		NM_019002	NP_061875	Q9NY74	ETAA1_HUMAN		4	AATTATCCACTG(	0.249	
+	7	806	p.P193L|CCT7_uc	NM_006429	NP_006420	Q99832	TCPH_HUMAN		0	,CAATCCCAAGAT	0.438	
+	10	2257	jg.2_Missense_Mu	NM_015120	NP_055935	Q8TCU4	ALMS1_HUMAN	ıpproximate tandem repeat	9	'CTACTCCCCAC'	0.478	
+	18	2821	ysg.1_Missense_I\	NM_004389	NP_004380	P26232	CTNA2_HUMAN		9	,CATTTCGCCTG'	0.368	
-	4	358	p.D130N|SFTPB_	NM_198843	NP_942140	P07988	PSPB_HUMAN	posin B-type 1.	2	AGTAGTCGTCAA(	0.617	rs45557339
-	13	2343		NM_004836	NP_004827	Q9NZJ5	E2AK3_HUMAN	Potential).|Protein kinase.	3	;GTGAAGGAGCT	0.453	
+	15	2401	;yn.1_RNA|VWA3E	NM_144992	NP_659429	Q502W6	VWA3B_HUMAN		6	;AAAAGGATGGA(	0.522	
+	11	2466		NM_001011552	NP_001011552	Q6AI14	SL9A4_HUMAN	lasmic (Potential).	3	:TGCAGGAAGAG	0.428	
+	20	7391		NM_006267	NP_006258	P49792	RBP2_HUMAN	RanBD1 3.	18	CTGTTCGTTTTAA	0.373	
-	7	1645		NM_000575	NP_000566	P01583	IL1A_HUMAN		1	'AGTGCCGTGAG'	0.468	
-	7	893	ı.1_Missense_Mut	NM_000576	NP_000567	P01584	IL1B_HUMAN		4	:TTTAGGAAGAC/	0.502	
-	17	5698	ttq.2_Missense_M	NM_207363	NP_997246	O14513	NCKP5_HUMAN		0	;TGGAGGAAGGC	0.597	
-	3	227	_p.P66S|YSK4_uc	NM_025052	NP_079328	Q56UN5	YSK4_HUMAN		5	:ACTGGGATCTT(	0.418	
+	4	443	10zbl.1_Missense_	NM_018460	NP_060930	Q53QZ3	RHG15_HUMAN	PH.	2	AAGAAACTAAGG	0.333	
-	131	18129	p.E2403K|NEB_uc	NM_004543	NP_004534	P20929	NEBU_HUMAN	Nebulin 163.	20	TGCTTTCCTCTA(	0.418	
-	11	1569	p.D284N|CCDC14	NM_138803	NP_620158	Q8NFR7	CC148_HUMAN		2	GAAGATCTCTCAT	0.303	
-	5	980	ɔs.2_Missense_Mu	NM_002349	NP_002340	O60449	LY75_HUMAN	Potential).|C-type lectin 1.	0	TTACCTGGATCC(	0.423	
-	4	363	:e|ITGB6_uc010zc	NM_000888	NP_000879	P18564	ITB6_HUMAN		3	:ACCACCTGCAA/	0.522	
-	23	4711	.Y1358D|SCN3A_ı	NM_006922	NP_008853	Q9NY46	SCN3A_HUMAN		10	:AAGATAGCCAG(	0.398	
-	13	2246	_p.W623*|SCN1A_	NM_006920	NP_008851	P35498	SCN1A_HUMAN	II.	13	TTTAACCAATATG	0.383	
+	3	461	ı_p.W123*|G6PC2	NM_021176	NP_066999	Q9NQR9	G6PC2_HUMAN	ical; (Potential).	1	TGTCTGGTATGT(	0.478	
+	7	1327	p.S256F|ITGA6_ι	NM_001079818	NP_001073286	P23229	ITA6_HUMAN	Extracellular (Potential).	2	AAGATTCTATGTT	0.358	
-	2	1268	_p.G67E|PDE11A	NM_016953	NP_058649	Q9HCR9	PDE11_HUMAN	GAF 1.	4	TTGTATCCAGTTA	0.408	

-	284	82389	84S|TTN_uc010z	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN			153	GAGAGGAGGAT	0.438	
-	275	76982_7698	282S|TTN_uc010z	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN			153	ACCTGGGGGAC	0.47	
-	275	71443	435*|TTN_uc010zf	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN			153	GAGACCATGTT	0.438	
-	275	68106	23A|TTN_uc010z	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN			153	TCACAGTAACTG	0.463	
-	275	63906	23Q|TTN_uc010z	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN			153	GATACTCTAATC	0.458	
-	238	48616	826E|TTN_uc010z	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN			153	TTGGTTCCTTCT	0.378	
-	220	43725	_uc010zfi.1_Misse	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN			153	AGGTTCCCAAG	0.398	
-	200	39450	.1_Missense_Muta	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN			153	CTTTTCCATGTT	0.363	
-	143	30597	z.1_Missense_Mu	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN			153	AACTTCCTCTT	0.453	
-	80	20457	_uc010zfj.1_Intro	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN			153	CTTGCGGATGA	0.512	
+	4	2903		NM_194250	NP_919226	Q7Z570	Z804A_HUMAN		p.R770Q(1)	11	TCTATCGAAAAC	0.333	
-	4	587	_p.K178*|CLK1_uc	NM_004071	NP_004062	P49759	CLK1_HUMAN			2	TTCTTTTCCTTC	0.443	
+	5	4094		NM_020923	NP_065974	Q9HCK1	ZDBF2_HUMAN			3	CTACAGATTCC	0.393	
-	2	90		NM_020989	NP_066269	P07315	CRGC_HUMAN	crystallin 'Greek key' 1.		0	GGTTTCGTAGC	0.522	rs145041511
+	11	4932	g.1_Missense_Mu	NM_002374	NP_002365	P11137	MAP2_HUMAN			17	AGAATTCCTTC	0.458	
-	3	320	b.2_Missense_M	NM_079420	NP_524144	P05976	MYL1_HUMAN	EF-hand 1.		1	CTGTTCTGTCA	0.438	
+	7	1185	.3_Missense_Muta	NM_005070	NP_005061	P48751	B3A3_HUMAN	Cytoplasmic.		5	TCCTTCGCAGG	0.652	rs140021661
+	10	1638	484S|SLC4A3_uc	NM_005070	NP_005061	P48751	B3A3_HUMAN	Cytoplasmic.		5	CAACTCCCAGC	0.612	
-	3	757	utation_p.W131R	NM_181457	NP_852122	P23760	PAX3_HUMAN	Paired.		766	TTTCCCAGCTGA	0.532	
-	8	4528	_Mutation_p.A14	NM_001142644	NP_001136116	Q2M3C7	SPKAP_HUMAN			10	CTTCAGCCTCT	0.552	
-	3	447	t.3_Missense_Mu	NM_001100818	NP_001094288	Q7Z2X4	PCLI1_HUMAN	PID.		4	GATTTCCAGGA	0.557	
+	5	653	se_Mutation_p.E1	NM_007237	NP_009168	Q13342	LY10_HUMAN			0	CTCAGGAAGCC	0.498	
+	5	818	_p.R196Q|ITM2C_	NM_030926	NP_112188	Q9NQX7	ITM2C_HUMAN			0	GCGCCGGGCAA	0.632	
-	2	361		NM_006056	NP_006047	Q9HB89	NMUR1_HUMAN	Name=1; (Potential).		5	GGATGACCAGA	0.632	
+	1	515	zmy.1_Intron|UG	NM_000463	NP_000454	P22309	UD11_HUMAN			2	TCTGCCCACTG	0.567	
-	3	443	ek.2_Missense_M	NM_001029871	NP_001025042	Q2I0M5	RSPO4_HUMAN	FU.		0	CTTCCCCTTGT	0.627	
+	3	187	RG1B_uc010gdr.1_RNA|FRG1B_uc010ztk.1_Missense_Mutation_p.L4S							0	TTTGTTGGCCT	0.353	
+	3	189	RG1B_uc010gdr.1_RNA|FRG1B_uc010ztk.1_Missense_Mutation_p.A5T							0	TTGTTGGCCTCA	0.353	
+	2	143		NM_001037730	NP_001032819	Q30KQ5	DB115_HUMAN			1	GAAATCATGCA	0.323	
-	2	116		NM_001037731	NP_001032820	Q30KQ4	DB116_HUMAN			0	TCACATGGATTC	0.468	
+	2	248		NM_182658	NP_872599	P59826	LPLC3_HUMAN	Leu-rich.		4	CCACGGAGGG	0.597	
-	5	446	_p.E65K|NECAB	NM_031232	NP_112509	Q96P71	NECA3_HUMAN			1	CGATTCCAATG	0.612	
+	7	924	S2_uc010gey.2_	NM_018677	NP_061147	Q9NR19	ACSA_HUMAN			0	GTCCCCCCCAA	0.537	
-	24	3507	.G1127A|PTPRT_	NM_007050	NP_008981	O14522	PTPRT_HUMAN	hatase 1.|Cytoplasmic (Po		20	CCACCCCTTCA	0.577	
-	22	3180	.R1018Q|PTPRT_	NM_007050	NP_008981	O14522	PTPRT_HUMAN	hatase 1.|Cytoplasmic (Po		20	CAGTATCGCACA	0.438	
-	21	3155	.E1010K|PTPRT_	NM_007050	NP_008981	O14522	PTPRT_HUMAN	hatase 1.|Cytoplasmic (Po		20	CACTTCCACCA	0.468	
-	8	1628	gj.2_Missense_M	NM_007050	NP_008981	O14522	PTPRT_HUMAN	tential).|Fibronectin type-III		20	GTCTTCCTCAG	0.552	
-	7	1154	gj.2_Missense_M	NM_007050	NP_008981	O14522	PTPRT_HUMAN	tential).|Fibronectin type-III		20	CACTTCCTTCA	0.567	
+	4	651		NM_004994	NP_004985	P14780	MMP9_HUMAN			2	GTGGTCCCTGG	0.637	
-	8	1852	hk.1_Missense_M	NM_021248	NP_067071	Q9UJ99	CAD22_HUMAN	(Potential).|Cadherin 4.		5	TTAGGGATGCC	0.552	
-	5	705	Missense_Mutatio	NM_022829	NP_073740	Q8WWT9	S13A3_HUMAN	lasmic (Potential).		1	ATCCTCCTTCCT	0.532	
-	12	2135	2_uc002xtq.2_Sp	NM_018837	NP_061325	Q8IWU5	SULF2_HUMAN			6	ACTCACCGATGT	0.594	
-	2	1634	s.1_Nonsense_M	NM_004975	NP_004966	Q14721	KCNB1_HUMAN	lasmic (Potential).		2	CTTTGTCCATTT	0.433	
+	7	2296	ze.1_Missense_M	NM_001164116	NP_001157588	Q9NQ75	CASS4_HUMAN			3	CATTTCACGGC	0.577	
+	1	917		NM_178457	NP_848552	Q5JPB2	ZN831_HUMAN			14	GAAGTCGCCGA	0.697	
+	2	3772		NM_178457	NP_848552	Q5JPB2	ZN831_HUMAN			14	TGCCCCAGCAC	0.498	
+	5	4780		NM_178457	NP_848552	Q5JPB2	ZN831_HUMAN			14	CCAGAGGCCAG	0.468	

+	7	724	co.2_Missense_M	NM_007002	NP_008933	Q16186	ADRM1_HUMAN	Ser-rich.	0	GGCAGCGGTCA	0.706	
+	11	1202	ion_p.R312*|ITSN	NM_003024	NP_003015	Q15811	ITSN1_HUMAN		4	GAGTTCGATCT	0.388	
-	15	3372	CAM_uc002yyr.1_	NM_001389	NP_001380	O60469	DSCAM_HUMAN	tential).|Fibronectin type-III	11	GAGCTCGTTGC	0.587	
+	2	173	c.2_RNA|UBASH3	NM_018961	NP_061834	P57075	UBS3A_HUMAN	UBA.	3	CACGGGGAGGA	0.607	
-	9	1614	p.H232Y|DGCR2_	NM_005137	NP_005128	P98153	IDD_HUMAN	lasmic (Potential).	1	CGGGTGGATGG	0.627	
+	6	1677	p.V489M|ZNF74_	NM_003426	NP_003417	Q16587	ZNF74_HUMAN	2H2-type 9.	1	TCATCGTGCAC	0.637	
+	26	4610	guz.1_Missense_	NM_032608	NP_115997	Q8IUG5	MY18B_HUMAN	otential.|Tail.	12	AAGGTGATGTG	0.612	
+	2	755		NM_020437	NP_065170	Q6ICH7	ASPH2_HUMAN	enal (Potential).	1	ACAACGAGGGC	0.637	
-	10	1209	.P292L|RBM9_uc	NM_001082578	NP_001076047	O43251	RFOX2_HUMAN	Ala-rich.	0	AGGCGGGGATG	0.512	
+	14	1907	aqc.3_Missense_	NM_000395	NP_000386	P32927	IL3RB_HUMAN	lasmic (Potential).	3	CCACAGAGCAG	0.637	
+	14	2411	aqc.3_Missense_	NM_000395	NP_000386	P32927	IL3RB_HUMAN	lasmic (Potential).	3	TAGTTCCCTCT	0.627	
-	5	2021	AP1_uc003azu.2_	NM_002883	NP_002874	P46060	RAGP1_HUMAN		0	CAAAGACCTTC	0.582	
-	8	840		NM_002676	NP_002667	Q92871	PMM1_HUMAN		1	CTCATGAGCTG	0.587	
-	7	640		NM_002676	NP_002667	Q92871	PMM1_HUMAN		1	CCTCGGGGAAG	0.592	
+	16	2991	BF2_uc003bbj.2_	NM_004599	NP_004590	Q12772	SRBP2_HUMAN	lasmic (Potential).	4	GAGTTCCTTCT	0.622	
-	3	448	ba.1_Intron|TNFR	NM_052945	NP_443177	Q96RJ3	TR13C_HUMAN	lasmic (Potential).	0	TTCCCGGAGAC	0.632	
-	5	815	.1_Intron|PHF21B	NM_138415	NP_612424	Q96EK2	PF21B_HUMAN		3	gggtgaaggggacagt	0.274	
+	4	381	E1_uc011aqz.1_5'	NM_016426	NP_057510	Q9NYZ3	GTSE1_HUMAN		1	TCGGACCCTTT	0.388	
+	3	417	1arp.1_Missense_	NM_018995	NP_061868	Q9BXT6	M10L1_HUMAN		3	GGAGTCCCTCA	0.512	
+	3	1711	p.E437K|PANX2_	NM_052839	NP_443071	Q96RD6	PANX2_HUMAN	lasmic (Potential).	1	AGAAGGAAATC	0.701	
+	1	1741		NM_138433	NP_612442	Q96G42	KLD7B_HUMAN	Kelch 5.	1	CACCACCCTGG	0.687	
+	3	551	_uc010hbh.1_Mis	NM_001097	NP_001088	P10323	ACRO_HUMAN	eptidase S1.	0	GGTGGCCGGCT	0.627	
+	10	1293		NM_001570	NP_001561	O43187	IRAK2_HUMAN	rotein kinase.	8	GTTGGCCGAGG	0.542	
-	7	2096	p.P574L|IQSEC1_	NM_014869	NP_055684	Q6DN90	IQEC1_HUMAN	SEC7.	1	CACGGGGAATG	0.527	
+	3	419_420	zi.2_Missense_M	NM_003298	NP_003289	P49116	NR2C2_HUMAN		0	TGGCTTCCCCA	0.554	
-	11	1677	.P495S|SCN5A_	NM_198056	NP_932173	Q14524	SCN5A_HUMAN		9	CTTGGGGAGCC	0.527	
-	27	5456		NM_006514	NP_006505	Q9Y5Y9	SCNAA_HUMAN		10	GAGAATCCAAC	0.448	
-	2	4092	2_3'UTR|XIRP1_	NM_194293	NP_919269	Q702N8	XIRP1_HUMAN	Pro-rich.	8	AAGAAGGGGGT	0.607	
+	8	992	YRIP_uc010hhw.2	NM_015460	NP_056275	Q8NFW9	MYRIP_HUMAN	yosin-binding.	5	CCGTGCTCCCG	0.597	
+	12	2230	ssense_Mutation_	NM_015460	NP_056275	Q8NFW9	MYRIP_HUMAN	ctin-binding.	5	TGGAAGAAAAT	0.507	
-	19	2006	w.2_Missense_Mu	NM_017886	NP_060356	Q96C45	ULK4_HUMAN		0	CCAAGGGAACA	0.448	
+	3	918	_Mutation_p.R24	NM_001296	NP_001287	O00590	CCBP2_HUMAN	lasmic (Potential).	5	AGGGCCGGGC	0.532	
-	9	1224		NM_000094	NP_000085	Q02388	CO7A1_HUMAN	(NC1).|Fibronectin type-III	11	TCAGGGAAGTG	0.647	
-	12	982	QARS_uc003cvy.	NM_005051	NP_005042	P47897	SYQ_HUMAN		1	GTAGCCTGGGG	0.547	
+	6	339		NM_004947	NP_004938	Q8IZD9	DOCK3_HUMAN		0	TTTCAGAAACA	0.388	
+	32	3386		NM_004947	NP_004938	Q8IZD9	DOCK3_HUMAN		0	GACATGATGGA	0.473	
+	42	5330	_Mutation_p.D17	NM_001128840	NP_001122312	Q01668	CAC1D_HUMAN	lasmic (Potential).	11	CAAGTGATACT	0.458	
+	37	3202		NM_018398	NP_060868	Q8IZS8	CA2D3_HUMAN	ellular (Potential).	7	GGCGCCCAGAA	0.443	
-	14	2699	RC2_uc003dht.1_	NM_015576	NP_056391	O15083	ERC2_HUMAN	Potential.	2	CAGTTCCTGTC	0.512	
+	6	762	e_Mutation_p.L11	NM_001098783	NP_001092253	O95059	RPP14_HUMAN		0	TTTCTTCTTGCA	0.393	
-	12	2359	lm.2_Missense_M	NM_003716	NP_003707	Q9ULU8	CAPS1_HUMAN		3	TAAATTCATCCAT	0.383	
-	8	1272	mh.1_Missense_	NM_182920	NP_891550	Q9P2N4	ATS9_HUMAN	ptidase M12B.	4	TATAGGGATCAC	0.403	
+	3	780	BD8_uc011bfv.1_I	NM_032505	NP_115894	Q8NFY9	KBTB8_HUMAN	BACK.	4	GTTTTCCTCTG	0.398	
-	8	998_999	M86D_uc003dpq.	NR_024241					0	GCCCGGCCTG	0.569	
+	17	3169	A3_uc010hon.1_	NM_005233	NP_005224	P29320	EPHA3_HUMAN	ntial).|PDZ-binding (Potent	33	CAGTTCCCGTG	0.493	rs147992008
+	6	1698		NM_001080448	NP_001073917	Q9UF33	EPHA6_HUMAN	III 2.|Extracellular (Potentia	16	AAAATAGCATTG	0.418	
+	7	1922	.3_5'UTR|EPHA6_	NM_001080448	NP_001073917	Q9UF33	EPHA6_HUMAN	III 2.|Extracellular (Potentia	16	AATTTGAAACAG	0.373	

-	36	5089		NM_014981	NP_055796	Q9Y2K3	MYH15_HUMAN	Potential.	7	TCAGATCACTGT	0.522	
+	7	1066	.1_Missense_Mut	NM_175862	NP_787058	P42081	CD86_HUMAN	lasmic (Potential).	2	AAGTTCGAAGA	0.333	rs141281931
+	4	453_454	bjq.1_Missense_M	NM_014367	NP_055182	Q96A26	F162A_HUMAN		1	ATTGAGGGCAAG	0.45	
+	3	633	ekj.2_Missense_M	NM_021937	NP_068756	P57772	SELB_HUMAN		1	AAGCTCCACAG	0.572	
-	1	1334		NM_025041	NP_079317	Q3SXR2	CC036_HUMAN		1	CCCCCCAGGTG	0.672	
+	2	370	.1_RNA|IL20RB_u	NM_144717	NP_653318	Q6UXL0	I20RB_HUMAN	III 1.|Extracellular (Potentia	1	AGAACCTCTCT	0.512	
+	17	2909		NM_022131	NP_071414	Q9H4D0	CSTN2_HUMAN	idic).|Cytoplasmic (Potenti	7	AGGAGGAAGAA	0.542	
-	38	6565	y.1_Missense_Mu	NM_001184	NP_001175	Q13535	ATR_HUMAN	FAT.	20	AAATTCGAGAG	0.343	
+	4	487	_p.S150F|MED12L	NM_053002	NP_443728	Q86YW9	MD12L_HUMAN		7	AATATTCTGTGCC	0.353	
-	3	1117	80_uc003fda.2_R	NM_173084	NP_775107	Q8IWR1	TRI59_HUMAN		0	TTGGAGAAATTT	0.308	
-	31	3780		NM_001041	NP_001032	P14410	SUIS_HUMAN	rase.|Lumenal.	14	TTCCCGAACCTC	0.343	
-	2	2627	fek.2_Missense_M	NM_014926	NP_055741	O94933	SLIK3_HUMAN	lasmic (Potential).	10	GAGAGGAAAGA	0.448	
-	1	140	_p.E38K|SERPIN	NM_006217	NP_006208	O75830	SPI2_HUMAN		3	CAAATTCGGTAT	0.368	rs147443553
-	2	388	_p.H81Y|WDR49_	NM_178824	NP_849146	Q8IV35	WDR49_HUMAN	WD 1.	3	GAGAGTGATAAT	0.378	
+	13	2193	_p.S331F|EIF2B5	NM_003907	NP_003898	Q13144	EI2BE_HUMAN	W2.	5	GGATTCCCCGC	0.532	
+	2	423	l.2_Intron|IGF2BP	NR_027317					0	GTAGGGAAGCA	0.562	
+	9	1660	w.1_Missense_Mu	NM_198485	NP_940887	Q6ZUI0	TPRG1_HUMAN		0	TCTATCGCATC	0.498	
-	4	1218_1219	p.A168T|C3orf21_	NM_152531	NP_689744	Q8NBI6	CC021_HUMAN		0	ATAGGCCTCGAA	0.624	
+	5	906	issense_Mutation	NM_000283	NP_000274	P35913	PDE6B_HUMAN	GAF 2.	0	CCCAGGAATTT	0.662	
+	17	3303	gee.3_RNA|WHS	NM_001042424	NP_001035889	O96028	NSD2_HUMAN	AWS.	9	GCCACCCGCAG	0.532	
+	17	3789	E1154K|SH3TC1_	NM_018986	NP_061859	Q8TE82	S3TC1_HUMAN		3	TTGACGAGGAG	0.632	
+	11	2045	p.S503L|CPZ_uc0	NM_001014447	NP_001014447	Q66K79	CBPZ_HUMAN		3	CACATCGCTGA	0.706	
-	3	2151		NM_053042	NP_444270	Q9C0D4	Z518B_HUMAN		4	TTGTAGATTCCA	0.433	
-	3	1452	F16_uc003gpo.2_	NM_017741	NP_060211	Q9NXF7	DCA16_HUMAN		1	GCTGGGACTTG	0.512	
+	20	2264	s.1_Missense_Mu	NM_004787	NP_004778	O94813	SLIT2_HUMAN	LRRCT 3.	11	CACGGGAAATC	0.438	
+	5	1316	_p.V102I|GBA3_u	NM_020973	NP_066024	Q9H227	GBA3_HUMAN		0	ATAAAGTCAAT	0.393	
-	7	1441		NM_001358	NP_001349	O43143	DHX15_HUMAN	case C-terminal.	1	ACGTCTCTGCTA	0.318	
-	7	705	3hdp.2_5'UTR|TM	NM_004262	NP_004253	O60235	TM11D_HUMAN	.|Extracellular (Potential).	1	GCTGCCTCCAC	0.532	
-	5	1309	e_Mutation_p.S28	NM_021139	NP_066962	P06133	UD2B4_HUMAN		2	TACTCGACATT	0.413	
+	6	201	_p.R51K|CSN1S1	NM_001890	NP_001881	P47710	CASA1_HUMAN		0	GAACAGGGTAA	0.274	
+	2	177		NM_021225	NP_067048	Q99935	PROL1_HUMAN		1	AGAATGAAATTA	0.299	
+	5	2791	3hkf.1_Missense_	NM_020859	NP_065910	Q8TF72	SHRM3_HUMAN		3	GCAAGCGGGTG	0.562	
+	56	8829		NM_025074	NP_079350	Q86XX4	FRAS1_HUMAN	|Extracellular (Potential).	5	CCAACGATGCC	0.537	
-	1	384		NM_032693	NP_116082	Q9BSU3	NAA11_HUMAN	cetyltransferase.	2	GCGCCGGTGTG	0.562	
-	10	1590	.S276F|ANTXR2_	NM_001145794	NP_001139266	P58335	ANTR2_HUMAN	ellular (Potential).	1	AGCATAGAATTA	0.269	
-	5	793	_p.E216K|RASGE	NM_152545	NP_689758	Q0VAM2	RGF1B_HUMAN	Ras-GEF.	0	CAGCTCTATATG	0.468	
-	17	3170		NM_014991	NP_055806	Q8IZQ1	WDFY3_HUMAN		3	GGGGCGGGTGC	0.502	
-	11	1433		NM_174952	NP_777612	Q8N412	CD037_HUMAN		0	AGATTTCCTTTC	0.269	
+	8	1787		NM_001977	NP_001968	Q07075	AMPE_HUMAN	ellular (Potential).	5	TGTAGGGATCTT	0.294	
-	4	796	X2_uc010iml.2_In	NM_153426	NP_700475	Q99697	PITX2_HUMAN		0	GTCCTCATTCT	0.592	
-	4	1047		NM_024574	NP_078850	Q8TB73	CD031_HUMAN		0	CTCAGGGTATG	0.483	
+	7	902	p.R224C|ADAD1_	NM_139243	NP_640336	Q96M93	ADAD1_HUMAN		0	TCTAATCGTTCA	0.269	
+	8	7432	e_Mutation_p.P77	NM_024582	NP_078858	Q6V0I7	FAT4_HUMAN	(Potential).|Cadherin 24.	18	CATCTCCTACT	0.383	
-	1	2734	.1_Intron|PCDH18	NM_019035	NP_061908	Q9HCL0	PCD18_HUMAN	lasmic (Potential).	5	GGTAGGAGATG	0.507	
-	1	2338	.1_Intron|PCDH18	NM_019035	NP_061908	Q9HCL0	PCD18_HUMAN	|Extracellular (Potential).	5	CCATTCTGTGT	0.438	rs141226164
-	5	872	k.1_Missense_Mu	NM_021833	NP_068605	P25874	UCP1_HUMAN	Solcar 3.	1	GAAAGCCGTTG	0.428	
-	3	521	k.1_Missense_Mu	NM_021833	NP_068605	P25874	UCP1_HUMAN	Solcar 2.	1	GATTCCGTGGA	0.468	

-	6	1693	_p.G305R|RNF150	NM_020724	NP_065775	Q9ULK6	RN150_HUMAN	lasmic (Potential).		1	ACCTCCCAGAG	0.542
-	3	304	.S30L|GYPA_uc0	NM_002099	NP_002090	P02724	GLPA_HUMAN	Extracellular.		2	ATTTCTGAAACT	0.413
+	7	1946		NM_022475	NP_071920	Q96QV1	HHIP_HUMAN			6	TCCACGATCCA	0.517
-	14	1947	_p.L576F|DDX60L_	NM_001012967	NP_001012985	Q5H9U9	DDX6L_HUMAN			1	TTTGAGAAATG	0.333
+	5	1556	irr.2_Missense_M	NM_014269	NP_055084	Q9UKF5	ADA29_HUMAN	B.|Extracellular (Potential).		16	TAAGAGGGTTA	0.428
-	5	1236		NM_005429	NP_005420	P49767	VEGFC_HUMAN			5	CATCTCCAGCA	0.398
+	4	350	RR_uc010isy.2_I	NM_013232	NP_037364	O75340	PDCD6_HUMAN	nd 2.|2 (Potential).		1	TCAGCGAGTTC	0.537
+	1	278		NM_182632	NP_872438	Q96N87	S6A18_HUMAN	Name=2; (Potential).		1	CTATGGAGGAG	0.637
-	7	2379	RT_uc003jcc.1_Mi	NM_198253	NP_937983	O14746	TERT_HUMAN	rse transcriptase.		12	ACTGTCGCATG	0.642
-	2	299		NM_001044	NP_001035	Q01959	SC6A3_HUMAN	lasmic (Potential).		6	CTCCCGATCCT	0.602
-	11	2084	_Mutation_p.M56	NM_004934	NP_004925	Q13634	CAD18_HUMAN	(Potential).|Cadherin 5.		7	GAGATCATAATG	0.498
-	5	654	_p.S192F|AGXT2_	NM_031900	NP_114106	Q9BYV1	AGT2_HUMAN			4	TGAAAGAAATG	0.448
-	10	1942	RLR_uc003jjj.1_In	NM_000949	NP_000940	P16471	PRLR_HUMAN	lasmic (Potential).		3	CCTTTCCCTCT	0.542
+	17	2734	jle.1_Missense_M	NM_152403	NP_689616	Q63HQ2	EGFLA_HUMAN	EGF-like 3.		7	GGAAGGAGGG	0.622
+	14	1939	7_uc011cpn.1_RN	NM_000587	NP_000578	P10643	CO7_HUMAN	Sushi 1.		0	GAAACCCAGTG	0.388
-	23	2840	jmi.3_Missense_	NM_173489	NP_775760	Q7Z745	HTRB2_HUMAN	HEAT 9.		8	TGTAACCAATCA	0.433
-	1	4		NM_000524	NP_000515	P08908	5HT1A_HUMAN	llular (By similarity).		4	CACATCCATGC	0.637
+	5	4571	x.1_Missense_Mu	NM_005909	NP_005900	P46821	MAP1B_HUMAN			5	TAAGTCCAGTT	0.413
+	2	132	1_5'Flank|GFM2_	NM_014886	NP_055701	O95478	NSA2_HUMAN			1	GATACCGTTTG	0.328
-	1	368		NR_004845						0	AGCTGGAGCC	0.542
+	20	3793_3794	98_uc003kjt.2_5'	NM_032119	NP_115495	Q8WXG9	GPR98_HUMAN	ellular (Potential).		16	TGGTTCCATTCA	0.421
+	36	8419	p.D481N|GPR98_	NM_032119	NP_115495	Q8WXG9	GPR98_HUMAN	.|Extracellular (Potential).		16	TGTTGGATGAC	0.338
+	38	8726	p.G583E|GPR98_	NM_032119	NP_115495	Q8WXG9	GPR98_HUMAN	ellular (Potential).		16	AGTAGGAAACC	0.393
+	45	9775	_p.R933*|GPR98_	NM_032119	NP_115495	Q8WXG9	GPR98_HUMAN	lar (Potential).|EAR 1.		16	TATCTCGAACT	0.393
+	5	1344	_Intron|SNCAIP_	NM_005460	NP_005451	Q9Y6H5	SNCAP_HUMAN	ANK 1.		2	TCAATGAGCGC	0.488
+	7	780	dd.1_Missense_M	NM_032446	NP_115822	Q96KG7	MEG10_HUMAN	self-assembly and formati		4	CCTGCGATGGT	0.582
-	2	321		NM_015082	NP_055897	Q6MZW2	FSTL4_HUMAN			2	CACACCCACAT	0.557
+	1	970	hd.2_Intron|PCDH	NM_018906	NP_061729	Q9Y5H8	PCDA3_HUMAN	|Extracellular (Potential).		8	CCACGGATAAA	0.373
+	1	217	lhh.1_Intron|PCD	NM_018910	NP_061733	Q9UN72	PCDA7_HUMAN	|Extracellular (Potential).		4	GTGGGGATCTT	0.612
+	1	1823	DHA7_uc003lhq.	NM_018904	NP_061727	Q9Y5I0	PCDAD_HUMAN	|Extracellular (Potential).		6	GGCTTTCGTATG	0.682
+	1	1932		NM_013340	NP_037472	Q9Y5F3	PCDB1_HUMAN	|Extracellular (Potential).		0	CTGTTCAAAGA	0.438
+	1	1974		NM_015669	NP_056484	Q9Y5E4	PCDB5_HUMAN	|Extracellular (Potential).		5	GGTGACCAAGG	0.697
+	1	1934		NM_018940	NP_061763	Q9Y5E2	PCDB7_HUMAN	|Extracellular (Potential).		6	GGTGACCAAGG	0.706
+	1	2177	daj.1_Missense_	NM_018931	NP_061754	Q9Y5F2	PCDBB_HUMAN	lasmic (Potential).		6	CTGCTCGGTGC	0.657
+	1	1997	dak.1_Missense_	NM_018932	NP_061755	Q9Y5F1	PCDBC_HUMAN	(Potential).|Cadherin 6.		3	GCTGTCGTACC	0.726
+	1	2011	35_uc003lkf.1_Int	NM_018928	NP_061751	Q9Y5F7	PCDGL_HUMAN	|Extracellular (Potential).		4	CTCATCCAGTT	0.488
-	4	3323		NM_032420	NP_115796	Q08174	PCDH1_HUMAN			5	TGGACGGCGTC	0.637
-	1	3399		NM_016580	NP_057664	Q9NPG4	PCD12_HUMAN	ical; (Potential).		3	CAACCCGAAGA	0.597
+	1	1303	TC2_uc003lpp.1_	NM_000024	NP_000015	P07550	ADRB2_HUMAN	Cytoplasmic.		1	CTACTCCAGCA	0.522
+	2	567		NM_000112	NP_000103	P50443	S26A2_HUMAN	lasmic (Potential).		0	GCTCCCAAAAT	0.423
-	1	587		NM_130899	NP_570969	Q8TC56	FA71B_HUMAN			6	GAGATCTTCCC	0.507
-	23	4448	jit.1_Missense_Mu	NM_025153	NP_079429	O94823	AT10B_HUMAN	ical; (Potential).		5	TGCATCCACCA	0.418
+	9	1539	lyv.2_Missense_M	NM_000811	NP_000802	Q16445	GBRA6_HUMAN	lasmic (Pro	p.P401L(1)	12	CAACACCTGTC	0.463
+	11	640		NM_001079529	NP_001072997	P0C7A2	F153B_HUMAN			1	TGGAGGAGCAT	0.507
+	14	2470		NM_133369	NP_588610	Q6ZN44	UNC5A_HUMAN	lasmic (Potential).		1	TCATTCGGCAG	0.637
+	10	491	mig.1_Missense_	NM_001079527	NP_001072995					0	TCCTTCCTCTG	0.527
+	13	1925_1926	q.1_Missense_Mu	NM_004415	NP_004406	P15924	DESP_HUMAN	plakophilin 1 and junction		9	GGTGTCCTGGC	0.525

+	2	1010		NM_001718	NP_001709	P22004	BMP6_HUMAN			3	ATTTATCAAGTCT	0.483
+	2	201		NM_002114	NP_002105	P15822	ZEP1_HUMAN			6	CAAATTCATCCCA	0.388
-	1	88		NM_005493	NP_005484	Q96S59	RANB9_HUMAN	Poly-Pro.		2	gctgctgcggcggcggc	0.517
+	6	720	.M133I|CAP2_uc0	NM_006366	NP_006357	P40123	CAP2_HUMAN			1	GGAGATGAATGAC	0.398
+	21	2121	p.G582E|LRRC16	NM_017640	NP_060110	Q5VZK9	LR16A_HUMAN	LRR 9.		4	GCAACGGAATGG	0.547
+	1	31		NM_003523	NP_003514	P62807	H2B1C_HUMAN			0	CCGCCCCGAAG	0.527
+	6	1262	2A3_uc011dkm.1_Intron							0	CTCTCTGGAGGA	0.507
+	7	1149		NM_001732	NP_001723	Q13410	BT1A1_HUMAN	.|Cytoplasmic (Potential).		2	TGTAGGGAGAAT	0.557
+	11	1396	njb.2_Missense_M	NM_005865	NP_005856	Q9NQE7	TSSP_HUMAN			5	TCCTCAGAATCA	0.567
+	2	166	se_Mutation_p.S5	NM_001509	NP_001500	O75715	GPX5_HUMAN			1	ATGTTTCCTTCAA	0.423
+	3	573	v.2_RNA|PPP1R11	NM_021959	NP_068778	O60927	PP1RB_HUMAN	Pro-rich.		3	ACCGACCCCCA	0.612
-	5	1323	MDC1_uc003nrh.1_	NM_014641	NP_055456	Q14676	MDC1_HUMAN	uclear localization (NLS1).		4	TCCAGGAGGTT	0.542
+	2	3502		NM_080870	NP_543146	Q3MIW9	DPCR1_HUMAN			0	CCACAGAACAC	0.463
-	2	508	1_5'Flank|PSORS	NM_014070	NP_054789	Q6UXA7	CF015_HUMAN			0	CTGGTGGAGGA	0.622
+	1	80	F_uc003nuj.2_5'Fl	NM_000594	NP_000585	P01375	TNFA_HUMAN			3	CTCAGACGCCAC	0.592
+	4	674	c003nuj.2_Silent_	NM_000594	NP_000585	P01375	TNFA_HUMAN	ellular (Potential).		3	GTCAACCTCCTC	0.632
+	6	468	IF1_uc003nva.2_M	NM_001623	NP_001614	P55008	AIF1_HUMAN			1	GAAAAGGAAAAG	0.488
+	10	1580	nzf.1_Missense_M	NM_000500	NP_000491	P08686	CP21A_HUMAN			0	ATGGGGGCCCAC	0.682
-	48	3769_3770	se_Mutation_p.P1	NM_080680	NP_542411	P13942	COBA2_HUMAN	le-helical region.		5	CTGGGGGGCCA	0.594
+	6	961	3_uc011dqu.1_5'F	NM_001077516	NP_001070984	Q92504	S39A7_HUMAN			1	GAAAAGGAAACA	0.488
+	60	9020		NM_001371	NP_001362					21	TTTCACGAATAAT	0.363
+	89	13573		NM_001371	NP_001362					21	TTCACTGAACTT	0.443
-	2	410	H_uc011dvl.1_5'Fl	NM_020750	NP_065801	Q9HAV4	XPO5_HUMAN	for interaction with Ran.		4	GAAGGCCAAAAT	0.418
-	10	944	.E230K|CRISP2_	NM_001142408	NP_001135880	P16562	CRIS2_HUMAN			1	ACTTTTCCTTGA	0.393
+	8	983		NM_018214	NP_060684	Q9BTT6	LRRC1_HUMAN	LRR 10.		1	AGACTTCCTGAA	0.378
+	5	1866		NM_001010872	NP_001010872	Q5T0W9	FA83B_HUMAN			6	GACACCCCTACG	0.473
+	5	2655		NM_001010872	NP_001010872	Q5T0W9	FA83B_HUMAN			6	AGTAAGGAAGAT	0.388
-	1	860	xf.1_Missense_Mu	NM_021073	NP_066551	P22003	BMP5_HUMAN			2	GTATTTCCCGTCT	0.453
-	5	532	BL2_uc011dxp.1_RNA							0	AGTTGCGATACC	0.507
-	10	2034	_p.A499V|EYS_uc	NM_001142800	NP_001136272	Q5T1H1	EYS_HUMAN			6	AAATAGGCATCA	0.343
+	18	3102	2_Missense_Mutat	NM_014989	NP_055804	Q86UR5	RIMS1_HUMAN			10	GATGTGGATAGT	0.363
-	9	1237	2CBP_uc011dyx.1_	NM_198920	NP_944602	Q7Z6J8	UB2CB_HUMAN	HECT-like.		1	ACGGCGAAGGG	0.463
-	14	2723	_p.E823K|EPHA7_	NM_004440	NP_004431	Q15375	EPHA7_HUMAN	Potential).|Protein kinase.		28	TAACTTCCCACAT	0.408
-	4	438	ub.2_Intron|DDO_	NM_003649	NP_003640	Q99489	OXDD_HUMAN			3	ATCTTTCGAAATC	0.468
+	4	886	E_uc003pwt.2_Nor	NM_001080976	NP_001074445	Q9UL01	DSE_HUMAN			1	CCTACTTATGGA	0.443
+	3	1553	0kfi.2_Missense_M	NM_052913	NP_443145	Q86VY9	T200A_HUMAN	lasmic (Potential).		1	GTGGAGGAGGAT	0.498
-	4	1209	.S317F|BCLAF1_	NM_014739	NP_055554	Q9NYF8	BCLF1_HUMAN			1	ACGAGGAACGG	0.403
-	3	780	_uc003qhk.2_Intro	NM_014432	NP_055247	Q9UHF4	I20RA_HUMAN	tential).|Fibronectin type-III		4	GTTCCCCAAATG	0.363
+	23	3910		NM_020340	NP_065073	Q5TH69	BIG3_HUMAN			2	GCCCTGGAAACA	0.493
-	143	26523	p.R8641W|SYNE1	NM_182961	NP_892006	Q8NF91	SYNE1_HUMAN	Cytoplasmic (Potential).		45	TGAGCCGATTTC	0.423
+	29	4232_4233	wc.1_Missense_M	NM_001040001	NP_001035090	P55196	AFAD_HUMAN	Pro-rich.		5	ACCTGCCTCCGC	0.614
-	13	2100		NM_032415	NP_115791	Q9BXL7	CAR11_HUMAN		p.I566I(1)	50	GGGGCTCGGCGC	0.622
+	7	672	8_uc010kst.2_Silent_p.A14A							0	CGGCCGCCCCG	0.617
-	15	1881	0ktd.1_Missense_	NM_173565	NP_775836	B2RC85	R10B2_HUMAN			3	AAATTGCCTAAA	0.338
+	2	326	ow.2_Missense_M	NM_006908	NP_008839	P63000	RAC1_HUMAN			2	GCATTTCCTGGA	0.353
-	13	3127		NM_015204	NP_056019	Q9UPZ6	THS7A_HUMAN	.|Extracellular (Potential).		3	TTTGTCACAAGG	0.388
-	1	484		NM_175886	NP_787082	P21108	PRPS3_HUMAN			1	AGCCCTGAATTT	0.448

+	10	2243	h.1_Missense_Mu	NM_002214	NP_002205	P26012	ITB8_HUMAN	epeats.|II.|Extracellular (P	3	CAAGTCACACA	0.373	
+	74	11997		NM_003777	NP_003768	Q96DT5	DYH11_HUMAN	6 (By similarity).	15	CAAAGGAGGAC	0.512	
-	9	819		NM_012294	NP_036426	Q92565	RPGF5_HUMAN		1	TGTCCGTCTGC	0.443	
-	3	481	tbc.2_RNA|GGCT_	NM_024051	NP_076956	O75223	GGCT_HUMAN		0	TATTTCTTTTCC	0.373	
+	16	1461	DCYAP1R1_uc0	NM_001118	NP_001109	P41586	PACR_HUMAN	lasmic (Potential).	1	CAAGCGAAAAT	0.612	
-	21	2270	.1_RNA|DPY19L2P1_uc010kwz.1_RNA						0	GATTTTCGACTA	0.274	
-	8	1287		NM_001077653	NP_001071121	Q9UMR3	TBX20_HUMAN		1	CCTGCTGAAAAT	0.517	
+	11	1124		NM_016616	NP_057700	Q8N427	TXND3_HUMAN	NDK 1.	3	CGAACGATCTG	0.443	
-	5	1091	.2_Intron|TBRG4_	NM_004749	NP_004740	Q969Z0	TBRG4_HUMAN		0	TGAGGGATAGC	0.592	
+	1	1202		NR_003595					0	AACTTCTCTCT	0.473	
+	1	470	_p.G22E|VSTM2	NM_182546	NP_872352	Q8TAG5	VTM2A_HUMAN		0	ACAAGGGCTTT	0.403	
-	4	488		NM_033273	NP_150376	Q96JC4	ZN479_HUMAN	KRAB.	4	GGACTCTTTATT	0.383	
+	4	680		NM_001159279	NP_001152751				2	AAAACGATGGC	0.328	
+	4	505		NM_153363	NP_699194	Q8IYX0	ZN679_HUMAN	KRAB.	1	AAAGAGAAATGA	0.393	
+	6	1033	3tvz.2_Missense_	NM_022479	NP_071924	Q6IS24	GLTL3_HUMAN	main B.|Lumenal (Potential	7	TGGATCCTGGC	0.502	
-	15	1835	n.2_Missense_Mu	NM_000601	NP_000592	P14210	HGF_HUMAN	eptidase S1.	4	CATCTCCTCTTC	0.363	
-	7	800	umu.1_Missense_	NM_001742	NP_001733	P30988	CALCR_HUMAN	Name=1; (Potential).	9	CTAGGGTGAAA	0.358	
+	13	4572		NM_014916	NP_055731	Q8IWU2	LMTK2_HUMAN		16	CCAGATCCTTTT	0.507	
+	29	3345	.3_Intron|GATS_u	NM_012447	NP_036579	Q9UJ98	STAG3_HUMAN		8	CAGCAGAGACC	0.632	
+	26	5158	AN_uc010lhh.2_	NM_003386	NP_003377	Q9Y493	ZAN_HUMAN	ar (Potential).|VWFD 2.	11	TGGTGGAAGTG	0.602	
+	3	7653	C17_uc010lho.1_	NM_001040105	NP_001035194	Q685J3	MUC17_HUMAN	X approximate tandem re	27	CTAGCACCCTT	0.488	
-	5	563	_Mutation_p.P77	NM_022777	NP_073614	Q9H7X7	RABL5_HUMAN		0	CTCAGGGTCAT	0.443	
-	34	5121	.2_Nonsense_Mut	NM_005045	NP_005036	P78509	RELN_HUMAN		19	AATCCCAGGTC	0.388	
-	30	4595	.2_Missense_Mut	NM_005045	NP_005036	P78509	RELN_HUMAN	p.D1479E(1)	19	GCCATCGTTAA	0.488	
-	24	3332	.2_Missense_Mut	NM_005045	NP_005036	P78509	RELN_HUMAN	EGF-like 2.	19	GCATTCAGTGC	0.527	
-	4	3362		NM_002711	NP_002702	Q16821	PPR3A_HUMAN		34	CTCTTCCCAGG	0.353	
-	4	949	ja.2_Missense_Mu	NM_003391	NP_003382	P09544	WNT2_HUMAN		7	CCTGAGAGTAC	0.552	
+	5	709	R_uc011knq.1_5'	NM_000492	NP_000483	P13569	CFTR_HUMAN	l).|ABC transmembrane ty	5	TTTGATGAAGTA	0.323	
+	12	4488	.2_Intron|PTPRZ1	NM_002851	NP_002842	P23471	PTPRZ_HUMAN	ellular (Potential).	9	CTGATCATTCT	0.403	
-	13	1407	.2_Missense_Mut	NM_004717	NP_004708	O75912	DGKI_HUMAN	DAGKc.	3	GAGTTCGAGCC	0.552	
-	15	1859_1860		NM_004333	NP_004324	P15056	BRAF_HUMAN	rotein kinas_R603>I(2)|p.T	18290	ATTTCACTGTAG	0.366	rs121913378
-	8	1160		NM_004333	NP_004324	P15056	BRAF_HUMAN		18290	ATTGGGAGCTG	0.393	
-	5	504	se_Mutation_p.G1	NM_013252	NP_037384	Q9NY25	CLC5A_HUMAN	.|Extracellular (Potential).	0	TGGATCCTTTTC	0.448	
-	1	149		NM_176817	NP_789787	P59533	T2R38_HUMAN	Name=1; (Potential).	2	GGACTGAAATG	0.438	
+	5	669	Intron|uc003wad.2	NM_002769	NP_002760	P07477	TRY1_HUMAN	eptidase S1.	2	GGGGTGATGGC	0.522	
+	2	189	.2_Intron|uc003wa	NR_001296					0	CTGTCCCCTAC	0.547	
+	1	644		NM_001001667	NP_001001667	Q8N148	OR6V1_HUMAN	Name=5; (Potential).	1	TCATCTCCTATG	0.552	
+	3	1008	_Intron|uc011kto.1	NM_001130025	NP_001123497	A6NFQ2	F115C_HUMAN		0	TAAAAGATCTG	0.562	
+	1	650		NM_012365	NP_036497	Q96R48	OR2A5_HUMAN	Name=5; (Potential).	3	GGTCTCCTACT	0.612	
+	43	6259		NM_198455	NP_940857	A2VEC9	SSPO_HUMAN	F5/8 type C.	0	AGCTGGAACAC	0.667	
+	3	207	IMAP4_uc011kuv.	NM_018326	NP_060796	Q9NUV9	GIMA4_HUMAN	TP (Potential).	1	AGCAGGAAAAA	0.463	
-	7	1717	p.W472*|KCNH2_	NM_000238	NP_000229	Q12809	KCNH2_HUMAN	=Segment S5; (Potential).	4	GCGTACCAGAT	0.617	
-	52	8270	_Mutation_p.S19	NM_033225	NP_150094	Q96PZ7	CSMD1_HUMAN	r (Potential).|Sushi 17.	25	GAAAGGAAAGG	0.398	
-	14	2275	wj.1_Missense_M	NM_033225	NP_150094	Q96PZ7	CSMD1_HUMAN	lar (Potential).|CUB 4.	25	CAAAATCATTAA	0.418	
+	8	1339	.2_Missense_Mut	NM_001715	NP_001706	P51451	BLK_HUMAN	se.|ATP (By similarity).	3	ATTCGGCGAAG	0.572	
-	1	464	.1_Intron|FAM66D	NM_201402	NP_958804	Q6R6M4	U17L2_HUMAN		3	TTGCCTCTATGG	0.522	
-	5	585		NM_003840	NP_003831	Q9UBN6	TR10D_HUMAN	(Potential).|TNFR-Cys 3.	0	CATCCCTCTGG	0.562	

+	12	1263	ec.2_Missense_Mu	NM_003817	NP_003808	Q9H2U9	ADAM7_HUMAN	B.|Extracellular (Potential).		5	TTGAAGGATTATA	0.353
-	13	1198	xek.2_Intron|EBF2	NM_022659	NP_073150	Q9HAK2	COE2_HUMAN			4	GCGGCTCGCTTC	0.488
-	10	999	xek.2_Intron|EBF2	NM_022659	NP_073150	Q9HAK2	COE2_HUMAN	IPT/TIG.		4	GGCTCCTTTGC	0.488
-	3	1765		NM_007257	NP_009188	Q9UL42	PNMA2_HUMAN			0	ctcttcttcccgtattacct	0.209
+	6	628	.Y135C|ADAM32_	NM_145004	NP_659441	Q8TC27	ADA32_HUMAN			3	TTTCTTATGGAAT	0.289
+	11	1255	se_Mutation_p.G7	NM_194294	NP_919270	Q6ZQW0	I23O2_HUMAN			2	ATCTGGACAGG	0.507
-	6	1334	3xpe.2_Missense_	NM_006749	NP_006740	Q08357	S20A2_HUMAN	ical; (Potential).		2	TATGGCCCACAT	0.537
+	4	2771	P1_uc011ldy.1_Intr	NM_006269	NP_006260	P56715	RP1_HUMAN			12	AAGGGGATAAA	0.358
+	3	1672		NM_052898	NP_443130	Q5GH76	XKR4_HUMAN			2	CCCTACGGTCCA	0.587
-	3	543	_p.L99F|CA8_uc	NM_004056	NP_004047	P35219	CAH8_HUMAN			0	CCGAAAGAACTG	0.393
-	3	1045_1046		NM_004820	NP_004811	O75881	CP7B1_HUMAN			3	CTATTTCAAGGT	0.366
+	15	1468	vt.2_Missense_Mu	NM_001033578	NP_001028750	Q96BR1	SGK3_HUMAN	rotein kinase.		4	CCTGGTCCATTC	0.428
-	7	2422	O5A1_uc011lfa.1_	NM_030958	NP_112220	Q9H2Y9	SO5A1_HUMAN	r (Potential).|Kazal-like.		4	CATCTGATCCAC	0.428
-	11	1308		NM_006540	NP_006531	Q15596	NCOA2_HUMAN			16	CGGATTCATCAC	0.408
-	5	451	ense_Mutation_p.F	NM_001738	NP_001729	P00915	CAH1_HUMAN			2	GAGAAAGGACCA	0.418
-	5	451	_p.P109L|CDH17_	NM_004063	NP_004054	Q12864	CAD17_HUMAN	r (Potential).|Cadherin 1.		6	GGACTGGACCC	0.483
-	8	1276	.1_Missense_Mut	NM_015668	NP_056483	Q8NE09	RGS22_HUMAN			7	TGCCATGAATAG	0.343
+	2	798	_p.R216Q|RIMS2_	NM_014677	NP_055492	Q9UQ26	RIMS2_HUMAN			15	ATCAGCGATCTT	0.458
+	4	471		NM_177531	NP_803875	Q86WI1	PKHL1_HUMAN	r (Potential).|IPT/TIG 1.		14	GTTACGGAAAAT	0.398
+	14	1429		NM_177531	NP_803875	Q86WI1	PKHL1_HUMAN	ellular (Potential).		14	ATTTTTCCAGTCC	0.353
+	38	5455		NM_177531	NP_803875	Q86WI1	PKHL1_HUMAN	r (Potential).|IPT/TIG 10.		14	TCATTGGAAATC	0.413
+	26	3547	uc003yqy.1_Intron	NM_001039112	NP_001034201	Q2WGJ9	FR1L6_HUMAN	lasmic (Potential).		11	AGATTCGCTAAC	0.527
-	2	331	_5'Flank|MGC708	NM_001001795	NP_001001795	Q6P1X6	CH082_HUMAN			0	ATTTTGGAATCAT	0.582
+	9	1154	_p.E343K|ADAMT	NM_001040272	NP_001035362	Q8N6G6	ATL1_HUMAN			5	ACCCAGAGAAC	0.453
-	1	745	zob.1_Missense_	NM_020344	NP_065077	Q9UI40	NCKX2_HUMAN	lasmic (Potential).		3	ATTTCTCTAGAAA	0.413
-	1	190	uc003zrh.1_Intron	NM_153809	NP_722516	Q8IZX4	TAF1L_HUMAN			26	TAAATGGGCCAC	0.567
+	2	1646		NM_000692	NP_000683	P30837	AL1B1_HUMAN			1	ATCAAGGTTCCT	0.517
+	5	378	_p.G102S|ANXA1_	NM_000700	NP_000691	P04083	ANXA1_HUMAN	Annexin 1.		2	CTTACAGGTCAC	0.403
-	25	3758	.1_Intron|TRPM6_	NM_017662	NP_060132	Q9BX84	TRPM6_HUMAN	lasmic (Potential).		8	TCACTCGGATTC	0.368
-	21	3003	1_Intron|TRPM6_	NM_017662	NP_060132	Q9BX84	TRPM6_HUMAN	ical; (Potential).		8	CAGCTGAAAAC	0.473
+	17	2706	_p.E590K|NTRK2_	NM_001018064	NP_001018074	Q16620	NTRK2_HUMAN	e.|Cytoplasmic (Potential).		16	AGGCCGAGCTC	0.542
+	4	4327		NM_178828	NP_849150	Q6ZUB1	CI079_HUMAN			3	CCATCCACAGC	0.607
-	2	726		NM_005384	NP_005375	Q16649	NFIL3_HUMAN	eucine-zipper.		0	CGTTTTCTTCTC	0.388
-	3	451	on_p.G129E|ECM	NM_001393	NP_001384	O94769	ECM2_HUMAN	VWFC.		2	ACTCTTCCATCT	0.522
+	9	1736	e_Mutation_p.E37	NM_001083536	NP_001077005	Q5JSP0	FGD3_HUMAN	PH 1.		2	GCCAATGAACTG	0.587
-	1	90	N3A_uc004bbq.1_	NM_147180	NP_671709	Q96LZ3	CANB2_HUMAN			2	GGCCTCGTTTC	0.592
-	3	2811	bq.1_Missense_M	NM_133445	NP_597702	Q8TCU5	NMD3A_HUMAN	lasmic (Potential).		7	CATTTTGGAGGT	0.448
-	2	1691	bq.1_Missense_M	NM_133445	NP_597702	Q8TCU5	NMD3A_HUMAN	ellular (Potential).		7	TCAGTTCCTCCA	0.512
-	1	278		NM_001001919	NP_001001919	Q8NGS5	O13C4_HUMAN	ellular (Potential).		1	GAGAAGGAAATG	0.448
-	17	2442	orf5_uc004bdr.3_	NM_032012	NP_114401	Q9H330	CI005_HUMAN			1	GGTAAGGATGGC	0.433
-	38	8688	ty.2_Missense_Mu	NM_153366	NP_699197	Q4LDE5	SVEP1_HUMAN	Sushi 23.	p.V2784I(1)	7	ATGGATCCATTC	0.478
-	38	7457	ty.2_Missense_Mu	NM_153366	NP_699197	Q4LDE5	SVEP1_HUMAN	Sushi 16.		7	AACAGGGAAAG	0.463
-	4	1344	eu.2_Missense_	NM_153366	NP_699197	Q4LDE5	SVEP1_HUMAN			7	CTGATTCCTCCT	0.522
-	2	923	P1_uc004beu.2_	NM_153366	NP_699197	Q4LDE5	SVEP1_HUMAN	VWFA.		7	ATCCATCAGTGAT	0.423
-	2	547	vf.2_Missense_Mu	NM_002160	NP_002151	P24821	TENA_HUMAN			7	ACTGGGATCCC	0.572
-	5	1058	d.2_Missense_Mu	NM_014618	NP_055433	O60477	DBC1_HUMAN	MACPF.		8	CCAGAGGCCCA	0.512
-	6	1353	p.E139K|TRAF1_	NM_005658	NP_005649	Q13077	TRAF1_HUMAN			3	CTCCTCCATGA	0.617

+	11	1721	mf.1_Missense_M	NM_000962	NP_000953	P23219	PGH1_HUMAN		2	CTTTTCCCTCA	0.512
+	1	349		NM_001005234	NP_001005234	Q8NH93	OR1L3_HUMAN	Name=3; (Potential).	1	TGGCGGCTATG	0.433
+	13	1978	p.L622F|GLE1_uc	NM_001003722	NP_001003722	Q53GS7	GLE1_HUMAN		0	CCCTCCTCTTT	0.502
+	6	1196	_Mutation_p.S26	NM_013355	NP_037487	Q6P5Z2	PKN3_HUMAN		4	GCCTTCAGGGA	0.612
+	12	1236	bf.2_Missense_M	NM_020822	NP_065873	Q5JUK3	KCNT1_HUMAN		4	TCATGGACTTC	0.647
+	6	1029	f.1_Missense_Mut	NM_004042	NP_004033	P54793	ARSF_HUMAN		2	TGAAGGAAGCG	0.408
+	6	586	_p.S22F|TBL1X_	NM_001139466	NP_001132938	O60907	TBL1X_HUMAN	LisH.	1	TTTTTCCCACT	0.552
-	2	1585	RHGAP6_uc004c	NM_013427	NP_038286	O43182	RHG06_HUMAN		2	ACAGTCCTGTT	0.557
+	3	791		NM_016562	NP_057646	Q9NYK1	TLR7_HUMAN	lar (Potential).|LRR 7.	5	TCACAGCCGTC	0.338
-	5	872	p.D177N|GEMIN8	NM_017856	NP_060326	Q9NWZ8	GEMI8_HUMAN		0	CAGGTCGTGGT	0.592
+	3	435	se_Mutation_p.G3	NM_001118885	NP_001112357	P23416	GLRA2_HUMAN	ellular (Probable).	2	GGTCTGGAAAA	0.418
+	3	507	se_Mutation_p.D5	NM_001118885	NP_001112357	P23416	GLRA2_HUMAN	ellular (Probable).	2	GATATGATGCA	0.378
-	3	1798	p.E410K|RAI2_uc	NM_021785	NP_068557	Q9Y5P3	RAI2_HUMAN		2	CATCTCGGTAG	0.557
+	3	291	_p.G46D|PDHA1_	NM_000284	NP_000275	P08559	ODPA_HUMAN		1	AGAAGGCCCTC	0.458
-	2	100	1mjl.1_Missense_	NM_004586	NP_004577	P51812	KS6A3_HUMAN		8	CTCTCCCATAG	0.348
-	2	320	w.2_RNA|APOO_	NM_024122	NP_077027	Q9BUR5	APOO_HUMAN		0	TGGGAGGTGAG	0.413
-	14	1897	.E577K|RPGR_uc	NM_001034853	NP_001030025	Q92834	RPGR_HUMAN	Glu-rich.	1	ATGCTTCGATAG	0.423
+	40	7412	c.2_Missense_Mu	NM_001039590	NP_001034679	Q93008	USP9X_HUMAN		6	TTTTGGTGATC	0.333
-	24	2345	.P587S|CASK_uc	NM_003688	NP_003679	O14936	CSKP_HUMAN	ylate kinase-like.	6	ACGTGGAATAG	0.303
-	1	161	dgi.3_Missense_M	NM_176819	NP_789789	Q9H7Y0	CX036_HUMAN		1	AGAAAGAACAG	0.592
-	7	794	it.2_Missense_M	NM_006962	NP_008893	P17025	ZN182_HUMAN		3	AACAAGGTTTG	0.338
+	12	1513		NM_000377	NP_000368	P42768	WASP_HUMAN	Glu-rich (acidic).	1	CAGACGAAGGG	0.582
+	8	1396	uq.2_Missense_M	NM_016656	NP_057740	Q5VZM2	RRAGB_HUMAN		0	AGCTGGAAATG	0.393
+	13	1557	_p.S477L|KIF4A_	NM_012310	NP_036442	O95239	KIF4A_HUMAN	Potential.	4	AGTTATCGGTAA	0.393
-	1	939	mqj.1_Missense_	NM_021963	NP_068798	Q9ULW6	NP1L2_HUMAN	u-rich (acidic).	1	CATATTCATGTA	0.338
-	1	525	1L2_uc011mqj.1_	NM_021963	NP_068798	Q9ULW6	NP1L2_HUMAN		1	TTCTTCCCCAA	0.592
-	4	498	se_Mutation_p.P	NM_022052	NP_071335	Q9H4D5	NXF3_HUMAN	RRM.	3	AACTGGGACGA	0.458
+	22	3977	.1_Missense_Mut	NM_198465	NP_940867	Q7Z2Y5	NRK_HUMAN	CNH.	14	GTTGGGAACCC	0.353
+	20	1421	_p.Q407*|COL4A	NM_033380	NP_203699	P29400	CO4A5_HUMAN	e-helical region.	4	GGGGTCAGAAA	0.527
+	24	1862	p.P554S|COL4A5	NM_033380	NP_203699	P29400	CO4A5_HUMAN	e-helical region.	4	ACTTTTCCAGGA	0.498
-	11	3395		NM_012471	NP_036603	Q9UL62	TRPC5_HUMAN	lasmic (Potential).	1	TGACTTTCCTTG	0.453
-	1	984		NM_016521	NP_057605	Q5H9I0	TFDP3_HUMAN	ating E2F activity.|DCB2 (	1	TCATGCCCATCC	0.478
+	18	2663	p.M801I|SAGE1_	NM_018666	NP_061136	Q9NXZ1	SAGE1_HUMAN		3	ATTAATGAAAGA	0.343
-	22	2767	n.1_Nonsense_Mu	NM_005369	NP_005360	P10911	MCF2_HUMAN		2	TAATTGATCCTG	0.333
+	6	676		NM_173493	NP_775764	Q8IV76	PASD1_HUMAN		3	AAGAGGAAATG	0.294
+	3	1086	_Mutation_p.R298	NM_005363	NP_005354	P43360	MAGA6_HUMAN	MAGE.	0	GACCTCGCATT	0.557
-	3	1149		NM_005362	NP_005353	P43357	MAGA3_HUMAN		0	TCACTCTTCCC	0.572
-	10	1717	zx.1_Missense_M	NM_012102	NP_036234	Q9P2R6	RERE_HUMAN	ELM2.	2	AGAAGGAAATG	0.443
+	1	136		NM_001080830	NP_001074299	O95522	PRA12_HUMAN		3	CTCTTTCCCCCA	0.627
-	4	1316		NM_001146344	NP_001139816	O60813	PRA11_HUMAN		0	GGCAGGATACA	0.498
+	4	1056		NM_001012276	NP_001012276	Q5VWM4	PRAM8_HUMAN	LRR 1.	0	AGCTGGACCTG	0.582
+	5	475	M50A_uc009vrr.2_	NM_014313	NP_055128	O95807	TM50A_HUMAN	ical; (Potential).	0	TCTCTGATTGCA	0.348
+	2	326	.L42F|TMEM57_	NM_018202	NP_060672	Q8N5G2	MACOI_HUMAN	ical; (Potential).	0	TTGTCCTCCTA	0.368
-	57	8859	m.1_Missense_M	NM_052896	NP_443128	Q7Z408	CSMD2_HUMAN	xtracellular (Potential).	12	AGGGTCACTGC	0.587
-	14	1748	lg.1_Missense_M	NM_003738	NP_003729	Q9Y6C5	PTC2_HUMAN	lasmic (Potential).	18	GCAGGATCTGA	0.592
-	6	1713	omj.1_Missense_	NM_014774	NP_055589	O75071	K0494_HUMAN		0	TGACGGAATGA	0.423
-	6	1289		NM_177414	NP_803133	O14495	LPP3_HUMAN	ical; (Potential).	0	GGGCTCCTTGA	0.502

+	2	291		NM_006252	NP_006243	P54646	AAPK2_HUMAN	rotein kinase.	6	CGTCATCCTCAT	0.254	
-	8	1565	u.1_Intron|C1orf16	NM_001004303	NP_001004303	Q5VWT5	CA168_HUMAN		5	GTTTTTCCTTCA	0.338	
-	3	1307	orf168_uc009vzv.	NM_001004303	NP_001004303	Q5VWT5	CA168_HUMAN		5	CTTGGGAACAG	0.607	
+	4	574		NM_000562	NP_000553	P07357	CO8A_HUMAN	MACPF.	3	TTCCAGGATCA	0.498	
+	10	1660		NM_000562	NP_000553	P07357	CO8A_HUMAN	EGF-like.	3	CCATCCTCGAG	0.617	
-	5	638	_p.L129F|C8B_uc	NM_000066	NP_000057	P07358	CO8B_HUMAN	MACPF.	4	ATCAAGAACTG	0.458	
+	2	775_776	s.1_Nonsense_Mu	NM_001134673	NP_001128145	Q12857	NFIA_HUMAN	CTF/NF-I.	2	ACAGGGAAAAAA	0.48	
+	6	983	K7_uc001dap.2_I	NM_014495	NP_055310	Q9Y5C1	ANGL3_HUMAN	ogen C-terminal.	0	TTCAGGAGAATT	0.318	
-	6	943	e_Mutation_p.G29	NM_024763	NP_079039	Q5VTH9	WDR78_HUMAN		2	GTGCTCCATTG	0.294	
-	7	1630	IQ3_uc001dfz.3_I	NM_001105659	NP_001099129	A6PVS8	LRIQ3_HUMAN		2	TGTTCTGAATTG	0.328	
+	3	2550	dnn.2_Missense_M	NM_001134479	NP_001127951	Q7L1W4	LRC8D_HUMAN	LRR 9.	2	ACTTGGAGTCA	0.348	
-	15	2127		NM_001013660	NP_001013682	Q6ZNA5	FRRS1_HUMAN	(Potential).|Cytochrome b5	1	ATCAGGAAGAT	0.448	
+	3	669	l.1_Missense_Mut	NM_000642	NP_000633	P35573	GDE_HUMAN	glucanotransferase.	3	CTGGTTCATTTC	0.308	
-	3	372	FM3_uc001dui.2_	NM_058170	NP_477518	Q96PB7	NOE3_HUMAN	Potential.	3	GACTTCAATAGA	0.348	
-	4	2465	eab.2_Missense_M	NM_018372	NP_060842	Q5T3J3	LRIF1_HUMAN		0	TTTCTTCTAACT	0.363	
-	7	763	e_Mutation_p.P19	NM_002557	NP_002548	Q12889	OVGP1_HUMAN		5	ATTTGGGGTCT	0.483	
-	2	332	98F|ATP5F1_uc00	NM_024102	NP_077007	Q9BQA1	MEP50_HUMAN	WD 1.	0	AATCGGAGGCC	0.582	
-	2	995	BN1_uc001edr.2_	NM_018364	NP_060834	Q5VWQ0	RSBN1_HUMAN		1	AAATTAATCGG	0.393	
-	3	404	e_Mutation_p.G16	NM_024626	NP_078902	Q7Z7D3	VTCN1_HUMAN	1.|Extracellular (Potential).	0	GCATTGCCAACT	0.473	
-	26	3783		NM_206996	NP_996879	Q6Q759	SPG17_HUMAN		6	TTGTCCAATGA	0.448	
-	2	261	RS2_uc010oxg.1_	NM_015836	NP_056651	Q9UGM6	SYWM_HUMAN		0	TAATGGAGTGG	0.502	
-	1	299	H2BE_uc001etc.2_	NM_175065	NP_778235	Q8IUE6	H2A2B_HUMAN		2	TGACACCCCCG	0.557	rs149336231
+	7	948	sense_Mutation_p.	NM_004425	NP_004416	Q16610	ECM1_HUMAN	roximate repeats.|1.	3	AGTTCTCGGTCA	0.632	
+	1	907		NM_017860	NP_060330	Q9BUN1	CA056_HUMAN		0	CACCAGTACCA	0.602	
-	3	1598		NM_001009931	NP_001009931	Q86YZ3	HORN_HUMAN	5	3	TAGATCCTTGTC	0.562	
-	3	428		NM_001009931	NP_001009931	Q86YZ3	HORN_HUMAN	1	3	TCTCCTCTTTTT	0.418	
-	3	682	uc001ezv.2_Intron	NM_002016	NP_002007	P20930	FILA_HUMAN	Potential.	16	CATAATCATATAC	0.353	
-	3	726		NM_016190	NP_057274	Q9UBG3	CRNN_HUMAN	Gln-rich.	3	TCTGTCCTGTT	0.582	
+	2	348		NM_178353	NP_848130	Q5T753	LCE1E_HUMAN	Cys-rich.	0	GCCAGCCCTCA	0.657	
+	12	1363	_p.P391L|UBAP2L	NM_014847	NP_055662	Q14157	UBP2L_HUMAN		2	ATCCCCATCAC	0.527	
+	10	1247	_p.T409I|DCST1_	NM_152494	NP_689707	Q5T197	DCST1_HUMAN	ical; (Potential).	2	CTGCACTTTCC	0.687	
-	9	1699	1fjn.2_Missense_	NM_006589	NP_006580	P81408	F189B_HUMAN		2	GGAGCGAAAGA	0.701	
+	1	308		NM_001004473	NP_001004473	Q8NGX5	O10K1_HUMAN	Name=3; (Potential).	1	TGTTTTCCTTCC	0.498	
-	8	1197		NM_003126	NP_003117	P02549	SPTA1_HUMAN	Spectrin 4.	8	GATGGGAAAGT	0.478	
-	1	85		NM_001004467	NP_001004467	Q5JRS4	O10J3_HUMAN	Name=1; (Potential).	2	CAACAAAGAAGA	0.448	
-	2	388		NM_030916	NP_112178	Q96NY8	PVRL4_HUMAN		2	CCGCGGGGCAC	0.632	
-	6	2161		NM_005099	NP_005090	O75173	ATS4_HUMAN	Cys-rich.	5	CACCTGAGCCA	0.627	
-	13	2279		NM_000130	NP_000121	P12259	FA5_HUMAN	B.	6	CTAAACGATCAT	0.403	
-	7	1088	f112_uc001ggj.2_	NM_000450	NP_000441	P16581	LYAM2_HUMAN	ar (Potential).|Sushi 3.	5	ATTCTGAGGCT	0.512	
+	16	3561	mh.1_Missense_	NM_015172	NP_055987	Q9Y520	PRC2C_HUMAN		0	AAAAACCATCT	0.468	
-	23	3997	N1_uc001glb.1_I	NM_004319	NP_004310	O14525	ASTN1_HUMAN		15	TCAAGTCCGTAG	0.567	
+	38	5309	1gox.1_Missense_	NM_000721	NP_000712	Q15878	CAC1E_HUMAN	Name=S6 of repeat IV.	6	GATGCTCAACC	0.547	
+	45	7370		NM_031935	NP_114141	Q96RW7	HMCN1_HUMAN		23	GTGTCCATGGT	0.408	
+	96	15201	rs.1_Missense_M	NM_031935	NP_114141	Q96RW7	HMCN1_HUMAN	en G2 beta-barrel.	23	TTGTGAGTGGCT	0.423	
+	5	617		NM_001039152	NP_001034241	Q2M5E4	RGS21_HUMAN		2	AAAATGGCTCC	0.333	
+	12	3161	_p.P953L|CAMSA	NM_203459	NP_982284	Q08AD1	CAMP2_HUMAN		4	CTCCCCTCGTC	0.453	
+	4	241	RPE_uc010pqn.1_	NM_003094	NP_003085	P62304	RUXE_HUMAN		0	GAGATTCATTCT	0.313	

+	6	727		NM_000715	NP_000706	P04003	C4BPA_HUMAN	Sushi 3.	3	GCCTCCTCCAG	0.448
-	11	1373	_p.R299K|INTS7_	NM_015434	NP_056249	Q9NVH2	INT7_HUMAN		0	GGGGCCTGCCC	0.453
-	64	14398		NM_206933	NP_996816	O75445	USH2A_HUMAN	II 32.|Extracellular (Potenti	26	ATAATTCGTAATA	0.418
-	63	13933		NM_206933	NP_996816	O75445	USH2A_HUMAN	II 30.|Extracellular (Potenti	26	ACCCCCTTGGC	0.502
-	10	993	.2_RNA|RAB3GA	NM_012414	NP_036546	Q9H2M9	RBGPR_HUMAN		1	AAAGGGGGACA	0.348
+	7	1186	e_Mutation_p.P33	NM_017898	NP_060368	Q969Z3	MOSC2_HUMAN	MOSC.	0	GTGACCCTGTG	0.458
+	30	8209	CN_uc001hsp.1_	NM_001098623	NP_001092093	Q5VST9	OBSCN_HUMAN	Ig-like 26.	28	GGGCTCCGAGG	0.692
+	2	464	hvy.1_Missense_	NM_173508	NP_775779	Q8IY50	S35F3_HUMAN	ical; (Potential).	2	CTCCTCGTGGG	0.637
+	37	5303		NM_001035	NP_001026	Q92736	RYR2_HUMAN	ilarity).|4 X approximate re	33	TGTCCCCATGAC	0.557
+	1	835		NM_001004698	NP_001004698	A6NFC9	OR2W5_HUMAN		3	TTCTACACCAT	0.517
+	3	1175		NM_175911	NP_787107	Q8N349	OR2LD_HUMAN	Name=7; (Potential).	4	CCATCCTTACC	0.468
-	4	855	ihz.2_Missense_	NM_024803	NP_079079	A6NHL2	TBAL3_HUMAN		1	AAATGTATTCTC	0.512
+	6	672	LAH_uc001int.2_	NM_001039702	NP_001034791	Q9NV23	SAST_HUMAN		0	TGGCATCGCATT	0.393
-	27	2827	b.1_Missense_Mu	NM_003638	NP_003629	P53708	ITA8_HUMAN	ellular (Potential).	6	GCTTTCTCCTC	0.478
-	20	2044	b.1_Missense_Mu	NM_003638	NP_003629	P53708	ITA8_HUMAN	ellular (Potential).	6	TGCTCCTTCCCC	0.363
-	2	419		NM_005028	NP_005019	P48426	PI42A_HUMAN	PIPK.	2	ACAGGGATTTG	0.353
-	1	343_344		NM_001034842	NP_001030014	Q3KNS1	PTHD3_HUMAN		4	CGGGGGGGTG	0.718
-	13	1342	_p.S313F|MPP7_u	NM_173496	NP_775767	Q5T2T1	MPP7_HUMAN		1	TGTTGGAAACT	0.408
+	31	2789		NM_052997	NP_443723	Q9BXX3	AN30A_HUMAN		9	TAAGTGGAAAAT	0.328
+	8	1780	.H321Y|ZNF37A_	NM_001007094	NP_001007095	P17032	ZN37A_HUMAN	2H2-type 4.	1	GAATTCATACAG	0.418
-	12	1524	_p.L442F|FRMPD	NM_001018071	NP_001018081	Q68DX3	FRPD2_HUMAN	FERM.	1	GGCAAGGACCC	0.537
-	11	1535	p.D408N|OGDHL_	NM_018245	NP_060715	Q9ULD0	OGDHL_HUMAN		1	GTCATCGGCAT	0.562
+	2	309	.1_Missense_Mut	NM_001145263	NP_001138735	Q13772	NCOA4_HUMAN		2	TTCTCCGGGCT	0.493
-	11	1515	p.P374S|PCDH15	NM_033056	NP_149045	Q96QU1	PCD15_HUMAN	|Extracellular (Potential).	13	AAGAGGATGAC	0.348
+	12	1636	j.1_Missense_Mu	NM_001080512	NP_001073981	Q9H694	BICC1_HUMAN		4	CTCCCCCTCCT	0.463
-	37	11398	K3_uc010qih.1_In	NM_020987	NP_066267	Q12955	ANK3_HUMAN		19	GGCCTTCTTTCT	0.418
+	37	2599	e_Mutation_p.G62	NM_005203	NP_005194	Q5TAT6	CODA1_HUMAN	l).|Triple-helical region 3 (	1	TAAAGGGGATA	0.428
-	4	370	0qkx.1_5'UTR|PL	NM_001001791	NP_001001791	Q5SWW7	CJ055_HUMAN		0	CCAGCGAACTG	0.562
+	6	492	TPA1_uc010qlt.1_	NM_005411	NP_005402	Q8IWL2	SFTA1_HUMAN		0	TCTCAGCCCTC	0.557
+	2	845	tt.2_Missense_Mu	NM_001548	NP_001539	P09914	IFIT1_HUMAN	TPR 5.	0	GACAGGAAGCT	0.453
+	2	562	9E|CYP2C19_uc	NM_000772	NP_000763	P33260	CP2CI_HUMAN	p.G79V(1)	5	TGCATGGATATG	0.423
+	5	2125	krs.2_Missense_	NM_018121	NP_060591	Q8IX21	F178A_HUMAN		0	AAAGACTAATA	0.428
+	9	6856	1lfz.2_Missense_	NM_206862	NP_996744	O95359	TACC2_HUMAN		10	CCAGTGGGGAG	0.562
+	13	1962	_p.P523S|C10orf1	NM_015608	NP_056423	Q3B7T1	EDRF1_HUMAN		10	TCTGATCCATCA	0.373
-	3	969	_p.P380R|C10orf9	NM_001004298	NP_001004298	Q96M02	CJ090_HUMAN		2	TTTTGGGGCTG	0.498
+	6	1275	ax.1_Intron|ZNF21	NM_013250	NP_037382	Q9UL58	ZN215_HUMAN	KRAB.	0	GAGAAAGAAAT	0.358
+	4	1110		NM_176822	NP_789792	Q86W24	NAL14_HUMAN	NACHT.	8	TTCGATGAACTG	0.453
+	11	3457		NM_176822	NP_789792	Q86W24	NAL14_HUMAN		8	GTAAACTACAAG	0.398
+	3	456		NM_003621	NP_003612	Q8ND30	LIPB2_HUMAN		4	AGGCACTAAAA	0.517
-	3	1348	e_Mutation_p.P38	NM_213618	NP_998783	P78524	ST5_HUMAN	Pro-rich.	1	TTTGGGGACAG	0.587
+	6	997	n_p.S30F|TEAD1	NM_021961	NP_068780	P28347	TEAD1_HUMAN		0	CATGTCCTCAG	0.577
-	8	1314	_Mutation_p.D33	NM_032320	NP_115696	Q9BSF8	BTBDA_HUMAN		0	CCACATCTCTGT	0.254
+	3	532	S2_uc001mqn.2_	NM_001143830	NP_001137302	O43903	GAS2_HUMAN	CH.	2	TGCAGGAGAAA	0.388
-	6	361	_p.G106E|CCDC7	NM_001008391	NP_001008392	Q6ZRK6	CCD73_HUMAN	Potential.	2	TATTTTCCCTTTA	0.259
-	9	791	1L1_uc001muf.1_	NM_001326	NP_001317	Q12996	CSTF3_HUMAN		0	TACTCCGATCTT	0.239
-	2	807	1_5'Flank|C11orf7	NM_000536	NP_000527	P55895	RAG2_HUMAN		5	GACATGAAAAG	0.423
+	1	246	e_Mutation_p.P18	NM_175732	NP_783859	Q8WUK0	PTPM1_HUMAN		1	CTACCCGACGC	0.776

+	3	485	go.3_Missense_M	NM_002843	NP_002834	Q12913	PTPRJ_HUMAN	ellular (Potential).	8	CAATTCCTGAC	0.418	
+	2	402		NM_024114	NP_077019	Q8IWZ4	TRI48_HUMAN	B box-type.	0	CTGAGGAGCAA	0.483	
+	3	224	C6_uc010rik.1_5'	NM_001004704	NP_001004704	Q8NH72	OR4C6_HUMAN		2	TATTTAGGATTCT	0.368	
+	1	221		NM_001004739	NP_001004739	Q8NGL0	OR5L2_HUMAN	Name=2; (Potential).	1	GCTACTCCTCAA	0.463	
+	1	932		NM_001001921	NP_001001921	Q8N127	O5AS1_HUMAN	lasmic (Potential).	5	ATATTCAAATGA	0.284	
+	1	740		NM_001005200	NP_001005200	Q8N162	OR8H2_HUMAN	Name=6; (Potential).	2	CTTGGGAGTCA	0.353	
+	1	692		NM_001005205	NP_001005205	Q8NGP2	OR8J1_HUMAN	lasmic (Potential).	2	TTCATCAGAAG	0.343	
+	5	925	no.2_Missense_M	NM_001142521	NP_001135993	Q96PZ2	F111A_HUMAN		3	TCTTTCCTTTCT	0.408	
+	1	326		NM_001004706	NP_001004706	Q8NGI4	OR4DB_HUMAN	Name=3; (Potential).	2	TGGTGGGGCAG	0.468	
+	1	694		NM_001004711	NP_001004711	Q8NGE8	OR4D9_HUMAN	lasmic (Potential).	0	GGGAAGGCAGG	0.502	
-	13	2614	BP_uc009ymr.1_	NM_002556	NP_002547	P22059	OSBP1_HUMAN		1	TGTGGGGGCAG	0.473	
+	6	677	A2_uc009ymu.2_3	NM_000139	NP_000130	Q01362	FCERB_HUMAN	ical; (Potential).	1	TCTGGGACTTG	0.403	
+	3	432	1_Intron|DAK_uc0	NM_015533	NP_056348	Q3LXA3	DHAK_HUMAN	cetone binding (By similari	0	CTGGCCATGAG	0.637	
-	5	10114	AK_uc001ntk.1_I	NM_001620	NP_001611	Q09666	AHNK_HUMAN		19	ATCTGGGCCAT	0.408	
-	4	655	A2_uc010rlx.1_5'	NM_004739	NP_004730	O94776	MTA2_HUMAN	BAH.	2	TTGCCGAGAAA	0.522	
-	7	1209	.1_RNA|SLC22A	NM_199352	NP_955384	Q6T423	S22AP_HUMAN	lasmic (Potential).	4	ACGGCTCATGTG	0.502	
+	1	213	A10_uc001nwu.3_	NM_001039752	NP_001034841	Q63ZE4	S22AA_HUMAN	lasmic (Potential).	2	AATGGCCTTTG	0.398	
+	9	1712	A10_uc001nwu.3	NM_001039752	NP_001034841	Q63ZE4	S22AA_HUMAN	ical; (Potential).	2	ATTTATGGAATCT	0.443	
+	1	1087	yps.1_Missense_	NM_144585	NP_653186	Q96S37	S22AC_HUMAN		1	ACACGGAGCC	0.667	
-	7	754		NM_017525	NP_059995	Q6DT37	MRCKG_HUMAN	rotein kinase.	4	GTAGTGGCCCT	0.592	
+	6	850	ense_Mutation_p.	NM_003273	NP_003264	O76062	ERG24_HUMAN		1	ACGTGGGTGAT	0.607	
+	10	1382	ense_Mutation_p.	NM_003273	NP_003264	O76062	ERG24_HUMAN		1	TTACCGCATCA	0.652	
+	7	2193	c.1_Missense_M	NM_178864	NP_849195	Q8IUM7	NPAS4_HUMAN		0	ACCTGTCCCTG	0.607	
-	7	753	_p.M160I|CABP2_	NM_016366	NP_057450	Q9NPB3	CABP2_HUMAN	EF-hand 4.	1	GACATCATTCG	0.572	
+	16	2306	.R703Q|PPFIA1_	NM_003626	NP_003617	Q13136	LIPA1_HUMAN		3	CCCACGAAGGA	0.602	
-	10	1949	a.2_5'UTR|SYTL2	NM_001162951	NP_001156423	Q9HCH5	SYTL2_HUMAN		3	CTCATCCTTTTG	0.398	
-	8	1079	e_Mutation_p.P26	NM_007166	NP_009097	Q13492	PICAL_HUMAN		2	GTCTGGTATAT	0.279	
-	9	2662	p.R630K|TRPC6_	NM_004621	NP_004612	Q9Y210	TRPC6_HUMAN	lasmic (Potential).	4	TTGGCCCTTGCA	0.428	
-	3	723		NM_000482	NP_000473				0	GAATTCGTCAG	0.622	rs145184607
+	5	530		NM_017425	NP_059121	Q15506	SP17_HUMAN	IQ.	0	CCAGAGAGGAG	0.403	
-	24	3071	_p.P980L|NFRKB_	NM_001143835	NP_001137307	Q6P4R8	NFRKB_HUMAN		3	AAGAGGGCGGC	0.547	
+	19	5657	_p.P1470L|WNK1_	NM_018979	NP_061852	Q9H4A3	WNK1_HUMAN		23	TTTACCACTAG	0.488	
-	3	532		NM_006248	NP_006239				0	TGTCTCCTTGT	0.607	
+	29	4033	se_Mutation_p.S1	NM_004570	NP_004561	O75747	P3C2G_HUMAN	PX.	21	CCTCTCTGAGG	0.289	
-	14	1824	se_Mutation_p.H2	NM_033123	NP_149114	Q86YW0	PLCZ1_HUMAN	C2.	3	GGACATGAATAA	0.308	
-	25	3156	.G1046S|ABCC9_	NM_005691	NP_005682	O60706	ABCC9_HUMAN	ntial).|ABC transmembrane	6	AATGCCTGCTC	0.413	
-	23	2759		NM_183378	NP_899234	Q7RTY7	OVCH1_HUMAN	CUB 3.	10	GTAATCCACCT	0.363	
+	13	1972	rf40_uc009zjv.1_	NM_001031748	NP_001026918	Q86WS4	CL040_HUMAN		6	TGAATCTGTAA	0.398	
-	6	895	_p.Q230*|ZNF641_	NM_152320	NP_689533	Q96N77	ZN641_HUMAN	ansactivation.	2	TTCCTGAAGAA	0.527	
+	13	1738	2B_uc009zlt.2_In	NM_173602	NP_775873	Q9P265	DIP2B_HUMAN		6	TAATGGGAGTT	0.378	
-	2	656	se_Mutation_p.A1	NM_007210	NP_009141	Q8NCL4	GALT6_HUMAN	enal (Potential).	2	CAAAGGCATTG	0.567	
-	7	1297		NM_005555	NP_005546	P04259	K2C6B_HUMAN	Rod.|Coil 2.	2	CATCTCCCCAC	0.562	
+	16	3041	p.L659F|ESPL1_	NM_012291	NP_036423	Q14674	ESPL1_HUMAN		3	AGGTTCTTTCA	0.527	
+	1	49		NM_001005183	NP_001005183	A6NM76	O6C76_HUMAN	ellular (Potential).	0	TGACGGATAAT	0.388	
+	8	1092	BB3_uc010sqc.1_	NM_001982	NP_001973	P21860	ERBB3_HUMAN	ellular (Potential).	8	AACATCCTGTG	0.507	
+	25	3155	RBB3_uc009zok.	NM_001982	NP_001973	P21860	ERBB3_HUMAN	lasmic (Potential).	8	TAGCCCCTGGG	0.502	
-	6	486	C3_uc010sqy.1_	NM_013251	NP_037383	Q9UHF0	TKNK_HUMAN		2	AGCTGGGGACG	0.517	

+	11	1561	sense_Mutation_p	NM_002392	NP_002383	Q00987	MDM2_HUMAN	or interaction with USP2.		3	AAGAAACCCAAG	0.393	
+	2	455	zm.1_Missense_M	NM_024560	NP_078836	Q9H6R3	ACSS3_HUMAN			4	CATATTGAAAATG	0.338	
+	2	23	Intron|SCYL2_uc0	NM_017988	NP_060458	Q6P3W7	SCYL2_HUMAN			6	TTTCTAGGTAACT	0.333	
-	15	2162		NM_145913	NP_666018	Q8N695	SC5A8_HUMAN	lasmic (Potential).		0	TTGAAAGCAGGA	0.383	
+	11	1561	p.D416N|CCDC63	NM_152591	NP_689804	Q8NA47	CCD63_HUMAN		p.D456N(1)	8	ACCAACGACCTG	0.597	rs138877502
-	18	3149	e_Mutation_p.T70	NM_002973	NP_002964	Q99700	ATX2_HUMAN	Pro-rich.		2	CTATATGTCTTGG	0.348	
-	2	321	uci.1_Missense_Mu	NM_002956	NP_002947	P30622	CLIP1_HUMAN			3	ATAAATCCAGGC	0.473	
+	12	1752	p.R118Q|DNAH10	NM_207437	NP_997320	Q8IVF4	DYH10_HUMAN	n (By similarity).		6	GGGAACGATCTCT	0.418	
-	11	1812	kb.2_Missense_M	NM_001122636	NP_001116108	Q9HCQ5	GALT9_HUMAN	ectin.|Lumenal (Potential).		0	GCAGCGGCCCG	0.622	
-	7	704	plice_Site_p.G207	NM_001161344	NP_001154816	Q96EP1	CHFR_HUMAN			1	CAGACCCTGTGA	0.557	
-	4	380	ense_Mutation_p.T	NM_001161344	NP_001154816	Q96EP1	CHFR_HUMAN			1	TCCCCAGTCTGTA	0.458	
-	2	469		NM_004004	NP_003995	P29033	CXB2_HUMAN	ical; (Potential).		0	GGCGTGGACACG	0.552	
+	13	1611	y.2_Nonsense_Mu	NM_175854	NP_787050	Q58A45	PAN3_HUMAN	se.|Interaction with PAN2.		1	ATGGCCCAGTACC	0.299	
-	5	727	RD13_uc001uux.2_	NM_178006	NP_821074	Q9Y3M8	STA13_HUMAN			4	TGCTTTCGCTGT	0.627	
-	4	1156	vo.2_Missense_Mu	NM_001142296	NP_001135768	Q8N0X7	SPG20_HUMAN			0	TATCAGGAAACAT	0.448	
-	9	1235		NM_012345	NP_036477	Q9UHK0	NUFP1_HUMAN			0	GCACTGCTATCA	0.328	
+	3	218	n_p.M16I|SCEL_uc	NM_144777	NP_659001	O95171	SCEL_HUMAN			5	AGAGATGAAGAG	0.443	
-	6	468	agl.2_Missense_M	NM_001845	NP_001836	P02462	CO4A1_HUMAN			6	CTGGCGGGCCGT	0.448	
-	3	509	vxk.2_Missense_M	NM_144568	NP_653169	Q86T03	TM55B_HUMAN			0	TTTTCCCTGGGG	0.473	
+	2	427	d.1_Missense_Mu	NM_173527	NP_775798	Q8IYK8	REM2_HUMAN	GTP.		2	AGTGGGGGAGA	0.607	
-	3	186_187	kp.1_Missense_M	NM_002471	NP_002462	P13533	MYH6_HUMAN	yosin head-like.		4	TCATCGGGCACG	0.579	
+	3	305	e_Mutation_p.P51	NM_173159	NP_071406	Q8IXF0	NPAS3_HUMAN	x-loop-helix motif.		2	CCTCTTCCTGCA	0.488	
+	11	1384	IPOL1_uc010ams.	NM_138731	NP_620059	Q8TD10	MIPO1_HUMAN	Potential.		2	AGACTTCAGCAA	0.433	
-	16	2673	e_Mutation_p.V82	NM_006939	NP_008870	Q07890	SOS2_HUMAN	Ras-GEF.		2	GAAAAACTTGCA	0.343	
+	2	976		NM_000953	NP_000944	Q13258	PD2R_HUMAN	cellular (Potential).		4	TTTAAGGATGTCA	0.398	
+	3	219	M20L_uc010trq.1_	NM_207377	NP_997260	Q6UXN7	TO20L_HUMAN	lasmic (Potential).		0	TTGTGGGATCCAA	0.308	
+	3	694	xex.3_Nonsense_	NM_021003	NP_066283	P35813	PPM1A_HUMAN			1	AATGTAAAGAAT	0.418	
+	4	1285_1286	ex.3_Missense_M	NM_021003	NP_066283	P35813	PPM1A_HUMAN			1	ATGCACCCAAAG	0.376	
-	21	2864	p.G123S|NEK9_uc	NM_033116	NP_149107	Q8TD19	NEK9_HUMAN	Potential.		5	CCAGACCCTGCA	0.502	
+	1	135	n_p.E18K|KIAA140	NM_020818	NP_065869	Q9P2D8	UNC79_HUMAN			17	TATCATTGAATATC	0.338	
-	21	3438	n_p.P1076S|DICER	NM_030621	NP_085124	Q9UPY3	DICER_HUMAN			5	CCGCAGGAAGTG	0.453	
+	9	2088	e_Mutation_p.S64	NM_014844	NP_055659	O15040	TCPR2_HUMAN			3	TGAACTCACTCA	0.602	
-	15	2293		NM_006035	NP_006026	Q9Y5S2	MRCKB_HUMAN	Potential.		11	CTCGGATTTGATT	0.463	
+	17	1827	TA1_uc001yrb.2_M	NM_004689	NP_004680	Q13330	MTA1_HUMAN	binding (Potential).		2	CCCGCCCCCCCA	0.682	
-	12	1913	q.2_Missense_Mut	NM_003257	NP_003248	Q07157	ZO1_HUMAN	PDZ 3.		6	TCTTCTCTTATGAT	0.368	
+	2	259		NM_001211	NP_001202	O60566	BUB1B_HUMAN			4	CCATGTCCCTGGA	0.413	
-	15	2095_2096	P1_uc001zoc.2_5'	NM_015540	NP_056355	Q9BWH6	RPAP1_HUMAN			1	TTCTTGGGGAGC	0.599	
+	17	2359		NM_198141	NP_937784	Q8TET4	GANC_HUMAN			2	GGTATTCTCTGTT	0.512	
+	2	565	1ztt.2_Missense_M	NM_016396	NP_057480	Q05D32	CTSL2_HUMAN			0	TGTTGTCTTCAAT	0.323	
-	5	942	_p.T173I|GABPB1_	NM_005254	NP_005245	Q06547	GABP1_HUMAN			1	GTCACAGTGTCAG	0.423	
-	8	845	ofi.1_Missense_Mu	NM_182758	NP_877435	Q3MJ13	WDR72_HUMAN			2	AGGATTCTGTGA	0.423	
+	1	561		NM_001080534	NP_001074003	Q8NB66	UN13C_HUMAN			7	AAAATGGAAAAA	0.458	
+	2	701	p.P141L|RNF111_	NM_017610	NP_060080	Q6ZNA4	RN111_HUMAN			2	CTTCTCCTTCATC	0.383	
-	30	5660		NM_003922	NP_003913	Q15751	HERC1_HUMAN			19	ATTGAACTACTTT	0.333	
-	7	1237	SNK1G1_uc002anl	NM_022048	NP_071331	Q9HCP0	KC1G1_HUMAN	rotein kinase.		0	GAGTCCTTGCCA	0.458	
-	3	400	02apj.3_Missense_	NM_005848	NP_005839	Q7Z401	MYCPP_HUMAN			4	AACACGAGGCC	0.363	
+	21	3051	on_p.V659I|IQCH_	NM_001031715	NP_001026885	Q86VS3	IQCH_HUMAN			4	CTAAGAGTAACAA	0.353	

+	15	1985	ukf.1_Missense_M	NM_017691	NP_060161	Q8IUZ0	LRC49_HUMAN			1	TCCAAAGGAAAA	0.308	
-	9	1150	o.2_RNA|PARP6_	NM_020214	NP_064599	Q2NL67	PARP6_HUMAN			0	CTGGGGGCTGG	0.597	
-	8	1566	se_Mutation_p.E3	NM_000781	NP_000772	P05108	CP11A_HUMAN			2	TCATCTCTAGCTC	0.562	
+	13	1864	unn.1_Missense_M	NM_018689	NP_061159	Q8WUJ3	K1199_HUMAN			3	GATTTAAGGCAG	0.542	
+	6	3070		NM_020778	NP_065829	Q96L96	ALPK3_HUMAN			12	GTTTCCCAAAAA	0.537	
+	7	1643	O3A1_uc010boc.1_	NM_013272	NP_037404	Q9UIG8	SO3A1_HUMAN	r (Potential).|Kazal-like.		1	CCGATTCCTTCA	0.468	
+	16	3186	e_Mutation_p.E104	NM_000875	NP_000866	P08069	IGF1R_HUMAN	e.|Cytoplasmic (Potential).		8	AGGATTGAGTTT	0.473	
-	15	6988	ot.1_Missense_Mut	NM_001009944	NP_001009944	P98161	PKD1_HUMAN	ular (Potential).|REJ.		3	CCCTCAATGATG	0.622	
-	12	3752		NM_032444	NP_115820	Q8IY92	SLX4_HUMAN	PLK1 and TERF2-TERF2IF		0	TCCCGCCCTGG	0.672	
-	5	920	wb.2_Missense_M	NM_015092	NP_055907	Q96Q15	SMG1_HUMAN	with SMG8 and SMG9.		16	TGTTTAACTAGTA	0.274	
+	2	1468		NM_006539	NP_006530	O60359	CCG3_HUMAN			0	GACTACGAACAG	0.562	
+	7	1615		NM_014712	NP_055527	O15047	SET1A_HUMAN	Ser-rich.	p.S310F(1)	3	CCTTTTCCCGCC	0.522	rs146035438
+	10	1452	_p.E353V|GPT2_	NM_133443	NP_597700	Q8TD30	ALAT2_HUMAN			2	TGTGGAGGCTG	0.582	
-	4	727	_p.G98E|CDH11_	NM_001797	NP_001788	P55287	CAD11_HUMAN	r (Potential).|Cadherin 1.		14	ATGGTTCCAGCT	0.433	
+	3	528	se_Mutation_p.N9	NM_001048251	NP_001041716	Q96MX0	CKLF3_HUMAN	MARVEL.		1	AGCTGAATGACA	0.592	
-	7	2151	ers.2_Missense_M	NM_001040715	NP_001035805	Q68EN5	K895L_HUMAN			0	CCAGCCGGTTG	0.637	
-	2	185	n_p.S29F|TAT_uc0	NM_000353	NP_000344	P17735	ATTY_HUMAN			2	GGCACAGAGCTT	0.527	
-	10	1415	ep.1_Missense_Mu	NM_012091	NP_036223	Q9BUB4	ADAT1_HUMAN	A to I editase.		2	CTGAAGAGTTCC	0.413	
+	11	1938		NM_022041	NP_071324	Q9H2C0	GAN_HUMAN			2	ATTCCCCTTGAG	0.527	
-	4	641_642	DL1_uc010vnv.1_In	NM_031463	NP_113651	Q3SXM5	HSDL1_HUMAN			0	ACACACCCACGT	0.475	rs144743188
-	11	3752	p.G1036E|NLRP1_	NM_033004	NP_127497	Q9C000	NALP1_HUMAN			9	GGTCCCCTTGA	0.567	
+	2	1231		NM_000676	NP_000667	P29275	AA2BR_HUMAN	smic (By similarity).		2	GCTACACTTTTC	0.488	
-	1	424	.1_Intron|uc002gy	NM_001004306	NP_001004306	Q6NUI1	C144L_HUMAN			0	TCCAGGAGCCA	0.627	
-	5	1332	F12_uc002hdj.1_M	NM_001033561	NP_001028733	Q96QT6	PHF12_HUMAN	action with SIN3A.		1	GTAAGGGAACGA	0.388	
+	50	7681	o.2_Nonsense_Mu	NM_001042492	NP_001035957	P21359	NF1_HUMAN		p.R2450*(1)	330	GAAGTTCGAAGT	0.363	
+	9	1214	hjc.2_Missense_M	NM_173167	NP_775259	Q8IWX7	UN45B_HUMAN			6	GAGCGCGATCAC	0.468	rs148057044
-	6	1268		NM_002278	NP_002269	Q14532	K1H2_HUMAN	Coil 2.|Rod.		0	AGTCCTCGTTCT	0.617	rs70964671
-	1	441	T14_uc010cxp.1_M	NM_000526	NP_000517	P02533	K1C14_HUMAN	Coil 1A.|Rod.		1	AGGAGGCCAGG	0.458	
+	1	265	.1_5'UTR|WNK4_	NM_032387	NP_115763	Q96J92	WNK4_HUMAN			7	CTCCGGACCCC	0.716	
-	3	697	SK|MEOX1_uc002i	NM_004527	NP_004518	P50221	MEOX1_HUMAN	Homeobox.		0	TTCATCCTTCGG	0.582	
-	1	486	ikd.2_Missense_M	NM_015443	NP_056258	Q7Z3B3	K1267_HUMAN			2	CTAAGGAAAACT	0.438	
+	2	722	h.2_5'UTR|HLF_u	NM_002126	NP_002117	Q16534	HLF_HUMAN			2	TCCTGGGGCCTA	0.488	
+	3	296	jgl.2_Missense_M	NM_002266	NP_002257	P52292	IMA2_HUMAN	IBB.		2	TAAGCTCATTTC	0.413	
+	2	207		NM_001545	NP_001536	Q14197	ICT1_HUMAN			2	CAAGCCGACAGT	0.269	
-	4	309	D2_uc010dfz.2_In	NM_006356	NP_006347	O75947	ATP5H_HUMAN			0	CCTCTGGCACG	0.448	
+	32	4292	lk.3_RNA|SMCHD	NM_015295	NP_056110	A6NHR9	SMHD1_HUMAN			0	AAAAACCCGTTC	0.353	
+	2	1157	XNDC2_uc002koh.	NM_001098529	NP_001091999	Q86VQ3	TXND2_HUMAN	repeat of Q-P-K-X-G-D-I-P		2	CAAGGAGAGTGA	0.562	
+	21	2215	D30B_uc010xak.1	NM_001145029	NP_001138501	Q9BXX2	AN30B_HUMAN			2	GAGTCTCCTGAT	0.289	
-	9	1728	_p.L286*|NPC1_u	NM_000271	NP_000262	O15118	NPC1_HUMAN			2	TAATTTAACACA	0.463	
-	9	1709	p.C280S|NPC1_u	NM_000271	NP_000262	O15118	NPC1_HUMAN			2	TGGTGCAGTTCG	0.448	
+	27	3373	ur.2_Missense_Mu	NM_198129	NP_937762	Q16787	LAMA3_HUMAN	IV 1 (domain IV B).		11	AGCAGTCGTCAC	0.438	
+	53	6901	kus.3_Missense_M	NM_198129	NP_937762	Q16787	LAMA3_HUMAN	omain II and I.		11	GAGATGGTCTTC	0.423	
-	13	2062	wi.3_Missense_Mu	NM_001941	NP_001932	Q14574	DSC3_HUMAN	r (Potential).|Cadherin 5.		4	TGATATGAAAGAC	0.333	
-	3	728	n_p.R92*|DSC2_u	NM_024422	NP_077740	Q02487	DSC2_HUMAN			3	AACTTCTCTTCTC	0.338	
-	12	2073	1012_uc002kxd.3_	NM_014939	NP_055754	Q9Y2L5	TPPC8_HUMAN			0	CTAAATCGATGGC	0.333	
-	13	1037	_uc002lbq.3_Silen	NM_024430	NP_077748	Q9H939	PPIP2_HUMAN			1	CTTTTAGGAATTG	0.249	
-	1	1626	NAL2_uc002lco.2_	NM_016427	NP_057511	Q8IYF1	ELOA2_HUMAN			4	CCGAATCCCAGG	0.547	

-	1	817	NAL2_uc002lco.2_	NM_016427	NP_057511	Q8IYF1	ELOA2_HUMAN		4	CACTTTCTCTCA	0.662	
+	3	1014	C_uc010xdr.1_5'U	NM_005215	NP_005206	P43146	DCC_HUMAN	otential).|Ig-like C2-type 2.	17	AGGTTCCTTTCA	0.388	
+	12	2494	_p.S484L|DCC_uc	NM_005215	NP_005206	P43146	DCC_HUMAN	tential).|Fibronectin type-III	17	TCAATTCAAGAG	0.408	
-	4	1859		NM_052947	NP_443179	Q86TB3	ALPK2_HUMAN		14	ATTCGGCTTCT	0.512	
+	6	632	xet.1_Missense_M	NM_001040147	NP_001035237	O75635	SPB7_HUMAN		3	CAAAGGCAAGT	0.393	
+	12	2390	b.2_Missense_Mu	NM_033646	NP_387450	Q9ULB5	CADH7_HUMAN	lasmic (Potential).	4	ACTCCAGAAATT	0.483	
+	7	1253	b.1_Missense_Mu	NM_004368	NP_004359	Q99439	CNN2_HUMAN		0	AGGTCCCTGAAT	0.637	
-	5	428	_p.P124L|PIP5K1	NM_012398	NP_036530	O60331	PI51C_HUMAN	PIPK.	4	GGGCGGGGGTG	0.622	
+	3	450	xib.1_Missense_M	NM_032607	NP_115996	Q68CJ9	CR3L3_HUMAN	lasmic (Potential).	2	CCGCCGGCTGC	0.657	rs145839480
+	5	702	_p.A80T|ZNF557_	NM_001044388	NP_001037853	Q8N988	ZN557_HUMAN	KRAB.	2	ACCTGGCCTCA	0.433	
-	5	36001		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).	57	AAATTCTGGGG	0.493	
-	5	35987		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).	57	CAACTGAAGTT	0.493	
-	3	18701		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).	57	CAAGAGATGTC	0.488	
-	6	1016	p.E248K|ZNF562_	NM_001130032	NP_001123504	Q6V9R5	ZN562_HUMAN		0	ACTTCTCTCCTT	0.348	
+	8	852		NM_173483	NP_775754	Q6NT55	CP4FN_HUMAN		2	AGTGATTATATCT	0.557	
-	9	1513	BP1_uc002nft.1_R	NM_031941	NP_114147	Q8N6Y0	USBP1_HUMAN		1	GGGTCCCCAGA	0.607	
-	3	1834		NM_001001411	NP_001001411	Q8N7Q3	ZN676_HUMAN	2H2-type 13.	0	ACATTTGTAGC	0.388	
+	6	2690	td.2_Nonsense_M	NM_001136156	NP_001129628	Q8TCN5	ZN507_HUMAN	2H2-type 8.	5	TATGTGGAAACAT	0.453	
+	15	2245	cd.3_Missense_M	NM_199180	NP_954649	Q6UWL6	KIRR2_HUMAN	ytoplasmic (Potential).	3	CACATCCTTTGG	0.617	
-	5	1009	p.H236Y|ZNF565_	NM_152477	NP_689690	Q8N9K5	ZN565_HUMAN	2H2-type 5.	2	TGTGTGGATTC	0.507	
+	8	1979	p.R402C|ZNF383_	NM_152604	NP_689817	Q8NA42	ZN383_HUMAN	2H2-type 11.	2	TCATTCGTCATC	0.378	
-	3	232		NM_001828	NP_001819	Q05315	LPPL_HUMAN	Galectin.	0	GAAATGGAAGAC	0.502	
+	9	738	2ooe.2_Missense_	NM_138392	NP_612401	Q8TBC3	SHKB1_HUMAN		2	GTTTTCCAGCC	0.627	
+	2	375	2orj.1_Missense_	NM_004363	NP_004354	P06731	CEAM5_HUMAN	Ig-like 1.	2	TAATAGGAACTCA	0.468	
-	3	750	_Mutation_p.E96	NM_182707	NP_874366	Q9UQ74	PSG8_HUMAN	like C2-type 1.	0	GTATTTCACATTC	0.512	
-	3	571	10eio.1_Missense_	NM_006905	NP_008836	P11464	PSG1_HUMAN	p.E145G(1)	2	AGTCTCCACTG	0.517	
-	5	1261	wf.3_Missense_Mu	NM_002784	NP_002775	Q00887	PSG9_HUMAN	like C2-type 3.	2	CGCTATGATTTC	0.443	
+	2	146		NM_015603	NP_056418	Q9Y3X0	CCDC9_HUMAN		0	CCTCAGTGCTG	0.542	
+	5	2330	c002pxc.1_5'Flan	NM_007147	NP_009078	Q9Y473	ZN175_HUMAN	2H2-type 14.	0	GGAAATCGTTCA	0.438	rs145951696
-	5	1020		NM_003830	NP_003821	O15389	SIGL5_HUMAN	otential).|Ig-like C2-type 2.	4	GTATTGGAGATG	0.622	
+	2	710	p.G222E|FPR2_u	NM_001005738	NP_001005738	P25090	FPR2_HUMAN	Name=5; (Potential).	4	GCTATGGGCTCAT	0.502	
+	2	496		NM_002030	NP_002021	P25089	FPR3_HUMAN	Name=3; (Potential).	6	TGTTATGATAGAC	0.468	
-	7	964	p.S147L|ZNF611_	NM_030972	NP_112234	Q8N823	ZN611_HUMAN		1	AGTAATGAAGAA	0.378	
+	5	623	L1_uc002qhl.3_In	NM_012314	NP_036446	P43632	KI2S4_HUMAN	otential).|Ig-like C2-type 2.	0	CCCACGGAGGG	0.592	
+	9	2952	tg.2_Missense_Mu	NM_176811	NP_789781	Q86W28	NALP8_HUMAN		13	GGCTGGAAAAC	0.512	
+	8	1918	uc002qnk.1_Intron	NM_020828	NP_065879	Q8NHY6	ZFP28_HUMAN		1	AGAAGCCTTTTG	0.428	
-	4	322	329_uc002qro.1_	NM_024620	NP_078896	Q86UD4	ZN329_HUMAN		1	GCAGGGAACTT	0.463	
-	16	2240	|ATAD2B_uc002re	NM_017552	NP_060022	Q9ULI0	ATD2B_HUMAN		1	GGGCACTAAGC	0.502	
+	11	883	_Mutation_p.E17	NM_007266	NP_009197	Q9HCN4	GPN1_HUMAN		0	GAATATGAACGT	0.373	
-	1	1027		NM_001029883	NP_001025054	A6NGG8	CB071_HUMAN		1	GGGGAGACCCT	0.587	
+	7	806	p.P193L|CCT7_uc	NM_006429	NP_006420	Q99832	TCPH_HUMAN		0	CAATCCCAAGAT	0.438	
+	6	1126	jf.1_Missense_Mu	NM_015120	NP_055935	Q8TCU4	ALMS1_HUMAN		9	TGTGATCGTTAT	0.378	
+	18	2821	ysg.1_Missense_M	NM_004389	NP_004380	P26232	CTNA2_HUMAN		9	ACATTTCGCCTG	0.368	
-	13	2343		NM_004836	NP_004827	Q9NZJ5	E2AK3_HUMAN	Potential).|Protein kinase.	3	GTGAAGGAGCT	0.453	
+	11	2466		NM_001011552	NP_001011552	Q6AI14	SL9A4_HUMAN	lasmic (Potential).	3	TGCAGGAAGAG	0.428	
-	7	1645		NM_000575	NP_000566	P01583	IL1A_HUMAN		1	AGTGCCGTGAG	0.468	
-	17	5698	ttq.2_Missense_M	NM_207363	NP_997246	O14513	NCKP5_HUMAN		0	TGGAGGAAGGC	0.597	

+	4	443	10zbl.1_Missense_	NM_018460	NP_060930	Q53QZ3	RHG15_HUMAN	PH.	2	AAGAAACTAAGG	0.333	
-	11	1569	p.D284N|CCDC14	NM_138803	NP_620158	Q8NFR7	CC148_HUMAN		2	GAAGATCTCTCA	0.303	
-	5	980	s.2_Missense_Mu	NM_002349	NP_002340	O60449	LY75_HUMAN	Potential).|C-type lectin 1.	0	TTACCTGGATCC	0.423	
-	4	363	ce|ITGB6_uc010z	NM_000888	NP_000879	P18564	ITB6_HUMAN		3	ACCACCTGCAA	0.522	
-	13	2246	_p.W623*|SCN1A_	NM_006920	NP_008851	P35498	SCN1A_HUMAN	II.	13	TTTAACCAATATG	0.383	
+	3	461	_p.W123*|G6PC	NM_021176	NP_066999	Q9NQR9	G6PC2_HUMAN	ical; (Potential).	1	TGTCTGGTATGT	0.478	
+	39	5582	e_Mutation_p.R71	NM_172070	NP_742067	Q6ZT12	UBR3_HUMAN		0	GGAAAGATACA	0.368	
+	7	1327	_p.S256F|ITGA6_	NM_001079818	NP_001073286	P23229	ITA6_HUMAN	Extracellular (Potential).	2	AAGATTCTATGTT	0.358	
-	306	92958	07K|TTN_uc010z	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	ATATTTCACTCC	0.388	
-	275	71443	435*|TTN_uc010zf	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	GAGACCATGTT	0.438	
-	275	68106	23A|TTN_uc010z	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	TCACAGTAACTG	0.463	
-	275	63906	23Q|TTN_uc010z	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	GATACTCTAATC	0.458	
-	220	43725	_uc010zfi.1_Miss	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	AGGTTCCCAAG	0.398	
-	200	39450	.1_Missense_Muta	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	CTTTTCCATGTTT	0.363	
-	157	32061	Intron|TTN_uc010	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	TTTGGGAGCCT	0.423	
-	143	30597	z.1_Missense_Mu	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	AACTTCCTCTT	0.453	
-	80	20457	_uc010zfj.1_Intro	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	CTTGCGGATGA	0.512	
+	4	2903		NM_194250	NP_919226	Q7Z570	Z804A_HUMAN	p.R770Q(1)	11	TCTATCGAAAAC	0.333	
-	4	587	_p.K178*|CLK1_uc	NM_004071	NP_004062	P49759	CLK1_HUMAN		2	TTCTTTTCCTTC	0.443	
+	5	4094		NM_020923	NP_065974	Q9HCK1	ZDBF2_HUMAN		3	CTACAGATTCC	0.393	
-	2	90		NM_020989	NP_066269	P07315	CRGC_HUMAN	a crystallin 'Greek key' 1.	0	GGTTTCGTAGC	0.522	rs145041511
+	7	2206	.1_Intron|MAP2_u	NM_002374	NP_002365	P11137	MAP2_HUMAN		17	ACCCAGTTCTC	0.443	
+	11	4932	g.1_Missense_Mu	NM_002374	NP_002365	P11137	MAP2_HUMAN		17	GAGAATTCCTTC	0.458	
-	3	320	eb.2_Missense_M	NM_079420	NP_524144	P05976	MYL1_HUMAN	EF-hand 1.	1	CTGTTCTGTCA	0.438	
-	7	970	vb.2_Intron|SLC23	NM_001144889	NP_001138361	Q6PIS1	S23A3_HUMAN	ical; (Potential).	0	CTGGGGGATAA	0.522	
+	7	1185	.3_Missense_Mut	NM_005070	NP_005061	P48751	B3A3_HUMAN	Cytoplasmic.	5	TCCTTCGCAGG	0.652	rs140021661
+	5	653	se_Mutation_p.E1	NM_007237	NP_009168	Q13342	LY10_HUMAN		0	CTCAGGAAGCC	0.498	
-	2	361		NM_006056	NP_006047	Q9HB89	NMUR1_HUMAN	Name=1; (Potential).	5	GGATGACCAGA	0.632	
+	8	1425		NM_018327	NP_060797	Q9NUV7	SPTC3_HUMAN		0	AGGTTACATAG	0.512	
-	2	258	_p.P53S|C20orf3_	NM_020531	NP_065392	Q9HDC9	APMAP_HUMAN	type II membrane protein;	1	CAGGGGAACGG	0.517	
-	2	116		NM_001037731	NP_001032820	Q30KQ4	DB116_HUMAN		0	TCACATGGATTC	0.468	
-	5	446	_p.E65K|NECAB	NM_031232	NP_112509	Q96P71	NECA3_HUMAN		1	CGATTCCAATG	0.612	
-	24	3507	.G1127A|PTPRT_	NM_007050	NP_008981	O14522	PTPRT_HUMAN	hatase 1.|Cytoplasmic (Po	20	ACCACCCCTTCA	0.577	
-	22	3180	.R1018Q|PTPRT_	NM_007050	NP_008981	O14522	PTPRT_HUMAN	hatase 1.|Cytoplasmic (Po	20	CAGTATCGCACA	0.438	
-	21	3155	p.E1010K|PTPRT_	NM_007050	NP_008981	O14522	PTPRT_HUMAN	hatase 1.|Cytoplasmic (Po	20	CACTTCCACCA	0.468	
+	4	651		NM_004994	NP_004985	P14780	MMP9_HUMAN		2	GTGGTCCCTGG	0.637	
-	8	1852	hk.1_Missense_M	NM_021248	NP_067071	Q9UJ99	CAD22_HUMAN	(Potential).|Cadherin 4.	5	TTAGGGATGCC	0.552	
-	5	705	Missense_Mutatio	NM_022829	NP_073740	Q8WWT9	S13A3_HUMAN	lasmic (Potential).	1	ATCCTCCTTCCT	0.532	
-	2	1634	s.1_Nonsense_M	NM_004975	NP_004966	Q14721	KCNB1_HUMAN	lasmic (Potential).	2	CTTTGTCCATTT	0.433	
+	2	3772		NM_178457	NP_848552	Q5JPB2	ZN831_HUMAN		14	TGCCCCAGCAC	0.498	
+	5	4780		NM_178457	NP_848552	Q5JPB2	ZN831_HUMAN		14	CCAGAGGCCAG	0.468	
+	11	1202	ion_p.R312*|ITSN	NM_003024	NP_003015	Q15811	ITSN1_HUMAN		4	GAGTTCGATCT	0.388	
-	15	3372	AM_uc002yyr.1_	NM_001389	NP_001380	O60469	DSCAM_HUMAN	tential).|Fibronectin type-III	11	GAGCTCGTTGC	0.587	
+	2	173	.2_RNA|UBASH3	NM_018961	NP_061834	P57075	UBS3A_HUMAN	UBA.	3	CACGGGGAGGA	0.607	
+	26	4610	guz.1_Missense_	NM_032608	NP_115997	Q8IUG5	MY18B_HUMAN	otential.|Tail.	12	AAGGTGATGTG	0.612	
+	2	755		NM_020437	NP_065170	Q6ICH7	ASPH2_HUMAN	enal (Potential).	1	ACAACGAGGGC	0.637	
-	4	1063	OX10_uc003auo.	NM_006941	NP_008872	P56693	SOX10_HUMAN		0	CCATGGAGCGC	0.627	

-	5	2021	AP1_uc003azu.2_	NM_002883	NP_002874	P46060	RAGP1_HUMAN		0	CAAAGACCTTC	0.582	
-	8	840		NM_002676	NP_002667	Q92871	PMM1_HUMAN		1	CTCATGAGCTG	0.587	
-	7	640		NM_002676	NP_002667	Q92871	PMM1_HUMAN		1	CCTCGGGGAAG	0.592	
-	3	283	3bde.3_Missense_	NM_007229	NP_009160	Q9UNF0	PACN2_HUMAN	FCH.	0	CCCGACCTAGG	0.642	
-	5	815	.1_Intron|PHF21B	NM_138415	NP_612424	Q96EK2	PF21B_HUMAN		3	ggtgaaggggacagt	0.274	
+	3	551	_uc010hbh.1_Mis	NM_001097	NP_001088	P10323	ACRO_HUMAN	eptidase S1.	0	GGTGGCCGGCT	0.627	
-	7	2096	_p.P574L|IQSEC1_	NM_014869	NP_055684	Q6DN90	IQEC1_HUMAN	SEC7.	1	CACGGGGAATG	0.527	
+	12	2230	ssense_Mutation_	NM_015460	NP_056275	Q8NFW9	MYRIP_HUMAN	ctin-binding.	5	TGGAAGAAAAT	0.507	
+	3	918	_Mutation_p.R24	NM_001296	NP_001287	O00590	CCBP2_HUMAN	lasmic (Potential).	5	AGGGCCGGGC	0.532	
+	5	526	c003cyw.2_5'UTR	NM_004636	NP_004627	Q13214	SEM3B_HUMAN	Sema.	6	GGCCCCTGTGG	0.642	
+	6	339		NM_004947	NP_004938	Q8IZD9	DOCK3_HUMAN		0	TTTCAGAAACA	0.388	
+	32	3386		NM_004947	NP_004938	Q8IZD9	DOCK3_HUMAN		0	GACATGATGGA	0.473	
+	42	5330	_Mutation_p.D17	NM_001128840	NP_001122312	Q01668	CAC1D_HUMAN	lasmic (Potential).	11	CAAGTGATACT	0.458	
-	14	2699	C2_uc003dht.1_	NM_015576	NP_056391	O15083	ERC2_HUMAN	Potential.	2	CAGTTCCTGTC	0.512	
-	12	2359	lm.2_Missense_M	NM_003716	NP_003707	Q9ULU8	CAPS1_HUMAN		3	TAAATTCATCCAT	0.383	
-	8	1272	mh.1_Missense_	NM_182920	NP_891550	Q9P2N4	ATS9_HUMAN	ptidase M12B.	4	TATAGGGATCAC	0.403	
+	7	1922	.3_5'UTR|EPHA6_	NM_001080448	NP_001073917	Q9UF33	EPHA6_HUMAN	III 2.|Extracellular (Potentia	16	AATTTGAAACAG	0.373	
-	14	2050	te.2_Missense_M	NM_080927	NP_563615	Q96PD2	DCBD2_HUMAN	lasmic (Potential).	3	GGTGCCTTCAG	0.378	
-	36	5089		NM_014981	NP_055796	Q9Y2K3	MYH15_HUMAN	Potential.	7	CAGATCACTGT	0.522	
+	4	438	_uc003eeo.2_Splic	NM_018456	NP_060926	Q96CJ1	EAF2_HUMAN		0	TTGCAGAGTTG	0.323	
+	7	1066	.1_Missense_Mut	NM_175862	NP_787058	P42081	CD86_HUMAN	lasmic (Potential).	2	AAGTTCGAAGA	0.333	rs141281931
+	3	633	ekj.2_Missense_M	NM_021937	NP_068756	P57772	SELB_HUMAN		1	AAGCTCCACAG	0.572	
+	2	370	.1_RNA|IL20RB_u	NM_144717	NP_653318	Q6UXL0	I20RB_HUMAN	III 1.|Extracellular (Potentia	1	AGAACCTCTCT	0.512	
-	38	6565	y.1_Missense_Mu	NM_001184	NP_001175	Q13535	ATR_HUMAN	FAT.	20	AAATTCGAGAG	0.343	
+	4	487	_p.S150F|MED12L	NM_053002	NP_443728	Q86YW9	MD12L_HUMAN		7	AATATTCTGTGC	0.353	
-	3	1117	80_uc003fda.2_R	NM_173084	NP_775107	Q8IWR1	TRI59_HUMAN		0	TTGGAGAAATTT	0.308	
-	1	140	_p.E38K|SERPIN	NM_006217	NP_006208	O75830	SPI2_HUMAN		3	CAAATTCGGTAT	0.368	rs147443553
-	2	388	_p.H81Y|WDR49_	NM_178824	NP_849146	Q8IV35	WDR49_HUMAN	WD 1.	3	GAGAGTGATAAT	0.378	
+	13	2193	_p.S331F|EIF2B5	NM_003907	NP_003898	Q13144	EI2BE_HUMAN	W2.	5	GGATTCCCCGC	0.532	
+	9	1660	w.1_Missense_M	NM_198485	NP_940887	Q6ZUI0	TPRG1_HUMAN		0	TCTATCGCATC	0.498	
+	17	3303	gee.3_RNA|WHS	NM_001042424	NP_001035889	O96028	NSD2_HUMAN	AWS.	9	GCCACCCGCAG	0.532	
-	8	1542	vl.1_Missense_M	NM_020972	NP_066023	Q9HCC9	LST2_HUMAN		3	CCGTCCCCTCC	0.701	
-	3	2151		NM_053042	NP_444270	Q9C0D4	Z518B_HUMAN		4	TTGTAGATTCCA	0.433	
-	3	1452	F16_uc003gpo.2_	NM_017741	NP_060211	Q9NXF7	DCA16_HUMAN		1	GCTGGGACTTG	0.512	
+	20	2264	s.1_Missense_Mu	NM_004787	NP_004778	O94813	SLIT2_HUMAN	LRRCT 3.	11	CACGGGAAATC	0.438	
-	7	1441		NM_001358	NP_001349	O43143	DHX15_HUMAN	case C-terminal.	1	ACGTCTCTGCTA	0.318	
-	14	1561		NM_003215	NP_003206	P42680	TEC_HUMAN		9	GGTTACCAGAT	0.433	
-	5	1422	ah.1_Missense_M	NM_004439	NP_004430	P54756	EPHA5_HUMAN	III 1.|Extracellular (Potentia	24	CATGACCGCCA	0.502	
-	7	705	3hdp.2_5'UTR|TM	NM_004262	NP_004253	O60235	TM11D_HUMAN	.|Extracellular (Potential).	1	GCTGCCTCCAC	0.532	
-	5	1309	e_Mutation_p.S28	NM_021139	NP_066962	P06133	UD2B4_HUMAN		2	TACTCGACATT	0.413	
+	6	201	_p.R51K|CSN1S1	NM_001890	NP_001881	P47710	CASA1_HUMAN		0	GAACAGGGTAA	0.274	
+	2	177		NM_021225	NP_067048	Q99935	PROL1_HUMAN		1	AGAATGAAATTA	0.299	
-	1	384		NM_032693	NP_116082	Q9BSU3	NAA11_HUMAN	cetyltransferase.	2	GCGCCGGTGTG	0.562	
-	10	1590	.S276F|ANTXR2_	NM_001145794	NP_001139266	P58335	ANTR2_HUMAN	ellular (Potential).	1	GCATAGAATTA	0.269	
-	17	3170		NM_014991	NP_055806	Q8IZQ1	WDFY3_HUMAN		3	GGGGCGGGTGC	0.502	
-	11	1433		NM_174952	NP_777612	Q8N412	CD037_HUMAN		0	AGATTTCCTTTC	0.269	
-	8	1385	ilr.2_Missense_Mu	NM_020395	NP_065128	Q96CB8	INT12_HUMAN	Ser-rich.	0	TAACTGAGCGA	0.448	

+	8	1787		NM_001977	NP_001968	Q07075	AMPE_HUMAN	ellular (Potential).		5	TGTAGGGATCTT	0.294	
-	4	796	X2_uc010iml.2_In	NM_153426	NP_700475	Q99697	PITX2_HUMAN			0	GTCCTCATTCTT	0.592	
+	2	865	e_Mutation_p.D11	NM_001128174	NP_001121646	Q16880	CGT_HUMAN			2	ACTGTGACCTG	0.443	
+	36	6028	AA1109_uc003iek	NM_015312	NP_056127	Q2LD37	K1109_HUMAN			12	CTCCAGATTCAT	0.368	
-	3	1434	_p.D211N|ANKRD5	NM_020337	NP_065070	Q9ULJ7	ANR50_HUMAN			1	GGATATCTAACTT	0.393	
+	1	2630		NM_024582	NP_078858	Q6V0I7	FAT4_HUMAN	(Potential).|Cadherin 8.		18	GAGACACTATGG	0.463	
+	8	7432	e_Mutation_p.P77	NM_024582	NP_078858	Q6V0I7	FAT4_HUMAN	(Potential).|Cadherin 24.		18	CATCTCCTACT	0.383	
-	1	2338	.1_Intron|PCDH18_	NM_019035	NP_061908	Q9HCL0	PCD18_HUMAN	|Extracellular (Potential).		5	CCATTCTGTGT	0.438	rs141226164
-	5	872	k.1_Missense_Mu	NM_021833	NP_068605	P25874	UCP1_HUMAN	Solcar 3.		1	GAAAGCCGTTG	0.428	
-	3	521	k.1_Missense_Mu	NM_021833	NP_068605	P25874	UCP1_HUMAN	Solcar 2.		1	GATTCCGTGGA	0.468	
-	6	1693	_p.G305R|RNF150_	NM_020724	NP_065775	Q9ULK6	RN150_HUMAN	lasmic (Potential).		1	ACCTCCCAGAG	0.542	
-	3	304	.S30L|GYPA_uc0	NM_002099	NP_002090	P02724	GLPA_HUMAN	Extracellular.		2	ATTTCTGAAACT	0.413	
+	7	1946		NM_022475	NP_071920	Q96QV1	HHIP_HUMAN			6	TCCACGATCCA	0.517	
-	14	1947	_p.L576F|DDX60L_	NM_001012967	NP_001012985	Q5H9U9	DDX6L_HUMAN			1	TTTGAGAAATG	0.333	
+	5	1556	irr.2_Missense_M	NM_014269	NP_055084	Q9UKF5	ADA29_HUMAN	B.|Extracellular (Potential).		16	TAAGAGGGTTA	0.428	
+	5	652	R17_uc003ium.3_	NM_170710	NP_733828	Q8IZU2	WDR17_HUMAN			6	ATTGTACACAAA	0.443	
-	5	1236		NM_005429	NP_005420	P49767	VEGFC_HUMAN			5	CATCTCCAGCAT	0.398	
+	4	350	RR_uc010isy.2_Ir	NM_013232	NP_037364	O75340	PDCD6_HUMAN	nd 2.|2 (Potential).		1	TCAGCGAGTTC	0.537	
+	1	278		NM_182632	NP_872438	Q96N87	S6A18_HUMAN	Name=2; (Potential).		1	CTATGGAGGAG	0.637	
-	1	680		NM_019599	NP_062545	Q9NYW7	TA2R1_HUMAN	lasmic (Potential).		3	ATATCCTCATCTT	0.453	
-	10	1942	RLR_uc003jjj.1_In	NM_000949	NP_000940	P16471	PRLR_HUMAN	lasmic (Potential).		3	GCCTTTCCCTCT	0.542	
-	23	2840	3jmi.3_Missense_	NM_173489	NP_775760	Q7Z745	HTRB2_HUMAN	HEAT 9.		8	TGTAACCAATCA	0.433	
-	3	385	X29_uc010ivw.2_	NM_019030	NP_061903	Q7Z478	DHX29_HUMAN			4	AATTACCACCTG	0.323	
-	6	564	CC8_uc011cqp.1_	NM_000082	NP_000073	Q13216	ERCC8_HUMAN			0	TGGGTCCTCTA	0.328	
+	5	4571	x.1_Missense_Mu	NM_005909	NP_005900	P46821	MAP1B_HUMAN			5	TAAGTCCAGTT	0.413	
+	2	743		NM_153217	NP_694949	Q8WUU8	TM174_HUMAN			1	TCTCTCCTCCCC	0.468	
-	1	368		NR_004845						0	AGCTGGAGCCC	0.542	
+	45	9775	_p.R933*|GPR98_	NM_032119	NP_115495	Q8WXG9	GPR98_HUMAN	lar (Potential).|EAR 1.		16	TATCTCGAACT	0.393	
+	6	1871	nw.1_Missense_M	NM_005575	NP_005566	Q9UIQ6	LCAP_HUMAN	ellular (Potential).		4	CAATGGCGGAT	0.473	
+	5	449	P19_uc011cvu.1_I	NM_003135	NP_003126	P09132	SRP19_HUMAN			0	AACAGGAGGTG	0.308	rs35400610
-	8	1022	_p.P123S|CEP120	NM_153223	NP_694955	Q8N960	CE120_HUMAN			1	GTTTGGAGGGT	0.493	
+	5	1269	NB1_uc010jdb.1_	NM_005573	NP_005564	P20700	LMNB1_HUMAN	Rod.|Coil 2.		2	GAATTGAGAGC	0.428	
+	7	780	dd.1_Missense_M	NM_032446	NP_115822	Q96KG7	MEG10_HUMAN	self-assembly and formati		4	CCTGCGATGGT	0.582	
+	23	4315	_Missense_Mutati	NM_020690	NP_065741	Q8IWZ2	Q8IWZ2_HUMAN			6	ACAATTACAGAT	0.318	
+	1	970	hd.2_Intron|PCDH	NM_018906	NP_061729	Q9Y5H8	PCDA3_HUMAN	|Extracellular (Potential).		8	CCACGGATAAA	0.373	
+	1	217	lhh.1_Intron|PCDH	NM_018910	NP_061733	Q9UN72	PCDA7_HUMAN	|Extracellular (Potential).		4	GTGGGGATCTT	0.612	
+	1	1823	CDHA7_uc003lhq.	NM_018904	NP_061727	Q9Y5I0	PCDAD_HUMAN	|Extracellular (Potential).		6	GGCTTTCGTATG	0.682	
+	1	2177	daj.1_Missense_	NM_018931	NP_061754	Q9Y5F2	PCDBB_HUMAN	lasmic (Potential).		6	CTGCTCGGTGC	0.657	
+	1	1997	dak.1_Missense_	NM_018932	NP_061755	Q9Y5F1	PCDBC_HUMAN	(Potential).|Cadherin 6.		3	GCTGTCGTACC	0.726	
-	4	3323		NM_032420	NP_115796	Q08174	PCDH1_HUMAN			5	TGGACGGCGTC	0.637	
+	2	567		NM_000112	NP_000103	P50443	S26A2_HUMAN	lasmic (Potential).		0	GCTCCCAAAAT	0.423	
-	23	4448	jit.1_Missense_Mu	NM_025153	NP_079429	O94823	AT10B_HUMAN	ical; (Potential).		5	TGCATCCACCAT	0.418	
+	9	1539	lyv.2_Missense_M	NM_000811	NP_000802	Q16445	GBRA6_HUMAN	lasmic (Prob	p.P401L(1)	12	CAACACCTGTC	0.463	
+	8	991	en.1_Missense_M	NM_015238	NP_056053	Q8IX03	KIBRA_HUMAN	Potential.		5	TGGCAGAGAAG	0.468	
-	34	4531	.2_Missense_Mut	NM_003062	NP_003053	O75094	SLIT3_HUMAN	EGF-like 8.		4	GCAGGGGTCCC	0.667	
+	10	491	mig.1_Missense_	NM_001079527	NP_001072995					0	TCCTTCCTCTG	0.527	
+	13	1925_1926	q.1_Missense_Mu	NM_004415	NP_004406	P15924	DESP_HUMAN	plakophilin 1 and junction		9	GGTGTCCTGGC	0.525	

+	2	201		NM_002114	NP_002105	P15822	ZEP1_HUMAN		6	CAAATTCATCCC	0.388
+	6	720	.M133I|CAP2_uc	NM_006366	NP_006357	P40123	CAP2_HUMAN		1	GAGATGAATGA	0.398
+	21	2121	p.G582E|LRRC16	NM_017640	NP_060110	Q5VZK9	LR16A_HUMAN	LRR 9.	4	CAACGGAATGG	0.547
+	1	31		NM_003523	NP_003514	P62807	H2B1C_HUMAN		0	CCGCCCCGAAG	0.527
+	6	1262	A3_uc011dkm.1_Intron						0	CTCTCTGGAGG	0.507
+	7	1149		NM_001732	NP_001723	Q13410	BT1A1_HUMAN	.|Cytoplasmic (Potential).	2	TGTAGGGAGAAT	0.557
+	11	1396	jb.2_Missense_M	NM_005865	NP_005856	Q9NQE7	TSSP_HUMAN		5	TCCTCAGAATCA	0.567
+	2	166	se_Mutation_p.S5	NM_001509	NP_001500	O75715	GPX5_HUMAN		1	TGTTTCCTTCAA	0.423
+	3	573	.2_RNA|PPP1R1	NM_021959	NP_068778	O60927	PP1RB_HUMAN	Pro-rich.	3	ACCGACCCCCA	0.612
-	5	1323	DC1_uc003nrh.1_	NM_014641	NP_055456	Q14676	MDC1_HUMAN	uclear localization (NLS1).	4	TCCAGGAGGTT	0.542
-	2	508	1_5'Flank|PSORS	NM_014070	NP_054789	Q6UXA7	CF015_HUMAN		0	CTGGTGGAGGA	0.622
-	9	1634	.D335N|BAT1_uc	NM_004640	NP_004631	Q13838	DX39B_HUMAN	case C-terminal.	0	GAAAATCTTTAA	0.413
+	4	674	c003nuj.2_Silent_	NM_000594	NP_000585	P01375	TNFA_HUMAN	ellular (Potential).	3	GTCAACCTCCTC	0.632
-	7	1044	p.P238S|BAT3_uc	NM_004639	NP_004630	P46379	BAG6_HUMAN	proximate repeats.|Pro-rich	0	GGCTGGGGCAC	0.607
+	6	961	B_uc011dqu.1_5'F	NM_001077516	NP_001070984	Q92504	S39A7_HUMAN		1	AAAAGGAAACA	0.488
+	80	12200	sense_Mutation_p	NM_001371	NP_001362				21	TAGGTCTTGGTG	0.338
+	89	13573		NM_001371	NP_001362				21	TTCACTGAACTT	0.443
-	2	410	H_uc011dvl.1_5'F	NM_020750	NP_065801	Q9HAV4	XPO5_HUMAN	for interaction with Ran.	4	AAGGCCAAAAT	0.418
-	10	944	.E230K|CRISP2_	NM_001142408	NP_001135880	P16562	CRIS2_HUMAN		1	ACTTTTCCTTGA	0.393
+	8	983		NM_018214	NP_060684	Q9BTT6	LRRC1_HUMAN	LRR 10.	1	AGACTTCCTGAA	0.378
+	5	1866		NM_001010872	NP_001010872	Q5T0W9	FA83B_HUMAN		6	GACACCCCTACG	0.473
+	5	2655		NM_001010872	NP_001010872	Q5T0W9	FA83B_HUMAN		6	AGTAAGGAAGAT	0.388
-	1	860	xf.1_Missense_M	NM_021073	NP_066551	P22003	BMP5_HUMAN		2	GTATTTCCCGTC	0.453
-	5	532	BL2_uc011dxp.1_RNA						0	AGTTGCGATACC	0.507
+	18	3102	2_Missense_Mutat	NM_014989	NP_055804	Q86UR5	RIMS1_HUMAN		10	GATGTGGATAGT	0.363
-	9	1237	CBP_uc011dyx.1_	NM_198920	NP_944602	Q7Z6J8	UB2CB_HUMAN	HECT-like.	1	ACGGCGAAGGG	0.463
-	14	2723	p.E823K|EPHA7_	NM_004440	NP_004431	Q15375	EPHA7_HUMAN	Potential).|Protein kinase.	28	TAACTTCCCACA	0.408
-	11	1895	u.2_Missense_Mu	NM_005068	NP_005059	P81133	SIM1_HUMAN	minded C-terminal.	4	TCAATTTTGCTG	0.453
-	4	438	ub.2_Intron|DDO_	NM_003649	NP_003640	Q99489	OXDD_HUMAN		3	ATCTTTCGAAAT	0.468
+	4	886	_uc003pwt.2_No	NM_001080976	NP_001074445	Q9UL01	DSE_HUMAN		1	CCTACTTATGGA	0.443
-	14	1929	ebw.1_Nonsense_	NM_033515	NP_277050	Q8N392	RHG18_HUMAN		3	CAACCCCACTAT	0.363
-	3	780	_uc003qhk.2_Intr	NM_014432	NP_055247	Q9UHF4	I20RA_HUMAN	tential).|Fibronectin type-III	4	GTTCCCCAAATG	0.363
+	23	3910		NM_020340	NP_065073	Q5TH69	BIG3_HUMAN		2	CCCTGGAAACA	0.493
-	143	26523	p.R8641W|SYNE1	NM_182961	NP_892006	Q8NF91	SYNE1_HUMAN	ytoplasmic (Potential).	45	TGAGCCGATTTC	0.423
+	29	4232_4233	c.1_Missense_M	NM_001040001	NP_001035090	P55196	AFAD_HUMAN	Pro-rich.	5	ACCTGCCTCCG	0.614
-	22	4531		NM_015204	NP_056019	Q9UPZ6	THS7A_HUMAN	Potential).|TSP type-1 15.	3	CAGCTGACACA	0.453
-	13	3127		NM_015204	NP_056019	Q9UPZ6	THS7A_HUMAN	.|Extracellular (Potential).	3	TTTGTCACAAGG	0.388
-	1	484		NM_175886	NP_787082	P21108	PRPS3_HUMAN		1	GCCCTGAATTT	0.448
+	13	1957	p.P642L|HDAC9_	NM_058176	NP_478056	Q9UKV0	HDAC9_HUMAN	ne deacetylase.	5	TGACCCCTTGA	0.438
+	10	2243	h.1_Missense_Mu	NM_002214	NP_002205	P26012	ITB8_HUMAN	epeats.|II.|Extracellular (P	3	CAAGTCACACA	0.373
-	9	819		NM_012294	NP_036426	Q92565	RPGF5_HUMAN		1	TGTCCGTCTGC	0.443
-	3	481	tbc.2_RNA|GGCT_	NM_024051	NP_076956	O75223	GGCT_HUMAN		0	TATTTCTTTTCC	0.373
+	16	1461	ADCYAP1R1_uc0	NM_001118	NP_001109	P41586	PACR_HUMAN	lasmic (Potential).	1	CAAGCGAAAAT	0.612
+	11	1124		NM_016616	NP_057700	Q8N427	TXND3_HUMAN	NDK 1.	3	CGAACGATCTG	0.443
+	1	470	_p.G22E|VSTM2	NM_182546	NP_872352	Q8TAG5	VTM2A_HUMAN		0	ACAAGGGCTTT	0.403
+	4	680		NM_001159279	NP_001152751				2	AAAACGATGGC	0.328
+	4	505		NM_153363	NP_699194	Q8IYX0	ZN679_HUMAN	KRAB.	1	AAAGAGAAATG	0.393

+	1	125	03tte.2_Translati	NM_016220	NP_057304	Q9UII5	ZN107_HUMAN			1	TAAGACGCCGG	0.602	
-	15	1835	n.2_Missense_Mu	NM_000601	NP_000592	P14210	HGF_HUMAN	eptidase S1.		4	CATCTCCTCTTC	0.363	
+	2	622	ense_Mutation_p.	NM_138290	NP_612147	Q96NL0	RUN3B_HUMAN	RUN.		1	ATTTTGGAACAG	0.328	
+	1	1396		NM_003505	NP_003496	Q9UP38	FZD1_HUMAN	Name=1; (Potential).		0	GTCAGTGCTGT	0.622	
-	7	800	umu.1_Missense_	NM_001742	NP_001733	P30988	CALCR_HUMAN	Name=1; (Potential).		9	CTAGGGTGAAA	0.358	
+	8	1079	a.2_Missense_Mut	NM_015908	NP_056992	Q9BXP5	SRRT_HUMAN	Glu-rich.		2	AGCAGGAGGAG	0.597	
+	3	7653	C17_uc010lho.1_	NM_001040105	NP_001035194	Q685J3	MUC17_HUMAN	X approximate tandem re		27	CTAGCACCCTT	0.488	
-	5	563	e_Mutation_p.P77	NM_022777	NP_073614	Q9H7X7	RABL5_HUMAN			0	CTCAGGGTCAT	0.443	
-	30	4595	.2_Missense_Mut	NM_005045	NP_005036	P78509	RELN_HUMAN		p.D1479E(1)	19	GCCATCGTTAA	0.488	
-	24	3332	.2_Missense_Mut	NM_005045	NP_005036	P78509	RELN_HUMAN	EGF-like 2.		19	GCATTCAGTGC	0.527	
-	4	3362		NM_002711	NP_002702	Q16821	PPR3A_HUMAN			34	CTCTTCCCAGG	0.353	
-	4	949	ja.2_Missense_Mu	NM_003391	NP_003382	P09544	WNT2_HUMAN			7	CCTGAGAGTAC	0.552	
+	5	709	R_uc011knq.1_5'	NM_000492	NP_000483	P13569	CFTR_HUMAN	l).|ABC transmembrane ty		5	TTTGATGAAGTAT	0.323	
+	12	4488	.2_Intron|PTPRZ1	NM_002851	NP_002842	P23471	PTPRZ_HUMAN	ellular (Potential).		9	CTGATCATTCTG	0.403	
-	13	1407	.2_Missense_Mut	NM_004717	NP_004708	O75912	DGKI_HUMAN	DAGKc.		3	GAGTTCGAGCC	0.552	
-	15	1859_1860		NM_004333	NP_004324	P15056	BRAF_HUMAN	rotein kinas	_R603>I(2)|p.T	18290	ATTTCACTGTAG	0.366	rs121913378
-	8	1160		NM_004333	NP_004324	P15056	BRAF_HUMAN			18290	ATTGGGAGCTG	0.393	
-	5	504	se_Mutation_p.G1	NM_013252	NP_037384	Q9NY25	CLC5A_HUMAN	.|Extracellular (Potential).		0	GGATCCTTTTC	0.448	
-	1	149		NM_176817	NP_789787	P59533	T2R38_HUMAN	Name=1; (Potential).		2	GGACTGAAATG	0.438	
+	5	669	Intron|uc003wad.2	NM_002769	NP_002760	P07477	TRY1_HUMAN	eptidase S1.		2	GGGGTGATGGC	0.522	
+	1	644		NM_001001667	NP_001001667	Q8N148	OR6V1_HUMAN	Name=5; (Potential).		1	TCATCTCCTATG	0.552	
+	3	1008	_Intron|uc011kto.1	NM_001130025	NP_001123497	A6NFQ2	F115C_HUMAN			0	TAAAAGATCTGT	0.562	
+	1	650		NM_012365	NP_036497	Q96R48	OR2A5_HUMAN	Name=5; (Potential).		3	GGTCTCCTACT	0.612	
-	18	2189	p.V680M|EZH2_u	NM_004456	NP_004447	Q15910	EZH2_HUMAN	SET.	p.N675K(1)	183	ATCCACCACAA	0.353	
+	43	6259		NM_198455	NP_940857	A2VEC9	SSPO_HUMAN	F5/8 type C.		0	AGCTGGAACAC	0.667	
+	8	1031	P343L|AGAP3_uc	NM_031946	NP_114152	Q96P47	AGAP3_HUMAN	all GTPase-like.		3	CACCCCCAGCA	0.657	
+	33	4042	wi.1_Missense_M	NM_003970	NP_003961	P54296	MYOM2_HUMAN			6	AAATACACTTTT	0.423	rs144413619
-	49	7828	p.G1809S|CSMD1	NM_033225	NP_150094	Q96PZ7	CSMD1_HUMAN	xtracellular (Potential).		25	CATGCCAAGTG	0.502	
-	14	2275	wj.1_Missense_M	NM_033225	NP_150094	Q96PZ7	CSMD1_HUMAN	lar (Potential).|CUB 4.		25	CAAAATCATTAA	0.418	
-	3	723	.1_RNA|FGF20_u	NM_019851	NP_062825	Q9NP95	FGF20_HUMAN			1	TTTCTGGATCC	0.423	
+	9	1436	_p.P322L|SH2D4A	NM_022071	NP_071354	Q9H788	SH24A_HUMAN	SH2.		0	CATGCCCGGCA	0.468	
+	9	1212	se_Mutation_p.G3	NM_001722	NP_001713	P05423	RPC4_HUMAN			0	TCCTGGGACAC	0.547	
+	12	1263	ec.2_Missense_M	NM_003817	NP_003808	Q9H2U9	ADAM7_HUMAN	B.|Extracellular (Potential).		5	TTGAAGGATTATA	0.353	
-	10	999	ek.2_Intron|EBF2	NM_022659	NP_073150	Q9HAK2	COE2_HUMAN	IPT/TIG.		4	GGCTCCTTTGC	0.488	
-	3	1765		NM_007257	NP_009188	Q9UL42	PNMA2_HUMAN			0	ctcttcttcccgtattacct	0.209	
+	4	502	1_uc003xnn.2_R	NM_002164	NP_002155	P14902	I23O1_HUMAN			2	ACTGTGTCTTG	0.383	
+	11	1255	se_Mutation_p.G7	NM_194294	NP_919270	Q6ZQW0	I23O2_HUMAN			2	ATCTGGACAGG	0.507	
+	3	352	ny.2_Missense_M	NM_032336	NP_115712	Q9BRT9	SLD5_HUMAN			1	GCAAGCCTGAG	0.463	
-	6	1334	xpe.2_Missense_	NM_006749	NP_006740	Q08357	S20A2_HUMAN	ical; (Potential).		2	TATGGCCCACA	0.537	
+	6	636	c003xql.1_Missen	NM_182746	NP_877423	P33991	MCM4_HUMAN			4	AAGAAGAAGAA	0.348	rs140307429
-	6	773	se_Mutation_p.P1	NM_024593	NP_078869	Q9HAE3	EFCB1_HUMAN			0	ATTTGGATCTTT	0.299	
+	4	2771	1_uc011ldy.1_Intr	NM_006269	NP_006260	P56715	RP1_HUMAN			12	AAGGGGATAAA	0.358	
-	3	543	_p.L99F|CA8_uc	NM_004056	NP_004047	P35219	CAH8_HUMAN			0	CGAAAGAACTG	0.393	
-	3	1045_1046		NM_004820	NP_004811	O75881	CP7B1_HUMAN			3	CTATTTCAAGGT	0.366	
+	15	1468	vt.2_Missense_Mu	NM_001033578	NP_001028750	Q96BR1	SGK3_HUMAN	rotein kinase.		4	CTGGTCCATTC	0.428	
-	5	451	ense_Mutation_p.	NM_001738	NP_001729	P00915	CAH1_HUMAN			2	AGAAAGGACCA	0.418	
-	8	1276	.1_Missense_Mut	NM_015668	NP_056483	Q8NE09	RGS22_HUMAN			7	GCCATGAATAG	0.343	

+	2	798	_p.R216Q|RIMS2_	NM_014677	NP_055492	Q9UQ26	RIMS2_HUMAN		15	ATCAGCGATCTT	0.458
+	4	471		NM_177531	NP_803875	Q86WI1	PKHL1_HUMAN	r (Potential).|IPT/TIG 1.	14	TTACGGAAAAT	0.398
+	14	1429		NM_177531	NP_803875	Q86WI1	PKHL1_HUMAN	ellular (Potential).	14	TTTTTCCAGTC	0.353
+	38	5455		NM_177531	NP_803875	Q86WI1	PKHL1_HUMAN	(Potential).|IPT/TIG 10.	14	CATTGGAAATC	0.413
+	26	3547	uc003yqy.1_Intron	NM_001039112	NP_001034201	Q2WGJ9	FR1L6_HUMAN	lasmic (Potential).	11	AGATTCGCTAAC	0.527
+	14	1590	2_uc003zda.2_5'	NM_145754	NP_665697	Q96AC6	KIFC2_HUMAN	inesin-motor.	3	CGCTGCAGTCG	0.667
-	2	331	_5'Flank|MGC708	NM_001001795	NP_001001795	Q6P1X6	CH082_HUMAN		0	TTTTGGAATCAT	0.582
+	9	1154	_p.E343K|ADAMT	NM_001040272	NP_001035362	Q8N6G6	ATL1_HUMAN		5	ACCCAGAGAAC	0.453
-	1	745	zob.1_Missense_	NM_020344	NP_065077	Q9UI40	NCKX2_HUMAN	lasmic (Potential).	3	TTTCTCTAGAAA	0.413
-	1	190	uc003zrh.1_Intron	NM_153809	NP_722516	Q8IZX4	TAF1L_HUMAN		26	AAATGGGCCAC	0.567
+	4	416	_p.D20Y|NUDT2_	NM_001161	NP_001152	P50583	AP4A_HUMAN	dix hydrolase.	0	AAGTGGACAAC	0.468
+	5	378	p.G102S|ANXA1_	NM_000700	NP_000691	P04083	ANXA1_HUMAN	Annexin 1.	2	TTACAGGTCAC	0.403
-	25	3758	.1_Intron|TRPM6_	NM_017662	NP_060132	Q9BX84	TRPM6_HUMAN	lasmic (Potential).	8	CACTCGGATTC	0.368
-	21	3003	1_Intron|TRPM6_	NM_017662	NP_060132	Q9BX84	TRPM6_HUMAN	ical; (Potential).	8	CAGCTGAAAAC	0.473
-	11	886	NRNPK_uc004ani.	NM_031262	NP_112552	P61978	HNRPK_HUMAN	DX1.|2 X 22 AA approxim	1	TGTGCACGTCCT	0.418
+	3	1955	p.3_Missense_Mu	NM_024945	NP_079221	Q9H9A7	RMI1_HUMAN		0	TGTAACCTTAAC	0.383
+	4	4327		NM_178828	NP_849150	Q6ZUB1	CI079_HUMAN		3	CCATCCACAGC	0.607
-	2	726		NM_005384	NP_005375	Q16649	NFIL3_HUMAN	eucine-zipper.	0	GTTTTCTTCTC	0.388
-	3	451	n_p.G129E|ECM	NM_001393	NP_001384	O94769	ECM2_HUMAN	VWFC.	2	CTCTTCCATCT	0.522
+	9	1736	e_Mutation_p.E37	NM_001083536	NP_001077005	Q5JSP0	FGD3_HUMAN	PH 1.	2	CCAATGAACTG	0.587
+	7	1712	_p.Q510*|PTPDC	NM_177995	NP_818931	A2A3K4	PTPC1_HUMAN		1	GGAGTCAGTCA	0.478
-	1	90	N3A_uc004bbq.1_	NM_147180	NP_671709	Q96LZ3	CANB2_HUMAN		2	GGCCTCGTTTC	0.592
-	3	2811	bq.1_Missense_	NM_133445	NP_597702	Q8TCU5	NMD3A_HUMAN	lasmic (Potential).	7	ATTTTGGAGGT	0.448
-	1	278		NM_001001919	NP_001001919	Q8NGS5	O13C4_HUMAN	ellular (Potential).	1	AGAAGGAAATG	0.448
-	28	4257		NM_005502	NP_005493	O95477	ABCA1_HUMAN		17	AGGACCCTTTG	0.473
-	15	2223	wc.1_Missense_M	NM_003640	NP_003631	O95163	ELP1_HUMAN		7	CTACTGACTTG	0.408
-	17	2442	orf5_uc004bdr.3_	NM_032012	NP_114401	Q9H330	CI005_HUMAN		1	GTAAGGATGGC	0.433
-	38	7457	ty.2_Missense_M	NM_153366	NP_699197	Q4LDE5	SVEP1_HUMAN	Sushi 16.	7	AACAGGGAAAG	0.463
-	2	923	P1_uc004beu.2_	NM_153366	NP_699197	Q4LDE5	SVEP1_HUMAN	VWFA.	7	TCCATCAGTGAT	0.423
-	15	1808	muc.1_Missense_	NM_001080398	NP_001073867				0	AATGTGGCATC	0.353
-	20	2186	lxc.1_Missense_M	NM_015258	NP_056073	Q5T1M5	FKB15_HUMAN	Potential.	3	CTGCACTTTGG	0.463
-	2	547	vf.2_Missense_Mu	NM_002160	NP_002151	P24821	TENA_HUMAN		7	ACTGGGATCCC	0.572
-	5	1058	d.2_Missense_Mu	NM_014618	NP_055433	O60477	DBC1_HUMAN	MACPF.	8	CCAGAGGCCCA	0.512
-	1	65	|LOC253039_uc0	NM_005047	NP_005038	Q16401	PSMD5_HUMAN		0	CGCTTCCAGCC	0.711
+	12	1236	bf.2_Missense_Mu	NM_020822	NP_065873	Q5JUK3	KCNT1_HUMAN		4	TCATGGACTTC	0.647
+	6	586	_p.S22F|TBL1X_	NM_001139466	NP_001132938	O60907	TBL1X_HUMAN	LisH.	1	TTTTTCCCACT	0.552
-	2	1585	RHGAP6_uc004c	NM_013427	NP_038286	O43182	RHG06_HUMAN		2	ACAGTCCTGTT	0.557
-	5	872	p.D177N|GEMIN8	NM_017856	NP_060326	Q9NWZ8	GEMI8_HUMAN		0	CAGGTCGTGGT	0.592
+	3	435	e_Mutation_p.G3	NM_001118885	NP_001112357	P23416	GLRA2_HUMAN	ellular (Probable).	2	GGTCTGGAAAA	0.418
+	3	507	e_Mutation_p.D5	NM_001118885	NP_001112357	P23416	GLRA2_HUMAN	ellular (Probable).	2	GATATGATGCA	0.378
-	3	1798	_p.E410K|RAI2_uc	NM_021785	NP_068557	Q9Y5P3	RAI2_HUMAN		2	CATCTCGGTAG	0.557
+	3	291	_p.G46D|PDHA1_	NM_000284	NP_000275	P08559	ODPA_HUMAN		1	AGAAGGCCCTC	0.458
-	2	100	1mjl.1_Missense_	NM_004586	NP_004577	P51812	KS6A3_HUMAN		8	CTCTCCCATAG	0.348
-	2	320	w.2_RNA|APOO_	NM_024122	NP_077027	Q9BUR5	APOO_HUMAN		0	TGGGAGGTGAG	0.413
-	4	1359		NM_030624	NP_085127	Q96M94	KLH15_HUMAN	Kelch 1.	2	AGCGTGGTACA	0.468
+	1	435		NM_001013736	NP_001013758	Q5HY64	FA47C_HUMAN		3	GAAGATATGCCT	0.572
+	40	7412	c.2_Missense_Mu	NM_001039590	NP_001034679	Q93008	USP9X_HUMAN		6	TTTTGGTGATC	0.333

-	24	2345	.P587S|CASK_uc	NM_003688	NP_003679	O14936	CSKP_HUMAN	ylate kinase-like.	6	ACGTGGAATAG	0.303	
-	7	794	dit.2_Missense_Mu	NM_006962	NP_008893	P17025	ZN182_HUMAN		3	AACAAGGTTTG	0.338	
-	10	1848	vq.1_Missense_M	NM_017677	NP_060147	Q96EF0	MTMR8_HUMAN		4	GACACGAGCCA	0.527	
+	2	1827	XO4_uc004dyt.1_	NM_005938	NP_005929	P98177	FOXO4_HUMAN		3	TCATGGATGAG	0.493	
+	8	1290	N1_uc011mpt.1_	NM_052957	NP_443189	Q96QF7	ACRC_HUMAN	sp/Ser-rich.	3	TCGGAAGCTCC	0.552	
-	1	939	mqj.1_Missense_	NM_021963	NP_068798	Q9ULW6	NP1L2_HUMAN	u-rich (acidic).	1	CATATTCATGTA	0.338	
-	1	525	1L2_uc011mqj.1_	NM_021963	NP_068798	Q9ULW6	NP1L2_HUMAN		1	TTCTTCCCCAA	0.592	
-	4	534	w.2_Missense_Mu	NM_183353	NP_899196	Q9NVW2	RNF12_HUMAN		2	TATTTTCATCTG	0.418	
-	3	1735		NM_001008537	NP_001008537	Q5QGS0	K2022_HUMAN		15	CCCCCCAGATG	0.468	
+	4	535	2_uc011mrh.1_5'	NM_001939	NP_001930	Q13474	DRP2_HUMAN		2	CTGGGGTTCCC	0.517	
+	5	1189	eib.1_Missense_	NM_016607	NP_057691	Q9UH62	ARMX3_HUMAN		2	CTCATCTGTGC	0.383	
-	4	498	se_Mutation_p.P	NM_022052	NP_071335	Q9H4D5	NXF3_HUMAN	RRM.	3	AACTGGGACGA	0.458	
-	38	3825	_Mutation_p.G121	NM_001847	NP_001838	Q14031	CO4A6_HUMAN	le-helical region.	8	GGAGACCAGCA	0.572	
-	11	793	msn.1_Splice_Sit	NM_001847	NP_001838	Q14031	CO4A6_HUMAN		8	TGTTTACCTTGA	0.398	
+	20	1421	_p.Q407*|COL4A	NM_033380	NP_203699	P29400	CO4A5_HUMAN	le-helical region.	4	GGGGTCAGAAA	0.527	
+	24	1862	p.P554S|COL4A5	NM_033380	NP_203699	P29400	CO4A5_HUMAN	le-helical region.	4	CTTTTCCAGGA	0.498	
-	13	2752	Y2F_uc011msq.1_	NM_001522	NP_001513	P51841	GUC2F_HUMAN	lasmic (Potential).	8	CATCCGAAGCA	0.353	rs145623152
-	11	3395		NM_012471	NP_036603	Q9UL62	TRPC5_HUMAN	lasmic (Potential).	1	TGACTTTCCTTG	0.453	
+	10	1573	splice|PLS3_uc01	NM_005032	NP_005023	P13797	PLST_HUMAN		2	AGAAGGTAACT	0.348	
-	4	1054	sv.2_Missense_M	NM_003588	NP_003579	Q13620	CUL4B_HUMAN		3	AATTTAGGCTTAT	0.313	
+	14	2383	e_Mutation_p.A69	NM_007325	NP_015564	P42263	GRIA3_HUMAN	ellular (Potential).	5	AATTGCTGTGT	0.408	
+	18	2663	p.M801I|SAGE1_	NM_018666	NP_061136	Q9NXZ1	SAGE1_HUMAN		3	TTAATGAAAGA	0.343	
-	12	2051	wc.1_Missense_	NM_024597	NP_078873	Q8IWC1	MA7D3_HUMAN		4	CCCATCTTTGA	0.418	
-	19	2351	n.1_Missense_Mu	NM_005369	NP_005360	P10911	MCF2_HUMAN		2	AGTTTCCCTAGA	0.408	
+	1	392		NM_001012989	NP_001013007	Q5JXB2	UE2NL_HUMAN		0	ATGATCCATTAG	0.443	
+	11	2350	.1_Missense_Mut	NM_002025	NP_002016	P51816	AFF2_HUMAN		5	TCAAAGGACAA	0.448	
+	3	1086	_Mutation_p.R298	NM_005363	NP_005354	P43360	MAGA6_HUMAN	MAGE.	0	GGACCTCGCATT	0.557	
-	3	1149		NM_005362	NP_005353	P43357	MAGA3_HUMAN		0	TCACTCTTCCC	0.572	
-	17	5851	.1_Missense_Mut	NM_000132	NP_000123	P00451	FA8_HUMAN	3.|Plastocyanin-like 6.	11	CAAATTCCTGTA	0.468	
-	14	2968		NM_000132	NP_000123	P00451	FA8_HUMAN	B.	11	GACTATCATAATG	0.378	
+	4	857		NM_017655	NP_060125	Q8TF65	GIPC2_HUMAN		1	GAAGGGCAACA	0.398	
+	1	301		NM_006536	NP_006527	Q9UQC9	CLCA2_HUMAN	ellular (Potential).	3	ATTGCAATTAATC	0.418	
+	5	3341		NM_001080426	NP_001073895	Q5VZP5	DUS27_HUMAN		3	TGCATCTGGAC	0.507	
+	6	1019	p.P192L|CACNA1	NM_000721	NP_000712	Q15878	CAC1E_HUMAN	cellular (Potential).	6	CGGCCCCAATG	0.517	
-	1	869		NM_001001966	NP_001001966	Q8NHC5	O14AG_HUMAN	lasmic (Potential).	0	TTGTTTCTCAAA	0.393	
-	1	475		NM_001001966	NP_001001966	Q8NHC5	O14AG_HUMAN	ellular (Potential).	0	GCCAGCTGTGT	0.473	
+	7	1156		NM_052997	NP_443723	Q9BXX3	AN30A_HUMAN		9	CGTGGGCAGCA	0.408	
-	2	1239	nj.2_Missense_M	NM_005674	NP_005665	Q16600	ZN239_HUMAN		0	ATATGGATGAC	0.438	
-	4	658		NM_001031746	NP_001026916	Q8IW00	CJ072_HUMAN	lasmic (Potential).	0	CTCTGGATTTC	0.517	
+	1	838		NM_001001916	NP_001001916	Q8NH60	O52J3_HUMAN	Name=7; (Potential).	3	GCCAATCTCTAT	0.393	rs138334057
-	6	682	22_uc001mpa.2_	NM_173588	NP_775859	Q8N9C0	IGS22_HUMAN	Lys-rich.	7	AAGTCCATTTT	0.517	
+	1	306		NM_001004703	NP_001004703	A6NHA9	O4C46_HUMAN	ellular (Potential).	1	GGAGAACATTT	0.463	
-	1	1081		NM_207374	NP_997257	Q8NGF6	O10W1_HUMAN	lasmic (Potential).	1	GGCCCGGTGGC	0.582	
+	6	1233	nwu.3_RNA|SLC2	NM_001039752	NP_001034841	Q63ZE4	S22AA_HUMAN	ellular (Potential).	2	GTTCCGCAACC	0.398	
+	7	1025		NM_207345	NP_997228	Q6UXN8	CLC9A_HUMAN	(Potential).|C-type lectin.	1	CCAGTCAAGAG	0.378	
-	4	942	B4_uc001qzf.1_In	NM_006249	NP_006240	Q04118	PRB3_HUMAN	Pro-rich.	1	GGGAGGTCTGT	0.537	
-	3	252		NM_006248	NP_006239				0	AGGAGGTGGGG	0.607	

+	1	236		NM_001004063	NP_001004063	Q8NGD4	OR4K1_HUMAN	Name=2; (Potential).	3	CACCCCCAAGA	0.398	
-	14	1683	gu.1_Missense_M	NM_024580	NP_078856	Q7Z2Z2	ETUD1_HUMAN		1	GCAATAAAAGACT	0.433	rs142283736
-	13	4054	yn.1_Missense_M	NM_001134407	NP_001127879	Q12879	NMDE1_HUMAN	lasmic (Potential).	45	GGGTTCCGGTTC	0.537	
+	1	225	PIRE2_uc010ciw.1	NM_032451	NP_115827	Q8WWL2	SPIR2_HUMAN	KIND.	1	CCGGCGCCTGC	0.483	
+	48	7584		NM_020877	NP_065928	Q9P225	DYH2_HUMAN	3 (By similarity).	13	CTCTAGGAAATG	0.597	
+	6	754		NM_001145127	NP_001138599	A8MZ36	EVPLL_HUMAN		0	CCAATACCGAGA	0.682	
+	5	445	CA_uc002iqj.2_M	NM_000023	NP_000014	Q16586	SGCA_HUMAN	ellular (Potential).	2	AAGCCGAGTTC	0.677	
+	1	977	uc010wna.1_RNA	NM_032559	NP_115948	Q8N4N8	KIF2B_HUMAN	inesin-motor.	8	CAAAGCCTCCA	0.557	
-	5	1201	.Q156H|CXXC1_u	NM_014593	NP_055408	Q9P0U4	CXXC1_HUMAN		2	ctgctgctgctggtgatg	0.468	
-	4	803	ntq.2_Missense_M	NM_145276	NP_660319	Q8TA94	ZN563_HUMAN	ype 2; degenerate.	0	GCACTACCATGT	0.423	
-	3	307	ILRA3_uc010erk.2	NM_006865	NP_006856	Q8N6C8	LIRA3_HUMAN	like C2-type p.G81G(1)	1	AACTGGCCCTTC	0.542	
+	4	403	p.2_RNA|SNTG2_	NM_018968	NP_061841	Q9NY99	SNTG2_HUMAN	PDZ.	3	AGGTTCTGAGC	0.393	
-	3	266	_p.E52K|REG1B_	NM_006507	NP_006498	P48304	REG1B_HUMAN	-type lectin.	2	GGTCTTCATTAA	0.532	
-	27	4708		NM_004525	NP_004516	P98164	LRP2_HUMAN	B 10.|Extracellular (Poten	29	TTCTGTCCGTTC	0.438	
-	225	45447	_uc010zfi.1_Misse	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	TCACCCGAAGTT	0.483	
-	2	356		NM_020760	NP_065811	Q9P2P5	HECW2_HUMAN		18	TGGAGCGGCTC	0.582	
-	4	999	uf.1_Missense_Mu	NM_003098	NP_003089	Q13424	SNTA1_HUMAN	PH 1.	1	TTGACCATCTG	0.597	
+	6	949	H26_uc010zzy.1_	NM_177980	NP_817089	Q8IXH8	CAD26_HUMAN	|Extracellular (Potential).	4	AAAGTGGTTTC	0.358	
+	18	2574	N_uc003ajn.1_Mis	NM_006932	NP_008863	P53814	SMTN_HUMAN		3	GCGCAGCCGTG	0.662	
-	13	2147	vw.2_Missense_M	NM_001001331	NP_001001331	Q01814	AT2B2_HUMAN	lasmic (Potential).	6	GCACTCCGTCT	0.642	
+	9	3930	6A6_uc003eni.3_5	NM_001102608	NP_001096078	A6NMZ7	CO6A6_HUMAN	.|Nonhelical region.	8	TGGTCCTTTTATT	0.333	
-	8	1822	GC1A_uc011bxp.	NM_013261	NP_037393	Q9UBK2	PRGC1_HUMAN	Arg/Ser-rich.	8	TGAACGAGAGC	0.453	
+	16	2807	cl.1_Nonsense_Mu	NM_005509	NP_005500	Q9Y485	DMXL1_HUMAN	WD 7.	2	GCACTCAAGACA	0.348	
+	1	960	.2_Intron|PCDHA6	NM_018903	NP_061726	Q9UN75	PCDAC_HUMAN	|Extracellular (Potential).	0	AAATTTCCTATG	0.368	
+	2	258		NM_005546	NP_005537	Q08881	ITK_HUMAN	PH.	26	TCTCCCGAATCA	0.458	
-	1	728		NM_033057	NP_149046	Q9GZK3	OR2B2_HUMAN	Name=6; (Potential).	0	GATGGGAGCCA	0.468	
+	58	8231	f125_uc003oez.1_	NM_002224	NP_002215	Q14573	ITPR3_HUMAN	lasmic (Potential).	19	TAGCCGCTGAG	0.612	
+	41	10444	_p.E3030*|AKAP9_	NM_005751	NP_005742	Q99996	AKAP9_HUMAN	Potential.	26	TGCATGAGCTC	0.443	
-	15	1860		NM_004333	NP_004324	P15056	BRAF_HUMAN	rotein kinas_R603>I(2)|p.T	18290	GATTTCACTGTA	0.368	
-	2	229		NM_001103176	NP_001096646	Q3B7I2	CNPY1_HUMAN		0	TTGGTATATTTTG	0.388	
-	13	1198	ek.2_Intron|EBF2	NM_022659	NP_073150	Q9HAK2	COE2_HUMAN		4	CGGCTCGCTTC	0.488	
-	5	1165	e_Mutation_p.G24	NM_014682	NP_055497	O60284	ST18_HUMAN		5	TTCCCCTGCTA	0.433	
+	32	4196	yoz.2_Missense_	NM_021110	NP_066933	Q05707	COEA1_HUMAN	ion (NC4).|TSP N-terminal.	12	TTAAATAAAAATT	0.393	
-	38	8675	ty.2_Missense_Mu	NM_153366	NP_699197	Q4LDE5	SVEP1_HUMAN	Sushi 23.	7	GACTGGATTTG	0.473	
-	7	8075		NM_015419	NP_056234	Q9NR99	MXRA5_HUMAN	like C2-type 11.	8	CTTGTTTGCTTC	0.637	
+	4	857		NM_017655	NP_060125	Q8TF65	GIPC2_HUMAN		1	GAAGGGCAACA	0.398	
+	1	301		NM_006536	NP_006527	Q9UQC9	CLCA2_HUMAN	ellular (Potential).	3	ATTGCAATTAATC	0.418	
-	9	502	25_splice|HORMA	NM_032132	NP_115508	Q86X24	HORM1_HUMAN		3	TTTTTACTAGAAG	0.308	
+	5	3341		NM_001080426	NP_001073895	Q5VZP5	DUS27_HUMAN		3	TGCATCTGGAC	0.507	
+	6	1019	_p.P192L|CACNA1	NM_000721	NP_000712	Q15878	CAC1E_HUMAN	cellular (Potential).	6	CGGCCCCAATG	0.517	
-	1	869		NM_001001966	NP_001001966	Q8NHC5	O14AG_HUMAN	lasmic (Potential).	0	TTGTTTCTCAAA	0.393	
-	1	475		NM_001001966	NP_001001966	Q8NHC5	O14AG_HUMAN	ellular (Potential).	0	GCCAGCTGTGT	0.473	
-	2	1239	nj.2_Missense_Mu	NM_005674	NP_005665	Q16600	ZN239_HUMAN		0	ATATGGATGAC	0.438	
-	4	658		NM_001031746	NP_001026916	Q8IW00	CJ072_HUMAN	lasmic (Potential).	0	CTCTGGATTTC	0.517	
+	2	273	_p.Q11*|BUB3_uc	NM_004725	NP_004716	O43684	BUB3_HUMAN	WD 1.	1	TGAACCAGCCA	0.627	
+	1	838		NM_001001916	NP_001001916	Q8NH60	O52J3_HUMAN	Name=7; (Potential).	3	GCCAATCTCTATT	0.393	rs138334057
-	6	682	22_uc001mpa.2_	NM_173588	NP_775859	Q8N9C0	IGS22_HUMAN	Lys-rich.	7	AAGTCCATTTT	0.517	

+	1	306		NM_001004703	NP_001004703	A6NHA9	O4C46_HUMAN	ellular (Potential).	1	GGAGAACATTT	0.463	
-	1	1081		NM_207374	NP_997257	Q8NGF6	O10W1_HUMAN	lasmic (Potential).	1	GGCCCGGTGGC	0.582	
+	7	1025		NM_207345	NP_997228	Q6UXN8	CLC9A_HUMAN	(Potential).|C-type lectin.	1	CCAGTCAAGAG	0.378	
+	25	2347	_Mutation_p.A756	NM_017901	NP_060371	Q9ULQ1	TPC1_HUMAN	S6 of repeat II; (Potential).	3	ATTGTCGCCTTT	0.597	
-	46	5946	.E1483K|CIT_uc0	NM_007174	NP_009105	O14578	CTRO_HUMAN		10	CAGCTCGGTCC	0.731	
+	38	3852	TC1_uc010taf.1_In	NM_014708	NP_055523	P50748	KNTC1_HUMAN		10	ATATCCCTTGG	0.204	
+	1	236		NM_001004063	NP_001004063	Q8NGD4	OR4K1_HUMAN	Name=2; (Potential).	3	CACCCCCAAGA	0.398	
-	2	600		NM_003814	NP_003805	O43506	ADA20_HUMAN		1	CTGTCCCCCAA	0.517	
-	22	8319	_Mutation_p.A270	NM_001009944	NP_001009944	P98161	PKD1_HUMAN	ular (Potential).|REJ.	3	GCCCGCGGTG	0.687	
-	13	4054	yn.1_Missense_M	NM_001134407	NP_001127879	Q12879	NMDE1_HUMAN	lasmic (Potential).	45	GGTTCCGGTTC	0.537	
+	48	7584		NM_020877	NP_065928	Q9P225	DYH2_HUMAN	3 (By similarity).	13	TCTAGGAAATG	0.597	
+	6	754		NM_001145127	NP_001138599	A8MZ36	EVPLL_HUMAN		0	CAATACCGAGA	0.682	
+	5	445	CA_uc002iqj.2_M	NM_000023	NP_000014	Q16586	SGCA_HUMAN	ellular (Potential).	2	AAGCCGAGTTC	0.677	
-	4	803	ntq.2_Missense_M	NM_145276	NP_660319	Q8TA94	ZN563_HUMAN	ype 2; degenerate.	0	CACTACCATGT	0.423	
+	4	1415	po.1_Intron|ZNF5	NM_001143939	NP_001137411	Q76KX8	ZN534_HUMAN	2H2-type 10.	0	CCTTACGAATGT	0.433	
-	3	307	ILRA3_uc010erk.2	NM_006865	NP_006856	Q8N6C8	LIRA3_HUMAN	like C2-type p.G81G(1)	1	ACTGGCCCTTC	0.542	
+	4	403	p.2_RNA|SNTG2_	NM_018968	NP_061841	Q9NY99	SNTG2_HUMAN	PDZ.	3	AGGTTCTGAGC	0.393	
-	225	45447	_uc010zfi.1_Misse	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	TCACCCGAAGTT	0.483	
-	10	1100	p.H236R|CSNK2A	NM_177559	NP_808227	P68400	CSK21_HUMAN	rotein kinase.	1	TGTCATGTCCAT	0.373	rs61730060
+	2	61	tj.1_RNA|FRG1B_uc010gdr.1_RNA|FRG1B_uc010ztk.1_Intron						0	CAGAATCGCCC	0.353	rs143761036
+	6	949	H26_uc010zzy.1_	NM_177980	NP_817089	Q8IXH8	CAD26_HUMAN	|Extracellular (Potential).	4	AAAGTGGTTTC	0.358	
+	1	299	.1_Intron|C21orf29	NM_198697	NP_941970	P60328	KR123_HUMAN	A approximate repeats.	1	TGCCCTCTGCA	0.617	
-	13	2147	vw.2_Missense_M	NM_001001331	NP_001001331	Q01814	AT2B2_HUMAN	lasmic (Potential).	6	GCACTCCGTCT	0.642	
-	1	666_667	pv.1_Missense_M	NM_198407	NP_940799	Q92847	GHSR_HUMAN	Name=5; (Potential).	5	GGAAGGAAGA	0.629	
+	21	3297		NM_006218	NP_006209	P42336	PK3CA_HUMAN	PI3K/PI4K. 2)|p.H1047Y(	3553	TGCACATCATG	0.378	rs121913279
-	16	2401	74_splice|ABCC5_	NM_005688	NP_005679	O15440	MRP5_HUMAN		4	AGGTACTGAAG	0.338	
-	8	1822	GC1A_uc011bxp.	NM_013261	NP_037393	Q9UBK2	PRGC1_HUMAN	Arg/Ser-rich.	8	TGAACGAGAGC	0.453	
-	12	1842	p.E468V|FSTL5_	NM_020116	NP_064501	Q8N475	FSTL5_HUMAN		8	TCACATTCTATGG	0.328	
+	11	2236		NM_020227	NP_064612	Q9NQV7	PRDM9_HUMAN	2H2-type 7.	6	GAGGACACACA	0.602	rs111488757
+	16	2807	cl.1_Nonsense_M	NM_005509	NP_005500	Q9Y485	DMXL1_HUMAN	WD 7.	2	GCACTCAAGAC	0.348	
+	1	960	.2_Intron|PCDHA6	NM_018903	NP_061726	Q9UN75	PCDAC_HUMAN	|Extracellular (Potential).	0	AAATTTCCTATG	0.368	
+	2	258		NM_005546	NP_005537	Q08881	ITK_HUMAN	PH.	26	TCTCCCGAATCA	0.458	
-	1	728		NM_033057	NP_149046	Q9GZK3	OR2B2_HUMAN	Name=6; (Potential).	0	GATGGGAGCCA	0.468	
-	1	18		NM_030903	NP_112165	Q9Y3N9	OR2W1_HUMAN	ellular (Potential).	3	AGAACTATAATTG	0.284	
+	5	704	55_splice|SYNGA	NM_006772	NP_006763	Q96PV0	SYGP1_HUMAN		4	GACCGGTACAG	0.517	
+	41	10444	p.E3030*|AKAP9_	NM_005751	NP_005742	Q99996	AKAP9_HUMAN	Potential.	26	TGCATGAGCTC	0.443	
-	15	1860		NM_004333	NP_004324	P15056	BRAF_HUMAN	rotein kinas_R603>I(2)|p.T	18290	ATTTCACTGTA	0.368	
+	6	397	p.R107*|SSBP1_	NM_003143	NP_003134	Q04837	SSBP_HUMAN	SSB.	1	GGTCTCGAATT	0.338	
-	2	229		NM_001103176	NP_001096646	Q3B7I2	CNPY1_HUMAN		0	TTGGTATATTTTG	0.388	
-	13	1198	ek.2_Intron|EBF2_	NM_022659	NP_073150	Q9HAK2	COE2_HUMAN		4	CGGCTCGCTTC	0.488	
-	11	1289		NM_000637	NP_000628	P00390	GSHR_HUMAN		5	CCTTATATTCAAA	0.388	
-	5	1165	e_Mutation_p.G24	NM_014682	NP_055497	O60284	ST18_HUMAN		5	TTCCCCTGCTA	0.433	
+	32	4196	yoz.2_Missense_	NM_021110	NP_066933	Q05707	COEA1_HUMAN	ion (NC4).|TSP N-terminal.	12	TTAAATAAAAATT	0.393	
-	12	1815		NM_001100878	NP_001094348	A6NGR9	CH073_HUMAN		1	GTATCGCTGAA	0.657	
-	38	8675	ty.2_Missense_M	NM_153366	NP_699197	Q4LDE5	SVEP1_HUMAN	Sushi 23.	7	GACTGGATTTG	0.473	
-	2	143	_5'Flank|COQ4_	NM_015679	NP_056494	O95900	TRUB2_HUMAN		1	GGAGCGGGAG	0.368	
-	7	8075		NM_015419	NP_056234	Q9NR99	MXRA5_HUMAN	ike C2-type 11.	8	CTTGTTTGCTT	0.637	

-	1	654	p.R191W|FAM120	NM_017848	NP_060318	Q9NX05	F120C_HUMAN			2	CTGCCGCTCGG	0.716	
-	37	2875	_p.P666L|COL16A	NM_001856	NP_001847	Q07092	COGA1_HUMAN	5 (COL5) with 3 imperfect		8	CAGGAGGTCCC	0.577	
+	3	511	bz.2_Missense_M	NM_203464	NP_982289	P27144	KAD4_HUMAN			0	CCTTGATGGTGA	0.448	
+	16	3063	12RB2_uc010oql.1	NM_001559	NP_001550	Q99665	I12R2_HUMAN	lasmic (Potential).		3	ATGACCTCCCC	0.567	rs17838066
+	3	542	l.1_Missense_Mut	NM_000642	NP_000633	P35573	GDE_HUMAN	-glucanotransferase.		3	GTGTATACAAATT	0.363	
-	5	1002	se_Mutation_p.E1	NM_030920	NP_112182	Q9BTT0	AN32E_HUMAN	-rich (highly acidic).		0	CTCCCTCTCCC	0.308	
-	4	587	L|GBA_uc001fjk.	NM_000157	NP_000148	P04062	GLCM_HUMAN			2	AAGTACGATTTA	0.383	
-	43	6503		NM_003292	NP_003283	P12270	TPR_HUMAN			7	GTGCTCGAGGG	0.512	
-	2	441	ot.1_Missense_M	NM_199051	NP_950252	Q76B58	FAM5C_HUMAN			5	CTAAATCCCTGC	0.448	
+	6	2111	b.1_Missense_Mu	NM_201253	NP_957705	P82279	CRUM1_HUMAN	Potential).|Laminin G-like 1.		9	ACATCTCGTCTG	0.448	
-	16	1772	KCQ_uc009xin.1_	NM_006257	NP_006248	Q04759	KPCT_HUMAN	rotein kinase.		6	GAACCCCGAAG	0.507	
-	8	2371	.2_Missense_Mut	NM_080599	NP_542166	Q9HAU5	RENT2_HUMAN	MIF4G 2.		3	AGACATGCAGG	0.338	
+	19	2792	1jrg.2_Missense_	NM_080722	NP_542453	Q8WXS8	ATS14_HUMAN	TSP type-1 3.		6	GACACGGGGGA	0.667	
-	2	1178	p.P369S|ITPRIP_	NM_033397	NP_203755	Q8IWB1	IPRI_HUMAN			0	AGAGGGCTCCC	0.567	
-	2	189	.S30P|RIC8A_uc0	NM_001098787	NP_001092257	Q9NYM9	BET1L_HUMAN	l).|t-SNARE coiled-coil ho		0	TTTGGAGGCCA	0.587	
+	1	29		NM_001003443	NP_001003443	Q8NH54	O56A3_HUMAN	cellular (Potential).		0	CCTCTCCACTG	0.453	
+	27	3091	n.1_Missense_Mu	NM_024662	NP_078938	Q9H0A0	NAT10_HUMAN	ion to the nucleolus and mi		2	CACAAGAAGGA	0.478	
-	8	1704	n_p.T362I|SLC1A	NM_004171	NP_004162	P43004	EAA2_HUMAN		p.T371fs*13(1)	3	GAAAGGTGACA	0.453	
+	1	343		NM_001001967	NP_001001967	Q8NGL4	OR5DD_HUMAN	Name=3; (Potential).		3	GAAACTTTCATG	0.418	
+	1	278		NM_001004730	NP_001004730	Q8NGP9	O5AR1_HUMAN	cellular (Potential).		0	TTATCTCCTTCTC	0.488	
+	9	2029	_p.E613_splice|T	NM_178031	NP_821174	Q24JP5	T132A_HUMAN			1	TGAGGTAAGCA	0.662	
-	5	7393_7394	AK_uc001ntk.1_I	NM_001620	NP_001611	Q09666	AHNK_HUMAN			19	CATTTGGGCCTT	0.465	
+	7	1034	A2_uc010rod.1_M	NM_002689	NP_002680	Q14181	DPOA2_HUMAN			0	GCGAACTCAAGG	0.358	
+	6	676	_p.P106S|FRMD8_	NM_031904	NP_114110	Q9BZ67	FRMD8_HUMAN	FERM.		2	GGTACCCGTGC	0.706	
+	1	488		NM_021046	NP_066384	O75690	KRA58_HUMAN	repeats of C-C-X-P.		0	CCTGCTGCTGC	0.602	
+	14	2615	uc001pen.1_Intro	NM_001098672	NP_001092142	Q6MZM0	HPHL1_HUMAN	e 5.|Extracellular (Potential		3	AGGTGGGCAAC	0.438	
+	6	481	.I126V|TTC12_uc	NM_017868	NP_060338	Q9H892	TTC12_HUMAN	TPR 1.		4	ACAGCTATCCTG	0.473	
+	1	843		NM_001007249	NP_001007250	Q15614	OR8G2_HUMAN			0	TCCATGGACCA	0.473	
-	13	1789	se_Mutation_p.R4	NM_003044	NP_003035	P48065	S6A12_HUMAN			1	CTTCCGGAGCT	0.647	
+	15	2300	1qik.1_Missense_	NM_173593	NP_775864	Q6L9W6	B4GN3_HUMAN	enal (Potential).		2	GAATACCCGGG	0.642	
-	53	7882	g.1_Missense_Mu	NM_002223	NP_002214	Q14571	ITPR2_HUMAN	cellular (Pote	p.V2489G(1)	14	CAGCACGGTGA	0.413	
+	20	2516	lt.2_Missense_Mu	NM_173602	NP_775873	Q9P265	DIP2B_HUMAN			6	TGTTGGGGATG	0.373	
+	30	5820	b.1_Missense_Mu	NM_014903	NP_055718	Q8IVL0	NAV3_HUMAN	Ser-rich.		17	TCATTAGGACTT	0.483	
+	7	1001		NM_198520	NP_940922	Q6ZTY8	CL063_HUMAN			7	AAAAATCCAAAT	0.423	
+	12	1856	ztx.2_Missense_	NM_139319	NP_647480	Q8NDX2	VGLU3_HUMAN	lasmic (Potential).		3	GAGAATCTCTCT	0.468	
-	2	320	1L2_uc009zup.2_	NM_001034173	NP_001029345	Q3SY69	AL1L2_HUMAN	GART.		1	CTCACCCAGAG	0.403	
+	1	13	001ufm.2_5'Flank|	NM_001516	NP_001507	Q13889	TF2H3_HUMAN			0	CTGAGGTGCTG	0.662	
+	29	5893	.V1952A|EP400_u	NM_015409	NP_056224	Q96L91	EP400_HUMAN	case C-terminal.		12	CCGTCGTGTTTT	0.493	
+	7	1325	O7_uc010thw.1_	NM_015842	NP_056667	Q8WWI1	LMO7_HUMAN			5	CATACCAAAATT	0.463	
-	1	1		NM_004196	NP_004187	Q00532	CDKL1_HUMAN			2	gctccatgggaactga	0.114	
-	10	2638		NM_024734	NP_079010	Q96JQ2	CLMN_HUMAN			0	TTTGGGGATTCC	0.443	
-	4	2014	gb.2_Missense_M	NM_138576	NP_612808	Q9C0K0	BC11B_HUMAN	Gly-rich.		10	CTTggccgcgccgcc	0.567	
-	14	1690	_Mutation_p.E23	NM_001012420	NP_001012420					0	CCCCCTCACTG	0.612	
-	7	897		NM_052955	NP_443187	Q96PF1	TGM7_HUMAN			2	AACACGGGTTG	0.413	
+	16	2410	|IQCH_uc002aqp.	NM_001031715	NP_001026885	Q86VS3	IQCH_HUMAN			4	TACCACCGTGC	0.507	
-	2	207		NM_001038640	NP_001033729	Q9NYA3	GOG6A_HUMAN	Potential.		0	TTGTCTCAGGGC	0.493	
+	3	356_357	REB2_uc002bdq.2	NM_004136	NP_004127	P48200	IREB2_HUMAN			0	TTATGAACATTTT	0.376	

-	26	3925	p.P1168S|RASGR	NM_002891	NP_002882	Q13972	RGRF1_HUMAN	Ras-GEF.	6	GGGTGGGTCAC	0.493	
+	21	3357	b.1_RNA|LRRK1_	NM_024652	NP_078928	Q38SD2	LRRK1_HUMAN		12	CAACACCATTC	0.557	
+	2	873	KN1_uc002chs.1_	NM_053284	NP_444514	Q96NZ8	WFKN1_HUMAN	-like C2-type.	0	TCAGCGGCCGC	0.677	
+	7	970	ua.2_Missense_M	NM_001042428	NP_001035893	O95201	ZN205_HUMAN		0	GCGTCCCGGAG	0.706	
-	3	447	T125I|RSL1D1_uc	NM_015659	NP_056474	O76021	RL1D1_HUMAN		0	AAACGGTTTTA	0.323	
-	12	2844		NM_022166	NP_071449	Q86Y38	XYLT1_HUMAN	enal (Potential).	4	TGGCACAGATG	0.667	
-	51	8231	bd.1_Missense_M	NM_017539	NP_060009	Q8TD57	DYH3_HUMAN	k (By similarity).	18	CAGCAACATTG	0.388	
+	3	544	efx.2_Missense_	NM_182922	NP_891552	Q7Z4Q2	HEAT3_HUMAN		2	CTCTGGTTGCG	0.378	
-	2	134	.1_5'UTR|SALL1_	NM_002968	NP_002959	Q9NSC2	SALL1_HUMAN		8	AGGGCGACTCG	0.448	
+	10	1139	ejc.2_Missense_M	NM_018233	NP_060703	Q8N543	OGFD1_HUMAN		1	CATGAAGTTATTT	0.423	
-	14	1993		NM_031885	NP_114091	Q9BXC9	BBS2_HUMAN		1	GACAGGAAAAT	0.368	
-	5	1286		NM_152342	NP_689555	Q8N8U2	CDYL2_HUMAN		1	AGGAGGAGCAG	0.632	
-	9	1393	fnc.1_Missense_	NM_013275	NP_037407	Q6UB99	ANR11_HUMAN		6	AACTGGAAGGT	0.577	
+	3	996	rf97_uc010vpz.1_	NM_001013672	NP_001013694	Q6ZQX7	CQ097_HUMAN	tandem repeat of A-L-K-G	1	CCACACTGACC	0.687	
-	1	532	X1_uc010ckm.1_5	NM_002558	NP_002549	P51575	P2RX1_HUMAN	Name=1; (Potential).	2	AGATAACGCCCA	0.657	
-	3	281		NM_031898	NP_114104	Q9BXF9	TEKT3_HUMAN		2	GTAGCTTGAGG	0.517	
-	2	171	se_Mutation_p.A3	NM_001042685	NP_001036150	Q3B8N2	LEG9B_HUMAN	Galectin 1.	1	AACGGCCCCAT	0.562	rs144269928
-	7	1670	_p.D357N|GHDC_	NM_032484	NP_115873	Q8N2G8	GHDC_HUMAN		0	AATATCTTCCCC	0.637	
-	5	318	10woz.1_RNA|uc010wpa.1_5'Flank						0	CCCGCCGAATT	0.562	
-	2	894		NM_003955	NP_003946	O14543	SOCS3_HUMAN		1	GGGGGACTCC	0.657	
-	12	1540		NM_006796	NP_006787	Q9Y4W6	AFG32_HUMAN		0	TGGTCCTTTAG	0.398	
-	5	620	nse_Mutation_p.S	NM_194281	NP_919257	Q6PI98	IN80C_HUMAN		0	ATGTAGGAAAAC	0.567	
+	17	3091	.1_Intron|DCC_uc	NM_005215	NP_005206	P43146	DCC_HUMAN	ellular (Potential).	17	CCCCACCTCGG	0.443	
+	9	1105	F11A_uc010dpv.2	NM_003839	NP_003830	Q9Y6Q6	TNR11_HUMAN	lasmic (Potential).	3	CCAGCCCACAG	0.532	
+	3	587	1G2_uc010dsu.2_	NM_001319	NP_001310	P78368	KC1G2_HUMAN		1	AGGCCGGCGGG	0.642	
-	9	1255	.R333W|DPP9_u	NM_139159	NP_631898	Q86TI2	DPP9_HUMAN		1	GTACCGATACG	0.622	
-	1	247		NM_001005191	NP_001005191	Q8NG98	OR7D4_HUMAN	ellular (Potential).	4	TGCTCACTAGCA	0.498	
-	4	545	_p.P35S|ILVBL_u	NM_006844	NP_006835	A1L0T0	ILVBL_HUMAN		2	GATTGGGGACT	0.642	
-	6	2332		NM_001080409	NP_001073878				2	CACATTCTTCAC	0.383	
+	2	714	oid.2_Missense_M	NM_004823	NP_004814	Q9Y257	KCNK6_HUMAN		1	AGCTTCTTGGAT	0.632	
-	8	4287		NM_003890	NP_003881	Q9Y6R7	FCGBP_HUMAN	VWFD 3.	9	GCAGGGAGAGT	0.627	
-	3	807	e_Site_p.P115_sp	NM_182707	NP_874366	Q9UQ74	PSG8_HUMAN		0	TACTCACGGAG	0.527	
+	2	211		NM_019612	NP_062558	Q6NXR0	IIGP5_HUMAN		3	CCAAGGAAAGG	0.642	
-	3	407	e_Mutation_p.P11	NM_007254	NP_009185	Q96T60	PNKP_HUMAN		2	AGGCGGAGTAT	0.592	
+	3	368	hn.1_Intron|KIR3	NM_006737	NP_006728	P43630	KI3L2_HUMAN	ellular (Potential).	2	CAACCCCCTGG	0.607	
-	7	2373		NM_176810	NP_789780	Q86W25	NAL13_HUMAN	LRR 2.	9	TCAGCTTGCTG	0.498	
-	7	1521		NM_017880	NP_060350	Q9NWW7	CB042_HUMAN		0	GCAGGGCATCA	0.418	
-	13	2089	of.1_Missense_M	NM_000122	NP_000113	P19447	ERCC3_HUMAN	case C-terminal.	7	TGTCCTGGGAT	0.423	
-	28	5629	nl.1_Missense_M	NM_018557	NP_061027	Q9NZR2	LRP1B_HUMAN	ellular (Potential).	50	ACAGGCAGCAC	0.408	
-	8	946	cl.1_Missense_M	NM_004288	NP_004279	O60759	CYTIP_HUMAN	Ser-rich.	3	AAAATCATCCC	0.532	
-	5	587	_p.T83N|ACVR1_	NM_001111067	NP_001104537	Q04771	ACVR1_HUMAN	ellular (Potential).	3	GCGGGGTCTTA	0.567	
-	245	50577	80N|TTN_uc010z	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	AGGTATCACCTT	0.418	
+	25	2848	_p.S472F|AOX1_u	NM_001159	NP_001150	Q06278	ADO_HUMAN		6	TTCCATCCAACA	0.498	
-	8	3364	p.E420K|COL6A3_	NM_004369	NP_004360	P12111	CO6A3_HUMAN	nhelical region.	18	CTTTTCACCTG	0.438	
+	18	2112	orf26_uc002wrw.2	NM_015585	NP_056400	Q8NHU2	CT026_HUMAN		4	GAATTTCCTTCC	0.333	
+	8	769		NM_020884	NP_065935	A7E2Y1	MYH7B_HUMAN	l-like.|ATP (By similarity).	2	GTAAGACGGTTA	0.602	
+	1	743	AS_uc002xzu.3_5	NM_016592	NP_057676	P63092	GNAS2_HUMAN		292	ACTTCGAGACC	0.642	

+	3	1040	4A1_uc002ydc.1_	NM_016354	NP_057438	Q96BD0	SO4A1_HUMAN	Name=5; (Potential).	1	CTGCCGGCTAC	0.677	
-	2	485	B46_uc002ygu.2_	NM_025224	NP_079500	Q86UZ6	ZBT46_HUMAN	BTB.	2	GCGCCAGGTGC	0.617	
+	8	1125	f.2_Missense_Mu	NM_005239	NP_005230	P15036	ETS2_HUMAN		4	TTCCTTCCTTCG	0.552	
+	1	97	.1_Intron|C21orf29	NM_198692	NP_941965	P60412	KR10B_HUMAN		1	CCTGGCAGGTG	0.642	
+	4	2223	H_uc003afp.2_5'	NM_021076	NP_066554	P12036	NFH_HUMAN	S-P-[AEPV]-[EAK]- [AEVK]	0	CAAAGTCCCCT	0.552	
+	4	2440	3afp.2_Translatio	NM_021076	NP_066554	P12036	NFH_HUMAN	S-P-[AEPV]-[EAK]- [AEVK]	0	TGTCAAGGAGG	0.532	
-	6	762	184B_uc003avh.	NM_012264	NP_036396	Q9Y519	T184B_HUMAN	ical; (Potential).	0	ACAGAACTGCA	0.612	
+	4	855	LA3_uc010gzm.1_	NM_025225	NP_079501	Q9NST1	PLPL3_HUMAN	enal (Potential).	0	TTGTCCCCCCG	0.547	
-	14	2026	se_Mutation_p.G5	NM_001145137	NP_001138609	Q92523	CPT1B_HUMAN	lasmic (Potential).	2	GGACCCCTCCA	0.612	
-	2	2548	_Mutation_p.R77	NM_194293	NP_919269	Q702N8	XIRP1_HUMAN		8	GAGTCCGCAGG	0.632	rs144904530
-	110	8130		NM_000094	NP_000085	Q02388	CO7A1_HUMAN	le-helical region.	11	GGAAGCCCCCA	0.602	
-	5	481		NM_138805	NP_620160	Q96BQ1	FAM3D_HUMAN		0	GGCTGGGCAGG	0.527	
-	7	975	M86D_uc003dpq.	NR_024241					0	CAGCTGGCACG	0.652	
+	1	160		NM_054106	NP_473447	Q9NZP5	O5AC2_HUMAN	lasmic (Potential).	1	GGAACGACCCC	0.448	
+	1	214		NM_001005479	NP_001005479	Q8NGV6	OR5H6_HUMAN	Name=2; (Potential).	3	CACCTTCATATC	0.423	
-	16	5611	d.2_Missense_Mu	NM_199420	NP_955452	O75417	DPOLQ_HUMAN		11	CATCAATTATGG	0.398	
-	10	1217	q.2_Missense_M	NM_053025	NP_444253	Q15746	MYLK_HUMAN		9	GCTGGCTGTTT	0.617	
+	3	605		NM_015720	NP_056535	Q9NZ53	PDXL2_HUMAN	ar (Potential).|Glu-rich.	2	TGAATGGATCCC	0.348	
-	3	2319	tron|ABCA11P_uc	NM_133474	NP_597731	D9N162	D9N162_HUMAN		1	AAAGGATTGCG	0.403	
-	3	2300	ron|ABCA11P_uc	NM_133474	NP_597731	D9N162	D9N162_HUMAN		1	TAAAGGCTTTGC	0.408	
-	6	1721		NM_177998	NP_819056	Q7RTM1	OTOP1_HUMAN	ical; (Potential).	3	GACAGCCAAAG	0.512	
-	2	288		NM_173536	NP_775807	Q8N1C3	GBRG1_HUMAN	ellular (Probable).	2	TTAAATCCTCAT	0.328	
-	7	979	A_uc011ceg.1_Mi	NM_000667	NP_000658	P07327	ADH1A_HUMAN		2	TTCATTGAGAGG	0.463	
-	14	2197	n.1_Missense_Mu	NM_001039580	NP_001034669	Q49MG5	MAP9_HUMAN		2	CACTTTTGCGA	0.348	
-	8	1073		NM_006598	NP_006589	Q9Y666	S12A7_HUMAN		4	GCGCGGAGGTG	0.657	
-	12	2472	_Mutation_p.P699	NM_004934	NP_004925	Q13634	CAD18_HUMAN	lasmic (Potential).	7	TCTGGGAGTGA	0.502	
+	7	1576	d.1_Missense_Mu	NM_004932	NP_004923	P55285	CADH6_HUMAN	(Potential).|Cadherin 4.	7	TCCTGTCAAGT	0.418	
-	51	9481	y.1_Missense_Mu	NM_023073	NP_075561	E9PH94	E9PH94_HUMAN		7	ACACGGAGCAT	0.373	rs144467995
-	2	513	.2_Intron|PPAP2A	NM_003711	NP_003702	O14494	LPP1_HUMAN	ellular (Potential).	2	GAAGGGGGTAT	0.348	
+	77	16598	.S3207F|GPR98_	NM_032119	NP_115495	Q8WXG9	GPR98_HUMAN	ellular (Potential).	16	TTTTTCTGTGG	0.438	
-	12	2172		NM_012081	NP_036213	O00472	ELL2_HUMAN		1	TTCATGGTAATT	0.353	
-	5	630	a.3_Missense_M	NM_018343	NP_060813	Q9BVS4	RIOK2_HUMAN		1	AACTGGAAATT	0.338	
-	15	2616	C_uc003kql.3_Mi	NM_002387	NP_002378	P23508	CRCM_HUMAN		1	ACACTCCTGAC	0.597	
+	3	1609		NM_175856	NP_787052	Q70JA7	CHSS3_HUMAN	enal (Potential).	3	GTGGAGTACATT	0.468	
-	8	957	wm.2_Missense_	NM_006638	NP_006629	O75818	RPP40_HUMAN		0	CCATGGAGCTA	0.348	
-	5	813	n_p.D167N|ETV7_	NM_016135	NP_057219	Q9Y603	ETV7_HUMAN		2	CTCACCAGCGA	0.597	
+	33	3736	e_Mutation_p.W8	NM_015255	NP_056070	Q8IWV8	UBR2_HUMAN		4	CTCAGTGGATT	0.318	
+	33	3778	se_Mutation_p.L9	NM_015255	NP_056070	Q8IWV8	UBR2_HUMAN		4	AGTTTCTTAGG	0.343	
+	3	637	.2_Missense_Mut	NM_005922	NP_005913	Q9Y6R4	M3K4_HUMAN		9	CTCATTCATGTT	0.418	
+	2	269	F25_uc003qwl.1_	NM_030615	NP_085118	Q9UIL4	KIF25_HUMAN	inesin-moto p.W3C(1)	2	TGACATGGACC	0.602	
+	19	2979	o.2_Missense_Mu	NM_152744	NP_689957	Q7Z5N4	SDK1_HUMAN	nectin type-III 3.	6	CACTTCCGTTCT	0.552	
-	17	2492_2493	ng.2_Missense_M	NM_033054	NP_149043	B0I1T2	MYO1G_HUMAN		4	TGGAAGGGCTG	0.614	
-	5	1584		NM_033273	NP_150376	Q96JC4	ZN479_HUMAN	2H2-type 10.	4	TCACATTTGTAG	0.453	
+	8	2094	_Mutation_p.P451	NM_015570	NP_056385	Q8WXX7	AUTS2_HUMAN		3	tccagccccccgcaca	0.244	
-	21	3202	kgz.1_Missense_	NM_001142749	NP_001136221	A8MWY0	K132L_HUMAN	lasmic (Potential).	7	CCAAAGATTTG	0.393	
+	1	1344		NM_012281	NP_036413	Q9NZV8	KCND2_HUMAN	lasmic (Potential).	5	TCCCGGAAATC	0.577	
-	15	1860		NM_004333	NP_004324	P15056	BRAF_HUMAN	rotein kinas _R603>I(2)|p.T	18290	ATTTCACTGTA	0.368	

+	1	608		NM_001001656	NP_001001656	Q8NGU2	OR9A4_HUMAN	Name=5; (Potential).		1	TAATGGCTGTTTT	0.413	
+	24	2765		NM_004668	NP_004659	O43451	MGA_HUMAN	(Potential).|Maltase.		2	TTAAAATTCTTGG	0.388	
+	4	538	1_Intron|uc010loj.	NR_001296						0	TCACAGCCGAC	0.493	
-	4	887_888	p.R214W|ZNF786	NM_152411	NP_689624	Q8N393	ZN786_HUMAN	2H2-type 2.		4	CTTCCGGCGGA	0.644	
+	8	1170	nse_Mutation_p.E	NM_012082	NP_036214	Q8WW38	FOG2_HUMAN	2H2-type 3.		5	ACCAGGAGCTC	0.507	
+	20	3414	3ywa.1_Missense_	NM_014957	NP_055772	A2RUS2	DEND3_HUMAN			1	TGTGGTGCTGT	0.622	
-	39	5437	.E1169K|PTPRD_	NM_002839	NP_002830	P23468	PTPRD_HUMAN	).|Tyrosine-protein phosph		22	TTTTTTCATGCT	0.388	
+	17	3283	p.D904E|TEK_uc	NM_000459	NP_000450	Q02763	TIE2_HUMAN	.|Cytoplasmic (Potential).		12	GCCGACGTGGC	0.552	rs56154987
+	3	1546	TL2_uc004awr.1_I	NM_001045477	NP_001038942	Q5VZR2	FA22G_HUMAN			1	TACGAGATGGC	0.652	
+	11	1438	FD1_uc004cvs.3_	NM_003611	NP_003602	O75665	OFD1_HUMAN	Potential.		0	AGGATGACTACA	0.378	
+	1	901		NM_001136234	NP_001129706					1	ATTTGGCCGTG	0.512	
-	2	1754	oo.1_Missense_M	NM_201286	NP_958443	Q70EK9	UBP51_HUMAN			3	CTCTGGCCTTG	0.483	
+	2	502		NM_003868	NP_003859	O43320	FGF16_HUMAN			1	ACAAAGATGGC	0.478	
+	5	546	_p.I144V|ARL13A_	NM_001012990	NP_001013008	Q5H913	AR13A_HUMAN			1	GATATTATTGACT	0.423	
-	5	562	F5_uc004eij.1_RN	NM_032946	NP_116564	Q9H1B4	NXF5_HUMAN	RRM.		1	TGACATCCTTCA	0.502	
+	4	2514	P2_uc004ejm.2_	NM_138437	NP_612446	Q96D09	GASP2_HUMAN			1	GGGCAGAAAAA	0.532	
+	1	365								1	CCATCACCTCC	0.622	
+	18	2945	c.1_Missense_Mu	NM_198465	NP_940867	Q7Z2Y5	NRK_HUMAN			14	AAATATCACCCC	0.413	
-	2	359	PL1_uc010nqa.2_	NM_178175	NP_835469	Q86WI0	LHPL1_HUMAN			0	GGGTTCCCACC	0.532	
-	18	3278	.P1071S|ODZ1_u	NM_014253	NP_055068	Q9UKZ4	TEN1_HUMAN	ellular (Potential).		23	GGCGGGAAACC	0.483	
+	1	494		NM_001727	NP_001718	P32247	BRS3_HUMAN	ellular (Potential).		1	CTGTTCGGAAG	0.448	
+	7	1405	_p.L171F|MAGEC	NM_138702	NP_619647	Q8TD91	MAGC3_HUMAN	MAGE 2.		3	CTTCTCCTCAAA	0.468	
-	3	500		NM_000808	NP_000799	P34903	GBRA3_HUMAN	ellular (Probable).		1	GACCTCCAAGC	0.448	
-	4	510	_1_uc009vka.2_5'	NM_004421	NP_004412	O14640	DVL1_HUMAN			0	ACCCTCCTCGC	0.652	
-	16	2006	vkz.1_Missense_	NM_001080484	NP_001073953	Q9C0B2	K1751_HUMAN			1	TCACCGAACAT	0.502	
-	7	963	HP4_uc009vlt.1_I	NM_015102	NP_055917	O75161	NPHP4_HUMAN			1	CTGGAGGCGAG	0.577	
+	2	226		NM_023013	NP_075389	O95521	PRAM1_HUMAN			0	TTCATGGAGGC	0.587	
+	6	728	522_uc010ohm.1_	NM_020888	NP_065939	Q9P206	K1522_HUMAN			0	GCATCCCCACA	0.721	
-	7	1328	IQ3_uc001dfz.3_	NM_001105659	NP_001099129	A6PVS8	LRIQ3_HUMAN			2	TATGCAGGAAAA	0.348	
-	10	1886	1_uc010ose.1_RN	NM_152890	NP_690850	Q17RW2	COOA1_HUMAN			5	GTGCACCTTTAG	0.338	
-	3	713		NM_205848	NP_995320	Q5T7P8	SYT6_HUMAN	mic (Potential).|C2 1.		5	GTAATCGTAGC	0.527	rs140277785
-	3	272		NM_002506	NP_002497	P01138	NGF_HUMAN			2	GTGGGCTTGGG	0.602	
+	25	2542	_Intron|SPAG17_	NM_006784	NP_006775	Q9UNX4	WDR3_HUMAN			1	TACTTGTGCTG	0.363	
-	4	703	D7B_uc001eto.2_	NM_020205	NP_064590	Q6GQQ9	OTU7B_HUMAN			3	CATTGGAGGAG	0.557	
+	9	1620	_Mutation_p.G39	NM_144618	NP_653219	Q8TAK5	GABP2_HUMAN			0	GACTGGGTCAG	0.473	
+	3	326		NM_176823	NP_789793	Q86SG5	S1A7A_HUMAN			1	GCAGAGCCATG	0.527	
-	4	555	LC39A1_uc001fdk	NM_014437	NP_055252	Q9NY26	S39A1_HUMAN	lasmic (Potential).		0	AGTGTGATCTGC	0.572	
-	11	1963_1964	p.P601F|YY1AP1_	NM_139118	NP_620829	Q9H869	YYAP1_HUMAN			3	ACAGGGGAAG	0.53	
-	4	562	_p.G150E|FCRL1_	NM_052938	NP_443170	Q96LA6	FCRL1_HUMAN	2.|Extracellular (Potential).		7	CAGCCCCTTTG	0.512	
+	2	828		NM_001763	NP_001754	P06126	CD1A_HUMAN	ellular (Potential).		3	GGAATTCGTAGA	0.468	
+	1	898		NM_001004473	NP_001004473	Q8NGX5	O10K1_HUMAN	lasmic (Potential).		1	AATCAGCCCTAC	0.279	
-	36	5318		NM_003126	NP_003117	P02549	SPTA1_HUMAN	Spectrin 16.		8	TTTTTCGTGGTG	0.443	
-	4	515	nse_Mutation_p.S	NM_016946	NP_058642	Q9Y624	JAM1_HUMAN	Potential).|Ig-like V-type 1.		2	TCATAGGAAGCT	0.537	
+	8	1017	q.1_Missense_Mu	NM_007348	NP_031374	P18850	ATF6A_HUMAN	|Cytoplasmi	p.R317*(1)	3	AAATCGAGAATC	0.378	
-	10	1233	EM3_uc010pom.1_	NM_025191	NP_079467	Q9BZQ6	EDEM3_HUMAN			1	AATATACCTCATT	0.403	
+	13	1547	p.S295L|PTPRC_	NM_002838	NP_002829	P08575	PTPRC_HUMAN	tential).|Fibronectin type-III		12	TTTTATCATTACA	0.308	
+	19	2400	_Mutation_p.R702	NM_001005388	NP_001005388	O94856	NFASC_HUMAN	tential).|Fibronectin type-III		6	CCTCCGGCTGT	0.582	rs151110151

-	18	4393	v.2_Missense_Mu	NM_206933	NP_996816	O75445	USH2A_HUMAN	III 3.|Extracellular (Potentia	26	TGAACTCATACTT	0.418
-	6	889		NM_000143	NP_000134	P07954	FUMH_HUMAN		5	CCAATTCTAGTAT	0.398
+	1	650		NM_001004689	NP_001004689	Q8NG83	OR2M3_HUMAN	Name=5; (Potential).	2	TTGCTTCCTATGC	0.423
+	33	4928	.1_RNA|MYO3A_	NM_017433	NP_059129	Q8NEV4	MYO3A_HUMAN		18	AAAACGAAGAC	0.239
-	6	834	RMC4_uc001itz.2	NM_018076	NP_060546	Q5T2S8	ARMC4_HUMAN		6	AAATTTCCCCACC	0.393
-	36	5324	hr.1_Missense_M	NM_001142771	NP_001136243	Q96QU1	PCD15_HUMAN		13	GTCAATCATGGAC	0.483
-	3	1067	p.A305T|EGR2_u	NM_001136177	NP_001129649	P11161	EGR2_HUMAN	Poly-Ala.	2	GGCGGCGGCTG	0.701
-	29	3879		NM_007055	NP_008986	O14802	RPC1_HUMAN		0	GGGCGGCCTCG	0.557
-	54	4469	7A1_uc001kxq.2_	NM_000494	NP_000485	Q9UMD9	COHA1_HUMAN	tential).|Triple-helical regio	5	GGCTCCATAAGC	0.498
+	21	3124	CS3_uc010qqz.1_	NM_014978	NP_055793	Q9UPU3	SORC3_HUMAN	enal (Potential).	10	GCATTTCCTTCAC	0.448
-	8	3800		NM_014881	NP_055696	Q6PJP8	DCR1A_HUMAN		2	CTGTAGGTCGA	0.358
+	15	2031		NM_014937	NP_055752	Q9Y2H2	SAC2_HUMAN		2	GCTGGGCCCTCA	0.473
-	29	3851		NM_005961	NP_005952	Q6W4X9	MUC6_HUMAN	-rich.|Thr-rich.	1	CCGAGGAGGCT	0.647
+	7	1076	p.W107*|KCNQ1_	NM_000218	NP_000209	P51787	KCNQ1_HUMAN	ellular (Potential).	1	GACGTGGGTCG	0.632
-	1	196		NM_001005238	NP_001005238	Q8NGK0	O51G2_HUMAN	Name=2; (Potential).	2	GGAAGAGATACAT	0.483
-	1	901		NM_001146033	NP_001139505	P0C7T3	O56A5_HUMAN	lasmic (Potential).	0	TGATCTCCTTGGT	0.443
-	14	2141		NM_000352	NP_000343	Q09428	ABCC8_HUMAN	smic (By similarity).	1	GCATCGCCATCT	0.652
-	8	725	e_Mutation_p.E20	NM_005709	NP_005700	Q9Y6N9	USH1C_HUMAN		1	TGTTTTCCCGATT	0.597
+	3	753		NM_020346	NP_065079	Q9P2U8	VGLU2_HUMAN		4	TCCATAGAAAGC	0.512
+	1	254		NM_001004727	NP_001004727	Q8NGF9	OR4X2_HUMAN	ellular (Potential).	0	TCATATCTTGGTG	0.502
-	7	1148	_Mutation_p.P281	NM_004476	NP_004467	Q04609	FOLH1_HUMAN	.|Extracellular (Probable).	3	CAATTGGATGAA	0.358
-	1	563		NM_001004471	NP_001004471	Q8NGQ4	O10Q1_HUMAN	ellular (Potential).	2	GGACGGGAGGC	0.622
+	5	617_618		NM_014207	NP_055022	P06127	CD5_HUMAN	ar (Potential).|SRCR 2.	1	GTGCCGGCGTGC	0.649
-	7	1554	wj.2_Missense_M	NM_004790	NP_004781	Q4U2R8	S22A6_HUMAN	ical; (Potential).	0	CCTGGGGTATCA	0.612
+	3	723	A10_uc001nwu.3_	NM_001039752	NP_001034841	Q63ZE4	S22AA_HUMAN	lasmic (Potential).	2	TTGGGCGAAGAT	0.403
-	1	1945	S_uc001oir.2_5'Fl	NM_018219	NP_060689	Q9NVE4	CCD87_HUMAN		2	CAGGGGCCACA	0.478
-	8	849	th.3_Missense_M	NM_014824	NP_055639	O94868	FCSD2_HUMAN		1	GATAATCATTCCT	0.373
-	2	500	p.P66L|DLG2_uc	NM_001364	NP_001355	Q15700	DLG2_HUMAN		6	TTCAGAGGAGAA	0.418
-	7	1945	m.2_Missense_M	NM_001143831	NP_001137303	P41594	GRM5_HUMAN	Name=1; (Potential).	9	ACAGCTGCAATG	0.493
+	14	4727		NM_005422	NP_005413	O75443	TECTA_HUMAN	VWFD 4.	10	AACTGGTTTGGC	0.353
+	24	3366	_uc001qkn.2_Mis	NM_199460	NP_955630	Q13936	CAC1C_HUMAN	=S4 of repeat III; (Potentia	11	CTTGCGAGTCCT	0.562
-	10	1657		NM_001733	NP_001724	P00736	C1R_HUMAN	eptidase S1.	0	TGATTTCCTAGC	0.552
-	11	2787	p.P887S|CD163_	NM_004244	NP_004235	Q86VB7	C163A_HUMAN	xtracellular (Potential).	8	ACATGGGAATGG	0.547
-	2	279	P_uc009zgl.2_5'U	NM_002864	NP_002855				5	CACAGTGGAATA	0.512
-	3	658		NM_006248	NP_006239				0	TGCCTCCTTGTG	0.602
-	4	791	1raj.1_Missense_	NM_018050	NP_060520	Q9H8J5	MANS1_HUMAN	ellular (Potential).	0	TCTGAGGATCCA	0.428
-	25	3058		NM_004963	NP_004954	P25092	GUC2C_HUMAN	lasmic (Potential).	6	TCAGTTCTCTTCA	0.428
-	16	2233		NM_021957	NP_068776	P54840	GYS2_HUMAN		2	CATCTTCCACATC	0.488
+	9	796	ssense_Mutation_	NM_020183	NP_064568	Q8WYA1	BMAL2_HUMAN		2	AAAGCTGGTTTG	0.388
+	3	1597		NM_032834	NP_116223	Q5BKT4	AG10A_HUMAN	ellular (Potential).	1	TTATAGGCTTAAC	0.338
-	40	13631		NM_003482	NP_003473	O14686	MLL2_HUMAN		41	CTGACCCCGTCC	0.627
-	8	1212	e_Mutation_p.L38	NM_000889	NP_000880	P26010	ITB7_HUMAN	tracellular (Potential).	8	GATGAGCTGTAC	0.552
+	1	192		NM_014212	NP_055027	O43248	HXC11_HUMAN		1	AGCGAGGGAGC	0.617
-	2	1474		NM_005447	NP_005438	O75901	RASF9_HUMAN		1	TGTTTTCCTTTAA	0.418
-	7	1034	e_Mutation_p.P12	NM_133503	NP_598010	P07585	PGS2_HUMAN	LRR 11.	4	AGGTGGGCAGA	0.408
-	14	1983	1tgp.2_Missense_	NM_015054	NP_055869	A0JNW5	UH1BL_HUMAN		2	CAGAAGGAATG	0.353
+	6	924	.1_Missense_Mut	NM_017915	NP_060385	Q9NWS1	PR1BP_HUMAN		0	AAATACCAAACC	0.299

+	2	356		NM_017564	NP_060034	Q8WWQ8	STAB2_HUMAN	ellular (Potential).	14	GGATGGTTACA	0.463	
-	14	1624	C3_uc010swd.1_5	NM_001031701	NP_001026871	Q86UY8	NT5D3_HUMAN		3	AGGCGGGCAGT	0.592	
+	3	280	ex.2_Missense_M	NM_020382	NP_065115	Q9NQR1	SETD8_HUMAN		0	ATCACGAAGTC	0.488	
-	49	6847	LE_uc001ukr.1_M	NM_006231	NP_006222	Q07864	DPOE1_HUMAN		8	GGTACGACATG	0.602	
+	6	693	p.E180K|SGCG_u	NM_000231	NP_000222	Q13326	SGCG_HUMAN	ellular (Potential).	0	CAGTGGAGACA	0.393	
+	1	91	se_Mutation_p.R1	NM_031277	NP_112567	Q9BXT8	RNF17_HUMAN		2	CCAGCGAATGG	0.617	
+	6	507		NM_000982	NP_000973	P46778	RL21_HUMAN		0	CTATTCCCTATG	0.403	
-	1	154	4P_uc001vwb.3_	NM_001145442	NP_001138914	A6NI47	POTEM_HUMAN		0	CTGCACCAGGG	0.587	
-	1	649		NM_001005465	NP_001005465	Q8NGC4	O10G3_HUMAN	Name=5; (Potential).	2	GGAGAGGAGGA	0.542	
+	13	1429	p.G446S|GALNTL	NM_020692	NP_065743	Q8N428	GLTL1_HUMAN	ectin.|Lumenal (Potential).	2	CTCAGGGCCAG	0.582	
-	4	929	2_uc010asx.2_3'U	NM_000793	NP_000784	Q92813	IOD2_HUMAN		1	AAGAGGAGTCC	0.557	
-	8	1267	e_Mutation_p.R26	NM_000153	NP_000144	P54803	GALC_HUMAN		0	AATGCGACCCC	0.338	
-	2	1052	1ycu.3_Missense_	NM_016186	NP_057270	Q9UK55	ZPI_HUMAN		3	CATTGCGAAAT	0.398	
+	3	534	ense_Mutation_p.	NM_000623	NP_000614	P30411	BKRB2_HUMAN	Name=2; (Potential).	5	CTTCTGGGCCA	0.592	
-	21	4656	.S1508F|TP53BP	NM_005657	NP_005648	Q12888	TP53B_HUMAN	h dimethylated histone H4.	7	TCCCAGAGTAA	0.473	
-	23	3139	un.2_Missense_M	NM_014080	NP_054799	Q9NRD8	DUOX2_HUMAN	teraction with TXNDC11 (B	5	CCAGTCCCTGG	0.597	
-	32	4062	5C_uc010uga.1_	NM_018728	NP_061198	Q9NQX4	MYO5C_HUMAN	Potential.	14	TGCTTCCTGCC	0.458	
+	1	1833_1834		NM_001080534	NP_001074003	Q8NB66	UN13C_HUMAN		7	GTTCAGGGTATC	0.5	
+	1	172	5'UTR|NOX5_uc0	NM_145658	NP_663633	Q6UW49	SPESP_HUMAN		0	GCCTTCGTCTG	0.642	
+	3	403	e_Mutation_p.G9	NM_001008226	NP_001008227	Q658L1	F154B_HUMAN		2	AAATTTGGAAAT	0.393	
+	1	405	_5'Flank|LOC146	NM_001053	NP_001044	P35346	SSR5_HUMAN	ellular (Potential).	1	CTGGCCCTTCG	0.622	
-	7	833	lo.2_Missense_Mutation_p.P61L|UNKL_uc002clp.2_Mi			Q9H9P5	UNKL_HUMAN		0	CGTTTGGACTT	0.657	
-	2	1867	p.D634H|IGFALS_	NM_004970	NP_004961	P35858	ALS_HUMAN	LRRCT.	0	GAGGTCCCGCA	0.682	
-	5	2693		NM_001116	NP_001107	O60503	ADCY9_HUMAN	lasmic (Potential).	6	GATGTTCTTGAA	0.547	rs72556388
-	28	3119	P7_uc010uyj.1_M	NM_003470	NP_003461	Q93009	UBP7_HUMAN		3	GATTTCCTGGG	0.488	
-	13	3942	uyn.1_Missense_	NM_001134407	NP_001127879	Q12879	NMDE1_HUMAN	lasmic (Potential).	45	GGGTGGATCTA	0.527	
+	3	657	IP2_uc010uyp.1_	NM_024997	NP_079273	Q5U623	MCAF2_HUMAN		0	AAAACGATTCTG	0.438	
-	1	231	CSM1_uc010bwg.	NM_052956	NP_443188	Q08AH1	ACSM1_HUMAN		2	CAGTACATAACT	0.483	
+	2	3236		NM_014699	NP_055514	O15015	ZN646_HUMAN		2	GTTCTGGGACT	0.577	
+	3	1084	eiu.3_Missense_M	NM_138736	NP_620073	P09471	GNAO_HUMAN		2	TCTCCGGAGAA	0.512	
+	29	4139	RC5_uc010ccs.1_	NM_032206	NP_115582	Q86WI3	NLRC5_HUMAN		7	GGCCTCAGTGA	0.572	
+	10	1460	G7_uc002fnk.1_R	NM_003119	NP_003110	Q9UQ90	SPG7_HUMAN	rial matrix (Potential).	0	TCTCCCCACGC	0.617	
+	2	133	.P34S|DPH1_uc0	NM_001383	NP_001374	Q9BZG8	DPH1_HUMAN		1	TCCCCCCTGAG	0.537	
+	3	466	e_Mutation_p.S89	NM_001042	NP_001033	P14672	GTR4_HUMAN	Name=2; (Potential).	0	CTTTTCCGTGG	0.622	
-	2	263		NM_004853	NP_004844	Q9UNK0	STX8_HUMAN	lasmic (Potential).	1	CCTTTGGTGCC	0.388	
+	6	446	7*|TBC1D3_uc002	NM_032258	NP_115634	Q8IZP1	TBC3A_HUMAN		0	TAGATCGAGCG	0.552	
-	1	516		NM_019016	NP_061889	Q2M2I5	K1C24_HUMAN	Rod.|Coil 1A.	0	TAGGTAATTGGC	0.527	
-	1	44		NM_181534	NP_853512	Q7Z3Z0	K1C25_HUMAN		2	AACGCGTTGCA	0.488	
-	3	249		NM_002634	NP_002625	P35232	PHB_HUMAN		0	CCCACGGGATG	0.498	
-	3	363		NM_018509	NP_060979	Q96AG4	LRC59_HUMAN	ytoplasmic (Potential).	1	TTCTTACTCAGG	0.458	
+	3	103		NM_153228	NP_694960	Q8N957	ANKF1_HUMAN		2	AATAGGAAGGA	0.398	
-	7	1201		NM_000250	NP_000241	P05164	PERM_HUMAN		4	GTACACCATGC	0.652	
-	4	874	dea.1_Missense_	NM_001098426	NP_001091896	Q92925	SMRD2_HUMAN		0	GAGGCTTTTTG	0.557	
+	7	1026	jth.2_Missense_M	NM_198955	NP_945193	Q3V5L5	MGT5B_HUMAN	enal (Potential).	3	GGAGTCCGGGG	0.672	
-	5	890	.D147N|NOL4_uc	NM_003787	NP_003778	O94818	NOL4_HUMAN		3	ATTCATCACTTT	0.328	
+	15	2721	mz.1_Nonsense_	NM_025135	NP_079411	Q2V2M9	FHOD3_HUMAN		8	GGGCTTAGGGT	0.557	
+	4	562	p.R81W|SLC14A	NM_007163	NP_009094	Q15849	UT2_HUMAN		4	CCCATCGGGAC	0.507	

-	4	694	ec.1_Missense_Mu	NM_001080467	NP_001073936	Q9ULV0	MYO5B_HUMAN	osin head-like.	5	GGGGTCCATGT	0.488	
+	5	1450	r.1_Missense_Mut	NM_005215	NP_005206	P43146	DCC_HUMAN	otential).|Ig-like C2-type 3.	17	AGTATTCTTTATT	0.358	
+	6	652	b.2_Missense_Mu	NM_001974	NP_001965	Q14246	EMR1_HUMAN	GF-like 4; calcium-binding	5	TGAATCCAGCA	0.478	
-	5	670		NM_198535	NP_940937	Q32M78	ZN699_HUMAN	ype 2; degenerate.	0	GCACTGATAGG	0.438	
-	2	974		NM_024527	NP_078803	Q96I13	ABHD8_HUMAN		0	ACATTTCGCTTC	0.592	
+	16	2019	AXL_uc010ehk.2_	NM_021913	NP_068713	P30530	UFO_HUMAN	Potential).|Protein kinase.	13	TGAACGAGAGA	0.597	
-	1	187	ssense_Mutation_	NM_006905	NP_008836	P11464	PSG1_HUMAN		2	GAGCCCCTTCC	0.562	
-	10	1541	0ejp.1_Missense_	NM_001102597	NP_001096067	Q6UY09	CEA20_HUMAN	lasmic (Potential).	2	CTCAGGACTCA	0.527	
-	1	1682		NM_032040	NP_114429	Q9H0W5	CCDC8_HUMAN	Poly-Arg.	3	TCCTGCGGCGC	0.627	
-	2	1895	rt.1_Missense_Mu	NM_004977	NP_004968	Q14003	KCNC3_HUMAN	=Segment S6; (Potential).	1	CACAGGCATGG	0.607	
+	3	388	_uc002pyz.3_Spli	NM_001161426	NP_001154898	Q8N9Z0	ZN610_HUMAN		3	CATTTAGGATTG	0.443	
+	7	1897	qr.1_Missense_M	NM_018555	NP_061025	Q9NQX6	ZN331_HUMAN		6	ATACTGGTGAG	0.413	
-	8	2661	.G862E|NLRP7_	NM_206828	NP_996611	Q8WX94	NALP7_HUMAN	LRR 6.	3	TCACCCCTGTA	0.507	
-	15	3486		NM_004304	NP_004295	Q9UM73	ALK_HUMAN	xtracellular (Potential).	1218	CCAGTCTCTCT	0.607	
+	1	366		NR_003663					0	GAGGTGGATTT	0.478	
+	11	1809	R1_uc002tbw.3_Ir	NM_016232	NP_057316	Q01638	ILRL1_HUMAN	oplasmic (Potential).	4	GTGGAGGGAGG	0.512	
+	9	1556	fiz.2_Missense_M	NM_003853	NP_003844	O95256	I18RA_HUMAN	ical; (Potential).	5	GAGGAGGTAAG	0.438	
+	16	1491	yf.1_Missense_M	NM_006770	NP_006761	Q9UEW3	MARCO_HUMAN	tracellular (Potential).	6	GCAAAATTCTGA	0.542	
+	1	789	uc002tpw.1_RNA	NM_032144	NP_115520	Q9H0N0	RAB6C_HUMAN		1	TGTCAGAACAG	0.428	
-	9	3768	_Mutation_p.R113	NM_025052	NP_079328	Q56UN5	YSK4_HUMAN	rotein kinase.	5	ATTTCCGTCCA	0.498	
+	14	2957	D7B_uc010zbj.1_	NM_001080427	NP_001073896				7	TTGTGGAATTG	0.418	
-	41	4956		NM_004543	NP_004534	P20929	NEBU_HUMAN		20	AAATCCAACTT	0.413	
-	11	1822	p.E444K|SCN3A_	NM_006922	NP_008853	Q9NY46	SCN3A_HUMAN		10	AAATTCGGCCT	0.413	
-	11	1757	p.R449Q|SCN1A_	NM_006920	NP_008851	P35498	SCN1A_HUMAN		13	TTGCTCGCCCT	0.478	
-	253	54795	86K|TTN_uc010z	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	AACTTCCTCTG	0.428	
-	225	45513	_uc010zfi.1_Miss	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	TGGTTCAGCCA	0.423	
-	143	30754	z.1_Missense_Mu	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	GTTTAACTTCT	0.438	
-	46	13716	.E4431K|TTN_uc0	NM_133437	NP_597681	Q8WZ42	TITIN_HUMAN		153	GTCTTCGGTAT	0.378	
-	16	2985	.G875R|TTN_uc0	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	GCGTCCGTGCA	0.527	
-	6	880		NM_173648	NP_775919	Q6ZP82	CC141_HUMAN		10	TGATGTCGACTC	0.502	
-	13	1676	0frt.2_Splice_Site_	NM_005795	NP_005786	Q16602	CALRL_HUMAN		4	CCATACCTGGA	0.388	
+	3	285	10ziu.1_5'Flank|E	NM_001037663	NP_001032752	P24534	EF1B_HUMAN	ST C-terminal.	0	TGTCCAGCCCA	0.468	
-	8	1349	F2_uc010fuw.2_	NM_016260	NP_057344	Q9UKS7	IKZF2_HUMAN		0	TTCCTGGGGTC	0.498	
+	12	1356	ver.2_Missense_M	NM_024532	NP_078808	Q8N0X2	SPG16_HUMAN	WD 2.	2	TTATGGGATCTAT	0.418	
-	3	961	C19A3_uc010zlv.1	NM_025243	NP_079519	Q9BZV2	S19A3_HUMAN	ical; (Potential).	2	TTAAAACCTGCT	0.458	
+	4	590	mp.1_Missense_	NM_001017915	NP_001017915	Q92835	SHIP1_HUMAN	p.F28L(1)	2	TTTTTCAAACG	0.587	
-	2	432	_p.R123*|SIRPG_	NM_018556	NP_061026	Q9P1W8	SIRPG_HUMAN	(Potential).|Ig-like V-type.	1	TTTTCGAAACT	0.498	
+	2	452	u.1_RNA|CSTL1_	NM_138283	NP_612140	Q9H114	CST1L_HUMAN		0	TAATTCGAAGTC	0.458	
+	1	63	G1B_uc010ztj.1_RNA|FRG1B_uc010gdr.1_RNA						0	TTGATACGTTGG	0.219	rs62197050
-	2	387	0gel.2_5'UTR|CD	NM_016408	NP_057492	Q96SZ6	CK5P1_HUMAN	activation inhibition.	5	GATAGGGAGGT	0.483	
+	9	1271	fo.1_Missense_Mu	NM_016436	NP_057520	Q9BVI0	PHF20_HUMAN		1	CCACTCCTTTG	0.473	
+	6	791	jz.1_Missense_Mu	NM_013396	NP_037528	Q9UHP3	UBP25_HUMAN		5	TTTTGGAATTTA	0.299	
-	25	4818_4819	AM_uc002yyr.1_	NM_001389	NP_001380	O60469	DSCAM_HUMAN	III 5.|Extracellular (Potentia	11	CCACTCCATTTT	0.475	
+	1	214		NM_000394	NP_000385	P02489	CRYAA_HUMAN		2	TACTACCGCCAG	0.632	rs74315441
+	1	59	.1_Intron|C21orf29	NM_198689	NP_941962	P60409	KR107_HUMAN		0	CCAGCGACCTG	0.532	
+	29	3671	fz.1_Missense_Mu	NM_015151	NP_055966	Q14689	DIP2A_HUMAN		2	TATTAGCGGGAG	0.493	
+	20	2849	_p.L843F|SGSM1	NM_001039948	NP_001035037	Q2NKQ1	SGSM1_HUMAN	ab-GAP TBC.	5	AAAGTCTCTTC	0.587	

+	11	1185_1186	_p.P120L|SAMM5	NM_015380	NP_056195	Q9Y512	SAM50_HUMAN		1	ATAAGCCGTCAA	0.361	
+	6	636	qx.1_Missense_Mu	NM_017931	NP_060401	Q5R3I4	TTC38_HUMAN	TPR 2.	1	TCTACTCTTTTG	0.383	
-	9	1184	_uc003bkh.2_Siler	NM_032019	NP_114408	Q969S8	HDA10_HUMAN	one deacetylase.	0	CTCAGGGTCCC	0.652	
+	9	1079	w.1_Missense_Mu	NM_006614	NP_006605	O00533	CHL1_HUMAN	3.|Extracellular (Potential).	12	CCAACTCCACAG	0.338	
+	3	507	M43_uc003byl.1_	NM_024334	NP_077310	Q9BTV4	TMM43_HUMAN	enal (Potential).	1	AGAATGAAGGA	0.597	
+	4	1721		NM_001039111	NP_001034200	Q2Q1W2	LIN41_HUMAN	Filamin.	3	TTACCGACCCC	0.577	
-	22	3904		NM_006514	NP_006505	Q9Y5Y9	SCNAA_HUMAN	=S5 of repeat III; (Potentia	10	GAAGAGGTTCA	0.502	
-	9	1412		NM_014139	NP_054858	Q9UI33	SCNBA_HUMAN		9	TCTGCTCCTCAT	0.473	
-	8	1106	e_Mutation_p.E25	NM_016598	NP_057682	Q9NYG2	ZDHC3_HUMAN	lasmic (Potential).	0	ATTGTTCTATTCC	0.458	
-	34	9424	kf.2_Missense_Mu	NM_001407	NP_001398	Q9NYQ7	CELR3_HUMAN	lasmic (Potential).	11	TGCGACCGTAA	0.647	
+	32	3423		NM_015136	NP_055951	Q9NY15	STAB1_HUMAN	xtracellular (Potential).	9	ACCAGGTCTTA	0.617	
+	31	2729	se_Mutation_p.S80	NM_018398	NP_060868	Q8IZS8	CA2D3_HUMAN	cellular (Potential).	7	GGGCTCCTTTA	0.403	
-	8	987	E1L3_uc003djp.1_	NM_004944	NP_004935	Q13609	DNSL3_HUMAN	lization signal (Potential).	3	TTCTTCCTTAGA	0.373	
-	8	1123	p.S265F|PLSCR4_	NM_001128305	NP_001121777	Q9NRQ2	PLS4_HUMAN	smic (By similarity).	0	TCAAGGGATTTG	0.388	
-	2	1052	HE_uc003fen.3_In	NM_000055	NP_000046	P06276	CHLE_HUMAN		4	TTTCTTGGGGAT	0.403	
-	12	1248	_p.E309K|ZBBX_u	NM_024687	NP_078963	A8MT70	ZBBX_HUMAN		2	TAAGTTCAATATT	0.279	
-	10	933	_p.E204K|ZBBX_u	NM_024687	NP_078963	A8MT70	ZBBX_HUMAN		2	TATTCTCCTCTTT	0.333	
-	3	12691	1bth.1_Intron|MU	NM_018406	NP_060876	Q99102	MUC4_HUMAN		0	GTGGCGTGACC	0.597	
+	7	310	_uc003fzv.1_Silent_	NM_001039127	NP_001034216	Q3SXZ3	ZN718_HUMAN	KRAB.	0	GCAAATAAAAGA	0.453	
+	3	859	3gdy.1_Missense_	NM_001042424	NP_001035889	O96028	NSD2_HUMAN	PWWP 1.	9	GTGGTCCAAAG	0.433	
+	7	1250	uc003ghf.2_Silent_	NM_173660	NP_775931	Q18PE1	DOK7_HUMAN		1	ACAGTCGAGTAC	0.701	
-	6	2123	D4_uc003gwm.2_	NM_207406	NP_997289	Q6ZU67	BEND4_HUMAN		0	GGTGATCGATCC	0.527	
+	5	847	zl.1_Nonsense_M	NM_025087	NP_079363	Q9H720	PG2IP_HUMAN		3	CAGATGGGCAG	0.527	
-	19	2934	t.1_Missense_Mut	NM_002253	NP_002244	P35968	VGFR2_HUMAN	e.|Cytoplasmic (Potential).	33	GATGCTCACTGT	0.468	
-	3	965	2A3_uc010ihp.1_	NM_024743	NP_079019	Q6UWM9	UD2A3_HUMAN	cellular (Potential).	2	ATTTTGAAACA	0.403	
-	6	862	DH1B_uc011ceh.1_	NM_000668	NP_000659	P00325	ADH1B_HUMAN		2	CTCCATCAGTCA	0.463	
-	6	862		NM_000673	NP_000664	P40394	ADH7_HUMAN		3	CCTTGGGACTGA	0.478	rs146193104
+	4	587	p.M138L|MTTP_u	NM_000253	NP_000244	P55157	MTP_HUMAN	Vitellogenin.	4	AAATAATGGGAA	0.398	
+	3	803	ill.2_Missense_Mu	NM_017935	NP_060405	Q8NDB2	BANK1_HUMAN		3	CTGGGGAAATA	0.368	
+	9	8267	_p.S1054L|FAT4_	NM_024582	NP_078858	Q6V0I7	FAT4_HUMAN	|Extracellular (Potential).	18	GTACTTCAGTAA	0.383	
+	9	9194	_p.G1363E|FAT4_	NM_024582	NP_078858	Q6V0I7	FAT4_HUMAN	(Potential).|Cadherin 29.	18	ATAAGGGAAACC	0.423	
+	9	10025	_p.R1640Q|FAT4_	NM_024582	NP_078858	Q6V0I7	FAT4_HUMAN	|Extracellular (Potential).	18	ATAGTCGAAAGA	0.413	
+	9	11284	_p.L2060F|FAT4_u	NM_024582	NP_078858	Q6V0I7	FAT4_HUMAN	cellular (Potential).	18	ACGTTTCTTTTGG	0.458	
-	5	764	mm.3_Missense_	NM_004564	NP_004555	O75879	GATB_HUMAN		0	ATGTTCGCCTGG	0.532	rs145476419
-	1	580	CH1_uc003iqs.1_	NM_012403	NP_036535	O43423	AN32C_HUMAN	-rich (highly acidic).	0	cctcttcaccttcctcctc	0.184	
+	15	2910	e.1_Missense_Mu	NM_001080477	NP_001073946	Q9P273	TEN3_HUMAN	cellular (Potential).	0	GAGTGGATTCG	0.418	
-	12	2569	_Mutation_p.P731	NM_004934	NP_004925	Q13634	CAD18_HUMAN	lasmic (Potential).	7	CATAAGGGGGA	0.478	
-	8	2597		NM_021072	NP_066550	O60741	HCN1_HUMAN	ic (Potential).|Poly-Pro.	1	TGCTGGAGGGA	0.587	
-	8	2513		NM_021072	NP_066550	O60741	HCN1_HUMAN	lasmic (Potential).	1	GCCCCCTGCCT	0.677	
-	4	636	_p.S188F|DEPDC	NM_018369	NP_060839	Q8WUY9	DEP1B_HUMAN		1	TCATAGACTTC	0.383	
+	9	1323		NM_003248	NP_003239	P35443	TSP4_HUMAN	alcium-binding (Potential).	0	ACCATCCCTGC	0.483	
+	8	9021	.2_Intron|VCAN_u	NM_004385	NP_004376	P13611	CSPG2_HUMAN	GAG-beta.	16	CTGAGCCTCCC	0.383	
-	8	1347	_p.E300K|EDIL3_	NM_005711	NP_005702	O43854	EDIL3_HUMAN	5/8 type C 1.	2	AAGTTCCATTC	0.368	
+	56	11785	.E1603K|GPR98_	NM_032119	NP_115495	Q8WXG9	GPR98_HUMAN	cellular (Potential).	16	GGAATGGAAATA	0.408	
+	6	1479	NB1_uc010jdb.1_	NM_005573	NP_005564	P20700	LMNB1_HUMAN	Rod.|Coil 2.	2	CCCTGGACATG	0.448	
+	7	1354		NM_133638	NP_598377	Q8TE59	ATS19_HUMAN		9	TGTTGGTAAGT	0.299	
+	1	2041	03lhf.2_Intron|PC	NM_018907	NP_061730	Q9UN74	PCDA4_HUMAN	|Extracellular (Potential).	6	ACCGCCTACTGG	0.677	

+	1	201		NM_013340	NP_037472	Q9Y5F3	PCDB1_HUMAN	|Extracellular (Potential).	0	AGAGCGGCTCG	0.537	
+	1	674		NM_015669	NP_056484	Q9Y5E4	PCDB5_HUMAN	|Extracellular (Potential).	5	GTGTTTCCCTTA	0.463	
+	5	886	_p.E243K|PPARG	NM_133263	NP_573570	Q86YN6	PRGC2_HUMAN		0	CCCAGGAAGAC	0.677	
-	9	1456_1457	dk.1_Missense_M	NM_015465	NP_056280	Q8TEQ6	GEMI5_HUMAN	WD 8.	3	TTGTTGGAGTAG	0.262	
-	7	772	_p.T185N|GABRB	NM_021911	NP_068711	P47870	GBRB2_HUMAN	ellular (Probable).	0	TCATCAGTTGTG	0.249	
-	11	1478	2_Missense_Muta	NM_003062	NP_003053	O75094	SLIT3_HUMAN	LRR 8.	4	TCAGGCCCTGG	0.522	
+	3	866	P3_uc003mil.1_5'	NM_015111	NP_055926	O15049	N4BP3_HUMAN		0	CTAGCCCCTTC	0.672	
-	54	4148	se_Mutation_p.P1	NM_080680	NP_542411	P13942	COBA2_HUMAN	e-helical region.	5	CGGTGGGACCA	0.622	
-	4	1650	f.1_Missense_Mu	NM_021073	NP_066551	P22003	BMP5_HUMAN		2	CGGATCGAAGA	0.453	
+	15	1575		NM_000947	NP_000938	P49643	PRI2_HUMAN		0	GAAATGGATATG	0.403	
+	16	2850	k.2_Missense_Mu	NM_001704	NP_001695	O60242	BAI3_HUMAN	ellular (Potential).	50	CGATTCGTTTCT	0.368	
+	13	4449	.P4_uc003qrg.2_I	NM_020245	NP_064630	Q9NRJ4	TULP4_HUMAN		1	GCCCCCACCTG	0.746	
+	18	3899	fz.1_RNA|MAP3K4	NM_005922	NP_005913	Q9Y6R4	M3K4_HUMAN		9	CAAGCCCCACG	0.438	
+	5	1433	_Mutation_p.A162	NM_003088	NP_003079	Q16658	FSCN1_HUMAN		1	CTCCGCGGTCA	0.617	rs17850070
+	7	951	szk.2_Missense_	NM_006024	NP_006015	Q86VP1	TAXB1_HUMAN	Potential.	1	CAACATGAAAGA	0.214	
-	1	577		NR_002789					0	TGTAAAGATTCC	0.463	
-	8	1126	.D161H|TYW1B_u	NM_001145440	NP_001138912	Q6NUM6	TYW1B_HUMAN		0	AGCATCGACTA	0.413	rs147711959
-	7	1425	se_Mutation_p.D4	NM_178125	NP_835226	Q86XT4	TRI50_HUMAN	B30.2/SPRY.	1	GTCATCGGGGC	0.682	
+	4	735		NM_001077621	NP_001071089	Q86XT2	VP37D_HUMAN		0	GGGGCCACCAG	0.766	
+	1	70	3ugm.2_5'Flank|u	NM_198467	NP_940869	Q6PCB5	RSBNL_HUMAN		1	CGTGCACTGTG	0.692	
+	4	2307		NM_181646	NP_857597	A4D1E1	Z804B_HUMAN		11	AAAGGATTGTG	0.378	
+	17	4633	lf.2_Missense_Mu	NM_005751	NP_005742	Q99996	AKAP9_HUMAN		26	AAAGAAAATACT	0.323	
-	6	741	ph.1_Missense_	NM_015395	NP_056210	Q7Z6L1	TCPR1_HUMAN		1	TCGAGGGGATC	0.637	
+	22	3141	p.E978K|TRRAP_	NM_003496	NP_003487	Q9Y4A5	TRRAP_HUMAN		37	GCCTGGAGGAC	0.562	
-	3	261	_p.W48*|CYP3A5	NM_000777	NP_000768	P20815	CP3A5_HUMAN		0	AATTTCCAGAG	0.398	
+	3	2248	56_uc003uxr.2_I	NM_030961	NP_112223	Q9BRZ2	TRI56_HUMAN		3	ACAAGGGGCCA	0.592	
+	8	1102	R_uc011knq.1_5'	NM_000492	NP_000483	P13569	CFTR_HUMAN	tial).|ABC transmembrane	5	TGCTTCCCTAT	0.463	
+	35	5979	.3_Missense_Mut	NM_001458	NP_001449	Q14315	FLNC_HUMAN	Filamin 17.	12	CGCCTGGAGAC	0.597	
+	4	523	R1D1_uc011kqe.	NM_005989	NP_005980	P51857	AK1D1_HUMAN		1	CTTGGGAGGTA	0.323	
-	15	1860		NM_004333	NP_004324	P15056	BRAF_HUMAN	rotein kinas_R603>I(2)|p.T	18290	ATTTCACTGTA	0.368	
-	7	1096		NM_001080392	NP_001073861	A4D1U4	LCHN_HUMAN		1	CTGCTCGTTGA	0.597	
+	1	454		NM_001001656	NP_001001656	Q8NGU2	OR9A4_HUMAN	Name=4; (Potential).	1	TGTTTGGGTTT	0.433	
+	10	1171		NM_004668	NP_004659	O43451	MGA_HUMAN	(Potential).|Maltase.	2	CCCTTCCCTCC	0.418	
+	1	351		NM_012365	NP_036497	Q96R48	OR2A5_HUMAN	Name=3; (Potential).	3	GTAATGATGTC	0.458	
-	4	1764		NM_001001661	NP_001001661	Q6IV72	ZN425_HUMAN	2H2-type 13.	3	TTCCAGGAGAAG	0.617	
-	4	1157		NM_001001661	NP_001001661	Q6IV72	ZN425_HUMAN	C2H2-type 6.	3	ACACTCGGGAC	0.607	
+	4	833		NM_006207	NP_006198	Q15198	PGFRL_HUMAN		0	TCTCCGTCAAG	0.567	
+	9	1605	sense_Mutation_p	NM_001128431	NP_001121903	Q15043	S39AE_HUMAN	ical; (Potential).	0	ATTCACCATCA	0.537	
+	3	1244	md.1_Intron|TACC	NM_006283	NP_006274	O75410	TACC1_HUMAN	with YEATS4.|SPAZ 1.	1	TCTCCCCCTGAC	0.542	
+	5	630	.1_RNA|IDO2_uc	NM_194294	NP_919270	Q6ZQW0	I23O2_HUMAN		2	TTGTCGAAGTC	0.473	
-	3	491		NM_014420	NP_055235	Q9UBT3	DKK4_HUMAN		1	GCTTCCTTTTG	0.448	
+	2	107	xpg.2_Missense_	NM_001135676	NP_001129148	Q96E16	CH040_HUMAN		0	TTCACGAAGCC	0.408	
+	2	235		NM_001007176	NP_001007177	Q8WWR9	PDPFL_HUMAN		0	TATTATCGAAGT	0.413	
-	17	3286_3287	NL_uc003xqt.3_	NM_144651	NP_653252	A1KZ92	PXDNL_HUMAN		2	AGAATAGGATTG	0.46	
+	4	1178	1_uc011ldy.1_Intr	NM_006269	NP_006260	P56715	RP1_HUMAN		12	AAGAGGAAGAA	0.338	
-	2	318	C1_uc011leo.1_5'	NM_018120	NP_060590	Q9NVT9	ARMC1_HUMAN		1	TTAACGGATCT	0.488	
-	1	2933		NM_025054	NP_079330	Q96JH7	VCIP1_HUMAN		8	ACATTTCTTTTTC	0.363	

+	4	3580	.E1091K|ZFHX4_	NM_024721	NP_078997	Q86UP3	ZFHX4_HUMAN		15	CAGAGGAGGAC	0.532	
-	5	1289	no.2_Missense_M	NM_001146	NP_001137	Q15389	ANGP1_HUMAN		7	TTTCCTCCCTTT	0.308	
+	49	8481		NM_177531	NP_803875	Q86WI1	PKHL1_HUMAN	ellular (Potential).	14	GAACATGAAATG	0.373	
-	1	1001		NM_031308	NP_112598	P58107	EPIPL_HUMAN	Plectin 7.	2	GGGGTCCACCA	0.672	
+	3	1316	kx.1_Missense_M	NM_198572	NP_940974	Q76KD6	SPERI_HUMAN		2	AGGTCCACGCA	0.617	
+	2	747		NM_021240	NP_067063	Q9NQL9	DMRT3_HUMAN		3	CCCTCGGGGACT	0.562	
-	37	7015	zlk.2_RNA|FREM1	NM_144966	NP_659403	Q5H8C1	FREM1_HUMAN	-type lectin.	5	GTTGAGAGGGC	0.478	
-	22	3847	q.2_Missense_Mu	NM_000264	NP_000255	Q13635	PTC1_HUMAN	lasmic (Potential).	379	CGGAGGAATCA	0.687	
-	4	723	bjg.2_Missense_	NM_005118	NP_005109	O95150	TNF15_HUMAN	ellular (Potential).	0	TACTTCGCATAC	0.527	rs150498686
-	8	1729	p.P543H|ASTN2_	NM_198187	NP_937830	O75129	ASTN2_HUMAN	r (Potential).|EGF-like 1.	9	GAACAGGGTCA	0.498	
-	12	1707	_p.P489L|FAM129	NM_022833	NP_073744	Q96TA1	NIBL1_HUMAN		0	GGAACGGGATG	0.632	
-	2	259	10_uc011mee.1_Missense_Mutation_p.A67V|LCN10_			Q6JVE6	LCN10_HUMAN		1	CGGACGCCCCC	0.632	
-	7	1523	clq.1_Missense_M	NM_013366	NP_037498	Q9UJX6	ANC2_HUMAN		1	CACAGGGTCCG	0.642	
-	5	1865		NM_015419	NP_056234	Q9NR99	MXRA5_HUMAN	like C2-type 1.	8	CAAGTACCCTAT	0.527	
-	4	424	nse_Mutation_p.P	NM_001033583	NP_001028755	Q9Y305	ACOT9_HUMAN		3	CCAAAGGCAAG	0.373	
+	8	1045	hq.2_Missense_M	NM_004651	NP_004642	P51784	UBP11_HUMAN		3	ACTTCCGCAAC	0.582	
-	20	2894		NM_001013742	NP_001013764	Q5KSL6	DGKK_HUMAN		2	AGAAGTTGATA	0.468	
+	2	976		NM_005448	NP_005439	O95972	BMP15_HUMAN		2	GTCTCCGAGTA	0.532	
+	10	1733	_p.K354N|DACH2_	NM_053281	NP_444511	Q96NX9	DACH2_HUMAN	tial.|DACHbox-C.	5	AAGAAGGAGAA	0.428	
-	4	1943	m.1_Missense_M	NM_012471	NP_036603	Q9UL62	TRPC5_HUMAN	ical; (Potential).	1	CATGGGAAACA	0.498	
+	3	380		NM_000686	NP_000677	P50052	AGTR2_HUMAN	Name=1; (Potential).	3	TAATTGGATTTCT	0.358	
-	15	2438	rt_Site|UTY_uc004	NM_007125	NP_009056	O14607	UTY_HUMAN		0	AATCAGTTATGG	0.433	
+	2	212		NM_021933	NP_068752	Q5JXC2	MIIP_HUMAN		1	GCTGCGGCTGC	0.682	
-	6	741	_Mutation_p.R19	NM_152372	NP_689585	Q5VTT5	MYOM3_HUMAN	like C2-type 1.	3	TCAATCCGTGTG	0.388	
-	4	349	_5'UTR|UBXN11_	NM_183008	NP_892120	Q5T124	UBX11_HUMAN		1	TCCTCGCCTCC	0.557	
-	5	1160	_p.R348C|ZNF683	NM_173574	NP_775845	Q8IZ20	ZN683_HUMAN		0	TGGACGCTCTC	0.597	
-	4	777	201H|CCDC17_	NM_001114938	NP_001108410	Q96LX7	CCD17_HUMAN		1	GAATGCGGGCC	0.701	
-	15	2232	r.1_Missense_Mut	NM_021080	NP_066566	O75553	DAB1_HUMAN		3	CTCTTCGCTTTT	0.423	rs142236626
+	7	2004	lsf.2_Missense_M	NM_017734	NP_060204	Q9NP74	PALMD_HUMAN		3	CATTCCCCATTT	0.448	
-	1	261	2_5'UTR|C1orf10	NM_018372	NP_060842	Q5T3J3	LRIF1_HUMAN		0	TTATTTGACATTT	0.562	
-	13	1795_1796	ff.1_Missense_M	NM_000036	NP_000027	P23109	AMPD1_HUMAN		4	GTGAGGTCGG	0.446	
-	11	1603	_Mutation_p.P55	NM_005060	NP_005051	P51449	RORG_HUMAN	gand-binding.	2	TGGAGGGAAAG	0.597	
-	2	109		NM_001008536	NP_001008536	Q5QJ38	TCHL1_HUMAN		2	TGTGGAATGTC	0.463	
+	5	1198	1C_uc001frv.2_Int	NM_001765	NP_001756	P29017	CD1C_HUMAN	ellular (Potential).	4	TTCCATGAATTG	0.378	
+	4	914	p.T136M|PBX1_u	NM_002585	NP_002576	P40424	PBX1_HUMAN		5	GAGCACGTGCG	0.607	
+	71	11133		NM_031935	NP_114141	Q96RW7	HMCN1_HUMAN	ike C2-type 35.	23	GTTACGGAACA	0.418	
+	4	607		NM_014359	NP_055174	Q9UBM4	OPT_HUMAN	LRR 1.	0	CAACCGCATCA	0.557	
-	4	1362		NM_173854	NP_776253	Q8IVJ1	S41A1_HUMAN		2	GTGTCCAATGTT	0.572	
-	4	1042	w.1_Missense_Mu	NM_003268	NP_003259	O60602	TLR5_HUMAN	ellular (Potential).	4	AAAAGGAGAGC	0.423	
-	31	5805	e_Mutation_p.R50	NM_014801	NP_055616	A6NKB5	PCX2_HUMAN		2	CTAATTCTGTCC	0.537	
-	13	2678	zu.2_Missense_M	NM_014812	NP_055627	Q5SW79	CE170_HUMAN		2	ACTGAGCCTCC	0.378	
+	12	5211	.R1209W|KIF26B_	NM_018012	NP_060482	Q2KJY2	KI26B_HUMAN		3	TGGCTCGGCCC	0.687	
+	3	528	zb.1_Missense_	NM_001001957	NP_001001957	Q7Z3T1	OR2W3_HUMAN	ellular (Potential).	3	TTAATGGATGT	0.567	
+	1	429	L13_uc001ids.2_I	NM_001001963	NP_001001963	Q8NGY9	OR2L8_HUMAN	Name=4; (Potential).	2	CTGATGATAAC	0.433	
+	17	2450	qy.2_Missense_M	NM_004641	NP_004632	P55197	AF10_HUMAN		2	AAGTCTCTCGC	0.423	
+	5	599	1izo.1_RNA|HSD17B7P2_uc001izp.1_Missense_Mutation_p.N173S						0	TCGCAATGCAA	0.453	rs2257765
-	1	741		NM_001057	NP_001048	P21452	NK2R_HUMAN	Name=1; (Potential).	1	TACCCGTCACG	0.607	rs140763069

+	53	8038	1jsh.3_Splice_Site_	NM_022124	NP_071407	Q9H251	CAD23_HUMAN		11	CTGCCAGAGGCC	0.627	
-	24	2464	e_Mutation_p.R768	NM_013451	NP_038479	Q9NZM1	MYOF_HUMAN	lasmic (Potential).	4	CTCCCCGGATCAT	0.502	
+	4	2300	_p.L556F|PLCE1_	NM_016341	NP_057425	Q9P212	PLCE1_HUMAN	Ras-GEF.	3	GACTACCTTTGCT	0.537	
+	7	1217	c010qol.1_Missens	NM_001776	NP_001767	P49961	ENTP1_HUMAN	cellular (Potential).	3	TTTACAAGACCCC	0.423	
-	7	1141	sn.2_Missense_Mu	NM_024895	NP_079171	Q9H5P4	PDZD7_HUMAN		3	TTACGTCGGTCCA	0.547	
+	11	1427	BP2_uc010qrz.1_F	NM_004132	NP_004123	Q14520	HABP2_HUMAN	Peptidase S1.	3	TCCTTTCCCTCTC	0.512	
+	8	1100	e_Mutation_p.W26	NM_198496	NP_940898	Q5GFL6	VWA2_HUMAN		5	CATGCTGGAGAG	0.642	
-	4	464	rf82_uc001lcs.1_3	NM_144661	NP_653262	Q8WW14	CJ082_HUMAN		0	CCAGGAAGTCCTT	0.552	
+	4	873		NM_020346	NP_065079	Q9P2U8	VGLU2_HUMAN	ical; (Potential).	4	TCAGGGTTTTCG	0.343	
+	2	461	o.1_Missense_Mu	NM_004265	NP_004256	O95864	FADS2_HUMAN	lasmic (Potential).	2	ACCACGGCAAGA	0.627	
-	2	179	.1_Silent_p.C67C|	NM_018093	NP_060563	Q6RFH5	WDR74_HUMAN		1	GCAGCAGCAGCC	0.652	
+	10	2258	cu.2_5'Flank|TM7S	NM_013265	NP_037397	Q9UID3	FFR_HUMAN		0	TACCTGTGGCGT	0.637	
-	1	1147		NM_053054	NP_444282	Q8NEC5	CTSR1_HUMAN	lasmic (Potential).	2	GGGCATCGTGAAT	0.562	
+	1	519		NM_005553	NP_005544	P26371	KRA59_HUMAN	repeats of C-C-X-P.	0	GTGGGTCATCCTC	0.627	
+	5	396	AF1_uc009ytx.1_RI	NM_025155	NP_079431	Q9BRP4	PAAF1_HUMAN	WD 1.	2	GGCAGGCTTCCA	0.453	
+	6	2112	A1_uc001ovm.2_I	NM_001098638	NP_001092108	Q8NCN4	RN169_HUMAN		1	CCTACGGTCCAC	0.498	
-	1	414	c.1_RNA|CREBZF	NM_001039618	NP_001034707	Q9NS37	ZHANG_HUMAN		1	GCCGGGAGATCC	0.726	
+	2	433		NM_153696	NP_710163	Q9HBA9	FOH1B_HUMAN		6	AGAATACGCTTAT	0.328	
+	11	2550	pfc.2_Missense_M	NM_130847	NP_570899	Q8IY63	AMOL1_HUMAN		2	CGCTCCGTTCCAT	0.537	
+	6	736	e_Mutation_p.R18	NM_015517	NP_056332	Q9BQA5	HINFP_HUMAN	C2H2-type 3.	4	AGGACCGCAGTA	0.547	
+	42	5298	I|CACNA1C_uc00	NM_199460	NP_955630	Q13936	CAC1C_HUMAN	lasmic (Potential).	11	AGGTCACCGTTGC	0.512	
+	11	1088	ses.1_Missense_M	NM_005002	NP_004993	Q16795	NDUA9_HUMAN		1	ACTTACCGCTGGC	0.542	rs3210083
-	3	276	_p.E50K|CD163_	NM_004244	NP_004235	Q86VB7	C163A_HUMAN	cellular (Potential).	8	TCAGCTCCTTGTC	0.438	
-	5	723		NM_018423	NP_060893	Q6J9G0	STYK1_HUMAN		8	TGGAGGAACAGC	0.527	rs140174760
-	4	579	zhz.2_Missense_M	NM_004963	NP_004954	P25092	GUC2C_HUMAN	cellular (Potential).	6	ACAATCCAAAACT	0.403	
+	8	816	zp.1_Missense_M	NM_181711	NP_859062	Q7Z6J2	GRASP_HUMAN	ith PSCD3 (By similarity).	2	CTGCTCCCGGGC	0.741	
-	8	661	IAA0748_uc010sp	NM_001098815	NP_001092285	A2RU30	K0748_HUMAN		2	AAAAATCGGGCG	0.517	
+	3	511	i.2_5'Flank|TSFM_	NM_015433	NP_056248	Q96AZ1	MT21B_HUMAN		0	AGGTGCGTGCCT	0.602	
+	7	895	p.A280D|SRGAP1	NM_020762	NP_065813	Q7Z6B7	SRGP1_HUMAN		4	ACAGAGCCCTAAC	0.328	
+	13	2635	qo.1_Nonsense_M	NM_014319	NP_055134	Q9Y2U8	MAN1_HUMAN	D1, SMAD2, SMAD3 and S	4	TTTCCCCAGGCTC	0.373	
+	25	3063	ax.2_Nonsense_Mu	NM_178826	NP_849148	Q32M45	ANO4_HUMAN	lasmic (Pote p.R796*(1)	6	GTATTTCGAATTT	0.483	rs145182702
+	1	912		NM_004316	NP_004307	P50553	ASCL1_HUMAN		0	GCCGCAGCAGCA	0.667	
-	7	475	x.3_Missense_Mu	NM_000432	NP_000423	P10916	MLRV_HUMAN	EF-hand 3.	1	TGGTCAACCTGCA	0.612	
+	12	1870	_p.G430*|ALDH2_	NM_000690	NP_000681	P05091	ALDH2_HUMAN		4	GTGTTTGGAGCCC	0.527	
-	8	1130	1tts.2_Missense_M	NM_001109662	NP_001103132				2	GAGAGTCCACTG	0.423	
+	4	889	ui.1_Missense_Mu	NM_016817	NP_058197	P29728	OAS2_HUMAN	OAS domain 1.	1	TCAGAACCGTACT	0.502	
-	4	731		NM_032656	NP_116045	Q8IY37	DHX37_HUMAN		1	CAGCCGGCACGC	0.697	
+	3	353	AP2_uc001vgu.2_In	NM_001098525	NP_001091995	Q8WWK9	CKAP2_HUMAN		2	TTTTTAAGTAGTA	0.378	
-	1	164		NR_027466					0	CAGTTCCCATGGA	0.488	
+	1	416		NM_001005483	NP_001005483	Q8NGD3	OR4K5_HUMAN	lasmic (Potential).	2	GCCGAAGGACATC	0.453	
-	1	1554		NM_175060	NP_778230	Q86T13	CLC14_HUMAN	ical; (Potential).	4	TGCTCACAAATAT	0.507	
+	20	2463	dq.2_Missense_M	NM_002892	NP_002883	P29374	ARI4A_HUMAN		6	GAAAATCCAAAGA	0.284	
-	7	5741	px.2_Missense_M	NM_138420	NP_612429	Q8IVF2	AHNK2_HUMAN		1	GGAGCGGAATGC	0.662	
+	1	496	on_p.P7L|MKRN3_	NM_005664	NP_005655	Q13064	MKRN3_HUMAN		10	CAGCTCCCTCAGA	0.642	
-	4	405	0bec.2_Missense_	NM_144565	NP_653166	Q1HG43	DOXA1_HUMAN	cellular (Potential).	1	CGTTGTAATTGAT	0.582	
+	2	728	e_Mutation_p.E16	NM_003645	NP_003636	O14975	S27A2_HUMAN	nenal (Potential).	2	GCTGTCGAAGAG	0.333	
-	29	7501	y.1_Missense_Mu	NM_015263	NP_056078	Q8TDJ6	DMXL2_HUMAN		9	TTCCAGGGACGA	0.413	

+	2	808	A|GCOM1_uc010	NM_015532	NP_056347	P0CAP1	GCOM1_HUMAN		0	TTCCAGTGGGA	0.448	
-	8	866	p.L249V|ALDH1A	NM_003888	NP_003879	O94788	AL1A2_HUMAN		1	GATAAGCTTTC	0.448	
-	10	1418	p.P351L|MEGF11	NM_032445	NP_115821	A6BM72	MEG11_HUMAN	EGF-like 7.	1	AGCCCGGAGCA	0.637	
+	16	2345	|IQCH_uc002aqp.	NM_001031715	NP_001026885	Q86VS3	IQCH_HUMAN		4	GGGAAAATCAG	0.517	
+	4	694	154N|CD276_uc0	NM_001024736	NP_001019907	Q5ZPR3	CD276_HUMAN	otential).|Ig-like C2-type 1.	1	ACAAGGACCTG	0.637	
+	13	2280	yj.3_Missense_Mu	NM_001130028	NP_001123500	P49761	CLK3_HUMAN	rotein kinase.	2	CTGCCCAGCGC	0.592	
-	5	1722_1723	k.2_RNA|DET1_u	NM_001144074	NP_001137546	Q7L5Y6	DET1_HUMAN		2	CAAAAGGGTGA	0.554	
+	18	3335	L_uc002cmf.2_S	NM_020825	NP_065876	Q96RY5	CRML_HUMAN		0	TGGCAGGTGAA	0.602	
-	13	4257	yn.1_Missense_M	NM_001134407	NP_001127879	Q12879	NMDE1_HUMAN	lasmic (Potential).	45	GGCATCGCACT	0.582	
+	3	533		NM_001039	NP_001030	P51170	SCNNG_HUMAN	llular (By similarity).	6	GCTTTCCAGAG	0.577	
-	2	1390		NM_020807	NP_065858	Q9P2F9	ZN319_HUMAN		0	AGGGCCGCTCG	0.622	
+	17	2104	p.I714M|FUK_uc0	NM_145059	NP_659496	Q8N0W3	FUK_HUMAN		1	CTGATCCGCCA	0.667	
+	2	494	o.2_Missense_Mu	NM_005769	NP_005760	Q8NCG5	CHST4_HUMAN	enal (Potential).	0	TGTGCGACATG	0.607	
+	8	1475	nw.1_Missense_M	NM_178452	NP_848547	Q8NEP3	DAAF1_HUMAN	Pro-rich.	0	AAGGAGAGGAC	0.617	rs144990549
+	2	250	1_5'Flank|CYB5D1	NM_203411	NP_981956	Q6PEY1	TMM88_HUMAN		0	GCACCGCGCAC	0.682	
-	32	4469		NM_003802	NP_003793	Q9UKX3	MYH13_HUMAN	Potential.	6	GCTTCCACTCT	0.512	
+	11	2443	CD_uc002gnp.1_	NM_153604	NP_705832	Q8IZQ8	MYCD_HUMAN		5	CAATTTCAGAGG	0.408	
+	2	3640_3641		NM_016239	NP_057323	Q9UKN7	MYO15_HUMAN	osin head-like.	9	CCTGCCCAAGG	0.678	
-	4	1128_1129	p.R229K|SLFN11	NM_001104588	NP_001098058	Q7Z7L1	SLN11_HUMAN		3	ATTGTCCTTTTT	0.391	
+	2	154	T_uc002hsi.1_5'F	NM_003673	NP_003664	O15273	TELT_HUMAN		0	CCAGAGACATG	0.677	
+	3	349	02hui.1_Nonsens	NM_133264	NP_573571	Q8TF74	WIPF2_HUMAN	WH2.	3	GGGGTCGAGGC	0.488	
+	4	782	on_p.S4*|KPNB1_	NM_002265	NP_002256	Q14974	IMB1_HUMAN	HEAT 1.	3	GGAGTCGACAT	0.453	
+	2	455	00A_uc010dfr.2_I	NM_007261	NP_009192	Q9UGN4	CLM8_HUMAN	(Potential).|Ig-like V-type.	2	GACCCTCAACA	0.537	
-	9	1915	e_Mutation_p.D44	NM_018414	NP_060884	Q9NSC7	SIA7A_HUMAN	enal (Potential).	0	TTCATCGTGTAG	0.532	
-	20	3382		NM_005406	NP_005397	Q13464	ROCK1_HUMAN	Glu-rich.	5	TCCAATAAAGTA	0.303	
+	61	8128	s.3_Missense_Mu	NM_198129	NP_937762	Q16787	LAMA3_HUMAN	minin G-like 2.	11	CCATTCGGTAC	0.383	
-	5	1201	.Q156H|CXXC1_u	NM_014593	NP_055408	Q9P0U4	CXXC1_HUMAN		2	ctgctgctgctggtgatg	0.468	
-	6	747_748		NM_005570	NP_005561	P49257	LMAN1_HUMAN	tential).|L-type lectin-like.	1	GTGCAGGGATA	0.356	
+	28	3198	a.2_Missense_Mu	NM_198531	NP_940933	O43861	ATP9B_HUMAN	lasmic (Potential).	3	TGACCGTCCGC	0.577	rs147969611
+	2	1162	_p.S237P|NFATC1	NM_006162	NP_006153	O95644	NFAC1_HUMAN	SP repeats.|2.	2	GGCACTCCCCC	0.701	
+	2	1191		NM_012283	NP_036415	Q9UJ96	KCNG2_HUMAN	=Segment S6; (Potential).	0	CTCATGGCCTT	0.682	
+	13	1737	dsu.2_Missense_	NM_001319	NP_001310	P78368	KC1G2_HUMAN		1	CAAGAGGAGAA	0.652	
+	20	2309	c002lvd.1_5'Flan	NM_032482	NP_115871	Q8TEK3	DOT1L_HUMAN		4	CCGGCCGCGCC	0.677	
+	2	339	p.2_Missense_Mu	NM_205843	NP_995315	P08651	NFIC_HUMAN	CTF/NF-I.	0	ACTTCGTGCTG	0.677	
-	7	1618_1619	p.Y504H|INSR_u	NM_000208	NP_000199	P06213	INSR_HUMAN		12	AATGTAAGAAA	0.45	
-	25	3245		NM_032447	NP_115823	Q75N90	FBN3_HUMAN	14; calcium-binding.	11	TTGCACACTCG	0.617	
+	7	827	mwa.1_Nonsense_	NM_005053	NP_005044	P54725	RD23A_HUMAN		1	AGCCCCAGTTC	0.642	
-	4	1518	.R366W|WIZ_uc0	NM_021241	NP_067064	O95785	WIZ_HUMAN		0	CACCCGTATTT	0.627	
+	1	493		NM_001004466	NP_001004466	Q8NGA6	O10H5_HUMAN	ellular (Potential).	1	ATTTTCCACCTC	0.597	
+	8	2016	w.3_Missense_M	NM_153221	NP_694953	Q8IUL8	CILP2_HUMAN		1	GTTCTCCGTGG	0.726	
-	4	1663		NM_001098626	NP_001092096	A6NK75	ZNF98_HUMAN		2	TTCTCTCCAGTA	0.388	
+	4	3673	d.1_Missense_Mu	NM_014717	NP_055532	O15090	ZN536_HUMAN		11	ACAACGATGAA	0.557	
-	3	279	nse_Mutation_p.R	NM_032816	NP_116205	Q96ST8	CEP89_HUMAN		0	CGTCCGCCCAG	0.547	
-	6	746	SGRP4_uc010xu	NM_170604	NP_733749	Q8TDF6	GRP4_HUMAN		3	TGGGGGGCCAG	0.617	
+	20	2646	u.2_Missense_Mu	NM_000540	NP_000531	P21817	RYR1_HUMAN	Cytoplasmic.	12	CCTGGTGGGCC	0.642	
+	13	1754	8F|LTBP4_uc002	NM_001042544	NP_001036009	Q8N2S1	LTBP4_HUMAN	rich.|EGF-like 3.	1	CCGATGCATTG	0.682	
-	2	123	2pav.2_Missense_Mutation_p.S49W			O75865	TPC6A_HUMAN		0	GGACCGACAGG	0.697	

-	7	660	e_Mutation_p.E17	NM_015953	NP_057037	Q9Y314	NOSIP_HUMAN		1	GGCTTCGGGCG	0.662	
+	11	1637	Missense_Mutatio	NM_007121	NP_009052	P55055	NR1H2_HUMAN	-binding (Potential).	0	GCTGTCGGAGA	0.647	
-	1	665	_p.R11W|SYT3_uc	NM_032298	NP_115674	Q9BQG1	SYT3_HUMAN	cular (Potential).	3	CCGCCGGCAGA	0.607	rs140892148
-	5	2581	P12_uc002qcj.3_	NM_144687	NP_653288	P59046	NAL12_HUMAN		7	CAGCATCATGCC	0.498	
+	8	1419	_p.D427N|LILRA2_	NM_001130917	NP_001124389	Q8N149	LIRA2_HUMAN	cellular (Potential).	1	CCCCAGGATTAC	0.587	
+	1	313	etg.2_Missense_M	NM_176811	NP_789781	Q86W28	NALP8_HUMAN	DAPIN.	13	CAGCTGGGCAG	0.522	
-	5	508	2orf43_uc010ykc.1	NM_021925	NP_068744	Q9H6V9	CB043_HUMAN		0	AGGCACGAATTA	0.383	
-	18	2821		NM_000384	NP_000375	P04114	APOB_HUMAN		27	TGGACCCCACTC	0.498	
+	2	1197	7L_uc010ymf.1_5'	NM_018158	NP_060628	Q9BWU0	NADAP_HUMAN		0	GAGAAGAAGAT	0.463	
+	3	798		NM_003124	NP_003115	P35270	SPRE_HUMAN		2	ACGAGTTCAAG	0.512	
+	9	4114		NM_144993	NP_659430	O43151	TET3_HUMAN		0	GAGGACGGCTG	0.677	
-	4	615	ssp.1_Missense_	NM_016618	NP_057702	Q9NPI7	KRCC1_HUMAN		1	TGCATGATCTTG	0.468	
+	4	700	n_p.P95S|CNGA3	NM_001298	NP_001289	Q16281	CNGA3_HUMAN		6	CAGGGACCGGA	0.602	
-	10	1797	_p.R571C|TBC1D8	NM_001102426	NP_001095896	O95759	TBCD8_HUMAN	ab-GAP TBC.	3	GGAGCGGTGCA	0.577	
+	2	625		NM_001099289	NP_001092759	Q8TEJ3	SH3R3_HUMAN	SH3 1.	1	GGAAGGAACCT	0.592	
+	1	362		NM_002193	NP_002184	P09529	INHBB_HUMAN		3	TCACGGCCCTG	0.731	
-	69	11682		NM_018557	NP_061027	Q9NZR2	LRP1B_HUMAN	ntial).|LDL-receptor class A	50	ACATTTCCATTTT	0.358	
-	55	10793		NM_004525	NP_004516	P98164	LRP2_HUMAN	A 26.|Extracellular (Potent	29	CAGATAGGAATG	0.498	
-	275	70159	007K|TTN_uc010z	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	GATGCTGTCTTC	0.393	
-	44	10570	_uc010zfj.1_Intro	NM_133437	NP_597681	Q8WZ42	TITIN_HUMAN		153	TGGATGGAACTT	0.378	
-	6	1476	se_Mutation_p.Q2	NM_015265	NP_056080	Q9UPW6	SATB2_HUMAN		1	ACTCCTGGCAC	0.313	
-	16	2734		NM_015049	NP_055864	O60296	TRAK2_HUMAN		0	TGGAGGGGGTTC	0.517	
+	16	2242	_Mutation_p.S659	NM_015690	NP_056505	Q9NRP7	STK36_HUMAN		11	CCATTTCCTCTG	0.572	
-	5	1353	e_Mutation_p.R31	NM_005689	NP_005680	Q9NP58	ABCB6_HUMAN	nsmembrane type-1.	2	GCCAGCGCAGT	0.672	
-	7	3168	.E1041K|SPHKA	NM_001142644	NP_001136116	Q2M3C7	SPKAP_HUMAN		10	CCACTTCATTGG	0.512	
+	1	1177	_p.R232K|GPR35_	NM_005301	NP_005292	Q9HC97	GPR35_HUMAN	lasmic (Potential).	3	CCAGAGGCCAC	0.657	
+	3	180	FRG1B_uc010gdr.1_RNA|FRG1B_uc010ztk.1_Missense_Mutation_p.A2P						0	AAAATGGCTTTG	0.333	rs145412486
+	16	2039	_Mutation_p.R511	NM_006892	NP_008823	Q9UBC3	DNM3B_HUMAN		5	AAGGCGGCCCA	0.587	rs143300013
+	3	428	2xew.2_Missense_	NM_012156	NP_036288	Q9H4G0	E41L1_HUMAN		3	AGAAATCGCCCC	0.567	
-	18	2164	2xgk.2_Missense_	NM_152503	NP_689716	Q9H579	CT132_HUMAN		0	CTTTTCCATGATG	0.453	
+	7	797	A3_uc002xtm.2_M	NM_181659	NP_858045	Q9Y6Q9	NCOA3_HUMAN		5	AATTGCCGTATGT	0.378	
-	68	9390		NM_005560	NP_005551	O15230	LAMA5_HUMAN	minin G-like 2.	3	CCTGTCGTGTTC	0.687	
-	21	1714	TE_uc002yir.1_Mi	NM_199261	NP_954870	P56180	TPTE_HUMAN	2 tensin-type.	5	CATTTTCCTAAT	0.318	
-	4	2618		NM_003489	NP_003480	P48552	NRIP1_HUMAN	ession domain 2.	0	TGAGAGCAAAG	0.393	
-	1	433		NM_001085455	NP_001078924	Q3LI83	KR241_HUMAN		0	GCATTTCGAGTG	0.353	
-	12	1616	_p.H318Y|ERG_uc	NM_001136155	NP_001129627	P11308	ERG_HUMAN		2828	AGGGTGGGGCG	0.577	
+	12	1571	.2_RNA|UBASH3	NM_018961	NP_061834	P57075	UBS3A_HUMAN	osphatase-like.	3	GAATCTTTGAAT	0.418	
+	11	1310	zmq.1_Nonsense_	NM_031481	NP_113669	Q9H1K4	GHC2_HUMAN	Solcar 3.	0	ACTCTGGATTCA	0.547	
+	1	1651	x.2_Missense_Mu	NM_004327	NP_004318	P11274	BCR_HUMAN	ling to ABL SH2-domain.	12	CAGCCGCGTGT	0.627	
+	43	7427	018B_uc011aka.1_	NM_032608	NP_115997	Q8IUG5	MY18B_HUMAN		12	TGGACGATGCG	0.597	
-	14	1891	h.1_Missense_Mu	NM_002473	NP_002464	P35579	MYH9_HUMAN	yosin head-like.	11	CTTGGGGTGGG	0.612	
-	3	692		NM_006078	NP_006069	Q9Y698	CCG2_HUMAN	ical; (Potential).	0	CCGGCACTCAGG	0.562	
+	7	2541	atq.1_Missense_M	NM_001039141	NP_001034230	Q9H2D6	TARA_HUMAN		1	GAGCCTCCTCTC	0.567	
+	5	799		NM_006855	NP_006846	O43731	ERD23_HUMAN		2	CCAATCTGAGGA	0.363	
+	16	2107	RNA|POLR3H_uc0	NM_001098	NP_001089	Q99798	ACON_HUMAN		4	ATCCACGGTGA	0.627	
+	3	378	ln.2_Missense_Mu	NM_007311	NP_009295	B1AH88	TSPOB_HUMAN		0	GCTGGCGTGGG	0.677	
-	8	1292	_p.I259F|PNPLA5	NM_138814	NP_620169	Q7Z6Z6	PLPL5_HUMAN		0	CCTGATGGGCC	0.672	

-	4	750	385D_uc010hfb.1_	NM_024697	NP_078973	Q9H6B1	Z385D_HUMAN		5	ATTTTTCATGGCT	0.463
-	2	994	e_Mutation_p.R25	NM_194293	NP_919269	Q702N8	XIRP1_HUMAN		8	CCTCCCGGCATC	0.612
-	7	865	MT_uc003cwy.2_M	NM_000481	NP_000472	P48728	GCST_HUMAN		1	GAATAGCTGTTGC	0.587
+	2	594	o.3_Intron|GRM2_	NM_000839	NP_000830	Q14416	GRM2_HUMAN	cellular (Potential).	1	TCACGCCACATC	0.582
+	49	7872		NM_015512	NP_056327	Q9P2D7	DYH1_HUMAN		3	ACAGATGATGCAC	0.398
-	5	588	hna.2_Missense_M	NM_017563	NP_060033	Q8NFM7	I17RD_HUMAN	cellular (Potential).	0	GGAAGGAAAAGC	0.408
+	21	3814	af.2_Missense_Mut	NM_001457	NP_001448	O75369	FLNB_HUMAN	with FBLP1.|Filamin 10.	19	CACTTCCCCGCCC	0.537
-	5	1284	np.2_Splice_Site_	NM_001033057	NP_001028229	Q96QZ7	MAGI1_HUMAN		6	AATCGGCTGCTTA	0.448
-	2	738	dzg.2_Missense_M	NM_199512	NP_955806	Q76M96	CCD80_HUMAN		2	ACACATCGTCCTT	0.567
+	4	457	_p.E100K|PLS1_uc	NM_001145319	NP_001138791	Q14651	PLSI_HUMAN		1	AGAGGGAAGGG	0.343
-	1	301		NM_033214	NP_149991	Q14410	GLPK2_HUMAN		4	TGGTTTCCCTCTC	0.428
+	4	698	se_Mutation_p.P17	NM_017912	NP_060382	Q8IVU3	HERC6_HUMAN	RCC1 3.	5	CAGCCCGCAGA	0.592
+	1	600	ku.2_Nonsense_M	NM_007351	NP_031377	Q13201	MMRN1_HUMAN		4	GGAAATCGAGCCC	0.353
-	2	285		NM_000134	NP_000125	P12104	FABPI_HUMAN		1	CAGTTCCGTCTGC	0.318
+	1	86		NM_024582	NP_078858	Q6V0I7	FAT4_HUMAN		18	TGTTTTGGCTACT	0.617
+	13	2708	ciu.1_Missense_M	NM_001083619	NP_001077088	P42262	GRIA2_HUMAN	cellular (Potential).	4	TGGATTCCAAAGC	0.438
-	4	546	orf45_uc010iqt.1_F	NM_152543	NP_689756	Q96LM5	CD045_HUMAN		0	ATAGCCCATTTGC	0.443
-	2	1017		NM_005958	NP_005949	P48039	MTR1A_HUMAN	lasmic (Potential).	5	CGGTTTCCATTTA	0.478
+	6	667		NM_004477	NP_004468	Q14331	FRG1_HUMAN		0	TAGATGCAATGA	0.368
-	4	448		NM_020040	NP_064424	Q99867	TBB4Q_HUMAN		0	GAGAAGGGTACC	0.557
-	20	3198		NM_001369	NP_001360	Q8TE73	DYH5_HUMAN	n (By similarity).	31	TTCACTGCTCCAC	0.483
-	1	361	3jif.3_Missense_M	NM_016180	NP_057264	Q9UMX9	S45A2_HUMAN	lasmic (Potential).	3	CTGGCCGATCCG	0.642
+	14	1645	oo.2_Missense_Mu	NM_024615	NP_078891	Q8N3A8	PARP8_HUMAN		5	GAGACCGTGGCT	0.294
+	1	1439	_p.A417T|SNX18_	NM_052870	NP_443102	Q96RF0	SNX18_HUMAN		0	CCCGCCGCTGCC	0.617
-	14	2212	oi.1_Missense_Mu	NM_000439	NP_000430	P29120	NEC1_HUMAN		2	GGAGTCGCAGC	0.542
-	9	2817	3kxy.1_Missense_I	NM_133456	NP_597713	Q2M3G4	SHRM1_HUMAN	ASD2.	1	GCAGCCGCTCC	0.682
-	14	2102	HL3_uc003lbr.3_M	NM_017415	NP_059111	Q9UH77	KLHL3_HUMAN	Kelch 6.	0	CCACCGAAGCC	0.532
-	10	2107	w.1_Missense_Mu	NM_004883	NP_004874	O14511	NRG2_HUMAN	lasmic (Potential).	6	CACGGCGTGCG	0.592
-	2	399	sense_Mutation_p	NM_014790	NP_055605	Q96AA8	JKIP2_HUMAN		2	TTATTTCGCCCT	0.458
-	2	828	FIP2_uc003lwr.2_I	NM_001001343	NP_001001343	Q8TBE3	FNDC9_HUMAN		0	GTGGGTCACCAC	0.572
-	9	1546		NM_005990	NP_005981	O94804	STK10_HUMAN		8	TGACACGGGTCC	0.612
-	13	2077	_p.S514L|UIMC1_u	NM_016290	NP_057374	Q96RL1	UIMC1_HUMAN		4	TCACCTGAAGTCT	0.483
+	13	1770		NM_003052	NP_003043	Q06495	NPT2A_HUMAN	lame=M8; (Potential).	1	GTGGTGCTCATCA	0.632
+	7	1619	wr.2_Missense_M	NM_006567	NP_006558	O95363	SYFM_HUMAN	FDX-ACB.	0	CCAGAGAGAGG	0.597
+	7	1584		NM_033229	NP_150232	Q9C019	TRI15_HUMAN	B30.2/SPRY.	0	TGGCCGGGGAG	0.731
+	2	261	n_p.G17R|MICB_u	NM_005931	NP_005922	Q29980	MICB_HUMAN	cellular (Potential).	0	GCTGAGGGACATC	0.562
-	1	807		NR_001444					0	GACAGGAGGCAC	0.577
+	76	11602	sense_Mutation_p	NM_001371	NP_001362				21	GTGGCTGCAGAA	0.507
+	6	1883	p.G599D|GPR115_	NM_153838	NP_722580	Q8IZF3	GP115_HUMAN	cellular (Potential).	8	AGAAAGGCTACAT	0.478
-	45	7257	pht.2_Missense_M	NM_004370	NP_004361	Q99715	COCA1_HUMAN	VWFA 4.	9	ACAAATGAAACCT	0.443
+	3	568	se_Mutation_p.L92	NM_001446	NP_001437	O15540	FABP7_HUMAN		0	GACAAACTTGTTC	0.353
-	12	1817	gv.2_Missense_Mu	NM_003980	NP_003971	Q14244	MAP7_HUMAN	Potential.	0	CGAGTCGTCCTC	0.582
-	2	173	AT2_uc003qjk.1_F	NM_182503	NP_872309	Q7Z6V5	ADAT2_HUMAN		0	CAACAGGAACTTC	0.388
+	8	3010	o.R847H|GRM1_uc	NM_000838	NP_000829	Q13255	GRM1_HUMAN	lasmic (Potential).	19	ATGTCCGCAGTG	0.512
+	11	1619		NM_000876	NP_000867	P11717	MPRI_HUMAN	menal (Potential).	3	CTGGTCCGCCATC	0.532
+	18	2589	wc.1_Missense_M	NM_001040001	NP_001035090	P55196	AFAD_HUMAN	Dilute.	5	GGGTGCGATTAT	0.537
-	16	1605	a.2_Missense_Mut	NM_004080	NP_004071	Q9Y6T7	DGKB_HUMAN	DAGKc.	12	CCATTTCCAGAAA	0.289

+	5	600	_uc011kcg.1_Miss	NM_181597	NP_853628	Q16831	UPP1_HUMAN			0	TAAATCCAAACAT	0.413	
+	17	4934	yr.2_Missense_Mu	NM_152701	NP_689914	Q86UQ4	ABCAD_HUMAN			10	ATAAGGATGTG	0.388	
-	7	925	n.1_Missense_Mu	NM_000601	NP_000592	P14210	HGF_HUMAN	Kringle 2.		4	AAAGCCCTTGT	0.493	
+	23	3676	1_uc011kkn.1_Int	NM_181552	NP_853530	P39880	CUX1_HUMAN			8	GCGGCGGCACA	0.657	
-	4	2400		NM_002711	NP_002702	Q16821	PPR3A_HUMAN			34	TATCTCGTTGA	0.398	
+	1	1383		NM_012281	NP_036413	Q9NZV8	KCND2_HUMAN	lasmic (Pote	p.R140H(1)	5	AGGATCGCAGG	0.602	
+	22	3290		NM_024913	NP_079189	A4D0V7	CG058_HUMAN			9	ACAGGGGAAGT	0.323	
-	15	1860		NM_004333	NP_004324	P15056	BRAF_HUMAN	rotein kinas	_R603>I(2)|p.T	18290	ATTTCACTGTA	0.368	
-	5	983	rl.1_Missense_Mu	NM_001008270	NP_001008271	A4D1T9	PRS37_HUMAN	eptidase S1.		1	TCGATTCCCTGG	0.443	
-	1	99		NM_001001658	NP_001001658	Q8NGT5	OR9A2_HUMAN	Name=1; (Potential).		1	TAAATAGAAGAA	0.433	
+	1	737		NM_001004685	NP_001004685	O95006	OR2F2_HUMAN	Name=6; (Potential).		4	CCTCACGGTGG	0.517	
-	2	271		NM_003840	NP_003831	Q9UBN6	TR10D_HUMAN	(Potential).|TNFR-Cys 1.		0	CCTGCCGGGGG	0.582	
-	5	1124_1125	_5'Flank|uc003xd	NM_002318	NP_002309	Q9Y4K0	LOXL2_HUMAN	SRCR 2.		3	TCCATGGAGAAT	0.604	
-	1	771	RG_uc003xim.1_	NM_013357	NP_037489	Q9UJV8	PURG_HUMAN	By similarity.		0	CCTCTTCGTTCT	0.453	
-	2	306	P2_uc010lzv.1_Int	NM_002677	NP_002668	P02689	MYP2_HUMAN			0	AAATTCCTGGC	0.398	
-	9	960	se_Mutation_p.G2	NM_001738	NP_001729	P00915	CAH1_HUMAN			2	TCTGCCCTTCA	0.448	rs121909577
-	13	1731	_p.P322S|CDH17_	NM_004063	NP_004054	Q12864	CAD17_HUMAN	(Potential).|Cadherin 5.		6	CTCAGGATTTT	0.403	
-	5	853	.D138N|MTERFD	NM_015942	NP_057026	Q96E29	MTER1_HUMAN			1	TGTTATCCAGTC	0.348	
-	2	481	ny.2_Missense_M	NM_014112	NP_054831	Q9UHF7	TRPS1_HUMAN			7	CAGAGGGGGGT	0.418	
+	7	1160	lid.1_Missense_M	NM_022783	NP_073620	Q8TB45	DPTOR_HUMAN			0	GGGCTCCGTAT	0.507	
-	17	2755	uc011llh.1_Intron	NM_013432	NP_038460	Q96HA7	TONSL_HUMAN			0	ACTGGGCTCTG	0.672	
+	7	956	rf68_uc003zik.2_I	NM_004170	NP_004161	P43005	EAA3_HUMAN			0	TTTCTTCAATGC	0.418	
-	1	2961	_p.I632L|RANBP	NM_012416	NP_036548	O60518	RNBP6_HUMAN	HEAT 7.		3	TCCCTATTGCTG	0.363	
-	1	368		NM_005454	NP_005445	O95813	CER1_HUMAN			0	GGGTCCCAGGT	0.493	
-	1	3853	c003zrh.1_5'Flan	NM_153809	NP_722516	Q8IZX4	TAF1L_HUMAN			26	GTTCCGCTTAA	0.463	
-	9	3304	p.R553W|PIGO_u	NM_032634	NP_116023	Q8TEQ8	PIGO_HUMAN			3	CTTCCGCAGCC	0.607	
-	2	443		NM_001100111	NP_001093581					0	CTTTTCTCTGG	0.438	
-	9	2001	ri.1_Missense_Mu	NM_004560	NP_004551	Q01974	ROR2_HUMAN	Potential).|Protein kinase.		20	TCCCCGCCGCG	0.622	
-	1	454		NM_001001961	NP_001001961	Q8NGS6	O13C3_HUMAN	lasmic (Potential).		1	CATAACGATCAA	0.473	
-	5	672	.V182M|UCK1_u	NM_031432	NP_113620	Q9HA47	UCK1_HUMAN			0	CTTCACGAAGG	0.617	
-	30	3780	LA7_uc010ncj.1_	NM_152286	NP_689499	Q6ZV29	PLPL7_HUMAN			1	GGCGCGTCTGA	0.662	
+	11	1647	rf.1_Missense_Mu	NM_004042	NP_004033	P54793	ARSF_HUMAN			2	CCCCGGTATTC	0.363	
-	7	7904		NM_015419	NP_056234	Q9NR99	MXRA5_HUMAN	ike C2-type 10.		8	CAGATCGGTGC	0.647	
+	1	683		NM_182699	NP_874358	Q86TM3	DDX53_HUMAN			3	GAAAGGAAAAT	0.388	
+	4	1045	p.R242H|MAGEB	NM_002363	NP_002354	P43366	MAGB1_HUMAN	MAGE.		0	AACCCCGTAAGT	0.488	
-	66	9884	n.2_Missense_Mu	NM_031407	NP_113584	Q7Z6Z7	HUWE1_HUMAN			17	TGTTATGGCTG	0.388	
-	17	3402	tc.1_Missense_Mu	NM_001002838	NP_001002838	Q9BYP7	WNK3_HUMAN			11	CAGCTGGAACT	0.443	
-	7	1047	_Mutation_p.T181	NM_144969	NP_659406	Q96MV8	ZDH15_HUMAN	ical; (Potential).		2	ACTGTCGTAGCA	0.373	
-	4	951		NM_153448	NP_703149	Q8N693	ESX1_HUMAN	n repeats of P-P-x-x-P-x- P		1	TGGGCGGCCAG	0.672	
-	3	627	pz.2_Missense_Mu	NM_020871	NP_065922	Q5VUJ6	LRCH2_HUMAN	LRR 5.		1	ACTTCCCAATTT	0.289	
+	32	3568	qq.2_Missense_M	NM_144658	NP_653259	Q5JSL3	DOC11_HUMAN			3	ACCTCCCCTTTG	0.333	
-	2	1117		NM_001145718	NP_001139190	P0C2W7	CT47B_HUMAN	Potential.		0	CCACATCCTTCT	0.448	
+	8	1011	uc.2_Missense_M	NM_006603	NP_006594	Q8N3U4	STAG2_HUMAN			5	GCTATGAAGTT	0.289	
-	4	339	fen.2_Intron|CD99	NM_031462	NP_113650	Q8TCZ2	C99L2_HUMAN	ellular (Potential).		3	CATCAGCCAAG	0.438	
+	16	3093		NM_017514	NP_059984	P51805	PLXA3_HUMAN	Extracellular (Potential).		3	ACAGCGAGTGC	0.697	
-	11	1854	lo.1_Missense_Mu	NM_007170	NP_009101	Q96S53	TESK2_HUMAN			5	GCGTGGTGGG	0.552	
+	6	813	HN2_uc001div.2_	NM_012302	NP_036434	O95490	LPHN2_HUMAN	otential).|Olfactomedin-like		9	TACTGGATTTG	0.358	

+	22	3137	p.P775Q|PKN2_u	NM_006256	NP_006247	Q16513	PKN2_HUMAN	kinase C-terminal.	3	AGCCACCATTTAT	0.358	
-	8	1208	hj.1_Missense_Mu	NM_152380	NP_689593	Q96SF7	TBX15_HUMAN		2	TGCTTCGGGCA	0.537	
+	12	1449	GA10_uc009wiw.2	NM_003637	NP_003628	O75578	ITA10_HUMAN	r (Potential).|FG-GAP 4.	8	ATCGAGGAAAAG	0.547	
-	3	1734		NM_001008536	NP_001008536	Q5QJ38	TCHL1_HUMAN		2	GCCTTCCTCTGA	0.542	
-	4	395	nv.1_Missense_M	NM_002928	NP_002919	O15492	RGS16_HUMAN	RGS.	1	GAAAGCGTGGA	0.532	
+	16	3192_3193		NM_002293	NP_002284	P11047	LAMC1_HUMAN	inin EGF-like 10.	5	CTGAAGGCTGCA	0.54	
-	2	130	zz.1_Missense_Mu	NM_005465	NP_005456	Q9Y243	AKT3_HUMAN	PH.	4	TATATTCTCCTAC	0.348	
+	22	3072		NM_000392	NP_000383	Q92887	MRP2_HUMAN	ame=12; (By similarity).	1	TGTTTTCGATATT	0.413	
+	2	206_207		NM_021801	NP_068573	Q9NRE1	MMP26_HUMAN		0	CCATCGGAATGG	0.525	
-	9	1089	kj.1_Missense_Mu	NM_004811	NP_004802	O60711	LPXN_HUMAN	l zinc-binding 3.	1	CAGAATGGACGT	0.517	
+	7	713	1rip.1_Missense_M	NM_018318	NP_060788	Q7Z6B0	CCD91_HUMAN	modimerization.	1	GCTATTGAAAAA	0.363	
-	13	1517_1518	24A6_uc001tva.2_	NM_024959	NP_079235	Q6J4K2	NCKX6_HUMAN	Name=9; (Potential).	1	GTGGCGGCCGC	0.619	
+	12	1707	aaa.2_Missense_M	NM_001676	NP_001667	P54707	AT12A_HUMAN	lasmic (Potential).	6	TCTCCATCCACGA	0.517	
-	1	511		NM_001004714	NP_001004714	Q8NH42	OR4KD_HUMAN	cellular (Potential).	2	ATTGGGACCACA	0.483	
-	2	1083	e_Mutation_p.R11	NM_183002	NP_892114	P57103	NAC3_HUMAN	lasmic (Potential).	7	ACCTCCCTCTCTT	0.478	
+	19	5338	mv.2_Missense_M	NM_015556	NP_056371	O43166	SI1L1_HUMAN		4	TGCCCGACCCT	0.587	
-	3	338		NM_014691	NP_055506	O60306	AQR_HUMAN		1	CAATCTCTTTTT	0.279	
+	13	3141	w.2_Missense_Mu	NM_032866	NP_116255	Q0VF96	CGNL1_HUMAN	Potential.	11	AGTTACGGGACT	0.537	
+	3	427	brb.2_Missense_M	NM_006011	NP_006002	Q92186	SIA8B_HUMAN	nenal (Potential).	0	CCAGACGCTCT	0.463	
-	11	3798		NM_001116	NP_001107	O60503	ADCY9_HUMAN	se 2.|Cytoplasmic (Potentia	6	GAGCTCGTTGA	0.587	
-	6	581	RN3_uc010uzq.1_	NM_018427	NP_060897	Q9NYV6	RRN3_HUMAN		1	ATCAGAATCTGA	0.239	
-	5	1338	002ffe.1_Missens	NM_199355	NP_955387	Q8TE60	ATS18_HUMAN	eptidase M12B.	18	GCTTTTCCACCA	0.463	
+	8	1530	nw.1_Missense_M	NM_178452	NP_848547	Q8NEP3	DAAF1_HUMAN	Pro-rich.	0	CACCCCCGCCAC	0.607	
+	8	1255	jf.2_Missense_Mu	NM_001005273	NP_001005273	Q12873	CHD3_HUMAN		1	GGGAGGAGGAG	0.438	
-	8	996	p.S264F|CCT6B_	NM_006584	NP_006575	Q92526	TCPW_HUMAN		1	TCTAAGGAAAAT	0.224	
-	49	6163	hno.2_Missense_	NM_198836	NP_942133	Q13085	ACACA_HUMAN	oxyltransferase.	2	ACTGTTCGGGTT	0.458	
+	3	436	e_Mutation_p.P13	NM_145273	NP_660316	Q6UXG3	CLM9_HUMAN	cellular (Potential).	0	GTCCTCCCTCCC	0.587	
+	10	1574	2lac.1_Nonsense_	NM_020776	NP_065827	Q86T90	K1328_HUMAN		1	TTGGTTCAGTCT	0.458	
-	4	1916	799_uc002mts.3_	NM_001080821	NP_001074290	Q96GE5	ZN799_HUMAN	C2H2-type 17.	6	TTACATTCATACG	0.413	
-	1	38		NM_001005190	NP_001005190	O76100	OR7AA_HUMAN	cellular (Potential).	0	AGGAGAAGAAAT	0.358	
-	4	743	pc.1_Missense_M	NM_001076675	NP_001070143	Q68DY1	ZN626_HUMAN		1	GGTTTCCCTCCA	0.363	
-	4	1027	rj.1_Missense_Mu	NM_003430	NP_003421	Q05481	ZNF91_HUMAN	C2H2-type 6.	0	GAAGAATGGCTA	0.413	
+	73	10887	iv.1_Missense_Mu	NM_000540	NP_000531	P21817	RYR1_HUMAN		12	GGACGCCGATG	0.652	
+	4	1894	po.1_Intron|ZNF53	NM_001143939	NP_001137411	Q76KX8	ZN534_HUMAN	C2H2-type 15.	0	TAGGAAAATTCAT	0.423	
+	4	2891	dw.1_Missense_M	NM_138374	NP_612383	Q96IR2	ZN845_HUMAN	C2H2-type 26.	0	CCTTCCGTCACA	0.363	rs150688663
+	7	1015	_p.T132I|ZNF761_	NM_001008401	NP_001008401	Q86XN6	ZN761_HUMAN		1	CCAAAACCCATA	0.358	
-	16	2414		NM_019024	NP_061897	Q9P2D3	HTR5B_HUMAN		8	GGAGGGGACCA	0.478	
+	2	1334	ense_Mutation_p.S	NM_014497	NP_055312	Q14966	ZN638_HUMAN		4	TTTTCGTCGGAA	0.398	
-	8	1996	e_Mutation_p.P47	NM_014795	NP_055610	O60315	ZEB2_HUMAN		9	TATTAGGAGAAG	0.413	
+	4	391_392	p.P131F|RQCD1_	NM_005444	NP_005435	Q92600	RCD1_HUMAN		2	CACGTCCCTTTG	0.426	
+	9	1223		NM_003245	NP_003236	Q08188	TGM3_HUMAN		9	GTGTTCGAGAG	0.567	
+	6	801	se_Mutation_p.P23	NM_022896	NP_075047	Q9BQK8	LPIN3_HUMAN		4	CCAGTCCCCTAA	0.632	
-	4	843	gf.1_Missense_Mu	NM_175878	NP_787074	Q5GH77	XKR3_HUMAN	ical; (Potential).	3	CTACACGTGAGA	0.423	
-	20	3679		NM_006514	NP_006505	Q9Y5Y9	SCNAA_HUMAN	e=S3 of repeat III; (Potentia	10	TCACATTCACAAT	0.537	
-	10	890		NM_004704	NP_004695	O43818	U3IP2_HUMAN	WD 4.	3	ACAGCGTCCTGG	0.632	
+	4	382	p.P104S|NISCH_	NM_007184	NP_009115	Q9Y2I1	NISCH_HUMAN	ositide-3-P; not sufficient fo	4	GCCTTCCCTGGC	0.517	
+	8	1057	gfk.3_Missense_M	NM_001122681	NP_001116153	P78314	3BP2_HUMAN		1	GCCACGGGGCC	0.672	rs141518457

+	1	225	_p.H18Y|LPHN3_	NM_015236	NP_056051	Q9HAR2	LPHN3_HUMAN		p.H18R(1)	18	ATAATTCATGGTA	0.383	
+	4	965	|MUC7_uc003hfj.	NM_001145006	NP_001138478	Q8TAX7	MUC7_HUMAN	3.|Thr-rich.		4	TCCACCATCTT	0.582	
+	8	3417	p.P419S|MMRN1_	NM_007351	NP_031377	Q13201	MMRN1_HUMAN	C1q.		4	CTGGTCCTATC	0.363	
-	5	551	x.2_Missense_M	NM_017639	NP_060109	Q6V1P9	PCD23_HUMAN	Cadherin 2.		4	TGCTCGTCACA	0.498	rs148693426
-	3	355	1cle.1_Missense_	NM_173553	NP_775824	Q8N7C3	TRIMM_HUMAN	Potential.		2	CATTTCCTGGA	0.403	
-	14	1925	x.2_Nonsense_M	NM_012334	NP_036466	Q9HD67	MYO10_HUMAN	osin head-like.		3	TCTATCCAGTCA	0.378	
-	8	858	loo.2_Missense_M	NM_001387	NP_001378	Q14195	DPYL3_HUMAN			1	GTAGAGAGGGC	0.498	
+	9	1018		NM_002269	NP_002260	O15131	IMA5_HUMAN	ARM 6.		4	TGATTCTGGAG	0.358	
+	16	1807	em.1_Nonsense_	NM_001029884	NP_001025055	Q9ULL1	PKHG1_HUMAN			2	CTCCCCAGCTG	0.493	rs35532326
+	17	5654	yr.2_Missense_M	NM_152701	NP_689914	Q86UQ4	ABCAD_HUMAN			10	ATGAAAGCTCC	0.418	
+	16	3678	sense_Mutation_p	NM_022742	NP_073579	Q96JN2	CC136_HUMAN	Glu-rich.		2	ACTCTTCCCTTG	0.338	
-	15	1860		NM_004333	NP_004324	P15056	BRAF_HUMAN	rotein kinas	_R603>I(2)|p.T	18290	GATTTCACTGTA	0.368	
+	17	3250		NM_014141	NP_054860	Q9UHC6	CNTP2_HUMAN	3.|Extracellular (Potential).		11	CAGAAGGCCAC	0.552	
-	4	2276		NM_001001661	NP_001001661	Q6IV72	ZN425_HUMAN	2H2-type 19.		3	CGCCCCCACGT	0.577	
-	16	1737_1738	_p.P457F|KIF13B_	NM_015254	NP_056069	Q9NQT8	KI13B_HUMAN			0	GGAGGGATCCT	0.431	
-	5	1072		NM_014729	NP_055544	O94900	TOX_HUMAN	HMG box.		4	CGTTTGGATTT	0.468	
-	4	574	_p.G173S|MPDZ_	NM_003829	NP_003820	O75970	MPDZ_HUMAN	PDZ 1.		6	ACTGCCCTCTT	0.443	
-	11	1306	_p.A361V|MAOB_	NM_000898	NP_000889	P27338	AOFB_HUMAN	Cytoplasmic.		2	CCAGAGCTTCT	0.458	
+	6	1681		NM_007137	NP_009068	P51508	ZNF81_HUMAN			0	TACAGGAGAGA	0.433	
-	42	5574_5575	lsn.2_Missense_M	NM_031407	NP_113584	Q7Z6Z7	HUWE1_HUMAN			17	TAGGGCCAAAG	0.426	
-	18	1919		NM_031407	NP_113584	Q7Z6Z7	HUWE1_HUMAN			17	GAAGTGCTGCT	0.398	
-	3	4644		NM_001008537	NP_001008537	Q5QGS0	K2022_HUMAN			15	GGGTTCCCAAA	0.478	
-	6	799	es.2_Missense_M	NM_024921	NP_079197	Q8WVV4	POF1B_HUMAN			0	TTATTTCCTGTG	0.438	
+	44	4182	_p.G1324E|COL4	NM_033380	NP_203699	P29400	CO4A5_HUMAN	le-helical region.		4	GAAAGGAGATC	0.433	
+	7	658	11_uc004eqq.2_	NM_144658	NP_653259	Q5JSL3	DOC11_HUMAN	PH.		3	AACTTCCTGAC	0.358	
+	4	551	EC1_uc010nsl.1_	NM_005462	NP_005453	O60732	MAGC1_HUMAN			4	CTGAGGGCGAC	0.582	
-	5	1421	4ffl.2_Missense_M	NM_001011543	NP_001011543	P43363	MAGAA_HUMAN			0	CTCTCTTCCTCA	0.468	
+	7	1049	agl.1_Missense_	NM_080875	NP_543151	Q96AX9	MIB2_HUMAN			0	GCAGGGTGAGT	0.677	
-	13	1413	nzr.1_Missense_	NM_001042663	NP_001036128	O94827	PKHG5_HUMAN	DH.		1	CAGGCGCTCCG	0.731	
+	8	3948	j.2_Intron|PRDM2_	NM_012231	NP_036363	Q13029	PRDM2_HUMAN	g (Potential).|Pro-rich.		1	CTCTCCCTCTC	0.498	
-	5	1003	C16_uc001awu.2_	NM_024758	NP_079034	Q9BSE5	SPEB_HUMAN			1	CTGTCCCTGGC	0.522	
-	1	402	C16_uc001awu.2_	NM_024758	NP_079034	Q9BSE5	SPEB_HUMAN			1	AGGCCGGTTGG	0.697	
-	57	8423	k.1_Missense_Mu	NM_020765	NP_065816	Q5T4S7	UBR4_HUMAN			25	AGGTGGGATGT	0.592	
+	4	370	p.G78R|LCK_uc01	NM_005356	NP_005347	P06239	LCK_HUMAN	SH3.		6	ACGACGGAGAT	0.602	
-	6	983	a.1_Missense_M	NM_000831	NP_000822	Q13003	GRIK3_HUMAN	ellular (Potential).		7	GAATCCGGAAT	0.572	
-	6	717	nv.1_Missense_M	NM_020365	NP_065098	Q9NR50	EI2BG_HUMAN			1	GACCCGTGTGG	0.388	
-	5	498	ont.1_Missense_	NM_002370	NP_002361	P61326	MGN_HUMAN			0	ATCCAATAAGA	0.378	
+	37	4957	se_Mutation_p.R4	NM_176877	NP_795352	Q8NI35	INADL_HUMAN	PDZ 9.		4	GACTCCGAGCT	0.473	
-	3	1069	3_Intron|KANK4_u	NM_181712	NP_859063	Q5T7N3	KANK4_HUMAN	Pro-rich.		6	CAGCTCCCTCC	0.547	
+	5	449	ote.1_Missense_	NM_001012425	NP_001012425	Q5VVC0	CA146_HUMAN			1	CAGTAAATGCTA	0.358	
-	20	2219	OL11A1_uc001dur	NM_001854	NP_001845	P12107	COBA1_HUMAN	le-helical region.		12	TCTTCTCCCTGT	0.284	
+	1	433		NM_018137	NP_060607	Q96LA8	ANM6_HUMAN			0	GGCCCGGGAGG	0.687	
-	4	454	orf194_uc009wew	NM_001122961	NP_001116433	Q5T5A4	CA194_HUMAN			1	AGTGTCTGATG	0.493	
+	14	1330	se_Mutation_p.S3	NM_003176	NP_003167	Q15431	SYCP1_HUMAN	Potential.		1	CTCATTCGTTTG	0.308	
+	11	1623	.L465F|PHGDH_	NM_006623	NP_006614	O43175	SERA_HUMAN			1	CCCTGCTCCTA	0.627	
+	5	1023	on|NBPF10_uc00	NM_203458	NP_982283	Q7Z3S9	NT2NL_HUMAN			1	TCTTTCCTAAGC	0.378	
+	10	1491	e_Mutation_p.H45	NM_001039703	NP_001034792	A6NDV3	A6NDV3_HUMAN			0	ATAGCCATGGC	0.468	

+	8	1210	_p.P311S|RPRD2_	NM_015203	NP_056018	Q5VT52	RPRD2_HUMAN		1	AGTCTCCTTTTC	0.502	
-	10	1044	nr.1_Missense_M	NM_001025603	NP_001020774	P48382	RFX5_HUMAN		1	TGTGGGCTCCA	0.522	
-	2	163		NM_001045479	NP_001038944				1	TTGGCGAAACAT	0.443	rs140012440
-	3	529		NM_017582	NP_060052	Q7Z7E8	UB2Q1_HUMAN		0	ATGCTGCAATAG	0.507	
+	1	540		NM_001004473	NP_001004473	Q8NGX5	O10K1_HUMAN	ellular (Potential).	1	TGTGACATCTCC	0.517	
+	6	944	_uc010pjo.1_Miss	NM_021181	NP_067004	Q9NQ25	SLAF7_HUMAN	lasmic (Potential).	3	AAATACCGAAAA	0.368	
+	6	829	nd.1_Missense_M	NM_001460	NP_001451	Q99518	FMO2_HUMAN		1	ACACCCGGTTT	0.473	
+	13	1813	_p.P503S|RABGA	NM_014857	NP_055672	Q5R372	RBG1L_HUMAN	ab-GAP TBC.	4	GGTGTCCCTGAA	0.473	
-	2	1083		NM_001009992	NP_001009992	Q5T619	ZN648_HUMAN	2H2-type 1.	1	GTGTGCCGCGG	0.697	
+	2	390		NM_130782	NP_570138	Q9NS28	RGS18_HUMAN		3	CCAAAGAAACA	0.348	
-	3	1195	pl.1_Missense_M	NM_001031725	NP_001026895	Q5T1V6	DDX59_HUMAN	ase ATP-binding.	4	CAGACGATAAA	0.408	
+	12	3444	.K1047N|CAMSA	NM_203459	NP_982284	Q08AD1	CAMP2_HUMAN		4	TCCAAAGGAC	0.408	
+	9	896	.2_RNA|LGR6_u	NM_001017403	NP_001017403	Q9HBX8	LGR6_HUMAN	tracellular (99_A300insG	10	GAAGATCGGCAT	0.488	
+	4	1226	C2_uc001hcb.1_	NM_014858	NP_055673	O75069	TMCC2_HUMAN		1	CCTCCCCGCCG	0.672	
-	31	4445	gh.1_Missense_	NM_018072	NP_060542	Q9H583	HEAT1_HUMAN		3	TGCTTCTAAAAT	0.368	
+	20	2710	.R836W|ACTN2_	NM_001103	NP_001094	P35609	ACTN2_HUMAN		5	TCCTTCCGGATC	0.502	
-	3	397	ibk.2_Missense_M	NM_022743	NP_073580	Q9H7B4	SMYD3_HUMAN		0	GAACGGAGTCT	0.398	
+	5	214	a.3_RNA|C1orf15	NM_145278	NP_660321	Q5JQS6	CA150_HUMAN		0	GGCAGGAAAAC	0.438	
+	15	3650	rf18_uc001iik.2_I	NM_017782	NP_060252	Q5VWN6	CJ018_HUMAN		2	ATGCAGCAGTG	0.448	
+	3	962		NM_031923	NP_114129	Q5VWG9	TAF3_HUMAN		1	aagagtcccaagagc	0.393	
+	4	593	iln.2_Missense_M	NM_153498	NP_705718	Q8IU85	KCC1D_HUMAN	rotein kinase.	2	AGAAGGATGCC	0.507	
+	11	1364	3A_uc009xkp.1_	NM_017433	NP_059129	Q8NEV4	MYO3A_HUMAN		18	TAATATCCAATCT	0.348	
+	13	1580		NM_019043	NP_061916	Q7Z5R6	AB1IP_HUMAN		7	GTATGGGAAGA	0.463	
-	15	2317_2318	dt.1_Nonsense_	NM_018076	NP_060546	Q5T2S8	ARMC4_HUMAN		6	CATTTCCATATA	0.446	
+	6	716		NM_052997	NP_443723	Q9BXX3	AN30A_HUMAN	ANK 6.	9	ATATACGAAAATT	0.269	
-	5	847	P22_uc010qgl.1_	NM_021226	NP_067049	Q7Z5H3	RHG22_HUMAN	Rho-GAP.	1	CTCCCGGATGA	0.647	
-	16	2273	gt.1_Missense_M	NM_018245	NP_060715	Q9ULD0	OGDHL_HUMAN		1	GACTCCGTACT	0.657	
-	1	237		NM_000242	NP_000233	P11226	MBL2_HUMAN	ollagen-like.	1	CTTTTCTCCCTT	0.532	
-	36	4893	ation_p.E1488K|P	NM_001142769	NP_001136241	Q96QU1	PCD15_HUMAN		13	TTCTTCCTCAGC	0.393	
-	15	1429	p.3_Missense_Mu	NM_013451	NP_038479	Q9NZM1	MYOF_HUMAN	mic (Potential).|C2 3.	4	TTTTTCACACAC	0.254	
+	8	1229	ut.2_Missense_M	NM_000771	NP_000762	P11712	CP2C9_HUMAN		6	AATTTCCCAACC	0.378	
+	6	1398		NM_005063	NP_005054	O00767	ACOD_HUMAN	lasmic (Potential).	0	CCACTCCTTTC	0.443	
+	7	3608	C1_uc010qqj.1_	NM_015062	NP_055877	Q5VV67	PPRC1_HUMAN		3	TCCTCCTCCGG	0.517	
-	23	3132	.P1042S|SORCS1	NM_052918	NP_443150	Q8WY21	SORC1_HUMAN	enal (Potential).	2	AGCTGGATCCT	0.542	
-	11	1565	qsp.1_Missense_	NM_001127211	NP_001120683	A0MZ66	SHOT1_HUMAN	Pro-rich.	0	aggaggaggtggtgg	0.333	
+	50	6431	p.G2108R|DMBT1	NM_007329	NP_015568	Q9UGM3	DMBT1_HUMAN	CUB 2.	7	GGAGAGGGTTC	0.527	
+	52	6879	_p.S2257Y|DMBT1	NM_007329	NP_015568	Q9UGM3	DMBT1_HUMAN	ZP.	7	ACATTTCCTTTT	0.463	
+	9	1405		NM_001105521	NP_001098991				1	ACGGCTCCTCC	0.587	
-	1	348	x.1_Intron|LOC33	NM_001005922	NP_001005922	Q6L8H4	KRA51_HUMAN	repeats of C-C-X-P.	0	CCTTGGAGCCC	0.672	
-	1	530		NM_001005329	NP_001005329	Q8NGJ6	O51A4_HUMAN	ellular (Potential).	3	GAATGGGATAATT	0.413	
-	2	465	BE1_uc001mam.1	NM_005330	NP_005321	P02100	HBE_HUMAN		0	CAAAGGAAGTC	0.512	
+	14	2456	q.2_Missense_M	NM_001003819	NP_001003819	B2RNG4	B2RNG4_HUMAN		1	CAAATCGTCAA	0.413	rs138080438
+	6	1151	2_uc010qzm.1_Mi	NM_006074	NP_006065	Q8IYM9	TRI22_HUMAN	30.2/SPRY.	0	TTAAAGGTAAG	0.443	
-	8	1859	p.G372D|TRIM3_	NM_006458	NP_006449	O75382	TRIM3_HUMAN	NHL 1.	5	GACACACCTTGT	0.498	
+	3	893		NM_006108	NP_006099	Q9HCB6	SPON1_HUMAN	Reelin.	0	TAGACGAAGAA	0.438	
-	1	1265	nb.3_Missense_	NM_000525	NP_000516	B4DWI4	B4DWI4_HUMAN		1	GTGGAGGGGCA	0.617	
+	7	1484	ic.2_Nonsense_M	NM_004211	NP_004202	Q9Y345	SC6A5_HUMAN	Name=4; (Potential).	4	GGCTTGGGTCA	0.453	

+	4	3577	p.P865S|QSER1_	NM_001076786	NP_001070254	Q2KHR3	QSER1_HUMAN			6	AGAATCCAAGG	0.413	
+	9	1085		NM_006133	NP_006124	Q9Y4D2	DGLA_HUMAN	lasmic (Potential).		3	CTGCTCGTGAG	0.642	
-	2	729		NM_203422	NP_981967	Q8ND94	LRN4L_HUMAN	-III.|Extracellular (Potential		0	GCCCCTTCAGT	0.677	
+	7	1397	R|PRDX5_uc001n	NM_004451	NP_004442	P11474	ERR1_HUMAN	F-2 domain.		0	GGGCAAGGTGC	0.647	
-	4	521	roz.1_Missense_	NM_004292	NP_004283	Q13671	RIN1_HUMAN	SH2.		3	GCCCTCCAAGG	0.662	
+	5	882	S4_uc010rpc.1_I	NM_178864	NP_849195	Q8IUM7	NPAS4_HUMAN	PAS 2.		0	TCCTAATCTAC	0.542	
-	3	413	PP1CA_uc001ok	NM_002708	NP_002699	P62136	PP1A_HUMAN			2	GCTTGCCCCTG	0.552	
+	7	807	p.P177S|IL18BP_	NM_001039659	NP_001034748	O95998	I18BP_HUMAN			0	CCTTGCCCCCC	0.597	
+	3	802	p.V157M|P2RY2_	NM_002564	NP_002555	P41231	P2RY2_HUMAN	Name=4; (Potential).		4	GGGCCGTGTG	0.726	
+	2	193	tion_p.R65W|MO	NM_025098	NP_079374	Q3SYC2	MOGT2_HUMAN			2	AGCCACGGCAG	0.562	
-	6	1423	a.3_Missense_Mu	NM_000795	NP_000786	P14416	DRD2_HUMAN	nteraction with PPP1R9B (		2	CTTCTCCTTCT	0.577	
+	5	665	_p.S100F|TMPR	NM_019894	NP_063947	Q9NRS4	TMPS4_HUMAN	lar (Potential).|SRCR.		2	GTTCTCTGCCT	0.552	
+	15	5059		NM_005422	NP_005413	O75443	TECTA_HUMAN	VWFD 4.		10	TGCAGGGTGAT	0.552	
+	8	1632		NM_025004	NP_079280	Q0P6D6	CCD15_HUMAN			2	TCTCCACAAAG	0.418	rs113451248
-	15	2057	_p.R313C|SLC2A1	NM_153449	NP_703150	Q8TDB8	GTR14_HUMAN	lasmic (Potential).		1	TGGGCGGGGGC	0.547	
-	14	2015	rey.2_Splice_Site_	NM_032941	NP_116559	P46063	RECQ1_HUMAN			2	TACATACTTAAG	0.358	
-	15	2107		NM_021957	NP_068776	P54840	GYS2_HUMAN			2	ATCTGGAAAAG	0.303	
-	10	1559	p.Q385K|BCAT1_	NM_005504	NP_005495	P54687	BCAT1_HUMAN			2	TACCTGGATATC	0.279	
-	12	1945	C1_uc001rja.2_N	NM_175861	NP_787057	Q8IUR5	TMTC1_HUMAN	TPR 4.		0	TTCTTTAAACC	0.328	
+	9	866	slz.1_Missense_	NM_000725	NP_000716	P54284	CACB3_HUMAN			0	CCTCTCCCTGG	0.582	
-	2	712		NM_175053	NP_778223	Q7RTS7	K2C74_HUMAN	oil 1B.|Rod.		2	CACCAGATCCC	0.572	
-	2	674	79_uc001sba.2_5'	NM_175834	NP_787028	Q5XKE5	K2C79_HUMAN	od.|Coil 1B.		4	GCCTCCCCCGC	0.617	
+	7	1689	cj.2_Missense_M	NM_012291	NP_036423	Q14674	ESPL1_HUMAN			3	GGCAGCCCTGC	0.552	
+	3	858	2_RNA|SLC26A1	NM_133489	NP_597996	Q8NG04	S2610_HUMAN			2	TCTCTCTCTTC	0.622	
-	14	3349	.A1325T|PTPRB_	NM_002837	NP_002828	P23467	PTPRB_HUMAN	II 13.|Extracellular (Potenti		3	TGAGGCGGTCC	0.552	
+	10	1533	p.G480E|ACSS3_	NM_024560	NP_078836	Q9H6R3	ACSS3_HUMAN			4	TCCCAGGATACA	0.403	
+	5	400	|RFX4_uc001tlt.2_	NM_213594	NP_998759	Q33E94	RFX4_HUMAN	type winged-helix.		1	CAGTTTCCTCAG	0.498	
-	20	2434	tul.2_Missense_M	NM_004658	NP_004649	O95294	RASL1_HUMAN			4	AGTCCCCCAGG	0.632	
-	13	1067	.2_Missense_Mut	NM_002150	NP_002141	P32754	HPPD_HUMAN			0	GGGCCGGTCCT	0.612	
-	8	2397	1uia.2_Missense_	NM_133448	NP_597705	Q14C87	T132D_HUMAN	ellular (Pote	p.I690I(1)	14	CAAAGATGGCC	0.577	
+	18	2425	h.2_Missense_M	NM_005766	NP_005757	Q9Y4F1	FARP1_HUMAN	DH.		2	TCCTGGAGCGG	0.622	
+	9	976		NM_182614	NP_872420	Q8WV15	FA70B_HUMAN	Pro-rich.		0	TTCCCCCGGGG	0.557	
+	1	839		NM_001004724	NP_001004724	Q8IXE1	OR4N5_HUMAN	Name=7; (Potential).		1	TCTTTCCTTTGAT	0.403	
-	10	1644	P1_uc010tlg.1_Mi	NM_007110	NP_009041	Q99973	TEP1_HUMAN	TROVE.		5	CAACCCGCAGC	0.522	
-	4	1916	p.D499N|ZNF219_	NM_016423	NP_057507	Q9P2Y4	ZN219_HUMAN	2H2-type 6.		1	ACAATCCTTGC	0.607	
-	35	6066	r.1_Nonsense_M	NM_020920	NP_065971	Q9HCK8	CHD8_HUMAN			10	CCATCAACTTG	0.408	
+	1	415	LHL28_uc001wvr.	NM_015091	NP_055906	Q9Y4F4	F179B_HUMAN			3	GGCCTCGGCCC	0.587	
-	2	469	dd.2_Missense_M	NM_001001872	NP_001001872	Q86TY3	CN037_HUMAN	ellular (Potential).		0	TGAGGGGACAC	0.488	
+	16	3033	p.V1043I|PLEKH	NM_015549	NP_056364	A1L390	PKHG3_HUMAN			1	AGCGCGTCAAG	0.632	
+	11	1219	p.D376N|GALNTL	NM_020692	NP_065743	Q8N428	GLTL1_HUMAN	enal (Potential).		2	TGGATGGATGAA	0.547	
+	2	1698		NM_018228	NP_060698	Q9H8Y1	VRTN_HUMAN			0	GGATGCCCCTG	0.672	
+	2	2208		NM_018228	NP_060698	Q9H8Y1	VRTN_HUMAN			0	ACAAGGAGTTC	0.567	
+	10	1037	e_Mutation_p.D27	NM_015072	NP_055887	Q6EMB2	TTLL5_HUMAN	TTL.		3	GTGGAGATTAC	0.468	
-	23	4085		NM_001080414	NP_001073883	Q9P219	DAPLE_HUMAN	Potential.		3	AGTTCCCCTTG	0.388	
+	9	882	e.2_Missense_Mu	NM_152328	NP_689541	Q8N142	PURA1_HUMAN			2	CCTTTGTGACT	0.587	
+	1	562		NM_001080841	NP_001074310					0	CAGCCGACAAG	0.453	
+	6	550		NM_004212	NP_004203	O43868	S28A2_HUMAN	ical; (Potential).		4	ACTGTGGTTGG	0.478	

+	16	4768	acl.2_Missense_M	NM_001080534	NP_001074003	Q8NB66	UN13C_HUMAN		7	AATTTGGATTTTT	0.393
-	6	1258	p.V238G|NPTN_u	NM_012428	NP_036560	Q9Y639	NPTN_HUMAN	ical; (Potential).	0	ATCACCACAAGG	0.522
-	26	3409	bbx.2_Missense_M	NM_020843	NP_065894	Q9BY12	SCAPE_HUMAN		3	AAGCAGGCACAC	0.488
+	2	243	0bmt.1_Missense_	NM_207517	NP_997400	P82987	ATL3_HUMAN		27	CGAGCCCCTGG	0.562
+	4	1439	592_uc010upb.1_	NM_014630	NP_055445	Q92610	ZN592_HUMAN		6	CAGCTCCCCAC	0.517
+	13	1289	C28A1_uc010upf	NM_004213	NP_004204	O00337	S28A1_HUMAN	ical; (Potential).	3	AGATCGATGCC	0.577
+	6	1389	AN_uc010upp.1_	NM_013227	NP_037359	E7EX88	E7EX88_HUMAN		3	TACCCCGACCCC	0.642
+	39	5911		NM_001271	NP_001262	O14647	CHD2_HUMAN		2	TACCCCCATTGC	0.542
+	5	787	ve.2_Missense_M	NM_005587	NP_005578	Q02078	MEF2A_HUMAN	Ser/Thr-rich.	1	AATGTCTGTCAC	0.433
+	6	765	010bqt.1_Translat	NM_006849	NP_006840	Q13087	PDIA2_HUMAN		2	AGTCCGTGTCT	0.557
-	3	627	002cgv.3_Translati	NM_021259	NP_067082	Q9HCN3	TMM8A_HUMAN	ellular (Potential).	3	AACTCGATCTTC	0.657
-	7	693	_uc002coe.1_Spli	NM_178167	NP_835461	Q86UK7	ZN598_HUMAN		2	AGTCGCTGGCA	0.657
-	3	288	p.G43D|PRSS33_	NM_152891	NP_690851	Q8NF86	PRS33_HUMAN	eptidase S1.	0	CCCGGCCATCC	0.711
-	13	3943	uyn.1_Missense_	NM_001134407	NP_001127879	Q12879	NMDE1_HUMAN	lasmic (Potential).	45	GGGGTGGATCT	0.532
-	7	1032		NM_174924	NP_777584	Q8N807	PDILT_HUMAN		1	AACTCGGAAATC	0.458
-	15	2410	a.1_Missense_Mu	NM_020718	NP_065769	Q70CQ4	UBP31_HUMAN	Ser-rich.	10	AGCTGCAGAGG	0.582
+	2	411	S2_uc002dlt.3_5'F	NM_019116	NP_061989	O14562	UBFD1_HUMAN		0	GGCCTCGGTCA	0.622
-	3	726		NM_001080417	NP_001073886	Q9UEG4	ZN629_HUMAN		0	CTCCCGTGTGG	0.682
+	23	2826	ap.1_Missense_Mu	NM_005353	NP_005344	Q13349	ITAD_HUMAN	ellular (Potential).	1	GATCAGCAGGT	0.552
-	16	1694	e.1_Nonsense_Mu	NM_013263	NP_037395	Q9NPI1	BRD7_HUMAN	Potential.	0	TCTTCTGGAATAT	0.453
+	3	405		NM_033119	NP_149110	Q969G9	NKD1_HUMAN		0	TAGGCCGAAGC	0.662
-	3	491	p.P102L|TOX3_uc	NM_001080430	NP_001073899	O15405	TOX3_HUMAN		0	GAGGGGGAAAC	0.532
+	5	1636	ense_Mutation_p.	NM_024731	NP_079007	Q8N4N3	KLH36_HUMAN	Kelch 5.	2	CCATCGGGGGC	0.677
-	9	1179	cjf.2_Intron|PRDM	NM_001098173	NP_001091643	Q9NQW5	PRDM7_HUMAN		1	CCCCATACCAG	0.522
-	9	1090	cjf.2_Intron|PRDM	NM_001098173	NP_001091643	Q9NQW5	PRDM7_HUMAN	SET.	1	CCCCAGACCAG	0.532
-	2	546	qa.1_Missense_M	NM_015721	NP_056536	P57678	GEMI4_HUMAN		4	AAAGCGCTCTA	0.562
-	22	2766	_Missense_Mutat	NM_001100112	NP_001093582	Q9UKX2	MYH2_HUMAN	Potential.	14	TTTCTTCCAGTTC	0.433
-	22	2755	_Missense_Mutat	NM_001100112	NP_001093582	Q9UKX2	MYH2_HUMAN	Potential.	14	TCCTTCCTTTTTG	0.428
+	11	2459	e_Mutation_p.E26	NM_014695	NP_055510	A2RUR9	C144A_HUMAN	Potential.	0	AAAAGGAACTA	0.333
+	12	1441		NM_004140	NP_004131	Q15334	L2GL1_HUMAN	WD 8.	6	TTCTGGGATGC	0.622
+	4	794	p.A170V|SMCR7_	NM_139162	NP_631901	Q96C03	SMCR7_HUMAN		0	ATGTGCGTCTC	0.706
-	3	1312	494_uc010waq.1_	NM_006461	NP_006452	Q96R06	SPAG5_HUMAN		1	TGGTGCCAACC	0.502
-	18	3581	p.P991L|SRCIN1_	NM_025248	NP_079524	Q9C0H9	SRCN1_HUMAN		0	TGTCGGGGCTG	0.672
+	4	505	ense_Mutation_p.	NM_133264	NP_573571	Q8TF74	WIPF2_HUMAN		3	TCTTCCAAGGA	0.517
-	2	1903		NM_018143	NP_060613	Q9NVR0	KLH11_HUMAN	Kelch 5.	0	AATATCGGTAGG	0.458
+	4	777	vha.1_Missense_	NM_173478	NP_775749	Q8N815	CNTD1_HUMAN		1	CACTCCCCTGG	0.443
-	23	2701	ilw.1_Missense_M	NM_145798	NP_665741	Q9BZF2	OSBL7_HUMAN		0	TCCCATAGCCTC	0.652
+	5	1137	p.A230T|KCNH6_	NM_030779	NP_110406	Q9H252	KCNH6_HUMAN	=Segment S3; (Potential).	1	TGGCCGCCATC	0.622
-	35	4574		NM_080284	NP_525023	Q8N139	ABCA6_HUMAN	C transporter 2.	7	CAGGAGGACAC	0.483
+	13	1862	IAI2_uc010dfp.2_	NM_023036	NP_075462	Q9GZS0	DNAI2_HUMAN		3	gaggagggagaggaa	0.373
-	3	795		NM_006678	NP_006669	Q08708	CLM6_HUMAN	xtracellular (Potential).	0	CCATGGAGCTC	0.617
+	4	1373		NM_020914	NP_065965	Q9HCF4	ALO17_HUMAN		21	ATGACGACCAC	0.532
-	22	3185	zj.1_Missense_Mu	NM_005559	NP_005550	P25391	LAMA1_HUMAN	inin EGF-like 11.	21	AGTGCCCATCCT	0.557
+	4	675	p.E197K|LAMA3_	NM_198129	NP_937762	Q16787	LAMA3_HUMAN	inin N-terminal.	11	TTAAAAGAATTTG	0.323
+	10	1446		NM_194449	NP_919431	O60346	PHLP1_HUMAN	LRR 12.	0	CTGCCCGGTGAG	0.368
+	12	2378	b.2_Missense_Mu	NM_033646	NP_387450	Q9ULB5	CADH7_HUMAN	lasmic (Potential).	4	GGAGGGATGTG	0.478
-	9	1672	p.G462E|NETO1_	NM_138966	NP_620416	Q8TDF5	NETO1_HUMAN	lasmic (Potential).	4	GGTTTTCCTGGC	0.488

+	5	408	PC5_uc002mhj.1_	NM_174918	NP_777578	Q8IX19	MCEM1_HUMAN	ellular (Pote	p.S128F(1)	1	AAACTCCGTAC	0.547	rs139191722
+	2	265	N16_uc002mqu.1_	NM_012466	NP_036598	Q9UKR8	TSN16_HUMAN	ical; (Potential).		1	AATGTGGAGGG	0.498	
-	4	1355		NM_145276	NP_660319	Q8TA94	ZN563_HUMAN	2H2-type 9.		0	ATAACGTTTTCC	0.413	
-	17	2589		NM_002918	NP_002909	P22670	RFX1_HUMAN	ary for dimerization.		2	CATCTGGTTGA	0.617	
-	37	4969	PAMD8_uc002nfd	NM_015692	NP_056507	Q8IZJ3	CPMD8_HUMAN			13	TTCATCCCCATG	0.572	
+	4	1529		NM_031218	NP_112495	P35789	ZNF93_HUMAN	2H2-type 12.		1	ATAAGAAAATTC	0.368	
-	7	1345	_p.D79N|LGI4_uc	NM_139284	NP_644813	Q8N135	LGI4_HUMAN	EAR 1.		1	GTAGTCCCAGG	0.677	
+	2	129	yb.1_RNA|FXYD1_	NM_021902	NP_068702	O00168	PLM_HUMAN			0	CCAAGGCAGGT	0.617	
-	3	759	02ovk.1_Missense	NM_002785	NP_002776	Q9UQ72	PSG11_HUMAN	like C2-type 1.		0	ATATTTCACATTC	0.507	
+	2	540	gk.1_Missense_Mu	NM_018485	NP_060955	Q9P296	C5ARL_HUMAN	ellular (Potential).		1	GCTGTCGGGCG	0.652	
+	4	3383		NM_020719	NP_065770	Q9ULL5	PRR12_HUMAN	Pro-rich.		2	CAGCTGCCGCT	0.701	
+	6	4435		NM_020719	NP_065770	Q9ULL5	PRR12_HUMAN	Pro-rich.		2	gccgccacagccagc	0.204	
-	8	1124		NM_016148	NP_057232	Q9Y566	SHAN1_HUMAN	ANK 5.		2	ACCTCGATACA	0.542	
-	4	1509	616_uc002pyn.2_	NM_178523	NP_848618	Q08AN1	ZN616_HUMAN	2H2-type 9.		0	ATTTGCAAGGT	0.393	
+	4	1894	po.1_Intron|ZNF5	NM_001143939	NP_001137411	Q76KX8	ZN534_HUMAN	2H2-type 15.		0	TAGGAAAATTCA	0.423	
-	5	1271	k.1_Intron|ZNF81	NM_001031665	NP_001026835	Q0VGE8	ZN816_HUMAN	2H2-type 4.		0	CTTCTCACTGA	0.443	rs141188407
+	1	820		NM_173856	NP_776255	Q8NFZ6	VN1R2_HUMAN	ellular (Potential).		0	GAGATTTGGGA	0.428	
-	3	2049	2qcj.3_Missense_	NM_144687	NP_653288	P59046	NAL12_HUMAN			7	CCAAGGAGCCC	0.567	
-	6	1228	ILRA3_uc010erk.2	NM_006865	NP_006856	Q8N6C8	LIRA3_HUMAN	like C2-type 4.		1	CCGAGGTCACA	0.587	
+	12	1838	_Mutation_p.D50	NM_006669	NP_006660	Q8NHL6	LIRB1_HUMAN	lasmic (Potential).		3	AGGCTGATTTC	0.607	
+	9	2527	p.T790M|NLRP2_	NM_017852	NP_060322	Q9NX02	NALP2_HUMAN	LRR 1.		2	CCTGACGTGCG	0.517	
-	8	318	_p.E77K|TNNT1_u	NM_003283	NP_003274	P13805	TNNT1_HUMAN			1	CAGCTCCAGCA	0.607	
-	8	1673	_p.E356K|PTPRH_	NM_002842	NP_002833	Q9HD43	PTPRH_HUMAN	tential).|Fibronectin type-III		4	CAGTTCCTTTA	0.577	
-	23	2880_2881	2qju.2_5'Flank|S	NM_014931	NP_055746	Q9UPN7	PP6R1_HUMAN			0	CTGGGAGCCT	0.653	
-	2	164	tation_p.S33F|uc0	NM_144690	NP_653291	Q96NG8	ZN582_HUMAN			4	CAAGGGACATG	0.448	
+	4	633	_p.E166K|ZNF324	NM_207395	NP_997278	Q6AW86	Z324B_HUMAN			1	CCAGGGAAAAG	0.662	
+	14	1633	512_uc010ylx.1_	NM_032434	NP_115810	Q96ME7	ZN512_HUMAN			1	TTCCCGAGACA	0.542	
-	11	1264	np.1_Missense_M	NM_144575	NP_653176	Q6MZZ7	CAN13_HUMAN			2	GTCCTCCTGCA	0.473	
+	2	568	1B_uc002rtv.2_In	NM_002706	NP_002697	O75688	PPM1B_HUMAN			2	TATTCCTCACG	0.453	
-	1	152	P2_uc002rxq.3_I	NM_001003937	NP_001003937	Q8N831	TSYL6_HUMAN			0	AGTAGCGGGGC	0.597	
-	19	3297	.2_Missense_Mut	NM_002285	NP_002276	P51826	AFF3_HUMAN			6	GGGGCCTTGTT	0.443	
-	8	1432	_p.S449F|TBC1D	NM_001102426	NP_001095896	O95759	TBCD8_HUMAN			3	TTTTGAGAAGAC	0.532	
-	6	1196	149_uc002tax.1_	NM_173647	NP_775918	Q8NC42	RN149_HUMAN			2	ATTCAGCAGGG	0.473	
+	11	1550	wd.1_Missense_	NM_003855	NP_003846	Q13478	IL18R_HUMAN	oplasmic (Potential).		3	TGGAAAGAAAAA	0.353	
+	7	1174	tdx.2_Missense_	NM_001056	NP_001047	O00338	ST1C2_HUMAN			1	ACAAATCGTTCT	0.403	rs112864909
+	5	480	_uc002tks.3_Miss	NM_007082	NP_009013	Q9UBK7	RBL2A_HUMAN			1	TGCCTCCTACT	0.582	
+	16	1427	yf.1_Missense_M	NM_006770	NP_006761	Q9UEW3	MARCO_HUMAN	tracellular (Potential).		6	TAACCGAGGCC	0.532	
-	6	691	flr.2_Missense_M	NM_014553	NP_055368	Q9NZI6	TF2L1_HUMAN			3	CATTCTCGTTCT	0.587	
-	3	707		NM_001099771	NP_001093241	A5A3E0	POTEF_HUMAN			5	GTGGCAGCACC	0.617	
-	3	687		NM_001099771	NP_001093241	A5A3E0	POTEF_HUMAN			5	ATCTTGTTCCTG	0.607	
-	3	596		NM_001099771	NP_001093241	A5A3E0	POTEF_HUMAN			5	GTGGCGGCACC	0.602	
+	17	2162	up.2_Missense_M	NM_015361	NP_056176	Q15032	R3HD1_HUMAN	Poly-Pro.		1	accgccaccaccacc	0.398	
+	2	599	HSD7B_uc002tvb.	NM_001080427	NP_001073896					7	CCATTTCCTGTC	0.458	
-	6	1090	_p.P175S|ZEB2_u	NM_014795	NP_055610	O60315	ZEB2_HUMAN			9	ATCTGGAGTTC	0.557	
-	21	2136	.1_Missense_Mut	NM_004543	NP_004534	P20929	NEBU_HUMAN			20	CACAGTAATTCA	0.358	
-	17	3502	.E1042K|SCN1A_	NM_006920	NP_008851	P35498	SCN1A_HUMAN			13	AGTTTCTTCAG	0.428	
+	7	576	_p.T119K|PPIG_uc	NM_004792	NP_004783	Q13427	PPIG_HUMAN	e cyclophilin-type.		3	AGGATACAAATG	0.269	

+	9	836	3A1_uc010frw.1_5'	NM_000090	NP_000081	P02461	CO3A1_HUMAN	le-helical region.	13	ACCTGGAGAGC	0.383	
+	18	2063	.1_Missense_Muta	NM_001080539	NP_001074008	Q8NCX0	CC150_HUMAN	Potential.	0	TAATGCGGCCC	0.428	
+	1	159	uc002uup.2_Intron	NM_138395	NP_612404	Q96GW9	SYMM_HUMAN		3	GCGATGATGCTT	0.627	
+	2	322	ce|CDK15_uc010f	NM_139158	NP_631897	Q96Q40	CDK15_HUMAN		5	AGTGGGTGAGT	0.512	
+	4	656	p.R144H|CXCR2_	NM_001557	NP_001548	P25025	CXCR2_HUMAN	lasmic (Potential).	2	GGACCGTTACC	0.532	
-	10	891	w.2_Missense_Mu	NM_022453	NP_071898	Q96BH1	RNF25_HUMAN		2	CAGGAGGCTAG	0.557	
-	3	329	zlm.1_Missense_M	NM_004438	NP_004429	P54764	EPHA4_HUMAN	cellular (Potential).	12	ACACCCTCTGAG	0.463	
-	22	2212		NM_000092	NP_000083	P53420	CO4A4_HUMAN	le-helical region.	11	GCCAGGGAGCC	0.587	
+	3	564	pe.2_Missense_M	NM_004504	NP_004495	P52594	AGFG1_HUMAN	Arf-GAP.	4	AATTCCAGACT	0.328	
+	16	2065	mp.1_Missense_M	NM_001017915	NP_001017915	Q92835	SHIP1_HUMAN		2	AAGAAATCACG	0.473	
+	4	1265	p.R291K|SH3BP4	NM_014521	NP_055336	Q9P0V3	SH3B4_HUMAN		4	CCACAGGAAGC	0.577	
-	21	3034	p.E936K|HDLBP_	NM_203346	NP_976221	Q00341	VIGLN_HUMAN	KH 11.	4	AGCCTCTCTCC	0.542	
-	16	2050	p.R608C|HDLBP_	NM_203346	NP_976221	Q00341	VIGLN_HUMAN	KH 7.	4	TTCACGAATCTA	0.502	
-	5	817	wrt.1_Missense_M	NM_016652	NP_057736	Q9BZJ0	CRNL1_HUMAN	HAT 2.	3	TGGATCGAGCC	0.388	
+	3	187	RG1B_uc010gdr.1_RNA|FRG1B_uc010ztk.1_Missense_Mutation_p.L4S						0	TTTGTTGGCCT	0.353	
+	3	189	RG1B_uc010gdr.1_RNA|FRG1B_uc010ztk.1_Missense_Mutation_p.A5T						0	TTGTTGGCCTCA	0.353	
+	9	1763	T2_uc002wzf.1_R	NM_005093	NP_005084	O43439	MTG8R_HUMAN		2	GCACAGCCCTG	0.498	
-	4	1844	1_5'Flank|EIF6_uc	NM_178468	NP_848563	Q9BQN1	FA83C_HUMAN		2	ATCACCAGGTC	0.642	
+	12	2112_2113	m.2_Missense_Mu	NM_181659	NP_858045	Q9Y6Q9	NCOA3_HUMAN	Ser-rich.	5	TTCCTCCTTGAC	0.47	
-	3	1304		NM_021035	NP_066363	Q9P2E3	ZNFX1_HUMAN		2	GCGAAGGAAGG	0.502	
+	15	1841	_p.T244M|SLC9A8	NM_015266	NP_056081	Q9Y2E8	SL9A8_HUMAN		1	GCTGACGCAGG	0.642	
-	15	1164	TE_uc002yir.1_Mi	NM_199261	NP_954870	P56180	TPTE_HUMAN	hatase tensin-type.	5	CAACTTCCTAAA	0.333	
-	3	422	GE_uc002yiw.1_R	NM_182482	NP_872288				0	GAAAGGTGTCG	0.423	rs4913558
-	4	362	SAMSN1_uc002yj	NM_022136	NP_071419	Q9NSI8	SAMN1_HUMAN		4	TCATCCTTCAG	0.413	
-	1	271		NM_001085455	NP_001078924	Q3LI83	KR241_HUMAN		0	TGGTACTGCAG	0.483	
-	1	349		NM_181621	NP_853652	Q52LG2	KR132_HUMAN		0	GGGAGCGGCAG	0.607	
+	8	1178	.2_RNA|UBASH3	NM_018961	NP_061834	P57075	UBS3A_HUMAN		3	GGCAAGGAGTC	0.448	
-	1	825	.1_Intron|C21orf29	NM_198688	NP_941961	P60371	KR106_HUMAN	repeats of C-C-X(3).	0	CAGGCGTGCTG	0.642	
-	1	551	zlh.1_5'UTR|POTE	NM_001136213	NP_001129685	Q6S545	POTEH_HUMAN		1	CGGCTCCATGA	0.587	
-	1	396	EH_uc002zlh.1_5	NM_001136213	NP_001129685	Q6S545	POTEH_HUMAN		1	CGTTGCTCTTG	0.592	
+	14	1899	v.1_Missense_Mu	NM_013430	NP_038347	P19440	GGT1_HUMAN	cellular (Potential).	0	GGGAGCTGCTG	0.652	
+	2	594		NM_001013618	NP_001013640				0	TGGTACCCCCA	0.582	
+	12	2704	sense_Mutation_p	NM_001017437	NP_001017437	Q569K6	CC157_HUMAN		1	CCCCACCTCGG	0.682	
-	24	3765		NM_014941	NP_055756	Q9Y6X9	MORC2_HUMAN		2	TGTATCAAGGC	0.597	
+	8	1078	_p.R271H|PPARA_	NM_005036	NP_005027	Q07869	PPARA_HUMAN		2	AGGTCCGCATCT	0.557	
-	1	2135		NM_014246	NP_055061	Q9NYQ6	CELR1_HUMAN	(Potential).|Cadherin 5.	11	GGTCGCGGGCC	0.637	
-	3	1039	GAP3_uc003bri.1_	NM_014850	NP_055665	O43295	SRGP2_HUMAN		9	ATTGTTCATGAA	0.542	
+	1	846	k.1_Missense_Mu	NM_152536	NP_689749	Q6ZNL6	FGD5_HUMAN	Glu-rich.	5	AGGATGCTGAG	0.632	
+	2	833	cdq.2_Missense_M	NM_052953	NP_443185	Q96PB8	LRC3B_HUMAN	LRR 1.	4	CCAATGAAATT	0.408	
+	5	878	chb.2_Missense_M	NM_178339	NP_848029	Q8IVJ8	APRG1_HUMAN		1	TGGACCTTTGG	0.448	
-	21	3695		NM_014139	NP_054858	Q9UI33	SCNBA_HUMAN	III.	9	CACCACCTTAT	0.448	
+	1	992		NM_152393	NP_689606	Q2TBA0	KBTB5_HUMAN		1	AGGAGGCCGAA	0.567	
+	3	618	0hiv.1_Missense_	NM_031200	NP_112477	P51686	CCR9_HUMAN	lasmic (Potential).	3	TGAGAGCACATA	0.473	
-	116	8537	2_uc003cty.1_5'F	NM_000094	NP_000085	Q02388	CO7A1_HUMAN	lical region (NC2).	11	AGGGGGTACCC	0.597	
-	2	367		NM_003335	NP_003326	P41226	UBA7_HUMAN	ximate repeats.|1-1.	2	GGTGGGGTGGG	0.657	
-	28	4388	3dmh.1_Splice_Si	NM_182920	NP_891550	Q9P2N4	ATS9_HUMAN		4	CCGTACCGAGC	0.468	
+	15	2743	A3_uc010hon.1_	NM_005233	NP_005224	P29320	EPHA3_HUMAN	Potential).|Protein kinase.	33	ATGAGGGCTAT	0.498	

-	26	2202	ul.2_Missense_Mu	NM_015429	NP_056244	Q7Z7G0	TARSH_HUMAN	Pro-rich.	4	GTGGGCGGCGA	0.403	
+	12	1925	_p.S462F|ALCAM_	NM_001627	NP_001618	Q13740	CD166_HUMAN	otential).|Ig-like C2-type 3.	3	AGGAATCTCCTT	0.343	
+	1	384		NM_032600	NP_115989	Q8NEL0	CCD54_HUMAN		0	GATATCCCACTGT	0.388	
-	4	645	A1C_uc003dxk.2_	NM_005459	NP_005450	O95843	GUC1C_HUMAN		0	AGGAGTCTGTCT	0.458	rs146701862
-	7	942		NM_138815	NP_620170	Q7Z7J5	DPPA2_HUMAN		3	CTGCCGAGAGA	0.512	rs151045476
+	2	318	xx.2_Missense_M	NM_198196	NP_937839	P40200	TACT_HUMAN	Potential).|Ig-like V-type 1.	3	CAGACAGTAGGC	0.443	
-	7	1734	eal.2_Missense_M	NM_001009899	NP_001009899	Q68DE3	K2018_HUMAN		3	AATAGTGTTTCCT	0.438	
+	10	1217	bik.1_Missense_M	NM_001690	NP_001681	P38606	VATA_HUMAN		3	TGGCCTCGTTTT	0.443	
+	4	1022		NM_000539	NP_000530	P08100	OPSD_HUMAN	Name=7; (Potential).	0	ATGATGAACAAG	0.612	
+	2	504		NM_001102608	NP_001096078	A6NMZ7	CO6A6_HUMAN	cal region.|VWFA 1.	8	AAGACGGAGTGA	0.498	
+	3	1216		NM_139209	NP_631948	Q8WTQ7	GRK7_HUMAN	rotein kinase.	5	GCCATGGGATGC	0.428	
+	4	1438		NM_139209	NP_631948	Q8WTQ7	GRK7_HUMAN	rotein kinase.	5	AAACATCATTTC	0.423	
-	4	573	_p.R82W|PLSCR4_	NM_001128305	NP_001121777	Q9NRQ2	PLS4_HUMAN	smic (By similarity).	0	GATACCGGACAG	0.517	rs149536276
+	10	1775		NM_006218	NP_006209	P42336	PK3CA_HUMAN	PI3K helical.	3553	GATCCTCTCTCT	0.328	
+	7	933	_Mutation_p.R261	NM_018358	NP_060828	Q9NUQ8	ABCF3_HUMAN	C transporter 1.	4	ACGGAGGGAGC	0.602	
-	2	370_371	2_Intron|MASP1_u	NM_001879	NP_001870	P48740	MASP1_HUMAN		4	GACAGGGAGAAG	0.47	
-	3	593	_6_uc010hza.2_5'	NM_001130845	NP_001124317	P41182	BCL6_HUMAN	BTB.	5	TTTTATGGGCTC	0.517	
+	3	307	D51N|ZNF595_uc	NM_182524	NP_872330	Q7Z3I0	Q7Z3I0_HUMAN		0	ACCCAGACCTG	0.403	
+	2	548	bwi.1_Missense_M	NM_020777	NP_065828	Q96PQ0	SORC2_HUMAN	Lumenal (Potential).	2	GTGGCGGTAAG	0.522	
-	5	1121		NM_001358	NP_001349	O43143	DHX15_HUMAN		1	CAACAGGATGT	0.403	
+	3	443	_Site_p.G58_splice	NM_018317	NP_060787	Q8N5T2	TBC19_HUMAN		1	AAACAGGTTGG	0.254	
-	4	1146		NM_001024611	NP_001019782	Q68CR7	LRC66_HUMAN	ical; (Potential).	3	ACACCGCCAGA	0.567	
+	3	506		NM_206919	NP_996802	Q6T311	ARL9_HUMAN		0	ATGTACCTATCCA	0.463	
+	4	1139	|MUC7_uc003hfj.2	NM_001145006	NP_001138478	Q8TAX7	MUC7_HUMAN	6.|Thr-rich.	4	CTGCCCCACCCA	0.577	
+	4	1629	e_Mutation_p.E41	NM_004885	NP_004876	Q9Y5X5	NPFF2_HUMAN	lasmic (Potential).	3	GTGATGGAAGAA	0.343	
-	2	893		NM_198281	NP_938022	Q6ZVF9	GRIN3_HUMAN		3	GTCAATGGTGTG	0.572	
-	11	949	.G244E|EMCN_u	NM_016242	NP_057326	Q9ULC0	MUCEN_HUMAN	lasmic (Potential).	0	GTTTTTCCTTGT	0.373	
+	12	1785	p.P470Q|HSPA4L_	NM_014278	NP_055093	O95757	HS74L_HUMAN		4	ATGCTCCAATGG	0.343	
-	1	1919	.1_Intron|PCDH18_	NM_019035	NP_061908	Q9HCL0	PCD18_HUMAN	r (Potential).|Cadherin 5.	5	GAACTTCCTAGA	0.418	
-	7	3217	ML3_uc011chd.1_	NM_018717	NP_061187	Q96JK9	MAML3_HUMAN	Gln-rich.	1	TCAGCCGTGAC	0.587	
-	13	2014	ckv.1_Missense_	NM_021069	NP_066547	O94875	SRBS2_HUMAN		1	GAGATCGTCAC	0.542	
-	58	9763	AH5_uc003jfc.2_5'	NM_001369	NP_001360	Q8TE73	DYH5_HUMAN		31	TAAGACCTAATT	0.413	
-	27	4360		NM_001369	NP_001360	Q8TE73	DYH5_HUMAN	.|Stem (By similarity).	31	TTTTTTCAATATT	0.313	
+	2	680	hm.2_Missense_M	NM_178140	NP_835260	O15018	PDZD2_HUMAN	PDZ 1.	9	TATGGTGAAAAG	0.567	
-	9	1634	0iuq.1_Missense_	NM_030955	NP_112217	P58397	ATS12_HUMAN	Disintegrin.	9	CTACTTCCTGGC	0.473	
+	6	981	jlb.1_Missense_M	NM_152403	NP_689616	Q63HQ2	EGFLA_HUMAN	onectin type-III 2.	7	GGCAATGAATTC	0.562	
+	8	1478		NM_003999	NP_003990	Q99650	OSMR_HUMAN	III 1.|Extracellular (Potentia	5	AACTCCATGGT	0.343	
+	5	1168	L21_uc003lbc.2_In	NM_012159	NP_036291	Q9UKT6	FXL21_HUMAN	LRR 7.	1	GCCTTCATCAGG	0.418	
+	1	946	03lhi.2_Intron|PC	NM_018908	NP_061731	Q9Y5H7	PCDA5_HUMAN	r (Potential).|Cadherin 3.	3	TCATATGAAATTA	0.323	
+	1	1318	03lhi.2_Intron|PCD	NM_018908	NP_061731	Q9Y5H7	PCDA5_HUMAN	r (Potential).|Cadherin 4.	3	GCCAGCGTGTCT	0.672	rs147205231
+	1	1755_1756	DHA7_uc003lhq.2	NM_018904	NP_061727	Q9Y5I0	PCDAD_HUMAN	|Extracellular (Potential).	6	TCGGTGGGTGC	0.693	
+	1	1197		NR_001280					0	AGAAAATTTCTAC	0.458	
-	3	754	loh.3_Missense_M	NM_004576	NP_004567	Q00005	2ABB_HUMAN		2	GGGTTCATGGC	0.373	
+	27	2630	ow.2_Nonsense_M	NM_006846	NP_006837	Q9NQ38	ISK5_HUMAN	Kazal-like 13.	4	GAATTTCGAAGC	0.388	
+	15	2394	e_Mutation_p.E75	NM_205836	NP_995308	Q6PIJ6	FBX38_HUMAN		6	GTCAGAGGACTC	0.597	
-	5	4004	2A_uc011dcs.1_In	NM_001447	NP_001438	Q9NYQ8	FAT2_HUMAN	(Potential).|Cadherin 11.	6	TAGCCGGACAC	0.572	
+	8	1540	|ODZ2_uc003lzr.3	NM_001122679	NP_001116151				10	TGGACGGGAAG	0.537	

-	7	1149	dy.2_Missense_M	NM_016356	NP_057440	Q9UHG0	DCDC2_HUMAN		1	AATTCACGTCTT	0.363
-	18	3061	1djq.1_Nonsense_	NM_014809	NP_055624	Q5VV43	K0319_HUMAN	ellular (Potential).	2	ACGCTGTATAAG	0.502
+	5	2314	5_uc003nki.3_Mis	NM_003447	NP_003438	P49910	ZN165_HUMAN	2H2-type 4.	0	ATTCAACCTGAA	0.463
+	5	806		NR_027822					0	CATCCCCATCG	0.602
-	9	850	AT5_uc003nvz.1_	NM_021160	NP_066983	O95870	ABHGA_HUMAN		0	CTCAGCTGTCC	0.592
-	7	895	e_Mutation_p.P52	NM_001145776	NP_001139248	Q13451	FKBP5_HUMAN	se FKBP-type 2.	1	AATTTAGGCTTC	0.358
+	6	2250	tj.1_RNA|BRPF3_	NM_015695	NP_056510	Q9ULD4	BRPF3_HUMAN	Bromo.	2	TTTTCCACCGA	0.408
-	2	246		NM_001010903	NP_001010903	P0C671	CF222_HUMAN		4	GGGCCTGCGGC	0.632
+	10	1117	wh.1_Missense_M	NM_005588	NP_005579	Q16819	MEP1A_HUMAN	lar (Potential).|MAM.	3	GACTCGTTGTC	0.488
+	5	1290		NM_001010872	NP_001010872	Q5T0W9	FA83B_HUMAN		6	CTGGGGAACAG	0.403
+	13	2532	k.2_Missense_Mu	NM_001704	NP_001695	O60242	BAI3_HUMAN	ellular (Potential).	50	AGAATTCATACTT	0.328
-	9	1058	OL9A1_uc003pff	NM_001851	NP_001842	P20849	CO9A1_HUMAN	lical region (COL3).	4	CCGGGGGGCC	0.572
-	17	2783	.1_RNA|GOPC_uc	NM_002944	NP_002935	P08922	ROS_HUMAN	ellular (Potential).	25	CCGAAGAACAG	0.378
+	3	532_533	BLD1_uc003pxr.1	NM_173674	NP_775945	Q8N8Z6	DCBD1_HUMAN	tracellular (Potential).	1	TGGATCCCACA	0.436
-	13	1866	p.G514R|SAMD3_	NM_001017373	NP_001017373	Q8N6K7	SAMD3_HUMAN		1	GAAATCCTACTT	0.368
+	3	1830	0kfi.2_Missense_	NM_052913	NP_443145	Q86VY9	T200A_HUMAN	lasmic (Potential).	1	GTCAAGGAATT	0.433
+	3	2157	0kfi.2_Missense_	NM_052913	NP_443145	Q86VY9	T200A_HUMAN	lasmic (Potential).	1	GCAAGGGATATA	0.463
-	2	398		NM_153235	NP_694967	Q8N3L3	TXLNB_HUMAN		2	TCTTTCCCTGCT	0.532
-	13	1781		NM_015718	NP_056533	Q9HBY0	NOX3_HUMAN	lasmic (Potential).	1	GAAATGAACACC	0.418
-	3	399	TR|TAGAP_uc003	NM_054114	NP_473455	Q8N103	TAGAP_HUMAN		1	ACATTCGATTAG	0.308
+	11	1508		NM_000876	NP_000867	P11717	MPRI_HUMAN	nal (Potential).|3.	3	GTTGACTGCACC	0.493
-	4	574	03qvc.1_Missens	NM_021135	NP_066958	Q15349	KS6A2_HUMAN	otein kinase 1.	8	GAAGGGGTGAT	0.408
-	4	424		NM_003247	NP_003238	P35442	TSP2_HUMAN	|Heparin-binding (Potential	5	CAAAGCGCACG	0.592
-	20	2213	.1_RNA|DPY19L2P1_uc010kwz.1_RNA						0	CGTAAAGTGGA	0.408
-	2	1141	bw.1_Missense_M	NM_013389	NP_037521	Q9UHC9	NPCL1_HUMAN	Name=2; (Potential).	5	CCACCGGGATG	0.627
-	22	3354	w.2_Missense_Mu	NM_022748	NP_073585	Q68CZ2	TENS3_HUMAN		4	GGAAAGGAGCC	0.677
+	4	1558		NM_001159522	NP_001152994	A8MUV8	ZN727_HUMAN	2H2-type 11.	0	GCAAAACCTTTA	0.428
+	4	1570		NM_001159522	NP_001152994	A8MUV8	ZN727_HUMAN	2H2-type 11.	0	CTGCTCCTCAA	0.418
+	2	1062	se_Mutation_p.V2	NM_003596	NP_003587	O60507	TPST1_HUMAN	enal (Potential).	0	TGTTGGTTCACT	0.418
+	6	906		NM_001099435	NP_001092905	A6NIY4	SPDE5_HUMAN	Arg-rich.	0	GAACCCGAGGG	0.592
+	5	517	ite|POR_uc011kg	NM_000941	NP_000932	P16435	NCPR_HUMAN	avodoxin-like.	1	GGTGAGGGAGA	0.627
-	5	7232	_Mutation_p.E231	NM_033026	NP_149015	Q9Y6V0	PCLO_HUMAN		7	AACTTCCAGAA	0.423
-	3	2720	v.2_Missense_Mu	NM_033026	NP_149015	Q9Y6V0	PCLO_HUMAN	Pro-rich.	7	TTTTTCCCCTG	0.433
+	13	1626	7orf63_uc011khj.1	NM_001039706	NP_001034795	A5D8W1	CG063_HUMAN		1	ACAGATCCGTTT	0.348
+	43	3267	1A2_uc011kib.1_I	NM_000089	NP_000080	P08123	CO1A2_HUMAN		9	GGGAACGATGG	0.488
-	23	3290		NM_015395	NP_056210	Q7Z6L1	TCPR1_HUMAN	TECPR 7.	1	GGACGGGATGT	0.592
+	4	649_650	T1_uc010ljj.1_Int	NM_021930	NP_068749	Q6NUQ1	RINT1_HUMAN		4	CGCAACCTTGG	0.396
+	4	1549	HRM2_uc003vtm	NM_001006630	NP_001006631	P08172	ACM2_HUMAN	smic (By similarity).	5	AGTTTCCACTT	0.463
-	15	1860		NM_004333	NP_004324	P15056	BRAF_HUMAN	rotein kinas_R603>I(2)|p.T	18290	ATTTCACTGTA	0.368
+	18	2177		NM_004668	NP_004659	O43451	MGA_HUMAN	(Potential).|Maltase.	2	GAATTCCTCCA	0.547
-	9	1451		NM_019841	NP_062815	Q9NQA5	TRPV5_HUMAN	ical; (Potential).	6	TCACAGCCCCA	0.537
+	6	734		NM_018487	NP_060957	Q96HP8	T176A_HUMAN		2	GTTCCCAACCA	0.542
+	4	507	_p.P75L|SLC4A2_	NM_003040	NP_003031	P04920	B3A2_HUMAN	ic (Potential).|Pro-rich.	0	TCACCCACTGT	0.692
-	1	143		NM_001005504	NP_001005504	O95013	O4F21_HUMAN	Name=1; (Potential).	0	TCACAGAAAAC	0.488
-	1	5470		NM_031271	NP_112561	Q9BXT5	TEX15_HUMAN		7	CAGGTCTTCTA	0.368
+	10	1131	se_Mutation_p.R3	NM_194294	NP_919270	Q6ZQW0	I23O2_HUMAN		2	GCATTCGTCATA	0.448
-	22	4294	NL_uc003xqt.3_	NM_144651	NP_653252	A1KZ92	PXDNL_HUMAN	VWFC.	2	CTCTAACATCT	0.517

+	4	3017	P1_uc011ldy.1_Intr	NM_006269	NP_006260	P56715	RP1_HUMAN			12	AATGATCCCCAT	0.323	
-	3	771	.2_5'UTR|RSPO2_	NM_178565	NP_848660	Q6UXX9	RSPO2_HUMAN			7	CAAATGGGATTT	0.358	
+	19	2139		NM_177531	NP_803875	Q86WI1	PKHL1_HUMAN	cellular (Potential).		14	TTGAAGAAGGA	0.289	
+	19	2759	lja.1_Nonsense_	NM_016018	NP_057102	A8MW92	P20L1_HUMAN			2	GGAAGCGAAAA	0.353	
-	10	1262	ion_p.E413K|NAP	NM_145201	NP_660202	Q6XQN6	PNCB_HUMAN			1	CTTCTCGGGGT	0.657	
-	13	1475	zo.1_Missense_Mu	NM_015356	NP_056171	Q14160	SCRIB_HUMAN	ens junction and to inhibit		5	CCGCCCCTCGA	0.682	
+	7	725	3zbi.3_Missense_	NM_032450	NP_115826	Q8NDA8	HTR7A_HUMAN	HEAT 2.		0	CCTGCCATCCG	0.692	
-	3	1243		NM_003923	NP_003914	O75593	FOXH1_HUMAN			0	AGGAAGGGGGC	0.682	
-	1	1323	_5'Flank|DOCK8_	NM_152569	NP_689782	Q5T8R8	CI066_HUMAN			1	TGCCTACATTCC	0.642	
-	1	101	uc003zrh.1_Intron	NM_153809	NP_722516	Q8IZX4	TAF1L_HUMAN			26	CGCAGCCGGGT	0.542	
-	4	884	on_p.E251D|ECM	NM_001393	NP_001384	O94769	ECM2_HUMAN	Poly-Glu.		2	ctcctcatcctcctcctc	0.398	
-	6	1128	rl.2_Missense_Mu	NM_000507	NP_000498	P09467	F16P1_HUMAN			0	TAGCGGGGTAC	0.358	
+	8	1817	x.1_Missense_Mu	NM_014290	NP_055105	Q8NHU6	TDRD7_HUMAN	Tudor 1.		3	GTTACGGGCAC	0.418	
+	4	760	c.2_Missense_Mu	NM_207299	NP_997182	Q8TBJ4	LPPR1_HUMAN			0	CCCTTACTTCGA	0.373	
-	3	1511	NB31_uc004bja.3	NM_015404	NP_056219	Q9P202	WHRN_HUMAN	PDZ 2.	p.R288W(1)	6	GGACCGGCCGT	0.632	
-	3	846	f.2_Missense_Mut	NM_002160	NP_002151	P24821	TENA_HUMAN			7	ACCGCTACAGA	0.557	
+	7	956	36_uc004cjk.1_RN	NM_024718	NP_078994	Q3YEC7	PARF_HUMAN	all GTPase-like.		0	AATATCCCATTTT	0.512	
-	25	3397	_p.W547L|MAP3K	NM_001001671	NP_001001671	Q6ZN16	M3K15_HUMAN			7	ACATCCAGTGG	0.423	
+	1	1320		NM_152577	NP_689790	Q8N7E2	ZN645_HUMAN			2	ATAGACGGTATT	0.463	
+	1	25		NM_004651	NP_004642	P51784	UBP11_HUMAN			3	TGTTTGGGGGG	0.562	
+	11	1741	lyz.2_Nonsense_	NM_005120	NP_005111	Q93074	MED12_HUMAN			4	AGCTGCAAGCG	0.527	
+	7	2564	ps.1_Missense_M	NM_018977	NP_061850	Q9NZ94	NLGN3_HUMAN	lasmic (Potential).		1	ACCACGAGTGT	0.687	
-	2	460	uc004esi.1_Intron	NM_032498	NP_115887	P0C7M4	RHF2B_HUMAN			0	TCCTTCCCATAG	0.607	
-	1	1311		NM_138289	NP_612146	Q8TDG2	ACTT1_HUMAN			5	TTCTTTGAACCA	0.478	
+	9	1374		NM_018558	NP_061028	Q9UN88	GBRT_HUMAN			3	TGAGCGATCTC	0.602	
-	2	214				Q8N1B3	FA58A_HUMAN			0	AGTACCTGCGC	0.527	
+	7	763	R1_uc001ajf.1_3'U	NM_007033	NP_008964	O15258	RER1_HUMAN			0	TGCCGGCAAGG	0.493	
-	21	2575	RSF25_uc001ani.	NM_001042663	NP_001036128	O94827	PKHG5_HUMAN			1	ACAGCGTGTCC	0.622	
+	10	1160	k.1_Missense_Mu	NM_002631	NP_002622	P52209	6PGD_HUMAN			1	TGGTGGCATCG	0.552	
+	8	3152	od.1_Missense_M	NM_012231	NP_036363	Q13029	PRDM2_HUMAN			1	CCGATGCCGGG	0.522	
+	8	3948	j.2_Intron|PRDM2_	NM_012231	NP_036363	Q13029	PRDM2_HUMAN	g (Potential).|Pro-rich.		1	CCTCTCCCTCTC	0.498	
-	5	1003	C16_uc001awu.2_	NM_024758	NP_079034	Q9BSE5	SPEB_HUMAN			1	CTGTCCCTGGC	0.522	
+	11	8698	p.1_Missense_Mu	NM_015001	NP_055816	Q96T58	MINT_HUMAN	h RBPSUH (By similarity).		15	ATCAGCGCCAAG	0.582	
-	16	2569	br.1_Missense_M	NM_003443	NP_003434	Q13105	ZBT17_HUMAN	ction with HCFC1.		0	GAGGGCGGAAG	0.677	rs34433473
-	5	784	BXO42_uc001ayf	NM_018994	NP_061867	Q6P3S6	FBX42_HUMAN	Kelch 2.		2	GCCACCAAACA	0.483	
+	8	1974	p.G457D|PAX7_u	NM_002584	NP_002575	P23759	PAX7_HUMAN			203	TGGCCGGCTATC	0.672	
-	21	2003	bew.2_Missense_	NM_002885	NP_002876	P47736	RPGP1_HUMAN			3	CCTCCGTCTCC	0.667	
-	2	839	vrj.2_Missense_M	NM_004350	NP_004341	Q13761	RUNX3_HUMAN	Runt.		0	CACTGCGGCCC	0.597	
-	12	1220	_Missense_Mutati	NM_183008	NP_892120	Q5T124	UBX11_HUMAN			1	TCCAAGGCCTTG	0.647	
-	14	1373	ik.1_Nonsense_M	NM_006802	NP_006793	Q12874	SF3A3_HUMAN	Matrin-type.		0	CCCTCGGTAGG	0.393	
+	30	12702	a.1_Missense_Mu	NM_033044	NP_149033	Q9UPN3	MACF1_HUMAN			16	TGTCCGATGCT	0.483	
+	11	1695	4A_uc010oki.1_I	NM_014663	NP_055478	O75164	KDM4A_HUMAN			1	ATCTTCTAGCCT	0.522	
+	22	1994	BPL9_uc001csw.	NM_024586	NP_078862	Q96SU4	OSBL9_HUMAN			1	TGGAAGATCAG	0.438	
+	4	1551		NM_000098	NP_000089	P23786	CPT2_HUMAN	ial matrix (By similarity).		0	ATGGGGATGGC	0.517	
+	37	4957	se_Mutation_p.R4	NM_176877	NP_795352	Q8NI35	INADL_HUMAN	PDZ 9.		4	GACTCCGAGCT	0.473	
-	3	1069	3_Intron|KANK4_u	NM_181712	NP_859063	Q5T7N3	KANK4_HUMAN	Pro-rich.		6	CAGCTCCCTCC	0.547	
+	5	449	ote.1_Missense_	NM_001012425	NP_001012425	Q5VVC0	CA146_HUMAN			1	CAGTAAATGCTA	0.358	

-	20	2219	OL11A1_uc001dur	NM_001854	NP_001845	P12107	COBA1_HUMAN	le-helical region.	12	TCTTCTCCCTGT	0.284	
-	10	1464	nse_Mutation_p.V	NM_001048210	NP_001041675	Q96S66	CLCC1_HUMAN		1	GTACCACCGTGG	0.468	
-	4	454	orf194_uc009wew	NM_001122961	NP_001116433	Q5T5A4	CA194_HUMAN		1	CAGTGTCTGATG	0.493	
+	4	491	9wey.2_Missense_	NM_020775	NP_065826	Q6UXG2	K1324_HUMAN	cellular (Potential).	5	CCCTCGGCACA	0.587	
-	1	791		NM_005549	NP_005540	Q16322	KCA10_HUMAN		4	GGGCCGGTTCC	0.448	
+	14	1330	se_Mutation_p.S3	NM_003176	NP_003167	Q15431	SYCP1_HUMAN	Potential.	1	CTCATTCGTTTG	0.308	
+	22	3382	splice|C1orf203_uc	NM_000701	NP_000692	P05023	AT1A1_HUMAN		1	CTGGCGGTAATT	0.493	
+	7	934	_p.R236H|PHGDH_	NM_006623	NP_006614	O43175	SERA_HUMAN	NAD.	1	TGCCCGTGGAG	0.617	
+	5	1023	ron|NBPF10_uc00	NM_203458	NP_982283	Q7Z3S9	NT2NL_HUMAN		1	TCTTTCCTAAGCT	0.378	
+	10	1491	e_Mutation_p.H45	NM_001039703	NP_001034792	A6NDV3	A6NDV3_HUMAN		0	AATAGCCATGGC	0.468	
+	2	237	A10_uc010oyv.1_M	NM_003637	NP_003628	O75578	ITA10_HUMAN	r (Potential).|FG-GAP 1.	8	GACAGCGATGGT	0.507	
+	8	1210	_p.P311S|RPRD2_	NM_015203	NP_056018	Q5VT52	RPRD2_HUMAN		1	GAGTCTCCTTTTC	0.502	
+	6	577	exn.2_Missense_M	NM_002810	NP_002801	P55036	PSMD4_HUMAN	VWFA.	0	GGTGACAGTGC	0.512	
-	10	1044	mr.1_Missense_Mu	NM_001025603	NP_001020774	P48382	RFX5_HUMAN		1	TGTGGGCTCCA	0.522	
-	2	2653	ne.1_Missense_Mu	NM_007113	NP_009044	Q07283	TRHY_HUMAN		5	GGCGGCGTCTCT	0.612	
-	2	163		NM_001045479	NP_001038944				1	ATTGGCGAAACAT	0.443	rs140012440
-	13	3445	i.2_Missense_Mut	NM_001111	NP_001102	P55265	DSRAD_HUMAN	A to I editase.	6	ACACGACAGCAA	0.453	
+	2	1319	'Flank|RUSC1_uc	NM_001105203	NP_001098673	Q9BVN2	RUSC1_HUMAN		2	CGGCACCTCCT	0.687	
-	3	1166	p.P229L|ASH1L_u	NM_018489	NP_060959	Q9NR48	ASH1L_HUMAN		11	TGGAAGGAGGA	0.453	
-	12	1222	sb.1_Missense_M	NM_178229	NP_839943	Q86VI3	IQGA3_HUMAN		6	GATCCGCTGCA	0.612	
+	3	1087		NM_001763	NP_001754	P06126	CD1A_HUMAN	ular (Potential).|Ig-like.	3	GCCCACGTTTCAT	0.468	rs142655599
+	1	540		NM_001004473	NP_001004473	Q8NGX5	O10K1_HUMAN	cellular (Potential).	1	CTGTGACATCTCC	0.517	
+	1	82	P12_uc001gbp.2_5	NM_007240	NP_009171	Q9UNI6	DUS12_HUMAN		1	GCTGTGCCGGGC	0.672	
+	7	958	md.1_Missense_M	NM_001460	NP_001451	Q99518	FMO2_HUMAN		1	ATGAAGGAACCT	0.408	
+	13	1813	_p.P503S|RABGA	NM_014857	NP_055672	Q5R372	RBG1L_HUMAN	ab-GAP TBC.	4	GGTGTCCCTGAA	0.473	
+	17	2915	p.Q867H|LAMC2_	NM_005562	NP_005553	Q13753	LAMC2_HUMAN	al.|Domain II and I.	3	CTTTCAGGTGAG	0.478	
+	2	390		NM_130782	NP_570138	Q9NS28	RGS18_HUMAN		3	GCCAAAGAAACA	0.348	
-	8	2173	pj.1_Missense_Mu	NM_014875	NP_055690	Q15058	KIF14_HUMAN	Kinesin-motor.	7	CTGGGTCATCAC	0.388	rs144936292
-	8	2151	pj.1_Missense_Mu	NM_014875	NP_055690	Q15058	KIF14_HUMAN	Kinesin-motor.	7	ACTGAATGAGAT	0.393	
-	3	1195	pl.1_Missense_Mu	NM_001031725	NP_001026895	Q5T1V6	DDX59_HUMAN	ase ATP-binding.	4	GCAGACGATAAA	0.408	
+	4	772	NPEP_uc001gxf.2	NM_020216	NP_064601	Q9H4A4	AMPB_HUMAN		1	GAGCCGGGTGT	0.502	
+	9	896	b.2_RNA|LGR6_uc	NM_001017403	NP_001017403	Q9HBX8	LGR6_HUMAN	xtracellular (I99_A300insGF	10	GAAGATCGGCAT	0.488	
-	1	475		NM_032833	NP_116222	Q5SWA1	PR15B_HUMAN		2	GGAAAAAGGGTG	0.627	
+	9	965	y.1_Intron|MDM4_	NM_002393	NP_002384	O15151	MDM4_HUMAN	|Asp/Glu-rich (acidic).	3	AAGTAGGGAAAG	0.353	
+	4	1226	C2_uc001hcb.1_M	NM_014858	NP_055673	O75069	TMCC2_HUMAN		1	GCCTCCCCGCCG	0.672	
+	3	288	_p.R60H|PFKFB2_	NM_006212	NP_006203	O60825	F262_HUMAN	phofructo-2-kinase.	1	TAACACGCTACCT	0.507	
-	29	4384		NM_004446	NP_004437	P07814	SYEP_HUMAN	-tRNA synthetase.	2	TATCACGTGGCC	0.383	rs113334654
+	3	355	se_Mutation_p.Q9	NM_032324	NP_115700	Q9BSD7	NTPCR_HUMAN		0	TTGAGCAGTTG	0.458	
-	3	397	ibk.2_Missense_M	NM_022743	NP_073580	Q9H7B4	SMYD3_HUMAN		0	GAACGGAGTCT	0.398	
+	5	214	a.3_RNA|C1orf15	NM_145278	NP_660321	Q5JQS6	CA150_HUMAN		0	GGCAGGAAAAC	0.438	
-	1	625		NM_001004692	NP_001004692	Q8NG77	O2T12_HUMAN	Name=5; (Potential).	3	GGAAAAGGGGA	0.547	
+	3	962		NM_031923	NP_114129	Q5VWG9	TAF3_HUMAN		1	caagagtcccaagagc	0.393	
+	4	593	iln.2_Missense_M	NM_153498	NP_705718	Q8IU85	KCC1D_HUMAN	rotein kinase.	2	AGAAGGATGCC	0.507	
-	8	1249	qcu.1_Missense_M	NM_005028	NP_005019	P48426	PI42A_HUMAN	PIPK.	2	ATGTTCGGATCG	0.537	
+	11	1364	O3A_uc009xkp.1_	NM_017433	NP_059129	Q8NEV4	MYO3A_HUMAN		18	TAATATCCAATCT	0.348	
+	13	1580		NM_019043	NP_061916	Q7Z5R6	AB1IP_HUMAN		7	AGTATGGGAAGA	0.463	
-	15	2317_2318	gdt.1_Nonsense_M	NM_018076	NP_060546	Q5T2S8	ARMC4_HUMAN		6	ACATTTCCATATA	0.446	

-	19	4504	u.1_Missense_Mu	NM_021738	NP_068506	O95425	SVIL_HUMAN		6	ACCTTCCAGGG	0.542	
+	17	1845	e_Mutation_p.D46	NM_024688	NP_078964	Q9H943	CJ068_HUMAN		3	GGAAGAGATATA	0.299	
+	6	716		NM_052997	NP_443723	Q9BXX3	AN30A_HUMAN	ANK 6.	9	ATATACGAAAATT	0.269	
-	1	237		NM_000242	NP_000233	P11226	MBL2_HUMAN	Collagen-like.	1	CCTTTTCTCCCTT	0.532	
-	36	4893	ation_p.E1488K|P	NM_001142769	NP_001136241	Q96QU1	PCD15_HUMAN		13	ATTCTTCCTCAGC	0.393	
-	27	5139_5140	G5_uc001jzj.2_Mis	NM_004747	NP_004738	Q8TDM6	DLG5_HUMAN		8	TTCCTCCGAAAA	0.53	rs146019787
-	8	1075	utation_p.T275M|A	NM_001613	NP_001604	P62736	ACTA_HUMAN		0	GGGCCGTGATC	0.517	
+	8	1229	xut.2_Missense_M	NM_000771	NP_000762	P11712	CP2C9_HUMAN		6	GAATTTCCCAACC	0.378	
+	1	240	ng.2_Missense_M	NM_004088	NP_004079	P04053	TDT_HUMAN		1	TTGATGGCCTCC	0.577	
-	7	842	h.1_Missense_Mu	NM_003061	NP_003052	O75093	SLIT1_HUMAN	LRR 6.	4	ACACGGGGATG	0.592	
+	6	1398		NM_005063	NP_005054	O00767	ACOD_HUMAN	lasmic (Potential).	0	ACCACTCCTTTC	0.443	
-	5	650	_uc001krw.1_Intror	NM_176792	NP_789762	Q8N983	RM43_HUMAN		1	GGGCTGGAGCA	0.453	
-	23	3132	.P1042S|SORCS1	NM_052918	NP_443150	Q8WY21	SORC1_HUMAN	enal (Potential).	2	CAGCTGGATCCT	0.542	
-	1	441	C2_uc009xxx.2_Ir	NR_026715					0	GCCAGGTGCCCC	0.537	
-	11	1565	qsp.1_Missense_	NM_001127211	NP_001120683	A0MZ66	SHOT1_HUMAN	Pro-rich.	0	aggaggaggtggtgg	0.333	
-	19	3423	p.M1059L|EIF3A_	NM_003750	NP_003741	Q14152	EIF3A_HUMAN	DE]-[DE]-R-[SEVGFPILV]-[	0	ATCCATGCCTCC	0.627	
+	50	6431	_p.G2108R|DMBT1	NM_007329	NP_015568	Q9UGM3	DMBT1_HUMAN	CUB 2.	7	GGAGAGGGTTC	0.527	
+	52	6879	_p.S2257Y|DMBT1	NM_007329	NP_015568	Q9UGM3	DMBT1_HUMAN	ZP.	7	ACATTTCCTTTT	0.463	
+	9	1238		NM_032182	NP_115558	Q15018	F175B_HUMAN		0	ATTCTCGACCCAT	0.448	
-	4	405	9_uc010qvv.1_5'l	NM_001012302	NP_001012302	A1A5B4	ANO9_HUMAN	lasmic (Potential).	4	GCGCGGCCAGC	0.647	
+	9	1150	tation_p.P327L|TN	NM_138567	NP_612634	Q8NBV8	SYT8_HUMAN	toplasmic (Potential).	1	TGAGCCCGTAG	0.687	
+	8	1963	_p.E467K|DNHD1_	NM_144666	NP_653267	Q96M86	DNHD1_HUMAN		2	GTTCACGAGGAC	0.522	
-	3	665	_p.A105D|CYP2R	NM_024514	NP_078790	Q6VVX0	CP2R1_HUMAN		2	GCACTGGCAGCT	0.388	
-	1	1265	nb.3_Missense_M	NM_000525	NP_000516	B4DWI4	B4DWI4_HUMAN		1	GTGGAGGGGCA	0.617	
+	7	1484	ic.2_Nonsense_M	NM_004211	NP_004202	Q9Y345	SC6A5_HUMAN	Name=4; (Potential).	4	GGCTTGGGTCA	0.453	
+	4	3577	p.P865S|QSER1_	NM_001076786	NP_001070254	Q2KHR3	QSER1_HUMAN		6	AGAATCCAAGG	0.413	
-	3	308	L1_uc001ocq.1_5'	NM_080668	NP_542399	Q96FF9	CDCA5_HUMAN		0	TGGGTGTCTGG	0.552	
+	5	882	S4_uc010rpc.1_Ir	NM_178864	NP_849195	Q8IUM7	NPAS4_HUMAN	PAS 2.	0	GTCCTAATCTACC	0.542	
-	6	1423	a.3_Missense_Mu	NM_000795	NP_000786	P14416	DRD2_HUMAN	nteraction with PPP1R9B (	2	TCTTCTCCTTCTG	0.577	
+	5	665	_p.S100F|TMPRS	NM_019894	NP_063947	Q9NRS4	TMPS4_HUMAN	lar (Potential).|SRCR.	2	GGTTCTCTGCCT	0.552	
-	14	1621	p.G495R|TREH_u	NM_007180	NP_009111	O43280	TREA_HUMAN		1	TCCCCCACCGG	0.617	
+	8	1632		NM_025004	NP_079280	Q0P6D6	CCD15_HUMAN		2	TCTCCACAAAG	0.418	rs113451248
-	5	761	R43H|RPUSD4_u	NM_032795	NP_116184	Q96CM3	RUSD4_HUMAN		1	GGCTGCGCCGC	0.547	
+	9	1226	p.G351D|FAM118	NM_024556	NP_078832	Q9BPY3	F118B_HUMAN		0	CTACAGGCTGTA	0.408	
-	16	2360	gy.1_Missense_M	NM_014987	NP_055802	Q9UPX0	TUTLB_HUMAN	cellular (Potential).	0	GCTGCGGGAAG	0.637	
+	14	2336	_uc001qkn.2_Miss	NM_199460	NP_955630	Q13936	CAC1C_HUMAN	acellular (Potential).	11	TTGGAGGAAAG	0.418	
+	3	778	eh.1_5'Flank|TUL	NR_027363					0	CCCCCGAGGAC	0.512	
-	22	3176	F_uc010set.1_Int	NM_000552	NP_000543	P04275	VWF_HUMAN	VWFD 3.	12	GTGGCGGTCCC	0.552	
+	26	3357	p.M667V|A2ML1_	NM_144670	NP_653271	A8K2U0	A2ML1_HUMAN		3	CAGCTATGAAG	0.448	
+	29	3634	_p.P759L|A2ML1_	NM_144670	NP_653271	A8K2U0	A2ML1_HUMAN		3	CTACTCCATCATC	0.478	
-	4	563	e_Mutation_p.F16	NM_001781	NP_001772	Q07108	CD69_HUMAN	.|Extracellular (Potential).	0	TTGTTAAATTCTT	0.398	
-	3	276		NM_006248	NP_006239				0	GGGTGGTCCTT	0.612	
-	23	4953	RP6_uc010shl.1_	NM_002336	NP_002327	O75581	LRP6_HUMAN	Potential).|PPPSP motif E.	12	GTGGCGGTGGG	0.517	
-	15	2107		NM_021957	NP_068776	P54840	GYS2_HUMAN		2	ATCTGGAAAAGC	0.303	
-	12	1945	C1_uc001rja.2_N	NM_175861	NP_787057	Q8IUR5	TMTC1_HUMAN	TPR 4.	0	CTTCTTTAAACCC	0.328	
-	2	641	rmf.2_Missense_M	NM_052885	NP_443117	Q96QE2	MYCT_HUMAN	Name=4; (Potential).	1	ACCTCCGCAATG	0.403	
+	21	2256	d.2_Missense_Mu	NM_000289	NP_000280	P08237	K6PF_HUMAN		4	AGTTACCGTAATC	0.527	

+	9	866	)slz.1_Missense_M	NM_000725	NP_000716	P54284	CACB3_HUMAN			0	ACCTCTCCCTGG	0.582
-	12	1269	1rvs.2_Missense_M	NM_013277	NP_037409	Q9H0H5	RGAP1_HUMAN	ol-ester/DAG-type.		1	ACCACACGACAG	0.463
-	6	1295	RT8_uc009zml.1_M	NM_002273	NP_002264	P05787	K2C8_HUMAN	Rod.|Coil 2.		2	TCTCCTCGCCCT	0.657
+	18	4145	_Mutation_p.R102	NM_012291	NP_036423	Q14674	ESPL1_HUMAN			3	CAGACCGGATC	0.577
+	3	458	5A_uc010srr.1_Int	NM_004984	NP_004975	Q12840	KIF5A_HUMAN	Kinesin-motor.		3	ATTTTTGCTTATG	0.488
+	6	494	n_p.M92V|RAP1B_	NM_001089704	NP_001083173	P61224	RAP1B_HUMAN			0	GTTCCAATGATT	0.303
-	14	3349	.A1325T|PTPRB_	NM_002837	NP_002828	P23467	PTPRB_HUMAN	II 13.|Extracellular (Potenti		3	TGAGGCGGTCC	0.552
-	2	301	se_Mutation_p.R8	NM_001109754	NP_001103224	P23467	PTPRB_HUMAN		p.R86H(1)	3	GAACAGCGGTCC	0.542
-	4	976	stq.1_Missense_M	NM_002849	NP_002840	Q15256	PTPRR_HUMAN	cellular (Potential).		3	GTGAACGAAGA	0.363
+	13	1527	swv.2_Splice_Site	NM_022771	NP_073608	Q8TC07	TBC15_HUMAN			0	CAAATGGTAAGA	0.308
+	10	1533	_p.G480E|ACSS3_	NM_024560	NP_078836	Q9H6R3	ACSS3_HUMAN			4	TCCCAGGATACA	0.403
-	1	720		NM_032148	NP_115524	Q96JW4	S41A2_HUMAN	Cytoplasmic.		2	CCACCTGTACTA	0.363
+	5	400	|RFX4_uc001tlt.2_	NM_213594	NP_998759	Q33E94	RFX4_HUMAN	type winged-helix.		1	CAGTTTCCTCAG	0.498
-	20	2434	tul.2_Missense_M	NM_004658	NP_004649	O95294	RASL1_HUMAN			4	AGTCCCCCAGG	0.632
+	11	2162	NF10_uc001tyq.3_	NM_014868	NP_055683	Q8N5U6	RNF10_HUMAN			2	GACAGCGTCACA	0.458
-	7	981	1uaf.2_RNA|ANAP	NM_016237	NP_057321	Q9UJX4	APC5_HUMAN			6	GCTTTCGGCTC	0.483
-	8	2397	)1uia.2_Missense_	NM_133448	NP_597705	Q14C87	T132D_HUMAN	cellular (Pote	p.I690I(1)	14	GCAAAGATGGCC	0.577
+	8	957	37_splice|NUPL1_	NM_014089	NP_054808	Q9BVL2	NUPL1_HUMAN			0	TTTCTTAGGGATA	0.308
-	5	1615	nse_Mutation_p.R	NM_183044	NP_898865	Q9Y252	RNF6_HUMAN			2	TCGGCGAAAGC	0.433
-	8	1327	c.3_Missense_Mu	NM_002019	NP_002010	P17948	VGFR1_HUMAN	4.|Extracellular (Potential).		24	TGCCAGCTACGG	0.408
+	8	979	|DGKH_uc010tfj.1_	NM_178009	NP_821077	Q86XP1	DGKH_HUMAN			2	CCGATGGTATGTA	0.338
-	19	4122	).R1257H|ATP7B_	NM_000053	NP_000044	P35670	ATP7B_HUMAN	lasmic (Potential).		3	TTGATGCGTATC	0.542
-	25	3343	hu.2_Missense_M	NM_001042517	NP_001035982	Q9NSV4	DIAP3_HUMAN	Potential.		2	TTGGCGTTCGA	0.323
+	12	2822	).Q587K|LMO7_uc	NM_015842	NP_056667	Q8WWI1	LMO7_HUMAN			5	CTAGCCAGAAAG	0.502
+	21	2636		NM_003291	NP_003282	P29144	TPP2_HUMAN			2	CTTTGTGAACTA	0.368
+	40	3936		NM_001846	NP_001837	P08572	CO4A2_HUMAN	le-helical region.		6	CATCCACGGAG	0.557
+	9	976		NM_182614	NP_872420	Q8WV15	FA70B_HUMAN	Pro-rich.		0	TTCCCCCGGGG	0.557
+	1	839		NM_001004724	NP_001004724	Q8IXE1	OR4N5_HUMAN	Name=7; (Potential).		1	TCTTTCCTTTGAT	0.403
-	35	6066	ar.1_Nonsense_Mu	NM_020920	NP_065971	Q9HCK8	CHD8_HUMAN			10	GCCATCAACTTG	0.408
+	5	304	se_Mutation_p.Q3	NM_178336	NP_848026	Q86TS9	RM52_HUMAN			0	CATGGCAGCTC	0.473
+	5	1439	ne.2_Missense_Mu	NM_014045	NP_054764	Q7Z4F1	LRP10_HUMAN	xtracellular (Potential).		1	AATGGTCGTGGC	0.582
+	2	379	nd.1_Missense_Mu	NM_173527	NP_775798	Q8IYK8	REM2_HUMAN			2	AGGGGAGGCAG	0.617
-	5	519	R91H|RBM23_uc0	NM_001077351	NP_001070819	Q86U06	RBM23_HUMAN	Arg-rich.		1	GTCGACGATCC	0.542
-	14	1604	MT5_uc010tng.1_	NM_006109	NP_006100	O14744	ANM5_HUMAN			1	GCAGCCGTACCA	0.507
-	2	469	dd.2_Missense_M	NM_001001872	NP_001001872	Q86TY3	CN037_HUMAN	cellular (Potential).		0	TGAGGGGACAC	0.488
+	2	606	HG3_uc001xhp.2_	NM_015549	NP_056364	A1L390	PKHG3_HUMAN	DH.		1	GACCTGCGCAGC	0.622
+	11	1219	p.D376N|GALNTL	NM_020692	NP_065743	Q8N428	GLTL1_HUMAN	nenal (Potential).		2	TGGATGGATGAA	0.547
+	9	2092	RS5_uc001xlp.2_	NM_006925	NP_008856	Q13243	SRSF5_HUMAN	r-rich (RS domain).		0	CAGCCGGTCAA	0.537
-	2	1415		NM_003814	NP_003805	O43506	ADA20_HUMAN	B.|Extracellular (Potential).		1	GTGGCCCAAAGT	0.428
+	2	2208		NM_018228	NP_060698	Q9H8Y1	VRTN_HUMAN			0	ACAAGGAGTTC	0.567
-	2	214	)tvf.1_Missense_M	NM_015305	NP_056120	Q9UNK9	ANGE1_HUMAN			4	TGTTCGCCAGA	0.537
-	23	4085		NM_001080414	NP_001073883	Q9P219	DAPLE_HUMAN	Potential.		3	AGTTCCCCTTG	0.388
+	4	487	u.3_Missense_Mu	NM_003836	NP_003827	P80370	DLK1_HUMAN	r (Potential).|EGF-like 3.		4	CTCTATGAATGC	0.582
+	1	562		NM_001080841	NP_001074310					0	CAGCCGACAAG	0.453
+	9	1995		NM_019074	NP_061947	Q9NR61	DLL4_HUMAN	lasmic (Potential).		2	TTCGACGGCCG	0.617
+	16	4768	acl.2_Missense_M	NM_001080534	NP_001074003	Q8NB66	UN13C_HUMAN			7	AATTTGGATTTTT	0.393
-	48	9705		NM_003922	NP_003913	Q15751	HERC1_HUMAN			19	TTCTGGCCAGA	0.483

-	6	550	uc010ujo.1_Misser	NM_017858	NP_060328	Q9BVW5	TIPIN_HUMAN		1	TTGCTAACAAAAT	0.219	
-	2	149	0bis.2_Missense_M	NM_001012642	NP_001012660	Q8IUY3	GRAM2_HUMAN		0	AGTCCGGGGGC	0.517	
-	11	1788	R521H|PKM2_uc01	NM_182471	NP_872271	P14618	KPYM_HUMAN	; part of allosteric site.|Inter	1	CAGGGCGCCAT	0.622	
-	6	1258	p.V238G|NPTN_u	NM_012428	NP_036560	Q9Y639	NPTN_HUMAN	ical; (Potential).	0	ATCACCACAAGG	0.522	
+	2	243	0bmt.1_Missense_	NM_207517	NP_997400	P82987	ATL3_HUMAN		27	CGAGCCCCTGG	0.562	
+	4	1439	592_uc010upb.1_	NM_014630	NP_055445	Q92610	ZN592_HUMAN		6	CAGCTCCCCAC	0.517	
+	12	5371	pc.1_Missense_M	NM_020778	NP_065829	Q96L96	ALPK3_HUMAN	type protein kinase.	12	TTCTCGGGAATG	0.547	
+	13	1289	LC28A1_uc010upf	NM_004213	NP_004204	O00337	S28A1_HUMAN	ical; (Potential).	3	CAGATCGATGCCA	0.577	
+	4	567	2_Missense_Mutat	NM_006122	NP_006113	P49641	MA2A2_HUMAN	nenal (Potential).	3	GGCAAGGCTTCG	0.602	
+	11	2328	R_uc010bon.2_Mi	NM_000875	NP_000866	P08069	IGF1R_HUMAN	cellular (Potential).	8	CGGCCGCAGAC	0.527	rs70958396
+	5	787	ve.2_Missense_M	NM_005587	NP_005578	Q02078	MEF2A_HUMAN	Ser/Thr-rich.	1	CAATGTCTGTCAC	0.433	
+	18	1718	p.R538H|BAIAP3_	NM_003933	NP_003924	O94812	BAIP3_HUMAN		1	GCAACCGTGAGT	0.443	
-	6	1859		NM_032444	NP_115820	Q8IY92	SLX4_HUMAN	C20orf94, ERCC4 and MSH	0	ACCTTCCGCCTCT	0.597	
-	13	3943	uyn.1_Missense_M	NM_001134407	NP_001127879	Q12879	NMDE1_HUMAN	lasmic (Potential).	45	GGGGTGGATCTA	0.532	
-	50	8796	p.M2671I|SMG1_u	NM_015092	NP_055907	Q96Q15	SMG1_HUMAN		16	TCCGCTCATACTG	0.532	
-	7	1032		NM_174924	NP_777584	Q8N807	PDILT_HUMAN		1	AACTCGGAAATCA	0.458	
-	3	253	_p.G15S|ACSM2E	NM_182617	NP_872423	Q68CK6	ACS2B_HUMAN		5	AGTACCCCACAC	0.498	
+	13	1998		NM_001039	NP_001030	P51170	SCNNG_HUMAN	smic (By similarity).	6	AGTGCCCGGCA	0.572	
-	2	144	ICE1_uc002doj.1_	NM_145080	NP_659547	Q8WV22	NSE1_HUMAN		0	GCGCCGGTGGA	0.547	
+	16	3232		NM_015202	NP_056017	O60303	K0556_HUMAN		8	GCCACGTTGCC	0.532	
-	16	1694	je.1_Nonsense_Mu	NM_013263	NP_037395	Q9NPI1	BRD7_HUMAN	Potential.	0	TCTTCTGGAATAT	0.453	
-	3	491	_p.P102L|TOX3_uc	NM_001080430	NP_001073899	O15405	TOX3_HUMAN		0	GAGGGGGAAAC	0.532	
-	3	378	nm.2_Missense_M	NM_001012398	NP_001012398	Q9H8T0	AKTIP_HUMAN		0	GGGCAGGAGAT	0.468	
+	5	1861	ation_p.R72*|NFAT	NM_173165	NP_775188	Q12968	NFAC3_HUMAN	RHD.	3	AACTTCGAAAAG	0.343	
-	6	3010	eyx.2_Missense_M	NM_006927	NP_008858	Q16842	SIA4B_HUMAN	nenal (Potential).	1	CTGTCGGCCCCG	0.697	
-	36	5718		NM_032821	NP_116210	Q4G0P3	HYDIN_HUMAN	p.D1816H(1)	2	GCTGATCAAATTC	0.443	
-	5	854	8B_uc010vmu.1_N	NM_001011880	NP_001011880	Q6UXF7	CL18B_HUMAN		0	ATGGTCCCAGGC	0.607	
+	4	2028	nn.1_Missense_Mu	NM_015251	NP_056066	O43313	ATMIN_HUMAN		0	GGACATAGAGAC	0.458	
-	8	1446	se_Mutation_p.E4	NM_020947	NP_065998	Q6P9B6	K1609_HUMAN		2	GCCCTTCGCTGT	0.632	
-	8	1131	se_Mutation_p.P2	NM_017740	NP_060210	Q9NXF8	ZDHC7_HUMAN		1	ATGTGGGCTTCT	0.572	
+	2	1176	H3_uc010vou.1_R	NM_020655	NP_065706	Q8WXH2	JPH3_HUMAN	ic (Potential).|MORN 7.	2	TCGGACGGGCTC	0.647	
-	24	2243	pn.1_Missense_M	NM_000135	NP_000126	O15360	FANCA_HUMAN		6	ACACTGGAGGCA	0.642	
-	9	1179	cjf.2_Intron|PRDM	NM_001098173	NP_001091643	Q9NQW5	PRDM7_HUMAN		1	TCCCCATACCAGA	0.522	
+	3	758	orf97_uc010vpz.1_	NM_001013672	NP_001013694	Q6ZQX7	CQ097_HUMAN	tandem repeat of A-L-K-G-	1	ACCCCGACCCCC	0.726	
-	11	1809	2fta.1_RNA|SCARF	NM_003693	NP_003684	Q14162	SREC_HUMAN	|Cytoplasmic (Potential).	1	ATGGCCGCTTGG	0.667	
+	9	1237	_p.L215H|CTNS_u	NM_004937	NP_004928	O60931	CTNS_HUMAN	ical; (Potential).	0	TTGTCCTCACGC	0.607	
+	20	3089	7M|USP6_uc010ck	NM_004505	NP_004496	P35125	UBP6_HUMAN	ab-GAP TBC.	5	TGGGACGTGTAT	0.587	
-	4	2644	p.G697R|NLRP1_	NM_033004	NP_127497	Q9C000	NALP1_HUMAN		9	TCCTCCCCTGAGA	0.562	
-	5	808	XE3_uc010vuo.1_	NM_021628	NP_067641	Q9BYJ1	LOXE3_HUMAN	ipoxygenase.	5	GATCTTCCAGCTT	0.473	
-	4	751	25A35_uc002gkt.2_	NM_201520	NP_958928	Q3KQZ1	S2535_HUMAN	Solcar 3.	0	GGGCTGGTTGTA	0.597	
-	34	4856	uc002gml.1_Intron	NM_017533	NP_060003	Q9Y623	MYH4_HUMAN	Potential.	13	TCTTTTTCAGCAA	0.408	
-	22	2766	3_Missense_Mutat	NM_001100112	NP_001093582	Q9UKX2	MYH2_HUMAN	Potential.	14	TTTCTTCCAGTTC	0.433	
-	22	2755	3_Missense_Mutat	NM_001100112	NP_001093582	Q9UKX2	MYH2_HUMAN	Potential.	14	TCCTTCCTTTTTG	0.428	
-	9	1701	ow.2_Missense_M	NM_006470	NP_006461	O95361	TRI16_HUMAN	B30.2/SPRY.	3	GTGTGCTGTGTC	0.557	
+	11	2459	e_Mutation_p.E26	NM_014695	NP_055510	A2RUR9	C144A_HUMAN	Potential.	0	CAAAAGGAACTA	0.333	
+	9	767	vyb.1_Missense_M	NM_001040078	NP_001035167	Q6DKI2	LEG9C_HUMAN	Galectin 2.	1	CCATTCCGGGA	0.587	
-	53	6774	no.2_Missense_M	NM_198836	NP_942133	Q13085	ACACA_HUMAN		2	CATCCGGCCTG	0.512	

-	8	1873	di.1_Missense_Mu	NM_000458	NP_000449	P35680	HNF1B_HUMAN		3	ATTACCTGTTTA	0.537	
+	2	219	q.2_Missense_Mu	NM_000759	NP_000750	P09919	CSF3_HUMAN		1	CGCAGCGCTCC	0.642	
+	4	505	ense_Mutation_p.	NM_133264	NP_573571	Q8TF74	WIPF2_HUMAN		3	TCTTCCAAGGA	0.517	
-	1	117		NM_030967	NP_112229	Q07627	KRA11_HUMAN		0	AGGTCCCACTG	0.607	
-	10	1604		NM_021078	NP_066564	Q92830	KAT2A_HUMAN	cetyltransferase.	2	ACACCCGCCGG	0.642	
+	4	561	_5'Flank|EFTUD2_	NM_213607	NP_998772	Q8IW40	CC103_HUMAN		1	CTGACCGGGCA	0.647	rs143476313
+	21	2888	p.R706Q|KPNB1_	NM_002265	NP_002256	Q14974	IMB1_HUMAN		3	AGGGCGGAGAT	0.428	
-	23	2701	ilw.1_Missense_M	NM_145798	NP_665741	Q9BZF2	OSBL7_HUMAN		0	TCCCATAGCCT	0.652	
+	14	1574	ense_Mutation_p.	NM_176096	NP_788276	Q96JB5	CK5P3_HUMAN		0	CGGGCGCCCTG	0.542	
-	2	870		NM_001080439	NP_001073908	Q4G112	HSF5_HUMAN		3	TATCTGAAAATG	0.478	
+	4	473	R11_uc002ixg.1_	NM_018304	NP_060774	Q96HE9	PRR11_HUMAN		2	AGGAAGCACTG.	0.234	
-	6	1305	EKHM1P_uc010w	NR_024386					0	TGAGGGAGAGA	0.657	
+	2	857	.R266C|BPTF_uc	NM_182641	NP_872579	Q12830	BPTF_HUMAN	DDT.	4	CTTTTCGCTTTG	0.443	
-	35	4574		NM_080284	NP_525023	Q8N139	ABCA6_HUMAN	C transporter 2.	7	TCAGGAGGACAC	0.483	
-	3	771		NM_006678	NP_006669	Q08708	CLM6_HUMAN	xtracellular (Potential).	0	CTGTGGTCGTC	0.592	
+	17	2389	195_uc010wsb.1_	NM_014738	NP_055553	Q12767	K0195_HUMAN		1	TGGCACCGCTG.	0.592	
-	7	784	_p.P201L|NPLOC	NM_017921	NP_060391	Q8TAT6	NPL4_HUMAN		2	CATTCGGCCAC	0.512	
+	19	2973	p.V849I|RBBP8_u	NM_002894	NP_002885	Q99708	COM1_HUMAN		3	AAGACGTCAGC	0.368	
+	4	675	p.E197K|LAMA3_	NM_198129	NP_937762	Q16787	LAMA3_HUMAN	inin N-terminal.	11	TAAAAGAATTTG	0.323	
-	15	2458	vi.3_Missense_Mu	NM_001941	NP_001932	Q14574	DSC3_HUMAN	lasmic (Potential).	4	CTGATCCCATAC	0.433	
+	4	555		NM_000371	NP_000362	P02766	TTHY_HUMAN		1	CACGGCTGTCG	0.537	
+	12	2378	b.2_Missense_Mu	NM_033646	NP_387450	Q9ULB5	CADH7_HUMAN	lasmic (Potential).	4	GGAGGGATGTG	0.478	
-	9	1672	p.G462E|NETO1_	NM_138966	NP_620416	Q8TDF5	NETO1_HUMAN	lasmic (Potential).	4	GGTTTTCCTGGC	0.488	
+	8	2176		NM_001194	NP_001185	Q9UL51	HCN2_HUMAN	lasmic (Potential).	0	GCTGGGTCAGC	0.567	
-	4	530	_p.T91M|DPP9_u	NM_139159	NP_631898	Q86TI2	DPP9_HUMAN		1	TCATCCGTCTTC	0.642	
-	2	1759		NM_182919	NP_891549	Q8IUC6	TCAM1_HUMAN		1	TGGCCGTGTCG	0.652	
-	2	1251		NM_182919	NP_891549	Q8IUC6	TCAM1_HUMAN	Pro-rich.	1	TTGGAGTGGCG	0.512	
-	5	874	jg.1_Missense_M	NM_005490	NP_005481	Q9BRG2	SH23A_HUMAN		2	GGGGACGTTCA	0.662	
+	5	408	C5_uc002mhj.1_	NM_174918	NP_777578	Q8IX19	MCEM1_HUMAN	ellular (Pote p.S128F(1)	1	AAACTCCGTAC	0.547	rs139191722
-	4	384	q.2_Missense_Mu	NM_021155	NP_066978	Q9NNX6	CD209_HUMAN	e).|7 X approximate tanden	1	TCAGCTGGGTC	0.562	
-	1	2819		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).	57	ACAGATGGATTC	0.488	
-	24	3703	e.2_Missense_Mu	NM_003331	NP_003322	P29597	TYK2_HUMAN	otein kinase 2.	9	GCTCAAGGAATT	0.373	
+	7	885	2_uc010dxk.2_5'F	NM_031209	NP_112486	Q9BXR0	TGT_HUMAN		1	GACAGCGGTGA	0.632	
+	2	265	N16_uc002mqu.1_	NM_012466	NP_036598	Q9UKR8	TSN16_HUMAN	ical; (Potential).	1	AATGTGGAGGG	0.498	
+	4	1932	e_Mutation_p.S62	NM_144566	NP_653167	Q9H0M5	ZN700_HUMAN	2H2-type 14.	0	CTTCAGTTGTGC	0.483	
+	4	1934	e_Mutation_p.C62	NM_144566	NP_653167	Q9H0M5	ZN700_HUMAN	2H2-type 14.	0	TCAGTTGTGCCT	0.483	
-	5	600		NM_001080404	NP_001073873	C9JN71	ZN878_HUMAN	2H2-type 2.	0	GGAAACCTGAA	0.423	
-	4	1916	799_uc002mts.3_	NM_001080821	NP_001074290	Q96GE5	ZN799_HUMAN	2H2-type 17.	6	TTACATTCATACG	0.413	
+	10	1708		NM_004843	NP_004834	Q6UWB1	I27RA_HUMAN	tential).|Fibronectin type-III	0	ATGCCCCTCCA	0.647	
+	11	1468	e_Mutation_p.R17	NM_173544	NP_775815	Q86XR2	NIBL2_HUMAN		0	CCGAGCGGAGC	0.607	
+	6	923	_p.V118I|RFXANK	NM_003721	NP_003712	O14593	RFXK_HUMAN	ANK 2.	2	AGACCGTTCGC	0.667	
+	8	3047	w.3_Missense_M	NM_153221	NP_694953	Q8IUL8	CILP2_HUMAN		1	CCTCGGCAGCC	0.697	
+	4	1529		NM_031218	NP_112495	P35789	ZNF93_HUMAN	2H2-type 12.	1	ATAAGAAAATTC	0.368	
+	4	1613		NM_031218	NP_112495	P35789	ZNF93_HUMAN	2H2-type 13.	1	ATAAGAAAATTC	0.348	
-	4	935		NM_001159293	NP_001152765	C9JHM3	C9JHM3_HUMAN		1	TCTCCACTATGA	0.403	
-	4	743	pc.1_Missense_M	NM_001076675	NP_001070143	Q68DY1	ZN626_HUMAN		1	GGTTTCCCTCCA	0.363	
-	4	1447	p.K353E|ZNF708_	NM_021269	NP_067092	P17019	ZN708_HUMAN		6	GTTTCTTTCCAG	0.343	

-	4	1111	rj.1_Missense_Mu	NM_003430	NP_003421	Q05481	ZNF91_HUMAN	2H2-type 7.	0	AAGAACGGCTA	0.393	rs410211
+	8	893	ss.2_Missense_M	NM_003796	NP_003787	O94763	RMP_HUMAN		2	TGAACTGTTCAG	0.279	
-	29	3224		NM_032139	NP_115515	Q96NW4	ANR27_HUMAN		5	CTACCGTGTGT	0.612	
-	3	613	LC7A10_uc010xrc	NM_019849	NP_062823	Q9NS82	AAA1_HUMAN		2	GGGGGGGATGC	0.632	
-	7	1345	_p.D79N|LGI4_uc	NM_139284	NP_644813	Q8N135	LGI4_HUMAN	EAR 1.	1	GTAGTCCCAGG	0.677	
+	2	129	yb.1_RNA|FXYD1_	NM_021902	NP_068702	O00168	PLM_HUMAN		0	CCAAGGCAGGT	0.617	
-	8	1186		NM_021232	NP_067055	Q9UF12	PROD2_HUMAN		2	GGCCACCGCTC	0.622	
-	5	1710		NM_133466	NP_597723	Q8N141	ZFP82_HUMAN	2H2-type 12.	2	ATAAGGGATGAA	0.388	
+	6	1744	.1_Missense_Mut	NM_181786	NP_861451	P10072	HKR1_HUMAN		2	ACACACGGGGG	0.537	
-	7	1908	_Mutation_p.Q40	NM_181882	NP_870998	Q9BXM0	PRAX_HUMAN	L]-[LIVMAP]- [AQKHRPE];	2	CAGCTGTACCT	0.587	
+	1	83	se_Mutation_p.P3	NM_001815	NP_001806	P40198	CEAM3_HUMAN		1	TGGGGCCCCCC	0.597	
-	3	759	2ovk.1_Missense	NM_002785	NP_002776	Q9UQ72	PSG11_HUMAN	like C2-type 1.	0	ATATTTCACATTC	0.507	
+	3	654	TL_uc010ekn.2_I	NM_017659	NP_060129	Q9NXS2	QPCTL_HUMAN		1	TGGGGCCAGTG	0.622	
+	19	2884	_p.G764S|TRPM4_	NM_017636	NP_060106	Q8TD43	TRPM4_HUMAN	ical; (Potential).	2	TCCTCGGCGTG	0.607	
+	8	954	_p.P88S|MED25_	NM_030973	NP_112235	Q71SY5	MED25_HUMAN	Pro-rich.	1	TGGGCCCTCGC	0.627	
-	8	1124		NM_016148	NP_057232	Q9Y566	SHAN1_HUMAN	ANK 5.	2	ACCTCGATACA	0.542	
+	1	820		NM_173856	NP_776255	Q8NFZ6	VN1R2_HUMAN	ellular (Potential).	0	GGAGATTTGGGA	0.428	
-	3	2049	2qcj.3_Missense_	NM_144687	NP_653288	P59046	NAL12_HUMAN		7	CCAAGGAGCCC	0.567	
-	6	1228	ILRA3_uc010erk.2	NM_006865	NP_006856	Q8N6C8	LIRA3_HUMAN	like C2-type 4.	1	CCGAGGTCACA	0.587	
-	8	318	_p.E77K|TNNT1_u	NM_003283	NP_003274	P13805	TNNT1_HUMAN		1	CAGCTCCAGCA	0.607	
-	8	1673	_p.E356K|PTPRH_	NM_002842	NP_002833	Q9HD43	PTPRH_HUMAN	tential).|Fibronectin type-III	4	CAGTTCCTTTAG	0.577	
-	23	2880_2881	2qju.2_5'Flank|S	NM_014931	NP_055746	Q9UPN7	PP6R1_HUMAN		0	ACTGGGAGCCTG	0.653	
+	3	981	tg.2_Missense_Mu	NM_176811	NP_789781	Q86W28	NALP8_HUMAN	NACHT.	13	TGAGTGAAGAC	0.493	
-	2	164	tation_p.S33F|uc0	NM_144690	NP_653291	Q96NG8	ZN582_HUMAN		4	ACAAGGGACATG	0.448	
+	2	187	NF324B_uc010eu	NM_207395	NP_997278	Q6AW86	Z324B_HUMAN	KRAB.	1	GTACCGCCACG	0.562	
-	2	604	_p.R60C|CHMP2A	NM_198426	NP_940818	O43633	CHM2A_HUMAN	ction with VPS4B.	0	GATGCGAACAG	0.522	
-	2	219	ya.2_Missense_M	NM_025203	NP_079479	Q9H6R7	CB044_HUMAN		2	CCCATCGGTCC	0.478	
+	2	240	rhv.3_Missense_	NM_020134	NP_064519	Q9BPU6	DPYL5_HUMAN		2	GCTGACGTCTAC	0.572	rs139435744
-	11	1264	np.1_Missense_M	NM_144575	NP_653176	Q6MZZ7	CAN13_HUMAN		2	GGTCCTCCTGCA	0.473	
+	2	568	1B_uc002rtv.2_In	NM_002706	NP_002697	O75688	PPM1B_HUMAN		2	GTATTCCTCACG	0.453	
-	2	790		NM_014482	NP_055297	O95393	BMP10_HUMAN		2	ACTTTTGCCAAC	0.502	
+	4	766		NM_178439	NP_848526	Q96IK5	GMCL1_HUMAN		3	TGGCAGCAGCT	0.398	
+	23	12476	.R4078_splice|AL	NM_015120	NP_055935	Q8TCU4	ALMS1_HUMAN		9	AAACGGTAAGA	0.448	
+	1	64	Mutation_p.R20Q|	NM_004389	NP_004380	P26232	CTNA2_HUMAN		9	AATCCGGACGC	0.408	
-	4	948	svr.2_Nonsense_	NM_017849	NP_060319	O75204	TM127_HUMAN		0	GTGGCTGGAACT	0.617	
-	7	2705		NM_207362	NP_997245	Q6NV74	CB055_HUMAN	Pro-rich.	0	CAGCTCCCCTG	0.701	
-	19	3297	.2_Missense_Muta	NM_002285	NP_002276	P51826	AFF3_HUMAN		6	GGGGCCTTGTT	0.443	
-	8	1432	_p.S449F|TBC1D8	NM_001102426	NP_001095896	O95759	TBCD8_HUMAN		3	TTTTGAGAAGAC	0.532	
+	11	1550	wd.1_Missense_	NM_003855	NP_003846	Q13478	IL18R_HUMAN	oplasmic (Potential).	3	TGGAAAGAAAAA	0.353	
+	2	229		NM_032411	NP_115787	Q9H1Z8	AUGN_HUMAN		0	AAAAACGAGAA	0.363	
+	7	1174	tdx.2_Missense_M	NM_001056	NP_001047	O00338	ST1C2_HUMAN		1	ACAAATCGTTCT	0.403	rs112864909
+	4	564	H2P_uc002tkd.2_	NM_182905	NP_878908				0	CATCCGCCAAG	0.522	
+	5	480	_uc002tks.3_Miss	NM_007082	NP_009013	Q9UBK7	RBL2A_HUMAN		1	ATGCCTCCTACT	0.582	
+	16	1427	yf.1_Missense_M	NM_006770	NP_006761	Q9UEW3	MARCO_HUMAN	tracellular (Potential).	6	TAACCGAGGCC	0.532	
-	6	691	flr.2_Missense_M	NM_014553	NP_055368	Q9NZI6	TF2L1_HUMAN		3	CATTCTCGTTCT	0.587	
+	2	599	SD7B_uc002tvb.	NM_001080427	NP_001073896				7	CCATTTCCTGTC	0.458	
-	6	1090	_p.P175S|ZEB2_u	NM_014795	NP_055610	O60315	ZEB2_HUMAN		9	ATCTGGAGTTC	0.557	

-	21	2136	/.1_Missense_Mut	NM_004543	NP_004534	P20929	NEBU_HUMAN		20	CACAGTAATTCAT	0.358	
-	1	370		NM_019845	NP_062819	Q9NS64	RPRM_HUMAN		0	CTCCCTCCGCGA	0.667	
-	17	3502	p.E1042K|SCN1A_	NM_006920	NP_008851	P35498	SCN1A_HUMAN		13	GAGTTTCTTCAG	0.428	
-	2	469		NM_013233	NP_037365	Q9UEW8	STK39_HUMAN	rotein kinase.	2	TTCATCCATACTG	0.458	
-	48	9207		NM_004525	NP_004516	P98164	LRP2_HUMAN	s A 23.|Extracellular (Potent	29	ACAGGTGAATTC	0.453	
-	4	695	ufp.2_Missense_M	NM_014168	NP_054887	Q9NRN9	METL5_HUMAN		1	GCTGTTCTTGCC	0.338	
+	9	836	3A1_uc010frw.1_5'	NM_000090	NP_000081	P02461	CO3A1_HUMAN	le-helical region.	13	ACCTGGAGAGC	0.383	
+	1	159	uc002uup.2_Intron	NM_138395	NP_612404	Q96GW9	SYMM_HUMAN		3	GCGATGATGCTT	0.627	
+	8	1252	ych.2_Missense_M	NM_001142300	NP_001135772	Q8N7R7	CCYL1_HUMAN		0	TTCATTGGTATTC	0.408	
+	1	133		NM_001927	NP_001918	P17661	DESM_HUMAN	Head.	2	CCGCCGCACCT	0.557	
-	3	329	zlm.1_Missense_M	NM_004438	NP_004429	P54764	EPHA4_HUMAN	cellular (Potential).	12	ACACCCTCTGAG	0.463	
-	22	2212		NM_000092	NP_000083	P53420	CO4A4_HUMAN	le-helical region.	11	GCCAGGGAGCC	0.587	
+	3	564	ype.2_Missense_M	NM_004504	NP_004495	P52594	AGFG1_HUMAN	Arf-GAP.	4	CAATTCCAGACTT	0.328	
+	16	2065	mp.1_Missense_M	NM_001017915	NP_001017915	Q92835	SHIP1_HUMAN		2	GAAGAAATCACG	0.473	
+	10	1145	n_p.L229I|LRRFIP	NM_001137552	NP_001131024	Q32MZ4	LRRF1_HUMAN		3	GAAGAGTTAAATC	0.458	
-	9	1161	as.2_Missense_Mu	NM_019609	NP_062555	Q96SM3	CPXM1_HUMAN		4	CCCGCCCCAGG	0.657	
+	1	160	010gbd.1_RNA|PAI	NM_153638	NP_705902	Q9BZ23	PANK2_HUMAN		0	TGGACGGAGGCA	0.652	
+	3	638	2_Missense_Mutat	NM_022096	NP_071379	Q9NU02	ANKR5_HUMAN		2	TGGGCTGTACTCC	0.438	
+	15	2481	se_Mutation_p.A73	NM_032819	NP_116208	Q9BYN7	ZN341_HUMAN		2	GACACGCTGAG	0.692	
+	9	1816	M2_uc010zuv.1_In	NM_006690	NP_006681	Q9Y5R2	MMP24_HUMAN	ical; (Potential).	0	GTGGCCGTGGTC	0.607	
-	4	1844	1_5'Flank|EIF6_uc	NM_178468	NP_848563	Q9BQN1	FA83C_HUMAN		2	GATCACCAGGTCT	0.642	
+	7	908	T_uc002xoi.1_RNA	NM_015937	NP_057021	Q969N2	PIGT_HUMAN	nenal (Potential).	1	GAGAGCCGAGTC	0.607	
+	12	2112_2113	m.2_Missense_Mu	NM_181659	NP_858045	Q9Y6Q9	NCOA3_HUMAN	Ser-rich.	5	TTCCTCCTTGAC	0.47	
-	24	3016	tv.1_Missense_Mu	NM_020820	NP_065871	Q8TCU6	PREX1_HUMAN		6	GGTTTGCGTCCA	0.527	
-	3	1304		NM_021035	NP_066363	Q9P2E3	ZNFX1_HUMAN		2	GCGAAGGAAGG	0.502	
+	15	1841	_p.T244M|SLC9A8	NM_015266	NP_056081	Q9Y2E8	SL9A8_HUMAN		1	GCTGACGCAGG	0.642	
-	4	1659	zyx.1_Missense_M	NM_173091	NP_775114	Q13469	NFAC2_HUMAN	RHD.	2	TCCCCGTGATTC	0.517	rs145327846
-	9	1880	wj.2_Missense_Mu	NM_199427	NP_955459	Q9NPA5	ZF64A_HUMAN	C2H2-type 7.	2	CACGCGCAGGG	0.657	
-	3	1956	gij.1_Missense_Mu	NM_006526	NP_006517	O75362	ZN217_HUMAN		6	GCACCATCAAAA	0.448	
-	3	436	j.3_Missense_Mut	NM_001336	NP_001327	Q9UBR2	CATZ_HUMAN		1	TGATCCGATCTG	0.622	
+	5	447	n_p.R121*|OGFR_	NM_007346	NP_031372	Q9NZT2	OGFR_HUMAN		0	CTCTGCGAGAA	0.622	
-	15	1164	TE_uc002yir.1_Mi	NM_199261	NP_954870	P56180	TPTE_HUMAN	hatase tensin-type.	5	CAACTTCCTAAA	0.333	
-	4	362	SAMSN1_uc002yjv	NM_022136	NP_071419	Q9NSI8	SAMN1_HUMAN		4	CTCATCCTTCAG	0.413	
-	6	953	F160_uc010gll.1_F	NM_015565	NP_056380	O94822	LTN1_HUMAN		0	GAGGTACACTGT	0.303	
+	8	874		NM_005441	NP_005432	Q13112	CAF1B_HUMAN	WD 5.	2	CCGACGGATCT	0.468	
-	1	551	zlh.1_5'UTR|POTE	NM_001136213	NP_001129685	Q6S545	POTEH_HUMAN		1	CGGCTCCATGA	0.587	
+	15	1204	vg.3_Missense_Mu	NM_148175	NP_680480	Q13356	PPIL2_HUMAN	e cyclophilin-type.	2	GGGCCGCGGCA	0.632	
+	5	1944	A2A_uc010guq.2_	NM_000675	NP_000666	P29274	AA2AR_HUMAN	Cytoplasmic.	0	AGTGTGCCCAG	0.607	
-	14	2096	jy.1_Missense_Mu	NM_001008496	NP_001008496	Q7Z3Z3	PIWL3_HUMAN		4	TATTTCCGTAATG	0.328	rs149915066
-	10	1571	jy.1_Missense_Mu	NM_001008496	NP_001008496	Q7Z3Z3	PIWL3_HUMAN	PAZ.	4	AGGCCCTTTTTC	0.468	
-	12	2430	k.2_Missense_Mut	NM_022081	NP_071364	Q9NQG7	HPS4_HUMAN		0	CCTGGGCAGCG	0.582	
-	3	749		NM_020530	NP_065391	P13725	ONCM_HUMAN		1	TCCTGCGCACCC	0.667	
+	3	1422	N3_uc003amy.2_In	NM_000362	NP_000353	P35625	TIMP3_HUMAN	NTR.	1	CCCATGTGCAGT	0.448	
-	15	2572	wp.2_Missense_M	NM_004737	NP_004728	O95461	LARGE_HUMAN	nenal (Potential).	3	AGTCACGTCTCA	0.572	
-	3	674	n_p.P12L|MYH9_u	NM_002473	NP_002464	P35579	MYH9_HUMAN	yosin head-like.	11	TGTGAGGGGGC	0.532	
-	3	475	aqe.2_Missense_M	NM_001163857	NP_001157329	O43247	EAN57_HUMAN		0	CCTCTCCCGAG	0.637	
-	7	1624		NM_152512	NP_689725	Q8IYW4	ENTD1_HUMAN		3	TAAAGGAGGTAC	0.468	

-	9	1682	ye.1_Missense_Mu	NM_020831	NP_065882	Q969V6	MKL1_HUMAN		p.S492S(1)	5	GTGGCGAGGCC	0.677	
+	23	3133	H7B_uc010gyl.1_I	NM_017590	NP_060060	Q9UGR2	Z3H7B_HUMAN	Poly-Ala.		1	CCACCGCCACC	0.662	rs140753362
-	1	2941		NM_014246	NP_055061	Q9NYQ6	CELR1_HUMAN	(Potential).|Cadherin 7.		11	CGAGGCGCTAA	0.567	
-	18	3075	_5'Flank|PLXNB2_	NM_012401	NP_036533	O15031	PLXB2_HUMAN	Extracellular	p.P1033R(1)	6	GTAGCGGCTCG	0.657	
+	11	1357	_p.A379V|CNTN4_	NM_175607	NP_783200	Q8IWV2	CNTN4_HUMAN	like C2-type 4.		7	AGATGCTGGCA	0.363	
-	3	1039	AP3_uc003bri.1_	NM_014850	NP_055665	O43295	SRGP2_HUMAN			9	ATTGTTCATGAA	0.542	
-	12	1499	vh.1_Missense_M	NM_001080423	NP_001073892	Q9C0E4	GRIP2_HUMAN			1	TGCAGGAAAAG	0.612	
+	4	1009	za.2_Missense_M	NM_032137	NP_115513	Q8ND61	CC020_HUMAN			4	CTACAGCAGCG	0.537	
-	21	2609	dj.2_Missense_Mu	NM_001068	NP_001059	Q02880	TOP2B_HUMAN			5	CTACACGTTGAT	0.383	
+	2	833	cdq.2_Missense_	NM_052953	NP_443185	Q96PB8	LRC3B_HUMAN	LRR 1.		4	CCAATGAAATTT	0.408	
-	5	1458		NM_015551	NP_056366	O60279	SUSD5_HUMAN	ellular (Potential).		2	GCCCCGAGGGA	0.527	rs113725248
+	5	878	chb.2_Missense_	NM_178339	NP_848029	Q8IVJ8	APRG1_HUMAN			1	TGGACCTTTGG	0.448	
-	21	3695		NM_014139	NP_054858	Q9UI33	SCNBA_HUMAN	III.		9	CACCACCTTAT	0.448	
+	1	992		NM_152393	NP_689606	Q2TBA0	KBTB5_HUMAN			1	AGGAGGCCGAA	0.567	
-	9	1515	_p.A114V|SLC6A2	NM_020208	NP_064593	Q9NP91	S6A20_HUMAN	ellular (Potential).		2	TGGCCGCGTAG	0.577	
-	1	1000	_5'Flank|ARIH2_	NM_001123040	NP_001116512	Q8N7S6	CC071_HUMAN			0	TGACCGTAAGT	0.572	
-	2	367		NM_003335	NP_003326	P41226	UBA7_HUMAN	ximate repeats.|1-1.		2	GGTGGGGTGGG	0.657	
-	4	1355	v.2_Missense_Mu	NM_033158	NP_149348	Q12891	HYAL2_HUMAN	EGF-like.		1	GTTGCGGCGCA	0.632	
+	38	3833_3834		NM_004947	NP_004938	Q8IZD9	DOCK3_HUMAN	DHR-2.		0	AGTGGGAGGAC	0.589	
+	15	2743	A3_uc010hon.1_	NM_005233	NP_005224	P29320	EPHA3_HUMAN	Potential).|Protein kinase.		33	ATGAGGGCTAT	0.498	
+	12	1925	_p.S462F|ALCAM_	NM_001627	NP_001618	Q13740	CD166_HUMAN	otential).|Ig-like C2-type 3.		3	AGGAATCTCCTT	0.343	
+	1	384		NM_032600	NP_115989	Q8NEL0	CCD54_HUMAN			0	GATATCCCACTG	0.388	
-	7	942		NM_138815	NP_620170	Q7Z7J5	DPPA2_HUMAN			3	CTGCCGAGAGA	0.512	rs151045476
+	2	318	xx.2_Missense_M	NM_198196	NP_937839	P40200	TACT_HUMAN	Potential).|Ig-like V-type 1.		3	AGACAGTAGGC	0.443	
+	10	1217	bik.1_Missense_	NM_001690	NP_001681	P38606	VATA_HUMAN			3	TGGCCTCGTTTT	0.443	
+	2	233	ehf.1_Missense_	NM_001024660	NP_001019831	O60229	KALRN_HUMAN	CRAL-TRIO.		6	GATGTCCTTCCT	0.468	
+	4	1022		NM_000539	NP_000530	P08100	OPSD_HUMAN	Name=7; (Potential).		0	ATGATGAACAAG	0.612	
+	2	504		NM_001102608	NP_001096078	A6NMZ7	CO6A6_HUMAN	cal region.|VWFA 1.		8	AGACGGAGTGA	0.498	
+	1	216		NM_001002026	NP_001002026	P56856	CLD18_HUMAN	ellular (Potential).		2	GTGTCCGAGAG	0.607	
+	4	1438		NM_139209	NP_631948	Q8WTQ7	GRK7_HUMAN	rotein kinase.		5	AAACATCATTTC	0.423	
+	2	1765		NM_003412	NP_003403	Q15915	ZIC1_HUMAN	2H2-type 4.		2	CGACCGCAAGA	0.542	
-	6	6215_6216	_p.W99*|IGSF10_	NM_178822	NP_849144	Q6WRI0	IGS10_HUMAN	like C2-type 7.		13	AAACTCCAAGAT	0.436	
+	10	1775		NM_006218	NP_006209	P42336	PK3CA_HUMAN	PI3K helical.		3553	GATCCTCTCTCT	0.328	
+	21	2733	_uc011bqm.1_Mis	NM_014616	NP_055431	Q9Y2G3	AT11B_HUMAN	lasmic (Potential).		3	AATGACGTAAGC	0.338	
+	18	1753	d.1_Missense_Mu	NM_015303	NP_056118	Q8N3P4	VPS8_HUMAN			1	CAAAAGCAGTA	0.443	
-	2	370_371	_Intron|MASP1_u	NM_001879	NP_001870	P48740	MASP1_HUMAN			4	ACAGGGAGAAG	0.47	
-	3	593	6_uc010hza.2_5'	NM_001130845	NP_001124317	P41182	BCL6_HUMAN	BTB.		5	TTTTATGGGCTC	0.517	
-	5	1428	fsg.2_Missense_	NM_018192	NP_060662	Q8IVL5	P3H2_HUMAN			4	TAGTAATCCACAT	0.418	
+	3	307	D51N|ZNF595_uc	NM_182524	NP_872330	Q7Z3I0	Q7Z3I0_HUMAN			0	ACCCAGACCTG	0.403	
+	8	3510	_p.K221R|RGS12_	NM_198229	NP_937872	O14924	RGS12_HUMAN			1	AAAAAAGGTGA	0.632	
-	2	252	X3_uc003gld.3_M	NM_003501	NP_003492	O15254	ACOX3_HUMAN			1	ACAGCGCCAGC	0.597	rs145529976
-	5	1121		NM_001358	NP_001349	O43143	DHX15_HUMAN			1	CAACAGGATGT	0.403	
+	3	443	_Site_p.G58_splice	NM_018317	NP_060787	Q8N5T2	TBC19_HUMAN			1	AAACAGGTTGG	0.254	
+	6	1427	_p.R264Q|KLHL5_	NM_015990	NP_057074	Q96PQ7	KLHL5_HUMAN			1	GAGACGACCCA	0.378	
-	5	860	_p.G85R|UGDH_u	NM_003359	NP_003350	O60701	UGDH_HUMAN			4	ATCCCCTCCAAT	0.512	
-	39	5347	L_uc003gyi.1_Mi	NM_015030	NP_055845	O94915	FRYL_HUMAN			1	ACGTAATCCACC	0.507	
+	3	474		NM_206919	NP_996802	Q6T311	ARL9_HUMAN	(By similarity).		0	GTGGCAGTAAAC	0.483	

+	4	965	.|MUC7_uc003hfj.2	NM_001145006	NP_001138478	Q8TAX7	MUC7_HUMAN	3.|Thr-rich.	4	CTCCACCATCTT	0.582	
+	4	1139	.|MUC7_uc003hfj.2	NM_001145006	NP_001138478	Q8TAX7	MUC7_HUMAN	6.|Thr-rich.	4	CTGCCCCACCCA	0.577	
+	4	1629	e_Mutation_p.E412	NM_004885	NP_004876	Q9Y5X5	NPFF2_HUMAN	lasmic (Potential).	3	GTGATGGAAGAA	0.343	
+	5	3504	3hkf.1_Missense_M	NM_020859	NP_065910	Q8TF72	SHRM3_HUMAN		3	AAAACGGGGAG	0.607	
-	8	937	T6L_uc003hkt.1_M	NM_144571	NP_653172	Q96LI5	CNO6L_HUMAN		1	ATTTTGGCACGT	0.398	
-	11	949	p.G244E|EMCN_u	NM_016242	NP_057326	Q9ULC0	MUCEN_HUMAN	lasmic (Potential).	0	GTTTTTCCTTGTG	0.373	
-	5	617	aa.2_Missense_M	NM_001130721	NP_001124193	Q9H5J4	ELOV6_HUMAN	ical; (Potential).	1	ACCAACCTCCC	0.522	
-	1	1919	.1_Intron|PCDH18	NM_019035	NP_061908	Q9HCL0	PCD18_HUMAN	r (Potential).|Cadherin 5.	5	GAACTTCCTAGA	0.418	
+	4	732	_p.C169*|FGB_uc	NM_005141	NP_005132	P02675	FIBB_HUMAN		3	CAGTTGCAATATT	0.383	
-	13	2014	ckv.1_Missense_M	NM_021069	NP_066547	O94875	SRBS2_HUMAN		1	GAGATCGTCACA	0.542	
+	8	1215		NM_001003841	NP_001003841	Q695T7	S6A19_HUMAN	cellular (Potential).	0	ATCAACGCCTTC	0.657	
+	2	1281		NM_024337	NP_077313	P78414	IRX1_HUMAN	Poly-Pro.	2	CACCTCCACCAC	0.701	
-	58	9763	AH5_uc003jfc.2_5'U	NM_001369	NP_001360	Q8TE73	DYH5_HUMAN		31	TAAGACCTAATT	0.413	
-	27	4360		NM_001369	NP_001360	Q8TE73	DYH5_HUMAN	.|Stem (By similarity).	31	TTTTTTCAATATT	0.313	
+	11	2068		NM_020227	NP_064612	Q9NQV7	PRDM9_HUMAN	C2H2-type 5.	6	GAGGAGACACA	0.612	rs112192848
-	11	2145	H10_uc011cnu.1_F	NM_006727	NP_006718	Q9Y6N8	CAD10_HUMAN	|Extracellular (Potential).	12	AGGGAGGAGCA	0.522	
-	9	1634	0iuq.1_Missense_	NM_030955	NP_112217	P58397	ATS12_HUMAN	Disintegrin.	9	CTACTTCCTGGCA	0.473	
+	6	981	3jlb.1_Missense_M	NM_152403	NP_689616	Q63HQ2	EGFLA_HUMAN	onectin type-III 2.	7	GGCAATGAATTC	0.562	
+	8	1478		NM_003999	NP_003990	Q99650	OSMR_HUMAN	III 1.|Extracellular (Potentia	5	GAACTCCATGGT	0.343	
-	6	818	d.2_Intron|IL6ST_u	NM_002184	NP_002175	P40189	IL6RB_HUMAN	tential).|Fibronectin type-III	2	TACACAGTAGAA	0.383	
+	28	4488	_Mutation_p.G140	NM_015183	NP_055998	O15021	MAST4_HUMAN		13	GGGAAGGCACG	0.602	
-	24	3656	v.2_Missense_Mut	NM_001999	NP_001990	P35556	FBN2_HUMAN	15; calcium-binding.	15	AGTTACCTTTGT	0.537	
+	5	1168	L21_uc003lbc.2_In	NM_012159	NP_036291	Q9UKT6	FXL21_HUMAN	LRR 7.	1	GCCTTCATCAGG	0.418	
+	6	1020	eq.2_Missense_M	NM_003339	NP_003330	P62837	UB2D2_HUMAN		1	GATAGAGAAAAG	0.403	
+	1	1755_1756	DHA7_uc003lhq.2	NM_018904	NP_061727	Q9Y5I0	PCDAD_HUMAN	|Extracellular (Potential).	6	TCGGTGGGTGCA	0.693	
+	1	1991		NM_013340	NP_037472	Q9Y5F3	PCDB1_HUMAN	|Extracellular (Potential).	0	CATGATGCAGAA	0.438	
+	1	1442	010jfx.1_Missense_	NM_018916	NP_061739	Q9Y5H0	PCDG3_HUMAN	r (Potential).|Cadherin 5.	1	CAGATAGCAACA	0.552	
+	1	2105	010jfx.1_Missense_	NM_018916	NP_061739	Q9Y5H0	PCDG3_HUMAN	ical; (Potential).	1	TCTCCTGCGTCT	0.682	
-	3	754	loh.3_Missense_M	NM_004576	NP_004567	Q00005	2ABB_HUMAN		2	GGGTTCATGGC	0.373	
+	9	1090	tion_p.R125*|G3B	NM_005754	NP_005745	Q13283	G3BP1_HUMAN		4	GAACAACGAATA	0.463	
+	14	1779	o.1_Missense_Mu	NM_002887	NP_002878	P54136	SYRC_HUMAN		3	ATTTTACGGTTC	0.398	
+	21	3259	q.1_Missense_Mu	NM_004415	NP_004406	P15924	DESP_HUMAN	Globular 1.	9	ATTCTGCAAGAG	0.299	
+	6	970	p.A222T|BTN3A3_	NM_006994	NP_008925	O00478	BT3A3_HUMAN	ical; (Potential).	0	CTTCTCGCAGGA	0.562	
-	10	4192	DC1_uc011dmp.1_I	NM_014641	NP_055456	Q14676	MDC1_HUMAN	on with the PRKDC comple	4	GAAGGCTGGAGC	0.527	
-	24	8474		NM_019105	NP_061978	P22105	TENX_HUMAN	nectin type-III 20.	0	GGGGATGGTCCA	0.672	
-	9	2791	e_Mutation_p.T566	NM_000841	NP_000832	Q14833	GRM4_HUMAN	lasmic (Potential).	6	TTCTGCGTGAAC	0.617	rs146041340
-	7	895	e_Mutation_p.P52	NM_001145776	NP_001139248	Q13451	FKBP5_HUMAN	ase FKBP-type 2.	1	AATTTAGGCTTC	0.358	
+	6	2250	tj.1_RNA|BRPF3_u	NM_015695	NP_056510	Q9ULD4	BRPF3_HUMAN	Bromo.	2	ATTTTCCACCGA	0.408	
-	2	246		NM_001010903	NP_001010903	P0C671	CF222_HUMAN		4	GGGCCTGCGGC	0.632	
+	9	1411	p.G439R|SLC22A7	NM_153320	NP_696961	Q9Y694	S22A7_HUMAN	ical; (Potential).	0	GTGATGGGGAAA	0.557	
+	11	1886	vh.1_Missense_Mu	NM_001146016	NP_001139488	Q5JTD0	TJAP1_HUMAN		0	ATTAACAGGGGCA	0.647	
-	2	273	PP5_uc011dvz.1_I	NM_021572	NP_067547	Q9UJA9	ENPP5_HUMAN		0	GGAGAGAAAAG	0.373	
+	10	1117	wh.1_Missense_M	NM_005588	NP_005579	Q16819	MEP1A_HUMAN	ular (Potential).|MAM.	3	AGACTCGTTGTC	0.488	
+	6	1238	e_Mutation_p.Q34	NM_153839	NP_722581	Q8IZF7	GP111_HUMAN	ular (Potential).|GPS.	1	ATGATTCAAGAA	0.443	
+	5	1290		NM_001010872	NP_001010872	Q5T0W9	FA83B_HUMAN		6	CTGGGGAACAG	0.403	
+	13	2532	k.2_Missense_Mu	NM_001704	NP_001695	O60242	BAI3_HUMAN	cellular (Potential).	50	AGAATTCATACTT	0.328	
-	9	1058	COL9A1_uc003pff	NM_001851	NP_001842	P20849	CO9A1_HUMAN	elical region (COL3).	4	CCCGGGGGGCC	0.572	

-	21	2243	zg.1_Missense_M	NM_153816	NP_722523	Q9Y5W7	SNX14_HUMAN	PX.	0	AGGGGAAAGAA	0.333	
+	16	2319	_Mutation_p.D59	NM_014942	NP_055757	Q9Y2G4	ANKR6_HUMAN		3	TTCGGGACACC	0.567	
-	14	6171	3L_uc003puz.3_	NM_002912	NP_002903	O60673	DPOLZ_HUMAN		6	AAGACGAAGTC	0.468	
-	17	2783	.1_RNA|GOPC_uc	NM_002944	NP_002935	P08922	ROS_HUMAN	ellular (Potential).	25	CCGAAGAACAG	0.378	
+	3	532_533	BLD1_uc003pxr.1	NM_173674	NP_775945	Q8N8Z6	DCBD1_HUMAN	tracellular (Potential).	1	TGGATCCCACA	0.436	
-	3	2099		NM_001012279	NP_001012279	Q5TF21	CF174_HUMAN	Potential.	6	GAGGCGGTACT	0.607	
-	13	1866	p.G514R|SAMD3_	NM_001017373	NP_001017373	Q8N6K7	SAMD3_HUMAN		1	GAAATCCTACTT	0.368	
+	3	1830	0kfi.2_Missense_	NM_052913	NP_443145	Q86VY9	T200A_HUMAN	lasmic (Potential).	1	GGTCAAGGAATT	0.433	
+	3	2157	0kfi.2_Missense_	NM_052913	NP_443145	Q86VY9	T200A_HUMAN	lasmic (Potential).	1	GCAAGGGATATA	0.463	
-	2	398		NM_153235	NP_694967	Q8N3L3	TXLNB_HUMAN		2	TCTTTCCCTGCT	0.532	
-	78	14828	ou.3_Missense_M	NM_182961	NP_892006	Q8NF91	SYNE1_HUMAN	lasmic (Potential).	45	CCTGTGCTGCG	0.512	
-	13	1781		NM_015718	NP_056533	Q9HBY0	NOX3_HUMAN	lasmic (Potential).	1	GAAATGAACAC	0.418	
-	3	399	TR|TAGAP_uc003	NM_054114	NP_473455	Q8N103	TAGAP_HUMAN		1	ACATTCGATTA	0.308	
+	11	1508		NM_000876	NP_000867	P11717	MPRI_HUMAN	nal (Potential).|3.	3	GTTGACTGCAC	0.493	
-	4	574	03qvc.1_Missens	NM_021135	NP_066958	Q15349	KS6A2_HUMAN	otein kinase 1.	8	GAAGGGGTGA	0.408	
-	17	2786		NM_003247	NP_003238	P35442	TSP2_HUMAN		5	CCTCACCTGGT	0.632	rs141075952
-	6	2535		NM_006092	NP_006083	Q9Y239	NOD1_HUMAN		2	TGGCCGCCAGC	0.617	
-	22	2449	.1_RNA|DPY19L2P1_uc010kwz.1_RNA						0	CCTGGCATCTT	0.453	
+	13	3931	hj.2_Nonsense_M	NM_003718	NP_003709	Q14004	CDK13_HUMAN		5	TCATTACAACTC	0.473	
+	7	1082	_Missense_Mutat	NM_031449	NP_113637	Q8NF64	ZMIZ2_HUMAN	Pro-rich.	5	GTCCCTGTCCG	0.697	
-	22	3354	w.2_Missense_Mu	NM_022748	NP_073585	Q68CZ2	TENS3_HUMAN		4	GGAAAGGAGCC	0.677	
+	4	1570		NM_001159522	NP_001152994	A8MUV8	ZN727_HUMAN	2H2-type 11.	0	CTGCTCCTCAA	0.418	
+	2	1062	se_Mutation_p.V2	NM_003596	NP_003587	O60507	TPST1_HUMAN	nal (Potential).	0	TGTTGGTTCACT	0.418	
+	11	2947	p.A718T|POM121_	NM_172020	NP_742017	Q96HA1	P121A_HUMAN	side (Potential).	0	GGGCCGCCAAG	0.652	
+	3	221	CF1B_uc011ker.1_	NM_000265	NP_000256				0	TACTGCGGCACG	0.622	
-	2	288	nse_Mutation_p.V	NM_178125	NP_835226	Q86XT4	TRI50_HUMAN	RING-type.	1	GCACACGGGGC	0.677	rs61743391
-	5	7232	_Mutation_p.E231	NM_033026	NP_149015	Q9Y6V0	PCLO_HUMAN		7	AAACTTCCAGAA	0.423	
-	3	2720	v.2_Missense_Mu	NM_033026	NP_149015	Q9Y6V0	PCLO_HUMAN	Pro-rich.	7	TTTTTCCCCTG	0.433	
-	2	1685	v.2_Missense_Mu	NM_033026	NP_149015	Q9Y6V0	PCLO_HUMAN		7	TGTTGGGCCAG	0.612	
+	13	1626	7orf63_uc011khj.1_	NM_001039706	NP_001034795	A5D8W1	CG063_HUMAN		1	CAGATCCGTTT	0.348	
+	43	3267	1A2_uc011kib.1_	NM_000089	NP_000080	P08123	CO1A2_HUMAN		9	GGGAACGATGG	0.488	
-	23	3290		NM_015395	NP_056210	Q7Z6L1	TCPR1_HUMAN	TECPR 7.	1	GGACGGGATGT	0.592	
+	4	649_650	T1_uc010ljj.1_Int	NM_021930	NP_068749	Q6NUQ1	RINT1_HUMAN		4	CGCAACCTTGG	0.396	
-	4	744		NM_033427	NP_219499	Q8WZ74	CTTB2_HUMAN	Potential.	5	TTCTTCGTTTCT	0.473	
-	1	386	PS2_uc010lkq.2_	NM_198085	NP_932351	Q8N7C7	RN148_HUMAN		0	TCTCTCCTAATT	0.453	
+	8	1513	a.3_Missense_Mu	NM_001458	NP_001449	Q14315	FLNC_HUMAN	Filamin 2.	12	CAGCACGTTCC	0.657	
-	12	1529	lmc.1_Missense_	NM_032842	NP_116231	Q96SK2	TM209_HUMAN		3	CGTCGGGATAC	0.358	rs17857472
+	4	1549	CHRM2_uc003vtm	NM_001006630	NP_001006631	P08172	ACM2_HUMAN	smic (By similarity).	5	AGTTTCCACTT	0.463	
-	15	1860		NM_004333	NP_004324	P15056	BRAF_HUMAN	rotein kinas R603>I(2)|p.T	18290	GATTTCACTGTA	0.368	
+	18	2177		NM_004668	NP_004659	O43451	MGA_HUMAN	(Potential).|Maltase.	2	GAATTCCTCCA	0.547	
-	9	1451		NM_019841	NP_062815	Q9NQA5	TRPV5_HUMAN	ical; (Potential).	6	TCACAGCCCCA	0.537	
+	4	507	_p.P75L|SLC4A2_	NM_003040	NP_003031	P04920	B3A2_HUMAN	ic (Potential).|Pro-rich.	0	TCACCCACTGT	0.692	
+	14	2932	_Mutation_p.G664	NM_053043	NP_444271	Q96EV2	RBM33_HUMAN		1	CAACGGTAACC	0.542	
-	2	826	wtw.2_Missense_	NM_053279	NP_444509	Q96KS9	F167A_HUMAN		0	AGCTCGCCTGT	0.697	
+	5	1124	nse_Mutation_p.	NM_020844	NP_065895	Q9P272	K1456_HUMAN		0	AAAACGGTCCC	0.458	
-	6	1319		NM_002318	NP_002309	Q9Y4K0	LOXL2_HUMAN	SRCR 3.	3	TCAGTCGCACC	0.642	
-	6	1867	p.E405K|CHRNA2	NM_000742	NP_000733	Q15822	ACHA2_HUMAN	Cytoplasmic.	1	GTCCTCCTCCT	0.657	

-	12	1510	e_Mutation_p.D38	NM_018250	NP_060720	Q9NV88	INT9_HUMAN			2	CCACGTCCCCG	0.493	
-	1	5470		NM_031271	NP_112561	Q9BXT5	TEX15_HUMAN			7	CAGGTCTTCTA	0.368	
-	6	565	ck.1_Missense_M	NM_001464	NP_001455	Q99965	ADAM2_HUMAN			2	TAAAGGACAGAT	0.308	
+	10	1131	se_Mutation_p.R3	NM_194294	NP_919270	Q6ZQW0	I23O2_HUMAN			2	GCATTCGTCAT	0.448	
-	22	4294	NL_uc003xqt.3_	NM_144651	NP_653252	A1KZ92	PXDNL_HUMAN	VWFC.		2	CCTCTAACATCT	0.517	
+	4	3017	1_uc011ldy.1_Intr	NM_006269	NP_006260	P56715	RP1_HUMAN			12	AATGATCCCCAT	0.323	
+	3	676	13_uc003ydf.1_R	NM_198584	NP_940986	Q8N1Q1	CAH13_HUMAN			0	TAGATGGAGTG	0.498	
-	4	397	nse_Mutation_p.S	NM_001738	NP_001729	P00915	CAH1_HUMAN			2	GGAAGGAATGC	0.378	
-	4	318	_Intron|SNORA72	NM_000989	NP_000980	P62888	RL30_HUMAN			0	ATGCTGTGCCC	0.378	
+	34	5573	iw.2_Missense_M	NM_017890	NP_060360	Q7Z7G8	VP13B_HUMAN			20	TGCCCGTCCCT	0.408	
-	3	771	.2_5'UTR|RSPO2_	NM_178565	NP_848660	Q6UXX9	RSPO2_HUMAN			7	AAATGGGATTT	0.358	
+	19	2139		NM_177531	NP_803875	Q86WI1	PKHL1_HUMAN	cellular (Potential).		14	TTGAAGAAGGA	0.289	
-	26	3627		NM_003184	NP_003175	Q6P1X5	TAF2_HUMAN			6	ATCTCCAAAGG	0.448	
+	20	2953	R67_uc003yps.1_	NM_145647	NP_663622	Q96DN5	WDR67_HUMAN			1	AGTTCCGTTTG	0.358	
-	10	1043	p.R19H|FAM49B_	NM_016623	NP_057707	Q9NUQ9	FA49B_HUMAN			0	TCATACGACTC	0.338	
-	6	1127	_uc011ljf.1_5'UT	NM_001045556	NP_001039021	Q13239	SLAP1_HUMAN	SH2.		2	CAGCTGCAGCA	0.582	
-	4	1185	M1_uc010mic.2_	NM_144966	NP_659403	Q5H8C1	FREM1_HUMAN	nent site (By similarity).		5	TCCACGAGGTT	0.517	
+	5	3148	SC2_uc003zwx.3	NM_014806	NP_055621	Q8N2Y8	RUSC2_HUMAN			1	ACCCCTTTTCC	0.507	
+	3	967	b.2_Missense_Mu	NM_003995	NP_003986	P20594	ANPRB_HUMAN	cellular (Potential).		3	TTGGTGTGGAG	0.517	
-	6	1109	_Mutation_p.R17	NM_016734	NP_057953	Q02548	PAX5_HUMAN		p.?(22)	147	CTTCCGGAGGA	0.572	
-	1	1064		NM_001126334	NP_001119806	Q5VV16	FX4L5_HUMAN			0	GCCGCCGCCGC	0.677	
+	8	1075	_Mutation_p.R25	NM_003558	NP_003549	O14986	PI51B_HUMAN	PIPK.		1	CTGCCGGGTAA	0.398	
+	20	4367	p.G1419A|WNK2_	NM_006648	NP_006639	Q9Y3S1	WNK2_HUMAN			12	AGGGGGTCCAG	0.672	
-	6	1128	rl.2_Missense_Mu	NM_000507	NP_000498	P09467	F16P1_HUMAN			0	TAGCGGGGTAC	0.358	
-	10	838	7B3_uc010msc.1_	NM_000197	NP_000188	P37058	DHB3_HUMAN			0	AGGTTTCACCTC	0.453	
+	4	760	c.2_Missense_Mu	NM_207299	NP_997182	Q8TBJ4	LPPR1_HUMAN			0	CCCTTACTTCGA	0.373	
+	3	1840	bbi.1_Missense_M	NM_003452	NP_003443	O75820	ZN189_HUMAN	2H2-type 13.		6	GCTTTAGTCAG	0.448	rs138924117
+	11	1817	mf.1_Missense_M	NM_000962	NP_000953	P23219	PGH1_HUMAN			2	GACGGCCACAC	0.562	
+	12	1130	al.1_Nonsense_M	NM_004957	NP_004948	Q05932	FOLC_HUMAN			0	GAGTGGCCGGG	0.721	
+	14	1777	p.R567H|SPTAN1	NM_003127	NP_003118	Q13813	SPTA2_HUMAN	Spectrin 6.		10	CCGCCGCAATG	0.512	rs139998823
-	3	627		NM_006336	NP_006327	Q7Z7L7	ZER1_HUMAN			1	TGTGGCTCGAAG	0.607	
-	8	874	bwx.1_Missense_	NM_020145	NP_064530	Q9NR46	SHLB2_HUMAN	BAR.		0	TGCTACTGATT	0.622	
-	4	576	co.1_Missense_M	NM_004269	NP_004260	Q6P2C8	MED27_HUMAN			1	ATGTTCCATTG	0.413	
+	7	956	6_uc004cjk.1_RN	NM_024718	NP_078994	Q3YEC7	PARF_HUMAN	all GTPase-like.		0	AATATCCCATTTT	0.512	
-	2	648	C2_uc011mer.1_	NM_013366	NP_037498	Q9UJX6	ANC2_HUMAN			1	CCCCTTCCCCC	0.592	
-	11	1496	py.1_Missense_M	NM_004192	NP_004183	O95671	ASML_HUMAN	ASMT-like.		0	CACCCGTGCAG	0.582	
+	2	742	fu.1_Missense_M	NM_173495	NP_775766	Q96NR3	PTHD1_HUMAN			6	CAACAGCAAAG	0.498	
+	1	25		NM_004651	NP_004642	P51784	UBP11_HUMAN			3	TGTTTGGGGGG	0.562	
+	11	2054	9_splice|MAGED	NM_001005332	NP_001005332	Q9Y5V3	MAGD1_HUMAN			3	CAGAGGTAATG	0.527	
-	2	674	xg.2_Intron|PJA1_	NM_145119	NP_660095	Q8NG27	PJA1_HUMAN			0	AGCCCCCTCCT	0.522	
+	7	2564	ps.1_Missense_M	NM_018977	NP_061850	Q9NZ94	NLGN3_HUMAN	lasmic (Potential).		1	ACCACGAGTGT	0.687	
-	25	6039	.K1898R|ATRX_u	NM_000489	NP_000480	P46100	ATRX_HUMAN	Poly-Lys.		30	TTCCCCTTTTTCC	0.318	
-	1	2479	p.G268D|PCDH1	NM_020766	NP_001098713	Q8TAB3	PCD19_HUMAN	|Extracellular (Potential).		7	TTGGTGCCCTCG	0.612	
-	5	694	utation_p.T163M|	NM_007052	NP_008983	Q9Y5S8	NOX1_HUMAN	ential).|Ferric oxidoreducta		1	TCACCGTGTTT	0.507	
+	6	1094	ejh.2_Missense_	NM_022838	NP_073749	Q6P1M9	ARMX5_HUMAN			1	GCTATGGCTGT	0.498	
+	3	4057	r.1_Missense_Mu	NM_020769	NP_065820	Q8NET4	RGAG1_HUMAN			4	TTCTACGGACC	0.522	
-	2	460	uc004esi.1_Intron	NM_032498	NP_115887	P0C7M4	RHF2B_HUMAN			0	TCCTTCCCATAG	0.607	

-	1	1311		NM_138289	NP_612146	Q8TDG2	ACTT1_HUMAN			5	TTCTTTGAACCA	0.478	
+	4	1055	EC1_uc010nsl.1_	NM_005462	NP_005453	O60732	MAGC1_HUMAN			4	AGAACTCAGAGT	0.498	
-	2	1936	fby.2_Missense_	NM_173078	NP_775101	Q8IW52	SLIK4_HUMAN	ellular (Potential).		2	AGATTGCAACTG	0.498	
+	4	649		NM_152578	NP_689791	Q8N0W7	FMR1N_HUMAN	ical; (Potential).		1	TTGGTGCGATCA	0.393	
+	3	309	_p.G53D|MAMLD	NM_005491	NP_005482	Q13495	MAMD1_HUMAN			0	ATGGGGGCTACC	0.423	
+	9	1374		NM_018558	NP_061028	Q9UN88	GBRT_HUMAN			3	TGAGCGATCTC	0.602	
-	2	214				Q8N1B3	FA58A_HUMAN			0	AGTACCTGCGC	0.527	
-	8	800	n.1_Missense_Mu	NM_003491	NP_003482	P41227	NAA10_HUMAN			1	CGGAGGCCTCT	0.602	
-	14	1523	EL1_uc009vlg.1_	NM_033467	NP_258428	Q495T6	MMEL1_HUMAN	enal (Potential).		0	TTCACGCCAGC	0.662	
+	18	3194	p.A1008T|PER3_	NM_016831	NP_058515	P56645	PER3_HUMAN	Ser-rich.		3	CCAGCGCTCTG	0.587	rs57875989
-	21	4456	.R1216C|RERE_	NM_012102	NP_036234	Q9P2R6	RERE_HUMAN		p.R1216C(1)	2	GAGGCGACCTT	0.642	
-	18	3430	ag.1_Missense_M	NM_001009566	NP_001009566	O94985	CSTN1_HUMAN	lasmic (Potential).		1	ATCCCGCATGG	0.612	rs148167401
+	6	1335	_uc001avj.2_RNA	NM_012231	NP_036363	Q13029	PRDM2_HUMAN			1	CGCCCGGAGCA	0.443	
-	3	519	cj.1_Nonsense_	NR_026567						0	CCGCCCCACAG	0.612	
+	6	571		NM_207421	NP_997304	Q6TGC4	PADI6_HUMAN			1	TGTCCCAGATG	0.507	
+	6	907	ACTR4_uc001bp	NM_001048183	NP_001041648	Q8IZ21	PHAR4_HUMAN			0	CACCCGCTGCC	0.572	
+	6	787	P4_uc010ohj.1_5'	NM_005610	NP_005601	Q09028	RBBP4_HUMAN			1	GTGCCGTTCCA	0.438	rs34196891
+	6	1818	522_uc010ohm.1_	NM_020888	NP_065939	Q9P206	K1522_HUMAN	Pro-rich.		0	TCTTCGCTCCC	0.642	
-	8	1143	ux.2_Missense_M	NM_022111	NP_071394	Q9HAW4	CLSPN_HUMAN			8	TCATTTCAGTAG	0.378	
+	3	315	_p.R31W|THRAP3_	NM_005119	NP_005110	Q9Y2W1	TR150_HUMAN	-rich.|Ser-rich.		9	AGTCTCGGTCC	0.463	
+	3	276	oir.1_Missense_M	NM_012090	NP_036222	Q9UPN3	MACF1_HUMAN	ctin-binding.		16	TGAGCGATCTT	0.627	
-	2	1296	_p.E107K|KIAA04	NM_014774	NP_055589	O75071	K0494_HUMAN			0	ATTTTTCCTTGA	0.333	
-	16	3081	nse_Mutation_p.	NM_003035	NP_003026	Q15468	STIL_HUMAN			3	GTAAACGTTTT	0.388	
-	3	1342		NM_147193	NP_671726	Q8NBF1	GLIS1_HUMAN			1	CTTCTCGCCCG	0.667	
+	1	1676		NM_001408	NP_001399	Q9HCU4	CELR2_HUMAN	|Extracellular (Potential).		8	ATGCCCGCCTG	0.587	rs138919468
+	12	5568		NM_001408	NP_001399	Q9HCU4	CELR2_HUMAN	ial).|EGF-like 6; calcium-bi		8	GAACCCGTGTG	0.572	
+	7	1455	A17_uc001dze.1_	NM_001010898	NP_001010898	Q9H1V8	S6A17_HUMAN	lasmic (Potential).		2	ACTTCGATGCC	0.547	
+	9	1920	dze.1_Missense_	NM_001010898	NP_001010898	Q9H1V8	S6A17_HUMAN	lasmic (Potential).		2	ATCATCGACACC	0.587	
+	10	1855	V10_uc001ecm.2	NM_001130079	NP_001123551	Q9HCE1	MOV10_HUMAN	(By similarity).		5	GCACCGGCAAG	0.592	
+	5	800	gn.1_Missense_M	NM_014813	NP_055628	O94898	LRIG2_HUMAN	tracellular (Potential).		3	TAAACCGTAACC	0.353	
+	3	612	e_Mutation_p.E19	NM_001767	NP_001758	P06729	CD2_HUMAN	Potential).|Ig-like C2-type.		1	GCAAGGAATCC	0.542	
-	11	2048	.G598R|NOTCH2_	NM_024408	NP_077719	Q04721	NOTC2_HUMAN	GF-like 15; calcium-binding		27	GTACCCGGGAT	0.522	
-	27	4457	E4DIP_uc001elm.	NM_014644	NP_055459	Q5VU43	MYOME_HUMAN		p.S1389S(1)	5	CTAGACGAATAA	0.517	
+	1	324	F10_uc001emp.3_	NM_153713	NP_714924	Q8IVB5	LIX1L_HUMAN			1	AGGCCGTGGTG	0.642	
+	8	3004	r.1_Missense_Mu	NM_004326	NP_004317	O00512	BCL9_HUMAN	Pro-rich.		6	TGGCTCAGACA	0.557	
-	2	923	B_uc001exu.2_Mi	NM_002651	NP_002642	Q9UBF8	PI4KB_HUMAN			4	GTCCTCGTTGC	0.493	
+	22	2343	n_p.E502K|INTS3_	NM_023015	NP_075391	Q68E01	INT3_HUMAN			3	TGTACGAGTCA	0.622	
+	5	637		NM_000748	NP_000739	P17787	ACHB2_HUMAN	ellular (Potential).		0	CTGACGGCATG	0.552	
-	3	387	fpx.1_Missense_	NM_024540	NP_078816	Q96A35	RM24_HUMAN	KOW.		0	AGTTTCGCTGC	0.562	
+	5	1275	Y9_uc001fwx.2_In	NM_002348	NP_002339	Q9HBG7	LY9_HUMAN	otential).|Ig-like C2-type 2.		1	AAGGGGAATCA	0.547	rs35268513
+	3	537	lb.1_Missense_M	NM_012474	NP_036606	Q9BZX2	UCK2_HUMAN			1	TTCCCGGTAAG	0.512	
+	2	258	x.1_Missense_Mu	NM_022093	NP_071376	Q9UQP3	TENN_HUMAN			9	AGATCGATGTG	0.627	
+	12	2665	.R988Q|RASAL2_	NM_004841	NP_004832	Q9UJF2	NGAP_HUMAN			5	CAGGCGGCACA	0.517	
+	7	1474	_Mutation_p.A382	NM_005807	NP_005798	Q92954	PRG4_HUMAN	ats of K-X-P-X-P-T-T-X.|17		1	AGCCTGCACCC	0.657	rs138528418
+	30	3500	p.S1059F|PTPRC_	NM_002838	NP_002829	P08575	PTPRC_HUMAN	hatase 2.|Cytoplasmic (Po		12	ACATTCCAAGG	0.363	
+	2	989		NM_004767	NP_004758	O60883	ETBR2_HUMAN	ellular (Potential).		2	CGCCCGCATGT	0.612	
-	4	501	pw.1_Missense_	NM_002832	NP_002823	P35236	PTN7_HUMAN	protein phosphatase.		1	GTATCGGTCCTT	0.547	

-	15	3117	ty.1_Missense_M	NM_005401	NP_005392	Q15678	PTN14_HUMAN	protein phosphatase.	5	TCTACTCGATTC	0.463	
+	5	1573	ense_Mutation_p.	NM_001098623	NP_001092093	Q5VST9	OBSCN_HUMAN		28	CAGGAAGCCTC	0.622	
+	10	1096	_Missense_Mutat	NM_001103	NP_001094	P35609	ACTN2_HUMAN	Spectrin 1.	5	GGATTCGTCGC	0.512	
+	2	517	o.3_Missense_M	NM_152609	NP_689822	Q6PJW8	CNST_HUMAN		0	GGGACGGGCAT	0.502	
+	1	55		NM_001004696	NP_001004696	Q8NH00	OR2T4_HUMAN	ellular (Potential).	1	TCCTGATGGGA	0.488	
+	3	1478	.R193Q|PGBD2_	NM_170725	NP_733843	Q6P3X8	PGBD2_HUMAN		1	AACGCGGACTC	0.542	rs138323244
+	6	704_705	ipx.2_Missense_	NM_201596	NP_963890	Q08289	CACB2_HUMAN		3	TAGTTCCAGAAA	0.366	
-	2	580	ense_Mutation_p.	NM_020848	NP_065899	Q9P266	K1462_HUMAN		4	ACATTCGCAAT	0.547	
+	7	794		NM_052997	NP_443723	Q9BXX3	AN30A_HUMAN		9	CTTGGCGGAAA	0.423	
+	7	1054		NM_052997	NP_443723	Q9BXX3	AN30A_HUMAN		9	CGTGGCCAGCA	0.423	
+	7	1156		NM_052997	NP_443723	Q9BXX3	AN30A_HUMAN		9	CGTGGGCAGCA	0.408	
-	2	1519	nse_Mutation_p.A	NM_170753	NP_736609	Q8N328	PGBD3_HUMAN		3	TGAGGCAACAG	0.403	
-	12	1632	p.R440Q|OGDHL_	NM_018245	NP_060715	Q9ULD0	OGDHL_HUMAN		1	CACGCCGGCG	0.572	
-	7	1309	GMS1_uc009xou.	NM_147156	NP_671512	Q86VZ5	SMS1_HUMAN		2	CATGGGGATCT	0.502	
-	21	7225	e_Mutation_p.R21	NM_032776	NP_116165	Q15652	JHD2C_HUMAN	JmjC.	6	AGGACGTACAA	0.363	
-	3	449	_p.R38C|PLA2G12	NM_032562	NP_115951	Q9BX93	PG12B_HUMAN		1	ACAGCGATATT	0.493	
+	18	3538	jvi.2_Missense_M	NM_015037	NP_055852	A7E2V4	K0913_HUMAN	Ser-rich.	1	CTGGGCCCCCA	0.612	
-	4	1609	_uc009xtu.1_Nons	NM_148977	NP_683878	Q8TE04	PANK1_HUMAN		0	CAAATCGTTCAT	0.468	
+	8	864	_p.R255Q|HECTD	NM_182765	NP_877497	Q5U5R9	HECD2_HUMAN		1	GCTACGACAGA	0.318	
+	2	384		NM_024954	NP_079230	Q9HAC8	UBTD1_HUMAN		0	GGGCCGCAAGG	0.622	
-	7	2025	2_Missense_Muta	NM_013274	NP_037406	Q9UGP5	DPOLL_HUMAN	mer binding (By similarity).	0	TTTCCCCGTCGG	0.607	
-	2	650	p.V193M|ITPRIP_	NM_033397	NP_203755	Q8IWB1	IPRI_HUMAN		0	GTCCACGCCAA	0.612	
-	1	441	C2_uc009xxx.2_I	NR_026715					0	CCAGGTGCCCC	0.537	
+	5	672		NM_006426	NP_006417	O14531	DPYL4_HUMAN		2	GGACCGGTGCC	0.632	
+	12	1479		NM_006426	NP_006417	O14531	DPYL4_HUMAN		2	GGGAGCGCCTG	0.657	
+	7	988	ra.2_Missense_M	NM_006755	NP_006746	P37837	TALDO_HUMAN		0	GATCCGCAAGT	0.552	rs143237187
-	2	492		NM_003141	NP_003132	P19474	RO52_HUMAN		4	AAGAGGGACCA	0.557	
-	1	34		NM_001004752	NP_001004752	A6NLW9	A6NLW9_HUMAN		2	AGGTTGGAAATT	0.443	
-	6	557	f.2_5'UTR|HPX_u	NM_000613	NP_000604	P02790	HEMO_HUMAN		0	CTCGCGGTCAC	0.333	
-	22	2758	ense_Mutation_p.L	NM_030962	NP_112224	Q86WG5	MTMRD_HUMAN	GRAM.	3	TCTAAGAATCTT	0.294	
-	8	739	A1_uc010rcp.1_	NM_002786	NP_002777	P25786	PSA1_HUMAN		2	GAAGCGTCTCT	0.313	
-	10	1702	cy.1_Missense_M	NM_000352	NP_000343	Q09428	ABCC8_HUMAN	ity).|ABC transmembrane	1	CCTGCGGGTCG	0.602	
+	2	250	e_Mutation_p.V61	NM_006157	NP_006148	Q92832	NELL1_HUMAN		3	ATATCGTCACC	0.473	
+	27	2979	s.1_Missense_Mu	NM_031418	NP_113606	Q9BYT9	ANO3_HUMAN	lasmic (Potential).	4	TGACCGAATAC	0.408	
+	7	845	2_uc001ndg.3_RN	NM_000506	NP_000497	P00734	THRB_HUMAN	Kringle 2.	3	ACGGGGATGAG	0.632	
+	1	365		NM_001004730	NP_001004730	Q8NGP9	O5AR1_HUMAN	lasmic (Potential).	0	TGGTCGTTTTG	0.512	rs143043362
+	1	446		NM_001004705	NP_001004705	Q8NGI6	OR4DA_HUMAN	Name=4; (Potential).	3	TGCCTGGTTGG	0.532	
-	22	2981	_p.D230N|DDB1_u	NM_001923	NP_001914	Q16531	DDB1_HUMAN	with CDT1 and CUL4A.	4	GAAGTCGCCCT	0.557	
+	18	2185	h.1_Missense_M	NM_000932	NP_000923	Q01970	PLCB3_HUMAN	C2.	2	CCTTGCGGGTC	0.662	
-	1	918		NM_020404	NP_065137	Q9HCU0	CD248_HUMAN	ellular (Potential).	3	TGGCCGGAAAC	0.642	
-	2	1285	jb.2_Missense_M	NM_031492	NP_113680	Q9BQ04	RBM4B_HUMAN	ith TNPO3 (By similarity).	0	TTCCCCGTAGC	0.512	
-	14	2361		NM_006946	NP_008877	O15020	SPTN2_HUMAN	Spectrin 5.	4	TCAACCAACCA	0.677	
+	2	239		NM_015516	NP_056331	Q8WUA8	TSK_HUMAN	LRRNT.	0	TCCCCGGGTGC	0.652	
+	7	924	m.1_Missense_M	NM_000260	NP_000251	Q13402	MYO7A_HUMAN	osin head-like.	4	TACATCGACATC	0.582	
-	4	671	p.G126E|MMP8_u	NM_002424	NP_002415	P22894	MMP8_HUMAN		4	TCTCCTCCAATA	0.413	
-	10	1258		NM_002426	NP_002417	P39900	MMP12_HUMAN	mopexin-like 3.	0	TCCTTTCATCATA	0.448	
-	1	80	e_Mutation_p.S5	NM_001680	NP_001671	P54710	ATNG_HUMAN		0	TCCATCGACAAC	0.617	

+	4	580	EM25_uc001pti.2_	NM_032780	NP_116169	Q86YD3	TMM25_HUMAN	ellular (Potential).	0	AAGTCGGCGCC	0.587	
-	7	1136	ze.1_Missense_M	NM_003455	NP_003446	O95125	ZN202_HUMAN	KRAB.	1	GGAAAAGCATA	0.453	
-	1	182		NM_001004474	NP_001004474	Q8NGN2	O10S1_HUMAN	lasmic (Potential).	2	CCACAGTTAGG	0.532	
-	1	366		NM_001004463	NP_001004463	Q8NGN6	O10G7_HUMAN	lasmic (Potential).	2	GCCAGGTAGCG	0.567	
-	2	205	nse_Mutation_p.G	NM_014231	NP_055046	P23763	VAMP1_HUMAN	lasmic (Potential).	0	GGGGACCCCCA	0.542	
+	5	1050	a.1_Missense_Mu	NM_001987	NP_001978	P41212	ETV6_HUMAN		250	CCCCCGGCAGG	0.607	
+	1	341		NR_003932					0	TTGACGGCATC	0.612	
+	9	1284	zip.2_Missense_M	NM_017435	NP_059131	Q9NYB5	SO1C1_HUMAN	lasmic (Potential).	7	TAATTCTTCCTC	0.388	
-	6	946	_p.V287I|IFLTD1_	NM_152590	NP_689803	Q8N9Z9	ILFT1_HUMAN		3	TTCAACGTCAG	0.373	
+	1	70	rf54_uc009zky.1_	NM_152319	NP_689532	Q6X4T0	CL054_HUMAN		0	AGCATCCCTGC	0.478	
+	13	1843	_p.C559Y|TROAP_	NM_005480	NP_005471	Q12815	TROAP_HUMAN	ate tandem repeats.|Cys-ri	1	GTCCTGCTGTA	0.597	
+	5	687	nse_Mutation_p.R	NM_015416	NP_056231	Q6P1Q0	LTMD1_HUMAN	membrane (Potential).|LET	2	GACTCCGGTGG	0.423	
+	6	1001	T81_uc001sac.2_I	NM_002284	NP_002275	O43790	KRT86_HUMAN	Rod.|Coil 2.	1	GTAGCCGGGCT	0.547	
+	9	1294	my.1_Nonsense_	NM_020547	NP_065434	Q16671	AMHR2_HUMAN	Potential).|Protein kinase.	2	CCCTCCGACGA	0.582	
-	1	569_570	fr.3_Missense_Mu	NM_006163	NP_006154	Q16621	NFE2_HUMAN	d for interaction with MAP	0	CTAGCTCTGAA	0.594	
+	2	289	_p.G30E|ACAD10	NM_025247	NP_079523	Q6JQN1	ACD10_HUMAN		2	CCAGGGGTCCC	0.597	
+	9	1531_1532	tation_p.417_418	NM_153348	NP_699179	Q8N3Y1	FBXW8_HUMAN	WD 5.	3	CAGATGGATGAC	0.594	
+	5	928	uc001txf.2_Intron	NM_178499	NP_848594	Q8IWA6	CCD60_HUMAN		3	TCTTCCGCCAG	0.517	rs147505092
-	5	1199	p.R214C|GOLGA	NM_005895	NP_005886	Q08378	GOGA3_HUMAN	-targeting domain.	6	GGTGCGCAGGA	0.512	
-	33	5015		NM_006437	NP_006428	Q9UKK3	PARP4_HUMAN	th the major vault protein.	4	TGGTGCGAATAA	0.383	rs148540630
+	1	656		NM_030979	NP_112241	Q9H361	PABP3_HUMAN	RRM 3.	4	AATTTTGGAGAA	0.428	
+	1	2894		NM_207361	NP_997244	Q5SZK8	FREM2_HUMAN	xtracellular (Potential).	11	ATGTTGCCCATA	0.507	
+	1	4846		NM_207361	NP_997244	Q5SZK8	FREM2_HUMAN	r (Potential).|CSPG 10.	11	TCACCGATGGA	0.453	
-	3	343		NM_018191	NP_060661	Q8NDN9	RCBT1_HUMAN		1	GGTGCCGAAGA	0.478	
+	1	1881		NR_003268					0	TGGACCACCAG	0.547	
-	1	402	P1_uc001vni.2_I	NM_178861	NP_849192	Q8IZP6	R113B_HUMAN		3	TCGGCGTATGG	0.652	
+	1	745		NM_001099780	NP_001093250	A5LHX3	PSB11_HUMAN		0	CGTGCGGGAGA	0.622	
-	18	1936	p.A466V|IPO4_uc	NM_024658	NP_078934	Q8TEX9	IPO4_HUMAN		1	GGGGCGCCAGG	0.607	
-	5	1736	wmz.1_5'UTR|TM	NM_006405	NP_006396	O15321	TM9S1_HUMAN		1	ATGACAGTAGAC	0.527	
-	30	5913	rb.1_5'UTR|HECT	NM_015382	NP_056197	Q9ULT8	HECD1_HUMAN		5	TCGACTTCTTC	0.343	
+	7	2884	ml.2_Missense_M	NM_004274	NP_004265	Q13023	AKAP6_HUMAN		21	GGAAGGGACTG	0.478	
+	13	6102		NM_004274	NP_004265	Q13023	AKAP6_HUMAN		21	CCTCTACTCCC	0.403	
-	3	857	_p.S229I|OTX2_u	NM_172337	NP_758840	P32243	OTX2_HUMAN		1	GATGGCTGGTG	0.512	
-	9	2532	se_Mutation_p.A2	NM_021136	NP_066959	Q16799	RTN1_HUMAN	Reticulon.	4	CTCAGCATGCC	0.393	
+	22	3342	ty.1_Missense_Mu	NM_173462	NP_775733	O95428	PPN_HUMAN	-like C2-type 2.	3	CCAGCGGATCC	0.642	rs138138992
-	2	2155	rf43_uc010tud.1_	NM_194278	NP_919254	Q6PJG2	CN043_HUMAN	Poly-Arg.	5	CCGGCGCCTCC	0.657	
-	2	1741	rf43_uc010tud.1_	NM_194278	NP_919254	Q6PJG2	CN043_HUMAN	Pro-rich.	5	CAGTTCTGGGT	0.667	
+	7	735	LL5_uc010ask.1_	NM_015072	NP_055887	Q6EMB2	TTLL5_HUMAN	TTL.	3	GACCTTGGATAG	0.413	
-	1	100	RS_uc001yhj.1_In	NM_173701	NP_776049	P23381	SYWC_HUMAN		1	TGCGGGCTCAC	0.547	
+	8	988	_Mutation_p.G18	NM_001112726	NP_001106197	Q9Y4F5	K0284_HUMAN		1	GGCAGGTGGGG	0.642	
-	10	2367		NM_024490	NP_077816	O60312	AT10A_HUMAN	lasmic (Potential).	5	GGTGCCGGATC	0.607	
+	10	1347		NM_033223	NP_150092	Q99928	GBRG3_HUMAN	lasmic (Probable).	0	CAATTCCGTTTA	0.423	
+	9	1986		NM_019074	NP_061947	Q9NR61	DLL4_HUMAN	lasmic (Potential).	2	AGCTGCGGCTT	0.632	
+	8	964	e_Mutation_p.R24	NM_014444	NP_055259	Q9UGJ1	GCP4_HUMAN		3	ACTAGCGCCTG	0.428	
-	37	7136		NM_003922	NP_003913	Q15751	HERC1_HUMAN		19	ATGGCGCCCAG	0.527	
+	3	1066_1067		NM_001031807	NP_001026977	P84550	SKOR1_HUMAN		0	GCTTCCCTACGG	0.579	
-	2	686		NM_002833	NP_002824	P43378	PTN9_HUMAN		2	GGCACGGAGCA	0.493	rs114183309

+	1	116	_5'Flank|SNX33_u	NM_153271	NP_695003	Q8WV41	SNX33_HUMAN	SH3.		1	CCGAGCCCTCT	0.557	
+	22	2968	b.1_Missense_Mu	NM_004136	NP_004127	P48200	IREB2_HUMAN			0	TCAGCGTGATT	0.363	
-	6	634	bgn.2_Missense_	NM_181900	NP_871629	Q9NSY2	STAR5_HUMAN	START.		1	TGGGAGGTAAC	0.522	
+	7	1505	IA2_uc002cgo.1_	NM_006849	NP_006840	Q13087	PDIA2_HUMAN	hioredoxin 1.		2	CGGAGGAGTAC	0.682	
+	4	1625	h.1_Missense_Mu	NM_005632	NP_005623	O75808	CAN15_HUMAN	anBP2-type 5.		2	TGCCTGTACCC	0.766	
-	29	4263	lz.2_Missense_Mu	NM_014714	NP_055529	Q96RY7	IF140_HUMAN			5	TTTGTCGTAGT	0.647	
-	22	3153	lz.2_Missense_Mu	NM_014714	NP_055529	Q96RY7	IF140_HUMAN	TPR 3.	p.R931C(1)	5	GAAGCGGTGCG	0.622	
+	2	343	24_uc002cqm.2_	NM_020705	NP_065756	Q9ULP9	TBC24_HUMAN	ab-GAP TBC.		0	GGTCACGCCTG	0.667	
+	2	864	24_uc002cqm.2_	NM_020705	NP_065756	Q9ULP9	TBC24_HUMAN	ab-GAP TBC.		0	TGTACCGCGTG	0.632	
+	11	7111	rl.1_Missense_Mu	NM_016333	NP_057417	Q9UQ35	SRRM2_HUMAN	-rich.|Ser-rich.		4	CAGCTATCAGT	0.572	
-	12	3145		NM_032444	NP_115820	Q8IY92	SLX4_HUMAN	PLK1 and TERF2-TERF2I		0	TTCTTCGTGGT	0.468	
+	5	1239	IP2_uc010uyp.1_	NM_024997	NP_079273	Q5U623	MCAF2_HUMAN	Potential.		0	CTATTTGATAAG	0.308	
+	8	962	IP_uc002dcx.3_R	NM_006985	NP_008916	Q9UND3	NPIP_HUMAN	Pro-rich.		0	AGCTCCACCCT	0.532	
-	33	4730		NM_017539	NP_060009	Q8TD57	DYH3_HUMAN			18	ACACACCTTCT	0.483	
-	2	273		NM_005003	NP_004994	O14561	ACPM_HUMAN			0	GAACACGGTCC	0.423	
+	15	4273	6A_uc002dmo.2_	NM_014494	NP_055309	Q8NDV7	TNR6A_HUMAN			2	ACAACGGTGGC	0.443	
+	7	1186	efx.2_Missense_	NM_182922	NP_891552	Q7Z4Q2	HEAT3_HUMAN			2	ACTTTCGTTTCA	0.353	
+	6	726	_uc010vhl.1_Silent_	NM_012106	NP_036238	Q9Y2Y0	AR2BP_HUMAN			0	ATCTGCGGCAC	0.483	
-	17	2354	.V739M|CDH16_	NM_004062	NP_004053	O75309	CAD16_HUMAN	Potential).|Ectodomain G.		3	GACACACGATCA	0.507	
-	1	2329	2L_uc002evj.2_5'	NM_018380	NP_060850	Q9NUL7	DDX28_HUMAN	case C-terminal.		1	CGCTCCCCACA	0.582	
-	5	852	_Splice_Site|VAC1	NM_018052	NP_060522	Q08AM6	VAC14_HUMAN			2	CCTTACCCAGG	0.522	
+	2	477	ao.2_Missense_M	NM_005769	NP_005760	Q8NCG5	CHST4_HUMAN	enal (Potential).		0	GATACGGGCCG	0.592	
-	8	1412	LPP2_uc010cgf.2_	NM_015020	NP_055835	Q6ZVD8	PHLP2_HUMAN	LRR 10.		2	GATTCCGCCCA	0.502	
+	2	274		NM_005752	NP_005743	O75596	CLC3A_HUMAN			0	CCCTGCAGACA	0.443	
-	13	2178	fhh.2_Missense_	NM_003791	NP_003782	Q14703	MBTP1_HUMAN	enal (Potential).		2	AGCCCGACCAA	0.537	
-	14	2210	1C_uc010vnz.1_	NM_005679	NP_005670	Q15572	TAF1C_HUMAN			1	TCTGGCGGTGG	0.672	
+	6	539_540	0vqr.1_Missense_	NM_000934	NP_000925	P08697	A2AP_HUMAN			0	AGGACCTGGGC	0.673	
+	8	719		NM_002945	NP_002936	P27694	RFA1_HUMAN			0	GTGCTCGTGTT	0.448	
-	1	227		NM_002550	NP_002541	P47881	OR3A1_HUMAN	Name=2; (Potential).		3	TGATGCACCCA	0.567	
+	8	1475	p.G518E|ZMYND1	NM_032265	NP_115641	Q9H091	ZMY15_HUMAN			0	GGCCGGGAAGG	0.532	
+	3	405	x.1_Missense_Mut	NM_019013	NP_061886	Q9BSJ6	FA64A_HUMAN			0	GGCCAGGAGGC	0.602	
+	7	1156	.R381Q|DNAH2_	NM_020877	NP_065928	Q9P225	DYH2_HUMAN	n (By similarity).		13	CACTCGGGAGA	0.542	
+	36	5749		NM_020877	NP_065928	Q9P225	DYH2_HUMAN	1 (By similarity).		13	TGGCCGCACAG	0.463	rs147216751
-	27	3829	uc002gml.1_Intron	NM_017533	NP_060003	Q9Y623	MYH4_HUMAN	Potential.		13	CAGTCTCCATGT	0.423	
+	9	1848		NM_001372	NP_001363	Q9NYC9	DYH9_HUMAN	n (By similarity).		20	AAGCAGAACTT	0.423	
-	2	480	n|NCRNA00188_u	NM_001113567	NP_001107039	Q8NAA5	CQ076_HUMAN			0	GTTCCGGAAGC	0.622	
-	2	526	L|SREBF1_uc002	NM_004176	NP_004167	P36956	SRBP1_HUMAN	|Cytoplasmic (Potential).		1	ATGGACGGGTAC	0.647	rs115855236
+	3	879	N2_uc010vyo.1_I	NM_014964	NP_055779	O95208	EPN2_HUMAN	ENTH.		1	TGAGAGGGCCC	0.582	
-	11	1214	g.1_Missense_Mu	NM_014030	NP_054749	Q9Y2X7	GIT1_HUMAN	milarity).|PTK2-binding (By		0	AAAGCGGGCCA	0.602	
+	4	893	uc010csm.2_Silen	NM_032322	NP_115698	Q8IUD6	RN135_HUMAN	B30.2/SPRY	p.?(1)	2	CTTCTCGGTTT	0.507	
-	6	1143	p.T221M|PIP4K2B	NM_003559	NP_003550	P78356	PI42B_HUMAN	PIPK.		1	CAACCGTAGAA	0.537	
+	11	1508	_p.V227I|ERBB2_	NM_004448	NP_004439	P04626	ERBB2_HUMAN	ellular (Potential).		143	TCAGCGTCTTC	0.577	rs142783371
-	4	1073	T23_uc010cxg.2_	NM_015515	NP_056330	Q9C075	K1C23_HUMAN	Rod.|Coil 1B.		1	CATTTTCATACCT	0.403	
+	7	1210	AP1_uc010wgs.1_	NM_003632	NP_003623	P78357	CNTP1_HUMAN	1.|Extracellular (Potential).		8	ACCGCGTCAAC	0.612	
-	3	696	.S1073S|WNK4_uc010wgx.1_Silent_p.S737S			Q9Y2R0	CCD56_HUMAN			0	GAGAGCGACCG	0.607	
-	7	882	_Mutation_p.S252	NM_001256	NP_001247	P30260	CDC27_HUMAN			5	ATATGGAAGTTC	0.383	
-	16	1822	ilw.1_Missense_M	NM_145798	NP_665741	Q9BZF2	OSBL7_HUMAN			0	AGACAGCAAAG	0.627	

-	3	281		NM_002634	NP_002625	P35232	PHB_HUMAN		0	AGAACGGCAGT	0.488	
+	9	2764	p.A845T|AKAP1_	NM_003488	NP_003479	Q92667	AKAP1_HUMAN		1	ATGCCGCCATG	0.557	
-	10	1434	ez.2_Nonsense_M	NM_080283	NP_525022	Q8IUA7	ABCA9_HUMAN	p.R431Q(1)	6	AACATCGATGTC	0.438	
-	11	1040	e_Mutation_p.R24	NM_001080542	NP_001074011	Q8TES7	FBF1_HUMAN		0	CGGGCGGGCCA	0.672	
+	7	2983		NM_032048	NP_114437	Q9BXX0	EMIL2_HUMAN	C1q.	3	GCACCGGTGAG	0.602	
-	60	8666	nl.2_Missense_Mu	NM_005559	NP_005550	P25391	LAMA1_HUMAN	minin G-like 4.	21	GGCAGGGATGC	0.522	
-	48	6978	zj.1_Missense_Mu	NM_005559	NP_005550	P25391	LAMA1_HUMAN	minin G-like 1.	21	ACCCACGGCAC	0.438	
+	7	1622	koc.2_Missense_	NM_006788	NP_006779	Q15311	RBP1_HUMAN	racts with RalA.	1	AGGATGTTTCC	0.333	
+	2	1410	NDC2_uc002koh.	NM_001098529	NP_001091999	Q86VQ3	TXND2_HUMAN	repeat of Q-P-K-X-G-D-I-	2	AAGAAGCCATC	0.597	
+	2	1425	NDC2_uc002koh.	NM_001098529	NP_001091999	Q86VQ3	TXND2_HUMAN	repeat of Q-P-K-X-G-D-I-	2	CCAAGGAGGGT	0.592	
-	27	4337	e_Mutation_p.H12	NM_014939	NP_055754	Q9Y2L5	TPPC8_HUMAN		0	TTGATGAAATG	0.353	
-	10	1547	dx.3_Missense_M	NM_006111	NP_006102	P42765	THIM_HUMAN		1	ACCTCCAATGC	0.448	
+	7	950	n_p.G136E|SERPI	NM_001143818	NP_001137290	P05120	PAI2_HUMAN		2	CAAAGGAAAGT	0.383	
-	11	1811	l.1_RNA|CDH19_	NM_021153	NP_066976	Q9H159	CAD19_HUMAN	|Extracellular (Potential).	2	GTGACGGGATT	0.443	
-	4	455	ED16_uc010xfw.1_	NM_005481	NP_005472	Q9Y2X0	MED16_HUMAN	WD 1.	0	CCCGTCGGCAT	0.637	
-	7	1144	va.1_Missense_M	NM_032737	NP_116126	Q03252	LMNB2_HUMAN	Rod.|Coil 2.	2	GTACTCGGCCA	0.657	
+	4	1228	wn.3_Missense_M	NM_152791	NP_690004	Q8NEP9	ZN555_HUMAN	2H2-type 8.	1	TTATCCCCAGT	0.463	
-	3	309	a.1_5'UTR|AES_u	NM_001130	NP_001121	Q08117	AES_HUMAN	rich (Q domain).	0	ACATTCGAGCTT	0.627	
-	10	1629		NM_001961	NP_001952	P13639	EF2_HUMAN		0	CAGGTCAGCCG	0.652	
-	3	3055	ub.1_Missense_M	NM_001080400	NP_001073869	Q96Q06	PLIN4_HUMAN		0	GAGCCCAGCGG	0.652	
-	3	2585	N4_uc010dub.1_In	NM_001080400	NP_001073869	Q96Q06	PLIN4_HUMAN	roximate tandem repeat.|24	0	CCTTTGGCCACT	0.582	
-	6	736	.R160W|DPP9_u	NM_139159	NP_631898	Q86TI2	DPP9_HUMAN		1	TTTCCGCTCCC	0.632	
-	2	522	o.2_Nonsense_M	NM_002034	NP_002025	Q11128	FUT5_HUMAN	enal (Potential).	0	AGATCCAGCGC	0.627	
-	6	916	_p.E35K|GTF2F1_	NM_002096	NP_002087	P35269	T2FA_HUMAN		0	GTCCTCCAGGT	0.637	
+	8	1096	_p.N211S|ZNF557_	NM_001044388	NP_001037853	Q8N988	ZN557_HUMAN	2H2-type 3.	2	ATGCAATGACTG	0.453	
+	5	607_608	_uc010dvs.2_Mis	NM_001144910	NP_001138382	Q9H2X3	CLC4M_HUMAN	|7 X approximate tandem r	1	TGACCCGGCT	0.584	
+	1	183	R40W|MAP2K7_u	NM_145185	NP_660186	O14733	MP2K7_HUMAN		11	GGCCCAGGCCC	0.373	
-	5	706		NM_001419	NP_001410	Q15717	ELAV1_HUMAN	RRM 2.	0	TCACTGTGATG	0.557	
-	14	1743		NM_032447	NP_115823	Q75N90	FBN3_HUMAN	7; calcium-binding.	11	CACTCGTCAAT	0.493	
-	3	23843		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	h.|Extracellular (Potential).	57	TCTGGTGATATT	0.493	
+	26	4452		NM_014975	NP_055790	Q9Y2H9	MAST1_HUMAN		7	CTGCGCGGCCC	0.726	
-	4	1218	p.D266N|WIZ_uc0	NM_021241	NP_067064	O95785	WIZ_HUMAN		0	CGTGTCGATGG	0.637	
+	9	1140	om.1_Missense_	NM_000896	NP_000887	Q08477	CP4F3_HUMAN		3	TGAAGGACCGT	0.582	
+	4	1812	.1_Intron|ZNF90_	NM_007138	NP_009069	Q03938	ZNF90_HUMAN	2H2-type 14.	2	GATAAGTCATAC	0.378	
+	5	1539	pk.2_Missense_	NM_025189	NP_079465	Q9H8G1	ZN430_HUMAN	2H2-type 10.	2	CATAAGGTAATT	0.373	
-	4	1717	p.K443E|ZNF708_	NM_021269	NP_067092	P17019	ZN708_HUMAN	2H2-type 14.	6	ATTCTTTACATTT	0.368	
-	4	1447	p.K353E|ZNF708_	NM_021269	NP_067092	P17019	ZN708_HUMAN		6	GTTTCTTTCCAG	0.343	
-	4	1363	p.E325K|ZNF708_	NM_021269	NP_067092	P17019	ZN708_HUMAN		6	TTTCTCTCCAG	0.368	
+	2	1494	_p.T533S|ZNF493_	NM_175910	NP_787106	Q6ZR52	ZN493_HUMAN	2H2-type 14.	1	CCCTTACTATAC	0.343	
-	4	1483		NM_001098626	NP_001092096	A6NK75	ZNF98_HUMAN	2H2-type 10.	2	TGAATTATCTTAT	0.363	
+	4	1782	rk.1_Missense_M	NM_203282	NP_975011	O75437	ZN254_HUMAN	2H2-type 13.	0	GTGAAAAATGT	0.358	
-	11	1445	p.G128R|NFKBID	NM_139239	NP_640332	Q8NI38	IKBD_HUMAN		0	CGGCCCGGGCC	0.701	
-	4	568	F_uc002otd.3_5'U	NM_006494	NP_006485	P50548	ERF_HUMAN		4	CACCCGACGGC	0.662	
+	5	678		NM_015125	NP_055940	Q96RK0	CIC_HUMAN	HMG box.	11	CAAGCGGCACC	0.617	
+	7	1115		NM_015125	NP_055940	Q96RK0	CIC_HUMAN		11	ACAGCGGGGTA	0.662	
-	5	1941	uc010eif.1_Intron	NM_005357	NP_005348	Q05469	LIPS_HUMAN		2	TGTTGGCCAGA	0.637	
-	2	386	SG2_uc010eiq.1_Missense_Mutation_p.R98Q|PSG2_			Q00889	PSG6_HUMAN	g-like V-type.	2	GTTTCTCGTCCA	0.448	rs150218743

-	1	1961		NM_032040	NP_114429	Q9H0W5	CCDC8_HUMAN		3	GGGCCTCTGCC	0.607	
+	1	1751		NM_004491	NP_004482	Q9NRY4	RHG35_HUMAN		1	TGACCGGAATC	0.488	
+	6	1231	.2_Missense_Mut	NM_020126	NP_064511	Q9NRA0	SPHK2_HUMAN	DAGKc.	1	ACCAGCACGGG	0.632	
-	6	1056	25D|IRF3_uc002p	NM_001571	NP_001562	Q14653	IRF3_HUMAN	in HERC5 binding.	2	GCAGGCCCTCC	0.652	
-	2	307	ydc.1_Missense_	NM_001245	NP_001236	O43699	SIGL6_HUMAN	(Potential).|Ig-like V-type.	1	GGGTACGAGGA	0.597	
+	7	1195	pzi.2_Missense_M	NM_032423	NP_115799	Q3MIS6	ZN528_HUMAN	2H2-type 2.	2	ACCTTTCACAA	0.388	
-	5	1746	k.1_Intron|ZNF81	NM_001031665	NP_001026835	Q0VGE8	ZN816_HUMAN	2H2-type 10.	0	TTACATGTGTAA	0.408	
-	5	934	_p.L275F|LILRB5_	NM_006840	NP_006831	O75023	LIRB5_HUMAN	3.|Extracellular (Potential).	2	GGAGAGCCCAG	0.637	
+	6	1417	.E228K|U2AF2_u	NM_013301	NP_037433	Q9BWC9	CC106_HUMAN		0	CCCCCGAGAAG	0.662	
+	5	377	_uc010eti.2_Splic	NM_033106	NP_149097	Q9UBC7	GALP_HUMAN		0	TGGAGGTAAAG	0.488	
+	5	1260		NM_152677	NP_689890	Q8NAM6	ZSCA4_HUMAN		1	TCACAGGATATG	0.373	
+	7	839	.G183S|COLEC1	NM_024027	NP_076932	Q9BWP8	COL11_HUMAN	-type lectin.	0	GCAGCGGTGAG	0.622	
+	12	1663	se_Mutation_p.G3	NM_198182	NP_937825	Q9NZI5	GRHL1_HUMAN		2	TGGAGGGTGAA	0.224	
-	26	10732		NM_000384	NP_000375	P04114	APOB_HUMAN		27	TGGAAGTGCCC	0.443	
-	2	614	D2B_uc010exx.1_	NM_017552	NP_060022	Q9ULI0	ATD2B_HUMAN		1	GTACTTCGTGAT	0.398	
+	12	2833	_p.A708T|NCOA1_	NM_003743	NP_003734	Q15788	NCOA1_HUMAN	tion with CREBBP.	11	CCACTGCCAGA	0.468	
+	37	5947	v.2_Missense_Mu	NM_004341	NP_004332	P27708	PYR1_HUMAN	artate transcarbamylase).	10	TGTCCGTCCAG	0.592	
-	35	3999		NM_000379	NP_000370	P47989	XDH_HUMAN		8	GCATTGCGGATC	0.582	rs138249576
+	36	7213		NM_016252	NP_057336	Q9NR09	BIRC6_HUMAN		14	TTGCACGCATTG	0.373	
-	16	1998	q.1_RNA|PSME4_	NM_014614	NP_055429	Q14997	PSME4_HUMAN		5	GTGGGGAACAA	0.318	
-	11	1449	4_uc010yoq.1_R	NM_014614	NP_055429	Q14997	PSME4_HUMAN		5	ACTGCGGGCTA	0.428	
+	1	378_379	.2_Intron|SPTBN1	NR_002229					0	TGAGTTTGCCAT	0.48	
-	4	411		NM_002056	NP_002047	Q06210	GFPT1_HUMAN	midotransferase type-2.	1	CCATATCTTGTTG	0.368	
-	8	1630	nc.2_Missense_M	NM_133637	NP_598376	Q8TE96	DQX1_HUMAN		2	CATCTCGTCCA	0.517	
-	3	543	_p.A9V|FAM176A	NM_001135032	NP_001128504	Q9H8M9	F176A_HUMAN	calization and biological ac	0	AGGCCGCTAGG	0.617	
-	7	1122	_p.A198V|IMMT_u	NM_006839	NP_006830	Q16891	IMMT_HUMAN	intermembrane (Potential).	1	GGACCGCAGCA	0.458	
-	5	682	yuv.1_Missense_	NM_030805	NP_110432	Q9H0V9	LMA2L_HUMAN	like.|Lumenal (Potential).	0	GTAGCGAATCA	0.562	
-	14	1950	p.A572T|AFF3_uc	NM_002285	NP_002276	P51826	AFF3_HUMAN		6	CTCCGCGGGCG	0.771	
+	7	707	2_uc002tjv.2_Spli	NM_172003	NP_742000	Q8IUF1	CBWD2_HUMAN		0	GTTTAGCATTTA	0.264	
+	5	674	H2P_uc002tkb.2_	NM_182905	NP_878908				0	GTGGGCACTTG	0.612	
+	1	275	TEE_uc002tsk.2_	NM_001083538	NP_001077007	Q6S8J3	POTEE_HUMAN		0	GGGGGAGTGGC	0.587	
-	12	1941	q.1_Missense_M	NM_000888	NP_000879	P18564	ITB6_HUMAN	ellular (Potential).	3	CTTCTCGGGCT	0.453	
-	2	257	fi.1_Missense_Mutation_p.P11L|TTN_uc010zfj.1_Misse			Q8WZ42	TITIN_HUMAN		153	GTAACGGCTGC	0.448	
-	9	1233		NM_182521	NP_872327	Q8NEG5	ZSWM2_HUMAN		3	CTGCTGAATTT	0.363	
+	28	4811	uzs.3_Splice_Site	NM_001114132	NP_001107604	Q6ZS30	NBEL1_HUMAN		2	CTAACGTAAGC	0.348	
-	3	441		NM_014617	NP_055432	P11844	CRGA_HUMAN	crystallin 'Greek key' 4.	0	CTGCCGCCCCC	0.577	
+	1	220	2R_uc010zjb.1_I	NM_005048	NP_005039	P49190	PTH2R_HUMAN		3	TGGCCGGGCTG	0.637	
+	33	7994		NM_005876	NP_005867	Q15772	SPEG_HUMAN	Ig-like 9.	14	GGGCAGCATCA	0.662	
+	3	597	1486_uc010fxa.1_	NM_020864	NP_065915	Q9P242	K1486_HUMAN		3	ACCACCCAAAC	0.577	
-	1	1929		NM_005544	NP_005535	P35568	IRS1_HUMAN		12	CCTTTCGGCCA	0.642	
+	48	4415	1418_splice|COL	NM_000091	NP_000082	Q01955	CO4A3_HUMAN		3	TTGAAGGACCA	0.378	
+	12	1178	se_Mutation_p.V3	NM_025139	NP_079415	Q7Z3E5	ARMC9_HUMAN		1	AGACCGTTCTG	0.493	
-	2	424		NM_006056	NP_006047	Q9HB89	NMUR1_HUMAN	Name=2; (Potential).	5	GGTCCGACACG	0.632	
+	1	46		NM_005383	NP_005374	Q9Y3R4	NEUR2_HUMAN		0	AGTCGGGAGCC	0.627	
+	2	815	_p.R151H|PRNP_	NM_001080122	NP_001073591	P04156	PRIO_HUMAN	2, ERI3 and SYN1 (By simi	1	CTATCGTGAAA	0.532	
-	17	2484	L1_uc002xgj.1_M	NM_002895	NP_002886	P28749	RBL1_HUMAN	ocket; binds T and E1A.	10	GTAAGCGTACA	0.348	
+	2	260	se_Mutation_p.V5	NM_022896	NP_075047	Q9BQK8	LPIN3_HUMAN	N-LIP.	4	TGGGCGTCCTG	0.637	

-	6	683	ox.2_Missense_M	NM_181510	NP_852611	Q8IUA0	WFDC8_HUMAN	WAP 3.	0	GCGTGGGCAGA	0.423	
+	9	1374		NM_004994	NP_004985	P14780	MMP9_HUMAN		2	GCCACGGCCTC	0.577	
-	18	1901	_Mutation_p.T49	NM_006045	NP_006036	O75110	ATP9A_HUMAN	lasmic (Potential).	4	TCACCGTGGCC	0.637	
+	2	2781		NM_173485	NP_775756	Q9NRE2	TSH2_HUMAN		6	AAGATGAAGCG	0.507	
+	5	1072	_p.E235K|EDN3_u	NM_000114	NP_000105	P14138	EDN3_HUMAN		1	TTCAGGAAGGA	0.562	
-	5	592		NM_020713	NP_065764	Q96KM6	Z512B_HUMAN		0	GGTGACCGGCC	0.602	
+	20	3541	DL1_uc002zag.1	NM_001004416	NP_001004416	Q5DID0	UROL1_HUMAN	llular (Potential).|ZP.	3	CTGTGCCCAAC	0.502	
+	28	5685	.2_Missense_Mut	NM_006031	NP_006022	O95613	PCNT_HUMAN	Potential.	8	AGTTCGAAGCG	0.612	
-	26	5112	_Mutation_p.A150	NM_015241	NP_056056	Q7RTP6	MICA3_HUMAN		0	TTCCGCGGACA	0.687	
-	2	984	NF6_uc003aqy.1_	NM_182486	NP_872292	Q9BXI9	C1QT6_HUMAN	C1q.	0	CGGTCGCCATG	0.552	
+	7	2145	tq.1_Missense_M	NM_001039141	NP_001034230	Q9H2D6	TARA_HUMAN		1	CCCCAGAACAT	0.592	
+	7	2376	tq.1_Missense_M	NM_001039141	NP_001034230	Q9H2D6	TARA_HUMAN		1	TGCCCAACGGG	0.582	
-	7	1038	e.1_Missense_M	NM_020831	NP_065882	Q969V6	MKL1_HUMAN	Gln-rich.	5	TGCTGCTGGTT	0.657	
-	9	1553	_p.A501T|SMC1B_	NM_148674	NP_683515	Q8NDV3	SMC1B_HUMAN	exible hinge.	2	CTCTGCTCTCT	0.348	
-	4	893	A_uc003bnd.3_M	NM_001085426	NP_001078895	P15289	ARSA_HUMAN		2	CTGGCGCTGGG	0.642	
+	2	819	c.1_RNA|GRM7_	NM_000844	NP_000835	Q14831	GRM7_HUMAN	ellular (Potential).	7	ATCAACGGCAC	0.502	
+	5	1326	0hcg.2_Missense	NM_000844	NP_000835	Q14831	GRM7_HUMAN	ellular (Potential).	7	CTTTACGTCCC	0.383	
-	5	1151	_Mutation_p.E23	NM_001001331	NP_001001331	Q01814	AT2B2_HUMAN	lasmic (Potential).	6	AGCTTTCATCAA	0.592	
+	2	1818		NM_001137674	NP_001131146	A6NHJ4	ZN860_HUMAN		1	GAAGAGAGATC	0.348	
+	14	1268	_Mutation_p.R30	NM_016300	NP_057384	Q9UBL0	ARP21_HUMAN		3	CAACAGAGATG	0.532	
-	3	1707		NM_014831	NP_055646	O15050	TRNK1_HUMAN		2	GAGGTCGATCA	0.542	
+	4	431	ko.2_Missense_	NM_001098414	NP_001091884	Q6ZSS3	ZN621_HUMAN	KRAB.	1	ATGGGGCCCAG	0.498	
+	3	1496		NM_152393	NP_689606	Q2TBA0	KBTB5_HUMAN	Kelch 3.	1	TCTACGTAATTG	0.577	
-	6	700	.2_Missense_Mut	NM_002343	NP_002334	P02788	TRFL_HUMAN	nsferrin-like 1.	4	CAGCCCCGTCT	0.537	
-	21	2535	pz.1_Missense_M	NM_147129	NP_667340	Q60I27	AL2CL_HUMAN		5	CCTCCCGCTCA	0.567	
-	1	987	uf.1_Missense_M	NM_001407	NP_001398	Q9NYQ7	CELR3_HUMAN	ellular (Potential).	11	CCCCTGGAAGAC	0.657	
-	5	697	MPPB_uc003cxl.1	NM_021971	NP_068806	Q9Y5P6	GMPPB_HUMAN		0	GAACCGGTGAA	0.572	
+	22	4422	bdu.1_Missense_	NM_015106	NP_055921	Q9Y4B4	ARIP4_HUMAN		3	TCCTACGGTCC	0.542	rs148251727
+	53	5710	1_5'UTR|STAB1_	NM_015136	NP_055951	Q9NY15	STAB1_HUMAN	ellular (Potential).	9	GACCCGGCCCC	0.652	
-	7	788	_p.S28L|TMEM11	NM_198563	NP_940965	Q86TL2	TM110_HUMAN		1	TCCTCGAGTCC	0.567	
+	1	646	E3_uc011bgd.1_5	NM_018971	NP_061844	Q9NS67	GPR27_HUMAN	lasmic (Potential).	1	TGCGGCCCGCG	0.751	
+	1	1055	.1_Intron|PPP4R2	NM_018029	NP_060499	Q6P2I7	EBLN2_HUMAN		0	GAGACGATTCA	0.473	
-	10	1846	_p.S282P|PDZRN	NM_015009	NP_055824	Q9UPQ7	PZRN3_HUMAN		7	CTCCGAGCTCT	0.637	
+	1	389		NM_001005515	NP_001005515	A6NDH6	O5H15_HUMAN	lasmic (Potential).	2	AACCTTTACTTT	0.368	
+	4	662	hpn.2_Missense_	NM_145037	NP_659474	Q969Y0	FA55C_HUMAN		3	AACTACGGCTT	0.448	
+	7	1630	pn.2_Nonsense_	NM_145037	NP_659474	Q969Y0	FA55C_HUMAN		3	CAGTGGAGGCC	0.358	
-	2	183	_p.E25K|ATG3_u	NM_022488	NP_071933	Q9NT62	ATG3_HUMAN		3	TTGATTCCTAAA	0.328	
+	10	2052		NM_020754	NP_065805	Q2M1Z3	RHG31_HUMAN		2	CAGCACGCCGT	0.592	
+	6	886	o.2_RNA|C3orf1_	NM_016589	NP_057673	Q9NPL8	TIDC1_HUMAN		0	AGGATCGAAAG	0.493	rs149481081
+	4	2224	rj.2_Missense_Mu	NM_138287	NP_612144	Q8TDB6	DTX3L_HUMAN		4	ATCCCGGTTTG	0.428	
-	8	1123	3eft.1_Missense_	NM_024610	NP_078886	Q96EW2	HBAP1_HUMAN		2	AGCGATCAAAAA	0.403	
+	2	1216	B3GNT5_uc003fll.	NM_032047	NP_114436	Q9BYG0	B3GN5_HUMAN	enal (Potential).	1	CCCCTCCCATTA	0.433	
-	15	1754	_p.V423I|IGF2BP	NM_006548	NP_006539	Q9Y6M1	IF2B2_HUMAN	KH 4.	0	TCTGACGATCA	0.507	
-	3	339	GF2BP2_uc010hyl	NM_006548	NP_006539	Q9Y6M1	IF2B2_HUMAN	RRM 2.	0	ATGTTTCGAATC	0.398	
-	3	12755	1bth.1_Intron|MU	NM_018406	NP_060876	Q99102	MUC4_HUMAN	Ser-rich.	0	GGTGACAGGAA	0.582	
-	3	12698	1bth.1_Intron|MU	NM_018406	NP_060876	Q99102	MUC4_HUMAN		0	AAGAGGGGTGG	0.597	
-	4	509	_5'Flank|KIAA022	NM_014687	NP_055502	Q92622	RUBIC_HUMAN	RUN.	0	TCTGGTCGTTC	0.572	

+	5	1113	141_uc003gab.2_I	NM_003441	NP_003432	Q15928	ZN141_HUMAN	C2H2-type 6.	0	CCTACAAATGTGA	0.398	
+	59	8084		NM_002111	NP_002102	P42858	HD_HUMAN		4	aggCCGACGCCC	0.423	
-	18	2245	gyk.2_Splice_Site_	NM_015030	NP_055845	O94915	FRYL_HUMAN		1	TACATACGTAATC	0.403	
+	3	791	e_Mutation_p.T79M	NM_001136258	NP_001129730	Q8NHU3	SMS2_HUMAN		1	GGAAAACGGGCA	0.478	
-	2	441	PC3_uc003ief.2_Mi	NM_001130698	NP_001124170	Q13507	TRPC3_HUMAN	nic (Potential).|ANK 1.	2	TGTTGCCGTACTC	0.667	
-	15	1457	jz.3_Missense_Mu	NM_001102653	NP_001096123	Q01804	OTUD4_HUMAN		3	ATTCTCCGCCTGC	0.383	
-	2	379	e_Mutation_p.D11	NM_178835	NP_849157	Q17R98	ZN827_HUMAN		0	GGTCATCGTCACA	0.582	
-	4	624_625	AP9_uc003iot.1_M	NM_001039580	NP_001034669	Q49MG5	MAP9_HUMAN		2	TTCACACCCATCA	0.332	
+	5	381		NM_005651	NP_005642	P48775	T23O_HUMAN		0	ATGAAAGGAACAT	0.423	
-	4	650		NM_001100389	NP_001093859	Q8IY95	TM192_HUMAN	ical; (Potential).	1	CATATCAGGGAAC	0.463	
+	5	1209		NM_001034845	NP_001030017	Q49A17	GLTL6_HUMAN	main A.|Lumenal (Potential	4	TCCTGCGGACCAT	0.428	rs149727048
+	4	391		NM_020227	NP_064612	Q9NQV7	PRDM9_HUMAN	KRAB-related.	6	CCACTCGACCAG	0.483	
-	5	1168	_p.A325T|UGT3A2	NM_174914	NP_777574	Q3SY77	UD3A2_HUMAN	cellular (Potential).	6	CCTTACCCAGGAC	0.527	
-	21	3512	o.2_RNA|ADAMTS	NM_197941	NP_922932	Q9UKP5	ATS6_HUMAN	TSP type-1 2.	0	AGGTGGGCAGG	0.378	
-	2	808	on_p.T159I|TAF9_u	NM_003187	NP_003178	Q16594	TAF9_HUMAN		0	GTGGGAGTACTTC	0.463	
-	11	1962	_p.S430L|MEF2C_	NM_002397	NP_002388	Q06413	MEF2C_HUMAN		7	TCGTACGAACTG	0.592	
-	40	4505		NM_014639	NP_055454	Q6PGP7	TTC37_HUMAN	TPR 20.	4	CCTTGGGATTGAT	0.438	
+	14	2119	_p.D646N|YTHDC2	NM_022828	NP_073739	Q9H6S0	YTDC2_HUMAN	case C-terminal.	3	TTTGATGACAAGC	0.368	
-	10	954	2_Intron|BRD8_uc0	NM_139199	NP_631938	Q9H0E9	BRD8_HUMAN		1	TCTACAGGGGGTC	0.537	
+	1	2177	lhd.2_Intron|PCDH	NM_018906	NP_061729	Q9Y5H8	PCDA3_HUMAN	lasmic (Potential).	8	CGCGCCGCCAA	0.637	
+	1	2359	CDHA5_uc003lhk.1	NM_018911	NP_061734	Q9Y5H6	PCDA8_HUMAN	ial).|5 X 4 AA repeats of P-X	2	GTAGGCGAAGAGC	0.453	
+	1	2364	2_Intron|PCDHA6_	NM_018903	NP_061726	Q9UN75	PCDAC_HUMAN	P-X-X-P.|Cytoplasmic (Pote	0	CCGTGGGGAGTT	0.672	
-	6	1145	se_Mutation_p.R13	NM_006058	NP_006049	Q15025	TNIP1_HUMAN	eracts with Nef.	2	CCATGCGGCCCAC	0.652	
-	9	969	35_splice|ADAM19	NM_033274	NP_150377	Q9H013	ADA19_HUMAN		8	CTATTTACGTGATT	0.493	
+	29	7960	.3_Nonsense_Mut	NM_001122679	NP_001116151				10	AGGACTCGAAGG	0.627	
-	11	1407	3_uc003mez.2_5'U	NM_002115	NP_002106	P52790	HXK3_HUMAN	Regulatory.	7	GCAGGACGCTGC	0.622	
+	18	2548	dfu.1_Missense_M	NM_002011	NP_002002	P22455	FGFR4_HUMAN	lasmic (Potential).	16	GCTCCTTCCCCTT	0.632	
-	3	939	_5'Flank|GRM6_u	NM_000843	NP_000834	O15303	GRM6_HUMAN	cellular (Potential).	8	TTGGTTCCCTGG	0.592	
-	23	3257	.3_Missense_Muta	NM_002020	NP_002011	P35916	VGFR3_HUMAN	Potential).|Protein kinase.	15	GTCCCGGGCAAC	0.617	rs68096331
+	1	646		NM_206880	NP_996763	Q96R30	OR2V2_HUMAN	Name=5; (Potential).	2	ATCATCGTGGCCT	0.522	
-	1	543	DC2_uc003mte.2_I	NM_148959	NP_683762	Q8NHY5	HUS1B_HUMAN		0	TGCCCACGTTCG	0.607	
-	4	1485	sense_Mutation_p.	NM_178012	NP_821080	Q9BVA1	TBB2B_HUMAN		1	CTTGTTCGTCGGC	0.657	
+	3	536	o.1_Intron|HLA-H_uc003nod.2_RNA						0	ACCTGGAGAACC	0.677	
-	7	986	R10_uc010jsc.1_5	NM_002714	NP_002705	Q96QC0	PP1RA_HUMAN	4 (By similarity).|TFIIS N-ter	4	GAGAGCGGATGA	0.478	
-	8	1573	HX16_uc011dmo.1	NM_003587	NP_003578	O60231	DHX16_HUMAN	ase ATP-binding.	4	CTCTCCGGGGT	0.522	
-	4	553	Flank|NRM_uc003	NM_007243	NP_009174	Q8IXM6	NRM_HUMAN	.|Nuclear (Potential).	0	GAGGCTCGCCCA	0.572	rs11539189
-	2	447	2_uc011doo.1_Intr	NM_181842	NP_862825	Q9Y330	ZBT12_HUMAN	BTB.	0	GGCGCCCGTGTA	0.607	
-	1	807		NR_001444					0	GACAGGAGGCAC	0.577	
+	38	5491		NM_001371	NP_001362				21	ATGGCCGTCATAT	0.358	rs149016705
+	11	1345		NM_032538	NP_115927	Q5TCY1	TTBK1_HUMAN		9	AACACCGAGGAT	0.662	
-	19	2581	2_Intron|TMEM151	NM_020745	NP_065796	Q5JTZ9	SYAM_HUMAN		1	GCTTACGGATGG	0.602	rs150351026
+	15	4463	o.Q1391H|PHF3_u	NM_015153	NP_055968	Q92576	PHF3_HUMAN		5	TGGTCAAGTATAT	0.388	
+	3	1151	_p.A72V|TPBG_u	NM_006670	NP_006661	Q13641	TPBG_HUMAN	lar (Potential).|LRRNT.	1	GGCAGCGCGCA	0.642	
+	4	515	1dzi.1_Missense_	NM_006416	NP_006407	P78382	S35A1_HUMAN	ical; (Potential).	0	CAGTGGGTTTCAC	0.403	
+	2	118	L_uc003pmg.2_M	NM_012381	NP_036513	Q9UBD5	ORC3_HUMAN		0	CTCTGCCAATAGC	0.333	
+	4	842	qo.3_Missense_Mu	NM_021956	NP_068775	Q13002	GRIK2_HUMAN	cellular (Potential).	5	ATCTTCGACTCAA	0.323	
-	4	1182	e_Mutation_p.W20	NM_031922	NP_114128	Q96D71	REPS1_HUMAN		2	GGAGACCAAAAT	0.383	

-	10	1323		NM_015718	NP_056533	Q9HBY0	NOX3_HUMAN	ical; (Potential).	1	TCCCCGCGGCA	0.527	
+	6	2346	p.R330H|TULP4_	NM_020245	NP_064630	Q9NRJ4	TULP4_HUMAN		1	TGTTCGTGGGG	0.483	
+	30	4701	_p.R797Q|SDK1_	NM_152744	NP_689957	Q7Z5N4	SDK1_HUMAN	nectin type-III 9.	6	GCCTCGGGGTG	0.667	
-	15	1967	on_p.P490L|OSBP	NM_015550	NP_056365	Q9H4L5	OSBL3_HUMAN		1	TGCTCGGGCAG	0.587	
-	3	346	_p.G76D|CPVL_u	NM_031311	NP_112601	Q9H3G5	CPVL_HUMAN		2	GGAAGCCGGC	0.458	
-	2	1078		NM_022728	NP_073565	Q96NK8	NDF6_HUMAN		2	AGAAGGATTCAT	0.483	
-	4	908	se_Mutation_p.R2	NM_000598	NP_000589	P17936	IBP3_HUMAN	oglobulin type-1.	3	AGCCCCGCTTC	0.582	
+	4	1013		NM_001159279	NP_001152751				2	AAGAATGTGGC	0.423	
+	4	968		NM_001159524	NP_001152996	P0CB33	ZN735_HUMAN		0	AGAGAAACCCT	0.418	
+	4	977		NM_001159524	NP_001152996	P0CB33	ZN735_HUMAN	2H2-type 7.	0	CTACACATGTG	0.433	
+	4	955_956	zu.2_Missense_Mu	NM_152626	NP_689839	Q03936	ZNF92_HUMAN	2H2-type 5.	0	CTCAACCCTTAC	0.351	
+	2	229	_uc003ukk.1_RN	NM_033107	NP_149098	A4D1E9	GTPBA_HUMAN		0	ATGACTTTAAAA	0.433	
+	48	7207	.T2315M|TRRAP_	NM_003496	NP_003487	Q9Y4A5	TRRAP_HUMAN	action with TP53.	37	GAAGACGCGCC	0.522	
-	2	1672	CHE_uc003uxg.2	NM_000665	NP_000656	P22303	ACES_HUMAN		2	CAGTCGCTGGG	0.612	
+	3	9609	C17_uc010lho.1_	NM_001040105	NP_001035194	Q685J3	MUC17_HUMAN	ich.|59 X approximate tand	27	TTTCAGCAACT	0.483	
+	6	836	R_uc011knq.1_5'	NM_000492	NP_000483	P13569	CFTR_HUMAN	tial).|ABC transmembrane	5	TGCCCTTTTTC	0.438	
-	4	1962		NM_033427	NP_219499	Q8WZ74	CTTB2_HUMAN		5	GCCTGCAGGTG	0.557	
-	15	1860		NM_004333	NP_004324	P15056	BRAF_HUMAN	rotein kinas_R603>I(2)|p.T	18290	GATTTCACTGTA	0.368	
+	6	1044	r.2_RNA|GALNTL	NM_145292	NP_660335	Q7Z4T8	GLTL5_HUMAN	enal (Potential).	2	TAAGGGGAACTT	0.433	
+	1	475		NM_001427	NP_001418	P19622	HME2_HUMAN		1	TCCTGCGGCCC	0.498	
+	19	2947	ni.3_Missense_Mu	NM_014671	NP_055486	Q15386	UBE3C_HUMAN	HECT.	5	AAGACGATGTG	0.527	rs141183982
+	2	839	pm.2_Missense_	NM_004745	NP_004736	Q9P1A6	DLGP2_HUMAN		0	GCTACCCCGAC	0.672	
-	4	289	Ilck.1_Missense_	NM_001464	NP_001455	Q99965	ADAM2_HUMAN		2	TGTAAACTCTAA	0.264	
-	4	351	ns.2_Missense_M	NM_024645	NP_078921	Q9H898	ZMAT4_HUMAN		3	CATGTCGGCAT	0.483	
-	14	1878	t.2_Missense_Mut	NM_000930	NP_000921	P00750	TPA_HUMAN	eptidase S1.	2	GTCACGAATCC	0.547	
+	4	541		NM_152419	NP_689632	Q68CP4	HGNAT_HUMAN		0	ACCTTCGTACGT	0.393	
+	2	472		NM_020697	NP_065748	Q9ULS6	KCNS2_HUMAN	lasmic (Potential).	1	CGAGACGCGCC	0.652	
+	38	5293		NM_177531	NP_803875	Q86WI1	PKHL1_HUMAN	xtracellular (Potential).	14	ACATGGAGTGC	0.438	
+	6	1019	p.V285M|GRINA_	NM_001009184	NP_001009184	Q7Z429	GRINA_HUMAN	ical; (Potential).	1	TGGGCGTGCTC	0.627	
+	2	1592		NM_022160	NP_071443	Q5VZB9	DMRTA_HUMAN		2	CTACCTAACAC	0.438	
+	18	2337	qx.3_Missense_M	NM_002197	NP_002188	P21399	ACOC_HUMAN		0	AACATTCGCTTG	0.493	
+	1	490	42421_uc004aed.1_RNA						0	TTAACCCCTTCC	0.582	
-	13	1979_1980	p.P547L|AGTPBP	NM_015239	NP_056054	Q9UPW5	CBPC1_HUMAN		7	TAATCGGGATAA	0.411	
+	11	976	_Mutation_p.R68	NM_020893	NP_065944				7	TGCCCGCATCG	0.572	
-	2	637	S6_uc004ayy.1_	NM_173551	NP_775822	Q68DC2	ANKS6_HUMAN	ANK 5.	2	CACCACGGCCT	0.687	
-	4	310	f80_uc010muk.2_	NM_021218	NP_067041	Q9NRY2	SOSSC_HUMAN		0	GAGTGCAATGC	0.413	
+	1	545		NM_001004457	NP_001004457	Q8NGR9	OR1N2_HUMAN	ellular (Potential).	4	GACCCGCGTGG	0.527	
+	10	1430	fc.1_Missense_Mu	NM_002957	NP_002948	P19793	RXRA_HUMAN	gand-binding.	2	CCTGCCGGCTC	0.607	
-	5	1336_1337	bh.2_Missense_	NM_144653	NP_653254	Q96BF6	NACC2_HUMAN	BEN.	0	CAGTCCCGCAG	0.668	
-	31	5780		NM_017617	NP_060087	P46531	NOTC1_HUMAN	nic (Potential).|ANK 1.	856	CGCCCGTGCGG	0.667	
-	4	1021	ense_Mutation_p.	NM_033290	NP_150632	O15344	TRI18_HUMAN		3	TCTGTCGTCTTT	0.388	
+	2	1423	d.2_Missense_Mu	NM_138636	NP_619542	Q9NR97	TLR8_HUMAN	ellular (Potential).	7	TATCCGGAAAC	0.388	
-	1	271		NM_001163264	NP_001156736	Q9Y5K3	PCY1B_HUMAN		0	GAGCGCGATTG	0.413	
+	3	270	ite_p.D89_splice|P	NM_016937	NP_058633	P09884	DPOLA_HUMAN		3	TGATGGTAGGT	0.507	
-	1	391		NM_001013742	NP_001013764	Q5KSL6	DGKK_HUMAN	imate tandem repeats of E-	2	cggttctggggccggc	0.02	
-	8	1634	nse_Mutation_p.R	NM_201599	NP_963893	Q14202	ZMYM3_HUMAN		1	CATTACGATCC	0.502	
+	26	4049	on_p.A507V|TAF1_	NM_138923	NP_620278	P21675	TAF1_HUMAN		17	TAGTGCGGATG	0.408	

-	1	981	nqj.1_Missense_M	NM_021963	NP_068798	Q9ULW6	NP1L2_HUMAN	u-rich (acidic).		1	CATAATCATAATA	0.343	
+	38	4097	qq.2_Missense_M	NM_144658	NP_653259	Q5JSL3	DOC11_HUMAN			3	CTTCGGAATAG	0.403	
-	1	1268		NM_138289	NP_612146	Q8TDG2	ACTT1_HUMAN			5	GTGACCCACAT	0.458	
+	3	925		NM_005364	NP_005355	P43361	MAGA8_HUMAN	MAGE.		0	TGGGAGGGAGC	0.587	
-	3	1639	se_Mutation_p.E4	NM_001142392	NP_001135864	P09131	P3_HUMAN	ical; (Potential).		2	CATCTCGGAGG	0.622	
-	2	405	nh.1_Nonsense_M	NM_020994	NP_066274	O75638	CTAG2_HUMAN			1	TGGTCGGGGGA	0.632	
+	2	238	9R_uc004fnu.1_M	NM_002186	NP_002177	Q01113	IL9R_HUMAN			0	GAGGCGAGACA	0.612	
-	20	2207	EL1_uc009vlg.1_F	NM_033467	NP_258428	Q495T6	MMEL1_HUMAN	enal (Potential).		0	CTGTTCGTCTG	0.637	
-	3	267_268	me.2_Missense_M	NM_000983	NP_000974	P35268	RL22_HUMAN			0	ACCTCGGATGTC	0.564	rs148093039
+	8	1153	obc.1_Missense_	NM_001243	NP_001234	P28908	TNR8_HUMAN	(Potential).|TNFR-Cys 6.		5	AGACGGTCACC	0.637	
+	6	808	se_Mutation_p.S4	NM_001066	NP_001057	P20333	TNR1B_HUMAN	ellular (Potential).		3	CACCTCCTTCC	0.562	
-	5	1213	ub.2_Missense_M	NM_004753	NP_004744	O75911	DHRS3_HUMAN			1	CTGTCCTCCGG	0.478	
+	4	1331		NM_023013	NP_075389	O95521	PRAM1_HUMAN			0	GCCTGGAGACG	0.537	
+	11	2227	p.1_Missense_Mu	NM_015001	NP_055816	Q96T58	MINT_HUMAN	g-rich.|Tyr-rich.		15	TACTACGATGAT	0.428	
+	10	991	ense_Mutation_p.R	NM_000085	NP_000076	P51801	CLCKB_HUMAN			1	TCAGCGAATCT	0.612	
+	14	1646		NM_016233	NP_057317	Q9ULW8	PADI3_HUMAN			2	ATAAAGACCTC	0.512	
-	7	752_753	cy.1_Missense_Mu	NM_201252	NP_957704					0	TGCAGGGCCTT	0.639	
-	3	326		NM_014589	NP_055404	Q9NZK7	PA2GE_HUMAN			0	ACGTTCGCTGA	0.577	
+	11	2126	gf.2_Missense_Mu	NM_017449	NP_059145	P29323	EPHB2_HUMAN	Potential).|Protein kinase.		5	ACACGGAGAAG	0.597	
-	15	1833	bio.2_Missense_M	NM_152372	NP_689585	Q5VTT5	MYOM3_HUMAN	nectin type-III 2.		3	TCGGGGATCTC	0.557	
+	13	1236	.R342H|RPS6KA	NM_002953	NP_002944	Q15418	KS6A1_HUMAN	kinase C-terminal.		1	GTCCCGCACAC	0.572	
+	12	1265	_p.R390C|KPNA6_	NM_012316	NP_036448	O60684	IMA7_HUMAN	(minor) (By similarity).|ARM		0	AGTTTCGTACA	0.463	
-	11	2039	_p.S663F|PHC2_	NM_198040	NP_932157	Q8IXK0	PHC2_HUMAN	FCS-type.		1	CCATGGAACAG	0.547	
-	51	7647	m.1_Missense_Mu	NM_052896	NP_443128	Q7Z408	CSMD2_HUMAN	r (Potential).|Sushi 15.		12	CATTCCATTCTT	0.488	
+	6	1429	xt.2_Missense_M	NM_032884	NP_116273	Q6P1W5	CA094_HUMAN			0	TACATCCCTTTT	0.557	
+	10	1119	YC_uc001cfy.3_In	NM_001142588	NP_001136060	Q13952	NFYC_HUMAN			3	CCCAGCAGAGC	0.627	
+	13	1966	p.R317Q|CCDC3	NM_001080850	NP_001074319	Q5VVM6	CCD30_HUMAN	Potential.		0	AGAGCGAATTAT	0.428	
+	4	465		NM_024097	NP_077002	Q9BV19	CA050_HUMAN			1	ATTTTTCCATCAT	0.388	
+	7	1278	ense_Mutation_p.	NM_152498	NP_689711	Q96MR6	WDR65_HUMAN			1	GTATCCATTGC	0.493	
-	1	177		NM_005764	NP_005755	Q13113	PDZ1I_HUMAN			0	GCTGAGGGCCG	0.642	
+	5	927	.A237V|ELAVL4_	NM_021952	NP_068771	P26378	ELAV4_HUMAN		p.A220A(1)	2	CCAGGCCCTGC	0.587	
+	19	3607	of.1_RNA|C1orf17	NM_001039464	NP_001034553	Q68CQ1	HEAT8_HUMAN	HEAT 3.		0	TCAGCGACGTG	0.592	
+	3	799	.1_RNA|PCSK9_u	NM_174936	NP_777596	Q8NBP7	PCSK9_HUMAN	eptidase S8.		4	CGGATGAATAC	0.622	
-	5	1109		NM_177414	NP_803133	O14495	LPP3_HUMAN	ical; (Potential).		0	ACATGGAGAAG	0.463	
-	18	2519	rf168_uc001cyl.2_	NM_001004303	NP_001004303	Q5VWT5	CA168_HUMAN			5	AATTACGACATAT	0.269	
+	7	1096		NM_000562	NP_000553	P07357	CO8A_HUMAN	MACPF.		3	AGCTTCCAGAT	0.403	
-	5	667		NM_152377	NP_689590	Q8N0U7	CA087_HUMAN			2	AGTTGGAACTC	0.448	
+	10	1288	au.2_Nonsense_M	NM_178221	NP_835739	Q96DT6	ATG4C_HUMAN			1	TCTTTTCGAAAA	0.308	rs41305874
-	8	1166		NM_022159	NP_071442	Q9HBW9	ELTD1_HUMAN	ellular (Potential).		2	AGACTGAAATT	0.333	
-	7	1000		NM_022159	NP_071442	Q9HBW9	ELTD1_HUMAN	ellular (Potential).		2	TTGGAAATATATT	0.279	
+	14	2778	R866Q|LPHN2_uc	NM_012302	NP_036434	O95490	LPHN2_HUMAN	lasmic (Potential).		9	GTGACCGAAATA	0.408	
+	3	763	D8_uc010otc.1_F	NM_183242	NP_899065	Q5XKL5	BTBD8_HUMAN			1	AGCATGAAATT	0.328	
-	10	1398	tn.1_Missense_Mu	NM_000350	NP_000341	P78363	ABCA4_HUMAN	Extracellular.		12	TTCTTCCCAGG	0.493	
+	7	1282	sf.2_Missense_Mu	NM_017734	NP_060204	Q9NP74	PALMD_HUMAN			3	CCCTGGACCAA	0.423	
+	11	1521	C14A_uc001dtf.2	NM_003672	NP_003663	Q9UNH5	CC14A_HUMAN			1	AAAATCGACCAT	0.323	
-	62	4873	1_splice|COL11A1	NM_001854	NP_001845	P12107	COBA1_HUMAN			12	GGTCCCTGTTA	0.423	
-	11	1698	nse_Mutation_p.G	NM_001048210	NP_001041675	Q96S66	CLCC1_HUMAN			1	CACACCTCTTG	0.582	

+	8	1545	r.1_Missense_Mut	NM_004037	NP_004028	Q01433	AMPD2_HUMAN		3	ACACCCGCAGG	0.652	
-	16	2852	ENND2C_uc001ef	NM_198459	NP_940861	Q68D51	DEN2C_HUMAN	DENN.	3	GTGAACGGATAC	0.463	
-	8	1171	eff.1_Missense_Mu	NM_000036	NP_000027	P23109	AMPD1_HUMAN		4	CAGCATGAACAT	0.418	
-	32	4678		NM_206996	NP_996879	Q6Q759	SPG17_HUMAN		6	AAAGAGAGCCT	0.388	
-	27	3842_3843		NM_206996	NP_996879	Q6Q759	SPG17_HUMAN		6	CTGACGGACCAT	0.48	
+	2	159	ehw.2_Missense_	NM_000862	NP_000853	P14060	3BHS1_HUMAN		2	GCTGGAGCTGCC	0.562	
-	1	1427		NM_021794	NP_068566	Q9UKF2	ADA30_HUMAN	Extracellular (Potential).	3	AACACCGATCTT	0.448	
+	19	2193	ation_p.E30G|NBP	NM_001037675	NP_001032764	Q3BBV1	NBPFK_HUMAN	NBPF 5.	0	GAAAGAGCCTG	0.483	
-	31	5299	E4DIP_uc001elm.3	NM_014644	NP_055459	Q5VU43	MYOME_HUMAN		5	GGATTCGGCCT	0.498	rs139225578
-	16	2504	_Missense_Mutatio	NM_014644	NP_055459	Q5VU43	MYOME_HUMAN		5	GATCTGGGTATG	0.368	
-	2	379	R|PDE4DIP_uc001	NM_014644	NP_055459	Q5VU43	MYOME_HUMAN		5	ATCTCCCCATCAT	0.403	
+	11	1314	GA10_uc009wiw.2	NM_003637	NP_003628	O75578	ITA10_HUMAN	cellular (Potential).	8	CCCACGAATGG	0.582	
-	9	1836	.3_Intron|FMO5_u	NM_001461	NP_001452	P49326	FMO5_HUMAN		3	AGCCCCATCCC	0.493	
-	9	1795	.3_Intron|FMO5_u	NM_001461	NP_001452	P49326	FMO5_HUMAN		3	TTGGAGTGCAG	0.532	
-	2	932	ot.1_Missense_Mu	NM_181703	NP_859054	P36382	CXA5_HUMAN	lasmic (Potential).	1	CGGGGGGTGGT	0.527	
-	5	802	lo.1_Missense_Mu	NM_005060	NP_005051	P51449	RORG_HUMAN	nge (Potential).	2	CAAAACGAAGTC	0.612	
-	3	906		NM_001008536	NP_001008536	Q5QJ38	TCHL1_HUMAN		2	CCTTTTCTGTTCT	0.453	
-	2	230	ne.1_Missense_M	NM_007113	NP_009044	Q07283	TRHY_HUMAN	and 2.|S-100-like.	5	AAAATAAATAGGA	0.483	
-	3	8603		NM_002016	NP_002007	P20930	FILA_HUMAN	rich.|Filaggrin 17.	16	GACGCGACCCT	0.577	
-	3	862		NM_016190	NP_057274	Q9UBG3	CRNN_HUMAN	Gln-rich.	3	TCTGGTCATTG	0.602	
+	2	239	faw.2_Missense_	NM_005987	NP_005978	P35321	SPR1A_HUMAN	oximate tandem repeats.|3.	0	AGTGCCTGAGC	0.637	
-	4	366	1fbp.2_Missense_	NM_020393	NP_065126	Q96LB8	PGRP4_HUMAN		4	GCAGTTCCCGCA	0.557	
-	3	992	HE_uc001ffc.2_RN	NM_001010846	NP_001010846	Q5VZ18	SHE_HUMAN		6	CTGCCCTGGGC	0.647	
-	21	2957	N4L_uc001fmb.3_	NM_001037533	NP_001032622	Q3T8J9	GON4L_HUMAN		3	GCTTCGATCTG	0.502	rs143360629
+	3	650	o.2_Missense_Mu	NM_021948	NP_068767	Q96GW7	PGCB_HUMAN	g-like V-type.	2	CCTACCGGTTCC	0.682	
+	6	585	e_Mutation_p.D19	NM_001080471	NP_001073940	Q5VY43	PEAR1_HUMAN		3	CGTGTGATCCC	0.622	
-	27	4037		NM_003126	NP_003117	P02549	SPTA1_HUMAN	Spectrin 12.	8	TACGATCCTTTGT	0.547	
-	22	3308		NM_003126	NP_003117	P02549	SPTA1_HUMAN		8	ACTCATCGTGGG	0.572	
-	6	878		NM_003126	NP_003117	P02549	SPTA1_HUMAN		8	GTTTTCCTGTTG	0.378	
+	3	137	_p.G39E|FCRL6_u	NM_001004310	NP_001004310	Q6DN72	FCRL6_HUMAN	1.|Extracellular (Potential).	3	TGAAGGAGATG	0.507	
-	9	1108	n_p.E279K|CCDC	NM_012337	NP_036469	Q9UL16	CCD19_HUMAN	Potential.	1	CTTTCTCCCTCC	0.547	
-	2	667		NM_002241	NP_002232	P78508	IRK10_HUMAN	smic (By similarity).	1	GCTTCTTGGGCC	0.547	
-	8	1031	e_Mutation_p.P33	NM_003874	NP_003865	Q9UIB8	SLAF5_HUMAN	lasmic (Potential).	4	GTCCCAGGAGGT	0.512	
-	2	525	tp.2_RNA|CD244_	NM_016382	NP_057466	Q9BZW8	CD244_HUMAN	ar (Potential).|Ig-like 1.	1	GTCTGAACTTTT	0.453	
-	3	176	se_Mutation_p.E39	NM_080878	NP_543154	Q8WWU7	ITLN2_HUMAN		1	AGGTTTCGAATT	0.478	
+	14	1579	e_Mutation_p.A41	NM_002697	NP_002688	P14859	PO2F1_HUMAN		5	GTGCAGCAACT	0.488	
-	14	1866	plj.1_Missense_M	NM_018417	NP_060887	Q96PN6	ADCYA_HUMAN		3	ATCTGGCTTTTT	0.358	
+	19	2763	lk.1_Missense_Mu	NM_001017977	NP_001017977	Q58WW2	DCAF6_HUMAN		3	CAGACCGGTTG	0.323	
-	13	3627		NM_000130	NP_000121	P12259	FA5_HUMAN	B.	6	TGACTTCGGTCA	0.488	
-	13	2225		NM_000130	NP_000121	P12259	FA5_HUMAN	B.	6	AAATCTCATATGA	0.388	
+	11	1511	se_Mutation_p.H3	NM_014283	NP_055098	Q9UBS9	OSPT_HUMAN	SUN.	2	ACTTTTCATGGT	0.303	
-	11	2677	u.1_Missense_Mu	NM_003285	NP_003276	Q92752	TENR_HUMAN	onectin type-III 7.	11	TGGGGGATCAA	0.433	
-	2	751	_p.E224K|TNR_uc	NM_003285	NP_003276	Q92752	TENR_HUMAN	-rich.|EGF-like 2.	11	TGTACTCGCTGT	0.627	
+	2	1486	e_Mutation_p.P10	NM_020318	NP_064714	Q9BXP8	PAPP2_HUMAN		16	CTTGTTCCCCCA	0.562	
+	3	3146	e_Mutation_p.S66	NM_020318	NP_064714	Q9BXP8	PAPP2_HUMAN	etalloprotease.	16	CTGACTCACCCA	0.498	
+	8	2146	lg.2_Missense_Mu	NM_021165	NP_066988	Q9C0B6	FAM5B_HUMAN		6	TTCCTGACTGG	0.527	
+	19	2345	orf125_uc001gmp.	NM_144696	NP_653297	Q5T1B0	AXDN1_HUMAN		0	GATATAGGAGTTG	0.428	

+	24	2903	mp.2_Missense_	NM_144696	NP_653297	Q5T1B0	AXDN1_HUMAN	Glu-rich.	0	GTAATTGAACAT	0.393	rs78751980
+	8	1468	e_Mutation_p.W40	NM_173533	NP_775804	Q8NAT2	TDRD5_HUMAN		5	TGTATGGAATTG	0.403	
+	14	2462	p.D792N|TDRD5_	NM_173533	NP_775804	Q8NAT2	TDRD5_HUMAN		5	GTGATGATATTT	0.423	
+	34	8886	p.P970S|CEP350	NM_014810	NP_055625	Q5VT06	CE350_HUMAN		4	TGTGTCCCAGA	0.368	
+	32	4735	1gox.1_Missense_	NM_000721	NP_000712	Q15878	CAC1E_HUMAN	me=S2 of repeat IV.|IV.	6	CCCTGGAATGT	0.478	
+	42	5747	.S1749F|CACNA	NM_000721	NP_000712	Q15878	CAC1E_HUMAN	lasmic (Potential).	6	AGCCTCTGACC	0.478	
+	18	2279	e_Mutation_p.V49	NM_001357	NP_001348	Q08211	DHX9_HUMAN	case C-terminal.	2	TTGGAGTAACC	0.388	
+	25	3216	X9_uc001gpt.2_Mi	NM_001357	NP_001348	Q08211	DHX9_HUMAN		2	AGGGCGTAATG	0.393	
-	14	2445	29A_uc001grb.1_	NM_052966	NP_443198	Q9BZQ8	NIBAN_HUMAN	Glu-rich.	4	TGGGCTCTTTTT	0.562	
+	18	2996	rr.1_Missense_Mu	NM_031935	NP_114141	Q96RW7	HMCN1_HUMAN	like C2-type 6.	23	AACGTCGGTGG	0.343	
-	33	4924		NM_003292	NP_003283	P12270	TPR_HUMAN	Potential.	7	TTGTCGGAGCT	0.408	
-	4	510		NM_001994	NP_001985	P05160	F13B_HUMAN	Sushi 3.	3	TTCAGGAGCCA	0.264	
-	18	5449	.2_Intron|ASPM_u	NM_018136	NP_060606	Q8IZT6	ASPM_HUMAN	IQ 6.	6	ATACAAGATTCC	0.373	
+	2	700	1_uc010ppa.1_R	NM_201253	NP_957705	P82279	CRUM1_HUMAN	GF-like 5; calcium-binding	9	TGGATGAATGT	0.473	
+	6	1343	B1_uc010ppb.1_	NM_201253	NP_957705	P82279	CRUM1_HUMAN	GF-like 10; calcium-binding	9	TTCTTCAAACC	0.353	
+	7	2366	1_uc010ppb.1_In	NM_201253	NP_957705	P82279	CRUM1_HUMAN	otential).|Laminin G-like 2.	9	TGTCCGAACGC	0.478	
-	8	2173	pj.1_Missense_M	NM_014875	NP_055690	Q15058	KIF14_HUMAN	inesin-motor.	7	TGGGTCATCAC	0.388	rs144936292
-	24	3207		NM_000069	NP_000060	Q13698	CAC1S_HUMAN	|Dihydropyridine binding (	5	GAAGTCGCTGT	0.602	
+	6	1674	p.E264K|ATP2B4_	NM_001684	NP_001675	P23634	AT2B4_HUMAN	lasmic (Potential).	3	TCATGGAAGGT	0.458	
+	3	1109	rf.1_Missense_M	NM_014858	NP_055673	O75069	TMCC2_HUMAN		1	TTCCTCCACCA	0.687	
+	16	2251	p.E640K|SRGAP	NM_015326	NP_056141	O75044	FNBP2_HUMAN		0	ATGACGGTACG	0.562	
+	2	305	YRK3_uc001hei.2_	NM_003582	NP_003573	O43781	DYRK3_HUMAN		3	CCCCTGTTCAA	0.398	
-	7	1992	z.2_Missense_Mu	NM_002644	NP_002635	P01833	PIGR_HUMAN	ellular (Potential).	3	AAAGCCTGGGA	0.537	
+	4	758	2_uc009xch.2_Mis	NM_001877	NP_001868	P20023	CR2_HUMAN	xtracellular (Potential).	8	GATTTCCCAAT	0.393	
+	2	330	g.1_Missense_Mu	NM_000573	NP_000564	P17927	CR1_HUMAN	xtracellular (Potential).	3	AGTTTCCCATTG	0.453	
+	2	493		NM_015714	NP_056529	P27469	G0S2_HUMAN		0	GCAAGCCCTGC	0.697	
-	6	756	ic.2_Missense_M	NM_172362	NP_758872	O95259	KCNH1_HUMAN	lasmic (Potential).	5	CTGGGGAAGGA	0.433	
+	14	2193	p.P585S|DTL_uc	NM_016448	NP_057532	Q9NZJ0	DTL_HUMAN		0	ATCAGTCCGTAT	0.463	
+	1	2013	uc010pth.1_RNA	NM_153606	NP_705834	Q8IYT1	FA71A_HUMAN		5	GCCAACCTTACT	0.552	
+	2	553	kg.1_Missense_	NM_002763	NP_002754	Q92786	PROX1_HUMAN		6	TAATTTCCCAGC	0.483	
-	44	9082		NM_206933	NP_996816	O75445	USH2A_HUMAN	ential).|Fibronectin type-III	26	TATATTCATAGGT	0.343	
-	4	1373		NM_024746	NP_079022	Q6UWX4	HIPL2_HUMAN		1	TATCCGGCCTC	0.582	
-	11	1674	BP2_uc010puz.1_	NM_001031685	NP_001026855	Q13625	ASPP2_HUMAN		3	AACGGACGCACT	0.428	
+	5	478	_5'UTR|GUK1_uc	NM_000858	NP_000849	Q16774	KGUA_HUMAN	ylate kinase-like.	0	CCAGGGAGGTG	0.632	
+	63	16470	p.E5476K|OBSCN	NM_001098623	NP_001092093	Q5VST9	OBSCN_HUMAN		28	AGCAGGAGAAA	0.607	
+	1	998		NM_001004342	NP_001004342	Q6ZTA4	TRI67_HUMAN	box-type 2.	4	CTGTCGAACCC	0.672	
-	13	4177	hvf.2_Missense_M	NM_020808	NP_065859	Q9P2F8	SI1L2_HUMAN	Ser-rich.	6	TGAGAGGATATC	0.587	
+	9	2560	hvu.3_Missense_	NM_032435	NP_115811	Q5TCX8	M3KL4_HUMAN		8	AGCGGGCTTCC	0.607	
-	5	1539	s.1_RNA|LYST_u	NM_000081	NP_000072	Q99698	LYST_HUMAN		12	AAACCAGCCAT	0.373	
+	73	10637	z.1_Missense_Mu	NM_001035	NP_001026	Q92736	RYR2_HUMAN		33	AAGTACGAGATA	0.333	
+	5	2523		NM_000740	NP_000731	P20309	ACM3_HUMAN	smic (By similarity).	5	TTTTTCACAAG	0.498	
+	5	2374	e.1_Missense_M	NM_020066	NP_064450	Q9NZ56	FMN2_HUMAN		12	TGACAGCCTCA	0.502	
+	5	3146	e.1_Missense_Mu	NM_020066	NP_064450	Q9NZ56	FMN2_HUMAN	ro-rich.|FH1.	12	GAGCAGGAATAC	0.711	
+	17	5363	N2_uc010pyg.1_	NM_020066	NP_064450	Q9NZ56	FMN2_HUMAN		12	ACTCTGGAATTG	0.279	
+	1	64		NM_001001914	NP_001001914	Q8NGZ4	OR2G3_HUMAN	ellular (Potential).	1	ACCCTCGTCTG	0.493	
+	6	1465	W3_uc001idp.1_I	NM_015431	NP_056246	Q8NG06	TRI58_HUMAN		7	TCCAGGGATCAT	0.463	
+	1	848		NM_017504	NP_059974	Q96R27	OR2M4_HUMAN	Name=7; (Potential).	2	CACCCCTATGCT	0.438	

-	1	425		NM_001004691	NP_001004691	Q8NG81	OR2M7_HUMAN	Name=4; (Potential).	2	ATAAGTCCACAA	0.478
+	1	613		NM_001004696	NP_001004696	Q8NH00	OR2T4_HUMAN	ellular (Potential).	1	TCCCGGGAGATT	0.498
+	1	16		NM_001005495	NP_001005495	Q8NH03	OR2T3_HUMAN	ellular (Potential).	1	GGAATCAGACT	0.458
+	15	2373	ig.2_Missense_M	NM_178150	NP_835363	Q8NFZ0	FBX18_HUMAN		3	CCGTACGGGTG	0.498
-	10	1505	_p.D262N|ITIH5_u	NM_030569	NP_085046	Q86UX2	ITIH5_HUMAN	VWFA.	4	TTTCATCGTAGA	0.522
+	19	4685	|KIAA1217_uc001	NM_019590	NP_062536	Q5T5P2	SKT_HUMAN		7	AAGAAGGGACT	0.478
+	11	2893	sk.2_Missense_M	NM_020752	NP_065803	Q5T848	GP158_HUMAN	lasmic (Potential).	8	AGAAATCACTCA	0.433
+	5	701	O3A_uc009xkq.1_	NM_017433	NP_059129	Q8NEV4	MYO3A_HUMAN	rotein kinase.	18	TGAAAGGATTTC	0.338
+	9	1437	q.2_Missense_Mu	NM_001134366	NP_001127838	Q05329	DCE2_HUMAN		2	ATGATTCCATCT	0.408
-	4	2358		NM_001034842	NP_001030014	Q3KNS1	PTHD3_HUMAN		4	CCCGGGAAGA	0.318
-	1	830		NM_001034842	NP_001030014	Q3KNS1	PTHD3_HUMAN		4	CAGATCCTGCA	0.622
-	3	927	RP1_uc001iwz.2_	NM_003873	NP_003864	O14786	NRP1_HUMAN	xtracellular (Potential).	4	GTATGGAAATC	0.343
+	7	1156		NM_052997	NP_443723	Q9BXX3	AN30A_HUMAN		9	CGTGGGCAGCA	0.408
+	34	3526		NM_052997	NP_443723	Q9BXX3	AN30A_HUMAN		9	TCACACCATCCT	0.398
+	3	708	_Mutation_p.S173	NM_020975	NP_066124	P07949	RET_HUMAN	xtracellular (Potential).	451	GCCCTCCTTCC	0.622
-	1	67		NR_002726					0	GGAGTCGGGCT	0.572
+	3	492	YR1_uc009xna.2	NM_005972	NP_005963	P50391	NPY4R_HUMAN	ellular (Potential).	2	CCCTGGGCACC	0.517
-	1	222	RC18_uc001jhe.1	NM_001006939	NP_001006940	Q8N456	LRC18_HUMAN	LRR 1.	2	AAGGCGCAGAA	0.507
-	4	266		NM_001080520	NP_001073989	A6NNA5	DRGX_HUMAN		0	CCCTTCTGTTC	0.547
-	8	1097	s.2_Missense_M	NM_019893	NP_063946	Q9NR71	ASAH2_HUMAN	enal (Potential).	0	ACTCTCCTGTG	0.433
-	37	5652	DH15_uc010qht.1_	NM_001142769	NP_001136241	Q96QU1	PCD15_HUMAN		13	ACTTTCGCTAC	0.488
-	9	1320	_p.Q309*|PCDH15_	NM_033056	NP_149045	Q96QU1	PCD15_HUMAN	|Extracellular (Potential).	13	GTCCTGATCAA	0.388
-	37	10597	K3_uc010qih.1_In	NM_020987	NP_066267	Q12955	ANK3_HUMAN		19	CTCCTCCTCGA	0.448
-	5	573	p.1_Missense_Mu	NM_032797	NP_116186	Q9BRQ8	AIFM2_HUMAN		1	GGACGGAGGGC	0.632
+	17	3176	_Mutation_p.E900	NM_170744	NP_734465	Q8IZJ1	UNC5B_HUMAN	nic (Potential).|Death.	3	TCTGGGAAGCT	0.607
+	6	801	rv.2_Missense_Mu	NM_022124	NP_071407	Q9H251	CAD23_HUMAN	|Extracellular (Potential).	11	GCATCCCTGAG	0.562
+	4	867	T3_uc009xqs.1_R	NM_152635	NP_689848	Q8WWZ8	OIT3_HUMAN	lcium-binding (Potential).	2	GAAGTGATGGC	0.488
+	4	244	10qkx.1_5'UTR|PL	NM_002658	NP_002649	P00749	UROK_HUMAN	EGF-like.	3	TGACTGTCTAA	0.537
+	2	194	S24_uc001jzp.2_	NM_001026	NP_001017	P62847	RS24_HUMAN		1	GACTACTTCAG	0.363
+	2	398	_p.W57*|OPN4_u	NM_033282	NP_150598	Q9UHM6	OPN4_HUMAN	ellular (Potential).	1	GCCTGGGTCCC	0.478
-	6	895		NM_144590	NP_653191	Q5VYY1	ANR22_HUMAN		0	ATCTCCGTGCA	0.403
-	7	924	utation_p.G225R|	NM_001613	NP_001604	P62736	ACTA_HUMAN		0	CCTACCGATGA	0.527
-	6	803	PA_uc010qnf.1_M	NM_000235	NP_000226	P38571	LICH_HUMAN		0	CCATAGGGCTA	0.478
+	2	777	.3_Intron|LIPA_uc	NM_001010987	NP_001010987	Q5T764	IFT1B_HUMAN		0	GACAGGAAGCT	0.433
+	1	307		NM_006204	NP_006195	P51160	PDE6C_HUMAN		4	AGGTGGAGGAG	0.627
+	2	748		NM_006204	NP_006195	P51160	PDE6C_HUMAN	GAF 1.	4	GCATCTGAATTTT	0.443
+	16	4799	.E1373K|PLCE1_	NM_016341	NP_057425	Q9P212	PLCE1_HUMAN		3	TCACAGGAGAAC	0.403
-	4	1185	_p.L190F|COX15_	NM_078470	NP_510870	Q7KZN9	COX15_HUMAN	ical; (Potential).	1	GACGAGGCCAC	0.458
+	4	765	R|SEMA4G_uc00	NM_017893	NP_060363	Q9NTN9	SEM4G_HUMAN	lar (Potential).|Sema.	1	AAAAAGGGAAA	0.507
+	10	4514	RC1_uc010qqj.1_	NM_015062	NP_055877	Q5VV67	PPRC1_HUMAN	-rich.|Ser-rich.	3	cttcgtcttcctcatcctc	0.443
+	7	1161		NM_001008723	NP_001008723	Q5T655	CC147_HUMAN	Potential.	5	AAGATCAAAAG	0.393
+	5	926	e_Mutation_p.S40	NM_024889	NP_079165	Q5SXH7	CJ081_HUMAN	PH.	1	TGGGTCTCCTTC	0.413
+	11	1616	0orf81_uc001las.	NM_024889	NP_079165	Q5SXH7	CJ081_HUMAN		1	GCCCCCCACGT	0.567
+	9	1163	_Mutation_p.R28	NM_198496	NP_940898	Q5GFL6	VWA2_HUMAN		5	GAAGAGAGTGT	0.498
-	10	1251_1252	n_p.D347N|ABLIM	NM_002313	NP_002304	O14639	ABLM1_HUMAN		1	TAAATCCTTGTA	0.416
+	12	1920	1lcc.2_Missense_	NM_020940	NP_065991	Q5W0V3	F16B1_HUMAN		1	GAAGATCCATTA	0.348
+	20	3607	e_Mutation_p.G2	NM_207303	NP_997186	Q5VV63	ATRN1_HUMAN	e 2.|Extracellular (Potential	7	CACAGGAAAAT	0.348

+	20	3630	se_Mutation_p.G2	NM_207303	NP_997186	Q5VV63	ATRN1_HUMAN	e 2.|Extracellular (Potential		7	ACTAAAGGAATAA	0.323	
+	3	357		NM_198515	NP_940917	P0C7W6	CJ096_HUMAN	Potential.		2	TGTCGTGAAAAA	0.338	
-	4	1442		NM_173791	NP_776152	Q8NEN9	PDZD8_HUMAN	PDZ.		0	TAAGTCGATCTCC	0.428	
-	2	1213	9xyz.1_Missense_	NM_014904	NP_055719	Q7L804	RFIP2_HUMAN			0	CCAAAGGAATCTA	0.388	
+	19	2741	fd.1_Missense_Mu	NM_018117	NP_060587	Q9BZH6	WDR11_HUMAN			0	GATGAACAAGAG	0.458	
+	9	6748	01lfz.2_Missense_	NM_206862	NP_996744	O95359	TACC2_HUMAN			10	AAAAACCGAGG	0.537	
+	52	6845	_p.E2246K|DMBT1	NM_007329	NP_015568	Q9UGM3	DMBT1_HUMAN	ZP.		7	GTCGAGGAAGTC	0.463	
-	3	749	_p.P307S|C10orf9	NM_001004298	NP_001004298	Q96M02	CJ090_HUMAN			2	CCTCGGGAACCT	0.582	
+	4	457		NM_002412	NP_002403	P16455	MGMT_HUMAN			2	TGATTTCTTACCA	0.498	
+	1	845		NM_001127389	NP_001120861	F5GZ66	F5GZ66_HUMAN			0	CACCGGCGCGT	0.786	
+	17	2683		NM_178537	NP_848632	Q76KP1	B4GN4_HUMAN	nenal (Potential).		1	AACTTCGAGCGC	0.692	
-	31	4256		NM_005961	NP_005952	Q6W4X9	MUC6_HUMAN	o-rich.|Thr-rich.		1	GTGGGGTTTGG	0.592	
+	25	3430		NM_002457	NP_002448	Q02817	MUC2_HUMAN			2	CACTATGAGCCA	0.622	
+	1	451		NM_001001480	NP_001001480	Q701N2	KRA55_HUMAN	repeats of C-C-X-P.		1	GGGGGGCTGTG	0.692	
+	1	230		NM_001005172	NP_001005172	Q8NGK3	O52K2_HUMAN	Name=2; (Potential).		2	TTTCCTCCTCAG	0.522	
+	1	319		NM_001005171	NP_001005171	Q8NGK4	O52K1_HUMAN	Name=3; (Potential).		0	TTCCTTCACTCC	0.517	
+	2	206		NM_152430	NP_689643	Q8TCB6	O51E1_HUMAN	cellular (Potential).		4	GCCTCCCTGGTT	0.488	
+	1	902		NM_001001916	NP_001001916	Q8NH60	O52J3_HUMAN	lasmic (Potential).		3	GATTCGAGAAC	0.378	rs146387387
-	1	731		NM_001005164	NP_001005164	Q8NGJ4	O52E2_HUMAN	Name=6; (Potential).		3	ACATGTGAACCA	0.458	
-	1	370		NM_001005160	NP_001005160	Q9H2C5	O52A5_HUMAN	lasmic (Potential).		4	CATAGCGATCCA	0.468	rs143161168
-	2	687	BG2_uc001maj.1_	NM_000559	NP_000550	P69892	HBG2_HUMAN			1	AGGTGCCCTTGA	0.522	
-	3	629	BE1_uc001mam.1_	NM_005330	NP_005321	P02100	HBE_HUMAN			0	GCACTTCAGGGG	0.512	
-	1	583	_uc001mam.1_Int	NM_001005288	NP_001005288	Q9H343	O51I1_HUMAN	cellular (Potential).		1	TAACATGGATGT	0.443	
-	1	343	_uc001mam.1_Int	NM_001005288	NP_001005288	Q9H343	O51I1_HUMAN	Name=3; (Potential).		1	GTATGCCTGACT	0.453	
+	1	886	M5_uc001mbq.1_I	NM_001005174	NP_001005174	Q8NGI0	O52N2_HUMAN	Name=7; (Potential).		2	GTTTATGGAGTCA	0.383	
+	4	1054	10rax.1_Translatio	NM_013250	NP_037382	Q9UL58	ZN215_HUMAN			0	GGCTCACGAACA	0.413	
+	1	239		NM_014469	NP_055284	O75526	HNRGT_HUMAN	RRM.		0	ACCTCGAAACC	0.607	
-	1	122		NM_001003745	NP_001003745	P58181	O10A3_HUMAN	Name=1; (Potential).		1	GCATTTCCCATCA	0.473	
-	12	2288	_p.P457S|STK33_	NM_030906	NP_112168	Q9BYT3	STK33_HUMAN			7	TTGCAGGAAATT	0.378	
-	1	1091	p.E58K|STK33_uc	NM_030906	NP_112168	Q9BYT3	STK33_HUMAN			7	TTCTCTCCAGTGA	0.373	
-	3	408	p.R110C|SCUBE2	NM_020974	NP_066025	Q9NQ36	SCUB2_HUMAN	alcium-binding (Potential).		2	TGCAACGATAATT	0.428	
+	13	2072		NM_006108	NP_006099	Q9HCB6	SPON1_HUMAN	TSP type-1 2.		0	GGTCGCCCTGC	0.652	
-	10	949	p.E312K|PLEKHA	NM_175058	NP_778228	Q6IQ23	PKHA7_HUMAN			3	CACATTCGTGAC	0.522	
-	10	1293	H1_uc009yhe.2_R	NM_004179	NP_004170	P17752	TPH1_HUMAN			0	GCAGCTCATTCA	0.443	
-	17	2814	F22_uc001mpa.2_	NM_173588	NP_775859	Q8N9C0	IGS22_HUMAN	onectin type-III 2.		7	ATAACTCGGAAT	0.552	rs144833584
-	6	879	C1_uc001msu.1_5	NM_181807	NP_861523	P59894	DCDC1_HUMAN	Doublecortin.		1	CTTCAGGTTCGA	0.428	
-	7	1313	se_Mutation_p.G3	NM_024426	NP_077744	P19544	WT1_HUMAN	H373fs*9(1)|p.V306fs*10(1)		687	CTACTCCAGGCA	0.527	
-	13	1026	ntw.1_Missense_	NM_001008391	NP_001008392	Q6ZRK6	CCD73_HUMAN	Potential.		2	CATTTTCTTTTAC	0.264	
-	11	2189	ew.1_Missense_M	NM_001001991	NP_001001991	Q6UXH9	PAMR1_HUMAN	Peptidase S1.		2	TCTTTCAATCCA	0.478	
-	2	415	1_5'Flank|C11orf7	NM_000536	NP_000527	P55895	RAG2_HUMAN			5	AAGTGGCTGGG	0.428	
-	4	1170		NM_003654	NP_003645	O43916	CHST1_HUMAN	nenal (Potential).		5	AGGGTCGCACA	0.706	
+	1	55		NM_001005512	NP_001005512	Q6IF82	O4A47_HUMAN	cellular (Potential).		2	CAGAATCCAAAG	0.418	
+	2	959	9ymb.2_Missense	NR_027044						0	TGAGGGTTGTG	0.463	
-	1	288		NM_001005272	NP_001005272	Q8NH83	OR4A5_HUMAN	cellular (Pote	p.M96I(1)	3	CTGGCCCATGCA	0.448	rs148710182
+	1	4		NM_001004124	NP_001004124	Q8NGL7	OR4P4_HUMAN	cellular (Potential).		1	ACCATGGAAAAA	0.303	
-	1	671		NM_001005491	NP_001005491	Q8NH19	O10AG_HUMAN	lasmic (Potential).		2	GCCTTTCCTCTGG	0.408	
-	1	472		NM_001005491	NP_001005491	Q8NH19	O10AG_HUMAN	cellular (Potential).		2	AAAAGGGCAAAA	0.393	rs77704611

+	1	19		NM_001005201	NP_001005201	Q8N146	OR8H3_HUMAN	cellular (Potential).	2	AGGAATGACACA	0.323	rs148197076
+	1	739		NM_001005210	NP_001005210	Q6ZSA7	LRC55_HUMAN	LRR 4.	0	GTGCATCCCCAG	0.627	
-	6	928		NM_001062	NP_001053	P20061	TCO1_HUMAN		2	CCTTGAGAAATT	0.448	
-	1	41	LC22A25_uc001nv	NM_199352	NP_955384	Q6T423	S22AP_HUMAN	Name=1; (Potential).	4	AATCTCCCCAGG	0.438	
+	3	2352	N3_uc001nxp.2_In	NM_201428	NP_958831	O95197	RTN3_HUMAN		1	GTGAGCCTCTAG	0.398	
+	2	522		NM_138471	NP_612480	Q9BUA3	CK084_HUMAN		0	TGTGGCGCTGAG	0.637	
+	1	693	1oaj.2_Missense_M	NM_018484	NP_060954	Q9NSA0	S22AB_HUMAN	cellular (Potential).	2	TGGAGCGAAGCT	0.682	
-	21	3170		NM_015104	NP_055919	Q2TAZ0	ATG2A_HUMAN		2	GGTTGGGGCCA	0.692	
+	2	425	0rob.1_Missense_N	NM_001004326	NP_001004326	A6NK97	S22AK_HUMAN	ical; (Potential).	1	CGCAGTCCGTCT	0.687	
-	3	436	CORO1B_uc001oll	NM_020441	NP_065174	Q9BR76	COR1B_HUMAN	WD 2.	2	CACTCGCTTGG	0.682	
+	7	856	ng.1_Missense_M	NM_000852	NP_000843	P09211	GSTP1_HUMAN	ST C-terminal.	1	AACCTCCCCATC	0.587	
-	13	1629	_Site_p.Y487_splic	NM_001876	NP_001867	P50416	CPT1A_HUMAN		2	GACGTACTGTCA	0.443	
-	1	901		NM_198923	NP_944605	Q8TDS7	MRGRD_HUMAN	lasmic (Potential).	1	CCTCGCGAAGCG	0.677	
-	17	3352		NM_015531	NP_056346	Q4AC94	C2CD3_HUMAN		7	ACACTGGATTGA	0.388	
-	4	975	oxf.1_Missense_Mu	NM_004626	NP_004617	O96014	WNT11_HUMAN		2	ATTCTTCATGCA	0.587	
+	28	3858_3859	se_Mutation_p.S1	NM_000260	NP_000251	Q13402	MYO7A_HUMAN	MyTH4 1.	4	TCGTGTCTCTCT	0.629	
-	13	1570		NM_182833	NP_878253	Q6W3E5	GDPD4_HUMAN	xtracellular (Potential).	1	TCCTGGAGCAC	0.468	
+	1	77		NM_003251	NP_003242	Q92748	THRSP_HUMAN		1	TGGACCGGTATG	0.622	
+	3	621	.E37K|CCDC83_u	NM_173556	NP_775827	Q8IWF9	CCD83_HUMAN	Potential.	1	ATAAAGGAAGAT	0.264	
+	3	582	pbw.1_Missense_N	NM_001156474	NP_001149946	Q6ZN84	CCD81_HUMAN		1	CAGATTCCAGCA	0.338	
-	8	1387		NM_020358	NP_065091	P0CI25	TRI49_HUMAN	B30.2/SPRY.	0	AAAGCCCAATTC	0.438	
-	4	405	A4_uc001pdm.2_	NM_152313	NP_689526	Q6YBV0	S36A4_HUMAN	ical; (Potential).	3	TGAACAGAAATA	0.303	
+	3	287	n_p.Q63*|CCDC67	NM_181645	NP_857596	Q05D60	CCD67_HUMAN		1	TTGGATCAGAAA	0.343	
+	14	1999	e_Mutation_p.E55	NM_014361	NP_055176	O94779	CNTN5_HUMAN	like C2-type 5.	8	GAGGGGAAAAC	0.408	
-	8	817	se_Mutation_p.W2	NM_152587	NP_689800	Q8NCR3	CK065_HUMAN		1	TTCCTTCCAGCT	0.328	
-	4	466		NM_006235	NP_006226	Q16633	OBF1_HUMAN		1	AACCTTCCATGT	0.642	
+	20	1885	C12_uc001pnw.2_	NM_017868	NP_060338	Q9H892	TTC12_HUMAN		4	AGTTATCATGAAG	0.388	
-	3	748	AM55A_uc001ppb.	NM_152315	NP_689528	Q8N323	FA55A_HUMAN		0	AGCCTCACAGG	0.438	
-	33	6334		NM_020693	NP_065744	Q8TD84	DSCL1_HUMAN	lasmic (Potential).	8	ACCAGGGTGTAG	0.617	
-	2	199	01prt.1_5'UTR|TM	NM_001077263	NP_001070731	Q9BYE2	TMPSD_HUMAN	epeats of A-S-P-A-[GLQR].	1	GGCTGGAGATG	0.637	
-	2	146	01prt.1_5'UTR|TM	NM_001077263	NP_001070731	Q9BYE2	TMPSD_HUMAN	5 AA repeats of A-S-P-A-[	1	GATGCTCCAGCT	0.617	
+	7	1477	p.S447L|IL10RA_	NM_001558	NP_001549	Q13651	I10R1_HUMAN	lasmic (Potential).	1	AAGAATCGCCCT	0.567	
+	3	613	L_uc001psz.1_Mi	NM_005933	NP_005924	Q03164	MLL1_HUMAN		25	TGTTTTCCCCTC	0.413	
-	6	2217	al.2_Nonsense_Mu	NM_182557	NP_872363	Q86UU0	BCL9L_HUMAN	teraction with CTNNB1 (By	2	GTCGCTCAATGT	0.687	
-	1	609	M29_uc001pxa.2_	NM_012101	NP_036233	Q14134	TRI29_HUMAN		4	ACCGTGAAAAA	0.642	
+	5	380	1S|POU2F3_uc01	NM_014352	NP_055167	Q9UKI9	PO2F3_HUMAN		2	TCCATCCGCTCC	0.572	
+	8	1859		NM_005422	NP_005413	O75443	TECTA_HUMAN	TIL 1.	10	GGCCTCGCGGA	0.662	
-	1	781		NM_001004474	NP_001004474	Q8NGN2	O10S1_HUMAN	Name=6; (Potential).	2	CACCCCAGTGA	0.607	
+	24	3384	K|CACNA1C_uc00	NM_199460	NP_955630	Q13936	CAC1C_HUMAN	=S4 of repeat III; (Potentia	11	ACTCAGGCCCC	0.592	
+	47	6155	K|CACNA1C_uc00	NM_199460	NP_955630	Q13936	CAC1C_HUMAN	lasmic (Potential).	11	GATGACGAAAAT	0.592	
-	2	452	ed.1_Missense_Mu	NM_031474	NP_113662	Q9BQI9	NRIP2_HUMAN		1	GGTTTCCCTCC	0.572	
-	17	2797	p.L871R|CHD4_u	NM_001273	NP_001264	Q14839	CHD4_HUMAN	ase ATP-binding.	2	TCTTCAGCCGAT	0.468	
-	5	544	RBP_uc010sfg.1_In	NM_032489	NP_115878	Q8NEB7	ACRBP_HUMAN		1	GGGCTGGAAGG	0.572	
+	1	79		NM_001080454	NP_001073923	P0C7M7	ACSM4_HUMAN		0	AAAGATCACCAG	0.463	
-	4	505	sge.1_Missense_M	NM_174941	NP_777601	Q9NR16	C163B_HUMAN	Extracellular (Potential).	11	TTGTTTCCATCC	0.443	
-	16	3472	.3_Intron|CD163_	NM_004244	NP_004235	Q86VB7	C163A_HUMAN		8	AATTTTCTGAAA	0.398	
-	5	661	p.E163K|CLEC4C	NM_130441	NP_569708	Q8WTT0	CLC4C_HUMAN	(Potential).|C-type lectin.	3	CATTTTCATTGTA	0.423	

-	1	51	P_uc009zgl.2_5'U	NM_002864	NP_002855					5	ATAAATGAAGAAC	0.493	
-	13	3022		NM_000834	NP_000825	Q13224	NMDE2_HUMAN	lasmic (Potential).		12	TTGTAGGATTTGC	0.552	
-	13	1627		NM_004963	NP_004954	P25092	GUC2C_HUMAN	Potential).|Protein kinase.		6	GTATCTCGTCTTT	0.473	
+	11	2078	cw.1_Missense_M	NM_030667	NP_109592	Q16827	PTPRO_HUMAN	III 7.|Extracellular (Potentia		9	TGGCTCCGGAAA	0.408	
+	6	667	_Mutation_p.R181	NM_019844	NP_062818	Q9NPD5	SO1B3_HUMAN	Name=4; (Potential).		4	ATGCTTCGTGGCA	0.378	rs143565471
-	12	2573	_p.Q776*|PKP2_uc	NM_004572	NP_004563	Q99959	PKP2_HUMAN	ARM 8.		2	TTTCTGGATGCC	0.493	
-	9	1970	_p.E575K|PKP2_uc	NM_004572	NP_004563	Q99959	PKP2_HUMAN			2	CTGCCTCCAGCTC	0.413	
+	10	1138	zjz.2_Missense_M	NM_013377	NP_037509	Q6ZMN7	PZRN4_HUMAN			11	GAGTAGGACGTAC	0.468	
-	27	4103	1rno.1_Missense_	NM_025003	NP_079279	P59510	ATS20_HUMAN	SP type-1 10.		19	ACTTCTCCCCAAT	0.398	
+	4	1305	_p.E72K|FAM113B_	NM_138371	NP_612380	Q96HM7	F113B_HUMAN			5	AAAAACGAAGTGC	0.582	
-	19	1340	OL2A1_uc001rqv.2	NM_001844	NP_001835	P02458	CO2A1_HUMAN	le-helical region.		2	GAGCACCTTCAGC	0.627	
-	6	605	rqv.2_Missense_M	NM_001844	NP_001835	P02458	CO2A1_HUMAN			2	CTTTTTCACCTTT	0.542	
+	13	2013	_p.P616S|TROAP_	NM_005480	NP_005471	Q12815	TROAP_HUMAN	A approximate tandem rep		1	TGCCCTCCAGCA	0.652	
-	4	356		NM_001037806	NP_001032895	Q9HCH0	NCK5L_HUMAN	Potential.		1	GGTTTTCGTTGGC	0.592	
-	12	1310	1rvs.2_Missense_I	NM_013277	NP_037409	Q9H0H5	RGAP1_HUMAN	ol-ester/DAG-type.		1	GCAGGGAAGGG	0.468	
-	10	1220	.2_Nonsense_Mut	NM_016293	NP_057377	Q9UBW5	BIN2_HUMAN			1	GGGTTCGGAGGA	0.592	
+	10	1292	4A8_uc001ryp.1_3	NM_001039960	NP_001035049	Q2Y0W8	S4A8_HUMAN	cellular (Potential).		5	CATGACGTAGCAT	0.438	
-	1	635	h.2_Missense_Mu	NM_000424	NP_000415	P13647	K2C5_HUMAN	Head.		0	TGGGGTCGATTTC	0.537	
-	1	99		NM_033448	NP_258259	Q3SY84	K2C71_HUMAN	lead.|Gly-rich.		2	GCAGCTCCCGAC	0.597	
-	1	94	av.1_Missense_Mu	NM_006121	NP_006112	P04264	K2C1_HUMAN	|Gly/Phe/Ser-rich.		2	CCACTTCGGTACC	0.552	
-	7	1317	ni.2_Missense_Mu	NM_175078	NP_778253	Q7Z794	K2C1B_HUMAN	Rod.|Coil 2.		1	CCAGGTCCTGCAC	0.612	
-	2	658	79_uc001sba.2_5'U	NM_175834	NP_787028	Q5XKE5	K2C79_HUMAN	Rod.|Coil 1B.		4	TCTGAAGTCTGTC	0.617	
+	1	561		NM_001005243	NP_001005243	Q8NGE7	OR9K2_HUMAN	cellular (Potential).		2	TAGCATGACATT	0.433	
+	2	629	_p.M70I|PA2G4_u	NM_006191	NP_006182	Q9UQ80	PA2G4_HUMAN			0	GGAAATGAAGAA	0.234	
+	9	1065	sqq.1_Missense_M	NM_002898	NP_002889	Q15434	RBMS2_HUMAN			0	TGTCTTCGTATCA	0.453	
+	2	1031		NM_005538	NP_005529	P55103	INHBC_HUMAN			0	AATCTTCTCAAGC	0.577	
+	10	2026	rj.2_Missense_Mut	NM_006654	NP_006645	Q8WU20	FRS2_HUMAN			2	ACTGATCTGCCCA	0.398	
-	1	448		NM_201550	NP_963844	Q5BKY1	LRC10_HUMAN			0	AGCGGCGTAACT	0.607	
-	10	1585	1svf.2_Missense_I	NM_032735	NP_116124	Q8N1M1	BEST3_HUMAN	lasmic (Potential).		0	AAGCAGGATTTCT	0.592	
-	8	1674	_p.R269C|PTPRR_	NM_002849	NP_002840	Q15256	PTPRR_HUMAN	sphatase.|Cytoplasmic (Pot		3	TATAGCGATTTTT	0.224	
-	10	1759		NM_032148	NP_115524	Q96JW4	S41A2_HUMAN	Extracellular.		2	TCCTTTCCTTTCC	0.468	
-	3	652	tmv.2_Missense_M	NM_001142345	NP_001135817	Q99788	CML1_HUMAN	lasmic (Potential).		5	CCAGGCGAACGC	0.562	
-	24	3988	_Mutation_p.G969	NM_002973	NP_002964	Q99700	ATX2_HUMAN			2	GGGACCGCCGG	0.557	
+	18	1928	e.1_Missense_Mu	NM_001143854	NP_001137326	Q9Y2J0	RP3A_HUMAN			7	TAAGATGAAACGT	0.483	
-	9	1480	_p.E329K|TBX5_uc	NM_181486	NP_852259	Q99593	TBX5_HUMAN		p.E329K(1)	8	ATTCTTCCTCTGT	0.493	rs142807139
-	19	2769		NM_173598	NP_775869	Q6VAB6	KSR2_HUMAN			15	CGGTTTCGCTTTC	0.498	
-	17	1635		NM_006836	NP_006827	Q92616	GCN1L_HUMAN			4	ACACAGTACACA	0.338	
-	5	1293	.R396Q|CLIP1_uc	NM_002956	NP_002947	P30622	CLIP1_HUMAN	Potential.		3	CGTCCCGGGCCA	0.622	
+	46	4862	TC1_uc010taf.1_In	NM_014708	NP_055523	P50748	KNTC1_HUMAN			10	ATTTCTCCTCCCC	0.368	
-	1	114	281_uc001ucw.1_In	NM_177551	NP_808219	Q8TDS4	HCAR2_HUMAN	cellular (Potential).		0	TCTTGTCTATTTC	0.537	
-	1	195	281_uc001ucw.1_In	NM_006018	NP_006009	P49019	HCAR3_HUMAN	cellular (Potential).		2	TCTTGTCTATTTC	0.532	
+	6	1975	_p.H49Y|ZNF664_	NM_152437	NP_689650	Q8N3J9	ZN664_HUMAN	C2H2-type 2.		0	CATATTCATTGGA	0.353	
-	5	1391		NM_006001	NP_005992	Q13748	TBA3C_HUMAN			5	ATTCTTCACCTTC	0.557	
-	19	1580	_p.D380N|TPTE2_	NM_199254	NP_954863	Q6XPS3	TPTE2_HUMAN	2 tensin-type.		0	TCACATCATCATA	0.333	
-	4	993	nr.3_Missense_Mu	NM_014572	NP_055387	Q9NRM7	LATS2_HUMAN			10	GTACGGCCGCG	0.701	
-	10	11921	E3631K|SACS_uc	NM_014363	NP_055178	Q9NZJ4	SACS_HUMAN			12	GGAATTCATATAT	0.388	
-	10	7383	S2118F|SACS_uc	NM_014363	NP_055178	Q9NZJ4	SACS_HUMAN			12	GAATGGGAATTT	0.353	

+	5	495	0tcu.1_Missense_	NM_018647	NP_061117	Q9NS68	TNR19_HUMAN	(Potential).|TNFR-Cys 3.	2	CTCCTCCTTACGA	0.458
+	13	2009	aa.2_Missense_M	NM_001676	NP_001667	P54707	AT12A_HUMAN	lasmic (Potential).	6	ATGATCGATCCCC	0.493
+	10	990	se_Mutation_p.E31	NM_031277	NP_112567	Q9BXT8	RNF17_HUMAN		2	CCCCAAGAAAATC	0.269
-	1	1791	p.G445E|FAM123A	NM_152704	NP_689917	Q8N7J2	F123A_HUMAN		4	GGACTTCCGTCCC	0.622
-	2	596	R12_uc010tdl.1_In	NM_005288	NP_005279	P47775	GPR12_HUMAN	Name=3; (Potential).	0	GAGGCAGAGAAA	0.527
-	19	2479	LT3_uc010tdn.1_M	NM_004119	NP_004110	P36888	FLT3_HUMAN	e.|Cytoplasmic (Potential).	8549	AAATTCCATTCCT	0.308
+	5	2951		NM_001033602	NP_001028774	Q5JR59	MTUS2_HUMAN	f microtubules.|Mediates int	0	TCATCTCCTAAGA	0.378
-	7	1415		NM_003045	NP_003036	P30825	CTR1_HUMAN	ical; (Potential).	0	AGAGGGAGCCC	0.617
+	2	199	aba.2_Missense_M	NM_130806	NP_570718	Q8WXD0	RXFP2_HUMAN	cellular (Potential).	0	TCACTCCTTCATG	0.398
+	16	1666	ba.2_Missense_Mu	NM_130806	NP_570718	Q8WXD0	RXFP2_HUMAN	lasmic (Potential).	0	ACATTCGACCTGC	0.453
+	22	9021		NM_000059	NP_000050	P51587	BRCA2_HUMAN		64	AATAATCACAGGC	0.363
+	5	2871		NM_004795	NP_004786	Q9UEF7	KLOT_HUMAN	cellular (Potential).	3	TCCCGGGCCCA	0.443
-	2	669	e_Mutation_p.P10	NM_001127217	NP_001120689	O15198	SMAD9_HUMAN	MH1.	0	TCCAGCGGCTTCA	0.607
-	23	2622	p.S778F|POSTN_	NM_006475	NP_006466	Q15063	POSTN_HUMAN		2	CACTGAGAACGAC	0.308
-	3	1098	p.R288K|TRPC4_u	NM_016179	NP_057263	Q9UBN4	TRPC4_HUMAN	Multimerization domain (By	6	TTTAGTCTTGCAA	0.388
+	1	3076		NM_207361	NP_997244	Q5SZK8	FREM2_HUMAN	Extracellular (Potential).	11	AGACATCATGTGC	0.507
-	3	945	p.D171N|HTR2A_	NM_000621	NP_000612	P28223	5HT2A_HUMAN	asmic (By similarity).	6	CAAGATCACTTAC	0.453
+	1	2488		NR_003268					0	GATTTTCCCCCCC	0.522
-	10	2684	TP7B_uc010tgu.1_	NM_000053	NP_000044	P35670	ATP7B_HUMAN	lasmic (Potential).	3	CTTTCCCATCCAC	0.542
+	4	606	gu.2_Missense_M	NM_001098525	NP_001091995	Q8WWK9	CKAP2_HUMAN		2	GATGATCCCCAAA	0.323
-	2	2248	nl.1_Missense_Mu	NM_203487	NP_982354	Q9HC56	PCDH9_HUMAN	r (Potential).|Cadherin 5.	6	GTTTTTCGGTCCA	0.433
-	8	2083	p.P406S|DACH1_	NM_080759	NP_542937	Q9UI36	DACH1_HUMAN		1	GAGATGGAAAACC	0.468
-	2	383		NM_001071775	NP_001065243	Q08AG7	MZT1_HUMAN		0	ATAACCGATGATA	0.343
-	1	1188		NM_052910	NP_443142	Q96PX8	SLIK1_HUMAN	lar (Potential).|LRR 2.	5	AGAAAAGCCCCCC	0.448
+	4	570	LDN10_uc010tii.1_	NM_006984	NP_008915	P78369	CLD10_HUMAN	ical; (Potential).	1	GAGCCTCACTGT	0.378
+	2	205	n_p.S64F|CLYBL_u	NM_206808	NP_996531	Q8N0X4	CLYBL_HUMAN		0	TTCCATCCCTGAA	0.408
-	10	1477	8_splice|TMTC4_u	NM_001079669	NP_001073137	Q5T4D3	TMTC4_HUMAN		3	TTGATACCTTTTT	0.498
-	4	578	e_Mutation_p.R15	NM_001079669	NP_001073137	Q5T4D3	TMTC4_HUMAN		3	GCCTCCGGCCTT	0.612
-	2	733	M_uc001vps.2_5'l	NM_024089	NP_076994	Q6UW63	KDEL1_HUMAN	Filamin.	1	GCCCTTGGAATT	0.318
-	4	545	TP1_uc010tkc.1_M	NM_024719	NP_078995	Q5TC63	GRTP1_HUMAN	ab-GAP TBC.	0	CCACTCCCTGGT	0.622
-	2	328	RHL1_uc001vtp.1_	NM_138430	NP_612439	Q8NDY3	ARHL1_HUMAN		0	TCTCCCGGTACAC	0.567
+	1	224		NM_001005483	NP_001005483	Q8NGD3	OR4K5_HUMAN	Name=2; (Potential).	2	AGGCTTCTTTTGC	0.408
+	1	283		NM_001004063	NP_001004063	Q8NGD4	OR4K1_HUMAN	cellular (Potential).	3	TCCTTTGAGGGTT	0.403
+	17	2782	p.P403S|RPGRIP	NM_020366	NP_065099	Q96KN7	RPGR1_HUMAN		7	AAGTTTCCCTACA	0.443
-	11	1935	DH24_uc010akf.2_	NM_022478	NP_071923	Q86UP0	CAD24_HUMAN	|Extracellular (Potential).	1	AGGGCCCAGAG	0.572
-	32	4698		NM_002471	NP_002462	P13533	MYH6_HUMAN	Potential.	4	GGGCTGACTGC	0.602
+	7	894	y.1_Missense_Mut	NM_001163484	NP_001156956	Q8TEB1	DCA11_HUMAN	WD 1.	0	ATGGCCGTTTCCC	0.488
-	4	493		NM_001911	NP_001902	P08311	CATG_HUMAN	Peptidase S1.	2	CCTCCTCATGCTC	0.617
-	5	865		NM_199047	NP_950248	Q6SJ96	TBPL2_HUMAN		0	TAAAATCGAGGAA	0.473
+	26	3294	e_Mutation_p.R10	NM_014992	NP_055807	Q9Y4D1	DAAM1_HUMAN	DAD.	1	CGGAATCGCAAA	0.368
+	43	6795	gl.2_Missense_Mu	NM_015180	NP_055995	Q8WXH0	SYNE2_HUMAN	Cytoplasmic (Potential).	14	AAATTCCTCAAGA	0.398
+	99	18235	n.2_Missense_Mu	NM_015180	NP_055995	Q8WXH0	SYNE2_HUMAN	Cytoplasmic (Potential).	14	ACGATCGTTGGCA	0.388
+	1	280		NM_003813	NP_003804	Q9UKJ8	ADA21_HUMAN		2	TACACAGATGACC	0.512
-	2	1426		NM_003814	NP_003805	O43506	ADA20_HUMAN	2B.|Extracellular (Potential).	1	GACCAAGCTCGT	0.418
+	14	1578	S6_uc001xmy.3_M	NM_004296	NP_004287	P49758	RGS6_HUMAN	RGS.	3	TTCTACGATTCCT	0.473
+	10	1307	p.R367C|RBM25_u	NM_021239	NP_067062	P49756	RBM25_HUMAN	peckle localization.|Glu-rich	4	gagaTCGTGACCC	0.214
+	18	2492	.1_RNA|PAPLN_u	NM_173462	NP_775733	O95428	PPN_HUMAN	I/Kunitz inhibitor.	3	TCTGTGGGCCAA	0.617

+	1	699		NM_019589	NP_062535	P49750	YLPM1_HUMAN		3	CCCTTCGCAGT	0.602	
-	15	1983	k.2_Missense_Mu	NM_033116	NP_149107	Q8TD19	NEK9_HUMAN	RCC1 4.	5	TAGCAGCTGTG	0.403	
+	5	1057	RXN3_uc010asv.1_	NM_004796	NP_004787	Q9Y4C0	NRX3A_HUMAN	otential).|Laminin G-like 3.	10	CAGGCGCACG	0.557	
+	2	1836	td.2_Missense_M	NM_013231	NP_037363	O43155	FLRT2_HUMAN	lar (Potential).|LRRCT.	4	TGAATCTTTTGT	0.542	
-	7	1994	_p.E518K|KCNK10	NM_021161	NP_066984	P57789	KCNKA_HUMAN	lasmic (Potential).	5	CAACTCAGCGT	0.502	
-	43	6032	d.2_Missense_Mu	NM_183387	NP_899243	Q05BV3	EMAL5_HUMAN	WD 29.	3	GTAAATCGAATA	0.433	
-	3	983	_p.S252F|DDX24_	NM_020414	NP_065147	Q9GZR7	DDX24_HUMAN	ase ATP-binding.	4	CATCAGACTCA	0.552	
+	24	2610		NM_058237	NP_478144	Q6NUP7	PP4R4_HUMAN		4	ATGATTCATTCC	0.403	
+	3	1085	nse_Mutation_p.R	NM_000623	NP_000614	P30411	BKRB2_HUMAN	cellular (Potential).	5	TGCATCGCCTC	0.577	
+	3	407	_p.S82F|EML1_uc	NM_004434	NP_004425	O00423	EMAL1_HUMAN		5	ACCATCCCCCTC	0.498	
+	3	997	se_Mutation_p.P3	NM_001161476	NP_001154948	Q64LD2	WDR25_HUMAN	WD 2.	0	GGGCTCCCTGT	0.622	
+	34	7089	1H1_uc001ykt.1_	NM_001376	NP_001367	Q14204	DYHC1_HUMAN	2 (By similarity).	10	TGGATCCAGAG	0.507	
+	11	1210		NM_015156	NP_055971	Q9UKL0	RCOR1_HUMAN	SANT 2.	1	TTCAGGCAATC	0.338	
+	15	2351	my.3_Missense_	NM_001128918	NP_001122390	P27448	MARK3_HUMAN		4	CAGTCGTAGCA	0.567	
+	35	4070	on.3_Nonsense_M	NM_153046	NP_694591	Q8NDG6	TDRD9_HUMAN		3	CGAGTGGAATC	0.488	
+	12	3800		NM_015656	NP_056471	Q9ULI4	KI26A_HUMAN		1	TGGCTCCCCCC	0.697	
-	7	5615	px.2_Missense_M	NM_138420	NP_612429	Q8IVF2	AHNK2_HUMAN		1	CGAACGACGGC	0.612	
+	1	961	KRN3_uc010ayi.1_	NM_005664	NP_005655	Q13064	MKRN3_HUMAN		10	CCCGGCTGCAT	0.647	
-	1	891		NM_002487	NP_002478	Q99608	NECD_HUMAN	MAGE.	0	GATTTCGCGGC	0.572	
-	4	458_459	v.2_Missense_Mu	NM_000275	NP_000266	Q04671	P_HUMAN	lasmic (Potential).	5	TGGATGGTAAAC	0.495	
+	2	194	ar.2_Missense_M	NM_001036	NP_001027	Q15413	RYR3_HUMAN	smic (By similarity).	10	CCGAGGGACTT	0.547	
+	6	566	ar.2_Nonsense_M	NM_001036	NP_001027	Q15413	RYR3_HUMAN	plasmic (By similarity).	10	AAGTTCGAATT	0.433	
+	54	8088	r.2_Missense_Mut	NM_001036	NP_001027	Q15413	RYR3_HUMAN	milarity).|4 X approximate r	10	TGCGCGAGAGT	0.527	
-	20	2457	se_Mutation_p.R7	NM_004573	NP_004564	Q00722	PLCB2_HUMAN	C2.	8	TTAGTTCGATAG	0.577	
-	16	1712	G397R|ATP8B4_	NM_024837	NP_079113	Q8TF62	AT8B4_HUMAN	lasmic (Potential).	8	TGTTCCCAATT	0.398	
+	7	1225	fz.1_Missense_M	NM_013243	NP_037375	Q8WXD2	SCG3_HUMAN		1	TTTGAGGAACTC	0.383	
+	1	1499		NM_001080534	NP_001074003	Q8NB66	UN13C_HUMAN		7	CAGCAGAATTT	0.388	
+	29	6145	3C_uc002acm.2_	NM_001080534	NP_001074003	Q8NB66	UN13C_HUMAN	C2 2.	7	CTGTTCATGTG	0.428	
+	2	1559	fw.2_Missense_M	NM_032866	NP_116255	Q0VF96	CGNL1_HUMAN	Head.	11	AGGAGGAGGAG	0.512	rs141642509
+	4	683	lv.2_Missense_M	NM_032857	NP_116246	P83111	LACTB_HUMAN		0	TGATTTCCCATTT	0.299	
-	6	785		NM_194272	NP_919248	Q6ZRY4	RBPS2_HUMAN		0	TGGCAGTTGGG	0.622	
-	20	4247	P8_uc002aoz.2_	NM_130434	NP_569118	Q6V1X1	DPP8_HUMAN		1	ATACGTGATCCA	0.388	
+	4	2007	AD6_uc002aqg.2_	NM_005585	NP_005576	O43541	SMAD6_HUMAN	MH2.	1	TACCTCAGGGC	0.667	
+	9	1347	p.A261T|IQCH_uc	NM_001031715	NP_001026885	Q86VS3	IQCH_HUMAN		4	TTCGAGCCAAG	0.433	
+	16	2467	|IQCH_uc002aqp.	NM_001031715	NP_001026885	Q86VS3	IQCH_HUMAN		4	AATTGGAAAAG	0.463	
+	6	2386		NM_001031807	NP_001026977	P84550	SKOR1_HUMAN		0	CAGGCGAAGAT	0.522	
-	26	3198	b.2_Nonsense_M	NM_001004439	NP_001004439	Q9UKX5	ITA11_HUMAN	cellular (Potential).	3	TTGCCCCAGAT	0.582	
+	12	1650	ukf.1_Missense_M	NM_017691	NP_060161	Q8IUZ0	LRC49_HUMAN		1	CTAATTCTCTGG	0.328	
-	4	811		NM_001102658	NP_001096128	P0C5K7	CT62_HUMAN		0	ACACTTCATGGG	0.488	
+	10	1086	ke.1_Missense_	NM_021819	NP_068591	Q9HAT1	LMA1L_HUMAN	enal (Potential).	0	AGATTCCATCC	0.612	
+	11	1164	ke.1_Missense_M	NM_021819	NP_068591	Q9HAT1	LMA1L_HUMAN	enal (Potential).	0	TCCATGGACAG	0.607	
-	18	3008	TS7_uc010und.1_	NM_014272	NP_055087	Q9UKP4	ATS7_HUMAN	SP type-1 3.	0	GGTTTCAGTAG	0.687	
+	12	1992	p.I581S|IL16_uc0	NM_172217	NP_757366	Q14005	IL16_HUMAN		4	GGACATCAGCA	0.627	
-	12	2005	.G568E|FSD2_uc	NM_001007122	NP_001007123	A1L4K1	FSD2_HUMAN	30.2/SPRY.	1	GATTTCCCATGA	0.527	
-	5	2973	s.1_Missense_Mu	NM_001717	NP_001708	Q01954	BNC1_HUMAN	2H2-type 6.	3	TTGCAGCCTGGT	0.502	
-	4	536	s.1_Nonsense_M	NM_001717	NP_001708	Q01954	BNC1_HUMAN		3	ACACCTTTCCTG	0.428	
+	5	625	se_Mutation_p.Q7	NM_003027	NP_003018	Q99963	SH3G3_HUMAN	BAR.	3	CCACTTCAGTTA	0.333	

-	19	2590	_p.E788K|NTRK3_	NM_001012338	NP_001012338	Q16288	NTRK3_HUMAN	Potential).|Protein kinase.	281	TGGTTCCCTCT	0.542	
-	2	268	se_Mutation_p.S4	NM_005928	NP_005919	Q08431	MFGM_HUMAN	EGF-like.	1	TGTACGAGGGG	0.542	rs145851768
-	13	1369	p.R248C|VPS33B	NM_018668	NP_061138	Q9H267	VP33B_HUMAN		2	CAGGCGGTGCT	0.562	rs140237411
+	3	1855	.2_5'Flank|PIGQ_	NM_145270	NP_660313	P0CG20	CP011_HUMAN		1	GCGTCCCACCC	0.697	
-	3	461		NM_001025190	NP_001020361	Q96KJ4	MSLNL_HUMAN		4	TGCACGGGTAG	0.557	
-	11	1151_1152		NM_020764	NP_065815	Q8WXD9	CSKI1_HUMAN		2	GATCTCCTCTGG	0.634	
+	11	7006	.1_Missense_Mut	NM_016333	NP_057417	Q9UQ35	SRRM2_HUMAN	Ser-rich.	4	AAGCCGGCGG	0.552	
-	3	1028	vw.2_Missense_	NM_004380	NP_004371	Q92793	CBP_HUMAN	ction with SRCAP.	127	CAAATGGACTT	0.498	
+	5	529		NM_014692	NP_055507	O43304	S14L5_HUMAN	RELI/MSF1.	0	AGGTCCACCCT	0.582	
-	13	4267	yn.1_Missense_	NM_001134407	NP_001127879	Q12879	NMDE1_HUMAN	lasmic (Potential).	45	TCCGCAGGCAG	0.582	
-	12	3114	yn.1_Missense_	NM_001134407	NP_001127879	Q12879	NMDE1_HUMAN	lasmic (Potential).	45	AGGCCGGTCGG	0.567	
-	5	1067		NM_144674	NP_653275	Q96M29	TEKT5_HUMAN	Potential.	2	TGCCTCCACATC	0.557	
-	4	557	M18A_uc010uyu.	NM_001079512	NP_001072980	A6NH52	FA18A_HUMAN		0	CATCTTCATCTAT	0.498	
+	9	1087	vam.1_Missense_	NR_003569					0	CCTCGCCGTGC	0.572	
-	51	9082	.L2767F|SMG1_u	NM_015092	NP_055907	Q96Q15	SMG1_HUMAN		16	CTGAAGAGATT	0.483	
+	14	2958	d.1_Missense_M	NM_001105248	NP_001098718	Q6UXY8	TMC5_HUMAN	ical; (Potential).	1	GGCTCCTTCTG	0.483	
-	53	10430	bd.1_Missense_M	NM_017539	NP_060009	Q8TD57	DYH3_HUMAN		18	AACATCGAAGG	0.527	
-	52	8263	bd.1_Missense_M	NM_017539	NP_060009	Q8TD57	DYH3_HUMAN	k (By similarity).	18	ACATTCGTTCT	0.597	
-	37	5399		NM_017539	NP_060009	Q8TD57	DYH3_HUMAN	2 (By simila p.W1800*(1)	18	CAATCCAAATA	0.403	
+	9	1017	A11_uc002dmt.2_	NM_052944	NP_443176	Q8WWX8	SC5AB_HUMAN	ellular (Potential).	2	TTTCCGAGATC	0.572	
+	2	1755		NM_006040	NP_006031	Q9Y661	HS3S4_HUMAN	enal (Potential).	2	AGGGTGATAAA	0.468	
-	4	784	_p.L81F|XPO6_u	NM_015171	NP_055986	Q96QU8	XPO6_HUMAN	ortin N-terminal.	2	CAAAAGGAGTT	0.408	
-	12	1258	12F|CLN3_uc002	NM_000086	NP_000077	Q13286	CLN3_HUMAN		0	TCAGGGAAGTG	0.617	
-	5	560	_uc010vef.1_RN	NM_003586	NP_003577	Q14183	DOC2A_HUMAN	C2 1.	2	CACGGGATTCA	0.562	
-	3	757	yr.1_Missense_M	NM_033410	NP_219363	Q96H86	ZN764_HUMAN		1	CCCACGATGGA	0.667	
-	3	1047	89_uc010bzy.2_5	NM_138447	NP_612456	Q96CS4	ZN689_HUMAN	2H2-type 4.	0	CCTCCGGAAGC	0.607	
+	25	5862	e_Mutation_p.S16	NM_006662	NP_006653	Q6ZRS2	SRCAP_HUMAN	Pro-rich.	4	GGTTTCGGCAT	0.378	
+	4	2161		NM_003414	NP_003405	Q14586	ZN267_HUMAN	2H2-type 12.	4	ACATCAGAGAA	0.438	
+	4	2173		NM_003414	NP_003405	Q14586	ZN267_HUMAN		4	TCATACTGGAG	0.453	
+	4	2329		NM_003414	NP_003405	Q14586	ZN267_HUMAN	2H2-type 14.	4	ACATCGGAGAA	0.433	rs146914846
+	4	2341		NM_003414	NP_003405	Q14586	ZN267_HUMAN		4	TCATAGTGGAG	0.418	
-	15	2537	C12_uc002efa.1_	NM_033226	NP_150229	Q96J65	MRP9_HUMAN		3	CATCTTCCTCTC	0.448	
-	13	2225	C12_uc002efa.1_	NM_033226	NP_150229	Q96J65	MRP9_HUMAN	C transporter 1.	3	GTCGTCCAGCA	0.632	
+	5	2575	_uc010cbn.1_Intro	NM_022162	NP_071445	Q9HC29	NOD2_HUMAN	LRR 2.	4	TGCGCGATAAC	0.408	rs61755272
+	7	1455	p.D306N|MMP2_	NM_004530	NP_004521	P08253	MMP2_HUMAN	pe-II 3.|Collagen-binding.	11	ACTACGATGAT	0.572	
-	4	589	p.E162K|CES1_u	NM_001025194	NP_001020365	P23141	EST1_HUMAN		0	GTTTTCATGGG	0.567	
+	46	5536	LRC5_uc002ekq.1	NM_032206	NP_115582	Q86WI3	NLRC5_HUMAN		7	TGCCCTGgaagta	0.294	
+	10	1563	n_p.W205*|SLC9	NM_004594	NP_004585	Q14940	SL9A5_HUMAN		2	AGGTGGGAGCA	0.597	
+	18	1836	p.G467R|WWP2_	NM_007014	NP_008945	O00308	WWP2_HUMAN	HECT.	6	ATGCCGGAAAG	0.463	
+	6	1558	vlr.1_Missense_M	NM_017990	NP_060460	Q8NCN5	PDPR_HUMAN		1	CCTCCCAAAAT	0.512	
-	8	4598	cl.2_Nonsense_M	NM_006885	NP_008816	Q15911	ZFHX3_HUMAN		4	ATCTCGATCTG	0.478	
-	5	814	8B_uc010vmu.1_	NM_001011880	NP_001011880	Q6UXF7	CL18B_HUMAN		0	AGAGCGAACAC	0.612	
-	4	409	n.2_Missense_Mu	NM_153486	NP_705690	Q86WU2	LDHD_HUMAN	inding PCMH-type.	0	GGATTCGGTCC	0.632	
-	20	3529	0chc.1_Missense_	NM_199355	NP_955387	Q8TE60	ATS18_HUMAN	SP type-1 3.	18	GCTCAGGTCTG	0.602	
-	9	1746	TS18_uc002ffe.1_	NM_199355	NP_955387	Q8TE60	ATS18_HUMAN	ptidase M12B.	18	CATACCAAAGC	0.393	
+	9	1242	fl.2_Missense_Mu	NM_016373	NP_057457	Q9NZC7	WWOX_HUMAN	ith MAPT (By similarity).	0	TGGGAGGGAT	0.547	
-	7	1588		NM_152342	NP_689555	Q8N8U2	CDYL2_HUMAN		1	GAAAAGGGAGT	0.557	

+	4	2069_2070	H3_uc010vou.1_R	NM_020655	NP_065706	Q8WXH2	JPH3_HUMAN	lasmic (Potential).	2	AGGAGGAGAA	0.653	
-	4	465	NA_uc010cju.2_T	NM_006224	NP_006215	Q00169	PIPNA_HUMAN		1	CAAACGTGGGT	0.517	
+	21	3233	_p.D335N|USP6_	NM_004505	NP_004496	P35125	UBP6_HUMAN		5	TGAACGATGAC	0.577	rs145087393
+	36	5951	.D1241N|USP6_	NM_004505	NP_004496	P35125	UBP6_HUMAN		5	TGGCTGACGCC	0.557	
-	20	3222	LG4_uc010cly.2_	NM_001365	NP_001356	P78352	DLG4_HUMAN	ylate kinase-like.	2	TGGCCGAGACA	0.687	
+	41	6548		NM_020877	NP_065928	Q9P225	DYH2_HUMAN	2 (By similarity).	13	AACATGAACTC	0.587	
+	50	7917		NM_020877	NP_065928	Q9P225	DYH2_HUMAN		13	TTCCATGATACC	0.522	
+	6	624	6B_uc002gix.2_5'	NM_001080424	NP_001073893	O15054	KDM6B_HUMAN	Pro-rich.	2	CACTCCAAGAC	0.637	rs141369717
+	10	1317	6B_uc002gix.2_5'	NM_001080424	NP_001073893	O15054	KDM6B_HUMAN	Pro-rich.	2	CATATCCATACC	0.642	
+	6	976	jf.2_Nonsense_Mu	NM_001005273	NP_001005273	Q12873	CHD3_HUMAN		1	GCCCCCGAGTG	0.522	
+	2	350_351	2gld.2_Missense_	NM_173728	NP_776089	O94989	ARHGF_HUMAN	Pro-rich.	3	TTTTGCCCCCCT	0.619	
-	15	1918	lr.1_RNA|PIK3R6_	NM_001010855	NP_001010855	Q5UE93	PI3R6_HUMAN		0	CAGTTCAATGA	0.468	
-	34	4937	uc002gml.1_Intron	NM_017533	NP_060003	Q9Y623	MYH4_HUMAN	Potential.	13	TCCTGATCTCA	0.453	
-	3	406		NM_002470	NP_002461	P11055	MYH3_HUMAN	osin head-like.	7	ATGTGTAACGG	0.567	
+	68	12994	.R3527Q|DNAH9	NM_001372	NP_001363	Q9NYC9	DYH9_HUMAN		20	TAGACGAGCCT	0.542	rs147022425
-	6	2638		NM_020787	NP_065838	Q9P2J8	ZN624_HUMAN	2H2-type 21.	2	GTACAGTAAGG	0.343	
-	3	411	sense_Mutation_p	NM_012452	NP_036584	O14836	TR13B_HUMAN	ellular (Potential).	2	TTCCCGAGTTG	0.532	
+	3	956		NM_207313	NP_997196	Q6IEE7	T132E_HUMAN	ellular (Potential).	1	TGCCAGACCGG	0.677	
+	5	1244		NM_207313	NP_997196	Q6IEE7	T132E_HUMAN	ellular (Potential).	1	ACTTTGAAATG	0.627	
-	5	702	oh.1_Missense_M	NM_007010	NP_008941	Q9Y2R4	DDX52_HUMAN	ase ATP-binding.	2	AATAGGAATGC	0.403	
+	4	679	tv.2_Missense_M	NM_003250	NP_003241	P10827	THA_HUMAN	eceptor.|NR C4-type.	0	ACTACCGCTGT	0.547	
-	5	923		NM_002280	NP_002271	Q92764	KRT35_HUMAN	Rod.|Coil 2.	2	CAGCTCCTCAC	0.507	
-	7	1370		NM_003771	NP_003762	O76013	KRT36_HUMAN	Tail.	0	TGGAGGAGATG	0.662	
-	8	1514	e_Mutation_p.G41	NM_021991	NP_068831	P14923	PLAK_HUMAN	ARM 5.	5	TGTGCCCGTGG	0.577	rs151226851
-	5	995	p.T158M|VAT1_uc	NM_006373	NP_006364	Q99536	VAT1_HUMAN		0	GGCCCGTCAGC	0.607	
-	8	989	p.P231S|GPATCH	NM_001002909	NP_001002909	Q9UKJ3	GPTC8_HUMAN		4	GACAGGAGCCT	0.463	
+	2	323	ikx.1_Missense_M	NM_003396	NP_003387	O14905	WNT9B_HUMAN		2	GGCATGAGCGC	0.672	
+	12	1980	B3_uc010wkr.1_R	NM_000212	NP_000203	P05106	ITB3_HUMAN	ellular (Potential).	6	ATGACGAAAAT	0.468	rs70940817
-	10	939	lbd.1_Splice_Site_	NM_003726	NP_003717	Q86WV1	SKAP1_HUMAN		0	TTCATCTGGGG	0.333	
-	31	2176		NM_000088	NP_000079	P02452	CO1A1_HUMAN	le-helical region.	382	ACGCTCGCCAG	0.642	
+	4	483_484	k.3_Missense_Mu	NM_003786	NP_003777	O15438	MRP3_HUMAN	ame=4; (By similarity).	4	CTTCGGGGGTC	0.599	
+	23	3358	C3_uc002isn.2_5'	NM_003786	NP_003777	O15438	MRP3_HUMAN	-1 2.|Helical; Name=14; (B	4	TCAATTCCTTCTT	0.542	
+	20	6666	_p.P2328Q|BPTF_	NM_182641	NP_872579	Q12830	BPTF_HUMAN		4	AATGCCAAATG	0.527	
-	35	4633	z.2_Missense_Mu	NM_080283	NP_525022	Q8IUA7	ABCA9_HUMAN	C transporter 2.	6	GCCTTCCTGAC	0.607	
+	3	295	k.2_Missense_Mu	NM_153209	NP_694941	Q2TAC6	KIF19_HUMAN	inesin-motor.	0	CCGACGACATC	0.647	
-	2	322		NM_001080466	NP_001073935	A6NE02	BTBDH_HUMAN	BTB.	0	TGGCTCCTGCA	0.632	
-	2	163		NM_001080466	NP_001073935	A6NE02	BTBDH_HUMAN		0	CAGCTCCTGCA	0.672	
-	7	881	63K|CD300LF_uc	NM_139018	NP_620587	Q8TDQ1	CLM1_HUMAN	lasmic (Potential).	1	CGGTTCCTGAT	0.617	
-	3	506	|C17orf28_uc002jr	NM_030630	NP_085133	Q8IV36	CQ028_HUMAN		0	GTGGACCAGAA	0.667	
-	22	3462	p.E1100D|EVPL_u	NM_001988	NP_001979	Q92817	EVPL_HUMAN	us rod domain.|Potential.	4	ACTACCTCTTT	0.597	
+	4	869	_p.S90F|TNRC6C	NM_018996	NP_061869	Q9HCJ0	TNR6C_HUMAN	on with argonaute family pr	2	TGCTTCCAACT	0.527	
+	2	285		NM_178543	NP_848638	Q6UWV6	ENPP7_HUMAN		3	ATATCGAGAACC	0.607	
+	3	666		NM_178543	NP_848638	Q6UWV6	ENPP7_HUMAN		3	AGATGGTGCGG	0.652	
+	15	2542	_p.D622N|CCDC4	NM_017950	NP_060420	Q4G0X9	CCD40_HUMAN	Potential. p.D839D(1)	3	ACAACGACCTG	0.527	
+	5	1003	wud.1_RNA|CARD	NM_024110	NP_077015	Q9BXL6	CAR14_HUMAN	Potential.	5	AGGAGGAGAAT	0.617	
-	14	1591	1_Missense_Muta	NM_017921	NP_060391	Q8TAT6	NPL4_HUMAN		2	GAAATGGATTTT	0.363	
+	4	480	_p.S164F|CLUL1_	NM_014410	NP_055225	Q15846	CLUL1_HUMAN		2	AGATTCCTGGG	0.423	

+	6	847		NM_015295	NP_056110	A6NHR9	SMHD1_HUMAN		0	TATGTTCGTCCA	0.373	
-	12	2150	lq.2_Missense_M	NM_003803	NP_003794	P52179	MYOM1_HUMAN		5	CGGATCCAGAG	0.433	
-	1	422	DLGAP1_uc002kn	NM_004746	NP_004737	O14490	DLGP1_HUMAN		4	GGTGTGATAGC	0.682	
-	56	8139	se_Mutation_p.A1	NM_005559	NP_005550	P25391	LAMA1_HUMAN		21	CGGGAGCCAGC	0.542	
+	1	481		NM_001105581	NP_001099051	A6NM36	LRC30_HUMAN	LRR 4.	2	TCGCCGACCTC	0.572	
-	1	609	TEC_uc010xaj.1_	NM_001137671	NP_001131143	B2RU33	POTEC_HUMAN		3	TAAAGGAGTCG	0.592	
+	34	4489	r.2_Missense_Mu	NM_198129	NP_937762	Q16787	LAMA3_HUMAN		11	CAGCTCACATA	0.428	
+	54	7062	us.3_Missense_M	NM_198129	NP_937762	Q16787	LAMA3_HUMAN	II and I.|Potential.	11	AGAACGAAGAC	0.478	rs148831718
+	68	9012	s.3_Missense_M	NM_198129	NP_937762	Q16787	LAMA3_HUMAN		11	GCTCACCACTT	0.547	
+	6	1287	uu.2_Missense_M	NM_001135993	NP_001129465	Q8N584	TT39C_HUMAN		1	TGGTATCATACT	0.423	
+	4	505_506		NM_001942	NP_001933	Q02413	DSG1_HUMAN	(Potential).|Cadherin 1.	7	ATATGGGATCTT	0.386	
+	8	1178		NM_001942	NP_001933	Q02413	DSG1_HUMAN	(Potential).|Cadherin 3.	7	GAAATGAATGA	0.279	
+	4	356	wr.2_Missense_M	NM_177986	NP_817123	Q86SJ6	DSG4_HUMAN	|Extracellular (Potential).	8	GATTCGATCAGA	0.333	rs145443659
+	16	3211	r.2_Nonsense_Mu	NM_177986	NP_817123	Q86SJ6	DSG4_HUMAN	lasmic (Potential).	8	CATCTCGACAC	0.438	
-	19	2666		NM_001080467	NP_001073936	Q9ULV0	MYO5B_HUMAN	IQ 1.|IQ 2.	5	GCAGGGTTAAG	0.597	
+	26	4459	f.1_Missense_Mut	NM_005215	NP_005206	P43146	DCC_HUMAN	lasmic (Potential).	17	GGACCGAGGTT	0.478	
-	10	1315	_p.Q211*|TCF4_u	NM_003199	NP_003190	P15884	ITF2_HUMAN		2	AGGCTGATTCA	0.493	
-	9	1050		NM_005570	NP_005561	P49257	LMAN1_HUMAN	enal (Potential).	1	AATACGATTCT	0.373	
-	8	1217	RPINB3_uc010dq	NM_006919	NP_008850	P29508	SPB3_HUMAN		3	TAGTTGAAGTAG	0.468	
+	3	277	ljq.1_Missense_M	NM_005024	NP_005015	P48595	SPB10_HUMAN		3	ACAGAGACCAG	0.274	
+	6	661	xew.1_Missense_	NM_005024	NP_005015	P48595	SPB10_HUMAN		3	TTAAAGGAATCT	0.393	
-	2	2330		NM_032160	NP_115536	Q8IZU8	DSEL_HUMAN		6	CTAACCAATTT	0.408	
+	3	307		NM_001972	NP_001963	P08246	ELNE_HUMAN	eptidase S1.	1	CCTCTCGCGGC	0.687	
-	7	1272	orf29_uc002lyi.3_	NM_001080543	NP_001074012	Q8WUQ7	CS029_HUMAN		0	CCCCTTGAACA	0.632	
+	16	1983	RP2_uc010dua.2_	NM_001001520	NP_001001520	Q7Z4V5	HDGR2_HUMAN		0	CCAAGGTGTGG	0.662	
+	13	1289	0duj.1_Missense_	NM_152784	NP_689997	Q86XM0	TM146_HUMAN	ellular (Potential).	3	AGCTGGAATTG	0.428	
-	2	538	o.2_Missense_M	NM_002034	NP_002025	Q11128	FUT5_HUMAN	enal (Potential).	0	GACTCCATGCT	0.627	
-	4	952	n_p.R210Q|MIR2	NM_006087	NP_006078	P04350	TBB4_HUMAN		2	GGGCCCGGTAC	0.677	
-	12	1462		NM_000064	NP_000055	P01024	CO3_HUMAN		5	CCCCGGGTCTG	0.602	
+	25	2387	a.1_Missense_Mu	NM_005428	NP_005419	P15498	VAV_HUMAN	SH2.	16	AGTTCCCCTTC	0.542	
-	14	36955		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	tracellular (Potential).	57	GGAGCCAGTGC	0.557	
-	3	17768		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).	57	TGGATCCTGTT	0.498	
-	3	11255		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).	57	AGATGCTCATC	0.428	
-	1	4115		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).	57	CAGGTGAAGAC	0.493	
+	1	323		NM_001079935	NP_001073404	Q6IFN5	O7E24_HUMAN	ellular (Potential).	1	CAGCAGAGTCA	0.493	
+	21	3279	p.D999N|SMARC	NM_003072	NP_003063	P51532	SMCA4_HUMAN	p.?(1)	67	AGTGCGACATG	0.617	
+	6	713	dya.2_Missense_	NM_002743	NP_002734	P14314	GLU2B_HUMAN		0	AGAGTCCCTGC	0.577	
+	4	1055		NM_152357	NP_689570	Q8IYI8	ZN440_HUMAN	2H2-type 6.	0	ATGTTCGTATAC	0.403	
+	4	2033_2034	e_Mutation_p.Q65	NM_144566	NP_653167	Q9H0M5	ZN700_HUMAN	2H2-type 15.	0	CCTTCAGATGCA	0.426	
+	4	1515	ym.1_Missense_	NM_001136501	NP_001129973	Q08AG5	ZN844_HUMAN		0	CTTCAGATCTG	0.423	
+	4	1542	ym.1_Missense_	NM_001136501	NP_001129973	Q08AG5	ZN844_HUMAN		0	GCATGGAAGGA	0.433	
+	4	1602	ym.1_Missense_	NM_001136501	NP_001129973	Q08AG5	ZN844_HUMAN		0	TCATTTTTTCCA	0.448	
+	4	1710	ym.1_Missense_	NM_001136501	NP_001129973	Q08AG5	ZN844_HUMAN		0	GCATGAAAGGA	0.413	
-	4	1409	709_uc002mtx.3_	NM_144976	NP_659413	Q8TBZ8	ZN564_HUMAN	2H2-type 11.	1	AGGCTCTACCA	0.433	
+	5	676		NM_017682	NP_060152	Q8NFU1	BEST2_HUMAN	ellular (Potential).	2	TCTTTCACTATG	0.502	
+	15	1795		NM_014975	NP_055790	Q9Y2H9	MAST1_HUMAN	rotein kinase.	7	CGCGCCCGAGG	0.657	
-	3	291	_p.G48E|EMR3_u	NM_032571	NP_115960	Q9BY15	EMR3_HUMAN	(Potential).|EGF-like 1.	6	GTATATCCATGG	0.398	

+	7	801		NM_173483	NP_775754	Q6NT55	CP4FN_HUMAN		2	AGTCTTCAGAAA	0.458
+	1	854		NM_001004465	NP_001004465	Q8NGA5	O10H4_HUMAN	Name=7; (Potential).	2	TCACCCCCTTCC	0.453
-	7	863	26_uc002nee.2_	NM_145046	NP_659483	Q96L12	CALR3_HUMAN	te repeats.|P-domain.|2-2.	0	CTTCTGGTTTCA	0.483
-	6	544		NM_001080421	NP_001073890	Q9UPW8	UN13A_HUMAN		3	CTCTCCAGGGC	0.632
-	8	1432	ih.3_Missense_M	NM_001098819	NP_001092289	Q08493	PDE4C_HUMAN		5	TTGCTCCTCCT	0.602
-	10	3312	_Mutation_p.G105	NM_014884	NP_055699	Q8IX01	SUGP2_HUMAN	G-patch.	0	CTGCCCGTCAG	0.557
-	7	2920	_p.P925L|SFRS14	NM_014884	NP_055699	Q8IX01	SUGP2_HUMAN		0	CGCCGGGAAGG	0.542
+	4	808	nse_Mutation_p.	NM_017660	NP_060130	Q86YP4	P66A_HUMAN	Potential.	0	AGTTGCGGCAG	0.527
+	4	1534		NM_031218	NP_112495	P35789	ZNF93_HUMAN	2H2-type 12.	1	AAATTCATACTG	0.368
-	4	1505		NM_001159293	NP_001152765	C9JHM3	C9JHM3_HUMAN		1	TTATGTGTAGTA	0.413
-	6	3352	208_uc002nqo.1_	NM_007153	NP_009084				7	TTGTAGAGTTTC	0.378
-	5	2403	208_uc002nqo.1_	NM_007153	NP_009084				7	TTACCTTATGTTT	0.373
-	4	1501	1_Intron|ZNF208_	NM_007153	NP_009084				7	AGGGTGTCTCT	0.373
-	4	1333	1_Intron|ZNF208_	NM_007153	NP_009084				7	AGGGTTTCTCT	0.383
+	4	1302	cy.2_Missense_M	NM_033468	NP_258429	Q9Y2Q1	ZN257_HUMAN	2H2-type 8.	0	GTGTGGAAAAG	0.373
-	3	1025		NM_001001411	NP_001001411	Q8N7Q3	ZN676_HUMAN	2H2-type 3.	0	AGGATCGATTA	0.363
-	6	2203		NM_001080409	NP_001073878				2	ATGTTTTCTAAG	0.343
-	5	605		NM_001080409	NP_001073878				2	TTAAAAGCTTTG	0.353
-	4	460	rj.1_Missense_M	NM_003430	NP_003421	Q05481	ZNF91_HUMAN		0	TCATGTCCACAT	0.353
-	4	1567		NM_138330	NP_612203	Q8TD23	ZN675_HUMAN	2H2-type 12.	2	GATTGGATAAA	0.368
-	4	1635	_p.R429K|ZNF681_	NM_138286	NP_612143	Q96N22	ZN681_HUMAN	2H2-type 12.	0	TGAATTCTCTTAT	0.358
+	4	878		NM_002295	NP_002286				0	AGATTCTCCTCT	0.542
+	2	1243	dd.1_Missense_M	NM_014717	NP_055532	O15090	ZN536_HUMAN		11	ACAAAGACTCC	0.607
+	5	1810	q.1_Missense_M	NM_194325	NP_919306	P17039	ZNF30_HUMAN	2H2-type 13.	2	AAAATTCATACT	0.438
+	3	549	e_Mutation_p.E12	NM_001037	NP_001028	Q07699	SCN1B_HUMAN	Potential).|Ig-like C2-type.	2	ACTACGAGTGC	0.562
+	3	684	_Mutation_p.S10	NM_144694	NP_653295	Q96NI8	ZN570_HUMAN	KRAB.	1	GGTATCACTGG	0.413
+	9	2875		NM_015073	NP_055888	O60292	SI1L3_HUMAN	Rap-GAP.	2	CAAATCCGACG	0.567
+	18	2370	jb.1_Missense_M	NM_004924	NP_004915	O43707	ACTN4_HUMAN	EF-hand 1.	0	AGTTCCGGGCG	0.637
-	10	1486_1487	E>IK|RINL_uc01	NM_198445	NP_940847	Q6ZS11	RINL_HUMAN	VPS9.	1	GAGCTCCATAAG	0.624
+	7	780	mr.2_Missense_M	NM_006503	NP_006494	P43686	PRS6B_HUMAN		1	GGTCCGGGATG	0.562
-	5	927	mv.2_Missense_	NM_001005851	NP_001005851	Q9Y6R6	Z780B_HUMAN	2H2-type 5.	2	ACCACGATTAA	0.373
-	2	513_514	onv.3_Missense_	NM_013368	NP_037500	Q9UJW9	SRTD3_HUMAN		0	CTCGGGGGGC	0.663
+	12	1559	_Missense_Mutat	NM_001042544	NP_001036009	Q8N2S1	LTBP4_HUMAN	Pro-rich.	1	cccgatccccggcccg	0.463
+	7	1044	nse_Mutation_p.S	NM_021913	NP_068713	P30530	UFO_HUMAN	tential).|Fibronectin type-III	13	CACCTCGCAAG	0.647
+	2	413	2orj.1_Nonsense_	NM_004363	NP_004354	P06731	CEAM5_HUMAN	Ig-like 1.	2	GTGGTCGAGAG	0.453
+	27	2691	76L|ARHGEF1_u	NM_004706	NP_004697	Q92888	ARHG1_HUMAN		4	CGGCCCCCTGA	0.682
-	2	478	_p.G2E|PSG8_uc	NM_182707	NP_874366	Q9UQ74	PSG8_HUMAN	g-like V-type.	0	TCACCTCCCATT	0.473
-	2	332_333	art_Site|PSG8_uc	NM_182707	NP_874366	Q9UQ74	PSG8_HUMAN	g-like V-type.	0	TGTAATGTAATG	0.416
+	6	1590	p.S421F|ZNF221_	NM_013359	NP_037491	Q9UK13	ZN221_HUMAN		1	AAAAATCCTTCA	0.413
-	4	651	0ejp.1_Missense_	NM_001102597	NP_001096067	Q6UY09	CEA20_HUMAN	2.|Extracellular (Potential).	2	TTCTCGTGGTG	0.537
+	6	1426	2ozq.2_Missense_	NM_001039213	NP_001034302	A7LI12	A7LI12_HUMAN		1	CGTCACAGTGC	0.617
+	14	1692	se_Mutation_p.P4	NM_007056	NP_008987	Q8N2M8	CLASR_HUMAN	r-rich.|Arg-rich.	0	cagagccccTCGC	0.438
-	6	816		NM_001824	NP_001815	P06732	KCRM_HUMAN	en kinase C-terminal.	1	AAACCTCCTTCA	0.572
-	2	372	pcz.2_Nonsense_	NM_001080469	NP_001073938	Q6PJ61	FBX46_HUMAN		3	GGACTCGACCCT	0.642
-	4	1481		NM_002516	NP_002507	Q9UNW9	NOVA2_HUMAN		0	CGTAGGTGACC	0.562
-	15	3067	H4_uc002pgb.1_	NM_015168	NP_055983	Q9UPT8	ZC3H4_HUMAN		6	GCCGGGGGTCC	0.726
+	14	1326	BL2_uc010emn.1	NM_006666	NP_006657	Q9Y230	RUVB2_HUMAN		0	GTCCCGCTCCA	0.597

-	3	381	D2_uc002pni.2_Mi	NM_003598	NP_003589	Q15562	TEAD2_HUMAN	TEA.	3	TGTTTTCGAGTT	0.512	
+	1	320	)yct.1_Missense_M	NM_014441	NP_055256	Q9Y336	SIGL9_HUMAN	(Potential).|Ig-like V-type.	1	TGTGGGAGGAG	0.567	
-	5	1806	e_Mutation_p.I534	NM_001136499	NP_001129971	Q6ZN19	ZN841_HUMAN	:2H2-type 10.	0	GGTATGAATTCT	0.398	
-	4	2233_2234	p.N652S|ZNF28_u	NM_006969	NP_008900	P17035	ZNF28_HUMAN	:2H2-type 18.	1	CAAGGTTTGACA	0.406	
-	5	1439	k.1_Intron|ZNF816	NM_001031665	NP_001026835	Q0VGE8	ZN816_HUMAN	C2H2-type 6.	0	ATTTCTGACTGAA	0.398	
+	4	1386	'dw.1_Missense_M	NM_138374	NP_612383	Q96IR2	ZN845_HUMAN	C2H2-type 8.	0	TCAGATGTCATC	0.413	
+	4	1553	ydw.1_Missense_M	NM_138374	NP_612383	Q96IR2	ZN845_HUMAN	:2H2-type 10.	0	GTCAGACATCAT	0.378	
+	7	1680	p.K354Q|ZNF761_	NM_001008401	NP_001008401	Q86XN6	ZN761_HUMAN		1	GGAGAGAAACCT	0.368	
+	6	1483	eqr.1_Nonsense_M	NM_018555	NP_061025	Q9NQX6	ZN331_HUMAN	KRAB.	6	TTTCTCAGGAG	0.517	
-	3	762	2qcj.3_Missense_M	NM_144687	NP_653288	P59046	NAL12_HUMAN		7	GTCCCCGGCCT	0.647	
+	3	266	_p.R40C|MYADM_	NM_001020820	NP_001018656	Q96S97	MYADM_HUMAN	MARVEL 1.	1	CTCCTTCGCCTG	0.667	
+	11	1285	S238F|CNOT3_uc	NM_014516	NP_055331	O75175	CNOT3_HUMAN	Pro-rich.	3	CCCCTCCGGCC	0.687	
+	4	696	_p.P203S|LILRA2_	NM_001130917	NP_001124389	Q8N149	LIRA2_HUMAN	otential).|Ig-like C2-type 2.	1	AACTCTCCCTAT	0.577	
+	4	525	LRA1_uc010yfh.1_	NM_006863	NP_006854	O75019	LIRA1_HUMAN	1.|Extracellular (Potential).	3	CCCTGGAGCTG	0.627	
+	1	72	2qid.2_Splice_Site_	NM_004829	NP_004820	O76036	NCTR1_HUMAN		2	CGTCGGTGAGT	0.607	
-	5	1868		NM_176810	NP_789780	Q86W25	NAL13_HUMAN		9	ATAATTCCTCCAT	0.408	
-	5	820	my.2_Missense_M	NM_144690	NP_653291	Q96NG8	ZN582_HUMAN	C2H2-type 2.	4	CAGAATGAATATT	0.343	
-	7	4532	.A1365V|PEG3_uc	NM_001146186	NP_001139658	Q9GZU2	PEG3_HUMAN	Glu-rich.	12	TCAGCAGCCTCT	0.483	
+	4	2391		NM_020903	NP_065954	Q9HBJ7	UBP29_HUMAN		11	CTTGTCGAGGTT	0.468	rs143453181
+	5	1589	ense_Mutation_p.I4	NM_024691	NP_078967	Q96HQ0	ZN419_HUMAN		0	TTCACATTGGAG	0.428	
+	5	1629	nse_Mutation_p.L4	NM_024691	NP_078967	Q96HQ0	ZN419_HUMAN	:2H2-type 10.	0	GAGATTGTTTAG	0.428	
-	4	1609	ense_Mutation_p.E	NM_024833	NP_079109	Q8TAW3	ZN671_HUMAN		1	CCTTTCCCCAG	0.493	rs144165618
-	3	1206	NF552_uc010yhg.1	NM_024762	NP_079038	Q9H707	ZN552_HUMAN	C2H2-type 7.	0	CAGTGTGAACTC	0.463	
+	7	758	PO_uc002qwx.2_M	NM_000547	NP_000538	P07202	PERT_HUMAN	cellular (Potential).	20	ACAGATGATGAC	0.537	
+	5	426		NM_018436	NP_060906	Q8N6M5	ALLC_HUMAN		1	CTCCTCGAGTG	0.547	rs148726288
+	7	669		NM_018436	NP_060906	Q8N6M5	ALLC_HUMAN		1	ATTTTCCCAGGT	0.403	
+	3	601	e_Mutation_p.G76	NM_002149	NP_002140	P37235	HPCL1_HUMAN	nd 2.|1 (Potential).	1	CAACGGCGACG	0.597	rs149639705
-	8	1428	2rda.2_Splice_Site_	NM_001002006	NP_001002006	Q96P26	5NT1B_HUMAN		3	CTAATACCTTCT	0.378	
-	26	6612		NM_000384	NP_000375	P04114	APOB_HUMAN	eparin-binding.	27	TGGCATCATCTAA	0.294	
-	15	1725	OF_uc002rhi.2_5'F	NM_194248	NP_919224	Q9HC10	OTOF_HUMAN	lasmic (Potential).	7	CTGGGCCCAGT	0.617	
+	8	1904		NM_018158	NP_060628	Q9BWU0	NADAP_HUMAN		0	TCATGTCAGAAA	0.368	
-	1	745		NM_001029883	NP_001025054	A6NGG8	CB071_HUMAN		1	GATCCTCCCTGA	0.552	
-	16	1779	N13_uc002rnm.2_	NM_144575	NP_653176	Q6MZZ7	CAN13_HUMAN		2	GTCCCCTGGAG	0.592	
-	21	2392		NM_000379	NP_000370	P47989	XDH_HUMAN		8	GGTCTTCATGGT	0.562	
-	3	246_247		NM_000379	NP_000370	P47989	XDH_HUMAN	S ferredoxin-type.	8	TACTTGGAGAGC	0.535	
-	4	626	e_Mutation_p.H82Y	NM_015955	NP_057039	Q9Y316	MEMO1_HUMAN		2	GCACATGATGAG	0.378	
+	14	1200	_p.S365L|SLC30A	NM_017964	NP_060434	Q6NXT4	ZNT6_HUMAN	lasmic (Potential).	0	AATTTTCATTTAA	0.408	
-	9	3111	XN1_uc002rxe.3_M	NM_001135659	NP_001129131	P58400	NRX1B_HUMAN		2	TCAAATGATATGG	0.418	
-	4	1732	CL11A_uc010ypj.1	NM_022893	NP_075044	Q9H165	BC11A_HUMAN	Glu-rich.	13	.Gctcctcctcctcttc	0.433	
+	2	860	LC1A4_uc010fcv.2	NM_003038	NP_003029	P43007	SATT_HUMAN	cellular (Potential).	1	CTGTTTCCCTCC	0.274	
+	5	1157		NM_019002	NP_061875	Q9NY74	ETAA1_HUMAN		4	AAACCCCACGAT	0.358	
+	6	635		NM_019617	NP_062563	Q9NS71	GKN1_HUMAN		1	ACATTTCCTTCT	0.393	
-	11	1598	DD2_uc010fdt.1_M	NM_001617	NP_001608	P35612	ADDB_HUMAN		3	CCTGTTCTGTAG	0.468	
+	5	525	_p.V135I|ACTG2_	NM_001615	NP_001606	P63267	ACTH_HUMAN		0	ATGTACGTCGCC	0.448	
-	11	2066	nc.2_Missense_Mu	NM_133637	NP_598376	Q8TE96	DQX1_HUMAN		2	GGAGCTCTGCGG	0.507	
-	10	1958	nc.2_Missense_Mu	NM_133637	NP_598376	Q8TE96	DQX1_HUMAN		2	AAGTATCCTGAC	0.473	
+	11	1650	_p.R549*|CTNNA2	NM_004389	NP_004380	P26232	CTNA2_HUMAN		9	GCAGCTCGAGTC	0.502	

-	4	778	_p.D89N|ST3GAL5	NM_003896	NP_003887	Q9UNP4	SIAT9_HUMAN	enal (Potential).	0	AACATCGAACT	0.333	
-	4	543	sp.1_Missense_	NM_016618	NP_057702	Q9NPI7	KRCC1_HUMAN		1	GAATTAACCTCT	0.413	
-	13	2553		NM_004836	NP_004827	Q9NZJ5	E2AK3_HUMAN	Potential).|Protein kinase.	3	CAAAGGAGTGC	0.458	
-	5	1192	ud.1_Missense_M	NM_032788	NP_116177	Q96K75	ZN514_HUMAN	2H2-type 3.	0	GAGACGAACTC	0.418	
+	1	20		NM_001011717	NP_001011717	Q5H8A3	NMS_HUMAN		1	ATCTTCGTCCC	0.552	
+	2	182	se_Mutation_p.W1	NM_003855	NP_003846	Q13478	IL18R_HUMAN		3	CCTTTGGGTGC	0.343	
+	8	961	wd.1_Missense_	NM_003855	NP_003846	Q13478	IL18R_HUMAN	3.|Extracellular (Potential).	3	ACAGGACTCCA	0.408	
+	10	1342	wd.1_Missense_	NM_003855	NP_003846	Q13478	IL18R_HUMAN	oplasmic (Potential).	3	CTGTGGAGATT	0.433	
+	4	462	D4_uc002tdu.2_5	NM_182588	NP_872394	Q7Z3J3	RGPD4_HUMAN		2	CCCAGGAAGTC	0.323	
+	11	1571	.2_5'UTR|RGPD4_	NM_182588	NP_872394	Q7Z3J3	RGPD4_HUMAN		2	CCAGCCACTTA	0.318	
+	2	539_540	sense_Mutation_p.	NM_001056	NP_001047	O00338	ST1C2_HUMAN		1	CAACTGGAGCC	0.55	rs140199800
+	20	5780		NM_006267	NP_006258	P49792	RBP2_HUMAN		18	GTCAACCAAAG	0.358	
-	4	239	.1_Missense_Mut	NM_000576	NP_000567	P01584	IL1B_HUMAN		4	AGATTCGTAGC	0.627	
+	6	701	yyf.1_Splice_Site	NM_006770	NP_006761	Q9UEW3	MARCO_HUMAN		6	TTCCAGGCCCC	0.542	
+	10	1711	.3_Missense_Mut	NM_005270	NP_005261	P10070	GLI2_HUMAN		13	CCAACGAGGTA	0.627	
+	12	2029	.3_Missense_Mut	NM_005270	NP_005261	P10070	GLI2_HUMAN		13	GCAGCGAGCCC	0.662	
-	17	1807	5_splice|BIN1_uc	NM_139343	NP_647593	O00499	BIN1_HUMAN		7	GAGCTCTGGTG	0.672	
-	15	2389	of.1_Missense_M	NM_000122	NP_000113	P19447	ERCC3_HUMAN		7	TGCTCCGCGAT	0.582	
-	3	673		NM_001099771	NP_001093241	A5A3E0	POTEF_HUMAN		5	TGTCTTCATAGC	0.617	
-	1	1178		NM_001077637	NP_001071105	Q53S08	Q53S08_HUMAN		0	AGCAATGATGAA	0.378	
-	11	4665		NM_002299	NP_002290	P09848	LPH_HUMAN	ial).|4.|4 X approximate re	13	AGCTGCTGTTC	0.512	
+	2	70	.1_RNA|THSD7B_	NM_001080427	NP_001073896				7	CAGGAGACTGT	0.488	
-	90	14533		NM_018557	NP_061027	Q9NZR2	LRP1B_HUMAN		50	tacctggcctgtatata	0.08	
-	8	1451	e_Mutation_p.S29	NM_014795	NP_055610	O60315	ZEB2_HUMAN	2-type 4; atypical.	9	TGTAGGAACCA	0.373	
+	4	711		NM_004522	NP_004513	O60282	KIF5C_HUMAN	inesin-motor.	1	CCCATGATATC	0.493	
-	103	15219	2_Missense_Muta	NM_004543	NP_004534	P20929	NEBU_HUMAN	Nebulin 137.	20	TCTCCGGACGT	0.423	
+	7	1395	0foc.1_Missense_	NM_052917	NP_443149	Q8IUC8	GLT13_HUMAN	enal (Potential).	6	GACAGGAGGAA	0.373	
+	1	586	.NT5_uc010zci.1_	NM_014568	NP_055383	Q7Z7M9	GALT5_HUMAN	enal (Potential).	4	AGAGGGAAAGA	0.527	
-	8	1076	cl.1_Missense_Mu	NM_004288	NP_004279	O60759	CYTIP_HUMAN		3	CACTTCCCTTT	0.502	
-	31	4553	.G1495E|LY75_uc	NM_002349	NP_002340	O60449	LY75_HUMAN	Potential).|C-type lectin 9.	0	AAGTTCCTTTT	0.348	
-	12	1844	s.2_Missense_Mu	NM_002349	NP_002340	O60449	LY75_HUMAN	Potential).|C-type lectin 3.	0	GGGAAGCTGG	0.428	
-	3	1623		NM_018086	NP_060556	Q5HY92	FIGN_HUMAN		4	AGAGAGGAGCT	0.517	
-	3	1540		NM_018086	NP_060556	Q5HY92	FIGN_HUMAN		4	CCAATGAATTT	0.498	
-	4	557	n_p.P7L|SLC38A	NM_173512	NP_775783	Q08AI6	S38AB_HUMAN	lasmic (Potential).	1	CCAAAGGAAAC	0.338	
-	13	2186	p.S565F|SCN3A_	NM_006922	NP_008853	Q9NY46	SCN3A_HUMAN		10	ACAGGGAGCCA	0.408	
+	26	5071	.W1594*|SCN2A_	NM_001040142	NP_001035232	Q99250	SCN2A_HUMAN	3 of repeat IV; (Potential).|	8	TTGGATGGAATA	0.333	
-	16	3079	_p.E901K|SCN1A_	NM_006920	NP_008851	P35498	SCN1A_HUMAN		13	TAAATTCATATAT	0.323	
-	11	1973	_p.S521F|SCN1A_	NM_006920	NP_008851	P35498	SCN1A_HUMAN		13	CCAAGGAAACC	0.493	
+	8	6112	e_Mutation_p.R18	NM_152381	NP_689594	A4UGR9	XIRP2_HUMAN		14	TAGATCGTGAA	0.388	
+	8	6820	se_Mutation_p.E2	NM_152381	NP_689594	A4UGR9	XIRP2_HUMAN		14	CAATGGAAAGG	0.418	
-	48	9202		NM_004525	NP_004516	P98164	LRP2_HUMAN	A 23.|Extracellular (Poten	29	TGAATTCATTTT	0.468	
-	10	1280	lf.1_Missense_Mu	NM_004525	NP_004516	P98164	LRP2_HUMAN	Extracellular (Potential).	29	CAAATTCCCCAT	0.423	
+	6	1797	ense_Mutation_p.	NM_144711	NP_653312	Q8NBE8	KLH23_HUMAN	Kelch 5.	0	AAAATGAATGG	0.418	rs149127224
+	2	1374	_Mutation_p.W68	NM_019558	NP_062458	P13378	HXD8_HUMAN	Homeobox.	0	AAATGGAAAAA	0.502	
-	8	1952	ls.1_Missense_M	NM_016953	NP_058649	Q9HCR9	PDE11_HUMAN	GAF 2.	4	AAAGTCGTTGA	0.378	
+	22	2707	.E746K|OSBPL6_	NM_032523	NP_115912	Q9BZF3	OSBL6_HUMAN		1	TGAATGAAGTC	0.448	
-	299	90093	52N|TTN_uc010z	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	GTCATCCTCTG	0.478	

-	281	81321	28R|TTN_uc010zf	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	CATTTCCTTTGAT	0.453
-	275	78339	34N|TTN_uc010zf	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	TTAGATCATAAAC	0.398
-	275	67530	31C|TTN_uc010zf	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	GGTCACGAGCCA	0.473
-	275	63658	40E|TTN_uc010zf	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	ACCTCTCCTACA	0.403
-	267	59629	_uc010zfi.1_Misse	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	AAGCAGAGTCTT	0.398
-	264	58748	203*|TTN_uc010zf	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	GGCTTCCAGCT	0.468
-	238	48616	826E|TTN_uc010z	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	TTGGTTCCTTCTT	0.378
-	228	46218	_uc010zfi.1_Misse	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	GTTTTTCAATGA	0.438
-	220	43909	_uc010zfi.1_Misse	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	ATTCTCCTCCAC	0.398
-	191	37215	.1_Missense_Muta	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	CAATTTCATACTT	0.408
-	188	36708	.1_Missense_Muta	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	AAGGGAGTGTA	0.398
-	179	34677	.1_Missense_Muta	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	AAGTTCGATTT	0.453
-	64	16107	_uc010zfj.1_Intro	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	AACTTCCAGAGA	0.393
-	63	15836	N_uc010zfj.1_Intro	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	TGCTTCATTACT	0.408
-	47	11262	N_uc010zfj.1_Intr	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	CCCATCTTTGCT	0.413
-	46	14103	N_uc010zfi.1_Intr	NM_133379	NP_596870	Q8WZ42	TITIN_HUMAN		153	CTGGATCTCCTA	0.378
-	46	11988	N_uc010zfi.1_Intr	NM_133379	NP_596870	Q8WZ42	TITIN_HUMAN		153	TCTGTTCGGTTTT	0.338
-	14	2565	1_Missense_Muta	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	TTTGATCAGTAG	0.478
-	10	1517		NM_173648	NP_775919	Q6ZP82	CC141_HUMAN		10	GCACTGAGGGT	0.433
-	7	700		NM_178123	NP_835224	Q86VW0	SESD1_HUMAN		1	TATCACTTCCATT	0.299
-	5	1097	F385B_uc002unl.	NM_152520	NP_689733	Q569K4	Z385B_HUMAN	atrin-type 2.	1	AAAGCGAAGCT	0.353
-	3	253	zfq.1_Missense_	NM_001003683	NP_001003683	P54750	PDE1A_HUMAN		3	CATATTCAATATT	0.373
+	4	3889		NM_194250	NP_919226	Q7Z570	Z804A_HUMAN		11	ACTATCCATCAC	0.358
-	7	891		NM_182521	NP_872327	Q8NEG5	ZSWM2_HUMAN		3	TCTAGTGATCTC	0.323
+	48	3880		NM_000090	NP_000081	P02461	CO3A1_HUMAN	lar collagen NC1.	13	GTTCTCGTAAA	0.398
-	54	4716	x.2_Missense_Mu	NM_000393	NP_000384	P05997	CO5A2_HUMAN	lar collagen NC1.	2	AACATCCACAG	0.453
-	22	2376	sk.2_Missense_M	NM_007315	NP_009330	P42224	STAT1_HUMAN	SH2.	10	TCAGGGGATTCT	0.448
-	42	7617		NM_018897	NP_061720	Q8WXX0	DYH7_HUMAN	4 (By similarity).	12	ATCTTCAGGCC	0.408
-	41	7554		NM_018897	NP_061720	Q8WXX0	DYH7_HUMAN	4 (By similarity).	12	AAGACGATTCC	0.428
-	41	7029		NM_018897	NP_061720	Q8WXX0	DYH7_HUMAN	4 (By similarity).	12	TCATGGGTTTTT	0.433
-	36	6062		NM_018897	NP_061720	Q8WXX0	DYH7_HUMAN		12	TACTTACCGTAA	0.338
+	4	1570	ftr.2_Missense_M	NM_001204	NP_001195	Q13873	BMPR2_HUMAN	ellular (Potential).	9	AGGTCCACCTC	0.234
+	7	955	p.E250K|PARD3B	NM_152526	NP_689739	Q8TEW8	PAR3L_HUMAN	PDZ 1.	4	TTCACGAAAAT	0.348
+	5	5225		NM_020923	NP_065974	Q9HCK1	ZDBF2_HUMAN		3	GCTGTGGATAT	0.393
-	7	542		NM_001099334	NP_001092804	Q0P641	CB080_HUMAN		1	TCGGGGAACCT	0.468
-	3	416	b.2_Missense_M	NM_079420	NP_524144	P05976	MYL1_HUMAN		1	GGTTTCCCAGA	0.408
-	23	2871_2872	zji.1_Missense_M	NM_005235	NP_005226	Q15303	ERBB4_HUMAN	.|Cytoplasmic (Potential).	33	GCGTTGGAATTC	0.381
-	15	1895_1896	_p.A600T|ERBB4_	NM_005235	NP_005226	Q15303	ERBB4_HUMAN	ar (Potential).|Cys-rich.	33	GTTTGCCCCCTG	0.47
+	10	3008		NM_005876	NP_005867	Q15772	SPEG_HUMAN	Ig-like 4.	14	GCTGTGCCGTG	0.622
+	37	8969		NM_005876	NP_005867	Q15772	SPEG_HUMAN	otein kinase 2.	14	GGGGCGAACGT	0.672
-	43	4784		NM_000092	NP_000083	P53420	CO4A4_HUMAN	e-helical region.	11	GGATTCGGGGA	0.582
+	8	788	e_Mutation_p.G22	NM_178821	NP_849143	Q8N136	WDR69_HUMAN	WD 4.	1	TCACGGGGTCT	0.418
-	7	818	_p.W257*|SPHKA	NM_001142644	NP_001136116	Q2M3C7	SPKAP_HUMAN		10	CAATTCCATTC	0.383
+	8	872_873	qn.2_Intron|SP14	NM_007237	NP_009168	Q13342	LY10_HUMAN		0	GCAACGGGATG	0.446
+	1	835	vur.2_Intron|UGT1	NM_019077	NP_061950	Q9HAW7	UD17_HUMAN		1	GTCATCAGGGA	0.388
+	3	955		NM_001080504	NP_001073973	Q6ZP01	RBM44_HUMAN		4	GAATATCATGAC	0.353
-	11	1089	_p.L315F|KIF1A_u	NM_004321	NP_004312	Q12756	KIF1A_HUMAN	inesin-motor.	1	CCGGAGGAGCC	0.567

+	15	2286	ml.2_Missense_M	NM_032485	NP_115874	Q9UJA3	MCM8_HUMAN		1	CTTCCGTACTTG	0.373	rs141935061
-	5	2061		NM_152611	NP_689824	Q8WUT4	LRRN4_HUMAN	tential).|Fibronectin type-II	3	GTAGCGGATCT	0.701	
+	18	1847	p.W615*|PLCB1_	NM_015192	NP_056007	Q9NQ66	PLCB1_HUMAN	I-PLC Y-box.	12	TCTTCTGGAATG	0.413	
+	30	2980	0_splice|PLCB4_	NM_182797	NP_877949	Q15147	PLCB4_HUMAN		15	CAAAGGTACAG	0.333	
-	3	1683	2wou.2_Intron|FL	NM_198391	NP_938205	Q9NZU0	FLRT3_HUMAN	tential).|Fibronectin type-II	1	TGAGGGACTCC	0.458	
-	7	721	ci.1_Missense_M	NM_024704	NP_078980	Q96L93	KI16B_HUMAN	inesin-motor.	8	TGTTTGGATAAAT	0.398	
+	6	1563_1564	_p.S186C|CSRP2	NM_020536	NP_065397	Q9H8E8	CSR2B_HUMAN		6	TTCCTCCTTGAG	0.52	
+	2	778	p.S242T|PAX1_uc	NM_006192	NP_006183	P15863	PAX1_HUMAN		2	CGCCGTCGCAG	0.667	
-	14	1842	_p.P590S|NINL_uc	NM_025176	NP_079452	Q9Y2I6	NINL_HUMAN		5	ATCCGGGCTCC	0.687	
+	1	63	G1B_uc010ztj.1_RNA|FRG1B_uc010gdr.1_RNA						0	TTGATACGTTGG	0.219	rs62197050
+	3	222	RG1B_uc010gdr.1_RNA|FRG1B_uc010ztk.1_Missense_Mutation_p.A16T						0	ATGAAGCAGGG	0.373	
+	3	1598		NM_001011718	NP_001011718	Q5GH72	XKR7_HUMAN		3	CAGGTCCCTGC	0.682	
+	22	2347		NM_020884	NP_065935	A7E2Y1	MYH7B_HUMAN	osin head-like.	2	GATCCGGATCT	0.632	
-	2	1678	_Missense_Mutati	NM_000557	NP_000548	P43026	GDF5_HUMAN		0	GAGTTCATCAG	0.597	
+	16	1599	wb.1_Missense_M	NM_021931	NP_068750	Q9H5Z1	DHX35_HUMAN		3	AGTCTCACGCA	0.473	
-	16	2597	_p.D824N|PTPRT	NM_007050	NP_008981	O14522	PTPRT_HUMAN	lasmic (Potential).	20	TTTGTCGGCAG	0.557	
+	8	870	2_Missense_Muta	NM_015478	NP_056293	Q9Y468	LMBL1_HUMAN	MBT 1.	0	CTGGTCGTGGG	0.532	rs143835872
+	2	1171	R312S|SEMG2_uc	NM_003007	NP_002998	P04279	SEMG1_HUMAN	AA repeat 2.	2	TCCCAACGCAGT	0.418	
+	2	1198	_p.Q381K|SEMG2_	NM_003008	NP_002999	Q02383	SEMG2_HUMAN	X 60 AA tandem repeats,	1	GAAGAGCAAATA	0.388	
-	6	943	xsg.1_Missense_	NM_022829	NP_073740	Q8WWT9	S13A3_HUMAN	lasmic (Potential).	1	GTCCCCCGTAC	0.502	
-	3	817_818	_p.T156N|SPATA2	NM_001135773	NP_001129245	Q9UM82	SPAT2_HUMAN		2	TGGAGGGTCTCC	0.535	
-	12	1157	_Mutation_p.S25	NM_006045	NP_006036	O75110	ATP9A_HUMAN	lasmic (Potential).	4	AGTACGAAATC	0.552	
+	2	1516		NM_173485	NP_775756	Q9NRE2	TSH2_HUMAN		6	CGTCTCGAAAC	0.557	
-	3	1253	p.N242H|BMP7_u	NM_001719	NP_001710	P18075	BMP7_HUMAN		1	CAGGTTGTGCC	0.637	
+	5	543		NM_020673	NP_065724	Q9UL26	RB22A_HUMAN		0	CATTTTCAACAT	0.353	
+	7	847_848	ah.1_Nonsense_	NM_144498	NP_653081	Q9H1P3	OSBL2_HUMAN		2	GAGCCCCGAGG	0.579	
+	1	790		NM_002531	NP_002522	P30989	NTR1_HUMAN	ellular (Potential).	4	CGCCGGCTGCC	0.687	
-	16	4178	ls.1_Missense_Mu	NM_033081	NP_149072	Q9BTC0	DIDO1_HUMAN		6	CAGACGAAGCG	0.597	
+	4	714	_uc002yei.2_Miss	NM_139317	NP_647478	Q96CA5	BIRC7_HUMAN		3	CGTGGGAAGAA	0.672	
-	7	2946	yfl.1_Missense_M	NM_001037335	NP_001032412	Q9BYK8	PR285_HUMAN		2	CGTGCGAGGCA	0.697	
-	8	573	e_Mutation_p.E51	NM_199261	NP_954870	P56180	TPTE_HUMAN		5	CATCTTCAACTT	0.343	rs141287188
+	15	2155	cb.1_Missense_M	NM_004540	NP_004531	O15394	NCAM2_HUMAN	III 2.|Extracellular (Potentia	4	ATAAGGAAGAC	0.348	
-	1	13		NM_012131	NP_036263	P56750	CLD17_HUMAN	lasmic (Potential).	2	CAAGGGATAAA	0.478	
+	5	647	1ado.1_Missense	NM_178817	NP_848932	Q8TCY5	MRAP_HUMAN	ellular (Potential).	0	CCCTCGTCAGG	0.602	
-	1	196	t_Site|C21orf59_u	NM_021254	NP_067077	P57076	CU059_HUMAN		0	GCACCGTGAGC	0.682	
+	3	1428	_Mutation_p.S460	NM_138927	NP_620305	P18583	SON_HUMAN		6	ACCATCCATGG	0.617	
+	38	5078	tj.2_Missense_Mu	NM_003024	NP_003015	Q15811	ITSN1_HUMAN	C2.	4	TGGTTGAAGGC	0.557	
+	6	768	eb.1_Missense_	NM_005128	NP_005119	Q9Y3R5	DOP2_HUMAN		2	TGAAGTCTTTGC	0.403	
+	4	1223	_p.W307*|KCNJ15	NM_002243	NP_002234	Q99712	IRK15_HUMAN	smic (By similarity).	6	TACTGGGGTTT	0.463	
-	21	4158	AM_uc002yyr.1_	NM_001389	NP_001380	O60469	DSCAM_HUMAN	III 4.|Extracellular (Potentia	11	AAACTCGCTGA	0.453	
-	20	4060	AM_uc002yyr.1_	NM_001389	NP_001380	O60469	DSCAM_HUMAN	III 4.|Extracellular (Potentia	11	CCATGGAGGCT	0.577	
-	9	2262	AM_uc002yyr.1_	NM_001389	NP_001380	O60469	DSCAM_HUMAN	otential).|Ig-like C2-type 7.	11	TGGAAACTCAA	0.468	
+	6	906	E_uc002zej.2_5'F	NM_000383	NP_000374	O43918	AIRE_HUMAN	SAND.	1	CAAGGGAGCCC	0.667	
-	1	242	.1_Intron|C21orf29	NM_181686	NP_859014	P59990	KR121_HUMAN	approximate repeats.	2	GGAGGGAGCCG	0.647	
-	3	400	_Mutation_p.P54L	NM_194255	NP_919231	P41440	S19A1_HUMAN	lasmic (Probable).	0	GCACCGGCGTG	0.647	
+	21	1703	6A2_uc002zhz.1_	NM_001849	NP_001840	P12110	CO6A2_HUMAN	(Potential).|Triple-helical re	8	CGAGGCGACTTT	0.557	rs138276378
+	3	600	e_Mutation_p.P47	NM_006031	NP_006022	O95613	PCNT_HUMAN		8	ACCACCCACCA	0.547	

-	1	1078		NM_014406	NP_055221	Q96SF2	TCPQM_HUMAN			1	TCGCTTCCTTTA	0.522	
-	5	815	NB1L_uc002zqf.1_	NM_053004	NP_443730	Q9BYB4	GNB1L_HUMAN			1	AATCTGAACCT	0.557	
-	9	2067	qy.2_Missense_M	NM_001670	NP_001661	O00192	ARVC_HUMAN	ARM 6.		1	CCAGGGGCCCG	0.662	
-	2	1475	ru.2_Missense_M	NM_023004	NP_075380	Q9BZR6	RTN4R_HUMAN			0	TGCGGGTGCG	0.721	
+	5	345	1_Missense_Muta	NM_012295	NP_036427	Q9Y6J0	CABIN_HUMAN			5	AGTTTCATCCG	0.522	
+	43	7424	D18B_uc011aka.1_	NM_032608	NP_115997	Q8IUG5	MY18B_HUMAN			12	CTGTGGACGAT	0.597	
+	43	7449	D18B_uc011aka.1_	NM_032608	NP_115997	Q8IUG5	MY18B_HUMAN			12	CCTTGGAAAGG	0.597	
-	15	2594	wp.2_Missense_M	NM_004737	NP_004728	O95461	LARGE_HUMAN	enal (Potential).		3	ACCTCCGGTCG	0.577	rs145736519
-	4	645	aqe.2_Missense_	NM_001163857	NP_001157329	O43247	EAN57_HUMAN			0	AATAGCCTTTTG	0.542	
-	2	208	_p.E23K|TMPRSS	NM_153609	NP_705837	Q8IU80	TMPS6_HUMAN	lasmic (Potential).		6	CGGCTCCGCTT	0.662	
-	2	192_193	2G6_uc003avb.2_	NM_003560	NP_003551	O60733	PA2G6_HUMAN			1	GGGTTAGAGAA	0.594	
+	30	3761	issense_Mutation	NM_152513	NP_689726	Q5TIA1	MEI1_HUMAN			2	GCCTTCCCCCT	0.602	
-	16	1988		NM_173050	NP_766638	Q8IWY4	SCUB1_HUMAN			5	AGGCCCACAGG	0.622	
-	22	2817	AB6_uc010gzi.1_	NM_022785	NP_073622	Q5THR3	EFCB6_HUMAN	EF-hand 9.		7	GCGTCGAAGAA	0.438	
-	2	245	fw.1_Missense_M	NM_001009880	NP_001009880	Q6ICG6	K0930_HUMAN			0	AGTACGCCAGC	0.617	
-	3	807	aa.2_Missense_M	NM_058238	NP_478679	P56706	WNT7B_HUMAN			1	GCCCTCGGCTT	0.687	
-	2	158		NM_001080447	NP_001073916					2	CATCCGGAATG	0.597	
+	16	2287	.R602C|CNTN6_	NM_014461	NP_055276	Q9UQ52	CNTN6_HUMAN	nectin type-III 1.		8	AATTTCGTGTTG	0.393	rs147761774
+	8	2054	_p.P594S|GRM7_	NM_000844	NP_000835	Q14831	GRM7_HUMAN	Name=1; (Potential).		7	GTGATTCCTGTC	0.547	
-	2	268	va.1_Missense_	NM_173472	NP_775743	Q96PS1	CC024_HUMAN			0	ACTCTCATCCA	0.537	
+	2	802	dt.2_Missense_Mu	NM_001098213	NP_001091683	P35367	HRH1_HUMAN	Name=4; (Potential).		2	TGGTTTCTCTCT	0.542	
+	10	2025	xj.2_Missense_M	NM_001162499	NP_001155971	O75155	CAND2_HUMAN	HEAT 14.		4	GGCCTCATTCCT	0.667	
+	12	3239	xj.2_Missense_Mu	NM_001162499	NP_001155971	O75155	CAND2_HUMAN	HEAT 23.		4	AGATCCGGCGG	0.582	
-	36	5178		NM_024923	NP_079199	Q8TEM1	PO210_HUMAN	enal (Probable).		11	TCAAAAGGATTT	0.607	rs137867919
-	25	3483		NM_024923	NP_079199	Q8TEM1	PO210_HUMAN	enal (Probable).		11	GTTCCCGATGG	0.473	rs149480023
+	12	723	f.1_RNA|SLC6A6_	NM_001134367	NP_001127839	P31641	SC6A6_HUMAN	ellular (Potential).		1	GCCTGGGCCAC	0.537	
+	2	926	dq.2_Missense_	NM_052953	NP_443185	Q96PB8	LRC3B_HUMAN			4	TAGCTGAAACC	0.448	
-	13	1365	fj.2_Missense_Mutation_p.S322F			Q6ZWH5	NEK10_HUMAN		p.E379K(1)	13	AAGAGGGATTTC	0.323	
+	2	1963		NM_001137674	NP_001131146	A6NHJ4	ZN860_HUMAN	2H2-type 9.		1	GTAATTCATAAG	0.408	
+	2	238	TAC_uc011aya.1_	NM_003149	NP_003140	Q99469	STAC_HUMAN			4	ACAGCGAAGAC	0.532	
-	12	4722		NM_014831	NP_055646	O15050	TRNK1_HUMAN			2	TGCTTCGTAGA	0.557	
-	15	2512	p.P773L|SCN5A_	NM_198056	NP_932173	Q14524	SCN5A_HUMAN			9	AGTAGGGGTCG	0.532	
-	27	5365		NM_006514	NP_006505	Q9Y5Y9	SCNAA_HUMAN			10	CAGGTCCATCT	0.468	
-	23	4136		NM_014139	NP_054858	Q9UI33	SCNBA_HUMAN			9	CTGTTGGTTGA	0.358	
-	1	456		NM_014139	NP_054858	Q9UI33	SCNBA_HUMAN			9	GATTTCGGTAG	0.428	
-	2	1513	e_Mutation_p.R43	NM_194293	NP_919269	Q702N8	XIRP1_HUMAN			8	CATCCCTCTGG	0.562	rs149251137
+	13	1962		NM_003241	NP_003232	P49221	TGM4_HUMAN			1	CATCTCCTCAC	0.383	
+	3	1504		NM_001123041	NP_001116513	P41597	CCR2_HUMAN	lasmic (Potential).		2	ACCAGGAAAGA	0.493	
-	9	1117	.2_Missense_Muta	NM_002343	NP_002334	P02788	TRFL_HUMAN			4	CACGCCGGGCA	0.667	
+	5	8258		NM_003458	NP_003449	Q9UPA5	BSN_HUMAN			8	GGAGAGCCTGG	0.652	
+	35	3571	123_uc003cxi.2_	NM_022064	NP_071347	Q5XPI4	RN123_HUMAN			7	GGTGCGTGGCC	0.582	
+	6	2851	se_Mutation_p.S2	NM_000839	NP_000830	Q14416	GRM2_HUMAN	lasmic (Potential).		1	GTCATCGCTTT	0.587	
+	38	3274		NM_018398	NP_060868	Q8IZS8	CA2D3_HUMAN	ical; (Potential).		7	AAGCCCAGACA	0.517	
-	11	2465	t.1_Missense_Mu	NM_015576	NP_056391	O15083	ERC2_HUMAN	Potential.		2	ATTCTCCACCT	0.478	
-	7	1817	2_uc003dht.1_5'U	NM_015576	NP_056391	O15083	ERC2_HUMAN	Potential.		2	TGTCCCCTTCT	0.393	
-	6	695	diu.2_Missense_M	NM_178504	NP_848599	Q6ZR08	DYH12_HUMAN	n (By similarity).		2	CTCCTTCATCTT	0.313	
-	3	372	RIG1_uc010hoa.2_	NM_015541	NP_056356	Q96JA1	LRIG1_HUMAN	lar (Potential).|LRR 3.		5	AAAGAGAGAGA	0.488	

-	15	2088		NM_020872	NP_065923	Q9P232	CNTN3_HUMAN	onectin type-III 1.	5	ATATTCCACCCA	0.438	
-	7	990	M86D_uc003dpq.	NR_024241					0	TAGCTCGGTGG	0.652	
+	1	704		NM_001005515	NP_001005515	A6NDH6	O5H15_HUMAN	lasmic (Potential).	2	GTGTAAGGAAAG	0.418	
+	1	432		NM_001005517	NP_001005517	A6NMS3	OR5K4_HUMAN	Name=4; (Potential).	1	CGGATGACCAC	0.468	
-	5	3768	on_p.K678I|FILIP1	NM_182909	NP_878913	Q4L180	FIL1L_HUMAN		1	GTTGTTTTGTTTA	0.448	
+	14	1814	bik.1_Missense_M	NM_001690	NP_001681	P38606	VATA_HUMAN		3	TTTCCTCCATGA	0.299	
-	7	1318	D3_uc003ebb.1_In	NM_000796	NP_000787	P35462	DRD3_HUMAN	Cytoplasmic.	4	GTTTTCGAACTT	0.532	
+	3	1592		NM_016298	NP_057382	Q9UH90	FBX40_HUMAN		5	CCACAGCGAGT	0.522	
+	11	831	A5_uc003egd.1_In	NM_006810	NP_006801	Q14554	PDIA5_HUMAN	hioredoxin 1.	1	CCAGTCCGCAG	0.612	
-	8	1220	_p.P240S|SLCO2A	NM_005630	NP_005621	Q92959	SO2A1_HUMAN	lasmic (Potential).	1	GCATGGAAACC	0.592	
-	4	342	1_Missense_Muta	NM_178554	NP_848649	Q8NBH2	KY_HUMAN		2	GGACTTCCACAG	0.488	
+	9	1301	T3_uc010hug.2_	NM_031913	NP_114119	A0FGR9	ESYT3_HUMAN	C2 1.	0	GGAACGAAGTG	0.582	
+	1	469		NM_152616	NP_689829	Q8IWZ5	TRI42_HUMAN	Cys-rich.	7	TGAGAGCCGCT	0.562	
-	38	6557	y.1_Missense_Mu	NM_001184	NP_001175	Q13535	ATR_HUMAN	FAT.	20	AGAGATCAATTG	0.338	
-	8	998	vw.1_Missense_M	NM_020359	NP_065092	Q9NRY7	PLS2_HUMAN	llular (By similarity).	0	CTAGTTCTTTCAA	0.343	
-	6	6577	p.H220Y|IGSF10_	NM_178822	NP_849144	Q6WRI0	IGS10_HUMAN	like C2-type 8.	13	TGGCATGAAATG	0.443	
-	4	1395		NM_178822	NP_849144	Q6WRI0	IGS10_HUMAN	like C2-type 1.	13	GGCCTCATCTC	0.448	
-	3	1408	fao.1_Missense_M	NM_004733	NP_004724	O00400	ACATN_HUMAN	ellular (Potential).	4	AATGTTCTTTGG	0.383	
-	4	355	se_Mutation_p.W1	NM_024687	NP_078963	A8MT70	ZBBX_HUMAN		2	TTTCCCCATGGA	0.279	
-	5	1014	p.G329E|SERPIN	NM_006217	NP_006208	O75830	SPI2_HUMAN		3	GTTATTCCAGAA	0.303	
-	2	632	ECOM_uc010hwn.	NM_004991	NP_004982	Q03112	EVI1_HUMAN		14	AGCAGGAATGG	0.478	
-	2	281	wp.1_Nonsense_	NM_024727	NP_079003	Q6UY01	LRC31_HUMAN		3	GGATCTCCATTC	0.383	
-	5	698	C39_uc003fkn.2_	NM_181426	NP_852091	Q9UFE4	CCD39_HUMAN	Potential.	4	TAAGTTCGTTGT	0.308	
+	19	2322	R273*|ATP11B_uc	NM_014616	NP_055431	Q9Y2G3	AT11B_HUMAN	lasmic (Potential).	3	AAAGTTCGAGAA	0.323	
+	13	1778	AP2_uc003fuv.2_RNA						0	TGAGGTGCACT	0.567	rs6583274
+	13	1780	AP2_uc003fuv.2_RNA						0	AGGTGCACTGG	0.567	rs6583275
-	2	6966	C4_uc003fvp.2_Int	NM_018406	NP_060876	Q99102	MUC4_HUMAN		0	TGGATGCTGAG	0.572	
+	2	247	1btu.1_Missense_	NM_152672	NP_689885	Q86UW1	OSTA_HUMAN		1	TACACAGCAGAT	0.617	
-	3	603	732_uc010ibb.1_I	NM_001137608	NP_001131080	B4DXR9	ZN732_HUMAN	type 3; degenerate.	0	ATTCTTCACATG	0.363	
+	5	1197	141_uc003gab.2_	NM_003441	NP_003432	Q15928	ZN141_HUMAN	C2H2-type 7.	0	CCTACACATGTG	0.408	
+	1	3043		NM_175918	NP_787114	Q8N1N5	CRPAK_HUMAN		0	ATGTGCCCATG	0.582	
-	3	1399	se_Mutation_p.S3	NM_024511	NP_078787	Q68CZ6	HAUS3_HUMAN	Potential.	4	TCATATGATAACT	0.299	
+	8	871	gfk.3_Missense_M	NM_001122681	NP_001116153	P78314	3BP2_HUMAN		1	TGGCTGCTGAG	0.682	
+	2	2000	vr.1_RNA|RGS12_	NM_198229	NP_937872	O14924	RGS12_HUMAN		1	CGGCCGACCCA	0.577	
-	10	1762	KMIP1_uc011bwc.	NM_144720	NP_653321	Q96N16	JKIP1_HUMAN	ith TYK2 and GABBR1.|P	4	GGCCTGGTACT	0.612	
+	8	2151	_p.S662F|WFS1_u	NM_001145853	NP_001139325	O76024	WFS1_HUMAN		2	CAACTCCACAC	0.617	
-	1	1405	3_5'Flank|TADA2B	NM_153376	NP_699207	Q2M329	CCD96_HUMAN		0	CTTTTCCTTCA	0.478	
+	13	1678	wi.1_Missense_M	NM_020777	NP_065828	Q96PQ0	SORC2_HUMAN	enal (Potential).	2	TTTGAGGAAGAG	0.577	
+	6	1094	.R186Q|CPZ_uc	NM_001014447	NP_001014447	Q66K79	CBPZ_HUMAN		3	GAACCGAAATT	0.647	
+	1	1570		NM_000798	NP_000789	P21918	DRD5_HUMAN	lasmic (Potential).	1	AGCAATGAGCTC	0.577	
+	2	271	_p.S22N|C1QTNF	NM_001135171	NP_001128643	Q9BXJ2	C1QT7_HUMAN		0	TGCCAGTGGAC	0.507	
-	2	768	sr.1_Missense_Mu	NM_015230	NP_056045	Q8WZ64	ARAP2_HUMAN		3	GCTTATCATCTG	0.423	
-	3	1217	_p.E213K|BEND4_	NM_207406	NP_997289	Q6ZU67	BEND4_HUMAN		0	AGTGCTCCTGTC	0.438	
-	1	160		NM_173536	NP_775807	Q8N1C3	GBRG1_HUMAN		2	TCAAAGGACCC	0.502	
-	9	1943	_p.V424I|GABRA2	NM_001114175	NP_001107647	P47869	GBRA2_HUMAN	ical; (Probable).	4	GAAAAACTATTCT	0.393	
+	9	1539	ze.1_Missense_M	NM_000812	NP_000803	P18505	GBRB1_HUMAN	lasmic (Probable).	2	TGAGCGACCCC	0.627	
+	5	1039	N2_uc003gyb.1_5	NM_020846	NP_065897	Q9P270	SLAI2_HUMAN		0	CGTCTCGGCGC	0.338	

+	5	1190	gyb.1_Missense_M	NM_020846	NP_065897	Q9P270	SLAI2_HUMAN			0	GCAATTCACCTCC	0.453	
+	15	2076	ozl.1_Missense_Mu	NM_025087	NP_079363	Q9H720	PG2IP_HUMAN			3	CATGCTGAACTGA	0.383	
+	2	955	FRA_uc003haa.2_	NM_133267	NP_573574	Q9BZM3	GSX2_HUMAN	Homeobox.		0	CGACTCCGGAGG	0.537	
+	21	2957	nbj.2_Missense_Mu	NM_025009	NP_079285	Q66GS9	CP135_HUMAN	Potential.		5	CAGTTCGACTGG	0.388	
+	15	2919	_p.L916F|LPHN3_	NM_015236	NP_056051	Q9HAR2	LPHN3_HUMAN	Name=2; (Potential).		18	AAGAACCTCTGCA	0.458	
-	9	795	p.R248Q|UBA6_uc	NM_018227	NP_060697	A0AVT1	UBA6_HUMAN			0	ATTTCTCGAAATG	0.299	
-	8	883	IPRSS11A_uc003h	NM_182606	NP_872412	Q6ZMR5	TM11A_HUMAN	.|Extracellular (Potential).		1	TCTTTTCATTAAG	0.373	
+	1	621	hq.2_Missense_M	NM_001074	NP_001065	P16662	UD2B7_HUMAN			2	CTCCTTCCTACGT	0.388	
-	2	869	uc003hei.1_Intron	NM_001073	NP_001064	O75310	UDB11_HUMAN			3	GTAGGGGTTTGC	0.368	rs138573352
+	13	1791	p.C582R|AFP_uc0	NM_001134	NP_001125	P02771	FETA_HUMAN	Albumin 3.		1	GAGAAATGCTGCC	0.418	
-	15	2581		NM_001042784	NP_001036249	Q5M9N0	CD158_HUMAN	Potential.		6	CCACTTCCATATT	0.323	
+	2	37		NM_006419	NP_006410	O43927	CXL13_HUMAN			0	CCCACAGCCTGG	0.493	
-	3	1218	x|HNRPDL_uc003h	NM_031372	NP_112740	O14979	HNRDL_HUMAN	RRM 1.		1	TCTTTCCCTTTTA	0.393	
+	3	572		NM_016323	NP_057407	Q9UII4	HERC5_HUMAN	RCC1 1.		9	AAAAAATAATTCA	0.279	
+	4	727_728		NM_016323	NP_057407	Q9UII4	HERC5_HUMAN	RCC1 2.		9	GAGTACCCTTGC	0.515	
-	2	371	c003hsi.2_Missens	NM_014883	NP_055698	O94988	FA13A_HUMAN	Rho-GAP.		2	CATTCTCGGTGAC	0.428	
-	2	2825		NM_198281	NP_938022	Q6ZVF9	GRIN3_HUMAN			3	GGGCAGGACGG	0.468	
+	7	3217	p.P352L|MMRN1_	NM_007351	NP_031377	Q13201	MMRN1_HUMAN	EGF-like.		4	GGCATCCGTGCC	0.413	
+	8	1052	3htz.3_Nonsense_	NM_001100427	NP_001093897	P52306	GDS1_HUMAN			3	ATTACTGAGCTCA	0.368	
-	29	3946	xc.1_Missense_Mu	NM_001813	NP_001804	Q02224	CENPE_HUMAN	Potential.		9	CCTCATGAAGCAC	0.313	
-	1	646		NM_001059	NP_001050	P29371	NK3R_HUMAN	Name=3; (Potential).		7	AACACAGCTGTG	0.527	
-	10	1292	1_Missense_Muta	NM_000204	NP_000195	P05156	CFAI_HUMAN	Peptidase S1.		0	TGATTCCACTGG	0.443	
+	1	616		NM_001977	NP_001968	Q07075	AMPE_HUMAN	cellular (Potential).		5	AACTTTCGACTGC	0.612	rs143343563
+	7	701_702	2_Nonsense_Muta	NM_020961	NP_066012	Q9HCE5	MTL14_HUMAN			0	CCCTTTAGAAGAA	0.337	
+	4	1520	e_Mutation_p.E442	NM_001128933	NP_001122405	Q9UMS6	SYNP2_HUMAN			2	GCAAGCGAATCAC	0.478	
+	9	8054	_p.R983Q|FAT4_u	NM_024582	NP_078858	Q6V0I7	FAT4_HUMAN	.|Extracellular (Potential).		18	CCCCTCGAAAAAT	0.348	
-	18	1676	jz.3_Missense_Mu	NM_001102653	NP_001096123	Q01804	OTUD4_HUMAN			3	TCTGGAGAAACTA	0.488	
-	2	401	se_Mutation_p.P11	NM_178835	NP_849157	Q17R98	ZN827_HUMAN			0	CTCAGGGGCTTG	0.582	
+	2	813	n_p.R41C|EDNRA	NM_001957	NP_001948	P25101	EDNRA_HUMAN	cellular (Pote	p.R41H(1)	2	ACTTTTCGTGGCA	0.463	rs139739379
+	16	2264	LK2_uc003ilo.3_M	NM_001040260	NP_001035350	Q8N568	DCLK2_HUMAN	Pro-rich.		3	CCAGTTCCTCCCT	0.647	
-	28	5014	.R173W|LRBA_uc0	NM_006726	NP_006717	P50851	LRBA_HUMAN			7	TAAGCCGATTAAT	0.368	
-	2	2143		NM_145720	NP_663772	Q8IY51	TIGD4_HUMAN			1	TCATCAGAAGTGT	0.403	
+	3	359	n_p.P47L|TLR2_uc	NM_003264	NP_003255	O60603	TLR2_HUMAN	cellular (Potential).		3	CCATTCCCTCAGC	0.493	
+	2	821	ior.2_Missense_Mu	NM_000910	NP_000901	P49146	NPY2R_HUMAN	cellular (Potential).		3	CTCTTACCTATAC	0.488	
+	4	1039		NM_006174	NP_006165	Q15761	NPY5R_HUMAN	lasmic (Potential).		7	AACACAGAAGAA	0.413	
-	3	747		NM_001012414	NP_001012414	Q5EBN2	TRI61_HUMAN	RING-type.		1	GTAGATCCTTCCA	0.463	
+	3	1123	qx.1_Missense_Mu	NM_152620	NP_689833	Q495X7	TRI60_HUMAN	B30.2/SPRY.		1	CTGTGCGATATGA	0.413	
+	18	3054	p.E826K|TLL1_uc	NM_012464	NP_036596	O43897	TLL1_HUMAN	CUB 4.		7	ACTTGGGAAATCA	0.488	rs150952504
+	18	3064	p.A829V|TLL1_uc	NM_012464	NP_036596	O43897	TLL1_HUMAN	CUB 4.		7	CAGCGCCACTCC	0.468	
-	18	2783		NM_017631	NP_060101	Q8IY21	DDX60_HUMAN	ase ATP-binding.		3	TAAAACGATTCTG	0.393	
-	34	4804		NM_001012967	NP_001012985	Q5H9U9	DDX6L_HUMAN			1	GACTTGGAAGCA	0.403	
-	19	2787	e_Mutation_p.R856	NM_001012967	NP_001012985	Q5H9U9	DDX6L_HUMAN	ase ATP-binding.		1	TTGGCGATGAGC	0.363	
-	15	2166	p.D649N|DDX60L_	NM_001012967	NP_001012985	Q5H9U9	DDX6L_HUMAN			1	TTAAATCTTTCGA	0.299	
+	6	1500	_p.R430Q|PALLD_	NM_016081	NP_057165	Q8WX93	PALLD_HUMAN			1	CTGCCGACCTGA	0.393	rs145571230
+	16	2889	e_Mutation_p.R49	NM_016081	NP_057165	Q8WX93	PALLD_HUMAN			1	AGGTCGAAGTCC	0.393	
+	5	2057	Dirr.2_Missense_Mu	NM_014269	NP_055084	Q9UKF5	ADA29_HUMAN	Extracellular (Potential).		16	GAATGTGATCTTC	0.448	
-	3	856_857		NM_005429	NP_005420	P49767	VEGFC_HUMAN			5	AAACTCCTTCCC	0.475	

+	9	1805	Z3_uc003ive.1_5'	NM_001080477	NP_001073946	Q9P273	TEN3_HUMAN	Extracellular (Potential).	0	GGGGTCGTGG	0.512	
+	3	1923	X2_uc003iwa.1_5'	NM_020225	NP_064610	Q9P2F5	STOX2_HUMAN		0	CGAGAGGATAC	0.527	
+	4	1179	n_p.L83F|TLR3_u	NM_003265	NP_003256	O15455	TLR3_HUMAN	|Lumenal (Potential).	5	AGCACCTTAAC	0.348	
+	4	345	LKB1_uc011cld.1_	NM_000892	NP_000883	P03952	KLKB1_HUMAN	Apple 1.	1	TACATCGAACA	0.348	
+	14	1707	e_Mutation_p.E34	NM_000892	NP_000883	P03952	KLKB1_HUMAN	eptidase S1.	1	CAAATGAAGAA	0.328	
+	12	1444	_p.P430S|PAPD7_	NM_006999	NP_008930	Q5XG87	PAPD7_HUMAN		1	CTGTTCCTTGC	0.542	
+	22	2446	jeu.1_Missense_	NM_005885	NP_005876	O60337	MARH6_HUMAN	ellular (Potential).	2	CAGACTCCTCTT	0.413	
-	44	7306		NM_001369	NP_001360	Q8TE73	DYH5_HUMAN	2 (By similarity).	31	GAATTTCTGCTT	0.428	
-	44	7300		NM_001369	NP_001360	Q8TE73	DYH5_HUMAN	2 (By similarity).	31	TGCTTCTTGAG	0.423	
-	38	6325		NM_001369	NP_001360	Q8TE73	DYH5_HUMAN	1 (By similarity).	31	GTTTTCAGGGA	0.438	
-	36	6062		NM_001369	NP_001360	Q8TE73	DYH5_HUMAN	1 (By similarity).	31	GGTCTGAACAA	0.463	
-	11	1405	AH5_uc003jfe.1_	NM_001369	NP_001360	Q8TE73	DYH5_HUMAN	n (By similarity).	31	GATTTTGTTTAA	0.308	
+	8	1426	e_Mutation_p.P42	NM_007118	NP_009049	O75962	TRIO_HUMAN		18	ACCTTCCCTCA	0.393	rs139674608
+	4	412		NM_020227	NP_064612	Q9NQV7	PRDM9_HUMAN	RAB-related.	6	TCACCGAAGGC	0.468	
+	2	804	m.2_Missense_M	NM_178140	NP_835260	O15018	PDZD2_HUMAN	PDZ 1.	9	ACTGCGGGATG	0.592	
+	7	1084	FLAM_uc003jle.1_	NM_152403	NP_689616	Q63HQ2	EGFLA_HUMAN		7	TCACCGACATG	0.488	rs147796862
-	10	1659	.2_Missense_Mut	NM_001127671	NP_001121143	P42702	LIFR_HUMAN	tential).|Fibronectin type-III	4	TAATATCCTTCA	0.269	
-	7	1020		NM_001737	NP_001728	P02748	CO9_HUMAN	MACPF.	0	CATCGCGATTTC	0.363	
-	10	1327	.2_Missense_Mu	NM_001343	NP_001334	P98082	DAB2_HUMAN		3	TCGAGGAAGAG	0.443	
-	39	4871	jmi.3_Missense_	NM_173489	NP_775760	Q7Z745	HTRB2_HUMAN		8	AAAGGGAATGC	0.483	
-	16	2552	1_Missense_Muta	NM_000065	NP_000056	P13671	CO6_HUMAN	nent control factor I module	7	TCAGATCCTGAT	0.368	
+	9	947	q.1_Missense_Mu	NM_000163	NP_000154	P10912	GHR_HUMAN	(Potential).|Box 1 motif.	6	CAGTTCCAGTT	0.318	
+	1	381		NM_006308	NP_006299	Q12988	HSPB3_HUMAN		0	CAAATCCCACT	0.577	
-	2	847		NM_152625	NP_689838	Q8N895	ZN366_HUMAN		2	GCTCTCCTGGG	0.652	
+	18	2196	izf.2_Missense_M	NM_001080479	NP_001073948	Q8N1W1	RGNEF_HUMAN		0	CTGGTCTCTCC	0.483	
+	2	2183		NM_153610	NP_705838	Q8N3K9	CMYA5_HUMAN		9	TCCATCACTGG	0.428	
+	2	6184		NM_153610	NP_705838	Q8N3K9	CMYA5_HUMAN		9	GCCAGGAAAAA	0.428	
+	2	6379		NM_153610	NP_705838	Q8N3K9	CMYA5_HUMAN		9	CATTGGAAGAA	0.438	
+	1	672	uc011ctk.1_Intron	NM_032567	NP_115956	Q9BXG8	SPZ1_HUMAN		1	AACAGGAGATG	0.358	
+	7	1108	98_uc003kjt.2_5'	NM_032119	NP_115495	Q8WXG9	GPR98_HUMAN	|Extracellular (Potential).	16	TTTATTCATGAAT	0.388	
+	56	11828	.G1617E|GPR98_	NM_032119	NP_115495	Q8WXG9	GPR98_HUMAN	ellular (Potential).	16	CAGAGGAATTT	0.423	
+	78	16748	.S3257F|GPR98_	NM_032119	NP_115495	Q8WXG9	GPR98_HUMAN	ellular (Potential).	16	TCATATCTCCAG	0.413	
-	3	570	nse_Mutation_p.P	NM_001142483	NP_001135955	Q16612	NP311_HUMAN		1	GACAGGAAGTC	0.458	
+	16	2858	cl.1_Missense_Mu	NM_005509	NP_005500	Q9Y485	DMXL1_HUMAN	WD 7.	2	TCAATTCCTGTC	0.328	
-	1	578	h.1_Missense_M	NM_020389	NP_065122	Q9HCX4	TRPC7_HUMAN	lasmic (Potential).	0	CGTGGGGCCGC	0.612	
+	1	533	03lhc.1_Missense	NM_018905	NP_061728	Q9Y5H9	PCDA2_HUMAN	ellular (Potential).	4	GGTTTCCCGAA	0.488	
+	1	104	c003lhi.2_Intron|P	NM_018908	NP_061731	Q9Y5H7	PCDA5_HUMAN	(Potential).|Cadherin 1.	3	GATCCCGGAGG	0.647	
+	1	1900	A6_uc003lhn.2_I	NM_018902	NP_061725	Q9Y5I1	PCDAB_HUMAN	(Potential).|Cadherin 3.	1	CTCCTGAAGTC	0.527	
+	1	526		NM_013340	NP_037472	Q9Y5F3	PCDB1_HUMAN	|Extracellular (Potential).	0	GGGTTCACGTT	0.537	
+	1	1024	uc003lin.2_Intron	NM_018937	NP_061760	Q9Y5E6	PCDB3_HUMAN	(Potential).|Cadherin 3.	2	TCAACGACAAC	0.478	
+	1	148	B6_uc011dah.1_	NM_018939	NP_061762	Q9Y5E3	PCDB6_HUMAN	(Potential).|Cadherin 1.	1	CAAAGGACCTG	0.502	
+	1	2174		NM_018940	NP_061763	Q9Y5E2	PCDB7_HUMAN	|Extracellular (Potential).	6	CTTCTCCCAGC	0.692	
+	1	1087	B16_uc003liv.2_5	NM_019120	NP_061993	Q9UN66	PCDB8_HUMAN	|Extracellular (Potential).	4	CAGGAGAAATT	0.403	
+	1	1571		NM_018933	NP_061756	Q9Y5F0	PCDBD_HUMAN	(Potential).|Cadherin 5.	3	TCCGCGAGAAC	0.602	
+	1	107	DHGA4_uc003ljq	NM_018919	NP_061742	Q9Y5G7	PCDG6_HUMAN	|Extracellular (Potential).	1	TATTCCCGAGG	0.657	
-	3	2258	p.Y714F|PCDH1_	NM_002587	NP_002578	Q08174	PCDH1_HUMAN	(Potential).|Cadherin 6.	5	GTGATATAGGGT	0.567	
-	7	1485	3loh.3_Splice_Sit	NM_004576	NP_004567	Q00005	2ABB_HUMAN		2	TCTATACCTGGT	0.483	

-	3	754	loh.3_Missense_M	NM_004576	NP_004567	Q00005	2ABB_HUMAN			2	GGGTTCATGGC	0.373	
-	6	862	y.1_Missense_Mut	NM_000870	NP_000861	Q13639	5HT4R_HUMAN	smic (By similarity).		1	AGGCTCCTGCC	0.547	
+	1	2438		NM_001099293	NP_001092763	Q2VIQ3	KIF4B_HUMAN	RC1 (By similarity).|Potenti		1	AGGAAGCCAAA	0.463	
+	1	2459		NM_001099293	NP_001092763	Q2VIQ3	KIF4B_HUMAN	RC1 (By similarity).|Potenti		1	AATGACCTCCTT	0.453	
-	2	661	vm.3_Missense_M	NM_001100816	NP_001094286	O43513	MED7_HUMAN			0	AGGTCCAAGAAA	0.373	
+	8	1613	|ODZ2_uc003lzr.3	NM_001122679	NP_001116151					10	ATGAAGCCGTGT	0.502	
+	9	1180	n_p.M206I|KCNIP	NM_001034837	NP_001030009	Q9NZI2	KCIP1_HUMAN	ith KCND2 (By similarity).		2	ATCATGAGGTC	0.468	
-	16	1717		NM_005110	NP_005101	O94808	GFPT2_HUMAN	SIS 2.		2	GCAGCGATCTC	0.527	
+	3	482	_p.A45S|CNOT6_	NM_015455	NP_056270	Q9ULM6	CNOT6_HUMAN			0	TTAAGCGCATCT	0.378	
-	1	235	C2_uc003mte.2_I	NM_148959	NP_683762	Q8NHY5	HUS1B_HUMAN			0	TCTTCCGAGACA	0.692	
+	2	339	P2L_uc011dim.1_	NM_001040274	NP_001035364	Q5T4T6	SYC2L_HUMAN			2	AGGAAGACAGG	0.279	
-	14	1434	p.G404R|FAM65B_	NM_014722	NP_055537	Q9Y4F9	FA65B_HUMAN			1	CCTTTCCATTTT	0.453	
+	1	257	2AA_uc003nfc.2_	NM_170610	NP_733759	Q96A08	H2B1A_HUMAN			1	CTACAGCAAGC	0.512	
+	11	1441	p.G379S|BTN3A3_	NM_006994	NP_008925	O00478	BT3A3_HUMAN	.|Cytoplasmic (Potential).		0	AAAAAGGTTGG	0.483	
+	1	23	uc003njq.2_5'Flank	NM_021968	NP_068803	P62805	H4_HUMAN			2	AGGCGGGAAGG	0.627	
-	4	1137	nl.3_Missense_Mu	NM_001109809	NP_001103279	Q9NU63	ZFP57_HUMAN			5	CCTGGGACCTG	0.557	
-	2	635	pd.2_Missense_M	NM_025236	NP_079512	Q9H2S5	RNF39_HUMAN			0	TTCCTCATATCC	0.527	
-	1	113	se_Mutation_p.E13	NM_006778	NP_006769	Q9UDY6	TRI10_HUMAN			0	GACTTCATCTGC	0.617	
+	3	868	st.2_Missense_Mu	NM_001077511	NP_001070979	Q9Y242	TCF19_HUMAN			0	CCCCTCGGAGT	0.562	
+	3	560_561	utation_p.116_117	NM_005931	NP_005922	Q29980	MICB_HUMAN	cellular (Potential).		0	ACTCAAGAATCG	0.525	
+	8	1143	nzf.1_Missense_M	NM_000500	NP_000491	P08686	CP21A_HUMAN			0	TGCACGGCTGC	0.667	
-	15	5498		NM_019105	NP_061978	P22105	TENX_HUMAN			0	TATCATCCATAGC	0.602	
-	6	381	dpz.1_Missense_M	NM_006781	NP_006772	Q5SRN2	CF010_HUMAN			1	GGTTATCATATGA	0.279	
-	9	1317	dw.2_Missense_M	NM_004761	NP_004752	O15211	RGL2_HUMAN	Ras-GEF.		6	CTCTGGGAATAA	0.547	
+	28	3857		NM_002224	NP_002215	Q14573	ITPR3_HUMAN	lasmic (Potential).		19	AGATCCCCTATG	0.577	
+	17	2104	_p.V699I|SCUBE3	NM_152753	NP_689966	Q8IX30	SCUB3_HUMAN			1	ACTCTGTAGAT	0.597	
+	5	769	lb.1_Missense_Mu	NM_145028	NP_659465	Q5T9G4	CF081_HUMAN			1	AAGAATGACCTT	0.493	
+	2	247	1_Missense_Muta	NM_173558	NP_775829	Q7Z6J4	FGD2_HUMAN			3	CCCCAGAAGCA	0.612	
+	76	11716	sense_Mutation_p	NM_001371	NP_001362					21	ATGTATCAGACG	0.507	
+	4	719	ense_Mutation_p.S	NM_001010873	NP_001010873	Q5TGU0	TSPO2_HUMAN	ical; (Potential).		0	TACCTAGCCTGG	0.607	
-	5	1155	_p.P37S|TRERF1	NM_033502	NP_277037	Q96PN7	TREF1_HUMAN			5	GGAAGGGATAG	0.637	
-	2	643	p.V166M|CUL7_uc	NM_014780	NP_055595	Q14999	CUL7_HUMAN			4	ACTTCACGTCGG	0.612	
+	1	4861	e.2_Missense_Mu	NM_001010870	NP_001010870	O60522	TDRD6_HUMAN	Tudor 7.		6	GCCATTCCTTCT	0.413	
+	6	1335	p.W416*|GPR115_	NM_153838	NP_722580	Q8IZF3	GP115_HUMAN	tracellular (F	p.W359*(1)	8	AGATGGGATGA	0.453	rs140327995
+	5	1085	TR2_uc010jzv.2_	NM_001526	NP_001517	O43614	OX2R_HUMAN	lasmic (Potential).		6	TCCCTGGAACAT	0.493	
+	8	1176		NM_207410	NP_997293	Q6UXV0	GFRAL_HUMAN	ical; (Potential).		2	ACCTGTGGAATC	0.358	
-	4	448	MGCLL1_uc011dx	NM_019036	NP_061909	Q8TB92	HMGC2_HUMAN			4	TGTAGGAACTAT	0.313	
-	1	1034	kf.1_Missense_Mu	NM_021073	NP_066551	P22003	BMP5_HUMAN			2	GGTCTCTTCTG	0.522	
-	10	1170	.1_Missense_Mut	NM_001144769	NP_001138241	Q03001	DYST_HUMAN	2.|Actin-binding.		14	ACAGCAACAGTA	0.348	
+	3	845	D6_uc003pdg.2_	NM_152731	NP_689944	Q5SZJ8	BEND6_HUMAN	Potential.		0	GGAAAGAAAAC	0.378	rs79968708
+	10	2358	sense_Mutation_p.	NM_001031623	NP_001026794	Q9Y4E5	ZN451_HUMAN			2	GATTTTCCAGTA	0.363	
+	11	1897	Q5_uc010kat.2_M	NM_019842	NP_062816	Q9NR82	KCNQ5_HUMAN			7	CCCCACCACTTA	0.403	
+	5	994	hq.2_Missense_Mu	NM_133493	NP_598000	Q6YHK3	CD109_HUMAN			4	TCATTTCCAAAA	0.368	
-	12	2496	L12A1_uc003phu	NM_004370	NP_004361	Q99715	COCA1_HUMAN	nectin type-III 4.		9	AGTGTTCTCCTC	0.433	
-	10	1860	L12A1_uc003phu	NM_004370	NP_004361	Q99715	COCA1_HUMAN	VWFA 2.		9	GAATTCCTCAGT	0.458	
-	5	2992	_p.M774I|FILIP1_	NM_015687	NP_056502	Q7Z7B0	FLIP1_HUMAN			4	CTTTCTCATCCAT	0.507	
-	4	1243	e_Mutation_p.E27	NM_001122769	NP_001116241	Q86VQ0	LCA5_HUMAN	Potential.		0	TATTTTCATCATG	0.333	

-	8	1491	_p.G322*|IBTK_u	NM_015525	NP_056340	Q9P2D0	IBTK_HUMAN		4	TTTCTCCATTGG	0.353	
+	17	2812	p.V842G|DOPEY	NM_015018	NP_055833	Q5JWR5	DOP1_HUMAN		4	CTGTGGTTATTA	0.448	
-	12	1419	_p.P363L|ME1_uc	NM_002395	NP_002386	P48163	MAOX_HUMAN		2	TGACTGGATCA	0.428	
-	20	1757	e_Mutation_p.G3	NM_020320	NP_064716	Q5T160	SYRM_HUMAN		3	TTCATTCCATTG	0.328	
-	6	574	nc.2_Missense_M	NM_016021	NP_057105	Q9Y385	UB2J1_HUMAN	lasmic (Potential).	0	CCTCAGGAGTG	0.388	
+	11	2243	e_Mutation_p.G14	NM_052904	NP_443136	Q96NJ5	KLH32_HUMAN	Kelch 6.	4	CCAATGGAATA	0.438	
-	11	2351	u.2_Missense_Mu	NM_005068	NP_005059	P81133	SIM1_HUMAN	minded C-terminal.	4	GCATATCCAGTT	0.453	
+	6	1148	o.3_Missense_Mu	NM_021956	NP_068775	Q13002	GRIK2_HUMAN	ellular (Potential).	5	GGAACGATTGC	0.413	
-	9	995	vr.2_Missense_Mu	NM_016262	NP_057346	Q9UJT0	TBE_HUMAN		1	GTTGAGGAAAA	0.333	
-	6	1586		NM_002031	NP_002022	P42685	FRK_HUMAN	rotein kinase.	6	CCACCTTAAAA	0.333	
+	6	2028	t.2_Missense_Mut	NM_001080976	NP_001074445	Q9UL01	DSE_HUMAN		1	AGAGATGGTCTC	0.488	rs141851816
-	1	1	plice_Site|GPRC6	NM_148963	NP_683766	Q5T6X5	GPC6A_HUMAN		6	TCAGTTCATGTG	0.403	
+	9	970		NM_173560	NP_775831	Q8HWS3	RFX6_HUMAN		3	ATCTCCTTCCC	0.348	
-	11	2142_2143		NM_005907	NP_005898	P33908	MA1A1_HUMAN	enal (Potential).	4	CAGGCCCATTTC	0.361	
+	6	619	_p.S53F|PKIB_uc	NM_181794	NP_861459	Q9C010	IPKB_HUMAN		0	TCTCTCCGTGA	0.473	
+	3	1314		NM_001010852	NP_001010852	Q5SYC1	CLVS2_HUMAN	CRAL-TRIO.	5	ATGATTGAAGAT	0.408	
+	5	1594		NM_001010852	NP_001010852	Q5SYC1	CLVS2_HUMAN	CRAL-TRIO.	5	TCATCCTGAGAT	0.448	
-	6	3437	174_uc003qbc.2_	NM_001012279	NP_001012279	Q5TF21	CF174_HUMAN		6	CTCCTCGTCCA	0.637	
-	4	827	bt.1_Missense_Mu	NM_001010923	NP_001010923	Q8N1K5	THMS1_HUMAN	CABIT 1.	4	TCCTTCTTGTG	0.378	
+	6	717		NM_006208	NP_006199	P22413	ENPP1_HUMAN	ase.|Extracellular (Potential	4	CTTCTTCCTGTT	0.398	
-	4	542	.2_Intron|IL22RA	NM_052962	NP_443194	Q969J5	I22R2_HUMAN		0	ccagcatccacttggct	0	
-	10	1930		NM_153235	NP_694967	Q8N3L3	TXLNB_HUMAN		2	GCATTGGGTTT	0.627	
+	3	636	_p.G188E|ULBP2_	NM_025217	NP_079493	Q9BZM5	N2DL2_HUMAN	lass I alpha-2 like.	0	AATGGGAGACT	0.478	
+	7	2388	p.P344L|TULP4_	NM_020245	NP_064630	Q9NRJ4	TULP4_HUMAN		1	GCGCCCCATCA	0.532	
+	7	1056	jw.1_Missense_Mu	NM_032532	NP_115921	Q4ZHG4	FNDC1_HUMAN	nectin type-III 3.	8	TTCTGGAAAAA	0.413	
+	8	1194	jw.1_Missense_Mu	NM_032532	NP_115921	Q4ZHG4	FNDC1_HUMAN	nectin type-III 3.	8	TGTATGAATTTG	0.468	
+	11	1000	sy.1_Missense_M	NM_173516	NP_775787	Q8NA58	PNDC1_HUMAN	lasmic (Potential).	0	AGCTACGATCAA	0.398	
+	29	4473	vc.1_Missense_Mu	NM_001040001	NP_001035090	P55196	AFAD_HUMAN	Potential.	5	GATGCGCACTC	0.567	
+	2	993	ense_Mutation_p.	NM_001098201	NP_001091671	Q99527	GPER_HUMAN	ellular (Potential).	1	ACACCGACGAG	0.657	
+	25	3734	o.2_Missense_Mu	NM_152744	NP_689957	Q7Z5N4	SDK1_HUMAN	nectin type-III 6.	6	TGCCGGATTCT	0.602	
+	42	6134	my.2_Nonsense_	NM_152744	NP_689957	Q7Z5N4	SDK1_HUMAN		6	CAGCTCAAGTG	0.597	
-	3	793	8A1_uc011jxe.1_	NM_001037763	NP_001032852	Q2UY09	COSA1_HUMAN	VWFA 1.	3	CAGACGATCTT	0.373	
+	10	1290	p.P373S|HDAC9_	NM_058176	NP_478056	Q9UKV0	HDAC9_HUMAN		5	GAGTTCCCTTA	0.343	
-	17	1552	1jyl.1_Missense_	NM_012294	NP_036426	Q92565	RPGF5_HUMAN		1	GCTATACTGGA	0.438	
-	5	627		NM_006547	NP_006538	O00425	IF2B3_HUMAN	RRM 2.	2	TACAACTGCAG	0.323	
-	6	984	plice_Site_p.R156	NM_013293	NP_037425	Q13595	TRA2A_HUMAN		1	CATTACCTGTAT	0.284	
-	4	696	_p.G60E|TRA2A_	NM_013293	NP_037425	Q13595	TRA2A_HUMAN	RRM.	1	CAAATCCTCGA	0.373	
+	6	859	r.3_Missense_Mu	NM_199136	NP_954587	A4D161	CG046_HUMAN		0	TTTCTTCATTAAG	0.279	
-	2	609	XA3_uc003syk.2_	NM_030661	NP_109377	O43365	HXA3_HUMAN	Pro-rich.	2	GGCAGGGGTAG	0.393	
+	16	1563	DCYAP1R1_uc0	NM_001118	NP_001109	P41586	PACR_HUMAN	lasmic (Potential).	1	GCTCTCCATCC	0.602	
+	11	3338	p.S633F|CCDC12	NM_194300	NP_919276	Q6ZRS4	CC129_HUMAN		0	CAAATCCGTCT	0.522	
-	9	1406	_p.E373K|PDE1C_	NM_005020	NP_005011	Q14123	PDE1C_HUMAN	ytic (By similarity).	4	TTCCTCGTCAT	0.413	
-	6	993	_p.S235F|PDE1C_	NM_005020	NP_005011	Q14123	PDE1C_HUMAN		4	TGAGGGAAAAG	0.468	
+	3	418	SR1_uc010kwv.1_	NM_207172	NP_997055	Q6W5P4	NPSR1_HUMAN	Name=2; (Potential).	4	TTTCACAGGAC	0.388	
-	9	905		NM_015283	NP_056098	Q2PZI1	D19L1_HUMAN	ical; (Potential).	0	CCAAGGAAGCA	0.343	
-	14	1606	.1_RNA|DPY19L2P1_uc010kwz.1_RNA						0	AAGATCACTCAG	0.323	
+	14	4413	thj.2_Missense_Mu	NM_003718	NP_003709	Q14004	CDK13_HUMAN		5	GTCTTTGGATAA	0.433	

-	44	6588	1_Intron|PKD1L1_	NM_138295	NP_612152	Q8TDX9	PK1L1_HUMAN	lasmic (Potential).		11	TCTTTTCCAAGC	0.507	
+	9	1612	p.G395S|IKZF1_u	NM_006060	NP_006051	Q13422	IKZF1_HUMAN	2H2-type 5.		148	ACATGGGCTGC	0.602	
-	7	1248	_p.E355*|COBL_	NM_015198	NP_056013	O75128	COBL_HUMAN			5	ATCCTCAGTGCC	0.592	
+	4	1558		NM_001159522	NP_001152994	A8MUV8	ZN727_HUMAN	2H2-type 11.		0	GCAAAACCTTTA	0.428	
-	1	697	C2_uc011kfa.1_Int	NM_001306	NP_001297	O15551	CLD3_HUMAN	ellular (Potential).		0	GCGCCCATCTCG	0.706	
+	23	1568	zs.2_Missense_M	NM_000501	NP_001075224	P15502	ELN_HUMAN	Ala-rich.		5	GTGGCTCCTGGT	0.547	
+	6	573	F4H_uc003uae.1_	NM_022170	NP_071496	Q15056	IF4H_HUMAN			0	GCCCTCCCCTC	0.612	
-	13	3290		NM_001099415	NP_001092885	A8CG34	P121C_HUMAN	side (Potential).		0	CGAAGGAGAAG	0.657	
+	4	597	_p.A145V|ZP3_uc0	NM_001110354	NP_001103824	P21754	ZP3_HUMAN	llular (Potential).|ZP.		0	ATGCAGCCCACC	0.498	
-	5	9347	_Mutation_p.D302	NM_033026	NP_149015	Q9Y6V0	PCLO_HUMAN			7	CTGTGTCAGTTC	0.398	
-	5	8672	_Mutation_p.V279	NM_033026	NP_149015	Q9Y6V0	PCLO_HUMAN			7	GGTCACTGTCT	0.433	
-	3	2757	v.2_Missense_Mu	NM_033026	NP_149015	Q9Y6V0	PCLO_HUMAN	Pro-rich.		7	CAGGTCGAGGT	0.438	
-	2	1835	v.2_Missense_Mu	NM_033026	NP_149015	Q9Y6V0	PCLO_HUMAN	n approximate repeats of P		7	TGCTGGGCCAG	0.597	
-	17	2744		NM_012431	NP_036563	O15041	SEM3E_HUMAN	Lys-rich (basic).		3	GGAACGGAGCT	0.448	
-	14	1913	hc.1_Missense_M	NM_000927	NP_000918	P08183	MDR1_HUMAN	r 1.|Cytoplasmic (Potential)		7	AATCTCATCCAT	0.443	
-	3	616	_p.D47N|CYP51A	NM_000786	NP_000777	Q16850	CP51A_HUMAN			0	GCACATCGTATG	0.378	
-	3	2294	mg.2_Missense_M	NM_017654	NP_060124	Q5K651	SAMD9_HUMAN			7	CTTCCTCTTTTG	0.363	
-	5	4116	D9L_uc003umk.1_	NM_152703	NP_689916	Q8IVG5	SAM9L_HUMAN			4	GTAGAATAAGTT	0.388	
-	2	178	10lff.2_Missense_	NM_001039372	NP_001034461	A8MVW5	HECA2_HUMAN	ellular (Potential).		5	GGACGGGTAGG	0.517	
-	4	488	umu.1_Missense_	NM_001742	NP_001733	P30988	CALCR_HUMAN	ellular (Potential).		9	TGCATTCGGTCA	0.388	rs144560846
+	6	1750	.H475Y|ZKSCAN	NM_003439	NP_003430	P17029	ZKSC1_HUMAN	2H2-type 5.		3	AGAATTCACACT	0.488	
-	6	1412	e_Mutation_p.E33	NM_032924	NP_116313	P17036	ZNF3_HUMAN	2H2-type 7	p.E369K(1)	1	TACATTCGTAGG	0.468	
+	14	2315	AN_uc003uwl.2_	NM_003386	NP_003377	Q9Y493	ZAN_HUMAN	ate) (mucin-like domain).|E		11	AAAAACCCACCA	0.507	
-	2	1447	_p.D431N|ACHE_	NM_000665	NP_000656	P22303	ACES_HUMAN			2	CACATCGCTCA	0.667	
+	3	7450	C17_uc010lho.1_	NM_001040105	NP_001035194	Q685J3	MUC17_HUMAN	ch.|59 X approximate tand		27	CACCACGCCGG	0.522	
+	3	7512	C17_uc010lho.1_	NM_001040105	NP_001035194	Q685J3	MUC17_HUMAN	X approximate tandem re		27	ACACCTATGACC	0.493	rs139444589
+	3	7514	C17_uc010lho.1_	NM_001040105	NP_001035194	Q685J3	MUC17_HUMAN	X approximate tandem re		27	ACCTATGACCAC	0.493	rs147944556
+	3	11748	C17_uc010lho.1_	NM_001040105	NP_001035194	Q685J3	MUC17_HUMAN	ellular (Potential).		27	ACACCTCCTCTT	0.468	
+	4	1711	_Intron|FBXL13_	NM_001031692	NP_001026862	Q8N6Y2	LRC17_HUMAN			1	AGTAGGATAAG	0.313	
-	8	1022	199N|FBXL13_uc	NM_145032	NP_659469	Q8NEE6	FXL13_HUMAN			0	AAAAATCAATCT	0.204	
+	5	1017	1kli.1_Missense_	NM_031905	NP_114111	Q8N2F6	ARM10_HUMAN			1	ACTGTTACCAAT	0.443	
-	4	675	ix.2_Missense_Mu	NM_014377	NP_055192	Q99543	DNJC2_HUMAN	J.		1	CTTTAGTTATGCA	0.328	
-	60	9915	.2_Missense_Mut	NM_005045	NP_005036	P78509	RELN_HUMAN	EGF-like 8.		19	GGAAGCTCTCG	0.393	
-	28	4206	.2_Missense_Mut	NM_005045	NP_005036	P78509	RELN_HUMAN			19	GAGTTTCCTTCG	0.478	
-	9	1394	y.2_Splice_Site_p	NM_019042	NP_061915	Q96PZ0	PUS7_HUMAN			1	ATACCAACCTTCC	0.373	
-	25	3746_3747	v.2_Missense_Mu	NM_002291	NP_002282	P07942	LAMB1_HUMAN	inin EGF-like 13.		8	AATGCCCCTGGG	0.53	
-	6	796	ex.2_Missense_M	NM_002291	NP_002282	P07942	LAMB1_HUMAN	inin N-terminal.		8	AGTCGGACGAT	0.433	
-	30	4696	p.D1538N|LAMB4_	NM_007356	NP_031382	A4D0S4	LAMB4_HUMAN	ential.|Domain I.		8	TTTCATCTGTCC	0.393	
-	25	3615	kg.3_Missense_M	NM_017954	NP_060424	Q86UW7	CAPS2_HUMAN			2	ATGGATGAAAAG	0.333	
+	37	6291	a.3_Missense_Mu	NM_001458	NP_001449	Q14315	FLNC_HUMAN	Filamin 18.		12	AACAGCCCCTTC	0.617	
+	8	1016	voq.1_Nonsense_	NM_178562	NP_848657	Q86UF1	TSN33_HUMAN	lasmic (Potential).		1	GTGAATCAGATC	0.532	
-	10	4047	.P1283L|KIAA154	NM_020910	NP_065961	Q9HCM3	K1549_HUMAN			230	GTGTCAGGCTGA	0.522	
-	2	2529	_p.S777F|KIAA15	NM_020910	NP_065961	Q9HCM3	K1549_HUMAN			230	AGAAAGAGGCC	0.522	
+	8	957	_p.E170K|TBXAS1	NM_001130966	NP_001124438	P24557	THAS_HUMAN	lasmic (Potential).		3	TTCTTCGAATTC	0.582	
-	15	1860		NM_004333	NP_004324	P15056	BRAF_HUMAN	rotein kinas	R603>I(2)|p.T	18290	GATTTCACTGTA	0.368	
+	1	469		NM_016944	NP_058640	Q9NYW5	TA2R4_HUMAN	ellular (Potential).		0	CCTTTTCCTGAA	0.458	
+	2	174	.2_Intron|uc003wa	NR_001296						0	CCTGTGAGGAG	0.547	

-	12	1582		NM_000420	NP_000411	P23276	KELL_HUMAN	ellular (Potential).	4	CCAGGGAAGGT	0.577	
-	8	976		NM_000420	NP_000411	P23276	KELL_HUMAN	ellular (Potential).	4	CAGCTGATTCA	0.542	
+	22	2612	tc.1_Missense_M	NM_000083	NP_000074	P35523	CLCN1_HUMAN	oplasmic (By similarity).	5	GTTTTCACTCC	0.572	
+	1	193		NM_012369	NP_036501	Q13607	OR2F1_HUMAN	lasmic (Potential).	3	GATCAGACTGG	0.532	
+	2	2691_2692	_Mutation_p.S858	NM_005435	NP_005426	Q12774	ARHG5_HUMAN		2	AAGTCCAGGG	0.589	
-	2	112		NM_001080413	NP_001073882	O60393	NOBOX_HUMAN		1	CACAGGAAATT	0.517	
-	4	221	PK1_uc003wer.2_	NM_022445	NP_071890	Q9H3S4	TPK1_HUMAN		2	TTAAAAGAGCTT	0.413	
+	12	2309		NM_014141	NP_054860	Q9UHC6	CNTP2_HUMAN	ential).|Fibrinogen C-termi	11	GCCTTCCTGTG	0.448	
-	4	750		NM_001001661	NP_001001661	Q6IV72	ZN425_HUMAN		3	TGGACGAGTTT	0.517	
-	6	2295		NM_015694	NP_056509	Q9ULD5	ZN777_HUMAN	2H2-type 5.	1	GGTGGCGCAGC	0.642	
-	5	1463		NM_015694	NP_056509	Q9ULD5	ZN777_HUMAN	Glu-rich.	1	CAGTTCGCTGA	0.652	
+	69	9659		NM_198455	NP_940857	A2VEC9	SSPO_HUMAN	SP type-1 11.	0	ATCCACCGTGG	0.672	
+	2	664		NM_175571	NP_783161	Q8ND71	GIMA8_HUMAN		7	ATGAGGAAACA	0.517	
+	4	1211		NM_175571	NP_783161	Q8ND71	GIMA8_HUMAN		7	CTGGAGAAAAA	0.468	
+	2	226		NM_153236	NP_694968	Q8NHV1	GIMA7_HUMAN		2	GAGGAAATCTT	0.502	
-	3	594	P6_uc003whm.2_	NM_024711	NP_078987	Q6P9H5	GIMA6_HUMAN		3	TGTTTCCTGTT	0.542	
+	7	989	p.S183F|UBE3C_	NM_014671	NP_055486	Q15386	UBE3C_HUMAN		5	AATATTCTGATTT	0.343	
+	4	465_466	M2_uc011kwi.1_I	NM_003970	NP_003961	P54296	MYOM2_HUMAN		6	CTGGCCCACTTG	0.634	
-	54	8753	p.P2117L|CSMD1	NM_033225	NP_150094	Q96PZ7	CSMD1_HUMAN	ar (Potential).|Sushi 19.	25	GCAGAGGGCTA	0.552	
-	52	8399	_Mutation_p.S19	NM_033225	NP_150094	Q96PZ7	CSMD1_HUMAN	ar (Potential).|Sushi 17.	25	TGCCGCTCCAG	0.463	
-	8	1444		NM_033225	NP_150094	Q96PZ7	CSMD1_HUMAN	ar (Potential).|Sushi 2.	25	CCCAGGATCTG	0.383	
-	3	360	.2_5'UTR|XKR5_	NM_207411	NP_997294	Q6UX68	XKR5_HUMAN		0	AGAGTCGAAGG	0.597	
-	4	6929		NM_178857	NP_849188	Q8IWN7	RP1L1_HUMAN		8	CCCTTCAGCCT	0.602	
-	4	3782		NM_178857	NP_849188	Q8IWN7	RP1L1_HUMAN		8	GGACCCAAGGT	0.617	
-	9	2790	.2_Missense_Mut	NM_005144	NP_005135	O43593	HAIR_HUMAN		2	TTGATTCCTTCT	0.502	
+	9	1275	e_Mutation_p.R3	NM_001722	NP_001713	P05423	RPC4_HUMAN		0	AACACCGGTAA	0.542	
-	3	830	uc003xdj.2_Intron	NM_002318	NP_002309	Q9Y4K0	LOXL2_HUMAN		3	ACCCAGGAATC	0.498	
+	11	1074	nse_Mutation_p.L	NM_014265	NP_055080	Q9UKQ2	ADA28_HUMAN	B.|Extracellular (Potential).	5	AATCTTCTTAGAG	0.358	
+	16	1770	ec.2_Missense_M	NM_003817	NP_003808	Q9H2U9	ADAM7_HUMAN	ar (Potential).|Cys-rich.	5	TCAGAGATGTC	0.453	
-	4	1546		NM_006158	NP_006149	P07196	NFL_HUMAN	subdomain B (acidic).	2	tcttccttgtccttctcctc	0.403	
-	3	1159		NM_007257	NP_009188	Q9UL42	PNMA2_HUMAN		0	tggctggagacacgcc	0	
-	4	938		NM_018310	NP_060780	Q9HAW0	BRF2_HUMAN		0	TCAGCCATCCG	0.582	
+	7	833	u.3_Nonsense_M	NM_004674	NP_004665	Q9UBL3	ASH2L_HUMAN		2	TTGGATCAGGTA	0.348	
-	38	4879	K1_uc003xoj.2_	NM_020476	NP_065209	P16157	ANK1_HUMAN	regulatory domain.	9	CCACTCGTGAC	0.597	
-	4	611	se_Mutation_p.E	NM_024593	NP_078869	Q9HAE3	EFCB1_HUMAN	EF-hand 3.	0	TTATTTCAACCA	0.333	
-	18	4810	rf.3_Missense_M	NM_014781	NP_055596	Q8TDY2	RBCC1_HUMAN		11	ACCTGGGAGTT	0.453	
+	2	639	.1_Missense_Mut	NM_006269	NP_006260	P56715	RP1_HUMAN	oublecortin 2.	12	CGACCCGAAGA	0.657	rs148346976
+	4	2922	1_uc011ldy.1_Intr	NM_006269	NP_006260	P56715	RP1_HUMAN		12	TAAATCCATATCC	0.333	
+	3	1332		NM_052898	NP_443130	Q5GH76	XKR4_HUMAN	ical; (Potential).	2	TGTTCGACATG	0.443	
+	3	1572		NM_052898	NP_443130	Q5GH76	XKR4_HUMAN		2	TTCTTTCATCCC	0.527	
+	2	2021		NM_017780	NP_060250	Q9P2D1	CHD7_HUMAN	Pro-rich.	9	CTGTCCTCCAC	0.587	
+	34	8064		NM_017780	NP_060250	Q9P2D1	CHD7_HUMAN		9	AGCCACAAACG	0.542	
+	10	1732	LF1_uc003xyf.2_	NM_015170	NP_055985	Q8IWU6	SULF1_HUMAN		7	ATATTCGTGTG	0.428	
+	13	2074	LF1_uc003xyf.2_	NM_015170	NP_055985	Q8IWU6	SULF1_HUMAN		7	AGACAGCCTGT	0.448	
-	5	921		NM_153225	NP_694957	Q8IVN8	RPESP_HUMAN		0	GACACCGAGGA	0.363	
+	3	358	_p.D30N|HNF4G_	NM_004133	NP_004124	Q14541	HNF4G_HUMAN	eceptor.|NR C4-type.	1	GCTGTGATGGG	0.458	
+	10	4672	.E1474K|ZFHX4_	NM_024721	NP_078997	Q86UP3	ZFHX4_HUMAN		15	AGAGCGAAACT	0.498	

+	10	4937	.S1562L|ZFHX4_	NM_024721	NP_078997	Q86UP3	ZFHX4_HUMAN	2H2-type 12.	15	ATAATTCAGTTTC	0.398
+	10	7831	.P2527S|ZFHX4_	NM_024721	NP_078997	Q86UP3	ZFHX4_HUMAN		15	ACTCTCCGTTCT	0.507
-	2	89	P12_uc003ycg.3_	NM_001105281	NP_001098751	A6NFH5	FBP12_HUMAN		0	TTCCTGCTGGCT	0.348
-	9	979	nse_Mutation_p.S	NM_001738	NP_001729	P00915	CAH1_HUMAN		2	AAAATGAAGCT	0.403
-	4	375	ense_Mutation_p.E	NM_001738	NP_001729	P00915	CAH1_HUMAN		2	TAATTTCTTTGGC	0.408
-	1	119		NM_019098	NP_061971	Q9NQW8	CNGB3_HUMAN	lasmic (Potential).	3	CCGACGAGAAC	0.423
-	1	420		NM_152418	NP_689631	Q8NA75	DC4L2_HUMAN		1	GGGTCGTCAGG	0.542
+	6	889	ense_Mutation_p.F	NM_052832	NP_439897	Q8TE54	S26A7_HUMAN	ical; (Potential).	2	AAATGCCATATAT	0.398
+	36	6442	iw.2_Missense_Mu	NM_017890	NP_060360	Q7Z7G8	VP13B_HUMAN		20	AAAATTCATGGT	0.393
+	50	9364	iw.2_Nonsense_M	NM_017890	NP_060360	Q7Z7G8	VP13B_HUMAN		20	GGACATCAGAAG	0.403
-	6	1678	e_Mutation_p.S50	NM_013437	NP_038465	Q9Y561	LRP12_HUMAN	lasmic (Potential).	0	TCAAATGATCTTT	0.363
+	8	1146	ense_Mutation_p.	NM_012082	NP_036214	Q8WW38	FOG2_HUMAN	2H2-type 3.	5	AGACTCAGAGG	0.502
-	2	1028		NM_139166	NP_631905	Q8N0Z2	ABRA_HUMAN		2	CATCTCGTCTGT	0.473
+	15	1549		NM_177531	NP_803875	Q86WI1	PKHL1_HUMAN	ellular (Potential).	14	AGTATCGAAATG	0.358
+	68	11010		NM_177531	NP_803875	Q86WI1	PKHL1_HUMAN	ellular (Potential).	14	ATGAGGATTTAC	0.284
-	50	8000	p.S2574F|CSMD3_	NM_198123	NP_937756	Q7Z407	CSMD3_HUMAN	ar (Potential).|Sushi 14.	63	CATAGGAAGAC	0.468
+	8	1290	Ilia.1_Missense_M	NM_173851	NP_776250	Q8IWU4	ZNT8_HUMAN	lasmic (Potential).	4	GAATCTCCAGTT	0.507
+	45	5261	yoz.2_Missense_M	NM_021110	NP_066933	Q05707	COEA1_HUMAN	lical region 2 (COL1).	12	CACCTGGAGCC	0.652
-	1	83	3yqt.2_Missense_	NM_004306	NP_004297	P27216	ANX13_HUMAN		3	ATGACGATTGC	0.353
-	42	3629	Iljo.1_Missense_M	NM_152888	NP_690848	Q8NFW1	COMA1_HUMAN	ly-rich.|Collagen-like 9.	13	CCGGGGATCCT	0.423
+	19	3112		NM_001702	NP_001693	O14514	BAI1_HUMAN	lasmic (Potential).	8	TACATTCGCTCA	0.592
-	24	2842	3zkl.2_Missense_	NM_002839	NP_002830	P23468	PTPRD_HUMAN	III 5.|Extracellular (Potentia	22	ACTAGGAACTG	0.433
-	9	2055	EM1_uc010mic.2_	NM_144966	NP_659403	Q5H8C1	FREM1_HUMAN	CSPG 2.	5	GGAGTCGCTGT	0.527
+	2	206	_p.R27C|ADAMT	NM_001040272	NP_001035362	Q8N6G6	ATL1_HUMAN		5	CCGCACGCTCC	0.582
-	1	3572	uc003zrh.1_5'Flan	NM_153809	NP_722516	Q8IZX4	TAF1L_HUMAN		26	TTGTTTCCTGAT	0.493
-	5	497	T1_uc003zxf.1_R	NM_014450	NP_055265	Q9Y3P8	SIT1_HUMAN	lasmic (Potential).	0	AGGAGGCCGCA	0.632
-	2	288	9orf128_uc011lpg	NM_001012446	NP_001012448	A6H8Z2	CI128_HUMAN		0	TGCTTCCATCTA	0.507
-	4	1113		NM_015667	NP_056482	Q5VU36	F75A5_HUMAN		0	GCAAATAATTTAA	0.438
+	44	5908	p.S1883F|VPS13	NM_033305	NP_150648	Q96RL7	VP13A_HUMAN		10	TAAATTCCCTTGG	0.338
-	2	499		NM_017594	NP_060064	Q96HU8	DIRA2_HUMAN		0	CACCTCGCGGC	0.577
-	9	2042	ri.1_Missense_Mu	NM_004560	NP_004551	Q01974	ROR2_HUMAN	Potential).|Protein kinase.	20	CAGGTCCTTGT	0.592
-	3	2700	bq.1_Missense_M	NM_133445	NP_597702	Q8TCU5	NMD3A_HUMAN	lasmic (Potential).	7	CAAATGGACTC	0.493
-	2	1670	bq.1_Missense_M	NM_133445	NP_597702	Q8TCU5	NMD3A_HUMAN	ellular (Potential).	7	ATCTCCCAGCA	0.507
+	1	280		NM_001004483	NP_001004483	Q8NGS7	O13C8_HUMAN	ellular (Potential).	2	TTTCCTTCTCTG	0.473
+	4	1743	lwx.1_Missense_	NM_133465	NP_597722	Q8N8K9	K1958_HUMAN		1	CATGTCGGGCG	0.567
+	6	1051	RY_uc010muw.2_	NM_017688	NP_060158	Q5W0U4	BSPRY_HUMAN	B30.2/SPRY.	1	AGTTTCGTTTC	0.617
-	8	2554		NM_014618	NP_055433	O60477	DBC1_HUMAN		8	GTCCCGAATAT	0.572
-	1	658	J2_uc004bmj.1_I	NM_001004451	NP_001004451	Q8NGS3	OR1J1_HUMAN	lasmic (Potential).	2	AATGTGACCAT	0.483
-	1	893		NM_001004454	NP_001004454	Q8NGR8	OR1L8_HUMAN	lasmic (Potential).	3	CCTGTTTCAGG	0.453
+	24	3982	bpr.2_Missense_	NM_015635	NP_056450	Q14C86	GAPD1_HUMAN		4	CACTCGTTGTC	0.413
-	4	487	NAC4_uc004bst.	NM_175039	NP_778204	Q9H4F1	SIA7D_HUMAN	enal (Potential).	0	GGGCTCGCGGA	0.632
+	3	172	wq.1_Nonsense_	NM_015354	NP_056169	Q5SRE5	NU188_HUMAN		7	TTACTACAAACCT	0.403
-	4	280	.Q16*|USP20_uc	NM_016520	NP_057604	Q9NZ63	CI078_HUMAN		0	TCATCTGAAAGG	0.408
+	30	2924		NM_000093	NP_000084	P20908	CO5A1_HUMAN	le-helical region.	11	AGGGTCGCGGA	0.637
-	5	747		NM_182974	NP_892019	Q7Z4J2	GL6D1_HUMAN	enal (Potential).	1	CACCTCGTCCT	0.602
-	7	939	be.2_Missense_	NM_001012415	NP_001012415	Q5JUK2	SOLH1_HUMAN		2	ACGCAGACCTG	0.617
-	11	1723	H1_uc004cia.1_5	NM_017617	NP_060087	P46531	NOTC1_HUMAN	GF-like 15; calcium-binding	856	GTGGCAGGGGT	0.672

+	42	5933	coi.2_Missense_M	NM_000718	NP_000709	Q00975	CAC1B_HUMAN	lasmic (Potential).	6	ACCAAGAGAGT	0.567	
+	8	908	F2RA_uc010ncu.2	NM_001161529	NP_001155001	P15509	CSF2R_HUMAN	ellular (Potential).	2	TTAACGGAACC	0.403	rs137852353
+	6	975	f.1_Missense_Mu	NM_004042	NP_004033	P54793	ARSF_HUMAN		2	GGCACGAGATC	0.478	
+	22	3306	1_uc010nen.2_N	NM_003611	NP_003602	O75665	OFD1_HUMAN	nteraction with SDCCAG8.	0	TGGTCCAAGAA	0.353	
-	7	913	B11_uc010nes.1_	NM_080873	NP_543149	Q8WXH4	ASB11_HUMAN	SOCS box.	3	TGGCTTGATGAC	0.488	
+	7	763		NM_007220	NP_009151	Q9Y2D0	CAH5B_HUMAN		0	TCATTTGACCCT	0.512	
-	4	494	fo.1_Missense_M	NM_152780	NP_689993	Q96T17	MA7D2_HUMAN		3	ATGTCCTCCGG	0.587	
+	12	1527	_p.V442I|PHEX_u	NM_000444	NP_000435	P78562	PHEX_HUMAN	ellular (Potential).	3	AGGGCGTTCGC	0.433	
+	1	1635		NM_182699	NP_874358	Q86TM3	DDX53_HUMAN	case C-terminal.	3	AAGCGGAAACA	0.373	
-	13	1213	se_Mutation_p.F3	NM_001033583	NP_001028755	Q9Y305	ACOT9_HUMAN		3	AAAGAAAGAGC	0.403	
-	4	1803		NM_030624	NP_085127	Q96M94	KLH15_HUMAN	Kelch 4.	2	TCTGGGTTGTAT	0.473	
+	2	1064		NM_173699	NP_775970	Q96M61	MAGBI_HUMAN	MAGE.	1	ATACATGATACC	0.527	
+	2	648	B6_uc010ngc.1_	NM_173523	NP_775794	Q8N7X4	MAGB6_HUMAN		3	AAATATGATGTG	0.498	
+	2	943		NM_001099921	NP_001093391	A2A368	MAGBG_HUMAN	MAGE.	7	CCACTGAAGAG	0.488	
+	1	1956		NM_001013736	NP_001013758	Q5HY64	FA47C_HUMAN		3	CTCCCAATACT	0.642	rs145580328
-	3	320	_p.E92K|CASK_u	NM_003688	NP_003679	O14936	CSKP_HUMAN	rotein kinase.	6	CAATTCGAAAA	0.358	
-	11	905	djk.3_Missense_M	NM_033518	NP_277053	Q8WUX1	S38A5_HUMAN	ellular (Potential).	3	GTTGAGTCCTT	0.522	
+	6	1598	E434K|CCNB3_u	NM_033031	NP_149020	Q8WWL7	CCNB3_HUMAN		9	CCCAGGAACCA	0.458	
-	20	2822		NM_001013742	NP_001013764	Q5KSL6	DGKK_HUMAN		2	TTTCTCCATCA	0.453	
-	5	1838	sc.2_Nonsense_M	NM_001111125	NP_001104595	Q5JU85	IQEC2_HUMAN	Pro-rich.	3	GCGCCCAGAAC	0.652	
-	33	4337	sn.2_Missense_M	NM_031407	NP_113584	Q7Z6Z7	HUWE1_HUMAN		17	CCCGGCGGGAG	0.557	
+	1	566		NM_015686	NP_056501	O75949	F155B_HUMAN		2	CCTTTCCCGTG	0.592	
-	3	3301		NM_001008537	NP_001008537	Q5QGS0	K2022_HUMAN		15	TGCCAGAAGTA	0.478	
-	25	6039	.K1898R|ATRX_u	NM_000489	NP_000480	P46100	ATRX_HUMAN	Poly-Lys.	30	TCCCCTTTTTCC	0.318	
+	9	2246	A_uc004ecw.2_3'	NM_000052	NP_000043	Q04656	ATP7A_HUMAN	ellular (Potential).	0	AACCTTCATTCT	0.388	
+	3	903	fc.3_Missense_M	NM_033048	NP_149037	Q8N123	CPXCR_HUMAN		3	ATCAGGAAAAT	0.413	
-	1	2802	p.R376C|PCDH1	NM_020766	NP_001098713	Q8TAB3	PCD19_HUMAN	|Extracellular (Potential).	7	GTCGCGATCAG	0.597	
-	9	1314	p.E370K|NOX1_u	NM_007052	NP_008983	Q9Y5S8	NOX1_HUMAN	type.|Extracellular (Potenti	1	TTGTTCGAAAG	0.463	
+	15	2008	h.1_Missense_Mu	NM_001939	NP_001930	Q13474	DRP2_HUMAN		2	TGGGTGAAGTG	0.507	
+	4	784	msz.1_Splice_Site_p.Q172_splice|ALG13_uc011mta.1_			Q9NP73	ALG13_HUMAN		1	GCAGGTAAAAG	0.443	
-	3	1281	4esz.2_Missense_	NM_152692	NP_689905	Q96EU7	C1GLC_HUMAN	enal (Potential).	0	ATTTGGAGGTA	0.388	
-	1	991		NM_138289	NP_612146	Q8TDG2	ACTT1_HUMAN		5	GGTCAGGTGCA	0.512	
+	5	632	num.1_Missense_	NM_003399	NP_003390	O43895	XPP2_HUMAN		0	ACTGGGAGCTC	0.542	
+	10	1252		NM_003399	NP_003390	O43895	XPP2_HUMAN		0	GAAATGATACCC	0.527	
-	18	3903	.G1216E|IGSF1_	NM_001555	NP_001546	Q8N6C5	IGSF1_HUMAN	otential).|Ig-like C2-type 12	5	TAGTTTCCAATG	0.498	
-	6	2076	vf.1_Missense_M	NM_031907	NP_114113	Q9BXU7	UBP26_HUMAN		8	CTGGTCATTCT	0.413	
+	21	8611	sb.1_Missense_M	NM_153834	NP_722576	Q8IZF6	GP112_HUMAN	lasmic (Potential).	12	GAAAAGATTATC	0.333	
-	17	2298	_p.M485I|ARHGE	NM_004840	NP_004831	Q15052	ARHG6_HUMAN		0	ATAAGACATCCT	0.338	
-	17	2195	n.1_Missense_Mu	NM_005369	NP_005360	P10911	MCF2_HUMAN	DH.	2	TGATTCGTTGCA	0.279	
-	2	271	NXC_uc004fbl.2_	NM_022661	NP_073152	Q9NY87	SPNXC_HUMAN		0	TCTCGGGCGTGG	0.448	
+	4	551	EC1_uc010nsl.1_	NM_005462	NP_005453	O60732	MAGC1_HUMAN		4	CTGAGGGCGAC	0.582	
-	3	907		NM_016249	NP_057333	Q9UBF1	MAGC2_HUMAN	MAGE.	2	GAACTCACGGG	0.483	
-	2	2513	fby.2_Missense_M	NM_173078	NP_775101	Q8IW52	SLIK4_HUMAN	lasmic (Potential).	2	AGGATCTGAAA	0.423	
-	2	2142	fby.2_Missense_M	NM_173078	NP_775101	Q8IW52	SLIK4_HUMAN	ellular (Potential).	2	ATGGTGCAGAC	0.443	
-	2	420	fby.2_Missense_	NM_173078	NP_775101	Q8IW52	SLIK4_HUMAN		2	TTGTCGAAGAA	0.388	
-	5	861	4ffl.2_Missense_	NM_001011543	NP_001011543	P43363	MAGAA_HUMAN	MAGE.	0	CTCCTTCATTTG	0.453	
+	8	988		NM_018558	NP_061028	Q9UN88	GBRT_HUMAN	p.S323F(1)	3	ACATTTCCTGTA	0.443	

+	9	1213		NM_018558	NP_061028	Q9UN88	GBRT_HUMAN			3	TCAGCTCTCTCC	0.587	
-	3	1078	AGEA12_uc004fg	NM_005367	NP_005358	P43365	MAGAC_HUMAN	MAGE.		1	CCTGGGATGCG	0.572	
-	3	966		NM_005362	NP_005353	P43357	MAGA3_HUMAN	MAGE.		0	AGTTTTCCTGCA	0.527	
+	5	826		NM_020061	NP_064445	P04000	OPSR_HUMAN	Cytoplasmic.		0	AGAAGGAAGTG	0.572	
+	8	1908		NM_017514	NP_059984	P51805	PLXA3_HUMAN	cellular (Potential).		3	AGGCGGCGGCG	0.692	
+	12	2906_2908	9vqi.1_In_Frame_	NM_001083621	NP_001077090	Q9NUA8	ZBT40_HUMAN			1	CCCCAAGAAGA	0.517	
+	8	890_892	.R259del|SFRS11	NM_004768	NP_004759	Q05519	SRS11_HUMAN	epeats of R-R-S-R- S-R-S-		0	TTCTAGGAGGA	0.3	
+	5	642_643	11A_uc001haf.2_	NM_014827	NP_055642	O75152	ZC11A_HUMAN	C3H1-type 1.		2	ACTGCTATTTTTT	0.371	
-	3	613	pzb.1_Frame_Shi	NM_001040151	NP_001035241	Q9NY72	SCN3B_HUMAN	e.|Extracellular (Potential).		6	CTTTACCGCCCT	0.587	
+	2	272	HB2_uc010sfu.1_	NM_006331	NP_006322	Q92979	NEP1_HUMAN			0	CCGTAGTTTATTG	0.569	857448;rs36063533
+	4	268_273	03ckr.2_In_Frame	NM_001904	NP_001895	P35222	CTNB1_HUMAN	el(1)|p.H24_G38del(1)|p.G		3166	TCTGGTGCCACT	0.5	
+	6	1385	1cam.1_Frame_Sh	NM_001075	NP_001066	P36537	UDB10_HUMAN			5	CAGTGAAGCCC	0.398	
+	11	2071_2072	.Q426fs|POM121	NM_172020	NP_742017	Q96HA1	P121A_HUMAN	side (Potential).		0	AACCCCAAGCC	0.614	
+	4	766_768	Q238del|SMARC	NM_003070	NP_003061	P51531	SMCA2_HUMAN	Poly-Gln.		3	cagcaacagcagcag	0.271	070757;rs62639301
+	13	2110_2112	E598del|GRIN1_uc	NM_007327	NP_015566	Q05586	NMDZ1_HUMAN	lasmic (Potential).		1	CAGCGAGGAGG	0.739	
+	12	2906_2908	9vqi.1_In_Frame_	NM_001083621	NP_001077090	Q9NUA8	ZBT40_HUMAN		NA	1	CCCCAAGAAGA	0.517	
+	6	945_947	n.2_RNA|CHGA_u	NM_001275	NP_001266	P10645	CMGA_HUMAN		NA	2	AGAgaagaggagga	0.557	
-	1	287_289	G1_uc002fcw.3_In_	NM_001145667	NP_001139139	Q92896	GSLG1_HUMAN	ar (Potential	NA	2	gttgctgttgctgctgctg	0.562	
-	13	1762_1764	ame_Del_p.S584d	NM_013403	NP_037535	Q9NRL3	STRN4_HUMAN	WD 3.	NA	0	CCGGGCTGCTG	0.7	
-	1	871_873	.S246del|TCF20_	NM_005650	NP_005641	Q9UGU0	TCF20_HUMAN	Ser-rich.	NA	5	AAGGGAaggagga	0.438	
+	3	532	ie.2_Frame_Shift_	NM_014346	NP_055161	Q8WUA7	TB22A_HUMAN		NA	1	CCTCACCCCCC	0.677	
-	25	3357	34_splice|MAP3K	NM_001001671	NP_001001671	Q6ZN16	M3K15_HUMAN		NA	7	atttacctaaaaaaaaa	0.421	
+	20	4967	1aoj.2_Frame_Shi	NM_015215	NP_056030	Q9Y6Y1	CMTA1_HUMAN	IQ 2.		9	ATGAACAAAAAA	0.473	
-	2	961	_p.D86fs|PIK3R3_	NM_003629	NP_003620	Q92569	P55G_HUMAN	SH2 1.		0	AAATATCCCCCC	0.353	
-	1	157_165	S_uc001dkd.2_5'	NM_004388	NP_004379	Q01459	DIAC_HUMAN			0	AGCCgcagcgccag	0.589	
-	2	1126	1fpt.1_Frame_Shi	NM_030980	NP_112242	Q9H9L3	I20L2_HUMAN	Exonuclease.		2	GTTGAGGGGGG	0.557	
+	16	4804	omh.1_Frame_Shi	NM_015172	NP_055987	Q9Y520	PRC2C_HUMAN			0	GGGATGAAAAAA	0.388	
+	7	1484_1486	e_Del_p.P386del|	NM_005807	NP_005798	Q92954	PRG4_HUMAN	ats of K-X-P-X-P-T-T-X.|17		1	CACCACTCCCAA	0.65	095882;rs143141440
-	11	1639	010pqc.1_Frame_	NM_021633	NP_067646	Q53G59	KLH12_HUMAN	n with DVL3.|Kelch 5.		0	CAAATCCCCCC	0.453	
+	1	753_754	y.2_Intron|DHDPS	NM_001009997	NP_001009997	Q5T681	CJ062_HUMAN	His-rich.		0	GCCAATCACACA	0.545	
+	1	310_312		NM_178168	NP_835462	Q9H207	O10A5_HUMAN	Name=3; (Potential).		3	TGTATTTCTTCTT	0.517	
-	1	258	RNA|PIK3C2A_uc	NM_002645	NP_002636	O00443	P3C2A_HUMAN	ction with clathrin.		10	CTGTGCTTTTTTT	0.398	
+	7	1983_1985	1qtt.1_In_Frame_	NM_018416	NP_060886	Q9P0K8	FOXJ2_HUMAN	Poly-Gln.		5	acctcaacagcagcag	0.478	
-	3	314_315		NM_006248	NP_006239					0	GGAGGTGGGG	0.614	
-	2	1302	raq.2_Frame_Shift	NM_006143	NP_006134	Q15760	GPR19_HUMAN	lasmic (Potential).		1	ACGTAGTTTTTTT	0.398	
+	4	669	|FAR2_uc009zjm.2	NM_018099	NP_060569	Q96K12	FACR2_HUMAN			0	GGAGCCAAAAAA	0.388	
+	2	685_687		NM_145657	NP_663632	Q9H4S2	GSX1_HUMAN	Poly-Gly.		1	CCATCgtggcggcgg	0.463	
+	3	707_710	vbk.2_Frame_Shi	NM_015116	NP_055931	Q9Y2L9	LRCH1_HUMAN	LRR 3.		2	CCGCCCTGCCTG	0.436	
-	5	1068	_p.L72fs|DZIP1_u	NM_198968	NP_945319	Q86YF9	DZIP1_HUMAN			2	GCGCTCAGCCG	0.662	
-	1	772_774		NM_001080396	NP_001073865	B1AL88	F155A_HUMAN	Poly-Gln.		1	cgctgcctctgctgctgc	0.404	
-	10	11252_1125	3_uc002fcl.2_In_F	NM_006885	NP_008816	Q15911	ZFHX3_HUMAN	Poly-Gly.		4	GTACGAgccgccg	0.394	
-	14	1600_1602	jca.2_In_Frame_	NM_017647	NP_060117	Q8IY81	RRMJ3_HUMAN			1	GGATTCTCCTCC	0.537	
-	5	1361_1363		NM_003655	NP_003646	O00257	CBX4_HUMAN	Interaction with BMI1.		2	CGACGGCgtggtgg	0.507	rs3833850
+	7	712_714		NM_001039887	NP_001034976	Q2NL68	CS055_HUMAN	Ser-rich.		1	TCCATCTCCTCC	0.631	
+	7	1058	me_Shift_Del_p.P	NM_021913	NP_068713	P30530	UFO_HUMAN	tential).|Fibronectin type-III		13	CCGTGCCCCCC	0.647	
+	14	2665_2666	NRNPUL1_uc002	NM_007040	NP_008971	Q9BUJ2	HNRL1_HUMAN	cessary for interaction with		2	GGTTACAACCCG	0.629	
+	1	96_98	2sda.2_In_Frame_	NM_203437	NP_982261	Q6ULP2	AFTIN_HUMAN			2	CAGAGGATGATG	0.409	

+	25	3447	mp.1_Frame_Shif	NM_001017915	NP_001017915	Q92835	SHIP1_HUMAN	Pro-rich.		2	GCCGGCGGGG	0.711	
-	4	308_310	02wle.2_RNA|RA	NM_170774	NP_739580	P50749	RASF2_HUMAN			6	TGCCAGGAGGA	0.611	
+	6	612_614	15_uc002zsr.2_In	NM_001003891	NP_001003891	Q96RN5	MED15_HUMAN	Poly-Gln.		1	gcgctacagcagcag	0.148	
-	30	4280_4282		NM_002473	NP_002464	P35579	MYH9_HUMAN	Potential.		11	TTGGCCTCCTC	0.65	
-	1	205_207	g.1_In_Frame_De	NM_004628	NP_004619	Q01831	XPC_HUMAN	lu.|Glu-rich (acidic).		3	TCACCCTCCTC	0.734	rs72561774
-	11	3554_3556	.Q639del|SATB1_	NM_002971	NP_002962	Q01826	SATB1_HUMAN	Poly-Gln.		4	CGGTGCctgctgc	0.468	
-	7	2209_2211	1blc.1_In_Frame_	NM_001017395	NP_001017395	O94876	TMCC1_HUMAN	Potential.		1	CCACCTGCTGC	0.581	
-	8	1759_1761	91DD>D|DBR1_u	NM_016216	NP_057300	Q9UK59	DBR1_HUMAN			0	TGCATCGTCAT	0.251	0114751;rs2622736
+	42	6369_6371	bnz.1_In_Frame_	NM_053002	NP_443728	Q86YW9	MD12L_HUMAN	Gln-rich.		7	GACCCAGCAGC	0.527	
+	1	3836_3837		NM_175918	NP_787114	Q8N1N5	CRPAK_HUMAN			0	CTGCTCACACGT	0.683	
+	1	3867_3868		NM_175918	NP_787114	Q8N1N5	CRPAK_HUMAN			0	CTGCTCACACGT	0.673	
+	1	3958_3959		NM_175918	NP_787114	Q8N1N5	CRPAK_HUMAN	9		0	CTGCTCACACA	0.668	
-	7	944		NM_173536	NP_775807	Q8N1C3	GBRG1_HUMAN	ellular (Probable).		2	AGGTCAAAAAA	0.294	
-	3	747_748	_Shift_Ins_p.K74f	NM_003948	NP_003939	Q92772	CDKL2_HUMAN	rotein kinase.		7	CCATCGTTTTTT	0.322	
-	1	479_480		NM_001085377	NP_001078846	P23508	CRCM_HUMAN			1	ctgccgctgccgccgc	0.391	
+	4	461_462	MRPS18B_uc011	NM_014046	NP_054765	Q9Y676	RT18B_HUMAN			1	TTGTTGGGAATC	0.401	
-	2	531_533	rb.3_In_Frame_De	NM_001134870	NP_001128342	Q6NYC8	PHTNS_HUMAN	Poly-Gln.		0	GTtgttgttgctgctgct	0.547	
+	15	2548_2549	p.R756fs|SYNGA	NM_006772	NP_006763	Q96PV0	SYGP1_HUMAN	inding (Potential).		4	TGGCTCGCCTCC	0.594	
-	3	422_424	ame_Del_p.40_41	NM_007162	NP_009093	P19484	TFEB_HUMAN	y-Gln.|Gln-rich.		1	gctgctgttgctgctgctg	0.547	rs150746914
+	10	1627_1629	ENP6_uc003pic.	NM_015571	NP_056386	Q9GZR1	SENP6_HUMAN			6	CCAGTGATGAT	0.296	
+	3	157		NM_001008395	NP_001008396	Q0VGL1	CG059_HUMAN			0	CATCTGGGGAC	0.448	
+	7	1118_1119	vuy.2_Frame_Shif	NM_016019	NP_057103	Q9Y383	LC7L2_HUMAN	Arg/Ser-rich.		0	GAGAAGAGAGA	0.391	
+	3	834_835	SCO2_uc003xgh.	NM_001017420	NP_001017420	Q56NI9	ESCO2_HUMAN			1	TCAGTGAAAAAA	0.396	rs80359852
+	14	1975	_Splice_Site|WDR	NM_145647	NP_663622	Q96DN5	WDR67_HUMAN			1	TTACAGTTTTTT	0.322	
+	4	766_768	Q238del|SMARC	NM_003070	NP_003061	P51531	SMCA2_HUMAN	Poly-Gln.		3	cagcaacagcagcag	0.271	070757;rs62639301
+	1	160_162		NM_001039792	NP_001034881	Q6UXD1	HRCT1_HUMAN	ical; (Potential).		0	GCGGTCctgctgct	0.601	
+	3	1021_1023	bag.1_In_Frame_	NM_006981	NP_008912	Q92570	NR4A3_HUMAN	Poly-His.		173	tcaccatcaccaccacc	0.483	
-	18	3468	Y2F_uc011msq.1_	NM_001522	NP_001513	P51841	GUC2F_HUMAN	lasmic (Potential).		8	AAGCCTTTTTTC	0.418	
+	1	50	el_p.M1fs|IQCC_	NM_018134	NP_060604	Q4KMZ1	IQCC_HUMAN			4	CCCATGGAGCC	0.652	
+	7	1484_1486	e_Del_p.P386del|	NM_005807	NP_005798	Q92954	PRG4_HUMAN	ats of K-X-P-X-P-T-T-X.|17		1	ACCACTCCCAA	0.65	095882;rs143141440
+	2	452_454	4A_uc002rca.1_5	NM_145175	NP_660158	Q96KN4	FA84A_HUMAN	Poly-His.		1	GCCGCCACCAC	0.64	
-	1	479_480		NM_001085377	NP_001078846	P23508	CRCM_HUMAN			1	ctgccgctgccgccgc	0.391	
-	11	2666_2668		NM_015117	NP_055932	Q8IXZ2	ZC3H3_HUMAN	Poly-Ser.	p.S879F(1)	1	ggggatgaggaggag	0.552	;rs2272753;rs137878905
+	4	753	ni.2_Frame_Shift_	NM_014874	NP_055689	O95140	MFN2_HUMAN	lasmic (Pote	NA	1	GTGGCTTTTTTT	0.537	
+	8	5294	.2_Intron|PRDM2_	NM_012231	NP_036363	Q13029	PRDM2_HUMAN		NA	1	TGTCCCAAAAAA	0.428	
+	3	345	_Shift_Del_p.D62fs	NM_018125	NP_060595	Q9HCE6	ARGAL_HUMAN		NA	3	ACAGACCCCCC	0.587	
-	4	4772	_Shift_Del_p.Q118	NM_024503	NP_078779	Q5T1R4	ZEP3_HUMAN		NA	6	GGCTTGAAATA	0.597	
+	4	741_743		NM_173642	NP_775913	Q8IXN7	RIMKA_HUMAN	ATP-grasp.	NA	0	TCCGGGTGGTG	0.542	
+	2	545_547	10okl.1_In_Frame	NM_003780	NP_003771	O60909	B4GT2_HUMAN	enal (Poten	NA	2	GCTGCTagcagcag	0.616	rs149892509
+	4	327_329	326_uc009wda.1_	NM_182976	NP_892021	Q5BKZ1	ZN326_HUMAN	l activation	NA	1	CACAGTGGTGG	0.409	
-	9	1607	0ovy.1_Frame_Sh	NM_004696	NP_004687	O15374	MOT5_HUMAN	ical; (Potent	NA	3	GGTACAAAAAAA	0.388	
-	1	273_274	_Shift_Del_p.P6fs|	NM_024408	NP_077719	Q04721	NOTC2_HUMAN		NA	27	GAGCGGGGCG	0.663	
+	4	724	3_5'UTR|NOTCH	NM_203458	NP_982283	Q7Z3S9	NT2NL_HUMAN	EGF-like 4.	NA	1	GGAAGTACCTG	0.498	
+	14	2499	_Shift_Del_p.G778	NM_019032	NP_061905	Q6UY14	ATL4_HUMAN	SP type-1 2	NA	2	AATTTGGGGGG	0.692	rs149280379
-	1	643_645	.E61del|MCL1_uc	NM_021960	NP_068779	Q07820	MCL1_HUMAN	PEST-like.	NA	0	CTCGTCCTCCT	0.635	
-	2	2734_2736	wne.1_In_Frame_	NM_007113	NP_009044	Q07283	TRHY_HUMAN	30 AA tande	NA	5	GTAGCTCCTCC	0.586	rs143222885
-	4	1374_1375		NM_006617	NP_006608	P48681	NEST_HUMAN	Tail.	NA	6	GGAGCAGAGAG	0.649	

-	6	1004_1006	X1A_uc001gcw.1_	NM_177398	NP_796372	Q8TE12	LMX1A_HUMAN	y-Gln.|Gln-r	NA	5	ATCTTGCTGCT	0.567	
-	11	1182_1192	MNAT2_uc001gq	NM_015039	NP_055854	Q9BZQ4	NMNA2_HUMAN		NA	1	TCCACAACATG	0.578	
+	5	701	.2_RNA|CR1L_uc	NM_175710	NP_783641	Q2VPA4	CR1L_HUMAN	Sushi 3.	NA	0	GAGGGAAAAG	0.507	
-	5	1798	AGT_uc009xff.2_F	NM_000029	NP_000020	P01019	ANGT_HUMAN		NA	0	AGCTCAAAAAA	0.562	
-	20	2528_2530	E813del|SFMBT2_	NM_001029880	NP_001025051	Q5VUG0	SMBT2_HUMAN		NA	8	AGTCTCTCCTCC	0.596	
+	16	3776_3778	_p.E1094del|KIAA	NM_019590	NP_062536	Q5T5P2	SKT_HUMAN		NA	7	GGAGGAAGAAG	0.552	
-	10	966_967	p.V188fs|MPP7_u	NM_173496	NP_775767	Q5T2T1	MPP7_HUMAN	PDZ.	NA	1	CGTTGACTTCCC	0.351	
-	2	2633_2635	e_Del_p.720_721	NM_020848	NP_065899	Q9P266	K1462_HUMAN	Ser-rich.	NA	4	TCCTCActgctgct	0.463	
-	15	1912	_p.K570fs|FRMPD	NM_001018071	NP_001018081	Q68DX3	FRPD2_HUMAN	FERM.	NA	1	TGAACTTTTTTT	0.463	
+	8	1926		NM_001077665	NP_001071133	Q5VW22	AGAP6_HUMAN		NA	1	GTCTTGGCCCC	0.527	
+	25	3716	_p.D924fs|ZMIZ1_	NM_020338	NP_065071	Q9ULJ6	ZMIZ1_HUMAN		NA	4	CTGGACCCCCC	0.557	
+	10	2052		NM_015188	NP_056003	O60347	TBC12_HUMAN	ab-GAP TB	NA	0	TTGGCCTTTTTT	0.418	
-	2	240_241	_Shift_Del_p.P47f	NM_001164	NP_001155	O00213	APBB1_HUMAN		NA	2	TCCTTGGGTCC	0.688	
-	3	345	rew.1_Frame_Shi	NM_001001991	NP_001001991	Q6UXH9	PAMR1_HUMAN		NA	2	AGGTACCCCCC	0.517	
-	24	2496_2498	PC3_uc010rhl.1_	NM_000256	NP_000247	Q14896	MYPC3_HUMAN	nectin type-	NA	3	GTAGCTCTTCTT	0.601	
+	18	2022_2023		NM_006133	NP_006124	Q9Y4D2	DGLA_HUMAN	lasmic (Pot	NA	3	GCCTTCAATGAG	0.594	
+	3	548_550	rlo.1_In_Frame_	NM_004265	NP_004256	O95864	FADS2_HUMAN	ical; (Potent	NA	2	TTCTTCCTCCT	0.537	
+	22	2657_2658	_5'Flank|PACS1_	NM_006842	NP_006833	Q13435	SF3B2_HUMAN		NA	3	TACAGCAAAAAA	0.515	
+	1	356_358	RFN4_uc001ojq.1	NM_024036	NP_076941	Q6PJG9	LRFN4_HUMAN		NA	0	GCTCCTGCTGC	0.719	
+	3	321_323	me_Del_p.E98del|	NM_033388	NP_203746	Q8NAA4	A16L2_HUMAN		NA	0	TGGCAGGAGGA	0.591	
-	2	308_322	prt.1_5'UTR|TMP	NM_001077263	NP_001070731	Q9BYE2	TMPSD_HUMAN	-A-[GLQR].|	NA	1	GGAGATGCCCG	0.67	
-	17	2397		NM_004818	NP_004809	Q9BUQ8	DDX23_HUMAN	case C-term	NA	6	CTTTTGTGAGG	0.572	
+	87	3755_13757		NM_002332	NP_002323	Q07954	LRP1_HUMAN	ical; (Potent	NA	22	CTGTTGCTGCT	0.557	
+	54	7280_7281		NM_014503	NP_055318	O75691	UTP20_HUMAN		NA	4	TGGAGCAAAAAA	0.386	
+	5	667_668	CHP_uc001tpp.2_	NM_001143852	NP_001137324	Q9BT92	TCHP_HUMAN	with keratin	NA	1	AAGAAGAAAAAA	0.48	
+	7	784_786	T81_uc001tqj.2_R	NM_001143779	NP_001137251	Q8WYA0	IFT81_HUMAN	Potential.	NA	1	AGAGAGAAGAA	0.35	
+	16	2686_2688	tbn.1_In_Frame_	NM_004592	NP_004583	Q12872	SFSWA_HUMAN	g/Ser-rich (	NA	0	CACGAGAAGAA	0.493	
+	4	523	aaa.2_Frame_Shi	NM_001676	NP_001667	P54707	AT12A_HUMAN	ical; (Potent	NA	6	ATGGTGGGGGG	0.587	
-	5	2069	ne_Shift_Del_p.L5	NM_183044	NP_898865	Q9Y252	RNF6_HUMAN		NA	2	TTTAGTAAAAAAA	0.403	
-	5	1432	ne_Shift_Del_p.R	NM_001142296	NP_001135768	Q8N0X7	SPG20_HUMAN		NA	0	TACCCTTTTTCC	0.373	
-	10	1917_1918	p.R637fs|ZC3H13	NM_015070	NP_055885	Q5T200	ZC3HD_HUMAN	Arg/Ser-rich	NA	2	CAAACCTCTCTC	0.337	
-	1	1020		NM_052910	NP_443142	Q96PX8	SLIK1_HUMAN	xtracellular (	NA	5	AGCCCTTTTTT	0.463	
-	3	1109		NM_000452	NP_000443	Q12908	NTCP2_HUMAN	ical; (Potent	NA	4	CGAGAGAAACC	0.398	
+	8	3011_3013	.Q981del|MGA_uc	NM_001080541	NP_001074010	Q8IWI9	MGAP_HUMAN	Gln-rich.	NA	12	GGCACAGCAGC	0.458	
-	22	2847_2848	a-mir-2116|MI001	NM_004998	NP_004989	Q12965	MYO1E_HUMAN		NA	3	CTGAGGGACA	0.559	
-	17	1884		NM_022450	NP_071895	Q96CC6	RHDF1_HUMAN	enal (Poten	NA	2	CGCTGTTTTTG	0.597	
-	8	1516_1518	_269LL>L|ABCA3_	NM_001089	NP_001080	Q99758	ABCA3_HUMAN	ical; (Potent	NA	16	GCTGAGCAGCA	0.611	rs145342500
-	10	895	NTAN1_uc010uzo.	NM_173474	NP_775745	Q96AB6	NTAN1_HUMAN		NA	0	TCTTCATTTTTTT	0.383	
+	9	1622_1633	C100132247_uc	NM_001135865	NP_001129337	A8MRT5	K220L_HUMAN	Pro-rich.	NA	0	TCCACCCTCAGC	0.571	
+	15	1993_1995	.S436del|SLC5A1	NM_052944	NP_443176	Q8WWX8	SC5AB_HUMAN	lasmic (Pot	NA	2	AGGCCAGCAGC	0.542	
+	17	2641	hift_Del_p.R819fs	NM_173201	NP_775293	O14983	AT2A1_HUMAN	smic (By si	NA	4	GACCGCCCCCC	0.657	
-	2	423_425	2dxs.2_In_Frame_	NM_006110	NP_006101	O95400	CD2B2_HUMAN		NA	1	CCCCCCATCATC	0.532	
+	13	3813_3815		NM_014712	NP_055527	O15047	SET1A_HUMAN	Ser-rich.	NA	3	Gctcctcatcctcctcct	0.389	
+	5	1317_1319	hx.2_In_Frame_D	NM_024335	NP_077311	P78412	IRX6_HUMAN		NA	6	gaggaagaggagga	0.493	
+	3	278_280	vho.1_In_Frame_	NM_020312	NP_064708	O75208	COQ9_HUMAN		NA	1	CGGCGAGGAGG	0.576	rs149029279
+	12	3846_3848	e_Del_p.Q812del|	NM_006599	NP_006590	O94916	NFAT5_HUMAN	Poly-Gln.	NA	0	AATcaacagcagca	0.389	
-	11	2790_2791	91B_uc002fuk.1_	NM_018128	NP_060598	Q2NL82	TSR1_HUMAN		NA	1	CTCTTCCTTGG	0.475	

+	3	449_451	F11_uc010vtw.1_In	NM_175734	NP_783861	Q0P670	CQ074_HUMAN	Arg-rich.	NA	0	TGTTcgtcgccgccg	0.424	
+	8	912_914	.L222del|CHRNB1	NM_000747	NP_000738	P11230	ACHB_HUMAN	ical; (Potent	NA	2	GTTCCTGCTGCT	0.498	
-	15	2000_2002	15_uc002ghy.1_5'I	NM_004860	NP_004851	P51116	FXR2_HUMAN	Poly-Arg.	NA	0	GTTACGGCGGC	0.547	
-	2	1324_1325	glg.1_Frame_Shift	NM_213597	NP_998762	Q6ZNG9	KRBA2_HUMAN	Potential.	NA	0	CAATTTCTAGCT	0.446	
+	5	773_775		NM_178170	NP_835464	Q86SG6	NEK8_HUMAN		NA	6	CCTCTGCATCCG	0.68	
-	1	1572_1573	18A_uc010csa.1_	NM_004740	NP_004731	O95411	TIAF1_HUMAN		NA	0	TGGTCCACACAC	0.564	
+	1	158_160	ime_Del_p.K7del|Z	NM_003457	NP_003448	O43670	ZN207_HUMAN		NA	0	TCGCAAGAAGA	0.542	
-	7	912	hift_Del_p.P262fs	NM_001256	NP_001247	P30260	CDC27_HUMAN		NA	5	GTTTTTGGTTTAT	0.373	
-	2	516_517		NM_004645	NP_004636	P38432	COIL_HUMAN		NA	1	CTCTTGTTTTTTT	0.366	
-	2	311_313	_47EE>E|TEX2_uc	NM_018469	NP_060939	Q8IWB9	TEX2_HUMAN	Poly-Glu.	NA	1	tcctcctcttcctcctcctc	0.468	
-	7	863	_p.P255fs|FECH_u	NM_000140	NP_000131	P22830	HEMH_HUMAN		NA	1	CAAGTGGAAAAT	0.413	
-	8	583	|DENND1C_uc002	NM_024898	NP_079174	Q8IV53	DEN1C_HUMAN	DENN.	NA	1	GGGTAGGGGGG	0.672	
-	23	2332	nnh.2_Frame_Shif	NM_001379	NP_001370	P26358	DNMT1_HUMAN		NA	6	GGTGCATTTTTTT	0.507	
-	23	3693_3694	lxe.2_Frame_Shift_	NM_003331	NP_003322	P29597	TYK2_HUMAN	otein kinase	NA	9	CACCGTGGGGG	0.48	
+	1	529		NM_012377	NP_036509	O60412	OR7C2_HUMAN	cellular (Pote	NA	3	CCGCACTTTTTTT	0.468	
-	11	1320_1321	nfg.1_Frame_Shift_	NM_033417	NP_219485	Q9BT25	HAUS8_HUMAN		NA	0	TGAACGAGAGAG	0.495	
-	2	503_504		NM_031310	NP_112600	Q9BX97	PLVAP_HUMAN	cellular (Pote	NA	0	GCTCTTGTTCAT	0.564	
-	3	909	_Shift_Del_p.I255fs	NM_014884	NP_055699	Q8IX01	SUGP2_HUMAN		NA	0	TGGGTATTTTTTT	0.502	
+	8	1243	mw.3_Frame_Shift	NM_153221	NP_694953	Q8IUL8	CILP2_HUMAN		NA	1	TGCGACCCCCG	0.647	
-	10	1444		NM_021232	NP_067055	Q9UF12	PROD2_HUMAN		NA	2	CACATACCCAGTC	0.582	
-	3	1139_1141	.1_Intron|B3GNT8	NM_198540	NP_940942	Q7Z7M8	B3GN8_HUMAN	.|Lumenal (P	NA	0	AGGCCAGCAGC	0.631	
+	2	1714_1715	osk.3_Frame_Shif	NM_022752	NP_073589	Q6ZN55	ZN574_HUMAN	ype 10; dege	NA	0	CTGCGCACACAC	0.609	
+	14	3239_3241	xyo.1_In_Frame_I	NM_014681	NP_055496	Q14147	DHX34_HUMAN		NA	5	AGCTGGAGGAG	0.66	
-	1	81_82	K1_uc010ycg.1_R	NM_002257	NP_002248	P06870	KLK1_HUMAN		NA	0	ACCAGTCCCCCC	0.653	
-	4	472	wl.2_Frame_Shift_	NM_001161748	NP_001155220	P55344	LMIP_HUMAN	ical; (Potent	NA	0	ACCCAGCCCAGG	0.607	
+	6	841	2_Frame_Shift_De	NM_002255	NP_002246	Q99706	KI2L4_HUMAN		NA	1	TGCTCCAAAAAA	0.532	rs66505238
-	11	1472_1474	1_In_Frame_Del_	NM_015317	NP_056132	Q8TB72	PUM2_HUMAN	Ala-rich.	NA	1	TCCAGCTGCTG	0.424	
-	11	2183	R113_uc010eyk.1_	NM_001145168	NP_001138640	Q8IZF5	GP113_HUMAN	tracellular (P	NA	4	ACCAACCCCCC	0.612	
-	29	4736	0ezy.1_Frame_Sh	NM_019024	NP_061897	Q9P2D3	HTR5B_HUMAN		NA	8	GACTCTGAGCAC	0.438	
-	2	234_236	HX57_uc002rrg.2_	NM_198963	NP_945314	Q6P158	DHX57_HUMAN	Gly-rich.	NA	3	gccacctccaccacca	0.384	
-	12	966	Shift_Del_p.P292fs	NM_003618	NP_003609	Q8IVH8	M4K3_HUMAN		NA	8	TGATCTGGATTAT	0.323	
-	6	747_749	l.2_In_Frame_Del_	NM_016079	NP_057163	Q9Y3E7	CHMP3_HUMAN	T-interacting	NA	1	CCTCTTCCTCCT	0.616	
-	7	1136	fos.2_Frame_Shift_	NM_002349	NP_002340	O60449	LY75_HUMAN	cellular (Pote	NA	0	TCTGAGTATGTCC	0.383	
+	1	285	D10_uc010zdh.1_	NM_006063	NP_006054	O60662	KBTBA_HUMAN	BTB.	NA	0	AGGCGAAAAAA	0.388	
-	8	1171_1172	02utu.2_Frame_Sh	NM_012086	NP_036218	Q9Y5Q9	TF3C3_HUMAN	TPR 6.	NA	7	CTGAAGTTTTTT	0.337	
-	16	2250_2251	_Shift_Del_p.L359f	NM_173076	NP_775099	Q86UK0	ABCAC_HUMAN		NA	11	TGATTGAGAATC	0.401	
+	17	2335	PM8_uc010fyj.2_In	NM_024080	NP_076985	Q7Z2W7	TRPM8_HUMAN	Name=3; (P	NA	4	CCACACCCCCC	0.577	
+	4	1257	d.2_RNA|PANK2_u	NM_153638	NP_705902	Q9BZ23	PANK2_HUMAN		NA	0	AGGAACTTTTTTT	0.343	
+	4	799_801	10zqz.1_Translatio	NM_001819	NP_001810	P05060	SCG1_HUMAN	Poly-Glu.	NA	6	GGATGAGGAGG	0.532	
+	3	1075_1077	.1_Intron|GZF1_u	NM_022482	NP_071927	Q9H116	GZF1_HUMAN		NA	1	gaggaagaggaggag	0.384	
+	3	254_256	FRG1B_uc010gdr.1_RNA|FRG1B_uc010ztk.1_In_Frame_Del_p.G27del						NA	0	CAGCAGGAGAA	0.355	rs142255283
+	1	369	.2_Intron|SGK2_u	NM_016276	NP_057360	Q9HBY8	SGK2_HUMAN		NA	6	CCTGTCCCCCA	0.617	
+	4	1167	002xpx.2_Frame_S	NM_033421	NP_219489	Q969T3	SNX21_HUMAN		NA	2	ACACCACCCCCC	0.617	
-	4	1934_1936	1aaq.1_In_Frame_	NM_017798	NP_060268	Q9BYJ9	YTHD1_HUMAN		NA	2	CACCACCTCCTC	0.557	
-	5	757		NM_144659	NP_653260	Q9NV44	CU077_HUMAN		NA	0	AGACACCCCCC	0.478	
+	11	1903_1905	K1A_uc002ywl.2_3	NM_001396	NP_001387	Q13627	DYR1A_HUMAN	Poly-His.	NA	4	tcaccatcaccaccacc	0.384	
+	7	2031_2033	3atq.1_In_Frame_	NM_001039141	NP_001034230	Q9H2D6	TARA_HUMAN		NA	1	CAGAGCCTCCTC	0.596	

+	13	1533_1535	aus.2_In_Frame_I	NM_012407	NP_036539	Q9NRD5	PICK1_HUMAN	Poly-Glu.	NA	0	AGATGGggaggag	0.562	
+	5	477_479		NM_001197	NP_001188	Q13323	BIK_HUMAN	Potential).|H	NA	0	ctgctggcgctgctgctg	0.562	
-	4	689	_p.Q58fs|PNPLA5_	NM_138814	NP_620169	Q7Z6Z6	PLPL5_HUMAN		NA	0	GCTCTGGGGGC	0.567	
+	2	818_820	tr.1_In_Frame_Del	NM_014760	NP_055575	Q93075	TATD2_HUMAN		NA	2	AATAACTCCTCC	0.635	
-	1	205_207	g.1_In_Frame_De	NM_004628	NP_004619	Q01831	XPC_HUMAN	lu.|Glu-rich (	NA	3	CTCACCCTCCTC	0.734	rs72561774
+	5	819	cko.2_Frame_Shif	NM_001098414	NP_001091884	Q6ZSS3	ZN621_HUMAN	C2H2-type 2	NA	1	AACCACATTGG	0.453	
+	26	3272	_p.L944fs|KIF15_	NM_020242	NP_064627	Q9NS87	KIF15_HUMAN	Potential.	NA	1	TATTCTGGATCTG	0.388	
-	14	1709_1710	3csi.1_Frame_Shif	NM_001789	NP_001780	P30304	MPIP1_HUMAN	Rhodanese.	NA	5	GGCGATCTCTCT	0.515	
+	10	1926_1928	njy.2_5'UTR|TREX	NM_130384	NP_569055	Q8WXE1	ATRIP_HUMAN		NA	1	GCCTCCTGCTGC	0.547	
+	7	1043	me_Shift_Del_p.G	NM_053002	NP_443728	Q86YW9	MD12L_HUMAN		NA	7	CCTGGCCCCCC	0.582	
+	21	2524_2526	buy.1_In_Frame_	NM_000283	NP_000274	P35913	PDE6B_HUMAN		NA	0	GAGAAGGAGGA	0.562	
-	1	340_348		NM_177998	NP_819056	Q7RTM1	OTOP1_HUMAN	ical; (Potent	NA	3	TCCACAGCAGC	0.727	245977;rs75328065
+	18	2813_2815	1_RNA|CRMP1_u	NM_153717	NP_714928	P57679	EVC_HUMAN		NA	2	CGCCCAGCAGC	0.478	
+	4	469	_p.P79fs|ADAD1_	NM_139243	NP_640336	Q96M93	ADAD1_HUMAN		NA	0	TCCTCCAAAAAA	0.358	
+	2	458	TU_uc011cgq.1_R	NM_015693	NP_056508	Q9ULD6	PDZD6_HUMAN		NA	1	TGCAATAAAAAA	0.358	
+	20	6410	nm.2_Frame_Shift_	NM_178140	NP_835260	O15018	PDZD2_HUMAN		NA	9	CTCTCTGAACCC	0.612	
-	5	1175	61fs|SLC45A2_uc	NM_016180	NP_057264	Q9UMX9	S45A2_HUMAN	cellular (Pote	NA	3	GTAGATGAGAAA	0.448	rs141120603
+	5	378_379	k.1_Frame_Shift_I	NM_006083	NP_006074	Q13123	RED_HUMAN		NA	1	AAATTGAGAGAG	0.46	
+	4	1770	3lnn.1_Frame_Shif	NM_020768	NP_065819	Q68DU8	KCD16_HUMAN		NA	4	GCAGCAAAAAA	0.468	
-	4	524	1_Splice_Site_p.N	NM_016290	NP_057374	Q96RL1	UIMC1_HUMAN		NA	4	ATATTTACATTCA	0.433	
-	5	1339	p.K176fs|ZNF184_	NM_007149	NP_009080	Q99676	ZN184_HUMAN		NA	1	GGGCCTTTTTC	0.408	
+	1	112		NM_030905	NP_112167	O76002	OR2J2_HUMAN	cellular (Pote	NA	0	ATGATTAAAAAA	0.358	
-	2	797_799	l.1_Intron|PSORS	NM_001264	NP_001255	Q15517	CDSN_HUMAN	Ser-rich.	NA	2	CTGGTCCACCAC	0.635	
+	14	2337_2338	AT2_uc003nvc.3_	NM_080686	NP_542417	P48634	PRC2A_HUMAN	X 57 AA typ	NA	0	GCTCCACCCCCG	0.594	
-	5	372_374	w.3_In_Frame_De	NM_003322	NP_003313	O00294	TULP1_HUMAN	Poly-Glu.	NA	3	tcctcctcttcctcctcctc	0.389	
-	8	1152	p.K221fs|ICK_uc0	NM_016513	NP_057597	Q9UPZ9	ICK_HUMAN	rotein kinas	NA	5	ATTACCTTTTTTG	0.502	
+	9	3342_3344	2_3'UTR|GRM1_u	NM_000838	NP_000829	Q13255	GRM1_HUMAN	lasmic (Pote	NA	19	CGTAGAGGAGG	0.586	
-	10	1313_1314		NM_015718	NP_056533	Q9HBY0	NOX3_HUMAN	ical; (Potent	NA	1	CAACGCACACA	0.53	
-	8	1134	p.R163fs|AGPAT4_	NM_020133	NP_064518	Q9NRZ5	PLCD_HUMAN		NA	0	CCGCCGGGGGG	0.627	
-	10	1122	p.E105fs|SKAP2_	NM_003930	NP_003921	O75563	SKAP2_HUMAN		NA	1	GTTCTTCCACTTT	0.398	
+	1	403_405	uc003tbl.3_5'Flank	NM_002047	NP_002038	P41250	SYG_HUMAN		NA	1	CCGCTCTGCTGC	0.749	
+	5	601_603	0kxo.2_In_Frame_	NM_007252	NP_009183	P78424	PO6F2_HUMAN	Gln-rich.	NA	1	cagctccagcagcag	0.365	
-	14	1383	_p.I348fs|DDC_uc	NM_000790	NP_000781	P20711	DDC_HUMAN		NA	2	AGTGGATTTTTTT	0.502	
-	2	83_85	_uc010lbj.1_In_Fr	NM_004603	NP_004594	Q16623	STX1A_HUMAN	lasmic (Pote	NA	0	AGCGACATCATC	0.586	
+	38	2779	.1_Intron|COL1A2	NM_000089	NP_000080	P08123	CO1A2_HUMAN		NA	9	ATGGTCCCCCC	0.453	
+	42	6364	.V2034fs|TRRAP_	NM_003496	NP_003487	Q9Y4A5	TRRAP_HUMAN	ite nuclear l	NA	37	TGTCCGTGGATT	0.517	
+	5	572	a.2_Frame_Shift_	NM_015908	NP_056992	Q9BXP5	SRRT_HUMAN		NA	2	ATGCTGGGGGG	0.607	
+	15	4762_4763	3wem.2_Frame_S	NM_005435	NP_005426	Q12774	ARHG5_HUMAN	SH3.	NA	2	TGGCTGGAGGG	0.569	
-	5	987_989		NM_014729	NP_055544	O94900	TOX_HUMAN	lization sign	NA	4	GGATCCTTCTTC	0.453	
-	2	136_138	_Del_p.24_25AA>	NM_078480	NP_510965	Q9UHX1	PUF60_HUMAN	homodimer	NA	0	caccactgccgccgcc	0.404	
-	30	4625	ae.1_Splice_Site_	NM_201380	NP_958782	Q15149	PLEC_HUMAN		NA	9	CTGTACCTCCTC	0.621	
-	1	20_21	3ziz.1_Frame_Shif	NM_134441	NP_604390	P04090	REL2_HUMAN		NA	0	AGGTGGAAAAAA	0.535	
+	2	2532	3zvv.2_Frame_Shi	NM_203299	NP_976044	Q5VYM1	CI131_HUMAN		NA	0	ATTTATCCCCCC	0.537	
+	1	417_419	8376_uc003zys.1_	NM_001039792	NP_001034881	Q6UXD1	HRCT1_HUMAN	His-rich.	NA	0	acccccaccgccacca	0.389	rs138232567
-	9	2947_2949	R2_uc004ari.1_Int	NM_004560	NP_004551	Q01974	ROR2_HUMAN	lasmic (Pote	NA	20	AGCCTTCCTCCT	0.645	
-	24	2709_2710	1lxc.1_Frame_Shif	NM_015258	NP_056073	Q5T1M5	FKB15_HUMAN	Potential.	NA	3	AGTTCCTTGATG	0.495	
-	3	308	.1_5'UTR|FKBP1	NM_015258	NP_056073	Q5T1M5	FKB15_HUMAN		NA	3	GTGCTGTTTTTG	0.378	

-	26	2978	_p.Y312fs|GOLGA	NM_004486	NP_004477	Q08379	GOGA2_HUMAN		NA	1	CCGGTAAAAAA	0.562	
+	11	1816_1818	zv.2_In_Frame_D	NM_005157	NP_005148	P00519	ABL1_HUMAN	n signal 1 (P	NA	817	GATCAAGAAGA	0.616	
-	2	873	.1_RNA|TTF1_uc	NM_007344	NP_031370	Q15361	TTF1_HUMAN	Poly-Lys.	NA	4	TTAGACTTTTTTT	0.473	
+	13	1980	512fs|ADAMTS13_	NM_139025	NP_620594	Q76LX8	ATS13_HUMAN		NA	6	AGTGGCCCCCG	0.637	rs75928689
-	33	6155_6156		NM_017617	NP_060087	P46531	NOTC1_HUMAN	nic (Potentia	NA	856	TTGTTAGCCCCG	0.604	
+	13	2110_2112	E598del|GRIN1_uc	NM_007327	NP_015566	Q05586	NMDZ1_HUMAN	lasmic (Pote	NA	1	CAGCGAGGAGG	0.739	
-	2	220	ZBED1_uc004cqh	NM_004729	NP_004720	O96006	ZBED1_HUMAN		NA	0	AGCTCTCCAGGC	0.597	
+	4	621_623	_In_Frame_Del_p	NM_005676	NP_005667	P98175	RBM10_HUMAN	Poly-Arg.	NA	5	CGTAGGCGGCG	0.65	
-	6	3494_3496	OM4_uc004dpd.3	NM_020717	NP_065768	Q9ULL8	SHRM4_HUMAN	Glu-rich.	NA	1	GCAGctcctcttcctcc	0.261	rs3747282
-	1			NM_018159	NP_060629	Q96G61	NUD11_HUMAN		NA	0	CTCGAGGCAGC	0.584	
-	4	299	4drf.2_Frame_Shif	NM_130776	NP_570132	Q8WTP9	GAGD4_HUMAN		NA	0	ATTCACCCCCA	0.423	
-	3	274_276	fen.2_Intron|CD9	NM_031462	NP_113650	Q8TCZ2	C99L2_HUMAN	ar (Potential	NA	3	GGTTGTGGTGG	0.552	
-	5	593_595	004ffl.2_In_Frame_	NM_001011543	NP_001011543	P43363	MAGAA_HUMAN	Poly-Ser.	NA	0	GATAGCaggagga	0.419	
+	3	719_721		NM_153812	NP_722519	Q86YI8	PHF13_HUMAN	lization signal (Probable).		0	caagctgaagaagaa	0.498	
+	1	1263_1265		NM_004455	NP_004446	Q92935	EXTL1_HUMAN	enal (Potential).		1	CCTGCCTCCTC	0.606	
+	20	5915	_p.G694fs|ARID1	NM_006015	NP_006006	O14497	ARI1A_HUMAN		p.G1848fs*6(3	142	TTGGTGGGGGG	0.582	rs140055856
+	2	1028_1030		NM_005281	NP_005272	P46089	GPR3_HUMAN	lasmic (Potential).		1	CTGTCTGCTGC	0.522	
+	9	2306	_p.K660fs|USP1_u	NM_001017415	NP_001017415	O94782	UBP1_HUMAN			1	TTGAACAAAAAA	0.373	
+	7	1426_1427	me_Shift_Del_p.H	NM_005012	NP_005003	Q01973	ROR1_HUMAN	xtracellular (Potential).		19	ATCCCCACACAC	0.554	
-	9	1232	_Shift_Del_p.M408	NM_005665	NP_005656	O60447	EVI5_HUMAN	Interaction with alpha-tubul		2	TTTTCATTTTTTT	0.318	
+	29	4304	.1_Frame_Shift_D	NM_000642	NP_000633	P35573	GDE_HUMAN	-glucanotransferase.		3	TTATCCAAAAAA	0.323	
+	10	2124	ova.1_Frame_Shif	NM_001144937	NP_001138409	Q5VTL7	FNDC7_HUMAN	nectin type-III 8.		2	CTGTCCAAAAAA	0.363	
-	1	2523		NM_021794	NP_068566	Q9UKF2	ADA30_HUMAN	lasmic (Potential).		3	GGTTACTTTTTT	0.358	
-	1	273_274	_Shift_Del_p.P6fs|	NM_024408	NP_077719	Q04721	NOTC2_HUMAN			27	GAGCGGGGCG	0.663	
-	11	1749	1elx.3_Frame_Shi	NM_014644	NP_055459	Q5VU43	MYOME_HUMAN	Potential.		5	AGAGCAACAGC	0.383	
+	14	2499	_Shift_Del_p.G778	NM_019032	NP_061905	Q6UY14	ATL4_HUMAN	TSP type-1 2.		2	AATTTGGGGGG	0.692	rs149280379
+	6	739	B4_uc001eyb.1_3	NM_002796	NP_002787	P28070	PSB4_HUMAN			2	CACCGAAAAAG	0.443	
-	2	2734_2736	wne.1_In_Frame_	NM_007113	NP_009044	Q07283	TRHY_HUMAN	30 AA tandem repeats.		5	GTAGCTCCTCC	0.586	rs143222885
-	3	1526_1527	uc001ezv.2_Intron	NM_001014342	NP_001014364	Q5D862	FILA2_HUMAN	Ser-rich.		17	CTGAGCCAGAC	0.52	
-	1	63	l_p.L13fs|CD84_u	NM_003874	NP_003865	Q9UIB8	SLAF5_HUMAN			4	GTTTGCAGGCA	0.448	
+	3	338_340		NM_001102566	NP_001096036	A6NKN8	PC4L1_HUMAN			0	AGGCGGAGGAG	0.488	
-	6	1004_1006	X1A_uc001gcw.1_	NM_177398	NP_796372	Q8TE12	LMX1A_HUMAN	y-Gln.|Gln-rich.		5	ATCTTGCTGCT	0.567	
+	4	474	hpl.2_Frame_Shift	NM_001136018	NP_001129490	P07099	HYEP_HUMAN			4	TGAAGCCCCCC	0.627	
-	3	615_616		NM_022735	NP_073572	Q9H3P7	GCP60_HUMAN	ential.|Glu-rich.		0	TTCACCTTTTTT	0.411	
-	20	2528_2530	E813del|SFMBT2_	NM_001029880	NP_001025051	Q5VUG0	SMBT2_HUMAN			8	AGTCTCTCCTCC	0.596	
-	4	3538_3539	uc001iqp.1_RNA	NM_207371	NP_997254	Q1XH10	DLN1_HUMAN	r-rich.|Glu-rich.		1	GCTGCccccctcct	0.441	rs138084841
-	2	2633_2635	e_Del_p.720_721	NM_020848	NP_065899	Q9P266	K1462_HUMAN	Ser-rich.		4	TCCTCActgctgct	0.463	
+	7	559	Shift_Del_p.K28fs|	NM_018063	NP_060533	Q9NRZ9	HELLS_HUMAN			2	GTGGCTAAAAAA	0.214	
+	1	754_755	y.2_Intron|DHDPS	NM_001009997	NP_001009997	Q5T681	CJ062_HUMAN	His-rich.		0	CCAATCACACAC	0.55	
+	9	6800	001lfz.2_Frame_S	NM_206862	NP_996744	O95359	TACC2_HUMAN			10	AGAGACCCCCC	0.522	
+	19	2126_2128	.Q620del|PTPRE_	NM_006504	NP_006495	P23469	PTPRE_HUMAN	hatase 2.|Cytoplasmic (Po		1	CAGAAGCAGCA	0.65	
+	13	1748	2_uc001ndg.3_RN	NM_000506	NP_000497	P00734	THRB_HUMAN	h is also known as the TP5		3	ACAGTGGGGGA	0.522	
+	3	548_550	rlo.1_In_Frame_D	NM_004265	NP_004256	O95864	FADS2_HUMAN	ical; (Potential).		2	TTCTTCCTCCT	0.537	
+	5	886	rlo.1_Frame_Shift_	NM_004265	NP_004256	O95864	FADS2_HUMAN	lasmic (Potential).		2	GGCAGCCCATC	0.527	
+	16	2803		NM_005188	NP_005179	P22681	CBL_HUMAN	n with CD2AP.|UBA.		149	ATGGCCAAAAAC	0.507	
-	22	3672_3674	1qfl.2_In_Frame_D	NM_020228	NP_064613	Q9NQV6	PRD10_HUMAN	Poly-Thr.		1	CCGTTGGTGGT	0.547	
+	7	948_950	.L125del|SLC39A	NM_173596	NP_775867	Q6ZMH5	S39A5_HUMAN	lasmic (Potential).		2	ATCCCTGCTGC	0.635	

+	87	13755_13757		NM_002332	NP_002323	Q07954	LRP1_HUMAN	ical; (Potential).	22	CTGTTGCTGCT	0.557	
+	6	1576	M19_uc009zru.1_	NM_018279	NP_060749	Q96HH6	TMM19_HUMAN	ical; (Potential).	0	TGGGGTTTTTG	0.433	
-	4	831		NM_173598	NP_775869	Q6VAB6	KSR2_HUMAN	Pro-rich.	15	TCCCCGGGGGC	0.682	rs36028047
+	16	2686_2688	tbn.1_In_Frame_	NM_004592	NP_004583	Q12872	SFSWA_HUMAN	g/Ser-rich (RS domain).	0	CACGAGAAGAA	0.493	
+	2	698	Y_uc010tdw.1_R	NM_023037	NP_075463	Q5TBA9	FRY_HUMAN		7	TCCTCAAAAGT	0.507	
+	4	541	1_Frame_Shift_De	NM_144595	NP_653196	Q8ND83	SLAI1_HUMAN		2	TCAGGAAAAAA	0.388	
+	16	4738_4740	1xmv.2_In_Frame	NM_015556	NP_056371	O43166	SI1L1_HUMAN	Ser-rich.	4	tcctcctcttcctcctcctc	0.468	
+	8	1064_1066	K_uc001ygg.3_In	NM_001099402	NP_001092872	O75909	CCNK_HUMAN	Poly-Gln.	0	AGCCCAGCAGC	0.621	
+	1	607_609		NM_003403	NP_003394	P25490	TYY1_HUMAN	Glu-rich (acidic).	0	gtgggcgaggaggag	0.34	
+	3	641		NM_001376	NP_001367	Q14204	DYHC1_HUMAN	n (By similarity).	10	GGCTCCTTTTTT	0.408	
+	10	1137	p.Q215fs|ADAL_u	NM_001159280	NP_001152752	Q6DHV7	ADAL_HUMAN		0	AAACCAAAAAA	0.453	
-	8	1516_1518	269LL>L|ABCA3_	NM_001089	NP_001080	Q99758	ABCA3_HUMAN	ical; (Potential).	16	GCTGAGCAGCA	0.611	rs145342500
-	1	295_296	e_Ins_p.16_16G>	NM_002094	NP_002085	P15170	ERF3A_HUMAN		3	ctgctgctcccgccgcc	0.332	rs71408216
-	3	553_555	20GG>G|KIAA043	NM_014647	NP_055462	Q9Y4F3	LKAP_HUMAN	Poly-Gly.	0	ACCGCCACCAC	0.532	
-	2	423_425	2dxs.2_In_Frame_	NM_006110	NP_006101	O95400	CD2B2_HUMAN		1	CCCCCCATCATC	0.532	
+	8	2801		NM_014712	NP_055527	O15047	SET1A_HUMAN		3	GCTGGCCCCCC	0.642	
+	9	1652	TO_uc010cbz.2_F	NM_001080432	NP_001073901	Q9C0B1	FTO_HUMAN		0	CTGGGAAAAGG	0.483	
+	5	1317_1319	hx.2_In_Frame_D	NM_024335	NP_077311	P78412	IRX6_HUMAN		6	gaggaagaggaggag	0.493	
+	3	278_280	vho.1_In_Frame_	NM_020312	NP_064708	O75208	COQ9_HUMAN		1	CGGCGAGGAGG	0.576	rs149029279
-	11	1150_1151		NM_001896	NP_001887	P19784	CSK22_HUMAN		1	TCTGCACAAGG	0.54	
-	1	625	S8_uc010vpv.1_I	NM_001214	NP_001205	O95177	CP003_HUMAN		0	AGGGTCCAGGC	0.184	
-	15	2000_2002	15_uc002ghy.1_5'	NM_004860	NP_004851	P51116	FXR2_HUMAN	Poly-Arg.	0	GTTACGGCGGC	0.547	
-	30	4166_4168	E1388del|MYH10_	NM_005964	NP_005955	P35580	MYH10_HUMAN	Potential.	2	CTGGCCTCCTC	0.596	
+	9	1849	p.S175fs|EPN2_u	NM_014964	NP_055779	O95208	EPN2_HUMAN	repeats of [DE]-P-W.	1	ACTTCAAAAAA	0.393	
+	1	158_160	me_Del_p.K7del|	NM_003457	NP_003448	O43670	ZN207_HUMAN		0	TCGCAAGAAGA	0.542	
+	5	1150	10_uc002hxw.1_	NM_021939	NP_068758	Q96AY3	FKB10_HUMAN		1	GAGCTCCCCCC	0.632	
-	10	1248	.1_Intron|BRCA1_	NM_007294	NP_009225	P38398	BRCA1_HUMAN		52	TCTACCTTTTTTT	0.438	rs80357618
-	7	912	hift_Del_p.P262fs	NM_001256	NP_001247	P30260	CDC27_HUMAN		5	GTTTTTGGTTTAT	0.373	
-	2	516_517		NM_004645	NP_004636	P38432	COIL_HUMAN		1	CTCTTGTTTTTTT	0.366	
+	15	2732_2734	2_uc002jae.2_5'F	NM_006039	NP_006030	Q9UBG0	MRC2_HUMAN	Potential).|C-type lectin 4.	3	CGGCACGACGA	0.645	
-	2	1200_1202	.E351del|CDC42E	NM_012121	NP_036253	Q9H3Q1	BORG4_HUMAN		0	TTTCATCCTCCT	0.64	
+	8	988	hift_Del_p.F267fs	NM_000213	NP_000204	P16144	ITB4_HUMAN	tracellular (Potential).	4	AGCCTTCCACTAT	0.647	
-	24	2552	p.N280fs|OSBPL1	NM_080597	NP_542164	Q9BXW6	OSBL1_HUMAN		4	TTATCATTTTTTT	0.393	
-	5	837	0xjg.1_Frame_Shi	NM_005490	NP_005481	Q9BRG2	SH23A_HUMAN		2	TGTCCGGGGGG	0.657	
-	11	1320_1321	nfg.1_Frame_Shift	NM_033417	NP_219485	Q9BT25	HAUS8_HUMAN		0	TGAACGAGAGAG	0.495	
+	15	3946_3948	nma.2_In_Frame_	NM_004386	NP_004377	O14594	NCAN_HUMAN		4	CGGCGAcaccacc	0.468	
-	4	491	p.K134fs|ZFP14_u	NM_020917	NP_065968	Q9HCL3	ZFP14_HUMAN		1	TGTTCCTTTTCCC	0.363	
+	2	648_650	egn.1_In_Frame_	NM_003407	NP_003398	P26651	TTP_HUMAN	P-P-P-P-G.	1	ACCTCACCACC	0.685	
-	6	472	_p.P16fs|C19orf47	NM_178830	NP_849152	Q8N9M1	CS047_HUMAN		2	CGCCTGGGGGG	0.612	
+	12	1271_1273	.Q407del|NUCB1_	NM_006184	NP_006175	Q02818	NUCB1_HUMAN	ential.|Poly-Gln.	0	agcggaagcagcag	0.522	
-	1	90_92	EC8_uc002pwu.2_	NM_014442	NP_055257	Q9NYZ4	SIGL8_HUMAN		5	agcaggggcagcagc	0.493	
+	4	1303_1305	2qlt.2_In_Frame_	NM_007279	NP_009210	P26368	U2AF2_HUMAN		1	CACGAGAAGAA	0.645	
-	11	1472_1474	1_In_Frame_Del_	NM_015317	NP_056132	Q8TB72	PUM2_HUMAN	Ala-rich.	1	TCCAGCTGCTG	0.424	
-	2	234_236	HX57_uc002rrg.2_	NM_198963	NP_945314	Q6P158	DHX57_HUMAN	Gly-rich.	3	gccacctccaccacca	0.384	
+	1	285	D10_uc010zdh.1_	NM_006063	NP_006054	O60662	KBTBA_HUMAN	BTB.	0	AGGCGAAAAAA	0.388	
+	6	820	Shift_Del_p.P197f	NM_025000	NP_079276	Q5H9S7	DCA17_HUMAN	ical; (Potential).	0	TCTACCTTTTTCA	0.343	
+	3	1075_1077	.1_Intron|GZF1_u	NM_022482	NP_071927	Q9H116	GZF1_HUMAN		1	gaggaagaggaggag	0.384	

-	3	691_692		NM_005225	NP_005216	Q01094	E2F1_HUMAN	box.|Potential.	0	TTCTTGGACTTC	0.589	
+	3	617_619	me_Del_p.A96del|	NM_016434	NP_057518	Q9NZ71	RTEL1_HUMAN	ase ATP-binding.	0	CAACGCTGCTG	0.645	
-	5	757		NM_144659	NP_653260	Q9NV44	CU077_HUMAN		0	AGACACCCCCC	0.478	
+	2	270_272		NM_004147	NP_004138	Q9Y295	DRG1_HUMAN	Poly-Gly.	1	AAAGGGTGGTG	0.409	
+	9	1570	amt.2_Frame_Shif	NM_012179	NP_036311	Q9Y3I1	FBX7_HUMAN		1	CCCCTTGCACCC	0.502	
+	19	2312_2314	3blc.2_In_Frame_	NM_014678	NP_055493	O75170	PP6R2_HUMAN		0	CCCTTTGATGAT	0.616	
+	40	5548	R1_uc011asu.1_I	NM_001099952	NP_001093422	Q14643	ITPR1_HUMAN	lasmic (Potential).	21	AGCCCGGGGGA	0.522	
+	7	1453	p.F219fs|EDEM1_	NM_014674	NP_055489	Q92611	EDEM1_HUMAN	enal (Potential).	3	CAGGCCTTTTTC	0.463	
-	1	205_207	g.1_In_Frame_De	NM_004628	NP_004619	Q01831	XPC_HUMAN	lu.|Glu-rich (acidic).	3	CTCACCCTCCTC	0.734	rs72561774
+	11	1433	3cig.2_Frame_Shi	NM_001106	NP_001097	Q13705	AVR2B_HUMAN	Potential).|Protein kinase.	1	CTTGTCCGCGG	0.597	
-	3	1288_1289	NB1_uc003csx.2_	NM_002673	NP_002664	O43157	PLXB1_HUMAN	lar (Potential).|Sema.	5	TGTAGCAGGCAT	0.629	
-	25	4571	e_Site_p.E1361_	NM_053025	NP_444253	Q15746	MYLK_HUMAN		9	GCTCTGGGGG	0.624	rs41431347
-	4	1041_1043	tg.2_In_Frame_De	NM_001017395	NP_001017395	O94876	TMCC1_HUMAN		1	AGACATgcagcag	0.404	
-	8	1759_1761	91DD>D|DBR1_u	NM_016216	NP_057300	Q9UK59	DBR1_HUMAN		0	CTGCATCGTCAT	0.251	0114751;rs2622736
+	21	2524_2526	buy.1_In_Frame_	NM_000283	NP_000274	P35913	PDE6B_HUMAN		0	GAGAAGGAGGA	0.562	
-	1	340_348		NM_177998	NP_819056	Q7RTM1	OTOP1_HUMAN	ical; (Potential).	3	TCCACAGCAGC	0.727	245977;rs75328065
+	3	794	p.F196fs|C1QTNF	NM_001135171	NP_001128643	Q9BXJ2	C1QT7_HUMAN	C1q.	0	GCTTTCCCAGG	0.448	
-	4	1088_1090	y.2_In_Frame_De	NM_001031732	NP_001026902	Q96MU7	YTDC1_HUMAN	Glu-rich.	2	tcttcttcttcctcctcctc	0.202	rs141105019
+	11	2218	2_uc011cdg.1_Fr	NM_000297	NP_000288	Q13563	PKD2_HUMAN	in.|Cytoplasmic (Potential).	1	AAACTGAAAAAA	0.348	
-	1	538_540	C3_uc011cdn.1_I	NM_153757	NP_715638	Q96NT1	NP1L5_HUMAN	Glu-rich.	1	tactcctcttcctcctcctc	0.369	
+	8	1187_1189	p.P363del|NPNT_	NM_001033047	NP_001028219	Q6UXI9	NPNT_HUMAN	Pro-rich.	1	TACTCCACCAC	0.522	
+	22	2560_2562	cgc.1_In_Frame_	NM_001148	NP_001139	Q01484	ANK2_HUMAN		14	AGGTCACCACC	0.443	
+	6	700	SC9_uc003ieb.2_	NM_005033	NP_005024	Q06265	EXOS9_HUMAN	ARE binding.	0	TTTGCCTTTTTC	0.358	
-	10	1909	10_uc011cnu.1_	NM_006727	NP_006718	Q9Y6N8	CAD10_HUMAN	|Extracellular (Potential).	12	AAACTGAAAAAA	0.313	
-	3	906	e_Shift_Del_p.K1	NM_014423	NP_055238	Q9UHB7	AFF4_HUMAN	Ser-rich.	5	TGGCCTTTTTTC	0.512	
+	26	4712	.1_Frame_Shift_	NM_020690	NP_065741	Q8IWZ2	Q8IWZ2_HUMAN		6	TTGGGAAAAAA	0.423	
+	5	378_379	k.1_Frame_Shift_	NM_006083	NP_006074	Q13123	RED_HUMAN		1	AAATTGAGAGAG	0.46	
-	12	1346_1349	.Q322fs|HNRNP	NM_005520	NP_005511	P31943	HNRH1_HUMAN	-rich approximate repeats.	0	GCTGCTGGCTG	0.5	
-	4	1510_1512	_Frame_Del_p.E3	NM_178012	NP_821080	Q9BVA1	TBB2B_HUMAN		1	TCGCCCTCCTC	0.65	
+	14	2337_2338	AT2_uc003nvc.3_	NM_080686	NP_542417	P48634	PRC2A_HUMAN	X 57 AA type A repeats.	0	GCTCCACCCCCG	0.594	
-	5	372_374	w.3_In_Frame_De	NM_003322	NP_003313	O00294	TULP1_HUMAN	Poly-Glu.	3	tcctcctcttcctcctcctc	0.389	
-	3	1001	_Shift_Del_p.K141	NM_031922	NP_114128	Q96D71	REPS1_HUMAN		2	GATCCCTTTTTC	0.478	
+	2	488_489	3qll.2_Frame_Shi	NM_000838	NP_000829	Q13255	GRM1_HUMAN		19	CCTTTTGTTTTTT	0.644	
-	10	1313_1314		NM_015718	NP_056533	Q9HBY0	NOX3_HUMAN	ical; (Potential).	1	CAACGCACACA	0.53	
-	1	915_917		NM_033224	NP_150093	Q96QR8	PURB_HUMAN		0	TCTTCGCCGCC	0.576	
-	2	390_392	kiw.1_In_Frame_	NM_015545	NP_056360	O75127	PTCD1_HUMAN		1	AAACTCTCCTCC	0.606	
+	5	572	a.2_Frame_Shift_	NM_015908	NP_056992	Q9BXP5	SRRT_HUMAN		2	ATGCTGGGGGG	0.607	
-	3	1170_1171	EPLD_uc011klj.1_	NM_198990	NP_945341	Q6IQ20	NAPEP_HUMAN		1	CCTGCGAAAAAA	0.46	rs147416689
+	9	1390	T1_uc010ljj.1_Int	NM_021930	NP_068749	Q6NUQ1	RINT1_HUMAN	RINT1/TIP20.	4	GCCACTGATATTC	0.388	
+	5	743	_p.E17fs|CBLL1_	NM_024814	NP_079090	Q75N03	HAKAI_HUMAN	RING-type.	5	ACATGAAAAAAA	0.269	
+	7	1118_1119	vuy.2_Frame_Shif	NM_016019	NP_057103	Q9Y383	LC7L2_HUMAN	Arg/Ser-rich.	0	AGAGAAGAGAGA	0.391	
+	1	528		NM_001001656	NP_001001656	Q8NGU2	OR9A4_HUMAN	ellular (Potential).	1	GAACAATTTTTTT	0.383	
-	3	436		NM_005431	NP_005422	O43543	XRCC2_HUMAN		2	TACACCAAAAAA	0.393	
-	5	3497_3498		NM_001080826	NP_001074295	Q86YV5	SG223_HUMAN	rotein kinase.	0	cgggagccggggcgg	0.609	rs143409664
-	10	1506	p.R384fs|NBN_uc	NM_002485	NP_002476	O60934	NBN_HUMAN	r localization signal.	7	CAGACCTTTTTTT	0.338	
-	45	6393_6394	ks.1_Frame_Shift_	NM_015902	NP_056986	O95071	UBR5_HUMAN		28	CCCTTCTTTTTT	0.381	
+	3	610_612	ysi.2_In_Frame_D	NM_002467	NP_002458	P01106	MYC_HUMAN	Poly-Gln.	6	CTACCAGCAGC	0.611	rs61752959

-	30	4625	ae.1_Splice_Site_	NM_201380	NP_958782	Q15149	PLEC_HUMAN			9	CTGTACCTCCTC	0.621	
-	1	2084	uc003zrh.1_RNA	NM_153809	NP_722516	Q8IZX4	TAF1L_HUMAN		p.K665fs*4(2)	26	TTGGCCTTTTTTT	0.478	
+	1	417_419	8376_uc003zys.1_	NM_001039792	NP_001034881	Q6UXD1	HRCT1_HUMAN	His-rich.		0	acccccaccgccacca	0.389	rs138232567
-	9	2947_2949	R2_uc004ari.1_Int	NM_004560	NP_004551	Q01974	ROR2_HUMAN	lasmic (Potential).		20	AGCCTTCCTCCT	0.645	
-	4	884_886	Del_p.E251del|EC	NM_001393	NP_001384	O94769	ECM2_HUMAN	Poly-Glu.		2	cctcctcatcctcctcctc	0.399	rs137929518
-	3	459		NM_022755	NP_073592	Q9H8X2	IPPK_HUMAN			2	ATGACATTTTTCC	0.438	
-	22	6093	vf.2_Frame_Shift_I	NM_002160	NP_002151	P24821	TENA_HUMAN	nectin type-III 15.		7	TGCCCGGGGGG	0.478	rs148674204
+	11	1816_1818	ozv.2_In_Frame_D	NM_005157	NP_005148	P00519	ABL1_HUMAN	n signal 1 (Potential).|Poly-		817	TGATCAAGAAGA	0.616	
-	9	916_918		NM_003086	NP_003077	Q5SXM2	SNPC4_HUMAN	TH myb-type 1.		0	AGCCGCTCCTCC	0.65	
-	40	5941	hift_Del_p.K1776fs	NM_004006	NP_003997	P11532	DMD_HUMAN	ction with SYNM (By similar		6	TGGCTAATTTTTTT	0.358	
-	1			NM_018159	NP_060629	Q96G61	NUD11_HUMAN			0	CCTCGAGGCAGC	0.584	
+	5	1012_1014	04elx.2_In_Frame_	NM_207318	NP_997201	Q6PEV8	F199X_HUMAN	Ser-rich.		1	GCGCCAGCAGC	0.567	
+	6	604_606	eoz.2_In_Frame_D	NM_001128173	NP_001121645	O75914	PAK3_HUMAN	Linker.		10	gaagaggaagaagaa	0.325	
-	2	574_575	P_uc004esg.2_5'F	NM_024528	NP_078804	Q8N5F7	NKAP_HUMAN			2	CCAATTCTCTCT	0.317	
-	3	274_276	fen.2_Intron|CD99	NM_031462	NP_113650	Q8TCZ2	C99L2_HUMAN	ar (Potential).|Poly-Thr.		3	GGTTGTGGTGGT	0.552	
-	5	593_595	004ffl.2_In_Frame_	NM_001011543	NP_001011543	P43363	MAGAA_HUMAN	Poly-Ser.		0	GATAGCaggagga	0.419	
-	4	601_603		NM_032656	NP_116045	Q8IY37	DHX37_HUMAN		NA	1	ATTCCGActcctcct	0.601	
-	1	1509_1511		NM_033132	NP_149123	Q96T25	ZIC5_HUMAN	Pro-rich.	NA	0	gggcggtggcggcggc	0.493	
+	15	5011_5013	2kae.2_In_Frame_	NM_001080519	NP_001073988	Q9P281	BAHC1_HUMAN		NA	1	GGCCAAGAAGA	0.621	
-	9	1261_1263	.E147del|GTF2F1_	NM_002096	NP_002087	P35269	T2FA_HUMAN	Glu-rich.	NA	0	TGccttcttctcctcctcc	0.542	
+	2	428	nk|MYCN_uc010yjr	NM_005378	NP_005369	P04198	MYCN_HUMAN		NA	5	CTCGACCCCCCC	0.657	
+	6	1052_1053	c002sta.3_Frame_	NM_018271	NP_060741	Q86YJ6	THNS2_HUMAN		NA	1	GAGACTTCTCTCT	0.545	
+	3	224_242		NM_001862	NP_001853	P10606	COX5B_HUMAN		NA	0	CCAAAGGGAGCT	0.397	
-	13	2025	p.W650fs|CLTCL1_	NM_007098	NP_009029	P53675	CLH2_HUMAN	gment.|Heav	NA	5	ACAAGCCACTGC	0.478	
-	6	1681_1683	Q376del|ARHGAP	NM_025251	NP_079527	Q9C0H5	RHG39_HUMAN		NA	0	CACTTCTGCTTGC	0.704	rs77462981
-	18	2477	akk.2_Frame_Shif	NM_001409	NP_001400	O75095	MEGF6_HUMAN	EGF-like 12.		1	TGGCAGGGGGC	0.697	
+	3	719_721		NM_153812	NP_722519	Q86YI8	PHF13_HUMAN	ization signal (Probable).		0	caagctgaagaagaa	0.498	
+	8	1246		NM_032283	NP_115659	Q9NUE0	ZDH18_HUMAN			0	GCATGGTAGGAG	0.612	
-	1	702_704		NM_001080418	NP_001073887	O95886	DLGP3_HUMAN	Poly-His.		3	CCGGGACtggtggt	0.537	
-	7	905	p.K51fs|TRIT1_uc0	NM_017646	NP_060116	Q9H3H1	MOD5_HUMAN			1	TGTGCATTTTCCC	0.453	
+	20	3859_3861	9vwt.2_In_Frame_	NM_002840	NP_002831	P10586	PTPRF_HUMAN	cellular (Potential).		10	AGCAGCGGCGG	0.631	
-	1	545	73fs|HHLA3_uc01	NM_030816	NP_110443	Q8N6S4	AN13C_HUMAN			0	GCGCCGGGGGC	0.637	
+	2	286_288	me_Del_p.Q49del|	NM_030965	NP_112227	Q9BVH7	SIA7E_HUMAN	.|Lumenal (Potential).		2	GCCCCCgcagcag	0.581	rs113832855
-	4	488	_p.D57fs|GSTM3_	NM_000849	NP_000840	P21266	GSTM3_HUMAN	ST N-terminal.		0	GAAAGTCCAGGT	0.488	
+	4	780	_p.L168fs|VANGL1	NM_138959	NP_620409	Q8TAA9	VANG1_HUMAN	Name=2; (Potential).		1	GGGCACTTTTTTT	0.493	
-	2	1768		NM_001004432	NP_001004432	Q6UY18	LIGO4_HUMAN	cellular (Potential).		1	TCCAGAAAAAAA	0.582	
+	11	2233	_p.D350fs|NPR1_u	NM_000906	NP_000897	P16066	ANPRA_HUMAN	Potential).|Protein kinase.		7	CACCGACCCCCC	0.493	
+	3	712	2_uc009xch.2_Fra	NM_001877	NP_001868	P20023	CR2_HUMAN	xtracellular (Potential).		8	TGCTGTCCCCCC	0.398	
+	4	635_646		NM_001104548	NP_001098018					0	gTagcagcagcagcag	0.283	30217;rs72359595;rs150848171
-	20	2967_2969	31QQ>Q|INTS7_u	NM_015434	NP_056249	Q9NVH2	INT7_HUMAN	Gln-rich.		0	TGCGTTGCTGCT	0.443	
-	5	1798	AGT_uc009xff.2_F	NM_000029	NP_000020	P01019	ANGT_HUMAN			0	AAGCTCAAAAAA	0.562	
+	14	1676_1678	xjw.1_In_Frame_D	NM_003473	NP_003464	Q92783	STAM1_HUMAN			2	CGCTACTGCTGCT	0.493	
-	5	1489_1491	_Del_p.445_446G	NM_000124	NP_000115	Q03468	ERCC6_HUMAN	Gly-rich.		16	TCCGACCTCCTC	0.458	rs4253047
+	7	608	el_p.G68fs|PLAU_	NM_002658	NP_002649	P00749	UROK_HUMAN	necting peptide.		3	TCCAGGAAAAAAC	0.517	
+	4	878_879	010qoq.1_Frame_	NM_019084	NP_061957	Q5T5M9	CCNJ_HUMAN			1	TGCTTGGAAAAG	0.441	
-	2	955_957	G2_uc001mak.1_Ir	NM_017481	NP_059509	Q9H347	UBQL3_HUMAN			3	TGGCTGGTGGT	0.537	rs2234451
+	2	732_733	001mcx.2_Frame_	NM_000543	NP_000534	P17405	ASM_HUMAN			0	AAGCCGCCCCCC	0.624	rs74053349

-	2	1347_1349		NM_002233	NP_002224	P22459	KCNA4_HUMAN	Poly-His.		4	TGACTGGTGGT	0.66	
+	2	423		NM_152316	NP_689529	Q8N8R7	CK046_HUMAN			0	TTAGCCAAAAAA	0.338	
-	16	1957		NM_001008391	NP_001008392	Q6ZRK6	CCD73_HUMAN			2	ACAGGATTTTTT	0.313	
-	8	778		NM_004308	NP_004299	Q07960	RHG01_HUMAN	SH3-binding.		1	GGCAGGGGGG	0.642	
-	17	2222	MTA2_uc010rlx.1_	NM_004739	NP_004730	O94776	MTA2_HUMAN			2	CGCCTTACCTGG	0.554	
+	14	1946	T491fs|KLC2_uc0	NM_001134775	NP_001128247	Q9H0B6	KLC2_HUMAN			0	GGGCACCCCCC	0.647	
-	5	631	SP1_uc010rvi.1_Ir	NM_033292	NP_150634	P29466	CASP1_HUMAN		p.N205I(1)	2	GTGAGATTTTTT	0.378	
-	2	308_322	prt.1_5'UTR|TMPI	NM_001077263	NP_001070731	Q9BYE2	TMPSD_HUMAN	-A-[GLQR].|Cytoplasmic (F		1	GGAGATGCCCG	0.67	
-	9	1657_1659	_554PP>P|IFFO1	NM_080730	NP_542768	Q0D2I5	IFFO1_HUMAN	Poly-Pro.		0	GCTTGGCGGCG	0.601	rs144019095
+	3	523_524	uc001qub.1_Intror	NM_016184	NP_057268	Q9UMR7	CLC4A_HUMAN	cellular (Potential).		0	TGTGTGAAAAA	0.332	
+	87	13755_13757		NM_002332	NP_002323	Q07954	LRP1_HUMAN	ical; (Potential).		22	CTGTTGCTGCT	0.557	
-	7	596_597	.Y221fs|TMBIM4_	NM_016056	NP_057140	Q9HC24	TMBI4_HUMAN			2	CACTATAAAAAA	0.351	
-	6	1097	me_Shift_Del_p.R	NM_198521	NP_940923	Q96LP6	CL042_HUMAN			2	TGGGCGGGGGG	0.587	
+	13	1752_1756	_Shift_Del_p.E98f	NM_033121	NP_149112	Q8IZ07	AN13A_HUMAN			0	TGGAGTCCAGC	0.449	
+	13	1903_1905		NM_194286	NP_919262	A7MD48	SRRM4_HUMAN	r-rich.|Arg-rich.		2	GGTACAGCAGC	0.532	
-	3	359	PS33A_uc001uce	NM_022916	NP_075067	Q96AX1	VP33A_HUMAN			1	TCTGACAAAAAA	0.383	
+	46	8261_8262	0_uc001ujm.2_In_	NM_015409	NP_056224	Q96L91	EP400_HUMAN	ith ZNF42 (By similarity).		12	agcagcaacagcagc	0.327	rs111782215
+	4	341		NM_194318	NP_919299	Q6Y288	B3GLT_HUMAN	enal (Potential).		2	CAGTTAAAAAA	0.373	rs141154947
+	20	3706_3707	.A881fs|LMO7_uc	NM_015842	NP_056667	Q8WWI1	LMO7_HUMAN			5	AGGCAGAGAG	0.386	
-	5	602_603	uc010tki.1_5'Flank	NM_000820	NP_000811	Q14393	GAS6_HUMAN	alcium-binding (Potential).		4	AGCCGGCCCCC	0.649	
+	5	648	me_Shift_Del_p.E	NM_002791	NP_002782	P60900	PSA6_HUMAN			0	TCCTTGAAAAAA	0.403	
+	36	3598	_p.E1099fs|KTN1_	NM_182926	NP_891556	Q86UP2	KTN1_HUMAN	(Potential).|Potential.		7	ATTTGAAAAAAA	0.318	
+	37	5712	gl.2_Frame_Shift_	NM_015180	NP_055995	Q8WXH0	SYNE2_HUMAN	lasmic (Potential).		14	ATACCAAAAAAA	0.318	
+	4	1996	p.Q522fs|ZBTB1_	NM_001123329	NP_001116801	Q9Y2K1	ZBTB1_HUMAN			1	TATCCAAAAAAA	0.378	
-	32	5066		NM_004667	NP_004658	O95714	HERC2_HUMAN			13	TTCTCATTTTTTC	0.398	
+	11	1696_1698	1znc.2_In_Frame_	NM_181642	NP_857593	O43278	SPIT1_HUMAN			1	CGGACACCACC	0.586	
+	4	6960		NM_002373	NP_002364	P78559	MAP1A_HUMAN			9	TTCCCTGCTTCA	0.622	
-	7	1388_1389	.G377fs|SIN3A_u	NM_015477	NP_056292	Q96ST3	SIN3A_HUMAN	on with REST (By similarity		5	ATTGTCCAAACT	0.406	
+	25	3086	90_uc002cil.1_RN	NM_145294	NP_660337	Q96KV7	WDR90_HUMAN			1	CGGGGCCCCCC	0.657	
+	7	1037_1039	.K238del|UBN1_u	NM_001079514	NP_001072982	Q9NPG3	UBN1_HUMAN	Lys-rich.		2	TAAGGAGAAGAA	0.453	
+	28	3366		NM_014287	NP_055102	Q15155	NOMO1_HUMAN	cellular (Potential).		1	CATTTCCCCCC	0.473	
+	12	1805	p.F559fs|TMC7_u	NM_024847	NP_079123	Q7Z402	TMC7_HUMAN	ical; (Potential).		3	GAGCCTTTTTCT	0.498	
+	19	2026	POLR3E_uc002dk	NM_018119	NP_060589	Q9NVU0	RPC5_HUMAN			2	AGTTTCCCCCC	0.562	
-	3	385_387	P2_uc010byn.2_Ir	NM_024816	NP_079092	Q9H5N1	RABE2_HUMAN	y-Gln.|Potential.		3	AGTCCTGCTGCT	0.527	
+	2	942	Frame_Shift_Del_	NM_145239	NP_660282	Q7Z6L0	PRRT2_HUMAN	ar (Potential).|Pro-rich.		0	TGGGGCCCCCC	0.652	
+	16	2021_2023	ne_Del_p.S561del	NM_014329	NP_055144	Q6P2E9	EDC4_HUMAN	Ser-rich.		4	agcggtagcagcagc	0.458	
+	10	1188	ss.1_Frame_Shift_	NM_053013	NP_443739	P13929	ENOB_HUMAN			1	TGGCTGGGGGG	0.567	
+	13	2245_2247	.K762del|CHD3_u	NM_001005273	NP_001005273	Q12873	CHD3_HUMAN	Poly-Lys.		1	AGTATAAGAAGA	0.488	
-	1	1572_1573	18A_uc010csa.1_	NM_004740	NP_004731	O95411	TIAF1_HUMAN			0	TGGTCCACACAC	0.564	
-	5	891		NM_139285	NP_644814	Q8NHY3	GA2L2_HUMAN			2	GGGCCGGGGGC	0.597	rs139867246
-	22	2927	nn.2_Frame_Shift	NM_198836	NP_942133	Q13085	ACACA_HUMAN			2	ACATTGGGGGG	0.473	
+	4	641_642	103_uc002ihp.1_5	NM_213607	NP_998772	Q8IW40	CC103_HUMAN			1	GGGCAGAGAGA	0.644	
-	5	1187_1189	.1_In_Frame_Del_	NM_007146	NP_009077	Q14119	VEZF1_HUMAN	Poly-Gln.		2	gttgttgttgctgctgctg	0.305	731354;rs73995411
-	33	4884	yn.1_Frame_Shift_	NM_032582	NP_115971	Q8NFA0	UBP32_HUMAN			5	TTTGGGTTTTTG	0.423	
+	4	2243_2245	.A552del|TNRC6C	NM_018996	NP_061869	Q9HCJ0	TNR6C_HUMAN	ith argonaute family protein		2	TAGTACTGCTGCT	0.591	
+	7	895_897	02jyd.1_In_Frame_	NM_173626	NP_775897	Q86WA9	S2611_HUMAN	ical; (Potential).		0	TGCATGCTGCT	0.675	
+	18	3129_3131	92_uc002kru.2_R	NM_032142	NP_115518	E9PF99	E9PF99_HUMAN			5	AGCTCAGCAGC	0.527	

+	2	160	ame_Shift_Del_p.	NM_020474	NP_065207	Q10472	GALT1_HUMAN	enal (Potential).		2	TGATGAAAAAAA	0.383	
-	5	1214_1216	Q161del|CXXC1_u	NM_014593	NP_055408	Q9P0U4	CXXC1_HUMAN	CXXC-type.		2	GTTTGATctgctgct	0.468	
-	15	2001_2002		NM_000064	NP_000055	P01024	CO3_HUMAN			5	TGCTCGTGAAGG	0.658	
+	6	480	2mpe.3_Frame_Sh	NM_020428	NP_065161	Q8IWA5	CTL2_HUMAN	ellular (Potential).		1	CGTGGAAAAATC	0.542	
+	8	1249_1251	.H387del|NFIX_uc002mwf.2_In_Frame_Del_p.H357del			Q14938	NFIX_HUMAN			2	CGCTACCACCA	0.645	
-	5	417_418	B3_uc010eaf.2_R	NM_054113	NP_473454	Q96Q77	CIB3_HUMAN			1	ACTCAGCCCCCC	0.564	
-	11	1923	HERP_uc010xpg.	NM_006387	NP_006378	Q8IWX8	CHERP_HUMAN	Pro-rich.		2	GCCATGGGGGG	0.672	
-	11	1320_1321	nfg.1_Frame_Shift	NM_033417	NP_219485	Q9BT25	HAUS8_HUMAN			0	TGAACGAGAGAG	0.495	
+	2	140	DHA_uc002oqp.1_	NM_000709	NP_000700	P12694	ODBA_HUMAN			0	CAGCACCCCCC	0.567	
+	4	376	FRS16_uc002pan	NM_007056	NP_008987	Q8N2M8	CLASR_HUMAN			0	ACTACACCCCCC	0.612	
+	4	656_658	E183del|KLC3_uc	NM_177417	NP_803136	Q6P597	KLC3_HUMAN	Poly-Glu.		1	CAGCGAGGAGG	0.645	
-	2	1402_1404	2per.3_In_Frame_	NM_018215	NP_060685	Q86V59	PNML1_HUMAN			0	CTCACCTTCTTC	0.562	
-	1	90_92	EC8_uc002pwu.2_	NM_014442	NP_055257	Q9NYZ4	SIGL8_HUMAN			5	agcaggggcagcagc	0.493	
+	11	1757_1759	me_Del_p.L480del	NM_006669	NP_006660	Q8NHL6	LIRB1_HUMAN	ical; (Potent	p.L479del(1)	3	tcctactgctcctcct	0.458	
-	1	839_841	ykm.1_In_Frame_	NM_004036	NP_004027	O60266	ADCY3_HUMAN			4	CCTCCTGCTGC	0.645	
-	2	164	T6B1_uc010yni.1_	NM_001032377	NP_001027549	Q6IMI4	ST6B1_HUMAN			3	TTATACTTTTTTT	0.323	
-	2	234_236	HX57_uc002rrg.2_	NM_198963	NP_945314	Q6P158	DHX57_HUMAN	Gly-rich.		3	gccacctccaccacca	0.384	
-	3	1648_1650	02sit.3_In_Frame	NM_015470	NP_056285	Q9BXF6	RFIP5_HUMAN			0	GCCTTGGTGGT	0.635	
-	4	878	ssp.1_Frame_Shif	NM_016618	NP_057702	Q9NPI7	KRCC1_HUMAN	Lys-rich.		1	GGTGCCTTTTCC	0.428	
+	6	1052_1053	002sta.3_Frame_	NM_018271	NP_060741	Q86YJ6	THNS2_HUMAN			1	AGACTTCTCTCT	0.545	
-	4	737_739	02svr.2_In_Frame_	NM_017849	NP_060319	O75204	TM127_HUMAN			0	TCTTATGCTGCTG	0.557	
+	3	224_242		NM_001862	NP_001853	P10606	COX5B_HUMAN			0	CCAAAGGGAGC	0.397	
-	20	2077	y.1_Frame_Shift_	NM_004543	NP_004534	P20929	NEBU_HUMAN	Nebulin 15.		20	TCTGGTTTTTGG	0.403	
-	15	3165	vdt.2_Frame_Shif	NM_152519	NP_689732	A0AUZ9	CB067_HUMAN			3	CACCTATTTTTTT	0.418	
+	7	931	.1_Frame_Shift_D	NM_000578	NP_000569	P49279	NRAM1_HUMAN	ical; (Potential).		4	GGAAGCTTTTTTT	0.418	
+	9	1386_1387	p.S210fs|FAM134	NM_024293	NP_077269	Q8NC44	F134A_HUMAN			2	AGGGTCCCCCC	0.604	
-	2	797	002wwn.2_Frame_	NM_138578	NP_612815	Q07817	B2CL1_HUMAN	BH1.		2	AGGAGAAAAAG	0.542	
-	2	361	_p.K64fs|EIF2S2_	NM_003908	NP_003899	P20042	IF2B_HUMAN			1	CGCACCTTTTTTC	0.483	
+	3	617_619	me_Del_p.A96del|	NM_016434	NP_057518	Q9NZ71	RTEL1_HUMAN	ase ATP-binding.		0	GCAACGCTGCTG	0.645	
-	10	1758	160_uc010gll.1_F	NM_015565	NP_056380	O94822	LTN1_HUMAN			0	TTACCATTTTTTT	0.378	
+	21	3378	p.G704fs|COL18A	NM_130444	NP_569711	P39060	COIA1_HUMAN	lical region 4 (COL4).		1	CCTGGCCCCCC	0.692	
-	4	542	l_p.G31fs|TBC1D	NM_031937	NP_114143	Q9BXI6	TB10A_HUMAN	ab-GAP TBC.		1	CGTGGCCCCCC	0.607	
+	5	1337	p.E279fs|HMGXB	NM_001003681	NP_001003681	Q9UGU5	HMGX4_HUMAN			2	CATAGTGAaaaaa	0.408	rs76572304
+	12	1563	aot.1_Frame_Shift	NM_015705	NP_056520	Q96HU1	SGSM3_HUMAN			2	ACCCCAAAAACT	0.617	
+	31	7059_7061		NM_001429	NP_001420	Q09472	EP300_HUMAN	ction with NCOA2.		64	ACCACAGCAGC	0.576	rs111265631
-	11	1376	11axh.1_Frame_Sh	NM_016141	NP_057225	Q9Y6G9	DC1L1_HUMAN			1	GATCAATTTTTTT	0.398	
+	13	2437	NKTR_uc003clq.1_	NM_005385	NP_005376	P30414	NKTR_HUMAN	Arg/Ser-rich.		3	GTGGGAAAAAA	0.378	rs150528581
+	4	842	pk.1_Frame_Shift	NM_178329	NP_847899	P51677	CCR3_HUMAN	ellular (Potential).		8	CTGGGTTTTTGC	0.488	
-	15	1367_1370	QARS_uc003cvy.2	NM_005051	NP_005042	P47897	SYQ_HUMAN			1	TGCAGAGTGAGT	0.593	rs144899098
+	14	2702_2703	A3_uc010hon.1_	NM_005233	NP_005224	P29320	EPHA3_HUMAN	Potential).|Protein kinase.		33	ATACTGGGAGAT	0.446	
+	13	1521_1522	p.T229fs|ZPLD1_u	NM_175056	NP_778226	Q8TCW7	ZPLD1_HUMAN	acellular (Potential).		5	AAAACCAAAGTA	0.351	rs148150314
+	1	507_509	me_Del_p.K22del|	NM_017548	NP_060018	Q9UKY7	CDV3_HUMAN	Poly-Lys.		0	GGACAAGAAGA	0.325	
-	9	782	me_Shift_Del_p.R	NM_178130	NP_835231	Q86XW9	TXND6_HUMAN	NDK.		5	GTCACGGGGGC	0.587	rs80092642
-	10	1701_1703	1bpf.1_In_Frame_	NM_014498	NP_055313	O00461	GOLI4_HUMAN	rich.|Lumenal (Potential).		5	TTGCCACctgctgct	0.374	rs61743912
-	28	3481_3482	3A3_uc003ftx.3_5	NM_024524	NP_078800	Q9H7F0	AT133_HUMAN			1	TGACCCAAAAAA	0.381	
+	21	2524_2526	buy.1_In_Frame_	NM_000283	NP_000274	P35913	PDE6B_HUMAN			0	GAGAAGGAGGA	0.562	
-	3	530_531	|UGDH_uc003gul.	NM_003359	NP_003350	O60701	UGDH_HUMAN			4	TGGTAGAAAAAA	0.297	

-	6	542	D2_uc003gyu.2_	NM_001014446	NP_001014446	Q56VL3	OCAD2_HUMAN	OCIA.		0	ATCTTCAAAAAA	0.393	
-	3	416_418	.1_5'UTR|NUP54_	NM_017426	NP_059122	Q7Z3B4	NUP54_HUMAN	ch.|9 X 2 AA repeats of F-G		2	AGTTTGCTGCT	0.394	
+	1	3100_3102	3igz.2_In_Frame_	NM_032961	NP_116586	Q9P2E7	PCD10_HUMAN	ytoplasmic (Potential).		2	GCCTCTGCTGC	0.581	
-	2	1076_1078	me_Del_p.P343d	NM_178835	NP_849157	Q17R98	ZN827_HUMAN	Pro-rich.		0	GGGATTgtggtggt	0.35	
-	10	7220		NM_005245	NP_005236	Q14517	FAT1_HUMAN	(Potential).|Cadherin 21.		12	CTGAGTAGTGA	0.483	
-	7	919	AH5_uc003jfe.1_	NM_001369	NP_001360	Q8TE73	DYH5_HUMAN	.|Stem (By similarity).		31	GAGTCTTTTTTT	0.517	
-	3	473_475	1_In_Frame_Del_	NM_016107	NP_057191	Q96KR1	ZFR_HUMAN	Ala-rich.		0	TGGGGGTGGTG	0.483	
-	1	479_480		NM_001085377	NP_001078846	P23508	CRCM_HUMAN			1	ctgccgctgccgccgc	0.391	
-	1	991_993	Frame_Del_p.E29	NM_020747	NP_065798	Q9ULD9	ZN608_HUMAN	Potential.		6	GGCTCTCCTCC	0.522	
+	4	743	l3B_uc010jew.1_5	NM_016604	NP_057688	Q7LBC6	KDM3B_HUMAN			11	GCTTTGATCAGT	0.398	
-	3	512_514	0jii.2_In_Frame_D	NM_138379	NP_612388	Q96H15	TIMD4_HUMAN	ar (Potential).|Thr-rich.		2	GGGCTTGTTGT	0.537	
-	2	823	IP2_uc003lwr.2_	NM_001001343	NP_001001343	Q8TBE3	FNDC9_HUMAN			0	CACCACCCCCC	0.582	
-	15	2057	BR1_uc003nmu.	NM_001470	NP_001461	Q9UBS5	GABR1_HUMAN	ellular (Potential).		7	CAGCTGGGGGG	0.363	
-	1	156_157		NM_032020	NP_114409	Q9BTY2	FUCO2_HUMAN			1	cggcggcggcagcag	0.599	
+	9	3753_3755	_3'UTR|GRM1_u	NM_000838	NP_000829	Q13255	GRM1_HUMAN	dic).|Cytoplasmic (Potentia		19	CGCGGACGACG	0.65	
+	9	3846_3848	_3'UTR|GRM1_u	NM_000838	NP_000829	Q13255	GRM1_HUMAN	dic).|Cytoplasmic (Potentia		19	GGAAGAGGAGG	0.64	
+	6	1162	lz.1_Frame_Shift_	NM_003751	NP_003742	P55884	EIF3B_HUMAN	teraction with EIF3E.|WD 1		0	TCTATGGGGGG	0.478	
-	3	1548	c003szu.1_5'Flan	NM_014817	NP_055632	Q7L0X0	TRIL_HUMAN	lar (Potential).|LRRCT.		0	GGCCGGGGGG	0.662	
+	1	403_405	c003tbl.3_5'Flank	NM_002047	NP_002038	P41250	SYG_HUMAN			1	CGCTCTGCTGC	0.749	
+	30	5386_5387	kbi.1_Frame_Shift	NM_015052	NP_055867	Q76N89	HECW1_HUMAN	HECT.		23	GCTGTTAACAGC	0.505	
+	7	890_892	3toi.3_In_Frame_	NM_001100159	NP_001093629	Q8NEG2	CG057_HUMAN			1	GGTTGCAGCAG	0.473	
-	4	453_455	_Frame_Del_p.D9	NM_016086	NP_057170	Q9Y6J8	STYL1_HUMAN	Rhodanese.		0	TCTGAATCATCA	0.389	
-	10	1091_1092	p.S339fs|ABCB4_	NM_018849	NP_061337	P21439	MDR3_HUMAN	).|ABC transmembrane typ		6	GGATTGAAAAAA	0.347	
-	7	1188	p.K237fs|CYP51A	NM_000786	NP_000777	Q16850	CP51A_HUMAN			0	ATAACATTTTTTT	0.398	
+	5	881	sk.2_Frame_Shift_	NM_153332	NP_699163	Q8IV48	ERI1_HUMAN	xonuclease.		0	GGTACTAAAAAA	0.328	
+	12	3531	uf.2_Frame_Shift_	NM_017780	NP_060250	Q9P2D1	CHD7_HUMAN	ase ATP-binding.		9	TGGCCCTTTTTT	0.418	
+	3	331	ame_Shift_Del_p.	NM_052832	NP_439897	Q8TE54	S26A7_HUMAN	lasmic (Potential).		2	GCATACCCCCC	0.398	
-	23	3681_3682	.K981fs|RGS22_	NM_015668	NP_056483	Q8NE09	RGS22_HUMAN	Potential.		7	TGCCAATTTTTT	0.312	rs7841915
-	45	6393_6394	ks.1_Frame_Shift_	NM_015902	NP_056986	O95071	UBR5_HUMAN			28	CCCTTCTTTTTT	0.381	
-	11	2666_2668		NM_015117	NP_055932	Q8IXZ2	ZC3H3_HUMAN	Poly-Ser.	p.S879F(1)	1	ggggatgaggaggag	0.552	;rs2272753;rs137878905
-	2	331		NM_015117	NP_055932	Q8IXZ2	ZC3H3_HUMAN			1	GCTGGCCCCCC	0.632	
-	6	1681_1683	Q376del|ARHGAP	NM_025251	NP_079527	Q9C0H5	RHG39_HUMAN			0	ACTTCTGCTTG	0.704	rs77462981
-	7	2587	IGO_uc003zwf.2_	NM_032634	NP_116023	Q8TEQ8	PIGO_HUMAN			3	GAGACGGGGGG	0.662	rs148341577
+	3	1021_1023	bag.1_In_Frame_	NM_006981	NP_008912	Q92570	NR4A3_HUMAN	Poly-His.		173	tcaccatcaccaccacc	0.483	
+	10	1284_1286	bhp.2_In_Frame_	NM_152786	NP_689999	Q8TAL5	CI043_HUMAN	Gln-rich.		0	gcagcggcagcagca	0.438	
-	22	6093	f.2_Frame_Shift_	NM_002160	NP_002151	P24821	TENA_HUMAN	nectin type-III 15.		7	TGCCCGGGGGG	0.478	rs148674204
-	3	128_129	_Shift_Ins_p.K34f	NM_016390	NP_057474	Q5T280	CI114_HUMAN			0	CTTCCATTTTTT	0.525	
+	43	5050		NM_015354	NP_056169	Q5SRE5	NU188_HUMAN			7	GTGCACCCCCG	0.587	
+	14	2226_2228	9orf86_uc004cjl.1	NM_024718	NP_078994	Q3YEC7	PARF_HUMAN	with CDKN2A.|Lys-rich.		0	CTaaggagaagaag	0.532	
+	13	2110_2112	598del|GRIN1_u	NM_007327	NP_015566	Q05586	NMDZ1_HUMAN	lasmic (Potential).		1	CAGCGAGGAGG	0.739	
+	7	563		NM_005635	NP_005626	Q16384	SSX1_HUMAN			1169	GACCCAAAAGG	0.493	
-	1	454_456	33A_uc004efr.1_5	NM_004538	NP_004529	Q99457	NP1L3_HUMAN	Ser-rich.		2	ccactagtgctgctgct	0.217	
+	2	431	P36_uc004ewb.2_	NM_144967	NP_659404	Q6ZRI8	RHG36_HUMAN			3	CCTTCATTTTTTT	0.542	
-	14	2723	p.A823fs|IGSF1_	NM_001555	NP_001546	Q8N6C5	IGSF1_HUMAN	otential).|Ig-like C2-type 8.		5	ACTGGCCCCCG	0.488	
+	2	555	cr.2_Frame_Shift_	NM_002025	NP_002016	P51816	AFF2_HUMAN			5	CACTTAAAAAAA	0.378	
+	2	368	_5'Flank|PNMA3_	NM_013364	NP_037496	Q9UL41	PNMA3_HUMAN			3	ctggtgtcgggggaa	0.07	
-	1	203	k|PEX14_uc010o	NM_004401	NP_004392	O00273	DFFA_HUMAN	CIDE-N.		0	GAGGCGGCCAC	0.706	

+	67	2633_1263	Shift_Del_p.V335	NM_015378	NP_056193	Q5THJ4	VP13D_HUMAN		5	AGTGTTATAACT	0.465	
-	23	3493	yz.1_Frame_Shift	NM_017940	NP_060410	Q3BBV0	NBPF1_HUMAN	NBPF 4.	0	TATGTCAACAG	0.488	
+	12	2906_2908	9vqi.1_In_Frame_	NM_001083621	NP_001077090	Q9NUA8	ZBT40_HUMAN		1	CCCCAAGAAGA	0.517	
+	1	1263_1265		NM_004455	NP_004446	Q92935	EXTL1_HUMAN	enal (Potential).	1	CCTGCCTCCTC	0.606	
+	4	552	9vws.1_Frame_Sh	NM_015284	NP_056099	Q5T011	SZT2_HUMAN		0	CTCTTCCCCCC	0.572	
-	2	836	01fs|ZCCHC11_u	NM_015269	NP_056084	Q5TAX3	TUT4_HUMAN		3	TTTCTCCCCCTA	0.388	
-	6	729	173_uc001dgi.3_5	NM_001002912	NP_001002912	Q5RHP9	CA173_HUMAN		5	TTACTGGGAAG	0.418	
-	2	368	1ebp.1_Frame_Sh	NM_019099	NP_061972	Q9NTI7	CA183_HUMAN		2	GTCCTGGGACC	0.622	
-	12	1907_1908		NM_020205	NP_064590	Q6GQQ9	OTU7B_HUMAN		3	CTTCTTGAGCTT	0.55	
-	2	3439	ne.1_Frame_Shift_	NM_007113	NP_009044	Q07283	TRHY_HUMAN	0 AA tandem repeats.	5	cctcctgctgcacctcct	0.174	
-	6	1404_1406	.V48del|PVRL4_u	NM_030916	NP_112178	Q96NY8	PVRL4_HUMAN	ical; (Potential).	2	TGAGCACCACC	0.571	
-	12	2457	1gjv.2_Splice_Site_	NM_172071	NP_742068	Q5TC82	RC3H1_HUMAN		2	TTGCTTACTTCT	0.277	
+	7	1456_1457	_Ins_p.378_379ins	NM_005807	NP_005798	Q92954	PRG4_HUMAN	ats of K-X-P-X-P-T-T-X.|17	1	CTGCACCCACC	0.653	rs149342058
+	7	1633_1634	_Ins_p.435_436ins	NM_005807	NP_005798	Q92954	PRG4_HUMAN	-X-P-X-P-T-T-X.|24; appro	1	CCACCAAGTCTG	0.639	
-	19	9180_9181	.L1390fs|ASPM_	NM_018136	NP_060606	Q8IZT6	ASPM_HUMAN	IQ 35.	6	TAGCTAGATATT	0.351	
-	4	586	_p.I113fs|TMEM9_	NM_016456	NP_057540	Q9P0T7	TMEM9_HUMAN	ellular (Potential).	0	ACCTTGATGGT	0.587	
-	4	2151		NM_025179	NP_079455	O75051	PLXA2_HUMAN	lar (Potential).|Sema.	3	ACCATGGGGGG	0.592	
+	5	950	FBXO28_uc010pv	NM_015176	NP_055991	Q9NVF7	FBX28_HUMAN		5	AAACTGCTAGA	0.473	
-	19	2298_2299	p.C122fs|DIP2C_	NM_014974	NP_055789	Q9Y2E4	DIP2C_HUMAN		7	AACTGCACACA	0.54	
-	14	1692		NM_015155	NP_055970	Q92615	LAR4B_HUMAN		3	TGTTTTCAAACA	0.413	
-	10	1480	p.Q352fs|GDI2_uc	NM_001494	NP_001485	P50395	GDIB_HUMAN		0	CACCTGGCTTT	0.453	
+	4	508	_Shift_Del_p.P24fs	NM_001008213	NP_001008214	Q96CV9	OPTN_HUMAN		2	ATGGACCCCCC	0.557	
+	5	1009	jrp.2_Frame_Shift	NM_170744	NP_734465	Q8IZJ1	UNC5B_HUMAN	.|Extracellular (Potential).	3	TGGCTCAAGAA	0.587	
-	5	868	009xvi.2_RNA|AR	NM_032900	NP_116289	Q14CB8	RHG19_HUMAN	Rho-GAP.	0	TCACATTTTTG	0.378	
-	2	441	1kov.2_Frame_Shi	NM_018058	NP_060528	Q9NQ79	CRAC1_HUMAN		5	CCGCTGGGACC	0.507	
-	3	1546	5_splice|CHST15	NM_015892	NP_056976	Q7LFX5	CHSTF_HUMAN		1	GCCTTACCGAT	0.554	
+	1	756	_uc001mam.1_Int	NM_001004750	NP_001004750	Q9H340	O51B6_HUMAN	Name=6; (Potential).	2	GTCACTGTAGT	0.443	
+	25	8653_8655	del|DNHD1_uc00	NM_144666	NP_653267	Q96M86	DNHD1_HUMAN	Glu-rich.	2	AGAGTgaggagg	0.507	
-	2	507_509		NM_003737	NP_003728	Q96JQ0	PCD16_HUMAN		5	AGCCCCcagcagc	0.527	
-	4	659	EIF4G2_uc001mjd	NM_001418	NP_001409	P78344	IF4G2_HUMAN	MIF4G.	2	CTCTTACTTTCC	0.433	
+	7	1258	hift_Del_p.V286fs	NM_018393	NP_060863	Q9NUJ3	T11L1_HUMAN		0	CCAGTGGGGGG	0.542	
+	30	3229	GKZ_uc009yky.1_	NM_001105540	NP_001099010	Q13574	DGKZ_HUMAN		3	TCCAGCCCCCC	0.649	rs3832759
+	1	578_579		NM_001005200	NP_001005200	Q8N162	OR8H2_HUMAN	ellular (Potential).	2	TACATACAACAC	0.406	rs147828358
-	12	2431	BP_uc009ymr.1_	NM_002556	NP_002547	P22059	OSBP1_HUMAN		1	AACATTCCATTTT	0.517	
-	5	593	N1_uc001nuk.2_	NM_015853	NP_056937	Q04323	UBXN1_HUMAN	nteraction with BRCA1.	0	CGGCCTTTTCC	0.537	
-	2	598_600	1orf95_uc001nxs.	NM_001144936	NP_001138408	C9JLR9	CK095_HUMAN	Glu-rich.	0	tcctcttcttcctcctcctc	0.532	
+	9	2328	_p.I493fs|SLC22A	NM_144585	NP_653186	Q96S37	S22AC_HUMAN		1	ACCATCCAAGA	0.602	
+	7	801	_5'Flank|C11orf6	NM_006442	NP_006433	Q14919	NC2A_HUMAN	Pro-rich.	0	CTTTGCCCCCA	0.647	
+	17	1651	5_splice|CTTN_u	NM_005231	NP_005222	Q14247	SRC8_HUMAN		1	CTTTTAGAGGAC	0.51	
-	16	2389	_p.E489fs|ARAP1_	NM_001040118	NP_001035207	Q96P48	ARAP1_HUMAN		1	CTTTTCCAGGG	0.627	
+	2	123	_Shift_Del_p.L41f	NM_025098	NP_079374	Q3SYC2	MOGT2_HUMAN	ical; (Potential).	2	GCCCTCCTGTT	0.597	
-	2	372	zg.2_Frame_Shif	NM_080491	NP_536739	Q9UQC2	GAB2_HUMAN		6	CCTGTGCTCTC	0.517	
-	29	5622	vb.1_Frame_Shift_	NM_001098816	NP_001092286	Q6N022	TEN4_HUMAN	ellular (Potential).	4	TGTCTGTATCA	0.537	
+	36	5710_5711	_Shift_Del_p.L427f	NM_000051	NP_000042	Q13315	ATM_HUMAN		240	TTTTTAGAAGTA	0.317	
+	3	2335	L_uc001psz.1_Fr	NM_005933	NP_005924	Q03164	MLL1_HUMAN		25	TCTCACCCCCC	0.453	
+	7	1236_1237	ne_Shift_Del_p.V2	NM_001655	NP_001646	P48444	COPD_HUMAN	MHD.	0	GTGACGTAGGG	0.436	
-	6	1503_1505	L1_uc001pwu.1_I	NM_002855	NP_002846	Q15223	PVRL1_HUMAN	ytoplasmic (Potential).	0	CACCGCcctcctc	0.576	

-	7	915	010sbo.1_5'Flank|	NM_003139	NP_003130	P08240	SRPR_HUMAN		0	AGCTGCCCCCC	0.527	
-	6	1100_1118	5A_uc010sdn.1_F	NM_001042603	NP_001036068	P29375	KDM5A_HUMAN		3	AGCCCACAACCT	0.342	
-	9	1657_1659	3_554PP>P|IFFO1	NM_080730	NP_542768	Q0D2I5	IFFO1_HUMAN	Poly-Pro.	0	GCTTGGCGGCG	0.601	rs144019095
-	4	745_747	.1_Intron|PRB1_u	NM_005039	NP_005030	P04280	PRP1_HUMAN	P-P-[PAQ]-Q-[GE]-[GD]- [N	0	TCCTGGAGGAG	0.611	
-	4	946	|LRP6_uc010shl.1	NM_002336	NP_002327	O75581	LRP6_HUMAN	eta-propeller 1.|LDL-recept	12	TCCATGGGAGA	0.433	
-	13	2119_2120	1rja.2_Frame_Shi	NM_175861	NP_787057	Q8IUR5	TMTC1_HUMAN	TPR 6.	0	GTCTTCCCAAGT	0.5	
-	10	1940		NM_003482	NP_003473	O14686	MLL2_HUMAN	f S/P-P-P-E/P-E/A.|Pro-rich	41	CAGGTGGGGGG	0.637	
-	27	3380_3382	a.2_Intron|SMARC	NM_003075	NP_003066	Q8TAQ2	SMRC2_HUMAN	Pro-rich.	6	GAGCAGGAGGA	0.591	
+	11	1468_1469	ntron|MDM2_uc00	NM_002392	NP_002383	Q00987	MDM2_HUMAN	or interaction with USP2.	3	ACAATCACAAGA	0.361	
+	6	1196_1198	me_Del_p.P402de	NM_007007	NP_008938	Q16630	CPSF6_HUMAN	Pro-rich.	0	TTCTTTCCTCCA	0.576	
-	12	1471	0_splice|NAP1L1_	NM_139207	NP_631946	P55209	NP1L1_HUMAN		2	GCTTACATCATC	0.345	
-	2	315	syn.2_Frame_Shift	NM_203394	NP_976328	Q96AV8	E2F7_HUMAN		3	CATTTTCCCCAT	0.373	
+	1	79		NM_001101421	NP_001094891	Q8N1T3	MYO1H_HUMAN		0	GAATCTGCCTTT	0.537	
+	11	1305	_Shift_Del_p.A322	NM_001114185	NP_001107657	Q03426	KIME_HUMAN		0	CGGTGCCCCCG	0.662	
+	9	1152	01trp.3_Frame_Sh	NM_001082537	NP_001076006	Q2MV58	TECT1_HUMAN		0	GTTCTGGGGAC	0.398	
-	6	1088	vq.2_Frame_Shift_	NM_181486	NP_852259	Q99593	TBX5_HUMAN	T-box.	8	GCTGTATTTTTTG	0.408	
-	9	1164	j.1_Splice_Site_p.	NM_007174	NP_009105	O14578	CTRO_HUMAN		10	CTACTTACAGTT	0.398	
-	5	948	1ufx.1_Frame_Shi	NM_025140	NP_079416	Q53HC0	CCD92_HUMAN		0	GCGATGGGGGG	0.682	rs147939560
+	6	2495_2496	p.T222fs|ZNF664_	NM_152437	NP_689650	Q8N3J9	ZN664_HUMAN		0	CCACACAGGAG	0.515	
-	2	1065_1067	_Intron|SALL2_uc	NM_005407	NP_005398	Q9Y467	SALL2_HUMAN	Poly-Ser.	3	gaggaagaggagga	0.512	
-	7	1366	p.P369fs|CDH24_	NM_022478	NP_071923	Q86UP0	CAD24_HUMAN	r (Potential).|Cadherin 3.	1	GGCTCTGGGGCA	0.642	
-	19	4033_4034	_uc001wiq.3_Fram	NM_014977	NP_055792	Q9UKV3	ACINU_HUMAN	Asp/Glu/Lys-rich.	4	TTTCTGAACGAT	0.421	
+	2	231		NM_004094	NP_004085	P05198	IF2A_HUMAN	S1 motif.	1	GAAATGGGGGC	0.279	
+	1	607_609		NM_003403	NP_003394	P25490	TYY1_HUMAN	Glu-rich (acidic).	0	gtgggcgaggagga	0.34	
-	11	1570_1571	zqp.2_Frame_Shift	NM_173500	NP_775771	Q6IQ55	TTBK2_HUMAN		7	TCCTGGGGACG	0.361	
-	18	2278	a.1_RNA|MYO5C_	NM_018728	NP_061198	Q9NQX4	MYO5C_HUMAN	osin head-like.	14	ACCTCCTTTTTAT	0.493	
-	4	629_630	LN6_uc010ujz.1_	NM_017882	NP_060352	Q9NWW5	CLN6_HUMAN		0	CGGCTTGAGATT	0.614	
+	5	471	.1_RNA|FANCI_u	NM_001113378	NP_001106849	Q9NVI1	FANCI_HUMAN		2	ATCTTTGGAGTT	0.393	
+	7	1157	_Shift_Del_p.K265	NM_018671	NP_061141	Q9H3U1	UN45A_HUMAN		2	GGTGTCAAAAAA	0.562	
+	8	947	rame_Shift_Del_p.	NM_000693	NP_000684	P47895	AL1A3_HUMAN		4	GAGCTGGGGGG	0.572	rs142377552
+	3	1065	dgb.3_Frame_Shift	NM_001105248	NP_001098718	Q6UXY8	TMC5_HUMAN	cellular (Potential).	1	CTCTACCAGAG	0.463	
+	15	1993_1995	.S436del|SLC5A1	NM_052944	NP_443176	Q8WWX8	SC5AB_HUMAN	lasmic (Potential).	2	AGGCCAGCAGC	0.542	
+	25	5954	e_Shift_Del_p.P16	NM_006662	NP_006653	Q6ZRS2	SRCAP_HUMAN	Pro-rich.	4	CTGGTCCCCCC	0.612	
-	6	3848	gn.1_Frame_Shift	NM_015069	NP_055884	Q2M1K9	ZN423_HUMAN	2H2-type 27.	4	GGATTTGGATCT	0.438	
-	2	506_508	me_Del_p.S62del	NM_002968	NP_002959	Q9NSC2	SALL1_HUMAN	Poly-Ser.	8	cgccgccgctgctgct	0.463	rs13336129
+	5	1317_1319	hx.2_In_Frame_D	NM_024335	NP_077311	P78412	IRX6_HUMAN		6	gaggaagaggagga	0.493	
-	14	1166_1168	h.2_In_Frame_Del	NM_001297	NP_001288	Q14028	CNGB1_HUMAN	ytoplasmic (Potential).	4	tcctcctcttcctcctcctc	0.414	
+	16	2002_2004	ne_Del_p.S549del	NM_014329	NP_055144	Q6P2E9	EDC4_HUMAN	Ser-rich.	4	CTCTCCcagcagc	0.453	
-	8	1497	KL_uc002fdc.2_Int	NM_152649	NP_689862	Q8NB16	MLKL_HUMAN	rotein kinase.	2	TTTCCTCAACTC	0.423	
+	1	90_92		NM_001005271	NP_001005271	Q12873	CHD3_HUMAN		1	ggcgacgaggagga	0.305	
+	13	2245_2247	.K762del|CHD3_u	NM_001005273	NP_001005273	Q12873	CHD3_HUMAN	Poly-Lys.	1	AGTATAAGAAGA	0.488	
+	1	149	ift_Del_p.G11fs|R	NM_016492	NP_057576	Q9HD47	MOG1_HUMAN		0	TGTTCGGGGGC	0.617	
-	30	4166_4168	E1388del|MYH10_	NM_005964	NP_005955	P35580	MYH10_HUMAN	Potential.	2	CTGGCCTCCTC	0.596	
+	4	1276_1278	SMCR7_uc010vx	NM_139162	NP_631901	Q96C03	SMCR7_HUMAN		0	GGCGGCTGCTG	0.685	
+	9	965_966	p.E205fs|MAP2K3	NM_145109	NP_659731	P46734	MP2K3_HUMAN	rotein kinase.	0	AGCCTGAGAGG	0.619	
-	13	1600	.K465fs|CCT6B_	NM_006584	NP_006575	Q92526	TCPW_HUMAN		1	AAGTTGTTTTTT	0.289	
+	6	1122	fe.1_Frame_Shift_	NM_000964	NP_000955	P10276	RARA_HUMAN	gand-binding.	3	ACATTGACCTC	0.572	

-	9	1271	hzi.3_Frame_Shif	NM_012448	NP_036580	P51692	STA5B_HUMAN			6	CACCTGGGGGG	0.577	rs144993426
-	11	1774_1775	K14_uc010daj.1_	NM_003954	NP_003945	Q99558	M3K14_HUMAN	th ZFP91.|Protein kinase.		8	AGGGATGTAGTC	0.574	
-	4	933	dbh.1_Frame_Shi	NM_018952	NP_061825	P17509	HXB6_HUMAN	Homeobox.		0	TCTCCTTTTTCC	0.602	
+	20	2951	195_uc010wsb.1_	NM_014738	NP_055553	Q12767	K0195_HUMAN			1	GAGATCCCCCC	0.612	
-	13	2084	jqe.2_Frame_Shif	NM_007292	NP_009223	Q15067	ACOX1_HUMAN			1	CGAATCAGAGT	0.408	rs79605652
+	26	4173	.P1237fs|PTPRM_	NM_002845	NP_002836	P28827	PTPRM_HUMAN	hatase 2.|Cytoplasmic (Po		6	TCCTGCCCCCA	0.597	
-	8	855		NM_005570	NP_005561	P49257	LMAN1_HUMAN			1	TGGGCTTTTTT	0.294	
+	4	1419_1420		NM_014913	NP_055728	Q6IQ32	ADNP2_HUMAN	Pro-rich.		8	CTCATTCCCCCC	0.644	
+	14	1937	409fs|HMHA1_uc0	NM_012292	NP_036424	Q92619	HMHA1_HUMAN			1	TAGGTCCCCCG	0.662	
+	8	1578_1579	p.T432fs|SMARC	NM_003072	NP_003063	P51532	SMCA4_HUMAN		p.?(1)	67	TGGAGACAGCC	0.629	
-	8	1346_1347	2mwy.3_Frame_Sh	NM_001127221	NP_001120693	O00555	CAC1A_HUMAN	lasmic (Potential).		2	GTTCTCCACCC	0.45	
+	10	1017_1018	_5'Flank|KIAA089	NM_015329	NP_056144	Q9Y6X3	SCC4_HUMAN			0	TGCTGGACTGC	0.639	
+	11	1955_1956	0xqv.1_Frame_Sh	NM_017660	NP_060130	Q86YP4	P66A_HUMAN			0	TCCGTCACCCAA	0.663	
-	2	120_122		NM_000704	NP_000695	P20648	ATP4A_HUMAN	lasmic (Potential).		1	CCGCCTTCTTC	0.601	
+	8	1917	p.S598fs|CEACAM	NM_004363	NP_004354	P06731	CEAM5_HUMAN	Ig-like 7.		2	CATTTCCCCCC	0.547	
-	3	1652	p.A536fs|DMWD_	NM_004943	NP_004934	Q09019	DMWD_HUMAN			0	CTCTGCCCCCC	0.706	
+	2	603_605		NM_014330	NP_055145	O75807	PR15A_HUMAN	alization in the endoplasmi		1	TTTTGGATGATG	0.571	
-	1	166_168		NM_178449	NP_848544	Q96A98	TIP39_HUMAN			0	CACCACcagcagc	0.596	
-	10	2162_2163	27A5_uc002qtb.2_	NM_012254	NP_036386	Q9Y2P5	S27A5_HUMAN	lasmic (Probable).		0	TCCCTCACACAC	0.604	
+	7	1087_1088	rbt.2_Frame_Shift_	NM_145693	NP_663731	Q14693	LPIN1_HUMAN			4	GAAATGCTTTGG	0.48	
+	7	1477	BL5_uc002rid.2_F	NM_021831	NP_068603	Q8NDL9	CBPC5_HUMAN			2	ACCATCCCCCC	0.512	
+	7	1438	v.2_Frame_Shift_	NM_206943	NP_996826	Q14766	LTBP1_HUMAN			8	TTTCCTCCTAAC	0.363	
+	8	1039	Shift_Del_p.L75fs|	NM_001130482	NP_001123954	Q86Y07	VRK2_HUMAN	rotein kinase.		1	TTATTTAGGAATT	0.279	
-	7	654_655	1_uc002sgl.3_RN	NM_022173	NP_071505	P31483	TIA1_HUMAN	RRM 2.		0	CCCTTAGACTTT	0.386	
+	54	6461	YSF_uc010fej.2_	NM_003494	NP_003485	O75923	DYSF_HUMAN	lasmic (Potential).		7	TGGTTTACCTCC	0.493	
+	1	147_152	2sjf.1_In_Frame_	NM_015120	NP_055935	Q8TCU4	ALMS1_HUMAN	Glu-rich.		9	AGCTggaggagg	0.403	rs72319667
-	2	269	4C_uc002sxg.3_5	NM_017789	NP_060259	Q9C0C4	SEM4C_HUMAN			2	ACTCACCCCCA	0.607	
+	22	3486_3487	yvq.1_Frame_Shi	NM_015904	NP_056988	O60841	IF2P_HUMAN			3	GTACATTTTTAA	0.401	
+	1	253	.3_Intron|TMEM18	NM_144632	NP_653233	Q6ZP80	TM182_HUMAN			0	TTTTTGGTGGC	0.383	
-	3	1148	c002too.1_5'Flank	NM_017969	NP_060439	Q96ST2	IWS1_HUMAN	pproximate tandem repeat		1	TCCTTGGGGGA	0.557	
+	11	1572	p.K327fs|ACVR2A	NM_001616	NP_001607	P27037	AVR2A_HUMAN	Potential).|Protein kinase.		13	TGCATAAAAAAA	0.368	
-	15	2279	0zcx.1_Frame_Sh	NM_014900	NP_055715	Q53SF7	COBL1_HUMAN			3	TCCCATCAAAAC	0.373	
-	4	986	Shift_Del_p.G87fs|	NM_022152	NP_071435	Q969X1	TMBI1_HUMAN			0	ACTCTCCAGGC	0.582	
+	4	350	p.L117fs|RQCD1_	NM_005444	NP_005435	Q92600	RCD1_HUMAN			2	TCCCACTTTTTTT	0.413	
-	16	1630	p.G552fs|FARSB_	NM_005687	NP_005678	Q9NSD9	SYFB_HUMAN			1	CATATCCCCCC	0.453	
+	20	2479	p.Y783fs|PSMD1_	NM_002807	NP_002798	Q99460	PSMD1_HUMAN			2	GGCTTATACCC	0.433	
+	26	3123	_Shift_Del_p.F993	NM_152879	NP_690618	Q16760	DGKD_HUMAN			5	AGCTTCGTCCT	0.597	
-	7	745_746	10zpi.1_Frame_Sh	NM_153269	NP_695001	Q9NUD7	CT096_HUMAN	Potential.		0	GGTCTTCTCAAT	0.545	
+	7	1231	wil.2_Frame_Shift_	NM_139321	NP_647537	O75882	ATRN_HUMAN	ar (Potential).|Kelch 1.		2	GGCTTCCACTA	0.373	
+	1	464_466	D3_uc010zrf.1_5'	NM_014962	NP_055777	Q9Y2F9	BTBD3_HUMAN	Poly-Ser.		3	AAATACcagcagc	0.335	
+	1	27_29		NM_080826	NP_543016	B1AKI9	ISM1_HUMAN			0	GGCCGAgctgctg	0.517	
-	2	446_447	CL2L1_uc002ww	NM_138578	NP_612815	Q07817	B2CL1_HUMAN			2	TCACTAAACTGA	0.525	
+	5	708	.E65fs|TM9SF4_	NM_014742	NP_055557	Q92544	TM9S4_HUMAN			2	GAAGGAAAAAG	0.557	
+	4	755_756		NM_176812	NP_789782	Q9H444	CHM4B_HUMAN			2	CCTACCATCAAA	0.485	
+	8	1393	02xiy.1_Frame_Sh	NM_020336	NP_065069	Q86X10	RLGPB_HUMAN			2	TACCACCCCCC	0.448	
+	6	840_842	me_Del_p.S121de	NM_001048225	NP_001041690					0	TCTAGGAcctcctcc	0.463	
+	7	1184	p.L300fs|LSM14B	NM_144703	NP_653304	Q9BX40	LS14B_HUMAN	FFD box.		0	GAACTCAAGAC	0.547	

+	1	216	3GR_uc002yxz.2_I	NM_007341	NP_031367	P55822	SH3BG_HUMAN		0	TGTGTTGGGGGG	0.552	
+	38	8691_8692	NT_uc002zjj.2_Int	NM_006031	NP_006022	O95613	PCNT_HUMAN	Potential.	8	CTCTGGAGAGAG	0.574	
-	10	847_849	y.1_In_Frame_Del	NM_005659	NP_005650	Q92890	UFD1_HUMAN		0	CCCCTTTCTTCTT	0.512	
+	6	612_614	015_uc002zsr.2_In	NM_001003891	NP_001003891	Q96RN5	MED15_HUMAN	Poly-Gln.	1	ggcgctacagcagcag	0.148	
-	2	658	ADORA2A_uc010guo.1_5'Flank|ADORA2A_uc010gup.2_5'Flank|ADORA2A_uc010guq.2_5'Flank|ADORA2A_uc003						0	GAGCATCAGGGA	0.602	
+	7	3642	atq.1_Frame_Shift	NM_001039141	NP_001034230	Q9H2D6	TARA_HUMAN		1	CCTCCTCCCCAC	0.627	
+	3	267	f32_uc003bca.2_5	NM_001002034	NP_001002034	Q6ICB4	SESQ2_HUMAN	PH.	0	CACCTGGGGGG	0.632	
+	2	378_380		NM_033318	NP_201575	Q9H4I9	CV032_HUMAN	Asp/Glu-rich.	1	CAGAGGATGATG	0.478	rs141840500
-	1	5454_5456	Q1774del|TCF20_	NM_005650	NP_005641	Q9UGU0	TCF20_HUMAN		5	TCCTTCTGCTGCT	0.601	
+	17	2268	N4_uc003bpe.2_F	NM_175607	NP_783200	Q8IWV2	CNTN4_HUMAN	onectin type-III 1.	7	GGATTGGGGAG	0.522	
-	6	806	ne_Shift_Del_p.P2	NM_022094	NP_071377	Q96AQ7	CIDEC_HUMAN		1	CCCTTGGGGGG	0.607	
+	40	4041	_Splice_Site_p.R1	NM_033084	NP_149075	Q9BXW9	FACD2_HUMAN		4	ACCGGGTAAGAG	0.473	
-	1	270_272	3P5_uc003bzq.1_I	NM_004844	NP_004835	O60239	3BP5_HUMAN	Glu-rich.	0	atcccctcttcctcctcctc	0.522	
-	8	1568_1570	3cum.2_In_Frame	NM_016453	NP_057537	Q9NZQ3	SPN90_HUMAN		0	TCTGTCTGCATGT	0.606	
-	10	1136_1137		NM_000884	NP_000875	P12268	IMDH2_HUMAN		1	CACCTTGTACAC	0.569	
-	5	491	p.G17fs|QARS_uc	NM_005051	NP_005042	P47897	SYQ_HUMAN		1	CATTTTGCCATCT	0.517	
+	14	1647	dgm.2_Frame_Shif	NM_006254	NP_006245	Q05655	KPCD_HUMAN	rotein kinase.	9	TCAACGGGGGG	0.602	
-	17	3333	dic.3_Frame_Shift	NM_015224	NP_056039	Q9UK61	CC063_HUMAN		5	GATCACTACACAC	0.433	
+	7	1003	128_uc011bhc.1_I	NM_032787	NP_116176	Q96K78	GP128_HUMAN	cellular (Potential).	4	GTCTTTGGGTAAT	0.368	
-	23	2582	p.V764fs|STAG1_	NM_005862	NP_005853	Q8WVM7	STAG1_HUMAN		2	TCAATACCAACA	0.373	
-	1	150_152	94A_uc003eyh.2_	NM_152394	NP_689607	Q7L0X2	F194A_HUMAN	Glu-rich.	3	ccacctcttcctcctcctc	0.232	
+	6	1672	2_Frame_Shift_De	NM_207293	NP_997176	Q9NR56	MBNL1_HUMAN		1	GTACTTCCCCCAT	0.393	
+	5	440_441	03fcr.1_Intron|IQC	NM_001042705	NP_001036170	Q1A5X6	IQCJ_HUMAN		0	CTCTTGGAGGTT	0.475	
-	26	3135_3137		NM_001041	NP_001032	P14410	SUIS_HUMAN	crase.|Lumenal.	14	TTTTTGTGATATTT	0.369	
+	2	210_212		NM_001145248	NP_001138720	C9JC47	F157A_HUMAN	Gln-rich.	0	GAACTGgcagcagc	0.399	
+	1	4021_4022		NM_175918	NP_787114	Q8N1N5	CRPAK_HUMAN		0	CCTGCTCACACG	0.653	
-	24	2669	cg.1_Frame_Shift_	NM_181808	NP_861524	Q7Z5Q5	DPOLN_HUMAN		4	GGGGTGGGGGC	0.637	
+	11	1685_1686	e_Shift_Del_p.V4	NM_001119	NP_001110	P35611	ADDA_HUMAN		1	GAGGTCCAGGAG	0.535	
+	8	2077	p.L637fs|WFS1_u	NM_001145853	NP_001139325	O76024	WFS1_HUMAN	ical; (Potential).	2	CATCCTGGTGTG	0.587	rs145163802
+	2	830		NM_001080505	NP_001073974	A0PJX4	SHSA3_HUMAN	lasmic (Potential).	2	CCACCTGGCTCAC	0.637	
+	4	2960_2961	p.N871fs|REST_u	NM_005612	NP_005603	Q13127	REST_HUMAN		9	GAAAATTTAAGA	0.441	
+	4	1178	s|MUC7_uc003hfj.	NM_001145006	NP_001138478	Q8TAX7	MUC7_HUMAN	6.|Thr-rich.	4	CGTCTTCCCCAG	0.557	
+	1	1079		NM_020368	NP_065101	Q9NQZ2	SAS10_HUMAN		0	GCACATGGACAT	0.428	
+	1	555		NM_031296	NP_112586	Q9H082	RB33B_HUMAN		0	GCGCTGGCCGC	0.607	rs149649513
+	1	413_414		NM_004575	NP_004566	Q12837	PO4F2_HUMAN		1	GCTggtggtggcggcg	0.386	907220;rs72269802
-	12	2150	cih.1_Frame_Shift_	NM_033632	NP_361014	Q969H0	FBXW7_HUMAN	p.S668fs*26(1)|p.S668	308	CCCACTCCCCCC	0.488	
-	21	4315	10iuq.1_Frame_Sh	NM_030955	NP_112217	P58397	ATS12_HUMAN	TSP type-1 6.	9	TATCTTGAAGCC	0.567	
-	15	2417	10iuq.1_Frame_Sh	NM_030955	NP_112217	P58397	ATS12_HUMAN	Spacer 1.	9	TCAGGTAATATTT	0.463	
-	6	1177_1194	AP2A_uc003jpz.2_	NM_003711	NP_003702	O14494	LPP1_HUMAN	lasmic (Potential).	2	CTTTCTTTAAAAG	0.381	
+	5	747	_p.L145fs|SFRS12	NM_139168	NP_631907	Q8WXA9	SREK1_HUMAN		0	CAGTTTGGGAGC	0.403	
+	7	1194	p.F311fs|BDP1_u	NM_018429	NP_060899	A6H8Y1	BDP1_HUMAN	Myb-like.	2	GATATGTTTTTTT	0.294	
+	2	237_240	_p.K19fs|AP3S1_	NM_001284	NP_001275	Q92572	AP3S1_HUMAN		0	ATCTAAGAGAGA	0.304	rs80118146
+	8	2534	p.C792fs|PPARG	NM_133263	NP_573570	Q86YN6	PRGC2_HUMAN		0	CCACTTGCTCTG	0.483	
+	4	546_547	c.2_RNA|GPX3_u	NM_002084	NP_002075	P22352	GPX3_HUMAN		0	ACCAGGAGAGA	0.49	
+	1	1090_1093		NM_000679	NP_000670	P35368	ADA1B_HUMAN	ame=6; (By similarity).	1	TTGTGCTGGCTA	0.485	
-	3	384_385	l_p.S77fs|SLU7_u	NM_006425	NP_006416	O95391	SLU7_HUMAN		1	CTTTTTGAAGGAT	0.337	
-	2	171	Shift_Del_p.G57fs	NM_016391	NP_057475	Q9Y3C1	NOP16_HUMAN		2	AGCCAACCCCAT	0.592	

-	6	1314	_uc003mfd.1_Intro	NM_016290	NP_057374	Q96RL1	UIMC1_HUMAN	AIR.	4	TCAAGCTTTTAAT	0.418	
+	23	6934	.K1997fs|NSD1_u	NM_022455	NP_071900	Q96L73	NSD1_HUMAN	Pro-rich.	3	CTCTCCAAAAAA	0.517	rs142030334
+	1	1122_1123		NM_001453	NP_001444	Q12948	FOXC1_HUMAN	Poly-Gly.	1	gcagctcgggcggcgg	0.49	rs71807729
+	6	1502	jqy.1_Frame_Shift	NM_006298	NP_006289	Q15776	ZN192_HUMAN	C2H2-type 5.	0	AGTGTGGGAAA	0.498	
-	3	758	npn.2_Frame_Shi	NM_006778	NP_006769	Q9UDY6	TRI10_HUMAN		0	AGATCTCCCCAG	0.532	
+	13	1843	ru.2_Intron|DDR1_	NM_013993	NP_054699	Q08345	DDR1_HUMAN	|Cytoplasmic (Potential).	9	CCGGGCCCCCC	0.682	
-	8	922_924	.1_In_Frame_Del_	NM_006709	NP_006700	Q96KQ7	EHMT2_HUMAN	Poly-Glu.	1	cctcctcttcctcctcctc	0.296	
+	2	246	oei.2_Frame_Shift	NM_024165	NP_077084	O43189	PHF1_HUMAN		0	CGCAGCCCCCC	0.557	
+	2	479		NM_152735	NP_689948	Q96C00	ZBTB9_HUMAN	BTB.	0	GCCTCTCCTTAC	0.557	
+	7	1266	_p.P268fs|FOXP4_	NM_001012426	NP_001012426	Q8IVH2	FOXP4_HUMAN		1	GTCTCACCCCCC	0.677	
-	65	11987_1198	.I3838fs|DST_uc0	NM_001144769	NP_001138241	Q03001	DYST_HUMAN	Spectrin 10.	14	GTCATGATTTTAT	0.366	
-	9	2112_2113	p.K585fs|FBXL4_	NM_012160	NP_036292	Q9UKA2	FBXL4_HUMAN	LRR 9.	2	AGATCTTTACAA	0.332	
+	1	939_941	.G270del|ARID1B_	NM_017519	NP_059989	Q8NFD5	ARI1B_HUMAN	Gly-rich.	2	ggcagcggaggagga	0.158	
-	4	650	sqc.2_Intron|DAG	NM_139179	NP_631918	Q8NCG7	DGLB_HUMAN	lasmic (Potential).	3	CATTTTCCCCCC	0.527	
-	14	3432		NM_015204	NP_056019	Q9UPZ6	THS7A_HUMAN	.|Extracellular (Potential).	3	CAGCCATTTAGA	0.498	
-	5	773	kug.2_Frame_Shif	NM_182762	NP_877439	Q6ZN28	MACC1_HUMAN		3	TACTCTGATGG	0.423	
+	8	2001_2002	Shift_Ins_p.P420fs	NM_015570	NP_056385	Q8WXX7	AUTS2_HUMAN		3	ccgccccacctcacatc	0.134	
+	5	1242_1243	_p.H229fs|DTX2_u	NM_020892	NP_065943	Q86UW9	DTX2_HUMAN		2	CCAGCACCCCC	0.649	rs143934697
-	2	786	.1_Intron|CCDC14	NM_006682	NP_006673	Q14314	FGL2_HUMAN	ogen C-terminal.	2	AGCCTCCCCCC	0.483	
+	11	1177	_p.I272fs|ZNF277_	NM_021994	NP_068834	Q9NRM2	ZN277_HUMAN		4	AATTTTATTCGG	0.358	
+	7	1118_1119	vuy.2_Frame_Shif	NM_016019	NP_057103	Q9Y383	LC7L2_HUMAN	Arg/Ser-rich.	0	AGAGAAGAGAG	0.391	
-	11	2513	vyy.2_Splice_Site_	NM_015310	NP_056125	Q9NYI0	PSD3_HUMAN		3	ATACTTACTCTT	0.323	
+	5	542	yar.2_Frame_Shif	NM_004133	NP_004124	Q14541	HNF4G_HUMAN		1	AAGCACCAGAA	0.433	
-	6	468	yhd.2_Frame_Shif	NM_057749	NP_477097	O96020	CCNE2_HUMAN		0	CTCTCCTTTTTT	0.323	
-	7	1565_1566	3yjk.1_Frame_Shi	NM_015435	NP_056250	Q9NV58	RN19A_HUMAN		4	ACCTGCTATGG	0.386	
-	7	1904	_p.W584fs|LRP12	NM_013437	NP_038465	Q9Y561	LRP12_HUMAN	lasmic (Potential).	0	CGGTTCCAAAT	0.453	
+	8	1139	e_Shift_Del_p.F1	NM_012082	NP_036214	Q8WW38	FOG2_HUMAN	C2H2-type 3.	5	GGCTTCCAGAC	0.502	
-	14	1846	p.P525fs|EIF2C2_	NM_012154	NP_036286	Q9UKV8	AGO2_HUMAN	Piwi.	0	CCGGCGGGGGG	0.647	rs148575703
-	4	773_774	3H_uc010mfk.1_5	NM_198488	NP_940890	Q6ZRV2	FA83H_HUMAN		3	CAGTCCACCAG	0.658	
-	4	737_738	_uc003zdk.1_3'UT	NM_001024678	NP_001019849	Q50LG9	LRC24_HUMAN		0	GTACCTGTGAGG	0.634	
+	1	568_569		NM_133497	NP_598004	Q8TDN2	KCNV2_HUMAN	lasmic (Potential).	2	GGCTTCCCCAAG	0.658	
+	13	2023	lb.2_Frame_Shift_	NM_003995	NP_003986	P20594	ANPRB_HUMAN	.|Cytoplasmic (Potential).	3	AACCTGATGAC	0.537	
+	5	647	ddo.2_Frame_Shif	NM_000950	NP_000941	O14668	TMG1_HUMAN	ic (Potential).|Poly-Pro.	2	CCCCACCCCCCC	0.488	
-	1	81	OM4_uc004dpd.3	NM_020717	NP_065768	Q9ULL8	SHRM4_HUMAN	PDZ.	1	GGGTGCCCCCC	0.642	
-	7	1047_1048	RMT2B_uc004egt	NM_024917	NP_079193	Q96GJ1	TRM2_HUMAN		1	GACTTAATTTCT	0.426	
+	3	1556_1558	Q477del|MAMLD1	NM_005491	NP_005482	Q13495	MAMD1_HUMAN	Poly-Gln.	0	cagcaacagcagca	0.433	
-	1	203	k|PEX14_uc010oa	NM_004401	NP_004392	O00273	DFFA_HUMAN	CIDE-N.	0	GAGGCGGCCAC	0.706	
+	12	2906_2908	9vqi.1_In_Frame_	NM_001083621	NP_001077090	Q9NUA8	ZBT40_HUMAN		1	CCCCAAGAAGA	0.517	
+	1	1263_1265		NM_004455	NP_004446	Q92935	EXTL1_HUMAN	enal (Potential).	1	GCCTGCCTCCTC	0.606	
-	31	5335	E4DIP_uc001elm	NM_014644	NP_055459	Q5VU43	MYOME_HUMAN		5	TATTCTGGGGAG	0.517	
+	6	700	hift_Del_p.F167fs|	NM_004425	NP_004416	Q16610	ECM1_HUMAN	roximate repeats.|1.	3	GGCTTCCCCCC	0.602	
-	18	1926	b.1_Frame_Shift_	NM_001668	NP_001659	P27540	ARNT_HUMAN		9	CGGCCGGGGGG	0.527	
-	11	1604	mr.1_Frame_Shift	NM_001025603	NP_001020774	P48382	RFX5_HUMAN		1	GTTTCCTTTTGG	0.537	
-	4	261_262	01fpl.2_Frame_Sh	NM_015590	NP_056405	Q5T3I0	GPTC4_HUMAN		1	CTTGTTGAAGAG	0.545	
-	6	1404_1406	.V48del|PVRL4_u	NM_030916	NP_112178	Q96NY8	PVRL4_HUMAN	ical; (Potential).	2	TGAGCACCACC	0.571	
+	20	6213	A2_uc009www.2_	NM_020318	NP_064714	Q9BXP8	PAPP2_HUMAN	Sushi 5.	16	GTAATCCCCCC	0.468	
+	20	2516	R_uc010pxx.1_Int	NM_000254	NP_000245	Q99707	METH_HUMAN	inding N-terminal.	3	TAAACCAAAAAA	0.279	

-	11	1419_1421	.P386del|ABI1_uc(	NM_005470	NP_005461	Q8IZP0	ABI1_HUMAN	Pro-rich.		1	CCACTGGTGGTC	0.478	
-	9	1366	Del_p.I412fs|PARD	NM_019619	NP_062565	Q8TEW0	PARD3_HUMAN			1	TGCCTATTTTTTT	0.433	
-	8	1142_1144	250TT>T|PCDH15	NM_033056	NP_149045	Q96QU1	PCD15_HUMAN	r (Potential).	p.T250N(1)	13	GAGAGTGGTGG	0.438	
+	10	1630	STAMBPL1_uc001	NM_020799	NP_065850	Q96FJ0	STALP_HUMAN			1	GCTTGTAAAAAAA	0.423	
-	13	1003		NM_024541	NP_078817	Q5T2E6	CJ076_HUMAN			0	AAGTGCCAGAAC	0.348	
-	12	2578_2579	rf118_uc001lbc.1_	NM_018017	NP_060487	Q7Z3E2	CJ118_HUMAN	Potential.		2	CTCTTTCAACAA	0.356	
-	25	3386_3388	Frame_Del_p.D83	NM_030962	NP_112224	Q86WG5	MTMRD_HUMAN			3	AGATACATCATCA	0.355	
-	5	7272	IAK_uc001ntk.1_Ir	NM_001620	NP_001611	Q09666	AHNK_HUMAN			19	GATTTTGGGTCC	0.458	
+	4	523_524	Shift_Del_p.P124fs	NM_006388	NP_006379	Q92993	KAT5_HUMAN			0	TCTCCAGAGAGA	0.564	
+	9	1355	.R394fs|NDUFV1	NM_007103	NP_009034	P49821	NDUV1_HUMAN			1	CGTGAGGGGGG	0.632	
-	6	1503_1505	L1_uc001pwu.1_Ir	NM_002855	NP_002846	Q15223	PVRL1_HUMAN	Cytoplasmic (Potential).		0	CCACCGCcctcctc	0.576	
-	4	605	ON_uc001qdd.3_F	NM_016952	NP_058648	Q4KMG0	CDON_HUMAN	Potential).|Ig-like C2-type 2.		6	CAGCCATTTTCCC	0.458	
-	3	440_442		NM_006248	NP_006239					0	TCCTGGAGGAG	0.601	
+	4	1243_1245		NM_018169	NP_060639	Q9HCM1	CL035_HUMAN			2	AAAGACCTCCTC	0.414	rs79406084
+	18	1613	fs|TENC1_uc001sl	NM_170754	NP_736610	Q63HR2	TENC1_HUMAN	Pro-rich.		2	GCAGACCCCCC	0.677	rs142183380
+	23	5212_5213	scj.2_Frame_Shift_	NM_012291	NP_036423	Q14674	ESPL1_HUMAN			3	GTGACTGTGTG	0.436	
+	1	592		NM_001005497	NP_001005497	A6NL08	O6C75_HUMAN	Name=5; (Potential).		3	ATGGCATTTTTTT	0.393	
-	27	3380_3382	a.2_Intron|SMARC	NM_003075	NP_003066	Q8TAQ2	SMRC2_HUMAN	Pro-rich.		6	GAGCAGGAGGA	0.591	
-	7	992	_p.E243fs|TMEM1	NM_001130963	NP_001124435	O14524	T194A_HUMAN			0	GGTGTTCCAGGT	0.453	
+	2	348	s|APEX1_uc001vx	NM_001641	NP_001632	P27695	APEX1_HUMAN	iation with rRNA, endoribo		4	GTGGGAAAAAG	0.557	
+	5	648	me_Shift_Del_p.E	NM_002791	NP_002782	P60900	PSA6_HUMAN			0	TCCTTGAAAAAAA	0.403	
-	2	873_874	1xki.1_Frame_Shi	NM_004926	NP_004917	Q07352	TISB_HUMAN			1	GGGTTATTGGTG	0.624	
+	8	1064_1066	NK_uc001ygg.3_In	NM_001099402	NP_001092872	O75909	CCNK_HUMAN	Poly-Gln.		0	AGCCCAGCAGC	0.621	
+	11	1696_1698	1znc.2_In_Frame_	NM_181642	NP_857593	O43278	SPIT1_HUMAN			1	CGGACACCACC	0.586	
+	4	271		NM_001013657	NP_001013679	Q6ZNW5	VTC2_HUMAN			0	TTGTTTATGGGCA	0.507	
+	15	1993_1995	.S436del|SLC5A1	NM_052944	NP_443176	Q8WWX8	SC5AB_HUMAN	lasmic (Potential).		2	AGGCCAGCAGC	0.542	
+	8	892	2dox.1_Frame_Sh	NM_015202	NP_056017	O60303	K0556_HUMAN			8	TTCGTTCCCACC	0.512	
+	25	5954	e_Shift_Del_p.P16	NM_006662	NP_006653	Q6ZRS2	SRCAP_HUMAN	Pro-rich.		4	CTGGTCCCCCC	0.612	
+	8	912_914	.L222del|CHRNB1	NM_000747	NP_000738	P11230	ACHB_HUMAN	ical; (Potential).		2	GTTCCTGCTGCT	0.498	
+	1	90_92		NM_001005271	NP_001005271	Q12873	CHD3_HUMAN			1	ggcgacgaggaggag	0.305	
+	10	2188_2189	2gjr.2_Frame_Shift	NM_053051	NP_444279	Q8N137	CNTRB_HUMAN	ed for centrosome localizati		2	GCTCGGAGAGAG	0.579	
+	15	2070	I_5'Flank|TRAF4_	NM_178170	NP_835464	Q86SG6	NEK8_HUMAN		p.P703fs*10(1)	6	CCGGTCCCCCC	0.582	
+	11	2096	hue.2_Frame_Shif	NM_007359	NP_031385	O15234	CASC3_HUMAN	tion in cytoplasmic stress g		1	CTCTATCCCCCA	0.483	
-	9	1271	2hzi.3_Frame_Shift	NM_012448	NP_036580	P51692	STA5B_HUMAN			6	CACCTGGGGGG	0.577	rs144993426
-	6	674	gd.2_Frame_Shift_	NM_014233	NP_055048	P17480	UBF1_HUMAN	HMG box 2.		0	GCTGCTGGGGGG	0.597	
-	2	169	igd.2_Frame_Shift	NM_014233	NP_055048	P17480	UBF1_HUMAN			0	GTTCTTCATGCAT	0.468	
-	9	1623_1625		NM_133373	NP_588614	Q8N3E9	PLCD3_HUMAN			3	cctcgtcatcctcctcc	0.527	
+	10	2507	.R787fs|CTDP1_	NM_004715	NP_004706	Q9Y5B0	CTDP1_HUMAN			0	CGCCCGGGGGC	0.672	
+	3	452	Frame_Shift_Del_	NM_030924	NP_112186	Q5FVE4	ACBG2_HUMAN			1	GAATGGCAAAAC	0.413	
-	1	625_627	xz.1_5'Flank|LGI4	NM_139284	NP_644813	Q8N135	LGI4_HUMAN			1	CAGCCAGCAGC	0.695	
+	28	3926	iu.2_Frame_Shift_	NM_000540	NP_000531	P21817	RYR1_HUMAN	6 X approximate repeats.		12	ACACGCCCCCC	0.667	
+	4	387_389	2qfw.2_In_Frame_Del_p.Q85del			Q96PV6	LENG8_HUMAN	Poly-Gln.		2	GCTTTGCAGCAG	0.532	
-	2	511	Shift_Del_p.R40fs|	NM_014795	NP_055610	O60315	ZEB2_HUMAN			9	GCACCGGGGGC	0.602	
-	16	1860_1861	2uua.1_Intron|ANK	NM_153697	NP_710181	Q8N8A2	ANR44_HUMAN			5	GGGTATGTGTGT	0.342	
+	9	1518	20A1_uc002uzy.3_	NM_177538	NP_803882	Q6UW02	CP20A_HUMAN			0	AAGTTCAAAAAA	0.348	
+	3	680	LA4_uc010fty.1_In	NM_005214	NP_005205	P16410	CTLA4_HUMAN	ical; (Potential).		0	GGGTTGTTTTTTT	0.478	
-	17	2374_2376	.Q659del|TNS1_	NM_022648	NP_072174	Q9HBL0	TENS1_HUMAN	Gln-rich.		4	GGCGAGgctgctg	0.562	

+	11	1399_1400	zmp.1_Frame_Shi	NM_001017915	NP_001017915	Q92835	SHIP1_HUMAN			2	GTAACGCCCCC	0.535	
-	3	556	_p.K61fs|DSN1_uc	NM_001145316	NP_001138788	Q9H410	DSN1_HUMAN			2	CCCCCTTTTTA	0.463	
-	4	583	MA7_uc002yby.1_F	NM_002792	NP_002783	O14818	PSA7_HUMAN			0	ACCTTCCAGGC	0.572	
-	3	1084_1085	p.G104fs|TCFL5_u	NM_006602	NP_006593	Q9UL49	TCFL5_HUMAN			1	TACCTCCCACTT	0.46	
-	15	1862_1864		NM_014227	NP_055042	Q9NY91	SC5A4_HUMAN	lasmic (Potential).		0	AGGCTTCCTCCT	0.502	
+	2	378_380		NM_033318	NP_201575	Q9H4I9	CV032_HUMAN	Asp/Glu-rich.		1	CAGAGGATGATG	0.478	rs141840500
-	7	811	03bfw.1_Frame_S	NM_001009880	NP_001009880	Q6ICG6	K0930_HUMAN			0	GCCCTGGGGGC	0.632	
-	20	3224	3brg.1_Frame_Shi	NM_014850	NP_055665	O43295	SRGP2_HUMAN			9	CCATCACCCCCC	0.557	
+	2	195_197	4L2_uc003dbh.2_	NM_015106	NP_055921	Q9Y4B4	ARIP4_HUMAN			3	gcggaagaggaggag	0.429	
+	14	1647	dgm.2_Frame_Shi	NM_006254	NP_006245	Q05655	KPCD_HUMAN	rotein kinase.		9	TCAACGGGGGG	0.602	
-	3	2530	Intron|ABCA11P_u	NM_133474	NP_597731	D9N162	D9N162_HUMAN			1	ACATTTGTAAAGT	0.408	
+	1	4021_4022		NM_175918	NP_787114	Q8N1N5	CRPAK_HUMAN			0	CCTGCTCACACG	0.653	
+	1	363_364	NUDT9_uc010ikl.2	NM_024047	NP_076952	Q9BW91	NUDT9_HUMAN			0	CGGTGTCTCTCT	0.649	rs151296797
+	22	2502	18_splice|KIAA092	NM_015196	NP_056011	A2VDJ0	T131L_HUMAN			2	ATTGTGTAAGCAT	0.383	
-	7	1606_1608	0irc.1_In_Frame_	NM_020870	NP_065921	Q7Z6J0	SH3R1_HUMAN	Poly-Ala.		3	CATTCCAGCAGC	0.601	
-	6	1177_1194	AP2A_uc003jpz.2_	NM_003711	NP_003702	O14494	LPP1_HUMAN	lasmic (Potential).		2	CTTTCTTTAAAAG	0.381	
+	5	424	IPH_uc010ixc.2_Ir	NM_022909	NP_075060	Q9H3R5	CENPH_HUMAN	Potential.		1	GCACTTAAAAAA	0.323	
-	3	491_492	cvb.1_Frame_Shi	NM_031438	NP_113626	Q9BQG2	NUD12_HUMAN			0	ATTATTTCTCTTTT	0.386	rs7734923
+	16	2438_2439	C_uc003kpy.3_Fra	NM_001127511	NP_001120983	P25054	APC_HUMAN	u-rich.|ARM	p.?(1)	2515	TGGAATCTCTCA	0.381	
+	2	237_240	_p.K19fs|AP3S1_u	NM_001284	NP_001275	Q92572	AP3S1_HUMAN			0	ATCTAAGAGAGA	0.304	rs80118146
-	2	322_323	wp.1_Frame_Shift	NM_000943	NP_000934	P45877	PPIC_HUMAN	e cyclophilin-type.		1	TTGCTAGAGCAA	0.361	rs150587688
+	4	653	F7_uc003kyx.2_5'U	NM_003202	NP_003193	P36402	TCF7_HUMAN			0	AATCAGCCCCCC	0.572	
-	22	12451	FAT2_uc003lud.3_	NM_001447	NP_001438	Q9NYQ8	FAT2_HUMAN	lasmic (Potential).		6	AGTCTGGGGGG	0.562	
-	1	189_191	lwl.2_In_Frame_D	NM_032782	NP_116171	Q8TDQ0	HAVR2_HUMAN			0	TAGTAGCAGCAC	0.291	
-	6	1314	_uc003mfd.1_Intro	NM_016290	NP_057374	Q96RL1	UIMC1_HUMAN	AIR.		4	TCAAGCTTTTAAT	0.418	
+	1	109_110		NM_016167	NP_057251	Q9UMY1	NOL7_HUMAN			0	GGCCTCGGAGGA	0.728	
+	15	3067_3069	.H937del|SYNGAF	NM_006772	NP_006763	Q96PV0	SYGP1_HUMAN			4	CTCccatcaccaccac	0.547	
-	4	624		NM_001085480	NP_001078949	Q5T6X4	F162B_HUMAN			0	GCTTTAGCCTGT	0.418	
+	1	939_941	.G270del|ARID1B_	NM_017519	NP_059989	Q8NFD5	ARI1B_HUMAN	Gly-rich.		2	ggcagcggaggagga	0.158	
+	7	1285_1286	.P401fs|EIF3B_uc	NM_003751	NP_003742	P55884	EIF3B_HUMAN	teraction with EIF3E.|WD 2		0	TGACCCTCAGGC	0.51	
-	4	864_866		NM_001002926	NP_001002926	Q3B726	RPA43_HUMAN	Lys-rich.		1	GCTTTTTCTTCTT	0.433	
+	1	403_405	uc003tbl.3_5'Flank	NM_002047	NP_002038	P41250	SYG_HUMAN			1	CGCTCTGCTGC	0.749	
-	1	280	thr.2_Frame_Shift_	NM_002192	NP_002183	P08476	INHBA_HUMAN			6	TATAATCCAGCAA	0.577	
+	52	8006_8007	.L2581fs|TRRAP_	NM_003496	NP_003487	Q9Y4A5	TRRAP_HUMAN			37	TTTCTGGACACT	0.495	
+	2	178	C8orf44_uc003xwq	NM_019607	NP_062553	Q96CB5	CH044_HUMAN			0	TATCTCAACCAGC	0.403	
-	13	1698	D2_uc003yqi.3_RI	NM_014109	NP_054828	Q6PL18	ATAD2_HUMAN			2	TTCGTCAAAAAA	0.413	
-	6	1030	ame_Shift_Del_p.K	NM_004323	NP_004314	Q99933	BAG1_HUMAN	with PPP1R15A.|BAG.		1	TGAACCTTTTTTA	0.358	
-	4	454_455	ar.1_5'UTR|CIZ1_u	NM_001131016	NP_001124488	Q9ULV3	CIZ1_HUMAN			4	aaactggtccagtccttt	0	
+	5	647	ddo.2_Frame_Shif	NM_000950	NP_000941	O14668	TMG1_HUMAN	ic (Potential).|Poly-Pro.		2	CCCCACCCCCCC	0.488	
-	14	2238	_Shift_Del_p.G663	NM_031206	NP_112483	Q9Y4W2	LAS1L_HUMAN			4	AGCTGCCCCTGG	0.512	
-	2	574_575	P_uc004esg.2_5'F	NM_024528	NP_078804	Q8N5F7	NKAP_HUMAN			2	CCAATTCTCTCT	0.317	
-	7	811_812	1_Intron|MST1P9_	NR_002729					NA	0	GGTACGCCGCGC	0.649	
-	3	1621_1622	CBL2_uc001dmr.2	NM_001162536	NP_001156008	Q96E39	RBMXL_HUMAN	Ser-rich.	NA	0	TAAGATGGCGGG	0.475	
-	3	1756_1759		NM_001122965	NP_001116437	Q6XPR3	RPTN_HUMAN	Gln-rich.	NA	0	GCCTTGTCTGTC	0.485	
+	2	137_139		NM_000427	NP_000418	P23490	LORI_HUMAN		NA	0	gcggcggcagcggcg	0.207	rs6661601
-	37	12084_12086	K3_uc010qih.1_In	NM_020987	NP_066267	Q12955	ANK3_HUMAN	Thr-rich.	NA	19	ggtggcagtggtggtgg	0.32	
-	9	1499_1501	XM2_uc001lhj.2_F	NM_198148	NP_937791	Q8N436	CPXM2_HUMAN	Poly-Leu.	NA	2	GCACCAGCAGC	0.626	

-	10	1133_1134	qfh.2_Frame_Shif	NM_001143835	NP_001137307	Q6P4R8	NFRKB_HUMAN	Lys-rich.	NA	3	CTTAACCTTTTTT	0.441	
+	1	998		NM_030979	NP_112241	Q9H361	PABP3_HUMAN	RRM 4.	NA	4	CGGAAAGCGTTT	0.408	
+	7	4096_4098		NM_015042	NP_055857	O15014	ZN609_HUMAN	Poly-His.	NA	3	CACACACCACC	0.576	
+	11	2629_2631	2gix.2_In_Frame_	NM_001080424	NP_001073893	O15054	KDM6B_HUMAN	-rich.|Thr-ri	NA	2	CGCCGTcaccacc	0.369	
+	1	111_113		NM_021175	NP_066998	P81172	HEPC_HUMAN		NA	1	TCCTGCTCCTCC	0.64	
+	11	1043_1044	V1C2_uc002rat.2_	NM_001039362	NP_001034451	Q8NEY4	VATC2_HUMAN		NA	1	CCGACAGAGAGA	0.604	
+	3	173_174	j.1_RNA|FRG1B_uc010gdr.1_RNA|FRG1B_uc010ztk.1_5'UTR						NA	0	TAGGGGAAAATG	0.322	
+	6	711_713	15_uc002zsr.2_In	NM_001003891	NP_001003891	Q96RN5	MED15_HUMAN	Poly-Gln.	NA	1	gcagctccagcagcag	0.187	
-	3	428_430	_19DD>D|TFIP11_	NM_012143	NP_036275	Q9UBB9	TFP11_HUMAN	Poly-Asp.	NA	0	GCTCGTCATCAT	0.532	rs145794160
+	7	1453	p.F219fs|EDEM1_	NM_014674	NP_055489	Q92611	EDEM1_HUMAN	enal (Poten	NA	3	CAGGCCTTTTTC	0.463	
+	16	1633_1634	el_p.R448fs|FIP1L	NM_030917	NP_112179	Q6UN15	FIP1_HUMAN	action with C	NA	2	GCACCAGAGAGA	0.292	
+	1	514_515		NM_015278	NP_056093	O94885	SASH1_HUMAN	Pro-rich.	NA	1	cggagcctgagcccga	0.381	
-	11	1327	xzp.2_Frame_Shi	NM_014393	NP_055208	Q9NUL3	STAU2_HUMAN	DRBM 4.	NA	0	GCAGCATTTTTTT	0.328	
-	14	2236	_Shift_Del_p.N28	NM_007126	NP_009057	P55072	TERA_HUMAN		NA	1	AACACATTTTTTT	0.512	
-	18	2564_2566	sw.2_In_Frame_D	NM_015107	NP_055922	Q9UPP1	PHF8_HUMAN		NA	3	GCGTTCTCCTCC	0.591	
-	1	1805_1806		NM_003604	NP_003595	O14654	IRS4_HUMAN		NA	10	CCTTTGCCCCCC	0.545	
-	3	274_276	fen.2_Intron|CD99	NM_031462	NP_113650	Q8TCZ2	C99L2_HUMAN	ar (Potential	NA	3	GGTTGTGGTGGT	0.552	
+	16	4351_4353	v.1_In_Frame_Del	NM_006015	NP_006006	O14497	ARI1A_HUMAN	Gln-rich.	334_R1335ins	142	CCCCCCgcagcag	0.512	
-	9	1499_1501	XM2_uc001lhj.2_F	NM_198148	NP_937791	Q8N436	CPXM2_HUMAN	Poly-Leu.		2	GCACCAGCAGCA	0.626	
+	1	55_56		NM_021046	NP_066384	O75690	KRA58_HUMAN			0	TCTGGAGGCTGT	0.649	379698;rs72145325
+	1	998		NM_030979	NP_112241	Q9H361	PABP3_HUMAN	RRM 4.		4	CGGAAAGCGTTT	0.408	
+	2	2046_2048	.L591del|SLC24A	NM_004727	NP_004718	O60721	NCKX1_HUMAN	ical; (Potential).		0	AGAGCCTGCTGC	0.547	
+	25	6010_6011	_Shift_Ins_p.Q16	NM_006662	NP_006653	Q6ZRS2	SRCAP_HUMAN	Pro-rich.		4	CGCCAGCCCCCC	0.569	
-	15	2000_2002	15_uc002ghy.1_5'I	NM_004860	NP_004851	P51116	FXR2_HUMAN	Poly-Arg.		0	GTTACGGCGGCG	0.547	
+	16	1978_1979	S_uc010cnw.1_Fra	NM_012393	NP_036525	O15067	PUR4_HUMAN			5	ATGGCCAGGGGC	0.604	
+	1	111_113		NM_021175	NP_066998	P81172	HEPC_HUMAN			1	TCCTGCTCCTCC	0.64	
+	9	1040	_Shift_Del_p.P156	NM_014516	NP_055331	O75175	CNOT3_HUMAN			3	CTCCCCTCCCAG	0.632	rs36665
+	11	1043_1044	V1C2_uc002rat.2_	NM_001039362	NP_001034451	Q8NEY4	VATC2_HUMAN			1	CCGACAGAGAGA	0.604	
+	3	171	plice_Site|FRG1B_uc010gdr.1_Splice_Site|FRG1B_uc010ztk.1_Splice_Site							0	CACTTAGGGGAA	0.318	rs78710112
+	3	173_174	j.1_RNA|FRG1B_uc010gdr.1_RNA|FRG1B_uc010ztk.1_5'UTR							0	TAGGGGAAAATG	0.322	
+	42	6369_6371	bnz.1_In_Frame_I	NM_053002	NP_443728	Q86YW9	MD12L_HUMAN	Gln-rich.		7	GACCCAGCAGC	0.527	
+	1	4123_4124		NM_175918	NP_787114	Q8N1N5	CRPAK_HUMAN	eraction with PAK1.		0	ACACACGTGCCC	0.624	
+	16	1633_1634	el_p.R448fs|FIP1L	NM_030917	NP_112179	Q6UN15	FIP1_HUMAN	action with CPSF1 and CST		2	GCACCAGAGAGA	0.292	
+	17	2312_2314	uc003kgi.3_Intron	NM_003248	NP_003239	P35443	TSP4_HUMAN	TSP type-3 7.		0	GAGTGTGATGAT	0.562	
+	1	1731_1743	uc003lin.2_5'Flank	NM_018937	NP_061760	Q9Y5E6	PCDB3_HUMAN	r (Potential).|Cadherin 6.		2	CGGGCGGCTGA	0.709	
-	1	210_212		NM_024807	NP_079083	Q5T2D2	TRML2_HUMAN			2	GCCACAGCAGCA	0.631	
-	18	2564_2566	sw.2_In_Frame_D	NM_015107	NP_055922	Q9UPP1	PHF8_HUMAN			3	GCGTTCTCCTCC	0.591	
+	3	432_433	PHACTR4_uc001b	NM_001048183	NP_001041648	Q8IZ21	PHAR4_HUMAN			0	TGGAGGAAAAAA	0.391	
-	5	924_925	RIQ3_uc001dfz.3_F	NM_001105659	NP_001099129	A6PVS8	LRIQ3_HUMAN			2	CTGCTGTTTTTT	0.327	
+	10	2124	ova.1_Frame_Shif	NM_001144937	NP_001138409	Q5VTL7	FNDC7_HUMAN	nectin type-III 8.		2	CTGTCCAAAAAA	0.363	
-	1	643_645	.E61del|MCL1_uc	NM_021960	NP_068779	Q07820	MCL1_HUMAN	PEST-like.		0	ACTCGTCCTCCT	0.635	
-	2	431	0qot.1_Frame_Shi	NM_020123	NP_064508	Q9HD45	TM9S3_HUMAN			0	TGATACTTTTTTT	0.363	
-	15	2895_2897	229PP>P|FNBP4_	NM_015308	NP_056123	Q8N3X1	FNBP4_HUMAN	Pro-rich.		1	ggtggtggaggagg	0.32	
-	2	60	ntron|CASP5_uc0	NM_004347	NP_004338	P51878	CASP5_HUMAN			3	TACGCCTTTTTTT	0.388	
-	9	1226	DDX6_uc001puc.2	NM_004397	NP_004388	P26196	DDX6_HUMAN			1	AATTCTGGGGGG	0.426	
-	3	314_315		NM_006248	NP_006239					0	TGGAGGTGGGGC	0.614	
+	1	199_201	C13_uc010sop.1_	NM_017410	NP_059106	P31276	HXC13_HUMAN	Gly-rich.		1	gcggcatcggcggcgg	0.498	

+	1	592		NM_001005497	NP_001005497	A6NL08	O6C75_HUMAN	Name=5; (Potential).		3	ATGGCATTTTTTT	0.393	
+	4	646_648	p.L194del|TPCN1_	NM_017901	NP_060371	Q9ULQ1	TPC1_HUMAN	=S1 of repeat I; (Potential).		3	GGCCCTGCTGC	0.64	
-	25	3416	SBNO1_uc010taq	NM_018183	NP_060653	A3KN83	SBNO1_HUMAN			9	CTTCCATTTTTTT	0.388	
-	25	5133	ECTD1_uc001wrd	NM_015382	NP_056197	Q9ULT8	HECD1_HUMAN	Ser-rich.		5	CCTTACAAAACT	0.468	
-	1	70_72	.2_5'UTR|NIPA1_	NM_144599	NP_653200	Q7RTP0	NIPA1_HUMAN	cellular (Potential).		0	TCCCCGgccgccg	0.626	
-	15	2121_2122	p.R660fs|SLTM_uc	NM_024755	NP_079031	Q9NWH9	SLTM_HUMAN	Glu-rich.|Potential.		1	TTCCATTCTCTCT	0.431	
+	9	960_962	ne_Del_p.E294del	NM_001099661	NP_001093131	B5ME19	B5ME19_HUMAN			0	GGATGAGGAGG	0.562	
-	3	385_387	P2_uc010byn.2_In	NM_024816	NP_079092	Q9H5N1	RABE2_HUMAN	y-Gln.|Potential.		3	AGTCCTGCTGC	0.527	
+	3	278_280	0vho.1_In_Frame_	NM_020312	NP_064708	O75208	COQ9_HUMAN			1	CGGCGAGGAGG	0.576	rs149029279
+	15	2170_2172	.E413del|SLC9A	NM_004594	NP_004585	Q14940	SL9A5_HUMAN			2	GTCTGAGGAGG	0.571	
+	12	3846_3848	e_Del_p.Q812del|	NM_006599	NP_006590	O94916	NFAT5_HUMAN	Poly-Gln.		0	AATcaacagcagcag	0.389	
+	3	433	l_p.T16fs|KIAA01	NM_014615	NP_055430	Q14687	GSE1_HUMAN			5	CAGCACCCCCC	0.687	
-	9	1952	a.3_RNA|CCDC14	NM_182568	NP_872374					2	TTGTTCATCAGC	0.406	rs66528329
-	9	2408_2410	0xyr.1_In_Frame_	NM_015063	NP_055878	Q9UPR5	NAC2_HUMAN	lasmic (Potential).		4	ACCCGTCCTCCT	0.616	
-	13	1581_1583	_Frame_Del_p.S1	NM_015541	NP_056356	Q96JA1	LRIG1_HUMAN	tial).|Ig-like C2-type 1.|Poly		5	GGGAGCTGCTG	0.547	
+	20	7008_7009	hm.2_Frame_Shift	NM_178140	NP_835260	O15018	PDZD2_HUMAN			9	CCCCTCGGGGG	0.584	rs138558075
+	7	1261	jlm.1_Frame_Shift	NM_003999	NP_003990	Q99650	OSMR_HUMAN	cellular (Potential).		5	CAAATAACTCAA	0.333	
+	16	2912	py.3_Frame_Shift_	NM_001127511	NP_001120983	P25054	APC_HUMAN	Ser-rich.	p.?(1)	2515	TAGTTCTCGTTCT	0.413	
-	3	512_514	0jii.2_In_Frame_D	NM_138379	NP_612388	Q96H15	TIMD4_HUMAN	ar (Potential).|Thr-rich.		2	GGGCTTGTTGT	0.537	
-	3	444	p.M121fs|SLC17A2_uc003nfl.2_Frame_Shift_Del_p.M1			O00624	NPT3_HUMAN			1	CAAGCATTTTTTT	0.453	
-	1	523_524		NM_052967	NP_443199	P35410	MAS1L_HUMAN	lasmic (Potential).		9	AGAGGACACAC	0.495	
+	7	1303_1304	tron|LOC285830_	NM_001098479	NP_001091949	P30511	HLAF_HUMAN			0	ATCTTGTTTTTTT	0.535	
-	1	210_212		NM_024807	NP_079083	Q5T2D2	TRML2_HUMAN			2	GCCACAGCAGC	0.631	
+	26	3025_3026	me_Shift_Ins_p.D	NM_015440	NP_056255	Q6UB35	C1TM_HUMAN	hydrofolate synthetase.		4	CCTGACAAAAAA	0.48	
+	8	2004_2005	srz.2_Frame_Shift	NM_014660	NP_055475	O94880	PHF14_HUMAN			3	TTGCAAGAGAGA	0.376	
+	3	342	_uc011kby.1_Intron	NM_002541	NP_002532	Q02218	ODO1_HUMAN			2	GGACATTTTTTT	0.577	
-	5	1204	.2_Frame_Shift_D	NM_000466	NP_000457	O43933	PEX1_HUMAN			2	ACCTAATTTTTTT	0.353	
+	5	927_929	10ljz.1_In_Frame_	NM_014491	NP_055306	O15409	FOXP2_HUMAN	Gln-rich.		8	cagcaacagcagcag	0.172	
-	7	1105_1107	r.2_In_Frame_Del	NM_018660	NP_061130	Q9H8N7	ZN395_HUMAN			0	CCTgcggcagcagc	0.507	rs142343457
+	10	6394_6396	2061del|ZFHX4_	NM_024721	NP_078997	Q86UP3	ZFHX4_HUMAN	Pro-rich.		15	accaccacctcctcct	0.286	
-	12	1824	mdt.2_Frame_Shif	NM_004519	NP_004510	O43525	KCNQ3_HUMAN			5	CTTGAATTTTTTT	0.453	
+	5	647	ddo.2_Frame_Shif	NM_000950	NP_000941	O14668	TMG1_HUMAN	ic (Potential).|Poly-Pro.		2	CCCCACCCCCC	0.488	
+	4	1940_1942	EC1_uc010nsl.1_	NM_005462	NP_005453	O60732	MAGC1_HUMAN			4	GAGCCCTCCTC	0.567	
+	3	460_483	PE104del|SPRR3_	NM_005416	NP_005407	Q9UBC9	SPRR3_HUMAN	proximate tandem repeats		1	TACACCAAGGTC	0.567	7;rs66616552;rs1970328
+	14	1901_1902	F7L2_uc010qro.1_	NM_001146274	NP_001139746	Q9NQB0	TF7L2_HUMAN	ecific activa	p.R465C(1)	4	TAGGAGAAAAAA	0.52	
-	2	1302	raq.2_Frame_Shift	NM_006143	NP_006134	Q15760	GPR19_HUMAN	lasmic (Potential).		1	ACGTAGTTTTTTT	0.398	
-	9	743_744	Shift_Ins_p.A195fs	NM_001136015	NP_001129487	P07355	ANXA2_HUMAN			1	CCCGAGCATCTT	0.317	
+	8	929_930	IP_uc002dcx.3_R	NM_006985	NP_008916	Q9UND3	NPIP_HUMAN	Pro-rich.		0	TCCCGAGTGTCT	0.559	
+	25	6010_6011	_Shift_Ins_p.Q16	NM_006662	NP_006653	Q6ZRS2	SRCAP_HUMAN	Pro-rich.		4	CGCCAGCCCCCC	0.569	
-	3	797_798	A10_uc002gut.1_	NM_001039999	NP_001035088	A6ND36	FA83G_HUMAN			2	GACGTTACTCTC	0.584	
-	9	1623_1625		NM_133373	NP_588614	Q8N3E9	PLCD3_HUMAN			3	cctcgtcatcctcctcct	0.527	
-	11	1313_1315		NM_001080421	NP_001073890	Q9UPW8	UN13A_HUMAN	-rich.|Potential.		3	TCAGGCAcctcctcc	0.433	
+	5	489_490	_p.Q50fs|LILRB1_	NM_006669	NP_006660	Q8NHL6	LIRB1_HUMAN	1.|Extracellular (Potential).		3	TGTCAGGGGGG	0.579	
+	12	2844		NM_001011552	NP_001011552	Q6AI14	SL9A4_HUMAN	lasmic (Potential).		3	TGCTCCAAAAAA	0.473	
-	4	358	UTR|SYS1-DBNDI	NM_014477	NP_055292	Q9Y2B4	T53G5_HUMAN			1	TTTTGTTTTATT	0.498	
-	10	1116	p.N255fs|ARFGAP	NM_014570	NP_055385	Q9NP61	ARFG3_HUMAN			1	TCAACATTTTTTT	0.224	
+	1	513_515		NM_020846	NP_065897	Q9P270	SLAI2_HUMAN	Poly-Glu.		0	GCTGGGAGGAG	0.754	

+	12	1499	ne_Shift_Del_p.S	NM_004100	NP_004091	O95677	EYA4_HUMAN			2	AGTTCTGGGTC	0.458	
+	14	2077	.Y360fs|BMP1_uc	NM_006129	NP_006120	P13497	BMP1_HUMAN	CUB 3.		3	GAGTACCCCCC	0.602	
-	2	655	_3'UTR|CDKN2A_	NM_000077	NP_000068	P42771	CD2A1_HUMAN	)|p.?(13)|p.R128fs*12(3)|p.		3678	CCTTCCGCGGC	0.597	
+	12	1615	Shift_Del_p.K373fs	NM_005392	NP_005383	O75151	PHF2_HUMAN	-rich.|Lys-rich.		1	TGTCCAAAAAA	0.448	rs76832193
-	7	7642		NM_015419	NP_056234	Q9NR99	MXRA5_HUMAN	like C2-type 9.		8	ACAGTGATCCG	0.572	
-	3	730	njg.1_5'UTR|CXor	NM_198279	NP_938020	A2AJT9	CX023_HUMAN			2	TGGGAGGGAAT	0.498	
+	15	2016_2017	09zfl.1_3'UTR|PTF	NM_002831	NP_002822	P29350	PTN6_HUMAN		NA	1	GTTCCCTCAAGA	0.559	
-	4	505	|CKB_uc010awr.1_	NM_001823	NP_001814	P12277	KCRB_HUMAN	gen kinase C	NA	0	GGGGGAGGCAG	0.577	
-	2	424	el_p.P9fs|SECTM1	NM_003004	NP_002995	Q8WVN6	SCTM1_HUMAN		NA	0	GGCCAGGGAAT	0.627	
+	9	2220	p.Q690fs|KIAA024	NM_015349	NP_056164	Q6AI39	K0240_HUMAN		NA	1	AGGACAAAAAA	0.388	
+	12	1499	ne_Shift_Del_p.S	NM_004100	NP_004091	O95677	EYA4_HUMAN		NA	2	AGTTCTGGGTC	0.458	
+	32	5375_5377		NM_001040001	NP_001035090	P55196	AFAD_HUMAN		NA	5	TACAATgaggagga	0.409	
-	3	730	njg.1_5'UTR|CXor	NM_198279	NP_938020	A2AJT9	CX023_HUMAN		NA	2	TGGGAGGGAAT	0.498	
+	4	1234_1235		NM_000314	NP_000305	P60484	PTEN_HUMAN	hatase tensi´(2)|p.Y68C(1)|		2334	GATATACAATCT	0.277	
-	1	106_108	n_Frame_Del_p.L	NM_139247	NP_640340	Q8NFM4	ADCY4_HUMAN	ical; (Potential).		3	TCCCCAGCAGC	0.7	
+	16	2611	Shift_Del_p.I555fs	NM_001013703	NP_001013725	Q9P2K8	E2AK4_HUMAN	otein kinase 2.		4	TCAACATTTTTTT	0.358	
+	16	3292_3294		NM_001145011	NP_001138483	C9JH24	C9JH24_HUMAN			0	ACCTCTGCTGC	0.675	
+	15	2866	p.K951fs|USP43_	NM_153210	NP_694942	Q70EL4	UBP43_HUMAN			5	ACTGGAAGGAG	0.547	
-	9	1016	18orf34_uc002kxc	NM_001105528	NP_001098998	Q5BJE1	CR034_HUMAN	Potential.		1	CCTCCATTTTTTT	0.318	
-	173	33412	Shift_Del_p.K4691	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN			153	TCTTCCTTAGGT	0.363	
-	27	3223	.2_RNA|CLASP2_	NM_015097	NP_055912	B2RTR1	B2RTR1_HUMAN			4	CACCCATTTTTTT	0.343	
-	1	220_222	3_5'Flank|TADA2B	NM_153376	NP_699207	Q2M329	CCD96_HUMAN	Glu-rich.		0	GCTTGCTCCTCC	0.729	
+	11	1154	p.*323fs|LIAS_uc	NM_006859	NP_006850	O43766	LIAS_HUMAN			0	TTCCTGAAAAATC	0.264	
+	25	3378	11csr.1_Frame_Sh	NM_001080479	NP_001073948	Q8N1W1	RGNEF_HUMAN	PH.		0	GACCAGAAATAC	0.313	
+	1	403_405	uc003tbl.3_5'Flank	NM_002047	NP_002038	P41250	SYG_HUMAN			1	CGCTCTGCTGC	0.749	
-	3	534_536	f.2_Intron|TP53IN	NM_033285	NP_150601	Q96A56	T53I1_HUMAN	Glu-rich.		0	CCTCCTCTTCTT	0.458	
-	3	615_616		NM_022735	NP_073572	Q9H3P7	GCP60_HUMAN	ential.|Glu-rich.		0	TTCACCTTTTTT	0.411	
+	4	1234_1235		NM_000314	NP_000305	P60484	PTEN_HUMAN	hatase tensi´(2)|p.Y68C(1)|		2334	GATATACAATCT	0.277	
+	1	515_516		NM_007129	NP_009060	O95409	ZIC2_HUMAN	transcriptional activation o		0	CTCGCAGAATGT	0.743	
-	6	961_963	.E208del|BEGAIN	NM_001159531	NP_001153003	Q9BUH8	BEGIN_HUMAN			0	CTCGGCCTCCTC	0.724	
-	5	630	_uc002cmq.1_5'Fl	NM_002513	NP_002504	Q13232	NDK3_HUMAN			0	CTGCGCGGAAC	0.652	
-	4	560_561	N1L_uc002fmi.2_	NM_001080487	NP_001073956	A6NDY0	EPAB2_HUMAN	RRM.		0	CCCTTGGGGTGT	0.564	
+	2	635_637		NM_033513	NP_277048	Q6ZTW0	TPGS1_HUMAN			1	CTCGGCCGCCG	0.768	
-	1	593		NM_005325	NP_005316	Q02539	H11_HUMAN			2	TTTGGGTTTTTTT	0.483	
-	2	967	11_uc003syy.2_R	NM_005523	NP_005514	P31270	HXA11_HUMAN	Homeobox.		2	TGTTAATTTTTTT	0.448	
-	3	534_536	f.2_Intron|TP53IN	NM_033285	NP_150601	Q96A56	T53I1_HUMAN	Glu-rich.		0	CCTCCTCTTCTT	0.458	
-	7	4513	3H_uc010mfk.1_	NM_198488	NP_940890	Q6ZRV2	FA83H_HUMAN			3	CCCCCCTGCCC	0.665	7;rs34283115;rs113442489
-	2	389_390	1bzw.1_Frame_Sh	NM_005202	NP_005193	P25067	CO8A2_HUMAN	le-helical region.		1	GCCCTGGGGGA	0.713	
-	2	598_600	me_Del_p.D166de	NM_001164	NP_001155	O00213	APBB1_HUMAN	Glu-rich.		2	cctcctcttcatcatcatc	0.414	
+	8	875_876	1mpj.2_Frame_Sh	NM_019028	NP_061901	Q8IUH4	ZDH13_HUMAN	ANK 6.		0	TATGGCTCTACA	0.332	
-	8	778		NM_004308	NP_004299	Q07960	RHG01_HUMAN	H3-binding.		1	GGGCAGGGGGG	0.642	
-	2	598_600	1orf95_uc001nxs.	NM_001144936	NP_001138408	C9JLR9	CK095_HUMAN	Glu-rich.		0	tcctcttcttcctcctcctc	0.532	
+	2	327		NM_025057	NP_079333	Q8ND07	CN045_HUMAN			0	CTTAAAGAAAAA	0.398	rs61752569
+	4	389	M_uc002lpn.1_Fra	NM_002579	NP_002570	O75781	PALM_HUMAN	Potential.		0	TCAGAGGGGGA	0.667	
-	58	4279_4280		NM_015719	NP_056534	P25940	CO5A3_HUMAN	le-helical region.		10	CCCTTGGGGCCA	0.584	
+	7	1953_1961	atq.1_In_Frame_D	NM_001039141	NP_001034230	Q9H2D6	TARA_HUMAN			1	GCCTCCAGAAC	0.589	
-	1	135	.1_Intron|LOC400	NM_018280	NP_060750	Q9NV39	CV026_HUMAN	Pro-rich.		0	GGGTTGGGGGG	0.751	

-	2	306_307	ame_Shift_Ins_p.K	NM_001024921	NP_001020092	P32969	RL9_HUMAN			1	ACCCTCTTTTTT	0.431	
+	1	140		NM_016167	NP_057251	Q9UMY1	NOL7_HUMAN			0	CTGTTGCTCGG	0.721	
-	3	444	p.M121fs|SLC17A2_uc003nfl.2_Frame_Shift_Del_p.M1			O00624	NPT3_HUMAN			1	CAAGCATTTTTT	0.453	
+	2	128_130	p.L24del|BTN2A2_	NM_006995	NP_008926	Q8WVV5	BT2A2_HUMAN			0	CAGCCTCcctcctc	0.483	
+	11	2081_2082	kvv.1_Frame_Shif	NM_053043	NP_444271	Q96EV2	RBM33_HUMAN	Pro-rich.		1	TGCCCACACAC	0.53	
-	7	4513	3H_uc010mfk.1_	NM_198488	NP_940890	Q6ZRV2	FA83H_HUMAN			3	CCCCCCTGCCC	0.665	7;rs34283115;rs113442489
-	4	773_774	3H_uc010mfk.1_5	NM_198488	NP_940890	Q6ZRV2	FA83H_HUMAN			3	CAGTCCACCAG	0.658	
-	6	1404_1406	.V48del|PVRL4_u	NM_030916	NP_112178	Q96NY8	PVRL4_HUMAN	ical; (Potent	NA	2	TGAGCACCACC	0.571	
-	1	205_207	p.G10del|KCNMA	NM_001161352	NP_001154824	Q12791	KCMA1_HUMAN	xtracellular	NA	3	cgctgctgccgccgcc	0.404	
-	14	2006_2008	21A_uc001rlz.2_	NM_017641	NP_060111	Q7Z4S6	KI21A_HUMAN		NA	7	GTCAtcttcctcctcc	0.281	
+	87	3755_13757		NM_002332	NP_002323	Q07954	LRP1_HUMAN	ical; (Potent	NA	22	CTGTTGCTGCT	0.557	
-	54	7655_7657	_uc001tao.2_3'UT	NM_025114	NP_079390	O15078	CE290_HUMAN	Potential.	NA	7	GAATATTCTTCTT	0.31	
+	9	1622_1633	C100132247_uc	NM_001135865	NP_001129337	A8MRT5	K220L_HUMAN	Pro-rich.	NA	0	TCCACCCTCAGC	0.571	
+	3	371_372	07_uc010csz.2_Fr	NM_003457	NP_003448	O43670	ZN207_HUMAN		NA	0	CAGACATAGAGT	0.332	
+	11	1321	xom.1_Frame_Shi	NM_000896	NP_000887	Q08477	CP4F3_HUMAN		NA	3	CAGTGTTTTTG	0.622	
+	2	151_152		NM_020813	NP_065864	Q9BX82	ZN471_HUMAN		NA	2	GTAGTAAAAGTC	0.401	
+	7	817_819		NM_005049	NP_005040	Q15269	PWP2_HUMAN	Poly-Glu.	NA	1	gaggaagaggaggag	0.527	
-	10	1116	p.N255fs|ARFGAP	NM_014570	NP_055385	Q9NP61	ARFG3_HUMAN		NA	1	TCAACATTTTTTT	0.224	
+	1	355_357		NM_000297	NP_000288	Q13563	PKD2_HUMAN	ytoplasmic	NA	1	AGGCCgaggagg	0.498	
+	10	1175_1178	.E360fs|HMGCR_	NM_000859	NP_000850	P04035	HMDH_HUMAN	Linker.	NA	1	TTTGAACAAACA	0.358	
-	6	1099_1101	.L118del|CSNK1A	NM_001892	NP_001883	P48729	KC1A_HUMAN	rotein kinas	NA	1	TATCCTAATGATT	0.335	
+	1	1207_1208	1463_uc003xvh.2	NM_152414	NP_689627	Q8NFJ8	BHE22_HUMAN	Basic motif.	NA	0	agcggcggcagcag	0.203	519836;rs34265378
+	3	719_721		NM_153812	NP_722519	Q86YI8	PHF13_HUMAN	ization signal (Probable).		0	caagctgaagaagaa	0.498	
-	28	4109	c001ayw.2_5'Flan	NM_017940	NP_060410	Q3BBV0	NBPF1_HUMAN	NBPF 7.		0	GCAGGCAGGAG	0.478	
+	1	136_137		NM_001008740	NP_001008740	Q7Z6W1	TMCO2_HUMAN			1	TAGAGTCTCTCT	0.406	
-	2	938_939	D1_uc001ctf.2_Fr	NM_002525	NP_002516	O43847	NRDC_HUMAN			0	CAGTAGTTTTTT	0.233	
-	4	884	xz.3_Frame_Shift	NM_001114108	NP_001107580	Q5TAA0	TTC22_HUMAN	TPR 4.		0	TGTCCTTCCGC	0.652	
+	1	152	ne_Shift_Del_p.E	NM_001902	NP_001893	P32929	CGL_HUMAN			1	GCAGGAAAAAG	0.547	
+	10	2124	ova.1_Frame_Shif	NM_001144937	NP_001138409	Q5VTL7	FNDC7_HUMAN	nectin type-III 8.		2	TGTCCAAAAAA	0.363	
+	2	1237_1238	ftp.3_Frame_Shift_	NM_002036	NP_002027	Q16570	DUFFY_HUMAN	lasmic (Potential).		2	CCCTTGGAAGC	0.54	
+	4	220_221	_p.P11fs|SDHC_u	NM_003001	NP_002992	Q99643	C560_HUMAN	al; (By similarity).		0	CTCTTCCCATGG	0.376	
+	8	1233_1234	9wxs.2_Frame_Sh	NM_000721	NP_000712	Q15878	CAC1E_HUMAN	lasmic (Potential).		6	CCAAAGAGAGA	0.51	
-	2	1361_1363	.2_Intron|RGL1_u	NM_203454	NP_982279	Q8WW27	ABEC4_HUMAN			0	TCCCTTTCTTCTT	0.419	rs141411396
+	7	1327_1328	_Ins_p.333_334ins	NM_005807	NP_005798	Q92954	PRG4_HUMAN	-X-P-X-P-T-T-X.|11; appro		1	CCACCAAGTCTG	0.658	
+	12	1394	0pos.1_Frame_Sh	NM_024420	NP_077734	P47712	PA24A_HUMAN	PLA2c.		3	AGTGCCTTTTCC	0.353	
-	5	865	1ird.2_Frame_Shi	NM_022365	NP_071760	Q96KC8	DNJC1_HUMAN	smic (By similarity).		1	CCAGTCTTTTTT	0.303	
+	7	2382	_p.A555fs|ZEB1_u	NM_030751	NP_110378	P37275	ZEB1_HUMAN			5	TGCGCAAAAAA	0.413	
-	4	784	01jod.1_Frame_S	NM_017987	NP_060457	Q8WXA3	RUFY2_HUMAN	RUN.		1	GGCCATTTTTTT	0.398	
+	25	3716	_p.D924fs|ZMIZ1_	NM_020338	NP_065071	Q9ULJ6	ZMIZ1_HUMAN			4	CTGGACCCCCC	0.557	
-	3	1279_1281	172PP>P|POLL_u	NM_013274	NP_037406	Q9UGP5	DPOLL_HUMAN			0	GGTGGGAGGAG	0.591	
-	1	213	.1_Intron|TRIM22_	NM_001001922	NP_001001922	Q8NH56	O52N5_HUMAN	Name=2; (Potential).		2	TGGCCAAAAAA	0.428	
+	1	525		NM_001003750	NP_001003750	Q8N0Y5	OR8I2_HUMAN	ellular (Potential).		1	CAATCATTTTTTT	0.443	rs112181516
-	12	1314	Splice_Site_p.C3	NM_016931	NP_058627	Q9NPH5	NOX4_HUMAN			2	GACACTAAAAA	0.292	rs56022003
-	6	1503_1505	L1_uc001pwu.1_I	NM_002855	NP_002846	Q15223	PVRL1_HUMAN	ytoplasmic (Potential).		0	CACCGCcctcctc	0.576	
-	10	1133_1134	qfh.2_Frame_Shift	NM_001143835	NP_001137307	Q6P4R8	NFRKB_HUMAN	Lys-rich.		3	TTAACCTTTTTT	0.441	
-	3	257_259		NM_006248	NP_006239					0	TCCTGGAGGAG	0.601	
+	4	669	|FAR2_uc009zjm.2	NM_018099	NP_060569	Q96K12	FACR2_HUMAN			0	GAGCCAAAAAA	0.388	

-	12	4127_4129	w.2_In_Frame_De	NM_004719	NP_004710	Q99590	SCAFB_HUMAN	Pro-rich.	0	AGGGGGTGGTG	0.483	
-	7	1132	.3_Frame_Shift_D	NM_016357	NP_057441	Q9UHB6	LIMA1_HUMAN		1	TTCCTGATGGG	0.428	
-	26	3234	p.P1074fs|SMARC	NM_003075	NP_003066	Q8TAQ2	SMRC2_HUMAN	Pro-rich.	6	GTCCAGGGGGG	0.577	
-	3	471	.F144fs|FBXO21_	NM_033624	NP_296373	O94952	FBX21_HUMAN		1	ATCCTCAAAAAA	0.373	
+	4	1848	_p.A605fs|EP400_	NM_015409	NP_056224	Q96L91	EP400_HUMAN		12	TCCCTGCACCG	0.632	
-	3	351	tcr.1_Frame_Shift_	NM_022459	NP_071904	Q9C0E2	XPO4_HUMAN		3	TTACTTGGGCCT	0.378	
-	10	3917	I963fs|SACS_uc0	NM_014363	NP_055178	Q9NZJ4	SACS_HUMAN		12	CTTCAATTTTTTT	0.383	
-	1	1994_1996	zo.1_In_Frame_De	NM_183422	NP_904358	Q15714	T22D1_HUMAN	Gln-rich.	0	gttgttgttgctgctgctg	0.409	613609;rs146722477
+	20	3706_3707	.A881fs|LMO7_uc	NM_015842	NP_056667	Q8WWI1	LMO7_HUMAN		5	GAGGCAGAGAG	0.386	
+	2	931	e_Shift_Del_p.P3	NM_144778	NP_659002	Q5VZF2	MBNL2_HUMAN	C3H1-type 1.	0	CTCATCCCCCC	0.413	
-	10	1212	1xae.2_Frame_Shi	NM_006832	NP_006823	Q96AC1	FERM2_HUMAN	FERM.|PH.	0	GTCAGCTTTTTG	0.343	
+	16	4738_4740	1xmv.2_In_Frame	NM_015556	NP_056371	O43166	SI1L1_HUMAN	Ser-rich.	4	tcctcctcttcctcctcctc	0.468	
+	11	1403_1404	.R399fs|RBM25_	NM_021239	NP_067062	P49756	RBM25_HUMAN	eckle localization.|Glu-rich	4	gcgggaaagagagaga	0.173	
-	2	365_367	c010twr.1_Intron|I	NM_020414	NP_065147	Q9GZR7	DDX24_HUMAN	Poly-Glu.	4	TTTCCCTCCTC	0.443	
-	7	1384	p.A457fs|C14orf4	NM_152592	NP_689805	Q6ZMZ3	SYNE3_HUMAN	lasmic (Potential).	1	CAGGGCCTTCC	0.652	
+	12	3276		NM_015656	NP_056471	Q9ULI4	KI26A_HUMAN		1	CCTGAGGGGGG	0.682	
+	19	3218	bbi.2_Frame_Shift	NM_003246	NP_003237	P07996	TSP1_HUMAN	SP C-terminal.	6	TTCTTCATCAA	0.488	
+	4	840	C4_uc001ztq.2_F	NM_138423	NP_612432	Q6P4E1	CASC4_HUMAN	(Potential).|Potential.	1	AATATTAAAAAGT	0.224	
-	17	3106	.K1025fs|SPG11_	NM_025137	NP_079413	Q96JI7	SPTCS_HUMAN	cellular (Potential).	5	TAACTCTTTTTTT	0.328	
+	2	214_216	p.Q15del|ARID3B_	NM_006465	NP_006456	Q8IVW6	ARI3B_HUMAN	Gln-rich.	0	CCACTTcagcagc	0.443	
+	29	4299_4300	so.1_Frame_Shift_	NM_001271	NP_001262	O14647	CHD2_HUMAN		2	CTGAAGAAAAAA	0.347	
-	2	667	_5'Flank|IQCK_uc	NM_001012991	NP_001013009	Q1ED39	CP088_HUMAN	Lys-rich.	0	GGTGGATTTTTT	0.532	
-	3	385_387	P2_uc010byn.2_I	NM_024816	NP_079092	Q9H5N1	RABE2_HUMAN	y-Gln.|Potential.	3	AGTCCTGCTGC	0.527	
+	7	485		NM_013292	NP_037424	Q96A32	MLRS_HUMAN	EF-hand 3.	0	GCCTTCCCCCC	0.672	
+	3	278_280	vho.1_In_Frame_	NM_020312	NP_064708	O75208	COQ9_HUMAN		1	CGGCGAGGAGG	0.576	rs149029279
+	5	2064_2065	02ewd.2_Frame_	NM_133458	NP_597715	Q8TF47	ZFP90_HUMAN	C2H2-type 12.	1	CTTCCGAAAAAA	0.411	
+	3	625	.2_Frame_Shift_D	NM_004937	NP_004928	O60931	CTNS_HUMAN	enal (Potential).	0	TTATCCTTTTTCC	0.393	
-	10	1079_1081	_63EE>E|C17orf85	NM_001114118	NP_001107590	Q53F19	CQ085_HUMAN	Glu-rich.	1	tcttcctcttcctcctcctc	0.379	
-	4	915	|PHF23_uc010vtt	NM_024297	NP_077273	Q9BUL5	PHF23_HUMAN		0	GTCTATCCCCCC	0.463	
+	2	3619_3620		NM_016239	NP_057323	Q9UKN7	MYO15_HUMAN	osin head-like.	9	GCCCATCAGGG	0.673	
-	8	1007	p.W57fs|MBTD1_	NM_017643	NP_060113	Q05BQ5	MBTD1_HUMAN	MBT 1.	2	TTGCACCAGAA	0.378	
-	11	1158_1160	.2_In_Frame_Del_	NM_017647	NP_060117	Q8IY81	RRMJ3_HUMAN		1	tcctcctcttcctcctcctc	0.463	
+	11	1393_1394	.G354fs|RBBP8_	NM_002894	NP_002885	Q99708	COM1_HUMAN		3	CCTGGGAAAAAA	0.361	
+	9	1222_1223	2lls.2_Frame_Shift	NM_032649	NP_116038	Q96KN2	CNDP1_HUMAN		0	GAGATTCTAATG	0.455	
-	13	1148	3_uc002ltq.2_Fra	NM_003200	NP_003191	P15923	TFE2_HUMAN		7	GCCCTGGGGGG	0.642	
+	12	2166	0xqv.1_Frame_Sh	NM_017660	NP_060130	Q86YP4	P66A_HUMAN		0	CTCCTGGACAT	0.667	
-	4	572_574		NM_018263	NP_060733	Q76L83	ASXL2_HUMAN	Ser-rich.	1	ATCACTGCTGC	0.463	
-	19	3112_3113	rrj.3_Frame_Shift_	NM_005633	NP_005624	Q07889	SOS1_HUMAN		10	TTGGGAGAGG	0.347	
+	16	3077_3078	sbz.2_Frame_Shift	NM_015252	NP_056067	Q8NDI1	EHBP1_HUMAN	Potential.	2	CAGCTGAGAGA	0.426	
-	2	607	GOLN2_uc002sp	NM_006464	NP_006455	O43493	TGON2_HUMAN	l).|14 X 14 AA tandem rep	0	GCTGCCTTTTTG	0.562	
+	1	1032_1033		NM_207364	NP_997247	Q8TDV2	GP148_HUMAN	lasmic (Potential).	1	GCCATCTTTACCA	0.525	
-	20	2071_2072	y.1_Frame_Shift_	NM_004543	NP_004534	P20929	NEBU_HUMAN	Nebulin 15.	20	TTTTTGGCCACC	0.411	
+	5	1589	_Shift_Del_p.P43	NM_022826	NP_073737	Q9H992	MARH7_HUMAN		0	GTCCCTCCAGC	0.428	rs1365803
-	1	244_246	p.L13del|PLA2R1	NM_007366	NP_031392	Q13018	PLA2R_HUMAN		3	CGCCCCcagcagc	0.601	
-	46	13588	N_uc010zfi.1_Intr	NM_133379	NP_596870	Q8WZ42	TITIN_HUMAN		153	TTCACCTTTTTCC	0.348	rs142304137
+	8	657_659	me_Del_p.G111de	NM_015575	NP_056390	Q6Y7W6	PERQ2_HUMAN	Poly-Gly.	7	GGACGAGGAGG	0.394	
-	1	1008_1009	TERFD2_uc010z	NM_182501	NP_872307	Q7Z6M4	MTER2_HUMAN		1	AAGACCACACAC	0.45	

+	4	1257	d.2_RNA|PANK2_u	NM_153638	NP_705902	Q9BZ23	PANK2_HUMAN		0	AGGAACTTTTTT	0.343	
+	4	651_654	el_p.L92fs|MCM8_u	NM_032485	NP_115874	Q9UJA3	MCM8_HUMAN		1	TCCTTTGATTGA	0.363	
+	11	1053	_p.P312fs|C20orf7	NM_024120	NP_077025	Q5TEU4	CT007_HUMAN		0	CCACCGGGGAA	0.323	
+	2	85_86	tj.1_RNA|FRG1B_uc010gdr.1_RNA|FRG1B_uc010ztk.1_Intron						0	ATGGAAAATATCT	0.342	
+	4	1167	002xpx.2_Frame_S	NM_033421	NP_219489	Q969T3	SNX21_HUMAN		2	ACACCACCCCC	0.617	
-	7	1206	_p.I184fs|STAU1_	NM_017453	NP_059347	O95793	STAU1_HUMAN		5	CTTTTTGATTCTA	0.433	
-	3	2331	me_Shift_Del_p.P7	NM_001098402	NP_001091872	Q9ULJ3	ZN295_HUMAN		3	TCTTTTGGTTTAG	0.438	
-	1	4423_4424		NM_002430	NP_002421	Q10571	MN1_HUMAN		10	CGCCTGAAGGAT	0.703	
+	5	1092	_p.L98fs|EDEM1_u	NM_014674	NP_055489	Q92611	EDEM1_HUMAN	nenal (Potential).	3	ACTCCTGGGGGA	0.532	
+	9	1152	ckz.3_Frame_Shif	NM_001042646	NP_001036111	Q9UPV9	TRAK1_HUMAN	al.|HAP1 N-terminal.	1	GCATCTGGGGGC	0.502	
-	4	457_458	03diu.2_Frame_Sh	NM_178504	NP_848599	Q6ZR08	DYH12_HUMAN	n (By similarity).	2	TCACTCCTTTTTT	0.248	
-	2	196_197		NM_005130	NP_005121	Q14512	FGFP1_HUMAN		0	TCTTCACTTTTTT	0.525	
-	4	2224_2225		NM_003263	NP_003254	Q15399	TLR1_HUMAN	smic (Potential).|TIR.	5	CTTCACCCAGAA	0.426	
-	3	747_748	e_Shift_Ins_p.K74f	NM_003948	NP_003939	Q92772	CDKL2_HUMAN	rotein kinase.	7	ACCATCGTTTTTT	0.322	
+	8	1279	ike.1_Frame_Shift	NM_001263	NP_001254	Q92903	CDS1_HUMAN		4	TTTGGATTTTTTT	0.308	
+	4	994_996	p.Q279del|MMRN1	NM_007351	NP_031377	Q13201	MMRN1_HUMAN	Poly-Gln.	4	GCTGAGCAGCA	0.448	
-	9	844	9_splice|EMCN_u	NM_016242	NP_057326	Q9ULC0	MUCEN_HUMAN		0	TGTGCCTAGGAG	0.396	
+	2	227	330_uc011chl.1_5'	NM_014487	NP_055302	Q9Y3S2	ZN330_HUMAN	lization signal (Potential).	0	ATGCCTAAAAAAA	0.353	
-	21	2860_2861	3ijz.3_Frame_Shift	NM_001102653	NP_001096123	Q01804	OTUD4_HUMAN		3	ACAGTTTCTCTCT	0.455	
-	10	1831	p.Q453fs|LRBA_uc	NM_006726	NP_006717	P50851	LRBA_HUMAN		7	GTACCTGGAGCAT	0.388	
-	10	1909	H10_uc011cnu.1_F	NM_006727	NP_006718	Q9Y6N8	CAD10_HUMAN	|Extracellular (Potential).	12	AAACTGAAAAAAA	0.313	
+	7	1394		NM_002439	NP_002430	P20585	MSH3_HUMAN		4	GGGACAAAAAAA	0.348	
+	26	4712	n.1_Frame_Shift_D	NM_020690	NP_065741	Q8IWZ2	Q8IWZ2_HUMAN		6	TTGGGAAAAAAA	0.423	
+	4	930_932	f25_uc011dfk.1_In_Frame_Del_p.S199del|uc003mdu.1			Q8NDZ2	CE025_HUMAN	Ser-rich.	0	agtaggagcagcagca	0.448	
+	9	1351	3nag.1_Frame_Shi	NM_030948	NP_112210	Q9C0D0	PHAR1_HUMAN		0	CTTCTTACCACAC	0.473	
-	8	966	_Shift_Del_p.K224f	NM_003472	NP_003463	P35659	DEK_HUMAN		1	GCTGTCTTTTTTG	0.373	
-	15	2057	BBR1_uc003nmu.3	NM_001470	NP_001461	Q9UBS5	GABR1_HUMAN	cellular (Potential).	7	CAGCTGGGGGG	0.363	
-	3	577_578	11ebw.1_Frame_S	NM_033515	NP_277050	Q8N392	RHG18_HUMAN		3	CTGTTTGTTTTTT	0.421	
-	1	648_649		NM_001129895	NP_001123367	Q9UM08	Q9UM08_HUMAN		0	GTTGGGAGGAGG	0.639	
+	8	2132_2134		NM_138426	NP_612435	Q86VQ1	GLCI1_HUMAN	Poly-Gln.	0	CATCCCAGCAGCA	0.562	
+	10	1645		NM_007252	NP_009183	P78424	PO6F2_HUMAN	POU-specific.	1	TCCTACCACAGC	0.488	
+	3	342	_uc011kby.1_Intron	NM_002541	NP_002532	Q02218	ODO1_HUMAN		2	GGGACATTTTTTT	0.577	
-	7	1188_1189	p.K237fs|CYP51A	NM_000786	NP_000777	Q16850	CP51A_HUMAN		0	AATAACATTTTTTT	0.396	
+	8	1031	_p.F215fs|DYNC1	NM_004411	NP_004402	O14576	DC1I1_HUMAN		4	GACATCTTTTTTG	0.383	
-	6	959	vst.2_Frame_Shift	NM_001008225	NP_001008226	O95628	CNOT4_HUMAN		0	CCTCATCCCCCA	0.393	
-	1	151_153	wnq.2_In_Frame_I	NM_002847	NP_002838	Q92932	PTPR2_HUMAN		7	cagcagtagcagcagca	0.478	
-	4	6567_6573		NM_178857	NP_849188	Q8IWN7	RP1L1_HUMAN		8	ATACCTTCTGCCT	0.604	rs139374902
-	6	418_419	ntron|CCDC25_uc	NM_018246	NP_060716	Q86WR0	CCD25_HUMAN		0	CATGTCAGCTGTT	0.485	
+	10	1740	LF1_uc003xyf.2_F	NM_015170	NP_055985	Q8IWU6	SULF1_HUMAN		7	TGTGCCTTTTTTT	0.408	
+	3	1173		NM_004770	NP_004761	Q92953	KCNB2_HUMAN	=Segment S1; (Potential).	7	GATCCTGGCCATC	0.458	
+	9	1450_1451	RRCC1_uc003ycx	NM_033402	NP_208325	Q9C099	LRCC1_HUMAN	Potential.	0	GACCAAGAGAGA	0.267	
+	19	2164	ame_Shift_Del_p.I	NM_052832	NP_439897	Q8TE54	S26A7_HUMAN	ytoplasmic (Potential).	2	AACCAATTTTTTT	0.343	
-	3	534_536	af.2_Intron|TP53IN	NM_033285	NP_150601	Q96A56	T53I1_HUMAN	Glu-rich.	0	CCTCCTCTTCTTC	0.458	
-	8	962	.1_Frame_Shift_D	NM_015668	NP_056483	Q8NE09	RGS22_HUMAN		7	GGGTCCTTTTTTC	0.279	
+	3	157_159	nc.2_In_Frame_De	NM_020189	NP_064574	Q9NPA8	ENY2_HUMAN		0	AGAGTTGCTGAGA	0.345	
-	2	473	yny.2_Frame_Shift	NM_014112	NP_054831	Q9UHF7	TRPS1_HUMAN		7	GGGTTCTTTTTCC	0.413	
-	6	524	3yqt.2_Frame_Shi	NM_004306	NP_004297	P27216	ANX13_HUMAN	Annexin 2.	3	CCAGGATTTTTTT	0.413	

-	3	757	zif.1_Frame_Shift_	NM_152629	NP_689842	Q8NEA6	GLIS3_HUMAN			1	GCTGCGGGGAC	0.672	
-	20	2893		NM_006289	NP_006280	Q9Y490	TLN1_HUMAN			13	ACTTTCCCCCT	0.562	
+	6	1019_1020	Shift_Del_p.Q191f	NM_018360	NP_060830	Q9NUQ3	TXLNG_HUMAN	Potential.		1	ACATCAGAGAGA	0.386	
-	13	1743_1744	p.V523fs|MAP7D2	NM_152780	NP_689993	Q96T17	MA7D2_HUMAN			3	TTTTCCACACAC	0.446	
-	7	3967	OM4_uc004dpd.3	NM_020717	NP_065768	Q9ULL8	SHRM4_HUMAN	ASD2.		1	TTTACCTTTTTTT	0.448	
-	2	352_353	AGT1_uc004ect.	NM_032121	NP_115497	Q9H0U3	MAGT1_HUMAN			1	GCTTTCACAAGG	0.421	
-	6	1039	emy.1_Frame_Shif	NM_018301	NP_060771	Q96IZ5	RBM41_HUMAN	RRM.		1	AGGTCCTTTTTT	0.433	
+	3	526	nzo.1_Frame_Shif	NM_001493	NP_001484	P31150	GDIA_HUMAN			0	AGGGGCCCCCT	0.577	
-	4	396_398	_In_Frame_Del_p.	NM_001042663	NP_001036128	O94827	PKHG5_HUMAN	Poly-Glu.	NA	1	AGCTCTCCTCC	0.631	
-	2	1126	1fpt.1_Frame_Shif	NM_030980	NP_112242	Q9H9L3	I20L2_HUMAN	xonuclease	NA	2	GTTGAGGGGGG	0.557	
-	4	521	yru.1_RNA|CORC	NM_020441	NP_065174	Q9BR76	COR1B_HUMAN	WD 2.	NA	2	TGCCCACATTC	0.592	
-	1	295_296	_Ins_p.16_16G>	NM_002094	NP_002085	P15170	ERF3A_HUMAN		NA	3	tgctgctcccgccgcc	0.332	rs71408216
-	12	5661_5663	2_In_Frame_Del_	NM_014071	NP_054790	Q14686	NCOA6_HUMAN	|Gln-rich.|C	NA	7	TCATTtgttgctgctgc	0.498	895426;rs140426729
-	4	1934_1936	1aaq.1_In_Frame_	NM_017798	NP_060268	Q9BYJ9	YTHD1_HUMAN		NA	2	ACCACCTCCTC	0.557	
-	3	428_430	_19DD>D|TFIP11_	NM_012143	NP_036275	Q9UBB9	TFP11_HUMAN	Poly-Asp.	NA	0	GCTCGTCATCAT	0.532	rs145794160
+	3	743_744	_103insS|TPRXL_	NR_002223					NA	0	gcagctctagcagcag	0	895893;rs138518200
+	13	1713_1714	_p.K518fs|PAPD7_	NM_006999	NP_008930	Q5XG87	PAPD7_HUMAN		NA	1	AAAAAACACACA	0.653	
+	1	616_617		NM_021614	NP_067627	Q9H2S1	KCNN2_HUMAN		NA	2	CCGCTGCCGCC	0.658	038013;rs34838882
-	7	739_740	_uc009vlz.2_Intron	NM_003790	NP_003781	Q93038	TNR25_HUMAN	ical; (Potent	NA	3	GGTGGCCCCAAG	0.634	
+	2	287	n|FDPS_uc001fke	NM_002004	NP_001995	P14324	FPPS_HUMAN		NA	0	ACCCCGGGAGA	0.682	
-	7	924_926	MARCH8_uc001jc	NM_001002266	NP_001002266	Q5T0T0	MARH8_HUMAN		NA	0	CCTTGAGTCTCT	0.384	
+	3	372	1kce.3_Frame_Sh	NM_032333	NP_115709	Q9BRX8	CJ058_HUMAN		NA	0	TATGGGAAAAAA	0.488	
+	1	354	_uc001mam.1_Int	NM_001004756	NP_001004756	B2RNI9	B2RNI9_HUMAN		NA	0	CCACTCTTTTTC	0.502	
-	3	345	rew.1_Frame_Shi	NM_001001991	NP_001001991	Q6UXH9	PAMR1_HUMAN		NA	2	AGGTACCCCCC	0.517	
-	3	635	sfi.3_Frame_Shift_	NM_001127322	NP_001120794	P45973	CBX5_HUMAN		NA	0	TCTCTCTTTTTTT	0.323	
+	3	353_355	e_Del_p.D88del|	NM_018559	NP_061029	Q8IXQ4	K1704_HUMAN	Poly-Asp.	NA	2	atgatgacgatgatgat	0.286	rs138421508
-	11	2527		NM_018353	NP_060823	Q6P0N0	M18BP_HUMAN		NA	0	TGGGACTTTTTTT	0.373	
+	4	1996	p.Q522fs|ZBTB1_	NM_001123329	NP_001116801	Q9Y2K1	ZBTB1_HUMAN		NA	1	TATCCAAAAAAA	0.378	
+	8	929_930	IP_uc002dcx.3_R	NM_006985	NP_008916	Q9UND3	NPIP_HUMAN	Pro-rich.	NA	0	TCCCGAGTGTCT	0.559	
+	12	1921_1923	vc.1_In_Frame_D	NM_016151	NP_057235	Q9UL54	TAOK2_HUMAN	Glu-rich.	NA	1	gaggaagaggagga	0.483	
-	2	401	exe.2_Frame_Shif	NM_005652	NP_005643	Q15554	TERF2_HUMAN	H dimerizat	NA	1	TCCTTCCCCAAC	0.592	
-	8	1040	N_uc010ezx.2_In	NM_003162	NP_003153	O43815	STRN_HUMAN		NA	1	ACCCCCTTTTTC	0.388	
+	8	2678_2679	ne_Shift_Ins_p.Q1	NM_005876	NP_005867	Q15772	SPEG_HUMAN	Ig-like 3.	NA	14	GTGCAGGGGG	0.594	
+	2	364_365	s_p.I20fs|DSTN_u	NM_006870	NP_006861	P60981	DEST_HUMAN	ADF-H.	NA	2	CTGTCATTTTTT	0.386	
-	6	827	Shift_Del_p.A279f	NM_178026	NP_821158	Q9UJ14	GGT7_HUMAN	ellular (Pote	NA	1	TTGGGCCACAG	0.597	
-	1	204		NM_181607	NP_853638	Q8IUB9	KR191_HUMAN	repeats of	NA	0	CCTCCAAAGCC	0.507	
-	7	944		NM_173536	NP_775807	Q8N1C3	GBRG1_HUMAN	ellular (Prob	NA	2	AGGTCAAAAAA	0.294	
-	25	3483	I1107fs|SEC31A_	NM_001077207	NP_001070675	O94979	SC31A_HUMAN	ction with P	NA	8	TGGTAATTTTTTT	0.388	
+	28	3960	hift_Del_p.Q1226	NM_015183	NP_055998	O15021	MAST4_HUMAN		NA	13	CGCTGCAGAGC	0.682	
+	11	2230		NM_014899	NP_055714	O94955	RHBT3_HUMAN	action with F	NA	2	TCAGTCAAAAG	0.328	
-	8	1188_1189	na.3_Frame_Shift	NM_018343	NP_060813	Q9BVS4	RIOK2_HUMAN	rotein kinas	NA	1	ATTCTTCTAGAC	0.416	
-	16	2124	_Shift_Del_p.S640	NM_016340	NP_057424	Q8TEU7	RPGF6_HUMAN		NA	3	GATTACTTTTTT	0.368	
-	7	1188	p.K237fs|CYP51A	NM_000786	NP_000777	Q16850	CP51A_HUMAN		NA	0	ATAACATTTTTTT	0.398	
+	14	2475_2476	16_uc004brr.1_3'U	NM_144965	NP_659402	Q8NEE8	TTC16_HUMAN		NA	0	TTCCACCAAGAC	0.609	rs139597416
+	11	1489_1490	A1B_uc011mfd.1_	NM_000718	NP_000709	Q00975	CAC1B_HUMAN	lasmic (Pote	NA	6	CCCTTCGCCCGC	0.609	
+	42	6439_6441	dza.2_In_Frame_	NM_005120	NP_005111	Q93074	MED12_HUMAN	Gln-rich.	NA	4	acatccggcagcagcag	0.256	
+	1	794	_5'Flank|BCAP31_	NM_000033	NP_000024	P33897	ABCD1_HUMAN	nteraction w	NA	0	TGGCTGGCAGC	0.667	rs74315280

-	2	90	ame.2_Frame_Shi	NM_000983	NP_000974	P35268	RL22_HUMAN			0	TGCTTCTTTTTTT	0.398	
+	20	5915	l_p.G694fs|ARID1	NM_006015	NP_006006	O14497	ARI1A_HUMAN		p.G1848fs*6(3	142	TTGGTGGGGGG	0.582	rs140055856
+	7	1312_1313	ame_Shift_Ins_p.S	NM_001048183	NP_001041648	Q8IZ21	PHAR4_HUMAN	Pro-rich.		0	CTCCGTCCCCCC	0.515	
-	8	1432	P2_uc001dmy.1_F	NM_207398	NP_997281	Q8N8V2	GBP7_HUMAN			2	TTGTGCCCCCCC	0.438	
-	9	1607_1608	0ovy.1_Frame_Sh	NM_004696	NP_004687	O15374	MOT5_HUMAN	ical; (Potential).		3	TGGTACAAAAAA	0.391	
-	2	1361_1363	.2_Intron|RGL1_u	NM_203454	NP_982279	Q8WW27	ABEC4_HUMAN			0	TCCCTTTCTTCTT	0.419	rs141411396
+	22	2922_2924		NM_018085	NP_060555	Q96P70	IPO9_HUMAN			2	gaggaagaggaggag	0.33	
+	5	2142_2143	33A_uc010qev.1_	NM_006974	NP_008905	Q06730	ZN33A_HUMAN	2H2-type 12.		3	ACATCAGAGAAC	0.391	
-	7	924_926	MARCH8_uc001j	NM_001002266	NP_001002266	Q5T0T0	MARH8_HUMAN			0	CCTTGAGTCTCT	0.384	
+	9	6800	001lfz.2_Frame_S	NM_206862	NP_996744	O95359	TACC2_HUMAN			10	AGAGACCCCCC	0.522	
+	1	303_304		NM_001005197	NP_001005197	Q8NGM9	OR8D4_HUMAN	Name=3; (Potential).		1	CAGCTGTTTTTT	0.436	rs79561639
+	13	1588	.1_3'UTR|GLB1L3	NM_001080407	NP_001073876	Q8NCI6	GLBL3_HUMAN			1	TGTATCCCCCC	0.602	
-	3	314_315		NM_006248	NP_006239					0	GGAGGTGGGG	0.614	
-	3	189_191		NM_006248	NP_006239					0	GAGGAGATGGG	0.557	
+	4	669	|FAR2_uc009zjm.2	NM_018099	NP_060569	Q96K12	FACR2_HUMAN			0	GAGCCAAAAAA	0.388	
-	9	1715_1735	av.1_Splice_Site_	NM_006121	NP_006112	P04264	K2C1_HUMAN	y/Ser-rich.|Tail.		2	gctgctacctccggagc	0	529359;rs61226348
-	3	635	sfi.3_Frame_Shift_	NM_001127322	NP_001120794	P45973	CBX5_HUMAN			0	TCTCTCTTTTTTT	0.323	
+	1	306_308		NM_001005280	NP_001005280	Q8NGE5	O10A7_HUMAN	Name=3; (Potential).		4	ATGTACTTCTTC	0.414	
+	3	227	nk|MARS_uc001s	NM_004990	NP_004981	P56192	SYMC_HUMAN			5	CAGATATTTTTTT	0.488	
+	6	694	sy.1_Frame_Shift	NM_007199	NP_009130	Q9Y616	IRAK3_HUMAN	rotein kinase.		8	AGGAGAAAAAA	0.303	
+	8	1314	C3_uc009zsm.2_	NM_181783	NP_861448	Q6ZXV5	TMTC3_HUMAN	ical; (Potential).		1	CGAACCTTTTTTT	0.303	
+	15	1554	1_uc009zuu.1_3'	NM_007062	NP_008993	Q13610	PWP1_HUMAN			0	GGCCCTTTTGG	0.373	
-	8	694	E2_uc001ume.2_I	NM_199254	NP_954863	Q6XPS3	TPTE2_HUMAN	ical; (Potential).		0	ATGTCAAAAAAA	0.303	
-	10	3917	I963fs|SACS_uc0	NM_014363	NP_055178	Q9NZJ4	SACS_HUMAN			12	CTTCAATTTTTTT	0.383	
-	5	1432	ne_Shift_Del_p.R	NM_001142296	NP_001135768	Q8N0X7	SPG20_HUMAN			0	TACCCTTTTTCC	0.373	
+	3	353_355	e_Del_p.D88del|	NM_018559	NP_061029	Q8IXQ4	K1704_HUMAN	Poly-Asp.		2	atgatgacgatgatgat	0.286	rs138421508
-	9	1177_1178	p.I309fs|DIAPH3_	NM_001042517	NP_001035982	Q9NSV4	DIAP3_HUMAN	GBD/FH3.		2	TGTCAATTTTTT	0.322	
+	7	1388_1390	Site|TOX4_uc010t	NM_014828	NP_055643	O94842	TOX4_HUMAN	ro-rich.|Poly-Ala.		1	AGCAGCTGCTG	0.581	
-	11	2527		NM_018353	NP_060823	Q6P0N0	M18BP_HUMAN			0	TGGGACTTTTTTT	0.373	
-	2	1971_1972	_Shift_Ins_p.K585	NM_001040108	NP_001035197	Q9UHC1	MLH3_HUMAN			2	TAGATTCTTTTTT	0.356	
-	7	1217_1219	339SS>S|FOXN3_	NM_001085471	NP_001078940	O00409	FOXN3_HUMAN			3	GGCTGAGGAGG	0.65	rs139532153
-	2	365_367	c010twr.1_Intron|I	NM_020414	NP_065147	Q9GZR7	DDX24_HUMAN	Poly-Glu.		4	TTTCCCTCCTC	0.443	
-	5	539_540	_Shift_Ins_p.I75fs|	NM_014226	NP_055041	Q9UQ07	MOK_HUMAN	rotein kinase.		4	TGCATAATTTTTT	0.322	rs145834415
+	7	998		NM_033223	NP_150092	Q99928	GBRG3_HUMAN			0	GGATCAAAAAAG	0.338	
-	12	2045_2061	p.A607fs|DMXL2_	NM_015263	NP_056078	Q8TDJ6	DMXL2_HUMAN	WD 5.		9	TCATTACTGTGG	0.438	rs139505079
+	7	2928_2930	10ujg.1_In_Frame	NM_004727	NP_004718	O60721	NCKX1_HUMAN	ic (Potential).|Poly-Glu.		0	gaggaagaggaggag	0.281	
+	10	2359	p.S379fs|BLM_uc	NM_000057	NP_000048	P54132	BLM_HUMAN	ase ATP-binding.		6	GTTATCAAAAAAA	0.269	
+	33	4739_4740	so.1_Frame_Shift_	NM_001271	NP_001262	O14647	CHD2_HUMAN			2	TCCAATgaaaaaa	0.158	
+	30	3476_3478	L1022del|ITGAL_	NM_002209	NP_002200	P20701	ITAL_HUMAN	ical; (Potential).		10	GGGGGCTGCTG	0.601	
+	2	171	ccz.1_Frame_Shi	NM_002987	NP_002978	Q92583	CCL17_HUMAN			1	CTCCTGGGGGC	0.662	
+	2	393_395		NM_018019	NP_060489	Q9NWA0	MED9_HUMAN	Potential.		0	CGAACAGCAGC	0.581	
-	2	1200_1202	.E351del|CDC42E	NM_012121	NP_036253	Q9H3Q1	BORG4_HUMAN			0	TTTCATCCTCCT	0.64	
-	2	140	Del_p.P27fs|SIRT	NM_016539	NP_057623	Q8N6T7	SIRT6_HUMAN			1	CCTCCGGGGGG	0.642	
+	3	1121_1123	002pbp.2_5'Flank|	NM_012099	NP_036231	O15446	RPA34_HUMAN	Poly-Lys.		4	TGCGGAAGAAG	0.581	
-	7	1091	me_Shift_Del_p.F	NM_002539	NP_002530	P11926	DCOR_HUMAN			1	ATGTCAAAAAC	0.473	
+	12	1349	RE_uc002rlt.2_Fr	NM_199194	NP_954664	Q9NXR7	BRE_HUMAN	UEV-like 2.		3	GGCCCAAAAAA	0.448	
-	4	596	ynd.1_5'Flank|FA	NM_015475	NP_056290	Q8NCA5	FA98A_HUMAN			1	TCTTACTTTTTTT	0.338	

+	12	2381	ruw.2_Frame_Shif	NM_001430	NP_001421	Q99814	EPAS1_HUMAN		2	TCCATGGGGGG	0.612	
+	1	96_98	2sda.2_In_Frame_	NM_203437	NP_982261	Q6ULP2	AFTIN_HUMAN		2	AGAGGATGATG	0.409	
+	19	2649	lice_Site_p.V850_	NM_001024457	NP_001019628	Q68DN6	RGPD1_HUMAN		0	tttttttAGTTGCAAC	0.312	
-	6	1386	.M392fs|REV1_u	NM_016316	NP_057400	Q9UBZ9	REV1_HUMAN		2	TTTTCATTTTTTT	0.348	
-	1	128	me_Shift_Del_p.P	NM_001087	NP_001078	Q13685	AAMP_HUMAN		1	CCAGTGGGGGG	0.617	
+	4	350	_p.L117fs|RQCD1_	NM_005444	NP_005435	Q92600	RCD1_HUMAN		2	TCCCACTTTTTT	0.413	
-	29	3477_3478	vul.2_Frame_Shift	NM_018218	NP_060688	Q9NVE5	UBP40_HUMAN		3	ATCTTGTTTTTT	0.317	
+	4	1257	.2_RNA|PANK2_	NM_153638	NP_705902	Q9BZ23	PANK2_HUMAN		0	AGGAACTTTTTT	0.343	
-	14	2158_2159	_p.K662fs|ZMYN	NM_012408	NP_036540	Q9ULU4	PKCB1_HUMAN		5	TTGGGCTTTTTT	0.49	
-	23	2501		NM_014258	NP_055073	Q9BX26	SYCP2_HUMAN		5	TCACCATTTTTT	0.323	
-	7	789_791		NM_016449	NP_057533	Q6PGQ1	CV043_HUMAN	Asp-rich.	1	CCTGGGcatcatc	0.261	
+	7	686_688	_Del_p.E197del|SH	NM_018957	NP_061830	Q9Y3L3	3BP1_HUMAN	BAR.	1	CTGAAGGAGGA	0.498	
+	12	3912	ayn.3_Frame_Shi	NM_001162501	NP_001155973	Q9UPQ9	TNR6B_HUMAN		0	TTATTTCCCCCC	0.448	
-	5	2710_2711	s_p.K325fs|FILIP	NM_182909	NP_878913	Q4L180	FIL1L_HUMAN	Potential.	1	ATTTAGTTTTTT	0.406	
-	6	1009		NM_013363	NP_037495	Q9UKZ9	PCOC2_HUMAN		3	GGCAGTTTTTTT	0.383	
-	3	1028	168_uc010iah.2_5	NM_152617	NP_689830	Q8IYW5	RN168_HUMAN	Glu-rich.	0	TTCGCCTTTTTT	0.448	
+	8	1111	gp.1_Frame_Shift_	NM_182982	NP_892027	P32298	GRK4_HUMAN	rotein kinase.	1	GCTACAAAAAA	0.393	
-	25	3567	tx.1_Frame_Shift_	NM_002913	NP_002904	P35251	RFC1_HUMAN		4	TCGAACTTTTTC	0.388	
+	4	1196_1198	.E415del|SEC24B	NM_006323	NP_006314	O95487	SC24B_HUMAN	Poly-Glu.	3	gaggaagaggagga	0.369	
-	8	596_598	3ijz.3_In_Frame_	NM_001102653	NP_001096123	Q01804	OTUD4_HUMAN		3	ACATCAGCAGC	0.34	
-	1	113_114		NM_001100389	NP_001093859	Q8IY95	TM192_HUMAN	lasmic (Potential).	1	ATCCTGCCCCCC	0.698	
-	7	1154		NM_016107	NP_057191	Q96KR1	ZFR_HUMAN		0	AGCTTCTTTTTT	0.348	
+	10	2028_2030	.MNB1_uc011cxb.	NM_005573	NP_005564	P20700	LMNB1_HUMAN	be involved in chromatin	2	AGAAGAGGAGG	0.325	
+	9	1679	uc003kwr.3_Intron	NM_003059	NP_003050	Q9H015	S22A4_HUMAN	ame=12; (Potential).	0	TCACCCTTTTTTT	0.418	
-	1	346_348	lew.1_In_Frame_	NM_004883	NP_004874	O14511	NRG2_HUMAN	Poly-Ser.	6	cgctctcgctgctgctg	0.291	
+	15	2605_2606	lny.2_Frame_Shif	NM_018989	NP_061862	Q9P2N5	RBM27_HUMAN	Potential.	3	GTGCTTAAAAAA	0.351	
-	2	531_533	rb.3_In_Frame_De	NM_001134870	NP_001128342	Q6NYC8	PHTNS_HUMAN	Poly-Gln.	0	GTTgttgttgctgctgct	0.547	
-	1	210_212		NM_024807	NP_079083	Q5T2D2	TRML2_HUMAN		2	GCCACAGCAGC	0.631	
+	7	1266	_p.P268fs|FOXP4_	NM_001012426	NP_001012426	Q8IVH2	FOXP4_HUMAN		1	TCTCACCCCCC	0.677	
+	15	2788	_p.K847fs|GRIK2_	NM_021956	NP_068775	Q13002	GRIK2_HUMAN	lasmic (Potential).	5	AATCCAAAAAAA	0.348	
-	13	1854	k.2_Frame_Shift_	NM_002037	NP_002028	P06241	FYN_HUMAN	rotein kinase.	7	GGTCCTTTTTC	0.562	
+	5	726	ISP3_uc003pvo.2	NM_003880	NP_003871	O95389	WISP3_HUMAN		0	ATTTGGAAAAAA	0.333	
-	5	2400		NM_001012279	NP_001012279	Q5TF21	CF174_HUMAN	Potential.	6	TGAGCCTTTTTT	0.294	
-	7	1235_1236	edm.1_Frame_Shi	NM_000416	NP_000407	P15260	INGR1_HUMAN	lasmic (Potential).	1	AAGAACTCTCT	0.431	
+	26	3025_3026	me_Shift_Ins_p.D	NM_015440	NP_056255	Q6UB35	C1TM_HUMAN	hydrofolate synthetase.	4	CCTGACAAAAAA	0.48	
+	6	694_695	_p.L112fs|ZDHHC4	NM_001134388	NP_001127860	Q9NPG8	ZDHC4_HUMAN	ical; (Potential).	2	AACCTGTTTTTT	0.45	
+	3	443	10ktk.1_Frame_S	NM_173565	NP_775836	B2RC85	R10B2_HUMAN		3	AACCCAAAAAA	0.468	
-	5	684_685	_Del_p.E93fs|OSB	NM_015550	NP_056365	Q9H4L5	OSBL3_HUMAN	PH.	1	CAGCTTCTCTCT	0.5	
+	21	3687_3689	.E707del|AEBP1_	NM_001129	NP_001120	Q8IUX7	AEBP1_HUMAN	y).|Glu-rich.|Interaction with	0	gaggaagaggagga	0.468	
-	2	458		NM_032936	NP_116325	Q9H2L4	TMM60_HUMAN		0	CCAGGCTTTTTT	0.408	
-	27	3637	.K1180fs|ABCB4_	NM_018849	NP_061337	P21439	MDR3_HUMAN	2.|Cytoplasmic (By similari	6	CTCTGTTTTTG	0.418	
-	10	1091_1092	_p.S339fs|ABCB4_	NM_018849	NP_061337	P21439	MDR3_HUMAN	).|ABC transmembrane typ	6	GGATTGAAAAAA	0.347	
-	7	1188	_p.K237fs|CYP51A	NM_000786	NP_000777	Q16850	CP51A_HUMAN		0	ATAACATTTTTT	0.398	
+	14	1294_1295	_p.Q359fs|CCDC1	NM_017667	NP_060137	Q96JG6	CC132_HUMAN		0	TATGGCAGGTTT	0.272	rs140810598
+	10	1383_1384		NM_014916	NP_055731	Q8IWU2	LMTK2_HUMAN	rotein kinase.	16	TCATTAGAGAGA	0.495	
+	28	3202	3_Intron|GATS_uc	NM_012447	NP_036579	Q9UJ98	STAG3_HUMAN		8	GTTTTCCCCCC	0.547	
+	1	528		NM_001001656	NP_001001656	Q8NGU2	OR9A4_HUMAN	ellular (Potential).	1	GAACAATTTTTT	0.383	

-	3	436		NM_005431	NP_005422	O43543	XRCC2_HUMAN		2	TACACCAAAAAA	0.393	
+	11	2081_2082	kvv.1_Frame_Shif	NM_053043	NP_444271	Q96EV2	RBM33_HUMAN	Pro-rich.	1	CTGCCCACACAC	0.53	
-	15	2035		NM_001010906	NP_001010906	Q68CJ6	SLIP_HUMAN		2	AGGAAATTTTTT	0.453	
-	7	1563	xon.3_Frame_Shif	NM_001099412	NP_001092882	Q92794	MYST3_HUMAN	tion with RUNX1-1.	7	ACCTGTTTTTG	0.398	
-	6	1263	_p.M308fs|PCMTD	NM_052937	NP_443169	Q96MG8	PCMD1_HUMAN		0	tcctcttccattttttcatcc	0.284	
-	7	735_736	p.K193fs|PTPLAD	NM_001010915	NP_001010915	Q5VWC8	HACD4_HUMAN	ic (Potential).|Poly-Lys.	1	CATCTTCTTTTTT	0.371	
+	2	306	|NDOR1_uc011me	NM_014434	NP_055249	Q9UHB4	NDOR1_HUMAN	avodoxin-like.	0	GGAGACCCCCC	0.527	
+	9	1017_1019		NM_173493	NP_775764	Q8IV76	PASD1_HUMAN	Poly-Ala.	3	TGAACCCgctgctg	0.355	
-	14	4550		NM_000132	NP_000123	P00451	FA8_HUMAN	B.	11	AGGTTATTTTTTT	0.413	
-	3	478_479	ocj.1_Frame_Shif	NR_026567					0	GCAGCCAGCTGA	0.663	rs141324796
+	1	1337_1339		NM_207334	NP_997217	Q6ZT52	FA43B_HUMAN		0	gaggacgaggaggag	0.567	
-	1	702_704		NM_001080418	NP_001073887	O95886	DLGP3_HUMAN	Poly-His.	3	CCGGGACtggtggt	0.537	
-	9	1732_1734	ows.1_In_Frame_	NM_015906	NP_056990	Q9UPN9	TRI33_HUMAN	Poly-Thr.	11	TGTTGTGTTGTT	0.429	
+	5	713	oyy.1_Frame_Shif	NM_006099	NP_006090	Q9Y6X2	PIAS3_HUMAN	PINIT.	1	TATTTTCCCCCCA	0.463	
-	13	1861	0pac.1_Intron|NBF	NM_017940	NP_060410	Q86T75	NBPFB_HUMAN	NBPF 3.	0	TCCTCCTTTTTCA	0.463	
+	1	171_176		NM_178356	NP_848133	Q5TA78	LCE4A_HUMAN	Cys-rich.	0	GGCTGTGGTTGC	0.578	269814;rs74871420;rs79268808
-	11	2245_2247	H700del|PBXIP1_	NM_020524	NP_065385	Q96AQ6	PBIP1_HUMAN	His-rich.	1	CCCCGGTGGTG	0.64	rs143592003
-	6	1004_1006	X1A_uc001gcw.1_	NM_177398	NP_796372	Q8TE12	LMX1A_HUMAN	y-Gln.|Gln-rich.	5	GATCTTGCTGCT	0.567	
+	16	4804	omh.1_Frame_Shi	NM_015172	NP_055987	Q9Y520	PRC2C_HUMAN		0	GGGATGAAAAAA	0.388	
+	7	1456_1457	_Ins_p.378_379ins	NM_005807	NP_005798	Q92954	PRG4_HUMAN	ats of K-X-P-X-P-T-T-X.|17	1	CTGCACCCACCA	0.653	rs149342058
+	7	1574_1576	e_Del_p.T418del|	NM_005807	NP_005798	Q92954	PRG4_HUMAN	ats of K-X-P-X-P-T-T-X.|21	1	GCACCCACCAC	0.645	
-	2	805	1hlg.3_Frame_Shi	NM_018040	NP_060510	Q9NW75	GPTC2_HUMAN		1	GGTCTGGTTCGT	0.313	
+	37	0073_1007	.S3343fs|OBSCN_	NM_001098623	NP_001092093	Q5VST9	OBSCN_HUMAN	Ig-like 33.	28	TACTCGTGTGTG	0.584	
-	20	2528_2530	E813del|SFMBT2_	NM_001029880	NP_001025051	Q5VUG0	SMBT2_HUMAN		8	AGTCTCTCCTCCT	0.596	
-	25	3723	_Shift_Del_p.D11	NM_033056	NP_149045	Q96QU1	PCD15_HUMAN	.|Extracellular (Potential).	13	GGAATCAGCTT	0.388	rs138363888
+	25	3716	_p.D924fs|ZMIZ1_	NM_020338	NP_065071	Q9ULJ6	ZMIZ1_HUMAN		4	CTGGACCCCCC	0.557	
+	3	410_412	ame_Del_p.I75del	NM_017787	NP_060257	Q9NX94	OPA1L_HUMAN	ical; (Potential).	1	TGGACCATCATC	0.606	
-	6	626		NM_005961	NP_005952	Q6W4X9	MUC6_HUMAN		1	TTGCCTGGGGTG	0.703	721287;rs63405860
+	25	8653_8655	del|DNHD1_uc00	NM_144666	NP_653267	Q96M86	DNHD1_HUMAN	Glu-rich.	2	GAGAGTgaggagga	0.507	
+	8	961	_p.Y171fs|PRMT3_	NM_005788	NP_005779	O60678	ANM3_HUMAN		0	CATATACCAAAAT	0.353	
-	24	2496_2498	PC3_uc010rhl.1_I	NM_000256	NP_000247	Q14896	MYPC3_HUMAN	nectin type-III 1.	3	GTAGCTCTTCTT	0.601	
+	5	886	rlo.1_Frame_Shift_	NM_004265	NP_004256	O95864	FADS2_HUMAN	lasmic (Potential).	2	GGCAGCCCATC	0.527	
-	4	1598_1600	.2_Intron|C11orf95	NM_001144936	NP_001138408	C9JLR9	CK095_HUMAN	-rich.|Glu-rich.	0	CACCCCActcctcct	0.547	
-	2	598_600	1orf95_uc001nxs.	NM_001144936	NP_001138408	C9JLR9	CK095_HUMAN	Glu-rich.	0	tcctcttcttcctcctcctc	0.532	
+	1	166		NM_003977	NP_003968	O00170	AIP_HUMAN		0	GGATCCAAAAAC	0.597	
+	3	285	zaa.1_Frame_Shi	NM_000073	NP_000064	P09693	CD3G_HUMAN	lar (Potential).|Ig-like.	0	GAAGATAAAAAA	0.403	
+	9	1502_1504		NM_005188	NP_005179	P22681	CBL_HUMAN	Glu-rich (acel(1)|p.E366_K	149	AAATTATGATGAT	0.473	
-	9	1657_1659	_554PP>P|IFFO1	NM_080730	NP_542768	Q0D2I5	IFFO1_HUMAN	Poly-Pro.	0	GCTTGGCGGCG	0.601	rs144019095
-	10	2162_2163		NM_001733	NP_001724	P00736	C1R_HUMAN	eptidase S1.	0	CTCCTCCATCTC	0.5	
-	3	441_442	.1_Intron|PRB1_u	NM_005039	NP_005030	P04280	PRP1_HUMAN	-[PAQ]-Q-[GE]-[GD]- [NKS]	0	TTTCCTGGAGGT	0.604	
-	3	812_814		NM_006248	NP_006239				0	TCCTGGAGGAG	0.606	
-	3	502_503		NM_006248	NP_006239				0	TTTCCTGGAGGT	0.594	
-	3	319_320		NM_006248	NP_006239				0	TTTCCTGGAGGT	0.614	
-	3	314_315		NM_006248	NP_006239				0	GGAGGTGGGG	0.614	
-	3	257_259		NM_006248	NP_006239				0	TCCTGGAGGAG	0.601	
-	4	730_731	.P215fs|IFLTD1_	NM_152590	NP_689803	Q8N9Z9	ILFT1_HUMAN		3	TGTTTGGAAGGA	0.371	
+	4	669	|FAR2_uc009zjm.	NM_018099	NP_060569	Q96K12	FACR2_HUMAN		0	GGAGCCAAAAAA	0.388	

+	11	1121	slz.1_Frame_Shif	NM_000725	NP_000716	P54284	CACB3_HUMAN		0	CTCCCGGGGGA	0.617	
+	2	347		NM_005430	NP_005421	P04628	WNT1_HUMAN		1	AGACTCCAAGA	0.562	
+	2	157	40B_uc001ruq.1_	NM_001031698	NP_001026868	Q6NWY9	PR40B_HUMAN	Pro-rich.	5	AGCTATCCCCCC	0.607	
+	27	4928		NM_002332	NP_002323	Q07954	LRP1_HUMAN	ntial).|LDL-receptor class	22	TGTACGGGGGG	0.587	rs139915490
-	5	654_655	_Shift_Del_p.L39fs	NM_139207	NP_631946	P55209	NP1L1_HUMAN		2	TTTTTGAGAGC	0.381	
-	6	1097	me_Shift_Del_p.R	NM_198521	NP_940923	Q96LP6	CL042_HUMAN		2	TGGGCGGGGG	0.587	
-	9	986		NM_001031701	NP_001026871	Q86UY8	NT5D3_HUMAN		3	GTCTTTCCCAAC	0.418	
+	35	3471_3472	C1_uc010taf.1_In	NM_014708	NP_055523	P50748	KNTC1_HUMAN		10	ATTGCTATTTCT	0.406	
-	25	3416	SBNO1_uc010taq	NM_018183	NP_060653	A3KN83	SBNO1_HUMAN		9	TTCCATTTTTTT	0.388	
+	1	998		NM_030979	NP_112241	Q9H361	PABP3_HUMAN	RRM 4.	4	GGAAAGCGTTT	0.408	
+	1	1058		NM_030979	NP_112241	Q9H361	PABP3_HUMAN	RRM 4.	4	GCAGCAAAGGG	0.428	
-	5	2069	ne_Shift_Del_p.L5	NM_183044	NP_898865	Q9Y252	RNF6_HUMAN		2	TTAGTAAAAAAA	0.403	
+	8	1137_1138	uqw.2_Frame_Shi	NM_006646	NP_006637	Q9UPY6	WASF3_HUMAN	Poly-Pro.	1	AGCCGCCCCC	0.678	rs141429361
+	3	707_710	vbk.2_Frame_Shi	NM_015116	NP_055931	Q9Y2L9	LRCH1_HUMAN	LRR 3.	2	CGCCCTGCCT	0.436	
+	20	3706_3707	.A881fs|LMO7_uc	NM_015842	NP_056667	Q8WWI1	LMO7_HUMAN		5	AGGCAGAGAG	0.386	
-	3	184	1zfl.2_5'Flank|TR	NM_002420	NP_002411	Q7Z4N2	TRPM1_HUMAN	ellular (Potential).	4	GCAGAGGGGG	0.507	
+	7	1140_1142	ame_Del_p.L345d	NM_024505	NP_078781	Q96PH1	NOX5_HUMAN	oreductase.|Helical; (Pote	2	CGCTCTGCTGC	0.626	
-	2	438_440	r.3_In_Frame_Del	NM_002693	NP_002684	P54098	DPOG1_HUMAN	Poly-Gln.	2	gctgctgttgctgctgct	0.458	
-	2	423_425	2dxs.2_In_Frame_	NM_006110	NP_006101	O95400	CD2B2_HUMAN		1	CCCCCCATCATC	0.532	
-	2	508_509	e_Ins_p.62_63ins	NM_002968	NP_002959	Q9NSC2	SALL1_HUMAN	Poly-Gly.	8	ccgccgccgctgctgc	0.46	rs113614842
+	8	759	p.G77fs|PLD2_uc	NM_002663	NP_002654	O14939	PLD2_HUMAN	PH.	5	TTCCTGGCCTC	0.617	
-	1	143_145	HX33_uc010clf.2_	NM_020162	NP_064547	Q9H6R0	DHX33_HUMAN		2	CCGGCCTCCTC	0.724	
+	8	912_914	.L222del|CHRNB1	NM_000747	NP_000738	P11230	ACHB_HUMAN	ical; (Potential).	2	GTTCCTGCTGC	0.498	
+	1	90_92		NM_001005271	NP_001005271	Q12873	CHD3_HUMAN		1	ggcgacgaggaggag	0.305	
+	13	2245_2247	.K762del|CHD3_u	NM_001005273	NP_001005273	Q12873	CHD3_HUMAN	Poly-Lys.	1	AGTATAAGAAGA	0.488	
+	4	1276_1278	SMCR7_uc010vx	NM_139162	NP_631901	Q96C03	SMCR7_HUMAN		0	GGCGGCTGCTG	0.685	
+	6	1142_1143	WSB1_uc002gze.	NM_015626	NP_056441	Q9Y6I7	WSB1_HUMAN	WD 5.	0	CATCTTATGATA	0.391	
+	3	202_204	10crt.2_In_Frame_	NM_003170	NP_003161	Q7KZ85	SPT6H_HUMAN	sp/Glu-rich.	3	AGATGAGGAGG	0.453	
+	1	158_160	me_Del_p.K7del|	NM_003457	NP_003448	O43670	ZN207_HUMAN		0	TCGCAAGAAGA	0.542	
+	10	1539		NM_001254	NP_001245	Q99741	CDC6_HUMAN		3	GATGGTAACAG	0.428	
-	1	96_98	_5'Flank|TMEM9	NM_000421	NP_000412	P13645	K1C10_HUMAN	ead.|Gly-rich.	0	ctccacatcctcctcct	0.409	
-	5	975_976		NM_012285	NP_036417	Q9UQ05	KCNH4_HUMAN	lasmic (Potential).	1	CGAGACCCCC	0.604	
+	8	1687	T2_uc010dbo.2_	NM_022167	NP_071450	Q9H1B5	XYLT2_HUMAN	enal (Potential).	1	AGCTACCCCCC	0.602	
+	1	488_490	E148del|BPTF_uc	NM_182641	NP_872579	Q12830	BPTF_HUMAN	Glu-rich.	4	gtctccgaggaggag	0.473	
+	14	1870_1871	.Q561fs|ITGB4_u	NM_000213	NP_000204	P16144	ITB4_HUMAN	tial).|Cysteine-rich tandem	4	GGCCAGTGTGT	0.604	rs121912463
-	6	817	p.Q195fs|SS18_u	NM_001007559	NP_001007560	Q15532	SSXT_HUMAN	Gln-rich.	1884	TCTCTGACCCA	0.423	
+	8	995	DR7_uc002lgl.1_	NM_015285	NP_056100	Q9Y4E6	WDR7_HUMAN		3	GGACCGGGGG	0.418	
-	4	1782		NM_052947	NP_443179	Q86TB3	ALPK2_HUMAN		14	AGTCCTTTCCC	0.522	
+	2	143_144	|CCDC159_uc010	NM_001080503	NP_001073972	P0C7I6	CC159_HUMAN		1	CTCTGGAGCGT	0.639	rs142796564
-	5	915_916	Ins_p.Q261fs|EC	NM_016581	NP_057665	Q9BQ95	ECSIT_HUMAN		1	GGGCTGGGGG	0.584	
-	3	330	_Shift_Del_p.P38f	NM_025249	NP_079525	Q9H0B3	K1683_HUMAN		2	TGAGCGGGGGC	0.622	rs116770984
-	1	207_208	ad.1_Frame_Shif	NM_198538	NP_940940	Q6UWP8	SBSN_HUMAN		1	CCCACCTCTCTC	0.579	
+	2	648_650	egn.1_In_Frame_	NM_003407	NP_003398	P26651	TTP_HUMAN	P-P-P-P-G.	1	ACCTCACCACC	0.685	
+	13	1226_1228	Frame_Del_p.S32	NM_007056	NP_008987	Q8N2M8	CLASR_HUMAN	r-rich.|Arg-rich.	0	CCGCCGctcctcc	0.522	
+	4	656_658	E183del|KLC3_uc	NM_177417	NP_803136	Q6P597	KLC3_HUMAN	Poly-Glu.	1	CAGCGAGGAGG	0.645	
+	8	2997	2phi.3_Frame_Sh	NM_015711	NP_056526	Q9NZM4	GSCR1_HUMAN	Poly-Pro.	3	CAGCACCCCCC	0.672	
+	5	2209_2210	c002pxc.1_5'Flan	NM_007147	NP_009078	Q9Y473	ZN175_HUMAN		0	ACACTAGAGAGA	0.436	

+	16	2225	OT3_uc002qdk.1_	NM_014516	NP_055331	O75175	CNOT3_HUMAN	Pro-rich.	3	GTACCTCCCCCG	0.617	rs145720928
-	1	324_326		NM_012344	NP_036476	O95665	NTR2_HUMAN	Name=2; (Potential).	0	CGACCAGCAGC	0.591	
-	1	1978_1980	KIF3C_uc010ykr.1_	NM_002254	NP_002245	O14782	KIF3C_HUMAN	y-Asn.|Potential.	4	CGGTGGTTGTTG	0.621	
-	4	596	ynd.1_5'Flank|FAI	NM_015475	NP_056290	Q8NCA5	FA98A_HUMAN		1	TCTTACTTTTTTT	0.338	
+	13	1538	F1_uc002txn.2_Fra	NM_018151	NP_060621	Q5UIP0	RIF1_HUMAN		15	CCTTCCTTTTTTT	0.343	
-	11	1904_1905	_p.F546fs|FN1_uc	NM_212482	NP_997647	P02751	FINC_HUMAN	ding.|Fibronectin type-I 8.	13	CTGACCGAAGCA	0.49	
+	7	931	.1_Frame_Shift_D	NM_000578	NP_000569	P49279	NRAM1_HUMAN	ical; (Potential).	4	GGAAGCTTTTTTT	0.418	
-	33	5621_5622	IIR375_hsa-mir-37	NM_194302	NP_919278	Q6ZU64	CC108_HUMAN	Glu-rich.	4	TCCTTCTCGTCC	0.604	
+	2	1083_1085		NM_024893	NP_079169	Q9H7V2	SYNG1_HUMAN	Cytoplasmic (Potential).	0	ATGTGGAGGAGC	0.547	
-	4	1604		NM_052846	NP_443078	Q9NT22	EMIL3_HUMAN		1	TCCCCACCCCCC	0.637	
-	3	293	C3_uc002xph.1_R	NM_080614	NP_542181	Q8IUB2	WFDC3_HUMAN	WAP 2.	0	ATACCCTTAGGA	0.527	
-	2	597	Shift_Del_p.Q166f	NM_020436	NP_065169	Q9UJQ4	SALL4_HUMAN		2	GTCCTGGGGGGT	0.577	
-	1	119		NM_181619	NP_853650	Q3LI58	KR211_HUMAN		1	caaacccacagccata	0.134	
-	3	356	N2_uc003apl.1_R	NM_012473	NP_036605	Q99757	THIOM_HUMAN	Thioredoxin.	0	GATCTTGCAGGG	0.552	
+	7	2100_2108	atq.1_In_Frame_D	NM_001039141	NP_001034230	Q9H2D6	TARA_HUMAN		1	AGCCTCCAGAAC	0.579	
+	5	474	2_3'UTR|POLR2F_	NM_021974	NP_068809	P61218	RPAB2_HUMAN		1	AGACTGGGGGGT	0.512	
-	13	2272_2274	p.2_In_Frame_Del	NM_001098504	NP_001091974	Q92841	DDX17_HUMAN	Poly-Pro.	4	ggagggggaggagga	0.36	
+	2	1222	gxy.2_Frame_Shif	NM_002409	NP_002400	Q09327	MGAT3_HUMAN	nenal (Potential).	0	GCGTCCTTTTCCT	0.642	
+	3	406_408	me_Del_p.E76del|	NM_012324	NP_036456	Q13387	JIP2_HUMAN	Glu-rich (acidic).	3	gaggaagaggaggag	0.483	
-	1	205_207	vg.1_In_Frame_De	NM_004628	NP_004619	Q01831	XPC_HUMAN	lu.|Glu-rich (acidic).	3	CTCACCCTCCTCC	0.734	rs72561774
-	27	3223	t.2_RNA|CLASP2_	NM_015097	NP_055912	B2RTR1	B2RTR1_HUMAN		4	CACCCATTTTTTT	0.343	
-	9	2297		NM_022842	NP_073753	Q9H5V8	CDCP1_HUMAN	lasmic (Potential).	3	TGAAACTTTTTTG	0.468	
-	11	2929	_p.S552fs|MAP4_u	NM_002375	NP_002366	P27816	MAP4_HUMAN		3	GCTCTTGGACCCA	0.577	
-	18	2397_2399	cwp.2_In_Frame_I	NM_003363	NP_003354	Q13107	UBP4_HUMAN		4	TGTGGTCTTCTTC	0.532	
+	2	195_197	4L2_uc003dbh.2_	NM_015106	NP_055921	Q9Y4B4	ARIP4_HUMAN		3	gcggaagaggaggag	0.429	
-	24	2792	hift_Del_p.P714fs	NM_002218	NP_002209	Q14624	ITIH4_HUMAN		3	CTCCCGGGGGC	0.582	rs140372968
-	2	584_586		NM_016206	NP_057290	A8MV65	VGLL3_HUMAN		0	TGGtctttctcctcctcc	0.394	
+	1	277_278		NM_001005514	NP_001005514	A6NHG9	O5H14_HUMAN	cellular (Potential).	1	ATGATATCTCTCTC	0.391	
+	7	1308	_Shift_Del_p.P256f	NM_001627	NP_001618	Q13740	CD166_HUMAN	Potential).|Ig-like C2-type 1.	3	GCCACCAAAAAAT	0.408	
+	3	425_426	F2_uc003eeo.2_In	NM_018456	NP_060926	Q96CJ1	EAF2_HUMAN		0	CACTGTAAAAAA	0.243	
+	1	1441		NM_002563	NP_002554	P47900	P2RY1_HUMAN	cellular (Potential).	1	TCACCTGTTACGA	0.537	
-	3	530_531	|UGDH_uc003gul.1	NM_003359	NP_003350	O60701	UGDH_HUMAN		4	TGGTAGAAAAAA	0.297	
-	6	542	AD2_uc003gyu.2_I	NM_001014446	NP_001014446	Q56VL3	OCAD2_HUMAN	OCIA.	0	ATCTTCAAAAAAA	0.393	
+	3	351		NM_006583	NP_006574	O14718	OPSX_HUMAN	Name=3; (Potential).	1	TGAATATTTTTTT	0.393	
-	17	2126	.2_Frame_Shift_D	NM_144643	NP_653244	Q96NL6	SCLT1_HUMAN	Potential.	5	TTTGGCTTTTTTT	0.353	
-	8	596_598	3ijz.3_In_Frame_I	NM_001102653	NP_001096123	Q01804	OTUD4_HUMAN		3	ACATCAGCAGCA	0.34	
+	20	2289_2291	10isc.2_In_Frame_	NM_021942	NP_068761	Q7Z392	CD041_HUMAN		0	GCAGGGAGGAGC	0.463	
+	20	6893_6895	jhm.2_In_Frame_I	NM_178140	NP_835260	O15018	PDZD2_HUMAN	Ser-rich.	9	TGGCGTCCTCCTC	0.527	744453;rs75551718
+	7	1394		NM_002439	NP_002430	P20585	MSH3_HUMAN		4	GGGACAAAAAAA	0.348	
+	2	237_240	_p.K19fs|AP3S1_u	NM_001284	NP_001275	Q92572	AP3S1_HUMAN		0	ATCTAAGAGAGA	0.304	rs80118146
+	3	465	XL21_uc003lbc.2_F	NM_012159	NP_036291	Q9UKT6	FXL21_HUMAN		1	GACCTTGGGCTT	0.428	
-	20	2629_2630	2_Intron|BRD8_uc	NM_139199	NP_631938	Q9H0E9	BRD8_HUMAN		1	TACAAAGAGAGA	0.505	
-	3	326		NM_145266	NP_660309	Q8WVJ2	NUDC2_HUMAN		0	TCCTCTAAAAAA	0.282	
+	5	668_670	3mdf.1_In_Frame_	NM_006650	NP_006641	Q6PUV4	CPLX2_HUMAN		1	GGACGAGGAGG	0.645	
+	7	2110	orf25_uc003mdr.3_RNA|C5orf25_uc003mdv.2_Frame_S			Q8NDZ2	CE025_HUMAN		0	GAGTCCTTTTCCT	0.488	
-	2	159	e_Shift_Del_p.L9fs	NM_018303	NP_060773	Q96KP1	EXOC2_HUMAN	IPT/TIG.	7	TCACAAGGGGGG	0.483	
+	1	422_423	AN4_uc011dlb.1_5	NM_001007531	NP_001007532	Q5M9Q1	NKAPL_HUMAN		2	TGAAGGAGAGAC	0.535	

+	4	957	nkz.2_Frame_Shif	NM_032507	NP_115896	Q96JS3	PGBD1_HUMAN		4	CCAGGAAAAAA	0.502	
-	2	381_382	3nnl.3_Frame_Shif	NM_001109809	NP_001103279	Q9NU63	ZFP57_HUMAN	KRAB.	5	TTCTTAAAGGTT	0.525	
+	5	799	_uc003nnz.3_Frar	NM_002127	NP_002118	P17693	HLAG_HUMAN	ar (Potential).|Alpha-3.	4	TCAGACCCCCC	0.537	
-	5	1557_1559	6_377EE>E|DAX	NM_001350	NP_001341	Q9UER7	DAXX_HUMAN	ial.|Necessary for interactic	23	tcttcttcttcctcctcctc	0.251	
+	1	499_501	_Del_p.17_18LL>	NM_006586	NP_006577	Q9BT09	CNPY3_HUMAN		1	CTTCCCTtgctgctg	0.606	
-	8	1152	p.K221fs|ICK_uc0	NM_016513	NP_057597	Q9UPZ9	ICK_HUMAN	rotein kinase.	5	ATTACCTTTTTTG	0.502	
+	9	1431	X43_uc011dyn.1_	NM_018665	NP_061135	Q9NXZ2	DDX43_HUMAN	ase ATP-binding.	4	GAGCTTAAAAAA	0.323	
-	3	477	SLC17A5_uc011dy	NM_012434	NP_036566	Q9NRA2	S17A5_HUMAN	ical; (Potential).	6	GCCATAAAAAAA	0.423	
+	22	2625_2626	jb.3_Frame_Shift_	NM_003318	NP_003309	P33981	TTK_HUMAN	p.R838fs*4(3)	11	CTTTTGAAAAAA	0.302	
+	11	1515	_p.K287fs|C6orf1	NM_001031743	NP_001026913	Q8IYR0	CF165_HUMAN		1	AAGGCCAAAAAA	0.269	
-	1	195_197	ob.1_In_Frame_	NM_145331	NP_663304	O43318	M3K7_HUMAN	Poly-Ser.	6	AGACGAGGAGG	0.655	
-	7	1235_1236	edm.1_Frame_Shi	NM_000416	NP_000407	P15260	INGR1_HUMAN	lasmic (Potential).	1	AAGAACTCTCTC	0.431	
-	1	307_309		NM_175747	NP_786923	Q7RTU3	OLIG3_HUMAN	Poly-His.	0	tggtggtggcggtggtg	0.488	
+	2	498	uc003qid.1_5'Flan	NM_015439	NP_056254	Q8IWP9	CC28A_HUMAN		0	AATGCCAAAAAA	0.413	
+	9	3753_3755	2_3'UTR|GRM1_u	NM_000838	NP_000829	Q13255	GRM1_HUMAN	dic).|Cytoplasmic (Potentia	19	CGCGGACGACG	0.65	
+	26	3025_3026	ame_Shift_Ins_p.D	NM_015440	NP_056255	Q6UB35	C1TM_HUMAN	hydrofolate synthetase.	4	CCTGACAAAAAA	0.48	
+	6	694_695	p.L112fs|ZDHHC4	NM_001134388	NP_001127860	Q9NPG8	ZDHC4_HUMAN	ical; (Potential).	2	AACCTGTTTTTT	0.45	
+	4	1034_1036		NM_001159279	NP_001152751				2	CCGCTCTTCAA	0.419	
-	5	964	2_Intron|GPC2_u	NM_152742	NP_689955	Q8N158	GPC2_HUMAN		2	GGGGACCCCCC	0.642	
-	9	2023_2025		NM_022574	NP_072096	O75420	PERQ1_HUMAN	Poly-Glu.	2	AGGTTCCTCCT	0.675	rs142340746
+	5	927_929	10ljz.1_In_Frame_	NM_014491	NP_055306	O15409	FOXP2_HUMAN	Gln-rich.	8	cagcaacagcagcag	0.172	
-	7	1685_1687	1kvs.1_In_Frame_	NM_007349	NP_031375	Q6ZW49	PAXI1_HUMAN	Gln-rich.	5	TTTGCATctgctgct	0.227	
+	11	2081_2082	kvv.1_Frame_Shif	NM_053043	NP_444271	Q96EV2	RBM33_HUMAN	Pro-rich.	1	CTGCCCACACAC	0.53	
+	4	381	p.K105fs|MCPH1_	NM_024596	NP_078872	Q8NEM0	MCPH1_HUMAN		2	CTAATTAAAAAA	0.274	
-	4	4130_4131		NM_178857	NP_849188	Q8IWN7	RP1L1_HUMAN		8	ATTGCACCTCTT	0.297	
-	7	1394_1395	ss.2_Frame_Shift_	NM_139167	NP_631906	Q96LD1	SGCZ_HUMAN	ellular (Potential).	3	CCTTCTGTAGAT	0.505	
+	3	289_290	_p.S58fs|ERLIN2_	NM_007175	NP_009106	O94905	ERLN2_HUMAN	enal (Potential).	0	ACATCATATAAG	0.515	
-	4	3431	ame_Shift_Del_p.	NM_001002814	NP_001002814	Q6WKZ4	RFIP1_HUMAN		3	TGTGGCTTTTTT	0.542	
-	18	3959	.E1139fs|MYST3_	NM_001099412	NP_001092882	Q92794	MYST3_HUMAN		7	TGGCTCAAGAG	0.428	
-	20	3283_3284	Shift_Del_p.Q419f	NM_006421	NP_006412	Q9Y6D6	BIG1_HUMAN		8	AATCTTGTAGAC	0.337	
+	17	2019	me_Shift_Del_p.F	NM_052832	NP_439897	Q8TE54	S26A7_HUMAN	toplasmic (Potential).	2	TTTACCTTTTTTG	0.403	
+	2	969		NM_030788	NP_110415	Q9H295	TM7S4_HUMAN	ical; (Potential).	4	CATCTGGGTGC	0.468	
-	13	1698	D2_uc003yqi.3_R	NM_014109	NP_054828	Q6PL18	ATAD2_HUMAN		2	TTCGTCAAAAAA	0.413	
+	28	3908	uc003yqy.1_Intron	NM_001039112	NP_001034201	Q2WGJ9	FR1L6_HUMAN	lasmic (Potential).	11	AAGGGAAAAAA	0.388	
-	12	2033		NM_152888	NP_690848	Q8NFW1	COMA1_HUMAN	ly-rich.|Collagen-like 2.	13	CACCCTTTTCCC	0.463	
-	30	4625	ae.1_Splice_Site_	NM_201380	NP_958782	Q15149	PLEC_HUMAN		9	CTGTACCTCCTC	0.621	
+	2	492_493	p.F109fs|GRINA_	NM_001009184	NP_001009184	Q7Z429	GRINA_HUMAN	Pro-rich.	1	CCCCTTCCCCCC	0.683	
+	11	1303_1304	p.C375fs|ADAMT	NM_001040272	NP_001035362	Q8N6G6	ATL1_HUMAN	TSP type-1 2.	5	TCGTGTGGGGG	0.584	
-	7	1190_1192	kh.1_5'UTR|VCP_	NM_007126	NP_009057	P55072	TERA_HUMAN		1	GATCAAGAAGA	0.463	
-	17	2544_2546	841del|RALGDS_	NM_006266	NP_006257	Q12967	GNDS_HUMAN	sociating.|Poly-Glu.	3	CCGGCTCCTCC	0.606	rs35200098
+	13	2110_2112	E598del|GRIN1_u	NM_007327	NP_015566	Q05586	NMDZ1_HUMAN	lasmic (Potential).	1	CAGCGAGGAGG	0.739	
-	4	458_459		NM_138462	NP_612471	Q96E35	ZMY19_HUMAN		1	GCCACGCCCCC	0.634	
-	9	1366	R3B_uc004cpf.2_	NM_013239	NP_037371	Q9Y5P8	P2R3B_HUMAN	EF-hand.	0	TCGGTGTTTTTT	0.567	
-	1	581	1L2_uc011mqj.1_	NM_021963	NP_068798	Q9ULW6	NP1L2_HUMAN		1	CCACCTTTTTTC	0.498	
-	1	1805_1806		NM_003604	NP_003595	O14654	IRS4_HUMAN		10	CCTTTGCCCCCC	0.545	
+	20	3644	me_Shift_Del_p.A	NM_001001344	NP_001001344	Q16720	AT2B3_HUMAN	lasmic (Potential).	1	CCGGGCCCCCC	0.587	rs149428057
-	5	924_925	RIQ3_uc001dfz.3_	NM_001105659	NP_001099129	A6PVS8	LRIQ3_HUMAN		2	CTGCTGTTTTTT	0.327	

+	2	286_288	me_Del_p.Q49del|	NM_030965	NP_112227	Q9BVH7	SIA7E_HUMAN	.|Lumenal (Potential).	2	GCCCCCgcagcag	0.581	rs113832855
-	7	878	otn.1_Frame_Shift	NM_000350	NP_000341	P78363	ABCA4_HUMAN	Extracellular.	12	AGTGTGGGAAG	0.368	
+	5	713	oyy.1_Frame_Shif	NM_006099	NP_006090	Q9Y6X2	PIAS3_HUMAN	PINIT.	1	TATTTTCCCCCC	0.463	
-	13	1861	0pac.1_Intron|NBF	NM_017940	NP_060410	Q86T75	NBPFB_HUMAN	NBPF 3.	0	TCCTCCTTTTTC	0.463	
-	2	3390_3392	vne.1_In_Frame_D	NM_007113	NP_009044	Q07283	TRHY_HUMAN	30 AA tandem repeats.	5	ggcgccttctcttctccc	0.241	
+	9	1814_1815	1_Frame_Shift_De	NM_170707	NP_733821	P02545	LMNA_HUMAN	Tail.	2	GGCTGCGGGA	0.624	rs149339264
-	1	356_358		NM_030916	NP_112178	Q96NY8	PVRL4_HUMAN		2	CAGTAGCAGCA	0.512	
+	7	1210_1211	_Ins_p.294_295ins	NM_005807	NP_005798	Q92954	PRG4_HUMAN	K-X-P-X-P-T-T-X.|6; appro	1	CCACCAAGTCTG	0.634	
-	8	1247		NM_001618	NP_001609	P09874	PARP1_HUMAN		10	TTTCTGGGGG	0.502	
+	1	255		NM_001004698	NP_001004698	A6NFC9	OR2W5_HUMAN		3	AACCTGGGGGG	0.532	
-	1	2290	vw.1_RNA|PGR_u	NM_000926	NP_000917	P06401	PRGR_HUMAN	ulating, Pro-Rich.	4	TGAGGCCGAGT	0.622	
-	23	3960	qie.1_Frame_Shift_	NM_001042603	NP_001036068	P29375	KDM5A_HUMAN	PHD-type 2.	3	GGATCCTTTTTT	0.478	
-	3	539_541		NM_006248	NP_006239				0	GGACTTGTTGT	0.596	
-	2	1302	raq.2_Frame_Shift	NM_006143	NP_006134	Q15760	GPR19_HUMAN	lasmic (Potential).	1	ACGTAGTTTTTT	0.398	
+	9	808_809	rame_Shift_Del_p	NM_020183	NP_064568	Q8WYA1	BMAL2_HUMAN		2	AAGTTCACAGTA	0.396	
-	15	2654	vfj.2_Frame_Shift_	NM_012141	NP_036273	Q9UL03	INT6_HUMAN		2	TGGTCCTTTTCC	0.398	
+	3	540_541	tka.1_Frame_Shi	NM_005561	NP_005552	P11279	LAMP1_HUMAN	ntial).|First lumenal domain	2	CTTCTGACCCC	0.436	
+	3	1978	_p.L550fs|ZNF828_	NM_001164144	NP_001157616	Q96JM3	ZN828_HUMAN	quired for the attachment o	2	TGCCCTTTTTCC	0.517	
+	9	960_962	ne_Del_p.E294del	NM_001099661	NP_001093131	B5ME19	B5ME19_HUMAN		0	GGATGAGGAGG	0.562	
+	2	942	Frame_Shift_Del_	NM_145239	NP_660282	Q7Z6L0	PRRT2_HUMAN	ar (Potential).|Pro-rich.	0	TGGGGCCCCCC	0.652	
-	14	1558	uc002hkz.1_5'Flan	NM_001001417	NP_001001417	Q8IZP1	TBC3A_HUMAN		0	ATGGCGGAACC	0.642	
-	2	513	BXO17_uc002okf	NM_024907	NP_079183	Q96EF6	FBX17_HUMAN	FBA.	0	CTCCGCAGGAG	0.532	
-	3	316	_p.P92fs|HS1BP3	NM_022460	NP_071905	Q53T59	H1BP3_HUMAN	PX.	1	GTAGTGGGGGG	0.537	rs77941615
+	30	3643_3645	k.2_In_Frame_De	NM_003494	NP_003485	O75923	DYSF_HUMAN	ic (Potential).|Arg-rich.	7	CCTTCCGCCGC	0.655	
+	6	1148		NM_173511	NP_775782	Q6P1L5	F117B_HUMAN		1	CTCCACCCCCC	0.488	
+	1	182_184	P_uc002vsr.2_5'F	NM_001632	NP_001623	P05187	PPB1_HUMAN		1	CCCTGCAtgctgct	0.542	
+	1	270_272	2wil.2_In_Frame_	NM_139321	NP_647537	O75882	ATRN_HUMAN	Leu-rich.	2	GCCACGgctgctg	0.424	
-	32	3210_3211		NM_014258	NP_055073	Q9BX26	SYCP2_HUMAN		5	TTTATAGTTTTTT	0.327	
-	5	575_592	RT_uc002yry.2_In	NM_000819	NP_000810	P22102	PUR2_HUMAN	similarity).|ATP-grasp.	1	GACCACTGGCCT	0.422	
+	8	833_835	zek.2_In_Frame_	NM_002626	NP_002617	P17858	K6PL_HUMAN		0	CTGAACATCATC	0.655	
-	4	571_573	j.1_RNA|PTTG1IP	NM_004339	NP_004330	P53801	PTTG_HUMAN	ytoplasmic (Potential).	1	TCCTGCAGCAG	0.616	
-	15	2101	_p.V281fs|TOP3B_	NM_003935	NP_003926	O95985	TOP3B_HUMAN		1	GGAGCACCAGCT	0.642	
-	3	591	_p.G163fs|DDX17_	NM_001098504	NP_001091974	Q92841	DDX17_HUMAN		4	ACATCTCCCCCC	0.378	
+	2	1890	.3_Intron|SYNGR	NM_006116	NP_006107	Q15750	TAB1_HUMAN		1	TGGGACCCCCC	0.592	
+	2	1293_1295	y.3_RNA|LNP1_uc	NM_001085451	NP_001078920	A1A4G5	LNP1_HUMAN	Poly-Asp.	0	ACAAAGATGATG	0.507	
+	10	1570_1572	3fns.2_In_Frame_	NM_198241	NP_937884	Q04637	IF4G1_HUMAN	Poly-Glu.	7	GAAATGgaagaag	0.443	
-	2	1333		NM_004488	NP_004479	P40197	GPV_HUMAN	lar (Potential).|LRRCT.	3	AGCCACCCCAG	0.756	
+	7	528_529	_p.C62fs|TMEM17	NM_032326	NP_115702	Q9BSA9	TM175_HUMAN	ical; (Potential).	0	TGTTCTGTGTGT	0.406	
+	1	3102_3103		NM_175918	NP_787114	Q8N1N5	CRPAK_HUMAN	1	0	CACACATGCCCA	0.644	rs144787346
+	1	3561_3562		NM_175918	NP_787114	Q8N1N5	CRPAK_HUMAN	5	0	CTGCTCACACGT	0.658	
-	8	1326	el_p.T164fs|NOP	NM_003703	NP_003694	P78316	NOP14_HUMAN		1	GTCTCTGGTAGC	0.537	
+	16	4429_4430	_p.G527fs|RGS12_	NM_198229	NP_937872	O14924	RGS12_HUMAN		1	ATTGGGAAAAA	0.332	
+	3	338_339		NM_021225	NP_067048	Q99935	PROL1_HUMAN	Pro-rich.	1	TGACTCAAGACT	0.495	
-	11	1436_1438	hnj.2_In_Frame_D	NM_001077207	NP_001070675	O94979	SC31A_HUMAN	ction with SEC13.	8	ATGGTGCTGCT	0.448	843621;rs140634448
+	29	7437_7438	jcl.1_Frame_Shift_	NM_005509	NP_005500	Q9Y485	DMXL1_HUMAN		2	ACTGGCGGTTA	0.421	rs17144964
+	1	1338_1340		NM_001453	NP_001444	Q12948	FOXC1_HUMAN	Poly-Gly.	1	GAGTCAcggcggc	0.537	
-	4	1405_1407	.E433del|TUBB2A	NM_001069	NP_001060	Q13885	TBB2A_HUMAN		1	TCGCCCTCCTC	0.532	

-	4	1510_1512	_Frame_Del_p.E36	NM_178012	NP_821080	Q9BVA1	TBB2B_HUMAN			1	TCGCCCTCCTC	0.65	
+	5	770_774	11dme.1_Intron|HLA-J_uc003nou.3_RNA|HLA-J_uc003nov.3_RNA							0	CTGACTTCTCTT	0.488	
-	5	559		NM_000846	NP_000837	P09210	GSTA2_HUMAN	ST C-terminal.		1	TTTTTCAAAGGC	0.433	
-	5	501		NM_145740	NP_665683	P08263	GSTA1_HUMAN	ST C-terminal.		1	TAGCGATTTTTT	0.433	
-	8	1152	p.K221fs|ICK_uc0	NM_016513	NP_057597	Q9UPZ9	ICK_HUMAN	rotein kinase.		5	ATTACCTTTTTG	0.502	
+	5	1030_1031	pre.2_Frame_Shif	NM_001198	NP_001189	O75626	PRDM1_HUMAN			56	AGGACCTCTACC	0.475	
+	26	3025_3026	ame_Shift_Ins_p.D	NM_015440	NP_056255	Q6UB35	C1TM_HUMAN	hydrofolate synthetase.		4	CCTGACAAAAAA	0.48	
+	6	695	p.F113fs|ZDHHC4	NM_001134388	NP_001127860	Q9NPG8	ZDHC4_HUMAN	ical; (Potential).		2	AACCTGTTTTTTT	0.453	
+	10	1740	LF1_uc003xyf.2_F	NM_015170	NP_055985	Q8IWU6	SULF1_HUMAN			7	TGTGCCTTTTTT	0.408	
+	17	2351	gr.1_RNA|INTS8_	NM_017864	NP_060334	Q75QN2	INT8_HUMAN			0	GTTTAATAAAACA	0.363	
-	11	2666_2668		NM_015117	NP_055932	Q8IXZ2	ZC3H3_HUMAN	Poly-Ser.	p.S879F(1)	1	aggggatgaggaggag	0.552	;rs2272753;rs137878905
+	8	1061	OFD1_uc004cvs.3	NM_003611	NP_003602	O75665	OFD1_HUMAN	Potential.		0	GAAGCAAAAAA	0.299	
+	20	2671_2673	.E837del|CNKSR2	NM_014927	NP_055742	Q8WXI2	CNKR2_HUMAN	ential.|Poly-Glu.		2	gaggaagaggaggag	0.379	
-	14	4550		NM_000132	NP_000123	P00451	FA8_HUMAN	B.		11	AGGTTATTTTTTT	0.413	
+	5	533	|PUSL1_uc010ny	NM_153339	NP_699170	Q8N0Z8	PUSL1_HUMAN			1	GGAAGCCGCCC	0.716	
+	3	360	jf.1_Nonsense_Mu	NM_007033	NP_008964	O15258	RER1_HUMAN	ical; (Potential).		0	ATGATTCGAGTTT	0.522	
-	49	6990	sc.2_Missense_Mu	NM_004958	NP_004949	P42345	MTOR_HUMAN	PI3K/PI4K.		29	TGACGGCATGCT	0.567	
+	11	2509	asi.1_Nonsense_M	NM_020780	NP_065831	Q9P2K9	PTHD2_HUMAN	cellular (Potential).		7	TGTTCCAGGAG	0.652	
+	3	512	.2_Missense_Muta	NM_033182	NP_149438	Q9H4M3	FBX44_HUMAN	FBA.		1	TTACTTCATATTA	0.527	
+	4	897	aug.1_Missense_	NM_001103170	NP_001096640	Q5VUY0	ADCL3_HUMAN			0	GTCTGGGAAAAG	0.478	
-	1	370	0obf.1_Missense_	NM_001146181	NP_001139653	B7ZW38	B7ZW38_HUMAN			0	TTTCCTCGGTTC	0.483	
-	1	273		NM_001136561	NP_001130033	B2RXH8	B2RXH8_HUMAN			0	TTTTCTCCTTATC	0.478	
-	10	1420	F1_uc001ayz.1_5'	NM_017940	NP_060410	Q3BBV0	NBPF1_HUMAN	NBPF 1.		0	AGCCTCCTCAA	0.438	
+	6	656		NM_016183	NP_057267	Q9UKD2	MRT4_HUMAN			0	CTTTCACTGTGA	0.587	
-	8	603_604	bew.2_Missense_	NM_002885	NP_002876	P47736	RPGP1_HUMAN			3	CTTGAGTGAGAA	0.604	
+	11	1401	AL3_uc009vrc.2_M	NM_020448	NP_065181	Q6P499	NPAL3_HUMAN			0	TTTGAGCCCTATA	0.448	
-	9	1071	ble.3_Missense_M	NM_000437	NP_000428	Q99487	PAFA2_HUMAN			2	GGCACATATCTT	0.483	
-	4	960	n_p.T281I|ZNF683	NM_173574	NP_775845	Q8IZ20	ZN683_HUMAN			0	AGTCGGTTGGG	0.647	
+	9	861	p.S255F|KPNA6_	NM_012316	NP_036448	O60684	IMA7_HUMAN	ARM 5.		0	TACTGTCTCGCC	0.507	
+	2	1044	p.P395L|GJA4_uc	NM_002060	NP_002051	P35212	CXA4_HUMAN	lasmic (Potential).		1	AAAAACCCCCAA	0.582	
-	4	395	ax.1_Missense_M	NM_000760	NP_000751	Q99062	CSF3R_HUMAN	e.|Extracellular (Potential).		3	CCTGCCCCCGG	0.602	
+	11	1439		NM_015284	NP_056099	Q5T011	SZT2_HUMAN			0	GGCTTCCCAGA	0.562	
+	7	1020	AH_uc001cpv.2_In	NM_001441	NP_001432	O00519	FAAH1_HUMAN	smic (By similarity).		2	CCTTGCCCTTCA	0.662	
+	3	764		NM_182532	NP_872338	Q8N0U2	TMM61_HUMAN			0	GGGATGCCCTG	0.637	
+	11	1803		NM_000562	NP_000553	P07357	CO8A_HUMAN	TSP type-1 2.		3	CAGGAAAGGAG	0.572	
-	44	3706	.E1142K|COL11A1	NM_001854	NP_001845	P12107	COBA1_HUMAN	le-helical region.		12	CAATTTCACCCT	0.318	
+	7	2014	v.3_Missense_Mut	NM_172212	NP_757351	P09603	CSF1_HUMAN	lasmic (Potential).		1	ATTCTCCCTTGG	0.637	
-	11	1869	p.P567S|OVGP1_	NM_002557	NP_002548	Q12889	OVGP1_HUMAN			5	CCTGGGGTGAG	0.517	
+	7	1205	p.P342S|MAGI3_	NM_001142782	NP_001136254	Q5TCQ9	MAGI3_HUMAN	WW 2.		6	GAGCTTCCTTATG	0.328	
-	6	1367	eu.2_Missense_Mu	NM_205848	NP_995320	Q5T7P8	SYT6_HUMAN	mic (Potential).|C2 2.		5	ATTGTGGCCCA	0.592	
+	11	951	se_Mutation_p.E2	NM_003176	NP_003167	Q15431	SYCP1_HUMAN	Potential.		1	GATTATGAAAAA	0.229	
-	29	4314		NM_206996	NP_996879	Q6Q759	SPG17_HUMAN			6	CAATGGGGTCA	0.398	
-	28	5279		NM_024408	NP_077719	Q04721	NOTC2_HUMAN	ion (NRR).|Extracellular (P		27	AGTGCGTTCTG	0.443	
+	23	2720	010oyd.1_Missens	NM_001037675	NP_001032764	Q3BBV1	NBPFK_HUMAN	NBPF 7.		0	CTGGATGGATGT	0.463	rs28736716
+	1	282		NM_017860	NP_060330	Q9BUN1	CA056_HUMAN			0	TGGCCGACGCC	0.657	
-	14	2518	.Q694E|POGZ_u	NM_015100	NP_055915	Q7Z3K3	POGZ_HUMAN			3	CTTCTGGATGCT	0.557	
-	8	1274	RC_uc010pdo.1_M	NM_005060	NP_005051	P51449	RORG_HUMAN	gand-binding.		2	AGGCTCGGAAC	0.552	

-	2	3373	e.1_Missense_Mu	NM_007113	NP_009044	Q07283	TRHY_HUMAN	30 AA tandem repeats.	5	gttcctctctcagcagctg	0.224	
-	3	754		NM_001122965	NP_001116437	Q6XPR3	RPTN_HUMAN	Gln-rich.	0	CACACCGATTTA	0.413	
-	3	9949		NM_002016	NP_002007	P20930	FILA_HUMAN	grin 20.|Ser-rich.	16	GTGGCGGGATC	0.567	
-	3	566	uc001ezv.2_Intron	NM_001014342	NP_001014364	Q5D862	FILA2_HUMAN	Ser-rich.	17	TACCTTGTCTTCC	0.493	
+	1	40		NM_178354	NP_848131	Q5T754	LCE1F_HUMAN	Pro-rich.	0	AGCCccctcccaagtg	0.358	
+	3	268	1_5'Flank|PEAR1_	NM_001080471	NP_001073940	Q5VY43	PEAR1_HUMAN	EMI.	3	GCTCCCCTCAG	0.672	
+	3	681	1C_uc001frv.2_5'U	NM_001765	NP_001756	P29017	CD1C_HUMAN	cellular (Potential).	4	CAGAAGGCTTCT	0.463	
-	1	864		NM_001004476	NP_001004476	Q6IF99	O10K2_HUMAN	Name=7; (Potential).	1	ATAAATCATTGGG	0.333	rs137874220
-	1	460		NM_001004467	NP_001004467	Q5JRS4	O10J3_HUMAN	Name=4; (Potential).	2	GCCAAGGCCAA	0.507	
+	15	5371	PA2_uc009www.2_	NM_020318	NP_064714	Q9BXP8	PAPP2_HUMAN	Sushi 1.	16	CTTGATCATGCT	0.507	
-	3	772	e_Mutation_p.P18	NM_004319	NP_004310	O14525	ASTN1_HUMAN		15	GCTGCGGGACC	0.612	
+	34	7491	_p.P505S|CEP350_	NM_014810	NP_055625	Q5VT06	CE350_HUMAN		4	TTGCTCCTAAAG	0.338	
+	1	406	gpx.2_Missense_M	NM_002293	NP_002284	P11047	LAMC1_HUMAN	inin N-terminal.	5	GCGCTGCATGC	0.522	
+	22	3592	p.V1093A|LAMC2_	NM_005562	NP_005553	Q13753	LAMC2_HUMAN	omain II and I.	3	CTGGGGTTACAA	0.483	
+	10	3451	_p.S644F|NAV1_u	NM_020443	NP_065176	Q8NEY1	NAV1_HUMAN		4	CCTGTCCCTGG	0.622	
+	5	1182_1183	_p.G242*|LAX1_uc	NM_017773	NP_060243	Q8IWV1	LAX1_HUMAN	lasmic (Potential).	2	GCAATGGAGAAG	0.5	
-	7	1500		NM_030952	NP_112214	Q9H093	NUAK2_HUMAN		5	TAGTAGCCAGAC	0.642	
-	15	1908	w.2_Missense_Mu	NM_006893	NP_008824	P41214	EIF2D_HUMAN		0	TCGAGGGAGCT	0.532	
+	3	381	jh.2_Missense_M	NM_001030287	NP_001025458	P18847	ATF3_HUMAN		0	TAGCCCCTGAAG	0.438	
+	11	1592_1593	.R431W|CAPN9_	NM_006615	NP_006606	O14815	CAN9_HUMAN	Domain III.	1	ATTACCCGGTGA	0.495	
-	1	68	RF2BP2_uc001hw	NM_182972	NP_892017	Q7Z5L9	I2BP2_HUMAN		0	CTGCCGCCGGG	0.647	
+	5	3220	e.1_Missense_Mu	NM_020066	NP_064450	Q9NZ56	FMN2_HUMAN	Pro-rich.|FH1.	12	ATACCCCCTCCG	0.711	
+	5	3352	e.1_Missense_Mu	NM_020066	NP_064450	Q9NZ56	FMN2_HUMAN	Pro-rich.|FH1.	12	ATACCCCCTCCG	0.731	
-	7	1172	n.3_Missense_Mutation_p.P139A|PLD5_uc001hzo.1_M			Q8N7P1	PLD5_HUMAN		6	AGATAGGCAGGT	0.483	
-	1	392		NM_001004734	NP_001004734	A6ND48	O14I1_HUMAN	lasmic (Potential).	0	CGGCTCTGTATT	0.517	
+	12	1255	P_uc009xhs.1_Mis	NM_002627	NP_002618	Q01813	K6PP_HUMAN		3	AGATCCCAAAG	0.602	
+	3	778	xig.2_Missense_M	NM_178150	NP_835363	Q8NFZ0	FBX18_HUMAN		3	CCTCCCGGTGG	0.423	
+	3	372_373	_p.P91F|MCM10_	NM_182751	NP_877428	Q7L590	MCM10_HUMAN		3	AAGTTCCCGCAT	0.485	
-	23	2732	j.2_RNA|NEBL_uc	NM_006393	NP_006384	O76041	NEBL_HUMAN	Nebulin 22.	2	AAATATGATTTTG	0.388	
-	1	225		NM_001034842	NP_001030014	Q3KNS1	PTHD3_HUMAN		4	ACTCCGATTCCT	0.687	
-	2	1455	nse_Mutation_p.G	NM_020848	NP_065899	Q9P266	K1462_HUMAN		4	TCCTCCATGAG	0.522	
+	2			NR_024524					0	GATGGTGAGAC	0.333	
-	5	1593	NF33B_uc001jag.	NM_006955	NP_008886	Q06732	ZN33B_HUMAN		0	TTATCTCCTATGT	0.393	
+	9	924	_p.V194M|RASSF	NM_032023	NP_114412	Q9H2L5	RASF4_HUMAN		1	TGGGCGTGGAA	0.582	
+	3	1189	qfq.1_Missense_M	NM_014696	NP_055511	O60269	GRIN2_HUMAN		0	CCAGTCCGTCC	0.672	
+	12	1865	y.1_Missense_Mu	NM_020549	NP_065574	P28329	CLAT_HUMAN		3	CATCAGATCGG	0.612	
-	10	1438	_p.E439K|CTNNA3	NM_001127384	NP_001120856	Q9UI47	CTNA3_HUMAN		8	CATCTTCATTTGT	0.308	
+	37	5425		NM_022124	NP_071407	Q9H251	CAD23_HUMAN	|Extracellular (Potential).	11	CACCTTCCGCA	0.572	
-	22	2827	xl.1_Missense_Mu	NM_001161352	NP_001154824	Q12791	KCMA1_HUMAN	lasmic (Potential).	3	GTACTCAATAG	0.498	
+	6	1308		NM_000314	NP_000305	P60484	PTEN_HUMAN	hatase tensifs*5(1)|p.H93D	2334	AAGACCATAAC	0.338	
-	17	2003		NM_022451	NP_071896	Q8WTT2	NOC3L_HUMAN		1	AATTTGGAAGAA	0.383	
-	9	1080_1081	uk.1_Missense_M	NM_022451	NP_071896	Q8WTT2	NOC3L_HUMAN		1	TTTAAGGAAACT	0.376	
-	1	103	C8_uc010qob.1_5'	NM_000770	NP_000761	P10632	CP2C8_HUMAN		0	CAAAAGGTTCC	0.453	
-	4	1353	00093_uc001kqk.	NM_015221	NP_056036	Q6XZF7	DNMBP_HUMAN		6	GGGATGAAAAG	0.527	
-	2	582		NM_001308	NP_001299	P15169	CBPN_HUMAN	Catalytic.	4	GTTCCGGAACT	0.602	rs146812654
-	4	860		NM_000102	NP_000093	P05093	CP17A_HUMAN		0	TTTTTCCAGGG	0.383	
+	17	2548	CS3_uc010qqz.1_	NM_014978	NP_055793	Q9UPU3	SORC3_HUMAN	enal (Potential).	10	CAATCCAGCAT	0.453	

-	1	441	C2_uc009xxx.2_Ir	NR_026715						0	CCAGGTGCCCC	0.537	
+	4	374	RNA|HABP2_uc01	NM_004132	NP_004123	Q14520	HABP2_HUMAN	EGF-like 1.		3	TCGTCCATGGG	0.537	
+	26	3119	R506*|DMBT1_uc	NM_007329	NP_015568	Q9UGM3	DMBT1_HUMAN	SRCR 8.		7	AGGGCCGAGTG	0.567	
-	8	1611	DD_uc001lrm.1_M	NM_145886	NP_665893	Q9HB75	PIDD_HUMAN	ZU5 2.		0	AGACTCGACGA	0.672	
-	13	1394	.1_Nonsense_Mut	NM_199292	NP_954986	P07101	TY3H_HUMAN			0	TGACTGGTACG	0.627	
-	1	28		NM_001005164	NP_001005164	Q8NGJ4	O52E2_HUMAN	ellular (Potential).		3	GGGGTGAAACT	0.498	
-	9	1419	.P30S|MRVI1_uc	NM_001100167	NP_001093637	Q9Y6F6	MRVI1_HUMAN			3	TCTCGGCAGAG	0.677	
-	3	803	e_Mutation_p.R15	NM_024514	NP_078790	Q6VVX0	CP2R1_HUMAN			2	GCTTTCTGTTG	0.378	
+	14	3375	AV2_uc001mpt.2_	NM_145117	NP_660093	Q8IVL1	NAV2_HUMAN			6	GAATTCCCTGT	0.537	
-	2	2065		NM_002233	NP_002224	P22459	KCNA4_HUMAN			4	TGCAGGACTGG	0.498	
+	21	2481	k.1_Missense_Mut	NM_001105540	NP_001099010	Q13574	DGKZ_HUMAN			3	TCCCGGTGCAG	0.687	
+	1	362		NM_001005275	NP_001005275	Q8NGL6	O4A15_HUMAN	ellular (Potential).		2	CATTTCCTTTC	0.388	
+	1	838		NM_001001967	NP_001001967	Q8NGL4	OR5DD_HUMAN	Name=7; (Potential).		3	TGTTTTACACAG	0.378	rs150799318
-	1	278		NM_001004058	NP_001004058	Q8NH50	OR8K5_HUMAN	ellular (Potential).		4	TAATAGGAAATA	0.398	
+	7	811		NM_000139	NP_000130	Q01362	FCERB_HUMAN	lasmic (Potential).		1	CAGGGGAAATG	0.418	
+	5	544		NM_017716	NP_060186	Q9NXJ0	M4A12_HUMAN	ical; (Potential).		0	GCCTGGGAATG	0.423	
-	2	2551	AB_uc001nuc.2_5'	NM_030628	NP_085131	Q6P9B9	INT5_HUMAN			2	CCTCGGGGGGC	0.647	
+	5	972	v.1_RNA|TSGA10	NM_152762	NP_689975	Q3SY00	T10IP_HUMAN			0	CCAAGGAGCTG	0.632	
+	3	757	nse_Mutation_p.A	NM_138768	NP_620123	Q96EZ4	MYEOV_HUMAN			0	CTGGAGCTGGT	0.652	
+	3	1325	_p.W380L|NEU3_	NM_006656	NP_006647	A8K327	A8K327_HUMAN			2	CTGCTGGTCCC	0.562	
+	4	680	xb.2_Missense_M	NM_032564	NP_115953	Q96PD7	DGAT2_HUMAN	lasmic (Potential).		0	TACTTTCCCATC	0.527	
+	32	4584	se_Mutation_p.A1	NM_000260	NP_000251	Q13402	MYO7A_HUMAN	FERM 1.		4	TCGCCGCCCAC	0.617	
+	47	6648	e_Mutation_p.P20	NM_000260	NP_000251	Q13402	MYO7A_HUMAN	FERM 2.		4	ACTTCCCTGAG	0.522	
+	2	500		NM_001098672	NP_001092142	Q6MZM0	HPHL1_HUMAN	e 1.|Extracellular (Potential		3	GTCATTCATTTAA	0.458	
-	5	422	se_Mutation_p.D6	NM_152587	NP_689800	Q8NCR3	CK065_HUMAN			1	GATGATCATTTT	0.358	
+	8	1234	.1_3'UTR|LAYN_	NM_178834	NP_849156	Q6UX15	LAYN_HUMAN	lasmic (Potential).		0	AAAGCGAAGCT	0.507	
-	5	1094	ppd.2_Missense_	NM_001077639	NP_001071107	Q6UWF7	FA55D_HUMAN			4	ATTTCTCTTTCAT	0.403	
+	2	458	se_Mutation_p.S2	NM_019854	NP_062828	Q9NR22	ANM8_HUMAN	H3-binding 1.		5	CCCCCTCCCAG	0.652	
-	5	906	p.G112R|EFCAB4	NM_032680	NP_116069	Q9BSW2	EFC4B_HUMAN	EF-hand 2.		2	AAATCCAGTAGT	0.532	
+	7	1766	u.2_Missense_Mu	NM_002286	NP_002277	P18627	LAG3_HUMAN	lasmic (Potential).		0	TTTCACCTTTGG	0.602	
-	25	3205	p.R73Q|A2M_uc0	NM_000014	NP_000005	P01023	A2MG_HUMAN			5	CATATCGCTCC	0.318	
-	1	335	H1_uc001qzc.2_I	NM_023922	NP_076411	Q9NYV8	T2R14_HUMAN	lasmic (Potential).		0	AATTGGCTATCT	0.348	
+	6	927	1467_uc009zhx.1_	NM_020853	NP_065904	A2RU67	K1467_HUMAN		p.R302*(1)	3	TGGGTCGACCT	0.507	
-	3	424		NM_182558	NP_872364					0	GGAACGATTCC	0.453	rs143075618
+	21	2889	se_Mutation_p.D	NM_004570	NP_004561	O75747	P3C2G_HUMAN	PI3K/PI4K.		21	GAGATGATCTT	0.368	
+	21	2895	se_Mutation_p.R	NM_004570	NP_004561	O75747	P3C2G_HUMAN	PI3K/PI4K.		21	ATCTTCGTCAG	0.363	
+	1	679	Z1_uc001rdw.3_5'	NM_033328	NP_201585	Q96KX2	CAZA3_HUMAN			2	TAAATGGATTTT	0.383	
-	14	1921		NM_021957	NP_068776	P54840	GYS2_HUMAN			2	GAACCGCCTGT	0.408	
+	5	751	_Mutation_p.R16	NM_152438	NP_689651	Q96FC9	DDX11_HUMAN	Helicase ATP-binding.		3	AGAAAGAGAGA	0.612	
-	1	325		NM_001040436	NP_001035526	Q9Y2Z4	SYYM_HUMAN	IGH region.		0	ATGAAGCGAGT	0.622	
+	10	1191	n.1_Missense_Mu	NM_001843	NP_001834	Q12860	CNTN1_HUMAN	like C2-type 4.		9	CCATCCCTACA	0.483	
-	2	619	se_Mutation_p.E1	NM_007210	NP_009141	Q8NCL4	GALT6_HUMAN	enal (Potential).		2	CTTTTCCTGGG	0.577	
+	7	1068	T81_uc001sac.2_I	NM_002284	NP_002275	O43790	KRT86_HUMAN	Rod.|Coil 2.		1	GCACGGGGAGA	0.602	
-	2	586	72_uc010sns.1_M	NM_001146225	NP_001139697	Q14CN4	K2C72_HUMAN	inker 1.|Rod.		6	TGCAGTTGTTC	0.567	
+	17	1715	_p.R88C|NCKAP1	NM_005337	NP_005328	P55160	NCKPL_HUMAN			4	CATCTTCGTATCT	0.393	
+	24	4326		NM_002332	NP_002323	Q07954	LRP1_HUMAN	ellular (Potential).		22	CAAAGGAGACT	0.597	
-	3	238	te|DCTN2_uc001s	NM_006400	NP_006391	Q13561	DCTN2_HUMAN			1	TCCTCCTGCAA	0.488	

-	5	963	7_splice|B4GALN	NM_001478	NP_001469	Q00973	B4GN1_HUMAN			0	TCTCACCTGGT	0.532	
-	8	2400	k.3_Missense_Mu	NM_013244	NP_037376	Q9UBM8	MGT4C_HUMAN	enal (Potential).		3	ATTTTCAAATAC	0.343	
-	6	1160		NM_145913	NP_666018	Q8N695	SC5A8_HUMAN	ical; (Potential).		0	CACCGTAGATG	0.388	
+	27	3226	0svs.1_Missense_	NM_206820	NP_996556	Q00872	MYPC1_HUMAN			4	ACTTTGATTTCT	0.358	
+	3	419		NM_017564	NP_060034	Q8WWQ8	STAB2_HUMAN	ellular (Potential).		14	GGTCAGAACAT	0.493	
+	4	454		NM_001101421	NP_001094891	Q8N1T3	MYO1H_HUMAN			0	GAAATGCCAGA	0.383	
-	2	810	u.2_Missense_Mut	NM_138451	NP_612460	Q96DY2	IQCD_HUMAN			1	GAGGCGGTCTC	0.522	rs141733272
-	15	1928	p.P595Q|RBM19_	NM_001146699	NP_001140171	Q9Y4C8	RBM19_HUMAN	RRM 4.		6	CTGCCGGGAG	0.632	
+	13	2435	F10_uc001tyq.3_	NM_014868	NP_055683	Q8N5U6	RNF10_HUMAN			2	CTGCTCCTCTG	0.512	
+	1	43	D8_uc001uex.2_5	NM_020382	NP_065115	Q9NQR1	SETD8_HUMAN			0	GAGCCATGGCT	0.667	
-	9	2808	1uia.2_Missense_	NM_133448	NP_597705	Q14C87	T132D_HUMAN	ellular (Potential).		14	TTTTTGGCCTT	0.522	
-	4	1462	nr.3_Missense_Mu	NM_014572	NP_055387	Q9NRM7	LATS2_HUMAN			10	GGACGGAGGTG	0.721	
-	3	387	T3_uc010tdn.1_M	NM_004119	NP_004110	P36888	FLT3_HUMAN	ellular (Potential).		8549	GACAGGAAATG	0.498	
+	9	970	ua.1_Missense_M	NM_000059	NP_000050	P51587	BRCA2_HUMAN			64	TATCGCTTCTGT	0.308	
+	3	838	ao.2_Missense_M	NM_152719	NP_689932	Q8NA61	SPERT_HUMAN	Potential.		2	GGAGGAGAATC	0.677	
-	9	995	se_Mutation_p.R	NM_152720	NP_689933	P51956	NEK3_HUMAN	ith VAV2.|Protein kinase.		2	GCCTCGAGAGA	0.478	
-	3	661	.N39S|THSD1_uc	NM_018676	NP_061146	Q9NS62	THSD1_HUMAN	ellular (Potential).		4	TGTCGTTGCTT	0.433	
+	2	165	sense_Mutation_	NM_024808	NP_079084	Q6PGQ7	BORA_HUMAN			0	AAACTCCAGGA	0.348	
+	15	3853_3854		NM_000123	NP_000114	P28715	ERCC5_HUMAN			7	AGCTCCCGTGA	0.485	
-	49	4668	4A1_uc010agl.2_	NM_001845	NP_001836	P02462	CO4A1_HUMAN	llagen IV NC1.		6	ATTTCGTGATG	0.507	
+	2	1169	.2_Missense_Mut	NM_005537	NP_005528	Q9UK53	ING1_HUMAN			1	CCGCACGCGGC	0.672	
+	9	1320	a.1_RNA|POTEG_	NM_001005356	NP_001005356	Q6S5H5	POTEG_HUMAN			1	GCACGGAAGTA	0.358	
+	1	344		NM_001004723	NP_001004723	Q8NGD1	OR4N2_HUMAN	Name=3; (Potential).		4	ACTCCTTGTTG	0.507	
+	2	383		NM_022360	NP_071755	P56851	EP3B_HUMAN			1	GTATGGGTCCA	0.408	
-	26	3419	wan.2_Missense_	NM_007192	NP_009123	Q9Y5B9	SP16H_HUMAN			0	GGCCCGAACTG	0.507	
+	9	5542		NM_025081	NP_079357	Q9P2P1	NYNRI_HUMAN	grase catalytic.		3	CCCTGCCTTTG	0.627	
-	3	671	A1_uc001wqa.2_5	NM_002515	NP_002506	P51513	NOVA1_HUMAN			5	ATTTTTTCTGCA	0.438	
+	2	1273	.2_Missense_Mut	NM_001173	NP_001025226	Q13017	RHG05_HUMAN			5	AAGAGCTTTTA	0.313	
+	4	798	y.1_Missense_Mu	NM_054024	NP_473365	Q96PC5	MIA2_HUMAN			2	TTGTTGAAAGT	0.428	
+	1	624	d.1_Missense_Mu	NM_031914	NP_114120	Q17RD7	SYT16_HUMAN			1	CGGAGGAAGAG	0.463	
-	32	6041	VE26_uc001xkc.	NM_015346	NP_056161	Q68DK2	ZFY26_HUMAN			11	CTCTGGGTTGG	0.582	
+	15	4505	xmv.2_Missense_	NM_015556	NP_056371	O43166	SI1L1_HUMAN	Ser-rich.		4	GGACCGGAAAA	0.552	
+	15	4547	xmv.2_Missense_	NM_015556	NP_056371	O43166	SI1L1_HUMAN	Ser-rich.		4	CAAGAGCCAAG	0.537	
-	10	1119	tion_p.P256S|NU	NM_001005743	NP_001005743	P49757	NUMB_HUMAN			4	AATTGGAGCAT	0.532	
-	4	1207	_p.E336*|STON2_	NM_033104	NP_149095	Q8WXE9	STON2_HUMAN			5	CTCCTCAAAGA	0.502	
-	4	981	_p.P180L|KCNK1	NM_021161	NP_066984	P57789	KCNKA_HUMAN		p.P175P(1)	5	TGCTCGGAGCA	0.393	
-	3	538		NM_001010854	NP_001010854	Q86TV6	TTC7B_HUMAN			2	TCACCCGCAGC	0.567	
-	7	1093	12_splice|FBLN5_	NM_006329	NP_006320	Q9UBX5	FBLN5_HUMAN			6	CACATCTGTGG	0.527	
+	1	175	CL1B_uc010avj.2	NM_004918	NP_004909	O95988	TCL1B_HUMAN			1	GTAGGGAATGG	0.677	
-	3	459	fb.3_Missense_Mu	NM_001098725	NP_001092195	P56279	TCL1A_HUMAN			1	GCAGCAGCTCG	0.552	
+	14	3425	.G1093C|TECPR	NM_014844	NP_055659	O15040	TCPR2_HUMAN			3	CCTCGGGCAAG	0.507	
+	4	578	_p.A93T|C14orf18	NM_001008404	NP_001008404	Q8N912	CN180_HUMAN			0	TCAGGGGTGAG	0.662	
-	7	14744	px.2_Missense_M	NM_138420	NP_612429	Q8IVF2	AHNK2_HUMAN			1	TTTGGGGGACT	0.498	
-	4	503	T14_uc001yqi.2_	NM_177533	NP_803877	O95848	NUD14_HUMAN	dix hydrolase.		1	CCAAGTGGTAG	0.597	
+	1	2978		NM_018958	NP_061831	Q9NZP6	CO002_HUMAN			8	TGTCATCTTGC	0.498	
+	5	1393	_p.Q224R|ARHGA	NM_014783	NP_055598	Q6P4F7	RHGBA_HUMAN	Rho-GAP.		6	ATTACAGGCTG	0.358	
+	35	4835	r.2_Missense_Mut	NM_001036	NP_001027	Q15413	RYR3_HUMAN	eats.|Cytoplasmic (By simil		10	CCCAGCTCTTC	0.607	

+	4	471	zkl.2_Missense_M	NM_001013703	NP_001013725	Q9P2K8	E2AK4_HUMAN		4	AGCCCCCTCCC	0.473	
-	9	880	LA2G4F_uc001zp	NM_213600	NP_998765	Q68DD2	PA24F_HUMAN		4	CCCCTCGCCCA	0.622	
+	2	209	fw.2_Missense_M	NM_032866	NP_116255	Q0VF96	CGNL1_HUMAN	ZIM (By similarity).	11	GTATTCGGGTC	0.507	
+	2	1022	fw.2_Missense_M	NM_032866	NP_116255	Q0VF96	CGNL1_HUMAN	Head.	11	TGGATGATCAG	0.522	
-	10	1763	_p.T373A|NARG2_	NM_024611	NP_078887	Q659A1	NARG2_HUMAN		2	CAGATGTTTTCA	0.328	
+	12	1662	_p.A287T|IQCH_u	NM_001031715	NP_001026885	Q86VS3	IQCH_HUMAN		4	CCTGAAGCTGTA	0.383	
-	2	622	zg.2_Missense_M	NM_020447	NP_065180	Q5XKK7	CO017_HUMAN		0	AGACCTTTTCC	0.602	
+	3	720	.3_RNA|IL16_uc0	NM_172217	NP_757366	Q14005	IL16_HUMAN		4	AAAGCCTGGAA	0.423	
+	9	1338	ql.2_Missense_M	NM_033544	NP_291022	A6NED2	RCCD1_HUMAN	RCC1 4.	0	TAAGCAACTCC	0.488	
+	11	1567	bok.2_Missense_	NM_018349	NP_060819	Q6DN12	MCTP2_HUMAN	C2 3.	3	GAACTCCCTGA	0.388	
+	14	3578	j.2_Missense_Mu	NM_005632	NP_005623	O75808	CAN15_HUMAN		2	CCCCCCACTCA	0.697	rs151328571
-	4	473	123W|CCDC78_u	NM_001031737	NP_001026907	A2IDD5	CCD78_HUMAN		1	TGCCCGGGGAT	0.622	rs144406163
+	35	6540	_p.D793N|CACNA	NM_021098	NP_066921	O95180	CAC1H_HUMAN	lasmic (Potential).	2	CAGCCGACGAG	0.741	
+	17	2378_2379		NM_016111	NP_057195	Q9Y4R8	TELO2_HUMAN		0	GTGGCCGGCC	0.649	
-	2	298		NM_001080524	NP_001073993	A8MZG2	CP090_HUMAN		0	CCAGGCTGTGC	0.677	
-	10	2704	uyn.1_Missense_	NM_001134407	NP_001127879	Q12879	NMDE1_HUMAN	ellular (Potential).	45	TCAGGCTGACC	0.463	
+	23	4218	zg.1_Intron|SRCA	NM_006662	NP_006653	Q6ZRS2	SRCAP_HUMAN	Pro-rich.	4	TTCTTCGACCC	0.667	
+	18	1751	u.3_Missense_Mu	NM_000293	NP_000284	Q93100	KPBB_HUMAN		3	ATTTATCGCATTC	0.343	
+	2	221	e_Mutation_p.V5	NM_024922	NP_079198	Q6UWW8	EST3_HUMAN		5	TGGGCGTGAAG	0.632	rs149175900
+	1	416		NM_002153	NP_002144	P37059	DHB2_HUMAN	(By similarity).	2	TGGATCAGAAG	0.468	
-	4	803	c.3_Missense_Mu	NM_001122890	NP_001116362	Q6P531	GGT6_HUMAN	ellular (Potential).	1	TGGCTCGGGCC	0.652	
+	7	1051	BG_uc010cmw.2	NM_001040	NP_001031	P04278	SHBG_HUMAN	minin G-like p.0?(1)|p.?(1)	0	TCCTTAACCTCT	0.547	
+	75	11502	m.1_Missense_M	NM_020877	NP_065928	Q9P225	DYH2_HUMAN	.6 (By similarity).	13	TGGAGGATTCA	0.597	
-	23	2834	uc002gml.1_Intron	NM_017533	NP_060003	Q9Y623	MYH4_HUMAN	Potential.	13	TCACATCTTTCC	0.373	
-	17	2062	uc002gml.1_Intron	NM_017533	NP_060003	Q9Y623	MYH4_HUMAN	osin head-like.	13	TGACACTGTCT	0.308	
-	13	1325	uc002gml.1_Intron	NM_017533	NP_060003	Q9Y623	MYH4_HUMAN	osin head-like.	13	CTCTGGGATAG	0.453	
+	3	1886		NM_021012	NP_066292	Q14500	IRK12_HUMAN	smic (By similarity).	4	GGACGGAGACC	0.657	
-	2	739	_p.P194L|MYO18A	NM_078471	NP_510880	Q92614	MY18A_HUMAN		0	GCTCAGGGGCT	0.687	
-	7	2864	_p.D808N|SLFN11	NM_001104588	NP_001098058	Q7Z7L1	SLN11_HUMAN		3	AACATCCTTTG	0.468	rs71366434
-	1	665		NM_000286	NP_000277	O00623	PEX12_HUMAN	lasmic (Potential).	0	TGGCTGGTCAT	0.502	
-	3	603		NM_019010	NP_061883	P35900	K1C20_HUMAN	oil 1B.|Rod.	3	ATCTGTTTTATGT	0.388	
+	8	1204	C25_uc010cxs.1_	NM_031421	NP_113609	Q96NG3	TTC25_HUMAN	TPR 6.	1	TGCCAGAGTTG	0.443	
+	11	1338	_p.P348S|ATP6V0	NM_001130021	NP_001123493	Q93050	VPP1_HUMAN	lasmic (Potential).	1	ATAAATCCAGGT	0.294	
+	4	565	938_uc002ibf.3_	NM_005854	NP_005845	O60895	RAMP2_HUMAN	ical; (Potential).	0	TAGTATGGAGGA	0.592	
+	14	1668	f.1_Missense_Mut	NM_006178	NP_006169	P46459	NSF_HUMAN		1	ATGGGGAGCTG	0.448	
-	14	1899	LL6_uc002ioc.2_	NM_001130918	NP_001124390	Q8N841	TTLL6_HUMAN		0	CGTGGGAGCCT	0.507	
+	4	703		NM_023079	NP_075567	Q9H832	UBE2Z_HUMAN		0	GGAGCCCAGCC	0.542	
+	2	2306	dbu.2_Missense_	NM_175575	NP_783165	Q8TEU8	WFKN2_HUMAN	NTR.	3	GCATGGCCATG	0.632	
+	4	959	ddd.2_Missense_	NM_014906	NP_055721	Q8WY54	PPM1E_HUMAN	PP2C-like.	5	GGGGAGTAGAT	0.502	
+	23	3724	utation_p.Q179*|	NM_006039	NP_006030	Q9UBG0	MRC2_HUMAN	ellular (Potential).	3	TCTGCCAGAAG	0.642	
-	2	163		NM_181449	NP_852114	Q496F6	CLM2_HUMAN	.|Extracellular (Potential).	4	TTGTACATGCTC	0.542	
-	15	2501	ense_Mutation_p.	NM_024421	NP_077739	Q08554	DSC1_HUMAN	lasmic (Potential).	4	TGCTTCCTAAAA	0.303	
+	7	879		NM_001943	NP_001934	Q14126	DSG2_HUMAN	(Potential).|Cadherin 2.	9	TGCAGGAACAC	0.403	
-	1	1630	AL2_uc002lco.2_	NM_016427	NP_057511	Q8IYF1	ELOA2_HUMAN		4	TAGCCGAATCC	0.547	rs150911848
+	3	1282	r.1_Missense_Mu	NM_005215	NP_005206	P43146	DCC_HUMAN	ellular (Potential).	17	TTTTATCAGGTAT	0.373	
-	4	1254		NM_052947	NP_443179	Q86TB3	ALPK2_HUMAN		14	GCAGGTTCCTT	0.453	
+	4	5021	qu.1_Missense_M	NM_017757	NP_060227	Q9C0G0	ZN407_HUMAN		2	AAAAGCCGTTTA	0.507	

-	10	1746	_uc010xfv.1_Intro	NM_005481	NP_005472	Q9Y2X0	MED16_HUMAN		0	AGAGCGAGGCC	0.667	
+	1	37_38	sense_Mutation_p.	NM_024100	NP_077005	Q9BV38	WDR18_HUMAN		1	GCGCCCATGG	0.728	
+	4	1232	wq.2_Missense_M	NM_024967	NP_079243	Q9HAH1	ZN556_HUMAN	2H2-type 8.	3	TTGGTCCTCAT	0.468	
+	4	1386	a.1_Missense_Mu	NM_173480	NP_775751	Q68EA5	ZNF57_HUMAN	2H2-type 9.	3	GAGGACGCACA	0.438	rs148390269
-	31	4924	w.2_Missense_Mu	NM_002850	NP_002841	Q13332	PTPRS_HUMAN	).|Tyrosine-protein phosph	4	CGTTGGGTATT	0.627	
-	14	1837	c.2_Missense_Mu	NM_000635	NP_000626	P48378	RFX2_HUMAN		6	GGGCCGCCTGC	0.657	
+	10	1081	_p.S296F|EMR1_	NM_001974	NP_001965	Q14246	EMR1_HUMAN	|Extracellular (Potential).	5	GGTCTCCTTTT	0.383	
-	58	7459	e.2_Missense_Mu	NM_032447	NP_115823	Q75N90	FBN3_HUMAN	40; calcium-binding.	11	CTGGTGGTGCT	0.567	
-	84	43654	wj.2_Missense_Mu	NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	lasmic (Potential).	57	TCCTTCCTTCTT	0.587	
-	33	38726	16_uc010xki.1_5'	NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	ellular (Potential).	57	AGGATGGAGTC	0.478	
-	28	38225		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	ellular (Potential).	57	AGGTCCCAGGA	0.498	
-	5	521	se_Mutation_p.I3	NM_152289	NP_689502	Q8N587	ZN561_HUMAN	KRAB.	1	TTTGTATCCCAC	0.338	
+	4	1515	ym.1_Missense_M	NM_001136501	NP_001129973	Q08AG5	ZN844_HUMAN		0	CTTCAGATCTG	0.423	
+	4	1710	ym.1_Missense_M	NM_001136501	NP_001129973	Q08AG5	ZN844_HUMAN		0	GCATGAAAGGA	0.413	
+	8	1511		NM_004843	NP_004834	Q6UWB1	I27RA_HUMAN	tential).|Fibronectin type-III	0	CCTGGAGAAAC	0.632	
+	16	3739	_p.S971L|NWD1_uc002nev.3_Missense_Mutation_p.S9			Q149M9	NWD1_HUMAN	WD 7.	7	AAGATCGGTGC	0.507	
-	28	3580		NM_001080421	NP_001073890	Q9UPW8	UN13A_HUMAN	MHD1.	3	TAGACGATGCT	0.562	
-	23	3098_3099		NM_001080421	NP_001073890	Q9UPW8	UN13A_HUMAN		3	TCAATCCGCAG	0.569	
+	5	1011	f.2_Missense_Mu	NM_002911	NP_002902	Q92900	RENT1_HUMAN	interaction with RENT2.	2	AGATCCCCTCC	0.657	
-	7	2699		NM_001080409	NP_001073878				2	GTCGAGAAATTG	0.353	rs55891931
-	6	2463		NM_001080409	NP_001073878				2	AATTAGCTTATGT	0.378	
-	2	821		NM_006003	NP_005994	P47985	UCRI_HUMAN	Rieske.	0	GGCAAGGGCA	0.478	
-	3	269	ntu.3_Missense_M	NM_001126335	NP_001119807	P82251	BAT1_HUMAN	ellular (Potential).	1	TGGGGGAAACG	0.602	
+	10	931	010xsh.1_Missens	NM_002151	NP_002142	P05981	HEPS_HUMAN	(Potential).|Peptidase S1.	2	CCACGGTCTGC	0.662	
-	26	3370	S1_uc010eem.1_	NM_004646	NP_004637	O60500	NPHN_HUMAN	lasmic (Potential).	5	AGTGTCCCGCT	0.602	
-	18	2335		NM_004646	NP_004637	O60500	NPHN_HUMAN	7.|Extracell p.G779*(1)	5	TTCTCCCTGGA	0.572	
-	5	1194	5B_uc002ofr.1_N	NM_152279	NP_689492	Q52M93	Z585B_HUMAN	2H2-type 6.	1	TACCTGAAGTT	0.388	
+	14	1584	PERG_uc002oif.3_	NM_021185	NP_067008	Q6ZRH7	CTSRG_HUMAN	ellular (Potential).	2	TGCAGCTCTAA	0.532	
+	7	1274	xp.3_Missense_M	NM_181845	NP_862828	Q8N7M2	ZN283_HUMAN	2H2-type 5.	0	TTGCTAAACAT	0.398	
-	6	1502_1503	_p.G11R|ZNF229_	NM_014518	NP_055333	Q9UJW7	ZN229_HUMAN	2H2-type 2.	4	GAACCCCTTTCC	0.515	
+	7	1020	.G301E|KLC3_uc	NM_177417	NP_803136	Q6P597	KLC3_HUMAN	TPR 3.	1	CTATGGGAAGC	0.657	
-	1	469		NM_015649	NP_056464	Q8IU81	I2BP1_HUMAN		0	GGTCCGCGCCC	0.706	
-	5	1342		NM_017708	NP_060178	Q2M2I3	FA83E_HUMAN		1	CCCACGGAGGT	0.667	
-	16	2379	m.2_Missense_Mu	NM_002103	NP_002094	P13807	GYS1_HUMAN		2	TGGCCGTGTCC	0.701	
+	12	1413	_p.P241S|MED25_	NM_030973	NP_112235	Q71SY5	MED25_HUMAN	16.|Interaction with CREB	1	TCATCCCCCAG	0.687	
+	4	293	e_Mutation_p.E9	NM_003121	NP_003112	Q01892	SPIB_HUMAN		2	ACCTCGAACTG	0.642	
-	17	2246	sw.1_Missense_M	NM_016148	NP_057232	Q9Y566	SHAN1_HUMAN	PDZ.	2	TTGGCGGATCA	0.602	
+	1	634		NM_001506	NP_001497	O75388	GPR32_HUMAN	ellular (Potential).	1	TGGAGGGACA	0.552	
-	6	864	.R216G|KLK5_uc	NM_001077491	NP_001070959	Q9Y337	KLK5_HUMAN	eptidase S1.	0	GCACCTTTTCT	0.507	
+	4	2891	dw.1_Missense_M	NM_138374	NP_612383	Q96IR2	ZN845_HUMAN	2H2-type 26.	0	CTTCCGTCACA	0.363	rs150688663
-	5	1012	_p.L301F|LILRB5_	NM_006840	NP_006831	O75023	LIRB5_HUMAN	3.|Extracellular (Potential).	2	GGAGAGGTTGT	0.692	
+	6	1069	_p.P304L|NLRP2_	NM_017852	NP_060322	Q9NX02	NALP2_HUMAN	NACHT.	2	GTTACCCAAGG	0.662	
+	4	2352		NM_020903	NP_065954	Q9HBJ7	UBP29_HUMAN		11	AAGATGGAGGG	0.483	
+	8	966	f39_uc010eym.1_	NM_145038	NP_659475	Q96MC2	CC164_HUMAN	Potential.	0	AGATTCTTGAG	0.279	
-	4	542		NM_000348	NP_000339	P31213	S5A2_HUMAN	ical; (Potential).	0	TATTCCCATTCC	0.403	
-	23	3675	j.3_Missense_Mut	NM_005633	NP_005624	Q07889	SOS1_HUMAN		10	TAAGGGAGGGC	0.502	
-	5	856	zj.2_Missense_Mu	NM_004105	NP_004096	Q12805	FBLN3_HUMAN	alcium-binding (Potential).	6	TGCACTCGTCTA	0.443	

-	1	199	A_uc002sbn.3_5'U	NM_032180	NP_115556	Q3B820	F161A_HUMAN		3	GGTCTTCGCGTT	0.652	
-	19	3333_3334	c.2_Missense_Mut	NM_016316	NP_057400	Q9UBZ9	REV1_HUMAN		2	CCTGCCTTTGTC	0.5	
+	3	314	81_splice|DBI_uc0	NM_001079862	NP_001073331	P07108	ACBP_HUMAN		0	GAAAGGTAATTG	0.443	
+	10	1026	02tvn.2_Missense_	NM_018460	NP_060930	Q53QZ3	RHG15_HUMAN	Rho-GAP.	2	AAAATTCCACAG	0.428	
-	46	6081		NM_004543	NP_004534	P20929	NEBU_HUMAN	Nebulin 51.	20	GTCTGGGTGCTC	0.433	
-	8	709	p.D196A|CACNB4	NM_000726	NP_000717	O00305	CACB4_HUMAN		2	ACAACATCGTAAG	0.473	
+	27	5801	ANC1_uc010fon.2_	NM_033394	NP_203752	Q9C0D5	TANC1_HUMAN		3	AAGCCCACAGGA	0.423	
-	22	3716	ip.2_Nonsense_Mu	NM_013450	NP_038478	Q9UIF8	BAZ2B_HUMAN	DDT.	4	CCTCTTGAAGAAC	0.428	
-	2	483	uci.2_Missense_M	NM_033272	NP_150375	Q9NS40	KCNH7_HUMAN	lasmic (Potential).	5	TCCTCTCTTCTGA	0.423	
-	28	6398	y.2_Missense_Mut	NM_006922	NP_008853	Q9NY46	SCN3A_HUMAN		10	CATAGGAAGGAG	0.358	
-	50	9967		NM_004525	NP_004516	P98164	LRP2_HUMAN	s B 30.|Extracellular (Potent	29	TTCTCTCAATGAC	0.413	
+	6	470	PIG_uc002ufb.2_M	NM_004792	NP_004783	Q13427	PPIG_HUMAN	e cyclophilin-type.	3	GAAATGGACGAG	0.264	
+	12	1396	fe.1_Missense_Mu	NM_032523	NP_115912	Q9BZF3	OSBL6_HUMAN		1	CCAGTTCGCTTG	0.423	
-	275	76663	175N|TTN_uc010z	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	ATAGTAATAGGAA	0.378	
-	46	15324	TN_uc010zfi.1_Intr	NM_133379	NP_596870	Q8WZ42	TITIN_HUMAN		153	CAACTTCCCCTAA	0.433	
-	46	14285	TN_uc010zfi.1_Intr	NM_133379	NP_596870	Q8WZ42	TITIN_HUMAN		153	CTCCACCATAGTT	0.328	
-	8	1447	ftt.2_Nonsense_Mu	NM_018256	NP_060726	Q9GZL7	WDR12_HUMAN	or nucleolar localization.	0	TGGTCGATTTGT	0.388	
-	6	1228	ftt.2_Missense_Mu	NM_018256	NP_060726	Q9GZL7	WDR12_HUMAN	nt for nucleolar localization.	0	AAGCACTCAATAA	0.378	
-	21	3081	e_Mutation_p.G63	NM_173076	NP_775099	Q86UK0	ABCAC_HUMAN		11	TTACTTCCAAAGA	0.388	
+	11	1378	su.3_Splice_Site_p	NM_001631	NP_001622	P09923	PPBI_HUMAN		1	TACCAGGGAGC	0.716	
-	1	316	T1A6_uc002vuu.2_	NM_001001394	NP_001001394	Q8WWF6	DNJB3_HUMAN		0	CTCCGCCCCCG	0.647	
-	19	6623	p.G1907D|COL6A3	NM_004369	NP_004360	P12111	CO6A3_HUMAN	l region.|Collagen-like 2.	18	TCCAGACCATCCA	0.408	
+	2	211		NM_153325	NP_697020	Q8N687	DB125_HUMAN		3	GCATTTCCTGTGA	0.363	
+	26	2537	_p.L813F|PLCB4_u	NM_182797	NP_877949	Q15147	PLCB4_HUMAN		15	ATTTCCCTTCGAA	0.413	
-	5	996	nj.2_Missense_Mu	NM_020341	NP_065074	Q9P286	PAK7_HUMAN	Linker.	23	CATAGAGACTCTT	0.493	
+	3	712	zf.1_RNA|CBFA2T	NM_005093	NP_005084	O43439	MTG8R_HUMAN	Pro-rich.	2	GAGGACCGAGG	0.502	
-	4	810		NM_016470	NP_057554	Q9NX31	CT111_HUMAN		0	CCAAGGGAGGGA	0.532	
+	2	3898		NM_173485	NP_775756	Q9NRE2	TSH2_HUMAN		6	GGTCTCCAGAAA	0.502	
-	16	2011	yfa.1_Missense_M	NM_172107	NP_742105	O43526	KCNQ2_HUMAN	lasmic (Potential).	2	GCAGCTCCGCCT	0.697	
-	13	1054	PTE_uc002yir.1_Mi	NM_199261	NP_954870	P56180	TPTE_HUMAN	hatase tensin-type.	5	GTGTATCGCCTTT	0.323	
+	1	176	.1_Intron|C21orf29	NM_198695	NP_941968	P60410	KR108_HUMAN	repeats of C-C-X(3).|1.	2	GCTGCGAGCCC	0.672	
+	30	6640	j.2_Missense_Muta	NM_006031	NP_006022	O95613	PCNT_HUMAN		8	ATTCTCCCATTCA	0.507	
-	9	1431	ise_Mutation_p.G1	NM_001136213	NP_001129685	Q6S545	POTEH_HUMAN		1	GTACTTCCGTGCT	0.358	
-	1	1554_1555		NM_014406	NP_055221	Q96SF2	TCPQM_HUMAN		1	TGGGCCCTTCCA	0.495	
-	2	1185	ru.2_Missense_Mu	NM_023004	NP_075380	Q9BZR6	RTN4R_HUMAN		0	CAGCGGCTCCTC	0.652	
+	12	1099	aeo.2_Splice_Site_	NM_133455	NP_597712	Q96A84	EMID1_HUMAN		0	ACACAGGGACTC	0.627	
+	17	2613	_p.S762L|MTMR3_	NM_021090	NP_066576	Q13615	MTMR3_HUMAN		5	TGTTCTCACAGG	0.577	
+	17	1316	EPDC5_uc003alt.2	NM_014662	NP_055477	O75140	DEPD5_HUMAN		8	GATTCTCGTCTGC	0.458	
+	3	831	ny.2_Missense_Mu	NM_014310	NP_055125	Q96D21	RHES_HUMAN	n GNB1, GNB2 and GNB3.	3	AGTACGGTGACG	0.627	
-	16	4134	GCP6_uc010har.1_	NM_020461	NP_065194	Q96RT7	GCP6_HUMAN	' AA tandem repeats.	4	GCCGGGTGGGAG	0.622	rs145066767
+	27	3631	PR1_uc011asu.1_I	NM_001099952	NP_001093422	Q14643	ITPR1_HUMAN	lasmic (Potential).	21	GAGGTGCTCCAG	0.567	
+	11	1508	plice_Site_p.D338_	NM_153461	NP_703191	Q8NAC3	I17RC_HUMAN		2	GTGGACGTAAGT	0.642	
+	19	4398	p.H1387Y|FGD5_u	NM_152536	NP_689749	Q6ZNL6	FGD5_HUMAN	PH 2.	5	ATTTTTCACCTTT	0.423	
-	5	940	385D_uc010hfb.1_	NM_024697	NP_078973	Q9H6B1	Z385D_HUMAN	Thr-rich.	5	TTTTTTCCACTTT	0.468	
-	4	3099		NM_014831	NP_055646	O15050	TRNK1_HUMAN		2	GTAAATCCACCAC	0.433	
+	13	1722	p.P479H|VILL_uc0	NM_015873	NP_056957	O15195	VILL_HUMAN		0	AGCCCCCCCACT	0.597	
+	11	1697_1698	.1_Missense_Muta	NM_007335	NP_031361	Q9Y238	DLEC1_HUMAN		9	GTTTTCCCCAAA	0.564	

-	27	4685		NM_006514	NP_006505	Q9Y5Y9	SCNAA_HUMAN	IV.		10	TGAAGTGACTTA	0.473	
+	11	1900	10hhw.2_Missense	NM_015460	NP_056275	Q8NFW9	MYRIP_HUMAN	Actin-binding.		5	CTGTACGAGTTA	0.493	
+	13	1715	kz.3_Missense_M	NM_001042646	NP_001036111	Q9UPV9	TRAK1_HUMAN	n with HGS.|Potential.		1	GCTGAGGCGGC	0.642	
-	2	996	R3_uc003cpg.1_In	NM_001295	NP_001286	P32246	CCR1_HUMAN	lasmic (Potential).		3	ACTTCCGGAACC	0.587	
+	1	190	_5'Flank|KIF9_uc	NM_025010	NP_079286	O94889	KLH18_HUMAN			0	TTGCCTAGTCGC	0.662	
+	5	3100		NM_003458	NP_003449	Q9UPA5	BSN_HUMAN			8	ACCTCTCCCACC	0.647	
+	1	364		NM_001005515	NP_001005515	A6NDH6	O5H15_HUMAN	lasmic (Potential).		2	TATGATCGCTATG	0.378	
+	5	2430	_p.G729R|COL8A1	NM_001850	NP_001841	P27658	CO8A1_HUMAN	helical region (NC1).		0	TATGCCGGGCAG	0.463	
+	4	424	ense_Mutation_p.P	NM_007072	NP_009003	Q9UM44	HHLA2_HUMAN	-like V-type 1.		1	AAGATCCCAGAT	0.408	
+	1	263	GSF11_uc010hqs	NM_152539	NP_689752	Q96M34	CC030_HUMAN			2	ACGGAGTAGCT	0.502	
-	2	156	on_p.S4F|PARP9_	NM_001146102	NP_001139574	Q8IXQ6	PARP9_HUMAN		p.S4S(1)	4	CCATGGAAAAG	0.418	
+	2	318	_p.E54K|FAIM_uc	NM_001033032	NP_001028204	Q9NVQ4	FAIM1_HUMAN			0	AAGATCGAATTT	0.363	
-	8	1212	p.H295Y|PLSCR4_	NM_001128305	NP_001121777	Q9NRQ2	PLS4_HUMAN	smic (By similarity).		0	GGAAGTGAATGT	0.428	rs138186262
-	9	1411	_p.L195F|SLC2A2_	NM_000340	NP_000331	P11168	GTR2_HUMAN	lasmic (Potential).		2	AAAGAGAGAAC	0.403	
-	4	445	SF10_uc003fie.2_I	NM_003810	NP_003801	P50591	TNF10_HUMAN	cellular (Potential).		5	GGACCTCTTTCT	0.403	
+	4	581	CNMB2_uc003fjf.2	NM_181361	NP_852006	Q9Y691	KCMB2_HUMAN	cellular (Potential).		1	TGGACCGAAGAG	0.483	
+	3	657		NM_004443	NP_004434	P54753	EPHB3_HUMAN	cellular (Potential).		11	ATGAATCCCATC	0.557	
+	8	1183	.2_Missense_Mut	NM_003722	NP_003713	Q9H3D4	P63_HUMAN	action with H	p.S365L(1)	12	AAGTTTCGGACA	0.537	rs147148566
-	8	1856	GC1A_uc011bxp.	NM_013261	NP_037393	Q9UBK2	PRGC1_HUMAN	Arg/Ser-rich.		8	ATCGGGAACAC	0.458	
-	5	1022		NM_000730	NP_000721	P32238	CCKAR_HUMAN	lasmic (Potential).		4	CTGCTGCTGCTG	0.602	
-	2	540	_p.D54A|TLR10_u	NM_030956	NP_112218	Q9BXR5	TLR10_HUMAN	lar (Potential).|LRR 2.		2	GATAAATCCAGTG	0.448	
+	2	928		NM_001080505	NP_001073974	A0PJX4	SHSA3_HUMAN	lasmic (Potential).		2	TCAGTTCCAGTT	0.557	
-	6	1266	zc.1_Nonsense_M	NM_001114175	NP_001107647	P47869	GBRA2_HUMAN	cellular (Probable).		4	TAAGTCCAAATAT	0.363	
-	14	1960	zg.1_Missense_Mu	NM_006587	NP_006578	Q9Y5Q5	CORIN_HUMAN	ential).|LDL-receptor class		2	GACATTCCCAAA	0.373	
-	3	345	gyu.2_Missense_M	NM_001014446	NP_001014446	Q56VL3	OCAD2_HUMAN	OCIA.		0	TTTCTTCCTGAC	0.383	
-	5	1070	3haf.3_Missense_M	NM_001126328	NP_001119800	Q8TBB1	LNX1_HUMAN			4	TGGTAATTTCAC	0.408	
+	21	3565	p.R1131Q|LPHN3_	NM_015236	NP_056051	Q9HAR2	LPHN3_HUMAN	lasmic (Potential).		18	AGGTACGAAAAG	0.373	
+	5	1325	cam.1_Missense_M	NM_001075	NP_001066	P36537	UDB10_HUMAN			5	ATTAATGATCCTT	0.383	
+	1	388	hq.2_Missense_M	NM_001074	NP_001065	P16662	UD2B7_HUMAN			2	ACAGGAAATCAT	0.303	
-	22	4180	_p.T1104A|ANKRD	NM_032217	NP_115593	O75179	ANR17_HUMAN	ANK 24.		10	ATGGAGTGTTCC	0.393	
-	1	1471		NM_033214	NP_149991	Q14410	GLPK2_HUMAN			4	ATCGTTCCATCCT	0.512	
+	21	2857	dm.1_Missense_M	NM_016323	NP_057407	Q9UII4	HERC5_HUMAN	HECT.		9	TCCACCCCGAA	0.328	
-	14	2564		NM_003728	NP_003719	O95185	UNC5C_HUMAN	lasmic (Potential).		4	CTTCTCCTTCCA	0.522	
+	21	3625	.1_Missense_Muta	NM_001963	NP_001954	P01133	EGF_HUMAN	lasmic (Potential).		4	CTACAGGTGAC	0.552	
-	4	877	X2_uc010iml.2_In	NM_153426	NP_700475	Q99697	PITX2_HUMAN	Homeobox.		0	CAGCTCCTGGA	0.612	rs1051887
-	25	7081		NM_017639	NP_060109	Q6V1P9	PCD23_HUMAN	Cadherin 21.		4	TTCCATGAGTGA	0.388	
-	3	424	x.2_Missense_Mu	NM_017639	NP_060109	Q6V1P9	PCD23_HUMAN	Cadherin 1.		4	TTACCCCATCCT	0.333	
+	7	1266	_p.I236F|CLCN3_	NM_001829	NP_001820	P51790	CLCN3_HUMAN			3	TTCATCATCAGA	0.363	
-	1	38		NM_080874	NP_543150	Q8WWX0	ASB5_HUMAN			2	ACGGCCGATTTT	0.443	
+	15	2831	e.1_Missense_Mu	NM_001080477	NP_001073946	Q9P273	TEN3_HUMAN	cellular (Potential).		0	TGGATTCCATGG	0.433	
-	5	667	ju.1_Missense_Mu	NM_001042625	NP_001036090	Q8WWF8	CAPSL_HUMAN	EF-hand 4.		1	TCAATGGATGCG	0.488	
-	19	2337	3jmi.3_Nonsense_	NM_173489	NP_775760	Q7Z745	HTRB2_HUMAN			8	GGCTTTCCAAAG	0.244	
-	3	385	f34_uc011cpx.1_I	NM_198566	NP_940968	Q96MH7	CE034_HUMAN			1	AATGTGGAACCA	0.383	
+	22	3419	2_Missense_Muta	NM_012343	NP_036475	Q13423	NNTM_HUMAN	chondrial matrix.		3	ACAATCCAATCT	0.428	
+	16	2029	cqi.1_Missense_M	NM_015360	NP_056175	P42285	SK2L2_HUMAN			2	AAAAATCCTTCTA	0.378	
+	28	5305_5306	_Mutation_p.P167	NM_015183	NP_055998	O15021	MAST4_HUMAN			13	TGACCCCAAGCT	0.624	
+	1	672	uc011ctk.1_Intron	NM_032567	NP_115956	Q9BXG8	SPZ1_HUMAN			1	AAACAGGAGATG	0.358	

-	3	682	sense_Mutation_p.	NM_001142483	NP_001135955	Q16612	NP311_HUMAN		1	GATTAAAAAAAGT	0.423	
+	9	1897	kuz.2_Missense_M	NM_014031	NP_054750	Q9Y2P4	S27A6_HUMAN		0	GTTATTGGAATGT	0.343	
-	13	1344	CSL6_uc003kvz.1_	NM_015256	NP_056071	Q9UKU0	ACSL6_HUMAN	lasmic (Potential).	3	TTACCTGAATCTT	0.453	
+	1	2530		NM_018930	NP_061753	Q9UN67	PCDBA_HUMAN	lasmic (Potential).	2	AAGGGTGAAGAA	0.428	
+	1	630	DHGA2_uc011dao	NM_018915	NP_061738	Q9Y5H1	PCDG2_HUMAN	r (Potential).|Cadherin 2.	3	ACGCCAGGATTC	0.458	
+	1	1936	DHGA2_uc011dac	NM_018915	NP_061738	Q9Y5H1	PCDG2_HUMAN	r (Potential).|Cadherin 6.	3	CAGAGCCCGGCT	0.662	
+	1	1416	ljs.1_Intron|PCDH	NM_032088	NP_114477	Q9Y5G5	PCDG8_HUMAN	r (Potential).|Cadherin 2.	0	AGCTCAGCCCCA	0.572	rs143622391
+	12	2365	se_Mutation_p.G5	NM_001114183	NP_001107655	P42261	GRIA1_HUMAN	cellular (Potential).	6	AAGCAGGATCTA	0.493	
-	7	928		NM_032782	NP_116171	Q8TDQ0	HAVR2_HUMAN	lasmic (Potential).	0	TGTTTTCTTCTGA	0.468	
+	4	855	l11_uc003lxf.1_5'F	NM_173491	NP_775762	P83369	LSM11_HUMAN		0	CTTCTTCCCTGCA	0.587	
+	10	1353	RP_uc011dev.1_3	NM_014211	NP_055026	O00591	GBRP_HUMAN	lasmic (Potential).	1	GACAATGAAAACC	0.403	
-	10	1007_1008	0jkt.2_Missense_M	NM_173465	NP_775736	Q86Y22	CONA1_HUMAN	ntial).|Collagen-like 1.|Gly-r	2	GCTCTCCTTTGG	0.46	
-	2	96	te|PECI_uc003mw	NM_206836	NP_996667	O75521	ECI2_HUMAN		0	GTGACCTGCAGA	0.403	
-	8	2028	e_Mutation_p.P35	NM_000332	NP_000323	P54253	ATX1_HUMAN		4	GGTGAGGAACCG	0.677	
-	5	2732	_p.P641S|ZNF184_	NM_007149	NP_009080	Q99676	ZN184_HUMAN		1	GGTAGGGTTTTT	0.428	
-	10	5242	DC1_uc011dmp.1_	NM_014641	NP_055456	Q14676	MDC1_HUMAN	vith the PRKDC complex.	4	CTATTTGTCCTG	0.587	
+	12	1855	AT2_uc003nvc.3_M	NM_080686	NP_542417	P48634	PRC2A_HUMAN	epeats.|2 X type B repeats.|	0	CCACCTCCAGCA	0.627	
-	10	1521	p.P397S|BAT3_uc	NM_004639	NP_004630	P46379	BAG6_HUMAN	9 AA approximate repeats.	0	GGGAGGTGCCT	0.622	
+	6	952	_p.P69S|LY6G6D_	NM_001003693	NP_001003693	Q5SQ64	LY66F_HUMAN		2	CAACATCCAGCC	0.562	
+	7	1195	Missense_Mutatio	NM_000063	NP_000054	P06681	CO2_HUMAN	VWFA.	2	CTGAACGACAAC	0.498	
-	21	7550		NM_019105	NP_061978	P22105	TENX_HUMAN	nectin type-III 17.	0	GCCGCCCGTCCC	0.657	
-	14	5291		NM_019105	NP_061978	P22105	TENX_HUMAN	nectin type-III 10.	0	CCTCAGGAACCG	0.662	
-	5	987	0jud.1_Intron|HLA	NM_002118	NP_002109	P28068	DMB_HUMAN	lasmic (Potential).	0	CCCAGGAAGAG	0.443	
-	10	1231	ltf.1_Missense_Mu	NM_001145776	NP_001139248	Q13451	FKBP5_HUMAN	TPR 2.	1	CCAAGGGCCTAG	0.423	
+	10	1308	GD2_uc011dtv.1_M	NM_173558	NP_775829	Q7Z6J4	FGD2_HUMAN	PH 1.	3	GCTGATGGATGC	0.652	
-	6	989	2_RNA|TMEM151E	NM_020745	NP_065796	Q5JTZ9	SYAM_HUMAN		1	AGTGTGCGGATG	0.642	
-	1	1258		NM_138733	NP_620061	P07205	PGK2_HUMAN		1	TCAGTGTTCCATT	0.507	
-	2	307	bal.1_Missense_Mu	NM_052872	NP_443104	Q96PD4	IL17F_HUMAN		1	GGGAGGTGGAG	0.418	
+	5	1155		NM_001010872	NP_001010872	Q5T0W9	FA83B_HUMAN		6	TTAAATGAACATG	0.348	
-	21	2225	utation_p.G50R|C	NM_030820	NP_110447	Q96P44	COLA1_HUMAN		2	GCATCCCTTGAA	0.313	
+	11	1617	.2_3'UTR|SMAP1_	NM_001044305	NP_001037770	Q8IYB5	SMAP1_HUMAN		0	AGCTCATCAGGT	0.488	
-	4	917	hz.2_Missense_M	NM_015687	NP_056502	Q7Z7B0	FLIP1_HUMAN		4	CTAACTCGTATAC	0.507	
+	8	4359	ense_Mutation_p.F	NM_001137667	NP_001131139	Q9UKL3	C8AP2_HUMAN		2	AAGGTCCATCTC	0.388	
+	1	532		NM_032602	NP_115991	Q969M2	CXA10_HUMAN	ical; (Potential).	0	TATATTCTCTATG	0.448	
+	20	5579	i.2_Missense_Mut	NM_001624	NP_001615	Q9Y4K1	AIM1_HUMAN	in B-type lectin.	9	CAGTATGATCAA	0.403	
+	17	2197		NM_173560	NP_775831	Q8HWS3	RFX6_HUMAN		3	CAGCCCCACTCC	0.512	
-	4	479	.1_RNA|GOPC_uc	NM_002944	NP_002935	P08922	ROS_HUMAN	cellular (Potential).	25	GTACTTCCTCTT	0.473	
+	2	451	.3_Intron|TFB1M_	NM_001001346	NP_001001346	P56880	CLD20_HUMAN	ical; (Potential).	0	TCACAGCCACTC	0.522	
-	12	2923	vc.1_Missense_Mu	NM_018059	NP_060529	Q96JH8	RADIL_HUMAN	Pro-rich.	7	AGTCGGGGTCC	0.711	
-	1	620		NM_175886	NP_787082	P21108	PRPS3_HUMAN		1	GCAATGGAGGTC	0.463	
+	4	643	n_p.E52K|CREB5_	NM_182898	NP_878901	Q02930	CREB5_HUMAN		2	GAGCACGAGTTC	0.557	
+	14	1300	orf10_uc003tho.1_	NM_024728	NP_079004	Q9HAC7	CG010_HUMAN		2	AGATACGATGACA	0.567	
+	6	1150	_p.S182L|HECW1_	NM_015052	NP_055867	Q76N89	HECW1_HUMAN		23	AAAACTCGGCAG	0.408	
-	4	947	4_uc003tmx.2_Intr	NM_004749	NP_004740	Q969Z0	TBRG4_HUMAN		0	GCAAGGGCACG	0.607	
-	13	1078_1079	p.G238R|TNS3_uc	NM_022748	NP_073585	Q68CZ2	TENS3_HUMAN	2 tensin-type.	4	ATCTCCCTTCAG	0.515	
+	23	3035	p.G885E|EGFR_u	NM_005228	NP_005219	P00533	EGFR_HUMAN	Potential).|Protein kinase.	9571	AGAAAGGAGAAC	0.532	
-	15	1860	p.R595Q|ABCB4_	NM_018849	NP_061337	P21439	MDR3_HUMAN	1.|Cytoplasmic (By similarit	6	GCATTTCGGACC	0.488	rs144398632

-	3	356	mg.2_Missense_M	NM_017654	NP_060124	Q5K651	SAMD9_HUMAN	SAM.	7	AAATTTCCCTGT	0.368
+	18	2329	p.S707F|TRRAP_	NM_003496	NP_003487	Q9Y4A5	TRRAP_HUMAN		37	GCTCTCCAACC	0.468
-	1	701		NM_001005276	NP_001005276	Q8NHA4	O2AE1_HUMAN	lasmic (Potential).	0	GCATTTCTCTTG	0.502
+	31	5890	wl.2_RNA|ZAN_u	NM_003386	NP_003377	Q9Y493	ZAN_HUMAN	xtracellular (Potential).	11	CCTGCAAACCC	0.632
+	3	11710	C17_uc010lho.1_	NM_001040105	NP_001035194	Q685J3	MUC17_HUMAN	ellular (Potential).	27	ACTTCCAACTA	0.468
-	6	938	AT3_uc010lhr.2_	NM_178176	NP_835470	Q86VF5	MOGT3_HUMAN		2	AGCTTCTTGAA	0.577
-	56	9314	.2_Missense_Mut	NM_005045	NP_005036	P78509	RELN_HUMAN		19	TGATTTCTGCTC	0.448
+	6	2477	8_splice|PIK3CG_	NM_002649	NP_002640	P48736	PK3CG_HUMAN		38	CTTACAGATTGA	0.363
-	13	1665	ves.2_Missense_M	NM_000111	NP_000102	P40879	S26A3_HUMAN	ical; (Potential).	4	CTAACCCGAGT	0.448
+	3	555	vjz.2_Missense_M	NM_002851	NP_002842	P23471	PTPRZ_HUMAN	tial).|Alpha-carbonic anhyd	9	AAATATCCAACA	0.299
-	3	1041	_p.A118T|SLC13A	NM_012450	NP_036582	Q9UKG4	S13A4_HUMAN	ical; (Potential).	0	CTTGGCTCCGG	0.602
-	20	5852	.L1869F|KIAA154	NM_020910	NP_065961	Q9HCM3	K1549_HUMAN		230	GAGGAGCTCCT	0.622
-	15	1860		NM_004333	NP_004324	P15056	BRAF_HUMAN	rotein kinas_R603>I(2)|p.T	18290	ATTTCACTGTA	0.368
-	7	1067		NM_001080392	NP_001073861	A4D1U4	LCHN_HUMAN		1	TGTCAGCACTG	0.582
+	2	429		NM_178829	NP_849151	Q96L11	CG034_HUMAN		0	CAGGAGGGCCA	0.542
+	14	1651	c.1_Missense_Mu	NM_000083	NP_000074	P35523	CLCN1_HUMAN		5	TACCTGGGGGC	0.443
+	3	603	xbp.3_Missense_	NM_001128431	NP_001121903	Q15043	S39AE_HUMAN	ellular (Potential).	0	GCAGACGGAGG	0.652
+	45	4716	xei.2_Nonsense_	NM_024940	NP_079216	Q9H7D0	DOCK5_HUMAN	DHR-2.	3	CCAACGAGAGG	0.562
+	4	2555	1_uc011ldy.1_Intr	NM_006269	NP_006260	P56715	RP1_HUMAN		12	TGTTTCCTCAC	0.299
+	19	2108	_p.F694S|PREX2_	NM_024870	NP_079146	Q70Z35	PREX2_HUMAN	PDZ 2.	17	GGGATTTGGCC	0.453
+	10	4867	.R1539C|ZFHX4_	NM_024721	NP_078997	Q86UP3	ZFHX4_HUMAN		15	CCATCTCGTCCA	0.388
-	3	1107	ydr.1_Missense_M	NM_138817	NP_620172	Q8TCU3	S7A13_HUMAN	Name=9; (Potential).	1	TGTAAATGGAG	0.348
-	15	2419	.1_Missense_Mut	NM_015668	NP_056483	Q8NE09	RGS22_HUMAN		7	CTTTTCCTGTTG	0.413
-	2	890	M74_uc003ymx.2_	NM_153015	NP_694560	Q96NL1	TMM74_HUMAN		4	TGTTTCGACGA	0.507
+	12	1638	uc003yqx.1_Intron	NM_001039112	NP_001034201	Q2WGJ9	FR1L6_HUMAN	lasmic (Potential).	11	AATGAGGAATTT	0.363
-	7	833	e_Mutation_p.S12	NM_015912	NP_056996	Q49AJ0	F135B_HUMAN		9	CTGAGGAAGTC	0.473
-	3	363	se_Mutation_p.S11	NM_023078	NP_075566	Q53H96	P5CR3_HUMAN		0	TCAGAGACACC	0.622
+	7	1050_1051	f.3_Missense_Mut	NM_173831	NP_776192	Q96C28	ZN707_HUMAN	2H2-type 3.	1	AAGGACCGCCT	0.629
+	4	385	3_uc011lmh.1_Int	NM_033439	NP_254274	O95760	IL33_HUMAN		0	CTTCATGATTCA	0.498
-	1	5058	uc003zrh.1_5'Flan	NM_153809	NP_722516	Q8IZX4	TAF1L_HUMAN		26	GGGGTCATTGG	0.443
-	1	754	.M77T|GBA2_uc01	NM_020944	NP_065995	Q9HCG7	GBA2_HUMAN	ellular (Potential).	4	TAGCCCATAGCT	0.537
-	8	1253		NM_015225	NP_056040	Q8WUY3	PRUN2_HUMAN		0	GAGGGGGGCAC	0.517
+	12	1490	_Mutation_p.A331	NM_005392	NP_005383	O75151	PHF2_HUMAN		1	CAAAGCCGTCC	0.602
+	6	828	h.1_Missense_Mu	NM_032558	NP_115947	Q5SR56	HIAL1_HUMAN	ical; (Potential).	2	ATTGGAGCATAT	0.562
-	4	1182	d.3_Missense_Mu	NM_001127610	NP_001121082	Q14032	BAAT_HUMAN		3	CCCCAGGGTAA	0.527
-	1	689		NM_001001919	NP_001001919	Q8NGS5	O13C4_HUMAN	lasmic (Potential).	1	TGGCCGAGTTC	0.418
+	58	5072_5073	.2_RNA|COL27A1_	NM_032888	NP_116277	Q8IZC6	CORA1_HUMAN	lar collagen NC1.	4	CTGCAGGGACC	0.594
+	3	1156	_p.R249*|TLR4_u	NM_138554	NP_612564	O00206	TLR4_HUMAN	ellular (Potential).	16	GAATTCCGATTA	0.363
+	4	1237	v.1_Missense_Mu	NM_054107	NP_473448	Q8NGS2	OR1J2_HUMAN	lasmic (Potential).	5	ATATGTCACCCT	0.428
+	1	589		NM_001004457	NP_001004457	Q8NGR9	OR1N2_HUMAN	ellular (Potential).	4	TATTGTGATCCTA	0.532
+	11	2972	v.2_Missense_Mut	NM_005157	NP_005148	P00519	ABL1_HUMAN	-binding.|Pro-rich.	817	ATCCTCGGCCC	0.662
+	18	3205		NM_006059	NP_006050	Q9Y6N6	LAMC3_HUMAN	omain II and I.	3	GGAGGGGTGGC	0.612
-	8	2368	HGAP6_uc004cu	NM_013427	NP_038286	O43182	RHG06_HUMAN	Rho-GAP.	2	CTGTTCCTCCG	0.532
+	1	1902		NM_018094	NP_060564	Q8IYD1	ERF3B_HUMAN		1	TAATCTCCTTGG	0.413
-	3	594		NM_001006938	NP_001006939	Q6IPX3	TCAL6_HUMAN		1	CACATCTCCAC	0.488
+	4	1349	mg.1_Missense_M	NM_152423	NP_689636	Q5H9M0	MUML1_HUMAN		4	AAGATGAAAAG	0.408
-	11	1699	su.1_Missense_M	NM_014289	NP_055104	Q9Y6Q1	CAN6_HUMAN		6	GCCACGAGCCA	0.423

+	5	915	A3_uc004ets.3_R	NM_007325	NP_015564	P42263	GRIA3_HUMAN	ellular (Potential).	5	TTGAAGAAATG	0.443	
-	3	462		NM_001013403	NP_001013421	Q5JRM2	CX066_HUMAN	ytoplasmic (Potential).	0	GTATGGATGGC	0.418	
+	5	533	|PUSL1_uc010ny	NM_153339	NP_699170	Q8N0Z8	PUSL1_HUMAN		1	GGAAGCCGCCC	0.716	
+	3	360	jf.1_Nonsense_Mu	NM_007033	NP_008964	O15258	RER1_HUMAN	ical; (Potential).	0	ATGATTCGAGTT	0.522	
-	22	2406	asb.2_Missense_M	NM_001001998	NP_001001998	Q01780	EXOSX_HUMAN		1	TGGGTCGCTTG	0.488	
-	28	4232		NM_004958	NP_004949	P42345	MTOR_HUMAN		29	CAGGGGGCCCT	0.527	
+	11	2509	asi.1_Nonsense_M	NM_020780	NP_065831	Q9P2K9	PTHD2_HUMAN	ellular (Potential).	7	TGTTCCAGGAG	0.652	
+	3	512	.2_Missense_Muta	NM_033182	NP_149438	Q9H4M3	FBX44_HUMAN	FBA.	1	TTACTTCATATTA	0.527	
+	4	897	aug.1_Missense_M	NM_001103170	NP_001096640	Q5VUY0	ADCL3_HUMAN		0	TCTGGGAAAAG	0.478	
-	1	370	0obf.1_Missense_	NM_001146181	NP_001139653	B7ZW38	B7ZW38_HUMAN		0	TTTCCTCGGTTC	0.483	
-	1	273		NM_001136561	NP_001130033	B2RXH8	B2RXH8_HUMAN		0	TTTTCTCCTTAT	0.478	
-	10	1420	F1_uc001ayz.1_5'	NM_017940	NP_060410	Q3BBV0	NBPF1_HUMAN	NBPF 1.	0	AGCCTCCTCAA	0.438	
+	5	506		NM_016233	NP_057317	Q9ULW8	PADI3_HUMAN		2	TGTGACCGTGAT	0.602	
+	15	1710		NM_016233	NP_057317	Q9ULW8	PADI3_HUMAN		2	GAAGCGGGAGC	0.592	rs138012325
-	66	9774	bk.1_Missense_Mu	NM_020765	NP_065816	Q5T4S7	UBR4_HUMAN		25	TGGCTGTAACC	0.587	
+	6	656		NM_016183	NP_057267	Q9UKD2	MRT4_HUMAN		0	TTTCACTGTGA	0.587	
+	5	842	qb.2_Missense_Mu	NM_032264	NP_115640	Q9H094	NBPF3_HUMAN	Potential.	2	ACCCAGTTAAG	0.502	
-	8	603_604	bew.2_Missense_	NM_002885	NP_002876	P47736	RPGP1_HUMAN		3	CTTGAGTGAGAA	0.604	
+	11	1401	AL3_uc009vrc.2_M	NM_020448	NP_065181	Q6P499	NPAL3_HUMAN		0	TTTGAGCCCTAT	0.448	
-	4	960	n_p.T281I|ZNF683	NM_173574	NP_775845	Q8IZ20	ZN683_HUMAN		0	AGTCGGTTGGG	0.647	
+	9	861	_p.S255F|KPNA6_	NM_012316	NP_036448	O60684	IMA7_HUMAN	ARM 5.	0	TACTGTCTCGCC	0.507	
-	3	1255		NM_018207	NP_060677	Q9BVG3	TRI62_HUMAN	Potential.	0	GCGTGCGGGCC	0.667	
+	2	1044	p.P395L|GJA4_uc	NM_002060	NP_002051	P35212	CXA4_HUMAN	lasmic (Potential).	1	AAAACCCCCAA	0.582	
-	4	395	ax.1_Missense_M	NM_000760	NP_000751	Q99062	CSF3R_HUMAN	.|Extracellular (Potential).	3	CCTGCCCCCGG	0.602	
-	2	269	ba.1_Missense_M	NM_000831	NP_000822	Q13003	GRIK3_HUMAN	ellular (Potential).	7	CCGTCCGCATAC	0.502	
-	4	792	PO1_uc009vvf.1_I	NM_001038633	NP_001033722	Q2MKA7	RSPO1_HUMAN		0	AAGCCGCATAG	0.642	
-	13	2296	.1_RNA|EPHA10_	NM_001099439	NP_001092909	Q5JZY3	EPHAA_HUMAN	Potential).|Protein kinase.	8	CGTGCCGCTGT	0.622	
+	1	3841	.1_Intron|MACF1_	NM_015038	NP_055853	O94854	K0754_HUMAN	Ala-rich.|2.	0	AGCCCACCTCC	0.721	
-	3	589	se_Mutation_p.T1	NM_148960	NP_683763	Q8N6F1	CLD19_HUMAN	ical; (Potential).	0	TCAAAGTGCAG	0.607	
+	3	268	_p.R75C|MPL_uc	NM_005373	NP_005364	P40238	TPOR_HUMAN	ellular (Potential).	363	AGCCCCGTGCT	0.597	
+	11	1439		NM_015284	NP_056099	Q5T011	SZT2_HUMAN		0	GGCTTCCCAGA	0.562	
+	6	889	T2_uc001coy.1_5	NM_015112	NP_055927	Q6P0Q8	MAST2_HUMAN		11	CCTTTGGACAG	0.488	
+	7	1020	AH_uc001cpv.2_In	NM_001441	NP_001432	O00519	FAAH1_HUMAN	smic (By similarity).	2	CTTGCCCTTCA	0.662	
+	11	1398	AH_uc001cpv.2_R	NM_001441	NP_001432	O00519	FAAH1_HUMAN	smic (By similarity).	2	GTCTCGGTAAG	0.577	
+	11	1803		NM_000562	NP_000553	P07357	CO8A_HUMAN	SP type-1 2.	3	CAGGAAAGGAG	0.572	
-	14	1971	r.1_Nonsense_Mu	NM_021080	NP_066566	O75553	DAB1_HUMAN		3	GGGCTGGTCGG	0.557	
+	9	975	df.2_Missense_M	NM_001077700	NP_001071168	Q8N108	MIER1_HUMAN	eraction with HDAC1.	1	ATATTTCTTAAAG	0.343	
+	4	786	sf.2_Missense_Mu	NM_017734	NP_060204	Q9NP74	PALMD_HUMAN		3	TTGAGCGGACA	0.333	
-	44	3706	.E1142K|COL11A1	NM_001854	NP_001845	P12107	COBA1_HUMAN	le-helical region.	12	CAATTTCACCCT	0.318	
-	6	956	dvm.2_Missense_	NM_013386	NP_037518	Q6NUK1	SCMC1_HUMAN	hondrial matrix (Potential).	1	CGAGCGGATAC	0.393	
+	7	2014	v.3_Missense_Mu	NM_172212	NP_757351	P09603	CSF1_HUMAN	lasmic (Potential).	1	ATTCTCCCTTGG	0.637	
-	11	1869	p.P567S|OVGP1_	NM_002557	NP_002548	Q12889	OVGP1_HUMAN		5	CCTGGGGTGAG	0.517	
-	2	589	bv.1_Missense_M	NM_004980	NP_004971	Q9UK17	KCND3_HUMAN	lasmic (Potential).	3	CTGCCGCTTGT	0.682	
+	7	1205	_p.P342S|MAGI3_	NM_001142782	NP_001136254	Q5TCQ9	MAGI3_HUMAN	WW 2.	6	AGCTTCCTTATG	0.328	
-	13	1883	ff.1_Missense_Mu	NM_000036	NP_000027	P23109	AMPD1_HUMAN		4	CTCACCTTTTTT	0.418	
+	11	951	se_Mutation_p.E2	NM_003176	NP_003167	Q15431	SYCP1_HUMAN	Potential.	1	GATTATGAAAAA	0.229	
-	29	4314		NM_206996	NP_996879	Q6Q759	SPG17_HUMAN		6	CAATGGGGTCA	0.398	

+	3	714	enm.1_Intron|TXN	NM_006472	NP_006463	Q9H3M7	TXNIP_HUMAN		2	TACTGGGTGAAG	0.428	
-	8	1274	RC_uc010pdo.1_M	NM_005060	NP_005051	P51449	RORG_HUMAN	gand-binding.	2	AGGCTCGGAAC	0.552	
-	3	754		NM_001122965	NP_001116437	Q6XPR3	RPTN_HUMAN	Gln-rich.	0	CACACCGATTTA	0.413	
-	3	566	uc001ezv.2_Intron	NM_001014342	NP_001014364	Q5D862	FILA2_HUMAN	Ser-rich.	17	TACCTTGTCTTCC	0.493	
+	1	40		NM_178354	NP_848131	Q5T754	LCE1F_HUMAN	Pro-rich.	0	AGCCccctcccaagtg	0.358	
-	7	1460		NM_020699	NP_065750	Q8WXI9	P66B_HUMAN	CR2.	0	CCTTACCTTGGC	0.423	
-	2	287	9A1_uc001fdk.2_M	NM_014437	NP_055252	Q9NY26	S39A1_HUMAN	ical; (Potential).	0	GGTGAGCACCA	0.647	
+	2	779	_uc001fkl.2_5'Flar	NM_001105203	NP_001098673	Q9BVN2	RUSC1_HUMAN		2	GCAACGCCCTG	0.622	
+	3	268	1_5'Flank|PEAR1_	NM_001080471	NP_001073940	Q5VY43	PEAR1_HUMAN	EMI.	3	GCTCCCCTCAG	0.672	
+	15	2067	fqk.1_Splice_Site_	NM_001080471	NP_001073940	Q5VY43	PEAR1_HUMAN		3	CCAGCGTATGT	0.622	
+	3	681	1C_uc001frv.2_5'U	NM_001765	NP_001756	P29017	CD1C_HUMAN	cellular (Potential).	4	CAGAAGGCTTCT	0.463	
-	1	864		NM_001004476	NP_001004476	Q6IF99	O10K2_HUMAN	Name=7; (Potential).	1	ATAAATCATTGG	0.333	rs137874220
+	1	931		NM_001005184	NP_001005184	Q8NGW6	OR6K6_HUMAN	Name=7; (Potential).	1	GCTCCCTTTTTCA	0.438	
-	1	460		NM_001004467	NP_001004467	Q5JRS4	O10J3_HUMAN	Name=4; (Potential).	2	GCCAAGGCCAA	0.507	
-	6	824	_p.H144Y|COPA_u	NM_004371	NP_004362	P53621	COPA_HUMAN	WD 4.	2	GGGGTGGAACT	0.468	
+	15	5371	PA2_uc009www.2_	NM_020318	NP_064714	Q9BXP8	PAPP2_HUMAN	Sushi 1.	16	CTTGATCATGCT	0.507	
-	3	772	e_Mutation_p.P18	NM_004319	NP_004310	O14525	ASTN1_HUMAN		15	GCTGCGGGACC	0.612	
+	34	7491	_p.P505S|CEP350_	NM_014810	NP_055625	Q5VT06	CE350_HUMAN		4	TTTGCTCCTAAAG	0.338	
+	2	923		NM_020950	NP_066001	Q5VZ46	K1614_HUMAN		4	TGGGCGCTGGG	0.627	
+	5	1415	e_Mutation_p.V71M	NM_020950	NP_066001	Q5VZ46	K1614_HUMAN		4	TCGCACGTGCGC	0.701	
+	22	3592	p.V1093A|LAMC2_	NM_005562	NP_005553	Q13753	LAMC2_HUMAN	omain II and I.	3	CTGGGGTTACAA	0.483	
-	8	2173	pj.1_Missense_Mu	NM_014875	NP_055690	Q15058	KIF14_HUMAN	Kinesin-motor.	7	CTGGGTCATCAC	0.388	rs144936292
+	10	3451	_p.S644F|NAV1_u	NM_020443	NP_065176	Q8NEY1	NAV1_HUMAN		4	CCTGTCCCTGG	0.622	
+	4	1341	_p.A153T|ATP2B4_	NM_001684	NP_001675	P23634	AT2B4_HUMAN	ical; (Potential).	3	AGGGGGCAGCC	0.502	
+	5	1182_1183	p.G242*|LAX1_uc	NM_017773	NP_060243	Q8IWV1	LAX1_HUMAN	lasmic (Potential).	2	GCAATGGAGAAG	0.5	
+	20	3030	_p.S805*|ZC3H11A	NM_014827	NP_055642	O75152	ZC11A_HUMAN		2	AGCTATCAGAAA	0.378	
-	7	1500		NM_030952	NP_112214	Q9H093	NUAK2_HUMAN		5	TAGTAGCCAGAC	0.642	
+	2	234	se_Mutation_p.R39	NM_001910	NP_001901	P14091	CATE_HUMAN		1	GGCACGGAGCC	0.557	
-	15	1908	w.2_Missense_Mu	NM_006893	NP_008824	P41214	EIF2D_HUMAN		0	TCGAGGGAGCT	0.532	
+	3	381	njh.2_Missense_M	NM_001030287	NP_001025458	P18847	ATF3_HUMAN		0	TAGCCCCTGAAG	0.438	
+	1	1922	uc010pth.1_RNA	NM_153606	NP_705834	Q8IYT1	FA71A_HUMAN		5	CTCTCACAAATCT	0.557	
+	17	5064	p.V1674M|OBSCN_	NM_001098623	NP_001092093	Q5VST9	OBSCN_HUMAN	Ig-like 17.	28	TGCGCGTGGAG	0.677	
+	5	3220	e.1_Missense_Mut	NM_020066	NP_064450	Q9NZ56	FMN2_HUMAN	Pro-rich.|FH1.	12	ATACCCCCTCCG	0.711	
+	5	3352	e.1_Missense_Mut	NM_020066	NP_064450	Q9NZ56	FMN2_HUMAN	Pro-rich.|FH1.	12	ATACCCCCTCCG	0.731	
-	4	1462	695_uc009xgt.1_In	NM_020394	NP_065127	Q8IW36	ZN695_HUMAN	C2H2-type 11.	0	ACATTCATCACAT	0.368	
+	1	26		NM_001004696	NP_001004696	Q8NH00	OR2T4_HUMAN	cellular (Potential).	1	GGCCAGCCACA	0.483	rs140989725
-	1	392		NM_001004734	NP_001004734	A6ND48	O14I1_HUMAN	lasmic (Potential).	0	ACGGCTCTGTATT	0.517	
+	3	778	xig.2_Missense_M	NM_178150	NP_835363	Q8NFZ0	FBX18_HUMAN		3	CCTCCCGGTGG	0.423	
+	3	607	KFB3_uc010qaw.1	NM_004566	NP_004557	Q16875	F263_HUMAN	phofructo-2-kinase.	3	GAGTATCGCCGG	0.507	
-	9	1524	HS1_uc001imi.2_I	NM_012247	NP_036379	P49903	SPS1_HUMAN		1	GGCCCCGGGTG	0.418	
-	9	1342	01ito.2_Missense_	NM_145698	NP_663736	Q5T8D3	ACBD5_HUMAN		0	TCTCCCGGTGT	0.453	
-	2	1455	nse_Mutation_p.G	NM_020848	NP_065899	Q9P266	K1462_HUMAN		4	TCCTCCATGAGC	0.522	
-	7	1541	_p.G340R|NRP1_u	NM_003873	NP_003864	O14786	NRP1_HUMAN	.|Extracellular (Potential).	4	GTGTCCCGACAG	0.488	
+	7	794		NM_052997	NP_443723	Q9BXX3	AN30A_HUMAN		9	CCTTGGCGGAAA	0.423	
+	2			NR_024524					0	GATGGTGAGACA	0.333	
-	10	1438	_p.E439K|CTNNA3	NM_001127384	NP_001120856	Q9UI47	CTNA3_HUMAN		8	CATCTTCATTTGT	0.308	
+	15	1877	PL1_uc009xqk.2_F	NM_003901	NP_003892	O95470	SGPL1_HUMAN	lasmic (Potential).	0	CAGCACCGACA	0.502	

-	3	685	_p.P179T|DNAJB1	NM_017626	NP_060096	Q9NXW2	DJB12_HUMAN	J.	0	ACCAGGTGCGT	0.562	
-	22	2827	xl.1_Missense_M	NM_001161352	NP_001154824	Q12791	KCMA1_HUMAN	lasmic (Potential).	3	GTACTCAATAG	0.498	
+	22	3133	n_p.I730T|ZMIZ1_	NM_020338	NP_065071	Q9ULJ6	ZMIZ1_HUMAN		4	AGATGATCATGC	0.632	
-	17	2003		NM_022451	NP_071896	Q8WTT2	NOC3L_HUMAN		1	ATTTGGAAGAA	0.383	
-	9	1080_1081	uk.1_Missense_M	NM_022451	NP_071896	Q8WTT2	NOC3L_HUMAN		1	TTTAAGGAAACT	0.376	
-	1	103	8_uc010qob.1_5'	NM_000770	NP_000761	P10632	CP2C8_HUMAN		0	ACAAAAGGTTCC	0.453	
-	4	1353	00093_uc001kqk.	NM_015221	NP_056036	Q6XZF7	DNMBP_HUMAN		6	GGGATGAAAAG	0.527	
-	2	582		NM_001308	NP_001299	P15169	CBPN_HUMAN	Catalytic.	4	GTTCCGGAACT	0.602	rs146812654
-	4	860		NM_000102	NP_000093	P05093	CP17A_HUMAN		0	TTTTTCCAGGG	0.383	
+	17	2548	CS3_uc010qqz.1_	NM_014978	NP_055793	Q9UPU3	SORC3_HUMAN	enal (Potential).	10	CAATCCAGCAT	0.453	
+	4	374	RNA|HABP2_uc01	NM_004132	NP_004123	Q14520	HABP2_HUMAN	EGF-like 1.	3	TCGTCCATGGG	0.537	
+	18	2490	lfd.1_Missense_M	NM_018117	NP_060587	Q9BZH6	WDR11_HUMAN	WD 7.	0	AAGTTGGGTGA	0.408	
+	26	3119	R506*|DMBT1_uc	NM_007329	NP_015568	Q9UGM3	DMBT1_HUMAN	SRCR 8.	7	AGGGCCGAGTG	0.567	
-	3	365	ASSF7_uc001lqb.	NM_173573	NP_775844	Q8IXW0	CK035_HUMAN		1	TGGGCGGAAGC	0.662	
+	14	2107	RF1_uc010qwe.1_	NM_020901	NP_065952	Q9P1Y6	PHRF1_HUMAN		0	ATGTCGCAGTG	0.592	
-	8	1611	DD_uc001lrm.1_M	NM_145886	NP_665893	Q9HB75	PIDD_HUMAN	ZU5 2.	0	AGACTCGACGA	0.672	
-	4	564		NM_004420	NP_004411	Q13202	DUS8_HUMAN		0	CATGGGTAGCA	0.652	
-	13	1394	1_Nonsense_Mut	NM_199292	NP_954986	P07101	TY3H_HUMAN		0	TGACTGGTACG	0.627	
-	19	2935	p.A976T|TRPM5_	NM_014555	NP_055370	Q9NZQ8	TRPM5_HUMAN	lasmic (Potential).	4	CATGGCGATGA	0.602	
-	1	576		NM_001005238	NP_001005238	Q8NGK0	O51G2_HUMAN	ellular (Potential).	2	ACAGGCCAATTT	0.448	
-	1	28		NM_001005164	NP_001005164	Q8NGJ4	O52E2_HUMAN	ellular (Potential).	3	GGGGTGAAACT	0.498	
-	9	1969	p.R409C|TRIM3_	NM_006458	NP_006449	O75382	TRIM3_HUMAN	NHL 2.	5	TGAGCGTCCTC	0.582	
-	9	1419	.P30S|MRVI1_uc	NM_001100167	NP_001093637	Q9Y6F6	MRVI1_HUMAN		3	TCTCGGCAGAG	0.677	
-	3	803	_Mutation_p.R15	NM_024514	NP_078790	Q6VVX0	CP2R1_HUMAN		2	GCTTTCTGTTG	0.378	
-	30	3808		NM_000352	NP_000343	Q09428	ABCC8_HUMAN	pe-1 2.|Cytoplasmic (By si	1	GTATTCGAGAA	0.542	
-	7	740	se_Mutation_p.P1	NM_006292	NP_006283	Q99816	TS101_HUMAN		0	GAGAAGGGTAC	0.428	
+	14	3375	AV2_uc001mpt.2_	NM_145117	NP_660093	Q8IVL1	NAV2_HUMAN		6	GAATTCCCTGT	0.537	
-	2	2065		NM_002233	NP_002224	P22459	KCNA4_HUMAN		4	TGCAGGACTGG	0.498	
-	3	764	_p.R102W|LMO2_	NM_001142316	NP_001135788	P25791	RBTN2_HUMAN	zinc-binding 2.	1	CACCCGCATTG	0.478	rs150071797
+	7	1675		NM_005456	NP_005447	Q9UQF2	JIP1_HUMAN	SH3.	4	GCCTCGACACG	0.577	
+	1	362		NM_001005275	NP_001005275	Q8NGL6	O4A15_HUMAN	ellular (Potential).	2	CATTTCCTTTC	0.388	
+	1	838		NM_001001967	NP_001001967	Q8NGL4	OR5DD_HUMAN	Name=7; (Potential).	3	TGTTTTACACA	0.378	rs150799318
-	1	278		NM_001004058	NP_001004058	Q8NH50	OR8K5_HUMAN	ellular (Potential).	4	TAATAGGAAATA	0.398	
+	1	757		NM_001005205	NP_001005205	Q8NGP2	OR8J1_HUMAN	Name=6; (Potential).	2	TTTATGGGACAT	0.363	
+	7	811		NM_000139	NP_000130	Q01362	FCERB_HUMAN	lasmic (Potential).	1	CAGGGGAAATG	0.418	
+	5	544		NM_017716	NP_060186	Q9NXJ0	M4A12_HUMAN	ical; (Potential).	0	GCCTGGGAATG	0.423	
+	5	844	o.1_Missense_Mu	NM_004265	NP_004256	O95864	FADS2_HUMAN	lasmic (Potential).	2	ATCCCGATGTG	0.562	
-	2	2551	AB_uc001nuc.2_5'	NM_030628	NP_085131	Q6P9B9	INT5_HUMAN		2	CCTCGGGGGC	0.647	
+	2	406	ilent_p.L128L|SA	NM_005146	NP_005137	O43290	SNUT1_HUMAN		1	TCCAGCTGCCA	0.517	
+	3	757	nse_Mutation_p.A	NM_138768	NP_620123	Q96EZ4	MYEOV_HUMAN		0	CTGGAGCTGGT	0.652	
+	3	1325	_p.W380L|NEU3_	NM_006656	NP_006647	A8K327	A8K327_HUMAN		2	CTGCTGGTCCC	0.562	
-	4	2365		NM_033063	NP_149052	Q96JE9	MAP6_HUMAN	Pro-rich.	0	TTGCTGGTACT	0.522	
+	4	680	xb.2_Missense_M	NM_032564	NP_115953	Q96PD7	DGAT2_HUMAN	lasmic (Potential).	0	ACTTTCCCATC	0.527	
+	47	6648	_Mutation_p.P20	NM_000260	NP_000251	Q13402	MYO7A_HUMAN	FERM 2.	4	ACTTCCCTGAG	0.522	
-	32	7160	.R458W|ODZ4_u	NM_001098816	NP_001092286	Q6N022	TEN4_HUMAN	lar (Potential).|YD 19.	4	GAGCCGTGCAC	0.592	
+	2	350	RSS23_uc010rts.	NM_007173	NP_009104	O95084	PRS23_HUMAN		2	AGTCTACCCTCA	0.532	
+	2	978		NM_000372	NP_000363	P14679	TYRO_HUMAN	elanosome (Potential).	3	ACGGCGTAATC	0.468	rs61754375

+	2	500		NM_001098672	NP_001092142	Q6MZM0	HPHL1_HUMAN	e 1.|Extracellular (Potential		3	GTCATTCATTTAA	0.458	
-	5	422	se_Mutation_p.D6	NM_152587	NP_689800	Q8NCR3	CK065_HUMAN			1	GATGATCATTTT	0.358	
+	4	622		NM_198498	NP_940900	Q8IXP5	CK053_HUMAN			0	CTGGGGCTCAG	0.622	
+	8	1234	.1_3'UTR|LAYN_	NM_178834	NP_849156	Q6UX15	LAYN_HUMAN	lasmic (Potential).		0	AAAGCGAAGCT	0.507	
-	5	1094	ppd.2_Missense_	NM_001077639	NP_001071107	Q6UWF7	FA55D_HUMAN			4	ATTTCTCTTTCAT	0.403	
-	1	586		NM_001004474	NP_001004474	Q8NGN2	O10S1_HUMAN	ellular (Potential).		2	AGGGGGTATGT	0.572	
+	7	1766	u.2_Missense_M	NM_002286	NP_002277	P18627	LAG3_HUMAN	lasmic (Potential).		0	TTCACCTTTGG	0.602	
-	25	3205	p.R73Q|A2M_uc0	NM_000014	NP_000005	P01023	A2MG_HUMAN			5	CATATCGCTCC	0.318	
-	1	335	H1_uc001qzc.2_I	NM_023922	NP_076411	Q9NYV8	T2R14_HUMAN	lasmic (Potential).		0	AATTGGCTATCT	0.348	
+	6	927	1467_uc009zhx.1_	NM_020853	NP_065904	A2RU67	K1467_HUMAN		p.R302*(1)	3	TGGGTCGACCT	0.507	
-	3	424		NM_182558	NP_872364					0	GGAACGATTCC	0.453	rs143075618
+	21	2889	nse_Mutation_p.D	NM_004570	NP_004561	O75747	P3C2G_HUMAN	PI3K/PI4K.		21	GGAGATGATCTT	0.368	
+	21	2895	nse_Mutation_p.R	NM_004570	NP_004561	O75747	P3C2G_HUMAN	PI3K/PI4K.		21	GATCTTCGTCAG	0.363	
+	1	679	Z1_uc001rdw.3_5'	NM_033328	NP_201585	Q96KX2	CAZA3_HUMAN			2	CTAAATGGATTTT	0.383	
-	1	325		NM_001040436	NP_001035526	Q9Y2Z4	SYYM_HUMAN	HIGH region.		0	ATGAAGCGAGT	0.622	
+	10	1191	n.1_Missense_M	NM_001843	NP_001834	Q12860	CNTN1_HUMAN	like C2-type 4.		9	CCATCCCTACA	0.483	
-	2	1273		NM_001008223	NP_001008224	Q86Z23	C1QL4_HUMAN	C1q.		0	CGCGTCCTGAG	0.642	
+	15	2952	mj.1_Missense_M	NM_012284	NP_036416	Q9ULD8	KCNH3_HUMAN	lasmic (Potential).		0	GGGAAGGACTG	0.662	
+	36	4462	lt.2_Missense_Mu	NM_173602	NP_775873	Q9P265	DIP2B_HUMAN			6	GGACAGGATAC	0.527	
-	15	1527	C11A2_uc001rxh.	NM_000617	NP_000608	P49281	NRAM2_HUMAN	lasmic (Potential).		1	CAATCCGCCAG	0.443	
-	7	1513	ryl.1_Missense_M	NM_007210	NP_009141	Q8NCL4	GALT6_HUMAN	enal (Potential).		2	CAGGCGCACTT	0.542	
-	2	619	nse_Mutation_p.E1	NM_007210	NP_009141	Q8NCL4	GALT6_HUMAN	enal (Potential).		2	CTTTTCCTGGG	0.577	
+	7	1068	T81_uc001sac.2_I	NM_002284	NP_002275	O43790	KRT86_HUMAN	Rod.|Coil 2.		1	GCACGGGGAGA	0.602	
-	2	586	72_uc010sns.1_M	NM_001146225	NP_001139697	Q14CN4	K2C72_HUMAN	inker 1.|Rod.		6	TGCAGTTGTTC	0.567	
+	17	1715	_p.R88C|NCKAP1	NM_005337	NP_005328	P55160	NCKPL_HUMAN			4	ATCTTCGTATCT	0.393	
+	2	314	RBB3_uc010sqc.1_	NM_001982	NP_001973	P21860	ERBB3_HUMAN	ellular (Potential).		8	CCGGCGATGCT	0.542	
+	3	271		NM_032786	NP_116175	Q96K80	ZC3HA_HUMAN	Gly-rich.		0	CCAGTGGGGCA	0.647	
+	24	4326		NM_002332	NP_002323	Q07954	LRP1_HUMAN	ellular (Potential).		22	CAAAGGAGACT	0.597	
-	3	238	te|DCTN2_uc001	NM_006400	NP_006391	Q13561	DCTN2_HUMAN			1	TCCTCCTGCAA	0.488	
+	3	1541	zs.1_Missense_M	NM_152588	NP_689801	Q8N394	TMTC2_HUMAN			2	CTTTGCATCCA	0.398	
-	8	2400	k.3_Missense_Mu	NM_013244	NP_037376	Q9UBM8	MGT4C_HUMAN	enal (Potential).		3	ATTTTCAAATAC	0.343	
-	6	1162		NM_145913	NP_666018	Q8N695	SC5A8_HUMAN	ical; (Potential).		0	GACACCGTAGA	0.388	
+	27	3226	0svs.1_Missense_	NM_206820	NP_996556	Q00872	MYPC1_HUMAN			4	ACTTTGATTTCT	0.358	
-	13	1680		NM_000277	NP_000268	P00439	PH4H_HUMAN			4	TGGCAGCAAAG	0.458	rs5030857
+	3	419		NM_017564	NP_060034	Q8WWQ8	STAB2_HUMAN	ellular (Potential).		14	GGTCAGAACAT	0.493	
-	2	810	u.2_Missense_Mu	NM_138451	NP_612460	Q96DY2	IQCD_HUMAN			1	GAGGCGGTCTC	0.522	rs141733272
+	13	2435	F10_uc001tyq.3_	NM_014868	NP_055683	Q8N5U6	RNF10_HUMAN			2	CTGCTCCTCTG	0.512	
+	13	1547	RX7_uc001tzp.2_	NM_002562	NP_002553	Q99572	P2RX7_HUMAN			5	CCTCCCATCTC	0.597	
+	1	43	D8_uc001uex.2_5'	NM_020382	NP_065115	Q9NQR1	SETD8_HUMAN			0	GAGCCATGGCT	0.667	
-	9	2808	1uia.2_Missense_	NM_133448	NP_597705	Q14C87	T132D_HUMAN	ellular (Potential).		14	TTTTTGGGCCTT	0.522	
+	28	5773	_uc001ujm.2_Miss	NM_015409	NP_056224	Q96L91	EP400_HUMAN	case C-terminal.		12	TGCCAGCAGTG	0.423	
-	4	1462	nr.3_Missense_M	NM_014572	NP_055387	Q9NRM7	LATS2_HUMAN			10	GGACGGAGGTG	0.721	
-	3	387	T3_uc010tdn.1_M	NM_004119	NP_004110	P36888	FLT3_HUMAN	ellular (Potential).		8549	GACAGGAAATG	0.498	
+	43	6248	Y_uc010tdw.1_R	NM_023037	NP_075463	Q5TBA9	FRY_HUMAN			7	AGGCGGCTGTG	0.408	
+	9	970	ua.1_Missense_M	NM_000059	NP_000050	P51587	BRCA2_HUMAN			64	TTATCGCTTCTGT	0.308	
-	9	1731	.A429G|ELF1_uc	NM_172373	NP_758961	P32519	ELF1_HUMAN			1	TGCTGGCTATA	0.448	
+	3	838	ao.2_Missense_M	NM_152719	NP_689932	Q8NA61	SPERT_HUMAN	Potential.		2	GGAGGAGAATC	0.677	

-	9	995	ıse_Mutation_p.R2	NM_152720	NP_689933	P51956	NEK3_HUMAN	ith VAV2.|Protein kinase.		2	GCCTCGAGAGA	0.478	
-	3	661	.N39S|THSD1_uc	NM_018676	NP_061146	Q9NS62	THSD1_HUMAN	cellular (Potential).		4	TGTCGTTGCTT	0.433	
+	2	165	sense_Mutation_	NM_024808	NP_079084	Q6PGQ7	BORA_HUMAN			0	AAACTCCAGGA	0.348	
-	4	618	e_Mutation_p.A17	NM_001079669	NP_001073137	Q5T4D3	TMTC4_HUMAN	ical; (Potential).		3	GCAGCGCGGCC	0.612	
+	15	3853_3854		NM_000123	NP_000114	P28715	ERCC5_HUMAN			7	AGCTCCCGTGA	0.485	
-	8	890	2_5'Flank|GAS6_	NM_000820	NP_000811	Q14393	GAS6_HUMAN	alcium-binding (Potential).		4	CACAGCGGCCC	0.662	rs78824256
+	9	1320	a.1_RNA|POTEG_	NM_001005356	NP_001005356	Q6S5H5	POTEG_HUMAN			1	GCACGGAAGTA	0.358	
+	1	344		NM_001004723	NP_001004723	Q8NGD1	OR4N2_HUMAN	Name=3; (Potential).		4	TACTCCTTGTTG	0.507	
+	2	383		NM_022360	NP_071755	P56851	EP3B_HUMAN			1	GTATGGGTCCA	0.408	
-	26	3419	wan.2_Missense_	NM_007192	NP_009123	Q9Y5B9	SP16H_HUMAN			0	GGCCCGAACTG	0.507	
-	35	5099		NM_000257	NP_000248	P12883	MYH7_HUMAN	Potential.		4	GTCGTCGTTGG	0.612	
-	8	1363	M1_uc010tog.1_In	NM_000359	NP_000350	P22735	TGM1_HUMAN			3	ATGTCCATGGT	0.572	
+	9	5542		NM_025081	NP_079357	Q9P2P1	NYNRI_HUMAN	grase catalytic.		3	TCCCTGCCTTTG	0.627	
-	3	671	A1_uc001wqa.2_5	NM_002515	NP_002506	P51513	NOVA1_HUMAN			5	ATTTTTTCTGCA	0.438	
+	2	1273	.2_Missense_Mut	NM_001173	NP_001025226	Q13017	RHG05_HUMAN			5	AAGAGCTTTTA	0.313	
+	4	798	y.1_Missense_Mu	NM_054024	NP_473365	Q96PC5	MIA2_HUMAN			2	TTGTTGAAAGT	0.428	
+	1	624	d.1_Missense_Mu	NM_031914	NP_114120	Q17RD7	SYT16_HUMAN			1	CGGAGGAAGAG	0.463	
-	32	6041	VE26_uc001xkc.	NM_015346	NP_056161	Q68DK2	ZFY26_HUMAN			11	CTCTGGGTTGG	0.582	
+	15	4547	xmv.2_Missense_	NM_015556	NP_056371	O43166	SI1L1_HUMAN	Ser-rich.		4	CAAGAGCCAAG	0.537	
+	2	251	ense_Mutation_p.	NM_015604	NP_056419	Q8WV16	DCAF4_HUMAN			3	GAAGACGACAT	0.473	
-	10	1119	tion_p.P256S|NU	NM_001005743	NP_001005743	P49757	NUMB_HUMAN			4	AATTGGAGCAT	0.532	
-	4	981	_p.P180L|KCNK1	NM_021161	NP_066984	P57789	KCNKA_HUMAN		p.P175P(1)	5	TGCTCGGAGCA	0.393	
+	17	2431	wy.2_Missense_M	NM_024824	NP_079100	Q6PJT7	ZC3HE_HUMAN			3	TCAGCGAATAG	0.333	rs144843433
-	29	4951	p.R142W|CCDC8	NM_001080414	NP_001073883	Q9P219	DAPLE_HUMAN			3	TTCCCGGGGCA	0.687	
-	7	1093	12_splice|FBLN5_	NM_006329	NP_006320	Q9UBX5	FBLN5_HUMAN			6	CACATCTGTGG	0.527	
+	1	2978		NM_018958	NP_061831	Q9NZP6	CO002_HUMAN			8	TGTCATCTTGC	0.498	
+	35	4835	r.2_Missense_Mu	NM_001036	NP_001027	Q15413	RYR3_HUMAN	eats.|Cytoplasmic (By simil		10	TCCCAGCTCTTC	0.607	
+	4	471	zkl.2_Missense_M	NM_001013703	NP_001013725	Q9P2K8	E2AK4_HUMAN			4	AGCCCCCTCCC	0.473	
-	9	880	LA2G4F_uc001zp	NM_213600	NP_998765	Q68DD2	PA24F_HUMAN			4	CCCCTCGCCCA	0.622	
+	2	209	fw.2_Missense_M	NM_032866	NP_116255	Q0VF96	CGNL1_HUMAN	ZIM (By similarity).		11	GTATTCGGGTC	0.507	
+	2	1022	fw.2_Missense_Mu	NM_032866	NP_116255	Q0VF96	CGNL1_HUMAN	Head.		11	TGGATGATCAG	0.522	
+	9	2590	_Mutation_p.R770	NM_017610	NP_060080	Q6ZNA4	RN111_HUMAN	Pro-rich.		2	ATGAACGCCCC	0.438	
+	4	1109		NM_015042	NP_055857	O15014	ZN609_HUMAN			3	CCGGGGTAGAG	0.493	
+	12	1662	_p.A287T|IQCH_u	NM_001031715	NP_001026885	Q86VS3	IQCH_HUMAN			4	CCTGAAGCTGTA	0.383	
-	15	2612	_p.T79M|TLE3_uc	NM_005078	NP_005069	Q04726	TLE3_HUMAN	WD 1.		2	GCCTCGTGGGG	0.657	
+	3	720	.3_RNA|IL16_uc0	NM_172217	NP_757366	Q14005	IL16_HUMAN			4	AAAGCCTGGAA	0.423	
+	12	1830	Mutation_p.R527	NM_172217	NP_757366	Q14005	IL16_HUMAN			4	CGGGCGGCCCA	0.552	
-	16	2032	587W|AP3B2_uc0	NM_004644	NP_004635	Q13367	AP3B2_HUMAN			5	GTCCCGGTCTA	0.602	
-	4	1566	s.1_Missense_Mu	NM_001717	NP_001708	Q01954	BNC1_HUMAN			3	GACTGCGGTAG	0.532	
+	12	2586	p.T455M|BLM_uc	NM_000057	NP_000048	P54132	BLM_HUMAN	ase ATP-bin	p.T830M(1)	6	TCTTACGGCCA	0.443	
+	8	1251	_p.R379H|MAN2A	NM_006122	NP_006113	P49641	MA2A2_HUMAN	enal (Potential).		3	TGGGCGCATCA	0.567	
+	9	1338	ql.2_Missense_Mu	NM_033544	NP_291022	A6NED2	RCCD1_HUMAN	RCC1 4.		0	ATAAGCAACTCC	0.488	
+	11	1567	bok.2_Missense_	NM_018349	NP_060819	Q6DN12	MCTP2_HUMAN	C2 3.		3	GAACTCCCTGA	0.388	
+	35	6540	_p.D793N|CACNA	NM_021098	NP_066921	O95180	CAC1H_HUMAN	lasmic (Potential).		2	CAGCCGACGAG	0.741	
+	17	2378_2379		NM_016111	NP_057195	Q9Y4R8	TELO2_HUMAN			0	CGTGGCCGGCC	0.649	
-	2	298		NM_001080524	NP_001073993	A8MZG2	CP090_HUMAN			0	CCAGGCTGTGC	0.677	
+	14	1391	h.2_Missense_Mu	NM_020686	NP_065737	P80404	GABT_HUMAN			1	ATGCAGCCCATG	0.632	

-	10	2704	uyn.1_Missense_	NM_001134407	NP_001127879	Q12879	NMDE1_HUMAN	ellular (Potential).	45	TCAGGCTGACC	0.463	
+	8	696	0uyu.1_RNA|FAM	NM_002484	NP_002475	P53384	NUBP1_HUMAN		2	TCATCGGGGTG	0.542	
-	18	2475	p.2_Missense_Mu	NM_033266	NP_150296	Q76MJ5	ERN2_HUMAN	.|Cytoplasmic (Potential).	6	GGTGGCTGCCA	0.582	
+	23	4218	zg.1_Intron|SRCA	NM_006662	NP_006653	Q6ZRS2	SRCAP_HUMAN	Pro-rich.	4	TTCTTCGACCC	0.667	
+	18	1751	u.3_Missense_Mu	NM_000293	NP_000284	Q93100	KPBB_HUMAN		3	ATTTATCGCATT	0.343	
+	5	1838	_p.G280*|CES2_u	NM_003869	NP_003860	O00748	EST2_HUMAN		0	ACTTTGGAGGC	0.582	
-	1	602	vjt.1_Missense_M	NM_001082486	NP_001075955	Q96AP0	ACD_HUMAN		1	CGAACCTGCCA	0.687	
+	1	416		NM_002153	NP_002144	P37059	DHB2_HUMAN	(By similarity).	2	TGGATCAGAAG	0.468	
+	5	761	i.2_Missense_Mut	NM_003119	NP_003110	Q9UQ90	SPG7_HUMAN	intermembrane (Potential).	0	CAAGCGAACAG	0.398	
+	10	1658	AFAH1B1_uc010v	NM_000430	NP_000421	P43034	LIS1_HUMAN	dynein and dynactin.|WD 6	1	CTACGCGTATGG	0.458	
+	7	1051	HBG_uc010cmw.2_	NM_001040	NP_001031	P04278	SHBG_HUMAN	minin G-like p.0?(1)|p.?(1)	0	TCCTTAACCTCT	0.547	
+	75	11502	m.1_Missense_M	NM_020877	NP_065928	Q9P225	DYH2_HUMAN	6 (By similarity).	13	TGGAGGATTCA	0.597	
+	82	12748		NM_020877	NP_065928	Q9P225	DYH2_HUMAN		13	ATACCCCTCAC	0.473	
-	23	2834	uc002gml.1_Intron	NM_017533	NP_060003	Q9Y623	MYH4_HUMAN	Potential.	13	TCACATCTTTCC	0.373	
-	13	1325	uc002gml.1_Intron	NM_017533	NP_060003	Q9Y623	MYH4_HUMAN	osin head-like.	13	CTCTGGGATAG	0.453	
+	4	530	0vvi.1_Missense_	NM_003010	NP_003001	P45985	MP2K4_HUMAN	rotein kinasR154W(2)|p.?(	58	TAATGCGGAGTA	0.363	
-	31	4573	|NCOR1_uc010vw	NM_006311	NP_006302	O75376	NCOR1_HUMAN	action with ETO.	5	GGAACGCACGG	0.522	
-	20	2494	.1_Missense_Mut	NM_002018	NP_002009	Q13045	FLII_HUMAN	tion with ACTL6A.	2	ATGGCGTGGCC	0.711	
+	3	1886		NM_021012	NP_066292	Q14500	IRK12_HUMAN	smic (By similarity).	4	GGACGGAGACC	0.657	
-	2	739	_p.P194L|MYO18A	NM_078471	NP_510880	Q92614	MY18A_HUMAN		0	GCTCAGGGGCT	0.687	
-	2	595	.1_Intron|NF1_uc	NM_006495	NP_006486	P34910	EVI2B_HUMAN	ellular (Potential).	2	TGTTGAGTAAAA	0.428	rs139629091
-	7	2864	_p.D808N|SLFN11_	NM_001104588	NP_001098058	Q7Z7L1	SLN11_HUMAN		3	AACATCCTTTG	0.468	rs71366434
-	3	603		NM_019010	NP_061883	P35900	K1C20_HUMAN	oil 1B.|Rod.	3	ATCTGTTTTATGT	0.388	
+	8	1204	C25_uc010cxs.1_	NM_031421	NP_113609	Q96NG3	TTC25_HUMAN	TPR 6.	1	TGCCAGAGTTG	0.443	
+	4	448	ys.2_Missense_	NM_001001349	NP_001001349	Q9NYR9	KBRS2_HUMAN	all GTPase-like.	1	GCAGCGGCGTG	0.582	
+	11	1338	_p.P348S|ATP6V0	NM_001130021	NP_001123493	Q93050	VPP1_HUMAN	lasmic (Potential).	1	ATAAATCCAGGT	0.294	
+	4	565	938_uc002ibf.3_	NM_005854	NP_005845	O60895	RAMP2_HUMAN	ical; (Potential).	0	TAGTATGGAGGA	0.592	
-	5	593	_Mutation_p.P134	NM_005374	NP_005365	Q14168	MPP2_HUMAN		0	CGGGAGGTACA	0.632	
-	14	1899	LL6_uc002ioc.2_	NM_001130918	NP_001124390	Q8N841	TTLL6_HUMAN		0	CGTGGGAGCCT	0.507	
+	2	2306	dbu.2_Missense_	NM_175575	NP_783165	Q8TEU8	WFKN2_HUMAN	NTR.	3	GCATGGCCATG	0.632	
+	1	51	_5'Flank|MBTD1_	NM_016001	NP_057085	Q9Y5J1	UTP18_HUMAN		0	AACGATGCCGC	0.706	
-	2	526	2iuk.3_Missense_	NM_018286	NP_060756	Q9NV29	TM100_HUMAN	ical; (Potential).	0	CCGCGGTGACC	0.527	
+	4	959	ddd.2_Missense_	NM_014906	NP_055721	Q8WY54	PPM1E_HUMAN	PP2C-like.	5	GGGGAGTAGAT	0.502	
+	23	3724	utation_p.Q179*|	NM_006039	NP_006030	Q9UBG0	MRC2_HUMAN	ellular (Potential).	3	TCTGCCAGAAG	0.642	
-	3	342	_p.R67C|ABCA9_	NM_080283	NP_525022	Q8IUA7	ABCA9_HUMAN		6	TACACGTCCCA	0.368	rs150105567
-	2	163		NM_181449	NP_852114	Q496F6	CLM2_HUMAN	.|Extracellular (Potential).	4	TTGTACATGCTC	0.542	
-	4	732	jqe.2_Nonsense_	NM_007292	NP_009223	Q15067	ACOX1_HUMAN		1	GCCTCGAAGGT	0.443	rs118204093
+	16	5305	ae.2_Missense_	NM_001080519	NP_001073988	Q9P281	BAHC1_HUMAN		1	AGAGGGCCACG	0.716	
-	4	676	wvd.1_Missense_	NM_006907	NP_008838	P32322	P5CR1_HUMAN		0	ACACGGTGGCC	0.647	
+	1	343		NM_018949	NP_061822	Q9UKP6	UR2R_HUMAN	ellular (Potential).	1	CCAAGGAGTGG	0.637	
+	7	879		NM_001943	NP_001934	Q14126	DSG2_HUMAN	(Potential).|Cadherin 2.	9	TGCAGGAACAC	0.403	
-	1	1630	AL2_uc002lco.2_	NM_016427	NP_057511	Q8IYF1	ELOA2_HUMAN		4	TAGCCGAATCC	0.547	rs150911848
+	3	1282	r.1_Missense_Mu	NM_005215	NP_005206	P43146	DCC_HUMAN	ellular (Potential).	17	TTTTATCAGGTAT	0.373	
-	4	1254		NM_052947	NP_443179	Q86TB3	ALPK2_HUMAN		14	GCAGGTTCCTT	0.453	
+	4	5021	qu.1_Missense_M	NM_017757	NP_060227	Q9C0G0	ZN407_HUMAN		2	AAAAGCCGTTTA	0.507	
+	3	3608	a.2_Missense_Mu	NM_171999	NP_741996	Q9BXA9	SALL3_HUMAN		4	AGCTCGGGCAA	0.582	
+	1	37_38	ense_Mutation_p.	NM_024100	NP_077005	Q9BV38	WDR18_HUMAN		1	GCGCCCATGG	0.728	

+	4	372	_p.R89*|GPX4_u	NM_002085	NP_002076	P36969	GPX4_HUMAN		0	ACGCCCGATAC	0.647	
+	4	1232	wq.2_Missense_M	NM_024967	NP_079243	Q9HAH1	ZN556_HUMAN	2H2-type 8.	3	TTGGTCCTCAT	0.468	
-	4	470	S10_uc002mkk.1	NM_030957	NP_112219	Q9H324	ATS10_HUMAN		4	GCCGCGGCGCT	0.682	
-	84	43654	wj.2_Missense_M	NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	lasmic (Potential).	57	TCCTTCCTTCTT	0.587	
-	28	38225		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	ellular (Potential).	57	AGGTCCCAGGA	0.498	
-	3	21530		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	h.|Extracellular (Potential).	57	TGGGAGGAGGT	0.522	
-	3	19546		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).	57	TGTTTGGGTGG	0.507	
+	7	1272	.3_Missense_Mut	NM_032497	NP_115886	Q9BR84	ZN559_HUMAN		1	ATGGTGGAGAG	0.383	
-	3	351	n_p.E73*|ECSIT_	NM_016581	NP_057665	Q9BQ95	ECSIT_HUMAN		1	GTCCTCAAAGG	0.657	
-	1	89		NM_006563	NP_006554	Q13351	KLF1_HUMAN	Pro-rich.	0	TGGAGGGCAAG	0.652	
+	5	686	mwa.1_Nonsense_	NM_005053	NP_005044	P54725	RD23A_HUMAN	UBA 1.	1	CCCACCGAGCC	0.647	
+	1	180		NM_001145160	NP_001138632	P67936	TPM4_HUMAN	By similarity.	13	CGACCGCGCGG	0.652	
-	28	3580		NM_001080421	NP_001073890	Q9UPW8	UN13A_HUMAN	MHD1.	3	TAGACGATGCT	0.562	
-	23	3098_3099		NM_001080421	NP_001073890	Q9UPW8	UN13A_HUMAN		3	TCAATCCGCAG	0.569	
-	4	1076		NM_001159293	NP_001152765	C9JHM3	C9JHM3_HUMAN		1	TAAGGATAGAG	0.413	
-	4	1019		NM_001159293	NP_001152765	C9JHM3	C9JHM3_HUMAN		1	TCTCCAGTATGA	0.413	
+	5	1464	pk.2_Missense_M	NM_025189	NP_079465	Q9H8G1	ZN430_HUMAN		2	TTCATACTGGA	0.383	
+	4	731		NM_020855	NP_065906	Q9P255	ZN492_HUMAN	2H2-type 1.	0	GAATTCATAGT	0.338	
-	6	2463		NM_001080409	NP_001073878				2	AATTAGCTTATGT	0.378	
-	2	821		NM_006003	NP_005994	P47985	UCRI_HUMAN	Rieske.	0	GGCAAGGGCA	0.478	
-	3	269	ntu.3_Missense_M	NM_001126335	NP_001119807	P82251	BAT1_HUMAN	ellular (Potential).	1	TGGGGGAAACG	0.602	
+	9	828	issense_Mutatio	NM_002151	NP_002142	P05981	HEPS_HUMAN	(Potential).|Peptidase S1.	2	TCTCCGGGGAC	0.672	
+	10	931	010xsh.1_Missens	NM_002151	NP_002142	P05981	HEPS_HUMAN	(Potential).|Peptidase S1.	2	CCACGGTCTGC	0.662	
+	8	878	_p.Q59K|USF2_u	NM_003367	NP_003358	Q15853	USF2_HUMAN	-loop-helix motif.	0	TCGTCCAGCTT	0.612	
+	4	465	M42_uc002oap.2_	NM_024321	NP_077297	Q9BTD8	RBM42_HUMAN		0	TGATCGGAGTC	0.597	
+	8	1203	p.2_Nonsense_M	NM_024321	NP_077297	Q9BTD8	RBM42_HUMAN	tion with HNRNPK (By sim	0	GGAGTGGGATG	0.617	
-	26	3370	S1_uc010eem.1_	NM_004646	NP_004637	O60500	NPHN_HUMAN	lasmic (Potential).	5	AGTGTCCCGCT	0.602	
-	18	2335		NM_004646	NP_004637	O60500	NPHN_HUMAN	7.|Extracell p.G779*(1)	5	TTCTCCCTGGA	0.572	
-	5	1194	5B_uc002ofr.1_N	NM_152279	NP_689492	Q52M93	Z585B_HUMAN	2H2-type 6.	1	TACCTGAAGTT	0.388	
+	7	1379	xp.3_Missense_M	NM_181845	NP_862828	Q8N7M2	ZN283_HUMAN		0	ATACTGGTAAG	0.378	
-	6	1502_1503	_p.G11R|ZNF229_	NM_014518	NP_055333	Q9UJW7	ZN229_HUMAN	2H2-type 2.	4	GAACCCCTTTCC	0.515	
+	7	1020	.G301E|KLC3_uc	NM_177417	NP_803136	Q6P597	KLC3_HUMAN	TPR 3.	1	CTATGGGAAGC	0.657	
-	20	2877	.R878W|SYMPK_	NM_004819	NP_004810	Q92797	SYMPK_HUMAN		1	ATCCCGGACCC	0.632	
+	2	548	2_uc010xyu.1_In	NM_014601	NP_055416	Q9NZN4	EHD2_HUMAN		2	TGGCCGTCATG	0.652	
-	5	1342		NM_017708	NP_060178	Q2M2I3	FA83E_HUMAN		1	CCCACGGAGGT	0.667	
-	1	166		NM_178449	NP_848544	Q96A98	TIP39_HUMAN		0	ACCACcagcagca	0.597	
+	12	1413	_p.P241S|MED25_	NM_030973	NP_112235	Q71SY5	MED25_HUMAN	16.|Interaction with CREB	1	TCATCCCCCAG	0.687	
+	4	293	e_Mutation_p.E9	NM_003121	NP_003112	Q01892	SPIB_HUMAN		2	ACCTCGAACTG	0.642	
+	4	262		NM_004533	NP_004524	Q14324	MYPC2_HUMAN	like C2-type 1.	1	CAGTGGTCGTG	0.582	
-	17	2246	sw.1_Missense_M	NM_016148	NP_057232	Q9Y566	SHAN1_HUMAN	PDZ.	2	TTGGCGGATCA	0.602	
+	1	634		NM_001506	NP_001497	O75388	GPR32_HUMAN	ellular (Potential).	1	TGGAGGGACA	0.552	
-	5	1468	NF614_uc010epj.2	NM_025040	NP_079316	Q8N883	ZN614_HUMAN	2H2-type 5.	5	ATAGCGCTTCA	0.428	
+	6	1175		NM_001099694	NP_001093164	Q96N58	ZN578_HUMAN		0	ACACTGGTGAG	0.418	
+	4	2891	dw.1_Missense_M	NM_138374	NP_612383	Q96IR2	ZN845_HUMAN	2H2-type 26.	0	CTTCCGTCACA	0.363	rs150688663
-	5	1012	_p.L301F|LILRB5_	NM_006840	NP_006831	O75023	LIRB5_HUMAN	3.|Extracellular (Potential).	2	GGAGAGGTTGT	0.692	
+	6	1069	_p.P304L|NLRP2_	NM_017852	NP_060322	Q9NX02	NALP2_HUMAN	NACHT.	2	GTTACCCAAGG	0.662	
+	4	607	2qkk.1_Missense	NM_032701	NP_116090	Q86Y97	SV422_HUMAN	SET.	0	CAACGGGGCCA	0.597	

+	2	1180	_Mutation_p.R155	NM_016535	NP_057619	Q9P0T4	ZN581_HUMAN	2H2-type 3.	0	CTTCCGGGATG	0.672	
+	4	2352		NM_020903	NP_065954	Q9HBJ7	UBP29_HUMAN		11	AAGATGGAGGG	0.483	
+	4	1003		NM_080657	NP_542388	Q8WXG1	RSAD2_HUMAN		0	TGCTTGGTGCC	0.393	
-	21	2268	AS_uc002rcd.1_R	NM_015909	NP_056993	A2RRP1	NBAS_HUMAN		4	AACCATGGTAAG	0.408	
+	4	655	mm.1_Nonsense_	NM_199280	NP_954974	Q6ZUX3	F179A_HUMAN		4	GGGACCAGCCC	0.607	
-	4	542		NM_000348	NP_000339	P31213	S5A2_HUMAN	ical; (Potential).	0	TATTCCCATTCC	0.403	
-	23	3675	j.3_Missense_Mut	NM_005633	NP_005624	Q07889	SOS1_HUMAN		10	TAAGGGAGGGC	0.502	
-	5	856	rzj.2_Missense_Mu	NM_004105	NP_004096	Q12805	FBLN3_HUMAN	alcium-binding (Potential).	6	TGCACTCGTCTA	0.443	
-	1	199	_uc002sbn.3_5'U	NM_032180	NP_115556	Q3B820	F161A_HUMAN		3	GTCTTCGCGTT	0.652	
+	14	1816	nb.1_Missense_Mu	NM_004263	NP_004254	O95754	SEM4F_HUMAN	ellular (Potential).	4	CAGAACGTCCA	0.527	
-	10	1540	n.2_Missense_Mu	NM_003203	NP_003194	P16383	GCF_HUMAN		2	AACAAAATATTC	0.318	
-	19	3333_3334	.2_Missense_Mut	NM_016316	NP_057400	Q9UBZ9	REV1_HUMAN		2	CCTGCCTTTGT	0.5	
+	2	490	.2_Missense_Mut	NM_012455	NP_036587	Q8NDX1	PSD4_HUMAN		2	GACAAGATGCT	0.637	
+	2	494	.2_Missense_Mut	NM_012455	NP_036587	Q8NDX1	PSD4_HUMAN		2	AGATGCTCCTC	0.637	
+	10	1026	2tvn.2_Missense_	NM_018460	NP_060930	Q53QZ3	RHG15_HUMAN	Rho-GAP.	2	AAATTCCACAG	0.428	
-	46	6081		NM_004543	NP_004534	P20929	NEBU_HUMAN	Nebulin 51.	20	GTCTGGGTGCT	0.433	
-	8	709	p.D196A|CACNB4	NM_000726	NP_000717	O00305	CACB4_HUMAN		2	CAACATCGTAA	0.473	
-	22	3716	p.2_Nonsense_Mu	NM_013450	NP_038478	Q9UIF8	BAZ2B_HUMAN	DDT.	4	CTCTTGAAGAA	0.428	
-	2	483	uci.2_Missense_M	NM_033272	NP_150375	Q9NS40	KCNH7_HUMAN	lasmic (Potential).	5	CCTCTCTTCTG	0.423	
-	28	6398	y.2_Missense_Mut	NM_006922	NP_008853	Q9NY46	SCN3A_HUMAN		10	CATAGGAAGGA	0.358	
-	49	9282		NM_004525	NP_004516	P98164	LRP2_HUMAN	A 23.|Extracellular (Potent	29	CTCTCGTCGCT	0.468	rs148612649
+	6	470	IG_uc002ufb.2_	NM_004792	NP_004783	Q13427	PPIG_HUMAN	e cyclophilin-type.	3	GAAATGGACGA	0.264	
+	5	753	fqf.1_Missense_M	NM_025000	NP_079276	Q5H9S7	DCA17_HUMAN		0	CTCAGCAGTGG	0.353	
+	12	1396	fe.1_Missense_Mu	NM_032523	NP_115912	Q9BZF3	OSBL6_HUMAN		1	CAGTTCGCTTG	0.423	
-	307	93765	76M|TTN_uc010z	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	GATCACGGTAT	0.428	
-	288	85204	22Q|TTN_uc010z	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	TAACTCGGAAT	0.448	
-	275	76663	175N|TTN_uc010z	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	TAGTAATAGGAA	0.378	
-	46	15324	N_uc010zfi.1_Intr	NM_133379	NP_596870	Q8WZ42	TITIN_HUMAN		153	AACTTCCCCTA	0.433	
-	46	14285	N_uc010zfi.1_Intr	NM_133379	NP_596870	Q8WZ42	TITIN_HUMAN		153	TCCACCATAGT	0.328	
-	3	331		NM_173648	NP_775919	Q6ZP82	CC141_HUMAN	Potential.	10	CAGCCGAAGGA	0.468	rs146458136
-	8	1447	ftt.2_Nonsense_Mu	NM_018256	NP_060726	Q9GZL7	WDR12_HUMAN	r nucleolar localization.	0	TGGTCGATTTGT	0.388	
+	7	1002	nse_Mutation_p.S	NM_005759	NP_005750	Q9NYB9	ABI2_HUMAN	Pro-rich.	0	TCGGAGCAGCA	0.473	
-	21	3081	_Mutation_p.G63	NM_173076	NP_775099	Q86UK0	ABCAC_HUMAN		11	TTACTTCCAAAG	0.388	
-	17	2034	kx.1_Missense_Mu	NM_024506	NP_078782	Q6UWU2	GLB1L_HUMAN		0	GTTGAGGGCTC	0.483	
-	8	1012	x.1_Missense_Mu	NM_024506	NP_078782	Q6UWU2	GLB1L_HUMAN		0	ATGGCCCATGG	0.493	
-	13	1836	p.A493S|PTPRN_	NM_002846	NP_002837	Q16849	PTPRN_HUMAN	ical; (Potential).	4	CAGGGCCACCA	0.652	
+	11	1378	su.3_Splice_Site_	NM_001631	NP_001622	P09923	PPBI_HUMAN		1	TACCAGGGAGC	0.716	
-	1	316	T1A6_uc002vuu.2_	NM_001001394	NP_001001394	Q8WWF6	DNJB3_HUMAN		0	CTCCGCCCCCG	0.647	
-	19	6623	.G1907D|COL6A	NM_004369	NP_004360	P12111	CO6A3_HUMAN	region.|Collagen-like 2.	18	CCAGACCATCC	0.408	
+	2	259		NM_005855	NP_005846	O60894	RAMP1_HUMAN	ellular (Potential).	0	TCACCCAGTTC	0.617	
+	8	1405	_Mutation_p.R177	NM_018226	NP_060696	Q9HAU8	RNPL1_HUMAN		2	CTGCCGGGCAG	0.642	
+	3	487		NM_032515	NP_115904	Q9UMX3	BOK_HUMAN	BH3.	1	TGATCCGGCCC	0.637	rs146987702
+	2	211		NM_153325	NP_697020	Q8N687	DB125_HUMAN		3	GCATTTCCTGTG	0.363	
+	4	578		NM_003245	NP_003236	Q08188	TGM3_HUMAN		9	GATGCCGGCATC	0.453	rs138092626
-	2	1078	tron|UBOX5_uc0	NM_021826	NP_068598	Q7L8L6	FAKD5_HUMAN		0	CTTTGCGGCCT	0.393	
+	9	1714	il.2_Missense_Mut	NM_139321	NP_647537	O75882	ATRN_HUMAN	ar (Potential).|Kelch 4.	2	ATACCCAGATG	0.433	
+	26	2537	p.L813F|PLCB4_	NM_182797	NP_877949	Q15147	PLCB4_HUMAN		15	TTTCCCTTCGA	0.413	

-	5	996	nj.2_Missense_Mu	NM_020341	NP_065074	Q9P286	PAK7_HUMAN	Linker.	23	CATAGAGACTCT	0.493	
+	5	722		NM_002862	NP_002853	P11216	PYGB_HUMAN		2	TCTACGGACGC	0.637	
+	2	71	tj.1_RNA|FRG1B_uc010gdr.1_RNA|FRG1B_uc010ztk.1_Intron						0	CCTGAAATCTGG	0.353	
+	12	3677	eb.2_Missense_Mu	NM_015338	NP_056153	Q8IXJ9	ASXL1_HUMAN		248	TGGCCAGTACTG	0.577	
+	14	1793	10gef.2_RNA|DNM	NM_006892	NP_008823	Q9UBC3	DNM3B_HUMAN	e PRC2/EED-EZH2 compl	5	TTGCAGCAACA	0.582	
+	3	712	zf.1_RNA|CBFA2T	NM_005093	NP_005084	O43439	MTG8R_HUMAN	Pro-rich.	2	GAGGACCGAGG	0.502	
+	13	1445	G1_uc010zwe.1_M	NM_182811	NP_877963	P19174	PLCG1_HUMAN	I-PLC X-box.	8	AGCCCGTGGAG	0.572	
-	24	3542	.R1139W|PTPRT_	NM_007050	NP_008981	O14522	PTPRT_HUMAN	hatase 1.|Cytoplasmic (Po	20	GGCCCGGAGCT	0.567	
-	4	810		NM_016470	NP_057554	Q9NX31	CT111_HUMAN		0	CAAGGGAGGGA	0.532	
-	11	1575	_p.H468Y|ZMYND	NM_012408	NP_036540	Q9ULU4	PKCB1_HUMAN		5	CGTGTGCACAG	0.597	
+	2	3898		NM_173485	NP_775756	Q9NRE2	TSH2_HUMAN		6	GGTCTCCAGAAA	0.502	
+	9	1050	p.E237K|RAE1_uc	NM_003610	NP_003601	P78406	RAE1L_HUMAN		0	AGTATCGAGGGG	0.413	
+	10	1624	.D22N|CDH26_uc	NM_177980	NP_817089	Q8IXH8	CAD26_HUMAN	r (Potential).|Cadherin 4.	4	AGCGTCGACAAA	0.378	rs144761668
-	13	1054	PTE_uc002yir.1_Mi	NM_199261	NP_954870	P56180	TPTE_HUMAN	hatase tensin-type.	5	GTGTATCGCCTT	0.323	
-	2	625	CAM_uc002yyr.1_	NM_001389	NP_001380	O60469	DSCAM_HUMAN	otential).|Ig-like C2-type 1.	11	AGGTACCATCTG	0.587	
+	16	2137		NM_005049	NP_005040	Q15269	PWP2_HUMAN		1	GGAGTCGCGATA	0.537	rs150290645
+	1	176	.1_Intron|C21orf29	NM_198695	NP_941968	P60410	KR108_HUMAN	repeats of C-C-X(3).|1.	2	GCTGCGAGCCC	0.672	
+	30	6640	j.2_Missense_Mut	NM_006031	NP_006022	O95613	PCNT_HUMAN		8	ATTCTCCCATTC	0.507	
-	9	1431	se_Mutation_p.G1	NM_001136213	NP_001129685	Q6S545	POTEH_HUMAN		1	GTACTTCCGTGC	0.358	
-	1	1554_1555		NM_014406	NP_055221	Q96SF2	TCPQM_HUMAN		1	TGGGCCCTTCC	0.495	
+	12	1099	aeo.2_Splice_Site_	NM_133455	NP_597712	Q96A84	EMID1_HUMAN		0	ACACAGGGACT	0.627	
+	17	2613	_p.S762L|MTMR3_	NM_021090	NP_066576	Q13615	MTMR3_HUMAN		5	TGTTCTCACAGG	0.577	
+	12	2704	sense_Mutation_p	NM_001017437	NP_001017437	Q569K6	CC157_HUMAN		1	CCCCACCTCGG	0.682	
+	17	1316	EPDC5_uc003alt.2	NM_014662	NP_055477	O75140	DEPD5_HUMAN		8	GATTCTCGTCTG	0.458	
+	6	670	M1_uc003anp.2_M	NM_005488	NP_005479	O60784	TOM1_HUMAN		1	TGTGGGCACTG	0.592	
+	3	831	ny.2_Missense_Mu	NM_014310	NP_055125	Q96D21	RHES_HUMAN	GNB1, GNB2 and GNB3.	3	AGTACGGTGACG	0.627	
-	39	5729		NM_002473	NP_002464	P35579	MYH9_HUMAN	Potential.	11	TGCAGGCTGCC	0.617	
+	7	1568	atq.1_Missense_M	NM_001039141	NP_001034230	Q9H2D6	TARA_HUMAN		1	CCTGCGCCCAG	0.582	
+	9	961	DSL_uc003ayr.3_M	NM_000026	NP_000017	P30566	PUR8_HUMAN		1	GCGTTCAGAAC	0.507	
+	5	515	aq.1_Missense_M	NM_001469	NP_001460	P12956	XRCC6_HUMAN		5	CTGTGGGTCTGT	0.473	
+	8	673	z.2_Missense_Mu	NM_014509	NP_055324	Q9H4I8	SEHL2_HUMAN		0	AGTGCGGGGAG	0.498	rs148540655
+	2	434	tron|SETMAR_uc	NM_006515	NP_006506	Q53H47	SETMR_HUMAN	-lysine N-methyltransferas	1	CTGTGCCGATGC	0.463	
+	27	3631	PR1_uc011asu.1_I	NM_001099952	NP_001093422	Q14643	ITPR1_HUMAN	lasmic (Potential).	21	GAGGTGCTCCAG	0.567	
-	3	960		NM_000916	NP_000907	P30559	OXYR_HUMAN	ellular (Potential).	0	CCAGGCGGCAC	0.642	
+	13	1481	p.R455H|ATG7_uc	NM_006395	NP_006386	O95352	ATG7_HUMAN		1	AGCCCGCAGAG	0.537	
+	13	3398	j.2_Missense_Mu	NM_001162499	NP_001155971	O75155	CAND2_HUMAN	HEAT 24.	4	AGGACGGGCTG	0.577	
+	19	4398	.H1387Y|FGD5_u	NM_152536	NP_689749	Q6ZNL6	FGD5_HUMAN	PH 2.	5	ATTTTTCACCTTT	0.423	
+	10	1899		NM_003884	NP_003875	Q92831	KAT2B_HUMAN		3	AGGCGGCAAGG	0.493	
+	15	1278	XL2_uc011axp.1_	NM_012157	NP_036289	Q9UKC9	FBXL2_HUMAN		1	CTCCCGTCACC	0.517	
-	7	1045	SP2_uc010hgb.2_	NM_015097	NP_055912	B2RTR1	B2RTR1_HUMAN		4	TCATACCGCCTG	0.284	
-	12	6279		NM_014831	NP_055646	O15050	TRNK1_HUMAN		2	AGTGGCGATACA	0.587	
-	4	3099		NM_014831	NP_055646	O15050	TRNK1_HUMAN		2	GTAAATCCACCA	0.433	
+	13	1722	p.P479H|VILL_uc	NM_015873	NP_056957	O15195	VILL_HUMAN		0	AGCCCCCCCACT	0.597	
+	11	1697_1698	.1_Missense_Muta	NM_007335	NP_031361	Q9Y238	DLEC1_HUMAN		9	GTTTTCCCCAAA	0.564	
-	27	4685		NM_006514	NP_006505	Q9Y5Y9	SCNAA_HUMAN	IV.	10	TGAAGTGACTTA	0.473	
+	11	1900	10hhw.2_Missense	NM_015460	NP_056275	Q8NFW9	MYRIP_HUMAN	Actin-binding.	5	CTGTACGAGTTA	0.493	
+	13	1715	kz.3_Missense_M	NM_001042646	NP_001036111	Q9UPV9	TRAK1_HUMAN	with HGS.|Potential.	1	GCTGAGGCGGC	0.642	

-	3	370	w.2_Intron|ANO10	NM_018075	NP_060545	Q9NW15	ANO10_HUMAN	lasmic (Potential).		2	AGTTCTGATTTTC	0.358	
-	2	996	R3_uc003cpg.1_In	NM_001295	NP_001286	P32246	CCR1_HUMAN	lasmic (Potential).		3	ACTTCCGGAACC	0.587	
+	1	190	_5'Flank|KIF9_uc	NM_025010	NP_079286	O94889	KLH18_HUMAN			0	TTGCCTAGTCGC	0.662	
-	102	7659		NM_000094	NP_000085	Q02388	CO7A1_HUMAN	.|Cell attachment site (Pote		11	CTCCCCGAGGT	0.602	
+	5	3100		NM_003458	NP_003449	Q9UPA5	BSN_HUMAN			8	ACCTCTCCCACC	0.647	
+	20	3692	dt.1_Missense_Mu	NM_015512	NP_056327	Q9P2D7	DYH1_HUMAN	n (By similarity).		3	CGAGAGCATCA	0.612	
+	67	11003	ldv.2_Missense_M	NM_015512	NP_056327	Q9P2D7	DYH1_HUMAN			3	ACCTGCCAACCT	0.582	
+	10	1699	z.2_Missense_Mu	NM_016483	NP_057567	Q9BWX1	PHF7_HUMAN			1	AGTGTGAGGAGT	0.582	
-	20	3024	dqd.2_Intron|ROB	NM_002941	NP_002932	Q9Y6N7	ROBO1_HUMAN	lasmic (Potential).		2	AAGACGGGACT	0.343	
+	1	364		NM_001005515	NP_001005515	A6NDH6	O5H15_HUMAN	lasmic (Potential).		2	TATGATCGCTAT	0.378	
+	5	2430	_p.G729R|COL8A1	NM_001850	NP_001841	P27658	CO8A1_HUMAN	helical region (NC1).		0	TATGCCGGGCAG	0.463	
+	4	424	ense_Mutation_p.P	NM_007072	NP_009003	Q9UM44	HHLA2_HUMAN	-like V-type 1.		1	AAGATCCCAGAT	0.408	
+	1	263	GSF11_uc010hqs	NM_152539	NP_689752	Q96M34	CC030_HUMAN			2	ACGGAGTAGCT	0.502	
-	2	156	on_p.S4F|PARP9_	NM_001146102	NP_001139574	Q8IXQ6	PARP9_HUMAN		p.S4S(1)	4	CCATGGAAAAG	0.418	
-	28	4962	olb.1_Missense_M	NM_015103	NP_055918	Q9Y4D7	PLXD1_HUMAN	lasmic (Potential).		1	AGGTCCCGAAGG	0.647	
+	2	318	_p.E54K|FAIM_uc	NM_001033032	NP_001028204	Q9NVQ4	FAIM1_HUMAN			0	AAGATCGAATTT	0.363	
-	8	1120		NM_173653	NP_775924	Q8IVB4	SL9A9_HUMAN	ical; (Potential).		3	GGCCGGTTTCC	0.493	
-	8	1212	p.H295Y|PLSCR4_	NM_001128305	NP_001121777	Q9NRQ2	PLS4_HUMAN	smic (By similarity).		0	GGAAGTGAATGT	0.428	rs138186262
+	39	5976	12L_uc011bnz.1_	NM_053002	NP_443728	Q86YW9	MD12L_HUMAN	Gln-rich.		7	ACCCCGTGCTA	0.587	
-	4	2338		NM_178822	NP_849144	Q6WRI0	IGS10_HUMAN			13	TGGGGGTGGGC	0.507	
-	9	1411	p.L195F|SLC2A2_	NM_000340	NP_000331	P11168	GTR2_HUMAN	lasmic (Potential).		2	AAAGAGAGAAC	0.403	
-	4	445	SF10_uc003fie.2_	NM_003810	NP_003801	P50591	TNF10_HUMAN	cellular (Potential).		5	GGACCTCTTTCT	0.403	
-	5	1412	ow.1_Missense_Mu	NM_001146276	NP_001139748	Q6PIU2	NCEH1_HUMAN	enal (Potential).		0	GGCCAGCTAGTG	0.493	
+	4	581	CNMB2_uc003fjf.2	NM_181361	NP_852006	Q9Y691	KCMB2_HUMAN	cellular (Potential).		1	GGACCGAAGAG	0.483	
+	1	1768	3foc.2_Missense_	NM_144635	NP_653236	Q6UXB0	F131A_HUMAN			1	GGCTCGCTTTG	0.448	
+	3	657		NM_004443	NP_004434	P54753	EPHB3_HUMAN	cellular (Potential).		11	ATGAATCCCATC	0.557	
+	8	1183	.2_Missense_Mut	NM_003722	NP_003713	Q9H3D4	P63_HUMAN	action with H	p.S365L(1)	12	AAGTTTCGGACA	0.537	rs147148566
+	6	897	.1_Missense_Mut	NM_002182	NP_002173	Q9NPH3	IL1AP_HUMAN	cellular (Potential).		1	CTGACTGTAAAG	0.328	
-	22	15657	bth.1_Missense_M	NM_018406	NP_060876	Q99102	MUC4_HUMAN			0	CTGACCGAGGCG	0.572	
-	3	2319	tron|ABCA11P_uc	NM_133474	NP_597731	D9N162	D9N162_HUMAN			1	AAAGGATTGCG	0.403	
-	3	2300	ron|ABCA11P_uc	NM_133474	NP_597731	D9N162	D9N162_HUMAN			1	TAAAGGCTTTGC	0.408	
+	6	1110	.P236L|PIGG_uc0	NM_001127178	NP_001120650	Q5H8A4	PIGG_HUMAN	enal (Potential).		4	GCTTACCGATTC	0.448	
-	3	459	on.2_Missense_Mu	NM_001347	NP_001338	P52824	DGKQ_HUMAN	l-ester/DAG-type 2.		1	GTGGAGCCCCC	0.677	
-	4	761	gey.3_Missense_M	NM_020972	NP_066023	Q9HCC9	LST2_HUMAN			3	GTCCCGCAGCG	0.647	
-	8	1856	GC1A_uc011bxp.	NM_013261	NP_037393	Q9UBK2	PRGC1_HUMAN	Arg/Ser-rich.		8	GATCGGGAACAC	0.458	
-	2	540	_p.D54A|TLR10_u	NM_030956	NP_112218	Q9BXR5	TLR10_HUMAN	lar (Potential).|LRR 2.		2	GATAAATCCAGTG	0.448	
+	2	928		NM_001080505	NP_001073974	A0PJX4	SHSA3_HUMAN	lasmic (Potential).		2	TCAGTTCCAGTT	0.557	
-	6	1266	zc.1_Nonsense_M	NM_001114175	NP_001107647	P47869	GBRA2_HUMAN	cellular (Probable).		4	TAAGTCCAAATAT	0.363	
-	14	1960	zg.1_Missense_Mu	NM_006587	NP_006578	Q9Y5Q5	CORIN_HUMAN	ential).|LDL-receptor class		2	GACATTCCCAAA	0.373	
-	3	345	gyu.2_Missense_M	NM_001014446	NP_001014446	Q56VL3	OCAD2_HUMAN	OCIA.		0	TTTCTTCCTGAC	0.383	
-	5	1070	haf.3_Missense_M	NM_001126328	NP_001119800	Q8TBB1	LNX1_HUMAN			4	TGGTAATTTCAC	0.408	
+	21	3565	p.R1131Q|LPHN3_	NM_015236	NP_056051	Q9HAR2	LPHN3_HUMAN	lasmic (Potential).		18	AGGTACGAAAAG	0.373	
+	5	1325	cam.1_Missense_M	NM_001075	NP_001066	P36537	UDB10_HUMAN			5	ATTAATGATCCTT	0.383	
+	1	388	hq.2_Missense_M	NM_001074	NP_001065	P16662	UD2B7_HUMAN			2	ACAGGAAATCAT	0.303	
+	4	965	|MUC7_uc003hfj.2	NM_001145006	NP_001138478	Q8TAX7	MUC7_HUMAN	3.|Thr-rich.		4	CTCCACCATCTT	0.582	
-	4	508	Nonsense_Mutati	NM_000583	NP_000574	P02774	VTDB_HUMAN	Albumin 1.		3	GCTTTCGTTCCA	0.532	
-	22	4180	_p.T1104A|ANKRD	NM_032217	NP_115593	O75179	ANR17_HUMAN	ANK 24.		10	ATGGAGTGTTCC	0.393	

-	15	2229	.2_RNA|PPEF2_u	NM_006239	NP_006230	O14830	PPE2_HUMAN			4	CTTGTACTCCAG	0.542	
-	1	1471		NM_033214	NP_149991	Q14410	GLPK2_HUMAN			4	TCGTTCCATCCT	0.512	
+	21	2857	dm.1_Missense_M	NM_016323	NP_057407	Q9UII4	HERC5_HUMAN	HECT.		9	TCCACCCCGAA	0.328	
-	14	2564		NM_003728	NP_003719	O95185	UNC5C_HUMAN	lasmic (Potential).		4	CTTCTCCTTCCA	0.522	
+	21	3625	.1_Missense_Muta	NM_001963	NP_001954	P01133	EGF_HUMAN	lasmic (Potential).		4	CTACAGGTGAC	0.552	
+	10	1918		NM_001977	NP_001968	Q07075	AMPE_HUMAN			5	ATCTTAGGCAA	0.343	
-	4	877	X2_uc010iml.2_In	NM_153426	NP_700475	Q99697	PITX2_HUMAN	Homeobox.		0	CAGCTCCTGGA	0.612	rs1051887
+	9	8053	_p.R983*|FAT4_u	NM_024582	NP_078858	Q6V0I7	FAT4_HUMAN	|Extracellular (Potential).		18	TCCCCTCGAAAA	0.343	
+	6	514		NM_153702	NP_714913	Q8IZ81	ELMD2_HUMAN	ELMO.		1	GCCCACGAAGA	0.373	
-	25	7081		NM_017639	NP_060109	Q6V1P9	PCD23_HUMAN	Cadherin 21.		4	TTCCATGAGTGA	0.388	
-	3	424	x.2_Missense_Mu	NM_017639	NP_060109	Q6V1P9	PCD23_HUMAN	Cadherin 1.		4	TTACCCCATCCT	0.333	
+	7	1266	_p.I236F|CLCN3_	NM_001829	NP_001820	P51790	CLCN3_HUMAN			3	TTCATCATCAGA	0.363	
-	6	785	p.1_Missense_Mu	NM_080874	NP_543150	Q8WWX0	ASB5_HUMAN	ANK 6.		2	TATCTGCTCCAA	0.408	
-	1	38		NM_080874	NP_543150	Q8WWX0	ASB5_HUMAN			2	ACGGCCGATTTT	0.443	
+	15	2831	e.1_Missense_Mu	NM_001080477	NP_001073946	Q9P273	TEN3_HUMAN	ellular (Potential).		0	TGGATTCCATGG	0.433	
+	3	2405	wa.1_Missense_M	NM_020225	NP_064610	Q9P2F5	STOX2_HUMAN			0	CTGACCGTGGAA	0.562	
+	11	1685	_p.P369L|FAM149	NM_015398	NP_056213	A5PLN7	F149A_HUMAN			1	CCCCCCGCTAG	0.537	rs141878617
+	1	900		NM_024563	NP_078839					0	CATGCAGTCAAC	0.418	
-	5	667	ju.1_Missense_Mu	NM_001042625	NP_001036090	Q8WWF8	CAPSL_HUMAN	EF-hand 4.		1	TCAATGGATGCG	0.488	
+	15	2479	3jle.1_Missense_M	NM_152403	NP_689616	Q63HQ2	EGFLA_HUMAN	minin G-like 2.		7	TGGAGGGAATG	0.443	
-	19	2337	3jmi.3_Nonsense_	NM_173489	NP_775760	Q7Z745	HTRB2_HUMAN			8	GGCTTTCCAAAG	0.244	
-	3	385	f34_uc011cpx.1_I	NM_198566	NP_940968	Q96MH7	CE034_HUMAN			1	ATGTGGAACCA	0.383	
+	16	2029	cqi.1_Missense_M	NM_015360	NP_056175	P42285	SK2L2_HUMAN			2	AAAATCCTTCT	0.378	
+	28	5305_5306	_Mutation_p.P167	NM_015183	NP_055998	O15021	MAST4_HUMAN			13	TGACCCCAAGC	0.624	
+	18	4678	_p.S1459N|ZFYVE	NM_001105251	NP_001098721	Q7Z3T8	ZFY16_HUMAN			0	CTTGTAGTGCTG	0.358	
+	24	3125	e_Mutation_p.V83	NM_002890	NP_002881	P20936	RASA1_HUMAN			5	ATTTGCGTGGCT	0.448	
-	34	3872		NM_014639	NP_055454	Q6PGP7	TTC37_HUMAN			4	CAACTCGAGAC	0.373	
+	18	1412	_uc011cut.1_Non	NM_001042443	NP_001035908	P20810	ICAL_HUMAN			5	ACAGTCAGCAC	0.537	
-	3	682	sense_Mutation_p.	NM_001142483	NP_001135955	Q16612	NP311_HUMAN			1	GATTAAAAAAAGT	0.423	
-	2	1108	LOX_uc011cwk.1_	NM_002317	NP_002308	P28300	LYOX_HUMAN	yl-oxidase li	p.L245Q(1)	1	GGCCAGACAGT	0.612	
+	9	1897	uz.2_Missense_M	NM_014031	NP_054750	Q9Y2P4	S27A6_HUMAN			0	GTTATTGGAATGT	0.343	
+	3	1580		NM_175856	NP_787052	Q70JA7	CHSS3_HUMAN	enal (Potential).		3	GCTACCGCAGAG	0.468	rs142677541
-	13	1344	CSL6_uc003kvz.1_	NM_015256	NP_056071	Q9UKU0	ACSL6_HUMAN	lasmic (Potential).		3	TTACCTGAATCT	0.453	
-	16	2053	de.2_Missense_M	NM_004134	NP_004125	P38646	GRP75_HUMAN			0	CATTTCGAACA	0.453	
+	1	2530		NM_018930	NP_061753	Q9UN67	PCDBA_HUMAN	lasmic (Potential).		2	AGGGTGAAGA	0.428	
+	1	630	DHGA2_uc011dao	NM_018915	NP_061738	Q9Y5H1	PCDG2_HUMAN	(Potential).|Cadherin 2.		3	CGCCAGGATTC	0.458	
+	1	1936	DHGA2_uc011da	NM_018915	NP_061738	Q9Y5H1	PCDG2_HUMAN	(Potential).|Cadherin 6.		3	AGAGCCCGGCT	0.662	
+	1	1416	ljs.1_Intron|PCDH	NM_032088	NP_114477	Q9Y5G5	PCDG8_HUMAN	(Potential).|Cadherin 2.		0	GCTCAGCCCCA	0.572	rs143622391
-	1	3019		NM_016580	NP_057664	Q9NPG4	PCD12_HUMAN	|Extracellular (Potential).		3	TGTCAGTGCCC	0.602	
+	4	671	2A_uc011dcr.1_Int	NM_000405	NP_000396	P17900	SAP3_HUMAN			0	ACTACCGCATAG	0.577	rs104893892
+	12	2365	e_Mutation_p.G5	NM_001114183	NP_001107655	P42261	GRIA1_HUMAN	ellular (Potential).		6	AAGCAGGATCTA	0.493	
-	7	928		NM_032782	NP_116171	Q8TDQ0	HAVR2_HUMAN	lasmic (Potential).		0	GTTTTCTTCTGA	0.468	
+	4	855	11_uc003lxf.1_5'F	NM_173491	NP_775762	P83369	LSM11_HUMAN			0	CTTCTTCCCTGC	0.587	
+	10	1353	RP_uc011dev.1_3	NM_014211	NP_055026	O00591	GBRP_HUMAN	lasmic (Potential).		1	ACAATGAAAAC	0.403	
-	1	1323	2_uc003mcn.1_5'F	NM_003714	NP_003705	O76061	STC2_HUMAN			3	CAGCCGCTCGG	0.512	
-	4	400		NM_005110	NP_005101	O94808	GFPT2_HUMAN	midotransferase type-2.		2	TGACAGCACTG	0.572	
-	6	855	_p.A172V|GNB2L	NM_006098	NP_006089	P63244	GBLP_HUMAN	WD 6.		0	TGGCAGCACAC	0.512	

-	8	2028	e_Mutation_p.P35	NM_000332	NP_000323	P54253	ATX1_HUMAN		4	GTGAGGAACCG	0.677	
+	9	1205	cn.1_Missense_M	NM_153042	NP_694587	Q8NB78	KDM1B_HUMAN		1	GGTACTCGGTG	0.512	rs148006516
-	5	2732	_p.P641S|ZNF184_	NM_007149	NP_009080	Q99676	ZN184_HUMAN		1	GGTAGGGTTTTT	0.428	
+	6	1036	nt_p.L346L|HLA-	NM_002116	NP_002107	P30443	1A01_HUMAN	lasmic (Potential).	2	ACACTCAGGCT	0.512	
-	10	5242	C1_uc011dmp.1_	NM_014641	NP_055456	Q14676	MDC1_HUMAN	ith the PRKDC complex.	4	CTATTTGTCCTG	0.587	
+	2	226	n_p.Q5R|MICB_uc	NM_005931	NP_005922	Q29980	MICB_HUMAN	ellular (Potential).	0	TGTCCCAGGATG	0.522	
+	12	1855	T2_uc003nvc.3_	NM_080686	NP_542417	P48634	PRC2A_HUMAN	peats.|2 X type B repeats.|	0	CACCTCCAGCA	0.627	
-	10	1521	p.P397S|BAT3_uc	NM_004639	NP_004630	P46379	BAG6_HUMAN	9 AA approximate repeats.	0	GGGAGGTGCCT	0.622	
+	6	952	_p.P69S|LY6G6D_	NM_001003693	NP_001003693	Q5SQ64	LY66F_HUMAN		2	AACATCCAGCC	0.562	
+	7	1195	Missense_Mutatio	NM_000063	NP_000054	P06681	CO2_HUMAN	VWFA.	2	TGAACGACAAC	0.498	
-	21	7550		NM_019105	NP_061978	P22105	TENX_HUMAN	nectin type-III 17.	0	CCGCCCGTCCC	0.657	
-	14	5291		NM_019105	NP_061978	P22105	TENX_HUMAN	nectin type-III 10.	0	CTCAGGAACCG	0.662	
-	5	987	0jud.1_Intron|HLA	NM_002118	NP_002109	P28068	DMB_HUMAN	lasmic (Potential).	0	CCCAGGAAGAG	0.443	
+	10	1308	D2_uc011dtv.1_	NM_173558	NP_775829	Q7Z6J4	FGD2_HUMAN	PH 1.	3	CTGATGGATGC	0.652	
+	5	378	10jyy.1_Missense	NM_018426	NP_060896	Q5T3F8	TM63B_HUMAN		3	TGACCGGTATG	0.607	
+	10	1104	dvn.1_Missense_	NM_007058	NP_008989	Q9UMQ6	CAN11_HUMAN	lpain catalytic.	2	AGGACGGGGA	0.632	
+	11	1625	dwh.1_Missense_	NM_005588	NP_005579	Q16819	MEP1A_HUMAN	tracellular (Potential).	3	TGTTCACTACCT	0.527	
-	2	307	al.1_Missense_M	NM_052872	NP_443104	Q96PD4	IL17F_HUMAN		1	GGGAGGTGGAG	0.418	
-	2	301	M3_uc011dwu.1_I	NM_002388	NP_002379	P25205	MCM3_HUMAN		3	TCTCACCGGTTA	0.502	
-	2	635		NM_001003760	NP_001003760	Q9H511	KLH31_HUMAN		1	TCTCCCGTATC	0.373	
+	5	1155		NM_001010872	NP_001010872	Q5T0W9	FA83B_HUMAN		6	TTAAATGAACATG	0.348	
-	21	2225	utation_p.G50R|C	NM_030820	NP_110447	Q96P44	COLA1_HUMAN		2	GCATCCCTTGAA	0.313	
+	11	1617	.2_3'UTR|SMAP1_	NM_001044305	NP_001037770	Q8IYB5	SMAP1_HUMAN		0	GCTCATCAGGT	0.488	
-	4	917	hz.2_Missense_M	NM_015687	NP_056502	Q7Z7B0	FLIP1_HUMAN		4	TAACTCGTATAC	0.507	
+	8	4359	nse_Mutation_p.	NM_001137667	NP_001131139	Q9UKL3	C8AP2_HUMAN		2	AGGTCCATCTC	0.388	
+	1	532		NM_032602	NP_115991	Q969M2	CXA10_HUMAN	ical; (Potential).	0	TATATTCTCTATG	0.448	
+	20	5579	i.2_Missense_Mut	NM_001624	NP_001615	Q9Y4K1	AIM1_HUMAN	in B-type lectin.	9	CAGTATGATCAA	0.403	
+	3	1283	OXO3_uc011ean.	NM_201559	NP_963853	O43524	FOXO3_HUMAN		6	GTGGCCGCCTG	0.607	rs145756480
-	36	5308	.G1660*|LAMA4_	NM_001105206	NP_001098676	Q16363	LAMA4_HUMAN	minin G-like 5.	9	TCAATCCAATATT	0.383	
+	17	2197		NM_173560	NP_775831	Q8HWS3	RFX6_HUMAN		3	AGCCCCACTCC	0.512	
-	4	479	.1_RNA|GOPC_uc	NM_002944	NP_002935	P08922	ROS_HUMAN	ellular (Potential).	25	GTACTTCCTCTT	0.473	
+	2	552	se_Mutation_p.R2	NM_000165	NP_000156	P17302	CXA1_HUMAN	lasmic (Potential).	2	GATGCGAAAGG	0.443	
+	12	1690	YNJ2_uc011efn.1_	NM_003898	NP_003889	O15056	SYNJ2_HUMAN	ytic (By similarity).	1	GGAACGTGAAC	0.582	
+	2	263	F25_uc003qwl.1_	NM_030615	NP_085118	Q9UIL4	KIF25_HUMAN	inesin-motor.	2	TCCCAGATGACA	0.582	
+	2	101	|GPR146_uc003s	NM_138445	NP_612454	Q96CH1	GP146_HUMAN	ellular (Potential).	1	TCAACGGCACA	0.687	
-	12	2923	c.1_Missense_Mu	NM_018059	NP_060529	Q96JH8	RADIL_HUMAN	Pro-rich.	7	AGTCGGGGTCC	0.711	
+	2	329	_uc003snx.2_Intr	NM_015610	NP_056425	Q9Y4P8	WIPI2_HUMAN		2	TGGCCGTCGCG	0.388	
-	1	620		NM_175886	NP_787082	P21108	PRPS3_HUMAN		1	CAATGGAGGTC	0.463	
+	4	643	_p.E52K|CREB5_	NM_182898	NP_878901	Q02930	CREB5_HUMAN		2	AGCACGAGTTC	0.557	
+	14	1300	rf10_uc003tho.1_	NM_024728	NP_079004	Q9HAC7	CG010_HUMAN		2	GATACGATGAC	0.567	
+	6	1150	_p.S182L|HECW1_	NM_015052	NP_055867	Q76N89	HECW1_HUMAN		23	AAACTCGGCAG	0.408	
-	4	947	_uc003tmx.2_Intr	NM_004749	NP_004740	Q969Z0	TBRG4_HUMAN		0	GCAAGGGCACG	0.607	
-	13	1078_1079	p.G238R|TNS3_uc	NM_022748	NP_073585	Q68CZ2	TENS3_HUMAN	2 tensin-type.	4	ATCTCCCTTCAG	0.515	
+	23	3035	p.G885E|EGFR_u	NM_005228	NP_005219	P00533	EGFR_HUMAN	Potential).|Protein kinase.	9571	GAAAGGAGAAC	0.532	
+	1	941	.1_Intron|CLDN4_	NM_001305	NP_001296	O14493	CLD4_HUMAN	lasmic (Potential).	0	TGCCCGCTCTG	0.627	
-	10	2107	dy.1_Missense_Mu	NM_012301	NP_036433	Q86UL8	MAGI2_HUMAN	PDZ 3.	11	CAATAGTGAAG	0.517	
-	15	1860	p.R595Q|ABCB4_	NM_018849	NP_061337	P21439	MDR3_HUMAN	1.|Cytoplasmic (By similarit	6	CATTTCGGACC	0.488	rs144398632

-	3	356	mg.2_Missense_M	NM_017654	NP_060124	Q5K651	SAMD9_HUMAN	SAM.	7	AAATTTCCCTGT	0.368	
+	18	2329	p.S707F|TRRAP_	NM_003496	NP_003487	Q9Y4A5	TRRAP_HUMAN		37	AGCTCTCCAACC	0.468	
-	1	701		NM_001005276	NP_001005276	Q8NHA4	O2AE1_HUMAN	lasmic (Potential).	0	GCATTTCTCTTG	0.502	
+	14	2378	ZAN_uc003uwl.2_F	NM_003386	NP_003377	Q9Y493	ZAN_HUMAN	ate) (mucin-like domain).|E	11	AAAAACCCACCA	0.522	
+	14	2798	ZAN_uc003uwl.2_F	NM_003386	NP_003377	Q9Y493	ZAN_HUMAN	ate) (mucin-like domain).|E	11	AAAAACTCACCA	0.502	
+	31	5890	uwl.2_RNA|ZAN_u	NM_003386	NP_003377	Q9Y493	ZAN_HUMAN	Extracellular (Potential).	11	ACCTGCAAACCC	0.632	
+	4	498	A9_uc003uwr.2_5'	NM_020246	NP_064631	Q9BXP2	S12A9_HUMAN	lasmic (Potential).	0	GGGCAGCATTG	0.463	
+	3	11710	C17_uc010lho.1_F	NM_001040105	NP_001035194	Q685J3	MUC17_HUMAN	ellular (Potential).	27	CACTTCCAACTA	0.468	
-	6	938	GAT3_uc010lhr.2_I	NM_178176	NP_835470	Q86VF5	MOGT3_HUMAN		2	AGCTTCTTGAA	0.577	
-	56	9314	.2_Missense_Muta	NM_005045	NP_005036	P78509	RELN_HUMAN		19	TGATTTCTGCTC	0.448	
+	6	2477	98_splice|PIK3CG_	NM_002649	NP_002640	P48736	PK3CG_HUMAN		38	CTTACAGATTGA	0.363	
-	13	1665	ves.2_Missense_M	NM_000111	NP_000102	P40879	S26A3_HUMAN	ical; (Potential).	4	CTAACCCGAGT	0.448	
-	12	1571	ves.2_Missense_M	NM_000111	NP_000102	P40879	S26A3_HUMAN	ical; (Potential).	4	CAAACTGCATCA	0.358	
+	3	555	vjz.2_Missense_M	NM_002851	NP_002842	P23471	PTPRZ_HUMAN	tial).|Alpha-carbonic anhyd	9	AAATATCCAACA	0.299	
-	3	1041	p.A118T|SLC13A	NM_012450	NP_036582	Q9UKG4	S13A4_HUMAN	ical; (Potential).	0	GCTTGGCTCCGG	0.602	
-	20	5852	.L1869F|KIAA154	NM_020910	NP_065961	Q9HCM3	K1549_HUMAN		230	GAGGAGCTCCT	0.622	
-	15	1860		NM_004333	NP_004324	P15056	BRAF_HUMAN	rotein kinas R603>I(2)|p.T	18290	GATTTCACTGTA	0.368	
+	2	429		NM_178829	NP_849151	Q96L11	CG034_HUMAN		0	CAGGAGGGCCA	0.542	
+	1	466		NM_001001667	NP_001001667	Q8N148	OR6V1_HUMAN	Name=4; (Potential).	1	ATGGTACCCACT	0.572	
+	12	1480	CN1_uc011ktc.1_In	NM_000083	NP_000074	P35523	CLCN1_HUMAN	al; (By similarity).	5	TTCTTCGTCATGA	0.502	rs139158852
+	14	1651	c.1_Missense_Mu	NM_000083	NP_000074	P35523	CLCN1_HUMAN		5	TACCTGGGGGC	0.443	
-	5	1013	p.P238S|KCNH2_	NM_000238	NP_000229	Q12809	KCNH2_HUMAN	lasmic (Potential).	4	TTTGGGGAATCT	0.587	
-	4	388	on_p.T75I|ENTPD	NM_004901	NP_004892	Q9Y227	ENTP4_HUMAN	enal (Potential).	2	TGTCGGTAACT	0.438	
+	45	4716	3xei.2_Nonsense_	NM_024940	NP_079216	Q9H7D0	DOCK5_HUMAN	DHR-2.	3	CCAACGAGAGG	0.562	
-	10	2478	p.D654N|WHSC1L	NM_023034	NP_075447	Q9BZ95	NSD3_HUMAN		1	TAGAATCGGAGT	0.418	
-	18	1985	ck.1_Missense_Mu	NM_001464	NP_001455	Q99965	ADAM2_HUMAN	r (Potential).|EGF-like.	2	ATGAAGCACTAC	0.378	rs147069631
+	4	2555	P1_uc011ldy.1_Intr	NM_006269	NP_006260	P56715	RP1_HUMAN		12	GTGTTTCCTCAC	0.299	
+	19	2108	p.F694S|PREX2_	NM_024870	NP_079146	Q70Z35	PREX2_HUMAN	PDZ 2.	17	GGGATTTGGCC	0.453	
+	10	4867	.R1539C|ZFHX4_	NM_024721	NP_078997	Q86UP3	ZFHX4_HUMAN		15	CCATCTCGTCCA	0.388	
-	3	1107	ydr.1_Missense_M	NM_138817	NP_620172	Q8TCU3	S7A13_HUMAN	Name=9; (Potential).	1	CTGTAAATGGAG	0.348	
-	15	2419	.1_Missense_Muta	NM_015668	NP_056483	Q8NE09	RGS22_HUMAN		7	CTTTTCCTGTTG	0.413	
-	2	890	M74_uc003ymx.2_	NM_153015	NP_694560	Q96NL1	TMM74_HUMAN		4	CTGTTTCGACGA	0.507	
-	7	833	se_Mutation_p.S12	NM_015912	NP_056996	Q49AJ0	F135B_HUMAN		9	CTGAGGAAGTC	0.473	
-	4	918	p.E204K|SLC45A	NM_001080431	NP_001073900	Q5BKX6	S45A4_HUMAN		2	CTCCTCGTCGA	0.662	
-	3	363	se_Mutation_p.S11	NM_023078	NP_075566	Q53H96	P5CR3_HUMAN		0	CTCAGAGACACC	0.622	
+	7	1050_1051	f.3_Missense_Mut	NM_173831	NP_776192	Q96C28	ZN707_HUMAN	C2H2-type 3.	1	AAGGACCGCCT	0.629	
-	21	2928	CRIB_uc003yzo.1	NM_015356	NP_056171	Q14160	SCRIB_HUMAN	ion with ARHGEF7.	5	GTGGTTATGCTG	0.682	
-	16	1494	nfl.2_Missense_Mu	NM_178564	NP_848659	Q9NSY0	NRBP2_HUMAN		2	CTGCCGGTGCA	0.736	
+	4	385	33_uc011lmh.1_Int	NM_033439	NP_254274	O95760	IL33_HUMAN		0	CTTCATGATTCA	0.498	
+	8	1029	p.W301*|ADAMTS	NM_001040272	NP_001035362	Q8N6G6	ATL1_HUMAN		5	CCGATGGAGGG	0.468	
-	1	5058	uc003zrh.1_5'Flan	NM_153809	NP_722516	Q8IZX4	TAF1L_HUMAN		26	GGGGTCATTGG	0.443	
-	1	754	.M77T|GBA2_uc01	NM_020944	NP_065995	Q9HCG7	GBA2_HUMAN	ellular (Potential).	4	TAGCCCATAGCT	0.537	
-	8	1253		NM_015225	NP_056040	Q8WUY3	PRUN2_HUMAN		0	GAGGGGGGCAC	0.517	
+	12	1490	_Mutation_p.A331	NM_005392	NP_005383	O75151	PHF2_HUMAN		1	CAAAGCCGTCC	0.602	
+	6	828	uh.1_Missense_Mu	NM_032558	NP_115947	Q5SR56	HIAL1_HUMAN	ical; (Potential).	2	ATTGGAGCATAT	0.562	
-	4	1182	od.3_Missense_Mu	NM_001127610	NP_001121082	Q14032	BAAT_HUMAN		3	GCCCCAGGGTAA	0.527	
+	4	527		NM_019592	NP_062538	Q5VTR2	BRE1A_HUMAN		8	TGACCGAGAGA	0.468	

-	1	555		NM_006686	NP_006677	Q9Y614	ACL7B_HUMAN		1	CTCCGCGTACT	0.622	
-	2	775		NM_001012993	NP_001013011	Q5JTZ5	CI152_HUMAN		0	CCATCGATTCTG	0.552	
-	9	965	_p.E215K|FKBP15_	NM_015258	NP_056073	Q5T1M5	FKB15_HUMAN	ase FKBP-type.	3	CACCTCGAACA	0.468	
+	58	5072_5073	.2_RNA|COL27A1_	NM_032888	NP_116277	Q8IZC6	CORA1_HUMAN	lar collagen NC1.	4	CTGCAGGGACC	0.594	
+	3	1156	_p.R249*|TLR4_u	NM_138554	NP_612564	O00206	TLR4_HUMAN	ellular (Potential).	16	GAATTCCGATTA	0.363	
+	4	1237	v.1_Missense_Mu	NM_054107	NP_473448	Q8NGS2	OR1J2_HUMAN	lasmic (Potential).	5	ATATGTCACCCT	0.428	
+	1	589		NM_001004457	NP_001004457	Q8NGR9	OR1N2_HUMAN	ellular (Potential).	4	TATTGTGATCCTA	0.532	
+	7	794	.R223Q|FAM125B	NM_033446	NP_258257	Q9H7P6	F125B_HUMAN		0	CACCCGGACGG	0.562	
+	11	2972	v.2_Missense_Mut	NM_005157	NP_005148	P00519	ABL1_HUMAN	-binding.|Pro-rich.	817	ATCCTCGGCCC	0.662	
+	18	3205		NM_006059	NP_006050	Q9Y6N6	LAMC3_HUMAN	omain II and I.	3	GGAGGGGTGGC	0.612	
+	7	1147	c.1_Missense_Mu	NM_002957	NP_002948	P19793	RXRA_HUMAN	gand-binding.	2	CCACCGGGCTG	0.682	
+	3	277	sense_Mutation_	NM_080877	NP_543153	Q8N130	NPT2C_HUMAN	lasmic (Potential).	0	GGACCTCCAGT	0.617	
-	5	443	ense_Mutation_p.	NM_006089	NP_006080	Q9UQR0	SCML2_HUMAN	MBT 1.	0	CAGTCGTAACC	0.448	
+	11	1313	_p.G377E|CNKSR	NM_014927	NP_055742	Q8WXI2	CNKR2_HUMAN	DUF1170.	2	TCAAGGAAGAC	0.313	
+	1	1902		NM_018094	NP_060564	Q8IYD1	ERF3B_HUMAN		1	TAATCTCCTTGG	0.413	
-	2	421		NM_152424	NP_689637	Q5JTC6	F123B_HUMAN	p.0?(40)	112	CCTACCTGGGC	0.527	
+	37	5411	0nle.1_RNA|TAF1_	NM_138923	NP_620278	P21675	TAF1_HUMAN	cidic tail).|Protein kinase 2.	17	CGGTGGGGAGG	0.517	
+	5	1035	dm.1_Missense_	NM_152630	NP_689843	Q8NEK8	FA46D_HUMAN		2	AGGTGGTGGCC	0.438	
-	3	594		NM_001006938	NP_001006939	Q6IPX3	TCAL6_HUMAN		1	ACACATCTCCAC	0.488	
+	4	1349	mg.1_Missense_	NM_152423	NP_689636	Q5H9M0	MUML1_HUMAN		4	AAGATGAAAAG	0.408	
-	11	1699	su.1_Missense_M	NM_014289	NP_055104	Q9Y6Q1	CAN6_HUMAN		6	GCCACGAGCCA	0.423	
+	5	915	A3_uc004ets.3_R	NM_007325	NP_015564	P42263	GRIA3_HUMAN	ellular (Potential).	5	TTGAAGAAATGG	0.443	
-	3	462		NM_001013403	NP_001013421	Q5JRM2	CX066_HUMAN	ytoplasmic (Potential).	0	GTATGGATGGC	0.418	
+	33	5728		NM_017514	NP_059984	P51805	PLXA3_HUMAN	lasmic (Potential).	3	TTGTCGGAAGC	0.597	
-	10	1309	za.1_Missense_M	NM_018216	NP_060686	Q9NVE7	PANK4_HUMAN		3	CGTGTCGGGCA	0.642	
+	5	1387		NM_004285	NP_004276	O95479	G6PE_HUMAN	1-dehydrogenase.	0	GGATCTTGTTC	0.612	
+	7	1606	4B_uc010oai.1_I	NM_001105562	NP_001099032	O95155	UBE4B_HUMAN		4	TTCCCGTGCAG	0.587	
+	10	1261		NM_021933	NP_068752	Q5JXC2	MIIP_HUMAN		1	ATCCAGGCCTC	0.642	
+	6	1170	av.1_Missense_	NM_032880	NP_116269	Q96ID5	IGS21_HUMAN		4	CCACAGAGAAC	0.672	
+	18	4770	e_Mutation_p.A10	NM_006015	NP_006006	O14497	ARI1A_HUMAN		142	CTCTGCACCCC	0.597	
-	3	810	d.2_Missense_Mu	NM_014654	NP_055469	O75056	SDC3_HUMAN	ntial).|Ser/Thr-rich (mucin-li	2	TGGCCGGGAGG	0.716	
+	2	125	4_uc001bxv.1_5'F	NM_005268	NP_005259	O95377	CXB5_HUMAN	lasmic (Potential).	1	AGGGACTCCTG	0.463	
+	4	990	B2_uc001bzd.1_I	NM_178548	NP_848643	Q6VUC0	AP2E_HUMAN		0	CCTCCGCAGGT	0.642	
-	14	2305	SLC6A9_uc010ok	NM_201649	NP_964012	P48067	SC6A9_HUMAN	lasmic (Potential).	0	TATCCGGGAGT	0.677	rs2286246
-	8	1454	oj.1_Missense_M	NM_014762	NP_055577	Q15392	DHC24_HUMAN		1	GCGGCTCCCCA	0.567	
-	1	1704	_5'Flank|uc010oo	NM_002228	NP_002219	P05412	JUN_HUMAN		0	CAGCCGCGGGT	0.716	
-	1	703	cj.1_Missense_M	NM_012152	NP_036284	Q9UBY5	LPAR3_HUMAN	lasmic (Potential).	5	ATGCGGAGACA	0.517	
-	7	1142	3_uc001dmu.2_M	NM_018284	NP_060754	Q9H0R5	GBP3_HUMAN		2	GACTGCGTTCT	0.512	rs113485304
+	3	675	dnn.2_Missense_	NM_001134479	NP_001127951	Q7L1W4	LRC8D_HUMAN		2	TGGAAGCAGCC	0.502	
-	2	634_635		NM_006492	NP_006483	O95076	ALX3_HUMAN	Homeobox.	0	CTCCCGGGCAT	0.594	rs121908168
+	12	1522	vkt.1_Missense_M	NM_001102663	NP_001096133				0	ATGTTATTCGAC	0.478	
+	7	726	M1_uc009wmn.2_	NM_024041	NP_076946	Q9BWG6	SCNM1_HUMAN		4	AGATGGACGAG	0.383	
-	3	1023		NM_001122965	NP_001116437	Q6XPR3	RPTN_HUMAN	Gln-rich.	0	CTGACTGTAGT	0.507	rs12117644
-	3	6751		NM_002016	NP_002007	P20930	FILA_HUMAN	ich.|Filaggrin 13.	16	TCCCCGGGGCC	0.577	
-	3	4489		NM_002016	NP_002007	P20930	FILA_HUMAN	Ser-rich.	16	CTGACCGTCTT	0.577	
-	6	2406	i.2_Missense_Mut	NM_001111	NP_001102	P55265	DSRAD_HUMAN	DRBM 3.	6	GGAGCGGGCGT	0.542	
-	2	843	2_Missense_Muta	NM_001111	NP_001102	P55265	DSRAD_HUMAN		6	TATGACCGTCTG	0.522	

+	4	895	ey.1_Intron|HCN3_	NM_020897	NP_065948	Q9P1Z3	HCN3_HUMAN	cellular (Potential).	2	GGGCCGCCAGT	0.592	rs137875525
-	2	688		NM_001093725	NP_001087194	A1L020	MEX3A_HUMAN	KH 2.	0	GGGCACCCGCA	0.627	
-	4	401	wsb.1_Missense_M	NM_178229	NP_839943	Q86VI3	IQGA3_HUMAN	CH.	6	GATAGCCAAAAG	0.463	
-	3	452	.L98F|FCRL5_uc	NM_031281	NP_112571	Q96RD9	FCRL5_HUMAN	otential).|Ig-like C2-type 1.	6	AAAATCCAAGTG	0.468	
+	7	866		NM_201563	NP_963857				0	CCAATTCCACTG	0.502	
-	13	4119		NM_000130	NP_000121	P12259	FA5_HUMAN	ndem repeats of [TNP]-L-S	6	GGCTGAGGTCT	0.512	
+	6	563		NM_139240	NP_640333	O95561	CA105_HUMAN		1	AAATTCCAGACT	0.373	
-	2	868	_p.E263K|TNR_uc	NM_003285	NP_003276	Q92752	TENR_HUMAN	Cys-rich.	11	CAGTTCCCTGC	0.637	
+	3	2723	e_Mutation_p.R52	NM_020318	NP_064714	Q9BXP8	PAPP2_HUMAN	etalloprotease.	16	CCTTCGGGGAG	0.537	
+	2	849	px.2_Missense_Mu	NM_002293	NP_002284	P11047	LAMC1_HUMAN	inin N-terminal.	5	CAGGAGGGGAC	0.577	
-	3	1109	se_Mutation_p.Q34	NM_015375	NP_056190	Q6XUX3	DUSTY_HUMAN		1	CACCTGGTGAG	0.522	
+	6	610	.H101Y|SMYD2_u	NM_020197	NP_064582	Q9NRG4	SMYD2_HUMAN	SET.	1	CTTTCTCATTTG	0.338	
-	4	1398	cf.2_Missense_Mu	NM_024804	NP_079080	Q96BR6	ZN669_HUMAN	C2H2-type 8.	0	TCTTTCGTGGA	0.423	
-	20	2446	_p.L172F|DIP2C_u	NM_014974	NP_055789	Q9Y2E4	DIP2C_HUMAN		7	GACGAGGCCTC	0.617	
-	6	1762		NM_018702	NP_061172	Q9NS39	RED2_HUMAN	to I editase.	3	AATATCGATCGC	0.527	
-	11	1377	_Mutation_p.S42	NM_001029880	NP_001025051	Q5VUG0	SMBT2_HUMAN	MBT 4.	8	CAACGGAGGCC	0.517	
-	4	4714	uc001iqp.1_Intron	NM_207371	NP_997254	Q1XH10	DLN1_HUMAN		1	AATCATCCAGTG	0.423	
-	14	2669	c001iwf.2_5'Flank	NM_025209	NP_079485	Q9H2F5	EPC1_HUMAN		4	ACCTTGGAAACT	0.433	
+	34	3410		NM_052997	NP_443723	Q9BXX3	AN30A_HUMAN	Potential.	9	TAAAAGGGCAT	0.333	
-	3	1599	sense_Mutation_p.	NM_001098208	NP_001091678	P52597	HNRPF_HUMAN		0	CTATACGCCCCA	0.552	
-	37	11068	K3_uc010qih.1_In	NM_020987	NP_066267	Q12955	ANK3_HUMAN		19	TCTCTTCAACAA	0.473	
+	9	1470	B3_uc001kdu.2_M	NM_007078	NP_009009	O75112	LDB3_HUMAN		1	CTGCGGAGCCT	0.468	
-	6	1976	_p.E260K|MMRN2	NM_024756	NP_079032	Q9H8L6	MMRN2_HUMAN		1	CACCTCCTCCC	0.731	
+	9	1103		NM_001010939	NP_001010939	Q5W064	LIPJ_HUMAN		1	TCATTGGAGTCA	0.348	
-	1	1710		NR_002319					0	CTTCTTAAATACC	0.498	
+	4	775	g.2_Missense_Mu	NM_004088	NP_004079	P04053	TDT_HUMAN	teraction with DNTTIP2.	1	CTCTGCCATTCA	0.438	
-	6	1286		NM_000102	NP_000093	P05093	CP17A_HUMAN		0	GTGGGGGATGA	0.622	
+	12	2030		NM_014978	NP_055793	Q9UPU3	SORC3_HUMAN	Lumenal (Potential).	10	ACATGGAGACA	0.443	
+	12	1486	h.2_Missense_Mu	NM_005308	NP_005299	P34947	GRK5_HUMAN	rotein kinase.	3	CCAAGTCCATCT	0.642	
+	8	1349	.1_Intron|WDR11_	NM_018117	NP_060587	Q9BZH6	WDR11_HUMAN	WD 3.	0	ATGCAGCCGCC	0.473	
+	4	2702	nse_Mutation_p.P	NM_206862	NP_996744	O95359	TACC2_HUMAN		10	ACATCCCCCCC	0.637	
+	29	3624	G674E|DMBT1_uc	NM_007329	NP_015568	Q9UGM3	DMBT1_HUMAN	SRCR 9.	7	CCCAGGAAATG	0.602	
-	1	655		NM_001012708	NP_001012726	Q6L8H2	KRA53_HUMAN	repeats of C-C-X-P.	2	gaacagcagggtttg	0.1	
+	1	928		NM_001004751	NP_001004751	Q8NGF3	O51D1_HUMAN	lasmic (Potential).	0	ACCAAAGAGATC	0.493	
-	1	793	2_uc001mak.1_Ir	NM_001005289	NP_001005289	Q8NGJ2	O52H1_HUMAN	Name=6; (Potential).	2	GGAGAAAAAGG	0.502	
-	3	867	1_5'Flank|APBB1_	NM_001164	NP_001155	O00213	APBB1_HUMAN	WW.	2	CAGCCGGCAGG	0.632	
+	22	2595	PFIBP2_uc010rbe	NM_003621	NP_003612	Q8ND30	LIPB2_HUMAN	SAM 3.	4	AGTATGCACCCA	0.517	
-	15	3017	_p.P524L|ST5_uc0	NM_213618	NP_998783	P78524	ST5_HUMAN	DENN.	1	GGGTGGGACAG	0.647	
-	19	3478	p.R418G|DENND5	NM_015213	NP_056028	Q6IQ26	DEN5A_HUMAN		1	ATGGCCTCTCAT	0.617	
+	22	2878		NM_014633	NP_055448	Q6PD62	CTR9_HUMAN	Lys-rich.	2	TTTAGCGTTCTAA	0.333	
-	12	1884	cy.1_Missense_Mu	NM_000352	NP_000343	Q09428	ABCC8_HUMAN	ilarity).|ABC transmembra	1	TGTGACCAAGAT	0.612	
+	5	892	nuc.2_Missense_M	NM_001077242	NP_001070710	Q96QD5	DEPD7_HUMAN		2	GCTCTCGGCAG	0.413	
+	8	1113	T_uc009ykc.1_R	NM_001752	NP_001743	P04040	CATA_HUMAN		3	GCATTGAGGCC	0.488	
+	3	946	GKZ_uc001ncl.2_	NM_001105540	NP_001099010	Q13574	DGKZ_HUMAN		3	CCGGAGTACAG	0.677	rs141189455
-	12	1002	_p.M144I|MTCH2_	NM_014342	NP_055157	Q9Y6C9	MTCH2_HUMAN		0	TGTAGCATGCA	0.269	
+	1	19		NM_001005200	NP_001005200	Q8N162	OR8H2_HUMAN	ellular (Potential).	2	GGAATAACACA	0.343	rs61746549
-	16	2188	_5'Flank|TNKS1B	NM_003146	NP_003137	Q08945	SSRP1_HUMAN	Ser-rich.	2	GCGTGGATTTCT	0.498	

-	3	790	_p.A80V|FADS1_	NM_013402	NP_037534	O60427	FADS1_HUMAN	ical; (Potential).	1	GCACCGCACAG	0.562	
-	6	1566	ay.3_Missense_M	NM_005609	NP_005600	P11217	PYGM_HUMAN		2	CATTGGGAGCC	0.622	
-	22	2510		NM_017525	NP_059995	Q6DT37	MRCKG_HUMAN		4	CATGCCTTGTG	0.647	
-	1	155	nt.1_Nonsense_	NM_015104	NP_055919	Q2TAZ0	ATG2A_HUMAN		2	CCGCTCTTTCA	0.642	
+	9	1710	1L1_uc001oep.1_	NM_001099409	NP_001092879	Q8N3D4	EH1L1_HUMAN		1	GCCCCCAGCGG	0.682	
+	12	1151	4Q|BBS1_uc001	NM_024649	NP_078925	Q8NFJ9	BBS1_HUMAN		1	TGGCCGGTACG	0.562	
+	7	818	SH3_uc001okl.2_	NM_017857	NP_060327	Q8TE77	SSH3_HUMAN		1	AGGCAGCTCTA	0.622	
-	10	1757	ense_Mutation_p.	NM_004910	NP_004901	O00562	PITM1_HUMAN		3	ATGAGGTGGCC	0.647	
+	1	351		NM_001012710	NP_001012728	Q6L8G5	KR510_HUMAN	repeats of C-C-X-P.	1	TGGGGGCTCCA	0.677	
-	1	901		NM_001005285	NP_001005285	A6NND4	O2AT4_HUMAN	lasmic (Potential).	1	TTACATCCCTGT	0.483	
+	2	602		NM_015516	NP_056331	Q8WUA8	TSK_HUMAN	LRR 4.	0	AGCTCCGGGAG	0.637	rs143993207
-	6	1042	tj.1_Missense_Mu	NM_001162951	NP_001156423	Q9HCH5	SYTL2_HUMAN		3	TCTAGGAAAAG	0.473	
+	1	699		NM_001008781	NP_001008781	Q8TDW7	FAT3_HUMAN	|Extracellular (Potential).	5	AGGTATGATCTG	0.388	
-	6	880	rvc.1_Missense_	NM_004347	NP_004338	P51878	CASP5_HUMAN		3	ACATCCGGTTTT	0.488	
+	17	1830	1L2_uc009zdg.1_	NM_138342	NP_612351	Q8IW92	GLBL2_HUMAN		3	ACATTACCTGCT	0.537	
-	9	1038		NM_020373	NP_065106	Q9NQ90	ANO2_HUMAN	lasmic (Potential).	7	GTCATTCATATC	0.483	
+	5	682	PS7A_uc001qqi.2	NM_001164094	NP_001157566	Q9UBW8	CSN7A_HUMAN	PCI.	1	CCAGCGCAACC	0.602	
+	1	104		NM_001080454	NP_001073923	P0C7M7	ACSM4_HUMAN		0	TGACTCTTGCTG	0.473	
-	3	276		NM_006248	NP_006239				0	GGGTGGTCCTT	0.612	
+	1	565	Z1_uc001rdw.3_5'	NM_033328	NP_201585	Q96KX2	CAZA3_HUMAN	p.G136A(1)	2	AAAAGGAAATTG	0.403	
-	33	2300	L2A1_uc001rqv.2	NM_001844	NP_001835	P02458	CO2A1_HUMAN	e-helical region.	2	GCCACGTTCAC	0.637	
-	9	1371	|CCNT1_uc009zk	NM_001240	NP_001231	O60563	CCNT1_HUMAN		6	AGTCCGATGAC	0.463	rs113480935
+	13	1843	_p.C559Y|TROAP_	NM_005480	NP_005471	Q12815	TROAP_HUMAN	ate tandem repeats.|Cys-ri	1	GTCCTGCTGTA	0.597	
-	10	1367	.2_Missense_Mut	NM_016293	NP_057377	Q9UBW5	BIN2_HUMAN	Pro-rich.	1	AGAGGCTGTAG	0.622	
+	25	5531	j.2_Missense_Mu	NM_012291	NP_036423	Q14674	ESPL1_HUMAN		3	AGCCCGGCCCT	0.607	
-	1	188	e_Mutation_p.R28	NM_003075	NP_003066	Q8TAQ2	SMRC2_HUMAN		6	CAGCCGCACGT	0.438	
+	12	1684	qk.1_Nonsense_	NM_173596	NP_775867	Q6ZMH5	S39A5_HUMAN	ical; (Potential).	2	TCCCTGGGTGT	0.652	
-	10	1690	sru.1_Missense_	NM_001478	NP_001469	Q00973	B4GN1_HUMAN	enal (Potential).	0	GTGGTGGAAGC	0.677	
+	6	780	se_Mutation_p.P2	NM_006812	NP_006803	Q13438	OS9_HUMAN		1	CTGCACCGCAG	0.617	
+	10	2051	_Mutation_p.A48	NM_181861	NP_863651	O14727	APAF_HUMAN		3	ACATGGCCAGT	0.378	
+	8	852	p.R209Q|GAS2L3_	NM_174942	NP_777602	Q86XJ1	GA2L3_HUMAN	GAR.	1	CTGTCGGCATG	0.398	rs147048300
-	8	2022		NM_004075	NP_004066	Q16526	CRY1_HUMAN	- mediated transcription (B	3	AATCTGCATCA	0.383	
+	7	946	HP_uc001tpp.2_M	NM_001143852	NP_001137324	Q9BT92	TCHP_HUMAN	Glu-rich.|Interaction with k	1	CCTTCCGGCAG	0.567	
+	21	3240	_Site_p.A1045_spli	NM_025247	NP_079523	Q6JQN1	ACD10_HUMAN		2	TGCCAGGCCTT	0.632	
-	10	1602		NM_173598	NP_775869	Q6VAB6	KSR2_HUMAN	Pro-rich.	15	GTAGGGGAGAA	0.652	
+	4	429	51_uc001ujy.3_5'	NM_024078	NP_076983	Q9BVI4	NOC4L_HUMAN		0	TGGAAGGAGCG	0.652	
-	25	2973	q.1_RNA|POLE_	NM_006231	NP_006222	Q07864	DPOE1_HUMAN		8	TTCCCCGCGGC	0.517	rs142563997
-	2	798		NM_021954	NP_068773	Q9Y6H8	CXA3_HUMAN	ical; (Potential).	1	CCACCGCCAGC	0.647	
-	17	2645	sa.3_Missense_M	NM_002019	NP_002010	P17948	VGFR1_HUMAN	lasmic (Potential).	24	CAGAAGAAGACT	0.383	
+	29	4869	i.2_Missense_Mu	NM_015678	NP_056493	Q8NFP9	NBEA_HUMAN		11	TCATAGGATGATA	0.343	
+	1	249	_p.A50T|COG3_u	NM_031431	NP_113619	Q96JB2	COG3_HUMAN		2	CGGCGGCAGAG	0.692	
+	1	1837		NR_003268					0	TCCAGGGGGAG	0.532	
-	4	714	orf1_uc010tgm.1_	NM_020456	NP_065189	Q5W111	SPRY7_HUMAN	B30.2/SPRY.	0	ATGCTGGACAA	0.328	
+	11	2091	p.Y435H|TDRD3_	NM_030794	NP_110421	Q9H7E2	TDRD3_HUMAN		2	GTAGATTATAATA	0.338	
-	7	1921	.1_Intron|DACH1_	NM_080759	NP_542937	Q9UI36	DACH1_HUMAN		1	CCCAGGAAGTA	0.408	
-	1	28	1vpk.2_Missense_	NM_001010977	NP_001010977	Q5VZV1	MT21C_HUMAN		0	CTGCGCGGAGC	0.577	
-	11	1783	1_3'UTR|TOX4_u	NM_019852	NP_062826	Q86U44	MTA70_HUMAN		2	TGAACCGTGCA	0.458	

+	2	753	se_Mutation_p.W1	NM_001126339	NP_001119811	Q9BU02	THTPA_HUMAN		0	TGCCTGGAAGC	0.617	
-	10	1318_1319	yv.2_Missense_Mu	NM_002863	NP_002854	P06737	PYGL_HUMAN		1	TCGAGGGAGCA	0.485	
-	7	1244	fz.1_Missense_Mu	NM_139318	NP_647479	Q8NCM2	KCNH5_HUMAN	ellular (Potential).	9	TATGGAGTCCCA	0.468	
+	2	208	.1_5'UTR|CHURC	NM_002028	NP_002019	P49356	FNTB_HUMAN	PFTB 2.	1	ACAAATCCTTGA	0.393	
+	17	2513	HH1_uc001xjn.1_	NM_020715	NP_065766	Q9ULM0	PKHH1_HUMAN	PH 2.	0	ACCACCTCACA	0.582	
+	34	6934	rf.1_Missense_Mu	NM_014982	NP_055797	Q96RV3	PCX1_HUMAN	Ser-rich.	1	TGCCATCATCCA	0.572	
+	15	4426	xmv.2_Missense_	NM_015556	NP_056371	O43166	SI1L1_HUMAN	Ser-rich.	4	AAGTGGCACCC	0.602	
+	2	521		NM_001037162	NP_001032239	Q3I5F7	ACOT6_HUMAN		0	TCGATGATCTA	0.403	
+	2	413	vj.1_5'Flank|VIPAF	NM_012111	NP_036243	O95433	AHSA1_HUMAN		0	GGAGCGTCAAA	0.423	
-	14	2305	rf145_uc010asz.1_	NM_152446	NP_689659	Q6ZU80	CE128_HUMAN	Potential.	0	CTGTTCGTGTTT	0.413	
-	4	1555	1ybp.2_Missense_	NM_001002860	NP_001002860	Q9P203	BTBD7_HUMAN		1	GATGAGAACTC	0.408	
+	24	3343	1409_uc001ybs.1_	NM_020818	NP_065869	Q9P2D8	UNC79_HUMAN		17	TCCAGCTCTCG	0.463	
+	23	2726	qv.2_Missense_M	NM_015197	NP_056012	Q86VP3	PACS2_HUMAN		1	TGCGGGGTGAG	0.617	
-	16	1840	v.2_Missense_Mu	NM_000275	NP_000266	Q04671	P_HUMAN	lasmic (Potential).	5	CCTTCCCCAGC	0.657	
-	30	3534	.2_Missense_Muta	NM_004573	NP_004564	Q00722	PLCB2_HUMAN	Potential.	8	ATGTGGGAGTTG	0.368	
+	4	771		NM_002373	NP_002364	P78559	MAP1A_HUMAN		9	GACTACTGCAG	0.542	
-	73	13664		NM_003922	NP_003913	Q15751	HERC1_HUMAN	HECT.	19	CAGGCGGAGGT	0.468	
-	8	3729		NM_005477	NP_005468	Q9Y3Q4	HCN4_HUMAN	lasmic (Potential).	6	GCGCCTTGTGG	0.726	
-	1	399	bfd.3_Missense_M	NM_004049	NP_004040	Q16548	B2LA1_HUMAN		1	TCACTTGGTTGA	0.393	
-	2	776		NM_032246	NP_115622	Q6ZN04	MEX3B_HUMAN		2	TGGGCGGCCCA	0.662	
+	6	642		NM_152336	NP_689549	Q96MI9	CBPC4_HUMAN		0	TGGCAGCACAG	0.622	
+	5	506	.1_RNA|FANCI_uc	NM_001113378	NP_001106849	Q9NVI1	FANCI_HUMAN		2	TGGCTACGAAAA	0.378	
+	2	1004	qa.1_Missense_M	NM_001039958	NP_001035047	Q0VG99	MESP2_HUMAN		0	ACTGCAGCCTC	0.637	
-	2	553		NM_001009606	NP_001009606	C9JH64	C9JH64_HUMAN		0	GTCCACGGGGC	0.716	
-	10	1021		NM_020764	NP_065815	Q8WXD9	CSKI1_HUMAN	SH3.	2	TCATTGCCCGTC	0.672	
-	4	554	S22_uc002crz.1_	NM_022119	NP_071402	Q9GZN4	BSSP4_HUMAN	eptidase S1.	1	GCATCAGGTAGG	0.587	
-	6	1528	KMYT1_uc002csp	NM_004203	NP_004194	Q99640	PMYT1_HUMAN		1	CCCGCGGCTGC	0.692	
+	3	456	e_Mutation_p.R82	NM_004221	NP_004212	P24001	IL32_HUMAN		1	AGGACGTGGAC	0.557	rs145687578
+	4	1183		NM_139170	NP_631909	Q8IYS4	CP071_HUMAN		1	AGTCAGCTCCC	0.657	
+	11	1531	.2_Missense_Mut	NM_000246	NP_000237	P33076	C2TA_HUMAN	NACHT.	1	CTGCAGGATCT	0.612	
-	12	2367	dbg.1_Missense_	NM_015914	NP_056998	Q6PKC3	TXD11_HUMAN	hioredoxin 2.	0	GCAGGGAAAAA	0.408	
-	10	1183	lbt.2_Missense_M	NM_001130007	NP_001123479	P15170	ERF3A_HUMAN		3	GACAAAGATTAT	0.373	
+	8	1029	p.P285L|ABCC1_	NM_004996	NP_004987	P33527	MRP1_HUMAN	Cytoplasmic.	4	CCAGCCGAAAG	0.557	
+	7	1520	fy.2_Missense_Mu	NM_016524	NP_057608	Q9BSW7	SYT17_HUMAN	C2 2.	1	AAGTTCCCCAA	0.458	
-	2	676	vaw.1_Missense_	NM_001002911	NP_001002911	Q6DWJ6	GP139_HUMAN	ellular (Potential).	2	GTCTTCAGTCC	0.517	
-	19	2099	ARHGAP17_uc00	NM_001006634	NP_001006635	Q68EM7	RHG17_HUMAN	Pro-rich.	0	GTGGCTTTGGT	0.692	
+	8	1100	9_splice|IL21R_u	NM_181078	NP_851564	Q9HBE5	IL21R_HUMAN		4	CAAGGTGAGCT	0.647	
-	16	2708	lou.2_Missense_M	NM_001520	NP_001511	Q12789	TF3C1_HUMAN		5	TGGGGGGATGT	0.562	
-	3	500	A2_uc002dqh.1_	NM_177528	NP_803564	P50226	ST1A2_HUMAN		0	GGTGCCTGGAG	0.627	
-	8	1697	10B_uc002dxt.2_	NM_015527	NP_056342	Q4KMP7	TB10B_HUMAN		0	GGCGCAGCAGG	0.602	
-	12	1846	fg.1_Missense_M	NM_173502	NP_775773	Q5K4E3	POLS2_HUMAN	eptidase S1 3.	1	CCACTGGAGCA	0.682	
-	6	2470		NM_153029	NP_694574	O75113	N4BP1_HUMAN		0	TGTACTGCAGCA	0.527	
-	7	704	e.1_Missense_Mu	NM_013263	NP_037395	Q9NPI1	BRD7_HUMAN	Bromo.	0	TCTCTGGTTTATT	0.333	
-	7	1433	p.T416M|TOX3_u	NM_001080430	NP_001073899	O15405	TOX3_HUMAN		0	ATGGTCGTTCCC	0.453	
-	2	466		NM_001796	NP_001787	P55286	CADH8_HUMAN	(Potential).|Cadherin 1.	9	CTCTTCCAGGA	0.423	
-	2	1501	uc002erg.1_5'UTR	NM_033309	NP_171608	Q6UX72	B3GN9_HUMAN	enal (Potential).	0	CTGCAGCGACAG	0.622	
-	19	3238	chc.1_Missense_	NM_199355	NP_955387	Q8TE60	ATS18_HUMAN	SP type-1 2.	18	GTACTCCATTCA	0.463	

+	8	1544	nw.1_Missense_	NM_178452	NP_848547	Q8NEP3	DAAF1_HUMAN	Pro-rich.	0	TGGAGGTTAAA	0.602	
-	16	2469	_p.R700Q|TRPV	NM_145068	NP_659505	Q8NET8	TRPV3_HUMAN	lasmic (Potential).	4	CCATCCGGAAT	0.532	
-	8	1246_1247	1_RNA|TRPV3_u	NM_145068	NP_659505	Q8NET8	TRPV3_HUMAN	lasmic (Potential).	4	AAGTCCTCGGC	0.579	
+	1	2119	3_Intron|ITGAE_u	NM_031965	NP_114171	Q8TF76	HASP_HUMAN	rotein kinase.	0	AACGGGATGGG	0.502	
-	2	1159		NM_032530	NP_115919	Q96JF6	ZN594_HUMAN	2H2-type 8.	3	TGTGCGCCCAC	0.463	
+	2	124		NM_153230	NP_694962	Q8N4B4	FBX39_HUMAN		2	GGATGGACGAA	0.507	rs143419082
-	4	433	vup.1_5'Flank|HE	NM_032580	NP_115969	Q9BYE0	HES7_HUMAN	Pro-rich.	0	GGATGGGCGCG	0.766	
-	3	1096	way.1_Missense_	NM_018182	NP_060652	Q8WU58	CQ063_HUMAN		1	CGTCTGGCAAA	0.587	
+	14	1434	OT1_uc002hgx.2	NM_018307	NP_060777	Q8IXI2	MIRO1_HUMAN	intermembrane (Potential).	4	TCAGCTGTTACA	0.368	
+	6	783	_p.G257S|RHBDL	NM_138328	NP_612201	P58872	RHBL3_HUMAN	ical; (Potential).	1	TGGCCGGTGTT	0.647	
-	2	207	Start_Site|DDX52_	NM_007010	NP_008941	Q9Y2R4	DDX52_HUMAN		2	CACACCTGGGA	0.413	
+	7	872	tf.2_Missense_Mu	NM_199321	NP_955353	Q6X784	ZPBP2_HUMAN		1	AGATCGAATAG	0.353	
-	14	1644	se_Mutation_p.S4	NM_014815	NP_055630	O75448	MED24_HUMAN		1	TCCCGGACAGC	0.582	
-	7	1275		NM_181534	NP_853512	Q7Z3Z0	K1C25_HUMAN	Tail.	2	CAGATCCATAAT	0.318	
-	1	104		NM_004138	NP_004129	O76009	KT33A_HUMAN	Head.	0	GGGGGGCACAC	0.642	
+	16	3241	.D738N|CCDC56_	NM_032387	NP_115763	Q96J92	WNK4_HUMAN		7	AGAGCGACCGT	0.607	
-	12	1638	.R477H|HDAC5_	NM_005474	NP_005465	Q9UQL6	HDAC5_HUMAN		1	CCACACGTTCA	0.652	rs143851045
-	28	2938	2B_uc002igu.1_3	NM_000419	NP_000410	P08514	ITA2B_HUMAN	ellular (Potential).	3	GCACCGCATAG	0.627	
+	1	1004		NM_001466	NP_001457	Q14332	FZD2_HUMAN	Name=2; (Potential).	3	GGTGTCGGTGG	0.602	
-	14	1520	_p.C385S|EFTUD2	NM_004247	NP_004238	Q15029	U5S1_HUMAN		1	TTTTTGCAGACC	0.547	
+	10	1329	p.A417P|ABCC3_	NM_003786	NP_003777	O15438	MRP3_HUMAN	rity).|ABC transmembrane	4	TGGATGCCCAG	0.552	
+	3	371	.G40R|NME1_uc0	NM_002512	NP_002503	P22392	NDKB_HUMAN	tion with AKAP13.	0	CAGATGGGGTC	0.493	
+	4	327		NM_153228	NP_694960	Q8N957	ANKF1_HUMAN		2	CCAAACGCCTG	0.453	
+	11	1958		NM_000502	NP_000493	P11678	PERE_HUMAN		2	CTTTTGCCGGG	0.517	rs144768455
-	2	360		NM_000334	NP_000325	P35499	SCN4A_HUMAN		3	GAGTACGATGA	0.473	
+	9	701	GS9_uc002jfd.2_	NM_003835	NP_003826	O75916	RGS9_HUMAN		4	TGGAATGGACAA	0.463	
+	2	783	C9A3R1_uc002jl	NM_004252	NP_004243	O14745	NHRF1_HUMAN	PDZ 2.	0	CTCCCCGGCTG	0.612	
-	20	3094	_p.E953K|RECQL	NM_004259	NP_004250	O94762	RECQ5_HUMAN		3	AGCTTCGCTCT	0.627	
-	18	3385	rl.3_Missense_Mu	NM_022066	NP_071349	Q9C0C9	UBE2O_HUMAN		5	CCACGCGGATC	0.577	
-	16	3092	e_Mutation_p.L53	NM_025090	NP_079366	Q9P275	UBP36_HUMAN		5	ACCAAGACCTT	0.582	
-	4	831	2_Missense_Muta	NM_001159772	NP_001153244	Q8WVQ1	CANT1_HUMAN	enal (Potential).	0	TAGCCCTTTTTC	0.577	
+	27	2444	D_uc002kgb.1_Mi	NM_005993	NP_005984	Q9BTW9	TBCD_HUMAN		0	ATGACTCGCTGT	0.632	
-	9	936	kod.1_Missense_	NM_001042388	NP_001035847	Q8TF05	PP4R1_HUMAN	HEAT 8.	1	ATTCAGCACAA	0.408	
+	2	867	XNDC2_uc002koh	NM_001098529	NP_001091999	Q86VQ3	TXND2_HUMAN	repeat of Q-P-K-X-G-D-I-P	2	TCAGAAAAAGCC	0.547	rs146821851
+	12	3446	xq.2_Missense_M	NM_030632	NP_085135	Q9C0F0	ASXL3_HUMAN		3	TTGCCTCCTCCG	0.478	
+	12	5622	q.2_Missense_Mu	NM_030632	NP_085135	Q9C0F0	ASXL3_HUMAN		3	TAAAGGGGTGC	0.458	
-	16	2029	x.1_Missense_Mu	NM_003199	NP_003190	P15884	ITF2_HUMAN		2	AACCGGAACCT	0.602	
-	1	135	_p.A37T|SERPINB3_uc010dqb.2_Missense_Mutation_			P48594	SPB4_HUMAN		3	TAATGCTGATG	0.418	
+	9	1262	.2_Missense_Mut	NM_001143818	NP_001137290	P05120	PAI2_HUMAN		2	CATACCCCAGT	0.418	
+	2	2441	ra.2_Missense_Mu	NM_171999	NP_741996	Q9BXA9	SALL3_HUMAN		4	GGACGCGGCCA	0.657	
+	10	1567		NM_182973	NP_892018	Q7Z410	TMPS9_HUMAN	Potential).|Peptidase S1 2.	2	TGAAGGAAGGG	0.677	
+	4	1371	a.1_Missense_Mu	NM_173480	NP_775751	Q68EA5	ZNF57_HUMAN	2H2-type 9.	3	ATTCCGAGGTC	0.428	rs149690257
-	4	840	lxx.2_Missense_M	NM_174983	NP_778148	Q6NUT3	CS028_HUMAN	ical; (Potential).	2	CACCACCAGCA	0.701	
-	2	390		NM_030662	NP_109587	P36507	MP2K2_HUMAN		0	GTCAAGTTCCA	0.572	
+	6	2302	.2_Missense_Mut	NM_020209	NP_064594	Q96IW2	SHD_HUMAN	SH2.	0	CAGGAGCAGCC	0.662	
-	1	38		NM_001080523	NP_001073992	A6NEK1	ARRD5_HUMAN		0	TGGGGGGTTGG	0.527	
-	11	1492	w.2_Missense_M	NM_002850	NP_002841	Q13332	PTPRS_HUMAN	III 1.|Extracellular (Potentia	4	TGTGCGGGTGA	0.697	

+	2	294	e_Mutation_p.R57	NM_020533	NP_065394	Q9GZU1	MCLN1_HUMAN		1	AGTTTCGAGCC	0.617
-	3	17776		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).	57	CCATTTCTGTGG	0.493
+	1	217		NM_001079935	NP_001073404	Q6IFN5	O7E24_HUMAN	Name=2; (Potential).	1	CCCACCTCCAC	0.572
+	4	1348	e_Mutation_p.H42	NM_144566	NP_653167	Q9H0M5	ZN700_HUMAN	2H2-type 7.	0	CGATATCATGAA	0.443
-	5	684		NM_001080404	NP_001073873	C9JN71	ZN878_HUMAN	2H2-type 3.	0	GGAAAACTGAA	0.403
+	4	1515	ym.1_Missense_M	NM_001136501	NP_001129973	Q08AG5	ZN844_HUMAN		0	CTTCAGATCTG	0.423
-	4	1577	709_uc002mtx.3_I	NM_144976	NP_659413	Q8TBZ8	ZN564_HUMAN	2H2-type 13.	1	AAGGCTTTACCA	0.388
-	6	1110	nwl.3_Missense_M	NM_017722	NP_060192	Q9NXH9	TRM1_HUMAN		2	CGTGGCAGGCC	0.642
-	9	1482	mwy.3_Missense_	NM_001127221	NP_001120693	O00555	CAC1A_HUMAN	lasmic (Potential).	2	AAAGGGATGCC	0.567
-	10	1716	BP1_uc002nft.1_F	NM_031941	NP_114147	Q8N6Y0	USBP1_HUMAN		1	TGCCCGTTCCC	0.687
-	17	3293	O8_uc010eap.2_F	NM_020959	NP_066010	Q9HCE9	ANO8_HUMAN	ellular (Potential).	3	TGGGCGGTGAG	0.682
-	10	1171	46_splice|COMP_	NM_000095	NP_000086	P49747	COMP_HUMAN		0	GCTCACGGTCG	0.687
-	1	381_382	5'Flank|NDUFA13_	NM_032037	NP_114426	Q9BXA6	TSSK6_HUMAN	rotein kinase.	1	AGTCCGGGGGC	0.614
-	4	827	pc.1_Missense_M	NM_001076675	NP_001070143	Q68DY1	ZN626_HUMAN		1	GGTTTCTCTCCA	0.393
-	18	2674	ee.1_Missense_M	NM_000704	NP_000695	P20648	ATP4A_HUMAN	enal (Potential).	1	ATTGCCGTGAAG	0.453
-	2	789	_Missense_Mutati	NM_152658	NP_689871	Q8NA92	THAP8_HUMAN	THAP-type.	0	GGAGGGCACTG	0.657
-	5	2544	5B_uc002ofr.1_Mi	NM_152279	NP_689492	Q52M93	Z585B_HUMAN	2H2-type 21.	1	TCTGATGAACAC	0.458
+	8	2763		NM_015073	NP_055888	O60292	SI1L3_HUMAN	Rap-GAP.	2	ATTGTCCGAGTC	0.592
-	1	230		NM_001080468	NP_001073937	Q0VAF6	SYCN_HUMAN		0	TGGCCCAGTTG	0.662
+	4	612	e_Mutation_p.P16	NM_017592	NP_060062	Q9NX70	MED29_HUMAN		2	CTGTGCCAAGG	0.632
-	6	2022	ense_Mutation_p.	NM_001010880	NP_001010880	O75290	Z780A_HUMAN	2H2-type 16.	0	AATAAGTTGCAT	0.403
+	27	5805	p.G1907S|SPTBN	NM_020971	NP_066022	Q9H254	SPTN4_HUMAN	Spectrin 16.	5	ATGCGGGTGAA	0.687
+	7	1112	YP2B6_uc010xvu.	NM_000767	NP_000758	P20813	CP2B6_HUMAN		2	GTGCCCCACATT	0.542
+	7	1055	YP2S1_uc010xvx.	NM_030622	NP_085125	Q96SQ9	CP2S1_HUMAN		1	CTGAATCGGGAG	0.657
+	4	879		NM_002483	NP_002474	P40199	CEAM6_HUMAN	like C2-type 2.	1	ATTTCCCCCTCA	0.527
-	12	1509	H4_uc002pgb.1_Ir	NM_015168	NP_055983	Q9UPT8	ZC3H4_HUMAN		6	ATCCTCGGCAC	0.617
-	18	1766	b.1_RNA|LIG1_uc	NM_000234	NP_000225	P18858	DNLI1_HUMAN		3	TGCCCCGGGTG	0.557
-	3	792		NM_017708	NP_060178	Q2M2I3	FA83E_HUMAN		1	GCCGTCCAGCA	0.657
-	11	1337	t.1_RNA|FUZ_uc0	NM_025129	NP_079405	Q9BT04	FUZZY_HUMAN	Leu-rich.	0	GCATGCAGAGTG	0.592
+	4	1385	dw.1_Missense_M	NM_138374	NP_612383	Q96IR2	ZN845_HUMAN	2H2-type 8.	0	GTCAGATGTCAT	0.408
+	7	1196	_p.P286S|LILRB1_	NM_006669	NP_006660	Q8NHL6	LIRB1_HUMAN	3.|Extracellular (Potential).	3	TGGGCCCTGTG	0.632
+	3	684	_p.Q21E|LILRB4_	NM_006847	NP_006838	Q8NHJ6	LIRB4_HUMAN	1.|Extracellular (Potential).	3	GGTCACAGCCC	0.607
-	9	1214	_p.P326S|PPP1R1	NM_017607	NP_060077	Q9BZL4	PP12C_HUMAN		2	CGGCGGGGAGG	0.612
+	5	431	_p.S89L|ZNF583_	NM_001159860	NP_001153332	Q96ND8	ZN583_HUMAN		1	AATTTTCATCAAA	0.313
+	8	1226	_p.G224D|ZNF274	NM_133502	NP_598009	Q96GC6	ZN274_HUMAN		1	CGAGGGCACCA	0.632
-	27	3894		NM_004850	NP_004841	O75116	ROCK2_HUMAN		4	ACCTGGAAACC	0.418
+	4	388	p.G124D|KRTCAP	NM_173853	NP_776252	Q53RY4	KCP3_HUMAN		0	CAACGGTGGCC	0.617
+	1	754		NM_005413	NP_005404	O95343	SIX3_HUMAN		0	GCGGCCGCCCA	0.637
+	7	1353		NM_001430	NP_001421	Q99814	EPAS1_HUMAN	PAS 2.	2	AGAACATGACC	0.413
+	5	431		NM_032118	NP_115494	Q9H977	WDR54_HUMAN	WD 1.	0	TGCCCGGGGAA	0.577
+	17	2173	_uc002suk.2_Splic	NM_144707	NP_653308	Q8N271	PROM2_HUMAN		1	CTTGTGGTCAGT	0.582
+	4	716	RAP_uc010fiz.2_I	NM_003853	NP_003844	O95256	I18RA_HUMAN	ellular (Potential).	5	AGTAACGACCTA	0.438
-	10	891	.R270C|UXS1_uc	NM_025076	NP_079352	Q8NBZ7	UXS1_HUMAN	enal (Potential).	2	CATGCGTGGCC	0.607
+	3	571	n_p.S14N|INSIG2_	NM_016133	NP_057217	Q9Y5U4	INSI2_HUMAN		2	ATGCCAGTGCTG	0.393
+	21	1957	p.E611*|EPB41L5	NM_020909	NP_065960	Q9HCM4	E41L5_HUMAN		1	CCCAAAGAGTCT	0.388
+	13	4402	.3_Nonsense_Mut	NM_005270	NP_005261	P10070	GLI2_HUMAN		13	AGGATGGAGGC	0.672
-	8	1279	_uc002uds.1_Mis	NM_002977	NP_002968	Q15858	SCN9A_HUMAN	I.	13	CAAAGGAGAGCA	0.328

+	8	1017	se_Mutation_p.T32	NM_002610	NP_002601	Q15118	PDK1_HUMAN	stidine kinase.	4	ATGTCACGCTGG	0.358	
+	2	858		NM_002148	NP_002139	P28358	HXD10_HUMAN		1	TCACTGCAAAGA	0.398	
-	80	20445	N_uc010zfj.1_Intro	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	GGAAGGAGGCA	0.488	
-	46	11869	.P3815L|TTN_uc0	NM_133437	NP_597681	Q8WZ42	TITIN_HUMAN		153	GTCTGTGGAAAA	0.478	
-	39	9510	.E3050K|TTN_uc0	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	GCAGTTCCTGGT	0.418	
-	13	1585	frt.2_Missense_Mu	NM_005795	NP_005786	Q16602	CALRL_HUMAN	Name=6; (Potential).	4	TCAATGCCAAGC	0.443	
+	8	907	usr.2_Missense_Mu	NM_001130158	NP_001123630	O43795	MYO1B_HUMAN	osin head-like.	8	TCTGAAGAGCTC	0.303	
-	18	2403		NM_018897	NP_061720	Q8WXX0	DYH7_HUMAN	n (By similarity).	12	AAGACGAAGATA	0.403	
+	29	3653	p.R1180Q|CPS1_u	NM_001875	NP_001866	P31327	CPSM_HUMAN	ATP-grasp 2.	13	GGCCCGAGAAG	0.423	
+	13	1504	_p.P169L|VIL1_uc	NM_007127	NP_009058	P09327	VILI_HUMAN	Core.	1	GGTCCCAATGG	0.542	
+	6	1220	vt.2_Missense_Mu	NM_001037131	NP_001032208	Q9UPQ3	AGAP1_HUMAN	all GTPase-like.	3	TACTACGAGACG	0.537	
-	11	1563	CA1_uc002vwa.1_	NM_024726	NP_079002	Q86XH1	IQCA1_HUMAN	Lys-rich.	1	CTGGGCGCTCCC	0.473	
-	11	1952	se_Mutation_p.L38	NM_006037	NP_006028	P56524	HDAC4_HUMAN		6	GGAAAAGGGAG	0.667	
+	18	2084		NM_001001891	NP_001001891	Q6IWH7	ANO7_HUMAN	cellular (Potential).	3	GAGGTCCTCATC	0.652	
-	6	541	D1_uc002wmd.3_	NM_019593	NP_062539	Q9NPB8	GPCP1_HUMAN	CBM20.	0	GTCCATCGTCAA	0.313	
+	5	1194	n_p.S63*|CSRP2B	NM_020536	NP_065397	Q9H8E8	CSR2B_HUMAN		6	CCGTTCAGGTG	0.478	
-	1	171		NM_001899	NP_001890	P01036	CYTS_HUMAN		1	CATTGAGGTCTG	0.572	
+	15	1673	_p.P453L|ITCH_uc	NM_031483	NP_113671	Q96J02	ITCH_HUMAN	WW 4.	6	GAATTCCATATTT	0.348	
+	35	7689	ve.1_Missense_Mu	NM_007186	NP_009117	Q9BV73	CP250_HUMAN	Potential.	5	GGAGAGGACAG	0.483	rs144859303
+	18	2123	we.1_Missense_M	NM_182811	NP_877963	P19174	PLCG1_HUMAN	SH2 2.	8	TCAGGTGGTAC	0.652	
-	7	1265	gj.2_Missense_Mu	NM_007050	NP_008981	O14522	PTPRT_HUMAN	tential).|Fibronectin type-III	20	TGAGGAGCACTC	0.577	
+	1	148	DC9_uc002xoy.2_I	NM_080753	NP_542791	Q9H1F0	WF10A_HUMAN		0	ACAAGAAGAGGA	0.587	
-	2	2409	us.1_Nonsense_M	NM_004975	NP_004966	Q14721	KCNB1_HUMAN	lasmic (Potential).	2	CCGCCTCAAAGT	0.572	
+	4	987	l_Missense_Mutat	NM_032527	NP_115916	Q8N5A5	ZGPAT_HUMAN		0	ACTGCGCACAG	0.637	
-	18	1404	TE_uc002yir.1_Mi	NM_199261	NP_954870	P56180	TPTE_HUMAN	hatase tensin-type.	5	TAGTTCCTGTTC	0.323	
-	1	238		NM_001085455	NP_001078924	Q3LI83	KR241_HUMAN		0	GATTTGCAGGTT	0.532	
-	15	1919	nd.2_Missense_Mu	NM_000819	NP_000810	P22102	PUR2_HUMAN	AIRS.	1	TGATCTCGCTCCA	0.488	
+	4	455	aeb.1_Missense_M	NM_005128	NP_005119	Q9Y3R5	DOP2_HUMAN		2	GTGCTGCTCACC	0.612	
+	6	694	zed.3_Missense_M	NM_004649	NP_004640	P30042	ES1_HUMAN		1	GTGGCAAGTGGC	0.627	
+	1	157	.1_Intron|C21orf29	NM_198692	NP_941965	P60412	KR10B_HUMAN	A repeats of C-C-X(3).	1	GCTGCGCCCCG	0.697	
+	1	220	.1_Intron|C21orf29	NM_198697	NP_941970	P60328	KR123_HUMAN	A approximate repeats.	1	GTGCCCGTGAGC	0.647	
-	5	655	_p.R204L|FTCD_u	NM_006657	NP_006648	O95954	FTCD_HUMAN	se C-subdomain (By simila	2	TGCTCCCGCAGG	0.657	rs144080295
+	22	4462	.2_Missense_Muta	NM_006031	NP_006022	O95613	PCNT_HUMAN	Potential.	8	ATCGCGGGTGTG	0.557	
-	2	330	70_uc002zxs.2_5'F	NM_013378	NP_037510	Q9UKI3	VPRE3_HUMAN	Ig-like.	0	GATCGGGGATGT	0.602	
+	14	2389		NM_019601	NP_062547	Q9UGT4	SUSD2_HUMAN	cellular (Potential).	1	AGGACGCAGCTA	0.657	
+	7	687	NF185_uc003akc.2	NM_152267	NP_689480	Q96GF1	RN185_HUMAN		0	GCTGTCCCTGGG	0.517	rs61743577
+	2	1072	gxy.2_Missense_Mu	NM_002409	NP_002400	Q09327	MGAT3_HUMAN	nenal (Potential).	0	CTTCCCGCCCG	0.672	
+	16	1986	aot.1_Missense_Mu	NM_015705	NP_056520	Q96HU1	SGSM3_HUMAN	RUN.	2	TTTATCGAGGAG	0.637	
+	24	4398		NM_001429	NP_001420	Q09472	EP300_HUMAN		64	GTGGAAGTAAAA	0.428	
-	1	771	p.R213W|TCF20_u	NM_005650	NP_005641	Q9UGU0	TCF20_HUMAN	Ser-rich.	5	GGGCCGCTGCA	0.498	
-	16	4134	GCP6_uc010har.1_	NM_020461	NP_065194	Q96RT7	GCP6_HUMAN	AA tandem repeats.	4	GCCGGGTGGGAG	0.622	rs145066767
-	25	4218	p.T163M|PLXNB2_	NM_012401	NP_036533	O15031	PLXB2_HUMAN	lasmic (Potential).	6	AAGAGCGTGTGC	0.527	
+	14	1293	ols.3_RNA|NCAPH	NM_152299	NP_689512	Q6IBW4	CNDH2_HUMAN		2	ATGGAGGTCCTG	0.607	
-	20	3128	brg.1_Missense_M	NM_014850	NP_055665	O43295	SRGP2_HUMAN		9	TGGCCTCGCTGT	0.572	
-	17	2493	ense_Mutation_p.V	NM_003615	NP_003606	Q9Y6M7	S4A7_HUMAN	cellular (Potential).	5	AGAATACACCAC	0.338	
+	4	289	003ckr.2_Missense	NM_001904	NP_001895	P35222	CTNB1_HUMAN	7del(1)|p.S45_S47>C(1)|p.	3166	GCTCCTTCTCTGA	0.502	rs121913407
+	3	780	e_Mutation_p.G20	NM_001296	NP_001287	O00590	CCBP2_HUMAN	cellular (Potential).	5	TCGGCGGGCAT	0.532	

-	3	437	on.2_Missense_M	NM_022842	NP_073753	Q9H5V8	CDCP1_HUMAN	cellular (Potential).	3	GGCCTGACATA	0.488	
-	19	2704	cqy.2_Missense_	NM_001134878	NP_001128350	Q9HAQ2	KIF9_HUMAN		1	GCACCCATGAG	0.592	
-	2	310	cm.1_Missense_M	NM_000581	NP_000572	P07203	GPX1_HUMAN		1	TGCACGGGAAG	0.617	
+	6	10564		NM_003458	NP_003449	Q9UPA5	BSN_HUMAN		8	AGCCCTCATCC	0.652	
-	2	158	n_p.T50I|CDHR4_	NM_001007540	NP_001007541	A6H8M9	CDHR4_HUMAN	cellular (Potential).	0	TGGGTGTGGGC	0.572	
+	15	1284		NM_004947	NP_004938	Q8IZD9	DOCK3_HUMAN	DHR-1.	0	ATATCCGCAAT	0.463	
+	1	2544		NM_013286	NP_037418	Q8NDT2	RB15B_HUMAN	stein-Barr virus BMLF1.|SP	0	GCCCGGTCTGC	0.637	
+	17	2860	.3_Missense_Muta	NM_007184	NP_009115	Q9Y2I1	NISCH_HUMAN		4	CCAACCGTGGC	0.647	
-	14	2750	RC2_uc003dht.1_	NM_015576	NP_056391	O15083	ERC2_HUMAN	Potential.	2	TTTTTCGGCCA	0.537	
+	6	1056		NM_022072	NP_071355	Q9H649	NSUN3_HUMAN		1	GGCTCTTAGTG	0.458	
+	10	1013	_p.C60F|ZPLD1_	NM_175056	NP_778226	Q8TCW7	ZPLD1_HUMAN	acellular (Potential).	5	TCTATTGTGGAG	0.363	
-	7	1150	_Mutation_p.N32	NM_170780	NP_740750	Q8TD46	MO2R1_HUMAN	lasmic (Potential).	3	ACCTTGTTTGTA	0.378	
+	3	470	RH_uc011bjb.1_I	NM_001125	NP_001116	P54922	ADPRH_HUMAN		1	ACACAGTGATG	0.542	
-	29	5197	_Missense_Mutati	NM_053025	NP_444253	Q15746	MYLK_HUMAN	rotein kinase.	9	GTAGCCGATGG	0.562	rs143900788
+	6	1557		NM_024768	NP_079044	Q9HA90	CCD48_HUMAN	Potential.	0	GTGGACGTGCT	0.627	
+	2	201	_Mutation_p.A41	NM_152395	NP_689608	Q96DE0	NUD16_HUMAN	dix hydrolase.	0	CTGCCGCTTTC	0.677	
-	7	1114	wp.1_Missense_	NM_024727	NP_079003	Q6UY01	LRC31_HUMAN	LRR 5.	3	TGGCTGATAAAT	0.393	
+	8	1553	hwy.1_Missense_	NM_207015	NP_996898	Q58DX5	NADL2_HUMAN	cellular (Potential).	1	AGACCGAACTA	0.408	
+	14	1380	.R367Q|FXR1_uc	NM_005087	NP_005078	P51114	FXR1_HUMAN	binding RGG-box.	1	GGGTCGAGGTC	0.488	
+	3	809	B5_uc003fmq.2_5	NM_003907	NP_003898	Q13144	EI2BE_HUMAN		5	ACTTTCTTCTG	0.463	
-	3	3308	tron|ABCA11P_uc	NM_133474	NP_597731	D9N162	D9N162_HUMAN		1	TAAAGGTTTTGC	0.418	
+	4	1357	417S|TACC3_uc	NM_006342	NP_006333	Q9Y6A5	TACC3_HUMAN		2	TCATCCCGTTC	0.622	
+	2	1093	PZ_uc003gll.2_R	NM_080819	NP_543009	Q96P69	GPR78_HUMAN	lasmic (Potential).	6	TGTGCGGCAGC	0.637	
-	10	4958	dr.1_Missense_Mu	NM_148894	NP_683692	Q8NFC6	BOD1L_HUMAN		6	CACTTTCCCCT	0.488	
-	3	654		NR_027277					0	CTTGGAGGTGT	0.597	
-	6	1433	_p.R457Q|UGT2A	NM_006798	NP_006789	Q9Y4X1	UD2A1_HUMAN	cellular (Potential).	1	CTGCTCGATCC	0.448	
-	12	2203		NM_003619	NP_003610	P56730	NETR_HUMAN	eptidase S1.	1	TCGGGTCGATAC	0.463	
+	5	6445	p.1_Missense_Mu	NM_024582	NP_078858	Q6V0I7	FAT4_HUMAN	.|Extracellular (Potential).	18	ATCAATGATAAC	0.378	
+	13	2668	_p.G776D|PLK4_u	NM_014264	NP_055079	O00444	PLK4_HUMAN		0	ACCTGGTAGTA	0.353	
-	10	2044		NM_015130	NP_055945	Q6ZT07	TBCD9_HUMAN	ab-GAP TBC.	1	GAAAAGCATAA	0.398	
+	5	1666	se_Mutation_p.T37	NM_032557	NP_115946	Q8NB14	UBP38_HUMAN		5	CAATTAACAGAA	0.333	
-	25	6607		NM_017639	NP_060109	Q6V1P9	PCD23_HUMAN	Cadherin 19.	4	ATTGACATCAA	0.488	rs141059888
+	13	2782		NM_020840	NP_065891	Q9P278	FNIP2_HUMAN	tion with PRKAA1.	0	TGGCTGGTGC	0.592	
+	24	5570		NM_001080477	NP_001073946	Q9P273	TEN3_HUMAN	cellular (Potential).	0	ATGACGGACAG	0.478	
-	6	4183		NM_005245	NP_005236	Q14517	FAT1_HUMAN	(Potential).|Cadherin 11.	12	GAGGGCGACCA	0.428	
+	3	624	_p.V127I|ZFP42_	NM_174900	NP_777560	Q96MM3	ZFP42_HUMAN	p.V127fs*0(1)	2	AAGGGGTAAAG	0.418	
-	11	2003	v.2_Missense_Mu	NM_001343	NP_001334	P98082	DAB2_HUMAN		3	CAGGAGCACTT	0.517	
-	3	297	jnt.2_RNA|CCL28_	NM_148672	NP_683513	Q9NRJ3	CCL28_HUMAN		2	TGTGCGGGCTG	0.403	
+	5	1553		NM_005921	NP_005912	Q13233	M3K1_HUMAN	SWIM-type.	2	TGCACGTGGAA	0.348	
+	10	3318		NM_152405	NP_689618	Q8N9B5	JMY_HUMAN	WH2.	0	AGGGGTAAAAT	0.408	
+	2	2755		NM_153610	NP_705838	Q8N3K9	CMYA5_HUMAN		9	ACACACCCTCT	0.468	
+	31	6929	_Mutation_p.D12	NM_032119	NP_115495	Q8WXG9	GPR98_HUMAN	cellular (Potential).	16	TAATGGACAGC	0.488	
+	5	1573	_uc003kmr.2_RNA	NM_022350	NP_071745	Q6P179	ERAP2_HUMAN	enal (Potential).	0	CTATGCATCCC	0.423	
+	12	1893	.R571H|DMXL1_	NM_005509	NP_005500	Q9Y485	DMXL1_HUMAN		2	CACCCGTTCCA	0.358	rs138186062
-	40	5639		NM_001999	NP_001990	P35556	FBN2_HUMAN		15	ACCTACCCATG	0.458	
+	11	1812	yo.1_Missense_M	NM_005733	NP_005724	O95235	KI20A_HUMAN	inesin-motor.	0	GGGCCGCTGTA	0.512	
+	1	815	3lhh.1_Intron|PC	NM_018909	NP_061732	Q9UN73	PCDA6_HUMAN	|Extracellular (Potential).	2	TTATCAGACTGA	0.408	

+	1	806	DHA5_uc003lhk.	NM_018911	NP_061734	Q9Y5H6	PCDA8_HUMAN	|Extracellular (Potential).	2	TGATCCGGATG	0.378	rs525886
+	1	266	.2_Intron|PCDHA	NM_018903	NP_061726	Q9UN75	PCDAC_HUMAN	|Extracellular (Potential).	0	TGGGCCGCATC	0.652	
+	1	1600	lka.1_Intron|PCD	NM_018914	NP_061737	Q9Y5H2	PCDGB_HUMAN	(Potential).|Cadherin 4.	0	ACAACGATAAC	0.537	
-	22	3569	jhd.2_Missense_M	NM_002609	NP_002600	P09619	PGFRB_HUMAN	lasmic (Potential).	17	CTCGTCAGCAA	0.537	
-	16	2339	NIP1_uc003ltg.2_	NM_006058	NP_006049	Q15025	TNIP1_HUMAN	Pro-rich.	2	GAGTGGGGGCG	0.662	
+	2	474		NM_000811	NP_000802	Q16445	GBRA6_HUMAN	ellular (Probable).	12	ACAATCGGCTG	0.493	
+	29	7954	.3_Missense_Mut	NM_001122679	NP_001116151				10	ACGGCAGGACT	0.627	
-	19	3097		NM_005990	NP_005981	O94804	STK10_HUMAN	Potential.	8	CTCCCGCTTCT	0.587	
-	11	1208	e_Mutation_p.R34	NM_005451	NP_005442	Q9NR12	PDLI7_HUMAN	zinc-binding 2.	1	GTTCCGGATGG	0.617	rs147300820
-	1	39	i.3_Intron|DOK3_	NM_024872	NP_079148	Q7L591	DOK3_HUMAN		0	GGCACGCGCGT	0.711	
-	5	947	_p.R217L|RASGE	NM_175062	NP_778232	Q8N431	RGF1C_HUMAN	Ras-GEF.	1	TGTGCCGCAGC	0.627	
+	2	106	32*|PRSS16_uc0	NM_005865	NP_005856	Q9NQE7	TSSP_HUMAN		5	TGGGTGAGCAC	0.632	
-	4	1073	nlb.2_Missense_	NM_001135216	NP_001128688	Q96LW9	ZN323_HUMAN		2	TGCCTTGCTGT	0.428	
-	6	592	X6_uc010jrg.1_R	NM_182701	NP_874360	P59796	GPX6_HUMAN		5	AGTTCCAGCGG	0.527	
-	2	413	qg.1_Nonsense_M	NM_018643	NP_061113	Q9NP99	TREM1_HUMAN	(Potential).|Ig-like V-type.	1	AGGCTGGTAGA	0.537	
-	5	1303	_p.G86E|TRERF1	NM_033502	NP_277037	Q96PN7	TREF1_HUMAN	Gln-rich.	5	GTCCTCCCTGC	0.602	
+	11	1334		NM_032538	NP_115927	Q5TCY1	TTBK1_HUMAN		9	GCTCCGGGAGA	0.662	
+	10	1678	us.2_Missense_M	NM_153320	NP_696961	Q9Y694	S22A7_HUMAN		0	AGGACGTGGAG	0.577	
-	7	922		NM_020750	NP_065801	Q9HAV4	XPO5_HUMAN		4	GACACCCAGTC	0.463	
+	25	3710	.2_Intron|RIMS1_	NM_014989	NP_055804	Q86UR5	RIMS1_HUMAN		10	AAACATCCTGC	0.517	
-	33	5780	pht.2_Missense_M	NM_004370	NP_004361	Q99715	COCA1_HUMAN	nectin type-III 14.	9	CTGACGAGGAT	0.448	
-	4	535	p.E129K|PPIL6_u	NM_173672	NP_775943	Q8IXY8	PPIL6_HUMAN	e cyclophilin-type.	0	TCACCTCAAAA	0.303	
-	11	1329	sh.1_Missense_M	NM_001013836	NP_001013858	Q9Y6D9	MD1L1_HUMAN	Potential.	2	GGTGACGGCGC	0.582	
-	8	1449		NM_032415	NP_115791	Q9BXL7	CAR11_HUMAN	Potential.	50	CTTGAGCTCCA	0.542	
-	3	985	w.1_Missense_M	NM_005924	NP_005915	P50222	MEOX2_HUMAN	Homeobox.	2	TTTTGGAACCAG	0.418	
+	3	651	kwc.1_RNA|INMT	NM_006774	NP_006765	O95050	INMT_HUMAN		0	AATTTTCCTGCG	0.597	
+	8	1328	_Mutation_p.K27	NM_198428	NP_940820	Q3SYG4	PTHB1_HUMAN		5	CCTTAAGGATA	0.373	
+	15	2020		NM_133468	NP_597725	Q8N8U9	BMPER_HUMAN	TIL.	3	TGTACGATACC	0.507	
-	5	3605	D9L_uc003umk.1_	NM_152703	NP_689916	Q8IVG5	SAM9L_HUMAN		4	CACAGGAATGT	0.383	
+	19	1812	_p.D532Y|CCDC1	NM_017667	NP_060137	Q96JG6	CC132_HUMAN		0	ACAGTGATGTT	0.378	
+	59	9150	.V2963M|TRRAP_	NM_003496	NP_003487	Q9Y4A5	TRRAP_HUMAN	FAT.	37	CCATCGTGTCT	0.418	
-	11	1147	3A5_uc003urs.2_I	NM_000765	NP_000756	P24462	CP3A7_HUMAN		1	AGTATCATAGG	0.378	
+	3	3880	C17_uc010lho.1_	NM_001040105	NP_001035194	Q685J3	MUC17_HUMAN	ch.|19.|59 X approximate t	27	TGAAGGAAGTA	0.502	
-	12	1772	lhs.2_Missense_M	NM_001084	NP_001075	O60568	PLOD3_HUMAN		2	AGCGGGCGTAG	0.701	
+	13	1787	zo.2_Missense_M	NM_152892	NP_690852	Q9UFC0	LRWD1_HUMAN		1	ATGGTCGTCCA	0.726	
-	14	1850	z.2_Missense_Mu	NM_005045	NP_005036	P78509	RELN_HUMAN		19	AGGGAGAACAG	0.438	
+	2	1878	p.W598*|PIK3CG_	NM_002649	NP_002640	P48736	PK3CG_HUMAN		38	GAAATGGGGAC	0.438	
+	12	2792	_p.A887T|MET_uc	NM_000245	NP_000236	P08581	MET_HUMAN	ellular (Potential).	159	CTGAAGCAGTT	0.368	
-	3	805	ja.2_Missense_M	NM_003391	NP_003382	P09544	WNT2_HUMAN	p.R169C(1)	7	TGCGCGGGCAA	0.438	rs149362965
-	25	3561	kg.3_Missense_M	NM_017954	NP_060424	Q86UW7	CAPS2_HUMAN		2	TCCAACACTGAA	0.348	
-	16	2858	nse_Mutation_p.R	NM_015689	NP_056504	Q9ULE3	DEN2A_HUMAN	dDENN.	4	GAAGCGGACAA	0.602	
-	15	1860		NM_004333	NP_004324	P15056	BRAF_HUMAN	rotein kinas_R603>I(2)|p.T	18290	ATTTCACTGTA	0.368	
+	5	705	1_Intron|uc010loj.	NR_001296					0	TGCAATGGACAG	0.493	rs143538588
+	3	5449	_p.H411Y|ABP1_u	NM_001091	NP_001082	P19801	ABP1_HUMAN		6	CGGTCCATTAT	0.577	
-	4	5590		NM_178857	NP_849188	Q8IWN7	RP1L1_HUMAN		8	TTCCCCCAACTC	0.572	
-	6	829	ense_Mutation_p.E	NM_001083537	NP_001077006	Q8N7N1	F86B1_HUMAN		0	TAGCTCGGTGG	0.647	
+	11	1110	se_Mutation_p.H1	NM_014265	NP_055080	Q9UKQ2	ADA28_HUMAN	B.|Extracellular (Potential).	5	TGGGCCACAAC	0.433	

-	6	1535	M35_uc010lup.1_3'	NM_171982	NP_741983	Q9UPQ4	TRI35_HUMAN	B30.2/SPRY.	0	ACTGATGTGCAA	0.632	
+	4	4548	P1_uc011ldy.1_Intr	NM_006269	NP_006260	P56715	RP1_HUMAN		12	TGGAATCTTTTGA	0.378	
+	4	534		NM_001077619	NP_001071087	Q14CS0	UBX2B_HUMAN		2	GAAAATCAGCTG	0.289	
+	11	1454	var.2_Missense_Mu	NM_004133	NP_004124	Q14541	HNF4G_HUMAN		1	AAGCATCAGTCA	0.413	
+	10	9004	.P2918S|ZFHX4_u	NM_024721	NP_078997	Q86UP3	ZFHX4_HUMAN		15	AGCAATCCCTTTA	0.493	
+	15	2546	p.G783R|RIMS2_	NM_014677	NP_055492	Q9UQ26	RIMS2_HUMAN		15	ATGACCGGACAT	0.388	rs147193181
+	8	1215	nse_Mutation_p.E	NM_012082	NP_036214	Q8WW38	FOG2_HUMAN		5	GACATGGAACAC	0.502	
-	1	706		NM_001081675	NP_001075144	Q2WGJ6	KLH38_HUMAN	BACK.	0	CTGGGTGGATGT	0.547	
-	1	445	ndt.2_Missense_M	NM_004519	NP_004510	O43525	KCNQ3_HUMAN		5	GTCGCGGCCGC	0.716	
-	13	2881	M135B_uc003yva	NM_015912	NP_056996	Q49AJ0	F135B_HUMAN		9	CCTTTGGGGTTT	0.463	
-	1	4272		NM_031308	NP_112598	P58107	EPIPL_HUMAN	Plectin 25.	2	CGCAGCGCTCC	0.607	
-	9	1176	PLAH_uc003zat.1	NM_017570	NP_060040	O14841	OPLA_HUMAN		0	AGAGGCCAGAC	0.647	
-	21	3290	uc011llh.1_5'Flank	NM_013432	NP_038460	Q96HA7	TONSL_HUMAN	LRR 1.	0	GGGCAGCCACC	0.682	
+	2	245	p.V30M|GPT_uc0	NM_005309	NP_005300	P24298	ALAT1_HUMAN		2	CGCGTGTGCGG	0.672	
-	20	1927	p.E396K|PTPRD_	NM_002839	NP_002830	P23468	PTPRD_HUMAN	III 1.|Extracellular (Potentia	22	AGGTTCGCTGG	0.542	
+	22	2685	zoh.1_Missense_	NM_017794	NP_060264	Q5VW36	K1797_HUMAN		10	GCTTTGGAGGA	0.378	
-	1	1261		NR_023917					0	TACTCCCTTTTTG	0.398	
-	14	1897	.1_RNA|SEMA4D	NM_006378	NP_006369	Q92854	SEM4D_HUMAN	tracellular (Potential).	2	CCTGTGCTGACA	0.507	
-	14	2727	e_Mutation_p.R67	NM_017746	NP_060216	Q9NXF1	TEX10_HUMAN	ical; (Potential).	2	GACTCGAGGCA	0.567	rs146070264
-	3	391	NAC4_uc004bst.	NM_175039	NP_778204	Q9H4F1	SIA7D_HUMAN	enal (Potential).	0	GTGGTCCAGGC	0.642	
+	4	939		NM_006059	NP_006050	Q9Y6N6	LAMC3_HUMAN	inin EGF-like 1.	3	AGTGCGGCCCC	0.667	
+	36	3276_3277		NM_000093	NP_000084	P20908	CO5A1_HUMAN	le-helical region.	11	GGGCCCCCCTG	0.589	
+	9	1388	A1B_uc011mfd.1_	NM_000718	NP_000709	Q00975	CAC1B_HUMAN	lasmic (Potential).	6	TGGACGGTAGG	0.602	
+	44	6227	coi.2_Missense_M	NM_000718	NP_000709	Q00975	CAC1B_HUMAN	lasmic (Potential).	6	CCCAGCGGCCC	0.697	
+	5	951	mij.1_Missense_M	NM_014728	NP_055543	Q14CM0	FRPD4_HUMAN	PDZ.	13	ATACTCCTCACT	0.393	
+	1	877	_5'Flank|MAGEB	NM_002367	NP_002358	O15481	MAGB4_HUMAN	MAGE.	1	AGTGATCCCCCA	0.502	
+	15	2563	rf22_uc010ngv.2_	NM_152632	NP_689845	Q6ZTR5	CX022_HUMAN		3	ACCCAGTGGAC	0.393	
-	2	362	dgi.3_Missense_M	NM_176819	NP_789789	Q9H7Y0	CX036_HUMAN		1	GATAAGAAAGC	0.483	
+	3	589	e_Mutation_p.E19	NM_003173	NP_003164	O43463	SUV91_HUMAN	Pre-SET.	0	GCTGCGAGTGC	0.637	
+	7	845	ense_Mutation_p.	NM_001032382	NP_001027554	O60828	PQBP1_HUMAN		1	GTCAACAGGAC	0.642	
+	10	3968	_p.R120C|CCNB	NM_033031	NP_149020	Q8WWL7	CCNB3_HUMAN		9	CACCTCGTGTG	0.463	
-	72	11618	p.R2547Q|HUWE	NM_031407	NP_113584	Q7Z6Z7	HUWE1_HUMAN		17	TAGCCCGGCGC	0.537	
-	1	51	RNA|EDA2R_uc0	NM_021783	NP_068555	Q9HAV5	TNR27_HUMAN	.|Extracellular (Potential).	1	ACACCGTCCCC	0.493	rs144036451
-	2	801	CC6L_uc004eap.1	NM_017669	NP_060139	Q2NKX8	ERC6L_HUMAN	ase ATP-binding.	3	GATGAGGTTTTT	0.413	rs140524285
-	2	341		NM_001012755	NP_001012773	Q5H9E4	MCAR6_HUMAN	Solcar 1.	0	TTGCCGGAACA	0.498	
+	5	410	P14_uc004esf.2_I	NM_178813	NP_848928	Q86UN6	AKA28_HUMAN		0	GTGTTTCTAAAA	0.353	
-	1	164		NM_001013628	NP_001013650	Q5VW00	DC122_HUMAN		7	GCGTCGCCGGC	0.741	
+	16	2536		NM_173493	NP_775764	Q8IV76	PASD1_HUMAN		3	TCGAGGGACCTC	0.532	
+	20	3656	nse_Mutation_p.P	NM_001001344	NP_001001344	Q16720	AT2B3_HUMAN	ic (Potential).|Poly-Pro.	1	GCCCCCGTCCC	0.602	
+	10	1022	Z_uc004flb.2_Miss	NM_000116	NP_000107	Q16635	TAZ_HUMAN		0	CTGATCGGGAAG	0.637	
+	4	1440		NM_017514	NP_059984	P51805	PLXA3_HUMAN	tracellular (Potential).	3	CCTACCGCCAG	0.657	
+	17	2494	p.E690K|SCNN1	NM_002978	NP_002969				0	CAGCCGAAGAG	0.672	
-	2	824		NM_020710	NP_065761	Q8N1G4	LRC47_HUMAN		2	CTTCCCGCCAC	0.433	
+	5	986	_p.E245D|DFFB_	NM_004402	NP_004393	O76075	DFFB_HUMAN		0	CCGGAAGGCTG	0.672	
+	20	2657	p.P816S|PIK3CD_	NM_005026	NP_005017	O00329	PK3CD_HUMAN	PI3K/PI4K.	7	GCCTCCCCACC	0.602	
-	1	373	0obf.1_Missense_	NM_001146181	NP_001139653	B7ZW38	B7ZW38_HUMAN		0	CGTTTCCTCGG	0.483	
+	4	436	_Mutation_p.G119	NM_004070	NP_004061	P51800	CLCKA_HUMAN		1	CTCTGGAGGTG	0.602	

-	6	582	plice_Site_p.G109_	NM_003760	NP_003751	O43432	IF4G3_HUMAN		1	GCGTTCCTAAAA	0.428	
+	5	891	gb.2_Missense_Mu	NM_032264	NP_115640	Q9H094	NBPF3_HUMAN	Potential.	2	TTGAATCAGCATC	0.567	
-	64	8502	gd.2_Missense_Mu	NM_005529	NP_005520	P98160	PGBM_HUMAN	ike C2-type 13.	9	CACCGGGGACG	0.647	
+	3	1229	p.R319H|PDIK1L_	NM_152835	NP_690048	Q8N165	PDK1L_HUMAN	rotein kinase.	0	AGGATCGTCCAG	0.378	
+	1	120		NM_006142	NP_006133	P31947	1433S_HUMAN		0	CAGGCCGAACGC	0.602	
-	2	666		NM_052943	NP_443175	Q96A09	FA46B_HUMAN		1	AGTGGCGTGATC	0.607	
+	3	700	BTB8A_uc001bvm.	NM_001040441	NP_001035531	Q96BR9	ZBT8A_HUMAN	BTB.	0	CTTTCTCCCCTG	0.423	
+	3	488		NM_017629	NP_060099	Q9HCK5	AGO4_HUMAN		1	ATTGGACGGGAT	0.343	
-	3	402_403	bw.3_Missense_M	NM_001099439	NP_001092909	Q5JZY3	EPHAA_HUMAN	cellular (Potential).	8	TGAACTGCAGTT	0.614	
+	23	2790	_uc001cdc.1_5'UT	NM_012090	NP_036222	Q9UPN3	MACF1_HUMAN		16	CACGCAGTCCAG	0.483	
+	1	311		NM_001008740	NP_001008740	Q7Z6W1	TMCO2_HUMAN		1	GAAACGAAGTAT	0.323	
-	8	960	1cim.2_Nonsense_	NM_006824	NP_006815	Q99848	EBP2_HUMAN		0	AGCCTTTCTTCTT	0.488	
+	16	3255	nse_Mutation_p.R5	NM_002840	NP_002831	P10586	PTPRF_HUMAN	III 7.|Extracellular (Potentia	10	ACACCCGCTTTA	0.592	
+	9	1138		NM_178134	NP_835235	Q86W10	CP4Z1_HUMAN	nenal (Potential).	1	GCACCGGTAGTA	0.473	
-	3	1083	se_Mutation_p.R1	NM_003189	NP_003180	P17542	TAL1_HUMAN		1	GGTCTCCTCTTC	0.577	
+	42	5452	ADL_uc009wag.2_	NM_176877	NP_795352	Q8NI35	INADL_HUMAN		4	TACCACCTTGGT	0.443	
+	7	1486	ense_Mutation_p.	NM_005012	NP_005003	Q01973	ROR1_HUMAN	xtracellular (Potential).	19	ACTGCCGCAAC	0.527	
-	3	185		NM_000329	NP_000320	Q16518	RPE65_HUMAN		1	CCACATCGAAGG	0.522	rs61751282
-	8	490	te_p.I74_splice|SL	NM_152697	NP_689910	Q8NCS7	CTL5_HUMAN		4	ACAGATCTGTGA	0.378	
+	17	2779	MPD2_uc010ovr.1_	NM_004037	NP_004028	Q01433	AMPD2_HUMAN		3	ATCACCGGAATC	0.612	
-	2	767	ebv.1_Missense_M	NM_004980	NP_004971	Q9UK17	KCND3_HUMAN	lasmic (Potential).	3	TAGAAGTTGAGC	0.612	
-	3	611		NM_205848	NP_995320	Q5T7P8	SYT6_HUMAN	lasmic (Potential).	5	TGATGCGGCCAA	0.572	
+	2	370	_p.G114E|CD2_uc	NM_001767	NP_001758	P06729	CD2_HUMAN	-3 (CD58) binding region 2.	1	CAAAAGGAAAAA	0.308	
-	3	644_645	MGCS2_uc001eie.	NM_005518	NP_005509	P54868	HMCS2_HUMAN		2	TAGACGGCAATG	0.475	
-	34	7295		NM_024408	NP_077719	Q04721	NOTC2_HUMAN	lasmic (Potential).	27	GCAAACGGGCCA	0.622	
-	32	6161		NM_024408	NP_077719	Q04721	NOTC2_HUMAN	nic (Potential).|ANK 4.	27	CACATCCGCTTG	0.527	
+	10	1256		NM_012113	NP_036245	Q9ULX7	CAH14_HUMAN	lasmic (Potential).	1	AGATTCGGTGAG	0.323	rs150286906
+	3	401	68S|ECM1_uc001	NM_004425	NP_004416	Q16610	ECM1_HUMAN		3	GCCCTCCCTTTC	0.572	
-	3	1840		NM_001008536	NP_001008536	Q5QJ38	TCHL1_HUMAN		2	GTATCTGGGTTA	0.537	
-	3	528		NM_001122965	NP_001116437	Q6XPR3	RPTN_HUMAN	Gln-rich.	0	GGGAATCTCTGT	0.517	
-	4	1527		NM_006617	NP_006608	P48681	NEST_HUMAN	Tail.	6	GCCAAGGAGGCA	0.627	
-	36	4743	_p.T651A|ARHGEF	NM_014784	NP_055599	O15085	ARHGB_HUMAN		9	TGGGTGTCAGGT	0.637	
-	7	1468	phw.1_Missense_M	NM_031281	NP_112571	Q96RD9	FCRL5_HUMAN	Potential).|Ig-like C2-type 4.	6	GTCAGAGAGAAG	0.582	
-	3	324	RL4_uc010phy.1_F	NM_031282	NP_112572	Q96PJ5	FCRL4_HUMAN	Potential).|Ig-like C2-type 1.	4	CTCCCCAGTAGT	0.517	
-	6	1075	se_Mutation_p.T32	NM_052938	NP_443170	Q96LA6	FCRL1_HUMAN	ical; (Potential).	7	CCACGGTGGCT	0.458	
+	3	714	1C_uc001frv.2_5'U	NM_001765	NP_001756	P29017	CD1C_HUMAN	cellular (Potential).	4	TAGATTTACTGA	0.478	
+	5	890	sz.1_Missense_Mu	NM_001004310	NP_001004310	Q6DN72	FCRL6_HUMAN	3.|Extracellular (Potential).	3	GTGTCTCCAGAG	0.557	
-	5	1615	_p.P524S|IGSF8_u	NM_052868	NP_443100	Q969P0	IGSF8_HUMAN	4.|Extracellular (Potential).	0	TCGGGGCCCCA	0.672	
-	7	963	R254*|NR1I3_uc00	NM_001077480	NP_001070948	Q14994	NR1I3_HUMAN		2	GTTTTCGTAGTG	0.527	rs144211465
+	4	673	gbp.2_Missense_M	NM_007240	NP_009171	Q9UNI6	DUS12_HUMAN		1	CAAGTGTAGAAA	0.318	
-	12	2869	u.1_Missense_Mu	NM_003285	NP_003276	Q92752	TENR_HUMAN	onectin type-III 7.	11	TGATTTCGTATTC	0.532	
-	10	2617	u.1_Missense_Mu	NM_003285	NP_003276	Q92752	TENR_HUMAN	onectin type-III 6.	11	GACAGCCACAA	0.552	
-	8	1388	wyj.2_Splice_Site_	NM_006469	NP_006460	Q9Y6Y0	NS1BP_HUMAN		5	TGTGTACCTGCA	0.403	
+	7	1183	_Mutation_p.P285	NM_005807	NP_005798	Q92954	PRG4_HUMAN	K-X-P-X-P-T-T-X.|4; appro	1	CCACCCCCAAG	0.637	
+	7	1369	_Mutation_p.P347	NM_005807	NP_005798	Q92954	PRG4_HUMAN	ats of K-X-P-X-P-T-T-X.|12	1	CCACCCCCAAG	0.652	
+	17	2841	2_Missense_Muta	NM_000573	NP_000564	P17927	CR1_HUMAN	ar (Potential).|Sushi 14.	3	CATGCGACCCC	0.512	
-	9	1406	CH2_uc009xdq.1_	NM_018040	NP_060510	Q9NW75	GPTC2_HUMAN		1	CTCCCGTGCATA	0.383	rs144624552

+	8	4116_4117		NM_032890	NP_116279	Q96F81	DISP1_HUMAN		0	GTCGAGGGCTTT	0.564	
+	91	20050	sr.1_Missense_Mu	NM_001098623	NP_001092093	Q5VST9	OBSCN_HUMAN	otein kinase 1.	28	GTGACCGTGCCA	0.627	
+	8	1174_1175	G251K|MTR_uc01	NM_000254	NP_000245	Q99707	METH_HUMAN	Hcy-binding.	3	CTCATGGAGAAC	0.465	
+	25	3044	x.1_Missense_Mu	NM_000254	NP_000245	Q99707	METH_HUMAN	B12-binding.	3	AGCTCCGAGATA	0.443	
+	6	1175	W3_uc001idp.1_Ir	NM_015431	NP_056246	Q8NG06	TRI58_HUMAN	B30.2/SPRY.	7	CGCCATCTCCTG	0.567	
+	6	1073	i.1_Missense_Mut	NM_030664	NP_109589	Q96BW5	PTER_HUMAN		2	GGGCTGTGAAG	0.413	
-	4	1575		NM_001034842	NP_001030014	Q3KNS1	PTHD3_HUMAN	Helical; (Potential).	4	ACTGCCGCTTTT	0.423	
-	7	575	T47M|ZNF438_uc0	NM_182755	NP_877432	Q7Z4V0	ZN438_HUMAN		2	TGGACGTTAGG	0.468	
-	12	1664	wr.3_Missense_Mu	NM_133376	NP_596867	P05556	ITB1_HUMAN	l).|I.|Cysteine-rich tandem r	2	TGTCTTCACTGTT	0.418	
+	7	1054		NM_052997	NP_443723	Q9BXX3	AN30A_HUMAN		9	CGTGGCCAGCA	0.423	
+	2	187	F4_uc009xmn.2_	NM_032023	NP_114412	Q9H2L5	RASF4_HUMAN		1	GCAAGTCCATTC	0.537	
+	3	383	N2_uc010qfq.1_5'	NM_014696	NP_055511	O60269	GRIN2_HUMAN		0	GGCGCGACCCA	0.697	rs149580948
+	4	615	nslation_Start_Site	NM_012207	NP_036339	P31942	HNRH3_HUMAN	Gly-rich.	2	TGGGCGTGGAA	0.438	
+	25	3558	AR1_uc010qjb.1_F	NM_018237	NP_060707	Q8IX12	CCAR1_HUMAN		7	GAGAATGGTGCC	0.274	
+	7	889	p.A267V|HK1_uc0	NM_000188	NP_000179	P19367	HXK1_HUMAN	Regulatory.	1	GGGAGCCTTTG	0.522	
-	2	418		NM_022146	NP_071429	Q9GZQ6	NPFF1_HUMAN	lasmic (Potential).	0	CCTTTCCACAG	0.572	
+	9	1625	p.2_Missense_Mu	NM_170744	NP_734465	Q8IZJ1	UNC5B_HUMAN	ical; (Potential).	3	TGGCGGTGGGG	0.622	
+	37	5403		NM_022124	NP_071407	Q9H251	CAD23_HUMAN	.|Extracellular (Potential).	11	TCGTCGCAGGC	0.582	rs56043301
+	5	1262	p.L229V|SH2D4B	NM_207372	NP_997255	Q5SQS7	SH24B_HUMAN		0	CGGGTCTGCCG	0.512	
-	12	1412	p.S405F|GPAM_u	NM_020918	NP_065969	Q9HCL2	GPAT1_HUMAN		2	TTTAAGGAAAATG	0.443	
+	6	1174	F7L2_uc001lah.2	NM_001146274	NP_001139746	Q9NQB0	TF7L2_HUMAN	tion with MAD2L2.|Pro-rich	4	CAGCCGACGTA	0.592	
+	4	317	RP1_uc001lcn.2_	NM_006229	NP_006220	P54315	LIPR1_HUMAN		2	CAAAGGAGATG	0.478	
-	8	892	qss.1_Nonsense_	NM_022063	NP_071346	Q9H8W3	F204A_HUMAN		0	TTTTCGGGCAG	0.368	
-	19	3423	p.M1059L|EIF3A_	NM_003750	NP_003741	Q14152	EIF3A_HUMAN	DE]-[DE]-R-[SEVGFPILV]-[	0	ATCCATGCCTCG	0.627	
+	4	560	ense_Mutation_p.S	NM_206862	NP_996744	O95359	TACC2_HUMAN		10	TGCCAGCCTGG	0.557	
-	12	2103	2_uc001lhj.2_Splic	NM_198148	NP_937791	Q8N436	CPXM2_HUMAN		2	CAGACCTGCCA	0.498	
+	8	1598	p.L431F|RIC8A_u	NM_021932	NP_068751	Q9NPQ8	RIC8A_HUMAN		0	GGGGCCTCATG	0.597	
+	8	1400	e_Mutation_p.D45	NM_025092	NP_079368	Q32M88	ATHL1_HUMAN	p.R429Q(1)	3	CCCCCGACGAG	0.607	
-	3	557		NM_001012709	NP_001012727	Q6L8H1	KRA54_HUMAN	repeats of C-C-X-P.	0	AGCCACAGCCC	0.672	
-	2	263		NR_001589					0	CGAAGGAGATC	0.493	
+	4	723	GA4_uc001mcn.2	NM_001037329	NP_001032406	Q8IV77	CNGA4_HUMAN	lasmic (Potential).	1	CGGACCCCGCG	0.577	
+	17	2930		NM_006108	NP_006099	Q9HCB6	SPON1_HUMAN	SP type-1 6.	0	caagaaggagatcag	0.234	
-	5	918	ws.1_Missense_M	NM_145803	NP_665802	Q9Y4K3	TRAF6_HUMAN	h TAX1BP1.|TRAF-type 1.	1	ATGCAGCACAG	0.378	
+	1	825		NM_001001955	NP_001001955	Q8NGP0	OR4CD_HUMAN	Name=7; (Potential).	4	CACTATGATAACT	0.363	
-	26	3464		NM_001923	NP_001914	Q16531	DDB1_HUMAN	with CDT1 and CUL4A.	4	CTTCCGCTCGG	0.512	
+	4	520	AK_uc009ynm.1_	NM_015533	NP_056348	Q3LXA3	DHAK_HUMAN	DhaK.	0	GGGCAGCATCC	0.652	
-	5	866	sn.2_Missense_M	NM_021727	NP_068373	Q9Y5Q0	FADS3_HUMAN	lasmic (Potential).	2	CGGGCGCCACC	0.647	
-	28	3223		NM_017525	NP_059995	Q6DT37	MRCKG_HUMAN		4	CCGGGGTCTTG	0.687	
+	11	1473	.3_RNA|MUS81_	NM_025128	NP_079404	Q96NY9	MUS81_HUMAN		0	GTTCCGTCCAC	0.637	
-	16	3286		NM_006946	NP_008877	O15020	SPTN2_HUMAN	Spectrin 8.	4	GCTGCGCAAGA	0.687	
-	17	2911	oly.2_Missense_M	NM_004910	NP_004901	O00562	PITM1_HUMAN		3	CGTGCGTTTTC	0.692	
+	14	3237	g.2_Missense_Mu	NM_002335	NP_002326	O75197	LRP5_HUMAN	eta-propeller 4.|Extracellula	7	CTGAGCGGGGA	0.662	
+	20	4241	g.2_Missense_Mu	NM_002335	NP_002326	O75197	LRP5_HUMAN	ical; (Potential).	7	CGGGCCCGTCA	0.602	
-	8	987	p.G273S|CPT1A_	NM_001876	NP_001867	P50416	CPT1A_HUMAN	lasmic (Potential).	2	GTTGCCGGCTC	0.418	rs144347513
-	21	4534	1opz.2_Missense_	NM_012309	NP_036441	Q9UPX8	SHAN2_HUMAN		5	GGCGACGGCGT	0.592	
-	13	1262	2A_uc001osn.2_	NM_002599	NP_002590	O00408	PDE2A_HUMAN	GAF 1.	4	GGTCAGTGGCC	0.567	
-	34	4511	ss.2_Missense_M	NM_001040118	NP_001035207	Q96P48	ARAP1_HUMAN		1	GGTCCGCGGTG	0.617	

-	16	4009	n.2_Missense_Mut	NM_016578	NP_057662	Q96T23	RSF1_HUMAN		4	TTTGCGGGATG	0.542	
-	4	842	g.2_Missense_Mu	NM_080491	NP_536739	Q9UQC2	GAB2_HUMAN		6	TGAGGCTGCCC	0.572	
+	13	2488	uc001pen.1_Intron	NM_001098672	NP_001092142	Q6MZM0	HPHL1_HUMAN	e 5.|Extracellular (Potential	3	AATTGGATTGG	0.423	
+	14	2047	e_p.E570_splice|	NM_014361	NP_055176	O94779	CNTN5_HUMAN		8	AAAGGTAAGAC	0.378	
+	3	974	gv.2_Missense_M	NM_001130145	NP_001123617	P46937	YAP1_HUMAN	WW 1.	3	AGGACCCCAGG	0.483	
+	7	1022		NM_015191	NP_056006	Q9H0K1	SIK2_HUMAN	UBA.	3	TTCTGCGACTG	0.438	
-	7	781	.P228S|ALG9_uc	NM_001077690	NP_001071158	Q9H6U8	ALG9_HUMAN	ical; (Potential).	2	GAATGGCCAGC	0.453	
+	3	433	O2_uc001poz.2_I	NM_015523	NP_056338	Q9Y3B8	ORN_HUMAN	xonuclease.	0	TTGGTGTAAGG	0.458	
-	5	1110	ppd.2_Missense_	NM_001077639	NP_001071107	Q6UWF7	FA55D_HUMAN		4	TCATTCCAAAC	0.413	
+	8	1231	sv.2_Missense_M	NM_004788	NP_004779	Q14139	UBE4A_HUMAN		5	AGGAGGCCAAC	0.463	
+	9	1192	w.1_Missense_Mu	NM_014619	NP_055434	Q16099	GRIK4_HUMAN	ellular (Potential).	3	GCCTGCGGTAA	0.577	
-	25	3829	zda.1_RNA|NCA	NM_015261	NP_056076	P42695	CNDD3_HUMAN		5	GGGGAACTTGT	0.443	
+	11	3053	.3_Intron|WNK1_	NM_018979	NP_061852	Q9H4A3	WNK1_HUMAN		23	AACTCCTCATGT	0.532	
-	3	133	_p.R24C|MLF2_u	NM_005439	NP_005430	Q15773	MLF2_HUMAN		1	CTGACGGTGAAT	0.542	
-	2	916		NM_020634	NP_065685	Q9NR23	GDF3_HUMAN		6	TCCATGGCAGT	0.527	
-	12	1500	k.1_Missense_Mut	NM_000014	NP_000005	P01023	A2MG_HUMAN		5	CATGGGCTCAA	0.512	
+	2	575	rad.2_Missense_	NM_138723	NP_620049	Q9BZR8	B2L14_HUMAN		1	AGATTCGCACA	0.512	
+	1	416		NR_003932					0	AGCCTGCAAGA	0.567	
+	5	840	1467_uc009zhx.1_	NM_020853	NP_065904	A2RU67	K1467_HUMAN		3	GTGTTCGAGAC	0.448	
-	6	576	GDIB_uc001rcp.1_	NM_001175	NP_001166	P52566	GDIR2_HUMAN		0	AACTGGAGTGA	0.522	
-	16	2179	sit.1_Missense_M	NM_014802	NP_055617	Q86YS7	K0528_HUMAN		4	TGAGCGTTGCC	0.353	
-	2	574		NM_001080406	NP_001073875	A8MTZ7	CL071_HUMAN		0	GCTGGCGGTTG	0.493	
-	53	4445	A1_uc009zkw.2_	NM_001844	NP_001835	P02458	CO2A1_HUMAN	lar collagen NC1.	2	TGCCCGGATCT	0.587	
+	1	61		NM_012404	NP_036536	O95626	AN32D_HUMAN	LRR 1.	2	TGAAAGAACTT	0.458	
+	1	563	smv.1_Missense_	NM_014033	NP_054752	Q9H8H3	MET7A_HUMAN		0	TGGGTGCAGGG	0.552	
-	13	1477	A5_uc010sow.1_	NM_002205	NP_002196	P08648	ITA5_HUMAN	tential).|Potential.|FG-GAP	2	GGATATCCATTG	0.562	
+	2	275	1_5'UTR|PDE1B_	NM_000924	NP_000915	Q01064	PDE1B_HUMAN	lin-binding (Potential).	2	TTCGGTCTCTG	0.637	
+	1	402		NM_054105	NP_473446	Q9NZP2	OR6C2_HUMAN	lasmic (Potential).	2	ATCATGAACAA	0.453	
+	2	434	qo.1_Missense_M	NM_207344	NP_997227	Q8WW59	SPRY4_HUMAN	B30.2/SPRY.	0	TGATCGTTCCT	0.562	
+	2	756	H4_uc009zpj.2_5'	NM_007224	NP_009155	O95158	NXPH4_HUMAN	(linker domain).	0	GCTGGGGATGG	0.756	
+	3	432	m.2_Missense_Mu	NM_006812	NP_006803	Q13438	OS9_HUMAN	PRKCSH.	1	GTTATGGACGC	0.433	
-	4	1826	sqx.2_Missense_	NM_178539	NP_848634	Q8N3H0	F19A2_HUMAN		1	TTCTTCTCCCT	0.413	
+	5	1405		NM_013381	NP_037513	Q9UKU6	TRHDE_HUMAN	ellular (Potential).	3	AAGACGTGTGG	0.403	
+	12	1734	yu.2_Splice_Site_	NM_001135805	NP_001129277	P21579	SYT1_HUMAN		6	TTTCAGAAAGT	0.453	
-	49	6990	lice_Site_p.E1276	NM_025114	NP_079390	O15078	CE290_HUMAN		7	GTTTCCTATCATT	0.279	
-	1	1060		NM_152638	NP_689851	Q8TC90	CL012_HUMAN	Potential.	2	GCTGACGCTCC	0.647	
+	35	4540		NM_014503	NP_055318	O75691	UTP20_HUMAN		4	TTAAAGAAATG	0.318	
-	39	5876	ttr.1_Missense_M	NM_001109662	NP_001103132				2	TGCAGGCTCGA	0.547	
-	12	1700	1tts.2_Missense_	NM_001109662	NP_001103132				2	CATCCGCCATG	0.478	
+	4	771	_p.Q180*|RNFT2_	NM_001109903	NP_001103373	Q96EX2	RNFT2_HUMAN	ellular (Potential).	0	TGCTTTCAGCAT	0.637	
+	2	556	uc001txf.2_Intron	NM_178499	NP_848594	Q8IWA6	CCD60_HUMAN		3	CATCAGGTCCC	0.443	
+	1	76		NM_004373	NP_004364	P12074	CX6A1_HUMAN		0	GTCCCGCCCAC	0.662	rs139069733
+	8	1106	p.R326C|ACADS_	NM_000017	NP_000008	P16219	ACADS_HUMAN		2	CCTGGCGCGCT	0.637	rs140853839
-	10	1434	uek.1_Missense_	NM_020845	NP_065896	Q9BZ72	PITM2_HUMAN		3	TGGTGCCTCCG	0.647	
+	66	11390	10_uc001ufu.3_5	NM_207437	NP_997320	Q8IVF4	DYH10_HUMAN		6	ACTTTGGGCAA	0.453	
+	1	262	.A41V|SFRS8_uc	NM_004592	NP_004583	Q12872	SFSWA_HUMAN		0	CTATGCCTGCA	0.672	
-	43	5944	LE_uc001ukr.1_M	NM_006231	NP_006222	Q07864	DPOE1_HUMAN		8	GATtcctccgcctcttc	0.313	

+	7	1209	p.R152*|SPATA13	NM_153023	NP_694568	Q96N96	SPT13_HUMAN	DH.	3	TATATCCGACAGT	0.363	
-	11	3143	p.E829K|TRPC4_u	NM_016179	NP_057263	Q9UBN4	TRPC4_HUMAN	and ITPR3.|Cytoplasmic (P	6	AATCTTCGTGGG	0.433	
-	2	570		NM_005780	NP_005771	Q9Y693	LHFP_HUMAN		4	GTGGCAGCACAA	0.527	
-	8	1314	p.S290L|ELF1_uc	NM_172373	NP_758961	P32519	ELF1_HUMAN		1	GATAGCGATGGA	0.418	
-	41	5090		NM_015058	NP_055873	A3KMH1	K0564_HUMAN		6	TAGCTTGATGTC	0.423	
+	13	1489	v.1_Missense_Mut	NM_031431	NP_113619	Q96JB2	COG3_HUMAN		2	GGAGCGGCTCG	0.458	
-	14	3347	_Mutation_p.E999	NM_000053	NP_000044	P35670	ATP7B_HUMAN	lasmic (Potential).	3	GGCCTCCGCAG	0.627	
+	15	1060	p.S277N|SCEL_uc	NM_144777	NP_659001	O95171	SCEL_HUMAN	imate tandem repeats.|3.	5	ATATGAGTACCCG	0.388	
+	6	1154	POTEG_uc010ah	NM_001005356	NP_001005356	Q6S5H5	POTEG_HUMAN		1	CTAAAAGTCTCT	0.214	
-	8	721_722	p.1_Missense_Mu	NM_002471	NP_002462	P13533	MYH6_HUMAN	osin head-like.	4	CTGGTCCTCCAG	0.609	
-	6	632		NM_016049	NP_057133	Q9Y3B6	F158A_HUMAN		0	CTGCCGTGACT	0.547	
-	4	805	lq.2_RNA|RIPK3_u	NM_006871	NP_006862	Q9Y572	RIPK3_HUMAN	rotein kinase.	4	TGTGGAGGCCT	0.582	
+	5	1985	r.1_Missense_Mut	NM_004554	NP_004545	Q14934	NFAC4_HUMAN	RHD.	3	GTTCCGGGTAC	0.602	
-	11	1799	.D470N|RALGAP	NM_014990	NP_055805	Q6GYQ0	RGPA1_HUMAN		4	ATGGTCTGTGA	0.343	
+	4	1684	ny.1_Missense_Mu	NM_054024	NP_473365	Q96PC5	MIA2_HUMAN		2	AAGAAACTGGAG	0.308	
+	5	1858		NM_054024	NP_473365	Q96PC5	MIA2_HUMAN		2	AACCATCAGTAG	0.393	
-	21	2002	sense_Mutation_p.	NM_004713	NP_004704	O60524	NEMF_HUMAN		0	AGGGAGGAAGA	0.294	
-	2	810		NM_005982	NP_005973	Q15475	SIX1_HUMAN		0	TGTTCTCCCTAA	0.428	
-	32	6484	p.D2144N|SPTB_u	NM_001024858	NP_001020029	P11277	SPTB1_HUMAN		11	TCTCATCCCCAG	0.647	
-	13	2508	YVE26_uc001xkc.	NM_015346	NP_056161	Q68DK2	ZFY26_HUMAN		11	TTGTACTTTCCA	0.453	
+	8	3051	.3_Intron|PCNX_u	NM_014982	NP_055797	Q96RV3	PCX1_HUMAN		1	TAGGCGGTAGC	0.463	
+	4	253	f80_uc001yrn.2_5'	NM_001311	NP_001302	P50238	CRIP1_HUMAN	M zinc-binding.	0	AGCACGAAGGC	0.572	
+	19	3414	bi.2_Missense_Mu	NM_003246	NP_003237	P07996	TSP1_HUMAN	SP C-terminal.	6	GGAACGCCCTG	0.592	
+	17	2709	_Mutation_p.G58	NM_001013703	NP_001013725	Q9P2K8	E2AK4_HUMAN	otein kinase 2.	4	AGACAGGAGAC	0.353	
-	8	1406	.2_5'UTR|CDAN1_	NM_138477	NP_612486	Q8IWY9	CDAN1_HUMAN		2	GAGACAGCTTGA	0.458	
-	19	4139	.G1336R|TP53BP	NM_005657	NP_005648	Q12888	TP53B_HUMAN		7	CTTTCCCTGAGC	0.572	
+	6	1030	2A1_uc010uex.1_	NM_000338	NP_000329	Q13621	S12A1_HUMAN	ical; (Potential).	2	GTGGCTGTTGCT	0.413	rs137853158
-	33	4383		NM_000138	NP_000129	P35555	FBN1_HUMAN	22; calcium-binding.	3	ACCCGGGACTG	0.403	
+	7	1301	jp.1_Missense_Mu	NM_002755	NP_002746	Q02750	MP2K1_HUMAN	n kinase.|Pro-rich.	0	ATGTTTGGGTGC	0.612	
-	18	3188	p.K271R|TLE3_uc	NM_005078	NP_005069	Q04726	TLE3_HUMAN	WD 5.	2	CAGGCTTGGTG	0.632	
-	2	871	nse_Mutation_p.R	NM_006901	NP_008832	B2RTY4	MYO9A_HUMAN		3	ATCATCCTGCGA	0.433	rs148320227
+	5	773	M202_uc002aur.2_	NM_001080462	NP_001073931	A6NGA9	TM202_HUMAN		2	TGGAATCTCTAA	0.458	
+	2	761		NM_000761	NP_000752	P05177	CP1A2_HUMAN		4	CCTCCGGGAAC	0.567	
+	15	1657	p.G400R|PSTPIP1	NM_003978	NP_003969	O43586	PPIP1_HUMAN	SH3.	1	GGAACGGGCAG	0.637	
+	7	3273	13_uc002blu.1_Mi	NM_007200	NP_009131	Q12802	AKP13_HUMAN		9	TGGGGGCAGAG	0.597	
+	5	2017		NM_198526	NP_940928	Q8N1W2	ZN710_HUMAN		1	GACTTCGAGGAG	0.577	
+	4	702	sc.1_RNA|LRRK1_	NM_024652	NP_078928	Q38SD2	LRRK1_HUMAN	ANK 2.	12	TGGCAGCGTATT	0.567	
+	21	3386	b.1_RNA|LRRK1_	NM_024652	NP_078928	Q38SD2	LRRK1_HUMAN		12	GCTTCGTTCCC	0.542	
+	16	2311		NM_016111	NP_057195	Q9Y4R8	TELO2_HUMAN		0	AGACCCAGCGG	0.677	
+	12	1501	p.E455K|MAPK8I	NM_015133	NP_055948	Q9UPT6	JIP3_HUMAN	Potential.	3	GGGGCGAGTTG	0.532	
-	3	506	3_uc002cmu.2_M	NM_080861	NP_543137	Q6PJ21	SPSB3_HUMAN	B30.2/SPRY.	0	TAGACGGGAGAG	0.662	
-	3	390		NM_005061	NP_005052	Q92901	RL3L_HUMAN		0	GCGCCGGCACT	0.637	
-	7	744		NM_020764	NP_065815	Q8WXD9	CSKI1_HUMAN	ANK 6.	2	CAGCCGCACCA	0.657	
-	6	886	crz.1_Missense_M	NM_022119	NP_071402	Q9GZN4	BSSP4_HUMAN	eptidase S1.	1	GTAGACCCCGG	0.726	
-	6	868	crz.1_Missense_M	NM_022119	NP_071402	Q9GZN4	BSSP4_HUMAN	eptidase S1.	1	GCGCTCGGCAC	0.721	
+	6	1148	uc002ctj.1_Intron	NM_022468	NP_071913	Q9NPA2	MMP25_HUMAN		0	GGCCTCGCCCA	0.652	
-	1	1069	ur.2_3'UTR|TIGD7_	NM_033208	NP_149985	Q6NT04	TIGD7_HUMAN	H CENPB-type.	0	AACACCGGCTG	0.507	

-	15	3227_3228	cvw.2_Missense_M	NM_004380	NP_004371	Q92793	CBP_HUMAN			127	GGATCGGGCTCA	0.599	rs144649776
-	13	4336	G1263E|GRIN2A_	NM_001134407	NP_001127879	Q12879	NMDE1_HUMAN	lasmic (Potential).		45	GCTCCCCGGTG	0.522	
-	6	1877	0uyn.1_Splice_Sit	NM_001134407	NP_001127879	Q12879	NMDE1_HUMAN			45	GAATTGCTGTAA	0.219	
+	3	409	IP2_uc010uyp.1_I	NM_024997	NP_079273	Q5U623	MCAF2_HUMAN			0	CTAGGACGACTG	0.373	rs75885887
-	11	2499	ense_Mutation_p.F	NM_014647	NP_055462	Q9Y4F3	LKAP_HUMAN			0	CAAGCGGGGAT	0.383	
+	3	463	dfp.2_Missense_M	NM_024847	NP_079123	Q7Z402	TMC7_HUMAN	cellular (Potential).		3	ACAAATGAAGTA	0.443	
+	3	1212	gb.3_Missense_Mu	NM_001105248	NP_001098718	Q6UXY8	TMC5_HUMAN	cellular (Potential).		1	CCAGATCATTTTG	0.493	rs148290322
-	3	745	I2_uc002dht.3_Int	NM_173475	NP_775746	Q8IWE4	DCNL3_HUMAN	DCUN1.		2	TTCCCGATGCAC	0.478	
+	5	368	se_Mutation_p.R7	NM_018119	NP_060589	Q9NVU0	RPC5_HUMAN			2	TTGCCGCAGCA	0.617	rs145630346
+	6	807	me.2_Missense_M	NM_212535	NP_997700	P05771	KPCB_HUMAN	C2.		9	CCGATCCCAAA	0.423	
+	34	7929	CAP_uc002dzg.1_	NM_006662	NP_006653	Q6ZRS2	SRCAP_HUMAN	Pro-rich.		4	cgcctccAGCCCAA	0.274	
+	2	1614		NM_014699	NP_055514	O15015	ZN646_HUMAN			2	AGCTCCCCTGC	0.602	
+	35	7605	p.P2466S|CHD9_	NM_025134	NP_079410	Q3L8U1	CHD9_HUMAN	ds A/T-rich D	p.I2481fs*71(1	7	GGAATTCCTGATA	0.388	
+	18	2886	_Mutation_p.R633	NM_005611	NP_005602	Q08999	RBL2_HUMAN	B.|Pocket; binds E1A.		5	GGCCCGGAGCC	0.413	
-	4	882	gq.2_Missense_M	NM_018124	NP_060594	Q6PCD5	RFWD3_HUMAN			3	TTTGGGGAGGG	0.279	
-	35	5723	.1_5'UTR|PKD1L2	NM_052892	NP_443124	Q7Z442	PK1L2_HUMAN	lasmic (Potential).		3	GCATAGGGGTCT	0.572	
+	3	462	hg.1_Missense_M	NM_002661	NP_002652	P16885	PLCG2_HUMAN	PH.		8	ACTCAGTTCGTC	0.498	
-	12	2603	CHC14_uc002fkb	NM_015144	NP_055959	Q8WYQ9	ZCH14_HUMAN			2	CTGGGGTCCCG	0.657	
-	13	1281	p.T396M|CAMKK	NM_172206	NP_757343	Q8N5S9	KKCC1_HUMAN	rotein kinase.		1	ATTCTCGTCTCG	0.567	
-	10	1401	fxz.3_Missense_M	NM_014520	NP_055335	Q9BQG0	MBB1A_HUMAN	with MYB (By similarity).		2	CAGCCGGAACA	0.493	
-	9	874	TA2_uc002gai.1_	NM_015099	NP_055914	O94983	CMTA2_HUMAN			1	CTCGGGGCTCCA	0.592	
+	2	992		NM_153230	NP_694962	Q8N4B4	FBX39_HUMAN			2	TGAACGGATCAT	0.542	
+	6	592		NM_014716	NP_055531	Q15027	ACAP1_HUMAN	omal tubule	p.R129Q(1)	3	CTGGCGGGGGG	0.637	
+	30	4186	rt.2_Missense_Mu	NM_003170	NP_003161	Q7KZ85	SPT6H_HUMAN	SH2.		3	GAGAACCACCTG	0.517	
+	1	1431	p.H392Y|LRRC37	NM_052888	NP_443120	Q96QE4	LR37B_HUMAN	cellular (Potential).		2	GCTCCTCATCCA	0.522	
+	6	1999	p.R581H|LRRC37	NM_052888	NP_443120	Q96QE4	LR37B_HUMAN	xtracellular (Potential).		2	CAATCGCAATCC	0.323	
-	7	1895	_Mutation_p.P411	NM_025248	NP_079524	Q9C0H9	SRCN1_HUMAN			0	CTGGCGGCCCG	0.706	
-	6	1050		NM_181537	NP_853515	Q7Z3Y8	K1C27_HUMAN	Rod.|Coil 2.		0	AGTTACTCTCGG	0.522	
-	4	459	hzi.3_Missense_M	NM_012448	NP_036580	P51692	STA5B_HUMAN			6	TCATACGTGTTC	0.537	
-	10	3464	ron|BRCA1_uc010	NM_007294	NP_009225	P38398	BRCA1_HUMAN			52	ATTTTGGCCCTC	0.373	
+	3	603	2igj.2_Missense_M	NM_001144825	NP_001138297	Q59EK9	RUN3A_HUMAN	RAP2A (By similarity).|RUN		0	TGTGAGCAGCA	0.612	
+	17	2226	_Mutation_p.D25	NM_005892	NP_005883	O95466	FMNL_HUMAN	FH2.		1	ATGAGTGATTTTG	0.597	
+	4	732	kx.1_Missense_Mu	NM_003396	NP_003387	O14905	WNT9B_HUMAN			2	GTTCCGTGAGA	0.637	
+	11	1780	B3_uc010wkr.1_R	NM_000212	NP_000203	P05106	ITB3_HUMAN	).|III.|Cysteine-rich tandem		6	ACTGTACCACGC	0.607	
+	6	1557		NM_013351	NP_037483	Q9UL17	TBX21_HUMAN			0	GGTTCCGCCCTA	0.677	
-	6	637	PL7_uc002ilw.1_5'	NM_145798	NP_665741	Q9BZF2	OSBL7_HUMAN			0	CCAGGCGGTGG	0.627	rs148584339
+	6	1241	c002irv.1_Missens	NM_018896	NP_061496	O43497	CAC1G_HUMAN	r (Potential).|Poly-Gly.|I.		1	GCGCGGGGACG	0.617	
-	13	1728	tf.2_Missense_Mu	NM_001130528	NP_001124000	O60271	JIP4_HUMAN	Potential.		5	CCATTTCTACTC	0.413	
+	1	259	2P1_uc002ivn.2_5'	NM_012374	NP_036506	Q15615	OR4D1_HUMAN	cellular (Potential).		1	TTCCTCCATGAG	0.512	
-	18	3198	s.1_Missense_Mu	NM_198393	NP_938207	Q8IWB6	TEX14_HUMAN			17	GTGAAGCTTCCA	0.378	
-	3	191	D3P2_uc010woz.1_RNA							0	CAGCTCGGTGTC	0.602	
-	15	1969		NM_001433	NP_001424	O75460	ERN1_HUMAN	Potential).|Protein kinase.		9	TCATCCGATTCTC	0.587	
-	2	439	_p.A89V|TEX2_u	NM_018469	NP_060939	Q8IWB9	TEX2_HUMAN			1	AGGCAGCAGGG	0.582	
-	4	732_733	1_RNA|MRPL38_	NM_032478	NP_115867	Q96DV4	RM38_HUMAN			1	GACTCGGGGCA	0.609	
-	4	1702	_Mutation_p.G43	NM_032134	NP_115510	Q9H0J4	QRIC2_HUMAN	Gln-rich.		5	TCTGCCAGGTTC	0.507	
+	2	142	GR2_uc002juv.1_M	NM_004710	NP_004701	O43760	SNG2_HUMAN	.|Helical; (Potential).		0	TTGATCGTGTTC	0.612	
+	7	1024	nse_Mutation_p.A	NM_024419	NP_077733	Q32NB8	PGPS1_HUMAN			0	ATGCAGCAGCT	0.532	

+	26	7690		NM_001080519	NP_001073988	Q9P281	BAHC1_HUMAN	BAH.	1	AGGTCGTGGCG	0.672	
+	6	935	p.G265S|KIAA080	NM_015210	NP_056025	Q9Y4B5	CC165_HUMAN	Potential.	0	CCTTCGGTGAC	0.642	
+	1	653		NM_005913	NP_005904	P33032	MC5R_HUMAN	lasmic (Potential).	6	CAAGCGGATCG	0.617	rs146841229
+	7	818	lbv.2_Splice_Site_	NM_138443	NP_612452	Q96CS2	HAUS1_HUMAN		1	ATGCCGGTAATA	0.328	
+	2	810	lbx.2_Missense_M	NM_145055	NP_659492	Q96B23	CR025_HUMAN		2	GGTCCCGATCTG	0.532	rs62096535
+	5	723	d.2_Missense_Mu	NM_002396	NP_002387	P23368	MAOM_HUMAN		0	ATGTTAAGGTAC	0.353	
-	2	840	h.1_Missense_Mu	NM_003927	NP_003918	Q9UBB5	MBD2_HUMAN	MBD.	0	AACTGCTGAGA	0.393	
+	25	3444	p.A1077T|KIAA14	NM_020854	NP_065905	Q9P260	K1468_HUMAN		6	CTAACGCAGAA	0.413	
-	8	1221	p.G312R|NETO1_	NM_138966	NP_620416	Q8TDF5	NETO1_HUMAN	ss A.|Extracellular (Potenti	4	GAGTCCATTGC	0.388	
-	7	878	APK3_uc002lzd.1_	NM_001348	NP_001339	O43293	DAPK3_HUMAN	rotein kinase.	7	ATTCTCCGCCTG	0.617	
+	3	295	if.1_Missense_Mu	NM_024333	NP_077309	Q9BTV5	FSD1_HUMAN	Potential.	1	ACCTCGAAGCA	0.577	
-	3	605	I4_uc010dub.1_5'	NM_001080400	NP_001073869	Q96Q06	PLIN4_HUMAN	roximate tandem repeat.|4	0	CTTTGGCCAAG	0.602	
+	9	1036	.R233W|PNPLA6_	NM_006702	NP_006693	Q8IY17	PLPL6_HUMAN	ytoplasmic (Potential).	3	CCCAGCGGACC	0.687	
-	18	2430		NM_020196	NP_064581	Q9HCS7	SYF1_HUMAN		4	GGAGGCGTCAC	0.677	
+	8	1155	345V|CLEC4M_uc	NM_001144910	NP_001138382	Q9H2X3	CLC4M_HUMAN	(Probable).|C-type lectin.	1	ACTGTGCGGAAT	0.512	
-	4	416	TS10_uc002mkk.1_	NM_030957	NP_112219	Q9H324	ATS10_HUMAN		4	GTGGTCCACGC	0.662	
-	3	25754		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	ch.|Extracellular (Potential).	57	AGGTTGTTGTT	0.502	
+	3	527	RM1_uc010dxn.2_	NM_199141	NP_954592	Q86X55	CARM1_HUMAN		0	GGAGCGGTCTG	0.642	
+	4	1515	ym.1_Missense_M	NM_001136501	NP_001129973	Q08AG5	ZN844_HUMAN		0	CTTCAGATCTG	0.423	
-	4	985		NM_005815	NP_005806	Q9Y2A4	ZN443_HUMAN	C2H2-type 5.	1	AAAAGGAAAGG	0.373	
-	2	268	on_p.T4I|ZNF709_	NM_152601	NP_689814	Q8N972	ZN709_HUMAN	KRAB.	0	CAAAGGTTTCT	0.438	
-	5	841		NM_020714	NP_065765	Q9ULM2	ZN490_HUMAN	C2H2-type 3.	0	GTTTCGAAAGG	0.423	
+	4	1316	_p.L362V|SYDE1_	NM_033025	NP_149014	Q6ZW31	SYDE1_HUMAN	Rho-GAP.	2	GAGGGCTGCGG	0.682	
+	6	918		NM_024074	NP_076979	Q9H6F2	TM38A_HUMAN	lasmic (Potential).	3	GCATTCGGCCA	0.642	rs147713228
+	10	2692	p.S622F|NWD1_uc002nev.3_Missense_Mutation_p.S5			Q149M9	NWD1_HUMAN		7	GATTTCCTGCC	0.597	
+	5	772	hu.2_Missense_M	NM_015683	NP_056498	Q8TBH0	ARRD2_HUMAN		1	CAACGGCTCCA	0.652	
+	5	1319	_p.K300T|ZNF431_	NM_133473	NP_597730	Q8TF32	ZN431_HUMAN	C2H2-type 8.	2	AACATAAAAGAA	0.348	
-	3	1913		NM_001001411	NP_001001411	Q8N7Q3	ZN676_HUMAN		0	TGTAGGGTTTC	0.418	
-	7	2699		NM_001080409	NP_001073878				2	GTCGAGAAATTG	0.353	rs55891931
-	1	667	.1_5'Flank|LGI4_	NM_139284	NP_644813	Q8N135	LGI4_HUMAN		1	ACTTTCCCTTTG	0.682	
+	3	203	AP33_uc002obt.1_	NM_052948	NP_443180	O14559	RHG33_HUMAN		4	CTCCTCGAGGC	0.607	
+	2	1314		NM_024509	NP_078785	Q9BTN0	LRFN3_HUMAN	xtracellular (Potential).	0	TGGGCGAGGA	0.736	
-	3	581		NM_001864	NP_001855	P24310	CX7A1_HUMAN	ial matrix (By similarity).	0	TACAACGGGATG	0.657	
-	6	2557	_p.C508R|ZNF569_	NM_152484	NP_689697	Q5MCW4	ZN569_HUMAN	2H2-type 18.	3	TGCCACACTCAA	0.413	
+	6	512	_p.R24W|ZNF793_	NM_001013659	NP_001013681	Q6ZN11	ZN793_HUMAN	KRAB.	0	GGCACCGGCTG	0.473	
-	4	1888	0_uc002ogq.2_Int	NM_016536	NP_057620	Q7Z3V5	ZN571_HUMAN	2H2-type 17.	0	GGACATCTAAAG	0.373	
+	48	7908	_Mutation_p.R259	NM_000540	NP_000531	P21817	RYR1_HUMAN	|6 X approximate repeats.	12	GGGTCGTTCGC	0.557	
-	18	2640	_p.P799L|ATP1A3_	NM_152296	NP_689509	P13637	AT1A3_HUMAN	lasmic (Potential).	2	TCCGCGGGTTC	0.627	
-	12	1653	p.A470V|ATP1A3_	NM_152296	NP_689509	P13637	AT1A3_HUMAN	lasmic (Potential).	2	TCGGGGGCACC	0.617	
-	9	1166	_p.A308T|ATP1A3_	NM_152296	NP_689509	P13637	AT1A3_HUMAN	lasmic (Potential).	2	CTTGGCGGTCA	0.488	
-	15	1795	vp.1_Missense_Mu	NM_006297	NP_006288	P18887	XRCC1_HUMAN	BRCT 2.	7	CCGCCGCTCGT	0.582	
+	2	1333		NM_019612	NP_062558	Q6NXR0	IIGP5_HUMAN		3	AGGACGCCCAG	0.647	
-	4	1112	_p.G338D|ZNF45_	NM_003425	NP_003416	Q02386	ZNF45_HUMAN	C2H2-type 7.	1	CTCTTGCCACAT	0.463	
-	5	345		NM_138568	NP_612635	Q2M3D2	EX3L2_HUMAN		1	CACACGCTGCT	0.632	
-	6	2154	xyr.1_Missense_M	NM_015063	NP_055878	Q9UPR5	NAC2_HUMAN	lasmic (Potential).	4	ATTGAGTAGCA	0.587	
+	4	765	e_Mutation_p.P36	NM_014601	NP_055416	Q9NZN4	EHD2_HUMAN		2	CTTCCCGGCCG	0.607	
+	3	250	Site|TRPM4_uc002	NM_017636	NP_060106	Q8TD43	TRPM4_HUMAN	lasmic (Potential).	2	TGACCGTGTGG	0.701	

-	2	304		NM_021733	NP_068379	Q9UJT2	TSKS_HUMAN		2	AGTCTGTCCCC	0.637	
+	7	801	ED25_uc002ppx.1	NM_030973	NP_112235	Q71SY5	MED25_HUMAN	Pro-rich.	1	CTCCCGCCGCA	0.662	
+	4	752	F766_uc002pyt.1	NM_001010851	NP_001010851	Q5HY98	ZN766_HUMAN	ype 2; degenerate.	0	AGAATTCGTACA	0.438	
-	3	1274	qcj.3_Missense_	NM_144687	NP_653288	P59046	NAL12_HUMAN	NACHT.	7	CAGACGGTGGA	0.547	
+	5	763	LRA1_uc010yfh.1_	NM_006863	NP_006854	O75019	LIRA1_HUMAN	2.|Extracellular (Potential).	3	GTGGTCGTACA	0.572	rs151320443
+	3	301	.1_Missense_Mut	NM_002000	NP_001991	P24071	FCAR_HUMAN	ellular (Potential).	2	CAAATCGAGTC	0.498	
+	6	613	_p.P152L|NLRP2_	NM_017852	NP_060322	Q9NX02	NALP2_HUMAN		2	CTGGCCTGGAG	0.512	
+	17	2241_2242	p.S671F|BRSK1_	NM_032430	NP_115806	Q8TDC3	BRSK1_HUMAN		6	CCCCTCCGTCT	0.639	
-	2	1005		NM_152600	NP_689813	Q8NAF0	ZN579_HUMAN	2H2-type 5.	0	GACGCGGCGGT	0.741	
+	10	3184	g.2_Missense_Mu	NM_176811	NP_789781	Q86W28	NALP8_HUMAN		13	CACGGGAAAA	0.512	
+	3	2002	47_uc002qpm.3_	NM_001023561	NP_001018855	O43361	ZN749_HUMAN		0	ACGGCGTTATG	0.433	rs148572975
+	3	1762	_p.R593C|ZNF211_	NM_198855	NP_942152	Q13398	ZN211_HUMAN	2H2-type 11.	2	AACACCGCAGA	0.453	rs12979532
+	3	1610	F776_uc002qqa.	NM_173632	NP_775903	Q68DI1	ZN776_HUMAN	pe 10; degenerate.	1	AGTGTGGAGAA	0.448	
+	9	1384	rs.1_Missense_M	NM_133502	NP_598009	Q96GC6	ZN274_HUMAN	KRAB 2.	1	CACAGAGGACC	0.607	
+	2	344	_p.G76A|ZNF446_	NM_017908	NP_060378	Q9NWS9	ZN446_HUMAN	SCAN box.	1	CCTGGGCACAC	0.672	
-	2	141	REF1_uc010eyr.	NM_006569	NP_006560	Q99674	CGRE1_HUMAN		1	ACATCCTTCCT	0.547	
+	7	940	rjn.2_Missense_M	NM_187841	NP_912730	Q9BYV2	TRI54_HUMAN	COS.	1	TCACCGTAAGG	0.652	rs142922734
+	12	1105	_p.V347I|GCKR_	NM_001486	NP_001477	Q14397	GCKR_HUMAN	SIS 2.	2	ATGGAGTAGAG	0.552	
-	4	373	PY30_uc002rob.1	NM_032574	NP_115963	Q9C005	DPY30_HUMAN		0	AGTTGGCAAAG	0.398	
+	2	515		NM_206943	NP_996826	Q14766	LTBP1_HUMAN		8	AGGGCGGTGCT	0.562	
+	18	1926		NM_032208	NP_115584	Q9H6X2	ANTR1_HUMAN	ic (Potential).|Pro-rich.	4	ccctcccccgcccccc	0.109	
+	7	2382	se_Mutation_p.C6	NM_014497	NP_055312	Q14966	ZN638_HUMAN	RRM 1.	4	ATGGTTGTACTG	0.338	
-	9	1025		NM_003584	NP_003575	O75319	DUS11_HUMAN		1	CAGGAGGAGG	0.423	
+	4	1926	uy.1_Missense_	NM_020184	NP_064569	Q6P4Q7	CNNM4_HUMAN		3	CGGCCGACTAC	0.592	
-	6	1623	tdr.2_Missense_M	NM_001142351	NP_001135823	Q96JF0	SIAT2_HUMAN	enal (Potential).	11	CAAATCCCCCT	0.592	
+	17	3241	.S641C|PSD4_uc	NM_012455	NP_036587	Q8NDX1	PSD4_HUMAN		2	ACTCGAGCCCG	0.632	
+	16	1687	yq.1_Missense_M	NM_001029996	NP_001025167	Q4G0U5	PCDP1_HUMAN		0	CTGTTCGTGAA	0.403	
+	3	731	flu.2_Missense_	NM_130773	NP_570129	Q8WYK1	CNTP5_HUMAN	|Extracellular (Potential).	10	AACAAGAAGAC	0.453	
-	17	2777		NM_001099771	NP_001093241	A5A3E0	POTEF_HUMAN	Actin-like.	5	CAGCTCGTTGT	0.572	
+	10	2302	SD7B_uc002tvb.2	NM_001080427	NP_001073896				7	GTATATCGGCAA	0.373	
+	12	4410	BD5_uc002two.2_	NM_018328	NP_060798	Q9P267	MBD5_HUMAN		5	TGTCAGTGCGG	0.512	
-	6	1184	_p.P227T|MMADH	NM_015702	NP_056517	Q9H3L0	MMAD_HUMAN		2	TGATGGGTCAA	0.328	
-	54	7621		NM_004543	NP_004534	P20929	NEBU_HUMAN	Nebulin 66.	20	CTCACATCACTC	0.299	
-	3	511	f.1_Missense_Mu	NM_004525	NP_004516	P98164	LRP2_HUMAN	s A 2.|Extracellular (Potenti	29	TTGACGTTCAT	0.478	rs138682237
+	11	1079	2uhe.1_Missense_	NM_001378	NP_001369	Q13409	DC1I2_HUMAN	WD 1.	1	AGATGCCCCTC	0.398	
+	11	1081	2uhe.1_Missense_	NM_001378	NP_001369	Q13409	DC1I2_HUMAN	WD 1.	1	ATGCCCCTCAT	0.403	
-	10	1256	.2_Missense_Mut	NM_004882	NP_004873	Q86X95	CIR1_HUMAN	r-rich (RS domain).	1	TTCTCCGGCTC	0.522	
+	4	905	umj.3_Splice_Sit	NM_001042702	NP_001036167	Q0ZLH3	PJVK_HUMAN		0	TGCGGGTAAAC	0.438	
-	301	90916	26L|TTN_uc010zf	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	CTTCTGGACTG	0.507	
-	42	10108	_uc010zfj.1_Miss	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	AAAGCGTGTAT	0.468	
-	6	1060	1_Missense_Mutation_p.R279W|TTN_uc010zfj.1_Miss			Q8WZ42	TITIN_HUMAN		153	CTGCCGAGCCA	0.587	rs138060032
-	62	11626	ti.3_Missense_M	NM_018897	NP_061720	Q8WXX0	DYH7_HUMAN		12	GGCTTGGGTAG	0.398	
-	35	5758		NM_018897	NP_061720	Q8WXX0	DYH7_HUMAN		12	GTATTTCGAGTT	0.358	rs13034775
+	14	1368	1_5'UTR|AOX1_u	NM_001159	NP_001150	Q06278	ADO_HUMAN		6	AGTGGGAATTT	0.483	
+	31	5155	zs.3_Nonsense_	NM_001114132	NP_001107604	Q6ZS30	NBEL1_HUMAN		2	AAAATCAGGAT	0.393	
-	3	459		NM_006891	NP_008822	P07320	CRGD_HUMAN	crystallin 'Greek key' 3.	0	GAAGCGGTCCT	0.567	
-	8	1272	ZF2_uc010fuw.2_	NM_016260	NP_057344	Q9UKS7	IKZF2_HUMAN		0	TGCTAATGGGT	0.502	

-	44	4901		NM_000092	NP_000083	P53420	CO4A4_HUMAN	le-helical region.	11	CCCTCCTGCCA	0.512	
+	1	1058		NM_152614	NP_689827	Q53QW1	CB057_HUMAN		1	GGTGGGAAGCG	0.662	
-	9	4402	p.A766T|COL6A3_	NM_004369	NP_004360	P12111	CO6A3_HUMAN	.|Nonhelical region.	18	GTCTGCGTTCC	0.607	rs112181324
-	6	816	pv.1_Missense_M	NM_198216	NP_937859	P14678	RSMB_HUMAN	eat-rich region.|	1	TTCCCGGAGGG	0.607	
+	8	899	w.1_Missense_Mu	NM_080751	NP_542789	Q8TDI7	TMC2_HUMAN	ellular (Potential).	3	GCCTCGGGCTG	0.428	
+	4	1212	zrf.1_Missense_M	NM_014962	NP_055777	Q9Y2F9	BTBD3_HUMAN		3	TTGTGGTTTTTG	0.443	
+	11	1051	2woz.2_Missense_	NM_080676	NP_542407	A1Z1Q3	MACD2_HUMAN	Glu-rich.	0	ACGGTCCAGAG	0.413	
+	5	2248	.S553L|ZNF133_	NM_003434	NP_003425	P52736	ZN133_HUMAN		2	AACCTTCGGATT	0.502	rs148089989
-	1	157		NM_001322	NP_001313	P09228	CYTT_HUMAN		0	GTGAAGGGCAC	0.592	
+	5	688	341_uc010geq.2_	NM_032819	NP_116208	Q9BYN7	ZN341_HUMAN		2	CAGTGCTGCTG	0.562	
+	14	1577	p.R421Q|ITCH_u	NM_031483	NP_113671	Q96J02	ITCH_HUMAN	ed for interaction with FYN.	6	CACACGAATTA	0.398	
+	2	216	0zvv.1_Missense_	NM_030877	NP_110517	Q8WYA6	CTBL1_HUMAN		2	CTATCGGGAAG	0.517	
+	19	2393	we.1_Missense_M	NM_182811	NP_877963	P19174	PLCG1_HUMAN		8	TCAACGAGGAG	0.557	
-	2	300	gj.2_Missense_M	NM_007050	NP_008981	O14522	PTPRT_HUMAN	lar (Potential).|MAM.	20	AGTTGCTGTAG	0.507	
+	3	596	1_Missense_Mutat	NM_024034	NP_076939	Q96MZ0	GD1L1_HUMAN	ST C-terminal.	1	AGTACGCCACG	0.597	
-	2	337		NM_001080472	NP_001073941	Q8N6M3	FITM2_HUMAN	lasmic (Potential).	2	AGTTGGTGAGG	0.567	
+	2	559	G2_uc010ggz.2_I	NM_003007	NP_002998	P04279	SEMG1_HUMAN		2	TGTGGGTTCAT	0.438	
+	25	3427	zyf.1_Missense_	NM_006420	NP_006411	Q9Y6D5	BIG2_HUMAN		4	TGTCCGCTGGC	0.502	rs151045115
+	5	1032	xn.1_Missense_M	NM_001033521	NP_001028693	Q05048	CSTF1_HUMAN	WD 4.	1	TGTACGTAACTG	0.398	rs140246355
-	7	761		NM_002772	NP_002763	P98073	ENTK_HUMAN	lar (Potential).|CUB 1.	8	GTTTTGGATAAT	0.368	
+	3	359	se_Mutation_p.K8	NM_001186	NP_001177	O14867	BACH1_HUMAN	BTB.	2	ACAGTTAAAGGA	0.318	
-	1	610		NM_001085455	NP_001078924	Q3LI83	KR241_HUMAN	]- [NRTS]-[SNTG]-X-[QHR	0	CTGTTGGAAATA	0.418	
-	21	4197	AM_uc002yyr.1_	NM_001389	NP_001380	O60469	DSCAM_HUMAN	III 4.|Extracellular (Potentia	11	GTTGGGAATTC	0.488	
-	13	1918	p.P175L|C2CD2_	NM_015500	NP_056315	Q9Y426	CU025_HUMAN		1	CTGGCGGGGCA	0.687	
+	21	2720	_5'Flank|C21orf3	NM_005049	NP_005040	Q15269	PWP2_HUMAN		1	AGTTTCCAAGC	0.577	
-	4	639	ef.2_Missense_M	NM_015259	NP_056074	O75144	ICOSL_HUMAN	Potential).|Ig-like C2-type.	0	GTACACGTTGG	0.577	
+	15	2305	pt.1_Missense_M	NM_003307	NP_003298	O94759	TRPM2_HUMAN	lasmic (Potential).	3	AGGACGAAGAG	0.627	rs150593294
+	5	601	11aga.1_Missense	NM_206962	NP_996845	P55345	ANM2_HUMAN	with RB1 (By similarity).	1	GGACACGTGGC	0.557	
-	1	1033		NM_014406	NP_055221	Q96SF2	TCPQM_HUMAN		1	GGGCCGTTGCT	0.502	rs147789853
-	6	1189	4_uc010gqs.1_3'	NM_001037814	NP_001032903	Q2WGN9	GAB4_HUMAN		2	CATGGGCACAC	0.562	
-	2	702	2zqh.2_Missense_	NM_024627	NP_078903	Q7L3V2	CV029_HUMAN		0	CCCAGGAGACG	0.637	
+	2	501	IR1306_hsa-mir-	NM_022720	NP_073557	Q8WYQ5	DGCR8_HUMAN	nd retention.|Necessary for	0	TGGACGTTGGC	0.597	
+	2	1147	R1_uc002zwt.2_I	NM_002073	NP_002064	P19086	GNAZ_HUMAN	(By similarity).	2	TGGGGGGGCAG	0.572	
+	8	1025	2A11_uc002zyo.3_	NM_001024938	NP_001020109	Q9BYW1	GTR11_HUMAN	ellular (Potential).	1	AAGCGAAGATCC	0.642	
+	9	2747	_p.V814I|CYTSA_	NM_015330	NP_056145	Q69YQ0	CYTSA_HUMAN		0	ATGCCGTTGAG	0.438	rs139167350
-	13	2507	sense_Mutation_p	NM_012143	NP_036275	Q9UBB9	TFP11_HUMAN		0	CCGGTTCATGAT	0.463	
-	11	1188_1189	n_p.K416E|CHEK	NM_007194	NP_009125	O96017	CHK2_HUMAN	rotein kinas73E(2)|p.S372	20	AATCTTGGAGTG	0.416	470496;rs146546850
+	14	2143	_Mutation_p.R698	NM_006932	NP_008863	P53814	SMTN_HUMAN		3	GGGGCGCGGC	0.687	rs141334834
-	4	1082		NM_015715	NP_056530	Q9NZ20	PA2G3_HUMAN		0	GCTTGGACCCT	0.672	
-	8	817	ion_p.R87C|BPIL	NM_174932	NP_777592	Q8NFQ6	BPIL2_HUMAN		2	GCTGCGTTCTG	0.488	rs149674580
+	4	1254		NM_138435	NP_612444	Q8NEG4	FA83F_HUMAN		1	GCCCCCCGTGG	0.657	
+	2	269	_Site_p.Q18_splic	NM_017590	NP_060060	Q9UGR2	Z3H7B_HUMAN		1	ATTCAGTAAGCC	0.592	
-	33	5283	p.T518M|PLXNB2_	NM_012401	NP_036533	O15031	PLXB2_HUMAN	lasmic (Potential).	6	GCTCCGTGCGC	0.622	
+	22	4337	p.R893K|SHANK3	NM_001080420	NP_001073889	F2Z3L0	F2Z3L0_HUMAN		1	CTTCAGGGACC	0.682	
+	14	1774	_p.P518L|CNTN4_	NM_175607	NP_783200	Q8IWV2	CNTN4_HUMAN	like C2-type 6.	7	TTTACCGTGCC	0.423	
-	2	386		NM_198560	NP_940962	Q7Z7J7	LHPL4_HUMAN	ical; (Potential).	3	GATGGCGAAGC	0.627	
+	4	698	.1_Missense_Mut	NM_000060	NP_000051	P43251	BTD_HUMAN	N hydrolase.	0	ATGTCGTGTTC	0.458	

-	11	3581	_p.Q648*|SATB1_	NM_002971	NP_002962	Q01826	SATB1_HUMAN			4	CTGCTGCTGTG	0.483	
+	13	2073		NM_178862	NP_849193	Q8TCJ2	STT3B_HUMAN			0	ATTCGGGTAAGA	0.383	
+	2	2024		NM_001137674	NP_001131146	A6NHJ4	ZN860_HUMAN	2H2-type 10.		1	CTTCCGTCACA	0.403	rs143925165
+	11	1475	e_Mutation_p.S40	NM_015442	NP_056257	Q9H9A5	CNOTA_HUMAN			2	GACTTCTGAAC	0.313	
+	3	847	10hiv.1_Missense_	NM_031200	NP_112477	P51686	CCR9_HUMAN	Name=5; (Potential).		3	GTCATGGCTTG	0.493	
+	12	2292	010hjy.2_5'UTR|T	NM_130384	NP_569055	Q8WXE1	ATRIP_HUMAN			1	TGCCGGGGGTC	0.607	
-	8	846	_Mutation_p.R234	NM_004567	NP_004558	Q16877	F264_HUMAN	-2,6-bisphosphatase.		1	GCCCCGAGGGG	0.652	
-	16	2295	e_Mutation_p.E80	NM_006677	NP_006668	O94966	UBP19_HUMAN	lasmic (Potential).		7	TACTTCGCTCG	0.542	
-	8	1082	MT_uc003cwy.2_M	NM_000481	NP_000472	P48728	GCST_HUMAN			1	GCCTCCGCTGC	0.597	
+	6	10538		NM_003458	NP_003449	Q9UPA5	BSN_HUMAN			8	GGAGCGACTTC	0.642	
-	14	1940		NM_003335	NP_003326	P41226	UBA7_HUMAN			2	CAGAAGCTGCA	0.617	
+	53	5661		NM_004947	NP_004938	Q8IZD9	DOCK3_HUMAN			0	TGGACGGCAGC	0.617	
+	3	378	.3_Intron|IQCF2_	NM_203424	NP_982248	Q8IXL9	IQCF2_HUMAN	IQ 2.		0	TGTGGCGTGTC	0.597	rs140755124
-	12	1585	_p.R363W|PCBP4_	NM_033010	NP_127503	P57723	PCBP4_HUMAN			0	CTGCCGCTCAG	0.652	
-	16	2140	on_p.R710*|PBRM	NM_181042	NP_060635	Q86U86	PB1_HUMAN	Bromo 5.	p.R710fs*13(1)	140	GACTTCGAATTT	0.438	
+	3	358	n_p.A2V|PRKCD_	NM_006254	NP_006245	Q05655	KPCD_HUMAN	C2.		9	CATGGCGCCGT	0.687	
-	12	1553	7_uc003dkv.1_Mis	NM_198463	NP_940865	Q6ZVT6	CC067_HUMAN			0	CTCTTTTAGATC	0.438	rs144152554
+	5	1365	BO2_uc011bgj.1_	NM_002942	NP_002933	Q9HCK4	ROBO2_HUMAN	3.|Extracellular (Potential).		11	AAGAAGCTGTAG	0.403	
-	3	1133		NM_016206	NP_057290	A8MV65	VGLL3_HUMAN			0	GGATGGATCCA	0.473	
-	6	492	.24_uc003dvi.1_3'	NM_000986	NP_000977	P83731	RL24_HUMAN			0	GGGGAGCTGAA	0.358	rs1804331
-	6	991		NM_018010	NP_060480	Q9NWB7	IFT57_HUMAN			3	GTTGCGGTAGT	0.383	
+	18	4100	_p.S1230L|PHLD	NM_001134438	NP_001127910	Q86SQ0	PHLB2_HUMAN	PH.		6	CCCATCGCCAG	0.423	
-	4	1126	BTB20_uc003ebl.	NM_015642	NP_056457	Q9HC78	ZBT20_HUMAN			5	AGGCCGGGGCT	0.617	
+	7	2821	ew.3_Missense_M	NM_000388	NP_000379	P41180	CASR_HUMAN	Name=6; (Potential).		7	TCATCGTCTGG	0.527	
+	60	8988	k.2_Missense_Mu	NM_001024660	NP_001019831	O60229	KALRN_HUMAN			6	CTCCCGCCTAG	0.552	
+	2	344	_p.D39G|ROPN1	NM_001012337	NP_001012337	Q9BZX4	ROP1B_HUMAN	RIIa.		0	GGCCGAGTACG	0.632	
+	28	5054	jh.2_Missense_Mu	NM_032242	NP_115618	Q9UIW2	PLXA1_HUMAN	lasmic (Potential).		3	CACACCGGGGC	0.632	
+	14	2857	_uc003epw.1_Intr	NM_001063	NP_001054	P02787	TRFE_HUMAN	ansferrin-like 2.		2	ATGAGTGGAGT	0.507	
-	13	2043	eqb.3_Missense_	NM_005630	NP_005621	Q92959	SO2A1_HUMAN	ellular (Potential).		1	CTCGCCTCCCC	0.607	
+	1	964	C22D2_uc003exx	NM_014779	NP_055594	O75157	T22D2_HUMAN			1	ACACAGCAGTA	0.617	
-	4	1891		NM_178822	NP_849144	Q6WRI0	IGS10_HUMAN	like C2-type 2.		13	ATATTCTTAATGT	0.413	
-	17	2090	_p.S656F|DHX36_	NM_020865	NP_065916	Q9H2U1	DHX36_HUMAN			1	TTATGGAGAGT	0.338	
-	6	1091	_p.V272L|PLCH1_	NM_001130960	NP_001124432	Q4KWH8	PLCH1_HUMAN			4	CAAGAACATTTTT	0.289	
-	14	2231	49_uc011bpd.1_	NM_178824	NP_849146	Q8IV35	WDR49_HUMAN			3	TCTGGTTCTTTC	0.433	
-	4	1064	1bpt.1_Intron|uc0	NM_020949	NP_066000	Q8TBB6	S7A14_HUMAN			5	CCAGCCGTGGG	0.502	
-	7	998	C39_uc003fkn.2_	NM_181426	NP_852091	Q9UFE4	CCD39_HUMAN			4	TGCCGTTCTAC	0.358	
+	4	749_750	tation_p.17_18W	NM_004721	NP_004712	O43283	M3K13_HUMAN			3	ACTTGGGAAGTG	0.525	
-	23	2671	4_uc010hzi.2_Spl	NM_032279	NP_115655	Q4VNC1	AT134_HUMAN			2	GAGCCTGAAAG	0.468	
+	20	4085	A_uc011bvm.1_M	NM_003704	NP_003695	P78312	F193A_HUMAN			3	GACCCGACAAA	0.507	
-	10	5032	dr.1_Missense_Mu	NM_148894	NP_683692	Q8NFC6	BOD1L_HUMAN			6	TGGCTTCGATTT	0.468	
-	2	281		NM_005130	NP_005121	Q14512	FGFP1_HUMAN			0	GTTCCCGGGCC	0.493	
+	10	1436	xs.1_Missense_Mu	NM_018323	NP_060793	Q8TCG2	P4K2B_HUMAN	PI3K/PI4K.		4	GAGACGGGAAG	0.408	
+	8	978	grn.3_Nonsense_	NM_024936	NP_079212	Q9H5U6	ZCHC4_HUMAN			2	TTTCTGGATTTTC	0.338	
+	5	1249	_p.R205C|KLHL5_	NM_015990	NP_057074	Q96PQ7	KLHL5_HUMAN			1	GGGTCCGTCAT	0.388	
-	31	3141	p.G196E|ATP8A1_	NM_006095	NP_006086	Q9Y2Q0	AT8A1_HUMAN	ellular (Potential).		3	CATTTCCAAATG	0.398	
+	4	745		NM_001080476	NP_001073945	A8MXD5	GRCR1_HUMAN			1	TTTCTTCCATGC	0.478	
-	8	1149	zr.1_Missense_Mu	NM_022832	NP_073743	P62068	UBP46_HUMAN			1	GAAGCCGTGAC	0.363	

-	3	735	3haf.3_Missense_I	NM_001126328	NP_001119800	Q8TBB1	LNX1_HUMAN		4	GGGAGGGAGCC	0.607	
+	1	54	ihe.2_Missense_M	NM_006947	NP_008878	O76094	SRP72_HUMAN		1	CGGCGGCAGCG	0.632	
-	14	2661	ah.1_Missense_Mi	NM_004439	NP_004430	P54756	EPHA5_HUMAN	Potential).|Protein kinase.	24	GTACCCGGGAA	0.428	
-	1	348	'2A3_uc010ihp.1_I	NM_024743	NP_079019	Q6UWM9	UD2A3_HUMAN	cellular (Potential).	2	TAACTGATTGCC	0.348	
-	2	833	_p.W126*|UGT2B4	NM_021139	NP_066962	P06133	UD2B4_HUMAN		2	AAAATCCCAGTAC	0.423	
-	4	463	se_Mutation_p.V1	NM_000583	NP_000574	P02774	VTDB_HUMAN	Albumin 1.	3	GTGAACGGGGA	0.493	
-	27	5236	hgq.2_Missense_I	NM_032217	NP_115593	O75179	ANR17_HUMAN		10	TTGCTACTGTTA	0.383	
+	2	331		NM_015393	NP_056208	Q6UWI2	PARM1_HUMAN	cellular (Potential).	1	GTTTCTCTTCCG	0.473	
-	10	1190	_p.R348Q|RASGE	NM_152545	NP_689758	Q0VAM2	RGF1B_HUMAN	Ras-GEF.	0	GCTGTTCGATAA	0.343	
+	13	1911	ej.1_Missense_Mu	NM_000253	NP_000244	P55157	MTP_HUMAN	Vitellogenin.	4	ACAATCCATCCTA	0.413	
-	2	369	nk.1_Missense_Mu	NM_021833	NP_068605	P25874	UCP1_HUMAN	Solcar 1.	1	GGACCGTGTCG	0.577	rs143645398
+	7	691	_p.H108Y|IL15_uc	NM_000585	NP_000576	P40933	IL15_HUMAN		0	AGTATTCATGATA	0.363	
+	6	1619	nh.2_Missense_Mu	NM_001130067	NP_001123539	Q9C040	TRIM2_HUMAN	NHL 1.	1	ATTTGATCTTTCG	0.537	
-	8	1437	F1_uc010iqw.1_Int	NM_138386	NP_612395	Q96HR8	NAF1_HUMAN		2	GATTATTTTGTCT	0.383	
-	7	1003	on_p.R261H|DDX6	NM_001012967	NP_001012985	Q5H9U9	DDX6L_HUMAN		1	GAACACGCTGG	0.398	
+	5	1359	Dirr.2_Missense_M	NM_014269	NP_055084	Q9UKF5	ADA29_HUMAN	2B.|Extracellular (Potential).	16	TTGTTAATATAGT	0.333	
-	7	1129	zk.1_Missense_Mu	NM_173553	NP_775824	Q8N7C3	TRIMM_HUMAN	B30.2/SPRY.	2	TGTCTCCATTTGC	0.458	
+	3	349	RIO_uc011cna.1_M	NM_007118	NP_009049	O75962	TRIO_HUMAN	CRAL-TRIO.	18	TGTATTCCCAGG	0.453	
+	2	451	nd.1_Missense_Mu	NM_004932	NP_004923	P55285	CADH6_HUMAN	p.G42A(1)	7	TCTCTGGAAACA	0.493	
+	20	5301	m.2_Missense_Mu	NM_178140	NP_835260	O15018	PDZD2_HUMAN		9	CACTCCGAGAG	0.582	
+	10	1366		NM_032637	NP_116026	Q13309	SKP2_HUMAN		4	GTATTTTTGTATG	0.328	
+	32	6361	kk.3_Splice_Site_p	NM_133433	NP_597677	Q6KC79	NIPBL_HUMAN		9	CAAAACGTGAGT	0.318	
-	3	580	MB_uc011cpy.1_Mi	NM_198449	NP_940851	Q6PCB8	EMB_HUMAN	Potential).|Ig-like V-type 1.	0	TATTCTCAAGTTG	0.368	
+	17	3393	p.V1044I|BDP1_uc	NM_018429	NP_060899	A6H8Y1	BDP1_HUMAN	E-M-E-T-D-L-K-X-T-G-R- E-	2	AGAGAAGTATCC	0.458	
-	2	134	se_Mutation_p.D31	NM_015566	NP_056381	Q9Y6X4	F169A_HUMAN		0	AGGGTCCCCAC	0.383	
-	10	1414	p.P289L|POC5_uc	NM_001099271	NP_001092741	Q8NA72	POC5_HUMAN		1	TCGGAGGAGCT	0.507	
+	3	750	_p.V132I|VCAN_uc	NM_004385	NP_004376	P13611	CSPG2_HUMAN	g-like V-type.	16	TGTGACGTCATG	0.522	
-	3	321	kp.2_Missense_M	NM_001145678	NP_001139150	Q8IV33	K0825_HUMAN		0	CTCCAGGAAATG	0.308	
+	20	2667	kks.2_Missense_M	NM_032290	NP_115666	Q9BQI6	ANR32_HUMAN	ANK 2.	2	TGCAACGTTGTC	0.458	
+	4	381	81B_uc010jbe.1_5	NM_152548	NP_689761	Q96LP2	FA81B_HUMAN		2	GAGAGGTCAGC	0.502	
-	15	1551	3kpp.1_Missense_	NM_022140	NP_071423	Q9HCS5	E41LA_HUMAN		1	CTGGGAGAATTG	0.512	
-	19	2915	3krv.3_Missense_M	NM_020796	NP_065847	Q9H2E6	SEM6A_HUMAN	lasmic (Potential).	2	GTTGCCGGGAG	0.612	
-	52	7010		NM_001999	NP_001990	P35556	FBN2_HUMAN	36; calcium-binding.	15	ATCCGTCGGTGT	0.413	
+	8	1832	kuz.2_Missense_M	NM_014031	NP_054750	Q9Y2P4	S27A6_HUMAN		0	GGACCGTACTGC	0.373	
+	6	1014	yj.1_Intron|WNT8A_	NM_058244	NP_490645	Q9H1J5	WNT8A_HUMAN		4	ACTGCGCACGCT	0.512	
+	12	1926	yo.1_Missense_Mu	NM_005733	NP_005724	O95235	KI20A_HUMAN	Kinesin-motor.	0	GAGGCCGTTCCT	0.488	
+	1	1445	CDHA7_uc003lhq.2	NM_018904	NP_061727	Q9Y5I0	PCDAD_HUMAN	|Extracellular (Potential).	6	GGACGCGGACG	0.667	
+	1	2159		NM_018940	NP_061763	Q9Y5E2	PCDB7_HUMAN	|Extracellular (Potential).	6	GCTCCTGGTGG	0.706	
+	1	713	l_Intron|PCDHGB4	NM_003735	NP_003726	O60330	PCDGC_HUMAN	r (Potential).|Cadherin 2.	4	CTCATCGTGCAA	0.582	
+	6	1408	uc010jgf.2_Missen	NM_001130029	NP_001123501	Q8NC24	RELL2_HUMAN		0	TGGCTCCCCCA	0.642	
-	12	3187	p.R559Q|SH3TC2	NM_024577	NP_078853	Q8TF17	S3TC2_HUMAN	TPR 4.	2	GGTTCCGATAAA	0.557	rs140666774
+	4	766	EL2_uc011dca.1_3	NM_152407	NP_689620	Q8TAA5	GRPE2_HUMAN		1	TTGCCCGAGTG	0.512	
+	5	842	_p.S228F|PPARGC	NM_133263	NP_573570	Q86YN6	PRGC2_HUMAN		0	GGACTCCCTAG	0.672	
-	21	2615		NM_000440	NP_000431	P16499	PDE6A_HUMAN		2	TGGCCGACTGC	0.408	
-	20	2956	F1R_uc010jhc.2_R	NM_005211	NP_005202	P07333	CSF1R_HUMAN	lasmic (Potential).	54	CACCCGCTCTC	0.632	
+	5	805	.A225T|GALNT10_	NM_198321	NP_938080	Q86SR1	GLT10_HUMAN	main A.|Lumenal (Potential	2	TGGGGGCCTCA	0.542	
-	4	649		NM_032782	NP_116171	Q8TDQ0	HAVR2_HUMAN	cellular (Potential).	0	ATCAGGGAGGCT	0.333	

+	7	989	_p.P174L|GABRA	NM_000806	NP_000797	P14867	GBRA1_HUMAN	ellular (Probable).	3	ACTTCCCTATGG	0.378	rs138145692
-	36	4917	.2_Missense_Mut	NM_003062	NP_003053	O75094	SLIT3_HUMAN	CTCK.	4	CACTGGAAGAC	0.637	
+	13	2372_2373		NM_133369	NP_588610	Q6ZN44	UNC5A_HUMAN	lasmic (Potential).	1	ATCACCAAGGT	0.658	
-	15	1591	03mhm.2_Missens	NM_016222	NP_057306	Q9UJV9	DDX41_HUMAN	case C-terminal.	0	GCGCCCGGTGC	0.607	
-	3	982	lm.1_Missense_M	NM_018434	NP_060904	Q86XS8	GOLI_HUMAN	ellular (Potential).	3	AGCCACGGCTG	0.383	
-	5	655	P2L_uc011dim.1_	NM_004752	NP_004743	O75603	GCM2_HUMAN		3	TTCTGCCTAGA	0.398	
+	3	265	49L|SLC17A4_uc	NM_005495	NP_005486	Q9Y2C5	S17A4_HUMAN		1	ATTTTTCAATTTA	0.478	
+	1	27		NM_001732	NP_001723	Q13410	BT1A1_HUMAN		2	ATGGCAGTTTTC	0.547	
+	18	1890	se_Mutation_p.P5	NM_001025091	NP_001020262	Q8NE71	ABCF1_HUMAN		2	AGGCCCCTGAG	0.562	
+	3	260	2B_uc003nvs.1_	NM_021221	NP_067044	Q8NDX9	LY65B_HUMAN	UPAR/Ly6.	0	CAACACCTACT	0.532	
-	6	1008	.2_Intron|C6orf27_	NM_025258	NP_079534	Q9Y334	G7C_HUMAN		3	CCCTCGGTGGC	0.602	
+	7	1141	Missense_Mutatio	NM_000063	NP_000054	P06681	CO2_HUMAN	VWFA.	2	TGAGCGTTGCC	0.517	
-	2	1000	_5'Flank|ATF6B_	NM_022110	NP_071393	Q9UIM3	FKBPL_HUMAN		0	TGGGGGTAAAG	0.592	
+	7	730_731	FL8_uc003oac.1_	NM_030652	NP_085155	Q99944	EGFL8_HUMAN	Potential.	0	AGCGGCTGGA	0.619	
+	5	398	WDR46_uc010juo.	NM_014260	NP_055075	O15212	PFD6_HUMAN		0	AGCTTCGGGAT	0.547	
+	58	8169	f125_uc003oez.1_	NM_002224	NP_002215	Q14573	ITPR3_HUMAN	lasmic (Potential).	19	TAGATGACGGA	0.617	
+	8	1100	D2_uc011dtv.1_5'U	NM_173558	NP_775829	Q7Z6J4	FGD2_HUMAN		3	CCTCGAGGACG	0.632	
-	5	634_635		NM_006653	NP_006644	O43559	FRS3_HUMAN		2	TCGAGGGAGGT	0.475	
+	8	870	_uc003orv.1_Miss	NM_138572	NP_612639	Q7Z7C8	TAF8_HUMAN		1	TGTCGGGTAGC	0.537	
-	6	862	b.2_Missense_Mu	NM_023932	NP_076421	Q6UY11	DLK2_HUMAN	GF-like 6; calcium-binding	0	GGCGGCTGGCA	0.612	
+	2	354	vx.1_Missense_M	NM_152732	NP_689945	Q9H1X1	RSPH9_HUMAN		2	TCATACGAATATG	0.527	rs150021750
-	7	2039	f.1_Missense_Mu	NM_021073	NP_066551	P22003	BMP5_HUMAN		2	TTCTATATTTTTT	0.343	
+	5	615	pje.2_Missense_M	NM_000056	NP_000047	P21953	ODBB_HUMAN		0	TATCCGGTCCC	0.483	rs79761867
-	3	657	pou.2_Missense_	NM_001143957	NP_001137429	Q9BZJ6	GPR63_HUMAN	ellular (Potential).	2	TCACGGTCAAG	0.433	
+	2	462		NM_021620	NP_067633	Q9H4Q3	PRD13_HUMAN	SET.	0	GAGTGGATAGG	0.617	
-	3	526	vt.2_Missense_M	NM_001105206	NP_001098676	Q16363	LAMA4_HUMAN		9	GGTGTGAAAGA	0.423	
+	4	664	_p.R79H|FAM26D_	NM_153036	NP_694581	Q5JW98	FA26D_HUMAN		0	ACATCCGCATTC	0.463	
+	9	954		NM_002269	NP_002260	O15131	IMA5_HUMAN	ARM 5.	4	CAGACGTGTGT	0.408	
+	2	472		NM_175057	NP_778227	Q96RI9	TAAR9_HUMAN	Name=4; (Potential).	0	TTTCCTGGTTCT	0.423	
+	12	1915		NM_020340	NP_065073	Q5TH69	BIG3_HUMAN	SEC7.	2	TAGCCGATGAA	0.567	rs147532213
+	3	1305	e_Mutation_p.T37	NM_015093	NP_055908	Q9NYJ8	TAB2_HUMAN		0	AAATACGGATG	0.493	
-	6	554	03qrb.2_Translati	NM_032861	NP_116250	Q96JX3	SRAC1_HUMAN		0	CTTCCGTAGGA	0.453	rs148861818
+	6	1120	qtd.2_Missense_M	NM_003057	NP_003048	O15245	S22A1_HUMAN	lasmic (Potential).	0	TGTTCCGCACG	0.592	
+	8	1725	p.R437W|HEATR	NM_017802	NP_060272	Q86Y56	HEAT2_HUMAN		1	TGGAGCGGGTG	0.637	
+	2	1291	ense_Mutation_p.	NM_001098201	NP_001091671	Q99527	GPER_HUMAN	ellular (Potential).	1	CCATGCCCACC	0.622	
-	8	1075	27_uc003smh.3_	NM_152743	NP_689956	Q6PJG6	BRAT1_HUMAN		0	GTCTGCCGTCC	0.682	
-	25	3818		NM_032415	NP_115791	Q9BXL7	CAR11_HUMAN	ylate kinase-like.	50	CCGATCTTGTC	0.647	
-	1	1967	DIL_uc011jwd.1_I	NM_020144	NP_064529	Q9NRJ5	PAPOB_HUMAN		1	GTGAGGAATAC	0.453	
-	2	263	on.3_Missense_M	NM_024963	NP_079239	Q96ME1	FXL18_HUMAN	F-box.	3	CTTCCGACAGG	0.527	
+	6	1625		NM_138426	NP_612435	Q86VQ1	GLCI1_HUMAN		0	AGGAGCGCAGC	0.537	rs145682662
-	18	3960		NM_015204	NP_056019	Q9UPZ6	THS7A_HUMAN	.|Extracellular (Potential).	3	GCCTTCTCACT	0.413	
+	13	1837	76_splice|ABCB5_	NM_178559	NP_848654	Q2M3G0	ABCB5_HUMAN		6	TTTATAAGATAGC	0.333	
-	2	1102	c003szc.1_5'Flan	NM_000522	NP_000513	P31271	HXA13_HUMAN	Homeobox.	1	TTCGTCGTGGCT	0.433	
+	11	1153		NM_016616	NP_057700	Q8N427	TXND3_HUMAN		3	AAGCCCAGGTT	0.448	
-	4	514		NM_032014	NP_114403	Q96EL2	RT24_HUMAN		0	TTGGAGGTGGA	0.478	
-	6	831	tron|POLM_uc003	NM_013284	NP_037416	Q9NP87	DPOLM_HUMAN		3	CACACCGACCC	0.602	
-	17	2375	g.2_Missense_M	NM_033054	NP_149043	B0I1T2	MYO1G_HUMAN		4	GTCTCCGGAAC	0.677	

-	8	1094	sense_Mutation_p	NM_033054	NP_149043	B0I1T2	MYO1G_HUMAN	osin head-like.	4	GGGGTGTGGCC	0.647	
+	11	1993		NM_021116	NP_066939	Q08828	ADCY1_HUMAN		6	TCACCCGGGTC	0.552	
-	8	1329_1330	c.2_Missense_Mu	NM_015198	NP_056013	O75128	COBL_HUMAN		5	CCTGCGGGGCT	0.629	
+	1	1880		NM_003508	NP_003499	O00144	FZD9_HUMAN	lasmic (Potential).	1	GGGCCCGGGCC	0.657	
+	20	1275	ELN_uc003tzr.2_I	NM_000501	NP_001075224	P15502	ELN_HUMAN	Ala-rich.	5	GCATTCCTACTT	0.627	
+	6	880		NM_001099435	NP_001092905	A6NIY4	SPDE5_HUMAN		0	GCGTCGGTTCC	0.587	
-	6	561	z.1_Missense_Mu	NM_005338	NP_005329	O00291	HIP1_HUMAN		8	TTCTCCAGCCT	0.552	
+	2	1463	.E120K|GRM3_uc	NM_000840	NP_000831	Q14832	GRM3_HUMAN	cellular (Potential).	13	TGGATGAAGCT	0.433	
-	15	1844	_p.R590*|ABCB4_	NM_018849	NP_061337	P21439	MDR3_HUMAN	1.|Cytoplasmic (By similarit	6	CAGTCGGTGTG	0.488	
+	4	989		NM_019004	NP_061877	Q9P2G1	AKIB1_HUMAN		1	TCTCACGGGAT	0.368	
+	18	1399	1A2_uc011kib.1_I	NM_000089	NP_000080	P08123	CO1A2_HUMAN		9	CCAAGGGTGCT	0.453	rs72656391
-	7	807	_p.A206S|SLC25	NM_014251	NP_055066	Q9UJS0	CMC2_HUMAN		4	AGCAGCCTCAA	0.308	
-	6	1131	e_Mutation_p.R23	NM_032924	NP_116313	P17036	ZNF3_HUMAN	2H2-type 3.	1	TCCTCCGATGC	0.498	
+	4	494	lgt.2_Intron|GATS_	NM_024070	NP_076975	Q6DKI7	PVRIG_HUMAN	ical; (Potential).	2	AGGGACCCCGG	0.637	
+	16	3566	AN_uc003uwl.2_	NM_003386	NP_003377	Q9Y493	ZAN_HUMAN	xtracellular (Potential).	11	TGGGACACACA	0.617	
+	3	4732	C17_uc010lho.1_	NM_001040105	NP_001035194	Q685J3	MUC17_HUMAN	ich.|59 X approximate tand	27	TGACGGTACCA	0.488	
+	3	12373	C17_uc010lho.1_	NM_001040105	NP_001035194	Q685J3	MUC17_HUMAN	cellular (Potential).	27	CCCCACGGTGA	0.537	rs150141937
-	10	1287	_uc003var.2_RNA	NM_145032	NP_659469	Q8NEE6	FXL13_HUMAN	LRR 3.	0	GCATCGTCCTG	0.463	
-	55	9102	.2_Missense_Mut	NM_005045	NP_005036	P78509	RELN_HUMAN	BNR 14.	19	CATCGGTAGAG	0.527	
-	52	5968	fw.2_Missense_M	NM_014705	NP_055520	Q8N1I0	DOCK4_HUMAN	Pro-rich.	4	GGGGCGGAGTC	0.711	
-	1	162		NM_002711	NP_002702	Q16821	PPR3A_HUMAN		34	AACCTCGTCTA	0.378	
+	6	745	R_uc011knq.1_5'	NM_000492	NP_000483	P13569	CFTR_HUMAN	tial).|ABC transmembrane	5	TCGCTCCTTTG	0.473	rs121908803
-	2	2083		NM_005302	NP_005293	O15354	GPR37_HUMAN	lasmic (Potential).	3	CCCTCGGGTAC	0.433	
-	11	1259	nse_Mutation_p.	NM_018077	NP_060547	Q9NW13	RBM28_HUMAN	RRM 3.	2	GAACTGGGCAA	0.448	
-	31	5721	qz.3_Missense_	NM_020911	NP_065962	Q9HCM2	PLXA4_HUMAN	lasmic (Potential).	1	GGTATGCGTTC	0.507	
-	15	3086		NM_020911	NP_065962	Q9HCM2	PLXA4_HUMAN		1	AGTGTCTGTGT	0.617	
-	15	1860		NM_004333	NP_004324	P15056	BRAF_HUMAN	rotein kinas _R603>I(2)|p.T	18290	ATTTCACTGTA	0.368	
-	3	750	xc.3_Missense_M	NM_001001317	NP_001001317	Q8IYP2	PRS58_HUMAN	eptidase S1.	0	GATATCACACA	0.433	
+	23	3014	tc.1_Missense_M	NM_000083	NP_000074	P35523	CLCN1_HUMAN	smic (By similarity).	5	CCTGCGATCCA	0.617	
+	1	796		NM_001004685	NP_001004685	O95006	OR2F2_HUMAN	ellular (Potential).	4	CTGGTCCCTCA	0.493	
+	12	1482_1483	d.1_Missense_Mu	NM_007188	NP_009119	Q9NUT2	ABCB8_HUMAN		3	TGCGTCCCCAA	0.649	
+	16	1907	3wpt.2_Missense	NM_014629	NP_055444	O15013	ARHGA_HUMAN	DH.	1	CACTAGCAGAG	0.483	
+	10	1280		NM_016353	NP_057437	Q9UIJ5	ZDHC2_HUMAN		0	TTTCCAACTTGC	0.373	rs2904682
-	3	1848	.2_Missense_Mut	NM_005144	NP_005135	O43593	HAIR_HUMAN		2	GCCGCGTGGA	0.662	
-	7	482	_p.E81K|BIN3_uc	NM_018688	NP_061158	Q9NQY0	BIN3_HUMAN	AR.|Potential.	0	CTGTTCCCGCC	0.612	
-	9	1143		NM_003844	NP_003835	O00220	TR10A_HUMAN	lasmic (Potential).	6	AGTGGGGTCAG	0.532	
-	1	834	fe.1_Missense_M	NM_000680	NP_000671	P35348	ADA1A_HUMAN	smic (By similarity).	5	GGTAGCGCAGC	0.617	
+	3	497	ense_Mutation_p.	NM_001135726	NP_001129198	Q6NT76	HMBX1_HUMAN		1	GGACCGTCTTG	0.438	
-	6	3688	3xkn.1_Missense_	NM_001002814	NP_001002814	Q6WKZ4	RFIP1_HUMAN	FIP-RBD.	3	TCCGAGGGGCT	0.448	
+	2	272	2L_uc003xku.3_5'	NM_004674	NP_004665	Q9UBL3	ASH2L_HUMAN		2	TAAGCGGTGGC	0.343	
-	7	1312	xrf.3_Missense_M	NM_014781	NP_055596	Q8TDY2	RBCC1_HUMAN		11	AAGATTCGTTAG	0.418	rs140425456
+	2	605	.1_Missense_Mut	NM_006269	NP_006260	P56715	RP1_HUMAN		12	GCCCCCCACGG	0.692	
-	11	1481	r.3_Missense_Mu	NM_020361	NP_065094	Q8N4T0	CBPA6_HUMAN		2	TGGGAGTAAAA	0.428	
+	39	4771		NM_024870	NP_079146	Q70Z35	PREX2_HUMAN		17	TGGGAGTCAGA	0.478	
-	3	393	ALB1_uc011lge.1_	NM_004929	NP_004920	P05937	CALB1_HUMAN	EF-hand 2.	1	TTTTTCCATCATC	0.289	
+	55	10130	iw.2_Missense_M	NM_017890	NP_060360	Q7Z7G8	VP13B_HUMAN		20	GCAGGTTGTGT	0.398	
+	16	2600	R1_uc010mch.2_	NM_018002	NP_060472	Q8N573	OXR1_HUMAN	TLD.	0	AATTTGCGCTTT	0.323	

-	2	1111		NM_139166	NP_631905	Q8N0Z2	ABRA_HUMAN	with actin (By similarity).	2	GGCACGCATGA	0.453	
+	5	3023	p.G281S|FAM83A	NM_032899	NP_116288	Q86UY5	FA83A_HUMAN	Ser-rich.	4	TCAGCGGCCGC	0.741	
+	9	1053		NM_001039112	NP_001034201	Q2WGJ9	FR1L6_HUMAN	toplasmic (Potential).	11	TTGTGGAGGTC	0.493	
+	3	1274	kx.1_Missense_M	NM_198572	NP_940974	Q76KD6	SPERI_HUMAN		2	ACCTCGTACCT	0.622	
+	2	70	K5_uc003zcg.2_	NM_174922	NP_777582	Q3MIX3	ADCK5_HUMAN		1	AGGTGCAGCTC	0.582	
-	2	398	f82_uc003zqb.2_5	NM_024828	NP_079104	Q9H8G2	CI082_HUMAN		0	CAGTCAGGTCC	0.343	
-	1	2962	uc003zrh.1_5'Flan	NM_153809	NP_722516	Q8IZX4	TAF1L_HUMAN		26	AGCAATGAAGG	0.473	
-	6	1009	ense_Mutation_p.A	NM_033655	NP_387504	Q9BZ76	CNTP3_HUMAN	otential).|Laminin G-like 1.	1	CAGGAGCAATA	0.498	
+	13	1340	b.1_RNA|TMC1_u	NM_138691	NP_619636	Q8TDI8	TMC1_HUMAN	ellular (Potential).	1	AATTGGATGGA	0.403	
-	8	2869		NM_015225	NP_056040	Q8WUY3	PRUN2_HUMAN		0	ATCTACCTTTTC	0.398	
-	1	357		NM_016848	NP_058544	Q92529	SHC3_HUMAN		4	CGACCGATGTC	0.562	
+	7	1643	.2_Missense_Mut	NM_006648	NP_006639	Q9Y3S1	WNK2_HUMAN		12	CTGGCCCGCGC	0.647	
+	2	227	axl.1_Missense_	NM_003275	NP_003266	P28289	TMOD1_HUMAN		0	CAGACGAGAAC	0.473	rs141454774
-	11	1543	nuc.1_Missense_	NM_001080398	NP_001073867				0	AGAGCGGAGGA	0.413	
-	3	417	4bjg.2_Missense_	NM_005118	NP_005109	O95150	TNF15_HUMAN	ellular (Potential).	0	CTTACCTGTCA	0.438	
+	54	7209	_p.E2346K|SPTAN	NM_003127	NP_003118	Q13813	SPTA2_HUMAN	EF-hand 2.	10	AAGGGGAACCT	0.567	
+	11	1306	wz.2_Intron|FAM7	NM_032809	NP_116198	Q7L4E1	FA73B_HUMAN		1	TCTTCGGGAAA	0.582	
+	5	1165		NM_006059	NP_006050	Q9Y6N6	LAMC3_HUMAN	inin EGF-like 2.	3	CTGCCGTGACC	0.637	rs45505601
+	18	2063	w.2_Missense_Mu	NM_007171	NP_009102	Q9Y6A1	POMT1_HUMAN		1	TCCGACGGCGA	0.428	rs150899645
-	5	618	TPD2_uc004ckx.	NM_203468	NP_982293	Q9Y5L3	ENTP2_HUMAN	ellular (Potential).	0	CCACCGGCCCA	0.677	
+	6	1104	la.3_Missense_M	NM_207309	NP_997192	Q3KQV9	UAP1L_HUMAN		1	TGGCTGTGAAG	0.532	
-	7	854	py.1_Missense_M	NM_004192	NP_004183	O95671	ASML_HUMAN		0	GAGTGGGCTCC	0.706	
-	2	2156	ED1_uc004cqh.1_	NM_004729	NP_004720	O96006	ZBED1_HUMAN		0	CACTCCGGGCG	0.672	
+	12	2514	id.1_Missense_M	NM_001830	NP_001821	P51793	CLCN4_HUMAN	smic (By similarity).	5	GCGGCGCATCC	0.592	
+	3	1158		NM_016562	NP_057646	Q9NYK1	TLR7_HUMAN	ar (Potential).|LRR 12.	5	TCTCCCCAGCC	0.398	
-	6	1334	v.2_Nonsense_Mu	NM_002641	NP_002632	P37287	PIGA_HUMAN	lasmic (Potential).	0	CAGTCGTTTGT	0.483	
-	28	3808	.1_3'UTR|PDHA1_	NM_001001671	NP_001001671	Q6ZN16	M3K15_HUMAN		7	GCAGCCGCAAC	0.408	
+	1	119	_5'Flank|MAGEB	NM_002367	NP_002358	O15481	MAGB4_HUMAN		1	TGCCCGTGAGA	0.572	
-	5	685	h.1_Missense_M	NM_006307	NP_006298	P78539	SRPX_HUMAN	HYR.	0	ACACCCGGACT	0.433	rs111307887
-	13	1681		NM_004229	NP_004220	O60244	MED14_HUMAN	EBF1.|Interaction with ST	4	TTATCGTAGGC	0.368	
+	14	2438	512H|DDX3X_uc	NM_001356	NP_001347	O00571	DDX3X_HUMAN	case C-terminal.	6	ACATCGTATTGG	0.373	
-	4	293	_p.L67F|SSX3_u	NM_021014	NP_066294	Q99909	SSX3_HUMAN	RAB-related.	0	TGGGAGGATGG	0.353	
+	4	504	dmu.2_Missense_	NM_024859	NP_079135	Q9H6Y5	MAGIX_HUMAN	PDZ.	0	TGGCCGTGCGC	0.632	
-	42	4992	nip.2_Missense_M	NM_005183	NP_005174	O60840	CAC1F_HUMAN	ic (Potential).|Poly-Glu.	6	gcccctcttcttcctcctc	0.383	
-	29	3606	nip.2_Missense_M	NM_005183	NP_005174	O60840	CAC1F_HUMAN	smic (Potential).|IV.	6	ACACACGATACT	0.562	
+	1	132		NM_198512	NP_940914	Q6ZPD8	DG2L6_HUMAN		1	GGAGGGCCTCC	0.463	
-	1	1962	a.1_Intron|RGAG4	NM_001024455	NP_001019626	Q5HYW3	RGAG4_HUMAN		3	CTGTGCGGCGA	0.587	
-	29	6830	.R2262C|ODZ1_u	NM_014253	NP_055068	Q9UKZ4	TEN1_HUMAN	tracellular (Potential).	23	GACACGTCGCC	0.448	
+	5	650	p.D139N|MST4_u	NM_016542	NP_057626	Q9P289	MST4_HUMAN	rotein kinase.	9	CATTTGATGAG	0.343	
+	5	2930	nwr.1_Missense_	NM_032539	NP_115928	Q9H156	SLIK2_HUMAN	lasmic (Potential).	7	ACGCCGAAAGG	0.428	rs147278885
+	3	1123		NM_005364	NP_005355	P43361	MAGA8_HUMAN	MAGE.	0	CATTTCCTACC	0.577	rs45578531
+	2	110	myi.1_Missense_	NM_007150	NP_009081	O15231	ZN185_HUMAN		3	AATAACGTTCTC	0.582	
-	8	2180	.R548W|PDZD4_u	NM_032512	NP_115901	Q76G19	PDZD4_HUMAN		1	CAGCCGATCTC	0.677	
+	13	2695		NM_017514	NP_059984	P51805	PLXA3_HUMAN	Extracellular (Potential).	3	CCCCCGCATCA	0.667	
+	22	4071		NM_017514	NP_059984	P51805	PLXA3_HUMAN	lasmic (Potential).	3	ACTACCGGACT	0.627	
+	17	2494	p.E690K|SCNN1	NM_002978	NP_002969				0	CAGCCGAAGAG	0.672	
+	5	986	_p.E245D|DFFB_	NM_004402	NP_004393	O76075	DFFB_HUMAN		0	CCGGAAGGCTG	0.672	

+	20	2657	p.P816S|PIK3CD_	NM_005026	NP_005017	O00329	PK3CD_HUMAN	PI3K/PI4K.		7	GCCTCCCCACC	0.602	
-	5	367	p.V103A|C1orf127	NM_173507	NP_775778	B7ZLG7	B7ZLG7_HUMAN			1	ATGTGAACTAAG	0.502	
-	1	373	0obf.1_Missense_	NM_001146181	NP_001139653	B7ZW38	B7ZW38_HUMAN			0	GCGTTTCCTCGG	0.483	
+	4	436	_Mutation_p.G119	NM_004070	NP_004061	P51800	CLCKA_HUMAN			1	CTCTGGAGGTG	0.602	
+	7	1662	p.R353H|PAX7_u	NM_002584	NP_002575	P23759	PAX7_HUMAN			203	GAGCCCGCCACA	0.667	
-	6	582	plice_Site_p.G109_	NM_003760	NP_003751	O43432	IF4G3_HUMAN			1	GCGTTCCTAAAA	0.428	
+	1	480	uc010ofi.1_RNA	NM_006142	NP_006133	P31947	1433S_HUMAN			0	GCCACCGGTGAC	0.622	
+	3	700	BTB8A_uc001bvm.	NM_001040441	NP_001035531	Q96BR9	ZBT8A_HUMAN	BTB.		0	CTTTCTCCCCTG	0.423	
-	3	402_403	bw.3_Missense_M	NM_001099439	NP_001092909	Q5JZY3	EPHAA_HUMAN	cellular (Potential).		8	TGAACTGCAGTT	0.614	
+	1	311		NM_001008740	NP_001008740	Q7Z6W1	TMCO2_HUMAN			1	GGAAACGAAGTA	0.323	
-	8	960	1cim.2_Nonsense_	NM_006824	NP_006815	Q99848	EBP2_HUMAN			0	AGCCTTTCTTCT	0.488	
+	2	189	ciy.2_Missense_M	NM_001255	NP_001246	Q12834	CDC20_HUMAN			0	GGCAGCGCAAA	0.692	
+	9	1138		NM_178134	NP_835235	Q86W10	CP4Z1_HUMAN	enal (Potential).		1	GCACCGGTAGTA	0.473	
-	27	2854		NM_015306	NP_056121	Q9UPU5	UBP24_HUMAN			13	GGCTGGATCAG	0.348	
+	42	5452	ADL_uc009wag.2_	NM_176877	NP_795352	Q8NI35	INADL_HUMAN			4	TACCACCTTGGT	0.443	
+	6	1003		NM_032437	NP_115813	A8K855	EFCB7_HUMAN			0	TGTCAGCAACC	0.378	
-	3	185		NM_000329	NP_000320	Q16518	RPE65_HUMAN			1	CCACATCGAAGG	0.522	rs61751282
-	8	490	te_p.I74_splice|SL	NM_152697	NP_689910	Q8NCS7	CTL5_HUMAN			4	ACAGATCTGTGA	0.378	
-	2	767	ebv.1_Missense_M	NM_004980	NP_004971	Q9UK17	KCND3_HUMAN	lasmic (Potential).		3	TAGAAGTTGAGC	0.612	
-	3	435		NM_002524	NP_002515	P01111	RASN_HUMAN	GTP.	)|p.Q61P(21)|	2607	CTTCTTGTCCAG	0.458	rs121913254
+	2	370	p.G114E|CD2_uc	NM_001767	NP_001758	P06729	CD2_HUMAN	-3 (CD58) binding region 2.		1	CAAAAGGAAAAA	0.308	
-	3	644_645	MGCS2_uc001eie.	NM_005518	NP_005509	P54868	HMCS2_HUMAN			2	TAGACGGCAATG	0.475	
-	32	6161		NM_024408	NP_077719	Q04721	NOTC2_HUMAN	nic (Potential).|ANK 4.		27	CACATCCGCTTG	0.527	
-	5	660		NR_024442						0	CAGATGCTCAG	0.498	
+	3	401	68S|ECM1_uc001	NM_004425	NP_004416	Q16610	ECM1_HUMAN			3	GCCCTCCCTTT	0.572	
-	2	3473	e.1_Missense_Mu	NM_007113	NP_009044	Q07283	TRHY_HUMAN	30 AA tandem repeats.		5	TTCTCCGGTTCC	0.174	rs113946258
-	3	528		NM_001122965	NP_001116437	Q6XPR3	RPTN_HUMAN	Gln-rich.		0	GGGAATCTCTGT	0.517	
-	4	1527		NM_006617	NP_006608	P48681	NEST_HUMAN	Tail.		6	GCCAAGGAGGCA	0.627	
+	13	1561	p.V201A|NTRK1_	NM_002529	NP_002520	P04629	NTRK1_HUMAN	lasmic (Potential).		17	CAGGTGTTCACC	0.567	
-	36	4743	p.T651A|ARHGEF	NM_014784	NP_055599	O15085	ARHGB_HUMAN			9	GGGTGTCAGGT	0.637	
-	7	1468	hw.1_Missense_M	NM_031281	NP_112571	Q96RD9	FCRL5_HUMAN	otential).|Ig-like C2-type 4.		6	GTCAGAGAGAAG	0.582	
+	3	714	1C_uc001frv.2_5'U	NM_001765	NP_001756	P29017	CD1C_HUMAN	cellular (Potential).		4	TAGATTTACTGAC	0.478	
+	6	1254	.L95F|CD1E_uc00	NM_030893	NP_112155	P15812	CD1E_HUMAN			3	AACATTCTTTCTC	0.328	
+	5	890	sz.1_Missense_Mu	NM_001004310	NP_001004310	Q6DN72	FCRL6_HUMAN	3.|Extracellular (Potential).		3	GTGTCTCCAGAG	0.557	
-	7	963	R254*|NR1I3_uc00	NM_001077480	NP_001070948	Q14994	NR1I3_HUMAN			2	GTTTTCGTAGTG	0.527	rs144211465
+	4	673	gbp.2_Missense_M	NM_007240	NP_009171	Q9UNI6	DUS12_HUMAN			1	CAAGTGTAGAA	0.318	
-	12	2869	u.1_Missense_Mu	NM_003285	NP_003276	Q92752	TENR_HUMAN	nectin type-III 7.		11	TGATTTCGTATT	0.532	
+	7	1744	_Mutation_p.P472	NM_005807	NP_005798	Q92954	PRG4_HUMAN	epeats of K-X-P-X-P-T-T-X		1	CCACTCCCAAG	0.637	
+	8	4116_4117		NM_032890	NP_116279	Q96F81	DISP1_HUMAN			0	GTCGAGGGCTTT	0.564	
+	2	541	C1_uc010pwr.1_M	NM_018662	NP_061132	Q9NRI5	DISC1_HUMAN	ction with MAP1A.		1	GGCAGCCTGCA	0.642	
+	8	1174_1175	G251K|MTR_uc01	NM_000254	NP_000245	Q99707	METH_HUMAN	Hcy-binding.		3	CTCATGGAGAAC	0.465	
+	6	1175	W3_uc001idp.1_In	NM_015431	NP_056246	Q8NG06	TRI58_HUMAN	B30.2/SPRY.		7	CGCCATCTCCTG	0.567	
+	3	356		NM_175911	NP_787107	Q8N349	OR2LD_HUMAN	cellular (Potential).		4	AATCACACTTCA	0.289	
+	7	1054		NM_052997	NP_443723	Q9BXX3	AN30A_HUMAN			9	CGTGGCCAGCA	0.423	
+	2	187	F4_uc009xmn.2_	NM_032023	NP_114412	Q9H2L5	RASF4_HUMAN			1	GCAAGTCCATTC	0.537	
+	3	383	N2_uc010qfq.1_5'	NM_014696	NP_055511	O60269	GRIN2_HUMAN			0	GGCGCGACCCA	0.697	rs149580948
+	7	889	p.A267V|HK1_uc0	NM_000188	NP_000179	P19367	HXK1_HUMAN	Regulatory.		1	GGGAGCCTTTG	0.522	

-	2	418		NM_022146	NP_071429	Q9GZQ6	NPFF1_HUMAN	lasmic (Potential).	0	ACCTTTCCACAG	0.572
-	12	1412	_p.S405F|GPAM_u	NM_020918	NP_065969	Q9HCL2	GPAT1_HUMAN		2	TTTAAGGAAAATG	0.443
+	4	317	PRP1_uc001lcn.2_	NM_006229	NP_006220	P54315	LIPR1_HUMAN		2	CAAAGGAGATG	0.478
+	1	427		NM_001001480	NP_001001480	Q701N2	KRA55_HUMAN	repeats of C-C-X-P.	1	GCTGTGGCTCCT	0.692
-	2	263		NR_001589					0	CGAAGGAGATC	0.493
+	2	674	08T|OLFML1_uc0	NM_198474	NP_940876	Q6UWY5	OLFL1_HUMAN	Potential.	2	GAGAGGCTGAC	0.473
+	17	2930		NM_006108	NP_006099	Q9HCB6	SPON1_HUMAN	TSP type-1 6.	0	caagaaggagatcag	0.234
+	10	1713	_p.S482N|CRY2_u	NM_021117	NP_066940	Q49AN0	CRY2_HUMAN		1	CTGGCAGCATGA	0.567
+	1	825		NM_001001955	NP_001001955	Q8NGP0	OR4CD_HUMAN	Name=7; (Potential).	4	CACTATGATAACT	0.363
-	1	94		NM_001005272	NP_001005272	Q8NH83	OR4A5_HUMAN	Name=1; (Potential).	3	AGTATGTGAGTA	0.433
+	2	1367		NM_004111	NP_004102	P39748	FEN1_HUMAN		1	GAGCCGCCAAG	0.547
+	20	4241	g.2_Missense_Mu	NM_002335	NP_002326	O75197	LRP5_HUMAN	ical; (Potential).	7	CGGGCCCGTCA	0.602
+	13	2488	uc001pen.1_Intron	NM_001098672	NP_001092142	Q6MZM0	HPHL1_HUMAN	e 5.|Extracellular (Potential	3	AAATTGGATTGG	0.423
+	14	2047	e_p.E570_splice|	NM_014361	NP_055176	O94779	CNTN5_HUMAN		8	AAAGGTAAGAC	0.378
+	3	974	gv.2_Missense_M	NM_001130145	NP_001123617	P46937	YAP1_HUMAN	WW 1.	3	AGGACCCCAGG	0.483
-	25	3829	zda.1_RNA|NCA	NM_015261	NP_056076	P42695	CNDD3_HUMAN		5	GGGGAACTTGT	0.443
-	2	916		NM_020634	NP_065685	Q9NR23	GDF3_HUMAN		6	CTCCATGGCAGT	0.527
+	5	840	1467_uc009zhx.1_	NM_020853	NP_065904	A2RU67	K1467_HUMAN		3	GGTGTTCGAGAC	0.448
-	6	576	GDIB_uc001rcp.1_	NM_001175	NP_001166	P52566	GDIR2_HUMAN		0	AACTGGAGTGA	0.522
+	1	61		NM_012404	NP_036536	O95626	AN32D_HUMAN	LRR 1.	2	GTGAAAGAACTT	0.458
-	1	194	_p.S59A|KRT8_uc	NM_002273	NP_002264	P05787	K2C8_HUMAN	ead.|Ser-rich.	2	GCGGGAACCGG	0.662
-	13	1477	A5_uc010sow.1_	NM_002205	NP_002196	P08648	ITA5_HUMAN	tential).|Potential.|FG-GAP	2	GGATATCCATTG	0.562
+	2	275	1_5'UTR|PDE1B_	NM_000924	NP_000915	Q01064	PDE1B_HUMAN	lin-binding (Potential).	2	CTTCGGTCTCTG	0.637
+	1	402		NM_054105	NP_473446	Q9NZP2	OR6C2_HUMAN	lasmic (Potential).	2	CATCATGAACAA	0.453
+	2	756	H4_uc009zpj.2_5'	NM_007224	NP_009155	O95158	NXPH4_HUMAN	(linker domain).	0	GCTGGGGATGG	0.756
+	3	432	m.2_Missense_Mu	NM_006812	NP_006803	Q13438	OS9_HUMAN	PRKCSH.	1	GTTATGGACGC	0.433
-	4	1826	sqx.2_Missense_	NM_178539	NP_848634	Q8N3H0	F19A2_HUMAN		1	ATTCTTCTCCCT	0.413
+	12	1734	yu.2_Splice_Site_	NM_001135805	NP_001129277	P21579	SYT1_HUMAN		6	CTTTCAGAAAGT	0.453
+	35	4540		NM_014503	NP_055318	O75691	UTP20_HUMAN		4	ATTAAAGAAATG	0.318
-	7	1477	pi.1_Missense_Mu	NM_021625	NP_067638	Q9HBA0	TRPV4_HUMAN	lasmic (Potential).	4	CACTTGTCCCGC	0.607
+	4	771	_p.Q180*|RNFT2_	NM_001109903	NP_001103373	Q96EX2	RNFT2_HUMAN	cellular (Potential).	0	TGCTTTCAGCAT	0.637
+	2	556	uc001txf.2_Intron	NM_178499	NP_848594	Q8IWA6	CCD60_HUMAN		3	CATCAGGTCCC	0.443
+	7	1042	D2_uc001udy.1_M	NM_024623	NP_078899	Q6N063	OGFD2_HUMAN		1	AGGAGCCCGCC	0.657
+	66	11390	H10_uc001ufu.3_5	NM_207437	NP_997320	Q8IVF4	DYH10_HUMAN		6	AACTTTGGGCAA	0.453
+	7	793	F3_uc001uqw.2_I	NM_006646	NP_006637	Q9UPY6	WASF3_HUMAN	Potential.	1	CCACCCGTGAG	0.468
-	11	3143	p.E829K|TRPC4_	NM_016179	NP_057263	Q9UBN4	TRPC4_HUMAN	and ITPR3.|Cytoplasmic (P	6	AATCTTCGTGGG	0.433
-	14	3347	_Mutation_p.E99	NM_000053	NP_000044	P35670	ATP7B_HUMAN	lasmic (Potential).	3	GGCCTCCGCAG	0.627
-	1	797		NM_001004714	NP_001004714	Q8NH42	OR4KD_HUMAN	cellular (Potential).	2	CTACCGAGTATC	0.383
-	8	721_722	p.1_Missense_Mu	NM_002471	NP_002462	P13533	MYH6_HUMAN	osin head-like.	4	CTGGTCCTCCAG	0.609
-	11	1799	.D470N|RALGAP	NM_014990	NP_055805	Q6GYQ0	RGPA1_HUMAN		4	CATGGTCTGTGA	0.343
+	4	1684	ny.1_Missense_Mu	NM_054024	NP_473365	Q96PC5	MIA2_HUMAN		2	AAGAAACTGGAG	0.308
+	4	1376	1_splice|MUDEN	NM_018229	NP_060699	Q9H0R1	MUDEN_HUMAN		1	CTTTTTAGGTCC	0.294
-	2	810		NM_005982	NP_005973	Q15475	SIX1_HUMAN		0	TGTTCTCCCTAA	0.428
-	13	2508	YVE26_uc001xkc.	NM_015346	NP_056161	Q68DK2	ZFY26_HUMAN		11	CTTGTACTTTCCA	0.453
+	5	499	0asq.1_Missense_	NM_020431	NP_065164	Q9P1W3	TM63C_HUMAN		0	AGACTTCCTTGG	0.517
-	91	14028	bi.2_Missense_Mu	NM_004667	NP_004658	O95714	HERC2_HUMAN	HECT.	13	TCAAATTCATGG	0.532
+	17	2709	_Mutation_p.G58	NM_001013703	NP_001013725	Q9P2K8	E2AK4_HUMAN	otein kinase 2.	4	CAGACAGGAGAC	0.353

-	8	1406	.2_5'UTR|CDAN1_	NM_138477	NP_612486	Q8IWY9	CDAN1_HUMAN		2	GAGACAGCTTGA	0.458	
-	19	4139	.G1336R|TP53BP	NM_005657	NP_005648	Q12888	TP53B_HUMAN		7	CTTTCCCTGAGC	0.572	
+	5	773	M202_uc002aur.2_	NM_001080462	NP_001073931	A6NGA9	TM202_HUMAN		2	TGGAATCTCTAA	0.458	
+	10	1821	_Mutation_p.E56	NM_002499	NP_002490	Q92859	NEO1_HUMAN	tential).|Fibronectin type-III	1	GTGGGAAACAC	0.438	
-	17	1874	utation_p.N17K|u	NR_027024					0	CAGCAGATTCAC	0.622	
+	5	2017		NM_198526	NP_940928	Q8N1W2	ZN710_HUMAN		1	GACTTCGAGGAG	0.577	
+	9	1988	p.2_Missense_Mut	NR_003659					0	GAGAAGAAGCAG	0.662	rs141089280
-	3	506	3_uc002cmu.2_M	NM_080861	NP_543137	Q6PJ21	SPSB3_HUMAN	B30.2/SPRY.	0	TAGACGGGAGAG	0.662	
-	6	868	rz.1_Missense_M	NM_022119	NP_071402	Q9GZN4	BSSP4_HUMAN	Peptidase S1.	1	GCGCTCGGCAC	0.721	
-	15	3227_3228	vw.2_Missense_M	NM_004380	NP_004371	Q92793	CBP_HUMAN		127	GGATCGGGCTC	0.599	rs144649776
-	13	4336	G1263E|GRIN2A_	NM_001134407	NP_001127879	Q12879	NMDE1_HUMAN	lasmic (Potential).	45	GCTCCCCGGTG	0.522	
+	3	1212	gb.3_Missense_Mu	NM_001105248	NP_001098718	Q6UXY8	TMC5_HUMAN	ellular (Potential).	1	CCAGATCATTTTG	0.493	rs148290322
+	6	807	me.2_Missense_M	NM_212535	NP_997700	P05771	KPCB_HUMAN	C2.	9	CCCGATCCCAAA	0.423	
+	2	1614		NM_014699	NP_055514	O15015	ZN646_HUMAN		2	CAGCTCCCCTGC	0.602	
+	35	7605	p.P2466S|CHD9_u	NM_025134	NP_079410	Q3L8U1	CHD9_HUMAN	ds A/T-rich Dp.I2481fs*71(1	7	GGAATTCCTGAT	0.388	
-	13	1670	p.Q533*|CDH16_u	NM_004062	NP_004053	O75309	CAD16_HUMAN	r (Potential).|Cadherin 5.	3	CACTCTGCACCA	0.637	
+	1	2620	LEKHG4_uc010ce	NM_015432	NP_056247	Q58EX7	PKHG4_HUMAN		2	AGTTTCAGGAT	0.597	
-	4	882	gq.2_Missense_M	NM_018124	NP_060594	Q6PCD5	RFWD3_HUMAN		3	GTTTGGGGAGGG	0.279	
-	35	5723	.1_5'UTR|PKD1L2	NM_052892	NP_443124	Q7Z442	PK1L2_HUMAN	lasmic (Potential).	3	GCATAGGGGTCT	0.572	
+	3	462	hg.1_Missense_M	NM_002661	NP_002652	P16885	PLCG2_HUMAN	PH.	8	ACTCAGTTCGTC	0.498	
-	13	1281	p.T396M|CAMKK	NM_172206	NP_757343	Q8N5S9	KKCC1_HUMAN	rotein kinase.	1	ATTCTCGTCTCG	0.567	
+	2	992		NM_153230	NP_694962	Q8N4B4	FBX39_HUMAN		2	TGAACGGATCAT	0.542	
-	3	617		NM_031898	NP_114104	Q9BXF9	TEKT3_HUMAN		2	GATTTTGGGTTG	0.393	
+	6	696	p.D115G|MAP2K3	NM_145109	NP_659731	P46734	MP2K3_HUMAN	rotein kinase.	0	TCATGGACACAT	0.567	
+	30	4186	rt.2_Missense_Mu	NM_003170	NP_003161	Q7KZ85	SPT6H_HUMAN	SH2.	3	GAGAACCACCTG	0.517	
+	1	1431	p.H392Y|LRRC37	NM_052888	NP_443120	Q96QE4	LR37B_HUMAN	ellular (Potential).	2	GCTCCTCATCCA	0.522	
+	13	1263	nse_Mutation_p.R	NM_006804	NP_006795	Q14849	STAR3_HUMAN	ytoplasmic (Potential).	0	TGTCCGGTGAG	0.617	rs140920637
-	6	1050		NM_181537	NP_853515	Q7Z3Y8	K1C27_HUMAN	Rod.|Coil 2.	0	AGTTACTCTCGG	0.522	
-	10	3464	ron|BRCA1_uc01	NM_007294	NP_009225	P38398	BRCA1_HUMAN		52	ATTTTGGCCCTC	0.373	
+	20	3131	.1_Missense_Mut	NM_004941	NP_004932	Q14562	DHX8_HUMAN		4	TTCTATAGGCCC	0.473	
+	17	2226	_Mutation_p.D25	NM_005892	NP_005883	O95466	FMNL_HUMAN	FH2.	1	ATGAGTGATTTTG	0.597	
+	6	1241	c002irv.1_Missens	NM_018896	NP_061496	O43497	CAC1G_HUMAN	r (Potential).|Poly-Gly.|I.	1	GCGCGGGGACG	0.617	
-	13	1728	tf.2_Missense_Mu	NM_001130528	NP_001124000	O60271	JIP4_HUMAN	Potential.	5	CCATTTCTACTC	0.413	
-	2	553	AG9_uc002itd.2_M	NM_001130528	NP_001124000	O60271	JIP4_HUMAN	Potential.	5	AAGTCCTTTTTTT	0.313	
+	1	259	2P1_uc002ivn.2_5	NM_012374	NP_036506	Q15615	OR4D1_HUMAN	ellular (Potential).	1	TTCCTCCATGAG	0.512	
-	4	732_733	1_RNA|MRPL38_	NM_032478	NP_115867	Q96DV4	RM38_HUMAN		1	GACTCGGGGCA	0.609	
+	4	688	ent_p.R164R|TMC	NM_152468	NP_689681	Q8IU68	TMC8_HUMAN	lasmic (Potential).	0	CCTCTTCGGCAC	0.692	
-	9	1633	n.1_Missense_Mu	NM_001792	NP_001783	P19022	CADH2_HUMAN	r (Potential).|Cadherin 3.	4	TCTCAGGAACTT	0.483	
-	5	416	2lft.2_Missense_M	NM_001143829	NP_001137301	Q9H2F9	CCD68_HUMAN		1	AAGGATCCATTT	0.358	rs148275303
-	8	1221	p.G312R|NETO1_	NM_138966	NP_620416	Q8TDF5	NETO1_HUMAN	ss A.|Extracellular (Potentia	4	GAGTCCATTGC	0.388	
-	1	204	A41_uc010dut.2_	NM_173637	NP_775908	Q8N5S1	S2541_HUMAN	Pro-rich.	0	CAggatgggggtgg	0.408	
+	8	1155	345V|CLEC4M_uc	NM_001144910	NP_001138382	Q9H2X3	CLC4M_HUMAN	(Probable).|C-type lectin.	1	ACTGTGCGGAAT	0.512	
-	4	416	TS10_uc002mkk.1_	NM_030957	NP_112219	Q9H324	ATS10_HUMAN		4	GTGGTCCACGC	0.662	
-	3	25754		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	h.|Extracellular (Potential).	57	AAGGTTGTTGTT	0.502	
-	25	2545	nh.2_Missense_M	NM_001379	NP_001370	P26358	DNMT1_HUMAN	BAH 1.	6	CTGCCCGTTGC	0.582	
+	4	1515	ym.1_Missense_M	NM_001136501	NP_001129973	Q08AG5	ZN844_HUMAN		0	CCTTCAGATCTG	0.423	
+	4	1602	ym.1_Missense_M	NM_001136501	NP_001129973	Q08AG5	ZN844_HUMAN		0	TCATTTTTTCCA	0.448	

-	2	268	on_p.T4I|ZNF709_	NM_152601	NP_689814	Q8N972	ZN709_HUMAN	KRAB.	0	ACAAAGGTTTCTT	0.438	
-	5	841		NM_020714	NP_065765	Q9ULM2	ZN490_HUMAN	C2H2-type 3.	0	GTTTCGAAAGGA	0.423	
-	20	3316	ao.1_Missense_M	NM_000435	NP_000426	Q9UM47	NOTC3_HUMAN	(Potential).|EGF-like 27.	21	CTCACAGTGGCTA	0.657	
+	10	2692	p.S622F|NWD1_uc002nev.3_Missense_Mutation_p.S5			Q149M9	NWD1_HUMAN		7	GGATTTCCTGCCC	0.597	
+	5	1319	_p.K300T|ZNF431_	NM_133473	NP_597730	Q8TF32	ZN431_HUMAN	C2H2-type 8.	2	AACATAAAAGAAT	0.348	
-	1	667	z.1_5'Flank|LGI4_u	NM_139284	NP_644813	Q8N135	LGI4_HUMAN		1	ACTTTCCCTTTGC	0.682	
-	6	2557	p.C508R|ZNF569_	NM_152484	NP_689697	Q5MCW4	ZN569_HUMAN	C2H2-type 18.	3	TGCCACACTCAAT	0.413	
-	4	1888	0_uc002ogq.2_Int	NM_016536	NP_057620	Q7Z3V5	ZN571_HUMAN	C2H2-type 17.	0	GGACATCTAAAGT	0.373	
+	14	1443	poe.2_Missense_M	NM_138392	NP_612401	Q8TBC3	SHKB1_HUMAN	WD 4.	2	GCATGATTTCCAC	0.612	
-	7	1144	n_p.K302N|CARD8	NM_014959	NP_055774	Q9Y2G2	CARD8_HUMAN		0	CATTACTTTCAGC	0.418	
-	1	166		NM_178449	NP_848544	Q96A98	TIP39_HUMAN		0	ACCACcagcagcag	0.597	
+	6	1161		NM_001099694	NP_001093164	Q96N58	ZN578_HUMAN	C2H2-type 3.	0	GCCATCGTAGATC	0.433	
+	4	1386	rdw.1_Missense_M	NM_138374	NP_612383	Q96IR2	ZN845_HUMAN	C2H2-type 8.	0	TCAGATGTCATCC	0.413	
+	5	763	LRA1_uc010yfh.1_	NM_006863	NP_006854	O75019	LIRA1_HUMAN	2.|Extracellular (Potential).	3	GGTGGTCGTACAC	0.572	rs151320443
+	11	1707	e_Mutation_p.G457	NM_006669	NP_006660	Q8NHL6	LIRB1_HUMAN	cellular (Potential).	3	GTCTGGGAAGGC	0.308	
+	3	301	v.1_Missense_Muta	NM_002000	NP_001991	P24071	FCAR_HUMAN	cellular (Potential).	2	CCAAATCGAGTCC	0.498	
+	6	613	p.P152L|NLRP2_u	NM_017852	NP_060322	Q9NX02	NALP2_HUMAN		2	GCTGGCCTGGAG	0.512	
+	17	2241_2242	p.S671F|BRSK1_u	NM_032430	NP_115806	Q8TDC3	BRSK1_HUMAN		6	GCCCCTCCGTCTT	0.639	
+	10	3184	g.2_Missense_Mu	NM_176811	NP_789781	Q86W28	NALP8_HUMAN		13	TCACGGGAAAAAC	0.512	
+	8	1520		NM_016441	NP_057525	Q9NZV1	CRIM1_HUMAN	1.|Extracellular (Potential).	3	GTTGTCGGACCTC	0.398	
-	31	3342	yob.1_Missense_M	NM_133259	NP_573566	P42704	LPPRC_HUMAN	PPR 16.	3	ATGTGGGTCTCCC	0.428	
+	18	1926		NM_032208	NP_115584	Q9H6X2	ANTR1_HUMAN	ic (Potential).|Pro-rich.	4	gccctcccccgcccccc	0.109	
+	7	1806	wf.2_Missense_Mu	NM_212481	NP_997646	Q03989	ARI5A_HUMAN		0	TTTGCCCGGCCT	0.642	
-	6	1623	2tdr.2_Missense_M	NM_001142351	NP_001135823	Q96JF0	SIAT2_HUMAN	enal (Potential).	11	GCAAATCCCCCTC	0.592	
+	3	533	0fki.1_Missense_M	NM_153214	NP_694946	Q53RD9	FBLN7_HUMAN	Sushi.	2	CCCCCGCAGACC	0.542	
+	17	3241	p.S641C|PSD4_uc	NM_012455	NP_036587	Q8NDX1	PSD4_HUMAN		2	CACTCGAGCCCG	0.632	
+	3	731	0flu.2_Missense_M	NM_130773	NP_570129	Q8WYK1	CNTP5_HUMAN	|Extracellular (Potential).	10	AACAAGAAGACA	0.453	
-	17	2777		NM_001099771	NP_001093241	A5A3E0	POTEF_HUMAN	Actin-like.	5	GCAGCTCGTTGTA	0.572	
+	10	2302	ISD7B_uc002tvb.2	NM_001080427	NP_001073896				7	GTATATCGGCAAC	0.373	
-	8	1118		NM_004688	NP_004679	Q13287	NMI_HUMAN		0	ATGCCTTCCATTC	0.353	
-	54	7621		NM_004543	NP_004534	P20929	NEBU_HUMAN	Nebulin 66.	20	CTCACATCACTCC	0.299	
+	11	1079	2uhe.1_Missense_	NM_001378	NP_001369	Q13409	DC1I2_HUMAN	WD 1.	1	AGATGCCCCTCA	0.398	
+	11	1081	2uhe.1_Missense_	NM_001378	NP_001369	Q13409	DC1I2_HUMAN	WD 1.	1	GATGCCCCTCATC	0.403	
-	301	90916	926L|TTN_uc010zf	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	CCTTCTGGACTGT	0.507	
-	42	10108	_uc010zfj.1_Misse	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	AAAAGCGTGTATT	0.468	
-	6	1060	1_Missense_Mutation_p.R279W|TTN_uc010zfj.1_Miss			Q8WZ42	TITIN_HUMAN		153	GCTGCCGAGCCA	0.587	rs138060032
-	62	11626	uti.3_Missense_Mu	NM_018897	NP_061720	Q8WXX0	DYH7_HUMAN		12	GGCTTGGGTAGC	0.398	
-	35	5758		NM_018897	NP_061720	Q8WXX0	DYH7_HUMAN		12	GTATTTCGAGTTC	0.358	rs13034775
+	14	1368	1_5'UTR|AOX1_u	NM_001159	NP_001150	Q06278	ADO_HUMAN		6	CAGTGGGAATTTC	0.483	
+	31	5155	uzs.3_Nonsense_M	NM_001114132	NP_001107604	Q6ZS30	NBEL1_HUMAN		2	GAAAATCAGGATC	0.393	
+	55	8392	p.E1328K|NBEAL1	NM_001114132	NP_001107604	Q6ZS30	NBEL1_HUMAN		2	GAAACTGAATATA	0.378	
-	8	1272	ZF2_uc010fuw.2_M	NM_016260	NP_057344	Q9UKS7	IKZF2_HUMAN		0	CTGCTAATGGGTC	0.502	
-	4	1470	h.1_Missense_Mu	NM_024536	NP_078812	Q8IZ52	CHSS2_HUMAN	enal (Potential).	0	CCCACGCAGTGC	0.672	
+	1	1058		NM_152614	NP_689827	Q53QW1	CB057_HUMAN		1	GGTGGGAAGCG	0.662	
-	9	4402	p.A766T|COL6A3_	NM_004369	NP_004360	P12111	CO6A3_HUMAN	7.|Nonhelical region.	18	GTCTGCGTTCCT	0.607	rs112181324
-	1	263	se_Mutation_p.A12	NM_001122962	NP_001116434	Q5JXA9	SIRB2_HUMAN		0	AGTGGGCCAGG	0.622	
+	11	1051	2woz.2_Missense_	NM_080676	NP_542407	A1Z1Q3	MACD2_HUMAN	Glu-rich.	0	ACGGTCCAGAG	0.413	

-	1	157		NM_001322	NP_001313	P09228	CYTT_HUMAN		0	GTGAAGGGCAC	0.592	
-	2	337		NM_001080472	NP_001073941	Q8N6M3	FITM2_HUMAN	lasmic (Potential).	2	AGTTGGTGAGG	0.567	
-	7	761		NM_002772	NP_002763	P98073	ENTK_HUMAN	lar (Potential).|CUB 1.	8	GTTTTGGATAAT	0.368	
+	3	359	se_Mutation_p.K8	NM_001186	NP_001177	O14867	BACH1_HUMAN	BTB.	2	ACAGTTAAAGGA	0.318	
-	1	610		NM_001085455	NP_001078924	Q3LI83	KR241_HUMAN	]- [NRTS]-[SNTG]-X-[QHR	0	CTGTTGGAAATA	0.418	
-	21	4197	CAM_uc002yyr.1_	NM_001389	NP_001380	O60469	DSCAM_HUMAN	III 4.|Extracellular (Potentia	11	GGTTGGGAATTC	0.488	
+	21	2720	_5'Flank|C21orf33	NM_005049	NP_005040	Q15269	PWP2_HUMAN		1	AGTTTCCAAGC	0.577	
+	15	2305	gpt.1_Missense_M	NM_003307	NP_003298	O94759	TRPM2_HUMAN	lasmic (Potential).	3	AGGACGAAGAG	0.627	rs150593294
+	9	1143	p.G217S|SLC25A1	NM_031481	NP_113669	Q9H1K4	GHC2_HUMAN		0	TCGCCGGTAAG	0.527	
-	2	702	2zqh.2_Missense_	NM_024627	NP_078903	Q7L3V2	CV029_HUMAN		0	CCCAGGAGACG	0.637	
-	4	826	6610_uc011aim.1_	NM_080764	NP_542942	Q86YH2	Z280B_HUMAN		2	TCTTGTATGTTC	0.413	
-	13	2507	sense_Mutation_p	NM_012143	NP_036275	Q9UBB9	TFP11_HUMAN		0	CCGGTTCATGAT	0.463	
-	11	1188_1189	n_p.K416E|CHEK	NM_007194	NP_009125	O96017	CHK2_HUMAN	rotein kinas73E(2)|p.S372	20	AATCTTGGAGTG	0.416	470496;rs146546850
-	4	1082		NM_015715	NP_056530	Q9NZ20	PA2G3_HUMAN		0	GCTTGGACCCT	0.672	
-	10	1490	se_Mutation_p.Q4	NM_003560	NP_003551	O60733	PA2G6_HUMAN		1	ATCCTGTAGTT	0.617	
+	4	1254		NM_138435	NP_612444	Q8NEG4	FA83F_HUMAN		1	GCCCCCCGTGG	0.657	
+	41	5683	R1_uc011asu.1_I	NM_001099952	NP_001093422	Q14643	ITPR1_HUMAN	lasmic (Potential).	21	GTGACCGAGTG	0.547	
+	11	1475	e_Mutation_p.S40	NM_015442	NP_056257	Q9H9A5	CNOTA_HUMAN		2	GACTTCTGAAC	0.313	
+	3	847	10hiv.1_Missense_	NM_031200	NP_112477	P51686	CCR9_HUMAN	Name=5; (Potential).	3	GTCATGGCTTG	0.493	
-	14	1700	csi.1_Nonsense_	NM_001789	NP_001780	P30304	MPIP1_HUMAN	Rhodanese.	5	TCTCTCTCACATA	0.507	
-	16	2140	on_p.R710*|PBR	NM_181042	NP_060635	Q86U86	PB1_HUMAN	Bromo 5. p.R710fs*13(1)	140	ACTTCGAATTT	0.438	
+	3	358	n_p.A2V|PRKCD_	NM_006254	NP_006245	Q05655	KPCD_HUMAN	C2.	9	CATGGCGCCGT	0.687	
-	7	868	_p.A20V|ACTR8_	NM_022899	NP_075050	Q9H981	ARP8_HUMAN		2	AGGTGGCACAC	0.493	
-	23	4446	f63_uc003dic.3_Mi	NM_015224	NP_056039	Q9UK61	CC063_HUMAN		5	TGAATCCAGAG	0.338	
-	12	1553	7_uc003dkv.1_Mis	NM_198463	NP_940865	Q6ZVT6	CC067_HUMAN		0	CTCTTTTAGATC	0.438	rs144152554
+	5	1365	BO2_uc011bgj.1_	NM_002942	NP_002933	Q9HCK4	ROBO2_HUMAN	3.|Extracellular (Potential).	11	AAGAAGCTGTAG	0.403	
-	3	1133		NM_016206	NP_057290	A8MV65	VGLL3_HUMAN		0	GGATGGATCCA	0.473	
-	6	492	24_uc003dvi.1_3'	NM_000986	NP_000977	P83731	RL24_HUMAN		0	GGGGAGCTGAA	0.358	rs1804331
+	9	2863	dyg.2_Nonsense_	NM_001134438	NP_001127910	Q86SQ0	PHLB2_HUMAN		6	GGGGGAAAGG	0.368	
+	18	4100	_p.S1230L|PHLD	NM_001134438	NP_001127910	Q86SQ0	PHLB2_HUMAN	PH.	6	CCCATCGCCAG	0.423	
+	13	2737	_p.G707S|BOC_uc	NM_033254	NP_150279	Q9BWV1	BOC_HUMAN	ellular (Potential).	6	TACAGCGGTCGC	0.622	
+	14	2857	_uc003epw.1_Intr	NM_001063	NP_001054	P02787	TRFE_HUMAN	ansferrin-like 2.	2	ATGAGTGGAGT	0.507	
-	13	2043	eqb.3_Missense_	NM_005630	NP_005621	Q92959	SO2A1_HUMAN	ellular (Potential).	1	CTCGCCTCCCC	0.607	
-	4	1891		NM_178822	NP_849144	Q6WRI0	IGS10_HUMAN	like C2-type 2.	13	ATATTCTTAATGT	0.413	
-	17	2090	_p.S656F|DHX36_	NM_020865	NP_065916	Q9H2U1	DHX36_HUMAN		1	TTATGGAGAGT	0.338	
-	6	1091	_p.V272L|PLCH1_	NM_001130960	NP_001124432	Q4KWH8	PLCH1_HUMAN		4	AAGAACATTTTT	0.289	
-	14	2231	49_uc011bpd.1_	NM_178824	NP_849146	Q8IV35	WDR49_HUMAN		3	TCTGGTTCTTTC	0.433	
-	7	998	C39_uc003fkn.2_	NM_181426	NP_852091	Q9UFE4	CCD39_HUMAN		4	TGCCGTTCTAC	0.358	
+	4	749_750	tation_p.17_18W	NM_004721	NP_004712	O43283	M3K13_HUMAN		3	CTTGGGAAGTG	0.525	
+	8	978	grn.3_Nonsense_	NM_024936	NP_079212	Q9H5U6	ZCHC4_HUMAN		2	TTTCTGGATTTTC	0.338	
-	31	3141	p.G196E|ATP8A1_	NM_006095	NP_006086	Q9Y2Q0	AT8A1_HUMAN	ellular (Potential).	3	CATTTCCAAATG	0.398	
+	4	745		NM_001080476	NP_001073945	A8MXD5	GRCR1_HUMAN		1	TTTCTTCCATGC	0.478	
-	8	1149	zr.1_Missense_M	NM_022832	NP_073743	P62068	UBP46_HUMAN		1	GAAGCCGTGAC	0.363	
-	3	735	haf.3_Missense_	NM_001126328	NP_001119800	Q8TBB1	LNX1_HUMAN		4	GGGAGGGAGCC	0.607	
-	1	348	2A3_uc010ihp.1_	NM_024743	NP_079019	Q6UWM9	UD2A3_HUMAN	ellular (Potential).	2	TAACTGATTGCC	0.348	
-	2	833	_p.W126*|UGT2B4	NM_021139	NP_066962	P06133	UD2B4_HUMAN		2	AAATCCCAGTA	0.423	
+	2	331		NM_015393	NP_056208	Q6UWI2	PARM1_HUMAN	ellular (Potential).	1	TTTCTCTTCCG	0.473	

+	13	1911	ej.1_Missense_Mu	NM_000253	NP_000244	P55157	MTP_HUMAN	Vitellogenin.		4	ACAATCCATCCTA	0.413	
+	1	3292	gz.2_Missense_M	NM_032961	NP_116586	Q9P2E7	PCD10_HUMAN	lasmic (Potential).		2	CTATCAGGTATGC	0.602	
+	7	691	_p.H108Y|IL15_uc	NM_000585	NP_000576	P40933	IL15_HUMAN			0	AGTATTCATGATA	0.363	
+	2	1033	_p.G114D|EDNRA_	NM_001957	NP_001948	P25101	EDNRA_HUMAN	Name=2; (Potential).		2	GAATGGCCCCA	0.423	
+	6	1619	nh.2_Missense_Mu	NM_001130067	NP_001123539	Q9C040	TRIM2_HUMAN	NHL 1.		1	ATTTGATCTTTCG	0.537	
+	5	1359	Dirr.2_Missense_M	NM_014269	NP_055084	Q9UKF5	ADA29_HUMAN	2B.|Extracellular (Potential).		16	TTGTTAATATAGT	0.333	
-	7	1129	zk.1_Missense_Mu	NM_173553	NP_775824	Q8N7C3	TRIMM_HUMAN	B30.2/SPRY.		2	TGTCTCCATTTGC	0.458	
+	4	396	RR_uc010isy.2_In	NM_020731	NP_065782	A9YTQ3	AHRR_HUMAN	PAS.		2	GGAAGGCTGCTG	0.632	
+	3	349	RIO_uc011cna.1_M	NM_007118	NP_009049	O75962	TRIO_HUMAN	CRAL-TRIO.		18	TGTATTCCCAGGT	0.453	
+	2	451	nd.1_Missense_Mu	NM_004932	NP_004923	P55285	CADH6_HUMAN		p.G42A(1)	7	TCTCTGGAAACA	0.493	
+	10	1366		NM_032637	NP_116026	Q13309	SKP2_HUMAN			4	GTATTTTTGTATG	0.328	
-	10	1549	1_Nonsense_Muta	NM_000065	NP_000056	P13671	CO6_HUMAN	MACPF.		7	TCCTTCCACCTC	0.418	
-	3	580	MB_uc011cpy.1_Mi	NM_198449	NP_940851	Q6PCB8	EMB_HUMAN	Potential).|Ig-like V-type 1.		0	TATTCTCAAGTTG	0.368	
+	17	3393	p.V1044I|BDP1_uc	NM_018429	NP_060899	A6H8Y1	BDP1_HUMAN	E-M-E-T-D-L-K-X-T-G-R- E-		2	AGAGAAGTATCC	0.458	
-	3	321	kkp.2_Missense_M	NM_001145678	NP_001139150	Q8IV33	K0825_HUMAN			0	CTCCAGGAAATGA	0.308	
+	4	381	81B_uc010jbe.1_5	NM_152548	NP_689761	Q96LP2	FA81B_HUMAN			2	AGAGAGGTCAGC	0.502	
+	11	2530	_Mutation_p.R844	NM_015288	NP_056103	Q9NQC1	JADE2_HUMAN			0	TGGTCCGCATGG	0.657	
+	1	1445	CDHA7_uc003lhq.2	NM_018904	NP_061727	Q9Y5I0	PCDAD_HUMAN	|Extracellular (Potential).		6	GGACGCGGACG	0.667	
+	6	1408	uc010jgf.2_Misser	NM_001130029	NP_001123501	Q8NC24	RELL2_HUMAN			0	ATGGCTCCCCCA	0.642	
+	5	842	_p.S228F|PPARGC	NM_133263	NP_573570	Q86YN6	PRGC2_HUMAN			0	GGGACTCCCTAG	0.672	
-	4	649		NM_032782	NP_116171	Q8TDQ0	HAVR2_HUMAN	cellular (Potential).		0	ATCAGGGAGGCT	0.333	
+	7	989	_p.P174L|GABRA1	NM_000806	NP_000797	P14867	GBRA1_HUMAN	cellular (Probable).		3	ACTTCCCTATGGA	0.378	rs138145692
+	13	2372_2373		NM_133369	NP_588610	Q6ZN44	UNC5A_HUMAN	lasmic (Potential).		1	CATCACCAAGGT	0.658	
-	11	1588	ez.2_Missense_Mu	NM_002115	NP_002106	P52790	HXK3_HUMAN	Catalytic.	p.A499V(1)	7	TGAACCGCAGCC	0.682	
+	1	41	ED9_uc010jko.2_F	NM_017510	NP_059980	Q9BVK6	TMED9_HUMAN			0	GCCCCGGCCCG	0.726	
-	9	1301	b.1_Nonsense_Mu	NM_000129	NP_000120	P00488	F13A_HUMAN			6	GCTTGCCAGCCT	0.478	
-	5	655	P2L_uc011dim.1_I	NM_004752	NP_004743	O75603	GCM2_HUMAN			3	CTTCTGCCTAGAA	0.398	
+	3	265	S49L|SLC17A4_uc	NM_005495	NP_005486	Q9Y2C5	S17A4_HUMAN			1	ATTTTTCAATTTA	0.478	
+	18	1890	se_Mutation_p.P56	NM_001025091	NP_001020262	Q8NE71	ABCF1_HUMAN			2	GAGGCCCCTGAG	0.562	
+	25	3286	_p.Y883C|VARS2_	NM_020442	NP_065175	Q5ST30	SYVM_HUMAN			4	CCCCCTACCCCA	0.667	
+	3	260	K2B_uc003nvs.1_3	NM_021221	NP_067044	Q8NDX9	LY65B_HUMAN	UPAR/Ly6.		0	GCAACACCTACTT	0.532	
+	7	730_731	FL8_uc003oac.1_I	NM_030652	NP_085155	Q99944	EGFL8_HUMAN	Potential.		0	GAGCGGCTGGA	0.619	
-	1	807		NR_001444						0	GACAGGAGGCA	0.577	
+	58	8169	f125_uc003oez.1_	NM_002224	NP_002215	Q14573	ITPR3_HUMAN	lasmic (Potential).		19	CTAGATGACGGA	0.617	
+	8	1100	D2_uc011dtv.1_5'U	NM_173558	NP_775829	Q7Z6J4	FGD2_HUMAN			3	GCCTCGAGGACG	0.632	
-	5	634_635		NM_006653	NP_006644	O43559	FRS3_HUMAN			2	TCGAGGGAGGT	0.475	
+	2	354	vx.1_Missense_Mu	NM_152732	NP_689945	Q9H1X1	RSPH9_HUMAN			2	TCATACGAATATG	0.527	rs150021750
-	1	603		NM_138733	NP_620061	P07205	PGK2_HUMAN			1	TGCCAAAAGCAT	0.458	
-	3	501	np.1_Nonsense_M	NM_014611	NP_055426	Q9NU22	MDN1_HUMAN			10	AACTCTCTAGGA	0.398	
-	3	657	pou.2_Missense_M	NM_001143957	NP_001137429	Q9BZJ6	GPR63_HUMAN	cellular (Potential).		2	TCACGGTCAAGC	0.433	
+	2	462		NM_021620	NP_067633	Q9H4Q3	PRD13_HUMAN	SET.		0	GGAGTGGATAGG	0.617	
+	2	269	F25_uc003qwl.1_I	NM_030615	NP_085118	Q9UIL4	KIF25_HUMAN	Kinesin-moto	p.W3C(1)	2	ATGACATGGACCT	0.602	
-	1	1967	DIL_uc011jwd.1_Ir	NM_020144	NP_064529	Q9NRJ5	PAPOB_HUMAN			1	CGTGAGGAATACT	0.453	
-	18	3960		NM_015204	NP_056019	Q9UPZ6	THS7A_HUMAN	2.|Extracellular (Potential).		3	TGCCTTCTCACTC	0.413	
+	13	1837	576_splice|ABCB5_	NM_178559	NP_848654	Q2M3G0	ABCB5_HUMAN			6	TTTATAAGATAGC	0.333	
-	3	1811	uc003szu.1_5'Flan	NM_014817	NP_055632	Q7L0X0	TRIL_HUMAN	cellular (Potential).		0	GCCTTAGGGCGCT	0.736	
-	17	2375	ng.2_Missense_Mu	NM_033054	NP_149043	B0I1T2	MYO1G_HUMAN			4	GTCTCCGGAAC	0.677	

-	8	1329_1330	c.2_Missense_Mu	NM_015198	NP_056013	O75128	COBL_HUMAN		5	CTGCGGGGCT	0.629	
-	6	641	_Mutation_p.R18	NM_006213	NP_006204	Q16816	PHKG1_HUMAN	rotein kinase.	1	GGTCCCGGTGC	0.537	
+	1	1880		NM_003508	NP_003499	O00144	FZD9_HUMAN	lasmic (Potential).	1	GGGCCCGGGCC	0.657	
+	20	1275	ELN_uc003tzr.2_I	NM_000501	NP_001075224	P15502	ELN_HUMAN	Ala-rich.	5	GCATTCCTACTT	0.627	
-	2	846	ERF_uc011khm.1	NM_006980	NP_008911	Q99551	MTERF_HUMAN		0	GTTCCTCACTGT	0.393	
+	18	1399	1A2_uc011kib.1_I	NM_000089	NP_000080	P08123	CO1A2_HUMAN		9	CCAAGGGTGCT	0.453	rs72656391
-	16	1808_1809	4_uc003uvi.2_RN	NM_002319	NP_002310	O75427	LRCH4_HUMAN	CH.	2	CACATGGATGAA	0.668	
-	18	2210	L13_uc003var.2_	NM_145032	NP_659469	Q8NEE6	FXL13_HUMAN	LRR 15.	0	CATATCTGACAG	0.418	
-	1	162		NM_002711	NP_002702	Q16821	PPR3A_HUMAN		34	AACCTCGTCTA	0.378	
+	6	745	R_uc011knq.1_5'	NM_000492	NP_000483	P13569	CFTR_HUMAN	tial).|ABC transmembrane	5	TCGCTCCTTTG	0.473	rs121908803
-	31	5721	qz.3_Missense_	NM_020911	NP_065962	Q9HCM2	PLXA4_HUMAN	lasmic (Potential).	1	GGTATGCGTTC	0.507	
-	15	3086		NM_020911	NP_065962	Q9HCM2	PLXA4_HUMAN		1	AGTGTCTGTGT	0.617	
-	15	1860		NM_004333	NP_004324	P15056	BRAF_HUMAN	rotein kinas_R603>I(2)|p.T	18290	ATTTCACTGTA	0.368	
-	3	750	xc.3_Missense_M	NM_001001317	NP_001001317	Q8IYP2	PRS58_HUMAN	eptidase S1.	0	GATATCACACA	0.433	
+	23	3014	tc.1_Missense_Mu	NM_000083	NP_000074	P35523	CLCN1_HUMAN	smic (By similarity).	5	CCTGCGATCCA	0.617	
+	1	796		NM_001004685	NP_001004685	O95006	OR2F2_HUMAN	ellular (Potential).	4	CTGGTCCCTCA	0.493	
+	12	1482_1483	d.1_Missense_Mu	NM_007188	NP_009119	Q9NUT2	ABCB8_HUMAN		3	TGCGTCCCCAA	0.649	
+	10	1280		NM_016353	NP_057437	Q9UIJ5	ZDHC2_HUMAN		0	TTTCCAACTTGC	0.373	rs2904682
+	4	364	60B2_uc011kyy.1	NM_022749	NP_073586	Q86V87	F16B2_HUMAN		0	GCATGCGGCAG	0.672	
-	9	1143		NM_003844	NP_003835	O00220	TR10A_HUMAN	lasmic (Potential).	6	AGTGGGGTCAG	0.532	
-	6	3688	3xkn.1_Missense_	NM_001002814	NP_001002814	Q6WKZ4	RFIP1_HUMAN	FIP-RBD.	3	TCCGAGGGGCT	0.448	
+	12	1080	AM18_uc010lwx.	NM_014237	NP_055052	Q9Y3Q7	ADA18_HUMAN	B.|Extracellular (Potential).	6	AACTGCAGCAT	0.353	
+	2	605	.1_Missense_Mut	NM_006269	NP_006260	P56715	RP1_HUMAN		12	GCCCCCCACGG	0.692	
+	55	10130	iw.2_Missense_M	NM_017890	NP_060360	Q7Z7G8	VP13B_HUMAN		20	GCAGGTTGTGT	0.398	
-	6	2235		NM_000127	NP_000118	Q16394	EXT1_HUMAN	enal (Potential).	4	GGGGGTCACCG	0.527	
+	9	1053		NM_001039112	NP_001034201	Q2WGJ9	FR1L6_HUMAN	toplasmic (Potential).	11	TTGTGGAGGTC	0.493	
-	1	2962	c003zrh.1_5'Flan	NM_153809	NP_722516	Q8IZX4	TAF1L_HUMAN		26	AGCAATGAAGG	0.473	
+	13	1340	b.1_RNA|TMC1_u	NM_138691	NP_619636	Q8TDI8	TMC1_HUMAN	ellular (Potential).	1	CAATTGGATGGA	0.403	
-	8	2869		NM_015225	NP_056040	Q8WUY3	PRUN2_HUMAN		0	ATCTACCTTTTC	0.398	
+	7	1643	.2_Missense_Mut	NM_006648	NP_006639	Q9Y3S1	WNK2_HUMAN		12	CTGGCCCGCGC	0.647	
+	22	3334	_Mutation_p.L101	NM_001042551	NP_001036016	O95347	SMC2_HUMAN	Potential.	9	AAAATTCTTACA	0.308	
-	14	2042		NM_005502	NP_005493	O95477	ABCA1_HUMAN	Extracellular.	17	AGGACCAGGGT	0.478	
-	3	615		NM_014334	NP_055149	Q9P0K9	CI004_HUMAN	DOMON.	0	TCTTACCATTTT	0.383	
-	11	1543	muc.1_Missense_	NM_001080398	NP_001073867				0	AGAGCGGAGGA	0.413	
-	8	800		NM_003086	NP_003077	Q5SXM2	SNPC4_HUMAN	Myb-like 1.	0	TCTTCTCCCAG	0.577	
+	4	394	2C_uc004cmg.1_	NM_006088	NP_006079	P68371	TBB2C_HUMAN		1	GTGCTGGGAAC	0.557	
-	7	854	py.1_Missense_M	NM_004192	NP_004183	O95671	ASML_HUMAN		0	GAGTGGGCTCC	0.706	
+	4	532		NM_173695	NP_775966	Q8N9S7	CX059_HUMAN		1	CAGCACAGACC	0.408	
-	29	3606	nip.2_Missense_M	NM_005183	NP_005174	O60840	CAC1F_HUMAN	smic (Potential).|IV.	6	CACACGATACT	0.562	
+	1	132		NM_198512	NP_940914	Q6ZPD8	DG2L6_HUMAN		1	GGAGGGCCTCC	0.463	
-	3	510	ir.2_Missense_Mu	NM_001159560	NP_001153032	Q5H9J7	BEX5_HUMAN		1	TGAACCGTTCCA	0.488	
+	5	650	p.D139N|MST4_u	NM_016542	NP_057626	Q9P289	MST4_HUMAN	rotein kinase.	9	CATTTGATGAG	0.343	
+	3	1123		NM_005364	NP_005355	P43361	MAGA8_HUMAN	MAGE.	0	CATTTCCTACC	0.577	rs45578531
-	6	659	e_Mutation_p.R17	NM_000425	NP_000416	P32004	L1CAM_HUMAN	otential).|Ig-like C2-type 2.	9	TCACCCGCTCG	0.612	rs137852521
+	9	1768		NM_198576	NP_940978	O00468	AGRIN_HUMAN	Kazal-like 6.	3	GCACACGTACC	0.687	
+	3	599	_5'Flank|CPSF3L_	NM_001029885	NP_001025056	Q5TA50	GLTD1_HUMAN		0	AGCTGCGGATC	0.652	
-	1	344	n_p.R7G|SSU72_	NM_014188	NP_054907	Q9NP77	SSU72_HUMAN		0	CACCCGCAGCG	0.701	

-	22	2132	.R640H|CDK11B_	NM_033486	NP_277021	P21127	CD11B_HUMAN	rotein kinase.	1	CGAAGCGCTTG	0.622	
+	5	523	jf.1_Missense_Mu	NM_007033	NP_008964	O15258	RER1_HUMAN		0	CCGCCCCTTCA	0.483	
-	11	1393	za.1_Missense_M	NM_018216	NP_060686	Q9NVE7	PANK4_HUMAN		3	TGCGCGCTTCA	0.642	
-	3	317	tion_p.R56C|ENO	NM_001428	NP_001419	P06733	ENOA_HUMAN	nized by CAR antibodies.	4	TATAGCGAGTCT	0.557	
+	3	1254	asi.1_Missense_	NM_020780	NP_065831	Q9P2K9	PTHD2_HUMAN	ellular (Potential).	7	GCCATGACTCA	0.592	
+	6	980	i.2_Missense_Mu	NM_014874	NP_055689	O95140	MFN2_HUMAN	lasmic (Potential).	1	TGCCGGCAGCC	0.572	
+	2	265		NM_021933	NP_068752	Q5JXC2	MIIP_HUMAN		1	CTGTGCGGCGG	0.632	
+	26	6358	73_splice|VPS13D	NM_015378	NP_056193	Q5THJ4	VP13D_HUMAN		5	TCCCAGGAATC	0.517	
+	10	2032		NM_015164	NP_055979	Q8IWE5	PKHM2_HUMAN		1	GTTCCGAGAAA	0.592	
+	12	10412	p.1_Missense_Mu	NM_015001	NP_055816	Q96T58	MINT_HUMAN	Pro-rich.	15	GCCTCGCCTCC	0.647	
-	8	1276	bs.1_Missense_	NM_003443	NP_003434	Q13105	ZBT17_HUMAN	2H2-type 2.	0	CGGCCGGGTCG	0.677	
+	7	755	e_Mutation_p.S19	NM_018125	NP_060595	Q9HCE6	ARGAL_HUMAN		3	AGTGTCCTTCC	0.592	
-	3	920		NM_152232	NP_689418	Q8TE23	TS1R2_HUMAN	ellular (Potential).	4	CGGGTCGATGG	0.637	
-	1	1002	2N1_uc001bdg.2_	NM_018584	NP_061054	Q7Z7J9	CK2N1_HUMAN	domain (By similarity).	0	CGATCTGGCCC	0.692	
+	7	1048	e_Mutation_p.R23	NM_005839	NP_005830	Q8IYB3	SRRM1_HUMAN	-rich.|Arg-rich.	3	GACCCGACCAC	0.502	rs17853564
-	2	323	n_p.F79L|RHCE_	NM_020485	NP_065231	P18577	RHCE_HUMAN	ical; (Potential).	0	AGGTTGAAGGC	0.597	
-	2	191	oge.1_Missense_	NM_004814	NP_004805	Q96DI7	SNR40_HUMAN		0	TGGAGGTCCCT	0.493	
+	6	1349	e_Mutation_p.Q35	NM_022753	NP_073590	Q96BU1	S1PBP_HUMAN		0	ATATGCAGCAC	0.443	
-	4	1496		NM_001080418	NP_001073887	O95886	DLGP3_HUMAN		3	GGCTCCGCATG	0.697	
-	7	1808	PQ_uc001byr.2_R	NM_005066	NP_005057	P23246	SFPQ_HUMAN	Poly-Arg.	8	TTCTACGTCGT	0.433	
+	11	1522	_Mutation_p.G36	NM_012199	NP_036331	Q9UL18	AGO1_HUMAN		3	TGCGGGGGAAA	0.562	
-	2	1778	zw.1_Missense_	NM_005202	NP_005193	P25067	CO8A2_HUMAN	helical region (NC1).	1	CACGGGCATGC	0.627	
-	15	2685	.1_RNA|EPHA10_	NM_001099439	NP_001092909	Q5JZY3	EPHAA_HUMAN	Potential).|Protein kinase.	8	GGGGGTGGCA	0.607	
-	1	346	CS_uc001chk.2_5	NM_032257	NP_115633	Q9H0C1	ZMY12_HUMAN	MYND-type.	1	CACCCGCTCGG	0.622	
+	5	610	.R177Q|DMAP1_	NM_001034024	NP_001029196	Q9NPF5	DMAP1_HUMAN	SANT.	0	TGACCGGTATG	0.507	
-	14	2030	lg.1_Missense_M	NM_003738	NP_003729	Q9Y6C5	PTC2_HUMAN	lasmic (Potential).	18	GATAGCGGGCG	0.607	
-	3	287	H2_uc010olg.1_5'	NM_003738	NP_003729	Q9Y6C5	PTC2_HUMAN	ellular (Pot p.R92P(1)	18	TCACCCGGCTG	0.607	
-	14	1860	ense_Mutation_p.	NM_024602	NP_078878	Q5T447	HECD3_HUMAN	HECT.	0	GGTTGGGTACAT	0.557	
+	5	695	AH_uc001cpv.2_R	NM_001441	NP_001432	O00519	FAAH1_HUMAN	smic (By similarity).	2	AGACCGTGAAC	0.657	
+	3	527	G11B_uc010onj.1_	NM_024646	NP_078922	Q9C0D3	ZY11B_HUMAN		4	ACTTGATGCCA	0.483	
-	5	498	ont.1_Missense_	NM_002370	NP_002361	P61326	MGN_HUMAN		0	ATCCAATAAGA	0.378	
+	7	1332		NM_006252	NP_006243	P54646	AAPK2_HUMAN		6	TTTACCGAGCT	0.383	
+	11	1972	ls.1_Missense_M	NM_001285	NP_001276	A8K7I4	CLCA1_HUMAN		1	ATATTCGCCAA	0.493	
+	1	217	D5_uc001dpo.2_	NM_206886	NP_996769	Q5T9S5	CCD18_HUMAN		5	AATGTAGTCCC	0.726	
-	5	1017	k.1_Missense_Mu	NM_001439	NP_001430	Q9UBQ6	EXTL2_HUMAN	enal (Potential).	1	TGCCTCTGAAAT	0.398	
-	6	1214	OL11A1_uc001dur	NM_001854	NP_001845	P12107	COBA1_HUMAN	nhelical region.	12	TTACCTCCGTCT	0.433	
+	12	2317		NM_001010898	NP_001010898	Q9H1V8	S6A17_HUMAN	ame=12; (Potential).	2	CATGGCACTCC	0.657	
+	1	2401	ense_Mutation_p.	NM_022768	NP_073605	Q96T37	RBM15_HUMAN		3	TGGGGGGACAG	0.542	
-	2	1686	NA2_uc009wfw.2_	NM_004974	NP_004965	P16389	KCNA2_HUMAN	=Segment S6; (Potential).	1	CACCTGCAATC	0.512	
-	1	472		NM_021794	NP_068566	Q9UKF2	ADA30_HUMAN		3	CTTTGGTATGTA	0.498	
+	32	4104	10_uc010oyl.1_Int	NM_001039703	NP_001034792	A6NDV3	A6NDV3_HUMAN		0	TGCTGGATGAG	0.478	
-	3	1114	th.2_Splice_Site_	NM_014849	NP_055664	Q7L0J3	SV2A_HUMAN		7	AGGCCTGGAAG	0.572	
-	2	424		NM_020205	NP_064590	Q6GQQ9	OTU7B_HUMAN		3	CTCGCGCTAGC	0.458	
-	2	134	.1_5'UTR|CTSK_u	NM_000396	NP_000387	P43235	CATK_HUMAN		1	CTTGAGCCCCC	0.493	
+	2	858		NM_020770	NP_065821	Q9P2M7	CING_HUMAN	ts with ZO-2.|Head.	3	CTCTAGCACAAA	0.587	
-	3	1061		NM_016190	NP_057274	Q9UBG3	CRNN_HUMAN	Gln-rich.	3	TGGATCTCAGT	0.602	
+	1	127		NM_012437	NP_036569	O95295	SNAPN_HUMAN		0	TGGCGGGGCCC	0.706	

+	7	717	.R206W|ADAM15_	NM_207197	NP_997080	Q13444	ADA15_HUMAN		6	AGAGGCGGGAT	0.587	
+	2	1041	11_uc010pgq.1_Ir	NM_152280	NP_689493	Q9BT88	SYT11_HUMAN	mic (Potential).|C2 1.	2	TTGGCGAGGTC	0.552	
+	1	329	1C_uc001frv.2_5'F	NM_001765	NP_001756	P29017	CD1C_HUMAN		4	TTCTTCTCCCA	0.458	
+	1	86		NM_001005184	NP_001005184	Q8NGW6	OR6K6_HUMAN	ellular (Potential).	1	GTTGACGGCCA	0.433	rs142721506
-	2	467		NM_002241	NP_002232	P78508	IRK10_HUMAN	llular (By similarity).	1	AGGGGGTGTGG	0.582	
-	2	167	_p.A41V|IGSF8_	NM_052868	NP_443100	Q969P0	IGSF8_HUMAN	1.|Extracellular (Potential).	0	TGCCAGCCACG	0.617	
+	9	1271	_p.T225I|ATP1A2	NM_000702	NP_000693	P50993	AT1A2_HUMAN	lasmic (Potential).	7	CCTCACCCAGA	0.607	
-	4	697	n.2_Missense_Mu	NM_003874	NP_003865	Q9UIB8	SLAF5_HUMAN	ellular (Potential).	4	CAACCCGGTGT	0.483	
-	4	342	F1_uc001fxj.2_Int	NM_007122	NP_009053	P22415	USF1_HUMAN		3	AAGACGTACTT	0.552	
-	9	1776	_5'Flank|ARHGAP	NM_030916	NP_112178	Q96NY8	PVRL4_HUMAN	lasmic (Potential).	2	GGCCCGTAGGG	0.597	rs138257801
-	9	1698	_5'Flank|ARHGAP	NM_030916	NP_112178	Q96NY8	PVRL4_HUMAN	lasmic (Potential).	2	GGCCCGCCCAG	0.582	rs139761589
+	5	502	LB_uc001gbl.2_Mi	NM_001002901	NP_001002901	Q6BAA4	FCRLB_HUMAN	like C2-type 1.	0	GGGGAGCACCC	0.572	
+	7	773	q.1_Missense_Mu	NM_007348	NP_031374	P18850	ATF6A_HUMAN	lasmic (Potential).	3	TTGCTGTCTCAG	0.498	
+	7	1048	1AP_uc010pks.1_	NM_014697	NP_055512	O75052	CAPON_HUMAN		3	ATGCGGTGGAG	0.592	
-	7	1275		NM_005814	NP_005805	Q99795	GPA33_HUMAN	lasmic (Potential).	0	ATTCACGCCCAG	0.612	rs139067139
-	5	689	f112_uc001ggj.2_	NM_000450	NP_000441	P16581	LYAM2_HUMAN	xtracellular (Potential).	5	AGTTCACAACTG	0.413	
+	12	1324	05_splice|C1orf12	NM_025063	NP_079339	Q5TGP6	CA129_HUMAN		1	TTGGCGGTAAAT	0.413	
+	2	1146	L13_uc001gib.2_	NM_015935	NP_057019	Q8N6R0	MTL13_HUMAN		1	TGGGGAGTGTG	0.657	
-	19	3731	.1_Missense_Mut	NM_003285	NP_003276	Q92752	TENR_HUMAN	nogen C-terminal.	11	GTGATCCTGTGT	0.572	
+	3	751	3A_uc010pnd.1_I	NM_022371	NP_071766	Q9H497	TOR3A_HUMAN		1	CGCCACGTTCC	0.597	rs146717666
+	10	1228		NM_015602	NP_056417	Q5JTV8	TOIP1_HUMAN	clear (Potential).	2	GAACCGGTGGT	0.433	
-	6	1195		NM_032360	NP_115736	Q9BR61	ACBD6_HUMAN		1	CCTACCCTAAAA	0.373	
+	11	1594	se_Mutation_p.R4	NM_004736	NP_004727	Q9UBH6	XPR1_HUMAN	mic (Potential).|EXS.	0	CGATATCGAGAC	0.468	
-	1	235	tart_Site|ASPM_u	NM_018136	NP_060606	Q8IZT6	ASPM_HUMAN		6	cccctcctggatctcctt	0.005	
+	14	1638		NM_018085	NP_060555	Q96P70	IPO9_HUMAN		2	ACACAGCCCCCA	0.502	
-	9	2838		NM_025179	NP_079455	O75051	PLXA2_HUMAN	ellular (Potential).	3	GATCCGGCCCT	0.562	
-	8	1728	ic.2_Missense_Mu	NM_172362	NP_758872	O95259	KCNH1_HUMAN	lasmic (Potential).	5	GTCCCGAACAC	0.463	
+	2	708	kg.1_Missense_M	NM_002763	NP_002754	Q92786	PROX1_HUMAN		6	TTTGGCAGGCCT	0.512	
+	4	484	e_Mutation_p.I64	NM_016121	NP_057205	Q9Y597	KCTD3_HUMAN	BTB.	3	ATATTTATTGATA	0.264	
-	3	1332	_p.R42W|DUSP10	NM_007207	NP_009138	Q9Y6W6	DUS10_HUMAN	protein phosphatase.	2	CTGCCGCAGGT	0.488	
-	2	759	h.2_Missense_M	NM_002221	NP_002212	P27987	IP3KB_HUMAN		5	TGCACGTTCTGC	0.672	
+	2	667	f69_uc010pvw.1_5	NM_001010867	NP_001010867	Q5T440	CAF17_HUMAN		0	AGCACGCATGG	0.692	
+	8	790	CE_uc010pxr.1_M	NM_003193	NP_003184	Q15813	TBCE_HUMAN	LRR 3.	0	TGCTGCGGTGT	0.507	rs75832955
+	1	1940	e_Mutation_p.R48	NM_006352	NP_006343	Q99592	ZN238_HUMAN	C2H2-type 4.	5	CGAGCGCAGGT	0.602	
+	2	449	o.3_Missense_M	NM_152609	NP_689822	Q6PJW8	CNST_HUMAN		0	TGACAGCGTGG	0.468	
+	8	1270	o.3_Missense_Mu	NM_152609	NP_689822	Q6PJW8	CNST_HUMAN		0	TTACTAGTGTCT	0.413	
+	1	512		NM_001004698	NP_001004698	A6NFC9	OR2W5_HUMAN		3	TGGACGTCGCA	0.562	rs145513251
-	3	282	ih.2_RNA|ASB13_	NM_024701	NP_078977	Q8WXK3	ASB13_HUMAN	ANK 2.	1	GCGAGCATCCA	0.577	
+	10	1224	iln.2_Missense_M	NM_153498	NP_705718	Q8IU85	KCC1D_HUMAN	Ser-rich.	2	TGGACAGTTCAA	0.473	
+	2	643	nse_Mutation_p.R	NM_024670	NP_078946	Q9H5I1	SUV92_HUMAN	SET.	3	TCTTTCGAACTA	0.428	
+	8	1590	e_Mutation_p.S26	NM_032812	NP_116201	Q6UX71	PXDC2_HUMAN	ellular (Potential).	4	CATTTCGGCTG	0.323	
+	12	1608	p.G509S|ARMC3_	NM_173081	NP_775104	Q5W041	ARMC3_HUMAN	ARM 12.	0	GTGCTGGTGAC	0.532	
-	3	505	p.T113R|ABI1_uc	NM_005470	NP_005461	Q8IZP0	ABI1_HUMAN		1	TTTGTTGTCAAA	0.328	
-	7	2138	.C568Y|ZNF438_	NM_182755	NP_877432	Q7Z4V0	ZN438_HUMAN	C2H2-type 3.	2	TCACAACACATG	0.478	
+	7	794		NM_052997	NP_443723	Q9BXX3	AN30A_HUMAN		9	CCTTGGCGGAAA	0.423	
+	7	1118		NM_052997	NP_443723	Q9BXX3	AN30A_HUMAN		9	AAATTATGAGTC	0.428	
+	1	134	0qev.1_Splice_Sit	NM_006974	NP_008905	Q06730	ZN33A_HUMAN		3	TGGGGTAAGCC	0.652	

+	5	599	1izo.1_RNA|HSD17B7P2_uc001izp.1_Missense_Mutation_p.N173S						0	TCGCAATGCAA	0.453	rs2257765
-	3	1103	_Mutation_p.R20	NM_001098208	NP_001091678	P52597	HNRPF_HUMAN		0	TGGCCGCTGCA	0.582	
+	3	397	jbl.2_Intron|TMEM	NM_001123376	NP_001116848	A0PK05	TMM72_HUMAN		0	GGCCATCTGCT	0.587	
-	4	601	T15_uc001jeb.2_	NM_031912	NP_114118	Q9BQS2	SYT15_HUMAN	mic (Potential).|C2 1.	0	CAGCCGCCCCA	0.612	
-	1	1894		NM_002900	NP_002891	P10745	RET3_HUMAN	nate tandem repeats.|2.	2	GACCGGCACGG	0.677	
-	18	3816	gr.1_Missense_M	NM_000124	NP_000115	Q03468	ERCC6_HUMAN		16	GGAATTCGAGTT	0.448	
-	2	555	p.R134Q|PGBD3_	NM_000124	NP_000115	Q03468	ERCC6_HUMAN		16	ACCGACCGATAC	0.537	
-	1	521	|TMEM26_uc001j	NM_178505	NP_848600	Q6ZUK4	TMM26_HUMAN	ical; (Potential).	0	TGAGCGCAGTC	0.642	
-	8	1218	se_Mutation_p.R	NM_022079	NP_071362	Q5GLZ8	HERC4_HUMAN	RCC1 6.	3	TTACCGTCCAC	0.383	
-	22	4723	kk.1_Missense_M	NM_152586	NP_689799	Q70EL1	UBP54_HUMAN		6	TGGCAGTGTAG	0.522	
+	23	3298	_Mutation_p.R28	NM_004922	NP_004913	P53992	SC24C_HUMAN		3	CTTACGGGCAC	0.468	
+	7	2889	p.R752L|PLCE1_	NM_016341	NP_057425	Q9P212	PLCE1_HUMAN	Ras-GEF.	3	ACAACGAGTGG	0.408	
+	6	890	qny.1_Missense_	NM_000769	NP_000760	P33261	CP2CJ_HUMAN		6	TGGAGCTGGGA	0.433	
+	23	3268		NM_000392	NP_000383	Q92887	MRP2_HUMAN	-1 2.|Helical; Name=13; (B	1	CATTTCTGGAG	0.433	
-	9	2874	nse_Mutation_p.R	NM_015221	NP_056036	Q6XZF7	DNMBP_HUMAN	DH.	6	GGTAACGCATTA	0.433	
-	10	1082		NM_001278	NP_001269	O15111	IKKA_HUMAN		7	TTTCACGCTCAA	0.383	
-	5	1122	wm.1_Missense_	NM_016112	NP_057196	Q9P0L9	PK2L1_HUMAN	ellular (Potential).	4	GTGGTATGTCC	0.552	
-	3	1377		NM_001085398	NP_001078867	P0CAT3	TLXNB_HUMAN		0	CCATGGCCTCT	0.662	
+	10	1950	p.K573R|NOLC1_	NM_004741	NP_004732	Q14978	NOLC1_HUMAN	lization signal (Potential).	1	GAAAAAGGCGG	0.502	
-	17	3591	.R391W|PSD_uc0	NM_002779	NP_002770	A5PKW4	PSD1_HUMAN		3	CTTCCGCCGCC	0.692	
-	6	563	_p.R78T|ACTR1A_	NM_005736	NP_005727	P61163	ACTZ_HUMAN		1	TGGTCCTGCCT	0.542	
+	3	466	se_Mutation_p.R9	NM_017787	NP_060257	Q9NX94	OPA1L_HUMAN		1	GCACCGCCTTC	0.562	
-	16	2157	10orf79_uc001kxx.	NM_025145	NP_079421	Q8NDM7	WDR96_HUMAN	WD 9.	0	CTGGTGAGAAT	0.403	
+	6	845	I1_uc010qrc.1_M	NM_005962	NP_005953	P50539	MXI1_HUMAN		0	TGGGAGTGACG	0.468	
+	8	1363	L2_uc001lah.2_M	NM_001146274	NP_001139746	Q9NQB0	TF7L2_HUMAN	tion with MAD2L2.|Pro-ric	4	TGACCGTCAAT	0.522	
+	3	918		NM_198514	NP_940916	Q8NBF2	NHLC2_HUMAN	NHL 1.	1	GTTACTGATAGA	0.353	
+	2	547	el.2_Missense_Mu	NM_004281	NP_004272	O95817	BAG3_HUMAN		2	CTAGGGAAGGC	0.572	
+	4	962	nse_Mutation_p.S	NM_206862	NP_996744	O95359	TACC2_HUMAN		10	AATGTCGCCAG	0.582	
+	4	5521	e_Mutation_p.S17	NM_206862	NP_996744	O95359	TACC2_HUMAN		10	GTGCGTCCGGT	0.607	
+	8	883	_Intron|DHX32_u	NM_016567	NP_057651	Q9P287	BCCIP_HUMAN		2	TTCACGGGGGC	0.433	
-	5	621		NM_004092	NP_004083	P30084	ECHM_HUMAN		0	CTTCCCAACAG	0.627	
-	4	308	09ybn.2_Missens	NM_001143764	NP_001137236	Q8N0S2	SYCE1_HUMAN	Potential.	1	GCTTTCTTTTTTG	0.498	
+	7	846	_p.A238T|PHRF1_	NM_020901	NP_065952	Q9P1Y6	PHRF1_HUMAN		0	TTGCCGCTGGT	0.627	
-	13	2017	.1_5'Flank|CDHR	NM_021924	NP_068743	Q9HBB8	CDHR5_HUMAN	epeats.|Extracellular (Pote	0	TCCTGGCTCTG	0.632	
-	13	1897	ycc.2_Missense_	NM_021924	NP_068743	Q9HBB8	CDHR5_HUMAN	em repeats.|2.|Extracellul	0	CCCACCGGGTG	0.672	rs139590704
+	13	1892	A2_uc009yco.1_R	NM_012305	NP_036437	O94973	AP2A2_HUMAN		0	GGAACGCAGAC	0.652	
-	31	6815		NM_005961	NP_005952	Q6W4X9	MUC6_HUMAN	r-rich.|Thr-rich.	1	TGGCCGTGGTC	0.612	
-	2	233	SD_uc009yda.1_R	NM_001909	NP_001900	P07339	CATD_HUMAN		0	GGTCCGGCGGA	0.622	
+	1	422	2_uc001mak.1_I	NM_001005162	NP_001005162	Q8NGF0	O52B6_HUMAN	lasmic (Potential).	1	TGACCGCTATG	0.517	
-	1	751	5_uc001mbq.1_I	NM_001005168	NP_001005168	Q6IFG1	O52E8_HUMAN	Name=6; (Potential).	2	TAACACCAATATG	0.408	
-	1	764		NM_001146033	NP_001139505	P0C7T3	O56A5_HUMAN	Name=6; (Potential).	0	CTGTGGTGAAG	0.488	
+	15	1937	p.Q606K|ZNF143_	NM_003442	NP_003433	P52747	ZN143_HUMAN		0	GCACCCAGATT	0.483	
-	7	1007	4_splice|COPB1_	NM_016451	NP_057535	P53618	COPB_HUMAN		2	CAGACCTGGAG	0.388	
-	15	2222	nf.2_Missense_M	NM_001145819	NP_001139291	P35712	SOX6_HUMAN		3	GTCTCCGAGAC	0.453	
+	32	6672	p.G1165D|NAV2_	NM_182964	NP_892009	Q8IVL1	NAV2_HUMAN	P (Potential).	6	CAGCGGCACTG	0.567	
-	1	248		NM_022725	NP_073562	Q9NPI8	FANCF_HUMAN		1	CCGCCCAAAGC	0.667	
-	4	1264	.1_Intron|MUC15_	NM_145650	NP_663625	Q8N387	MUC15_HUMAN	lasmic (Potential).	3	TATACAGAAGTAC	0.383	

-	2	1252	_uc009yiz.2_Intro	NM_001143816	NP_001137288	P23560	BDNF_HUMAN		0	CTCGGCGGGCA	0.552
+	2	418	.1_Intron|DGKZ_u	NM_001105540	NP_001099010	Q13574	DGKZ_HUMAN		3	TACCACCGTGG	0.657
+	2	127	2_uc001ndg.3_RN	NM_000506	NP_000497	P00734	THRB_HUMAN		3	GTGTTCCTGGC	0.657
+	5	890	32_uc001nee.2_In	NM_000107	NP_000098	Q92466	DDB2_HUMAN		3	GGACGGCAAAG	0.572
+	1	861		NM_001005496	NP_001005496	Q8NGK9	OR5DG_HUMAN	Name=7; (Potential).	5	TTGTTGAATCC	0.403
-	1	283		NM_001004746	NP_001004746	Q8NGG2	OR5T2_HUMAN	Name=2; (Potential).	2	TTTGTGGAGCT	0.393
-	5	725		NM_005142	NP_005133	P27352	IF_HUMAN		2	GGCCAGTACTG	0.358
-	4	589		NM_014502	NP_055317	Q9UMS4	PRP19_HUMAN		1	TTCTCGGGCAG	0.582
+	2	666		NM_138471	NP_612480	Q9BUA3	CK084_HUMAN		0	TGAGAGCTGAG	0.587
+	6	1098	_RNA|KCNK4_uc	NM_033310	NP_201567	Q9NYG8	KCNK4_HUMAN	lasmic (Potential).	0	TGCGAGTAGTG	0.642
+	2	1396	nv.1_Missense_M	NM_013299	NP_037431				0	AGGACGTACCC	0.622
+	17	1927	p.A321T|POLA2_	NM_002689	NP_002680	Q14181	DPOA2_HUMAN		0	TTTACGCACAG	0.493
+	6	789	rot.1_Missense_M	NM_005146	NP_005137	O43290	SNUT1_HUMAN		1	TTTGGTGTCAGC	0.602
-	3	395	e_Site|RIN1_uc01	NM_004292	NP_004283	Q13671	RIN1_HUMAN		3	AACGTCTGCAA	0.637
+	10	931	TN3_uc010rpi.1_	NM_001104	NP_001095	Q08043	ACTN3_HUMAN	Spectrin 1.	0	GGATCCGCCGC	0.647
-	17	3692		NM_006946	NP_008877	O15020	SPTN2_HUMAN	Spectrin 9.	4	CATCAGCAGCC	0.557
+	8	738	10C_uc001okz.2_	NM_198517	NP_940919	Q8IV04	TB10C_HUMAN	ab-GAP TBC.	0	CGCACGTGCAC	0.697
+	5	1074	nse_Mutation_p.E	NM_020811	NP_065862	A5YM72	CRNS1_HUMAN		0	TGGTGGAGGCT	0.657
+	4	277	FS8_uc009ysb.1_	NM_002496	NP_002487	O00217	NDUS8_HUMAN		1	AGCCCGCACCC	0.652
-	11	2418	1onn.1_Missense_	NM_017635	NP_060105	Q4FZB7	SV421_HUMAN		3	GCCTACGAAGA	0.383
-	9	1123	p.P318R|CPT1A_	NM_001876	NP_001867	P50416	CPT1A_HUMAN	lasmic (Potential).	2	CTCCTGGGATC	0.483
-	3	1251	op.3_Missense_	NM_001098515	NP_001091985	Q96AM1	MRGRF_HUMAN	lasmic (Potential).	0	CCCTCCCGGCC	0.687
+	16	2548	L817P|C11orf30_u	NM_020193	NP_064578	Q7Z589	EMSY_HUMAN		6	TGACCTGAGTC	0.388
+	45	6453	_Mutation_p.R20	NM_000260	NP_000251	Q13402	MYO7A_HUMAN	FERM 2.	4	TGCTGCGGGAG	0.637
+	2	433		NM_153696	NP_710163	Q9HBA9	FOH1B_HUMAN		6	GAATACGCTTAT	0.328
+	5	728		NM_153696	NP_710163	Q9HBA9	FOH1B_HUMAN		6	TGGGAGGTCAC	0.418
+	4	546	p.N146S|NAALAD	NM_005467	NP_005458	Q9Y3Q0	NALD2_HUMAN	ellular (Potential).	2	TTACAAATATTGT	0.328
+	18	11029	i.3_Missense_Mu	NM_001008781	NP_001008781	Q8TDW7	FAT3_HUMAN	ellular (Potential).	5	CCGGCGCACCC	0.587
+	11	2520	pfc.2_Missense_M	NM_130847	NP_570899	Q8IY63	AMOL1_HUMAN		2	AGACAGACTCC	0.502
+	12	2797	pfc.2_Missense_M	NM_130847	NP_570899	Q8IY63	AMOL1_HUMAN		2	CAGCAGCACAC	0.672
+	9	1228	fz.2_Missense_M	NM_014361	NP_055176	O94779	CNTN5_HUMAN		8	TGGGAGAATAT	0.368
+	2	788	G140W|YAP1_uc	NM_001130145	NP_001123617	P46937	YAP1_HUMAN		3	CTCCTGGGACA	0.542
-	1	70	n_p.A8V|MMP7_	NM_002423	NP_002414	P09237	MMP7_HUMAN		1	ACACAGCACAC	0.552
-	16	3055	_p.P888S|ARHGA	NM_020809	NP_065860	Q9P2F6	RHG20_HUMAN		5	TGGGGGTAAAA	0.488
-	5	829		NM_017589	NP_060059	Q9NY30	BTG4_HUMAN		0	TGCATAGCAGGC	0.557
+	9	1385	ol.2_Missense_M	NM_006028	NP_006019	O95264	5HT3B_HUMAN	ellular (Potential).	0	GGGGCGGCGTG	0.493
+	2	131	utation_p.A10V|P	NM_002572	NP_002563	P68402	PA1B2_HUMAN		1	AGCAGCTATTC	0.408
+	6	687	qg.2_Missense_M	NM_001040455	NP_001035545	Q8NBJ9	SIDT2_HUMAN	ellular (Potential).	0	ACAACGTAGCC	0.592
-	9	1276		NM_004716	NP_004707	Q16549	PCSK7_HUMAN	xtracellular (Potential).	0	CATGCGTCCCT	0.567
-	12	2701		NM_020693	NP_065744	Q8TD84	DSCL1_HUMAN	otential).|Ig-like C2-type 9.	8	TTGGTGGCGATG	0.642
-	7	1701	rzi.1_Missense_M	NM_012101	NP_036233	Q14134	TRI29_HUMAN		4	TTGTCAGAGTTC	0.612
+	13	1615	w.1_Missense_M	NM_014619	NP_055434	Q16099	GRIK4_HUMAN	ellular (Potential).	3	TGACCGCTACG	0.547
-	9	1967	yp.2_Missense_M	NM_006597	NP_006588	P11142	HSP7C_HUMAN		8	GAGGAGCTCCA	0.507
+	6	760	p.A184G|VWA5A_	NM_001130142	NP_001123614	O00534	VMA5A_HUMAN		2	TGGTCGCCACCA	0.502
+	2	168	_5'Flank|SIAE_uc	NM_017425	NP_059121	Q15506	SP17_HUMAN		0	CTACCGAATTC	0.423
+	9	1588		NM_022370	NP_071765	Q96MS0	ROBO3_HUMAN	5.|Extracellular (Potential).	2	TTGGCTCCTCC	0.607
+	1	691	2_3'UTR|HEPACA	NM_001037558	NP_001032647	Q6WQI6	HEPN1_HUMAN		0	TCCTATGAACTG	0.488

+	4	354	X2_uc010sba.1_	NM_022062	NP_071345	Q96KN3	PKNX2_HUMAN		3	CGATGATGGCC	0.662	
-	2	511	CRV1_uc001qco.	NM_001612	NP_001603	P26436	ASPX_HUMAN	peats of S-E-H-[GA]-S.	0	GTGCTCGGCCA	0.517	
-	5	843	p.R161H|KIRREL	NM_032531	NP_115920	Q8IZU9	KIRR3_HUMAN	2.|Extracellular (Potential).	3	CCGCACGCAGG	0.652	
+	9	1176	_p.L207F|LOC100288778_uc010sdf.1_Missense_Mutation_p.L207F|LOC100288778_uc010sdg.1_Missense_Mutati						0	CACTTGATGTC	0.607	
-	19	2158	CNA2D4_uc009z	NM_172364	NP_758952	Q7Z3S7	CA2D4_HUMAN	ellular (Potential).	1	GGTGTCGCTGA	0.478	
+	1	1081		NM_002235	NP_002226	P17658	KCNA6_HUMAN		3	TGGCCGGCGAG	0.622	
+	2	451	ev.1_Missense_M	NM_001769	NP_001760	P21926	CD9_HUMAN	lasmic (Potential).	1	TGCCGGTCAAA	0.632	
+	12	1523	sew.1_Missense_	NM_018173	NP_060643	Q3KR16	PKHG6_HUMAN	PH.	2	TGCTGGAGAAG	0.592	
-	11	1896	_p.T486I|ZNF384_	NM_001135734	NP_001129206	Q8TF68	ZN384_HUMAN		8	TGACAGTGAGG	0.582	
-	3	119	qqg.1_Missense_	NM_153685	NP_710152	Q8IYJ0	CL053_HUMAN		0	AGGGAGGAGGT	0.672	
-	13	3381	ge.1_Missense_M	NM_174941	NP_777601	Q9NR16	C163B_HUMAN	xtracellular (Potential).	11	CCAGCCGCGGG	0.617	rs149805278
-	2	285	raq.2_Missense_	NM_006143	NP_006134	Q15760	GPR19_HUMAN	ellular (Potential).	1	TGGCTGTTTCA	0.468	
-	3	424		NM_182558	NP_872364				0	GGAACGATTCC	0.453	rs143075618
+	2	412	_p.Q68R|C12orf72	NM_001135864	NP_001129336	Q8IXQ9	MET20_HUMAN		0	AATCCAGTTGC	0.552	
+	4	751	GD4_uc010ske.1_	NM_139241	NP_640334	Q96M96	FGD4_HUMAN	t-binding (By similarity).	3	CCAACGGTGTA	0.483	
-	13	1821		NM_004818	NP_004809	Q9BUQ8	DDX23_HUMAN	ase ATP-binding.	6	TGTCTGGCTTC	0.527	
-	12	1347	_p.M335I|LMBR1L	NM_018113	NP_060583	Q6UX01	LMBRL_HUMAN	ellular (Potential).	1	ACCTGCATGCC	0.617	
-	19	2503	rut.1_Missense_M	NM_175736	NP_783863	Q8IVF7	FMNL3_HUMAN	FH2.	4	CTTGACGGAAG	0.547	
+	21	2981	ryo.2_Missense_	NM_001039960	NP_001035049	Q2Y0W8	S4A8_HUMAN	ellular (Potential).	5	TGCCCGCAAAG	0.507	rs146086054
+	10	1541	81_uc001sac.2_5'	NM_002284	NP_002275	O43790	KRT86_HUMAN	Tail.	1	ACGCCTGCGCC	0.672	
-	9	1523		NM_004693	NP_004684	O95678	K2C75_HUMAN	Tail.	0	GTAGCCGCTGC	0.627	
-	6	1268	T8_uc009zml.1_	NM_002273	NP_002264	P05787	K2C8_HUMAN	Rod.|Coil 2.	2	GGTGGCGATCT	0.667	
-	9	1097	s.3_Nonsense_M	NM_015665	NP_056480	Q9NRG9	AAAS_HUMAN	WD 4.	1	TCACCGAAAGA	0.562	rs121918547
+	11	1588	R2_uc009zmy.1_3	NM_020547	NP_065434	Q16671	AMHR2_HUMAN	Potential).|Protein kinase.	2	AGCAGCGCCTG	0.597	
-	8	1229	.P84S|MMP19_uc	NM_002429	NP_002420	Q99542	MMP19_HUMAN	mopexin-like 2.	1	CTTGGGGAAGC	0.458	
+	12	1237	e_Mutation_p.R32	NM_001345	NP_001336	P23743	DGKA_HUMAN		4	TGCTCCGGGAT	0.602	
-	10	1254	_Mutation_p.P289	NM_004077	NP_004068	O75390	CISY_HUMAN		0	ATCGCGGATCA	0.413	
-	18	2324		NM_003920	NP_003911	Q9UNS1	TIM_HUMAN		8	TGTGGGCACTA	0.493	rs138087467
-	5	446	2_RNA|TAC3_uc0	NM_013251	NP_037383	Q9UHF0	TKNK_HUMAN		2	TGGCTGGACGC	0.502	
+	81	12924		NM_002332	NP_002323	Q07954	LRP1_HUMAN	|Extracellular (Potential).	22	TGACCGCAAGA	0.642	
-	4	526		NM_000619	NP_000610	P01579	IFNG_HUMAN		0	GTTCATGTATTG	0.433	
+	9	1732	_p.E578G|CPSF6_	NM_007007	NP_008938	Q16630	CPSF6_HUMAN	uclear targeting.|Arg-rich.	0	gaccgagagcgtgac	0.353	
+	2	977	C2_uc001szs.1_M	NM_152588	NP_689801	Q8N394	TMTC2_HUMAN	ical; (Potential).	2	ATGCAGCATGT	0.478	
-	1	1649		NM_152638	NP_689851	Q8TC90	CL012_HUMAN		2	TAACAGTTAAA	0.368	
-	10	1578	_p.A412G|SART3_	NM_014706	NP_055521	Q15020	SART3_HUMAN		1	TAAAGGCGGCC	0.458	
+	53	7398	CB_uc001tod.2_	NM_001093	NP_001084	O00763	ACACB_HUMAN		8	TGGCCGTGGAC	0.622	
-	68	11872		NM_001109662	NP_001103132				2	CGGTACCTGCT	0.617	
-	28	4117		NM_001109662	NP_001103132				2	TGTGGCTCGGG	0.542	
-	11	1276	24A6_uc001tva.2_	NM_024959	NP_079235	Q6J4K2	NCKX6_HUMAN	ellular (Potential).	1	GGGCCGTTTCC	0.622	
-	8	1223		NM_015335	NP_056150	Q71F56	MD13L_HUMAN		8	GGACTGGGTTC	0.418	
-	7	885		NM_015335	NP_056150	Q71F56	MD13L_HUMAN		8	CCATCCGAACA	0.428	
-	4	1241		NM_019086	NP_061959	Q8N0Z9	VSI10_HUMAN	3.|Extracellular (Potential).	0	GCAGCTGGCGC	0.522	
-	45	5710	.A1405V|CIT_uc0	NM_007174	NP_009105	O14578	CTRO_HUMAN		10	AGGACGCCAAG	0.607	
-	5	602	RPLP0_uc001txr.	NM_053275	NP_444505	P05388	RLA0_HUMAN		1	GCACAGTGACT	0.532	
+	3	869	yw.2_Missense_M	NM_001033677	NP_001028849	Q9NZU7	CABP1_HUMAN	EF-hand 2.	1	TCATCGAACTG	0.512	
-	2	651	ci.1_Missense_Mu	NM_002956	NP_002947	P30622	CLIP1_HUMAN	Ser-rich.	3	GAGGCGTAGCT	0.507	
-	1	451	PH9_uc010tam.1	NM_022782	NP_073619	Q99550	MPP9_HUMAN		0	CAGGAGAAATG	0.353	

+	20	2787		NM_012463	NP_036595	Q9Y487	VPP2_HUMAN	lasmic (Potential).		2	TTTCATCAAAGT	0.348	
-	3	1334		NM_133448	NP_597705	Q14C87	T132D_HUMAN	ellular (Potential).		14	GGCTCGCACGC	0.552	
+	3	852	jh.2_Missense_Mu	NM_025215	NP_079491	Q9Y606	TRUA_HUMAN			2	TCAGGCTGTATT	0.517	
+	5	1374	jh.2_Missense_Mu	NM_025215	NP_079491	Q9Y606	TRUA_HUMAN			2	TGGTCGGCCTG	0.622	
-	39	5422	ukr.1_Missense_M	NM_006231	NP_006222	Q07864	DPOE1_HUMAN			8	GGCACCTGAAG	0.552	
+	5	1614	NF10_uc001ulq.2_	NM_015394	NP_056209	P21506	ZNF10_HUMAN	2H2-type 6.		3	CAGAGCACACA	0.438	
-	2	423		NM_004004	NP_003995	P29033	CXB2_HUMAN	ellular (Potential).		0	GATGGGGAAGT	0.592	
+	18	1777	q.1_Missense_Mu	NM_175605	NP_783195	Q13099	IFT88_HUMAN	TPR 6.		1	GTGCAGCTGCA	0.343	
-	10	3641	.E871Q|SACS_uc	NM_014363	NP_055178	Q9NZJ4	SACS_HUMAN			12	ATTCTCAAGGA	0.348	
+	1	4159		NM_207361	NP_997244	Q5SZK8	FREM2_HUMAN	xtracellular	p.G1284G(1)	11	CAGATGGGAAG	0.408	
-	3	337	tez.1_Missense_	NM_145286	NP_660329	Q8TAV4	STML3_HUMAN	lasmic (Potential).		1	GATGCGTCCCA	0.473	rs139159531
-	1	200		NM_198849	NP_942146	Q8IW03	SIAH3_HUMAN			2	TGTGGGGTTGA	0.542	
-	13	2328	l8_uc010acm.2_M	NM_025113	NP_079389	Q9H714	CM018_HUMAN			0	CAGCAGCCCTT	0.542	
-	11	2011	.S334L|C13orf18_	NM_025113	NP_079389	Q9H714	CM018_HUMAN			0	TGCACGACTCT	0.517	
-	1	363	P1_uc001vni.2_I	NM_178861	NP_849192	Q8IZP6	R113B_HUMAN			3	CAGCGGTGGCC	0.692	
+	24	2025		NM_001846	NP_001837	P08572	CO4A2_HUMAN	e-helical region.		6	AGGCCGCGATG	0.632	
+	29	2682		NM_001846	NP_001837	P08572	CO4A2_HUMAN	e-helical region.		6	AGGCCTTCCCG	0.692	
+	2	1117	g.2_Missense_Mu	NM_005537	NP_005528	Q9UK53	ING1_HUMAN			1	TGGGCGACGAG	0.662	
+	19	2304	1A_uc001vsm.1_	NM_015205	NP_056020	P98196	AT11A_HUMAN	lasmic (Potential).		4	CAGCGGGAGCC	0.657	
+	1	53	gr.1_Missense_Mu	NM_003891	NP_003882	P22891	PROZ_HUMAN			0	TCCTCGCCCTC	0.607	
+	4	330	r.1_Missense_Mu	NM_003891	NP_003882	P22891	PROZ_HUMAN	EGF-like 1.		0	CTGGGGCTACA	0.607	
+	9	831	.2_Missense_Mut	NM_001008895	NP_001008895	Q13619	CUL4A_HUMAN			3	GACAGAGTAATC	0.413	
-	8	1061	u.2_Missense_Mu	NM_138376	NP_612385	Q8N0Z6	TTC5_HUMAN			1	TGACGGCACCG	0.527	
+	2	457	vyl.1_Missense_M	NM_002934	NP_002925	P10153	RNAS2_HUMAN			1	CACCAGCAAAC	0.458	
+	17	3783	10357_uc010aij.2_	NM_018071	NP_060541	Q8TER5	ARH40_HUMAN	DH.		0	GCAGAGACCTG	0.622	
+	4	581		NM_020366	NP_065099	Q96KN7	RPGR1_HUMAN			7	ACCCAGTGAAC	0.423	
-	2	349		NM_001344	NP_001335	P61803	DAD1_HUMAN			1	GCTCTGGGGAG	0.418	
-	11	1223	_p.R308*|RBM23	NM_001077351	NP_001070819	Q86U06	RBM23_HUMAN			1	CAGTCGCTCAG	0.547	
+	3	625	se_Mutation_p.G6	NM_182908	NP_878912	Q13268	DHRS2_HUMAN	ADP (By similarity).		2	GGGACGGGGCC	0.647	
+	11	1328	.1_Missense_Mut	NM_001163484	NP_001156956	Q8TEB1	DCA11_HUMAN			0	TGGGTGCACTG	0.562	
+	2	150	np.2_RNA|IRF9_u	NM_006084	NP_006075	Q00978	IRF9_HUMAN			1	ACGCTGCACCC	0.567	
-	2	319	IPK3_uc010toi.1_	NM_006871	NP_006862	Q9Y572	RIPK3_HUMAN	rotein kinas	p.R37R(1)	4	CGCCCGGAACA	0.627	
+	8	2971	ml.2_Missense_Mu	NM_004274	NP_004265	Q13023	AKAP6_HUMAN			21	TGTACAGCGAGC	0.443	
-	4	1936		NM_203301	NP_976046	Q7Z6M2	FBX33_HUMAN			0	TGAGTGATTCG	0.443	
-	1	292	14orf104_uc001w	NM_018139	NP_060609	Q9NVR5	KTU_HUMAN			0	CGGGTGCACGA	0.711	
+	8	601	qw.1_Missense_M	NM_002806	NP_002797	P62333	PRS10_HUMAN			1	GAGCCGTTGCT	0.289	
-	17	1632	apo.2_Missense_	NM_174978	NP_777638	Q08AQ4	Q08AQ4_HUMAN			4	TTCTTGCAGAAT	0.279	
-	25	5456	.R1801H|SPTB_u	NM_000347	NP_000338	P11277	SPTB1_HUMAN	Spectrin 15.		11	AGTAGCGGTGC	0.652	
+	6	1775	T8_uc001xir.3_R	NM_178155	NP_835368	Q9BYC5	FUT8_HUMAN	enal (Potential).		1	TTCAGCGGAGAA	0.373	
+	2	362	010aqz.2_Translat	NM_014734	NP_055549	Q92537	K0247_HUMAN			3	TTGCCGTGGCC	0.478	
-	7	2138	_p.A85T|ZFYVE1_	NM_021260	NP_067083	Q9HBF4	ZFYV1_HUMAN			1	TTTTGCGAGAC	0.512	
+	4	407	25_uc010ttu.1_M	NM_021239	NP_067062	P49756	RBM25_HUMAN			4	TGGGCGCAAGA	0.378	rs143840737
+	6	720	se_Mutation_p.V1	NM_182476	NP_872282	Q9Y2Z9	COQ6_HUMAN			0	CCGGAGTACGG	0.493	
+	1	500		NM_019589	NP_062535	P49750	YLPM1_HUMAN	Pro-rich.		3	AACACCAGATG	0.667	
-	1	857	X2_uc001xqq.1_I	NM_001080408	NP_001073877	Q3B8N5	PROX2_HUMAN			0	AGGCAGCCAAA	0.577	
-	2	3239	e_Mutation_p.P10	NM_001040108	NP_001035197	Q9UHC1	MLH3_HUMAN			2	TCTACCGGATTC	0.393	
+	4	579	1xtc.1_Missense_	NM_033426	NP_219494	Q9C0C6	K1737_HUMAN			0	CACCTGTACCA	0.512	

+	4	991	xtc.1_Missense_	NM_033426	NP_219494	Q9C0C6	K1737_HUMAN		0	AGACAGCACTC	0.567	
-	4	998	2_uc010asx.2_3'U	NM_000793	NP_000784	Q92813	IOD2_HUMAN		1	GCTCCAGAAGC	0.557	
-	7	1544	_p.D10N|C14orf10	NM_017970	NP_060440	Q9H7Z3	CN102_HUMAN		3	GCTGTCGGGTT	0.552	
+	5	500	LM1_uc010atr.1_	NM_006888	NP_008819	P62158	CALM_HUMAN	F-hand 3.|3.	1	AATGGTTATATC	0.398	
+	6	1901	_p.S508R|RIN3_u	NM_024832	NP_079108	Q8TB24	RIN3_HUMAN		3	CTGAGCTTTGC	0.592	
-	6	588	_p.S84P|BEGAIN_	NM_001159531	NP_001153003	Q9BUH8	BEGIN_HUMAN		0	ATCCGAGGGCA	0.672	
+	9	1799		NM_015656	NP_056471	Q9ULI4	KI26A_HUMAN	inesin-motor.	1	CCGACGCAGCT	0.701	
+	4	250	80_uc001yrn.2_5'	NM_001311	NP_001302	P50238	CRIP1_HUMAN		0	TTGCAGCACGA	0.567	
-	19	2892	2P2_uc001yvo.3_5'Flank|HERC2P2_uc001yvp.3_Intron						0	TCTCCATGAGGC	0.493	
+	2	308		NM_207444	NP_997327	Q8NAA6	CO053_HUMAN		0	GCTGGGTCCAA	0.483	
+	3	1668	p.1_Missense_M	NM_014952	NP_055767	Q8TBE0	BAHD1_HUMAN		0	TAGCCCGTGCG	0.667	
+	9	1110	_p.A272T|RAD51_	NM_002875	NP_002866	Q06609	RAD51_HUMAN		0	TGGTAGCTCAA	0.453	
-	19	2419	80_uc010ucu.1_	NM_017553	NP_060023	Q9ULG1	INO80_HUMAN	served components INO8	4	CATGTGTAAGC	0.373	
+	13	1291	_p.C628Y|JMJD7	NM_001114633	NP_001108105	P0C869	PA24B_HUMAN	PLA2c.	1	AAGCTGCTTCA	0.483	
+	16	1675	_p.R756H|JMJD7-	NM_001114633	NP_001108105	P0C869	PA24B_HUMAN	PLA2c.	1	GGACCGCTGGG	0.637	
+	8	1117	e_Mutation_p.L29	NM_014444	NP_055259	Q9UGJ1	GCP4_HUMAN		3	TGAACCTGACT	0.433	
+	10	1319	_Mutation_p.A325	NM_017434	NP_059130	Q9NRD9	DUOX1_HUMAN	roxidase activity.|Extracellu	8	TGGCGGCCTCT	0.572	
-	55	6987	N1_uc010beo.1_R	NM_000138	NP_000129	P35555	FBN1_HUMAN	38; calcium-binding.	3	CACATCGGAAG	0.458	
-	10	1051	xm.2_Missense_	NM_152647	NP_689860	Q96M60	CO033_HUMAN		1	AACAATCAGGAT	0.254	
-	13	1223	8B4_uc010ufd.1_	NM_024837	NP_079113	Q8TF62	AT8B4_HUMAN	lasmic (Potential).	8	CTTCCGGTCCC	0.393	
+	5	1019	AQP9_uc010ugx.	NM_020980	NP_066190	O43315	AQP9_HUMAN	ellular (Potential).	1	AGACCTGAGTC	0.557	
+	4	834	_Mutation_p.G76	NM_000236	NP_000227	P11150	LIPC_HUMAN		1	AGTGCGGCTTC	0.473	
+	6	1634		NM_032857	NP_116246	P83111	LACTB_HUMAN		0	TCAATAGCACCG	0.378	
+	8	710	ih.1_Missense_M	NM_016530	NP_057614	Q92930	RAB8B_HUMAN		2	TTGCTCGCTAC	0.458	
-	5	652	6A_uc002amu.1_	NM_032231	NP_115607	Q9H5X1	FA96A_HUMAN		0	CACTCGCTCTT	0.413	
+	1	184	OX5_uc002aro.2_	NM_024505	NP_078781	Q96PH1	NOX5_HUMAN	cts with the C-terminal cat	2	TGCCGGCTTAT	0.632	
-	18	3110	_p.S245L|TLE3_u	NM_005078	NP_005069	Q04726	TLE3_HUMAN	WD 5.	2	CCAGCGAGAAG	0.622	
-	16	2933	_p.L186P|TLE3_u	NM_005078	NP_005069	Q04726	TLE3_HUMAN	WD 3.	2	TGTGCAGGTCC	0.592	
-	7	1174	.R325Q|STOML1_	NM_004809	NP_004800	Q9UBI4	STML1_HUMAN	mic (Potential).|SCP2.	1	GGGGCCGCAGC	0.642	
-	2	1104	cu.1_Missense_M	NM_032808	NP_116197	Q96FE5	LIGO1_HUMAN	lar (Potential).|LRR 11.	2	ATTCCTCCAGT	0.652	
-	18	3032	TS7_uc010und.1_	NM_014272	NP_055087	Q9UKP4	ATS7_HUMAN		0	ACAGGGTACAT	0.662	
+	2	148	0unk.1_Missense_	NM_015206	NP_056021	Q9UPX6	K1024_HUMAN		4	AATACCGTTTCT	0.478	
+	7	567	n.1_Missense_Mu	NM_000137	NP_000128	P16930	FAAA_HUMAN		0	TGGCCGTGCCT	0.527	
-	4	1733	s.1_Missense_Mu	NM_001717	NP_001708	Q01954	BNC1_HUMAN		3	CAGCTTCTTTCT	0.458	
-	7	804	A|WDR73_uc010	NM_032856	NP_116245	Q6P4I2	WDR73_HUMAN		0	CTGAGCTCACA	0.617	
+	7	3273	13_uc002blu.1_Mi	NM_007200	NP_009131	Q12802	AKP13_HUMAN		9	TGGGGGCAGAG	0.597	
-	11	1962		NM_001150	NP_001141	P15144	AMPN_HUMAN	ular.|Metalloprotease.	4	CCGTGCTGGTA	0.597	
+	8	1199	L13_uc002bpe.1_	NM_001029964	NP_001025135	A6NNM8	TTL13_HUMAN	TTL.	0	TGTCCGGGATG	0.522	
-	12	1647	o.2_Missense_Mu	NM_003981	NP_003972	O43663	PRC1_HUMAN	tured, Arg/Lys rich.	2	TGGCCGTAGCAT	0.517	
+	30	4362	.1_Missense_Mut	NM_001271	NP_001262	O14647	CHD2_HUMAN		2	GGGGGGTGGAA	0.408	
-	10	1476	2bvx.1_Missense_	NM_139057	NP_620688	Q8TE56	ATS17_HUMAN	Disintegrin.	3	TGCCCGGCAGC	0.582	rs144488545
-	5	593	_p.T123M|TM2D3_	NM_078474	NP_510883	Q9BRN9	TM2D3_HUMAN	ical; (Potential).	1	GAGCCGTAGAC	0.393	
-	4	506	xj.2_Missense_M	NM_078474	NP_510883	Q9BRN9	TM2D3_HUMAN		1	GCACCGTGCAG	0.498	rs144526936
+	7	1578	3P_uc002cdp.2_	NR_003659					0	CCTGCCCGGCA	0.582	
+	2	1428	KN1_uc002chs.1_	NM_053284	NP_444514	Q96NZ8	WFKN1_HUMAN	Kunitz inhibitor 2.	0	GCAACGGCAAC	0.731	
+	19	1877	ation_p.A383T|R	NM_138769	NP_620124	Q8IXI1	MIRO2_HUMAN	type IV membrane protein;	1	TGGCCGCAGTC	0.642	
+	4	982	c010bra.1_5'Flan	NM_024042	NP_076947	Q9UJH8	METRN_HUMAN		0	CCTGCGAGGTG	0.672	

-	7	1487		NM_001025190	NP_001020361	Q96KJ4	MSLNL_HUMAN			4	CCATCCTGCCC	0.756
+	22	2511	v.1_Missense_Mu	NM_000548	NP_000539	P49815	TSC2_HUMAN		p.E793fs*9(1)	10	TGCCAGCCAGT	0.632
-	15	4689	t.1_Missense_Mut	NM_001009944	NP_001009944	P98161	PKD1_HUMAN	ar (Potential).|PKD 10.		3	GGGGCGCCCAC	0.652
+	1	1034		NM_020982	NP_066192	O95484	CLD9_HUMAN	ellular (Potential).		0	TGGTGGCCCAG	0.667
+	1	411		NR_002169						0	TGACCGCTTTG	0.512
-	22	4045	vw.2_Missense_M	NM_004380	NP_004371	Q92793	CBP_HUMAN	Cys/His-rich.		127	AATCAACGAAAC	0.512
-	2	2032		NM_001116	NP_001107	O60503	ADCY9_HUMAN	tential).|Guanylate cyclase		6	GGATGCCGCAA	0.557
-	2	1162		NM_001116	NP_001107	O60503	ADCY9_HUMAN	ellular (Potential).		6	TGGCCGTAAGG	0.582
-	20	2119	uxh.1_Missense_M	NM_024535	NP_078811	P57737	CORO7_HUMAN	WD 7.		0	ACTCCGGGGC	0.647
+	4	431	ws.3_Missense_M	NM_001127206	NP_001120678	P30519	HMOX2_HUMAN			0	GGAGCGCAACA	0.562
+	11	1828	g.2_Missense_Mu	NM_000246	NP_000237	P33076	C2TA_HUMAN	NACHT.		1	TTTGAGCTGTC	0.627
-	14	3097	uzv.1_Missense_M	NM_014647	NP_055462	Q9Y4F3	LKAP_HUMAN			0	TTCTAACTCTTC	0.478
-	14	1716	dx.2_Missense_Mu	NM_002474	NP_002465	P35749	MYH11_HUMAN	osin head-like.		15	TTCCTCGTCCA	0.572
+	16	2222	vl.2_Missense_Mu	NM_004996	NP_004987	P33527	MRP1_HUMAN	ter 1.|ATP 1.|Cytoplasmic.		4	GCTGCGGAAAG	0.612
-	2	874	vav.1_Missense_M	NM_016235	NP_057319	Q9NZH0	GPC5B_HUMAN	ellular (Potential).		3	GCCGAAGAGGT	0.607
-	13	3651		NM_024675	NP_078951	Q86YC2	PALB2_HUMAN	RAD51 and BRCA2.|WD 6		11	TGGGAGGAGGG	0.458
-	1	284	e_Mutation_p.P39	NM_033266	NP_150296	Q76MJ5	ERN2_HUMAN			6	GCCAGGTCCCT	0.741
+	4	1052	_uc002drl.2_Misse	NM_001145795	NP_001139267	Q9NRF2	SH2B1_HUMAN	phosphorylation) (By simil		2	CTGGCGGGGCT	0.647
+	4	443	p.S72N|KIF22_uc	NM_007317	NP_015556	Q14807	KIF22_HUMAN	inesin-motor.		0	GGGCAGCCCAG	0.602
+	7	899	_uc010vdz.1_RN	NM_005115	NP_005106	Q14764	MVP_HUMAN	MVP 5.	p.P272L(1)	4	TTGTGCCCATCA	0.642
+	7	1298	_uc002dvc.1_Miss	NM_016151	NP_057235	Q9UL54	TAOK2_HUMAN	rotein kinase.		1	TTGGTTCTGCGT	0.557
+	2	2768		NM_014699	NP_055514	O15015	ZN646_HUMAN	2H2-type 14.		2	ACTGTGGGCAT	0.612
-	15	2361	fg.1_Missense_Mu	NM_173502	NP_775773	Q5K4E3	POLS2_HUMAN	eptidase S1 3.		1	GGGCGGTGCTG	0.637
-	6	678	vfq.1_Missense_M	NM_022744	NP_073581	Q96GQ5	CP058_HUMAN			2	ATGTTGTTCCT	0.637
-	3	561	ETO2_uc002ees.	NM_018092	NP_060562	Q8NC67	NETO2_HUMAN	lar (Potential).|CUB 1.		0	TTGGCGAAGCA	0.383
+	11	1818	NP2_uc002efj.1_	NM_031490	NP_113678	Q86WA8	LONP2_HUMAN			0	TGGCCGTGAAG	0.483
-	2	545	_RNA|SIAH1_uc00	NM_003031	NP_003022	Q8IUQ4	SIAH1_HUMAN	AH-type.|SBD.		1	ATTACAGCATCC	0.468
-	1	498		NM_004352	NP_004343	P23435	CBLN1_HUMAN			0	ACAGAGATGCC	0.627
-	5	1149	gn.1_Missense_M	NM_015069	NP_055884	Q2M1K9	ZN423_HUMAN	2H2-type 6.		4	GGCGGGTGAGC	0.607
-	3	508	_p.L108F|TOX3_u	NM_001080430	NP_001073899	O15405	TOX3_HUMAN			0	AGGGAGGTCCA	0.483
+	1	729	.3_Intron|LPCAT2_	NM_032330	NP_115706	Q96L46	CPNS2_HUMAN	EF-hand 4.		0	GGTCCGCCTGG	0.438
+	45	5444	LRC5_uc002ekq.1	NM_032206	NP_115582	Q86WI3	NLRC5_HUMAN			7	GCTCCCGCTGC	0.617
-	2	1321		NM_020807	NP_065858	Q9P2F9	ZN319_HUMAN	2H2-type 5.		0	ACAGCGTGCAC	0.607
+	2	337	se_Mutation_p.P6	NM_001160305	NP_001153777	Q8TBK2	SETD6_HUMAN	SET.		1	GGTGCCGCGGG	0.682
-	1	106	0vim.1_Translatio	NM_002080	NP_002071	P00505	AATM_HUMAN			2	GGACCGTAGGA	0.716
+	5	634	e_Mutation_p.S18	NM_024922	NP_079198	Q6UWW8	EST3_HUMAN			5	CCCAGCACTGG	0.587
-	3	1479	|KIAA0895L_uc00	NM_001040715	NP_001035805	Q68EN5	K895L_HUMAN			0	CAGCGCAGCCC	0.587
+	12	4264	cef.2_Missense_M	NM_015432	NP_056247	Q58EX7	PKHG4_HUMAN			2	TGTTGGCAGAG	0.527
-	8	1220		NM_013304	NP_037436	Q8WTX9	ZDHC1_HUMAN			0	GGGCCGCATCT	0.627
-	8	1097	FBP1_uc002fce.2_	NM_031293	NP_112583	Q8TBY8	PMFBP_HUMAN	Potential.		2	GTGCTTCAGTA	0.512
-	19	3119	1L2_uc002fgg.1_	NM_052892	NP_443124	Q7Z442	PK1L2_HUMAN	racellular (Potential).		3	TGACTCGAAGC	0.562
+	13	1273	g.1_Nonsense_M	NM_002661	NP_002652	P16885	PLCG2_HUMAN	I-PLC X-box.		8	TGGCTGGACGC	0.577
+	13	1279	g.1_Missense_Mu	NM_002661	NP_002652	P16885	PLCG2_HUMAN	I-PLC X-box.		8	GACGCGGACTA	0.557
-	8	1185	se_Mutation_p.P3	NM_017740	NP_060210	Q9NXF8	ZDHC7_HUMAN			1	GGGGGGCCCCC	0.572
-	9	6220	_Mutation_p.T192	NM_013275	NP_037407	Q6UB99	ANR11_HUMAN	Pro-rich.		6	CGGCCGTCGCC	0.692
+	18	1694	cke.2_Missense_	NM_015085	NP_055900	Q684P5	RPGP2_HUMAN			1	CAACAGCATGG	0.667
-	7	1845	_p.L438V|TRPV1_	NM_080706	NP_542437	Q8NER1	TRPV1_HUMAN	ical; (Potential).		1	GACCAGGAAGT	0.582

-	16	2484	_p.T778M|ATP2A3	NM_174955	NP_777615	Q93084	AT2A3_HUMAN	nal (By similarity).	5	ATTGCCGTGAGG	0.642	
-	18	2535	_p.R834*|ANKFY1_	NM_016376	NP_057460	Q9P2R3	ANFY1_HUMAN		3	TGTCTCGTACATT	0.537	
-	3	488	zz.2_Missense_Mu	NM_005022	NP_005013	P07737	PROF1_HUMAN		0	GGACACCTTCTTT	0.552	
-	16	2884	_p.A925T|CAMTA2	NM_015099	NP_055914	O94983	CMTA2_HUMAN		1	TGTCAGCGTCCT	0.577	rs142999940
-	4	343		NM_016041	NP_057125	Q9GZP9	DERL2_HUMAN		0	AGGATACGGTCAT	0.428	
+	6	571	2gfh.1_Missense_M	NM_203415	NP_981960	Q8TE02	DERP6_HUMAN		0	GTGACAGCTCCT	0.537	
+	7	1091	.V311M|TNK1_uc0	NM_003985	NP_003976	Q13470	TNK1_HUMAN	rotein kinase.	3	TTGGGGTGACG	0.672	
+	3	423	F11_uc010vtw.1_In	NM_175734	NP_783861	Q0P670	CQ074_HUMAN		0	ATCACAGTAGCA	0.423	
-	4	1839	hd.3_Missense_Mu	NM_001128833	NP_001122305	Q9P1Z0	ZBTB4_HUMAN	Pro-rich.	4	GTGGCTGCAGGC	0.667	rs144969522
+	48	7656		NM_020877	NP_065928	Q9P225	DYH2_HUMAN	3 (By similarity).	13	CGGAGTCGCTTC	0.587	
+	11	1561	e_Mutation_p.R52	NM_153210	NP_694942	Q70EL4	UBP43_HUMAN		5	AGGAGCGAGCG	0.577	
-	30	4176	_Missense_Mutatio	NM_001100112	NP_001093582	Q9UKX2	MYH2_HUMAN	Potential.	14	TTCCCGCAGCA	0.547	
+	8	904	0vvi.1_Missense_M	NM_003010	NP_003001	P45985	MP2K4_HUMAN	rotein kinas.?(3)|p.A279T(	58	CCAAGCGCATCA	0.428	
-	3	430	vq.1_Missense_Mu	NM_018127	NP_060597	Q9BQ52	RNZ2_HUMAN		0	TGCATTCGTGTCA	0.418	
-	4	952	e_Mutation_p.P13	NM_006470	NP_006461	O95361	TRI16_HUMAN	B box-type 2.	3	TGGGCAGGGCAG	0.572	
-	5	744	n.2_3'UTR|UNC11	NM_005148	NP_005139	Q13432	U119A_HUMAN		0	CAGCCGGTCAT	0.612	
+	7	806	crt.2_Missense_Mu	NM_003170	NP_003161	Q7KZ85	SPT6H_HUMAN	Asp/Glu-rich.	3	AGGAAGAGTATG	0.468	
-	3	660	se_Mutation_p.T1	NM_001017368	NP_001017368	Q8WZ73	RFFL_HUMAN		0	GCTGGGTCAGGA	0.597	
-	5	956		NM_139285	NP_644814	Q8NHY3	GA2L2_HUMAN		2	TGATGGTCATTG	0.617	
+	7	633	F15_uc002hkc.2_M	NM_139215	NP_631961	Q92804	RBP56_HUMAN	Gly/Ser/Tyr-rich.	35	AGGGAGGAGGT	0.428	
+	11	1785	e_Mutation_p.L26	NM_005937	NP_005928	P55198	AF17_HUMAN		6	CCGCCTCAGCC	0.687	
+	6	902	B2_uc010cwb.2_M	NM_004448	NP_004439	P04626	ERBB2_HUMAN	cellular (Potential).	143	GTGCCGGTGGC	0.647	
+	5	773	vc.2_Missense_Mu	NM_005310	NP_005301	Q14451	GRB7_HUMAN	as-associating.	5	GTGGGCGGAGAT	0.597	
+	3	929		NM_001552	NP_001543	P22692	IBP4_HUMAN	oglobulin type-1.	0	CGACCGCAACG	0.667	
-	1	520		NM_033059	NP_149048	Q9BYQ6	KR411_HUMAN	C-[GIKRQVHEL]- [SPTR]-[	0	GACGCAGGcagc	0.323	rs141357429
-	1	216		NM_033188	NP_149445	Q9BYR2	KRA45_HUMAN	[GRQVCHIEK]- [SPTR]-[V	0	gagatgcagcagctag	0.274	
-	1	215		NM_032524	NP_115913	Q9BYR3	KRA44_HUMAN	f C-C-[GRQVCH]-[SPT]- [V	0	GCAGGTGGTCC	0.667	
-	8	1326	P_uc010wfs.1_Intr	NM_000422	NP_000413	Q04695	K1C17_HUMAN	Tail.	2	GTCACCGCTGCA	0.632	
+	3	395	1_3'UTR|GRN_uc	NM_002087	NP_002078	P28799	GRN_HUMAN		5	GGGTGGCCCCT	0.582	
-	11	1005	2B_uc002igu.1_5'	NM_000419	NP_000410	P08514	ITA2B_HUMAN	Extracellular (Potential).	3	TGACAGCCACTG	0.562	
+	11	1425	MT1_uc002iia.2_RI	NM_021079	NP_066565	P30419	NMT1_HUMAN		0	GGCATAGGGGA	0.517	
+	17	2372	p.R534H|KPNB1_	NM_002265	NP_002256	Q14974	IMB1_HUMAN		3	TGTGCCGTGCCC	0.468	
-	45	3406		NM_000088	NP_000079	P02452	CO1A1_HUMAN	(Potential).|Triple-helical re	382	GTCACCACGGG	0.582	
+	16	2602	BPAP_uc002iqz.2_	NM_032133	NP_115509	Q8TBZ2	MYBPP_HUMAN		6	CGAGATGTGATT	0.537	
+	9	2435	c002irv.1_Nonsens	NM_018896	NP_061496	O43497	CAC1G_HUMAN	lasmic (Potential).	1	CTGACTCAGACA	0.652	
-	9	1610		NM_000250	NP_000241	P05164	PERM_HUMAN		4	CGGTACGTGGGC	0.567	
-	1	435		NM_001080439	NP_001073908	Q4G112	HSF5_HUMAN	By similarity.	3	CCATTGCCTGCC	0.652	
-	1	1134	l_5'Flank|SEPT4_	NM_001038704	NP_001033793	Q8NEP4	CQ047_HUMAN		1	ACCCTGCGGCCA	0.542	
-	20	3540	_p.L714F|HEATR6_	NM_022070	NP_071353	Q6AI08	HEAT6_HUMAN		2	CTGGGAGTGCCC	0.498	
+	25	4393	TANC2_uc002jao.3	NM_025185	NP_079461	Q9HCD6	TANC2_HUMAN		2	TCTCCAGCTCAC	0.602	
-	8	695		NM_001433	NP_001424	O75460	ERN1_HUMAN	nenal (Potential).	9	GGACATCTCTGTA	0.507	
-	17	2378	_p.D423Y|SMURF2	NM_022739	NP_073576	Q9HAU4	SMUF2_HUMAN	HECT.	4	CTTCATCAAAAA	0.458	
-	3	2773	37A3_uc010wqf.1_	NM_199340	NP_955372	O60309	L37A3_HUMAN	cellular (Potential).	0	CTGGAAGCTGAG	0.517	
-	1	117	D12_uc002jfz.2_5	NM_002816	NP_002807	O00232	PSD12_HUMAN		0	GCGCCCGTCAG	0.677	
+	24	8268	gg.2_Missense_Mu	NM_182641	NP_872579	Q12830	BPTF_HUMAN		4	AGGAAACTAAGA	0.388	
+	3	1194	SG_uc002jhb.1_5'U	NM_014960	NP_055775	Q96EG1	ARSG_HUMAN		1	TCACTGGGATAAT	0.547	
-	29	4300	se_Mutation_p.G13	NM_080282	NP_525021	Q8WWZ4	ABCAA_HUMAN		4	CATTTCCATACTT	0.259	

+	6	1450	rq.1_Missense_M	NM_178233	NP_839947	Q7RTS5	OTOP3_HUMAN		1	CCGAGGGCCTG	0.657	
+	13	1642	p.R466H|KIAA019	NM_014738	NP_055553	Q12767	K0195_HUMAN		1	CACCCGCTCCT	0.637	
-	14	1991	vsc.1_Missense_M	NM_020753	NP_065804	Q8WXE0	CSKI2_HUMAN		1	TGGCCGCACGT	0.642	
-	4	508	ra.2_Missense_M	NM_052916	NP_443148	Q96PX1	RN157_HUMAN		1	CCTGGCAATAC	0.483	
-	9	1555	_p.S497F|UBE2O_	NM_022066	NP_071349	Q9C0C9	UBE2O_HUMAN		5	TGGCAGAGGAG	0.562	
-	8	1753	se_Mutation_p.L39	NM_018414	NP_060884	Q9NSC7	SIA7A_HUMAN	enal (Potential).	0	AGTGAGCAGCA	0.577	
-	5	1724		NM_003655	NP_003646	O00257	CBX4_HUMAN	action with BMI1.	2	GGCCTCGGCTG	0.488	
-	2	259		NM_019020	NP_061893	Q8TBP0	TBC16_HUMAN		0	CCGGCGGGTGC	0.672	
-	33	5785	N_uc002kdv.1_5'F	NM_004104	NP_004095	P49327	FAS_HUMAN	y similarity).|NADP (KR) (B	1	CACCAGCGATGA	0.632	rs139792253
+	29	2702	e_Mutation_p.D18	NM_005993	NP_005984	Q9BTW9	TBCD_HUMAN		0	TGGACGACTAC	0.567	
-	18	2930	M1_uc002klq.2_I	NM_003803	NP_003794	P52179	MYOM1_HUMAN		5	TGGCGGGGAGG	0.557	
-	3	295	A70V|EPB41L3_uc	NM_012307	NP_036439	Q9Y2J2	E41L3_HUMAN		5	TGGCAGCAAAC	0.403	
-	35	6092	.1_Intron|KIAA163	NM_020964	NP_066015	Q9HCE0	EPG5_HUMAN		0	GCTTGAGGCCA	0.438	
-	5	1565	lbo.1_Missense_M	NM_020964	NP_066015	Q9HCE0	EPG5_HUMAN		0	AACACCAGCGG	0.428	
-	7	1254	y.1_Missense_Mu	NM_013305	NP_037437	O15466	SIA8E_HUMAN	enal (Potential).	3	GCCGCCGCCAC	0.647	
-	2	273		NM_145020	NP_659457	Q96M91	CCD11_HUMAN		3	TCAAGCGATCC	0.468	
-	5	4930	k.1_Missense_M	NM_052947	NP_443179	Q86TB3	ALPK2_HUMAN		14	CTCAACTATGTC	0.458	
-	3	450	se_Mutation_p.K1	NM_021153	NP_066976	Q9H159	CAD19_HUMAN	|Extracellular (Potential).	2	TCAAGCTTCTG	0.433	
-	2	3764		NM_032160	NP_115536	Q8IZU8	DSEL_HUMAN		6	TTCCCTCAGCC	0.428	
-	3	1024		NM_001044369	NP_001037834	Q0P6D2	FA69C_HUMAN	enal (Potential).	0	CTGCGCTCCGC	0.488	
-	2	1947	sr.1_Missense_Mu	NM_020695	NP_065746	Q8N1G1	REXO1_HUMAN		0	GATCCGCAGGC	0.612	
-	2	822	sr.1_Missense_Mu	NM_020695	NP_065746	Q8N1G1	REXO1_HUMAN		0	GTGCCGGGCCG	0.692	
+	6	550	_p.S59N|HMG20B_	NM_006339	NP_006330	Q9P0W2	HM20B_HUMAN		0	CTCGAGCTCTG	0.622	
-	2	281	lzd.1_Missense_M	NM_001348	NP_001339	O43293	DAPK3_HUMAN	rotein kinase.	7	CCTCCCGCTCG	0.627	
-	3	1385	4_uc010dub.1_5'F	NM_001080400	NP_001073869	Q96Q06	PLIN4_HUMAN	roximate tandem repeat.|12	0	TCGCAGCACCG	0.582	
-	29	4601	v.2_Missense_Mut	NM_002850	NP_002841	Q13332	PTPRS_HUMAN	).|Tyrosine-protein phosph	4	GACACCGGTAG	0.607	
-	10	1145	w.2_Missense_M	NM_002850	NP_002841	Q13332	PTPRS_HUMAN	3.|Extracellular (Potential).	4	AGTCCTTGACA	0.622	
-	15	1581	mdz.2_Nonsense_	NM_007322	NP_015561	Q9H6Z4	RANB3_HUMAN	RanBD1.	1	CAGTCGCAGGC	0.617	
-	2	148	.2_5'UTR|DENND	NM_024898	NP_079174	Q8IV53	DEN1C_HUMAN		1	AGGCCGCTTCG	0.617	
+	2	328		NM_003811	NP_003802	P41273	TNFL9_HUMAN	ellular (Potential).	1	GGTGGCCCAAA	0.577	
-	41	4955	2_Missense_Muta	NM_000064	NP_000055	P01024	CO3_HUMAN	NTR.	5	TCGGGCCAGTG	0.612	
+	13	1466	e_Mutation_p.W41	NM_004240	NP_004231	Q15642	CIP4_HUMAN	raction with PDE6G (By sin	1	GGCGTGGCTGG	0.672	
+	5	585	41_splice|ZNF557_	NM_001044388	NP_001037853	Q8N988	ZN557_HUMAN		2	CTTTAGGGCTT	0.587	
-	9	1185		NM_020196	NP_064581	Q9HCS7	SYF1_HUMAN	HAT 9.	4	GAAGGGGTCCA	0.562	
-	4	453	vq.2_Missense_M	NM_021155	NP_066978	Q9NNX6	CD209_HUMAN	|2.|7 X approximate tanden	1	TCAGCCGGGTC	0.567	
-	3	25945		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	h.|Extracellular (Potential).	57	TGCTCTCTGGTA	0.532	
-	11	1303	pd.2_Missense_M	NM_005498	NP_005489	Q9Y6Q5	AP1M2_HUMAN	MHD.	2	CCAGGGCAGGG	0.582	
+	7	599	npe.3_Nonsense_	NM_020428	NP_065161	Q8IWA5	CTL2_HUMAN	ellular (Potential).	1	TGCTTCAAGAT	0.597	
-	26	3274	xlq.1_Missense_M	NM_020812	NP_065863	Q96HP0	DOCK6_HUMAN		3	GGGAGGTGGTG	0.607	
+	4	1602	ym.1_Missense_M	NM_001136501	NP_001129973	Q08AG5	ZN844_HUMAN		0	TCATTTTTTCCA	0.448	
+	12	1392	vk.2_Missense_M	NM_014975	NP_055790	Q9Y2H9	MAST1_HUMAN	rotein kinase.	7	TTTGTGGAGCGC	0.567	
-	20	3381	wy.3_Missense_M	NM_001127221	NP_001120693	O00555	CAC1A_HUMAN	lasmic (Potential).	2	TGGCCGGGTGG	0.582	
+	12	1684	F15_uc002mxu.2_	NM_138353	NP_612362	Q66K64	DCA15_HUMAN		1	TGGTCATGAAG	0.667	
-	6	1170	ense_Mutation_p.	NM_001008701	NP_001008701	O94910	LPHN1_HUMAN	ke.|Extracellular (Potential)	5	GCTCACCACCA	0.637	
-	6	665	X39_uc010dzl.2_F	NM_005804	NP_005795	O00148	DX39A_HUMAN	ase ATP-binding.	0	CCCGCCGCATG	0.627	
-	11	1572	_p.P423L|EMR3_u	NM_032571	NP_115960	Q9BY15	EMR3_HUMAN	Name=4; (Potential).	6	CAGCGGGAACG	0.522	
-	14	2313	_p.L83F|RASAL3_	NM_022904	NP_075055	Q86YV0	RASL3_HUMAN		0	CACAAGCACAG	0.612	

+	1	25		NM_001004466	NP_001004466	Q8NGA6	O10H5_HUMAN	cellular (Potential).		1	ACCTCCGTGTCT	0.572	
+	3	1064		NM_016270	NP_057354	Q9Y5W3	KLF2_HUMAN			0	GCACACGGGCC	0.622	
+	11	2916	p.Q697K|NWD1_uc002nev.3_Missense_Mutation_p.Q6			Q149M9	NWD1_HUMAN			7	CTATGCCAACAG	0.612	
-	1	90	nhx.1_Missense_	NM_005535	NP_005526	P42701	I12R1_HUMAN			1	GGGGGACCACC	0.672	
-	3	491	_p.P140L|LASS1_	NM_021267	NP_067090	P27539	GDF1_HUMAN			0	ATGCCCGGCGTC	0.617	
+	11	1172	392_uc010ecd.2_	NM_015329	NP_056144	Q9Y6X3	SCC4_HUMAN			0	ACCATGCAGCAC	0.552	
-	4	1319		NM_001159293	NP_001152765	C9JHM3	C9JHM3_HUMAN			1	GAGGACCAGTTG	0.418	
-	4	743	pc.1_Missense_M	NM_001076675	NP_001070143	Q68DY1	ZN626_HUMAN			1	GGTTTCCCTCCA	0.363	
+	2	903	_p.P336L|ZNF493_	NM_175910	NP_787106	Q6ZR52	ZN493_HUMAN	type 7; degenerate.		1	CAACCCCTACTA	0.348	rs142651314
+	2	1049	_p.A385T|ZNF493_	NM_175910	NP_787106	Q6ZR52	ZN493_HUMAN	C2H2-type 9.		1	GGCAAAGCCTTT	0.363	
-	5	1807	208_uc002nqo.1_	NM_007153	NP_009084					7	TGTGTAGTAAGG	0.383	
-	4	1122	_p.R258T|ZNF681_	NM_138286	NP_612143	Q96N22	ZN681_HUMAN	type 6; degenerate.		0	TATGTCTGGTAA	0.378	
+	5	467	nso.2_Missense_M	NM_001238	NP_001229	P24864	CCNE1_HUMAN		p.R95W(1)	2	AGCCTCGGATTA	0.547	
-	2	2859		NM_020856	NP_065907	Q63HK5	TSH3_HUMAN	neobox; atypical.		8	CATCCGCTCCTG	0.587	
+	1	126	PI_uc010xrw.1_Mi	NM_000175	NP_000166	P06744	G6PI_HUMAN			2	GGACCCCCAGT	0.657	
+	16	1517	PI_uc010xrw.1_Mis	NM_000175	NP_000166	P06744	G6PI_HUMAN			2	GGAAATCGCCCA	0.527	
+	5	652	dq.1_Missense_M	NM_194325	NP_919306	P17039	ZNF30_HUMAN			2	GAAGATGATACA	0.299	
+	5	1445		NM_144689	NP_653290	Q8TAQ5	ZN420_HUMAN	C2H2-type 10.		0	ACATCAGAGAATA	0.413	
+	95	13979	.2_Missense_Mut	NM_000540	NP_000531	P21817	RYR1_HUMAN			12	GGGCCGGAGAG	0.622	
-	3	610	e_Mutation_p.L67	NM_001533	NP_001524	P14866	HNRPL_HUMAN	RRM 2.		0	GGGTTCAGGATG	0.542	
+	19	3705	KHG2_uc002olj.2_	NM_022835	NP_073746	Q9H7P9	PKHG2_HUMAN	Pro-rich.		4	CCAACGCCCCAC	0.587	
-	6	2952		NM_003890	NP_003881	Q9Y6R7	FCGBP_HUMAN	VWFD 2.		9	TCCAGTCATAAGT	0.597	
+	9	1302	CYP2B6_uc010xvu	NM_000767	NP_000758	P20813	CP2B6_HUMAN			2	CCACAGGGAAG	0.567	
+	1	201	sense_Mutation_p.	NM_021913	NP_068713	P30530	UFO_HUMAN			13	GTGGCGGTGCC	0.726	
-	5	591	1_Intron|BCKDHA_	NM_020158	NP_064543	Q9NQT4	EXOS5_HUMAN			0	GCTTCCGTTCCA	0.582	
+	5	1254	E|ZNF155_uc010xv	NM_003445	NP_003436	Q12901	ZN155_HUMAN	C2H2-type 7.		2	AGTGTGGAAAAG	0.418	
+	5	821	F284_uc010ejd.2_	NM_001037813	NP_001032902	Q2VY69	ZN284_HUMAN			0	AGAAACGCTATA	0.408	
+	15	1731	ba.1_Missense_Mutation_p.D576N			Q96L34	MARK4_HUMAN			3	TCCGGGACCGG	0.662	
-	2	483		NM_000960	NP_000951	P43119	PI2R_HUMAN	lasmic (Potential).		0	GTAGGGGTGGC	0.692	
+	1	3440		NM_004491	NP_004482	Q9NRY4	RHG35_HUMAN			1	GAGGGCGCAAGG	0.557	
-	8	923	A_uc002phc.1_Mis	NM_003827	NP_003818	P54920	SNAA_HUMAN			0	GCCGCCTTGAAG	0.602	
+	6	1364	_p.H236Y|EHD2_u	NM_014601	NP_055416	Q9NZN4	EHD2_HUMAN			2	AAGTTTCACTCG	0.632	
-	13	1238	G1_uc010xzf.1_Mis	NM_000234	NP_000225	P18858	DNLI1_HUMAN			3	CGGCTGCCTCAC	0.687	
+	3	1139		NM_000836	NP_000827	O15399	NMDE4_HUMAN	cellular (Potential).		6	GCGCCCAGAAC	0.642	
-	4	852	C1_uc010ema.2_	NM_001217	NP_001208	O75493	CAH11_HUMAN			0	GTTCCCCGGAGC	0.547	
+	2	1012	c.2_Missense_Mu	NM_001097638	NP_001091107	Q10981	FUT2_HUMAN	menal (Potential).		1	CGGGCGGAGAC	0.557	rs144269088
-	3	224	2_uc002pkt.2_Intr	NM_001190	NP_001181	O15382	BCAT2_HUMAN			1	TGTGGTCGGTAA	0.592	
-	19	2565	uc002pkw.1_Miss	NM_020904	NP_065955	Q9H4M7	PKHA4_HUMAN			3	GAACCCGCTCCC	0.443	
+	3	322	_p.G50S|CCDC15	NM_144688	NP_653289	Q8N6L0	CC155_HUMAN			2	GGACAGGTGGT	0.642	
+	8	1134	Dyas.1_Missense_	NM_153329	NP_699160	Q8IZ83	A16A1_HUMAN			1	GGGCCGTGGAC	0.682	
+	16	1902	_p.A404P|MED25_	NM_030973	NP_112235	Q71SY5	MED25_HUMAN	n with RARA.|Pro-rich.		1	CCAGGTGCCCCT	0.726	
+	11	1378	LD1_uc010enx.2_	NM_002691	NP_002682	P28340	DPOD1_HUMAN			2	GCAGACGGGCC	0.622	
-	2	175		NM_001080457	NP_001073926	Q9NT99	LRC4B_HUMAN			2	CGGGCGGCAGC	0.716	
+	6	1236		NM_001099694	NP_001093164	Q96N58	ZN578_HUMAN	C2H2-type 4.		0	CCCTTACATGCC	0.423	
+	6	1320		NM_001099694	NP_001093164	Q96N58	ZN578_HUMAN	C2H2-type 5.		0	CCCTTAGATGCC	0.388	
+	7	619	Start_Site|ZNF761_	NM_001008401	NP_001008401	Q86XN6	ZN761_HUMAN	KRAB.		1	ATGCACGATGA	0.368	rs143107546
+	4	717	5'Flank|TSEN34_u	NM_024075	NP_076980	Q9BSV6	SEN34_HUMAN			0	ACTGGCGTGTCC	0.652	

-	4	629	gfi.2_Missense_Mu	NM_012276	NP_036408	P59901	LIRA4_HUMAN	Potential).|Ig-like C2-type 2.	2	AATGTACCCCTG	0.572	
-	5	1646	n.1_Missense_Mut	NM_003180	NP_003171	O00445	SYT5_HUMAN	mic (Potential).|C2 1.	0	AGTCGTACACCG	0.647	
-	19	2421	|SAPS1_uc002qjv.	NM_014931	NP_055746	Q9UPN7	PP6R1_HUMAN	Pro-rich.	0	TCGGGGGCTGG	0.687	
-	5	844	jjv.2_Missense_Mu	NM_014931	NP_055746	Q9UPN7	PP6R1_HUMAN	ction with PPP6C.	0	TCGACGGGTGG	0.577	
+	9	1977	lt.2_Missense_Mu	NM_007279	NP_009210	P26368	U2AF2_HUMAN	RRM 2.	1	GAGTACGTGGAC	0.627	
-	5	1865	b.2_Missense_Mut	NM_145007	NP_659444	P59045	NAL11_HUMAN	NACHT.	6	TGGCAGTAAGT	0.512	
+	3	1106		NM_021216	NP_067039	Q9NQZ8	ZNF71_HUMAN	C2H2-type 6.	1	CACCAGCGCACG	0.662	
-	10	2127	27A5_uc002qtb.2_	NM_012254	NP_036386	Q9Y2P5	S27A5_HUMAN	lasmic (Probable).	0	GGGCCGGAAGG	0.592	
-	24	4166	p.Q1111H|MYT1L_	NM_015025	NP_055840	Q9UL68	MYT1L_HUMAN	Potential.	6	CTCGTTCTGCTG	0.532	
+	1	1106		NM_002236	NP_002227	Q9H3M0	KCNF1_HUMAN		1	ATCCCCGAGCTG	0.672	
+	11	1483	hv.3_Missense_M	NM_020134	NP_064519	Q9BPU6	DPYL5_HUMAN		2	CAGCCGGGGGC	0.617	
-	3	613	2rkj.2_Missense_M	NM_144631	NP_653232	Q8N8E2	ZN513_HUMAN	Gly-rich.	1	CCACCCGGCCCT	0.706	
+	1	5386	1_5'Flank|ZNF512_	NM_032266	NP_115642	Q68DN1	CB016_HUMAN	m repeat of P-S-E-R-S-H-H	1	CCCTCTGAGAGA	0.527	
+	4	667	ymm.1_Missense_	NM_199280	NP_954974	Q6ZUX3	F179A_HUMAN		4	CTGGTGCTCCTC	0.617	
-	9	2724		NM_004304	NP_004295	Q9UM73	ALK_HUMAN	xtracellular (Potential).	1218	GCCTACCTGTCA	0.517	
-	5	680		NM_019024	NP_061897	Q9P2D3	HTR5B_HUMAN		8	ACTGCACATCGA	0.393	
+	9	1384		NM_005400	NP_005391	Q02156	KPCE_HUMAN		10	AAGTCCGGCAAG	0.587	
+	16	2805		NM_000251	NP_000242	P43246	MSH2_HUMAN		55	GAGAGACAGAAC	0.468	
+	16	3277	rxx.2_Missense_M	NM_003128	NP_003119	Q01082	SPTB2_HUMAN	Spectrin 7.	8	ATTGAGGCAAAG	0.652	
+	15	1559	OLG_uc002sak.2_I	NM_022894	NP_075045	Q9BWT3	PAPOG_HUMAN		2	TTTTCGGAGAGT	0.299	
+	8	855	_p.V285L|MDH1_u	NM_005917	NP_005908	P40925	MDHC_HUMAN		2	GAGTTTGTGTCC	0.378	
+	4	626		NM_014181	NP_054900	Q3ZCW2	LEGL_HUMAN	Galectin.	0	TGTGTTCACAGAT	0.473	
-	13	978	_uc010fet.2_Silent	NM_144579	NP_653180	Q8TD22	SFXN5_HUMAN		1	GGGGCGTGCCT	0.682	
+	10	1261	p.R345W|CCT7_uc	NM_006429	NP_006420	Q99832	TCPH_HUMAN		0	ACAGAGCGGTCC	0.547	
+	4	439	_p.L106P|ACTG2_	NM_001615	NP_001606	P63267	ACTH_HUMAN		0	CCCTGCTCACAG	0.527	
+	1	52	2_uc002slo.2_RNA	NM_022492	NP_071937	Q49AM3	TTC31_HUMAN		0	TGGGGCGGATCA	0.562	
+	3	511	ue.1_Missense_M	NM_021088	NP_066574	Q9BSG1	ZNF2_HUMAN	KRAB.	0	ACATTCGAAGAC	0.453	
+	8	1310	syl.1_5'UTR|VWA3	NM_144992	NP_659429	Q502W6	VWA3B_HUMAN		6	CCTGCAGCACGC	0.602	
-	7	1338	_p.D418N|TBC1D8	NM_001102426	NP_001095896	O95759	TBCD8_HUMAN		3	AGGTGTCGTAGT	0.602	
+	10	1400	ot.2_Missense_Mu	NM_003854	NP_003845	Q9HB29	ILRL2_HUMAN	oplasmic (Potential).	2	TATTCGGCAGAG	0.458	
+	3	655	Missense_Mutation	NM_001056	NP_001047	O00338	ST1C2_HUMAN		1	GGGACGTGGAG	0.468	rs17036055
+	2	682	ice_Site|BCL2L11_	NM_138621	NP_619527	O43521	B2L11_HUMAN		0	AATGGGTAAGCA	0.488	
-	1	1659		NR_002826					0	GCCGCAGGACC	0.637	
+	1	1046		NM_001508	NP_001499	O43194	GPR39_HUMAN	cellular (Potential).	0	TGCAACCGCTCC	0.632	
+	13	2774	HSD7B_uc002tvb.2	NM_001080427	NP_001073896				7	CAGACAGCAAAG	0.498	
+	14	2941	D7B_uc010zbj.1_I	NM_001080427	NP_001073896				7	GGGTCTTGCAGT	0.403	
+	12	4241	MBD5_uc002two.2_	NM_018328	NP_060798	Q9P267	MBD5_HUMAN		5	GCTTCCGTAGAT	0.502	
+	3	394	wz.2_RNA|LYPD6_	NM_194317	NP_919298	Q86Y78	LYPD6_HUMAN	UPAR/Ly6.	0	GCTCCAGACATC	0.463	
-	5	424		NM_004543	NP_004534	P20929	NEBU_HUMAN	Nebulin 1.	20	TTTGAAGGATCC	0.483	
-	2	163	_p.R14M|CACNB4	NM_000726	NP_000717	O00305	CACB4_HUMAN		2	TCAACCTGCTCC	0.662	
-	3	659	Ofof.2_Intron|ACVR	NM_145259	NP_660302	Q8NER5	ACV1C_HUMAN	lasmic (Potential).	7	CACTGTCGACCC	0.483	
+	27	5229	.R1647C|SCN2A_	NM_001040142	NP_001035232	Q99250	SCN2A_HUMAN	Name=S4 of repeat IV; (Pot	8	GGGATCCGCACG	0.493	
+	5	853	6PC2_uc010fpv.2_	NM_021176	NP_066999	Q9NQR9	G6PC2_HUMAN	ienal (Potential).	1	ACACCACGCCTT	0.522	
+	30	3673	O3B_uc002ufz.2_M	NM_138995	NP_620482	Q8WXR4	MYO3B_HUMAN		19	ATGGCCGTACAC	0.453	
+	7	731	_p.V54I|HAT1_uc	NM_003642	NP_003633	O14929	HAT1_HUMAN		2	GCGACCGTAGGC	0.438	
+	3	556	dy.1_Missense_Mu	NM_001079818	NP_001073286	P23229	ITA6_HUMAN	r (Potential).|FG-GAP 2.	2	GGGTCACCGTCC	0.522	
+	2	153	CA7_uc010zej.1_S	NM_145810	NP_665809	Q9BWT1	CDCA7_HUMAN		1	TTTGCAGCAGAA	0.348	

-	8	827	2ujr.2_RNA|ATF2_u	NM_001880	NP_001871	P15336	ATF2_HUMAN		3	AAGGTACTGCCT	0.438	
+	1	352		NM_152945	NP_694453	Q8IUH3	RBM45_HUMAN	RRM 1.	0	AGATGCATGGCC	0.652	
-	230	46720	194F|TTN_uc010z	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	GTGGGGATGGG	0.418	
-	225	45481	l_uc010zfi.1_Misse	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	CAGGCGGTCCT	0.438	
-	46	12490	.A4022V|TTN_uc0	NM_133437	NP_597681	Q8WZ42	TITIN_HUMAN		153	ATGAGCGCACTT	0.478	
-	46	16876	TN_uc010zfi.1_Intr	NM_133379	NP_596870	Q8WZ42	TITIN_HUMAN		153	AATTTTCCATCTT	0.413	
-	16	2923	p.K854R|TTN_uc0	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	ACTTCCTTTTTCA	0.547	
-	20	2995	_p.R421*|CWC22_	NM_020943	NP_065994	Q9HCG8	CWC22_HUMAN		0	TCTTCGCCGGT	0.348	
+	11	2639	FA2_uc010zfo.1_	NM_001130445	NP_001123917	P28290	SSFA2_HUMAN		2	TTCACCTATAAGT	0.448	
-	1	477		NM_005259	NP_005250	O14793	GDF8_HUMAN		1	GTTTCCGTTGTAG	0.438	
-	3	762	_p.E82G|KCTD18_	NM_152387	NP_689600	Q6PI47	KCD18_HUMAN		1	GTTTGCTCATCT	0.438	
+	3	679	D28_uc010ftx.2_M	NM_006139	NP_006130	P10747	CD28_HUMAN	ical; (Potential).	0	AGCCCTTTTGG	0.443	
+	20	3233	nse_Mutation_p.P	NM_152526	NP_689739	Q8TEW8	PAR3L_HUMAN		4	ACCATCCACTGG	0.433	
+	5	489	ank|NDUFS1_uc0	NM_001037663	NP_001032752	P24534	EF1B_HUMAN		0	TTACAGGAAAGT	0.358	
+	5	4932		NM_020923	NP_065974	Q9HCK1	ZDBF2_HUMAN		3	ATATCAGCTGTAT	0.388	
-	13	2739	dt.2_Missense_Mu	NM_152519	NP_689732	A0AUZ9	CB067_HUMAN		3	TGCTCCCATAGT	0.398	
-	11	1388	_p.S312F|USP37_	NM_020935	NP_065986	Q86T82	UBP37_HUMAN		5	TAACAGAAAGAG	0.438	
+	7	679	p.R227S|RQCD1_	NM_005444	NP_005435	Q92600	RCD1_HUMAN		2	TCTGCCCGTCTG	0.428	
-	8	4430	t.2_Missense_Mut	NM_001105537	NP_001099007	P52746	ZN142_HUMAN	C2H2-type 21.	4	ACAGCGGGAAC	0.657	
+	3	456	TLL4_uc010fvx.2_	NM_014640	NP_055455	Q14679	TTLL4_HUMAN		3	CAGTACCTGCCA	0.562	
-	9	3269	0zli.1_Missense_M	NM_015311	NP_056126	O75147	OBSL1_HUMAN	Ig-like 8.	0	GTGACAGTGAAG	0.632	
+	5	844	3_Missense_Muta	NM_005070	NP_005061	P48751	B3A3_HUMAN	Cytoplasmic.	5	GGTGGGCCCAC	0.637	
-	40	4435		NM_000092	NP_000083	P53420	CO4A4_HUMAN	le-helical region.	11	GATCTCCAGGTG	0.542	
-	28	2861		NM_000092	NP_000083	P53420	CO4A4_HUMAN	le-helical region.	11	GACCCCTTTTCA	0.498	
-	9	4723	.2_Intron|SPHKAF	NM_001142644	NP_001136116	Q2M3C7	SPKAP_HUMAN		10	TCCAGATCCATAA	0.448	
+	1	169	2vur.2_Intron|UGT	NM_019077	NP_061950	Q9HAW7	UD17_HUMAN		1	GTGGTCGTAGTC	0.547	
-	14	6298	p.P1799S|COL6A3	NM_004369	NP_004360	P12111	CO6A3_HUMAN	0.|Nonhelical region.	18	TCAGGGGCCTGT	0.493	
-	5	1100	Intron|ANKMY1_u	NM_016552	NP_057636	Q9P2S6	ANKY1_HUMAN		1	CTTTGCGTCCG	0.567	rs148452586
-	21	2106	p.E663K|KIF1A_u	NM_004321	NP_004312	Q12756	KIF1A_HUMAN	Potential.	1	CTCCTCCCGCT	0.721	
+	3	912	dn.2_Missense_Mu	NM_021158	NP_066981	Q96RU7	TRIB3_HUMAN	rotein kinase.	2	TACGCCTTTTTCA	0.672	
+	12	1925	M6_uc010gal.1_In	NM_198994	NP_945345	O95932	TGM3L_HUMAN		4	GTGGCAGTTACA	0.597	
+	16	1622	_p.R381Q|VPS16_	NM_022575	NP_072097	Q9H269	VPS16_HUMAN		4	CTGCACGAGCCT	0.592	rs143701351
-	6	662	20orf27_uc002wjh.	NM_001039140	NP_001034229	Q9GZN8	CT027_HUMAN		0	TGCCGTGGTGCC	0.662	
+	13	1679		NM_002862	NP_002853	P11216	PYGB_HUMAN		2	CTGCTGCCGCTG	0.617	
-	4	369	IL_uc010gdo.1_5'U	NM_025176	NP_079452	Q9Y2I6	NINL_HUMAN		5	TGGAGGGATGG	0.572	
-	2	793	2wwn.2_Missense	NM_138578	NP_612815	Q07817	B2CL1_HUMAN	BH1.	2	AGAAAAAGGCCA	0.537	
+	12	2773	eb.2_Missense_Mu	NM_015338	NP_056153	Q8IXJ9	ASXL1_HUMAN		248	TTGCATCCGGAT	0.562	
-	5	918	0gec.2_Missense_	NM_080616	NP_542183	Q96MY1	CT112_HUMAN		0	ACCATCTCCATG	0.642	
+	3	458	0zvp.1_Missense_	NM_014902	NP_055717	Q9Y2H0	DLGP4_HUMAN		3	CAGCCGCCCCC	0.711	
-	3	1562	khm.2_Missense_M	NM_014657	NP_055472	O43156	TTI1_HUMAN		0	AGAGTTCCAACG	0.498	
+	12	1198	wb.1_Missense_M	NM_021931	NP_068750	Q9H5Z1	DHX35_HUMAN	case C-terminal.	3	GTGGTCGTAGTC	0.507	
-	7	1785	hk.1_Missense_Mu	NM_021248	NP_067071	Q9UJ99	CAD22_HUMAN	r (Potential).|Cadherin 4.	5	GCCGGCCGTCT	0.622	
+	30	4284	0zyf.1_Missense_M	NM_006420	NP_006411	Q9Y6D5	BIG2_HUMAN		4	AGAATCGTGTTT	0.463	
+	11	1214	C9A8_uc010gic.2_I	NM_015266	NP_056081	Q9Y2E8	SL9A8_HUMAN		1	ACTACACGCACC	0.552	
-	3	1734		NM_002237	NP_002228	Q9UIX4	KCNG1_HUMAN	lasmic (Potential).	2	GCCCTCCGGAAC	0.572	
+	2	240	K1_uc010zzm.1_5'	NM_002591	NP_002582	P35558	PCKGC_HUMAN		1	CCAGGCAGTGA	0.582	
-	3	409	0zzp.1_Missense_	NM_153360	NP_699191	Q8NCL9	APCDL_HUMAN		1	GGCGCGGGTCA	0.677	

+	3	851	_p.C161F|EDN3_u	NM_000114	NP_000105	P14138	EDN3_HUMAN	ndothelin-like.	1	CGCTTGTGTGG	0.562
+	5	477	ion_p.T80M|OSBP	NM_144498	NP_653081	Q9H1P3	OSBL2_HUMAN		2	AGATCACGATGC	0.602
+	13	1503	.R422Q|OSBPL2_	NM_144498	NP_653081	Q9H1P3	OSBL2_HUMAN		2	AGCACGGAGGG	0.617
+	4	510	M1_uc002yco.2_M	NM_007002	NP_008933	Q16186	ADRM1_HUMAN	Gly-rich.	0	GCAGCGGCCAC	0.607
-	10	1391		NM_005560	NP_005551	O15230	LAMA5_HUMAN	inin EGF-like 3.	3	CAGGTCCTCGC	0.657
+	34	3714	1aav.1_Splice_Site	NM_020882	NP_065933	Q9P218	COKA1_HUMAN		1	CCACAGCACAC	0.662
-	9	3705	yfl.1_Missense_M	NM_001037335	NP_001032412	Q9BYK8	PR285_HUMAN		2	TGTGCCGCTCC	0.706
-	5	550		NM_020713	NP_065764	Q96KM6	Z512B_HUMAN		0	GGGTCGGTCCA	0.632
+	6	872	_p.P66L|NCAM2_	NM_004540	NP_004531	O15394	NCAM2_HUMAN	3.|Extracellular (Potential).	4	AGTGCCGCCAG	0.423
+	11	1320	P16_uc011acm.1_	NM_006447	NP_006438	Q9Y5T5	UBP16_HUMAN		4	ATGCAGAACTG	0.323
+	5	614		NM_005441	NP_005432	Q13112	CAF1B_HUMAN	WD 3.	2	ATGTCAGCAAAG	0.343
-	5	373	zfx.2_Missense_M	NM_003343	NP_003334	P60604	UB2G2_HUMAN		4	CATGGGGTCAT	0.627
-	14	2285	nk.1_Missense_M	NM_015241	NP_056056	Q7RTP6	MICA3_HUMAN		0	CTGGCTATCAG	0.532
-	4	458	T2_uc002zyx.3_M	NM_000854	NP_000845	P0CG30	GSTT2_HUMAN	ST C-terminal.	0	CCTCGGGCACC	0.637
+	13	2244		NM_019601	NP_062547	Q9UGT4	SUSD2_HUMAN	tracellular (Potential).	1	CCAACGGACAA	0.627
+	19	2321	_p.S667G|SGSM1	NM_001039948	NP_001035037	Q2NKQ1	SGSM1_HUMAN	ab-GAP TBC.	5	TGCACAGCGAC	0.642
-	1	1524		NM_002430	NP_002421	Q10571	MN1_HUMAN		10	GCAGGCATGGG	0.711
+	4	2181	H_uc003afp.2_5'	NM_021076	NP_066554	P12036	NFH_HUMAN	S-P-[AEPV]-[EAK]- [AEVK]	0	CAAAGTCCCCT	0.557
-	9	981	n.1_Missense_Mu	NM_014303	NP_055118	O00541	PESC_HUMAN		0	CCCATCGGTGG	0.607
+	3	380	NF185_uc003akc.	NM_152267	NP_689480	Q96GF1	RN185_HUMAN	RING-type.	0	AGTTGGCCGTG	0.458
-	15	2020	h.1_Missense_Mu	NM_002473	NP_002464	P35579	MYH9_HUMAN	osin head-like.	11	TGTGGCGATGT	0.587
+	3	508	utation_p.R28H|M	NM_001161572	NP_001155044	Q9ULX9	MAFF_HUMAN	Basic motif.	0	GCGCCGCACAC	0.682
-	13	1970	xp.2_Missense_M	NM_001098504	NP_001091974	Q92841	DDX17_HUMAN		4	TGGACTTCCAT	0.517
+	7	905	_Mutation_p.R19	NM_031488	NP_113676	Q969R5	LMBL2_HUMAN		3	CCCACGGAGTG	0.537
+	22	2759	H7B_uc010gyl.1_I	NM_017590	NP_060060	Q9UGR2	Z3H7B_HUMAN	C2H2-type.	1	CTGCGGCAAGA	0.637
+	9	1256	aq.1_Missense_M	NM_001469	NP_001460	P12956	XRCC6_HUMAN	Ku.	5	TTGCAGCATTG	0.488
+	3	186	_uc011apk.1_Intro	NM_152613	NP_689826	Q6ICG8	WBP2L_HUMAN	GRAM.	2	ATACCGGGTAA	0.378
-	7	1128	YP2D7P1_uc010	NR_002570					0	TGCCCTATCAC	0.607
-	19	2484		NM_173050	NP_766638	Q8IWY4	SCUB1_HUMAN	CUB.	5	CGCCGCCGCAG	0.677
-	16	2121		NM_173050	NP_766638	Q8IWY4	SCUB1_HUMAN		5	CGTTGCGGGCA	0.642
+	5	1453	_p.G81C|NUP50_	NM_007172	NP_009103	Q9UKX7	NUP50_HUMAN		0	ACAGTGGTGAA	0.358
+	6	769	zy.2_Missense_M	NM_006953	NP_008884	O75631	UPK3A_HUMAN	lasmic (Potential).	0	AGGCTGTTCCC	0.597
+	1	131		NM_001082967	NP_001076436	Q7Z5A7	F19A5_HUMAN		1	ATCGCCCAGGA	0.423
-	7	992	_uc003bkh.2_Sile	NM_032019	NP_114408	Q969S8	HDA10_HUMAN	ne deacetylase.	0	CTCTCGCAGGA	0.547
-	11	984	.S131T|MAPK11_	NM_002751	NP_002742	Q15759	MK11_HUMAN		2	ACTGGCTGAAG	0.617
-	25	4139	p.R137C|PLXNB2_	NM_012401	NP_036533	O15031	PLXB2_HUMAN	lasmic (Potential).	6	GGCGCGGGCCG	0.662
-	19	3113	_5'Flank|PLXNB2	NM_012401	NP_036533	O15031	PLXB2_HUMAN	xtracellular (Potential).	6	CGTGACGTTGA	0.701
-	5	739	_uc011asa.1_Miss	NM_001145137	NP_001138609	Q92523	CPT1B_HUMAN	lasmic (Potential).	2	GGGGCGCACAG	0.542
+	14	1717	bnf.1_Missense_M	NM_001080420	NP_001073889	F2Z3L0	F2Z3L0_HUMAN		1	TCCTACGACAGC	0.632
+	14	1736	bnf.1_Missense_M	NM_001080420	NP_001073889	F2Z3L0	F2Z3L0_HUMAN		1	ACACAGGTACG	0.627
+	2	1852	F1_uc003bps.1_I	NM_020873	NP_065924	Q6UXK5	LRRN1_HUMAN	ellular (Potential).	1	TCTGCGTGAGA	0.488
-	3	1082		NM_000916	NP_000907	P30559	OXYR_HUMAN	lasmic (Potential).	0	CAGGCGGTCGG	0.706
+	1	227	bvy.1_Missense_M	NM_014229	NP_055044	P48066	S6A11_HUMAN	Name=1; (Potential).	4	TGGCCGGGGA	0.537
+	3	212	50_splice|MKRN2	NM_014160	NP_054879	Q9H000	MKRN2_HUMAN		0	TTGTTTAGATATG	0.572
-	10	1412	p.R118C|RAF1_uc	NM_002880	NP_002871	P04049	RAF1_HUMAN		14	TCCACGAGGCC	0.413
+	8	1197	xj.2_Missense_Mu	NM_001162499	NP_001155971	O75155	CAND2_HUMAN	HEAT 9.	4	TCATCCGCCGCT	0.627
+	16	2930	ex.1_Missense_M	NM_144633	NP_653234	Q96L42	KCNH8_HUMAN	lasmic (Potential).	5	GCACAGCACCT	0.522

+	3	341	cei.2_Nonsense_	NM_001040432	NP_001035522	Q504Y3	ZCPW2_HUMAN	CW-type.	2	ACCATGGTACT	0.363	
-	3	2038		NM_033403	NP_208382	Q9C098	DCLK3_HUMAN	rotein kinase.	9	TTGGGGTCCCA	0.413	
+	5	570	e_Mutation_p.R10	NM_173826	NP_776187	Q8N3R3	CC023_HUMAN		3	GATTTCGAGCA	0.303	
+	2	344		NM_144638	NP_653239	Q69YG0	TMM42_HUMAN	ical; (Potential).	0	CCTCAGCTCGG	0.498	
+	9	1124		NM_003241	NP_003232	P49221	TGM4_HUMAN		1	TGGACGCAACG	0.627	
-	3	413	S45_uc011bam.1_	NM_199183	NP_954652	Q7RTY3	PRS45_HUMAN	eptidase S1.	0	TCATGTCCCCC	0.537	
+	28	4485	Site_p.Q813_splic	NM_015175	NP_055990	Q6ZNJ1	NBEL2_HUMAN		1	CCACAGCAAAC	0.642	
+	40	6669	AL2_uc010hjn.1_	NM_015175	NP_055990	Q6ZNJ1	NBEL2_HUMAN	BEACH.	1	ATGCAGCAGGC	0.602	
+	2	1700	EX1_uc010hjz.2_	NM_033629	NP_338599	Q9NSU2	TREX1_HUMAN		0	GCTGGCAGCGC	0.632	
-	23	3117		NM_000094	NP_000085	Q02388	CO7A1_HUMAN	(NC1).|Fibronectin type-III	11	ATGCCTCAGGA	0.597	
-	11	1340	cuc.1_Missense_M	NM_003365	NP_003356	P31930	QCR1_HUMAN		0	CAATCCGGCTT	0.617	
-	5	846	p.G109C|DALRD3	NM_001009996	NP_001009996	Q5D0E6	DALD3_HUMAN		0	GCAGCCGCCTG	0.517	
+	2	890		NM_203370	NP_976248	Q96EL1	CC054_HUMAN		0	CATGCCCACCT	0.627	
-	2	315	D10_uc003dah.1_	NM_015896	NP_056980	O75800	ZMY10_HUMAN		5	AATGGGCTCGC	0.597	
-	12	1293	dap.2_Missense_	NM_006030	NP_006021	Q9NY47	CA2D2_HUMAN	tracellular (Potential).	1	CGTCCGGTTTG	0.582	
+	1	422		NM_080865	NP_543141	Q9BZJ7	GPR62_HUMAN	Name=1; (Potential).	1	GGGGGCACTGC	0.677	
+	58	9616	H1_uc003ddv.2_5	NM_015512	NP_056327	Q9P2D7	DYH1_HUMAN	Potential.	3	GCCGAGCTGGC	0.662	
+	51	5329	1_5'UTR|STAB1_	NM_015136	NP_055951	Q9NY15	STAB1_HUMAN	lar (Potential).|FAS1 6.	9	GCCCCTGCTTC	0.637	
+	56	6065	se_Mutation_p.C1	NM_015136	NP_055951	Q9NY15	STAB1_HUMAN	tential).|Laminin EGF-like	9	TCTGTGCCGTTC	0.642	
-	10	1533	bev.1_Missense_	NM_019555	NP_062455	Q9NR81	ARHG3_HUMAN		1	GCCCGGCAGCA	0.507	
+	1	470	iv.2_Missense_Mu	NM_177966	NP_808881	Q6L8Q7	PDE12_HUMAN		0	TGAGCCGGCTG	0.672	
+	1	240	djd.1_Missense_M	NM_007159	NP_009090	Q14BN4	SLMAP_HUMAN	somes (By similarity).|Cyto	0	CCGCCCGAACT	0.602	
+	36	6176	_Mutation_p.R198	NM_001457	NP_001448	O75369	FLNB_HUMAN	with the cytoplasmic tail of	19	CCGCCGAGCCA	0.577	
+	43	7348	ense_Mutation_p.	NM_001457	NP_001448	O75369	FLNB_HUMAN	Interaction with INPPL1.	19	GACTCGAAGGG	0.592	rs142023538
-	4	970		NM_000097	NP_000088	P36551	HEM6_HUMAN		0	GACAGCGTCTT	0.433	
-	39	5615		NM_014981	NP_055796	Q9Y2K3	MYH15_HUMAN	Potential.	7	GTCTGCGGGCT	0.547	
-	5	850	b.1_Missense_Mu	NM_000796	NP_000787	P35462	DRD3_HUMAN	Cytoplasmic.	4	TCTGTCCCGTGC	0.562	
-	9	1909	e_Mutation_p.T32	NM_001146156	NP_001139628	P49841	GSK3B_HUMAN	rotein kinase.	2	GTGGAGTTCGG	0.418	
-	19	6137	d.2_Missense_Mu	NM_199420	NP_955452	O75417	DPOLQ_HUMAN		11	GAGTCGGCTCC	0.438	
+	12	1901	_p.R359K|PARP15	NM_001113523	NP_001106995	Q460N3	PAR15_HUMAN	ARP catalytic.	5	TGGGAGAAAGC	0.478	
+	60	9012	k.2_Missense_Mu	NM_001024660	NP_001019831	O60229	KALRN_HUMAN		6	ACGTCGCAAGC	0.552	rs144099513
-	3	649		NM_002213	NP_002204	P18084	ITB5_HUMAN	cellular (Potential).	2	CCGGAGGTTCA	0.592	
-	2	162	ko.1_Missense_M	NM_001003794	NP_001003794	Q99685	MGLL_HUMAN		0	TGGGGGAACTT	0.522	
+	7	1705	EC_uc003ekj.2_3	NM_021937	NP_068756	P57772	SELB_HUMAN		1	TGGCCGTGGGG	0.647	
+	14	1554	b.2_Missense_Mu	NM_016128	NP_057212	Q9Y678	COPG_HUMAN		4	GCATGAGGAGG	0.552	
+	6	755	elv.2_Missense_M	NM_020187	NP_064572	Q96FZ2	CC037_HUMAN		1	AGGCAGTTTCT	0.468	
+	4	850		NM_000539	NP_000530	P08100	OPSD_HUMAN	Cytoplasmic.	0	TCACCCGCATGG	0.622	
-	5	1084	1_Missense_Muta	NM_001017395	NP_001017395	O94876	TMCC1_HUMAN		1	CAACCGTTCGA	0.478	
+	34	6467	ni.3_Nonsense_M	NM_001102608	NP_001096078	A6NMZ7	CO6A6_HUMAN	.|Nonhelical region.	8	CTTGGCCGAATT	0.443	
-	1	462	2_5'Flank|UBA5_	NM_032169	NP_115545	Q709F0	ACD11_HUMAN		1	TAGGTAGGCCT	0.587	
+	20	3509	_uc003epw.1_Intr	NM_001063	NP_001054	P02787	TRFE_HUMAN	ansferrin-like 2.	2	GTATGCGAACT	0.498	
-	1	402	6B_uc011blu.1_5'	NM_016577	NP_057661	Q9NRW1	RAB6B_HUMAN		1	ATTCCCAAAATC	0.388	
+	3	572	f72_uc011bmr.1_3	NM_001040061	NP_001035150	Q6ZUU3	CC072_HUMAN		0	CGGGAGAGAAT	0.627	
+	8	3198	_p.S739N|ZBTB38	NM_001080412	NP_001073881	Q8NAP3	ZBT38_HUMAN		3	CAGCAGCAACC	0.522	
+	10	958	03eua.1_Missense	NM_006506	NP_006497	Q15283	RASA2_HUMAN		6	ACTACGTGCTT	0.368	
-	2	528	ns.1_Missense_M	NM_015472	NP_056287	Q9GZV5	WWTR1_HUMAN		4	TGACGGCAGGG	0.413	
+	10	1378		NM_001004316	NP_001004316	Q6ZMV7	LEKR1_HUMAN		0	TGTCAACAGATA	0.328	

-	5	765		NM_206963	NP_996846	P49788	TIG1_HUMAN	cellular (Potential).		0	CAAAATCAATTGT	0.254	
-	2	262	CC5_uc010hxm.2_	NM_005688	NP_005679	O15440	MRP5_HUMAN			4	CTTCACGGTCTCT	0.443	rs146572786
+	7	932	p.R141Q|PSMD2_	NM_002808	NP_002799	Q13200	PSMD2_HUMAN			0	AGGCCGGCATGC	0.517	
+	12	1678	RD_uc003foy.2_M	NM_003741	NP_003732	Q9H2X0	CHRD_HUMAN	CHRD 3.		3	CAGGAGGACAC	0.612	
+	1	44	003fqv.2_5'UTR|EI	NM_001967	NP_001958	Q14240	IF4A2_HUMAN			4	TCATGTCTGGTGC	0.577	
+	6	841	.1_Missense_Muta	NM_002182	NP_002173	Q9NPH3	IL1AP_HUMAN	Potential).|Ig-like C2-type 2.		1	ACACATGTGTTGT	0.353	
+	5	1038	3fsv.2_Splice_Site	NM_174908	NP_777568	Q8IVM0	CCD50_HUMAN			0	ATGGAGGTAACA	0.383	
-	3	447	p.N55S|TFRC_uc	NM_003234	NP_003225	P02786	TFR1_HUMAN	h SH3BP4.|Cytoplasmic (P		3	GTGACATTGGCCT	0.423	
-	6	576	wh.2_Missense_M	NM_005017	NP_005008	P49585	PCY1A_HUMAN	alytic (Potential).		0	GGACTGCGTCATA	0.532	
-	8	1304	t.2_Missense_Mut	NM_203314	NP_976059	Q02338	BDH_HUMAN			1	GTGACAGCATCGA	0.572	
+	1	3222		NM_175918	NP_787114	Q8N1N5	CRPAK_HUMAN			0	CTGCTCACATGTC	0.647	
+	1	3663		NM_175918	NP_787114	Q8N1N5	CRPAK_HUMAN	6		0	CGTGCCGATGCC	0.672	
-	13	1664	N_uc010ich.1_Intr	NM_181808	NP_861524	Q7Z5Q5	DPOLN_HUMAN			4	GTTACCTTTTTCA	0.313	
+	38	4952		NM_002111	NP_002102	P42858	HD_HUMAN			4	AATGAAGACAAGT	0.493	
+	12	3960	_p.S218N|RGS12_	NM_198229	NP_937872	O14924	RGS12_HUMAN	RBD 1.		1	AAGACAGTAGCAT	0.587	
-	9	1472	p.N361D|PPP2R2	NM_020416	NP_065149	Q9Y2T4	2ABG_HUMAN	WD 6.		4	TGGTGTTCCGATC	0.647	
-	1	982	3_5'Flank|TADA2B	NM_153376	NP_699207	Q2M329	CCD96_HUMAN	Potential.		0	GCTCCTGGTGGTA	0.622	
+	15	3447	A1040T|SH3TC1_	NM_018986	NP_061859	Q8TE82	S3TC1_HUMAN			3	AGGCGGCTGGA	0.637	
-	8	1386	se_Mutation_p.P32	NM_001290	NP_001281	O43679	LDB2_HUMAN			0	GTGGCGGGAGGT	0.542	
+	13	1594		NM_015907	NP_056991	P28838	AMPL_HUMAN			0	AAGTGGGCACATT	0.453	
-	7	1124	gqn.1_Missense_M	NM_145290	NP_660333	Q8IWK6	GP125_HUMAN	lar (Potential).|Ig-like.		1	ATTCATCGGTTTC	0.378	rs138542858
-	4	734	p.R31W|GPR125_	NM_145290	NP_660333	Q8IWK6	GP125_HUMAN	lar (Potential).|LRR 4.		1	CAGCCGAACCAC	0.353	rs147434497
-	9	2017	GC1A_uc003gqt.2	NM_013261	NP_037393	Q9UBK2	PRGC1_HUMAN	Arg/Ser-rich.		8	TTACCTGGGCCC	0.473	
+	11	1338	BPJ_uc003gsa.1_	NM_005349	NP_005340	Q06330	SUH_HUMAN	IPT/TIG.		3	GGGGACGTAGCA	0.363	
-	5	1442	ah.1_Missense_Mu	NM_004439	NP_004430	P54756	EPHA5_HUMAN	III 1.|Extrace	p.R417Q(1)	24	TTGCCGGGGAA	0.493	
+	5	554	.S146N|SLC4A4_	NM_001098484	NP_001091954	Q9Y6R1	S4A4_HUMAN	lasmic (Potential).		5	GATGGAGCAAGC	0.443	
-	5	924	bc.1_Missense_M	NM_173827	NP_776188	Q8N8Q8	COX18_HUMAN	ical; (Potential).		0	GGTACCGTTGCAC	0.413	rs138323566
-	26	5015	hgq.2_Missense_M	NM_032217	NP_115593	O75179	ANR17_HUMAN	Ser-rich.		10	CTCTTACGACTGC	0.463	
-	3	1083	n.1_Missense_Mut	NM_020803	NP_065854	Q9P2G9	KLHL8_HUMAN			0	ATGGCAGCATTAT	0.418	
+	5	376	.2_Intron|SPP1_uc	NM_001040058	NP_001035147	P10451	OSTP_HUMAN			1	TTTAAACAAGAGC	0.398	
+	26	3189	3_uc011cdo.1_Mis	NM_014606	NP_055421	Q15034	HERC3_HUMAN	HECT.		4	CAGCGGGGAGG	0.577	
+	1	899		NM_005172	NP_005163	Q92858	ATOH1_HUMAN			0	GGACAGCGCCC	0.607	rs142131282
-	8	1309	p.I404M|UNC5C_	NM_003728	NP_003719	O95185	UNC5C_HUMAN	ical; (Potential).		4	CACTGCTATCACA	0.438	
-	16	2459	es.1_Missense_M	NM_005908	NP_005899	O00462	MANBA_HUMAN			1	GTGGTAGTTGGT	0.557	
+	18	2057	p.A653T|ANK2_uc	NM_001148	NP_001139	Q01484	ANK2_HUMAN	ANK 19.		14	TATGGAGCAGAG	0.438	
+	9	1595	ey.2_Missense_Mu	NM_145207	NP_660208	Q8NB90	SPAT5_HUMAN			0	GATGCTGCTCTCC	0.428	
+	1	1940	10_uc003igz.2_Mis	NM_032961	NP_116586	Q9P2E7	PCD10_HUMAN	|Extracellular (Potential).		2	GCGCGGCGCCC	0.622	
+	7	1958	se_Mutation_p.S47	NM_032557	NP_115946	Q8NB14	UBP38_HUMAN			5	GTATTATCTTTAAA	0.284	
+	4	649	se_Mutation_p.L70	NM_001040876	NP_001035809	P61221	ABCE1_HUMAN	ferredoxin-type 2.		1	GCGCCTTATCAAT	0.303	
+	7	1018		NM_033393	NP_203751	Q9C0D6	FHDC1_HUMAN	FH2.		2	AATGCAGTAGGA	0.303	
+	18	3224		NM_014247	NP_055062	Q9Y4G8	RPGF2_HUMAN			4	GATGCCCAAATGC	0.443	
-	1	815	n.1_Intron|KLHL2_	NM_000167	NP_000158					0	TAAGTGCTAAGTC	0.418	
+	12	2820	p.V754M|CLCN3_	NM_001829	NP_001820	P51790	CLCN3_HUMAN	oplasmic (By similarity).		3	GAGATCGTGGTG	0.488	
+	3	1789	X2_uc003iwa.1_5'	NM_020225	NP_064610	Q9P2F5	STOX2_HUMAN			0	CGGCACACGCTC	0.443	
+	3	3984	va.1_Missense_Mu	NM_020225	NP_064610	Q9P2F5	STOX2_HUMAN			0	CAGCAGCAGCAT	0.552	
-	4	1231		NM_020040	NP_064424	Q99867	TBB4Q_HUMAN			0	GCTCTCGGCCTC	0.557	
-	37	5027	.P1692L|RICTOR	NM_152756	NP_689969	Q6R327	RICTR_HUMAN			10	GACACGGAAGT	0.338	rs77464125

-	29	3471	3jmi.3_Missense_I	NM_173489	NP_775760	Q7Z745	HTRB2_HUMAN	HEAT 10.	8	ATTACCTTAGCTA	0.413	
+	1	564	uc003joq.1_5'Flanl	NM_002202	NP_002193	P61371	ISL1_HUMAN		3	ATGGGAGATCCA	0.527	
+	2	1158	GA1_uc003jou.2_Ir	NM_015946	NP_057030	Q9BRX2	PELO_HUMAN		0	GGGCAGCAACC	0.617	
+	20	1993	h.3_Missense_Mu	NM_001136034	NP_001129506	Q9NQI0	DDX4_HUMAN	case C-terminal.	2	GCAGAGCAATTT	0.358	
+	2	299		NM_001029875	NP_001025046	Q6MZT1	R7BP_HUMAN		0	GGCCCGTCAGG	0.493	
+	3	344	7BP_uc011cqu.1_5	NM_001029875	NP_001025046	Q6MZT1	R7BP_HUMAN		0	AAGATGGTGAGA	0.453	
-	21	3468	o.2_RNA|ADAMTS	NM_197941	NP_922932	Q9UKP5	ATS6_HUMAN	TSP type-1 2.	0	GGCTTACTGTCA	0.438	
-	4	1409	c003jtq.2_RNA|AD	NM_197941	NP_922932	Q9UKP5	ATS6_HUMAN		0	GATGTCGTTGTTG	0.398	
+	17	3393	p.V1044I|BDP1_u	NM_018429	NP_060899	A6H8Y1	BDP1_HUMAN	E-M-E-T-D-L-K-X-T-G-R- E-	2	AGAGAAGTATCC	0.458	
-	9	989	sz.1_Missense_Mu	NM_018268	NP_060738	Q9HAD4	WDR41_HUMAN	WD 4.	0	AAAACTCAAATCT	0.438	
+	2	6593		NM_153610	NP_705838	Q8N3K9	CMYA5_HUMAN		9	AGAAAGGAATTT	0.453	
-	4	988	kin.2_Missense_M	NM_001884	NP_001875	P10915	HPLN1_HUMAN	Link 2.	5	CAGCCCGCATCA	0.557	
+	2	1004	nw.1_Missense_M	NM_005575	NP_005566	Q9UIQ6	LCAP_HUMAN	cellular (Potential).	4	CCATGGGCACAG	0.463	
-	5	672		NM_173666	NP_775937	Q8NBA8	DTWD2_HUMAN		0	TGCATCCGAATT	0.313	
+	28	7106	l.1_Missense_Mut	NM_005509	NP_005500	Q9Y485	DMXL1_HUMAN		2	CTGGCGAGGAA	0.378	
+	6	1407	CAIP_uc010jcu.2_	NM_005460	NP_005451	Q9Y6H5	SNCAP_HUMAN	ANK 2.	2	GAGTGCGTACGC	0.403	
+	8	1145	MD3_uc011cwx.1_	NM_023927	NP_076416	Q96HH9	GRAM3_HUMAN		1	GCAGACCGCCCT	0.393	
-	9	746	_p.G164S|BRD8_u	NM_139199	NP_631938	Q9H0E9	BRD8_HUMAN		1	GGACACCTGTAC	0.527	
+	4	937	P156L|FAM53C_u	NM_001135647	NP_001129119	Q9NYF3	FA53C_HUMAN		1	GTGGGCCGCAGG	0.677	
+	4	498	se_Mutation_p.V1	NM_001903	NP_001894	P35221	CTNA1_HUMAN	TNNB1.|Involved in homod	11	TCTGCTGTTACC	0.468	
+	1	241	003lhf.2_Intron|PC	NM_018907	NP_061730	Q9UN74	PCDA4_HUMAN	|Extracellular (Potential).	6	GGGCCGCATCG	0.662	
+	1	1957	03lhf.2_Intron|PCD	NM_018907	NP_061730	Q9UN74	PCDA4_HUMAN	|Extracellular (Potential).	6	GCGCGCGCATCC	0.672	
+	1	755	HB16_uc003liv.2_5	NM_019120	NP_061993	Q9UN66	PCDB8_HUMAN	|Extracellular (Potential).	4	ATGGCAGGAAATA	0.502	
+	1	1744	3ljq.1_Intron|PCDH	NM_018920	NP_061743	Q9Y5G6	PCDG7_HUMAN	r (Potential).|Cadherin 6.	0	GCTCCGCAGAG	0.632	
+	1	1820	Intron|PCDHGB4_	NM_018927	NP_061750	Q9Y5F8	PCDGJ_HUMAN	r (Potential).|Cadherin 5.	2	ACAACGCACCG	0.711	
+	1	1793	1_Intron|PCDHGB	NM_003735	NP_003726	O60330	PCDGC_HUMAN	r (Potential).|Cadherin 5.	4	CCGCCCCTCAGC	0.622	
+	7	728	p.S231R|ARHGAP	NM_015071	NP_055886	Q9UNA1	RHG26_HUMAN		1	CATTAGCATACAG	0.473	
+	4	504	p.R155H|TCERG1	NM_006706	NP_006697	O14776	TCRG1_HUMAN	WW 1.	2	GGACACGTGAAT	0.313	
-	2	2255		NM_001012301	NP_001012301	Q5FYB1	ARSI_HUMAN		2	GAAAAAGGATCC	0.537	
-	8	811	ense_Mutation_p.E	NM_003118	NP_003109	P09486	SPRC_HUMAN	EF-hand.	1	AATGCTCCATGG	0.607	
+	1	557		NR_024356					0	CCGGCCGCGATC	0.662	
-	13	1819		NM_001017995	NP_001017995	A1X283	SPD2B_HUMAN		4	GCCCCGGAGCT	0.662	
+	7	1132	kg.1_Missense_M	NM_133369	NP_588610	Q6ZN44	UNC5A_HUMAN	ical; (Potential).	1	GTGGCCGTCTGC	0.622	
+	13	1809	lfu.1_Missense_Mu	NM_002011	NP_002002	P22455	FGFR4_HUMAN	e.|Cytoplasmic (Potential).	16	CTGTACGTGATC	0.716	
-	9	899	p.R162H|DDX41_	NM_016222	NP_057306	Q9UJV9	DDX41_HUMAN	ase ATP-binding.	0	CGCAGCGCAGG	0.657	
-	18	2687		NM_014244	NP_055059	O95450	ATS2_HUMAN	TSP type-1 2.	4	GGGCGGCACAG	0.642	
+	2	1522	nkn.1_Missense_M	NM_014757	NP_055572	Q92585	MAML1_HUMAN		6	CACCCCGGCAC	0.657	rs141578236
-	4	396	003mwc.2_5'UTR|	NM_206836	NP_996667	O75521	ECI2_HUMAN	ACB.	0	AATGAAGGACTC	0.483	
-	2	201	on_p.K25R|PECI_	NM_206836	NP_996667	O75521	ECI2_HUMAN	ACB.	0	GGATCCTTTTTCA	0.398	
-	5	602	am.2_Missense_Mu	NM_016495	NP_057579	Q9P0N9	TBCD7_HUMAN	ab-GAP TBC.	1	CTGGGGCAAGG	0.483	
+	5	655	P2_uc011djb.1_Mis	NM_006366	NP_006357	P40123	CAP2_HUMAN		1	GTCAGCGAAAGC	0.473	
+	9	875	p.P234Q|CDKAL1	NM_017774	NP_060244	Q5VV42	CDKAL_HUMAN		2	GTTATCCAATTGA	0.323	
-	2	632	RL_uc003ndq.2_M	NM_000948	NP_000939	P01236	PRL_HUMAN		0	GGCATCGGGCA	0.587	
+	4	978	dkk.1_Missense_M	NM_007048	NP_008979	O00481	BT3A1_HUMAN	2.|Extracellular (Potential).	2	TATGCAGTAGCA	0.547	
+	4	837	A-E_uc011dmh.1_	NM_005516	NP_005507	P13747	HLAE_HUMAN	pha-3.|Extracellular (Potent	5	GGGCAGCTGTG	0.622	
-	10	2331	nj.1_Missense_Mu	NM_005275	NP_005266	P36915	GNL1_HUMAN		3	CTGGGCGATAG	0.602	
-	5	412	2_5'Flank|VARS_u	NM_021177	NP_067000	Q9Y333	LSM2_HUMAN		0	ACGTATCGGACC	0.512	

+	3	563	f.2_Missense_Mut	NM_001710	NP_001701	P00751	CFAB_HUMAN		1	AGTGCGGACAG	0.632	
+	43	6133	ey.2_Missense_Mu	NM_002224	NP_002215	Q14573	ITPR3_HUMAN	lasmic (Potential).	19	TCACCGCACTG	0.592	
+	6	872	_p.R278H|DEF6_u	NM_022047	NP_071330	Q9H4E7	DEFI6_HUMAN	PH.	0	AAAGCGCTGCA	0.657	
+	8	1519	tb.1_Missense_M	NM_006238	NP_006229	Q03181	PPARD_HUMAN	gand-binding.	1	AGATGGCTGAC	0.602	
-	8	806	w.3_Missense_Mu	NM_003322	NP_003313	O00294	TULP1_HUMAN		3	TTGCCCTTTTGA	0.597	
-	5	715	.2_Intron|TRERF1	NM_033502	NP_277037	Q96PN7	TREF1_HUMAN		5	TTGGCGAGGCC	0.577	
+	4	357	23_uc003owo.2_	NM_153246	NP_694978	Q8N319	CF223_HUMAN		0	CGGATGTCGCG	0.602	
+	19	1760	se_Mutation_p.G4	NM_018426	NP_060896	Q5T3F8	TM63B_HUMAN	ical; (Potential).	3	ACAACGGCGCC	0.632	
-	4	1165	_Intron|TMEM151	NM_182539	NP_872345	Q5JU00	TCTE1_HUMAN	LRR 2.	4	CACACGCAGGC	0.607	rs146631063
+	2	618		NM_014936	NP_055751	Q9Y6X5	ENPP4_HUMAN	ellular (Potential).	4	TATTTGGGTGA	0.423	
-	5	845	wx.1_Missense_M	NM_021814	NP_068586	Q9NYP7	ELOV5_HUMAN		0	CTTGCGCAGGA	0.488	
+	5	1320	k.2_Missense_Mut	NM_001704	NP_001695	O60242	BAI3_HUMAN	.|Extracellular (Potential).	50	AGGTGAATCTG	0.423	
-	6	856	A1_uc003pff.3_5'	NM_001851	NP_001842	P20849	CO9A1_HUMAN		4	TCAAACTGGAG	0.463	
+	10	1355	_5'Flank|PPIL6_u	NM_003080	NP_003071	O60906	NSMA_HUMAN		0	AGGCTCGCTGG	0.647	
-	3	556	186_uc003pub.2_	NM_001123364	NP_001116836	Q5JXM2	CF186_HUMAN		0	TCACCCTAAGG	0.438	
-	19	2764	_p.R812*|LAMA4_	NM_001105206	NP_001098676	Q16363	LAMA4_HUMAN	omain II and I.	9	CTCTCGGATCC	0.502	rs148409597
+	3	577		NM_001029858	NP_001025029	Q5T1Q4	S35F1_HUMAN		1	ATTTTACGACGA	0.378	
+	3	644	au.2_Missense_Mu	NM_030963	NP_112225	Q9NTX7	RN146_HUMAN	WWE.	1	TGGACGTCGCA	0.388	
+	20	2346	on_p.L630F|EYA4	NM_004100	NP_004091	O95677	EYA4_HUMAN		2	TGGCTCTCCAC	0.328	
-	7	1665	hk.2_Missense_Mu	NM_014432	NP_055247	Q9UHF4	I20RA_HUMAN	lasmic (Potential).	4	CCGCACAAATG	0.512	
-	1	75	1_5'Flank|PEX3_u	NM_182503	NP_872309	Q7Z6V5	ADAT2_HUMAN		0	TTGCAGCTGGC	0.697	
-	9	2297	_p.A633V|SHPRH_	NM_001042683	NP_001036148	Q149N8	SHPRH_HUMAN		3	ATTCAGCACAG	0.403	
+	7	755	p.P220S|RBM16_	NM_014892	NP_055707	Q9UPN6	SCAF8_HUMAN		0	GCTTACCTGAT	0.448	
-	1	561	p.A124V|RSPH3_	NM_031924	NP_114130	Q86UC2	RSPH3_HUMAN		2	TGGGCGCTAAG	0.652	
+	17	3672	.1_RNA|MAP3K4_	NM_005922	NP_005913	Q9Y6R4	M3K4_HUMAN		9	CACTCGGAGCA	0.408	
+	2	142	wr.1_Missense_M	NM_022138	NP_071421	Q9H3U7	SMOC2_HUMAN	Kazal-like.	1	ATTGTAGCTTGG	0.448	
+	7	1069	sjr.1_Missense_Mu	NM_017781	NP_060251	Q8TAV3	CP2W1_HUMAN		0	CTCCACGAGGT	0.726	
+	11	1307	p.V94M|TTYH3_u	NM_025250	NP_079526	Q9C0H2	TTYH3_HUMAN	ellular (Potential).	0	ACTACGTGCAA	0.642	
+	13	1647	p.E207G|TTYH3_u	NM_025250	NP_079526	Q9C0H2	TTYH3_HUMAN	lasmic (Potential).	0	CTGTGAGAACA	0.652	
-	24	3634		NM_032415	NP_115791	Q9BXL7	CAR11_HUMAN	ylate kinase-like.	50	ACACCCGGATG	0.592	
-	27	8433		NM_001080495	NP_001073964	O15417	TNC18_HUMAN		0	CCTGCGCGGAA	0.637	
-	3	1329	on.3_Missense_M	NM_024963	NP_079239	Q96ME1	FXL18_HUMAN	LRR 7.	3	GACGCAGCCGG	0.572	
+	5	709	42_uc011jwp.1_M	NM_032172	NP_115548	Q9H9J4	UBP42_HUMAN		5	ACCAAGAAGAT	0.413	
-	2	830		NM_001037163	NP_001032240	Q7Z4H9	SIPAR_HUMAN		0	CAACACCACTG	0.612	
-	10	1088	a.2_Missense_Mu	NM_004080	NP_004071	Q9Y6T7	DGKB_HUMAN		12	TTTTGGACTTCA	0.448	
+	7	1397	R_uc003stt.3_R	NM_001621	NP_001612	P35869	AHR_HUMAN		3	CACCTCAGTTG	0.373	
-	11	1402	26A_uc003svn.3_	NM_032581	NP_115970	Q9BYI3	HYCCI_HUMAN		1	TGACCGTCTGT	0.438	
+	12	1671	_p.A458T|MPP6_u	NM_016447	NP_057531	Q9NZW5	MPP6_HUMAN	ylate kinase-like.	0	TTGCGGCTCCG	0.423	
-	8	1083	03tjx.2_Intron|PO	NM_013284	NP_037416	Q9NP87	DPOLM_HUMAN	NA binding (By similarity).	3	GTCCACGTCAT	0.652	
+	1	1334		NR_003595					0	GGCGAAGACAA	0.458	
+	4	647	_Mutation_p.I216	NM_182633	NP_872439	Q8N859	ZN713_HUMAN		2	CAGCATCAAACA	0.343	
+	4	365_366	f.1_Missense_Mut	NM_001483	NP_001474	O75323	NIPS2_HUMAN		1	TATGGCGAGCA	0.406	
+	4	1013		NM_001159279	NP_001152751				2	AAGAATGTGGC	0.423	
+	4	995		NM_001159524	NP_001152996	P0CB33	ZN735_HUMAN	2H2-type 7.	0	TGGCAAAGCCT	0.428	
-	4	640	3tzc.2_Missense_	NM_148912	NP_683710	Q8NFV4	ABHDB_HUMAN		0	GGAGCGGGGCA	0.552	
-	2	656	.3_5'UTR|POM121C_uc003udl.1_RNA			A8CG34	P121C_HUMAN	and nuclear pore complex.	0	CCCCCGGACAG	0.527	
-	1		POM121C_uc003udk.3_Intron			A8CG34	P121C_HUMAN		0	TCACCTGCATA	0.458	

-	2	879	.1_Intron|CCDC14	NM_006682	NP_006673	Q14314	FGL2_HUMAN	ogen C-terminal.	2	ATTCCCTTCTG	0.458	
-	17	2258	.R740W|SEMA3	NM_152754	NP_689967	O95025	SEM3D_HUMAN	Lys-rich (basic).	5	TCTCCGCTTCT	0.507	
-	2	444	ERF_uc011khm.1	NM_006980	NP_008911	Q99551	MTERF_HUMAN		0	GAGTACGTGTTA	0.413	
+	46	11474	.T3373M|AKAP9_	NM_005751	NP_005742	Q99996	AKAP9_HUMAN		26	TTTCACGGATC	0.532	
+	8	780	_Mutation_p.G191	NM_003496	NP_003487	Q9Y4A5	TRRAP_HUMAN		37	ATGGTTGGTATG	0.448	
+	4	465	6_uc011kji.1_5'F	NM_152755	NP_689968	Q8N129	CNPY4_HUMAN		0	CATGGCAACAC	0.542	
+	1	553	.1_5'Flank|ZCWP	NM_019606	NP_062552	Q7L2J0	MEPCE_HUMAN	Gly-rich.	1	CGGGGGCAAG	0.672	
+	1	926	.1_5'Flank|ZCWP	NM_019606	NP_062552	Q7L2J0	MEPCE_HUMAN		1	CACCAGCAGCA	0.647	
-	7	973	i.2_RNA|LRCH4_	NM_002319	NP_002310	O75427	LRCH4_HUMAN		2	TGCCACTATCA	0.602	
+	36	6688	wl.2_RNA|ZAN_u	NM_003386	NP_003377	Q9Y493	ZAN_HUMAN	ellular (Potential).	11	TCGGAGGTCTC	0.662	
+	45	8224	h.2_RNA|ZAN_u	NM_003386	NP_003377	Q9Y493	ZAN_HUMAN	xtracellular (Potential).	11	TGTGTGAGCCC	0.632	
-	2	1550	CHE_uc003uxg.2	NM_000665	NP_000656	P22303	ACES_HUMAN		2	TGGAAGCACGG	0.652	
+	3	6600	C17_uc010lho.1_	NM_001040105	NP_001035194	Q685J3	MUC17_HUMAN	ch.|59 X approximate tand	27	TTTCAACAACT	0.483	rs147644870
+	3	6777	C17_uc010lho.1_	NM_001040105	NP_001035194	Q685J3	MUC17_HUMAN	X approximate tandem re	27	TTTCAGCAACT	0.498	
-	4	960	xz.1_Missense_M	NM_198571	NP_940973	Q8N8M0	CG052_HUMAN		1	GATGGTCCCGC	0.726	
-	1	1261	.2_Intron|CADPS2	NM_139175	NP_631914	Q8WVZ7	RN133_HUMAN		1	CTGCAGGAGAA	0.403	
-	12	1454	64_splice|RBM28_	NM_018077	NP_060547	Q9NW13	RBM28_HUMAN		2	ACTCACAGCCT	0.498	
+	5	572	e_Mutation_p.S79	NM_001868	NP_001859	P15085	CBPA1_HUMAN		1	GGGCAGTAAGC	0.622	
-	2	1182	p.A318V|PLXNA4	NM_020911	NP_065962	Q9HCM2	PLXA4_HUMAN	lar (Potential).|Sema.	1	CCCCCGCTTTG	0.582	
-	3	405	1B1_uc003vrq.1_	NM_001628	NP_001619	P15121	ALDR_HUMAN		3	CCAGTGAATAA	0.552	
-	15	1860		NM_004333	NP_004324	P15056	BRAF_HUMAN	rotein kinas_R603>I(2)|p.T	18290	ATTTCACTGTA	0.368	
+	33	4064		NM_004668	NP_004659	O43451	MGA_HUMAN	se.|Lumenal (Potential).	2	GGAGGATGACG	0.493	
+	15	2948	bt.2_Missense_M	NM_004445	NP_004436	O15197	EPHB6_HUMAN	Potential).|Protein kinase.	19	GGGCCGCAGTG	0.687	
+	6	803	ta.1_Missense_M	NM_032982	NP_116764	P42575	CASP2_HUMAN		3	ATTTCGCTCTG	0.527	
+	1	355		NM_001001659	NP_001001659	Q96R47	O2A14_HUMAN	Name=3; (Potential).	0	ATGTCCTATGAT	0.483	
-	4	1101	p.G285R|ZNF786_	NM_152411	NP_689624	Q8N393	ZN786_HUMAN		4	CGGCCCCTCCC	0.716	
+	5	860	1_uc003wga.2_R	NM_032534	NP_115923	A5PL33	KRBA1_HUMAN		2	TCTCCCCATCA	0.612	
+	43	6245		NM_198455	NP_940857	A2VEC9	SSPO_HUMAN	F5/8 type C.	0	TGCATCGTCCC	0.672	
+	53	7674		NM_198455	NP_940857	A2VEC9	SSPO_HUMAN	SP type-1 5.	0	GCATGGGCCAT	0.662	
+	4	773	p.R152P|REPIN1_	NM_013400	NP_037532	Q9BWE0	REPI1_HUMAN	2H2-type 2.	1	CTTTCGCCATG	0.677	
-	11	1411	jo.1_Missense_M	NM_007189	NP_009120	Q9UG63	ABCF2_HUMAN	er 2.|ATP 2 (By similarity).	1	CCCTGCTCCAT	0.507	
+	1	314	_p.T52M|uc003wl	NM_024012	NP_076917	P47898	5HT5A_HUMAN	ame=2; (By similarity).	3	TGGCCGTCTCG	0.687	
+	5	763	me.2_Missense_M	NM_053043	NP_444271	Q96EV2	RBM33_HUMAN	Glu-rich.	1	CAAATCTGATG	0.408	
+	15	3442	n_p.T835M|RBM	NM_053043	NP_444271	Q96EV2	RBM33_HUMAN		1	GGTGACGCTGA	0.657	
-	49	7853	p.T1817M|CSMD1	NM_033225	NP_150094	Q96PZ7	CSMD1_HUMAN	xtracellular (Potential).	25	GTGGCGTGAGG	0.463	
-	2	581		NM_178857	NP_849188	Q8IWN7	RP1L1_HUMAN		8	TGGCCGGCCTG	0.637	
-	2	1386	p.A305V|EGR3_u	NM_004430	NP_004421	Q06889	EGR3_HUMAN	2H2-type 3.	0	TGCGCGCAAAC	0.647	
+	5	752	SF10C_uc011kzr.1	NM_003841	NP_003832	O14798	TR10C_HUMAN	TAPE 2.	0	AATGAACACCA	0.602	rs61736405
+	2	180	ea.1_Nonsense_	NM_003817	NP_003808	Q9H2U9	ADAM7_HUMAN	ellular (Potential).	5	TCCTTGGAGTA	0.403	
+	26	2799	p.Y664C|PTK2B_	NM_173174	NP_775266	Q14289	FAK2_HUMAN	rotein kinase.	5	GGACTACGACC	0.647	
+	6	599	1lce.1_Missense_	NM_021623	NP_067636	Q9HB19	PKHA2_HUMAN		0	GGGCCTACCCA	0.562	
-	3	294	t.2_Nonsense_M	NM_000930	NP_000921	P00750	TPA_HUMAN		2	GAATCGGGCAT	0.582	
-	85	12013	_Mutation_p.H39	NM_006904	NP_008835	P78527	PRKDC_HUMAN	PI3K/PI4K.	34	TGCGTGTACCA	0.498	
+	13	1116	TG1_uc010lxz.1_	NM_018967	NP_061840	Q9NSN8	SNTG1_HUMAN		5	TCTCTGCTGAA	0.433	
-	17	3153	NL_uc003xqt.3_	NM_144651	NP_653252	A1KZ92	PXDNL_HUMAN		2	AGGCAGCCAGT	0.592	
+	3	617	1_uc010lyh.2_5'	NM_024831	NP_079107	Q96RS0	TGS1_HUMAN		3	TGACAGCAAAG	0.423	
+	3	2005		NM_004770	NP_004761	Q92953	KCNB2_HUMAN	lasmic (Potential).	7	AGGCCGGAGAG	0.527	

+	10	8022	C2590W|ZFHX4_	NM_024721	NP_078997	Q86UP3	ZFHX4_HUMAN		15	AATTGCAGTGA	0.473	
+	10	8675	.T2808M|ZFHX4_	NM_024721	NP_078997	Q86UP3	ZFHX4_HUMAN		15	TTAATACGGCAAT	0.473	
+	7	1051	13_uc003ydf.1_Int	NM_198584	NP_940986	Q8N1Q1	CAH13_HUMAN		0	AGGGTGAAGCA	0.463	
+	11	1496	Splice_Site_p.M4	NM_052832	NP_439897	Q8TE54	S26A7_HUMAN		2	CATGGTACGGT	0.343	
+	6	829	q.1_RNA|INTS8_	NM_017864	NP_060334	Q75QN2	INT8_HUMAN		0	AAACTGAGAGT	0.373	
+	2	1161		NM_020697	NP_065748	Q9ULS6	KCNS2_HUMAN	=Segment S3; (Potential).	1	TCCCCTTTTAC	0.537	
-	15	2581	nt.2_Nonsense_M	NM_198123	NP_937756	Q7Z407	CSMD3_HUMAN	lar (Potential).|CUB 4.	63	CAATCGCAGTAT	0.408	
+	16	1533	_p.S491N|FAM91A	NM_144963	NP_659400	Q658Y4	F91A1_HUMAN		2	TTGCAGCAGAG	0.473	
+	1	497	c003yrb.2_5'Flan	NM_007218	NP_009149	Q8WU17	RN139_HUMAN	ical; (Potential).	1	GCATCGTGCTC	0.647	
+	3	835	i.2_Missense_Mut	NM_002467	NP_002458	P01106	MYC_HUMAN		6	TGGGAGGAGAC	0.607	
-	3	931		NM_152888	NP_690848	Q8NFW1	COMA1_HUMAN	ly-Ala.|VWFA.	13	CGCCGCGGCGT	0.721	
-	9	1518	_p.R560C|TRAPP	NM_001160372	NP_001153844	Q96Q05	TPPC9_HUMAN		2	CAAACGCATCT	0.522	
-	2	286	_p.R149P|TRAPP	NM_001160372	NP_001153844	Q96Q05	TPPC9_HUMAN		2	GGACTCGCTGG	0.572	
-	8	1368	e.1_Missense_M	NM_201380	NP_958782	Q15149	PLEC_HUMAN	ar 1.|Actin-binding.	9	GCGGGGCATGG	0.687	
+	3	621	c003zce.1_Misse	NM_024531	NP_078807	Q9HAB3	RFT3_HUMAN	ical; (Potential).	0	GAGTGCCCTGC	0.652	
-	19	2978	uc011llh.1_5'Flan	NM_013432	NP_038460	Q96HA7	TONSL_HUMAN		0	GTGGGGCCAGC	0.706	
-	6	1723	p.R438W|ZNF34_	NM_030580	NP_085057	Q8IZ26	ZNF34_HUMAN	2H2-type 12.	0	GTGCCGGAAGG	0.582	
-	4	608	u.2_Missense_M	NM_001029976	NP_001025147	P17020	ZNF16_HUMAN		5	CCCCATGGCAG	0.552	
+	1	203	gu.1_Missense_	NM_021951	NP_068770	Q9Y5R6	DMRT1_HUMAN		1	CCTCACGCCCC	0.711	
+	2	598		NM_212558	NP_997723	Q68D42	TM215_HUMAN		0	GGTCCGCAAAT	0.597	
+	4	422	m.1_Missense_M	NM_012144	NP_036276	Q9UI46	DNAI1_HUMAN		0	CACACGCACCC	0.498	
+	2	185	3zvr.2_Missense_	NM_015297	NP_056112	Q9UPV7	K1045_HUMAN		1	TGGGGGTGTTG	0.552	
-	5	1333	_Mutation_p.E31	NM_032634	NP_116023	Q8TEQ8	PIGO_HUMAN		3	CACCTCTGGTG	0.527	
+	13	1587	wr.2_Nonsense_	NM_006377	NP_006368	O14795	UN13B_HUMAN		5	ACAGTCACTGG	0.522	
+	18	2490	wr.2_Missense_M	NM_006377	NP_006368	O14795	UN13B_HUMAN		5	GGGGGAGGAGA	0.527	
-	56	7726		NM_006289	NP_006280	Q9Y490	TLN1_HUMAN		13	GCAGCCTGGGC	0.517	
-	3	418	ense_Mutation_p.	NM_005476	NP_005467	Q9Y223	GLCNE_HUMAN	glucosamine 2-epimerase.	0	TGTTAATGTCA	0.443	
+	4	518	jh.2_Missense_M	NM_006914	NP_008845	Q92753	RORB_HUMAN	ge (Potential).	4	GGCACGTCATT	0.542	
+	6	1218	Splice_Site|TLE4_	NM_007005	NP_008936	O60756	BCE1_HUMAN		5	TTGGGGTACGT	0.468	
-	12	1990	CHC6_uc004aot.	NM_024617	NP_078893	Q5VYS8	TUT7_HUMAN	P-associated 1.	2	CAATGCGCTTTT	0.368	
-	4	991	ion_p.P287L|ECM	NM_001393	NP_001384	O94769	ECM2_HUMAN	LRRNT.	2	TGGGAGGAGCA	0.458	
+	3	698	P4_uc010msh.2_	NM_014282	NP_055097	Q5JVS0	HABP4_HUMAN		1	TGAGAGGACGT	0.488	
+	3	1172	ag.1_Missense_M	NM_006981	NP_008912	Q92570	NR4A3_HUMAN		173	GGCCTTCCCCC	0.721	
+	1	676		NM_006687	NP_006678	Q9Y615	ACL7A_HUMAN		0	TCCTACGTGGTC	0.622	
-	6	913	uc.1_Missense_	NM_001080398	NP_001073867				0	CTGCTGTGGCT	0.408	
+	2	764	lwx.1_Missense_	NM_133465	NP_597722	Q8N8K9	K1958_HUMAN		1	AGCAATGATGTC	0.473	
+	4	657	nse_Mutation_p.R	NM_000177	NP_000168	P06396	GELS_HUMAN	elsolin-like 2.	3	GGTCCGTGCCA	0.592	rs150617780
-	19	1611	1A_uc004boa.1_	NM_020946	NP_065997	Q8TEH3	DEN1A_HUMAN		2	GGGGGCGCAG	0.622	
-	4	766	ion_p.R145C|MAP	NM_001006617	NP_001006618	Q9BPZ7	SIN1_HUMAN	tion with MAP3K2.	4	TAGGCGTACAG	0.393	
-	5	630	p.T130M|FAM129	NM_022833	NP_073744	Q96TA1	NIBL1_HUMAN	PH.	0	TTGCCGTGGTC	0.577	
+	6	843	_p.L252F|DNM1_u	NM_004408	NP_004399	Q05193	DYN1_HUMAN		2	GCCTTGGCTGC	0.552	
+	1	179		NM_021619	NP_067632	Q9H4Q4	PRD12_HUMAN		0	CGGCCGCTGGC	0.677	
+	8	1528		NM_006059	NP_006050	Q9Y6N6	LAMC3_HUMAN	inin EGF-like 4.	3	TGGCTGCAGCA	0.592	
-	5	660	D27_uc011mco.1	NM_004269	NP_004260	Q6P2C8	MED27_HUMAN		1	TTTACTATTGTTC	0.443	
-	5	715	22_uc004cdd.2_3	NM_133640	NP_598395	Q15528	MED22_HUMAN		1	AGAGTCTGTGT	0.642	
-	3	1118	C2_uc010nbh.2_5	NM_144653	NP_653254	Q96BF6	NACC2_HUMAN		0	TGGCAGGTAGG	0.662	
-	5	684		NM_181701	NP_859052	Q6ZRP7	QSOX2_HUMAN		1	TGCTTTCAAAGA	0.527	

+	11	1254	p.G286R|PMPCA_	NM_015160	NP_055975	Q10713	MPPA_HUMAN			0	TGGGCGGAACC	0.552
+	4	929	Missense_Mutatior	NM_014172	NP_054891	Q9NRX4	PHP14_HUMAN			0	CAGCACGCCATT	0.617
-	22	2676	|EXD3_uc010ncf.1	NM_017820	NP_060290	Q8N9H8	MUT7_HUMAN			0	AGCACCGCAGC	0.682
+	25	3569	coe.2_Missense_M	NM_024757	NP_079033	Q9H9B1	EHMT1_HUMAN	with histone H3.|SET.		3	GATCTCGACAATA	0.502
+	29	4589	p.A1012T|CACNA	NM_000718	NP_000709	Q00975	CAC1B_HUMAN	1 of repeat IV; (Potential).|I		6	ATGATAGCCCTC	0.562
-	7	1106	mha.1_Missense_	NM_013239	NP_037371	Q9Y5P8	P2R3B_HUMAN			0	ATGTCCGCCTCC	0.637
-	8	1280	SD_uc004cqz.1_In	NM_001669	NP_001660	P51689	ARSD_HUMAN			0	CGGGAGCACCC	0.632
+	2	133		NM_001011719	NP_001011719	Q5FYA8	ARSH_HUMAN			1	GTGAGGCTTACC	0.502
-	3	503	se_Mutation_p.D9	NM_012080	NP_036212	Q08623	HDHD1_HUMAN			0	TTCGGGGTCATC	0.572
+	6	926	cyd.2_Missense_	NM_001037540	NP_001032629	Q9UN30	SCML1_HUMAN			3	GATGGTGCAACG	0.537
+	12	1584	yn.2_Missense_Mu	NM_003159	NP_003150	O76039	CDKL5_HUMAN			6	AGAACCGCCACT	0.463
-	17	2181	czj.1_Missense_M	NM_001001671	NP_001001671	Q6ZN16	M3K15_HUMAN	rotein kinase.		7	TATTGCGGTGCT	0.453
-	1	1213		NM_153270	NP_695002	Q8N239	KLH34_HUMAN	BACK.		1	CCAAAGCGGACA	0.677
+	1	542		NM_019886	NP_063939	Q9NS84	CHST7_HUMAN	nenal (Potential).		3	TTAACCAGCACC	0.632
-	6	617	dit.2_Missense_M	NM_006962	NP_008893	P17025	ZN182_HUMAN	KRAB.		3	AAAATGGGATTT	0.488
+	14	1206	_Missense_Mutati	NM_006044	NP_006035	Q9UBN7	HDAC6_HUMAN	ne deacetylase 1.		4	CTGCTCATGGGT	0.597
+	1	804		NM_181532	NP_853510	Q7Z444	RASE_HUMAN			5	AAACACGGCAA	0.622
-	6	555	p.Y186H|TIMM17	NM_005834	NP_005825	O60830	TI17B_HUMAN			1	CTGTGTAGCGAG	0.592
+	7	893	se_Mutation_p.A2	NM_001032382	NP_001027554	O60828	PQBP1_HUMAN			1	CACAGCAGCTG	0.637
-	5	3101	lw.1_Missense_Mu	NM_004979	NP_004970	Q9NSA2	KCND1_HUMAN	lasmic (Potential).		3	GCGGCCACCCG	0.657
-	25	2401		NM_020137	NP_064522	Q4V328	GRAP1_HUMAN	Potential.		3	ATCTCCCGAAGG	0.587
-	4	348	se_Mutation_p.R5	NM_001029896	NP_001025067	Q9Y484	WIPI4_HUMAN			1	TGGAGCGGTGC	0.607
-	1	171		NM_015698	NP_056513	Q92917	GPKOW_HUMAN			2	AGCTCCCTCCCT	0.627
+	2	243	4dpi.3_Missense_	NM_153183	NP_694853	Q8NFP7	NUD10_HUMAN			0	ACCAGACACGGA	0.677
+	13	1323	L3L_uc004dti.2_R	NM_019067	NP_061940	Q9NVN8	GNL3L_HUMAN			1	CAGCGGGAAGA	0.507
+	1	2518		NM_007157	NP_009088	P98169	ZXDB_HUMAN			0	TCTTTGGACAG	0.473
-	2	865		NM_152424	NP_689637	Q5JTC6	F123B_HUMAN		p.0?(40)	112	CCTCTCAGGCC	0.577
-	15	1564	pg.1_Missense_M	NM_002547	NP_002538	O60890	OPHN1_HUMAN	Rho-GAP.		2	CAAAAAAGGCATT	0.388
+	1	206	12_uc004dyz.2_M	NM_005120	NP_005111	Q93074	MED12_HUMAN			4	ATGGCGGCCTTC	0.677
+	8	1290	RN1_uc011mpt.1_	NM_052957	NP_443189	Q96QF7	ACRC_HUMAN	Asp/Ser-rich.		3	TCGGAAGCTCC	0.552
+	8	1292	RN1_uc011mpt.1_	NM_052957	NP_443189	Q96QF7	ACRC_HUMAN	Asp/Ser-rich.		3	GGAAGCTCCCG	0.557
-	2	333	XCR3_uc011mpx.	NM_001504	NP_001495	P49682	CXCR3_HUMAN	lasmic (Potential).		3	AGGTGTCGGTGC	0.672
-	1	1402	en.2_Missense_Mu	NM_001163541	NP_001157013	Q86VE3	SATL1_HUMAN	Gln-rich.		2	CTGTTTGGTTCT	0.572
+	6	1243	_p.P191Q|DACH2	NM_053281	NP_444511	Q96NX9	DACH2_HUMAN			5	ACAGTCCACTCT	0.403
-	8	2011	Y2F_uc011msq.1_	NM_001522	NP_001513	P51841	GUC2F_HUMAN	e.|Cytoplasmic (Potential).		8	AATCTCCAAGGG	0.373
-	1	1303		NM_138289	NP_612146	Q8TDG2	ACTT1_HUMAN			5	ACCACAGATGTC	0.468
-	10	1278	0nrf.1_Missense_	NM_017666	NP_060136	Q8ND82	Z280C_HUMAN	C2H2-type 2.		3	GTGTGTGTACTC	0.438
+	4	344		NM_016024	NP_057108	Q9Y388	RBMX2_HUMAN	RRM.		4	CTGGCCGTCGAC	0.443
-	5	854	wf.2_Missense_Mu	NM_001555	NP_001546	Q8N6C5	IGSF1_HUMAN	2.|Extracellular (Potential).		5	TGGGGAGCATCT	0.542
-	2	1044		NM_001009615	NP_001009615	Q5MJ10	SPXN2_HUMAN			1	TCCTCCTGTGAA	0.517
-	8	1581	.A348V|PDZD4_u	NM_032512	NP_115901	Q76G19	PDZD4_HUMAN			1	CTGGCCGCCAGG	0.632
-	22	3754	NA_uc010nuu.1_	NM_001110556	NP_001104026	P21333	FLNA_HUMAN	Filamin 10.		6	CAGCCCGGGGC	0.642
-	17	2731	u.1_Missense_Mu	NM_001110556	NP_001104026	P21333	FLNA_HUMAN	Filamin 6.		6	CATTGCGGATGA	0.622
+	9	764	nb.2_Missense_M	NM_024332	NP_077308	P46736	BRCC3_HUMAN			6	TCACTATCGGGA	0.448
-	25	3879	5_uc001ama.1_R	NM_015557	NP_056372	Q8TDI0	CHD5_HUMAN			12	ATGGCCGCATCG	0.572
+	15	2067	p.G632D|PER3_u	NM_016831	NP_058515	P56645	PER3_HUMAN	ing domain (By similarity).		3	AATGCGGTTACA	0.507
+	17	2900	_p.A910T|PER3_u	NM_016831	NP_058515	P56645	PER3_HUMAN			3	GGGAGGCACAA	0.527

+	7	1050	apx.2_Missense_	NM_032315	NP_115691	Q9BSK2	S2533_HUMAN	Solcar 3.	0	GGCGCGCCTGG	0.498	
+	2	256	P7_uc009vms.2_	NM_052960	NP_443192	Q96R05	RET7_HUMAN		0	TGAAATTTAAAGT	0.333	
+	11	1266	bb.1_Missense_M	NM_000302	NP_000293	Q02809	PLOD1_HUMAN		3	CAACAGCCTGC	0.637	
+	17	2189	tw.2_Missense_M	NM_015378	NP_056193	Q5THJ4	VP13D_HUMAN		5	GATGCAGACCA	0.473	
-	7	794	1_Intron|MST1P9_	NR_002729					0	TATTGGCTGTG	0.617	
-	13	1599	dy.1_Nonsense_	NM_016287	NP_057371	Q5SSJ5	HP1B3_HUMAN	Lys-rich.	2	CCGCTGGGCAG	0.552	
-	7	1532		NM_004091	NP_004082	Q14209	E2F2_HUMAN	tivation (Potential).	4	GCCTCCAAGGG	0.652	
-	1	77	slation_Start_Site|	NM_020485	NP_065231	P18577	RHCE_HUMAN		0	TGTCCGTCTCT	0.592	
+	15	1641	es.1_Missense_M	NM_020451	NP_065184	Q9NZV5	SELN_HUMAN		2	CTGCCTGCCCA	0.637	
+	2	257	lice_Site|PDIK1L_	NM_152835	NP_690048	Q8N165	PDK1L_HUMAN		0	TTTCCAGAAAC	0.418	
-	6	1651	p.E228Q|AHDC1_	NM_001029882	NP_001025053	Q5TGY3	AHDC1_HUMAN	Pro-rich.	1	AGGCTCTGGGG	0.647	
-	33	4936	_Mutation_p.S111	NM_001703	NP_001694	O60241	BAI2_HUMAN	lasmic (Potential).	13	AGGGCTGGGCT	0.378	
+	10	1367		NM_017629	NP_060099	Q9HCK5	AGO4_HUMAN		1	TTGTTGTCCAC	0.428	
+	4	738	1bzu.2_Missense_	NM_017825	NP_060295	Q9NX46	ARHL2_HUMAN		1	AGTCCGTCTTG	0.602	
+	6	1472	cbc.1_Missense_	NM_025079	NP_079355	Q5D1E8	ZC12A_HUMAN		2	CATTGGCTCCC	0.657	
+	30	3809	89_splice|MACF1_	NM_012090	NP_036222	Q9UPN3	MACF1_HUMAN		16	CCACAGCACTG	0.448	
+	61	17263	.R80H|MACF1_uc	NM_033044	NP_149033	Q9UPN3	MACF1_HUMAN	tail (By similarity).|GAR.	16	TGGTCCGTATTC	0.438	
-	14	2065	5_splice|FOXJ3_	NM_014947	NP_055762	Q9UPW0	FOXJ3_HUMAN		2	TCTTACCTGCC	0.428	
+	5	1075		NM_173642	NP_775913	Q8IXN7	RIMKA_HUMAN		0	TGGCTGTCCTC	0.532	
+	7	1289	ense_Mutation_p.	NM_152498	NP_689711	Q96MR6	WDR65_HUMAN	WD 5.	1	ACTCAGCACCC	0.488	
+	10	1279		NM_015284	NP_056099	Q5T011	SZT2_HUMAN		0	GTGGGGCTCCC	0.557	
+	21	2930		NM_015284	NP_056099	Q5T011	SZT2_HUMAN		0	GCACCGCGCAG	0.562	
+	15	1518	c.1_Missense_Mut	NM_006845	NP_006836	Q99661	KIF2C_HUMAN	inesin-motor.	1	TTCCTCCCGCT	0.522	
+	5	765	p.S171N|CYP4X1_	NM_178033	NP_828847	Q8N118	CP4X1_HUMAN		2	TTGCAGCACTC	0.498	
+	5	570		NM_006252	NP_006243	P54646	AAPK2_HUMAN	rotein kinase.	6	TCAGATGGTGAA	0.308	
+	2	261	FGGY_uc001czj.3	NM_018291	NP_060761	Q96C11	FGGY_HUMAN		1	TGGACGTTGGA	0.502	
-	1	93	11_uc010oqo.1_5	NM_017768	NP_060238	Q9H9A6	LRC40_HUMAN		1	AACCAGCGCGG	0.597	
+	11	1972	ls.1_Missense_M	NM_001285	NP_001276	A8K7I4	CLCA1_HUMAN		1	ATATTCGCCAAG	0.493	
+	5	441	.1_Intron|ZNF326	NM_182976	NP_892021	Q5BKZ1	ZN326_HUMAN	l activation (By similarity).|	1	ACAAAGCCGCT	0.507	
+	4	536				P26439	3BHS2_HUMAN		2	TGTCGGTCGTC	0.512	
+	4	1599	HFE2_uc001enk.	NM_213653	NP_998818	Q6ZVN8	RGMC_HUMAN		1	TTTGCATTCAGT	0.463	
+	27	3191	08_splice|ITGA10_	NM_003637	NP_003628	O75578	ITA10_HUMAN		8	CTGTTAGAATGG	0.522	
-	3	3458	c001ezv.2_5'Flan	NM_002016	NP_002007	P20930	FILA_HUMAN	Ser-rich.	16	CTTGTCTTCGT	0.602	
-	17	1909	n_p.G592V|THBS	NM_007112	NP_009043	P49746	TSP3_HUMAN	SP type-3 6.	5	CATCCCCATCG	0.512	
-	3	442	CRL5_uc010phw.	NM_031281	NP_112571	Q96RD9	FCRL5_HUMAN	otential).|Ig-like C2-type 1.	6	GCACAGGGCTA	0.458	
-	3	210		NM_005894	NP_005885	O43866	CD5L_HUMAN		1	CACTCCAGATG	0.597	
+	2	751		NM_004983	NP_004974	Q92806	IRK9_HUMAN	smic (By similarity).	2	AGCCACGCTCG	0.652	
+	1	351		NM_001231	NP_001222	P31415	CASQ1_HUMAN		1	CAGGGGTACAG	0.552	
-	23	2777	v.3_Missense_Mu	NM_004371	NP_004362	P53621	COPA_HUMAN		2	CTGGAGCAGCT	0.433	
-	4	582	5_uc010plr.1_RN	NM_000130	NP_000121	P12259	FA5_HUMAN	1.|Plastocyanin-like 1.	6	ATTCTCGGCCT	0.512	rs145625079
+	27	7445	2L2_uc010pmi.1_	NM_015172	NP_055987	Q9Y520	PRC2C_HUMAN	Gln-rich.	0	ATGGACACAAG	0.408	
+	5	985	_p.G80D|KLHL20_	NM_014458	NP_055273	Q9Y2M5	KLH20_HUMAN	BACK.	1	GGTCGGCACAG	0.373	
+	38	9718	.G1247E|CEP350	NM_014810	NP_055625	Q5VT06	CE350_HUMAN		4	GCAGGGGAGAA	0.463	
-	6	995		NM_000069	NP_000060	Q13698	CAC1S_HUMAN	llular (Potential).|I.	5	CCATTGATGGT	0.617	
-	2	764		NM_002479	NP_002470	P15173	MYOG_HUMAN		2	CGCTGGGCACC	0.607	
+	4	957	xcw.2_Missense_	NM_019605	NP_062551	Q9NUC0	SRTD4_HUMAN		2	GCCAGATACCT	0.363	
-	4	578	pte.1_Missense_	NM_018252	NP_060722	Q9H813	TM206_HUMAN	ellular (Potential).	1	TCAGAGGAGGA	0.542	

-	2	2213	h.2_Missense_Mu	NM_002221	NP_002212	P27987	IP3KB_HUMAN			5	GGTGCGCTCAG	0.562	rs34777857
+	4	821	.1_Intron|ZNF678_	NM_178549	NP_848644	F5GXA7	F5GXA7_HUMAN			1	AATGTGGCAAAG	0.333	rs145397350
+	26	7101	CN_uc001hsp.1_	NM_001098623	NP_001092093	Q5VST9	OBSCN_HUMAN	Ig-like 23.		28	TCCACGCAGAG	0.607	
-	14	2314		NM_005646	NP_005637	Q13395	TARB1_HUMAN			3	TACCCCTTTTCC	0.398	
+	5	538	BCE_uc010pxr.1_	NM_003193	NP_003184	Q15813	TBCE_HUMAN			0	TGTGCAGTAAGT	0.438	
+	13	6345		NM_018012	NP_060482	Q2KJY2	KI26B_HUMAN			3	CAGGCGTCCGC	0.602	
+	1	635	L13_uc001ids.2_I	NM_001001963	NP_001001963	Q8NGY9	OR2L8_HUMAN	Name=5; (Potential).		2	TCATTGGTATTT	0.498	
+	1	383		NM_001013355	NP_001013373	Q5TZ20	OR2G6_HUMAN	lasmic (Potential).		3	CTGCCGGCCAC	0.597	
-	6	976	_p.Q206R|SEPHS	NM_012247	NP_036379	P49903	SPS1_HUMAN			1	CCACCTGTGTC	0.522	
-	22	2874	9xjf.1_Missense_M	NM_018027	NP_060497	Q9P2Q2	FRM4A_HUMAN			3	CCCTCGATGTAC	0.527	
+	7	794		NM_052997	NP_443723	Q9BXX3	AN30A_HUMAN			9	CCTTGGCGGAAA	0.423	
+	7	1156		NM_052997	NP_443723	Q9BXX3	AN30A_HUMAN			9	CGTGGGCAGCA	0.408	
+	5	599	01izo.1_RNA|HSD17B7P2_uc001izp.1_Missense_Mutation_p.N173S							0	TCGCAATGCAA	0.453	rs2257765
+	2	262	_p.D55N|ALOX5_	NM_000698	NP_000689	P09917	LOX5_HUMAN	PLAT.		2	TCATACGACGTG	0.448	
-	6	1923	oi.2_Intron|PARG_	NM_003631	NP_003622	Q86W56	PARG_HUMAN			2	AACATACCTTCA	0.433	
+	13	2023	_p.I645T|HK1_uc0	NM_000188	NP_000179	P19367	HXK1_HUMAN	Catalytic.		1	ATGCGATAAAAA	0.368	
+	18	1564	ljqc.1_Missense_M	NM_005203	NP_005194	Q5TAT6	CODA1_HUMAN	al).|Triple-helical region 2 (		1	GGATGAAGGTCA	0.597	
+	11	1730	p.R580Q|ADAMT	NM_080722	NP_542453	Q8WXS8	ATS14_HUMAN	TSP type-1 1.		6	CAGCCGGAGCT	0.667	
+	21	2962	_Mutation_p.R176	NM_004922	NP_004913	P53992	SC24C_HUMAN			3	ATGACCGTGCCT	0.498	
+	2	165	S24_uc001jzp.2_	NM_001026	NP_001017	P62847	RS24_HUMAN			1	CTATCCGCACTA	0.383	
-	19	2370	p.R210Q|IDE_uc0	NM_004969	NP_004960	P14735	IDE_HUMAN			3	CTATACCGAACCA	0.428	
-	2	142	5'Flank|ZDHHC16	NM_016046	NP_057130	Q9Y3B2	EXOS1_HUMAN			0	GACAGCCGGCA	0.577	
+	2	67	1_uc001lcn.2_Sp	NM_006229	NP_006220	P54315	LIPR1_HUMAN			2	CCAAAGGTAAGA	0.498	
+	4	2654	nse_Mutation_p.P	NM_206862	NP_996744	O95359	TACC2_HUMAN			10	CGGGCCGGCGT	0.617	
+	14	1498	p.L407M|PTPRE_	NM_006504	NP_006495	P23469	PTPRE_HUMAN	lasmic (Potential).		1	CCTCCCTGGAG	0.592	
-	19	2149	_p.V765F|ADAM8_uc009ybi.2_Missense_Mutation_p.C			P78325	ADAM8_HUMAN			3	TGTAGACAGGAA	0.652	
-	13	1897	9ycc.2_Missense_	NM_021924	NP_068743	Q9HBB8	CDHR5_HUMAN	dem repeats.|2.|Extracellula		0	CCCACCGGGTG	0.672	rs139590704
-	6	1257	p.P226L|LRDD_u	NM_145886	NP_665893	Q9HB75	PIDD_HUMAN	ZU5 1.		0	CATGAGGACCC	0.706	
+	48	9956	b.2_Missense_Mu	NM_017511	NP_059981	Q9HC84	MUC5B_HUMAN	approximate tandem repeat		0	CACCACACCCA	0.637	
-	7	1607	e_Mutation_p.R23	NM_018073	NP_060543	Q6AZZ1	TRI68_HUMAN	B30.2/SPRY.		1	GAGGCGCCCAG	0.522	
-	8	1636	p.L426P|FAM160	NM_001098794	NP_001092264	Q8N612	F16A2_HUMAN			2	GGAACAAGATAC	0.507	
-	1	593		NM_003696	NP_003687	O95222	OR6A2_HUMAN	lasmic (Potential).		5	ATAGCAGATGGC	0.532	
-	2	541		NM_020646	NP_065697	Q9NQ33	ASCL3_HUMAN			0	CTTTTCCAGGGT	0.433	
-	11	1923	VI1_uc001miz.2_	NM_001100167	NP_001093637	Q9Y6F6	MRVI1_HUMAN		p.R486C(1)	3	GTTTGCGCAGCA	0.498	rs116772600
-	7	1060	miz.2_Missense_	NM_001100167	NP_001093637	Q9Y6F6	MRVI1_HUMAN			3	ATGGCGGGCCA	0.622	
+	11	1458		NM_014633	NP_055448	Q6PD62	CTR9_HUMAN	TPR 8.		2	GAACAGCAACA	0.458	
-	18	3234	rk.3_Missense_Mu	NM_018490	NP_060960	Q9BXB1	LGR4_HUMAN	lasmic (Potential).		1	GTCTGAGACAA	0.512	
+	4	478	_Mutation_p.K86R	NM_005693	NP_005684	Q13133	NR1H3_HUMAN			3	GAAAAAGGGGC	0.567	
-	10	1179	hm.1_Missense_M	NM_001025596	NP_001020767	Q92879	CELF1_HUMAN			3	CCAGCAGCACCA	0.557	
+	1	403		NM_001004701	NP_001004701	Q8NGL9	OR4CG_HUMAN	lasmic (Potential).		2	ATCATAAGCCAG	0.507	
-	1	846	NR_uc001njn.3_	NM_005161	NP_005152	P35414	APJ_HUMAN	lasmic (Potential).		6	CTGGCCTCACGA	0.637	
-	5	622		NM_006093	NP_006084	Q9Y2Y8	PRG3_HUMAN	C-type lectin.		0	TTCCACAGGAAC	0.557	
-	3	426		NM_006093	NP_006084	Q9Y2Y8	PRG3_HUMAN			0	GCACCTTGGAC	0.532	
-	10	1524	p.H383Y|SF1_uc0	NM_004630	NP_004621	Q15637	SF01_HUMAN	Pro-rich.		3	CTCCATGCATGC	0.617	
-	1	163		NM_138456	NP_612465	Q8N1L9	BATF2_HUMAN			1	TCTGGGTCAGC	0.597	
+	2	584		NM_006779	NP_006770	O14613	BORG1_HUMAN			0	TGGCAGTGGCG	0.617	
+	4	966	fq.2_Missense_Mu	NM_004561	NP_004552	O14753	OVOL1_HUMAN	C2H2-type 4.		1	TGAGGAGTGCG	0.622	

-	2	620	gw.2_Missense_	NM_033036	NP_149025	Q96A11	G3ST3_HUMAN	enal (Potential).	1	GGCCGGCTCGC	0.701	
+	3	2048	ri.2_3'UTR|RBM4_	NM_006328	NP_006319	Q96PK6	RBM14_HUMAN		3	ACCGTCGCCTG	0.587	
+	4	981	e_Mutation_p.R19	NM_018043	NP_060513	Q5XXA6	ANO1_HUMAN	lasmic (Potential).	2	TCTCCCGGGAG	0.517	
+	13	1176	on_p.F287L|CTTN	NM_005231	NP_005222	Q14247	SRC8_HUMAN	actin 7; truncated.	1	TCAACCTTTGAG	0.557	
+	6	884	IT_uc009yta.2_RN	NM_145309	NP_660352	Q96E66	LRC51_HUMAN	LRRCT.	0	AGACCGCACCA	0.552	
-	19	2794	_p.P624S|ARAP1_	NM_001040118	NP_001035207	Q96P48	ARAP1_HUMAN		1	GTAGGGTAGGC	0.662	
+	3	1044		NM_153614	NP_705842	P59910	DJB13_HUMAN		0	TGAAAAGGTGT	0.498	
-	26	5318	_uc001out.2_Spli	NM_015531	NP_056346	Q4AC94	C2CD3_HUMAN		7	ATAGCCTATTAAG	0.279	
-	19	2481	K|XRRA1_uc001o	NM_182969	NP_892014	Q6P2D8	XRRA1_HUMAN		1	CCGTTCTGTCC	0.587	
+	9	1799	s.1_Missense_Mu	NM_007256	NP_009187	O94956	SO2B1_HUMAN	ellular (Potential).	2	GATTGCGGGCA	0.642	rs146532688
+	11	1396	m.1_Missense_Mu	NM_000260	NP_000251	Q13402	MYO7A_HUMAN	osin head-like.	4	CACCCTCATCA	0.672	
+	1	426	11_uc009yuu.2_Ir	NM_173039	NP_766627	Q8NBQ7	AQP11_HUMAN	Name=1; (Potential).	0	GCTGTCGGTGG	0.701	
+	2	433		NM_153696	NP_710163	Q9HBA9	FOH1B_HUMAN		6	GAATACGCTTAT	0.328	
+	1	229		NM_017516	NP_059986	Q14964	RB39A_HUMAN	(By similarity).	0	CGGCGGGACAG	0.741	
+	1	203	uc001pnh.2_5'Flar	NM_031938	NP_114144	Q9BYV7	BCDO2_HUMAN		0	GCTCCCAGGTA	0.488	
+	6	716	gg.2_Missense_Mu	NM_001040455	NP_001035545	Q8NBJ9	SIDT2_HUMAN	ellular (Potential).	0	ACGATGACCAA	0.567	
+	15	2390		NM_005188	NP_005179	P22681	CBL_HUMAN	D2AP.|Asp/Glu-rich (acidic	149	TCCAGGTGAAG	0.463	
-	24	3608	.A1159V|NFRKB_	NM_001143835	NP_001137307	Q6P4R8	NFRKB_HUMAN		3	ACAGCAGCATTC	0.612	
+	8	966	se_Mutation_p.R2	NM_014384	NP_055199	Q9UKU7	ACAD8_HUMAN		0	TGTCCGGAAGC	0.612	rs121908422
+	5	1881	TM2_uc001qju.2_	NM_001039029	NP_001034118	Q8N967	LRTM2_HUMAN	lasmic (Potential).	1	AGGGCGAGCAC	0.662	
-	7	926	dy.1_Missense_Mu	NM_152640	NP_689853	Q8IZD4	DCP1B_HUMAN		1	GGTGAGTGTCT	0.473	
-	15	2361	p.G726S|CHD4_u	NM_001273	NP_001264	Q14839	CHD4_HUMAN		2	CAGGCCCTCCA	0.522	
-	4	548	|PHB2_uc001qse.	NM_001144831	NP_001138303	Q99623	PHB2_HUMAN		3	GAGCATTGGGT	0.547	
+	3	488		NM_001080454	NP_001073923	P0C7M7	ACSM4_HUMAN		0	GGCCAAGTGCA	0.562	
-	4	1067	1raj.1_Missense_	NM_018050	NP_060520	Q9H8J5	MANS1_HUMAN	xtracellular (Potential).	0	TTACAGGTGGA	0.562	
-	32	3952	.E1311G|ABCC9_	NM_005691	NP_005682	O60706	ABCC9_HUMAN	lasmic (Potential).	6	TGATCTCCCCTT	0.398	
-	13	1821		NM_004818	NP_004809	Q9BUQ8	DDX23_HUMAN	ase ATP-binding.	6	TGTCTGGCTTC	0.527	
+	3	699	zmd.2_Missense_	NM_021934	NP_068753	Q9BSB4	ATGA1_HUMAN		0	TCGTGCCCTGC	0.572	
-	5	992		NM_175053	NP_778223	Q7RTS7	K2C74_HUMAN	Rod.|Coil 2.	2	GCATGCGGACC	0.592	
-	2	643	fr.3_Nonsense_Mu	NM_006163	NP_006154	Q16621	NFE2_HUMAN	d for interaction with MAP	0	TGGCTCACTTG	0.512	
-	2	441	.A74V|ITGA7_uc0	NM_001144996	NP_001138468	Q13683	ITA7_HUMAN	Extracellular (Potential).	5	GGGGAGCACCC	0.627	
+	41	6960		NM_002332	NP_002323	Q07954	LRP1_HUMAN	Extracellular (Potential).	22	TGGCGGGTGCC	0.687	
+	2	675		NM_031479	NP_113667	P58166	INHBE_HUMAN		3	GGAGGCGCCAA	0.617	rs145766269
+	8	1182	u.2_Missense_Mu	NM_001135805	NP_001129277	P21579	SYT1_HUMAN	hospholipid binding (Proba	6	TGCCCGCCTTG	0.423	
+	1	193	p.2_RNA|C12orf2	NM_001009894	NP_001009894	Q8N999	CL029_HUMAN		0	AATGCCGTGTG	0.642	
+	5	897	PT1_uc001tip.1_	NM_020244	NP_064629	Q8WUD6	CHPT1_HUMAN		0	ATTGAAGATCCT	0.313	
-	9	1211	_p.A166G|FOXN4_	NM_213596	NP_998761	Q96NZ1	FOXN4_HUMAN		2	GATGTGCCTGG	0.701	
+	13	1846	E3B_uc001too.1_	NM_130466	NP_569733	Q7Z3V4	UBE3B_HUMAN		4	CCCACGCACAG	0.572	
-	4	583	|C12orf76_uc010s	NM_207435	NP_997318	Q8N812	CL076_HUMAN		1	TTTCAGCAAAG	0.512	
+	7	725	T81_uc001tqj.2_R	NM_001143779	NP_001137251	Q8WYA0	IFT81_HUMAN	Potential.	1	AGACAGCTCAG	0.363	
-	44	6746	ttr.1_Missense_M	NM_001109662	NP_001103132				2	AGGGATGtcatcat	0.428	
-	31	4702		NM_001109662	NP_001103132				2	GGCGCCAGTAC	0.478	
+	7	1775		NM_004416	NP_004407	Q86Y01	DTX1_HUMAN		4	GACGGGTACGC	0.647	
+	3	654		NM_012240	NP_036372	Q9Y6E7	SIRT4_HUMAN	tylase sirtuin-type.	0	AGCAAGTCCGG	0.557	
-	19	2763	.2_Missense_Muta	NM_032590	NP_115979	Q8NHM5	KDM2B_HUMAN		2	GCGCCGGAGGG	0.716	
-	17	2783	NM2_uc001uek.1_	NM_020845	NP_065896	Q9BZ72	PITM2_HUMAN	DDHD.	3	GGTGGTGGGGC	0.687	
-	1	451	PH9_uc010tam.1	NM_022782	NP_073619	Q99550	MPP9_HUMAN		0	CAGGAGAAATG	0.353	

-	4	752	tbd.1_Missense_M	NM_005505	NP_005496	Q8WTV0	SCRB1_HUMAN	cellular (Potential).	1	TTCGCCGAGGG	0.547	
-	20	2258	LE_uc009zyu.1_M	NM_006231	NP_006222	Q07864	DPOE1_HUMAN		8	TTCCACCTTGGT	0.577	
+	4	489	AM5_uc010tbr.1_F	NM_018663	NP_061133	Q9NR77	PXMP2_HUMAN	isomal (Potential).	0	TCGCCGCCAAG	0.597	rs142063460
-	10	1053	ct.1_Missense_Mu	NM_152726	NP_689939	Q8IYU8	EFHA1_HUMAN		0	TGACAGGACGA	0.328	
-	1	165	TR2A_uc010acr.2_	NM_000621	NP_000612	P28223	5HT2A_HUMAN	llular (By similarity).	6	AGCTCAAAGAAG	0.388	
+	1	298		NM_001507	NP_001498	O43193	MTLR_HUMAN	cellular (Potential).	0	TCTGGCGCTCG	0.687	
+	7	1609	p.P223T|SETDB2_	NM_031915	NP_114121	Q96T68	SETB2_HUMAN		2	AATTACCCAAAG	0.378	
-	3	522	nse_Mutation_p.A	NM_020121	NP_064506	Q9NYU1	UGGG2_HUMAN		3	AATAGCTGGGG	0.358	rs143906515
-	1	743		NM_001080396	NP_001073865	B1AL88	F155A_HUMAN	Poly-Gln.	1	gctgccgctgctgctgc	0.353	
-	42	3714	4A1_uc010agl.2_I	NM_001845	NP_001836	P02462	CO4A1_HUMAN	le-helical region.	6	GCTCCCGGCTA	0.577	
-	1	261		NM_017817	NP_060287	Q9NX57	RAB20_HUMAN	(By similarity).	0	GCGACGTCTTC	0.657	
+	13	2358		NM_017905	NP_060375	Q6UWJ1	TMCO3_HUMAN		0	CACGAGGTGTG	0.602	
+	34	3602	16B_uc001wlk.2_	NM_138360	NP_612369	Q8ND23	LR16B_HUMAN		5	GGACAGCACAG	0.607	
+	4	995	RS1_uc001woj.1_	NM_174913	NP_777573	Q86U38	CN021_HUMAN		4	TCGCGGTTCCT	0.502	
+	13	2375	M_uc001wwe.3_M	NM_020937	NP_065988	Q8IYD8	FANCM_HUMAN		7	ATTTTATAGGCC	0.413	
-	1	412		NM_080746	NP_542784	Q96L21	RL10L_HUMAN		1	TGTCAGCCCCA	0.542	
-	6	2155	_p.Q460*|TRIM9_	NM_015163	NP_055978	Q9C026	TRIM9_HUMAN	onectin type-III.	3	TGGCTGTTTCC	0.532	
-	5	1615	ah.2_Missense_M	NM_001160148	NP_001153620	Q8NEL9	DDHD1_HUMAN		2	TCAAGAGTAAGT	0.323	
+	1	660	0tsa.1_Intron|uc00	NM_006255	NP_006246	P24723	KPCL_HUMAN		6	CCTTCGAGGGT	0.627	
+	3	539	PP5_uc001xjb.1_	NM_022474	NP_071919	Q8N3R9	MPP5_HUMAN	th PARD6B (By similarity).	1	TTGCATCACCA	0.463	
+	20	3119	ty.1_Missense_Mu	NM_173462	NP_775733	O95428	PPN_HUMAN	-like C2-type 1.	3	GCCGCGACTCC	0.647	rs145618706
+	1	923		NM_017791	NP_060261	Q9UPI3	FLVC2_HUMAN	ical; (Potential).	0	TGGTGGGCCAG	0.627	
-	2	1211	sd.2_Nonsense_M	NM_003239	NP_003230	P10600	TGFB3_HUMAN		2	CAGTTCGTCTA	0.532	
-	4	736		NM_004863	NP_004854	O15270	SPTC2_HUMAN		2	TATTCCGTGCA	0.418	
-	22	3989		NM_001080414	NP_001073883	Q9P219	DAPLE_HUMAN	Potential.	3	GGGCCTGCCAG	0.627	
+	2	343	L_uc001ygu.2_Mis	NM_016337	NP_057421	Q9UI08	EVL_HUMAN	WH1.	3	CAGCCGGATCA	0.507	
+	5	738	PP2R5C_uc001y	NM_002719	NP_002710	Q13362	2A5G_HUMAN		2	CTTACATCAGA	0.428	
+	12	2390		NM_015656	NP_056471	Q9ULI4	KI26A_HUMAN		1	CGGTGGGGCGG	0.697	
-	1	113		NM_207379	NP_997262	Q6ZVK1	T179A_HUMAN		0	GTGGCCGTTCT	0.642	
+	1	582	n_p.E36*|MKRN3_	NM_005664	NP_005655	Q13064	MKRN3_HUMAN		10	TCTGTGAGCCC	0.687	
-	2	162	ense_Mutation_p.	NM_003134	NP_003125	P37108	SRP14_HUMAN		0	TTCTTCAAGGT	0.637	
+	2	366	_p.S92N|MGA_uc	NM_001080541	NP_001074010	Q8IWI9	MGAP_HUMAN	T-box.	12	TCGAAGCACAG	0.388	
+	15	5172	GA_uc010uda.1_	NM_001164273	NP_001157745	Q8IWI9	MGAP_HUMAN	Thr-rich.	12	AACCACTGGGA	0.488	
-	2	310	DAN1_uc010bcx.	NM_138477	NP_612486	Q8IWY9	CDAN1_HUMAN		2	CGGGAGGACGC	0.741	
-	15	1900	un.2_Missense_M	NM_014080	NP_054799	Q9NRD8	DUOX2_HUMAN	-like; mediates peroxidase	5	AGGGTGCACCT	0.562	
-	6	1293	_p.R193*|GATM_u	NM_001482	NP_001473	P50440	GATM_HUMAN		0	TGGTCGGTCAG	0.403	
+	18	2473	_p.A753T|SLC12A	NM_000338	NP_000329	Q13621	S12A1_HUMAN		2	TGGCGGCAGAC	0.458	
-	16	1697	.T392P|ATP8B4_u	NM_024837	NP_079113	Q8TF62	AT8B4_HUMAN	lasmic (Potential).	8	CTATTGTTATGGT	0.408	
-	2	235		NM_001007595	NP_001007596	A6NLJ0	C2C4B_HUMAN		0	CGGCGGGATGC	0.721	
+	7	1033	axp.2_Missense_	NM_025055	NP_079331	Q8N5R6	CCD33_HUMAN		5	CCCAGGGTCAG	0.637	
+	2	2886	p.R856W|C15orf3	NM_015492	NP_056307	Q6ZRI6	CO039_HUMAN		0	TCCCTCGGCTG	0.682	
+	4	467		NM_001101404	NP_001094874	A6NKC9	SH2D7_HUMAN		0	CACCCGGGGCC	0.617	
+	6	520	_p.V115M|IDH3A_	NM_005530	NP_005521	P50213	IDH3A_HUMAN		0	GAGTCGTGCAG	0.552	
-	4	550	2bjj.2_Missense_M	NM_199330	NP_955362	Q9NSB8	HOME2_HUMAN	Potential.	0	AGGTCTCGATTT	0.423	
+	7	754	.G14V|LRRC28_u	NM_144598	NP_653199	Q86X40	LRC28_HUMAN	LRR 8.	0	ATTTAGGTCGAT	0.338	
+	8	1648	p.Q25H|PDIA2_u	NM_006849	NP_006840	Q13087	PDIA2_HUMAN		2	TTCCAGGTGAG	0.716	
+	8	1793	p.E189G|RAB11FI	NM_014700	NP_055515	O75154	RFIP3_HUMAN	F-binding domain (ABD).	0	CGGTGAGCAAC	0.652	

-	11	1678	MF1_uc010bri.2_M	NM_022773	NP_073610	Q96S06	LMF1_HUMAN	enal (Potential).	0	CCACGGTCCCT	0.677	
+	7	790	_p.R93K|NUBP2_	NM_012225	NP_036357	Q9Y5Y2	NUBP2_HUMAN		0	CATGAGGACCC	0.667	
-	18	3411		NM_020764	NP_065815	Q8WXD9	CSKI1_HUMAN	Pro-rich.	2	GATGCGCCTCT	0.682	
+	5	1032	2cpp.2_Missense_	NM_001374	NP_001365	Q92874	DNSL2_HUMAN		0	TGTGCGGGCGC	0.682	
+	4	659		NM_032575	NP_115964	Q9BZE0	GLIS2_HUMAN		0	TGCGGGGTACT	0.607	
+	4	1023		NM_014117	NP_054836	Q14CZ0	CP072_HUMAN		1	AGTGGATCGAAT	0.438	
+	3	336	6P1_uc010vam.1_	NR_003569					0	GCCCCAGAATTC	0.567	
-	5	672	gx.2_Nonsense_M	NM_001007240	NP_001007241	P55259	GP2_HUMAN	EGF-like.	4	CTCCTCGGGGC	0.577	
-	53	9586	bd.1_Missense_M	NM_017539	NP_060009	Q8TD57	DYH3_HUMAN	5 (By similarity).	18	GGTGATCATGA	0.473	
+	6	728	uc002dsc.2_Intron	NM_014387	NP_055202	O43561	LAT_HUMAN	lasmic (Potential).	0	GGTGGGGAGTC	0.607	
-	1	112	dyr.1_Missense_M	NM_033410	NP_219363	Q96H86	ZN764_HUMAN		1	GTCCCGGGGAG	0.726	
+	12	1447	_Mutation_p.G45	NM_000632	NP_000623	P11215	ITAM_HUMAN	Extracellular (Potential).	1	CAAGGGCACCC	0.567	
+	3	254	D_uc010cap.1_Mis	NM_005353	NP_005344	Q13349	ITAD_HUMAN	r (Potential).|FG-GAP 1.	1	GCGCAGCTGCC	0.652	
-	3	206		NM_001001436	NP_001001436	Q6PH81	CP087_HUMAN		0	CTCTGTTCGCC	0.378	
-	2	2252	_Mutation_p.R64	NM_002968	NP_002959	Q9NSC2	SALL1_HUMAN	2H2-type 4.	8	AGCCCGGCCAC	0.547	
-	2	444	e_Mutation_p.G41	NM_002968	NP_002959	Q9NSC2	SALL1_HUMAN		8	AAGTGCCGCTG	0.463	
-	2	1707		NM_020807	NP_065858	Q9P2F9	ZN319_HUMAN	2H2-type 9.	0	GCGCCGGTGGC	0.642	
+	11	1756		NM_001795	NP_001786	P33151	CADH5_HUMAN	|Extracellular (Potential).	6	ACACGGCCAAC	0.572	
+	1	363	cdu.2_Missense_M	NM_144673	NP_653274	Q8TAZ6	CKLF2_HUMAN		1	GGGGTGTCGCC	0.542	
-	1	386	0vjt.1_Missense_M	NM_001082486	NP_001075955	Q96AP0	ACD_HUMAN		1	GGATGCTGGCC	0.672	
+	6	1077	A2G15_uc010vlf.	NM_012320	NP_036452	Q8NCC3	PAG15_HUMAN		1	TGCCTCTATGGT	0.567	
+	15	1914	ewt.3_Missense_M	NM_032830	NP_116219	Q969X6	CIR1A_HUMAN		0	CTGCATCATTGA	0.423	
+	12	4695	_Mutation_p.A10	NM_006599	NP_006590	O94916	NFAT5_HUMAN		0	TTGCAGCACCG	0.428	
-	9	1549	n_p.T4I|RFWD3_	NM_018124	NP_060594	Q6PCD5	RFWD3_HUMAN		3	TTGGCAGTACTC	0.433	
+	3	751	1B_uc010vng.1_I	NM_014940	NP_055755	Q7L1V2	MON1B_HUMAN		0	TGACCGCCCTG	0.587	
+	18	1601	0cke.2_Missense_	NM_015085	NP_055900	Q684P5	RPGP2_HUMAN		1	CGTACGCAGCC	0.642	
-	11	1542	2RX5_uc002fwj.2_	NM_002561	NP_002552	Q93086	P2RX5_HUMAN	lasmic (Potential).	0	CTCACCTGTGGG	0.667	
-	13	1720	.R276M|C17orf85	NM_001114118	NP_001107590	Q53F19	CQ085_HUMAN		1	GCGCCCTGTGA	0.502	
-	11	2247	clo.2_Missense_M	NM_014804	NP_055619	Q2KHM9	K0753_HUMAN	Potential.	0	CTTGGCTTTTAA	0.388	
+	3	1271	11_uc010vtw.1_In	NM_175734	NP_783861	Q0P670	CQ074_HUMAN		0	CTGACTACCTCT	0.667	
-	6	1086	se_Mutation_p.S2	NM_002616	NP_002607	O15534	PER1_HUMAN		9	CTGCTGAGGCC	0.627	
+	2	972		NM_004822	NP_004813	O95631	NET1_HUMAN	inin EGF-like 1.	0	GCAACGGCCAC	0.706	
-	14	1462	_Mutation_p.R445	NM_001100112	NP_001093582	Q9UKX2	MYH2_HUMAN	osin head-li p.R445H(1)	14	TGATGCGGGCA	0.473	
+	29	5998	o.2_Missense_Mu	NM_001372	NP_001363	Q9NYC9	DYH9_HUMAN	1 (By similarity).	20	GCTATGCTGGCC	0.488	
+	10	806	D26_uc002gpb.3_	NM_178571	NP_848666	Q86UD7	TBC26_HUMAN	ab-GAP TBC.	0	TGGGCTACCAC	0.592	
-	6	1320		NM_020787	NP_065838	Q9P2J8	ZN624_HUMAN		2	GTTTCTCACCAT	0.388	
+	14	1909	p.R618Q|MPRIP_	NM_201274	NP_958431	Q6WCQ1	MPRIP_HUMAN	ction with RHOA.	0	GGACCGGAGCC	0.657	
+	10	1579	_Mutation_p.D40	NM_001037330	NP_001032407	Q309B1	TR16L_HUMAN	B30.2/SPRY.	0	GAGTATGATTCC	0.498	
+	6	980	p.R261G|RNF112_	NM_007148	NP_009079	Q7Z5V9	Q7Z5V9_HUMAN		2	GAAACAAGGATC	0.617	
-	31	4936	_Mutation_p.R113	NM_078471	NP_510880	Q92614	MY18A_HUMAN	Potential.	0	TCATCCCGACTC	0.557	
-	21	2716	nn.2_Missense_Mu	NM_198836	NP_942133	Q13085	ACACA_HUMAN		2	GTGCCGTGCTC	0.458	
-	7	948	v.1_Missense_Mu	NM_014815	NP_055630	O75448	MED24_HUMAN		1	GACTCCGGAGC	0.587	
-	1	452		NM_030966	NP_112228	Q8IUG1	KRA13_HUMAN		0	GGCCTCGGCGT	0.662	
-	1	520		NM_033059	NP_149048	Q9BYQ6	KR411_HUMAN	C-[GIKRQVHEL]- [SPTR]-[	0	GACGCAGGcagc	0.323	rs141357429
-	1	430	vfr.1_Missense_Mu	NM_153490	NP_705694	P13646	K1C13_HUMAN	oil 1A.|Rod.	5	GGCGCGCACCT	0.527	
+	1	536	1_5'UTR|WNK4_	NM_032387	NP_115763	Q96J92	WNK4_HUMAN		7	TGGCCGATACC	0.607	
-	3	460	wis.1_Missense_	NM_032376	NP_115752	Q96IK0	TM101_HUMAN	ical; (Potential).	2	AACACCTGGCC	0.607	

-	7	1240		NM_133373	NP_588614	Q8N3E9	PLCD3_HUMAN	I-PLC X-box.	3	TCCCTGGGCAA	0.652	
-	2	509	e.3_Missense_Mu	NM_006807	NP_006798	P83916	CBX1_HUMAN		0	CTCCACTTTCT	0.448	
-	2	881		NM_002144	NP_002135	P14653	HXB1_HUMAN		1	CTTCCGGGGAG	0.652	
+	11	933	m.1_Missense_Mu	NM_138962	NP_620412	Q96DH6	MSI2H_HUMAN	Poly-Ala.	2	TGGCAGCAGCG	0.627	rs144586096
-	9	1610		NM_000250	NP_000241	P05164	PERM_HUMAN		4	GGTACGTGGGC	0.567	
+	15	1377	.S419N|BCAS3_u	NM_001099432	NP_001092902	Q9H6U6	BCAS3_HUMAN	WD 3.	5	GGTCAGTACTC	0.463	
+	15	2787	2_uc002jae.2_5'F	NM_006039	NP_006030	Q9UBG0	MRC2_HUMAN	Potential).|C-type lectin 4.	3	CAGTGGGTGGC	0.662	
+	12	1860	_Mutation_p.Y52	NM_025185	NP_079461	Q9HCD6	TANC2_HUMAN		2	AGGCTTACATC	0.423	
+	19	3325	p.R1011H|TANC2_	NM_025185	NP_079461	Q9HCD6	TANC2_HUMAN	ANK 8.	2	GGGCCGCACTC	0.512	
-	5	2478	.R776W|TEX2_uc	NM_018469	NP_060939	Q8IWB9	TEX2_HUMAN		1	CTGCCGCACGC	0.632	
+	1	659	.Y200H|BPTF_uc	NM_182641	NP_872579	Q12830	BPTF_HUMAN		4	GTACCTACAGC	0.597	
+	3	1194	G_uc002jhb.1_5'U	NM_014960	NP_055775	Q96EG1	ARSG_HUMAN		1	TCACTGGGATAA	0.547	
-	10	1554		NM_080284	NP_525023	Q8N139	ABCA6_HUMAN		7	CAGAGGGATGC	0.373	
+	4	2562	p.N654K|TNRC6C	NM_018996	NP_061869	Q9HCJ0	TNR6C_HUMAN	on with argonaute family pr	2	ACAAACTGGGG	0.512	
-	9	1353		NM_178493	NP_848588	Q6P988	NOTUM_HUMAN		0	CAGCCGCAGGC	0.692	
+	2	272	_p.V46M|PSMG2_	NM_020232	NP_064617	Q969U7	PSMG2_HUMAN		0	CTGAAGGTATG	0.323	
-	15	2487	vi.3_Missense_Mu	NM_001941	NP_001932	Q14574	DSC3_HUMAN	lasmic (Potential).	4	AATGGTTTCCT	0.502	
+	1	17	1_Missense_Muta	NM_018255	NP_060725	Q6IA86	ELP2_HUMAN		4	TGGTGGCACCC	0.612	
-	18	3365	_5'UTR|KIAA1632	NM_020964	NP_066015	Q9HCE0	EPG5_HUMAN		0	GTGTAGGAACA	0.517	
+	4	564	lfk.3_Nonsense_M	NM_007195	NP_009126	Q9UNA4	POLI_HUMAN	UmuC.	3	GACTACAGCAG	0.373	
+	20	3545	236_uc002lmj.2_	NM_007345	NP_031371	Q9UL36	ZN236_HUMAN		4	TTTCACGGAGG	0.532	
-	9	1524	_Mutation_p.S447	NM_005481	NP_005472	Q9Y2X0	MED16_HUMAN		0	AAGGTGAGAGG	0.682	
-	9	713	.2_Missense_Muta	NM_003200	NP_003191	P15923	TFE2_HUMAN		7	TGCCACGTAGA	0.692	
-	29	4046	_Mutation_p.R12	NM_138813	NP_620168	O60423	AT8B3_HUMAN	lasmic (Potential).	0	CCCTCCGCAGA	0.557	
-	2	925	0dsw.1_Intron|uc0	NM_001101391	NP_001094861	P0C6S8	LIGO3_HUMAN	lar (Potential).|LRR 8.	0	GCCGCAGCGCG	0.726	
-	1	244	wa.1_Missense_M	NM_032737	NP_116126	Q03252	LMNB2_HUMAN	oil 1A.|Rod.	2	GAGCCGGTCGT	0.562	
+	4	1554	a.1_Missense_Mu	NM_173480	NP_775751	Q68EA5	ZNF57_HUMAN	2H2-type 11.	3	GAGGATGCACA	0.443	
+	6	400	6_uc010dtg.2_Mis	NM_024760	NP_079036	Q9H808	TLE6_HUMAN		1	GACATCATGGC	0.637	
+	3	362	_p.G99R|MPND_u	NM_032868	NP_116257	Q8N594	MPND_HUMAN		1	TGCAGGGGAAG	0.642	
+	19	2954	p.G944S|KDM4B_	NM_015015	NP_055830	O94953	KDM4B_HUMAN		1	CGGGGGGTCAC	0.716	
-	16	2529		NM_014649	NP_055464	Q14151	SAFB2_HUMAN	Interacts with SAFB1.	0	GCCCCGGTCTC	0.587	
-	2	446	nse_Mutation_p.F	NM_001097641	NP_001091110	P21217	FUT3_HUMAN	enal (Potential).	0	CTTAGGGTTGG	0.627	
+	13	1493	p.R385H|PNPLA6_	NM_006702	NP_006693	Q8IY17	PLPL6_HUMAN	lasmic (Potential).	3	CCCCCGCTCCG	0.537	
-	10	1355	wr.1_Missense_M	NM_152476	NP_689689	Q96MR9	ZN560_HUMAN	2H2-type 3.	6	TTTTGCCACAG	0.418	
+	10	1068	_Mutation_p.A30	NM_146387	NP_666499	Q9BYD3	RM04_HUMAN	p.A306fs>4(1)	1	CCCAGCGGCCA	0.657	
-	7	1168	p.E79Q|TYK2_uc	NM_003331	NP_003322	P29597	TYK2_HUMAN	FERM.	9	CCGCTCGAGTG	0.677	
-	2	251	_p.H73Y|RTBDN_	NM_001080997	NP_001074466	Q9BSG5	RTBDN_HUMAN		0	ATGGTGTTGCT	0.632	
+	16	2266	_p.G706S|PKN1_	NM_002741	NP_002732	Q16512	PKN1_HUMAN	rotein kinase.	8	CGGCCGGTGGG	0.642	
+	16	2817	3B_uc010xpi.1_Mi	NM_015260	NP_056075	O75182	SIN3B_HUMAN		2	CTGCTAGGGAG	0.657	
-	3	1952	p.K579R|KIAA168	NM_025249	NP_079525	Q9H0B3	K1683_HUMAN		2	TGATCTTCCCC	0.572	
+	4	1547		NM_031218	NP_112495	P35789	ZNF93_HUMAN		1	AGAGAAACCCT	0.368	
+	4	1631		NM_031218	NP_112495	P35789	ZNF93_HUMAN		1	AGAGAAACCCT	0.358	
+	4	1449	co.2_Missense_M	NM_003429	NP_003420	Q03923	ZNF85_HUMAN	ype 11; degenerate.	1	AAAACTTACTG	0.323	
+	2	903	_p.P336L|ZNF493_	NM_175910	NP_787106	Q6ZR52	ZN493_HUMAN	ype 7; degenerate.	1	AACCCCTACTA	0.348	rs142651314
-	5	2403	208_uc002nqo.1_	NM_007153	NP_009084				7	TTACCTTATGTTT	0.373	
+	4	1578	cy.2_Missense_M	NM_033468	NP_258429	Q9Y2Q1	ZN257_HUMAN	2H2-type 11.	0	TTAACCAGTCTT	0.408	
-	4	1355	p.K336Q|ZNF681_	NM_138286	NP_612143	Q96N22	ZN681_HUMAN	2H2-type 9.	0	GGACTTGTTAA	0.403	rs1852431

-	2	2509		NM_020856	NP_065907	Q63HK5	TSH3_HUMAN		8	TTGCCGGGGCT	0.532	
+	4	2466	rn.1_Missense_M	NM_001136156	NP_001129628	Q8TCN5	ZN507_HUMAN		5	CTTCTAATGAG	0.378	
+	5	652	dq.1_Missense_M	NM_194325	NP_919306	P17039	ZNF30_HUMAN		2	AAGATGATACA	0.299	
+	2	343	ea.2_Missense_M	NM_005306	NP_005297	O15552	FFAR2_HUMAN	Name=3; (Potential).	1	TTTTGGCTTCT	0.617	
-	9	1353	NL_uc010xuo.1_M	NM_198445	NP_940847	Q6ZS11	RINL_HUMAN	VPS9.	1	AGACATCTCTG	0.682	
-	14	1754	c002ole.1_Silent_	NM_019088	NP_061961	Q8N7H5	PAF1_HUMAN		1	ACTATCAGCTT	0.567	
-	1	206	A|MED29_uc010x	NM_019088	NP_061961	Q8N7H5	PAF1_HUMAN		1	CTCCCGCTGGG	0.687	
-	6	2952		NM_003890	NP_003881	Q9Y6R7	FCGBP_HUMAN	VWFD 2.	9	CCAGTCATAAG	0.597	
-	3	1231		NM_144685	NP_653286	Q8NE63	HIPK4_HUMAN	rotein kinase.	2	GAGGTCGGCGT	0.607	
-	5	755	se_Mutation_p.E4	NM_000762	NP_000753	P11509	CP2A6_HUMAN		2	AGTCCTCCAGC	0.542	
+	7	952	2F1_uc010xvv.1_	NM_000774	NP_000765	P24903	CP2F1_HUMAN		0	TGGCGGCACCA	0.582	
-	4	527	0ejp.1_Missense_	NM_001102597	NP_001096067	Q6UY09	CEA20_HUMAN	2.|Extracellular (Potential).	2	GGCAACACCAG	0.498	
+	6	1364	_p.H236Y|EHD2_	NM_014601	NP_055416	Q9NZN4	EHD2_HUMAN		2	AGTTTCACTCG	0.632	
+	2	240	_5'Flank|NOSIP_	NM_000951	NP_000942	O14669	TMG2_HUMAN		1	GAGGAGACAGA	0.468	
+	1	245	2A1_uc002ppo.2_	NM_014203	NP_055018	O95782	AP2A1_HUMAN		2	TGCGGGGGCTC	0.706	
+	17	2110	_p.L473P|MED25_	NM_030973	NP_112235	Q71SY5	MED25_HUMAN	with RARA.|Pro-rich.	1	GGGCCTGGGGC	0.726	
+	19	2429	p.Q835H|MYH14_	NM_024729	NP_079005	Q7Z406	MYH14_HUMAN	osin head-like.	1	GCCCAGCTGGA	0.647	
-	3	303	H2_uc002prv.3_I	NM_004851	NP_004842	O96009	NAPSA_HUMAN		0	TTCCCAGCCCAA	0.547	
+	7	976	se_Mutation_p.A2	NM_007121	NP_009052	P55055	NR1H2_HUMAN	-binding (Potential).	0	TGGCGGCCCAA	0.607	
-	5	888	77_uc010ydf.1_5'	NM_023074	NP_075562	Q9BS31	ZN649_HUMAN	2H2-type 2.	3	TACACACGTGG	0.488	
-	5	2929	p.N909D|ZNF841_	NM_001136499	NP_001129971	Q6ZN19	ZN841_HUMAN		0	CACATTGAGTT	0.318	
-	3	1808		NM_198457	NP_940859	Q6ZNG1	ZN600_HUMAN	2H2-type 13.	0	CAGACGGAAGG	0.443	
+	5	806	ek.1_Missense_M	NM_015629	NP_056444	Q8WWY3	PRP31_HUMAN		1	CATCCGCACGG	0.577	rs147725190
+	3	2269	p.S674R|ZNF304_	NM_020657	NP_065708	Q9HCX3	ZN304_HUMAN	2H2-type 16.	1	AGAAGCTCCCA	0.478	
-	3	640		NM_001037160	NP_001032237	Q717R9	CYS1_HUMAN		0	CGATGCTCGCC	0.667	
-	2	811		NM_012344	NP_036476	O95665	NTR2_HUMAN	lasmic (Potential).	0	TGCCCGGGGTA	0.612	rs151252387
-	2	481	xu.1_Missense_M	NM_002381	NP_002372	O15232	MATN3_HUMAN	VWFA.	0	TGTGTAGGCCT	0.567	
+	13	2131	D_uc010eyw.2_Int	NM_004341	NP_004332	P27708	PYR1_HUMAN	ate synthase).|CPSase A.|	10	TGACCCAGCAC	0.532	
-	3	952	rkj.2_Missense_M	NM_144631	NP_653232	Q8N8E2	ZN513_HUMAN		1	TGGGAGGCCGG	0.672	
+	6	623	512_uc010ylx.1_	NM_032434	NP_115810	Q96ME7	ZN512_HUMAN		1	GGGGAGGAAG	0.423	
+	5	579	.2_Missense_Mut	NM_053276	NP_444506	Q6UXI7	VITRN_HUMAN	LCCL.	2	CCAACGGTGTC	0.428	
+	1	414	fam.1_Missense_	NM_152390	NP_689603	Q8NBL3	TM178_HUMAN	ellular (Potential).	0	CACCCTCATCC	0.383	
-	31	3372	ob.1_Missense_M	NM_133259	NP_573566	P42704	LPPRC_HUMAN	PPR 17.	3	TGGCAGCATCG	0.433	
+	9	1012	p.E337A|MDH1_u	NM_005917	NP_005908	P40925	MDHC_HUMAN		2	AAAGGAACTGA	0.353	
-	1	38		NM_000682	NP_000673	P18089	ADA2B_HUMAN	ame=1; (By similarity).	3	TGGCCGCTGTG	0.677	
-	17	2209	fhz.2_Nonsense_	NM_001115016	NP_001108488	Q9P2N6	K1310_HUMAN	Ser-rich.	0	CCACTGAAGGG	0.592	
+	10	2061		NM_003048	NP_003039	Q9UBY0	SL9A2_HUMAN	lasmic (Potential).	8	TCGCCGGCGAC	0.493	rs144961744
+	2	438	fki.1_Missense_M	NM_153214	NP_694946	Q53RD9	FBLN7_HUMAN		2	CATCCGCCACA	0.682	
+	4	869		NM_198581	NP_940983	P61129	ZC3H6_HUMAN		4	GTAACTACGGT	0.363	
+	17	1997	p.G482W|UGGT1_	NM_020120	NP_064505	Q9NYU2	UGGG1_HUMAN		1	TTTTGGGGATT	0.393	
-	14	3223	AP5_uc002ttq.2_I	NM_207363	NP_997246	O14513	NCKP5_HUMAN		0	AAGGTGCTGGT	0.592	
-	12	4696		NM_002299	NP_002290	P09848	LPH_HUMAN	tial).|4.|4 X approximate rep	13	GGGCAGTGCCA	0.502	
-	7	1843		NM_002299	NP_002290	P09848	LPH_HUMAN	tial).|4 X approximate repe	13	TCTCTGGAGAC	0.592	rs145074769
+	5	561	p.L144R|KYNU_u	NM_003937	NP_003928	Q16719	KYNU_HUMAN		2	ATCTTCTAATGGT	0.308	
+	8	1511	foc.1_Missense_	NM_052917	NP_443149	Q8IUC8	GLT13_HUMAN	main B.|Lumenal (Potential	6	TATCTGGGGTG	0.383	
-	1	779		NM_152275	NP_689488	Q86WT1	TT30A_HUMAN	TPR 3.	0	ATGCAGCTTCAT	0.557	
-	46	16876	N_uc010zfi.1_Intr	NM_133379	NP_596870	Q8WZ42	TITIN_HUMAN		153	AATTTTCCATCT	0.413	

-	22	2442	sk.2_Missense_Mu	NM_007315	NP_009330	P42224	STAT1_HUMAN		10	CTTCCTTTGGC	0.458	
-	1	616		NM_004657	NP_004648	O95810	SDPR_HUMAN		2	TGAGGTCATTCT	0.592	
-	14	2633		NM_213589	NP_998754	Q70E73	RAPH1_HUMAN		10	GTGGGTGGTGCA	0.602	
+	12	1985	p.E593G|PARD3B	NM_152526	NP_689739	Q8TEW8	PAR3L_HUMAN		4	GCCAGAGAGAC	0.488	
+	5	7038		NM_020923	NP_065974	Q9HCK1	ZDBF2_HUMAN		3	GGCGAAGAGAA	0.463	
-	20	3352	gs.2_Missense_Mu	NM_022648	NP_072174	Q9HBL0	TENS1_HUMAN		4	GTTTCAGGCCC	0.652	
-	45	5249	voa.2_Missense_M	NM_014689	NP_055504	Q96BY6	DOC10_HUMAN	DHR-2.	2	CTTCATCTGAGC	0.527	
-	20	2581	vob.2_Missense_M	NM_014689	NP_055504	Q96BY6	DOC10_HUMAN	DHR-1.	2	AGAGCCTCCTTC	0.408	
+	3	512	16L1_uc002vub.2_	NM_030803	NP_110430	Q676U5	A16L1_HUMAN	Potential.	0	GAAATGGCCCA	0.463	
-	15	2138	nt.1_Missense_Mu	NM_018218	NP_060688	Q9NVE5	UBP40_HUMAN		3	ATGGCCGTCCAA	0.502	
-	1	288	ng.1_Missense_Mu	NM_001485	NP_001476	P52951	GBX2_HUMAN		0	GCTGGGGATCT	0.642	
-	10	1402	CA1_uc002vwa.1_	NM_024726	NP_079002	Q86XH1	IQCA1_HUMAN	Lys-rich.	1	TTTTTCATCCAG	0.313	
-	10	1331	R2_uc010znw.1_M	NM_022817	NP_073728	O15055	PER2_HUMAN	PAS 2.	2	AGCACTGGGGTT	0.552	
+	2	177		NM_001040445	NP_001035535	Q9Y576	ASB1_HUMAN		0	GTGATCATCCGC	0.557	
+	5	1149		NM_002081	NP_002072	P35052	GPC1_HUMAN		1	CGGGTGTGGAG	0.627	
+	17	1955		NM_001001891	NP_001001891	Q6IWH7	ANO7_HUMAN	cellular (Potential).	3	TACCCAGGCAAC	0.562	
+	2	205		NM_173821	NP_776182	Q14D33	CB085_HUMAN		1	TCCGGGGACCT	0.682	
+	5	1022	il.2_Nonsense_Mu	NM_139321	NP_647537	O75882	ATRN_HUMAN	cellular (Potential).	2	GCTTCTCAGACT	0.388	
+	1	310	10gbd.1_RNA|PA	NM_153638	NP_705902	Q9BZ23	PANK2_HUMAN		0	CTGCCGCGGAG	0.736	
-	1	92		NM_033176	NP_149416	Q9H2Z4	NKX24_HUMAN		0	GCCGCTGAACT	0.522	
+	1	797		NM_001052	NP_001043	P31391	SSR4_HUMAN	lasmic (Potential).	1	TGCGCGCTGGC	0.627	
-	11	830		NM_080675	NP_542406	Q8TC36	SUN5_HUMAN	SUN.	1	GGTGTCACGTTG	0.522	
+	2	477	OCR_uc010zuw.1	NM_006404	NP_006395	Q9UNN8	EPCR_HUMAN	cellular (Potential).	0	CGTGCGCCTGG	0.498	
-	2	138	on_p.L8F|SCAND1	NM_033630	NP_361012	P57086	SCND1_HUMAN		0	GCCGCCAAGAT	0.667	
-	4	530		NM_015474	NP_056289	Q9Y3Z3	SAMH1_HUMAN		0	GATTCGGACGA	0.393	
+	11	1849	wj.1_Missense_Mu	NM_002466	NP_002457	P10244	MYBB_HUMAN		5	GGACTTGAAGG	0.627	
-	5	601	DA_uc010ggt.2_R	NM_000022	NP_000013	P00813	ADA_HUMAN		3	TGGGCTGGTGG	0.692	
-	4	518	UTR|SYS1-DBND	NM_014477	NP_055292	Q9Y2B4	T53G5_HUMAN		1	ATTGCCGCCAAT	0.507	
-	1	989	gj.3_5'Flank|CTSA	NM_080749	NP_542787	Q9BR09	NEUL2_HUMAN	NHR.	0	CAAGGCGCACGC	0.637	
+	14	1841		NM_017895	NP_060365	Q96GQ7	DDX27_HUMAN		2	CAAGGTGAGCA	0.463	
-	7	1082		NM_004776	NP_004767	O43286	B4GT5_HUMAN	nenal (Potential).	1	CCACCCCAACC	0.443	
+	2	322	sense_Mutation_p	NM_015266	NP_056081	Q9Y2E8	SL9A8_HUMAN		1	CGACCCCTGGC	0.577	
-	3	1743	p.R465C|SPATA2	NM_001135773	NP_001129245	Q9UM82	SPAT2_HUMAN		2	TGGGCGGTTGC	0.597	
-	4	570	MEM189_uc010gi	NM_199203	NP_954673	Q13404	UB2V1_HUMAN		0	GTCCCCGTTGG	0.612	
+	7	2554	ze.1_Missense_Mu	NM_001164116	NP_001157588	Q9NQ75	CASS4_HUMAN		3	AGCAACACACG	0.617	
-	2	330	P1_uc002xyp.2_In	NM_030776	NP_110403	Q9H171	ZBP1_HUMAN	DRADA 1.	2	GGATTCTTTGTT	0.617	
+	9	1019	L1_uc002ybz.1_R	NM_198935	NP_945173	O75177	CREST_HUMAN	Gln-rich.	2	GTGCCGCGCAG	0.662	rs142989416
+	3	206		NM_020882	NP_065933	Q9P218	COKA1_HUMAN	onectin type-III 1.	1	CTGGCTGTGCTG	0.622	
-	4	1814		NM_003489	NP_003480	P48552	NRIP1_HUMAN		0	TTTCCTCAAAAAT	0.368	
-	5	803	p.N229S|SYNJ1_	NM_003895	NP_003886	O43426	SYNJ1_HUMAN	SAC.	5	CAAAATTGGCA	0.338	
+	5	709	X2_uc011aer.1_R	NM_002463	NP_002454	P20592	MX2_HUMAN		2	TGGCCGGGGCA	0.587	
-	4	555	ef.2_Missense_Mu	NM_015259	NP_056074	O75144	ICOSL_HUMAN	Potential).|Ig-like C2-type.	0	GACGGGCACGC	0.577	
+	19	1649	6A2_uc002zhz.1_	NM_001849	NP_001840	P12110	CO6A2_HUMAN	le-helical region.	8	GAGGAGCACCC	0.637	
-	1	61	0gqs.1_Translatio	NM_001037814	NP_001032903	Q2WGN9	GAB4_HUMAN		2	AGGGCGTTGCT	0.677	
-	26	5641	_Mutation_p.T167	NM_015241	NP_056056	Q7RTP6	MICA3_HUMAN		0	AGGGGGTGCTG	0.647	
-	26	5101	_Mutation_p.P149	NM_015241	NP_056056	Q7RTP6	MICA3_HUMAN		0	CCAAGGGCAGC	0.706	
+	5	686	_Mutation_p.G19	NM_013373	NP_037505	Q9ULC8	ZDHC8_HUMAN	ical; (Potential).	2	TGGCCGGCCTC	0.632	

-	6	1625	hr.1_Missense_Mu	NM_032775	NP_116164	Q53GT1	KLH22_HUMAN	Kelch 5.	1	TGTATCCGGCAT	0.587	
+	2	145		NM_001144931	NP_001138403				0	TGACGGTACGG	0.667	
+	30	5012	zzl.1_Missense_M	NM_012295	NP_036427	Q9Y6J0	CABIN_HUMAN		5	CCATGCTTCAG	0.647	
-	5	1142	T5_uc002zzq.3_M	NM_004121	NP_004112	P36269	GGT5_HUMAN	ellular (Potential).	3	GCATCTGGCCC	0.637	
+	6	816	169P|EWSR1_uc	NM_005243	NP_005234	Q01844	EWS_HUMAN	).|31 X approximate tande	3254	CAGCCTAGGAT	0.502	
+	2	672	afc.1_Missense_M	NM_152236	NP_689422	Q99501	GA2L1_HUMAN		0	CCTCGTGCAGT	0.701	
+	5	684		NM_182527	NP_872333	Q86V35	CABP7_HUMAN	IV membrane protein; (Pc	0	CATTGCGGCCA	0.647	
+	11	1206	M1_uc003anp.2_	NM_005488	NP_005479	O60784	TOM1_HUMAN		1	CTGGTCGACTG	0.602	
+	3	308		NM_002305	NP_002296	P09382	LEG1_HUMAN	oside binding.|Galectin.	0	GGGGGACCGAG	0.657	
-	2	477		NM_145912	NP_666017	Q8NET5	NFAM1_HUMAN	(Potential).|Ig-like V-type.	0	CAGGATGAAGG	0.572	
+	1	191	ANX2_uc003bjo.3	NM_052839	NP_443071	Q96RD6	PANX2_HUMAN	ical; (Potential).	1	CATCCTGCTGG	0.577	
-	9	1211	1_Missense_Mutat	NM_001145137	NP_001138609	Q92523	CPT1B_HUMAN	lasmic (Potential).	2	CGCCCTCATAG	0.612	
+	2	500	tron|SETMAR_uc	NM_006515	NP_006506	Q53H47	SETMR_HUMAN	ysine N-methyltransferase.	1	GTGTTCAAGACG	0.453	
-	15	1968	p.R303P|RAF1_uc	NM_002880	NP_002871	P04049	RAF1_HUMAN	rotein kinase.	14	TGCATTCGGATC	0.478	rs149580968
+	6	872		NM_015141	NP_055956	Q8N335	GPD1L_HUMAN	bstrate binding.	0	AGGGCGGAACC	0.617	
-	3	1953		NM_033403	NP_208382	Q9C098	DCLK3_HUMAN	rotein kinase.	9	CTCATTTCGCT	0.408	
-	3	3882	v.2_Missense_Mu	NM_014159	NP_054878	Q9BYW2	SETD2_HUMAN		32	ATAGCTACTGT	0.473	
+	1	169	_Mutation_p.V715	NM_033629	NP_338599	Q9NSU2	TREX1_HUMAN		0	ACTGCGTGGAG	0.607	
+	5	3338		NM_003458	NP_003449	Q9UPA5	BSN_HUMAN	Potential.	8	GACCCGGCGGG	0.657	
+	37	3738		NM_004947	NP_004938	Q8IZD9	DOCK3_HUMAN	DHR-2.	0	TATATCCGCTAC	0.428	
+	12	2339	nv.2_Missense_Mu	NM_000333	NP_000324	O15265	ATX7_HUMAN		0	TGGCAGCAGCC	0.537	
-	1	21	dmh.1_5'Flank|A	NM_182920	NP_891550	Q9P2N4	ATS9_HUMAN		4	TCCCACCCCTC	0.751	
-	3	577	G2_uc011bhe.1_5'	NM_016247	NP_057331	Q9BZV3	IMPG2_HUMAN	ellular (Potential).	3	GATCCCAAAAA	0.403	
+	5	1187	jb.1_Missense_M	NM_001125	NP_001116	P54922	ADPRH_HUMAN		1	GAGCCTTTTTC	0.547	
+	4	1516	w.3_Missense_Mu	NM_000388	NP_000379	P41180	CASR_HUMAN	ellular (Potential).	7	GTGGCGACAGG	0.493	
-	13	2844	C14_uc010hrt.2_	NM_022757	NP_073594	Q49A88	CCD14_HUMAN		0	ACGTTGAAAAC	0.443	
+	1	785		NM_032242	NP_115618	Q9UIW2	PLXA1_HUMAN	tracellular (Potential).	3	TCGTGCGGCTC	0.602	
+	10	1709	M2_uc010hsl.2_	NM_004526	NP_004517	P49736	MCM2_HUMAN	MCM.	4	GGGGGCGTCGG	0.617	
-	11	1272	Y_uc011blx.1_Mis	NM_178554	NP_848649	Q8NBH2	KY_HUMAN		2	GGTACACCTCCA	0.532	
-	2	691	rr.1_Nonsense_M	NM_173543	NP_775814	Q8IYY4	DZI1L_HUMAN		2	CAGCTGGGCAA	0.662	
+	7	1345	tm.2_Missense_	NM_022131	NP_071414	Q9H4D0	CSTN2_HUMAN	ellular (Potential).	7	TGGATGAAACA	0.562	
+	15	2280	m.1_Missense_M	NM_003875	NP_003866	P49915	GUAA_HUMAN		3	CTGGTATACCT	0.383	
-	3	789	1bpt.1_Intron|uc0	NM_020949	NP_066000	Q8TBB6	S7A14_HUMAN		5	AGTCAAACATG	0.562	
+	1	44	003fqv.2_5'UTR|E	NM_001967	NP_001958	Q14240	IF4A2_HUMAN		4	TCATGTCTGGTG	0.577	
-	3	1518	732_uc010ibb.1_I	NM_001137608	NP_001131080	B4DXR9	ZN732_HUMAN	2H2-type 14.	0	ACATTCGTAAG	0.398	
+	12	1836	06_splice|TBC1D1	NM_001113361	NP_001106832	Q9P2M4	TBC14_HUMAN		2	GATTGGTAAGAC	0.408	
+	12	2682	Q785*|SH3TC1_u	NM_018986	NP_061859	Q8TE82	S3TC1_HUMAN		3	AGGACCAGGAG	0.687	
-	10	6986	dr.1_Missense_Mu	NM_148894	NP_683692	Q8NFC6	BOD1L_HUMAN		6	TGGCGGTGTCA	0.557	
+	1	2314	_p.V389I|PCDH7_	NM_002589	NP_002580	O60245	PCDH7_HUMAN	(Potential).|Cadherin 4.	4	AGGACGTTCTG	0.622	
-	4	2469		NM_001024611	NP_001019782	Q68CR7	LRC66_HUMAN		3	TGCCCGGAAAC	0.463	
-	3	408		NM_002704	NP_002695	P02775	CXCL7_HUMAN		4	GGGAGCATCTG	0.428	
+	17	2400	58_splice|FRAS1_	NM_025074	NP_079350	Q86XX4	FRAS1_HUMAN		5	AAAGGTATCGT	0.478	
+	25	3502	w.2_Missense_Mu	NM_025074	NP_079350	Q86XX4	FRAS1_HUMAN	tracellular (Potential).	5	CCGCTGCAAAG	0.512	
+	2	1212		NM_152618	NP_689831	Q6ZW61	BBS12_HUMAN		2	TGTCAGTATCTA	0.403	
-	2	1993	L3_uc011chd.1_I	NM_018717	NP_061187	Q96JK9	MAML3_HUMAN		1	GGACAGCACAG	0.562	
+	2	6593		NM_153610	NP_705838	Q8N3K9	CMYA5_HUMAN		9	AGAAAGGAATTT	0.453	
+	3	500	ksn.2_Missense_	NM_182761	NP_877438	A1A519	F170A_HUMAN		1	TCCTCCCCGCT	0.483	

+	1	178		NM_016048	NP_057132	Q96CN7	ISOC1_HUMAN		0	CAGAAGTTCCTC	0.602	
+	4	1161		NM_032289	NP_115665	Q9BQI7	PSD2_HUMAN	SEC7.	1	TGGCACGCCGTC	0.652	
+	15	2163	_p.A623P|SLC4A9	NM_031467	NP_113655	Q96Q91	B3A4_HUMAN	al).|Membrane (anion exch	1	TTGGAGCCAAC	0.597	
+	3	1513	lgh.1_Missense_M	NM_080670	NP_542401	Q96G79	S35A4_HUMAN	(Potential).|Leu-rich.	0	AGGCACTAAATG	0.592	
+	1	1385	03lhc.1_Missense_	NM_018905	NP_061728	Q9Y5H9	PCDA2_HUMAN	|Extracellular (Potential).	4	TGACCGCACGG	0.632	
+	1	1279	CDHA7_uc003lhq.2	NM_018904	NP_061727	Q9Y5I0	PCDAD_HUMAN	|Extracellular (Potential).	6	TGACCGCGCGG	0.657	
+	1	101	GA8_uc003lkd.1_	NM_018928	NP_061751	Q9Y5F7	PCDGL_HUMAN	|Extracellular (Potential).	4	CTACCCGGTCC	0.552	
-	16	2252	_p.P695L|DIAPH1_	NM_005219	NP_005210	O60610	DIAP1_HUMAN	FH1.	1	GAGGAGGTGGG	0.642	
-	8	1310	_p.L188P|CSNK1A	NM_001892	NP_001883	P48729	KC1A_HUMAN	rotein kinase.	1	TGCCTCAGATAC	0.373	
+	10	1532	ition_p.G308D|uc0	NM_198321	NP_938080	Q86SR1	GLT10_HUMAN	ential).|Ricin B-type lectin.	2	TGTGGGCACAG	0.607	
+	2	925	c.1_Intron|SAP30L	NM_024632	NP_078908	Q9HAJ7	SP30L_HUMAN		0	AAGACAAGTGAC	0.423	
-	4	750	P1_uc003map.2_	NM_004137	NP_004128	Q16558	KCMB1_HUMAN	cellular (Potential).	2	CGGCCCGGGCC	0.577	
-	14	1474		NM_005110	NP_005101	O94808	GFPT2_HUMAN	SIS 1.	2	CAGTCGGTCTCG	0.701	
-	10	1823	7M|SLC22A23_uc	NM_015482	NP_056297	A1A5C7	S22AN_HUMAN	ical; (Potential).	1	GATGAGCGtgcag	0.453	
-	2	632	RL_uc003ndq.2_M	NM_000948	NP_000939	P01236	PRL_HUMAN		0	GGCATCGGGCA	0.587	
-	2	507	0jrf.1_Intron|ZSCA	NM_001012455	NP_001012458	Q3MJ62	ZSC23_HUMAN	SCAN box.	0	GCTGTCTGACC	0.582	
+	3	727	p.R652Q|CFB_uc	NM_001710	NP_001701	P00751	CFAB_HUMAN	Sushi 2.	1	TGGCCGATGGA	0.587	
+	8	1279	u.1_5'Flank|SLC3	NM_001077516	NP_001070984	Q92504	S39A7_HUMAN	ical; (Potential).	1	TGACAGCAGTAC	0.552	
+	16	2027		NM_002224	NP_002215	Q14573	ITPR3_HUMAN	lasmic (Potential).	19	CAACCGCAAGC	0.612	
-	1	119	_5'Flank|LEMD2_	NM_181336	NP_851853	Q8NC56	LEMD2_HUMAN	LEM.	1	GCGGCGCAGCT	0.741	
+	16	2054	D2_uc011dtv.1_Mi	NM_173558	NP_775829	Q7Z6J4	FGD2_HUMAN	PH 2.	3	GGAGCTGAAGG	0.682	
+	18	2383	ox.2_Missense_M	NM_015345	NP_056160	Q86T65	DAAM2_HUMAN	FH2.	3	CGTGCTGACCGC	0.577	
-	4	2494	318_uc003ouw.2_	NM_014345	NP_055160	Q5VUA4	ZN318_HUMAN		7	AGGTGGGATACAT	0.527	
-	5	1620	3ovj.1_Missense_M	NM_001012974	NP_001012992	Q5JTD7	CF154_HUMAN	LRR 7.	0	ATGCTGTTCTCAC	0.547	
-	13	1577		NM_020750	NP_065801	Q9HAV4	XPO5_HUMAN		4	TAGTTTTGGGAT	0.438	
+	2	541	g.2_RNA|SPATS1_	NM_145026	NP_659463	Q496A3	SPAS1_HUMAN		1	CAACACCCTCTG	0.433	
+	1	1342	ze.2_Missense_Mu	NM_001010870	NP_001010870	O60522	TDRD6_HUMAN		6	GTCCTTCAGAGC	0.468	
-	35	5963	ai.2_Missense_Mu	NM_138694	NP_619639	P08F94	PKHD1_HUMAN	cellular (Potential).	44	TGGGCGTCTCAC	0.428	rs140996978
-	6	856	9A1_uc003pff.3_5'	NM_001851	NP_001842	P20849	CO9A1_HUMAN		4	TCAAACTGGAG	0.463	
-	22	2762	HIP_uc011dyp.1_M	NM_017934	NP_060404	Q8WWQ0	PHIP_HUMAN		6	TTTACCTAGAACT	0.363	
-	6	740	p.R137W|ME1_uc	NM_002395	NP_002386	P48163	MAOX_HUMAN		2	CTGCCGTAGTC	0.269	rs141363376
+	6	834	_Mutation_p.S165F	NM_014942	NP_055757	Q9Y2G4	ANKR6_HUMAN	ANK 5.	3	CCGGGTCCCGC	0.542	
-	16	2607	e|USP45_uc003pp	NM_001080481	NP_001073950	Q70EL2	UBP45_HUMAN		2	GCCAGCCTTAAA	0.323	
-	6	961	p.G218R|LAMA4_	NM_001105206	NP_001098676	Q16363	LAMA4_HUMAN	inin EGF-like 3.	9	GAATCCGGTGG	0.483	
+	46	6788	o.2_Missense_Mu	NM_000426	NP_000417	P24043	LAMA2_HUMAN	minin G-like 1.	10	ACTCATATTGGTA	0.373	
+	3	2160	0kfi.2_Missense_M	NM_052913	NP_443145	Q86VY9	T200A_HUMAN	lasmic (Potential).	1	AGGGATATATGA	0.458	
+	3	1688		NM_016217	NP_057301	Q9UBI9	HDC_HUMAN		0	GGATGGCAGCT	0.552	
-	10	1883		NM_153235	NP_694967	Q8N3L3	TXLNB_HUMAN		2	AGGGAGGTTCA	0.602	
+	3	583	n_p.P58T|GPR12	NM_020455	NP_065188	Q86SQ4	GP126_HUMAN	tracellular (Potential).	1	TGCTACCCTAAC	0.502	
+	3	208	rf72_uc010kie.1_Ir	NM_138785	NP_620140	Q9NU53	CF072_HUMAN	cellular (Potential).	0	TTTAAGGTTGTTC	0.318	
-	5	738	M231I|KATNA1_u	NM_007044	NP_008975	O75449	KTNA1_HUMAN		1	TTCGGGCATCCA	0.388	
-	1	561	p.A124V|RSPH3_	NM_031924	NP_114130	Q86UC2	RSPH3_HUMAN		2	GTGGGCGCTAAG	0.652	
-	10	1674	qte.1_Missense_M	NM_003058	NP_003049	O15244	S22A2_HUMAN	ical; (Potential).	2	CAAGCACGCCTG	0.393	rs140033522
-	1	88	uc003quy.1_5'Flan	NM_145169	NP_660152	Q8WV19	SFT2A_HUMAN	lasmic (Potential).	1	CTGCGCAGTCA	0.731	
-	38	5418	1_uc003skm.1_5'	NM_001080453	NP_001073922	Q8N201	INT1_HUMAN		0	CTCATCGTCCC	0.697	
+	25	3948	o.2_Missense_Mu	NM_152744	NP_689957	Q7Z5N4	SDK1_HUMAN	onectin type-III 6.	6	GGGCCGGACGC	0.647	
+	3	860	_p.A121T|FOXK1_	NM_001037165	NP_001032242	P85037	FOXK1_HUMAN		2	TTGCAGCAAAG	0.662	

-	8	1276	nse_Mutation_p.V	NM_139179	NP_631918	Q8NCG7	DGLB_HUMAN	lasmic (Potential).	3	ACCACAACAGAC	0.572	
+	4	315	tp.1_Missense_M	NM_019005	NP_061878	Q9NXC5	MIO_HUMAN		0	TGAGCGGTACC	0.338	
+	5	902	POLR2J4_uc010k	NM_175064	NP_778234	Q8NFV5	SPDE1_HUMAN	Arg-rich.	1	TGAACCCGAGG	0.552	
-	18	2530	g.2_Missense_Mu	NM_033054	NP_149043	B0I1T2	MYO1G_HUMAN		4	GGCCCGCCACC	0.637	
+	9	1526	p.S366N|IKZF1_u	NM_006060	NP_006051	Q13422	IKZF1_HUMAN		148	GGTCAGCACCA	0.662	
-	12	1420	b.2_Missense_Mu	NM_005311	NP_005302	Q13322	GRB10_HUMAN		6	CTTACCCTCCA	0.642	
-	8	1138	.E165K|TYW1B_u	NM_001145440	NP_001138912	Q6NUM6	TYW1B_HUMAN		0	CCTCTCCCTCG	0.418	
-	2	656	.3_5'UTR|POM121C_uc003udl.1_RNA			A8CG34	P121C_HUMAN	and nuclear pore complex.	0	CCCCCGGACAG	0.527	
-	6	526	I20A_uc003ueb.1_	NM_031925	NP_114131	Q9BXJ8	T120A_HUMAN	ical; (Potential).	0	ATGATGGTGAGG	0.637	
+	2	314	.1_5'UTR|CDK14_	NM_012395	NP_036527	O94921	CDK14_HUMAN		4	TTATAGCTTTGAA	0.313	
+	2	1188		NM_001040152	NP_001035242	Q86TG7	PEG10_HUMAN	or interaction with ALK1.	1	AGCTCGCAAGC	0.647	
-	3	651		NM_001185	NP_001176	P25311	ZA2G_HUMAN		2	TTGCCGGTCCA	0.542	rs146685912
+	3	379	51_uc003uve.1_5'	NM_173564	NP_775835	Q6ZVC0	CG051_HUMAN		1	ACCCCTGCCGC	0.731	
+	9	1552	11kka.1_Missense_	NM_033506	NP_277041	O75426	FBX24_HUMAN	RCC1.	4	CTCCCTGGTGC	0.682	
-	23	4008		NM_022574	NP_072096	O75420	PERQ1_HUMAN		2	TGCCCTCCCCG	0.677	
+	3	8506	C17_uc010lho.1_	NM_001040105	NP_001035194	Q685J3	MUC17_HUMAN	ch.|59 X approximate tand	27	TGTCAACCACA	0.493	
-	2	895		NM_003378	NP_003369	O15240	VGF_HUMAN		0	Agggggccgggggcg	0.557	
-	4	859	xz.1_Missense_	NM_198571	NP_940973	Q8N8M0	CG052_HUMAN		1	AGAAGGTGCCA	0.741	
-	11	1667	D3_uc010lhs.2_5'	NM_001084	NP_001075	O60568	PLOD3_HUMAN		2	GGATACGCAGG	0.667	rs137857342
-	2	261		NM_138403	NP_612412	Q9BUA6	MYL10_HUMAN		2	TTCTCGGTGCC	0.597	
-	20	3239	g.3_RNA|DPY19L	NR_003561					0	CTTGACACTTGC	0.373	
-	1	689	|DUS4L_uc003ve	NM_181733	NP_859422	Q9UP83	COG5_HUMAN		4	GGACTGTAGCT	0.667	
+	14	2483	q.1_Missense_Mu	NM_000492	NP_000483	P13569	CFTR_HUMAN	lasmic (Potential).	5	ACATTCACCGAA	0.498	
-	2	1018	lt.2_Missense_Mut	NM_000845	NP_000836	O00222	GRM8_HUMAN	ellular (Potential).	23	ATCTGGGTGAAG	0.493	
-	2	211	1B1_uc003vrq.1_	NM_001628	NP_001619	P15121	ALDR_HUMAN		3	ACATGGGCACAG	0.587	
-	15	3764	d.3_Missense_Mu	NM_022740	NP_073577	Q9H2X6	HIPK2_HUMAN	bitory domain (AID).	7	TATATGTAAGGGT	0.418	
-	15	1860		NM_004333	NP_004324	P15056	BRAF_HUMAN	rotein kinas_R603>I(2)|p.T	18290	GATTTCACTGTA	0.368	
-	15	1935	_p.A595V|EZH2_u	NM_004456	NP_004447	Q15910	EZH2_HUMAN	Cys-rich.	183	CAGCGGCTCCA	0.527	
+	36	5351		NM_198455	NP_940857	A2VEC9	SSPO_HUMAN	SP type-1 2.	0	GGGCCGCACCT	0.657	
+	6	603	e_Mutation_p.R17	NM_024596	NP_078872	Q8NEM0	MCPH1_HUMAN		2	AGAAGAGATTA	0.333	
-	1	1358	.1_Intron|FAM66D	NM_201402	NP_958804	Q6R6M4	U17L2_HUMAN		3	ACTTTTCTGACG	0.478	
+	7	1226	xbp.3_Missense_	NM_001128431	NP_001121903	Q15043	S39AE_HUMAN	lasmic (Potential).	0	TCATCGATGGCC	0.542	
+	30	3152	_Mutation_p.E78	NM_173174	NP_775266	Q14289	FAK2_HUMAN		5	AGGAGGAGGAC	0.567	
+	5	1387	gb.1_Missense_	NM_016240	NP_057324	Q6AZY7	SCAR3_HUMAN	ellular (Potential).	4	GGGAGCGCTTC	0.597	
-	1	182		NR_003129					0	GGCCACACACA	0.592	
+	5	1359		NM_147189	NP_671722	Q8TC76	F110B_HUMAN		1	CTTCGCGGAGT	0.697	
+	2	899	u.1_Missense_Mu	NM_024721	NP_078997	Q86UP3	ZFHX4_HUMAN		15	CCTGGCATCTG	0.468	
+	44	8156	iw.2_Missense_Mu	NM_017890	NP_060360	Q7Z7G8	VP13B_HUMAN		20	TTGGGGCAACT	0.433	
+	58	11285	iw.2_Missense_Mu	NM_017890	NP_060360	Q7Z7G8	VP13B_HUMAN		20	GGACCGGCTCT	0.637	
+	62	10245		NM_177531	NP_803875	Q86WI1	PKHL1_HUMAN	ellular (Potential).	14	CCAACCGAGTC	0.383	
-	1	191		NM_024094	NP_076999	Q9BVC3	DCC1_HUMAN		1	TCGGCCGCATTC	0.731	
+	29	3809	yoz.2_Missense_	NM_021110	NP_066933	Q05707	COEA1_HUMAN	VWFA 2.	12	TTGGCAGTAAG	0.438	
+	3	2781		NM_014943	NP_055758	Q9Y6X8	ZHX2_HUMAN		2	CTCTGCGAAGA	0.532	
-	4	791	G1_uc010mef.2_	NM_001135242	NP_001128714	Q92597	NDRG1_HUMAN		4	AACTTACGGTT	0.557	
+	14	2539	_p.G715V|DENND	NM_014957	NP_055772	A2RUS2	DEND3_HUMAN		1	GCCAGGCTACT	0.468	
-	2	850		NM_005293	NP_005284	Q99678	GPR20_HUMAN	Name=6; (Potential).	1	GCGTGAAGCAG	0.682	
+	23	3554		NM_001702	NP_001693	O14514	BAI1_HUMAN	lasmic (Potential).	8	CATCACGGACA	0.662	

-	4	608	eu.2_Missense_Mu	NM_001029976	NP_001025147	P17020	ZNF16_HUMAN			5	GCCCCATGGCAG	0.552	
+	7	1440		NM_000550	NP_000541	P17643	TYRP1_HUMAN			1	AATTTAGATATAT	0.328	
-	1	1175	v.2_Intron|KLHL9_	NM_018847	NP_061335	Q9P2J3	KLHL9_HUMAN	BACK.		4	GGAAAGCACAA	0.408	
-	3	1346	e_Mutation_p.R44	NM_012166	NP_036298	Q9UK96	FBX10_HUMAN	PbH1 3.		5	CTTGCGGATGA	0.602	
-	16	2519	ahy.2_Missense_M	NM_001007471	NP_001007472	Q9HCF6	TRPM3_HUMAN	lasmic (Potential).		9	CATGTCGGTGA	0.632	
+	5	1579		NM_194320	NP_919301	Q14929	ZN169_HUMAN	2H2-type 10.		2	AGTGTGGGCGT	0.567	rs150911311
+	3	5415	.R1557H|ZNF462_	NM_021224	NP_067047	Q96JM2	ZN462_HUMAN	2H2-type 16.		5	CATCCGCAAAG	0.557	
-	47	5570		NM_001080398	NP_001073867					0	AGCTCCTTTTCC	0.453	
-	21	4211	A1278V|AKNA_uc	NM_030767	NP_110394	Q7Z591	AKNA_HUMAN			6	GCAGGCGCATAG	0.637	
-	3	512	3XW2_uc004bkm.	NM_012164	NP_036296	Q9UKT8	FBXW2_HUMAN			4	CAGTGCAAAGC	0.438	
-	3	442	_NAC4_uc004bst.	NM_175039	NP_778204	Q9H4F1	SIA7D_HUMAN	nenal (Potential).		0	ACTGAAGTGCA	0.512	
-	4	1019		NM_006336	NP_006327	Q7Z7L7	ZER1_HUMAN			1	CGGCCGCAGCA	0.612	
+	21	2477	p.L756M|USP20_	NM_001110303	NP_001103773	Q9Y2K6	UBP20_HUMAN	DUSP 1.		2	GTCATCCTGCCC	0.627	
+	13	1375	zs.1_Missense_Mu	NM_003934	NP_003925	Q96I24	FUBP3_HUMAN			1	ATAGATGAGAAA	0.567	
+	10	1410	mzj.1_Missense_M	NM_013318	NP_037450	Q5JSZ5	PRC2B_HUMAN			0	CCCTCAGCCAC	0.607	
-	7	2217	F1_uc004cbm.2_M	NM_007344	NP_031370	Q15361	TTF1_HUMAN	Myb-like 2.		4	TCTACCCAAGATA	0.418	
+	20	3025	861R|ADAMTS13_	NM_139025	NP_620594	Q76LX8	ATS13_HUMAN			6	TGTGTCGGGATG	0.642	
+	2	479		NM_000787	NP_000778	P09172	DOPO_HUMAN	ntragranular (Potential).		4	ACCCCAAGGATT	0.592	
-	3	345	y.2_5'UTR|FBXW5	NM_018998	NP_061871	Q969U6	FBXW5_HUMAN			0	TGGCCGCTGCG	0.682	
+	16	2627	.S766N|GRIN1_uc	NM_007327	NP_015566	Q05586	NMDZ1_HUMAN	cellular (Potential).		1	AGACAGCCCCT	0.652	
+	11	1632		NM_015456	NP_056271	Q8WX92	NELFB_HUMAN			0	GAATTTGCCCTT	0.612	
+	4	359	uc010ncq.2_Silent_p.T210T							0	GGGACGCTACA	0.592	
-	16	1159	n_p.T308I|GPR64_	NM_001079858	NP_001073327	Q8IZP9	GPR64_HUMAN	cellular (Potential).		0	ACATGGGTTTGG	0.577	
+	18	2054	p.C617*|PHEX_u	NM_000444	NP_000435	P78562	PHEX_HUMAN	cellular (Potential).		3	AAAATGCATGATT	0.363	
-	1	794		NM_001017930	NP_001017930	A6NGE4	DC8L1_HUMAN	WD 1.	p.R227P(1)	4	CTGCCGCACCC	0.512	
-	61	9335	_Missense_Mutati	NM_004006	NP_003997	P11532	DMD_HUMAN	Spectrin 22.		6	CTCGACGGCCA	0.423	rs143426249
+	1	721		NM_001013736	NP_001013758	Q5HY64	FA47C_HUMAN			3	CCACCTGGAGC	0.637	
-	1	163	dgv.1_Missense_M	NM_032591	NP_115980	Q96T83	SL9A7_HUMAN			2	TGGCGCTGCTG	0.582	
+	10	1053	n.1_Missense_Mu	NM_012280	NP_036412	Q9UET6	RRMJ1_HUMAN			0	AGCTCCTATGATT	0.572	
+	11	1258	n.1_Missense_Mu	NM_012280	NP_036412	Q9UET6	RRMJ1_HUMAN			0	CTCAGTGCCACA	0.617	
-	14	1780	nip.2_Missense_M	NM_005183	NP_005174	O60840	CAC1F_HUMAN	=S2 of repeat II; (Potential		6	CCACCGTGAAC	0.532	
+	3	218	L3L_uc004dti.2_R	NM_019067	NP_061940	Q9NVN8	GNL3L_HUMAN	r nucleolar localization.		1	TACCCTCAGGTA	0.453	
+	7	539	L3L_uc004dti.2_R	NM_019067	NP_061940	Q9NVN8	GNL3L_HUMAN			1	GTGGAATACTCT	0.532	
+	12	2555	RO_uc011mok.1_	NM_001039705	NP_001034794	Q12816	TROP_HUMAN	proximate tandem repeats.		1	TGGCATGCCTTG	0.542	
+	6	1102	uq.2_Missense_M	NM_016656	NP_057740	Q5VZM2	RRAGB_HUMAN			0	CTGATTTATGTCT	0.398	
-	13	1513	_4_uc004ege.3_M	NM_080737	NP_542775	Q96C24	SYTL4_HUMAN	C2 1.		2	TCATCAGCATAG	0.537	
+	1	576		NM_001031834	NP_001027004	P0C0E4	RB40L_HUMAN	SOCS box.		2	TGCTGCGGCAC	0.587	
+	4	1265		NM_017416	NP_059112	Q9NP60	IRPL2_HUMAN	2.|Extracellular (Potential).		3	TTAAAAAGTCCG	0.423	
+	4	2662	nrd.1_Missense_M	NM_021946	NP_068765	Q5H9F3	BCORL_HUMAN			7	GTGCCGGGCAG	0.617	
+	11	2821	b.1_Missense_Mu	NM_002025	NP_002016	P51816	AFF2_HUMAN			5	CACCTATTCCTGT	0.458	
+	3	991	_XNB3_uc010nuk.	NM_005393	NP_005384	Q9ULL4	PLXB3_HUMAN	ılar (Potential).|Sema.		1	ACCAACCTGTAC	0.612	
+	29	5008	NB3_uc011mzd.1_	NM_005393	NP_005384	Q9ULL4	PLXB3_HUMAN	lasmic (Potential).		1	GCCAGGTCCCA	0.537	
-	21	2944	.G946S|L1CAM_	NM_000425	NP_000416	P32004	L1CAM_HUMAN	tential).|Fibronectin type-III		9	CACGCCGTTGT	0.711	
-	7	1393	ve.1_Missense_Mu	NM_080612	NP_542179	Q8WWW8	GAB3_HUMAN			1	GTGGCCGTGCTA	0.488	
-	19	1803	p.R307C|ACAP3_	NM_030649	NP_085152	Q96P50	ACAP3_HUMAN			0	CTCGGCGGAACT	0.667	
-	4	496	K4_uc010nza.1_Ir	NM_018216	NP_060686	Q9NVE7	PANK4_HUMAN			3	CATGGGGGATGT	0.532	
+	21	3619	E4B_uc010oaj.1_	NM_001105562	NP_001099032	O95155	UBE4B_HUMAN			4	TACCTTCCCTGAT	0.458	

+	4	966		NM_001012276	NP_001012276	Q5VWM4	PRAM8_HUMAN		0	TCCTTGGAGATG	0.552	
+	5	805	M1_uc001axg.1_M	NM_017556	NP_060026	Q8WUP2	FBLI1_HUMAN	Pro-rich.	1	GGAGGCTCCTG	0.667	
+	7	884	ki.1_Missense_Mu	NM_014663	NP_055478	O75164	KDM4A_HUMAN	JmjC.	1	TCCGCCACAAG	0.388	
-	9	1667	u.1_RNA|C1orf16	NM_001004303	NP_001004303	Q5VWT5	CA168_HUMAN		5	TCATCTGAATTT	0.458	
-	3	429	_p.R59Q|C8B_uc	NM_000066	NP_000057	P07358	CO8B_HUMAN	receptor class A.	4	TCACATCGCACT	0.483	
-	10	1481	73_uc001dgi.3_Mi	NM_001002912	NP_001002912	Q5RHP9	CA173_HUMAN	Glu-rich.	5	TCCTCTCCTTTC	0.413	
+	6	1139	HN2_uc001div.2_	NM_012302	NP_036434	O95490	LPHN2_HUMAN	otential).|Olfactomedin-like	9	GCGGAGTCCTC	0.393	
-	10	1919	_p.P443S|TGFBR	NM_003243	NP_003234	Q03167	TGBR3_HUMAN	acellular (Potential).	3	GGTAGGATCCA	0.537	
-	36	3107	_p.P942L|COL11A	NM_001854	NP_001845	P12107	COBA1_HUMAN	le-helical region.	12	GTCCAGGGAAT	0.388	
+	21	3815	.1_3'UTR|MAGI3_	NM_001142782	NP_001136254	Q5TCQ9	MAGI3_HUMAN		6	AAGTAGAAAATG	0.408	
-	3	460		NM_152380	NP_689593	Q96SF7	TBX15_HUMAN	T-box.	2	ATGTGGATCTA	0.443	
-	7	1015	_p.T175A|C1orf43	NM_001098616	NP_001092086	Q9BWL3	CA043_HUMAN		0	ACTGAGTTAGGT	0.507	
+	6	1992	ion_p.P119L|RUS	NM_001105203	NP_001098673	Q9BVN2	RUSC1_HUMAN	RUN.	2	AGCCCCGCTGA	0.642	
+	1	274		NM_001231	NP_001222	P31415	CASQ1_HUMAN		1	AGACAGGATGG	0.632	
-	4	314		NM_001013625	NP_001013647	Q5VTH2	CA192_HUMAN		0	CCTTGAGTAAA	0.478	
+	6	918		NM_018122	NP_060592	Q6PI48	SYDM_HUMAN		2	CTCTTCGGTTG	0.323	
+	2	123		NM_020950	NP_066001	Q5VZ46	K1614_HUMAN		4	AGGGCCCAAGA	0.612	
+	46	6392	.S1964F|CACNA	NM_000721	NP_000712	Q15878	CAC1E_HUMAN	lasmic (Potential).	6	TCAATCCAGGT	0.587	
-	32	4698	zl.1_Missense_Mu	NM_017596	NP_060066	O75037	KI21B_HUMAN	WD 4.	6	GGTGACCGTCA	0.622	
+	13	1162	.2_RNA|LGR6_u	NM_001017403	NP_001017403	Q9HBX8	LGR6_HUMAN	xtracellular (p.E388K(1)	10	TCTGGGAAATT	0.647	rs143455603
-	4	839	z.2_Missense_Mu	NM_002644	NP_002635	P01833	PIGR_HUMAN	2.|Extracellular (Potential).	3	GCAGAGATACT	0.502	
-	10	1627		NM_018040	NP_060510	Q9NW75	GPTC2_HUMAN	G-patch.	1	TAGAGGAAATC	0.473	
-	4	796	w.1_Missense_Mu	NM_003268	NP_003259	O60602	TLR5_HUMAN	lar (Potential).|LRR 2.	4	ACAGTCCCTGA	0.403	
-	14	1632	13_uc001hug.3_	NM_024525	NP_078801	Q8NBP0	TTC13_HUMAN		2	ATGCGGCCAAA	0.468	
+	5	1075	hvy.1_Missense_	NM_173508	NP_775779	Q8IY50	S35F3_HUMAN	ical; (Potential).	2	TGCATTCCTATT	0.418	
-	9	2113	d.2_Missense_Mu	NM_002508	NP_002499	P14543	NID1_HUMAN	EGF-like 2.	2	GCAGGGATTCT	0.562	
+	36	4966		NM_001035	NP_001026	Q92736	RYR2_HUMAN	ilarity).|4 X approximate re	33	GCCAAGGCTGG	0.527	
+	3	235	_p.P33S|NLRP3_	NM_001079821	NP_001073289	Q96P20	NALP3_HUMAN	DAPIN.	26	ACTATCCTCCC	0.547	
+	1	481		NM_001001914	NP_001001914	Q8NGZ4	OR2G3_HUMAN	ellular (Potential).	1	ATGCAACTTTT	0.488	
-	14	1773		NM_001081	NP_001072	O60494	CUBN_HUMAN	CUB 1.	19	CCATTTCTTAAAT	0.403	
-	3	455	s.2_Missense_Mu	NM_019893	NP_063946	Q9NR71	ASAH2_HUMAN	enal (Potential).	0	CTGTTCGATTG	0.473	
+	10	2170		NM_032199	NP_115575	Q14865	ARI5B_HUMAN		4	ACCCCCTTTGA	0.552	
+	2	1481	jmx.3_Intron|CTN	NM_178011	NP_821079	Q86VH5	LRRT3_HUMAN	ellular (Potential).	3	CTTGCTGGGAAT	0.423	
+	5	1062	C19_uc009xus.1_	NM_000772	NP_000763	P33260	CP2CI_HUMAN		5	TATTGGAGAGA	0.338	
+	2	417	42F|C10orf137_uc	NM_015608	NP_056423	Q3B7T1	EDRF1_HUMAN		10	TTATTTCTTGGA	0.388	
+	14	2283	u.3_Missense_Mu	NM_025092	NP_079368	Q32M88	ATHL1_HUMAN		3	GGGTTCCTCCA	0.612	
+	47	6781	b.2_Missense_Mu	NM_017511	NP_059981	Q9HC84	MUC5B_HUMAN	in repeats.|Cys-rich subdo	0	GAGGGGACGTT	0.602	
+	1	370		NM_001001480	NP_001001480	Q701N2	KRA55_HUMAN	repeats of C-C-X-P.	1	TGGCTCCTGTG	0.697	
+	8	1186	p.R144G|KCNQ1_	NM_000218	NP_000209	P51787	KCNQ1_HUMAN	lasmic (Potential).	1	AGCAGAGGCAG	0.602	
+	2	246	8_uc001lwy.2_No	NM_183233	NP_899056	Q96BI1	S22AI_HUMAN		3	GGGACCAGGGC	0.652	
-	1	871		NM_001004758	NP_001004758	Q8NGJ8	O51S1_HUMAN	Name=7; (Potential).	4	TGGAGGAAGAA	0.448	
-	1	483_484		NM_001005329	NP_001005329	Q8NGJ6	O51A4_HUMAN	Name=4; (Potential).	3	AAAGGGAAGG	0.436	
-	1	329	_uc001mam.1_Int	NM_001005288	NP_001005288	Q9H343	O51I1_HUMAN	Name=3; (Potential).	1	TGAAGGAGAAA	0.443	
-	1	1304	2_uc001mak.1_Ir	NM_145053	NP_659490	Q8IYU4	UBQLN_HUMAN		3	TTGAAGAGAAA	0.507	
-	1	344	.1_Intron|TRIM22_	NM_001001922	NP_001001922	Q8NH56	O52N5_HUMAN	Name=3; (Potential).	2	TGAACCCATGA	0.493	rs143745000
+	13	2012	hm.2_Missense_	NM_001142307	NP_001135779	P32780	TF2H1_HUMAN		0	GGGCACTTATG	0.463	
-	2	485	mri.1_Missense_	NM_030771	NP_110398	Q96HJ3	CCD34_HUMAN		0	CCCATGGTGTC	0.418	

+	2	146	rf74_uc001mwx.1_	NM_138787	NP_620142	Q86VG3	CK074_HUMAN		0	AAATTCCTTAATT	0.358	
-	4	1035		NM_003654	NP_003645	O43916	CHST1_HUMAN	enal (Potential).	5	GAGGTCGCGGC	0.662	
-	5	1046	.1_Intron|RAPSN_	NM_005055	NP_005046	Q13702	RAPSN_HUMAN	TPR 6.	1	GATCTCGGTCA	0.652	
+	1	586		NM_001004708	NP_001004708	Q8NGJ1	OR4D6_HUMAN	Name=5; (Potential).	1	CTTTGGAGCTT	0.527	
-	5	15458_1545	AK_uc001ntk.1_I	NM_001620	NP_001611	Q09666	AHNK_HUMAN		19	AGGCTGGCATC	0.441	
+	5	352	v.1_RNA|TSGA10	NM_152762	NP_689975	Q3SY00	T10IP_HUMAN		0	CTTCCCCTTCC	0.662	
-	3	566	HA3_uc010rrj.1_	NM_182904	NP_878907	Q7Z4N8	P4HA3_HUMAN		1	GAGCCGTTTGG	0.507	
+	2	113	on_p.E5D|C11orf6	NM_024684	NP_078960	Q9H7C9	CK067_HUMAN		0	CCTGAAATTGC	0.378	
-	22	3614		NM_001098816	NP_001092286	Q6N022	TEN4_HUMAN	ellular (Potential).	4	GATTTCCTCCT	0.582	
-	2	1005	_p.T194A|TRPC6_	NM_004621	NP_004612	Q9Y210	TRPC6_HUMAN	lasmic (Potential).	4	GCTGGTTGCTA	0.463	
-	6	5135	z.1_Missense_Mu	NM_015065	NP_055880	Q8NEV8	EXPH5_HUMAN		5	CAGTAATGGGG	0.453	
-	9	937	P28_uc001poi.2_5	NM_020886	NP_065937	Q96RU2	UBP28_HUMAN		7	TTCACGAACCC	0.358	
+	3	556		NM_182495	NP_872301	Q96DL1	FA55B_HUMAN		1	GGCCAGGATGT	0.552	
-	7	1417	1pri.1_Missense_	NM_020693	NP_065744	Q8TD84	DSCL1_HUMAN	otential).|Ig-like C2-type 5.	8	AGGACGAGACG	0.682	
+	1	650		NM_001001965	NP_001001965	Q8NGN0	OR4D5_HUMAN	Name=5; (Potential).	1	GGGATCGTACA	0.517	rs138187932
+	10	1311	_p.E368K|VWA5A_	NM_001130142	NP_001123614	O00534	VMA5A_HUMAN	VWFA.	2	GCACTGAAATC	0.522	
-	1	158		NM_012378	NP_036510	Q15620	OR8B8_HUMAN	lasmic (Potential).	1	AGTGAGAGTTG	0.478	
+	2	1064	_p.V134I|NTM_u	NM_016522	NP_057606	Q9P121	NTRI_HUMAN		6	TGCAAGGTAGG	0.552	
-	7	1237	dy.1_Missense_M	NM_152640	NP_689853	Q8IZD4	DCP1B_HUMAN		1	GAGCTCTGCTG	0.572	
-	1	46	0sge.1_Missense_	NM_174941	NP_777601	Q9NR16	C163B_HUMAN		11	GCCACGAGTTTT	0.378	
+	3	660		NM_024865	NP_079141	Q9H9S0	NANOG_HUMAN	Homeobox.	0	AGAATGAAATC	0.373	
-	1	206	RC3_uc010shc.1	NM_002261	NP_002252	Q07444	NKG2E_HUMAN	lasmic (Potential).	3	CAATCCCTTGAT	0.348	
-	6	855	_p.P279S|ABCC9_	NM_005691	NP_005682	O60706	ABCC9_HUMAN	lasmic (Potential).	6	ATTTGGATGAT	0.353	
-	2	655	10_uc009zju.1_5'	NM_198992	NP_945343	Q6XYQ8	SYT10_HUMAN	lasmic (Potential).	2	GCTTTTCATTTT	0.398	
-	35	5221		NM_025003	NP_079279	P59510	ATS20_HUMAN		19	ATAAATCTAAAG	0.303	
-	1	82		NM_025003	NP_079279	P59510	ATS20_HUMAN		19	CCTGGGGTGGA	0.652	
-	2	1381	7L_uc001rns.3_M	NM_001098615	NP_001092085	Q9H0K6	PUS7L_HUMAN		1	TTTTCCTTCTTG	0.348	
-	11	893	qv.2_Missense_M	NM_001844	NP_001835	P02458	CO2A1_HUMAN	e-helical region.	2	CATGGGACCCT	0.478	
-	5	654		NM_014470	NP_055285	Q92730	RND1_HUMAN		1	GCATGGATGCC	0.552	
-	6	1186		NM_033045	NP_149034	Q9NSB2	KRT84_HUMAN	Rod.|Coil 2.	1	GATCTCGTTCC	0.547	rs145550883
-	2	616		NM_005555	NP_005546	P04259	K2C6B_HUMAN	oil 1A.|Rod.	2	CAGAACCTTGT	0.537	
-	2	948		NM_005554	NP_005545	P02538	K2C6A_HUMAN	oil 1B.|Rod.	5	GTCCTCCACCA	0.542	
+	1	478		NM_001005497	NP_001005497	A6NL08	O6C75_HUMAN	Name=4; (Potential).	3	TAATGCTTCTG	0.438	
+	8	877	q.2_Missense_Mu	NM_005269	NP_005260	P08151	GLI1_HUMAN		15	GGAAGGAGTTC	0.597	
+	3	336	_p.P85L|MSRB3_	NM_198080	NP_932346	Q8IXL7	MSRB3_HUMAN		2	AACTCCATTGT	0.318	
-	2	335	va.3_Missense_M	NM_002837	NP_002828	P23467	PTPRB_HUMAN	III 1.|Extracellular (Potentia	3	ACTGTTCTCTCT	0.458	
-	1	734		NM_152638	NP_689851	Q8TC90	CL012_HUMAN		2	GAATTTCCAGAA	0.647	
+	6	935	zth.1_Missense_M	NM_152435	NP_689648	Q96NU7	HUTI_HUMAN		1	AACTGGGAGCG	0.483	
-	3	291	.2_RNA|MMAB_uc	NM_052845	NP_443077	Q96EY8	MMAB_HUMAN		0	TTTCTCCTGTG	0.393	
-	9	620	.2_Missense_Mu	NM_002150	NP_002141	P32754	HPPD_HUMAN		0	GGACACCATCT	0.582	
-	14	1485	_p.V214I|ZCCHC8	NM_017612	NP_060082	Q6NZY4	ZCHC8_HUMAN		0	TGGTACCTCCA	0.413	
+	11	739	au.1_Missense_M	NM_001516	NP_001507	Q13889	TF2H3_HUMAN		0	TCAGAGATCTC	0.393	
-	8	1272	_p.C278G|RIMBP	NM_015347	NP_056162	O15034	RIMB2_HUMAN	nectin type-III 1.	11	GACGCACTGCA	0.627	
-	3	338		NM_006001	NP_005992	Q13748	TBA3C_HUMAN		5	ATCTTCCTTCC	0.522	
+	10	1663	w.2_Missense_M	NM_006646	NP_006637	Q9UPY6	WASF3_HUMAN		1	TGTCCCGGCGC	0.617	
-	2	666	12_uc010tdl.1_5'	NM_005288	NP_005279	P47775	GPR12_HUMAN	lasmic (Potential).	0	GAATGGTACGT	0.577	
+	42	6907	_p.R27Q|NBEA_	NM_015678	NP_056493	Q8NFP9	NBEA_HUMAN		11	AAACCGAAGTA	0.343	

-	10	1246	z.2_Missense_Mu	NM_052867	NP_443099	Q8IZF0	NALCN_HUMAN	lasmic (Potential).		16	CATCTTCATGAA	0.448	
-	5	1085	p.A232V|NOVA1_	NM_002515	NP_002506	P51513	NOVA1_HUMAN		p.A256D(1)	5	ACATTGGCATAA	0.458	
+	7	903	rt.2_Missense_Mu	NM_173159	NP_071406	Q8IXF0	NPAS3_HUMAN			2	TCAAATCATCAG	0.478	
-	16	2499	p.V703A|RALGAP	NM_014990	NP_055805	Q6GYQ0	RGPA1_HUMAN			4	GTCCAACTCCT	0.413	
+	9	1025_1026		NM_002687	NP_002678	Q9H307	PININ_HUMAN	ential.|Glu-rich.		1	AGAGGGTAAG	0.351	
-	9	1304	L1_uc001wxz.2_I	NM_004196	NP_004187	Q00532	CDKL1_HUMAN			2	taggagggggatgcct	0	
-	11	2661	H5_uc001xfy.2_3'	NM_139318	NP_647479	Q8NCM2	KCNH5_HUMAN	lasmic (Potential).		9	GTCACTTTTTGT	0.507	
-	5	557	nse_Mutation_p.P	NM_015346	NP_056161	Q68DK2	ZFY26_HUMAN			11	CCTTGGATTTC	0.572	
-	8	785	ri.1_Missense_Mu	NM_012074	NP_036206	Q92784	DPF3_HUMAN			1	ATTGGGAATGA	0.512	
-	5	516	ri.1_Missense_Mu	NM_012074	NP_036206	Q92784	DPF3_HUMAN			1	TCTTTCGCTTG	0.448	
+	5	1298	RXN3_uc010asv.1	NM_004796	NP_004787	Q9Y4C0	NRX3A_HUMAN	ellular (Potential).		10	CGGATGAGTGC	0.567	
-	3	1347	1ycu.3_Missense_	NM_016186	NP_057270	Q9UK55	ZPI_HUMAN			3	CATTTCCTTGG	0.502	
-	3	980	RPINA1_uc010au	NM_000295	NP_000286	P01009	A1AT_HUMAN			1	CCTTCACGGTG	0.542	
-	2	828	ydg.2_Missense_	NM_175739	NP_783866	Q86WD7	SPA9_HUMAN			2	AATGTGGTTCA	0.388	
+	3	612		NM_003246	NP_003237	P07996	TSP1_HUMAN	P N-terminal.		6	TGGAAGAAGCT	0.582	
+	9	1879		NM_019074	NP_061947	Q9NR61	DLL4_HUMAN	ellular (Potential).		2	GTTCCCCGTGG	0.652	
+	1	775		NM_001080534	NP_001074003	Q8NB66	UN13C_HUMAN			7	AAACAGAACTT	0.463	
+	8	3781	acl.2_Missense_	NM_001080534	NP_001074003	Q8NB66	UN13C_HUMAN	C2 1.		7	ATTTTTGGAAAT	0.313	
+	24	5650		NM_001080534	NP_001074003	Q8NB66	UN13C_HUMAN			7	CAATGGATGCA	0.338	
+	2	1600	rh.2_Missense_M	NM_015322	NP_056137	Q9UK73	FEM1B_HUMAN			0	AAGGCCTTATA	0.418	
-	3	989		NM_001897	NP_001888	Q6UVK1	CSPG4_HUMAN	obular or compact configur		3	CCACGGAGATT	0.607	
+	21	2806	b.1_Missense_Mu	NM_004136	NP_004127	P48200	IREB2_HUMAN			0	AAAGATCATTTG	0.368	
+	11	1430	G3_uc010uud.1_	NM_032039	NP_114428	Q9H0X4	ITFG3_HUMAN	ellular (Potential).		1	CCTAGCCCTCC	0.672	
-	2	469		NM_001013658	NP_001013680	Q96A99	PTX4_HUMAN			0	GCTGTGGACGA	0.736	
+	4	546	e_Mutation_p.I12	NM_004996	NP_004987	P33527	MRP1_HUMAN	Cytoplasmic.		4	TTTAATTCAGCT	0.383	
-	19	2721		NM_017539	NP_060009	Q8TD57	DYH3_HUMAN	n (By similarity).		18	TGTCCTCCACAT	0.458	
+	17	3624	e_Mutation_p.P82	NM_006910	NP_008841	Q7Z6E9	RBBP6_HUMAN			4	TTTCTCCAGAG	0.418	
+	1	71		NM_144602	NP_653203	Q8WTQ4	CP078_HUMAN			1	TGAAGGATTTA	0.532	
-	7	820	e_Mutation_p.P25	NM_000512	NP_000503	P34059	GALNS_HUMAN			2	AGAAGGGTTTG	0.602	
-	5	540	e_Mutation_p.P15	NM_000512	NP_000503	P34059	GALNS_HUMAN			2	CAGGGGGTGGA	0.567	
-	2	885	L|TRPV1_uc010v	NM_080706	NP_542437	Q8NER1	TRPV1_HUMAN	nic (Potential).|ANK 1.		1	GGCTTCAAAGA	0.567	
-	6	1220	k.1_Missense_Mu	NM_015113	NP_055928	O43149	ZZEF1_HUMAN	DOC.		4	AGACTTCTTAA	0.483	
-	11	1743	cb.2_Missense_	NM_020162	NP_064547	Q9H6R0	DHX33_HUMAN			2	ATTCTCTTTGC	0.358	rs147158339
-	6	775	nse_Mutation_p.P	NM_020360	NP_065093	Q9NRY6	PLS3_HUMAN	smic (By similarity).		0	GGAAGGGATGC	0.612	
+	1	67	2R_uc010cog.1_	NM_004246	NP_004237	O95838	GLP2R_HUMAN	ellular (Potential).		3	TCCACGAGCTG	0.647	
+	9	1907	bj.2_Missense_Mu	NM_003593	NP_003584	O15353	FOXN1_HUMAN			1	ATCTTCGATGC	0.612	
-	3	617		NM_001045	NP_001036	P31645	SC6A4_HUMAN	lasmic (Potential).		4	AACTCCGTTTT	0.502	
-	3	402	nse_Mutation_p.D	NM_152781	NP_689994	A2RTY3	CQ066_HUMAN			3	CAGGTCGTGCC	0.512	
-	8	1386	P_uc010wfs.1_Int	NM_000422	NP_000413	Q04695	K1C17_HUMAN	Tail.		2	GGGAGGAGATG	0.652	
-	12	1651	o.1_Missense_Mu	NM_005374	NP_005365	Q14168	MPP2_HUMAN	ylate kinase-like.		0	ATATTCCACTCT	0.617	
+	26	3423	c010dag.2_Intron|	NM_005892	NP_005883	O95466	FMNL_HUMAN	DAD.		1	AGACGGTGCCC	0.582	
-	5	1746	ikd.2_Missense_M	NM_015443	NP_056258	Q7Z3B3	K1267_HUMAN			2	AGACAGGCTGA	0.343	
-	15	2627	s.1_Missense_Mu	NM_198393	NP_938207	Q8IWB6	TEX14_HUMAN			17	TTTTCCAGGGT	0.423	
+	26	3881_3882	ug.1_Missense_M	NM_020761	NP_065812	Q8N122	RPTOR_HUMAN	WD 1.		6	GCGTCCCCTCT	0.559	
+	1	471	L_uc010dkz.2_In	NM_020412	NP_065145	Q7LBR1	CHM1B_HUMAN			0	TGGACAAATTC	0.517	
+	1	59		NM_005913	NP_005904	P33032	MC5R_HUMAN	ellular (Potential).		6	GGGCAACCTTT	0.463	
+	14	1990		NM_005925	NP_005916	Q16820	MEP1B_HUMAN	ellular (Potential).		2	AGGCTCCACCC	0.463	

-	5	696	2_uc010dnf.2_3'	NM_002930	NP_002921	Q99578	RIT2_HUMAN		1	GCCATGAAAAG	0.423	
+	20	3706	p.R868K|DCC_uc	NM_005215	NP_005206	P43146	DCC_HUMAN	tential).|Fibronectin type-III	17	CTTCAGGACTC	0.388	
-	8	1143	p.E332K|SERPIN	NM_002974	NP_002965	P48594	SPB4_HUMAN		3	ATAATTCGACTA	0.463	
+	6	689	xet.1_Missense_	NM_001040147	NP_001035237	O75635	SPB7_HUMAN		3	ATCTCCCAAGG	0.408	
-	6	820	p.S178F|NETO1_	NM_138966	NP_620416	Q8TDF5	NETO1_HUMAN	tracellular (Potential).	4	CTTCGGAACCG	0.428	
+	2	1120		NM_173481	NP_775752	Q8IVT2	CS021_HUMAN		1	AGGGCGCCCGT	0.682	
+	13	1539	.G432D|FSD1_uc	NM_024333	NP_077309	Q9BTV5	FSD1_HUMAN	B30.2/SPRY.	1	GTATGGTGTGG	0.677	
-	11	1183	p.G382E|SEMA6	NM_032108	NP_115484	Q9H3T3	SEM6B_HUMAN	lar (Potential).|Sema.	1	GCATCCCGGGG	0.612	
+	2	924	edk.1_Missense_	NM_014686	NP_055501	O15063	K0355_HUMAN		1	CGGGTCCAAGC	0.627	
+	10	2221	efi.2_Missense_Mutation_p.E373G|uc010efj.2_Missens			Q3ZCX4	ZN568_HUMAN		2	ATGTGAAAAGG	0.448	rs1363752
-	5	717	85B_uc002ofr.1_	NM_152279	NP_689492	Q52M93	Z585B_HUMAN		1	TTTTTCTCCTG	0.393	
-	1	688		NM_020862	NP_065913	Q9P244	LRFN1_HUMAN	tracellular (Potential).	2	GAAGAGCCCGT	0.667	
+	27	3502_3503	se_Mutation_p.P4	NM_001042544	NP_001036009	Q8N2S1	LTBP4_HUMAN	Pro-rich.	1	GCCGACCCAGC	0.693	
-	3	574	G4_uc002owb.2_	NM_002780	NP_002771	Q00888	PSG4_HUMAN	like C2-type 1.	1	CCTGGGATTTA	0.532	
+	3	311	e_Mutation_p.Q54	NM_001007270	NP_001007271	Q9H840	GEMI7_HUMAN		1	AATCCCAGGAG	0.627	
+	2	232	pgk.1_Missense_	NM_018485	NP_060955	Q9P296	C5ARL_HUMAN	ellular (Potential).	1	ACGATTCTGTCA	0.607	
+	4	379	p.P69S|CCDC15	NM_144688	NP_653289	Q8N6L0	CC155_HUMAN		2	AGGGCCCCCAG	0.642	
+	14	1964	e_Mutation_p.E54	NM_006669	NP_006660	Q8NHL6	LIRB1_HUMAN	lasmic (Potential).	3	AGCCTGAGGAT	0.612	
-	5	1190	ne.2_Missense_M	NM_022103	NP_071386	Q5HYK9	ZN667_HUMAN	2H2-type 6.	1	GGGGTGAAATC	0.388	
-	11	1775	61T|ZIM2_uc002q	NM_015363	NP_056178	Q9NZV7	ZIM2_HUMAN		3	GCAGGCTCTCT	0.483	
+	3	362		NM_182626	NP_872432	Q96LS8	CB048_HUMAN		0	tttctaaggggatgaga	0	
-	4	459	dx.2_Missense_M	NM_022460	NP_071905	Q53T59	H1BP3_HUMAN	PX.	1	CCCTGGGGATC	0.557	
-	26	7173		NM_000384	NP_000375	P04114	APOB_HUMAN		27	CTACTTCATACC	0.378	
-	16	2333	i.1_RNA|ATAD2B_	NM_017552	NP_060022	Q9ULI0	ATD2B_HUMAN		1	GTGGTCTTATG	0.448	
+	1	331	7L_uc010ymf.1_5'	NM_018158	NP_060628	Q9BWU0	NADAP_HUMAN		0	CTTCACCATCG	0.522	
-	38	5970_5971	DA_uc002rsx.3_	NM_001083953	NP_001077422	Q6YHU6	THADA_HUMAN		3	ACCATCCTTTGA	0.525	
-	10	1796	p.M512I|FSHR_u	NM_000145	NP_000136	P23945	FSHR_HUMAN	Name=6; (Potential).	8	ATGGCCATGCG	0.527	
+	10	7466	g.2_Missense_Mu	NM_015120	NP_055935	Q8TCU4	ALMS1_HUMAN		9	TGTTTCACCCA	0.448	
+	12	1129	.R335*|EPB41L5_	NM_020909	NP_065960	Q9HCM4	E41L5_HUMAN		1	TCTCATCGATCA	0.378	
+	6	1253	flu.2_Missense_	NM_130773	NP_570129	Q8WYK1	CNTP5_HUMAN	1.|Extracellular (Potential).	10	AGGGCGAGACG	0.562	
-	17	2633		NM_001099771	NP_001093241	A5A3E0	POTEF_HUMAN	Actin-like.	5	GCCCCCCATCA	0.622	
-	1	1637		NR_002826					0	CAGCTCCGGGA	0.642	
-	73	12143		NM_018557	NP_061027	Q9NZR2	LRP1B_HUMAN	ntial).|LDL-receptor class A	50	TTATTTCTGCATC	0.383	
+	9	1760	.2_Missense_Mut	NM_018328	NP_060798	Q9P267	MBD5_HUMAN		5	GTTTTCATGGA	0.448	
-	123	17284	.G2121E|NEB_uc	NM_004543	NP_004534	P20929	NEBU_HUMAN		20	GATTTTCCTTTC	0.403	
+	3	1180	J3_uc010zce.1_3'	NM_002239	NP_002230	P48549	IRK3_HUMAN	smic (By similarity).	2	TTTTTTCCTGTA	0.388	
-	22	4263	uc002udp.2_Intro	NM_002977	NP_002968	Q15858	SCN9A_HUMAN	III.	13	GGAAGGAATTG	0.353	
-	309	99378	lissense_Mutation_	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	ACCTTCGTTTAT	0.418	
-	292	87727	63E|TTN_uc010z	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	CTCCTCCGTCT	0.527	
-	275	74985	16A|TTN_uc010z	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	CCCATGTTACTA	0.483	
-	181	35412	.1_Missense_Mut	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN	p.E5233K(1)	153	CATATTCGCCTT	0.428	
-	42	10036	_uc010zfj.1_Miss	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	ACCAGGAAATT	0.527	
-	13	2269	1_Missense_Muta	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	TCTTGTCTAGTA	0.368	
+	7	2914	p.Q934L|SGOL2_	NM_152524	NP_689737	Q562F6	SGOL2_HUMAN		4	TGTCCAAGAAA	0.279	
+	3	646	D28_uc010ftx.2_M	NM_006139	NP_006130	P10747	CD28_HUMAN	ellular (Potential).	0	TTTGTCCAAGT	0.438	
-	2	300		NM_006891	NP_008822	P07320	CRGD_HUMAN	crystallin 'Greek key' 2.	0	ATAGTCGCCGC	0.657	
+	13	1433	_Mutation_p.S44	NM_001875	NP_001866	P31327	CPSM_HUMAN		13	TCTGTCCATTG	0.373	

+	11	1230	_p.Q78K|VIL1_uc	NM_007127	NP_009058	P09327	VILI_HUMAN	Core.	1	GCTGCCCAGCAG	0.567	
-	11	4921	e_Mutation_p.R15	NM_001142644	NP_001136116	Q2M3C7	SPKAP_HUMAN		10	TGGCTCGGAGC	0.542	
+	12	1514	yc.2_Missense_Mu	NM_000751	NP_000742	Q07001	ACHD_HUMAN		3	TTTCCTGGGGAC	0.617	
+	9	1048	fye.1_Missense_M	NM_005199	NP_005190	P07510	ACHG_HUMAN	lasmic (Potential).	0	GAGGGGTCCGC	0.617	
+	2	256		NM_173821	NP_776182	Q14D33	CB085_HUMAN		1	GGACAGGGCCA	0.706	
-	7	1194	gj.2_Missense_M	NM_007050	NP_008981	O14522	PTPRT_HUMAN	tential).|Fibronectin type-III	20	ATGTGGGTCTCT	0.557	
-	2	861	hk.1_Missense_M	NM_021248	NP_067071	Q9UJ99	CAD22_HUMAN	r (Potential).|Cadherin 1.	5	GATGAACTCCG	0.632	
-	9					P56180	TPTE_HUMAN		5	ATTTTACCTAGCT	0.299	rs4041777
+	6	770	yxz.2_Missense_M	NM_007341	NP_031367	P55822	SH3BG_HUMAN	u-rich (acidic).	0	AAGATTCCTAGG	0.493	
-	25	4734	CAM_uc002yyr.1_	NM_001389	NP_001380	O60469	DSCAM_HUMAN	III 5.|Extracellular (Potentia	11	TGATTGGAAAAC	0.488	
+	9	1092	zbj.2_Missense_M	NM_018964	NP_061837	P57057	GLPT_HUMAN	ical; (Potential).	0	GCCTGGAGCCA	0.592	
-	1	469	.1_Intron|C21orf2	NM_198688	NP_941961	P60371	KR106_HUMAN	repeats of C-C-X(3).	0	GCAGGGGGAGG	0.602	
-	2	331	4R_uc002zru.2_5'	NM_023004	NP_075380	Q9BZR6	RTN4R_HUMAN	LRRNT.	0	CTGGGGGCAGC	0.667	
-	18	2565	B1_uc003afl.2_Mi	NM_001127	NP_001118	Q10567	AP1B1_HUMAN		2	GGCAGGGAGATC	0.657	
-	4	887	_p.S103F|LARGE_	NM_004737	NP_004728	O95461	LARGE_HUMAN	nenal (Potential).	3	TCCATGGAGTAG	0.672	
-	6	1043	ssense_Mutation_	NR_002570					0	GTGGTCAAGGTG	0.627	rs1800754
-	31	4207		NM_024923	NP_079199	Q8TEM1	PO210_HUMAN	nenal (Probable).	11	GGTAGGAAACA	0.572	rs147706980
+	1	2110	k.1_Missense_Mu	NM_152536	NP_689749	Q6ZNL6	FGD5_HUMAN		5	CGGAGAACAAAT	0.517	
-	5	1039	p.V170A|UBP1_uc	NM_014517	NP_055332	Q9NZI7	UBIP1_HUMAN		2	AATTCAACCGCA	0.358	
-	12	4842		NM_014831	NP_055646	O15050	TRNK1_HUMAN		2	CCATTTCCTTCTC	0.493	
-	13	1066	2_uc003cgr.2_Intr	NM_006309	NP_006300	Q9Y608	LRRF2_HUMAN	-binding.|Ser-rich.	1	GACCATAAGGGT	0.358	
-	11	1388	lx.2_Missense_Mu	NM_020707	NP_065758	Q9HCP6	HHATL_HUMAN		3	TCAATTCGTGCT	0.577	
-	3	478	DA_uc010hku.2_5'	NM_001664	NP_001655	P61586	RHOA_HUMAN		2	TCAGGCGATCAT	0.493	
+	19	2720	_p.M853L|CACNA	NM_001128840	NP_001122312	Q01668	CAC1D_HUMAN	lasmic (Potential).	11	TTGAACATGAAG	0.428	rs138798164
+	1	189	rf26_uc003dtk.1_	NM_032359	NP_115735	Q9BQ75	CC026_HUMAN		1	CGACTGGAGCA	0.662	
+	4	2336		NM_016298	NP_057382	Q9UH90	FBX40_HUMAN		5	ACGTCTCCTAAA	0.488	
+	1	226	bjn.1_Nonsense_	NM_021082	NP_066568	Q16348	S15A2_HUMAN		1	CACCTCGACCA	0.502	
-	6	784	fk.2_Missense_Mu	NM_005241	NP_005232	Q03112	EVI1_HUMAN	MAPK9, SMAD3 and proba	14	CCGACGAAGTG	0.552	
+	2	211	z.2_Missense_Mu	NM_003722	NP_003713	Q9H3D4	P63_HUMAN	cription activation.	12	CATGTCCCAGA	0.373	
+	4	1205	P366L|TACC3_uc	NM_006342	NP_006333	Q9Y6A5	TACC3_HUMAN		2	GCCTCCCTTGA	0.602	
-	1	387	2A3_uc010ihp.1_	NM_024743	NP_079019	Q6UWM9	UD2A3_HUMAN	cellular (Potential).	2	AAAGTTCCTCTT	0.338	
+	2	689		NM_015393	NP_056208	Q6UWI2	PARM1_HUMAN	cellular (Potential).	1	TCATCTCCCCTC	0.572	
-	1	413		NM_032693	NP_116082	Q9BSU3	NAA11_HUMAN	cetyltransferase.	2	CTGGTCCATCAG	0.557	
+	5	966	n_p.L78F|ARHGA	NM_001025616	NP_001020787	Q8N264	RHG24_HUMAN	Rho-GAP.	0	GAGGGTCTCTTT	0.488	
+	7	978		NM_004967	NP_004958	P21815	SIAL_HUMAN		0	GCCTATGAAGAT	0.478	
+	2	687	190A_uc010ikv.2_	NM_001145065	NP_001138537	Q9C0I3	F190A_HUMAN		2	GACATTCTGTTG	0.368	
-	2	183	R38C|ADH1A_uc	NM_000667	NP_000658	P07327	ADH1A_HUMAN		2	TAATACGAACTTC	0.348	
-	7	582		NM_000669	NP_000660	P00326	ADH1G_HUMAN		0	CCAGGGGCGAG	0.522	
+	9	10628	p.P1841L|FAT4_u	NM_024582	NP_078858	Q6V0I7	FAT4_HUMAN	|Extracellular (Potential).	18	AAGGTCCCTTTA	0.498	
-	1	2501	.1_Intron|PCDH18	NM_019035	NP_061908	Q9HCL0	PCD18_HUMAN	ical; (Potential).	5	CCTAAGGAAATA	0.423	
-	7	1247	p.R258K|LRBA_u	NM_006726	NP_006717	P50851	LRBA_HUMAN		7	CTGGTTCTGAAA	0.323	
-	15	2172	p.G578V|FSTL5_u	NM_020116	NP_064501	Q8N475	FSTL5_HUMAN		8	ACATTCCCACTG	0.413	
-	6	1287	3iqr.1_Missense_M	NM_017923	NP_060393	Q8TCQ1	MARH1_HUMAN	ING-CH-type.	2	CAAAGCGCAGTG	0.527	rs146337383
+	8	688	irn.2_Nonsense_M	NM_007193	NP_009124	Q9UJ72	ANX10_HUMAN	Annexin 3.	0	CCTATGGGAAGC	0.502	
+	12	2015	kb.1_Missense_M	NM_017423	NP_059119	Q86SF2	GALT7_HUMAN	ectin.|Lumenal (Potential).	1	CAGTAAAACGAC	0.363	
+	12	1865	_p.L330S|SNX25_	NM_031953	NP_114159	Q9H3E2	SNX25_HUMAN	PX.	5	GAATTTACACC	0.403	
-	10	1686		NM_003966	NP_003957	Q13591	SEM5A_HUMAN	tracellular (Potential).	2	ATGGCGCTCAGG	0.602	

-	2	198	z.1_5'UTR|CTNN	NM_001332	NP_001323	Q9UQB3	CTND2_HUMAN		8	GGTCTGGAACA	0.493	
-	62	10543	H5_uc003jfc.2_5'	NM_001369	NP_001360	Q8TE73	DYH5_HUMAN		31	ATCTTTCTTTTTC	0.413	
-	40	6625		NM_001369	NP_001360	Q8TE73	DYH5_HUMAN		31	CCTCATCAATCT	0.373	
-	7	1557	p.E394K|CDH18_	NM_004934	NP_004925	Q13634	CAD18_HUMAN	(Potential).|Cadherin 4.	7	CATTTTCGTAGA	0.433	
+	12	1107	_p.S233L|RAI14_	NM_015577	NP_056392	Q9P0K7	RAI14_HUMAN		1	AGGAATCGGTAT	0.313	
-	4	542	GT3A1_uc011cor.	NM_152404	NP_689617	Q6NUS8	UD3A1_HUMAN	ellular (Potential).	3	TTATATCCTTTCT	0.303	
+	10	1905	_p.R370C|SLC1A3	NM_004172	NP_004163	P43003	EAA1_HUMAN		0	GGGATCGCCTC	0.547	
+	2	293		NM_138453	NP_612462	Q96E17	RAB3C_HUMAN	region (By similarity).	2	GGATCGATTTC	0.408	
-	22	3708	o.2_RNA|ADAMT	NM_197941	NP_922932	Q9UKP5	ATS6_HUMAN	SP type-1 4.	0	CCAAAGCCACC	0.453	
+	20	4120	98_uc003kjt.2_5'	NM_032119	NP_115495	Q8WXG9	GPR98_HUMAN	ellular (Potential).	16	GTTAATCCAAAA	0.463	
-	1	511	C_uc003kql.3_Int	NM_032028	NP_114417	Q9BXA7	TSSK1_HUMAN	rotein kinase.	5	CAGGGCTCCCC	0.557	
+	5	1117	TS19_uc003kvc.1	NM_133638	NP_598377	Q8TE59	ATS19_HUMAN	ptidase M12B.	9	AATCTTCGTGTG	0.294	
-	5	712		NM_015082	NP_055897	Q6MZW2	FSTL4_HUMAN		2	TGTCTCCTTCTT	0.577	
-	6	1192	loh.3_Missense_	NM_004576	NP_004567	Q00005	2ABB_HUMAN	WD 4.	2	CACCTCCGTGA	0.562	
-	9	1051	oo.2_Missense_M	NM_001387	NP_001378	Q14195	DPYL3_HUMAN		1	AGTCCGGAGTA	0.567	
+	4	588	A6_uc003lyv.2_5'	NM_000811	NP_000802	Q16445	GBRA6_HUMAN	ellular (Probable).	12	TTTTCCGCCAG	0.408	
+	15	2754	lzt.3_Splice_Site_	NM_001122679	NP_001116151				10	TTCTCAGCTTGG	0.507	
+	2	250	tion_p.P62L|MIR1	NM_173664	NP_775935	Q8N8L6	ARL10_HUMAN		1	GCAGCCCGAGG	0.701	
-	12	1673	9_splice|RASGEF	NM_175062	NP_778232	Q8N431	RGF1C_HUMAN		1	ACTCACCTTAG	0.507	
-	7	998	A|MAK_uc010jou.	NM_005906	NP_005897	P20794	MAK_HUMAN	rotein kinase.	3	GAATAGCTTCAT	0.428	
-	4	4456_4457		NM_052923	NP_443155	Q6R2W3	SCND3_HUMAN		1	agagaatccggtctca	0	rs140560647
-	4	3499		NM_052923	NP_443155	Q6R2W3	SCND3_HUMAN		1	atttaaattccaaaccac	0	
+	1	600		NM_030905	NP_112167	O76002	OR2J2_HUMAN	ellular (Potential).	0	TTCTGGGTACC	0.478	
+	9	1269	_Missense_Mutat	NM_013993	NP_054699	Q08345	DDR1_HUMAN	ellular (Potential).	9	AGTGCCCCTTG	0.667	
-	22	7854		NM_019105	NP_061978	P22105	TENX_HUMAN	nectin type-III 18.	0	TGAAGGAGTCA	0.692	
+	2	409	3obi.2_Splice_Sit	NM_019111	NP_061984	P01903	DRA_HUMAN		2	AATGGTACCTC	0.463	
-	52	4075	se_Mutation_p.P1	NM_080680	NP_542411	P13942	COBA2_HUMAN	e-helical region.	5	CCGAGGGCCAC	0.602	
-	7	1749	b.2_Missense_Mu	NM_001142883	NP_001136355	Q96PC2	IP6K3_HUMAN		0	GATATCCTGCA	0.478	
+	11	1235	h.2_RNA|GLP1R_	NM_002062	NP_002053	P43220	GLP1R_HUMAN	Name=7; (Potential).	5	CACCTCCTTCC	0.527	
+	2	241	ML4_uc003oqd.2_	NM_198153	NP_937796	Q6UXN2	TRML4_HUMAN	g-like V-type.	1	CAAGAGAGGGC	0.537	
+	1	3325	e.2_Nonsense_M	NM_001010870	NP_001010870	O60522	TDRD6_HUMAN		6	TACCAGAAGAA	0.373	
+	6	1150	_p.L355V|GPR115	NM_153838	NP_722580	Q8IZF3	GP115_HUMAN	ellular (Potential).	8	CAACCTTGGGG	0.473	
+	2	268		NM_001010872	NP_001010872	Q5T0W9	FA83B_HUMAN		6	GGAACGAGTTT	0.383	
+	2	237		NM_207410	NP_997293	Q6UXV0	GFRAL_HUMAN	ellular (Potential).	2	TGCAATGATTCA	0.318	
+	4	1963	dxm.1_Missense_	NM_020931	NP_065982	Q9HCI6	K1586_HUMAN		0	ATAAATTTAATGC	0.264	
-	27	1961	_p.G174E|COL9A1	NM_001851	NP_001842	P20849	CO9A1_HUMAN	lical region (COL2).	4	AATTTCCCATC	0.423	
-	11	1175	OL9A1_uc003pff.	NM_001851	NP_001842	P20849	CO9A1_HUMAN	lical region (COL3).	4	CCTTTGACCCA	0.388	
+	34	5092	gg.2_Missense_	NM_014989	NP_055804	Q86UR5	RIMS1_HUMAN		10	TCCCCTCACCC	0.512	
-	1	86	1A1_uc003phh.2_	NM_001402	NP_001393	P68104	EF1A1_HUMAN	(By similarity).	0	CGAATCTACGT	0.423	
-	2	3738	_p.Q59*|CNR1_u	NM_001160260	NP_001153732	P21554	CNR1_HUMAN	ellular (Potential).	2	CTCTTGGAAGG	0.453	
-	5	940	qi.1_Missense_M	NM_001040179	NP_001035269	Q969V1	MCHR2_HUMAN	Name=5; (Potential).	8	TAGAGGGAAAA	0.279	
+	18	2506		NM_173560	NP_775831	Q8HWS3	RFX6_HUMAN		3	GGCTCGGATCA	0.428	
-	9	2354		NM_001042475	NP_001035940	Q5SZL2	CF204_HUMAN	Potential.	1	AGGCATCTTTCT	0.323	
+	4	837	as.1_Missense_M	NM_032784	NP_116173	Q9BXY4	RSPO3_HUMAN	TSP type-1.	0	AGCATCCTTCA	0.453	
-	12	2397	u.1_Missense_M	NM_002844	NP_002835	Q15262	PTPRK_HUMAN	tential).|Fibronectin type-III	8	GGTTTCCCGGG	0.542	
+	19	2044	qbu.2_Missense_	NM_032438	NP_115814	Q96JM7	LMBL3_HUMAN		6	CTTCTTCCCCTG	0.348	
-	13	1756	p.R477K|SAMD3_	NM_001017373	NP_001017373	Q8N6K7	SAMD3_HUMAN		1	TCAATCCTAAAT	0.413	

-	7	1084	kgh.2_Missense_	NM_022568	NP_072090	Q9H2A2	AL8A1_HUMAN		4	GAGCTCTCTTG	0.463	
+	6	1352	qe.2_Missense_M	NM_012454	NP_036586	Q8IVF5	TIAM2_HUMAN		4	AAATTCCTTGC	0.433	
+	18	4911	.E1547K|ARID1B_	NM_017519	NP_059989	Q8NFD5	ARI1B_HUMAN	Pro-rich.	2	GAAGGGAGATC	0.512	
+	34	5543		NM_001040001	NP_001035090	P55196	AFAD_HUMAN		5	TGACATTCAAG	0.418	
-	41	5823	km.1_Missense_M	NM_001080453	NP_001073922	Q8N201	INT1_HUMAN		0	CAGGAAGCAGC	0.682	
+	20	3092	o.2_Missense_Mu	NM_152744	NP_689957	Q7Z5N4	SDK1_HUMAN	nectin type-III 4.	6	ATCTTGGACACA	0.423	
+	8	911	e.1_Missense_Mu	NM_031414	NP_113602	Q9BXU1	STK31_HUMAN		9	ATAGGGAAAGTT	0.323	
-	2	904	A3_uc003syk.2_5'	NM_002141	NP_002132	Q00056	HXA4_HUMAN		1	AGGCCGAATTG	0.398	
+	4	871	_p.S89F|HECW1_	NM_015052	NP_055867	Q76N89	HECW1_HUMAN		23	CTATTCCATCGG	0.592	
-	5	569	_p.P126L|VOPP1	NM_030796	NP_110423	Q96AW1	VOPP1_HUMAN	ytoplasmic (Potential).	0	CGACAGGGTTC	0.632	
+	5	1216		NM_153363	NP_699194	Q8IYX0	ZN679_HUMAN	2H2-type 6.	1	CAAGAGAATTC	0.408	
+	11	1750	tvz.2_Missense_	NM_022479	NP_071924	Q6IS24	GLTL3_HUMAN	ctin.|Lumenal (Potential).	7	TCCTCCGCAGC	0.627	
-	7	12903	p.P4205L|PCLO_u	NM_033026	NP_149015	Q9Y6V0	PCLO_HUMAN		7	TGAATAGGTGAA	0.383	
+	2	1152	.G16E|GRM3_uc	NM_000840	NP_000831	Q14832	GRM3_HUMAN		13	AAAGGGATTTT	0.398	
-	3	1046	TEAP4_uc003ujt.2_	NM_024636	NP_078912	Q687X5	STEA4_HUMAN	oxidoreductase.	0	TAATATCGAATAG	0.428	
+	12	1524	_p.C379Y|DYNC1	NM_004411	NP_004402	O14576	DC1I1_HUMAN	WD 3.	4	AATGTGTTCCT	0.433	
-	2	346		NM_018842	NP_061330	Q9UHR4	BI2L1_HUMAN	IMD.	1	AATTTCGCAGCC	0.299	
-	1	493	_p.G113S|ACHE_	NM_000665	NP_000656	P22303	ACES_HUMAN		2	GGTGCCCTCAA	0.597	
+	6	853	R_uc011knq.1_5'	NM_000492	NP_000483	P13569	CFTR_HUMAN	tial).|ABC transmembrane	5	GGCTAGGGAG	0.433	
+	1	1022		NM_012281	NP_036413	Q9NZV8	KCND2_HUMAN	NIP2.|Cytoplasmic (Potent	5	GGGTGGATGCC	0.612	
-	1	638	PS2_uc010lkq.2_	NM_198085	NP_932351	Q8N7C7	RN148_HUMAN	PA.	0	ACATGGGAAATA	0.448	
-	8	686	GA14_uc003vqa.	NM_018718	NP_061188	Q9BYV8	CEP41_HUMAN	Rhodanese.	0	TACATATTCAAG	0.368	
+	17	3000	ub.2_Missense_M	NM_015905	NP_056989	O15164	TIF1A_HUMAN		8	CTGTTCCTCTA	0.323	
-	15	1860		NM_004333	NP_004324	P15056	BRAF_HUMAN	rotein kinas_R603>I(2)|p.T	18290	ATTTCACTGTA	0.368	
-	1	719		NM_176817	NP_789787	P59533	T2R38_HUMAN	lasmic (Potential).	2	CAGAAGAAACC	0.458	
-	4	617	TRPV6_uc010lou.	NM_018646	NP_061116	Q9H1D0	TRPV6_HUMAN	ytoplasmic (Potential).	2	GGGCTCGCACC	0.572	rs150734746
-	7	1114	bz.2_Missense_M	NM_019841	NP_062815	Q9NQA5	TRPV5_HUMAN	lasmic (Potential).	6	GGAGTCGATCT	0.557	
+	5	682	LCN1_uc010lox.1	NM_000083	NP_000074	P35523	CLCN1_HUMAN		5	TACTTCGTGGG	0.507	rs143506735
+	1	840		NM_012369	NP_036501	Q13607	OR2F1_HUMAN	ellular (Potential).	3	CCAGTCCCTCT	0.478	
+	3	4687	_p.E157K|ABP1_u	NM_001091	NP_001082	P19801	ABP1_HUMAN		6	TGCAGGAAGCC	0.602	
-	4	690	ense_Mutation_p.	NM_173833	NP_776194	Q6ZMJ2	SCAR5_HUMAN	ellular (Potential).	2	GCGCGGCCTGG	0.577	
-	7	854		NM_000637	NP_000628	P00390	GSHR_HUMAN		5	CTTAGAACCCA	0.413	
+	7	762	2_uc010lwz.1_Intr	NM_194294	NP_919270	Q6ZQW0	I23O2_HUMAN		2	CTGGGGGAGAG	0.478	
-	17	2585	NL_uc003xqt.3_	NM_144651	NP_653252	A1KZ92	PXDNL_HUMAN		2	CGCCCATCCGA	0.662	
-	5	541		NM_144651	NP_653252	A1KZ92	PXDNL_HUMAN	LRR 5.	2	TCTAATCTCAGA	0.433	
+	4	1274	1_uc011ldy.1_Intr	NM_006269	NP_006260	P56715	RP1_HUMAN		12	AAAGTCGATCA	0.408	
+	4	2679	1_uc011ldy.1_Intr	NM_006269	NP_006260	P56715	RP1_HUMAN		12	TGGCATCTGGGT	0.333	
+	10	1775	nse_Mutation_p.	NM_184085	NP_908973	Q9BYV6	TRI55_HUMAN		5	CCCTCCAGGGA	0.468	
-	4	588	A6_uc003xxs.2_	NM_020361	NP_065094	Q8N4T0	CBPA6_HUMAN		2	TGAAGATCTTCT	0.383	
+	2	620		NM_004770	NP_004761	Q92953	KCNB2_HUMAN	lasmic (Potential).	7	TAAACAGGAAGA	0.507	
+	1	339		NM_003301	NP_003292	P34981	TRFR_HUMAN	Name=3; (Potential).	3	ATTTGGGAATTA	0.463	
+	46	7005		NM_177531	NP_803875	Q86WI1	PKHL1_HUMAN	ular (Potential).|G8 1.	14	GGACTCGCTTG	0.383	rs73309320
-	48	7683	.E2468D|CSMD3_	NM_198123	NP_937756	Q7Z407	CSMD3_HUMAN	xtracellular (Potential).	63	ATCAAATTCCTT	0.328	
-	38	6280	nt.2_Missense_M	NM_198123	NP_937756	Q7Z407	CSMD3_HUMAN	ar (Potential).|CUB 11.	63	AAGATGAAATCC	0.274	
+	22	3001	uc003yqy.1_Intron	NM_001039112	NP_001034201	Q2WGJ9	FR1L6_HUMAN	lasmic (Potential).	11	TGAGCCCCCCA	0.488	
-	61	4742	ljo.1_Missense_M	NM_152888	NP_690848	Q8NFW1	COMA1_HUMAN	y-rich.|Collagen-like 14.	13	GTAGTCCTTGG	0.602	
-	40	5798	.G1289E|PTPRD_	NM_002839	NP_002830	P23468	PTPRD_HUMAN	).|Tyrosine-protein phosph	22	TCAGATCCTTCT	0.388	

-	2	384	KN2A_uc010miu.	NM_000077	NP_000068	P42771	CD2A1_HUMAN	ANK 2.	)|p.V28_V51de	3678	CACTCGGGCGC	0.677	rs121913387
-	1	2639	c003zrh.1_5'Flan	NM_153809	NP_722516	Q8IZX4	TAF1L_HUMAN			26	GCTTTTTTTATAT	0.453	
-	1	637		NM_019897	NP_063950	Q9NQN1	OR2S1_HUMAN	ellular (Potential).		1	TGATGGAAATG	0.473	
+	2	121_122	aah.1_Missense_	NM_014907	NP_055722	Q5SYB0	FRPD1_HUMAN			9	CTTCGGCGCTC	0.525	rs146611803
-	4	1896		NM_001145196	NP_001138668	Q5VVP1	F75A6_HUMAN			0	GTCCCGAAGCT	0.542	rs138779714
+	21	2415	kq.3_Missense_	NM_033305	NP_150648	Q96RL7	VP13A_HUMAN			10	AGCTGCTTTAC	0.323	
-	6	679	wo.1_Missense_	NM_014930	NP_055745	Q9Y2H8	ZN510_HUMAN			0	AGCTACATGCA	0.333	
-	1	208		NM_001001956	NP_001001956	Q8NGT0	O13C9_HUMAN	Name=2; (Potential).		0	GATGTCCAAGA	0.478	
+	2	193	TGS1_uc004bmf.	NM_000962	NP_000953	P23219	PGH1_HUMAN			2	CGCTCCCCGTC	0.672	
+	27	2939	wu.2_Nonsense_	NM_015354	NP_056169	Q5SRE5	NU188_HUMAN			7	AAGATCGATAC	0.547	
+	15	3182	p.P626S|BAT2L1_	NM_013318	NP_037450	Q5JSZ5	PRC2B_HUMAN			0	TTCCCCCCATG	0.562	
-	3	436		NM_006753	NP_006744	O75683	SURF6_HUMAN			1	CAGTCGCTGTC	0.632	
-	2	240	10_uc011mee.1_Missense_Mutation_p.D61N|LCN10_			Q6JVE6	LCN10_HUMAN			1	CTTGTCCCTGG	0.647	
-	5	3009		NM_015419	NP_056234	Q9NR99	MXRA5_HUMAN			8	GTGACGATCCA	0.502	
+	2	115	Intron|ARHGAP6_	NM_001142	NP_001133	Q99217	AMELX_HUMAN			0	TTTTGCCATGC	0.403	
-	5	1109	se_Mutation_p.P1	NM_002641	NP_002632	P37287	PIGA_HUMAN	lasmic (Potential).		0	CTCAGGAATTC	0.373	
+	5	825	PS2_uc010nfr.2_5	NM_206923	NP_996806	O15391	TYY2_HUMAN			2	CATTTGCAACTT	0.343	
+	2	692		NM_173699	NP_775970	Q96M61	MAGBI_HUMAN	MAGE.		1	TGGATCCCATC	0.438	
+	1	277		NM_000531	NP_000522	P00480	OTC_HUMAN			2	TTCATGGTTCG	0.383	
-	4	568	rf38_uc004dev.1_	NM_144970	NP_659407	Q8TB03	CX038_HUMAN			1	TCAGAAAATTTT	0.358	
-	10	1213	TMR8_uc004dvt.	NM_017677	NP_060147	Q96EF0	MTMR8_HUMAN	ularin phosphatase.		4	TTTGGGAAAAC	0.343	
+	4	928	p.P229H|EDA_uc	NM_001399	NP_001390	Q92838	EDA_HUMAN	(Potential).|Collagen-like.		3	ACCCCCTGGCC	0.453	
-	3	4825		NM_001008537	NP_001008537	Q5QGS0	K2022_HUMAN			15	GTTTTCCCATTG	0.453	
+	2	512		NM_005296	NP_005287	Q99677	LPAR4_HUMAN	ellular (Potential).		3	ATGATTCCTTCA	0.403	
+	5	352	OL_uc010nmp.2_	NM_198450	NP_940852	Q6UXV4	APOOL_HUMAN			0	TCTTCCGAAAAT	0.338	
+	6	1339	fa.2_Missense_M	NM_019117	NP_061990	Q9C0H6	KLHL4_HUMAN			5	TGAAACCAGTT	0.378	
+	13	2432	mj.3_Missense_M	NM_018015	NP_060485	Q6NSI4	CX057_HUMAN			3	ACCATGAGATA	0.269	
-	2	439		NM_031273	NP_112563	Q9BXU2	TX13B_HUMAN			1	CTGTTCCTTGA	0.567	
-	11	2623		NM_020721	NP_065772	Q9ULL0	K1210_HUMAN			5	TCTGAGAGGCA	0.453	
-	2	438	e.3_Missense_M	NM_001421	NP_001412	Q99607	ELF4_HUMAN			1	CCATCCCGTTG	0.527	
-	5	737	f.2_Missense_Mu	NM_001555	NP_001546	Q8N6C5	IGSF1_HUMAN	2.|Extracellular (Potential).		5	CATATCCCTCTT	0.502	
+	4	1601	EC1_uc010nsl.1_	NM_005462	NP_005453	O60732	MAGC1_HUMAN			4	GTTTTCCCCAG	0.458	
+	15	1663	R1_uc004fcl.3_M	NM_002024	NP_002015	Q06787	FMR1_HUMAN	tion with RANBP9.		3	ATAGGAACTAAT	0.388	
+	3	739	_p.Q195*|MAGEA	NM_002362	NP_002353	P43358	MAGA4_HUMAN	MAGE.		3	AATAATCAGATC	0.547	
-	3	993		NM_005362	NP_005353	P43357	MAGA3_HUMAN	MAGE.		0	GCCGGGGACCT	0.527	
+	26	4744		NM_017514	NP_059984	P51805	PLXA3_HUMAN	lasmic (Potential).		3	GCGTCCCAAAG	0.607	
-	18	6092	1_Missense_Muta	NM_000132	NP_000123	P00451	FA8_HUMAN	3.|Plastocyanin-like 6.		11	TGAATAGAATGG	0.403	
-	6	1023	_p.P286L|TMLHE_	NM_018196	NP_060666	Q9NVH6	TMLH_HUMAN			1	CCTCAGGTGCC	0.418	
-	19	1803	p.R307C|ACAP3_	NM_030649	NP_085152	Q96P50	ACAP3_HUMAN			0	TCGGCGGAACT	0.667	
-	4	496	K4_uc010nza.1_I	NM_018216	NP_060686	Q9NVE7	PANK4_HUMAN			3	ATGGGGGATGT	0.532	
+	9	1355	p.D383N|PIK3CD_	NM_005026	NP_005017	O00329	PK3CD_HUMAN			7	TCTGCGACCTG	0.617	rs149331749
+	21	3619	E4B_uc010oaj.1_	NM_001105562	NP_001099032	O95155	UBE4B_HUMAN			4	ACCTTCCCTGA	0.458	
-	4	1248		NM_001146344	NP_001139816	O60813	PRA11_HUMAN	LRR 6.		0	CCATGCAGATG	0.532	rs143004725
+	4	966		NM_001012276	NP_001012276	Q5VWM4	PRAM8_HUMAN			0	CCTTGGAGATG	0.552	
+	5	805	M1_uc001axg.1_	NM_017556	NP_060026	Q8WUP2	FBLI1_HUMAN	Pro-rich.		1	GGAGGCTCCTG	0.667	
-	8	949	1_Intron|MST1P9_	NR_002729						0	GTTCCAGCAGA	0.662	rs1806514
+	3	519	_p.L63P|PIGV_u	NM_017837	NP_060307	Q9NUD9	PIGV_HUMAN	enal (Potential).		1	CGGCCTGTCTC	0.552	

+	6	682	_p.A160V|SYTL1_	NM_032872	NP_116261	Q8IYJ3	SYTL1_HUMAN			1	GGAGGCGTCCC	0.612	
+	1	4075	.1_Intron|MACF1_	NM_015038	NP_055853	O94854	K0754_HUMAN	Ala-rich.|8.		0	AGCCCACCTCC	0.726	rs783822
-	7	1547	.2_Intron|PPIE_uc	NM_001720	NP_001711	P34820	BMP8B_HUMAN			0	GCGGTGCTTGC	0.632	
+	7	884	ki.1_Missense_M	NM_014663	NP_055478	O75164	KDM4A_HUMAN	JmjC.		1	TCCGCCACAAG	0.388	
+	3	765		NM_057176	NP_476517	Q8WZ55	BSND_HUMAN	lasmic (Potential).		2	GGGGAAAGACG	0.612	
-	9	1667	u.1_RNA|C1orf16	NM_001004303	NP_001004303	Q5VWT5	CA168_HUMAN			5	TCATCTGAATTT	0.458	
-	3	429	_p.R59Q|C8B_uc	NM_000066	NP_000057	P07358	CO8B_HUMAN	receptor class A.		4	TCACATCGCACT	0.483	
-	10	1481	73_uc001dgi.3_Mi	NM_001002912	NP_001002912	Q5RHP9	CA173_HUMAN	Glu-rich.		5	TCCTCTCCTTTC	0.413	
+	6	1139	HN2_uc001div.2_	NM_012302	NP_036434	O95490	LPHN2_HUMAN	otential).|Olfactomedin-like		9	GCGGAGTCCTC	0.393	
-	10	1919	_p.P443S|TGFBR	NM_003243	NP_003234	Q03167	TGBR3_HUMAN	acellular (Potential).		3	GGTAGGATCCA	0.537	
+	6	428	DC76_uc009wea	NM_019083	NP_061956	Q9NUP7	TRM13_HUMAN	Potential.		1	TCTACACTTAAA	0.373	
-	36	3107	_p.P942L|COL11A	NM_001854	NP_001845	P12107	COBA1_HUMAN	le-helical region.		12	GTCCAGGGAAT	0.388	
+	10	5328		NM_001408	NP_001399	Q9HCU4	CELR2_HUMAN	otential).|Laminin G-like 2.		8	GGCCCGTGGCT	0.672	rs142723500
+	21	3815	.1_3'UTR|MAGI3_	NM_001142782	NP_001136254	Q5TCQ9	MAGI3_HUMAN			6	AAGTAGAAAATG	0.408	
-	3	435		NM_002524	NP_002515	P01111	RASN_HUMAN	GTP.	)|p.Q61P(21)|	2607	TTCTTGTCCAG	0.458	rs121913254
-	3	460		NM_152380	NP_689593	Q96SF7	TBX15_HUMAN	T-box.		2	ATGTGGATCTA	0.443	
-	5	1313		NM_001047980	NP_001041445	P0C2Y1	NBPF7_HUMAN	NBPF 1.		2	TTTGAATAAGTG	0.468	
-	1	80	2AC_uc001etd.2_	NM_003528	NP_003519	Q16778	H2B2E_HUMAN			1	AGCCCTTTTTA	0.537	
-	3	883		NM_016190	NP_057274	Q9UBG3	CRNN_HUMAN	Gln-rich.		3	CGTGGGTCTCA	0.612	rs3814301
-	3	862		NM_016190	NP_057274	Q9UBG3	CRNN_HUMAN	Gln-rich.		3	TCTGGTCATTG	0.602	
-	7	1015	_p.T175A|C1orf43	NM_001098616	NP_001092086	Q9BWL3	CA043_HUMAN			0	ACTGAGTTAGGT	0.507	
-	7	1100	|CLK2_uc001fjx.2_	NM_003993	NP_003984	P49760	CLK2_HUMAN	rotein kinase.		0	AAGGCCATGTG	0.567	
+	6	1992	ion_p.P119L|RUS	NM_001105203	NP_001098673	Q9BVN2	RUSC1_HUMAN	RUN.		2	AGCCCCGCTGA	0.642	
+	1	274		NM_001231	NP_001222	P31415	CASQ1_HUMAN			1	AGACAGGATGG	0.632	
-	4	314		NM_001013625	NP_001013647	Q5VTH2	CA192_HUMAN			0	CCTTGAGTAAA	0.478	
+	5	1928		NM_001080426	NP_001073895	Q5VZP5	DUS27_HUMAN			3	GTCTATGGCAA	0.642	
+	6	918		NM_018122	NP_060592	Q6PI48	SYDM_HUMAN			2	CTCTTCGGTTG	0.323	
+	2	123		NM_020950	NP_066001	Q5VZ46	K1614_HUMAN			4	AGGGCCCAAGA	0.612	
+	46	6392	.S1964F|CACNA	NM_000721	NP_000712	Q15878	CAC1E_HUMAN	lasmic (Potential).		6	TCAATCCAGGT	0.587	
-	32	4698	zl.1_Missense_Mu	NM_017596	NP_060066	O75037	KI21B_HUMAN	WD 4.		6	GGTGACCGTCA	0.622	
+	13	1162	.2_RNA|LGR6_u	NM_001017403	NP_001017403	Q9HBX8	LGR6_HUMAN	xtracellular (	p.E388K(1)	10	TCTGGGAAATT	0.647	rs143455603
-	4	839	z.2_Missense_Mu	NM_002644	NP_002635	P01833	PIGR_HUMAN	2.|Extracellular (Potential).		3	GCAGAGATACT	0.502	
-	10	1627		NM_018040	NP_060510	Q9NW75	GPTC2_HUMAN	G-patch.		1	TAGAGGAAATC	0.473	
-	4	796	w.1_Missense_Mu	NM_003268	NP_003259	O60602	TLR5_HUMAN	lar (Potential).|LRR 2.		4	ACAGTCCCTGA	0.403	
-	16	2384		NM_001618	NP_001609	P09874	PARP1_HUMAN	P alpha-helical.		10	TCAGGGTGTAA	0.562	
-	14	1632	13_uc001hug.3_	NM_024525	NP_078801	Q8NBP0	TTC13_HUMAN			2	ATGCGGCCAAA	0.468	
+	5	1075	hvy.1_Missense_	NM_173508	NP_775779	Q8IY50	S35F3_HUMAN	ical; (Potential).		2	TGCATTCCTATT	0.418	
-	9	2113	d.2_Missense_Mu	NM_002508	NP_002499	P14543	NID1_HUMAN	EGF-like 2.		2	GCAGGGATTCT	0.562	
+	36	4966		NM_001035	NP_001026	Q92736	RYR2_HUMAN	ilarity).|4 X approximate re		33	GCCAAGGCTGG	0.527	
+	3	235	_p.P33S|NLRP3_	NM_001079821	NP_001073289	Q96P20	NALP3_HUMAN	DAPIN.		26	ACTATCCTCCC	0.547	
+	1	481		NM_001001914	NP_001001914	Q8NGZ4	OR2G3_HUMAN	ellular (Potential).		1	ATGCAACTTTT	0.488	
+	1	788		NM_001005495	NP_001005495	Q8NH03	OR2T3_HUMAN	Name=6; (Potential).		1	TCTACACCTACAT	0.542	
-	7	2002		NM_018702	NP_061172	Q9NS39	RED2_HUMAN	to I editase.		3	GGACGCCGTCC	0.682	
+	12	1590	R1C3_uc001ihr.2	NM_001353	NP_001344	Q04828	AK1C1_HUMAN	P (By similarity).		2	CAAGCGAACCC	0.597	rs140396306
+	10	1991		NM_018706	NP_061176	Q96HY7	DHTK1_HUMAN			2	GTTTCTAGAGG	0.478	
-	14	1773		NM_001081	NP_001072	O60494	CUBN_HUMAN	CUB 1.		19	CCATTTCTTAAAT	0.403	
+	14	1925	NB2_uc001ipw.2_	NM_201596	NP_963890	Q08289	CACB2_HUMAN			3	GTGCAACAAGC	0.552	

+	11	1796	e_Mutation_p.E33	NM_032812	NP_116201	Q6UX71	PXDC2_HUMAN	ar (Potential).|Thr-rich.		4	CAGTGGAAACT	0.423	
+	7	794		NM_052997	NP_443723	Q9BXX3	AN30A_HUMAN			9	CTTGGCGGAAA	0.423	
+	3	1179		NM_199459	NP_955629	Q711Q0	CJ071_HUMAN			0	TCATGGAATGC	0.527	
-	3	455	s.2_Missense_Mu	NM_019893	NP_063946	Q9NR71	ASAH2_HUMAN	enal (Potential).		0	CTGTTCGATTG	0.473	
+	10	2170		NM_032199	NP_115575	Q14865	ARI5B_HUMAN			4	ACCCCCTTTGA	0.552	
+	2	1481	mx.3_Intron|CTN	NM_178011	NP_821079	Q86VH5	LRRT3_HUMAN	ellular (Potential).		3	CTTGCTGGGAAT	0.423	
+	6	1401		NM_000314	NP_000305	P60484	PTEN_HUMAN	hatase tensi	p.Y27_N212>	2334	ATTCACTGTAAA	0.408	rs121909223
+	5	1062	C19_uc009xus.1_	NM_000772	NP_000763	P33260	CP2CI_HUMAN			5	TATTGGAGAGA	0.338	
+	1	1222		NM_000684	NP_000675	P08588	ADRB1_HUMAN	smic (By similarity).		0	CTGCCGCAGCC	0.701	
+	2	417	42F|C10orf137_uc	NM_015608	NP_056423	Q3B7T1	EDRF1_HUMAN			10	TTATTTCTTGGA	0.388	
+	14	2283	u.3_Missense_Mu	NM_025092	NP_079368	Q32M88	ATHL1_HUMAN			3	GGGTTCCTCCA	0.612	
+	47	6781	b.2_Missense_Mu	NM_017511	NP_059981	Q9HC84	MUC5B_HUMAN	in repeats.|Cys-rich subdo		0	GAGGGGACGTT	0.602	
-	1	542		NM_001012708	NP_001012726	Q6L8H2	KRA53_HUMAN	repeats of C-C-X-P.		2	GGGAGCAGCTG	0.388	
+	1	370		NM_001001480	NP_001001480	Q701N2	KRA55_HUMAN	repeats of C-C-X-P.		1	TGGCTCCTGTG	0.697	
+	8	1186	p.R144G|KCNQ1_	NM_000218	NP_000209	P51787	KCNQ1_HUMAN	lasmic (Potential).		1	AGCAGAGGCAG	0.602	
+	2	246	8_uc001lwy.2_Nor	NM_183233	NP_899056	Q96BI1	S22AI_HUMAN			3	GGGACCAGGGC	0.652	
-	1	871		NM_001004758	NP_001004758	Q8NGJ8	O51S1_HUMAN	Name=7; (Potential).		4	TGGAGGAAGAA	0.448	
-	1	483_484		NM_001005329	NP_001005329	Q8NGJ6	O51A4_HUMAN	Name=4; (Potential).		3	AAAGGGAAGG	0.436	
-	1	329	_uc001mam.1_Int	NM_001005288	NP_001005288	Q9H343	O51I1_HUMAN	Name=3; (Potential).		1	TGAAGGAGAAA	0.443	
-	1	1304	2_uc001mak.1_Ir	NM_145053	NP_659490	Q8IYU4	UBQLN_HUMAN			3	TTTGAAGAGAAA	0.507	
-	1	344	.1_Intron|TRIM22_	NM_001001922	NP_001001922	Q8NH56	O52N5_HUMAN	Name=3; (Potential).		2	TGAACCCATGA	0.493	rs143745000
+	13	2012	hm.2_Missense_	NM_001142307	NP_001135779	P32780	TF2H1_HUMAN			0	GGGCACTTATG	0.463	
-	2	485	mri.1_Missense_	NM_030771	NP_110398	Q96HJ3	CCD34_HUMAN			0	CCCATGGTGTC	0.418	
+	2	146	rf74_uc001mwx.1_	NM_138787	NP_620142	Q86VG3	CK074_HUMAN			0	AAATTCCTTAATT	0.358	
-	4	1035		NM_003654	NP_003645	O43916	CHST1_HUMAN	enal (Potential).		5	GAGGTCGCGGC	0.662	
+	20	2395	k.1_Missense_Mu	NM_001105540	NP_001099010	Q13574	DGKZ_HUMAN			3	GACGTCGTTGG	0.657	
-	5	1046	.1_Intron|RAPSN_	NM_005055	NP_005046	Q13702	RAPSN_HUMAN	TPR 6.		1	GATCTCGGTCA	0.652	
+	1	986		NM_001004702	NP_001004702	Q8NH37	OR4C3_HUMAN	lasmic (Potential).		1	TTACATGGTAAG	0.328	
-	1	1122	NR_uc001njn.3_	NM_005161	NP_005152	P35414	APJ_HUMAN	lasmic (Potential).		6	TTGGGCGATGA	0.627	
+	1	586		NM_001004708	NP_001004708	Q8NGJ1	OR4D6_HUMAN	Name=5; (Potential).		1	CTTTGGAGCTT	0.527	
-	5	5458_1545	AK_uc001ntk.1_Ir	NM_001620	NP_001611	Q09666	AHNK_HUMAN			19	AGGCTGGCATC	0.441	
+	5	352	v.1_RNA|TSGA10	NM_152762	NP_689975	Q3SY00	T10IP_HUMAN			0	CTTCCCCTTCC	0.662	
-	1	2139		NM_020404	NP_065137	Q9HCU0	CD248_HUMAN	ical; (Potential).		3	GTACACGATGC	0.602	
-	3	566	HA3_uc010rrj.1_	NM_182904	NP_878907	Q7Z4N8	P4HA3_HUMAN			1	GAGCCGTTTGG	0.507	
+	8	637	09yuo.1_Nonsens	NM_018367	NP_060837	Q9NUN7	ACER3_HUMAN	ical; (Potential).		0	ATACATCATTGG	0.318	
+	2	113	n_p.E5D|C11orf6	NM_024684	NP_078960	Q9H7C9	CK067_HUMAN			0	CCTGAAATTGC	0.378	
-	17	2082	yp.2_Intron|INTS4_	NM_033547	NP_291025	Q96HW7	INT4_HUMAN			2	AATACAAAGGG	0.478	
-	22	3614		NM_001098816	NP_001092286	Q6N022	TEN4_HUMAN	ellular (Potential).		4	GATTTCCTCCT	0.582	
-	2	1005	p.T194A|TRPC6_	NM_004621	NP_004612	Q9Y210	TRPC6_HUMAN	lasmic (Potential).		4	GCTGGTTGCTA	0.463	
-	6	5135	z.1_Missense_Mu	NM_015065	NP_055880	Q8NEV8	EXPH5_HUMAN			5	CAGTAATGGGG	0.453	
-	9	937	P28_uc001poi.2_5	NM_020886	NP_065937	Q96RU2	UBP28_HUMAN			7	TTCACGAACCC	0.358	
+	3	556		NM_182495	NP_872301	Q96DL1	FA55B_HUMAN			1	GGCCAGGATGT	0.552	
-	7	1417	1pri.1_Missense_	NM_020693	NP_065744	Q8TD84	DSCL1_HUMAN	otential).|Ig-like C2-type 5.		8	AGGACGAGACG	0.682	
-	2	206	1prt.1_5'UTR|TM	NM_001077263	NP_001070731	Q9BYE2	TMPSD_HUMAN	epeats of A-S-P-A-[GLQR].		1	ATGCCTGGGCT	0.637	
-	2	203	1prt.1_5'UTR|TM	NM_001077263	NP_001070731	Q9BYE2	TMPSD_HUMAN	epeats of A-S-P-A-[GLQR].		1	CCTGGGCTGGA	0.632	
+	1	650		NM_001001965	NP_001001965	Q8NGN0	OR4D5_HUMAN	Name=5; (Potential).		1	GGGATCGTACA	0.517	rs138187932
+	10	1311	p.E368K|VWA5A_	NM_001130142	NP_001123614	O00534	VMA5A_HUMAN	VWFA.		2	GCACTGAAATC	0.522	

-	1	158		NM_012378	NP_036510	Q15620	OR8B8_HUMAN	lasmic (Potential).		1	AGTGAGAGTTG	0.478	
+	2	1064	_p.V134I|NTM_u	NM_016522	NP_057606	Q9P121	NTRI_HUMAN			6	TGCAAGGTAGG	0.552	
-	7	1237	dy.1_Missense_M	NM_152640	NP_689853	Q8IZD4	DCP1B_HUMAN			1	GAGCTCTGCTG	0.572	
-	1	46	0sge.1_Missense_	NM_174941	NP_777601	Q9NR16	C163B_HUMAN			11	GCCACGAGTTTT	0.378	
+	3	660		NM_024865	NP_079141	Q9H9S0	NANOG_HUMAN	Homeobox.		0	AGAATGAAATC	0.373	
-	1	206	RC3_uc010shc.1_	NM_002261	NP_002252	Q07444	NKG2E_HUMAN	lasmic (Potential).		3	CAATCCCTTGAT	0.348	
-	3	630		NM_006248	NP_006239					0	CTTTCCTGGAG	0.592	
-	6	855	_p.P279S|ABCC9_	NM_005691	NP_005682	O60706	ABCC9_HUMAN	lasmic (Potential).		6	ATTTGGATGAT	0.353	
-	2	655	10_uc009zju.1_5'	NM_198992	NP_945343	Q6XYQ8	SYT10_HUMAN	lasmic (Potential).		2	GCTTTTCATTTT	0.398	
-	35	5221		NM_025003	NP_079279	P59510	ATS20_HUMAN			19	ATAAATCTAAAG	0.303	
-	1	82		NM_025003	NP_079279	P59510	ATS20_HUMAN			19	CCTGGGGTGGA	0.652	
-	2	1381	7L_uc001rns.3_M	NM_001098615	NP_001092085	Q9H0K6	PUS7L_HUMAN			1	TTTTCCTTCTTG	0.348	
-	11	893	qv.2_Missense_M	NM_001844	NP_001835	P02458	CO2A1_HUMAN	le-helical region.		2	CATGGGACCCT	0.478	
-	5	654		NM_014470	NP_055285	Q92730	RND1_HUMAN			1	GCATGGATGCC	0.552	
-	6	1186		NM_033045	NP_149034	Q9NSB2	KRT84_HUMAN	Rod.|Coil 2.		1	GATCTCGTTCC	0.547	rs145550883
-	2	616		NM_005555	NP_005546	P04259	K2C6B_HUMAN	oil 1A.|Rod.		2	CAGAACCTTGT	0.537	
-	2	948		NM_005554	NP_005545	P02538	K2C6A_HUMAN	oil 1B.|Rod.		5	GTCCTCCACCA	0.542	
+	1	478		NM_001005497	NP_001005497	A6NL08	O6C75_HUMAN	Name=4; (Potential).		3	TAATGCTTCTG	0.438	
+	8	877	q.2_Missense_Mu	NM_005269	NP_005260	P08151	GLI1_HUMAN			15	GGAAGGAGTTC	0.597	
+	3	336	_p.P85L|MSRB3_	NM_198080	NP_932346	Q8IXL7	MSRB3_HUMAN			2	AACTCCATTGT	0.318	
-	2	335	va.3_Missense_M	NM_002837	NP_002828	P23467	PTPRB_HUMAN	III 1.|Extracellular (Potentia		3	ACTGTTCTCTCT	0.458	
-	1	734		NM_152638	NP_689851	Q8TC90	CL012_HUMAN			2	GAATTTCCAGAA	0.647	
+	6	935	zth.1_Missense_M	NM_152435	NP_689648	Q96NU7	HUTI_HUMAN			1	AACTGGGAGCG	0.483	
+	12	1507		NM_017564	NP_060034	Q8WWQ8	STAB2_HUMAN	lar (Potential).|FAS1 1.		14	TTGCTGGTCAG	0.378	
-	3	291	.2_RNA|MMAB_uc	NM_052845	NP_443077	Q96EY8	MMAB_HUMAN			0	TTTCTCCTGTG	0.393	
-	10	1584	tqp.3_Missense_M	NM_016238	NP_057322	Q9UJX3	APC7_HUMAN	TPR 7.		0	TCCATTGCCTCC	0.517	
+	8	1819		NM_006187	NP_006178	Q9Y6K5	OAS3_HUMAN	AS domain 2.		1	AGGGCGAGCAT	0.557	
-	9	620	k.2_Missense_Mut	NM_002150	NP_002141	P32754	HPPD_HUMAN			0	GGACACCATCT	0.582	
-	14	1485	_p.V214I|ZCCHC8	NM_017612	NP_060082	Q6NZY4	ZCHC8_HUMAN			0	TGGTACCTCCA	0.413	
-	2	614	AP1_uc001uep.2_	NM_004642	NP_004633	O14519	CDKA1_HUMAN			0	AAGACGTTGCC	0.622	
+	11	739	au.1_Missense_M	NM_001516	NP_001507	Q13889	TF2H3_HUMAN			0	ATCAGAGATCTC	0.393	
-	8	1272	_p.C278G|RIMBP	NM_015347	NP_056162	O15034	RIMB2_HUMAN	nectin type-III 1.		11	GACGCACTGCA	0.627	
-	3	338		NM_006001	NP_005992	Q13748	TBA3C_HUMAN			5	ATCTTCCTTCC	0.522	
+	10	1663	w.2_Missense_M	NM_006646	NP_006637	Q9UPY6	WASF3_HUMAN			1	TGTCCCGGCGC	0.617	
-	2	666	12_uc010tdl.1_5'	NM_005288	NP_005279	P47775	GPR12_HUMAN	lasmic (Potential).		0	GAATGGTACGT	0.577	
+	42	6907	_p.R27Q|NBEA_	NM_015678	NP_056493	Q8NFP9	NBEA_HUMAN			11	AAACCGAAGTA	0.343	
-	2	748	_uc010aez.1_Mis	NM_001122659	NP_001116131	P24530	EDNRB_HUMAN	ellular (Potential).		0	CTCTGCCAGCA	0.463	
-	10	1246	z.2_Missense_Mu	NM_052867	NP_443099	Q8IZF0	NALCN_HUMAN	lasmic (Potential).		16	CATCTTCATGAA	0.448	
-	5	1085	p.A232V|NOVA1_	NM_002515	NP_002506	P51513	NOVA1_HUMAN		p.A256D(1)	5	ACATTGGCATAA	0.458	
+	7	903	vrt.2_Missense_M	NM_173159	NP_071406	Q8IXF0	NPAS3_HUMAN			2	TCAAATCATCAG	0.478	
-	16	2499	p.V703A|RALGAP	NM_014990	NP_055805	Q6GYQ0	RGPA1_HUMAN			4	GTCCAACTCCT	0.413	
+	9	1025_1026		NM_002687	NP_002678	Q9H307	PININ_HUMAN	ential.|Glu-rich.		1	AAGAGGGTAAG	0.351	
-	9	1304	L1_uc001wxz.2_I	NM_004196	NP_004187	Q00532	CDKL1_HUMAN			2	taggaggggatgcct	0	
-	11	2661	H5_uc001xfy.2_3'	NM_139318	NP_647479	Q8NCM2	KCNH5_HUMAN	lasmic (Potential).		9	GTCACTTTTTGT	0.507	
-	5	557	nse_Mutation_p.P	NM_015346	NP_056161	Q68DK2	ZFY26_HUMAN			11	TCCTTGGATTTC	0.572	
-	8	785	ri.1_Missense_Mu	NM_012074	NP_036206	Q92784	DPF3_HUMAN			1	TATTGGGAATGA	0.512	
-	5	516	ri.1_Missense_Mu	NM_012074	NP_036206	Q92784	DPF3_HUMAN			1	TTCTTTCGCTTG	0.448	

+	5	1298	RXN3_uc010asv.1	NM_004796	NP_004787	Q9Y4C0	NRX3A_HUMAN	ellular (Potential).	10	CGGATGAGTGC	0.567	
-	3	1347	1ycu.3_Missense_	NM_016186	NP_057270	Q9UK55	ZPI_HUMAN		3	CATTTCCTTGG	0.502	
-	3	980	RPINA1_uc010au	NM_000295	NP_000286	P01009	A1AT_HUMAN		1	CCTTCACGGTG	0.542	
-	2	828	ydg.2_Missense_	NM_175739	NP_783866	Q86WD7	SPA9_HUMAN		2	AATGTGGTTCA	0.388	
-	2	617	RF1_uc010axg.1_	NM_001519	NP_001510	Q92994	TF3B_HUMAN		4	GCAGGGTCTGC	0.592	
-	1	104		NM_002487	NP_002478	Q99608	NECD_HUMAN		0	CAGATCCTTACT	0.647	
+	3	612		NM_003246	NP_003237	P07996	TSP1_HUMAN	P N-terminal.	6	TGGAAGAAGCT	0.582	
+	9	1879		NM_019074	NP_061947	Q9NR61	DLL4_HUMAN	ellular (Potential).	2	GTTCCCCGTGG	0.652	
+	1	775		NM_001080534	NP_001074003	Q8NB66	UN13C_HUMAN		7	AAACAGAACTT	0.463	
+	8	3781	acl.2_Missense_	NM_001080534	NP_001074003	Q8NB66	UN13C_HUMAN	C2 1.	7	ATTTTTGGAAAT	0.313	
+	24	5650		NM_001080534	NP_001074003	Q8NB66	UN13C_HUMAN		7	CAATGGATGCA	0.338	
+	2	1600	rh.2_Missense_M	NM_015322	NP_056137	Q9UK73	FEM1B_HUMAN		0	AAGGCCTTATA	0.418	
-	3	989		NM_001897	NP_001888	Q6UVK1	CSPG4_HUMAN	obular or compact configur	3	CCACGGAGATT	0.607	
+	21	2806	b.1_Missense_M	NM_004136	NP_004127	P48200	IREB2_HUMAN		0	AAAGATCATTTG	0.368	
+	22	3205	unn.1_Missense_	NM_018689	NP_061159	Q8WUJ3	K1199_HUMAN		3	GGTCCGGCACC	0.582	
+	11	1430	G3_uc010uud.1_	NM_032039	NP_114428	Q9H0X4	ITFG3_HUMAN	ellular (Potential).	1	CCTAGCCCTCC	0.672	
-	2	469		NM_001013658	NP_001013680	Q96A99	PTX4_HUMAN		0	GCTGTGGACGA	0.736	
+	4	546	se_Mutation_p.I12	NM_004996	NP_004987	P33527	MRP1_HUMAN	Cytoplasmic.	4	TTTAATTCAGCT	0.383	
-	19	2721		NM_017539	NP_060009	Q8TD57	DYH3_HUMAN	n (By similarity).	18	TGTCCTCCACAT	0.458	
+	17	3624	e_Mutation_p.P82	NM_006910	NP_008841	Q7Z6E9	RBBP6_HUMAN		4	TTTCTCCAGAG	0.418	
+	1	291	_Missense_Mutati	NM_173201	NP_775293	O14983	AT2A1_HUMAN	smic (By similarity).	4	GAAATACGGCC	0.547	
+	1	71		NM_144602	NP_653203	Q8WTQ4	CP078_HUMAN		1	CTGAAGGATTTA	0.532	
+	1	11	ank|IRX5_uc010cc	NM_005853	NP_005844	P78411	IRX5_HUMAN		0	CTATCCGCAGG	0.627	
-	6	681_682	p.G130F|CNOT1_	NM_016284	NP_057368	A5YKK6	CNOT1_HUMAN		6	CAAGGCCAAAA	0.351	rs113031066
-	7	820	e_Mutation_p.P25	NM_000512	NP_000503	P34059	GALNS_HUMAN		2	AGAAGGGTTTG	0.602	
-	5	540	e_Mutation_p.P15	NM_000512	NP_000503	P34059	GALNS_HUMAN		2	CAGGGGGTGGA	0.567	
+	12	1666	.1_RNA|SPG7_uc	NM_003119	NP_003110	Q9UQ90	SPG7_HUMAN	rial matrix (Potential).	0	ACGCCGTGGAG	0.627	rs147706568
-	2	885	L|TRPV1_uc010v	NM_080706	NP_542437	Q8NER1	TRPV1_HUMAN	nic (Potential).|ANK 1.	1	GGCTTCAAAGA	0.567	
-	6	1220	k.1_Missense_Mu	NM_015113	NP_055928	O43149	ZZEF1_HUMAN	DOC.	4	AGACTTCTTAA	0.483	
-	11	1743	cb.2_Missense_	NM_020162	NP_064547	Q9H6R0	DHX33_HUMAN		2	ATTCTCTTTGC	0.358	rs147158339
-	6	775	nse_Mutation_p.P	NM_020360	NP_065093	Q9NRY6	PLS3_HUMAN	smic (By similarity).	0	GGAAGGGATGC	0.612	
+	25	4093	issense_Mutatio	NM_001005273	NP_001005273	Q12873	CHD3_HUMAN		1	TGGACCCTGAC	0.507	
+	1	67	2R_uc010cog.1_	NM_004246	NP_004237	O95838	GLP2R_HUMAN	ellular (Potential).	3	TCCACGAGCTG	0.647	
+	2	1186		NM_016239	NP_057323	Q9UKN7	MYO15_HUMAN	osin head-like.	9	CCCGCCCGAGG	0.637	
+	9	1907	bj.2_Missense_M	NM_003593	NP_003584	O15353	FOXN1_HUMAN		1	ATCTTCGATGC	0.612	
-	3	617		NM_001045	NP_001036	P31645	SC6A4_HUMAN	lasmic (Potential).	4	AACTCCGTTTT	0.502	
-	3	402	nse_Mutation_p.D	NM_152781	NP_689994	A2RTY3	CQ066_HUMAN		3	CAGGTCGTGCC	0.512	
+	5	659	nse_Mutation_p.S	NM_133264	NP_573571	Q8TF74	WIPF2_HUMAN		3	AGACAGCAGCC	0.617	
-	8	1386	P_uc010wfs.1_Int	NM_000422	NP_000413	Q04695	K1C17_HUMAN	Tail.	2	GGGAGGAGATG	0.652	
-	12	1651	o.1_Missense_Mu	NM_005374	NP_005365	Q14168	MPP2_HUMAN	ylate kinase-like.	0	ATATTCCACTCT	0.617	
+	26	3423	c010dag.2_Intron|	NM_005892	NP_005883	O95466	FMNL_HUMAN	DAD.	1	AGACGGTGCCC	0.582	
+	6	1302	PT_uc002ijx.3_In	NM_016835	NP_058519	P10636	TAU_HUMAN		1	CATTTCCAGGG	0.622	
-	5	1746	ikd.2_Missense_M	NM_015443	NP_056258	Q7Z3B3	K1267_HUMAN		2	AGACAGGCTGA	0.343	
-	15	2627	s.1_Missense_Mu	NM_198393	NP_938207	Q8IWB6	TEX14_HUMAN		17	TTTTCCAGGGT	0.423	
-	4	831	2_Missense_Muta	NM_001159772	NP_001153244	Q8WVQ1	CANT1_HUMAN	enal (Potential).	0	TAGCCCTTTTTC	0.577	
+	26	3881_3882	ug.1_Missense_M	NM_020761	NP_065812	Q8N122	RPTOR_HUMAN	WD 1.	6	GCGTCCCCTCT	0.559	
+	1	471	L_uc010dkz.2_In	NM_020412	NP_065145	Q7LBR1	CHM1B_HUMAN		0	TGGACAAATTC	0.517	

+	1	59		NM_005913	NP_005904	P33032	MC5R_HUMAN	cellular (Potential).	6	GGGCAACCTTT	0.463
+	14	1990		NM_005925	NP_005916	Q16820	MEP1B_HUMAN	cellular (Potential).	2	AGGCTCCACCC	0.463
-	5	696	2_uc010dnf.2_3'U	NM_002930	NP_002921	Q99578	RIT2_HUMAN		1	GCCATGAAAAG	0.423
+	20	3706	p.R868K|DCC_uc	NM_005215	NP_005206	P43146	DCC_HUMAN	tential).|Fibronectin type-III	17	CTTCAGGACTC	0.388
-	8	1143	p.E332K|SERPIN	NM_002974	NP_002965	P48594	SPB4_HUMAN		3	ATAATTCGACTA	0.463
+	6	689	xet.1_Missense_	NM_001040147	NP_001035237	O75635	SPB7_HUMAN		3	ATCTCCCAAGG	0.408
-	6	820	p.S178F|NETO1_	NM_138966	NP_620416	Q8TDF5	NETO1_HUMAN	xtracellular (Potential).	4	CTTCGGAACCG	0.428
+	4	1262	a.1_Missense_M	NM_173480	NP_775751	Q68EA5	ZNF57_HUMAN	C2H2-type 8.	3	GGAAAGCCTTC	0.443
+	13	1539	.G432D|FSD1_uc	NM_024333	NP_077309	Q9BTV5	FSD1_HUMAN	B30.2/SPRY.	1	GTATGGTGTGG	0.677
-	11	1183	p.G382E|SEMA6	NM_032108	NP_115484	Q9H3T3	SEM6B_HUMAN	lar (Potential).|Sema.	1	GCATCCCGGGG	0.612
+	4	1710	ym.1_Missense_	NM_001136501	NP_001129973	Q08AG5	ZN844_HUMAN		0	GCATGAAAGGA	0.413
+	6	441	2mzl.3_Splice_Sit	NM_032433	NP_115809	Q96JL9	ZN333_HUMAN		3	TGCCAGGGGCC	0.602
-	11	1300		NM_001080421	NP_001073890	Q9UPW8	UN13A_HUMAN	-rich.|Potential.	3	ctcctcctcctccagct	0.433
+	4	456	_p.M5K|ZNF431_	NM_133473	NP_597730	Q8TF32	ZN431_HUMAN	KRAB.	2	GTGGATGAACC	0.418
-	4	1122	p.R258T|ZNF681_	NM_138286	NP_612143	Q96N22	ZN681_HUMAN	type 6; degenerate.	0	TATGTCTGGTAA	0.378
-	2	147	81_uc002nrj.3_Int	NM_138286	NP_612143	Q96N22	ZN681_HUMAN		0	ATGGTTCCTGA	0.284
+	2	924	edk.1_Missense_	NM_014686	NP_055501	O15063	K0355_HUMAN		1	CGGGTCCAAGC	0.627
+	3	368	odk.2_Missense_	NM_001749	NP_001740	P04632	CPNS1_HUMAN		0	GCAGCGAGGCG	0.657
-	5	717	85B_uc002ofr.1_	NM_152279	NP_689492	Q52M93	Z585B_HUMAN		1	TTTTTCTCCTG	0.393
-	1	688		NM_020862	NP_065913	Q9P244	LRFN1_HUMAN	xtracellular (Potential).	2	GAAGAGCCCGT	0.667
+	27	3502_3503	se_Mutation_p.P4	NM_001042544	NP_001036009	Q8N2S1	LTBP4_HUMAN	Pro-rich.	1	GCCGACCCAGC	0.693
+	3	311	e_Mutation_p.Q54	NM_001007270	NP_001007271	Q9H840	GEMI7_HUMAN		1	AATCCCAGGAG	0.627
+	2	232	pgk.1_Missense_	NM_018485	NP_060955	Q9P296	C5ARL_HUMAN	cellular (Potential).	1	ACGATTCTGTCA	0.607
+	4	379	_p.P69S|CCDC15	NM_144688	NP_653289	Q8N6L0	CC155_HUMAN		2	AGGGCCCCCAG	0.642
+	4	507	131I|ALDH16A1_u	NM_153329	NP_699160	Q8IZ83	A16A1_HUMAN		1	GGGCTGTTCGA	0.627
+	4	943	d.2_Missense_Mu	NM_012068	NP_036200	Q9Y2D1	ATF5_HUMAN	on with PTP4A1 (By similar	2	caccaccctccccgcc	0.488
+	5	954	e_Mutation_p.H28	NM_001130917	NP_001124389	Q8N149	LIRA2_HUMAN	3.|Extracellular (Potential).	1	CCTCCCACGGG	0.647
+	14	1964	e_Mutation_p.E54	NM_006669	NP_006660	Q8NHL6	LIRB1_HUMAN	lasmic (Potential).	3	AGCCTGAGGAT	0.612
-	5	1190	ne.2_Missense_M	NM_022103	NP_071386	Q5HYK9	ZN667_HUMAN	C2H2-type 6.	1	GGGGTGAAATC	0.388
-	11	1775	61T|ZIM2_uc002q	NM_015363	NP_056178	Q9NZV7	ZIM2_HUMAN		3	GCAGGCTCTCT	0.483
+	4	746		NM_020903	NP_065954	Q9HBJ7	UBP29_HUMAN		11	AATTGACAAAAC	0.358
+	28	3290	zi.2_Missense_Mu	NM_003887	NP_003878	O43150	ASAP2_HUMAN	SH3.	0	AGATTGGCCAC	0.403
+	3	362		NM_182626	NP_872432	Q96LS8	CB048_HUMAN		0	atttctaaggggatgaga	0
-	4	459	dx.2_Missense_M	NM_022460	NP_071905	Q53T59	H1BP3_HUMAN	PX.	1	CCCCTGGGGATC	0.557
-	26	7173		NM_000384	NP_000375	P04114	APOB_HUMAN		27	CTACTTCATACC	0.378
-	16	2333	i.1_RNA|ATAD2B_	NM_017552	NP_060022	Q9ULI0	ATD2B_HUMAN		1	AGTGGTCTTATG	0.448
+	1	331	7L_uc010ymf.1_5'	NM_018158	NP_060628	Q9BWU0	NADAP_HUMAN		0	ACTTCACCATCG	0.522
+	11	1919		NM_016441	NP_057525	Q9NZV1	CRIM1_HUMAN	Extracellular (Potential).	3	GTGCCGGGAAT	0.592
-	38	5970_5971	DA_uc002rsx.3_	NM_001083953	NP_001077422	Q6YHU6	THADA_HUMAN		3	ACCATCCTTTGA	0.525
-	10	1796	_p.M512I|FSHR_u	NM_000145	NP_000136	P23945	FSHR_HUMAN	Name=6; (Potential).	8	ATGGCCATGCG	0.527
+	10	7466	g.2_Missense_Mu	NM_015120	NP_055935	Q8TCU4	ALMS1_HUMAN		9	TGTTTCACCCA	0.448
+	12	1129	.R335*|EPB41L5_	NM_020909	NP_065960	Q9HCM4	E41L5_HUMAN		1	TCTCATCGATCA	0.378
+	6	1253	flu.2_Missense_	NM_130773	NP_570129	Q8WYK1	CNTP5_HUMAN	1.|Extracellular (Potential).	10	AGGGCGAGACG	0.562
-	17	2633		NM_001099771	NP_001093241	A5A3E0	POTEF_HUMAN	Actin-like.	5	GCCCCCCATCA	0.622
-	1	1637		NR_002826					0	CAGCTCCGGGA	0.642
-	73	12143		NM_018557	NP_061027	Q9NZR2	LRP1B_HUMAN	ntial).|LDL-receptor class A	50	TTATTTCTGCATC	0.383
+	9	1760	.2_Missense_Mut	NM_018328	NP_060798	Q9P267	MBD5_HUMAN		5	GTTTTCATGGA	0.448

-	123	17284	.G2121E|NEB_uc	NM_004543	NP_004534	P20929	NEBU_HUMAN			20	GATTTTCCTTTCT	0.403	
+	3	1180	J3_uc010zce.1_3'	NM_002239	NP_002230	P48549	IRK3_HUMAN	smic (By similarity).		2	TTTTTTCCTGTA	0.388	
-	22	4263	uc002udp.2_Intron	NM_002977	NP_002968	Q15858	SCN9A_HUMAN	III.		13	GGAAGGAATTG	0.353	
+	1	425	_p.S76N|DLX1_uc	NM_178120	NP_835221	P56177	DLX1_HUMAN			0	GGTCAGCAGCC	0.672	
-	309	99378	lissense_Mutation_	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN			153	ACCTTCGTTTAT	0.418	
-	292	87727	63E|TTN_uc010z	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN			153	CTCCTCCGTCTT	0.527	
-	275	74985	16A|TTN_uc010z	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN			153	CCCATGTTACTA	0.483	
-	181	35412	.1_Missense_Muta	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		p.E5233K(1)	153	CATATTCGCCTT	0.428	
-	42	10036	_uc010zfj.1_Misse	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN			153	ACCAGGAAATTT	0.527	
-	28	6502	TN_uc010zfj.1_Mi	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN			153	CATCAGATCCTT	0.463	
-	13	2269	1_Missense_Muta	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN			153	CTTGTCTAGTAG	0.368	
+	7	2914	_p.Q934L|SGOL2_	NM_152524	NP_689737	Q562F6	SGOL2_HUMAN			4	TGTCCAAGAAA	0.279	
+	3	646	D28_uc010ftx.2_M	NM_006139	NP_006130	P10747	CD28_HUMAN	ellular (Potential).		0	TTTGTCCAAGT	0.438	
-	2	300		NM_006891	NP_008822	P07320	CRGD_HUMAN	crystallin 'Greek key' 2.		0	ATAGTCGCCGC	0.657	
+	13	1433	_Mutation_p.S44	NM_001875	NP_001866	P31327	CPSM_HUMAN			13	TCTGTCCATTG	0.373	
+	11	1230	_p.Q78K|VIL1_uc	NM_007127	NP_009058	P09327	VILI_HUMAN	Core.		1	CTGCCCAGCAG	0.567	
-	11	4921	_Mutation_p.R15	NM_001142644	NP_001136116	Q2M3C7	SPKAP_HUMAN			10	TGGCTCGGAGC	0.542	
+	12	1514	yc.2_Missense_M	NM_000751	NP_000742	Q07001	ACHD_HUMAN			3	TTCCTGGGGAC	0.617	
+	9	1048	fye.1_Missense_M	NM_005199	NP_005190	P07510	ACHG_HUMAN	lasmic (Potential).		0	GAGGGGTCCGC	0.617	
+	1	835	_p.P118L|GPR35_	NM_005301	NP_005292	Q9HC97	GPR35_HUMAN	ellular (Potential).		3	CACGCCGCTGT	0.642	
-	5	635	wtu.2_Missense_	NM_178312	NP_842564	Q9BX51	GGTL1_HUMAN			1	CGTGACGTTGG	0.622	
-	10	4975	w.2_Missense_M	NM_014071	NP_054790	Q14686	NCOA6_HUMAN	n.|NCOA6IP-binding region		7	ATCACCATGCT	0.542	
-	7	1194	gj.2_Missense_M	NM_007050	NP_008981	O14522	PTPRT_HUMAN	tential).|Fibronectin type-III		20	TGTGGGTCTCT	0.557	
-	2	861	hk.1_Missense_M	NM_021248	NP_067071	Q9UJ99	CAD22_HUMAN	(Potential).|Cadherin 1.		5	GATGAACTCCG	0.632	
-	3	480	GE_uc002yiw.1_R	NM_182482	NP_872288					0	CTTTCAGGAGC	0.388	
+	6	770	yxz.2_Missense_	NM_007341	NP_031367	P55822	SH3BG_HUMAN	u-rich (acidic).		0	AAGATTCCTAGG	0.493	
-	25	4734	AM_uc002yyr.1_	NM_001389	NP_001380	O60469	DSCAM_HUMAN	III 5.|Extracellular (Potentia		11	TGATTGGAAAAC	0.488	
+	9	1092	zbj.2_Missense_M	NM_018964	NP_061837	P57057	GLPT_HUMAN	ical; (Potential).		0	GCCTGGAGCCA	0.592	
-	1	469	.1_Intron|C21orf29	NM_198688	NP_941961	P60371	KR106_HUMAN	repeats of C-C-X(3).		0	GCAGGGGGAGG	0.602	
-	2	331	4R_uc002zru.2_5'	NM_023004	NP_075380	Q9BZR6	RTN4R_HUMAN	LRRNT.		0	CTGGGGGCAGC	0.667	
-	18	2565	B1_uc003afl.2_Mi	NM_001127	NP_001118	Q10567	AP1B1_HUMAN			2	GCAGGGAGATC	0.657	
-	4	887	_p.S103F|LARGE_	NM_004737	NP_004728	O95461	LARGE_HUMAN	enal (Potential).		3	TCCATGGAGTAG	0.672	
-	15	1894	_p.R231C|SBF1_u	NM_002972	NP_002963	O95248	MTMR5_HUMAN			0	GTTGCGCACAA	0.627	
-	31	4207		NM_024923	NP_079199	Q8TEM1	PO210_HUMAN	enal (Probable).		11	GGTAGGAAACA	0.572	rs147706980
+	1	2110	k.1_Missense_Mu	NM_152536	NP_689749	Q6ZNL6	FGD5_HUMAN			5	GGAGAACAAAT	0.517	
-	5	1039	p.V170A|UBP1_uc	NM_014517	NP_055332	Q9NZI7	UBIP1_HUMAN			2	AATTCAACCGCA	0.358	
-	12	4842		NM_014831	NP_055646	O15050	TRNK1_HUMAN			2	CATTTCCTTCT	0.493	
-	13	1066	2_uc003cgr.2_Intr	NM_006309	NP_006300	Q9Y608	LRRF2_HUMAN	-binding.|Ser-rich.		1	GACCATAAGGGT	0.358	
-	11	1388	lx.2_Missense_Mu	NM_020707	NP_065758	Q9HCP6	HHATL_HUMAN			3	CAATTCGTGCTA	0.577	
-	12	6025	_Mutation_p.E20	NM_014159	NP_054878	Q9BYW2	SETD2_HUMAN			32	CACTCTCCACAT	0.443	
-	3	478	A_uc010hku.2_5'	NM_001664	NP_001655	P61586	RHOA_HUMAN			2	TCAGGCGATCAT	0.493	
+	25	4430		NM_015512	NP_056327	Q9P2D7	DYH1_HUMAN	n (By similarity).		3	CTACCCCTCCA	0.602	
+	19	2720	_p.M853L|CACNA	NM_001128840	NP_001122312	Q01668	CAC1D_HUMAN	lasmic (Potential).		11	TTGAACATGAAG	0.428	rs138798164
-	11	1461		NM_020872	NP_065923	Q9P232	CNTN3_HUMAN	like C2-type 5.		5	CTCCATCGTTTA	0.318	
+	1	189	rf26_uc003dtk.1_	NM_032359	NP_115735	Q9BQ75	CC026_HUMAN			1	CGACTGGAGCA	0.662	
+	4	2336		NM_016298	NP_057382	Q9UH90	FBX40_HUMAN			5	ACGTCTCCTAAA	0.488	
+	1	226	bjn.1_Nonsense_	NM_021082	NP_066568	Q16348	S15A2_HUMAN			1	CACCTCGACCA	0.502	

+	4	1112		NM_001080440	NP_001073909	A6NHN0	OTOL1_HUMAN	C1q.	0	CCAAGGGAATT	0.468	
-	6	784	fk.2_Missense_Mu	NM_005241	NP_005232	Q03112	EVI1_HUMAN	MAPK9, SMAD3 and proba	14	CCGACGAAGTG	0.552	
+	2	211	z.2_Missense_Mut	NM_003722	NP_003713	Q9H3D4	P63_HUMAN	cription activation.	12	CATGTCCCAGA	0.373	
-	3	10394	h.1_5'Flank|MUC4	NM_018406	NP_060876	Q99102	MUC4_HUMAN		0	AACAGGGGTGG	0.592	
-	2	6986	C4_uc003fvp.2_Int	NM_018406	NP_060876	Q99102	MUC4_HUMAN		0	AAGAGAGGTGG	0.587	
-	3	919	A_uc003gbz.2_Int	NM_213613	NP_998778	Q9H2B4	S26A1_HUMAN	ical; (Potential).	1	GGTGGCGACAC	0.687	rs144893723
+	4	1205	366L|TACC3_uc0	NM_006342	NP_006333	Q9Y6A5	TACC3_HUMAN		2	GCCTCCCTTGA	0.602	
+	2	79		NM_001040448	NP_001035538	P59861	DB131_HUMAN		0	TCTAATGATGAAT	0.308	
-	1	387	2A3_uc010ihp.1_	NM_024743	NP_079019	Q6UWM9	UD2A3_HUMAN	ellular (Potential).	2	AAGTTCCTCTT	0.338	
+	2	689		NM_015393	NP_056208	Q6UWI2	PARM1_HUMAN	ellular (Potential).	1	TCATCTCCCCTC	0.572	
-	1	413		NM_032693	NP_116082	Q9BSU3	NAA11_HUMAN	cetyltransferase.	2	TGGTCCATCAG	0.557	
+	5	966	n_p.L78F|ARHGA	NM_001025616	NP_001020787	Q8N264	RHG24_HUMAN	Rho-GAP.	0	AGGGTCTCTTT	0.488	
+	5	1454		NM_014208	NP_055023	Q9NZW4	DSPP_HUMAN	Asp/Ser-rich.	1	TGACAGCAATA	0.403	
+	7	978		NM_004967	NP_004958	P21815	SIAL_HUMAN		0	CCTATGAAGAT	0.478	
+	2	687	190A_uc010ikv.2_	NM_001145065	NP_001138537	Q9C0I3	F190A_HUMAN		2	GACATTCTGTTG	0.368	
-	7	582		NM_000669	NP_000660	P00326	ADH1G_HUMAN		0	CAGGGGCGAG	0.522	
+	9	10628	p.P1841L|FAT4_u	NM_024582	NP_078858	Q6V0I7	FAT4_HUMAN	.|Extracellular (Potential).	18	AGGTCCCTTTA	0.498	
-	1	2501	.1_Intron|PCDH18	NM_019035	NP_061908	Q9HCL0	PCD18_HUMAN	ical; (Potential).	5	CCTAAGGAAATA	0.423	
-	7	1247	p.R258K|LRBA_uc	NM_006726	NP_006717	P50851	LRBA_HUMAN		7	TGGTTCTGAAA	0.323	
-	15	2172	p.G578V|FSTL5_u	NM_020116	NP_064501	Q8N475	FSTL5_HUMAN		8	CATTCCCACTG	0.413	
-	6	1287	iqr.1_Missense_	NM_017923	NP_060393	Q8TCQ1	MARH1_HUMAN	ING-CH-type.	2	AAAGCGCAGTG	0.527	rs146337383
+	8	688	irn.2_Nonsense_	NM_007193	NP_009124	Q9UJ72	ANX10_HUMAN	Annexin 3.	0	CTATGGGAAGC	0.502	
+	12	2015	kb.1_Missense_M	NM_017423	NP_059119	Q86SF2	GALT7_HUMAN	ectin.|Lumenal (Potential).	1	AGTAAAACGAC	0.363	
+	12	1865	_p.L330S|SNX25_	NM_031953	NP_114159	Q9H3E2	SNX25_HUMAN	PX.	5	GAATTTACACCG	0.403	
-	10	1686		NM_003966	NP_003957	Q13591	SEM5A_HUMAN	tracellular (Potential).	2	TGGCGCTCAGG	0.602	
-	2	198	z.1_5'UTR|CTNN	NM_001332	NP_001323	Q9UQB3	CTND2_HUMAN		8	GGTCTGGAACA	0.493	
-	75	13103	fc.2_Missense_Mu	NM_001369	NP_001360	Q8TE73	DYH5_HUMAN		31	CCACCGCCTCC	0.577	
-	40	6625		NM_001369	NP_001360	Q8TE73	DYH5_HUMAN		31	CTCATCAATCT	0.373	
-	7	1557	p.E394K|CDH18_	NM_004934	NP_004925	Q13634	CAD18_HUMAN	r (Potential).|Cadherin 4.	7	CATTTTCGTAGA	0.433	
+	12	1107	_p.S233L|RAI14_	NM_015577	NP_056392	Q9P0K7	RAI14_HUMAN		1	AGGAATCGGTAT	0.313	
-	4	542	GT3A1_uc011cor.	NM_152404	NP_689617	Q6NUS8	UD3A1_HUMAN	ellular (Potential).	3	TTATATCCTTTCT	0.303	
+	10	1905	_p.R370C|SLC1A3	NM_004172	NP_004163	P43003	EAA1_HUMAN		0	GGGATCGCCTC	0.547	
-	9	1338		NM_006622	NP_006613	Q9NYY3	PLK2_HUMAN		4	AAGTCTTTTTC	0.353	
+	2	293		NM_138453	NP_612462	Q96E17	RAB3C_HUMAN	region (By similarity).	2	GGATCGATTTC	0.408	
-	22	3708	o.2_RNA|ADAMT	NM_197941	NP_922932	Q9UKP5	ATS6_HUMAN	TSP type-1 4.	0	CCAAAGCCACC	0.453	
-	13	1512	_p.P430L|FAM169	NM_015566	NP_056381	Q9Y6X4	F169A_HUMAN		0	TACGTGGGGTC	0.373	
+	1	816	uc011ctk.1_RNA	NM_032567	NP_115956	Q9BXG8	SPZ1_HUMAN	notif (By similarity).	1	AACAGCAGATG	0.353	
+	20	4120	98_uc003kjt.2_5'	NM_032119	NP_115495	Q8WXG9	GPR98_HUMAN	ellular (Potential).	16	GTTAATCCAAAA	0.463	
-	1	511	C_uc003kql.3_Int	NM_032028	NP_114417	Q9BXA7	TSSK1_HUMAN	rotein kinase.	5	CAGGGCTCCCC	0.557	
+	5	1117	TS19_uc003kvc.1	NM_133638	NP_598377	Q8TE59	ATS19_HUMAN	ptidase M12B.	9	AATCTTCGTGTG	0.294	
-	5	712		NM_015082	NP_055897	Q6MZW2	FSTL4_HUMAN		2	TGTCTCCTTCTT	0.577	
+	14	2091	ldi.2_Missense_	NM_001903	NP_001894	P35221	CTNA1_HUMAN		11	TAGCTGGCCAG	0.542	
+	1	1192		NR_001280					0	ACCTTAGAAAAT	0.473	
-	6	1192	loh.3_Missense_	NM_004576	NP_004567	Q00005	2ABB_HUMAN	WD 4.	2	CACCTCCGTGA	0.562	
-	9	1051	oo.2_Missense_M	NM_001387	NP_001378	Q14195	DPYL3_HUMAN		1	AGTCCGGAGTA	0.567	
-	9	1800	jhd.2_Missense_	NM_002609	NP_002600	P09619	PGFRB_HUMAN	otential).|Ig-like C2-type 5.	17	TGTTCGGCTGG	0.597	
+	4	588	A6_uc003lyv.2_5'	NM_000811	NP_000802	Q16445	GBRA6_HUMAN	ellular (Probable).	12	TTTTCCGCCAG	0.408	

+	15	2754	lzt.3_Splice_Site_	NM_001122679	NP_001116151				10	TTCTCAGCTTGG	0.507	
+	2	250	tion_p.P62L|MIR1	NM_173664	NP_775935	Q8N8L6	ARL10_HUMAN		1	GCAGCCCGAGG	0.701	
-	12	1673	9_splice|RASGEF	NM_175062	NP_778232	Q8N431	RGF1C_HUMAN		1	GACTCACCTTAG	0.507	
+	1	470		NM_001453	NP_001444	Q12948	FOXC1_HUMAN	Fork-head.	1	CCCGGACTCCT	0.622	
+	23	4640	P_uc003mxq.1_Int	NM_004415	NP_004406	P15924	DESP_HUMAN	us rod domain.|Potential.	9	ACAAGTCACTC	0.463	
-	7	998	A|MAK_uc010jou.	NM_005906	NP_005897	P20794	MAK_HUMAN	rotein kinase.	3	GAATAGCTTCAT	0.428	
+	4	3169	EP1_uc011diq.1_	NM_002114	NP_002105	P15822	ZEP1_HUMAN		6	AGAACCTGAGC	0.463	
-	4	4456_4457		NM_052923	NP_443155	Q6R2W3	SCND3_HUMAN		1	agagaatccggtctca	0	rs140560647
-	4	3499		NM_052923	NP_443155	Q6R2W3	SCND3_HUMAN		1	atttaaattccaaaccac	0	
+	1	600		NM_030905	NP_112167	O76002	OR2J2_HUMAN	ellular (Potential).	0	TTCTGGGTACC	0.478	
-	10	5112	C1_uc011dmp.1_	NM_014641	NP_055456	Q14676	MDC1_HUMAN	ith the PRKDC complex.	4	CCTGCCCCTAG	0.582	
+	9	1269	_Missense_Mutat	NM_013993	NP_054699	Q08345	DDR1_HUMAN	ellular (Potential).	9	AGTGCCCCTTG	0.667	
-	22	7854		NM_019105	NP_061978	P22105	TENX_HUMAN	nectin type-III 18.	0	TGAAGGAGTCA	0.692	
+	2	409	3obi.2_Splice_Sit	NM_019111	NP_061984	P01903	DRA_HUMAN		2	AATGGTACCTC	0.463	
-	52	4075	se_Mutation_p.P1	NM_080680	NP_542411	P13942	COBA2_HUMAN	le-helical region.	5	CCGAGGGCCAC	0.602	
-	1	807		NR_001444					0	GACAGGAGGCA	0.577	
-	7	1749	b.2_Missense_Mu	NM_001142883	NP_001136355	Q96PC2	IP6K3_HUMAN		0	GATATCCTGCA	0.478	
+	11	1235	h.2_RNA|GLP1R_	NM_002062	NP_002053	P43220	GLP1R_HUMAN	Name=7; (Potential).	5	CACCTCCTTCC	0.527	
+	2	241	ML4_uc003oqd.2_	NM_198153	NP_937796	Q6UXN2	TRML4_HUMAN	g-like V-type.	1	CAAGAGAGGGC	0.537	
-	3	1244	318_uc003ouw.2_	NM_014345	NP_055160	Q5VUA4	ZN318_HUMAN		7	ATTATGTCCACC	0.483	
+	11	2316	LH_uc011dvl.1_R	NM_006502	NP_006493	Q9Y253	POLH_HUMAN		2	AAACCCCCAGG	0.498	
+	1	3325	e.2_Nonsense_Mu	NM_001010870	NP_001010870	O60522	TDRD6_HUMAN		6	TACCAGAAGAA	0.373	
+	6	1150	_p.L355V|GPR115_	NM_153838	NP_722580	Q8IZF3	GP115_HUMAN	ellular (Potential).	8	CAACCTTGGGG	0.473	
+	2	268		NM_001010872	NP_001010872	Q5T0W9	FA83B_HUMAN		6	GGAACGAGTTT	0.383	
+	2	237		NM_207410	NP_997293	Q6UXV0	GFRAL_HUMAN	ellular (Potential).	2	TGCAATGATTCA	0.318	
+	4	1963	dxm.1_Missense_	NM_020931	NP_065982	Q9HCI6	K1586_HUMAN		0	ATAAATTTAATGC	0.264	
-	27	1961	_p.G174E|COL9A1	NM_001851	NP_001842	P20849	CO9A1_HUMAN	elical region (COL2).	4	GAATTTCCCATC	0.423	
-	11	1175	OL9A1_uc003pff.	NM_001851	NP_001842	P20849	CO9A1_HUMAN	elical region (COL3).	4	CCTTTGACCCA	0.388	
+	34	5092	gg.2_Missense_	NM_014989	NP_055804	Q86UR5	RIMS1_HUMAN		10	TCCCCTCACCC	0.512	
-	1	86	1A1_uc003phh.2_	NM_001402	NP_001393	P68104	EF1A1_HUMAN	(By similarity).	0	CGAATCTACGT	0.423	
-	2	3738	_p.Q59*|CNR1_u	NM_001160260	NP_001153732	P21554	CNR1_HUMAN	ellular (Potential).	2	CTCTTGGAAGG	0.453	
+	18	2506		NM_173560	NP_775831	Q8HWS3	RFX6_HUMAN		3	GGCTCGGATCA	0.428	
-	9	2354		NM_001042475	NP_001035940	Q5SZL2	CF204_HUMAN	Potential.	1	AGGCATCTTTCT	0.323	
-	2	1204	_p.D166N|FAM184	NM_024581	NP_078857	Q8NB25	F184A_HUMAN		7	TAAGATCAGCTT	0.378	
+	4	837	as.1_Missense_M	NM_032784	NP_116173	Q9BXY4	RSPO3_HUMAN	TSP type-1.	0	AGCATCCTTCA	0.453	
-	12	2397	u.1_Missense_Mu	NM_002844	NP_002835	Q15262	PTPRK_HUMAN	tential).|Fibronectin type-III	8	GGTTTCCCGGG	0.542	
+	19	2044	qbu.2_Missense_	NM_032438	NP_115814	Q96JM7	LMBL3_HUMAN		6	TTCTTCCCCTG	0.348	
-	13	1756	p.R477K|SAMD3_	NM_001017373	NP_001017373	Q8N6K7	SAMD3_HUMAN		1	TCAATCCTAAAT	0.413	
-	7	1084	kgh.2_Missense_	NM_022568	NP_072090	Q9H2A2	AL8A1_HUMAN		4	GAGCTCTCTTG	0.463	
-	2	780	uc003qky.1_Intron	NM_032145	NP_115521	Q8TB52	FBX30_HUMAN		3	CAGCAGCCAAA	0.403	
+	6	1352	qe.2_Missense_M	NM_012454	NP_036586	Q8IVF5	TIAM2_HUMAN		4	AAATTCCTTGC	0.433	
+	18	4911	.E1547K|ARID1B_	NM_017519	NP_059989	Q8NFD5	ARI1B_HUMAN	Pro-rich.	2	GAAGGGAGATC	0.512	
+	34	5543		NM_001040001	NP_001035090	P55196	AFAD_HUMAN		5	TGACATTCAAG	0.418	
-	41	5823	km.1_Missense_M	NM_001080453	NP_001073922	Q8N201	INT1_HUMAN		0	CAGGAAGCAGC	0.682	
+	20	3092	o.2_Missense_Mu	NM_152744	NP_689957	Q7Z5N4	SDK1_HUMAN	nectin type-III 4.	6	ATCTTGGACACA	0.423	
+	6	873	5_uc010ksp.2_Sp	NM_014855	NP_055670	O43299	K0415_HUMAN		1	CACAGGTGTGC	0.701	
+	8	911	e.1_Missense_Mu	NM_031414	NP_113602	Q9BXU1	STK31_HUMAN		9	ATAGGGAAAGTT	0.323	

-	2	904	A3_uc003syk.2_5'	NM_002141	NP_002132	Q00056	HXA4_HUMAN		1	AGGCCGAATTG	0.398	
+	4	871	_p.S89F|HECW1_	NM_015052	NP_055867	Q76N89	HECW1_HUMAN		23	CTATTCCATCGG	0.592	
-	5	569	_p.P126L|VOPP1	NM_030796	NP_110423	Q96AW1	VOPP1_HUMAN	ytoplasmic (Potential).	0	CGACAGGGTTC	0.632	
+	5	1216		NM_153363	NP_699194	Q8IYX0	ZN679_HUMAN	2H2-type 6.	1	ACAAGAGAATTC	0.408	
+	11	1750	tvz.2_Missense_	NM_022479	NP_071924	Q6IS24	GLTL3_HUMAN	ectin.|Lumenal (Potential).	7	TCCTCCGCAGC	0.627	
-	7	12903	p.P4205L|PCLO_u	NM_033026	NP_149015	Q9Y6V0	PCLO_HUMAN		7	TGAATAGGTGAA	0.383	
+	2	1152	.G16E|GRM3_uc	NM_000840	NP_000831	Q14832	GRM3_HUMAN		13	AAAGGGATTTTT	0.398	
-	3	1046	TEAP4_uc003ujt.2	NM_024636	NP_078912	Q687X5	STEA4_HUMAN	oxidoreductase.	0	TAATATCGAATAG	0.428	
+	12	1524	_p.C379Y|DYNC1	NM_004411	NP_004402	O14576	DC1I1_HUMAN	WD 3.	4	AATGTGTTCCT	0.433	
-	2	346		NM_018842	NP_061330	Q9UHR4	BI2L1_HUMAN	IMD.	1	AATTTCGCAGCC	0.299	
-	1	493	_p.G113S|ACHE_	NM_000665	NP_000656	P22303	ACES_HUMAN		2	GGTGCCCTCAA	0.597	
-	4	571	n_p.L29F|NRCAM	NM_001037132	NP_001032209	Q92823	NRCAM_HUMAN	ellular (Potential).	5	ATCAAGAGGTA	0.458	
+	6	853	R_uc011knq.1_5'	NM_000492	NP_000483	P13569	CFTR_HUMAN	tial).|ABC transmembrane	5	GGCTAGGGAG	0.433	
+	1	1022		NM_012281	NP_036413	Q9NZV8	KCND2_HUMAN	NIP2.|Cytoplasmic (Potent	5	GGGTGGATGCC	0.612	
-	1	638	PS2_uc010lkq.2_	NM_198085	NP_932351	Q8N7C7	RN148_HUMAN	PA.	0	ACATGGGAAATA	0.448	
-	8	686	GA14_uc003vqa.	NM_018718	NP_061188	Q9BYV8	CEP41_HUMAN	Rhodanese.	0	TACATATTCAAG	0.368	
+	17	3000	ub.2_Missense_M	NM_015905	NP_056989	O15164	TIF1A_HUMAN		8	CTGTTCCTCTA	0.323	
-	15	1860		NM_004333	NP_004324	P15056	BRAF_HUMAN	rotein kinas_R603>I(2)|p.T	18290	GATTTCACTGTA	0.368	
-	1	719		NM_176817	NP_789787	P59533	T2R38_HUMAN	lasmic (Potential).	2	CAGAAGAAACC	0.458	
-	4	617	TRPV6_uc010lou.	NM_018646	NP_061116	Q9H1D0	TRPV6_HUMAN	ytoplasmic (Potential).	2	GGGCTCGCACC	0.572	rs150734746
-	7	1114	bz.2_Missense_M	NM_019841	NP_062815	Q9NQA5	TRPV5_HUMAN	lasmic (Potential).	6	GGAGTCGATCT	0.557	
+	1	934		NM_001001667	NP_001001667	Q8N148	OR6V1_HUMAN	lasmic (Potential).	1	GCAAGGCACAA	0.542	
+	5	682	LCN1_uc010lox.1	NM_000083	NP_000074	P35523	CLCN1_HUMAN		5	TACTTCGTGGG	0.507	rs143506735
+	1	840		NM_012369	NP_036501	Q13607	OR2F1_HUMAN	ellular (Potential).	3	TCCAGTCCCTCT	0.478	
+	3	4687	_p.E157K|ABP1_u	NM_001091	NP_001082	P19801	ABP1_HUMAN		6	TGCAGGAAGCC	0.602	
+	5	707	SF10C_uc011kzr.1	NM_003841	NP_003832	O14798	TR10C_HUMAN	TAPE 1.	0	AATGAACACCA	0.557	
-	4	690	ense_Mutation_p.	NM_173833	NP_776194	Q6ZMJ2	SCAR5_HUMAN	ellular (Potential).	2	GCGCGGCCTGG	0.577	
-	7	854		NM_000637	NP_000628	P00390	GSHR_HUMAN		5	CTTAGAACCCA	0.413	
+	7	762	2_uc010lwz.1_Intr	NM_194294	NP_919270	Q6ZQW0	I23O2_HUMAN		2	CTGGGGGAGAG	0.478	
-	17	2585	NL_uc003xqt.3_	NM_144651	NP_653252	A1KZ92	PXDNL_HUMAN		2	CGCCCATCCGA	0.662	
-	5	541		NM_144651	NP_653252	A1KZ92	PXDNL_HUMAN	LRR 5.	2	TCTAATCTCAGA	0.433	
+	4	1274	1_uc011ldy.1_Intr	NM_006269	NP_006260	P56715	RP1_HUMAN		12	AAAGTCGATCA	0.408	
+	4	2679	1_uc011ldy.1_Intr	NM_006269	NP_006260	P56715	RP1_HUMAN		12	TGGCATCTGGGT	0.333	
+	10	1775	ense_Mutation_p.	NM_184085	NP_908973	Q9BYV6	TRI55_HUMAN		5	CCCTCCAGGGA	0.468	
-	4	588	A6_uc003xxs.2_	NM_020361	NP_065094	Q8N4T0	CBPA6_HUMAN		2	TGAAGATCTTCTA	0.383	
+	2	620		NM_004770	NP_004761	Q92953	KCNB2_HUMAN	lasmic (Potential).	7	TAAACAGGAAGA	0.507	
-	9	985	s.1_Missense_Mu	NM_015902	NP_056986	O95071	UBR5_HUMAN		28	TTCACGTAAAC	0.453	
+	1	339		NM_003301	NP_003292	P34981	TRFR_HUMAN	Name=3; (Potential).	3	ATTTGGGAATTA	0.463	
+	46	7005		NM_177531	NP_803875	Q86WI1	PKHL1_HUMAN	ular (Potential).|G8 1.	14	GGACTCGCTTG	0.383	rs73309320
-	48	7683	.E2468D|CSMD3_	NM_198123	NP_937756	Q7Z407	CSMD3_HUMAN	xtracellular (Potential).	63	ATCAAATTCCTTT	0.328	
-	38	6280	nt.2_Missense_M	NM_198123	NP_937756	Q7Z407	CSMD3_HUMAN	ar (Potential).|CUB 11.	63	AAGATGAAATCC	0.274	
+	22	3001	uc003yqy.1_Intron	NM_001039112	NP_001034201	Q2WGJ9	FR1L6_HUMAN	lasmic (Potential).	11	TGAGCCCCCCA	0.488	
-	61	4742	ljo.1_Missense_M	NM_152888	NP_690848	Q8NFW1	COMA1_HUMAN	y-rich.|Collagen-like 14.	13	GTAGTCCTTGG	0.602	
-	2	682	_p.E281G|TRAPP	NM_001160372	NP_001153844	Q96Q05	TPPC9_HUMAN		2	TTTTTCTCAAACG	0.532	
-	17	2211	e_Mutation_p.V64	NM_012154	NP_036286	Q9UKV8	AGO2_HUMAN	Piwi.	0	TCCCAACCTTCG	0.622	
-	40	5798	.G1289E|PTPRD_	NM_002839	NP_002830	P23468	PTPRD_HUMAN	).|Tyrosine-protein phosph	22	TCAGATCCTTCTA	0.388	
+	23	3714	_p.V1231I|CNTLN_	NM_017738	NP_060208	Q9NXG0	CNTLN_HUMAN	Potential.	1	TCCTAGTATCAA	0.348	

-	2	384	KN2A_uc010miu.	NM_000077	NP_000068	P42771	CD2A1_HUMAN	ANK 2.	)|p.V28_V51de	3678	CACTCGGGCGC	0.677	rs121913387
-	1	2639	uc003zrh.1_5'Flan	NM_153809	NP_722516	Q8IZX4	TAF1L_HUMAN			26	GCTTTTTTTATAT	0.453	
-	1	637		NM_019897	NP_063950	Q9NQN1	OR2S1_HUMAN	ellular (Potential).		1	TGATGGAAATG	0.473	
+	2	121_122	aah.1_Missense_	NM_014907	NP_055722	Q5SYB0	FRPD1_HUMAN			9	CTTCGGCGCTC	0.525	rs146611803
+	21	2415	akq.3_Missense_	NM_033305	NP_150648	Q96RL7	VP13A_HUMAN			10	AGCTGCTTTAC	0.323	
-	5	1086		NM_017561	NP_060031	A1L443	FA22F_HUMAN	Pro-rich.		0	TGGGCCTTGGT	0.706	
-	6	679	wo.1_Missense_	NM_014930	NP_055745	Q9Y2H8	ZN510_HUMAN			0	AGCTACATGCA	0.333	
-	1	208		NM_001001956	NP_001001956	Q8NGT0	O13C9_HUMAN	Name=2; (Potential).		0	GATGTCCAAGA	0.478	
+	2	193	TGS1_uc004bmf.1	NM_000962	NP_000953	P23219	PGH1_HUMAN			2	CGCTCCCCGTC	0.672	
+	27	2939	wu.2_Nonsense_	NM_015354	NP_056169	Q5SRE5	NU188_HUMAN			7	AAGATCGATAC	0.547	
+	15	3182	p.P626S|BAT2L1_	NM_013318	NP_037450	Q5JSZ5	PRC2B_HUMAN			0	TTCCCCCCATG	0.562	
-	3	436		NM_006753	NP_006744	O75683	SURF6_HUMAN			1	CAGTCGCTGTC	0.632	
+	4	699	sense_Mutation_p.	NM_016034	NP_057118	Q9Y399	RT02_HUMAN			0	TGGCCGTGAGA	0.607	
-	2	240	10_uc011mee.1_Missense_Mutation_p.D61N|LCN10_			Q6JVE6	LCN10_HUMAN			1	CTTGTCCCTGG	0.647	
-	5	3009		NM_015419	NP_056234	Q9NR99	MXRA5_HUMAN			8	GTGACGATCCA	0.502	
+	2	115	Intron|ARHGAP6_	NM_001142	NP_001133	Q99217	AMELX_HUMAN			0	TTTTGCCATGC	0.403	
-	5	1109	se_Mutation_p.P1	NM_002641	NP_002632	P37287	PIGA_HUMAN	lasmic (Potential).		0	CTCAGGAATTC	0.373	
+	5	825	PS2_uc010nfr.2_5	NM_206923	NP_996806	O15391	TYY2_HUMAN			2	CATTTGCAACTT	0.343	
+	10	1102		NM_001415	NP_001406	P41091	IF2G_HUMAN			1	GTGCAGTCGGA	0.423	
+	2	692		NM_173699	NP_775970	Q96M61	MAGBI_HUMAN	MAGE.		1	TGGATCCCATC	0.438	
+	1	1557		NM_001013736	NP_001013758	Q5HY64	FA47C_HUMAN			3	AGCCTTCTGAG	0.612	rs141294322
+	1	277		NM_000531	NP_000522	P00480	OTC_HUMAN			2	TTCATGGTTCG	0.383	
-	4	568	orf38_uc004dev.1_	NM_144970	NP_659407	Q8TB03	CX038_HUMAN			1	TCAGAAAATTTT	0.358	
+	3	272	M3_uc004dkg.2_	NM_006743	NP_006734	P98179	RBM3_HUMAN	RRM.		1	CTCAGCGGTCC	0.552	
-	10	1213	TMR8_uc004dvt.1	NM_017677	NP_060147	Q96EF0	MTMR8_HUMAN	ularin phosphatase.		4	TTTGGGAAAAC	0.343	
+	4	928	p.P229H|EDA_uc	NM_001399	NP_001390	Q92838	EDA_HUMAN	(Potential).|Collagen-like.		3	ACCCCCTGGCC	0.453	
+	11	1892	p.S185G|DLG3_u	NM_021120	NP_066943	Q92796	DLG3_HUMAN	SH3.		2	TGCCAAGCCAG	0.522	
-	3	4825		NM_001008537	NP_001008537	Q5QGS0	K2022_HUMAN			15	GTTTTCCCATTG	0.453	
+	2	512		NM_005296	NP_005287	Q99677	LPAR4_HUMAN	ellular (Potential).		3	ATGATTCCTTCA	0.403	
+	5	352	OL_uc010nmp.2_	NM_198450	NP_940852	Q6UXV4	APOOL_HUMAN			0	TCTTCCGAAAAT	0.338	
+	6	1339	fa.2_Missense_M	NM_019117	NP_061990	Q9C0H6	KLHL4_HUMAN			5	TGAAACCAGTT	0.378	
+	13	2432	mj.3_Missense_M	NM_018015	NP_060485	Q6NSI4	CX057_HUMAN			3	ACCATGAGATA	0.269	
-	2	439		NM_031273	NP_112563	Q9BXU2	TX13B_HUMAN			1	CTGTTCCTTGA	0.567	
-	11	2623		NM_020721	NP_065772	Q9ULL0	K1210_HUMAN			5	TCTGAGAGGCA	0.453	
-	2	438	e.3_Missense_M	NM_001421	NP_001412	Q99607	ELF4_HUMAN			1	CCATCCCGTTG	0.527	
-	5	737	f.2_Missense_M	NM_001555	NP_001546	Q8N6C5	IGSF1_HUMAN	2.|Extracellular (Potential).		5	CATATCCCTCTT	0.502	
+	4	1601	EC1_uc010nsl.1_	NM_005462	NP_005453	O60732	MAGC1_HUMAN			4	GTTTTCCCCAG	0.458	
+	15	1663	R1_uc004fcl.3_M	NM_002024	NP_002015	Q06787	FMR1_HUMAN	tion with RANBP9.		3	ATAGGAACTAAT	0.388	
+	3	739	_p.Q195*|MAGEA	NM_002362	NP_002353	P43358	MAGA4_HUMAN	MAGE.		3	AATAATCAGATC	0.547	
-	3	993		NM_005362	NP_005353	P43357	MAGA3_HUMAN	MAGE.		0	GCCGGGGACCT	0.527	
+	26	4744		NM_017514	NP_059984	P51805	PLXA3_HUMAN	lasmic (Potential).		3	GCGTCCCAAAG	0.607	
-	18	6092	1_Missense_Muta	NM_000132	NP_000123	P00451	FA8_HUMAN	3.|Plastocyanin-like 6.		11	TGAATAGAATGG	0.403	
-	6	1023	_p.P286L|TMLHE_	NM_018196	NP_060666	Q9NVH6	TMLH_HUMAN			1	CCTCAGGTGCC	0.418	
+	12	1867	5'Flank|PLEKHN1_	NM_198317	NP_938073	Q6TDP4	KLH17_HUMAN	on with F-actin (By similarit		0	CGACGGTAGCT	0.647	
+	6	817	_Mutation_p.R24	NM_022114	NP_071397	Q9HAZ2	PRD16_HUMAN	2-type 1; atypical.		7	CCTGCGGCGCC	0.632	
+	2	520	pv.2_Nonsense_	NM_025106	NP_079382	Q96BD6	SPSB1_HUMAN	B30.2/SPRY.		0	ACGACCGATCG	0.562	
+	9	1083	_p.D290E|PEX14_	NM_004565	NP_004556	O75381	PEX14_HUMAN			1	GGGGATGGGC	0.582	

+	8	1273		NM_015207	NP_056022	Q5T2D3	OTUD3_HUMAN		0	GAACACGCAGG	0.552	
-	18	2156	se_Mutation_p.S6	NM_001397	NP_001388	P42892	ECE1_HUMAN	ellular (Potential).	3	GGAGCGAGTGC	0.552	
-	61	7974	d.2_Missense_M	NM_005529	NP_005520	P98160	PGBM_HUMAN	ike C2-type 12.	9	AGGTCTGCCCT	0.632	
+	7	896	A3B_uc009vqf.2_	NM_007352	NP_031378	P08861	CEL3B_HUMAN	eptidase S1.	1	TTCATTGACTGG	0.607	
+	15	2713_2714		NM_020526	NP_065387	P29322	EPHA8_HUMAN	Potential).|Protein kinase.	13	GGCTGCCCCC	0.673	
+	4	1126	vry.1_Missense_	NM_020379	NP_065112	Q9NR34	MA1C1_HUMAN	enal (Potential).	1	ACATCGGGGGA	0.423	
-	6	2965	sz.1_Missense_M	NM_001029882	NP_001025053	Q5TGY3	AHDC1_HUMAN	Gly-rich.	1	CCGCCGGAAGC	0.677	
+	6	847	_p.G105D|EIF3I_u	NM_003757	NP_003748	Q13347	EIF3I_HUMAN		1	TGGGGGCAACA	0.547	
+	4	391	p.G85R|LCK_uc01	NM_005356	NP_005347	P06239	LCK_HUMAN	SH3.	6	AGAAGGGGGAA	0.617	
-	21	3392	byw.2_Missense_	NM_024874	NP_079150	Q8IZA0	K319L_HUMAN	lasmic (Potential).	2	CCTCCCGCGGG	0.637	
+	4	336	001cfy.3_Nonsen	NM_001142588	NP_001136060	Q13952	NFYC_HUMAN		3	TTTGATCAGTTT	0.413	
-	4	5294	e_Mutation_p.P13	NM_024503	NP_078779	Q5T1R4	ZEP3_HUMAN		6	TGGGGGTTCCT	0.562	
+	22	4241	wt.2_Missense_M	NM_002840	NP_002831	P10586	PTPRF_HUMAN	lasmic (Potential).	10	CGATCGGACTG	0.587	
-	3	355	ob.2_Missense_M	NM_181697	NP_859048	Q06830	PRDX1_HUMAN	Thioredoxin.	0	GCTTCGGGTCT	0.458	
+	2	541	.1_RNA|PCSK9_u	NM_174936	NP_777596	Q8NBP7	PCSK9_HUMAN		4	TGAAGGAGGAG	0.622	
+	3	706	i.3_Missense_Mu	NM_005012	NP_005003	Q01973	ROR1_HUMAN	.|Extracellular (Potential).	19	AGCCCCGGAGG	0.572	
-	6	1673	ose.1_RNA|COL2	NM_152890	NP_690850	Q17RW2	COOA1_HUMAN		5	GTTGACCTGGG	0.308	
-	27	3017_3018	M1_uc001dob.3_	NM_001017975	NP_001017975	A2PYH4	HFM1_HUMAN	SEC63.	0	CAAAGGGGGGAT	0.257	
-	6	1160	_p.V190I|TGFBR	NM_003243	NP_003234	Q03167	TGBR3_HUMAN	ellular (Potential).	3	TGTGTACTTCCT	0.458	
-	4	679		NM_144988	NP_659425	Q96F25	ALG14_HUMAN	lasmic (Potential).	0	TACACCGATTTG	0.408	
-	10	1257		NM_000110	NP_000101	Q12882	DPYD_HUMAN		8	CTCAGGGACAG	0.408	
-	2	1097		NM_020703	NP_065754	Q86WK6	AMGO1_HUMAN	xtracellular (Potential).	2	CTGCCGATACT	0.517	
-	15	1382	_Mutation_p.R41	NM_133181	NP_573444	Q8TE67	ES8L3_HUMAN		3	TCCCCGCCTAA	0.572	
+	1	2401	ense_Mutation_p.	NM_022768	NP_073605	Q96T37	RBM15_HUMAN		3	TGGGGGGACAG	0.542	
+	3	584	_Mutation_p.R20	NM_001688	NP_001679	P24539	AT5F1_HUMAN		0	AAAGTTCGTTAT	0.438	
+	6	475	1A_uc001ebl.2_	NM_002884	NP_002875	P62834	RAP1A_HUMAN		0	TGAGCGAGTAG	0.383	rs139066408
+	2	445	_uc010owp.1_5'F	NM_022836	NP_073747	Q9H816	DCR1B_HUMAN		0	ATGACCGTAACC	0.468	
+	19	1806	se_Mutation_p.E5	NM_003176	NP_003167	Q15431	SYCP1_HUMAN	Potential.	1	CACAGGAAACA	0.239	
+	4	506		NM_152367	NP_689580	Q8N8X9	MB213_HUMAN		0	TGGCCGGGTAC	0.587	
+	18	2989	a-mir-942|MI0005	NM_003594	NP_003585	Q9UNY4	TTF2_HUMAN		1	AGAGAGCACCA	0.478	
-	19	2691		NM_206996	NP_996879	Q6Q759	SPG17_HUMAN		6	TTTTCTCATTCAT	0.318	
+	4	466				P26439	3BHS2_HUMAN		2	CAAGATCAAGCT	0.473	
+	76	9465	BPF10_uc010oyl.1	NM_001039703	NP_001034792	A6NDV3	A6NDV3_HUMAN		0	ATGAGAAAGGG	0.493	
-	1	143	2AC_uc001etd.2_	NM_003528	NP_003519	Q16778	H2B2E_HUMAN		1	CTTTGCGGCTG	0.572	
-	3	1161		NM_001122965	NP_001116437	Q6XPR3	RPTN_HUMAN	Gln-rich.	0	GTAGTGGGAAC	0.473	
-	33	4690	p.H449Y|NUP210	NM_207308	NP_997191	Q5VU65	P210L_HUMAN		11	TGTCATGAAAAA	0.428	
-	8	2697	i.2_Missense_Mut	NM_001111	NP_001102	P55265	DSRAD_HUMAN		6	AGGGAGCTGTG	0.567	
-	3	130	CRL2_uc009wsp.	NM_030764	NP_110391	Q96LA5	FCRL2_HUMAN	1.|Extracellular (Potential).	2	AGGGCGCCACA	0.498	rs144041840
+	9	2232	_uc010pmx.1_3'	NM_022093	NP_071376	Q9UQP3	TENN_HUMAN	nectin type-III 6.	9	CAGACAGGTAAG	0.557	
-	8	1716	_Mutation_p.E50	NM_004319	NP_004310	O14525	ASTN1_HUMAN		15	CCCATTCGTTCC	0.493	
+	1	1132		NM_016545	NP_057629	Q5VY09	IER5_HUMAN		1	CCCGCCGGAACT	0.498	
-	28	3413	.R1051K|KCNT2_	NM_198503	NP_940905	Q6UVM3	KCNT2_HUMAN	lasmic (Potential).	7	CTGTTTCTTCGAC	0.358	
+	2	1192		NM_004767	NP_004758	O60883	ETBR2_HUMAN	Name=6; (Potential).	2	GAGAACGTCTGC	0.627	
-	2	921	ha.3_Missense_	NM_025179	NP_079455	O75051	PLXA2_HUMAN	lar (Potential).|Sema.	3	GTGGACGGTCA	0.607	
-	5	823	K2_uc001his.3_	NM_002497	NP_002488	P51955	NEK2_HUMAN	rotein kinase.	3	TTTTCCCAGCG	0.343	
-	3	614	47_uc001hrf.2_5'F	NM_023007	NP_075383	Q9H9V9	JMJD4_HUMAN	JmjC.	0	CAGTCGGACGAG	0.612	
-	7	1416	k|TRIM17_uc001h	NM_016102	NP_057186	Q9Y577	TRI17_HUMAN	B30.2/SPRY.	1	AGGCCGTCTGG	0.637	

+	1	935		NM_001004342	NP_001004342	Q6ZTA4	TRI67_HUMAN	box-type 2.		4	GGCCCGCAAGT	0.711	
-	44	10178	i.2_Missense_Mut	NM_000081	NP_000072	Q99698	LYST_HUMAN	BEACH.		12	AAGACGAGGAT	0.448	
+	1	659		NM_001004690	NP_001004690	A3KFT3	OR2M5_HUMAN	lasmic (Potential).		3	TGCTCGAGTTAT	0.423	rs148081072
+	16	1717	s.1_Missense_Mu	NM_002627	NP_002618	Q01813	K6PP_HUMAN			3	TCACCGACGTA	0.602	
-	2	297	ense_Mutation_p.	NM_031453	NP_113641	Q9H098	F107B_HUMAN			4	TTTCTGAGGCC	0.393	
-	55	8753	UBN_uc009xjr.1_	NM_001081	NP_001072	O60494	CUBN_HUMAN	CUB 21.		19	GAAGACGGCAG	0.577	
+	12	1205	DSS1_uc010qdf.1_	NM_014317	NP_055132	Q5T2R2	DPS1_HUMAN			0	ATGAAGCAATA	0.423	
-	4	1153	1iwc.1_Missense_	NM_018287	NP_060757	Q8IWW6	RHG12_HUMAN	WW 1.		0	AGGAGGTTTCC	0.448	
+	11	1661	p.R489H|ALOX5_	NM_000698	NP_000689	P09917	LOX5_HUMAN	ipoxygenase.		2	GGGCCGCAAGT	0.692	
+	4	897	pp.2_Missense_M	NM_012238	NP_036370	Q96EB6	SIRT1_HUMAN	tylase sirtuin-type.		0	ATGCTCGCCTT	0.378	
+	21	4038	YPN_uc009xpt.2_	NM_032578	NP_115967	Q86TC9	MYPN_HUMAN	action with ACTN.		5	GCTACGGATCT	0.488	
+	17	2242	nse_Mutation_p.P	NM_033100	NP_149091	Q96JP9	CDHR1_HUMAN	lasmic (Potential).		1	CTGCGCCCCGC	0.567	
+	17	2496	nse_Mutation_p.M	NM_033100	NP_149091	Q96JP9	CDHR1_HUMAN	lasmic (Potential).		1	ACTATGGGAAG	0.567	
+	6	978		NM_004329	NP_004320	P36894	BMR1A_HUMAN			8	TCATAGGTAGGT	0.433	
+	6	1417		NM_000314	NP_000305	P60484	PTEN_HUMAN	hatase tensi	|p.K128fs*47(1	2334	AAAGGGACGAA	0.413	rs121909218
-	9	875	_Mutation_p.E210	NM_013314	NP_037446	Q8WV28	BLNK_HUMAN	Pro-rich.		2	GGTTTCCCAGG	0.587	
-	13	1782	qot.1_Missense_M	NM_020123	NP_064508	Q9HD45	TM9S3_HUMAN	ical; (Potential).		0	ATGCAGCAGAG	0.333	
-	2	450_451	AP19_uc001kmy.2	NM_003061	NP_003052	O75093	SLIT1_HUMAN	LRR 1.		4	AGTTCCCTGGA	0.619	
+	5	2935	RC1_uc010qqj.1_	NM_015062	NP_055877	Q5VV67	PPRC1_HUMAN	Pro-rich.		3	CACCCCCTCCT	0.622	
+	9	1278	x.2_Missense_Mu	NM_016169	NP_057253	Q9UMX1	SUFU_HUMAN		p.S377fs*7(1)	7	AGTCCGGAGCC	0.587	
-	13	1550	08L|ABLIM1_uc0	NM_002313	NP_002304	O14639	ABLM1_HUMAN			1	TGGACGGCTCA	0.473	
+	23	3826	e_Mutation_p.S27	NM_207303	NP_997186	Q5VV63	ATRN1_HUMAN	ellular (Potential).		7	ATATATCAATTAA	0.279	
+	17	1982	T1_uc009xzz.1_	NM_007329	NP_015568	Q9UGM3	DMBT1_HUMAN	SRCR 5.		7	GCACCGTGTGT	0.597	
+	2	847		NM_003577	NP_003568	Q5T230	UTF1_HUMAN			0	ACACCGCCCTG	0.378	
+	5	687		NM_030783	NP_110410	Q9BVG9	PTSS2_HUMAN	ellular (Potential).		0	ACTACGGGGGA	0.612	
-	1	602		NM_001005161	NP_001005161	Q8NGK2	O52B4_HUMAN	Name=5; (Potential).		0	AAAACCCATAC	0.373	
+	1	451	_uc001mam.1_Int	NM_001004756	NP_001004756	B2RNI9	B2RNI9_HUMAN			0	CTGGCCAGCAA	0.527	
-	1	327	.1_Intron|TRIM22_	NM_001001922	NP_001001922	Q8NH56	O52N5_HUMAN	Name=3; (Potential).		2	AACATCTGGGC	0.488	
-	6	1482	f16_uc001mhc.3_	NM_020643	NP_065694	Q9NQ32	CK016_HUMAN			2	TGACTCCGCTTT	0.537	
+	12	1675	_p.R256Q|TEAD1_	NM_021961	NP_068780	P28347	TEAD1_HUMAN	al activation (Potential).		0	TATACCGAATAAA	0.373	
+	1	766	E3B_uc010rcr.1_M	NM_000922	NP_000913	Q13370	PDE3B_HUMAN			0	CACCCGGACCA	0.687	
-	1	376	mri.1_Missense_M	NM_030771	NP_110398	Q96HJ3	CCD34_HUMAN			0	GCTCGCCACTT	0.557	
-	10	1641	ew.1_Missense_M	NM_001001991	NP_001001991	Q6UXH9	PAMR1_HUMAN	eptidase S1.		2	TCATCCCGGTCA	0.527	
+	3	390	rik.1_Missense_M	NM_001004704	NP_001004704	Q8NH72	OR4C6_HUMAN	Name=1; (Potential).		2	ATCTACTTATTGT	0.393	
-	6	874	q.1_Missense_Mu	NM_003146	NP_003137	Q08945	SSRP1_HUMAN			2	CTCCCGGAAGA	0.527	
+	5	1801	_Mutation_p.R12	NM_015457	NP_056272	Q9C0B5	ZDHC5_HUMAN			1	GGTCCGCACGG	0.517	rs141814126
+	4	540		NM_023945	NP_076434	Q9H3V2	MS4A5_HUMAN	ellular (Potential).		2	CTCACCAAAATA	0.353	
+	20	2933		NM_006133	NP_006124	Q9Y4D2	DGLA_HUMAN	lasmic (Potential).		3	CGAGAGCCCCA	0.627	
+	14	1854	ym.2_Missense_	NM_178443	NP_848537	Q86UX7	URP2_HUMAN			1	AAGACGAGATC	0.632	
-	20	3263	9ypw.2_5'Flank|R	NM_005609	NP_005600	P11217	PYGM_HUMAN		p.R816G(1)	2	GGTGCGGTCAC	0.622	rs143177272
-	9	1423	p.P349L|SF1_uc0	NM_004630	NP_004621	Q15637	SF01_HUMAN	Pro-rich.		3	TGGCGGGAGCA	0.642	
-	28	3151		NM_017525	NP_059995	Q6DT37	MRCKG_HUMAN	PH.		4	CCCCTCGCTCT	0.697	
+	13	1552	dg.1_Nonsense_	NM_005186	NP_005177	P07384	CAN1_HUMAN	Domain III.		1	ACCTGCGAGAG	0.642	
+	13	1330	64*|BBS1_uc001oi	NM_024649	NP_078925	Q8NFJ9	BBS1_HUMAN			1	CACTGCGAGAG	0.602	
-	21	3553	1opz.2_Missense_	NM_012309	NP_036441	Q9UPX8	SHAN2_HUMAN			5	GCCACCCACGA	0.677	
-	3	667	IE3_uc009yvk.2_	NM_001014811	NP_001014811	Q16798	MAON_HUMAN			1	TAGGCGTGTAC	0.587	
+	18	2602	gb.2_Missense_M	NM_014361	NP_055176	O94779	CNTN5_HUMAN	nectin type-III 1.		8	CTATTGGGACA	0.468	

-	7	865		NM_002426	NP_002417	P39900	MMP12_HUMAN		0	TGTCAGGATTTG	0.403	
-	3	297	.R87W|MPZL3_uc	NM_198275	NP_938016	Q6UWV2	MPZL3_HUMAN	g-like V-type.	0	AAATCCGATCCC	0.413	
-	4	1023	p.T284M|PVRL1_	NM_002855	NP_002846	Q15223	PVRL1_HUMAN	otential).|Ig-like C2-type 2.	0	ACTTACGTGGTC	0.577	
+	8	447	10rzn.1_Missense_	NM_015313	NP_056128	Q9NZN5	ARHGC_HUMAN	PDZ.	7	GGGACGCCCAC	0.502	
-	4	353	sbj.1_Missense_Mu	NM_212555	NP_997720	Q6UY27	PATE2_HUMAN		0	TACTATGATCACA	0.453	
-	24	3376	p.R1082C|NFRKB_	NM_001143835	NP_001137307	Q6P4R8	NFRKB_HUMAN		3	TCAAGCGAAAAG	0.552	
+	19	4441	p.R1065C|WNK1_	NM_018979	NP_061852	Q9H4A3	WNK1_HUMAN		23	CTTAGACGTGCC	0.468	
+	10	1733	_uc001qkn.2_Miss	NM_199460	NP_955630	Q13936	CAC1C_HUMAN	lasmic (Potential).	11	GAGTCCGTCAAC	0.597	
+	9	944	_p.L180V|TEAD4_	NM_003213	NP_003204	Q15561	TEAD4_HUMAN		0	TCCAAGCTCTGG	0.677	
+	1	973		NM_002235	NP_002226	P17658	KCNA6_HUMAN		3	GCGGGGGCTGCT	0.667	
-	28	4488	VF_uc010set.1_Int	NM_000552	NP_000543	P04275	VWF_HUMAN	site for platelet glycoprotein	12	CCCACCGGGATC	0.597	rs61750079
-	30	3892	p.A302V|A2M_uc0	NM_000014	NP_000005	P01023	A2MG_HUMAN		5	ACAGAGCATGG	0.478	
-	5	807	n.2_Intron|GSG1_	NM_001080555	NP_001074024	Q2KHT4	GSG1_HUMAN	ical; (Potential).	0	ACTCACCTGACA	0.567	
+	10	2042	cw.1_Missense_Mu	NM_030667	NP_109592	Q16827	PTPRO_HUMAN	cellular (Potential).	9	GTGACAGCTCTA	0.473	
-	21	3055	_p.E173K|ADAMTS	NM_025003	NP_079279	P59510	ATS20_HUMAN	TSP type-1 4.	19	AAAATTCATTGC	0.403	
-	2	233		NM_025003	NP_079279	P59510	ATS20_HUMAN		19	TAGTGGGTTCGG	0.617	
+	13	1773	_p.V480M|ANO6_u	NM_001025356	NP_001020527	Q4KMQ2	ANO6_HUMAN	cellular (Potential).	2	CTCTCGGTGTTC	0.438	
+	10	1301	ARID2_uc009zkh.1	NM_152641	NP_689854	Q68CP9	ARID2_HUMAN		10	CTTGCACAAAAA	0.368	
+	11	1150	slz.1_Missense_M	NM_000725	NP_000716	P54284	CACB3_HUMAN		0	CTGACCGTACAG	0.607	
-	31	6284		NM_003482	NP_003473	O14686	MLL2_HUMAN		41	GTCTTACGGGCT	0.662	
-	5	754	E138Q|LMBR1L_u	NM_018113	NP_060583	Q6UX01	LMBRL_HUMAN	lasmic (Potential).	1	AGCCCTCAGACT	0.328	
-	2	143	B7_uc010snz.1_R	NM_000889	NP_000880	P26010	ITB7_HUMAN	cellular (Potential).	8	TGGGATCTTGGC	0.562	
-	8	1305	p.R274C|RARG_u	NM_000966	NP_000957	P13631	RARG_HUMAN	gand-binding.	4	AGATACGCAGCA	0.597	
+	24	5343	j.2_Missense_Mut	NM_012291	NP_036423	Q14674	ESPL1_HUMAN		3	ATCTGCGTTCAG	0.542	
+	2	466		NM_021191	NP_067014	Q9HD90	NDF4_HUMAN		4	CAAAATGAGGTG	0.398	
+	1	593		NM_001005243	NP_001005243	Q8NGE7	OR9K2_HUMAN	cellular (Potential).	2	TCGGGCTGTTG	0.393	
+	1	49		NM_001005518	NP_001005518	A6NJZ3	O6C65_HUMAN	cellular (Potential).	0	TTTACAGATAAC	0.323	
-	5	824	P19_uc001sid.2_F	NM_002429	NP_002420	Q99542	MMP19_HUMAN		1	AGCCCTCGTAGA	0.622	
+	2	233	zog.2_Missense_M	NM_002868	NP_002859	P61020	RAB5B_HUMAN		0	TATTACGTTTTGT	0.478	
+	10	1308	sqk.1_Missense_M	NM_173596	NP_775867	Q6ZMH5	S39A5_HUMAN	lasmic (Potential).	2	CAGGGGCTCAG	0.582	
-	17	2813	se_Mutation_p.R8	NM_001127460	NP_001120932	Q504Q3	PAN2_HUMAN		6	TCATGCGAATGG	0.428	
-	17	1771_1772	sxi.3_Missense_M	NM_032606	NP_115995	Q9BXY5	CAYP2_HUMAN	EF-hand 3.	2	ATAAAGGCCTAA	0.243	
-	3	1664	_p.G507E|USP44_	NM_001042403	NP_001035862	Q9H0E7	UBP44_HUMAN		3	TCTTTTCCACTG	0.393	
+	15	1913		NM_017564	NP_060034	Q8WWQ8	STAB2_HUMAN	lar (Potential).|FAS1 2.	14	TCCTTTCTCCAG	0.423	
+	6	587	tlq.2_Missense_M	NM_018082	NP_060552	Q9NW08	RPC2_HUMAN		2	CCGAGGCAGCC	0.463	
+	3	1958	_p.M479I|BTBD11_	NM_001018072	NP_001018082	A6QL63	BTBDB_HUMAN		3	ACAAATGGAATG	0.577	
-	3	544	RAP_uc009zvv.2_	NM_006768	NP_006759	Q7Z569	BRAP_HUMAN		1	ACGGAGAATCT	0.413	
-	13	1750	NO1_uc001ueu.2_	NM_018183	NP_060653	A3KN83	SBNO1_HUMAN		9	TCATTCGTTGCT	0.443	
-	11	1650	RB1_uc010tbd.1_	NM_005505	NP_005496	Q8WTV0	SCRB1_HUMAN	lasmic (Potential).	1	ACTTGGCTCCGG	0.647	
-	8	2346_2347	se_Mutation_p.D62	NM_178006	NP_821074	Q9Y3M8	STA13_HUMAN	Rho-GAP.	4	GAGGTCCCGGA	0.465	
-	11	2780	PC4_uc010abw.2_	NM_016179	NP_057263	Q9UBN4	TRPC4_HUMAN	and ITPR3.|Cytoplasmic (P	6	GTCTATGAAATAA	0.443	
+	3	5613		NM_207361	NP_997244	Q5SZK8	FREM2_HUMAN	|Extracellular (Potential).	11	GAATTGGGCATG	0.343	
+	26	3603	C3A_uc001vco.2_	NM_001079673	NP_001073141	Q9Y2H6	FND3A_HUMAN	onectin type-III 9.	2	GGTCCCGACTCT	0.438	rs142361918
-	1	466	_p.P15S|DACH1_	NM_080759	NP_542937	Q9UI36	DACH1_HUMAN		1	AGGGGGGACCA	0.622	
-	35	4952	ev.2_Missense_M	NM_015057	NP_055872	O75592	MYCB2_HUMAN		14	CTTCACGGAAGC	0.413	
-	13	2057	g.1_Missense_Mu	NM_000359	NP_000350	P22735	TGM1_HUMAN		3	TCACACGGTCCG	0.622	rs144517528
-	7	952	_p.R2W|ADCY4_u	NM_139247	NP_640340	Q8NFM4	ADCY4_HUMAN	lasmic (Potential).	3	TGATCCGCATGC	0.572	

+	4	1833	ml.2_Nonsense_M	NM_004274	NP_004265	Q13023	AKAP6_HUMAN			21	TCACTTGAGCCT	0.438	
-	1	1830		NM_001012706	NP_001012724	A1A4T8	CN182_HUMAN			0	CGGTTCGTGAA	0.537	
-	6	1263	h.1_Nonsense_Mu	NM_021818	NP_068590	Q9H4B6	SAV1_HUMAN	RAH.|Potential.		1	CTTTCGGTTTT	0.343	
-	3	273	xae.2_Missense_	NM_006832	NP_006823	Q96AC1	FERM2_HUMAN			0	TCTTCAGAAGC	0.408	
-	3	1275	arj.2_Missense_M	NM_021260	NP_067083	Q9HBF4	ZFYV1_HUMAN			1	GGGTCGGGGAG	0.493	
+	2	584	S_uc010asi.2_Mis	NM_005252	NP_005243	P01100	FOS_HUMAN			3	GGAGGGGCAAG	0.632	
-	5	2740	_p.V847M|STON2_	NM_033104	NP_149095	Q8WXE9	STON2_HUMAN	MHD.		5	TCTCACGCTGG	0.507	
+	2	620		NR_015340						2	TTCTGGGATCTG	0.672	
+	11	1480	_p.R376Q|TRAF3_	NM_145725	NP_663777	Q13114	TRAF3_HUMAN			3	GGCTCGGAACA	0.672	
+	10	1887	0txz.1_Missense_	NM_006291	NP_006282	Q03169	TNAP2_HUMAN			1	TCATTCGCCTG	0.637	
-	7	5530	x.2_Missense_Mu	NM_138420	NP_612429	Q8IVF2	AHNK2_HUMAN			1	CAGCCGCACAC	0.622	
-	88	13671	bi.2_Missense_Mu	NM_004667	NP_004658	O95714	HERC2_HUMAN	HECT.		13	CGGCCGGGCTG	0.632	
-	48	7734	bk.1_Missense_M	NM_004667	NP_004658	O95714	HERC2_HUMAN		p.A2543V(1)	13	CAACAGCACCA	0.333	rs139970998
+	8	1072		NM_033510	NP_277045	A7MBM2	DISP2_HUMAN			2	CCAGCGGACAG	0.637	
+	20	2440	LA2G4B_uc010bc	NM_001114633	NP_001108105	P0C869	PA24B_HUMAN	PLA2c.		1	CAGGCCCCACT	0.622	
-	3	313	adf.1_Missense_M	NM_015617	NP_056432	Q9Y3Y4	PYGO1_HUMAN	Pro-rich.		2	TTGACGAAGGT	0.443	rs144572806
-	8	1998	RC1_uc010bgt.1_	NM_003922	NP_003913	Q15751	HERC1_HUMAN	RCC1 5.		19	CTTTGCGAATG	0.373	
-	11	1726	2apj.3_Missense_	NM_005848	NP_005839	Q7Z401	MYCPP_HUMAN	DENN.		4	GAGAGGAACAT	0.413	
+	14	1932	ukf.1_Missense_M	NM_017691	NP_060161	Q8IUZ0	LRC49_HUMAN			1	TGATTTCCATTCT	0.368	
+	2	700	h.1_Missense_Mu	NM_005545	NP_005536	O14498	ISLR_HUMAN	LRR 4.		4	CCCGCGACGCC	0.612	
+	7	825	_p.V160I|ZFAND6	NM_019006	NP_061879	Q6FIF0	ZFAN6_HUMAN	AN1-type.		0	GTGGTGTACAC	0.373	
+	8	927	se_Mutation_p.I17	NM_003027	NP_003018	Q99963	SH3G3_HUMAN	n with ARC (By similarity).		3	AGAATATCAGCT	0.463	
+	3	675	AN_uc010upp.1_	NM_013227	NP_037359	E7EX88	E7EX88_HUMAN			3	CCTATCAGGAC	0.617	
-	6	905	G_uc002boa.2_R	NM_016321	NP_057405	Q9UBD6	RHCG_HUMAN	ical; (Potential).		1	CGGTACCCACG	0.617	
-	17	2606		NM_001150	NP_001141	P15144	AMPN_HUMAN	ular.|Metalloprotease.		4	AGAGACCATCT	0.592	
-	9	1170	.1_Missense_Mut	NM_002168	NP_002159	P48735	IDHP_HUMAN			711	GGGCCGGCCCT	0.667	
+	10	2648	2ckt.2_Missense_	NM_021098	NP_066921	O95180	CAC1H_HUMAN	=S1 of repeat II; (Potential		2	ATCATGATGGC	0.662	
+	35	6837	_p.P892S|CACNA	NM_021098	NP_066921	O95180	CAC1H_HUMAN	lasmic (Potential).		2	AACCCCCTGCG	0.721	
-	4	685	sense_Mutation_p	NM_002952	NP_002943	P15880	RS2_HUMAN			0	CTCTGCGCACG	0.647	
+	7	628	.3_uc010bsc.1_Mi	NM_006453	NP_006444	Q12788	TBL3_HUMAN	WD 3.		0	ATGCCGCCATC	0.677	
-	23	8898	e_Mutation_p.V28	NM_001009944	NP_001009944	P98161	PKD1_HUMAN	ellular (Potential).		3	CACAACGGAGT	0.682	rs145532417
-	23	8672	_Mutation_p.D28	NM_001009944	NP_001009944	P98161	PKD1_HUMAN	ular (Potential).|REJ.		3	ACCACGTCACT	0.622	
+	7	985	p.E313K|E4F1_uc	NM_004424	NP_004415	Q66K89	E4F1_HUMAN			1	CAGGCGAGCCT	0.592	
-	6	856	rz.1_Missense_M	NM_022119	NP_071402	Q9GZN4	BSSP4_HUMAN	eptidase S1.		1	GCCCTCGCCCC	0.701	
-	14	1704	|TRAP1_uc010uxf	NM_016292	NP_057376	Q12931	TRAP1_HUMAN			1	ACGAAGGTGCA	0.562	
-	25	2614	_p.A612T|CORO7_	NM_024535	NP_078811	P57737	CORO7_HUMAN			0	CACAGCCGTGT	0.617	
+	6	685		NM_014692	NP_055507	O43304	S14L5_HUMAN	RELI/MSF1.		0	TGAATGAGCTC	0.627	
+	3	317	AT_uc010buh.2_In	NM_020686	NP_065737	P80404	GABT_HUMAN			1	AAGTCCCAGGG	0.478	
-	3	721	.3_Intron|CPPED	NM_018340	NP_060810	Q9BRF8	CPPED_HUMAN			0	GTGCTGGAAGA	0.592	
-	44	7483	p.R2234*|SMG1_u	NM_015092	NP_055907	Q96Q15	SMG1_HUMAN	PI3K/PI4K.		16	TCATTCGAAAAG	0.373	
-	3	272	_p.T48M|UMOD_	NM_003361	NP_003352	P07911	UROM_HUMAN	EGF-like 1.		2	ACGTCGTAACG	0.612	
-	4	564	se_Mutation_p.S1	NM_001888	NP_001879	Q14894	CRYM_HUMAN			0	TAAAGGAGAAC	0.527	
+	8	1435		NM_000336	NP_000327	P51168	SCNNB_HUMAN	llular (By similarity).		7	GGACTTCCCAG	0.617	
+	6	2696	p.S608L|TNRC6A_	NM_014494	NP_055309	Q8NDV7	TNR6A_HUMAN	ction with EIF2C1 and EIF		2	AAACTTCAAGGA	0.468	
+	2	1570		NM_006040	NP_006031	Q9Y661	HS3S4_HUMAN	enal (Potential).		2	CAAGGGGTTCC	0.512	
+	12	1512	_Missense_Mutati	NM_001142448	NP_001135920	Q9H2V7	SPNS1_HUMAN			0	AGTTCCGGGCT	0.652	
+	3	1559	C5_uc002eca.3_	NM_001105247	NP_001098717	Q96C12	ARMC5_HUMAN	ARM 5.		1	CAACCTCCCAG	0.652	

+	1	108	5A2_uc010car.2_	NM_003041	NP_003032	P31639	SC5A2_HUMAN	ical; (Potential).	1	TCATTGCTGCAT	0.587	
+	4	495		NM_144602	NP_653203	Q8WTQ4	CP078_HUMAN		1	ATTCCGTCGAC	0.493	
+	9	1401	j.2_Missense_Mut	NM_005611	NP_005602	Q08999	RBL2_HUMAN	A.|Pocket; binds E1A.	5	GAGTCGTCTTC	0.453	
+	2	612	eld.2_Missense_M	NM_133368	NP_588609	Q96DX4	RSPRY_HUMAN		1	GTAATACGGACT	0.502	
+	3	422	_uc010vjt.1_5'Flan	NM_016948	NP_058644	Q9NPB6	PAR6A_HUMAN	vith PRKCI and PRKCZ.	1	CTCTGCAGCGG	0.617	
-	11	1503	_p.P437S|RANBP	NM_020850	NP_065901	Q6VN20	RBP10_HUMAN		1	GTTGGGGTAGT	0.602	
+	3	480	33Q|TSNAXIP1_uc	NM_018430	NP_060900	Q2TAA8	TXIP1_HUMAN		0	CTACCGGAAGC	0.592	
+	5	1931	2ewd.2_Missense_	NM_133458	NP_597715	Q8TF47	ZFP90_HUMAN	2H2-type 10.	1	GAACCCACACT	0.438	
-	10	1599		NM_005652	NP_005643	Q15554	TERF2_HUMAN	b-type.|H-T-H motif.	1	GGTCCGCCAGC	0.443	
+	10	995	_Mutation_p.D345	NM_145059	NP_659496	Q8N0W3	FUK_HUMAN		1	TTCGCGATCAG	0.642	
+	23	3135	.G1032D|FUK_uc	NM_145059	NP_659496	Q8N0W3	FUK_HUMAN		1	AGGCGGTGGAG	0.622	
+	3	268	DT7_uc010vnj.1_In	NM_001105663	NP_001099133	P0C024	NUDT7_HUMAN	udix hydrolase.	2	GAAGGGCCCCT	0.418	
-	5	717	se_Mutation_p.P1	NM_020947	NP_065998	Q6P9B6	K1609_HUMAN		2	ATGGGGGACCC	0.562	
+	4	1322	L36_uc010chl.2_In	NM_024731	NP_079007	Q8N4N3	KLH36_HUMAN	Kelch 2.	2	TGCCTCCATCG	0.567	
-	19	2787	p.G918S|ANKFY1	NM_016376	NP_057460	Q9P2R3	ANFY1_HUMAN	ANK 17.	3	TGAGCCTGCTT	0.438	
+	10	970	fym.2_Missense_	NM_004313	NP_004304	P32121	ARRB2_HUMAN	ction with TRAF6.	0	GCACCGCCCAG	0.567	
+	27	4402		NM_020877	NP_065928	Q9P225	DYH2_HUMAN	n (By similarity).	13	CATCCGCAAGC	0.517	rs146287609
-	12	1662	ER1_uc010vur.1_	NM_002616	NP_002607	O15534	PER1_HUMAN		9	TGGGGGCCGGG	0.657	
+	13	3051	p.D966N|MYOCD	NM_153604	NP_705832	Q8IZQ8	MYCD_HUMAN		5	ACATCGATTTC	0.517	
+	9	1614	.G272S|ALDH3A	NM_000382	NP_000373	P51648	AL3A2_HUMAN	ical; (Potential).	2	AACTCGGTCTC	0.473	
-	9	1113	277N|SLC47A2_uc	NM_152908	NP_690872	Q86VL8	S47A2_HUMAN	ellular (Potential).	0	GGAAGCTCCCG	0.647	
-	1	124		NM_032854	NP_116243	Q6QEF8	CORO6_HUMAN		0	TGACGGCACAG	0.587	
+	9	981	_p.R289H|RHBDL	NM_138328	NP_612201	P58872	RHBL3_HUMAN	ical; (Potential).	1	GGGCCGTGTGG	0.662	
-	12	1410	E1_uc002hiz.1_	NM_018096	NP_060566	Q9NVX2	NLE1_HUMAN	WD 8.	4	TCAACAGCATAT	0.592	
-	1	427		NM_031960	NP_114166	Q9BYQ9	KRA48_HUMAN	-[IKRQVHEC]- [SPRT]-[S	0	gagatgctgcagctgg	0.124	
+	20	3104	.1_Missense_Mut	NM_004941	NP_004932	Q14562	DHX8_HUMAN		4	TATCCATGCTG	0.502	
-	23	3095	f.1_Missense_Mut	NM_005474	NP_005465	Q9UQL6	HDAC5_HUMAN	ne deacetylase.	1	AAACCCGGCGG	0.572	
-	5	965	_Mutation_p.T30	NM_002055	NP_002046	P14136	GFAP_HUMAN	Coil 2B.|Rod.	2	TCACCGTGCCG	0.716	
-	13	1723	LL6_uc002ioc.2_	NM_001130918	NP_001124390	Q8N841	TTLL6_HUMAN		0	TTCTTTCTCACT	0.527	
+	2	329	se_Mutation_p.L5	NM_006151	NP_006142	P22079	PERL_HUMAN		2	GTCCTTCTCCAT	0.488	
+	8	1319	se_Mutation_p.E2	NM_006151	NP_006142	P22079	PERL_HUMAN		2	ACCAGGAGGTC	0.617	
-	8	3242	_p.A429V|RNF43_	NM_017763	NP_060233	Q68DV7	RNF43_HUMAN	lasmic (Potential).	1	AAGCAGCAGGG	0.657	
-	5	735	.1_Missense_Muta	NM_004574	NP_004565	O43236	SEPT4_HUMAN		0	GAGCCGCAGCC	0.532	
-	13	1718	n.1_Missense_Mu	NM_032582	NP_115971	Q8NFA0	UBP32_HUMAN	DUSP.	5	TTTACCGCTGCC	0.333	rs147383770
-	2	688	ddt.2_Missense_	NM_001915	NP_001906	P49447	CY561_HUMAN	ntial).|Cytochrome b561.	1	GATGACGAGCG	0.617	
+	4	1088	wqx.1_Missense_	NM_181790	NP_861455	Q7Z601	GP142_HUMAN	Name=6; (Potential).	4	CATCACCACAC	0.667	
-	18	3635	wsc.1_Missense_	NM_020753	NP_065804	Q8WXE0	CSKI2_HUMAN	Pro-rich.	1	AGACTCGCCAG	0.692	
-	23	3913	se_Mutation_p.A516T|DNAH17_uc002jvs.2_RNA						9	AAAGGCGACTA	0.537	
-	5	386	s.2_Missense_Mu	NM_014740	NP_055555	P38919	IF4A3_HUMAN	ase ATP-binding.	1	TTCACGAACCT	0.393	
-	23	3117	1_Missense_Muta	NM_014984	NP_055799	Q9UPN4	AZI1_HUMAN		4	CTGCCGCACAA	0.697	
-	5	442		NM_016286	NP_057370	Q7Z4W1	DCXR_HUMAN		0	AGTTACTGCCC	0.438	
+	30	4802	.D1446E|PTPRM_	NM_002845	NP_002836	P28827	PTPRM_HUMAN	hatase 2.|Cytoplasmic (Po	6	GTCGACCTCCT	0.418	
-	9	957	kod.1_Missense_	NM_001042388	NP_001035847	Q8TF05	PP4R1_HUMAN	HEAT 8.	1	CACATGAAACC	0.413	
+	37	6670	nse_Mutation_p.S	NM_032142	NP_115518	E9PF99	E9PF99_HUMAN		5	CTAATTCCTCCT	0.328	
-	4	1704	CO1_uc002kti.1_	NM_052911	NP_443143	Q5FWF5	ESCO1_HUMAN		0	TTTTCGGGACC	0.413	
+	15	2780	nz.1_Missense_M	NM_025135	NP_079411	Q2V2M9	FHOD3_HUMAN	FH2.	8	ACCATCCGTTTG	0.502	
+	8	1279	_Mutation_p.E332	NM_014772	NP_055587	O43310	CTIF_HUMAN		0	TTCCCGAGCGC	0.562	

+	4	1315		NM_015879	NP_056963	O43173	SIA8C_HUMAN	nenal (Potential).	2	TTGTATGGATTTT	0.423	
+	8	1144	n_p.E201K|SERPI	NM_001143818	NP_001137290	P05120	PAI2_HUMAN		2	CCAGATGAAATTG	0.413	
+	3	651	_p.R109K|CDH7_u	NM_033646	NP_387450	Q9ULB5	CADH7_HUMAN	r (Potential).|Cadherin 1.	4	CCAAGAGACTGG	0.498	
-	24	3115	TN_uc010xfb.1_M	NM_173630	NP_775901	Q86VV8	RTTN_HUMAN		8	ACACCGGCTTCA	0.418	
-	5	354	p.P96L|TCF3_uc0	NM_003200	NP_003191	P15923	TFE2_HUMAN		7	AGTCCCGGTCCC	0.637	
+	4	469	p.R131H|C19orf36	NM_001039846	NP_001034935	Q1ZYL8	IZUM4_HUMAN		0	AGCACCGCTGTG	0.672	
-	9	909		NM_198492	NP_940894	Q6UXB4	CLC4G_HUMAN	(Potential).|C-type lectin.	0	CTTCTCGCTGTCA	0.627	
+	10	1161	S4_uc002mji.2_M	NM_024552	NP_078828	Q9HA82	CERS4_HUMAN	TLC.	1	CTCTTTCCCACC	0.567	
-	5	35849		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).	57	GCTGAAGAGCTG	0.498	
-	3	22243		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	ch.|Extracellular (Potential).	57	GAGTGGTTGATG	0.478	
-	3	20990		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).	57	GATGTGGAAACA	0.463	
-	1	9472		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).	57	GAGGCTCCTCCT	0.493	
-	1	7184		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	ch.|Extracellular (Potential).	57	TGGGGGAAGTG	0.473	
-	19	3002	e.2_Missense_Mu	NM_003331	NP_003322	P29597	TYK2_HUMAN	otein kinase 1.	9	ACGTCAGCAAGA	0.582	
+	4	1934	e_Mutation_p.C62	NM_144566	NP_653167	Q9H0M5	ZN700_HUMAN	2H2-type 14.	0	TCAGTTGTGCCT	0.483	
-	2	67		NM_001105578	NP_001099048	Q6PIF2	SYCE2_HUMAN		0	GCTGCGGTTCCT	0.612	
-	3	645	mwy.3_Missense_	NM_001127221	NP_001120693	O00555	CAC1A_HUMAN	=S2 of repeat I; (Potential)	2	ATGGTTCTGTGT	0.478	
+	12	2270	ng.1_Missense_M	NM_023072	NP_075560	Q9H7M6	ZSWM4_HUMAN		2	GGTGCGCTGGC	0.607	rs139232826
+	3	464	naf.2_Missense_M	NM_012114	NP_036246	P31944	CASPE_HUMAN		4	CACCATGAAAAGA	0.542	
+	1	121		NM_001004713	NP_001004713	O60431	OR1I1_HUMAN	Name=1; (Potential).	3	ATCATTGGAAATG	0.483	
-	5	973	26_uc002nee.2_I	NM_024881	NP_079157	Q96K37	S35E1_HUMAN	ical; (Potential).	2	CAGGACGTTGG	0.597	
+	6	1318	_p.R164H|NWD1_uc002nev.3_Missense_Mutation_p.R			Q149M9	NWD1_HUMAN	WD 1.	7	AGATCCGCCACC	0.622	rs61737596
-	2	457		NM_005234	NP_005225	P10588	NR2F6_HUMAN	eceptor.|NR C4-type.	0	TGAGACGGCAG	0.627	
+	8	2360	cc.1_Missense_Mu	NM_004386	NP_004377	O14594	NCAN_HUMAN		4	GTATCCCGGGGT	0.597	
+	4	1702		NM_031218	NP_112495	P35789	ZNF93_HUMAN	2H2-type 14.	1	AAAATTCATACTA	0.358	
-	4	935		NM_001159293	NP_001152765	C9JHM3	C9JHM3_HUMAN		1	TCTCCACTATGA	0.403	
-	4	1447	_p.K353E|ZNF708_	NM_021269	NP_067092	P17019	ZN708_HUMAN		6	GTTTCTTTCCAG	0.343	
-	4	1110	1_Intron|ZNF208_	NM_007153	NP_009084				7	GAAGGCTTTGC	0.413	
+	4	1398		NM_020855	NP_065906	Q9P255	ZN492_HUMAN	C2H2-type 9.	0	ATAAGAGAATTCA	0.378	
+	3	2263	rn.1_Missense_Mu	NM_001136156	NP_001129628	Q8TCN5	ZN507_HUMAN		5	TCCATCGACAGA	0.493	rs143809236
+	6	956	_p.V230I|KCTD1	NM_001129994	NP_001123466	Q96SI1	KCD15_HUMAN		1	AACTCGGTACAG	0.692	
+	5	2103		NM_144689	NP_653290	Q8TAQ5	ZN420_HUMAN	2H2-type 18.	0	TCACATCTTTCTC	0.433	
+	11	3705		NM_015073	NP_055888	O60292	SI1L3_HUMAN		2	GAGCAGGAAAGC	0.622	
+	66	10022	iv.1_Missense_Mu	NM_000540	NP_000531	P21817	RYR1_HUMAN		12	TGCCCGCCGGC	0.642	
+	2	1002	gn.1_Missense_Mu	NM_003407	NP_003398	P26651	TTP_HUMAN		1	CCCGGCGACTCC	0.617	
+	5	840	.1_Intron|CYP2S1	NM_030622	NP_085125	Q96SQ9	CP2S1_HUMAN		1	ATGCTTCGGGCC	0.652	
+	14	1385	F8_uc002otl.3_5'F	NM_173633	NP_775904	Q8NBT3	TM145_HUMAN		0	GGGAACGTGACG	0.667	
-	3	617	e_Mutation_p.A13	NM_005619	NP_005610	O75298	RTN2_HUMAN		3	GAGGCGCGGTG	0.682	
-	26	3819	6A_uc002pdm.2_	NM_004819	NP_004810	Q92797	SYMPK_HUMAN		1	CCTCCCGGAAAT	0.602	
+	6	683		NM_015603	NP_056418	Q9Y3X0	CCDC9_HUMAN	Potential.	0	GGAGCGGCGCA	0.567	
+	7	2811	_p.E722K|NLRP4_	NM_134444	NP_604393	Q96MN2	NALP4_HUMAN		15	TGCTGCGAATAC	0.512	
+	9	1149	zi.2_Missense_Mu	NM_003887	NP_003878	O43150	ASAP2_HUMAN	Potential.	0	AGCTTCGAGATAT	0.408	
+	31	5695	bp.1_Missense_Mu	NM_014668	NP_055483	Q4ZG55	GREB1_HUMAN		1	GTGCCCCGGAC	0.647	
+	3	1154	w.2_Missense_Mu	NM_002252	NP_002243	Q9BQ31	KCNS3_HUMAN	=Segment S2; (Potential).	4	TCACCGGGGAG	0.517	
-	19	3050	_p.M869I|PUM2_u	NM_015317	NP_056132	Q8TB72	PUM2_HUMAN	M-HD.|Pumilio 8.	1	TTCAGCCATATCA	0.413	
-	3	360	_p.E107K|HS1BP3	NM_022460	NP_071905	Q53T59	H1BP3_HUMAN	PX.	1	TCCTCTCCCGGA	0.562	
-	26	7584		NM_000384	NP_000375	P04114	APOB_HUMAN		27	GGTGTCCTGTAC	0.418	

-	4	436	n_p.T58I|POMC_u	NM_001035256	NP_001030333	P01189	COLI_HUMAN			1	TGGGAGTCTCG	0.692	
+	8	1472	P1_uc002rkp.2_M	NM_013392	NP_037524	Q9UHY1	NRBP_HUMAN	rotein kinase.		3	CACAACGGACTC	0.582	
-	2	224	Flank|GPN1_uc01	NM_024584	NP_078860	Q6ZUS5	CC121_HUMAN	Potential.		0	TTTCCGCTGGG	0.433	
+	3	473		NM_030915	NP_112177	Q53QV2	LBH_HUMAN			0	TCCAGGAGGAT	0.567	
-	3	428	_p.K61R|NLRC4_	NM_021209	NP_067032	Q9NPP4	NLRC4_HUMAN	CARD.		6	GAACCCTTTTTC	0.398	
+	10	1945	v.2_Nonsense_Mu	NM_206943	NP_996826	Q14766	LTBP1_HUMAN	alcium-bindi	p.R649*(1)	8	AGCTATCGATGT	0.378	
+	7	961	_p.E112K|RASGR	NM_170672	NP_733772	Q8IV61	GRP3_HUMAN	rminal Ras-GEF.		5	GATATGAAAAC	0.443	
-	8	902	RS7_uc010ynp.1_	NM_001031684	NP_001026854	Q16629	SRSF7_HUMAN	f R-R-S-R-S-X-S-X.|Arg/Se		0	GGAACGACTAA	0.378	
-	5	955	HX57_uc002rrg.2_	NM_198963	NP_945314	Q6P158	DHX57_HUMAN			3	ATTTGCGGAATC	0.343	
-	3	1662	2sit.3_Missense_	NM_015470	NP_056285	Q9BXF6	RFIP5_HUMAN			0	CGCTCCGACTT	0.637	
+	5	479	_p.A132S|REG3G	NM_198448	NP_940850	Q6UW15	REG3G_HUMAN	C-type lectin.		0	ACTTTGCATGG	0.507	
-	6	1221	svl.2_Missense_	NM_020151	NP_064536	Q9NQZ5	STAR7_HUMAN	START.		0	GGGACGGATAA	0.468	
-	34	4974	NP200_uc010yuj.1_	NM_014014	NP_054733	O75643	U520_HUMAN	ase C-terminal 2.		10	CAGGCGTCGCT	0.577	
-	15	2643	SEMA4C_uc002sx	NM_017789	NP_060259	Q9C0C4	SEM4C_HUMAN	lasmic (Potential).		2	CCTCGGGGTTG	0.652	
+	7	1009	70_uc002sye.1_Mi	NM_001079	NP_001070	P43403	ZAP70_HUMAN	nterdomain B.		6	GCTGCTCCCACA	0.706	
-	5	739		NM_004854	NP_004845	O43529	CHSTA_HUMAN	ble).|Lumenal (Potential).		1	ACTTTGGGAGTC	0.498	
-	4	909	se_Mutation_p.T1	NM_152515	NP_689728	Q8IYA6	CKP2L_HUMAN			0	GAACCGTCCTT	0.403	
-	7	1049	se_Mutation_p.H2	NM_025181	NP_079457	Q8WV83	S35F5_HUMAN			0	ATGCATGACTTG	0.388	
+	13	3842	nt.3_Missense_Mu	NM_005270	NP_005261	P10070	GLI2_HUMAN			13	CTGCAGCAACA	0.627	
+	18	2418	.2_Missense_Mut	NM_004522	NP_004513	O60282	KIF5C_HUMAN			1	TTCCAGGATAAG	0.413	
-	116	16579	_Mutation_p.R188	NM_004543	NP_004534	P20929	NEBU_HUMAN	Nebulin 149.		20	TAGTACGCAGG	0.299	rs16830171
+	6	1148	p.R194Q|GALNT1	NM_052917	NP_443149	Q8IUC8	GLT13_HUMAN	tial).|Catalytic subdomain A		6	TCTTCGAGGAG	0.423	
-	10	1412	P4_uc010fpb.2_5'U	NM_001935	NP_001926	P27487	DPP4_HUMAN	cellular (Potential).		3	TGTATGGAAGTT	0.393	
+	4	539	.2_Missense_Mut	NM_138995	NP_620482	Q8WXR4	MYO3B_HUMAN	rotein kinase.		19	AGCAATGATCTC	0.493	
-	2	711	K1_uc002ugp.2_M	NM_012290	NP_036422	Q9UKI8	TLK1_HUMAN			1	TGCAACTGCCC	0.393	
+	1	134	zew.1_Missense_	NM_021193	NP_067016	P35452	HXD12_HUMAN			0	CTACCCGCGCG	0.706	
-	6	688	NKRD44_uc002uu	NM_153697	NP_710181	Q8N8A2	ANR44_HUMAN	ANK 6.		5	CACGCCGGTCC	0.418	
+	2	1180	uv.3_Missense_Mu	NM_001114661	NP_001108133	Q15111	PLCL1_HUMAN			2	CCACCCGCGTG	0.373	
+	2	539	_p.S98P|GPBAR1	NM_170699	NP_733800	Q8TDU6	GPBAR_HUMAN	Name=3; (Potential).		1	TTCCTCTCCCTG	0.637	
+	13	1975		NM_032726	NP_116115	Q9BRC7	PLCD4_HUMAN	I-PLC Y-box.		3	CATTTCCGCCAG	0.532	
-	14	2162_2163	p.G602R|PTPRN_	NM_002846	NP_002837	Q16849	PTPRN_HUMAN	lasmic (Potential).		4	GTGTCCCGTGGA	0.663	rs145338513
+	17	3001	wm.2_Missense_	NM_005070	NP_005061	P48751	B3A3_HUMAN	al).|Membrane (anion exch		5	CCTGCGCAAGT	0.637	
-	7	2775	_p.L910F|SPHKA	NM_001142644	NP_001136116	Q2M3C7	SPKAP_HUMAN			10	AGGAAGCAGCA	0.483	
-	21	3119	IP12_uc002vpy.1_	NM_004238	NP_004229	Q14669	TRIPC_HUMAN			9	GCAGTCGTTTTC	0.398	
+	1	286		NM_152614	NP_689827	Q53QW1	CB057_HUMAN			1	ACGGCCAGAAG	0.532	
+	13	1288	FARP2_uc010zor.	NM_014808	NP_055623	O94887	FARP2_HUMAN			3	CATTCCCCGAG	0.478	
+	9	1283		NM_003245	NP_003236	Q08188	TGM3_HUMAN			9	ATGCCGACCGC	0.562	
+	7	1017	al.1_Missense_Mu	NM_198994	NP_945345	O95932	TGM3L_HUMAN			4	CGGGCGGACCC	0.612	rs148376598
-	5	1033	.1_Intron|VSX1_u	NM_014588	NP_055403	Q9NZR4	VSX1_HUMAN			0	CCTGCCGGGCA	0.592	
-	24	4051	p.S977F|NINL_uc	NM_025176	NP_079452	Q9Y2I6	NINL_HUMAN	Potential.		5	AGGTCGGACTTC	0.567	
+	2	91	tj.1_RNA|FRG1B_uc010gdr.1_RNA|FRG1B_uc010ztk.1_Intron							0	AATATCTTGGTA	0.333	rs137871677
+	3	187	RG1B_uc010gdr.1_RNA|FRG1B_uc010ztk.1_Missense_Mutation_p.L4S							0	CTTTGTTGGCCT	0.353	
+	3	189	RG1B_uc010gdr.1_RNA|FRG1B_uc010ztk.1_Missense_Mutation_p.A5T							0	TTGTTGGCCTCA	0.353	
+	1	135		NM_153324	NP_697019	Q8N688	DB123_HUMAN			0	TCTTATCCCAGC	0.537	
+	15	1934	tz.1_Missense_Mu	NM_006892	NP_008823	Q9UBC3	DNM3B_HUMAN	ADD.		5	GCGGCGCCGGA	0.637	
-	6	675	_Missense_Mutati	NM_018217	NP_060687	Q9BV94	EDEM2_HUMAN			0	CTGCCGTACAG	0.542	
+	14	1592	uc002xjn.1_Intron	NM_003286	NP_003277	P11387	TOP1_HUMAN		p.R449W(1)	7	TCGGCGGCTGA	0.468	

-	4	646		NM_016470	NP_057554	Q9NX31	CT111_HUMAN		0	ACTTGGGTAGCG	0.498	
+	8	1104	2_RNA|PABPC1L_	NM_001124756	NP_001118228	Q4VXU2	PAP1L_HUMAN	RRM 4.	1	GTTTTTCCTCCC	0.587	
-	2	399	se_Mutation_p.R17	NM_001135773	NP_001129245	Q9UM82	SPAT2_HUMAN		2	ACTTCCGAAATA	0.552	rs77667957
-	6	1341	nse_Mutation_p.R	NM_018197	NP_060667	Q9NPA5	ZF64A_HUMAN	C2H2-type 6.	2	GCTTCCGGAGG	0.582	
-	2	233	B46_uc002ygu.2_	NM_025224	NP_079500	Q86UZ6	ZBT46_HUMAN		2	TGGGACGTGATT	0.572	
-	7	1031		NM_198996	NP_945347	Q6XZB0	LIPI_HUMAN		2	TCCTAAGAGGTC	0.303	
+	2	266	se_Mutation_p.V5	NM_001186	NP_001177	O14867	BACH1_HUMAN	BTB.	2	GGTCCGTGCTG	0.522	rs149732438
-	13	2310	_p.V616M|GRIK1_	NM_000830	NP_000821	P39086	GRIK1_HUMAN	lasmic (Potential).	3	CACCACGTCTG	0.448	
+	13	1136	_p.G298D|PDE9A_	NM_002606	NP_002597	O76083	PDE9A_HUMAN	ytic (By similarity).	2	ATCCCGGCTACA	0.498	
-	3	378	v.3_Missense_Mu	NM_000071	NP_000062	P35520	CBS_HUMAN		0	GGGCCGGATCC	0.667	
-	3	1589	2zii.2_Missense_M	NM_001142854	NP_001136326	Q9H0A9	CU056_HUMAN		1	TAGCTCCTCCTG	0.662	
-	1	450	TEH_uc002zlh.1_5	NM_001136213	NP_001129685	Q6S545	POTEH_HUMAN		1	ATCTTGCTCCTG	0.607	
+	1	1646	R14_uc002zou.2_	NM_053006	NP_443732	Q96PF2	TSSK2_HUMAN		1	GAGCTGAGGTG	0.617	
-	2	868	4R_uc002zru.2_5'	NM_023004	NP_075380	Q9BZR6	RTN4R_HUMAN	LRR 7.	0	GTCACGGAAGG	0.647	
-	2	75	zue.2_Missense_M	NM_004173	NP_004164	O43246	CTR4_HUMAN		2	CCCCCGGGCCA	0.652	
+	14	1912	p.P490L|NF2_uc0	NM_000268	NP_000259	P35240	MERL_HUMAN	p.P490fs*25(2)|p.P483fs*	728	AGCACCGTTGC	0.463	
+	7	1702_1703	ense_Mutation_p.F	NM_030758	NP_110385	Q969R2	OSBP2_HUMAN		2	CGGCCGGGAGC	0.609	
-	3	497	03K|PIK3IP1_uc0	NM_052880	NP_443112	Q96FE7	P3IP1_HUMAN	cellular (Potential).	1	AGGTACCTGGAC	0.736	
-	3	486	aqe.2_Nonsense_	NM_001163857	NP_001157329	O43247	EAN57_HUMAN		0	ATGGCTGAGCCC	0.622	
+	15	1983	_Mutation_p.V536	NM_013365	NP_037497	Q9UJY5	GGA1_HUMAN	GAE.	3	CCGACGTGCTG	0.622	
+	2	425		NM_004286	NP_004277	O00178	GTPB1_HUMAN		1	GGATGCGGAGAG	0.393	rs11547402
-	4	282	xc.2_Nonsense_M	NM_175709	NP_783640	O95931	CBX7_HUMAN	Chromo.	1	ATGCTCGGTCTC	0.592	
+	18	4668	yn.3_Nonsense_M	NM_001162501	NP_001155973	Q9UPQ9	TNR6B_HUMAN		0	TGCCATGGAAAG	0.413	
-	3	317	gye.1_Missense_M	NM_020831	NP_065882	Q969V6	MKL1_HUMAN	on with SCAI and ACTB (B	5	AGCTCCGATCTC	0.473	
-	2	199	nse_Mutation_p.V	NM_032311	NP_115687	Q9BY77	PDIP3_HUMAN		0	CCCAACTCGAG	0.502	
-	15	1805		NM_173050	NP_766638	Q8IWY4	SCUB1_HUMAN		5	TGCTCGCTTCC	0.537	
-	1	286	v.1_RNA|LOC400	NM_018280	NP_060750	Q9NV39	CV026_HUMAN	Pro-rich.	0	ACGGAGGACGG	0.756	
-	12	2029		NM_001080447	NP_001073916				2	CGGGAGCTCCA	0.677	
-	4	720	_p.E26K|IL5RA_u	NM_000564	NP_000555	Q01344	IL5RA_HUMAN	cellular (Potential).	1	TCTTTTCATCAGG	0.348	
+	5	668	uc003bru.2_Transl	NM_001080517	NP_001073986	Q9C0A6	SETD5_HUMAN		2	ACGCTGTGGAG	0.567	
-	16	2769	vw.2_Missense_M	NM_001001331	NP_001001331	Q01814	AT2B2_HUMAN	lasmic (Potential).	6	TCAATTCGCTCC	0.488	
-	34	4761		NM_024923	NP_079199	Q8TEM1	PO210_HUMAN	enal (Probable).	11	GTGACGGGCCA	0.443	
-	13	2448	p.V589M|XPC_uc	NM_004628	NP_004619	Q01831	XPC_HUMAN	NA; required for formation	3	GGCCACGCGGT	0.592	
+	10	3411	_p.V1101I|FGD5_u	NM_152536	NP_689749	Q6ZNL6	FGD5_HUMAN		5	ACAGCGTCCGG	0.627	
-	9	882	eq.1_Missense_Mu	NM_207359	NP_997242	Q6ZQY3	GADL1_HUMAN		0	AGCTCCCAACA	0.438	
+	2	679_680	Missense_Mutatio	NM_002468	NP_002459	Q99836	MYD88_HUMAN	e domain (By similarity).	94	GATGACCCCCTG	0.525	
+	12	1499	kz.3_Missense_M	NM_001042646	NP_001036111	Q9UPV9	TRAK1_HUMAN	action with HGS.	1	CGGCTCCAACC	0.572	
-	4	517	.R145W|CCDC13	NM_144719	NP_653320	Q8IYE1	CCD13_HUMAN	Potential.	1	ACAGCCGGTTCT	0.512	
-	3	654	1_uc003cpf.2_Mis	NM_005283	NP_005274	P46094	XCR1_HUMAN	Name=4; (Potential).	1	GCAGCGGAGGG	0.597	
+	4	415	.H82N|PTPN23_u	NM_015466	NP_056281	Q9H3S7	PTN23_HUMAN	BRO1.	3	TGGCCCATGAG	0.582	
-	4	1671	ro.3_Intron|CSPG	NM_006574	NP_006565	O95196	CSPG5_HUMAN	lasmic (Potential).	2	ATGGGGGGAGG	0.517	
+	5	8215		NM_003458	NP_003449	Q9UPA5	BSN_HUMAN		8	GAGATCGTCAGG	0.652	
+	43	7072		NM_015512	NP_056327	Q9P2D7	DYH1_HUMAN	3 (By similarity).	3	TTGACAGCAAG	0.582	
+	51	8239	H1_uc003ddv.2_5'	NM_015512	NP_056327	Q9P2D7	DYH1_HUMAN	4 (By similarity).	3	ACAACGTCCTA	0.537	
-	16	2626	ej.1_Missense_Mu	NM_003157	NP_003148	P51957	NEK4_HUMAN		1	GCAAACGTACCT	0.249	rs147140852
+	4	590	_p.E79D|PRKCD_	NM_006254	NP_006245	Q05655	KPCD_HUMAN	C2.	9	GAGGAGCCAGT	0.592	
+	1	695	BO2_uc011bgj.1_	NM_002942	NP_002933	Q9HCK4	ROBO2_HUMAN		11	ATGTTCGGGTTG	0.373	

+	4	784		NM_173824	NP_776185	Q5JPI3	CC038_HUMAN			0	AGAATCCTTTTCT	0.393	
+	3	1130	rp.1_Missense_Mu	NM_001080448	NP_001073917	Q9UF33	EPHA6_HUMAN	cellular (Potential).		16	ACAGGATATGAA	0.343	
-	7	614	hn.1_Missense_M	NM_014429	NP_055244	Q86VD1	MORC1_HUMAN			8	TTAAATGGGGAG	0.343	
+	16	3136	.R840W|BOC_uc	NM_033254	NP_150279	Q9BWV1	BOC_HUMAN	cellular (Potential).		6	TAGAGCGGCCG	0.617	
-	4	466	BTB20_uc003ebl.	NM_015642	NP_056457	Q9HC78	ZBT20_HUMAN			5	CTGCTCGTTGA	0.597	
+	3	623	o.2_RNA|C3orf1_u	NM_016589	NP_057673	Q9NPL8	TIDC1_HUMAN	ical; (Potential).		0	CTGGCGCTGGG	0.398	rs142096113
+	9	1301	T3_uc010hug.2_	NM_031913	NP_114119	A0FGR9	ESYT3_HUMAN	C2 1.		0	GGAACGAAGTG	0.582	
-	17	2298	nm.1_Missense_M	NM_000935	NP_000926	O00469	PLOD2_HUMAN			2	ATATACGGCTAT	0.358	
+	4	580	_p.G45E|AGTR1_	NM_031850	NP_114038	P30556	AGTR1_HUMAN	Name=1; (Potential).		0	TATTTGGAAACA	0.353	
-	7	1559	_uc003ewz.2_Nor	NM_000096	NP_000087	P00450	CERU_HUMAN	in-like 3.|F5/8 type A 2.		1	CTTTCGATTTGT	0.453	
-	1	333	_uc003ewz.2_Mis	NM_000096	NP_000087	P00450	CERU_HUMAN	1.|Plastocyanin-like 1.		1	ATAATTCCAATG	0.353	
-	19	2433	_p.E743K|ZBBX_u	NM_024687	NP_078963	A8MT70	ZBBX_HUMAN	Potential.		2	GTAATTCTTTTTC	0.328	
-	13	2579	.R851C|PHC3_uc	NM_024947	NP_079223	Q8NDX5	PHC3_HUMAN			2	ACGACGGCCAC	0.423	
-	7	1210	_p.R128*|SLC2A2_	NM_000340	NP_000331	P11168	GTR2_HUMAN	lasmic (Potential).		2	CTGTCGGTAGC	0.418	rs121909743
+	13	2196	_p.P332L|EIF2B5_	NM_003907	NP_003898	Q13144	EI2BE_HUMAN	W2.		5	TTCCCCGCTTG	0.527	
+	7	930	_Mutation_p.R260	NM_018358	NP_060828	Q9NUQ8	ABCF3_HUMAN	C transporter 1.		4	GCTACGGAGGG	0.602	
+	2	199	.2_Missense_Mut	NM_003722	NP_003713	Q9H3D4	P63_HUMAN	cription activation.		12	TTACCGATCCA	0.373	
-	3	319		NM_198505	NP_940907	Q4VNC0	AT135_HUMAN			11	ATTCTTCCCACT	0.408	
-	13	1981		NM_018385	NP_060855	Q9H089	LSG1_HUMAN			0	AAGTTACAGGAT	0.438	
-	3	9356	C4_uc003fvp.2_In	NM_018406	NP_060876	Q99102	MUC4_HUMAN			0	GGAAAGGCTGG	0.602	
-	3	3298	ron|ABCA11P_uc	NM_133474	NP_597731	D9N162	D9N162_HUMAN			1	CCACATTCTCC	0.413	
-	3	1955	ron|ABCA11P_uc0	NM_133474	NP_597731	D9N162	D9N162_HUMAN			1	TGCCACGATCTT	0.378	
+	5	1505	Site|ZBTB49_uc01	NM_145291	NP_660334	Q6ZSB9	ZBT49_HUMAN	C2H2-type 2.		2	TACGACGGCAT	0.408	
+	19	2574	.V728I|CC2D2A_u	NM_001080522	NP_001073991	Q9P2K1	C2D2A_HUMAN			3	AGGGAGTTGGA	0.418	
+	16	1798	s.1_Missense_Mu	NM_004787	NP_004778	O94813	SLIT2_HUMAN	LRRNT 3.		11	CACATTCCCCAG	0.448	
-	11	1866	qn.1_Missense_M	NM_145290	NP_660333	Q8IWK6	GP125_HUMAN	cellular (Potential).		1	ACTGTTGAATAAA	0.488	
+	12	2071	N7_uc003gvi.3_3'	NM_024677	NP_078953					0	CTGCAGCCAAG	0.428	
-	2	240	.1_RNA|NMU_uc	NM_006681	NP_006672	P48645	NMU_HUMAN			0	TGTAATCCTTGA	0.308	
-	6	1370		NM_001076	NP_001067	P54855	UDB15_HUMAN			0	TAATTTCATGAC	0.363	
+	5	1203	cam.1_Missense_	NM_001075	NP_001066	P36537	UDB10_HUMAN		p.P393S(1)	5	GCATTCCATTGT	0.448	
+	3	962	_p.L141F|RUFY3_	NM_014961	NP_055776	Q7L099	RUFY3_HUMAN	RUN.		0	CTTTTCTCGGA	0.259	
+	5	608	LB_uc003hgu.3_	NM_000477	NP_000468	P02768	ALBU_HUMAN	Albumin 1.		6	GAACTCCTTTTC	0.353	
-	13	2312		NM_001042784	NP_001036249	Q5M9N0	CD158_HUMAN	Potential.		6	TCAGATCCTTCC	0.294	
+	16	2894	PAQR3_uc003hln.	NM_198892	NP_942595	Q9NSY1	BMP2K_HUMAN			1	AATGTACAAGAA	0.478	
-	8	1011	_p.G237E|AGXT2L	NM_031279	NP_112569	Q8TBG4	AT2L1_HUMAN			1	GTTTTCCCATT	0.468	
+	11	2152	p.R525H|EGF_uc	NM_001963	NP_001954	P01133	EGF_HUMAN	s B 7.|Extracellular (Potenti		4	TTGGCCGTAGAT	0.453	
-	9	2573	ST4_uc010imw.2_	NM_022569	NP_072091	Q9H3R1	NDST4_HUMAN	eparan sulfate N-sulfotrans		4	GAACTTCCTCAA	0.318	
+	1	3845		NM_024582	NP_078858	Q6V0I7	FAT4_HUMAN	.|Extracellular (Potential).		18	CCTATTCCCTTG	0.363	
+	8	7405	e_Mutation_p.H76	NM_024582	NP_078858	Q6V0I7	FAT4_HUMAN	(Potential).|Cadherin 24.		18	AGCATCACCCA	0.453	
+	17	13949	p.S2891L|FAT4_u	NM_024582	NP_078858	Q6V0I7	FAT4_HUMAN	lasmic (Potential).		18	AATTTTCAATCCA	0.498	
-	5	764	mm.3_Missense_	NM_004564	NP_004555	O75879	GATB_HUMAN			0	TGTTCGCCTGG	0.532	rs145476419
+	11	2396		NM_033393	NP_203751	Q9C0D6	FHDC1_HUMAN			2	CATCTCGGACA	0.622	
+	5	960	p.D134N|CLCN3_	NM_001829	NP_001820	P51790	CLCN3_HUMAN	al; (By similarity).		3	CTGCCGATTGG	0.418	
+	11	2189	e.1_Missense_Mu	NM_001080477	NP_001073946	Q9P273	TEN3_HUMAN	r (Potential).|EGF-like 7.		0	GTGCCGAGCAC	0.617	
+	2	585		NM_207352	NP_997235	Q6ZWL3	CP4V2_HUMAN			0	CTGGGTCGGGC	0.423	
-	9	978	nk.1_Missense_M	NM_017755	NP_060225	Q08J23	NSUN2_HUMAN			1	CCCGCGTGTTG	0.468	rs149296511
-	2	565	e.3_5'Flank|MTRF	NM_024091	NP_076996	Q14CZ7	FAKD3_HUMAN			4	CATCCTTTTTTT	0.418	

+	11	2205		NM_020227	NP_064612	Q9NQV7	PRDM9_HUMAN	2H2-type 7.	6	TTTAGCTGGCAG	0.617	
+	11	2236		NM_020227	NP_064612	Q9NQV7	PRDM9_HUMAN	2H2-type 7.	6	GAGGACACACA	0.602	rs111488757
+	2	645	LC1A3_uc010iuy.	NM_004172	NP_004163	P43003	EAA1_HUMAN	ical; (Potential).	0	TCACCGCTGTC	0.418	rs143571478
+	3	2111	A1_uc003jou.2_Ir	NM_015946	NP_057030	Q9BRX2	PELO_HUMAN		0	CTGACCAAGAG	0.438	
+	2	5636		NM_153610	NP_705838	Q8N3K9	CMYA5_HUMAN		9	AGTTTTCACTTAT	0.333	
+	5	821	SGRF2_uc003khb	NM_006909	NP_008840	O14827	RGRF2_HUMAN	DH.	12	CCTGCGTATGG	0.498	
+	4	857	yo.1_Missense_M	NM_005733	NP_005724	O95235	KI20A_HUMAN	inesin-motor.	0	ACAGGTTCACC	0.473	
+	1	1384	03lhf.2_Intron|PCD	NM_018907	NP_061730	Q9UN74	PCDA4_HUMAN	|Extracellular (Potential).	6	CGCGCGAGACG	0.617	
+	1	2321	DHA7_uc003lhq.	NM_018904	NP_061727	Q9Y5I0	PCDAD_HUMAN	XXP 2.|6 X 4 AA repeats	6	TCAGTCCCAGCC	0.567	
+	19	1840	p.T602M|ARHGA	NM_015071	NP_055886	Q9UNA1	RHG26_HUMAN	Ser-rich.	1	CCTGACGCTCT	0.597	rs146092149
+	6	747	3lrz.2_Splice_Site	NM_001135243	NP_001128715	Q13428	TCOF_HUMAN		3	TGGAGGTAATT	0.617	
-	3	331	.2_5'UTR|CCDC6	NM_015621	NP_056436	A6NI79	CCD69_HUMAN	Potential.	2	TCTTTTCCTCCT	0.502	
+	6	1440	IPAL4_uc011ddq.	NM_001099287	NP_001092757	Q0D2K0	NIPA4_HUMAN	lasmic (Potential).	0	AGAACGTCCTT	0.493	
+	49	5220	e_Mutation_p.A12	NM_004946	NP_004937	Q92608	DOCK2_HUMAN		7	AGAAAGCAGCT	0.577	
+	9	1803	_p.P459Q|RIPK1_	NM_003804	NP_003795	Q13546	RIPK1_HUMAN	tion with SQSTM1.	5	GCCACCAACAG	0.413	
+	10	3620	p.S1077L|RREB1_	NM_001003698	NP_001003698	Q92766	RREB1_HUMAN		11	ATCCTCGGCCC	0.627	
+	1	811_812		NM_030905	NP_112167	O76002	OR2J2_HUMAN	lasmic (Potential).	0	TTCAGAAAGTG	0.45	
+	4	482	_Mutation_p.G36	NM_001517	NP_001508	Q92759	TF2H4_HUMAN		3	GAGCGGCCTCC	0.582	
-	10	874	_uc003nvz.1_Spli	NM_021160	NP_066983	O95870	ABHGA_HUMAN		0	TCACCTAGGAA	0.597	
-	10	1733_1734	RS_uc011doi.1_R	NM_006295	NP_006286	P26640	SYVC_HUMAN		3	TCCAAGGAGCT	0.594	
-	21	7671		NM_019105	NP_061978	P22105	TENX_HUMAN	nectin type-III 17.	0	ACACCGGGCCC	0.637	
-	2	467	se_Mutation_p.S8	NM_016593	NP_057677	Q9NYL5	CP39A_HUMAN		1	TTTTTGGATTTTA	0.323	
+	6	908	e_Mutation_p.G23	NM_153839	NP_722581	Q8IZF7	GP111_HUMAN	ellular (Potential).	1	AACATTGGAAAA	0.398	
-	6	921		NM_152688	NP_689901	Q5VWX1	KHDR2_HUMAN	Pro-rich.	11	TGCTTCCCCGA	0.607	
+	13	2596	_Missense_Mutati	NM_001162529	NP_001156001	Q9P2D6	F135A_HUMAN		1	GGAAATCATTG	0.353	
-	56	8558	ht.2_Missense_M	NM_004370	NP_004361	Q99715	COCA1_HUMAN	n (COL2) with 1 imperfecti	9	GAGTCCATTGG	0.488	
+	7	1040	60_splice|DOPEY	NM_015018	NP_055833	Q5JWR5	DOP1_HUMAN		4	AGTCAGGTAAAA	0.373	
+	1	268		NM_021620	NP_067633	Q9H4Q3	PRD13_HUMAN	SET.	0	TGCACGGAGCC	0.692	
-	1	205	.1_RNA|GOPC_u	NM_002944	NP_002935	P08922	ROS_HUMAN		25	AATGTTCTTCAT	0.383	
-	5	1614	bt.1_Missense_M	NM_001010923	NP_001010923	Q8N1K5	THMS1_HUMAN	CABIT 2.	4	AACCTCCTTCC	0.443	
+	10	1892	he.2_Missense_	NM_020455	NP_065188	Q86SQ4	GP126_HUMAN	ellular (Potential).	1	GGAAGGAAAAA	0.393	
+	3	446		NM_025218	NP_079494	Q9BZM6	N2DL1_HUMAN	lass I alpha-2 like.	1	GACACGGCAGA	0.517	
+	3	1031	R265H|OPRM1_u	NM_000914	NP_000905	P35372	OPRM_HUMAN	lasmic (Potential).	1	TGTCCGCATGC	0.502	
+	29	5994	|TIAM2_uc011efl.1	NM_012454	NP_036586	Q8IVF5	TIAM2_HUMAN		4	TGATGACCACC	0.527	
-	13	1951	.1_Missense_Mut	NM_003379	NP_003370	P15311	EZRI_HUMAN	ction with SCYL3.	1	CGATGCGCTGC	0.607	
-	8	1148	utation_p.A305S	NM_030752	NP_110379	P17987	TCPA_HUMAN		1	CATAGCACCAG	0.408	
+	3	1338	LL2_uc011egr.1_R	NM_031949	NP_114155	Q9BWV7	TTLL2_HUMAN	TTL.	3	TTTACTTAAATG	0.433	
+	12	1767	wc.1_Missense_M	NM_001040001	NP_001035090	P55196	AFAD_HUMAN		5	TAGTGGGACAG	0.413	
+	14	1562	e_Mutation_p.V40	NM_001130965	NP_001124437	O94901	SUN1_HUMAN	ear space.|Potential.	0	GACACGTGAAG	0.483	
-	7	1678	LL2_uc003ski.3_	NM_182924	NP_891554	Q8IY33	MILK2_HUMAN		1	CGAAGGGAGGC	0.627	rs146347352
+	7	1457	a.1_Missense_M	NM_001037165	NP_001032242	P85037	FOXK1_HUMAN		2	TGGCCGTGCCT	0.667	
+	15	3196	wq.1_Missense_M	NM_032172	NP_115548	Q9H9J4	UBP42_HUMAN	Arg-rich.	5	GACACCGGAGC	0.726	
-	11	1625	_p.L446F|PDE1C_	NM_005020	NP_005011	Q14123	PDE1C_HUMAN	ytic (By similarity).	4	ATGGAGGTCCC	0.443	
+	17	2432	_Mutation_p.T393	NM_031449	NP_113637	Q8NF64	ZMIZ2_HUMAN	Pro-rich.	5	CCCAACCCTTG	0.632	
+	54	14090_1409	A13_uc010kyt.1_	NM_152701	NP_689914	Q86UQ4	ABCAD_HUMAN		10	TACTCTCCAAG	0.391	
-	6	626	e_Mutation_p.L17	NM_006213	NP_006204	Q16816	PHKG1_HUMAN	rotein kinase.	1	ATGTTGAGTTTG	0.527	
+	2	526	3udv.1_Missense_	NM_001040456	NP_001035546	Q6NTF9	RHBD2_HUMAN		0	CCACCGTCCGT	0.612	

-	10	13870	4527R|PCLO_uc	NM_033026	NP_149015	Q9Y6V0	PCLO_HUMAN		7	TCTCCACTATGT	0.378	
-	2	501	iw.1_Missense_M	NM_015545	NP_056360	O75127	PTCD1_HUMAN		1	CTCCGGTTCCA	0.542	
-	2	1375	e_Mutation_p.R12	NM_024637	NP_078913	Q96RP7	G3ST4_HUMAN	enal (Potential).	3	TGGGCGGTAGC	0.612	rs116867043
+	4	1252	ve.1_Missense_M	NM_173564	NP_775835	Q6ZVC0	CG051_HUMAN	Pro-rich.	1	CCAAGGAGCCA	0.687	
+	2	249	e_Mutation_p.R1	NM_024653	NP_078929	Q9H875	PKRI1_HUMAN	NA-binding (By similarity).	1	TGTCCGAGATG	0.279	
+	13	1678	kmc.1_Missense_	NM_000441	NP_000432	O43511	S26A4_HUMAN	ellular (Potential).	7	TGTTTACGTGTA	0.373	
-	32	4954	_p.R1624*|LAMB4	NM_007356	NP_031382	A4D0S4	LAMB4_HUMAN	ential.|Domain I.	8	TGATCGCTGCT	0.453	
+	21	4123	30_splice|MET_uc	NM_000245	NP_000236	P08581	MET_HUMAN		159	GAACAGATATG	0.423	
-	8	2538	RM8_uc003vlt.2_M	NM_000845	NP_000836	O00222	GRM8_HUMAN	ellular (Potential).	23	AATGTCACACT	0.468	
+	5	587	1_uc011kpa.1_5'	NM_005011	NP_005002	Q16656	NRF1_HUMAN		1	GGTGCGTAAGT	0.557	
-	8	2211		NM_020911	NP_065962	Q9HCM2	PLXA4_HUMAN	tracellular (Potential).	1	ACTTACGAATTG	0.512	
+	3	663		NM_020299	NP_064695	O60218	AK1BA_HUMAN		5	CACAGGGATTC	0.507	rs146306673
-	10	1892	st.2_Missense_M	NM_001008225	NP_001008226	O95628	CNOT4_HUMAN		0	TGGCGGGAGAT	0.453	
+	15	4802	wem.2_Missense_	NM_005435	NP_005426	Q12774	ARHG5_HUMAN	SH3.	2	GGTTTCCTGTG	0.572	
+	5	740	1_uc003wga.2_R	NM_032534	NP_115923	A5PL33	KRBA1_HUMAN		2	TCTCCGAGGCC	0.622	
+	7	889	PO_uc010lpl.1_5'	NM_198455	NP_940857	A2VEC9	SSPO_HUMAN	VWFD 1.	0	TGGGGGTCGTG	0.632	
-	3	915	hm.2_Missense_	NM_024711	NP_078987	Q6P9H5	GIMA6_HUMAN		3	CCTTCCGGGTG	0.622	
+	10	1852	.R495Q|ACCN3_u	NM_004769	NP_004760	Q9UHC3	ACCN3_HUMAN	lasmic (Potential).	2	CCATCGAACCC	0.632	
+	3	680	8_uc003xcf.2_Mis	NM_001013842	NP_001013864	Q8NAV2	CH058_HUMAN		1	GTCTTCGCTAT	0.647	
-	18	2362		NM_001010906	NP_001010906	Q68CJ6	SLIP_HUMAN		2	CATCCCCCTGG	0.512	
+	6	393	M18_uc010lww.2_	NM_014237	NP_055052	Q9Y3Q7	ADA18_HUMAN		6	GTAGAATCTTC	0.294	
+	4	3992	1_uc011ldy.1_Intr	NM_006269	NP_006260	P56715	RP1_HUMAN		12	TTTTTTCCTAGT	0.408	
-	5	1153		NM_000780	NP_000771	P22680	CP7A1_HUMAN		1	TGTCCGGATGT	0.348	rs149291486
+	3	301	lyy.1_Nonsense_	NM_052958	NP_443190	Q49A92	CH034_HUMAN		1	AAGCTATGATAA	0.343	
+	9	1120	hu.1_Missense_	NM_014754	NP_055569	P48651	PTSS1_HUMAN		1	TACTACGCTTAC	0.418	
+	1	345		NM_003301	NP_003292	P34981	TRFR_HUMAN	Name=3; (Potential).	3	GAATTAATGCAT	0.463	
+	16	1825		NM_022045	NP_071328	Q96DY7	MTBP_HUMAN	ith MDM2 (By similarity).	3	AGGGTCCTCGG	0.398	
+	21	3311	lja.1_Missense_M	NM_016018	NP_057102	A8MW92	P20L1_HUMAN		2	TTAAACGCCAC	0.423	
+	2	240	GPR172A_uc003z	NM_024531	NP_078807	Q9HAB3	RFT3_HUMAN	ical; (Potential).	0	GGTCAATGGGA	0.662	rs141698844
-	14	2235		NM_004260	NP_004251	O94761	RECQ4_HUMAN	case C-terminal.	4	GGCACGACCTT	0.662	
+	1	271		NM_002170	NP_002161	P32881	IFNA8_HUMAN		0	TCCTCCATGAG	0.473	
-	2	403	uc004ags.1_RNA	NM_153237	NP_694969	Q8N6L7	CI071_HUMAN		0	AGGCCTCTCTC	0.522	
-	5	1143		NM_004297	NP_004288	O95837	GNA14_HUMAN		2	TTTCCGATCGT	0.453	
+	18	2648	p.G717E|PHF2_uc	NM_005392	NP_005383	O75151	PHF2_HUMAN		1	GAATGGGGGTG	0.637	
-	9	2182	_p.R668C|TBC1D2	NM_018421	NP_060891	Q9BYX2	TBD2A_HUMAN	ab-GAP TBC.	3	TGGCGGGCAG	0.667	rs147662482
+	9	1108	3_splice|HSDL2_	NM_032303	NP_115679	Q6YN16	HSDL2_HUMAN		0	CTCCGGTAAGG	0.418	
+	3	428	2_RNA|COL27A1_	NM_032888	NP_116277	Q8IZC6	CORA1_HUMAN	-like.|TSP N-terminal.	4	CCGGCGCTCAG	0.677	
-	14	1826	_p.W599*|C5_uc0	NM_001735	NP_001726	P01031	CO5_HUMAN		2	CCACCCAGGAA	0.448	
-	17	1676	c004buh.2_Misse	NM_004486	NP_004477	Q08379	GOGA2_HUMAN	Potential.	1	AAATCCGCTCT	0.612	
-	3	334	SEC16A_uc010nb	NM_014866	NP_055681	O15027	SC16A_HUMAN	action with SEC23A.|Pro-r	0	AGACGGGACCG	0.567	
-	1	512		NM_031297	NP_112587	Q9H0X6	RN208_HUMAN		0	CCGCCGAAGAA	0.672	
+	1	474		NM_152577	NP_689790	Q8N7E2	ZN645_HUMAN		2	AGCTCGAAAAC	0.448	
-	4	1769		NM_030624	NP_085127	Q96M94	KLH15_HUMAN	Kelch 4.	2	AGATTCGAAAG	0.473	
+	2	568	B6_uc010ngc.1_	NM_173523	NP_775794	Q8N7X4	MAGB6_HUMAN	Ser-rich.	3	TTCCCATGATG	0.537	
+	2	574	B6_uc010ngc.1_	NM_173523	NP_775794	Q8N7X4	MAGB6_HUMAN	Ser-rich.	3	TGATGTCTCCG	0.532	
+	7	1025	nse_Mutation_p.D	NM_005676	NP_005667	P98175	RBM10_HUMAN	anBP2-type.	5	ATGAGGACTGG	0.507	
+	9	1648	q.1_Missense_M	NM_000084	NP_000075	P51795	CLCN5_HUMAN	al; (By similarity).	4	AGGTCGACTTC	0.488	

-	22	3460	e.1_Missense_Mu	NM_006306	NP_006297	Q14683	SMC1A_HUMAN	sp-rich (DA-box).	6	CTCCCCGCCTG	0.577	
+	4	894	_p.V95I|NLGN3_	NM_018977	NP_061850	Q9NZ94	NLGN3_HUMAN	ellular (Potential).	1	TCATCGTCATC	0.537	
-	3	4938		NM_001008537	NP_001008537	Q5QGS0	K2022_HUMAN		15	TCGGTCCGTTAT	0.453	
+	3	299	jw.3_Missense_Mu	NM_001080425	NP_001073894	Q9NWD9	BEX4_HUMAN		1	AAAACGAAGGA	0.532	
+	4	731	sz.1_Nonsense_Mutation_p.R155*|ALG13_uc011mta.1			Q9NP73	ALG13_HUMAN	OTU.	1	TGTTTCGAAAG	0.443	
-	5	1273	p.G398E|KLHL13_	NM_033495	NP_277030	Q9P2N7	KLH13_HUMAN	Kelch 2.	2	GTTTTTCCTTTT	0.433	
-	14	2498	p.D811N|ODZ1_u	NM_014253	NP_055068	Q9UKZ4	TEN1_HUMAN	ellular (Potential).	23	ACTCACCTCCAT	0.443	
+	5	418	ur.2_Missense_Mu	NM_000276	NP_000267	Q01968	OCRL_HUMAN		4	AAATTCGGGTT	0.423	
+	14	1549	.R433S|FMR1_uc	NM_002024	NP_002015	Q06787	FMR1_HUMAN	tion with RANBP9.	3	CCAAATCGTACA	0.448	
-	3	518	p.A55V|CSAG1_u	NM_005367	NP_005358	P43365	MAGAC_HUMAN		1	CGGCAGCAGGC	0.622	
+	1	927	_p.E54K|PCDH11	NM_032973	NP_116755	Q9BZA8	PC11Y_HUMAN	(Potential).|Cadherin 1.	0	GAGAAGAAATT	0.463	
+	2	590		NM_002760	NP_002751				0	ATTCCCGACGTC	0.577	
-	3	304	adf.2_Missense_M	NM_003327	NP_003318	P43489	TNR4_HUMAN	.|Extracellular (Potential).	0	TGGCCGTGCAC	0.697	
+	9	1083	p.D290E|PEX14_	NM_004565	NP_004556	O75381	PEX14_HUMAN		1	GGGGATGGGC	0.582	
-	78	10851	d.2_Missense_Mu	NM_005529	NP_005520	P98160	PGBM_HUMAN	ike C2-type 22.	9	TGTCAGGAGTG	0.592	
-	61	7974	d.2_Missense_Mu	NM_005529	NP_005520	P98160	PGBM_HUMAN	ike C2-type 12.	9	AGGTCTGCCCT	0.632	
+	4	391	p.G85R|LCK_uc01	NM_005356	NP_005347	P06239	LCK_HUMAN	SH3.	6	AGAAGGGGGAA	0.617	
-	14	2619	.1_RNA|EPHA10_	NM_001099439	NP_001092909	Q5JZY3	EPHAA_HUMAN	Potential).|Protein kinase.	8	AGGCCGCTCCC	0.602	
+	4	336	001cfy.3_Nonsen	NM_001142588	NP_001136060	Q13952	NFYC_HUMAN		3	TTTGATCAGTTT	0.413	
+	2	541	.1_RNA|PCSK9_u	NM_174936	NP_777596	Q8NBP7	PCSK9_HUMAN		4	TGAAGGAGGAG	0.622	
-	27	3017_3018	M1_uc001dob.3_	NM_001017975	NP_001017975	A2PYH4	HFM1_HUMAN	SEC63.	0	CAAAGGGGGGA	0.257	
-	10	1257		NM_000110	NP_000101	Q12882	DPYD_HUMAN		8	CTCAGGGACAG	0.408	
+	3	584	_Mutation_p.R20	NM_001688	NP_001679	P24539	AT5F1_HUMAN		0	AAAGTTCGTTAT	0.438	
+	19	1806	e_Mutation_p.E5	NM_003176	NP_003167	Q15431	SYCP1_HUMAN	Potential.	1	CACAGGAAACA	0.239	
-	19	2691		NM_206996	NP_996879	Q6Q759	SPG17_HUMAN		6	TTTTCTCATTCA	0.318	
+	4	466				P26439	3BHS2_HUMAN		2	AAGATCAAGCT	0.473	
+	76	9459	PF10_uc010oyl.1	NM_001039703	NP_001034792	A6NDV3	A6NDV3_HUMAN		0	TGCTGGATGAG	0.483	
+	13	2422	uc010ozk.1_5'UT	NM_017940	NP_060410	A6NDV3	A6NDV3_HUMAN		0	CCGGACAAGTC	0.587	
-	3	1161		NM_001122965	NP_001116437	Q6XPR3	RPTN_HUMAN	Gln-rich.	0	GTAGTGGGAAC	0.473	
-	33	4690	p.H449Y|NUP210	NM_207308	NP_997191	Q5VU65	P210L_HUMAN		11	TGTCATGAAAA	0.428	
+	9	2232	_uc010pmx.1_3'	NM_022093	NP_071376	Q9UQP3	TENN_HUMAN	nectin type-III 6.	9	AGACAGGTAAG	0.557	
-	8	1716	_Mutation_p.E50	NM_004319	NP_004310	O14525	ASTN1_HUMAN		15	CCATTCGTTCC	0.493	
+	18	2070	_p.V538I|CAPN2_	NM_001748	NP_001739	P17655	CAN2_HUMAN	n IV.|EF-hand 2.|2.	5	TCGACGTTGAC	0.418	
-	3	614	7_uc001hrf.2_5'F	NM_023007	NP_075383	Q9H9V9	JMJD4_HUMAN	JmjC.	0	AGTCGGACGAG	0.612	
+	1	127		NM_001001914	NP_001001914	Q8NGZ4	OR2G3_HUMAN	Name=1; (Potential).	1	GGAAACTTCACC	0.443	
+	1	659		NM_001004690	NP_001004690	A3KFT3	OR2M5_HUMAN	lasmic (Potential).	3	TGCTCGAGTTAT	0.423	rs148081072
+	21	2894		NM_002216	NP_002207	P19823	ITIH2_HUMAN		3	GTTTGGAACGG	0.488	
+	6	1417		NM_000314	NP_000305	P60484	PTEN_HUMAN	hatase tensi|p.K128fs*47(1	2334	AAAGGGACGAA	0.413	rs121909218
-	1	3044		NR_002319					0	GGGAGCCCACA	0.547	
-	9	875	_Mutation_p.E210	NM_013314	NP_037446	Q8WV28	BLNK_HUMAN	Pro-rich.	2	GGTTTCCCAGG	0.587	
+	1	2998		NM_015652	NP_056467	Q8N655	CJ012_HUMAN		2	TGGCAGTGATG	0.488	
-	2	450_451	AP19_uc001kmy.2	NM_003061	NP_003052	O75093	SLIT1_HUMAN	LRR 1.	4	AGTTCCCTGGA	0.619	
+	5	2935	RC1_uc010qqj.1_	NM_015062	NP_055877	Q5VV67	PPRC1_HUMAN	Pro-rich.	3	CACCCCCTCCT	0.622	
-	1	341	C2_uc009xxx.2_I	NR_026715					0	GATGCAGTCAA	0.592	
+	23	3826	e_Mutation_p.S27	NM_207303	NP_997186	Q5VV63	ATRN1_HUMAN	ellular (Potential).	7	ATATATCAATTAA	0.279	
-	7	555	NO9_uc010qvv.1_	NM_001012302	NP_001012302	A1A5B4	ANO9_HUMAN	lasmic (Potential).	4	GTCCCTCCCCC	0.647	
-	1	602		NM_001005161	NP_001005161	Q8NGK2	O52B4_HUMAN	Name=5; (Potential).	0	AAAACCCATAC	0.373	

-	1	659		NM_001003745	NP_001003745	P58181	O10A3_HUMAN	lasmic (Pote	p.R220*(1)	1	AGAACTCGAATG	0.448	
-	2	1300	S_uc009yiz.2_Intr	NM_001143816	NP_001137288	P23560	BDNF_HUMAN			0	CTGCTGCCGTT	0.552	
+	9	1689	n.1_Missense_Mu	NM_003682	NP_003673	Q8WXG6	MADD_HUMAN	dDENN.		11	ATTCCGCCAAC	0.522	
+	3	390	rik.1_Missense_M	NM_001004704	NP_001004704	Q8NH72	OR4C6_HUMAN	Name=1; (Potential).		2	ATCTACTTATTGT	0.393	
-	5	6119	AK_uc001ntk.1_Ir	NM_001620	NP_001611	Q09666	AHNK_HUMAN			19	ACATCCACATCC	0.502	
+	4	526		NM_199337	NP_955369	Q7Z7N9	T179B_HUMAN			0	ATGCTGAAGTG	0.483	
-	21	3553	1opz.2_Missense_	NM_012309	NP_036441	Q9UPX8	SHAN2_HUMAN			5	GCCACCCACGA	0.677	
-	7	865		NM_002426	NP_002417	P39900	MMP12_HUMAN			0	GTCAGGATTTG	0.403	
-	24	4338		NM_020693	NP_065744	Q8TD84	DSCL1_HUMAN	III 5.|Extracellular (Potentia		8	GGGCTGGTCCG	0.642	
+	2	690	uf.2_Missense_Mu	NM_001716	NP_001707	P32302	CXCR5_HUMAN	ellular (Potential).		1	CAAGGCCATCAC	0.577	rs138622461
-	6	2266	al.2_Missense_Mu	NM_182557	NP_872363	Q86UU0	BCL9L_HUMAN	teraction with CTNNB1 (By		2	CTGGGGGCCCC	0.672	
-	4	353	bj.1_Missense_Mu	NM_212555	NP_997720	Q6UY27	PATE2_HUMAN			0	TACTATGATCACA	0.453	
-	24	3376	.R1082C|NFRKB_	NM_001143835	NP_001137307	Q6P4R8	NFRKB_HUMAN			3	CAAGCGAAAAG	0.552	
+	3	191	C77_uc010sdp.1_	NM_032358	NP_115734	Q9BR77	CCD77_HUMAN			1	CTTTACCCCAA	0.363	
-	5	807	n.2_Intron|GSG1_	NM_001080555	NP_001074024	Q2KHT4	GSG1_HUMAN	ical; (Potential).		0	CTCACCTGACA	0.567	
-	23	3357	_p.E273D|ADAMT	NM_025003	NP_079279	P59510	ATS20_HUMAN	SP type-1 6.		19	ACTAGCTTCATG	0.383	
-	21	3055	_p.E173K|ADAMT	NM_025003	NP_079279	P59510	ATS20_HUMAN	SP type-1 4.		19	AAAATTCATTGC	0.403	
+	13	1773	_p.V480M|ANO6_u	NM_001025356	NP_001020527	Q4KMQ2	ANO6_HUMAN	ellular (Potential).		2	TCTCGGTGTTC	0.438	
-	2	143	B7_uc010snz.1_R	NM_000889	NP_000880	P26010	ITB7_HUMAN	ellular (Potential).		8	GGGATCTTGGC	0.562	
+	2	466		NM_021191	NP_067014	Q9HD90	NDF4_HUMAN			4	AAAATGAGGTG	0.398	
+	1	593		NM_001005243	NP_001005243	Q8NGE7	OR9K2_HUMAN	ellular (Potential).		2	TCGGGCTGTTG	0.393	
+	1	49		NM_001005518	NP_001005518	A6NJZ3	O6C65_HUMAN	ellular (Potential).		0	TTTACAGATAAC	0.323	
-	17	1771_1772	sxi.3_Missense_M	NM_032606	NP_115995	Q9BXY5	CAYP2_HUMAN	EF-hand 3.		2	ATAAAGGCCTAA	0.243	
-	3	1664	_p.G507E|USP44_	NM_001042403	NP_001035862	Q9H0E7	UBP44_HUMAN			3	CTTTTCCACTG	0.393	
+	6	824		NM_198520	NP_940922	Q6ZTY8	CL063_HUMAN			7	TTGCCGAAATT	0.308	
+	12	2027	ztx.2_Nonsense_	NM_139319	NP_647480	Q8NDX2	VGLU3_HUMAN	lasmic (Potential).		3	TTGATGAGGAA	0.438	
+	15	1913		NM_017564	NP_060034	Q8WWQ8	STAB2_HUMAN	lar (Potential).|FAS1 2.		14	CCTTTCTCCAG	0.423	
+	3	1958	_p.M479I|BTBD11_	NM_001018072	NP_001018082	A6QL63	BTBDB_HUMAN			3	ACAAATGGAATG	0.577	
-	14	2543		NM_015335	NP_056150	Q71F56	MD13L_HUMAN			8	TGAGCGCAGAG	0.443	
+	6	518		NM_207437	NP_997320	Q8IVF4	DYH10_HUMAN	n (By similarity).		6	TGGGAGTCACA	0.428	
-	8	2346_2347	e_Mutation_p.D6	NM_178006	NP_821074	Q9Y3M8	STA13_HUMAN	Rho-GAP.		4	AGGTCCCGGA	0.465	
-	11	2780	PC4_uc010abw.2_	NM_016179	NP_057263	Q9UBN4	TRPC4_HUMAN	and ITPR3.|Cytoplasmic (P		6	GTCTATGAAATA	0.443	
+	3	5613		NM_207361	NP_997244	Q5SZK8	FREM2_HUMAN	|Extracellular (Potential).		11	AATTGGGCATG	0.343	
-	8	1153		NM_012345	NP_036477	Q9UHK0	NUFP1_HUMAN			0	TGAAAGACTGC	0.448	
-	1	743		NM_001080396	NP_001073865	B1AL88	F155A_HUMAN	Poly-Gln.		1	gctgccgctgctgctgc	0.353	
+	6	644	_p.E186K|ATP11A_	NM_015205	NP_056020	P98196	AT11A_HUMAN	lasmic (Potential).		4	ATGGAGAATCC	0.552	
-	1	82	R5A_uc010tpk.1_	NM_080664	NP_542395	Q96FN9	DTD2_HUMAN			0	AGCCATGGCTT	0.706	
-	3	273	xae.2_Missense_	NM_006832	NP_006823	Q96AC1	FERM2_HUMAN			0	TCTTCAGAAGC	0.408	
+	2	1732	mu.2_Missense_	NM_015556	NP_056371	O43166	SI1L1_HUMAN			4	TGGCAGTACTT	0.423	
+	2	620		NR_015340						2	TTCTGGGATCTG	0.672	
+	21	3726	2_uc001ypc.2_Mi	NM_022489	NP_071934	Q27J81	INF2_HUMAN			0	TCTCCGAGGAT	0.687	
-	8	1054	e_Mutation_p.Q2	NM_002420	NP_002411	Q7Z4N2	TRPM1_HUMAN	ellular (Potential).		4	GAAGCTGCTCC	0.338	
+	20	2440	LA2G4B_uc010bc	NM_001114633	NP_001108105	P0C869	PA24B_HUMAN	PLA2c.		1	CAGGCCCCACT	0.622	
-	15	3759	nse_Mutation_p.L	NM_173500	NP_775771	Q6IQ55	TTBK2_HUMAN			7	AGAAAAGGTCT	0.418	
-	11	1726	2apj.3_Missense_	NM_005848	NP_005839	Q7Z401	MYCPP_HUMAN	DENN.		4	GAGAGGAACAT	0.413	
+	14	1932	ukf.1_Missense_M	NM_017691	NP_060161	Q8IUZ0	LRC49_HUMAN			1	TGATTTCCATTCT	0.368	
-	23	3531	_Missense_Mutati	NM_006901	NP_008832	B2RTY4	MYO9A_HUMAN			3	GCGGAGCACCT	0.453	

+	2	700	h.1_Missense_Mut	NM_005545	NP_005536	O14498	ISLR_HUMAN	LRR 4.	4	CCCGCGACGCC	0.612	
+	8	927	se_Mutation_p.I17	NM_003027	NP_003018	Q99963	SH3G3_HUMAN	n with ARC (By similarity).	3	AGAATATCAGCT	0.463	
+	3	675	AN_uc010upp.1_	NM_013227	NP_037359	E7EX88	E7EX88_HUMAN		3	CCTATCAGGAC	0.617	
+	10	2648	2ckt.2_Missense_	NM_021098	NP_066921	O95180	CAC1H_HUMAN	=S1 of repeat II; (Potential	2	ATCATGATGGC	0.662	
+	35	6837	_p.P892S|CACNA	NM_021098	NP_066921	O95180	CAC1H_HUMAN	lasmic (Potential).	2	AACCCCCTGCG	0.721	
-	23	8672	_Mutation_p.D28	NM_001009944	NP_001009944	P98161	PKD1_HUMAN	ular (Potential).|REJ.	3	ACCACGTCACT	0.622	
+	11	6782	l.1_Missense_Mut	NM_016333	NP_057417	Q9UQ35	SRRM2_HUMAN	-rich.|Ser-rich.	4	CAGGCGTTCTG	0.542	
-	25	2614	_p.A612T|CORO7_	NM_024535	NP_078811	P57737	CORO7_HUMAN		0	CACAGCCGTGT	0.617	
+	3	317	AT_uc010buh.2_In	NM_020686	NP_065737	P80404	GABT_HUMAN		1	AAGTCCCAGGG	0.478	
+	5	481	uh.2_Missense_M	NM_020686	NP_065737	P80404	GABT_HUMAN		1	CCCATAGGTAA	0.473	
-	1	397		NM_015092	NP_055907	Q96Q15	SMG1_HUMAN	with SMG8 and SMG9.	16	cgccgctgcTCAGC	0.627	
-	4	564	se_Mutation_p.S1	NM_001888	NP_001879	Q14894	CRYM_HUMAN		0	TAAAGGAGAAC	0.527	
+	6	2696	p.S608L|TNRC6A_	NM_014494	NP_055309	Q8NDV7	TNR6A_HUMAN	ction with EIF2C1 and EIF	2	AAACTTCAAGGA	0.468	
+	2	1570		NM_006040	NP_006031	Q9Y661	HS3S4_HUMAN	enal (Potential).	2	CAAGGGGTTCC	0.512	
-	10	1379	uc010vct.1_Intron	NM_003321	NP_003312	P49411	EFTU_HUMAN		1	CTGCCGCAAGA	0.547	
-	1	165	R762_hsa-mir-762|	NM_004765	NP_004756	Q8WUZ0	BCL7C_HUMAN		0	GCTCCGGGTCT	0.453	
+	7	761	r.2_RNA|C16orf58_	NM_003041	NP_003032	P31639	SC5A2_HUMAN	ellular (Potential).	1	CAGCCGTGGGA	0.662	
+	12	1793	|SLC9A5_uc010vji	NM_004594	NP_004585	Q14940	SL9A5_HUMAN		2	TGGCAGTGGAG	0.592	
+	10	1401	sense_Mutation_p	NM_018430	NP_060900	Q2TAA8	TXIP1_HUMAN		0	AGAGCGCTGGC	0.647	
+	2	786	et.2_Missense_M	NM_006742	NP_006733	P11801	KPSH1_HUMAN	rotein kinase.	0	ATGGCGTCCGG	0.587	
-	3	228		NM_001907	NP_001898	P40313	CTRL_HUMAN	eptidase S1.	0	GGGCAGCAGTG	0.662	
+	5	1931	ewd.2_Missense_	NM_133458	NP_597715	Q8TF47	ZFP90_HUMAN	2H2-type 10.	1	GAACCCACACT	0.438	
+	3	268	T7_uc010vnj.1_In	NM_001105663	NP_001099133	P0C024	NUDT7_HUMAN	dix hydrolase.	2	GAAGGGCCCCT	0.418	
+	4	1322	L36_uc010chl.2_In	NM_024731	NP_079007	Q8N4N3	KLH36_HUMAN	Kelch 2.	2	TGCCTCCATCG	0.567	
-	19	2787	p.G918S|ANKFY1_	NM_016376	NP_057460	Q9P2R3	ANFY1_HUMAN	ANK 17.	3	TGAGCCTGCTT	0.438	
+	4	520		NM_000697	NP_000688	P18054	LOX12_HUMAN	ipoxygenase.	1	AGACCGTAAGG	0.502	
+	13	3051	p.D966N|MYOCD_	NM_153604	NP_705832	Q8IZQ8	MYCD_HUMAN		5	ACATCGATTTCC	0.517	
-	1	355		NM_031960	NP_114166	Q9BYQ9	KRA48_HUMAN	IKRQVHEC]- [SPRT]-[STC	0	ctggacacacagcag	0.204	
-	1	457		NM_033059	NP_149048	Q9BYQ6	KR411_HUMAN	-[GIKRQVHEL]- [SPTR]-[S	0	gagatgctgcagctgg	0.129	
-	13	1723	LL6_uc002ioc.2_	NM_001130918	NP_001124390	Q8N841	TTLL6_HUMAN		0	TTCTTTCTCACT	0.527	
+	8	1319	se_Mutation_p.E2	NM_006151	NP_006142	P22079	PERL_HUMAN		2	ACCAGGAGGTC	0.617	
+	1	508	.D149E|BPTF_uc	NM_182641	NP_872579	Q12830	BPTF_HUMAN	-rich.|Asp-rich.	4	gaggaCGGCGAC	0.448	
+	4	1088	wqx.1_Missense_	NM_181790	NP_861455	Q7Z601	GP142_HUMAN	Name=6; (Potential).	4	CATCACCACAC	0.667	
-	9	957	kod.1_Missense_	NM_001042388	NP_001035847	Q8TF05	PP4R1_HUMAN	HEAT 8.	1	CACATGAAACC	0.413	
+	37	6670	nse_Mutation_p.S	NM_032142	NP_115518	E9PF99	E9PF99_HUMAN		5	CTAATTCCTCCT	0.328	
+	4	1315		NM_015879	NP_056963	O43173	SIA8C_HUMAN	enal (Potential).	2	TTGTATGGATTTT	0.423	
+	8	1144	n_p.E201K|SERPI	NM_001143818	NP_001137290	P05120	PAI2_HUMAN		2	CAGATGAAATT	0.413	
+	3	651	p.R109K|CDH7_u	NM_033646	NP_387450	Q9ULB5	CADH7_HUMAN	(Potential).|Cadherin 1.	4	CAAGAGACTGG	0.498	
-	27	3673	TN_uc010xfb.1_M	NM_173630	NP_775901	Q86VV8	RTTN_HUMAN		8	TGACAGCAGTC	0.398	
+	23	2744	A6_uc002mgr.1_M	NM_006702	NP_006693	Q8IY17	PLPL6_HUMAN	lasmic (Potential).	3	ACACCGTATCG	0.662	
+	10	1161	S4_uc002mji.2_M	NM_024552	NP_078828	Q9HA82	CERS4_HUMAN	TLC.	1	TCTTTCCCACC	0.567	
-	5	35849		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).	57	CTGAAGAGCTG	0.498	
-	3	20990		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).	57	ATGTGGAAACA	0.463	
-	1	9472		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).	57	AGGCTCCTCCT	0.493	
-	1	7184		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	h.|Extracellular (Potential).	57	TGGGGGAAGTG	0.473	
-	8	1152		NM_015719	NP_056534	P25940	CO5A3_HUMAN	nhelical region.	10	TGCCCGGAAGT	0.537	rs147076757
-	3	645	mwy.3_Missense_	NM_001127221	NP_001120693	O00555	CAC1A_HUMAN	=S2 of repeat I; (Potential)	2	TGGTTCTGTGT	0.478	

+	3	464	2naf.2_Missense_M	NM_012114	NP_036246	P31944	CASPE_HUMAN			4	CACCATGAAAAG	0.542	
-	3	420	t_Site|ILVBL_uc01	NM_006844	NP_006835	A1L0T0	ILVBL_HUMAN			2	ACGGCCGTGACC	0.622	
+	8	2360	cc.1_Missense_Mu	NM_004386	NP_004377	O14594	NCAN_HUMAN			4	GTATCCCGGGGT	0.597	
+	4	1702		NM_031218	NP_112495	P35789	ZNF93_HUMAN	C2H2-type 14.		1	AAAATTCATACTA	0.358	
-	4	1464	p.N439I|ZNF43_u	NM_003423	NP_003414	P17038	ZNF43_HUMAN	C2H2-type 10.		2	ATTCTGTTATGTT	0.383	
-	4	1110	1_Intron|ZNF208_	NM_007153	NP_009084					7	TGAAGGCTTTGC	0.413	
+	5	2103		NM_144689	NP_653290	Q8TAQ5	ZN420_HUMAN	C2H2-type 18.		0	TCACATCTTTCTC	0.433	
+	11	3705		NM_015073	NP_055888	O60292	SI1L3_HUMAN			2	GAGCAGGAAAGC	0.622	
+	66	10022	piv.1_Missense_Mu	NM_000540	NP_000531	P21817	RYR1_HUMAN			12	TGCCCGCCGGC	0.642	
+	3	219		NM_001042507	NP_001035972	P47929	LEG7_HUMAN	Galectin.		0	AGCAAGGCTCC	0.667	
+	3	1369	02pbp.2_5'Flank|C	NM_012099	NP_036231	O15446	RPA34_HUMAN			4	GCAAAAGGGGA	0.557	
-	5	2086	ydj.1_Missense_M	NM_001102657	NP_001096127	Q6ZNA1	ZN836_HUMAN	C2H2-type 13.		0	TTATGAATTGAAA	0.383	
+	7	2811	_p.E722K|NLRP4_	NM_134444	NP_604393	Q96MN2	NALP4_HUMAN			15	TGCTGCGAATAC	0.512	
+	31	5695	bp.1_Missense_Mu	NM_014668	NP_055483	Q4ZG55	GREB1_HUMAN			1	GTGCCCCGGAC	0.647	
-	3	360	_p.E107K|HS1BP3	NM_022460	NP_071905	Q53T59	H1BP3_HUMAN	PX.		1	TCCTCTCCCGGA	0.562	
-	26	7584		NM_000384	NP_000375	P04114	APOB_HUMAN			27	GGTGTCCTGTAC	0.418	
+	3	473		NM_030915	NP_112177	Q53QV2	LBH_HUMAN			0	GTCCAGGAGGAT	0.567	
+	10	1945	v.2_Nonsense_Mu	NM_206943	NP_996826	Q14766	LTBP1_HUMAN	alcium-bindi	p.R649*(1)	8	AGCTATCGATGT	0.378	
+	7	961	_p.E112K|RASGRI	NM_170672	NP_733772	Q8IV61	GRP3_HUMAN	rminal Ras-GEF.		5	GGATATGAAAAAC	0.443	
-	5	955	HX57_uc002rrg.2_	NM_198963	NP_945314	Q6P158	DHX57_HUMAN			3	ATTTGCGGAATC	0.343	
+	5	738		NR_003683						0	tAAGGAATCGCT	0.388	
-	2	959	j.1_Intron|CTNNA2	NM_178839	NP_849161	Q86UE6	LRRT1_HUMAN	Lumenal (Potential).		5	GGCGCGGGAAG	0.582	
-	15	2643	SEMA4C_uc002sx	NM_017789	NP_060259	Q9C0C4	SEM4C_HUMAN	lasmic (Potential).		2	CCTCGGGGTTG	0.652	
+	7	1009	70_uc002sye.1_Mi	NM_001079	NP_001070	P43403	ZAP70_HUMAN	nterdomain B.		6	GCTGCTCCCACA	0.706	
-	5	739		NM_004854	NP_004845	O43529	CHSTA_HUMAN	ble).|Lumenal (Potential).		1	ACTTTGGGAGTC	0.498	
-	7	1049	ise_Mutation_p.H2	NM_025181	NP_079457	Q8WV83	S35F5_HUMAN			0	ATGCATGACTTGA	0.388	
-	26	5146	nl.1_Missense_Mu	NM_018557	NP_061027	Q9NZR2	LRP1B_HUMAN	ntial).|LDL-receptor class B		50	CAGAAAAGAATTC	0.249	
+	18	2418	.2_Missense_Muta	NM_004522	NP_004513	O60282	KIF5C_HUMAN			1	TTCCAGGATAAG	0.413	
+	6	1148	p.R194Q|GALNT1	NM_052917	NP_443149	Q8IUC8	GLT13_HUMAN	tial).|Catalytic subdomain A		6	GTCTTCGAGGAG	0.423	
-	1	470	sense_Mutation_p.	NM_020711	NP_065762	Q8TAM6	ERMIN_HUMAN			2	AGTTGAGCAGCA	0.423	
-	10	1412	P4_uc010fpb.2_5'U	NM_001935	NP_001926	P27487	DPP4_HUMAN	cellular (Potential).		3	TGTATGGAAGTT	0.393	
+	4	539	z.2_Missense_Mut	NM_138995	NP_620482	Q8WXR4	MYO3B_HUMAN	rotein kinase.		19	AGCAATGATCTC	0.493	
+	1	134	zew.1_Missense_	NM_021193	NP_067016	P35452	HXD12_HUMAN			0	CTACCCGCGCG	0.706	
-	46	13657	.K4411T|TTN_uc0	NM_133437	NP_597681	Q8WZ42	TITIN_HUMAN			153	TTGAACTTTTCAT	0.378	
+	11	2073	SFA2_uc010zfo.1_	NM_001130445	NP_001123917	P28290	SSFA2_HUMAN			2	CAGCAGCAGTTG	0.473	
+	4	2269		NM_194250	NP_919226	Q7Z570	Z804A_HUMAN			11	GAAACAGAAAAG	0.323	
-	61	11484	uti.3_Missense_Mu	NM_018897	NP_061720	Q8WXX0	DYH7_HUMAN			12	TCAGTAACTTATT	0.383	
+	12	5211	g.1_Missense_Mu	NM_002374	NP_002365	P11137	MAP2_HUMAN			17	CTCCTGCGACT	0.502	
-	9	1370	se_Mutation_p.P4	NM_001144889	NP_001138361	Q6PIS1	S23A3_HUMAN	cellular (Potential).		0	GCAGTGGGATG	0.552	
-	14	2162_2163	p.G602R|PTPRN_	NM_002846	NP_002837	Q16849	PTPRN_HUMAN	lasmic (Potential).		4	GTGTCCCGTGGA	0.663	rs145338513
-	3	327	PTPRN_uc002vla.2	NM_002846	NP_002837	Q16849	PTPRN_HUMAN	cellular (Potential).		4	TTGGAGAACTG	0.567	
+	1	286		NM_152614	NP_689827	Q53QW1	CB057_HUMAN			1	CACGGCCAGAAG	0.532	
+	22	2615	e_Mutation_p.E76	NM_015575	NP_056390	Q6Y7W6	PERQ2_HUMAN	n-rich.|Glu-rich.		7	CAGGAAGAACTC	0.468	
+	4	829	NL_uc010fyw.2_5'	NM_194312	NP_919288	Q6ZVH7	ESPNL_HUMAN	ANK 8.		1	GGGGGCCACGG	0.657	
-	17	2257	p.R677C|HDLBP_	NM_203346	NP_976221	Q00341	VIGLN_HUMAN	KH 8.		4	GGAGCGGATCAC	0.587	
+	13	1288	FARP2_uc010zor.	NM_014808	NP_055623	O94887	FARP2_HUMAN			3	CATTCCCCGAG	0.478	
-	24	4051	p.S977F|NINL_uc	NM_025176	NP_079452	Q9Y2I6	NINL_HUMAN	Potential.		5	AGGTCGGACTTC	0.567	

+	2	91	tj.1_RNA|FRG1B_uc010gdr.1_RNA|FRG1B_uc010ztk.1_Intron							0	AATATCTTGGTAT	0.333	rs137871677
+	1	135		NM_153324	NP_697019	Q8N688	DB123_HUMAN			0	TCTTATCCCAGCT	0.537	
+	8	1104	2_RNA|PABPC1L_	NM_001124756	NP_001118228	Q4VXU2	PAP1L_HUMAN	RRM 4.		1	GTTTTTCCTCCC	0.587	
+	2	1198	_p.Q381K|SEMG2_	NM_003008	NP_002999	Q02383	SEMG2_HUMAN	X 60 AA tandem repeats,		1	GAAGAGCAAATA	0.388	
+	1	986		NM_178457	NP_848552	Q5JPB2	ZN831_HUMAN			14	GGATGCCAAGG	0.721	
-	1	87	GE_uc002yix.2_R	NM_182482	NP_872288					0	acgagccacggtgtta	0	
-	7	1031		NM_198996	NP_945347	Q6XZB0	LIPI_HUMAN			2	TCCTAAGAGGTC	0.303	
-	1	211		NM_181617	NP_853648	Q3LI59	KR212_HUMAN			0	TGGTCGGTAGC	0.279	rs147814118
+	20	1590	issense_Mutation_	NM_148175	NP_680480	Q13356	PPIL2_HUMAN			2	AGCGAGCAGCA	0.612	
+	7	1702_1703	ense_Mutation_p.	NM_030758	NP_110385	Q969R2	OSBP2_HUMAN			2	GGCCGGGAGC	0.609	
-	3	497	03K|PIK3IP1_uc0	NM_052880	NP_443112	Q96FE7	P3IP1_HUMAN	ellular (Potential).		1	GGTACCTGGAC	0.736	
-	3	486	aqe.2_Nonsense_	NM_001163857	NP_001157329	O43247	EAN57_HUMAN			0	TGGCTGAGCCC	0.622	
+	18	4668	n.3_Nonsense_M	NM_001162501	NP_001155973	Q9UPQ9	TNR6B_HUMAN			0	TGCCATGGAAAG	0.413	
-	3	317	ye.1_Missense_M	NM_020831	NP_065882	Q969V6	MKL1_HUMAN	on with SCAI and ACTB (B		5	GCTCCGATCTC	0.473	
-	10	5302	arc.1_Missense_M	NM_014246	NP_055061	Q9NYQ6	CELR1_HUMAN	otential).|Laminin G-like 2.		11	CACCCGCAACC	0.587	
-	4	720	_p.E26K|IL5RA_u	NM_000564	NP_000555	Q01344	IL5RA_HUMAN	ellular (Potential).		1	TCTTTTCATCAG	0.348	
-	16	2769	vw.2_Missense_M	NM_001001331	NP_001001331	Q01814	AT2B2_HUMAN	lasmic (Potential).		6	TCAATTCGCTCC	0.488	
-	9	882	eq.1_Missense_M	NM_207359	NP_997242	Q6ZQY3	GADL1_HUMAN			0	AGCTCCCAACA	0.438	
+	2	679_680	Missense_Mutatio	NM_002468	NP_002459	Q99836	MYD88_HUMAN	e domain (By similarity).		94	GATGACCCCCTG	0.525	
+	12	1499	kz.3_Missense_M	NM_001042646	NP_001036111	Q9UPV9	TRAK1_HUMAN	action with HGS.		1	CGGCTCCAACC	0.572	
-	14	4030	al.1_Missense_Mu	NM_024513	NP_078789	Q9BQS8	FYCO1_HUMAN			1	CGTCCGGTGGC	0.517	
-	4	1671	ro.3_Intron|CSPG	NM_006574	NP_006565	O95196	CSPG5_HUMAN	lasmic (Potential).		2	ATGGGGGGAGG	0.517	
-	3	457		NM_012234	NP_036366	Q8N488	RYBP_HUMAN			0	TGCTTCACTAGG	0.368	
+	1	695	BO2_uc011bgj.1_	NM_002942	NP_002933	Q9HCK4	ROBO2_HUMAN			11	ATGTTCGGGTTG	0.373	
+	4	784		NM_173824	NP_776185	Q5JPI3	CC038_HUMAN			0	AGAATCCTTTTCT	0.393	
+	3	1130	rp.1_Missense_M	NM_001080448	NP_001073917	Q9UF33	EPHA6_HUMAN	ellular (Potential).		16	ACAGGATATGAA	0.343	
-	7	614	hn.1_Missense_M	NM_014429	NP_055244	Q86VD1	MORC1_HUMAN			8	TTAAATGGGGAG	0.343	
+	9	1301	T3_uc010hug.2_	NM_031913	NP_114119	A0FGR9	ESYT3_HUMAN	C2 1.		0	GGAACGAAGTG	0.582	
+	4	580	_p.G45E|AGTR1_	NM_031850	NP_114038	P30556	AGTR1_HUMAN	Name=1; (Potential).		0	TATTTGGAAACA	0.353	
-	6	1355	_uc003ewz.2_Mis	NM_000096	NP_000087	P00450	CERU_HUMAN			1	GCTTCCCACGGA	0.418	
-	1	333	_uc003ewz.2_Mis	NM_000096	NP_000087	P00450	CERU_HUMAN	1.|Plastocyanin-like 1.		1	ATAATTCCAATGT	0.353	
-	19	2433	_p.E743K|ZBBX_u	NM_024687	NP_078963	A8MT70	ZBBX_HUMAN	Potential.		2	GTAATTCTTTTTC	0.328	
-	3	319		NM_198505	NP_940907	Q4VNC0	AT135_HUMAN			11	ATTCTTCCCACT	0.408	
-	8	1079	3A3_uc003ftz.1_5	NM_024524	NP_078800	Q9H7F0	AT133_HUMAN	ical; (Potential).		1	GTGCTCCACAGT	0.333	
-	3	12755	1bth.1_Intron|MU	NM_018406	NP_060876	Q99102	MUC4_HUMAN	Ser-rich.		0	GGTGACAGGAA	0.582	
-	3	1350	732_uc010ibb.1_I	NM_001137608	NP_001131080	B4DXR9	ZN732_HUMAN	2H2-type 12.		0	CACATTTGTAAG	0.418	
-	3	1955	ron|ABCA11P_uc0	NM_133474	NP_597731	D9N162	D9N162_HUMAN			1	TGCCACGATCTT	0.378	
+	11	1639	G452R|FAM193A_	NM_003704	NP_003695	P78312	F193A_HUMAN			3	CAGCCGGAGCC	0.502	
+	16	1798	s.1_Missense_Mu	NM_004787	NP_004778	O94813	SLIT2_HUMAN	LRRNT 3.		11	CACATTCCCCAG	0.448	
-	11	1866	qn.1_Missense_M	NM_145290	NP_660333	Q8IWK6	GP125_HUMAN	ellular (Potential).		1	ACTGTTGAATAAA	0.488	
+	12	2071	N7_uc003gvi.3_3'	NM_024677	NP_078953					0	GCTGCAGCCAAG	0.428	
-	2	240	.1_RNA|NMU_uc	NM_006681	NP_006672	P48645	NMU_HUMAN			0	TGTAATCCTTGA	0.308	
-	6	1370		NM_001076	NP_001067	P54855	UDB15_HUMAN			0	TAATTTCATGACA	0.363	
+	5	1203	cam.1_Missense_	NM_001075	NP_001066	P36537	UDB10_HUMAN		p.P393S(1)	5	GCATTCCATTGT	0.448	
+	3	962	_p.L141F|RUFY3_	NM_014961	NP_055776	Q7L099	RUFY3_HUMAN	RUN.		0	ACTTTTCTCGGA	0.259	
+	5	608	LB_uc003hgu.3_M	NM_000477	NP_000468	P02768	ALBU_HUMAN	Albumin 1.		6	GAACTCCTTTTC	0.353	
+	12	1444	p.Q258H|USO1_u	NM_003715	NP_003706	O60763	USO1_HUMAN	8.|Globular head.		3	TGGCCAGTTATT	0.383	

-	13	2312		NM_001042784	NP_001036249	Q5M9N0	CD158_HUMAN	Potential.	6	TCAGATCCTTCC	0.294	
-	5	665		NM_174952	NP_777612	Q8N412	CD037_HUMAN		0	TATAGTCGTGGG	0.269	rs147933911
-	8	1011	_p.G237E|AGXT2L	NM_031279	NP_112569	Q8TBG4	AT2L1_HUMAN		1	GGTTTTCCCATTG	0.468	
-	9	2573	ST4_uc010imw.2_	NM_022569	NP_072091	Q9H3R1	NDST4_HUMAN	eparan sulfate N-sulfotrans	4	GAACTTCCTCAA	0.318	
+	1	3845		NM_024582	NP_078858	Q6V0I7	FAT4_HUMAN	.|Extracellular (Potential).	18	CCTATTCCCTTG	0.363	
+	8	7405	e_Mutation_p.H76	NM_024582	NP_078858	Q6V0I7	FAT4_HUMAN	(Potential).|Cadherin 24.	18	CAGCATCACCCA	0.453	
+	17	13949	_p.S2891L|FAT4_u	NM_024582	NP_078858	Q6V0I7	FAT4_HUMAN	lasmic (Potential).	18	AATTTTCAATCCA	0.498	
+	19	3303	09_splice|TLL1_uc	NM_012464	NP_036596	O43897	TLL1_HUMAN		7	TACAGGTCAGCA	0.368	
+	12	2360	ve.1_Missense_Mu	NM_001080477	NP_001073946	Q9P273	TEN3_HUMAN	cellular (Potential).	0	TGTGACGTAGCC	0.517	
+	2	585		NM_207352	NP_997235	Q6ZWL3	CP4V2_HUMAN		0	CTGGGTCGGGC	0.423	
-	10	8199		NM_005245	NP_005236	Q14517	FAT1_HUMAN	(Potential).|Cadherin 24.	12	CAAAGAAAGTGA	0.378	
+	2	5636		NM_153610	NP_705838	Q8N3K9	CMYA5_HUMAN		9	AGTTTTCACTTAT	0.333	
+	1	389	tron|SLC22A4_uc	NM_003059	NP_003050	Q9H015	S22A4_HUMAN	cellular (Potential).	0	CGGCCGCGAGG	0.746	
+	1	1384	03lhf.2_Intron|PCD	NM_018907	NP_061730	Q9UN74	PCDA4_HUMAN	|Extracellular (Potential).	6	CGCGCGAGACG	0.617	
+	1	2321	CDHA7_uc003lhq.	NM_018904	NP_061727	Q9Y5I0	PCDAD_HUMAN	PXXP 2.|6 X 4 AA repeats o	6	TCAGTCCCAGCC	0.567	
+	1	1511		NM_018930	NP_061753	Q9UN67	PCDBA_HUMAN	|Extracellular (Potential).	2	TCAATGACAACG	0.587	
-	5	857	ense_Mutation_p.S	NM_022481	NP_071926	Q8WWN8	ARAP3_HUMAN		7	GTGGGCGATAAG	0.607	rs144278581
-	3	331	.2_5'UTR|CCDC6	NM_015621	NP_056436	A6NI79	CCD69_HUMAN	Potential.	2	TCTTTTCCTCCT	0.502	
+	7	2110	orf25_uc003mdr.3_RNA|C5orf25_uc003mdv.2_Missense			Q8NDZ2	CE025_HUMAN		0	GAGTCCTTTTCC	0.488	
+	10	3620	p.S1077L|RREB1_	NM_001003698	NP_001003698	Q92766	RREB1_HUMAN		11	TATCCTCGGCCC	0.627	
+	1	811_812		NM_030905	NP_112167	O76002	OR2J2_HUMAN	lasmic (Potential).	0	TTCAGAAAGTGT	0.45	
-	10	1733_1734	RS_uc011doi.1_R	NM_006295	NP_006286	P26640	SYVC_HUMAN		3	TCCAAGGAGCTG	0.594	
-	2	467	se_Mutation_p.S8	NM_016593	NP_057677	Q9NYL5	CP39A_HUMAN		1	TTTTTGGATTTTA	0.323	
+	6	908	e_Mutation_p.G23	NM_153839	NP_722581	Q8IZF7	GP111_HUMAN	cellular (Potential).	1	AACATTGGAAAA	0.398	
+	3	732		NM_003221	NP_003212	Q92481	AP2B_HUMAN		0	CAGCGGCATGA	0.333	
-	6	921		NM_152688	NP_689901	Q5VWX1	KHDR2_HUMAN	Pro-rich.	11	TGCTTCCCCGA	0.607	
+	13	2596	_Missense_Mutati	NM_001162529	NP_001156001	Q9P2D6	F135A_HUMAN		1	GGAAATCATTGT	0.353	
-	56	8558	ht.2_Missense_M	NM_004370	NP_004361	Q99715	COCA1_HUMAN	n (COL2) with 1 imperfecti	9	GAGTCCATTGG	0.488	
-	1	205	.1_RNA|GOPC_uc	NM_002944	NP_002935	P08922	ROS_HUMAN		25	AATGTTCTTCAT	0.383	
-	5	1614	ebt.1_Missense_M	NM_001010923	NP_001010923	Q8N1K5	THMS1_HUMAN	CABIT 2.	4	AAACCTCCTTCC	0.443	
+	10	1892	khe.2_Missense_M	NM_020455	NP_065188	Q86SQ4	GP126_HUMAN	cellular (Potential).	1	GGAAGGAAAAA	0.393	
+	29	5975	M|TIAM2_uc011efl.	NM_012454	NP_036586	Q8IVF5	TIAM2_HUMAN		4	GACATCCTGAGC	0.537	
+	12	1767	wc.1_Missense_M	NM_001040001	NP_001035090	P55196	AFAD_HUMAN		5	ATAGTGGGACAG	0.413	
-	7	1678	LL2_uc003ski.3_	NM_182924	NP_891554	Q8IY33	MILK2_HUMAN		1	CGAAGGGAGGC	0.627	rs146347352
+	17	2432	_Mutation_p.T393	NM_031449	NP_113637	Q8NF64	ZMIZ2_HUMAN	Pro-rich.	5	CCCCAACCCTTG	0.632	
-	1	908		NM_033224	NP_150093	Q96QR8	PURB_HUMAN		0	GCCGCCGCTGC	0.587	
+	54	14090_1409	CA13_uc010kyt.1_	NM_152701	NP_689914	Q86UQ4	ABCAD_HUMAN		10	CTACTCTCCAAG	0.391	
-	6	626	e_Mutation_p.L17	NM_006213	NP_006204	Q16816	PHKG1_HUMAN	rotein kinase.	1	ATGTTGAGTTTG	0.527	
+	5	1255	an.2_Missense_Mu	NM_003388	NP_003379	Q9UDT6	CLIP2_HUMAN		3	GTGTCAGCACTG	0.632	
-	10	13870	S4527R|PCLO_uc	NM_033026	NP_149015	Q9Y6V0	PCLO_HUMAN		7	TTCTCCACTATGT	0.378	
+	9	1090	u.2_Missense_Mu	NM_021151	NP_066974	Q9UKG9	OCTC_HUMAN		3	ATAGCAGTCCAC	0.353	
+	4	1252	ve.1_Missense_M	NM_173564	NP_775835	Q6ZVC0	CG051_HUMAN	Pro-rich.	1	CCAAGGAGCCA	0.687	
+	3	6600	C17_uc010lho.1_	NM_001040105	NP_001035194	Q685J3	MUC17_HUMAN	ich.|59 X approximate tand	27	CTTTCAACAACT	0.483	rs147644870
+	21	4123	30_splice|MET_uc	NM_000245	NP_000236	P08581	MET_HUMAN		159	GGAACAGATATG	0.423	
-	8	2538	RM8_uc003vlt.2_M	NM_000845	NP_000836	O00222	GRM8_HUMAN	cellular (Potential).	23	AAATGTCACACT	0.468	
+	3	663		NM_020299	NP_064695	O60218	AK1BA_HUMAN		5	CCACAGGGATTC	0.507	rs146306673
+	15	4802	wem.2_Missense_	NM_005435	NP_005426	Q12774	ARHG5_HUMAN	SH3.	2	TGGTTTCCTGTG	0.572	

-	3	915	hm.2_Missense_	NM_024711	NP_078987	Q6P9H5	GIMA6_HUMAN		3	CCTTCCGGGTG	0.622	
-	18	2362		NM_001010906	NP_001010906	Q68CJ6	SLIP_HUMAN		2	CATCCCCCTGG	0.512	
+	4	3992	1_uc011ldy.1_Intr	NM_006269	NP_006260	P56715	RP1_HUMAN		12	TTTTTTCCTAGTG	0.408	
+	2	467	n_p.A46V|GRHL2_	NM_024915	NP_079191	Q6ISB3	GRHL2_HUMAN	cription activation.	3	GACAGCAGCCA	0.547	
+	1	209		NM_024410	NP_077721	Q14990	ODFP1_HUMAN	eats of [RC]-C-L-C-D.|1.	2	CACACGGTGCC	0.507	rs117958007
+	1	345		NM_003301	NP_003292	P34981	TRFR_HUMAN	Name=3; (Potential).	3	GAATTAATGCAT	0.463	
+	16	1825		NM_022045	NP_071328	Q96DY7	MTBP_HUMAN	ith MDM2 (By similarity).	3	AGGGTCCTCGG	0.398	
+	10	2457		NM_003129	NP_003120	Q14534	ERG1_HUMAN		2	CTTTCTGTGTAA	0.388	
+	1	271		NM_002170	NP_002161	P32881	IFNA8_HUMAN		0	TCCTCCATGAG	0.473	
-	6	1225	e_Mutation_p.A2	NM_005476	NP_005467	Q9Y223	GLCNE_HUMAN	glucosamine 2-epimerase.	0	TGTCAGCATCC	0.393	
+	1	474		NM_152577	NP_689790	Q8N7E2	ZN645_HUMAN		2	AGCTCGAAAAC	0.448	
-	3	4938		NM_001008537	NP_001008537	Q5QGS0	K2022_HUMAN		15	TCGGTCCGTTAT	0.453	
-	5	1273	p.G398E|KLHL13_	NM_033495	NP_277030	Q9P2N7	KLH13_HUMAN	Kelch 2.	2	GTTTTTCCTTTT	0.433	
+	5	418	ur.2_Missense_M	NM_000276	NP_000267	Q01968	OCRL_HUMAN		4	AAATTCGGGTT	0.423	
+	1	927	_p.E54K|PCDH11	NM_032973	NP_116755	Q9BZA8	PC11Y_HUMAN	r (Potential).|Cadherin 1.	0	GAGAAGAAATT	0.463	
-	4	389	_p.R78L|KIAA17	NM_001080484	NP_001073953	Q9C0B2	K1751_HUMAN		1	TCTGCCGCAGG	0.502	
-	4	1018	ad.1_Missense_	NM_024980	NP_079256	Q5UAW9	GP157_HUMAN	lasmic (Potential).	0	AGAGAGAGAAG	0.607	
+	16	1818	KA_uc010obw.1_	NM_004070	NP_004061	P51800	CLCKA_HUMAN	CBS 1.	1	AGTATCCCCTG	0.557	
-	20	3350	.E752K|EIF4G3_u	NM_003760	NP_003751	O43432	IF4G3_HUMAN		1	ACCTTCGTCCA	0.448	
+	4	768	b.2_Missense_M	NM_032264	NP_115640	Q9H094	NBPF3_HUMAN	Potential.	2	TTGCAGAGGAG	0.552	
+	2	344	HD_uc001bkb.2_	NM_016124	NP_057208	Q02161	RHD_HUMAN	ical; (Potential).	1	TGGACGGCTTC	0.577	
-	11	1079	.F27Y|UBXN11_u	NM_183008	NP_892120	Q5T124	UBX11_HUMAN	SEP.	1	AGGGAAAGAAG	0.582	
+	20	6984	_p.A1050V|ARID1	NM_006015	NP_006006	O14497	ARI1A_HUMAN		142	CCTTGCCGCCA	0.642	
+	8	1440	_p.A266V|HCRTR1	NM_001525	NP_001516	O43613	OX1R_HUMAN	Name=7; (Potential).	1	CAGCGCTGCCA	0.592	
+	2	288	_p.R41C|ZSCAN	NM_145238	NP_660281	P17040	ZSC20_HUMAN		4	AGGACCGTGGC	0.597	
-	64	9804	m.1_Missense_M	NM_052896	NP_443128	Q7Z408	CSMD2_HUMAN	ellular (Potential).	12	CTCCCGGGCAG	0.502	rs149656829
-	55	8419	m.1_Missense_M	NM_052896	NP_443128	Q7Z408	CSMD2_HUMAN	xtracellular (Potential).	12	TGTACCGCACC	0.597	rs149704396
-	9	1231	xm.1_Missense_M	NM_052896	NP_443128	Q7Z408	CSMD2_HUMAN	ar (Potential).|Sushi 2.	12	CACCTCGGCAG	0.632	
-	2	567		NM_152374	NP_689587	Q8TAB5	CA216_HUMAN		1	TTGGAGCTCGG	0.567	
-	6	1692	4_uc001cdm.2_M	NM_003819	NP_003810	Q13310	PABP4_HUMAN	RRM 3.	0	GTGCACGGCCT	0.398	
+	4	599	_p.R102Q|ZNF642	NM_198494	NP_940896	Q49AA0	ZN642_HUMAN	KRAB.	0	ATACCGAGAGG	0.458	rs145832267
-	4	586	c001cnh.2_Misse	NM_012222	NP_036354	Q9UIF7	MUTYH_HUMAN		0	ATATGCCCGCC	0.632	
+	6	1127	5'Flank|MUTYH_u	NM_025077	NP_079353	Q96GM8	TOE1_HUMAN		1	TAATCCGAGCC	0.552	
+	14	3698	tp.2_Missense_M	NM_004799	NP_004790	O95405	ZFYV9_HUMAN		8	TGTGTGTACAG	0.423	
-	3	438		NM_023077	NP_075565	Q96BR5	SELR1_HUMAN	Sel1-like 3.	0	TGGCCTTTCCC	0.537	
-	3	986		NM_147193	NP_671726	Q8NBF1	GLIS1_HUMAN		1	CCTTCCGGCAG	0.657	
-	3	383	_p.E44K|C8B_uc	NM_000066	NP_000057	P07358	CO8B_HUMAN	SP type-1 1.	4	GACTTCCTTGT	0.498	
+	12	1845	pc.1_Missense_M	NM_014787	NP_055602	O75061	AUXI_HUMAN	Pro-rich.	3	CACCACGCCGC	0.537	
+	16	1775	C7_uc009wbg.2_I	NM_020794	NP_065845	Q96NW7	LRRC7_HUMAN		14	TAAAATCTGTTC	0.338	
-	11	1844	73_uc001dgi.3_Mi	NM_001002912	NP_001002912	Q5RHP9	CA173_HUMAN	Glu-rich.	5	TCTCTTTTTCAG	0.403	
+	6	919	ls.1_Missense_M	NM_001285	NP_001276	A8K7I4	CLCA1_HUMAN		1	AGCAAAATCAA	0.373	
+	9	1380	dly.2_Nonsense_	NM_016009	NP_057093	Q9Y371	SHLB1_HUMAN	SH3.	0	GAAACCAGAAG	0.388	
-	15	1954	RHGAP29_uc001	NM_004815	NP_004806	Q52LW3	RHG29_HUMAN		11	TATAAAGGAAG	0.358	
+	4	263	va.1_Missense_M	NM_001040033	NP_001035122	P19397	CD53_HUMAN	ical; (Potential).	0	CTTTGGGATCT	0.483	
+	23	2095	e_Mutation_p.G6	NM_003176	NP_003167	Q15431	SYCP1_HUMAN	Potential.	1	AAAAGGTACAG	0.254	
-	11	1315	vu.1_Missense_M	NM_001232	NP_001223	O14958	CASQ2_HUMAN		1	GAAGATCGTCAT	0.403	
-	25	3982	4DIP_uc001elm.3	NM_014644	NP_055459	Q5VU43	MYOME_HUMAN	Potential.	5	TCTCCTGGAGAT	0.507	

-	3	474	P_uc001eln.3_Miss	NM_014644	NP_055459	Q5VU43	MYOME_HUMAN		5	CCTTTTCACCAC	0.433	
+	29	3792	I0_uc010oyl.1_Intr	NM_001039703	NP_001034792	A6NDV3	A6NDV3_HUMAN		0	GACCCACCATGC	0.453	
+	76	9445	BPF10_uc010oyl.1	NM_001039703	NP_001034792	A6NDV3	A6NDV3_HUMAN		0	GCTCAGCAGGG	0.463	
-	9	1214	).R276Q|LASS2_u	NM_181746	NP_859530	Q96G23	CERS2_HUMAN	Helical; (Potential).	0	ACCAGTCGGGTG	0.512	
+	2	1046		NM_001025231	NP_001020402	Q5T749	KPRP_HUMAN	Pro-rich.	5	GAGATTTCCTCCC	0.632	
-	4	472	A6_uc001fbw.1_5'	NM_002962	NP_002953	P33763	S10A5_HUMAN	2; high affinity (Potential).	0	CTGGTCGCTGT	0.547	rs140492850
+	4	1026	|HCN3_uc010pfz.	NM_020897	NP_065948	Q9P1Z3	HCN3_HUMAN	=Segment S6; (Potential).	2	TGCTACGCCATG	0.607	
-	6	1103	L3_uc009wsn.2_In	NM_052939	NP_443171	Q96P31	FCRL3_HUMAN	cellular (Potential).	4	TCCTTTTTTTGAT	0.547	
+	12	2169	TP1A4_uc001fvg.2	NM_144699	NP_653300	Q13733	AT1A4_HUMAN	lasmic (Potential).	4	TTCTGCTTCTTG	0.468	
-	6	1046	244_uc009wtp.2_F	NM_016382	NP_057466	Q9BZW8	CD244_HUMAN	lasmic (Potential).	1	CTCCAGGAAAG	0.502	
-	12	2250	p.G481E|ARHGAF	NM_001025598	NP_001020769	Q7Z6I6	RHG30_HUMAN		3	GCCTCTCCCTCC	0.587	
+	7	845	on_p.A221T|NIT1_	NM_005600	NP_005591	Q86X76	NIT1_HUMAN	CN hydrolase.	0	GCAGCAGCACAG	0.572	
-	2	220	wux.1_Missense_I	NM_178550	NP_848645	Q86UF4	CA110_HUMAN	Potential.	0	CTCCAAATCAAA	0.433	
+	4	551	K2_uc010plb.1_Int	NM_012474	NP_036606	Q9BZX2	UCK2_HUMAN		1	GAGACAGTTACT	0.547	
+	6	977	geq.2_Missense_M	NM_003953	NP_003944	O95297	MPZL1_HUMAN	lasmic (Potential).	2	AGTCAGAGTCT	0.443	
-	7	1179	nse_Mutation_p.K	NM_000655	NP_000646	P14151	LYAM1_HUMAN	cellular (Potential).	0	ACCCTCCTTAAT	0.393	
-	13	1918	YL3_uc001ggt.2_M	NM_181093	NP_851607	Q8IZE3	PACE1_HUMAN	action with EZR.	2	GGGCTCGCAGT	0.473	
+	9	1572	_Mutation_p.G47	NM_002021	NP_002012	Q01740	FMO1_HUMAN		1	GCCCAGGAAAAT	0.507	
-	22	3130	vwe.2_Missense_M	NM_178527	NP_848622	Q5TAH2	S9A11_HUMAN	cNMP.	2	AGATTCCTTGTG	0.303	
+	8	1565	lg.2_Nonsense_Mu	NM_021165	NP_066988	Q9C0B6	FAM5B_HUMAN		6	ACTGGTGGAACC	0.512	
+	7	477	orf49_uc001glv.1_F	NM_032126	NP_115502	Q5T0J7	CA049_HUMAN		0	CAAAGGAGCAGC	0.557	
+	16	1712	_p.E317K|C1orf12	NM_144696	NP_653297	Q5T1B0	AXDN1_HUMAN		0	AAAGAAGAGTTT	0.368	
-	2	300	onv.1_Missense_M	NM_002928	NP_002919	O15492	RGS16_HUMAN		1	TCTTTGCTGTGT	0.537	
+	71	11181		NM_031935	NP_114141	Q96RW7	HMCN1_HUMAN	ike C2-type 35.	23	CCCCACCTGTAA	0.413	
+	11	1793		NM_000186	NP_000177	P08603	CFAH_HUMAN	Sushi 9.	6	gaatgccagaactaaa	0.249	
+	2	205	HR2_uc001gtr.1_In	NM_005666	NP_005657	P36980	FHR2_HUMAN	Sushi 1.	3	CATTTTCCCAAG	0.348	
+	8	1276		NM_030787	NP_110414	Q9BXR6	FHR5_HUMAN	Sushi 6.	2	TGTAGAAAAAAG	0.348	
+	12	4160	se_Mutation_p.S1	NM_201253	NP_957705	P82279	CRUM1_HUMAN	cellular (Potential).	9	TGATCTCCGACA	0.428	
-	29	4657	qv.1_Missense_Mu	NM_002646	NP_002637	O00750	P3C2B_HUMAN	PX.	7	TTCTCTCGCATC	0.532	
-	2	1032		NM_173854	NP_776253	Q8IVJ1	S41A1_HUMAN		2	GGCCCGAGACT	0.652	
-	10	1663	MB3_uc001hhh.2_	NM_001017402	NP_001017402	Q13751	LAMB3_HUMAN	ninin EGF-like 3.	6	CTGCGGGTTGG	0.652	
-	6	926	pte.1_Missense_M	NM_018252	NP_060722	Q9H813	TM206_HUMAN	cellular (Potential).	1	GCTTCCCGCCCA	0.562	
+	7	694	PATA17_uc001hli.2	NM_138796	NP_620151	Q96L03	SPT17_HUMAN		1	CAAGCGCCCGTT	0.408	
-	6	395	_uc010pvd.1_Intr	NM_002533	NP_002524	O15381	NVL_HUMAN		2	TCATGTGATTTG	0.353	
-	9	1304	130331_uc010pyc	NM_021186	NP_067009	Q12836	ZP4_HUMAN	acellular (Potential).	3	GTCCCCTGAGG	0.532	
+	12	2875	_p.S430L|KIF26B_	NM_018012	NP_060482	Q2KJY2	KI26B_HUMAN		3	CAGCTCGTCCG	0.652	
+	3	893	o.3_Missense_Mu	NM_152609	NP_689822	Q6PJW8	CNST_HUMAN		0	TGCAGTCTCTGT	0.453	
-	32	6364	CTF1_uc009xgs.1_	NM_015446	NP_056261	Q8WYP5	ELYS_HUMAN	lear localization (By similar	7	TGGAGAAAATAA	0.433	
+	16	1687	ns.1_Missense_Mu	NM_002627	NP_002618	Q01813	K6PP_HUMAN		3	GCATCGGGGCA	0.642	
+	13	1658		NM_002216	NP_002207	P19823	ITIH2_HUMAN		3	GCTCCGGAATG	0.408	
-	8	2208		NM_001010924	NP_001010924	Q5VUB5	F1711_HUMAN	lasmic (Potential).	4	TTACTTCCGTTC	0.532	
-	55	8723	UBN_uc009xjr.1_M	NM_001081	NP_001072	O60494	CUBN_HUMAN	CUB 21.	19	GATAACGGGAC	0.552	rs150488625
-	43	6540		NM_001081	NP_001072	O60494	CUBN_HUMAN	CUB 15.	19	GGTGGAGAACAG	0.383	
-	1	818		NM_001034842	NP_001030014	Q3KNS1	PTHD3_HUMAN		4	CGCGCCGTCCA	0.627	
+	7	767		NM_052997	NP_443723	Q9BXX3	AN30A_HUMAN		9	CTGCAGGAACAC	0.348	
+	7	860		NM_052997	NP_443723	Q9BXX3	AN30A_HUMAN		9	CCTTGGTGGAAA	0.502	
+	15	1949	PRKG1_uc009xow	NM_001098512	NP_001091982	Q13976	KGP1_HUMAN	rotein kinase.	6	TGCCAAAAATGC	0.313	

+	18	2460	j.1_Missense_Mu	NM_001080512	NP_001073981	Q9H694	BICC1_HUMAN		4	CCGAAATGGAAT	0.458	
+	3	772	e_Mutation_p.S19	NM_032578	NP_115967	Q86TC9	MYPN_HUMAN	action with CARP.	5	AAAACAGCTCCA	0.448	
+	7	1220	ow.1_Missense_M	NM_004728	NP_004719	Q9NR30	DDX21_HUMAN	ase ATP-binding.	3	TGCAACTTGCC	0.368	
+	25	3447	p.V640M|CDH23_	NM_022124	NP_071407	Q9H251	CAD23_HUMAN	.|Extracellular (Potential).	11	ACGACGTGGGC	0.657	
+	6	944	STAMBPL1_uc001	NM_020799	NP_065850	Q96FJ0	STALP_HUMAN		1	TAGAATCGGAGC	0.443	rs148096389
-	4	649	sense_Mutation_p.	NM_000770	NP_000761	P10632	CP2C8_HUMAN		0	AATCGTTTCTGG	0.388	
-	3	688	kmp.2_Missense_	NM_152309	NP_689522	Q6ZUJ8	BCAP_HUMAN	DBB.	5	CACAGCGAATG	0.547	
-	27	3026		NM_003061	NP_003052	O75093	SLIT1_HUMAN		4	CACACTTGGCC	0.542	
+	14	2260	.43_uc010qpu.1_I	NM_017893	NP_060363	Q9NTN9	SEM4G_HUMAN	Potential).|Ig-like C2-type.	1	GTTACAGATGCA	0.627	
-	6	1917	.2_Missense_Muta	NM_013274	NP_037406	Q9UGP5	DPOLL_HUMAN		0	GTTCCAGGAAG	0.572	
+	25	3838		NM_014976	NP_055791	Q14690	RRP5_HUMAN	S1 motif 11.	7	TCCTTCCCCTTT	0.557	
-	4	467	se_Mutation_p.T13	NM_024928	NP_079204	Q9H668	STN1_HUMAN	OB.	1	GGATCGTGTCC	0.458	
+	4	4130	se_Mutation_p.S12	NM_206862	NP_996744	O95359	TACC2_HUMAN		10	TGTTTCCTCTG	0.592	
-	3	1405	_p.V298I|CHST15	NM_015892	NP_056976	Q7LFX5	CHSTF_HUMAN	enal (Potential).	1	GCGGACGATTC	0.547	
+	14	1916		NM_198075	NP_932341	Q8IYG6	LRC56_HUMAN		1	TCGACAGACCTG	0.687	
+	20	2240	_p.E620K|EPS8L2	NM_022772	NP_073609	Q9H6S3	ES8L2_HUMAN		1	AGGAGGAGCTG	0.677	
+	44	14641		NM_002457	NP_002448	Q02817	MUC2_HUMAN	VWFC 1.	2	CCACGGAGGTC	0.622	
+	39	4906	ltb.2_Missense_M	NM_017511	NP_059981	Q9HC84	MUC5B_HUMAN	VWFD 3.	0	GGACCTTCCGC	0.652	
+	3	426	_p.V70M|SLC22A	NM_183233	NP_899056	Q96BI1	S22AI_HUMAN	ical; (Potential).	3	TCGGGGTGCTG	0.637	
-	1	543	.1_Intron|HBE1_uc	NM_033180	NP_149420	Q9Y5P1	O51B2_HUMAN	cellular (Potential).	3	AAAATGAAAAAA	0.398	
-	1	519		NM_153444	NP_703145	Q8WZ92	OR5P2_HUMAN	cellular (Potential).	5	ACAGAAAAAATG	0.383	
+	6	689	k.1_Nonsense_M	NM_018222	NP_060692	Q9NVD7	PARVA_HUMAN		3	CCATCCAAGTG	0.498	
-	7	946	n_p.P140L|PTPN	NM_006906	NP_008837	P54829	PTN5_HUMAN		2	TGGGTGGCTCT	0.632	
-	16	2715		NM_031217	NP_112494	Q8NI77	KI18A_HUMAN		2	TTACGTCTGCAG	0.318	
+	10	1835	_p.L514F|EXT2_uc	NM_207122	NP_997005	Q93063	EXT2_HUMAN	enal (Potential).	5	GATTCTCTCTGG	0.383	
-	5	854	MBRA1_uc001ncv.	NM_017749	NP_060219	Q9C0C7	AMRA1_HUMAN	WD 3.	3	GACTCCAGTCC	0.567	
-	9	861_862		NM_004308	NP_004299	Q07960	RHG01_HUMAN	Rho-GAP.	1	AGTCTCCCTGAC	0.653	
+	7	674	2_uc001ndg.3_RN	NM_000506	NP_000497	P00734	THRB_HUMAN		3	CATTGGAGCAG	0.607	
-	30	4725	uc001ndl.2_RNA	NM_002334	NP_002325	O75096	LRP4_HUMAN	ntial).|LDL-receptor class B	4	ACCTGCGGGTAT	0.498	
+	6	941	32_uc001nee.2_In	NM_000107	NP_000098	Q92466	DDB2_HUMAN	WD 3.	3	ATGTGGCCCTGA	0.542	
-	1	52		NM_001004743	NP_001004743	Q8NGP3	OR5M9_HUMAN	cellular (Potential).	4	CTGACGACAGG	0.428	
-	1	188		NM_001005489	NP_001005489	Q8NGF7	OR5BH_HUMAN	Name=2; (P p.N63S(1)	3	GACAGGTTACTG	0.468	
+	8	1093	Mutation_p.Q308*	NM_053023	NP_444251	Q96JP5	ZFP91_HUMAN		1	CAATCCAGTAT	0.408	
-	8	1323		NM_001062	NP_001053	P20061	TCO1_HUMAN		2	TGGTTCGCCTC	0.527	rs140632800
+	6	1197	na.1_Missense_M	NM_017670	NP_060140	Q96FW1	OTUB1_HUMAN	OTU.	1	TGGACGGACTG	0.657	
+	9	781	ph.1_Missense_M	NM_000932	NP_000923	Q01970	PLCB3_HUMAN		2	CTCAACGAAGTG	0.622	
-	17	3820		NM_006946	NP_008877	O15020	SPTN2_HUMAN	Spectrin 9.	4	TTTCCCGAATCT	0.557	
+	8	1808	P5_uc009ysg.2_5'U	NM_002335	NP_002326	O75197	LRP5_HUMAN	ptor class B 10.|Extracellula	7	CAGCCGGGACG	0.622	
+	14	4730		NM_014786	NP_055601	Q96PE2	ARHGH_HUMAN		0	TCCGTCGCTGA	0.726	
+	5	1272		NM_153614	NP_705842	P59910	DJB13_HUMAN		0	CTCCACCATCA	0.527	
-	15	2086	n_p.V595I|DLG2_u	NM_001364	NP_001355	Q15700	DLG2_HUMAN	SH3.	6	GGATGACCCCCA	0.468	rs149247541
+	1	216		NM_001098672	NP_001092142	Q6MZM0	HPHL1_HUMAN		3	GTCTGGGCTGG	0.502	
+	17	3150	v.2_3'UTR|GRIA4_	NM_000829	NP_000820	P48058	GRIA4_HUMAN	lasmic (Potential).	8	GACCTACCATAA	0.493	
-	12	2600_2601		NM_020693	NP_065744	Q8TD84	DSCL1_HUMAN	otential).|Ig-like C2-type 9.	8	TAGCTCCTTCGC	0.639	
+	3	411	sbq.1_5'UTR|FOX	NM_017547	NP_060017	Q96CU9	FXRD1_HUMAN		0	TCATTGCCTGAG	0.488	
+	8	900	sense_Mutation_p.	NM_017547	NP_060017	Q96CU9	FXRD1_HUMAN		0	GAATGCGCCATT	0.642	
+	5	670	_p.V149I|LTBR_uc	NM_002342	NP_002333	P36941	TNR3_HUMAN	(Potential).|TNFR-Cys 3.	2	ACTGCGTCCCC	0.637	rs145130663

-	2	101	DA_uc001quq.1_	NM_020661	NP_065712	Q9GZX7	AICDA_HUMAN		2	CCTCCGGTTCA	0.473	
+	1	114		NM_144670	NP_653271	A8K2U0	A2ML1_HUMAN		3	AGCTCCTTCTA	0.507	
-	3	510	B4_uc001qzf.1_In	NM_006249	NP_006240	Q04118	PRB3_HUMAN	[PQS]-P-[PS]-Q-[GE]-G-N-	1	GGACGAGGCG	0.647	
-	13	3619		NM_000834	NP_000825	Q13224	NMDE2_HUMAN	lasmic (Potential).	12	CGTGCTCCCAG	0.582	
+	21	2437_2438	MP_uc001rgi.2_R	NM_006152	NP_006143	Q12912	LRMP_HUMAN	enal (Potential).	2	TGTGGATGCCG	0.495	
-	12	963_964	_Mutation_p.R215	NM_002733	NP_002724	P54619	AAKG1_HUMAN	CBS 4.	1	AGTCGGTGAAC	0.54	
-	5	1439		NM_002272	NP_002263	B4DRS2	B4DRS2_HUMAN		6	CTCCTCGTACT	0.592	
+	6	979	2_Nonsense_Mut	NM_199187	NP_954657	P05783	K1C18_HUMAN	.|Rod.|Necessary for inter	1	CAGTCCAGTCC	0.572	
+	19	2765	.2_Missense_Mut	NM_170754	NP_736610	Q63HR2	TENC1_HUMAN	Pro-rich.	2	GGAGCCGGTGT	0.627	
+	8	1153	my.1_Missense_M	NM_020547	NP_065434	Q16671	AMHR2_HUMAN	Potential).|Protein kinase.	2	TGCTCCCTGGC	0.577	
-	2	800		NM_020370	NP_065103	Q9NQS5	GPR84_HUMAN	lasmic (Potential).	2	GGAAACGACCA	0.582	
-	2	232	|KIAA0748_uc010	NM_001098815	NP_001092285	A2RU30	K0748_HUMAN		2	GATCTGGGACA	0.597	
+	1	539		NM_054104	NP_473445	Q9NZP0	OR6C3_HUMAN	ellular (Potential).	1	ATTTTCCCCTCT	0.403	
+	8	1102	d.1_Missense_Mu	NM_022465	NP_071910	Q9H2S9	IKZF4_HUMAN		1	TCGATCGTCTG	0.512	
+	3	466		NM_032786	NP_116175	Q96K80	ZC3HA_HUMAN	3H1-type 2.	0	AATTGCCGTTTC	0.542	
-	8	1724	se_Mutation_p.R	NM_001127460	NP_001120932	Q504Q3	PAN2_HUMAN		6	ATTGCGCAGCC	0.537	
+	2	261		NM_003725	NP_003716	O14756	H17B6_HUMAN	(By similarity).	2	TGGATGCACGA	0.617	
+	6	1531_1532	p.G411E|SLC16A	NM_004731	NP_004722	O60669	MOT2_HUMAN	ical; (Potential).	1	TGTGGGGCTAT	0.391	
-	2	290	uc001srx.2_Intron	NM_001099676	NP_001093146	Q8IXR9	CL056_HUMAN		0	ATTTCTCTATCTG	0.328	
-	12	2411	_Mutation_p.R53	NM_182767	NP_877499	Q9H2J7	S6A15_HUMAN	ame=12; (Potential).	3	GCGACGAACAA	0.443	
-	2	1403		NM_005447	NP_005438	O75901	RASF9_HUMAN		1	TATTCTTTTGCTT	0.398	
-	3	1396	M_uc001tbn.2_R	NM_002345	NP_002336	P51884	LUM_HUMAN		2	TAAGAGTGACTT	0.353	
-	19	1999	_Mutation_p.R36	NM_002108	NP_002099	P42357	HUTH_HUMAN		3	GGGACGTAGAA	0.473	
+	47	6341		NM_014503	NP_055318	O75691	UTP20_HUMAN		4	GCTTCCCCCAA	0.493	
+	8	1016	swi.1_Splice_Site_	NM_003211	NP_003202	Q13569	TDG_HUMAN		6	ATTCTAGCTCT	0.323	
+	3	1266		NM_007076	NP_009007	Q9BVA6	FICD_HUMAN	Fido.	0	CCTCCCGTCTG	0.562	
+	8	840	xn.1_Missense_Mutation_p.D998N			Q8N1T3	MYO1H_HUMAN		0	TTTTCGACACT	0.368	
-	2	151	s.2_Missense_Mu	NM_016301	NP_057385	Q9UHW5	GPN3_HUMAN		0	CAGACCGGTTG	0.522	
+	14	1843	.3_Missense_Mut	NM_001082537	NP_001076006	Q2MV58	TECT1_HUMAN		0	GGCTGCCCTTT	0.512	
+	8	2023	f.2_Missense_Mu	NM_005475	NP_005466	Q9UQQ2	SH2B3_HUMAN		1	ACTACGAAATG	0.592	
-	17	1995	un.1_Nonsense_M	NM_004658	NP_004649	O95294	RASL1_HUMAN	PH.	4	TTCTCGAACAA	0.637	rs61740514
-	17	3495		NM_015335	NP_056150	Q71F56	MD13L_HUMAN		8	ATGTAAAGCCCG	0.463	
-	6	1379	SL_uc001tzk.1_3'	NM_003733	NP_003724	Q15646	OASL_HUMAN	biquitin-like 2.	1	TCAGACCCAGG	0.552	
-	2	162_163	y.2_Missense_Mu	NM_006549	NP_006540	Q96RR4	KKCC2_HUMAN		3	GCGGCCCGGTT	0.668	
+	17	2814		NM_144668	NP_653269	Q8TBY9	WDR66_HUMAN	WD 9.	2	CCACCCGAACG	0.522	
-	2	425	_Mutation_p.R39	NM_019625	NP_062571	Q9NP78	ABCB9_HUMAN		0	GTGGCGGATGT	0.602	
+	2	397	P35_uc009zxz.2_	NM_022717	NP_073208	Q16560	U1SBP_HUMAN	RRM.	0	GGGCTACGCCT	0.507	
+	12	1728		NM_012463	NP_036595	Q9Y487	VPP2_HUMAN	lasmic (Potential).	2	GCCACCCACCC	0.532	
+	19	3024	p.W542*|DNAH10	NM_207437	NP_997320	Q8IVF4	DYH10_HUMAN	(By similarity).	6	TCTCTGGAAAT	0.383	
+	1	554		NM_001136103	NP_001129575	Q8N3T6	T132C_HUMAN	ellular (Potential).	1	GTCCATGGACC	0.667	
+	10	1193	ij.1_Missense_Mu	NM_004764	NP_004755	Q96J94	PIWL1_HUMAN	PAZ.	2	CAAGAGAAGGC	0.547	
-	19	3298		NM_015347	NP_056162	O15034	RIMB2_HUMAN		11	TCTTCTTCTGT	0.308	
+	2	132		NM_152325	NP_689538	Q8N6G2	CM026_HUMAN		3	ATTCACGCCTA	0.373	
-	5	608	D13_uc001uux.2_	NM_178006	NP_821074	Q9Y3M8	STA13_HUMAN		4	GCAGCGTGTAG	0.572	
-	1	1204	A_uc010tee.1_Int	NM_005584	NP_005575	Q13394	MB211_HUMAN		2	AGGAGTGGCAC	0.642	
-	8	819	se_Mutation_p.S2	NM_013338	NP_037470	Q9Y673	ALG5_HUMAN	enal (Potential).	0	GAGATGAAAAC	0.448	
-	2	239		NM_198849	NP_942146	Q8IW03	SIAH3_HUMAN		2	AGTGACGGCGC	0.443	

-	14	4304	_p.S17F|ZC3H13_	NM_015070	NP_055885	Q5T200	ZC3HD_HUMAN		2	CTCTCGGATTTAT	0.408	
+	1	2386		NR_003268					0	TTTTCCACCAAG	0.517	
+	5	737	e_Mutation_p.G13	NM_052950	NP_443182	Q96P53	WDFY2_HUMAN	WD 3.	0	GCACAGGACAG	0.532	
-	6	2191	m.1_Missense_Mu	NM_020866	NP_065917	Q9NR64	KLHL1_HUMAN	Kelch 1.	0	CCATTCCTCCTA	0.343	
-	8	2044	_p.S393P|DACH1_	NM_080759	NP_542937	Q9UI36	DACH1_HUMAN		1	TTAGAGAGAGTT	0.443	
-	6	762	_Missense_Mutati	NM_024546	NP_078822	Q5W0B1	RN219_HUMAN	Potential.	2	GAGGCGATTGG	0.383	
+	1	541		NM_153456	NP_703157	Q8IZP7	H6ST3_HUMAN	ienal (Potential).	2	CTGGAGCAGCCT	0.607	
+	2	784		NM_153456	NP_703157	Q8IZP7	H6ST3_HUMAN	ienal (Potential).	2	TGAGCGAGTGG	0.478	
+	13	1709		NM_003291	NP_003282	P29144	TPP2_HUMAN		2	ACCTCCGAGAT	0.443	
+	2	452	vyc.2_Missense_	NM_006683	NP_006674	Q14507	EP3A_HUMAN		0	GTGGCGTAGAT	0.433	rs146022737
-	2	2221	510C|SALL2_uc0	NM_005407	NP_005398	Q9Y467	SALL2_HUMAN	C2H2-type 3.	3	AAGGCGTAGGG	0.572	
-	21	2403		NM_000257	NP_000248	P12883	MYH7_HUMAN	ling.|Myosin head-like.	4	CGGCCTTGAAG	0.592	
-	12	1946	g.1_Missense_Mu	NM_000359	NP_000350	P22735	TGM1_HUMAN		3	TGTGCGGCGGC	0.562	
-	12	1784	g.1_Missense_Mu	NM_000359	NP_000350	P22735	TGM1_HUMAN		3	CTTCCGCTCTG	0.617	
-	4	2006		NM_203301	NP_976046	Q7Z6M2	FBX33_HUMAN		0	AAAAAGCTAAAT	0.358	
+	5	861	_p.R110C|PRPF39	NM_017922	NP_060392	Q86UA1	PRP39_HUMAN	HAT 4.	2	ATGATCGTATTC	0.388	
+	107	19669	|SYNE2_uc001xg	NM_015180	NP_055995	Q8WXH0	SYNE2_HUMAN	lasmic (Potential).	14	CTGTTCCCCCTG	0.502	
+	16	3061	.R1052H|PLEKH	NM_015549	NP_056364	A1L390	PKHG3_HUMAN		1	GGCCCGCCAGT	0.632	
-	2	803	se_Mutation_p.G1	NM_183002	NP_892114	P57103	NAC3_HUMAN		7	CAGCCCAAAAT	0.542	
-	9	906	_Mutation_p.R18	NM_001005743	NP_001005743	P49757	NUMB_HUMAN		4	TGACACGGAATG	0.448	
-	19	2103	aub.1_Missense_	NM_024764	NP_079040	Q9H7T0	CTSRB_HUMAN		5	TCTTCTCTATAT	0.403	
+	11	909	n_p.M276I|SLC24	NM_153646	NP_705932	Q8NFF2	NCKX4_HUMAN	cellular (Potential).	3	ATTATGAGCTC	0.532	
-	1	412_413	R20_uc010txu.1_5	NM_001017963	NP_001017963	P07900	HS90A_HUMAN		7	GGCGGGACAG	0.698	
-	14	3041	R13B_uc010awv.1	NM_015316	NP_056131	Q96KQ4	ASPP1_HUMAN	ANK 1.	1	CCCTTCGTCGT	0.617	
+	14	1404	TA1_uc001yrb.2_	NM_004689	NP_004680	Q13330	MTA1_HUMAN	A-type; atypical.	2	GTATTCTTGGG	0.493	
-	111								0	ACTGCGTCTTT	0.527	rs144392595
-	10	1158	A2_uc010ayv.2_In	NM_000275	NP_000266	Q04671	P_HUMAN	lasmic (Potential).	5	GTGCACGATCT	0.547	
+	11	1915	at.1_Nonsense_M	NM_005503	NP_005494	Q99767	APBA2_HUMAN	PDZ 1.	0	AGCTGCAGCTG	0.637	
-	10	1624	AN1_uc001zqk.2_	NM_138477	NP_612486	Q8IWY9	CDAN1_HUMAN		2	AAGCCGAACAA	0.522	
-	6	1064		NM_005926	NP_005917	P55081	MFAP1_HUMAN		1	CTTCTCGATCTT	0.418	
+	3	493		NM_024908	NP_079184	Q9H967	WDR76_HUMAN		0	ATTTTTCGGGAT	0.343	rs139119504
-	10	1178	e_Mutation_p.R10	NM_002112	NP_002103	P19113	DCHS_HUMAN		6	AGAGCGAAACC	0.547	
-	25	3830	w.1_Missense_Mu	NM_017672	NP_060142	Q96QT4	TRPM7_HUMAN	lasmic (Potential).	10	GAATGAAATTTG	0.333	
-	10	1186	gb.1_RNA|MYO5C	NM_018728	NP_061198	Q9NQX4	MYO5C_HUMAN	osin head-like.	14	TCATCCTCCTTC	0.582	
+	2	738	fw.2_Missense_M	NM_032866	NP_116255	Q0VF96	CGNL1_HUMAN	Head.	11	CAGCTCCGTGG	0.542	
-	7	1068	NIP2_uc010uhb.1_	NM_004330	NP_004321	Q12982	BNIP2_HUMAN	CRAL-TRIO.	1	CCTTCTATCAATT	0.303	
-	4	528	ense_Mutation_p.	NM_024611	NP_078887	Q659A1	NARG2_HUMAN		2	AACGAGAGAAA	0.398	
+	7	585	X22_uc002ana.1_	NM_024798	NP_079074	Q96L94	SNX22_HUMAN		0	GCCCAGATAAA	0.577	
-	2	189		NM_003613	NP_003604	O75339	CILP1_HUMAN		7	TTGGTCCCCACC	0.552	
-	2	2126		NM_005477	NP_005468	Q9Y3Q4	HCN4_HUMAN	r; Name=Segment S4; (Po	6	GAAGCGGACAA	0.537	
+	2	1475		NM_005576	NP_005567	Q08397	LOXL1_HUMAN	yl-oxidase like.	0	TGTGCAAGCAT	0.572	
+	2	1012	h.1_Missense_Mu	NM_005545	NP_005536	O14498	ISLR_HUMAN	Ig-like.	4	AGGATGGTGCC	0.652	
+	2	435		NM_025055	NP_079331	Q8N5R6	CCD33_HUMAN		5	AGAGGAGCCCC	0.433	
+	6	948	2axp.2_Missense_	NM_025055	NP_079331	Q8N5R6	CCD33_HUMAN		5	CTTTCTCCGGG	0.582	
+	2	521	_p.V107A|ARID3B_	NM_006465	NP_006456	Q8IVW6	ARI3B_HUMAN		0	TGAAGTTGCAG	0.517	
-	4	562	_p.D38N|CIB2_uc	NM_006383	NP_006374	O75838	CIB2_HUMAN	EF-hand 1.	0	ACCATCCTCGG	0.532	
+	4	520	_p.S58N|ZFAND6	NM_019006	NP_061879	Q6FIF0	ZFAN6_HUMAN	Ser-rich.	0	TGGCAGTGTGC	0.413	

+	10	1242	_p.P119S|AGBL1_	NM_152336	NP_689549	Q96MI9	CBPC4_HUMAN			0	AAATCCTGGA	0.478	
-	7	956		NM_000326	NP_000317	P12271	RLBP1_HUMAN	CRAL-TRIO.		1	TGAGTTTCCTC	0.468	
+	6	1571	e_Mutation_p.S48	NM_145728	NP_663780	O15061	SYNEM_HUMAN	Tail.		4	TGCTTCGGAAA	0.532	
+	2	321	_5'Flank|SNRNP2	NM_024571	NP_078847	Q9BV90	SNR25_HUMAN			0	TAATGCGTAAGT	0.512	
+	32	3154	p.V1017L|BAIAP3	NM_003933	NP_003924	O94812	BAIP3_HUMAN	C2 2.		1	TGATCGTGGAG	0.627	
-	3	299	q.2_Missense_Mu	NM_001037125	NP_001032202	Q9H9P5	UNKL_HUMAN	3H1-type 1.		0	TAGGGACACCT	0.607	
-	2	353	2ctw.1_Intron|ZSC	NM_032805	NP_116194	Q96SZ4	ZSC10_HUMAN			1	TGCACGGGGAC	0.562	
-	10	1198	e_Mutation_p.D30	NM_144605	NP_653206	Q8IYM1	SEP12_HUMAN			1	AGAATCGTCATG	0.662	
-	22	4862		NM_002705	NP_002696	O60437	PEPL_HUMAN	Potential.		6	TTTCCGTCGCT	0.552	rs145419671
+	8	799_800	g.2_Missense_Mu	NM_000246	NP_000237	P33076	C2TA_HUMAN			1	AATCTCCCTGAG	0.515	
+	10	1143	ch.2_Missense_Mu	NM_014048	NP_054767	Q9ULH7	MKL2_HUMAN			5	GCCTGCTCCAG	0.527	
+	29	4325	l.2_Missense_Mu	NM_004996	NP_004987	P33527	MRP1_HUMAN	porter 2.|Cytoplasmic.		4	GTTCCCTCCGA	0.552	
+	4	609	dfy.2_Missense_M	NM_016524	NP_057608	Q9BSW7	SYT17_HUMAN			1	AAGACGCTCGT	0.577	
-	19	2803		NM_017539	NP_060009	Q8TD57	DYH3_HUMAN	n (By similarity).		18	ACTTATCGATCTT	0.488	
+	2	1372		NM_006040	NP_006031	Q9Y661	HS3S4_HUMAN	enal (Potential).		2	TGCTTCCTGGA	0.542	
+	2	1001	on|APOB48R_uc0	NM_018690	NP_061160	Q0VD83	APOBR_HUMAN	Glu-rich.		0	GGACAGCCTCG	0.716	
+	16	4270	_Intron|TAOK2_uc	NM_016151	NP_057235	Q9UL54	TAOK2_HUMAN			1	TGGCACGGGCC	0.682	
-	2	390	dxs.2_Missense_	NM_006110	NP_006101	O95400	CD2B2_HUMAN			1	CCAAAGAGTGT	0.522	
-	3	1032		NM_001080417	NP_001073886	Q9UEG4	ZN629_HUMAN	2H2-type 5.		0	GGTCCGAGCTG	0.637	
+	4	749	1_uc002ebo.2_5'	NM_001008274	NP_001008275	Q6ZMU5	TRI72_HUMAN			0	TGGGGGAGCAG	0.667	
+	6	908	m.2_Missense_Mu	NM_133443	NP_597700	Q8TD30	ALAT2_HUMAN			2	GGAACCCCACA	0.542	
+	16	1653	u.3_Missense_Mu	NM_000293	NP_000284	Q93100	KPBB_HUMAN			3	GGAGCTTGTGA	0.378	
+	1	267	_p.R80W|SLC12A	NM_001126108	NP_001119580	P55017	S12A3_HUMAN	lasmic (Potential).		3	AGCCCCGGAAG	0.488	
+	2	105		NM_002990	NP_002981	O00626	CCL22_HUMAN			0	ACATGGAAGAC	0.642	
-	6	939	.R109W|KIFC3_u	NM_005550	NP_005541	Q9BVG8	KIFC3_HUMAN	Potential.		3	GGCCCGCAGGC	0.677	
+	10	2799		NM_002428	NP_002419	P51511	MMP15_HUMAN	ellular (Pot	p.G609R(1)	3	GGACGGGGGCA	0.701	
+	6	784		NM_001950	NP_001941	Q16254	E2F4_HUMAN			1	CCTCACGTCCA	0.597	rs142389152
-	1	525	vjt.1_Missense_M	NM_001082486	NP_001075955	Q96AP0	ACD_HUMAN			1	CCTCGGAAGA	0.741	
-	6	921		NM_000229	NP_000220	P04180	LCAT_HUMAN			0	GAAGCGTTGGA	0.572	
-	62	10515		NM_032821	NP_116210	Q4G0P3	HYDIN_HUMAN			2	CACGAGGCCTC	0.562	
-	3	645	gq.2_Nonsense_	NM_018124	NP_060594	Q6PCD5	RFWD3_HUMAN			3	CACCTGAAAGT	0.413	
+	6	897	.R146Q|CNTNAP	NM_033401	NP_207837	Q9C0A0	CNTP4_HUMAN	(Potential).|F5/8 type C.		2	AATGCGAATCG	0.408	
+	11	1818	_p.P405L|CNTNA	NM_033401	NP_207837	Q9C0A0	CNTP4_HUMAN	otential).|Laminin G-like 2.		2	TGCTCCTCTGC	0.478	
-	2	579		NM_003791	NP_003782	Q14703	MBTP1_HUMAN			2	TCTTTTCCAGT	0.453	
+	8	1355	AFAH1B1_uc010	NM_000430	NP_000421	P43034	LIS1_HUMAN	n with dynein and dynacti		1	GGGTCGTAGCA	0.498	
+	10	1275	_p.R228C|CTNS_	NM_004937	NP_004928	O60931	CTNS_HUMAN	lasmic (Potential).		0	CCCAGCGCGGT	0.682	
-	6	1001		NM_002558	NP_002549	P51575	P2RX1_HUMAN	ellular (Potential).		2	TGAAAAGAGTG	0.622	
-	3	515	O1_uc010vsi.1_3'	NM_182566	NP_872372	Q7Z5L0	VMO1_HUMAN			1	ACAGCGGAAGC	0.657	
-	5	979	c002gcb.2_Misse	NM_020162	NP_064547	Q9H6R0	DHX33_HUMAN	case C-terminal.		2	ACAGAGGAAGG	0.607	
+	3	523	ghe.2_Missense_	NM_000937	NP_000928	P24928	RPB1_HUMAN			1	TTCACGTGGGC	0.542	
+	34	5403		NM_020877	NP_065928	Q9P225	DYH2_HUMAN	1 (By similarity).		13	TGCACCGAGGG	0.582	
-	39	5741		NM_003802	NP_003793	Q9UKX3	MYH13_HUMAN	Potential.		6	CCTGCCTCTTG	0.587	
+	27	5721	o.2_Missense_Mu	NM_001372	NP_001363	Q9NYC9	DYH9_HUMAN	1 (By similarity).		20	TGGGCCGCGCA	0.627	
-	9	2166	nse_Mutation_p.S	NM_006470	NP_006461	O95361	TRI16_HUMAN	B30.2/SPRY.		3	CTTGGAAAGCC	0.512	
+	1	1858		NM_144775	NP_658988	Q8TEV9	SMCR8_HUMAN			1	GTTTCGACCCC	0.473	
+	9	874	_p.L169F|PRPSA	NM_002767	NP_002758	O60256	KPRB_HUMAN			1	GACTTGGTGGA	0.582	
+	13	1240_1241	sense_Mutation_p	NM_018242	NP_060712	Q96FL8	S47A1_HUMAN	ical; (Potential).		0	TGTTTCCCACCT	0.431	

+	4	1224	e_Mutation_p.S27	NM_001033553	NP_001028725	Q5M775	CYTSB_HUMAN	Ser-rich.		0	TGGGAGTTCCC	0.488	
+	3	1304		NM_021012	NP_066292	Q14500	IRK12_HUMAN	smic (By similarity).		4	CAACGCCGTGG	0.612	
-	4	597	se_Mutation_p.D1	NM_005148	NP_005139	Q13432	U119A_HUMAN			0	GAAGTCGAAGC	0.557	
-	3	458	ro.2_Missense_M	NM_005165	NP_005156	P09972	ALDOC_HUMAN			1	GCCCACGACGA	0.517	rs139497270
-	21	3315	2_5'Flank|ALDOC_	NM_006461	NP_006452	Q96R06	SPAG5_HUMAN	Potential.		1	GGTAAGGTGGG	0.542	
-	2	277	_p.G28E|SEZ6_uc	NM_178860	NP_849191	Q53EL9	SEZ6_HUMAN	ellular (Potential).		2	CTTTCCCCACG	0.582	
+	53	8180	se_Mutation_p.Q8	NM_001042492	NP_001035957	P21359	NF1_HUMAN			330	GATCCAGGCGC	0.403	
-	10	814	t.2_Missense_Mu	NM_018428	NP_060898	Q9NYH9	UTP6_HUMAN			1	CAATCGAAAGC	0.333	rs146623373
-	10	1686	w.1_RNA|MMP28_	NM_024302	NP_077278	Q9H239	MMP28_HUMAN	mopexin-like 4.		1	TGATGGAGCCA	0.677	
+	7	1368	_p.S358F|CASC3_	NM_007359	NP_031385	O15234	CASC3_HUMAN			1	GACTTCTGTGA	0.572	
+	1	235_236		NM_031961	NP_114167	Q9BYQ4	KRA92_HUMAN	-C-[RQVSGE]-[SPTQ]- [T		1	TGCTGCCAGCC	0.644	
-	3	534	n.2_Missense_M	NM_002277	NP_002268	Q15323	K1H1_HUMAN	od.|Coil 1B.		0	CAGACCGTTGA	0.597	
-	6	1637		NM_006771	NP_006762	O76015	KRT38_HUMAN	Coil 2.|Rod.		2	GGTTCCGGTAC	0.552	
-	1	115		NM_002278	NP_002269	Q14532	K1H2_HUMAN	Head.		0	CGGGGGCAGC	0.612	
+	1	450	586_uc002ibx.2_	NR_002773						0	CCAAGGCTGCA	0.657	
+	3	312	HX8_uc010wig.1_	NM_004941	NP_004932	Q14562	DHX8_HUMAN			4	AGGATTCTCTTA	0.433	
+	5	811	e_Mutation_p.E21	NM_032133	NP_115509	Q8TBZ2	MYBPP_HUMAN			6	CTGCTGAAGGA	0.522	
+	8	936	02itm.2_Missense_	NM_002512	NP_002503	P22392	NDKB_HUMAN			0	AGGCCGAGTGA	0.527	
+	6	657		NM_153228	NP_694960	Q8N957	ANKF1_HUMAN	Potential.		2	GCCTGGAAAGC	0.468	
+	9	1533		NM_000502	NP_000493	P11678	PERE_HUMAN			2	TGTTCCGCTTG	0.592	
-	17	2197	ixa.3_Splice_Site_	NM_001005207	NP_001005207	O94972	TRI37_HUMAN			7	TCATTACCTGCG	0.428	
+	6	504	nse_Mutation_p.P	NM_001099432	NP_001092902	Q9H6U6	BCAS3_HUMAN			5	TGCTCCACAGT	0.413	
-	10	785	10woz.1_RNA|uc010wpb.1_5'Flank							0	GCTGTGAAATC	0.572	
-	24	5295		NM_000334	NP_000325	P35499	SCN4A_HUMAN	IQ.		3	GTGCCGGCGGT	0.642	
-	13	1959	_p.D594N|ABCA8_	NM_007168	NP_009099	O94911	ABCA8_HUMAN	C transporter 1.		3	CTTTATCCACTT	0.333	
-	30	4441	e_Mutation_p.P1	NM_080282	NP_525021	Q8WWZ4	ABCAA_HUMAN			4	GTTTGGAGCAG	0.423	
+	5	589	jip.2_Nonsense_	NM_018658	NP_061128	Q9NPI9	IRK16_HUMAN	smic (By similarity).		3	AGAAGACGATTA	0.453	
+	2	174	n_p.V8I|RAB37_u	NM_001006638	NP_001006639	Q96AX2	RAB37_HUMAN	(By similarity).		1	CAGGCGTCGGC	0.567	
-	2	994	ro.1_Missense_M	NM_173477	NP_775748	Q495M9	USH1G_HUMAN			2	GAGCGGGGCTC	0.706	
-	7	1224_1225	wtb.1_Missense_	NM_002766	NP_002757	Q14558	KPRA_HUMAN			1	TACATGGCAACT	0.347	
+	3	924		NM_178543	NP_848638	Q6UWV6	ENPP7_HUMAN			3	TCAAGGACGCC	0.597	
+	4	3302		NM_020914	NP_065965	Q9HCF4	ALO17_HUMAN			21	GGCTTCGTGAC	0.507	
+	10	1951	p.W197*|RPTOR_	NM_020761	NP_065812	Q8N122	RPTOR_HUMAN			6	GCCTGGGACCT	0.612	
+	11	1220	p.A372V|GPS1_uc	NM_004127	NP_004118	Q13098	CSN1_HUMAN	PCI.		1	GGCAGCCTTCA	0.632	
+	6	625	_p.A102S|USP14_	NM_005151	NP_005142	P54578	UBP14_HUMAN			2	GGTATGCAGGT	0.378	
-	13	1717	s.1_Intron|EPB41L	NM_012307	NP_036439	Q9Y2J2	E41L3_HUMAN	ctin-binding (Potential).		5	TGGACGGCTCA	0.577	
-	11	1022	_p.F288I|L3MBTL	NM_173464	NP_775735	Q8NA19	LMBL4_HUMAN	MBT 3.		3	TTTTAAAAACTTT	0.323	
+	14	1612	76_splice|ARHGAP28_uc002kne.2_Splice_Site_p.M47			B4DXL2	B4DXL2_HUMAN			1	GAATGGTAAGA	0.284	
-	58	8363	l.2_Missense_Mut	NM_005559	NP_005550	P25391	LAMA1_HUMAN	minin G-like 4.		21	TCTGATGAGCCA	0.552	
+	3	748	dkv.2_Missense_M	NM_002845	NP_002836	P28827	PTPRM_HUMAN	tracellular (Potential).		6	GAGAGCCCACC	0.458	
+	5	397		NM_021074	NP_066552	P19404	NDUV2_HUMAN			1	TCCAATGAGAGT	0.328	
-	9	1299	vi.3_Missense_Mu	NM_001941	NP_001932	Q14574	DSC3_HUMAN	|Extracellular (Potential).		4	TTAAATCCTTATC	0.308	
-	8	1452	vk.3_Missense_Mu	NM_024422	NP_077740	Q02487	DSC2_HUMAN	(Potential).|Cadherin 2.		3	GACCAAAATACT	0.313	
+	8	1077		NM_001942	NP_001933	Q02413	DSG1_HUMAN	(Potential).|Cadherin 3.		7	TGCTCGAGATTA	0.328	
+	12	1937	vr.2_Missense_Mu	NM_177986	NP_817123	Q86SJ6	DSG4_HUMAN	ellular (Pot	p.A601V(1)	8	TGCCGCGGGCA	0.507	
+	14	2281	uc002kwv.3_Intron	NM_001943	NP_001934	Q14126	DSG2_HUMAN	lasmic (Potential).		9	GAAAGGAAGTA	0.512	
+	11	1436	q.2_Missense_Mu	NM_030632	NP_085135	Q9C0F0	ASXL3_HUMAN			3	AGACTAGTATCT	0.393	

+	11	1914	xq.2_Missense_Mu	NM_030632	NP_085135	Q9C0F0	ASXL3_HUMAN	Ser-rich.	3	CAGAGGGAGCCT	0.483
-	1	1111	NAL2_uc002lco.2_	NM_145653	NP_663628	Q8NG57	ELOA3_HUMAN		0	TGGGAGGTCATG	0.617
-	27	3827	ea.2_Missense_Mu	NM_001080467	NP_001073936	Q9ULV0	MYO5B_HUMAN	Potential.	5	GGTTCCGCCTGC	0.498
+	13	2601	_p.E520K|DCC_uc	NM_005215	NP_005206	P43146	DCC_HUMAN	tential).|Fibronectin type-III	17	GAGATGGAAACA	0.428
-	8	1009	_p.R304*|FECH_u	NM_000140	NP_000131	P22830	HEMH_HUMAN		1	CAGTCGGTAGG	0.493
+	7	1010		NM_152721	NP_689934	Q6PKX4	DOK6_HUMAN		3	ATCACTCGTCAG	0.438
-	11	1464	p.1_5'UTR|RTTN_	NM_173630	NP_775901	Q86VV8	RTTN_HUMAN		8	GCACAAGCATCA	0.473
+	3	519		NM_004359	NP_004350	P49427	UB2R1_HUMAN		0	GAGCGGGGAGC	0.642
+	13	1834	sb.1_Missense_Mu	NM_019112	NP_061985	Q8IZY2	ABCA7_HUMAN	llular (By similarity).	9	CCCTATCCGTGC	0.697
+	27	4496	vc.1_Missense_Mu	NM_032482	NP_115871	Q8TEK3	DOT1L_HUMAN		4	CGGCTCCGTGG	0.726
+	4	1228	wn.3_Missense_M	NM_152791	NP_690004	Q8NEP9	ZN555_HUMAN	C2H2-type 8.	1	TTTATCCCCAGTC	0.463
-	16	1764	02_splice|TLE2_u	NM_003260	NP_003251	Q04725	TLE2_HUMAN		0	CGGTTCTGGGG	0.617
-	3	1937	l4_uc010dub.1_5'F	NM_001080400	NP_001073869	Q96Q06	PLIN4_HUMAN	roximate tandem repeat.|17	0	CCTGTCGCGATA	0.572
+	14	1733	n_p.F513L|EMR1_	NM_001974	NP_001965	Q14246	EMR1_HUMAN	ular (Potential).|Ser/Thr-rich	5	ATCCTTTGGCTG	0.443
-	40	39365_3936	C16_uc010dwj.2_5	NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN		57	ACACTGGAGTTC	0.515
-	3	28000		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	ch.|Extracellular (Potential).	57	ATGTGAGAACAT	0.468
-	3	19028		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).	57	GAGGTGAACGA	0.488
-	3	15362		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).	57	ATCAGGGAAGGT	0.478
-	10	1817	wr.1_Missense_M	NM_152476	NP_689689	Q96MR9	ZN560_HUMAN	C2H2-type 7.	6	TGAGTTCGCATG	0.408
-	6	1212	_p.P267L|ZNF561	NM_152289	NP_689502	Q8N587	ZN561_HUMAN		1	TCATAGGGTTTT	0.418
-	29	2307		NM_015719	NP_056534	P25940	CO5A3_HUMAN	le-helical region.	10	CCACATCGCCCT	0.627
+	2	59	z.1_Missense_Mut	NM_001040664	NP_001035754	Q9NQ55	SSF1_HUMAN		2	AGCTCCGCAACC	0.726
-	1	204	ense_Mutation_p.F	NM_007065	NP_008996	Q16543	CDC37_HUMAN		0	GCCAGCGGAAGA	0.632
+	4	719		NM_152357	NP_689570	Q8IYI8	ZN440_HUMAN	C2H2-type 2.	0	GTGTTCGAAGAC	0.393
+	4	1651	ym.1_Missense_M	NM_001136501	NP_001129973	Q08AG5	ZN844_HUMAN		0	GAAACCCTATGA	0.413
+	9	978	_p.V301M|GCDH_	NM_000159	NP_000150	Q92947	GCDH_HUMAN		0	TGGGGCGTGCTT	0.647
+	12	2239	xng.1_Missense_M	NM_023072	NP_075560	Q9H7M6	ZSWM4_HUMAN		2	CTGAACGTAATG	0.617
-	3	1199	D26_uc002nee.2_	NM_004831	NP_004822	O95402	MED26_HUMAN	Pro-rich.	2	GGTGACGGCACC	0.682
+	5	1472	0xpn.1_Intron|ANK	NM_152363	NP_689576	Q8NAG6	ANKL1_HUMAN	LEM.	0	TTGCTCCTGGTT	0.572
-	11	1540		NM_001080421	NP_001073890	Q9UPW8	UN13A_HUMAN		3	TCTCCTCGTCCT	0.667
+	7	1236	nhu.2_Missense_M	NM_015683	NP_056498	Q8TBH0	ARRD2_HUMAN		1	CAGGACCCCGAC	0.632
-	7	2677	_p.T844M|SFRS14_	NM_014884	NP_055699	Q8IX01	SUGP2_HUMAN		0	GATGACGTGAAA	0.473
-	8	1113	nse_Mutation_p.G	NM_172231	NP_757386	Q8IWZ8	SUGP1_HUMAN	Pro-rich.	0	GCTTCCCGGGGG	0.672
+	4	835	se_Mutation_p.K1	NM_021047	NP_066385	O75346	ZN253_HUMAN	C2H2-type 3.	0	ATAAGAAAATTC	0.403
+	4	837	se_Mutation_p.I17	NM_021047	NP_066385	O75346	ZN253_HUMAN	C2H2-type 3.	0	AAGAAAATTCATA	0.398
+	4	1046		NM_031218	NP_112495	P35789	ZNF93_HUMAN		1	AGAAGCCCTACG	0.373
-	4	827	pc.1_Missense_M	NM_001076675	NP_001070143	Q68DY1	ZN626_HUMAN		1	GGTTTCTCTCCA	0.393
+	4	1725	eco.2_Missense_M	NM_003429	NP_003420	Q03923	ZNF85_HUMAN		1	TCATACTGGAG	0.353
-	5	1789	208_uc002nqo.1_	NM_007153	NP_009084				7	ACCTTAATAAAG	0.398
-	4	916	1_Intron|ZNF208_	NM_007153	NP_009084				7	TTGTAGGATTTCT	0.358
-	4	1086	rj.1_Missense_Mu	NM_003430	NP_003421	Q05481	ZNF91_HUMAN	C2H2-type 7.	0	ATTCTTCACATT	0.388
-	4	1136	_p.H263Y|ZNF681_	NM_138286	NP_612143	Q96N22	ZN681_HUMAN	type 6; degenerate.	0	CAGTATGAATTA	0.388
-	3	359	681_uc002nrj.3_M	NM_138286	NP_612143	Q96N22	ZN681_HUMAN	KRAB.	0	GGGGTTCGGCCA	0.418
+	19	3054	nuh.1_Missense_M	NM_018025	NP_060495	Q9BRR8	GPTC1_HUMAN		1	GCAGACGTGTCG	0.498
+	4	485		NM_032346	NP_115722	Q9BRP1	PDD2L_HUMAN		1	ATGCCAGCAGTG	0.587
-	2	784	z.1_5'Flank|LGI4_	NM_139284	NP_644813	Q8N135	LGI4_HUMAN	LRR 1.	1	GGGTGACTCCCG	0.607
+	22	4762		NM_014727	NP_055542	Q9UMN6	MLL4_HUMAN		11	AAATACGGGGAT	0.607

+	15	2322	651F|KIRREL2_uc	NM_199180	NP_954649	Q6UWL6	KIRR2_HUMAN	lasmic (Pote p.L704L(1)	3	CGCGTCTCCAG	0.562	
+	14	1768	p.E545K|APLP1_	NM_005166	NP_005157	P51693	APLP1_HUMAN	ellular (Potential).	2	CGCTGGAACAG	0.338	
-	11	1439	p.R126W|NFKBID	NM_139239	NP_640332	Q8NI38	IKBD_HUMAN		0	GGGCCGCAGCA	0.701	
+	11	1232	iu.2_Missense_Mu	NM_000540	NP_000531	P21817	RYR1_HUMAN	plasmic.|MIR 5.	12	TGCGGCTCGGC	0.393	
-	3	459	xuj.1_Missense_M	NM_006149	NP_006140	P56470	LEG4_HUMAN	Galectin 1.	2	ACTTCCCGCCC	0.582	
-	8	657	_p.R133C|SIRT2_	NM_012237	NP_036369	Q8IXJ6	SIRT2_HUMAN	tylase sirtuin-type.	0	CAGGCGCATGA	0.582	
+	3	194		NM_013268	NP_037400	Q9UHV8	PP13_HUMAN	Galectin.	1	TTGCCTTCCGTT	0.512	
-	7	3507	_Mutation_p.R94	NM_181882	NP_870998	Q9BXM0	PRAX_HUMAN		2	GGCACGATCAC	0.632	
-	7	2893	_Mutation_p.K73	NM_181882	NP_870998	Q9BXM0	PRAX_HUMAN		2	CCATTTTAGCG	0.627	
+	10	1593		NM_015125	NP_055940	Q96RK0	CIC_HUMAN	Pro-rich.	11	GCCCCCGGATC	0.627	
-	5	1174	j.3_Missense_Mu	NM_182707	NP_874366	Q9UQ74	PSG8_HUMAN	like C2-type 3.	0	GTGGGTTAGAG	0.463	
-	2	191	se_Mutation_p.W34*|PSG11_uc002ovm.1_Nonsense_			Q00889	PSG6_HUMAN		2	AAGTTCCAGAA	0.483	
-	2	231		NM_145296	NP_660339	Q8NFZ8	CADM4_HUMAN	.|Extracellular (Potential).	0	TCTGCCGGGCT	0.453	
+	5	670	n_p.V60I|ZNF225_	NM_013362	NP_037494	Q9UK10	ZN225_HUMAN		0	TTCACGTAAGAC	0.423	
-	4	1867		NM_145056	NP_659493	Q96B18	DACT3_HUMAN		0	TGGCGGGGCCT	0.622	
+	3	1239	lc.1_Missense_Mu	NM_014681	NP_055496	Q14147	DHX34_HUMAN	ase ATP-binding.	5	TGTTGCCCACG	0.587	
+	2	603	2_uc010xyu.1_In	NM_014601	NP_055416	Q9NZN4	EHD2_HUMAN		2	GGACCCGGACA	0.602	rs144834998
+	5	951		NM_031485	NP_113673	Q9BQ67	GRWD1_HUMAN	WD 1.	1	ACATCCACCTC	0.642	
-	9	914		NM_001080434	NP_001073903				6	GGTCAGAGGTC	0.687	
-	7	1135	LEKHA4_uc010er	NM_020904	NP_065955	Q9H4M7	PKHA4_HUMAN	Pro-rich.	3	CTTCCGGTGAT	0.692	
+	4	221	BL2_uc002pls.1_	NM_006666	NP_006657	Q9Y230	RUVB2_HUMAN		0	TTGCCGGTCGG	0.652	
+	5	2407	_p.H724Y|ZNF473_	NM_001006656	NP_001006657	Q8WTR7	ZN473_HUMAN	2H2-type 15.	2	GAATTCACTCA	0.512	
-	3	1368		NM_001080457	NP_001073926	Q9NT99	LRC4B_HUMAN	Potential).|Ig-like C2-type.	2	GCGCACGCGGT	0.637	
-	22	3585	sw.1_Missense_M	NM_016148	NP_057232	Q9Y566	SHAN1_HUMAN	Poly-Gly.	2	CGCCTCCCGTG	0.473	
+	5	782		NM_007147	NP_009078	Q9Y473	ZN175_HUMAN		0	CATTTTAGAAG	0.393	
-	6	385	10ydp.1_Missense	NM_030972	NP_112234	Q8N823	ZN611_HUMAN		1	TCAAGCGTCCC	0.388	rs141987068
-	5	411	qbg.1_Missense_M	NM_182609	NP_872415	Q86XU0	ZN677_HUMAN	KRAB.	1	ATAATTCCTCTT	0.348	
+	4	1151	.2_Intron|ZNF765_	NR_003699					0	CTTACGAATGT	0.388	rs61743769
+	1	73		NM_001012728	NP_001012746	A6NFQ7	DPRX_HUMAN		0	GATCTTCGTAAA	0.507	rs148896232
-	4	1216_1217	p.E381K|NLRP7_	NM_206828	NP_996611	Q8WX94	NALP7_HUMAN	NACHT.	3	GTCCTCCCCCT	0.683	
+	5	2459	_p.F604L|NLRP4_	NM_134444	NP_604393	Q96MN2	NALP4_HUMAN		15	TCCTTTTCTGG	0.428	
+	3	1043	tg.2_Missense_M	NM_176811	NP_789781	Q86W28	NALP8_HUMAN	NACHT.	13	ACGATGCTTCC	0.502	
-	7	4528	.E1364K|PEG3_uc	NM_001146186	NP_001139658	Q9GZU2	PEG3_HUMAN	Glu-rich.	12	AGCCTCTACGT	0.478	
-	7	2577	_p.E713D|PEG3_	NM_001146186	NP_001139658	Q9GZU2	PEG3_HUMAN		12	TCACTTTCAAG	0.408	
-	3	2631	.2_Intron|ZNF814	NM_001144989	NP_001138461	B7Z6K7	ZN814_HUMAN	2H2-type 21.	0	TGTGAAACTGG	0.413	
-	7	1679	hp.1_Missense_M	NM_025027	NP_079303	Q8WXB4	ZN606_HUMAN		2	AAATAAAAGATAT	0.338	
+	3	1281	.R359C|TTC15_u	NM_016030	NP_057114	Q8WVT3	TTC15_HUMAN		4	TGCTTCGCTTT	0.393	
+	8	1161	qyt.2_Missense_	NM_014746	NP_055561	P50876	R144A_HUMAN		2	CTCCCGGGCAT	0.468	
-	32	3747	e_Mutation_p.R31	NM_015909	NP_056993	A2RRP1	NBAS_HUMAN		4	GATCCGATCAG	0.478	
+	5	946	mm.1_Missense_	NM_199280	NP_954974	Q6ZUX3	F179A_HUMAN		4	TACCGGGGAGC	0.622	
-	9	1095	np.1_Missense_M	NM_144575	NP_653176	Q6MZZ7	CAN13_HUMAN	lpain catalytic.	2	CCGTTTCTTATG	0.443	
-	29	2238	p.F695Y|MAP4K3	NM_003618	NP_003609	Q8IVH8	M4K3_HUMAN	CNH.	8	ATAGGAAAATCT	0.333	
-	18	2907	p.S801F|AAK1_uc	NM_014911	NP_055726	Q2M2I8	AAK1_HUMAN		0	GAAGAGAAGTG	0.408	
+	5	685	se_Mutation_p.R7	NM_002357	NP_002348	Q05195	MAD1_HUMAN		0	GATCCGGATGG	0.597	
+	6	825	e_Mutation_p.R12	NM_002357	NP_002348	Q05195	MAD1_HUMAN		0	ACGAGCGGGGC	0.557	
-	4	1256		NM_017880	NP_060350	Q9NWW7	CB042_HUMAN		0	AGATACTTCATC	0.378	
-	16	2591	D2_uc002sha.2_	NM_001617	NP_001608	P35612	ADDB_HUMAN	ith calmodulin (Potential).	3	GTTCGGAATTTC	0.527	

-	3	472	DD2_uc010fdt.1_M	NM_001617	NP_001608	P35612	ADDB_HUMAN			3	TCTCTTCGCTCA	0.617	
-	3	1622	2sit.3_Missense_M	NM_015470	NP_056285	Q9BXF6	RFIP5_HUMAN			0	CATCCGGGGCT	0.647	
+	4	399	e_Mutation_p.G10	NM_198448	NP_940850	Q6UW15	REG3G_HUMAN	C-type lectin.		0	GATTGGGCTCC	0.562	
-	1	292	lank|ELMOD3_uc	NM_017750	NP_060220	Q6NUM9	RETST_HUMAN			2	TCTTCGGAGAAA	0.597	
+	6	705	.1_Intron|SMYD1_	NM_198274	NP_938015	Q8NB12	SMYD1_HUMAN	SET.		4	GAATTGAGCTCC	0.502	
-	14	2381_2382	.G716S|AFF3_uc	NM_002285	NP_002276	P51826	AFF3_HUMAN			6	ACTGCCCCCGTT	0.624	
+	20	2874	e_Mutation_p.G11	NM_182588	NP_872394	Q7Z3J3	RGPD4_HUMAN			2	ACCAGGAAATC	0.408	
+	5	938	JLT1C4_uc002teb.	NM_006588	NP_006579	O75897	ST1C4_HUMAN			0	GGGAAGCCAAA	0.463	
-	12	1682	.Q449H|EDAR_uc	NM_022336	NP_071731	Q9UNE0	EDAR_HUMAN	ytoplasmic (Potential).		1	CTCAATCTGCAC	0.572	
+	7	1670		NM_001099289	NP_001092759	Q8TEJ3	SH3R3_HUMAN			1	CAGTGGGAGTC	0.682	
+	4	993_994	2toz.2_Intron|LIMS	NM_001161415	NP_001154887	Q13304	GPR17_HUMAN	cellular (Potential).		0	CATTTGGGGAA	0.589	
+	12	1367	_p.G272R|UGGT1_	NM_020120	NP_064505	Q9NYU2	UGGG1_HUMAN			1	ATCAATGGACTTC	0.328	
+	3	868	SD7B_uc002tvb.2	NM_001080427	NP_001073896					7	TGCCTTCAAGATT	0.443	
+	17	3445	D7B_uc010zbj.1_I	NM_001080427	NP_001073896					7	CTGAATGAAAATT	0.453	
-	39	7123		NM_018557	NP_061027	Q9NZR2	LRP1B_HUMAN	ntial).|LDL-receptor class B		50	TATTTTCCTAAAT	0.353	
-	7	1985	P1B_uc010fnl.1_In	NM_018557	NP_061027	Q9NZR2	LRP1B_HUMAN			50	TTCTTACCCTGC	0.363	
+	10	1355	m.1_Missense_Mu	NM_033394	NP_203752	Q9C0D5	TANC1_HUMAN			3	TTGCTCCCTACA	0.333	
-	33	6080	p.2_Missense_Mu	NM_013450	NP_038478	Q9UIF8	BAZ2B_HUMAN			4	CTGTGCAGCAC	0.358	
+	7	992	C4A10_uc002uby.	NM_022058	NP_071341	Q6U841	S4A10_HUMAN	lasmic (Potential).		5	TGTGTTGAAAAT	0.373	
+	3	837		NM_006898	NP_008829	P31249	HXD3_HUMAN	Homeobox.		0	TGTGCCGGCCG	0.592	
-	253	54771	378K|TTN_uc010z	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN			153	CACTTTCCCCAC	0.398	
-	230	46884	9249I|TTN_uc010	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN			153	CTCTACAGCAG	0.368	
-	27	4965	TTN_uc010zfj.1_M	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN			153	GGTTACCCGTAG	0.378	
-	5	708	_p.N152Y|STAT4_	NM_003151	NP_003142	Q14765	STAT4_HUMAN			9	CACTGTTTTTAAT	0.408	
+	3	285	010ziu.1_5'Flank|E	NM_001037663	NP_001032752	P24534	EF1B_HUMAN	ST C-terminal.		0	GTGTCCAGCCCA	0.468	
-	17	2465	e_Mutation_p.P43	NM_173076	NP_775099	Q86UK0	ABCAC_HUMAN			11	CTTTTGGCCTCTC	0.383	
+	4	838	_p.A205T|CXCR2_	NM_001557	NP_001548	P25025	CXCR2_HUMAN	cellular (Potential).		2	ATACAGCAAACT	0.542	
+	32	2737	utation_p.G859R|C	NM_000091	NP_000082	Q01955	CO4A3_HUMAN	le-helical region.		3	CACCAGGAATTC	0.483	
+	46	4279	tation_p.G1373R|	NM_000091	NP_000082	Q01955	CO4A3_HUMAN	le-helical region.		3	TGCAGGGAGAA	0.542	
-	12	5064	e_Mutation_p.H164	NM_001142644	NP_001136116	Q2M3C7	SPKAP_HUMAN			10	CTGCATGGAAGA	0.483	
-	4	812	nse_Mutation_p.G	NM_152527	NP_689740	Q7RTX9	MOT14_HUMAN	cellular (Potential).		6	ACCTGCCCACC	0.612	
+	7	731	RND_uc010fyc.2_M	NM_000751	NP_000742	Q07001	ACHD_HUMAN	cellular (Pote	p.R243H(1)	3	TCATCCGCCGC	0.612	
-	10	1429	mt.1_Missense_Mu	NM_018218	NP_060688	Q9NVE5	UBP40_HUMAN			3	GCTGTTCAATATC	0.413	
+	4	335	ense_Mutation_p.P	NM_024080	NP_076985	Q7Z2W7	TRPM8_HUMAN	lasmic (Potential).		4	GAATTTCCTACCC	0.468	
+	14	1790	0fyj.2_Splice_Site_	NM_024080	NP_076985	Q7Z2W7	TRPM8_HUMAN			4	AAAAAGACCAGC	0.358	
+	14	1857	_p.P424S|MLPH_u	NM_024101	NP_077006	Q9BV36	MELPH_HUMAN			1	GCTGTGCCCTATC	0.468	
+	17	2055	2vyf.2_Missense_M	NM_015650	NP_056465	Q8TDR0	MIPT3_HUMAN	SC1-interaction domain.		1	GAGCCCTTAAAG	0.478	
-	3	1535_1536	vbs.2_Missense_M	NM_015963	NP_057047	Q8WY91	THAP4_HUMAN			0	CGGCTCCAGGTC	0.594	
-	2	432	_p.R123*|SIRPG_u	NM_018556	NP_061026	Q9P1W8	SIRPG_HUMAN	(Potential).|Ig-like V-type.		1	CTTTTCGAAACTT	0.498	
+	11	1746	al.1_Missense_Mu	NM_198994	NP_945345	O95932	TGM3L_HUMAN			4	AGAAGAGAATCC	0.448	rs148419172
-	6	834	pv.1_Missense_M	NM_198216	NP_937859	P14678	RSMB_HUMAN	eat-rich region.|		1	CAGGGGGAGGA	0.572	
+	8	1463	il.2_Missense_Mut	NM_139321	NP_647537	O75882	ATRN_HUMAN	cellular (Potential).		2	TGGCCGAGTGG	0.448	
+	6	553		NM_001009608	NP_001009608	Q5VYV7	CT094_HUMAN			0	TTCAGTCGTGATC	0.318	
+	1	621	Mutation_p.L27F|E	NM_014962	NP_055777	Q9Y2F9	BTBD3_HUMAN			3	CAGAATCTCAGT	0.473	
-	2	497		NM_001008693	NP_001008693	Q5W186	CST9_HUMAN			1	GAGGAAAGCTGA	0.527	
+	12	3229	eb.2_Missense_Mu	NM_015338	NP_056153	Q8IXJ9	ASXL1_HUMAN			248	GCTGCTCCCACC	0.542	
+	2	388	0gee.2_RNA|DNM	NM_006892	NP_008823	Q9UBC3	DNM3B_HUMAN	th DNMT1 and DNMT3A.		5	TCCTCGTCAACC	0.642	

+	11	1181		NM_182658	NP_872599	P59826	LPLC3_HUMAN		4	TCCCTCGGCTA	0.572	rs79150816
+	9	1675	T2_uc002wzf.1_R	NM_005093	NP_005084	O43439	MTG8R_HUMAN		2	CAGATCGTGAA	0.532	
-	3	2028	dk.2_Intron|CPNE	NM_152838	NP_690051	Q9NTZ6	RBM12_HUMAN		3	ACTTACGTGCA	0.398	
+	4	545	ggc.2_Missense_	NM_015568	NP_056383	Q96T49	PP16B_HUMAN	ANK 1.	3	GAAGCTGCTCC	0.597	
+	4	617	o.1_Missense_Mu	NM_182811	NP_877963	P19174	PLCG1_HUMAN	hand.|Potential.	8	TGGATCGGAAT	0.582	
+	7	815	y.2_Missense_Mu	NM_006282	NP_006273	Q13043	STK4_HUMAN	rotein kinase.	2	TCCTCCCACAT	0.393	
+	2	1081	G2_uc010ggz.2_I	NM_003007	NP_002998	P04279	SEMG1_HUMAN	AA repeat 2.	2	GCCAAAAGGCA	0.393	
-	4	592	UTR|SYS1-DBND	NM_014477	NP_055292	Q9Y2B4	T53G5_HUMAN		1	GACTCCAGGGT	0.537	
+	22	2975	xrb.2_Missense_	NM_001134771	NP_001128243	Q9H2X9	S12A5_HUMAN	lasmic (Potential).	5	GGAGAAAGAAT	0.572	
+	2	405		NM_005985	NP_005976	O95863	SNAI1_HUMAN		1	TTCGTCCTTCT	0.642	
-	2	1981	2_Intron|SALL4_u	NM_020436	NP_065169	Q9UJQ4	SALL4_HUMAN	2H2-type 5.	2	GGCACGAATGC	0.522	
+	4	950	zzi.1_Missense_	NM_003222	NP_003213	Q92754	AP2C_HUMAN		1	CAGCTCTACGT	0.532	
-	74	10328		NM_005560	NP_005551	O15230	LAMA5_HUMAN	minin G-like 4.	3	AGGCCGGGAGC	0.697	
-	16	5737	s.1_Missense_Mu	NM_033081	NP_149072	Q9BTC0	DIDO1_HUMAN	Pro-rich.	6	GGGGCCTCTGC	0.617	
-	3	640	fb.1_Missense_M	NM_172107	NP_742105	O43526	KCNQ2_HUMAN	lasmic (Potential).	2	GCCACGGTACC	0.617	
-	9	5610	fl.1_Missense_Mu	NM_001037335	NP_001032412	Q9BYK8	PR285_HUMAN		2	GCACCCGGTCC	0.721	
-	2	291	D10_uc002yhn.2_	NM_080621	NP_542188	Q9BYL1	SAM10_HUMAN		0	GGGTCCGGCAG	0.637	
+	2	295	yim.3_Missense_	NM_018257	NP_060727	Q9NV79	PCMD2_HUMAN		0	GCAGGCTTTCA	0.428	
-	21	1708	TE_uc002yir.1_Mi	NM_199261	NP_954870	P56180	TPTE_HUMAN	2 tensin-type.	5	CTAATGAAATAG	0.328	
-	18	2439	h.1_Missense_Mu	NM_000484	NP_000475	P05067	A4_HUMAN	tial).|Interaction with G(o)-a	1	GTGGCGCTCCT	0.478	
-	3	348	wo.2_Missense_	NM_002240	NP_002231	P48051	IRK6_HUMAN	me=M1; (By similarity).	1	GTAAACCATGA	0.483	
-	1	5803_5804	E2_uc002yyx.2_I	NM_182832	NP_878252	Q8WY50	PLAC4_HUMAN		0	gtgaACGTGTCC	0.317	
-	13	1949_1950	p.L186F|C2CD2_u	NM_015500	NP_056315	Q9Y426	CU025_HUMAN		1	GCAAGGGATG	0.698	
-	3	2795	zy.3_Missense_M	NM_001098402	NP_001091872	Q9ULJ3	ZN295_HUMAN		3	AGAGGAATCTT	0.488	
+	13	1716	_uc002zap.2_Misse	NM_004915	NP_004906	P45844	ABCG1_HUMAN	.|ABC transmembrane type	3	GCTGTTTGCCG	0.647	
-	14	2400		NM_173354	NP_775490	P57059	SIK1_HUMAN		7	CCAGGGGCTCA	0.692	
+	1	222	.1_Intron|C21orf29	NM_198695	NP_941968	P60410	KR108_HUMAN	repeats of C-C-X(3).|3.	2	CTGTGCCCCAG	0.662	
+	9	837	_p.P304L|PCBP3_	NM_020528	NP_065389	P57721	PCBP3_HUMAN		1	CTCACCCGGAT	0.512	
-	7	1325	_p.A167T|GNB1L_	NM_053004	NP_443730	Q9BYB4	GNB1L_HUMAN	WD 6.	1	GCCCGCGGCCA	0.687	
+	5	2125	11aiz.1_RNA|LOC	NM_153615	NP_705843	Q8IZJ4	RGDSR_HUMAN	Ras-GEF.	1	TCATCGTCTCT	0.572	
-	1	529	T5_uc002zzq.3_	NM_004121	NP_004112	P36269	GGT5_HUMAN	ellular (Potential).	3	CTGGGGGCCAC	0.657	
+	5	451		NM_000496	NP_000487	P43320	CRBB2_HUMAN	a crystallin 'Greek key' 3.	0	ACGCCCATGGC	0.493	
-	9	976	n.1_Missense_Mu	NM_014303	NP_055118	O00541	PESC_HUMAN		0	CGGTGGGAAAC	0.622	
-	4	443	.2_5'UTR|BPIL2_u	NM_174932	NP_777592	Q8NFQ6	BPIL2_HUMAN		2	CATTTCGGGTT	0.493	rs78469100
+	3	895	ny.2_Missense_M	NM_014310	NP_055125	Q96D21	RHES_HUMAN	GNB1, GNB2 and GNB3.	3	GGCATGGTCTC	0.647	
-	5	1339	ense_Mutation_p.	NM_024955	NP_079231	Q8IWF2	FXRD2_HUMAN		2	GAGCCGGTGAA	0.627	rs143694562
-	3	1460		NM_052906	NP_443138	Q5R3F8	LRFN6_HUMAN	xtracellular (Potential).	2	GCAGCGGGTAG	0.667	
+	7	2024	atq.1_Missense_M	NM_001039141	NP_001034230	Q9H2D6	TARA_HUMAN		1	ACAATCCCAGA	0.587	
-	2	1066	axe.2_Missense_	NM_002608	NP_002599	P01127	PDGFB_HUMAN		373	CCTCGGGAATG	0.597	
+	5	671	RVG_uc010gzr.1_	NM_001137605	NP_001131077	Q9HBI0	PARVG_HUMAN	CH 1.	0	TATTCCGTAAG	0.562	rs147016590
+	1	1017		NM_138433	NP_612442	Q96G42	KLD7B_HUMAN		1	AGGGGGGCCGC	0.756	
+	2	835	sg.2_Missense_M	NM_004634	NP_004625	P55201	BRPF1_HUMAN	ith MYST3 and MYST4.	3	CTACTCCCAAG	0.547	
+	6	738	byl.1_Missense_	NM_024334	NP_077310	Q9BTV4	TMM43_HUMAN	enal (Potential).	1	ACTTCGACCGA	0.498	rs150425166
+	5	503	_p.G138R|C3orf19	NM_016474	NP_057558	Q6PII3	CC019_HUMAN		0	AGGCAGGAGAA	0.473	
+	2	357	.1_5'Flank|METT	NM_033083	NP_149074	Q96JC9	EAF1_HUMAN		1	CACTTCCTGTG	0.373	
-	10	3465	_p.H577L|SATB1_	NM_002971	NP_002962	Q01826	SATB1_HUMAN		4	CGCCATGGTGA	0.483	
+	10	1904	hex.1_Missense_	NM_144633	NP_653234	Q96L42	KCNH8_HUMAN	toplasmic (Potential).	5	AACCTCTTTCT	0.502	

-	8	947	_p.L325V|NEK10_uc010hfj.2_Missense_Mutation_p.L2			Q6ZWH5	NEK10_HUMAN		13	TCTTTAAAATGTC	0.284	
-	16	2074	j.1_Missense_Mut	NM_000404	NP_000395	P16278	BGAL_HUMAN		1	GGAGGGATGAT	0.498	
+	2	256	TAC_uc011aya.1_I	NM_003149	NP_003140	Q99469	STAC_HUMAN		4	TGCAAGCACAC	0.537	
-	12	6541		NM_014831	NP_055646	O15050	TRNK1_HUMAN		2	AACAGAGCAGG	0.542	
-	3	423	se_Mutation_p.P7	NM_147129	NP_667340	Q60I27	AL2CL_HUMAN		5	AGTCCGGGTAA	0.627	
+	20	2813	N23_uc011bax.1_I	NM_015466	NP_056281	Q9H3S7	PTN23_HUMAN	Pro-rich.|His.	3	TCCTCCCCCGC	0.672	
-	18	2668	wf.1_Missense_Mu	NM_002292	NP_002283	P55268	LAMB2_HUMAN	ninin EGF-like 6.	3	TCAGTGAACCT	0.597	
-	17	2316	wp.2_Missense_M	NM_003363	NP_003354	Q13107	UBP4_HUMAN		4	TCCGAGTTTCA	0.512	
+	5	2867		NM_003458	NP_003449	Q9UPA5	BSN_HUMAN		8	GGCTACCGATG	0.622	
+	9	1067	cyk.2_Missense_M	NM_004186	NP_004177	Q13275	SEM3F_HUMAN	Sema.	2	GAGCCCCGCGG	0.602	
+	19	2371	cyk.2_Missense_M	NM_004186	NP_004177	Q13275	SEM3F_HUMAN		2	CAACGCCTCCT	0.682	
-	6	549	03dap.2_Splice_Si	NM_006030	NP_006021	Q9NY47	CA2D2_HUMAN		1	TCGTCCTGCAG	0.552	
+	32	5501		NM_015512	NP_056327	Q9P2D7	DYH1_HUMAN	1 (By similarity).	3	CAGCTCCCAGG	0.438	
+	6	655	k.1_Missense_Mu	NM_002217	NP_002208	Q06033	ITIH3_HUMAN		3	CCAACGACCTC	0.532	
+	18	1893	l1bfa.1_Missense_	NM_007159	NP_009090	Q14BN4	SLMAP_HUMAN	ic (Potential).|Potential.	0	TCTCCGGGAGG	0.418	rs138744399
+	37	6358	e_Mutation_p.V20	NM_001457	NP_001448	O75369	FLNB_HUMAN	.|Interaction with the cytopl	19	CTACCGTGCCT	0.542	
-	14	1846	ense_Mutation_p.R	NM_015541	NP_056356	Q96JA1	LRIG1_HUMAN	otential).|Ig-like C2-type 2.	5	GTGGTCCGGATG	0.562	
+	4	1813	ofv.1_Missense_M	NM_032505	NP_115894	Q8NFY9	KBTB8_HUMAN	Kelch 5.	4	TGAATGTGCTG	0.438	
-	14	1392	ense_Mutation_p.	NM_015123	NP_055938	Q9Y2L6	FRM4B_HUMAN		4	CTGAAGGAATTT	0.363	
+	3	322		NM_032359	NP_115735	Q9BQ75	CC026_HUMAN		1	ACAACCAAAGG	0.239	
+	5	1205	npn.2_Missense_M	NM_145037	NP_659474	Q969Y0	FA55C_HUMAN		3	TCCACCCCAGT	0.458	
-	36	5224		NM_014981	NP_055796	Q9Y2K3	MYH15_HUMAN	Potential.	7	TTCTTTCTGTTG	0.527	
-	5	564	PPA4_uc011bhp.1_	NM_018189	NP_060659	Q7L190	DPPA4_HUMAN		1	GAGGAAGAGCC	0.498	
-	7	5569	eal.2_Missense_M	NM_001009899	NP_001009899	Q68DE3	K2018_HUMAN		3	CACACGACCCT	0.423	
-	7	3914	eal.2_Missense_M	NM_001009899	NP_001009899	Q68DE3	K2018_HUMAN		3	ACAATGATGCTT	0.463	
-	1	615	e_Mutation_p.L16	NM_022135	NP_071418	Q9HBU9	POPD2_HUMAN		1	AGAGAGCAGCA	0.527	
+	11	1151	_p.V330I|ABTB1_	NM_172027	NP_742024	Q969K4	ABTB1_HUMAN		0	TGAGCGTCGCC	0.647	
-	4	1118	_p.P228L|GATA2_	NM_001145661	NP_001139133	P23769	GATA2_HUMAN		15	GCAGGGGACTG	0.632	
+	2	217	_p.R43W|ACPP_u	NM_001099	NP_001090	P15309	PPAP_HUMAN		1	TGTTTCGGCAT	0.428	
+	1	332		NM_003571	NP_003562	Q13515	BFSP2_HUMAN	Head.	0	TGGGTGCATAG	0.662	
-	11	1801_1802	_p.P434S|SLCO2	NM_005630	NP_005621	Q92959	SO2A1_HUMAN	cellular (Potential).	1	ACAGGGGACAG	0.559	
+	5	1320	31_uc011bly.1_3'U	NM_004441	NP_004432	P54762	EPHB1_HUMAN	tential).|Fibronectin type-III	30	AGACCGCCGGA	0.612	
+	4	1101	p.Y321H|HPS3_u	NM_032383	NP_115759	Q969F9	HPS3_HUMAN		6	CCATTTACCAG	0.478	
-	1	306	_uc003ewz.2_Nor	NM_000096	NP_000087	P00450	CERU_HUMAN		1	TCGCCCAGGCT	0.373	
-	5	1055	e_Mutation_p.N21	NM_033169	NP_149359	O75752	B3GL1_HUMAN	nenal (Potential).	1	GGAATAATTATCA	0.353	
-	18	2116	_p.F598Y|ZBBX_u	NM_024687	NP_078963	A8MT70	ZBBX_HUMAN		2	AAAATAAAGAAT	0.308	
-	9	2292	OM_uc003ffk.2_In	NM_005241	NP_005232	Q03112	EVI1_HUMAN		14	ATCAGGCAGTT	0.313	
-	8	1103	q.1_Missense_Mu	NM_024947	NP_079223	Q8NDX5	PHC3_HUMAN	o-rich.|Gln-rich.	2	TGGGGGTGGGT	0.488	
+	4	947	B5_uc003fmq.2_5	NM_003907	NP_003898	Q13144	EI2BE_HUMAN		5	CAACTCGTTGC	0.483	rs113994055
+	4	583	.R148Q|DVL3_uc	NM_004423	NP_004414	Q92997	DVL3_HUMAN		3	ACGCCGGAGGG	0.617	
-	3	586	_p.P153S|TBCCD	NM_018138	NP_060608	Q9NVR7	TBCC1_HUMAN		2	GTCAGGAGACT	0.408	
+	5	852	b.2_Missense_Mu	NM_003722	NP_003713	Q9H3D4	P63_HUMAN		12	TCAACGAGGGT	0.498	
-	2	75		NM_004488	NP_004479	P40197	GPV_HUMAN		3	GGGCGCGCAGA	0.667	
-	8	1174		NM_018385	NP_060855	Q9H089	LSG1_HUMAN		0	AGCTGGGAGAT	0.478	
-	16	1953	zy.2_Missense_Mu	NM_003234	NP_003225	P02786	TFR1_HUMAN	cellular (Potential).	3	CGCAAAAACAG	0.229	
+	3	1280		NM_198565	NP_940967	Q86YC3	LRC33_HUMAN	ar (Potential).|LRR 13.	3	GCTGCACCTGGC	0.657	
+	5	1113	141_uc003gab.2_I	NM_003441	NP_003432	Q15928	ZN141_HUMAN	C2H2-type 6.	0	CCTACAAATGTG	0.398	

-	12	1750	sense_Mutation_p	NM_003703	NP_003694	P78316	NOP14_HUMAN		1	GAAGTCGGAAG	0.527	
-	3	3536		NM_053042	NP_444270	Q9C0D4	Z518B_HUMAN		4	TTTTATGAACTTT	0.418	
-	8	1628	GC1A_uc011bxp.	NM_013261	NP_037393	Q9UBK2	PRGC1_HUMAN		8	AGTCCTGAATTT	0.428	
-	2	299		NM_001358	NP_001349	O43143	DHX15_HUMAN		1	TATCACGTTCTC	0.363	rs145564625
-	13	2324_2325	grv.2_Missense_Mu	NM_015187	NP_056002	Q68CR1	SE1L3_HUMAN	Sel1-like 3.	0	ATCCTCCGTCTC	0.49	
+	1	651	.1_Missense_Muta	NM_175737	NP_783864	Q86Z14	KLOTB_HUMAN	ential).|Glycosyl hydrolase-	1	TGCTTAGAAACAT	0.413	
+	8	1615	gvi.3_Missense_Mu	NM_024677	NP_078953				0	CTGCTACCTCGT	0.303	
-	9	1470	p.E390K|KDR_uc	NM_002253	NP_002244	P35968	VGFR2_HUMAN	4.|Extracellular (Potential).	33	CTCTTTCACTCA	0.408	
+	1	203	n_p.M10I|LPHN3_	NM_015236	NP_056051	Q9HAR2	LPHN3_HUMAN		18	TTTCATGATGCTC	0.363	
-	8	823		NM_182502	NP_872308	Q86T26	TM11B_HUMAN		1	TTTTCCTAGAGG	0.323	
+	4	1524	n_p.Q15*|SHROO	NM_020859	NP_065910	Q8TF72	SHRM3_HUMAN		3	GGCACCAAAGC	0.473	
+	37	5395	_p.R1652K|FRAS	NM_025074	NP_079350	Q86XX4	FRAS1_HUMAN	xtracellular (Potential).	5	CCGAAGGCCGA	0.493	
+	10	1747	du.1_Missense_Mu	NM_001510	NP_001501	O43424	GRID2_HUMAN	ellular (Potential).	6	AATACGGAAGC	0.393	
+	1	111		NM_005390	NP_005381	P29803	ODPAT_HUMAN		1	CAGAAATCAGC	0.537	
-	9	981		NM_000669	NP_000660	P00326	ADH1G_HUMAN		0	TCTGGGAATCA	0.448	
+	7	1536	_p.F320I|EGF_uc	NM_001963	NP_001954	P01133	EGF_HUMAN	g (Potential).|Extracellular	4	TGTGCTTTTTGG	0.398	
+	7	776	.V226M|ANK2_uc	NM_001148	NP_001139	Q01484	ANK2_HUMAN		14	ATGATGGTGAAT	0.353	
-	7	995	ine.2_Missense_M	NM_018699	NP_061169	Q9NQX1	PRDM5_HUMAN	2-type 3; atypical.	2	GCTCAAAACTAC	0.478	
+	7	875	p.E215K|ADAD1_	NM_139243	NP_640336	Q96M93	ADAD1_HUMAN		0	GTTAAAGAAAGA	0.323	
-	1	126	TA5_uc003iez.3_	NM_007083	NP_009014	P53370	NUDT6_HUMAN		0	CTGTGCGCCCG	0.711	
+	1	1846		NM_024582	NP_078858	Q6V0I7	FAT4_HUMAN	r (Potential).|Cadherin 6.	18	ACAACGGAACA	0.547	
+	11	11909	p.G2233E|FAT4_u	NM_024582	NP_078858	Q6V0I7	FAT4_HUMAN	Extracellular (Potential).	18	TCTTTGGAAAAC	0.289	
+	11	1277	u.2_Missense_Mu	NM_001039717	NP_001034806	Q0P651	CD029_HUMAN		1	AAGTCGCAACC	0.388	
+	10	1337		NM_057175	NP_476516	Q9BXJ9	NAA15_HUMAN		2	TTTAACCCCAATG	0.323	
-	7	792	10A7_uc010ipa.2_	NM_001029998	NP_001025169	Q0GE19	NTCP7_HUMAN	ical; (Potential).	0	GAGAGGAACCA	0.353	
+	11	2576		NM_033393	NP_203751	Q9C0D6	FHDC1_HUMAN		2	TCCTGCCCCCG	0.622	
-	15	3677		NM_017639	NP_060109	Q6V1P9	PCD23_HUMAN	Cadherin 10.	4	CCAAAGGACAG	0.378	
-	14	3434		NM_017639	NP_060109	Q6V1P9	PCD23_HUMAN	Cadherin 9.	4	TCAGTCGCCGG	0.463	
-	5	1053	e_Mutation_p.G33	NM_000508	NP_000499	P02671	FIBA_HUMAN	By similarity.	3	AGCTTCCAGTA	0.567	
-	2	224		NM_001334	NP_001325	P43234	CATO_HUMAN		0	ACTGGGAAATA	0.333	
+	3	1539	qx.1_Missense_Mu	NM_152620	NP_689833	Q495X7	TRI60_HUMAN	B30.2/SPRY.	1	GAACAGATTCC	0.353	
-	12	1360	p.D404N|SPOCK3	NM_016950	NP_058646	Q9BQ16	TICN3_HUMAN	Asp-rich.	3	tcataatatcgtcttcatc	0.075	
-	11	1737		NM_017631	NP_060101	Q8IY21	DDX60_HUMAN		3	TTATACCTCTTTA	0.348	
+	6	722		NM_004477	NP_004468	Q14331	FRG1_HUMAN		0	AGAAATGATCAA	0.363	
-	10	1771	RLR_uc003jjj.1_In	NM_000949	NP_000940	P16471	PRLR_HUMAN	lasmic (Potential).	3	CATGTTGAACAT	0.532	
+	3	372	se_Mutation_p.E9	NM_002185	NP_002176	P16871	IL7RA_HUMAN	ellular (Potential).	5	TCATCGAGACAA	0.383	
-	7	1400	_p.A402V|UGT3A2	NM_174914	NP_777574	Q3SY77	UD3A2_HUMAN	ellular (Potential).	6	CTGCCGCGGAC	0.562	
+	6	919	jlb.1_Missense_M	NM_152403	NP_689616	Q63HQ2	EGFLA_HUMAN	nectin type-III 2.	7	AGATGGACTCC	0.507	
-	7	1803		NM_021072	NP_066550	O60741	HCN1_HUMAN	lasmic (Potential).	1	CTATTCGATCTA	0.378	
+	1	315		NM_006308	NP_006299	Q12988	HSPB3_HUMAN		0	GAGGAAAACCA	0.567	
+	8	844	CR_uc003kdq.2_	NM_000859	NP_000850	P04035	HMDH_HUMAN		1	AGGGTCGTCCA	0.413	
+	2	9180		NM_153610	NP_705838	Q8N3K9	CMYA5_HUMAN		9	TTCAGAAACTGA	0.323	
-	7	832	.1_Missense_Mut	NM_032042	NP_114431	Q8WUF8	F172A_HUMAN		0	TCTTCGGCTTTT	0.328	
+	5	683	81B_uc010jbe.1_5	NM_152548	NP_689761	Q96LP2	FA81B_HUMAN		2	GAGATCTTCGA	0.433	
-	9	1351	jbi.1_Missense_M	NM_000439	NP_000430	P29120	NEC1_HUMAN	Catalytic.	2	AGGCCGAGGTG	0.557	
+	2	127	e_Mutation_p.S10	NM_001744	NP_001735	Q16566	KCC4_HUMAN		5	CCTGCTCCGCC	0.597	
+	12	1311	bv.2_Missense_Mu	NM_001744	NP_001735	Q16566	KCC4_HUMAN		5	AGTTAAAGGTGC	0.527	

+	2	627	_p.R132Q|PRR16_	NM_016644	NP_057728	Q569H4	PRR16_HUMAN	Pro-rich.	3	TCTACGAAATG	0.493	
-	1	371	ense_Mutation_p.	NM_001182	NP_001173	P49419	AL7A1_HUMAN		3	GGCCTCCCCAG	0.652	
+	2	184		NM_207408	NP_997291	Q6ZNM6	CE048_HUMAN		1	AAACATGATATTC	0.303	
-	6	945		NM_198282	NP_938023	Q86WV6	TM173_HUMAN	lasmic (Potential).	1	AGCATGGTCAC	0.557	
-	12	1518	_p.R459H|HARS_	NM_002109	NP_002100	P12081	SYHC_HUMAN		2	CTGAACGGAGC	0.552	
+	1	1028	.2_Intron|PCDHA6	NM_018903	NP_061726	Q9UN75	PCDAC_HUMAN	|Extracellular (Potential).	0	ACAGGTGAAATT	0.378	
+	1	1928	.2_Intron|PCDHA6	NM_018903	NP_061726	Q9UN75	PCDAC_HUMAN	|Extracellular (Potential).	0	CTGACTCCGG	0.677	
+	1	388	uc003lin.2_Intron	NM_018937	NP_061760	Q9Y5E6	PCDB3_HUMAN	(Potential).|Cadherin 1.	2	ACCATTCTCCG	0.418	
+	1	2365	uc003lin.2_5'Flan	NM_018937	NP_061760	Q9Y5E6	PCDB3_HUMAN	lasmic (Potential).	2	CCAGTTTCAGG	0.453	
+	1	647	B16_uc003liv.2_5	NM_019120	NP_061993	Q9UN66	PCDB8_HUMAN	|Extracellular (Potential).	4	GTTTCCTCTGA	0.438	
+	1	1895	_5'Flank|PCDHB1	NM_019120	NP_061993	Q9UN66	PCDB8_HUMAN	|Extracellular (Potential).	4	TGGCTCCGCGC	0.721	
-	1	736		NM_031947	NP_114153	Q9BXI2	ORNT2_HUMAN	=4; (Potential).|Solcar 2.	1	GAAAAAGAAAT	0.453	
+	1	1972	q.1_Intron|PCDH	NM_018924	NP_061747	Q9Y5G1	PCDGF_HUMAN	(Potential).|Cadherin 6.	0	CCACCGTCATG	0.617	
+	3	481	IP1_uc003lmj.1_I	NM_030571	NP_085048	Q9BT67	NFIP1_HUMAN	lasmic (Potential).	0	CTATCCCTTTG	0.428	
+	4	1779	nn.1_Missense_M	NM_020768	NP_065819	Q68DU8	KCD16_HUMAN		4	AAAAAGCTGTT	0.448	
+	8	1520	p.P473S|TCERG1	NM_006706	NP_006697	O14776	TCRG1_HUMAN	Glu-rich.	2	AGGATCCTAAA	0.403	
-	3	244	_Mutation_p.S27L	NM_000870	NP_000861	Q13639	5HT4R_HUMAN	ame=1; (By similarity).	1	CCGTCGAGAGA	0.537	
+	13	1381	lqc.1_Missense_	NM_014945	NP_055760	O94929	ABLM3_HUMAN		3	GTACATAGACT	0.627	
+	2	558		NM_014228	NP_055043	Q99884	SC6A7_HUMAN	Name=1; (Potential).	0	GGCGCTTCCCC	0.602	
-	6	1903	M_uc011dcl.1_Int	NM_052860	NP_443092	Q96RE9	ZN300_HUMAN		2	TTTCTCTCCTG	0.433	
+	11	1581	2A_uc011dcs.1_In	NM_078483	NP_510968	Q7Z2H8	S36A1_HUMAN	ame=11; (Potential).	1	TGAGGCTCTCT	0.552	
-	2	410	lwl.2_Missense_	NM_032782	NP_116171	Q8TDQ0	HAVR2_HUMAN	.|Extracellular (Potential).	0	CTTTGCGGAAA	0.473	
+	25	2731	p.R865W|CYFIP2_	NM_001037333	NP_001032410	Q96F07	CYFP2_HUMAN		0	TTGTGCGGACT	0.473	
+	1	597		NM_000679	NP_000670	P35368	ADA1B_HUMAN	smic (By similarity).	1	CCATCGATCGC	0.617	
-	7	1411	se_Mutation_p.P3	NM_024565	NP_078841	Q8IV13	CCNJL_HUMAN		0	CAAGGGCTGCA	0.622	
-	3	661	NMB1_uc003mar	NM_004137	NP_004128	Q16558	KCMB1_HUMAN	ellular (Potential).	2	ACAGCCCACCT	0.592	
+	4	773	on_p.E71K|KCNIP	NM_001034837	NP_001030009	Q9NZI2	KCIP1_HUMAN	nd 1; degenerate.	2	TCAACGAAGAC	0.547	rs145371121
-	14	1516	03mhm.2_Missens	NM_016222	NP_057306	Q9UJV9	DDX41_HUMAN	case C-terminal.	0	GGCAGGGAAGT	0.577	
+	5	612		NM_014594	NP_055409	Q86Y25	Z354C_HUMAN		1	ATTGGGGAAAA	0.353	
-	16	2631	_p.R41Q|TBC1D	NM_198868	NP_942568	Q66K14	TBC9B_HUMAN		2	GTTCCCGGAAC	0.647	
-	12	1446	lc.2_Missense_Mu	NM_002752	NP_002743	P45984	MK09_HUMAN		4	TGATCGATGAA	0.483	
-	18	2044		NM_005110	NP_005101	O94808	GFPT2_HUMAN	SIS 2.	2	CGCTCAGGATG	0.527	
-	7	1220	p.R177C|TRIM7_	NM_203293	NP_976038	Q9C029	TRIM7_HUMAN	B30.2/SPRY.	3	GACGCGGGTGT	0.697	
-	3	321	se_Mutation_p.R6	NM_018303	NP_060773	Q96KP1	EXOC2_HUMAN	IPT/TIG.	7	CCACTCGACATA	0.423	
-	10	1358	ib.1_Missense_Mu	NM_000129	NP_000120	P00488	F13A_HUMAN		6	AGGCGGGGCCA	0.512	
+	4	2241	EP1_uc011diq.1_	NM_002114	NP_002105	P15822	ZEP1_HUMAN		6	TGAGTCCACCA	0.512	
-	3	342	djz.1_Missense_	NM_006632	NP_006623	O00476	NPT4_HUMAN		0	GGAATCATTGA	0.433	
+	2	319	se_Mutation_p.P3	NM_024493	NP_077819	Q9BRR0	ZKSC3_HUMAN		2	GTTTTCCCAGT	0.607	
-	1	880		NM_030903	NP_112165	Q9Y3N9	OR2W1_HUMAN	lasmic (Potential).	3	CTTATTTCTTAA	0.423	
+	4	729	_3'UTR|MOG_uc	NM_206809	NP_996532	Q16653	MOG_HUMAN	lasmic (Potential).	1	TTTAGGAAAACT	0.493	
-	8	1177	R10_uc010jsc.1_	NM_002714	NP_002705	Q96QC0	PP1RA_HUMAN	ith TOX4 (By similarity).	4	GGAACGGAACT	0.567	
+	3	612	B_uc011dos.1_3'	NM_001710	NP_001701	P00751	CFAB_HUMAN	Sushi 2.	1	AGAACGGGGAA	0.532	
-	2	1831	dz.2_5'Flank|TAP	NM_005453	NP_005444	O15209	ZBT22_HUMAN	2H2-type 3.	1	GTCCTCGGTGG	0.647	
+	8	2033	f.1_Missense_Mu	NM_002263	NP_002254	Q9BW19	KIFC1_HUMAN	inesin-motor.	0	GGCCCGCACAG	0.607	
+	4	467	_p.R154Q|SCUBE	NM_152753	NP_689966	Q8IX30	SCUB3_HUMAN		1	CCAGCGGCCAG	0.612	
+	5	1562	b.2_Intron|PI16_u	NM_153370	NP_699201	Q6UXB8	PI16_HUMAN	ellular (Potential).	0	CACGGGTGGG	0.617	
+	10	1104	dvn.1_Missense_	NM_007058	NP_008989	Q9UMQ6	CAN11_HUMAN	lpain catalytic.	2	AGGACGGGGAG	0.632	

-	8	1072	se_Mutation_p.M2	NM_001098518	NP_001091988	Q8IZF2	GP116_HUMAN	racellular (Potential).	2	TAGTCCATTTT	0.353
-	2	615		NM_014452	NP_055267	O75509	TNR21_HUMAN	(Potential).|TNFR-Cys 1.	0	GGCCGGTGGCA	0.547
+	2	214		NM_207410	NP_997293	Q6UXV0	GFRAL_HUMAN	ellular (Potential).	2	TTGGAGAGTAA	0.328
-	7	839	98L|HMGCLL1_u	NM_019036	NP_061909	Q8TB92	HMGC2_HUMAN		4	TTTTGCGGTGTA	0.318
-	40	6556_6557	S1_uc011ebi.1_R	NM_002944	NP_002935	P08922	ROS_HUMAN	.|Cytoplasmic (Potential).	25	GCCTTCCCCTC	0.436
-	1	89	.2_5'UTR|VNN3_	NM_078625	NP_523239				0	TTTGGAAAATGT	0.358
-	11	1157	CEF1_uc003qpw.	NM_015553	NP_056368	Q8WWN9	ICEF1_HUMAN		0	TAGTCGAAGGT	0.383
-	7	1655	LL2_uc003ski.3_	NM_182924	NP_891554	Q8IY33	MILK2_HUMAN		1	GAGACGAGGA	0.622
+	2	1036	md.2_Missense_	NM_018641	NP_061111	Q9NRB3	CHSTC_HUMAN	enal (Potential).	1	TCCTTCGCCAAC	0.677
-	6	1125		NM_032415	NP_115791	Q9BXL7	CAR11_HUMAN	Potential.	50	ATTCCTCCTCCA	0.483
+	7	1012	0415_uc010ksp.2_	NM_014855	NP_055670	O43299	K0415_HUMAN		1	TAACCGACGTG	0.682
-	14	2156	V1_uc003ssw.3_	NM_004956	NP_004947	P50549	ETV1_HUMAN		35	GCCTTCGTTGT	0.478
-	2	195_196	xy.1_Missense_M	NM_006408	NP_006399	O95994	AGR2_HUMAN		0	GGAATTTTCTCC	0.47
+	51	8334		NM_003777	NP_003768	Q96DT5	DYH11_HUMAN		15	TCAGAGAAGAA	0.363
+	6	518	e.1_Missense_Mu	NM_031414	NP_113602	Q9BXU1	STK31_HUMAN		9	ACATTCCTTCT	0.328
-	9	952	8_splice|SKAP2_	NM_003930	NP_003921	O75563	SKAP2_HUMAN		1	CCATATCTATAAA	0.294
-	1	397_398		NM_001126493	NP_001119965				0	GCCTTCTTTCAC	0.485
+	2	490	_p.G62R|AQP1_u	NM_198098	NP_932766	P29972	AQP1_HUMAN	l; Name=Helix 4.	0	TCATCGGGACC	0.652
-	13	1588	.1_RNA|DPY19L2P1_uc010kwz.1_RNA						0	GTGGTCTGAAA	0.219
-	1	908		NM_033224	NP_150093	Q96QR8	PURB_HUMAN		0	GCCGCCGCTGC	0.587
+	1	401	tart_Site|VSTM2	NM_182546	NP_872352	Q8TAG5	VTM2A_HUMAN		0	CCTTTTTGGAA	0.483
+	4	968		NM_001159279	NP_001152751				2	CTAACTACAAG	0.408
+	4	993		NM_001159279	NP_001152751				2	AGAGAAACCCT	0.413
+	4	1002		NM_001159279	NP_001152751				2	CTACACATGTG	0.428
+	4	997		NM_001159524	NP_001152996	P0CB33	ZN735_HUMAN	2H2-type 7.	0	GCAAAGCCTTT	0.428
+	7	1696	x.3_Missense_M	NM_015570	NP_056385	Q8WXX7	AUTS2_HUMAN		3	AGCTCCTTCTC	0.632
+	10	2031	fj.3_Missense_Mu	NM_020892	NP_065943	Q86UW9	DTX2_HUMAN		2	TATTACGGTTCC	0.577
-	7	1113	_p.F202Y|SEMA3	NM_006379	NP_006370	Q99985	SEM3C_HUMAN	Sema.	1	CAGAGAAAAGC	0.328
-	7	960_961	n.1_Nonsense_M	NM_000601	NP_000592	P14210	HGF_HUMAN	Kringle 2.	4	CGGCTGGCCAT	0.475
+	11	1260	e_Mutation_p.R22	NM_001142327	NP_001135799	Q9Y222	DMTF1_HUMAN	CND3 (By similarity).|HTH	2	CTGAACGAGTC	0.478
+	23	2332	_p.S705F|CCDC1	NM_017667	NP_060137	Q96JG6	CC132_HUMAN		0	GGAATCCTTGT	0.403
-	17	1953	_p.R589*|SLC25A	NM_014251	NP_055066	Q9UJS0	CMC2_HUMAN	ical; Name=6; (Potential).	4	AGGATCGAAATA	0.338
-	3	293	_p.G59E|CYP3A5_	NM_000777	NP_000768	P20815	CP3A5_HUMAN		0	ATTTTTCCATAC	0.413
-	4	420	3uvz.2_RNA|uc00	NM_016188	NP_057272	O94805	ACL6B_HUMAN		1	TTTGCTGTAGG	0.602
+	14	2461	AN_uc003uwl.2_	NM_003386	NP_003377	Q9Y493	ZAN_HUMAN	ate) (mucin-like domain).|E	11	AAAAACCCACC	0.522
+	14	2470	AN_uc003uwl.2_	NM_003386	NP_003377	Q9Y493	ZAN_HUMAN	ate) (mucin-like domain).|E	11	CCATCTCCCCA	0.522
+	14	2489	AN_uc003uwl.2_R	NM_003386	NP_003377	Q9Y493	ZAN_HUMAN	ate) (mucin-like domain).|E	11	CACCATCCCCA	0.532
-	13	2683	_p.L638R|EPHB4	NM_004444	NP_004435	P54760	EPHB4_HUMAN	Potential).|Protein kinase.	15	CGGCAAGGTAC	0.587
+	3	3876	C17_uc010lho.1_	NM_001040105	NP_001035194	Q685J3	MUC17_HUMAN	ch.|19.|59 X approximate t	27	CTAGTGAAGGA	0.498
-	2	316	zm.2_Missense_	NM_017621	NP_060091	Q9NXW9	ALKB4_HUMAN		0	TCCTCCGTCCA	0.642
-	20	2460	ves.2_Missense_	NM_000111	NP_000102	P40879	S26A3_HUMAN		4	GTAATCCTCCAT	0.333
-	30	4558	p.E1492K|LAMB4	NM_007356	NP_031382	A4D0S4	LAMB4_HUMAN	Domain I.	8	CGTTTTCCTCTT	0.398
-	52	5974	fw.2_Missense_M	NM_014705	NP_055520	Q8N1I0	DOCK4_HUMAN	Pro-rich.	4	TGTACGGGGGC	0.716
-	4	3120		NM_002711	NP_002702	Q16821	PPR3A_HUMAN		34	ACTAATCCTTCA	0.403
-	4	2443		NM_002711	NP_002702	Q16821	PPR3A_HUMAN		34	ACGTGATTCCTT	0.378
-	4	2441		NM_002711	NP_002702	Q16821	PPR3A_HUMAN		34	GTGATTCCTTTT	0.373
+	7	612	e_Mutation_p.H1	NM_019071	NP_061944	Q9NXR8	ING3_HUMAN		1	ACAGATCATATT	0.299

+	41	7167	a.3_Missense_Mut	NM_001458	NP_001449	Q14315	FLNC_HUMAN	Filamin 21.	12	GGGCCGGAGGC	0.677	
+	10	1548	p.R384Q|IRF5_uc	NM_002200	NP_002191	Q13568	IRF5_HUMAN		0	GCAGCGGTTGC	0.592	
+	20	2111	_p.A691T|FAM40B	NM_020704	NP_065755	Q9ULQ0	FA40B_HUMAN		0	AATCGGCACCA	0.438	
-	21	4124		NM_020911	NP_065962	Q9HCM2	PLXA4_HUMAN	lasmic (Potential).	1	GATGTCCGTCTC	0.562	
+	2	529		NM_020299	NP_064695	O60218	AK1BA_HUMAN		5	GAAGCGGGAGG	0.517	
+	11	1965	uv.2_Missense_Mu	NM_173569	NP_775840	Q6ZU65	UBN2_HUMAN		2	CTGGATGCAGGC	0.348	
-	19	2660	M1D_uc010lng.2_	NM_030647	NP_085150	Q6ZMT4	KDM7_HUMAN		1	AGAAGGAAGTTT	0.483	
-	15	1860		NM_004333	NP_004324	P15056	BRAF_HUMAN	rotein kinas_R603>I(2)|p.T	18290	GATTTCACTGTAC	0.368	
-	1	170		NM_176817	NP_789787	P59533	T2R38_HUMAN	Name=1; (Potential).	2	AGAAACCCCACT	0.463	
-	4	759	xc.3_Missense_Mu	NM_001001317	NP_001001317	Q8IYP2	PRS58_HUMAN	eptidase S1.	0	GCTCTTTGTCTA	0.353	
-	4	734	bz.2_Missense_Mu	NM_019841	NP_062815	Q9NQA5	TRPV5_HUMAN	lasmic (Potential).	6	GGTTGCGGGGA	0.627	
+	1	373	uc003wda.2_Intror	NM_177437	NP_803186	P59551	T2R60_HUMAN	lasmic (Potential).	6	CTACCTTCACCC	0.498	
+	9	1777	CN3_uc003wip.2_	NM_004769	NP_004760	Q9UHC3	ACCN3_HUMAN	lasmic (Potential).	2	TCCTGGGATATT	0.612	
-	21	3602	p.S463F|CSMD1_	NM_033225	NP_150094	Q96PZ7	CSMD1_HUMAN	xtracellular (Potential).	25	AGCAGGAAAAC	0.557	
-	2	460		NM_001080826	NP_001074295	Q86YV5	SG223_HUMAN		0	ACAGCGAGAAT	0.642	
-	3	439		NM_004686	NP_004677	Q9Y216	MTMR7_HUMAN		1	GGCATCCGGTA	0.433	
+	18	2079	xbw.3_Missense_	NM_005775	NP_005766	O60504	VINEX_HUMAN		0	CCAGACCCAGG	0.657	
+	2	424	7_uc003xdp.2_RN	NM_016612	NP_057696	Q9NYZ2	MFRN1_HUMAN	Solcar 1.	0	GAGCCCTCAAG	0.522	
+	2	286		NM_004095	NP_004086	Q13541	4EBP1_HUMAN		0	CACCCCCAAGG	0.562	
+	6	682	ny.2_Missense_Mu	NM_032336	NP_115712	Q9BRT9	SLD5_HUMAN		1	TGGACCTCTTT	0.507	
-	29	3512	K1_uc003xoj.2_M	NM_020476	NP_065209	P16157	ANK1_HUMAN		9	TGGGGCGGTGG	0.657	
-	8	1917	xpe.2_Missense_	NM_006749	NP_006740	Q08357	S20A2_HUMAN	lasmic (Potential).	2	GGGCCGATGAG	0.602	
-	23	4432	DNL_uc003xqt.3_	NM_144651	NP_653252	A1KZ92	PXDNL_HUMAN	VWFC.	2	CAGGTTCCTTTC	0.517	
-	17	3339_3340	DNL_uc003xqt.3_	NM_144651	NP_653252	A1KZ92	PXDNL_HUMAN		2	GAACGGAAGGT	0.495	
+	2	494	S1_uc010lyh.2_Int	NM_024831	NP_079107	Q96RS0	TGS1_HUMAN		3	GGGATCGAAAAT	0.313	
-	2	419	ta.3_Missense_Mu	NM_006211	NP_006202	P01210	PENK_HUMAN		4	TCCATTTTCTTC	0.498	
+	2	700	/S1_uc003xui.2_In	NM_173519	NP_775790	Q8IUQ0	CLVS1_HUMAN	CRAL-TRIO.	5	ATGGGTTCCCC	0.483	
+	5	744	_uc003yam.2_Miss	NM_015886	NP_056970	O43692	PI15_HUMAN		3	GCAATTCATACTT	0.428	
-	8	763	nse_Mutation_p.S1	NM_001738	NP_001729	P00915	CAH1_HUMAN		2	GGGATGAAGGA	0.428	
-	1	825		NM_172239	NP_758439	Q8IX06	GOR_HUMAN	R1-125 epitope.	0	CACAGCGGCCC	0.662	
-	4	1072	no.2_Missense_M	NM_001146	NP_001137	Q15389	ANGP1_HUMAN	Potential.	7	TTCCTTCCATTTC	0.313	
-	26	2712	_p.P706L|ASAP1_	NM_018482	NP_060952	Q9ULH1	ASAP1_HUMAN	Pro-rich.	4	AGTTTAGGAAGA	0.294	
-	9	2438	Y8_uc010mds.2_	NM_001115	NP_001106	P40145	ADCY8_HUMAN	ical; (Potential).	6	GTATTGCCGTGA	0.353	
+	20	4326	v.2_Missense_Mut	NM_003235	NP_003226	P01266	THYG_HUMAN		15	GGGACCACTTT	0.567	
+	21	3531	ywa.1_Missense_	NM_014957	NP_055772	A2RUS2	DEND3_HUMAN	WD 2.	1	CTCCTTCCTGAG	0.577	
-	2	174		NM_205545	NP_991108	Q6UXB3	LYPD2_HUMAN	UPAR/Ly6.	0	TGTGGGCTCCG	0.637	
-	4	689	c003yxj.2_Missen	NM_000497	NP_000488	P15538	C11B1_HUMAN		3	GACCTCCAGGG	0.607	
-	7	2023		NM_015117	NP_055932	Q8IXZ2	ZC3H3_HUMAN		1	CCCTGCGCTGC	0.677	
+	2	240	GPR172A_uc003z	NM_024531	NP_078807	Q9HAB3	RFT3_HUMAN	ical; (Potential).	0	CGGTCAATGGGA	0.662	rs141698844
-	3	1516		NM_003923	NP_003914	O75593	FOXH1_HUMAN	eraction domain (SID).	0	GGCCACCCCCC	0.612	
+	5	563	.V136M|GPT_uc0	NM_005309	NP_005300	P24298	ALAT1_HUMAN		2	AGGACGTGGCG	0.647	
+	23	2901	DCK8_uc010mgw.	NM_203447	NP_982272	Q8NF50	DOCK8_HUMAN		6	CGATCGCAACT	0.463	
-	15	2467	e_Mutation_p.R36	NM_007126	NP_009057	P55072	TERA_HUMAN		1	AAGCACGCTGG	0.512	
-	4	1620		NM_001145196	NP_001138668	Q5VVP1	F75A6_HUMAN		0	GGAGAGAGCTT	0.478	
+	3	1718	p.3_Missense_Mu	NM_024945	NP_079221	Q9H9A7	RMI1_HUMAN		0	AGCCATTCCttaa	0.284	
+	11	2058	ry.1_Missense_M	NM_001010895	NP_001010895	Q5T890	RAD26_HUMAN	case C-terminal.	0	TATGGCGTCTG	0.403	
-	1	671		NM_001001919	NP_001001919	Q8NGS5	O13C4_HUMAN	lasmic (Potential).	1	AAGATGGTGTAG	0.408	

+	2	518	lwx.1_Missense_M	NM_133465	NP_597722	Q8N8K9	K1958_HUMAN		1	GTAACCGGACC	0.483	
-	5	1323	_p.E408K|ASTN2_	NM_198187	NP_937830	O75129	ASTN2_HUMAN	lasmic (Potential).	9	AGTTTCATCGT	0.537	
+	11	1761	bkz.1_Missense_	NM_007018	NP_008949	Q7Z7A1	CNTRL_HUMAN	Potential.	0	AAGTCGTTTGG	0.358	
-	5	453	e_Mutation_p.R74	NM_004099	NP_004090	P27105	STOM_HUMAN	lasmic (Potential).	0	AACGCGGTAAT	0.443	
+	4	664	ous.2_Missense_	NM_016035	NP_057119	Q9Y3A0	COQ4_HUMAN		0	GGATTTCGACAT	0.597	
+	7	965_966	_p.R297*|SPTAN1	NM_003127	NP_003118	Q13813	SPTA2_HUMAN	Spectrin 4.	10	TTGGCCGAGAC	0.48	
+	13	1315	s.1_Missense_M	NM_003934	NP_003925	Q96I24	FUBP3_HUMAN	KH 4.	1	ACCTGCGGAGA	0.607	
-	10	1159		NM_013379	NP_037511	Q9UHL4	DPP2_HUMAN		0	GCGGAGCTCGT	0.667	
-	1	170	1mer.1_Missense_	NM_013366	NP_037498	Q9UJX6	ANC2_HUMAN		1	CGGCGGCACCA	0.721	
+	5	499	sense_Mutation_p.	NM_080877	NP_543153	Q8N130	NPT2C_HUMAN	ellular (Potential).	0	AAGTGGCCGGA	0.647	
-	4	306	v.1_RNA|FAM9B_	NM_205849	NP_995321	Q8IZU0	FAM9B_HUMAN		0	TTTTATCCATTTT	0.274	
+	9	1385	mij.1_Missense_M	NM_014728	NP_055543	Q14CM0	FRPD4_HUMAN	FERM.	13	AAAGATCCAATT	0.393	
-	7	1167	P7_uc004cxu.2_M	NM_002893	NP_002884	Q16576	RBBP7_HUMAN		2	TGTGCGCATCC	0.498	
+	37	4399		NM_016937	NP_058633	P09884	DPOLA_HUMAN		3	TTGTGCCGTGA	0.507	
+	1	876		NM_001013736	NP_001013758	Q5HY64	FA47C_HUMAN		3	CTCCCAAGACT	0.607	
+	19	3304	fc.2_Nonsense_M	NM_001039590	NP_001034679	Q93008	USP9X_HUMAN		6	TAGTTCGATTTC	0.408	
+	3	393	oq.1_Missense_	NM_000084	NP_000075	P51795	CLCN5_HUMAN	smic (By similarity).	4	TTAATTCACAGT	0.363	
+	4	701	kc.1_Nonsense_	NM_177433	NP_803182	Q9UNF1	MAGD2_HUMAN		3	GTGGCCGAAGG	0.587	
-	7	1300	lyo.2_Missense_M	NM_032803	NP_116192	Q8WY07	CTR3_HUMAN	lasmic (Potential).	2	GGGTGCGTGTG	0.557	
+	16	2489	lyz.2_Nonsense_	NM_005120	NP_005111	Q93074	MED12_HUMAN		4	AGCAGCGAGAT	0.537	
+	1	1198		NM_020932	NP_065983	Q9HCI5	MAGE1_HUMAN	Pro-rich.	6	GCACCTCCGTG	0.701	
+	4	1789	eh.1_Missense_M	NM_021118	NP_066941	P35663	CYLC1_HUMAN		5	TCAATGAAAAAG	0.418	
+	5	972	11_uc004eeq.2_M	NM_021998	NP_068838	Q9Y462	ZN711_HUMAN		4	TAGTGGATGATG	0.313	
-	3	1271	p.E306K|ARMCX2	NM_177949	NP_808818	Q7L311	ARMX2_HUMAN		6	CAGTTCGTCTA	0.587	
-	1	419		NM_001002916	NP_001002916	Q7Z2G1	H2BWT_HUMAN		1	TGATGGTCTGG	0.647	
+	11	2788		NM_017416	NP_059112	Q9NP60	IRPL2_HUMAN	lasmic (Potential).	3	CCAAAGAGCTT	0.408	
-	2	353	Y2F_uc011msq.1_	NM_001522	NP_001513	P51841	GUC2F_HUMAN		8	CAAGGCCATGG	0.572	
-	5	2180	m.1_Missense_M	NM_012471	NP_036603	Q9UL62	TRPC5_HUMAN	lasmic (Potential).	1	ACATTTCCTTAAT	0.443	
+	6	1653	_Mutation_p.A30	NM_000868	NP_000859	P28335	5HT2C_HUMAN	smic (By similarity).	3	GAAAAGCTTCG	0.438	
+	12	1660		NM_007231	NP_009162	Q9UN76	S6A14_HUMAN		3	GAGGTGGATAT	0.363	
-	18	3313	.W1082*|ODZ1_u	NM_014253	NP_055068	Q9UKZ4	TEN1_HUMAN	ellular (Potential).	23	TTGTTCCAAGC	0.448	
+	9	1158	k.1_Missense_M	NM_001015877	NP_001015877	Q8IWS0	PHF6_HUMAN	ype 2; degenerate.	1	GTCACGAGGAA	0.348	
-	4	1143	p.R171C|FGF13_	NM_004114	NP_004105	Q92913	FGF13_HUMAN		3	GCTGACGGTATA	0.398	
+	7	887		NM_018558	NP_061028	Q9UN88	GBRT_HUMAN	ical; (Potential).	3	TTGGATGAACTA	0.443	
-	13	2123	K1_uc004fjt.1_Mis	NM_001569	NP_001560	P51617	IRAK1_HUMAN		9	GCTGTCCAGGG	0.637	
+	2	247		NM_004699	NP_004690	Q14320	FA50A_HUMAN		1	GTTCTCTGCGC	0.622	
+	2	583		NM_017514	NP_059984	P51805	PLXA3_HUMAN	tracellular (Potential).	3	CCACCGCAAGG	0.667	
-	4	389	_p.R78L|KIAA17	NM_001080484	NP_001073953	Q9C0B2	K1751_HUMAN		1	TCTGCCGCAGG	0.502	
-	4	1018	ad.1_Missense_	NM_024980	NP_079256	Q5UAW9	GP157_HUMAN	lasmic (Potential).	0	AGAGAGAGAAG	0.607	
+	18	2269	_Mutation_p.R710	NM_015378	NP_056193	Q5THJ4	VP13D_HUMAN		5	CCGTGCGGCTG	0.428	rs139539467
+	16	1818	KA_uc010obw.1_	NM_004070	NP_004061	P51800	CLCKA_HUMAN	CBS 1.	1	AGTATCCCCTG	0.557	
+	4	768	b.2_Missense_M	NM_032264	NP_115640	Q9H094	NBPF3_HUMAN	Potential.	2	TTGCAGAGGAG	0.552	
-	3	930		NM_004091	NP_004082	Q14209	E2F2_HUMAN	per.|DEF box.|Potential.	4	GATGCGCCGCT	0.592	
-	4	459	.1_Missense_Mut	NM_001127621	NP_001121093	Q14376	GALE_HUMAN		0	ACCGCCATAAA	0.552	
+	13	1921	e_Mutation_p.P53	NM_005839	NP_005830	Q8IYB3	SRRM1_HUMAN	s and matrix localization.|A	3	CCCTCCTCCTC	0.537	
+	13	1933	e_Mutation_p.R54	NM_005839	NP_005830	Q8IYB3	SRRM1_HUMAN	s and matrix localization.|A	3	ACGGCGCAGGA	0.532	rs78787676
-	11	1079	.F27Y|UBXN11_u	NM_183008	NP_892120	Q5T124	UBX11_HUMAN	SEP.	1	AGGGAAAGAAG	0.582	

+	20	6984	_p.A1050V|ARID1	NM_006015	NP_006006	O14497	ARI1A_HUMAN			142	CCTTGCCGCCA	0.642	
+	2	288	_p.R41C|ZSCAN	NM_145238	NP_660281	P17040	ZSC20_HUMAN			4	AGGACCGTGGC	0.597	
-	9	1231	xm.1_Missense_M	NM_052896	NP_443128	Q7Z408	CSMD2_HUMAN	ar (Potential).|Sushi 2.		12	CACCTCGGCAG	0.632	
+	4	599	_p.R102Q|ZNF642	NM_198494	NP_940896	Q49AA0	ZN642_HUMAN	KRAB.		0	ATACCGAGAGG	0.458	rs145832267
+	10	1725	ense_Mutation_p.	NM_152498	NP_689711	Q96MR6	WDR65_HUMAN	WD 8.		1	ATGGTGCTGTGT	0.463	
+	15	2893	1orf175_uc010oc	NM_001039464	NP_001034553	Q68CQ1	HEAT8_HUMAN			0	TGGGCCGTGTG	0.647	
-	3	383	_p.E44K|C8B_uc	NM_000066	NP_000057	P07358	CO8B_HUMAN	SP type-1 1.		4	GACTTCCTTGT	0.498	
+	16	1775	C7_uc009wbg.2_I	NM_020794	NP_065845	Q96NW7	LRRC7_HUMAN			14	TAAAATCTGTTC	0.338	
-	11	1844	73_uc001dgi.3_Mi	NM_001002912	NP_001002912	Q5RHP9	CA173_HUMAN	Glu-rich.		5	TCTCTTTTTCAG	0.403	
+	6	919	ls.1_Missense_M	NM_001285	NP_001276	A8K7I4	CLCA1_HUMAN			1	AGCAAAATCAA	0.373	
+	9	1380	dly.2_Nonsense_	NM_016009	NP_057093	Q9Y371	SHLB1_HUMAN	SH3.		0	GAAACCAGAAG	0.388	
-	15	1954	RHGAP29_uc001	NM_004815	NP_004806	Q52LW3	RHG29_HUMAN			11	TATAAAGGAAG	0.358	
+	4	263	wa.1_Missense_M	NM_001040033	NP_001035122	P19397	CD53_HUMAN	ical; (Potential).		0	CTTTGGGATCT	0.483	
-	3	435		NM_002524	NP_002515	P01111	RASN_HUMAN	GTP.	)|p.Q61P(21)|	2607	TTCTTGTCCAG	0.458	rs121913254
+	23	2095	e_Mutation_p.G62	NM_003176	NP_003167	Q15431	SYCP1_HUMAN	Potential.		1	AAAAGGTACAG	0.254	
-	11	1315	wu.1_Missense_M	NM_001232	NP_001223	O14958	CASQ2_HUMAN			1	AAGATCGTCAT	0.403	
-	25	4713		NM_024408	NP_077719	Q04721	NOTC2_HUMAN	(NRR).|LNR 2.|Extracellula		27	CGACCGTGTTG	0.517	
-	25	3982	4DIP_uc001elm.3	NM_014644	NP_055459	Q5VU43	MYOME_HUMAN	Potential.		5	TCTCCTGGAGAT	0.507	
-	3	474	_uc001eln.3_Mis	NM_014644	NP_055459	Q5VU43	MYOME_HUMAN			5	CCTTTTCACCAC	0.433	
+	14	1889	10_uc010oyi.1_Int	NM_001039703	NP_001034792	A6NDV3	A6NDV3_HUMAN			0	TTCCACGCTCAG	0.453	rs61816394
+	11	1769	se_Mutation_p.S2	NM_007259	NP_009190	Q9NRW7	VPS45_HUMAN			2	ACACAGCAGCA	0.443	
+	8	877	xn.2_Missense_M	NM_002810	NP_002801	P55036	PSMD4_HUMAN			0	TGGCCGCACTG	0.547	
+	2	247		NM_178428	NP_848515	Q5TA79	LCE2A_HUMAN	Cys-rich.		0	GTGGCGGCTGC	0.687	
+	2	1046		NM_001025231	NP_001020402	Q5T749	KPRP_HUMAN	Pro-rich.		5	AGATTTCCTCCC	0.632	
+	9	1007	p.R329H|DCST1_	NM_152494	NP_689707	Q5T197	DCST1_HUMAN	ellular (Potential).		2	GTGCCGCAATC	0.592	
-	19	3609	_Mutation_p.R28	NM_014215	NP_055030	P14616	INSRR_HUMAN	Potential).|Protein kinase.		20	GTTGCGGGCTG	0.512	
-	6	1103	3_uc009wsn.2_In	NM_052939	NP_443171	Q96P31	FCRL3_HUMAN	ellular (Potential).		4	TCCTTTTTTTGAT	0.547	
+	12	2169	TP1A4_uc001fvg.2	NM_144699	NP_653300	Q13733	AT1A4_HUMAN	lasmic (Potential).		4	TTCTGCTTCTTG	0.468	
-	6	1046	244_uc009wtp.2_	NM_016382	NP_057466	Q9BZW8	CD244_HUMAN	lasmic (Potential).		1	TCCAGGAAAAG	0.502	
-	12	2250	p.G481E|ARHGA	NM_001025598	NP_001020769	Q7Z6I6	RHG30_HUMAN			3	CCTCTCCCTCC	0.587	
+	3	651	1AP_uc010pks.1_	NM_014697	NP_055512	O75052	CAPON_HUMAN	PID.		3	AAGAAGAAAAA	0.448	
-	2	220	wux.1_Missense_	NM_178550	NP_848645	Q86UF4	CA110_HUMAN	Potential.		0	TCCAAATCAAA	0.433	
+	6	977	eq.2_Missense_M	NM_003953	NP_003944	O95297	MPZL1_HUMAN	lasmic (Potential).		2	AGTCAGAGTCT	0.443	
+	9	1572	_Mutation_p.G47	NM_002021	NP_002012	Q01740	FMO1_HUMAN			1	CCCAGGAAAAT	0.507	
-	22	3130	we.2_Missense_	NM_178527	NP_848622	Q5TAH2	S9A11_HUMAN	cNMP.		2	AGATTCCTTGTG	0.303	
+	8	1565	lg.2_Nonsense_M	NM_021165	NP_066988	Q9C0B6	FAM5B_HUMAN			6	CTGGTGGAACC	0.512	
+	7	477	rf49_uc001glv.1_	NM_032126	NP_115502	Q5T0J7	CA049_HUMAN			0	AAAGGAGCAGC	0.557	
+	2	495		NM_014864	NP_055679	O75063	XYLK_HUMAN	enal (Potential).		3	TTGCAGCCCAG	0.582	
+	16	1712	_p.E317K|C1orf12	NM_144696	NP_653297	Q5T1B0	AXDN1_HUMAN			0	AAGAAGAGTTT	0.368	
+	71	11181		NM_031935	NP_114141	Q96RW7	HMCN1_HUMAN	ike C2-type 35.		23	CCCCACCTGTAA	0.413	
+	11	1793		NM_000186	NP_000177	P08603	CFAH_HUMAN	Sushi 9.		6	aatgccagaactaaa	0.249	
+	2	205	R2_uc001gtr.1_In	NM_005666	NP_005657	P36980	FHR2_HUMAN	Sushi 1.		3	ATTTTCCCAAG	0.348	
+	8	1276		NM_030787	NP_110414	Q9BXR6	FHR5_HUMAN	Sushi 6.		2	TGTAGAAAAAG	0.348	
+	12	4160	se_Mutation_p.S1	NM_201253	NP_957705	P82279	CRUM1_HUMAN	ellular (Potential).		9	TGATCTCCGACA	0.428	
-	53	10838		NM_206933	NP_996816	O75445	USH2A_HUMAN	II 19.|Extracellular (Potenti		26	GTCCTCGCCCA	0.443	
+	7	694	ATA17_uc001hli.2	NM_138796	NP_620151	Q96L03	SPT17_HUMAN			1	AAGCGCCCGTT	0.408	
+	5	1575	.Y336H|TGFB2_u	NM_003238	NP_003229	P61812	TGFB2_HUMAN			0	CGGCCTATTGC	0.448	

+	1	48	_uc001hls.3_5'UTR	NM_138794	NP_620149	Q5VWZ2	LYPL1_HUMAN			0	TGGCGGCTGCG	0.662	
-	6	395	_uc010pvd.1_Intr	NM_002533	NP_002524	O15381	NVL_HUMAN			2	TCATGTGATTTGC	0.353	
-	12	2614	.2_Intron|NID1_uc	NM_002508	NP_002499	P14543	NID1_HUMAN	alcium-binding (Potential).		2	GCAACGGAAGC	0.572	
-	9	1304	130331_uc010pyc	NM_021186	NP_067009	Q12836	ZP4_HUMAN	acellular (Potential).		3	GTCCCCTGAGG	0.532	
-	2	653	.2_RNA|OPN3_uc	NM_014322	NP_055137	Q9H1Y3	OPN3_HUMAN	Name=4; (Potential).		0	TGCTCCTGCCC	0.537	
+	3	893	o.3_Missense_Mu	NM_152609	NP_689822	Q6PJW8	CNST_HUMAN			0	TGCAGTCTCTGT	0.453	
-	32	6364	TF1_uc009xgs.1_	NM_015446	NP_056261	Q8WYP5	ELYS_HUMAN	lear localization (By similar		7	TGGAGAAAATAA	0.433	
+	1	943		NM_001013355	NP_001013373	Q5TZ20	OR2G6_HUMAN	lasmic (Potential).		3	GCCACAAGGAC	0.488	
+	15	6938	iik.2_Missense_Mu	NM_017782	NP_060252	Q5VWN6	CJ018_HUMAN			2	GAATCTCGGAAT	0.338	
+	2	232	1ind.2_5'UTR|HSF	NM_016299	NP_057383	Q0VDF9	HSP7E_HUMAN			5	ATGCCGGTGAC	0.403	
-	8	2208		NM_001010924	NP_001010924	Q5VUB5	F1711_HUMAN	lasmic (Potential).		4	TTACTTCCGTTCC	0.532	
+	7	767		NM_052997	NP_443723	Q9BXX3	AN30A_HUMAN			9	TGCAGGAACAC	0.348	
+	2	279	jbl.2_Intron|TMEM	NM_001123376	NP_001116848	A0PK05	TMM72_HUMAN	ical; (Potential).		0	TCGGCGTGGGC	0.547	
-	8	2011	.2_Intron|PARG_u	NM_003631	NP_003622	Q86W56	PARG_HUMAN			2	TTCTGCTTCTT	0.318	
+	15	1949	PRKG1_uc009xow	NM_001098512	NP_001091982	Q13976	KGP1_HUMAN	rotein kinase.		6	GCCAAAAATGC	0.313	
+	18	2460	j.1_Missense_Mu	NM_001080512	NP_001073981	Q9H694	BICC1_HUMAN			4	CGAAATGGAAT	0.458	
+	3	772	_Mutation_p.S19	NM_032578	NP_115967	Q86TC9	MYPN_HUMAN	action with CARP.		5	AAACAGCTCCA	0.448	
-	1	534		NM_003956	NP_003947	O95992	CH25H_HUMAN			0	ACTGCGTTGCC	0.582	
-	4	649	ense_Mutation_p.	NM_000770	NP_000761	P10632	CP2C8_HUMAN			0	ATCGTTTCTGG	0.388	
-	27	3026		NM_003061	NP_003052	O75093	SLIT1_HUMAN			4	CACACTTGGCC	0.542	
+	14	2260	43_uc010qpu.1_I	NM_017893	NP_060363	Q9NTN9	SEM4G_HUMAN	Potential).|Ig-like C2-type.		1	TTACAGATGCA	0.627	
-	6	1917	.2_Missense_Muta	NM_013274	NP_037406	Q9UGP5	DPOLL_HUMAN			0	GTTCCAGGAAG	0.572	
-	4	429		NM_006993	NP_008924	O75607	NPM3_HUMAN			0	GTGCCGCCCAG	0.617	
+	5	486	_p.R74Q|NFKB2_	NM_001077494	NP_001070962	Q00653	NFKB2_HUMAN	RHD.		3	GGGCCGAAAG	0.597	
+	25	3838		NM_014976	NP_055791	Q14690	RRP5_HUMAN	S1 motif 11.		7	TCCTTCCCCTTT	0.557	
-	7	1399	_Mutation_p.R251	NM_000141	NP_000132	P21802	FGFR2_HUMAN	cellular (Pot	p.R251Q(1)	96	GCGATCGCTCT	0.562	
+	4	4130	se_Mutation_p.S12	NM_206862	NP_996744	O95359	TACC2_HUMAN			10	TGTTTCCTCTG	0.592	
+	8	1393		NM_002775	NP_002766	Q92743	HTRA1_HUMAN	PDZ.		0	TACCCCAGCAG	0.498	
+	1	845		NM_001127389	NP_001120861	F5GZ66	F5GZ66_HUMAN			0	CACCGGCGCGT	0.786	
+	14	1916		NM_198075	NP_932341	Q8IYG6	LRC56_HUMAN			1	CGACAGACCTG	0.687	
+	44	14641		NM_002457	NP_002448	Q02817	MUC2_HUMAN	VWFC 1.		2	CCACGGAGGTC	0.622	
+	39	4906	ltb.2_Missense_M	NM_017511	NP_059981	Q9HC84	MUC5B_HUMAN	VWFD 3.		0	GGACCTTCCGC	0.652	
+	48	9914	b.2_Missense_Mu	NM_017511	NP_059981	Q9HC84	MUC5B_HUMAN	pproximate tandem repeat		0	CCCAGGGACGG	0.642	
-	1	543	.1_Intron|HBE1_uc	NM_033180	NP_149420	Q9Y5P1	O51B2_HUMAN	cellular (Potential).		3	AAAATGAAAAAA	0.398	
+	1	742	_uc001mam.1_Int	NM_001004754	NP_001004754	Q9H344	O51I2_HUMAN	Name=6; (Potential).		4	TGGCTGTACTT	0.493	
-	1	519		NM_153444	NP_703145	Q8WZ92	OR5P2_HUMAN	cellular (Potential).		5	CAGAAAAAATG	0.383	
+	6	689	k.1_Nonsense_M	NM_018222	NP_060692	Q9NVD7	PARVA_HUMAN			3	CCATCCAAGTG	0.498	
+	8	1496	_Mutation_p.D366	NM_018393	NP_060863	Q9NUJ3	T11L1_HUMAN			0	AGGCCGACTTT	0.527	rs149395795
+	10	1835	_p.L514F|EXT2_uc	NM_207122	NP_997005	Q93063	EXT2_HUMAN	enal (Potential).		5	ATTCTCTCTGG	0.383	
-	5	854	BRA1_uc001ncv.	NM_017749	NP_060219	Q9C0C7	AMRA1_HUMAN	WD 3.		3	GACTCCAGTCC	0.567	
-	4	650	ncv.2_Missense_	NM_017749	NP_060219	Q9C0C7	AMRA1_HUMAN	WD 2.		3	ATGGAGTACGG	0.478	
-	9	861_862		NM_004308	NP_004299	Q07960	RHG01_HUMAN	Rho-GAP.		1	AGTCTCCCTGA	0.653	
+	7	674	2_uc001ndg.3_RN	NM_000506	NP_000497	P00734	THRB_HUMAN			3	CATTGGAGCAG	0.607	
+	6	941	32_uc001nee.2_In	NM_000107	NP_000098	Q92466	DDB2_HUMAN	WD 3.		3	TGTGGCCCTGA	0.542	
+	2	199	D5_uc010riq.1_5'	NM_032681	NP_116070	Q9BSJ1	SPRY5_HUMAN	RING-type.		0	TTGCCGGCCCT	0.512	
-	1	52		NM_001004743	NP_001004743	Q8NGP3	OR5M9_HUMAN	cellular (Potential).		4	CTGACGACAGG	0.428	
-	1	188		NM_001005489	NP_001005489	Q8NGF7	OR5BH_HUMAN	Name=2; (P	p.N63S(1)	3	ACAGGTTACTG	0.468	

+	8	1093	Mutation_p.Q308*	NM_053023	NP_444251	Q96JP5	ZFP91_HUMAN		1	CCAATCCAGTAT	0.408	
-	5	806	CE_uc001nrb.2_F	NM_152718	NP_689931	Q96DN2	VWCE_HUMAN	alcium-binding (Potential).	1	TGTGGCGGTCG	0.458	
+	8	815	TN3_uc010rpi.1_F	NM_001104	NP_001095	Q08043	ACTN3_HUMAN		0	CGGGGCTGAGC	0.597	
-	17	3820		NM_006946	NP_008877	O15020	SPTN2_HUMAN	Spectrin 9.	4	TTTCCCGAATCT	0.557	
+	14	4730		NM_014786	NP_055601	Q96PE2	ARHGH_HUMAN		0	TCCGTCGCTGA	0.726	
+	5	1272		NM_153614	NP_705842	P59910	DJB13_HUMAN		0	CTCCACCATCA	0.527	
+	1	216		NM_001098672	NP_001092142	Q6MZM0	HPHL1_HUMAN		3	GTCTGGGCTGG	0.502	
-	6	1178	hp.2_Missense_M	NM_025208	NP_079484	Q9GZP0	PDGFD_HUMAN		2	CTGTAACGCTTG	0.458	
+	17	3150	v.2_3'UTR|GRIA4_	NM_000829	NP_000820	P48058	GRIA4_HUMAN	lasmic (Potential).	8	GACCTACCATAA	0.493	
+	2	86		NM_000040	NP_000031	P02656	APOC3_HUMAN		0	TGGCGCTCCTG	0.647	
-	12	2600_2601		NM_020693	NP_065744	Q8TD84	DSCL1_HUMAN	otential).|Ig-like C2-type 9.	8	TAGCTCCTTCGC	0.639	
+	4	733	MKLB_uc010sgl.1_	NM_020734	NP_065785	Q9ULI2	RIMKB_HUMAN	p.|ATP (By similarity).	0	TACGCGGGGTC	0.363	
+	1	114		NM_144670	NP_653271	A8K2U0	A2ML1_HUMAN		3	CAGCTCCTTCTA	0.507	
-	13	3619		NM_000834	NP_000825	Q13224	NMDE2_HUMAN	lasmic (Potential).	12	CGTGCTCCCAG	0.582	
+	21	2437_2438	MP_uc001rgi.2_R	NM_006152	NP_006143	Q12912	LRMP_HUMAN	enal (Potential).	2	TGTGGATGCCGC	0.495	
-	12	963_964	_Mutation_p.R215	NM_002733	NP_002724	P54619	AAKG1_HUMAN	CBS 4.	1	AGTCGGTGAAC	0.54	
-	5	1439		NM_002272	NP_002263	B4DRS2	B4DRS2_HUMAN		6	CTCCTCGTACT	0.592	
+	6	979	2_Nonsense_Muta	NM_199187	NP_954657	P05783	K1C18_HUMAN	.|Rod.|Necessary for intera	1	CAGTCCAGTCC	0.572	
+	8	1153	my.1_Missense_M	NM_020547	NP_065434	Q16671	AMHR2_HUMAN	Potential).|Protein kinase.	2	TGCTCCCTGGC	0.577	
-	2	232	|KIAA0748_uc010	NM_001098815	NP_001092285	A2RU30	K0748_HUMAN		2	GATCTGGGACA	0.597	
+	1	539		NM_054104	NP_473445	Q9NZP0	OR6C3_HUMAN	ellular (Potential).	1	ATTTTCCCCTCT	0.403	
+	7	1064	|RAB5B_uc001siv	NM_001798	NP_001789	P24941	CDK2_HUMAN	rotein kinase.	2	GATTTCGGCCA	0.522	
+	8	1102	d.1_Missense_Mu	NM_022465	NP_071910	Q9H2S9	IKZF4_HUMAN		1	TCGATCGTCTG	0.512	
-	9	1236	_p.T324M|TMEM1	NM_001130963	NP_001124435	O14524	T194A_HUMAN		0	TTGGCGTGAGG	0.433	
-	7	828	n_p.A83T|STAT6_	NM_003153	NP_003144	P42226	STAT6_HUMAN		4	CTTTGGCTGCCT	0.632	
+	6	1531_1532	_p.G411E|SLC16A	NM_004731	NP_004722	O60669	MOT2_HUMAN	ical; (Potential).	1	CTGTGGGGCTAT	0.391	
-	2	290	uc001srx.2_Intron	NM_001099676	NP_001093146	Q8IXR9	CL056_HUMAN		0	ATTTCTCTATCTG	0.328	
+	6	1126	e_Mutation_p.P37	NM_007007	NP_008938	Q16630	CPSF6_HUMAN	Pro-rich.	0	AGCTCCTCCTC	0.627	
-	2	1403		NM_005447	NP_005438	O75901	RASF9_HUMAN		1	TATTCTTTTGCTT	0.398	
-	3	1396	JM_uc001tbn.2_R	NM_002345	NP_002336	P51884	LUM_HUMAN		2	TAAGAGTGACTT	0.353	
+	8	840	xn.1_Missense_Mutation_p.D998N			Q8N1T3	MYO1H_HUMAN		0	TTTTCGACACT	0.368	
+	14	1843	.3_Missense_Mut	NM_001082537	NP_001076006	Q2MV58	TECT1_HUMAN		0	AGGCTGCCCTTT	0.512	
+	8	2023	sf.2_Missense_Mu	NM_005475	NP_005466	Q9UQQ2	SH2B3_HUMAN		1	GACTACGAAATG	0.592	
-	17	1995	un.1_Nonsense_M	NM_004658	NP_004649	O95294	RASL1_HUMAN	PH.	4	CTTCTCGAACAAT	0.637	rs61740514
-	17	3495		NM_015335	NP_056150	Q71F56	MD13L_HUMAN		8	ATGTAAAGCCCG	0.463	
+	2	397	IP35_uc009zxz.2_	NM_022717	NP_073208	Q16560	U1SBP_HUMAN	RRM.	0	GGGCTACGCCT	0.507	
+	19	3024	_p.W542*|DNAH10	NM_207437	NP_997320	Q8IVF4	DYH10_HUMAN	n (By similarity).	6	CTCTCTGGAAAT	0.383	
+	9	3108	1uhf.1_Missense_	NM_052907	NP_443139	Q14DG7	T132B_HUMAN	lasmic (Potential).	19	TCCTCCCAGAG	0.478	
+	10	1193	ij.1_Missense_Mu	NM_004764	NP_004755	Q96J94	PIWL1_HUMAN	PAZ.	2	CAAGAGAAGGC	0.547	
-	19	3298		NM_015347	NP_056162	O15034	RIMB2_HUMAN		11	CTCTTCTTCTGT	0.308	
-	1	1204	A_uc010tee.1_Int	NM_005584	NP_005575	Q13394	MB211_HUMAN		2	AGGAGTGGCAC	0.642	
-	8	819	se_Mutation_p.S2	NM_013338	NP_037470	Q9Y673	ALG5_HUMAN	enal (Potential).	0	GAGATGAAAAC	0.448	
-	14	4304	_p.S17F|ZC3H13_	NM_015070	NP_055885	Q5T200	ZC3HD_HUMAN		2	CTCTCGGATTTA	0.408	
+	1	2386		NR_003268					0	TTTTCCACCAAG	0.517	
-	6	2191	m.1_Missense_Mu	NM_020866	NP_065917	Q9NR64	KLHL1_HUMAN	Kelch 1.	0	CCATTCCTCCTA	0.343	
-	8	2044	_p.S393P|DACH1_	NM_080759	NP_542937	Q9UI36	DACH1_HUMAN		1	TTAGAGAGAGTT	0.443	
-	10	2772	IN1_uc001wir.3_M	NM_014977	NP_055792	Q9UKV3	ACINU_HUMAN		4	GCAGCGAGCTC	0.458	

-	21	2403		NM_000257	NP_000248	P12883	MYH7_HUMAN	ling.|Myosin head-like.	4	CGGCCTTGAAG	0.592	
-	2	369	DHRS1_uc001wol	NM_138452	NP_612461	Q96LJ7	DHRS1_HUMAN		0	GTAAACTGTGG	0.592	
-	18	3003	sl.2_Missense_M	NM_013448	NP_038476	Q9NRL2	BAZ1A_HUMAN	ion with SMARCA5.	7	TATCGTCTATAC	0.418	
-	4	2006		NM_203301	NP_976046	Q7Z6M2	FBX33_HUMAN		0	AAAAAGCTAAAT	0.358	
+	5	861	_p.R110C|PRPF3	NM_017922	NP_060392	Q86UA1	PRP39_HUMAN	HAT 4.	2	ATGATCGTATTC	0.388	
-	8	1045	A0831_uc001xbw	NM_014924	NP_055739	Q6ZNE5	BAKOR_HUMAN		0	ATTTTCGCCAC	0.289	
-	2	803	se_Mutation_p.G1	NM_183002	NP_892114	P57103	NAC3_HUMAN		7	CAGCCCAAAAT	0.542	
-	19	2103	aub.1_Missense_	NM_024764	NP_079040	Q9H7T0	CTSRB_HUMAN		5	TCTTCTCTATAT	0.403	
+	11	909	n_p.M276I|SLC24	NM_153646	NP_705932	Q8NFF2	NCKX4_HUMAN	ellular (Potential).	3	ATTATGAGCTC	0.532	
-	1	412_413	R20_uc010txu.1_5	NM_001017963	NP_001017963	P07900	HS90A_HUMAN		7	GGCGGGACAG	0.698	
+	8	2008	1ylr.2_Missense_	NM_018335	NP_060805	A8K0R7	ZN839_HUMAN		2	CAATGGGAGCG	0.542	
-	32	4775		NM_006035	NP_006026	Q9Y5S2	MRCKB_HUMAN		11	GTTGAGGAGGT	0.602	
+	14	1404	TA1_uc001yrb.2_	NM_004689	NP_004680	Q13330	MTA1_HUMAN	A-type; atypical.	2	GTATTCTTGGG	0.493	
+	1	851	43_splice|ARHGA	NM_014783	NP_055598	Q6P4F7	RHGBA_HUMAN		6	TAGGGGTAAGT	0.463	
-	3	1602	ck.1_Missense_M	NM_007223	NP_009154	Q14439	GP176_HUMAN	lasmic (Potential).	6	GGTCCGGAGCG	0.577	
-	6	1064		NM_005926	NP_005917	P55081	MFAP1_HUMAN		1	CTTCTCGATCTT	0.418	
+	3	493		NM_024908	NP_079184	Q9H967	WDR76_HUMAN		0	TTTTTCGGGAT	0.343	rs139119504
-	10	1178	e_Mutation_p.R10	NM_002112	NP_002103	P19113	DCHS_HUMAN		6	AGAGCGAAACC	0.547	
-	25	3830	w.1_Missense_M	NM_017672	NP_060142	Q96QT4	TRPM7_HUMAN	lasmic (Potential).	10	GAATGAAATTTG	0.333	
-	10	1186	gb.1_RNA|MYO5C	NM_018728	NP_061198	Q9NQX4	MYO5C_HUMAN	osin head-like.	14	TCATCCTCCTTC	0.582	
+	2	738	fw.2_Missense_M	NM_032866	NP_116255	Q0VF96	CGNL1_HUMAN	Head.	11	CAGCTCCGTGG	0.542	
-	7	1068	NIP2_uc010uhb.1_	NM_004330	NP_004321	Q12982	BNIP2_HUMAN	CRAL-TRIO.	1	CCTTCTATCAATT	0.303	
-	4	528	ense_Mutation_p.	NM_024611	NP_078887	Q659A1	NARG2_HUMAN		2	AACGAGAGAAA	0.398	
+	7	585	X22_uc002ana.1_	NM_024798	NP_079074	Q96L94	SNX22_HUMAN		0	GCCCAGATAAA	0.577	
-	2	189		NM_003613	NP_003604	O75339	CILP1_HUMAN		7	TTGGTCCCCACC	0.552	
+	2	1475		NM_005576	NP_005567	Q08397	LOXL1_HUMAN	yl-oxidase like.	0	TGTGCAAGCAT	0.572	
+	2	1012	.1_Missense_Mu	NM_005545	NP_005536	O14498	ISLR_HUMAN	Ig-like.	4	AGGATGGTGCC	0.652	
+	2	435		NM_025055	NP_079331	Q8N5R6	CCD33_HUMAN		5	AGAGGAGCCCC	0.433	
+	6	948	2axp.2_Missense_	NM_025055	NP_079331	Q8N5R6	CCD33_HUMAN		5	CTTTCTCCGGG	0.582	
+	2	521	p.V107A|ARID3B_	NM_006465	NP_006456	Q8IVW6	ARI3B_HUMAN		0	TGAAGTTGCAG	0.517	
-	4	562	_p.D38N|CIB2_uc	NM_006383	NP_006374	O75838	CIB2_HUMAN	EF-hand 1.	0	ACCATCCTCGG	0.532	
+	4	1973	592_uc010upb.1_	NM_014630	NP_055445	Q92610	ZN592_HUMAN		6	GAAAAAGGCTG	0.572	
+	10	1242	_p.P119S|AGBL1_	NM_152336	NP_689549	Q96MI9	CBPC4_HUMAN		0	AAAATCCTGGA	0.478	
-	7	956		NM_000326	NP_000317	P12271	RLBP1_HUMAN	CRAL-TRIO.	1	TTGAGTTTCCTC	0.468	
-	4	490	5orf38_uc002bou.	NM_182616	NP_872422	P59780	AP3S2_HUMAN		0	CGGGCGTGAGC	0.632	
+	7	1670	3A1_uc010boc.1_	NM_013272	NP_037404	Q9UIG8	SO3A1_HUMAN	r (Potential).|Kazal-like.	1	CAGATGGCATCA	0.463	
-	7	2054	q.1_Missense_Mu	NM_003502	NP_003493	O15169	AXIN1_HUMAN	F111.|Interaction with PPP	2	TCTCCGCATCC	0.617	
-	3	299	q.2_Missense_Mu	NM_001037125	NP_001032202	Q9H9P5	UNKL_HUMAN	3H1-type 1.	0	TAGGGACACCT	0.607	
+	4	682	PK8IP3_uc002cm	NM_015133	NP_055948	Q9UPT6	JIP3_HUMAN		3	AGGTCGGAGGA	0.393	
-	27	9714	_Mutation_p.R316	NM_001009944	NP_001009944	P98161	PKD1_HUMAN	toplasmic (Potential).	3	GATCCGGAAGA	0.657	
-	4	581	cpi.1_Missense_	NM_182563	NP_872369	Q6PL45	CP079_HUMAN	BRICHOS.	1	TCTCCCGATCA	0.692	
-	2	353	2ctw.1_Intron|ZSC	NM_032805	NP_116194	Q96SZ4	ZSC10_HUMAN		1	TGCACGGGGAC	0.562	
-	15	3134	vw.2_Missense_	NM_004380	NP_004371	Q92793	CBP_HUMAN		127	CCACCGAGGAG	0.532	
-	10	1198	e_Mutation_p.D30	NM_144605	NP_653206	Q8IYM1	SEP12_HUMAN		1	AGAATCGTCATG	0.662	
+	8	799_800	g.2_Missense_Mu	NM_000246	NP_000237	P33076	C2TA_HUMAN		1	AATCTCCCTGAG	0.515	
+	10	1143	ch.2_Missense_M	NM_014048	NP_054767	Q9ULH7	MKL2_HUMAN		5	GCCTGCTCCAG	0.527	
+	29	4325	l.2_Missense_Mu	NM_004996	NP_004987	P33527	MRP1_HUMAN	porter 2.|Cytoplasmic.	4	GTTCCCTCCGA	0.552	

-	1	397		NM_015092	NP_055907	Q96Q15	SMG1_HUMAN	with SMG8 and SMG9.	16	cgccgctgcTCAGC	0.627	
-	19	2803		NM_017539	NP_060009	Q8TD57	DYH3_HUMAN	n (By similarity).	18	ACTTATCGATCTT	0.488	
+	4	2011		NM_006539	NP_006530	O60359	CCG3_HUMAN		0	GGGACCCCTCA	0.567	
+	2	1372		NM_006040	NP_006031	Q9Y661	HS3S4_HUMAN	enal (Potential).	2	TGCTTCCTGGA	0.542	
+	2	1001	on|APOB48R_uc0	NM_018690	NP_061160	Q0VD83	APOBR_HUMAN	Glu-rich.	0	GGACAGCCTCG	0.716	
-	2	390	dxs.2_Missense_	NM_006110	NP_006101	O95400	CD2B2_HUMAN		1	CCAAAGAGTGT	0.522	
+	3	499	BXL19_uc002eaa.	NM_001099784	NP_001093254	Q6PCT2	FXL19_HUMAN	PHD-type.	4	GGAGTGTACAA	0.607	
+	4	749	1_uc002ebo.2_5'	NM_001008274	NP_001008275	Q6ZMU5	TRI72_HUMAN		0	TGGGGGAGCAG	0.667	
+	4	2173		NM_003414	NP_003405	Q14586	ZN267_HUMAN		4	TCATACTGGAG	0.453	
+	4	2329		NM_003414	NP_003405	Q14586	ZN267_HUMAN	2H2-type 14.	4	ACATCGGAGAA	0.433	rs146914846
+	2	105		NM_002990	NP_002981	O00626	CCL22_HUMAN		0	ACATGGAAGAC	0.642	
-	29	3000	dh.2_Missense_M	NM_001297	NP_001288	Q14028	CNGB1_HUMAN	(Potential).|cAMP (By simil	4	AGAGCGAAGCC	0.562	
+	10	2799		NM_002428	NP_002419	P51511	MMP15_HUMAN	ellular (Pot p.G609R(1)	3	GGACGGGGGCA	0.701	
-	1	525	vjt.1_Missense_M	NM_001082486	NP_001075955	Q96AP0	ACD_HUMAN		1	TCCTCGGAAGA	0.741	
-	62	10515		NM_032821	NP_116210	Q4G0P3	HYDIN_HUMAN		2	CACGAGGCCTC	0.562	
-	3	645	gq.2_Nonsense_	NM_018124	NP_060594	Q6PCD5	RFWD3_HUMAN		3	TCACCTGAAAGT	0.413	
+	6	897	.R146Q|CNTNAP	NM_033401	NP_207837	Q9C0A0	CNTP4_HUMAN	(Potential).|F5/8 type C.	2	AATGCGAATCG	0.408	
+	11	1818	_p.P405L|CNTNA	NM_033401	NP_207837	Q9C0A0	CNTP4_HUMAN	otential).|Laminin G-like 2.	2	TGCTCCTCTGC	0.478	
-	2	579		NM_003791	NP_003782	Q14703	MBTP1_HUMAN		2	TTCTTTTCCAGT	0.453	
+	12	1170	hy.2_Missense_M	NM_014861	NP_055676	O75185	AT2C2_HUMAN	ellular (Potential).	2	GTCATCGTGAAG	0.582	
-	6	1001		NM_002558	NP_002549	P51575	P2RX1_HUMAN	ellular (Potential).	2	TGAAAAGAGTG	0.622	
-	3	515	O1_uc010vsi.1_3'	NM_182566	NP_872372	Q7Z5L0	VMO1_HUMAN		1	ACAGCGGAAGC	0.657	
-	5	979	c002gcb.2_Misse	NM_020162	NP_064547	Q9H6R0	DHX33_HUMAN	case C-terminal.	2	ACAGAGGAAGG	0.607	
+	9	1391	1_splice|DNAH2_	NM_020877	NP_065928	Q9P225	DYH2_HUMAN		13	GTGCAGGTTCC	0.592	
+	8	1249	f.2_Missense_Mu	NM_001005273	NP_001005273	Q12873	CHD3_HUMAN		1	TGGCCGGGGAG	0.438	
+	24	3931	issense_Mutatio	NM_001005273	NP_001005273	Q12873	CHD3_HUMAN		1	CCATCGCTCGG	0.512	
-	39	5741		NM_003802	NP_003793	Q9UKX3	MYH13_HUMAN	Potential.	6	CCTGCCTCTTG	0.587	
+	27	5721	o.2_Missense_M	NM_001372	NP_001363	Q9NYC9	DYH9_HUMAN	1 (By similarity).	20	TGGGCCGCGCA	0.627	
-	9	2166	nse_Mutation_p.S	NM_006470	NP_006461	O95361	TRI16_HUMAN	B30.2/SPRY.	3	CTTGGAAAGCC	0.512	
-	5	542	2_uc010cpr.2_Intr	NM_001082968	NP_001076437	Q6ZVM7	TM1L2_HUMAN	VHS.	0	TGCTTCGAAAGG	0.512	
+	13	1240_1241	sense_Mutation_p	NM_018242	NP_060712	Q96FL8	S47A1_HUMAN	ical; (Potential).	0	TGTTTCCCACCT	0.431	
+	3	1063		NM_021012	NP_066292	Q14500	IRK12_HUMAN	llular (By similarity).	4	GGGGCCGCACA	0.652	
+	3	1304		NM_021012	NP_066292	Q14500	IRK12_HUMAN	smic (By similarity).	4	CAACGCCGTGG	0.612	
-	6	941	p.A182S|PIGS_uc	NM_033198	NP_149975	Q96S52	PIGS_HUMAN	enal (Potential).	4	CTGGGCCACCT	0.587	
-	21	3315	2_5'Flank|ALDOC_	NM_006461	NP_006452	Q96R06	SPAG5_HUMAN	Potential.	1	GGTAAGGTGGG	0.542	
-	2	277	_p.G28E|SEZ6_uc	NM_178860	NP_849191	Q53EL9	SEZ6_HUMAN	ellular (Potential).	2	CTTTCCCCACG	0.582	
-	10	814	t.2_Missense_Mu	NM_018428	NP_060898	Q9NYH9	UTP6_HUMAN		1	CAATCGAAAGC	0.333	rs146623373
-	10	1686	w.1_RNA|MMP28_	NM_024302	NP_077278	Q9H239	MMP28_HUMAN	mopexin-like 4.	1	TGATGGAGCCA	0.677	
-	20	2875	v.2_Intron|MYO19	NM_001163735	NP_001157207	Q96H55	MYO19_HUMAN	osin head-like.	1	TCTGCGCCTGG	0.587	
+	7	1368	_p.S358F|CASC3_	NM_007359	NP_031385	O15234	CASC3_HUMAN		1	GACTTCTGTGA	0.572	
-	1	393		NM_033059	NP_149048	Q9BYQ6	KR411_HUMAN	GIKRQVHEL]- [SPTR]-[ST	0	tgcagcagctggaca	0.129	
+	1	235_236		NM_031961	NP_114167	Q9BYQ4	KRA92_HUMAN	-C-[RQVSGE]-[SPTQ]- [T	1	TGCTGCCAGCC	0.644	
-	1	115		NM_002278	NP_002269	Q14532	K1H2_HUMAN	Head.	0	CGGGGGCAGC	0.612	
+	1	450	586_uc002ibx.2_	NR_002773					0	CCAAGGCTGCA	0.657	
+	3	312	HX8_uc010wig.1_	NM_004941	NP_004932	Q14562	DHX8_HUMAN		4	AGGATTCTCTTA	0.433	
-	2	639		NM_025237	NP_079513	Q9BQB4	SOST_HUMAN		0	GGCGCGGGGCC	0.552	
+	5	811	e_Mutation_p.E21	NM_032133	NP_115509	Q8TBZ2	MYBPP_HUMAN		6	CTGCTGAAGGA	0.522	

+	6	657		NM_153228	NP_694960	Q8N957	ANKF1_HUMAN	Potential.		2	GCCTGGAAAGC	0.468	
-	1	520	M25_uc010dcj.2_5'	NM_005082	NP_005073	Q14258	TRI25_HUMAN			3	GCGGCGCAACA	0.632	
-	20	4470	.P1140L|BZRAP1	NM_004758	NP_004749	O95153	RIMB1_HUMAN			3	AGGCCGGACAG	0.677	rs142431736
+	3	735	I1E_uc010ddd.2_I	NM_014906	NP_055721	Q8WY54	PPM1E_HUMAN			5	GGCCCGTTCTG	0.468	
+	6	504	nse_Mutation_p.P	NM_001099432	NP_001092902	Q9H6U6	BCAS3_HUMAN			5	TGCTCCACAGT	0.413	
-	10	785	10woz.1_RNA|uc010wpb.1_5'Flank							0	GCTGTGAAATC	0.572	
-	11	1291		NM_001433	NP_001424	O75460	ERN1_HUMAN	enal (Potential).		9	AATCAGCAGGA	0.393	
+	11	4553	.2_Nonsense_Mu	NM_182641	NP_872579	Q12830	BPTF_HUMAN			4	ACTACCGAGAT	0.423	
-	13	1959	_p.D594N|ABCA8_	NM_007168	NP_009099	O94911	ABCA8_HUMAN	C transporter 1.		3	CTTTATCCACTT	0.333	
-	30	4441	e_Mutation_p.P1	NM_080282	NP_525021	Q8WWZ4	ABCAA_HUMAN			4	GTTTGGAGCAG	0.423	
-	2	994	ro.1_Missense_M	NM_173477	NP_775748	Q495M9	USH1G_HUMAN			2	GAGCGGGGCTC	0.706	
-	7	1224_1225	wtb.1_Missense_	NM_002766	NP_002757	Q14558	KPRA_HUMAN			1	TACATGGCAACT	0.347	
+	3	924		NM_178543	NP_848638	Q6UWV6	ENPP7_HUMAN			3	TCAAGGACGCC	0.597	
+	4	3302		NM_020914	NP_065965	Q9HCF4	ALO17_HUMAN			21	GGCTTCGTGAC	0.507	
+	10	1951	p.W197*|RPTOR_	NM_020761	NP_065812	Q8N122	RPTOR_HUMAN			6	GCCTGGGACCT	0.612	
-	11	1022	_p.F288I|L3MBTL	NM_173464	NP_775735	Q8NA19	LMBL4_HUMAN	MBT 3.		3	TTTTAAAAACTTT	0.323	
+	14	1612	76_splice|ARHGAP28_uc002kne.2_Splice_Site_p.M47			B4DXL2	B4DXL2_HUMAN			1	GAATGGTAAGA	0.284	
-	58	8363	l.2_Missense_Mut	NM_005559	NP_005550	P25391	LAMA1_HUMAN	minin G-like 4.		21	TCTGATGAGCCA	0.552	
+	3	748	dkv.2_Missense_	NM_002845	NP_002836	P28827	PTPRM_HUMAN	tracellular (Potential).		6	GAGAGCCCACC	0.458	
-	9	1299	vi.3_Missense_Mu	NM_001941	NP_001932	Q14574	DSC3_HUMAN	|Extracellular (Potential).		4	TTAAATCCTTATC	0.308	
-	8	1452	vk.3_Missense_M	NM_024422	NP_077740	Q02487	DSC2_HUMAN	(Potential).|Cadherin 2.		3	GACCAAAATAC	0.313	
+	8	1077		NM_001942	NP_001933	Q02413	DSG1_HUMAN	(Potential).|Cadherin 3.		7	TGCTCGAGATT	0.328	
+	12	1937	vr.2_Missense_Mu	NM_177986	NP_817123	Q86SJ6	DSG4_HUMAN	ellular (Pot	p.A601V(1)	8	TGCCGCGGGC	0.507	
+	14	2281	uc002kwv.3_Intro	NM_001943	NP_001934	Q14126	DSG2_HUMAN	lasmic (Potential).		9	GAAAGGAAGTA	0.512	
+	11	1436	q.2_Missense_M	NM_030632	NP_085135	Q9C0F0	ASXL3_HUMAN			3	AGACTAGTATC	0.393	
+	11	1914	q.2_Missense_M	NM_030632	NP_085135	Q9C0F0	ASXL3_HUMAN	Ser-rich.		3	AGAGGGAGCCT	0.483	
-	1	1111	AL2_uc002lco.2_	NM_145653	NP_663628	Q8NG57	ELOA3_HUMAN			0	GGGAGGTCATG	0.617	
-	27	3827	ea.2_Missense_M	NM_001080467	NP_001073936	Q9ULV0	MYO5B_HUMAN	Potential.		5	GTTCCGCCTGC	0.498	
+	13	2601	_p.E520K|DCC_uc	NM_005215	NP_005206	P43146	DCC_HUMAN	tential).|Fibronectin type-III		17	AGATGGAAACA	0.428	
-	8	1009	_p.R304*|FECH_u	NM_000140	NP_000131	P22830	HEMH_HUMAN			1	CAGTCGGTAGG	0.493	
+	16	2225		NM_194449	NP_919431	O60346	PHLP1_HUMAN	PP2C-like.		0	TGTCGGTGAAT	0.537	
+	7	1010		NM_152721	NP_689934	Q6PKX4	DOK6_HUMAN			3	TCACTCGTCAG	0.438	
+	21	2439	.1_Nonsense_Mut	NM_198531	NP_940933	O43861	ATP9B_HUMAN	lasmic (Potential).		3	CATTTCGAAGG	0.473	rs147932692
+	13	1834	sb.1_Missense_M	NM_019112	NP_061985	Q8IZY2	ABCA7_HUMAN	llular (By similarity).		9	CCTATCCGTGC	0.697	
+	27	4496	c.1_Missense_Mu	NM_032482	NP_115871	Q8TEK3	DOT1L_HUMAN			4	CGGCTCCGTGG	0.726	
-	3	259	lvj.1_Missense_M	NM_144616	NP_653217	Q96MG2	JSPR1_HUMAN	with CACNA1S (By simila		1	CTGGGGTCCCC	0.612	
+	4	1262	a.1_Missense_M	NM_173480	NP_775751	Q68EA5	ZNF57_HUMAN	2H2-type 8.		3	GGAAAGCCTTC	0.443	
+	4	1322	a.1_Missense_M	NM_173480	NP_775751	Q68EA5	ZNF57_HUMAN	2H2-type 9.		3	CAGCTCTATAAA	0.438	
+	4	1490	a.1_Missense_M	NM_173480	NP_775751	Q68EA5	ZNF57_HUMAN	2H2-type 11.		3	CAGCTCCATAAA	0.443	
-	16	1764	02_splice|TLE2_u	NM_003260	NP_003251	Q04725	TLE2_HUMAN			0	CGGTTCTGGGG	0.617	
-	3	1937	l4_uc010dub.1_5'	NM_001080400	NP_001073869	Q96Q06	PLIN4_HUMAN	roximate tandem repeat.|1		0	CTGTCGCGATA	0.572	
-	9	1050		NM_000064	NP_000055	P01024	CO3_HUMAN			5	GATGACGGTGG	0.612	
+	14	1733	_p.F513L|EMR1_	NM_001974	NP_001965	Q14246	EMR1_HUMAN	lar (Potential).|Ser/Thr-rich		5	TCCTTTGGCTG	0.443	
-	40	9365_3936	16_uc010dwj.2_	NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN			57	ACACTGGAGTT	0.515	
-	3	28000		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	h.|Extracellular (Potential)		57	TGTGAGAACAT	0.468	
-	3	19028		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).		57	GAGGTGAACGA	0.488	
-	3	15362		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).		57	TCAGGGAAGGT	0.478	

-	10	1817	wr.1_Missense_M	NM_152476	NP_689689	Q96MR9	ZN560_HUMAN	C2H2-type 7.		6	TGAGTTCGCATG	0.408	
-	6	1212	_p.P267L|ZNF561	NM_152289	NP_689502	Q8N587	ZN561_HUMAN			1	TCATAGGGTTTTA	0.418	
-	29	2307		NM_015719	NP_056534	P25940	CO5A3_HUMAN	le-helical region.		10	CCACATCGCCCT	0.627	
-	1	204	ense_Mutation_p.R	NM_007065	NP_008996	Q16543	CDC37_HUMAN			0	GCCAGCGGAAGA	0.632	
-	2	613	nor.1_Missense_M	NM_012289	NP_036421	Q14145	KEAP1_HUMAN			17	GTGGAGGACAC	0.582	
+	4	539	e_Mutation_p.R43	NM_022737	NP_073574	Q96GM1	LPPR2_HUMAN			1	GCCAGCCGAGTG	0.627	
-	6	1455		NM_138783	NP_620138	Q96CK0	ZN653_HUMAN	C2H2-type 1.		0	GCAGTGGAACAT	0.692	
+	4	719		NM_152357	NP_689570	Q8IYI8	ZN440_HUMAN	C2H2-type 2.		0	GTGTTCGAAGACA	0.393	
+	4	1515	ym.1_Missense_M	NM_001136501	NP_001129973	Q08AG5	ZN844_HUMAN			0	CCTTCAGATCTG	0.423	
+	4	1710	ym.1_Missense_M	NM_001136501	NP_001129973	Q08AG5	ZN844_HUMAN			0	TGCATGAAAGGA	0.413	
+	5	1472	xpn.1_Intron|ANK	NM_152363	NP_689576	Q8NAG6	ANKL1_HUMAN	LEM.		0	TTGCTCCTGGTTA	0.572	
-	11	1540		NM_001080421	NP_001073890	Q9UPW8	UN13A_HUMAN			3	TCTCCTCGTCCTT	0.667	
+	7	1236	hu.2_Missense_M	NM_015683	NP_056498	Q8TBH0	ARRD2_HUMAN			1	CAGGACCCCGAC	0.632	
+	4	1046		NM_031218	NP_112495	P35789	ZNF93_HUMAN			1	AGAAGCCCTACG	0.373	
-	4	1649	pc.1_Missense_M	NM_001076675	NP_001070143	Q68DY1	ZN626_HUMAN	ype 12; degenerate.		1	ATTCTCTCATGTG	0.398	rs71332197
-	4	916	1_Intron|ZNF208_	NM_007153	NP_009084					7	TTGTAGGATTTCT	0.358	
-	4	1136	_p.H263Y|ZNF681_	NM_138286	NP_612143	Q96N22	ZN681_HUMAN	type 6; degenerate.		0	CAGTATGAATTAT	0.388	
+	17	1926	Y19L3_uc002nti.1	NM_207325	NP_997208	Q6ZPD9	D19L3_HUMAN			4	TGGCCGGAGTC	0.537	
+	6	946		NM_032346	NP_115722	Q9BRP1	PDD2L_HUMAN			1	TGCCAGCACTG	0.433	rs141281403
-	2	784	z.1_5'Flank|LGI4_	NM_139284	NP_644813	Q8N135	LGI4_HUMAN	LRR 1.		1	GGTGACTCCCG	0.607	
+	15	2322	651F|KIRREL2_uc	NM_199180	NP_954649	Q6UWL6	KIRR2_HUMAN	lasmic (Pote	p.L704L(1)	3	CCGCGTCTCCAG	0.562	
+	14	1768	_p.E545K|APLP1_u	NM_005166	NP_005157	P51693	APLP1_HUMAN	cellular (Potential).		2	CCGCTGGAACAG	0.338	
+	11	1232	iu.2_Missense_Mu	NM_000540	NP_000531	P21817	RYR1_HUMAN	oplasmic.|MIR 5.		12	CTGCGGCTCGGC	0.393	
-	3	459	xuj.1_Missense_M	NM_006149	NP_006140	P56470	LEG4_HUMAN	Galectin 1.		2	CACTTCCCGCCC	0.582	
-	8	657	_p.R133C|SIRT2_u	NM_012237	NP_036369	Q8IXJ6	SIRT2_HUMAN	etylase sirtuin-type.		0	GCAGGCGCATGA	0.582	
+	3	194		NM_013268	NP_037400	Q9UHV8	PP13_HUMAN	Galectin.		1	ATTGCCTTCCGTT	0.512	
-	7	3507	e_Mutation_p.R94	NM_181882	NP_870998	Q9BXM0	PRAX_HUMAN			2	TGGCACGATCAC	0.632	
-	7	2893	e_Mutation_p.K73	NM_181882	NP_870998	Q9BXM0	PRAX_HUMAN			2	CCATTTTAGCGG	0.627	
+	9	1159	MRTC2_uc010xwe.	NM_001040283	NP_001035373	Q8IXT2	DMRTD_HUMAN			0	TGGCCGTCTGG	0.572	
-	3	1701	_uc002ots.1_Misse	NM_005357	NP_005348	Q05469	LIPS_HUMAN			2	GCAGGCGTGAAC	0.607	rs143861703
-	5	1174	j.3_Missense_Mu	NM_182707	NP_874366	Q9UQ74	PSG8_HUMAN	like C2-type 3.		0	GGTGGGTTAGAG	0.463	
-	2	191	se_Mutation_p.W34*|PSG11_uc002ovm.1_Nonsense_			Q00889	PSG6_HUMAN			2	CAAGTTCCAGAA	0.483	
-	2	496	se_Mutation_p.G1	NM_002780	NP_002771	Q00888	PSG4_HUMAN	g-like V-type.		1	CTCCTCCAGTCC	0.498	
-	2	231		NM_145296	NP_660339	Q8NFZ8	CADM4_HUMAN	.|Extracellular (Potential).		0	GTCTGCCGGGCT	0.453	
-	4	1867		NM_145056	NP_659493	Q96B18	DACT3_HUMAN			0	TGGCGGGGCCT	0.622	
+	5	951		NM_031485	NP_113673	Q9BQ67	GRWD1_HUMAN	WD 1.		1	AACATCCACCTCT	0.642	
-	9	914		NM_001080434	NP_001073903					6	AGGTCAGAGGTC	0.687	
-	1	166		NM_178449	NP_848544	Q96A98	TIP39_HUMAN			0	ACCACcagcagca	0.597	
+	8	1029	V1_uc002pqa.2_R	NM_017432	NP_059128	Q86YD1	PTOV1_HUMAN	ction with FLOT1.		0	GTCTACGTGAAC	0.657	
+	5	2407	_p.H724Y|ZNF473_	NM_001006656	NP_001006657	Q8WTR7	ZN473_HUMAN	C2H2-type 15.		2	AGAATTCACTCA	0.512	
-	22	3585	sw.1_Missense_M	NM_016148	NP_057232	Q9Y566	SHAN1_HUMAN	Poly-Gly.		2	CCGCCTCCCGTG	0.473	
+	5	782		NM_007147	NP_009078	Q9Y473	ZN175_HUMAN			0	CCATTTTAGAAGA	0.393	
-	5	2254	ydj.1_Missense_M	NM_001102657	NP_001096127	Q6ZNA1	ZN836_HUMAN	C2H2-type 15.		0	TTATGATTTGAAA	0.408	
-	5	2235	ydj.1_Missense_M	NM_001102657	NP_001096127	Q6ZNA1	ZN836_HUMAN	C2H2-type 15.		0	CACTGTCATTGAA	0.423	
-	4	2233_2234	p.N652S|ZNF28_u	NM_006969	NP_008900	P17035	ZNF28_HUMAN	C2H2-type 18.		1	CAAGGTTTGACA	0.406	
-	5	411	qbg.1_Missense_M	NM_182609	NP_872415	Q86XU0	ZN677_HUMAN	KRAB.		1	TATAATTCCTCTTT	0.348	
+	4	1553	dw.1_Missense_M	NM_138374	NP_612383	Q96IR2	ZN845_HUMAN	C2H2-type 10.		0	GTCAGACATCAT	0.378	

+	7	1834	_p.R405L|ZNF761_	NM_001008401	NP_001008401	Q86XN6	ZN761_HUMAN	2H2-type 9.	1	TAGACGTCATA	0.393	
+	7	1848	_p.Q410K|ZNF761_	NM_001008401	NP_001008401	Q86XN6	ZN761_HUMAN		1	GAGAGCAACC	0.393	rs146851069
+	1	73		NM_001012728	NP_001012746	A6NFQ7	DPRX_HUMAN		0	GATCTTCGTAAA	0.507	rs148896232
-	4	1217	p.E381K|NLRP7_	NM_206828	NP_996611	Q8WX94	NALP7_HUMAN	NACHT.	3	GTCCTCCCCC	0.687	
+	5	2459	_p.F604L|NLRP4_	NM_134444	NP_604393	Q96MN2	NALP4_HUMAN		15	TCCTTTTCTGG	0.428	
+	3	1043	tg.2_Missense_M	NM_176811	NP_789781	Q86W28	NALP8_HUMAN	NACHT.	13	ACGATGCTTCC	0.502	
-	7	4528	.E1364K|PEG3_uc	NM_001146186	NP_001139658	Q9GZU2	PEG3_HUMAN	Glu-rich.	12	AGCCTCTACG	0.478	
-	7	2577	_p.E713D|PEG3_	NM_001146186	NP_001139658	Q9GZU2	PEG3_HUMAN		12	TCACTTTCAAG	0.408	
+	5	1421	nse_Mutation_p.T	NM_024691	NP_078967	Q96HQ0	ZN419_HUMAN		0	TCACACTGGAG	0.433	
+	5	1461	nse_Mutation_p.F	NM_024691	NP_078967	Q96HQ0	ZN419_HUMAN	2H2-type 8.	0	GAGATTCTTTAG	0.423	
-	7	1679	hp.1_Missense_M	NM_025027	NP_079303	Q8WXB4	ZN606_HUMAN		2	AAATAAAAGATA	0.338	
+	3	1281	.R359C|TTC15_u	NM_016030	NP_057114	Q8WVT3	TTC15_HUMAN		4	TGCTTCGCTTT	0.393	
+	22	4093	p.1_Missense_M	NM_014668	NP_055483	Q4ZG55	GREB1_HUMAN		1	AGCTCGTGTAC	0.672	
+	5	688	sense_Mutation_p	NM_181713	NP_859064	P68543	UBX2A_HUMAN	SEP.	0	TCACCGTCAAC	0.323	rs13386425
+	2	383	BL5_uc002rid.2_	NM_021831	NP_068603	Q8NDL9	CBPC5_HUMAN		2	TCAACGTGTGG	0.527	
+	5	946	mm.1_Missense_	NM_199280	NP_954974	Q6ZUX3	F179A_HUMAN		4	TACCGGGGAGC	0.622	
-	9	1095	np.1_Missense_M	NM_144575	NP_653176	Q6MZZ7	CAN13_HUMAN	lpain catalytic.	2	CCGTTTCTTAT	0.443	
-	29	2238	p.F695Y|MAP4K3_	NM_003618	NP_003609	Q8IVH8	M4K3_HUMAN	CNH.	8	ATAGGAAAATCT	0.333	
-	16	2591	D2_uc002sha.2_	NM_001617	NP_001608	P35612	ADDB_HUMAN	ith calmodulin (Potential).	3	GTTCGGAATTTC	0.527	
-	3	472	DD2_uc010fdt.1_	NM_001617	NP_001608	P35612	ADDB_HUMAN		3	TCTCTTCGCTCA	0.617	
-	3	1245	2sit.3_Missense_	NM_015470	NP_056285	Q9BXF6	RFIP5_HUMAN		0	AGAGCGAAGAG	0.622	
+	4	399	e_Mutation_p.G1	NM_198448	NP_940850	Q6UW15	REG3G_HUMAN	-type lectin.	0	GATTGGGCTCC	0.562	
-	2	782	OLN2_uc002spb.	NM_006464	NP_006455	O43493	TGON2_HUMAN	l).|8.|14 X 14 AA tandem r	0	GCTAGGGCTGT	0.597	
-	2	777	OLN2_uc002spb.	NM_006464	NP_006455	O43493	TGON2_HUMAN	l).|8.|14 X 14 AA tandem r	0	GGCTGTCTTTT	0.592	
-	1	292	lank|ELMOD3_uc	NM_017750	NP_060220	Q6NUM9	RETST_HUMAN		2	CTTCGGAGAAA	0.597	
+	21	1829	_Mutation_p.R178	NM_017952	NP_060422	Q96EY7	PTCD3_HUMAN	PPR 10.	1	TGGGAGAACTC	0.448	
+	6	705	.1_Intron|SMYD1_	NM_198274	NP_938015	Q8NB12	SMYD1_HUMAN	SET.	4	GAATTGAGCTC	0.502	
+	5	534	uq.2_Missense_M	NM_013434	NP_038462	Q9Y2W7	CSEN_HUMAN	EF-hand 2.	3	TGATGCGGACG	0.622	
-	14	2381_2382	.G716S|AFF3_uc	NM_002285	NP_002276	P51826	AFF3_HUMAN		6	ACTGCCCCCGTT	0.624	
+	20	2874	e_Mutation_p.G11	NM_182588	NP_872394	Q7Z3J3	RGPD4_HUMAN		2	ACCAGGAAATC	0.408	
+	5	938	LT1C4_uc002teb.	NM_006588	NP_006579	O75897	ST1C4_HUMAN		0	GGGAAGCCAAA	0.463	
-	12	1682	.Q449H|EDAR_uc	NM_022336	NP_071731	Q9UNE0	EDAR_HUMAN	toplasmic (Potential).	1	TCAATCTGCAC	0.572	
+	7	1670		NM_001099289	NP_001092759	Q8TEJ3	SH3R3_HUMAN		1	CAGTGGGAGTC	0.682	
+	4	993_994	2toz.2_Intron|LIM	NM_001161415	NP_001154887	Q13304	GPR17_HUMAN	ellular (Potential).	0	CATTTGGGGAA	0.589	
+	12	1367	_p.G272R|UGGT1_	NM_020120	NP_064505	Q9NYU2	UGGG1_HUMAN		1	TCAATGGACTT	0.328	
+	3	868	SD7B_uc002tvb.2	NM_001080427	NP_001073896				7	GCCTTCAAGAT	0.443	
+	17	3445	D7B_uc010zbj.1_	NM_001080427	NP_001073896				7	CTGAATGAAAAT	0.453	
-	39	7123		NM_018557	NP_061027	Q9NZR2	LRP1B_HUMAN	ntial).|LDL-receptor class B	50	TATTTTCCTAAAT	0.353	
-	7	1985	1B_uc010fnl.1_In	NM_018557	NP_061027	Q9NZR2	LRP1B_HUMAN		50	TTCTTACCCTGC	0.363	
-	112	16168	.2_Missense_Muta	NM_004543	NP_004534	P20929	NEBU_HUMAN	Nebulin 145.	20	TGACTGCTCGG	0.383	
+	10	1355	m.1_Missense_M	NM_033394	NP_203752	Q9C0D5	TANC1_HUMAN		3	TTGCTCCCTAC	0.333	
-	8	1347	e_Mutation_p.A33	NM_013450	NP_038478	Q9UIF8	BAZ2B_HUMAN		4	CAGACGCAAGA	0.448	
+	7	992	C4A10_uc002uby.	NM_022058	NP_071341	Q6U841	S4A10_HUMAN	lasmic (Potential).	5	TGTGTTGAAAAT	0.373	
-	16	1919	b.2_Missense_Mu	NM_001935	NP_001926	P27487	DPP4_HUMAN	ellular (Potential).	3	GACACCTTTCC	0.458	
+	3	837		NM_006898	NP_008829	P31249	HXD3_HUMAN	Homeobox.	0	TGTGCCGGCCG	0.592	
-	253	54771	78K|TTN_uc010z	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	ACTTTCCCCAC	0.398	
-	27	4965	TTN_uc010zfj.1_	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	GTTACCCGTAG	0.378	

+	7	995	NAJC10_uc002uoz	NM_018981	NP_061854	Q8IXB1	DJC10_HUMAN	'hioredoxin 1.	4	CTTTGCCGAATGA	0.378	
-	5	708	_p.N152Y|STAT4_u	NM_003151	NP_003142	Q14765	STAT4_HUMAN		9	CACTGTTTTTAAT	0.408	
-	17	2465	e_Mutation_p.P43	NM_173076	NP_775099	Q86UK0	ABCAC_HUMAN		11	CTTTTGGCCTCTC	0.383	
+	10	1828	ense_Mutation_p.F	NM_018089	NP_060559	Q9H8Y5	ANKZ1_HUMAN	ANK 2.	2	GTGGTTCGTCTG	0.542	
+	32	2737	utation_p.G859R|C	NM_000091	NP_000082	Q01955	CO4A3_HUMAN	le-helical region.	3	TCACCAGGAATTC	0.483	
+	46	4279	tation_p.G1373R|	NM_000091	NP_000082	Q01955	CO4A3_HUMAN	le-helical region.	3	ATGCAGGGAGAA	0.542	
-	12	5064	e_Mutation_p.H164	NM_001142644	NP_001136116	Q2M3C7	SPKAP_HUMAN		10	CTGCATGGAAGA	0.483	
-	4	812	nse_Mutation_p.G	NM_152527	NP_689740	Q7RTX9	MOT14_HUMAN	cellular (Potential).	6	TACCTGCCCACC	0.612	
-	10	1429	mt.1_Missense_Mu	NM_018218	NP_060688	Q9NVE5	UBP40_HUMAN		3	GCTGTTCAATATC	0.413	
+	4	335	ense_Mutation_p.F	NM_024080	NP_076985	Q7Z2W7	TRPM8_HUMAN	lasmic (Potential).	4	GAATTTCCTACCC	0.468	
+	14	1790	0fyj.2_Splice_Site_	NM_024080	NP_076985	Q7Z2W7	TRPM8_HUMAN		4	TAAAAGACCAGC	0.358	
+	14	1857	_p.P424S|MLPH_u	NM_024101	NP_077006	Q9BV36	MELPH_HUMAN		1	GCTGTGCCCTAT	0.468	
+	17	2055	2vyf.2_Missense_N	NM_015650	NP_056465	Q8TDR0	MIPT3_HUMAN	SC1-interaction domain.	1	GAGCCCTTAAAG	0.478	
-	3	1535_1536	vbs.2_Missense_M	NM_015963	NP_057047	Q8WY91	THAP4_HUMAN		0	CGGCTCCAGGTC	0.594	
-	2	432	_p.R123*|SIRPG_u	NM_018556	NP_061026	Q9P1W8	SIRPG_HUMAN	(Potential).|Ig-like V-type.	1	CTTTTCGAAACTT	0.498	
+	11	1746	al.1_Missense_Mu	NM_198994	NP_945345	O95932	TGM3L_HUMAN		4	AGAAGAGAATCC	0.448	rs148419172
+	1	621	Mutation_p.L27F|E	NM_014962	NP_055777	Q9Y2F9	BTBD3_HUMAN		3	CAGAATCTCAGT	0.473	
-	2	497		NM_001008693	NP_001008693	Q5W186	CST9_HUMAN		1	GAGGAAAGCTGA	0.527	
+	1	58	j.1_Intron|FRG1B_uc010gdr.1_Intron|FRG1B_uc010ztk.1_Intron						0	TTCCAGGTGAGC	0.289	rs75468660
+	2	78	tj.1_RNA|FRG1B_uc010gdr.1_RNA|FRG1B_uc010ztk.1_Intron						0	TCTGGCTATGGA	0.348	
+	12	3229	eb.2_Missense_Mu	NM_015338	NP_056153	Q8IXJ9	ASXL1_HUMAN		248	CTGCTCCCACC	0.542	
+	9	1675	2T2_uc002wzf.1_R	NM_005093	NP_005084	O43439	MTG8R_HUMAN		2	TCAGATCGTGAA	0.532	
-	8	930	c002xdu.1_Missen	NM_021100	NP_066923	Q9Y697	NFS1_HUMAN		2	ATACCCCGCTCC	0.617	
+	4	545	0ggc.2_Missense_	NM_015568	NP_056383	Q96T49	PP16B_HUMAN	ANK 1.	3	GAAGCTGCTCC	0.597	
+	7	815	gy.2_Missense_Mu	NM_006282	NP_006273	Q13043	STK4_HUMAN	'rotein kinase.	2	CTCCTCCCACATT	0.393	
+	2	1081	G2_uc010ggz.2_Ir	NM_003007	NP_002998	P04279	SEMG1_HUMAN	3 AA repeat 2.	2	AGCCAAAAGGCA	0.393	
-	4	592	UTR|SYS1-DBNDI	NM_014477	NP_055292	Q9Y2B4	T53G5_HUMAN		1	GGACTCCAGGGT	0.537	
+	2	1629	zxg.1_Missense_M	NM_080752	NP_542790	Q96MP5	ZSWM3_HUMAN		2	CAGACGCACAG	0.577	rs139419541
+	22	2975	xrb.2_Missense_M	NM_001134771	NP_001128243	Q9H2X9	S12A5_HUMAN	lasmic (Potential).	5	GGAGAAAGAATC	0.572	
+	36	5049	0zyf.1_Missense_M	NM_006420	NP_006411	Q9Y6D5	BIG2_HUMAN		4	ATTACGAGCAGC	0.473	
+	2	405		NM_005985	NP_005976	O95863	SNAI1_HUMAN		1	CTTCGTCCTTCTC	0.642	
-	2	1981	2_Intron|SALL4_u	NM_020436	NP_065169	Q9UJQ4	SALL4_HUMAN	C2H2-type 5.	2	GGCACGAATGC	0.522	
+	4	950	0zzi.1_Missense_M	NM_003222	NP_003213	Q92754	AP2C_HUMAN		1	TCAGCTCTACGT	0.532	
-	74	10328		NM_005560	NP_005551	O15230	LAMA5_HUMAN	minin G-like 4.	3	AGGCCGGGAGC	0.697	
-	16	5737	s.1_Missense_Mu	NM_033081	NP_149072	Q9BTC0	DIDO1_HUMAN	Pro-rich.	6	GGGGCCTCTGC	0.617	
+	2	207	2yim.3_Missense_	NM_018257	NP_060727	Q9NV79	PCMD2_HUMAN		0	TGGGCGGTGCT	0.378	
+	2	295	2yim.3_Missense_N	NM_018257	NP_060727	Q9NV79	PCMD2_HUMAN		0	GCAGGCTTTCA	0.428	
-	21	1708	PTE_uc002yir.1_Mi	NM_199261	NP_954870	P56180	TPTE_HUMAN	2 tensin-type.	5	CCTAATGAAATAG	0.328	
-	13	1949_1950	p.L186F|C2CD2_u	NM_015500	NP_056315	Q9Y426	CU025_HUMAN		1	GGCAAGGGATGC	0.698	
-	3	2795	vzy.3_Missense_M	NM_001098402	NP_001091872	Q9ULJ3	ZN295_HUMAN		3	AGAGGAATCTTC	0.488	
+	13	1716	_uc002zap.2_Misse	NM_004915	NP_004906	P45844	ABCG1_HUMAN	).|ABC transmembrane type	3	GCTGTTTGCCGC	0.647	
+	9	837	_p.P304L|PCBP3_	NM_020528	NP_065389	P57721	PCBP3_HUMAN		1	CTCACCCGGATC	0.512	
+	26	3278	2A_uc011afz.1_Mi	NM_015151	NP_055966	Q14689	DIP2A_HUMAN		2	CGCGGCTCTGA	0.572	
-	1	529	GT5_uc002zzq.3_M	NM_004121	NP_004112	P36269	GGT5_HUMAN	cellular (Potential).	3	CTGGGGGCCAC	0.657	
-	9	976	n.1_Missense_Mu	NM_014303	NP_055118	O00541	PESC_HUMAN		0	TCGGTGGGAAAC	0.622	
-	8	1094	ISD_uc011alr.1_M	NM_014338	NP_055153	Q9UG56	PISD_HUMAN		3	TGGGGACGCCCT	0.577	
-	4	443	.2_5'UTR|BPIL2_u	NM_174932	NP_777592	Q8NFQ6	BPIL2_HUMAN		2	TCATTTCGGGTT	0.493	rs78469100

+	3	895	ny.2_Missense_M	NM_014310	NP_055125	Q96D21	RHES_HUMAN	GNB1, GNB2 and GNB3.	3	GGCATGGTCTC	0.647	
-	5	1339	ense_Mutation_p.	NM_024955	NP_079231	Q8IWF2	FXRD2_HUMAN		2	GAGCCGGTGAA	0.627	rs143694562
+	7	2024	atq.1_Missense_M	NM_001039141	NP_001034230	Q9H2D6	TARA_HUMAN		1	ACAATCCCAGA	0.587	
-	2	1066	axe.2_Missense_	NM_002608	NP_002599	P01127	PDGFB_HUMAN		373	CCTCGGGAATG	0.597	
+	11	2092	aye.2_Missense_	NM_021096	NP_066919	Q9P0X4	CAC1I_HUMAN	asmic (Potential).|II.	2	TCTTCGACTAC	0.567	
+	5	671	RVG_uc010gzr.1_	NM_001137605	NP_001131077	Q9HBI0	PARVG_HUMAN	CH 1.	0	TATTCCGTAAG	0.562	rs147016590
-	10	1997		NM_012401	NP_036533	O15031	PLXB2_HUMAN	ellular (Potential).	6	GCTCACGCAGG	0.662	
+	1	1017		NM_138433	NP_612442	Q96G42	KLD7B_HUMAN		1	AGGGGGGCCGC	0.756	
+	2	835	sg.2_Missense_M	NM_004634	NP_004625	P55201	BRPF1_HUMAN	ith MYST3 and MYST4.	3	CTACTCCCAAG	0.547	
+	2	357	.1_5'Flank|METTI	NM_033083	NP_149074	Q96JC9	EAF1_HUMAN		1	CACTTCCTGTG	0.373	
-	10	3465	_p.H577L|SATB1_	NM_002971	NP_002962	Q01826	SATB1_HUMAN		4	CGCCATGGTGA	0.483	
+	10	1904	hex.1_Missense_	NM_144633	NP_653234	Q96L42	KCNH8_HUMAN	toplasmic (Potential).	5	AACCTCTTTCT	0.502	
-	8	947	_p.L325V|NEK10_uc010hfj.2_Missense_Mutation_p.L2			Q6ZWH5	NEK10_HUMAN		13	TCTTTAAAATGTC	0.284	
-	16	2074	j.1_Missense_Mut	NM_000404	NP_000395	P16278	BGAL_HUMAN		1	GGAGGGATGAT	0.498	
+	2	256	TAC_uc011aya.1_	NM_003149	NP_003140	Q99469	STAC_HUMAN		4	TGCAAGCACAC	0.537	
-	12	6541		NM_014831	NP_055646	O15050	TRNK1_HUMAN		2	AACAGAGCAGG	0.542	
-	12	6087		NM_014831	NP_055646	O15050	TRNK1_HUMAN		2	GAACCGGAAAT	0.478	
-	18	2668	wf.1_Missense_M	NM_002292	NP_002283	P55268	LAMB2_HUMAN	inin EGF-like 6.	3	TCAGTGAACCT	0.597	
-	17	2316	wp.2_Missense_M	NM_003363	NP_003354	Q13107	UBP4_HUMAN		4	TCCGAGTTTCA	0.512	
+	9	1067	cyk.2_Missense_	NM_004186	NP_004177	Q13275	SEM3F_HUMAN	Sema.	2	GAGCCCCGCGG	0.602	
+	19	2371	cyk.2_Missense_	NM_004186	NP_004177	Q13275	SEM3F_HUMAN		2	CAACGCCTCCT	0.682	
-	6	549	03dap.2_Splice_Si	NM_006030	NP_006021	Q9NY47	CA2D2_HUMAN		1	TCGTCCTGCAG	0.552	
-	5	356	dbg.1_Splice_Site	NM_014703	NP_055518	Q9Y4B6	VPRBP_HUMAN		2	TCGACCTACCAA	0.443	
+	32	5501		NM_015512	NP_056327	Q9P2D7	DYH1_HUMAN	1 (By similarity).	3	CAGCTCCCAGG	0.438	
+	6	655	k.1_Missense_Mu	NM_002217	NP_002208	Q06033	ITIH3_HUMAN		3	CCAACGACCTC	0.532	
-	21	2977	nse_Mutation_p.R	NM_001005159	NP_001005159	Q9UHJ3	SMBT1_HUMAN	SAM.	1	TGAACCGCACA	0.418	
-	11	1264	_p.A83V|LRIG1_uc	NM_015541	NP_056356	Q96JA1	LRIG1_HUMAN	ar (Potential).|LRR 15.	5	TGATCGCATTC	0.433	
+	4	1813	fv.1_Missense_M	NM_032505	NP_115894	Q8NFY9	KBTB8_HUMAN	Kelch 5.	4	TGAATGTGCTG	0.438	
-	14	1392	ense_Mutation_p.	NM_015123	NP_055938	Q9Y2L6	FRM4B_HUMAN		4	TGAAGGAATTT	0.363	
-	17	2325	_p.E668K|FOXP1_	NM_032682	NP_116071	Q9H334	FOXP1_HUMAN		2	CATCTTCGTAAT	0.478	
+	5	1205	pn.2_Missense_	NM_145037	NP_659474	Q969Y0	FA55C_HUMAN		3	TCCACCCCAGT	0.458	
-	36	5224		NM_014981	NP_055796	Q9Y2K3	MYH15_HUMAN	Potential.	7	TTCTTTCTGTTG	0.527	
-	5	564	PA4_uc011bhp.1_	NM_018189	NP_060659	Q7L190	DPPA4_HUMAN		1	GAGGAAGAGCC	0.498	
-	7	3914	eal.2_Missense_	NM_001009899	NP_001009899	Q68DE3	K2018_HUMAN		3	ACAATGATGCTT	0.463	
+	16	5119	RP14_uc003efr.2_	NM_017554	NP_060024	Q460N5	PAR14_HUMAN	ARP catalytic.	6	TGCCGGCTCCG	0.493	
+	2	293		NM_015720	NP_056535	Q9NZ53	PDXL2_HUMAN	ellular (Potential).	2	GTCTCGGATTC	0.582	
-	4	1118	_p.P228L|GATA2_	NM_001145661	NP_001139133	P23769	GATA2_HUMAN		15	GCAGGGGACTG	0.632	
+	22	2922	emq.2_Missense_	NM_052989	NP_443715	Q9HBG6	IF122_HUMAN		2	ATGCCGTGGCG	0.527	
+	2	217	_p.R43W|ACPP_u	NM_001099	NP_001090	P15309	PPAP_HUMAN		1	TGTTTCGGCAT	0.428	
-	11	1801_1802	_p.P434S|SLCO2	NM_005630	NP_005621	Q92959	SO2A1_HUMAN	ellular (Potential).	1	ACAGGGGACAG	0.559	
+	5	1320	31_uc011bly.1_3'U	NM_004441	NP_004432	P54762	EPHB1_HUMAN	tential).|Fibronectin type-III	30	AGACCGCCGGA	0.612	
+	4	1101	p.Y321H|HPS3_u	NM_032383	NP_115759	Q969F9	HPS3_HUMAN		6	CCATTTACCAG	0.478	
-	1	306	_uc003ewz.2_Nor	NM_000096	NP_000087	P00450	CERU_HUMAN		1	TCGCCCAGGCT	0.373	
-	5	1055	e_Mutation_p.N21	NM_033169	NP_149359	O75752	B3GL1_HUMAN	enal (Potential).	1	GGAATAATTATCA	0.353	
-	18	2116	_p.F598Y|ZBBX_u	NM_024687	NP_078963	A8MT70	ZBBX_HUMAN		2	AAAATAAAGAAT	0.308	
+	7	1246	ffb.3_Missense_	NM_001122752	NP_001116224	Q99574	NEUS_HUMAN		1	GCTCAGAAGCT	0.373	
-	9	2292	OM_uc003ffk.2_In	NM_005241	NP_005232	Q03112	EVI1_HUMAN		14	ATCAGGCAGTT	0.313	

-	3	586	_p.P153S|TBCCD	NM_018138	NP_060608	Q9NVR7	TBCC1_HUMAN			2	GTCAGGAGACT	0.408
+	5	852	b.2_Missense_Mu	NM_003722	NP_003713	Q9H3D4	P63_HUMAN			12	TCAACGAGGGT	0.498
-	8	1174		NM_018385	NP_060855	Q9H089	LSG1_HUMAN			0	AGCTGGGAGAT	0.478
-	16	1953	zy.2_Missense_Mu	NM_003234	NP_003225	P02786	TFR1_HUMAN	ellular (Potential).		3	CGCAAAAACAG	0.229
+	3	1280		NM_198565	NP_940967	Q86YC3	LRC33_HUMAN	ar (Potential).|LRR 13.		3	CTGCACCTGGC	0.657
-	22	3227	se_Mutation_p.D1	NM_005255	NP_005246	O14976	GAK_HUMAN			4	GAAGTCGGCGC	0.627
+	9	1412		NM_053044	NP_444272	P83110	HTRA3_HUMAN	PDZ.		1	CATCCAAGATG	0.647
-	3	3536		NM_053042	NP_444270	Q9C0D4	Z518B_HUMAN			4	TTTTATGAACTTT	0.418
-	8	1628	GC1A_uc011bxp.	NM_013261	NP_037393	Q9UBK2	PRGC1_HUMAN			8	AGTCCTGAATTT	0.428
-	13	2324_2325	rv.2_Missense_Mu	NM_015187	NP_056002	Q68CR1	SE1L3_HUMAN	Sel1-like 3.		0	ATCCTCCGTCTC	0.49
+	1	651	.1_Missense_Muta	NM_175737	NP_783864	Q86Z14	KLOTB_HUMAN	ential).|Glycosyl hydrolase-		1	TGCTTAGAAACA	0.413
-	9	1470	p.E390K|KDR_uc	NM_002253	NP_002244	P35968	VGFR2_HUMAN	4.|Extracellular (Potential).		33	TCTTTCACTCA	0.408
+	1	203	n_p.M10I|LPHN3_	NM_015236	NP_056051	Q9HAR2	LPHN3_HUMAN			18	TTCATGATGCTC	0.363
-	8	823		NM_182502	NP_872308	Q86T26	TM11B_HUMAN			1	TTTTCCTAGAGG	0.323
+	4	1524	_p.Q15*|SHROO	NM_020859	NP_065910	Q8TF72	SHRM3_HUMAN			3	GGCACCAAAGC	0.473
+	37	5395	_p.R1652K|FRAS	NM_025074	NP_079350	Q86XX4	FRAS1_HUMAN	xtracellular (Potential).		5	CCGAAGGCCGA	0.493
+	10	1747	u.1_Missense_Mu	NM_001510	NP_001501	O43424	GRID2_HUMAN	ellular (Potential).		6	AATACGGAAGC	0.393
+	1	111		NM_005390	NP_005381	P29803	ODPAT_HUMAN			1	CAGAAATCAGC	0.537
-	9	981		NM_000669	NP_000660	P00326	ADH1G_HUMAN			0	TCTGGGAATCA	0.448
+	5	818	p.G171C|GAR1_u	NM_018983	NP_061856	Q9NY12	GAR1_HUMAN	RGG-box 2.		0	aagaggtggtggcag	0.264
+	7	1536	_p.F320I|EGF_uc	NM_001963	NP_001954	P01133	EGF_HUMAN	g (Potential).|Extracellular		4	TGTGCTTTTTGG	0.398
+	7	776	.V226M|ANK2_uc	NM_001148	NP_001139	Q01484	ANK2_HUMAN			14	TGATGGTGAAT	0.353
+	33	4222	50_splice|ANK2_	NM_001148	NP_001139	Q01484	ANK2_HUMAN			14	TGGAGGTACTG	0.323
-	7	995	ine.2_Missense_M	NM_018699	NP_061169	Q9NQX1	PRDM5_HUMAN	-type 3; atypical.		2	CTCAAAACTAC	0.478
+	7	875	p.E215K|ADAD1_	NM_139243	NP_640336	Q96M93	ADAD1_HUMAN			0	GTTAAAGAAAGA	0.323
+	11	11909	p.G2233E|FAT4_u	NM_024582	NP_078858	Q6V0I7	FAT4_HUMAN	Extracellular (Potential).		18	TCTTTGGAAAAC	0.289
+	10	1337		NM_057175	NP_476516	Q9BXJ9	NAA15_HUMAN			2	TTTAACCCCAAT	0.323
-	7	792	10A7_uc010ipa.2_	NM_001029998	NP_001025169	Q0GE19	NTCP7_HUMAN	ical; (Potential).		0	GAGAGGAACCA	0.353
-	15	3677		NM_017639	NP_060109	Q6V1P9	PCD23_HUMAN	Cadherin 10.		4	CCAAAGGACAG	0.378
-	5	1053	e_Mutation_p.G33	NM_000508	NP_000499	P02671	FIBA_HUMAN	By similarity.		3	AGCTTCCAGTA	0.567
-	2	224		NM_001334	NP_001325	P43234	CATO_HUMAN			0	ACTGGGAAATA	0.333
+	3	1539	qx.1_Missense_Mu	NM_152620	NP_689833	Q495X7	TRI60_HUMAN	B30.2/SPRY.		1	GAACAGATTCC	0.353
-	12	1360	p.D404N|SPOCK3	NM_016950	NP_058646	Q9BQ16	TICN3_HUMAN	Asp-rich.		3	tcataatatcgtcttcatc	0.075
-	11	1737		NM_017631	NP_060101	Q8IY21	DDX60_HUMAN			3	TTATACCTCTTTA	0.348
+	27	3231	0isc.2_Splice_Sit	NM_021942	NP_068761	Q7Z392	CD041_HUMAN			0	TGCAGGTAGCG	0.373
+	6	722		NM_004477	NP_004468	Q14331	FRG1_HUMAN			0	GAAATGATCAA	0.363
-	8	1113	.1_Missense_Muta	NM_023924	NP_076413	Q9H8M2	BRD9_HUMAN			0	GAACCGGTTGA	0.637
-	10	1771	RLR_uc003jjj.1_In	NM_000949	NP_000940	P16471	PRLR_HUMAN	lasmic (Potential).		3	CATGTTGAACAT	0.532
+	3	372	se_Mutation_p.E9	NM_002185	NP_002176	P16871	IL7RA_HUMAN	ellular (Potential).		5	TCATCGAGACA	0.383
+	6	919	jlb.1_Missense_M	NM_152403	NP_689616	Q63HQ2	EGFLA_HUMAN	nectin type-III 2.		7	AGATGGACTCC	0.507
+	5	613	2_Missense_Muta	NM_003432	NP_003423	P52739	ZN131_HUMAN			0	CTTCTGCCAAG	0.463
-	7	1803		NM_021072	NP_066550	O60741	HCN1_HUMAN	lasmic (Potential).		1	CTATTCGATCTA	0.378
+	1	315		NM_006308	NP_006299	Q12988	HSPB3_HUMAN			0	GAGGAAAACCA	0.567
+	9	1617	jvd.2_Missense_M	NM_181523	NP_852664	P27986	P85A_HUMAN	SH2 1.	p.?(1)	101	CAGACGGGACC	0.373
+	5	6732	x.1_Missense_Mu	NM_005909	NP_005900	P46821	MAP1B_HUMAN			5	TCCCCCGGAGA	0.577
+	8	844	CR_uc003kdq.2_	NM_000859	NP_000850	P04035	HMDH_HUMAN			1	AGGGTCGTCCA	0.413
+	2	9180		NM_153610	NP_705838	Q8N3K9	CMYA5_HUMAN			9	TTCAGAAACTGA	0.323

+	1	672	uc011ctk.1_Intron	NM_032567	NP_115956	Q9BXG8	SPZ1_HUMAN		1	AAACAGGAGATG	0.358	
-	7	832	n.1_Missense_Mut	NM_032042	NP_114431	Q8WUF8	F172A_HUMAN		0	TCTTCGGCTTTT	0.328	
+	5	683	81B_uc010jbe.1_5	NM_152548	NP_689761	Q96LP2	FA81B_HUMAN		2	GAGATCTTCGA	0.433	
-	9	1351	jbi.1_Missense_M	NM_000439	NP_000430	P29120	NEC1_HUMAN	Catalytic.	2	AGGCCGAGGTG	0.557	
+	12	1311	bv.2_Missense_M	NM_001744	NP_001735	Q16566	KCC4_HUMAN		5	AGTTAAAGGTGC	0.527	
-	1	371	ense_Mutation_p.	NM_001182	NP_001173	P49419	AL7A1_HUMAN		3	GGCCTCCCCAG	0.652	
+	2	184		NM_207408	NP_997291	Q6ZNM6	CE048_HUMAN		1	AAACATGATATTC	0.303	
+	1	1028	.2_Intron|PCDHA6	NM_018903	NP_061726	Q9UN75	PCDAC_HUMAN	|Extracellular (Potential).	0	ACAGGTGAAATT	0.378	
+	1	1928	.2_Intron|PCDHA6	NM_018903	NP_061726	Q9UN75	PCDAC_HUMAN	|Extracellular (Potential).	0	GCTGACTCCGG	0.677	
+	1	388	uc003lin.2_Intron	NM_018937	NP_061760	Q9Y5E6	PCDB3_HUMAN	(Potential).|Cadherin 1.	2	GACCATTCTCCG	0.418	
+	1	2365	uc003lin.2_5'Flank	NM_018937	NP_061760	Q9Y5E6	PCDB3_HUMAN	lasmic (Potential).	2	CCAGTTTCAGG	0.453	
+	1	647	B16_uc003liv.2_5	NM_019120	NP_061993	Q9UN66	PCDB8_HUMAN	|Extracellular (Potential).	4	CGTTTCCTCTGA	0.438	
+	1	1895	_5'Flank|PCDHB1	NM_019120	NP_061993	Q9UN66	PCDB8_HUMAN	|Extracellular (Potential).	4	TGGCTCCGCGC	0.721	
-	1	736		NM_031947	NP_114153	Q9BXI2	ORNT2_HUMAN	e=4; (Potential).|Solcar 2.	1	AGAAAAAGAAAT	0.453	
+	1	1489	DHGB2_uc003ljs.1	NM_003736	NP_003727	Q9UN71	PCDGG_HUMAN	|Extracellular (Potential).	0	AGCAGCGGGAG	0.622	
+	3	481	IP1_uc003lmj.1_I	NM_030571	NP_085048	Q9BT67	NFIP1_HUMAN	lasmic (Potential).	0	ACTATCCCTTTG	0.428	
+	4	1779	nn.1_Missense_M	NM_020768	NP_065819	Q68DU8	KCD16_HUMAN		4	AAAAAAGCTGTT	0.448	
+	8	1520	p.P473S|TCERG1	NM_006706	NP_006697	O14776	TCRG1_HUMAN	Glu-rich.	2	GAGGATCCTAAA	0.403	
-	3	244	_Mutation_p.S27L	NM_000870	NP_000861	Q13639	5HT4R_HUMAN	ame=1; (By similarity).	1	CCGTCGAGAGA	0.537	
+	13	1381	lqc.1_Missense_M	NM_014945	NP_055760	O94929	ABLM3_HUMAN		3	GGTACATAGACT	0.627	
+	4	518		NM_001001669	NP_001001669	A1IGU5	ARH37_HUMAN	DH.	0	AGGCGGTGGTG	0.597	
+	2	558		NM_014228	NP_055043	Q99884	SC6A7_HUMAN	Name=1; (Potential).	0	GGCGCTTCCCC	0.602	
-	6	1903	M_uc011dcl.1_Int	NM_052860	NP_443092	Q96RE9	ZN300_HUMAN		2	GTTTCTCTCCTG	0.433	
+	11	1581	2A_uc011dcs.1_In	NM_078483	NP_510968	Q7Z2H8	S36A1_HUMAN	Name=11; (Potential).	1	ATGAGGCTCTCT	0.552	
+	9	1489	tion_p.V294M|uc0	NM_198321	NP_938080	Q86SR1	GLT10_HUMAN	nenal (Potential).	2	CACCCGTGGAG	0.274	rs117925322
+	1	597		NM_000679	NP_000670	P35368	ADA1B_HUMAN	smic (By similarity).	1	TCCATCGATCGC	0.617	
-	3	661	CNMB1_uc003mar	NM_004137	NP_004128	Q16558	KCMB1_HUMAN	cellular (Potential).	2	ACAGCCCACCT	0.592	
+	4	773	on_p.E71K|KCNIP	NM_001034837	NP_001030009	Q9NZI2	KCIP1_HUMAN	nd 1; degenerate.	2	GTCAACGAAGAC	0.547	rs145371121
-	14	1516	03mhm.2_Missens	NM_016222	NP_057306	Q9UJV9	DDX41_HUMAN	case C-terminal.	0	GGCAGGGAAGT	0.577	
+	5	612		NM_014594	NP_055409	Q86Y25	Z354C_HUMAN		1	AATTGGGGAAAA	0.353	
-	18	2044		NM_005110	NP_005101	O94808	GFPT2_HUMAN	SIS 2.	2	CGCTCAGGATG	0.527	
-	7	1220	p.R177C|TRIM7_	NM_203293	NP_976038	Q9C029	TRIM7_HUMAN	B30.2/SPRY.	3	GACGCGGGTGT	0.697	
+	5	1776	ua.2_Missense_M	NM_020135	NP_064520	Q96S55	WRIP1_HUMAN		2	AGGGAGGAGAG	0.607	
+	4	2241	EP1_uc011diq.1_	NM_002114	NP_002105	P15822	ZEP1_HUMAN		6	GTGAGTCCACCA	0.512	
+	2	319	se_Mutation_p.P3	NM_024493	NP_077819	Q9BRR0	ZKSC3_HUMAN		2	GGTTTTCCCAGT	0.607	
-	1	880		NM_030903	NP_112165	Q9Y3N9	OR2W1_HUMAN	lasmic (Potential).	3	CCTTATTTCTTAA	0.423	
+	4	729	_3'UTR|MOG_uc	NM_206809	NP_996532	Q16653	MOG_HUMAN	lasmic (Potential).	1	TTTTAGGAAAACT	0.493	
-	7	1214	10_uc003npn.2_	NM_006778	NP_006769	Q9UDY6	TRI10_HUMAN	B30.2/SPRY.	0	CACGGTGCAGC	0.662	
+	14	1795	p.R311Q|SKIV2L_	NM_006929	NP_008860	Q15477	SKIV2_HUMAN	ase ATP-binding.	4	CAGGCGGCTGA	0.577	
-	5	777	c.2_Missense_M	NM_001093728	NP_001087197	Q8WWU5	TCP11_HUMAN		5	GGATCCGTAATG	0.478	rs146246778
+	2	1017	j.1_RNA|BRPF3_	NM_015695	NP_056510	Q9ULD4	BRPF3_HUMAN		2	CCTCCCGGCCT	0.597	
+	6	2254	tj.1_RNA|BRPF3_	NM_015695	NP_056510	Q9ULD4	BRPF3_HUMAN		2	CCACCGAGCAG	0.408	
+	5	1562	b.2_Intron|PI16_u	NM_153370	NP_699201	Q6UXB8	PI16_HUMAN	cellular (Potential).	0	CCACGGGTGGG	0.617	
-	8	1072	se_Mutation_p.M2	NM_001098518	NP_001091988	Q8IZF2	GP116_HUMAN	racellular (Potential).	2	GTAGTCCATTTTG	0.353	
-	11	1407	dwl.1_Missense_M	NM_153840	NP_722582	Q5T601	GP110_HUMAN	cellular (Potential).	3	GTAACCGTGAG	0.443	
+	2	214		NM_207410	NP_997293	Q6UXV0	GFRAL_HUMAN	cellular (Potential).	2	CTTGGAGAGTAAT	0.328	
-	40	6556_6557	S1_uc011ebi.1_R	NM_002944	NP_002935	P08922	ROS_HUMAN	e.|Cytoplasmic (Potential).	25	GCCTTCCCCTC	0.436	

-	1	89	.2_5'UTR|VNN3_	NM_078625	NP_523239				0	TTTGGAAAATGT	0.358	
+	11	1393		NM_000301	NP_000292	P00747	PLMN_HUMAN	Kringle 4.	4	CCAGCGTCAGG	0.502	
-	7	1655	LL2_uc003ski.3_	NM_182924	NP_891554	Q8IY33	MILK2_HUMAN		1	GAGACGAGGA	0.622	
-	6	1125		NM_032415	NP_115791	Q9BXL7	CAR11_HUMAN	Potential.	50	ATTCCTCCTCCA	0.483	
-	14	2156	V1_uc003ssw.3_	NM_004956	NP_004947	P50549	ETV1_HUMAN		35	GCCTTCGTTGT	0.478	
-	2	195_196	xy.1_Missense_M	NM_006408	NP_006399	O95994	AGR2_HUMAN		0	GGAATTTTCTCC	0.47	
+	51	8334		NM_003777	NP_003768	Q96DT5	DYH11_HUMAN		15	TCAGAGAAGAA	0.363	
+	6	518	e.1_Missense_Mu	NM_031414	NP_113602	Q9BXU1	STK31_HUMAN		9	ACATTCCTTCT	0.328	
-	9	952	8_splice|SKAP2_	NM_003930	NP_003921	O75563	SKAP2_HUMAN		1	CCATATCTATAAA	0.294	
-	1	397_398		NM_001126493	NP_001119965				0	GCCTTCTTTCAC	0.485	
-	13	1588	.1_RNA|DPY19L2P1_uc010kwz.1_RNA						0	GTGGTCTGAAA	0.219	
-	2	583	e_Mutation_p.T61	NM_001637	NP_001628	P28039	AOAH_HUMAN	aposin B-type.	1	GGACCGTCGAG	0.507	rs148515077
+	11	2850	kbi.1_Missense_M	NM_015052	NP_055867	Q76N89	HECW1_HUMAN		23	AGTCGGTACCC	0.662	
+	4	376	.1_5'UTR|DBNL_u	NM_001014436	NP_001014436	Q9UJU6	DBNL_HUMAN	ADF-H.	1	TGTGCGGAAGG	0.622	
+	2	242	tnc.2_Missense_M	NM_005856	NP_005847	O60896	RAMP3_HUMAN	ellular (Potential).	0	TGTCCGAGTTC	0.602	
+	1	401	tart_Site|VSTM2	NM_182546	NP_872352	Q8TAG5	VTM2A_HUMAN		0	CCCTTTTTGGAA	0.483	
+	7	1696	vx.3_Missense_M	NM_015570	NP_056385	Q8WXX7	AUTS2_HUMAN		3	AGCTCCTTCTC	0.632	
-	7	1113	_p.F202Y|SEMA3	NM_006379	NP_006370	Q99985	SEM3C_HUMAN	Sema.	1	CAGAGAAAAGC	0.328	
-	7	960_961	n.1_Nonsense_M	NM_000601	NP_000592	P14210	HGF_HUMAN	Kringle 2.	4	CGGCTGGCCAT	0.475	
-	10	1073		NM_000722	NP_000713	P54289	CA2D1_HUMAN	lar (Potential).|VWFA.	6	ATGTTCGGATCA	0.348	
+	23	2332	_p.S705F|CCDC1	NM_017667	NP_060137	Q96JG6	CC132_HUMAN		0	CGGAATCCTTGT	0.403	
-	3	293	_p.G59E|CYP3A5	NM_000777	NP_000768	P20815	CP3A5_HUMAN		0	ATTTTTCCATAC	0.413	
+	2	342		NM_005837	NP_005828	O75817	POP7_HUMAN		1	GCTTCCCAGCC	0.607	
-	13	2683	_p.L638R|EPHB4	NM_004444	NP_004435	P54760	EPHB4_HUMAN	Potential).|Protein kinase.	15	CGGCAAGGTAC	0.587	
+	8	1241	_Mutation_p.R103	NM_020246	NP_064631	Q9BXP2	S12A9_HUMAN	lasmic (Potential).	0	CCTCCCGCATC	0.632	rs143596115
+	3	3876	C17_uc010lho.1_	NM_001040105	NP_001035194	Q685J3	MUC17_HUMAN	ch.|19.|59 X approximate t	27	CTAGTGAAGGA	0.498	
+	3	6600	C17_uc010lho.1_	NM_001040105	NP_001035194	Q685J3	MUC17_HUMAN	ch.|59 X approximate tand	27	TTTCAACAACT	0.483	rs147644870
+	3	7335	C17_uc010lho.1_	NM_001040105	NP_001035194	Q685J3	MUC17_HUMAN	ch.|59 X approximate tand	27	CACCTGTCACC	0.517	
+	3	9432	C17_uc010lho.1_	NM_001040105	NP_001035194	Q685J3	MUC17_HUMAN	ch.|50.|59 X approximate t	27	TTTCAACAACT	0.498	
-	20	2460	ves.2_Missense_	NM_000111	NP_000102	P40879	S26A3_HUMAN		4	GTAATCCTCCAT	0.333	
-	30	4558	p.E1492K|LAMB4	NM_007356	NP_031382	A4D0S4	LAMB4_HUMAN	Domain I.	8	CGTTTTCCTCTT	0.398	
-	52	5974	fw.2_Missense_M	NM_014705	NP_055520	Q8N1I0	DOCK4_HUMAN	Pro-rich.	4	TGTACGGGGGC	0.716	
-	4	3120		NM_002711	NP_002702	Q16821	PPR3A_HUMAN		34	ACTAATCCTTCA	0.403	
-	4	2443		NM_002711	NP_002702	Q16821	PPR3A_HUMAN		34	CGTGATTCCTT	0.378	
-	4	2441		NM_002711	NP_002702	Q16821	PPR3A_HUMAN		34	GTGATTCCTTTT	0.373	
+	7	612	e_Mutation_p.H1	NM_019071	NP_061944	Q9NXR8	ING3_HUMAN		1	ACAGATCATATT	0.299	
-	5	1244	_p.V61M|CADPS2	NM_017954	NP_060424	Q86UW7	CAPS2_HUMAN		2	TACCACGTCGG	0.388	
-	5	2076	vly.1_Missense_	NM_176814	NP_789784	Q2TB10	ZN800_HUMAN		1	ACCGACGTCAG	0.373	
+	41	7167	.3_Missense_Mut	NM_001458	NP_001449	Q14315	FLNC_HUMAN	Filamin 21.	12	GGGCCGGAGGC	0.677	
+	20	2111	_p.A691T|FAM40B	NM_020704	NP_065755	Q9ULQ0	FA40B_HUMAN		0	AATCGGCACCA	0.438	
-	21	4124		NM_020911	NP_065962	Q9HCM2	PLXA4_HUMAN	lasmic (Potential).	1	GATGTCCGTCT	0.562	
-	19	2660	M1D_uc010lng.2_	NM_030647	NP_085150	Q6ZMT4	KDM7_HUMAN		1	GAAGGAAGTTT	0.483	
-	15	1860		NM_004333	NP_004324	P15056	BRAF_HUMAN	rotein kinas_R603>I(2)|p.T	18290	ATTTCACTGTA	0.368	
-	7	1067		NM_001080392	NP_001073861	A4D1U4	LCHN_HUMAN		1	TGTCAGCACTG	0.582	
-	1	170		NM_176817	NP_789787	P59533	T2R38_HUMAN	Name=1; (Potential).	2	GAAACCCCACT	0.463	
-	4	759	xc.3_Missense_M	NM_001001317	NP_001001317	Q8IYP2	PRS58_HUMAN	eptidase S1.	0	GCTCTTTGTCTA	0.353	
+	11	1333	tc.1_Missense_M	NM_000083	NP_000074	P35523	CLCN1_HUMAN		5	TGGCTGGAGAG	0.463	

+	1	373	uc003wda.2_Intror	NM_177437	NP_803186	P59551	T2R60_HUMAN	lasmic (Potential).	6	CTACCTTCACCC	0.498	
-	4	825		NM_001001661	NP_001001661	Q6IV72	ZN425_HUMAN	2H2-type 2.	3	TTCTCACACTCA	0.577	
+	9	1777	N3_uc003wip.2_	NM_004769	NP_004760	Q9UHC3	ACCN3_HUMAN	lasmic (Potential).	2	TCCTGGGATATT	0.612	
+	3	1150		NM_018941	NP_061764	Q9UBY8	CLN8_HUMAN		3	GCTGCGGAAGA	0.592	
-	21	3602	p.S463F|CSMD1_	NM_033225	NP_150094	Q96PZ7	CSMD1_HUMAN	xtracellular (Potential).	25	AGCAGGAAAAC	0.557	
-	3	439		NM_004686	NP_004677	Q9Y216	MTMR7_HUMAN		1	GGCATCCGGTA	0.433	
+	13	1652	p.G502R|PIWIL2_	NM_018068	NP_060538	Q8TC59	PIWL2_HUMAN		1	TGACCGGAATCC	0.468	rs138817329
+	18	2079	xbw.3_Missense_	NM_005775	NP_005766	O60504	VINEX_HUMAN		0	CCAGACCCAGG	0.657	
+	2	424	7_uc003xdp.2_RN	NM_016612	NP_057696	Q9NYZ2	MFRN1_HUMAN	Solcar 1.	0	GAGCCCTCAAG	0.522	
+	19	2124	p.G377R|DOCK5_	NM_024940	NP_079216	Q9H7D0	DOCK5_HUMAN	DHR-1.	3	ATGGAGGAGAG	0.333	
+	24	2474	p.L556M|PTK2B_	NM_173174	NP_775266	Q14289	FAK2_HUMAN	rotein kinase.	5	ACATCCTGGTG	0.572	
+	2	286		NM_004095	NP_004086	Q13541	4EBP1_HUMAN		0	CACCCCCAAGG	0.562	
-	8	1917	xpe.2_Missense_	NM_006749	NP_006740	Q08357	S20A2_HUMAN	lasmic (Potential).	2	GGGCCGATGAG	0.602	
-	23	4432	NL_uc003xqt.3_	NM_144651	NP_653252	A1KZ92	PXDNL_HUMAN	VWFC.	2	AGGTTCCTTTC	0.517	
-	17	3339_3340	NL_uc003xqt.3_	NM_144651	NP_653252	A1KZ92	PXDNL_HUMAN		2	GAACGGAAGGT	0.495	
-	2	419	ta.3_Missense_M	NM_006211	NP_006202	P01210	PENK_HUMAN		4	TCCATTTTCTTC	0.498	
+	2	700	S1_uc003xui.2_I	NM_173519	NP_775790	Q8IUQ0	CLVS1_HUMAN	RAL-TRIO.	5	ATGGGTTCCCC	0.483	
+	5	744	uc003yam.2_Miss	NM_015886	NP_056970	O43692	PI15_HUMAN		3	GCAATTCATACTT	0.428	
-	8	763	se_Mutation_p.S1	NM_001738	NP_001729	P00915	CAH1_HUMAN		2	GGGATGAAGGA	0.428	
-	15	1862	s.1_Missense_M	NM_015902	NP_056986	O95071	UBR5_HUMAN		28	ATGGTGGAGGA	0.378	
-	26	2712	_p.P706L|ASAP1_	NM_018482	NP_060952	Q9ULH1	ASAP1_HUMAN	Pro-rich.	4	GTTTAGGAAGA	0.294	
-	9	2438	Y8_uc010mds.2_	NM_001115	NP_001106	P40145	ADCY8_HUMAN	ical; (Potential).	6	GTATTGCCGTGA	0.353	
+	20	4326	.2_Missense_Mut	NM_003235	NP_003226	P01266	THYG_HUMAN		15	GGGACCACTTT	0.567	
+	21	3531	ywa.1_Missense_	NM_014957	NP_055772	A2RUS2	DEND3_HUMAN	WD 2.	1	TCCTTCCTGAG	0.577	
-	2	174		NM_205545	NP_991108	Q6UXB3	LYPD2_HUMAN	UPAR/Ly6.	0	TGTGGGCTCCG	0.637	
-	5	939	c003yxj.2_Missen	NM_000497	NP_000488	P15538	C11B1_HUMAN		3	GCAGTGAGTTCC	0.622	
-	4	689	c003yxj.2_Missen	NM_000497	NP_000488	P15538	C11B1_HUMAN		3	GACCTCCAGGG	0.607	
-	6	737	e_Mutation_p.R2	NM_023078	NP_075566	Q53H96	P5CR3_HUMAN		0	TGAGCGCAGCT	0.697	
-	3	1516		NM_003923	NP_003914	O75593	FOXH1_HUMAN	raction domain (SID).	0	GGCCACCCCCC	0.612	
-	4	1620		NM_001145196	NP_001138668	Q5VVP1	F75A6_HUMAN		0	GGAGAGAGCTT	0.478	
-	2	688		NM_001163	NP_001154	Q02410	APBA1_HUMAN		1	CTCGGCGTGCT	0.687	
+	3	1718	p.3_Missense_Mu	NM_024945	NP_079221	Q9H9A7	RMI1_HUMAN		0	AGCCATTCCttaa	0.284	
+	2	243	e.2_RNA|C9orf89_	NM_032310	NP_115686	Q96LW7	BINCA_HUMAN	CARD.	0	TGGGCGCTTGA	0.557	rs117047073
-	1	671		NM_001001919	NP_001001919	Q8NGS5	O13C4_HUMAN	lasmic (Potential).	1	AGATGGTGTAG	0.408	
-	5	1323	p.E408K|ASTN2_	NM_198187	NP_937830	O75129	ASTN2_HUMAN	lasmic (Potential).	9	AGTTTCATCGT	0.537	
+	2	215	wa.2_Missense_	NM_138777	NP_620132	Q96E11	RRFM_HUMAN		3	AGACAGTGCAT	0.478	
+	4	664	ous.2_Missense_	NM_016035	NP_057119	Q9Y3A0	COQ4_HUMAN		0	GGATTTCGACAT	0.597	
+	7	965_966	_p.R297*|SPTAN1	NM_003127	NP_003118	Q13813	SPTA2_HUMAN	Spectrin 4.	10	TTGGCCGAGAC	0.48	
+	5	499	ense_Mutation_p.	NM_080877	NP_543153	Q8N130	NPT2C_HUMAN	ellular (Potential).	0	AAGTGGCCGGA	0.647	
-	2	191		NM_015419	NP_056234	Q9NR99	MXRA5_HUMAN		8	CACCACGGAGA	0.622	
-	4	306	v.1_RNA|FAM9B_	NM_205849	NP_995321	Q8IZU0	FAM9B_HUMAN		0	TTTTATCCATTTT	0.274	
+	9	1385	mij.1_Missense_M	NM_014728	NP_055543	Q14CM0	FRPD4_HUMAN	FERM.	13	AAAGATCCAATT	0.393	
+	8	786	n.2_Missense_M	NM_003159	NP_003150	O76039	CDKL5_HUMAN	rotein kinase.	6	GTATCGGTCCC	0.408	
+	17	2144	s.2_Missense_M	NM_006240	NP_006231	O14829	PPE1_HUMAN		0	TACAAGAGGCA	0.373	
+	37	4399		NM_016937	NP_058633	P09884	DPOLA_HUMAN		3	TTGTGCCGTGA	0.507	
+	1	876		NM_001013736	NP_001013758	Q5HY64	FA47C_HUMAN		3	CTCCCAAGACT	0.607	
-	10	775	.T137R|GRIPAP1	NM_020137	NP_064522	Q4V328	GRAP1_HUMAN	Potential.	3	TTTCTGTCTGC	0.507	

+	3	393	oq.1_Missense_M	NM_000084	NP_000075	P51795	CLCN5_HUMAN	smic (By similarity).	4	TTAATTCACAGT	0.363	
-	9	1187	_p.G362S|ABCB7	NM_004299	NP_004290	O75027	ABCB7_HUMAN	ane type-1.|Helical; (Potenti	1	TTAAACCGACAC	0.398	
+	4	1789	eh.1_Missense_M	NM_021118	NP_066941	P35663	CYLC1_HUMAN		5	TCAATGAAAAAG	0.418	
+	5	972	11_uc004eeq.2_M	NM_021998	NP_068838	Q9Y462	ZN711_HUMAN		4	TAGTGGATGATG	0.313	
-	1	419		NM_001002916	NP_001002916	Q7Z2G1	H2BWT_HUMAN		1	GTGATGGTCTGG	0.647	
+	11	2788		NM_017416	NP_059112	Q9NP60	IRPL2_HUMAN	lasmic (Potential).	3	TCCAAAGAGCTT	0.408	
-	2	878	Y2F_uc011msq.1_	NM_001522	NP_001513	P51841	GUC2F_HUMAN	ellular (Potential).	8	TGGCTGTATGC	0.532	
-	2	353	Y2F_uc011msq.1_	NM_001522	NP_001513	P51841	GUC2F_HUMAN		8	CAAGGCCATGG	0.572	
-	5	2180	om.1_Missense_M	NM_012471	NP_036603	Q9UL62	TRPC5_HUMAN	lasmic (Potential).	1	ACATTTCCTTAAT	0.443	
+	6	1653	e_Mutation_p.A30	NM_000868	NP_000859	P28335	5HT2C_HUMAN	smic (By similarity).	3	GAAAAGCTTCG	0.438	
+	12	1660		NM_007231	NP_009162	Q9UN76	S6A14_HUMAN		3	GAGGTGGATAT	0.363	
-	18	3313	.W1082*|ODZ1_u	NM_014253	NP_055068	Q9UKZ4	TEN1_HUMAN	ellular (Potential).	23	TTGTTCCAAGC	0.448	
+	4	2104	EC1_uc010nsl.1_	NM_005462	NP_005453	O60732	MAGC1_HUMAN		4	TCCATGTCTCC	0.572	
-	2	420	fby.2_Missense_	NM_173078	NP_775101	Q8IW52	SLIK4_HUMAN		2	TTGTCGAAGAA	0.388	
+	7	887		NM_018558	NP_061028	Q9UN88	GBRT_HUMAN	ical; (Potential).	3	TTGGATGAACTA	0.443	
+	2	247		NM_004699	NP_004690	Q14320	FA50A_HUMAN		1	GTTCTCTGCGC	0.622	
+	5	557	n.2_Missense_Mu	NM_001215	NP_001206	P23280	CAH6_HUMAN		2	TTACAGCAACT	0.498	
+	1	4118	.1_Intron|MACF1_	NM_015038	NP_055853	O94854	K0754_HUMAN	9.|Ala-rich.	0	CGCCTCCCCAG	0.726	
-	17	932	cfi.1_Missense_M	NM_001852	NP_001843	Q14055	CO9A2_HUMAN	lical region 3 (COL3).	2	TCCACGAATAC	0.622	
+	14	1698	kt.1_Missense_M	NM_001102663	NP_001096133				0	AGCTGCTGGAG	0.488	
+	6	818		NM_002001	NP_001992	P12319	FCERA_HUMAN	lasmic (Potential).	5	AACCAGGAAAG	0.383	
+	2	439	_p.D114N|ALOX5_	NM_000698	NP_000689	P09917	LOX5_HUMAN	PLAT.	2	TGAGGGATGGA	0.582	
+	14	2035	.1_Missense_Mut	NM_020549	NP_065574	P28329	CLAT_HUMAN		3	CACTGCGGGAG	0.572	rs116097791
+	17	2097	PRKG1_uc009xo	NM_001098512	NP_001091982	Q13976	KGP1_HUMAN	kinase C-terminal.	6	ACACCTCCTATA	0.333	
-	6	1433	ij.1_RNA|TMEM2	NM_178505	NP_848600	Q6ZUK4	TMM26_HUMAN		0	AGCCCCGCAAA	0.582	
-	5	1915	xyz.1_Missense_	NM_014904	NP_055719	Q7L804	RFIP2_HUMAN	1A, subcellular location, en	0	TGGGCGTTTCT	0.423	
+	3	577	R2D_uc001lkt.2_5	NM_018461	NP_060931	Q66LE6	2ABD_HUMAN		1	AAGACGAAGAT	0.368	
+	1	637	_uc001mam.1_Int	NM_001004757	NP_001004757	Q8NH59	O51Q1_HUMAN	Name=5; (Potential).	1	GTGGATCCTCTG	0.498	
-	2	1441	16_uc010sqx.1_5'	NM_014830	NP_055645	O15060	ZBT39_HUMAN		1	GCGCATTTCAGC	0.552	
-	6	1717_1718	nse_Mutation_p.R	NM_019600	NP_062546	Q32MH5	K1370_HUMAN		0	AACTCCTAAACA	0.401	
-	4	621	DC2_uc002eyb.2_RNA|PDXDC2_uc002eyc.2_RNA						0	GTTCTTTGGCG	0.363	
+	47	7485		NM_020877	NP_065928	Q9P225	DYH2_HUMAN	3 (By similarity).	13	GCTAAGGACATG	0.517	
+	2	487	.1_Intron|CNP_uc	NM_033133	NP_149124	P09543	CN37_HUMAN		0	GCCGGGACATC	0.602	
-	4	392		NM_002634	NP_002625	P35232	PHB_HUMAN		0	GGTGAAGATGC	0.527	
-	8	915	p.L219R|SBNO2_	NM_014963	NP_055778	Q9Y2G9	SBNO2_HUMAN		0	TGGACAGTGTG	0.657	
-	284	82270	44E|TTN_uc010z	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	CCAACTCCATTT	0.413	
-	25	2584	p.R822Q|KIF1A_u	NM_004321	NP_004312	Q12756	KIF1A_HUMAN	Potential.	1	TCTCCCGCATC	0.652	
+	10	1244	_p.A325T|RTEL1_	NM_016434	NP_057518	Q9NZ71	RTEL1_HUMAN		0	TCAGCGCGGAC	0.662	rs144255879
-	21	3384	EMA5B_uc003eg	NM_001031702	NP_001026872	Q9P283	SEM5B_HUMAN	ellular (Potential).	7	AGTCGGTGGCC	0.632	
-	3	501	L39L_uc003frf.1_	NM_052969	NP_443201	Q96EH5	RL39L_HUMAN		0	GACCCAGCTTG	0.418	
-	18	3142	_p.D470N|EVC2_u	NM_147127	NP_667338	Q86UK5	LBN_HUMAN	Potential.	5	CTGGTCCTCCA	0.642	
-	146	26926	_uc003qou.3_Mis	NM_182961	NP_892006	Q8NF91	SYNE1_HUMAN	space (Potential).|KASH.	45	AGAGGGCACAG	0.552	
-	12	1832	g.1_Missense_Mu	NM_000168	NP_000159	P10071	GLI3_HUMAN	C2H2-type 4.	19	ACCTTCGTGCT	0.473	
-	16	2319		NM_012431	NP_036563	O15041	SEM3E_HUMAN	-like C2-type.	3	TCACGTCCTTTC	0.368	
-	15	1860		NM_004333	NP_004324	P15056	BRAF_HUMAN	rotein kinas_R603>I(2)|p.T	18290	GATTTCACTGTA	0.368	
-	5	817	T3_uc011lnf.1_Mi	NM_004529	NP_004520	P42568	AF9_HUMAN	Poly-Ser.	3	ctgctgctgctgctgct	0.164	
-	2	143	_5'Flank|COQ4_u	NM_015679	NP_056494	O95900	TRUB2_HUMAN		1	AGGAGCGGGAG	0.368	

+	4	614	P5_uc010ncq.2_3'UTR						0	AGTCCACCAGC	0.517	rs77284214
+	1	1543		NM_001136234	NP_001129706				1	ctgctgctgctgctgct	0.104	
+	42	6425	za.2_Nonsense_	NM_005120	NP_005111	Q93074	MED12_HUMAN	Gln-rich.	4	gcagcagcagtacca	0.264	
+	2	457		NM_207422	NP_997305	Q56UQ5	TPT1L_HUMAN		1	AGGTGGAAGG	0.512	
-	8	1138	AA0562_uc001ak	NM_014704	NP_055519	O60308	CE104_HUMAN	Potential.	0	CCACGGCACAG	0.498	
+	16	2279	i.2_Missense_Mu	NM_014874	NP_055689	O95140	MFN2_HUMAN	Name=1; (Potential).	1	TGGCCTCCTTGA	0.642	
-	3	530		NM_001146344	NP_001139816	O60813	PRA11_HUMAN		0	AAAGTTCTACAA	0.498	
+	1	112	a.2_Intron|CD52_	NM_001803	NP_001794	P31358	CD52_HUMAN		0	GCTTCCTCTTCC	0.522	
+	5	1036		NM_031459	NP_113647	P58004	SESN2_HUMAN		7	TGCCCCCCAGG	0.622	
-	4	1204	d.2_Missense_Mu	NM_014654	NP_055469	O75056	SDC3_HUMAN	ellular (Potential).	2	CTACGAGCACC	0.637	
-	2	945	e_Mutation_p.Q29	NM_144569	NP_653170	Q6ZMY3	SPOC1_HUMAN		6	CTGGCTGGGGC	0.642	
+	6	977	sense_Mutation_p	NM_018056	NP_060526	Q9GZU3	TM39B_HUMAN		0	GAGTTCCTCAA	0.587	
-	52	7819	m.1_Missense_Mu	NM_052896	NP_443128	Q7Z408	CSMD2_HUMAN	xtracellular (Potential).	12	TGCTACTGACAT	0.473	
-	45	6887	p.F2284L|CSMD2_	NM_052896	NP_443128	Q7Z408	CSMD2_HUMAN	ar (Potential).|CUB 13.	12	CCGGAGAAAGC	0.313	
-	25	3961	p.G1351E|CSMD2	NM_052896	NP_443128	Q7Z408	CSMD2_HUMAN	tracellular (Potential).	12	CTTACCCAATG	0.577	
-	8	1265	a.1_Missense_Mu	NM_000831	NP_000822	Q13003	GRIK3_HUMAN	ellular (Potential).	7	CAATTCGTCCA	0.498	
-	4	4823	_Mutation_p.H12	NM_024503	NP_078779	Q5T1R4	ZEP3_HUMAN		6	GAGATGGAGTT	0.607	
-	12	2458	DC1_uc001dek.3_	NM_001114120	NP_001107592	Q5TB30	DEP1A_HUMAN		0	CGTGGTTGGAA	0.353	
-	2	426	P2_uc001dmy.1_	NM_004120	NP_004111	P32456	GBP2_HUMAN	(By similarity).	1	GGTAGGATTTG	0.542	
+	4	950		NM_001010898	NP_001010898	Q9H1V8	S6A17_HUMAN	Name=3; (Potential).	2	GGGTGGAGCAT	0.577	
-	7	1579		NM_001047980	NP_001041445	P0C2Y1	NBPF7_HUMAN	NBPF 2.	2	CTCCGGGGAGT	0.483	
+	2	232	D1L_uc009wjh.2_	NM_004284	NP_004275	Q86WJ1	CHD1L_HUMAN		6	ACTGGCTCGCC	0.507	
-	3	2464	c001ezv.2_5'Flan	NM_002016	NP_002007	P20930	FILA_HUMAN	Ser-rich.	16	CCCTGTCCATC	0.567	
-	2	843	2_Missense_Muta	NM_001111	NP_001102	P55265	DSRAD_HUMAN		6	TATGACCGTCTG	0.522	
-	1	491		NM_001005185	NP_001005185	Q8NGY5	OR6N1_HUMAN	ellular (Potential).	1	GGCGTGAAATC	0.502	
+	10	2380		NM_022093	NP_071376	Q9UQP3	TENN_HUMAN	nectin type-III 6.	9	GGTGGGGAAGG	0.647	
+	3	907	1_uc010ppa.1_R	NM_201253	NP_957705	P82279	CRUM1_HUMAN	g (Potential).|Extracellular	9	GGGATCACTGT	0.512	
+	4	419	1_Intron|PTPRC_	NM_002838	NP_002829	P08575	PTPRC_HUMAN	ellular (Potential).	12	ATACTTCCACCC	0.423	
+	9	1208	p.Q316Q|CTSE_	NM_001910	NP_001901	P14091	CATE_HUMAN		1	CTCCAGCTGGG	0.542	
+	4	856	_p.E267K|RASSF	NM_182663	NP_872604	Q8WWW0	RASF5_HUMAN		1	TCAAGGAGGTG	0.592	
+	9	1388	o.3_Missense_Mu	NM_152609	NP_689822	Q6PJW8	CNST_HUMAN		0	CAGTCCCTGCT	0.488	
+	6	1162	W3_uc001idp.1_I	NM_015431	NP_056246	Q8NG06	TRI58_HUMAN	B30.2/SPRY p.E372K(1)	7	AGGGGGAAACC	0.562	rs143805378
+	1	698_699		NM_001005471	NP_001005471	Q8NHC8	OR2T6_HUMAN	lasmic (Potential).	3	TGAAGGGAGGA	0.51	
-	1	577		NM_001001964	NP_001001964	Q8NH01	O2T11_HUMAN	Name=5; (Potential).	1	AGTTTCATACAA	0.483	
+	12	1778	P11_uc001kef.2_I	NM_133447	NP_597704	Q8TF27	AGA11_HUMAN	PH.	0	CCTGCGCACCC	0.473	
-	7	1385	01kgl.2_Missense_	NM_213606	NP_998771	Q6ZSM3	MOT12_HUMAN	ical; (Potential).	1	GCAGAGCCCAT	0.463	
+	6	3472	klq.2_Missense_	NM_014803	NP_055618	Q6AHZ1	Z518A_HUMAN		1	AGATGTGAGAG	0.373	
-	7	1170		NM_032211	NP_115587	Q96JB6	LOXL4_HUMAN	SRCR 3.	5	GGTTCCACCTG	0.682	
+	20	2992	CS3_uc010qqz.1_	NM_014978	NP_055793	Q9UPU3	SORC3_HUMAN	enal (Potential).	10	AGTTCCATTTG	0.448	
+	8	842		NM_000936	NP_000927	P16233	LIPP_HUMAN		3	TAGACGGAATC	0.398	rs62623373
-	5	521	llu.2_Missense_M	NM_173572	NP_775843	Q5SR76	CJ093_HUMAN		1	GTGACGATATC	0.527	
+	5	532		NM_206893	NP_996776	Q96PG2	M4A10_HUMAN	ellular (Potential).	2	AGGATCTCTTT	0.512	
-	2	1247	_5'Flank|BRMS1_	NM_006876	NP_006867	O43505	B3GN1_HUMAN	enal (Potential).	0	ACCTTCGTTCA	0.473	
+	2	517	nse_Mutation_p.	NM_002896	NP_002887	Q9BWF3	RBM4_HUMAN	RRM 1.	1	CCTGCCCCGGG	0.493	
-	10	2304	p.G726S|CD163_	NM_004244	NP_004235	Q86VB7	C163A_HUMAN	xtracellular (Potential).	8	AGCGACCTCCTC	0.458	
+	13	2713	e.2_Missense_M	NM_004426	NP_004417	P78364	PHC1_HUMAN		2	CTCGCGTTCGC	0.537	
-	3	1091	ju.1_Missense_M	NM_198992	NP_945343	Q6XYQ8	SYT10_HUMAN	mic (Potential).|C2 1.	2	AAGTTCCTGTG	0.358	

-	8	2299		NM_005164	NP_005155	Q9UBJ2	ABCD2_HUMAN	C transporter.	6	ACTTATGATAAA	0.368	
+	1	82	lutation_p.H28Y|L	NM_152641	NP_689854	Q68CP9	ARID2_HUMAN	ARID.	10	TCCACCACAGC	0.677	
-	39	11948		NM_003482	NP_003473	O14686	MLL2_HUMAN	Gln-rich.	41	GTAAAGTTCGA	0.333	
-	51	6918		NM_006836	NP_006827	Q92616	GCN1L_HUMAN		4	CCACGGAGGGC	0.622	
-	11	1438	p.S414L|KDM2B_	NM_032590	NP_115979	Q8NHM5	KDM2B_HUMAN		2	TGGGTGAAGTG	0.542	
-	12	1570	33A_uc001ucc.2_	NM_022916	NP_075067	Q96AX1	VP33A_HUMAN		1	ACATACGATATGT	0.527	
+	4	942	h.2_Missense_Mu	NM_025215	NP_079491	Q9Y606	TRUA_HUMAN		2	GCCAGGTGGTA	0.557	
-	5	1217		NM_006001	NP_005992	Q13748	TBA3C_HUMAN		5	CAGGCGAGCCC	0.647	
-	3	1055	_p.K168E|GJB6_u	NM_006783	NP_006774	O95452	CXB6_HUMAN	ellular (Potential).	1	ACATTTCAACA	0.443	
+	3	243		NM_144578	NP_653179	Q8NDC0	MISSL_HUMAN	Pro-rich.	0	CAAAACCTGGC	0.517	
+	8	1945	s.1_Missense_M	NM_001024218	NP_001019389	Q9NQX3	GEPH_HUMAN	GABARAP (By similarity).	2	TCAGGCTACAT	0.498	
+	3	910	_p.N155S|PCNX_	NM_014982	NP_055797	Q96RV3	PCX1_HUMAN		1	AAGCAACCAGG	0.483	
+	8	809	LL5_uc010ask.1_	NM_015072	NP_055887	Q6EMB2	TTLL5_HUMAN	TTL.	3	CCCTGGAAGAG	0.398	
+	25	3125	r.2_Missense_Mut	NM_001036	NP_001027	Q15413	RYR3_HUMAN	c (By similarity).|4 X appro	10	CCCGTCTGGTG	0.453	
-	2	268	.2_Missense_Mut	NM_033503	NP_277038	Q96LC9	BMF_HUMAN		1	TGGGTCGAAGG	0.622	
-	17	1881		NM_178034	NP_828848	Q86XP0	PA24D_HUMAN	PLA2c.	2	GGGCCTGCCTG	0.677	
+	12	2313	te.2_Nonsense_M	NM_024817	NP_079093	Q6ZMP0	THSD4_HUMAN	SP type-1 3.	2	CGACTGGACCT	0.637	
+	2	2182	unk.1_Missense_	NM_015206	NP_056021	Q9UPX6	K1024_HUMAN		4	AAAGCCTCTTC	0.547	
-	2	367	_p.L67P|FSD2_uc	NM_001007122	NP_001007123	A1L4K1	FSD2_HUMAN		1	TCTTGAAGGTCT	0.443	
+	17	1568	_Missense_Mutati	NM_138769	NP_620124	Q8IXI1	MIRO2_HUMAN	rial intermembrane (Potent	1	AGTCCTTTGCA	0.632	
+	6	1507	_p.N40S|ZNF263	NM_005741	NP_005732	O14978	ZN263_HUMAN	2H2-type 1.	4	ACTCAAACCTAA	0.478	
-	13	4513	G1322E|GRIN2A_	NM_001134407	NP_001127879	Q12879	NMDE1_HUMAN	lasmic (Potential).	45	AATTTCCCTCC	0.527	
+	11	1514		NM_017888	NP_060358	Q6NUN0	ACSM5_HUMAN		2	GGACCGAGCTC	0.483	
+	15	1913	_p.D405N|SLC5A1	NM_052944	NP_443176	Q8WWX8	SC5AB_HUMAN	lasmic (Potential).	2	GTCACGACCCC	0.577	
+	1	114_115	B3_uc010cja.1_R	NM_006086	NP_006077	Q13509	TBB3_HUMAN		3	GATCGGGGCC	0.347	
+	32	7129		NM_016239	NP_057323	Q9UKN7	MYO15_HUMAN	Tail.	9	CGGCTGGACCG	0.602	
-	5	1584		NM_001145045	NP_001138517	P0CG31	Z286B_HUMAN	2H2-type 8.	0	TTTTCCCACATT	0.388	
+	1	285	L3_uc002hit.2_5'F	NM_017559	NP_060029	Q8TC99	FNDC8_HUMAN	p.N68I(1)	2	CCATCAACCTAC	0.284	
-	3	336	16_uc002hkm.2_	NM_004590	NP_004581	O15467	CCL16_HUMAN		0	TTGGGATCCTTG	0.507	
-	14	1865	hrl.1_Missense_M	NM_000723	NP_000714	Q02641	CACB1_HUMAN		2	AGTAGCGGGC	0.647	
-	1	181		NM_033062	NP_149051	Q9BYR5	KRA42_HUMAN	C-C-[GRQVS]-[SPT]- [VS	0	GTCTGCAGCAG	0.677	rs147637076
+	4	479	0cze.1_Missense_	NM_145041	NP_659478	Q96A25	T106A_HUMAN		0	TCATTCCCTATG	0.572	
+	3	705	.1_3'UTR|ARMC7	NM_024585	NP_078861	Q9H6L4	ARMC7_HUMAN	ARM 2.	1	TCCCAGAGCTG	0.632	
+	9	1427	jth.2_Missense_M	NM_198955	NP_945193	Q3V5L5	MGT5B_HUMAN	enal (Potential).	3	TGTTTCGTGAG	0.622	
+	14	2094		NM_005925	NP_005916	Q16820	MEP1B_HUMAN	lasmic (Potential).	2	AAATATCGTGAA	0.408	
-	21	3916	32_uc010xcr.1_S	NM_020964	NP_066015	Q9HCE0	EPG5_HUMAN		0	TTTGTACCTTCA	0.433	
+	7	1794	_p.E251K|DCC_u	NM_005215	NP_005206	P43146	DCC_HUMAN	otential).|Ig-like C2-type 4.	17	TGGCTGAAAAT	0.438	
-	5	2855	k.1_Missense_Mu	NM_052947	NP_443179	Q86TB3	ALPK2_HUMAN		14	GCCGTCCTTGC	0.428	
-	11	1263	_p.V409M|SEMA6	NM_032108	NP_115484	Q9H3T3	SEM6B_HUMAN	lar (Potential).|Sema.	1	GGGCACCGCCT	0.652	
-	8	892		NM_032447	NP_115823	Q75N90	FBN3_HUMAN		11	GGCCCGGTAGT	0.383	rs138686141
-	3	21008		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).	57	CAGAGGAAACA	0.458	
-	1	6323		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	h.|Extracellular (Potential)	57	TTGTGGAATCC	0.488	
+	10	2692	_p.S622F|NWD1_uc002nev.3_Missense_Mutation_p.S5			Q149M9	NWD1_HUMAN		7	GATTTCCTGCC	0.597	
-	2	132	1_uc010xpk.1_5'	NM_031941	NP_114147	Q8N6Y0	USBP1_HUMAN		1	GGGCCGCGTGG	0.632	
-	13	2081	.R249Q|PDE4C_	NM_001098819	NP_001092289	Q08493	PDE4C_HUMAN		5	TGGATTCGGTCG	0.378	
+	19	2420	dd.2_Missense_M	NM_173636	NP_775907	O43379	WDR62_HUMAN		0	GCCACCCCAGG	0.453	
-	3	1425		NM_003890	NP_003881	Q9Y6R7	FCGBP_HUMAN	VWFD 1.	9	GGCGCGGCAGA	0.677	

-	5	506	oo.2_Missense_M	NM_004756	NP_004747	Q9Y6R0	NUMBL_HUMAN	PID.	5	TCACGGACTTT	0.652	
+	1	550	rf54_uc002oox.1_	NM_004596	NP_004587	P09012	SNRPA_HUMAN		4	CCCGAGACCCG	0.498	
-	4	855_856	.E160K|PSG9_uc	NM_002784	NP_002775	Q00887	PSG9_HUMAN	like C2-type 2.	2	ATTCTCCCTGGG	0.51	
+	2	654	yct.1_Missense_M	NM_014441	NP_055256	Q9Y336	SIGL9_HUMAN	otential).|Ig-like C2-type 1.	1	CTCCTCGGTGC	0.657	rs141688796
-	3	1129	_p.R240Q|SIGLE	NM_053003	NP_443729	Q96PQ1	SIG12_HUMAN	1.|Extracellular (Potential).	5	TGAGTCGGACA	0.602	
+	3	1399	tg.2_Missense_Mu	NM_176811	NP_789781	Q86W28	NALP8_HUMAN	NACHT.	13	ACTTTTCCAGAA	0.473	
-	11	2299	113_uc010eyk.1_	NM_001145168	NP_001138640	Q8IZF5	GP113_HUMAN	ellular (Potential).	4	GGGTTCTTCCG	0.627	
+	7	1007	_p.P253L|SPTBN1	NM_003128	NP_003119	Q01082	SPTB2_HUMAN	2.|Actin-binding.	8	GGACCCCGAAG	0.423	
+	7	865		NM_031283	NP_112573	Q9HCS4	TF7L1_HUMAN	Pro-rich.	3	TCCTCCCGGTG	0.612	
+	11	1213	se_Mutation_p.T1	NM_001135021	NP_001128493	Q96FG2	ELMD3_HUMAN	ELMO.	2	GCTGACCGGCT	0.547	
+	3	224	1A_uc002sqv.2_5'	NM_017952	NP_060422	Q96EY7	PTCD3_HUMAN		1	CATTAGGGATTG	0.284	
-	2	151	_p.R11Q|ST6GAL	NM_001142351	NP_001135823	Q96JF0	SIAT2_HUMAN	lasmic (Potential).	11	AGCATTCGTTGT	0.507	
-	4	371	h.1_Missense_Mu	NM_000576	NP_000567	P01584	IL1B_HUMAN		4	TGAAGGGAAAG	0.532	
-	4	527	se_Mutation_p.P5	NM_013450	NP_038478	Q9UIF8	BAZ2B_HUMAN		4	TAAACGGTTGAT	0.433	
+	27	5425	p.T1712I|SCN2A_	NM_001040142	NP_001035232	Q99250	SCN2A_HUMAN	IV.	8	TACAACCTCTG	0.458	
-	225	45318	_uc010zfi.1_Miss	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	AATTTCCCCAC	0.473	
-	75	19126	_uc010zfj.1_Intro	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	TGATTCGCATC	0.408	rs72648969
-	2	1412		NM_004657	NP_004648	O95810	SDPR_HUMAN		2	CCCTGGAGGTC	0.577	
+	20	2263_2264	_p.R277K|AOX1_	NM_001159	NP_001150	Q06278	ADO_HUMAN		6	AGAAAGGAAACT	0.426	
+	26	2973	p.E514K|AOX1_u	NM_001159	NP_001150	Q06278	ADO_HUMAN		6	TACAAGGAAATT	0.368	
+	11	2663	0fvx.2_Missense_	NM_014640	NP_055455	Q14679	TTLL4_HUMAN	TTL.	3	TTTGACCTGCGG	0.488	
-	8	2241	nj.2_Missense_Mu	NM_020341	NP_065074	Q9P286	PAK7_HUMAN	rotein kinase.	23	CCTGTGAATCA	0.443	
-	2	776	xcb.1_Missense_M	NM_178468	NP_848563	Q9BQN1	FA83C_HUMAN		2	GAGGTCCATCT	0.647	
-	3	2822	dk.2_Intron|CPNE	NM_152838	NP_690051	Q9NTZ6	RBM12_HUMAN	RRM 3.	3	TAAAGGGCATGT	0.353	
+	11	1414	ggc.2_Missense_	NM_015568	NP_056383	Q96T49	PP16B_HUMAN		3	CTACTCTCCGAA	0.567	
-	5	521	3_uc002xph.1_In	NM_080614	NP_542181	Q8IUB2	WFDC3_HUMAN	WAP 3.	0	TATGCCCCTGG	0.547	
+	6	2719	'Flank|GHRLOS_	NM_014760	NP_055575	Q93075	TATD2_HUMAN		2	CCTCCCTCGCC	0.622	
+	6	2721	5'Flank|GHRLOS_	NM_014760	NP_055575	Q93075	TATD2_HUMAN		2	TCCCTCGCCAG	0.617	rs150215933
+	3	300	_p.S95N|MOBP_u	NM_182935	NP_891980	Q13875	MOBP_HUMAN		2	AACCAGCCGCC	0.667	
-	11	1701		NM_003500	NP_003491	Q99424	ACOX2_HUMAN		0	GCTTACCTTACT	0.597	rs145582569
-	6	1088	y.2_Missense_Mu	NM_001015887	NP_001015887	Q5DX21	IGS11_HUMAN	lasmic (Potential).	0	ATTAGGAATTTC	0.323	
-	9	1787	jg.1_Missense_M	NM_153002	NP_694547	Q8NFN8	GP156_HUMAN	lasmic (Potential).	2	TGTAAGGGCTA	0.602	
-	16	4783	d.2_Missense_Mu	NM_199420	NP_955452	O75417	DPOLQ_HUMAN		11	ATCATTGGAAC	0.333	
-	9	1581	wp.1_Missense_M	NM_024727	NP_079003	Q6UY01	LRC31_HUMAN		3	TCTAAACCATT	0.448	
-	3	10637	h.1_5'Flank|MUC4	NM_018406	NP_060876	Q99102	MUC4_HUMAN		0	AGGAAGAGGGG	0.597	
-	5	820	zh.1_Missense_M	NM_006587	NP_006578	Q9Y5Q5	CORIN_HUMAN	ular (Potential).|FZ 1.	2	TTCTAAACTGGG	0.468	
+	32	5717	p.S1727F|PTPN1	NM_080683	NP_542414	Q12923	PTN13_HUMAN	Poly-Ser.	6	TGCTTCCTCTA	0.393	
+	3	378	se_Mutation_p.P5	NM_001033047	NP_001028219	Q6UXI9	NPNT_HUMAN	EGF-like 1.	1	CACAGCTGTGT	0.388	
-	7	866	e.1_Missense_Mu	NM_176824	NP_789794	Q8IWZ6	BBS7_HUMAN		1	GAATTTCCCACT	0.338	
-	17	1850	hn.1_Missense_M	NM_003866	NP_003857	O15327	INP4B_HUMAN		2	GTAGTTGATTGA	0.383	
-	14	2299	.R609W|LRBA_u	NM_006726	NP_006717	P50851	LRBA_HUMAN		7	TCTCCGAATGG	0.418	
-	6	1580	_p.M230I|LRP2BP	NM_018409	NP_060879	Q9P2M1	LR2BP_HUMAN	Sel1-like 5.	0	AAATTTCATCTTA	0.308	
-	2	1212	.1_Missense_Mut	NM_005245	NP_005236	Q14517	FAT1_HUMAN	ellular (Potential).	12	GAGTTCCTTTAT	0.458	
-	12	2291	v.1_Missense_Mu	NM_016279	NP_057363	Q9ULB4	CADH9_HUMAN	lasmic (Potential).	9	ATTTTCCCACAG	0.418	
+	2	465	ELD2_uc003jwr.1_	NM_001038603	NP_001033692	Q8N4S9	MALD2_HUMAN	lasmic (Potential).	0	AAGATCCCTAC	0.542	
-	2	287	RAP3_uc003llo.1_	NM_022481	NP_071926	Q8WWN8	ARAP3_HUMAN		7	CCAGGGAGCCC	0.642	
-	1	313		NM_001080516	NP_001073985	A6NFK2	GRCR2_HUMAN		0	TGTAATCGTTGA	0.498	

+	16	3055	se_Mutation_p.S8	NM_001114183	NP_001107655	P42261	GRIA1_HUMAN	lasmic (Potential).		6	CAGTTCAGGGA	0.622	rs144882662
+	49	5154	e_Mutation_p.E11	NM_004946	NP_004937	Q92608	DOCK2_HUMAN			7	TGCCTGAGGTC	0.587	
-	4	1055	2A23_uc003mvp.1	NM_015482	NP_056297	A1A5C7	S22AN_HUMAN	ical; (Potential).		1	GGAAGGGGCA	0.662	
-	3	537	A-DRB5_uc003ob	NM_002125	NP_002116	Q30154	DRB5_HUMAN	eta-2.|Extracellular (Potenti		0	ATTCTGAATCA	0.552	
+	8	884	plice_Site|GLP1R_	NM_002062	NP_002053	P43220	GLP1R_HUMAN			5	TCTTAGGTGTT	0.617	
+	6	1041	_p.E238K|MDFI_u	NM_005586	NP_005577	Q99750	MDFI_HUMAN	Cys-rich.		0	GCATGGAGTGC	0.672	
-	4	502	pai.2_Missense_M	NM_138694	NP_619639	P08F94	PKHD1_HUMAN	tential).|IPT/TIG 1; atypica		44	ACAGGGAACAC	0.507	
+	5	1539		NM_001010872	NP_001010872	Q5T0W9	FA83B_HUMAN			6	ATATCCGCTTTT	0.408	
-	3	677	nse_Mutation_p.D1	NM_030820	NP_110447	Q96P44	COLA1_HUMAN	VWFA.		2	GTCATCTTGGG	0.443	
-	5	965	VL4_uc011dyt.1_I	NM_022726	NP_073563	Q9GZR5	ELOV4_HUMAN			2	GTATCGTTTCC	0.343	
+	17	2230		NM_173560	NP_775831	Q8HWS3	RFX6_HUMAN			3	ACACCGAGCAT	0.527	
-	10	1976		NM_153235	NP_694967	Q8N3L3	TXLNB_HUMAN			2	GCTTCCAGGAC	0.622	
+	12	1641	ense_Mutation_p.G	NM_015440	NP_056255	Q6UB35	C1TM_HUMAN	hydrofolate synthetase.		4	CCAAGGACCGA	0.488	
-	3	625	AD1L1_uc010ksj.	NM_013393	NP_037525	Q9UI43	RRMJ2_HUMAN			1	TTTGACTTCCA	0.512	
-	5	1154	p.K373T|ACTB_u	NM_001101	NP_001092	P60709	ACTB_HUMAN			0	AGCATTTGCGG	0.512	
+	9	1187	_p.R210C|OGDH_	NM_002541	NP_002532	Q02218	ODO1_HUMAN			2	TCAATCGTGTC	0.557	
-	9	1391	_p.S305F|CYP51A	NM_000786	NP_000777	Q16850	CP51A_HUMAN			0	TGGGAGAAACA	0.413	
-	7	627	n_p.V134I|CYP3A	NM_017460	NP_059488	P08684	CP3A4_HUMAN			4	AAAGACGCTGA	0.448	
-	15	1860		NM_004333	NP_004324	P15056	BRAF_HUMAN	rotein kinas	_R603>I(2)|p.T	18290	ATTTCACTGTA	0.368	
+	1	662	uc003wda.2_Intro	NM_177437	NP_803186	P59551	T2R60_HUMAN	lasmic (Potential).		6	TCTGGGAAGAC	0.458	
+	1	829	C61_uc003wgx.2_I	NM_138434	NP_612443	Q96FA7	CG029_HUMAN			1	CCATGGGGGCC	0.542	
-	45	7153	_p.Q1647*|CSMD1	NM_033225	NP_150094	Q96PZ7	CSMD1_HUMAN	ar (Potential).|CUB 13.		25	GAGCTGAAATG	0.338	
-	2	91		NM_001033018	NP_001028190	Q30KP8	DB136_HUMAN			0	GGTGCGAACTT	0.458	
+	2	522	.1_Missense_Mut	NM_006269	NP_006260	P56715	RP1_HUMAN			12	CCCGCGGCCCT	0.706	
-	2	477	_p.S146T|JPH1_u	NM_020647	NP_065698	Q9HDC5	JPH1_HUMAN	ic (Potential).|MORN 5.		1	GCACGCTCTGG	0.687	
-	1	673	ydr.1_Missense_M	NM_138817	NP_620172	Q8TCU3	S7A13_HUMAN	cellular (Potential).		1	TGAAATCGTTCT	0.413	
-	10	940	p.R285K|ENPP2_	NM_001040092	NP_001035181	Q13822	ENPP2_HUMAN			7	ATATTCTCCGCT	0.428	
-	25	3413	0_splice|KIAA019	NM_014846	NP_055661	Q12768	STRUM_HUMAN			2	TTACTCACCTTAT	0.443	
-	6	846	RC6_uc003ytl.2_R	NM_012472	NP_036604	Q86X45	LRRC6_HUMAN			2	ATTCAGGAGTAA	0.403	
-	3	981	RPIN_uc003zbb.2_	NM_030974	NP_112236	Q9H0F6	SHRPN_HUMAN	ciation (By similarity).		1	TTCCAGGGCTC	0.627	
+	4	334	.2_RNA|ADCK5_	NM_174922	NP_777582	Q3MIX3	ADCK5_HUMAN			1	AGGTCGGCCTG	0.637	
-	23	2707	3zkl.2_Missense_	NM_002839	NP_002830	P23468	PTPRD_HUMAN	III 4.|Extracellular (Potentia		22	CGAAGGAATTC	0.478	
-	1	436		NM_002175	NP_002166	P01568	IFN21_HUMAN			2	TCTCTTCCACCC	0.468	
-	1	490	.1_5'UTR|PAX5_u	NM_016734	NP_057953	Q02548	PAX5_HUMAN		p.?(9)	147	CCTGTCCTGCT	0.547	
-	4	434		NM_000035	NP_000026	P05062	ALDOB_HUMAN			1	TGTTCCTGCAA	0.408	
-	10	876	PN3_uc010mtu.2_	NM_002829	NP_002820	P26045	PTN3_HUMAN	FERM.		3	ACTTACCAAGGA	0.343	
-	2	422	_p.L57F|PHF19_u	NM_015651	NP_056466	Q5T6S3	PHF19_HUMAN			2	CCCGAGGTAGT	0.562	
-	4	532	CL_uc004bna.2_3'	NM_005388	NP_005379	Q13371	PHLP_HUMAN			0	TCTCTTCCATTC	0.478	
-	9	1270	b.2_Missense_Mu	NM_021804	NP_068576	Q9BYF1	ACE2_HUMAN	cellular (Potential).		3	GAAGTCGTCCA	0.408	
-	6	1131	D2_uc010nfb.2_I	NM_153346	NP_699177	Q8NDZ0	BEND2_HUMAN			5	TAATTTCCCATTA	0.294	
+	13	1511		NM_001654	NP_001645	P10398	ARAF_HUMAN	rotein kinase.		7	GCGGGGCCCAG	0.627	
-	5	1372	w.2_Missense_Mu	NM_183353	NP_899196	Q9NVW2	RNF12_HUMAN			2	AACCTCCTCGT	0.458	
-	3	942	npd.2_Missense_	NM_000354	NP_000345	P05543	THBG_HUMAN			0	AAATGGAAAAC	0.428	
+	16	2728	C4_uc004emp.3_I	NM_017752	NP_060222	Q0IIM8	TBC8B_HUMAN			4	GGGCTCATTCT	0.408	
-	1	901		NM_005634	NP_005625	P41225	SOX3_HUMAN			1	CGTAGCGGTGC	0.448	
+	4	416	EC1_uc010nsl.1_	NM_005462	NP_005453	O60732	MAGC1_HUMAN			4	CTGAGAGCGAC	0.587	rs147626195
+	3	958	.2_Nonsense_Mu	NM_002025	NP_002016	P51816	AFF2_HUMAN			5	GTGGTCACGTG	0.468	

+	5	506	utation_p.N99S|S	NM_001363	NP_001354	O60832	DKC1_HUMAN		0	CTCTAACCCCT	0.453	
+	6	2110		NM_152228	NP_689414	Q7RTX0	TS1R3_HUMAN	ellular (Potential).	0	CCTTCCCGCCG	0.706	rs142424158
+	16	2279	i.2_Missense_Mu	NM_014874	NP_055689	O95140	MFN2_HUMAN	Name=1; (Potential).	1	TGGCCTCCTTGA	0.642	
-	3	530		NM_001146344	NP_001139816	O60813	PRA11_HUMAN		0	AAAGTTCTACAA	0.498	
+	1	112	na.2_Intron|CD52_	NM_001803	NP_001794	P31358	CD52_HUMAN		0	GCTTCCTCTTCC	0.522	
+	5	1036		NM_031459	NP_113647	P58004	SESN2_HUMAN		7	TGCCCCCCAGG	0.622	
-	4	1204	d.2_Missense_Mu	NM_014654	NP_055469	O75056	SDC3_HUMAN	ellular (Potential).	2	CTACGAGCACC	0.637	
+	6	977	sense_Mutation_p	NM_018056	NP_060526	Q9GZU3	TM39B_HUMAN		0	GAGTTCCTCAA	0.587	
-	52	7819	m.1_Missense_Mu	NM_052896	NP_443128	Q7Z408	CSMD2_HUMAN	xtracellular (Potential).	12	ATGCTACTGACA	0.473	
-	45	6887	p.F2284L|CSMD2_	NM_052896	NP_443128	Q7Z408	CSMD2_HUMAN	ar (Potential).|CUB 13.	12	CCGGAGAAAGC	0.313	
-	25	3961	p.G1351E|CSMD2	NM_052896	NP_443128	Q7Z408	CSMD2_HUMAN	tracellular (Potential).	12	CTTACCCAATG	0.577	
-	13	2155	a.1_Missense_Mu	NM_000831	NP_000822	Q13003	GRIK3_HUMAN	ellular (Potential).	7	GTCATCAGCAG	0.547	
-	8	1265	a.1_Missense_Mu	NM_000831	NP_000822	Q13003	GRIK3_HUMAN	ellular (Potential).	7	ACAATTCGTCCA	0.498	
+	3	1362	orf175_uc010oof.1	NM_001039464	NP_001034553	Q68CQ1	HEAT8_HUMAN	Ser-rich.	0	TTCAGCGACAC	0.562	
-	12	2458	DC1_uc001dek.3_	NM_001114120	NP_001107592	Q5TB30	DEP1A_HUMAN		0	CGTGGTTGGAA	0.353	
-	2	426	P2_uc001dmy.1_	NM_004120	NP_004111	P32456	GBP2_HUMAN	(By similarity).	1	GGTAGGATTTG	0.542	
-	44	6129	qi.1_Missense_Mu	NM_000350	NP_000341	P78363	ABCA4_HUMAN	porter 2.|Cytoplasmic.	12	GACTTCAGAAA	0.438	
+	4	950		NM_001010898	NP_001010898	Q9H1V8	S6A17_HUMAN	Name=3; (Potential).	2	GGGTGGAGCAT	0.577	
+	5	531	wge.1_Missense_	NM_181643	NP_857594	Q8TCI5	CA088_HUMAN		2	AATTTGGATCTC	0.418	
-	7	1579		NM_001047980	NP_001041445	P0C2Y1	NBPF7_HUMAN	NBPF 2.	2	CTCCGGGGAGT	0.483	
-	2	297	UDT17_uc001eof.	NM_001012758	NP_001012776	P0C025	NUD17_HUMAN	dix hydrolase.	0	AATGACGGCCA	0.647	
+	2	232	D1L_uc009wjh.2_	NM_004284	NP_004275	Q86WJ1	CHD1L_HUMAN		6	ACTGGCTCGCC	0.507	
+	12	1487	kt.1_Missense_M	NM_001102663	NP_001096133				0	AAAGAGCCTGA	0.473	
-	3	2464	c001ezv.2_5'Flan	NM_002016	NP_002007	P20930	FILA_HUMAN	Ser-rich.	16	CCCTGTCCATC	0.567	
-	24	3138	_p.D116Y|ARHGE	NM_014784	NP_055599	O15085	ARHGB_HUMAN		9	CAGATCATCCT	0.572	
+	10	2380		NM_022093	NP_071376	Q9UQP3	TENN_HUMAN	nectin type-III 6.	9	GGTGGGGAAGG	0.647	
-	2	838	_p.E253K|TNR_uc	NM_003285	NP_003276	Q92752	TENR_HUMAN	-like 3.|Cys-rich.	11	CTCTTCACAGA	0.622	
+	14	2405		NM_000186	NP_000177	P08603	CFAH_HUMAN	Sushi 12.	6	CAGAATCATTTA	0.418	
+	3	907	1_uc010ppa.1_R	NM_201253	NP_957705	P82279	CRUM1_HUMAN	g (Potential).|Extracellular	9	GGGATCACTGT	0.512	
+	4	419	1_Intron|PTPRC_	NM_002838	NP_002829	P08575	PTPRC_HUMAN	ellular (Potential).	12	ATACTTCCACCC	0.423	
-	3	464	hat.1_Missense_	NM_198447	NP_940849	Q6ZVE7	GOT1A_HUMAN	enal (Potential).	0	AGAATCCGTAG	0.552	
+	9	1208	p.Q316Q|CTSE_u	NM_001910	NP_001901	P14091	CATE_HUMAN		1	CTCCAGCTGGG	0.542	
+	4	856	_p.E267K|RASSF	NM_182663	NP_872604	Q8WWW0	RASF5_HUMAN		1	TCAAGGAGGTG	0.592	
-	2	502		NM_152485	NP_689698	Q96LT6	CA074_HUMAN		1	AATCTCAAGGA	0.507	
+	13	4051	3_uc001hnm.2_	NM_198551	NP_940953	Q5JRA6	MIA3_HUMAN	ytoplasmic (Potential).	5	GCCATCGGGTT	0.383	
+	9	1388	o.3_Missense_Mu	NM_152609	NP_689822	Q6PJW8	CNST_HUMAN		0	CAGTCCCTGCT	0.488	
+	6	1162	W3_uc001idp.1_I	NM_015431	NP_056246	Q8NG06	TRI58_HUMAN	B30.2/SPRY p.E372K(1)	7	AGGGGGAAACC	0.562	rs143805378
+	1	698_699		NM_001005471	NP_001005471	Q8NHC8	OR2T6_HUMAN	lasmic (Potential).	3	TGAAGGGAGGA	0.51	
-	1	577		NM_001001964	NP_001001964	Q8NH01	O2T11_HUMAN	Name=5; (Potential).	1	AGTTTCATACAA	0.483	
-	12	1700_1701	F692_uc001ifd.1_	NM_017865	NP_060335	Q9BU19	ZN692_HUMAN		0	TGGAGCCTGAG	0.604	
+	10	1740	ig.2_Missense_M	NM_178150	NP_835363	Q8NFZ0	FBX18_HUMAN		3	AGGGTGGATTC	0.453	
-	10	1117	_p.S306F|FRMPD	NM_001018071	NP_001018081	Q68DX3	FRPD2_HUMAN		1	AAATAGGATTTC	0.323	
-	2	372	f.3_Missense_Mu	NM_001083116	NP_001076585	P14222	PERF_HUMAN	MACPF.	3	GGTGCCGTCGG	0.697	rs142059134
+	6	503	_Mutation_p.G16	NM_033100	NP_149091	Q96JP9	CDHR1_HUMAN	|Extracellular (Potential).	1	TGGAGGGAGTG	0.612	
-	7	1385	01kgl.2_Missense_	NM_213606	NP_998771	Q6ZSM3	MOT12_HUMAN	ical; (Potential).	1	GCAGAGCCCAT	0.463	
-	3	459	ense_Mutation_p.	NM_000770	NP_000761	P10632	CP2C8_HUMAN		0	GGATCTCCTTCC	0.488	
+	6	3472	klq.2_Missense_	NM_014803	NP_055618	Q6AHZ1	Z518A_HUMAN		1	AGATGTGAGAG	0.373	

-	7	1170		NM_032211	NP_115587	Q96JB6	LOXL4_HUMAN	SRCR 3.		5	GGTTCCACCTG	0.682	
+	20	2992	CS3_uc010qqz.1_	NM_014978	NP_055793	Q9UPU3	SORC3_HUMAN	enal (Potential).		10	AGTTCCATTTG	0.448	
+	8	842		NM_000936	NP_000927	P16233	LIPP_HUMAN			3	TAGACGGAATC	0.398	rs62623373
+	8	807	e_Mutation_p.G26	NM_006541	NP_006532	O76003	GLRX3_HUMAN	lutaredoxin 2.		0	ATGTGGATTCA	0.299	
-	5	521	llu.2_Missense_M	NM_173572	NP_775843	Q5SR76	CJ093_HUMAN			1	GTGACGATATC	0.527	
+	1	835		NM_001127389	NP_001120861	F5GZ66	F5GZ66_HUMAN			0	CCTTCGCCCAC	0.776	rs150899513
-	12	2132	lissense_Mutation_	NM_145886	NP_665893	Q9HB75	PIDD_HUMAN			0	GCCCTCGAACA	0.677	
+	5	532		NM_206893	NP_996776	Q96PG2	M4A10_HUMAN	ellular (Potential).		2	AGGATCTCTTT	0.512	
-	8	1303	rp.2_Missense_M	NM_001136040	NP_001129512	Q8N684	CPSF7_HUMAN			1	GGACACGGCAA	0.517	
-	2	1247	_5'Flank|BRMS1_	NM_006876	NP_006867	O43505	B3GN1_HUMAN	enal (Potential).		0	ACCTTCGTTCA	0.473	
+	2	517	ense_Mutation_p.F	NM_002896	NP_002887	Q9BWF3	RBM4_HUMAN	RRM 1.		1	CCTGCCCCGGG	0.493	
-	11	1274		NM_006946	NP_008877	O15020	SPTN2_HUMAN	Spectrin 1.		4	CCAGCCGCTCC	0.672	
-	21	2765	1opz.2_Missense_	NM_012309	NP_036441	Q9UPX8	SHAN2_HUMAN	Pro-rich.		5	GGGACGGGGGC	0.587	
+	17	5357		NM_014786	NP_055601	Q96PE2	ARHGH_HUMAN			0	CAGGTATCTGA	0.473	
+	27	3762	e_Mutation_p.R11	NM_000260	NP_000251	Q13402	MYO7A_HUMAN	MyTH4 1.		4	TCCTGCGGCCA	0.577	
+	10	1970	uc001pen.1_Intron	NM_001098672	NP_001092142	Q6MZM0	HPHL1_HUMAN	e 4.|Extracellular (Potential		3	GGCATCCCTTC	0.383	
+	29	4622	pke.1_Splice_Site	NM_000051	NP_000042	Q13315	ATM_HUMAN			240	TTTCTAGGATTC	0.274	
+	8	879	gg.2_Missense_Mu	NM_001040455	NP_001035545	Q8NBJ9	SIDT2_HUMAN	ellular (Potential).		0	AAAACCCTGTCA	0.532	
+	2	354	4_uc010sca.1_5'F	NM_021978	NP_068813	Q9Y5Y6	ST14_HUMAN	lasmic (Pote	p.R54C(1)	5	GGGGCGCTGGG	0.607	
-	25	2774		NM_020373	NP_065106	Q9NQ90	ANO2_HUMAN	ellular (Pote	p.R902H(1)	7	CCAGACGGGCG	0.507	
-	10	2304	p.G726S|CD163_	NM_004244	NP_004235	Q86VB7	C163A_HUMAN	xtracellular (Potential).		8	GCGACCTCCTC	0.458	
-	3	305	zt.2_Missense_Mu	NM_002723	NP_002714	P10163	PRB4_HUMAN	R]-[PR]-P-Q-G-G-N-Q-[PS		1	GGGACCTTGGG	0.602	rs1063751
-	3	1091	ju.1_Missense_Mu	NM_198992	NP_945343	Q6XYQ8	SYT10_HUMAN	mic (Potential).|C2 1.		2	AAGTTCCTGTG	0.358	
-	8	2299		NM_005164	NP_005155	Q9UBJ2	ABCD2_HUMAN	C transporter.		6	ACTTATGATAAA	0.368	
+	4	324	nn.1_Missense_M	NM_001843	NP_001834	Q12860	CNTN1_HUMAN	like C2-type 1.		9	CCAGCCCTTTC	0.428	
-	1	82		NM_025003	NP_079279	P59510	ATS20_HUMAN			19	CCTGGGGTGGA	0.652	
+	1	82	utation_p.H28Y|L	NM_152641	NP_689854	Q68CP9	ARID2_HUMAN	ARID.		10	TCCACCACAGC	0.677	
+	4	1242	p.E51K|FAM113B_	NM_138371	NP_612380	Q96HM7	F113B_HUMAN			5	GCGAGGAAGTC	0.617	
+	26	2868_2869	p.S472F|NCKAP1	NM_005337	NP_005328	P55160	NCKPL_HUMAN			4	TTTCTCCTCCCA	0.416	
+	1	226		NM_002469	NP_002460	P23409	MYF6_HUMAN			1	CAGCGGAGAGG	0.622	
+	13	3257	ab.1_Missense_M	NM_001079910	NP_001073379	Q96JM4	LRIQ1_HUMAN	LRR 8.		6	TTCAACTGTGG	0.308	
+	3	369	Site|C12orf23_uc0	NM_152261	NP_689474	Q8WUH6	CL023_HUMAN			0	TTTTAGGAGATC	0.323	
-	8	1363	.2_Nonsense_Mu	NM_181486	NP_852259	Q99593	TBX5_HUMAN			8	GTATTGGGACC	0.577	
-	51	6918		NM_006836	NP_006827	Q92616	GCN1L_HUMAN			4	CCACGGAGGGC	0.622	
-	12	1570	33A_uc001ucc.2_	NM_022916	NP_075067	Q96AX1	VP33A_HUMAN			1	ACATACGATATGT	0.527	
-	1	943	81_uc001ucw.1_I	NM_006018	NP_006009	P49019	HCAR3_HUMAN	ellular (Potential).		2	TCTGCGTGCCC	0.537	
-	5	1217		NM_006001	NP_005992	Q13748	TBA3C_HUMAN			5	CAGGCGAGCCC	0.647	
-	3	1055	p.K168E|GJB6_u	NM_006783	NP_006774	O95452	CXB6_HUMAN	ellular (Potential).		1	ACATTTCAACAC	0.443	
-	1	409	A_uc010tee.1_Int	NM_005584	NP_005575	Q13394	MB211_HUMAN			2	TGCAGCGTTGGT	0.373	
-	3	1121		NM_000452	NP_000443	Q12908	NTCP2_HUMAN	ical; (Potential).		4	AAACAGGAACA	0.393	
-	3	797	p.R126C|ZNF219_	NM_016423	NP_057507	Q9P2Y4	ZN219_HUMAN		p.R126R(1)	1	CGCGCGCTCTT	0.721	
-	34	5016		NM_000257	NP_000248	P12883	MYH7_HUMAN	Potential.		4	CCTCGGCGGCC	0.597	
+	3	243		NM_144578	NP_653179	Q8NDC0	MISSL_HUMAN	Pro-rich.		0	CAAAACCTGGC	0.517	
+	3	275		NM_002306	NP_002297	P17931	LEG3_HUMAN	epeats of Y-P-G-X(3)-P- G-		0	TCCTATCCTGGG	0.662	
+	3	910	p.N155S|PCNX_	NM_014982	NP_055797	Q96RV3	PCX1_HUMAN			1	AAGCAACCAGG	0.483	
+	5	3218	M1_uc001xql.3_F	NM_019589	NP_062535	P49750	YLPM1_HUMAN	Arg-rich.		3	ACACACGGGAT	0.493	
+	8	809	LL5_uc010ask.1_	NM_015072	NP_055887	Q6EMB2	TTLL5_HUMAN	TTL.		3	CCCTGGAAGAG	0.398	

+	16	2086	ybs.1_Missense_	NM_020818	NP_065869	Q9P2D8	UNC79_HUMAN		p.I654_H670del(	17	GGGGGGATCCC	0.448
-	4	1604	gb.2_Missense_M	NM_138576	NP_612808	Q9C0K0	BC11B_HUMAN	2H2-type 2.		10	TGCGCCGGTGC	0.652
+	75	13614		NM_001376	NP_001367	Q14204	DYHC1_HUMAN			10	TCAGCGAGAGG	0.612
+	25	3125	r.2_Missense_Mut	NM_001036	NP_001027	Q15413	RYR3_HUMAN	c (By similarity).|4 X appro		10	CCCGTCTGGTG	0.453
-	2	268	.2_Missense_Mut	NM_033503	NP_277038	Q96LC9	BMF_HUMAN			1	TGGGTCGAAGG	0.622
+	23	7980	.1_Missense_Mut	NM_001164273	NP_001157745	Q8IWI9	MGAP_HUMAN			12	GACTCCGCAAG	0.433
+	9	1219	sa.2_Missense_M	NM_017705	NP_060175	Q9NXK6	MPRG_HUMAN	lasmic (Potential).		2	GGAAGGAATGG	0.498
+	12	2313	te.2_Nonsense_M	NM_024817	NP_079093	Q6ZMP0	THSD4_HUMAN	SP type-1 3.		2	CGACTGGACCT	0.637
+	2	1531	h.1_Nonsense_Mu	NM_005545	NP_005536	O14498	ISLR_HUMAN			4	TGGGCCAAAGC	0.617
+	2	2182	unk.1_Missense_	NM_015206	NP_056021	Q9UPX6	K1024_HUMAN			4	AAAGCCTCTTC	0.547
-	2	367	_p.L67P|FSD2_uc	NM_001007122	NP_001007123	A1L4K1	FSD2_HUMAN			1	CTTGAAGGTCT	0.443
+	17	1568	_Missense_Mutati	NM_138769	NP_620124	Q8IXI1	MIRO2_HUMAN	rial intermembrane (Potent		1	AGTCCTTTGCA	0.632
+	6	1507	_p.N40S|ZNF263	NM_005741	NP_005732	O14978	ZN263_HUMAN	2H2-type 1.		4	CTCAAACCTAA	0.478
+	7	1444	_p.A369T|UBN1_u	NM_001079514	NP_001072982	Q9NPG3	UBN1_HUMAN			2	AGCTGGCTCAG	0.577
-	13	4513	1322E|GRIN2A_	NM_001134407	NP_001127879	Q12879	NMDE1_HUMAN	lasmic (Potential).		45	AATTTCCCTCC	0.527
+	11	1514		NM_017888	NP_060358	Q6NUN0	ACSM5_HUMAN			2	GGACCGAGCTC	0.483
-	7	984	_p.W258*|ACSM2	NM_182617	NP_872423	Q68CK6	ACS2B_HUMAN			5	TATGGTCCACA	0.443
+	15	1913	_p.D405N|SLC5A1	NM_052944	NP_443176	Q8WWX8	SC5AB_HUMAN	lasmic (Potential).		2	GTCACGACCCC	0.577
-	2	371	ou.2_Nonsense_	NM_001520	NP_001511	Q12789	TF3C1_HUMAN			5	GCCCTGGATGC	0.463
-	1	298	vq.1_Missense_M	NM_024939	NP_079215	Q9H6T0	ESRP2_HUMAN			1	CCGCCGTAGCC	0.413
-	3	669	_p.L83F|SMPD3_	NM_018667	NP_061137	Q9NY59	NSMA2_HUMAN	ical; (Potential).		1	GAAGAGAAAGC	0.642
-	10	1600		NM_005652	NP_005643	Q15554	TERF2_HUMAN	b-type.|H-T-H motif.		1	TGGTCCGCCAG	0.438
+	12	5035	_Mutation_p.M12	NM_006599	NP_006590	O94916	NFAT5_HUMAN			0	ATACCATGGCTA	0.299
+	4	485	NTNAP4_uc002fe	NM_033401	NP_207837	Q9C0A0	CNTP4_HUMAN	(Potential).|F5/8 type C.		2	ATGATCCTCTT	0.473
-	5	762	_p.G68S|FBXO31	NM_024735	NP_079011	Q5XUX0	FBX31_HUMAN			1	CCCGCCGGACA	0.557
-	4	284	D_uc002flf.1_5'Fl	NM_002461	NP_002452	P53602	MVD1_HUMAN			0	CCTCCGCTTCC	0.697
+	1	114_115	B3_uc010cja.1_R	NM_006086	NP_006077	Q13509	TBB3_HUMAN			3	GATCGGGGCC	0.347
+	37	5690	_Mutation_p.S181	NM_001005273	NP_001005273	Q12873	CHD3_HUMAN	interaction with PCNT.		1	CCTCTCCAAGG	0.607
+	32	7129		NM_016239	NP_057323	Q9UKN7	MYO15_HUMAN	Tail.		9	CGGCTGGACCG	0.602
-	5	1584		NM_001145045	NP_001138517	P0CG31	Z286B_HUMAN	2H2-type 8.		0	TTTTCCCACATT	0.388
+	1	285	L3_uc002hit.2_5'F	NM_017559	NP_060029	Q8TC99	FNDC8_HUMAN		p.N68I(1)	2	CATCAACCTAC	0.284
-	3	336	16_uc002hkm.2_	NM_004590	NP_004581	O15467	CCL16_HUMAN			0	TTGGGATCCTTG	0.507
-	14	1884	nn.2_Missense_M	NM_198836	NP_942133	Q13085	ACACA_HUMAN	in carboxylation.		2	GTTTTCTCCCC	0.393
-	1	196	39_uc010wfm.1_5	NM_213656	NP_998821	Q6A163	K1C39_HUMAN	Head.		0	CCAGGGAATTC	0.502
+	4	479	0cze.1_Missense_	NM_145041	NP_659478	Q96A25	T106A_HUMAN			0	CATTCCCTATGG	0.572
-	4	450	37A2_uc002ikn.1_	NM_016632	NP_057716	Q8IVW1	ARL17_HUMAN			0	TGCCGGTGACC	0.403
+	1	2104	uc010wna.1_RNA	NM_032559	NP_115948	Q8N4N8	KIF2B_HUMAN	Potential.		8	AAAATTGATGCT	0.458
+	11	1305	te_p.P300_splice|	NM_005486	NP_005477	O75674	TM1L1_HUMAN			1	CCCCCGTAAGT	0.318
+	13	2750_2751	pm.1_Missense_	NM_030779	NP_110406	Q9H252	KCNH6_HUMAN	lasmic (Potential).		1	CCCCAGGGCTT	0.619
+	8	1106	l.2_Missense_Mu	NM_002266	NP_002257	P52292	IMA2_HUMAN	ing site (minor) (By similari		2	TACAGATGAAC	0.438
+	4	1291	qx.1_Missense_	NM_181790	NP_861455	Q7Z601	GP142_HUMAN	lasmic (Potential).		4	TCCACGATGCC	0.607
+	3	705	.1_3'UTR|ARMC7_	NM_024585	NP_078861	Q9H6L4	ARMC7_HUMAN	ARM 2.		1	TCCCAGAGCTG	0.632
+	7	849	g.3_Missense_Mu	NM_001258	NP_001249	Q00526	CDK3_HUMAN	rotein kinase.		1	GCCAGAGGGCA	0.582
+	9	1427	jth.2_Missense_M	NM_198955	NP_945193	Q3V5L5	MGT5B_HUMAN	enal (Potential).		3	TGTTTCGTGAG	0.622
-	10	1985	TEC_uc010xaj.1_	NM_001137671	NP_001131143	B2RU33	POTEC_HUMAN	Potential.		3	ATACCTCAGAAT	0.269
-	10	1973	TEC_uc010xaj.1_	NM_001137671	NP_001131143	B2RU33	POTEC_HUMAN	Potential.		3	TCATTTTCTTTTC	0.284
+	15	2956	p.1_Missense_Mu	NM_001942	NP_001933	Q02413	DSG1_HUMAN	ential).|Desmoglein repeat		7	TCCTAGAGAGT	0.468

+	14	2094		NM_005925	NP_005916	Q16820	MEP1B_HUMAN	lasmic (Potential).	2	AAATATCGTGAA	0.408	
-	8	1490	_Mutation_p.E347K	NM_003787	NP_003778	O94818	NOL4_HUMAN		3	AGTTTTCATCTAC	0.478	
-	7	2067	kzj.2_Missense_M	NM_012319	NP_036451	Q13433	S39A6_HUMAN	lasmic (Potential).	2	AGTGGCGACGC	0.318	
+	7	1794	_p.E251K|DCC_uc	NM_005215	NP_005206	P43146	DCC_HUMAN	otential).|Ig-like C2-type 4.	17	TGGCTGAAAAT	0.438	
-	5	2855	k.1_Missense_Mu	NM_052947	NP_443179	Q86TB3	ALPK2_HUMAN		14	TGCCGTCCTTGC	0.428	
-	2	220	_p.N65S|SERPINB3_uc010dqb.2_Missense_Mutation_p			P48594	SPB4_HUMAN		3	TGGTGTTCTCT	0.428	
-	2	1244		NM_032160	NP_115536	Q8IZU8	DSEL_HUMAN		6	ATGGGGGAGCT	0.383	
-	4	363	uc010dvi.1_5'Flank	NM_020196	NP_064581	Q9HCS7	SYF1_HUMAN	HAT 3.	4	TAGCCACAGACG	0.657	
-	3	21008		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).	57	CAGAGGAAACA	0.458	
-	1	6323		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	h.|Extracellular (Potential).	57	ATTGTGGAATCC	0.488	
-	2	333	n_p.R16L|ICAM3_	NM_002162	NP_002153	P32942	ICAM3_HUMAN	otential).|Ig-like C2-type 1.	3	AGGATCCGACTG	0.552	
-	4	1744	3_uc002msz.1_Mi	NM_001080411	NP_001073880	Q8N7K0	ZN433_HUMAN	2H2-type 14.	0	TCCTTCCATGAT	0.443	
+	1	143	xf.2_Missense_Mu	NM_001031727	NP_001026897	Q9BV20	MTNA_HUMAN		1	GAGCCGCTACG	0.537	
+	10	2692	_p.S622F|NWD1_uc002nev.3_Missense_Mutation_p.S5			Q149M9	NWD1_HUMAN		7	GATTTCCTGCC	0.597	
-	13	2081	.R249Q|PDE4C_u	NM_001098819	NP_001092289	Q08493	PDE4C_HUMAN		5	TGGATTCGGTCG	0.378	
+	19	2420	dd.2_Missense_M	NM_173636	NP_775907	O43379	WDR62_HUMAN		0	GCCACCCCAGG	0.453	
-	5	506	oo.2_Missense_M	NM_004756	NP_004747	Q9Y6R0	NUMBL_HUMAN	PID.	5	TCACGGACTTT	0.652	
+	1	550	rf54_uc002oox.1_	NM_004596	NP_004587	P09012	SNRPA_HUMAN		4	CCCGAGACCCG	0.498	
-	2	253	on_p.L41Q|PSG5_	NM_002781	NP_002772	Q15238	PSG5_HUMAN	g-like V-type.	3	GTGGCAGGGCT	0.468	
-	4	855_856	.E160K|PSG9_uc	NM_002784	NP_002775	Q00887	PSG9_HUMAN	like C2-type 2.	2	ATTCTCCCTGGG	0.51	
-	1	1154	2peu.1_Silent_p.L	NM_020709	NP_065760	Q9ULN7	PNML2_HUMAN		1	ACTGCCTAACC	0.637	
-	9	2649	xyr.1_Missense_M	NM_015063	NP_055878	Q9UPR5	NAC2_HUMAN	.|Helical; (Potential).	4	GCCCAGGGCAA	0.602	
+	1	58		NM_033068	NP_149059	Q9BZG2	PPAT_HUMAN		0	tgctgctgctggtgctg	0.622	
+	2	654	yct.1_Missense_M	NM_014441	NP_055256	Q9Y336	SIGL9_HUMAN	otential).|Ig-like C2-type 1.	1	CTCCTCGGTGC	0.657	rs141688796
-	3	1129	_p.R240Q|SIGLEC	NM_053003	NP_443729	Q96PQ1	SIG12_HUMAN	1.|Extracellular (Potential).	5	TGAGTCGGACA	0.602	
+	7	2416	qr.1_Missense_M	NM_018555	NP_061025	Q9NQX6	ZN331_HUMAN	2H2-type 8.	6	CTCACGAATGT	0.507	
+	4	621	010esf.2_Missense	NM_013289	NP_037421	P43629	KI3L1_HUMAN	otential).|Ig-like C2-type 2.	5	ATGATGCTTGC	0.547	
+	3	1399	tg.2_Missense_Mu	NM_176811	NP_789781	Q86W28	NALP8_HUMAN	NACHT.	13	ACTTTTCCAGAA	0.473	
-	11	2299	113_uc010eyk.1_	NM_001145168	NP_001138640	Q8IZF5	GP113_HUMAN	ellular (Potential).	4	GGGTTCTTCCG	0.627	
+	7	900	se_Mutation_p.R2	NM_015701	NP_056516	Q96DZ1	ERLEC_HUMAN		2	GCCCAGATCAA	0.378	
-	3	329	_p.R40K|TPRKB_	NM_016058	NP_057142	Q9Y3C4	TPRKB_HUMAN		2	AGAGTTCTTGTC	0.353	
+	7	865		NM_031283	NP_112573	Q9HCS4	TF7L1_HUMAN	Pro-rich.	3	TCCTCCCGGTG	0.612	
+	3	224	1A_uc002sqv.2_5'	NM_017952	NP_060422	Q96EY7	PTCD3_HUMAN		1	CATTAGGGATTG	0.284	
-	2	1056	p.E313K|ST6GAL	NM_001142351	NP_001135823	Q96JF0	SIAT2_HUMAN	enal (Potential).	11	TATTTCCTCGCC	0.667	
-	2	151	_p.R11Q|ST6GAL	NM_001142351	NP_001135823	Q96JF0	SIAT2_HUMAN	lasmic (Potential).	11	AGCATTCGTTGT	0.507	
-	4	371	h.1_Missense_Mu	NM_000576	NP_000567	P01584	IL1B_HUMAN		4	TGAAGGGAAAG	0.532	
-	19	3556		NM_018383	NP_060853	Q9C0J8	WDR33_HUMAN		0	ACCAGGAAAAC	0.567	
-	4	527	se_Mutation_p.P5	NM_013450	NP_038478	Q9UIF8	BAZ2B_HUMAN		4	TAAACGGTTGAT	0.433	
+	27	5425	p.T1712I|SCN2A_	NM_001040142	NP_001035232	Q99250	SCN2A_HUMAN	IV.	8	TACAACCTCTGC	0.458	
-	8	1706	STKD1_uc002uex	NM_024622	NP_078898	Q53R41	FAKD1_HUMAN		4	GGCTTCAATTC	0.418	
-	3	1016		NM_001080458	NP_001073927	Q03828	EVX2_HUMAN		2	GGAAGGGGTAG	0.522	
-	225	45318	_uc010zfi.1_Misse	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	AATTTCCCCAC	0.473	
-	75	19126	_uc010zfj.1_Intro	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	TGATTCGCATC	0.408	rs72648969
-	46	13470	.E4349K|TTN_uc0	NM_133437	NP_597681	Q8WZ42	TITIN_HUMAN		153	AACCTCCTCAG	0.453	
-	46	14139	N_uc010zfi.1_Intr	NM_133379	NP_596870	Q8WZ42	TITIN_HUMAN		153	CTGTTCCCTAG	0.373	
-	2	1412		NM_004657	NP_004648	O95810	SDPR_HUMAN		2	CCCTGGAGGTC	0.577	
+	20	2263_2264	_p.R277K|AOX1_u	NM_001159	NP_001150	Q06278	ADO_HUMAN		6	AGAAAGGAAACT	0.426	

+	26	2973	p.E514K|AOX1_u	NM_001159	NP_001150	Q06278	ADO_HUMAN		6	TACAAGGAAATT	0.368	
+	10	1862	xm.1_Missense_M	NM_032974	NP_116756	Q92851	CASPA_HUMAN		6	CAATGGAAATCA	0.512	
+	11	2663	0fvx.2_Missense_	NM_014640	NP_055455	Q14679	TTLL4_HUMAN	TTL.	3	TTTGACCTGCGG	0.488	
-	1	421	ls.1_Missense_Mu	NM_003590	NP_003581	Q13618	CUL3_HUMAN		4	GGTGTCCTTCC	0.602	rs2969802
-	3	1640	zoj.1_Missense_M	NM_182501	NP_872307	Q7Z6M4	MTER2_HUMAN		1	cattgtcatcctcatcatt	0.224	
-	8	2241	nj.2_Missense_Mu	NM_020341	NP_065074	Q9P286	PAK7_HUMAN	rotein kinase.	23	CCTGTGAATCA	0.443	
-	8	2152	e_Mutation_p.W2	NM_032501	NP_115890	Q9NUB1	ACS2L_HUMAN		2	ACTCCCAGGCC	0.527	
+	2	127	tj.1_RNA|FRG1B_uc010gdr.1_RNA|FRG1B_uc010ztk.1_Intron						0	ATTCAGATGCAA	0.333	
-	2	776	xcb.1_Missense_M	NM_178468	NP_848563	Q9BQN1	FA83C_HUMAN		2	GAGGTCCATCT	0.647	
-	3	2822	dk.2_Intron|CPNE	NM_152838	NP_690051	Q9NTZ6	RBM12_HUMAN	RRM 3.	3	TAAAGGGCATGT	0.353	
+	11	1414	ggc.2_Missense_	NM_015568	NP_056383	Q96T49	PP16B_HUMAN		3	CTACTCTCCGAA	0.567	
-	5	521	3_uc002xph.1_In	NM_080614	NP_542181	Q8IUB2	WFDC3_HUMAN	WAP 3.	0	TATGCCCCTGG	0.547	
-	3	1323		NM_080617	NP_542184	Q9NTU7	CBLN4_HUMAN	C1q.	4	TTTCTCCAGTTT	0.453	
-	21	3392	TCL1_uc011agu.1_	NM_007098	NP_009029	P53675	CLH2_HUMAN	gment.|Heavy chain arm.	5	ACACAGCAGGC	0.527	
+	6	2719	'Flank|GHRLOS_	NM_014760	NP_055575	Q93075	TATD2_HUMAN		2	CCTCCCTCGCC	0.622	
+	6	2721	5'Flank|GHRLOS_	NM_014760	NP_055575	Q93075	TATD2_HUMAN		2	TCCCTCGCCAG	0.617	rs150215933
+	6	574	vl.1_Missense_Mu	NM_133625	NP_598328	Q92777	SYN2_HUMAN		2	TCCTTGGAGATT	0.433	
-	20	3063	ense_Mutation_p.	NM_003615	NP_003606	Q9Y6M7	S4A7_HUMAN	cellular (Potential).	5	TTGTTCCCCTG	0.433	
-	11	1701		NM_003500	NP_003491	Q99424	ACOX2_HUMAN		0	CTTACCTTACT	0.597	rs145582569
-	10	1127	hob.2_Missense_	NM_003848	NP_003839	Q96I99	SUCB2_HUMAN		2	GTTGACGATAC	0.448	rs115935149
-	5	780	p.R12W|KIAA152	NM_020890	NP_065941	Q8TCG1	CIP2A_HUMAN		3	GTGCCGACAAA	0.299	
-	6	1088	y.2_Missense_Mu	NM_001015887	NP_001015887	Q5DX21	IGS11_HUMAN	lasmic (Potential).	0	ATTAGGAATTTC	0.323	
-	9	1787	jg.1_Missense_M	NM_153002	NP_694547	Q8NFN8	GP156_HUMAN	lasmic (Potential).	2	TGTAAGGGCTA	0.602	
-	9	1417		NM_199420	NP_955452	O75417	DPOLQ_HUMAN	case C-terminal.	11	GGCTCCTTCAA	0.378	
+	8	899	bjn.1_Missense_M	NM_021082	NP_066568	Q16348	S15A2_HUMAN		1	TGAAGGAAACA	0.338	
-	13	2948		NM_022776	NP_073613	Q9BXB4	OSB11_HUMAN		5	TATTTTCCAAAGT	0.358	
-	3	1977	c003ekl.1_5'Flan	NM_153330	NP_699161	Q8NHS0	DNJB8_HUMAN		0	CAGGCCACCAA	0.637	
-	8	1344	1257_uc003elh.1_	NM_020741	NP_065792	Q9ULG3	K1257_HUMAN		0	TGACGGCCAGC	0.592	
-	9	1581	wp.1_Missense_M	NM_024727	NP_079003	Q6UY01	LRC31_HUMAN		3	TCTAAACCATT	0.448	
-	3	12753	1bth.1_Intron|MU	NM_018406	NP_060876	Q99102	MUC4_HUMAN	Ser-rich.	0	TGACAGGAAGA	0.587	
-	3	941		NM_025163	NP_079439	Q86VD9	PIGZ_HUMAN	ical; (Potential).	3	GGGCTGCCCCA	0.612	rs149492566
+	1	31		NM_001040448	NP_001035538	P59861	DB131_HUMAN		0	GAGTCCTTTCC	0.368	
+	30	3352	s.1_Missense_Mut	NM_004787	NP_004778	O94813	SLIT2_HUMAN	EGF-like 4.	11	AGCACGATTCA	0.483	
+	15	1255	iet.1_Missense_M	NM_013367	NP_037499	Q9UJX5	APC4_HUMAN		5	CAAAAATATGAA	0.343	
-	5	820	zh.1_Missense_M	NM_006587	NP_006578	Q9Y5Q5	CORIN_HUMAN	ular (Potential).|FZ 1.	2	TTCTAAACTGGG	0.468	
+	16	2235	zl.1_Missense_Mu	NM_025087	NP_079363	Q9H720	PG2IP_HUMAN		3	AATTATGAAAAC	0.259	
-	33	5653		NM_014991	NP_055806	Q8IZQ1	WDFY3_HUMAN		3	AGCATCTCGGT	0.458	
+	32	5717	p.S1727F|PTPN1	NM_080683	NP_542414	Q12923	PTN13_HUMAN	Poly-Ser.	6	TGCTTCCTCTA	0.393	
+	3	378	se_Mutation_p.P5	NM_001033047	NP_001028219	Q6UXI9	NPNT_HUMAN	EGF-like 1.	1	CACAGCTGTGT	0.388	
-	7	1075	D_uc003icl.2_RN	NM_014822	NP_055637	O94855	SC24D_HUMAN	Pro-rich.	0	CCTGGATCTGA	0.478	
-	7	866	e.1_Missense_Mu	NM_176824	NP_789794	Q8IWZ6	BBS7_HUMAN		1	GAATTTCCCACT	0.338	
+	13	1451	_Mutation_p.R22	NM_015312	NP_056127	Q2LD37	K1109_HUMAN		12	CCCCCGAATAT	0.378	
-	17	1850	hn.1_Missense_M	NM_003866	NP_003857	O15327	INP4B_HUMAN		2	GTAGTTGATTGA	0.383	
-	14	2299	.R609W|LRBA_u	NM_006726	NP_006717	P50851	LRBA_HUMAN		7	TCTCCGAATGG	0.418	
+	12	1881	p.D114N|ETFDH_	NM_004453	NP_004444	Q16134	ETFD_HUMAN		3	GTTTTGACCTC	0.438	
+	12	1920	p.E127K|ETFDH_	NM_004453	NP_004444	Q16134	ETFD_HUMAN		3	ATCATGAACATG	0.468	
+	8	1646	Z3_uc003ive.1_5'	NM_001080477	NP_001073946	Q9P273	TEN3_HUMAN	r (Potential).|EGF-like 1.	0	TGTTTTCCAGGA	0.408	

-	6	1580	_p.M230I|LRP2BP	NM_018409	NP_060879	Q9P2M1	LR2BP_HUMAN	Sel1-like 5.	0	AAATTTCATCTTA	0.308	
-	2	1212	.1_Missense_Mut	NM_005245	NP_005236	Q14517	FAT1_HUMAN	ellular (Potential).	12	GAGTTCCTTTAT	0.458	
+	4	796		NM_007277	NP_009208	O60645	EXOC3_HUMAN		0	AAATTGACAGGC	0.517	
+	2	770		NM_024337	NP_077313	P78414	IRX1_HUMAN		2	GCGACCAGAGC	0.667	
+	13	1949		NM_015325	NP_056140	Q9Y2F5	K0947_HUMAN		2	TGAACCAGACC	0.388	
-	71	12215	fc.2_Missense_Mu	NM_001369	NP_001360	Q8TE73	DYH5_HUMAN	6 (By similarity).	31	ATGATGGAATCT	0.517	
-	27	4193		NM_001369	NP_001360	Q8TE73	DYH5_HUMAN	n (By similarity).	31	GTATATGTGATG	0.313	
+	31	4632	IO_uc003jfh.1_Mis	NM_007118	NP_009049	O75962	TRIO_HUMAN	PH 1.	18	GAGTTGGGTGT	0.393	
+	3	965		NM_012304	NP_036436	Q9UJT9	FBXL7_HUMAN		3	CGGGCGAGACC	0.662	
+	11	2037		NM_020227	NP_064612	Q9NQV7	PRDM9_HUMAN	2H2-type 5.	6	TTAGCCGGCAG	0.622	rs111393391
-	12	2291	v.1_Missense_Mu	NM_016279	NP_057363	Q9ULB4	CADH9_HUMAN	lasmic (Potential).	9	ATTTTCCCACAG	0.418	
-	7	1200		NM_016279	NP_057363	Q9ULB4	CADH9_HUMAN	|Extracellular (Potential).	9	CTTAAAGTATAG	0.328	
+	10	1903	d.1_Missense_Mu	NM_004932	NP_004923	P55285	CADH6_HUMAN	(Potential).|Cadherin 5.	7	GTTTTCCTTGG	0.413	
+	1	671	z.1_Intron|NPR3_	NM_000908	NP_000899	P17342	ANPRC_HUMAN	ellular (Potential).	2	TGGGACCTGCC	0.701	
-	6	900		NM_001737	NP_001728	P02748	CO9_HUMAN	MACPF.	0	AAACCGAAAAC	0.323	
+	2	465	ELD2_uc003jwr.1_	NM_001038603	NP_001033692	Q8N4S9	MALD2_HUMAN	lasmic (Potential).	0	AAGATCCCTAC	0.542	
+	8	5143	.2_Intron|VCAN_u	NM_004385	NP_004376	P13611	CSPG2_HUMAN	GAG-beta.	16	TGTTTCAGAGG	0.428	
-	6	957	e_Mutation_p.R1	NM_001239	NP_001230	P51946	CCNH_HUMAN		3	CAAGTTCTGTTC	0.294	
-	20	2359		NM_014639	NP_055454	Q6PGP7	TTC37_HUMAN	TPR 12.	4	CTTTTTCTATGT	0.284	
-	13	2337		NM_180991	NP_851322	Q6ZQN7	SO4C1_HUMAN	ame=12; (Potential).	4	AAATCCATTGA	0.308	
+	11	2215	kuz.2_Missense_	NM_014031	NP_054750	Q9Y2P4	S27A6_HUMAN		0	CCAGGGAACTT	0.338	
-	11	2476	se_Mutation_p.E7	NM_020389	NP_065122	Q9HCX4	TRPC7_HUMAN	lasmic (Potential).	0	TTTTTCCTCAA	0.478	
-	10	1342_1343	bp.2_Missense_M	NM_004598	NP_004589	Q08629	TICN1_HUMAN		1	AAATCCCCTGA	0.505	rs139421454
-	5	930	o.2_Missense_Mu	NM_001496	NP_001487	O60609	GFRA3_HUMAN		1	CAGGCGTGATC	0.318	
+	1	975		NM_013340	NP_037472	Q9Y5F3	PCDB1_HUMAN	|Extracellular (Potential).	0	ATGGAGAAGTT	0.463	
+	1	2541		NM_018933	NP_061756	Q9Y5F0	PCDBD_HUMAN	lasmic (Potential).	3	TACAAGGAAATT	0.443	
+	1	2351	dal.1_Missense_	NM_018934	NP_061757	Q9Y5E9	PCDBE_HUMAN	lasmic (Potential).	1	TATGGGGGAAA	0.373	
+	1	1024	jfx.1_Intron|PCDH	NM_018923	NP_061746	Q9Y5G2	PCDGE_HUMAN	(Potential).|Cadherin 3.	0	ACAACGATTGT	0.443	
-	2	287	RAP3_uc003llo.1_	NM_022481	NP_071926	Q8WWN8	ARAP3_HUMAN		7	CCAGGGAGCCC	0.642	
-	1	313		NM_001080516	NP_001073985	A6NFK2	GRCR2_HUMAN		0	TGTAATCGTTGA	0.498	
-	4	1058	sense_Mutation_	NM_014790	NP_055605	Q96AA8	JKIP2_HUMAN	Potential.	2	CAGTTCCTTTT	0.423	
+	15	2714	.1_Intron|FBXO38	NM_205836	NP_995308	Q6PIJ6	FBX38_HUMAN		6	CCCTCGGAGGC	0.572	
+	16	3055	se_Mutation_p.S8	NM_001114183	NP_001107655	P42261	GRIA1_HUMAN	lasmic (Potential).	6	CAGTTCAGGGA	0.622	rs144882662
-	2	1523	p.S489F|PWWP2	NM_001130864	NP_001124336	Q96N64	PWP2A_HUMAN		0	TTCAGAGAAGAG	0.522	
+	49	5154	e_Mutation_p.E11	NM_004946	NP_004937	Q92608	DOCK2_HUMAN		7	TGCCTGAGGTC	0.587	
-	6	991	tion_p.H63Y|MGA	NM_014275	NP_055090	Q9UQ53	MGT4B_HUMAN	enal (Potential).	0	AGAATGGATCT	0.632	
-	4	1055	2A23_uc003mvp.1	NM_015482	NP_056297	A1A5C7	S22AN_HUMAN	ical; (Potential).	1	GGAAGGGGCA	0.662	
+	3	337	bh.2_Missense_M	NM_004233	NP_004224	Q01151	CD83_HUMAN	(Potential).|Ig-like V-type.	0	TTATTGGAGGG	0.507	
-	6	695	se_Mutation_p.C1	NM_005074	NP_005065	Q14916	NPT1_HUMAN	ical; (Potential).	4	AGATTCACAGAT	0.368	
-	3	537	A-DRB5_uc003ob	NM_002125	NP_002116	Q30154	DRB5_HUMAN	ta-2.|Extracellular (Potenti	0	ATTCTGAATCA	0.552	
+	8	884	plice_Site|GLP1R_	NM_002062	NP_002053	P43220	GLP1R_HUMAN		5	TCTTAGGTGTT	0.617	
+	6	1041	_p.E238K|MDFI_u	NM_005586	NP_005577	Q99750	MDFI_HUMAN	Cys-rich.	0	GCATGGAGTGC	0.672	
-	4	502	pai.2_Missense_M	NM_138694	NP_619639	P08F94	PKHD1_HUMAN	tential).|IPT/TIG 1; atypica	44	ACAGGGAACAC	0.507	
+	5	1539		NM_001010872	NP_001010872	Q5T0W9	FA83B_HUMAN		6	ATATCCGCTTTT	0.408	
-	3	677	se_Mutation_p.D1	NM_030820	NP_110447	Q96P44	COLA1_HUMAN	VWFA.	2	GTCATCTTGGG	0.443	
-	20	2514	p.1_Missense_Mu	NM_017934	NP_060404	Q8WWQ0	PHIP_HUMAN		6	TCTTTTGGAACA	0.323	
-	5	965	VL4_uc011dyt.1_I	NM_022726	NP_073563	Q9GZR5	ELOV4_HUMAN		2	GGTATCGTTTCC	0.343	

+	12	1542	_uc010kcd.2_Mis	NM_014942	NP_055757	Q9Y2G4	ANKR6_HUMAN			3	GCAAGGATGGG	0.517	
-	17	3102	ai.1_Missense_Mu	NM_006828	NP_006819	Q8N3C0	HELC1_HUMAN			6	TCATCCGTACAT	0.343	
-	3	418	ense_Mutation_p.F	NM_198081	NP_932347	Q8N228	SCML4_HUMAN			1	GAACCCGAGAC	0.562	
-	13	1530	p.S426L|CDK19_	NM_015076	NP_055891	Q9BWU1	CDK19_HUMAN	Ser-rich.		4	GAGACGAGGAA	0.587	
+	17	2230		NM_173560	NP_775831	Q8HWS3	RFX6_HUMAN			3	ACACCGAGCAT	0.527	
+	3	686	L2_uc003pxo.2_Ir	NM_182645	NP_872586	Q8N8G2	VGLL2_HUMAN			1	CCGCGCACTCG	0.746	
+	12	1641	nse_Mutation_p.G	NM_015440	NP_056255	Q6UB35	C1TM_HUMAN	hydrofolate synthetase.		4	CCAAGGACCGA	0.488	
-	3	625	AD1L1_uc010ksj.	NM_013393	NP_037525	Q9UI43	RRMJ2_HUMAN			1	TTTGACTTCCA	0.512	
-	17	1637	a.2_Missense_Mu	NM_004080	NP_004071	Q9Y6T7	DGKB_HUMAN	DAGKc.		12	ATCACGGAAAA	0.368	
-	5	657	MY2_uc010ktz.2_	NM_020319	NP_064715	Q8IV38	ANKY2_HUMAN			1	TGGCTCTTTATC	0.438	
+	6	438	e.1_Missense_Mu	NM_031414	NP_113602	Q9BXU1	STK31_HUMAN	Tudor.		9	TAAATCGATCTG	0.358	
-	1	510		NM_000162	NP_000153	P35557	HXK4_HUMAN			4	CTTCTCCTTCTT	0.562	
+	6	623	F1_uc011kck.1_M	NM_006060	NP_006051	Q13422	IKZF1_HUMAN	2H2-type 2	p.?(74)	148	CGGGGCCTCAT	0.602	
+	12	1698	W1_uc011kef.1_M	NM_018264	NP_060734	Q9NV66	TYW1_HUMAN			1	AATTTCCTGCG	0.423	
+	10	1129	o.1_Missense_Mu	NM_033107	NP_149098	A4D1E9	GTPBA_HUMAN			0	CACTTCATAAG	0.368	
-	5	4043	D9L_uc003umk.1_	NM_152703	NP_689916	Q8IVG5	SAM9L_HUMAN			4	ATATTTCACACTG	0.378	
+	4	586	kib.1_Missense_M	NM_000089	NP_000080	P08123	CO1A2_HUMAN			9	ATAGAGGACCA	0.368	
-	7	627	n_p.V134I|CYP3A	NM_017460	NP_059488	P08684	CP3A4_HUMAN			4	AAAGACGCTGA	0.448	
-	1	620		NM_002711	NP_002702	Q16821	PPR3A_HUMAN	CBM21.		34	ATAAGGAGGAA	0.333	
+	7	1318	_p.T291A|C7orf5	NM_024913	NP_079189	A4D0V7	CG058_HUMAN			9	ATTCGACGGGC	0.418	
-	15	1860		NM_004333	NP_004324	P15056	BRAF_HUMAN	rotein kinas	R603>I(2)|p.T	18290	GATTTCACTGTAC	0.368	
+	1	662	uc003wda.2_Intror	NM_177437	NP_803186	P59551	T2R60_HUMAN	lasmic (Potential).		6	TCTGGGAAGAC	0.458	
-	4	1890	p.R548C|ZNF786_	NM_152411	NP_689624	Q8N393	ZN786_HUMAN	2H2-type 10.		4	CACGCGCAAGT	0.642	
-	5	551_552		NM_001040135	NP_001035225	Q9C0K3	ARP3C_HUMAN			0	ACTTCTGGGGAT	0.411	rs28634863
+	1	829	C61_uc003wgx.2_I	NM_138434	NP_612443	Q96FA7	CG029_HUMAN			1	CCATGGGGGCC	0.542	
-	45	7153	p.Q1647*|CSMD1	NM_033225	NP_150094	Q96PZ7	CSMD1_HUMAN	ar (Potential).|CUB 13.		25	GAGCTGAAATG	0.338	
+	7	1123	p.G218R|SH2D4A	NM_022071	NP_071354	Q9H788	SH24A_HUMAN			0	CCCTCGGGGCC	0.537	
+	3	272	xgb.1_Missense_M	NM_016240	NP_057324	Q6AZY7	SCAR3_HUMAN	lasmic (Potential).		4	CAGCCGCTGCC	0.622	
+	2	522	.1_Missense_Muta	NM_006269	NP_006260	P56715	RP1_HUMAN			12	CCCGCGGCCCT	0.706	
-	2	477	_p.S146T|JPH1_u	NM_020647	NP_065698	Q9HDC5	JPH1_HUMAN	ic (Potential).|MORN 5.		1	GCACGCTCTGG	0.687	
-	1	673	ydr.1_Missense_M	NM_138817	NP_620172	Q8TCU3	S7A13_HUMAN	ellular (Potential).		1	TGAAATCGTTCT	0.413	
-	3	986		NM_203390	NP_976324	Q8IXT5	RB12B_HUMAN			0	GTTTTCGAAAAT	0.403	
+	7	1001	p.P301S|POP1_u	NM_001145860	NP_001139332	Q99575	POP1_HUMAN			2	AATATCCCAGAC	0.512	
-	1	508		NM_139166	NP_631905	Q8N0Z2	ABRA_HUMAN			2	GCTGTGGAGGA	0.587	
-	10	940	p.R285K|ENPP2_	NM_001040092	NP_001035181	Q13822	ENPP2_HUMAN			7	ATATTCTCCGCT	0.428	
+	18	2258		NM_022045	NP_071328	Q96DY7	MTBP_HUMAN	ith MDM2 (By similarity).		3	GAGATCTAAAG	0.363	
-	25	3413	0_splice|KIAA019	NM_014846	NP_055661	Q12768	STRUM_HUMAN			2	TTACTCACCTTAT	0.443	
-	6	846	RC6_uc003ytl.2_R	NM_012472	NP_036604	Q86X45	LRRC6_HUMAN			2	TTCAGGAGTAA	0.403	
-	3	981	RPIN_uc003zbb.2_	NM_030974	NP_112236	Q9H0F6	SHRPN_HUMAN	ciation (By similarity).		1	TTCCAGGGCTC	0.627	
-	1	1338	_5'Flank|DOCK8_	NM_152569	NP_689782	Q5T8R8	CI066_HUMAN			1	GGGCTCCCCCG	0.607	
+	1	256		NM_017913	NP_060383	Q7L3B6	CD37L_HUMAN	lf-association.		0	CTCGGGCCGAG	0.687	
-	1	2808	p.A581S|RANBP6	NM_012416	NP_036548	O60518	RNBP6_HUMAN	HEAT 6.		3	AGCAGCAGCTT	0.418	
-	23	2707	zkl.2_Missense_M	NM_002839	NP_002830	P23468	PTPRD_HUMAN	III 4.|Extracellular (Potentia		22	CGAAGGAATTC	0.478	
-	1	436		NM_002175	NP_002166	P01568	IFN21_HUMAN			2	TCTCTTCCACCC	0.468	
+	2	1059		NM_212558	NP_997723	Q68D42	TM215_HUMAN			0	ACCACGAGACC	0.488	rs147544032
-	3	564_565	pt.2_Missense_Mu	NM_001039803	NP_001034892	Q8IZL9	CDK20_HUMAN	rotein kinase.		1	CAGATCCGACAC	0.599	rs139270796
+	7	1254	sh.2_Missense_M	NM_014282	NP_055097	Q5JVS0	HABP4_HUMAN			1	TGGGCGTGGAG	0.552	rs141094261

-	4	434		NM_000035	NP_000026	P05062	ALDOB_HUMAN			1	TGTTCCTGCAAG	0.408	
-	2	422	_p.L57F|PHF19_u	NM_015651	NP_056466	Q5T6S3	PHF19_HUMAN			2	CCCGAGGTAGTA	0.562	
-	4	532	CL_uc004bna.2_3'U	NM_005388	NP_005379	Q13371	PHLP_HUMAN			0	TCTCTTCCATTCG	0.478	
-	3	284	_uc004brb.1_5'Fla	NM_000976	NP_000967	P30050	RL12_HUMAN			0	GTCTGTTCTGAAT	0.502	
-	9	1270	b.2_Missense_Mu	NM_021804	NP_068576	Q9BYF1	ACE2_HUMAN	cellular (Potential).		3	GGAAGTCGTCCA	0.408	
-	6	1131	ID2_uc010nfb.2_Ir	NM_153346	NP_699177	Q8NDZ0	BEND2_HUMAN			5	TAATTTCCCATTA	0.294	
-	6	650	p.P159S|MAP7D2	NM_152780	NP_689993	Q96T17	MA7D2_HUMAN			3	AAGAGGGCCAA	0.443	
-	1	2311		NM_153270	NP_695002	Q8N239	KLH34_HUMAN	Kelch 6.		1	CGTTGCGGGTA	0.692	
+	1	2650		NM_001013736	NP_001013758	Q5HY64	FA47C_HUMAN			3	AGTGCAGAGCAA	0.458	
-	2	2527		NM_152424	NP_689637	Q5JTC6	F123B_HUMAN		p.0?(40)	112	GATCTTCAGGGG	0.512	
-	5	1372	w.2_Missense_Mu	NM_183353	NP_899196	Q9NVW2	RNF12_HUMAN			2	AACCTCCTCGT	0.458	
-	3	942	0npd.2_Missense_	NM_000354	NP_000345	P05543	THBG_HUMAN			0	GAAATGGAAAAC	0.428	
+	16	2728	C4_uc004emp.3_I	NM_017752	NP_060222	Q0IIM8	TBC8B_HUMAN			4	TGGGCTCATTCT	0.408	
+	27	3429	p.Y1054F|ALG13_uc011mta.1_Missense_Mutation_p.Y			Q9NP73	ALG13_HUMAN			1	CTCATTATGTACC	0.393	
+	31	3359	eqq.2_Missense_M	NM_144658	NP_653259	Q5JSL3	DOC11_HUMAN			3	CAGATTCAAATC	0.299	
+	2	295	I_5'Flank|LOC100	NM_001152	NP_001143	P05141	ADT2_HUMAN	Solcar 1.		1	TGGTCCGTATTC	0.512	
-	1	1146		NM_138289	NP_612146	Q8TDG2	ACTT1_HUMAN			5	CCACTTCCTTCAT	0.493	
+	7	752	num.1_Missense_	NM_003399	NP_003390	O43895	XPP2_HUMAN			0	AGTTATGATCTG	0.507	
+	5	1249	p.R242C|ZNF449_	NM_152695	NP_689908	Q6P9G9	ZN449_HUMAN	C2H2-type 2.		2	TTCCTTCGTAGTT	0.433	
-	19	2219	P11C_uc004fba.2	NM_173694	NP_775965	Q8NB49	AT11C_HUMAN	lasmic (Potential).		8	TCAATGGTTTTTG	0.408	
+	4	551	EC1_uc010nsl.1_I	NM_005462	NP_005453	O60732	MAGC1_HUMAN			4	CTGAGGGCGAC	0.582	
+	3	958	r.2_Nonsense_Mut	NM_002025	NP_002016	P51816	AFF2_HUMAN			5	AGTGGTCACGTG	0.468	
-	9	1523	u.1_Missense_Mu	NM_001110556	NP_001104026	P21333	FLNA_HUMAN	Filamin 2.		6	TTCTGTCCCATG	0.682	
+	5	506	lutation_p.N99S|S	NM_001363	NP_001354	O60832	DKC1_HUMAN			0	CCTCTAACCCCT	0.453	
-	2	720		NM_171998	NP_741995	Q96DA2	RB39B_HUMAN			0	GTACTTCATGCC	0.483	
-	1	436		NM_171998	NP_741995	Q96DA2	RB39B_HUMAN			0	TGGCTCGATCT	0.622	
-	13	1569	p.V301M|NOC2L_	NM_015658	NP_056473	Q9Y3T9	NOC2L_HUMAN			2	GATCACGGAGA	0.637	
-	8	883	_p.R72Q|NOC2L_	NM_015658	NP_056473	Q9Y3T9	NOC2L_HUMAN			2	TGTGCCGCAGC	0.622	
+	17	2883		NM_198576	NP_940978	O00468	AGRIN_HUMAN	Kazal-like 9.		3	CATACGGCAAC	0.627	
+	5	944		NM_138705	NP_619650	Q8TD86	CALL6_HUMAN	and 4.|Potential.		0	ACCATCGACTAT	0.632	
-	18	2317	vkz.1_Missense_M	NM_001080484	NP_001073953	Q9C0B2	K1751_HUMAN			1	GCTCCTCCTCCT	0.697	
-	14	1977	kk.2_Missense_M	NM_001409	NP_001400	O75095	MEGF6_HUMAN	EGF-like 10.		1	GCAGCGGCAGG	0.582	
+	9	1094		NM_015215	NP_056030	Q9Y6Y1	CMTA1_HUMAN			9	AGGGGGGTACG	0.617	
+	2	215	6_uc009vmn.2_Int	NM_001215	NP_001206	P23280	CAH6_HUMAN			2	CCTTGAAGGGGC	0.602	
+	5	1212	.R167C|UBE4B_u	NM_001105562	NP_001099032	O95155	UBE4B_HUMAN			4	ATCTTCCGTGTC	0.463	
+	27	3098	qz.2_Nonsense_M	NM_015074	NP_055889	O60333	KIF1B_HUMAN			3	ACGACCGATCC	0.532	
-	11	1360		NM_006610	NP_006601	O00187	MASP2_HUMAN	Peptidase S1.		4	GCCCTCCATATAT	0.448	
+	8	1255	ni.2_Missense_Mu	NM_014874	NP_055689	O95140	MFN2_HUMAN	lasmic (Potential).		1	GAGCCCGAGTAC	0.567	
+	6	791	0obc.1_Missense_	NM_001243	NP_001234	P28908	TNR8_HUMAN	cellular (Potential).		5	GTGCCAGCACCA	0.622	rs151315213
+	19	4402	p.R1421C|VPS13D	NM_015378	NP_056193	Q5THJ4	VP13D_HUMAN			5	GTGACCGTCTG	0.488	rs148968489
+	63	12049	S13D_uc001atx.2_	NM_015378	NP_056193	Q5THJ4	VP13D_HUMAN			5	ACCTCCATGAA	0.358	
+	3	1466		NM_001080830	NP_001074299	O95522	PRA12_HUMAN			3	GTCAGGGTGGAT	0.498	
+	4	1385		NM_023013	NP_075389	O95521	PRAM1_HUMAN			0	AATTGGGAGATC	0.572	
-	1	474		NM_001136561	NP_001130033	B2RXH8	B2RXH8_HUMAN			0	GTGCTGGGAAAC	0.517	
-	14	2254	obr.1_Missense_M	NM_003443	NP_003434	Q13105	ZBT17_HUMAN	MYC.|Interaction with HCFC		0	GCTGTCGCTGCC	0.652	rs148819837
-	2	412	I_5'Flank|ARHGEF	NM_153213	NP_694945	Q8IW93	ARHGJ_HUMAN			3	ATCCCCCCGCTG	0.682	
-	20	2417	ense_Mutation_p.F	NM_022089	NP_071372	Q9NQ11	AT132_HUMAN	lasmic (Potential).		4	GGATGCGGGTCC	0.627	

+	7	1452	av.1_Missense_Mu	NM_032880	NP_116269	Q96ID5	IGS21_HUMAN	Ig-like 2.	4	GTAGGGGACACA	0.582	
-	45	6630_6631	se_Mutation_p.A14	NM_020765	NP_065816	Q5T4S7	UBR4_HUMAN		25	ACCTTCGCTTTA	0.436	
-	33	4680	m.1_Missense_Mu	NM_020765	NP_065816	Q5T4S7	UBR4_HUMAN		25	ACAGCAGCATTAT	0.473	
+	4	593	.2_Missense_Muta	NM_017765	NP_060235	Q6ZP29	PQLC2_HUMAN	1.|Helical; (Potential).	0	ATTGGCGGAGAC	0.617	
-	14	1585	oco.1_Missense_M	NM_181719	NP_859070	Q5TGY1	TMCO4_HUMAN		0	ACCTTCCGGAAA	0.502	
-	5	586	oda.1_Missense_M	NM_001161729	NP_001155201	P14555	PA2GA_HUMAN		0	TAGGTCGTCTTG	0.458	rs148324464
-	3	313	)oda.1_Missense_I	NM_001161729	NP_001155201	P14555	PA2GA_HUMAN		0	CCTGTCGTCAAC	0.552	
-	68	9092	vqd.2_Splice_Site_	NM_005529	NP_005520	P98160	PGBM_HUMAN		9	TACTCACGGTAG	0.652	
+	13	1720	ogj.2_Missense_Mu	NM_015013	NP_055828	O60341	KDM1A_HUMAN	ethylase activity.	2	CATCAAGAGACA	0.383	
-	13	1232	nse_Mutation_p.R2	NM_017707	NP_060177	Q8TDY4	ASAP3_HUMAN	PH.	3	ACGTCCGGTTGT	0.677	
-	3	976		NM_004091	NP_004082	Q14209	E2F2_HUMAN	box.|Potential.	4	TTCTTGCGGATG	0.602	
+	11	1401	p.R447Q|GRHL3_	NM_021180	NP_067003	Q8TE85	GRHL3_HUMAN		1	ACCTTCGGCCAG	0.632	
+	1	65	P3S|CNKSR1_uc0	NM_006314	NP_006305	Q969H4	CNKR1_HUMAN		2	ATGGAACCGGTA	0.637	
+	12	1727	TC1_uc001bnp.1_	NM_015023	NP_055838	Q8N5D0	WDTC1_HUMAN	TPR 2.	2	GCCATGCTTTATG	0.552	
+	2	753		NM_005281	NP_005272	P46089	GPR3_HUMAN	lasmic (Potential).	1	CGCATCGTCTGC	0.587	
-	2	434	RNA|MATN1_uc001	NM_002379	NP_002370	P21941	MATN1_HUMAN	VWFA 1.	1	CTGCATCGCCGA	0.617	
-	5	514	_p.V126L|NKAIN1	NM_024522	NP_078798	Q4KMZ8	NKAI1_HUMAN	lasmic (Potential).	1	GGAACACTTTGC	0.627	
-	6	864	OL16A1_uc001btl.	NM_001856	NP_001847	Q07092	COGA1_HUMAN	SP N-terminal.	8	CCAACGCAAGT	0.637	
-	16	2893	on_p.R780C|BAI2_	NM_001703	NP_001694	O60241	BAI2_HUMAN	cellular (Potential).	13	GGGGCGCACAG	0.627	
-	10	2291	o.R745W|SPOCD1	NM_144569	NP_653170	Q6ZMY3	SPOC1_HUMAN		6	TGTCCCGCTGAA	0.368	
-	5	1840		NM_018207	NP_060677	Q9BVG3	TRI62_HUMAN	B30.2/SPRY.	0	GGCTCCGTGCAG	0.592	
-	3	1272		NM_018207	NP_060677	Q9BVG3	TRI62_HUMAN	Potential.	0	TCTGCTCGATGT	0.672	
+	2	419	oxt.2_Missense_Mu	NM_032884	NP_116273	Q6P1W5	CA094_HUMAN		0	CAGCAGGCAGG	0.577	
-	3	576	bw.3_Missense_M	NM_001099439	NP_001092909	Q5JZY3	EPHAA_HUMAN	cellular (Potential).	8	GGTCGCCCTGCG	0.687	
+	7	731	P11L_uc010oil.1_F	NM_016037	NP_057121	Q9Y3A2	UTP11_HUMAN		0	TTGTTCGTTATTG	0.398	
+	14	1573	cda.1_Splice_Site_	NM_012090	NP_036222	Q9UPN3	MACF1_HUMAN		16	CAGGCTGTAAGT	0.418	
+	1	3841	.1_Intron|MACF1_	NM_015038	NP_055853	O94854	K0754_HUMAN	Ala-rich.|2.	0	GAGCCCACCTCC	0.721	
+	4	528	n.2_Intron|CCDC3	NM_001080850	NP_001074319	Q5VVM6	CCD30_HUMAN		0	ACAGAGGAACTC	0.299	
+	15	2538	q.2_Missense_Mut	NM_005424	NP_005415	P35590	TIE1_HUMAN	lasmic (Potential).	7	TACCCGGCGGC	0.607	
+	11	1472		NM_015284	NP_056099	Q5T011	SZT2_HUMAN		0	GGACCCGGTGTC	0.592	
+	47	6587	0467_uc001cjl.1_5	NM_015284	NP_056099	Q5T011	SZT2_HUMAN		0	CGCCCGCAGGT	0.567	
-	5	737	A9_uc009vxd.2_RN	NM_201649	NP_964012	P48067	SC6A9_HUMAN		0	CCATAGCCCACT	0.478	
+	4	426	okt.1_Missense_M	NM_001034024	NP_001029196	Q9NPF5	DMAP1_HUMAN		0	GGCGACGTGCA	0.572	rs145929825
+	10	1348	ym.2_Missense_M	NM_000779	NP_000770	P13584	CP4B1_HUMAN		2	CCGACCCTGAG	0.582	
+	4	551	p.R167Q|CYP4A2	NM_001010969	NP_001010969	Q5TCH4	CP4AM_HUMAN		4	CTGTACGAGTGA	0.567	
-	4	1208	AL1_uc001cqy.2_M	NM_003189	NP_003180	P17542	TAL1_HUMAN	-loop-helix motif.	1	CTTGCGGAGCT	0.567	
+	2	399	_p.S61N|ELAVL4_	NM_021952	NP_068771	P26378	ELAV4_HUMAN		2	ATGACAGCAAAA	0.463	
+	8	1127	nr.1_Missense_Mu	NM_153703	NP_714914	Q7Z5L7	PODN_HUMAN	LRR 10.	2	GTGGACGCGAAT	0.602	
-	4	1390		NM_147193	NP_671726	Q8NBF1	GLIS1_HUMAN	C2H2-type 3.	1	CAGCCGTGAGA	0.627	rs148564902
+	8	944	p.V166M|ACOT11_	NM_015547	NP_056362	Q8WXI4	ACO11_HUMAN	nzyme A hydrolase 2.	1	GCCATCGTGAAC	0.597	rs139645585
-	2	481		NM_152268	NP_689481	Q7L3T8	SYPM_HUMAN		2	TCCCACCGGTTG	0.557	
-	6	769	m.1_Nonsense_M	NM_002227	NP_002218	P23458	JAK1_HUMAN	FERM.	61	GGTCTCGAATAG	0.498	
-	11	1844	73_uc001dgi.3_Mi	NM_001002912	NP_001002912	Q5RHP9	CA173_HUMAN	Glu-rich.	5	CTCTCTTTTTCAG	0.403	
-	10	1690	73_uc001dgi.3_Mi	NM_001002912	NP_001002912	Q5RHP9	CA173_HUMAN	Glu-rich.	5	TATTTTCCTGGT	0.358	
-	2	722	uc001dla.1_5'Flank	NM_003921	NP_003912	O95999	BCL10_HUMAN		2	GGGACGGTGCG	0.726	
-	8	1565	P2_uc001dmy.1_F	NM_004120	NP_004111	P32456	GBP2_HUMAN		1	AGAGACGGTAAC	0.443	
-	27	4218		NM_000350	NP_000341	P78363	ABCA4_HUMAN	Cytoplasmic.	12	GGAAGTCCTTGT	0.607	

-	13	1706	RHGAP29_uc001c	NM_004815	NP_004806	Q52LW3	RHG29_HUMAN		11	TGTAAACTGTCTC	0.438	
-	8	792	qz.3_Missense_Mu	NM_001839	NP_001830	Q15417	CNN3_HUMAN		0	TCCACCGGCTGT	0.448	
-	1	96	FM3_uc001dui.2_I	NM_058170	NP_477518	Q96PB7	NOE3_HUMAN		3	AGCGCCAAGCT	0.547	
-	40	3380	p.G1033E|COL11A	NM_001854	NP_001845	P12107	COBA1_HUMAN	le-helical region.	12	GCTGGTCCATCT	0.378	
+	19	2588	g.1_Missense_Mu	NM_020775	NP_065826	Q6UXG2	K1324_HUMAN	cellular (Potential).	5	ATCCGCGTCAGG	0.532	
+	8	915	ao.2_Missense_Mu	NM_004000	NP_003991	Q15782	CH3L2_HUMAN		1	CCACCGTGGGG	0.577	rs140247314
+	8	1832	whg.1_Missense_M	NM_006699	NP_006690	O60476	MA1A2_HUMAN	nenal (Potential).	0	ATGGATCGTCCA	0.333	
-	2	316	ehg.2_Missense_M	NM_017686	NP_060156	Q9NXN4	GDAP2_HUMAN		2	GAAGGTGCACCT	0.398	
-	3	532		NM_001080470	NP_001073939	Q5TEC3	ZN697_HUMAN		1	AAGTACGGGAG	0.682	
-	1	754		NM_001047980	NP_001041445	P0C2Y1	NBPF7_HUMAN		2	GGGGGCGCAATT	0.483	
-	11	2088	p.C611Y|NOTCH2_	NM_024408	NP_077719	Q04721	NOTC2_HUMAN	GF-like 16; calcium-binding	27	CTGTAACATTCAT	0.542	
-	1	242		NM_001123068	NP_001116540	A2BFH1	PAL4G_HUMAN	e cyclophilin-type.	0	CCATTAGGGTGT	0.468	
+	12	1397	_RNA|NBPF9_uc	NM_001037675	NP_001032764	Q3BBV1	NBPFK_HUMAN	NBPF 2.	0	AACGATGACAATC	0.423	
+	4	1320	HFE2_uc001enk.2_	NM_213653	NP_998818	Q6ZVN8	RGMC_HUMAN		1	AGAGCGCAATC	0.542	
+	15	1818	sb.1_Missense_M	NM_173638	NP_775909	Q8N660	NBPFF_HUMAN	NBPF 4.	0	TAGATGTTATTCA	0.473	
-	20	2194	b.1_Missense_Mu	NM_001668	NP_001659	P27540	ARNT_HUMAN		9	TTGGGGCACCA	0.547	
-	8	940	p.R266Q|ARNT_u	NM_001668	NP_001659	P27540	ARNT_HUMAN		9	CTCATTCGGCAA	0.438	
-	3	5923		NM_002016	NP_002007	P20930	FILA_HUMAN	Ser-rich.	16	CTCTGTCTTCGT	0.567	
+	3	296	_p.G49E|SPRR3_	NM_005416	NP_005407	Q9UBC9	SPRR3_HUMAN	pproximate tandem repeats	1	AACCTGGAAACA	0.547	
+	14	2579	p.G466S|NPR1_u	NM_000906	NP_000897	P16066	ANPRA_HUMAN	Potential).|Protein kinase.	7	CAGGCTGGTGAC	0.602	
-	7	1245		NM_020699	NP_065750	Q8WXI9	P66B_HUMAN		0	GTGGCGAGGAC	0.522	
+	7	2065	_uc001fgg.1_3'UT	NM_025207	NP_079483	Q8NFF5	FAD1_HUMAN		3	ACATACCGTCCA	0.607	
-	9	1107	_p.R362W|THBS3	NM_007112	NP_009043	P49746	TSP3_HUMAN	alcium-binding (Potential).	5	GGCCCGGGCAT	0.597	rs35484178
+	2	848	_uc001fkl.2_5'Flar	NM_001105203	NP_001098673	Q9BVN2	RUSC1_HUMAN		2	CAGGATCTCCCT	0.567	
-	21	4514	N4L_uc001fmb.3_	NM_001037533	NP_001032622	Q3T8J9	GON4L_HUMAN	Glu-rich.	3	CATCTTCCTCATC	0.478	
+	5	1108	T|LMNA_uc010pg	NM_170707	NP_733821	P02545	LMNA_HUMAN	Coil 2.|Rod.	2	TGGGGGCTGCC	0.637	
+	15	1966	p.G336E|NTRK1_	NM_002529	NP_002520	P04629	NTRK1_HUMAN	Potential).|Protein kinase.	17	CTGCGGGGATGG	0.642	
+	18	2517	qk.1_Missense_Mu	NM_001080471	NP_001073940	Q5VY43	PEAR1_HUMAN		3	CTGGACGGCTCC	0.607	
-	11	2622	sm.2_Missense_M	NM_031281	NP_112571	Q96RD9	FCRL5_HUMAN	otential).|Ig-like C2-type 8.	6	CATTGTCGGCCT	0.557	
-	29	4223		NM_003126	NP_003117	P02549	SPTA1_HUMAN	Spectrin 13.	8	GGGAGCCTCTG	0.483	
+	1	1263		NR_024151					0	TCCACTCGCATC	0.607	
+	5	1541	p.R389Q|POGK_u	NM_017542	NP_060012	Q9P215	POGK_HUMAN	DDE.	1	CTTCCGGGGCC	0.393	
+	2	135		NM_002995	NP_002986	P47992	XCL1_HUMAN		0	CCCAGCGACTG	0.468	
+	8	1827	N_uc010pmx.1_Int	NM_022093	NP_071376	Q9UQP3	TENN_HUMAN	onectin type-III 4.	9	GACCAAGAGACC	0.602	
+	7	1364	p.R101Q|FAM5B_	NM_021165	NP_066988	Q9C0B6	FAM5B_HUMAN		6	ATGACCGGTTCC	0.567	
-	3	933	|ANGPTL1_uc001	NM_004673	NP_004664	O95841	ANGL1_HUMAN	Potential.	0	CAGTTGGGAAA	0.388	
-	2	100	C_uc001grz.2_5'Fl	NM_002597	NP_002588	P20941	PHOS_HUMAN		1	TTCCTCCAAACT	0.318	
+	12	4303	se_Mutation_p.R1	NM_201253	NP_957705	P82279	CRUM1_HUMAN	lasmic (Potential).	9	GCTCCCGAGTG	0.532	
-	8	2173	pj.1_Missense_Mu	NM_014875	NP_055690	Q15058	KIF14_HUMAN	inesin-motor.	7	TGGGTCATCAC	0.388	rs144936292
-	18	3003	zl.1_Nonsense_M	NM_017596	NP_060066	O75037	KI21B_HUMAN		6	TTACCGGGCAG	0.647	
+	11	1286	IA4_uc010pqf.1_5'UTR			O75335	LIPA4_HUMAN		5	TCAGCGGGACC	0.642	
-	16	2551	HA6_uc009xau.1_	NM_014935	NP_055750	Q9Y2H5	PKHA6_HUMAN		4	CTCTGGGGGTG	0.517	
-	6	753	bv.1_Missense_M	NM_005057	NP_005048	Q15291	RBBP5_HUMAN	WD 4.	1	CCTTCCGGGCA	0.383	
+	3	1142	rf.1_Missense_Mu	NM_014858	NP_055673	O75069	TMCC2_HUMAN		1	CGACGGCAGCA	0.677	
+	4	503	z.2_RNA|CR1L_uc	NM_175710	NP_783641	Q2VPA4	CR1L_HUMAN	Sushi 2.	0	GATACCGACTC	0.343	
-	29	5946	IA2_uc001hgy.2_5	NM_025179	NP_079455	O75051	PLXA2_HUMAN	lasmic (Potential).	3	GTCATGGATGC	0.572	
+	9	1388		NM_016343	NP_057427	P49454	CENPF_HUMAN	localization to the cytoplas	13	AACAGCGTTCTT	0.532	

-	63	13784		NM_206933	NP_996816	O75445	USH2A_HUMAN	II 30.|Extracellular (Potentia	26	TTGGAGGTTTC	0.453	
+	8	831	ATA17_uc001hli.2	NM_138796	NP_620151	Q96L03	SPT17_HUMAN		1	CCAATCGATGAG	0.468	
-	8	849	.2_RNA|RAB3GAP	NM_012414	NP_036546	Q9H2M9	RBGPR_HUMAN		1	AAGCACGAAGAG	0.299	rs144569017
+	3	1284		NM_021958	NP_068777	Q14774	HLX_HUMAN	Homeobox.	2	GGAAGCGTTCAT	0.562	
-	7	1103	42C|TP53BP2_uc	NM_001031685	NP_001026855	Q13625	ASPP2_HUMAN		3	GAGGCGATCAA	0.488	
+	4	1572	d.1_Missense_Mu	NM_014777	NP_055592	Q14146	URB2_HUMAN		3	TCTGTCGTCCAG	0.572	
+	6	1702		NM_001004342	NP_001004342	Q6ZTA4	TRI67_HUMAN	onectin type-III.	4	ACGACGGTGCC	0.632	
-	10	3555	hvf.2_Missense_M	NM_020808	NP_065859	Q9P2F8	SI1L2_HUMAN		6	CCCGCCGGGTC	0.522	
-	7	2978	1L2_uc001hvf.2_5'	NM_020808	NP_065859	Q9P2F8	SI1L2_HUMAN		6	TACTTACTACTAA	0.393	
-	5	1565	u.2_RNA|PCNXL2	NM_014801	NP_055616	A6NKB5	PCX2_HUMAN		2	GACAGGGAACAC	0.577	
-	5	965	u.2_RNA|PCNXL2	NM_014801	NP_055616	A6NKB5	PCX2_HUMAN		2	CACCCTCGGATC	0.498	
-	30	4744		NM_005646	NP_005637	Q13395	TARB1_HUMAN		3	CACAAACGTCC	0.458	
+	1	905	L13_uc001ids.2_I	NM_001001963	NP_001001963	Q8NGY9	OR2L8_HUMAN	lasmic (Potential).	2	GACACGAGTGA	0.473	
+	1	28	L13_uc001ids.2_I	NM_001004491	NP_001004491	Q8NG84	O2AK2_HUMAN	cellular (Potential).	2	CCTTTGATATTTT	0.189	
+	1	120		NM_001004690	NP_001004690	A3KFT3	OR2M5_HUMAN	Name=1; (Potential).	3	CTTCATGGGAAA	0.522	
+	1	571		NM_017504	NP_059974	Q96R27	OR2M4_HUMAN	cellular (Potential).	2	GCACAGAAACA	0.408	
-	1	47		NM_001004692	NP_001004692	Q8NG77	O2T12_HUMAN	cellular (Potential).	3	TGGTTAAAGAGT	0.448	
-	5	667	ion_p.R167K|ZNF	NM_017865	NP_060335	Q9BU19	ZN692_HUMAN		0	TGAGTCCTCTCA	0.507	
-	4	1118	p.A336D|TUBB8_	NM_177987	NP_817124	Q3ZCM7	TBB8_HUMAN		1	TGGATGGCCGTA	0.532	
-	21	2617	p.V229M|DIP2C_u	NM_014974	NP_055789	Q9Y2E4	DIP2C_HUMAN		7	AGCCACGATCA	0.647	
-	3	274	uc009xhk.1_Silent_	NM_014974	NP_055789	Q9Y2E4	DIP2C_HUMAN		7	CCGGCGTTCTT	0.572	
-	3	370	h.2_RNA|ASB13_	NM_024701	NP_078977	Q8WXK3	ASB13_HUMAN	ANK 3.	1	CCTTGGCCCCG	0.662	
-	4	616	.1_Intron|IL2RA_u	NM_000417	NP_000408	P01589	IL2RA_HUMAN	xtracellular (Potential).	2	CTGGACGCACT	0.532	
+	3	1738		NM_031923	NP_114129	Q5VWG9	TAF3_HUMAN	Lys-rich.	1	GAATTTCTTAAAG	0.264	
+	7	2716		NM_031923	NP_114129	Q5VWG9	TAF3_HUMAN	PHD-type.	1	AGATGCAGTGG	0.507	
-	8	1223		NM_001010924	NP_001010924	Q5VUB5	F1711_HUMAN	lasmic (Potential).	4	TTCGCCGCCCG	0.617	
-	53	8393	JBN_uc009xjr.1_M	NM_001081	NP_001072	O60494	CUBN_HUMAN	CUB 20.	19	AGTCACGACCA	0.428	
+	5	581	ivu.3_Missense_M	NM_030751	NP_110378	P37275	ZEB1_HUMAN	C2H2-type 1.	5	CCTGTCCATATT	0.318	
-	19	2551	AP12_uc001iwc.1_	NM_018287	NP_060757	Q8IWW6	RHG12_HUMAN	Rho-GAP.	0	GACTCGCTGTC	0.413	
-	14	2618	p.E693K|NRP1_uc	NM_003873	NP_003864	O14786	NRP1_HUMAN	lar (Potential).|MAM.	4	ATTTTCGTCAG	0.493	rs139081795
-	1	79		NM_031866	NP_114072	Q9H461	FZD8_HUMAN		0	CCGCAGCGCCC	0.647	
+	5	958	|TMEM72_uc009x	NM_001123376	NP_001116848	A0PK05	TMM72_HUMAN		0	ACACGACACCCA	0.602	
-	7	1704	L1_uc009xmu.2_M	NM_001128324	NP_001121796	Q86XD8	ANUB1_HUMAN		0	GTTTCACCAGAG	0.418	
-	4	3617		NM_002900	NP_002891	P10745	RET3_HUMAN	mate tandem repeats.|4.	2	CCTCCCCAATG	0.622	
-	4	3602		NM_002900	NP_002891	P10745	RET3_HUMAN	mate tandem repeats.|4.	2	GGGCCCGGCCC	0.612	
+	4	2435		NM_199459	NP_955629	Q711Q0	CJ071_HUMAN		0	acacacacacacaca	0.433	
+	14	2036	y.1_Missense_Mut	NM_020549	NP_065574	P28329	CLAT_HUMAN		3	ACTGCGGGAGC	0.577	rs114545628
-	7	1360	ron|uc001jin.2_Intr	NM_001077685	NP_001071153	Q5VUJ5	AGAP7_HUMAN	PH.	0	TTGGACCCATG	0.547	
-	37	11059	K3_uc010qih.1_In	NM_020987	NP_066267	Q12955	ANK3_HUMAN		19	AAAATCCCTCTT	0.463	
-	4	878	ij.1_RNA|TMEM26	NM_178505	NP_848600	Q6ZUK4	TMM26_HUMAN	ical; (Potential).	0	CTCGAGTGATCC	0.438	
+	1	240	qip.1_Missense_M	NM_030759	NP_110386	Q96F24	NRBF2_HUMAN		0	TGGAAGGACCC	0.637	
+	12	2244	PN_uc009xpt.2_M	NM_032578	NP_115967	Q86TC9	MYPN_HUMAN		5	CTAAGGAGTTT	0.453	
+	14	2676	rp.2_Missense_Mu	NM_170744	NP_734465	Q8IZJ1	UNC5B_HUMAN	lasmic (Potential).	3	GAAACCGCTAA	0.617	
-	14	2065	y.2_Missense_Mu	NM_007265	NP_009196	O95905	SGT1_HUMAN		1	AGCTATAGGATT	0.463	
-	7	742	_p.A242V|USP54	NM_152586	NP_689799	Q70EL1	UBP54_HUMAN		6	GTGGAGCATTC	0.468	
-	7	727	_p.R237H|USP54	NM_152586	NP_689799	Q70EL1	UBP54_HUMAN		6	ACACACGGCGA	0.468	
-	31	4141		NM_007055	NP_008986	O14802	RPC1_HUMAN		0	ATTCCCATGAT	0.453	

+	1	387	uc010qls.1_5'Flan	NM_001099692	NP_001093162	Q6IS14	IF5AL_HUMAN			0	CCTTCGTCTCC	0.547	
-	3	1383	nc.1_Missense_M	NM_001017924	NP_001017924	A6NDA9	LRIT2_HUMAN			2	ACGTGCCTCTA	0.617	
+	2	406	.3_Intron|LIPA_uc	NM_001010987	NP_001010987	Q5T764	IFT1B_HUMAN	TPR 2.		0	CATGGGCAGAT	0.473	
+	13	1562	.R362H|HELLS_u	NM_018063	NP_060533	Q9NRZ9	HELLS_HUMAN			2	GAACCGTACAA	0.338	
-	7	978	M1_uc009xuv.2_3	NM_020992	NP_066272	O00151	PDLI1_HUMAN	zinc-binding.		0	TGGTGCCACAG	0.537	
+	9	1402	g.2_Missense_M	NM_004088	NP_004079	P04053	TDT_HUMAN	teraction with DNTTIP2.		1	GCCTCGTCAAA	0.483	rs151142894
-	13	1484	h.1_Missense_Mu	NM_003061	NP_003052	O75093	SLIT1_HUMAN	LRR 11.		4	ACAGGGAGAGC	0.587	
-	13	1668	ou.1_Missense_M	NM_015179	NP_055994	Q5JTH9	RRP12_HUMAN			3	CCTTCCTCATC	0.478	
-	18	1868	_Mutation_p.Q38	NM_022362	NP_071757	Q96T76	MMS19_HUMAN			0	AGCATTGGGTG	0.527	
+	1	122	2A_uc010qoy.1_I	NM_018425	NP_060895	Q9BTU6	P4K2A_HUMAN			2	CCCGTCGGGCT	0.776	
-	3	975		NM_003015	NP_003006	Q5T4F7	SFRP5_HUMAN	NTR.		1	CTTTGCGGCCC	0.592	
+	20	2883		NM_000392	NP_000383	Q92887	MRP2_HUMAN	smic (By similarity).		1	TAGCCGCAGGT	0.483	
+	3	1075	e_Mutation_p.R33	NM_032429	NP_115805	Q9BRK4	LZTS2_HUMAN	Potential.		4	GAGACCGGGAG	0.632	
+	9	1324	_p.V98I|TMEM18	NM_024789	NP_079065	Q14CX5	TM180_HUMAN			1	ACCGCGTCTTC	0.612	
+	19	3734	.1_Nonsense_Mut	NM_014720	NP_055535	Q9H2G2	SLK_HUMAN			8	CCACCGGATCA	0.438	
-	5	440	_p.P91S|COL17A	NM_000494	NP_000485	Q9UMD9	COHA1_HUMAN	tial).|Nonhelical region (N		5	GTTGGGCAGAG	0.517	
+	9	1459		NM_001008723	NP_001008723	Q5T655	CC147_HUMAN	Potential.		5	GGAGCGTGACC	0.498	
-	5	325	EP1_uc001kyq.1_	NM_020383	NP_065116	Q9NQW7	XPP1_HUMAN			4	TGGCTGTGCCT	0.478	
+	12	1186	_p.P405S|ACSL5_	NM_203379	NP_976313	Q9ULC5	ACSL5_HUMAN	lasmic (Potential).		3	TGTTTCCCGCG	0.507	
-	13	1573	16F|ABLIM1_uc0	NM_002313	NP_002304	O14639	ABLM1_HUMAN			1	AGGGAGAGGG	0.507	
-	12	1444	p.R411W|ABLIM1_	NM_002313	NP_002304	O14639	ABLM1_HUMAN			1	GGACCGATGGA	0.552	
+	6	1387	se_Mutation_p.L3	NM_207303	NP_997186	Q5VV63	ATRN1_HUMAN	ar (Potential).|Kelch 1.		7	GGTCCTAAAGT	0.328	
+	12	2315		NM_207303	NP_997186	Q5VV63	ATRN1_HUMAN	tracellular (Potential).		7	TCTTGGGAATC	0.358	
+	6	1247		NM_002775	NP_002766	Q92743	HTRA1_HUMAN	PDZ.		0	GCCAAAGGTAG	0.537	
-	15	2044	_p.A544V|ADAM1	NM_003474	NP_003465	O43184	ADA12_HUMAN	ar (Potential).|Cys-rich.		9	CAGGGGCAGGT	0.463	
+	27	2799	un.1_Missense_M	NM_001380	NP_001371	Q14185	DOCK1_HUMAN			9	TCTCCGGACCG	0.483	
-	1	332		NM_152311	NP_689524	Q8NCR9	CLRN3_HUMAN			1	CCCACGAAAAA	0.383	
-	3	558	c.1_Missense_Mu	NM_173575	NP_775846	Q86UX6	ST32C_HUMAN	rotein kinase.		5	CTCCCGGAAGA	0.582	
+	3	302		NM_178537	NP_848632	Q76KP1	B4GN4_HUMAN	enal (Potential).		1	TGGGGGGGCTG	0.597	
+	3	578		NM_007183	NP_009114	Q9Y446	PKP3_HUMAN		p.G168G(1)	1	AGCGCGGTGGG	0.716	
-	10	2000	AF1_uc009ycf.1_	NM_021008	NP_066288	O75398	DEAF1_HUMAN	Pro-rich.		0	GTGCCGCTTTG	0.557	
+	1	439		NM_001001480	NP_001001480	Q701N2	KRA55_HUMAN	repeats of C-C-X-P.		1	TGGGGGGTCCA	0.692	
+	1	451		NM_001001480	NP_001001480	Q701N2	KRA55_HUMAN	repeats of C-C-X-P.		1	GGGGGGCTGTG	0.692	
-	6	662	5_uc010qxr.1_Mis	NM_001130520	NP_001123992	O14628	ZN195_HUMAN	Spacer.		0	TATGCCCTGCT	0.353	
-	3	332	1_5'UTR|CHRNA1	NM_020402	NP_065135	Q9GZZ6	ACH10_HUMAN	ellular (Potential).		1	CATCTGTCCAC	0.552	rs138195713
-	1	368		NM_001005177	NP_001005177	Q8NGF1	O52R1_HUMAN	Name=1; (Potential).		1	ATATTTCCAACA	0.522	
-	1	11		NM_001005238	NP_001005238	Q8NGK0	O51G2_HUMAN	ellular (Potential).		2	GGGATCCCAGG	0.547	
-	1	660	.1_Intron|HBE1_u	NM_033180	NP_149420	Q9Y5P1	O51B2_HUMAN	Name=5; (Potential).		3	TTAAAGAGATC	0.398	
+	1	712	_uc001mam.1_Int	NM_001004757	NP_001004757	Q8NH59	O51Q1_HUMAN	lasmic (Potential).		1	GACTCCGTGCC	0.488	
-	3	862	p.S168N|FAM160	NM_001098794	NP_001092264	Q8N612	F16A2_HUMAN			2	GGCTACTGGGC	0.597	
+	4	1055	15_uc010rax.1_5'	NM_013250	NP_037382	Q9UL58	ZN215_HUMAN			0	CTCACGAACAG	0.408	
+	2	664	fd.2_RNA|SYT9_u	NM_175733	NP_783860	Q86SS6	SYT9_HUMAN	lasmic (Potential).		3	AGACGGGGATC	0.602	
+	1	371	7R|OLFML1_uc0	NM_198474	NP_940876	Q6UWY5	OLFL1_HUMAN			2	TTCGAGGAGCT	0.567	
+	16	1872	nse_Mutation_p.	NM_003621	NP_003612	Q8ND30	LIPB2_HUMAN			4	TAAACGGAATC	0.453	
-	1	233		NM_001003745	NP_001003745	P58181	O10A3_HUMAN	ellular (Potential).		1	CAGGCGTAATG	0.448	rs150971423
-	22	3808	_p.V528I|DENND5	NM_015213	NP_056028	Q6IQ26	DEN5A_HUMAN	RUN 2.		1	GGACTACTTCAT	0.463	
+	5	766	L2_uc010rci.1_Mi	NM_014632	NP_055447	O94851	MICA2_HUMAN		p.R160H(1)	2	GTATTCGCCAA	0.483	

+	9	1210	_p.S101L|TEAD1_	NM_021961	NP_068780	P28347	TEAD1_HUMAN	ctivation (Potential).|Pro-ric		0	TGCATCGGCCC	0.567	
+	18	2012	NTL_uc001mkt.2_	NM_001178	NP_001169	O00327	BMAL1_HUMAN			0	TTCTCCAGGAG	0.498	
-	19	3308	cw.1_Missense_M	NM_002645	NP_002636	O00443	P3C2A_HUMAN		p.R1081*(1)	10	TGTACTCGTTCC	0.333	
-	5	610		NM_003476	NP_003467	P50461	CSRP3_HUMAN	zinc-binding 2.		0	AAGTTCCCCAT	0.478	
-	1	62	1mri.1_Missense_	NM_030771	NP_110398	Q96HJ3	CCD34_HUMAN			0	CCGCCGCCCA	0.706	
-	14	2535		NM_031217	NP_112494	Q8NI77	KI18A_HUMAN			2	TTGTTCGGGT	0.318	
+	3	628		NM_152316	NP_689529	Q8N8R7	CK046_HUMAN			0	ATTTACGAATCC	0.368	
+	1	1718	un.1_Missense_	NM_012194	NP_036326	Q6ZVL6	CK041_HUMAN			2	ATTCCGTGTCT	0.483	
-	2	361	d.1_Missense_M	NM_198381	NP_938195	Q9UKW6	ELF5_HUMAN	PNT.		1	AGGCAGGGTAG	0.552	
+	11	2229		NM_005456	NP_005447	Q9UQF2	JIP1_HUMAN	PID.		4	AGTCCGTGGG	0.632	
-	10	1459	2_uc001ndv.1_5'	NM_016223	NP_057307	Q9UKS6	PACN3_HUMAN	SH3.		0	CAGCGTAGTCA	0.617	
+	23	3789	yln.1_Intron|MAD	NM_003682	NP_003673	Q8WXG6	MADD_HUMAN	Ser-rich.		11	GCACCGTGGTA	0.517	
-	4	1057	TBD4_uc001nfz.2	NM_016506	NP_057590	Q9NVX7	KBTB4_HUMAN	Kelch 2.		2	GCGCCGTGGGA	0.587	
-	6	1010	160_uc009ylw.2_	NM_015231	NP_056046	Q12769	NU160_HUMAN			7	ACATTCGTAGTT	0.403	
+	1	886		NM_001004727	NP_001004727	Q8NGF9	OR4X2_HUMAN	lasmic (Potential).		0	TGGATTAGGACA	0.438	
+	4	379	1nni.1_Missense_Mutation_p.M1I|GLYATL1_uc001nnj.			Q969I3	GLYL1_HUMAN			1	AGAATGATCCT	0.433	
+	8	942	L1_uc001nni.1_Missense_Mutation_p.G189E|GLYATL1			Q969I3	GLYL1_HUMAN			1	GCGAGGGAAGA	0.502	
+	8	1124	L1_uc001nni.1_Nonsense_Mutation_p.R250*|GLYATL1			Q969I3	GLYL1_HUMAN			1	TGGTGCGATAC	0.458	
+	8	1584	r.2_Intron|CD6_uc	NM_006725	NP_006716	P30203	CD6_HUMAN	lasmic (Potential).		1	TCAACCGGTCC	0.587	
-	6	1023	_p.P340S|CPSF7_	NM_001136040	NP_001129512	Q8N684	CPSF7_HUMAN	Pro-rich.		1	TGGGGGGAAGA	0.567	
-	5	589	_p.T198M|EEF1G_	NM_001404	NP_001395	P26641	EF1G_HUMAN	ST C-terminal.		0	TCCTCGTCTTC	0.473	
+	2	238	_p.E46G|TAF6L_	NM_006473	NP_006464	Q9Y6J9	TAF6L_HUMAN			3	GAGAGAGGCCA	0.582	
-	6	942	om.2_Missense_	NM_004254	NP_004245	Q8TCC7	S22A8_HUMAN	lasmic (Potential).		3	TTCGAGGACTTT	0.572	
+	3	636	1nxd.2_Missense_	NM_033101	NP_149092	Q96DT0	LEG12_HUMAN	Galectin 1.		2	ACCCTCGCTTC	0.622	
+	3	824	N3_uc001nxp.2_I	NM_201428	NP_958831	O95197	RTN3_HUMAN			1	AGAAACCACCT	0.408	
-	41	5838	_uc001obw.2_Mi	NM_015104	NP_055919	Q2TAZ0	ATG2A_HUMAN			2	TGGACGTGGCC	0.701	
-	2	112	1orf85_uc001ocd.	NM_001037225	NP_001032302	Q3KP22	CK085_HUMAN			0	ACCTCGTCTCT	0.383	rs146063063
+	7	815		NM_006782	NP_006773	O95159	ZFPL1_HUMAN	lasmic (Potential).		1	TGATACGCGGG	0.597	
+	17	1964	_p.P333L|POLA2_	NM_002689	NP_002680	Q14181	DPOA2_HUMAN			0	CATCCCGTCAG	0.512	
+	6	974		NM_032223	NP_115599	Q9H6A9	PCX3_HUMAN			0	GGACAGCCCCC	0.647	
-	9	1094	p.A310V|FIBP_uc	NM_198897	NP_942600	O43427	FIBP_HUMAN			1	GAACCGCACGT	0.597	
-	2	375	L1_uc010ros.1_I	NM_005438	NP_005429	P15407	FOSL1_HUMAN			0	GGTAACTGCTG	0.617	
-	2	1337	_5'Flank|BRMS1_	NM_006876	NP_006867	O43505	B3GN1_HUMAN	enal (Potential).		0	CTGGCGATATA	0.507	
+	8	1207	p.R324H|PELI3_u	NM_145065	NP_659502	Q8N2H9	PELI3_HUMAN			1	TGGCCGCACAG	0.731	
-	1	676	S_uc001oir.2_5'F	NM_018219	NP_060689	Q9NVE4	CCD87_HUMAN			2	TGAACGTCCCA	0.617	
+	3	261	S_uc001ois.2_5'F	NM_005125	NP_005116	O14618	CCS_HUMAN	HMA.		0	GCAGGCGGTAC	0.617	
-	12	1631	_uc001ojp.1_Miss	NM_022172	NP_071504	P11498	PYC_HUMAN			4	GACAACGGGGT	0.622	
-	2	307	_p.V40M|PITPNM	NM_004910	NP_004901	O00562	PITM1_HUMAN			3	CTCCACGCCGC	0.642	
-	2	269	mn.2_Missense_M	NM_181843	NP_862826	Q8WV74	NUDT8_HUMAN	ox.|Nudix hydrolase.		0	TTCCCGCAGGG	0.647	
-	3	259	5332_uc001omu.	NR_024249						0	GCCCGCTGGTG	0.627	
-	12	1583	k.2_Missense_Mu	NM_001277	NP_001268	P35790	CHKA_HUMAN			2	TCACACCCCAA	0.582	
+	6	1345	5_uc009ysg.2_5'	NM_002335	NP_002326	O75197	LRP5_HUMAN	ta-propeller 2.|Extracellula		7	CGGTCGACTGG	0.667	
-	8	1032	p.R288W|CPT1A_	NM_001876	NP_001867	P50416	CPT1A_HUMAN	lasmic (Potential).		2	CTCCCGGTCCA	0.343	
+	3	1042	nse_Mutation_p.R	NM_138768	NP_620123	Q96EZ4	MYEOV_HUMAN			0	GGGCGCGAATG	0.612	
+	8	709	p.R168Q|CTTN_u	NM_005231	NP_005222	Q14247	SRC8_HUMAN	Cortactin 3.		1	CGACCGAGTAG	0.597	
-	9	1577	ql.2_Missense_Mu	NM_001163817	NP_001157289	Q9UBM7	DHCR7_HUMAN			2	GCAGCGGTGGG	0.667	
-	5	1825	rz.1_Missense_M	NM_004705	NP_004696	O43422	P52K_HUMAN			3	TGAGGGTACCA	0.438	

+	21	3955	loxn.2_Missense_	NM_020193	NP_064578	Q7Z589	EMSY_HUMAN		6	CAGCTCCAATG	0.468	
-	6	1328	zg.2_Missense_Mu	NM_080491	NP_536739	Q9UQC2	GAB2_HUMAN		6	TGTCCGATCGG	0.478	
+	9	4996		NM_001008781	NP_001008781	Q8TDW7	FAT3_HUMAN	.|Extracellular (Potential).	5	GCATTTCCGTCA	0.438	
+	23	12640	di.3_Missense_Mut	NM_001008781	NP_001008781	Q8TDW7	FAT3_HUMAN	lasmic (Potential).	5	GCATCCCGTTCC	0.652	
-	8	1312		NM_178127	NP_835228	Q86XS5	ANGL5_HUMAN	nogen C-terminal.	1	AAACTGGTATTTT	0.274	
+	10	1620	w.2_Missense_Mu	NM_000829	NP_000820	P48058	GRIA4_HUMAN	cellular (Potential).	8	TGGAATGATATG	0.358	
-	7	1025	rwj.1_Missense_M	NM_002716	NP_002707	P30154	2AAB_HUMAN	HEAT 8.	0	GGGCAGCAGCT	0.408	
+	5	834	ono.2_Missense_M	NM_001076682	NP_001070150	P13591	NCAM1_HUMAN	2.|Extracellular (Potential).	1	TAGTCCGATTCAT	0.502	
+	2	716	p.R151Q|ZBTB16_	NM_006006	NP_005997	Q05516	ZBT16_HUMAN		2	AGGCTCGGTACC	0.607	
+	2	977	_p.V238A|ZBTB16_	NM_006006	NP_005997	Q05516	ZBT16_HUMAN		2	TGGGGTGGCTG	0.637	
-	3	340	55D_uc001ppd.2_5	NM_001077639	NP_001071107	Q6UWF7	FA55D_HUMAN		4	GGGAATAAGGA	0.398	
+	3	2607	L_uc001psz.1_No	NM_005933	NP_005924	Q03164	MLL1_HUMAN		25	AAAGATCGAGAT	0.303	
+	11	1498	_p.G437R|HINFP_	NM_015517	NP_056332	Q9BQA5	HINFP_HUMAN	action with NPAT.	4	GAGCCAGGACGT	0.587	
+	12	1762	ar.2_Missense_Mu	NM_022169	NP_071452	Q9H172	ABCG4_HUMAN	ype-2.|Helical; Name=3; (P	2	GCTGACGTGCCC	0.542	
-	6	1568	rzi.1_Missense_Mu	NM_012101	NP_036233	Q14134	TRI29_HUMAN		4	TGTCCGGACCC	0.537	
+	46	6429	_p.D963N|SORL1_	NM_003105	NP_003096	Q92673	SORL_HUMAN	tential).|Fibronectin type-III	15	TGTACGATGAG	0.478	rs144806633
-	1	320		NM_001004474	NP_001004474	Q8NGN2	O10S1_HUMAN	cellular (Potential).	2	TCAAAGGAGATC	0.547	
+	12	2017	2_5'Flank|ROBO3_	NM_022370	NP_071765	Q96MS0	ROBO3_HUMAN	III 1.|Extracellular (Potentia	2	GATGGCGTGCAG	0.587	
-	7	2958	e_Mutation_p.V24	NM_014758	NP_055573	Q92543	SNX19_HUMAN		4	TGGCACGGCTG	0.557	
+	29	4016	M|CACNA1C_uc00	NM_199460	NP_955630	Q13936	CAC1C_HUMAN	asmic (Potential).|IV.	11	GGTACGTGGTC	0.592	
+	1	532	nk.3_Missense_Mu	NM_002527	NP_002518	P20783	NTF3_HUMAN		1	AGTACTCGGTAT	0.577	
-	13	1721	t.1_Missense_Mut	NM_000552	NP_000543	P04275	VWF_HUMAN	VWFD 2.	12	GAGGCGCACGG	0.677	
-	8	1218	.2_Intron|ZNF384_	NM_001135734	NP_001129206	Q8TF68	ZN384_HUMAN	C2H2-type 4.	8	GGATACGGAGG	0.617	
-	4	251	n_p.A63V|MLF2_u	NM_005439	NP_005430	Q15773	MLF2_HUMAN		1	GAGACAGCTCCA	0.463	
+	9	1297	_p.R313Q|PTPN6_	NM_002831	NP_002822	P29350	PTN6_HUMAN	-protein phosphatase.	1	CACCCGAGAGG	0.622	
+	12	1600		NM_001080454	NP_001073923	P0C7M7	ACSM4_HUMAN		0	TTAACTCTTGAA	0.368	
-	31	4204	p.S406F|A2M_uc0	NM_000014	NP_000005	P01023	A2MG_HUMAN		5	CTTAGGGAGATT	0.448	
-	3	637	B4_uc001qzf.1_Int	NM_006249	NP_006240	Q04118	PRB3_HUMAN	[PQS]-P-[PS]-Q-[GE]-G-N-[	1	CCGGACGAGGT	0.637	rs28628341
+	1	372		NR_003932					0	AAAGCGGATGG	0.597	
-	13	4539		NM_000834	NP_000825	Q13224	NMDE2_HUMAN	lasmic (Potential).	12	ACAGGGGTTGG	0.532	
+	25	3607	rcy.1_Missense_M	NM_030667	NP_109592	Q16827	PTPRO_HUMAN	al).|Tyrosine-protein phosph	9	ACAGGAACATTC	0.443	
-	15	2044	_uc001rew.2_3'UT	NM_032941	NP_116559	P46063	RECQ1_HUMAN		2	AAATGGTAGCAT	0.348	
-	5	636	_p.E206*|ABCC9_	NM_005691	NP_005682	O60706	ABCC9_HUMAN	lasmic (Potential).	6	GGTCTTCAGGAG	0.358	
-	3	466	m.2_Missense_Mu	NM_198966	NP_945317	P12272	PTHR_HUMAN		1	GTCGCCGTAAAT	0.468	
+	3	1566		NM_032834	NP_116223	Q5BKT4	AG10A_HUMAN	cellular (Potential).	1	AATTTCGTTACT	0.348	
-	19	2650	nse_Mutation_p.R8	NM_017641	NP_060111	Q7Z4S6	KI21A_HUMAN		7	CTTGCCGACGA	0.443	
-	8	2299		NM_005164	NP_005155	Q9UBJ2	ABCD2_HUMAN	BC transporter.	6	ACTTATGATAAA	0.368	
+	49	7449	.R1281Q|LRRK2_	NM_198578	NP_940980	Q5S007	LRRK2_HUMAN		24	CTCGTCGACTTA	0.398	
+	11	1201	t.1_Missense_Mut	NM_016488	NP_057572	Q8NEY8	PPHLN_HUMAN		2	aacccccgaaaacga	0.01	
+	15	4460	_p.P943L|ARID2_u	NM_152641	NP_689854	Q68CP9	ARID2_HUMAN		10	AGTTCCCGACT	0.458	
-	5	632	_p.G78E|SLC38A	NM_018018	NP_060488	Q969I6	S38A4_HUMAN	lasmic (Potential).	4	GACATTCCAAAG	0.428	
+	4	1696	rpq.2_Missense_M	NM_138371	NP_612380	Q96HM7	F113B_HUMAN	Pro-rich.	5	gcctcctcctcccATTC	0.249	
-	5	921	GEF3_uc009zkr.2_	NM_001098532	NP_001092002	A8K2G5	A8K2G5_HUMAN		4	AGCTTCGGCCA	0.657	
-	1	1178	_p.P173L|ADCY6_	NM_015270	NP_056085	O43306	ADCY6_HUMAN		0	GGGCGGGTGCG	0.647	
-	2	490	_uc001rtj.1_5'Flan	NM_018113	NP_060583	Q6UX01	LMBRL_HUMAN	.|Cytoplasmic (Potential).	1	GGTGAACTCAG	0.522	
-	9	750	e_Mutation_p.T15	NM_012306	NP_036438	Q9BWQ8	FAIM2_HUMAN	ical; (Potential).	3	GGGCCGTGATG	0.652	
-	10	1010	n.2_Missense_Mut	NM_016293	NP_057377	Q9UBW5	BIN2_HUMAN	Potential.	1	CTATTTCCTCCT	0.532	

+	8	1404	.R374Q|ACVRL1_	NM_000020	NP_000011	P37023	ACVL1_HUMAN	Potential).|Protein kinase.	2	CAAGCGGTACA	0.617	
-	5	1181	h.2_Missense_Mu	NM_000424	NP_000415	P13647	K2C5_HUMAN	Rod.|Coil 2.	0	CTCAGCGATGA	0.577	
-	4	836		NM_033448	NP_258259	Q3SY84	K2C71_HUMAN	oil 1B.|Rod.	2	GGATTCCACCT	0.527	
-	5	445	D3_uc010snw.1_	NM_032840	NP_116229	Q8NCJ5	SPRY3_HUMAN	30.2/SPRY.	1	GTCCCCGGAGT	0.567	
+	30	6227	lank|PFDN5_uc0	NM_012291	NP_036423	Q14674	ESPL1_HUMAN		3	GCATCGTGCTC	0.622	
+	2	731		NM_173860	NP_776272	P31275	HXC12_HUMAN	Homeobox.	1	GCGCCGGAGG	0.522	
+	11	1100	KAP1L_uc010so	NM_005337	NP_005328	P55160	NCKPL_HUMAN		4	AACGGCGGCAA	0.517	
-	1	327	.2_5'UTR|RDH16_	NM_003708	NP_003699	O75452	RDH16_HUMAN	ity).|Cytoplasmic (Potential	0	AGCCTCGTGCA	0.602	
+	41	6984		NM_002332	NP_002323	Q07954	LRP1_HUMAN	Extracellular (Potential).	22	GTACCGGGGCC	0.697	
+	16	2138	b.1_Missense_Mu	NM_006313	NP_006304	Q9Y4E8	UBP15_HUMAN		3	AAAAACGATTGT	0.373	
+	6	1096	_p.P228L|TMEM5_	NM_014254	NP_055069	Q9Y2B1	TMEM5_HUMAN	ellular (Potential).	0	GTGCCCGGTCG	0.458	
-	3	436	q.1_Missense_Mut	NM_002076	NP_002067	P15586	GNS_HUMAN		1	AGAGAGCACTT	0.448	
+	12	2745	z.1_RNA|HELB_u	NM_033647	NP_387467	Q8NG08	HELB_HUMAN		2	GGGCCGCCAGC	0.532	rs149917565
+	15	1978	rp.2_Missense_Mu	NM_014515	NP_055330	Q9NZN8	CNOT2_HUMAN		0	TTTAACCGTGATT	0.358	
+	3	885		NM_031435	NP_113623	Q9H0W7	THAP2_HUMAN		1	AGCTATGCCTTT	0.348	
+	15	3484	ub.1_Missense_M	NM_014903	NP_055718	Q8IVL0	NAV3_HUMAN	Ser-rich.	17	TGGCGGGAAGT	0.478	
-	12	2538	_Mutation_p.P57	NM_182767	NP_877499	Q9H2J7	S6A15_HUMAN	lasmic (Potential).	3	TCGCTCGGTATT	0.443	
-	1	285	tbg.2_Missense_M	NM_001682	NP_001673	P20020	AT2B1_HUMAN	lasmic (Potential).	3	GAGCCCGCAGC	0.443	
-	1	904		NM_152638	NP_689851	Q8TC90	CL012_HUMAN		2	GGTAGGAGTGG	0.716	
+	10	2315		NM_005761	NP_005752	O60486	PLXC1_HUMAN	ellular (Potential).	3	TACCCGGGCAT	0.408	
+	12	1486		NM_014503	NP_055318	O75691	UTP20_HUMAN		4	CTCTGGCCATT	0.418	
+	4	533	sense_Mutation_p.	NM_018413	NP_060883	Q9NPF2	CHSTB_HUMAN	enal (Potential).	0	GATGCGGCGGG	0.567	
+	14	1501	t.2_Missense_Mut	NM_213594	NP_998759	Q33E94	RFX4_HUMAN	ary for dimerization.	1	GCCAATGAGCTC	0.448	
-	12	2555		NM_004075	NP_004066	Q16526	CRY1_HUMAN		3	AGGACGTTTCC	0.398	
+	3	299	WP1_uc009zuu.1_	NM_007062	NP_008993	Q13610	PWP1_HUMAN		0	GGCACGCCCAA	0.517	
+	3	1014		NM_007076	NP_009007	Q9BVA6	FICD_HUMAN	Fido.	0	GCGACGTGCTG	0.612	
-	2	694	M119_uc001tnf.2_	NM_181724	NP_859075	Q4V9L6	TM119_HUMAN	lasmic (Potential).	1	GCGGCCAAGAT	0.627	
+	2	218	_p.R22H|DAO_uc	NM_001917	NP_001908	P14920	OXDA_HUMAN		2	TGAGCGCTACC	0.622	
+	13	2142	c.2_Missense_Mu	NM_001093	NP_001084	O00763	ACACB_HUMAN	in carboxylation.	8	ATTTCCGGAGC	0.512	
+	26	3882	c.2_Missense_Mu	NM_001093	NP_001084	O00763	ACACB_HUMAN		8	TGTACGGCCAC	0.597	
+	9	1123	HP_uc001tpp.2_M	NM_001143852	NP_001137324	Q9BT92	TCHP_HUMAN	Glu-rich.|Interaction with ke	1	TGGCCGATGTG	0.662	
+	5	698	ense_Mutation_p.	NM_033121	NP_149112	Q8IZ07	AN13A_HUMAN		0	TCTGTCGCATC	0.458	
-	16	1991	q.3_Missense_Mu	NM_024072	NP_076977	Q8TDD1	DDX54_HUMAN		3	CTTCCGGCCCA	0.662	
-	3	948		NM_138451	NP_612460	Q96DY2	IQCD_HUMAN		1	CCAGCGAGATC	0.607	
-	13	1442	p.D213N|TAOK3_	NM_016281	NP_057365	Q9H2K8	TAOK3_HUMAN	Ser-rich.	6	GTCATCGTGCA	0.502	
+	2	500	e_Mutation_p.R1	NM_207311	NP_997194	Q6ZP65	BICR1_HUMAN	Potential.	2	AGAACCGAGAA	0.463	
+	9	1015	RX7_uc001tzp.2_	NM_002562	NP_002553	Q99572	P2RX7_HUMAN		5	AGAAACGGACT	0.448	
-	5	749	_splice|CAMKK2_	NM_006549	NP_006540	Q96RR4	KKCC2_HUMAN		3	ACTCACGTGGA	0.488	
+	5	577	zxh.2_Missense_	NM_001080825	NP_001074294	A0PK00	T120B_HUMAN	ical; (Potential).	0	GTGCCGTGGCA	0.612	
+	31	3198	k.1_Missense_Mu	NM_003959	NP_003950	O75146	HIP1R_HUMAN		1	GCGTGGCCCCC	0.682	
+	9	1126		NM_207437	NP_997320	Q8IVF4	DYH10_HUMAN	n (By similarity).	6	GCCATGATGAG	0.577	
+	18	2793	p.R465Q|DNAH10	NM_207437	NP_997320	Q8IVF4	DYH10_HUMAN	n (By similarity).	6	TGTCCGGAATT	0.428	
+	18	2121	ACS_uc009zyh.2_	NM_023928	NP_076417	Q86V21	AACS_HUMAN		3	TTGCCGTCAAA	0.532	
+	4	1236		NM_052907	NP_443139	Q14DG7	T132B_HUMAN	ellular (Potential).	19	TCTCCGAGATC	0.522	
-	2	731		NM_133448	NP_597705	Q14C87	T132D_HUMAN	ellular (Potential).	14	GTCCCGCAGGA	0.537	rs138159153
-	35	4573	_p.A314V|POLE_	NM_006231	NP_006222	Q07864	DPOE1_HUMAN		8	CGGATGCCCTG	0.597	
+	2	248	AM5_uc001uku.2_	NM_138575	NP_612642	Q96HS1	PGAM5_HUMAN		0	CGTGCGGAAGA	0.498	rs142758535

+	3	559	_p.V38M|ZNF10_uc001ulq.2_Missense_Mutation_p.V3			Q14587	ZN268_HUMAN		1	CAGATCGTGTAC	0.438	
+	5	1442	NF10_uc001ulq.2_	NM_015394	NP_056209	P21506	ZNF10_HUMAN	C2H2-type 4.	3	TCAGCTGGTTCT	0.418	
+	5	1574	NF10_uc001ulq.2_	NM_015394	NP_056209	P21506	ZNF10_HUMAN		3	AGAAACCCTATG	0.428	
+	10	2059	1umg.2_Nonsense	NM_017520	NP_059990	Q99549	MPP8_HUMAN	ANK 3.	0	ATCGTACGACTC	0.443	
-	1	397	j.1_RNA|PSPC1_	NM_001042414	NP_001035879	Q8WXF1	PSPC1_HUMAN		1	GCTTGAGGAAAC	0.652	
+	4	477	aaa.2_Missense_	NM_001676	NP_001667	P54707	AT12A_HUMAN	lasmic (Potential).	6	TCACCCCTCCCA	0.577	
-	5	878	p.2_Missense_M	NM_183044	NP_898865	Q9Y252	RNF6_HUMAN		2	CTTGTTCGCCTA	0.423	rs138864245
+	1	2169		NM_001033602	NP_001028774	Q5JR59	MTUS2_HUMAN	teraction with MAPRE1.	0	CTGCCAACCTCT	0.552	
-	5	808	D13_uc001uux.2_	NM_178006	NP_821074	Q9Y3M8	STA13_HUMAN		4	GCTGACGAGTG	0.602	rs146112751
-	4	1190	PC4_uc010abw.2_	NM_016179	NP_057263	Q9UBN4	TRPC4_HUMAN	lasmic (Potential).	6	AGCCTGGAAACT	0.458	
-	4	728	_p.R119*|ELF1_uc	NM_172373	NP_758961	P32519	ELF1_HUMAN		1	TTATTCGTTTTTC	0.363	
-	11	2825	p.V890M|ATP7B_	NM_000053	NP_000044	P35670	ATP7B_HUMAN	lasmic (Potential).	3	GCCCACGTGGG	0.443	
+	5	431	jr.2_Missense_M	NM_006002	NP_005993	P15374	UCHL3_HUMAN		0	AAGAACGAGCCA	0.398	rs11555620
+	20	3690	.R876K|LMO7_uc	NM_015842	NP_056667	Q8WWI1	LMO7_HUMAN		5	GCAAAGGGCCA	0.383	
-	2	1732	lj.2_Nonsense_M	NM_005842	NP_005833	O43597	SPY2_HUMAN	PR.|Cys-rich.	2	ACCATCGTGTAC	0.473	
-	20	3034	se_Mutation_p.E	NM_198968	NP_945319	Q86YF9	DZIP1_HUMAN		2	CGATTTCGCTTC	0.547	
+	9	1028	k.1_Nonsense_M	NM_002271	NP_002262	O00410	IPO5_HUMAN		3	GACTGGGCAAA	0.418	
-	25	3060		NM_052867	NP_443099	Q8IZF0	NALCN_HUMAN	S3 of repeat III; (Potential)	16	TATGTCCATTACT	0.358	
+	22	2575	qu.1_Missense_	NM_015011	NP_055826	Q9Y6X6	MYO16_HUMAN	osin head-like 1.	10	CAAGTGGAATGT	0.368	
-	27	2107	4A1_uc010agl.2_	NM_001845	NP_001836	P02462	CO4A1_HUMAN	le-helical region.	6	CTTGGGGACCT	0.542	
+	27	3201	_Mutation_p.S10	NM_015205	NP_056020	P98196	AT11A_HUMAN	ical; (Potential).	4	GGGGTCGCTGC	0.418	
+	8	957	r.1_Missense_Mu	NM_003891	NP_003882	P22891	PROZ_HUMAN	eptidase S1.	0	CACGCGGCCTG	0.637	
+	1	597		NM_001005500	NP_001005500	Q8NGD0	OR4M1_HUMAN	Name=5; (Potential).	0	AGTGATGATCTG	0.478	
-	24	3503	.1_RNA|TEP1_uc	NM_007110	NP_009041	Q99973	TEP1_HUMAN		5	TCAGCCGTTGCA	0.637	
+	5	1749	he.2_Missense_M	NM_014045	NP_054764	Q7Z4F1	LRP10_HUMAN	s A 4.|Extracellular (Potenti	1	GCATTGCCAGC	0.607	
-	17	3858	IN1_uc001wir.3_M	NM_014977	NP_055792	Q9UKV3	ACINU_HUMAN	Asp/Glu/Lys-rich.	4	CTTGATCGGGAA	0.567	
-	2	788	jb.2_Missense_M	NM_020834	NP_065885	Q8IX15	HOMEZ_HUMAN		0	GGTAGGGGAATG	0.527	
+	2	694	R84C|CMTM5_uc	NM_138460	NP_612469	Q96DZ9	CKLF5_HUMAN	MARVEL.	0	ACCAGCGCTTC	0.557	rs147365003
-	12	1169		NM_000257	NP_000248	P12883	MYH7_HUMAN	osin head-like.	4	GATGGCGCCTG	0.547	
-	4	1786	e_Mutation_p.R29	NM_032452	NP_115828	Q96JJ6	JPH4_HUMAN	lasmic (Potential).	2	GCGCCGATCTG	0.637	
+	35	3746	wlk.2_Missense_	NM_138360	NP_612369	Q8ND23	LR16B_HUMAN		5	ACGACGCAGGT	0.542	
-	3	679	A1_uc001wqa.2_5	NM_002515	NP_002506	P51513	NOVA1_HUMAN		5	TTTCTCGAATTT	0.438	
+	6	563	.S181C|SIP1_uc0	NM_003616	NP_003607	O14893	GEMI2_HUMAN		0	TTGCTTAGTATT	0.259	
+	3	2013	a.2_Missense_M	NM_152447	NP_689660	Q96NI6	LRFN5_HUMAN	lar (Potential).|LRRCT.	8	TGGCCGCTACT	0.468	
-	1	1774		NM_001012706	NP_001012724	A1A4T8	CN182_HUMAN		0	CTCTTCCTCCAA	0.493	
-	10	2866		NM_015163	NP_055978	Q9C026	TRIM9_HUMAN	B30.2/SPRY.	3	GAAGTCGGGGA	0.602	
+	6	1121		NM_021255	NP_067078	Q9HAT8	PELI2_HUMAN		1	TTAACGCCGCC	0.577	
+	15	1459	xdq.2_Missense_	NM_002892	NP_002883	P29374	ARI4A_HUMAN		6	GCCGTTCGGCAA	0.323	
-	11	2806	H5_uc001xfy.2_3'	NM_139318	NP_647479	Q8NCM2	KCNH5_HUMAN	bly) (By similarity).|Cytopla	9	TGTCCTCTTTGA	0.512	
-	11	2474	H5_uc001xfy.2_3'	NM_139318	NP_647479	Q8NCM2	KCNH5_HUMAN	lasmic (Potential).	9	CCTTTTCCATTT	0.453	
+	28	3736	l.2_Missense_Mu	NM_015180	NP_055995	Q8WXH0	SYNE2_HUMAN	lasmic (Potential).	14	TGCTCGCTGGA	0.294	
+	105	19221	E2_uc010aqa.2_	NM_015180	NP_055995	Q8WXH0	SYNE2_HUMAN	Cytoplasmic (Potential).	14	CTCCACCGCTAC	0.587	
+	2	1571	k.3_Missense_M	NM_021979	NP_068814	P54652	HSP72_HUMAN		1	AGCACCGGTAAG	0.562	
-	24	5086	.V1678M|SPTB_u	NM_000347	NP_000338	P11277	SPTB1_HUMAN	Spectrin 14.	11	CGCCACGTCCT	0.557	
-	9	1981	q.2_Missense_M	NM_003861	NP_003852	Q96JK2	DCAF5_HUMAN		2	GCGCCGCATGG	0.552	
-	2	477		NM_001105579	NP_001099049	A6NDD5	SYN1L_HUMAN		0	CTTGTCTCTCCC	0.697	
+	26	3047	se_Mutation_p.H5	NM_015072	NP_055887	Q6EMB2	TTLL5_HUMAN		3	GCCTACATCCC	0.517	

+	3	542	e_Mutation_p.R15	NM_004452	NP_004443	A2VDJ2	A2VDJ2_HUMAN		2	GCCTGCCGCTTC	0.577	
-	5	1305	EL1_uc010tvf.1_I	NM_015305	NP_056120	Q9UNK9	ANGE1_HUMAN		4	CCGGCGTGGGT	0.592	
+	6	703	ss.2_Missense_M	NM_145870	NP_665877	O43708	MAAI_HUMAN	ST C-terminal.	0	TTTAACGGTGAG	0.577	
-	4	452	e_Mutation_p.R94	NM_152446	NP_689659	Q6ZU80	CE128_HUMAN		0	ATAAACGTTGA	0.368	
+	4	460	2_Missense_Muta	NM_024824	NP_079100	Q6PJT7	ZC3HE_HUMAN		3	CAACTGGTAAG	0.299	
-	11	4302	uf.1_Missense_Mu	NM_004239	NP_004230	Q15643	TRIPB_HUMAN	Potential.	13	CTATTTCGATGT	0.333	rs145498019
+	6	1509	_p.A378T|RIN3_uc	NM_024832	NP_079108	Q8TB24	RIN3_HUMAN	Pro-rich.	3	GGACAGCCAAA	0.627	
-	19	3166	_p.S985L|DICER1_	NM_030621	NP_085124	Q9UPY3	DICER_HUMAN	PAZ.	5	TACCTTGAAGAT	0.468	
-	9	2616		NM_024734	NP_079010	Q96JQ2	CLMN_HUMAN		0	GCTGTCCATGG	0.557	
+	4	329	ygn.1_Missense_	NM_006668	NP_006659	Q9Y6A2	CP46A_HUMAN		0	GTACCGTGCGC	0.537	
-	3	371	|RAGE_uc001yln.	NM_014226	NP_055041	Q9UQ07	MOK_HUMAN	rotein kinase.	4	TCTCTCGTAGGT	0.378	rs141604419
+	9	1184	on.3_Missense_Mu	NM_153046	NP_694591	Q8NDG6	TDRD9_HUMAN	case C-terminal.	3	GGAGCGAAGCA	0.408	
+	13	4020	196S|KIAA0284_u	NM_001112726	NP_001106197	Q9Y4F5	K0284_HUMAN		1	ccccggcccccgggA	0.552	
+	7	1036	l.1_Missense_Mut	NM_138790	NP_620145	Q96BZ4	PLD4_HUMAN		2	ATGGGGTGCCC	0.607	
-	7	3148	ypx.2_Missense_M	NM_138420	NP_612429	Q8IVF2	AHNK2_HUMAN		1	CCGATACCCCGA	0.607	
-	4	314	T14_uc001yqi.2_	NM_177533	NP_803877	O95848	NUD14_HUMAN	udix hydrolase.	1	TCACCCGCATAC	0.682	
-	17	2359	Mutation_p.D462N	NM_001519	NP_001510	Q92994	TF3B_HUMAN		4	CCCACCGTTGC	0.607	
-	7	915	zba.2_Missense_M	NM_000814	NP_000805	P28472	GBRB3_HUMAN	ical; (Probable).	5	AGAATCGTTATC	0.408	
-	61	9538		NM_004667	NP_004658	O95714	HERC2_HUMAN	RCC1 9.	13	ATCACCATTTTG	0.483	
+	3	296	_p.E65K|TMCO5A	NM_152453	NP_689666	Q8N6Q1	TMC5A_HUMAN	Potential.	1	AGTGGGAGAAG	0.522	
-	11	1569	.2_Intron|RASGRF	NM_005739	NP_005730	O95267	GRP1_HUMAN		2	GTTTTTGGATCA	0.448	
+	12	1518	_p.R365H|IVD_uc	NM_002225	NP_002216	P26440	IVD_HUMAN		1	GGGCCGCTTTC	0.512	
+	15	5980	ot.1_Missense_Mu	NM_170589	NP_733468	Q8NG31	CASC5_HUMAN	ation and for interaction wit	5	TTTACCGACCCA	0.383	
+	30	4013	PKBP1_uc010udb	NM_001128608	NP_001122080	O60336	MABP1_HUMAN		10	CCGTCTCGGCCT	0.627	
-	33	6085	-4310|MI0015840_	NM_016642	NP_057726	Q9NRC6	SPTN5_HUMAN	Spectrin 16.	2	GTCACGCACCT	0.667	
-	3	415		NM_001080490	NP_001073959	Q3MJ16	PA24E_HUMAN		0	ACTTCACGTGGG	0.502	
-	20	2842	AN1_uc001zqk.2_	NM_138477	NP_612486	Q8IWY9	CDAN1_HUMAN		2	GGTCTCCCCCTT	0.627	
-	7	980	gp.2_Nonsense_M	NM_173500	NP_775771	Q6IQ55	TTBK2_HUMAN	rotein kinase.	7	CAGCTCGAGGCT	0.418	
+	4	2743		NM_002373	NP_002364	P78559	MAP1A_HUMAN		9	TGAGCCGGAGG	0.557	
+	4	5518		NM_002373	NP_002364	P78559	MAP1A_HUMAN		9	TTGGAGGGGCA	0.582	
+	10	1592_1593	T1B_uc001zsd.3_	NM_020990	NP_066270	P12532	KCRU_HUMAN		0	CGTCTGGAGAG	0.5	
-	30	4051	n.2_Missense_Mu	NM_014080	NP_054799	Q9NRD8	DUOX2_HUMAN	ential).|FAD-binding FR-typ	5	GTCACTCCTGGA	0.592	
+	19	2758	_Mutation_p.A744	NM_153618	NP_705871	Q8NFY4	SEM6D_HUMAN	lasmic (Potential).	4	CATGGAGCTTCA	0.522	
-	9	1170	_p.A307T|CYP19A	NM_031226	NP_112503	P11511	CP19A_HUMAN		3	AGGAGCTGCGA	0.398	
+	3	585	_p.D122N|GLDN_	NM_181789	NP_861454	Q6ZMI3	GLDN_HUMAN	Potential).|Collagen-like 1.	2	TTGTAGGACCTT	0.502	
-	32	7991	y.1_Missense_Mut	NM_015263	NP_056078	Q8TDJ6	DMXL2_HUMAN		9	TTATTTCGAAGA	0.303	
-	38	4833	10uga.1_RNA|uc0	NM_018728	NP_061198	Q9NQX4	MYO5C_HUMAN	Dilute.	14	CCAGGCCGTTCT	0.592	
+	3	936	gd.2_Missense_M	NM_004751	NP_004742	O95395	GCNT3_HUMAN	enal (Potential).	2	GTGTCCATGTG	0.443	
-	4	605		NM_003613	NP_003604	O75339	CILP1_HUMAN		7	CTTACCTGGTG	0.612	
-	8	934	.G190R|MEGF11_	NM_032445	NP_115821	A6BM72	MEG11_HUMAN		1	TGTCCCTGGTG	0.567	
+	12	2092	p.A610T|DIS3L_u	NM_001143688	NP_001137160	Q8TF46	DI3L1_HUMAN		2	GGGTCGCCAAA	0.547	
+	15	2696	_p.R811K|DIS3L_u	NM_001143688	NP_001137160	Q8TF46	DI3L1_HUMAN		2	TACCAAGGTATGT	0.323	
+	4	686	x.1_Missense_Mu	NM_016166	NP_057250	O75925	PIAS1_HUMAN	PINIT.	2	CAGTACAGGTCC	0.353	
+	25	3884	_p.Q1248*|NEO1_	NM_002499	NP_002490	Q92859	NEO1_HUMAN	lasmic (Potential).	1	CCCCAGCGTAAG	0.458	
+	4	479	bjb.2_Missense_M	NM_001042367	NP_001035826	Q7Z4M0	CO060_HUMAN		1	CCTGATGGAAAC	0.537	
+	12	1229	_p.P349L|CSK_uc	NM_001127190	NP_001120662	P41240	CSK_HUMAN	rotein kinase.	3	GCTGCCAGTCA	0.652	
+	14	1537	e_Mutation_p.L50	NM_021819	NP_068591	Q9HAT1	LMA1L_HUMAN	lasmic (Potential).	0	GGCCCTGGGGA	0.627	

-	1	1318		NM_017793	NP_060263	Q9BUL9	RPP25_HUMAN			0	GATGGGGATTC	0.672	
+	2	1064	unk.1_Missense_	NM_015206	NP_056021	Q9UPX6	K1024_HUMAN			4	CGAAAGCTTAG	0.522	
-	3	1423	k.2_Intron|DET1_u	NM_001144074	NP_001137546	Q7L5Y6	DET1_HUMAN			2	CTTACCGGCGC	0.448	
+	1	217	CTP2_uc010bok.2	NM_018349	NP_060819	Q6DN12	MCTP2_HUMAN			3	CCTCTCTGTGC	0.582	
+	8	1833	on.2_Missense_M	NM_000875	NP_000866	P08069	IGF1R_HUMAN	nectin type-III 1.		8	ATATCCGTGGG	0.557	
+	21	4026	n.2_Missense_Mu	NM_000875	NP_000866	P08069	IGF1R_HUMAN	lasmic (Potential).		8	AGGCCGAGAAC	0.682	
+	6	2412	e_Mutation_p.F76	NM_145728	NP_663780	O15061	SYNEM_HUMAN	Tail.		4	GGAGTTTTCCGT	0.572	
-	12	1385	DF1_uc010utz.1_	NM_022450	NP_071895	Q96CC6	RHDF1_HUMAN	ical; (Potential).		2	GTGCACGAAGG	0.672	
+	5	1870		NM_005632	NP_005623	O75808	CAN15_HUMAN	lpain catalytic.		2	GCTTCCCCGCG	0.647	
+	3	796	192W|STUB1_uc0	NM_003961	NP_003952	O75783	RHBL1_HUMAN			0	ACGTTGGGTGA	0.632	
-	6	1453	XL16_uc002cjb.2	NM_153350	NP_699181	Q8N461	FXL16_HUMAN	LRR 6.		0	GGAGGTGCTTC	0.642	
-	3	896		NM_001013658	NP_001013680	Q96A99	PTX4_HUMAN	Pentaxin.		0	CCGTGCGGACC	0.662	rs61751878
+	3	872	g.1_Missense_M	NM_016111	NP_057195	Q9Y4R8	TELO2_HUMAN			0	CGTCCGGGTGC	0.667	
+	15	1604	R290H|TBL3_uc0	NM_006453	NP_006444	Q12788	TBL3_HUMAN	WD 10.		0	GGACCGCACGG	0.637	
+	22	2522	v.1_Missense_Mu	NM_000548	NP_000539	P49815	TSC2_HUMAN		p.E793fs*9(1)	10	GCGTCGTGGCC	0.622	
+	23	2727	v.1_Missense_Mu	NM_000548	NP_000539	P49815	TSC2_HUMAN			10	CCTGCCGTACA	0.657	rs138527121
+	42	5414	vw.1_Missense_M	NM_000548	NP_000539	P49815	TSC2_HUMAN			10	TGCACCCTCCG	0.642	
-	44	12237	_p.R4009C|MIR1	NM_001009944	NP_001009944	P98161	PKD1_HUMAN	lasmic (Potential).		3	CTGGCGCACGA	0.677	
-	24	9004	_Mutation_p.H29	NM_001009944	NP_001009944	P98161	PKD1_HUMAN	ellular (Potential).		3	GGTAGTGGCCT	0.672	
-	12	2031	_p.P382L|ABCA3_	NM_001089	NP_001080	Q99758	ABCA3_HUMAN			16	TGACGGGACTC	0.642	
+	11	7425_7426	.1_Missense_Mut	NM_016333	NP_057417	Q9UQ35	SRRM2_HUMAN	-rich.|Ser-rich.		4	ACAGCCCCAGC	0.634	
+	11	8042	.1_Missense_Mut	NM_016333	NP_057417	Q9UQ35	SRRM2_HUMAN	Ser-rich.		4	CCCTGCCCCTG	0.647	
+	2	682	F213_uc010bth.2	NM_004220	NP_004211	O14771	ZN213_HUMAN	SCAN box.		0	AGCTGCGTACC	0.657	
+	2	799	F213_uc010bth.2_	NM_004220	NP_004211	O14771	ZN213_HUMAN	SCAN box.		0	CTGTCGCCTTG	0.642	
+	6	2268	p.R294W|ZNF263	NM_005741	NP_005732	O14978	ZN263_HUMAN	2H2-type 8.		4	TCCAATCGGATT	0.478	
+	3	307	AT15_uc010uxc.1	NM_001083601	NP_001077070	Q9H7X0	NAT15_HUMAN	etyltransferase.		0	TGCCACGATGAC	0.627	
+	9	869	N1_uc002cxb.2_	NM_001142290	NP_001135762	O60291	MGRN1_HUMAN			2	TGGACCGGGTC	0.572	
+	11	1698	v.1_Missense_Mu	NM_018723	NP_061193	Q9NWB1	RFOX1_HUMAN			0	GGAGGGATCTT	0.488	
-	1	571		NM_144674	NP_653275	Q96M29	TEKT5_HUMAN	Potential.		2	GTTCTGGTTCT	0.612	
+	24	3240	2dap.2_Missense_	NM_015226	NP_056041	Q2KHT3	CL16A_HUMAN			2	TGAGCGTCGAA	0.706	
-	7	940	dbg.1_Missense_	NM_015914	NP_056998	Q6PKC3	TXD11_HUMAN			0	CTAGGTAATCT	0.383	
+	4	746	va.2_Missense_M	NM_005236	NP_005227	Q92889	XPF_HUMAN	ucine-zipper 1.		10	CCCATCGCTTG	0.333	
-	16	2024	C6_uc010bvo.2_	NM_001171	NP_001162	O95255	MRP6_HUMAN	nsporter 1.|Cytoplasmic (B		3	TGGACCGACAA	0.632	rs72653780
+	8	1200	ssense_Mutation_	NM_024847	NP_079123	Q7Z402	TMC7_HUMAN	lasmic (Potential).		3	CAATACGCATTT	0.413	
+	1	1347	IPL2_uc002dft.2_	NM_001034841	NP_001030013	Q3MIP1	IPIL2_HUMAN	lasmic (Potential).		2	AGGGGCGCTGT	0.652	rs145325211
+	5	983	fy.2_Missense_Mu	NM_016524	NP_057608	Q9BSW7	SYT17_HUMAN	C2 1.		1	CCCACGATGGC	0.612	
-	1	120	TL9_uc002djf.2_In	NM_005849	NP_005840	O95976	IGSF6_HUMAN			0	CTTACCGACAC	0.393	rs143387566
+	13	1400	_uc002dji.2_Miss	NM_144672	NP_653273	Q7RTW8	OTOAN_HUMAN			3	TGAAACGCAAG	0.582	
+	12	994	p.D280N|POLR3	NM_018119	NP_060589	Q9NVU0	RPC5_HUMAN			2	TGGCCGATCAG	0.642	
+	3	580	_uc010byo.1_Miss	NM_001770	NP_001761	P15391	CD19_HUMAN	ellular (Potential).		3	TCCGTGTCTCC	0.647	
+	2	834	_uc002dtn.2_Mis	NM_001030288	NP_001025459	P16150	LEUK_HUMAN	ellular (Potential).		2	GATGTCTCCAA	0.592	
-	6	1127	226L|SEZ6L2_uc	NM_201575	NP_963869	Q6UXD5	SE6L2_HUMAN	xtracellular (Potential).		2	GGCCGGCCGG	0.637	
-	3	909	89_uc010bzy.2_	NM_138447	NP_612456	Q96CS4	ZN689_HUMAN	2H2-type 2.		0	TGCCCGCCGGT	0.587	
+	16	5370		NM_014712	NP_055527	O15047	SET1A_HUMAN			3	CTCAACCAGCT	0.468	
+	6	1002		NM_001008274	NP_001008275	Q6ZMU5	TRI72_HUMAN			0	CCCACCCGCCC	0.617	
+	30	3551	AX_uc002ebt.2_In	NM_000887	NP_000878	P20702	ITAX_HUMAN	lasmic (Potential).		4	CCAGTGAGAAA	0.552	
-	5	527	PS35_uc002eee.	NM_018206	NP_060676	Q96QK1	VPS35_HUMAN			0	TCAAGGATGT	0.393	

-	5	3207	gn.1_Missense_M	NM_015069	NP_055884	Q2M1K9	ZN423_HUMAN	2H2-type 23.	4	GCAGCGAAGGG	0.617	
+	2	558	_p.A97V|ADCY7_	NM_001114	NP_001105	P51828	ADCY7_HUMAN	ical; (Potential).	1	CTTGGCGCTGC	0.642	
-	13	1731	q.2_Missense_Mu	NM_001143685	NP_001137157	Q6NT32	EST5A_HUMAN		0	CTGTCCGAGGC	0.527	
+	2	286	3_uc002ejg.2_3'U	NM_005954	NP_005945	P25713	MT3_HUMAN	Beta.	0	CTGCGCGGACT	0.647	
+	16	2066	79_splice|SLC12A	NM_001126108	NP_001119580	P55017	S12A3_HUMAN		3	TCATCGTGAGT	0.428	
-	16	2264_2265	on_p.550_551SR	NM_005550	NP_005541	Q9BVG8	KIFC3_HUMAN	inesin-motor.	3	AGGCGGCTGC	0.693	
-	5	694	m.1_Missense_Mu	NM_002080	NP_002071	P00505	AATM_HUMAN		2	CACAGCGCCTG	0.488	
+	7	1488	p.R175W|HSF4_u	NM_001040667	NP_001035757	Q9ULV5	HSF4_HUMAN	obic repeat HR-A/B.	0	CACTTCGGCAG	0.637	
+	16	2393	_p.S482L|SLC9A	NM_004594	NP_004585	Q14940	SL9A5_HUMAN		2	GTCCTCGGAAA	0.607	
+	2	230	_uc010vjt.1_5'Fla	NM_016948	NP_058644	Q9NPB6	PAR6A_HUMAN	PRKCI and PRKCZ.|OPR	1	TGCTGCGGGCG	0.667	
-	2	468	.E133K|NIP7_uc0	NM_032382	NP_115758	Q96MW5	COG8_HUMAN		1	CTCCTCGGCTT	0.398	
-	8	777	ezk.1_Missense_	NM_138383	NP_612392	Q765P7	MTSSL_HUMAN	IMD.	1	CATGTCGTTGA	0.667	
-	46	7449		NM_032821	NP_116210	Q4G0P3	HYDIN_HUMAN		2	CCCTTCACTGT	0.478	
+	8	789	.A156V|KIAA0174_uc002fbn.1_Missense_Mutation_p.			P53990	IST1_HUMAN	teraction with CHMP1A an	1	GGAAGCCCCAC	0.393	
+	18	2747	mp.1_Missense_	NM_014003	NP_054722	Q92620	PRP16_HUMAN	case C-terminal.	1	ATGGCGTTCGG	0.507	
+	2	360		NM_020927	NP_065978	Q9HCJ6	VAT1L_HUMAN		1	GGTGCGACAAG	0.443	
-	1	85		NM_001080442	NP_001073911	A6NNN8	S38A8_HUMAN	ical; (Potential).	0	GACAGCGCCCA	0.642	
-	12	1699	CHC14_uc002fkb	NM_015144	NP_055959	Q8WYQ9	ZCH14_HUMAN		2	CATGGCGCTGC	0.557	rs141001038
-	1	150		NM_001739	NP_001730	P35218	CAH5A_HUMAN		0	CCATCGCCCTG	0.512	
+	2	126	|TRAPPC2L_uc00	NM_016209	NP_057293	Q9UL33	TPC2L_HUMAN		0	AGAACGAGCTG	0.562	
+	3	473	_p.G141S|SPIRE2	NM_032451	NP_115827	Q8WWL2	SPIR2_HUMAN	KIND.	1	ACAGCGGCTGC	0.711	
+	7	844	8_uc010vpq.1_Mi	NM_207514	NP_997397	Q6ZN54	DEFI8_HUMAN		1	TGTGAGCTCCA	0.567	
-	21	3394		NM_006445	NP_006436	Q6P2Q9	PRP8_HUMAN		6	GATGCGATCAA	0.507	
-	2	812	d.1_Missense_Mu	NM_017575	NP_060045	Q86US8	EST1A_HUMAN	n with telomeric DNA.	4	GTAGCGATTCC	0.652	rs147212426
-	7	1301	V1_uc010vru.1_5'	NM_013276	NP_037408	Q9UHJ6	SHPK_HUMAN		1	AGCCCGGGTCA	0.647	
-	4	703	e_Mutation_p.A11	NM_002561	NP_002552	Q93086	P2RX5_HUMAN	ellular (Potential).	0	TAACCGCTTCC	0.647	
-	13	1562		NM_002208	NP_002199	P38570	ITAE_HUMAN	Extracellular (Potential).	4	ACACGGCCCCA	0.577	
-	4	802	c.3_Nonsense_M	NM_001122890	NP_001116362	Q6P531	GGT6_HUMAN	ellular (Potential).	1	GGCTCGGGCCC	0.652	
+	25	3114	sn.1_Missense_M	NM_153827	NP_722549	Q8N4C8	MINK1_HUMAN	teraction wi p.E973V(1)	6	GGCAGCCCTAG	0.587	
+	22	2910		NM_006612	NP_006603	O43896	KIF1C_HUMAN	Potential.	2	CCCTGCGGGAC	0.642	
-	3	931	72B_uc010ckw.2_	NM_001104577	NP_001098047	Q9NWF4	RFT_HUMAN		0	TGCCCGGGGCC	0.662	rs137937212
-	11	1609	UP88_uc010cle.1	NM_002532	NP_002523	Q99567	NUP88_HUMAN		1	CAAAGGAATCT	0.463	
+	9	1447	lt.1_Missense_Mu	NM_181844	NP_862827	Q8N143	BCL6B_HUMAN		1	AACACGGAGCT	0.632	
-	26	4211	RL4_uc002gfy.1_	NM_032442	NP_115818	Q96JN8	NEUL4_HUMAN		2	GTACCTGAGGT	0.572	
+	3	731	EM102_uc002ggy.	NM_178518	NP_848613	Q8N9M5	TM102_HUMAN	ellular (Potential).	0	CGGAACCCCCA	0.572	
-	4	1554	hd.3_Missense_M	NM_001128833	NP_001122305	Q9P1Z0	ZBTB4_HUMAN	Pro-rich.	4	CCTCCGGGGCT	0.662	
+	7	1328	ghe.2_Missense_	NM_000937	NP_000928	P24928	RPB1_HUMAN		1	CCGTACTGTCA	0.607	
+	14	2479		NM_000937	NP_000928	P24928	RPB1_HUMAN		1	ATGCCCGAGAC	0.502	
+	70	10747	nm.1_Missense_	NM_020877	NP_065928	Q9P225	DYH2_HUMAN	5 (By similarity).	13	TGCATACCTCCA	0.607	
-	13	1060	AB3_uc010vul.1_	NM_004732	NP_004723	O43448	KCAB3_HUMAN		1	ACTGCGGAGAC	0.577	
+	18	3369	p.R817Q|CNTRO	NM_053051	NP_444279	Q8N137	CNTRB_HUMAN	centrosome localization.	2	GGCTCGGGGCT	0.582	
-	8	797	_uc002glu.3_5'U	NM_014308	NP_055123	Q8WYR1	PI3R5_HUMAN		5	ATCCCCGATGC	0.617	
-	23	3018	uc002gml.1_Intro	NM_002472	NP_002463	P13535	MYH8_HUMAN	Potential.	11	GTTCTCCGTGG	0.393	
-	30	4267	uc002gml.1_Intro	NM_017533	NP_060003	Q9Y623	MYH4_HUMAN	Potential.	13	TGTGCGCTGGA	0.527	
-	16	1892	uc002gml.1_Intro	NM_017533	NP_060003	Q9Y623	MYH4_HUMAN	osin head-like.	13	AGCCGGCGATG	0.552	
-	12	1124	uc002gml.1_Intro	NM_017533	NP_060003	Q9Y623	MYH4_HUMAN	osin head-like.	13	CCACAGCACTC	0.468	
-	15	1649	uc002gml.1_Intro	NM_005963	NP_005954	P12882	MYH1_HUMAN	osin head-like.	21	CAGGTCCATCC	0.448	

-	24	3189	_Missense_Mutati	NM_001100112	NP_001093582	Q9UKX2	MYH2_HUMAN	Potential.	14	CTTTGTCCTCCTC	0.478	
-	26	3670		NM_002470	NP_002461	P11055	MYH3_HUMAN	Potential.	7	CTATCCGCATGC	0.597	
-	13	1426		NM_002470	NP_002461	P11055	MYH3_HUMAN	yosin head-like.	7	AGCTTCGTATCC	0.383	
+	58	11298	2gnf.2_Missense_	NM_001372	NP_001363	Q9NYC9	DYH9_HUMAN		20	CCATCCGCGGG	0.502	
+	7	972	_p.L225I|MYOCD_	NM_153604	NP_705832	Q8IZQ8	MYCD_HUMAN		5	AGGGGCTTGGC	0.582	
-	27	3803	S1095L|NCOR1_	NM_006311	NP_006302	O75376	NCOR1_HUMAN	action with ETO.	5	ATTCTCGAAATG	0.498	
+	11	1965	oz.2_Missense_Mu	NM_016113	NP_057197	Q9Y5S1	TRPV2_HUMAN	lasmic (Potential).	1	CCTGCGGGACC	0.622	
+	3	1256	n.1_Missense_Mu	NM_030665	NP_109590	Q7Z5J4	RAI1_HUMAN	Gln-rich.	2	CAGCGGGTCCAG	0.527	
-	3	423	MT1_uc010vxt.1_5'	NM_004169	NP_004160	P34896	GLYC_HUMAN		1	GGCCCGGGTAC	0.478	
-	5	539	AP4_uc002gvs.2_	NM_002404	NP_002395	P55083	MFAP4_HUMAN	nogen C-terminal.	0	TGCCCCGCCAT	0.627	
+	6	974	p.E259K|RNF112_	NM_007148	NP_009079	Q7Z5V9	Q7Z5V9_HUMAN		2	GCAGGGAAACA	0.612	
-	3	444	90L|SLC47A2_uc0	NM_152908	NP_690872	Q86VL8	S47A2_HUMAN	lasmic (Potential).	0	ATGCCGAAGAC	0.567	
-	1	395	22L|ALDH3A1_uc	NM_001135168	NP_001128640	P30838	AL3A1_HUMAN		2	GCAGCGGACGG	0.697	
+	12	3085	99_splice|CYTSB_	NM_001033553	NP_001028725	Q5M775	CYTSB_HUMAN		0	ATGCGGTAAGG	0.527	
-	2	756	EZ6_uc002hdq.1_	NM_178860	NP_849191	Q53EL9	SEZ6_HUMAN	xtracellular (Potential).	2	TCCAGGACCCT	0.642	
-	2	337	_p.P48L|SEZ6_uc	NM_178860	NP_849191	Q53EL9	SEZ6_HUMAN	cellular (Potential).	2	GCTCAGGTGTG	0.577	
+	19	2589	p.Q651K|TAOK1_	NM_020791	NP_065842	Q7L7X3	TAOK1_HUMAN	Potential.	4	GAGTGCCAGGTT	0.443	
+	3	1123	e_Mutation_p.R12	NM_001304	NP_001295	O75976	CBPD_HUMAN	ntial).|Carboxypeptidase-lik	2	AACAATCGTGAG	0.398	
+	5	953	2hgo.2_Missense_	NM_032932	NP_116321	Q86YS3	RFIP4_HUMAN	subcellular location, homo-	1	CCAACGTCTAC	0.552	
-	22	2933		NM_015194	NP_056009	O94832	MYO1D_HUMAN		3	TCTTCCCGTGC	0.597	
+	2	224		NM_002988	NP_002979	P55774	CCL18_HUMAN		0	GTGCCCCAAGC	0.552	
+	9	1274	_p.T342I|GGNBP2	NM_024835	NP_079111	Q9H3C7	GGNB2_HUMAN		2	GATGACCGTGG	0.274	
-	27	3478	n.2_Missense_Mu	NM_198836	NP_942133	Q13085	ACACA_HUMAN		2	TTATGGCGAAGC	0.368	
-	10	1141	n.2_Missense_Mu	NM_198836	NP_942133	Q13085	ACACA_HUMAN	n.|ATP (Potential).|ATP-gra	2	TTCCCTCCTCCT	0.378	
+	10	1122	2_Intron|MLLT6_u	NM_005937	NP_005928	P55198	AF17_HUMAN		6	GTACTCCAAGC	0.602	
-	2	294		NM_001008777	NP_001008777	Q5MNV8	FBX47_HUMAN		0	TGAGCCAAGGG	0.358	
+	13	1530	B7_uc010cwc.2_M	NM_005310	NP_005301	Q14451	GRB7_HUMAN		5	CCACCGCACCC	0.607	
-	3	341		NM_001838	NP_001829	P32248	CCR7_HUMAN	lasmic (Potential).	1	GTATCGGTCATG	0.547	
-	5	959		NM_181539	NP_853517	Q7Z3Y9	K1C26_HUMAN	Rod.|Coil 2.	0	TTAATTCGGTCA	0.448	
-	6	1316		NM_000223	NP_000214	Q99456	K1C12_HUMAN	Rod.|Coil 2.	1	GCAGGCGGCGG	0.632	
-	1	244		NM_000223	NP_000214	Q99456	K1C12_HUMAN	lead.|Gly-rich.	1	ACTTCCGGAGC	0.602	rs138169839
-	1	61		NM_000223	NP_000214	Q99456	K1C12_HUMAN	Head.	1	GGTGCGCACTG	0.577	
-	1	514	uc002hwo.1_RNA	NM_003770	NP_003761	O76014	KRT37_HUMAN	Rod.|Coil 1B.	1	ATTGTACGGAAG	0.597	
-	7	1377		NM_002278	NP_002269	Q14532	K1H2_HUMAN	Tail.	0	GAGCAAGGCATG	0.647	
+	2	593	10_uc002hxw.1_5	NM_021939	NP_068758	Q96AY3	FKB10_HUMAN	se FKBP-type 1.	1	TGGTGGCCATC	0.617	
-	4	1316	HDC_uc002hze.3_	NM_032484	NP_115873	Q8N2G8	GHDC_HUMAN		0	GGCCCCGAGGG	0.652	
+	11	1482	JBG2_uc002ias.2_	NM_016437	NP_057521	Q9NRH3	TBG2_HUMAN		1	GTTCCGTAAGG	0.512	
-	19	5483	A1_uc002icu.2_N	NM_007294	NP_009225	P38398	BRCA1_HUMAN	p.R1751*(1)	52	TGCTCGCTTTG	0.463	rs80357123
-	5	388	plice_Site_p.D74_	NM_001932	NP_001923	Q13368	MPP3_HUMAN		2	GGCTTACGTCCT	0.542	
+	14	1650	f.1_Nonsense_Mu	NM_006178	NP_006169	P46459	NSF_HUMAN		1	GTTACTCGAGTT	0.458	
+	6	855	BP1_uc010dbj.2_	NM_006546	NP_006537	Q9NZI8	IF2B1_HUMAN		1	CTCTCGGGGTC	0.657	
-	2	234	orf67_uc002iuq.2_	NM_001085430	NP_001078899	Q0P5P2	CQ067_HUMAN		0	CTCACCCGCATT	0.498	
-	2	212	orf67_uc002iuq.2_	NM_001085430	NP_001078899	Q0P5P2	CQ067_HUMAN		0	GGAATCCGGGTT	0.493	
+	1	602		NM_001004707	NP_001004707	P58180	OR4D2_HUMAN	Name=5; (Potential).	2	GATCTCCAACA	0.512	
-	17	3582	_p.P844L|BZRAP1	NM_004758	NP_004749	O95153	RIMB1_HUMAN	onectin type-III 2.	3	TGCCGGGCACC	0.642	
-	7	970	xa.3_Missense_M	NM_001005207	NP_001005207	O94972	TRI37_HUMAN	Potential.	7	GCTCATCTTTTG	0.353	
+	13	1128	iyw.3_Missense_M	NM_001099432	NP_001092902	Q9H6U6	BCAS3_HUMAN		5	CTGACAGTGATG	0.418	

-	9	1653	zp.2_Missense_Mu	NM_005121	NP_005112	Q9UHV7	MED13_HUMAN		2	CATTTCGGTGC	0.458	
-	8	1284	izp.2_Missense_M	NM_005121	NP_005112	Q9UHV7	MED13_HUMAN		2	CTTCTTCGCATA	0.363	
-	6	464	10woz.1_RNA|uc010wpa.1_5'Flank						0	TTCCTCAATGTT	0.552	
+	2	303	E_uc010wpi.1_Mi	NM_000789	NP_000780	P12821	ACE_HUMAN	Potential).|Peptidase M2 1.	4	GTTTGCGGAGG	0.617	
-	2	186	se_Mutation_p.R4	NM_002059	NP_002050	P01242	SOM2_HUMAN		3	GGCGCGGAGC	0.562	
+	4	821	vqx.1_Missense_M	NM_181790	NP_861455	Q7Z601	GP142_HUMAN	lasmic (Potential).	4	AGGCCGGACCC	0.662	
+	14	1967		NM_001080419	NP_001073888	Q9C0B0	UNK_HUMAN		0	CCCTCCCGTCA	0.602	
-	7	955	5_uc002jpx.2_5'Fl	NM_032478	NP_115867	Q96DV4	RM38_HUMAN		1	CACCCGGTTAC	0.617	
-	19	2032	sense_Mutation_p.	NM_052916	NP_443148	Q96PX1	RN157_HUMAN		1	GGCGCTGGGCAT	0.597	
-	11	1022	jra.2_Missense_M	NM_052916	NP_443148	Q96PX1	RN157_HUMAN		1	GGAAGGCTGTG	0.512	
-	4	1486	_Mutation_p.R36	NM_032134	NP_115510	Q9H0J4	QRIC2_HUMAN	Gln-rich.	5	ccaggccggaccaaa	0.139	rs143499534
-	4	608		NM_001008528	NP_001008528	P84157	MXRA7_HUMAN		0	CACGTCGCCGT	0.577	
+	4	521	1_uc002jvn.2_5'Fl	NM_024419	NP_077733	Q32NB8	PGPS1_HUMAN		0	GCTCACGAGGTA	0.537	
-	3	381	.2_Intron|LGALS3	NM_005567	NP_005558	Q08380	LG3BP_HUMAN	SRCR.	4	GTTCTCGAAGC	0.657	rs11548453
-	6	1583	j.2_Missense_Mut	NM_001159772	NP_001153244	Q8WVQ1	CANT1_HUMAN	nenal (Potential).	0	GAAGCGCCCGT	0.547	
+	4	2591		NM_020914	NP_065965	Q9HCF4	ALO17_HUMAN		21	ATGACGACAGC	0.502	
-	3	669		NM_178520	NP_848615	Q8N8V8	TM105_HUMAN	ical; (Potential).	1	CAGGCTGTGAAC	0.597	
-	7	1231	_p.R22H|P4HB_uc	NM_000918	NP_000909	P07237	PDIA1_HUMAN		0	GGAAGCGGTGG	0.652	
+	5	645	p.G155E|TBCD_u	NM_005993	NP_005984	Q9BTW9	TBCD_HUMAN		0	TGACGGGAACC	0.468	
-	4	427	F1_uc002kkv.3_M	NM_017512	NP_059982	Q7L5Y1	ENOF1_HUMAN		1	TAGGACGGCCG	0.502	
-	23	3834	lq.2_Missense_Mu	NM_003803	NP_003794	P52179	MYOM1_HUMAN	like C2-type 3.	5	ACTCGGACTTT	0.413	
-	9	822	p.R221H|L3MBTL	NM_173464	NP_775735	Q8NA19	LMBL4_HUMAN	MBT 2.	3	GTAAGCGATCT	0.393	
-	8	1335	p.R233W|MPPE1_	NM_023075	NP_075563	Q53F39	MPPE1_HUMAN		0	ACACCGGCTGG	0.637	
+	3	519	dlb.1_Missense_M	NM_014214	NP_055029	O14732	IMPA2_HUMAN		2	CGACCCCATCG	0.562	
+	11	1402		NM_005925	NP_005916	Q16820	MEP1B_HUMAN	lar (Potential).|MATH.	2	GCCCTCCATTTTA	0.408	
+	14	2116		NM_005925	NP_005916	Q16820	MEP1B_HUMAN	lasmic (Potential).	2	CAAATCGACCAA	0.383	
+	12	5363	q.2_Missense_Mu	NM_030632	NP_085135	Q9C0F0	ASXL3_HUMAN		3	GATTGGGAGCC	0.517	
+	6	911	_p.S197L|SLC14A	NM_007163	NP_009094	Q15849	UT2_HUMAN		4	TGTTCTCGGAGA	0.532	
+	16	2290	lbe.2_Missense_M	NM_007163	NP_009094	Q15849	UT2_HUMAN	ical; (Potential).	4	ATGGCCGTGTTC	0.557	
-	9	1225	la.1_Missense_Mu	NM_004671	NP_004662	O75928	PIAS2_HUMAN	P-RING-type.	4	GGCATGGGATT	0.438	
-	16	2272	ec.1_Missense_Mu	NM_001080467	NP_001073936	Q9ULV0	MYO5B_HUMAN	e.|Actin-binding (Potential)	5	TCTCATCGTTGG	0.577	
+	2	638		NM_015879	NP_056963	O43173	SIA8C_HUMAN	nenal (Potential).	2	TAATCGGACAG	0.368	
-	4	423		NM_133459	NP_597716	Q6UXH8	CCBE1_HUMAN		3	TCATATCGGTATC	0.512	rs115982879
-	4	618	ky.1_Missense_Mu	NM_138966	NP_620416	Q8TDF5	NETO1_HUMAN	xtracellular (Potential).	4	TTATTGGAGAAA	0.373	
+	2	2389	ra.2_Missense_Mu	NM_171999	NP_741996	Q9BXA9	SALL3_HUMAN		4	AGCTACGATGAC	0.662	rs143920432
+	7	1906		NM_001194	NP_001185	Q9UL51	HCN2_HUMAN	ytoplasmic (Potential).	0	CCGCCGCACGG	0.726	
-	5	857	Mutation_p.A225T	NM_005481	NP_005472	Q9Y2X0	MED16_HUMAN	WD 2.	0	CGACGCGCTGC	0.692	
-	3	408	te|REEP6_uc010x	NM_017573	NP_060043	Q6UW60	PCSK4_HUMAN		0	CACCACGACAG	0.682	rs143050585
-	5	566	p.A182T|MBD3_u	NM_003926	NP_003917	O95983	MBD3_HUMAN		3	GCTGGCGATGG	0.667	
-	20	2446	e_Mutation_p.E70	NM_138813	NP_620168	O60423	AT8B3_HUMAN	lasmic (Potential).	0	TGTCCTCGATGG	0.627	
-	4	1044	2lue.2_Missense_	NM_001130111	NP_001123583	Q96GS6	F18A1_HUMAN		0	TGAGCGGCGAG	0.607	
-	18	2280	_p.S595L|AP3D1_	NM_003938	NP_003929	O14617	AP3D1_HUMAN		0	GATGGCGAGCTC	0.652	
-	3	787	xgy.1_Missense_	NM_144564	NP_653165	Q9BRY0	S39A3_HUMAN	ical; (Potential).	0	GGGCCGACAGC	0.721	
+	2	579	xp.2_Missense_Mu	NM_205843	NP_995315	P08651	NFIC_HUMAN	CTF/NF-I.	0	TGGCCGTCAAG	0.687	
-	13	1987	_p.R393C|LONP1_	NM_004793	NP_004784	P36776	LONM_HUMAN		0	CATACGGTCTC	0.662	
-	17	1915	mdz.2_Missense_	NM_007322	NP_015561	Q9H6Z4	RANB3_HUMAN		1	CGGTCGTCTGC	0.706	
-	10	1039		NM_003685	NP_003676	Q92945	FUBP2_HUMAN	Gly-rich.	1	CAAAGCCGCCT	0.637	

-	2	393	5A41_uc010dut.2_	NM_173637	NP_775908	Q8N5S1	S2541_HUMAN	ical; Name=1; (Potential).	0	CGCCCCGGCCA	0.612	
-	4	1345	on_p.S341N|MIR2	NM_006087	NP_006078	P04350	TBB4_HUMAN		2	TGTTGCTCTCGC	0.627	
-	3	418	D3A_uc010xjg.1_I	NM_005490	NP_005481	Q9BRG2	SH23A_HUMAN	SH2.	2	GGGCTGTGGGT	0.647	
+	8	1096	_p.N211S|ZNF557_	NM_001044388	NP_001037853	Q8N988	ZN557_HUMAN	C2H2-type 3.	2	ATGCAATGACTG	0.453	
+	5	982	rf45_uc010xjo.1_5	NM_198534	NP_940936	Q8NA69	CS045_HUMAN		0	GTGACGGCCTC	0.587	
+	1	60	10dvs.2_Translatio	NM_001144910	NP_001138382	Q9H2X3	CLC4M_HUMAN		1	CAGAGGGTGGAA	0.507	
+	3	2470	1_5'Flank|MAP2K7	NM_025061	NP_079337	Q6NSJ5	LRC8E_HUMAN		2	AGTGCGGGACA	0.552	rs145323217
-	22	2791		NM_032447	NP_115823	Q75N90	FBN3_HUMAN	TB 5.	11	ACTCATCCTCAT	0.647	
+	4	517	S4_uc002mji.2_5'	NM_024552	NP_078828	Q9HA82	CERS4_HUMAN		1	GAGCCGGTGGC	0.582	
-	9	1000	kh.2_Nonsense_M	NM_012335	NP_036467	O00160	MYO1F_HUMAN	osin head-like.	3	CCACTCGGGCGT	0.612	
-	5	33544		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).	57	GAATTGGAATAGT	0.507	
-	3	11903		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).	57	TGGAGGAGCTG	0.458	
-	1	1382		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).	57	GTACCTGGACTT	0.522	
-	8	1009	ws.2_Missense_M	NM_024106	NP_077011	Q9BUY5	ZN426_HUMAN		1	GTTTTTCTCCATT	0.388	
-	3	502		NM_133452	NP_597709	Q8IY67	RAVR1_HUMAN	RRM 1.	1	GCACCGACAGT	0.672	
-	19	3023	e.2_Missense_Mu	NM_003331	NP_003322	P29597	TYK2_HUMAN		9	AGTCCGGGTTC	0.572	rs1140385
-	4	715	3_uc002msz.1_Mi	NM_001080411	NP_001073880	Q8N7K0	ZN433_HUMAN	C2H2-type 2.	0	TTGAATGGGAAA	0.388	
-	7	989	lyv.1_Missense_M	NM_000528	NP_000519	O00754	MA2B1_HUMAN		6	ATACCGGCCCT	0.527	
+	2	189	nuw.2_Missense_	NM_004317	NP_004308	O43681	ASNA_HUMAN		2	TGGCAGTCCAG	0.537	
+	8	735	e_Mutation_p.D22	NM_000159	NP_000150	Q92947	GCDH_HUMAN		0	ATGGCCGATCTG	0.622	
+	9	1293	_uc002mvz.1_5'Fl	NM_004343	NP_004334	P27797	CALR_HUMAN	in.|Asp/Glu/Lys-rich.	1	ggaagatgaggagga	0.348	
-	4	619	tation_p.S108L|uc	NM_001008701	NP_001008701	O94910	LPHN1_HUMAN	in.|Extracellular (Potential).	5	CATCCGAGCCG	0.587	
+	35	5703	nfj.1_Missense_Mu	NM_004145	NP_004136	Q13459	MYO9B_HUMAN	Rho-GAP.|Tail.	1	TCTTCGCACCCT	0.647	
+	5	1640	_p.A544V|MAP1S_	NM_018174	NP_060644	Q66K74	MAP1S_HUMAN	tubule-organizing center loc	1	CCGGGCAGCCT	0.662	
+	5	894	hu.2_Missense_M	NM_015683	NP_056498	Q8TBH0	ARRD2_HUMAN		1	GCCCCGGGCAG	0.701	
-	3	1624		NM_001001411	NP_001001411	Q8N7Q3	ZN676_HUMAN	C2H2-type 10.	0	AGTAAGGCTTGA	0.438	
+	4	1512		NM_020855	NP_065906	Q9P255	ZN492_HUMAN	C2H2-type 11.	0	ACAAATGTGAAG	0.373	
+	3	552	xrn.1_Nonsense_M	NM_001136156	NP_001129628	Q8TCN5	ZN507_HUMAN		5	GTAATCCAGTCAC	0.438	
+	4	389	123_uc002ntz.1_5	NM_152266	NP_689479	Q9BTP7	FAP24_HUMAN		0	GTAGTCGTTGAA	0.418	
+	6	2893		NM_014727	NP_055542	Q9UMN6	MLL4_HUMAN	CXXC-type.	11	ATGGCTCGATGT	0.622	
+	12	1646	_p.S503N|APLP1_u	NM_005166	NP_005157	P51693	APLP1_HUMAN	cellular (Potential).	2	GGGCAGCAGCG	0.587	
+	14	1874	dd.2_Nonsense_M	NM_173636	NP_775907	O43379	WDR62_HUMAN	WD 9.	0	GACATCCAGATG	0.627	
+	30	4013	dd.2_Missense_Mu	NM_173636	NP_775907	O43379	WDR62_HUMAN		0	CCCCCCGTGGAT	0.682	rs144440621
+	4	1839	p.G106R|ZNF146_	NM_007145	NP_009076	Q15072	OZF_HUMAN	C2H2-type 4.	0	ATTGCGGGAAA	0.418	rs145747574
-	6	1552	345_uc002oez.2_I	NM_001037232	NP_001032309	Q3KNS6	ZN829_HUMAN	C2H2-type 9.	0	TGATGTCGAGTA	0.403	
+	6	1444	.1_Missense_Mut	NM_181786	NP_861451	P10072	HKR1_HUMAN	C2H2-type 4.	2	TGGGCGTGGCT	0.527	
+	2	140	527_uc010xtq.1_F	NM_032453	NP_115829	Q8NB42	ZN527_HUMAN		2	CCATGTCCCAGG	0.433	
-	6	689	tu.1_Missense_M	NM_004647	NP_004638	Q92782	DPF1_HUMAN		0	ACATACGGCTTG	0.612	
+	5	599	.1_Intron|FAM98C	NM_174905	NP_777565	Q17RN3	FA98C_HUMAN		1	CTCTGCCCCCA	0.587	
+	68	10427	iv.1_Missense_Mu	NM_000540	NP_000531	P21817	RYR1_HUMAN		12	CGGAGGAGCTG	0.682	
-	13	1044	ense_Mutation_p.F	NM_012237	NP_036369	Q8IXJ6	SIRT2_HUMAN	tylase sirtuin-type.	0	CAGGCGAGGGG	0.657	
-	3	588	BXO17_uc002okf.1	NM_024907	NP_079183	Q96EF6	FBX17_HUMAN	FBA.	0	GCACCGGTGTT	0.582	
+	4	602	gl.2_Missense_Mu	NM_001004318	NP_001004318	Q6ZNF0	PAPL_HUMAN		0	GTTTATCGCTGTG	0.652	
+	2	570	M50_uc002olt.1_F	NM_001001563	NP_001001563	Q3ZCQ8	TIM50_HUMAN		1	GAGCCGCGGGA	0.612	
+	7	723	mt.2_Missense_M	NM_178544	NP_848639	Q86UE3	ZN546_HUMAN		3	TCAATTGCAGAC	0.313	
-	7	4462	_Mutation_p.A125	NM_181882	NP_870998	Q9BXM0	PRAX_HUMAN		2	TGGGGGCTGCA	0.697	
+	29	3760	_p.V127M|LTBP4_	NM_001042544	NP_001036009	Q8N2S1	LTBP4_HUMAN	alcium-binding (Potential).	1	CAGACGTGGAC	0.502	

+	2	295	)ehh.1_Missense_Mutation_p.S96F|CYP2B7P1_uc002opq.2_RNA						2	CCTTCTCTGGCC	0.627	
+	8	1086	2F1_uc010xvv.1_	NM_000774	NP_000765	P24903	CP2F1_HUMAN		0	ACCGCGCGGCC	0.667	
+	4	505	ense_Mutation_p.	NM_000709	NP_000700	P12694	ODBA_HUMAN	yrophosphate binding.	0	GTACCGGGAGG	0.582	
-	9	1237	se_Mutation_p.P2	NM_019884	NP_063937	P49840	GSK3A_HUMAN	rotein kinase.	4	CTGGCGGCGTT	0.582	
-	3	612	xwj.1_Missense_M	NM_002573	NP_002564	Q15102	PA1B3_HUMAN		0	GGGCCGGATGT	0.562	
+	14	1334	F8_uc002otl.3_5'F	NM_173633	NP_775904	Q8NBT3	TM145_HUMAN		0	GACCCGGAGGG	0.617	
+	9	2203	tm.3_Missense_M	NM_001410	NP_001401	Q7Z7M0	MEGF8_HUMAN	ellular (Potential).	1	TGGTGGCAGCG	0.637	
-	4	829	11_uc002oty.2_Mis	NM_001712	NP_001703	P13688	CEAM1_HUMAN	2.|Extracellular (Potential).	2	TGGGGGTGTCC	0.562	
-	4	1015	uj.3_Missense_M	NM_182707	NP_874366	Q9UQ74	PSG8_HUMAN	like C2-type 2.	0	TAGGGTCCTGTT	0.498	
+	8	814	R_uc010xxp.1_M	NM_000164	NP_000155	P48546	GIPR_HUMAN	Name=3; (Potential).	1	AGGGCGTCTAC	0.687	
-	14	2106	_p.A621T|SYMPK_	NM_004819	NP_004810	Q92797	SYMPK_HUMAN		1	CCAGGCGAAGG	0.642	
-	2	445	per.3_Missense_	NM_018215	NP_060685	Q86V59	PNML1_HUMAN		0	tggggagaggacccc	0	
-	6	1810	pfq.2_Missense_M	NM_005628	NP_005619	Q15758	AAAT_HUMAN	ical; (Potential).	0	CTGCGGCCACG	0.607	
+	1	2288		NM_004491	NP_004482	Q9NRY4	RHG35_HUMAN		1	TAAGCGTAACT	0.433	
+	2	3763		NM_004491	NP_004482	Q9NRY4	RHG35_HUMAN	Rho-GAP.	1	CTGTCGTGACT	0.443	
+	14	3049	yo.1_Missense_M	NM_014681	NP_055496	Q14147	DHX34_HUMAN		5	TCAGTCCCTCC	0.642	
-	1	150		NM_003167	NP_003158	Q06520	ST2A1_HUMAN		2	GAAATCGTCCG	0.468	
+	4	1069	n.1_5'Flank|FGF2	NM_019113	NP_061986	Q9NSA1	FGF21_HUMAN		1	CCTGCCACTAC	0.692	
-	9	1083	p.R309Q|BCAT2_	NM_001190	NP_001181	O15382	BCAT2_HUMAN		1	GGATTCGGTGC	0.652	
+	5	521	X_uc010xzx.1_R	NM_138761	NP_620116	Q07812	BAX_HUMAN	BH2.	3	GGGCTGGATCC	0.448	
-	3	828	c.2_Intron|CGB7_	NM_033142	NP_149133	P01233	CGHB_HUMAN		0	CCCCGGGAGTC	0.627	rs142903731
+	13	1700	g.2_Missense_M	NM_152359	NP_689572	Q8TCG5	CPT1C_HUMAN	lasmic (Potential).	3	CAGACGGCCAC	0.612	
-	23	6275	sw.1_Missense_M	NM_016148	NP_057232	Q9Y566	SHAN1_HUMAN		2	GTCCGGGGGCA	0.667	
-	3	479	e_Mutation_p.E14	NM_017509	NP_059979	Q9H2R5	KLK15_HUMAN	eptidase S1.	2	AGGCTCGTTGT	0.687	
-	7	946	.G243D|KLK5_uc	NM_001077491	NP_001070959	Q9Y337	KLK5_HUMAN	eptidase S1.	0	AATCACCCTGC	0.343	
-	3	248	l.2_Missense_Mu	NM_001161748	NP_001155220	P55344	LMIP_HUMAN	ical; (Potential).	0	AGGATCATGAA	0.587	
+	6	1161		NM_001099694	NP_001093164	Q96N58	ZN578_HUMAN	2H2-type 3.	0	CCATCGTAGAT	0.433	
-	5	659	k.1_Intron|ZNF81	NM_001031665	NP_001026835	Q0VGE8	ZN816_HUMAN		0	TTCAACTTCTTG	0.398	
+	1	788		NM_173856	NP_776255	Q8NFZ6	VN1R2_HUMAN	ellular (Potential).	0	CAAATGGAGCA	0.418	
+	7	1715	eqr.1_Missense_M	NM_018555	NP_061025	Q9NQX6	ZN331_HUMAN		6	ACAGCGCTCCA	0.428	
-	10	1139	n.1_Missense_Mu	NM_002287	NP_002278	Q6GTX8	LAIR1_HUMAN	lasmic (Potential).	4	GGACTCGGCCA	0.602	
+	6	747	plice_Site_p.G21	NM_002255	NP_002246	Q99706	KI2L4_HUMAN		1	CTCCAGGTATC	0.468	
+	6	771	id.2_Missense_Mu	NM_004829	NP_004820	O76036	NCTR1_HUMAN	ellular (Potential).	2	AGAAAGGTAAG	0.498	
-	13	2497	ense_Mutation_p.	NM_002842	NP_002833	Q9HD43	PTPRH_HUMAN	lasmic (Potential).	4	CTGACGTGGTC	0.552	rs143797290
+	6	1337	.R201Q|U2AF2_u	NM_013301	NP_037433	Q9BWC9	CC106_HUMAN		0	GTCGCGGGCCT	0.667	
+	2	557	d.2_Missense_Mu	NM_001130072	NP_001123544	Q9Y6I3	EPN1_HUMAN	ENTH.	0	CTGGCGTCACG	0.592	
+	5	476		NM_020813	NP_065864	Q9BX82	ZN471_HUMAN		2	GCTATGGACTT	0.368	
-	7	4738	E1434Q|PEG3_uc	NM_001146186	NP_001139658	Q9GZU2	PEG3_HUMAN	Glu-rich.	12	TCTTTCTTCTG	0.547	
-	5	1009		NM_052882	NP_443114	Q96PE6	ZIM3_HUMAN	2H2-type 2.	2	GCTTCCACTTC	0.433	
+	4	1230		NM_152677	NP_689890	Q8NAM6	ZSCA4_HUMAN		1	GACTTCCCAAG	0.443	
+	3	803	yhz.1_Missense_	NM_181846	NP_862829	P10073	ZSC22_HUMAN		1	CCAGCGTGGCC	0.517	
-	3	542	DAM17_uc010exb	NM_003183	NP_003174	P78536	ADA17_HUMAN		2	AACCAACCACG	0.438	
+	4	554	se_Mutation_p.Y1	NM_182625	NP_872431	Q17RS7	GEN_HUMAN	I-domain.	8	TCCTTTATGGG	0.408	
-	9	1797	DH14_uc002rcx.3_	NM_033253	NP_150278	Q96P26	5NT1B_HUMAN		3	TTGTCCGTACAA	0.473	
-	5	811	_p.S176L|NT5C1B	NM_001002006	NP_001002006	Q96P26	5NT1B_HUMAN		3	TGCGCGAATAT	0.662	
+	8	988	hv.3_Missense_M	NM_020134	NP_064519	Q9BPU6	DPYL5_HUMAN		2	TGCCACGCTGA	0.522	
-	11	1207	.R365W|IFT172_	NM_015662	NP_056477	Q9UG01	IF172_HUMAN		2	TAAGCCGATTAG	0.493	

+	34	2336	j.1_Missense_Mut	NM_153021	NP_694566	Q6P1J6	PLB1_HUMAN	ate repeats.|Extracellular (	9	GGACGGCTCCC	0.522	
+	1	269		NM_016441	NP_057525	Q9NZV1	CRIM1_HUMAN	nal.|Extracellular (Potential)	3	CGGCACCTTCG	0.667	
+	3	597	MIN6_uc002rrb.2_	NM_024775	NP_079051	Q8WXD5	GEMI6_HUMAN		0	TTGAAGGACAT	0.398	
+	15	1857	q.2_Missense_Mu	NM_020744	NP_065795	Q9BTC8	MTA3_HUMAN		2	AGTCCGAAACA	0.478	
+	8	1621	_p.S513F|PLEKHH	NM_172069	NP_742066	Q8IVE3	PKHH2_HUMAN		3	TATTTTCCTATGA	0.458	
+	4	545	oa.1_Missense_Mu	NM_022437	NP_071882	Q9H221	ABCG8_HUMAN	er.|Cytoplasmic (Potential).	4	CGTGCGCCAGC	0.627	
+	9	1459	C7A_uc010fbc.2_	NM_020458	NP_065191	Q9ULT0	TTC7A_HUMAN		2	GAGCCGGGTGC	0.592	
+	5	595	pt.1_Missense_Mu	NM_014562	NP_055377	P32242	OTX1_HUMAN		2	AGTGCGGGAGA	0.647	
+	5	1332	LC1A4_uc010fcv.2	NM_003038	NP_003029	P43007	SATT_HUMAN	ical; (Potential).	1	CATTTGCGACAG	0.488	
+	6	867	f.2_Missense_Mut	NM_173545	NP_775816	Q8IW19	APLF_HUMAN		2	AGCAAGGAAGA	0.363	
+	11	2213	sew.2_Missense_	NM_001007231	NP_001007232	P42331	RHG25_HUMAN	Potential.	4	GCTCCCGGGAG	0.507	
-	3	584	p.R178Q|CYP26B	NM_019885	NP_063938	Q9NR63	CP26B_HUMAN		2	GCACCCGGATG	0.617	
+	20	11897	.W3885*|ALMS1_	NM_015120	NP_055935	Q8TCU4	ALMS1_HUMAN		9	TTCTTGGTCAG	0.418	
-	4	895	1_uc002smc.2_5'	NM_133637	NP_598376	Q8TE96	DQX1_HUMAN		2	CACCCGATCAG	0.522	
+	18	2739	ysg.1_Missense_M	NM_004389	NP_004380	P26232	CTNA2_HUMAN		9	CTCCAGAGAAG	0.483	
+	7	914	gk.2_Missense_Mu	NM_005911	NP_005902	P31153	METK2_HUMAN		0	TGGACGCAAAA	0.453	
-	31	5043	ytb.1_Missense_M	NM_015425	NP_056240	O95602	RPA1_HUMAN		3	TGGTCGCATAG	0.493	
-	5	759	RPS5_uc010yud.1_	NM_031902	NP_114108	P82675	RT05_HUMAN		3	CTTTCGGTCCC	0.532	
-	3	345	ense_Mutation_p.	NM_207328	NP_997211	Q6NUI2	GPAT2_HUMAN		0	ACTTCCCCAGG	0.587	
-	6	1221	svl.2_Missense_M	NM_020151	NP_064536	Q9NQZ5	STAR7_HUMAN	START.	0	GGGACGGATAA	0.468	
-	34	4971	NP200_uc010yuj.1_	NM_014014	NP_054733	O75643	U520_HUMAN	ase C-terminal 2.	10	GCGTCGCTCCA	0.572	
-	11	1314		NM_005735	NP_005726	P42025	ACTY_HUMAN		1	TAGCACGGGAG	0.542	
-	5	404	LYG1_uc010yvo.1_	NM_174898	NP_777558	Q8N1E2	LYG1_HUMAN		0	AGCACGAACTC	0.463	
+	11	1310	vt.1_Missense_Mu	NM_002518	NP_002509	Q99743	NPAS2_HUMAN	PAC.	4	AGCCCGAGTTC	0.607	
-	5	909	L2_uc002tcx.2_Mis	NM_201557	NP_963851	Q14192	FHL2_HUMAN	zinc-binding 3.	1	TCCTGCAGGCG	0.607	
+	8	2147	e.2_Missense_Mut	NM_012455	NP_036587	Q8NDX1	PSD4_HUMAN	SEC7.	2	GGAACGGGAGC	0.602	rs149806578
+	19	2130	p.R554Q|DPP10_	NM_020868	NP_065919	Q8N608	DPP10_HUMAN	cellular (Potential).	10	GGACCGAAACC	0.284	
+	16	2879	0flu.2_Nonsense_	NM_130773	NP_570129	Q8WYK1	CNTP5_HUMAN	3.|Extracellular (Potential).	10	TTCATTCGACTC	0.289	
-	9	2194	VS1_uc010yzl.1_R	NM_017969	NP_060439	Q96ST2	IWS1_HUMAN	IIS N-terminal.	1	CTTGAGTGCAG	0.438	
+	1	207	e.1_Intron|UGGT1_	NM_020120	NP_064505	Q9NYU2	UGGG1_HUMAN		1	CGGTGCGTGTG	0.721	
+	2	438	_p.G83E|FAM123	NM_152698	NP_689911	Q8N944	F123C_HUMAN		3	CTGTGGAGCCA	0.652	
+	8	1144	nse_Mutation_p.R	NM_001100623	NP_001094093	Q96CS7	PKHB2_HUMAN		2	CTATCGAGACA	0.517	
-	14	4185	AP5_uc002ttq.2_I	NM_207363	NP_997246	O14513	NCKP5_HUMAN		0	CTTTGGCGCCAT	0.532	
-	14	2784	AP5_uc002ttq.2_I	NM_207363	NP_997246	O14513	NCKP5_HUMAN		0	TGGGAGGTATTT	0.463	
+	13	1859		NM_002410	NP_002401	Q09328	MGT5A_HUMAN	enal (Potential).	3	TCATCGGGCGG	0.438	
-	4	478	M163_uc002tty.2_	NM_030923	NP_112185	Q8TC26	TM163_HUMAN		0	GTAACGCCACA	0.512	
-	57	10031		NM_018557	NP_061027	Q9NZR2	LRP1B_HUMAN	cellular (Potential).	50	TGATCAGCAAGA	0.333	
-	53	9391		NM_018557	NP_061027	Q9NZR2	LRP1B_HUMAN	ntial).|LDL-receptor class A	50	CATTTTCATCAC	0.388	
-	7	1889	P1B_uc010fnl.1_In	NM_018557	NP_061027	Q9NZR2	LRP1B_HUMAN	ntial).|LDL-receptor class	50	AGATCCGGTCA	0.413	
-	5	1024	of.2_Missense_Mu	NM_145259	NP_660302	Q8NER5	ACV1C_HUMAN	e.|Cytoplasmic (Potential).	7	AAGTTCCATTAT	0.313	
+	23	3980	om.1_Missense_M	NM_033394	NP_203752	Q9C0D5	TANC1_HUMAN	ANK 10.	3	GAGCCGTGATC	0.607	
-	7	994	e_Mutation_p.R28	NM_152528	NP_689741	Q8N9V3	WSDU1_HUMAN	WD 7.	0	CAGACCTGGTG	0.294	
-	26	5005	se_Mutation_p.Q1	NM_006922	NP_008853	Q9NY46	SCN3A_HUMAN		10	TTTCTGAGGTT	0.388	
+	9	1417	_p.S376F|SCN2A_	NM_001040142	NP_001035232	Q99250	SCN2A_HUMAN	I.	8	TTTTGTCCTTATT	0.403	
+	7	1458	udg.2_Missense_M	NM_024969	NP_079245	Q8WYN3	CSRN3_HUMAN	Glu-rich.	5	TAGCACGCAAA	0.418	
-	2	355	3_5'Flank|SCN1A_	NM_006920	NP_008851	P35498	SCN1A_HUMAN	I.	13	GAAGGGAGTTA	0.353	
-	70	13081		NM_004525	NP_004516	P98164	LRP2_HUMAN	cellular (Potential).	29	CCTTTTCCTTAG	0.398	

-	56	11128		NM_004525	NP_004516	P98164	LRP2_HUMAN	A 29.|Extracellular (Potent	29	AAACTGGCCCG	0.542	
-	54	10709		NM_004525	NP_004516	P98164	LRP2_HUMAN	(Potential).|EGF-like 13.	29	GAAGGGTGCGG	0.537	
-	23	3691	f.1_Nonsense_Mut	NM_004525	NP_004516	P98164	LRP2_HUMAN	A 11.|Extracellular (Potent	29	TACATCGATGATT	0.398	
+	15	2188	no.1_Missense_Mu	NM_001079818	NP_001073286	P23229	ITA6_HUMAN	cellular (Potential).	2	GTGTACCAGAAC	0.378	
-	307	98674	010zfi.1_Missense	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	GATACCTTCTCAT	0.373	
-	293	88087	83H|TTN_uc010zf	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	TGACACGTGTCC	0.483	
-	246	50929	97D|TTN_uc010zf	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	CAGAAACCTTTC	0.393	
-	10	1567_1568		NM_173648	NP_775919	Q6ZP82	CC141_HUMAN		10	ATAAGTGCTGAG	0.446	
-	4	337	ense_Mutation_p.	NM_001003683	NP_001003683	P54750	PDE1A_HUMAN		3	CAGTCTGAATGT	0.353	
-	9	1848		NM_182521	NP_872327	Q8NEG5	ZSWM2_HUMAN		3	CATTTTCGTGTA	0.338	
+	20	3701	AR_uc002uqx.1_F	NM_144708	NP_653309	Q7Z5J8	ANKAR_HUMAN		4	TCATTCGTATAA	0.368	
+	7	1424	p.G242S|INPP1_u	NM_001128928	NP_001122400	P49441	INPP_HUMAN		2	GAAACGGCAGT	0.463	rs140787085
+	3	1378		NM_017694	NP_060164	Q6ZSS7	MFSD6_HUMAN	ical; (Potential).	2	CACATCGAAGTG	0.567	
+	20	2405	01B_uc002usr.2_M	NM_001130158	NP_001123630	O43795	MYO1B_HUMAN	IQ 1.	8	TCGGGGGTGGA	0.418	
+	12	3558	PR2_uc010ftr.2_In	NM_001204	NP_001195	Q13873	BMPR2_HUMAN	lasmic (Potential).	9	GTGACAGTCACC	0.448	
+	12	1900	p.E565K|PARD3B	NM_152526	NP_689739	Q8TEW8	PAR3L_HUMAN	PDZ 3.	4	ACCACGAAGCT	0.473	
-	13	1497	zis.1_Missense_M	NM_005006	NP_004997	P28331	NDUS1_HUMAN		1	CTTCCCGAAGCA	0.378	
-	6	674	p.T200M|LANCL1	NM_001136574	NP_001130046	O43813	LANC1_HUMAN		0	TTTGCCGTGAAG	0.403	rs141178650
-	8	1089_1090	_p.P331K|ERBB4_	NM_005235	NP_005226	Q15303	ERBB4_HUMAN	xtracellular (Potential).	33	CTTTTGGGCAAA	0.376	
+	6	588	f62_uc002vhs.2_I	NM_198559	NP_940961	Q7Z7H3	CB062_HUMAN		0	CCTGGCGGCGG	0.582	
-	7	931	vif.2_Nonsense_M	NM_020935	NP_065986	Q86T82	UBP37_HUMAN	D-box 3.	5	CTTTTCGAAATG	0.363	
+	2	672		NM_025216	NP_079492	Q9GZT5	WN10A_HUMAN		2	CCGGCGGCAGA	0.607	
-	11	1528	ense_Mutation_p.F	NM_194302	NP_919278	Q6ZU64	CC108_HUMAN		4	GGAGCGCTCCC	0.577	
+	9	1300	vkh.2_Missense_M	NM_018089	NP_060559	Q9H8Y5	ANKZ1_HUMAN		2	AGAAGCCTACT	0.453	
-	4	702	200H|TUBA4B_uc	NM_006000	NP_005991	P68366	TBA4A_HUMAN		3	GGTTGCGGCGG	0.557	
+	4	771	.1_Intron|KIAA148	NM_020864	NP_065915	Q9P242	K1486_HUMAN		3	GAAATCCGAACA	0.507	
+	11	980	40L_uc010fxo.1_I	NM_138402	NP_612411	Q9H930	LY10L_HUMAN	SAND.	1	ACTGTGGATTTTC	0.423	
+	2	271	P_uc002vsr.2_5'F	NM_001632	NP_001623	P05187	PPB1_HUMAN		1	GGAACCGCGAG	0.632	
+	7	964	P_uc002vsr.2_5'F	NM_001632	NP_001623	P05187	PPB1_HUMAN		1	GGTGCCCGGTAT	0.677	
+	18	2163	3_Missense_Mutat	NM_015575	NP_056390	Q6Y7W6	PERQ2_HUMAN	Gln-rich.	7	GGAACGACTGA	0.428	
+	28	3370	e_Mutation_p.V10	NM_152879	NP_690618	Q16760	DGKD_HUMAN		5	GCCTCGTGACC	0.522	
+	1	177	UGT1A7_uc002vu	NM_007120	NP_009051	P22310	UD14_HUMAN		1	TGCGGGAGCTC	0.597	
+	7	767	M8_uc010fyj.2_5'	NM_024080	NP_076985	Q7Z2W7	TRPM8_HUMAN	lasmic (Potential).	4	CTTATGGATGACT	0.398	
+	12	1527	vyf.2_Missense_M	NM_015650	NP_056465	Q8TDR0	MIPT3_HUMAN	-interaction domain.	1	CTCCCCGGGTC	0.507	
+	2	705	dn.2_Missense_M	NM_021158	NP_066981	Q96RU7	TRIB3_HUMAN		2	CCTCCCGTCTT	0.667	
+	4	1015	p.R219C|SIRPA_u	NM_001040022	NP_001035111	P78324	SHPS1_HUMAN	1.|Extracellular (Potential).	1	TGACCCGCGAG	0.587	
+	9	1712	p.T451M|SIRPA_u	NM_001040022	NP_001035111	P78324	SHPS1_HUMAN	lasmic (Potential).	1	CCACACGGAGT	0.582	
+	9	1280	al.1_Missense_Mu	NM_198994	NP_945345	O95932	TGM3L_HUMAN		4	ACGAGGATGAG	0.597	
+	9	1087	w.1_Nonsense_M	NM_080751	NP_542789	Q8TDI7	TMC2_HUMAN	lasmic (Potential).	3	GTCATTCGATCGT	0.552	rs143970919
-	10	937	_p.P310S|IDH3B_u	NM_006899	NP_008830	O43837	IDH3B_HUMAN		0	AAATGGGTGCC	0.597	
-	11	1602	M1_uc010gas.2_I	NM_019609	NP_062555	Q96SM3	CPXM1_HUMAN		4	ACGGGGTGCGA	0.597	
+	4	392	se_Mutation_p.P6	NM_033453	NP_258412	Q9BY32	ITPA_HUMAN		1	GGCTCCCCGGC	0.567	
+	6	1286	Mutation_p.Q58*|C	NM_021873	NP_068659	P30305	MPIP2_HUMAN		5	ACTCCCAGGCG	0.667	
-	3	524	u.2_Missense_Mu	NM_017545	NP_060015	Q9UJM8	HAOX1_HUMAN	xy acid dehydrogenase.	3	CCAGACGGTTG	0.448	rs143166500
+	27	2643	p.S848L|PLCB4_u	NM_182797	NP_877949	Q15147	PLCB4_HUMAN		15	CTTTATCAGATCC	0.348	
+	4	1819	0zrf.1_Missense_M	NM_014962	NP_055777	Q9Y2F9	BTBD3_HUMAN		3	GCATGACAGAAG	0.493	
+	17	1698	p.R459C|XRN2_u	NM_012255	NP_036387	Q9H0D6	XRN2_HUMAN		1	AAATTCCGTCGG	0.408	rs34008581

+	6	1870	_p.R90C|GZF1_u	NM_022482	NP_071927	Q9H116	GZF1_HUMAN	2H2-type 9.	1	GCCACCGCCGC	0.632	rs139522387
-	2	522		NM_001008693	NP_001008693	Q5W186	CST9_HUMAN		1	TGCAGCATCCA	0.537	
-	6	1950	.2_Intron|ACSS1_	NM_032501	NP_115890	Q9NUB1	ACS2L_HUMAN		2	AAGGACGCTGG	0.567	
+	3	487		NM_033118	NP_149109	Q9H1R3	MYLK2_HUMAN		6	GGGTGGGCAAG	0.632	
+	17	2167	_Mutation_p.V554	NM_006892	NP_008823	Q9UBC3	DNM3B_HUMAN		5	GAACCGTGAAG	0.502	
+	2	162	1_uc010geq.2_Spl	NM_032819	NP_116208	Q9BYN7	ZN341_HUMAN		2	ATTGGGTGAGT	0.577	
+	31	6322	ve.1_Missense_M	NM_007186	NP_009117	Q9BV73	CP250_HUMAN	lu-rich.|Potential.	5	CCAGGCCCTGG	0.607	
+	12	1549	xew.2_Missense_	NM_012156	NP_036288	Q9H4G0	E41L1_HUMAN		3	ATGGCGAGTCT	0.592	
-	16	1049	vq.1_Missense_M	NM_032013	NP_114402	Q9UGV2	NDRG3_HUMAN		1	GAGCCGAGTCA	0.532	
+	1	21		NM_080628	NP_542195	A0PJX2	CT118_HUMAN		0	GCCTCCGCTGG	0.622	
-	4	512		NM_015474	NP_056289	Q9Y3Z3	SAMH1_HUMAN		0	GTGGAGCTCAA	0.398	
+	16	1602	wb.1_Missense_M	NM_021931	NP_068750	Q9H5Z1	DHX35_HUMAN		3	TCTCACGCAGTA	0.473	
+	9	929	270C|PLCG1_uc0	NM_182811	NP_877963	P19174	PLCG1_HUMAN		8	TTGATCGCCTC	0.602	
+	22	2657	ve.1_Missense_M	NM_182811	NP_877963	P19174	PLCG1_HUMAN	SH3.	8	ACTACGTGGAA	0.592	
-	3	3013	e_Mutation_p.V87	NM_015035	NP_055850	Q9H4I2	ZHX3_HUMAN	omeobox 5.	3	CTTGACCTGCT	0.562	
-	17	2708	d.2_Missense_Mu	NM_032221	NP_115597	Q8TD26	CHD6_HUMAN	case C-terminal.	14	GAACCGGTCGA	0.537	
-	7	1055	gj.2_Missense_M	NM_007050	NP_008981	O14522	PTPRT_HUMAN	tential).|Fibronectin type-III	20	AATGGGCGTGG	0.512	
+	1	49		NM_002638	NP_002629	P19957	ELAF_HUMAN		0	TGATCGTGGTG	0.572	
+	15	1949	C12A5_uc002xrb.	NM_001134771	NP_001128243	Q9H2X9	S12A5_HUMAN	lasmic (Potential).	5	TCCTGGGCATG	0.557	
-	3	764	_Missense_Mutati	NM_173179	NP_775271	Q9NQQ7	S35C2_HUMAN		1	CACACGGGCCC	0.632	
+	5	1695		NM_030777	NP_110404	O95528	GTR10_HUMAN	lasmic (Potential).	1	GTACAGCCGCA	0.602	
+	12	1494	o.2_Missense_Mu	NM_005244	NP_005235	O00167	EYA2_HUMAN		1	GCGGCGTGGAC	0.612	
-	15	2623	ND8_uc002xtb.1_	NM_012408	NP_036540	Q9ULU4	PKCB1_HUMAN		5	GGGCCGGGGC	0.677	
+	9	1155	m.2_Missense_M	NM_181659	NP_858045	Q9Y6Q9	NCOA3_HUMAN		5	GAAACGTCACT	0.294	
-	16	6139	s.1_Missense_Mu	NM_033081	NP_149072	Q9BTC0	DIDO1_HUMAN	Pro-rich.	6	CCTGGGACCTG	0.577	
-	15	3625	lt.1_Missense_Mu	NM_033081	NP_149072	Q9BTC0	DIDO1_HUMAN		6	GAAGCGGATCA	0.502	
-	3	769	lv.1_Missense_Mu	NM_033081	NP_149072	Q9BTC0	DIDO1_HUMAN	lization signal (Potential).	6	CCTGCGAAGGC	0.602	
+	6	629	_p.G60S|ARFGAP	NM_018209	NP_060679	Q8N6T3	ARFG1_HUMAN		1	ACCTCGGCTCC	0.602	rs148044740
-	5	921	p.P274S|EEF1A2_	NM_001958	NP_001949	Q05639	EF1A2_HUMAN		0	GCCCGGCCGCA	0.672	
+	15	2128	F6_uc002yhp.2_I	NM_012469	NP_036601	O94906	PRP6_HUMAN	HAT 6.	2	AGTCCGAGAAT	0.662	
+	9	1139	25_uc002yjz.1_M	NM_013396	NP_037528	Q9UHP3	UBP25_HUMAN		5	TGGGAGTACTT	0.333	
+	6	871	_p.P66S|NCAM2_	NM_004540	NP_004531	O15394	NCAM2_HUMAN	3.|Extracellular (Potential).	4	CAGTGCCGCCA	0.423	
+	10	1497	f.2_Missense_Mu	NM_005239	NP_005230	P15036	ETS2_HUMAN	ETS.	4	GACGTCGGGGA	0.582	
-	12	1283	.1_5'UTR|BRWD1_	NM_018963	NP_061836	Q9NSI6	BRWD1_HUMAN	WD 5.	4	TTACCGATCAC	0.328	
+	8	1647	R345Q|BACE2_uc	NM_012105	NP_036237	Q9Y5Z0	BACE2_HUMAN	ellular (Potential).	2	TTACCGATTCG	0.517	
-	8	1936		NM_020639	NP_065690	P57078	RIPK4_HUMAN		7	GTTGACGTCGG	0.687	
-	3	1536	aa.3_Missense_M	NM_001098402	NP_001091872	Q9ULJ3	ZN295_HUMAN		3	TGTCCGAGGGG	0.562	
+	19	3464	DL1_uc002zag.1_	NM_001004416	NP_001004416	Q5DID0	UROL1_HUMAN	llular (Potential).|ZP.	3	CCTGACGGAGT	0.572	
+	3	256	02zdx.2_Missens	NM_020132	NP_064517	Q9NRZ7	PLCC_HUMAN	lasmic (Potential).	0	AGTTCGTGCTG	0.642	
-	4	535	ol.3_Missense_M	NM_016335	NP_057419	O43272	PROD_HUMAN		1	TTATTCGTGCCT	0.622	
-	14	2624	qy.2_Missense_M	NM_001670	NP_001661	O00192	ARVC_HUMAN	ARM 10.	1	GATTTCGTGGA	0.682	rs144187900
+	7	1153	nse_Mutation_p.R	NM_003073	NP_003064	Q12824	SNF5_HUMAN	.|2.|2 X ap)|p.L266_*386	407	GCATCCGGGGA	0.542	
-	3	333	.2_RNA|GSTT1_u	NM_000853	NP_000844	P30711	GSTT1_HUMAN	ST C-terminal.	1	CACACGGGCAC	0.622	
+	13	2896	L_uc011akd.1_Mi	NM_021115	NP_066938	Q9BYH1	SE6L1_HUMAN	xtracellular (Potential).	6	CCATCCGCTGC	0.557	
-	4	547	p.G33S|TBC1D10	NM_031937	NP_114143	Q9BXI6	TB10A_HUMAN	ab-GAP TBC.	1	TCACCCGTGGC	0.612	
-	10	1597		NM_005877	NP_005868	Q15459	SF3A1_HUMAN		5	CTCACCGATCT	0.512	
-	2	889	gwa.1_RNA|DUSP	NM_152511	NP_689724	Q8NEJ0	DUS18_HUMAN	protein phosphatase.	0	GTGGGCGTCCA	0.592	

+	2	1140	R283H|RFPL3S_u	NM_001098535	NP_001092005	O75679	RFPL3_HUMAN		1	AGTCCGTCCTG	0.458	
-	9	1224		NM_014306	NP_055121	Q9Y3I0	RTCB_HUMAN		0	CTTTCCGTCCA	0.498	
-	8	1045	h.1_Missense_Mu	NM_002473	NP_002464	P35579	MYH9_HUMAN	osin head-like.	11	AGGTCCGTTCTT	0.537	
-	13	1384	p.T423M|EIF3D_u	NM_003753	NP_003744	O15371	EIF3D_HUMAN		1	GCTCCGTGGCA	0.562	
-	3	673		NM_006078	NP_006069	Q9Y698	CCG2_HUMAN		0	GTGTCGAGTTTT	0.562	
+	7	1827	atq.1_Missense_M	NM_001039141	NP_001034230	Q9H2D6	TARA_HUMAN		1	TCCCAATAGAG	0.587	
+	7	2067	atq.1_Missense_M	NM_001039141	NP_001034230	Q9H2D6	TARA_HUMAN		1	ACCCCACAACAT	0.582	
+	2	155	2_5'UTR|POLR2F	NM_021974	NP_068809	P61218	RPAB2_HUMAN		1	GCGACGACTTT	0.408	
-	2	1340	vt.1_Missense_Mu	NM_004981	NP_004972	P48050	IRK4_HUMAN	smic (By similarity).	0	CATCCGGATGA	0.682	
+	30	5452		NM_001429	NP_001420	Q09472	EP300_HUMAN	or E1A adenovirus.|ZZ-typ	64	TGTCTGTGAGG	0.572	
+	3	421	gyr.2_Missense_	NM_145733	NP_663786	Q9UH03	SEPT3_HUMAN		0	GGAACCGGGAG	0.572	
-	10	1323	p.V396M|NAGA_u	NM_000262	NP_000253	P17050	NAGAB_HUMAN		1	CATCACTACCC	0.552	
+	3	376	e.2_Missense_Mu	NM_014346	NP_055161	Q8WUA7	TB22A_HUMAN		1	ATGAGCTCCTG	0.647	
-	11	1339		NM_001080447	NP_001073916				2	GCTGCGGCCC	0.662	
+	2	998	p.R199H|PANX2_	NM_052839	NP_443071	Q96RD6	PANX2_HUMAN	lasmic (Potential).	1	GACGCGCCGGC	0.562	
+	8	1808	jy.2_Missense_Mu	NM_031454	NP_113642	Q9BVL4	SELO_HUMAN		0	AGCACGTGCGC	0.652	
-	9	888	bkl.1_Missense_	NM_002969	NP_002960	P53778	MK12_HUMAN	rotein kinase.	0	CAGCCGGAGGC	0.667	rs141322209
+	7	643	utation_p.G177R|	NM_017584	NP_060054	Q9UGB7	MIOX_HUMAN		0	AGCTCGGGATG	0.582	
+	16	1431	.R436H|MTMR14_	NM_001077525	NP_001070993	Q8NCE2	MTMRE_HUMAN		1	GGACCGTGGCA	0.562	
-	7	1428	sy.2_Missense_Mu	NM_006354	NP_006345	O75528	TADA3_HUMAN		0	TGCCCCGTCAG	0.507	
-	5	628	ion_p.A173V|CIDE	NM_022094	NP_071377	Q96AQ7	CIDEC_HUMAN		1	AAGTCGCCTTC	0.502	
+	9	1376	xj.2_Missense_Mu	NM_001162499	NP_001155971	O75155	CAND2_HUMAN	HEAT 10.	4	TGCAGCGGCA	0.647	
-	13	1765	RIP2_uc011avh.1	NM_001080423	NP_001073892	Q9C0E4	GRIP2_HUMAN	PDZ 4.	1	AGGCTCGATGA	0.567	
+	8	822	rf19_uc010hej.2_I	NM_016474	NP_057558	Q6PII3	CC019_HUMAN		0	GGCCCGGCAAC	0.423	
+	6	3156	p.A1016T|FGD5_	NM_152536	NP_689749	Q6ZNL6	FGD5_HUMAN	DH.	5	TGGCAGCTGCT	0.582	
-	7	995	ation_p.R112Q|S	NM_004844	NP_004835	O60239	3BP5_HUMAN		0	ATCCCCGAGGC	0.597	
+	2	497	M8_uc010hfu.2_I	NM_178868	NP_849199	Q8IZV2	CKLF8_HUMAN	MARVEL.	0	GGTCCCCGCAT	0.502	
-	12	1716	cfr.3_Missense_M	NM_014517	NP_055332	Q9NZI7	UBIP1_HUMAN		2	TAAGTCGGCAC	0.368	
+	16	2296	p.A719V|PDCD6I	NM_013374	NP_037506	Q8WUM4	PDC6I_HUMAN	EIAV p9.|Self-association.	2	CATTGCCAGAG	0.328	
+	7	820	AC_uc011aya.1_	NM_003149	NP_003140	Q99469	STAC_HUMAN		4	ATCCAGAAAATG	0.373	
-	8	3732		NM_014831	NP_055646	O15050	TRNK1_HUMAN		2	TCTTAACGAACA	0.408	
+	23	3313	se_Mutation_p.L11	NM_007335	NP_031361	Q9Y238	DLEC1_HUMAN		9	AGGAGCTCCGC	0.592	
+	8	1093	cig.2_Missense_M	NM_001106	NP_001097	Q13705	AVR2B_HUMAN	Potential).|Protein kinase.	1	CCCACGGACAG	0.562	
-	27	4780		NM_006514	NP_006505	Q9Y5Y9	SCNAA_HUMAN	r; Name=S4 of repeat IV; (	10	TGTGCGGATCC	0.532	
-	5	1977	cjh.2_Missense_M	NM_033027	NP_149016	Q96S65	CSRN1_HUMAN		5	ACACCGGCACA	0.557	
-	2	175	_p.P24L|HIGD1A_	NM_001099669	NP_001093139	Q9Y241	HIG1A_HUMAN	mic (Potential).|HIG1.	0	ATGAAGGAAGG	0.383	
-	5	1261		NM_022842	NP_073753	Q9H5V8	CDCP1_HUMAN	ellular (Potential).	3	ACACACGAAAC	0.502	rs148426340
-	6	4845	v.2_Nonsense_Mu	NM_014159	NP_054878	Q9BYW2	SETD2_HUMAN	SET.	32	GTTTCGTGCATA	0.388	
-	3	1911	qv.2_Nonsense_M	NM_014159	NP_054878	Q9BYW2	SETD2_HUMAN		32	TTAATCGATTTGA	0.313	rs148810823
+	9	1399	av.1_Missense_M	NM_025010	NP_079286	O94889	KLH18_HUMAN	Kelch 3.	0	CTGGGGTTACA	0.517	rs139615876
+	3	302	.R44H|PTPN23_u	NM_015466	NP_056281	Q9H3S7	PTN23_HUMAN	BRO1.	3	TCCTCCGCAAGT	0.637	
+	10	1378	ss.2_Missense_M	NM_207102	NP_996985	Q6X9E4	FBW12_HUMAN	WD 5.	0	CATCCGAGAAC	0.507	rs140417083
-	94	7178		NM_000094	NP_000085	Q02388	CO7A1_HUMAN	le-helical region.	11	AGGGAGGCCC	0.612	
-	9	1167		NM_000094	NP_000085	Q02388	CO7A1_HUMAN	(NC1).|Fibronectin type-III	11	AGTCCGTGCCA	0.642	
-	55	12371	cuk.2_Missense_	NM_001407	NP_001398	Q9NYQ7	CELR3_HUMAN		11	TGACAGCATCA	0.547	
-	12	6148	_Mutation_p.P202	NM_001407	NP_001398	Q9NYQ7	CELR3_HUMAN	ial).|EGF-like 5; calcium-bi	11	GAGGTGGGCAG	0.667	
-	1	441	62_uc003cwm.2_5	NM_198562	NP_940964	Q6ZUJ4	CC062_HUMAN		0	AGCAGCAAAAG	0.582	

-	3	461_462	1_uc011bcm.1_3'	NM_000581	NP_000572	P07203	GPX1_HUMAN			1	AGGAAGGCGA	0.639	
+	19	2249	w.1_Missense_M	NM_001640	NP_001631	P13798	ACPH_HUMAN			1	ACATCGCCTCC	0.577	
+	17	1652		NM_004947	NP_004938	Q8IZD9	DOCK3_HUMAN	DHR-1.		0	ATTCACGAGCT	0.483	
+	50	5383		NM_004947	NP_004938	Q8IZD9	DOCK3_HUMAN			0	ATACCGGGACC	0.537	
-	14	2258	BP_uc003dbf.1_5'	NM_014703	NP_055518	Q9Y4B6	VPRBP_HUMAN			2	ATACTGGATATTC	0.463	
+	2	511	ARP3_uc003dbz.	NM_005485	NP_005476	Q9Y6F1	PARP3_HUMAN			1	AATCCGCGTGG	0.627	
-	2	3519	.2_Missense_Mut	NM_017442	NP_059138	Q9NR96	TLR9_HUMAN	oplasmic (Potential).		4	CCTTGCGGTCC	0.701	
-	11	1481	p.V390M|NT5DC	NM_022908	NP_075059	Q9H857	NT5D2_HUMAN			0	AGCACGCGGG	0.647	
-	13	1661	k.2_Missense_Mu	NM_052859	NP_443091	Q96AA3	RFT1_HUMAN			1	CAGTGCGTCTG	0.552	
+	2	309	F_uc003dob.2_M	NM_198159	NP_937802	O75030	MITF_HUMAN			2	TCATGCGTGAG	0.597	
-	15	2100		NM_020872	NP_065923	Q9P232	CNTN3_HUMAN	nectin type-III 1.		5	AACCCGAAATT	0.418	
+	22	4046	BO2_uc011bgk.1_	NM_002942	NP_002933	Q9HCK4	ROBO2_HUMAN	lasmic (Potential).		11	CTGTTCGAGGC	0.517	
+	7	1790	e_Mutation_p.R52	NM_005233	NP_005224	P29320	EPHA3_HUMAN	tential).|Fibronectin type-III		33	CAGCCGCAAGT	0.458	
-	2	459	2_5'UTR|PROS1_	NM_000313	NP_000304	P07225	PROS_HUMAN			1	ACGACGCTTCC	0.358	
-	12	1675	he.1_Missense_M	NM_016247	NP_057331	Q9BZV3	IMPG2_HUMAN	ellular (Potential).		3	CTGCCGGGGTG	0.473	
-	5	857	b.1_Missense_Mu	NM_000796	NP_000787	P35462	DRD3_HUMAN	Cytoplasmic.		4	AGGAGCTCTGT	0.562	
-	3	563	bb.1_Missense_M	NM_000796	NP_000787	P35462	DRD3_HUMAN	elical; Name=1.		4	GGCCATTGCCG	0.622	
-	4	595	BTB20_uc003ebl.	NM_015642	NP_056457	Q9HC78	ZBT20_HUMAN	BTB.		5	GATGTCGCTGT	0.612	
+	2	114	PK1B_uc003ecd.	NM_006952	NP_008883	O75841	UPK1B_HUMAN	lasmic (Potential).		0	CTGTTCGTTGC	0.393	
+	5	1122	jb.1_Missense_M	NM_001125	NP_001116	P54922	ADPRH_HUMAN			1	TGCCCCCATGA	0.577	
-	9	1847	jg.1_Missense_M	NM_153002	NP_694547	Q8NFN8	GP156_HUMAN	lasmic (Potential).		2	AGGGTGCAGAG	0.617	
+	4	467	bji.1_Missense_M	NM_014980	NP_055795	Q9Y2K9	STB5L_HUMAN			9	CATGAAAGTGG	0.373	
+	3	442		NM_016298	NP_057382	Q9UH90	FBX40_HUMAN	TRAF-type.	p.R78H(1)	5	TGTCCCGCCAC	0.597	rs137929409
+	3	778		NM_016298	NP_057382	Q9UH90	FBX40_HUMAN			5	CTAATGGGGAG	0.493	
+	14	2577	p.R817Q|KALRN_	NM_001024660	NP_001019831	O60229	KALRN_HUMAN			6	AGAACGGAAGC	0.552	
+	16	3118		NM_032242	NP_115618	Q9UIW2	PLXA1_HUMAN			3	TTCCAGCGGTG	0.627	
+	47	5590		NM_015268	NP_056083	O75165	DJC13_HUMAN			2	GACATCGAGTA	0.333	
+	12	2448	qu.2_Missense_M	NM_004441	NP_004432	P54762	EPHB1_HUMAN	Potential).|F	p.R743Q(1)	30	GCATCGGGACC	0.552	
+	2	754	esi.3_Missense_M	NM_012219	NP_036351	O14807	RASM_HUMAN			4	TGGACGGTGAG	0.493	
-	6	1603		NM_001184	NP_001175	Q13535	ATR_HUMAN			20	CAACAGCAATT	0.388	
+	11	2084	_p.Q616*|TRPC1_	NM_003304	NP_003295	P48995	TRPC1_HUMAN			2	GCTTTCAGTTG	0.363	
+	4	1110	p.G324S|HPS3_u	NM_032383	NP_115759	Q969F9	HPS3_HUMAN			6	AGACCGGTAAG	0.483	
-	6	1413	_uc003ewz.2_Mis	NM_000096	NP_000087	P00450	CERU_HUMAN	in-like 3.|F5/8 type A 2.		1	CAGAGGGAGCA	0.403	
+	1	1722	C22D2_uc003exx	NM_014779	NP_055594	O75157	T22D2_HUMAN			1	GAGTGCCCCCG	0.736	
+	1	162	FSD1_uc011bow.1	NM_022736	NP_073573	Q9H3U5	MFSD1_HUMAN	ical; (Potential).		0	CTTTTGGTGCT	0.652	
-	17	2298	80_uc003fdd.1_	NM_020800	NP_065851	Q9P2H3	IFT80_HUMAN			1	CCATAGCAGCT	0.343	
-	4	957		NM_031955	NP_114161	Q9BXB7	SPT16_HUMAN			3	TTGACGAAGAT	0.348	rs141658177
+	7	2074	ip.1_Missense_Mu	NM_014932	NP_055747	Q8N2Q7	NLGN1_HUMAN	ellular (Potential).		7	TTAGTGACCCA	0.328	
+	14	1320	.R347Q|FXR1_uc	NM_005087	NP_005078	P51114	FXR1_HUMAN			1	CAGCCGACATC	0.542	
+	15	1527	p.R416H|FXR1_uc	NM_005087	NP_005078	P51114	FXR1_HUMAN	Poly-Arg.		1	TAACCGTCGTAG	0.443	
-	11	1204	ce|MCF2L2_uc011	NM_015078	NP_055893	Q86YR7	MF2L2_HUMAN			5	GGCTCCTGCAA	0.602	
-	15	2233	p.R218C|ABCC5_	NM_005688	NP_005679	O15440	MRP5_HUMAN	C transporter 1.		4	CTGGCGCTGCC	0.597	
+	9	1083	e_Mutation_p.T31	NM_018358	NP_060828	Q9NUQ8	ABCF3_HUMAN	C transporter 1.		4	CTTTACCCCTA	0.527	
-	8	1163	d.1_Missense_Mu	NM_005787	NP_005778	Q92685	ALG3_HUMAN			0	CCAGCGTGCAG	0.577	
+	11	1720	p.G443E|ECE2_u	NM_014693	NP_055508	O60344	ECE2_HUMAN	dothelin-converting enzyme		4	TTTGGGGTCCC	0.498	
+	24	3694	_Mutation_p.R117	NM_198241	NP_937884	Q04637	IF4G1_HUMAN			7	GTGAACGGGGA	0.597	
+	24	3707	_Mutation_p.R117	NM_198241	NP_937884	Q04637	IF4G1_HUMAN			7	GGACCGTGGGG	0.627	

-	15	1839	p.R555H|CLCN2_	NM_004366	NP_004357	P51788	CLCN2_HUMAN	smic (By similarity).	0	GGTGGCGGCCC	0.627	
+	1	385	qr.2_Missense_Mu	NM_001102416	NP_001095886	P01042	KNG1_HUMAN	Cystatin 1.	1	GTACCGCATAA	0.403	
+	8	1489	i.1_Missense_Mut	NM_005578	NP_005569	Q93052	LPP_HUMAN	zinc-binding 1.	165	CAGGCCGCTGT	0.483	
-	7	763	_Mutation_p.S21	NM_032279	NP_115655	Q4VNC1	AT134_HUMAN	lasmic (Potential).	2	TTCACTAAACC	0.338	
+	3	784		NM_198565	NP_940967	Q86YC3	LRC33_HUMAN	lar (Potential).|LRR 7.	3	CACGCGGCTGC	0.642	
+	6	587	_Mutation_p.R189	NM_033029	NP_149018	Q96KR4	LMLN_HUMAN		1	TCTACCGTGGG	0.502	
+	21	2541	uy.1_Missense_M	NM_000283	NP_000274	P35913	PDE6B_HUMAN		0	AGAGGGTGGCA	0.552	
+	1	3709		NM_175918	NP_787114	Q8N1N5	CRPAK_HUMAN	7	0	TGCCCGCCTGC	0.682	rs143316662
+	29	3795		NM_002111	NP_002102	P42858	HD_HUMAN		4	TGATACCTCAG	0.358	
+	2	948	bvr.1_RNA|RGS1	NM_198229	NP_937872	O14924	RGS12_HUMAN		1	TGGGCCGTCGC	0.607	
-	7	663	_p.L188F|CRMP1_	NM_001313	NP_001304	Q14194	DPYL1_HUMAN		2	CTTAAGGAAGG	0.428	
-	3	1005		NM_053042	NP_444270	Q9C0D4	Z518B_HUMAN	2H2-type 1.	4	CCTTTCGTATAC	0.398	
-	8	1429		NM_018176	NP_060646	Q8N0V4	LGI2_HUMAN	EAR 5.	0	GACCCGGGAGT	0.522	
+	1	2873	p.S575N|PCDH7_	NM_002589	NP_002580	O60245	PCDH7_HUMAN	|Extracellular (Potential).	4	GGGCAGCACTA	0.493	
+	6	1197		NM_016531	NP_057615	P57682	KLF3_HUMAN		2	AAAAACCCTAC	0.353	
+	3	314		NM_017581	NP_060051	Q9UGM1	ACHA9_HUMAN	ellular (Potential).	7	AGTACGATGGC	0.483	
-	5	1990	ve.2_RNA|RBM4	NM_001098634	NP_001092104	A0AV96	RBM47_HUMAN		3	AATTCGGCACC	0.473	
+	4	385	_p.H16Y|UCHL1_	NM_004181	NP_004172	P09936	UCHL1_HUMAN		2	TTATTCACGCA	0.443	
-	14	2355	t.1_Missense_Mut	NM_002253	NP_002244	P35968	VGFR2_HUMAN	7.|Extracellular (Potential).	33	GACTTCGATGC	0.448	
+	7	767	P72_uc003hbw.1	NM_006947	NP_008878	O76094	SRP72_HUMAN	TPR 3.	1	GAACAGAGGAG	0.398	
-	8	1284	can.1_Missense_Mutation_p.S299L			P36537	UDB10_HUMAN		5	TACTCGACATT	0.383	
-	3	979	_p.S175L|UGT2B4	NM_021139	NP_066962	P06133	UD2B4_HUMAN		2	CCATCGACCCC	0.373	
-	3	920	p.E155D|UGT2B4	NM_021139	NP_066962	P06133	UD2B4_HUMAN		2	TTCCATTTCCTG	0.363	
+	9	1205	LB_uc003hgu.3_	NM_000477	NP_000468	P02768	ALBU_HUMAN	Albumin 2.	6	ACATATGAAACC	0.388	rs76593094
-	4	392	0iik.1_Missense_	NM_201431	NP_958834	Q6ZTQ3	RASF6_HUMAN		2	AGCATTCCTTCA	0.348	
-	3	315		NM_002416	NP_002407	Q07325	CXCL9_HUMAN		1	CACCAACCTGT	0.318	
-	24	3432		NM_001042784	NP_001036249	Q5M9N0	CD158_HUMAN	Potential.	6	TCTGATCATTGA	0.328	
-	11	1500	g.1_Nonsense_M	NM_006259	NP_006250	Q13237	KGP2_HUMAN	rotein kinase.	7	ATGCTCCTGCT	0.408	
+	3	294	e_Mutation_p.G43	NM_014606	NP_055421	Q15034	HERC3_HUMAN	RCC1 1.	4	TGGGGGAAACC	0.542	
-	2	817		NM_198281	NP_938022	Q6ZVF9	GRIN3_HUMAN		3	CTGGGGATTGC	0.552	
+	6	2635	MRN1_uc011cds.1	NM_007351	NP_031377	Q13201	MMRN1_HUMAN	Potential.	4	AGATTTCCAAAA	0.333	
+	9	1325	_p.A67S|PDLIM5_	NM_006457	NP_006448	Q96HC4	PDLI5_HUMAN		2	ACTCAGCTTTG	0.478	
-	3	406		NM_145244	NP_660287	Q96D03	DDT4L_HUMAN		1	TGCTTTGATTTG	0.453	
+	3	2665	T2_uc010ilp.1_M	NM_001127208	NP_001120680	Q6N021	TET2_HUMAN	Gln-rich.	733	GACTTTTCCTC	0.393	
-	6	825	e_Mutation_p.P91	NM_001163435	NP_001156907	Q8TEA7	TBCK_HUMAN	rotein kinase.	5	CGAGGGATACC	0.373	
-	10	1487		NM_005443	NP_005434	O43252	PAPS1_HUMAN	lyl-sulfate kinase.	1	TTCATACGCCAC	0.547	
+	4	654	H_uc010ily.2_5'U	NM_005327	NP_005318	Q16836	HCDH_HUMAN		1	CTGGCCTCCAT	0.502	
-	3	646	ml.2_5'UTR|PITX	NM_153426	NP_700475	Q99697	PITX2_HUMAN		0	TTCAACGGCCG	0.667	
-	6	995	aw.2_Missense_M	NM_018392	NP_060862	Q6ZU11	YD002_HUMAN		0	TGATTCGGACT	0.373	rs150615137
-	10	2627	T4_uc010imw.2_	NM_022569	NP_072091	Q9H3R1	NDST4_HUMAN	paran sulfate N-sulfotrans	4	AAAAGTCCATAT	0.338	
+	4	1193	e_Mutation_p.L43	NM_019050	NP_061923	Q70EK8	UBP53_HUMAN		4	TGCTTTCTTAATA	0.353	
-	16	2129	e_Mutation_p.V59	NM_018699	NP_061169	Q9NQX1	PRDM5_HUMAN		2	AGCTACACCAT	0.413	
-	12	2817	f.2_Missense_Mu	NM_001130698	NP_001124170	Q13507	TRPC3_HUMAN	ellular (Potential).	2	TGCTGGGATTCA	0.378	
-	1	851	_uc011cgz.1_Intr	NM_019035	NP_061908	Q9HCL0	PCD18_HUMAN	(Potential).|Cadherin 2.	5	GAATGCGAGTC	0.433	
-	2	1327	NF150_uc003iip.1	NM_020724	NP_065775	Q9ULK6	RN150_HUMAN	ical; (Potential).	1	CCATGCGAGGG	0.423	
+	3	493	_p.A125T|TRIM2_	NM_001130067	NP_001123539	Q9C040	TRIM2_HUMAN		1	GCAACGCTGAG	0.577	
+	10	1553		NM_000824	NP_000815	P48167	GLRB_HUMAN	lasmic (Probable).	2	GGAAATCTCAG	0.408	

+	14	2843	se_Mutation_p.G1	NM_001083619	NP_001077088	P42262	GRIA2_HUMAN	cellular (Potential).	4	GTGCGGCAGCG	0.468	
+	4	1083	e_Mutation_p.P14	NM_012464	NP_036596	O43897	TLL1_HUMAN		7	GAGTTCCCAGA	0.423	
+	5	2981	irr.2_Missense_Mu	NM_014269	NP_055084	Q9UKF5	ADA29_HUMAN	).|4.|9 X 9 AA approximate	16	CAACCTCGGGTG	0.577	rs144239698
+	15	2276	_p.R412Q|SNX25_	NM_031953	NP_114159	Q9H3E2	SNX25_HUMAN		5	ACTTCGAGGAA	0.378	
-	2	257		NM_005958	NP_005949	P48039	MTR1A_HUMAN	Name=2; (Potential).	5	GGGTACGGATAA	0.502	
+	12	2082	uc003jbb.1_5'Flan	NM_007277	NP_009208	O60645	EXOC3_HUMAN		0	GAAGACGTGGAC	0.617	
-	2	323	FS6_uc003jcy.2_5'	NM_032479	NP_115868	Q9P0J6	RM36_HUMAN		0	TACCACCGACCC	0.562	
-	17	3077	ND2_uc011cmz.1_	NM_001332	NP_001323	Q9UQB3	CTND2_HUMAN	ARM 9.	8	CCTTGGCGTTCT	0.512	
-	6	666	_uc011cmy.1_Intro	NM_001332	NP_001323	Q9UQB3	CTND2_HUMAN		8	TGGTTGCTATGG	0.592	
-	2	198	z.1_5'UTR|CTNN	NM_001332	NP_001323	Q9UQB3	CTND2_HUMAN		8	TGGTCTGGAACA	0.493	
-	28	4541		NM_001369	NP_001360	Q8TE73	DYH5_HUMAN	n (By similarity).	31	AGGGTGGTTATC	0.463	
+	3	253	IO_uc011cna.1_M	NM_007118	NP_009049	O75962	TRIO_HUMAN	CRAL-TRIO.	18	GATAAACGTGGA	0.408	
+	3	330		NM_020227	NP_064612	Q9NQV7	PRDM9_HUMAN	RAB-related.	6	AAAACTCGCTAT	0.438	
+	11	2370		NM_020227	NP_064612	Q9NQV7	PRDM9_HUMAN	C2H2-type 9.	6	GGCTTTAGCAAT	0.592	
+	11	2373		NM_020227	NP_064612	Q9NQV7	PRDM9_HUMAN	C2H2-type 9.	6	TTTAGCAATAAG	0.592	rs58979818
-	13	1494	_p.R442C|MTMR1	NM_001040446	NP_001035536	Q9C0I1	MTMRC_HUMAN	ularin phosphatase.	1	CTGGCGGAGAT	0.498	
+	31	4603	_p.V984M|SPEF2_	NM_024867	NP_079143	Q9C093	SPEF2_HUMAN		4	GATTTGGTGACC	0.358	
-	14	1225	_p.R401C|RICTOR	NM_152756	NP_689969	Q6R327	RICTR_HUMAN		10	CATTACGAATAA	0.269	
+	2	669	uc003joq.1_5'Flan	NM_002202	NP_002193	P61371	ISL1_HUMAN	l zinc-binding 1.	3	CATGCGGCATGT	0.418	
+	3	369	A2_uc011cqc.1_5'	NM_002203	NP_002194	P17301	ITA2_HUMAN	Extracellular (Potential).	1	GAGAACCGAATG	0.358	
-	10	1155	3jqt.2_Missense_M	NM_024669	NP_078945	Q3KP44	ANR55_HUMAN		1	GGGCCGACTGC	0.502	
+	14	3476		NM_005921	NP_005912	Q13233	M3K1_HUMAN		2	CCCCATCTGTAC	0.463	
-	11	1004		NM_014473	NP_055288	Q9UNQ2	DIMT1_HUMAN		1	CCATGGAACGG	0.353	
+	17	1842	_p.V575L|MAST4_	NM_015183	NP_055998	O15021	MAST4_HUMAN	rotein kinase.	13	GGATGCGTGCCA	0.463	
+	5	6470	x.1_Missense_Mu	NM_005909	NP_005900	P46821	MAP1B_HUMAN		5	GAAGCCCGTCAG	0.478	
+	13	1780	RGNEF_uc010izf.2	NM_001080479	NP_001073948	Q8N1W1	RGNEF_HUMAN		0	GCTTATCGGAGC	0.378	
+	15	2093	2_Missense_Muta	NM_000859	NP_000850	P04035	HMDH_HUMAN	Catalytic.	1	ATATCCGTTTCCA	0.353	
+	3	820	e_Mutation_p.D15	NM_018046	NP_060516	Q8N302	AGGF1_HUMAN		3	GGTACCGATAGA	0.353	
+	3	1808	w.1_Missense_Mu	NM_152405	NP_689618	Q8N9B5	JMY_HUMAN		0	AAAGCTCACATG	0.373	
+	4	1890	v.1_Missense_Mut	NM_152405	NP_689618	Q8N9B5	JMY_HUMAN		0	ATGATCGAATGC	0.363	
+	11	1685	se_Mutation_p.S35	NM_002890	NP_002881	P20936	RASA1_HUMAN	PH.	5	GATCTCAGTGTAT	0.323	
-	3	926	_p.V85M|MEF2C_	NM_002397	NP_002388	Q06413	MEF2C_HUMAN	2-type (Potential).	7	CCTCCACGATGT	0.542	
+	4	497	R98_uc003kjt.2_5'	NM_032119	NP_115495	Q8WXG9	GPR98_HUMAN	cellular (Potential).	16	CTGTTACTGTGA	0.249	
-	22	2169	se_Mutation_p.S25	NM_022140	NP_071423	Q9HCS5	E41LA_HUMAN		1	GCATCCGAAGAA	0.393	
+	7	1069	p.R230H|APC_uc	NM_001127511	NP_001120983	P25054	APC_HUMAN	u-rich.|Potential.	2515	TACTTCGTATACG	0.303	
+	12	1876	PC_uc003kpy.3_Mi	NM_001127511	NP_001120983	P25054	APC_HUMAN	Leu-rich. .R499*(2)|p.?(	2515	TAAGACGATATG	0.368	
+	11	944	e_Mutation_p.K29	NM_000414	NP_000405	P51659	DHB4_HUMAN	acyl-CoA dehydrogenase.	2	ACTGGAAGAAGA	0.488	
-	17	2349	_p.R565H|CEP120	NM_153223	NP_694955	Q8N960	CE120_HUMAN	Potential.	1	GCCCTACGGATA	0.428	rs74938108
+	3	2155		NM_175856	NP_787052	Q70JA7	CHSS3_HUMAN	nenal (Potential).	3	TGTGATGTTGACT	0.428	
-	3	495	f.1_Missense_Mut	NM_007054	NP_008985	Q9Y496	KIF3A_HUMAN	Kinesin-motor.	1	ATAGCTCGAACA	0.373	
-	11	1730	IL3_uc011cyd.1_In	NM_017415	NP_059111	Q9UH77	KLHL3_HUMAN	Kelch 3.	0	CGCCGCGTGTTC	0.597	
-	15	1840	03lde.2_Translatio	NM_004134	NP_004125	P38646	GRP75_HUMAN		0	CAACTCGTTCCT	0.368	
+	2	909	et.2_Missense_Mu	NM_016463	NP_057547	Q7LFL8	CXXC5_HUMAN		1	CAGTCCGACTTC	0.662	
+	3	1410	lgh.1_Missense_M	NM_080670	NP_542401	Q96G79	S35A4_HUMAN	(Potential).|Leu-rich.	0	ACTTTTGGTGTG	0.587	
+	1	1256	_p.S419L|PCDHA1	NM_018900	NP_061723	Q9Y5I3	PCDA1_HUMAN	|Extracellular (Potential).	1	GCCTGTCGGTCT	0.627	
+	1	1861	CDHA1_uc003lgz.2	NM_018900	NP_061723	Q9Y5I3	PCDA1_HUMAN	|Extracellular (Potential).	1	CGCATCCCGTTC	0.657	
+	1	1867	hd.2_Intron|PCDH	NM_018906	NP_061729	Q9Y5H8	PCDA3_HUMAN	|Extracellular (Potential).	8	CGTTTCGCGTG	0.662	

+	1	1526	CDHA5_uc003lhk.	NM_018911	NP_061734	Q9Y5H6	PCDA8_HUMAN	|Extracellular (Potential).	2	ACATTTCGGTGCA	0.687	
+	1	1229	CDHA6_uc003lhn.2	NM_018901	NP_061724	Q9Y5I2	PCDAA_HUMAN	|Extracellular (Potential).	5	TGGACAGCGCTC	0.632	
+	1	975		NM_013340	NP_037472	Q9Y5F3	PCDB1_HUMAN	|Extracellular (Potential).	0	AATGGAGAAGTT	0.463	
+	1	1564	uc003lin.2_5'Flank	NM_018937	NP_061760	Q9Y5E6	PCDB3_HUMAN	r (Potential).|Cadherin 5.	2	GACTACGAGGCC	0.692	
+	1	1978		NM_018938	NP_061761	Q9Y5E5	PCDB4_HUMAN	|Extracellular (Potential).	3	CACGTGCTCCTG	0.692	
+	1	1358	dah.1_Missense_M	NM_018939	NP_061762	Q9Y5E3	PCDB6_HUMAN	cellular (Potential).	1	AAACCTCCTACA	0.592	
+	1	1564	HB16_uc010jfw.1_	NM_020957	NP_066008	Q9NRJ7	PCDBG_HUMAN	cellular (Potential).	2	GAAAAGGAAATG	0.373	
+	1	2096	daj.1_Missense_M	NM_018931	NP_061754	Q9Y5F2	PCDBB_HUMAN	ical; (Potential).	6	TGTCTTCGCTCT	0.682	
-	1	2952		NM_016580	NP_057664	Q9NPG4	PCD12_HUMAN	cellular (Potential).	3	CATTCACAAGCA	0.612	
-	2	398		NM_001080516	NP_001073985	A6NFK2	GRCR2_HUMAN		0	GGGGTTCGAATG	0.403	
+	7	1518	427Q|SH3RF2_uc0	NM_152550	NP_689763	Q8TEC5	SH3R2_HUMAN	SH3 3.	2	CGGGCGAGTCG	0.612	rs146377978
+	8	1689	_uc011dbm.1_5'UT	NM_152550	NP_689763	Q8TEC5	SH3R2_HUMAN		2	TCAAATCCGTCTT	0.567	
-	9	1721	jhd.2_Nonsense_M	NM_002609	NP_002600	P09619	PGFRB_HUMAN	Potential).|Ig-like C2-type 5.	17	GCACTCGGACAG	0.617	
-	5	709	_Mutation_p.R146C	NM_001025071	NP_001020242	P62263	RS14_HUMAN		1	CACGGCGACCCC	0.522	
-	23	12797	AT2_uc003lud.3_M	NM_001447	NP_001438	Q9NYQ8	FAT2_HUMAN	lasmic (Potential).	6	CAGGCGCTCCC	0.647	
-	2	1615	.3_Intron|PWWP2A	NM_001130864	NP_001124336	Q96N64	PWP2A_HUMAN		0	TGAAGGGGCCT	0.542	
-	2	469	3lyf.1_Missense_M	NM_022090	NP_071373	Q8IZ13	CE054_HUMAN		1	cgtttcttcgacatggcac	0	
+	19	3562	t.3_Missense_Mut	NM_001122679	NP_001116151				10	ACAAAGGCACTC	0.582	
+	26	5704	t.3_Missense_Muta	NM_001122679	NP_001116151				10	ATGAGCGAGAGG	0.607	
-	25	2998	g.2_Missense_Mut	NM_003062	NP_003053	O75094	SLIT3_HUMAN	LRRCT 4.	4	CACAGTGGAGTG	0.622	
+	11	1714	eq.1_Nonsense_M	NM_017785	NP_060255	Q96EA4	SPDLY_HUMAN		2	GTTTATCGATTAC	0.443	
-	2	2309		NM_052899	NP_443131	Q7Z2K8	GRIN1_HUMAN		2	TCAGGGGGACCA	0.637	
+	10	1138		NM_003052	NP_003043	Q06495	NPT2A_HUMAN	cellular (Potential).	1	GCCTACCGGACC	0.627	
-	3	245	2_uc003mgn.3_5'	NM_000505	NP_000496	P00748	FA12_HUMAN	ronectin type-II.	0	CTGGCCGGCCCT	0.602	
+	6	623	gq.2_Missense_Mu	NM_002082	NP_002073	P43250	GRK6_HUMAN	terminal.|RGS.	3	CTGAGCGTGGCC	0.632	
+	3	316	ED9_uc010jko.2_F	NM_017510	NP_059980	Q9BVK6	TMED9_HUMAN	Lumenal (Potential).	0	GCTCCGAGGGC	0.527	
-	16	1887	p.R585C|EXOC2_	NM_018303	NP_060773	Q96KP1	EXOC2_HUMAN		7	GCAACGTACTCG	0.463	
+	23	4099	P_uc003mxq.1_Int	NM_004415	NP_004406	P15924	DESP_HUMAN	us rod domain.|Potential.	9	GAAAACGCCCTT	0.498	
-	7	1339	RNA|TFAP2A_uc0	NM_003220	NP_003211	P05549	AP2A_HUMAN	span-helix), dimerization.	1	TGGGCCGTGAGT	0.617	
-	8	2881	e_Mutation_p.R63	NM_000332	NP_000323	P54253	ATX1_HUMAN	USP7.|RNA-binding.|AXH.	4	GGGCTCGGTGC	0.572	
-	8	951	slation_Start_Site|	NM_000332	NP_000323	P54253	ATX1_HUMAN		4	CCTCCACGGTGA	0.527	
+	7	1312		NM_001732	NP_001723	Q13410	BT1A1_HUMAN	.|Cytoplasmic (Potential).	2	AATCAGGAGACAT	0.517	
+	5	941	G_uc003nnz.3_Mis	NM_002127	NP_002118	P17693	HLAG_HUMAN	ntial).|Ig-like C1-type.|Alpha	4	GAGCTCGTGGAG	0.627	
+	1	492	2_5'Flank|TRIM10_	NM_033229	NP_150232	Q9C019	TRI15_HUMAN		0	GCAACCCCGTCC	0.627	
-	1	58	l.2_Missense_Mut	NM_002341	NP_002332	Q06643	TNFC_HUMAN	lasmic (Potential).	0	AGGGAACCCCTC	0.642	
+	3	223	K2B_uc003nvs.1_3	NM_021221	NP_067044	Q8NDX9	LY65B_HUMAN	UPAR/Ly6.	0	TGTGGACAGTAC	0.502	
-	20	1661	p.C511F|BAT5_uc	NM_021160	NP_066983	O95870	ABHGA_HUMAN		0	GGGTGCAGTGA	0.577	
-	1	106	LC44A4_uc011dor	NM_025257	NP_079533	Q53GD3	CTL4_HUMAN	lasmic (Potential).	4	TCTCACCGTAGG	0.662	
+	29	3874	.1_Missense_Muta	NM_007293	NP_009224	P0C0L4	CO4A_HUMAN		0	CTGCTTCACGAG	0.672	
-	27	9446		NM_019105	NP_061978	P22105	TENX_HUMAN	nectin type-III 23.	0	GGCCCTCGGGAA	0.667	
-	6	884		NM_002120	NP_002111	P13765	DOB_HUMAN	lasmic (Potential).	1	TGAGACCTGGA	0.572	
-	2	331	3ocz.1_Missense_I	NM_080680	NP_542411	P13942	COBA2_HUMAN	SP N-terminal.	5	CCCGGAGCACAT	0.592	
-	15	1741	dn.1_Missense_Mu	NM_022553	NP_072047	Q8N1B4	VPS52_HUMAN		5	AGCGGCGTGTGA	0.537	
+	7	902	GAP1_uc010juy.2_	NM_006772	NP_006763	Q96PV0	SYGP1_HUMAN	PH.	4	GGTCTGCGGCCG	0.507	
-	2	213	:.1_5'Flank|C6orf12	NM_032340	NP_115716	Q9BRT2	CF125_HUMAN		0	AGCTCTCGTACAT	0.483	
-	7	1569	fb.2_Missense_Mu	NM_001142883	NP_001136355	Q96PC2	IP6K3_HUMAN		0	CGTGAGGATGCG	0.552	
-	15	1067	D42N|CPNE5_uc0	NM_020939	NP_065990	Q9HCH3	CPNE5_HUMAN	VWFA.	1	TGAAATCAATGG	0.592	

+	60	9013		NM_001371	NP_001362				21	AAACAGATTTC	0.363	
+	1	555	e_Mutation_p.G36	NM_006586	NP_006577	Q9BT09	CNPY3_HUMAN		1	AGGCCGGAGCT	0.602	
-	4	1019	_Intron|TMEM151	NM_182539	NP_872345	Q5JU00	TCTE1_HUMAN		4	TGCTTCGGGTC	0.537	
-	19	2563	_Intron|TMEM151	NM_020745	NP_065796	Q5JTZ9	SYAM_HUMAN		1	GGCACGCCGCT	0.587	
+	11	1473	AG_uc010jzt.2_R	NM_014464	NP_055279	Q9UJW2	TINAG_HUMAN		4	CATGGGGAGAG	0.403	
+	5	1011		NM_001010872	NP_001010872	Q5T0W9	FA83B_HUMAN		6	GAAAAGCCCTC	0.428	
+	5	2599		NM_001010872	NP_001010872	Q5T0W9	FA83B_HUMAN		6	ATCTCCTAGAA	0.393	
+	39	2651		NM_001858	NP_001849	Q14993	COJA1_HUMAN	lical region 5 (COL5).	4	ACCCGGTCCTC	0.323	
+	7	1109		NM_024576	NP_078852	Q5TC84	OGRL1_HUMAN		0	CGCCTCGAAAA	0.468	
+	14	2184	kat.2_Splice_Site	NM_019842	NP_062816	Q9NR82	KCNQ5_HUMAN		7	TTCTAGGTACA	0.408	
-	5	1472		NM_138441	NP_612450	Q8N884	M21D1_HUMAN		0	TACATACGTGAA	0.413	
-	26	4924	pht.2_Missense_M	NM_004370	NP_004361	Q99715	COCA1_HUMAN	nectin type-III 11.	9	GGTTCCCAAAA	0.403	
-	14	2945	2A1_uc003pht.2_	NM_004370	NP_004361	Q99715	COCA1_HUMAN	nectin type-III 6.	9	AGCAGATGTCC	0.393	
-	13	1926		NM_001563	NP_001554	Q17R60	IMPG1_HUMAN	SEA 2.	3	GAGCTCGGTAC	0.458	
+	2	396		NM_031469	NP_113657	Q9UJC5	SH3L2_HUMAN		0	ATGGCGACCGA	0.468	
+	3	369	b.3_Missense_Mu	NM_003318	NP_003309	P33981	TTK_HUMAN		11	CGCTTCCCCCA	0.348	
+	8	2621		NM_015021	NP_055836	O60281	ZN292_HUMAN		4	CAGAACACAGC	0.398	
-	92	15463		NM_014611	NP_055426	Q9NU22	MDN1_HUMAN		10	GCACACGCTCA	0.478	
-	61	9580		NM_014611	NP_055426	Q9NU22	MDN1_HUMAN		10	CCTGCCGCCGG	0.622	rs142328599
-	21	3021	o.1_Missense_Mu	NM_014611	NP_055426	Q9NU22	MDN1_HUMAN		10	GGCCCGGCACA	0.502	
+	5	1422		NM_024641	NP_078917	Q5SRI9	MANEA_HUMAN	able).|Lumenal (Potential).	3	ATTACCGTCCT	0.408	
+	7	1529	317R|KLHL32_u	NM_052904	NP_443136	Q96NJ5	KLH32_HUMAN	Kelch 2.	4	CAGGAGGGGAA	0.577	
+	5	1654	re.2_Missense_M	NM_001198	NP_001189	O75626	PRDM1_HUMAN		56	CAGATGGAGCC	0.677	
-	5	996	dr.2_Missense_M	NM_022765	NP_073602	Q8TDZ2	MICA1_HUMAN		3	GGTGCGTCCAT	0.547	
-	13	1922	_p.A531V|LAMA4_	NM_001105206	NP_001098676	Q16363	LAMA4_HUMAN	omain II and I.	9	AGTCCGCAGAT	0.443	
-	3	515	_p.R48Q|HDAC2_	NM_001527	NP_001518	Q92769	HDAC2_HUMAN	ne deacetylase.	4	TTGACCGTAGA	0.348	
-	3	830	_p.Q270*|GPRC6	NM_148963	NP_683766	Q5T6X5	GPC6A_HUMAN	ellular (Potential).	6	AACCTGGGCTT	0.363	
+	11	1103		NM_173560	NP_775831	Q8HWS3	RFX6_HUMAN		3	ACATAAGAAATT	0.308	
-	43	7110	S1_uc011ebi.1_R	NM_002944	NP_002935	P08922	ROS_HUMAN	lasmic (Potential).	25	CTTCTTTCCTCA	0.473	
-	2	1244	_p.R179Q|FAM184	NM_024581	NP_078857	Q8NB25	F184A_HUMAN	Potential.	7	TTTTTCGTAAAA	0.393	
+	1	274	L_uc003pzq.2_RNA			Q8TC41	RN217_HUMAN		0	TGGACGTGCTG	0.701	
-	2	509	issense_Mutation	NM_002844	NP_002835	Q15262	PTPRK_HUMAN	lar (Potential).|MAM.	8	CTGGTGGTAAT	0.438	
-	14	1787	_Site_p.S179_splic	NM_004830	NP_004821	Q9ULK4	MED23_HUMAN		3	AACATACCTCATT	0.373	
-	13	1991	v.2_Missense_Mu	NM_003980	NP_003971	Q14244	MAP7_HUMAN	Potential.	0	CCTGCCGGACC	0.567	
-	7	950	kgs.2_Missense_	NM_003980	NP_003971	Q14244	MAP7_HUMAN		0	GGAACGAATGT	0.527	
-	3	1001	e_Mutation_p.K14	NM_031922	NP_114128	Q96D71	REPS1_HUMAN		2	ATCCCTTTTTC	0.478	
+	2	185	.1_RNA|VTA1_uc	NM_016485	NP_057569	Q9NP79	VTA1_HUMAN	HMP5.|Interaction with IS	0	AATGTCGCAAAT	0.299	
-	9	6940_6941		NM_006734	NP_006725	P31629	ZEP2_HUMAN	repeats of S-P-[RGMKC]- [	6	CCTTTGGGTATC	0.465	
-	5	3987		NM_006734	NP_006725	P31629	ZEP2_HUMAN		6	TTGCCGCACCA	0.562	
-	10	1572		NM_173515	NP_775786	Q6P9H4	CNKR3_HUMAN	DUF1170.	4	ACCGGGGAGAG	0.483	
+	8	1183	_p.G83R|SYNJ2_u	NM_003898	NP_003889	O15056	SYNJ2_HUMAN	SAC.	1	CAAAGGGGGAG	0.582	
+	8	2810	_p.V485I|TULP4_	NM_020245	NP_064630	Q9NRJ4	TULP4_HUMAN		1	AGTTCGTCATC	0.632	
+	9	977	se_Mutation_p.G2	NM_007045	NP_008976	O95684	FR1OP_HUMAN		1	TGGCGGGAGCC	0.453	
-	1	901		NM_005299	NP_005290	O00270	GPR31_HUMAN	lasmic (Potential).	0	GCCTCGGAGGG	0.592	rs148093951
+	2	365	GPR146_uc003sj	NM_138445	NP_612454	Q96CH1	GP146_HUMAN	ellular (Potential).	1	GGAGTGTGGGC	0.652	
-	3	1613	on.3_Missense_M	NM_024963	NP_079239	Q96ME1	FXL18_HUMAN		3	GTTGCGGATGG	0.662	
+	4	590	42_uc011jwp.1_Mi	NM_032172	NP_115548	Q9H9J4	UBP42_HUMAN		5	TATGATGTGTAC	0.378	

+	7	862		NM_001163941	NP_001157413	Q2M3G0	ABCB5_HUMAN			6	ACCCTAGTGACT	0.448	
+	8	1294	uh.2_Missense_Mu	NM_178559	NP_848654	Q2M3G0	ABCB5_HUMAN	).|ABC transmembrane type		6	GTTCTGGGGACA	0.299	
+	10	1310	e.1_Missense_Mu	NM_031414	NP_113602	Q9BXU1	STK31_HUMAN			9	ATAATATGGGCA	0.383	
+	8	1754	CDC129_uc011kae	NM_194300	NP_919276	Q6ZRS4	CC129_HUMAN			0	GAATGGGTAAAC	0.473	
-	4	2367	L9_uc011kai.1_Int	NM_015483	NP_056298	Q8IY47	KBTB2_HUMAN	Kelch 5.		0	GTACACGTTCAG	0.468	
+	1	820	uc003tfl.2_Intron	NM_181791	NP_861456	Q7Z602	GP141_HUMAN	Name=7; (Potential).		3	GTAACAGCAATT	0.388	
+	4	254	BE2D4_uc003tjb.1	NM_015983	NP_057067	Q9Y2X8	UB2D4_HUMAN			0	CACTTTCCTACA	0.502	
+	3	276	G60R|DBNL_uc01	NM_001014436	NP_001014436	Q9UJU6	DBNL_HUMAN	ADF-H.		1	ACAGCGGGAAG	0.577	
+	8	1377	3_5'Flank|AEBP1_	NM_001129	NP_001120	Q8IUX7	AEBP1_HUMAN			0	GGGCAGTGGAG	0.627	
+	16	2266	e_Mutation_p.R22	NM_001129	NP_001120	Q8IUX7	AEBP1_HUMAN	with PTEN (By similarity).		0	GTGTGCGCAGCC	0.632	
+	9	1180	nq.2_RNA|CCM2_	NM_031443	NP_113631	Q9BSQ5	CCM2_HUMAN			0	GGACAGCCGCA	0.592	
-	27	4153		NM_138295	NP_612152	Q8TDX9	PK1L1_HUMAN	ular (Potential).|REJ.		11	TAAAGCCTAGCT	0.493	
+	51	13664	CA13_uc010kyt.1_	NM_152701	NP_689914	Q86UQ4	ABCAD_HUMAN	ical; (Potential).		10	CTTTTCGGGTAT	0.483	
-	7	1201	_p.P339L|COBL_	NM_015198	NP_056013	O75128	COBL_HUMAN	Pro-rich.		5	GTGGAGGGGGA	0.532	
-	7	874		NM_207366	NP_997249	Q6ZU15	SEP14_HUMAN			0	TCACTTCATCTG	0.428	
+	4	980		NM_001159279	NP_001152751					2	AGAATTCATACT	0.408	
+	7	1198	3tvz.2_Missense_	NM_022479	NP_071924	Q6IS24	GLTL3_HUMAN	nenal (Potential).		7	GCTCTTCGCGTT	0.537	
+	1	1170		NM_003508	NP_003499	O00144	FZD9_HUMAN	cellular (Potential).		1	GCTGCACGCTGG	0.657	
+	1	98	S|ELN_uc003tzr.2_	NM_000501	NP_001075224	P15502	ELN_HUMAN			5	ATGGCGGGTCT	0.507	
+	18	1041	e|ELN_uc003tzr.2_	NM_000501	NP_001075224	P15502	ELN_HUMAN			5	TCCACAGGAGC	0.567	
+	5	717	n_p.R56Q|LAT2_u	NM_032464	NP_115853	Q9GZY6	NTAL_HUMAN	lasmic (Potential).		0	GGTCCCGGACCT	0.612	
+	17	2508	p.G508D|CCDC14	NM_020879	NP_065930	Q8IYE0	CC146_HUMAN	Potential.		2	TCAGGGCTGCA	0.512	
-	6	10547	_p.R3420*|PCLO_	NM_033026	NP_149015	Q9Y6V0	PCLO_HUMAN			7	GTCCTCGGACTT	0.428	
-	17	1977	p.T646M|SEMA3D	NM_152754	NP_689967	O95025	SEM3D_HUMAN	g-like C2-typ	p.T646M(1)	5	TATTCCGTTTTG	0.408	rs139389337
-	26	3506	.R1137W|ABCB4_	NM_018849	NP_061337	P21439	MDR3_HUMAN	2.|Cytoplasm	p.I1144T(1)	6	AACCCGGCTGT	0.473	
-	20	2798	hc.1_Nonsense_M	NM_000927	NP_000918	P08183	MDR1_HUMAN	smembrane type-1 2.		7	GGATCGGAAAA	0.552	
+	2	417	011khj.1_Missense	NM_001039706	NP_001034795	A5D8W1	CG063_HUMAN			1	CTCCTCGAAGAG	0.333	rs145263721
+	12	981	C132_uc003umr.2_	NM_017667	NP_060137	Q96JG6	CC132_HUMAN			0	AACACCGTGTTT	0.363	
-	11	1786	p.S427F|ASNS_u	NM_133436	NP_597680	P08243	ASNS_HUMAN	ragine synthetase.		1	TAATAGGAAGAA	0.343	
-	2	358	iw.1_Missense_Mu	NM_015545	NP_056360	O75127	PTCD1_HUMAN			1	GTGGCCGTGGAG	0.622	
+	7	1916	_p.V598I|ZKSCAN	NM_145102	NP_659570	Q9Y2L8	ZKSC5_HUMAN	C2H2-type 6.		1	AGCGCGTCCAC	0.517	rs4729542
+	4	578	uc011kjm.1_5'Flan	NM_001004351	NP_001004351	A6NKU9	SPDE3_HUMAN			0	TATGCCGTCCCA	0.547	
+	3	797	uxr.2_Missense_M	NM_030961	NP_112223	Q9BRZ2	TRI56_HUMAN	B box-type 2.		3	GCTGTGCAGAG	0.701	
-	5	471	k|CLDN15_uc003	NM_016068	NP_057152	Q9Y3D6	FIS1_HUMAN	ical; (Potential).		0	CTCCCACGATGG	0.662	
-	4	327	sense_Mutation_p.	NM_022777	NP_073614	Q9H7X7	RABL5_HUMAN			0	GGGCCGGCCAG	0.458	
+	24	4482	1_uc011kkn.1_Intr	NM_181552	NP_853530	P39880	CUX1_HUMAN			8	AGGCCGCGAAC	0.716	
+	4	638	uzm.2_5'Flank|LR	NM_152892	NP_690852	Q9UFC0	LRWD1_HUMAN			1	CCAGGCGGACT	0.627	
-	14	1983	vex.2_Missense_M	NM_002291	NP_002282	P07942	LAMB1_HUMAN	minin IV type B.		8	GGGTGGCAAAGT	0.557	
-	15	1913	ey.2_Missense_Mu	NM_007356	NP_031382	A4D0S4	LAMB4_HUMAN	minin IV type B.		8	TTGACAGCAAAT	0.493	
-	4	1284	nse_Mutation_p.R1	NM_015723	NP_056538	Q9NP80	PLPL8_HUMAN			2	GGGACGAGAAA	0.408	
+	1	543		NR_002144						0	GGCCAGGAAGC	0.602	
+	4	605	.R49Q|CALD1_uc	NM_033138	NP_149129	Q05682	CALD1_HUMAN	odulin-binding (By similarity		0	GGAACGGCTGC	0.577	
-	15	1859_1860		NM_004333	NP_004324	P15056	BRAF_HUMAN	rotein kinas	_R603>I(2)|p.T	18290	GATTTCACTGTAG	0.366	rs121913378
-	7	736	n_p.R179H|CLEC5	NM_013252	NP_037384	Q9NY25	CLC5A_HUMAN	.|Extracellular (Potential).		0	ATCCTGCGGTAG	0.408	
+	5	705	1_Intron|uc010loj.	NR_001296						0	TGCAATGGACAG	0.493	rs143538588
-	15	2143	p.R429W|TRPV6_	NM_018646	NP_061116	Q9H1D0	TRPV6_HUMAN	lasmic (Potential).		2	GATCCGCTGCC	0.557	
+	1	436		NM_012369	NP_036501	Q13607	OR2F1_HUMAN	lasmic (Potential).		3	CCTGCGATACT	0.552	rs141056144

+	4	1198	p.Q294*|REPIN1_	NM_013400	NP_037532	Q9BWE0	REPI1_HUMAN	C2H2-type 6.	1	CCCTTCCAGTGT	0.527
+	3	1651	3743_uc003whg.2_	NM_173680	NP_775951	Q96BV0	ZN775_HUMAN	C2H2-type 11.	0	CGGCCGCGGCT	0.721
+	4	1423	M1_uc010lqp.1_5'F	NM_138400	NP_612409	Q5C9Z4	NOM1_HUMAN	MIF4G.	0	GTCATTGCCCAT	0.443
-	60	9769	.G2456S|CSMD1_	NM_033225	NP_150094	Q96PZ7	CSMD1_HUMAN	Extracellular (Potential).	25	GGTAACCGTCCA	0.567
-	1	721		NM_004225	NP_004216	Q9Y4C4	MFHA1_HUMAN		0	GGGGGGAGGCG	0.582
+	2	751	p.G249D|TNKS_u	NM_003747	NP_003738	O95271	TNKS1_HUMAN	ANK 2.	7	TGGAGGTCTCA	0.443
+	7	1101	se_Mutation_p.R31	NM_004462	NP_004453	P37268	FDFT_HUMAN		0	AGATTCGGAAA	0.448
-	9	3313	wl.1_Missense_Mu	NM_182643	NP_872584	Q96QB1	RHG07_HUMAN		7	TTCGGTCGTTGT	0.582
-	1	173	ltg.1_Missense_Mu	NM_021020	NP_066300	Q9Y250	LZTS1_HUMAN		1	ACTGCGAAGCC	0.642
-	8	1454	.2_Missense_Muta	NM_139278	NP_644807	Q8N145	LGI3_HUMAN	EAR 4.	1	CAGCCGTGGCT	0.627
+	4	750	BS3_uc011kzk.1_	NM_005775	NP_005766	O60504	VINEX_HUMAN	SoHo.	0	CCCCCGATCCG	0.632
+	5	1660	|RHOBTB2_uc011	NM_015178	NP_055993	Q9BYZ6	RHBT2_HUMAN	BTB 1.	2	GCAACGGAACA	0.612
-	9	1153	dm.2_Missense_M	NM_004901	NP_004892	Q9Y227	ENTP4_HUMAN	enal (Potential).	2	GCATTGCCACCA	0.423
+	4	1033	010ltz.2_RNA|SLC	NM_016612	NP_057696	Q9NYZ2	MFRN1_HUMAN	Solcar 3.	0	TCAACGGCCTG	0.577
+	11	1128	se_Mutation_p.H1	NM_014265	NP_055080	Q9UKQ2	ADA28_HUMAN	B.|Extracellular (Potential).	5	ATGTTTCATGAC	0.458
+	3	2559	p.K624N|NEFM_u	NM_005382	NP_005373	P07197	NFM_HUMAN	Tail.	1	GAAAAGAAGGG	0.338
-	40	5512	az.1_Missense_Mu	NM_015254	NP_056069	Q9NQT8	KI13B_HUMAN		0	TTCTCAGGGTTC	0.692
+	12	2043	se_Mutation_p.S2	NM_013964	NP_039258	Q02297	NRG1_HUMAN	lasmic (Potential).	0	ATGACAGTAACA	0.552
+	27	3298		NM_001031836	NP_001027006	A8MYU2	KCNU1_HUMAN	lasmic (Potential).	1	CATTCAGACACA	0.388
+	19	3208	vy.2_Missense_Mu	NM_032777	NP_116166	Q96PE1	GP124_HUMAN	lasmic (Potential).	5	GGCTACGCTTA	0.637
+	6	901	p.R196C|LETM2_	NM_144652	NP_653253	Q2VYF4	LETM2_HUMAN	hondrial matrix (Potential).	0	TTAGATCGCCCT	0.502
+	12	1382	se_Mutation_p.S1	NM_001556	NP_001547	O14920	IKKB_HUMAN		7	GATCTCCCCAC	0.408
-	5	551	lcw.1_Missense_M	NM_004198	NP_004189	Q15825	ACHA6_HUMAN	Extracellular.	0	TTTGATGATCAAA	0.363
+	19	2597	gf.2_RNA|KIAA014	NM_001080394	NP_001073863	Q14159	K0146_HUMAN		0	GTTTGCCGCCG	0.592
+	5	1125	_p.I214K|YTHDF3	NM_152758	NP_689971	Q7Z739	YTHD3_HUMAN		0	CTCCTATAAAAC	0.488
+	2	244	orf44_uc003xwq.1	NM_019607	NP_062553	Q96CB5	CH044_HUMAN		0	CACTTCGAAAAC	0.294
+	9	1085	yb.2_Missense_M	NM_052958	NP_443190	Q49A92	CH034_HUMAN		1	ATACTCCATTCTC	0.328
+	5	871	_p.D52N|SULF1_	NM_015170	NP_055985	Q8IWU6	SULF1_HUMAN		7	ACCGATGATCAA	0.468
+	22	3283	on_p.G856R|SULI	NM_015170	NP_055985	Q8IWU6	SULF1_HUMAN		7	ATGGAGGAAGC	0.328
-	6	740	h.1_Missense_Mu	NM_000971	NP_000962	P18124	RL7_HUMAN		0	TGTTGATCTGGT	0.428
-	2	933	p.R298H|JPH1_uc	NM_020647	NP_065698	Q9HDC5	JPH1_HUMAN	ic (Potential).|MORN 6.	1	TGGAGCGCTCG	0.542
-	3	710	p.V90M|TPD52_u	NM_001025252	NP_001020423	P55327	TPD52_HUMAN		1	CTGTCACGTCTT	0.443
-	5	334	_Mutation_p.R107	NM_024699	NP_078975	Q8TCF1	ZFAN1_HUMAN	AN1-type 2.	1	GCCATTCGAGGC	0.413
+	7	1054	13_uc003ydf.1_Int	NM_198584	NP_940986	Q8N1Q1	CAH13_HUMAN		0	GGTGAAGCAGCA	0.473
-	4	739	ec.2_Missense_Mu	NM_005941	NP_005932	P51512	MMP16_HUMAN	cellular (Potential).	8	CACGGCGAATAG	0.373
-	9	1093	DH17_uc011lgp.1_	NM_004063	NP_004054	Q12864	CAD17_HUMAN	r (Potential).|Cadherin 3.	6	CCAGCGGATAT	0.413
-	24	5336	1429_uc010maz.1	NM_015496	NP_056311	Q69YN4	VIR_HUMAN		2	CCCCACGACCTC	0.478
+	20	2500	r.1_RNA|INTS8_uc	NM_017864	NP_060334	Q75QN2	INT8_HUMAN		0	GATATTACAGCT	0.269
+	6	1223	vid.2_Missense_M	NM_002380	NP_002371	O00339	MATN2_HUMAN	EGF-like 3.	2	ACGGATGTGAAC	0.428
-	1	171	10_uc011lhj.1_5'F	NM_005655	NP_005646	Q13118	KLF10_HUMAN		0	GAGAGGCACCG	0.453
-	7	1618	no.2_Nonsense_M	NM_001146	NP_001137	Q15389	ANGP1_HUMAN	ogen C-terminal.	7	GGCTCGGTTCC	0.428
-	3	375	p.V131M|EIF3H_	NM_003756	NP_003747	O15372	EIF3H_HUMAN	MPN.	3	GCCCACGTGAA	0.438
-	2	600	F11B_uc010mdc.	NM_002546	NP_002537	O00300	TR11B_HUMAN	TNFR-Cys 2.	2	GCTTGACGTACT	0.577
-	6	1049		NM_003184	NP_003175	Q6P1X5	TAF2_HUMAN		6	ATGTATGGATCTA	0.353
+	7	961		NM_015137	NP_055952	Q14156	EFR3A_HUMAN		5	AATGCTGTTAGA	0.378
-	15	2240	dt.2_Missense_M	NM_004519	NP_004510	O43525	KCNQ3_HUMAN		5	TCCTCCTTCTTC	0.532
+	3	237		NM_003235	NP_003226	P01266	THYG_HUMAN	globulin type-1 1.	15	AGAACGACGGC	0.637

-	13	2173	M135B_uc003yva	NM_015912	NP_056996	Q49AJ0	F135B_HUMAN		9	GAGTTCCTCCT	0.527	
-	2	191	slation_Start_Site|	NM_015912	NP_056996	Q49AJ0	F135B_HUMAN		9	TCAACCGTTCCT	0.323	
-	2	565		NM_005293	NP_005284	Q99678	GPR20_HUMAN	lasmic (Potential).	1	AGCGGCGGGAG	0.692	
-	2	227		NM_003695	NP_003686	Q14210	LY6D_HUMAN		0	TACCCACCTGTG	0.637	
-	7	1158	p.R100Q|CYP11B	NM_000497	NP_000488	P15538	C11B1_HUMAN		3	CCACTCGCTCC	0.602	
-	3	259	_p.G75S|TSTA3_	NM_003313	NP_003304	Q13630	FCL_HUMAN		1	CAGGCCCCCA	0.552	
-	32	11511	e.1_Missense_Mu	NM_201380	NP_958782	Q15149	PLEC_HUMAN	Globular 2.	9	GCGGCGCACGT	0.607	
+	2	273	GPR172A_uc003z	NM_024531	NP_078807	Q9HAB3	RFT3_HUMAN		0	TGGTCAAAGAGC	0.647	
+	7	2525	gp.1_Missense_M	NM_015158	NP_055973	Q14678	KANK1_HUMAN		4	AAGTGCGGTCT	0.537	
-	28	3305	_p.F819L|UBAP2_	NM_018449	NP_060919	Q5T6F2	UBAP2_HUMAN		3	TGTAGGAATGGT	0.652	
+	15	1923	e_Mutation_p.R4	NM_021111	NP_066934	O95980	RECK_HUMAN		3	TCTACCCGCCTT	0.473	
+	4	870	se_Mutation_p.R2	NM_032226	NP_115602	Q8N3Z6	ZCHC7_HUMAN		3	CCCAGCGGTAC	0.368	
+	5	751		NM_015110	NP_055925	Q8IY18	SMC5_HUMAN	Potential.	3	AAATATCACTGT	0.368	
-	9	1337	c.1_Nonsense_M	NM_017662	NP_060132	Q9BX84	TRPM6_HUMAN	lasmic (Potential).	8	AATTTGGAAAAG	0.383	
+	32	3653	_Mutation_p.M113	NM_033305	NP_150648	Q96RL7	VP13A_HUMAN		10	TTACATGGATGC	0.318	
-	4	1516	_p.R458*|KIF27_u	NM_017576	NP_060046	Q86VH2	KIF27_HUMAN		5	TTCCTCGAAATG	0.463	
-	9	2126	ri.1_Missense_Mu	NM_004560	NP_004551	Q01974	ROR2_HUMAN	Potential).|Protein kinase.	20	ATCGGCGGCAT	0.567	
+	30	3090		NM_001855	NP_001846	P39059	COFA1_HUMAN	ical region 6 (NC6).	6	CCGTCCGACCA	0.493	
-	2	131	bd.3_Missense_M	NM_001127610	NP_001121082	Q14032	BAAT_HUMAN		3	CACAGGGGTAG	0.443	rs147241373
-	2	455	uc004bbl.1_5'Flan	NM_032342	NP_115718	Q9BRR3	CI125_HUMAN		0	AAGTCGGTGAC	0.582	
-	1	909		NM_006686	NP_006677	Q9Y614	ACL7B_HUMAN		1	GAGCTCGTAGT	0.632	
-	17	2405	vc.1_Missense_M	NM_003640	NP_003631	O95163	ELP1_HUMAN		7	AAAGCGACACC	0.408	
-	38	8148	ty.2_Missense_M	NM_153366	NP_699197	Q4LDE5	SVEP1_HUMAN	Sushi 20.	7	GGATGGAACTT	0.458	
-	25	3708	_Mutation_p.W11	NM_173521	NP_775792	Q5VXU9	CI084_HUMAN		2	TCTTTCCAGTA	0.363	
+	2	319	nuw.2_Missense_	NM_017688	NP_060158	Q5W0U4	BSPRY_HUMAN		1	CGGACGTCCTG	0.458	
+	7	929	hp.2_Missense_M	NM_152786	NP_689999	Q8TAL5	CI043_HUMAN		0	AACACGAGTAG	0.473	rs148106673
+	21	2967	_p.E259K|RGS3_	NM_144488	NP_652759	P49796	RGS3_HUMAN		3	TGATCGAGACG	0.532	
+	6	2059	2_Intron|COL27A1	NM_032888	NP_116277	Q8IZC6	CORA1_HUMAN	|Triple-helical region.	4	CCCACGATGGG	0.522	
-	13	3143	_uc004bir.3_Miss	NM_030767	NP_110394	Q7Z591	AKNA_HUMAN		6	TCTGCCGGAGA	0.602	
-	3	1794	f.2_Missense_Mut	NM_002160	NP_002151	P24821	TENA_HUMAN	EGF-like 11.	7	GCGGCCGTGCT	0.587	rs149285218
-	20	3522	se_Mutation_p.R	NM_198187	NP_937830	O75129	ASTN2_HUMAN	tential).|Fibronectin type-II	9	GCTTCGACCAG	0.512	
+	1	888		NM_001005234	NP_001005234	Q8NH93	OR1L3_HUMAN	lasmic (Potential).	1	GACATGAAACG	0.363	
-	7	1011	nww.2_Missense_	NM_002721	NP_002712	O00743	PPP6_HUMAN		2	ACAACGATAGC	0.403	
+	10	1948	p.S541L|GAPVD1	NM_015635	NP_056450	Q14C86	GAPD1_HUMAN		4	GCTTTCGGATG	0.373	rs139685989
+	3	177	e_Mutation_p.R3	NM_030914	NP_112176	Q9BTM9	URM1_HUMAN		0	ACATCCGGAAC	0.527	
+	11	1034	p.R249Q|FUBP3_	NM_003934	NP_003925	Q96I24	FUBP3_HUMAN	KH 3.	1	GGATCGGTGTC	0.532	
+	4	529	_p.L140F|C9orf9_	NM_018956	NP_061829	Q96E40	CI009_HUMAN	p.?(1)	0	TCAGCCTCATC	0.617	
+	4	428	e_Mutation_p.A1	NM_017586	NP_060056	Q9UGQ2	FLOWR_HUMAN	ical; (Potential).	0	GATGGCGGTCG	0.637	
+	3	463	cfc.1_Missense_	NM_002957	NP_002948	P19793	RXRA_HUMAN	ating (By similarity).	2	ACCCCGTCAGC	0.627	rs137938878
-	12	1731		NM_181701	NP_859052	Q6ZRP7	QSOX2_HUMAN		1	GTTGTCGCGGC	0.582	
+	5	459	CA_uc010nbl.2_M	NM_015160	NP_055975	Q10713	MPPA_HUMAN		0	TGTATGCTGTG	0.577	
-	4	3958	w.2_Missense_Mu	NM_014866	NP_055681	O15027	SC16A_HUMAN	plasmic reticulum localizati	0	GGGCTCGGGAT	0.642	
-	5	865		NM_017617	NP_060087	P46531	NOTC1_HUMAN		856	TACGCGCCTGT	0.622	
-	1	490	_5'Flank|NDOR1_	NM_053045	NP_444273	Q969S6	TM203_HUMAN	ical; (Potential).	0	GGACCGTAAGT	0.602	
+	12	1571	es.1_Missense_M	NM_014434	NP_055249	Q9UHB4	NDOR1_HUMAN		0	CTGCCGCTGGC	0.597	
+	4	569	mg.1_Missense_	NM_006088	NP_006079	P68371	TBB2C_HUMAN		1	GATCCGGGAGG	0.597	
-	6	787		NM_138462	NP_612471	Q96E35	ZMY19_HUMAN	MYND-type.	1	GCAGCGCCCAC	0.607	

+	4	1084	3P5_uc010ncq.2_3'UTR						0	TTCCCCGACAAC	0.512	rs147421666
-	13	1856	Mutation_p.G506D	NM_004192	NP_004183	O95671	ASML_HUMAN	ASMT-like.	0	TCCTTGCCTTCA	0.642	
-	7	8087		NM_015419	NP_056234	Q9NR99	MXRA5_HUMAN	like C2-type 11.	8	GGTTATGATACT	0.632	
+	3	182		NM_016562	NP_057646	Q9NYK1	TLR7_HUMAN		5	CTTATCCTTTTTA	0.353	
+	7	919	_p.T196M|GLRA2_	NM_001118885	NP_001112357	P23416	GLRA2_HUMAN	cellular (Probable).	2	GGTACACGATGA	0.383	
-	7	958	B11_uc010nes.1_	NM_080873	NP_543149	Q8WXH4	ASB11_HUMAN	SOCS box.	3	ATAGGAGGAATC	0.493	rs145057594
+	1	161	11mjr.1_Translatior	NM_000444	NP_000435	P78562	PHEX_HUMAN		3	AACCACGAAAA	0.517	
+	1	2193		NM_001013736	NP_001013758	Q5HY64	FA47C_HUMAN		3	ATCTCTGCCCG	0.637	
-	4	308	_p.R72C|SSX3_u	NM_021014	NP_066294	Q99909	SSX3_HUMAN	RAB-related.	0	TATTACGCATGA	0.398	
-	5	1038	v.2_Missense_Mut	NM_017602	NP_060072	Q96G74	OTUD5_HUMAN	OTU.	1	CTAACACGAATG	0.512	
-	23	4030	ion_p.R1099H|KD	NM_004187	NP_004178	P41229	KDM5C_HUMAN		18	TGGTGCGACGC	0.607	
-	8	1292		NM_198510	NP_940912	Q6UXX5	ITH5L_HUMAN	VWFA.	6	GATACCCTGTGG	0.592	
-	13	1413	p.R256W|PFKFB1_	NM_002625	NP_002616	P16118	F261_HUMAN	-2,6-bisphosphatase.	1	TCTCCCGGTGTG	0.557	
+	4	1379	xe.2_Missense_Mu	NM_004429	NP_004420	P98172	EFNB1_HUMAN	cellular (Potential).	0	TCGGGGCTCCC	0.572	rs149648624
+	16	1830	ipl.1_Missense_Mu	NM_017711	NP_060181	Q9HCC8	GDPD2_HUMAN	lasmic (Potential).	2	AAACAGCAGTG	0.537	
+	37	5403	p.R1735H|MED12_	NM_005120	NP_005111	Q93074	MED12_HUMAN	tion with CTNNB1 and GLI	4	GGCCCCGCGCCT	0.642	
+	8	1294	RN1_uc011mpt.1_	NM_052957	NP_443189	Q96QF7	ACRC_HUMAN	Asp/Ser-rich.	3	AAGCTCCCGAC	0.557	
-	1	1012	mqj.1_Missense_M	NM_021963	NP_068798	Q9ULW6	NP1L2_HUMAN	u-rich (acidic).	1	tcctcctcctcctcct	0.323	
+	21	4226		NM_000052	NP_000043	Q04656	ATP7A_HUMAN	lasmic (Potential).	0	AGGATTCGGATA	0.343	
-	2	4825	n.2_Missense_Mut	NM_032441	NP_115817	Q5H9K5	ZMAT1_HUMAN		1	CTTTCCTGTGCTT	0.383	
+	5	4379	R1193Q|GPRASP	NM_014710	NP_055525	Q5JY77	GASP1_HUMAN	PRD1-binding.	2	TCATTCGAGATTC	0.368	
+	13	2484	mj.3_Missense_M	NM_018015	NP_060485	Q6NSI4	CX057_HUMAN		3	ATATTCGAACAT	0.398	
-	23	1989	nsn.1_Missense_M	NM_001847	NP_001838	Q14031	CO4A6_HUMAN	le-helical region.	8	CACGGGGTCCA	0.547	
-	22	1731	nsn.1_Missense_M	NM_001847	NP_001838	Q14031	CO4A6_HUMAN	le-helical region.	8	TTCTTTCCTTTG	0.512	
-	8	2020_2021	Y2F_uc011msq.1_	NM_001522	NP_001513	P51841	GUC2F_HUMAN	e.|Cytoplasmic (Potential).	8	GGTCTCCAAAAT	0.376	
-	8	2011	Y2F_uc011msq.1_	NM_001522	NP_001513	P51841	GUC2F_HUMAN	e.|Cytoplasmic (Potential).	8	ATCTCCAAGGG	0.373	
+	2	665	MEM164_uc010np	NM_032227	NP_115603	Q5U3C3	TM164_HUMAN	ical; (Potential).	3	AAGACCGTCATC	0.522	
+	3	464		NM_001004308	NP_001004308	Q6ZR62	ZCH16_HUMAN		1	AATCATCATCTA	0.468	
-	1	390		NM_001145718	NP_001139190	P0C2W7	CT47B_HUMAN		0	GGCACCATGTC	0.751	
-	1	387		NM_001145718	NP_001139190	P0C2W7	CT47B_HUMAN		0	CACCATGTCGCT	0.741	
+	7	701	ur.2_Missense_Mu	NM_000276	NP_000267	Q01968	OCRL_HUMAN		4	CCCCACCTCCAC	0.348	
+	15	1750	ur.2_Missense_Mu	NM_000276	NP_000267	Q01968	OCRL_HUMAN		4	GTTAGCGCCCTC	0.393	
+	9	4480	evc.1_Missense_M	NM_021946	NP_068765	Q5H9F3	BCORL_HUMAN	ANK 1.	7	ATGCTGGCTAC	0.567	
-	1	427		NM_016521	NP_057605	Q5H9I0	TFDP3_HUMAN	Potential.	1	AAAGACGGCAC	0.582	
+	2	586	R61C|FAM122C_	NM_138819	NP_620174	Q6P4D5	F222C_HUMAN		0	ATCGACGCTCT	0.303	
+	1	1527		NM_003413	NP_003404	O60481	ZIC3_HUMAN	Nuclear localization signal.	3	TGCCCGTTCTG	0.582	
+	17	2020	p.R565C|FMR1_u	NM_002024	NP_002015	Q06787	FMR1_HUMAN	tion with RANBP9.	3	AAAGATCGTAAC	0.433	
+	21	4345	p.1_Missense_Mut	NM_002025	NP_002016	P51816	AFF2_HUMAN		5	ACAGCAGCATGA	0.498	
-	4	724	se_Mutation_p.R7	NM_032508	NP_115897	Q8NFB2	T185A_HUMAN		1	GTGACCTGTCAT	0.328	
+	3	1731	_p.P527L|MAMLD1	NM_005491	NP_005482	Q13495	MAMD1_HUMAN		0	TGAGCCGGGTC	0.592	
+	2	944	3_5'Flank|PNMA3_	NM_013364	NP_037496	Q9UL41	PNMA3_HUMAN		3	aaagaggcggaggctg	0	
-	16	3170		NM_005334	NP_005325	P51610	HCFC1_HUMAN	TB17.|Interaction with GAE	2	GGGTCGTGACA	0.652	
-	18	2317	vkz.1_Missense_M	NM_001080484	NP_001073953	Q9C0B2	K1751_HUMAN		1	GCTCCTCCTCCT	0.697	
+	22	4128	CH2_uc001ajj.1_3	NM_014638	NP_055453	O75038	PLCH2_HUMAN		5	GGGAGGGACAC	0.667	
-	11	1360		NM_006610	NP_006601	O00187	MASP2_HUMAN	Peptidase S1.	4	GCCCTCCATATAT	0.448	
+	13	1557	TNFRSF8_uc001a	NM_001243	NP_001234	P28908	TNR8_HUMAN		5	TCAACGGTAAGT	0.577	
+	50	10145	p.T3310M|VPS13D	NM_015378	NP_056193	Q5THJ4	VP13D_HUMAN		5	GCTGCACGATGA	0.483	

+	3	1466		NM_001080830	NP_001074299	O95522	PRA12_HUMAN		3	GTCAGGGTGGAT	0.498	
+	4	1385		NM_023013	NP_075389	O95521	PRAM1_HUMAN		0	AATTGGGAGATC	0.572	
+	3	350_351		NM_001013641	NP_001013663	A0PJX8	TMM82_HUMAN	Leu-rich.	2	GGCCTCCCTGG	0.678	
-	2	412	_5'Flank|ARHGE	NM_153213	NP_694945	Q8IW93	ARHGJ_HUMAN		3	ATCCCCCCGCTG	0.682	
+	7	1452	av.1_Missense_M	NM_032880	NP_116269	Q96ID5	IGS21_HUMAN	Ig-like 2.	4	GTAGGGGACACA	0.582	
+	1	65	P3S|CNKSR1_uc0	NM_006314	NP_006305	Q969H4	CNKR1_HUMAN		2	ATGGAACCGGTA	0.637	
-	11	1662	p.E506Q|FGR_uc	NM_005248	NP_005239	P09769	FGR_HUMAN	rotein kinase.	2	GGTACTCGAAGG	0.627	
-	5	514	_p.V126L|NKAIN1	NM_024522	NP_078798	Q4KMZ8	NKAI1_HUMAN	lasmic (Potential).	1	GGAACACTTTGC	0.627	
+	7	1170	DC_uc001bww.2_	NM_052998	NP_443724	Q96A70	ADC_HUMAN		2	GTGGGTGTGAGG	0.557	
-	3	576	bw.3_Missense_	NM_001099439	NP_001092909	Q5JZY3	EPHAA_HUMAN	cellular (Potential).	8	GGTCGCCCTGCG	0.687	
+	5	785		NM_005857	NP_005848	O75844	FACE1_HUMAN		0	AAATTGGGGGT	0.348	
-	6	691	ng.2_Nonsense_M	NM_014947	NP_055762	Q9UPW0	FOXJ3_HUMAN	Fork-head.	2	TATGTCGTATGG	0.313	
+	4	528	in.2_Intron|CCDC	NM_001080850	NP_001074319	Q5VVM6	CCD30_HUMAN		0	ACAGAGGAACTC	0.299	
+	7	1135		NM_004559	NP_004550	P67809	YBOX1_HUMAN		5	AGGGCGGGGCT	0.542	
-	5	737	A9_uc009vxd.2_R	NM_201649	NP_964012	P48067	SC6A9_HUMAN		0	CATAGCCCACT	0.478	
+	10	1348	ym.2_Missense_M	NM_000779	NP_000770	P13584	CP4B1_HUMAN		2	CCGACCCTGAG	0.582	
-	4	1208	AL1_uc001cqy.2_	NM_003189	NP_003180	P17542	TAL1_HUMAN	-loop-helix motif.	1	CTTGCGGAGCT	0.567	
-	5	498	ont.1_Missense_	NM_002370	NP_002361	P61326	MGN_HUMAN		0	AATCCAATAAGA	0.378	
-	5	1627		NM_147193	NP_671726	Q8NBF1	GLIS1_HUMAN	localization signal (Potentia	1	CTTACGCACCT	0.637	rs59283679
-	2	558		NM_152268	NP_689481	Q7L3T8	SYPM_HUMAN		2	CTTCCTCGTGAG	0.522	
-	11	1844	73_uc001dgi.3_Mi	NM_001002912	NP_001002912	Q5RHP9	CA173_HUMAN	Glu-rich.	5	CTCTCTTTTCAG	0.403	
-	10	1690	73_uc001dgi.3_Mi	NM_001002912	NP_001002912	Q5RHP9	CA173_HUMAN	Glu-rich.	5	TATTTTCCTGGT	0.358	
-	27	4218		NM_000350	NP_000341	P78363	ABCA4_HUMAN	Cytoplasmic.	12	GGAAGTCCTTGT	0.607	
-	1	96	FM3_uc001dui.2_	NM_058170	NP_477518	Q96PB7	NOE3_HUMAN		3	AGCGCCAAGCT	0.547	
-	40	3380	.G1033E|COL11	NM_001854	NP_001845	P12107	COBA1_HUMAN	le-helical region.	12	GCTGGTCCATCT	0.378	
+	7	4763		NM_001408	NP_001399	Q9HCU4	CELR2_HUMAN	otential).|Laminin G-like 1.	8	GGCACCGTGCCT	0.627	rs144272839
-	8	1324	edm.2_Missense_	NM_006608	NP_006599	Q9UMS5	PHTF1_HUMAN		1	CTCCTACGCAAT	0.413	
+	8	1832	vhg.1_Missense_	NM_006699	NP_006690	O60476	MA1A2_HUMAN	nenal (Potential).	0	ATGGATCGTCCA	0.333	
+	9	994	uc010oyd.1_Intron|	NM_001037675	NP_001032764	Q3BBV1	NBPFK_HUMAN		0	GCAGTTCAGAAA	0.468	
+	2	231	1_Intron|NBPF10_	NM_001039703	NP_001034792	A6NDV3	A6NDV3_HUMAN		0	AAAGACCTCATA	0.527	
+	78	9695	BPF10_uc010oyl.1	NM_001039703	NP_001034792	A6NDV3	A6NDV3_HUMAN		0	GAAAGAGCCTGA	0.473	
+	2	302		NM_016074	NP_057158	Q9Y3E2	BOLA1_HUMAN		1	CGGTCCCGCCT	0.677	
-	3	5923		NM_002016	NP_002007	P20930	FILA_HUMAN	Ser-rich.	16	CTCTGTCTTCGT	0.567	
-	3	4937	R1486H|ASH1L_	NM_018489	NP_060959	Q9NR48	ASH1L_HUMAN		11	TGTGACGGTGC	0.502	
+	15	1966	p.G336E|NTRK1_	NM_002529	NP_002520	P04629	NTRK1_HUMAN	Potential).|Protein kinase.	17	CTGCGGGGATGG	0.642	
+	11	1749	1fyg.2_5'Flank|PP	NM_001014443	NP_001014443	Q9UK80	UBP21_HUMAN		5	CCTCGAATCCTC	0.398	
+	10	1364	cg.2_Missense_Mu	NM_001014796	NP_001014796	Q16832	DDR2_HUMAN	cellular (Potential).	6	TCTTTAAGGAGG	0.507	
+	2	915	0794_uc001gdd.2	NM_001005214	NP_001005214	Q8N7C0	LRC52_HUMAN	lasmic (Potential).	1	AGGACGAGGCC	0.572	
+	8	1827	N_uc010pmx.1_In	NM_022093	NP_071376	Q9UQP3	TENN_HUMAN	onectin type-III 4.	9	GACCAAGAGACC	0.602	
+	38	5408	1gox.1_Nonsense_	NM_000721	NP_000712	Q15878	CAC1E_HUMAN	Cytoplasmic (Potential).	6	GCGTCTGGGCAG	0.602	
+	16	3105		NM_002293	NP_002284	P11047	LAMC1_HUMAN	inin EGF-like 10.	5	GACATCCGCACC	0.532	
-	4	341		NM_014176	NP_054895	Q9NPD8	UBE2T_HUMAN		0	GAAATCGGATCT	0.343	rs149154798
-	16	2551	KHA6_uc009xau.1_	NM_014935	NP_055750	Q9Y2H5	PKHA6_HUMAN		4	CTCTGGGGGTG	0.517	
-	29	5946	A2_uc001hgy.2_5	NM_025179	NP_079455	O75051	PLXA2_HUMAN	lasmic (Potential).	3	TGTCATGGATGC	0.572	
+	12	2449		NM_016343	NP_057427	P49454	CENPF_HUMAN	Potential.	13	CATGCCGAATATG	0.428	
+	11	1282	ub.1_Missense_M	NM_016121	NP_057205	Q9Y597	KCTD3_HUMAN	WD 3.	3	CTTCTGCTTGGA	0.308	
+	8	831	ATA17_uc001hli.2	NM_138796	NP_620151	Q96L03	SPT17_HUMAN		1	CCAATCGATGAG	0.468	

-	5	704	p.R172Q|TAF1A_u	NM_139352	NP_647603	Q15573	TAF1A_HUMAN		0	TTTCCCGGGAAG	0.383	rs145721552
-	2	1211	_p.L235F|AGT_uc	NM_000029	NP_000020	P01019	ANGT_HUMAN		0	TGGGAGGACCA	0.592	
-	5	1565	u.2_RNA|PCNXL2	NM_014801	NP_055616	A6NKB5	PCX2_HUMAN		2	ACAGGGAACAC	0.577	
+	1	538	L13_uc001ids.2_I	NM_001001963	NP_001001963	Q8NGY9	OR2L8_HUMAN	cellular (Potential).	2	GTGATGTCCCA	0.473	
+	1	905	L13_uc001ids.2_I	NM_001001963	NP_001001963	Q8NGY9	OR2L8_HUMAN	lasmic (Potential).	2	GACACGAGTGA	0.473	
+	1	28	L13_uc001ids.2_I	NM_001004491	NP_001004491	Q8NG84	O2AK2_HUMAN	cellular (Potential).	2	CCTTTGATATTTT	0.189	
+	1	120		NM_001004690	NP_001004690	A3KFT3	OR2M5_HUMAN	Name=1; (Potential).	3	TTCATGGGAAA	0.522	
+	1	571		NM_017504	NP_059974	Q96R27	OR2M4_HUMAN	cellular (Potential).	2	GCACAGAAACAT	0.408	
-	1	47		NM_001004692	NP_001004692	Q8NG77	O2T12_HUMAN	cellular (Potential).	3	TGGTTAAAGAGT	0.448	
-	5	667	ion_p.R167K|ZNF	NM_017865	NP_060335	Q9BU19	ZN692_HUMAN		0	TGAGTCCTCTCAT	0.507	
-	7	736	TRM1_uc001igu.1_Missense_Mutation_p.T259M|PITRI			E7ES23	E7ES23_HUMAN		1	CGTACGTGAAG	0.393	
+	7	2716		NM_031923	NP_114129	Q5VWG9	TAF3_HUMAN	PHD-type.	1	AGATGCAGTGG	0.507	
+	6	1671	e_Mutation_p.A27	NM_019590	NP_062536	Q5T5P2	SKT_HUMAN		7	TCATTGCATATCA	0.507	
+	5	581	ivu.3_Missense_M	NM_030751	NP_110378	P37275	ZEB1_HUMAN	C2H2-type 1.	5	CCTGTCCATATT	0.318	
+	18	2515	j.1_Missense_Mut	NM_001080512	NP_001073981	Q9H694	BICC1_HUMAN		4	CCTAAGCGTAAA	0.433	
+	12	2244	PN_uc009xpt.2_M	NM_032578	NP_115967	Q86TC9	MYPN_HUMAN		5	CCTAAGGAGTTT	0.453	
+	1	100	qnu.1_Missense_M	NM_181745	NP_859529	Q5NUL3	O3FA1_HUMAN	cellular (Potential).	0	CTTGCGCAGCC	0.701	
-	13	1484	h.1_Missense_Mu	NM_003061	NP_003052	O75093	SLIT1_HUMAN	LRR 11.	4	ACAGGGAGAGC	0.587	
-	16	2001	RP12_uc010qou.1	NM_015179	NP_055994	Q5JTH9	RRP12_HUMAN		3	TTACCTGCCAC	0.592	
-	18	1868	e_Mutation_p.Q38	NM_022362	NP_071757	Q96T76	MMS19_HUMAN		0	AGCATTGGGTG	0.527	
-	4	688	sn.2_Missense_Mu	NM_024895	NP_079171	Q9H5P4	PDZD7_HUMAN	PDZ 1.	3	GCAGGCGGCTG	0.627	
-	4	773	p.L255F|SORCS1	NM_052918	NP_443150	Q8WY21	SORC1_HUMAN	nenal (Potential).	2	GATCAATAAACT	0.388	
+	12	1186	_p.P405S|ACSL5_	NM_203379	NP_976313	Q9ULC5	ACSL5_HUMAN	lasmic (Potential).	3	TGTTTCCCGCG	0.507	
-	19	3422_3423	p.M1059L|EIF3A_	NM_003750	NP_003741	Q14152	EIF3A_HUMAN	DE]-[DE]-R-[SEVGFPILV]-[	0	TCCATGCCTCG	0.629	
+	6	1247		NM_002775	NP_002766	Q92743	HTRA1_HUMAN	PDZ.	0	GCCAAAGGTAG	0.537	
-	1	332		NM_152311	NP_689524	Q8NCR9	CLRN3_HUMAN		1	CCCACGAAAAA	0.383	
+	5	609		NM_002412	NP_002403	P16455	MGMT_HUMAN		2	TGGCCGTGAAG	0.667	
-	4	734	pc.1_Nonsense_M	NM_173575	NP_775846	Q86UX6	ST32C_HUMAN	rotein kinase.	5	CATCTCGCAGAT	0.632	
+	3	578		NM_007183	NP_009114	Q9Y446	PKP3_HUMAN	p.G168G(1)	1	AGCGCGGTGGG	0.716	
-	2	230	SD_uc009yda.1_R	NM_001909	NP_001900	P07339	CATD_HUMAN		0	CCGGCGGATGG	0.617	
+	2	1063		NM_152430	NP_689643	Q8TCB6	O51E1_HUMAN	lasmic (Potential).	4	ATCCTTCGACTT	0.463	
-	1	368		NM_001005177	NP_001005177	Q8NGF1	O52R1_HUMAN	Name=1; (Potential).	1	ATATTTCCAACAA	0.522	
-	1	77		NM_000518	NP_000509	P68871	HBB_HUMAN		1	GCAGACTTCTC	0.507	rs35198910
+	1	712	_uc001mam.1_Int	NM_001004757	NP_001004757	Q8NH59	O51Q1_HUMAN	lasmic (Potential).	1	GACTCCGTGCC	0.488	
+	2	664	fd.2_RNA|SYT9_u	NM_175733	NP_783860	Q86SS6	SYT9_HUMAN	lasmic (Potential).	3	AGACGGGGATC	0.602	
-	2	806		NM_198516	NP_940918	Q6P9A2	GLTL4_HUMAN	nenal (Potential).	0	CAGGCGGTCGC	0.657	
+	18	2012	NTL_uc001mkt.2_	NM_001178	NP_001169	O00327	BMAL1_HUMAN		0	TTCTCCAGGAG	0.498	
-	9	1410	_p.R295W|PTPN5	NM_006906	NP_008837	P54829	PTN5_HUMAN	protein phosphatase.	2	TGTACCGGTTCTT	0.577	
-	5	610		NM_003476	NP_003467	P50461	CSRP3_HUMAN	I zinc-binding 2.	0	AAAGTTCCCCAT	0.478	
-	12	2669	F8_uc001mpn.3_M	NM_024680	NP_078956	A0AVK6	E2F8_HUMAN		1	AGAGCCGGGCTG	0.527	
-	10	1893	F8_uc001mpn.3_M	NM_024680	NP_078956	A0AVK6	E2F8_HUMAN		1	CACTTTCTGTCT	0.473	
-	2	361	xd.1_Missense_Mu	NM_198381	NP_938195	Q9UKW6	ELF5_HUMAN	PNT.	1	AGGCAGGGTAG	0.552	
+	2	376	-CNTF_uc010rkm.	NM_000614	NP_000605	P26441	CNTF_HUMAN		1	ATTTTACCCCAA	0.483	
+	4	379	1nni.1_Missense_Mutation_p.M1I|GLYATL1_uc001nnj.			Q969I3	GLYL1_HUMAN		1	CAGAATGATCCT	0.433	
-	6	942	om.2_Missense_M	NM_004254	NP_004245	Q8TCC7	S22A8_HUMAN	lasmic (Potential).	3	TTCGAGGACTTT	0.572	
+	3	824	N3_uc001nxp.2_I	NM_201428	NP_958831	O95197	RTN3_HUMAN		1	CAGAAACCACCT	0.408	
+	8	1042	cj.2_Missense_Mu	NM_013306	NP_037438	Q9NRS6	SNX15_HUMAN	PX.	1	TGACCCGACCCT	0.622	

-	6	1225	lodr.1_Missense_	NM_001077241	NP_001070709	Q8N413	S2545_HUMAN	e=6; (Potential).|Solcar 3.	0	AGGCGCGGGC	0.617	
-	6	1325	p.Q93E|RIN1_uc0	NM_004292	NP_004283	Q13671	RIN1_HUMAN	-3 protein binding region.	3	GCCCTGCAGCT	0.711	
+	11	1045	e_Mutation_p.L47	NM_018161	NP_060631	Q6IA69	NADE_HUMAN		2	TTTGCCCTCTCG	0.597	
+	11	4247		NM_014786	NP_055601	Q96PE2	ARHGH_HUMAN		0	ACTGCGGGACC	0.657	
-	6	1328	g.2_Missense_Mu	NM_080491	NP_536739	Q9UQC2	GAB2_HUMAN		6	TGTCCGATCGG	0.478	
+	4	546	p.N146S|NAALAD	NM_005467	NP_005458	Q9Y3Q0	NALD2_HUMAN	ellular (Potential).	2	TTACAAATATTGT	0.328	
+	4	566	p.A153S|NAALAD	NM_005467	NP_005458	Q9Y3Q0	NALD2_HUMAN	ellular (Potential).	2	TATAATGCTTTCT	0.348	
-	5	787	yvz.2_Missense_	NM_012124	NP_036256	Q9UHD1	CHRD1_HUMAN	AA1 and HSP90AB1 (By si	0	GTTTTAGGGAG	0.279	
+	9	4996		NM_001008781	NP_001008781	Q8TDW7	FAT3_HUMAN	|Extracellular (Potential).	5	GCATTTCCGTCA	0.438	
-	1	684	p.D147E|CCDC82	NM_024725	NP_079001	Q8N4S0	CCD82_HUMAN		1	CTGATCATCCTC	0.318	
-	1	918	vw.1_RNA|PGR_u	NM_000926	NP_000917	P06401	PRGR_HUMAN	ulating, Pro-Rich.	4	GAAGAGTAGCC	0.647	
-	8	1312		NM_178127	NP_835228	Q86XS5	ANGL5_HUMAN	ogen C-terminal.	1	AACTGGTATTTT	0.274	
+	10	1620	w.2_Missense_Mu	NM_000829	NP_000820	P48058	GRIA4_HUMAN	ellular (Potential).	8	TGGAATGATATG	0.358	
-	3	340	5D_uc001ppd.2_	NM_001077639	NP_001071107	Q6UWF7	FA55D_HUMAN		4	GGGAATAAGGA	0.398	
-	2	236	1prt.1_5'UTR|TM	NM_001077263	NP_001070731	Q9BYE2	TMPSD_HUMAN	toplasmic (Potential).|12 X	1	GTGTCCCAGCT	0.677	
+	4	794	.2_RNA|FOXR1_	NM_181721	NP_859072	Q6PIV2	FOXR1_HUMAN	Fork-head.	1	CAGTTCCCCCT	0.632	
-	4	383	qhi.2_Missense_	NM_001037305	NP_001032382	Q9P016	THYN1_HUMAN		0	TAGTTACGAACA	0.488	
+	6	908	_p.R183Q|GLB1L	NM_001080407	NP_001073876	Q8NCI6	GLBL3_HUMAN		1	CCCCCGGTTAC	0.567	
-	19	3040	_p.R893*|KDM5A_	NM_001042603	NP_001036068	P29375	KDM5A_HUMAN		3	TCAGTCGTGGTA	0.468	
-	12	2041	p.R619Q|CHD4_u	NM_001273	NP_001264	Q14839	CHD4_HUMAN	Chromo 2.	2	GGATTCGGTGG	0.507	
+	12	1600		NM_001080454	NP_001073923	P0C7M7	ACSM4_HUMAN		0	TTAACTCTTGAA	0.368	
+	2	294	MKLB_uc010sgl.1	NM_020734	NP_065785	Q9ULI2	RIMKB_HUMAN		0	CAGATCGTCGC	0.453	
-	31	4204	.S406F|A2M_uc0	NM_000014	NP_000005	P01023	A2MG_HUMAN		5	TTAGGGAGATT	0.448	
+	5	884	/6_uc001raa.1_5'	NM_001987	NP_001978	P41212	ETV6_HUMAN		250	GGTCCCCCCTG	0.632	
-	1	718		NM_018654	NP_061124	Q9NZD1	GPC5D_HUMAN	Name=7; (Potential).	0	GACCGGGTCGT	0.557	
-	13	4539		NM_000834	NP_000825	Q13224	NMDE2_HUMAN	lasmic (Potential).	12	ACAGGGGTTGG	0.532	
-	9	1231		NM_004963	NP_004954	P25092	GUC2C_HUMAN	ellular (Potential).	6	CTGGACCGTCA	0.448	
+	25	3607	rcy.1_Missense_M	NM_030667	NP_109592	Q16827	PTPRO_HUMAN	l).|Tyrosine-protein phosp	9	ACAGGAACATTC	0.443	
-	8	1412		NM_021957	NP_068776	P54840	GYS2_HUMAN		2	TGTTTTCGCACT	0.383	
+	2	215	SF8_uc009zjd.1_	NM_007211	NP_009142	Q8NHQ8	RASF8_HUMAN		0	GGCCGGTGCAC	0.502	
-	8	2299		NM_005164	NP_005155	Q9UBJ2	ABCD2_HUMAN	C transporter.	6	ACTTATGATAAA	0.368	
+	22	2970	_Mutation_p.R57	NM_198578	NP_940980	Q5S007	LRRK2_HUMAN		24	GAAAAAGAAAAA	0.289	
-	4	646	p.A120V|PRICKLE	NM_001144881	NP_001138353	Q96MT3	PRIC1_HUMAN	PET.	4	TGACTGCTCTG	0.522	
+	13	1648	e_Mutation_p.L6F	NM_152641	NP_689854	Q68CP9	ARID2_HUMAN	type winged-helix.	10	AATACCTCTCG	0.333	
+	15	4460	_p.P943L|ARID2_u	NM_152641	NP_689854	Q68CP9	ARID2_HUMAN		10	AGTTCCCGACT	0.458	
-	1	1180	_p.A174T|ADCY6_	NM_015270	NP_056085	O43306	ADCY6_HUMAN		0	GCGGGCGGGTG	0.652	
-	2	490	_uc001rtj.1_5'Flan	NM_018113	NP_060583	Q6UX01	LMBRL_HUMAN	.|Cytoplasmic (Potential).	1	GGTGAACTCAG	0.522	
-	2	1327		NM_001008223	NP_001008224	Q86Z23	C1QL4_HUMAN	C1q.	0	GCCCACGTCCA	0.602	
-	10	1010	.2_Missense_Mut	NM_016293	NP_057377	Q9UBW5	BIN2_HUMAN	Potential.	1	TATTTCCTCCT	0.532	
+	27	5980	c001rzb.1_5'Flan	NM_014191	NP_055006	Q9UQD0	SCN8A_HUMAN		7	GAGAAAAAAGA	0.522	
-	9	1654		NM_033045	NP_149034	Q9NSB2	KRT84_HUMAN	Tail.	1	GGCTCCACCCA	0.706	
-	4	836		NM_033448	NP_258259	Q3SY84	K2C71_HUMAN	oil 1B.|Rod.	2	GGATTCCACCTT	0.527	
-	2	208	_p.R22W|CALCO	NM_020898	NP_065949	Q9P1Z2	CACO1_HUMAN	rminal AD (CTNNB1 bindi	1	GGTCCGGGCTA	0.527	
+	50	8607		NM_002332	NP_002323	Q07954	LRP1_HUMAN	A 15.|Extracellular (Potent	22	CTGGACGTGTG	0.622	rs141905136
+	88	13934		NM_002332	NP_002323	Q07954	LRP1_HUMAN	Interaction with MAFB (By	22	TGGACGCTGAC	0.602	
+	18	2924		NM_013381	NP_037513	Q9UKU6	TRHDE_HUMAN	ellular (Potential).	3	TGGTGTCACAG	0.269	
-	6	639		NM_001321	NP_001312	Q16527	CSRP2_HUMAN	Gly-rich.	1	CCCTGCTCCTT	0.433	

+	18	2290		NM_017988	NP_060458	Q6P3W7	SCYL2_HUMAN	vith clathrin is necessary fo	6	CTTTCACTTCTGT	0.393	
+	14	1501	t.2_Missense_Mut	NM_213594	NP_998759	Q33E94	RFX4_HUMAN	ary for dimerization.	1	GCCAATGAGCTC	0.448	
-	5	1461	M4_uc001tmq.2_I	NM_012406	NP_036538	Q9UKN5	PRDM4_HUMAN		2	CTACATGACCTGT	0.468	
+	9	964	_Mutation_p.C256	NM_032663	NP_116052	Q70CQ3	UBP30_HUMAN	lasmic (Potential).	1	ACAACTGTACAA	0.507	
+	2	379	oc.2_Missense_M	NM_001093	NP_001084	O00763	ACACB_HUMAN		8	CGGTCGGCGGA	0.632	
-	11	2578		NM_000620	NP_000611	P29475	NOS1_HUMAN		7	GGTCCTTCCAC	0.507	
+	3	331		NM_176818	NP_789788	O43716	GATCL_HUMAN		0	GCGTCGTGGAG	0.463	
+	9	1263	ufq.1_Missense_	NM_012463	NP_036595	Q9Y487	VPP2_HUMAN	lasmic (Potential).	2	ACCTGCGCCGG	0.537	
+	9	1126		NM_207437	NP_997320	Q8IVF4	DYH10_HUMAN	n (By similarity).	6	CGCCATGATGAG	0.577	
-	18	2473		NM_032656	NP_116045	Q8IY37	DHX37_HUMAN		1	GTTGTCGGCTCA	0.652	
+	5	1574	NF10_uc001ulq.2_	NM_015394	NP_056209	P21506	ZNF10_HUMAN		3	AGAAACCCTATG	0.428	
+	1	2169		NM_001033602	NP_001028774	Q5JR59	MTUS2_HUMAN	teraction with MAPRE1.	0	CTGCCAACCTCT	0.552	
+	4	325	0tdr.1_Missense_	NM_001629	NP_001620	P20292	AL5AP_HUMAN	Helical.	0	CTGCTGCGTTTG	0.438	
+	11	4303		NM_000059	NP_000050	P51587	BRCA2_HUMAN		64	TATTTACTGATCA	0.328	rs80359424
-	5	808	RD13_uc001uux.2_	NM_178006	NP_821074	Q9Y3M8	STA13_HUMAN		4	GCTGACGAGTG	0.602	rs146112751
-	2	1248	se_Mutation_p.A3	NM_000053	NP_000044	P35670	ATP7B_HUMAN	ytoplasmic (Potential).	3	GCAATGGCAATC	0.562	
+	20	3690	p.R876K|LMO7_uc	NM_015842	NP_056667	Q8WWI1	LMO7_HUMAN		5	GCAAAGGGCCA	0.383	
+	13	1536	_p.S366P|IPO5_uc	NM_002271	NP_002262	O00410	IPO5_HUMAN		3	CTGCATTCCATTA	0.408	
+	1	478	0agj.2_Missense_	NM_006573	NP_006564	Q9Y275	TN13B_HUMAN	cellular (Potential).	0	TGGCCGCCCTG	0.662	
+	22	2575	qu.1_Missense_	NM_015011	NP_055826	Q9Y6X6	MYO16_HUMAN	sin head-like 1.	10	CAAGTGGAATGT	0.368	
-	27	2107	4A1_uc010agl.2_I	NM_001845	NP_001836	P02462	CO4A1_HUMAN	le-helical region.	6	CTTGGGGACCT	0.542	
-	12	1886	P1_uc010tlg.1_Mis	NM_007110	NP_009041	Q99973	TEP1_HUMAN	TROVE.	5	CTGACGGCTTA	0.488	
-	4	774		NM_017807	NP_060277	Q9NPF4	OSGEP_HUMAN		0	AGTATGCAATCA	0.453	
-	2	788	jb.2_Missense_M	NM_020834	NP_065885	Q8IX15	HOMEZ_HUMAN		0	GTAGGGGAATG	0.527	
-	4	1786	e_Mutation_p.R29	NM_032452	NP_115828	Q96JJ6	JPH4_HUMAN	lasmic (Potential).	2	GCGCCGATCTG	0.637	
-	3	679	A1_uc001wqa.2_5	NM_002515	NP_002506	P51513	NOVA1_HUMAN		5	TTTCTCGAATTTT	0.438	
-	11	2806	H5_uc001xfy.2_3'	NM_139318	NP_647479	Q8NCM2	KCNH5_HUMAN	bly) (By similarity).|Cytopla	9	TGTCCTCTTTGA	0.512	
-	11	2474	H5_uc001xfy.2_3'	NM_139318	NP_647479	Q8NCM2	KCNH5_HUMAN	lasmic (Potential).	9	CCTTTTCCATTT	0.453	
-	3	484	s.2_Missense_Mu	NM_000347	NP_000338	P11277	SPTB1_HUMAN	1.|Actin-binding.	11	CAGGCGGTGGT	0.612	
+	2	305		NM_004094	NP_004085	P05198	IF2A_HUMAN	S1 motif.	1	GAAGGCGTATCC	0.403	
-	7	1863	tua.1_Missense_	NM_203309	NP_976054				1	GGCTGGTGGCA	0.418	
-	29	4672		NM_000428	NP_000419	Q14767	LTBP2_HUMAN	TB 3.	2	GTTCCGGCCCA	0.662	rs150484024
+	1	620		NM_019589	NP_062535	P49750	YLPM1_HUMAN	Pro-rich.	3	ACATGCCCCCA	0.627	
-	9	1791	_p.R92H|C14orf10	NM_017970	NP_060440	Q9H7Z3	CN102_HUMAN		3	GGTCACGGGAA	0.557	rs149932737
+	12	2980	49M|KIAA0284_u	NM_001112726	NP_001106197	Q9Y4F5	K0284_HUMAN		1	GGAGACGGCCC	0.677	
+	13	4020	196S|KIAA0284_u	NM_001112726	NP_001106197	Q9Y4F5	K0284_HUMAN		1	ccccggcccccgggA	0.552	
+	1	77	ar.2_Missense_M	NM_001036	NP_001027	Q15413	RYR3_HUMAN	smic (By similarity).	10	TGGCCGAAGGG	0.706	
+	36	5673	r.2_Nonsense_Mu	NM_001036	NP_001027	Q15413	RYR3_HUMAN	eats.|Cytoplasmic (By simil	10	CCGCTCACCCC	0.557	
+	5	1272	p.D401Y|C15orf5	NM_175741	NP_786883	Q86Y26	NUT_HUMAN		30	TATGTTGACATC	0.587	
+	3	296	_p.E65K|TMCO5A	NM_152453	NP_689666	Q8N6Q1	TMC5A_HUMAN	Potential.	1	AGTGGGAGAAG	0.522	
+	26	7032	bt.1_Missense_Mu	NM_170589	NP_733468	Q8NG31	CASC5_HUMAN	ation and for interaction wit	5	CCATCTGTACCAT	0.378	
+	4	3112		NM_002373	NP_002364	P78559	MAP1A_HUMAN		9	TGAAGCTACGC	0.552	
+	10	1592_1593	T1B_uc001zsd.3_	NM_020990	NP_066270	P12532	KCRU_HUMAN		0	CGTCTGGAGAG	0.5	
-	30	4051	n.2_Missense_Mu	NM_014080	NP_054799	Q9NRD8	DUOX2_HUMAN	ential).|FAD-binding FR-ty	5	GTCACTCCTGGA	0.592	
-	2	572		NM_138356	NP_612365	Q7M4L6	SHF_HUMAN		1	GCCCCGGAGAC	0.662	
-	4	605		NM_003613	NP_003604	O75339	CILP1_HUMAN		7	CTTACCTGGTG	0.612	
+	15	2696	_p.R811K|DIS3L_u	NM_001143688	NP_001137160	Q8TF46	DI3L1_HUMAN		2	ACCAAGGTATGT	0.323	

-	17	1874	utation_p.N17K|u	NR_027024					0	AGCAGATTCAC	0.622
+	4	1322		NM_152259	NP_689472	Q7Z2Z1	TICRR_HUMAN		7	TGACAGCCCCC	0.493
+	6	2412	e_Mutation_p.F76	NM_145728	NP_663780	O15061	SYNEM_HUMAN	Tail.	4	GGAGTTTTCCGT	0.572
+	1	343		NM_001001674	NP_001001674	Q8NGB8	O4F15_HUMAN	Name=3; (Potential).	0	GTGCTGCTCATA	0.453
+	2	280	_p.V60M|PIGQ_u	NM_148920	NP_683721	Q9BRB3	PIGQ_HUMAN		1	TGGGCGTGGCC	0.701
-	6	1453	XL16_uc002cjb.2	NM_153350	NP_699181	Q8N461	FXL16_HUMAN	LRR 6.	0	GGAGGTGCTTC	0.642
-	20	8061	_Mutation_p.V261	NM_001009944	NP_001009944	P98161	PKD1_HUMAN	ular (Potential).|REJ.	3	CAGCACGGTGA	0.647
+	11	7425_7426	.1_Missense_Mut	NM_016333	NP_057417	Q9UQ35	SRRM2_HUMAN	-rich.|Ser-rich.	4	ACAGCCCCAGC	0.634
+	11	1698	v.1_Missense_Mu	NM_018723	NP_061193	Q9NWB1	RFOX1_HUMAN		0	GGAGGGATCTT	0.488
-	1	571		NM_144674	NP_653275	Q96M29	TEKT5_HUMAN	Potential.	2	GTTCTGGTTCT	0.612
-	7	940	dbg.1_Missense_	NM_015914	NP_056998	Q6PKC3	TXD11_HUMAN		0	CTAGGTAATCT	0.383
+	4	746	va.2_Missense_M	NM_005236	NP_005227	Q92889	XPF_HUMAN	ucine-zipper 1.	10	CCCATCGCTTG	0.333
-	40	6739	wa.2_Missense_	NM_015092	NP_055907	Q96Q15	SMG1_HUMAN		16	GGTTCCGCCCA	0.438
-	1	397		NM_015092	NP_055907	Q96Q15	SMG1_HUMAN	with SMG8 and SMG9.	16	cgccgctgcTCAGC	0.627
+	3	580	_uc010byo.1_Miss	NM_001770	NP_001761	P15391	CD19_HUMAN	ellular (Potential).	3	TCCGTGTCTCC	0.647
+	8	783	_p.V236I|TGFB1	NM_001042454	NP_001035919	O43294	TGFI1_HUMAN	zinc-binding 1.	0	ACTTCGTTTGC	0.657
-	5	527	PS35_uc002eee.	NM_018206	NP_060676	Q96QK1	VPS35_HUMAN		0	TCAAGGGATGT	0.393
+	2	558	_p.A97V|ADCY7_	NM_001114	NP_001105	P51828	ADCY7_HUMAN	ical; (Potential).	1	CTTGGCGCTGC	0.642
-	16	2264_2265	on_p.550_551SR	NM_005550	NP_005541	Q9BVG8	KIFC3_HUMAN	inesin-motor.	3	AGGCGGCTGC	0.693
+	8	1052	.E327K|CES3_uc	NM_024922	NP_079198	Q6UWW8	EST3_HUMAN		5	CCAAGGAACTC	0.537
-	14	2616	27_splice|KCTD1	NM_001100915	NP_001094385	Q17RG1	KCD19_HUMAN		1	ACATACCCACA	0.562
+	1	840	PT_uc002eun.3_I	NM_020457	NP_065190	Q96EK4	THA11_HUMAN	Ala-rich.	0	CAGCCGCAGAG	0.667
+	3	289	4_uc002eut.1_3'	NM_198443	NP_940845	Q496H8	NRN1L_HUMAN		1	CTGTCCGGAGG	0.572
+	8	1346	.1_Intron|DHX38_	NM_014003	NP_054722	Q92620	PRP16_HUMAN		1	TGGACGAGGGC	0.562
-	2	3245	X3_uc002fcl.2_In	NM_006885	NP_008816	Q15911	ZFHX3_HUMAN		4	GGCCTCGGCGG	0.567
-	2	2063	X3_uc002fcl.2_In	NM_006885	NP_008816	Q15911	ZFHX3_HUMAN	Poly-Glu.	4	cttcctcctccgcctcct	0.318
+	2	360		NM_020927	NP_065978	Q9HCJ6	VAT1L_HUMAN		1	GGTGCGACAAG	0.443
+	2	327	hg.1_Missense_M	NM_002661	NP_002652	P16885	PLCG2_HUMAN	PH.	8	CCGCTGACAAG	0.627
-	4	476	_uc010vnz.1_5'U	NM_005679	NP_005670	Q15572	TAF1C_HUMAN		1	GGTCCCGGGCA	0.672
+	4	314	p.E62Q|USP10_u	NM_005153	NP_005144	Q14694	UBP10_HUMAN	tion with p53/TP53.	0	GAATTGAGTTT	0.398
+	3	796	rf97_uc010vpz.1_	NM_001013672	NP_001013694	Q6ZQX7	CQ097_HUMAN	tandem repeat of A-L-K-G-	1	CCCGAGGCTCT	0.711
-	11	1335	su.2_Missense_M	NM_152346	NP_689559	Q8N370	LAT4_HUMAN		0	CTGCCGGTCCC	0.607
-	26	4231		NM_006445	NP_006436	Q6P2Q9	PRP8_HUMAN		6	TGGCTGTATGTA	0.512
-	13	1562		NM_002208	NP_002199	P38570	ITAE_HUMAN	Extracellular (Potential).	4	ACACGGCCCCA	0.577
+	21	2630	sn.1_Missense_M	NM_153827	NP_722549	Q8N4C8	MINK1_HUMAN		6	TGGACGAGGCC	0.642
-	11	1609	UP88_uc010cle.1	NM_002532	NP_002523	Q99567	NUP88_HUMAN		1	CAAAGGAATCT	0.463
-	6	841	th.1_Missense_M	NM_053285	NP_444515	Q969V4	TEKT1_HUMAN		2	GGATTCGATCC	0.537
+	4	498		NM_000697	NP_000688	P18054	LOX12_HUMAN	ipoxygenase.	1	GGGTTACCCCTG	0.448
-	11	2069	88_splice|NEURL	NM_032442	NP_115818	Q96JN8	NEUL4_HUMAN		2	CCTCACCCACG	0.642
+	26	3472	p.V687M|PFAS_u	NM_012393	NP_036525	O15067	PUR4_HUMAN	midotransferase type-1.	5	GTGGCGTGGCC	0.622
-	9	1022	.1_RNA|PIK3R6_	NM_001010855	NP_001010855	Q5UE93	PI3R6_HUMAN		0	CCGCGGGACCC	0.706
-	23	3018	uc002gml.1_Intron	NM_002472	NP_002463	P13535	MYH8_HUMAN	Potential.	11	GTTCTCCGTGG	0.393
-	34	5023	uc002gml.1_Intron	NM_017533	NP_060003	Q9Y623	MYH4_HUMAN	Potential.	13	CTGGCGGTTGG	0.453
-	16	1892	uc002gml.1_Intron	NM_017533	NP_060003	Q9Y623	MYH4_HUMAN	osin head-like.	13	AGCCGGCGATG	0.552
-	30	4172	uc002gml.1_Intron	NM_005963	NP_005954	P12882	MYH1_HUMAN	Potential.	21	TAGCTCGGCCT	0.592
-	15	1649	uc002gml.1_Intron	NM_005963	NP_005954	P12882	MYH1_HUMAN	osin head-like.	21	CAGGTCCATCC	0.448
-	24	3189	_Missense_Mutati	NM_001100112	NP_001093582	Q9UKX2	MYH2_HUMAN	Potential.	14	TTTGTCCTCCT	0.478

+	7	972	_p.L225I|MYOCD_	NM_153604	NP_705832	Q8IZQ8	MYCD_HUMAN		5	AGGGGCTTGGC	0.582	
+	6	974	p.E259K|RNF112_	NM_007148	NP_009079	Q7Z5V9	Q7Z5V9_HUMAN		2	GCAGGGAAACA	0.612	
-	1	395	22L|ALDH3A1_uc	NM_001135168	NP_001128640	P30838	AL3A1_HUMAN		2	GCAGCGGACGG	0.697	
+	2	420	1_Intron|WSB1_uc	NM_015626	NP_056441	Q9Y6I7	WSB1_HUMAN	WD 1.	0	TGGTCGTGAAA	0.403	
+	8	1518	ARM1_uc002hbe.1	NM_015077	NP_055892	Q6SZW1	SARM1_HUMAN		0	CGACCGCAGCA	0.657	
-	5	1363	.1_3'UTR|SLC46	NM_080669	NP_542400	Q96NT5	PCFT_HUMAN	ical; (Potential).	0	GGAACCCCTTCA	0.562	
-	2	756	EZ6_uc002hdq.1_	NM_178860	NP_849191	Q53EL9	SEZ6_HUMAN	xtracellular (Potential).	2	TCCAGGACCCT	0.642	
-	2	337	_p.P48L|SEZ6_uc	NM_178860	NP_849191	Q53EL9	SEZ6_HUMAN	ellular (Potential).	2	GCTCAGGTGTG	0.577	
+	13	1498	bf.1_Missense_M	NM_020791	NP_065842	Q7L7X3	TAOK1_HUMAN		4	GTAATCGAGAAC	0.398	
+	1	902	B_uc010ctg.2_5'F	NM_052857	NP_443089	Q96NB3	ZN830_HUMAN		1	ATTTCCGAAGCC	0.502	
-	5	923		NM_139285	NP_644814	Q8NHY3	GA2L2_HUMAN		2	CATCCTGTACCC	0.587	
+	2	224		NM_002988	NP_002979	P55774	CCL18_HUMAN		0	GTGCCCCAAGC	0.552	
+	10	1122	2_Intron|MLLT6_u	NM_005937	NP_005928	P55198	AF17_HUMAN		6	GTACTCCAAGC	0.602	
+	15	1796	37_uc010cwc.2_M	NM_005310	NP_005301	Q14451	GRB7_HUMAN	SH2.	5	TGAACCGCGGC	0.667	
-	5	959		NM_181539	NP_853517	Q7Z3Y9	K1C26_HUMAN	Rod.|Coil 2.	0	TTAATTCGGTCA	0.448	
+	1	284		NM_033061	NP_149050				0	agctgctgcaagcccc	0.199	
-	1	469		NM_031854	NP_114060	Q9BQ66	KR412_HUMAN	C-C-[GRQVIL]-[SPTR]- [V	0	ctggggcggcagcag	0.144	rs146088137
-	12	1566	gg.3_Missense_M	NM_000342	NP_000333	P02730	B3AT_HUMAN	exchange).|Helical; (Potent	3	GGCTTCCTCAA	0.612	
+	14	1650	f.1_Nonsense_Mu	NM_006178	NP_006169	P46459	NSF_HUMAN		1	GTTACTCGAGTT	0.458	
-	6	1045	RN2_uc002imf.2_	NM_138355	NP_612364	Q96FV2	SCRN2_HUMAN		1	CGTGGCGGTAA	0.597	
+	3	760	se_Mutation_p.G	NM_003110	NP_003101	Q02086	SP2_HUMAN		0	GGGCGGCAATG	0.632	
-	5	530		NM_002634	NP_002625	P35232	PHB_HUMAN		0	AAGGTCGTCGC	0.587	
+	10	840	_p.V201M|MSI2_u	NM_138962	NP_620412	Q96DH6	MSI2H_HUMAN		2	ACTTCGTGGCG	0.537	
+	1	602		NM_001004707	NP_001004707	P58180	OR4D2_HUMAN	Name=5; (Potential).	2	GATCTCCAACA	0.512	
-	1	768	_5'Flank|SEPT4_	NM_001038704	NP_001033793	Q8NEP4	CQ047_HUMAN		1	GTAGTCGTAATT	0.512	rs142981278
-	7	970	xa.3_Missense_M	NM_001005207	NP_001005207	O94972	TRI37_HUMAN	Potential.	7	GCTCATCTTTTG	0.353	
-	6	1737	_Mutation_p.D538	NM_001100875	NP_001094345	Q8NA82	MARHA_HUMAN		0	CTGAGTCTGAG	0.428	
-	5	734	dds.2_Nonsense_	NM_001100875	NP_001094345	Q8NA82	MARHA_HUMAN		0	ACTGCTGTTTCT	0.532	
-	25	3575		NM_080284	NP_525023	Q8N139	ABCA6_HUMAN	ical; (Potential).	7	AAAGAAGTAAA	0.289	
+	7	1215		NM_178160	NP_835454	Q7RTS6	OTOP2_HUMAN	ical; (Potential).	4	GTGCCGCCCTG	0.637	
+	12	1983	_p.P337L|MFSD11	NM_024311	NP_077287	O43934	MFS11_HUMAN		1	TTGCTCCTGTTA	0.463	
-	3	381	.2_Intron|LGALS3	NM_005567	NP_005558	Q08380	LG3BP_HUMAN	SRCR.	4	GTTCTCGAAGC	0.657	rs11548453
+	5	1374	wuf.1_Missense_	NM_020761	NP_065812	Q8N122	RPTOR_HUMAN		6	CCCGTCGATCT	0.542	
+	29	4248	_p.R990Q|RPTOR	NM_020761	NP_065812	Q8N122	RPTOR_HUMAN	WD 3.	6	CGTCCGGATCT	0.627	
+	10	1283	_p.T392I|BAIAP2_	NM_017451	NP_059345	Q9UQB8	BAIP2_HUMAN	SH3.	0	CAGCACCCTCC	0.617	
-	12	1416	_p.A412T|NPLOC4	NM_017921	NP_060391	Q8TAT6	NPL4_HUMAN		2	CTTGGCGTAGC	0.493	
-	23	3834	lq.2_Missense_M	NM_003803	NP_003794	P52179	MYOM1_HUMAN	like C2-type 3.	5	AACTCGGACTTT	0.413	
+	3	519	llb.1_Missense_M	NM_014214	NP_055029	O14732	IMPA2_HUMAN		2	CGACCCCATCG	0.562	
+	56	7254	us.3_Missense_M	NM_198129	NP_937762	Q16787	LAMA3_HUMAN	minin G-like 1.	11	CTGTCCCCATG	0.458	
-	15	2468	vi.3_Missense_M	NM_001941	NP_001932	Q14574	DSC3_HUMAN	lasmic (Potential).	4	ATTTTTCATTCCT	0.443	
+	11	1402		NM_005925	NP_005916	Q16820	MEP1B_HUMAN	lar (Potential).|MATH.	2	CCCTCCATTTTA	0.408	
+	12	5363	q.2_Missense_Mu	NM_030632	NP_085135	Q9C0F0	ASXL3_HUMAN		3	GATTGGGAGCC	0.517	
-	4	423		NM_133459	NP_597716	Q6UXH8	CCBE1_HUMAN		3	TCATATCGGTAT	0.512	rs115982879
+	25	3468	p.F1085L|KIAA14	NM_020854	NP_065905	Q9P260	K1468_HUMAN		6	ATGAGTGTAAG	0.393	
-	4	618	ky.1_Missense_M	NM_138966	NP_620416	Q8TDF5	NETO1_HUMAN	tracellular (Potential).	4	TTATTGGAGAAA	0.373	
+	2	89		NM_002777	NP_002768	P24158	PRTN3_HUMAN		1	AGGTGCTGCCC	0.726	
+	4	1228	wn.3_Missense_M	NM_152791	NP_690004	Q8NEP9	ZN555_HUMAN	2H2-type 8.	1	TTTATCCCCAGT	0.463	

+	8	1195	_p.T369M|NFIC_uc	NM_205843	NP_995315	P08651	NFIC_HUMAN		0	CTACGACGTCCAT	0.647	
+	1	60	10dvs.2_Translatic	NM_001144910	NP_001138382	Q9H2X3	CLC4M_HUMAN		1	CAGAGGGTGGAA	0.507	
-	22	2791		NM_032447	NP_115823	Q75N90	FBN3_HUMAN	TB 5.	11	ACTCATCCTCATC	0.647	
-	3	22655		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	ch.|Extracellular (Potential).	57	CTGGAAGTTCCA	0.478	
-	3	11903		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).	57	TGGAGGAGCTG	0.458	
-	5	772		NM_015719	NP_056534	P25940	CO5A3_HUMAN	nhelical region.	10	GCTGCCGGTGCC	0.572	
+	6	778	AM129C_uc002ng	NM_173544	NP_775815	Q86XR2	NIBL2_HUMAN		0	GCACAGCATGCC	0.637	
+	16	2515	b.1_RNA|PIK3R2_	NM_005027	NP_005018	O00459	P85B_HUMAN	SH2 2.	6	AGCACTGCGTCAT	0.677	
-	21	2740	ank|GMIP_uc010xr	NM_016573	NP_057657	Q9P107	GMIP_HUMAN		1	ACCGCCCCGGG	0.632	
+	4	1631		NM_031218	NP_112495	P35789	ZNF93_HUMAN		1	GAGAGAAACCCT	0.358	
-	5	1776	208_uc002nqo.1_I	NM_007153	NP_009084				7	TTTTGCCACATT	0.393	
+	4	1512		NM_020855	NP_065906	Q9P255	ZN492_HUMAN	C2H2-type 11.	0	ACAAATGTGAAG	0.373	
+	5	1631	p.R376W|CHST8_u	NM_001127895	NP_001121367	Q9H2A9	CHST8_HUMAN	nenal (Potential).	4	AGGACCGGCAC	0.617	
+	10	2483		NM_014686	NP_055501	O15063	K0355_HUMAN		1	ACATCCCGGTTCA	0.463	
-	8	1201	4A_uc010eee.1_5'I	NM_000704	NP_000695	P20648	ATP4A_HUMAN	lasmic (Potential).	1	GTGAGAGTCCCT	0.582	
+	14	1874	dd.2_Nonsense_M	NM_173636	NP_775907	O43379	WDR62_HUMAN	WD 9.	0	GACATCCAGATGA	0.627	
+	2	140	527_uc010xtq.1_F	NM_032453	NP_115829	Q8NB42	ZN527_HUMAN		2	CCATGTCCCAGG	0.433	
+	20	2530	jb.1_Missense_Mu	NM_004924	NP_004915	O43707	ACTN4_HUMAN	nd 2.|2 (Potential).	0	ATAGCGGCCTTGT	0.607	
+	7	723	omt.2_Missense_M	NM_178544	NP_848639	Q86UE3	ZN546_HUMAN		3	TCAATTGCAGAC	0.313	
+	2	295	Dehh.1_Missense_Mutation_p.S96F|CYP2B7P1_uc002opq.2_RNA						2	CCTTCTCTGGCC	0.627	
+	8	1214		NM_000766	NP_000757	Q16696	CP2AD_HUMAN		3	GAGACCCCAGGT	0.547	rs140896123
+	37	7093	e_Mutation_p.R176	NM_001410	NP_001401	Q7Z7M0	MEGF8_HUMAN	cellular (Potential).	1	TGTGCCGCCCTG	0.662	
-	4	1015	ouj.3_Missense_Mu	NM_182707	NP_874366	Q9UQ74	PSG8_HUMAN	-like C2-type 2.	0	TAGGGTCCTGTT	0.498	
-	4	531	obu.1_Missense_M	NM_001983	NP_001974	P07992	ERCC1_HUMAN		2	CATAGTCGGGAAT	0.617	
+	11	1096	PR_uc010xxp.1_M	NM_000164	NP_000155	P48546	GIPR_HUMAN	lasmic (Potential).	1	GCTGCCGGGAT	0.602	
-	2	445	2per.3_Missense_M	NM_018215	NP_060685	Q86V59	PNML1_HUMAN		0	tggggagaggacccca	0	
+	14	3049	xyo.1_Missense_M	NM_014681	NP_055496	Q14147	DHX34_HUMAN		5	TTCAGTCCCTCCT	0.642	
-	1	150		NM_003167	NP_003158	Q06520	ST2A1_HUMAN		2	AGAAATCGTCCGA	0.468	
+	4	1069	n.1_5'Flank|FGF21	NM_019113	NP_061986	Q9NSA1	FGF21_HUMAN		1	TCCTGCCACTACC	0.692	
-	6	1021	LEKHA4_uc010en	NM_020904	NP_065955	Q9H4M7	PKHA4_HUMAN		3	TAGTCGTCCCCCT	0.657	
+	17	2100	LD1_uc010enx.2_F	NM_002691	NP_002682	P28340	DPOD1_HUMAN		2	CCCTCCGGCGC	0.667	
+	25	3047		NM_004533	NP_004524	Q14324	MYPC2_HUMAN	onectin type-III 3.	1	TCGTGGGCAATGA	0.542	
-	3	479	se_Mutation_p.E14	NM_017509	NP_059979	Q9H2R5	KLK15_HUMAN	Peptidase S1.	2	CAGGCTCGTTGTC	0.687	
-	7	946	p.G243D|KLK5_uc	NM_001077491	NP_001070959	Q9Y337	KLK5_HUMAN	Peptidase S1.	0	GAATCACCCTGC	0.343	
-	3	248	vl.2_Missense_Mu	NM_001161748	NP_001155220	P55344	LMIP_HUMAN	ical; (Potential).	0	CAGGATCATGAAC	0.587	
-	5	1840	vdj.1_Missense_Mu	NM_001102657	NP_001096127	Q6ZNA1	ZN836_HUMAN	C2H2-type 10.	0	ATTCTCCGATGCC	0.413	
+	6	1161		NM_001099694	NP_001093164	Q96N58	ZN578_HUMAN	C2H2-type 3.	0	GCCATCGTAGATC	0.433	
+	1	788		NM_173856	NP_776255	Q8NFZ6	VN1R2_HUMAN	cellular (Potential).	0	GCAAATGGAGCA	0.418	
+	3	284	ation_p.V8L|ZIK1_u	NM_001010879	NP_001010879	Q3SY52	ZIK1_HUMAN	KRAB.	2	GCCCTTGTAGCCT	0.493	
+	4	1230		NM_152677	NP_689890	Q8NAM6	ZSCA4_HUMAN		1	AGACTTCCCAAG	0.443	
+	2	716	1_Intron|TRIM28_	NM_005762	NP_005753	Q13263	TIF1B_HUMAN	BCC domain.	3	AGGCTGCCACC	0.577	
-	3	542	DAM17_uc010exb	NM_003183	NP_003174	P78536	ADA17_HUMAN		2	AACCAACCACGT	0.438	
+	31	5696	bp.1_Missense_M	NM_014668	NP_055483	Q4ZG55	GREB1_HUMAN		1	TGCCCCGGACAC	0.652	rs34299689
+	4	554	se_Mutation_p.Y1	NM_182625	NP_872431	Q17RS7	GEN_HUMAN	I-domain.	8	TCCTTTATGGGG	0.408	
+	8	1621	_p.S513F|PLEKHH	NM_172069	NP_742066	Q8IVE3	PKHH2_HUMAN		3	TATTTTCCTATGA	0.458	
-	1	19	n|CCDC142_uc00	NM_032779	NP_116168	Q17RM4	CC142_HUMAN		1	CTGAACGTTTCGA	0.607	
+	6	578	_p.A165T|REG3G_	NM_198448	NP_940850	Q6UW15	REG3G_HUMAN	C-type lectin.	0	TGTGATGCAAAGT	0.498	

+	18	2739	ysg.1_Missense_	NM_004389	NP_004380	P26232	CTNA2_HUMAN		9	CTCCAGAGAAG	0.483	
+	12	2074	p.V583M|KDM3A_	NM_018433	NP_060903	Q9Y4C1	KDM3A_HUMAN		5	ATGGTGTGTTG	0.318	
-	2	194	4C_uc002sxg.3_5	NM_017789	NP_060259	Q9C0C4	SEM4C_HUMAN		2	CCTTGCTGCCA	0.637	
-	5	404	YG1_uc010yvo.1_	NM_174898	NP_777558	Q8N1E2	LYG1_HUMAN		0	AGCACGAACTC	0.463	
+	8	2147	e.2_Missense_Mu	NM_012455	NP_036587	Q8NDX1	PSD4_HUMAN	SEC7.	2	GGAACGGGAGC	0.602	rs149806578
+	16	2879	flu.2_Nonsense_	NM_130773	NP_570129	Q8WYK1	CNTP5_HUMAN	3.|Extracellular (Potential).	10	TTCATTCGACTC	0.289	
+	45	6147	_p.R142*|MYO7B_	NM_001080527	NP_001073996	Q6PIF6	MYO7B_HUMAN	FERM 2.	2	TCAACCGACAT	0.667	
-	14	2784	AP5_uc002ttq.2_I	NM_207363	NP_997246	O14513	NCKP5_HUMAN		0	GGGAGGTATTT	0.463	
-	53	9391		NM_018557	NP_061027	Q9NZR2	LRP1B_HUMAN	ntial).|LDL-receptor class A	50	CATTTTCATCAC	0.388	
-	5	1024	of.2_Missense_Mu	NM_145259	NP_660302	Q8NER5	ACV1C_HUMAN	.|Cytoplasmic (Potential).	7	AAGTTCCATTAT	0.313	
-	6	822	B6_uc010zcq.1_I	NM_000888	NP_000879	P18564	ITB6_HUMAN	lar (Potential).|VWFA.	3	CACTCACAAAG	0.458	
+	9	1417	_p.S376F|SCN2A_	NM_001040142	NP_001035232	Q99250	SCN2A_HUMAN	I.	8	TTTTGTCCTTATT	0.403	
-	2	355	3_5'Flank|SCN1A_	NM_006920	NP_008851	P35498	SCN1A_HUMAN	I.	13	GAAGGGAGTTA	0.353	
+	8	8564	_p.A2674V|XIRP2_	NM_152381	NP_689594	A4UGR9	XIRP2_HUMAN		14	ATCAGCACCAA	0.378	
-	70	13081		NM_004525	NP_004516	P98164	LRP2_HUMAN	ellular (Potential).	29	CCTTTTCCTTAG	0.398	
-	56	11128		NM_004525	NP_004516	P98164	LRP2_HUMAN	A 29.|Extracellular (Potent	29	AAACTGGCCCG	0.542	
+	14	1637	B_uc002ufz.2_Mi	NM_138995	NP_620482	Q8WXR4	MYO3B_HUMAN	osin head-like.	19	GAAATGATGTT	0.433	
+	6	698	fe.1_Missense_M	NM_032523	NP_115912	Q9BZF3	OSBL6_HUMAN	PH.	1	GCAGCGTTTTT	0.363	
-	307	98674	10zfi.1_Missense_	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	ATACCTTCTCAT	0.373	
-	246	50929	97D|TTN_uc010z	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	AGAAACCTTTC	0.393	
-	10	1567_1568		NM_173648	NP_775919	Q6ZP82	CC141_HUMAN		10	TAAGTGCTGAG	0.446	
-	4	337	ense_Mutation_p.	NM_001003683	NP_001003683	P54750	PDE1A_HUMAN		3	AGTCTGAATGT	0.353	
+	12	1900	p.E565K|PARD3B_	NM_152526	NP_689739	Q8TEW8	PAR3L_HUMAN	PDZ 3.	4	ACCACGAAGCT	0.473	
+	13	1432	_p.V361I|ATIC_uc	NM_004044	NP_004035	P31939	PUR9_HUMAN		29	TCATCGTAGCC	0.473	
+	4	1068		NM_006522	NP_006513	Q9Y6F9	WNT6_HUMAN		3	ACCTCCTCTAC	0.746	
+	2	470	G_uc010fwh.1_5'	NM_005876	NP_005867	Q15772	SPEG_HUMAN		14	CAGCACCCCCA	0.607	
+	12	1876	nj.2_Nonsense_M	NM_004457	NP_004448	O95573	ACSL3_HUMAN	lasmic (Potential).	2	GGATACGGGCT	0.522	
-	6	614		NM_020830	NP_065881	Q8IWB7	WDFY1_HUMAN	WD 4.	1	AACACGTGTTC	0.428	
-	4	1477	nse_Mutation_p.	NM_152527	NP_689740	Q7RTX9	MOT14_HUMAN	ical; (Potential).	6	TATGACGCCCA	0.423	
+	11	980	40L_uc010fxo.1_I	NM_138402	NP_612411	Q9H930	LY10L_HUMAN	SAND.	1	CTGTGGATTTTC	0.423	
+	1	177	UGT1A7_uc002v	NM_007120	NP_009051	P22310	UD14_HUMAN		1	TGCGGGAGCTC	0.597	
+	7	767	M8_uc010fyj.2_5'	NM_024080	NP_076985	Q7Z2W7	TRPM8_HUMAN	lasmic (Potential).	4	TTATGGATGAC	0.398	
-	19	3133	v.1_Missense_Mu	NM_022817	NP_073728	O15055	PER2_HUMAN	Pro-rich.	2	GGCCCGGGTG	0.667	
+	21	2468		NM_014808	NP_055623	O94887	FARP2_HUMAN	PH 1.	3	GCTGTACACAA	0.517	
+	2	941	HC3_uc002wdg.2_	NM_033089	NP_149080	Q9NUD5	ZCHC3_HUMAN		0	CCAGGGGGAGG	0.632	
+	3	499	_p.A47T|SIRPA_u	NM_001040022	NP_001035111	P78324	SHPS1_HUMAN	.|Extracellular (Potential).	1	TTGCAGCTGGA	0.562	
+	9	1280	l.1_Missense_Mu	NM_198994	NP_945345	O95932	TGM3L_HUMAN		4	ACGAGGATGAG	0.597	
+	4	392	se_Mutation_p.P6	NM_033453	NP_258412	Q9BY32	ITPA_HUMAN		1	GGCTCCCCGGC	0.567	
-	11	1439	wlh.1_Missense_	NM_005116	NP_005107	Q9UGH3	S23A2_HUMAN		2	GAAGCACGCCT	0.552	
+	27	2643	_p.S848L|PLCB4_	NM_182797	NP_877949	Q15147	PLCB4_HUMAN		15	TTTATCAGATC	0.348	
+	9	1233	p.V286M|PCSK2_	NM_002594	NP_002585	P16519	NEC2_HUMAN	Catalytic.	7	TCTACGTGTGG	0.682	
+	3	487		NM_033118	NP_149109	Q9H1R3	MYLK2_HUMAN		6	GGGTGGGCAAG	0.632	
-	10	5002	aw.2_Missense_M	NM_014071	NP_054790	Q14686	NCOA6_HUMAN	n.|NCOA6IP-binding region	7	TGACATCGTTAT	0.537	
+	31	6322	ve.1_Missense_M	NM_007186	NP_009117	Q9BV73	CP250_HUMAN	lu-rich.|Potential.	5	CCAGGCCCTGG	0.607	
+	9	929	270C|PLCG1_uc0	NM_182811	NP_877963	P19174	PLCG1_HUMAN		8	TTGATCGCCTC	0.602	
-	7	1055	gj.2_Missense_M	NM_007050	NP_008981	O14522	PTPRT_HUMAN	tential).|Fibronectin type-III	20	AATGGGCGTGG	0.512	
+	3	351	_p.G61S|TOX2_	NM_001098798	NP_001092268	Q96NM4	TOX2_HUMAN	iptional activation (By simil	1	CCAACGGTCTG	0.652	

+	6	951	wm.1_Missense_	NM_024034	NP_076939	Q96MZ0	GD1L1_HUMAN	ST C-terminal.	1	CAGCCGGCCCA	0.607	
+	3	518	utation_p.V132M|	NM_024331	NP_077307	Q9BTX7	TTPAL_HUMAN	CRAL-TRIO.	1	TCACCGTGCTG	0.557	
+	15	1949	C12A5_uc002xrb.	NM_001134771	NP_001128243	Q9H2X9	S12A5_HUMAN	lasmic (Potential).	5	TCCTGGGCATG	0.557	
-	2	808	_Mutation_p.R23	NM_020436	NP_065169	Q9UJQ4	SALL4_HUMAN		2	GGATGCGGATC	0.627	
+	4	464		NM_020673	NP_065724	Q9UL26	RB22A_HUMAN		0	AGTTTCGTGCC	0.343	
-	16	6139	s.1_Missense_Mu	NM_033081	NP_149072	Q9BTC0	DIDO1_HUMAN	Pro-rich.	6	CCTGGGACCTG	0.577	
-	4	1612	aaq.1_Missense_	NM_017798	NP_060268	Q9BYJ9	YTHD1_HUMAN	YTH.	2	ATTGACGCTGA	0.602	rs147453582
-	1	433		NM_001085455	NP_001078924	Q3LI83	KR241_HUMAN		0	CATTTCGAGTG	0.353	
-	30	3707	2yqg.2_Missense	NM_003895	NP_003886	O43426	SYNJ1_HUMAN	Pro-rich.	5	GAATCGTCTAC	0.438	rs145937537
+	1	728	f.1_Missense_Mu	NM_053277	NP_444507	Q96NY7	CLIC6_HUMAN	NG]- [VIM]-[DEQ]-A-[EAG]	2	GCGGAGGGCC	0.761	
-	19	2659	yzp.2_Missense_	NM_022115	NP_071398	P57071	PRD15_HUMAN		0	CTTGTCGCCGT	0.547	
-	10	1210	ol.3_Missense_M	NM_016335	NP_057419	O43272	PROD_HUMAN		1	ACTTCCGCTGC	0.622	
-	2	305	cx.2_Missense_	NM_003595	NP_003586	O60704	TPST2_HUMAN	enal (Potential).	1	CAGGCCGCATG	0.697	
-	4	462		NM_001887	NP_001878	P53674	CRBB1_HUMAN	crystallin 'Greek key' 2.	1	TGCGGTAGCTG	0.607	
+	7	1967	akv.1_Missense_	NM_001017437	NP_001017437	Q569K6	CC157_HUMAN	Potential.	1	GGCCCGTGTCG	0.662	
-	3	272	n.3_Nonsense_M	NM_014338	NP_055153	Q9UG56	PISD_HUMAN		3	CTCTCGCTCCC	0.582	
+	11	1446	_Mutation_p.R40	NM_006739	NP_006730	P33992	MCM5_HUMAN	MCM.	1	GATGCGAGAAG	0.542	rs151176258
+	7	2067	tq.1_Missense_M	NM_001039141	NP_001034230	Q9H2D6	TARA_HUMAN		1	CCCCACAACAT	0.582	
+	22	2741	H7B_uc010gyl.1_I	NM_017590	NP_060060	Q9UGR2	Z3H7B_HUMAN	C2H2-type.	1	GGGCTACCACT	0.637	
-	7	730	3bfw.1_Missense	NM_001009880	NP_001009880	Q6ICG6	K0930_HUMAN		0	GGCCACGCTCA	0.662	
-	2	314	1_uc011arm.1_Mi	NM_139202	NP_631941	Q15049	MLC1_HUMAN		1	GCATCCGGTCA	0.627	
+	8	914		NM_001080420	NP_001073889	F2Z3L0	F2Z3L0_HUMAN		1	CTTCCGTGGAG	0.587	
-	6	539	_uc003bnn.1_Miss	NM_001130922	NP_001124394	Q9UNT1	RBL2B_HUMAN		0	TATAGGTGACT	0.502	
+	1	1888	k.1_Missense_Mu	NM_152536	NP_689749	Q6ZNL6	FGD5_HUMAN		5	CTCTGGGAGTT	0.562	
-	26	2913	1_Missense_Muta	NM_015199	NP_056014	O15084	ANR28_HUMAN		1	GGCTGCGTTGG	0.323	rs149481554
+	2	497	M8_uc010hfu.2_I	NM_178868	NP_849199	Q8IZV2	CKLF8_HUMAN	MARVEL.	0	GGTCCCCGCAT	0.502	
-	23	2605	gb.2_RNA|CLASP	NM_015097	NP_055912	B2RTR1	B2RTR1_HUMAN		4	AATACGACTGC	0.468	
+	16	2296	p.A719V|PDCD6I	NM_013374	NP_037506	Q8WUM4	PDC6I_HUMAN	EIAV p9.|Self-association.	2	CATTGCCAGAG	0.328	
-	2	175	_p.P24L|HIGD1A_	NM_001099669	NP_001093139	Q9Y241	HIG1A_HUMAN	mic (Potential).|HIG1.	0	ATGAAGGAAGG	0.383	
-	2	970	mr.1_Missense_M	NM_032806	NP_116195	Q8NAT1	AGO61_HUMAN		2	GCTCACGTTCA	0.557	
-	3	1911	qv.2_Nonsense_M	NM_014159	NP_054878	Q9BYW2	SETD2_HUMAN		32	TAATCGATTTGA	0.313	rs148810823
+	8	1285	av.1_Missense_M	NM_025010	NP_079286	O94889	KLH18_HUMAN	Kelch 3.	0	TCTACGTCTGT	0.592	
-	12	6148	_Mutation_p.P202	NM_001407	NP_001398	Q9NYQ7	CELR3_HUMAN	al).|EGF-like 5; calcium-bi	11	GAGGTGGGCAG	0.667	
-	3	461_462	1_uc011bcm.1_3'	NM_000581	NP_000572	P07203	GPX1_HUMAN		1	AGGAAGGCGA	0.639	
-	8	1151	T_uc003cwy.2_M	NM_000481	NP_000472	P48728	GCST_HUMAN		1	TGGTACCCTCC	0.617	
+	3	1859		NM_004393	NP_004384	Q14118	DAG1_HUMAN	-glycosylated at seven site	2	GTATTCGCACC	0.592	
-	14	2258	BP_uc003dbf.1_5'	NM_014703	NP_055518	Q9Y4B6	VPRBP_HUMAN		2	ATACTGGATATTC	0.463	
+	2	133	TK_uc003ddn.2_	NM_145262	NP_660305	Q8IVS8	GLCTK_HUMAN		0	TGGCCCGAGCC	0.657	
-	9	1293	.R395W|TKT_uc0	NM_001135055	NP_001128527	P29401	TKT_HUMAN		2	GGCCCGCGTGA	0.627	
-	10	967	na.2_Missense_M	NM_017563	NP_060033	Q8NFM7	I17RD_HUMAN	ellular (Potential).	0	CCCACGGGGAG	0.468	rs150457965
-	2	268	oa.2_Missense_M	NM_015541	NP_056356	Q96JA1	LRIG1_HUMAN	lar (Potential).|LRR 1.	5	CAGCAGGGTCA	0.458	
-	15	2100		NM_020872	NP_065923	Q9P232	CNTN3_HUMAN	nectin type-III 1.	5	AACCCGAAATT	0.418	
+	22	4046	BO2_uc011bgk.1_	NM_002942	NP_002933	Q9HCK4	ROBO2_HUMAN	lasmic (Potential).	11	CTGTTCGAGGC	0.517	
+	10	838		NM_020202	NP_064587	Q9NQR4	NIT2_HUMAN	N hydrolase.	1	AAATACGCCAGC	0.423	
-	13	1775	C9A10_uc010hq	NM_183061	NP_898884	Q4G0N8	S9A10_HUMAN		5	AGAGACGCCTG	0.358	
-	5	857	b.1_Missense_M	NM_000796	NP_000787	P35462	DRD3_HUMAN	Cytoplasmic.	4	AGGAGCTCTGT	0.562	
-	3	563	bb.1_Missense_M	NM_000796	NP_000787	P35462	DRD3_HUMAN	lical; Name=1.	4	GGCCATTGCCG	0.622	

+	5	1122	ɔjb.1_Missense_M	NM_001125	NP_001116	P54922	ADPRH_HUMAN			1	ATGCCCCCATGA	0.577	
+	3	442		NM_016298	NP_057382	Q9UH90	FBX40_HUMAN	TRAF-type.	p.R78H(1)	5	ATGTCCCGCCAC	0.597	rs137929409
+	3	778		NM_016298	NP_057382	Q9UH90	FBX40_HUMAN			5	ACTAATGGGGAG	0.493	
-	11	2266	_p.Q389*|ADCY5_	NM_183357	NP_899200	O95622	ADCY5_HUMAN	lasmic (Potential).		4	CTACCTGCTTGG	0.602	
-	19	2274	nse_Mutation_p.G	NM_012190	NP_036322	O75891	AL1L1_HUMAN	de dehydrogenase.		4	CTCATCCCCTTC	0.537	
+	11	2084	_p.Q616*|TRPC1_	NM_003304	NP_003295	P48995	TRPC1_HUMAN			2	AGCTTTCAGTTG	0.363	
-	8	1116	53_splice|PLSCR4_	NM_001128305	NP_001121777	Q9NRQ2	PLS4_HUMAN			0	TTGACCTGGAAT	0.378	
-	6	1413	P_uc003ewz.2_Mis	NM_000096	NP_000087	P00450	CERU_HUMAN	in-like 3.|F5/8 type A 2.		1	CAGAGGGAGCA	0.403	
+	23	3394	.1_Intron|P2RY12_	NM_053002	NP_443728	Q86YW9	MD12L_HUMAN			7	GGATGCGGACG	0.512	
-	4	1799		NM_001038705	NP_001033794	Q86SP6	GP149_HUMAN	lasmic (Potential).		6	ATAGGGTTTTCC	0.453	
-	10	1753	ɔpf.1_Missense_M	NM_014498	NP_055313	O00461	GOLI4_HUMAN	-rich.|Lumenal (Potential).		5	GCGGCCGGCCC	0.418	
+	8	1344	_p.L359F|SAMD7_	NM_182610	NP_872416	Q7Z3H4	SAMD7_HUMAN	SAM.		1	AACTTTGCCATT	0.348	
+	19	2264	fhz.3_Missense_M	NM_022763	NP_073600	Q53EP0	FND3B_HUMAN	onectin type-III 5.		3	CATCGGAAAGT	0.502	
-	4	957		NM_031955	NP_114161	Q9BXB7	SPT16_HUMAN			3	CTTGACGAAGAT	0.348	rs141658177
+	5	1262	_p.R320H|NLGN1_	NM_014932	NP_055747	Q8N2Q7	NLGN1_HUMAN	cellular (Potential).		7	GTAACCGTTGGA	0.423	rs143069241
+	10	1791		NM_006218	NP_006209	P42336	PK3CA_HUMAN	PI3K helical	5)|p.E545?(19)	3553	CACTGAGCAGG	0.353	rs121913274
+	18	2309		NM_003940	NP_003931	Q92995	UBP13_HUMAN	UBA 2.		1	TCAGCGAAATC	0.408	
-	11	1204	ce|MCF2L2_uc011	NM_015078	NP_055893	Q86YR7	MF2L2_HUMAN			5	GGCTCCTGCAA	0.602	
+	11	1720	_p.G443E|ECE2_u	NM_014693	NP_055508	O60344	ECE2_HUMAN	dothelin-converting enzyme		4	CTTTGGGGTCCC	0.498	
-	6	1067	jc.2_Missense_Mu	NM_001346	NP_001337	P49619	DGKG_HUMAN	EF-hand 1.		5	TTATCCTGAGGC	0.537	
-	2	3765	C4_uc003fvp.2_Int	NM_018406	NP_060876	Q99102	MUC4_HUMAN	Ser-rich.		0	AGGTGGCGTGA	0.582	
-	14	1715	k.1_Missense_Mut	NM_005255	NP_005246	O14976	GAK_HUMAN	hatase tensin-type.		4	GTGCACGACGC	0.592	
-	7	663	_p.L188F|CRMP1_	NM_001313	NP_001304	Q14194	DPYL1_HUMAN			2	CCTTAAGGAAGG	0.428	
+	6	1197		NM_016531	NP_057615	P57682	KLF3_HUMAN			2	GAAAAACCCTAC	0.353	
+	3	314		NM_017581	NP_060051	Q9UGM1	ACHA9_HUMAN	cellular (Potential).		7	CAGTACGATGGC	0.483	
+	4	385	n_p.H16Y|UCHL1_	NM_004181	NP_004172	P09936	UCHL1_HUMAN			2	CTTATTCACGCA	0.443	
-	16	2225	p.H572R|CORIN_	NM_006587	NP_006578	Q9Y5Q5	CORIN_HUMAN	ılar (Potential).|SRCR.		2	ACATGGTGTTCT	0.453	
+	21	2954	.2_Missense_Muta	NM_000222	NP_000213	P10721	KIT_HUMAN	lasmic (Pote	p.R956Q(1)	5118	CTGTGCGGATCA	0.532	rs139694927
-	3	920	_p.E155D|UGT2B4	NM_021139	NP_066962	P06133	UD2B4_HUMAN			2	TTCCATTTCCTG	0.363	
+	9	1205	LB_uc003hgu.3_M	NM_000477	NP_000468	P02768	ALBU_HUMAN	Albumin 2.		6	ACATATGAAACC	0.388	rs76593094
-	4	392	0iik.1_Missense_M	NM_201431	NP_958834	Q6ZTQ3	RASF6_HUMAN			2	AGCATTCCTTCA	0.348	
-	2	197		NM_002619	NP_002610	P02776	PLF4_HUMAN			0	TGGGACGGACC	0.607	
-	3	315		NM_002416	NP_002407	Q07325	CXCL9_HUMAN			1	TCACCAACCTGT	0.318	
-	2	817		NM_198281	NP_938022	Q6ZVF9	GRIN3_HUMAN			3	CTGGGGATTGC	0.552	
+	6	2635	MRN1_uc011cds.1	NM_007351	NP_031377	Q13201	MMRN1_HUMAN	Potential.		4	AGATTTCCAAAA	0.333	
+	4	677	003htd.3_Missense	NM_020159	NP_064544	Q9H4L7	SMRCD_HUMAN			4	CACGTAGAAATG	0.234	
+	3	2665	ET2_uc010ilp.1_M	NM_001127208	NP_001120680	Q6N021	TET2_HUMAN	Gln-rich.		733	AGACTTTTCCTC	0.393	
+	4	654	DH_uc010ily.2_5'U	NM_005327	NP_005318	Q16836	HCDH_HUMAN			1	GCTGGCCTCCAT	0.502	
-	10	2627	ST4_uc010imw.2_	NM_022569	NP_072091	Q9H3R1	NDST4_HUMAN	eparan sulfate N-sulfotrans		4	AAAAGTCCATAT	0.338	
+	4	1193	e_Mutation_p.L43	NM_019050	NP_061923	Q70EK8	UBP53_HUMAN			4	TGCTTTCTTAATA	0.353	
-	12	2817	ef.2_Missense_Mu	NM_001130698	NP_001124170	Q13507	TRPC3_HUMAN	cellular (Potential).		2	TGCTGGGATTCA	0.378	
-	3	1070		NM_003013	NP_003004	Q96HF1	SFRP2_HUMAN	NTR.		2	CCTTCTGCCACC	0.607	
-	10	956	_p.P289L|PLRG1_	NM_002669	NP_002660	O43660	PLRG1_HUMAN	WD 3.		0	ATTGTCGGGTGC	0.373	
+	10	1553		NM_000824	NP_000815	P48167	GLRB_HUMAN	lasmic (Probable).		2	GGAAATCTCAG	0.408	
+	22	4224		NM_014247	NP_055062	Q9Y4G8	RPGF2_HUMAN			4	ATAGCACAAAGT	0.463	
+	4	1083	e_Mutation_p.P14	NM_012464	NP_036596	O43897	TLL1_HUMAN			7	GAGTTCCCAGA	0.423	
-	18	2076	iwu.1_Splice_Site_	NM_001995	NP_001986	P33121	ACSL1_HUMAN			2	CACATACCTGCA	0.468	

-	2	257		NM_005958	NP_005949	P48039	MTR1A_HUMAN	Name=2; (Potential).	5	GGTACGGATAA	0.502
+	7	1211	_p.A358E|ADAMT	NM_139056	NP_620687	Q8TE57	ATS16_HUMAN	ptidase M12B.	8	CCACGCAGACC	0.483
-	21	3514	ND2_uc011cmz.1_	NM_001332	NP_001323	Q9UQB3	CTND2_HUMAN		8	CTATACAAAGTT	0.343
-	6	666	_uc011cmy.1_Intro	NM_001332	NP_001323	Q9UQB3	CTND2_HUMAN		8	TGGTTGCTATGG	0.592
-	4	1027	DH12_uc003jgk.2_	NM_004061	NP_004052	P55289	CAD12_HUMAN	(Potential).|Cadherin 2.	2	AGGTCGGGTCA	0.403
+	3	330		NM_020227	NP_064612	Q9NQV7	PRDM9_HUMAN	RAB-related.	6	AAAACTCGCTAT	0.438
+	3	1310	_p.R308C|PDZD2_	NM_178140	NP_835260	O15018	PDZD2_HUMAN		9	ACAAACGCCGC	0.493
+	31	4603	_p.V984M|SPEF2_	NM_024867	NP_079143	Q9C093	SPEF2_HUMAN		4	ATTTGGTGACC	0.358
+	28	5864	.3_Nonsense_Mu	NM_133433	NP_597677	Q6KC79	NIPBL_HUMAN	HEAT 1.	9	CTGTTCGAACA	0.328
-	28	3314	.R1007*|NUP155_	NM_153485	NP_705618	O75694	NU155_HUMAN		1	CATTCGGACTA	0.378
+	4	1867		NM_153361	NP_699192	Q8IY84	NIM1_HUMAN		9	GGTGCCATACC	0.498
+	11	1745	.2_Missense_Mut	NM_012343	NP_036475	Q13423	NNTM_HUMAN		3	ATCTAGCCTTTT	0.507
-	10	1155	jqt.2_Missense_	NM_024669	NP_078945	Q3KP44	ANR55_HUMAN		1	GGGCCGACTGC	0.502
-	11	1004		NM_014473	NP_055288	Q9UNQ2	DIMT1_HUMAN		1	CCATGGAACGG	0.353
+	3	1808	.1_Missense_Mu	NM_152405	NP_689618	Q8N9B5	JMY_HUMAN		0	AAGCTCACATG	0.373
-	4	799		NM_001962	NP_001953	P52803	EFNA5_HUMAN		0	AACACGATCAT	0.328
+	11	944	e_Mutation_p.K29	NM_000414	NP_000405	P51659	DHB4_HUMAN	acyl-CoA dehydrogenase.	2	CTGGAAGAAGA	0.488
+	7	1459	_p.R423W|SLC22	NM_003060	NP_003051	O76082	S22A5_HUMAN	lasmic (Potential).	0	TGCCCCGGCGC	0.542
-	12	1754	8_uc003lch.2_Mi	NM_139199	NP_631938	Q9H0E9	BRD8_HUMAN		1	TCTCATCGCCTT	0.473
+	5	1560	V364M|FAM53C_	NM_001135647	NP_001129119	Q9NYF3	FA53C_HUMAN	p.V364V(1)	1	GGGCTGTGCGG	0.612
+	1	1861	DHA1_uc003lgz.	NM_018900	NP_061723	Q9Y5I3	PCDA1_HUMAN	|Extracellular (Potential).	1	GCATCCCGTTC	0.657
+	1	1867	hd.2_Intron|PCDH	NM_018906	NP_061729	Q9Y5H8	PCDA3_HUMAN	|Extracellular (Potential).	8	CGTTTCGCGTG	0.662
+	1	1229	DHA6_uc003lhn.	NM_018901	NP_061724	Q9Y5I2	PCDAA_HUMAN	|Extracellular (Potential).	5	GGACAGCGCTC	0.632
+	1	975		NM_013340	NP_037472	Q9Y5F3	PCDB1_HUMAN	|Extracellular (Potential).	0	ATGGAGAAGTT	0.463
+	1	1564	uc003lin.2_5'Flan	NM_018937	NP_061760	Q9Y5E6	PCDB3_HUMAN	(Potential).|Cadherin 5.	2	ACTACGAGGCC	0.692
+	1	1564	B16_uc010jfw.1_	NM_020957	NP_066008	Q9NRJ7	PCDBG_HUMAN	ellular (Potential).	2	AAAAGGAAATG	0.373
+	1	2096	daj.1_Missense_	NM_018931	NP_061754	Q9Y5F2	PCDBB_HUMAN	ical; (Potential).	6	TGTCTTCGCTCT	0.682
-	1	3690		NM_016580	NP_057664	Q9NPG4	PCD12_HUMAN	lasmic (Potential).	3	ATTACGCAGCG	0.622
+	8	1689	_uc011dbm.1_5'U	NM_152550	NP_689763	Q8TEC5	SH3R2_HUMAN		2	TCAAATCCGTCT	0.567
+	19	3562	.3_Missense_Mut	NM_001122679	NP_001116151				10	ACAAAGGCACT	0.582
-	2	2309		NM_052899	NP_443131	Q7Z2K8	GRIN1_HUMAN		2	CAGGGGGACCA	0.637
-	8	2959	mhu.2_Missense_	NM_019057	NP_061930	E9PET5	E9PET5_HUMAN		0	CACTGAAGCTG	0.577
+	6	928	_uc003mix.2_Miss	NM_031266	NP_112556	Q99729	ROAA_HUMAN	RRM 2.	0	TTAGTGTGAGA	0.557
-	11	1224	NRNPH1_uc003	NM_005520	NP_005511	P31943	HNRH1_HUMAN		0	GTGTTCTGAAAT	0.418
+	4	1474	EP1_uc011diq.1_	NM_002114	NP_002105	P15822	ZEP1_HUMAN		6	AGAGCGACCCT	0.398
+	7	1312		NM_001732	NP_001723	Q13410	BT1A1_HUMAN	|Cytoplasmic (Potential).	2	ATCAGGAGACA	0.517
-	11	1481	nmu.3_Missense_	NM_001470	NP_001461	Q9UBS5	GABR1_HUMAN	ellular (Potential).	7	AGAGACGCTCC	0.428
+	1	492	_5'Flank|TRIM10_	NM_033229	NP_150232	Q9C019	TRI15_HUMAN		0	CAACCCCGTCC	0.627
-	1	58	l.2_Missense_Mut	NM_002341	NP_002332	Q06643	TNFC_HUMAN	lasmic (Potential).	0	GGGAACCCCTC	0.642
+	29	3874	.1_Missense_Mut	NM_007293	NP_009224	P0C0L4	CO4A_HUMAN		0	TGCTTCACGAG	0.672
-	50	3887	se_Mutation_p.S1	NM_080680	NP_542411	P13942	COBA2_HUMAN	le-helical region.	5	CTGGAGATCCT	0.547
+	3	586	B_uc011dqu.1_5'F	NM_001077516	NP_001070984	Q92504	S39A7_HUMAN	ical; (Potential).	1	TTATCCCCGTG	0.547
-	7	1569	b.2_Missense_Mu	NM_001142883	NP_001136355	Q96PC2	IP6K3_HUMAN		0	GTGAGGATGCG	0.552
-	15	1067	D42N|CPNE5_uc	NM_020939	NP_065990	Q9HCH3	CPNE5_HUMAN	VWFA.	1	TGAAATCAATGG	0.592
+	60	9013		NM_001371	NP_001362				21	AAAACAGATTTC	0.363
-	10	1687	u.1_Missense_Mu	NM_007162	NP_009093	P19484	TFEB_HUMAN		1	GGCTGCTGGCC	0.667
-	4	1181	p.A252T|SLC35B	NM_178148	NP_835361	Q8TB61	S35B2_HUMAN		2	ACATGCGGAGC	0.582

-	4	1019	2_Intron|TMEM151	NM_182539	NP_872345	Q5JU00	TCTE1_HUMAN		4	TTGCTTCGGGTC	0.537	
+	11	1473	NAG_uc010jzt.2_R	NM_014464	NP_055279	Q9UJW2	TINAG_HUMAN		4	CATGGGGAGAG	0.403	
+	2	124		NM_001010872	NP_001010872	Q5T0W9	FA83B_HUMAN		6	TGGAGACCTCAT	0.388	
+	5	1011		NM_001010872	NP_001010872	Q5T0W9	FA83B_HUMAN		6	GAAAAGCCCTC	0.428	
+	5	2599		NM_001010872	NP_001010872	Q5T0W9	FA83B_HUMAN		6	CATCTCCTAGAAG	0.393	
+	7	804	sense_Mutation_p.	NM_001031623	NP_001026794	Q9Y4E5	ZN451_HUMAN	C2H2-type 1.	2	AGGTTCGATCAC	0.353	
+	14	2184	0kat.2_Splice_Site_	NM_019842	NP_062816	Q9NR82	KCNQ5_HUMAN		7	CTTCTAGGTACA	0.408	
+	13	2196	p.R666Q|MTO1_u	NM_133645	NP_598400	Q9Y2Z2	MTO1_HUMAN		6	CTCAACGAAGAC	0.423	
-	14	2945	12A1_uc003pht.2_	NM_004370	NP_004361	Q99715	COCA1_HUMAN	onectin type-III 6.	9	GAGCAGATGTCC	0.393	
-	13	1926		NM_001563	NP_001554	Q17R60	IMPG1_HUMAN	SEA 2.	3	GAGCTCGGTAC	0.458	
+	3	1240	p.Q102K|TPBG_u	NM_006670	NP_006661	Q13641	TPBG_HUMAN	lar (Potential).|LRR 1.	1	GCAACCAGCTG	0.721	
+	2	705	bm.2_Missense_M	NM_153362	NP_699193	Q8N3Z0	PRS35_HUMAN	Peptidase S1.	1	AAGGGAGTAAAA	0.478	
+	1	611	_p.V19M|NT5E_u	NM_002526	NP_002517	P21589	5NTD_HUMAN		4	GCGCGGTGCTG	0.701	
+	11	1103		NM_173560	NP_775831	Q8HWS3	RFX6_HUMAN		3	ACATAAGAAATT	0.308	
-	9	1071	INC1_uc003pyx.1_	NM_020755	NP_065806	Q9NRX5	SERC1_HUMAN	lasmic (Potential).	1	GAAGTACGGATG	0.323	
+	7	718	PD52L1_uc003pzy	NM_003287	NP_003278	Q16890	TPD53_HUMAN		0	GTAGGCGGTACG	0.478	
-	2	1052		NM_145176	NP_660159	Q8TD20	GTR12_HUMAN	ical; (Potential).	1	TTGGTTGGCCA	0.418	
+	4	4928	_Mutation_p.R146	NM_005100	NP_005091	Q02952	AKA12_HUMAN		8	TTGTACGTACAG	0.448	
-	78	14481	ou.3_Nonsense_M	NM_182961	NP_892006	Q8NF91	SYNE1_HUMAN	lasmic (Potential).	45	GGTCTGCCCAG	0.393	
+	7	975	jw.1_Missense_Mu	NM_032532	NP_115921	Q4ZHG4	FNDC1_HUMAN	onectin type-III 3.	8	GAGGACGAATTG	0.488	
-	37	5719		NM_005577	NP_005568	P08519	APOA_HUMAN	Peptidase S1.	6	GCCTTGAGGACC	0.502	
+	29	4793	wc.1_Missense_Mu	NM_001040001	NP_001035090	P55196	AFAD_HUMAN	Potential.	5	GCGCCGAGGAG	0.483	
-	11	1683	DR27_uc003qwy.2_Missense_Mutation_p.S261L|WDR2			A2RRH5	WDR27_HUMAN		1	GCACACGATCCG	0.547	
-	23	3210	xp.1_Missense_Mu	NM_001080453	NP_001073922	Q8N201	INT1_HUMAN		0	CAGAGGCAGGC	0.692	
+	4	1273	p.V109M|FSCN1_	NM_003088	NP_003079	Q16658	FSCN1_HUMAN		1	ATCATCGTGTTCC	0.617	
+	8	1294	uh.2_Missense_Mu	NM_178559	NP_848654	Q2M3G0	ABCB5_HUMAN	).|ABC transmembrane type	6	GTTCTGGGGACA	0.299	
+	5	971		NM_003777	NP_003768	Q96DT5	DYH11_HUMAN	n (By similarity).	15	AGCAGCTATTTT	0.388	
+	10	1310	e.1_Missense_Mu	NM_031414	NP_113602	Q9BXU1	STK31_HUMAN		9	ATAATATGGGCA	0.383	
+	8	1322		NM_002047	NP_002038	P41250	SYG_HUMAN		1	CTTTTGCTGCTG	0.398	
-	3	703	p.K167*|KIAA089	NM_001100425	NP_001093895	Q8NCT3	K0895_HUMAN		0	GAGGCTTTGGCT	0.408	
+	4	254	BE2D4_uc003tjb.1	NM_015983	NP_057067	Q9Y2X8	UB2D4_HUMAN		0	CACTTTCCTACA	0.502	
-	7	874		NM_207366	NP_997249	Q6ZU15	SEP14_HUMAN		0	TCACTTCATCTG	0.428	
-	5	1584		NM_033273	NP_150376	Q96JC4	ZN479_HUMAN	C2H2-type 10.	4	TCACATTTGTAGG	0.453	
-	4	2184		NM_015852	NP_056936	Q03924	ZN117_HUMAN		1	TCTCCACTATGA	0.363	
+	7	1198	3tvz.2_Missense_	NM_022479	NP_071924	Q6IS24	GLTL3_HUMAN	nenal (Potential).	7	GCTCTTCGCGTT	0.537	
+	6	1216	uap.2_Missense_	NM_016328	NP_057412	Q9UHL9	GT2D1_HUMAN		4	GAAGCACCTTCC	0.657	
-	6	10547	_p.R3420*|PCLO_	NM_033026	NP_149015	Q9Y6V0	PCLO_HUMAN		7	GTCCTCGGACTT	0.428	
-	2	1266	nv.2_Missense_Mu	NM_033026	NP_149015	Q9Y6V0	PCLO_HUMAN		7	GGCCCAGGCTGT	0.552	
-	11	1786	_p.S427F|ASNS_u	NM_133436	NP_597680	P08243	ASNS_HUMAN	ragine synthetase.	1	TAATAGGAAGAA	0.343	
-	21	2788	e_Mutation_p.P90	NM_007356	NP_031382	A4D0S4	LAMB4_HUMAN	minin EGF-like 8.	8	AAGAAGGATTTC	0.438	
+	12	1790	TR_uc011knq.1_5'U	NM_000492	NP_000483	P13569	CFTR_HUMAN	otential).|ABC transporter 1	5	GTCAACGAGCAA	0.338	rs121909044
+	12	3708	.2_Intron|PTPRZ1_	NM_002851	NP_002842	P23471	PTPRZ_HUMAN	cellular (Potential).	9	CTTGCTCATACC	0.403	
+	4	338	_p.D16N|ASB15_u	NM_080928	NP_563616	Q8WXK1	ASB15_HUMAN		3	AGTTATGATATTC	0.353	
+	1	543		NR_002144					0	GGCCAGGAAGC	0.602	
+	6	1768	.1_Intron|CALD1_	NM_033138	NP_149129	Q05682	CALD1_HUMAN		0	AAAAGGGAGAA	0.403	
-	2	1298	.1_5'Flank|PARP1	NM_022750	NP_073587	Q9H0J9	PAR12_HUMAN		3	AGAGTTGGCATA	0.512	
-	15	1859_1860		NM_004333	NP_004324	P15056	BRAF_HUMAN	rotein kinas_R603>I(2)|p.T	18290	GATTTCACTGTAG	0.366	rs121913378

+	13	1606		NM_004668	NP_004659	O43451	MGA_HUMAN	(Potential).|Maltase.		2	CTTTTTCACAATC	0.363	
+	23	3268	l.1_Missense_Mut	NM_198455	NP_940857	A2VEC9	SSPO_HUMAN	VWFD 3.		0	ATGGGGTGAGC	0.642	
+	5	876	C3_uc003wwv.2_	NM_006765	NP_006756	Q13454	TUSC3_HUMAN	ical; (Potential).		3	CAACTTGGAGTT	0.398	
-	8	1470	.2_Missense_Mut	NM_139278	NP_644807	Q8N145	LGI3_HUMAN	EAR 4.		1	GAGCTGCTGGAC	0.612	
+	11	1128	se_Mutation_p.H1	NM_014265	NP_055080	Q9UKQ2	ADA28_HUMAN	B.|Extracellular (Potential).		5	ATGTTTCATGAC	0.458	
+	3	2559	p.K624N|NEFM_u	NM_005382	NP_005373	P07197	NFM_HUMAN	Tail.		1	GAAAAGAAGGG	0.338	
+	27	3298		NM_001031836	NP_001027006	A8MYU2	KCNU1_HUMAN	lasmic (Potential).		1	CATTCAGACACA	0.388	
+	6	901	p.R196C|LETM2_	NM_144652	NP_653253	Q2VYF4	LETM2_HUMAN	hondrial matrix (Potential).		0	TTAGATCGCCCT	0.502	
+	12	1382	se_Mutation_p.S1	NM_001556	NP_001547	O14920	IKKB_HUMAN			7	GATCTCCCCAC	0.408	
-	5	551	lcw.1_Missense_M	NM_004198	NP_004189	Q15825	ACHA6_HUMAN	Extracellular.		0	TTTGATGATCAAA	0.363	
-	20	4148	fb.1_Missense_Mu	NM_006540	NP_006531	Q15596	NCOA2_HUMAN			16	CCATTCGGGGT	0.512	
+	13	2305	R1_uc010mch.2_	NM_018002	NP_060472	Q8N573	OXR1_HUMAN	TLD.		0	TATCCATGGACT	0.368	
-	4	621	.1_Intron|SAMD12	NM_207506	NP_997389	Q8N8I0	SAM12_HUMAN			1	CCATCCATCCA	0.423	
-	6	1049		NM_003184	NP_003175	Q6P1X5	TAF2_HUMAN			6	ATGTATGGATCTA	0.353	
-	15	2240	dt.2_Missense_M	NM_004519	NP_004510	O43525	KCNQ3_HUMAN			5	TCCTCCTTCTTC	0.532	
-	13	2173	M135B_uc003yva	NM_015912	NP_056996	Q49AJ0	F135B_HUMAN			9	GAGTTCCTCCT	0.527	
-	7	1158	p.R100Q|CYP11B	NM_000497	NP_000488	P15538	C11B1_HUMAN			3	CCACTCGCTCC	0.602	
-	5	627	AH_uc003zat.1_5'	NM_017570	NP_060040	O14841	OPLA_HUMAN			0	ATGCCTCGAGAT	0.677	
+	6	632	.2_RNA|ADCK5_	NM_174922	NP_777582	Q3MIX3	ADCK5_HUMAN	rotein kinase.		1	GGCCCTCCCCC	0.637	
-	1	263	TR|APTX_uc003z	NM_175072	NP_778242	Q7Z2E3	APTX_HUMAN	with ADPRT and NCL.		1	TGCTTCCAAATG	0.468	
-	28	3305	p.F819L|UBAP2_	NM_018449	NP_060919	Q5T6F2	UBAP2_HUMAN			3	TGTAGGAATGG	0.652	
+	12	4678	SC2_uc003zwx.3_	NM_014806	NP_055621	Q8N2Y8	RUSC2_HUMAN	SH3.		1	TCCTACGAGTG	0.642	
-	2	1001_1002		NM_001163	NP_001154	Q02410	APBA1_HUMAN	c-18-1 binding.		1	CCGTCGGAGCG	0.713	
+	5	751		NM_015110	NP_055925	Q8IY18	SMC5_HUMAN	Potential.		3	AAATATCACTGT	0.368	
-	9	1337	c.1_Nonsense_M	NM_017662	NP_060132	Q9BX84	TRPM6_HUMAN	lasmic (Potential).		8	AATTTGGAAAAG	0.383	
-	5	445	nsc.1_Missense_	NM_000197	NP_000188	P37058	DHB3_HUMAN			0	GCATTCCGACAT	0.388	
+	5	1847	ag.1_Missense_M	NM_006981	NP_008912	Q92570	NR4A3_HUMAN			173	GAGGTCGTCTGC	0.458	
-	2	131	bd.3_Missense_M	NM_001127610	NP_001121082	Q14032	BAAT_HUMAN			3	CACAGGGGTAG	0.443	rs147241373
+	3	917	n_p.V58I|ZNF462_	NM_021224	NP_067047	Q96JM2	ZN462_HUMAN			5	CGCCCGTATCA	0.507	
+	6	531	rf6_uc010mtr.2_R	NM_017832	NP_060302	Q9NX38	CI006_HUMAN			1	AGTTGTGTTAC	0.363	
+	6	558	rf6_uc010mtr.2_R	NM_017832	NP_060302	Q9NX38	CI006_HUMAN			1	GTAAAAGCATAA	0.368	
-	38	8148	ty.2_Missense_M	NM_153366	NP_699197	Q4LDE5	SVEP1_HUMAN	Sushi 20.		7	GGATGGAACTT	0.458	
-	47	5534		NM_001080398	NP_001073867					0	TTGTCCGGACC	0.418	rs145249965
-	25	3708	_Mutation_p.W11	NM_173521	NP_775792	Q5VXU9	CI084_HUMAN			2	GTCTTTCCAGTA	0.363	
-	20	4079	A1234V|AKNA_uc	NM_030767	NP_110394	Q7Z591	AKNA_HUMAN			6	ACCCCGCCTGC	0.632	
+	2	1320	TN2_uc004bjt.1_I	NM_001099679	NP_001093149	Q13049	TRI32_HUMAN	NHL 1.		3	TAGTCGCTGAC	0.493	
+	11	1817	mf.1_Missense_M	NM_000962	NP_000953	P23219	PGH1_HUMAN			2	GACGGCCACAC	0.562	
+	1	888		NM_001005234	NP_001005234	Q8NH93	OR1L3_HUMAN	lasmic (Potential).		1	GACATGAAACG	0.363	
-	4	788	nse_Mutation_p.A	NM_001100588	NP_001094058	Q9HBD1	RC3H2_HUMAN			4	GACAGCGGCCC	0.478	
-	7	1011	nww.2_Missense_	NM_002721	NP_002712	O00743	PPP6_HUMAN			2	ACAACGATAGC	0.403	
+	10	1948	p.S541L|GAPVD1	NM_015635	NP_056450	Q14C86	GAPD1_HUMAN			4	GCTTTCGGATG	0.373	rs139685989
+	7	1267	zv.2_Missense_Mu	NM_005157	NP_005148	P00519	ABL1_HUMAN	rotein kinase.		817	CCGACGTCTGG	0.507	
-	22	3059	1_uc011mcq.1_M	NM_000368	NP_000359	Q92574	TSC1_HUMAN	Potential.	p.?(1)	14	CGGCCTGCAGC	0.448	
-	6	880		NM_138462	NP_612471	Q96E35	ZMY19_HUMAN			1	ATGCTGGAAGG	0.647	
+	41	5895	coi.2_Missense_M	NM_000718	NP_000709	Q00975	CAC1B_HUMAN	lasmic (Potential).		6	GAGTTCCACCT	0.592	
+	3	493	XD1_uc011mgx.1_	NM_018390	NP_060860	Q9NUJ7	PLCX1_HUMAN	I-PLC X-box.		0	CGCACGAGGAG	0.622	
+	3	536	XD1_uc011mgx.1_	NM_018390	NP_060860	Q9NUJ7	PLCX1_HUMAN	I-PLC X-box.		0	GCCCTGCATCA	0.637	

-	7	8087		NM_015419	NP_056234	Q9NR99	MXRA5_HUMAN	like C2-type 11.		8	GGTTATGATACT	0.632	
+	3	182		NM_016562	NP_057646	Q9NYK1	TLR7_HUMAN			5	CTTATCCTTTTTA	0.353	
-	5	683	SB9_uc010ner.2_	NM_001031739	NP_001026909	Q96DX5	ASB9_HUMAN	ANK 4.		0	CACGTGGCCTG	0.453	
-	7	958	B11_uc010nes.1_	NM_080873	NP_543149	Q8WXH4	ASB11_HUMAN	SOCS box.		3	TAGGAGGAATC	0.493	rs145057594
+	5	494	yn.2_Missense_M	NM_003159	NP_003150	O76039	CDKL5_HUMAN	rotein kinase.		6	TTCGTCGGAGG	0.383	
+	3	246	lv.1_Missense_Mu	NM_173357	NP_775493					0	TGAAATTCTCG	0.408	
-	56	8018	sn.2_Missense_Mu	NM_031407	NP_113584	Q7Z6Z7	HUWE1_HUMAN			17	GGGTGAGACGA	0.587	
-	8	1292		NM_198510	NP_940912	Q6UXX5	ITH5L_HUMAN	VWFA.		6	ATACCCTGTGG	0.592	
-	20	3235	se_Mutation_p.R1	NM_201599	NP_963893	Q14202	ZMYM3_HUMAN			1	GTCCCGGGAGC	0.537	
+	8	952	RN1_uc011mpt.1_	NM_052957	NP_443189	Q96QF7	ACRC_HUMAN	Asp/Ser-rich.		3	CCGACGACAAC	0.473	
+	8	1294	RN1_uc011mpt.1_	NM_052957	NP_443189	Q96QF7	ACRC_HUMAN	Asp/Ser-rich.		3	AAGCTCCCGAC	0.557	
-	30	6839	.E2165K|ATRX_u	NM_000489	NP_000480	P46100	ATRX_HUMAN	case C-terminal.		30	TAAGCTCATTCA	0.393	
-	7	928	Mutation_p.R241H|	NM_007052	NP_008983	Q9Y5S8	NOX1_HUMAN	tase.|Extracellular (Potenti		1	ACTTGCGAGGA	0.498	rs35242502
-	22	1731	sn.1_Missense_M	NM_001847	NP_001838	Q14031	CO4A6_HUMAN	le-helical region.		8	TTCTTTCCTTTG	0.512	
+	3	464		NM_001004308	NP_001004308	Q6ZR62	ZCH16_HUMAN			1	AATCATCATCTA	0.468	
+	4	511		NM_173798	NP_776159	Q6PEW1	ZCH12_HUMAN			1	CCGGCGGCTGA	0.493	
+	13	1621	e_Mutation_p.T45	NM_018666	NP_061136	Q9NXZ1	SAGE1_HUMAN			3	CATTACTCACA	0.448	
+	17	2020	.R565C|FMR1_u	NM_002024	NP_002015	Q06787	FMR1_HUMAN	tion with RANBP9.		3	AAGATCGTAAC	0.433	
+	2	3807	fqm.1_Missense_	NM_032973	NP_116755	Q9BZA8	PC11Y_HUMAN	lasmic (Potential).		0	GTTTCTGACTGT	0.458	
-	13	1636	vkz.1_Missense_M	NM_001080484	NP_001073953	Q9C0B2	K1751_HUMAN			1	CAGCCGCTCCA	0.642	
+	9	1378		NM_015215	NP_056030	Q9Y6Y1	CMTA1_HUMAN			9	TGATGGGGAGC	0.642	
-	9	686	bew.2_Missense_	NM_002885	NP_002876	P47736	RPGP1_HUMAN			3	AGATGGGGATG	0.592	
+	3	376	_Missense_Mutati	NM_005839	NP_005830	Q8IYB3	SRRM1_HUMAN	toplasmic accumulation.|N		3	GCCTTGGATAA	0.338	
-	11	1603	p.S486Y|FGR_uc	NM_005248	NP_005239	P09769	FGR_HUMAN	rotein kinase.		2	ACAGGGATGCT	0.592	
+	3	1183		NM_018053	NP_060523	Q9H6D3	XKR8_HUMAN			0	GCTGCCTCAGA	0.577	
+	10	1288	ogj.1_Missense_M	NM_022164	NP_071447	Q9GZM7	TINAL_HUMAN			0	TGAGCCTTGGG	0.567	
+	29	5117	e_Mutation_p.P16	NM_015112	NP_055927	Q6P0Q8	MAST2_HUMAN			11	CCATCCCTCCT	0.632	
-	3	692	GBL4_uc001crv.1	NM_024603	NP_078879	Q7L4P6	BEND5_HUMAN	Potential.		1	AGCTTCTTGGC	0.607	
-	1	389_390	ddy.2_Missense_	NM_001018067	NP_001018077	Q8NC51	PAIRB_HUMAN			1	CTGGGGGGCA	0.634	
-	6	867		NM_002053	NP_002044	P32455	GBP1_HUMAN			2	GTTTCATCTTTTT	0.303	
-	24	3451	E4DIP_uc001elm.	NM_014644	NP_055459	Q5VU43	MYOME_HUMAN			5	CTCAAGGCAAA	0.493	
+	10	2038	KRD35_uc010oy	NM_144698	NP_653299	Q8N283	ANR35_HUMAN	Potential.		5	AGAGGGAGCTA	0.612	
+	11	1550	_p.E419*|SNX27_	NM_030918	NP_112180	Q96L92	SNX27_HUMAN			3	TGCATGAGTGC	0.418	
+	2	1053		NM_001025231	NP_001020402	Q5T749	KPRP_HUMAN	Pro-rich.		5	CTCCCCGTGCT	0.637	rs147332234
-	4	451		NM_052891	NP_443123	Q96LB9	PGRP3_HUMAN			4	ATAAGGCAGCA	0.512	
+	20	2176		NM_020452	NP_065185	P98198	AT8B2_HUMAN	lasmic (Potential).		2	TGACGGATGAC	0.562	
-	3	635	.2_Intron|SLAMF	NM_033438	NP_254273	Q96A28	SLAF9_HUMAN	.|Extracellular (Potential).		1	TATCCCCCCGG	0.577	
-	3	541		NM_005717	NP_005708	O15511	ARPC5_HUMAN			0	CAGACGGGCTC	0.338	rs144388879
-	5	732	.1_Intron|FAM129	NM_052966	NP_443198	Q9BZQ8	NIBAN_HUMAN			4	AGCCTCGTGGA	0.582	
+	6	1075	D4_uc010prl.1_R	NM_181644	NP_857595	Q8N468	MFSD4_HUMAN			3	TTCCGCCTTCG	0.627	
+	7	1238	m.2_RNA|KCNK2_	NM_001017425	NP_001017425	O95069	KCNK2_HUMAN	ed for basal channel activit		0	TCCAGCGGGCC	0.547	
-	54	11020		NM_206933	NP_996816	O75445	USH2A_HUMAN	ential).|Fibrc	p.R3545W(1)	26	TCCCCGAAAAC	0.383	rs145718329
+	18	4537	m.2_Missense_Mu	NM_198551	NP_940953	Q5JRA6	MIA3_HUMAN	ic (Potential).|Potential.		5	GACTGGAAGAT	0.403	
-	1	256		NM_001005487	NP_001005487	Q8NGZ3	O13G1_HUMAN	ellular (Potential).		1	TATTTTCTGATGT	0.488	
+	2	292		NM_002216	NP_002207	P19823	ITIH2_HUMAN			3	AAATTTCAATTG	0.318	
-	4	723		NM_000242	NP_000233	P11226	MBL2_HUMAN	-type lectin.		1	AATCTTCATCAG	0.488	
-	2	672		NM_001308	NP_001299	P15169	CBPN_HUMAN	Catalytic.		4	GGCAGCAGCCA	0.572	

+	1	337		NM_001005172	NP_001005172	Q8NGK3	O52K2_HUMAN	Name=3; (Potential).	2	ATCATGGAGTCA(	0.522	
-	2	95		NM_054030	NP_473371	Q96LB1	MRGX2_HUMAN	:ellular (Potential).	1	TGGTTGGATCCA	0.453	
+	6	1128	nuc.2_Missense_N	NM_001077242	NP_001070710	Q96QD5	DEPD7_HUMAN		2	CAGCTCCTTCTA/	0.333	
-	10	2118	_p.R500Q|SLC1A2	NM_004171	NP_004162	P43004	EAA2_HUMAN		3	GCACTCGATGCT	0.443	
+	1	593		NM_001005275	NP_001005275	Q8NGL6	O4A15_HUMAN	:ellular (Potential).	2	CTGTGGACCCA,	0.423	
-	1	585		NM_001005489	NP_001005489	Q8NGF7	OR5BH_HUMAN	Name=5; (Potential).	3	AAGAATCAACTC,	0.373	
+	4	328	n_p.P14L|POU2F3	NM_014352	NP_055167	Q9UKI9	PO2F3_HUMAN		2	GGAAACCAAATG	0.517	
-	4	798	B4_uc001qzf.1_Int	NM_006249	NP_006240	Q04118	PRB3_HUMAN	PQS]-P-[PS]-Q-[GE]-G-N-[(	1	TGTTACCTTCTTG	0.607	
-	5	629	:ion_p.E118K|END	NM_006025	NP_006016	P21128	ENDOU_HUMAN		3	TGTCTTCCTTCTG	0.507	
-	1	150		NM_004693	NP_004684	O95678	K2C75_HUMAN	3ly-rich.|Head.	0	CCACTCCCTGCT(	0.672	
-	6	604		NM_006741	NP_006732	Q13522	PPR1A_HUMAN	ion with PPP1R15A.	0	CTCTCTCGTGAG	0.542	
+	2	1126		NM_021191	NP_067014	Q9HD90	NDF4_HUMAN		4	CCTTATGAGGGC(	0.498	
+	2	702		NM_004416	NP_004407	Q86Y01	DTX1_HUMAN	WWE 2.	4	CTACGATATGGA(	0.622	
-	17	3262	wn.1_Missense_Mu	NM_000620	NP_000611	P29475	NOS1_HUMAN	avodoxin-like.	7	TTTGGGAGTCA(	0.572	
+	2	48	SNORD102_uc001	NM_000982	NP_000973	P46778	RL21_HUMAN		0	AATGACGAACA(	0.418	
-	5	275	tion_p.S28F|NDRC	NM_201540	NP_963834	Q9UN36	NDRG2_HUMAN		2	CCACAGAGTGA(	0.567	
+	20	2723	ybs.1_Nonsense_N	NM_020818	NP_065869	Q9P2D8	UNC79_HUMAN	p.W880*(1)	17	GACTGGAAGAT(	0.488	
+	15	1659		NM_152327	NP_689540	Q96M32	KAD7_HUMAN		1	ACCTTCCTGAG/	0.527	
+	8	996	e_Mutation_p.G18	NM_001112726	NP_001106197	Q9Y4F5	K0284_HUMAN		1	GGGGCGGAGCG	0.622	
-	7	840	zba.2_Missense_N	NM_000814	NP_000805	P28472	GBRB3_HUMAN	:ellular (Probable).	5	AGTGACAGTCGA	0.433	
-	8	1068	19A1_uc001zzb.2_	NM_031226	NP_112503	P11511	CP19A_HUMAN		3	ATTCTTCCAGTTT	0.388	
+	9	1405	Fz.1_Missense_Mu	NM_013243	NP_037375	Q8WXD2	SCG3_HUMAN		1	TTGGATGAAATG/	0.313	rs137873046
-	2	1308		NM_004498	NP_004489	Q9UBC0	HNF6_HUMAN	Homeobox.	0	GGACATCTGTGA/	0.453	
-	9	2813		NM_003613	NP_003604	O75339	CILP1_HUMAN		7	TGGCCATGCTAA	0.547	rs149553691
-	7	1430		NM_002833	NP_002824	P43378	PTN9_HUMAN	protein phosphatase.	2	TGTCTTCATATTC	0.478	
-	13	2759	bla.2_Missense_N	NM_144572	NP_653173	Q9UPU7	TBD2B_HUMAN	p.D903N(1)	3	CGCGTCGGTTC	0.617	rs117285325
-	5	323	ll.1_Intron|CTSH_u	NM_148979	NP_683880	P09668	CATH_HUMAN		3	TTCAGCAAAGCT	0.343	
-	2	146	cyh.2_RNA|NAGPA	NM_016256	NP_057340	Q9UK23	NAGPA_HUMAN	ienal (Potential).	0	GCGCGCGTGGA	0.766	
+	9	1323	teih.2_Nonsense_N	NM_001043	NP_001034	P23975	SC6A2_HUMAN	Name=8; (Potential).	8	ATTCTGGGCTGT	0.532	
-	3	354	nse_Mutation_p.E9	NM_032821	NP_116210	Q4G0P3	HYDIN_HUMAN		2	AGAGTTCGATGAT	0.468	
-	26	2903	_p.S379L|WDR59_	NM_030581	NP_085058	Q6PJI9	WDR59_HUMAN		2	TGGACGATCCC(	0.622	
-	21	3330	fhh.2_Missense_N	NM_003791	NP_003782	Q14703	MBTP1_HUMAN	ienal (Potential).	2	ACCTGGGCGCC	0.532	
-	5	1133	xa.2_Missense_M	NM_002275	NP_002266	P19012	K1C15_HUMAN	Rod.|Coil 2.	0	CTGGATCATTTCT	0.592	
-	1	643	P_uc010wfs.1_Intr	NM_000226	NP_000217	P35527	K1C9_HUMAN	Rod.|Linker 1.	3	CAGGTCCCTTCT	0.478	
-	17	3209	_p.P720S|BZRAP1	NM_004758	NP_004749	O95153	RIMB1_HUMAN		3	GTGATGGGCTCA(	0.687	
-	18	2499	m.2_Missense_Mu	NM_020748	NP_065799	Q9H0H0	INT2_HUMAN		3	AGAATTCTCCGT(	0.368	
-	9	1840	zp.2_Missense_Mu	NM_005121	NP_005112	Q9UHV7	MED13_HUMAN		2	TATTGAGGTGGG/	0.413	
-	6	465	se_Mutation_p.E4(	NM_001009905	NP_001009905	Q67FW5	B3GNL_HUMAN		2	ATCGTTCGGTGG.	0.562	rs151094014
-	1	827	TEC_uc010xaj.1_F	NM_001137671	NP_001131143	B2RU33	POTEC_HUMAN		3	CGCTGTCGTCGT.	0.607	
+	8	1073		NM_001944	NP_001935	P32926	DSG3_HUMAN	|Extracellular (Potential).	9	ACTGATCCTAGA/	0.348	
+	2	850	C_uc010xdr.1_5'U	NM_005215	NP_005206	P43146	DCC_HUMAN	Potential).|Ig-like C2-type 1.	17	ATGAAAGGAAGC/	0.483	
+	25	4255	of.1_Missense_Mut	NM_005215	NP_005206	P43146	DCC_HUMAN	lasmic (Potential).	17	GAGGTCGCTGG	0.517	
-	10	1357_1358	_p.P225L|TCF4_u	NM_003199	NP_003190	P15884	ITF2_HUMAN		2	GACTGTGGAATAT	0.505	
-	3	967	m.3_Missense_Mu	NM_006566	NP_006557	Q15762	CD226_HUMAN	2.|Extracellular (Potential).	0	GAGGTCGATCT(	0.512	
-	32	5206	w.2_Missense_Mu	NM_002850	NP_002841	Q13332	PTPRS_HUMAN	lasmic (Potential).	4	TGCGTGCGGGCA	0.627	
+	20	2605	850_splice|SAFB_	NM_002967	NP_002958	Q15424	SAFB1_HUMAN		3	CTTCCAGGTGG(	0.627	
-	5	478	ı.2_5'UTR|TIMM44	NM_006351	NP_006342	O43615	TIM44_HUMAN		1	CGGCCGACTGC	0.607	

-	3	13372		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).	57	:TGTTTGGGTGG	0.458	
+	7	1330	e.3_Missense_Mut	NM_032497	NP_115886	Q9BR84	ZN559_HUMAN		1	:AGCCCTTTTTGT	0.388	
-	4	394		NM_001105578	NP_001099048	Q6PIF2	SYCE2_HUMAN		0	GCTTTTCCTGGAT	0.428	
-	2	339	:no.1_Missense_M	NM_001008701	NP_001008701	O94910	LPHN1_HUMAN		5	GACGGCGGTGA	0.677	
-	12	1953	nao.1_Missense_M	NM_000435	NP_000426	Q9UM47	NOTC3_HUMAN	GF-like 16; calcium-binding	21	GGGTTGCTGGCA	0.582	
+	1	524		NM_001004466	NP_001004466	Q8NGA6	O10H5_HUMAN	:ellular (Potential).	1	AGATCCACCATT	0.602	
+	1	526		NM_001004466	NP_001004466	Q8NGA6	O10H5_HUMAN	:ellular (Potential).	1	ATCCACCATTTCT	0.602	
+	12	2149	xqv.1_Nonsense_I	NM_017660	NP_060130	Q86YP4	P66A_HUMAN		0	GACCGCCAGCGA	0.657	
+	4	1624		NM_031218	NP_112495	P35789	ZNF93_HUMAN		1	:ATACTGGAGAG/	0.353	
+	7	600	_p.Y137H|SUPT5H	NM_001111020	NP_001104490	O00267	SPT5H_HUMAN		4	GAGTATTACATG/	0.587	
-	31	14440		NM_003890	NP_003881	Q9Y6R7	FCGBP_HUMAN		9	:ACTCAGGGCCC	0.657	
-	5	1028	0ejp.1_Missense_	NM_001102597	NP_001096067	Q6UY09	CEA20_HUMAN	Potential).|Ig-like C2-type 3.	2	GCTCAAGGGGCT	0.557	
-	7	2429	_p.L785I|NLRP7_u	NM_206828	NP_996611	Q8WX94	NALP7_HUMAN		3	:TTTGAGGACAT/	0.527	
+	1	218		NM_001105569	NP_001099039	A6NI15	MSGN1_HUMAN		1	CGGCGGGGCCA	0.632	
-	12	1879	UM2_uc010yjy.1_I	NM_015317	NP_056132	Q8TB72	PUM2_HUMAN	Ser-rich.	1	GACTTGGAGAG	0.463	
+	3	272		NM_019617	NP_062563	Q9NS71	GKN1_HUMAN	BRICHOS.	1	CAACGGATGGG/	0.373	
-	3	576	_p.P49S|EDAR_uc	NM_022336	NP_071731	Q9UNE0	EDAR_HUMAN	.|Extracellular (Potential).	1	:ACACGGGGGGC	0.627	
-	8	3123	_Mutation_p.R918	NM_025052	NP_079328	Q56UN5	YSK4_HUMAN		5	TATATCCTGAGCC	0.398	
-	8	1520	_p.W438*|PLA2R1_	NM_007366	NP_031392	Q13018	PLA2R_HUMAN	Potential).|C-type lectin 2.	3	CCAATCCATGTTT	0.338	
+	7	1133	_p.S372F|XIRP2_u	NM_152381	NP_689594	A4UGR9	XIRP2_HUMAN		14	AAAGTCTGCCC/	0.378	
+	4	811	ufi.1_Missense_Mu	NM_144711	NP_653312	Q8NBE8	KLH23_HUMAN	BACK.	0	AGGAATCTCGAA	0.373	
-	46	16617	'N_uc010zfi.1_Intr	NM_133379	NP_596870	Q8WZ42	TITIN_HUMAN		153	ATCCCCGACAGAT	0.408	
+	27	3702	nv.2_Missense_Mu	NM_000885	NP_000876	P13612	ITA4_HUMAN	ical; (Potential).	6	TAGTGATTATTTC	0.313	
-	42	3058	frx.2_Missense_M	NM_000393	NP_000384	P05997	CO5A2_HUMAN		2	:CCGCAGGTCCT	0.577	
-	3	972		NM_005259	NP_005250	O14793	GDF8_HUMAN		1	:AGCATCGTGATT	0.418	
+	37	9014		NM_005876	NP_005867	Q15772	SPEG_HUMAN	otein kinase 2.	14	CAAGCGGCGGG	0.647	
+	1	338	/uq.3_Intron|UGT1	NM_021027	NP_066307	O60656	UD19_HUMAN		5	AAGCACAAGTAC	0.353	
-	3	299	xox.2_Missense_M	NM_181510	NP_852611	Q8IUA0	WFDC8_HUMAN	WAP 1.	0	GGTATTCCTTGCA	0.478	
+	6	770	op.1_Missense_Mu	NM_001794	NP_001785	P55283	CADH4_HUMAN	|Extracellular (Potential).	6	GGACATGAATGG	0.607	
-	69	9465		NM_005560	NP_005551	O15230	LAMA5_HUMAN	minin G-like 3.	3	GGCGAAGGAAG	0.682	
-	15	1763		NM_002772	NP_002763	P98073	ENTK_HUMAN	lar (Potentia p.D578N(1)	8	CTACATCGTTAAT	0.308	
-	1	160		NM_181617	NP_853648	Q3LI59	KR212_HUMAN		0	gccagagccgtatcca	0.169	rs144960846
+	42	5564	p.P1820L|TTC3_u	NM_001001894	NP_001001894	P53804	TTC3_HUMAN		9	GAAGCCCTGTGG	0.587	
+	6	724	yxz.2_Missense_M	NM_007341	NP_031367	P55822	SH3BG_HUMAN	u-rich (acidic).	0	GAGGAGGAGGAA	0.453	
+	1	745	.1_Intron|C21orf29	NM_181688	NP_859016	P60014	KR10A_HUMAN		0	GTGTTTCCCTCCT	0.682	
+	22	3086	_p.Y922H|SGSM1_	NM_001039948	NP_001035037	Q2NKQ1	SGSM1_HUMAN	ab-GAP TBC.	5	ATCGGCTATGTCC	0.473	
-	2	1321	GCP6_uc010has.1_	NM_020461	NP_065194	Q96RT7	GCP6_HUMAN		4	GACTGGGAATCA	0.597	
+	1	2373	'k.1_Missense_Mu	NM_152536	NP_689749	Q6ZNL6	FGD5_HUMAN		5	TTCCTGCCCTTG	0.547	
-	16	2419	wf.1_Missense_M	NM_002292	NP_002283	P55268	LAMB2_HUMAN	minin IV type B.	3	GAGTAGGGAGTC	0.547	
-	16	3618	e_Mutation_p.P10	NM_016247	NP_057331	Q9BZV3	IMPG2_HUMAN	otif involved in chondroitin	3	TGAAGGGACTCT	0.323	
-	16	3582	se_Mutation_p.L99	NM_016247	NP_057331	Q9BZV3	IMPG2_HUMAN	involved in chondroitin sulf	3	:TTGGAGAGTCCT	0.413	
+	25	3307	1bky.1_Missense_I	NM_052989	NP_443715	Q9HBG6	IF122_HUMAN		2	AAAGTCCATTGA	0.617	
-	8	936	_p.P153S|MRPL3_	NM_007208	NP_009139	P09001	RM03_HUMAN		0	TTCCAGGCATTTT	0.353	
+	5	1141	hvn.2_Missense_M	NM_207365	NP_997248	Q6P093	ADCL2_HUMAN		0	:AACATGATCTCT	0.383	
+	8	1467	bru.1_Missense_M	NM_004721	NP_004712	O43283	M3K13_HUMAN	rotein kinase.	3	TCTTTTCGGCAG/	0.408	
-	21	15410	nse_Mutation_p.G	NM_018406	NP_060876	Q99102	MUC4_HUMAN		0	GCTCCCCAGAG	0.612	
+	15	1782	p.W624*|LMLN_uc	NM_033029	NP_149018	Q96KR4	LMLN_HUMAN		1	ATGGCTGGATTC/	0.512	

+	5	2931	28M|RGS12_uc00	NM_198229	NP_937872	O14924	RGS12_HUMAN			1	GTTGACGGGCG	0.692
+	1	1684		NM_000798	NP_000789	P21918	DRD5_HUMAN	lasmic (Potential).		1	ACGAGGAGGAG	0.577
-	3	881	n.1_Missense_Mu	NM_020803	NP_065854	Q9P2G9	KLHL8_HUMAN			0	GGAGGGATGAA	0.438
-	7	1179	M13A_uc003hsh.	NM_014883	NP_055698	O94988	FA13A_HUMAN			2	TCTGCTGAATTC	0.458
-	6	840	e_Mutation_p.E25	NM_000667	NP_000658	P07327	ADH1A_HUMAN			2	TCATTTCCTTTAG	0.463
-	39	6365	e_Mutation_p.S19	NM_001813	NP_001804	Q02224	CENPE_HUMAN	Potential.		9	TCAGGCTTTCC	0.408
+	38	5438	3_Intron|ANK2_uc	NM_001148	NP_001139	Q01484	ANK2_HUMAN			14	AAGATGAACAG	0.507
+	8	1869	Y1A3_uc003ioz.2_	NM_000856	NP_000847	Q02108	GCYA3_HUMAN			4	TGGAGGAGGAG	0.532
+	15	3047	Mutation_p.S816L	NM_001083619	NP_001077088	P42262	GRIA2_HUMAN	lasmic (Potential).		4	AGAATTCACAGA	0.403
-	2	218	se_Mutation_p.R47	NM_031900	NP_114106	Q9BYV1	AGT2_HUMAN			4	GCATTCTGGGCT	0.438
+	20	4902	.3_Missense_Mut	NM_133433	NP_597677	Q6KC79	NIPBL_HUMAN			9	CAAGAGGAGTT	0.308
-	8	1883		NM_021072	NP_066550	O60741	HCN1_HUMAN	lasmic (Potential).		1	GATTTCGTTCT	0.418
-	11	1697	d.2_Intron|IL6ST_	NM_002184	NP_002175	P40189	IL6RB_HUMAN	tential).|Fibronectin type-III		2	TTAAATAGGTG	0.373
+	2	314	AF2_uc003jso.3_	NM_174889	NP_777549	Q8N183	MIMIT_HUMAN			0	ACTATGAAGCA	0.318
+	4	781	p.S160F|ZFYVE1	NM_001105251	NP_001098721	Q7Z3T8	ZFY16_HUMAN			0	AGATTCCTTGAT	0.348
+	3	1142	nse_Mutation_p.R	NM_182761	NP_877438	A1A519	F170A_HUMAN			1	CCTGAGGAGAT	0.343
+	11	2080	kuz.2_Missense_	NM_014031	NP_054750	Q9Y2P4	S27A6_HUMAN			0	TACAGGAAAAA	0.289
+	1	2392	A6_uc003lhn.2_I	NM_018902	NP_061725	Q9Y5I1	PCDAB_HUMAN	(Potential).|Cadherin 5.		1	ACGCGGAGAGC	0.706
+	1	2583	A7_uc003lhq.2_I	NM_018898	NP_061721	Q9H158	PCDC1_HUMAN	lasmic (Potential).		5	GGAAAGGGGAT	0.453
+	1	927		NM_001099293	NP_001092763	Q2VIQ3	KIF4B_HUMAN	inesin-motor.		1	GGATCGTCTAA	0.438
+	33	3868	lws.2_Missense_	NM_001037333	NP_001032410	Q96F07	CYFP2_HUMAN			0	AGCCACCCATC	0.522
+	2	182	L1_uc003mkn.1_	NM_145867	NP_665874	Q16873	LTC4S_HUMAN	Lumenal.		0	CTCGGCGCGCA	0.726
-	2	621	C90A_uc010jpf.2_	NM_001031713	NP_001026883	Q96AQ8	CC90A_HUMAN			0	GAAGTAGAGTT	0.453
-	4	708	dpv.1_RNA|NOTC	NM_004557	NP_004548	Q99466	NOTC4_HUMAN	r (Potential).|EGF-like 4.		22	CACAGGCATGG	0.612
-	51	3976	se_Mutation_p.P1	NM_080680	NP_542411	P13942	COBA2_HUMAN	le-helical region.		5	TGGTGGCCCTG	0.627
+	7	1464	NF8_uc011dtx.1_	NM_003958	NP_003949	O76064	RNF8_HUMAN	RING-type.		1	TCTGCTCCTACT	0.433
+	25	2627	e_Mutation_p.P52	NM_015255	NP_056070	Q8IWV8	UBR2_HUMAN			4	ACCTCCGGTGT	0.398
+	6	1014	AG_uc010jzt.2_In	NM_014464	NP_055279	Q9UJW2	TINAG_HUMAN			4	GCATCGATAGG	0.428
+	6	1656	t.2_Missense_Mut	NM_001080976	NP_001074445	Q9UL01	DSE_HUMAN			1	TTTCCCCAGCT	0.453
+	4	310	se_Mutation_p.W8	NM_000265	NP_000256	P14598	NCF1_HUMAN	PX.		1	AAGTGGTTTGA	0.677
-	22	15233		NM_033026	NP_149015	Q9Y6V0	PCLO_HUMAN			7	TCTGTCCCATCT	0.323
+	48	7282	.S2340L|TRRAP_	NM_003496	NP_003487	Q9Y4A5	TRRAP_HUMAN	action with TP53.		37	AAAATCACCAG	0.532
-	13	1698	z.2_Missense_Mu	NM_005045	NP_005036	P78509	RELN_HUMAN			19	AATAGGAAAGG	0.433
-	3	392	cv.2_Missense_M	NM_182691	NP_872633	P78362	SRPK2_HUMAN			6	TGGATGATATC	0.353
-	14	2404	vkg.3_Missense_	NM_017954	NP_060424	Q86UW7	CAPS2_HUMAN			2	CTCTTTTATCTC	0.289
-	7	616	ue.2_Missense_M	NM_001139456	NP_001132928	Q8N434	SVOPL_HUMAN	ical; (Potential).		0	GACGCGAATGA	0.612	rs143755972
-	15	1860		NM_004333	NP_004324	P15056	BRAF_HUMAN	rotein kinas	_R603>I(2)|p.T	18290	GATTTCACTGTA	0.368
+	44	5117		NM_004668	NP_004659	O43451	MGA_HUMAN	se.|Lumenal (Potential).		2	TCCAGGGTGTG	0.522
+	8	1315	1_uc003wga.2_R	NM_032534	NP_115923	A5PL33	KRBA1_HUMAN			2	GGAAAAGGGGT	0.627
+	5	1841	nse_Mutation_p.K	NM_020844	NP_065895	Q9P272	K1456_HUMAN			0	GAAAAAGAGAG	0.433
+	19	2184	ec.2_Missense_M	NM_003817	NP_003808	Q9H2U9	ADAM7_HUMAN	lasmic (Pote	p.R691H(1)	5	TAGTTCGTTACC	0.373
-	6	830	c.1_Missense_Mu	NM_001007243	NP_001007244	P49675	STAR_HUMAN	START.		1	TGTTCCCGAAG	0.617
-	6	1341	xpe.2_Missense_	NM_006749	NP_006740	Q08357	S20A2_HUMAN	ical; (Potential).		2	TGAGGGCTATG	0.517
-	15	2726	xrf.3_Missense_M	NM_014781	NP_055596	Q8TDY2	RBCC1_HUMAN			11	CTAATGAATCC	0.348
+	4	3434	.P1042L|ZFHX4_	NM_024721	NP_078997	Q86UP3	ZFHX4_HUMAN			15	TGAATCCCGAAT	0.483
-	3	616	3H_uc010mfk.1_5	NM_198488	NP_940890	Q6ZRV2	FA83H_HUMAN			3	TCATCTCATCCA	0.622
-	26	5586	zlk.2_RNA|FREM	NM_144966	NP_659403	Q5H8C1	FREM1_HUMAN	CSPG 12.		5	CTGATCGTCCT	0.458

-	1	110	sense_Mutation_p.	NM_001001790	NP_001001790	Q8N4H5	TOM5_HUMAN		0	CGGAACATCGC	0.627	
-	26	3875	.1_Intron|TRPM6_	NM_017662	NP_060132	Q9BX84	TRPM6_HUMAN	lasmic (Potential).	8	AGAGATCCTGCA	0.468	
-	3	710	1_5'UTR|IKBKAP_	NM_003640	NP_003631	O95163	ELP1_HUMAN		7	CTCTGGGAGAA	0.453	
+	1	1462	T1_uc011mei.1_5'I	NM_001080482	NP_001073951	C9J069	CI172_HUMAN		0	AAGGCCGGCGC	0.751	
+	1	1465	T1_uc011mei.1_5'I	NM_001080482	NP_001073951	C9J069	CI172_HUMAN		0	GCCGGCGCCCG	0.751	
+	4	425	rf173_uc011mev.1_Missense_Mutation_p.R138H|C9orf			Q8N7X2	CI173_HUMAN		1	TGGCCGCAGGG	0.622	rs73668205
+	4	736	lhh.2_Missense_M	NM_005676	NP_005667	P98175	RBM10_HUMAN	Poly-Glu.	5	aggaggaggatgagg	0.522	
-	4	459	_p.I121V|PSMD1	NM_002814	NP_002805	O75832	PSD10_HUMAN	nteraction with RELA.	1	AGCGATCTGGA	0.448	
+	1	1669		NM_012084	NP_036216	P49448	DHE4_HUMAN		1	CCTGGGATTGG	0.468	
-	5	804_805	adb.2_Missense_	NM_004195	NP_004186	Q9Y5U5	TNR18_HUMAN	lasmic (Potential).	0	CTCTTCCTCGG	0.713	
+	7	1329	_p.S140F|PLCH2_	NM_014638	NP_055453	O75038	PLCH2_HUMAN	I-PLC X-box.	5	CATGTCCCAGT	0.627	
+	2	367	nv.2_Missense_M	NM_138697	NP_619642	Q7RTX1	TS1R1_HUMAN	ellular (Potential).	3	TGCCAGGGCAA	0.587	
-	4	1505		NM_018948	NP_061821	Q9UJM3	ERRFI_HUMAN		1	GCGCCTCCATTT	0.438	
-	19	3038	x.1_Missense_Mu	NM_012102	NP_036234	Q9P2R6	RERE_HUMAN	Pro-rich.	2	TGGGAGCCTGC	0.692	
-	11	1214		NM_207420	NP_997303	Q6PXP3	GTR7_HUMAN	lasmic (Potential).	0	CGGTCCTCACC	0.657	
+	21	2082	_p.G601D|KIF1B_	NM_015074	NP_055889	O60333	KIF1B_HUMAN		3	CATGGGTAAAA	0.423	
-	7	928		NM_006610	NP_006601	O00187	MASP2_HUMAN	Sushi 1.	4	CCATCGGATAAG	0.507	
+	4	1430		NM_023013	NP_075389	O95521	PRAM1_HUMAN		0	TGAGGGAAGTC	0.562	
+	2	580	N_uc010obp.1_5'F	NM_015001	NP_055816	Q96T58	MINT_HUMAN	ich.|By similarity.	15	CACGAGAAGGA	0.468	
-	14	2283	_p.D69N|ARHGEF	NM_153213	NP_694945	Q8IW93	ARHGJ_HUMAN	SH3.	3	TACTACCTTCCC	0.622	rs146123988
-	3	718	_5'Flank|ARHGEF	NM_153213	NP_694945	Q8IW93	ARHGJ_HUMAN		3	AGCGCCTCCGC	0.657	
-	23	3415	yz.1_Missense_Mu	NM_017940	NP_060410	Q3BBV0	NBPF1_HUMAN	NBPF 4.	0	TTCAGGAGGAA	0.512	
-	2	140	azy.2_Missense_	NM_002403	NP_002394	P55001	MFAP2_HUMAN		0	GGCAGCTCTCA	0.607	
-	1	92		NM_152232	NP_689418	Q8TE23	TS1R2_HUMAN	ellular (Potential).	4	ATCCCCAGGCA	0.582	
-	101	14704_1470	w.1_Missense_Mu	NM_020765	NP_065816	Q5T4S7	UBR4_HUMAN		25	TTCCCGGCCTCG	0.554	
-	8	926	uc010ocy.1_Silent_	NM_201252	NP_957704				0	CAGCCGGCTCC	0.607	
+	10	1330	_p.A303V|ALPL_u	NM_000478	NP_000469	P05186	PPBT_HUMAN		5	CCGGGCCATCG	0.607	
+	13	3825	_uc001bmw.1_Mis	NM_006015	NP_006006	O14497	ARI1A_HUMAN		142	AACCAGCAGTT	0.532	
+	15	2270	TC1_uc001bnp.1_	NM_015023	NP_055838	Q8N5D0	WDTC1_HUMAN	WD 7.	2	AAGGGGATGAG	0.592	
+	2	535		NM_000911	NP_000902	P41143	OPRD_HUMAN	Name=2; (Potential).	2	GCTGGCCACCA	0.478	
+	5	617	gj.1_Missense_M	NM_022164	NP_071447	Q9GZM7	TINAL_HUMAN		0	CAGCGCCTTCT	0.592	
+	3	262	uj.2_Missense_M	NM_175852	NP_787048	P40222	TXLNA_HUMAN		2	GTCTGGGGCCC	0.567	
-	9	1616	.1_Missense_Mut	NM_198040	NP_932157	Q8IXK0	PHC2_HUMAN		1	CCTGCCCTGTC	0.607	
-	22	3480	_p.L1191F|CSMD	NM_052896	NP_443128	Q7Z408	CSMD2_HUMAN	lar (Potential).|CUB 7.	12	CTTGAGGACAT	0.423	
-	3	472	sense_Mutation_p	NM_024874	NP_079150	Q8IZA0	K319L_HUMAN	xtracellular (Potential).	2	AGAGGTGATTTT	0.512	
-	9	884	_p.P173S|MKNK1_	NM_003684	NP_003675	Q9BUB5	MKNK1_HUMAN	rotein kinase.	2	TTCTGGTTTCAG	0.358	
+	5	580	vym.2_Splice_Sit	NM_000779	NP_000770	P13584	CP4B1_HUMAN		2	CTCCAGGACAA	0.562	
+	17	2286	cp.2_Missense_M	NM_001037341	NP_001032418	Q07343	PDE4B_HUMAN		3	AGGGACACAG	0.483	
+	13	954	SGIP1_uc001dct.2	NM_032291	NP_115667	Q9BQI5	SGIP1_HUMAN	Pro-rich.	3	CACTGGAAGTA	0.403	
+	19	1895	dct.2_Missense_M	NM_032291	NP_115667	Q9BQI5	SGIP1_HUMAN		3	ACACTCTCCCT	0.433	
-	7	1242	wbk.2_Missense_	NM_030816	NP_110443	Q8N6S4	AN13C_HUMAN		0	CTCATGATGTAT	0.343	
+	12	1435		NM_033055	NP_149044	Q96MC6	HIAT1_HUMAN	ellular (Potential).	0	CAGGAGAGGCC	0.448	
+	19	2562	g.1_Missense_Mu	NM_020775	NP_065826	Q6UXG2	K1324_HUMAN	ellular (Potential).	5	CTGCAGTTCTG	0.537	
+	3	346		NM_032414	NP_115790	P58294	PROK1_HUMAN		0	TCCATGGACTTG	0.527	
-	19	2708	_p.P717S|CSDE1_	NM_001007553	NP_001007554	O75534	CSDE1_HUMAN		1	TCGAGGAGCTG	0.498	
+	5	891		NM_001767	NP_001758	P06729	CD2_HUMAN	ic (Potential).|Pro-rich.	1	CTGGTCATCGT	0.587	
+	5	990		NM_001767	NP_001758	P06729	CD2_HUMAN	ic (Potential).|Pro-rich.	1	AAGTTCACCAG	0.582	

+	9	1948	vhg.1_Nonsense_	NM_006699	NP_006690	O60476	MA1A2_HUMAN	enal (Potential).		0	AGCATGGTTGAT	0.373
-	9	1305		NM_206996	NP_996879	Q6Q759	SPG17_HUMAN			6	TGGTGGAGCTT	0.448
-	8	1366	hj.1_Missense_Mu	NM_152380	NP_689593	Q96SF7	TBX15_HUMAN			2	GCCAGGCAACG	0.567
-	30	5567		NM_024408	NP_077719	Q04721	NOTC2_HUMAN			27	TCAGCCTGAAA	0.517
-	41	7084	4DIP_uc001elm.3_	NM_014644	NP_055459	Q5VU43	MYOME_HUMAN			5	CACAGGGATGT	0.572
-	39	6670	E4DIP_uc001elm.	NM_014644	NP_055459	Q5VU43	MYOME_HUMAN			5	GAAGACCAGAG	0.517
-	36	6154	DE4DIP_uc001el	NM_014644	NP_055459	Q5VU43	MYOME_HUMAN	Potential.		5	TTTCCACCTTCT	0.542
-	3	412	DE4DIP_uc001el	NM_014644	NP_055459	Q5VU43	MYOME_HUMAN			5	AAAAGCTGTCA	0.398
+	4	1293	HFE2_uc001enk.2	NM_213653	NP_998818	Q6ZVN8	RGMC_HUMAN			1	CCCTCCAAGTC	0.572
+	10	4593	.1_Missense_Mut	NM_004326	NP_004317	O00512	BCL9_HUMAN	Pro-rich.		6	AGAATGGGACTA	0.597
+	6	1002	9wlw.2_Nonsense_	NM_019032	NP_061905	Q6UY14	ATL4_HUMAN			2	GAGCCCAGGCC	0.642
+	9	1210	e|BNIPL_uc009w	NM_138278	NP_612122	Q7Z465	BNIPL_HUMAN			0	AGACAGTGAGT	0.458
-	7	1315	Z_uc010pdc.1_Mi	NM_015100	NP_055915	Q7Z3K3	POGZ_HUMAN			3	CACCACTGGCC	0.507
-	2	1755		NM_001004432	NP_001004432	Q6UY18	LIGO4_HUMAN	ellular (Potential).		1	GCCCTGGGATC	0.587
-	3	1483		NM_001122965	NP_001116437	Q6XPR3	RPTN_HUMAN	Gln-rich.		0	AGTGGGAACTC	0.512
-	3	2572	c001ezv.2_5'Flan	NM_002016	NP_002007	P20930	FILA_HUMAN	Ser-rich.		16	TGACCCCGGGT	0.582
-	3	528		NM_014624	NP_055439	P06703	S10A6_HUMAN	F-hand 2.|2.		1	ATACTCCTGGA	0.493
+	6	1653	7A3_uc009won.2_	NM_024330	NP_077306	Q5K4L6	S27A3_HUMAN			1	CTCCAGGTTGG	0.592
-	3	591		NM_020699	NP_065750	Q8WXI9	P66B_HUMAN			0	TTCCTCGCTCT	0.408
+	16	1597		NM_020452	NP_065185	P98198	AT8B2_HUMAN	lasmic (Potential).		2	CCCTGGTCACC	0.572
-	2	200	BAP1_uc001fjf.3_Intron|GBAP1_uc001fje.3_5'UTR							0	ATGATGCTTACC	0.562
-	18	2492	4L_uc001fmb.3_5'	NM_001037533	NP_001032622	Q3T8J9	GON4L_HUMAN			3	TGTGGCCAGAA	0.428
-	5	815	C1orf85_uc009wr	NM_144580	NP_653181	Q8WWB7	NCUG1_HUMAN	enal (Potential).		2	CTGGTCCAACT	0.592
-	5	358	1fpl.2_Missense_	NM_015590	NP_056405	Q5T3I0	GPTC4_HUMAN			1	GTTGGGCTTGG	0.458
-	38	5185	_uc001fqn.2_Miss	NM_014784	NP_055599	O15085	ARHGB_HUMAN			9	GGGGGCTCATG	0.607
-	1	803		NM_001004467	NP_001004467	Q5JRS4	O10J3_HUMAN	ellular (Pote	p.S268F(1)	2	CCAGGGAACTC	0.532
-	23	2793	v.3_Missense_Mu	NM_004371	NP_004362	P53621	COPA_HUMAN			2	TGATAGGTGCA	0.428
+	2	110	pjo.1_Missense_	NM_021181	NP_067004	Q9NQ25	SLAF7_HUMAN	ellular (Potential).		3	CGGTTCCGTTG	0.498
+	6	937	pjo.1_Missense_	NM_021181	NP_067004	Q9NQ25	SLAF7_HUMAN	lasmic (Potential).		3	CTGTGGAAATA	0.368
+	4	790	_Mutation_p.A24	NM_002348	NP_002339	Q9HBG7	LY9_HUMAN	ellular (Potential).		1	AGGAGCCTCCA	0.602
-	5	515		NM_001013625	NP_001013647	Q5VTH2	CA192_HUMAN			0	GGGGACCTGGA	0.527
+	2	1720	aq.2_Missense_M	NM_002155	NP_002146	P17066	HSP76_HUMAN			1	TGCAGGACTTC	0.602
-	3	345	_p.G67D|CD247_	NM_198053	NP_932170	P20963	CD3Z_HUMAN	ic (Potential).|ITAM 1.		0	TTCTGGCCCTGC	0.627
+	4	565	2_uc010pmd.1_5'	NM_001460	NP_001451	Q99518	FMO2_HUMAN			1	GCCACCACATT	0.488
+	7	1234	p.S163N|KLHL20_	NM_014458	NP_055273	Q9Y2M5	KLH20_HUMAN	Kelch 1.		1	AATGAGCAAAA	0.458
+	9	1207		NM_018122	NP_060592	Q6PI48	SYDM_HUMAN			2	TTATCGAGATG	0.338
-	12	3364	g.3_Missense_Mu	NM_007314	NP_009298	P42684	ABL2_HUMAN	tin-binding (By similarity).		14	CCAGAGCTGCC	0.577
+	5	733	_p.E181Q|XPR1_u	NM_004736	NP_004727	Q9UBH6	XPR1_HUMAN	lasmic (Potential).		0	ACGTAGAGGTG	0.398
+	28	3846	pt.2_Missense_Mu	NM_001357	NP_001348	Q08211	DHX9_HUMAN	NTD.		2	TAGAGGCAACT	0.582
+	21	3420	p.A1036T|LAMC2_	NM_005562	NP_005553	Q13753	LAMC2_HUMAN	al.|Domain II and I.		3	TGACAGCAGAT	0.522
+	7	2992	_Mutation_p.L888	NM_005807	NP_005798	Q92954	PRG4_HUMAN			1	CTACTCTTGCA	0.353
-	19	2641		NM_003292	NP_003283	P12270	TPR_HUMAN	Potential.		7	AATTTTCTGCTC	0.308
-	12	1591	p.1_Missense_Mu	NM_003292	NP_003283	P12270	TPR_HUMAN	Potential.		7	CTTTGGCTTCCA	0.383
-	8	1553	ot.1_Missense_Mu	NM_199051	NP_950252	Q76B58	FAM5C_HUMAN			5	TGTGCAGGGCA	0.622
-	8	1356		NM_001994	NP_001985	P05160	F13B_HUMAN	Sushi 7.		3	GCAACGAGATA	0.413
-	22	2449	D1B_uc010ppf.1_	NM_001142795	NP_001136267	Q6P3S1	DEN1B_HUMAN			0	AAGTCGATGAA	0.423
+	12	1446	pqf.1_Splice_Site_p.Q42_splice			O75335	LIPA4_HUMAN			5	GCCAGGTACCT	0.602

-	11	1255	_p.L149F|CHIT1_u	NM_003465	NP_003456	Q13231	CHIT1_HUMAN		0	.TGGAAGACCTG(	0.572	
+	5	1582	ɔ.G375D|LAX1_uc	NM_017773	NP_060243	Q8IWV1	LAX1_HUMAN	lasmic (Potential).	2	GGCCTGGCACTC	0.483	
-	3	1950	_p.P521L|LRRN2_	NM_006338	NP_006329	O75325	LRRN2_HUMAN	cellular (Potential).	2	:TGCCTGGCTGG/	0.617	
+	16	2269	_p.A558V|CNTN2_	NM_005076	NP_005067	Q02246	CNTN2_HUMAN	ɔnectin type-III 1.	1	GCAATGCCGAGA	0.517	
-	1	594		NM_203376	NP_976310	Q6P7N7	TMM81_HUMAN	:tracellular (Potential).	0	CATACTCCTGAG	0.468	
+	9	1312		NM_000715	NP_000706	P04003	C4BPA_HUMAN	Sushi 6.	3	ATAATGGTGAAAT	0.383	
+	12	1966		NM_000715	NP_000706	P04003	C4BPA_HUMAN		3	GACAATCCACTT	0.413	
+	14	2443	.2_Missense_Muta	NM_000573	NP_000564	P17927	CR1_HUMAN	Extracellular (Potential).	3	TTCACCCGGGC/	0.577	
+	8	1412	ҝcu.1_Missense_M	NM_014388	NP_055203	Q68CQ4	DIEXF_HUMAN		0	TCCTCGGATATC(	0.463	
+	7	872	:OR3_uc010psw.1	NM_018254	NP_060724	Q9P2K3	RCOR3_HUMAN		1	'GTAGTCCCAATG	0.418	
+	11	2735	_p.T647I|RPS6KC	NM_012424	NP_036556	Q96S38	KS6C1_HUMAN	otein kinase 2.	8	AACCAACTTCTT	0.368	rs144436274
+	2	792	ҝg.1_Missense_Mu	NM_002763	NP_002754	Q92786	PROX1_HUMAN		6	ATAATTCGGGGTA	0.498	
-	63	13946		NM_206933	NP_996816	O75445	USH2A_HUMAN	II 30.|Extracellular (Potentia	26	AGAGGACTCAAA	0.512	
-	10	2038	kv.2_Missense_Mu	NM_206933	NP_996816	O75445	USH2A_HUMAN	e 1.|Extracellular (Potential	26	AGCAGCGATCAC	0.368	
-	2	347	se_Mutation_p.S3ε	NM_001438	NP_001429	P62508	ERR3_HUMAN		2	:TGAAGAGCCAC(	0.562	
+	6	1092	ɔun.1_Splice_Site_	NM_018650	NP_061120	Q9P0L2	MARK1_HUMAN		10	GGCAGGTATGG/	0.368	
+	12	1549	_p.G364E|CAPN2_	NM_001748	NP_001739	P17655	CAN2_HUMAN	Domain III.	5	'AAGTGGGCAGA(	0.498	
-	12	2590	09xes.2_Splice_Si	NM_003607	NP_003598	Q5VT25	MRCKA_HUMAN		11	'ATTTTACCTTATT	0.274	
+	10	3174	sn.2_Missense_Mu	NM_001098623	NP_001092093	Q5VST9	OBSCN_HUMAN	Ig-like 10.	28	:AGCAGGCAGGC	0.577	
-	1	390		NM_020808	NP_065859	Q9P2F8	SI1L2_HUMAN		6	:CCTTGCTCTCA(	0.522	
+	1	305		NM_003272	NP_003263	O60478	G137B_HUMAN	lasmic (Potential).	0	'ACCGCCACAAG(	0.587	
+	28	3364		NM_001035	NP_001026	Q92736	RYR2_HUMAN	4 X approximate repeats.|B	33	GGCACCGGGGAA	0.517	
+	89	12001	ɔya.1_Splice_Site_	NM_001035	NP_001026	Q92736	RYR2_HUMAN		33	'TTTCAGGATTCC	0.343	
-	8	1292	n.3_Missense_Mutation_p.D179N|PLD5_uc001hzo.1_M			Q8N7P1	PLD5_HUMAN		6	GGGGATCAGTTT(	0.383	
-	3	384	)1ibx.2_Missense_	NM_020394	NP_065127	Q8IW36	ZN695_HUMAN	KRAB.	0	GTCTTCTCTGTG	0.468	
+	1	790		NM_001001918	NP_001001918	Q8NHC7	O14CZ_HUMAN	cellular (Potential).	3	GCGATACCTGCA(	0.458	
-	5	1015	)pzq.1_Missense_I	NM_030645	NP_085148	Q7L8J4	3BP5L_HUMAN		0	:CTGCTCAGCCA(	0.632	
+	12	2045	ɔrf18_uc001iik.2_Ir	NM_017782	NP_060252	Q5VWN6	CJ018_HUMAN		2	;AGAACCCCAGA/	0.373	
+	3	828	ҝig.2_Missense_M	NM_178150	NP_835363	Q8NFZ0	FBX18_HUMAN		3	'GGAGGGAGATC/	0.498	
+	2	412	009xja.2_Missense	NM_006023	NP_006014	O75794	CD123_HUMAN		1	ATGGAACTCTGG	0.303	
-	6	831		NM_001010924	NP_001010924	Q5VUB5	F1711_HUMAN	cellular (Potential).	4	'GGGGGGCAATG	0.557	
-	55	8690	JBN_uc009xjr.1_M	NM_001081	NP_001072	O60494	CUBN_HUMAN	CUB 21.	19	:AGTGGCTAGCA(	0.532	
-	8	1108	1ird.2_Splice_Site	NM_022365	NP_071760	Q96KC8	DNJC1_HUMAN		1	TCTGTTCTAAAA/	0.254	
+	34	5011	.1_Intron|MYO3A_	NM_017433	NP_059129	Q8NEV4	MYO3A_HUMAN		18	'CTGGACCAAAG(	0.348	
-	5	742	ARMC4_uc001itz.2	NM_018076	NP_060546	Q5T2S8	ARMC4_HUMAN		6	TGGTTTCCTTTTC	0.308	
-	7	1690	ɔ.P419S|ZNF438_	NM_182755	NP_877432	Q7Z4V0	ZN438_HUMAN		2	:TTGGGGATCAT	0.403	
-	14	2213	wr.3_Missense_Mu	NM_133376	NP_596867	P05556	ITB1_HUMAN	cellular (Potential).	2	:CTTCTCCTTACA	0.443	
-	37	6921	K3_uc010qih.1_In	NM_020987	NP_066267	Q12955	ANK3_HUMAN		19	GTGAGTCTCTTC	0.403	
+	2	605	jmx.3_Intron|CTN	NM_178011	NP_821079	Q86VH5	LRRT3_HUMAN		3	GTTATAGCCCCC/	0.408	
+	5	682	jrv.2_Missense_M	NM_022124	NP_071407	Q9H251	CAD23_HUMAN	|Extracellular (Potential).	11	AGTTCACCGTGG/	0.617	
+	45	6448		NM_022124	NP_071407	Q9H251	CAD23_HUMAN	.|Extracellular (Potential).	11	GGTCAGGTGTCA	0.627	
+	13	1975	_Mutation_p.T599	NM_004922	NP_004913	P53992	SC24C_HUMAN		3	TTATCACCAGGT/	0.512	
+	18	4553	ɔ.E1062K|MYST4_	NM_012330	NP_036462	Q8WYB5	MYST4_HUMAN	Poly-Glu.	16	ggaagaggaagagga	0.234	
+	2	398	jwy.1_Missense_M	NM_144660	NP_653261	Q96LT4	SAMD8_HUMAN		0	ATGACCCCTTTC/	0.438	
+	10	1739	kew.2_Splice_Site	NM_004670	NP_004661	O95340	PAPS2_HUMAN		2	ACAGAGGTGAGC	0.507	
-	5	1701_1702	32W|PANK1_uc00	NM_148977	NP_683878	Q8TE04	PANK1_HUMAN		0	GGCCCGGGCGA(	0.49	rs140753322
-	6	773	ҝuk.1_Missense_M	NM_022451	NP_071896	Q8WTT2	NOC3L_HUMAN		1	TTTCTGGATCTG/	0.348	rs138770211

+	10	1563	.1_Intron|WDR11_	NM_018117	NP_060587	Q9BZH6	WDR11_HUMAN		0	ACATCCCAGAG	0.428
+	9	7514	_p.S89F|TACC2_u	NM_206862	NP_996744	O95359	TACC2_HUMAN	SPAZ.	10	CATCCTCTAAGAC	0.522
-	13	2319	XM2_uc001lhj.2_F	NM_198148	NP_937791	Q8N436	CPXM2_HUMAN		2	TTAATGCCTTCTA	0.423
-	2	213		NM_004092	NP_004083	P30084	ECHM_HUMAN		0	TCAACCCCACGG	0.512
+	21	2339	_p.E653K|EPS8L2	NM_022772	NP_073609	Q9H6S3	ES8L2_HUMAN		1	GAGCTGGAAGAA	0.632
+	29	3575	ltb.2_Missense_Mu	NM_017511	NP_059981	Q9HC84	MUC5B_HUMAN	VWFD 2.	0	GCAGGCCATCC	0.692
+	7	897	_Missense_Mutatio	NM_138567	NP_612634	Q8NBV8	SYT8_HUMAN	toplasmic (Potential).	1	ACGTGCCCAGC	0.667
+	3	459	b.1_Missense_Mu	NM_004314	NP_004305	P52961	NAR1_HUMAN		0	CTCCTGGCCTAC	0.677
+	3	816	b.1_Missense_Mu	NM_004314	NP_004305	P52961	NAR1_HUMAN		0	GAGAGGAAGAG	0.607
-	1	1211	32_uc001mak.1_Ir	NM_145053	NP_659490	Q8IYU4	UBQLN_HUMAN		3	GGGGTGAAGAC	0.483
-	1	382		NM_001004490	NP_001004490	A6NM03	O2AG2_HUMAN	lasmic (Potential).	4	GAGGATGACAAT	0.522
-	6	560		NM_198185	NP_937828				0	CGCCACCTGAAA	0.473
+	6	1472	ht.2_Missense_Mu	NM_003390	NP_003381	P30291	WEE1_HUMAN	rotein kinase.	5	GATCTCCTTTTG	0.363
+	3	575	sense_Mutation_p.	NM_001025389	NP_001020560	Q01432	AMPD3_HUMAN		2	CAAGATGATTCGC	0.532
-	3	568	on_p.I73L|CYP2R1	NM_024514	NP_078790	Q6VVX0	CP2R1_HUMAN		2	TGGTTATGTTTGA	0.328
-	20	2869	_p.S55T|PLEKHA	NM_175058	NP_778228	Q6IQ23	PKHA7_HUMAN		3	CACAGATGTGT	0.677
+	3	426	_p.L20F|BBOX1_u	NM_003986	NP_003977	O75936	BODG_HUMAN		1	CAGATCCTCTGG	0.498
-	11	1677		NM_031217	NP_112494	Q8NI77	KI18A_HUMAN		2	CCTCCTCCCTCC	0.403
-	4	1092	e_Mutation_p.S29	NM_024426	NP_077744	P19544	WT1_HUMAN	p.D299Y(1)|p.D299fs	687	GCTGGGATGTC	0.368
+	2	738	_p.G56E|PDHX_u	NM_003477	NP_003468	O00330	ODPX_HUMAN	ipoyl-binding.	1	AGAAGGAAACA	0.363
-	2	735	on_p.T39I|SLC1A2	NM_004171	NP_004162	P43004	EAA2_HUMAN	ical; (Potential).	3	TCAGGGTGAGC	0.622
+	6	1413	73_splice|EXT2_uc	NM_207122	NP_997005	Q93063	EXT2_HUMAN		5	GAAGAGGTGGGT	0.428
-	27	4008		NM_002334	NP_002325	O75096	LRP4_HUMAN	ntial).|LDL-receptor class B	4	TCACGAGGATGA	0.597
+	25	4050	.G1202R|MADD_u	NM_003682	NP_003673	Q8WXG6	MADD_HUMAN		11	ATGAGGGACTC	0.527
+	1	325		NM_001004747	NP_001004747	Q8NGG3	OR5T3_HUMAN	cellular (Potential).	0	GTCACTCCAAAA	0.368
+	3	719		NM_178570	NP_848665	Q86UN3	R4RL2_HUMAN	LRR 8.	0	CCTGGCCTCGC	0.731
+	2	772		NM_001105565	NP_001099035	E9PPJ3	E9PPJ3_HUMAN		1	CGGAGGATGCA	0.567
-	3	547	nsn.2_Missense_M	NM_021727	NP_068373	Q9Y5Q0	FADS3_HUMAN	lasmic (Potential).	2	GGTGGGACTGG	0.627
-	5	10334	IAK_uc001ntk.1_Ir	NM_001620	NP_001611	Q09666	AHNK_HUMAN		19	GACTTGCCTTCG	0.423
-	6	826	A2_uc010rlx.1_5'U	NM_004739	NP_004730	O94776	MTA2_HUMAN	ELM2.	2	ACCAACTCTAAT	0.403
+	4	523		NM_004585	NP_004576	Q9UL19	TIG3_HUMAN		1	GATGCTCTTTTG	0.517
-	11	1647		NM_015104	NP_055919	Q2TAZ0	ATG2A_HUMAN		2	TGCTGGTTGTC	0.667
+	15	3115	_p.S881F|SIPA1_u	NM_006747	NP_006738	Q96FS4	SIPA1_HUMAN	Potential.	0	GGAGTCCATGC	0.632
-	7	683	79_splice|BRMS1	NM_015399	NP_056214	Q9HCU9	BRMS1_HUMAN		0	CCATTCTGCCC	0.602
-	2	1285	jb.2_Missense_Mu	NM_031492	NP_113680	Q9BQ04	RBM4B_HUMAN	ith TNPO3 (By similarity).	0	ATTCCCCGTAGC	0.512
-	22	4201	CD3_uc001out.2_F	NM_015531	NP_056346	Q4AC94	C2CD3_HUMAN		7	TCTTTTGTTGGA	0.378
-	23	3954		NM_001098816	NP_001092286	Q6N022	TEN4_HUMAN	cellular (Potential).	4	GACGCGTCAATT	0.453
+	8	3515	u.1_Missense_Mut	NM_015885	NP_056969	O94913	PCF11_HUMAN	Gly-rich.	1	ACATGGTCAGC	0.512
+	16	4837		NM_015885	NP_056969	O94913	PCF11_HUMAN		1	AGACACCAGTT	0.373
-	2	526	_p.A84T|SYTL2_u	NM_001162951	NP_001156423	Q9HCH5	SYTL2_HUMAN		3	CACCTGCTATCTG	0.473
+	3	815	eq.2_Missense_M	NM_015368	NP_056183	Q96RD7	PANX1_HUMAN	lasmic (Potential).	0	ATCATGGAAGAA	0.502
+	20	2849	gb.2_Missense_Mu	NM_014361	NP_055176	O94779	CNTN5_HUMAN	onectin type-III 2.	8	TTTATCGAGATGA	0.433
-	10	1420	uc001phh.1_Intror	NM_002422	NP_002413	P08254	MMP3_HUMAN	mopexin-like 4.	2	GAAGATCCAGTA	0.338
+	89	12974	p.R4284K|DYNC2	NM_001080463	NP_001073932	Q8NCM8	DYHC2_HUMAN		0	CTGAAAGGATC	0.398
+	2	96	_Start_Site|PAFAH	NM_002572	NP_002563	P68402	PA1B2_HUMAN		1	CTCAGGTGTAG	0.373
+	21	2055	e_Mutation_p.L69	NM_001040455	NP_001035545	Q8NBJ9	SIDT2_HUMAN	cellular (Potential).	0	CACGTGCTCTAC	0.622
-	9	2155		NM_020693	NP_065744	Q8TD84	DSCL1_HUMAN	otential).|Ig-like C2-type 7.	8	GAGACGCTAGAG	0.602

+	4	498	aa.1_Missense_Mu	NM_000073	NP_000064	P09693	CD3G_HUMAN	lasmic (Potential).	0	GACAGGATGGA	0.473	
+	35	3380	rzn.1_Missense_M	NM_015313	NP_056128	Q9NZN5	ARHGC_HUMAN	PH.	7	TGGCAGGACCTA	0.383	
+	10	3406		NM_005422	NP_005413	O75443	TECTA_HUMAN	VWFD 3.	10	AGCTCAGACTCT	0.567	rs147890616
+	9	2599		NM_024806	NP_079082	Q6NUN7	CK063_HUMAN		3	AACAGGCTGTG	0.413	
+	10	1498		NM_002014	NP_002005	Q02790	FKBP4_HUMAN		0	GAGACCATCCC	0.532	
+	5	529	seg.1_RNA|TULP3	NM_003324	NP_003315	O75386	TULP3_HUMAN		0	CAGTCAGCATGT	0.383	
-	13	1451		NM_020373	NP_065106	Q9NQ90	ANO2_HUMAN	lasmic (Potential).	7	CCAGTCGCATC	0.418	
-	16	2510	01qpd.1_5'Flank|N	NM_001033714	NP_001028886	P46087	NOP2_HUMAN		2	GAGGCTGAGGC	0.577	
+	14	1778	grb.1_Missense_M	NM_014262	NP_055077	Q8IVL6	P3H3_HUMAN	OG dioxygenase.	0	GTCACCCAGTG	0.647	
+	7	970	sl.2_Missense_Mut	NM_201442	NP_958850	P09871	C1S_HUMAN	CUB 1.	1	CTGTGGACAGA	0.403	
-	12	3204	.V1026M|CD163_u	NM_004244	NP_004235	Q86VB7	C163A_HUMAN	xtracellular (Potential).	8	AATTCACTGCAG	0.512	
-	12	3136	p.S1003F|CD163_u	NM_004244	NP_004235	Q86VB7	C163A_HUMAN	xtracellular (Potential).	8	AGGAAGACTCA	0.522	
-	7	1757	quh.2_Missense_M	NM_018088	NP_060558	Q86YD7	F90A1_HUMAN		1	CGTTTTCCAGTC	0.622	
+	27	3417	p.E687K|A2ML1_u	NM_144670	NP_653271	A8K2U0	A2ML1_HUMAN		3	TGCTGGAGATG	0.517	
+	10	2407	ve.2_Missense_Mu	NM_004426	NP_004417	P78364	PHC1_HUMAN		2	CTTTCCCGGTG	0.478	
-	3	266	n_p.P77S|PRB1_u	NM_005039	NP_005030	P04280	PRP1_HUMAN	P-P-[PAQ]-Q-[GE]-[GD]- [NK	0	CTTGTGGCTTTC	0.622	
-	8	1752	LRP6_uc010shl.1_	NM_002336	NP_002327	O75581	LRP6_HUMAN	ular (Potential).|LDL-recept	12	GTAAATCCAAATA	0.403	
-	4	856	1raj.1_Missense_M	NM_018050	NP_060520	Q9H8J5	MANS1_HUMAN	cellular (Potential).	0	CTTTTTCCTTATA	0.453	
-	9	1485		NM_024829	NP_079105	Q6P4A8	PLBL1_HUMAN		0	CTTTCCCTTGGT	0.418	
-	18	2085		NM_004963	NP_004954	P25092	GUC2C_HUMAN	Potential).|Protein kinase.	6	GGTGCTCTGGAG	0.483	
+	1	157	e_Mutation_p.G24	NM_019012	NP_061885	Q9HAU0	PKHA5_HUMAN	WW 1.	3	GGGCGGCCGAG	0.637	
+	24	3309	sif.1_Missense_M	NM_019012	NP_061885	Q9HAU0	PKHA5_HUMAN		3	TCAACTCCTGAG	0.368	
-	7	967	_p.T107I|SLCO1A	NM_021094	NP_066580	P46721	SO1A2_HUMAN	cellular (Potential).	4	CAACGAGTGTCA	0.378	
+	1	198	_p.G59E|ETNK1_	NM_018638	NP_061108	Q9HBU6	EKI1_HUMAN		0	CCCCGGGACGG	0.532	
-	3	628	_p.W74*|BCAT1_	NM_005504	NP_005495	P54687	BCAT1_HUMAN		2	GAGGACCACTC	0.453	
+	3	232	D21_uc009zjh.1_F	NM_004264	NP_004255	Q13503	MED21_HUMAN		0	GCAAAAGACATT	0.368	
+	11	1308	p.A291T|PPFIBP1	NM_003622	NP_003613	Q86W92	LIPB1_HUMAN	Potential.	5	AAAAAGCTGTG	0.348	
-	3	590	im.2_Missense_Mu	NM_198966	NP_945317	P12272	PTHR_HUMAN		1	CAGACCCAAATC	0.512	
-	8	2412	p.S221N|CAPRIN2	NM_001002259	NP_001002259	Q6IMN6	CAPR2_HUMAN		2	TTTTGACTCTCA	0.468	
+	24	3096	nn.1_Missense_M	NM_001843	NP_001834	Q12860	CNTN1_HUMAN	onectin type-III 4.	9	CAGGTGCACCC	0.468	rs143416044
-	16	2351	nse_Mutation_p.G	NM_001145108	NP_001138580	Q99435	NELL2_HUMAN	alcium-binding (Potential).	4	GGTAGCCATCTCT	0.433	
+	7	433	orf54_uc009zky.1_	NM_152319	NP_689532	Q6X4T0	CL054_HUMAN		0	ACCCTGGACCC	0.517	
+	17	2402	ryo.2_Missense_M	NM_001039960	NP_001035049	Q2Y0W8	S4A8_HUMAN	ical; (Potential).	5	ACAATGGTGATT	0.413	
+	11	1712_1713	p.P377F|SCN8A_	NM_014191	NP_055006	Q9UQD0	SCN8A_HUMAN		7	GGGATCCCGAGA	0.45	
+	5	937	zm.2_Missense_M	NM_004302	NP_004293	P36896	ACV1B_HUMAN	e.|Cytoplasmic (Potential).	9	TACACAGTGACA	0.532	
-	9	1347	e_Mutation_p.G45	NM_182507	NP_872313	Q6KB66	K2C80_HUMAN	Tail.	0	GAGGCCTGATC	0.547	
+	2	597	sdq.2_5'UTR|TAR	NM_134323	NP_599150	Q15633	TRBP2_HUMAN	action with PRKRA.|DRBM	1	TGCAGGAGTATC	0.592	
-	4	1031	pa.2_Missense_Mu	NM_003708	NP_003699	O75452	RDH16_HUMAN	lasmic (Potential).	0	GCTTGGCATCCC	0.572	
-	19	2290	p.P521S|MYO1A_	NM_005379	NP_005370	Q9UBC5	MYO1A_HUMAN		7	TCTTGGGGCTTC	0.532	
+	3	737	nb.2_Missense_Mu	NM_002332	NP_002323	Q07954	LRP1_HUMAN	ential).|LDL-receptor class A	22	CCCGCCTCTGC	0.592	
-	13	1820	se_Mutation_p.S46	NM_153377	NP_700356	Q6UXM1	LRIG3_HUMAN	-like C2-type 1.	4	CACTGCTGCTG	0.458	
+	20	2577	srv.2_Missense_M	NM_020762	NP_065813	Q7Z6B7	SRGP1_HUMAN		4	CGTCATCCTGAC	0.587	
-	12	2175	TPRR_uc009zrs.2_	NM_002849	NP_002840	Q15256	PTPRR_HUMAN	sphatase.|Cytoplasmic (Pot	3	GCAGTGGACAA	0.522	
+	13	2284		NM_013381	NP_037513	Q9UKU6	TRHDE_HUMAN	cellular (Potential).	3	GATTTTCTTCCTT	0.368	
+	5	882	zm.1_Missense_M	NM_024560	NP_078836	Q9H6R3	ACSS3_HUMAN		4	CGGTTCCTTTGG	0.398	
-	5	496	tan.2_Missense_M	NM_152589	NP_689802	Q8NA57	CL050_HUMAN		3	TTTCTTCAATTTC	0.259	
-	14	2190	se_Mutation_p.W5	NM_016122	NP_057206	Q9Y592	CCD41_HUMAN	Potential.	0	TCCAACCACTGT	0.363	

-	10	1119	e_Mutation_p.W66	NM_002108	NP_002099	P42357	HUTH_HUMAN		3	GGAGACCACAT	0.522
+	11	3132	mj.2_Missense_M	NM_001018072	NP_001018082	A6QL63	BTBDB_HUMAN		3	ATGTTTGAGATC	0.517
-	12	1619	1tts.2_Missense_	NM_001109662	NP_001103132				2	GCCTTAGTAACT	0.423
-	3	206		NM_002442	NP_002433	O43347	MSI1H_HUMAN	RRM 1.	3	GACACTCCTTCA	0.502
-	19	3237	.2_Missense_Mut	NM_032590	NP_115979	Q8NHM5	KDM2B_HUMAN	Pro-rich.	2	GGGTGGCCGG	0.697
+	3	348	uby.2_Missense_	NM_030765	NP_110392	Q9C0J1	B3GN4_HUMAN	type II membrane protein;	1	TGCTCGGCTGC	0.682
-	28	3677	BNO1_uc010taq.1_	NM_018183	NP_060653	A3KN83	SBNO1_HUMAN		9	TTTTTAGGATTCA	0.264
+	8	1497	bm.1_Missense_	NM_198827	NP_942122	Q6QNK2	GP133_HUMAN	ellular (Potential).	10	CCTCTCGGAGC	0.453
+	45	8037	0_uc001ujm.2_No	NM_015409	NP_056224	Q96L91	EP400_HUMAN	ith ZNF42 (By similarity).	12	GTGTTCGAGCG	0.667
-	11	1622		NM_175066	NP_778236	Q8N8A6	DDX51_HUMAN	case C-terminal.	2	CACCCCCAAAA	0.627
-	31	4355		NM_006437	NP_006428	Q9UKK3	PARP4_HUMAN		4	TCCAGGATGTT	0.532
+	1	980		NM_001033602	NP_001028774	Q5JR59	MTUS2_HUMAN		0	AACTGGAAGCA	0.507
-	11	1928		NM_003045	NP_003036	P30825	CTR1_HUMAN	ellular (Potential).	0	GCACGGTCACA	0.562
+	41	6769	e_Mutation_p.A84	NM_015678	NP_056493	Q8NFP9	NBEA_HUMAN		11	ATTCTGCCTTCA	0.488
-	19	1750	.2_Missense_Muta	NM_001014286	NP_001014308	Q8NEM7	FA48A_HUMAN		0	TTGATGGCTTA	0.403
-	19	2256	uyk.2_Missense_	NM_015058	NP_055873	A3KMH1	K0564_HUMAN		6	AGAGTTCCAGAT	0.413
-	11	1468	e_Mutation_p.Q3	NM_001127615	NP_001121087	Q8TC92	ENOX1_HUMAN		2	GAGCTGCTCAC	0.458
-	1	1915	uzo.1_Missense_	NM_183422	NP_904358	Q15714	T22D1_HUMAN		0	AGTGTGCTGACA	0.398
+	7	838	nse_Mutation_p.P	NM_031431	NP_113619	Q96JB2	COG3_HUMAN		2	ATTATCCCATATA	0.358
-	9	999	ron|CPB2_uc001v	NM_001872	NP_001863	Q96IY4	CBPB2_HUMAN		2	GAGTATGAATGC	0.378
+	5	846	_p.T139I|CDADC	NM_030911	NP_112173	Q9BWV3	CDAC1_HUMAN		1	TGATGACTATAG	0.323
+	2	901	U2_uc001vdo.1_In	NM_173605	NP_775876	Q8N5I3	KCNRG_HUMAN		0	TAAAGGAAGGC	0.383
+	1	319	f.1_Intron|DLEU1_	NR_002183					0	AGAAGGTGTGA	0.408
-	1	284	aed.1_Missense_	NM_001042517	NP_001035982	Q9NSV4	DIAP3_HUMAN		2	AGGAAGGGTAG	0.711
-	1	515	n_p.T31I|DACH1_	NM_080759	NP_542937	Q9UI36	DACH1_HUMAN		1	TGGAGGTGGTG	0.667
-	1	518	_p.W57*|TBC1D4_	NM_014832	NP_055647	O60343	TBCD4_HUMAN	PID 1.	6	ATGAGCCAGGG	0.577
+	12	2879	.P606S|LMO7_uc	NM_015842	NP_056667	Q8WWI1	LMO7_HUMAN		5	ACATCCCCCTTC	0.493
-	46	6644	ev.2_Missense_M	NM_015057	NP_055872	O75592	MYCB2_HUMAN		14	CAAGTGCTTCTA	0.373
-	1	446	fh.2_Missense_Mu	NM_001922	NP_001913	P40126	TYRP2_HUMAN		5	AAACCCCCACC	0.388
+	1	212	afz.1_Missense_	NM_004800	NP_004791	Q99805	TM9S2_HUMAN		1	GGGCGGTTCCT	0.652
+	4	464	3A_uc001vur.2_R	NM_023011	NP_075387	Q9H1J1	REN3A_HUMAN		1	GGCCTAGAATAT	0.388
-	2	270	ahw.2_Missense_	NM_145250	NP_660293	Q8TAA1	RNS11_HUMAN		3	TAAATTCTTCTT	0.403
+	2	454	vyl.1_Missense_M	NM_002934	NP_002925	P10153	RNAS2_HUMAN		1	CAGACACCAGCA	0.453
-	7	636	ax.2_Missense_M	NM_032846	NP_116235	Q8WUD1	RAB2B_HUMAN		1	CATTGTGGACAT	0.408
-	2	2009	439L|SALL2_uc0	NM_005407	NP_005398	Q9Y467	SALL2_HUMAN		3	CATAGGGGAAG	0.547
+	7	2513	10_uc001whe.2_I	NM_014045	NP_054764	Q7Z4F1	LRP10_HUMAN	ytoplasmic (Potential).	1	CTGGAGTGGTG	0.677
+	9	828		NM_138360	NP_612369	Q8ND23	LR16B_HUMAN		5	CAAGGACTTGC	0.592
-	3	980	10tob.1_Missense	NM_006405	NP_006396	O15321	TM9S1_HUMAN		1	CTGAAGTCTCA	0.542
+	1	1799	ense_Mutation_p.	NM_019839	NP_062813	Q9NPC1	LT4R2_HUMAN	Name=1; (Potential).	0	GCTGGCGGCGC	0.697
+	2	335		NM_025081	NP_079357	Q9P2P1	NYNRI_HUMAN		3	TGGGGGCGATC	0.667
-	33	5469	LGAPA1_uc010tp	NM_014990	NP_055805	Q6GYQ0	RGPA1_HUMAN	binds to TCF3/E12 (By sim	4	CATTCAGGACTA	0.358
-	2	551	pz.1_Missense_M	NM_004496	NP_004487	P55317	FOXA1_HUMAN		0	CTGCGCCGGGA	0.677
-	16	2114	_p.P517S|SEC23A	NM_006364	NP_006355	Q15436	SC23A_HUMAN		5	TGGTGGTCCAC	0.348
+	11	1253	te_p.D277_splice|	NM_005930	NP_005921	O15320	CTGE5_HUMAN		0	ACTGTAGATAATC	0.328
+	7	1149	Missense_Mutatio	NM_017922	NP_060392	Q86UA1	PRP39_HUMAN		2	AGCATGAAGTT	0.259
-	2	321	j.1_Intron|MGAT2_	NM_001001	NP_000992	Q969Q0	RL36L_HUMAN		0	TCAACACATTCC	0.483
+	2	841	5S_uc001wxx.1_	NM_001003803	NP_001003803	Q99766	ATP5S_HUMAN		2	TGTTTAATAAGT	0.383

-	4	802	'h.1_Missense_Mu	NM_021818	NP_068590	Q9H4B6	SAV1_HUMAN	WW 1.	1	TATTTTCTCCCTC	0.453	
-	7	2005	.1_Missense_Muta	NM_007361	NP_031387	Q14112	NID2_HUMAN	en G2 beta-barrel.	7	GCCAGCCAAACA(	0.582	
-	2	556	:.1_Missense_Muta	NM_007361	NP_031387	Q14112	NID2_HUMAN	NIDO.	7	GAAAAGGGGCGA	0.642	
+	7	1184	1wzt.3_Missense_I	NM_001099652	NP_001093122	Q8N3F9	G137C_HUMAN	lasmic (Potential).	0	CAGTCACTCCCC/	0.418	
+	16	2598	336_splice|KIAA05	NM_014749	NP_055564	E9PGW8	E9PGW8_HUMAN		1	ATAAAGGTATATT	0.318	
+	51	10500	o.L3424F|SYNE2_	NM_015180	NP_055995	Q8WXH0	SYNE2_HUMAN	ic (Potential).|Potential.	14	CAGATCCTTAGA(	0.393	
+	69	13462	ipy.2_Missense_M	NM_015180	NP_055995	Q8WXH0	SYNE2_HUMAN	lasmic (Potential).	14	TGTGGCCCCAGT/	0.348	
+	10	809	f50_uc001xhm.1_	NM_172365	NP_758953	Q96LQ0	CN050_HUMAN		1	TGTAGTCCTTTT/	0.393	
+	7	779		NM_020715	NP_065766	Q9ULM0	PKHH1_HUMAN		0	CTGAAGGCAGCT	0.612	
-	38	7126	e|ZFYVE26_uc001	NM_015346	NP_056161	Q68DK2	ZFY26_HUMAN		11	ATGTGCCTGTGGT	0.517	
-	11	1957_1958	nse_Mutation_p.G	NM_015346	NP_056161	Q68DK2	ZFY26_HUMAN		11	TCTTCCCCTCAAT	0.525	rs142015707
+	3	208	.2_5'UTR|DNAL1_	NM_031427	NP_113615	Q4LDG9	DNAL1_HUMAN		0	TCATAGGAAGAG/	0.403	
+	2	432		NM_018228	NP_060698	Q9H8Y1	VRTN_HUMAN		0	GCAAGGGGGAG	0.672	
-	3	580	1_uc001xru.2_Spli	NM_007176	NP_009107	Q9UKR5	ERG28_HUMAN		0	CATTCACTGTGT/	0.498	
-	42	5837	xd.2_Missense_Mu	NM_183387	NP_899243	Q05BV3	EMAL5_HUMAN		3	TCATCTCCTAGA/	0.418	
-	6	1430	14orf102_uc001xy	NM_017970	NP_060440	Q9H7Z3	CN102_HUMAN		3	TGGCCTCTTCCGT	0.408	
-	11	5137	uf.1_Missense_Mu	NM_004239	NP_004230	Q15643	TRIPB_HUMAN	Potential.	13	AATATTCTCTCCT	0.338	
+	21	2791	lybs.1_Missense_I	NM_020818	NP_065869	Q9P2D8	UNC79_HUMAN		17	CAGTAACCAAAA/	0.468	
-	18	2935	sense_Mutation_p.	NM_030621	NP_085124	Q9UPY3	DICER_HUMAN	PAZ.	5	AAGGGTGTTTCTT	0.338	
+	3	650	avn.2_Nonsense_M	NM_000710	NP_000701	P46663	BKRB1_HUMAN	lasmic (Potential).	3	GGAGGCAGCAG	0.642	
-	1	458	R20_uc010txu.1_5	NM_001017963	NP_001017963	P07900	HS90A_HUMAN		7	CTTCCTGGGCGG	0.637	
-	10	1207	_uc001ylh.2_Intron	NM_014226	NP_055041	Q9UQ07	MOK_HUMAN		4	TTAGTACCTGCTT	0.612	
+	2	1045	NF839_uc001ylq.1	NM_018335	NP_060805	A8K0R7	ZN839_HUMAN		2	TGCTGTCTGAGA/	0.582	
+	9	1114		NM_015156	NP_055971	Q9UKL0	RCOR1_HUMAN	ction with KDM1A.	1	TATCGACTTCCAG	0.308	
-	22	3220	01ymj.1_Splice_Si	NM_006035	NP_006026	Q9Y5S2	MRCKB_HUMAN		11	GTCTCACCTCCT(	0.592	
-	7	6868	px.2_Missense_M	NM_138420	NP_612429	Q8IVF2	AHNK2_HUMAN		1	TGAGGTCCACTTT	0.602	
+	1	286	727924_uc001yub	NM_001004719	NP_001004719	Q8NGB6	OR4M2_HUMAN	cellular (Potential).	1	TTTGATGGATGC/	0.458	
+	1	3712		NM_018958	NP_061831	Q9NZP6	CO002_HUMAN		8	GTATTTGGATATA	0.537	
+	36	5582	r.2_Nonsense_Mu	NM_001036	NP_001027	Q15413	RYR3_HUMAN	eats.|Cytoplasmic (By simil	10	AAGCTGCAGGCA	0.552	
+	7	1309		NM_152594	NP_689807	Q7Z699	SPRE1_HUMAN		5	CAAAACGAAGAA/	0.413	
-	32	4077	080_uc010ucu.1_F	NM_017553	NP_060023	Q9ULG1	INO80_HUMAN	nserved components INO8(	4	TTCCTCCTGTTG(	0.473	
+	18	2229	_Mutation_p.G642	NM_001128608	NP_001122080	O60336	MABP1_HUMAN	WD 10.	10	CAGTGGAAAGC/	0.517	
-	13	5295	:pv.2_Missense_M	NM_022473	NP_071918	Q9H2Y7	ZF106_HUMAN	WD 3.	3	GGCCATGGCATT(	0.463	
+	8	1045	e_Mutation_p.P26	NM_014444	NP_055259	Q9UGJ1	GCP4_HUMAN		3	TACATTCCAGTGA	0.428	
-	2	333	01zsj.2_Missense_	NM_172095	NP_742093	Q96P56	CTSR2_HUMAN	lasmic (Potential).	1	CCGCGGCACAG	0.453	
-	25	4329	uei.1_Missense_M	NM_025137	NP_079413	Q96JI7	SPTCS_HUMAN	lasmic (Potential).	5	TTGCTTCCTTGA/	0.488	
+	26	3750	oee.1_Missense_M	NM_017434	NP_059130	Q9NRD9	DUOX1_HUMAN	TXNDC11 (By similarity).|(	8	TGCCTCCACCG(	0.657	
+	8	1700	_p.E437K|SLC27A	NM_003645	NP_003636	O14975	S27A2_HUMAN	lasmic (Potential).	2	AAAGGGGAAAT(	0.453	
-	3	644	GABPB1_uc001zyc	NM_005254	NP_005245	Q06547	GABP1_HUMAN	ANK 3.	1	GTAATGGTGTTCG	0.453	
+	2	536	.1_Intron|GLDN_u	NM_181789	NP_861454	Q6ZMI3	GLDN_HUMAN	cellular (Potential).	2	CAGATCCGAGTG	0.572	
-	18	3035		NM_173814	NP_776175	Q2VWP7	PRTG_HUMAN		3	AGGAGGCACTG	0.418	
-	18	2330	e_Mutation_p.D70	NM_017661	NP_060131	Q6N043	Z280D_HUMAN		3	TATTATCTAAGCC	0.308	
-	8	867	se_Mutation_p.S21	NM_017661	NP_060131	Q6N043	Z280D_HUMAN		3	CCTGGGAAGAA(	0.328	
-	18	2492	p.G784R|SLTM_u	NM_024755	NP_079031	Q9NWH9	SLTM_HUMAN	Arg/Glu-rich.	1	TTTTCCCCTCACT	0.423	
-	69	12992		NM_003922	NP_003913	Q15751	HERC1_HUMAN	RCC1 13. p.P4282P(1)	19	GTTGCGGTCGATT	0.468	
-	38	7406		NM_003922	NP_003913	Q15751	HERC1_HUMAN		19	ATTCATGTCGGT(	0.483	
+	4	935	ujp.1_Missense_M	NM_002755	NP_002746	Q02750	MP2K1_HUMAN	rotein kinase.	0	GATCAAGTCCTG/	0.353	

-	9	1133	_p.G161D|LCTL_u	NM_207338	NP_997221	Q6UWM7	LCTL_HUMAN	cellular (Potential).	2	GATGTGCCTTTA	0.498	
-	6	1070	M2_uc002atw.1_M	NM_182471	NP_872271	P14618	KPYM_HUMAN		1	TCCGAACCCCCT	0.532	
-	1	413	1_Missense_Muta	NM_052840	NP_443072	Q96J87	CELF6_HUMAN		3	CGGGACCGGGGT	0.721	
+	3	716	O1_uc010uky.1_Mi	NM_002499	NP_002490	Q92859	NEO1_HUMAN	Potential).|Ig-like C2-type 2.	1	CAACCCCTTCTT	0.443	
-	10	1933	p.P482L|EDC3_u	NM_001142443	NP_001135915	Q96F86	EDC3_HUMAN	eF N-terminal.	1	TGCTGGGGAATG	0.577	
+	3	333	.2_5'UTR|C15orf2	NM_152335	NP_689548	Q2M3C6	CO027_HUMAN		0	CCACGGCGGGC	0.522	
+	5	1075		NM_001101404	NP_001094874	A6NKC9	SH2D7_HUMAN		0	GAAGGCCTCCTG	0.617	
-	10	1805	Dblm.1_Missense_	NM_002891	NP_002882	Q13972	RGRF1_HUMAN	PH 2.	6	AGGCGCCCCCTG	0.562	
+	21	3142	p.A973V|ADAMTS	NM_207517	NP_997400	P82987	ATL3_HUMAN	-like C2-type 1.	27	GTCTTGCTGCCC	0.552	
+	4	2428	592_uc010upb.1_	NM_014630	NP_055445	Q92610	ZN592_HUMAN		6	GCCTTGCCACTC	0.592	
+	8	4285	olu.1_Missense_M	NM_007200	NP_009131	Q12802	AKP13_HUMAN		9	TAGGGAGCATAG	0.463	
-	2	169	nk.2_RNA|DET1_u	NM_001144074	NP_001137546	Q7L5Y6	DET1_HUMAN		2	ATGGTAGAAACAT	0.403	
-	7	1048	c.1_Missense_Mu	NM_002168	NP_002159	P48735	IDHP_HUMAN		711	CCTGGGCCAGG	0.562	
+	24	3009		NM_003870	NP_003861	P46940	IQGA1_HUMAN	C1.	8	AAGTTGGAAGCT	0.358	
-	19	1890	ense_Mutation_p.G	NM_001287	NP_001278	P51798	CLCN7_HUMAN	al; (By similarity).	4	CGTCGCCCACGA	0.632	
+	16	1725	v.1_Missense_Mu	NM_000548	NP_000539	P49815	TSC2_HUMAN		10	CCTCTCCCCAC	0.577	
-	15	5859	t.1_Missense_Mut	NM_001009944	NP_001009944	P98161	PKD1_HUMAN	xtracellular (Potential).	3	CTCCTCCGCCG	0.637	
+	11	1628	rl.1_Missense_Mu	NM_016333	NP_057417	Q9UQ35	SRRM2_HUMAN	-rich.|Ser-ri p.G360D(1)	4	CACAGGCCCAG	0.577	
-	2	639	2cuk.2_Missense_	NM_003454	NP_003445	P98182	ZN200_HUMAN		0	TGCAGCCATCAT	0.542	
-	10	2316		NM_000243	NP_000234	O15553	MEFV_HUMAN	B30.2/SPRY.	6	GTGTCCCAGGG	0.527	
-	5	1068	_p.R12Q|ZNF434_	NM_017810	NP_060280	Q9NX65	ZN434_HUMAN		2	GGGTCCGCAGA	0.502	
+	4	469	ws.3_Missense_M	NM_001127206	NP_001120678	P30519	HMOX2_HUMAN		0	ACTTCCCCATGC	0.567	
+	14	1517	N1_uc002cxb.2_	NM_001142290	NP_001135762	O60291	MGRN1_HUMAN		2	TCTTCCCCCATC	0.652	
+	12	1776	v.1_Missense_Mu	NM_018723	NP_061193	Q9NWB1	RFOX1_HUMAN		0	CACCGCCGCGG	0.592	
-	4	256	_Intron|NTAN1_uc	NM_173474	NP_775745	Q96AB6	NTAN1_HUMAN		0	CATTACCTGAAG	0.527	
-	7	1087	p.P293S|ACSM2E	NM_182617	NP_872423	Q68CK6	ACS2B_HUMAN		5	CAGTGGGTCAA	0.408	
+	15	1919	dme.2_Splice_Site	NM_212535	NP_997700	P05771	KPCB_HUMAN		9	AAGGGGTAAGT	0.299	
+	2	184	issense_Mutation_	NM_007074	NP_009005	P31146	COR1A_HUMAN	WD 1.	0	CAAGGCCGACC	0.592	
+	8	1228	za.2_Missense_M	NM_024031	NP_076936	Q9BWN1	PRR14_HUMAN	Pro-rich.	0	CTTCTCCCTAAG	0.677	
+	2	483	et.2_Missense_Mu	NM_006742	NP_006733	P11801	KPSH1_HUMAN	nilarity).|Protein kinase.	0	CTAATTGGCCGA	0.587	
-	72	12372	DIN_uc010cfy.2_R	NM_032821	NP_116210	Q4G0P3	HYDIN_HUMAN		2	AGATGAGAGGTT	0.483	
+	6	639	74_uc002fbl.1_Missense_Mutation_p.A106V|KIAA0174			P53990	IST1_HUMAN	nteraction with CHMP1A an	1	CTGGGCTGCTC	0.368	
+	7	984_985	p.S175F|CNTNAF	NM_033401	NP_207837	Q9C0A0	CNTP4_HUMAN	cellular (Potential).	2	AAAATCCCTGAG	0.381	
+	4	689	on_p.V158I|BCMO	NM_017429	NP_059125	Q9HAY6	BCDO1_HUMAN		0	GAGAAGGTATCA	0.517	rs149750747
+	4	551	.1_Missense_Muta	NM_001257	NP_001248	P55290	CAD13_HUMAN	Cadherin 1.	1	TATCTCCCATTT	0.358	
+	7	1362	_p.L244F|OSGIN1	NM_013370	NP_037502	Q9UJX0	OSGI1_HUMAN		0	TGGTCCTCGCC	0.701	
+	11	1286	oc.2_Missense_Mu	NM_014972	NP_055787	Q9BQ70	TCF25_HUMAN		0	ATCCGCCTCTTC	0.627	
-	5	1282	tn.1_Missense_Mu	NM_052928	NP_443160	Q8IYR2	SMYD4_HUMAN		5	TCTTATCACAAAG	0.433	
-	5	480	_p.R110H|ATP2A3	NM_174955	NP_777615	Q93084	AT2A3_HUMAN	ame=2; (By similarity).	5	GCGTTGCGTTCC	0.652	
-	17	2399	p.Q788H|ANKFY1	NM_016376	NP_057460	Q9P2R3	ANFY1_HUMAN	ANK 13.	3	AAGACACTGTAC	0.562	
+	5	573		NM_006612	NP_006603	O43896	KIF1C_HUMAN	Kinesin-motor.	2	ATGCTGCTCCAC	0.552	
-	3	1004	gat.2_Missense_M	NM_014519	NP_055334	Q9UNY5	ZN232_HUMAN	SCAN box.	2	GTTTCTCTGGCC	0.592	
-	2	93	onsense_Mutation	NM_207103	NP_996986	Q6UWF3	CQ087_HUMAN	ical; (Potential).	1	GATGATCCAGAA	0.473	
-	17	4894	se_Mutation_p.A1	NM_033004	NP_127497	Q9C000	NALP1_HUMAN	CARD.	9	CAGGGCTTGGT	0.572	
-	29	4544	_uc002gfy.1_Splic	NM_032442	NP_115818	Q96JN8	NEUL4_HUMAN		2	CACACACCTGGA	0.552	
+	7	777	_p.L174F|CHRNB	NM_000747	NP_000738	P11230	ACHB_HUMAN	ical; (Potential).	2	AAGCCTCTCTTC	0.577	
+	11	1674	r.2_Missense_Mut	NM_001143990	NP_001137462	Q9BUR4	WAP53_HUMAN		0	CGCGCCACGTC	0.642	

+	12	2103	p.P661L|ARHGEF	NM_173728	NP_776089	O94989	ARHGF_HUMAN			3	TCACCCCTCTTT	0.637
-	24	3061	ve.1_Missense_M	NM_003802	NP_003793	Q9UKX3	MYH13_HUMAN	Potential.		6	TGTTTTCTTCAA	0.378
+	35	6955	o.2_Missense_Mu	NM_001372	NP_001363	Q9NYC9	DYH9_HUMAN	2 (By similarity).		20	GAACCCTCCAG	0.443
-	8	1937	gov.3_Splice_Site_p.E224_splice			O95361	TRI16_HUMAN			3	ACTTACCAGGG	0.303
-	1	262	M16_uc002gor.1_I	NM_006382	NP_006373	O95170	CDRT1_HUMAN			0	TAGAGGGATGG	0.463
-	3	460	COR1_uc010coz.1	NM_006311	NP_006302	O75376	NCOR1_HUMAN	ith ZBTB33 and HEXIM1.		5	AAATTCTGAAA	0.388
-	1	447		NM_181716	NP_859067	Q7Z7K6	CENPV_HUMAN			0	GGCGGCACCCT	0.617
-	4	422	rl.2_Splice_Site_	NM_148173	NP_680478	Q9UBM1	PEMT_HUMAN			0	TCTTACCTAGG	0.672
+	12	1154	sense_Mutation_p	NM_018242	NP_060712	Q96FL8	S47A1_HUMAN	ical; (Potential).		0	TTAAGCTGTAA	0.408
-	26	3592		NM_000625	NP_000616	P35228	NOS2_HUMAN			4	CTCGACCTGCT	0.602
-	16	2814	sa.1_Missense_M	NM_078471	NP_510880	Q92614	MY18A_HUMAN	osin head-like.		0	AGCCTCCTCTT	0.587
-	5	1122		NM_001045	NP_001036	P31645	SC6A4_HUMAN	ellular (Potential).		4	GCTGGTCCGTG	0.527
+	11	1551	45B_uc002hjc.2_	NM_173167	NP_775259	Q8IWX7	UN45B_HUMAN			6	TCAGGGACTCT	0.458
-	10	1999		NM_001004334	NP_001004334	Q6PRD1	GP179_HUMAN	lasmic (Potential).		3	GCCAAGGTAGG	0.622
-	3	265	T40_uc002hvq.1_	NM_182497	NP_872303	Q6A162	K1C40_HUMAN	Head.		0	TACCGGGGAGA	0.577
-	1	216		NM_033188	NP_149445	Q9BYR2	KRA45_HUMAN	[GRQVCHIEK]- [SPTR]-[V		0	gagatgcagcagcta	0.274
+	12	2014	458*|STAT5A_uc	NM_003152	NP_003143	P42229	STA5A_HUMAN			1	TGTTCCAGGTG	0.607
+	14	2156	474L|STAT5A_uc	NM_003152	NP_003143	P42229	STA5A_HUMAN			1	GTGGCCGCAGC	0.552
+	6	1920		NM_000263	NP_000254	P54802	ANAG_HUMAN			0	TGAATACCAGCA	0.632
+	10	2015	ibk.1_Missense_M	NM_032387	NP_115763	Q96J92	WNK4_HUMAN			7	CCCAGGGAGG	0.552
+	1	294		NM_003734	NP_003725	Q16853	AOC3_HUMAN	ellular (Potential).		4	TGTATCTCCCA	0.622
-	8	4535	.G1413S|GPATCH	NM_001002909	NP_001002909	Q9UKJ3	GPTC8_HUMAN			4	CTGACCTGAGA	0.607
+	14	1748	4B_uc010wjc.1_I	NM_145663	NP_663696	Q8NFT6	DBF4B_HUMAN			0	TTCGTCCCTTTC	0.552
-	17	1948	_p.A528T|EFTUD2	NM_004247	NP_004238	Q15029	U5S1_HUMAN			1	GGTTGCTGTCT	0.498
+	6	1749		NM_013351	NP_037483	Q9UL17	TBX21_HUMAN			0	CTCCTCCCCTG	0.522
+	2	1004	inb.3_Missense_M	NM_003204	NP_003195	Q14494	NF2L1_HUMAN			1	TCAGCCCAACT	0.607
+	7	2576	p.S782F|AKAP1_	NM_003488	NP_003479	Q92667	AKAP1_HUMAN	Tudor.		1	TGCCTCCTACG	0.607
-	15	2798	p.P583S|BZRAP1	NM_004758	NP_004749	O95153	RIMB1_HUMAN			3	AGCTGGGAGCA	0.647
+	25	5802	NC2_uc002jao.3_	NM_025185	NP_079461	Q9HCD6	TANC2_HUMAN			2	TGCTGGCTAAC	0.527
-	14	1713	LZ_uc002jfx.3_Mi	NM_014877	NP_055692					2	AGCGACCAAAA	0.413
+	4	1914	.G618V|BPTF_uc	NM_182641	NP_872579	Q12830	BPTF_HUMAN	ction with KEAP1.		4	GCAAGGAAAAT	0.318
+	7	888	6_splice|PRKAR1	NM_212471	NP_997636	P10644	KAP0_HUMAN			12	TCATGGTAAGA	0.368
-	22	3096	wqq.1_Splice_Site_	NM_007168	NP_009099	O94911	ABCA8_HUMAN			3	TCCATTCTGAAA	0.353
+	2	131	g.2_RNA|DNAI2_u	NM_023036	NP_075462	Q9GZS0	DNAI2_HUMAN			3	GAAGCGCAGCG	0.637
+	9	1459	p.A426V|GAA_uc	NM_001079803	NP_001073271	P10253	LYAG_HUMAN			1	CCCGGCCATGG	0.647
+	10	1512	p.P444S|GAA_uc	NM_001079803	NP_001073271	P10253	LYAG_HUMAN			1	AGGATCCTGCC	0.642
+	32	3015	_Mutation_p.P287	NM_005993	NP_005984	Q9BTW9	TBCD_HUMAN			0	TGCACCTTCCC	0.657
+	11	969	o.2_Missense_Mu	NM_003826	NP_003817	Q99747	SNAG_HUMAN			0	ACCAAGATCAG	0.453
-	29	4390		NM_005406	NP_005397	Q13464	ROCK1_HUMAN	|Auto-inhibitory.		5	AACAAAATTTTTT	0.338
+	3	940	ABLES1_uc002ku	NM_001100619	NP_001094089	Q8TDN4	CABL1_HUMAN	th CDK3 (By similarity).		1	GTTCACCCAGA	0.438
-	10	1847	n.1_Missense_Mu	NM_001792	NP_001783	P19022	CADH2_HUMAN	(Potential).|Cadherin 3.		4	CTGCAGCAACA	0.403
-	13	2190	m.2_Missense_M	NM_024421	NP_077739	Q08554	DSC1_HUMAN	(Potential).	p.S643F(1)	4	GCACAGAATAA	0.358
-	9	980	18orf34_uc002kxo.	NM_001105528	NP_001098998	Q5BJE1	CR034_HUMAN	Potential.		1	AAGTTCCTGAT	0.323
+	1	177	rf21_uc002kzd.2_	NM_031446	NP_113634	Q32NC0	CR021_HUMAN			0	GCTACCTCCTG	0.637
-	9	1201	Mutation_p.D173	NM_003199	NP_003190	P15884	ITF2_HUMAN			2	CGAGTCCCTAT	0.512
+	18	2699		NM_194449	NP_919431	O60346	PHLP1_HUMAN	PP2C-like.		0	TGGTGCCTCGC	0.602
+	6	688	xet.1_Missense_	NM_001040147	NP_001035237	O75635	SPB7_HUMAN			3	AATCTCCCAAG	0.413

-	6	941	2llf.2_Missense_M	NM_152676	NP_689889	Q8NCQ5	FBX15_HUMAN		3	GATATGGTCAAAT	0.468	
+	4	371	lo.2_Missense_Mu	NM_018235	NP_060705	Q96KP4	CNDP2_HUMAN		3	AGCTCCCTGATGC	0.517	
-	2	233	ense_Mutation_p.A	NM_025078	NP_079354	Q8N2U9	PQLC1_HUMAN	1.|Helical; (Potential).	2	GGCCGCGCCCC	0.711	
+	21	3169	sb.1_Missense_Mu	NM_019112	NP_061985	Q8IZY2	ABCA7_HUMAN	C transporter 1.	9	ATTTGGGAGCTGC	0.408	
-	4	649	DAMTSL5_uc010x	NM_213604	NP_998769	Q6ZMM2	ATL5_HUMAN	TSP type-1.	0	ACGGTTCTTCCCC	0.677	
-	5	2446_2447	O1_uc010xgs.1_5	NM_020695	NP_065746	Q8N1G1	REXO1_HUMAN		0	ATGGTGGTGGTA	0.644	
-	14	2147		NM_015174	NP_055989	Q9UPR6	ZFR2_HUMAN		2	GGTCGGAGGAG	0.542	
-	5	1113	JS3L_uc010duk.2_	NM_020175	NP_064560	Q96G46	DUS3L_HUMAN		0	TGGTGCAGACG	0.607	
+	3	1929		NM_025061	NP_079337	Q6NSJ5	LRC8E_HUMAN	LRR 5.	2	CAGGAACTTGAC	0.632	
-	3	14698		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).	57	TGGTAACTACTGT	0.453	
-	1	3155		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).	57	GAAACAGTGGTTC	0.463	
-	1	2849		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).	57	ACTCTGGAAACAC	0.483	
-	8	1222	ws.2_Missense_M	NM_024106	NP_077011	Q9BUY5	ZN426_HUMAN	C2H2-type 4.	1	AGTTGGAATAATT	0.433	
-	26	2815	nh.2_Missense_M	NM_001379	NP_001370	P26358	DNMT1_HUMAN	BAH 1.	6	TGGAGGGGACT	0.572	
-	25	2997	lq.1_Missense_Mu	NM_020812	NP_065863	Q96HP0	DOCK6_HUMAN		3	CCACATCCTGGGC	0.617	
+	3	349		NM_152356	NP_689569	Q8N8L2	ZN491_HUMAN		2	CAGGTTCCGGAA	0.398	
-	5	1592		NM_020714	NP_065765	Q9ULM2	ZN490_HUMAN	C2H2-type 12.	0	TTCAGGGAATTTA	0.413	
-	9	3261	p.E1039K|SFRS14	NM_014884	NP_055699	Q8IX01	SUGP2_HUMAN	G-patch.	0	CCGGCTCCCTGAT	0.642	
+	3	307		NM_004386	NP_004377	O14594	NCAN_HUMAN	g-like V-type.	4	AGCGCAGCCCGA	0.652	rs2228601
+	6	1204	714_uc010ecp.1_M	NM_182515	NP_872321	Q96N38	ZN714_HUMAN		0	GTTAAAGAAAAAC	0.348	
+	2	903	_p.P336L|ZNF493_	NM_175910	NP_787106	Q6ZR52	ZN493_HUMAN	type 7; degenerate.	1	CAACCCCTACTAA	0.348	rs142651314
-	3	1700		NM_001001411	NP_001001411	Q8N7Q3	ZN676_HUMAN	C2H2-type 11.	0	CTTGAGGACCAGC	0.418	
-	4	1151_1152	_p.P268F|ZNF681_	NM_138286	NP_612143	Q96N22	ZN681_HUMAN		0	TGTAGGGTTTCTC	0.401	
+	7	613	c010xsh.1_Missens	NM_002151	NP_002142	P05981	HEPS_HUMAN	xtracellular (Potential).	2	CGAGGGGAGGC	0.692	
+	6	1388	p.G389D|ZNF567_	NM_152603	NP_689816	Q8N184	ZN567_HUMAN		0	ATACAGGTGAGAA	0.438	
+	11	1035	oe.2_Missense_M	NM_138392	NP_612401	Q8TBC3	SHKB1_HUMAN	WD 3.	2	TCACCAGTTATGA	0.647	
+	9	2266	M5_uc002orl.2_Sp	NM_004363	NP_004354	P06731	CEAM5_HUMAN		2	AGACTGGTAGGT	0.507	
-	1	1756		NM_015649	NP_056464	Q8IU81	I2BP1_HUMAN		0	CGTTGCGGGCC	0.741	
-	3	2001		NM_001080457	NP_001073926	Q9NT99	LRC4B_HUMAN	lasmic (Potential).	2	GCTCGTCCTCCAC	0.731	
-	5	755	p.C225Y|KLK10_u	NM_145888	NP_665895	O43240	KLK10_HUMAN	Peptidase S1.	2	CCTGGCAAGGG	0.512	
+	5	819	p.V243M|TTYH1_	NM_020659	NP_065710	Q9H313	TTYH1_HUMAN	Name=4; (Potential).	0	TGGCTGGTGATC	0.632	
-	19	2386_2387	|SAPS1_uc002qjv	NM_014931	NP_055746	Q9UPN7	PP6R1_HUMAN	Pro-rich.	0	TCAAAGGTGGCT	0.668	
-	2	341		NM_176820	NP_789790	Q7RTR0	NALP9_HUMAN		7	ATGTTTCCTTCAT	0.348	
+	3	1839	etg.2_Missense_M	NM_176811	NP_789781	Q86W28	NALP8_HUMAN		13	CTGAAAGTCATAC	0.488	
+	7	2209	ni.2_Missense_Mu	NM_153447	NP_703148	P59047	NALP5_HUMAN	LRR 2.	7	AAAATTCGGGTG	0.498	
+	7	1335	446_uc010eur.2_3	NM_017908	NP_060378	Q9NWS9	ZN446_HUMAN	C2H2-type 2.	1	AGCTGGAAGTCC	0.652	
-	6	2425	on|MZF1_uc002qt	NM_198055	NP_932172	P28698	MZF1_HUMAN		1	GCTTTTCGCCGG	0.672	
+	2	1003	vm.1_Missense_M	NM_016030	NP_057114	Q8WVT3	TTC15_HUMAN		4	CCATGCGAGGGC	0.577	
+	1	482		NM_080657	NP_542388	Q8WXG1	RSAD2_HUMAN		0	AAGCTGGTGAGT	0.512	
+	7	971	2qyt.2_Missense_M	NM_014746	NP_055561	P50876	R144A_HUMAN		2	ATGGAAGAAGATC	0.567	
+	7	665	2rat.2_Missense_I	NM_001039362	NP_001034451	Q8NEY4	VATC2_HUMAN		1	CTTCTGGTCATCC	0.562	
-	31	3682	e_Mutation_p.A29	NM_015909	NP_056993	A2RRP1	NBAS_HUMAN		4	CCAACGGCTTGG	0.378	
-	15	2254		NM_000384	NP_000375	P04114	APOB_HUMAN		27	AAAAATCCTTGCT	0.418	
-	1	420	km.1_Missense_M	NM_004036	NP_004027	O60266	ADCY3_HUMAN	lasmic (Potential).	4	TCGTGGCGCTGC	0.597	
-	3	376		NM_018263	NP_060733	Q76L83	ASXL2_HUMAN		1	GCAAGAGGAGAAC	0.373	
+	14	1905		NM_145038	NP_659475	Q96MC2	CC164_HUMAN	Glu-rich.	0	gaagaggaggagAC	0.358	
+	11	1661	v.2_Missense_Mut	NM_004341	NP_004332	P27708	PYR1_HUMAN	phosphate synthase).|CPS	10	GGTCCGGGTCCT	0.627	

+	6	673	NX17_uc010ylm.	NM_014748	NP_055563	Q15036	SNX17_HUMAN	s-associating.		1	AGCTGGATCTT	0.468
+	37	7450		NM_016252	NP_057336	Q9NR09	BIRC6_HUMAN			14	TGTAGGTGCGA	0.443
-	8	1473	nd.1_Missense_	NM_015475	NP_056290	Q8NCA5	FA98A_HUMAN	Gly-rich.		1	gcctccacgaccacct	0.393
-	4	601	g.2_Missense_Mu	NM_005102	NP_005093	Q9UHY8	FEZ2_HUMAN			1	GTGTAGGGGTT	0.418
+	4	817	_p.G250E|MSH2_	NM_000251	NP_000242	P43246	MSH2_HUMAN			55	AAAGGGAGAGC	0.318
+	5	3565	i.1_Missense_Mut	NM_000179	NP_000170	P52701	MSH6_HUMAN	P (Potential).		168	TATGGGGGGCA	0.378
-	9	1754	zd.2_Missense_M	NM_001122964	NP_001116436	Q5MIZ7	P4R3B_HUMAN			1	ATTCACTTTTTT	0.318
+	18	1969		NM_032208	NP_115584	Q9H6X2	ANTR1_HUMAN	c (Potential).|Pro-rich.		4	cccaccttccacccttc	0.09
-	8	1674		NM_017880	NP_060350	Q9NWW7	CB042_HUMAN			0	TCTGGGGTATCT	0.428
+	10	2199		NM_005791	NP_005782	O00566	MPP10_HUMAN			3	TAGCTTCGGAGA	0.423
+	10	5698	g.2_Missense_Mu	NM_015120	NP_055935	Q8TCU4	ALMS1_HUMAN	approximate tandem repea		9	CTTATGAGCAG	0.453
-	3	909	_p.S130N|MOGS_	NM_006302	NP_006293	Q13724	MOGS_HUMAN	enal (Potential).		0	CTGGACTGGTT	0.527
-	6	683	th.1_Missense_M	NM_022912	NP_075063	Q9H902	REEP1_HUMAN			0	GTTTGCCGCTG	0.647
-	9	1852		NM_004836	NP_004827	Q9NZJ5	E2AK3_HUMAN			3	TCTTACCCTGTG	0.254
-	33	4699	NP200_uc010yuj.1	NM_014014	NP_054733	O75643	U520_HUMAN		p.R1538C(1)	10	GCAGGCGGGTT	0.557
+	11	1727	bt.2_Missense_Mu	NM_003854	NP_003845	Q9HB29	ILRL2_HUMAN	oplasmic (Potential).		2	GAGATACCACAT	0.572
-	6	1265	_p.S164F|TGFBR	NM_004257	NP_004248	Q8WUH2	TGFA1_HUMAN			2	AGGAGGAGGTG	0.547
-	7	705	b.2_Missense_Mu	NM_004336	NP_004327	O43683	BUB1_HUMAN			7	CTGAAGATATC	0.323
+	5	1448	D4_uc002tje.2_In	NM_012455	NP_036587	Q8NDX1	PSD4_HUMAN			2	GGGTGGACACC	0.642
+	13	3572	t.3_Missense_Mu	NM_005270	NP_005261	P10070	GLI2_HUMAN			13	CTTTGGCCAGT	0.692
+	13	1673	|POTEE_uc002tsl.	NM_001083538	NP_001077007	Q6S8J3	POTEE_HUMAN			0	TCGAAGAAATG	0.373
+	9	783	GAP1_uc010fng.	NM_012233	NP_036365	Q15042	RB3GP_HUMAN			2	AGATGCCCTTG	0.363
+	19	2141	GAP1_uc010fng.2	NM_012233	NP_036365	Q15042	RB3GP_HUMAN			2	CCCGGGATTAT	0.423
-	54	9568		NM_018557	NP_061027	Q9NZR2	LRP1B_HUMAN	ntial).|LDL-receptor class A		50	TCCATCACACT	0.403
+	7	1112	D2_uc002tzd.3_M	NM_001083112	NP_001076581	P43304	GPDM_HUMAN			1	AGTGAGCTTGC	0.572
-	3	1327		NM_018086	NP_060556	Q5HY92	FIGN_HUMAN			4	GTTGGCCATAG	0.448
+	7	1869	dg.2_Missense_	NM_024969	NP_079245	Q8WYN3	CSRN3_HUMAN			5	CAACCCCTCTG	0.517
-	8	1147	_p.R246*|SCN1A_	NM_006920	NP_008851	P35498	SCN1A_HUMAN	I.		13	TAGTCGAAACA	0.388
+	3	384	.2_Missense_Mut	NM_138995	NP_620482	Q8WXR4	MYO3B_HUMAN	rotein kinase.		19	CTAATCATCCC	0.418
+	14	1488	0fqo.2_Missense_	NM_007023	NP_008954	Q8WZA2	RPGF4_HUMAN	cAMP 2.		6	AGCTGCCTCTA	0.488
-	1	882		NM_152275	NP_689488	Q86WT1	TT30A_HUMAN	TPR 4.		0	GTGCTGAGGCA	0.552
-	275	71319	94G|TTN_uc010z	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN			153	AAGCTCTTAAA	0.378
-	275	62973	12T|TTN_uc010z	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN			153	GGTGGCTGTGG	0.438
-	253	52930	T11264I|TTN_uc0	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN			153	TTAATGGTAAGT	0.438
-	194	37684	.1_Missense_Mut	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN			153	GGTTTGGAGACT	0.398
-	66	16515	_uc010zfj.1_Intro	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN			153	GGAGGCTTCTA	0.373
-	46	15582	N_uc010zfi.1_Intr	NM_133379	NP_596870	Q8WZ42	TITIN_HUMAN			153	CAGTAGGAATAG	0.478
-	46	13311	N_uc010zfi.1_Intr	NM_133379	NP_596870	Q8WZ42	TITIN_HUMAN		p.A4363A(1)	153	TCTCTCTTTCC	0.383
-	46	13143	N_uc010zfi.1_Intr	NM_133379	NP_596870	Q8WZ42	TITIN_HUMAN			153	ATAGTCCCTTA	0.418
+	9	1301		NM_018471	NP_060941	Q8WU90	ZC3HF_HUMAN			1	CATATACTTCAG	0.308
+	8	1455	_Mutation_p.E415	NM_177454	NP_803237	Q6P995	F171B_HUMAN	lasmic (Potential).		10	AACAGAAGAAA	0.348
-	17	1791	k.1_Missense_Mu	NM_003151	NP_003142	Q14765	STAT4_HUMAN			9	TTGATCTGAGT	0.453
+	6	1821	_p.T536I|SLC39A	NM_001127257	NP_001120729	Q9ULF5	S39AA_HUMAN			2	GAACACAGAAG	0.338
-	46	8787		NM_018897	NP_061720	Q8WXX0	DYH7_HUMAN			12	TAGCTCCAGAG	0.488
-	36	5971		NM_018897	NP_061720	Q8WXX0	DYH7_HUMAN	3 (By simila	p.R1957*(1)	12	AGTATCGAATT	0.378
+	21	2361	_p.E310K|AOX1_u	NM_001159	NP_001150	Q06278	ADO_HUMAN			6	ATATGGAAACCC	0.433
+	10	1088		NM_015934	NP_057018	Q9Y2X3	NOP58_HUMAN	Nop.		0	ATGCAGCTTCTA	0.393

+	10	1319	10zib.1_Missense_	NM_001104586	NP_001098056	Q8N187	AL2S8_HUMAN		2	TGGAGCAGGAG	0.308
+	12	1679	ıse_Mutation_p.P	NM_001104586	NP_001098056	Q8N187	AL2S8_HUMAN		2	TTTTTTCCAACTG	0.328
-	25	3132	zji.1_Missense_Mu	NM_005235	NP_005226	Q15303	ERBB4_HUMAN	lasmic (Potential).	33	CCAAATCCTCTTC	0.433
-	28	4878	_uc002vfg.2_Splic	NM_212482	NP_997647	P02751	FINC_HUMAN		13	AAGTTACCTGTT	0.438
+	17	3416	x.2_Missense_Mut	NM_014640	NP_055455	Q14679	TTLL4_HUMAN		3	GAAGATGAGTTTT	0.458
+	22	4838		NM_005876	NP_005867	Q15772	SPEG_HUMAN	se 1.|ATP (By similarity).	14	CTTTCTCCTACTT	0.642
-	4	845	ER_uc010zly.1_5'U	NM_139072	NP_620711	Q8NFT8	DNER_HUMAN	cellular (Potential).	8	GAGGCAGTGGCA	0.453
+	5	887	p.R152K|CAB39_u	NM_016289	NP_057373	Q9Y376	CAB39_HUMAN		1	GCATCAGACATGA	0.333
+	17	2219	mp.1_Missense_M	NM_001017915	NP_001017915	Q92835	SHIP1_HUMAN		2	GTCAGTCTTATGC	0.488
-	8	1293	_p.W348*|HJURP_	NM_018410	NP_060880	Q8NCD3	HJURP_HUMAN		1	AATTAACCATTTT	0.398
+	8	1413	vt.2_Missense_Mu	NM_001037131	NP_001032208	Q9UPQ3	AGAP1_HUMAN	all GTPase-like.	3	GAGGTGGGAGTT	0.498
-	18	2548	CA1_uc002vwa.1_	NM_024726	NP_079002	Q86XH1	IQCA1_HUMAN		1	TTAAAGCTCTCTT	0.478
+	17	2272	D1_uc002waj.1_5'F	NM_001080437	NP_001073906	Q8TER0	SNED1_HUMAN	alcium-binding (Potential).	2	AGTGCCGGTCT	0.562
+	8	1248	DH_uc002wcg.1_	NM_152783	NP_689996	Q8N465	D2HDH_HUMAN		0	TCCTGGAGCAC	0.612
-	8	1368	PT4_uc010zpn.1_	NM_015985	NP_057069	Q9Y264	ANGP4_HUMAN	ıogen C-terminal.	2	CCAGGCTGCTC	0.617
-	12	1118	DH3B_uc002wgr.2_	NM_006899	NP_008830	O43837	IDH3B_HUMAN		0	AGTCGGTTGTG	0.562
+	4	1283	zqz.1_Missense_M	NM_001819	NP_001810	P05060	SCG1_HUMAN		6	GAGGGACCACC	0.537
-	8	1810	ERMT1_uc002wms	NM_017671	NP_060141	Q9BQL6	FERM1_HUMAN	FERM.	3	TTCATCAACCTC	0.413
+	10	1546	F341_uc010geq.2_	NM_032819	NP_116208	Q9BYN7	ZN341_HUMAN	C2H2-type 6.	2	CTGCGGCAAGG	0.587
-	2	960	_Missense_Mutati	NM_000557	NP_000548	P43026	GDF5_HUMAN		0	CGGGACCTCGG	0.612
+	2	1432		NM_080552	NP_542119	Q9H598	VIAAT_HUMAN	ical; (Potential).	0	CCAAGGCGCTGT	0.617
+	3	334	xmu.2_Missense_	NM_003404	NP_003395	P31946	1433B_HUMAN		4	GAGCAGGCTGAG	0.463
-	1	121	W1_uc002xot.2_5	NM_020398	NP_065131	O95925	EPPI_HUMAN	WAP.	1	TTACTGGGAAATA	0.507
+	2	209	xpo.2_Splice_Site	NM_007019	NP_008950	O00762	UBE2C_HUMAN		0	CTCATGGTGAGT	0.498
+	12	2361	m.2_Missense_Mu	NM_181659	NP_858045	Q9Y6Q9	NCOA3_HUMAN		5	GGGACGGAAATG	0.473
-	2	1608	us.1_Missense_Mu	NM_004975	NP_004966	Q14721	KCNB1_HUMAN	lasmic (Potential).	2	ACAAGTGGTTAT	0.428
-	6	865	xvc.2_Intron|UBE2	NM_199203	NP_954673	Q13404	UB2V1_HUMAN		0	TGCGAGGGACT	0.458
+	12	2089	p.S500N|PHACTR	NM_080672	NP_542403	Q96KR7	PHAR3_HUMAN		3	ACAAAAGTAATGA	0.333
-	23	2487		NM_014258	NP_055073	Q9BX26	SYCP2_HUMAN		5	GTTTCGAATCCC	0.328
-	16	1908		NM_002772	NP_002763	P98073	ENTK_HUMAN	lar (Potential).|CUB 2.	8	TTAAACCCTCCTC	0.458
+	21	2652	|ITSN1_uc002ysx.	NM_003024	NP_003015	Q15811	ITSN1_HUMAN	SH3 1.	4	AGGGTGGTTCC	0.483
-	4	2230	uk.3_Missense_Mu	NM_001001890	NP_001001890	Q01196	RUNX1_HUMAN	o/Ser/Thr-ricp.H242fs*14(2)	387	CGTGGGGGCTG	0.627
+	10	1269	aeb.1_Missense_M	NM_005128	NP_005119	Q9Y3R5	DOP2_HUMAN		2	CTGCAGAGATGC	0.453
-	11	2727	CAM_uc002yyr.1_F	NM_001389	NP_001380	O60469	DSCAM_HUMAN	Potential).|Ig-like C2-type 8.	11	TGTCTTCCTCCAC	0.517
-	5	1302	CAM_uc002yyr.1_F	NM_001389	NP_001380	O60469	DSCAM_HUMAN	Potential).|Ig-like C2-type 3.	11	AGGGGCGAATGT	0.542
+	6	577	ı_p.P12S|RRP1_u	NM_003683	NP_003674	P56182	RRP1_HUMAN		0	AGGCCCCCAAC	0.597
-	15	2311	l.1_Missense_Mut	NM_001127491	NP_001120963	P05107	ITB2_HUMAN	lasmic (Potential).	9	GTGGCGCTCTTG	0.557
+	33	7306	.2_Missense_Muta	NM_006031	NP_006022	O95613	PCNT_HUMAN		8	GGTGCGTGACG	0.642
-	2	334	4R_uc002zru.2_5'	NM_023004	NP_075380	Q9BZR6	RTN4R_HUMAN	LRRNT.	0	CTGCTGGGGGC	0.672
-	10	1717	zsk.1_Missense_M	NM_153334	NP_699165	Q96GP6	SREC2_HUMAN	lasmic (Potential).	1	CAGCCCTGAGG	0.612
+	5	1859		NM_152612	NP_689825	Q8IYX3	CC116_HUMAN		2	ATAAAGCCGAGA	0.438
+	13	3250	y.1_Missense_Mut	NM_004327	NP_004318	P11274	BCR_HUMAN	C2.	12	CCAACTCGTGTG	0.567
+	5	506	C2A11_uc011ajc.	NM_001024938	NP_001020109	Q9BYW1	GTR11_HUMAN	Name=4; (Potential).	1	GTCCAGGTGTGA	0.642
+	4	1533	309L|MYO18B_uc	NM_032608	NP_115997	Q8IUG5	MY18B_HUMAN		12	GGAGTCGCCAG	0.632
+	15	3143	guz.1_Missense_M	NM_032608	NP_115997	Q8IUG5	MY18B_HUMAN	osin head-like.	12	TTGAGGAGCTG	0.612
+	4	3000	uc003afp.2_Silent_	NM_021076	NP_066554	P12036	NFH_HUMAN	Tail.	0	GCCAAGGAAGAT	0.507
+	7	859	ua.1_Missense_Mu	NM_014291	NP_055106	O75600	KBL_HUMAN		0	CTGGGCCCCTGG	0.657

+	8	1373		NM_004286	NP_004277	O00178	GTPB1_HUMAN		1	TGGCAGGGTGT	0.612	
+	6	1417	gxz.1_Missense_M	NM_019008	NP_061881	Q9NQG6	SMC7L_HUMAN		1	GACAAACATCTC	0.577	
+	2	730		NM_001429	NP_001420	Q09472	EP300_HUMAN	action with ALX1.	64	AGAGCAGTCCTG	0.512	
-	10	1279	p.R381Q|NAGA_u	NM_000262	NP_000253	P17050	NAGAB_HUMAN		1	CATCTCGGAGG	0.562	rs144771084
-	3	1225	gzd.2_Nonsense_M	NM_017436	NP_059132	Q9NPC4	A4GAT_HUMAN	nenal (Potential).	2	TGCCCTGGCTCT	0.617	
-	5	564	1_uc003bdj.2_Spli	NM_012263	NP_036395	O95922	TTLL1_HUMAN		1	CAAAGTCTGCAA	0.552	
+	2	65		NM_001197	NP_001188	Q13323	BIK_HUMAN		0	AAATGTCTGAAG	0.532	
+	12	1683	2_splice|ATXN10_	NM_013236	NP_037368	Q9UBB4	ATX10_HUMAN		2	TCTTTAGTGAATG	0.343	
-	3	727	aa.2_Missense_M	NM_058238	NP_478679	P56706	WNT7B_HUMAN		1	GTGACGGCGTGC	0.692	
-	9	1199	p.V212M|LMF2_u	NM_033200	NP_149977	Q9BU23	LMF2_HUMAN		1	CCGCACCTGGG	0.652	
+	15	1279		NM_153635	NP_705899	Q8IYJ1	CPNE9_HUMAN	VWFA.	2	CAGTTCCCCCTG	0.522	
+	4	2096	sg.2_Missense_M	NM_004634	NP_004625	P55201	BRPF1_HUMAN	iptional activation.|Interacti	3	TGCAATCTCAGA	0.547	
+	15	1450	'Flank|IL17RC_uc	NM_153483	NP_705616	Q8NFR9	I17RE_HUMAN	cellular (Potential).	1	AAGCACCTCTTG	0.607	
+	16	1366	D2_uc003buy.1_M	NM_033084	NP_149075	Q9BXW9	FACD2_HUMAN		4	CTTAAGGATATGT	0.398	
-	22	3753	_Mutation_p.P106	NM_001001331	NP_001001331	Q01814	AT2B2_HUMAN	lasmic (Potential).	6	TCCTCCGGGATC	0.637	
-	3	749	e_Mutation_p.Q10	NM_001001331	NP_001001331	Q01814	AT2B2_HUMAN	ical; (Potential).	6	GTCCTGCAGCG	0.557	
-	5	530	_Missense_Mutati	NM_012260	NP_036392	Q9UJ83	HACL1_HUMAN		0	GAAACTCCTGGA	0.244	
+	5	1614	caq.3_Missense_M	NM_054110	NP_473451	Q8N3T1	GLTL2_HUMAN	tial).|Catalytic subdomain E	1	ACACTGGAGCGT	0.547	
+	6	1773	3caq.3_Missense_I	NM_054110	NP_473451	Q8N3T1	GLTL2_HUMAN	nenal (Potential).	1	AGGCCACCCTGA	0.552	
-	2	526	385D_uc010hfb.1_	NM_024697	NP_078973	Q9H6B1	Z385D_HUMAN		5	CAAGAGGAAAGG	0.502	
+	2	608		NM_001137674	NP_001131146	A6NHJ4	ZN860_HUMAN		1	CTCTTCCTCAGG	0.483	
+	11	1088	P21_uc011axy.1_I	NM_016300	NP_057384	Q9UBL0	ARP21_HUMAN		3	AGATGACAGAC	0.378	
+	2	334	TAC_uc011aya.1_I	NM_003149	NP_003140	Q99469	STAC_HUMAN		4	CCAGGGCTGGT	0.562	
+	2	337	AC_uc011aya.1_M	NM_003149	NP_003140	Q99469	STAC_HUMAN		4	AGGGCTGGTCTG	0.562	
-	12	6694		NM_014831	NP_055646	O15050	TRNK1_HUMAN		2	CATGCCCTCCTC	0.582	
+	14	2164	_p.V715M|DLEC1	NM_007335	NP_031361	Q9Y238	DLEC1_HUMAN		9	CAGATGGTGCTA	0.587	
+	3	430	99K|MYRIP_uc01	NM_015460	NP_056275	Q8NFW9	MYRIP_HUMAN	E-type.|RabBD.	5	AGCACGAAAAG	0.557	
+	4	966_967	cnr.2_Missense_M	NM_003420	NP_003411	P13682	ZNF35_HUMAN		0	AGAAACCCTTTG	0.465	
+	26	3312	p.D958N|KIF15_u	NM_020242	NP_064627	Q9NS87	KIF15_HUMAN	Potential.	1	CTGAGGACATA	0.383	
-	8	2362	al.1_Missense_Mu	NM_024513	NP_078789	Q9BQS8	FYCO1_HUMAN	Potential.	1	GCTGGCACTGC	0.607	
-	3	1433_1434	ro.3_Nonsense_M	NM_006574	NP_006565	O95196	CSPG5_HUMAN	cellular (Potential).	2	CACCTGGAAGTC	0.589	
+	2	2297	p.G153D|TREX1_u	NM_033629	NP_338599	Q9NSU2	TREX1_HUMAN		0	CACTGGGTCTGC	0.577	
-	1	320	PRKAR2A_uc003c	NM_004157	NP_004148	P13861	KAP2_HUMAN	on and phosphorylation.	1	GTCAGGCGGCT	0.711	
-	5	475	_p.L12P|QARS_uc	NM_005051	NP_005042	P47897	SYQ_HUMAN		1	CACTTCAGCACA	0.527	
+	3	2071		NM_004393	NP_004384	Q14118	DAG1_HUMAN	eptidase S72.	2	GTCCTGGGTACA	0.567	
-	10	1240	c011bcs.1_Silent_	NM_020998	NP_066278	P26927	HGFL_HUMAN	Kringle 4.	1	CTGCTCCCCTG	0.706	
-	4	1078	_p.A156T|MON1A_	NM_032355	NP_115731	Q86VX9	MON1A_HUMAN		2	CCACCGCCACTA	0.612	
+	5	999	3ddt.1_Splice_Site_	NM_015512	NP_056327	Q9P2D7	DYH1_HUMAN		3	TGAAGGTGAGC	0.597	
+	4	483	ei.1_Missense_Mu	NM_015136	NP_055951	Q9NY15	STAB1_HUMAN	Extracellular (Potential).	9	ACCTGTGTGTGC	0.637	
+	7	773	1_uc003dft.2_5'Fla	NM_002215	NP_002206	P19827	ITIH1_HUMAN		3	CTACATCCTTACT	0.572	
-	14	1887	ense_Mutation_p.H	NM_015541	NP_056356	Q96JA1	LRIG1_HUMAN	Potential).|Ig-like C2-type 2.	5	TGGGTGACCTG	0.562	
-	6	776	.A124V|C3orf64_u	NM_173654	NP_775925	Q5NDL2	AER61_HUMAN		1	TCTCTGGCATAT	0.363	
-	2	192		NM_020872	NP_065923	Q9P232	CNTN3_HUMAN	like C2-type 1.	5	CAACAGGGAAAA	0.363	
+	5	1344	_p.V367I|COL8A1	NM_001850	NP_001841	P27658	CO8A1_HUMAN	elical region (COL1).	0	GAGGTGTTCCT	0.637	
+	5	458	ıc003dvc.2_RNA|F	NM_020357	NP_065090	Q8WW12	PCNP_HUMAN		0	CAAACTCCTTCA	0.338	
+	11	2413	l.1_Missense_Mut	NM_024548	NP_078824	Q8IW35	CEP97_HUMAN		2	GAGACAAGAGAT	0.413	
+	2	1067	p.D161N|PLCXD2	NM_001134478	NP_001127950	Q0VAA5	PLCX2_HUMAN	I-PLC X-box.	1	TCCTGGATTTCA	0.502	

+	7	871	bjd.1_Missense_	NM_033364	NP_203528	Q7Z4T9	AAT1_HUMAN	Potential.	3	TGAGAAGAGGA	0.522
+	13	1277	bjn.1_Missense_	NM_021082	NP_066568	Q16348	S15A2_HUMAN		1	CTTCTCGTAAGT	0.378
+	8	947	ense_Mutation_p.V	NM_013336	NP_037468	P61619	S61A1_HUMAN	ical; (Potential).	1	CAGTGGTCATC	0.532
-	19	2312	rc.1_Missense_Mu	NM_005862	NP_005853	Q8WVM7	STAG1_HUMAN		2	GTCTTCCACAG	0.343
-	5	1019	ns.1_Missense_M	NM_015472	NP_056287	Q9GZV5	WWTR1_HUMAN		4	TCTCATCCACATT	0.463
-	6	7096	_p.P393S|IGSF10_	NM_178822	NP_849144	Q6WRI0	IGS10_HUMAN	ike C2-type 10.	13	AGGTGGTGGGT	0.383
+	1	94		NM_001101337	NP_001094807	P0CE67	CC079_HUMAN		0	TGGTCAGGATCC	0.443
+	12	1216	d.1_Missense_Mut	NM_015938	NP_057022	Q96D46	NMD3_HUMAN		1	ATTTGGGACATC	0.373
+	2	152		NM_130770	NP_570126	Q8WXA8	5HT3C_HUMAN	cellular (Potential).	3	ATGGGGTTGAC	0.527
+	5	852	b.2_Missense_Mu	NM_003722	NP_003713	Q9H3D4	P63_HUMAN		12	TCAACGAGGGT	0.498
-	4	376_377	IAP1_uc003fvx.3_RNA						0	ATTATGGGTCTAT	0.406
+	12	1590	_p.E513K|PDE6B_	NM_000283	NP_000274	P35913	PDE6B_HUMAN		0	GCACCGAACTG	0.582
-	8	1299	329W|MFSD10_uc	NM_001120	NP_001111	Q14728	MFS10_HUMAN		0	GATCCGCCGGG	0.662
+	12	1523	cw.2_Missense_Mu	NM_001528	NP_001519	Q04756	HGFA_HUMAN	Peptidase S1.	2	GAAAGGGGACC	0.667
-	6	1711		NM_177998	NP_819056	Q7RTM1	OTOP1_HUMAN	ical; (Potential).	3	GGCGGGAGGTA	0.537
-	16	2461	e_Mutation_p.E47	NM_001099433	NP_001092903	Q96N16	JKIP1_HUMAN		4	GTTCTTCATTTCT	0.458
+	7	1093	53_splice|MAN2B2	NM_015274	NP_056089	Q9Y2E5	MA2B2_HUMAN		2	CACAGGTACAG	0.617
-	25	2794	003gou.2_Intron|P	NM_006017	NP_006008	O43490	PROM1_HUMAN		7	GCTTTACCTTGT	0.383
-	4	758	p.A181V|SEPSEC	NM_153825	NP_722547	Q9HD40	SPCS_HUMAN		0	TTACCTGCAGTG	0.303
+	10	1081	_Mutation_p.M309	NM_025132	NP_079408	Q8NEZ3	WDR19_HUMAN	WD 5.	1	AGACATGTATGTT	0.274
-	21	2909_2910	x.1_Missense_Mut	NM_002913	NP_002904	P35251	RFC1_HUMAN		4	ACTCCGGATCTG	0.495
+	2	754	n_p.Q87*|NSUN7_	NM_024677	NP_078953				0	TCCTTTCAGCGT	0.448
+	8	2538	ozz.1_Missense_	NM_020722	NP_065773	Q6ZU35	K1211_HUMAN		2	CAGTCAATGCAA	0.577
-	5	1219	_p.V386I|UGT2A	NM_006798	NP_006789	Q9Y4X1	UD2A1_HUMAN	cellular (Potential).	1	AGGGACTCCGT	0.458
-	2	156	0ihv.1_Missense_	NM_005420	NP_005411	P49888	ST1E1_HUMAN		1	TCCCATGGACTT	0.343
+	5	1594	OM3_uc003hkf.1_	NM_020859	NP_065910	Q8TF72	SHRM3_HUMAN		3	GAGCCCTGACC	0.547
+	27	3976	w.2_Missense_Mu	NM_025074	NP_079350	Q86XX4	FRAS1_HUMAN	xtracellular (Potential).	5	AGTGCGTTTTG	0.478
+	41	6036	_p.L1866F|FRAS1	NM_025074	NP_079350	Q86XX4	FRAS1_HUMAN	xtracellular (Potential).	5	ACAACCTCCAG	0.428
-	1	314	R3_uc003hln.2_R	NM_001040202	NP_001035292	Q6TCH7	PAQR3_HUMAN	lasmic (Potential).	0	ACCCGGGGATC	0.632
-	6	352	1ccj.1_Missense_	NM_001080506	NP_001073975	B9EJG8	T150C_HUMAN		1	CTTCGGTTTCA	0.418
-	21	2704	i.2_Missense_Mut	NM_001077207	NP_001070675	O94979	SC31A_HUMAN	with PDCD6.|Pro-rich.	8	ACATTTCCATGC	0.473
-	15	1864	.G567E|SEC31A_	NM_001077207	NP_001070675	O94979	SC31A_HUMAN		8	TACCCCCACTG	0.289
-	33	5797		NM_014991	NP_055806	Q8IZQ1	WDFY3_HUMAN		3	GACAGGCACAC	0.498
+	4	854		NM_014208	NP_055023	Q9NZW4	DSPP_HUMAN		1	TGGGAGTCCTA	0.468
-	3	699	ense_Mutation_p.	NM_004827	NP_004818	Q9UNQ0	ABCG2_HUMAN	er.|Cytoplasmic (Potential).	1	ATGATCCCACTGT	0.393
-	5	629	DH1B_uc011ceh.1	NM_000668	NP_000659	P00325	ADH1B_HUMAN		2	CAGACCCATAA	0.483
-	15	1549	xc.1_Missense_M	NM_001813	NP_001804	Q02224	CENPE_HUMAN	Potential.	9	TTGTTGCTGGAT	0.289
-	2	235	SS1_uc011cfh.1_	NM_005443	NP_005434	O43252	PAPS1_HUMAN	ylyl-sulfate kinase.	1	ACCACGAAAGC	0.463
-	28	2092	25A1_uc003hzd.2_	NM_198721	NP_942014	Q9BXS0	COPA1_HUMAN	cellular (Potential).	2	TGGACCCGGCA	0.448
+	9	1809	_p.P411S|EGF_uc	NM_001963	NP_001954	P01133	EGF_HUMAN	Extracellular (Potential).	4	TGCGTTCCTCTT	0.423
-	3	1956	_p.L385F|ANKRD	NM_020337	NP_065070	Q9ULJ7	ANR50_HUMAN	ANK 3.	1	AGACAAGTAAATT	0.398
-	3	3127	25_splice|PCDH1	NM_019035	NP_061908	Q9HCL0	PCD18_HUMAN		5	TCTTACCTGCT	0.398
+	7	1037		NM_033393	NP_203751	Q9C0D6	FHDC1_HUMAN	FH2.	2	TGTCTTCTTTGCT	0.343
-	25	7555		NM_017639	NP_060109	Q6V1P9	PCD23_HUMAN	Cadherin 22.	4	CAAAAACAGTGC	0.418
+	18	2217	cjd.1_Missense_M	NM_021634	NP_067647	Q9HBX9	RXFP1_HUMAN	lasmic (Potential).	0	AGAAAACATATG	0.413
+	10	1370	irc.2_Missense_M	NM_007246	NP_009177	O95198	KLHL2_HUMAN	Kelch 2.	0	ACTGTAGATTCC	0.463
+	21	4439	e.1_Missense_Mu	NM_001080477	NP_001073946	Q9P273	TEN3_HUMAN	lar (Potential).|NHL 5.	0	CCAAGGATGCC	0.498

+	1	122	ssense_Mutation_	NM_004168	NP_004159	P31040	DHSA_HUMAN		0	TGTCGGGGGTC	0.637	
-	20	2782		NM_006598	NP_006589	Q9Y666	S12A7_HUMAN	lasmic (Potential).	4	CTCGGCGCTGA	0.408	
-	3	408		NM_001044	NP_001035	Q01959	SC6A3_HUMAN		6	GGCACCTGTGG	0.607	
+	13	5801		NM_015325	NP_056140	Q9Y2F5	K0947_HUMAN		2	AACCAGGGGAG	0.507	
-	9	1548		NM_003966	NP_003957	Q13591	SEM5A_HUMAN	tracellular (Potential).	2	GACGGGAGCAG	0.517	
-	47	7834		NM_001369	NP_001360	Q8TE73	DYH5_HUMAN	3 (By similarity).	31	TTATTACTGTTTT	0.308	
-	11	2085	H10_uc011cnu.1_	NM_006727	NP_006718	Q9Y6N8	CAD10_HUMAN	|Extracellular (Potential).	12	ACACTCGAATGG	0.512	
-	7	1574	T3A1_uc003jjw.1_	NM_152404	NP_689617	Q6NUS8	UD3A1_HUMAN	ellular (Potential).	3	ATAGGGCTTGA	0.597	
+	10	1615	LAM_uc003jle.1_	NM_152403	NP_689616	Q63HQ2	EGFLA_HUMAN	minin G-like 1.	7	AGAACGAACAC	0.498	rs140240157
-	29	2857	p.E945K|RICTOR	NM_152756	NP_689969	Q6R327	RICTR_HUMAN		10	TTTCTTCCTGTA	0.348	
-	13	2156	.1_Missense_Muta	NM_000065	NP_000056	P13671	CO6_HUMAN	C5b-binding domain.	7	CTGGAGGAACT	0.398	
-	8	1337	_p.S58F|HMGCS1	NM_001098272	NP_001091742	Q01581	HMCS1_HUMAN		0	AAACCAGAACCA	0.403	
+	3	714		NM_152687	NP_689900	Q8N292	GAPT_HUMAN		0	AAAAACCGATA	0.413	
+	6	715	qu.1_Missense_	NM_001029875	NP_001025046	Q6MZT1	R7BP_HUMAN		0	CCTACCCCCTG	0.468	
+	3	399	_Mutation_p.S101	NM_015342	NP_056157	Q96BP3	PPWD1_HUMAN	WD 2.	1	TCGTAGTCACCT	0.289	
+	28	7258	p.S2325F|MAST4_	NM_015183	NP_055998	O15021	MAST4_HUMAN		13	GCCATCCCCAG	0.597	
+	10	1302	_p.E431K|RGNEF	NM_001080479	NP_001073948	Q8N1W1	RGNEF_HUMAN		0	TTAGTGAAAAT	0.507	
+	8	1041		NM_006633	NP_006624	Q13576	IQGA2_HUMAN		7	TGAAGGTGCTT	0.338	
+	7	1931	u.2_Missense_Mu	NM_004385	NP_004376	P13611	CSPG2_HUMAN	minoglycan attachment do	16	AGAATGATCCT	0.398	rs146518697
-	10	1603	p.1_Missense_Mu	NM_005711	NP_005702	O43854	EDIL3_HUMAN	5/8 type C 2.	2	TTAGCTCCTTGT	0.388	
+	83	17932	.A3652T|GPR98_	NM_032119	NP_115495	Q8WXG9	GPR98_HUMAN	ical; (Potential).	16	TGATGGCAGCC	0.433	
+	7	1620	q.2_RNA|AQPEP_	NM_173800	NP_776161	Q6Q4G3	AMPQ_HUMAN	enal (Potential).	0	ATGAAGGTGGAA	0.353	
-	3	883	krx.3_Missense_	NM_020796	NP_065847	Q9H2E6	SEM6A_HUMAN	tracellular (Potential).	2	ATCTGGATGTCC	0.507	
+	1	213	3ksn.2_Missense_	NM_182761	NP_877438	A1A519	F170A_HUMAN		1	TATCATGAAACG	0.448	
+	2	868	2_Missense_Muta	NM_004384	NP_004375	Q9Y6M4	KC1G3_HUMAN	se.|ATP (By similarity).	0	AATTGGATGTG	0.348	
+	4	292	218P|IRF1_uc003kxb.2_Silent_p.P218P|IRF1_uc010jdt.			Q8N8D9	CE056_HUMAN		0	GTGGAGGGCAT	0.577	
+	12	1803		NM_002154	NP_002145	P34932	HSP74_HUMAN		2	ATGAGGAGCCA	0.423	
+	3	534	F7_uc003kyx.2_5'	NM_003202	NP_003193	P36402	TCF7_HUMAN		0	GTGCACCAGCG	0.627	
+	6	813	se_Mutation_p.T2	NM_058244	NP_490645	Q9H1J5	WNT8A_HUMAN		4	ATGGCACAGAG	0.572	
+	19	3072	yo.1_Missense_M	NM_005733	NP_005724	O95235	KI20A_HUMAN	ular (Potential).	0	ACCAACCTGCC	0.502	
+	1	3118	lhk.1_Intron|PCDH	NM_031857	NP_114063	Q9Y5H5	PCDA9_HUMAN		5	GGAAGGTGGGT	0.418	
+	1	2329	DHA7_uc003lhq.	NM_018904	NP_061727	Q9Y5I0	PCDAD_HUMAN	XXP 2.|6 X 4 AA repeats	6	AGCCTTCCTCCT	0.552	
+	1	2800		NM_020957	NP_066008	Q9NRJ7	PCDBG_HUMAN	(Potential).|Cadherin 5.	2	TGCGCGTGCTG	0.711	
+	1	727	ljm.1_Intron|PCD	NM_018922	NP_061745	Q9Y5G3	PCDGD_HUMAN	(Potential).|Cadherin 3.	0	AGGAGGTATAC	0.562	
+	1	657	DHGB1_uc003ljo.	NM_018918	NP_061741	Q9Y5G8	PCDG5_HUMAN	(Potential).|Cadherin 2.	4	GGAGACCCGGT	0.577	
+	1	1222	ju.1_Intron|PCDH	NM_018921	NP_061744	Q9Y5G4	PCDG9_HUMAN	|Extracellular (Potential).	0	CGGCCCAAATT	0.423	
+	1	1917	1_Intron|PCDHGA	NM_002588	NP_002579	Q9UN70	PCDGK_HUMAN	(Potential).|Cadherin 6.	2	TGCAGGGCACA	0.597	
+	2	956		NM_000112	NP_000103	P50443	S26A2_HUMAN	ical; (Potential).	0	TAGCTGGAGTT	0.353	
-	3	308	.2_5'UTR|CCDC6	NM_015621	NP_056436	A6NI79	CCD69_HUMAN	Potential.	2	AGAATTCTGGTT	0.453	
+	2	565	vb.2_Missense_M	NM_001128209	NP_001121681	Q92629	SGCD_HUMAN	lasmic (Potential).	0	CTGGCGGAAAC	0.483	
-	34	4360	.2_Missense_Mut	NM_003062	NP_003053	O75094	SLIT3_HUMAN	aminin G-like.	4	CAGCTCGTTGT	0.662	
-	19	3067		NM_005990	NP_005981	O94804	STK10_HUMAN	Potential.	8	CAGAGCCTAGG	0.587	
+	7	2101	rf25_uc003mdr.3_RNA|C5orf25_uc003mdv.2_Missens			Q8NDZ2	CE025_HUMAN		0	GCCTGGGCGAG	0.488	
-	3	929	_5'Flank|GRM6_u	NM_000843	NP_000834	O15303	GRM6_HUMAN	ellular (Potential).	8	GGAATCTTGAT	0.602	
-	14	1635	_p.D501N|EXOC2_	NM_018303	NP_060773	Q96KP1	EXOC2_HUMAN		7	TAAAATCATTTTG	0.318	
+	4	1560	w.2_RNA|PRPF4	NM_003913	NP_003904	Q13523	PRP4B_HUMAN	Lys-rich (basic).	5	CGGTGGTCGTA	0.423	
+	7	1064	q.1_Missense_Mu	NM_004415	NP_004406	P15924	DESP_HUMAN	plakophilin 1 and junction p	9	AGCGTCCTTTG	0.483	

+	25	2415	ow.2_Missense_M	NM_001040274	NP_001035364	Q5T4T6	SYC2L_HUMAN		2	ATTCTCCCAACC	0.318	
+	6	915	div.1_Splice_Site_	NM_004973	NP_004964	Q92833	JARD2_HUMAN		4	TTTCTAGTTTTCA	0.373	
+	1	782		NM_016255	NP_057339	Q9UBU6	FA8A1_HUMAN		0	GACGAGGGTAG	0.711	
-	18	3303	p.P1066S|NUP15	NM_005124	NP_005115	P49790	NU153_HUMAN		9	AGCAGGAGCAG	0.453	
+	1	653	z.2_Missense_Mu	NM_001949	NP_001940	O00716	E2F3_HUMAN	K2 binding (Potential).	1	CAGCAGAGCCG	0.662	
+	11	1084	4_splice|CDKAL1	NM_017774	NP_060244	Q5VV42	CDKAL_HUMAN		2	TTTAAGGAAATG	0.393	
-	3	847	_p.A204T|KIAA03	NM_014809	NP_055624	Q5VV43	K0319_HUMAN	ellular (Potential).	2	CACCGCAGGAC	0.622	
-	1	76	H3C_uc003nfv.2_	NM_021062	NP_066406	P33778	H2B1B_HUMAN		0	TACCATCCTTCTT	0.488	
+	1	287		NM_003540	NP_003531	P62805	H4_HUMAN		0	AGGGACGCACTC	0.552	
+	4	1538	_p.V152M|ZNF165	NM_003447	NP_003438	P49910	ZN165_HUMAN		0	AAAAAAGTGTCA	0.428	
-	6	1001	pn.2_Missense_M	NM_006778	NP_006769	Q9UDY6	TRI10_HUMAN	B30.2/SPRY.	0	TACCTGGCTCAT	0.373	
-	10	4492	C1_uc011dmp.1_	NM_014641	NP_055456	Q14676	MDC1_HUMAN	on with the PRKDC compl	4	CTCCTAGTGGTC	0.557	
+	6	454	9E|PSORS1C1_uc	NM_014068	NP_054787	Q9UIG5	PS1C1_HUMAN		1	GGGGACCTCCA	0.572	
+	6	629	8S|PSORS1C1_u	NM_014068	NP_054787	Q9UIG5	PS1C1_HUMAN		1	CTTCCTCCTCCC	0.562	
+	6	926	_p.P60L|LY6G6D_	NM_001003693	NP_001003693	Q5SQ64	LY66F_HUMAN		2	CTCAGCCCCAG	0.537	
-	17	1807	J1_uc003nxr.3_5'F	NM_025257	NP_079533	Q53GD3	CTL4_HUMAN	ical; (Potential).	4	GCATGAGTAGCAT	0.532	
-	17	2153	ssense_Mutation_	NM_006709	NP_006700	Q96KQ7	EHMT2_HUMAN		1	GTTTGTCCACTG	0.617	
+	2	418	s.1_Missense_Mu	NM_001710	NP_001701	P00751	CFAB_HUMAN	Sushi 1.	1	AGGCGGCTCCT	0.592	
+	18	2563	.1_Missense_Muta	NM_001710	NP_001701	P00751	CFAB_HUMAN		1	ATTTGGGTTTTC	0.517	
-	2	404	AT1_uc003oag.2_	NM_006411	NP_006402	Q99943	PLCA_HUMAN		1	TGGGGCTGCAG	0.468	
-	4	629	dpv.1_RNA|NOTC	NM_004557	NP_004548	Q99466	NOTC4_HUMAN	r (Potential).|EGF-like 4.	22	ACATGGGTTGG	0.567	
-	4	753	QB1_uc003obv.2_	NM_002123	NP_002114	P01920	DQB1_HUMAN	|Ig-like C1-type.|Connectin	0	ATTCAGACTGA	0.547	
-	1	358	9_uc011dqj.1_5'F	NM_000593	NP_000584	Q03518	TAP1_HUMAN	lasmic (Potential).	1	GGGGAGCGGG	0.726	
-	18	2030	dn.1_Missense_M	NM_022553	NP_072047	Q8N1B4	VPS52_HUMAN		5	AAGGGGGAGAC	0.473	
+	4	336	8_uc003odq.1_Sp	NM_022551	NP_072045	P62269	RS18_HUMAN		0	GCCAGGTGTGT	0.493	
-	3	351	_uc010juo.1_RN	NM_005452	NP_005443	O15213	WDR46_HUMAN		0	GACGGGGGCGG	0.582	
-	2	1419	dz.2_5'Flank|TAP	NM_005453	NP_005444	O15209	ZBT22_HUMAN		1	GTTGCCCTGCA	0.622	
-	7	2296	ation_p.L623F|DA	NM_001350	NP_001341	Q9UER7	DAXX_HUMAN	action with SPOP.	23	GCAGAGGGAGC	0.627	
+	27	3740		NM_002224	NP_002215	Q14573	ITPR3_HUMAN	lasmic (Potential).	19	CAAGGGCGTGA	0.647	
+	5	546	se_Mutation_p.T7	NM_145899	NP_665906	P17096	HMGA1_HUMAN	ith HIPK2 (By similarity).	0	GAAAACCACCA	0.507	
+	11	1679	dst.1_Missense_	NM_015245	NP_056060	Q92625	ANS1A_HUMAN		4	AGGTGGGGCAG	0.697	
+	2	463	ml.2_Missense_M	NM_000389	NP_000380	P38936	CDN1A_HUMAN		2	ACCTGTCACTGT	0.657	
+	25	3556		NM_001371	NP_001362				21	AGTTGGTCCTG	0.468	
+	57	8581		NM_001371	NP_001362				21	AATCTTCGAGAT	0.393	rs149070832
+	79	12136	sense_Mutation_p	NM_001371	NP_001362				21	AGGAGGAAATT	0.388	
-	6	3041	318_uc003ouw.2_	NM_014345	NP_055160	Q5VUA4	ZN318_HUMAN		7	TTCTGGGATTTAT	0.448	
+	18	4123	p.R1275Q|ABCC1	NM_033450	NP_258261	Q5T3U5	MRP7_HUMAN	C transporter 2.	7	AGGGCGAGTGC	0.642	
-	15	2391	yp.3_Missense_	NM_001098518	NP_001091988	Q8IZF2	GP116_HUMAN	ellular (Potential).	2	TCCCGCCAATG	0.537	
-	3	1662	wn.1_Missense_	NM_001013732	NP_001013754	Q6ZW05	CF138_HUMAN		1	AATCCACTACAG	0.468	
-	2	352	_p.V97A|RHAG_u	NM_000324	NP_000315	Q02094	RHAG_HUMAN	ical; (Potential).	2	CCTGTACAATAG	0.388	
-	1	1078		NM_138733	NP_620061	P07205	PGK2_HUMAN		1	TGAGCATGATTC	0.483	
-	23	2563	ai.2_Missense_Mu	NM_138694	NP_619639	P08F94	PKHD1_HUMAN	ellular (Potential).	44	AGTGGGCACAG	0.542	
+	2	649		NM_133367	NP_588608	Q8TEZ7	MPRB_HUMAN	lasmic (Potential).	0	GCAGTGCTTTG	0.527	
-	9	1242	_p.P251L|ICK_uc0	NM_016513	NP_057597	Q9UPZ9	ICK_HUMAN	rotein kinase.	5	CATTGGGAATC	0.458	
+	2	369		NM_001010872	NP_001010872	Q5T0W9	FA83B_HUMAN		6	TGTGATGATACC	0.433	
-	28	3867	y.3_Missense_Mu	NM_001144769	NP_001138241	Q03001	DYST_HUMAN		14	AACACACTTTCAT	0.383	
+	11	4430	i.2_Missense_Mut	NM_001624	NP_001615	Q9Y4K1	AIM1_HUMAN		9	CAATAGGATTTTT	0.313	

-	4	623	k.2_Missense_Mu	NM_002037	NP_002028	P06241	FYN_HUMAN	SH3.	7	TCCGTGCTTCAT	0.393	
+	3	1039		NM_001013734	NP_001013756	Q6ZWI9	RFPLB_HUMAN	B30.2/SPRY.	0	TTGTGTCCATTC	0.443	
-	9	1024	D3_uc003qbw.2_	NM_001017373	NP_001017373	Q8N6K7	SAMD3_HUMAN		1	GGTCTTCGAACA	0.343	
+	14	2512	khe.2_Missense_	NM_020455	NP_065188	Q86SQ4	GP126_HUMAN	ellular (Potential).	1	GGTCTTCCAAGC	0.348	
+	11	2902	jw.1_Missense_M	NM_032532	NP_115921	Q4ZHG4	FNDC1_HUMAN		8	GCAGCCCATCT	0.607	
-	3	408	44L_uc003qva.2_	NM_016098	NP_057182	Q9Y5U8	BR44L_HUMAN		1	CCGCCCTCCCT	0.433	
+	7	801	.2_Missense_Mut	NM_001159767	NP_001153239	Q9Y6E2	BZW2_HUMAN		2	TTTGAGAAAAG	0.418	
+	15	2239	ui.2_Missense_Mu	NM_058176	NP_478056	Q9UKV0	HDAC9_HUMAN	ne deacetylase.	5	TGGTGGACTTG	0.269	
+	8	1628	_p.T211I|CCDC12	NM_194300	NP_919276	Q6ZRS4	CC129_HUMAN		0	ATGTGACCAATG	0.473	
-	1	808		NM_003014	NP_003005	Q6FHJ7	SFRP4_HUMAN		1	CGATGGCTTCA	0.657	
+	3	461	nc.2_Missense_Mu	NM_005856	NP_005847	O60896	RAMP3_HUMAN	ical; (Potential).	0	CCATGGCTGGC	0.612	
-	4	398		NM_138295	NP_612152	Q8TDX9	PK1L1_HUMAN		11	TGACATACCTATC	0.388	
+	53	14067	A13_uc010kyt.1_	NM_152701	NP_689914	Q86UQ4	ABCAD_HUMAN		10	TCTGCGATGGC	0.493	
+	28	3605	.1_Missense_Mut	NM_005228	NP_005219	P00533	EGFR_HUMAN	lasmic (Potential).	9571	GCCCAGCAGAG	0.532	
+	4	534		NM_001159279	NP_001152751				2	AAGGAGGTTATA	0.338	
+	16	1318	r.2_Missense_Mut	NM_000048	NP_000039	P04424	ARLY_HUMAN		2	AGGGGGTCGCC	0.642	
-	5	809		NM_016038	NP_057122	Q9Y3A5	SBDS_HUMAN		1	GACATACCTGAA	0.403	
+	2	1197	_p.R152*|AUTS2_	NM_015570	NP_056385	Q8WXX7	AUTS2_HUMAN		3	TCAGATCGAGAA	0.512	
-	2	185	k|SBDSP1_uc011	NM_001145440	NP_001138912	Q6NUM6	TYW1B_HUMAN		0	GAGAGGTCCCAT	0.348	
-	5	1149	gr.1_Missense_Mu	NM_012301	NP_036433	Q86UL8	MAGI2_HUMAN		11	GTTCCTCATTGT	0.488	
-	15	1548	uc003uhs.1_Intron	NM_000722	NP_000713	P54289	CA2D1_HUMAN	ellular (Potential).	6	GGTCTTCCCAAA	0.348	
+	4	1008		NM_181646	NP_857597	A4D1E1	Z804B_HUMAN		11	ATGGCAGAAAGG	0.438	
-	5	2658	D9L_uc003umk.1_	NM_152703	NP_689916	Q8IVG5	SAM9L_HUMAN		4	TTCTCCCACATG	0.413	
+	22	1675	1A2_uc011kib.1_I	NM_000089	NP_000080	P08123	CO1A2_HUMAN		9	GGTAGTCCTGGT	0.448	
-	12	1982	2_splice|ASNS_u	NM_133436	NP_597680	P08243	ASNS_HUMAN		1	ATTATACCTGAT	0.338	
+	9	1213	py.1_Missense_M	NM_006409	NP_006400	Q92747	ARC1A_HUMAN	WD 6.	1	ATTTGGGATTTC	0.274	
+	2	550	AN1_uc003usl.1_	NM_003439	NP_003430	P17029	ZKSC1_HUMAN	SCAN box.	3	CCAAGGAGCTC	0.517	
+	2	233	1kjf.1_Splice_Site	NM_006833	NP_006824	Q7L5N1	CSN6_HUMAN		0	GCAGGGTGAGT	0.592	
+	14	1307	td.2_Missense_Mu	NM_004722	NP_004713	O00189	AP4M1_HUMAN	MHD.	0	TGCCTCGGGTG	0.632	
-	3	670	68T|STAG3_uc01	NM_152742	NP_689955	Q8N158	GPC2_HUMAN		2	GCTGTGCCCAGA	0.592	
-	3	505	13K|STAG3_uc01	NM_152742	NP_689955	Q8N158	GPC2_HUMAN		2	GCATCTCCAGAA	0.557	
-	1	176	3V|STAG3_uc010l	NM_152742	NP_689955	Q8N158	GPC2_HUMAN		2	GCAGCGCGGAC	0.657	rs138935052
-	7	1896	.V469I|EPHB4_uc	NM_004444	NP_004435	P54760	EPHB4_HUMAN	tential).|Fibronectin type-III	15	ATTTGACCTCGT	0.602	
+	12	1815	p.G294E|SLC12A	NM_020246	NP_064631	Q9BXP2	S12A9_HUMAN	ellular (Potential).	0	GGGGGGGCTGT	0.627	
+	14	2155	_p.P670S|CDHR3	NM_152750	NP_689963	Q6ZTQ4	CDHR3_HUMAN	|Extracellular (Potential).	1	CCCACCCAACC	0.493	
+	3	570		NM_002736	NP_002727	P31323	KAP3_HUMAN	n and phosphorylation.	1	AGTCCAGGGTAT	0.299	
+	6	1486	_p.P265S|CBLL1_	NM_024814	NP_079090	Q75N03	HAKAI_HUMAN	Pro-rich.	5	TAACCCCTCCC	0.547	
+	3	452	n.2_Missense_Mu	NM_000230	NP_000221	P41159	LEP_HUMAN		0	CCTGGGGGGTG	0.627	
-	3	340	_p.M153I|IMPDH1	NM_001142573	NP_001136045	P20839	IMDH1_HUMAN		4	AATGGCCATGTC	0.607	
+	9	1129	_p.W299*|METTL2	NM_018396	NP_060866	Q6P1Q9	MTL2B_HUMAN		1	GGTTTGGATTCA	0.517	
+	8	1037	F5_uc003voi.2_Mi	NM_002200	NP_002191	Q13568	IRF5_HUMAN		0	GCTTCCCCAGC	0.637	
+	16	1871	p.P503L|AHCYL2_	NM_015328	NP_056143	Q96HN2	SAHH3_HUMAN		2	TCAAGCCTAATT	0.527	
+	2	219	ow.2_Missense_	NM_020704	NP_065755	Q9ULQ0	FA40B_HUMAN		0	AGATGGGCATG	0.507	
+	10	1193	h.2_Missense_Mu	NM_013255	NP_037387	Q9UL63	MKLN1_HUMAN	Kelch 2.	1	GTGAGGATACT	0.403	
-	3	445	2_5'Flank|WDR91_	NM_014149	NP_054868	A4D1P6	WDR91_HUMAN		4	ACAAACCAATCC	0.532	
-	13	4440	.S1414F|KIAA154	NM_020910	NP_065961	Q9HCM3	K1549_HUMAN		230	AGATGGAGGCT	0.572	
-	15	1860		NM_004333	NP_004324	P15056	BRAF_HUMAN	rotein kinas_R603>I(2)|p.T	18290	GATTTCACTGTA	0.368	

+	11	845_846	GK_uc011krg.1_RN	NM_018238	NP_060708	Q53H12	AGK_HUMAN			2	GTACTGGTATCT	0.332	
-	4	852		NM_005232	NP_005223	P21709	EPHA1_HUMAN	ar (Potential).|Cys-rich.		5	CACCAGCCACTC	0.657	
+	1	538		NM_012365	NP_036497	Q96R48	OR2A5_HUMAN	cellular (Potential).		3	TTCTGTGAAATCC	0.557	
+	1	808		NM_001005480	NP_001005480	Q6IF42	OR2A2_HUMAN	cellular (Potential).		2	GAGCAGGAGAAA	0.517	
-	7	950	3whv.3_Missense_	NM_001101313	NP_001094783	Q3YBM2	T176B_HUMAN			1	TCTGCTCCCTAGA	0.567	
-	6	818	3whv.3_Missense_	NM_001101313	NP_001094783	Q3YBM2	T176B_HUMAN	ical; (Potential).		1	CAATGACCTTCAA	0.542	
-	14	2119		NM_170606	NP_733751	Q8NEZ4	MLL3_HUMAN			63	GCTTCACTTCAGA	0.353	
+	18	3864	mg.2_Missense_M	NM_053043	NP_444271	Q96EV2	RBM33_HUMAN	RRM.		1	ATGTGGCCCTGA	0.507	
-	63	10166	p.L2588P|CSMD1_	NM_033225	NP_150094	Q96PZ7	CSMD1_HUMAN	ar (Potential).|Sushi 27.		25	TGGCAAGGCAGC	0.438	
-	1	117		NM_001926	NP_001917	Q01524	DEF6_HUMAN			0	GATCATCCTCAGC	0.582	
-	1	1198	.1_Intron|FAM66D	NM_201402	NP_958804	Q6R6M4	U17L2_HUMAN			3	GCCTGTCTGTGT	0.567	
-	6	1088	_p.G297D|MSR1_u	NM_138715	NP_619729	P21757	MSRE_HUMAN	.|Extracellular (Potential).		1	ATTGGACCTGGA	0.398	
+	15	2030	60B2_uc011kyy.1_	NM_022749	NP_073586	Q86V87	F16B2_HUMAN			0	TATTCTCCGTGTT	0.642	
+	2	653	on_p.T61I|RHOBTE	NM_015178	NP_055993	Q9BYZ6	RHBT2_HUMAN	Rho-like.	p.T39T(1)	2	ATGCCACCCTCAC	0.582	
-	5	463	aj.1_Missense_Mutation_p.A108T|STMN4_uc011lak.1_M			Q9H169	STMN4_HUMAN	Potential.		2	TCTCTGCTAGGTC	0.493	
-	3	8018		NM_031271	NP_112561	Q9BXT5	TEX15_HUMAN			7	GTAATGGCATTGC	0.433	
+	7	2106	CC1_uc010lwo.1_M	NM_006283	NP_006274	O75410	TACC1_HUMAN			1	TGGAGTCCTCTGC	0.532	
+	11	991	DAM18_uc010lwx.2	NM_014237	NP_055052	Q9Y3Q7	ADA18_HUMAN	2B.|Extracellular (Potential).		6	TATGATGACATCA	0.318	
-	4	751		NM_014420	NP_055235	Q9UBT3	DKK4_HUMAN	KK-type Cys-2.		1	TTAATCGAGCATG	0.398	
-	7	1605	xpe.2_Missense_M	NM_006749	NP_006740	Q08357	S20A2_HUMAN	lasmic (Potential).		2	TGGCTGCCCGCA	0.612	
-	14	1817_1818		NM_144651	NP_653252	A1KZ92	PXDNL_HUMAN	-like C2-type 4.		2	GTCAGGGAACCC	0.475	
-	5	1015	se_Mutation_p.A19	NM_014682	NP_055497	O60284	ST18_HUMAN			5	TACTGCCAGGCT	0.532	
+	4	2174	P1_uc011ldy.1_Intr	NM_006269	NP_006260	P56715	RP1_HUMAN			12	AAAAAATCTCGAC	0.328	
+	4	5817	P1_uc011ldy.1_Intr	NM_006269	NP_006260	P56715	RP1_HUMAN			12	ACCAACCATTGCC	0.398	
-	2	759	n_p.E41K|SDR16C	NM_138969	NP_620419	Q8N3Y7	RDHE2_HUMAN			3	CTATTTCACCAGC	0.448	
+	4	580	JC5B_uc003xvt.1_	NM_033105	NP_149096	Q9UF47	DNJ5B_HUMAN			0	GGAGACGAAAAC	0.448	
-	7	2376	O5A1_uc011lfa.1_	NM_030958	NP_112220	Q9H2Y9	SO5A1_HUMAN	ar (Potential).|Kazal-like.		4	AATTAACGTTGCA	0.413	
-	2	1171	CO5A1_uc003xyk	NM_030958	NP_112220	Q9H2Y9	SO5A1_HUMAN	cellular (Potential).		4	TCAATGGTGGTA	0.547	
+	3	2630		NM_004770	NP_004761	Q92953	KCNB2_HUMAN	lasmic (Potential).		7	ATGCCAGTGGCTC	0.542	
+	10	1427	_p.G163D|CRISPLI	NM_031461	NP_113649	Q9H336	CRLD1_HUMAN	LCCL 1.		2	ATGGTGGCTGGG	0.333	
+	3	308	n_p.A13V|HNF4G_	NM_004133	NP_004124	Q14541	HNF4G_HUMAN	receptor.|NR C4-type.		1	TGTGTGCTATCTG	0.448	
+	1	178		NM_152565	NP_689778	Q8N8Y2	VA0D2_HUMAN			0	ACCTGGTCCAGT	0.483	
-	5	689	0maj.2_Splice_Site	NM_019098	NP_061971	Q9NQW8	CNGB3_HUMAN			3	ATAATACCTGTGT	0.378	
-	5	453	ygp.2_Missense_M	NM_015496	NP_056311	Q69YN4	VIR_HUMAN	Pro-rich.		2	GGGAggtggtggcg	0.323	
+	2	366		NM_024613	NP_078889	Q9H8W4	PKHF2_HUMAN	PH.		2	GAGAAGGAGTATT	0.363	
+	15	2582	_p.R795C|RIMS2_	NM_014677	NP_055492	Q9UQ26	RIMS2_HUMAN			15	AGACATCGTGTCA	0.393	
+	1	496		NM_003301	NP_003292	P34981	TRFR_HUMAN	Name=4; (Potential).		3	GCTCTGGTTCTTC	0.408	
-	3	599	hx.1_Missense_Mu	NM_198123	NP_937756	Q7Z407	CSMD3_HUMAN	lar (Potential).|CUB 1.		63	GATTTGGTACTTG	0.358	
+	9	1041		NM_001039112	NP_001034201	Q2WGJ9	FR1L6_HUMAN	toplasmic (Potential).		11	CTGGTGGATCCC	0.507	
-	11	786	ense_Mutation_p.W	NM_032026	NP_114415	Q6P1N9	TATD1_HUMAN			0	ACTTTCCCACTT	0.383	
-	23	3122	p.F783L|KIAA0196	NM_014846	NP_055661	Q12768	STRUM_HUMAN			2	GGCGGAAAAATA	0.363	
-	6	2126	FAT_uc010mei.2_F	NM_020863	NP_065914	Q9P243	ZFAT_HUMAN			1	GGCTCTGGGCGC	0.587	
-	13	3364	M135B_uc003yva	NM_015912	NP_056996	Q49AJ0	F135B_HUMAN		p.P1065P(1)	9	TGATGGGAAACAC	0.517	rs35639744
-	13	1727	AM135B_uc003yva	NM_015912	NP_056996	Q49AJ0	F135B_HUMAN			9	CCAGTCCAACATT	0.473	
-	11	1214	se_Mutation_p.S24	NM_015912	NP_056996	Q49AJ0	F135B_HUMAN			9	GCCTCAGAAAAC	0.383	
-	4	1132		NM_152888	NP_690848	Q8NFW1	COMA1_HUMAN			13	CTCCTTCTACACG	0.453	
+	3	792		NM_030895	NP_112157	Q9H7X3	ZN696_HUMAN	C2H2-type 1.		0	GTGCGGCGCCT	0.687	

+	1	1234	D_uc011lkk.1_5'Fl	NM_032862	NP_116251	Q53EQ6	TIGD5_HUMAN		0	ACCTGGCTGGC	0.687	
-	24	3543		NM_017570	NP_060040	O14841	OPLA_HUMAN		0	CGCTCACCGGCT	0.647	
-	17	2381	zas.1_Missense_M	NM_017570	NP_060040	O14841	OPLA_HUMAN		0	GACGCTCCTTGAT	0.647	
-	23	2515		NM_013291	NP_037423	Q10570	CPSF1_HUMAN		1	CTGCCCCACAG	0.667	
-	5	1010	uc003zco.2_Nonse	NM_130849	NP_570901	Q6P5W5	S39A4_HUMAN	cellular (Potential).	0	TCAGCTGCTGTTC	0.662	
-	17	2786	uc011llh.1_Intron	NM_013432	NP_038460	Q96HA7	TONSL_HUMAN		0	CCAAGGGCTGG	0.677	
+	20	2468	CK8_uc010mgw.1_	NM_203447	NP_982272	Q8NF50	DOCK8_HUMAN		6	GCCTGGAGCCG	0.607	
+	33	4793	n_p.P229L|SMARC	NM_003070	NP_003061	P51531	SMCA2_HUMAN		3	CCAAACCTGTAGT	0.498	
-	10	2442	IS3_uc010mhf.1_M	NM_152629	NP_689842	Q8NEA6	GLIS3_HUMAN		1	TTCAGCCCCGCT	0.532	
-	2	949		NM_001017969	NP_001017969	Q5HYC2	K2026_HUMAN		3	TAGATTCAAAAAC	0.398	
-	43	6233	.S1434L|PTPRD_	NM_002839	NP_002830	P23468	PTPRD_HUMAN	).|Tyrosine-protein phospha	22	TGGACTGAAATGC	0.403	
-	39	5566	.E1212K|PTPRD_	NM_002839	NP_002830	P23468	PTPRD_HUMAN	lasmic (Potential).	22	GCACTTCGGTATT	0.408	
+	18	2669	3znr.2_Missense_	NM_017925	NP_060395	Q5VZ89	DEN4C_HUMAN		2	GTATGTCTGAAAG	0.453	
+	10	1160		NM_017794	NP_060264	Q5VW36	K1797_HUMAN		10	GCTTACCCAGAT	0.393	
+	10	2015	|NFX1_uc003zsp.1	NM_002504	NP_002495	Q12986	NFX1_HUMAN	NF-X1-type 4.	1	TGTGGACCATGCT	0.368	
+	2	942	zvv.2_Missense_M	NM_203299	NP_976044	Q5VYM1	CI131_HUMAN		0	GAGGCACCCACA	0.537	
+	6	1295	lb.2_Missense_Mu	NM_003995	NP_003986	P20594	ANPRB_HUMAN	cellular (Potential).	3	GGCTCCTCCCT	0.582	
-	2	1177		NM_014872	NP_055687	O15062	ZBTB5_HUMAN		2	ACCACTCTCATGT	0.502	
-	2	600		NM_014872	NP_055687	O15062	ZBTB5_HUMAN		2	CTCCTGAACGC	0.547	
-	3	1070	e_Mutation_p.G35	NM_012166	NP_036298	Q9UK96	FBX10_HUMAN		5	CACTACCCACCTC	0.607	
-	13	2121	ense_Mutation_p.A	NM_033655	NP_387504	Q9BZ76	CNTP3_HUMAN	ninal.|Extracellular (Potentia	1	CGCGGCGTCTG	0.637	rs1758272
-	1	589	mp.1_Missense_M	NM_152573	NP_689786	Q8IZ41	RASEF_HUMAN		3	CCGCGTCCTCGT	0.741	
-	11	1057	ltv.1_Missense_Mu	NM_006415	NP_006406	O15269	SPTC1_HUMAN	lasmic (Potential).	2	GGTAACGAAGCT	0.428	
-	3	430	tion_p.T122I|ECM	NM_001393	NP_001384	O94769	ECM2_HUMAN	VWFC.	2	CAGGTAGTGCAG	0.483	
+	5	595	tc.2_Missense_Mu	NM_145006	NP_659443	Q96L08	SUSD3_HUMAN	lasmic (Potential).	6	CACAGAGACCATC	0.597	
-	12	1055	p.G280S|SLC35D2	NM_007001	NP_008932	Q76EJ3	S35D2_HUMAN	lasmic (Potential).	0	CTTCACCCACAG	0.453	
-	7	1410	n_p.L82F|TSTD2_	NM_139246	NP_640339	Q5T7W7	TSTD2_HUMAN	Rhodanese.	2	AATCAAGAAGGA	0.353	
-	6	945	4_uc004ayg.1_Mi	NM_033220	NP_150089	Q14142	TRI14_HUMAN	B30.2/SPRY.	1	CACTTGCCAGAG	0.746	
-	15	2958	_p.I754V|TEX10_u	NM_017746	NP_060216	Q9NXF1	TEX10_HUMAN		2	CAGTGATATACAC	0.438	
-	2	1845	bq.1_Missense_M	NM_133445	NP_597702	Q8TCU5	NMD3A_HUMAN	cellular (Potential).	7	TCGTGCTGGGA	0.478	
-	1	1094	bq.1_Missense_M	NM_133445	NP_597702	Q8TCU5	NMD3A_HUMAN	cellular (Potential).	7	GAAGGGCAAAA	0.597	
-	10	2343	_p.S669N|SVEP1_	NM_153366	NP_699197	Q4LDE5	SVEP1_HUMAN	HYR 2.	7	CCCAGCTTGCG	0.448	
-	4	1115	_p.A378T|ZFP37_	NM_003408	NP_003399	Q9Y6Q3	ZFP37_HUMAN	2-type 3; atypical.	2	TGAGTGCATGTT	0.413	
-	1	160		NM_001244	NP_001235	P32971	TNFL8_HUMAN		6	ATCACACCTTATC	0.507	
-	3	1413	1mac.1_Intron|RAL	NM_012098	NP_036230	Q9UKU9	ANGL2_HUMAN	nogen C-terminal.	0	CCACACCTGCAT	0.617	
+	2	942		NM_032728	NP_116117	Q8NBV4	PPAC3_HUMAN	ical; (Potential).	1	GGTGCCCCTGC	0.677	
+	1	323		NM_000787	NP_000778	P09172	DOPO_HUMAN	ntragranular (Potential).	4	CTGGACCGATGC	0.602	
+	3	815		NM_000093	NP_000084	P20908	CO5A1_HUMAN	rminal.|Laminin G-like.	11	ACACGGGGAAG	0.627	
+	3	248	fh.1_Missense_Mu	NM_004108	NP_004099	Q15485	FCN2_HUMAN	Collagen-like p.P80L(1)	1	GACCTCCTGGG	0.617	
-	4	722	mdx.1_Missense_I	NM_052813	NP_434700	Q9H257	CARD9_HUMAN	Potential.	3	GCATGGCCAGGT	0.692	
-	22	3566	cia.1_Missense_M	NM_017617	NP_060087	P46531	NOTC1_HUMAN	GF-like 31; calcium-binding	856	GGTGGGAGAGG	0.692	
-	3	296	|LCN10_uc011me	NM_198946	NP_945184	P62502	LCN6_HUMAN		0	ATGACACTCTGGT	0.612	
-	16	2469	e_Mutation_p.G70	NM_001606	NP_001597	Q9BZC7	ABCA2_HUMAN		0	CCTGGCCGTACT	0.602	
-	3	238	eq.1_Missense_M	NM_013379	NP_037511	Q9UHL4	DPP2_HUMAN		0	GATGGGCCCCTC	0.527	
+	5	1011	MT1_uc004cob.1_I	NM_024757	NP_079033	Q9H9B1	EHMT1_HUMAN		3	CTGTGGGTTCCA	0.448	
-	5	5607		NM_015419	NP_056234	Q9NR99	MXRA5_HUMAN		8	ATAAAGGAGATAG	0.512	
-	5	3479		NM_015419	NP_056234	Q9NR99	MXRA5_HUMAN		8	TAACTGGAGACAT	0.502	

+	1	1946		NM_182699	NP_874358	Q86TM3	DDX53_HUMAN			3	GAAAACCTGGA	0.378	
+	1	499		NM_181532	NP_853510	Q7Z444	RASE_HUMAN			5	GTTGACCCTGG	0.602	
-	1	298		NM_018159	NP_060629	Q96G61	NUD11_HUMAN	udix hydrolase.		0	ACGATCCAGCG	0.692	
-	5	1750	lsc.2_Missense_M	NM_001111125	NP_001104595	Q5JU85	IQEC2_HUMAN			3	GAGGGGAAGAT	0.632	
-	4	533	dyp.1_RNA|uc004	NM_013346	NP_037478	Q9UMY4	SNX12_HUMAN			0	TAGTTCCTGTCA	0.507	
-	1	513	1L2_uc011mqj.1_I	NM_021963	NP_068798	Q9ULW6	NP1L2_HUMAN			1	CCCAGCGGCAG	0.567	
-	3	424	39B_uc004eli.1_In	NM_016370	NP_057454	Q9NP90	RAB9B_HUMAN			3	GATCTCGATTTA	0.498	
-	1	652		NM_003604	NP_003595	O14654	IRS4_HUMAN			10	CGTGCCGCAGC	0.657	
-	14	1863	muk.1_Missense_	NM_003069	NP_003060	P28370	SMCA1_HUMAN	case C-terminal.		4	CACTTGCCAGGT	0.368	
+	18	2346	p.E696K|SAGE1_	NM_018666	NP_061136	Q9NXZ1	SAGE1_HUMAN			3	AGGAGGAGATG	0.428	
-	3	770	1_5'UTR|ARHGEF	NM_004840	NP_004831	Q15052	ARHG6_HUMAN	CH.		0	GCTAAAAGAGTA	0.393	
-	9	1280	C|RBMX_uc004faf	NM_002139	NP_002130	P38159	HNRPG_HUMAN			1	GAGGGTACCCC	0.567	
-	2	236		NM_001009609	NP_001009609	Q5MJ09	SPXN3_HUMAN			2	TTATTGGATATTC	0.383	
-	1	577	hn.1_Missense_M	NM_017518	NP_059988	Q99871	HAUS7_HUMAN			0	CGCTCCGAGCC	0.721	
-	7	1264	u.1_Missense_Mu	NM_001110556	NP_001104026	P21333	FLNA_HUMAN	Filamin 1.		6	TGCGGTTCTTGT	0.622	
-	14	3706		NM_000132	NP_000123	P00451	FA8_HUMAN	B.		11	CTACGTCCTTTG	0.338	
+	6	960	40_splice|IL9R_uc	NM_002186	NP_002177	Q01113	IL9R_HUMAN			0	CAAGGTGGGCA	0.617	
-	6	847	e_Mutation_p.D13	NM_004653	NP_004644	Q9BY66	KDM5D_HUMAN			1	CTTATCTTTTAC	0.408	
-	8	1137	_p.R360*|C1orf127	NM_173507	NP_775778	B7ZLG7	B7ZLG7_HUMAN			1	AGGTCGTTCAG	0.622	rs146743970
-	10	1754		NR_026567						0	GCAGCGGCTGA	0.687	rs11260887
+	8	1145_1146	_p.P311L|SERINC	NM_178865	NP_849196	Q96SA4	SERC2_HUMAN			0	AGGCCCCGAGG	0.589	
+	11	1953	_p.F583Y|ZMYM1_	NM_024772	NP_079048	Q5SVZ6	ZMYM1_HUMAN			0	AAACATTTCGAC	0.308	
+	3	331		NM_007102	NP_009033	Q16661	GUC2B_HUMAN			0	ACTGTGAGCTG	0.627	
+	9	1592	_p.S263L|PGM1_u	NM_002633	NP_002624	P36871	PGM1_HUMAN			3	GTTCTCAGCAA	0.473	
+	2	247	2_5'UTR|CLCA4_	NM_012128	NP_036260	Q14CN2	CLCA4_HUMAN			2	CCACAGAAAAAA	0.328	
-	11	1731	e|COL11A1_uc00	NM_001854	NP_001845	P12107	COBA1_HUMAN			12	ACTTACCCTATC	0.403	
+	4	1008		NM_020440	NP_065173	Q9P2B2	FPRP_HUMAN	3.|Extracellular (Potential).		1	TGGCTGAAGGA	0.493	
+	9	1128	GA10_uc009wiw.	NM_003637	NP_003628	O75578	ITA10_HUMAN	ellular (Potential).		8	ACTAGGAGATC	0.473	
+	8	1567	r.1_Missense_Mut	NM_004326	NP_004317	O00512	BCL9_HUMAN	Pro-rich.		6	GGACCGGGAGA	0.592	
+	2	228	_p.V74A|TARS2_	NM_025150	NP_079426	Q9BW92	SYTM_HUMAN			1	TGCTGTGGCAT	0.502	
-	5	767	eh.1_Missense_	NM_207308	NP_997191	Q5VU65	P210L_HUMAN		p.R232*(1)	11	TGAATTCGAACT	0.368	
-	2	990	2_Missense_Muta	NM_001111	NP_001102	P55265	DSRAD_HUMAN			6	TATGACTGTCTG	0.488	
-	8	879_880	PATCH4_uc001fp	NM_015590	NP_056405	Q5T3I0	GPTC4_HUMAN			1	AATTCCCCAAG	0.485	
+	15	1826	rf92_uc001fql.2_3'	NM_144702	NP_653303	Q8N4P6	LRC71_HUMAN			0	GGGAGGATGAG	0.562	
+	1	364		NM_001004473	NP_001004473	Q8NGX5	O10K1_HUMAN	lasmic (Potential).		1	TATGATCGCTAT	0.527	
-	6	981	f112_uc001ggj.2_I	NM_000450	NP_000441	P16581	LYAM2_HUMAN	xtracellular (Potential).		5	TCAAATCCTTCTT	0.473	
+	5	1010		NM_031935	NP_114141	Q96RW7	HMCN1_HUMAN			23	GAAATTCGCAAT	0.358	
-	6	930		NM_001994	NP_001985	P05160	F13B_HUMAN	Sushi 5.		3	CTATTTCTCCATG	0.368	
-	27	3258	issense_Mutation	NM_012414	NP_036546	Q9H2M9	RBGPR_HUMAN			1	AAAAACGTGCTT	0.308	
+	3	1031		NM_021205	NP_067028	Q7L0Q8	RHOU_HUMAN			0	CTTCCAGAACG	0.522	
+	5	328	1hxv.1_Missense_	NM_145861	NP_665860	Q8WWZ3	EDAD_HUMAN			0	CTCTTCCAGGTA	0.294	
-	3	499	icp.2_Missense_	NM_032752	NP_116141	Q96IT1	ZN496_HUMAN			2	CTTCGGAGCCA	0.592	
+	1	518		NM_001001915	NP_001001915	Q8NGZ5	OR2G2_HUMAN	ellular (Potential).		0	CTGTGGGCATC	0.552	
-	2	327	se_Mutation_p.N	NM_002189	NP_002180	Q13261	I15RA_HUMAN	tracellular (Potential).		0	CGACATTCGTG	0.572	
-	22	3153	xjf.1_Missense_M	NM_018027	NP_060497	Q9P2Q2	FRM4A_HUMAN			3	TGGAACGCTGG	0.701	
-	23	2732	j.2_RNA|NEBL_uc	NM_006393	NP_006384	O76041	NEBL_HUMAN	Nebulin 22.		2	AAATATGATTTTG	0.388	
-	9	1215	_p.S67F|ANKRD2	NM_014915	NP_055730	Q9UPS8	ANR26_HUMAN			4	TGTGGGAAGGT	0.403	

-	15	1927	_p.E573Q|ANK3_	NM_020987	NP_066267	Q12955	ANK3_HUMAN	ANK 16.	19	GACTTCAAGCT	0.363	
-	12	1606	9xpr.2_Missense_	NM_022079	NP_071362	Q5GLZ8	HERC4_HUMAN		3	CAGAGGAAGAA	0.244	
-	8	861	_Mutation_p.P220	NM_022129	NP_071412	P30039	PBLD_HUMAN		3	CCACGGTGCAA	0.448	
+	34	4767	CDH23_uc001jsc.	NM_022124	NP_071407	Q9H251	CAD23_HUMAN	|Extracellular (Potential).	11	ACATCGCGGGG	0.602	
+	17	2544	ag.2_Nonsense_M	NM_020338	NP_065071	Q9ULJ6	ZMIZ1_HUMAN		4	TGTGCCAGCCG	0.677	
+	3	549	M20_uc001kjh.2_Ir	NM_001134658	NP_001128130	Q2M3R5	TMM20_HUMAN	(Potential).|DUF6 1.	1	TTATCACGTTTAG	0.438	
+	17	4988	.H1436Y|PLCE1_	NM_016341	NP_057425	Q9P212	PLCE1_HUMAN	I-PLC X-box.	3	ATTTATCATGGA	0.423	
-	4	652	nse_Mutation_p.R	NM_000770	NP_000761	P10632	CP2C8_HUMAN		0	CAAATCGTTTCT	0.388	
-	4	731	L2_uc009xvf.1_Int	NM_012465	NP_036597	Q9Y6L7	TLL2_HUMAN	otease (By similarity).	3	CCCTCCAATGA	0.572	
-	1	196		NM_001004758	NP_001004758	Q8NGJ8	O51S1_HUMAN	Name=2; (Potential).	4	CATTGGGCGGT	0.567	
+	1	493	_uc001mam.1_Int	NM_001004750	NP_001004750	Q9H340	O51B6_HUMAN	ellular (Potential).	2	GGTTTCCCTAC	0.488	
-	2	1185	S_uc009yiz.2_Intr	NM_001143816	NP_001137288	P23560	BDNF_HUMAN		0	GTATTCCTCCAG	0.522	
+	24	3427	l.2_Missense_Mu	NM_018259	NP_060729	Q96AE7	TTC17_HUMAN		5	GGGACGGCGCT	0.428	rs143797065
+	1	48		NM_001001952	NP_001001952	Q8NGL1	OR5DI_HUMAN	ellular (Potential).	3	CTCTTGGGCTT	0.433	
+	1	285_286		NM_001005200	NP_001005200	Q8N162	OR8H2_HUMAN	ellular (Potential).	2	TTTACGGGCTGC	0.446	
+	7	1951	c.1_Missense_Mu	NM_178864	NP_849195	Q8IUM7	NPAS4_HUMAN		0	CCTAGCCCAGC	0.587	
-	19	3080	oly.2_Missense_	NM_004910	NP_004901	O00562	PITM1_HUMAN		3	TGCCCGACAGC	0.647	
+	24	3303	se_Mutation_p.G1	NM_000260	NP_000251	Q13402	MYO7A_HUMAN		4	TCCAGGGGACA	0.602	
+	5	776	s.1_Missense_Mu	NM_006169	NP_006160	P40261	NNMT_HUMAN		1	CTGCCCAGACC	0.632	
+	7	1375	2_Missense_Muta	NM_015157	NP_055972	Q86UU1	PHLB1_HUMAN		0	CTTGGCGGAGG	0.657	
+	1	722		NM_001004464	NP_001004464	Q8NGN5	O10G8_HUMAN	Name=6; (Potential).	2	CTGTGCCTCCC	0.547	
+	2	315		NM_138342	NP_612351	Q8IW92	GLBL2_HUMAN		3	GCCATCGACAG	0.622	
-	2	768		NM_004054	NP_004045	Q16581	C3AR_HUMAN	ellular (Potential).	1	AGTGGGGACTG	0.408	
-	1	157	H1_uc001qzc.2_Ir	NM_176889	NP_795370	P59543	T2R20_HUMAN	Name=2; (Potential).	0	GGAGACTGCCA	0.343	
+	15	2016		NM_006446	NP_006437	Q9Y6L6	SO1B1_HUMAN	ame=12; (Potential).	8	CATCACTTGttttat	0.289	
+	3	1295	p.D356N|ALG10B_	NM_001013620	NP_001013642	Q5I7T1	AG10B_HUMAN	ical; (Potential).	3	TAGCTGACTCA	0.308	
-	3	1660		NM_005164	NP_005155	Q9UBJ2	ABCD2_HUMAN		6	GTACCTCTTTGT	0.328	
+	4	766	1rze.2_Nonsense	NM_001130015	NP_001123487	Q7Z3H0	ANR33_HUMAN		0	GGGACCAGCGG	0.652	
+	5	851	f.1_Missense_Mu	NM_005556	NP_005547	P08729	K2C7_HUMAN	od.|Linker 12.	0	TCTCCGACACA	0.592	
-	6	1180		NM_033045	NP_149034	Q9NSB2	KRT84_HUMAN	Rod.|Coil 2.	1	GTTCCGTATGTT	0.552	
+	1	244		NM_001005519	NP_001005519	A6NDL8	O6C68_HUMAN	ellular (Potential).	1	GTGTTCCAAGA	0.363	
-	6	2024	p.G607D|DNAJC1	NM_032364	NP_115740	Q6Y2X3	DJC14_HUMAN		4	AGATACCTACA	0.468	
-	22	2990	.R684W|GRIP1_u	NM_021150	NP_066973	Q9Y3R0	GRIP1_HUMAN		2	GCTCCGAGTTG	0.537	
-	3	572	.1_Intron|MDM1_u	NM_017440	NP_059136	Q8TC05	MDM1_HUMAN		5	ATTAACTGGTG	0.408	
+	5	437	se_Mutation_p.D7	NM_001089704	NP_001083173	P61224	RAP1B_HUMAN		0	TTTAACGATTTAC	0.328	
+	1	198	i.1_RNA|ZDHHC1	NM_015336	NP_056151	Q8IUH5	ZDH17_HUMAN	lasmic (Potential).	0	GATGGCGGACG	0.672	
-	9	1343	do.3_Missense_M	NM_003297	NP_003288	P13056	NR2C1_HUMAN		1	CTTTTTCGGTGT	0.428	
+	5	731	5A3_uc001tfr.2_Mi	NM_005888	NP_005879	Q00325	MPCP_HUMAN	hondrial matrix (Potential).	0	TGCAGCTCCCA	0.373	
-	2	1546		NM_006825	NP_006816	Q07065	CKAP4_HUMAN		0	CAGCTCCTCCA	0.657	
-	35	4513	.Q1006P|CIT_uc0	NM_007174	NP_009105	O14578	CTRO_HUMAN	PH.	10	GCCTCTGTCCA	0.313	
-	9	1424	c.3_Missense_Mu	NM_002019	NP_002010	P17948	VGFR1_HUMAN	4.|Extracellular (Potential).	24	GAGCAGATTTC	0.403	
-	2	1472	_p.R168*|SLC46A	NM_181785	NP_861450	Q7Z3Q1	S46A3_HUMAN	lasmic (Potential).	2	CTATTCGAATTG	0.373	
+	7	1268	.P287A|SLAIN1_	NM_144595	NP_653196	Q8ND83	SLAI1_HUMAN		2	CAAAGCCTCTG	0.393	
-	7	1053	se_Mutation_p.P3	NM_022118	NP_071401	Q5T8P6	RBM26_HUMAN	Pro-rich.	1	TGGGGGGAGTC	0.552	
+	8	1066	nh.2_Missense_M	NM_005766	NP_005757	Q9Y4F1	FARP1_HUMAN	FERM.	2	TGGCCGTTGCC	0.537	
-	8	845	OCK9_uc010tis.1_	NM_015296	NP_056111	Q9BZ29	DOCK9_HUMAN	PH.	1	ACTGTCTGCTG	0.398	
+	4	669	RG2_uc010tll.1_In	NM_173846	NP_776245	P59282	TPPP2_HUMAN		0	ACAAGGGTTCT	0.542	

-	15	1612	PO4_uc001wmy.1_	NM_024658	NP_078934	Q8TEX9	IPO4_HUMAN	HEAT 4.	1	CCCGGGGACTG	0.627	
-	4	406	xfz.1_Missense_M	NM_139318	NP_647479	Q8NCM2	KCNH5_HUMAN	toplasmic (Potential).	9	CCTTTTCATGTT	0.378	
+	64	12657	apy.2_Missense_M	NM_015180	NP_055995	Q8WXH0	SYNE2_HUMAN	lasmic (Potential).	14	TCTTCACTTTGG	0.473	
-	15	2626		NM_001080414	NP_001073883	Q9P219	DAPLE_HUMAN	Potential.	3	CAGCCGCTTGG	0.612	
-	12	2683	se_Mutation_p.I60	NM_032560	NP_115949	Q6IN85	P4R3A_HUMAN		0	TTTCAATTACATG	0.289	
+	2	149	_p.G18E|PPP2R5	NM_001161725	NP_001155197	Q13362	2A5G_HUMAN		2	AGAGTGGAAAAA	0.353	
-	6	710	ypx.2_Missense_	NM_138420	NP_612429	Q8IVF2	AHNK2_HUMAN		1	CCTGTGGGGCA	0.542	
+	6	574	P_uc010bcd.1_5'F	NM_007236	NP_009167	Q99653	CHP1_HUMAN	EF-hand 3.	1	ATGGTCGGAGTA	0.473	
+	21	7610	p.Q2268*|MGA_uc	NM_001164273	NP_001157745	Q8IWI9	MGAP_HUMAN		12	CAGATCAGGCA	0.363	
-	30	4203	02aca.1_Splice_Si	NM_000259	NP_000250	Q9Y4I1	MYO5A_HUMAN		4	AACTTACCTATTT	0.303	
-	2	279	ace.1_Missense_M	NM_006628	NP_006619	P56211	ARP19_HUMAN		0	TGCAACCGTTTC	0.403	
+	2	287	jx.1_Missense_Mu	NM_016166	NP_057250	O75925	PIAS1_HUMAN	lization signal (Potential).	2	GCGGCGGTTCC	0.483	
+	14	2002	se_Mutation_p.A6	NM_024505	NP_078781	Q96PH1	NOX5_HUMAN	cellular (Potential).	2	CCAGGCCGAGG	0.502	
-	6	937	CG_uc002boa.2_R	NM_016321	NP_057405	Q9UBD6	RHCG_HUMAN	ical; (Potential).	1	GGCACCGTAAG	0.617	rs146143065
+	13	1556	_p.M457I|WDR93_	NM_020212	NP_064597	Q6P2C0	WDR93_HUMAN		2	CAAATGAAATGT	0.488	
-	5	932	pd.2_3'UTR|MLST	NM_182563	NP_872369	Q6PL45	CP079_HUMAN	ical; (Potential).	1	AGACCGACACG	0.637	
-	5	952		NM_178844	NP_849172	Q7RTR2	NLRC3_HUMAN	NACHT.	6	GAGATCCCGGA	0.672	
-	4	275	RL_uc002cvy.3_R	NM_001098814	NP_001092284	Q86TD4	SRCA_HUMAN		5	CTCTCCATCTGT	0.468	
-	11	1561	CSM1_uc010bwg.1	NM_052956	NP_443188	Q08AH1	ACSM1_HUMAN		2	CCACGGCTGAC	0.607	
+	2	493	Missense_Mutatio	NM_007245	NP_009176	Q8WWM7	ATX2L_HUMAN	action with MPL.	2	GACCCCCACAG	0.403	
+	8	800	p.R240Q|PHKG2_	NM_000294	NP_000285	P15735	PHKG2_HUMAN	rotein kinase.	1	GCACCGGCGGC	0.607	rs143915773
-	11	2304	ge.1_Missense_M	NM_182493	NP_872299	Q32MK0	MYLK3_HUMAN	rotein kinase.	7	CAAAATCCCAGC	0.468	
-	3	580		NM_001796	NP_001787	P55286	CADH8_HUMAN	r (Potential).|Cadherin 1.	9	TTATTTGAAATAT	0.418	
-	9	1141	p.R302C|SPATA22	NM_032598	NP_115987	Q8NHS9	SPT22_HUMAN		0	GTTCACGATCCT	0.348	
-	48	7743	F1_uc002fxg.1_5'F	NM_015113	NP_055928	O43149	ZZEF1_HUMAN		4	GGGTTCGATTCA	0.592	
-	3	878	6F|ZMYND15_uc0	NM_022059	NP_071342	Q9H2A7	CXL16_HUMAN	(Potential).|Chemokine.	0	GATCAAGACAGC	0.547	
-	37	5472	uc002gml.1_Intron	NM_002472	NP_002463	P13535	MYH8_HUMAN	Potential.	11	CCTTCACCGTCT	0.557	
-	19	2186	uc002gml.1_Intron	NM_017533	NP_060003	Q9Y623	MYH4_HUMAN	yosin head-like.	13	GGACAAGCTCA	0.493	
-	30	4154_4155	_Missense_Mutati	NM_001100112	NP_001093582	Q9UKX2	MYH2_HUMAN	Potential.	14	GTGGCGGGAAG	0.52	rs145911509
+	3	1399		NM_021012	NP_066292	Q14500	IRK12_HUMAN	smic (By similarity).	4	GCGCAGCTCATC	0.637	
+	15	1860	R1_uc002gzm.2_M	NM_014238	NP_055053	Q8IVT5	KSR1_HUMAN		4	ACATCCCCTTCG	0.716	
+	3	791	ATF_uc002hnj.2_R	NM_012138	NP_036270	Q9NY61	AATF_HUMAN	Glu-rich.	0	GGCATGGAAGA	0.517	
-	8	768	v.1_Missense_Mut	NM_001143780	NP_001137252	Q9BZJ4	S2539_HUMAN	Solcar 2.	1	ACTGCAGTTCGA	0.642	
-	9	1389	_p.E253*|SPOP_u	NM_003563	NP_003554	O43791	SPOP_HUMAN	BTB.	6	TCATTTCCTTAAA	0.383	
+	11	854	sense_Mutation_p.	NM_001099432	NP_001092902	Q9H6U6	BCAS3_HUMAN		5	TTGATTCGATGT	0.428	
+	3	459		NM_000727	NP_000718	Q06432	CCG1_HUMAN		0	CCCTCGGGAAG	0.612	rs142384274
+	5	394	FMID_uc002juz.3_	NM_001010982	NP_001010982	Q63HM1	AFMID_HUMAN		2	GCTTACGGCATC	0.582	
+	5	1499		NM_005189	NP_005180	Q14781	CBX2_HUMAN		0	CAGTGTCCGTTC	0.627	
-	17	2758	dw.1_Missense_Mu	NM_004104	NP_004095	P49327	FAS_HUMAN		1	ACCGTCGAGGG	0.672	
-	58	8407_8408	nl.2_Missense_Mu	NM_005559	NP_005550	P25391	LAMA1_HUMAN	minin G-like 4.	21	GAGGCGGCCCC	0.574	
-	5	804	HD3_uc010xao.1_	NM_138340	NP_612213	Q8WU67	ABHD3_HUMAN		1	ACCCTCCCATTG	0.433	
+	1	124	MA8_uc002kvp.2_N	NM_144662	NP_653263	Q8TAA3	PSA7L_HUMAN		1	GCGTCTCGATAT	0.602	
+	15	2574	p.1_Missense_Mu	NM_001942	NP_001933	Q02413	DSG1_HUMAN	lasmic (Potential).	7	CTCAGGAAACA	0.488	
-	11	2316	2lbo.1_Missense_M	NM_020964	NP_066015	Q9HCE0	EPG5_HUMAN		0	AGGAGGAGAGC	0.577	
+	7	1794	_p.E251K|DCC_uc	NM_005215	NP_005206	P43146	DCC_HUMAN	otential).|Ig-like C2-type 4.	17	GTGGCTGAAAAT	0.438	
-	12	6497		NM_052947	NP_443179	Q86TB3	ALPK2_HUMAN	type protein kinase.	14	CCAGCGTTGCTA	0.498	rs149775332
+	5	1025	p.D234N|CDH7_u	NM_033646	NP_387450	Q9ULB5	CADH7_HUMAN	r (Potential).|Cadherin 2.	4	GCAAAGGATATG	0.423	

+	37	5339	_Mutation_p.M156	NM_019112	NP_061985	Q8IZY2	ABCA7_HUMAN	ical; (Potential).	9	TGACATGGTGC	0.577	
-	4	751	D2_uc002luo.1_5'	NM_017797	NP_060267	Q9BX70	BTBD2_HUMAN		2	GGCGTCTGCAG	0.672	
+	2	418	va.1_Splice_Site_	NM_005428	NP_005419	P15498	VAV_HUMAN		16	GCAAGGTGAGC	0.51	
-	3	14392		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).	57	CACGTCCTTGA	0.488	
+	6	700		NM_138353	NP_612362	Q66K64	DCA15_HUMAN		1	CCTTCCAGCCC	0.622	
-	5	1866	208_uc002nqo.1_	NM_007153	NP_009084				7	AAAGGCTTTGC	0.383	
-	5	920	p.R206K|ZNF565_	NM_152477	NP_689690	Q8N9K5	ZN565_HUMAN	2H2-type 4.	2	TGAGTTCTTTGA	0.463	
-	1	97		NM_001080468	NP_001073937	Q0VAF6	SYCN_HUMAN		0	CTTGAGGTCGG	0.706	
+	18	1780	2osb.2_Missense_	NM_004706	NP_004697	Q92888	ARHG1_HUMAN	DH.	4	GACATGATCCC	0.667	
-	2	340	g.1_Intron|PSG3_	NM_021016	NP_066296	Q16557	PSG3_HUMAN	g-like V-type.	2	TTGCCCTTTGTA	0.433	
-	1	166		NM_178449	NP_848544	Q96A98	TIP39_HUMAN		0	ACCACcagcagca	0.597	
-	2	454	wk.2_Missense_M	NM_005601	NP_005592	Q16617	NKG7_HUMAN	ical; (Potential).	1	GGTGGTTGAGA	0.617	
-	2	543	ydc.1_Nonsense_	NM_001245	NP_001236	O43699	SIGL6_HUMAN	ellular (Potential).	1	TTTCATCCATTTG	0.537	
+	4	1821	313_uc010eqq.1_	NM_001004301	NP_001004301	Q6ZN06	ZN813_HUMAN	2H2-type 13.	1	AAGCACACCTT	0.368	
-	2	664	gn.1_Missense_M	NM_001005850	NP_001005850				4	CTTGCCGCAGT	0.731	
-	3	919	issense_Mutation_	NM_198458	NP_940860	Q6ZNH5	ZN497_HUMAN		2	CGGCCGCGCGC	0.697	
-	11	2916		NM_004304	NP_004295	Q9UM73	ALK_HUMAN	ellular (Potential).	1218	TTGGTGAATTT	0.468	
+	15	1657	p.L445S|KLRAQ1_	NM_001135629	NP_001129101	Q6ZMI0	KLRAQ_HUMAN		1	ACAATTTGGACT	0.343	
+	6	579	_p.V153I|ACTG2_	NM_001615	NP_001606	P63267	ACTH_HUMAN		0	GCATCGTCCTG	0.507	
+	10	1411	YD1_uc002sss.2	NM_198274	NP_938015	Q8NB12	SMYD1_HUMAN		4	CCAGCCCATGC	0.602	
+	2	381	RTK_uc002thl.1_In	NM_006343	NP_006334	Q12866	MERTK_HUMAN	otential).|Ig-like C2-type 1.	9	TCTGTCGAATCA	0.483	
-	4	554		NM_032494	NP_115883	Q8N5P1	ZC3H8_HUMAN		0	AGGGCCAGGCC	0.383	
-	3	317	_Mutation_p.L51F|	NM_003466	NP_003457	Q06710	PAX8_HUMAN	Paired.	2	GCGGAGCTGGC	0.627	
-	10	1205	z.2_Nonsense_Mu	NM_002980	NP_002971	P47872	SCTR_HUMAN	lasmic (Potential).	3	TTTCTTGGGTTC	0.328	
-	14	2785	AP5_uc002ttq.2_I	NM_207363	NP_997246	O14513	NCKP5_HUMAN		0	TGGGAGGTATT	0.458	
-	2	451	p.N123S|CXCR4_	NM_003467	NP_003458	P61073	CXCR4_HUMAN	lical; Name=3.	3	TAGAGGTTGACT	0.542	
+	9	3414	se_Mutation_p.P8	NM_018328	NP_060798	Q9P267	MBD5_HUMAN		5	TACATCCCAATC	0.453	
-	34	3806		NM_004543	NP_004534	P20929	NEBU_HUMAN	Nebulin 30.	20	GGAATCCAGCC	0.453	
+	7	1246	s.2_Missense_Mu	NM_004180	NP_004171	Q92844	TANK_HUMAN		1	AATCCGAGGAC	0.413	
-	275	70825	29K|TTN_uc010z	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	TCATTTCTTTTAA	0.423	
-	259	57436	66Q|TTN_uc010zfi	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	CAAATCGGTTTT	0.468	
-	51	12415	N_uc010zfj.1_Intro	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	CTTATTCGGTAT	0.473	rs146847928
-	63	11862	ti.3_Missense_Mu	NM_018897	NP_061720	Q8WXX0	DYH7_HUMAN		12	ACCATCCTCAG	0.413	
+	1	799		NM_152614	NP_689827	Q53QW1	CB057_HUMAN		1	GCCCCCACGAG	0.637	
+	2	250		NM_022134	NP_071417	Q9H3Q3	G3ST2_HUMAN		0	ACACCGTAAGT	0.632	
-	8	724	D1_uc002wmd.3_	NM_019593	NP_062539	Q9NPB8	GPCP1_HUMAN	Poly-Asp.	0	TATCATCGTCAT	0.418	
-	5	1501		NM_152611	NP_689824	Q8WUT4	LRRN4_HUMAN	ellular (Potential).	3	CCTCCCGTGCA	0.672	
-	2	234	uc002wqu.1_RNA	NM_001099407	NP_001092877	Q9NVP4	CT012_HUMAN		1	CTGAGGGACAC	0.328	
-	12	6122	w.2_Missense_Mu	NM_014071	NP_054790	Q14686	NCOA6_HUMAN	1-binding region.	7	AGGGGGTTGC	0.552	
-	4	1501	zzp.1_Missense_	NM_153360	NP_699191	Q8NCL9	APCDL_HUMAN		1	GGTATCGGGAC	0.612	
+	1	493	NAS_uc002xzu.3_	NM_080425	NP_536350	P63092	GNAS2_HUMAN		292	GTGGACCCCCA	0.632	
+	3	798	ks.2_Nonsense_	NM_003195	NP_003186	Q15560	TCEA2_HUMAN	IIS N-terminal.	0	CCACCCGAGTC	0.617	
-	14	1163	e|TPTE_uc002yir.	NM_199261	NP_954870	P56180	TPTE_HUMAN		5	CCTTACCTTGA	0.313	
-	3	603	.1_Missense_Mut	NM_198996	NP_945347	Q6XZB0	LIPI_HUMAN		2	TTCTTCCAAGTT	0.284	
+	11	1984	1A_uc002ywl.2_3	NM_001396	NP_001387	Q13627	DYR1A_HUMAN		4	CTCCAACGAAT	0.408	
-	33	6235	AM_uc002yyr.1_	NM_001389	NP_001380	O60469	DSCAM_HUMAN	lasmic (Potential).	11	TCCAAGCATGCT	0.572	
+	8	890	abj.2_Missense_M	NM_001039948	NP_001035037	Q2NKQ1	SGSM1_HUMAN		5	ACTACGTGGAG	0.562	

-	14	2808	sense_Mutation_p	NM_012143	NP_036275	Q9UBB9	TFP11_HUMAN		0	CCGGTCGATGT	0.572	
+	12	1597	_p.Q320*|SFI1_uc	NM_001007467	NP_001007468	A8K8P3	SFI1_HUMAN	HAT 5.	1	ATCTCCAGCAA	0.468	
+	18	3689		NM_001429	NP_001420	Q09472	EP300_HUMAN	Bromo.	64	CATGGATCTTTC	0.393	
-	1	88		NM_002676	NP_002667	Q92871	PMM1_HUMAN		1	TCCTGCGGGCT	0.672	
-	13	1690	p.G146R|TTLL12_	NM_015140	NP_055955	Q14166	TTL12_HUMAN	TTL.	1	AGGCCCGGAAG	0.667	
+	14	1872	blc.2_Missense_M	NM_014678	NP_055493	O75170	PP6R2_HUMAN		0	GGATCGCCAAC	0.667	rs140951188
+	5	1532	asw.1_Missense_M	NM_003670	NP_003661	O14503	BHE40_HUMAN		1	ACTTAGAAACC	0.478	rs147880359
-	22	2965	RIP2_uc011avh.1_	NM_001080423	NP_001073892	Q9C0E4	GRIP2_HUMAN		1	CAGTTCCCTCA	0.627	
-	22	3871	ev.2_Nonsense_M	NM_014744	NP_055559	Q92609	TBCD5_HUMAN		1	AGGCTGGGCCT	0.587	rs150988847
+	5	3340		NM_003458	NP_003449	Q9UPA5	BSN_HUMAN	Potential.	8	CCCGGCGGGAC	0.657	
-	3	471	717_uc003dpw.3_	NM_001128223	NP_001121695	C9JSV9	C9JSV9_HUMAN		0	CATCACGTCCC	0.502	rs147946451
-	1	469	1_uc003dty.3_5'Fl	NM_014820	NP_055635	O94826	TOM70_HUMAN	intermembrane (Potential).	1	GGCTGCGACCA	0.716	
+	10	1082	se_Mutation_p.H1	NM_017577	NP_060047	Q8IYS0	GRM1C_HUMAN		3	ATTTTTCATATCA	0.338	
+	16	1627	bjn.1_Missense_M	NM_021082	NP_066568	Q16348	S15A2_HUMAN		1	TCATTCGTGAA	0.398	
-	14	2356		NM_173543	NP_775814	Q8IYY4	DZI1L_HUMAN		2	GCCCTGGCCAG	0.612	
+	8	761		NM_001870	NP_001861	P15088	CBPA3_HUMAN		2	AAAAATCGTTCC	0.383	
-	4	1922	HE_uc003fen.3_R	NM_000055	NP_000046	P06276	CHLE_HUMAN		4	TAAATTGATTTTT	0.333	
+	13	2826		NM_004443	NP_004434	P54753	EPHB3_HUMAN		11	CACCAGGGCGG	0.662	
-	3	12753	1bth.1_Intron|MU	NM_018406	NP_060876	Q99102	MUC4_HUMAN	Ser-rich.	0	TGACAGGAAGA	0.587	
-	8	796	wh.2_Missense_M	NM_005017	NP_005008	P49585	PCY1A_HUMAN	lytic (Potential).	0	ACAATTCGGGTG	0.483	
-	5	1222	53A_uc010ibw.2_3	NM_001013622	NP_001013644	Q6NSI3	FA53A_HUMAN		0	GAGGCCCCTCT	0.657	
+	67	9249		NM_002111	NP_002102	P42858	HD_HUMAN		4	GGTCCGGGACT	0.647	
-	1	588		NM_198353	NP_938167	Q6ZWB6	KCTD8_HUMAN	BTB.	3	GCCGTCCCGGT	0.567	
-	3	410	cw.2_Missense_M	NM_001010874	NP_001010874	Q5HYJ1	TECRL_HUMAN		0	AGAAGGGTACC	0.318	
+	3	752		NM_021225	NP_067048	Q99935	PROL1_HUMAN	Thr-rich.	1	CATATCAGCAG	0.498	
-	9	1289	.2_Missense_Mut	NM_000583	NP_000574	P02774	VTDB_HUMAN	Albumin 2.	3	AGTCTTCAACA	0.308	
+	6	968		NM_016599	NP_057683	Q9NPC6	MYOZ2_HUMAN		0	CGAACCTACAG	0.373	
+	83	14728	em.2_Missense_M	NM_015312	NP_056127	Q2LD37	K1109_HUMAN		12	AAAAGTCCAATT	0.338	
+	5	6625	p.1_Missense_Mut	NM_024582	NP_078858	Q6V0I7	FAT4_HUMAN	|Extracellular (Potential).	18	TCACAGGTGCC	0.463	
-	6	725	ivv.1_Missense_M	NM_152682	NP_689895	Q6NW29	RWDD4_HUMAN		0	TCGAGGAAGTT	0.284	
+	22	3214	jp.1_Missense_Mu	NM_024867	NP_079143	Q9C093	SPEF2_HUMAN		4	CTAATAGAAAAT	0.333	
-	34	6788	orf42_uc011coz.1_	NM_023073	NP_075561	E9PH94	E9PH94_HUMAN		7	AAAACGAAGTG	0.423	
+	28	3537	A1_uc003jow.2_M	NM_181501	NP_852478	P56199	ITA1_HUMAN	ical; (Potential).	3	TTTAGCACTGTG	0.318	
+	4	765	zx.2_Missense_Mu	NM_001882	NP_001873	P24387	CRHBP_HUMAN		0	CTTCCGAGTCC	0.468	rs139472454
+	11	2210	R98_uc003kjt.2_5'U	NM_032119	NP_115495	Q8WXG9	GPR98_HUMAN	ellular (Potential).	16	CCCCGGATGATA	0.428	
-	6	786	kpw.1_Missense_	NM_022140	NP_071423	Q9HCS5	E41LA_HUMAN	FERM.	1	AGTTCTTCCTTC	0.358	
+	1	2159		NM_018935	NP_061758	Q9Y5E8	PCDBF_HUMAN	lasmic (Potential).	5	GGCGGCCTCAG	0.652	
+	1	185	ljm.1_Intron|PCDH	NM_018922	NP_061745	Q9Y5G3	PCDGD_HUMAN	|Extracellular (Potential).	0	AACTCGAAAAC	0.522	
+	11	2912	_p.S918F|PPARG	NM_133263	NP_573570	Q86YN6	PRGC2_HUMAN	RRM.	0	CCCTCTCTTTGA	0.612	
+	4	477	RS_uc011deo.1_In	NM_002887	NP_002878	P54136	SYRC_HUMAN		3	ACCTCCCAGAC	0.328	
+	2	199		NM_197975	NP_932079	Q6UXE8	BTNL3_HUMAN	ellular (Potential).	0	TGGACCGGGCA	0.552	
+	8	1099	ag.1_Missense_M	NM_030948	NP_112210	Q9C0D0	PHAR1_HUMAN		0	AGACCTCTCAC	0.607	
-	8	2712	e_Mutation_p.Q5	NM_000332	NP_000323	P54253	ATX1_HUMAN	tion with USP7.|RNA-bindi	4	CAACTGGATGA	0.572	
-	8	1631	e_Mutation_p.Q22	NM_000332	NP_000323	P54253	ATX1_HUMAN	Poly-Gln.	4	ctgctgctgctgctgctg	0.363	
-	8	1625	e_Mutation_p.Q21	NM_000332	NP_000323	P54253	ATX1_HUMAN	Poly-Gln.	4	ctgctgctgctgctgctg	0.368	
+	6	697	.P126S|CAP2_uc	NM_006366	NP_006357	P40123	CAP2_HUMAN		1	CCAAACCTGGT	0.413	
+	1	278		NM_012367	NP_036499	P58173	OR2B6_HUMAN	ellular (Potential).	1	TAATCAGTTATCG	0.408	

-	7	1524	HX16_uc011dmo.	NM_003587	NP_003578	O60231	DHX16_HUMAN	ase ATP-binding.		4	CTCCTCAAAGA	0.408	
+	2	226	n_p.Q5R|MICB_u	NM_005931	NP_005922	Q29980	MICB_HUMAN	ellular (Potential).		0	GTCCCAGGATG	0.522	
-	15	2667	oca.2_Missense_	NM_018833	NP_061313	Q03519	TAP2_HUMAN			0	GATTCCCACCA	0.517	
-	2	461	dsq.1_Missense_	NM_012391	NP_036523	O95238	SPDEF_HUMAN			5	CAGGAGGTGGC	0.677	
+	6	1294	_p.V337L|PNPLA1	NM_001145717	NP_001139189	Q8N8W4	PLPL1_HUMAN	Pro-rich.	p.P432A(1)	4	CAACTGTGGGG	0.592	
-	4	498		NM_006708	NP_006699	Q04760	LGUL_HUMAN			1	CTTACCGAATC	0.338	
+	5	706	ML4_uc003oqd.2_	NM_198153	NP_937796	Q6UXN2	TRML4_HUMAN			1	GTTGTGAGTCC	0.582	
+	5	1657		NM_001010872	NP_001010872	Q5T0W9	FA83B_HUMAN			6	TGGATCAGCTT	0.403	
-	4	945	YS_uc003per.1_M	NM_001142800	NP_001136272	Q5T1H1	EYS_HUMAN			6	AATTAACAGTG	0.413	
+	18	2053	0776_uc010kck.2_	NM_015323	NP_056138	O94874	UFL1_HUMAN			1	AACATCGACAA	0.378	rs141416978
-	5	779	.1_Intron|ROS1_u	NM_001017408	NP_001017408	Q9HD26	GOPC_HUMAN			1	TTTGCCTAGGT	0.333	
-	7	2147		NM_015204	NP_056019	Q9UPZ6	THS7A_HUMAN	ellular (Potential).		3	CTTTCGGGCAT	0.537	
-	9	1006	uc.2_Nonsense_Mutation_p.Q62*|SNX13_uc003stx.1_			Q9Y5W8	SNX13_HUMAN	PXA.		3	TGAGTTGATTTA	0.269	
+	3	607	e_Mutation_p.E1	NM_018685	NP_061155	Q9NQW6	ANLN_HUMAN	tion.|Interaction with CD2A		3	GATTGGAAGCA	0.493	
+	10	1110	A13_uc010kyr.2_5	NM_152701	NP_689914	Q86UQ4	ABCAD_HUMAN			10	ACAGGGTAGCC	0.423	
+	2	574	0ldj.1_RNA|uc003	NM_001540	NP_001531	P04792	HSPB1_HUMAN	h TGFB1I1 (By similarity).		0	CACGCGGAAAT	0.647	
+	13	1692	ldp.2_Missense_	NM_020879	NP_065930	Q8IYE0	CC146_HUMAN			2	CATTCGAAATG	0.303	
-	2	643	ERF_uc011khm.1_	NM_006980	NP_008911	Q99551	MTERF_HUMAN			0	GAGGGGCATTG	0.403	
-	6	843	L13_uc003var.2_	NM_145032	NP_659469	Q8NEE6	FXL13_HUMAN			0	AACTTCGTTCA	0.318	
-	18	2293	ey.2_Missense_M	NM_007356	NP_031382	A4D0S4	LAMB4_HUMAN	inin IV type B.		8	CAATTTCAACAC	0.473	
+	15	2824_2825		NM_173569	NP_775840	Q6ZU65	UBN2_HUMAN	Ser-rich.		2	TGTCTCCATTAC	0.465	
-	15	1860		NM_004333	NP_004324	P15056	BRAF_HUMAN	rotein kinas	R603>I(2)|p.T	18290	ATTTCACTGTA	0.368	
-	2	1788	ion_p.G28S|FAM1	NM_014690	NP_055505	Q86XD5	F131B_HUMAN			0	GATGCCGTCCC	0.577	
+	7	805	M2_uc011kwi.1_I	NM_003970	NP_003961	P54296	MYOM2_HUMAN	like C2-type 1.		6	TTGACGACACT	0.537	
+	15	1282	TG1_uc010lxz.1_	NM_018967	NP_061840	Q9NSN8	SNTG1_HUMAN	PH.		5	GTACTCCCCGA	0.478	
-	9	860	_p.A32T|SNX31_u	NM_152628	NP_689841	Q8N9S9	SNX31_HUMAN			0	GTTTGGCCCATC	0.363	
-	5	1389	e_Mutation_p.R41	NM_013437	NP_038465	Q9Y561	LRP12_HUMAN	ntial).|LDL-receptor class		0	GCAGCGATCAG	0.413	
-	2	1304	cw.2_Missense_M	NM_014379	NP_055194	Q6PIU1	KCNV1_HUMAN	r; Name=Segment S4; (Po		2	GCATGCGCAGA	0.502	
-	16	1450	p.C285W|ASAP1_	NM_018482	NP_060952	Q9ULH1	ASAP1_HUMAN	-GAP.|C4-type.		4	TTCTATACAGGT	0.388	
-	1	1378		NM_015193	NP_056008	Q7LC44	ARC_HUMAN			1	CTGGGTCCGGT	0.711	
-	5	2192		NM_138367	NP_612376	Q9BRH9	ZN251_HUMAN			0	CTCTCCAACAC	0.403	
+	21	3000	.2_Missense_Mu	NM_004972	NP_004963	O60674	JAK2_HUMAN	otein kinase 2.		28641	CATAGGGTATG	0.318	
+	1	257		NM_022160	NP_071443	Q5VZB9	DMRTA_HUMAN			2	AGACCGAGGC	0.667	
+	3	196	1P1_uc010mjq.1_	NM_014471	NP_055286	O60575	ISK4_HUMAN	Kazal-like.		0	CATATACGAATG	0.557	rs149166930
+	7	1722	P1_uc011loj.1_Mi	NM_016525	NP_057609	Q9NZ09	UBAP1_HUMAN	UBA 2.		0	CCTCATGGCTC	0.532	
+	1	58	lb.2_Missense_M	NM_003995	NP_003986	P20594	ANPRB_HUMAN			3	GTCCTCCCGGG	0.677	
-	13	2140	nse_Mutation_p.Q	NM_033655	NP_387504	Q9BZ76	CNTP3_HUMAN	inal.|Extracellular (Potenti		1	CGTGCTGCACC	0.701	rs1758271
-	5	1086		NM_017561	NP_060031	A1L443	FA22F_HUMAN	Pro-rich.		0	TGGGCCTTGGT	0.706	
+	25	2784		NM_001855	NP_001846	P39059	COFA1_HUMAN	lical region 4 (COL4).		6	AGGGCGAGAAG	0.512	
+	1	1270		NM_006687	NP_006678	Q9Y615	ACL7A_HUMAN			0	ACGAGGAACAC	0.587	
+	14	2342	kz.1_Missense_	NM_007018	NP_008949	Q7Z7A1	CNTRL_HUMAN	Potential.		0	GTGAGCTCCAT	0.418	
-	17	1470	.G381R|DENND1	NM_020946	NP_065997	Q8TEH3	DEN1A_HUMAN			2	TTGCTCCACTTC	0.408	
+	1	679		NM_032728	NP_116117	Q8NBV4	PPAC3_HUMAN	ical; (Potential).		1	CCCTGGATCGG	0.687	
+	26	4113	53_splice|CACNA	NM_000718	NP_000709	Q00975	CAC1B_HUMAN			6	TGCAGGTAAAC	0.542	
+	4	524		NM_001011719	NP_001011719	Q5FYA8	ARSH_HUMAN	ical; (Potential).		1	CCTTGCCCTGG	0.532	
+	9	1703	id.1_Missense_M	NM_001830	NP_001821	P51793	CLCN4_HUMAN			5	CTCGGCCTGTG	0.542	
+	8	781		NM_005089	NP_005080	Q15696	U2AFM_HUMAN	RRM.		3	TGCCCGAGTTC	0.522	

+	5	662	_p.P190L|SYAP1_	NM_032796	NP_116185	Q96A49	SYAP1_HUMAN	BSD.		1	TCGTTCCTAAAC	0.488	
+	9	2561	se_Mutation_p.S8	NM_003410	NP_003401	P17010	ZFX_HUMAN	2H2-type 12.		2	TTATTTCCATTCA	0.433	
+	11	1504		NM_173695	NP_775966	Q8N9S7	CX059_HUMAN			1	gagaaaggaagatat	0	
-	5	1254_1255		NM_176819	NP_789789	Q9H7Y0	CX036_HUMAN			1	TGGGCGGATGC	0.569	
+	1	530		NM_019886	NP_063939	Q9NS84	CHST7_HUMAN	enal (Potential).		3	TGGGCGAACTC	0.627	
+	4	736	lhh.2_Missense_M	NM_005676	NP_005667	P98175	RBM10_HUMAN	Poly-Glu.		5	aggaggaggatgagg	0.522	
+	6	2909	E871K|CCNB3_u	NM_033031	NP_149020	Q8WWL7	CCNB3_HUMAN		p.E871>*(1)	9	AGCAGGAGGCC	0.527	
-	12	2736	oi.1_Missense_Mu	NM_004463	NP_004454	P98174	FGD1_HUMAN	PH 1.		6	GAGCTCGAGGG	0.552	
+	5	1810	p.D560N|STARD8	NM_014725	NP_055540	Q92502	STAR8_HUMAN			6	GGCGCGATTCA	0.607	
-	4	416	F5_uc004eij.1_RN	NM_032946	NP_116564	Q9H1B4	NXF5_HUMAN	RRM.		1	CATAAGGAATC	0.413	
+	6	1444	ejh.2_Missense_M	NM_022838	NP_073749	Q6P1M9	ARMX5_HUMAN			1	CTGGCCTGAAG	0.458	
-	8	1613		NM_005334	NP_005325	P51610	HCFC1_HUMAN			2	CTTTTCTGTGG	0.632	
+	5	648	.2_Missense_Mut	NM_017765	NP_060235	Q6ZP29	PQLC2_HUMAN	1.|Helical; (Potential).		0	ACAGACCTACA	0.284	
+	11	1953	_p.F583Y|ZMYM1_	NM_024772	NP_079048	Q5SVZ6	ZMYM1_HUMAN			0	AAACATTTCGAC	0.308	
-	12	1456	r.1_Missense_Mu	NM_021080	NP_066566	O75553	DAB1_HUMAN			3	CGGGGGGAGA	0.363	
+	9	1592	_p.S263L|PGM1_u	NM_002633	NP_002624	P36871	PGM1_HUMAN			3	GTTCTCAGCAA	0.473	
+	2	247	2_5'UTR|CLCA4_	NM_012128	NP_036260	Q14CN2	CLCA4_HUMAN			2	CACAGAAAAAA	0.328	
+	9	1128	GA10_uc009wiw.	NM_003637	NP_003628	O75578	ITA10_HUMAN	ellular (Potential).		8	ACTAGGAGATC	0.473	
-	8	879_880	PATCH4_uc001fp	NM_015590	NP_056405	Q5T3I0	GPTC4_HUMAN			1	AATTCCCCAAG	0.485	
+	15	1826	rf92_uc001fql.2_3'	NM_144702	NP_653303	Q8N4P6	LRC71_HUMAN			0	GGGAGGATGAG	0.562	
+	1	364		NM_001004473	NP_001004473	Q8NGX5	O10K1_HUMAN	lasmic (Potential).		1	TATGATCGCTAT	0.527	
-	6	981	f112_uc001ggj.2_	NM_000450	NP_000441	P16581	LYAM2_HUMAN	xtracellular (Potential).		5	TCAAATCCTTCTT	0.473	
+	5	1010		NM_031935	NP_114141	Q96RW7	HMCN1_HUMAN			23	AAATTCGCAAT	0.358	
-	6	930		NM_001994	NP_001985	P05160	F13B_HUMAN	Sushi 5.		3	TATTTCTCCATG	0.368	
+	3	1031		NM_021205	NP_067028	Q7L0Q8	RHOU_HUMAN			0	CTTCCAGAACG	0.522	
+	5	328	1hxv.1_Missense_	NM_145861	NP_665860	Q8WWZ3	EDAD_HUMAN			0	TCTTCCAGGTA	0.294	
-	2	211	1ibx.2_Missense_	NM_020394	NP_065127	Q8IW36	ZN695_HUMAN	KRAB.		0	GCTGGGTCCAG	0.453	
-	3	499	icp.2_Missense_M	NM_032752	NP_116141	Q96IT1	ZN496_HUMAN			2	CTTCGGAGCCA	0.592	
-	2	327	nse_Mutation_p.N	NM_002189	NP_002180	Q13261	I15RA_HUMAN	tracellular (Potential).		0	CGACATTCGTG	0.572	
-	9	1215	_p.S67F|ANKRD2	NM_014915	NP_055730	Q9UPS8	ANR26_HUMAN			4	TGTGGGAAGGT	0.403	
-	12	1606	9xpr.2_Missense_	NM_022079	NP_071362	Q5GLZ8	HERC4_HUMAN			3	CAGAGGAAGAA	0.244	
-	8	861	_Mutation_p.P220	NM_022129	NP_071412	P30039	PBLD_HUMAN			3	CCACGGTGCAA	0.448	
+	17	4988	.H1436Y|PLCE1_	NM_016341	NP_057425	Q9P212	PLCE1_HUMAN	I-PLC X-box.		3	ATTTATCATGGA	0.423	
-	4	652	nse_Mutation_p.R	NM_000770	NP_000761	P10632	CP2C8_HUMAN			0	CAAATCGTTTCT	0.388	
+	1	283	uc001kwr.2_Intron	NM_001143909	NP_001137381	Q2QD12	Q2QD12_HUMAN			0	CCTTCGAAAGC	0.498	rs61746133
+	31	11879		NM_002457	NP_002448	Q02817	MUC2_HUMAN			2	accaccaccactacg	0.129	
-	1	196		NM_001004758	NP_001004758	Q8NGJ8	O51S1_HUMAN	Name=2; (Potential).		4	CATTGGGCGGT	0.567	
+	1	493	_uc001mam.1_Int	NM_001004750	NP_001004750	Q9H340	O51B6_HUMAN	ellular (Potential).		2	GGTTTCCCTAC	0.488	
-	2	1185	S_uc009yiz.2_Int	NM_001143816	NP_001137288	P23560	BDNF_HUMAN			0	GTATTCCTCCAG	0.522	
+	24	3427	l.2_Missense_Mu	NM_018259	NP_060729	Q96AE7	TTC17_HUMAN			5	GGGACGGCGCT	0.428	rs143797065
+	1	285_286		NM_001005200	NP_001005200	Q8N162	OR8H2_HUMAN	ellular (Potential).		2	TTTACGGGCTGC	0.446	
+	7	1951	c.1_Missense_Mu	NM_178864	NP_849195	Q8IUM7	NPAS4_HUMAN			0	CCTAGCCCAGC	0.587	
+	24	3303	e_Mutation_p.G1	NM_000260	NP_000251	Q13402	MYO7A_HUMAN			4	TCCAGGGGACA	0.602	
+	5	776	s.1_Missense_Mu	NM_006169	NP_006160	P40261	NNMT_HUMAN			1	CTGCCCAGACC	0.632	
+	1	722		NM_001004464	NP_001004464	Q8NGN5	O10G8_HUMAN	Name=6; (Potential).		2	CTGTGCCTCCC	0.547	
-	3	252		NM_006248	NP_006239					0	AGGAGGTGGGG	0.607	
+	3	1295	p.D356N|ALG10B_	NM_001013620	NP_001013642	Q5I7T1	AG10B_HUMAN	ical; (Potential).		3	TAGCTGACTCA	0.308	

-	3	1660		NM_005164	NP_005155	Q9UBJ2	ABCD2_HUMAN		6	GTACCTCTTTGT	0.328	
+	4	766	1rze.2_Nonsense	NM_001130015	NP_001123487	Q7Z3H0	ANR33_HUMAN		0	GGGACCAGCGG	0.652	
+	5	851	f.1_Missense_Mu	NM_005556	NP_005547	P08729	K2C7_HUMAN	od.|Linker 12.	0	TCTCCGACACA	0.592	
+	1	244		NM_001005519	NP_001005519	A6NDL8	O6C68_HUMAN	ellular (Potential).	1	GTGTTCCAAGA	0.363	
-	6	2024	p.G607D|DNAJC1	NM_032364	NP_115740	Q6Y2X3	DJC14_HUMAN		4	AGATACCTACA	0.468	
-	22	2990	.R684W|GRIP1_u	NM_021150	NP_066973	Q9Y3R0	GRIP1_HUMAN		2	GCTCCGAGTTG	0.537	
-	3	572	.1_Intron|MDM1_u	NM_017440	NP_059136	Q8TC05	MDM1_HUMAN		5	ATTAACTGGTGT	0.408	
-	35	4513	.Q1006P|CIT_uc0	NM_007174	NP_009105	O14578	CTRO_HUMAN	PH.	10	GCCTCTGTCCA	0.313	
+	11	770	e_Mutation_p.S16	NM_144669	NP_653270	Q96MS3	GL1D1_HUMAN		0	TAGCTCTGTCT	0.468	
-	9	1424	c.3_Missense_Mu	NM_002019	NP_002010	P17948	VGFR1_HUMAN	4.|Extracellular (Potential).	24	GAGCAGATTTC	0.403	
-	2	1472	_p.R168*|SLC46A	NM_181785	NP_861450	Q7Z3Q1	S46A3_HUMAN	lasmic (Potential).	2	CTATTCGAATTG	0.373	
-	8	845	OCK9_uc010tis.1	NM_015296	NP_056111	Q9BZ29	DOCK9_HUMAN	PH.	1	ACTGTCTGCTG	0.398	
-	1	78		NM_001004712	NP_001004712	Q8NGD5	OR4KE_HUMAN	Name=1; (Potential).	3	AAGAAAAAATTT	0.423	
+	14	1516	p.2_Missense_Mu	NM_022734	NP_073571	Q9H7H0	MET17_HUMAN		0	TGTGCTTACTC	0.532	
+	4	669	RG2_uc010tll.1_In	NM_173846	NP_776245	P59282	TPPP2_HUMAN		0	ACAAGGGTTCT	0.542	
-	12	2683	se_Mutation_p.I6	NM_032560	NP_115949	Q6IN85	P4R3A_HUMAN		0	TTCAATTACATG	0.289	
+	2	149	_p.G18E|PPP2R5	NM_001161725	NP_001155197	Q13362	2A5G_HUMAN		2	GAGTGGAAAAA	0.353	
+	21	7610	.Q2268*|MGA_uc	NM_001164273	NP_001157745	Q8IWI9	MGAP_HUMAN		12	CAGATCAGGCA	0.363	
-	2	279	ace.1_Missense_	NM_006628	NP_006619	P56211	ARP19_HUMAN		0	GCAACCGTTTC	0.403	
+	14	2002	se_Mutation_p.A6	NM_024505	NP_078781	Q96PH1	NOX5_HUMAN	ellular (Potential).	2	CCAGGCCGAGG	0.502	
+	13	1556	_p.M457I|WDR93_	NM_020212	NP_064597	Q6P2C0	WDR93_HUMAN		2	CAAATGAAATGT	0.488	
-	5	952		NM_178844	NP_849172	Q7RTR2	NLRC3_HUMAN	NACHT.	6	GAGATCCCGGA	0.672	
-	3	439	_p.L104V|UMOD_	NM_003361	NP_003352	P07911	UROM_HUMAN	lcium-binding (Potential).	2	GCCGAGACCGG	0.627	
-	11	1561	SM1_uc010bwg.1	NM_052956	NP_443188	Q08AH1	ACSM1_HUMAN		2	CCACGGCTGAC	0.607	
+	2	493	Missense_Mutatio	NM_007245	NP_009176	Q8WWM7	ATX2L_HUMAN	action with MPL.	2	GACCCCCACAG	0.403	
+	18	2586		NM_001114	NP_001105	P51828	ADCY7_HUMAN	ical; (Potential).	1	CCAAGGCCTGG	0.662	
-	3	580		NM_001796	NP_001787	P55286	CADH8_HUMAN	(Potential).|Cadherin 1.	9	TTATTTGAAATAT	0.418	
-	48	7743	F1_uc002fxg.1_5'	NM_015113	NP_055928	O43149	ZZEF1_HUMAN		4	GGTTCGATTCA	0.592	
-	3	878	6F|ZMYND15_uc0	NM_022059	NP_071342	Q9H2A7	CXL16_HUMAN	(Potential).|Chemokine.	0	ATCAAGACAGC	0.547	
-	37	5472	uc002gml.1_Intro	NM_002472	NP_002463	P13535	MYH8_HUMAN	Potential.	11	CTTCACCGTCT	0.557	
-	19	2186	uc002gml.1_Intro	NM_017533	NP_060003	Q9Y623	MYH4_HUMAN	osin head-like.	13	GGACAAGCTCA	0.493	
+	3	1399		NM_021012	NP_066292	Q14500	IRK12_HUMAN	smic (By similarity).	4	CGCAGCTCATC	0.637	
+	15	1860	R1_uc002gzm.2_	NM_014238	NP_055053	Q8IVT5	KSR1_HUMAN		4	CATCCCCTTCG	0.716	
+	3	791	TF_uc002hnj.2_R	NM_012138	NP_036270	Q9NY61	AATF_HUMAN	Glu-rich.	0	GGCATGGAAGA	0.517	
-	1	384	15_uc002hxa.2_5	NM_002275	NP_002266	P19012	K1C15_HUMAN	ly-rich.|Head.	0	GACCCTCATGC	0.323	
-	5	1186	P_uc010wfs.1_Int	NM_000226	NP_000217	P35527	K1C9_HUMAN	Rod.|Coil 2.	3	GTGCCGGAGCT	0.547	rs116216460
-	9	1389	_p.E253*|SPOP_u	NM_003563	NP_003554	O43791	SPOP_HUMAN	BTB.	6	TCATTTCCTTAA	0.383	
+	11	854	sense_Mutation_p.	NM_001099432	NP_001092902	Q9H6U6	BCAS3_HUMAN		5	TTGATTCGATGT	0.428	
+	5	1499		NM_005189	NP_005180	Q14781	CBX2_HUMAN		0	AGTGTCCGTTC	0.627	
-	58	8407_8408	l.2_Missense_Mu	NM_005559	NP_005550	P25391	LAMA1_HUMAN	minin G-like 4.	21	AGGCGGCCCC	0.574	
+	1	124	A8_uc002kvp.2_	NM_144662	NP_653263	Q8TAA3	PSA7L_HUMAN		1	CGTCTCGATAT	0.602	
+	15	2574	p.1_Missense_Mu	NM_001942	NP_001933	Q02413	DSG1_HUMAN	lasmic (Potential).	7	CTCAGGAAACA	0.488	
-	11	2316	lbo.1_Missense_	NM_020964	NP_066015	Q9HCE0	EPG5_HUMAN		0	AGGAGGAGAGC	0.577	
+	7	1794	_p.E251K|DCC_u	NM_005215	NP_005206	P43146	DCC_HUMAN	otential).|Ig-like C2-type 4.	17	TGGCTGAAAAT	0.438	
-	12	6497		NM_052947	NP_443179	Q86TB3	ALPK2_HUMAN	ype protein kinase.	14	CAGCGTTGCTA	0.498	rs149775332
+	5	1025	p.D234N|CDH7_u	NM_033646	NP_387450	Q9ULB5	CADH7_HUMAN	(Potential).|Cadherin 2.	4	CAAAGGATATG	0.423	
+	37	5339	_Mutation_p.M156	NM_019112	NP_061985	Q8IZY2	ABCA7_HUMAN	ical; (Potential).	9	TGACATGGTGC	0.577	

+	2	418	dva.1_Splice_Site_	NM_005428	NP_005419	P15498	VAV_HUMAN			16	GGCAAGGTGAGC	0.51	
-	3	17809		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).		57	TAGTCCCTATAGC	0.502	
-	5	920	p.R206K|ZNF565_	NM_152477	NP_689690	Q8N9K5	ZN565_HUMAN	C2H2-type 4.		2	TGAGTTCTTTGAT	0.463	
-	11	2916		NM_004304	NP_004295	Q9UM73	ALK_HUMAN	cellular (Potential).		1218	CTTGGTGAATTTT	0.468	
+	15	1657	p.L445S|KLRAQ1_	NM_001135629	NP_001129101	Q6ZMI0	KLRAQ_HUMAN			1	ACAATTTGGACTA	0.343	
-	3	345	yqv.1_Missense_M	NM_173535	NP_775806	Q8N1N0	CLC4F_HUMAN	cellular (Potential).		5	ACTCACTGTTGG	0.527	
+	10	1411	MYD1_uc002sss.2	NM_198274	NP_938015	Q8NB12	SMYD1_HUMAN			4	ACCAGCCCATGCA	0.602	
+	2	381	RTK_uc002thl.1_In	NM_006343	NP_006334	Q12866	MERTK_HUMAN	Potential).|Ig-like C2-type 1.		9	TCTGTCGAATCAA	0.483	
+	4	564	SH2P_uc002tkd.2_	NM_182905	NP_878908					0	CATCCGCCAAG	0.522	
-	10	1205	z.2_Nonsense_Mu	NM_002980	NP_002971	P47872	SCTR_HUMAN	lasmic (Potential).		3	TTTCTTGGGTTCT	0.328	
-	14	2785	AP5_uc002ttq.2_I	NM_207363	NP_997246	O14513	NCKP5_HUMAN			0	CTGGGAGGTATT	0.458	
+	9	3414	se_Mutation_p.P8	NM_018328	NP_060798	Q9P267	MBD5_HUMAN			5	TACATCCCAATCC	0.453	
-	11	1862	p.G484E|SCN1A_	NM_006920	NP_008851	P35498	SCN1A_HUMAN			13	CTCTCTCCGTGTC	0.527	
-	275	70825	229K|TTN_uc010z	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN			153	TCATTTCTTTTAA	0.423	
-	259	57436	66Q|TTN_uc010zf	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN			153	CCAAATCGGTTTT	0.468	
-	51	12415	N_uc010zfj.1_Intro	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN			153	CTTATTCGGTATT	0.473	rs146847928
-	63	11862	uti.3_Missense_Mu	NM_018897	NP_061720	Q8WXX0	DYH7_HUMAN			12	TACCATCCTCAGC	0.413	
+	1	799		NM_152614	NP_689827	Q53QW1	CB057_HUMAN			1	GCCCCCACGAG	0.637	
-	4	1501	zzp.1_Missense_M	NM_153360	NP_699191	Q8NCL9	APCDL_HUMAN			1	GGTATCGGGACT	0.612	
-	14	1163	e|TPTE_uc002yir.	NM_199261	NP_954870	P56180	TPTE_HUMAN			5	CCCTTACCTTGAT	0.313	
-	3	603	v.1_Missense_Mut	NM_198996	NP_945347	Q6XZB0	LIPI_HUMAN			2	ATTCTTCCAAGTT	0.284	
-	33	6235	CAM_uc002yyr.1_F	NM_001389	NP_001380	O60469	DSCAM_HUMAN	lasmic (Potential).		11	TCCAAGCATGCTT	0.572	
+	12	1597	_p.Q320*|SFI1_uc	NM_001007467	NP_001007468	A8K8P3	SFI1_HUMAN	HAT 5.		1	CATCTCCAGCAA	0.468	
-	22	2965	RIP2_uc011avh.1_	NM_001080423	NP_001073892	Q9C0E4	GRIP2_HUMAN			1	CAGTTCCCTCAC	0.627	
-	22	3871	nev.2_Nonsense_M	NM_014744	NP_055559	Q92609	TBCD5_HUMAN			1	AGGCTGGGCCT	0.587	rs150988847
+	2	127		NM_153215	NP_694947	Q8N112	CC045_HUMAN			1	GGGGGCCATTG	0.617	
-	2	7628	C4_uc003fvp.2_Int	NM_018406	NP_060876	Q99102	MUC4_HUMAN			0	GGAAGCGTCGG	0.592	
+	5	1022	p.R176Q|NSUN7_	NM_024677	NP_078953					0	GATGTCGAATCA	0.378	
+	3	752		NM_021225	NP_067048	Q99935	PROL1_HUMAN	Thr-rich.		1	CCATATCAGCAGC	0.498	
-	9	1289	e.2_Missense_Mut	NM_000583	NP_000574	P02774	VTDB_HUMAN	Albumin 2.		3	GAGTCTTCAACAT	0.308	
+	83	14728	em.2_Missense_M	NM_015312	NP_056127	Q2LD37	K1109_HUMAN			12	AAAAGTCCAATTA	0.338	
+	5	6625	p.1_Missense_Mut	NM_024582	NP_078858	Q6V0I7	FAT4_HUMAN	.|Extracellular (Potential).		18	GTCACAGGTGCC	0.463	
-	6	725	3ivv.1_Missense_M	NM_152682	NP_689895	Q6NW29	RWDD4_HUMAN			0	CTCGAGGAAGTT	0.284	
+	1	1318	003lhf.2_Intron|PCI	NM_018907	NP_061730	Q9UN74	PCDA4_HUMAN	|Extracellular (Potential).		6	CTACTCGTTGGT	0.622	rs143891810
+	1	2159		NM_018935	NP_061758	Q9Y5E8	PCDBF_HUMAN	lasmic (Potential).		5	GGCGGCCTCAG	0.652	
-	9	6462	2A_uc011dcs.1_In	NM_001447	NP_001438	Q9NYQ8	FAT2_HUMAN	(Potential).|Cadherin 18.		6	GATGGCGTTCCT	0.418	rs147595273
-	8	2712	e_Mutation_p.Q5	NM_000332	NP_000323	P54253	ATX1_HUMAN	ction with USP7.|RNA-bindi		4	CCAACTGGATGAT	0.572	
+	6	697	.P126S|CAP2_uc	NM_006366	NP_006357	P40123	CAP2_HUMAN			1	CCCAAACCTGGT	0.413	
+	1	278		NM_012367	NP_036499	P58173	OR2B6_HUMAN	cellular (Potential).		1	TAATCAGTTATCG	0.408	
-	15	2667	oca.2_Missense_M	NM_018833	NP_061313	Q03519	TAP2_HUMAN			0	GATTCCCACCAC	0.517	
-	2	461	dsq.1_Missense_M	NM_012391	NP_036523	O95238	SPDEF_HUMAN			5	CAGGAGGTGGC	0.677	
+	6	1294	p.V337L|PNPLA1_	NM_001145717	NP_001139189	Q8N8W4	PLPL1_HUMAN	Pro-rich.	p.P432A(1)	4	CAACTGTGGGG	0.592	
-	8	1165	p.S288R|GTPBP2	NM_019096	NP_061969	Q9BX10	GTPB2_HUMAN			2	GACACACTGGA	0.532	
+	5	1657		NM_001010872	NP_001010872	Q5T0W9	FA83B_HUMAN			6	ATGGATCAGCTTT	0.403	
+	10	889	_p.V252L|C7orf10_	NM_024728	NP_079004	Q9HAC7	CG010_HUMAN			2	TATATTGTAGTTG	0.333	
+	10	1110	A13_uc010kyr.2_5	NM_152701	NP_689914	Q86UQ4	ABCAD_HUMAN			10	AACAGGGTAGCC	0.423	
-	6	843	L13_uc003var.2_R	NM_145032	NP_659469	Q8NEE6	FXL13_HUMAN			0	GAACTTCGTTCAC	0.318	

-	18	2293	ey.2_Missense_Mu	NM_007356	NP_031382	A4D0S4	LAMB4_HUMAN	ninin IV type B.		8	CAATTTCAACAC	0.473	
+	4	718	CHRM2_uc003vtm	NM_001006630	NP_001006631	P08172	ACM2_HUMAN	ame=1; (By similarity).		5	CTGGATCCCTCA	0.423	
-	15	1860		NM_004333	NP_004324	P15056	BRAF_HUMAN	rotein kinas	R603>I(2)|p.T	18290	GATTTCACTGTAC	0.368	
+	7	805	OM2_uc011kwi.1_I	NM_003970	NP_003961	P54296	MYOM2_HUMAN	like C2-type 1.		6	TTGACGACACT	0.537	
-	2	212	3wso.3_Missense_	NM_024607	NP_078883	Q86XI6	PPR3B_HUMAN		p.S16F(1)	2	GCAAGGAAGGA	0.493	rs142670074
-	9	860	_p.A32T|SNX31_u	NM_152628	NP_689841	Q8N9S9	SNX31_HUMAN			0	GTTTGGCCCATC	0.363	
-	5	1389	e_Mutation_p.R41	NM_013437	NP_038465	Q9Y561	LRP12_HUMAN	ential).|LDL-receptor class		0	GCAGCGATCAG	0.413	
-	16	1450	p.C285W|ASAP1_	NM_018482	NP_060952	Q9ULH1	ASAP1_HUMAN	-GAP.|C4-type.		4	TTCTATACAGGT	0.388	
-	1	1378		NM_015193	NP_056008	Q7LC44	ARC_HUMAN			1	CTGGGTCCGGT	0.711	
-	5	2192		NM_138367	NP_612376	Q9BRH9	ZN251_HUMAN			0	CTCTCCAACAC	0.403	
+	7	1722	P1_uc011loj.1_Mi	NM_016525	NP_057609	Q9NZ09	UBAP1_HUMAN	UBA 2.		0	CCTCATGGCTC	0.532	
-	16	1981	pc.1_Intron|TRPM	NM_017662	NP_060132	Q9BX84	TRPM6_HUMAN	lasmic (Potential).		8	AAGGACTATAGA	0.363	
+	4	892		NR_026851						0	ATATTTCCCAGG	0.483	
-	17	1470	.G381R|DENND1	NM_020946	NP_065997	Q8TEH3	DEN1A_HUMAN			2	TTGCTCCACTTC	0.408	
+	9	1703	id.1_Missense_Mu	NM_001830	NP_001821	P51793	CLCN4_HUMAN			5	CTCGGCCTGTG	0.542	
+	5	662	_p.P190L|SYAP1_	NM_032796	NP_116185	Q96A49	SYAP1_HUMAN	BSD.		1	TCGTTCCTAAAC	0.488	
+	9	2561	se_Mutation_p.S8	NM_003410	NP_003401	P17010	ZFX_HUMAN	2H2-type 12.		2	TTATTTCCATCA	0.433	
-	3	366	kh.1_Missense_M	NM_006307	NP_006298	P78539	SRPX_HUMAN	Sushi 1.		0	GCAGCTCGTAGC	0.542	
-	7	923	dit.2_Missense_Mu	NM_006962	NP_008893	P17025	ZN182_HUMAN			3	CAGTATGGAAGA	0.348	
+	6	2909	E871K|CCNB3_uc	NM_033031	NP_149020	Q8WWL7	CCNB3_HUMAN		p.E871>*(1)	9	AGCAGGAGGCC	0.527	
+	5	1810	p.D560N|STARD8	NM_014725	NP_055540	Q92502	STAR8_HUMAN			6	GGCGCGATTCA	0.607	
+	8	1294	RN1_uc011mpt.1_	NM_052957	NP_443189	Q96QF7	ACRC_HUMAN	Asp/Ser-rich.		3	AAGCTCCCGAC	0.557	
+	28	4498	_Mutation_p.P78	NM_014675	NP_055490	Q5TZA2	CROCC_HUMAN			5	ACAGCCCCAGC	0.627	
-	10	1254	xm.1_Missense_	NM_052896	NP_443128	Q7Z408	CSMD2_HUMAN	xtracellular (Potential).		12	CTCGAAGGTGGG	0.537	
+	25	11625	a.1_Nonsense_Mu	NM_033044	NP_149033	Q9UPN3	MACF1_HUMAN	Spectrin 7.		16	GATGATCGAAAG	0.428	rs145098670
-	8	2050		NM_020883	NP_065934	Q9P217	ZSWM5_HUMAN			0	GATGGGATCCAC	0.522	
-	3	710		NM_023077	NP_075565	Q96BR5	SELR1_HUMAN			0	GGACACCTTTCT	0.527	
-	5	498	ont.1_Missense_	NM_002370	NP_002361	P61326	MGN_HUMAN			0	AATCCAATAAGA	0.378	
+	3	709		NM_057176	NP_476517	Q8WZ55	BSND_HUMAN	lasmic (Potential).		2	GTTCAGGCCTGG	0.627	
-	2	498	1orf168_uc009vzv.	NM_001004303	NP_001004303	Q5VWT5	CA168_HUMAN			5	CCTGCTGGGAAT	0.458	
+	15	2222	HD1_uc001dbq.1_	NM_020925	NP_065976	Q5VU97	CAHD1_HUMAN	ellular (Potential).		2	CTAGGAGACAAT	0.448	
+	6	1132	.2_Missense_Mut	NM_174858	NP_777283	Q9Y6K8	KAD5_HUMAN			1	GGAAAAGGGGC	0.433	
+	12	1400	_RNA|NBPF9_uc	NM_001037675	NP_001032764	Q3BBV1	NBPFK_HUMAN	NBPF 2.		0	GATGACAATGAA	0.423	
+	14	1889	10_uc010oyi.1_Int	NM_001039703	NP_001034792	A6NDV3	A6NDV3_HUMAN			0	TTCCACGCTCAG	0.453	rs61816394
-	3	6171	uc001ezv.2_Intron	NM_001014342	NP_001014364	Q5D862	FILA2_HUMAN	Filaggrin 9.		17	TCACTGTACTCA	0.537	
-	3	4318	uc001ezv.2_Intron	NM_001014342	NP_001014364	Q5D862	FILA2_HUMAN			17	GTTGTCCTGGA	0.527	
-	3	883		NM_016190	NP_057274	Q9UBG3	CRNN_HUMAN	Gln-rich.		3	CGTGGGTCTCA	0.612	rs3814301
+	2	336	_uc001fht.1_RNA	NM_025058	NP_079334	Q7Z4K8	TRI46_HUMAN			3	CCCCTTCCACC	0.682	
+	8	1629	sense_Mutation_p.	NM_025058	NP_079334	Q7Z4K8	TRI46_HUMAN	onectin type-III.		3	TACGGCGAATAC	0.657	
-	6	1176	L2_uc010phz.1_M	NM_030764	NP_110391	Q96LA5	FCRL2_HUMAN	4.|Extracellular (Potential).		2	CAGGCCGTTGT	0.577	rs149829829
-	27	3994		NM_003126	NP_003117	P02549	SPTA1_HUMAN	Spectrin 12.		8	CAGCTCCATTTC	0.552	
-	1	431	pmk.1_Splice_Site	NM_000261	NP_000252	Q99972	MYOC_HUMAN	Potential.		1	CAACTCTCTGG	0.597	
+	16	5609	PA2_uc009www.2_	NM_020318	NP_064714	Q9BXP8	PAPP2_HUMAN	Sushi 2.		16	CAGAGGGAACCA	0.522	
-	5	1502	pl.1_Missense_M	NM_001031725	NP_001026895	Q5T1V6	DDX59_HUMAN	case C-terminal.		4	AAAATAATCTGA	0.358	
-	2	251	se_Mutation_p.R6	NM_001438	NP_001429	P62508	ERR3_HUMAN			2	TGTGTCGATCTT	0.373	
+	46	12282	sn.2_Missense_Mu	NM_001098623	NP_001092093	Q5VST9	OBSCN_HUMAN	Ig-like 42.		28	AGCAGGAGACA	0.622	
+	1	99	L13_uc001ids.2_I	NM_001004686	NP_001004686	Q8NH16	OR2L2_HUMAN	ellular (Potential).		3	CCCATGGAAAA	0.289	

+	1	560		NR_002141					0	AGCAGGTTTGT	0.517	
-	4	477	hz.2_Missense_M	NM_024803	NP_079079	A6NHL2	TBAL3_HUMAN		1	AGCTTCGGAAA	0.448	
-	12	1462	qie.1_Missense_M	NM_198215	NP_937858	Q8NE31	FA13C_HUMAN		2	CAATTGTTGGA	0.378	rs148740536
+	46	7072	_5'Flank|CDH23_	NM_022124	NP_071407	Q9H251	CAD23_HUMAN	|Extracellular (Potential).	11	CCTTTGCTGTGA	0.363	
+	9	1943	p.R442Q|NRG3_u	NM_001010848	NP_001010848	P56975	NRG3_HUMAN	lasmic (Potential).	6	AGATCCGAATTC	0.483	
+	11	4067	p.P1145S|PLCE1_	NM_016341	NP_057425	Q9P212	PLCE1_HUMAN		3	CCCTCCCTTCC	0.532	
+	9	1722	407N|CYP2C19_u	NM_000772	NP_000763	P33260	CP2CI_HUMAN		5	CCAAAGGATATT	0.498	
+	1	845		NM_001127389	NP_001120861	F5GZ66	F5GZ66_HUMAN		0	CACCGGCGCGT	0.786	
-	13	1990	DHR5_uc009ycc.	NM_021924	NP_068743	Q9HBB8	CDHR5_HUMAN	dem repeats.|3.|Extracellula	0	CCCACCGGGTG	0.652	rs140290184
+	39	13975		NM_002457	NP_002448	Q02817	MUC2_HUMAN	VWFD 4.	2	CTGACCAGTGG	0.657	
-	1	742		NM_001012708	NP_001012726	Q6L8H2	KRA53_HUMAN	repeats of C-C-X-P.	2	AGGAGCAGGGC	0.313	
+	4	660		NM_024114	NP_077019	Q8IWZ4	TRI48_HUMAN		0	ATATTATACAGGT	0.338	
-	5	6119	AK_uc001ntk.1_I	NM_001620	NP_001611	Q09666	AHNK_HUMAN		19	ACATCCACATCC	0.502	
-	4	504		NM_030930	NP_112192	Q9H1C4	UN93B_HUMAN	ical; (Potential).	0	CACAGCGAGGA	0.602	
-	31	3007	sn.2_Missense_M	NM_002599	NP_002590	O00408	PDE2A_HUMAN		4	AGGCACCTCGT	0.612	
+	24	3499	p.G980R|CNTN5_	NM_014361	NP_055176	O94779	CNTN5_HUMAN	nectin type-III 4.	8	GAGATGGAACA	0.383	
+	9	1165	e_Mutation_p.A26	NM_019894	NP_063947	Q9NRS4	TMPS4_HUMAN	(Potential).|Peptidase S1.	2	ACATCGCCCTC	0.498	rs140795322
-	1	43		NM_001004474	NP_001004474	Q8NGN2	O10S1_HUMAN	ellular (Potential).	2	GTTCTCCGTTG	0.473	
-	9	2222	p.L698F|CD163_	NM_004244	NP_004235	Q86VB7	C163A_HUMAN	ellular (Potential).	8	GGGCCCAAAGA	0.448	
-	3	384	.1_Intron|PRB1_u	NM_005039	NP_005030	P04280	PRP1_HUMAN	-P-[PAQ]-Q-[GE]-[GD]- [N	0	GCTTTCCTGGA	0.612	
-	29	3654	p.L1212F|ABCC9_	NM_005691	NP_005682	O60706	ABCC9_HUMAN	l).|ABC transmembrane ty	6	CTGAGAGAAATA	0.438	
-	22	2749	p.Q349P|IPO8_uc	NM_006390	NP_006381	O15397	IPO8_HUMAN		3	ACAATCTGTCCC	0.438	
+	5	751	_Mutation_p.R167	NM_152438	NP_689651	Q96FC9	DDX11_HUMAN	Helicase ATP-binding.	3	AGAAAGAGAGA	0.612	
-	4	1551	TUBA1B_uc001rtl.	NM_006082	NP_006073	P68363	TBA1B_HUMAN		0	CTCACCCTCTC	0.483	
+	7	934	p.T293S|SRGAP1	NM_020762	NP_065813	Q7Z6B7	SRGP1_HUMAN		4	TGAAACCTCCA	0.423	
+	9	1063	rj.2_Missense_Mu	NM_006654	NP_006645	Q8WU20	FRS2_HUMAN		2	CACATCCTTTG	0.458	
+	9	2028	.S577L|ZMYM2_u	NM_003453	NP_003444	Q9UBW7	ZMYM2_HUMAN	MYM-type 5.	6	AAAATCACAAA	0.289	
-	2	686		NM_005780	NP_005771	Q9Y693	LHFP_HUMAN		4	CTGCCGACTCT	0.582	
+	9	2614	se_Mutation_p.S7	NM_000123	NP_000114	P28715	ERCC5_HUMAN		7	AAGATTCGCTCC	0.488	
+	1	386		NM_001004717	NP_001004717	Q8NH43	OR4L1_HUMAN	lasmic (Potential).	5	TAAACCCCTGC	0.438	
+	2	218		NM_002687	NP_002678	Q9H307	PININ_HUMAN	ternative 5' splicing.|Neces	1	CCATCCAAGCC	0.423	
-	11	2254	H5_uc001xfy.2_3'	NM_139318	NP_647479	Q8NCM2	KCNH5_HUMAN	lasmic (Potential).	9	TACCTGGAGTT	0.552	
+	8	956	k.1_Missense_Mu	NM_012111	NP_036243	O95433	AHSA1_HUMAN		0	AGGTCCCTGAG	0.388	
+	3	526	XN3_uc010asv.1_	NM_004796	NP_004787	Q9Y4C0	NRX3A_HUMAN	2.|Extracellular (Potential).	10	AGGAGGAAGCC	0.502	
-	3	918		NM_206918	NP_996801	Q6QHC5	DEGS2_HUMAN		0	ATCTTCCGCACC	0.657	
+	2	633	ujp.1_Missense_	NM_002755	NP_002746	Q02750	MP2K1_HUMAN		0	GGCCTTTCTTA	0.547	rs121908594
-	13	3226	t.1_Missense_Mu	NM_001009944	NP_001009944	P98161	PKD1_HUMAN	lar (Potential).|PKD 4.	3	TCACGGTGACG	0.637	
-	22	3012	p.2_Missense_Mu	NM_033266	NP_150296	Q76MJ5	ERN2_HUMAN	toplasmic (Potential).	6	AGGCGCAGCTC	0.647	
+	4	2173		NM_003414	NP_003405	Q14586	ZN267_HUMAN		4	TCATACTGGAG	0.453	
-	5	440	A10P_uc002edi.1_RNA						0	GTGTTTTTGTA	0.512	
-	5	423	A10P_uc002edi.1_RNA						0	CGGCTTGTAGT	0.453	rs79284655
+	5	794	H1_uc010cfg.1_M	NM_004360	NP_004351	P12830	CADH1_HUMAN	|Extracellular (Potential).	243	GAGAACGCATT	0.488	
-	5	814	8B_uc010vmu.1_	NM_001011880	NP_001011880	Q6UXF7	CL18B_HUMAN		0	AGAGCGAACAC	0.612	
+	10	1278	n_p.G285S|SPNS	NM_182538	NP_872344	Q6ZMD2	SPNS3_HUMAN	ical; (Potential).	1	CGGTGGGCCAC	0.652	
-	1	25	1_5'UTR|PLSCR3_	NM_152766	NP_689979	Q8N2U0	CQ061_HUMAN		1	AGCTGGCCCGG	0.667	
+	3	1353	11_uc010vtw.1_In	NM_175734	NP_783861	Q0P670	CQ074_HUMAN		0	TTCCTCCCAGC	0.652	
-	30	4153	.E1384Q|MYH10_	NM_005964	NP_005955	P35580	MYH10_HUMAN	Potential.	2	CTCCTCCTGCT	0.587	

+	1	287		NM_033061	NP_149050				0	ctgctgcaagccccag	0.194	
-	1	363		NM_031960	NP_114166	Q9BYQ9	KRA48_HUMAN	IKRQVHEC]- [SPRT]-[STC	0	ttgcagcagctggaca	0.179	
-	1	457		NM_033059	NP_149048	Q9BYQ6	KR411_HUMAN	-[GIKRQVHEL]- [SPTR]-[S	0	gagatgctgcagctgg	0.129	
-	1	393		NM_033059	NP_149048	Q9BYQ6	KR411_HUMAN	GIKRQVHEL]- [SPTR]-[ST	0	tgcagcagctggaca	0.129	
-	6	495	fz.2_Intron|ATP5H	NM_006356	NP_006347	O75947	ATP5H_HUMAN		0	TCTAATTTGGTTT	0.393	
-	10	1973	TEC_uc010xaj.1_	NM_001137671	NP_001131143	B2RU33	POTEC_HUMAN	Potential.	3	TCATTTTCTTTTC	0.284	
+	1	736	ES1_uc002kub.2_	NM_001100619	NP_001094089	Q8TDN4	CABL1_HUMAN	th CDK3 (By similarity).	1	CTCAGGGAATC	0.672	
+	17	3190	_p.S696F|DCC_uc	NM_005215	NP_005206	P43146	DCC_HUMAN	tential).|Fibronectin type-III	17	ACAACTCTGTCC	0.527	
+	4	1336	a.1_Missense_Mu	NM_173480	NP_775751	Q68EA5	ZNF57_HUMAN	C2H2-type 9.	3	GAACAATGTGG	0.428	
+	4	1371	a.1_Missense_Mu	NM_173480	NP_775751	Q68EA5	ZNF57_HUMAN	C2H2-type 9.	3	CATTCCGAGGTC	0.428	rs149690257
+	4	1386	a.1_Missense_Mu	NM_173480	NP_775751	Q68EA5	ZNF57_HUMAN	C2H2-type 9.	3	GAGGACGCACA	0.438	rs148390269
-	4	453	vq.2_Missense_M	NM_021155	NP_066978	Q9NNX6	CD209_HUMAN	|2.|7 X approximate tanden	1	TCAGCCGGGTC	0.567	
-	3	28508		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	ch.|Extracellular (Potential).	57	CCAGGGAAGAT	0.507	
-	3	20909		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).	57	CAGAGGATTGT	0.488	
+	4	1651	ym.1_Missense_M	NM_001136501	NP_001129973	Q08AG5	ZN844_HUMAN		0	GAAACCCTATGA	0.413	
+	4	1710	ym.1_Missense_M	NM_001136501	NP_001129973	Q08AG5	ZN844_HUMAN		0	GCATGAAAGGA	0.413	
-	4	1355		NM_145276	NP_660319	Q8TA94	ZN563_HUMAN	C2H2-type 9.	0	ATAACGTTTTCC	0.413	
-	6	3184	208_uc002nqo.1_	NM_007153	NP_009084				7	TGTAGGGTTTCT	0.368	
-	3	545	p.P16S|ZNF599_u	NM_001007248	NP_001007249	Q96NL3	ZN599_HUMAN	KRAB.	2	GTTTGGGAACAG	0.458	
-	16	7944		NM_003890	NP_003881	Q9Y6R7	FCGBP_HUMAN	VWFD 6.	9	ACTCCTCGCTGG	0.657	
+	4	799	P62_uc002pqz.2_	NM_012068	NP_036200	Q9Y2D1	ATF5_HUMAN		2	CTCCTCCCTCTG	0.577	
-	3	2328	rt.1_Missense_Mu	NM_004977	NP_004968	Q14003	KCNC3_HUMAN	lasmic (Potential).	1	ATGGCTGGGCAG	0.642	
-	4	613	K8_uc002put.1_Int	NM_007196	NP_009127	O60259	KLK8_HUMAN	Peptidase S1.	1	TGGGTGCAATGA	0.592	
-	5	1439	k.1_Intron|ZNF81	NM_001031665	NP_001026835	Q0VGE8	ZN816_HUMAN	C2H2-type 6.	0	ATTTCTGACTGA	0.398	
+	3	1399	NF17_uc002qop.1	NM_006959	NP_008890	P17021	ZNF17_HUMAN	C2H2-type 8.	1	GCAACGAATGT	0.393	
+	3	1622_1623	47_uc002qpm.3_	NM_001023561	NP_001018855	O43361	ZN749_HUMAN	2H2-type 10.	0	CAGCACCAGAA	0.421	
+	2	321	.3_Intron|ZNF776_	NM_138347	NP_612356	Q7Z340	ZN551_HUMAN	KRAB.	1	ATGAGTCTCAGA	0.483	
-	7	2374	hp.1_Missense_M	NM_025027	NP_079303	Q8WXB4	ZN606_HUMAN	C2H2-type 9.	2	TCTGATGGGCAA	0.423	
-	2	189	e_Mutation_p.E29	NM_001002006	NP_001002006	Q96P26	5NT1B_HUMAN		3	CAGATTCCTTTC	0.393	
-	3	867	kj.2_Missense_Mu	NM_144631	NP_653232	Q8N8E2	ZN513_HUMAN	C2H2-type 3.	1	GATGCCGCCTCA	0.677	
+	10	1436	S1_uc010yqh.1_R	NM_002398	NP_002389	O00470	MEIS1_HUMAN	eobox; TALE-type.	0	ATGCCCGGAGA	0.448	
+	5	674	SH2P_uc002tkb.2_	NM_182905	NP_878908				0	GGTGGGCACTTG	0.612	
+	13	4582	.3_Missense_Muta	NM_005270	NP_005261	P10070	GLI2_HUMAN		13	ATGGATGATGGC	0.627	
-	63	10974		NM_018557	NP_061027	Q9NZR2	LRP1B_HUMAN	ntial).|LDL-receptor class A	50	ACATTTCCACCA	0.338	
+	2	392	on_p.P98S|PDK1_	NM_002610	NP_002601	Q15118	PDK1_HUMAN		4	CTCCTTCCAGAT	0.393	
-	40	9583	R3074Q|TTN_uc0	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	ACATCCGGGTG	0.453	rs72647894
+	8	1892	_p.H561Y|FAM171	NM_177454	NP_803237	Q6P995	F171B_HUMAN	lasmic (Potential).	10	CATTCTCATGCAC	0.478	
-	40	6558		NM_018897	NP_061720	Q8WXX0	DYH7_HUMAN	3 (By similarity).	12	CATTTACGATTTG	0.318	
+	13	1535		NM_015934	NP_057018	Q9Y2X3	NOP58_HUMAN	Lys-rich.	0	AAAAAGCCAAGA	0.328	
-	17	2526	e_Mutation_p.S45	NM_173076	NP_775099	Q86UK0	ABCAC_HUMAN		11	TATTTTGAAGCA	0.348	
+	17	1697	P140_uc002vqm.2	NM_007237	NP_009168	Q13342	LY10_HUMAN		0	CCGACGGCCAG	0.478	
-	7	1266	_p.E63K|NGEF_u	NM_019850	NP_062824	Q8N5V2	NGEF_HUMAN	DH.	7	CTCCTCCATCCG	0.587	
+	1	67	B_uc010ztj.1_Splice_Site|FRG1B_uc010gdr.1_Splice_Site						0	CGTTGGTGAGT	0.219	rs137860963
+	2	127	tj.1_RNA|FRG1B_uc010gdr.1_RNA|FRG1B_uc010ztk.1_Intron						0	ATTCAGATGCAA	0.333	
+	3	264	RG1B_uc010gdr.1_RNA|FRG1B_uc010ztk.1_Nonsense_Mutation_p.E30*						0	GAAGAAGAAATG	0.373	
-	4	2461		NM_052846	NP_443078	Q9NT22	EMIL3_HUMAN	Potential.	1	CATCCCGGAGG	0.652	
+	2	1229	e_Mutation_p.R39	NM_003008	NP_002999	Q02383	SEMG2_HUMAN	X 60 AA tandem repeats,	1	AGGTAAGAATTC	0.403	

-	38	4807	tv.1_Missense_Mu	NM_020820	NP_065871	Q8TCU6	PREX1_HUMAN		6	CCAGGGACACG	0.687	
-	8	1214	yi.1_Missense_Mu	NM_000961	NP_000952	Q16647	PTGIS_HUMAN		3	GGAAGGGGAAG	0.557	
+	2	3406		NM_173485	NP_775756	Q9NRE2	TSH2_HUMAN		6	GGTCCCCCCCA	0.552	
-	8	976	nse_Mutation_p.L2	NM_006052	NP_006043	O14972	DSCR3_HUMAN		0	CAGAGAGGCCC	0.602	
+	2	98	.1_Missense_Muta	NM_018943	NP_061816	Q9NY65	TBA8_HUMAN		0	TCCACGTGGGC	0.572	
+	7	1731	atq.1_Missense_M	NM_001039141	NP_001034230	Q9H2D6	TARA_HUMAN		1	ACAATCCCAGAG	0.592	
-	16	3082		NM_006514	NP_006505	Q9Y5Y9	SCNAA_HUMAN		10	CTGTCCTTTGG	0.542	
+	3	1576		NM_001123041	NP_001116513	P41597	CCR2_HUMAN	lasmic (Potential).	2	AGCCCCTGAAG	0.488	
-	8	1442	ip.1_Missense_Mu	NM_001142733	NP_001136205	A6NK59	ASB14_HUMAN	ANK 11.	0	AACATCGCTCT	0.428	
+	25	4525	f.2_Missense_Mu	NM_001457	NP_001448	O75369	FLNB_HUMAN	Interaction with FBLP1.	19	TGGCTCCGCTG	0.657	
+	6	1109	M2_uc010hsl.2_	NM_004526	NP_004517	P49736	MCM2_HUMAN	type (Potential).	4	AGGCTCCTGTC	0.582	
-	33	5520	LXND1_uc011blb.	NM_015103	NP_055918	Q9Y4D7	PLXD1_HUMAN	lasmic (Potential).	1	AGATGGAGCAG	0.602	
-	15	1760	p.Q529K|CLCN2_	NM_004366	NP_004357	P51788	CLCN2_HUMAN	al; (By similarity).	0	ACTCTGGGCGA	0.612	
+	3	377	.P74L|ZNF595_uc	NM_182524	NP_872330	Q7Z3I0	Q7Z3I0_HUMAN		0	CAAACCCCCAG	0.498	
-	3	1553_1554	732_uc010ibb.1_I	NM_001137608	NP_001131080	B4DXR9	ZN732_HUMAN	2H2-type 14.	0	GTATGTGGACC	0.386	
-	3	1518	732_uc010ibb.1_I	NM_001137608	NP_001131080	B4DXR9	ZN732_HUMAN	2H2-type 14.	0	ACATTCGTAAG	0.398	
-	3	1350	732_uc010ibb.1_I	NM_001137608	NP_001131080	B4DXR9	ZN732_HUMAN	2H2-type 12.	0	ACATTTGTAAG	0.418	
-	4	2300		NM_001024611	NP_001019782	Q68CR7	LRC66_HUMAN		3	CCCTGGAATTG	0.478	
+	4	860	|MUC7_uc003hfj.	NM_001145006	NP_001138478	Q8TAX7	MUC7_HUMAN	2.|Thr-rich.	4	AGCTGCCCCAC	0.587	
-	16	2186	_p.Q320K|FAM13	NM_014883	NP_055698	O94988	FA13A_HUMAN		2	CCTCTTGCTCAT	0.522	
+	3	5443	p.1_Missense_Mu	NM_024582	NP_078858	Q6V0I7	FAT4_HUMAN	.|Extracellular (Potential).	18	TAGTTCGTGCT	0.468	
+	7	940	e_Mutation_p.R17	NM_001040157	NP_001035247	Q9C0F1	CEP44_HUMAN		0	GTGATTCGTCAC	0.289	rs148258730
+	20	4001	e.1_Missense_Mu	NM_001080477	NP_001073946	Q9P273	TEN3_HUMAN	ellular (Potential).	0	TCTAACGATTTG	0.393	
+	8	1174	R_uc011cop.1_R	NM_002185	NP_002176	P16871	IL7RA_HUMAN	lasmic (Potential).	5	CTTTGGAAGAG	0.537	
+	1	672	uc011ctk.1_Intron	NM_032567	NP_115956	Q9BXG8	SPZ1_HUMAN		1	AAACAGGAGATG	0.358	
+	8	1039	_p.P70S|DCP2_u	NM_152624	NP_689837	Q8IU60	DCP2_HUMAN		0	TTATTTCCTGAC	0.373	
+	4	1033	uc003nkk.1_Intro	NM_025231	NP_079507	Q9H4T2	ZSC16_HUMAN	C2H2-type 3.	1	CATCAGAGAAT	0.418	
-	10	4459	C1_uc011dmp.1_	NM_014641	NP_055456	Q14676	MDC1_HUMAN	on with the PRKDC comple	4	CAGGTTGGTCT	0.537	
-	9	1487	se_Mutation_p.D9	NM_025258	NP_079534	Q9Y334	G7C_HUMAN		3	GGCATCCGTGA	0.582	
-	25	8843		NM_019105	NP_061978	P22105	TENX_HUMAN	nectin type-III 21.	0	CTGCCCATCCC	0.627	
-	7	1674	X6_uc010jya.2_R	NM_000287	NP_000278	Q13608	PEX6_HUMAN		1	GTGAGCAACAG	0.642	
-	11	1839	wl.1_Missense_M	NM_153840	NP_722582	Q5T601	GP110_HUMAN	tracellular (Potential).	3	GGCAgcctgcatcgt	0.264	
-	63	10098		NM_014611	NP_055426	Q9NU22	MDN1_HUMAN		10	CTCCTGAACCA	0.572	
+	10	1582	qo.3_Missense_M	NM_021956	NP_068775	Q13002	GRIK2_HUMAN	ellular (Potential).	5	TATGTCCTTTTTA	0.343	
-	5	2449		NM_001080450	NP_001073919	Q5T5X7	BEND3_HUMAN	BEN 3.	3	CCAGGGAGCCG	0.637	
+	6	1896	t.2_Missense_Mut	NM_001080976	NP_001074445	Q9UL01	DSE_HUMAN		1	TTCTCCTTGTA	0.498	
+	13	5311_5312	.P4_uc003qrg.2_I	NM_020245	NP_064630	Q9NRJ4	TULP4_HUMAN		1	GAAGTCCTCTCC	0.584	
-	3	465	1egc.1_Missense_	NM_020133	NP_064518	Q9NRZ5	PLCD_HUMAN		0	GGCGCGCGGGT	0.527	
+	2	976	md.2_Missense_	NM_018641	NP_061111	Q9NRB3	CHSTC_HUMAN	enal (Potential).	1	CCAACCACACC	0.647	
-	2	802		NM_015204	NP_056019	Q9UPZ6	THS7A_HUMAN	ellular (Potential).	3	CTGCTCCAGGA	0.537	
-	19	2454	n_p.W647*|OSBP	NM_015550	NP_056365	Q9H4L5	OSBL3_HUMAN		1	TTTGTTCCACTC	0.403	
-	11	1499	sense_Mutation_p	NM_033054	NP_149043	B0I1T2	MYO1G_HUMAN	osin head-like.	4	CAATGGTGGCG	0.622	
-	4	688	n_p.H67Y|MYO1	NM_033054	NP_149043	B0I1T2	MYO1G_HUMAN	osin head-like.	4	GCTGTGGATGT	0.602	
-	9	1101	b.2_Missense_Mu	NM_005311	NP_005302	Q13322	GRB10_HUMAN	PH.	6	TCTGTAGGGGCG	0.597	
-	6	801	ph.1_Missense_M	NM_015395	NP_056210	Q7Z6L1	TCPR1_HUMAN		1	TCTCCCAGCCC	0.622	
-	3	1904	GAL3ST4_uc003u	NM_024637	NP_078913	Q96RP7	G3ST4_HUMAN	enal (Potential).	3	AGACAGAGTCC	0.532	
+	14	2903	AN_uc003uwl.2_	NM_003386	NP_003377	Q9Y493	ZAN_HUMAN	ate) (mucin-like domain).|E	11	AAAAACCCACCA	0.507	

-	5	574	do.2_Nonsense_M	NM_006754	NP_006745	Q16563	SYPL1_HUMAN	.|Helical; (Potential).	0	CACCAACCACAA	0.343	
-	15	1860		NM_004333	NP_004324	P15056	BRAF_HUMAN	rotein kinas_R603>I(2)|p.T	18290	GATTTCACTGTAC	0.368	
-	5	551		NM_001040135	NP_001035225	Q9C0K3	ARP3C_HUMAN		0	ACTTCTGGGGAT	0.413	
-	28	3497_3498	uc003xhi.1_Intron	NM_015254	NP_056069	Q9NQT8	KI13B_HUMAN		0	AGAGGGGACCAT	0.54	
-	16	3579	R1012Q|MYST3_	NM_001099412	NP_001092882	Q92794	MYST3_HUMAN		7	ACCTTTCGCTTCA	0.498	
-	3	1130	p.R252H|OPRK1_	NM_000912	NP_000903	P41145	OPRK_HUMAN	lasmic (Potential).	2	TTGAGACGCAGG	0.552	
+	7	812	p.D255N|C8orf34_	NM_052958	NP_443190	Q49A92	CH034_HUMAN		1	TCTCAAGATTCT	0.368	
-	2	710	_p.R224C|JPH1_u	NM_020647	NP_065698	Q9HDC5	JPH1_HUMAN	lasmic (Potential).	1	ACTTGCGAAGTT	0.587	
-	6	575_576	p.P164S|ENPP2_	NM_001040092	NP_001035181	Q13822	ENPP2_HUMAN		7	GGAGGGCGAAC	0.376	
-	5	1584		NM_138367	NP_612376	Q9BRH9	ZN251_HUMAN	C2H2-type 9.	0	CTCCGACGAAAG	0.493	
-	1	609		NM_207305	NP_997188	Q12950	FOXD4_HUMAN	Fork-head.	1	GGGGCTTTGCC	0.677	
+	3	405	laza.2_Missense_	NM_001855	NP_001846	P39059	COFA1_HUMAN	SP N-terminal.	6	CGGCCTACAGT	0.617	
+	5	906		NM_001340	NP_001331	Q14093	CYLC2_HUMAN	A repeats of K-K-X.	1	CCAGTAGTACAG	0.254	
+	10	7190	sense_Mutation_p	NM_021224	NP_067047	Q96JM2	ZN462_HUMAN	2H2-type 25.	5	GTTTTCCGCTGT	0.448	
-	1	1051		NM_006686	NP_006677	Q9Y614	ACL7B_HUMAN		1	AGCCCGTGTCC	0.667	
+	6	1179		NM_000093	NP_000084	P20908	CO5A1_HUMAN	nhelical region.	11	GGAAGGAGACG	0.602	
-	20	3080	_Mutation_p.G909	NM_001606	NP_001597	Q9BZC7	ABCA2_HUMAN		0	CATGCCACGGG	0.637	
+	5	521		NM_000377	NP_000368	P42768	WASP_HUMAN		1	CCACAGACAGA	0.572	
+	17	2020	eqq.2_Missense_M	NM_144658	NP_653259	Q5JSL3	DOC11_HUMAN	DHR-1.	3	AATACGATAGCC	0.308	
+	9	1615		NM_018558	NP_061028	Q9UN88	GBRT_HUMAN		3	CAGGCTGGGACC	0.527	
+	7	1141	hs.1_Missense_M	NM_001001344	NP_001001344	Q16720	AT2B3_HUMAN	lasmic (Potential).	1	CGGAGGGTGGG	0.592	
-	5	582	_1_uc009vka.2_5'F	NM_004421	NP_004412	O14640	DVL1_HUMAN		0	GGTGGACGCGC	0.667	
+	10	1727	_p.E273K|PLCH2_	NM_014638	NP_055453	O75038	PLCH2_HUMAN		5	AAGGCGAGGTG	0.617	
-	22	3432	uc001ama.1_RNA|	NM_015557	NP_056372	Q8TDI0	CHD5_HUMAN	case C-terminal.	12	CCGCCGTGGCC	0.632	
+	17	2267	p.E686K|PIK3CD_	NM_005026	NP_005017	O00329	PK3CD_HUMAN		7	AGGGGGAAGCA	0.667	
-	21	5001		NM_001079843	NP_001073312	Q86V15	CASZ1_HUMAN		1	GCAGTCGGGCA	0.647	
+	2	233	e_Mutation_p.R38	NM_015291	NP_056106	Q9Y2G8	DJC16_HUMAN	asmic (Potential).|J.	3	TCAGCCGAACAG	0.438	
-	26	3845	yz.1_Missense_M	NM_017940	NP_060410	Q3BBV0	NBPF1_HUMAN	NBPF 6.	0	GTTGAATAACAT	0.488	
+	28	4498	_Mutation_p.P78	NM_014675	NP_055490	Q5TZA2	CROCC_HUMAN		5	ACAGCCCCAGC	0.627	
-	6	768	_Mutation_p.G20	NM_152372	NP_689585	Q5VTT5	MYOM3_HUMAN	like C2-type 1.	3	TATTTTCCGGCA	0.478	
+	13	1921	e_Mutation_p.P53	NM_005839	NP_005830	Q8IYB3	SRRM1_HUMAN	s and matrix localization.|A	3	CCCTCCTCCTC	0.537	
+	13	1933	e_Mutation_p.R54	NM_005839	NP_005830	Q8IYB3	SRRM1_HUMAN	s and matrix localization.|A	3	ACGGCGCAGGA	0.532	rs78787676
+	3	346	uj.2_Missense_M	NM_175852	NP_787048	P40222	TXLNA_HUMAN		2	GGGGGGCCCCG	0.597	
-	10	1254	xm.1_Missense_M	NM_052896	NP_443128	Q7Z408	CSMD2_HUMAN	xtracellular (Potential).	12	CTCGAAGGTGGG	0.537	
+	25	11625	a.1_Nonsense_M	NM_033044	NP_149033	Q9UPN3	MACF1_HUMAN	Spectrin 7.	16	ATGATCGAAAG	0.428	rs145098670
-	5	768	T1_uc010ojg.1_M	NM_000310	NP_000301	P50897	PPT1_HUMAN		1	ACATACCGTTCC	0.458	
-	8	2050		NM_020883	NP_065934	Q9P217	ZSWM5_HUMAN		0	GATGGGATCCA	0.522	
-	28	4547	ctz.2_Missense_M	NM_015269	NP_056084	Q5TAX3	TUT4_HUMAN	n-rich.|Pro-rich.	3	ACTGGGAAGAG	0.433	
+	25	3559	e_Mutation_p.G11	NM_176877	NP_795352	Q8NI35	INADL_HUMAN	PDZ 6.	4	ATGCAGGAAAC	0.403	
+	15	2222	HD1_uc001dbq.1_	NM_020925	NP_065976	Q5VU97	CAHD1_HUMAN	cellular (Potential).	2	CTAGGAGACAAT	0.448	
+	11	1440	_p.T348M|KIAA13	NM_020775	NP_065826	Q6UXG2	K1324_HUMAN	cellular (Potential).	5	GGAAACGACCG	0.537	rs143784237
+	9	994	uc010oyd.1_Intron|	NM_001037675	NP_001032764	Q3BBV1	NBPFK_HUMAN		0	GCAGTTCAGAAA	0.468	
-	1	92	H2BF_uc010pbk.1_	NM_001123375	NP_001116847	Q71DI3	H32_HUMAN		0	TGGCCGGCGCG	0.692	
+	3	279	odf.1_Missense_M	NM_020127	NP_064512	Q9NNX1	TUFT1_HUMAN		0	CATGATGGACATC	0.483	
+	2	336	5_uc001fht.1_RNA	NM_025058	NP_079334	Q7Z4K8	TRI46_HUMAN		3	CCCCTTCCACC	0.682	
+	8	1629	sense_Mutation_p.	NM_025058	NP_079334	Q7Z4K8	TRI46_HUMAN	onectin type-III.	3	TACGGCGAATAC	0.657	
-	2	921	_5'Flank|RUSC1_	NM_001039517	NP_001034606	Q66K80	RUAS1_HUMAN		0	AGCTACGCCAC	0.657	

-	6	1176	L2_uc010phz.1_M	NM_030764	NP_110391	Q96LA5	FCRL2_HUMAN	4.|Extracellular (Potential).	2	CAGGCCGTTGT	0.577	rs149829829
-	27	3994		NM_003126	NP_003117	P02549	SPTA1_HUMAN	Spectrin 12.	8	AGCTCCATTTTC	0.552	
-	7	854	_p.R194Q|CCDC	NM_012337	NP_036469	Q9UL16	CCD19_HUMAN	Potential.	1	GCTCCCGCTGC	0.512	
+	7	1208	nd.1_Nonsense_M	NM_001460	NP_001451	Q99518	FMO2_HUMAN		1	CAAGTCAACCC	0.433	
-	1	431	pmk.1_Splice_Site	NM_000261	NP_000252	Q99972	MYOC_HUMAN	Potential.	1	CAACTCTCTGG	0.597	
+	72	11228		NM_031935	NP_114141	Q96RW7	HMCN1_HUMAN	ike C2-type 35.	23	CACCTCGAGTG	0.393	
+	8	1006		NM_024529	NP_078805	Q6P1J9	CDC73_HUMAN		49	TTCAATCTGTAA	0.333	
+	3	509	R1_uc001gtm.2_I	NM_002113	NP_002104	Q03591	FHR1_HUMAN	Sushi 2.	0	AGAACGGGGCT	0.393	
-	5	1502	pl.1_Missense_M	NM_001031725	NP_001026895	Q5T1V6	DDX59_HUMAN	case C-terminal.	4	AAAATAATCTGA	0.358	
+	8	4114		NM_032890	NP_116279	Q96F81	DISP1_HUMAN		0	CTGTCGAGGGC	0.562	rs149927406
+	9	2836	nsn.2_Missense_M	NM_001098623	NP_001092093	Q5VST9	OBSCN_HUMAN	ly-Ser.|Ig-like 9.	28	GCTGAGCTCCA	0.647	
+	46	12282	sn.2_Missense_Mu	NM_001098623	NP_001092093	Q5VST9	OBSCN_HUMAN	Ig-like 42.	28	AGCAGGAGACA	0.622	
+	5	3587	e.1_Missense_Mu	NM_020066	NP_064450	Q9NZ56	FMN2_HUMAN	ro-rich.|FH1.	12	CCCTCCTCCCC	0.716	
+	1	99	L13_uc001ids.2_I	NM_001004686	NP_001004686	Q8NH16	OR2L2_HUMAN	ellular (Potential).	3	CCCATGGAAAA	0.289	
+	1	55		NM_001004696	NP_001004696	Q8NH00	OR2T4_HUMAN	ellular (Potential).	1	TCCTGATGGGA	0.488	
+	15	5595	iik.2_Missense_M	NM_017782	NP_060252	Q5VWN6	CJ018_HUMAN		2	TCCCCACGCTTT	0.458	
+	4	1055	p.R120H|MAP3K8	NM_005204	NP_005195	P41279	M3K8_HUMAN		4	ATGGACGTTACC	0.433	
+	7	860		NM_052997	NP_443723	Q9BXX3	AN30A_HUMAN		9	CTTGGTGGAAA	0.502	
-	12	1462	qie.1_Missense_M	NM_198215	NP_937858	Q8NE31	FA13C_HUMAN		2	CAATTGTTGGA	0.378	rs148740536
-	12	1808	mw.2_Missense_M	NM_001127384	NP_001120856	Q9UI47	CTNA3_HUMAN		8	TGTAAGCCCCT	0.458	
+	9	1943	p.R442Q|NRG3_u	NM_001010848	NP_001010848	P56975	NRG3_HUMAN	lasmic (Potential).	6	AGATCCGAATTC	0.483	
+	9	1722	407N|CYP2C19_u	NM_000772	NP_000763	P33260	CP2CI_HUMAN		5	CCAAAGGATATT	0.498	
-	1	341	C2_uc009xxx.2_I	NR_026715					0	GATGCAGTCAA	0.592	
+	1	427		NM_001001480	NP_001001480	Q701N2	KRA55_HUMAN	repeats of C-C-X-P.	1	CTGTGGCTCCT	0.692	
-	9	1140	_p.D260N|OSBPL	NM_020896	NP_065947	Q9H0X9	OSBL5_HUMAN		3	CTGGTCGCTGC	0.637	
+	1	664		NM_001005172	NP_001005172	Q8NGK3	O52K2_HUMAN	lasmic (Potential).	2	TATATCTTTATTC	0.483	
-	1	167		NM_001005164	NP_001005164	Q8NGJ4	O52E2_HUMAN	lasmic (Potential).	3	GTAGGCTGCTG	0.488	
-	5	538	lutation_p.R40H|	NM_012402	NP_036534	P53365	ARFP2_HUMAN	AH.	0	TCTCACGCAGC	0.567	
+	15	2449	yic.2_Missense_M	NM_004211	NP_004202	Q9Y345	SC6A5_HUMAN	ame=12; (Potential).	4	TGTTCCGTCATC	0.478	rs138848148
-	15	1916	160_uc009ylw.2_	NM_015231	NP_056046	Q12769	NU160_HUMAN		7	CAGCCGGAGGC	0.383	
-	1	586		NM_001005282	NP_001005282	Q8NGP6	OR5M8_HUMAN	Name=5; (Potential).	1	TGACAACTCCT	0.418	
+	14	1766	p.W571*|CCDC88	NM_032251	NP_115627	A6NC98	CC88B_HUMAN		4	GACTGGTCCCC	0.642	
+	8	889	p.A206V|RPS6KA	NM_003942	NP_003933	O75676	KS6A4_HUMAN	otein kinase 1.	5	CGTGGCGCAGG	0.667	rs142374327
+	14	1846	US81_uc001ofx.3_	NM_025128	NP_079404	Q96NY9	MUS81_HUMAN		0	ATACAGCACCC	0.607	
-	4	1410	ns.2_Missense_M	NM_022338	NP_071733	Q96F05	CK024_HUMAN	ar (Potential).|Pro-rich.	0	GTGTCGTGGGG	0.627	rs138575739
+	33	5319	ke.1_Missense_M	NM_000051	NP_000042	Q13315	ATM_HUMAN		240	TTATGGTGAAAC	0.259	
+	11	915	rzn.1_Missense_	NM_015313	NP_056128	Q9NZN5	ARHGC_HUMAN		7	GCCCAGTAGTG	0.428	
+	48	6705	_p.V1055I|SORL1_	NM_003105	NP_003096	Q92673	SORL_HUMAN	lasmic (Potential).	15	ATGACGTCCCC	0.393	
-	10	1455		NM_170601	NP_733746	Q9HAT2	SIAE_HUMAN		0	GCATCGATGGT	0.498	
-	1	101		NM_020996	NP_066276	P10767	FGF6_HUMAN		3	GTGCCCTGCAG	0.607	
-	9	2222	_p.L698F|CD163_	NM_004244	NP_004235	Q86VB7	C163A_HUMAN	ellular (Potential).	8	GGGCCCAAAGA	0.448	
-	3	384	.1_Intron|PRB1_u	NM_005039	NP_005030	P04280	PRP1_HUMAN	-P-[PAQ]-Q-[GE]-[GD]- [N	0	GCTTTCCTGGA	0.612	
-	29	3654	p.L1212F|ABCC9_	NM_005691	NP_005682	O60706	ABCC9_HUMAN	l).|ABC transmembrane ty	6	CTGAGAGAAATA	0.438	
-	22	2749	p.Q349P|IPO8_uc	NM_006390	NP_006381	O15397	IPO8_HUMAN		3	CAATCTGTCCC	0.438	
-	1	256		NM_001013699	NP_001013721	Q6NXT2	H3C_HUMAN		0	GATGAGCAGCT	0.602	
-	4	1551	TUBA1B_uc001rtl.	NM_006082	NP_006073	P68363	TBA1B_HUMAN		0	CTCACCCTCTC	0.483	
+	13	2025	p.G620R|TROAP_	NM_005480	NP_005471	Q12815	TROAP_HUMAN	A approximate tandem rep	1	AACCCGGGCCC	0.642	

+	9	1552	A211V|TARBP2_u	NM_134323	NP_599150	Q15633	TRBP2_HUMAN	l.|DRBM 3.|Sufficient for int		1	CCGTGCCCTGC	0.627	
+	8	1098	_p.Q348*|SRGAP1	NM_020762	NP_065813	Q7Z6B7	SRGP1_HUMAN			4	GTGCCCAGCAG	0.532	
+	9	1063	rj.2_Missense_Mu	NM_006654	NP_006645	Q8WU20	FRS2_HUMAN			2	CACATCCTTTG	0.458	
+	18	2666	se_Mutation_p.S8	NM_003667	NP_003658	O75473	LGR5_HUMAN	lasmic (Pote	p.S873I(1)	9	TTACCAGCTCCA	0.478	
+	1	112	Mutation_p.A3T|L	NM_003299	NP_003290	P14625	ENPL_HUMAN			3	TGAGGGCCCTG	0.682	
-	3	861	tmv.2_Missense_M	NM_001142345	NP_001135817	Q99788	CML1_HUMAN	ellular (Potential).		5	GAAGCGGGTGA	0.582	
+	5	455	wh.2_Missense_M	NM_138432	NP_612441	Q96GA7	SDSL_HUMAN			0	CTATGCTGCTA	0.637	
-	2	686		NM_005780	NP_005771	Q9Y693	LHFP_HUMAN			4	CTGCCGACTCT	0.582	
+	14	1497	p.R414H|COG6_u	NM_020751	NP_065802	Q9Y2V7	COG6_HUMAN			2	TGCTCGTCAAG	0.363	
+	9	2614	se_Mutation_p.S7	NM_000123	NP_000114	P28715	ERCC5_HUMAN			7	AAGATTCGCTCC	0.488	
+	1	386		NM_001004717	NP_001004717	Q8NH43	OR4L1_HUMAN	lasmic (Potential).		5	TAAACCCCTGC	0.438	
-	23	3675	.R1090H|CHD8_u	NM_020920	NP_065971	Q9HCK8	CHD8_HUMAN			10	TCATACGTCGC	0.428	
+	2	218		NM_002687	NP_002678	Q9H307	PININ_HUMAN	ternative 5' splicing.|Neces		1	CCATCCAAGCC	0.423	
-	11	2254	IH5_uc001xfy.2_3'	NM_139318	NP_647479	Q8NCM2	KCNH5_HUMAN	lasmic (Potential).		9	TACCTGGAGTT	0.552	
+	8	956	vk.1_Missense_Mu	NM_012111	NP_036243	O95433	AHSA1_HUMAN			0	AGGTCCCTGAG	0.388	
+	2	242		NM_207322	NP_997205	Q8NCU7	C2C4A_HUMAN			0	CACCACCGCCG	0.682	
+	2	633	ujp.1_Missense_M	NM_002755	NP_002746	Q02750	MP2K1_HUMAN			0	GGCCTTTCTTA	0.547	rs121908594
+	2	2964	p.R882W|C15orf3	NM_015492	NP_056307	Q6ZRI6	CO039_HUMAN			0	AGGAGCGGGCA	0.672	
+	9	1102		NM_002569	NP_002560	P09958	FURIN_HUMAN			7	GGAACGGGGGC	0.627	
-	3	645	_p.R16C|RGMA_	NM_020211	NP_064596	Q96B86	RGMA_HUMAN			0	CAGGCGTGGCT	0.662	
-	13	3226	t.1_Missense_Mu	NM_001009944	NP_001009944	P98161	PKD1_HUMAN	lar (Potential).|PKD 4.		3	TCACGGTGACG	0.637	
-	8	737	cya.2_Missense_M	NM_032569	NP_115958	Q49A26	GLYR1_HUMAN			0	GATTGCCTGGT	0.453	
-	25	4940	zv.1_Missense_M	NM_014647	NP_055462	Q9Y4F3	LKAP_HUMAN			0	GCGCTCGCCCT	0.547	
+	3	411		NM_014669	NP_055484	Q8N1F7	NUP93_HUMAN			2	CACTGACATTC	0.527	
-	3	627	ex.2_Missense_M	NM_022357	NP_071752	Q9H4B8	DPEP3_HUMAN			3	GCACGGCAGTC	0.607	
-	2	366	_Mutation_p.R41	NM_001128	NP_001119	O43747	AP1G1_HUMAN			2	GGTTCGGGCTG	0.463	
-	5	814	8B_uc010vmu.1_	NM_001011880	NP_001011880	Q6UXF7	CL18B_HUMAN			0	AGAGCGAACAC	0.612	
-	6	787	n.2_Missense_Mu	NM_153486	NP_705690	Q86WU2	LDHD_HUMAN	inding PCMH-type.		0	CGGAGCCCACG	0.652	
+	3	796	rf97_uc010vpz.1_	NM_001013672	NP_001013694	Q6ZQX7	CQ097_HUMAN	tandem repeat of A-L-K-G-		1	CCCGAGGCTCT	0.711	
-	5	1295	tn.1_Missense_Mu	NM_052928	NP_443160	Q8IYR2	SMYD4_HUMAN			5	TCCTTGTTACTA	0.423	
-	14	2478	_Mutation_p.R731	NM_015229	NP_056044	O75153	K0664_HUMAN			2	GCTCCGCAGCA	0.711	
-	8	1019	_p.R290C|ATP2A3	NM_174955	NP_777615	Q93084	AT2A3_HUMAN	nal (By similarity).		5	GCCACGCAGCC	0.672	
+	10	1278	n_p.G285S|SPNS	NM_182538	NP_872344	Q6ZMD2	SPNS3_HUMAN	ical; (Potential).		1	CGGTGGGCCAC	0.652	
-	6	787	'Flank|RNF167_u	NM_003562	NP_003553	Q02978	M2OM_HUMAN	=5; (Potential).|Solcar 3.		0	TGCTGGCACAG	0.617	
-	7	3364	_p.V937I|NLRP1_	NM_033004	NP_127497	Q9C000	NALP1_HUMAN	LRR 5.		9	GCCAACGTCAT	0.622	
+	3	1353	11_uc010vtw.1_In	NM_175734	NP_783861	Q0P670	CQ074_HUMAN			0	TTCCTCCCAGC	0.652	
-	30	4135		NM_003802	NP_003793	Q9UKX3	MYH13_HUMAN	Potential.		6	CTGTTCCCGCA	0.592	
-	9	1914	grr.1_Missense_M	NM_004176	NP_004167	P36956	SRBP1_HUMAN	lasmic (Potential).		1	GTGGGGCCGTG	0.667	
+	2	1028	p.A304V|SLFN5_u	NM_144975	NP_659412	Q08AF3	SLFN5_HUMAN			3	CTGTGCGGTGT	0.493	rs149363506
+	2	233	hse.2_Missense_	NM_006804	NP_006795	Q14849	STAR3_HUMAN	lasmic (Potential).		0	ACCTCCTTCCG	0.642	
-	2	375	nse_Mutation_p.R	NM_001042471	NP_001035936	Q8TAX9	GSDMB_HUMAN			2	ATATCCGGTTCT	0.488	rs144892352
-	1	235	39_uc010wfm.1_5	NM_213656	NP_998821	Q6A163	K1C39_HUMAN	Head.		0	CTTGCGACAAA	0.517	
-	1	363		NM_031960	NP_114166	Q9BYQ9	KRA48_HUMAN	IKRQVHEC]- [SPRT]-[STC		0	ttgcagcagctggaca	0.179	
-	1	216		NM_033188	NP_149445	Q9BYR2	KRA45_HUMAN	[GRQVCHIEK]- [SPTR]-[V		0	gagatgcagcagcta	0.274	
-	1	428	T17_uc010wft.1_M	NM_000422	NP_000413	Q04695	K1C17_HUMAN	keratinocyte proliferation a		2	GGCACGCACCT	0.632	
-	16	2186		NM_012448	NP_036580	P51692	STA5B_HUMAN	SH2.		6	TGGCCGATCAG	0.428	
+	19	3427	AP1_uc010wgs.1	NM_003632	NP_003623	P78357	CNTP1_HUMAN	ellular (Potential).		8	TGCCCGGTTAC	0.637	

-	26	3467	.1_Missense_Mut	NM_005474	NP_005465	Q9UQL6	HDAC5_HUMAN	ear export signal.		1	GCTCACAGTCT	0.677	
+	3	545		NM_016001	NP_057085	Q9Y5J1	UTP18_HUMAN			0	ATGATGAAAAATG	0.303	
-	6	495	fz.2_Intron|ATP5H	NM_006356	NP_006347	O75947	ATP5H_HUMAN			0	TCTAATTTGGTTT	0.393	
+	3	422		NM_032048	NP_114437	Q9BXX0	EMIL2_HUMAN	EMI.		3	GGTATCGAGTGA	0.502	
+	10	2513	.R750W|KIAA080	NM_015210	NP_056025	Q9Y4B5	CC165_HUMAN			0	ACTCCCGGGTG	0.672	rs144721445
+	3	886		NM_153000	NP_694545	Q8J025	APCD1_HUMAN	ellular (Potential).		0	CAGACGGGGGT	0.627	
-	40	5738	p.M387T|MYO5B_	NM_001080467	NP_001073936	Q9ULV0	MYO5B_HUMAN			5	GGAAACATGTGC	0.423	
+	2	254	DR7_uc002lgl.1_	NM_015285	NP_056100	Q9Y4E6	WDR7_HUMAN			3	GGGGTCGAAAA	0.413	
+	11	1647	ls.2_Missense_Mu	NM_032649	NP_116038	Q96KN2	CNDP1_HUMAN			0	AACATTCGCAGA	0.512	
+	1	1577	qu.1_Missense_M	NM_017757	NP_060227	Q9C0G0	ZN407_HUMAN			2	GTGCCCGTCCTC	0.572	
+	2	1555		NM_005786	NP_005777	Q6ZSZ6	TSH1_HUMAN			0	TGGCCCTGAGTG	0.617	
+	9	1072	.V245M|PNPLA6_	NM_006702	NP_006693	Q8IY17	PLPL6_HUMAN	ytoplasmic (Potential).		3	TCCACGGTGCTG	0.687	
-	3	28508		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	h.|Extracellular (Potential).		57	CCAGGGAAGAT	0.507	
-	3	20909		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).		57	ACAGAGGATTGT	0.488	
+	8	1035	p.S210N|C19orf66	NM_018381	NP_060851	Q9NUL5	CS066_HUMAN			0	ACATTAGCAGTG	0.557	
-	13	2818	nqo.3_Missense_M	NM_015493	NP_056308	Q63ZY3	KANK2_HUMAN	ANK 3.		0	TGACAACGTCCA	0.632	
-	4	765	si.3_Missense_Mu	NM_001611	NP_001602	P13686	PPA5_HUMAN			1	ACACGGGGTAGT	0.667	
+	14	1938	dzh.2_Missense_M	NM_017721	NP_060191	Q6P1N0	C2D1A_HUMAN			0	ATCACCAAGGTG	0.552	
+	5	1455	pk.2_Missense_M	NM_025189	NP_079465	Q9H8G1	ZN430_HUMAN	2H2-type 9.		2	ACATAAGATAATT	0.378	
+	5	1464	pk.2_Missense_M	NM_025189	NP_079465	Q9H8G1	ZN430_HUMAN			2	ATTCATACTGGAG	0.383	
-	3	1913		NM_001001411	NP_001001411	Q8N7Q3	ZN676_HUMAN			0	TTGTAGGGTTTCT	0.418	
-	18	1883		NM_032139	NP_115515	Q96NW4	ANR27_HUMAN	ANK 5.		5	GGTAGCCCCAG	0.532	
-	9	1058	_p.A180V|RHPN2_	NM_033103	NP_149094	Q8IUC4	RHPN2_HUMAN	BRO1.		6	CCGGCGCCTGG	0.622	
-	3	545	p.P16S|ZNF599_u	NM_001007248	NP_001007249	Q96NL3	ZN599_HUMAN	KRAB.		2	GTTTGGGAACAG	0.458	
+	6	1891	p.G557S|ZNF567_	NM_152603	NP_689816	Q8N184	ZN567_HUMAN			0	CATACCGGCCAG	0.418	
-	16	7944		NM_003890	NP_003881	Q9Y6R7	FCGBP_HUMAN	VWFD 6.		9	ACTCCTCGCTGG	0.657	
-	1	1071	c.2_Missense_Mut	NM_175875	NP_787071	Q8N196	SIX5_HUMAN	Homeobox.		1	CGTGGGGTAGC	0.687	
+	11	1288	_p.V277I|PPP5C_	NM_006247	NP_006238	P53041	PPP5_HUMAN	Catalytic.		2	CTGACGTCACC	0.612	
-	19	2941	_p.D387N|PRKD2_	NM_001079881	NP_001073350	Q9BZL6	KPCD2_HUMAN			7	GCATGTCGTGGT	0.652	
-	11	1841	KD2_uc002pfi.2_	NM_001079881	NP_001073350	Q9BZL6	KPCD2_HUMAN	PH.		7	GTCTCCCAGCCC	0.692	
-	4	472	pfu.1_Missense_M	NM_004069	NP_004060	P53680	AP2S1_HUMAN			0	CACAGACATTGT	0.507	
+	4	799	P62_uc002pqz.2_	NM_012068	NP_036200	Q9Y2D1	ATF5_HUMAN			2	CTCCTCCCTCTG	0.577	
+	4	1437	dn.1_Missense_M	NM_018260	NP_060730	Q9NV72	ZN701_HUMAN			0	AGAAACCTTACA	0.348	rs142390931
-	4	403	_p.A75T|OSCAR_	NM_206818	NP_996554	Q8IYS5	OSCAR_HUMAN	Ig-like 1.		0	GGGGAGCGATCT	0.582	
-	5	988	LRA3_uc010erk.2	NM_006865	NP_006856	Q8N6C8	LIRA3_HUMAN	like C2-type 3.		1	GGGCCGACCAC	0.677	
-	6	1154	fi.2_Missense_Mu	NM_012276	NP_036408	P59901	LIRA4_HUMAN	4.|Extracellular (Potential).		2	TCAGACGCAACC	0.587	rs139101339
+	5	495	_Mutation_p.T11	NM_017852	NP_060322	Q9NX02	NALP2_HUMAN			2	CAGAAACGAAA	0.323	
+	2	321	.3_Intron|ZNF776_	NM_138347	NP_612356	Q7Z340	ZN551_HUMAN	KRAB.		1	ATGAGTCTCAGA	0.483	
-	7	2374	hp.1_Missense_M	NM_025027	NP_079303	Q8WXB4	ZN606_HUMAN	2H2-type 9.		2	TCTGATGGGCAA	0.423	
+	3	840	.2_Missense_Mut	NM_000221	NP_000212	P50053	KHK_HUMAN			0	GTAGCCGCACCA	0.557	rs138367050
-	4	533	p.A150V|ATL2_uc	NM_001135673	NP_001129145	Q8NHH9	ATLA2_HUMAN	ytoplasmic.		3	AGCACAGCAACC	0.363	
+	3	682	svy.2_Missense_	NM_001008949	NP_001008949	Q6GPH6	IPIL1_HUMAN	ical; (Potent	p.G124V(1)	3	ACACTGGCCTCT	0.572	
-	3	336		NM_016466	NP_057550	Q53RE8	ANR39_HUMAN	ANK 3.		0	CTCGGTGCAGAG	0.622	
-	11	1379	xe.2_5'Flank|SEM	NM_017789	NP_060259	Q9C0C4	SEM4C_HUMAN	effect on m	p.R407W(1)	2	TCCACCGAGGCC	0.622	
+	13	4582	.3_Missense_Mut	NM_005270	NP_005261	P10070	GLI2_HUMAN			13	ATGGATGATGGC	0.627	
+	1	207	.1_Intron|UGGT1_	NM_020120	NP_064505	Q9NYU2	UGGG1_HUMAN			1	CGGTGCGTGTG	0.721	
-	63	10974		NM_018557	NP_061027	Q9NZR2	LRP1B_HUMAN	ntial).|LDL-receptor class A		50	ACATTTCCACCA	0.338	

+	2	392	n_p.P98S|PDK1_	NM_002610	NP_002601	Q15118	PDK1_HUMAN		4	CTCCTTCCAGAT	0.393	
-	46	15972	N_uc010zfi.1_Intr	NM_133379	NP_596870	Q8WZ42	TITIN_HUMAN		153	TCCCCCTTCTC	0.403	
-	40	9583	R3074Q|TTN_uc0	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	ACATCCGGGTG	0.453	rs72647894
-	40	6558		NM_018897	NP_061720	Q8WXX0	DYH7_HUMAN	3 (By similarity).	12	CATTTACGATTT	0.318	
+	3	285	10ziu.1_5'Flank|E	NM_001037663	NP_001032752	P24534	EF1B_HUMAN	ST C-terminal.	0	TGTCCAGCCCA	0.468	
-	17	2526	e_Mutation_p.S45	NM_173076	NP_775099	Q86UK0	ABCAC_HUMAN		11	TATTTTGAAGCA	0.348	
+	17	1697	140_uc002vqm.2	NM_007237	NP_009168	Q13342	LY10_HUMAN		0	CCGACGGCCAG	0.478	
+	3	247	c010fyc.2_Splice_	NM_000751	NP_000742	Q07001	ACHD_HUMAN		3	AGCACGTAAGA	0.284	
-	7	1266	_p.E63K|NGEF_	NM_019850	NP_062824	Q8N5V2	NGEF_HUMAN	DH.	7	CTCCTCCATCC	0.587	
+	2	673		NM_005383	NP_005374	Q9Y3R4	NEUR2_HUMAN		0	AAGTCGAGACT	0.652	
-	10	4652	p.R1250Q|COL6A	NM_004369	NP_004360	P12111	CO6A3_HUMAN	.|Nonhelical region.	18	AATCTCGAATAT	0.458	
-	9	817	_p.P270S|IDH3B_	NM_006899	NP_008830	O43837	IDH3B_HUMAN		0	ATTGGGCATCA	0.527	
+	2	959	K2_uc002wkd.2_I	NM_153638	NP_705902	Q9BZ23	PANK2_HUMAN		0	GTGGAGCGTAC	0.383	
+	4	620	zrc.1_Missense_	NM_012261	NP_036393	Q9UJQ1	CT103_HUMAN	ellular (Potential).	3	CCAAGGGACCT	0.582	
+	10	1488	fw.2_Splice_Site_	NM_002951	NP_002942	P04844	RPN2_HUMAN		3	ACCCGGTAGGT	0.517	
+	2	349	2xix.2_Missense_	NM_020336	NP_065069	Q86X10	RLGPB_HUMAN		2	TGGACGAGAGG	0.488	
-	38	4807	tv.1_Missense_M	NM_020820	NP_065871	Q8TCU6	PREX1_HUMAN		6	CCAGGGACACG	0.687	
-	8	1214	yi.1_Missense_M	NM_000961	NP_000952	Q16647	PTGIS_HUMAN		3	GGAAGGGGAAG	0.557	
+	2	3406		NM_173485	NP_775756	Q9NRE2	TSH2_HUMAN		6	GGTCCCCCCCA	0.552	
+	21	2975	CRNA00176_uc0	NM_012469	NP_036601	O94906	PRP6_HUMAN		2	CGGCCGCATCA	0.617	
-	6	2187		NM_006988	NP_008919	Q9UHI8	ATS1_HUMAN	SP type-1 1.	6	GACTCCTCCAC	0.498	
-	11	1188_1189	n_p.K416E|CHEK	NM_007194	NP_009125	O96017	CHK2_HUMAN	rotein kinas73E(2)|p.S372	20	AATCTTGGAGTG	0.416	470496;rs146546850
-	16	2130		NM_173050	NP_766638	Q8IWY4	SCUB1_HUMAN		5	ATTCCGACACG	0.647	
-	13	1598	qk.1_Missense_M	NM_138415	NP_612424	Q96EK2	PF21B_HUMAN		3	GGCCCGCAGGC	0.652	
-	3	557		NM_012401	NP_036533	O15031	PLXB2_HUMAN	lar (Potential).|Sema.	6	GGCCACGCCCT	0.637	
+	9	885	aux.1_Missense_	NM_024827	NP_079103	Q96DB2	HDA11_HUMAN	ne deacetylase.	2	CCTGCCCGACG	0.617	
+	8	1321	C22A13_uc011ay	NM_004256	NP_004247	Q9Y226	S22AD_HUMAN	ellular (Potential).	1	TGGCTGTGGTG	0.612	
-	16	3082		NM_006514	NP_006505	Q9Y5Y9	SCNAA_HUMAN		10	CTGTCCTTTGG	0.542	
+	10	1513	NB1_uc011azf.1_	NM_001904	NP_001895	P35222	CTNB1_HUMAN	ARM 8.	3166	TCCTTCGGGCT	0.502	
+	3	1576		NM_001123041	NP_001116513	P41597	CCR2_HUMAN	lasmic (Potential).	2	AGCCCCTGAAG	0.488	
+	47	6293	_Mutation_p.P20	NM_001128840	NP_001122312	Q01668	CAC1D_HUMAN	lasmic (Potential).	11	CTGTCCCCAGC	0.622	
-	8	1442	ip.1_Missense_Mu	NM_001142733	NP_001136205	A6NK59	ASB14_HUMAN	ANK 11.	0	AACATCGCTCT	0.428	
+	25	4525	f.2_Missense_Mu	NM_001457	NP_001448	O75369	FLNB_HUMAN	|Interaction with FBLP1.	19	TGGCTCCGCTG	0.657	
+	1	374		NM_001005482	NP_001005482	Q8NGV7	OR5H2_HUMAN	lasmic (Potential).	3	TGGCATATGATC	0.378	
-	9	980	h.1_Missense_Mu	NM_007085	NP_009016	Q12841	FSTL1_HUMAN	VWFC.	1	CTCACCGTCAC	0.517	
+	6	1109	M2_uc010hsl.2_	NM_004526	NP_004517	P49736	MCM2_HUMAN	type (Potential).	4	AGGCTCCTGTC	0.582	
+	1	3723		NM_175918	NP_787114	Q8N1N5	CRPAK_HUMAN	7	0	CGTGCCGATGT	0.687	
-	4	2300		NM_001024611	NP_001019782	Q68CR7	LRC66_HUMAN		3	CCCTGGAATTG	0.478	
-	7	695	003hdl.3_Intron|uc	NM_207407	NP_997290	Q6ZWK6	TM11F_HUMAN	.|Extracellular (Potential).	1	ATTCCCCTTCCA	0.522	
+	19	3830	k.3_Missense_Mu	NM_005935	NP_005926	P51825	AFF1_HUMAN		1	GAATATGACATC	0.537	
+	38	5850	3_Intron|ANK2_uc	NM_001148	NP_001139	Q01484	ANK2_HUMAN	ich region.|Repeat A.	14	TGTATCGCCCT	0.512	
+	3	5443	p.1_Missense_Mu	NM_024582	NP_078858	Q6V0I7	FAT4_HUMAN	.|Extracellular (Potential).	18	TAGTTCGTGCT	0.468	
+	13	2650	ciu.1_Missense_	NM_001083619	NP_001077088	P42262	GRIA2_HUMAN	ellular (Potential).	4	ATGAACGAGTAC	0.507	
+	20	4001	e.1_Missense_Mu	NM_001080477	NP_001073946	Q9P273	TEN3_HUMAN	ellular (Potential).	0	TCTAACGATTTG	0.393	
-	6	1180	10_uc011cnu.1_	NM_006727	NP_006718	Q9Y6N8	CAD10_HUMAN	|Extracellular (Potential).	12	CAACTGGGGAG	0.313	
+	8	1174	R_uc011cop.1_R	NM_002185	NP_002176	P16871	IL7RA_HUMAN	lasmic (Potential).	5	CTTTGGAAGAG	0.537	
-	4	321	TARD4_uc003kpi.	NM_139164	NP_631903	Q96DR4	STAR4_HUMAN	START.	1	CTGTCCCAATC	0.398	

+	8	1039	_p.P70S|DCP2_u	NM_152624	NP_689837	Q8IU60	DCP2_HUMAN		0	TTATTTCCTGAC	0.373	
-	5	1421	nse_Mutation_p.L	NM_020389	NP_065122	Q9HCX4	TRPC7_HUMAN	ical; (Potential).	0	AAATCTAGCAGG	0.582	
-	1	463	h.1_Missense_Mu	NM_020389	NP_065122	Q9HCX4	TRPC7_HUMAN	lasmic (Potential).	0	CCTCGTCGTAGG	0.662	
+	3	801		NM_032289	NP_115665	Q9BQI7	PSD2_HUMAN		1	GGTTGGGCATTG	0.687	
+	21	2029	e_Mutation_p.P66	NM_015071	NP_055886	Q9UNA1	RHG26_HUMAN	Ser-rich.	1	GCCCCCCGAATC	0.587	
+	22	3698	.A1159V|TCOF1_	NM_001135243	NP_001128715	Q13428	TCOF_HUMAN		3	GGTGGCGCCAT	0.632	
-	2	3165		NM_052899	NP_443131	Q7Z2K8	GRIN1_HUMAN	th GNAO1 (By similarity).	2	ACCGCGGCCGG	0.672	
-	16	1807	_p.T558I|EXOC2_	NM_018303	NP_060773	Q96KP1	EXOC2_HUMAN		7	TCATGAGTAAGT	0.458	
+	1	109		NM_003540	NP_003531	P62805	H4_HUMAN		0	TCCGTCGCTTG	0.577	
+	3	612	2A1_uc003nid.1_	NM_007049	NP_008980	Q7KYR7	BT2A1_HUMAN	(Potential).|Ig-like V-type.	2	TCCTACGATGAG	0.532	
+	4	1033	uc003nkk.1_Intror	NM_025231	NP_079507	Q9H4T2	ZSC16_HUMAN	C2H2-type 3.	1	GCATCAGAGAAT	0.418	
+	16	3979	T2_uc003nvc.3_N	NM_080686	NP_542417	P48634	PRC2A_HUMAN	X 57 AA type A repeats.	0	GGAGGCGACAT	0.632	
-	9	1487	se_Mutation_p.D9	NM_025258	NP_079534	Q9Y334	G7C_HUMAN		3	AGGCATCCGTGA	0.582	
-	25	8843		NM_019105	NP_061978	P22105	TENX_HUMAN	nectin type-III 21.	0	GCTGCCCATCCC	0.627	
-	1	483	aw.2_Missense_M	NM_002586	NP_002577	P40425	PBX2_HUMAN		1	CCTGGGCCTCG	0.647	
+	10	1582	qo.3_Missense_M	NM_021956	NP_068775	Q13002	GRIK2_HUMAN	cellular (Potential).	5	TATGTCCTTTTTA	0.343	
-	5	2449		NM_001080450	NP_001073919	Q5T5X7	BEND3_HUMAN	BEN 3.	3	CCAGGGAGCCG	0.637	
+	13	5311_5312	.P4_uc003qrg.2_In	NM_020245	NP_064630	Q9NRJ4	TULP4_HUMAN		1	GAAGTCCTCTCC	0.584	
+	5	775	jw.1_Missense_M	NM_032532	NP_115921	Q4ZHG4	FNDC1_HUMAN	nectin type-III 2.	8	GATCACGGGGTT	0.542	
+	18	1637	sy.1_Nonsense_M	NM_173516	NP_775787	Q8NA58	PNDC1_HUMAN	lasmic (Potential).	0	GCTACTGGAGGC	0.622	
-	3	465	l1egc.1_Missense_	NM_020133	NP_064518	Q9NRZ5	PLCD_HUMAN		0	GGCGCGCGGGT	0.527	
-	19	2454	n_p.W647*|OSBPL	NM_015550	NP_056365	Q9H4L5	OSBL3_HUMAN		1	TTTGTTCCACTC	0.403	
+	11	1814		NM_002047	NP_002038	P41250	SYG_HUMAN		1	ACCTCTGAAAG	0.433	
-	11	1499	sense_Mutation_p	NM_033054	NP_149043	B0I1T2	MYO1G_HUMAN	osin head-like.	4	CAATGGTGGCG	0.622	
+	4	1052		NM_001159279	NP_001152751				2	CTAACCACAAG	0.398	
-	20	2777	c.1_Missense_Mu	NM_000927	NP_000918	P08183	MDR1_HUMAN	smembrane type-1 2.	7	GAGCCGCTTGG	0.522	
+	8	2347	p.V689I|PPP1R9A	NM_017650	NP_060120	Q9ULJ8	NEB1_HUMAN	N38 (By similarity).|Potenti	4	CATGCAGTTACA	0.318	
-	6	741	_p.R184*|SLC25	NM_014251	NP_055066	Q9UJS0	CMC2_HUMAN	EF-hand 4.	4	GTCTCGGAAGT	0.453	rs80338716
-	3	1904	GAL3ST4_uc003u	NM_024637	NP_078913	Q96RP7	G3ST4_HUMAN	enal (Potential).	3	AGACAGAGTCC	0.532	
+	4	713	ntron|AGFG2_uc0	NM_006076	NP_006067	O95081	AGFG2_HUMAN		1	CCACCTCGAGC	0.552	
-	2	477	KI_uc003vtu.2_Int	NM_004717	NP_004708	O75912	DGKI_HUMAN		3	TGGCTGGACCA	0.478	
-	15	1860		NM_004333	NP_004324	P15056	BRAF_HUMAN	rotein kinas_R603>I(2)|p.T	18290	GATTTCACTGTA	0.368	
+	3	5767	p.R517C|ABP1_u	NM_001091	NP_001082	P19801	ABP1_HUMAN		6	CACTACCGCGTA	0.567	
-	1	871	.1_Intron|FAM66D	NM_201402	NP_958804	Q6R6M4	U17L2_HUMAN		3	GGCAAGTTTGTT	0.498	
-	28	3497_3498	uc003xhi.1_Intron	NM_015254	NP_056069	Q9NQT8	KI13B_HUMAN		0	AGAGGGGACCA	0.54	
+	2	430	HD2_uc003xlc.2_M	NM_015214	NP_056029	O94830	DDHD2_HUMAN		2	CATCTCCGTCAC	0.408	rs143549962
-	16	3579	R1012Q|MYST3_	NM_001099412	NP_001092882	Q92794	MYST3_HUMAN		7	CCTTTCGCTTC	0.498	
-	3	1130	p.R252H|OPRK1_	NM_000912	NP_000903	P41145	OPRK_HUMAN	lasmic (Potential).	2	TTGAGACGCAGG	0.552	
+	5	1103		NM_147189	NP_671722	Q8TC76	F110B_HUMAN		1	AGCCCGTGAAG	0.677	
+	7	812	.D255N|C8orf34_	NM_052958	NP_443190	Q49A92	CH034_HUMAN		1	TCTCAAGATTCT	0.368	
-	2	80	IF2C2_uc010meo.	NM_012154	NP_036286	Q9UKV8	AGO2_HUMAN		0	CGGCGGCGCAG	0.582	
-	31	6907	e.1_Missense_Mu	NM_201380	NP_958782	Q15149	PLEC_HUMAN	us rod domain.|Potential.	9	CCTGCCGCCGG	0.761	
-	5	1584		NM_138367	NP_612376	Q9BRH9	ZN251_HUMAN	C2H2-type 9.	0	CTCCGACGAAAG	0.493	
-	5	780	T3_uc011lnf.1_Mi	NM_004529	NP_004520	P42568	AF9_HUMAN	Poly-Ser.	3	ctgctgctgctgctgctg	0.139	
-	7	1177	p.A288V|ELAVL2_	NM_004432	NP_004423	Q12926	ELAV2_HUMAN	RRM 3.	3	TGACAGCTCCA	0.468	
-	3	730	ense_Mutation_p.	NM_004323	NP_004314	Q99933	BAG1_HUMAN	.|Interaction with HSPA8.	1	TGACCCGGCAA	0.368	
+	7	1613	|NFX1_uc003zsp.	NM_002504	NP_002495	Q12986	NFX1_HUMAN	NF-X1-type 2.	1	CATGGGGGTCAG	0.493	rs35268125

-	16	2167	ssense_Mutation_	NM_022917	NP_075068	Q9H6R4	NOL6_HUMAN		2	GGTGAGCTCCC	0.617	rs139620819
-	3	797		NM_017561	NP_060031	A1L443	FA22F_HUMAN		0	TGGCCTGCCAC	0.617	
+	3	285	4brk.2_Splice_Site	NM_001032221	NP_001027392	P61764	STXB1_HUMAN		1	CTTGCAGGTGC	0.517	
-	7	1089	dn.1_Missense_M	NM_001134707	NP_001128179	Q9UL12	SARDH_HUMAN		0	GCGGAGGTAGA	0.577	
+	6	1179		NM_000093	NP_000084	P20908	CO5A1_HUMAN	nhelical region.	11	GGAAGGAGACG	0.602	
-	2	367	n_p.C59F|MID1_u	NM_033290	NP_150632	O15344	TRI18_HUMAN	RING-type.	3	GCCGGCAGGTG	0.587	
+	5	521		NM_000377	NP_000368	P42768	WASP_HUMAN		1	CCACAGACAGA	0.572	
-	2	795		NM_019003	NP_061876	Q99865	SPI2A_HUMAN		0	AGAACCATGCT	0.423	
-	14	1938	_p.S612L|ABCB7	NM_004299	NP_004290	O75027	ABCB7_HUMAN	C transporter.	1	TCTAACGATGAA	0.353	
+	17	2020	qq.2_Missense_M	NM_144658	NP_653259	Q5JSL3	DOC11_HUMAN	DHR-1.	3	AATACGATAGCC	0.308	
+	4	2019	EC1_uc010nsl.1_	NM_005462	NP_005453	O60732	MAGC1_HUMAN		4	TCCTCACTACT	0.582	
+	8	602	5_uc011myj.1_Mis	NM_007150	NP_009081	O15231	ZN185_HUMAN		3	GGACAGCTCCC	0.488	
-	7	904	ku.1_Missense_M	NM_006730	NP_006721	P49184	DNSL1_HUMAN		0	GCAGACTCCGG	0.662	
-	9	875	se_Mutation_p.E1	NM_017871	NP_060341	Q5TA45	INT11_HUMAN		0	CTTCTCGGTCA	0.562	
-	4	545	P2_uc001arw.2_3	NM_006610	NP_006601	O00187	MASP2_HUMAN	e; calcium-binding.	4	TTGTTACGGTGC	0.687	
+	5	857	i.2_Missense_Mu	NM_014874	NP_055689	O95140	MFN2_HUMAN	lasmic (Potential).	1	CCTGCGGGTAG	0.582	
-	13	2091	_p.Q5*|ARHGEF	NM_153213	NP_694945	Q8IW93	ARHGJ_HUMAN	PH.	3	CACCTGCAGCT	0.657	
+	6	1125	av.1_Missense_M	NM_032880	NP_116269	Q96ID5	IGS21_HUMAN		4	CCTCCCGTGGC	0.637	
-	94	13667	se_Mutation_p.G2	NM_020765	NP_065816	Q5T4S7	UBR4_HUMAN		25	TGCACCCCCAC	0.537	
-	65	8547	d.2_Missense_Mu	NM_005529	NP_005520	P98160	PGBM_HUMAN	ike C2-type 14.	9	CTCGGGAGGAG	0.677	
+	15	2948	gf.2_Missense_Mu	NM_017449	NP_059145	P29323	EPHB2_HUMAN	mic (Potential).|SAM.	5	GCTTCGCCAAT	0.592	
+	8	534	c001bhs.1_Silent	NM_007260	NP_009191	O95372	LYPA2_HUMAN		2	CCACCCTCTGG	0.682	
+	13	1933	e_Mutation_p.R54	NM_005839	NP_005830	Q8IYB3	SRRM1_HUMAN	s and matrix localization.|A	3	ACGGCGCAGGA	0.532	rs78787676
+	13	1157	.R316C|RPS6KA	NM_002953	NP_002944	Q15418	KS6A1_HUMAN	kinase C-terminal.	1	ACCGTCGTGAG	0.597	
+	3	1442	_p.D371N|PIGV_u	NM_017837	NP_060307	Q9NUD9	PIGV_HUMAN	lasmic (Potential).	1	AGCCCGATCTT	0.537	
+	4	879	ofh.1_Missense_	NM_032283	NP_115659	Q9NUE0	ZDH18_HUMAN		0	CGTTGCGTGAG	0.567	
+	11	1671	p.D267Y|ADC_uc	NM_052998	NP_443724	Q96A70	ADC_HUMAN		2	CGGTTGATGGC	0.617	
-	13	2278	_p.D743H|PHC2_u	NM_198040	NP_932157	Q8IXK0	PHC2_HUMAN		1	GTTATCTGAGC	0.572	
-	14	2437	_p.L169F|KIAA031	NM_024874	NP_079150	Q8IZA0	K319L_HUMAN	tracellular (Potential).	2	TCCAGAGGTAGC	0.557	
-	7	1117	a.1_Missense_Mu	NM_000831	NP_000822	Q13003	GRIK3_HUMAN	ellular (Potential).	7	GGCGTCGTACA	0.652	
-	2	425	ba.1_Missense_M	NM_000831	NP_000822	Q13003	GRIK3_HUMAN	ellular (Potential).	7	TCACCCTTTTTG	0.547	
+	34	4383	_p.T480M|MACF1_	NM_012090	NP_036222	Q9UPN3	MACF1_HUMAN		16	CTACACGGCAT	0.418	
-	9	2205	.R436H|PABPC4_	NM_003819	NP_003810	Q13310	PABP4_HUMAN		0	GCCAGCGTGGA	0.527	
-	4	825	fv.1_Missense_Mu	NM_014747	NP_055562	Q9UJD0	RIMS3_HUMAN		0	ACGTGCCGTCG	0.667	
+	8	1174				Q5T011	SZT2_HUMAN		0	CTGCGGTGAG	0.577	
+	7	987	js.2_Missense_Mu	NM_002840	NP_002831	P10586	PTPRF_HUMAN	otential).|Ig- p.R206H(1)	10	CACACGTTACT	0.607	
+	4	1074	okl.1_Missense_	NM_003780	NP_003771	O60909	B4GT2_HUMAN	enal (Potential).	2	ACCCCGCCACT	0.617	rs145778728
+	2	844	lw.1_Missense_M	NM_018150	NP_060620	Q5VTB9	RN220_HUMAN		2	GCAAGGAATAT	0.517	
+	6	822	e_Mutation_p.R12	NM_006066	NP_006057	P14550	AK1A1_HUMAN		0	TCAGGCGGGGA	0.557	
-	17	3570	se_Mutation_p.E1	NM_003035	NP_003026	Q15468	STIL_HUMAN		3	GTTCCTCTTCAT	0.393	
-	9	1754	u.1_RNA|C1orf16	NM_001004303	NP_001004303	Q5VWT5	CA168_HUMAN		5	CTCAGGGCAG	0.463	
+	19	3394	_p.A406T|LRRC7_	NM_020794	NP_065845	Q96NW7	LRRC7_HUMAN		14	TGAGCGCCACA	0.587	rs144289156
+	5	1043	NAC5_uc009wbw.	NM_030965	NP_112227	Q9BVH7	SIA7E_HUMAN	enal (Potential).	2	GAGGACGCAAG	0.443	
-	3	415	dkr.2_Missense_M	NM_018298	NP_060768	Q8TDD5	MCLN3_HUMAN		1	TTCGGTCCATAT	0.378	
-	17	2111	nse_Mutation_p.R	NM_001017975	NP_001017975	A2PYH4	HFM1_HUMAN	case C-terminal.	0	TTAATCGAGTCA	0.373	
+	7	1416	dur.2_Missense_	NM_020978	NP_066188	P19961	AMY2B_HUMAN		0	TGGCCGGGTGA	0.378	
+	7	4649		NM_001408	NP_001399	Q9HCU4	CELR2_HUMAN	otential).|Laminin G-like 1.	8	TGCCTGACCTG	0.642	

+	17	3083	gn.1_Missense_M	NM_014813	NP_055628	O94898	LRIG2_HUMAN	lasmic (Potential).	3	TGATACCGTCAG	0.488	
-	1	461	wu.1_Missense_M	NM_001232	NP_001223	O14958	CASQ2_HUMAN		1	TTTTGCGTGACC	0.473	
-	5	1864	_p.G387R|IGSF3_	NM_001007237	NP_001007238	O75054	IGSF3_HUMAN	ellular (Potential).	2	TTCCCCGGTCA	0.517	
-	4	532	_p.A31V|REG4_u	NM_001159352	NP_001152824	Q9BYZ8	REG4_HUMAN		1	CAGGAGCACAG	0.373	
+	32	4104	10_uc010oyl.1_Int	NM_001039703	NP_001034792	A6NDV3	A6NDV3_HUMAN		0	TGCTGGATGAG	0.478	
+	74	9249	.1_Intron|NBPF10	NM_001039703	NP_001034792	A6NDV3	A6NDV3_HUMAN		0	GGCCTAAAGTC	0.473	
+	4	613	_uc001enz.1_5'Fla	NM_003846	NP_003837	O96011	PX11B_HUMAN		0	TGGCTCGAGTC	0.582	
+	19	2327		NM_173638	NP_775909	Q8N660	NBPFF_HUMAN	NBPF 6.	0	TTATTCGACTC	0.458	
-	2	1030	pcr.1_Missense_M	NM_212551	NP_997716	Q96S90	LYSM1_HUMAN		0	GGCACGTCCTG	0.502	
-	3	11572		NM_002016	NP_002007	P20930	FILA_HUMAN	grin 23.|Ser-rich.	16	CTGGCCGGACT	0.592	rs143233744
-	12	1520	01fde.3_RNA|CR	NM_181715	NP_859066	Q53ET0	CRTC2_HUMAN		2	TGGGGGTAACC	0.542	rs35857186
-	7	2205	fo.2_Missense_M	NM_002249	NP_002240	Q9UGI6	KCNN3_HUMAN	-binding (By similarity).	1	GGAAAGGTCCA	0.552	
+	3	757	_p.R234H|ZBTB7B	NM_015872	NP_056956	O15156	ZBT7B_HUMAN		0	CCGCCGCAGCC	0.657	
+	20	2677	k.1_Missense_M	NM_001080471	NP_001073940	Q5VY43	PEAR1_HUMAN	Pro-rich.	3	AGGTGGGGCCC	0.667	
-	21	3114		NM_003126	NP_003117	P02549	SPTA1_HUMAN		8	CCACTGGTGCA	0.507	
-	16	2415		NM_003126	NP_003117	P02549	SPTA1_HUMAN	Spectrin 8.	8	CCTGACGAGCA	0.463	rs145972324
-	4	415		NM_017625	NP_060095	Q8WWA0	ITLN1_HUMAN	ogen C-terminal.	7	TGGACCAGCGA	0.627	
+	8	1334	_p.V326M|UHMK1	NM_175866	NP_787062	Q8TAS1	UHMK1_HUMAN	RRM.	0	TTTGTTGTGGCT	0.433	
+	3	478	cr.1_Nonsense_M	NM_145697	NP_663735	Q9BZD4	NUF2_HUMAN	the N-terminus of NDC80.	4	GAATTCGACTG	0.348	
-	13	3971		NM_000130	NP_000121	P12259	FA5_HUMAN	ndem repeats of [TNP]-L-S	6	AGAAAGGGGCA	0.502	rs140018525
+	6	643	_p.C62S|FAM163	NM_173509	NP_775780	Q96GL9	F163A_HUMAN		1	CCACCTGCAAT	0.667	
+	16	2338	h.2_Missense_M	NM_173156	NP_775179	Q92540	SMG7_HUMAN	Gln/Pro-rich.	3	GCCACCTTCCC	0.537	
+	6	999		NM_030787	NP_110414	Q9BXR6	FHR5_HUMAN	Sushi 5.	2	ATGGAGTTTCA	0.378	
-	2	2245	p.T713M|ZNF281_	NM_012482	NP_036614	Q9Y2X9	ZN281_HUMAN		2	GGAGACGTAGTG	0.433	
-	2	636	_Mutation_p.L177	NM_012482	NP_036614	Q9Y2X9	ZN281_HUMAN		2	ACTGAGGTCCT	0.547	
-	8	2173	pj.1_Missense_M	NM_014875	NP_055690	Q15058	KIF14_HUMAN	inesin-motor.	7	TGGGTCATCAC	0.388	rs144936292
+	5	1011	_p.S29P|RNPEP_	NM_020216	NP_064601	Q9H4A4	AMPB_HUMAN		1	AGATCTCCCAC	0.537	
-	8	2175	z.2_Missense_Mu	NM_002644	NP_002635	P01833	PIGR_HUMAN	lasmic (Potential).	3	TGTGCCGGGCT	0.652	
-	10	2155	kv.2_Missense_M	NM_206933	NP_996816	O75445	USH2A_HUMAN	e 2.|Extracellular (Potential	26	GTCTACAGAGA	0.423	
+	1	996		NM_021958	NP_068777	Q14774	HLX_HUMAN		2	TTGACCGCATTT	0.597	
+	4	552	d.1_Missense_Mu	NM_014777	NP_055592	Q14146	URB2_HUMAN		3	TCATCTACACGG	0.572	
+	4	2297	d.1_Missense_Mu	NM_014777	NP_055592	Q14146	URB2_HUMAN		3	CGACGGCTTCC	0.463	
+	1	55		NM_001004696	NP_001004696	Q8NH00	OR2T4_HUMAN	ellular (Potential).	1	TCCTGATGGGA	0.488	
+	9	992	F18_uc001imq.2_	NM_003675	NP_003666	Q99633	PRP18_HUMAN		1	CCATCGGTGTC	0.413	
-	22	3080		NM_001081	NP_001072	O60494	CUBN_HUMAN	CUB 5.	19	TGGCGGGATCG	0.393	
+	7	860		NM_052997	NP_443723	Q9BXX3	AN30A_HUMAN		9	CTTGGTGGAAA	0.502	
-	6	957	_p.E188*|PCDH15	NM_033056	NP_149045	Q96QU1	PCD15_HUMAN	(Potential).|Cadherin 2.	13	ATACTCTATCTG	0.333	
+	8	994		NM_001080512	NP_001073981	Q9H694	BICC1_HUMAN	KH 2.	4	TCTACCGTCTAC	0.413	
+	15	2308	50_uc010qjc.1_3'	NM_024045	NP_076950	Q9BQ39	DDX50_HUMAN		1	ACAAACGGAGTT	0.423	
-	1	812		NM_001057	NP_001048	P21452	NK2R_HUMAN	Name=2; (Potential).	1	ATTGACGATGA	0.572	
+	27	2022	jqc.1_Missense_M	NM_005203	NP_005194	Q5TAT6	CODA1_HUMAN	l).|Triple-helical region 3 (	1	GACACGATGGG	0.502	
-	6	1327	bt.1_Missense_M	NM_145869	NP_665876	P50995	ANX11_HUMAN		1	GCTCGGCACTG	0.701	
+	3	456	70_splice|PCGF5_	NM_032373	NP_115749	Q86SE9	PCGF5_HUMAN		1	TTGAGGTAAGG	0.318	
-	2	562		NM_005398	NP_005389	Q9UQK1	PPR3C_HUMAN	ction with EPM2A.	1	GTAATCGGTTGA	0.428	
-	3	283		NM_006993	NP_008924	O75607	NPM3_HUMAN		0	GGTTCCGGGCC	0.542	
-	6	978	kxy.1_Missense_M	NM_025145	NP_079421	Q8NDM7	WDR96_HUMAN	WD 3.	0	AAGTACAGTCAC	0.408	
-	5	2445		NM_173791	NP_776152	Q8NEN9	PDZD8_HUMAN		0	TATTCCGTGTTT	0.453	

+	4	3076	ıse_Mutation_p.P9	NM_206862	NP_996744	O95359	TACC2_HUMAN		10	:AGCTCCCCAAA(	0.493	
-	8	1099	AT_uc001lhr.2_Mis	NM_000274	NP_000265	P04181	OAT_HUMAN		0	;CCACTCGGCAG	0.488	
-	7	1008	›c.1_Nonsense_M	NM_173575	NP_775846	Q86UX6	ST32C_HUMAN	rotein kinase.	5	ATCCTCGCAGCA(	0.662	
+	6	756	lra.2_Missense_M	NM_006755	NP_006746	P37837	TALDO_HUMAN		0	TGGGCGCCTCC	0.527	
+	12	2169	›q.2_Missense_Mu	NM_001003819	NP_001003819	B2RNG4	B2RNG4_HUMAN		1	TGCTGCAAATGT	0.428	
+	2	508		NM_173525	NP_775796	Q8N5U0	CK042_HUMAN		1	'GGCTCCGAAGC.	0.597	
-	7	1475	d.2_Missense_Mu	NM_006458	NP_006449	O75382	TRIM3_HUMAN	Filamin.	5	'CTGCACGCAGC	0.657	
+	1	117	ıkh.2_Missense_M	NM_018222	NP_060692	Q9NVD7	PARVA_HUMAN	on with ARHGAP31.	3	;GTCCCGCAAGA	0.697	
-	9	1043	F22_uc001mpa.2_	NM_173588	NP_775859	Q8N9C0	IGS22_HUMAN	Ig-like 2.	7	TCACATCGTACTT	0.527	
+	8	1467	_p.S282L|NAV2_u	NM_145117	NP_660093	Q8IVL1	NAV2_HUMAN		6	:CTCCTCGGCCA	0.607	
+	2	198		NM_152316	NP_689529	Q8N8R7	CK046_HUMAN		0	CAGCTTCGTACT/	0.383	
+	2	2063	nun.1_Missense_M	NM_012194	NP_036326	Q6ZVL6	CK041_HUMAN		2	;CAGCAGCTGCC	0.512	
-	40	5566	dj.1_Missense_Mu	NM_001008938	NP_001008938	Q14008	CKAP5_HUMAN		2	ACTATTCGAGATG	0.498	
+	8	1342	›.2_Missense_Mut	NM_207341	NP_997224	P60852	ZP1_HUMAN	llular (Potential).|ZP.	0	AGGTCCGGCTTC	0.622	
+	8	1116	nxd.2_Missense_M	NM_033101	NP_149092	Q96DT0	LEG12_HUMAN	Galectin 2.	2	TCCTTCGCAGAC.	0.572	
+	1	99	_uc001ocy.1_5'Fla	NM_004927	NP_004918	Q13405	RM49_HUMAN		0	TGGCAGCTACCA	0.677	
-	7	1584	›.R439W|LTBP3_u	NM_001130144	NP_001123616	Q9NS15	LTBP3_HUMAN	TB 2.	3	;ACACCGCGCGC	0.637	
+	5	684	›_Mutation_p.R178	NM_006388	NP_006379	Q92993	KAT5_HUMAN		0	ACCACCGCTCAA(	0.592	
+	2	256	_p.R65H|DPP3_uc	NM_005700	NP_005691	Q9NY33	DPP3_HUMAN		2	'CAGCCGCCTCT	0.642	
+	3	414		NM_014578	NP_055393	O00212	RHOD_HUMAN		0	TAACCGGGTAG(	0.547	
+	6	713	ı_p.R155*|ANKRD	NM_207354	NP_997237	Q6ZTN6	AN13D_HUMAN		1	AGCCTGCGAGTA(	0.607	
-	3	713	_p.A157V|LRRC32	NM_005512	NP_005503	Q14392	LRC32_HUMAN	ılar (Potential).|LRR 5.	0	TCTCCGCCAGT(	0.642	
+	18	2739	JL5_uc001pju.2_R	NM_003478	NP_003469	Q93034	CUL5_HUMAN		1	TGGACGTTTGC/	0.343	
+	6	599	.1_Missense_Muta	NM_014956	NP_055771	Q9UPV0	CE164_HUMAN	action with ATRIP.	2	;TTTACGAGGTC	0.537	
+	27	10365	.2_Missense_Muta	NM_005933	NP_005924	Q03164	MLL1_HUMAN		25	GCAGACGAACAC	0.537	rs139366882
-	2	804	P2_uc001pwn.3_In	NM_004205	NP_004196	O75604	UBP2_HUMAN	or interaction with MDM4.	4	AGCATGGGGCTG(	0.627	
+	4	693		NM_003105	NP_003096	Q92673	SORL_HUMAN	cellular (Potential).	15	;CATTTCGGGCA(	0.512	
-	2	242	ıat.2_Missense_Mu	NM_014312	NP_055127	Q96IQ7	VSIG2_HUMAN	(Potential).|Ig-like V-type.	4	;CAGGGCGAAGC	0.632	
+	11	1314	bg.1_Missense_M	NM_152713	NP_689926	P46977	STT3A_HUMAN	ical; (Potential).	0	TCAGCTGTAATGG	0.428	rs140314352
+	5	1227	ıjk.2_Missense_Mu	NM_032642	NP_116031	Q9H1J7	WNT5B_HUMAN		1	AGAGCGTGCAG(	0.602	
-	43	7686	/F_uc010set.1_Int	NM_000552	NP_000543	P04275	VWF_HUMAN	VWFC 2.	12	;TCACCGACCGA(	0.577	
+	14	1851	_p.G498R|PTPN6_	NM_002831	NP_002822	P29350	PTN6_HUMAN		1	GAGTACGGGAAC	0.652	
-	10	2433	sge.1_Missense_M	NM_174941	NP_777601	Q9NR16	C163B_HUMAN	Extracellular (Potential).	11	AGCAGGGCATAT(	0.453	
+	6	648	IM1L_uc010skh.1_	NM_012062	NP_036192	O00429	DNM1L_HUMAN	TPase domain.	2	GATATTGAGCTT(	0.388	
+	17	2220	nn.1_Missense_Mu	NM_001843	NP_001834	Q12860	CNTN1_HUMAN		9	ACAGACGGTGCT(	0.368	
-	11	1222	FRS2IP_uc001roy.	NM_004719	NP_004710	Q99590	SCAFB_HUMAN		0	GGTTTTCGTCTT(	0.428	
-	1	367		NM_001004134	NP_001004134	Q8NGE0	O10AD_HUMAN	lasmic (Potential).	1	CATAACGGTCATA	0.488	
-	4	1485	TUBA1B_uc001rtl.	NM_006082	NP_006073	P68363	TBA1B_HUMAN		0	TTCACGGGCCT(	0.512	
+	4	1269	'UBA1C_uc010sm	NM_032704	NP_116093	Q9BQE3	TBA1C_HUMAN		0	;GGCTCGCCTGG	0.592	
-	5	1089		NM_030809	NP_110436	Q9H175	CSRN2_HUMAN		0	;GGACCCGGATT(	0.592	
+	22	5078	:j.2_Missense_Mut	NM_012291	NP_036423	Q14674	ESPL1_HUMAN		3	;TTCAGGAGATG(	0.592	
-	2	1134	_p.R325C|SP7_uc(	NM_152860	NP_690599	Q8TDD2	SP7_HUMAN	C2H2-type 2.	0	CATGACGCTCCA(	0.612	
+	7	780	tation_p.R144W|P	NM_001128911	NP_001122383	Q15366	PCBP2_HUMAN	KH 2.	0	ACTGAGCGGGCC	0.473	
-	2	863	zob.1_Missense_M	NM_032364	NP_115740	Q6Y2X3	DJC14_HUMAN		4	;GATGTCGACCA(	0.597	
-	9	988	ıse_Mutation_p.D2	NM_145064	NP_659501	Q96MF2	STAC3_HUMAN	SH3 1.	3	CCAGATCGTCCT	0.567	
-	3	357		NM_018402	NP_060872	Q9NPH9	IL26_HUMAN		0	CCTCCACAAAGC	0.388	
-	1	661		NM_201550	NP_963844	Q5BKY1	LRC10_HUMAN	LRR 3.	0	GGGGAGGTCGC.	0.577	

+	3	905		NM_032790	NP_116179	Q96D31	CRCM1_HUMAN	ical; (Potential).		0	CCATCGCCTCG	0.642	
+	6	664	zxh.2_Missense_	NM_001080825	NP_001074294	A0PK00	T120B_HUMAN	ical; (Potential).		0	CCATTCGGGAG	0.572	
-	3	769	_p.R27H|RILPL1_	NM_178314	NP_847884	Q5EBL4	RIPL1_HUMAN	Potential.		0	TGGCGCGGATC	0.617	
-	12	2436		NM_015347	NP_056162	O15034	RIMB2_HUMAN			11	CTCCTCCATGA	0.612	
+	6	719		NM_003565	NP_003556	O75385	ULK1_HUMAN	rotein kinase.		4	CCGCCGGCCGC	0.473	
-	5	1441	_p.D294E|GOLGA	NM_005895	NP_005886	Q08378	GOGA3_HUMAN			6	CGGTCGTCAGT	0.597	rs143511800
-	14	2075	R6_uc001uqe.1_	NM_004685	NP_004676	Q9Y217	MTMR6_HUMAN			4	TGCCCTCTATAG	0.423	
-	5	1531	se_Mutation_p.R4	NM_183044	NP_898865	Q9Y252	RNF6_HUMAN	Arg-rich.		2	TATCCCGATCTC	0.463	
+	1	2516		NM_207361	NP_997244	Q5SZK8	FREM2_HUMAN	xtracellular (Potential).		11	TGACCGAGAAC	0.562	
+	7	771	p.E172G|COG6_u	NM_020751	NP_065802	Q9Y2V7	COG6_HUMAN			2	CTTATGAAAGAC	0.264	
-	2	233		NM_198849	NP_942146	Q8IW03	SIAH3_HUMAN			2	GGCGCGCCGAC	0.443	
-	13	3281	se_Mutation_p.S	NM_015070	NP_055885	Q5T200	ZC3HD_HUMAN			2	GGGTACTACCA	0.373	
-	5	650		NM_002267	NP_002258	O00505	IMA3_HUMAN			0	GCATTCTGCAAT	0.328	
-	13	2665	0aer.2_Missense_	NM_014832	NP_055647	O60343	TBCD4_HUMAN			6	GCTGCCGCCAG	0.517	
-	3	727		NM_012158	NP_036290	Q9UKT7	FBXL3_HUMAN	LRR 1.		0	TGCTGCTGTCC	0.348	
-	13	1642	_p.L475F|TUBGC	NM_006322	NP_006313	Q96CW5	GCP3_HUMAN			1	CCTATCAAAAG	0.358	
-	9	688	_p.D203N|PCID2_	NM_001127203	NP_001120675	Q5JVF3	PCID2_HUMAN			0	TGTAATCGTCTTT	0.333	
+	2	470	vtt.3_Missense_M	NM_017905	NP_060375	Q6UWJ1	TMCO3_HUMAN			0	TGCACCGCGGG	0.627	
-	10	1144	_p.E32K|GAS6_u	NM_000820	NP_000811	Q14393	GAS6_HUMAN	minin G-like 1.		4	GCCCTCGGGGT	0.652	
-	9	1247	u.2_Missense_Mu	NM_138376	NP_612385	Q8N0Z6	TTC5_HUMAN			1	TGTGCTGAATTC	0.428	
+	2	807	ASE4_uc001vya.	NM_002937	NP_002928	P34096	RNAS4_HUMAN			1	AACATTCGTAGT	0.463	
-	1	166		NM_001005466	NP_001005466	Q8NGC3	O10G2_HUMAN	lasmic (Potential).		1	CGGGTCAGCCC	0.527	
-	15	1958		NM_002471	NP_002462	P13533	MYH6_HUMAN	osin head-like.		4	GCTTACCAGTAT	0.567	
-	1	25		NM_199047	NP_950248	Q6SJ96	TBPL2_HUMAN			0	AACCCGCTCCG	0.692	
+	8	2096	.3_Intron|FUT8_u	NM_178155	NP_835368	Q9BYC5	FUT8_HUMAN	tential).|Lumenal (Potential		1	TCCCCGTCCTC	0.458	
+	22	3258	_p.P759S|GPHN_	NM_001024218	NP_001019389	Q9NQX3	GEPH_HUMAN	denylyltransferase.		2	TGCTACCTCCA	0.473	
+	6	736	_p.E215K|GALNTL	NM_020692	NP_065743	Q8N428	GLTL1_HUMAN	main A.|Lumenal (Potential		2	ACTGCGAAGTG	0.627	
-	1	1111		NR_003951						0	TATCAACTCCAC	0.403	
+	8	906	AF4_uc010tts.1_	NM_015604	NP_056419	Q8WV16	DCAF4_HUMAN			3	TGAATTCGGTGT	0.507	
-	7	830	_Mutation_p.H67Q	NM_005050	NP_005041	O14678	ABCD4_HUMAN	nsmembrane type-1.		4	TGCATGTGCTT	0.552	
+	13	5711	M1_uc001xqm.1_	NM_019589	NP_062535	P49750	YLPM1_HUMAN			3	TTGGAGGACCT	0.378	
+	10	1301		NM_000369	NP_000360	P16473	TSHR_HUMAN	ellular (Pote	p.D382H(1)	299	CTTTTGACAGCC	0.458	
-	3	951		NM_206918	NP_996801	Q6QHC5	DEGS2_HUMAN			0	GCTGCGGCAGG	0.637	
+	8	1852		NM_001376	NP_001367	Q14204	DYHC1_HUMAN	similarity).|Stem (By simila		10	GACCCGGATCA	0.532	
-	2	452		NM_207379	NP_997262	Q6ZVK1	T179A_HUMAN			0	GGGTACGGTGC	0.657	
+	7	1316	|OR4N4_uc010tzv	NM_001005241	NP_001005241	Q8N0Y3	OR4N4_HUMAN	Name=3; (Potential).		5	GGAGGGATTAC	0.512	
+	1	95		NM_001080841	NP_001074310					0	GGAGGGATTAC	0.493	
+	6	561	p.V153M|CYFIP1_	NM_014608	NP_055423	Q7L576	CYFP1_HUMAN			9	ACTTCGTGTCA	0.537	
-	5	551	C2_uc001zbl.1_5'	NM_004667	NP_004658	O95714	HERC2_HUMAN			13	ATAGCGCTCCA	0.502	
-	16	2034	se_Mutation_p.E5	NM_002420	NP_002411	Q7Z4N2	TRPM1_HUMAN	lasmic (Potential).		4	CTCTTCCCCTC	0.592	
+	4	1192		NM_020857	NP_065908	Q9P253	VPS18_HUMAN			3	CCTTCGCCTGG	0.637	
+	8	1058	_p.E290G|SQRDL_	NM_021199	NP_067022	Q9Y6N5	SQRD_HUMAN			1	AGTATGAAATGC	0.448	
-	4	663		NM_000138	NP_000129	P35555	FBN1_HUMAN	EGF-like 1.		3	TGGAGCCACAG	0.408	
-	9	4299	.1_Intron|RFX7_u	NM_022841	NP_073752	Q2KHR2	RFX7_HUMAN			0	TTCACTGCAAAT	0.368	
+	4	801	se_Mutation_p.R6	NM_000236	NP_000227	P11150	LIPC_HUMAN			1	CAGATTCGAATC	0.488	
-	77	14256	1_uc002amo.2_5	NM_003922	NP_003913	Q15751	HERC1_HUMAN	HECT.		19	CTTCTCGGACT	0.597	
-	1	133	PX_uc010bhg.1_	NM_006660	NP_006651	O76031	CLPX_HUMAN			0	GGCGAGTGAGG	0.706	

-	4	791		NM_001102658	NP_001096128	P0C5K7	CT62_HUMAN			0	CATTCCGTCTG	0.493	
-	2	739		NM_001039614	NP_001034703	Q2T9L4	CO059_HUMAN			1	TGGCCGAGTCG	0.627	rs138123176
-	2	1379		NM_032246	NP_115622	Q6ZN04	MEX3B_HUMAN			2	GGCAGCCGTCG	0.652	
-	18	2305	678S|AP3B2_uc01	NM_004644	NP_004635	Q13367	AP3B2_HUMAN	Glu/Ser-rich.		5	AGAGCCGCTCT	0.562	
-	4	1128	s.1_Missense_Mu	NM_001717	NP_001708	Q01954	BNC1_HUMAN			3	CTATTCCTCTCA	0.473	
+	10	1038		NM_003870	NP_003861	P46940	IQGA1_HUMAN			8	AATATCGACCTG	0.473	
+	18	3513	e_Mutation_p.R76	NM_000057	NP_000048	P54132	BLM_HUMAN			6	TTCACGACACA	0.368	
+	5	1217	3A1_uc010boc.1_	NM_013272	NP_037404	Q9UIG8	SO3A1_HUMAN	lasmic (Potential).		1	GATCCCGAAGG	0.582	
-	9	1434	_p.E374K|PCSK6_	NM_002570	NP_002561	P29122	PCSK6_HUMAN	Catalytic.		2	ATTCTCGGTGG	0.567	
+	5	1855		NM_005632	NP_005623	O75808	CAN15_HUMAN	lpain cataly	p.E498fs*15(1)	2	GGCCCGAGTCT	0.657	
+	25	3152	.R1005H|MAPK8I	NM_015133	NP_055948	Q9UPT6	JIP3_HUMAN			3	AGGCCGTGTGC	0.701	
-	10	1977		NM_000243	NP_000234	O15553	MEFV_HUMAN	30.2/SPRY.		6	AACTCGGAGAG	0.522	rs104895107
+	6	1347	IP2_uc010uyp.1_	NM_024997	NP_079273	Q5U623	MCAF2_HUMAN	Potential.		0	AAAGACGTATT	0.289	
+	25	3845	l.2_Missense_Mut	NM_004996	NP_004987	P33527	MRP1_HUMAN	ne type-1 2.|Helical; Name		4	GGCACAGCCTC	0.567	
+	12	1778	p.G550R|TMC7_u	NM_024847	NP_079123	Q7Z402	TMC7_HUMAN	ellular (Potential).		3	TTTACGGGCAA	0.498	
+	5	936	fy.2_Missense_M	NM_016524	NP_057608	Q9BSW7	SYT17_HUMAN	C2 1.		1	CCTCACCGTGC	0.607	
+	7	1252	2K_uc002dkh.2_	NM_013302	NP_037434	O00418	EF2K_HUMAN	ype protein kinase.		1	GCCGCAGGTGA	0.607	
+	15	2162	Mutation_p.D660N	NM_173201	NP_775293	O14983	AT2A1_HUMAN	smic (By similarity).		4	TCGACGACCTG	0.632	
+	15	2183	utation_p.R667W	NM_173201	NP_775293	O14983	AT2A1_HUMAN	smic (By similarity).		4	AACAGCGGGAA	0.622	
-	4	571	_Intron|TBX6_uc0	NM_004608	NP_004599	O95947	TBX6_HUMAN	T-box.		2	GACACGGTCAG	0.632	
-	3	945	89_uc010bzy.2_5	NM_138447	NP_612456	Q96CS4	ZN689_HUMAN	2H2-type 3.		0	ACACTGGTCAC	0.602	
+	18	2771	_p.R215Q|RNF40_	NM_014771	NP_055586	O75150	BRE1B_HUMAN	Potential.		1	GACTCGGCTGC	0.642	
-	2	532	efh.1_Missense_	NM_033151	NP_149163	Q96J66	ABCCB_HUMAN	lasmic (Potential).		6	TCCCCCACGGT	0.552	
+	3	748	_p.R70H|MMP2_	NM_004530	NP_004521	P08253	MMP2_HUMAN	lagenase-like 1.		11	TGCTCGTGCCT	0.478	
-	5	545		NM_001896	NP_001887	P19784	CSK22_HUMAN	rotein kinase.		1	AAACCGGATATC	0.343	
-	18	2955	_p.R7H|FHOD1_u	NM_013241	NP_037373	Q9Y613	FHOD1_HUMAN	FH2.		3	CACGGCGGTG	0.617	
-	3	1322	_p.A163T|TPPP3_	NM_016140	NP_057224	Q9BW30	TPPP3_HUMAN			1	GTAGGCGCTCA	0.627	
-	3	812	OD2_uc002euc.2	NM_030819	NP_110446	Q3B7J2	GFOD2_HUMAN			3	GCCCCCGCCGC	0.612	
+	4	1029	S3_uc002ewl.2_	NM_005329	NP_005320	O00219	HAS3_HUMAN	lasmic (Potential).		0	TCAACGTGGAG	0.567	
-	3	237	dn.2_Missense_M	NM_153486	NP_705690	Q86WU2	LDHD_HUMAN	inding PCMH-type.		0	AGGTTCGCACC	0.632	
+	4	1202	ng.1_Missense_M	NM_014940	NP_055755	Q7L1V2	MON1B_HUMAN			0	GGAGCGAAATG	0.657	
+	23	2649		NM_002661	NP_002652	P16885	PLCG2_HUMAN			8	ACTTCGAGGAG	0.512	
+	5	761	voj.1_Missense_	NM_014732	NP_055547	O60268	K0513_HUMAN			1	AGAACCTCATG	0.522	
-	3	268	V72I|MTHFSD_uc	NM_001159377	NP_001152849	Q2M296	MTHSD_HUMAN			0	CCGAACGCCTT	0.537	
-	12	1445	CHC14_uc002fkb.	NM_015144	NP_055959	Q8WYQ9	ZCH14_HUMAN			2	GGGCCGTGGGT	0.587	
-	9	1179	jf.2_Intron|PRDM	NM_001098173	NP_001091643	Q9NQW5	PRDM7_HUMAN			1	CCCCATACCAG	0.522	
-	8	984	_p.V299I|SLC43A	NM_152346	NP_689559	Q8N370	LAT4_HUMAN			0	GTCGACGGTGG	0.697	
-	5	1099	tn.1_Missense_Mu	NM_052928	NP_443160	Q8IYR2	SMYD4_HUMAN	MYND-type.		5	GCATCCGTCAC	0.542	
-	28	3250	3_Intron|GSG2_u	NM_002208	NP_002199	P38570	ITAE_HUMAN	ellular (Potential).		4	CCATTCTTCCA	0.458	
-	3	657	k.1_Missense_Mu	NM_015113	NP_055928	O43149	ZZEF1_HUMAN			4	TCACCGCGCTG	0.512	
-	17	3016	2gag.1_Missense_	NM_015099	NP_055914	O94983	CMTA2_HUMAN			1	CTCCCGCATTG	0.612	
-	12	1834		NM_001139	NP_001130	O75342	LX12B_HUMAN	ipoxygenase.		0	GGCTGCGTCAC	0.577	
-	14	1697	_p.L544P|MYH10_	NM_005964	NP_005955	P35580	MYH10_HUMAN	osin head-like.		2	CCAAAAGGGCC	0.428	
+	16	2919	o.2_Missense_M	NM_001372	NP_001363	Q9NYC9	DYH9_HUMAN	n (By similarity).		20	TTGAGGGTCTC	0.502	
+	12	1374	p.D440N|MPRIP_	NM_201274	NP_958431	Q6WCQ1	MPRIP_HUMAN	PH 2.		0	TGTTACGATGTC	0.488	rs144918812
-	6	880	n.2_Missense_Mu	NM_001142610	NP_001136082	Q8IYT8	ULK2_HUMAN	rotein kinase.		4	CTTTGCTGTGC	0.453	
+	2	342	2_5'UTR|MAP2K3	NM_145109	NP_659731	P46734	MP2K3_HUMAN			0	ATCTACGGATAT	0.557	rs144032462

+	3	986		NM_021012	NP_066292	Q14500	IRK12_HUMAN	me=M1; (By similarity).	4	TGCCTCCTGGC	0.627	
+	26	3675	sn.1_Missense_Mu	NM_001042492	NP_001035957	P21359	NF1_HUMAN	p.?(2)	330	CCTTTTGAATGA	0.433	
+	2	675	e_Mutation_p.L15	NM_003885	NP_003876	Q15078	CD5R1_HUMAN		1	AGCTGCTTCGC	0.682	
-	26	3736	.R715Q|MYO19_	NM_001163735	NP_001157207	Q96H55	MYO19_HUMAN	hondrial targeting.	1	GCGCTCGGATG	0.567	
+	11	2057	ue.2_Missense_M	NM_007359	NP_031385	O15234	CASC3_HUMAN	tion in cytoplasmic stress g	1	ATCCCCACCAG	0.498	
-	3	274		NM_001838	NP_001829	P32248	CCR7_HUMAN	Name=1; (Potential).	1	GCCCACGAAAC	0.502	
-	4	864		NM_181537	NP_853515	Q7Z3Y8	K1C27_HUMAN	Rod.|Coil 2.	0	CTCCGCGTCCC	0.652	
+	3	310		NM_030975	NP_112237	B5MDD6	B5MDD6_HUMAN		0	CTACCCGACGA	0.637	
-	5	848		NM_002279	NP_002270	Q14525	KT33B_HUMAN	Coil 2.|Rod.	0	CCTGGTAGGAC	0.592	
+	6	688	p.L154Q|MLX_uc	NM_170607	NP_733752	Q9UH92	MLX_HUMAN		0	CGCCCTAAAGA	0.502	
-	3	723	p.R174K|MEOX1_	NM_004527	NP_004518	P50221	MEOX1_HUMAN		0	CTGACCTCCCT	0.567	
-	6	1906	e_Mutation_p.S4	NM_001145365	NP_001138837	Q9Y2D9	ZN652_HUMAN	ype 9; degenerate.	1	TGTTCGAGAAG	0.567	
+	5	746	ird.2_Missense_M	NM_022827	NP_073738	Q8TB22	SPT20_HUMAN		0	AATACGAGAAC	0.627	
+	1	490		NM_001004707	NP_001004707	P58180	OR4D2_HUMAN	ellular (Potential).	2	TGATGCTCCCA	0.552	
-	2	219	02jcu.1_Missense	NM_001317	NP_001308	P01243	CSH_HUMAN		1	AAAAAGCCTGG	0.612	
-	24	4596		NM_000334	NP_000325	P35499	SCN4A_HUMAN	=S5 of repeat IV; (Potentia	3	CTTGACGTAGG	0.557	rs140517911
-	11	2458	HM1P_uc002jev.3	NR_024386					0	AGCGGGGGCAG	0.637	
+	4	697		NM_000727	NP_000718	Q06432	CCG1_HUMAN		0	GCCCCGGAACC	0.632	
-	35	4600	z.2_Missense_Mu	NM_080283	NP_525022	Q8IUA7	ABCA9_HUMAN	C transporter 2.	6	ACACCGCCTCA	0.572	
+	10	1267	k.2_Nonsense_Mu	NM_153209	NP_694941	Q2TAC6	KIF19_HUMAN	Potential.	0	TCCAGCGACTC	0.632	
-	10	1794	_p.H577Y|UBE2O_	NM_022066	NP_071349	Q9C0C9	UBE2O_HUMAN		5	GTGGTGCACAG	0.597	
-	4	585		NM_001008528	NP_001008528	P84157	MXRA7_HUMAN		0	CAAACGTCTCC	0.567	
+	2	703	_p.H178Y|FOXK2_	NM_004514	NP_004505	Q01167	FOXK2_HUMAN		0	AGCCACACATC	0.592	
-	3	2287	D_uc002kfy.1_In	NM_024702	NP_078978	Q32MQ0	ZN750_HUMAN		1	GTTCCGGGGCC	0.642	
-	10	894	e_Mutation_p.V18	NM_001009905	NP_001009905	Q67FW5	B3GNL_HUMAN		2	GTCCACGTCAC	0.637	
+	4	1118		NM_032048	NP_114437	Q9BXX0	EMIL2_HUMAN	Potential.	3	GGACAGTAAGA	0.562	
-	1	438	N2_uc002klo.2_In	NR_026659					0	TAATTCCAAATTT	0.338	
-	18	1766	.R536W|L3MBTL	NM_173464	NP_775735	Q8NA19	LMBL4_HUMAN		3	GGCCCGGATGT	0.632	
+	36	4728	r.2_Missense_Mu	NM_198129	NP_937762	Q16787	LAMA3_HUMAN	ninin IV type A.	11	CTGGCGACATG	0.448	
-	6	898	a.1_5'UTR|PIAS2_	NM_004671	NP_004662	O75928	PIAS2_HUMAN	PINIT.	4	TAGGCGGTGGT	0.398	
+	2	1024	HC2_uc002lio.2_	NM_017742	NP_060212	Q9C0B9	ZCHC2_HUMAN		2	TTACCGTGGCA	0.418	
-	2	2804		NM_032160	NP_115536	Q8IZU8	DSEL_HUMAN		6	GTTGACCTTCC	0.493	
+	6	787	p.G125S|CNDP2_	NM_018235	NP_060705	Q96KP4	CNDP2_HUMAN		3	CCTACGGCCTC	0.483	
-	5	685	_p.R217*|PPAP2C	NM_003712	NP_003703	O43688	LPP2_HUMAN		1	GGGTCGCAGCA	0.612	
+	4	1194	wn.3_Missense_M	NM_152791	NP_690004	Q8NEP9	ZN555_HUMAN	2H2-type 8.	1	CCTACGAATGC	0.453	
-	3	250	_p.A65T|PIP5K1	NM_012398	NP_036530	O60331	PI51C_HUMAN		4	GGATGCGTCCA	0.617	
-	29	38320	16_uc010xki.1_5'	NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	tracellular (Potential).	57	GATGGTGAAGT	0.498	
-	1	136		NM_001005192	NP_001005192	Q8NGA0	OR7G1_HUMAN	Name=1; (Potential).	2	CAGGAGAATGA	0.493	
-	2	339	02mog.1_Missens	NM_007065	NP_008996	Q16543	CDC37_HUMAN		0	GCCCTCGGCCA	0.652	
-	2	595	nrx.1_Missense_M	NM_001420	NP_001411	Q14576	ELAV3_HUMAN	RRM 1.	3	TGTCCCGAACC	0.562	
-	5	909	on_p.P259S|ECSI	NM_016581	NP_057665	Q9BQ95	ECSIT_HUMAN		1	GGGGGGATCTG	0.582	rs139421495
+	2	253		NR_027049					0	CCAGACGAGTG	0.473	
+	19	2301		NM_014975	NP_055790	Q9Y2H9	MAST1_HUMAN		7	AGCACGAGCCC	0.657	
-	19	2717	R2_uc002mzr.1_	NM_013447	NP_038475	Q9UHX3	EMR2_HUMAN	Name=6; (Potential).	4	CAGCCGGACCC	0.572	
+	5	848	_p.R115W|YJEF	NM_015965	NP_057049	Q9P0J0	NDUAD_HUMAN		0	TCTCCCGGAAG	0.517	
+	17	1903	A576V|DPY19L3_	NM_207325	NP_997208	Q6ZPD9	D19L3_HUMAN		4	GTTTGCGGGAA	0.488	
+	5	304	yf.1_Missense_Mu	NM_022006	NP_071289	P58549	FXYD7_HUMAN		0	CTTCAGGTGAG	0.542	

+	4	456	e_Mutation_p.G14	NM_174905	NP_777565	Q17RN3	FA98C_HUMAN		1	TGAAGGGGTAG	0.632	
+	7	615	_p.A142T|SUPT5H	NM_001111020	NP_001104490	O00267	SPT5H_HUMAN		4	AAATACGCCAAG	0.582	
-	2	535	0xwd.1_Splice_Si	NM_001817	NP_001808	O75871	CEAM4_HUMAN		0	ACTCACGGTGT	0.547	
-	4	1182	d.3_Missense_Mu	NM_006494	NP_006485	P50548	ERF_HUMAN		4	CTGGGGCTGGG	0.657	
-	9	2880	uc010eif.1_Intron	NM_005357	NP_005348	Q05469	LIPS_HUMAN		2	AATCCGTGCCC	0.617	
+	5	1145	284_uc010ejd.2_	NM_013361	NP_037493	Q9UK11	ZN223_HUMAN	2H2-type 5.	1	GCTTCCGTCTT	0.443	
+	4	1083	p.A262T|PVR_uc	NM_006505	NP_006496	P15151	PVR_HUMAN	otential).|Ig-like C2-type 2.	0	ATGAGGCCACC	0.448	
-	17	2643	_p.M287I|PRKD2_	NM_001079881	NP_001073350	Q9BZL6	KPCD2_HUMAN	rotein kinase.	7	GGGTACATGAA	0.637	
-	12	2942		NM_001080434	NP_001073903				6	TCTCGGGGGAC	0.652	
-	7	772	p.V240M|IL4I1_uc	NM_152899	NP_690863	Q96RQ9	OXLA_HUMAN		3	CATCACGTCTC	0.587	
+	4	331		NM_033068	NP_149059	Q9BZG2	PPAT_HUMAN	ellular (Potential).	0	TTGACCGCACG	0.682	
-	5	637		NM_022046	NP_071329	Q9P0G3	KLK14_HUMAN	eptidase S1.	1	CCTCCCGATCC	0.652	
+	4	1000	218Y|SIGLEC7_	NM_014385	NP_055200	Q9Y286	SIGL7_HUMAN	2.|Extracellular (Potential).	1	AAGTGCACCTG	0.587	
-	3	590	EC6_uc010ydc.1_	NM_001245	NP_001236	O43699	SIGL6_HUMAN	ellular (Potential).	1	TCAGGGCTGGT	0.622	
+	2	344		NM_002030	NP_002021	P25089	FPR3_HUMAN	lasmic (Potential).	6	GATTCCGGATG	0.542	
+	7	1279	pzi.2_Missense_M	NM_032423	NP_115799	Q3MIS6	ZN528_HUMAN	2H2-type 3.	2	AGCTTGCACAA	0.368	
-	3	663		NM_198457	NP_940859	Q6ZNG1	ZN600_HUMAN		0	GAAATTCTTTGG	0.388	
-	4	1042	2qah.2_Missense	NM_207333	NP_997216	A2RRD8	ZN320_HUMAN	2H2-type 5.	0	AATTTCGAGCG	0.423	
-	4	603	|LILRB2_uc002qf	NM_005874	NP_005865	Q8N423	LIRB2_HUMAN	otential).|Ig-like C2-type 2.	1	CACCAGGGGGT	0.612	
-	7	1009	ff.2_Missense_Mu	NM_021250	NP_067073	A6NI73	LIRA5_HUMAN	lasmic (Potential).	1	TCCAGCTGCAG	0.537	
+	4	508	_p.T140I|LILRA2_	NM_001130917	NP_001124389	Q8N149	LIRA2_HUMAN	otential).|Ig-like C2-type 2.	1	CGTGACCCTCC	0.557	
+	3	142	8_uc010yga.1_Mis	NM_000991	NP_000982	P46779	RL28_HUMAN		0	TGAAGGCCCGC	0.597	rs147614077
-	2	384	256_uc010euj.2_I	NM_005773	NP_005764	Q9Y2P7	ZN256_HUMAN	KRAB.	2	AGGTTGTAAGT	0.522	
+	4	275	135_uc002qrf.2_M	NM_003436	NP_003427	B4DHH9	B4DHH9_HUMAN		1	GAAGCCGAATG	0.582	
+	3	1247	cw.2_Missense_M	NM_002252	NP_002243	Q9BQ31	KCNS3_HUMAN	=Segment S3; (Potential).	4	TTCCCTTCTATG	0.498	
+	12	1269		NM_001080473	NP_001073942	A6NFX1	MFS2B_HUMAN	ical; (Potential).	2	TCCTACGTCTTC	0.607	
-	12	4254	gt.1_Missense_Mu	NM_018263	NP_060733	Q76L83	ASXL2_HUMAN		1	TGGTACAGCAG	0.498	
+	2	260		NM_001105519	NP_001098989	A6NJV1	CB070_HUMAN		1	CGCCAGCACCC	0.592	
+	5	731	u.2_RNA|ABHD1_	NM_032604	NP_115993	Q96SE0	ABHD1_HUMAN		0	AGCATCGTTATC	0.522	rs138157315
+	1	4967	1_5'Flank|ZNF512	NM_032266	NP_115642	Q68DN1	CB016_HUMAN	dem repeat of P-S-E-R-S-H	1	CCATCGCGGTC	0.572	
-	23	3624	j.3_Nonsense_Mu	NM_005633	NP_005624	Q07889	SOS1_HUMAN		10	ATATCGTGGTG	0.443	
-	3	441		NM_017880	NP_060350	Q9NWW7	CB042_HUMAN		0	GTCCCCGGGTT	0.488	
+	3	2628		NM_001080474	NP_001073943	A6NCI8	CB078_HUMAN		2	TCTCCGGTCAC	0.512	
-	4	1964	rt.1_Nonsense_M	NM_006302	NP_006293	Q13724	MOGS_HUMAN	enal (Potential).	0	ACATCGCAGGT	0.632	
-	2	1478	DC142_uc002slo	NM_032779	NP_116168	Q17RM4	CC142_HUMAN		1	TAAGCGACTGA	0.537	
-	1	742		NM_000682	NP_000673	P18089	ADA2B_HUMAN	smic (By similarity).	3	GTGTCCGTTGA	0.647	
+	4	566	se_Mutation_p.T1	NM_003855	NP_003846	Q13478	IL18R_HUMAN	2.|Extracellular (Potential).	3	GATAACCTGTG	0.279	rs34216045
+	15	3774	kp.2_Missense_M	NM_019014	NP_061887	Q9H9Y6	RPA2_HUMAN		1	TCGGTCGGTAG	0.512	
-	4	516		NM_001009993	NP_001009993	A1KXE4	F168B_HUMAN		0	CATACGGGCTC	0.617	
+	4	479	wz.2_RNA|LYPD6_	NM_194317	NP_919298	Q86Y78	LYPD6_HUMAN	UPAR/Ly6.	0	CAAACGCTGTG	0.478	
-	6	1674	cf.1_Missense_Mu	NM_006186	NP_006177	P43354	NR4A2_HUMAN	-binding (Potential).	3	GCCCCGGATGA	0.502	
-	3	586		NM_018086	NP_060556	Q5HY92	FIGN_HUMAN		4	TGTCCGAATAG	0.463	
+	18	2264	.A598V|OSBPL6_	NM_032523	NP_115912	Q9BZF3	OSBL6_HUMAN		1	CGTTGCCGCAT	0.438	
-	44	10527	.1_Missense_Mut	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	TTTACCTTCCAG	0.378	
-	28	6232	TN_uc010zfj.1_Mi	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	TTCTGCGCTTG	0.443	
-	51	4155	frx.2_Missense_M	NM_000393	NP_000384	P05997	CO5A2_HUMAN	lar collagen NC1.	2	CGTGCGGGCTG	0.498	
-	25	2576	_p.N647S|PGAP1	NM_024989	NP_079265	Q75T13	PGAP1_HUMAN	ical; (Potential).	4	GTAAGTTAATCA	0.353	

+	2	1192		NM_153689	NP_710156	Q8N8R5	CB069_HUMAN		1	CAAGTACGTGAT	0.388	
+	23	3749	sense_Mutation_p.	NM_152526	NP_689739	Q8TEW8	PAR3L_HUMAN		4	GCCCCGTGGGG	0.627	
-	6	411	l_uc010fvj.1_Miss	NM_022648	NP_072174	Q9HBL0	TENS1_HUMAN	hatase tensin-type.	4	GGTCCGGCTCA	0.582	
+	17	3393	k.2_Missense_Mut	NM_014640	NP_055455	Q14679	TTLL4_HUMAN		3	ATGTTCGGATTC	0.483	
+	3	233	p.G53S|STK11IP_	NM_052902	NP_443134	Q8N1F8	S11IP_HUMAN		1	CCATGGGGCCCT	0.577	
+	23	2859	F2_uc002vth.3_M	NM_015575	NP_056390	Q6Y7W6	PERQ2_HUMAN	n-rich.|Glu-rich.	7	GTTACGCAAACA	0.403	
+	8	842	e_Mutation_p.S144	NM_152879	NP_690618	Q16760	DGKD_HUMAN	l-ester/DAG-type 2.	5	ACACATCGTGTA	0.552	
+	4	1549	p.E386Q|SH3BP4	NM_014521	NP_055336	Q9P0V3	SH3B4_HUMAN		4	AACCTGGAGGTG	0.537	
-	4	1702	vbs.2_Missense_M	NM_015963	NP_057047	Q8WY91	THAP4_HUMAN		0	CACCTTGTTGGT	0.627	
+	4	1048	p.V230M|SIRPA_u	NM_001040022	NP_001035111	P78324	SHPS1_HUMAN	1.|Extracellular (Potential).	1	GCGAGGTGGCC	0.612	
+	4	1057	_p.V233I|SIRPA_u	NM_001040022	NP_001035111	P78324	SHPS1_HUMAN	1.|Extracellular (Potential).	1	GCCCACGTCACC	0.617	
+	9	1199		NM_003245	NP_003236	Q08188	TGM3_HUMAN		9	AGTGCGGCCCC	0.592	
+	21	2081	PS16_uc002whd.2	NM_022575	NP_072097	Q9H269	VPS16_HUMAN		4	CCTACGGCTGC	0.587	
-	3	3341	2wib.1_Missense_	NM_014731	NP_055546	O60299	PRIP1_HUMAN		1	GTGGGCGTGCTT	0.652	
-	2	176		NR_003678					0	GCCTCCAAATG	0.373	rs76611503
-	20	2927	L1_uc002xgj.1_Mi	NM_002895	NP_002886	P28749	RBL1_HUMAN		10	CCAAGTCGTATT	0.323	
+	3	465	38*|WISP2_uc002	NM_003881	NP_003872	O76076	WISP2_HUMAN	FBP N-terminal.	1	CTCCCCGATGC	0.667	
+	13	1733	02xmw.2_Missense	NM_001124756	NP_001118228	Q4VXU2	PAP1L_HUMAN	PABC.	1	GGGAGCGTCTC	0.572	
-	9	924	p.1_Missense_Mu	NM_006227	NP_006218	P55058	PLTP_HUMAN		1	CGCCCGGAAGT	0.602	
+	2	922	yfk.2_Missense_M	NM_024059	NP_076964	Q9BVV2	CT195_HUMAN		0	CCAACCGATCCT	0.647	
+	5	1179	l_Missense_Mutat	NM_032527	NP_115916	Q8N5A5	ZGPAT_HUMAN	G-patch.	0	ACACGCGAGGTA	0.602	
-	13	2171		NM_020713	NP_065764	Q96KM6	Z512B_HUMAN		0	TGGTCCAGTCG	0.711	
+	16	2816	EY2_uc011aeb.1_	NM_005128	NP_005119	Q9Y3R5	DOP2_HUMAN		2	ATCTGCGAGGAC	0.607	
+	6	973	ywl.2_Missense_M	NM_001396	NP_001387	Q13627	DYR1A_HUMAN	rotein kinase.	4	CCCAAACGCAGT	0.383	
-	8	2083		NM_020639	NP_065690	P57078	RIPK4_HUMAN		7	GTTGCGGGCAG	0.687	
-	15	1669	w.3_Missense_Mu	NM_000071	NP_000062	P35520	CBS_HUMAN	CBS.	0	CTGACGGCTGC	0.577	
+	9	955	p.D138N|RRP1_u	NM_003683	NP_003674	P56182	RRP1_HUMAN		0	GTGACGACAGG	0.637	
+	4	1334	RB1_uc002zgt.2_	NM_015833	NP_056648	P78563	RED1_HUMAN		1	CTTGCACTTGG	0.557	
+	38	4843	P2A_uc002zjs.2_	NM_015151	NP_055966	Q14689	DIP2A_HUMAN		2	ACCTGCGGGAC	0.632	
+	7	724	1_RNA|SEPT5_uc	NM_002688	NP_002679	Q99719	SEPT5_HUMAN		1	GATCCGGAAGC	0.602	
+	9	903	1_RNA|SEPT5_uc	NM_002688	NP_002679	Q99719	SEPT5_HUMAN		1	AGCGGGTCCGG	0.682	
-	5	763	p.D110N|TOP3B_	NM_003935	NP_003926	O95985	TOP3B_HUMAN	Toprim.	1	GTAGTCGCAGC	0.597	
+	43	7532	D18B_uc011aka.1_	NM_032608	NP_115997	Q8IUG5	MY18B_HUMAN		12	GGAAACTCCCA	0.567	
+	8	1130	se_Mutation_p.R21	NM_005243	NP_005234	Q01844	EWS_HUMAN	em repeats.|EAD (Gln/Pro/	3254	TCATTCCGACAG	0.517	
+	2	209		NM_182527	NP_872333	Q86V35	CABP7_HUMAN	ntial).|1 (Potential).|EF-han	0	TTGACCGTGAC	0.597	
+	15	1205	EPDC5_uc003alt.2	NM_014662	NP_055477	O75140	DEPD5_HUMAN		8	ACCAAGCAGCGG	0.512	
-	1	355	EP3_uc011aoy.1_	NM_145174	NP_660157	Q7Z6W7	DNJB7_HUMAN		1	CACCTCCGTTTA	0.363	
-	3	361	22orf9_uc003bfw.	NM_001009880	NP_001009880	Q6ICG6	K0930_HUMAN		0	CCAGTCGATGT	0.642	
+	3	358	had.2_Missense_	NM_015124	NP_055939	Q6IC98	GRAM4_HUMAN	Potential.	1	CCAACGCGGAG	0.652	
-	6	2663	p.D775N|BRD1_u	NM_014577	NP_055392	O95696	BRD1_HUMAN		1	GAGGTCGAGCA	0.592	
+	2	258	.3_RNA|NCAPH2_	NM_152299	NP_689512	Q6IBW4	CNDH2_HUMAN		2	TTGACGAAGGC	0.537	
-	16	2194	e_Mutation_p.L64	NM_001145137	NP_001138609	Q92523	CPT1B_HUMAN	lasmic (Potential).	2	CCGAGAGCACCT	0.617	
+	43	6127	R1_uc011asu.1_I	NM_001099952	NP_001093422	Q14643	ITPR1_HUMAN	lasmic (Potential).	21	ATCATGCAGCCC	0.647	
+	7	1701	e_Mutation_p.R47	NM_000844	NP_000835	Q14831	GRM7_HUMAN	cellular (Potential).	7	CTGGGCGTTATG	0.463	
-	6	978	OL1_uc003cbx.2_	NM_001012410	NP_001012410	Q5FBB7	SGOL1_HUMAN		0	GTAAACGTTCCTG	0.269	rs148005116
+	4	1550	en.2_Missense_M	NM_003242	NP_003233	P37173	TGFR2_HUMAN	.|Cytoplasmic (Potential).	26	AGAACGACCTA	0.552	
-	18	2221	axu.1_Missense_	NM_015097	NP_055912	B2RTR1	B2RTR1_HUMAN		4	TTCGCACAGACT	0.522	

-	12	4389		NM_014831	NP_055646	O15050	TRNK1_HUMAN			2	CCTGTTCAGCA	0.547	
+	36	5047	_p.Q1679*|DLEC1_	NM_007335	NP_031361	Q9Y238	DLEC1_HUMAN			9	GCCAGCAGGAG	0.617	
+	2	185	u.1_Missense_Mut	NM_020839	NP_065890	Q8TAF3	WDR48_HUMAN	WD 1.		2	GGAGTGTCAATC	0.413	
+	12	1220	NKTR_uc003clq.1_	NM_005385	NP_005376	P30414	NKTR_HUMAN			3	ATGACAGCAGTG	0.388	
+	50	7837	0hjn.1_Missense_M	NM_015175	NP_055990	Q6ZNJ1	NBEL2_HUMAN	WD 4.		1	GCATGGGGCTG	0.587	rs144664865
-	1	2272	cuf.1_Missense_M	NM_001407	NP_001398	Q9NYQ7	CELR3_HUMAN	r (Potential).|Cadherin 4.		11	AAGGGAGCATTT	0.517	
+	5	1049	5'Flank|MIR191_hs	NM_199069	NP_951032	Q9BU61	NDUF3_HUMAN			0	GCCAAGCTGCTC	0.522	
-	4	1600_1601	p.Q435P|QRICH1	NM_198880	NP_942581	Q2TAL8	QRIC1_HUMAN	Gln-rich.		1	ctgctgctgctgtggtggt	0.361	
+	4	528	yl.2_Missense_Mu	NM_144499	NP_653082	P11488	GNAT1_HUMAN			3	TTGAGCGCGCC	0.478	
-	21	2333	.G561E|ITIH4_uc	NM_002218	NP_002209	Q14624	ITIH4_HUMAN			3	CAACCCCTGGG	0.602	
+	12	2348	nv.2_Missense_M	NM_000333	NP_000324	O15265	ATX7_HUMAN			0	GCCACCGTCTCT	0.537	
-	22	3100		NM_020872	NP_065923	Q9P232	CNTN3_HUMAN			5	ACATTCGAGATG	0.338	
-	2	610	dzg.2_Missense_M	NM_199512	NP_955806	Q76M96	CCD80_HUMAN			2	GGGAAACGCAAC	0.582	
+	9	1556		NM_020754	NP_065805	Q2M1Z3	RHG31_HUMAN			2	ACTATCCGACCA	0.383	
+	12	4208		NM_020754	NP_065805	Q2M1Z3	RHG31_HUMAN			2	AATGGGGTTCAG	0.587	
-	13	3686	.R1153H|GOLGB1	NM_004487	NP_004478	Q14789	GOGB1_HUMAN	ic (Potential).|Potential.		10	CCTTGCGGGAG	0.413	rs146898283
-	14	2115	MA5B_uc003egb.	NM_001031702	NP_001026872	Q9P283	SEM5B_HUMAN	cellular (Potential).		7	ACATTCCGCACC	0.562	
-	8	1056	egb.1_Missense_M	NM_001031702	NP_001026872	Q9P283	SEM5B_HUMAN	ular (Potential).|Sema.		7	ATGACCGTGGCT	0.592	
-	3	1247	TL2_uc003eqh.1_M	NM_016201	NP_057285	Q9Y2J4	AMOL2_HUMAN	Potential.		1	TCTCCCTCAGC	0.662	
+	14	2673	GEF_uc011boi.1_	NM_015595	NP_056410	Q96DR7	ARHGQ_HUMAN	SH3.		1	TCAACGTGTCA	0.527	
+	22	4135	3gee.3_RNA|WHS	NM_001042424	NP_001035889	O96028	NSD2_HUMAN			9	CGGGCGGTCCT	0.612	
+	2	549	.E32K|GRK4_uc0	NM_182982	NP_892027	P32298	GRK4_HUMAN	N-terminal.		1	GGAAGGAGATA	0.403	
+	17	2688	1_RNA|CRMP1_u	NM_153717	NP_714928	P57679	EVC_HUMAN			2	CCCTTCGTCGG	0.552	
-	14	1520	07_splice|ABLIM2_	NM_001130084	NP_001123556	Q6H8Q1	ABLM2_HUMAN			3	GCATTACCTTCC	0.493	
-	3	2171		NM_053042	NP_444270	Q9C0D4	Z518B_HUMAN			4	TTACAGGAATATT	0.423	
-	12	1940	qn.1_Missense_M	NM_145290	NP_660333	Q8IWK6	GP125_HUMAN	cellular (Potential).		1	GAACACGGTAC	0.468	
-	3	703		NM_001358	NP_001349	O43143	DHX15_HUMAN	ase ATP-binding.		1	ATGATCGCATGT	0.418	
-	4	1814	3M47_uc011bys.1_	NM_001098634	NP_001092104	A0AV96	RBM47_HUMAN			3	TCCCTGTTGGG	0.637	
-	3	714	3haf.3_Missense_M	NM_001126328	NP_001119800	Q8TBB1	LNX1_HUMAN			4	GGCTCGCACAG	0.597	
+	13	970		NM_016519	NP_057603	Q9NP70	AMBN_HUMAN			4	GCTATGGGCGGT	0.592	
+	11	1366	A4_uc003hgc.3_Mi	NM_001098484	NP_001091954	Q9Y6R1	S4A4_HUMAN	lasmic (Potential).		5	ATGAATGGGGAT	0.443	
+	55	8445		NM_025074	NP_079350	Q86XX4	FRAS1_HUMAN	(Potential).|Calx-beta 2.		5	TCAACGATACCG	0.448	
+	7	1168	C5_uc011cdm.1_5'	NM_016323	NP_057407	Q9UII4	HERC5_HUMAN	RCC1 5.		9	CTGATGCCGCTT	0.398	
+	3	3267	ET2_uc010ilp.1_Mi	NM_001127208	NP_001120680	Q6N021	TET2_HUMAN	Gln-rich.	p.E961*(1)	733	AGCAAGAACAG	0.512	
+	27	3994	1109_uc010ins.1_	NM_015312	NP_056127	Q2LD37	K1109_HUMAN			12	CCACCCGTCTT	0.463	
-	12	1600	se_Mutation_p.S4	NM_031956	NP_114162	Q8NA56	TTC29_HUMAN			0	CGTTCTGAGTTT	0.308	
-	11	1346		NM_004564	NP_004555	O75879	GATB_HUMAN			0	GTGACAGGACTG	0.502	
-	13	1342	nz.2_Missense_Mu	NM_002669	NP_002660	O43660	PLRG1_HUMAN	WD 6.		0	ATACAAGCACTC	0.294	
-	3	572		NM_144644	NP_653245	Q8NEY3	SPAT4_HUMAN			0	ACTCTCGATGTG	0.279	rs144504100
-	5	4020		NM_005245	NP_005236	Q14517	FAT1_HUMAN	(Potential).|Cadherin 11.		12	CTTGTCGGTGG	0.498	
-	4	628		NM_024830	NP_079106	Q8NF37	PCAT1_HUMAN	nenal (Potential).		2	CAGGCCGTATAT	0.577	
-	2	316	FS6_uc003jcy.2_5'	NM_032479	NP_115868	Q9P0J6	RM36_HUMAN			0	GACCCCGCCTCT	0.557	
+	5	744	_p.R173*|DNAJC2	NM_001012339	NP_001012339	Q5F1R6	DJC21_HUMAN			2	ATACACGACAG	0.413	rs150576702
+	10	3303	p.P935L|NIPBL_u	NM_133433	NP_597677	Q6KC79	NIPBL_HUMAN			9	CACACCCTGACA	0.373	
+	13	2009	M_uc003jle.1_Spl	NM_152403	NP_689616	Q63HQ2	EGFLA_HUMAN			7	GTATTTAGGGGA	0.507	
+	28	3604	_Mutation_p.R110	NM_015183	NP_055998	O15021	MAST4_HUMAN			13	AAGGCGAAAGT	0.692	
+	5	817	cy.1_Missense_M	NM_001080479	NP_001073948	Q8N1W1	RGNEF_HUMAN			0	TCTTCCGGAAAT	0.433	

-	5	751	splice|DMGDH_uc	NM_013391	NP_037523	Q9UI17	M2GD_HUMAN		4	GCTTACCTGCA	0.403	
+	2	2213		NM_005654	NP_005645	P10589	COT1_HUMAN		3	CCAACGGGAC	0.607	
+	20	1576	Missense_Mutatio	NM_001042443	NP_001035908	P20810	ICAL_HUMAN	bitory domain 3.	5	TTGGTGAAAAA	0.328	
-	13	2000		NM_001270	NP_001261	O14646	CHD1_HUMAN	ase ATP-binding.	5	TAATCGGTGTG	0.338	
+	18	2558	e.2_Missense_M	NM_015216	NP_056031	O43314	VIP2_HUMAN		2	ACATCGAATGG	0.284	
+	16	2068	R36_uc010jbu.2_	NM_139281	NP_644810	Q8NI36	WDR36_HUMAN	WD 8.	2	GGGACCTTCCT	0.313	
-	2	410	nse_Mutation_p.N	NM_001182	NP_001173	P49419	AL7A1_HUMAN		3	CGTTGTTAGCA	0.313	
+	16	2554	ense_Mutation_p.	NM_001046	NP_001037	P55011	S12A2_HUMAN	ellular (Potential).	3	AGGTGCTCCAA	0.343	
+	4	1150	uz.2_Missense_	NM_014031	NP_054750	Q9Y2P4	S27A6_HUMAN		0	CTTTTGGTTGT	0.418	
-	1	33		NM_000879	NP_000870	P05113	IL5_HUMAN		0	GAAACGTTCTG	0.438	
+	3	1278	y.1_RNA|TXNDC1	NM_024715	NP_078991	Q96J42	TXD15_HUMAN	(Potential).| p.G207S(1)	2	AAACGGTAGTG	0.448	
-	12	1804	e_Mutation_p.R37	NM_017415	NP_059111	Q9UH77	KLHL3_HUMAN	Kelch 4.	0	CTGGCGGGAAG	0.557	
+	12	1875	yo.1_Missense_M	NM_005733	NP_005724	O95235	KI20A_HUMAN	inesin-motor.	0	CTTCCGTGACA	0.502	
-	2	430	lcs.1_Missense_	NM_001790	NP_001781	P30307	MPIP3_HUMAN		3	CCAAGAAATTTG	0.388	
+	6	1347		NM_032289	NP_115665	Q9BQI7	PSD2_HUMAN	SEC7.	1	AGAGCGTGAGC	0.587	
+	8	1037	p.C130Y|HARS2_	NM_012208	NP_036340	P49590	SYHM_HUMAN		0	CCAGTGTCATG	0.463	
+	1	2125		NM_018935	NP_061758	Q9Y5E8	PCDBF_HUMAN	ical; (Potential).	5	TGTTCGTGGCA	0.682	
-	3	1326	p.N403K|PCDH1_	NM_002587	NP_002578	Q08174	PCDH1_HUMAN	(Potential).|Cadherin 4.	5	GAGATGTTAGC	0.567	
-	18	1564	_p.R471Q|ANXA6	NM_001155	NP_001146	P08133	ANXA6_HUMAN	Annexin 6.	0	TGGCCCGGATT	0.562	
-	9	1067	_Silent_p.L39L|C5	NM_032385	NP_115761	Q96IV6	CE004_HUMAN		1	TGTCAGTCCCA	0.592	
-	3	625	jii.2_Missense_Mu	NM_138379	NP_612388	Q96H15	TIMD4_HUMAN	ar (Potential).|Thr-rich.	2	GAAGACGGCAA	0.547	
-	31	3949	.2_Nonsense_Mu	NM_003062	NP_003053	O75094	SLIT3_HUMAN	aminin G-like.	4	GGGTCGGACCT	0.607	rs141058025
+	2	170	2A3_uc011dkm.1_RNA						0	CACTACGTTAC	0.547	
-	18	1568	p.W480L|BAT5_uc	NM_021160	NP_066983	O95870	ABHGA_HUMAN		0	CGCTCCAGGGG	0.602	
+	9	923	L8_uc003oac.1_	NM_030652	NP_085155	Q99944	EGFL8_HUMAN		0	GCCTCGGCGTC	0.552	
+	9	1033	se_Mutation_p.C2	NM_024165	NP_077084	O43189	PHF1_HUMAN		0	TTGCTGTAAGA	0.468	
+	15	1898	p.R630H|SCUBE	NM_152753	NP_689966	Q8IX30	SCUB3_HUMAN		1	GCACCGTGCTG	0.632	
-	3	340	BP5_uc003oky.2_	NM_001145776	NP_001139248	Q13451	FKBP5_HUMAN	se FKBP-type 1.	1	TCGGCGTTTCC	0.338	
-	6	906	EML1_uc011dud.	NM_178174	NP_835468	Q86YW5	TRML1_HUMAN	lasmic (Potential).	1	CCCTCCCGGGA	0.537	
-	4	1419	318_uc003ouw.2_	NM_014345	NP_055160	Q5VUA4	ZN318_HUMAN		7	TTGCCCTGAGG	0.483	
+	5	762	_p.R171C|SLC25	NM_004277	NP_004268	O95847	UCP4_HUMAN	Solcar 2.	0	GATTTCGTGGT	0.388	
-	2	932		NM_014452	NP_055267	O75509	TNR21_HUMAN	(Potential).|TNFR-Cys 3.	0	ACACCGCACAT	0.542	
+	3	446		NM_002190	NP_002181	Q16552	IL17_HUMAN		0	CTTCCGGCTGG	0.597	rs147810050
-	10	1593	u.1_Missense_Mu	NM_002388	NP_002379	P25205	MCM3_HUMAN	MCM.	3	CTCCCGATCCT	0.498	rs148636199
-	14	1173	ite_p.R196_splice	NM_020320	NP_064716	Q5T160	SYRM_HUMAN		3	GCACCTAAAAG	0.413	
-	1	1	_uc003qab.1_Spli	NM_016063	NP_057147	Q7Z4H3	HDDC2_HUMAN		0	ccccacttccgctttctc	0	
-	4	794	bt.1_Missense_Mu	NM_001010923	NP_001010923	Q8N1K5	THMS1_HUMAN	CABIT 1.	4	GAGTTTGATGAT	0.388	
+	59	8503	ense_Mutation_p.	NM_000426	NP_000417	P24043	LAMA2_HUMAN	minin G-like 4.	10	AATCCGGCTTG	0.413	
+	8	937	B_uc003qgr.2_Mis	NM_018945	NP_061818	Q9NP56	PDE7B_HUMAN	ytic (By similarity).	1	CAGCAGCACAC	0.478	
+	2	641		NM_016217	NP_057301	Q9UBI9	HDC_HUMAN		0	GTGCAACAACG	0.612	
+	3	637		NM_025218	NP_079494	Q9BZM6	N2DL1_HUMAN	lass I alpha-2 like.	1	TTTTTGATGTAC	0.408	
+	18	2124	nse_Mutation_p.T	NM_015440	NP_056255	Q6UB35	C1TM_HUMAN	hydrofolate synthetase.	4	CCTGACGGACA	0.597	rs143492706
+	17	2483		NM_000876	NP_000867	P11717	MPRI_HUMAN	menal (Potential).	3	AGTACGACCTC	0.577	
+	10	2052	sjb.2_Missense_	NM_017802	NP_060272	Q86Y56	HEAT2_HUMAN		1	CTGCCGTGTCC	0.692	
+	2	464	PR146_uc003sjx.	NM_138445	NP_612454	Q96CH1	GP146_HUMAN	lasmic (Potential).	1	ACATCGAGCGT	0.642	
+	2	871	md.2_Missense_	NM_018641	NP_061111	Q9NRB3	CHSTC_HUMAN	larity).|Lumenal (Potential).	1	TGCGCGACCCC	0.602	
+	6	937	g.2_Missense_Mu	NM_001040167	NP_001035257	Q8NES3	LFNG_HUMAN	enal (Potential).	0	CATCCGCAGCG	0.667	

-	10	1275	p.H376Y|EIF2AK1	NM_014413	NP_055228	Q9BQI3	E2AK1_HUMAN	rotein kinase.		4	CAGGTGGTACT	0.443	
-	2	402	Mutation_p.R86C|E	NM_014413	NP_055228	Q9BQI3	E2AK1_HUMAN			4	TGAACGAAGTG	0.348	
-	9	1514	se_Mutation_p.E2	NM_004956	NP_004947	P50549	ETV1_HUMAN			35	TGGGTTCCTGTT	0.493	
-	13	1762	swf.2_Missense_M	NM_006547	NP_006538	O00425	IF2B3_HUMAN	KH 4.		2	TGCCAGCAGCA	0.413	
+	11	1462	L9_uc010kwj.1_M	NM_015060	NP_055875	Q8NBF6	AVL9_HUMAN			0	TTTTTCGACAAC	0.453	rs145306409
-	3	771	p.V100M|GCK_uc	NM_000162	NP_000153	P35557	HXK4_HUMAN			4	CTTCACGCTCC	0.627	
-	5	521	MK2B_uc003tku.	NM_001220	NP_001211	Q13554	KCC2B_HUMAN	rotein kinase.		2	TCTCTCGCCACA	0.542	
+	11	1791	3tvz.2_Missense_	NM_022479	NP_071924	Q6IS24	GLTL3_HUMAN	enal (Potential).		7	CTCCATCAAGTA	0.652	
-	6	690	p.R217Q|SEMA3D	NM_152754	NP_689967	O95025	SEM3D_HUMAN	Sema.		5	GGGATCGAGTG	0.408	
-	8	939	N2_uc010lfk.2_R	NM_000305	NP_000296	Q15165	PON2_HUMAN			0	GAAGGATCAATA	0.398	
+	3	476	I3_uc011kip.1_Int	NM_015379	NP_056194	O95415	BRI3_HUMAN			0	GCGACGATGCC	0.512	
+	7	2081	p.R653*|ZKSCAN	NM_145102	NP_659570	Q9Y2L8	ZKSC5_HUMAN	2H2-type 8.		1	ATCTTCGACTC	0.512	
-	2	668	.2_5'Flank|C7orf43	NM_018275	NP_060745	Q8WVR3	CG043_HUMAN			0	TCCCTGGGGGC	0.527	
-	2	557		NM_001004323	NP_001004323	Q8IZ16	CG061_HUMAN			0	TCCTCGGCAGC	0.632	
+	1	309	XO24_uc003uvl.1_	NM_033506	NP_277041	O75426	FBX24_HUMAN			4	AGGCGGTCCCT	0.582	
+	4	12489	C17_uc010lho.1_	NM_001040105	NP_001035194	Q685J3	MUC17_HUMAN	r (Potential).|EGF-like.		27	CCTCTCGCTGC	0.532	
-	8	845		NM_138403	NP_612412	Q9BUA6	MYL10_HUMAN	EF-hand 3.		2	CTCTTCACCGT	0.547	
+	9	1061	p.D257N|ASB15_	NM_080928	NP_563616	Q8WXK1	ASB15_HUMAN	ANK 5.		3	AATCCCGACTGC	0.522	
-	9	1615	0lly.1_Missense_M	NM_012470	NP_036602	Q9Y5L0	TNPO3_HUMAN			5	ACCCTATCAAG	0.413	
-	5	523	_p.R53*|ZC3HC1	NM_016478	NP_057562	Q86WB0	NIPA_HUMAN			0	AAATCGGTCTG	0.318	
-	15	1860		NM_004333	NP_004324	P15056	BRAF_HUMAN	rotein kinas	_R603>I(2)|p.T	18290	ATTTCACTGTA	0.368	
+	12	1345	N1_uc011ktc.1_In	NM_000083	NP_000074	P35523	CLCN1_HUMAN			5	TGATGCCCCGC	0.522	
+	3	301	PO_uc010lpl.1_Int	NM_198455	NP_940857	A2VEC9	SSPO_HUMAN	EMI.		0	GGGGCGCCCAC	0.627	
+	22	3136	y.1_Missense_Mu	NM_000603	NP_000594	P29474	NOS3_HUMAN	-binding FR-type.		8	ACCCAGCACCC	0.652	
+	4	648	p.A122V|SLC4A2	NM_003040	NP_003031	P04920	B3A2_HUMAN	ic (Potential).|Pro-rich.		0	TGAGGCCAGCG	0.697	
-	9	1390	_p.M423I|PTPRN	NM_002847	NP_002838	Q92932	PTPR2_HUMAN	ellular (Potential).		7	CTCTCCATGTCG	0.592	
-	4	1664		NM_178857	NP_849188	Q8IWN7	RP1L1_HUMAN			8	CACCCCGTCCT	0.692	
-	4	2904	ense_Mutation_p.	NM_001002814	NP_001002814	Q6WKZ4	RFIP1_HUMAN			3	TCAGATCGGCCA	0.448	rs146977784
+	3	947	1_uc003xmd.1_I	NM_006283	NP_006274	O75410	TACC1_HUMAN	ction with TDRD7.		1	CAGACGCCCTC	0.587	
+	6	577	1_uc003xnn.2_R	NM_002164	NP_002155	P14902	I23O1_HUMAN			2	TCATTTCGTGATG	0.358	
-	9	846	p.V179L|LYPLA1_	NM_006330	NP_006321	O75608	LYPA1_HUMAN			1	CTTGACATCCA	0.353	
+	3	3299		NM_004770	NP_004761	Q92953	KCNB2_HUMAN	lasmic (Potential).		7	TTATTGTCCCA	0.348	
-	5	491	h.1_Missense_Mu	NM_000971	NP_000962	P18124	RL7_HUMAN			0	ACCACGCTTGT	0.358	
-	3	1005	j.1_Missense_Mu	NM_005655	NP_005646	Q13118	KLF10_HUMAN			0	CAACAGGGTTG	0.587	
+	15	2582	_p.R795C|RIMS2_	NM_014677	NP_055492	Q9UQ26	RIMS2_HUMAN			15	GACATCGTGTC	0.393	
-	2	395	74_uc003ymx.2_	NM_153015	NP_694560	Q96NL1	TMM74_HUMAN		p.R97W(1)	4	CTTTCCGTTCC	0.502	
+	3	2122		NM_014943	NP_055758	Q9Y6X8	ZHX2_HUMAN			2	GACACGGTCGC	0.522	rs137944558
-	1	506		NM_001081675	NP_001075144	Q2WGJ6	KLH38_HUMAN	BACK.		0	AGGACGTCAGT	0.582	
+	2	273	GPR172A_uc003	NM_024531	NP_078807	Q9HAB3	RFT3_HUMAN			0	TGGTCAAAGAGC	0.647	
+	7	1364	K_uc011lno.1_Intr	NM_000459	NP_000450	Q02763	TIE2_HUMAN	Extracellular (Potential).		12	TTTACGGGCCA	0.473	
-	10	1286	U1_uc010mjp.1_I	NM_018225	NP_060695	Q2TAY7	SMU1_HUMAN	WD 5.		1	CTGCGGTGCTG	0.398	
+	8	882	T_uc003zvh.2_Mis	NM_000155	NP_000146	P07902	GALT_HUMAN			0	TGAGCGTGATG	0.617	rs111033831
-	2	709	se_Mutation_p.R5	NM_013390	NP_037522	Q9UHN6	TMEM2_HUMAN			2	TGCCCGGTCTT	0.468	
-	3	575	p.1_Missense_Mu	NM_015250	NP_056065	Q8TD16	BICD2_HUMAN	Potential.		1	CTTCCCGGAAT	0.562	
-	12	1803	orf5_uc004bdr.3_	NM_032012	NP_114401	Q9H330	CI005_HUMAN			1	CTGACGACTGA	0.323	
+	15	2444	kz.1_Missense_M	NM_007018	NP_008949	Q7Z7A1	CNTRL_HUMAN			0	TGGTTCGTCCA	0.413	rs149200288
+	9	1253	mf.1_Missense_M	NM_000962	NP_000953	P23219	PGH1_HUMAN			2	ATACCGCAACC	0.537	

+	8	864	vj.2_Missense_Mu	NM_014397	NP_055212	Q9HC98	NEK6_HUMAN	rotein kinase.	3	TGTACGAGGTG	0.587	
+	15	1668	_p.R401*|GARNL	NM_032293	NP_115669	Q5VVW2	GARL3_HUMAN		3	AATAGACGATCT	0.408	
+	7	1185	.2_Intron|C9orf117	NM_001012502	NP_001012520	Q5JU67	CI117_HUMAN		0	GCACCGCGATG	0.592	
-	17	1362	OLGA2_uc004bu	NM_004486	NP_004477	Q08379	GOGA2_HUMAN	ential.|Poly-Pro.	1	GGGGCGGGGGT	0.597	
-	5	713	mzn.2_Missense_	NM_005312	NP_005303	Q13905	RPGF1_HUMAN		7	CAGCACAGCCT	0.562	
+	4	464	bo.2_Nonsense_	NM_207417	NP_997300	Q6ZQR2	CI171_HUMAN		5	ACGCTGGAACG	0.647	
-	13	3980	.R1217Q|CAMSA	NM_015447	NP_056262	Q5T5Y3	CAMP1_HUMAN		3	GCACCCGGTCT	0.657	
-	26	4647	cia.1_Nonsense_	NM_017617	NP_060087	P46531	NOTC1_HUMAN	lar (Potential).|LNR 3.	856	CTGTTGCAGCC	0.706	
+	13	2069	orf86_uc004cjl.1_	NM_024718	NP_078994	Q3YEC7	PARF_HUMAN		0	CTGACGAGGAT	0.647	
-	17	2202	mfa.1_Intron|PNP	NM_152286	NP_689499	Q6ZV29	PLPL7_HUMAN	cNMP 3.	1	CAGAGCGCAGC	0.682	
+	7	1057	XD1_uc011mgx.1_	NM_018390	NP_060860	Q9NUJ7	PLCX1_HUMAN		0	TGTTCGTGGCC	0.612	
+	2	560	.P122S|SFRS17A_	NM_005088	NP_005079	Q02040	AK17A_HUMAN		0	ACTTCCCCACC	0.647	
-	9	1412	p.R334C|ARSE_u	NM_000047	NP_000038	P51690	ARSE_HUMAN		2	CACGCGGATCC	0.602	
+	11	1453	se_Mutation_p.D8	NM_015691	NP_056506	Q9ULE0	WWC3_HUMAN	Ser-rich.	4	CCTTCGACTCT	0.647	
+	6	847	p.P194Q|HCCS_u	NM_005333	NP_005324	P53701	CCHL_HUMAN		0	TTCACCAAGGG	0.448	
-	8	2449	HGAP6_uc004cu	NM_013427	NP_038286	O43182	RHG06_HUMAN	Rho-GAP.	2	GGAGAGGAACT	0.562	
+	5	725		NM_000531	NP_000522	P00480	OTC_HUMAN	rbamoyl phosphate bindin	2	CTATCCAGATC	0.393	
+	5	1492	N_uc010nho.1_Mi	NM_152869	NP_690608	Q15493	RGN_HUMAN		0	ACTCCGTGGAT	0.413	
+	4	504	dmu.2_Missense_	NM_024859	NP_079135	Q9H6Y5	MAGIX_HUMAN	PDZ.	0	TGGCCGTGCGC	0.632	
-	3	624	yo.2_Missense_M	NM_032803	NP_116192	Q8WY07	CTR3_HUMAN	ellular (Potential).	2	GGGCACGTGCA	0.552	
+	6	1696	zc.2_Missense_M	NM_018977	NP_061850	Q9NZ94	NLGN3_HUMAN	ellular (Potential).	1	CGGCTCGCCTA	0.562	
+	10	1801	nse_Mutation_p.R	NM_001145408	NP_001138880	Q15233	NONO_HUMAN	tential.|DBHS.	4	GATGCGGCGAC	0.517	
+	2	3355	efm.1_Missense_	NM_032968	NP_116750	Q9BZA7	PC11X_HUMAN	lasmic (Potential).	2	ATGTCGCCAGG	0.433	
-	11	3180	s.2_Missense_M	NM_001113490	NP_001106962	Q4VCS5	AMOT_HUMAN		1	AGAGTATTGGA	0.428	
-	1	439		NM_001145718	NP_001139190	P0C2W7	CT47B_HUMAN		0	CTCCCCGAGGC	0.697	
+	19	1944		NM_003399	NP_003390	O43895	XPP2_HUMAN		0	GATCCGTCTCG	0.542	
-	22	3127	R1007W|L1CAM_	NM_000425	NP_000416	P32004	L1CAM_HUMAN	tential).|Fibronectin type-III	9	TTCCCGTACGA	0.627	
-	13	2099	u.1_Missense_M	NM_001110556	NP_001104026	P21333	FLNA_HUMAN	Filamin 4.	6	CCTGCGATGGC	0.637	
+	10	919		NM_004699	NP_004690	Q14320	FA50A_HUMAN		1	ACGGGGGAAGA	0.642	
+	28	4881		NM_017514	NP_059984	P51805	PLXA3_HUMAN	lasmic (Potential).	3	CAGACGGTTCC	0.627	
-	3	189	001aeh.1_Intron|C	NM_017871	NP_060341	Q5TA45	INT11_HUMAN		0	GGAAGCGTCGC	0.617	
+	22	3926	CH2_uc001ajj.1_	NM_014638	NP_055453	O75038	PLCH2_HUMAN		5	CTGACGAACTG	0.687	
+	7	733	k.1_Missense_Mu	NM_002631	NP_002622	P52209	6PGD_HUMAN		1	AGGACGAGATG	0.562	
-	21	2602	lice_Site_p.K799_	NM_022089	NP_071372	Q9NQ11	AT132_HUMAN		4	CCTCACCTTAA	0.632	
+	6	1125	av.1_Missense_M	NM_032880	NP_116269	Q96ID5	IGS21_HUMAN		4	CCTCCCGTGGC	0.637	
-	37	4307	.R275C|MYOM3_	NM_152372	NP_689585	Q5VTT5	MYOM3_HUMAN	like C2-type 4.	3	CATGCGGTATC	0.542	
+	11	1428	L3_uc009vrc.2_S	NM_020448	NP_065181	Q6P499	NPAL3_HUMAN		0	GCCAGGTAAGG	0.473	
+	11	1671	p.D267Y|ADC_uc	NM_052998	NP_443724	Q96A70	ADC_HUMAN		2	CGGTTGATGGC	0.617	
-	31	4891	p.G1661E|CSMD2	NM_052896	NP_443128	Q7Z408	CSMD2_HUMAN	ar (Potential).|CUB 10.	12	ACTGTCCCCCA	0.547	
+	16	2758	yu.2_Missense_M	NM_005095	NP_005086	Q5VZL5	ZMYM4_HUMAN		5	ATTGGCAAGTG	0.423	
+	3	278		NM_024097	NP_077002	Q9BV19	CA050_HUMAN	Potential.	1	TCATCCGAGCA	0.358	rs150987262
-	3	676		NM_006516	NP_006507	P11166	GTR1_HUMAN	ellular (Potential).	5	ATAGCGGTGGA	0.597	
+	19	3119	q.2_Missense_Mu	NM_005424	NP_005415	P35590	TIE1_HUMAN	Potential).|Protein kinase.	7	AGGGGCGTCTC	0.582	rs144134618
+	2	844	lw.1_Missense_M	NM_018150	NP_060620	Q5VTB9	RN220_HUMAN		2	GCAAGGAATAT	0.517	
-	17	3570	se_Mutation_p.E1	NM_003035	NP_003026	Q15468	STIL_HUMAN		3	GTTCCTCTTCAT	0.393	
-	9	1754	u.1_RNA|C1orf16	NM_001004303	NP_001004303	Q5VWT5	CA168_HUMAN		5	CTCAGGGCAGG	0.463	
+	6	1087	5_splice|PGM1_u	NM_002633	NP_002624	P36871	PGM1_HUMAN		3	CCCAAGGATCG	0.383	

-	8	1360	m.1_Nonsense_M	NM_002227	NP_002218	P23458	JAK1_HUMAN	FERM.	61	TGATTTCAGGGA	0.373	
+	12	1301	_p.R400*|SFRS11_	NM_004768	NP_004759	Q05519	SRS11_HUMAN		0	aagagaacgatcaac	0.159	
+	12	1365	73A_uc010orl.1_M	NM_198549	NP_940951	Q8NAN2	FA73A_HUMAN		1	AGACCGATCAC	0.294	rs146380219
-	9	1183	1eal.1_Missense_M	NM_024901	NP_079177	Q9H6A0	DEN2D_HUMAN	DENN.	1	GATTGACCAGC	0.458	
+	3	332	nse_Mutation_p.C	NM_003176	NP_003167	Q15431	SYCP1_HUMAN	Glu-rich (acidic).	1	AAATGTACTGA	0.318	
-	4	574		NM_052891	NP_443123	Q96LB9	PGRP3_HUMAN		4	TCCTGGGCATC	0.532	
+	20	2677	qk.1_Missense_Mu	NM_001080471	NP_001073940	Q5VY43	PEAR1_HUMAN	Pro-rich.	3	AGGTGGGGCCC	0.667	
-	16	2415		NM_003126	NP_003117	P02549	SPTA1_HUMAN	Spectrin 8.	8	CCTGACGAGCA	0.463	rs145972324
+	10	1469	g.2_Missense_Mu	NM_001014796	NP_001014796	Q16832	DDR2_HUMAN	cellular (Potential).	6	TGTCACGGTGC	0.522	rs147483979
-	7	1074	gcw.1_Missense_	NM_177398	NP_796372	Q8TE12	LMX1A_HUMAN		5	TGATTCCTTCCAT	0.577	
+	2	725	0794_uc001gdd.2	NM_001005214	NP_001005214	Q8N7C0	LRC52_HUMAN	lar (Potential).|LRRCT.	1	GGGTGGCCCAT	0.552	
-	13	3971		NM_000130	NP_000121	P12259	FA5_HUMAN	ndem repeats of [TNP]-L-S	6	AGAAAGGGGCA	0.502	rs140018525
+	7	654	G4A_uc010pos.1_	NM_024420	NP_077734	P47712	PA24A_HUMAN	binding (Probable).|PLA2c.	3	GGCTCTGTGTG	0.443	
+	2	499	jx.2_Missense_Mu	NM_001136475	NP_001129947	Q86V25	VASH2_HUMAN		0	AGGTCCCAAAC	0.542	
+	4	552	d.1_Missense_Mu	NM_014777	NP_055592	Q14146	URB2_HUMAN		3	TCATCTACACGG	0.572	
+	8	2129		NM_001004342	NP_001004342	Q6ZTA4	TRI67_HUMAN	B30.2/SPRY.	4	CAACCGCAGCT	0.607	
+	1	55		NM_001004696	NP_001004696	Q8NH00	OR2T4_HUMAN	cellular (Potential).	1	ATCCTGATGGGA	0.488	
+	9	992	F18_uc001imq.2_	NM_003675	NP_003666	Q99633	PRP18_HUMAN		1	CCATCGGTGTC	0.413	
+	4	856	i.1_Missense_Mut	NM_030664	NP_109589	Q96BW5	PTER_HUMAN		2	ATATTGCAAGAA	0.473	
-	32	6413	010qdw.1_Missen	NM_021738	NP_068506	O95425	SVIL_HUMAN	elsolin-like 4.	6	CTCCACGCACG	0.627	
+	7	794		NM_052997	NP_443723	Q9BXX3	AN30A_HUMAN		9	CTTGGCGGAAA	0.423	
+	7	860		NM_052997	NP_443723	Q9BXX3	AN30A_HUMAN		9	CTTGGTGGAAA	0.502	
+	7	1120		NM_052997	NP_443723	Q9BXX3	AN30A_HUMAN		9	ATTATGAGTCCC	0.428	
-	6	957	_p.E188*|PCDH15	NM_033056	NP_149045	Q96QU1	PCD15_HUMAN	(Potential).|Cadherin 2.	13	ATACTCTATCTG	0.333	
+	3	413	D1_uc001jkd.3_R	NM_018464	NP_060934	Q9NZ45	CISD1_HUMAN	lasmic (Potential).	0	ATAACGAAGAG	0.403	
-	19	3921	_Mutation_p.R69	NM_004747	NP_004738	Q8TDM6	DLG5_HUMAN		8	ACACTCCGCGGA	0.502	
+	9	2379	ug.1_Missense_M	NM_017580	NP_060050	Q9UGI0	ZRAN1_HUMAN		2	CTCGGCGGCGA	0.547	
-	13	7474	.1_Missense_Mut	NM_002417	NP_002408	P46013	KI67_HUMAN	approximate repeats.|12.	7	CTTAGGAGTCTG	0.453	
+	12	2169	eq.2_Missense_Mu	NM_001003819	NP_001003819	B2RNG4	B2RNG4_HUMAN		1	TGCTGCAAATGT	0.428	
-	5	917	cy.1_Missense_Mu	NM_000352	NP_000343	Q09428	ABCC8_HUMAN	smic (By similarity).	1	AGCCGTTGGTAG	0.547	
-	5	501	se_Mutation_p.G1	NM_005709	NP_005700	Q9Y6N9	USH1C_HUMAN	PDZ 1.	1	CGTCCCCTACC	0.552	
+	1	317	86_uc001nqb.2_	NM_024098	NP_077003	Q9H6F5	CCD86_HUMAN	Pro-rich.	0	CTCCGAGTGTG	0.662	
+	25	2969	ph.1_Missense_M	NM_000932	NP_000923	Q01970	PLCB3_HUMAN		2	CACCCGCCGCC	0.677	
-	2	1150	vv.2_Missense_Mu	NM_033063	NP_149052	Q96JE9	MAP6_HUMAN	-binding (By similarity).	0	TAGAGGCTGCGT	0.512	
-	11	1351	.R388W|MRE11A	NM_005591	NP_005582	P49959	MRE11_HUMAN		5	TACCCGATCCA	0.353	
-	5	667	A154G|CASP5_uc	NM_004347	NP_004338	P51878	CASP5_HUMAN		3	AGTGAGCCCCA	0.498	
+	6	850	3A_uc009yyx.2_I	NM_213621	NP_998786	P46098	5HT3A_HUMAN	cellular (Potential).	0	CGACAGGAGTG	0.493	
-	22	4741	ense_Mutation_p.F	NM_001142685	NP_001136157	A7KAX9	RHG32_HUMAN	action with GAB2.	5	TCTCCGGATGG	0.557	
+	13	1608	_p.G332E|LEPREL	NM_014262	NP_055077	Q8IVL6	P3H3_HUMAN		0	GGCTGGGACAG	0.662	
+	13	1779	_p.A474T|PTPN6_	NM_002831	NP_002822	P29350	PTN6_HUMAN	protein phosphatase.	1	CCATCGCCCAG	0.617	
-	5	504	_p.R96C|KLRC1_	NM_002259	NP_002250	P26715	NKG2A_HUMAN	cellular (Potential).	0	AATGACGTGCTA	0.338	
-	20	2511	sit.1_Missense_M	NM_014802	NP_055617	Q86YS7	K0528_HUMAN		4	TCGTAGTTTAAA	0.274	
-	3	971		NM_021044	NP_066382	O43323	DHH_HUMAN		2	GTCTCCGCGGT	0.677	
-	2	573		NM_175068	NP_778238	Q86Y46	K2C73_HUMAN	Rod.|Linker 1.	6	TGGGCTCCAGGT	0.607	
+	19	2385	r.1_Missense_Mut	NM_004984	NP_004975	Q12840	KIF5A_HUMAN		3	AGCAGAAGACCA	0.597	
+	17	2202		NM_007235	NP_009166	O43592	XPOT_HUMAN	ytoplasmic localization and	2	TGATCAACTTTT	0.373	
+	15	3579	ub.1_Missense_Mu	NM_014903	NP_055718	Q8IVL0	NAV3_HUMAN	Ser-rich.	17	AATATCGCAGC	0.512	

+	3	1201		NM_007076	NP_009007	Q9BVA6	FICD_HUMAN	Fido.	0	AGTTTGCAGCCT	0.542	
-	1	191	utation_p.V40M|M	NM_052845	NP_443077	Q96EY8	MMAB_HUMAN		0	TTCCACGCCCT	0.692	
-	2	284	uq.3_Missense_M	NM_024072	NP_076977	Q8TDD1	DDX54_HUMAN		3	GGCACGCACCA	0.617	
-	3	418	NO1_uc001ueu.2_	NM_018183	NP_060653	A3KN83	SBNO1_HUMAN		9	ATTTCGTACTG	0.418	
-	12	2436		NM_015347	NP_056162	O15034	RIMB2_HUMAN		11	CTCCTCCATGA	0.612	
+	21	2472	5B_uc010abg.2_	NM_015032	NP_055847	Q9NTI5	PDS5B_HUMAN		4	ATTGGTCATATTG	0.393	
-	11	3433	wz.2_Missense_	NM_025138	NP_079414	Q86XN7	CM023_HUMAN		5	ATACCCGGCTT	0.433	
+	7	771	p.E172G|COG6_u	NM_020751	NP_065802	Q9Y2V7	COG6_HUMAN		2	CTTATGAAAGAC	0.264	
+	1	447		NM_001004724	NP_001004724	Q8IXE1	OR4N5_HUMAN	Name=4; (Potential).	1	CTGTGGCTTGG	0.488	
+	21	4348	j.2_RNA|FLJ1035	NM_018071	NP_060541	Q8TER5	ARH40_HUMAN		0	GCCGGGAGCCT	0.687	
+	12	1166	6_uc001wlm.2_M	NM_006032	NP_006023	O95741	CPNE6_HUMAN	VWFA.	3	ATAAGCGGTTCC	0.582	rs146313186
+	7	870	mp.2_RNA|IRF9_	NM_006084	NP_006075	Q00978	IRF9_HUMAN		1	GCCCTCAGGCT	0.642	
+	8	2096	.3_Intron|FUT8_uc	NM_178155	NP_835368	Q9BYC5	FUT8_HUMAN	tential).|Lumenal (Potential	1	ATCCCCGTCCTC	0.458	
-	2	445	kr.3_Missense_M	NM_003861	NP_003852	Q96JK2	DCAF5_HUMAN	WD 1.	2	CCGGCGGTCAT	0.488	
+	3	527	aqz.2_Missense_	NM_014734	NP_055549	Q92537	K0247_HUMAN	tracellular (Potential).	3	GTCATCGAATAC	0.557	
-	7	830	_Mutation_p.H67Q	NM_005050	NP_005041	O14678	ABCD4_HUMAN	nsmembrane type-1.	4	TGCATGTGCTT	0.552	
-	4	2590	_p.R797*|STON2_	NM_033104	NP_149095	Q8WXE9	STON2_HUMAN	MHD.	5	CAGTCGGTTTA	0.473	
-	21	3415	_p.A1068V|DICE	NM_030621	NP_085124	Q9UPY3	DICER_HUMAN		5	CGCCAGCATCG	0.498	
+	3	1209	nse_Mutation_p.R	NM_000623	NP_000614	P30411	BKRB2_HUMAN	lasmic (Potential).	5	CAAGCGCTTCC	0.567	rs148172749
+	7	1316	|OR4N4_uc010tzv	NM_001005241	NP_001005241	Q8N0Y3	OR4N4_HUMAN	Name=3; (Potential).	5	GGAGGGATTAC	0.512	
-	17	2760	.2_Missense_Mut	NM_003257	NP_003248	Q07157	ZO1_HUMAN	ylate kinase-like.	6	TTTTACGAAGTT	0.373	
-	3	253	_p.A48V|ATPBD4	NM_080650	NP_542381	Q7L8W6	ATBD4_HUMAN		0	CCATTGCTTCT	0.438	
+	6	810	p.K207N|SQRDL_	NM_021199	NP_067022	Q9Y6N5	SQRD_HUMAN		1	TCAGAAGATCAT	0.478	
-	11	1359	_p.S442L|CEP152	NM_014985	NP_055800	O94986	CE152_HUMAN	Potential.	2	GTACTGACCCT	0.453	
-	16	1722	.V400D|ATP8B4_u	NM_024837	NP_079113	Q8TF62	AT8B4_HUMAN	lasmic (Potential).	8	AAGTAACTAGT	0.388	
-	15	1738		NM_032802	NP_116191	Q8TCT8	PSL2_HUMAN		0	TTATTGCTGGAC	0.333	
-	40	5648	.R1775C|MYO5A_	NM_000259	NP_000250	Q9Y4I1	MYO5A_HUMAN	Dilute.	4	AGTACGAATGA	0.333	
+	10	1927	p.S440N|LIPC_uc	NM_000236	NP_000227	P11150	LIPC_HUMAN	PLAT.	1	ATGGAGCACAG	0.512	rs6079
+	3	858	jp.1_Missense_M	NM_002755	NP_002746	Q02750	MP2K1_HUMAN	rotein kinase.	0	CGTGGGCTTCT	0.507	rs121908596
+	13	2163	_p.R674Q|NEO1_	NM_002499	NP_002490	Q92859	NEO1_HUMAN	tential).|Fibronectin type-III	1	CTACCGAAAGG	0.483	
-	6	687	aq.2_Missense_M	NM_005701	NP_005692	O95149	SPN1_HUMAN		1	TACCTGGCAATC	0.502	
+	20	4889	rf42_uc010upv.1_	NM_152259	NP_689472	Q7Z2Z1	TICRR_HUMAN		7	CCTCTCCCACA	0.607	
+	9	1943	p.2_Missense_Mu	NR_003659					0	GCATCGGCAAG	0.652	
+	6	1347	IP2_uc010uyp.1_	NM_024997	NP_079273	Q5U623	MCAF2_HUMAN	Potential.	0	AAAGACGTATT	0.289	
+	6	872	p.2_Missense_Mu	NM_024847	NP_079123	Q7Z402	TMC7_HUMAN	ellular (Potential).	3	TTTTACGGACAT	0.498	
+	8	1136	se_Mutation_p.A3	NM_024847	NP_079123	Q7Z402	TMC7_HUMAN	lasmic (Potential).	3	TTCAGGCAGAT	0.393	
+	3	546	sense_Mutation_p.	NM_020422	NP_065155	Q96B96	TM159_HUMAN	ical; (Potential).	1	CATGTCGGCCG	0.527	rs145147020
-	5	2714		NM_024675	NP_078951	Q86YC2	PALB2_HUMAN		11	TTGTACCTGTTC	0.438	
+	15	1869	me.2_Missense_	NM_212535	NP_997700	P05771	KPCB_HUMAN	rotein kinase.	9	ACAACGTAGCC	0.443	
+	4	1020	ae.1_Missense_	NM_014712	NP_055527	O15047	SET1A_HUMAN	RRM.	3	TGAAGGATATG	0.547	
+	24	5152	_p.P1663L|CHD9_	NM_025134	NP_079410	Q3L8U1	CHD9_HUMAN		7	GGTACCAGAAC	0.338	
+	2	470	S3_uc002enj.3_I	NM_022770	NP_073607	Q9BRX5	PSF3_HUMAN		0	TGGAACTCCCC	0.502	
+	2	1005	o.2_Missense_M	NM_005769	NP_005760	Q8NCG5	CHST4_HUMAN	enal (Potential).	0	TGTGCGCTATG	0.552	
-	9	1179	jf.2_Intron|PRDM	NM_001098173	NP_001091643	Q9NQW5	PRDM7_HUMAN		1	CCCCATACCAG	0.522	
+	3	996	rf97_uc010vpz.1_	NM_001013672	NP_001013694	Q6ZQX7	CQ097_HUMAN	tandem repeat of A-L-K-G	1	CCACACTGACC	0.687	
+	22	3359	USP6_uc010ckz.1	NM_004505	NP_004496	P35125	UBP6_HUMAN		5	CACGTGGTGGG	0.637	
-	7	1644	_Mutation_p.A10	NM_001365	NP_001356	P78352	DLG4_HUMAN	PDZ 1.	2	GGGCCGCAGCC	0.612	

-	6	858	e_Mutation_p.P199	NM_004489	NP_004480	Q13227	GPS2_HUMAN		3	TGTGGGCCCAT	0.567	
-	11	2310	cry.1_Missense_M	NM_178860	NP_849191	Q53EL9	SEZ6_HUMAN	ellular (Potential).	2	ATTGCGGGGCA	0.612	
-	1	112		NM_002279	NP_002270	Q14525	KT33B_HUMAN	Head.	0	GGGGGGCACAC	0.647	
+	4	598	_5'Flank|EFTUD2_	NM_213607	NP_998772	Q8IW40	CC103_HUMAN		1	GGCGAGCACTG	0.632	
-	18	2284	tf.2_Missense_Mu	NM_001130528	NP_001124000	O60271	JIP4_HUMAN		5	TGACTCCAACA	0.363	
+	1	904		NM_203425	NP_982249	Q86X59	CQ082_HUMAN		0	CCACCGACACA	0.756	
-	4	369	e_Mutation_p.R10	NM_002059	NP_002050	P01242	SOM2_HUMAN		3	GATGCGGAGCA	0.647	
-	25	3508	A9_uc010dez.2_I	NM_080283	NP_525022	Q8IUA7	ABCA9_HUMAN	ical; (Potential).	6	CATATGTCAAG	0.313	
-	4	1648	e_Mutation_p.G41	NM_032134	NP_115510	Q9H0J4	QRIC2_HUMAN	Gln-rich.	5	CTGACCTGTGC	0.368	
-	10	1794	_p.H577Y|UBE2O_	NM_022066	NP_071349	Q9C0C9	UBE2O_HUMAN		5	GTGGTGCACAG	0.597	
+	5	4530		NM_020914	NP_065965	Q9HCF4	ALO17_HUMAN		21	AGTCCGGTGAG	0.592	
+	6	1764		NM_001194	NP_001185	Q9UL51	HCN2_HUMAN	toplasmic (Potential).	0	GACTACATCATC	0.592	
+	19	2378	jz.1_Missense_Mu	NM_145245	NP_660288	Q96CN4	EVI5L_HUMAN		1	TTGGCGTAGGC	0.701	
-	11	1300	nse_Mutation_p.E	NM_004461	NP_004452	Q9Y285	SYFA_HUMAN		1	CACCTCCATGC	0.612	
+	1	288		NM_001098622	NP_001092092	P60323	NANO3_HUMAN		1	TGCCGGGACCC	0.657	
-	5	701	p.E167D|SLC1A6_	NM_005071	NP_005062	P48664	EAA4_HUMAN	ellular (Potential).	6	CCGTTCTCCAC	0.587	
-	15	2525	.A397G|PDE4C_	NM_001098819	NP_001092289	Q08493	PDE4C_HUMAN		5	TCTTTGGCTAAA	0.443	
-	4	1447	p.K353E|ZNF708_	NM_021269	NP_067092	P17019	ZN708_HUMAN		6	GTTTCTTTCCAG	0.343	
-	4	1419	.E424V|ZNF43_u	NM_003423	NP_003414	P17038	ZNF43_HUMAN	2H2-type 10.	2	CCACATTCTTCA	0.398	
-	5	1782	208_uc002nqo.1_	NM_007153	NP_009084				7	AAAGGTTTTGC	0.398	
+	4	342	_uc002nxs.1_Intro	NM_002151	NP_002142	P05981	HEPS_HUMAN	type II membrane protein;	2	CCATCGGGGCG	0.657	
-	5	608		NM_004646	NP_004637	O60500	NPHN_HUMAN	2.|Extracellular (Potential).	5	CACACCTGGCT	0.547	
-	7	2439	e_Mutation_p.L58	NM_181882	NP_870998	Q9BXM0	PRAX_HUMAN	L]-[LIVMAP]- [AQKHRPE];	2	TGGGAGCTTCA	0.577	
+	7	726	p.V206M|RAB4B_	NM_080732	NP_542770	Q96KS0	EGLN2_HUMAN		2	AGGCCGTGGCC	0.682	rs138801573
+	2	669	gk.1_Missense_M	NM_018485	NP_060955	Q9P296	C5ARL_HUMAN	Name=4; (Potential).	1	GCGGGGTGCAG	0.687	
-	12	2942		NM_001080434	NP_001073903				6	TCTCGGGGGAC	0.652	
+	1	282	yct.1_Missense_	NM_014441	NP_055256	Q9Y336	SIGL9_HUMAN	(Potential).|Ig-like V-type.	1	GGATGCTCCAG	0.597	
-	4	603	|LILRB2_uc002qf	NM_005874	NP_005865	Q8N423	LIRB2_HUMAN	otential).|Ig-like C2-type 2.	1	CACCAGGGGGT	0.612	
-	7	1009	qff.2_Missense_M	NM_021250	NP_067073	A6NI73	LIRA5_HUMAN	lasmic (Potential).	1	TCCAGCTGCAG	0.537	
+	6	1683	.G509W|NLRP2_	NM_017852	NP_060322	Q9NX02	NALP2_HUMAN		2	ACATTGGGGAC	0.557	
+	3	1256	gv.1_Missense_M	NM_006635	NP_006626	Q14592	ZN460_HUMAN	2H2-type 5.	0	GCAGCGAATGT	0.463	rs146815063
-	16	3293	e_Mutation_p.D82	NM_015025	NP_055840	Q9UL68	MYT1L_HUMAN		6	GTGTAGTCTAC	0.537	
-	30	5059	nse_Mutation_p.R	NM_020738	NP_065789	Q9ULH0	KDIS_HUMAN	lasmic (Potential).	4	TTCCCCGCTTT	0.483	
+	3	1247	cw.2_Missense_M	NM_002252	NP_002243	Q9BQ31	KCNS3_HUMAN	=Segment S3; (Potential).	4	TTCCCTTCTATG	0.498	
-	12	4254	gt.1_Missense_M	NM_018263	NP_060733	Q76L83	ASXL2_HUMAN		1	TGGTACAGCAG	0.498	
+	1	4409	1_5'Flank|ZNF512_	NM_032266	NP_115642	Q68DN1	CB016_HUMAN		1	TCTTCGACTGC	0.502	
-	20	1541	_p.P463S|MAP4K	NM_003618	NP_003609	Q8IVH8	M4K3_HUMAN		8	TGGGGGTAATC	0.453	
+	14	1845	2_Missense_Muta	NM_019063	NP_061936	Q9HC35	EMAL4_HUMAN	WD 5.	250	AGGAGGGAAAG	0.338	
+	52	6168	YSF_uc010fej.2_M	NM_003494	NP_003485	O75923	DYSF_HUMAN	lasmic (Potential).	7	CAACCGCATGC	0.547	
-	7	867		NM_014014	NP_054733	O75643	U520_HUMAN		10	ATCCCGAGGGT	0.478	
+	5	674	H2P_uc002tkb.2_	NM_182905	NP_878908				0	GGTGGGCACTTG	0.612	
+	16	1433	yf.1_Missense_M	NM_006770	NP_006761	Q9UEW3	MARCO_HUMAN	tracellular (Potential).	6	AGGCCGGGCTG	0.527	
+	17	2361	p.F243L|PTPN4_	NM_002830	NP_002821	P29074	PTN4_HUMAN	PDZ.	2	TGGATTCAATGT	0.264	
-	34	4103	yy.1_RNA|CLASP	NM_015282	NP_056097	Q7Z460	CLAP1_HUMAN		2	CTGTCCGGCCT	0.652	
+	6	590		NM_001080527	NP_001073996	Q6PIF6	MYO7B_HUMAN	osin head-like.	2	ATCAGTGGCCA	0.622	
-	7	914	nse_Mutation_p.P	NM_032143	NP_115519	Q5FWF4	ZRAB3_HUMAN		2	TAGGGGGTAGC	0.378	
-	45	5689		NM_004543	NP_004534	P20929	NEBU_HUMAN		20	GGAAGCCAATG	0.443	rs34778227

+	6	1987	p.N221K|DHRS9_	NM_005771	NP_005762	Q9BPW9	DHRS9_HUMAN		0	TATTAATGTCTCC	0.428	
-	25	2576	_p.N647S|PGAP1_	NM_024989	NP_079265	Q75T13	PGAP1_HUMAN	ical; (Potential).	4	AGTAAGTTAATCA	0.353	
-	3	2599		NM_020814	NP_065865	Q9P2E8	MARH4_HUMAN	ical; (Potential).	1	CATCCCGTAGC	0.557	
+	9	1816	_Splice_Site_p.A4	NM_014140	NP_054859	Q9NZC9	SMAL1_HUMAN		7	CCACAGGCCTT	0.557	
-	1	3044		NM_005544	NP_005535	P35568	IRS1_HUMAN		12	CTGACGGGGAC	0.632	
+	10	1224	yc.2_Missense_Mu	NM_000751	NP_000742	Q07001	ACHD_HUMAN	lasmic (Potential).	3	AGAGCGGCATG	0.632	
+	8	842	e_Mutation_p.S144	NM_152879	NP_690618	Q16760	DGKD_HUMAN	l-ester/DAG-type 2.	5	ACACATCGTGTA	0.552	
+	4	1549	p.E386Q|SH3BP4_	NM_014521	NP_055336	Q9P0V3	SH3B4_HUMAN		4	ACCTGGAGGTG	0.537	
+	4	1048	p.V230M|SIRPA_	NM_001040022	NP_001035111	P78324	SHPS1_HUMAN	1.|Extracellular (Potential).	1	GCGAGGTGGCC	0.612	
-	36	3425	p.G864V|C20orf19	NM_001009984	NP_001009984	Q5TEA3	CT194_HUMAN		0	TGGGTGCCATTA	0.453	
-	3	495	zrn.1_Missense_	NM_001195	NP_001186	Q12934	BFSP1_HUMAN	Rod.|Coil 1B.	1	ATGCAGCAAGGC	0.488	
+	2	133	tj.1_RNA|FRG1B_uc010gdr.1_RNA|FRG1B_uc010ztk.1_Intron						0	ATGCAATTGGAC	0.343	
+	7	1117	MT3B_uc010gef.2_	NM_006892	NP_008823	Q9UBC3	DNM3B_HUMAN	n with DNMT1 and DNMT	5	TTGGCGATGGC	0.617	
+	3	223	ud.1_Missense_M	NM_174897	NP_777557	Q8NFQ5	BPIL3_HUMAN		2	AGCTGCCCGTC	0.562	
-	2	303	10gel.2_Intron|CD	NM_016408	NP_057492	Q96SZ6	CK5P1_HUMAN	activation inhibition.	5	CAGCAGCCAGC	0.522	
-	4	999	uf.1_Missense_Mu	NM_003098	NP_003089	Q13424	SNTA1_HUMAN	PH 1.	1	TTGACCATCTG	0.597	
+	30	3958		NM_020884	NP_065935	A7E2Y1	MYH7B_HUMAN	Potential.	2	GACCCGCGCCA	0.617	
-	12	2869		NM_003185	NP_003176	O00268	TAF4_HUMAN		3	CTTCCTCTGCT	0.527	
+	5	1468	p.V356M|OPRL1_	NM_182647	NP_872588	P41146	OPRX_HUMAN	lasmic (Potential).	2	AGGACGTGGCC	0.652	
+	7	1487		NM_014586	NP_055401	P57058	HUNK_HUMAN		2	TCCTGGCCATCT	0.547	
+	19	3348	DL1_uc002zag.1_	NM_001004416	NP_001004416	Q5DID0	UROL1_HUMAN	llular (Potential).|ZP.	3	GAAATGCAGTT	0.517	
-	1	881	.1_Intron|C21orf29	NM_198691	NP_941964	P60331	KR101_HUMAN		1	CCGGGCGGGAG	0.716	
+	15	2865	jj.2_Missense_Mut	NM_006031	NP_006022	O95613	PCNT_HUMAN		8	AGCTCGAGGCC	0.642	
-	4	424	.2_5'UTR|BPIL2_u	NM_174932	NP_777592	Q8NFQ6	BPIL2_HUMAN		2	GATACCGGTAAA	0.498	
+	4	1154		NM_030642	NP_085145	Q9BWW9	APOL5_HUMAN		0	GCCTGTTGTGG	0.592	
+	10	3566	ayn.3_Missense_M	NM_001162501	NP_001155973	Q9UPQ9	TNR6B_HUMAN		0	GGTTCCGTCCA	0.408	
-	12	3585	R1082Q|BRD1_uc	NM_014577	NP_055392	O95696	BRD1_HUMAN		1	CGATCCGCACG	0.582	
+	2	552	R1D2_uc011awk.1	NM_005126	NP_005117	Q14995	NR1D2_HUMAN		3	GAAAACAAGCA	0.378	
-	18	2221	axu.1_Missense_	NM_015097	NP_055912	B2RTR1	B2RTR1_HUMAN		4	TTCGCACAGACT	0.522	
-	12	4389		NM_014831	NP_055646	O15050	TRNK1_HUMAN		2	CCTGTTCAGCA	0.547	
+	10	985		NM_018725	NP_061195	Q9NRM6	I17RB_HUMAN	lasmic (Potential).	3	GGCACGGTAAG	0.458	rs61751221
+	7	1211	u.2_Nonsense_Mu	NM_007072	NP_009003	Q9UM44	HHLA2_HUMAN	ical; (Potential).	1	CTTATGGATTTTG	0.413	
+	3	1386		NM_032242	NP_115618	Q9UIW2	PLXA1_HUMAN	tracellular (Potential).	3	GGGCAGCCCCA	0.662	
-	6	855	.Y171C|THPO_uc	NM_000460	NP_000451	P40225	TPO_HUMAN		1	AGCCAGTAGTTC	0.542	
+	16	2033	buy.1_Missense_	NM_000283	NP_000274	P35913	PDE6B_HUMAN		0	CTGATGGACAT	0.692	
+	2	549	.E32K|GRK4_uc0	NM_182982	NP_892027	P32298	GRK4_HUMAN	N-terminal.	1	GGAAGGAGATA	0.403	
+	7	920	oi.2_Missense_Mu	NM_004334	NP_004325	Q10588	BST1_HUMAN		1	AAGGCAGCATGA	0.393	
+	1	230		NM_001079827	NP_001073296	A0PK11	CLRN2_HUMAN		0	GACTGGAGTGG	0.537	
-	2	477	GDH_uc003gul.1_	NM_003359	NP_003350	O60701	UGDH_HUMAN		4	TTTACCTCATAAA	0.303	
-	7	1026	zr.1_Missense_Mu	NM_022832	NP_073743	P62068	UBP46_HUMAN		1	GAGCCGGAGTT	0.547	
-	8	1169	can.1_Missense_Mutation_p.T261A			P36537	UDB10_HUMAN		5	AGATTGTCTCGT	0.403	rs13118402
+	11	1366	A4_uc003hgc.3_Mi	NM_001098484	NP_001091954	Q9Y6R1	S4A4_HUMAN	lasmic (Potential).	5	ATGAATGGGGAT	0.443	
+	21	2914	kw.2_Missense_M	NM_025074	NP_079350	Q86XX4	FRAS1_HUMAN	tracellular (Potential).	5	TGGGAGCATCT	0.577	
+	5	942	_p.C157R|NUDT9_	NM_024047	NP_076952	Q9BW91	NUDT9_HUMAN	udix hydrolase.	0	AAGACTGTGGA	0.348	
-	4	1250	K2_uc003hyj.1_3'U	NM_014421	NP_055236	Q9UBU2	DKK2_HUMAN		5	GGCAGGGGTCT	0.433	
+	6	822	.R169Q|PHF17_u	NM_199320	NP_955352	Q6IE81	JADE1_HUMAN		0	GCAGCGATGCT	0.428	
-	3	540	hx.2_Missense_M	NM_030648	NP_085151	Q8WTS6	SETD7_HUMAN		2	CATACGTGCCC	0.507	rs139666025

-	12	1600	se_Mutation_p.S4	NM_031956	NP_114162	Q8NA56	TTC29_HUMAN			0	CGTTCTGAGTTT	0.308	
+	10	1491	irc.2_Missense_M	NM_007246	NP_009177	O95198	KLHL2_HUMAN	Kelch 3.		0	ATGGGAGTACAG	0.418	
-	3	732	clx.1_Missense_Mu	NM_004174	NP_004165	P48764	SL9A3_HUMAN	lasmic (Potential).		0	AGGACCTCGTTG	0.642	
+	11	2236		NM_020227	NP_064612	Q9NQV7	PRDM9_HUMAN	C2H2-type 7.		6	GAGGACACACA	0.602	rs111488757
-	7	1588	_uc011cnu.1_Spli	NM_006727	NP_006718	Q9Y6N8	CAD10_HUMAN			12	CACTTACCTAATG	0.259	
+	5	744	_p.R173*|DNAJC2	NM_001012339	NP_001012339	Q5F1R6	DJC21_HUMAN			2	ATACACGACAGC	0.413	rs150576702
+	10	3303	p.P935L|NIPBL_u	NM_133433	NP_597677	Q6KC79	NIPBL_HUMAN			9	CACACCCTGACA	0.373	
+	2	762	ELD2_uc003jwr.1_	NM_001038603	NP_001033692	Q8N4S9	MALD2_HUMAN	.|Helical; (Potential).		0	TGGGAGGCGTT	0.498	
+	16	4383	_p.R1361*|ZFYVE	NM_001105251	NP_001098721	Q7Z3T8	ZFY16_HUMAN			0	GCTTTACGAGAA	0.388	
+	77	16610	.R3211Q|GPR98_	NM_032119	NP_115495	Q8WXG9	GPR98_HUMAN	cellular (Potential).		16	GTTCTCGGCTGG	0.448	
+	21	2812	kks.2_Missense_	NM_032290	NP_115666	Q9BQI6	ANR32_HUMAN			2	GGGAGAATTGC	0.378	
+	23	5344	.R1371H|KDM3B_	NM_016604	NP_057688	Q7LBC6	KDM3B_HUMAN	JmjC.		11	GTTTCCGCCTGA	0.428	
-	9	1654	loh.3_Missense_M	NM_004576	NP_004567	Q00005	2ABB_HUMAN			2	CGAAGCCTCAA	0.527	
-	2	1340		NM_001012301	NP_001012301	Q5FYB1	ARSI_HUMAN			2	GGTAGCGGTACA	0.627	
-	13	1991	gx.2_Missense_Mu	NM_004395	NP_004386	Q16643	DREB_HUMAN			6	ATTGGGCAAACT	0.582	
-	7	1429	nlm.1_Nonsense_	NM_018434	NP_060904	Q86XS8	GOLI_HUMAN	lasmic (Potential).		3	AGGGCTGATCTT	0.522	
+	2	924		NM_001718	NP_001709	P22004	BMP6_HUMAN			3	GGGTGAGGTGG	0.438	
-	5	917	on.2_Missense_Mu	NM_006778	NP_006769	Q9UDY6	TRI10_HUMAN			0	AGTCCCGAATCC	0.512	
+	9	1411	p.R337W|TRIM39_	NM_021253	NP_067076	Q9HCM9	TRI39_HUMAN	B30.2/SPRY.		3	AGACTCCGGGAT	0.577	
-	2	188	n_p.F8L|HLA-DO	NM_002119	NP_002110	P06340	DOA_HUMAN	ar (Potential).|Alpha-1.		0	GTAGAAGGCGG	0.522	
-	4	779	_p.T9M|CCND3_u	NM_001760	NP_001751	P30281	CCND3_HUMAN			0	TGCCCGTGGCG	0.577	
+	3	717		NM_003221	NP_003212	Q92481	AP2B_HUMAN			0	TTGAAGATGCCA	0.343	
-	2	217_218	jzr.2_Missense_Mu	NM_003643	NP_003634	Q9NP62	GCM1_HUMAN			1	TCGTCAGGTTCC	0.396	
+	18	3042	2_Missense_Mutat	NM_014989	NP_055804	Q86UR5	RIMS1_HUMAN		p.S989S(1)	10	TCACGTTCTCCA	0.383	
+	10	1550		NM_003080	NP_003071	O60906	NSMA_HUMAN			0	GGCCCAGGCT	0.622	
-	4	888	bt.1_Missense_Mu	NM_001010923	NP_001010923	Q8N1K5	THMS1_HUMAN	CABIT 1.		4	ATCTTCCATTCA	0.353	
+	7	1368	0khi.2_Missense_	NM_014721	NP_055536	O75167	PHAR2_HUMAN			2	TGCCTCAGCTAC	0.517	
+	13	1822	szk.2_Missense_M	NM_006024	NP_006015	Q86VP1	TAXB1_HUMAN	Potential.		1	ATAAATATGCTGA	0.279	
+	3	660	kwc.1_RNA|INMT_	NM_006774	NP_006765	O95050	INMT_HUMAN			0	CGTGGCCCTGG	0.587	
+	11	1791	3tvz.2_Missense_	NM_022479	NP_071924	Q6IS24	GLTL3_HUMAN	nenal (Potential).		7	CTCCATCAAGTAC	0.652	
+	4	1042	n.2_Missense_Mu	NM_003388	NP_003379	Q9UDT6	CLIP2_HUMAN	CAP-Gly 2.		3	ACGTGGGGGAG	0.647	
-	6	690	p.R217Q|SEMA3D	NM_152754	NP_689967	O95025	SEM3D_HUMAN	Sema.		5	GGGATCGAGTG	0.408	
-	23	3801	y.2_Missense_Mu	NM_000466	NP_000457	O43933	PEX1_HUMAN			2	TGCAGTCATTAA	0.388	
-	8	939	N2_uc010lfk.2_RI	NM_000305	NP_000296	Q15165	PON2_HUMAN			0	GAAGGATCAATA	0.398	
+	6	634	is.1_Missense_Mu	NM_003496	NP_003487	Q9Y4A5	TRRAP_HUMAN			37	CAAACAGTTCAC	0.313	
+	8	1352	498_uc003urn.2_	NM_145115	NP_660090	Q6NSZ9	ZN498_HUMAN			2	CCACAGCTCCT	0.602	
-	3	809		NM_001004323	NP_001004323	Q8IZ16	CG061_HUMAN			0	GGGCAGCATGG	0.637	
+	14	2911	ZAN_uc003uwl.2_	NM_003386	NP_003377	Q9Y493	ZAN_HUMAN	ate) (mucin-like domain).|E		11	ACCATCTCCACG	0.502	
+	23	4529	ZAN_uc010lhh.2_	NM_003386	NP_003377	Q9Y493	ZAN_HUMAN	tracellular (Potential).		11	AGACCGGTGCG	0.622	
+	3	6234	C17_uc010lho.1_	NM_001040105	NP_001035194	Q685J3	MUC17_HUMAN	X approximate tandem re		27	CTGAGGGTAAC	0.488	
+	10	1156	mh.1_Splice_Site_	NM_000108	NP_000099	P09622	DLDH_HUMAN			1	CCAAAGTAAGT	0.308	
-	2	172		NM_001024607	NP_001019778	A4D0T2	CG066_HUMAN	ical; (Potential).		2	TGGTGCAGAAA	0.463	
+	1	263	/1_uc003vig.1_RN	NM_001753	NP_001744	Q03135	CAV1_HUMAN			0	TTCATCCAGCC	0.607	
-	9	1615	0lly.1_Missense_M	NM_012470	NP_036602	Q9Y5L0	TNPO3_HUMAN			5	ACCCTATCAAG	0.413	
+	7	835	p.D129G|TBXAS1	NM_001130966	NP_001124438	P24557	THAS_HUMAN	lasmic (Potential).		3	CATTTGACATCC	0.443	
-	15	1860		NM_004333	NP_004324	P15056	BRAF_HUMAN	rotein kinas_R603>I(2)|p.T		18290	GATTTCACTGTA	0.368	
-	9	1390	_p.M423I|PTPRN2	NM_002847	NP_002838	Q92932	PTPR2_HUMAN	cellular (Potential).		7	CTCTCCATGTCG	0.592	

+	6	577	1_uc003xnn.2_R	NM_002164	NP_002155	P14902	I23O1_HUMAN		2	TCATTTCGTGATG	0.358	
+	5	508	rf45_uc011lew.1_	NM_173518	NP_775789	Q4G0Z9	CH045_HUMAN		1	TATGGTCTTGATC	0.313	
-	3	1005	j.1_Missense_Mu	NM_005655	NP_005646	Q13118	KLF10_HUMAN		0	CAACAGGGTTGT	0.587	
+	2	398	_uc003ylg.2_Miss	NM_024812	NP_079088	Q8WXS3	BAALC_HUMAN		0	ATGGTGTGCCC	0.557	
-	7	1618	no.2_Nonsense_M	NM_001146	NP_001137	Q15389	ANGP1_HUMAN	ogen C-terminal.	7	GGCTCGGTTCC	0.428	
+	5	478	.2_RNA|ADCK5_u	NM_174922	NP_777582	Q3MIX3	ADCK5_HUMAN		1	GCAACGGGGGC	0.657	
+	1	1137		NM_006570	NP_006561	Q7L523	RRAGA_HUMAN		0	TTCTGCGGCCA	0.493	
+	2	211	_p.R59W|DNAJB5	NM_012266	NP_036398	O75953	DNJB5_HUMAN	J.	0	CCTACCGGAAG	0.498	
+	1	490	42421_uc004aed.1_RNA						0	TTAACCCCTTCC	0.582	
+	4	637		NM_001001670	NP_001001670	Q6ZQQ2	F75D1_HUMAN	Pro-rich.	0	ACCCCCCTTAA	0.557	
-	27	4202		NM_005502	NP_005493	O95477	ABCA1_HUMAN		17	CTATGTCAGAAT	0.488	
+	17	4640	q.1_Missense_Mu	NM_002581	NP_002572	Q13219	PAPP1_HUMAN	Sushi 4.	9	CTCCACCAAAAT	0.527	
+	4	1036	HD1_uc004bwm.2_	NM_001100876	NP_001094346	Q5SRE7	PHYD1_HUMAN		0	AACAAAGGATTG	0.552	rs149087529
+	4	853		NM_014811	NP_055626	Q5T8A7	K0649_HUMAN		3	GTCTCGTTGCT	0.612	
+	5	725		NM_000531	NP_000522	P00480	OTC_HUMAN	rbamoyl phosphate bindin	2	CTATCCAGATCC	0.393	
+	6	1596	_p.I557V|MAGED	NM_001005332	NP_001005332	Q9Y5V3	MAGD1_HUMAN	MAGE.	3	AGAGATATCATC	0.537	
-	19	2948	oe.1_Missense_M	NM_006306	NP_006297	Q14683	SMC1A_HUMAN		6	AGTCCTCCCCC	0.527	
-	3	624	lyo.2_Missense_M	NM_032803	NP_116192	Q8WY07	CTR3_HUMAN	ellular (Potential).	2	GGGCACGTGCA	0.552	
+	8	1304_1305	N1_uc011mpt.1_	NM_052957	NP_443189	Q96QF7	ACRC_HUMAN	sp/Ser-rich.	3	CGACAGCAGTG	0.554	
-	11	3180	s.2_Missense_Mu	NM_001113490	NP_001106962	Q4VCS5	AMOT_HUMAN		1	AGAGTATTGGAG	0.428	
+	11	1631	zm.1_Missense_M	NM_012253	NP_036385	P51854	TKTL1_HUMAN		4	TGGAGCTGGAA	0.468	
-	9	972	y.2_Nonsense_Mu	NM_002074	NP_002065	P62873	GBB1_HUMAN		0	TTCTCGCACATC	0.567	
-	16	3113	oag.1_Missense_	NM_001009566	NP_001009566	O94985	CSTN1_HUMAN	ellular (Potential).	1	CAAGCAAGGAC	0.557	
-	17	2499	xm.1_Missense_M	NM_052896	NP_443128	Q7Z408	CSMD2_HUMAN	tracellular (Potential).	12	GGTCCCGTGGT	0.542	
+	5	538	Nonsense_Mutatio	NM_000374	NP_000365	P06132	DCUP_HUMAN		0	GACAACGACTG	0.587	
+	5	953	l.1_RNA|PCSK9_u	NM_174936	NP_777596	Q8NBP7	PCSK9_HUMAN	eptidase S8.	4	GGCCAGCAAGT	0.627	
-	10	2107	tation_p.D655G|A	NM_006594	NP_006585	Q9Y6B7	AP4B1_HUMAN		4	GGGTGTCAGGA	0.498	
-	4	529	_p.C30S|REG4_u	NM_001159352	NP_001152824	Q9BYZ8	REG4_HUMAN		1	GAGCACAGCTG	0.363	
+	8	1168	.1_Intron|NBPF10	NM_001039703	NP_001034792	A6NDV3	A6NDV3_HUMAN		0	AGCTGACCCAGT	0.507	
+	74	9249	.1_Intron|NBPF10	NM_001039703	NP_001034792	A6NDV3	A6NDV3_HUMAN		0	GGCCTAAAGTC	0.473	
+	78	9695	BPF10_uc010oyl.1	NM_001039703	NP_001034792	A6NDV3	A6NDV3_HUMAN		0	AAAGAGCCTGA	0.473	
+	10	1949	KRD35_uc010oyx	NM_144698	NP_653299	Q8N283	ANR35_HUMAN	Potential.	5	GCTGGAGAAGG	0.587	
-	2	1066	e.1_Missense_Mu	NM_007113	NP_009044	Q07283	TRHY_HUMAN	eats of R-R-E-Q-E-E- E-R-	5	tctcctcctcctgctcgc	0	
-	2	624	si.1_Intron|INSRR	NM_014215	NP_055030	P14616	INSRR_HUMAN		20	GTCACGCAGAT	0.622	
-	13	3971		NM_000130	NP_000121	P12259	FA5_HUMAN	ndem repeats of [TNP]-L-S	6	AGAAAGGGGCA	0.502	rs140018525
-	20	2807	e_Mutation_p.G3	NM_178527	NP_848622	Q5TAH2	S9A11_HUMAN		2	CACGACCCTCA	0.308	
+	8	2597	lg.2_Missense_Mu	NM_021165	NP_066988	Q9C0B6	FAM5B_HUMAN		6	GTCCTCCCTGA	0.557	
+	18	3028		NM_000186	NP_000177	P08603	CFAH_HUMAN	Sushi 16.	6	GCCTTCCTTGT	0.299	
+	1	520		NM_001105517	NP_001098987	P0C7Q3	FA58B_HUMAN		0	TGAACTGCCAC	0.617	
-	4	1167	w.1_Missense_Mu	NM_003268	NP_003259	O60602	TLR5_HUMAN	ellular (Potential).	4	GATGTCCACTG	0.468	
+	10	1796		NM_014753	NP_055568	Q14692	BMS1_HUMAN		3	TGGCTGTTAAG	0.458	
+	4	802	y.1_Missense_Mu	NM_020549	NP_065574	P28329	CLAT_HUMAN		3	GCCCTGCCGTG	0.612	
+	2	1161	T11_uc001juz.1_	NM_173540	NP_775811	Q495W5	FUT11_HUMAN	enal (Potential).	0	GGAGTGGGGAG	0.512	
+	4	496	_p.P31S|CYP2C1	NM_000769	NP_000760	P33261	CP2CJ_HUMAN		6	TGTGATCCCACT	0.328	
+	4	347	1lgg.1_Missense_	NM_001001974	NP_001001974	Q9HB21	PKHA1_HUMAN	PH 1.	1	AAGGCCAAAGG	0.328	
+	2	793		NM_001105574	NP_001099044	A6NHT5	HMX3_HUMAN	Homeobox.	0	TCCCTGCACCTC	0.652	
-	8	769	e_Mutation_p.R279W|ADAM8_uc010qvb.1_Missense_			P78325	ADAM8_HUMAN		3	TGTCCGTTGCC	0.522	

+	1	556		NM_001004702	NP_001004702	Q8NH37	OR4C3_HUMAN	cellular (Potential).	1	CAGCTCCTCCTG	0.522	
-	1	554		NM_006637	NP_006628	Q13606	OR5I1_HUMAN	cellular (Potential).	1	GCAGGGGAGGG	0.403	
+	11	2328	on_p.G713D|TMEN	NM_178031	NP_821174	Q24JP5	T132A_HUMAN	ilization similar to full-length	1	AGCCTGGTGCCA	0.687	
+	6	467	GFB_uc001nyx.2_In	NM_003377	NP_003368	P49765	VEGFB_HUMAN		0	CCCACCACCGT	0.672	
+	6	554	yx.2_Missense_M	NM_003377	NP_003368	P49765	VEGFB_HUMAN		0	CAGCCCCAGGC	0.726	
+	14	1737		NM_006842	NP_006833	Q13435	SF3B2_HUMAN		3	TGACATCGACTA	0.493	
-	3	259	5332_uc001omu.3	NR_024249					0	GCCCGCTGGTG	0.627	
+	5	617	ofz.2_Missense_M	NM_014361	NP_055176	O94779	CNTN5_HUMAN		8	TACAGAAAGTGT	0.313	
-	2	203	01prt.1_5'UTR|TMP	NM_001077263	NP_001070731	Q9BYE2	TMPSD_HUMAN	epeats of A-S-P-A-[GLQR].	1	CCTGGGCTGGA	0.632	
+	9	1567		NM_005188	NP_005179	P22681	CBL_HUMAN	Pro-rich. E366_K477del	149	GGTGCCAAGGTA	0.433	
+	8	1632		NM_025004	NP_079280	Q0P6D6	CCD15_HUMAN		2	TTCTCCACAAAG	0.418	rs113451248
-	12	2974	_p.S949F|CD163_u	NM_004244	NP_004235	Q86VB7	C163A_HUMAN	Extracellular (Potential).	8	CCCAGGAACCT	0.483	
-	11	1138	l.2_Missense_Muta	NM_002864	NP_002855				5	CCTTTTCCATCCA	0.428	
-	3	198	zt.2_Missense_Mu	NM_002723	NP_002714	P10163	PRB4_HUMAN	PR]-[PR]-P-Q-G-G-N-Q-[PS]	1	GCTTTCCTGGAC	0.607	
+	66	10859		NM_002332	NP_002323	Q07954	LRP1_HUMAN	ntial).|LDL-receptor class A	22	CCAAACGGTGCA	0.627	
-	3	741	bg.2_Missense_Mu	NM_001682	NP_001673	P20020	AT2B1_HUMAN	lasmic (Potential).	3	CAATTCGGCTCT	0.418	
-	4	1007	NKS1B_uc009ztt.1	NM_152788	NP_690001	Q7Z6G8	ANS1B_HUMAN	ANK 6.	0	GAAGTGGCGTG	0.522	
+	1	2071		NR_003268					0	CTAATTGTGCTAG	0.433	rs150112365
-	1	1408		NM_175060	NP_778230	Q86T13	CLC14_HUMAN	cellular (Potential).	4	GACATCGTGCTCT	0.493	
+	4	2672	N5_uc010ana.2_In	NM_152447	NP_689660	Q96NI6	LRFN5_HUMAN	otential).|Fibronectin type-II	8	TATGATGATGGCA	0.443	
+	1	411		NM_000956	NP_000947	P43116	PE2R2_HUMAN	lasmic (Potential).	2	GGGACGTGGGG	0.697	
+	2	1635	XO34_uc010aoo.2	NM_017943	NP_060413	Q9NWN3	FBX34_HUMAN		5	AAGGTAGACAAA	0.433	
-	14	1393	PERB_uc010aub.1_	NM_024764	NP_079040	Q9H7T0	CTSRB_HUMAN		5	CTTCGGGGATGA	0.413	
+	8	2491	01ylr.2_Nonsense_	NM_018335	NP_060805	A8K0R7	ZN839_HUMAN		2	ATGGATCACTATT	0.582	
-	26	3808	e_Mutation_p.R53	NM_002226	NP_002217	Q9Y219	JAG2_HUMAN	lasmic (Potential).	5	GGTTGCGGATG	0.527	
-	1	545		NR_024387					0	TCACTTCCAATTT	0.393	
+	7	1124	A|OR4N4_uc010tzv	NM_001005241	NP_001005241	Q8N0Y3	OR4N4_HUMAN	Name=1; (Potential).	5	TTTCACCATAAG	0.458	
-	7	927	GM5_uc001zre.1_	NM_201631	NP_963925	O43548	TGM5_HUMAN		1	CTGTATCGTGGC	0.453	
-	11	1729	lzza.3_Missense_I	NM_031226	NP_112503	P11511	CP19A_HUMAN		3	CTTGGGGTAAAG	0.448	
-	17	3061	e_Mutation_p.P94	NM_015263	NP_056078	Q8TDJ6	DMXL2_HUMAN		9	TTTCTGGAGAAG	0.393	
-	34	3642	ahb.1_Missense_M	NM_020821	NP_065872	Q709C8	VP13C_HUMAN		2	AGACAATCTGAAT	0.308	
+	7	1178	ujs.1_Missense_M	NM_005902	NP_005893	P84022	SMAD3_HUMAN	teraction with XPO4.|MH2.	5	AGAGGCGTGCGG	0.572	
+	4	319	se_Mutation_p.V53	NM_138967	NP_620417	Q8TAC9	SCAM5_HUMAN	ical; (Potential).	1	CTGGCCGTGAAC	0.617	
+	8	842	PIP_uc002dcx.3_R	NM_006985	NP_008916	Q9UND3	NPIP_HUMAN	Pro-rich.	0	TACCCTCAGCGG	0.522	
+	2	1064		NM_001451	NP_001442	Q12946	FOXF1_HUMAN		0	GTGACCGAAAG	0.607	
-	13	4201	cj.2_Missense_Mu	NM_033004	NP_127497	Q9C000	NALP1_HUMAN		9	GACTCCCAAGG	0.547	
+	4	978	D1_uc002gja.2_5'F	NM_144607	NP_653208	Q6P9G0	CB5D1_HUMAN		1	GGATCCGGGAT	0.463	rs62059715
+	8	1322	va.1_Missense_M	NM_153210	NP_694942	Q70EL4	UBP43_HUMAN		5	AGGTCCGCCATC	0.373	
-	20	2432	.3_Splice_Site_p.K	NM_001100112	NP_001093582	Q9UKX2	MYH2_HUMAN		14	AAAATTACCTTGG	0.413	
-	19	2707		NM_000342	NP_000333	P02730	B3AT_HUMAN	.|Membrane (anion exchan	3	GCCGGCGTGGAC	0.637	
+	4	1207	.2_Missense_Muta	NM_003110	NP_003101	Q02086	SP2_HUMAN		0	CATCCGCACGC	0.592	
+	9	1177	_RNA|HILS1_uc01	NM_000023	NP_000014	Q16586	SGCA_HUMAN	lasmic (Potential).	2	CAGGTGCCCCTC	0.637	
+	12	1456		NM_153228	NP_694960	Q8N957	ANKF1_HUMAN		2	GTTCTATTACACA	0.328	
-	12	3477	_p.I1109L|TEX2_uc	NM_018469	NP_060939	Q8IWB9	TEX2_HUMAN		1	GCATTATAGTGAT	0.473	
-	2	382		NM_181449	NP_852114	Q496F6	CLM2_HUMAN	.|Extracellular (Potential).	4	GACCATGAATCCA	0.552	
-	2	576	lxx.2_Missense_M	NM_174983	NP_778148	Q6NUT3	CS028_HUMAN	ical; (Potential).	2	AGATCACGATGAA	0.637	
-	4	453	vq.2_Missense_M	NM_021155	NP_066978	Q9NNX6	CD209_HUMAN	|2.|7 X approximate tandem	1	TCAGCCGGGTC	0.567	

-	10	1810	lwr.1_Missense_M	NM_152476	NP_689689	Q96MR9	ZN560_HUMAN	C2H2-type 7.		6	GCATGTGAATAC	0.403	
-	4	1916	799_uc002mts.3_I	NM_001080821	NP_001074290	Q96GE5	ZN799_HUMAN	2H2-type 17.		6	TTACATTCATACG	0.413	
-	14	2453	O8_uc010eap.2_R	NM_020959	NP_066010	Q9HCE9	ANO8_HUMAN	ical; (Potential).		3	GGGGGAAGGCG	0.652	
+	4	1594		NM_031218	NP_112495	P35789	ZNF93_HUMAN	2H2-type 13.		1	TCCTCTTCCCTT	0.358	
-	4	935		NM_001159293	NP_001152765	C9JHM3	C9JHM3_HUMAN			1	TCTCCACTATGA	0.403	
-	5	1789	208_uc002nqo.1_I	NM_007153	NP_009084					7	ACCTTAATAAAG	0.398	
+	4	1004	ecy.2_Missense_M	NM_033468	NP_258429	Q9Y2Q1	ZN257_HUMAN	C2H2-type 4.		0	AGAATTCATAATA	0.378	
-	3	1798		NM_001001411	NP_001001411	Q8N7Q3	ZN676_HUMAN	2H2-type 12.		0	TATGTTTAGTAAG	0.383	
+	4	1398		NM_020855	NP_065906	Q9P255	ZN492_HUMAN	C2H2-type 9.		0	ATAAGAGAATTC	0.378	
-	5	1402		NM_001080409	NP_001073878					2	CAGTATGAATTAT	0.338	
-	4	1086	rj.1_Missense_Mu	NM_003430	NP_003421	Q05481	ZNF91_HUMAN	C2H2-type 7.		0	ATTCTTCACATTT	0.388	
-	6	2022	ense_Mutation_p.	NM_001010880	NP_001010880	O75290	Z780A_HUMAN	2H2-type 16.		0	AATAAGTTGCAT	0.403	
+	3	527		NM_005178	NP_005169	P20749	BCL3_HUMAN	ANK 1.	p.R145W(1)	2	GTGCACCGGCTG	0.507	
-	7	1641	_p.R409C|ZNF160_	NM_001102603	NP_001096073	Q9HCG1	ZN160_HUMAN	C2H2-type 6.		1	TTGAACGAACAC	0.408	
+	4	2891	dw.1_Missense_M	NM_138374	NP_612383	Q96IR2	ZN845_HUMAN	2H2-type 26.		0	CCTTCCGTCACA	0.363	rs150688663
+	4	2950	dw.1_Missense_M	NM_138374	NP_612383	Q96IR2	ZN845_HUMAN	2H2-type 27.		0	TACAAGTGTAAT	0.348	
+	4	1772	313_uc010eqq.1_I	NM_001004301	NP_001004301	Q6ZN06	ZN813_HUMAN			1	TGGAGATAAACC	0.378	
+	5	657	LRA1_uc010yfh.1_	NM_006863	NP_006854	O75019	LIRA1_HUMAN	2.|Extracellular (Potential).		3	GTAAGGAAGGA	0.592	
+	7	1096_1097	god.2_Missense_M	NM_001015878	NP_001015878	Q9UQB9	AURKC_HUMAN			6	TGCCTCCCTGTG	0.569	
-	3	2715	.2_Intron|ZNF814_	NM_001144989	NP_001138461	B7Z6K7	ZN814_HUMAN	2H2-type 22.		0	AGTGAGACTGG	0.403	
+	65	13161		NM_016252	NP_057336	Q9NR09	BIRC6_HUMAN			14	GAAGCTCAGTCA	0.418	
+	5	1019	.2_Missense_Muta	NM_001007231	NP_001007232	P42331	RHG25_HUMAN	Rho-GAP.	p.A210fs*4(1)	4	GGGAGCGGCCC	0.607	
+	8	7097	se_Mutation_p.S2	NM_152381	NP_689594	A4UGR9	XIRP2_HUMAN	Pro-rich.		14	AAAGTTCATCGA	0.493	
-	2	122	nse_Mutation_p.L2	NM_012433	NP_036565	O75533	SF3B1_HUMAN			6	TCATCAAGAGCT	0.393	
+	13	1554	ver.2_Missense_M	NM_024532	NP_078808	Q8N0X2	SPG16_HUMAN	WD 4.		2	TTTTTTCCTTTCT	0.363	
+	12	1533	_p.A468T|PSMD1_	NM_002807	NP_002798	Q99460	PSMD1_HUMAN	PC 2.		2	AGAACGCCAGC	0.363	
+	10	1177	se_Mutation_p.E25	NM_152879	NP_690618	Q16760	DGKD_HUMAN	DAGKc.		5	CTCTCCGAAATC	0.532	
-	6	454		NM_080675	NP_542406	Q8TC36	SUN5_HUMAN			1	GTAAGTGAATAG	0.383	
+	7	788		NM_017895	NP_060365	Q96GQ7	DDX27_HUMAN	Q motif.		2	CCCACCCCGATC	0.577	
-	2	640	xys.2_Missense_M	NM_020182	NP_064567	Q969W9	PMEPA_HUMAN	lasmic (Potential).		1	CATCTTCTCTCC	0.537	
+	1	2068	u.3_Intron|GNAS_u	NM_080425	NP_536350	P63092	GNAS2_HUMAN			292	AGCATCGGCGA	0.637	
-	3	332	GE_uc002yiw.1_R	NM_182482	NP_872288					0	CAAAATGCACATC	0.388	
-	3	326	GE_uc002yiw.1_R	NM_182482	NP_872288					0	CACATCGCTGAA	0.383	
+	1	756	.1_Intron|C21orf29	NM_198695	NP_941968	P60410	KR108_HUMAN			2	cggcctcctgcctgtcct	0.199	
-	20	1965	2_Nonsense_Muta	NM_001001438	NP_001001438	P48449	ERG7_HUMAN	PFTB 4.		0	TCCCCCCAGCCT	0.607	
+	3	765		NM_138435	NP_612444	Q8NEG4	FA83F_HUMAN			1	GTGTCCGCTCTG	0.602	
+	4	840	.1_Missense_Muta	NM_178329	NP_847899	P51677	CCR3_HUMAN	cellular (Potential).		8	TAACTGGGTTTTT	0.488	
-	2	2235	b.2_Missense_Mu	NM_017442	NP_059138	Q9NR96	TLR9_HUMAN	xtracellular (Potential).		4	TAGAGGTCCAGC	0.617	
-	8	869	.G244R|GLT8D1_	NM_152932	NP_690909	Q68CQ7	GL8D1_HUMAN	nenal (Potential).		0	AAACTCCAGGAT	0.358	
-	4	4145		NM_178822	NP_849144	Q6WRI0	IGS10_HUMAN			13	GTTTCGGCTGTG	0.468	
-	2	1388	fek.2_Missense_M	NM_014926	NP_055741	O94933	SLIK3_HUMAN	cellular (Potential).		10	ACAGAGGATAGC	0.478	
-	5	609	SF10_uc003fie.2_3	NM_003810	NP_003801	P50591	TNF10_HUMAN	cellular (Potential).		5	GTTCACCATTCCT	0.408	
-	7	1350		NM_031955	NP_114161	Q9BXB7	SPT16_HUMAN			3	TTTTTTCCAAAA	0.408	
+	24	3643	_Mutation_p.E115	NM_198241	NP_937884	Q04637	IF4G1_HUMAN			7	GCCGAGAACGA	0.572	
-	31	4108	_p.N1168S|FRYL_	NM_015030	NP_055845	O94915	FRYL_HUMAN			1	ATCAGGTTGCTC	0.527	
-	5	628	cw.2_Missense_M	NM_001010874	NP_001010874	Q5HYJ1	TECRL_HUMAN			0	AGCACTCTCTTTT	0.279	
-	6	1083	_p.G197E|ABCG2_	NM_004827	NP_004818	Q9UNQ0	ABCG2_HUMAN	er.|Cytoplasmic (Potential).		1	TCCATTCCTATA	0.408	

-	3	1116	ef.2_Missense_M	NM_001130698	NP_001124170	Q13507	TRPC3_HUMAN	lasmic (Potential).	2	GAGATCCAGCA	0.433	
+	3	988	_Mutation_p.R11	NM_012464	NP_036596	O43897	TLL1_HUMAN		7	AGACAGGATAA	0.348	
-	17	3140	D2_uc011cmz.1_	NM_001332	NP_001323	Q9UQB3	CTND2_HUMAN	ARM 9.	8	CTTATCTCCTTT	0.483	
+	4	655	jlb.1_Missense_M	NM_152403	NP_689616	Q63HQ2	EGFLA_HUMAN	nectin type-III 1.	7	AATATCGTGTG	0.458	
+	12	1981	LAM_uc003jle.1_	NM_152403	NP_689616	Q63HQ2	EGFLA_HUMAN	minin G-like 1.	7	CCCTGGGAAAA	0.557	
-	19	2398	g.2_Missense_Mu	NM_003062	NP_003053	O75094	SLIT3_HUMAN		4	CAGGAGGTTTC	0.602	
+	3	421	p.P38S|PPARD_u	NM_006238	NP_006229	Q03181	PPARD_HUMAN		1	CACTTCCTTCC	0.627	rs147861745
+	10	1134		NM_016224	NP_057308	Q9Y5X1	SNX9_HUMAN	PX.	0	TTTGAAGAGGAA	0.423	
-	1	315		NM_006735	NP_006726	O43364	HXA2_HUMAN		2	GCTGGCTATTGA	0.498	
-	12	1455	nse_Mutation_p.S	NM_001883	NP_001874	Q13324	CRFR2_HUMAN	lasmic (Potential).	4	TGATGCTGTGG	0.637	
+	7	1486	_p.P164S|CCDC1	NM_194300	NP_919276	Q6ZRS4	CC129_HUMAN		0	AAATCCCAGCC	0.483	
+	4	955	zu.2_Missense_M	NM_152626	NP_689839	Q03936	ZNF92_HUMAN	2H2-type 5.	0	CCTCAACCCTTA	0.353	
+	12	2644	TS2_uc011keg.1	NM_015570	NP_056385	Q8WXX7	AUTS2_HUMAN		3	CCCGAGGGTAC	0.527	
-	7	984	ex.2_Missense_M	NM_002291	NP_002282	P07942	LAMB1_HUMAN	inin N-terminal.	8	GATCTTCTATTTT	0.259	
+	37	5231	205_uc003vsx.2_	NM_015135	NP_055950	Q92621	NU205_HUMAN		6	AATTTCAAGAC	0.383	
-	16	3008	nse_Mutation_p.F	NM_015689	NP_056504	Q9ULE3	DEN2A_HUMAN	dDENN.	4	CCGAAACATCT	0.607	
-	15	1859_1860		NM_004333	NP_004324	P15056	BRAF_HUMAN	rotein kinas_R603>I(2)|p.T	18290	ATTTCACTGTAG	0.366	rs121913378
+	4	567	1_Intron|uc010loj.	NR_001296					0	GCCTGGACGCT	0.502	
+	1	352_353		NM_054028	NP_473369	Q96KT7	AMCL2_HUMAN	.|Helical; (Potential).	0	CGATGCCTCTTC	0.624	rs148317481
-	2	659	_p.N95S|OPRK1_	NM_000912	NP_000903	P41145	OPRK_HUMAN	lasmic (Potential).	2	AAATGTTGGTTG	0.388	
-	1	444		NM_152418	NP_689631	Q8NA75	DC4L2_HUMAN		1	TGTGCGGGTAT	0.547	
-	14	1957		NM_003184	NP_003175	Q6P1X5	TAF2_HUMAN		6	AAGTGGTCCCT	0.318	
-	31	6339	.1_Missense_Mut	NM_201380	NP_958782	Q15149	PLEC_HUMAN	us rod domain.|Potential.	9	CCGCCGCTGCC	0.687	
+	6	880	0mnn.2_Missense	NM_001012419	NP_001012419	Q5VUR7	A20A3_HUMAN		0	TAAAAAGAAGAT	0.234	
+	16	2435	p.T141M|TLE4_u	NM_007005	NP_008936	O60756	BCE1_HUMAN		5	GTACACGGGTG	0.602	
+	4	2303	lwx.1_Missense_	NM_133465	NP_597722	Q8N8K9	K1958_HUMAN		1	GGCTTGGCTCC	0.607	
-	18	1981	A1_uc010mws.2	NM_002077	NP_002068	Q92805	GOGA1_HUMAN	Potential.	1	CTCGGCCTGCA	0.672	
+	3	635		NM_014506	NP_055321	O14657	TOR1B_HUMAN		0	CAAGCCGTTTC	0.498	
+	30	2906		NM_000093	NP_000084	P20908	CO5A1_HUMAN	le-helical region.	11	ATGGCCCTGAA	0.617	
+	27	3460	mej.1_Missense_	NM_206920	NP_996803	Q6UXC1	AEGP_HUMAN	lasmic (Potential).	7	TGATCCGTAGA	0.502	
+	1	721		NM_001013736	NP_001013758	Q5HY64	FA47C_HUMAN		3	CCACCTGGAGC	0.637	
+	1	2230		NM_001013736	NP_001013758	Q5HY64	FA47C_HUMAN		3	TCTCCGCCCAG	0.637	
-	5	705	kh.1_Missense_M	NM_006307	NP_006298	P78539	SRPX_HUMAN	HYR.	0	TCCTTCGGGTG	0.443	
+	8	1294	RN1_uc011mpt.1_	NM_052957	NP_443189	Q96QF7	ACRC_HUMAN	Asp/Ser-rich.	3	AAGCTCCCGAC	0.557	
-	3	567	as.2_Missense_	NM_001144887	NP_001138359	Q99966	CITE1_HUMAN		0	AGAAGGAGAGA	0.627	
-	13	1625	42_splice|PHKA1_	NM_002637	NP_002628	P46020	KPB1_HUMAN		4	ACATACCTTGA	0.378	
-	2	323	1_uc004evh.2_Int	NM_004208	NP_004199	O95831	AIFM1_HUMAN		5	CATCTGGAGTT	0.383	
+	4	2019	EC1_uc010nsl.1_	NM_005462	NP_005453	O60732	MAGC1_HUMAN		4	TCCTCACTACT	0.582	
-	3	503		NM_021049	NP_066387	P43359	MAGA5_HUMAN	MAGE.	0	TGGGTCAGGGG	0.542	
+	5	820		NM_152492	NP_689705	Q2M243	CCD27_HUMAN	Potential.	1	AGATACAGGTT	0.587	
-	6	961_962	mx.2_Missense_	NM_001079843	NP_001073312	Q86V15	CASZ1_HUMAN		1	CCGGGGTGGA	0.604	
+	19	3059	p.R973Q|VPS13D	NM_015378	NP_056193	Q5THJ4	VP13D_HUMAN		5	TGGCCGGTACA	0.502	
-	9	1112	1_Intron|MST1P9_	NR_002729					0	CACCCTTGCGG	0.731	
+	9	1023_1024		NM_016233	NP_057317	Q9ULW8	PADI3_HUMAN		2	GCCAGGAAGG	0.653	
-	3	578	s.3_Missense_Mu	NM_020816	NP_065867	Q9P2E2	KIF17_HUMAN	inesin-motor.	4	GGTGTCAGCCC	0.577	
-	8	1355	e_Mutation_p.G32	NM_001103160	NP_001096630	Q6ZV89	SH2D5_HUMAN	SH2.	0	CTGGCCGCTAG	0.662	rs74703877
-	8	924	RNP40_uc010og	NM_004814	NP_004805	Q96DI7	SNR40_HUMAN	WD 6.	0	GTGACCAAGAA	0.373	

-	4	2501	se_Mutation_p.A43	NM_024503	NP_078779	Q5T1R4	ZEP3_HUMAN	TRAF-dependent NF-Kapp	6	CATGGCGGTCC	0.622	
+	11	1718	14A_uc010oki.1_Ir	NM_014663	NP_055478	O75164	KDM4A_HUMAN		1	TCTTCACGGGAT	0.517	
+	5	731	K3_uc001cmo.2_R	NM_004073	NP_004064	Q9H4B4	PLK3_HUMAN	rotein kinase.	0	GGTTGGAGCCT	0.498	
-	8	989	nv.1_Missense_M	NM_020365	NP_065098	Q9NR50	EI2BG_HUMAN		1	CCTGTCTCCTC	0.493	
-	42	5991	dqi.1_Missense_M	NM_000350	NP_000341	P78363	ABCA4_HUMAN	sporter 2.|Cytoplasmic.	12	AGGGCGAACTC	0.522	
-	6	913		NM_152380	NP_689593	Q96SF7	TBX15_HUMAN		2	TTCTCCCAGAAT	0.378	
-	5	724		NM_152380	NP_689593	Q96SF7	TBX15_HUMAN	T-box.	2	AACTCGAGGCT	0.438	
+	3	201	enu.1_Missense_M	NM_005105	NP_005096	Q9Y5S9	RBM8A_HUMAN		0	GCGTGGAGCAG	0.488	
+	14	1711	vkt.1_Missense_M	NM_001102663	NP_001096133				0	TAGTAGAGCCTG	0.473	
-	44	6536		NM_003126	NP_003117	P02549	SPTA1_HUMAN	Spectrin 20.	8	GCACACCTAAGG	0.517	
-	43	6158		NM_003126	NP_003117	P02549	SPTA1_HUMAN	Spectrin 19.	8	GATCTCGGGAA	0.498	
+	13	1668	p.P377L|NCSTN_	NM_015331	NP_056146	Q92542	NICA_HUMAN	cellular (Potential).	2	TGATCCCCAAA	0.552	
-	18	2573	plj.1_Missense_M	NM_018417	NP_060887	Q96PN6	ADCYA_HUMAN		3	TCTTTTCCTCAG	0.438	
-	3	512	f112_uc001ggj.2_I	NM_000450	NP_000441	P16581	LYAM2_HUMAN	(Potential).|C-type lectin.	5	TTTTTCTCTCTT	0.493	rs142216825
+	6	958	wb.2_Missense_M	NM_015569	NP_056384	Q9UQ16	DYN3_HUMAN		1	CCTTTCCCACCC	0.473	
-	2	421	|PIGC_uc001gin.2	NM_153747	NP_714969	Q92535	PIGC_HUMAN		1	CAATATTGGTATT	0.483	
+	22	3568	1gox.1_Missense_	NM_000721	NP_000712	Q15878	CAC1E_HUMAN	lasmic (Potential).	6	TGTTCATCTTCA	0.458	
+	1	143		NM_005298	NP_005289	O00155	GPR25_HUMAN	Name=1; (Potential).	1	CCTGGCGGCCT	0.587	
+	6	787	ion_p.T116M|DTL_	NM_016448	NP_057532	Q9NZJ0	DTL_HUMAN	WD 3.	0	CTGTACGGGTG	0.328	
-	2	410		NM_024746	NP_079022	Q6UWX4	HIPL2_HUMAN		1	GGCGTCGTAGA	0.567	
-	7	2012	p.P460S|SUSD4_	NM_017982	NP_060452	Q5VX71	SUSD4_HUMAN	lasmic (Potential).	0	GTCAGGGTTGT	0.582	
+	65	16687	p.S5548L|OBSCN	NM_001098623	NP_001092093	Q5VST9	OBSCN_HUMAN		28	GGTATCGGCCA	0.642	
-	3	392	tr.2_Nonsense_M	NM_014409	NP_055224	O75529	TAF5L_HUMAN		1	CAGTCGTCCAA	0.373	
-	5	723	.1_Missense_Mut	NM_030569	NP_085046	Q86UX2	ITIH5_HUMAN		4	CCCCGCGCCCA	0.617	
+	7	1473	e_Mutation_p.G23	NM_032812	NP_116201	Q6UX71	PXDC2_HUMAN	cellular (Potential).	4	AGTCGGACTGT	0.423	
+	7	926	YO3A_uc009xkq.1	NM_017433	NP_059129	Q8NEV4	MYO3A_HUMAN	rotein kinase.	18	AACACCGTTTT	0.443	
+	8	2452	TL_uc009xkw.1_M	NM_032844	NP_116233	Q96GX5	GWL_HUMAN	rotein kinase.	3	ATATTGAAGATC	0.373	
-	6	624	_p.A74T|MPP7_u	NM_173496	NP_775767	Q5T2T1	MPP7_HUMAN	L27 2.	1	CAAGGCCGCCG	0.512	
-	5	556	ZNF33B_uc001jag	NM_006955	NP_008886	Q06732	ZN33B_HUMAN		0	AAACTCATTCC	0.328	
+	7	1642		NM_000314	NP_000305	P60484	PTEN_HUMAN	2 tensin-typ_N212>Y(2)|p.	2334	CTATTCCAATGTT	0.358	
-	3	643	se_Mutation_p.A85	NM_018058	NP_060528	Q9NQ79	CRAC1_HUMAN		5	CGACCGCGATG	0.662	
+	10	1517	p.E237K|C10orf81	NM_024889	NP_079165	Q5SXH7	CJ081_HUMAN		1	AAGTGGAGAAA	0.428	
+	2	1391	g.2_5'Flank|EMX2	NM_004098	NP_004089	Q04743	EMX2_HUMAN	Homeobox.	0	CACACAGCCTC	0.632	
+	1	731		NM_001127389	NP_001120861	F5GZ66	F5GZ66_HUMAN		0	TCGAAGGGCCA	0.701	
+	9	1051	_p.S306F|PHRF1_	NM_020901	NP_065952	Q9P1Y6	PHRF1_HUMAN	Arg-rich.	0	GTCTTCCCTGC	0.672	
+	8	1197	nt_p.H143H|EFCA	NM_020376	NP_065109	Q96AD5	PLPL2_HUMAN	enal (Potential).	0	GGCCACGGCCA	0.711	
-	13	1921	.W638G|TRPM5_	NM_014555	NP_055370	Q9NZQ8	TRPM5_HUMAN	lasmic (Pote p.W638*(1)	4	CCCCCACCAGA	0.642	
-	1	14		NM_001005238	NP_001005238	Q8NGK0	O51G2_HUMAN	cellular (Potential).	2	CCAGGGATCCC	0.552	rs150566249
+	10	1335	p.H402Y|TUB_uc	NM_177972	NP_813977	P50607	TUB_HUMAN		1	TGGTTCATGAG	0.547	
+	1	140		NM_001005205	NP_001005205	Q8NGP2	OR8J1_HUMAN	lasmic (Potential).	2	TCATCACCCTCA	0.502	
+	6	1047	e.2_Nonsense_Mu	NM_207341	NP_997224	P60852	ZP1_HUMAN	llular (Potential).|ZP.	0	GCGACCAGCTC	0.612	
-	3	495	GAT3_uc001ntx.2_	NM_012200	NP_036332	O94766	B3GA3_HUMAN	enal (Potential).	0	ACCACGGGGAT	0.682	
+	28	4579	ez.2_Missense_M	NM_032223	NP_115599	Q9H6A9	PCX3_HUMAN		0	ACTCGGATCCC	0.622	
+	21	2507	nu.2_Missense_M	NM_001164161	NP_001157633	Q5H9R7	PP6R3_HUMAN		0	AACCAGCACTG	0.512	
-	22	5119	ssense_Mutation_	NM_012309	NP_036441	Q9UPX8	SHAN2_HUMAN		5	GGGGCGAACAG	0.602	
-	5	778	tj.1_Missense_Mu	NM_001162951	NP_001156423	Q9HCH5	SYTL2_HUMAN		3	TTCTGGCAACT	0.333	
+	23	3601	_Mutation_p.R115	NM_001080463	NP_001073932	Q8NCM8	DYHC2_HUMAN	n (By similarity).	0	ACTTTTCGGTTT	0.323	

-	5	243	FXYD2_uc001prk.	NM_001680	NP_001671	P54710	ATNG_HUMAN		0	ATTTGCCTGGTG	0.584	
+	46	6278	_p.S912R|SORL1_	NM_003105	NP_003096	Q92673	SORL_HUMAN	tential).|Fibronectin type-III	15	TGATAGTGCCAT	0.393	
-	16	2931	_p.P312S|CDON_	NM_016952	NP_058648	Q4KMG0	CDON_HUMAN	cellular (Potential).	6	TGACAGGATATTC	0.428	
-	17	2793	p.R870W|CHD4_u	NM_001273	NP_001264	Q14839	CHD4_HUMAN	ase ATP-binding.	2	CAGCCGATGGG	0.468	
-	8	469	_p.D76N|MFAP5_	NM_003480	NP_003471	Q13361	MFAP5_HUMAN		1	CTCATCCCAGC	0.443	
-	6	604	gl.2_Missense_Mu	NM_002864	NP_002855				5	AGAGGGGAAAG	0.502	
-	5	740	i.2_Intron|CLEC7A	NM_197947	NP_922938	Q9BXN2	CLC7A_HUMAN	.|Extracellular (Potential).	1	GGGCCGAGAAA	0.368	
-	1	645	B4_uc001qzf.1_Int	NM_181429	NP_852094	Q7RTR8	T2R42_HUMAN	lasmic (Potential).	1	ACTGAGCTTCAA	0.413	
-	13	3180		NM_000834	NP_000825	Q13224	NMDE2_HUMAN	lasmic (Potential).	12	CCCATCGATGG	0.587	
-	8	992	_p.E264K|CASC1_	NM_001082973	NP_001076442	Q6TDU7	CASC1_HUMAN		2	CTCTTTCTTGTT	0.358	
-	34	9446		NM_003482	NP_003473	O14686	MLL2_HUMAN		41	CCAAGGGAATTG	0.607	
+	8	1341	ln.2_Missense_Mu	NM_001095	NP_001086	P78348	ACCN2_HUMAN	llular (By similarity).	1	TGACCCGCTATG	0.532	
+	2	586	ch.1_Missense_M	NM_032889	NP_116278	Q6N075	MFSD5_HUMAN	ical; (Potential).	3	GCTAGTGGGGC	0.537	
-	1	151		NM_001005493	NP_001005493	A6NF89	OR6C6_HUMAN	lasmic (Potential).	2	CCGGGGATCCA	0.408	rs138420259
+	1	209		NM_001005182	NP_001005182	Q96RD1	OR6C1_HUMAN	Name=2; (Potential).	2	AAATTTCGTTCAC	0.378	
+	1	116		NM_001005494	NP_001005494	Q8NGE1	OR6C4_HUMAN	Name=1; (Potential).	0	TCCTAGGAAATCT	0.418	
+	4	512	5A_uc010srr.1_Int	NM_004984	NP_004975	Q12840	KIF5A_HUMAN	Kinesin-motor.	3	CTGCACGACCCT	0.507	
+	9	1894		NM_013381	NP_037513	Q9UKU6	TRHDE_HUMAN	cellular (Potential).	3	ATCTATGATATCA	0.323	
-	18	2308	ui.1_RNA|PPFIA2	NM_003625	NP_003616	B7Z663	B7Z663_HUMAN		6	GGAGATGAACTG	0.547	
-	1	715		NM_152638	NP_689851	Q8TC90	CL012_HUMAN		2	GGGGTGGGCGC	0.652	
+	4	762	nse_Mutation_p.E2	NM_178826	NP_849148	Q32M45	ANO4_HUMAN	cellular (Potential).	6	TTTGATGAATTAG	0.403	
+	5	669	tz.1_Nonsense_M	NM_014503	NP_055318	O75691	UTP20_HUMAN	HEAT 1.	4	TATATACAGGTAA	0.418	
+	39	4454		NM_017564	NP_060034	Q8WWQ8	STAB2_HUMAN	cellular (Potential).	14	CTGGCGAGGAG	0.443	
+	4	654	n_p.V94I|C12orf23	NM_152261	NP_689474	Q8WUH6	CL023_HUMAN	ical; (Potential).	0	GGAGGTGTTACA	0.478	
+	3	993_994		NM_007076	NP_009007	Q9BVA6	FICD_HUMAN		0	GCATCGGCTCCG	0.624	
+	10	1163_1164	_p.S361F|TPCN1_	NM_017901	NP_060371	Q9ULQ1	TPC1_HUMAN	cellular (Potential).	3	GCCCTCCTACTC	0.545	
+	2	420	se_Mutation_p.P47	NM_153348	NP_699179	Q8N3Y1	FBXW8_HUMAN	F-box.	3	ATGTGCCTTTCTT	0.338	
-	3	948	IABLO_uc010tad.	NM_019887	NP_063940	Q9NR28	DBLOH_HUMAN		0	AAGCCAATCGTC	0.458	
+	3	339	udi.1_Missense_M	NM_003959	NP_003950	O75146	HIP1R_HUMAN	ENTH.	1	AGGTCCTTCGA	0.642	
+	1	912		NM_001033602	NP_001028774	Q5JR59	MTUS2_HUMAN		0	ACACATCACATT	0.517	
+	34	5904	bi.2_Missense_Mu	NM_015678	NP_056493	Q8NFP9	NBEA_HUMAN		11	CTTCTTCGTGAA	0.303	
+	1	5230		NM_207361	NP_997244	Q5SZK8	FREM2_HUMAN	ar (Potential).|CSPG 12.	11	GGAGACCCCAA	0.493	
+	7	1864		NM_004466	NP_004457	P78333	GPC5_HUMAN		5	TGTGATGATGAA	0.458	
-	11	1427	oz.2_Missense_Mu	NM_052867	NP_443099	Q8IZF0	NALCN_HUMAN	cellular (Potential).	16	TACTGCCTCCTG	0.552	
+	1	157		NM_001004723	NP_001004723	Q8NGD1	OR4N2_HUMAN	lasmic (Potential).	4	CAGACCCTGGG	0.463	
+	1	447		NM_001004717	NP_001004717	Q8NH43	OR4L1_HUMAN	Name=4; (Potential).	5	TTCATGGATAATT	0.398	
-	33	5636	Mutation_p.Q1744	NM_020920	NP_065971	Q9HCK8	CHD8_HUMAN		10	CATCTTGGGACAT	0.483	
-	35	5330		NM_002471	NP_002462	P13533	MYH6_HUMAN	Potential.	4	CCTTCTCCTCGG	0.582	
+	33	3294	wlk.2_Missense_M	NM_138360	NP_612369	Q8ND23	LR16B_HUMAN		5	TGCCTCCACTCC	0.652	
+	33	3312	wlk.2_Missense_M	NM_138360	NP_612369	Q8ND23	LR16B_HUMAN		5	GAGGCGCCGGG	0.682	
+	2	3216	n.2_Missense_Mut	NM_001173	NP_001025226	Q13017	RHG05_HUMAN		5	TATAGTCCAATTG	0.403	
+	14	1943	vze.2_Missense_M	NM_152330	NP_689543	Q96NE9	FRMD6_HUMAN		3	CCAGAAAGACTT	0.478	
+	3	453		NM_144578	NP_653179	Q8NDC0	MISSL_HUMAN	Pro-rich.	0	GTCCCCCACCT	0.602	
-	3	498	xbt.2_Missense_M	NM_014750	NP_055565	Q15398	DLGP5_HUMAN	Potential.	2	TTTTGGAGCATCT	0.338	
+	10	1056	xke.2_Missense_M	NM_133509	NP_598193	O15315	RA51B_HUMAN		0	CCTTCACCTCATT	0.468	
-	2	436		NM_001080451	NP_001073920	Q86U17	SPA11_HUMAN		1	GGCAAGGGTGT	0.557	
+	2	1050	nk|uc001ykg.2_5'Fl	NM_001362	NP_001353	P55073	IOD3_HUMAN	cellular (Potential).	3	GGCCCCGGAGG	0.597	

+	4	607	PR2_uc010awl.2_	NM_014844	NP_055659	O15040	TCPR2_HUMAN	WD 2.	3	TGTTTATTCTTCT	0.338	
-	3089	_uc001ysq.2_5'Flank|KIAA0125_uc001ysr.2_5'Flank							0	ACAGTGACACG	0.567	
-	3	185	as.2_Missense_M	NM_000462	NP_000453	Q05086	UBE3A_HUMAN		3	CCATACGAAGA	0.433	
-	9	1368	ba.2_Missense_M	NM_000814	NP_000805	P28472	GBRB3_HUMAN	lasmic (Probable).	5	CTTCTCGAGGC	0.488	
+	7	3208_3209	.S1046F|C15orf5	NM_175741	NP_786883	Q86Y26	NUT_HUMAN		30	ACTCTCCAACTT	0.505	
+	15	2538	bj.1_Nonsense_	NM_001013703	NP_001013725	Q9P2K8	E2AK4_HUMAN	otein kinase 2.	4	CTTTTTCGAGAG	0.378	
-	3	395	utation_p.R111Q|	NM_001080792	NP_001074261	Q9BV29	CO057_HUMAN		1	GAGTTCGAAGC	0.438	rs139886034
-	5	1159	d.2_Missense_Mu	NM_138792	NP_620147	Q8WVC0	LEO1_HUMAN		0	CTGAGAAAGTT	0.338	
+	1	730		NM_001080534	NP_001074003	Q8NB66	UN13C_HUMAN		7	TCATGGAAATG	0.448	
-	2	175	1_uc010bkk.2_Mis	NM_006715	NP_006706	Q9NTJ4	MA2C1_HUMAN		0	GAAGTCTCTCC	0.706	
+	16	7690	_Mutation_p.T24	NM_013227	NP_037359	E7EX88	E7EX88_HUMAN		3	CTTCACGTGTA	0.507	
+	8	1236	_p.R374P|MAN2A	NM_006122	NP_006113	P49641	MA2A2_HUMAN	enal (Potential).	3	CAAACGCCTGC	0.557	
+	8	908	e_Mutation_p.D18	NM_020664	NP_065715	Q9NUI1	DECR2_HUMAN		0	TGGCCGATGGC	0.627	
+	9	2642	H_uc002chj.2_5'F	NM_005632	NP_005623	O75808	CAN15_HUMAN	lpain catalytic.	2	CCTGCGTGGCG	0.677	rs139791573
+	4	727	H1_uc002csc.2_	NM_032296	NP_115672	Q4VC44	FWCH1_HUMAN	YWCH-type 1.	0	CATTCGGGGGC	0.612	
+	4	730	EN2_uc010bsx.2	NM_172229	NP_757384	Q8NCW0	KREM2_HUMAN	lar (Potential).|WSC.	2	CAGCGGCACCT	0.647	
+	4	2388		NM_005223	NP_005214	P24855	DNAS1_HUMAN		0	ACTGGGACGGA	0.597	
+	17	2070	B_uc002dme.2_	NM_212535	NP_997700	P05771	KPCB_HUMAN	kinase C-terminal.	9	ACAAGAGAGAC	0.453	
-	17	2779	FHOD1_uc010ced	NM_013241	NP_037373	Q9Y613	FHOD1_HUMAN		3	GCTAACCTTGG	0.587	
-	6	836	.R287W|ATP6V0	NM_004691	NP_004682	P61421	VA0D1_HUMAN		0	GAGCCGCCCAC	0.597	
+	13	1790	.1_RNA|SPG7_uc	NM_003119	NP_003110	Q9UQ90	SPG7_HUMAN	rial matrix (Potential).	0	GGAGGCCGTGA	0.617	
-	4	685	S156F|YWHAE_u	NM_006761	NP_006752	P62258	1433E_HUMAN		3	ATACGGAAAAA	0.483	
-	4	474	NA_uc010cju.2_5	NM_006224	NP_006215	Q00169	PIPNA_HUMAN		1	GCATTCGAACA	0.522	
+	8	1415	sense_Mutation_p	NM_001114974	NP_001108446	Q2TAL5	SMTL2_HUMAN	CH.	0	CCTACGTCCAG	0.592	rs144468111
+	22	2866	vsn.1_Splice_Site_	NM_153827	NP_722549	Q8N4C8	MINK1_HUMAN		6	AGCGCGTGAGT	0.657	rs112125089
-	11	1923_1924	_p.L605F|CAMTA	NM_015099	NP_055914	O94983	CMTA2_HUMAN	IPT/TIG.	1	GAAAGGGGCCC	0.594	
+	11	1793	.S540G|TNK1_uc	NM_003985	NP_003976	Q13470	TNK1_HUMAN	Pro-rich.	3	CCTCTAGCTCT	0.617	
+	76	11805	m.1_Missense_M	NM_020877	NP_065928	Q9P225	DYH2_HUMAN	6 (By similarity).	13	TCCCCCACCCA	0.552	
-	5	829		NM_001128076	NP_001121548	A6NLX3	SPDE4_HUMAN		0	TACCTCCTCCA	0.622	
-	6	735	_Mutation_p.S14	NM_001082968	NP_001076437	Q6ZVM7	TM1L2_HUMAN		0	GCGAGGAATAG	0.582	
+	2	153	S9C_uc010vyb.1_	NM_001040078	NP_001035167	Q6DKI2	LEG9C_HUMAN	Galectin 1.	1	GGACGGATTTC	0.567	
+	4	999	n_p.R66C|MAPK7_	NM_139033	NP_620602	Q13164	MK07_HUMAN	zation (By similarity).|Protei	9	TGGCTCGTGGC	0.552	
+	5	679	F4_uc002hcq.1_I	NM_004295	NP_004286	Q9BUZ4	TRAF4_HUMAN	TRAF-type 2.	2	CCAAGCGCACT	0.592	
+	18	3134	AP1_uc010wgs.1_	NM_003632	NP_003623	P78357	CNTP1_HUMAN	Extracellular (Potential).	8	AGGCCGCTGCG	0.597	
-	3	549	p.E150K|KIF18B_	NM_001080443	NP_001073912				2	CACCTCGAAGT	0.647	
+	6	842	BP1_uc010dbj.2_	NM_006546	NP_006537	Q9NZI8	IF2B1_HUMAN		1	GAGGGGGCTTT	0.647	
-	25	1820_1821		NM_000088	NP_000079	P02452	CO1A1_HUMAN	e-helical region.	382	GTCCGGGGCG	0.614	
+	5	2288	P1_uc002iuy.2_R	NM_003488	NP_003479	Q92667	AKAP1_HUMAN		1	CGCTCCCCCAT	0.527	
-	17	2654	_p.P806L|RECQL	NM_004259	NP_004250	O94762	RECQ5_HUMAN		3	TGGGCGGGCAG	0.652	
+	8	1830	ense_Mutation_p.	NM_001142602	NP_001136074	Q9NYA1	SPHK1_HUMAN		1	CAGTGGATGGG	0.592	
-	18	3474	l.3_Missense_Mu	NM_022066	NP_071349	Q9C0C9	UBE2O_HUMAN		5	CAGCCGCCAGC	0.657	
-	7	738_739	_p.H255Y|PCYT2_	NM_002861	NP_002852	Q99447	PCY2_HUMAN	lytic 2 (Potential).	0	GATACGGAACA	0.609	
+	66	8737	s.3_Missense_Mu	NM_198129	NP_937762	Q16787	LAMA3_HUMAN	minin G-like 3.	11	GCAGTCTCTGC	0.463	
-	2	1156	m.1_Missense_Mu	NM_020783	NP_065834	Q9H2B2	SYT4_HUMAN	Probable).|Cytoplasmic (P	5	AATTCCCGAGA	0.328	
+	17	3094	.1_Intron|DCC_uc	NM_005215	NP_005206	P43146	DCC_HUMAN	ellular (Potential).	17	CACCTCGGTCC	0.453	
+	25	4248	f.1_Missense_Mut	NM_005215	NP_005206	P43146	DCC_HUMAN	lasmic (Potential).	17	CTCTGGAGAGG	0.522	
+	2	465	LN_uc002lxh.1_R	NM_020170	NP_064555	Q969V3	NCLN_HUMAN	enal (Potential).	0	GCAGTCGGCGG	0.721	

+	15	2351_2352	p.G743K|KDM4B_	NM_015015	NP_055830	O94953	KDM4B_HUMAN		1	CCCTCGGAAAGG	0.649	
+	5	454	nse_Mutation_p.S8	NM_001974	NP_001965	Q14246	EMR1_HUMAN	EGF-like 3; calcium-binding	5	TCACCAGCAGCG	0.483	
+	3	624	mgu.3_Missense_I	NM_020902	NP_065953	Q9P1Y5	CAMP3_HUMAN	CH.	1	GTGGACACGGTA	0.652	
-	4	659	q.2_Missense_Mut	NM_021155	NP_066978	Q9NNX6	CD209_HUMAN	|5.|7 X approximate tanden	1	TCAGCCGGGTCA	0.562	rs141131967
+	4	424	Site_p.A115_splice	NM_005968	NP_005959	P52272	HNRPM_HUMAN		0	ATGTGCGTAAGT	0.378	
-	26	3527	2mki.1_Nonsense_	NM_030957	NP_112219	Q9H324	ATS10_HUMAN	PLAC.	4	AGAACTGAAATT	0.627	
-	3	24249		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	ch.|Extracellular (Potential).	57	GTGCAACATATCT	0.473	
-	67	5182		NM_015719	NP_056534	P25940	CO5A3_HUMAN	lar collagen NC1.	10	CCTTTCCGGAGC	0.592	
+	9	824	xoj.1_Missense_M	NM_007253	NP_009184	P98187	CP4F8_HUMAN		1	TGTGGACGGCGC	0.552	
+	2	682	p.T177M|MYO9B_	NM_004145	NP_004136	Q13459	MYO9B_HUMAN	yosin head-like.	1	TCTACACGTACGC	0.547	
-	4	305	n_p.V92E|TMEM16	NM_017814	NP_060284	Q9NX61	T161A_HUMAN	cellular (Potential).	2	GCATCCACGGTC	0.607	
+	4	1536	s.1_Intron|ZNF90_u	NM_007138	NP_009069	Q03938	ZNF90_HUMAN	C2H2-type 11.	2	GCTCCTCAAACC	0.418	
-	4	800	p.N218H|ZNF43_u	NM_003423	NP_003414	P17038	ZNF43_HUMAN	type 2; degenerate.	2	CAGTATTAATTCT	0.323	
-	1	1166		NM_002152	NP_002143	P23327	SRCH_HUMAN	.|2-6.|6 X approximate tand	1	CCTCTTCCTTTCT	0.532	
-	4	349	K7_uc010yco.1_5'U	NM_139277	NP_644806	P49862	KLK7_HUMAN	Peptidase S1.	0	GCGTATCACTGCC	0.572	
-	5	563		NM_022046	NP_071329	Q9P0G3	KLK14_HUMAN	Peptidase S1.	1	GGGTGCGTCACC	0.647	
+	2	187		NM_002030	NP_002021	P25089	FPR3_HUMAN	cellular (Potential).	6	GAAGATGGAAAC	0.483	
-	4	576		NM_052882	NP_443114	Q96PE6	ZIM3_HUMAN	KRAB.	2	CCTTTCCTTGTTC	0.468	
+	4	747		NM_182626	NP_872432	Q96LS8	CB048_HUMAN		0	CCATTCTCAGACC	0.587	
+	13	1029	e_Mutation_p.L227	NM_007266	NP_009197	Q9HCN4	GPN1_HUMAN		0	TGATTTGATCCTG	0.483	
-	7	1056		NM_018079	NP_060549	Q8N5C6	SRBD1_HUMAN		1	TGTCTTGCTCTCT	0.423	
+	21	2412	M2_uc002suk.2_M	NM_144707	NP_653308	Q8N271	PROM2_HUMAN	cellular (Potential).	1	CCCTCTCCGGAG	0.622	
-	1	137		NM_000682	NP_000673	P18089	ADA2B_HUMAN	asmic (By similarity).	3	TCTGAGGGGCG	0.632	
-	3	1144	uc002too.1_5'Flank	NM_017969	NP_060439	Q96ST2	IWS1_HUMAN	approximate tandem repeat	1	TTGGGGGATCCT	0.557	
-	4	1062	uci.2_Missense_M	NM_033272	NP_150375	Q9NS40	KCNH7_HUMAN	lasmic (Potential).	5	GGTGGACGCCGA	0.398	
-	240	49420	094S|TTN_uc010z	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	GCAGCATTGATT	0.433	
-	230	46866	243K|TTN_uc010z	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	TGACTTCCTCCC	0.393	
+	19	2857	vap.1_Missense_M	NM_152526	NP_689739	Q8TEW8	PAR3L_HUMAN	Lys-rich.	4	AAAGAGGATAAG	0.423	
-	14	2220	ve.1_Missense_Mu	NM_005689	NP_005680	Q9NP58	ABCB6_HUMAN	BC transporter.	2	TCTATTCGGATGC	0.537	rs13402964
-	14	1474	rmd.3_Missense_M	NM_019593	NP_062539	Q9NPB8	GPCP1_HUMAN	GDPD.	0	CTTTCCGATCCTT	0.348	
+	4	591	p.R26Q|TM9SF4_u	NM_014742	NP_055557	Q92544	TM9S4_HUMAN		2	AGAGCCGACTCG	0.577	rs139891092
+	2	296	n_p.R80Q|SEMG2_	NM_003008	NP_002999	Q02383	SEMG2_HUMAN	at-rich region.|3-1.	1	GGACCCGAAAAA	0.368	
-	1	364		NM_181621	NP_853652	Q52LG2	KR132_HUMAN		0	CTCGATCCATAGC	0.582	
-	1	208		NM_181611	NP_853642	Q3LI72	KR195_HUMAN		0	AAAATCCAGAGAA	0.502	rs73186218
+	2	316	AR1_uc011adv.1_5	NM_000629	NP_000620	P17181	INAR1_HUMAN	cellular (Potential).	2	TCTGTCGGGAATC	0.348	
+	12	1334	zbj.2_Missense_M	NM_018964	NP_061837	P57057	GLPT_HUMAN	ical; (Potential).	0	ATTCTCCCCGGGC	0.572	
+	17	2399	p.E708K|CABIN1_	NM_012295	NP_036427	Q9Y6J0	CABIN_HUMAN		5	TGTTTTGAGTGTT	0.587	
+	4	1238	xd.1_Missense_Mu	NM_021115	NP_066938	Q9BYH1	SE6L1_HUMAN	xtracellular (Potential).	6	TAATCCGAAGCCC	0.632	
-	5	1753	mf.3_Missense_Mu	NM_001098527	NP_001091997	O75678	RFPL2_HUMAN	B30.2/SPRY.	1	CAAGCTCTGTGGT	0.582	
-	3	314		NM_002872	NP_002863	P15153	RAC2_HUMAN		4	CGGAGACGGTCG	0.403	
-	7	1507		NM_152512	NP_689725	Q8IYW4	ENTD1_HUMAN		3	GATAAAGGAGAAA	0.398	
-	1	1839		NM_006071	NP_006062	Q9NTG1	PKDRE_HUMAN	ular (Potential).|REJ.	5	GTTCTCTTTTACT	0.433	
-	33	5283	p.T518M|PLXNB2_	NM_012401	NP_036533	O15031	PLXB2_HUMAN	lasmic (Potential).	6	GCTCCGTGCGCC	0.622	
+	31	4087	PR1_uc011asu.1_In	NM_001099952	NP_001093422	Q14643	ITPR1_HUMAN	lasmic (Potential).	21	TCTGCGCAGGCA	0.453	
-	1	97	l_5'Flank|GRIP2_u	NM_001080423	NP_001073892	Q9C0E4	GRIP2_HUMAN		1	CACGCGGGAAG	0.597	
-	21	2637	cdj.2_Missense_M	NM_001068	NP_001059	Q02880	TOP2B_HUMAN		5	GGAATTATAGGA	0.408	
+	2	1352		NM_152393	NP_689606	Q2TBA0	KBTB5_HUMAN	Kelch 2.	1	TGGTCGGTGGCA	0.642	

+	5	481	C36_uc011bck.1_	NM_178173	NP_835467	Q8IYA8	CCD36_HUMAN		2	AAAATGATTATT	0.363	
-	12	1522	_p.P342S|PCBP4_	NM_033010	NP_127503	P57723	PCBP4_HUMAN		0	CGGCGGCGGCC	0.622	
-	2	1584	b.2_Missense_Mu	NM_017442	NP_059138	Q9NR96	TLR9_HUMAN	xtracellular (Potential).	4	AGTTCTCACTC	0.527	
+	6	664	k.1_Missense_Mu	NM_002217	NP_002208	Q06033	ITIH3_HUMAN		3	TCCTGGGAAGC	0.532	
+	2	464	_p.R101*|CACNA	NM_001128840	NP_001122312	Q01668	CAC1D_HUMAN	lasmic (Potential).	11	ACAGCCGACCT	0.488	
+	19	3095	.1_3'UTR|MINA_u	NM_153605	NP_705833				0	TGGAGGGAGAA	0.318	
+	6	739		NM_017945	NP_060415	Q9BS91	S35A5_HUMAN	ical; (Potential).	1	CTTGACTGCCG	0.438	
+	16	3165		NM_032242	NP_115618	Q9UIW2	PLXA1_HUMAN	r (Potential).|IPT/TIG 3.	3	TGTCCGTGAAC	0.647	
+	28	5144	6A6_uc003eni.3_5	NM_001102608	NP_001096078	A6NMZ7	CO6A6_HUMAN	le-helical region.	8	CAGGAGAGATG	0.343	
+	2	382	P1B3_uc003euh.	NM_001679	NP_001670	P54709	AT1B3_HUMAN	ellular (Potential).	0	AGGTTCCAAAA	0.333	rs41265475
-	1	137		NM_178822	NP_849144	Q6WRI0	IGS10_HUMAN	LRRNT.	13	GGTACCGAAAT	0.552	rs148699040
-	26	2991		NM_001041	NP_001032	P14410	SUIS_HUMAN	|P-type 2.|Isomaltase.	14	TCTGGGAAAGT	0.363	
+	21	2843	y.2_Missense_Mu	NM_003741	NP_003732	Q9H2X0	CHRD_HUMAN		3	GCAGGCTGATG	0.612	
+	7	1364	frw.1_Missense_M	NM_198485	NP_940887	Q6ZUI0	TPRG1_HUMAN		0	GTCAAGTGTGA	0.453	
+	20	2198	s.1_Missense_Mu	NM_004787	NP_004778	O94813	SLIT2_HUMAN	LRRCT 3.	11	CCAATCCTTTTA	0.463	
+	21	2683	p.Q717*|LIMCH1_	NM_014988	NP_055803	Q9UPQ0	LIMC1_HUMAN		4	CATTCCAGGGA	0.398	
+	9	825	1D4_uc003gzg.2_	NM_001040402	NP_001035492	Q92564	DCNL4_HUMAN	DCUN1.	2	GCCCCTTTTTC	0.383	
+	4	471		NM_001432	NP_001423	O14944	EREG_HUMAN	r (Potential).|EGF-like.	2	TGTCCGATGTG	0.358	
+	2	765	bv.1_3'UTR|STBD	NM_003943	NP_003934	O95210	STBD1_HUMAN	lasmic (Potential).	1	AAGTTGCCTTC	0.448	
-	2	200	.E36K|ADH6_uc0	NM_000672	NP_000663	P28332	ADH6_HUMAN		3	AACTTCCTTTG	0.388	
-	5	1437	w.1_Missense_M	NM_178833	NP_849155	Q86UD5	NHDC2_HUMAN		0	AAGGCCAGCAC	0.388	
-	4	1784	T4_uc010imw.2_	NM_022569	NP_072091	Q9H3R1	NDST4_HUMAN	Heparan sulfate N-deacety	4	AGACCGAAGTA	0.388	
-	5	1098		NM_003619	NP_003610	P56730	NETR_HUMAN	SRCR 2.	1	ATTCCCAGTGC	0.478	
+	3	5551	p.1_Missense_Mu	NM_024582	NP_078858	Q6V0I7	FAT4_HUMAN	.|Extracellular (Potential).	18	ACATTCCTGAG	0.403	
+	2	152	XFP1_uc011cjd.1_	NM_021634	NP_067647	Q9HBX9	RXFP1_HUMAN	ellular (Potential).	0	GACAGGATGTC	0.507	
+	2	179	XFP1_uc011cjd.1_	NM_021634	NP_067647	Q9HBX9	RXFP1_HUMAN	ential).|LDL-receptor class	0	TATTTCCCCTGT	0.517	
-	14	9951		NM_005245	NP_005236	Q14517	FAT1_HUMAN	(Potential).|Cadherin 30.	12	ACTTGCTGCAT	0.413	
-	63	10660	H5_uc003jfc.2_5'	NM_001369	NP_001360	Q8TE73	DYH5_HUMAN		31	AAGATCACGAA	0.373	
-	2	822	uc003jfp.2_5'Flan	NM_001102562	NP_001096032	A6NNE9	MARHB_HUMAN	ING-CH-type.	0	CTGATCCATTTT	0.428	
+	3	539	lm.1_Missense_M	NM_003999	NP_003990	Q99650	OSMR_HUMAN	ellular (Potential).	5	AACCTTCCTTAT	0.388	
-	8	1293		NM_001737	NP_001728	P02748	CO9_HUMAN	MACPF.	0	CATCTTTATTAAA	0.413	
+	7	747	q.1_Missense_Mu	NM_000163	NP_000154	P10912	GHR_HUMAN	tential).|Fibronectin type-II	6	ACAACGAAACT	0.373	
+	8	1105	OLK_uc010izr.2_	NM_016218	NP_057302	Q9UBT6	POLK_HUMAN	UmuC.	4	ATTCTTCCCAATA	0.323	
-	3	908	_p.R79W|MEF2C_	NM_002397	NP_002388	Q06413	MEF2C_HUMAN	-type (Potential).	7	TGTCCGGCTCT	0.557	
-	3	906	_p.S78T|MEF2C_	NM_002397	NP_002388	Q06413	MEF2C_HUMAN	-type (Potential).	7	TCCGGCTCTCAT	0.557	
+	29	6413	98_uc003kjt.2_5'	NM_032119	NP_115495	Q8WXG9	GPR98_HUMAN	ellular (Pot p.A2106V(1)	16	CTATTGCGCAAC	0.413	
+	1	2356	A6_uc003lhn.2_I	NM_018902	NP_061725	Q9Y5I1	PCDAB_HUMAN	(Potential).|Cadherin 5.	1	TGGGCGACCGC	0.677	
-	20	2950	e.1_Missense_M	NM_022481	NP_071926	Q8WWN8	ARAP3_HUMAN	Rho-GAP.	7	CCGACGGAACT	0.622	
+	2	198		NM_197975	NP_932079	Q6UXE8	BTNL3_HUMAN	ellular (Potential).	0	CTGGACCGGGC	0.552	
+	1	1530	C5_uc003mxw.2_	NR_027712					0	ACCATGGAGGC	0.498	
-	21	4476	.A1457T|NUP153	NM_005124	NP_005115	P49790	NU153_HUMAN		9	TGAGGCTGCAG	0.458	
-	3	1934_1935		NM_052923	NP_443155	Q6R2W3	SCND3_HUMAN	grase catalytic.	1	TCCCTCCCATTG	0.421	
-	31	10704	1_5'Flank|TNXB_u	NM_019105	NP_061978	P22105	TENX_HUMAN	nectin type-III 27.	0	CTACGGTGACT	0.637	
-	2	456	qg.1_Missense_M	NM_018643	NP_061113	Q9NP99	TREM1_HUMAN	(Potential).|Ig-like V-type.	1	CCACCAAGCGG	0.567	
+	4	463	_p.A45V|MDFI_u	NM_005586	NP_005577	Q99750	MDFI_HUMAN		0	CCCTGCGGAGG	0.627	rs144261097
+	4	662	p.G151E|RUNX2_	NM_001024630	NP_001019801	Q13950	RUNX2_HUMAN	Runt.	3	AGATGGGACTG	0.438	
-	2	834	vz.1_Missense_M	NM_021572	NP_067547	Q9UJA9	ENPP5_HUMAN		0	TATCTGAAATGA	0.438	

-	30	3800	ai.2_Missense_Mu	NM_138694	NP_619639	P08F94	PKHD1_HUMAN	tential).|IPT/TIG 6; atypica	44	AGACGGAAATT	0.527
-	21	1651	_p.P71S|COL9A1_	NM_001851	NP_001842	P20849	CO9A1_HUMAN	elical region (COL2).	4	ACCAGGAAGAC	0.403
-	5	698	_p.E123K|ME1_uc	NM_002395	NP_002386	P48163	MAOX_HUMAN		2	ATTTTCGGTTC	0.393
-	58	9007		NM_014611	NP_055426	Q9NU22	MDN1_HUMAN		10	TCTGGGGTTGT	0.433
+	4	466	SP3_uc003pvo.2_	NM_003880	NP_003871	O95389	WISP3_HUMAN		0	TGTAGCTGTTG	0.453
+	13	1423	PP3_uc010kfq.2_	NM_005021	NP_005012	O14638	ENPP3_HUMAN	tential).|Phosphodiesteras	4	GCAGCGGAATT	0.348
-	3	587_588		NM_001901	NP_001892	P29279	CTGF_HUMAN	VWFC.	0	CCGTCCAGGC	0.639
+	4	625	ense_Mutation_p.	NM_004100	NP_004091	O95677	EYA4_HUMAN		2	AAAAATCTAATCT	0.423
-	3	884		NM_001143676	NP_001137148	O00141	SGK1_HUMAN		6	CTCACCTTTAAA	0.373
+	11	1075	e_Mutation_p.L34	NM_018341	NP_060811	Q5T6L9	CF070_HUMAN		1	TTTTCCTTGGA	0.328
+	4	408_409	n_p.T59I|IQCE_uc	NM_152558	NP_689771	Q6IPM2	IQCE_HUMAN		0	CCTGACCCCGC	0.584
-	20	3056_3057		NM_032415	NP_115791	Q9BXL7	CAR11_HUMAN		50	GCTGACCCGGG	0.55
+	4	852	2_3'UTR|EIF2AK1	NM_006303	NP_006294	Q13155	AIMP2_HUMAN	ST C-terminal.	1	AAGAGGGAAGC	0.473
-	4	773	y.2_Missense_Mut	NM_001101426	NP_001094896	A4D126	ISPD_HUMAN		1	TCAGGTGATCCT	0.418
+	24	3183	uj.2_Missense_Mu	NM_178425	NP_848512	Q9UKV0	HDAC9_HUMAN		5	ATGTGGAACAG	0.532
+	3	651	kwc.1_RNA|INMT	NM_006774	NP_006765	O95050	INMT_HUMAN		0	ATTTTCCTGCG	0.597
+	7	1565	p.M190K|CCDC12	NM_194300	NP_919276	Q6ZRS4	CC129_HUMAN		0	GCGAATGGACA	0.488
+	4	445	kaf.1_Missense_M	NM_006658	NP_006649	O96001	GSUB_HUMAN		3	ACATCCAAAGG	0.423
-	1	229		NM_000290	NP_000281	P15259	PGAM2_HUMAN		0	GGGTGCGGATG	0.632
-	14	3137	1kbw.1_Splice_Sit	NM_013389	NP_037521	Q9UHC9	NPCL1_HUMAN		5	GGCCGCTGCAA	0.577
+	1	429		NM_182595	NP_872401	Q8N7R1	P1L12_HUMAN		0	GGTGACCATCG	0.577
+	11	998	_splice|LAT2_uc0	NM_032464	NP_115853	Q9GZY6	NTAL_HUMAN		0	ACAGGTGAGGC	0.617
-	11	1548	n.2_Nonsense_Mu	NM_000601	NP_000592	P14210	HGF_HUMAN	Kringle 4.	4	ATAATCCCAAGG	0.383
+	17	2162	_p.R592C|DYNC1	NM_004411	NP_004402	O14576	DC1I1_HUMAN		4	GAAATTCGTGCT	0.488
+	1	95	X6AS_uc003uol.2_	NM_005222	NP_005213	P56179	DLX6_HUMAN		2	agcagcagcaacagc	0.313
+	6	1028	t.2_Intron|GATS_	NM_024070	NP_076975	Q6DKI7	PVRIG_HUMAN		2	AGCATGGGTGA	0.677
+	3	443	_Intron|SLC12A9_	NM_020246	NP_064631	Q9BXP2	S12A9_HUMAN	lasmic (Potential).	0	TGCAGGGGGGC	0.612
-	2	904	e_Mutation_p.T17	NM_022484	NP_071929	Q9H0V1	TM168_HUMAN		2	ACATAGTTGTG	0.423
-	15	1860		NM_004333	NP_004324	P15056	BRAF_HUMAN	rotein kinas_R603>I(2)|p.T	18290	GATTTCACTGTA	0.368
+	19	2368		NM_004668	NP_004659	O43451	MGA_HUMAN	(Potential).|Maltase.	2	CTGGATGAAGTA	0.488
+	7	760		NM_018487	NP_060957	Q96HP8	T176A_HUMAN		2	AGAAGGAAATG	0.522
+	3	4885	_p.H223Y|ABP1_u	NM_001091	NP_001082	P19801	ABP1_HUMAN		6	TGGATCATGGG	0.597
-	1	486_487	_Mutation_p.D12	NM_001142459	NP_001135931	Q8WXI3	ASB10_HUMAN		0	GGAGTCCGCGA	0.644
-	4	1180	_Mutation_p.R146	NM_016203	NP_057287	Q9UGJ0	AAKG2_HUMAN		2	TAGATGCGATTC	0.592
-	27	4666	.G818R|CSMD1_	NM_033225	NP_150094	Q96PZ7	CSMD1_HUMAN	ar (Potential).|Sushi 8.	25	TTGTCCTTGGA	0.493
-	3	1205		NM_015310	NP_056125	Q9NYI0	PSD3_HUMAN		3	TGAAGGAGCTT	0.468
+	4	3519	1_uc011ldy.1_Intr	NM_006269	NP_006260	P56715	RP1_HUMAN		12	GTAATTCATCCA	0.418
+	12	1609_1610	.3_Missense_Mut	NM_002350	NP_002341	P07948	LYN_HUMAN	rotein kinase.	3	AAATTCCCTACC	0.371
+	4	488	p.2_RNA|STMN2_	NM_007029	NP_008960	Q93045	STMN2_HUMAN	Potential.	2	AAAACCGTGAGG	0.453
-	1	293		NM_152418	NP_689631	Q8NA75	DC4L2_HUMAN		1	GGAGGGATCCC	0.517
+	18	1995		NM_181787	NP_861452	Q7Z388	D19L4_HUMAN		2	AAAGCGATCTG	0.279
-	33	4313_4314	.1_Missense_Mut	NM_015902	NP_056986	O95071	UBR5_HUMAN		28	AGAAACCTCATT	0.351
-	2	914	cw.2_Missense_M	NM_014379	NP_055194	Q6PIU1	KCNV1_HUMAN	lasmic (Potential).	2	GAACAGTGGGA	0.488
-	12	1891	dt.2_Missense_M	NM_004519	NP_004510	O43525	KCNQ3_HUMAN		5	CATGTCGAGAT	0.453
-	10	1312	1_5'Flank|OPLAH_	NM_017570	NP_060040	O14841	OPLA_HUMAN		0	GGCCCAAAAAT	0.642
-	6	378	p.R109W|VPS28_	NM_016208	NP_057292	Q9UK41	VPS28_HUMAN	S28 N-terminal.	0	GATCCGCTCCAT	0.667
-	5	1132	1_5'Flank|LRRC14	NM_004260	NP_004251	O94761	RECQ4_HUMAN		4	GTGCCCGGCCC	0.642

-	3	588	zif.1_Missense_M	NM_152629	NP_689842	Q8NEA6	GLIS3_HUMAN	Ser-rich.	1	GTGCCGAGGAC	0.542	
+	8	1312	_p.S429L|CNTLN_	NM_017738	NP_060208	Q9NXG0	CNTLN_HUMAN		1	GGAATCACAGG	0.368	
-	1	3217	c003zrh.1_5'Flan	NM_153809	NP_722516	Q8IZX4	TAF1L_HUMAN		26	CACTTCCCAGC	0.478	
-	24	2805	f.1_Missense_Mu	NM_018449	NP_060919	Q5T6F2	UBAP2_HUMAN		3	CTGCTGGGCTG	0.587	
+	16	2348	_p.P112L|TLE4_uc	NM_007005	NP_008936	O60756	BCE1_HUMAN		5	AATCCCCCGGC	0.607	
+	4	4092		NM_178828	NP_849150	Q6ZUB1	CI079_HUMAN		3	CCCAGGAGAAT	0.597	
-	8	1693	1_splice|ASTN2_	NM_198187	NP_937830	O75129	ASTN2_HUMAN		9	CTCTCCTGTAA	0.468	
+	5	1886	qb.2_RNA|ASMT_	NM_005088	NP_005079	Q02040	AK17A_HUMAN		0	CCTGCGAGCAG	0.647	
+	2	394		NM_001099921	NP_001093391	A2A368	MAGBG_HUMAN		7	CCCTCCTCTCC	0.557	
-	4	424	p.P86S|RPGR_uc	NM_001034853	NP_001030025	Q92834	RPGR_HUMAN	RCC1 1.	1	TTCAGGTTTTA	0.299	
+	1	38		NM_207320	NP_997203	Q7L8S5	OTU6A_HUMAN		2	TCATGGATGAT	0.547	
-	13	1548	p.G416E|PHKA1_	NM_002637	NP_002628	P46020	KPB1_HUMAN		4	AAAATCCCTAA	0.398	
+	13	2135	c.1_Missense_Mu	NM_198465	NP_940867	Q7Z2Y5	NRK_HUMAN		14	CATTCCAGTAG	0.498	
+	33	3102	p.G967E|COL4A5	NM_033380	NP_203699	P29400	CO4A5_HUMAN	e-helical region.	4	GAAGGGGGAAC	0.413	
-	6	699	zh.1_Missense_M	NM_002910	NP_002901	P51606	RENBP_HUMAN		2	GGGCCGGCCCA	0.692	
-	15	1833	1_uc009vka.2_Mi	NM_004421	NP_004412	O14640	DVL1_HUMAN		0	GCCGGCCGGAC	0.726	
-	4	1279	pa.1_Missense_M	NM_018948	NP_061821	Q9UJM3	ERRFI_HUMAN	RBB2 and regulation of EG	1	TGACCCCATTGA	0.537	
-	1	138	|PEX14_uc010oar	NM_004401	NP_004392	O00273	DFFA_HUMAN		0	GATCTCGCCAG	0.667	
-	28	3638	d.2_Missense_Mu	NM_005529	NP_005520	P98160	PGBM_HUMAN	inin EGF-like 6.	9	CCCCCGCTGGG	0.667	
-	5	707	vrb.1_Missense_	NM_021258	NP_067081	Q8N6P7	I22R1_HUMAN	ellular (Potential).	1	TCACCTGGCAGT	0.562	
+	4	253		NM_001010980	NP_001010980	Q5T1S8	CA130_HUMAN		0	GGCGGGAACTA	0.587	
-	6	3478	sz.1_Missense_M	NM_001029882	NP_001025053	Q5TGY3	AHDC1_HUMAN		1	GCCGGTGAAGA	0.632	
-	2	433		NM_032881	NP_116270	Q969L4	LSM10_HUMAN		0	CTGCTCAATGG	0.557	
+	47	15372	s.1_Nonsense_M	NM_033044	NP_149033	Q9UPN3	MACF1_HUMAN		16	TTGTCCAGCGA	0.443	
+	11	1528		NM_015284	NP_056099	Q5T011	SZT2_HUMAN		0	TGGTTGGCATG	0.607	
+	16	3030	se_Mutation_p.R4	NM_002840	NP_002831	P10586	PTPRF_HUMAN	tential).|Fibronectin type-III	10	GAACCGGGCTG	0.602	rs149018733
+	1	278	3_uc001cmo.2_5'	NM_004073	NP_004064	Q9H4B4	PLK3_HUMAN		0	GCGGCCGCACC	0.677	
+	21	2729	e_Mutation_p.R49	NM_015112	NP_055927	Q6P0Q8	MAST2_HUMAN	kinase C-terminal.	11	CAGCCCGCTCA	0.552	
-	3	556		NM_032027	NP_114416	Q9BX74	TM2D1_HUMAN		1	GGGTGCTGGAA	0.353	
+	3	401	e_Mutation_p.P63	NM_144701	NP_653302	Q5VWK5	IL23R_HUMAN	ellular (Potential).	0	AATGTCCCAAA	0.358	
-	6	1066	IQ3_uc001dfz.3_	NM_001105659	NP_001099129	A6PVS8	LRIQ3_HUMAN		2	GATAATATATATT	0.169	
+	10	1685	q.2_Nonsense_M	NM_001001933	NP_001001933	Q68G74	LHX8_HUMAN		3	GACTCCAGCCC	0.328	
+	16	2229		NM_002440	NP_002431	O15457	MSH4_HUMAN		5	ATATCGAAACA	0.289	
+	6	716	HN2_uc001div.2_	NM_012302	NP_036434	O95490	LPHN2_HUMAN	otential).|Olfactomedin-like	9	CCTATCGTACC	0.398	
+	7	1321	ue.1_Missense_M	NM_014839	NP_055654	Q7Z2D5	LPPR4_HUMAN		3	CCCATGGGGAA	0.488	
+	7	776		NM_033055	NP_149044	Q96MC6	HIAT1_HUMAN	Name=7; (Potential).	0	CCTACCGGAGG	0.383	
-	7	703	tu.2_RNA|DPH5_u	NM_015958	NP_057042	Q9H2P9	DPH5_HUMAN		0	ATACCGTGGAG	0.418	rs116634893
-	8	1480	_p.E400K|COL11A	NM_001854	NP_001845	P12107	COBA1_HUMAN	nhelical region.	12	CATATTCTTTATA	0.363	
+	3	216	M5_uc010ovu.1_5	NM_000851	NP_000842	P46439	GSTM5_HUMAN	(By similarity).|GST N-term	6	CTGAATGAAAAA	0.572	
-	4	430	ff.1_Nonsense_M	NM_000036	NP_000027	P23109	AMPD1_HUMAN		4	TCTCTGAAAAT	0.463	
+	4	488	hr.1_Missense_M	NM_001005783	NP_001005783	Q9NYQ3	HAOX2_HUMAN	xy acid dehydrogenase.	4	GAATTCGCCTC	0.552	
+	17	1995	441S|NBPF9_uc	NM_001037675	NP_001032764	Q3BBV1	NBPFK_HUMAN	NBPF 4.	0	ATGTTATTCAAC	0.483	
+	4	2006	10_uc001emp.3_	NM_001039888	NP_001034977	Q69YU3	AN34A_HUMAN	Pro-rich.	0	CCATCCCCCAA	0.612	
+	12	1521	vkt.1_Missense_M	NM_001102663	NP_001096133				0	GATGTTATTCG	0.478	
-	1	381	CL1_uc001eva.2_	NM_021960	NP_068779	Q07820	MCL1_HUMAN		0	CCTCGGCGCCA	0.771	
-	2	991	e.1_Missense_M	NM_007113	NP_009044	Q07283	TRHY_HUMAN	-E-Q-E-E- E-R-R-E-Q-Q-L	5	tctcctcctgctgctcgc	0	
-	3	1734		NM_001009931	NP_001009931	Q86YZ3	HORN_HUMAN	5	3	ACTGCCTGGAA	0.592	

-	2	65		NM_002964	NP_002955	P05109	S10A8_HUMAN		0	CAGCTCGGTCA	0.512	
+	7	1821	ite_p.D213_splic	NM_000906	NP_000897	P16066	ANPRA_HUMAN		7	ctGCAGATCACC	0.348	
+	7	1183	b.1_Missense_M	NM_001002294	NP_001002294	P31513	FMO3_HUMAN		1	GTATTTCCTCCT	0.453	
-	4	1339_1340	_Mutation_p.G42	NM_003285	NP_003276	Q92752	TENR_HUMAN	nectin type-III 2.	11	TAGCCCTTGAG	0.495	
+	31	6580	50_uc001gnv.2_	NM_014810	NP_055625	Q5VT06	CE350_HUMAN	Potential.	4	AAAATCAGTTG	0.393	
+	12	1783	_Mutation_p.E570	NM_002826	NP_002817	O00391	QSOX1_HUMAN		2	CCCTGGAGCTG	0.622	
+	38	5392	1gox.1_Missense_	NM_000721	NP_000712	Q15878	CAC1E_HUMAN	ytoplasmic (Potential).	6	TGGACGAGTTT	0.607	
+	6	1103	tm.2_Missense_M	NM_002113	NP_002104	Q03591	FHR1_HUMAN		0	AAAAAGATAGA	0.323	
+	5	748		NM_030787	NP_110414	Q9BXR6	FHR5_HUMAN	Sushi 4.	2	TACGATCATGTG	0.318	
+	12	2092	p.G597S|CAMSA	NM_203459	NP_982284	Q08AD1	CAMP2_HUMAN		4	CGAAAGGTGCC	0.353	
+	5	425		NM_006335	NP_006326	Q99595	TI17A_HUMAN	ical; (Potential).	0	AGCTGGTATCT	0.398	
+	20	2717	1gyb.1_Missense	NM_002481	NP_002472	O60237	MYPT2_HUMAN		3	AAGAGCCCGTC	0.473	
-	8	1369	gyr.3_Missense_	NM_015999	NP_057083	Q96A54	ADR1_HUMAN	ellular (Potential).	0	ACAGCCGCCTT	0.512	
-	7	1162	e_Mutation_p.R2	NM_001017402	NP_001017402	Q13751	LAMB3_HUMAN	inin EGF-like 1.	6	GCAGCGATCAG	0.677	rs145575474
+	3	1409		NM_021958	NP_068777	Q14774	HLX_HUMAN	Homeobox.	2	CGGACGCACAG	0.642	
+	20	2278	p.G607E|CAPN2_	NM_001748	NP_001739	P17655	CAN2_HUMAN	ain IV.|EF-hand 3.	5	TACTGGAACAA	0.502	
-	4	1014	_Mutation_p.G27	NM_003240	NP_003231	O00292	LFTY2_HUMAN		0	CGGCCCCAGAA	0.657	
-	7	1796	xes.2_Missense_	NM_003607	NP_003598	Q5VT25	MRCKA_HUMAN	rotein kinase.	11	GCGATTCTGCAT	0.368	
+	4	821	.1_Intron|ZNF678_	NM_178549	NP_848644	F5GXA7	F5GXA7_HUMAN		1	AATGTGGCAAAG	0.333	rs145397350
+	4	854	.1_Intron|ZNF678_	NM_178549	NP_848644	F5GXA7	F5GXA7_HUMAN		1	TAACTAACCATA	0.333	
+	10	1335	0pyl.1_Missense_	NM_006642	NP_006633	Q86SQ7	SDCG8_HUMAN	r homodimerization (By si	0	ATGATGAAAAA	0.433	
-	8	858_859	z.1_Missense_Mu	NM_005465	NP_005456	Q9Y243	AKT3_HUMAN	rotein kinase.	4	ATAGTCCAAGGC	0.416	
+	1	548		NM_001004690	NP_001004690	A3KFT3	OR2M5_HUMAN	ellular (Potential).	3	TCCCTTCCCTAC	0.418	
-	1	548		NM_001004691	NP_001004691	Q8NG81	OR2M7_HUMAN	ellular (Potential).	2	GTAGGGAAGGG	0.428	
+	1	74		NM_001004697	NP_001004697	Q6IEZ7	OR2T5_HUMAN	ellular (Potential).	0	ACGATCCAAAC	0.498	
+	4	773		NM_002438	NP_002429	P22897	MRC1_HUMAN	ellular (Potential).	0	AAGACCCGCTG	0.433	
+	10	1321	g.2_Nonsense_M	NM_005180	NP_005171	P35226	BMI1_HUMAN	action with E4F1.	2	GAGTTCGACCT	0.373	
-	12	1635	_p.R458*|ABI1_uc	NM_005470	NP_005461	Q8IZP0	ABI1_HUMAN	SH3.	1	TCACTCGATTGC	0.348	
-	7	1310	t.2_Missense_Mut	NM_025209	NP_079485	Q9H2F5	EPC1_HUMAN		4	CAGACGATGGT	0.443	
-	1	634		NM_002900	NP_002891	P10745	RET3_HUMAN	ate tandem repeats.|1.	2	GCCTCCTGTGC	0.607	
-	10	1432	.2_Missense_Mut	NM_138932	NP_620310	Q9NQ94	A1CF_HUMAN		1	TGTCTCCTTTG	0.498	
-	33	6235	sense_Mutation_p	NM_033056	NP_149045	Q96QU1	PCD15_HUMAN	lasmic (Potential).	13	TGAGATTGTTTT	0.353	
-	37	6532	K3_uc010qih.1_In	NM_020987	NP_066267	Q12955	ANK3_HUMAN		19	AAAGTCATCAG	0.433	
+	39	5614		NM_022124	NP_071407	Q9H251	CAD23_HUMAN	.|Extracellular (Potential).	11	CCCCCGGGACT	0.577	rs111033270
+	24	3627	e_Mutation_p.G89	NM_020338	NP_065071	Q9ULJ6	ZMIZ1_HUMAN		4	AGGCCGGAGCG	0.692	
-	4	311	an.3_Missense_	NM_006926	NP_008857	Q8IWL1	SFPA2_HUMAN	ollagen-like.	0	ATTATTCCCAG	0.622	
+	3	582	4_uc010qmk.1_M	NM_033282	NP_150598	Q9UHM6	OPN4_HUMAN	Name=2; (Potential).	1	TTCCTCATGTCC	0.567	
-	2	567	t_Site|GLUD1_uc0	NM_005271	NP_005262	P00367	DHE3_HUMAN		0	TCTACACTCACAT	0.418	
-	7	738	utation_p.R163C|	NM_001613	NP_001604	P62736	ACTA_HUMAN		0	CTCACGCTCAG	0.493	
-	13	1324	ip.3_Missense_M	NM_013451	NP_038479	Q9NZM1	MYOF_HUMAN	mic (Potential).|C2 3.	4	GGAAACTTCTA	0.373	
+	4	562	_p.D53N|CYP2C1	NM_000769	NP_000760	P33261	CP2CJ_HUMAN		6	CGTTTCGATTAT	0.403	
-	10	1501	po.1_Missense_M	NM_021828	NP_068600	Q8WWQ2	HPSE2_HUMAN		1	GAGCATAAATCC	0.572	
+	12	1186	_p.P405S|ACSL5_	NM_203379	NP_976313	Q9ULC5	ACSL5_HUMAN	lasmic (Potential).	3	TGTTTCCCGCG	0.507	
-	17	2730	_Mutation_p.E57	NM_000141	NP_000132	P21802	FGFR2_HUMAN	Potential).|Protein kinase.	96	GATCTCCCACA	0.517	
+	49	6119	4_splice|DMBT1_	NM_007329	NP_015568	Q9UGM3	DMBT1_HUMAN		7	CAGCAGATTAT	0.448	
+	35	3521	p.L1174F|DOCK1_	NM_001380	NP_001371	Q14185	DOCK1_HUMAN	DHR-2.	9	TCAGCCTTCTG	0.343	
+	8	1288	p.G220R|CYP2E1	NM_000773	NP_000764	P05181	CP2E1_HUMAN		3	AAAATGGAAAG	0.448	

-	1	505		NM_001005237	NP_001005237	Q8NGK1	O51G1_HUMAN	cellular (Potential).	2	AGTATTGGAAGC	0.512	
-	1	482		NM_001005160	NP_001005160	Q9H2C5	O52A5_HUMAN	Name=4; (Potential).	4	CCTAAGGAAGGT	0.458	
-	1	641	.1_Intron|HBE1_uc	NM_033179	NP_149419	Q9Y5P0	O51B4_HUMAN	Name=5; (Potential).	2	ATATAAGAAAAGA	0.378	
-	1	78	.1_Intron|HBE1_uc	NM_033180	NP_149420	Q9Y5P1	O51B2_HUMAN	cellular (Potential).	3	AAGGGGCTGCA	0.488	
-	2	373	G2_uc001mak.1_Ir	NM_017481	NP_059509	Q9H347	UBQL3_HUMAN	Ubiquitin-like.	3	ATGGCACGGTGC	0.582	
+	1	842	.1_Intron|TRIM22_	NM_001005180	NP_001005180	Q8NGI3	O56B1_HUMAN	cellular (Potential).	2	TGATTCCAGTTCT	0.428	
+	22	2607	PFIBP2_uc010rbe	NM_003621	NP_003612	Q8ND30	LIPB2_HUMAN	SAM 3.	4	ATCTTCGAGGGA	0.502	
+	5	750	_p.M217I|SWAP70	NM_015055	NP_055870	Q9UH65	SWP70_HUMAN	PH.	3	TTACATGATGAAA	0.343	
-	11	1461_1462	rcv.1_Missense_M	NM_175058	NP_778228	Q6IQ23	PKHA7_HUMAN		3	GGAGCCCCCCGA	0.629	
-	30	3781		NM_000352	NP_000343	Q09428	ABCC8_HUMAN	ype-1 2.|Cytoplasmic (By si	1	GGCCTCATACCT	0.567	
+	5	1074	p.R219C|RCN1_u	NM_002901	NP_002892	Q15293	RCN1_HUMAN	EF-hand 5.	1	GAGATTCGCCACT	0.473	
-	15	2146	ykx.2_Missense_M	NM_001101802	NP_001095272	Q96BD5	PF21A_HUMAN	criptional repression.|PHD-t	2	ATACACGGGAACA	0.468	
-	2	554		NM_031909	NP_114115	Q9BXJ3	C1QT4_HUMAN	C1q 1.	0	CGGTTTCGCACC	0.711	
+	3	486	ngo.3_Missense_M	NM_002843	NP_002834	Q12913	PTPRJ_HUMAN	cellular (Potential).	8	CAATTCCTGACC	0.418	
+	4	660		NM_024114	NP_077019	Q8IWZ4	TRI48_HUMAN		0	ATATTATACAGGT	0.338	
-	1	782		NM_001004700	NP_001004700	Q6IEV9	OR4CB_HUMAN	cellular (Potential).	1	AAGTGGTCGGG	0.433	
+	3	712_713	ik.1_Missense_Mu	NM_001004704	NP_001004704	Q8NH72	OR4C6_HUMAN	Name=4; (Potential).	2	GTGGGGGGATT	0.465	
+	1	449		NM_001001967	NP_001001967	Q8NGL4	OR5DD_HUMAN	Name=4; (Potential).	3	CTGGGTCCTATA	0.418	
-	1	865		NM_006637	NP_006628	Q13606	OR5I1_HUMAN	Name=7; (Potential).	1	CAACGGATTCAG	0.368	
-	1	241		NM_001004742	NP_001004742	Q8NGP4	OR5M3_HUMAN	cellular (Potential).	2	GGTTTTCCAACA	0.368	
+	4	1670	n_p.T446I|FAM111	NM_198947	NP_945185	Q6SJ93	F111B_HUMAN		2	ATGCTACTTGCTT	0.388	
-	12	1466	p.R381Q|GANAB_	NM_198334	NP_938148	Q14697	GANAB_HUMAN		5	GAACTCGGTAG	0.562	
+	3	982	N3_uc001nxp.2_Ir	NM_201428	NP_958831	O95197	RTN3_HUMAN		1	CTCATATAAGGAG	0.363	
+	18	3039	2_Missense_Mutat	NM_032251	NP_115627	A6NC98	CC88B_HUMAN	Potential.	4	TGCAGGGGCAG	0.682	
-	16	1921		NM_017525	NP_059995	Q6DT37	MRCKG_HUMAN	Potential.	4	GGTTTTCCTCCTC	0.667	
+	8	1711	P5_uc009ysg.2_5'U	NM_002335	NP_002326	O75197	LRP5_HUMAN	eta-propeller 2.|Extracellular	7	AAGCTCCCGCAC	0.602	
-	2	413		NM_005169	NP_005160	O14813	PHX2A_HUMAN		0	CGGATGGCTCTG	0.637	
+	10	2873	sp.1_Missense_Mu	NM_020798	NP_065849	Q9P2H5	UBP35_HUMAN		3	CTGCCGCTTCTCT	0.587	
+	6	2321	su.1_Missense_Mu	NM_015885	NP_056969	O94913	PCF11_HUMAN		1	CTCTTGCAAGCAA	0.328	
+	2	986		NM_000372	NP_000363	P14679	TYRO_HUMAN	melanosome (Potential).	3	AATCCTGGAAAC	0.473	
+	85	12584	p.R4154H|DYNC2I	NM_001080463	NP_001073932	Q8NCM8	DYHC2_HUMAN		0	TGCCCGTGCCCT	0.423	
-	7	784	SP28_uc001poj.3_	NM_020886	NP_065937	Q96RU2	UBP28_HUMAN		7	GCTGTTCCTCAG	0.423	
+	6	629	09yzm.2_Intron|PA	NM_002572	NP_002563	P68402	PA1B2_HUMAN		1	ATACCGACGGGG	0.542	
+	14	1321	e_Mutation_p.E344	NM_173593	NP_775864	Q6L9W6	B4GN3_HUMAN	menal (Potential).	2	GCAGAGGAGACC	0.517	
+	49	6572	S|CACNA1C_uc00	NM_199460	NP_955630	Q13936	CAC1C_HUMAN	Cytoplasmic (Potential).	11	GCGGGGGCAGC	0.701	
+	6	857	_p.P138L|CD9_uc0	NM_001769	NP_001760	P21926	CD9_HUMAN	cellular (Potential).	1	ATGAGCCCCAGC	0.542	
+	2	272_273	HG6_uc010sew.1_	NM_018173	NP_060643	Q3KR16	PKHG6_HUMAN		2	CCCGAGGATACC	0.619	
-	5	813	sense_Mutation_p.	NM_001065	NP_001056	P19438	TNR1A_HUMAN	.|Extracellular (Potential).	3	CACACTCGTTTT	0.547	
-	2	178	ense_Mutation_p.G	NM_014231	NP_055046	P23763	VAMP1_HUMAN	lasmic (Potential).	0	CTGTCCCTTCAG	0.502	
-	3	673	B4_uc001qzf.1_Int	NM_006249	NP_006240	Q04118	PRB3_HUMAN	[PQS]-P-[PS]-Q-[GE]-G-N-[	1	TGGTTTCCTCCTT	0.622	
+	6	769	O1C1_uc009zip.2_	NM_017435	NP_059131	Q9NYB5	SO1C1_HUMAN	cellular (Potential).	7	CAAATATGAGAG	0.373	rs145524055
-	18	2332	n_p.T771I|ABCC9_	NM_005691	NP_005682	O60706	ABCC9_HUMAN	otential).|ABC transporter 1	6	CCAAAAGTAATAT	0.328	
-	14	1985		NM_025003	NP_079279	P59510	ATS20_HUMAN	Cys-rich.	19	TGGTTCCAGCAA	0.348	
+	15	4175	_p.P848L|ARID2_u	NM_152641	NP_689854	Q68CP9	ARID2_HUMAN		10	TATCTCCAATGGA	0.358	
+	13	1852	n_p.S562I|TROAP_	NM_005480	NP_005471	Q12815	TROAP_HUMAN	ate tandem repeats.|Cys-ri	1	GTAGGAGTGAGC	0.592	
+	13	1942	e_Mutation_p.Y59	NM_005480	NP_005471	Q12815	TROAP_HUMAN	approximate tandem repea	1	AGTCCTACTGTAC	0.617	
+	5	1047	smj.1_Missense_M	NM_012284	NP_036416	Q9ULD8	KCNH3_HUMAN	=Segment S2; (Potential).	0	CCCAGCGTCTGT	0.662	

-	2	532		NM_004693	NP_004684	O95678	K2C75_HUMAN	Coil 1A.|Rod.	0	CTGCTCCAAGAA	0.498	
-	7	1472		NM_173086	NP_775109	P48668	K2C6C_HUMAN		2	TTACCTACCTGC	0.567	
-	7	617	AD_uc001sbz.2_M	NM_015989	NP_057073	Q9Y600	CSAD_HUMAN		1	TGATAGCGGGCC	0.617	
-	9	1291	se_Mutation_p.S40	NM_000889	NP_000880	P26010	ITB7_HUMAN	cellular (Potential).	8	TCGTAAGAAATG	0.552	
+	1	341		NM_017409	NP_059105	Q9NYD6	HXC10_HUMAN		1	GGCGACCCCAA	0.637	
-	5	709	w.1_RNA|ITGA5_	NM_002205	NP_002196	P08648	ITA5_HUMAN	r (Potential).|FG-GAP 3.	2	CCTTGGTGAAC	0.582	
+	1	460		NM_001005280	NP_001005280	Q8NGE5	O10A7_HUMAN	Name=4; (Potential).	4	GGTGTTCCTGTG	0.488	
+	1	812		NM_054105	NP_473446	Q9NZP2	OR6C2_HUMAN	Name=7; (Potential).	2	ATAAAGGAGTTTC	0.423	
-	10	2149	.R650Q|BAZ2A_	NM_013449	NP_038477	Q9UIF9	BAZ2A_HUMAN	A.T hook 1.	0	CGACCCCGTTTG	0.527	
-	5	743		NM_001686	NP_001677	P06576	ATPB_HUMAN	(By similarity).	1	AGTACAGTCTTG	0.408	
+	8	1450		NM_032230	NP_115606	Q8N6Q8	CL026_HUMAN		0	TTCTATCGTGCT	0.284	
-	1	1178_1179	sun.1_Intron|GAL	NM_003774	NP_003765	Q8N4A0	GALT4_HUMAN	main B.|Lumenal (Potential	0	TCCAAGGTACTG	0.49	
+	32	3649		NM_017564	NP_060034	Q8WWQ8	STAB2_HUMAN	lar (Potential).|FAS1 4.	14	TCCGGGGCTAC	0.507	
-	4	487	PL2_uc010swu.1	NM_018171	NP_060641	Q8NEU8	DP13B_HUMAN	AB5A binding (By similarity)	1	ACTTTGGAAAAA	0.343	
-	3	705	1_Missense_Muta	NM_001145374	NP_001138846	Q6NS38	ALKB2_HUMAN	bstrate binding.	0	GTGCCACTTCCC	0.572	
+	2	378	oc.2_Missense_M	NM_001093	NP_001084	O00763	ACACB_HUMAN		8	CCGGTCGGCGG	0.637	
+	17	2567		NM_015267	NP_056082	O14529	CUX2_HUMAN	Poly-Ser.	6	GTCGCCCTCGC	0.731	
-	38	5776	ttr.1_Missense_M	NM_001109662	NP_001103132				2	AGTCCCGGTAGA	0.592	
+	10	1147	e.1_Missense_Mu	NM_001143854	NP_001137326	Q9Y2J0	RP3A_HUMAN	Pro-rich.	7	CAGCCGGAGCC	0.532	
-	15	2643		NM_015335	NP_056150	Q71F56	MD13L_HUMAN		8	AACATCCTTTGC	0.403	
-	7	1227		NM_173598	NP_775869	Q6VAB6	KSR2_HUMAN	ol-ester/DAG-type.	15	GACATCCAGTAC	0.458	
-	4	526	SRC2_uc001ucs.	NM_023012	NP_075388	Q7L4I2	RSRC2_HUMAN	Ser-rich.	1	CTAGATCTTGAG	0.378	
+	16	2447	p.P350S|DNAH10	NM_207437	NP_997320	Q8IVF4	DYH10_HUMAN	n (By similarity).	6	GAACTCCCAGGT	0.299	
+	1	1954	_5'Flank|uc001ui	NM_007197	NP_009128	Q9ULW2	FZD10_HUMAN	cellular (Potential).	5	TCCCCGCCGTG	0.552	
-	11	2244	_p.E602K|RIMBP2	NM_015347	NP_056162	O15034	RIMB2_HUMAN		11	TTCTCTCTAGGA	0.587	
+	19	1904		NM_003565	NP_003556	O75385	ULK1_HUMAN		4	CTCCCCGCACT	0.701	
-	10	14105	A4359T|SACS_uc	NM_014363	NP_055178	Q9NZJ4	SACS_HUMAN	HEPN.	12	CTGAGCAAGTG	0.388	
+	7	6406	ww.2_Missense_M	NM_207361	NP_997244	Q5SZK8	FREM2_HUMAN	(Potential).|Calx-beta 3.	11	GGAGAACGGGC	0.493	
-	8	1597	.D384E|ELF1_uc	NM_172373	NP_758961	P32519	ELF1_HUMAN		1	GTTTCATCCTGC	0.428	
+	1	1542		NR_003268					0	ATTATATACCATG	0.383	
+	1	61	hk.1_Missense_M	NM_006418	NP_006409	Q6UX06	OLFM4_HUMAN		1	CAGGGGATTTG	0.478	
-	1	632	h.2_Missense_Mu	NM_001922	NP_001913	P40126	TYRP2_HUMAN	elanosome (Potential).	5	GGGCCTTGTGT	0.607	
-	19	2858	nse_Mutation_p.P	NM_198968	NP_945319	Q86YF9	DZIP1_HUMAN		2	TTTCTGGGAAAA	0.279	
-	3	1121		NM_000452	NP_000443	Q12908	NTCP2_HUMAN	ical; (Potential).	4	AAACAGGAACA	0.393	
-	5	707		NM_004093	NP_004084	P52799	EFNB2_HUMAN	cellular (Potential).	1	CTGCAAATAAGG	0.493	
+	1	167	a.1_RNA|POTEG_	NM_001005356	NP_001005356	Q6S5H5	POTEG_HUMAN		1	GGAGCGGCAAG	0.592	
+	1	686		NM_001004717	NP_001004717	Q8NH43	OR4L1_HUMAN	lasmic (Potential).	5	AAAAATCATCAC	0.438	
-	16	2380	EP1_uc010tlf.1_R	NM_007110	NP_009041	Q99973	TEP1_HUMAN		5	GACCCTGTCCAC	0.468	
-	5	1021	se_Mutation_p.S1	NM_019852	NP_062826	Q86U44	MTA70_HUMAN		2	CCTAAAGACTCA	0.398	
-	34	5039		NM_002471	NP_002462	P13533	MYH6_HUMAN	Potential.	4	CAGCTGGATCT	0.627	
-	22	2813		NM_002471	NP_002462	P13533	MYH6_HUMAN	Potential.	4	CCAGCTGAATCT	0.517	
-	28	3888	a-mir-208b|MI000	NM_000257	NP_000248	P12883	MYH7_HUMAN	Potential.	4	GCCTTGCTCCGG	0.582	
+	1	144		NM_203402	NP_981947	A5D6W6	FITM1_HUMAN	lasmic (Potential).	0	gggcCCGAATCC	0.443	
-	12	1878	p.S496F|RALGAP	NM_014990	NP_055805	Q6GYQ0	RGPA1_HUMAN		4	CAACTGGAATTT	0.413	
-	10	1287	yv.2_Missense_M	NM_002863	NP_002854	P06737	PYGL_HUMAN		1	GCCAGCGCTCC	0.522	
-	1	238	_p.D23N|OTX2_u	NM_172337	NP_758840	P32243	OTX2_HUMAN		1	GCAAGTCCATAC	0.587	
-	20	4430	.R1459Q|SPTB_u	NM_000347	NP_000338	P11277	SPTB1_HUMAN	Spectrin 12.	11	AGGAACCGCTTC	0.567	rs148127231

+	7	2579	_p.P744L|SIPA1L1	NM_015556	NP_056371	O43166	SI1L1_HUMAN	Rap-GAP.		4	ACAATCCGTGCT	0.512	
+	10	3566	p.S1073N|SIPA1L	NM_015556	NP_056371	O43166	SI1L1_HUMAN			4	CGCCAGCAAGG	0.507	
+	10	1314	.R369Q|RBM25_	NM_021239	NP_067062	P49756	RBM25_HUMAN	eckle localization.|Glu-rich		4	TGACCGGGATA	0.234	
+	2	1779		NM_018228	NP_060698	Q9H8Y1	VRTN_HUMAN			0	GCTTCCGCCTC	0.652	
+	2	1509		NM_022054	NP_071337	Q9HB14	KCNKD_HUMAN	lasmic (Potential).		1	AGCCAACAAGG	0.602	
-	15	1978_1979		NM_001080414	NP_001073883	Q9P219	DAPLE_HUMAN	Potential.		3	GCTCCCCCTTCT	0.629	
+	9	1338	_p.Q292*|UBR7_u	NM_175748	NP_786924	Q8N806	UBR7_HUMAN			0	GAGTCCAGCAA	0.413	
+	2	334	_p.W55*|PPP2R5	NM_002719	NP_002710	Q13362	2A5G_HUMAN			2	TAAAGTGGAAGG	0.408	
+	1	122	727924_uc001yu	NM_001004719	NP_001004719	Q8NGB6	OR4M2_HUMAN	Name=1; (Potential).		1	TACCAGGAAATAT	0.413	
-	23	4569	.2_Missense_Mut	NM_003257	NP_003248	Q07157	ZO1_HUMAN			6	AAACTTCTTCGG	0.428	
+	20	3510	bi.2_Missense_Mu	NM_003246	NP_003237	P07996	TSP1_HUMAN	SP C-terminal.		6	GATGGCGTCTC	0.463	
-	3	1115	FAF1_uc010bcf.2_	NM_016013	NP_057097	Q9Y375	CIA30_HUMAN			1	TCCCCCGCGGG	0.383	
+	15	5207	GA_uc010uda.1_	NM_001164273	NP_001157745	Q8IWI9	MGAP_HUMAN	Thr-rich.		12	GCTTTTCCTAAG	0.478	
-	4	558		NM_052955	NP_443187	Q96PF1	TGM7_HUMAN			2	CTGCCCGTAGT	0.493	
-	12	2495	_p.D788N|TP53BP	NM_005657	NP_005648	Q12888	TP53B_HUMAN			7	GGAATCTGAGC	0.433	
+	4	243		NM_004212	NP_004203	O43868	S28A2_HUMAN			4	GGAGTCGGTGG	0.408	rs144302819
+	4	541	r.2_RNA|PLDN_u	NM_012388	NP_036520	Q9UL45	PLDN_HUMAN	Potential.		1	AGTTTGCTGAG	0.279	
-	5	2140	D4_uc010ugj.1_	NM_198400	NP_006145	P46934	NEDD4_HUMAN	eraction with TNIK (By simil		4	CCCTGGAGGTA	0.473	
-	7	780	DH1A2_uc010ugw	NM_003888	NP_003879	O94788	AL1A2_HUMAN			1	CCATATCCTGGC	0.473	
+	11	1526	axp.2_Missense_	NM_025055	NP_079331	Q8N5R6	CCD33_HUMAN			5	GCAAGGCTCTT	0.398	
-	1	1396		NM_017793	NP_060263	Q9BUL9	RPP25_HUMAN			0	TCGCGGAGCCT	0.687	
-	4	3938		NM_001897	NP_001888	Q6UVK1	CSPG4_HUMAN	noglycan attachment doma		3	CACTCGGTGGG	0.627	
+	9	1047	_p.Q275*|ADAMTS	NM_207517	NP_997400	P82987	ATL3_HUMAN			27	CACTTCAAGGA	0.333	
+	4	1541	592_uc010upb.1_	NM_014630	NP_055445	Q92610	ZN592_HUMAN			6	ATCCAAGTAAGT	0.532	
+	2	202		NM_152336	NP_689549	Q96MI9	CBPC4_HUMAN			0	CCTAAGAGGTA	0.522	
+	2	256	_p.S52F|WDR93_	NM_020212	NP_064597	Q6P2C0	WDR93_HUMAN			2	TGGATTCCTTGC	0.502	
+	29	3682		NM_003870	NP_003861	P46940	IQGA1_HUMAN	as-GAP.|C1.		8	ATTATCGATACAT	0.438	
+	5	694		NM_023933	NP_076422	Q9BQD7	F173A_HUMAN			1	TGGACCGAGTA	0.687	
-	3	495	TG_uc002clm.2_5'	NM_001001410	NP_001001410	Q9UJK0	TSR3_HUMAN			0	CAGGCGCAAGT	0.637	
+	6	1220	vg.1_Missense_M	NM_016111	NP_057195	Q9Y4R8	TELO2_HUMAN			0	CCGGCTCACGG	0.597	
+	2	630		NM_014117	NP_054836	Q14CZ0	CP072_HUMAN			1	GGGTCCCCTTC	0.458	
-	20	2752	H7A_uc002dbl.2_	NM_014153	NP_054872	Q8IWR0	Z3H7A_HUMAN		p.E852Q(1)	4	TAACTTCAGCAT	0.328	rs150604583
-	2	862	_5'Flank|IQCK_uc	NM_001012991	NP_001013009	Q1ED39	CP088_HUMAN	Lys-rich.		0	TGGCTCCTCGA	0.473	
+	4	629	hd.1_Missense_M	NM_017888	NP_060358	Q6NUN0	ACSM5_HUMAN			2	GGCGTCCAGGG	0.562	
-	49	7777	bd.1_Nonsense_	NM_017539	NP_060009	Q8TD57	DYH3_HUMAN	4 (By similarity).		18	AGGACTGGAACC	0.473	
+	2	1746		NM_006040	NP_006031	Q9Y661	HS3S4_HUMAN	enal (Potential).		2	AACAGGAAGAG	0.463	
-	2	153	uc010vct.1_Intron	NM_145659	NP_663634	Q8NEV9	IL27A_HUMAN			0	CCTCCGCAGCT	0.647	
+	7	782	_uc010vdz.1_RN	NM_005115	NP_005106	Q14764	MVP_HUMAN	MVP 5.		4	TCGGCGGAACT	0.627	
-	7	2097	lank|INO80E_uc0	NM_003609	NP_003600	Q9BW71	HIRP3_HUMAN			1	GCCACGCATAT	0.597	rs139557944
+	10	1021	_p.P315L|TGFB1I1	NM_001042454	NP_001035919	O43294	TGFI1_HUMAN	zinc-binding 2.		0	CCGCCCCTACT	0.682	
+	4	2245		NM_003414	NP_003405	Q14586	ZN267_HUMAN	2H2-type 13.		4	ACATCGGAGAA	0.443	
-	2	3356	_Mutation_p.P101	NM_002968	NP_002959	Q9NSC2	SALL1_HUMAN			8	AGACGGGACGT	0.562	
+	5	536		NM_001950	NP_001941	Q16254	E2F4_HUMAN	ization (Potential).		1	CATCCGGGCCC	0.627	
-	11	1504	_p.P437L|RANBP	NM_020850	NP_065901	Q6VN20	RBP10_HUMAN			1	CGTTGGGGTAG	0.602	
+	10	3361	n_p.Q572*|NFATC	NM_173165	NP_775188	Q12968	NFAC3_HUMAN			3	TTTCCCAAGGA	0.493	
+	10	716	ALB2_uc002fac.3_	NM_001740	NP_001731	P22676	CALB2_HUMAN	bable).|EF-hand 5.		0	TACATTGACGAG	0.567	
-	2	2477	X3_uc002fcl.2_In	NM_006885	NP_008816	Q15911	ZFHX3_HUMAN			4	TGGTGCTGTGG	0.582	

-	3	2426	ej.1_Missense_Mu	NM_024533	NP_078809	Q9GZS9	CHST5_HUMAN	enal (Potential).		0	CTAGACGAAGTAT	0.657	
+	5	1095		NM_012213	NP_036345	O95822	DCMC_HUMAN			0	GATTCGGAATGTA	0.522	
+	3	689	orf97_uc010vpz.1_	NM_001013672	NP_001013694	Q6ZQX7	CQ097_HUMAN	tandem repeat of A-L-K-G-		1	AGGGCTTCCACC	0.647	
-	2	397		NM_001212	NP_001203	Q07021	C1QBP_HUMAN			1	AACCTCCAGACA	0.448	
-	9	1191	e_Mutation_p.T311	NM_031220	NP_112497	Q9BZ71	PITM3_HUMAN			4	TCATAGGTGGAG	0.582	
-	7	848	e_Mutation_p.V197	NM_031220	NP_112497	Q9BZ71	PITM3_HUMAN			4	TGGCGACAGCAT	0.627	
-	5	616	jgo.1_Missense_M	NM_020360	NP_065093	Q9NRY6	PLS3_HUMAN	smic (By similarity).		0	GCAGCGGCCGG	0.721	
+	6	1542		NM_000180	NP_000171	Q02846	GUC2D_HUMAN	lasmic (Potential).		1	AGGCACCGGCTA	0.587	
+	14	2331	p.G737E|ARHGEF	NM_173728	NP_776089	O94989	ARHGF_HUMAN			3	GCTGGGAGCCT	0.582	
+	5	701	_p.K134N|MYOCD	NM_153604	NP_705832	Q8IZQ8	MYCD_HUMAN			5	TGTGAAAGAGGC	0.488	
+	11	1086	_p.G234D|LGALS9	NM_009587	NP_033665	O00182	LEG9_HUMAN	Galectin 2.		0	TGGATGGTCAGC	0.552	rs145626584
+	3	365	vag.1_5'Flank|TME	NM_152464	NP_689677	Q6SZW1	SARM1_HUMAN			0	ATCACCCGCAAC	0.468	
-	5	1562	p.G374R|SLFN11_	NM_001104588	NP_001098058	Q7Z7L1	SLN11_HUMAN			3	GAGGCCCACTAG	0.383	
-	1	403		NM_139285	NP_644814	Q8NHY3	GA2L2_HUMAN	CH.		2	GATGCCCATCTC	0.592	
+	5	792	n_p.G76R|PPP1R1	NM_032192	NP_115568	Q9UD71	PPR1B_HUMAN			0	AGCTGGGGGAG	0.418	
+	2	421	e.1_Intron|DHX40_	NM_024612	NP_078888	Q8IX18	DHX40_HUMAN	ase ATP-binding.		0	CTATATGAAGCAG	0.323	
-	4	865	C|CYB561_uc010d	NM_001915	NP_001906	P49447	CY561_HUMAN	tochrome b561.		1	GTAGCGGCTCC	0.617	
-	8	973	jfz.2_Missense_M	NM_002816	NP_002807	O00232	PSD12_HUMAN	PCI.		0	TCTTCTAACTTCT	0.353	
-	5	444	p.T110M|SLC39A	NM_001159770	NP_001153242	Q8N1S5	S39AB_HUMAN			1	GGGTCGTCTGG	0.542	
-	4	1486	e_Mutation_p.R362	NM_032134	NP_115510	Q9H0J4	QRIC2_HUMAN	Gln-rich.		5	ccaggccggaccaaa	0.139	rs143499534
+	14	4319	uf.2_Missense_Mu	NM_018996	NP_061869	Q9HCJ0	TNR6C_HUMAN	Pro-rich.		2	CCCCTCGCACC	0.647	
-	10	1342	ZI1_uc002jzo.1_Mi	NM_014984	NP_055799	Q9UPN4	AZI1_HUMAN			4	TGGGGGACAGC	0.677	
-	3	795		NM_178520	NP_848615	Q8N8V8	TM105_HUMAN			1	TGTCTTCGCCTT	0.662	rs75774881
-	5	1788	orf70_uc010wuq.1_	NM_001109760	NP_001103230	Q0VG06	FP100_HUMAN			2	CCTCCCGCCGA	0.682	
-	12	1672	ssense_Mutation_	NM_022156	NP_071439	Q6P1R4	DUS1L_HUMAN			1	AGGCTCGCTTC	0.672	
-	16	2368	tion_p.T33I|EPB41	NM_012307	NP_036439	Q9Y2J2	E41L3_HUMAN	ctin-binding (Potential).		5	GGGAGGTGGAA	0.512	
-	6	392	0dkt.2_Missense_M	NM_173464	NP_775735	Q8NA19	LMBL4_HUMAN	MBT 1.		3	CTCTGGAAAGG	0.343	
-	23	3438	wzj.1_Missense_M	NM_005559	NP_005550	P25391	LAMA1_HUMAN	inin EGF-like 13.		21	GCCCCGGTTTCC	0.572	
+	17	2503	o.2_Missense_Mut	NM_020774	NP_065825	Q86YT6	MIB1_HUMAN	RING-type 1.		4	CCATGTGGACAT	0.383	
+	5	589	vr.2_Missense_Mu	NM_177986	NP_817123	Q86SJ6	DSG4_HUMAN	|Extracellular (Potential).		8	ATAAATGATAACG	0.408	
-	4	1513	o.R221H|SMAD7_	NM_005904	NP_005895	O15105	SMAD7_HUMAN	MH2.		0	ACTGGCGGGTG	0.622	
+	7	1422	fb.3_Missense_Mu	NM_005359	NP_005350	Q13485	SMAD4_HUMAN	SAD.	p.0?(35)|p.?(2)	369	CTATGCCGCCCC	0.433	
+	3	557	2lfp.1_Missense_M	NM_173629	NP_775900	Q8N1N2	CR026_HUMAN			0	TGTCCACCTACA	0.468	
+	5	959	if.2_Missense_Mu	NM_031891	NP_114097	Q9HBT6	CAD20_HUMAN	r (Potential).|Cadherin 3.		5	GGATGGAGATG	0.423	
-	2	641	km.3_Missense_M	NM_006566	NP_006557	Q15762	CD226_HUMAN	1.|Extracellular (Potential).		0	TGAGTAGGGCTG	0.448	
-	8	1251	p.E322K|NETO1_	NM_138966	NP_620416	Q8TDF5	NETO1_HUMAN	ss A.|Extracellular (Potentia		4	GATTTTCATCCCA	0.378	
-	5	770	kfs.1_Missense_M	NM_214710	NP_999875	Q6UWY2	PRS57_HUMAN	Peptidase S1.		0	GTACACGTCGG	0.711	
+	41	5794	e_Mutation_p.G30	NM_019112	NP_061985	Q8IZY2	ABCA7_HUMAN	C transporter 2.		9	TGGCAGGCCAC	0.647	
+	1	780		NM_003775	NP_003766	O95977	S1PR4_HUMAN	smic (By similarity).		2	GAAGACGGTGC	0.687	
+	7	737	p.V235M|FZR1_uc	NM_001136198	NP_001129670	Q9UM11	FZR_HUMAN	WD 2.		2	CCTCCGTGGGC	0.632	
+	8	1561_1562		NM_005483	NP_005474	Q13111	CAF1A_HUMAN			2	GCTTTCCATCCA	0.594	
-	2	792	dj.2_Missense_Mu	NM_001097641	NP_001091110	P21217	FUT3_HUMAN	enal (Potential).		0	TGGTCCCCTTG	0.607	
-	3	448	f.1_Missense_Mut	NM_001252	NP_001243	P32970	CD70_HUMAN	cellular (Potential).		0	CATCACGATGGA	0.637	
-	4	521	q.2_Missense_Mut	NM_021155	NP_066978	Q9NNX6	CD209_HUMAN	|7 X approximate tandem r		1	CAGCCAGGTCA	0.557	
-	11	1068	o.Q96*|TIMM44_uc	NM_006351	NP_006342	O43615	TIM44_HUMAN			1	CTGCTGGATGG	0.642	
+	2	182	xkd.1_Missense_M	NM_004218	NP_004209	Q15907	RB11B_HUMAN			0	GCTGTCGCGCT	0.642	
-	5	35792		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).		57	GAAGTTGGAATC	0.488	

-	5	32182		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).	57	TGTCCCCGAAA	0.498	
-	3	30874		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	h.|Extracellular (Potential).	57	CACTGGAATTT	0.458	
-	3	26695		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	h.|Extracellular (Potential).	57	TCATAGGAGTGG	0.527	
-	1	9503		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).	57	CTGCAATGGTC	0.478	
-	1	4672		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).	57	TAGGTGGAAAAA	0.423	
+	4	1932	e_Mutation_p.S62	NM_144566	NP_653167	Q9H0M5	ZN700_HUMAN	2H2-type 14.	0	TTCAGTTGTGC	0.483	
+	4	1934	e_Mutation_p.C62	NM_144566	NP_653167	Q9H0M5	ZN700_HUMAN	2H2-type 14.	0	TCAGTTGTGCCT	0.483	
-	4	901		NM_005815	NP_005806	Q9Y2A4	ZN443_HUMAN	C2H2-type 4.	1	AAAAGAAAAGG	0.378	
+	1	905		NM_012377	NP_036509	O60412	OR7C2_HUMAN	lasmic (Potential).	3	GGGGAGACTCC	0.542	
-	1	501		NM_013940	NP_039228	Q9Y4A9	O10H1_HUMAN	lasmic (Potential).	0	CCGCGGGCTCA	0.647	
-	23	2976		NM_015692	NP_056507	Q8IZJ3	CPMD8_HUMAN		13	GGGGACTCCTT	0.602	
+	10	1530		NM_000453	NP_000444	Q92911	SC5A5_HUMAN	ical; (Potential).	4	TCTACGGATCG	0.607	rs121909180
-	4	1316		NM_021030	NP_066358	P17017	ZNF14_HUMAN		3	TTTCTCTCCAG	0.378	
+	4	1280		NM_031218	NP_112495	P35789	ZNF93_HUMAN	C2H2-type 9.	1	GAGAGTTCATA	0.393	
-	4	1019		NM_001159293	NP_001152765	C9JHM3	C9JHM3_HUMAN		1	TCTCCAGTATGA	0.413	
-	4	1000		NM_001159293	NP_001152765	C9JHM3	C9JHM3_HUMAN		1	TATGTGTAGTAA	0.398	rs57947174
+	4	1244	co.2_Missense_M	NM_003429	NP_003420	Q03923	ZNF85_HUMAN	C2H2-type 9.	1	AATGTGAAAAA	0.358	
+	6	1631	714_uc010ecp.1_	NM_182515	NP_872321	Q96N38	ZN714_HUMAN		0	AGAAACTCTACA	0.368	
-	5	1663	qh.2_Missense_M	NM_173531	NP_775802	Q8IYN0	ZN100_HUMAN	2H2-type 12.	0	ACATTCCTCACA	0.398	
-	6	2775	208_uc002nqo.1_	NM_007153	NP_009084				7	ATTCTTCACATT	0.368	
-	4	822	1_Intron|ZNF208_	NM_007153	NP_009084				7	TCTCTCCAGTAT	0.353	
-	5	1066		NM_001080409	NP_001073878				2	CAGTATGAATTA	0.368	rs34442493
-	4	1111	rj.1_Missense_Mu	NM_003430	NP_003421	Q05481	ZNF91_HUMAN	C2H2-type 7.	0	AAGAACGGCTA	0.393	rs410211
-	4	1486		NM_138330	NP_612203	Q8TD23	ZN675_HUMAN	2H2-type 11.	2	AGGATCGGTTA	0.378	
-	4	1655	_p.S436P|ZNF681_	NM_138286	NP_612143	Q96N22	ZN681_HUMAN		0	TGTAGGATTTCT	0.373	
+	4	2677	dd.1_Missense_M	NM_014717	NP_055532	O15090	ZN536_HUMAN		11	TCCCTGGAATC	0.572	
-	15	2117	_p.S533F|RHPN2_	NM_033103	NP_149094	Q8IUC4	RHPN2_HUMAN		6	ACCAAGAACTG	0.502	
-	7	1102	nul.2_Missense_	NM_019849	NP_062823	Q9NS82	AAA1_HUMAN	ical; (Potential).	2	GACAGGCATGA	0.612	
-	2	251	_p.A39V|PEPD_u	NM_000285	NP_000276	P12955	PEPD_HUMAN		2	TGCACAGCAGG	0.662	
+	2	243	ea.2_Missense_M	NM_005306	NP_005297	O15552	FFAR2_HUMAN	Name=2; (Potential).	1	TGGCCGACCTC	0.662	
+	5	1902		NM_144689	NP_653290	Q8TAQ5	ZN420_HUMAN	2H2-type 16.	0	GTAAGGAATGT	0.428	
+	4	284	xtq.1_RNA|ZNF52	NM_032453	NP_115829	Q8NB42	ZN527_HUMAN	KRAB.	2	CATTTCTAAGC	0.483	
-	14	1703	_p.E419K|AKT2_u	NM_001626	NP_001617	P31751	AKT2_HUMAN	kinase C-terminal.	2	TCACTCGCGGA	0.597	
-	7	4471	_Mutation_p.S126	NM_181882	NP_870998	Q9BXM0	PRAX_HUMAN		2	CGGGGGACTTG	0.692	
+	2	894	sk.3_Missense_M	NM_022752	NP_073589	Q6ZN55	ZN574_HUMAN		0	TGTACCCGAGT	0.617	
-	5	858	p.D175N|PAFAH1	NM_002573	NP_002564	Q15102	PA1B3_HUMAN		0	AGGGTCGGCAT	0.597	
+	3	1277	.2_Missense_Mut	NM_199285	NP_954979	A6NJB7	PRR19_HUMAN	Pro-rich.	0	TCGGCCCTGGG	0.647	
+	4	716		NM_005178	NP_005169	P20749	BCL3_HUMAN	ANK 3.	2	AGCACCGCAGC	0.682	
-	1	707	g.1_Intron|DMPK_	NM_001081563	NP_001075032	Q09013	DMPK_HUMAN		3	GAACCGAGGGT	0.602	
-	1	1352	uc002peu.1_5'UTF	NM_020709	NP_065760	Q9ULN7	PNML2_HUMAN		1	CGTCCGGGGTG	0.572	
-	6	705	t.2_Missense_Mu	NM_001190	NP_001181	O15382	BCAT2_HUMAN		1	CCCCGCCCACC	0.647	
-	1	77	K1_uc010ycg.1_R	NM_002257	NP_002248	P06870	KLK1_HUMAN		0	TCCCCCCCAGG	0.642	
+	3	642	33_uc010eot.1_	NM_001772	NP_001763	P20138	CD33_HUMAN	Potential).|Ig-like C2-type.	0	ACCCCACGGC	0.612	
-	2	1102		NM_002029	NP_002020	P21462	FPR1_HUMAN	lasmic (Potential).	3	AATTGGTAGCT	0.582	
-	5	1531	.2_Intron|uc002py	NM_021632	NP_067645	Q9GZX5	ZN350_HUMAN		1	GATTTTCCACCT	0.493	
+	5	649	sense_Mutation_p	NM_144684	NP_653285	Q8WV37	ZN480_HUMAN		1	CAAGAACAGAA	0.358	
+	4	1437	dn.1_Missense_M	NM_018260	NP_060730	Q9NV72	ZN701_HUMAN		0	AGAAACCTTACA	0.348	rs142390931

-	7	2131	p.R536H|ZNF611_	NM_030972	NP_112234	Q8N823	ZN611_HUMAN	2H2-type 14.	1	ACCTGCGACTG	0.448	rs145568781
-	4	2277	_p.*666C|ZNF28_	NM_006969	NP_008900	P17035	ZNF28_HUMAN		1	CACTTTCAAGG	0.403	
+	8	2341	.R728Q|NLRP2_	NM_017852	NP_060322	Q9NX02	NALP2_HUMAN		2	TCTTCGAGGTC	0.453	
+	10	2787	p.T877P|NLRP2_	NM_017852	NP_060322	Q9NX02	NALP2_HUMAN	LRR 4.	2	TGCAGACCTTG	0.552	
+	3	214	5D_uc002qlg.3_5'	NM_020378	NP_065111	Q8WUY8	NAT14_HUMAN	cetyltransferase.	2	GGCCCTGCTCC	0.701	
-	5	1369	b.2_Missense_Mu	NM_145007	NP_659444	P59045	NAL11_HUMAN	NACHT.	6	GGGATCAGACA	0.478	
+	7	1604	mi.2_Missense_M	NM_153447	NP_703148	P59047	NALP5_HUMAN	NACHT.	7	TATGGCTGTGG	0.557	
+	6	397	LP_uc010eti.2_3'	NM_033106	NP_149097	Q9UBC7	GALP_HUMAN		0	AGCATGAAAAT	0.368	
-	2	865	gn.1_Missense_M	NM_001005850	NP_001005850				4	GTGGCGGATGA	0.682	
-	5	1758		NM_052882	NP_443114	Q96PE6	ZIM3_HUMAN	2H2-type 11.	2	CCTGTCAGCGA	0.408	
-	5	499		NM_001012729	NP_001012747	A6NLW8	DUXA_HUMAN	omeobox 2.	1	TCTTCGATTTTG	0.383	
+	3	1610	F776_uc002qqa.	NM_173632	NP_775903	Q68DI1	ZN776_HUMAN	ype 10; degenerate.	1	AGTGTGGAGAA	0.448	
+	10	1622	_p.V363M|TRIM28	NM_005762	NP_005753	Q13263	TIF1B_HUMAN		3	TGGAGGTGCAG	0.607	
-	10	1533	e_Mutation_p.D23	NM_015025	NP_055840	Q9UL68	MYT1L_HUMAN		6	ACTATCGTCTTC	0.443	
+	1	1302		NM_002236	NP_002227	Q9H3M0	KCNF1_HUMAN		1	CCTCACGCTCA	0.627	
-	8	1338	da.2_Missense_M	NM_001002006	NP_001002006	Q96P26	5NT1B_HUMAN		3	TTTTCCCCCGG	0.393	
-	26	10625		NM_000384	NP_000375	P04114	APOB_HUMAN	parin-binding.	27	TTGACATCTCC	0.458	
-	26	8053		NM_000384	NP_000375	P04114	APOB_HUMAN		27	CTGGATGGGATT	0.358	
+	4	2634	lank|KHK_uc002r	NM_007046	NP_008977	Q9Y6C2	EMIL1_HUMAN	Potential.	1	GTGAACGGTTG	0.657	rs139887250
+	4	1510	mi.1_Missense_M	NM_005253	NP_005244	P15408	FOSL2_HUMAN		3	GTCCTCGTCGG	0.682	
+	8	932	nk.1_Missense_M	NM_144736	NP_653337	Q7L592	MIDA_HUMAN		1	AACTTTCTCAAC	0.413	
+	8	934	nk.1_Nonsense_	NM_144736	NP_653337	Q7L592	MIDA_HUMAN		1	TTTCTCAACGC	0.413	
+	25	5363	x.2_Missense_M	NM_003128	NP_003119	Q01082	SPTB2_HUMAN	with ANK2.|Spectrin 14.	8	CAACCGGGAGG	0.547	
+	8	955	sff.2_Missense_M	NM_032208	NP_115584	Q9H6X2	ANTR1_HUMAN	lar (Potential).|VWFA.	4	GTTTCCCGTGA	0.488	
+	2	1034	10feb.1_Missense_	NM_005791	NP_005782	O00566	MPP10_HUMAN	Potential.	3	ATAATGATGAG	0.323	
+	51	6134	SF_uc010fej.2_M	NM_003494	NP_003485	O75923	DYSF_HUMAN	lasmic (Potential).	7	TTTGATGATTTTC	0.522	
+	8	739		NM_032118	NP_115494	Q9H977	WDR54_HUMAN	WD 3.	0	TAGCAGCAGGC	0.557	
-	1	124	P39_uc010ysv.1_	NM_001013649	NP_001013671	Q2NKX9	CB068_HUMAN		1	CAGCCGCCCCC	0.731	
-	4	909	svr.2_Missense_	NM_017849	NP_060319	O75204	TM127_HUMAN		0	GGGCTCGTTCT	0.622	
+	7	1083		NM_004804	NP_004795	O76071	CIAO1_HUMAN		0	CTTCTCCCTGA	0.612	
-	22	2922		NM_022662	NP_073153	Q9H1A4	APC1_HUMAN		2	GTGAGGATTCAT	0.289	
-	6	797	2orf76_uc002tlt.2_	NM_001017927	NP_001017927	Q3KRA6	CB076_HUMAN		0	GTCTTTCGTCAT	0.448	
+	3	408	LI2_uc002tmu.3_	NM_005270	NP_005261	P10070	GLI2_HUMAN		13	CACATGGAGCA	0.647	
-	3	387	IMS2_uc010yzm.1	NM_001161403	NP_001154875	Q7Z4I7	LIMS2_HUMAN	zinc-binding 1.	0	AGCACGGAGCA	0.602	
-	14	2946	AP5_uc002ttq.2_	NM_207363	NP_997246	O14513	NCKP5_HUMAN		0	TAATTCAAAGAG	0.532	
-	6	1158		NM_002299	NP_002290	P09848	LPH_HUMAN	ial).|4 X approximate repe	13	TTCAGGGAAAG	0.602	
+	27	4684		NM_001080427	NP_001073896				7	CACCTCCCCAA	0.418	
-	89	14518		NM_018557	NP_061027	Q9NZR2	LRP1B_HUMAN	lasmic (Potential).	50	GGTCTATCATAA	0.373	
+	1	1118		NR_026904					0	AGACAGCTATG	0.388	
+	9	1616	foc.1_Missense_	NM_052917	NP_443149	Q8IUC8	GLT13_HUMAN	enal (Potential).	6	CAACTCCATACA	0.413	
+	3	1630	J3_uc010zce.1_3'	NM_002239	NP_002230	P48549	IRK3_HUMAN	smic (By similarity).	2	TGGCTGGAGGA	0.428	
+	6	1000	zd.3_Missense_M	NM_001083112	NP_001076581	P43304	GPDM_HUMAN		1	TGGTAGGAGCA	0.393	
-	12	2539		NM_022168	NP_071451	Q9BYX4	IFIH1_HUMAN	case C-terminal.	1	TGACTTCTTTTTG	0.294	
-	16	3400	p.E1008K|SCN1A_	NM_006920	NP_008851	P35498	SCN1A_HUMAN		13	TTTCTTCCAGAT	0.284	
+	8	2470	udy.2_Missense_	NM_152381	NP_689594	A4UGR9	XIRP2_HUMAN	Xin 8.	14	CCTTTGGAGAAA	0.378	
+	2	910		NM_020981	NP_066191	Q9Y5Z6	B3GT1_HUMAN	enal (Potential).	4	GACAATCTTATT	0.408	
-	2	229		NM_020675	NP_065726	Q9HBM1	SPC25_HUMAN	omplex.|Interaction with th	1	GTATCTCTTAGTC	0.373	

-	36	6052		NM_004525	NP_004516	P98164	LRP2_HUMAN	B 18.|Extracellular (Potent	29	CCACGTTTCCTC	0.343	
-	4	405	.2_Intron|SLC25A	NM_003705	NP_003696	O75746	CMC1_HUMAN	.|EF-hand 2.	0	ATGTCACCTCTC	0.363	
-	254	55829	230I|TTN_uc010z	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	GGTCTCATTTCC	0.453	
-	253	54483	782K|TTN_uc010z	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	TGTTTCGATGG	0.393	
-	250	52053	72C|TTN_uc010z	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	CATTACGAATTT	0.388	
-	238	48717	860F|TTN_uc010z	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	ATAGAGAACAG	0.433	
-	65	16329	_uc010zfj.1_Intro	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	AAGTTCCACAT	0.408	
-	65	16228	_uc010zfj.1_Intro	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	CAGGTTTCACT	0.338	
+	3	884		NM_194250	NP_919226	Q7Z570	Z804A_HUMAN	p.R97Q(1)	11	TGCTCGAAATG	0.368	rs145158210
-	7	911	frt.2_Nonsense_M	NM_005795	NP_005786	Q16602	CALRL_HUMAN	ellular (Potential).	4	TTTGTCCATGTT	0.333	
-	44	8356		NM_018897	NP_061720	Q8WXX0	DYH7_HUMAN	k (By similarity).	12	CATGAAGTGACT	0.373	
-	41	7050		NM_018897	NP_061720	Q8WXX0	DYH7_HUMAN	4 (By similarity).	12	AAATCGAAACA	0.443	rs115474479
-	36	6037		NM_018897	NP_061720	Q8WXX0	DYH7_HUMAN	milarity).|ATP (Potential).	12	CAGTTCCTGTT	0.368	
-	8	1165	W2_uc002utl.1_I	NM_020760	NP_065811	Q9P2P5	HECW2_HUMAN		18	ACCTTCATGAA	0.403	
+	11	2709	tr.2_Missense_Mu	NM_001204	NP_001195	Q13873	BMPR2_HUMAN	lasmic (Potential).	9	ATCCAATGTCT	0.423	
+	11	1748	_p.V393I|ABI2_uc	NM_005759	NP_005750	Q9NYB9	ABI2_HUMAN	SH3.	0	AATTACGTTGAG	0.453	
+	3	285	10ziu.1_5'Flank|E	NM_001037663	NP_001032752	P24534	EF1B_HUMAN	ST C-terminal.	0	TGTCCAGCCCA	0.468	
-	7	979	_p.P294L|ERBB4_	NM_005235	NP_005226	Q15303	ERBB4_HUMAN	xtracellular (Potential).	33	TACGTGGACAT	0.318	
+	4	392	_p.P131L|RQCD1_	NM_005444	NP_005435	Q92600	RCD1_HUMAN		2	ACGTCCCTTTG	0.423	
-	4	575	_5'UTR|ZNF142_	NM_001105537	NP_001099007	P52746	ZN142_HUMAN		4	GTCCCGGGAAG	0.602	
-	10	1868	.R555W|ECEL1_	NM_004826	NP_004817	O95672	ECEL1_HUMAN	enal (Potential).	2	CTGCCGAATCT	0.567	
+	12	1227	F2_uc002vtk.3_M	NM_015575	NP_056390	Q6Y7W6	PERQ2_HUMAN		7	AAGAAATGGGTA	0.448	
+	1	900	_p.A140T|GPR35_	NM_005301	NP_005292	Q9HC97	GPR35_HUMAN	Name=3; (Potential).	3	TCACGGCCATC	0.697	
+	3	469		NM_032515	NP_115904	Q9UMX3	BOK_HUMAN	BH3.	1	CAGGCGATGAG	0.647	
-	2	471		NM_015963	NP_057047	Q8WY91	THAP4_HUMAN	THAP-type.	0	AGATGGATGGC	0.582	
+	4	582	al.1_Missense_Mu	NM_198994	NP_945345	O95932	TGM3L_HUMAN		4	ACGAGCCCAGG	0.622	
-	5	1408	nj.2_Missense_Mu	NM_020341	NP_065074	Q9P286	PAK7_HUMAN	Linker.	23	AGCCTGACCTG	0.552	
-	5	1064	nj.2_Missense_Mu	NM_020341	NP_065074	Q9P286	PAK7_HUMAN	Linker.	23	CATTTTCATTACG	0.463	
-	3	679		NM_021220	NP_067043	Q9BRP0	OVOL2_HUMAN		1	GTGTCTTTTCA	0.592	
+	3	302	OLR3F_uc002wqx	NM_006466	NP_006457	Q9H1D9	RPC6_HUMAN		0	AGGGTCAGTTG	0.303	
-	1	1496	HBD_uc002wsu.1_	NM_000361	NP_000352	P07204	TRBM_HUMAN	g (Potential).|Extracellular	0	GTTTTCGCACT	0.642	
-	17	3072	L_uc010gdn.1_In	NM_025176	NP_079452	Q9Y2I6	NINL_HUMAN		5	GGCCCGGGCCT	0.677	
+	15	2497	lv.1_Missense_Mu	NM_012112	NP_036244	Q9ULW0	TPX2_HUMAN		2	CAGAAGAGGTG	0.488	
+	6	991	eb.2_Missense_Mu	NM_015338	NP_056153	Q8IXJ9	ASXL1_HUMAN		248	CATCAGGTATG	0.507	
+	3	228_229		NM_182519	NP_872325	P59827	LPLC4_HUMAN		0	GGACCCCCCCC	0.485	rs145261889
-	3	594		NM_005225	NP_005216	Q01094	E2F1_HUMAN	Potential.	0	CAGGTCGACGA	0.577	
+	15	2212	v.2_Nonsense_Mu	NM_012156	NP_036288	Q9H4G0	E41L1_HUMAN		3	CGGATCGAGGG	0.652	
-	6	680	gu.2_Missense_M	NM_182970	NP_892015	Q9H426	RIMS4_HUMAN		5	CCAGGGTGGTC	0.657	
+	1	100		NM_002638	NP_002629	P19957	ELAF_HUMAN		0	TCACGGGAGGT	0.597	
-	5	922	p.P274L|EEF1A2_	NM_001958	NP_001949	Q05639	EF1A2_HUMAN		0	TGCCCGGCCGC	0.672	
+	2	545	nk|ARFRP1_uc011	NM_032527	NP_115916	Q8N5A5	ZGPAT_HUMAN	Poly-Glu.	0	ggaagagggagagg	0.542	
+	18	2522	P25_uc002yjz.1_M	NM_013396	NP_037528	Q9UHP3	UBP25_HUMAN		5	AGCATGAAGAT	0.378	
-	2	276	orf59_uc010glx.2_	NM_021254	NP_067077	P57076	CU059_HUMAN		0	TATGCCATGTTC	0.328	
+	4	476	yri.1_Missense_M	NM_000628	NP_000619	Q08334	I10R2_HUMAN	-III.|Extracellular (Potential	0	CTGATTCTTTAC	0.348	
+	4	1278	p.D326N|KCNJ15	NM_002243	NP_002234	Q99712	IRK15_HUMAN	smic (By similarity).	6	TGGCTGATTTC	0.443	
-	6	1522	AM_uc002yyr.1_	NM_001389	NP_001380	O60469	DSCAM_HUMAN	otential).|Ig-like C2-type 4.	11	TTTTTTCCAGGG	0.507	
-	5	857		NM_020639	NP_065690	P57078	RIPK4_HUMAN		7	CTCGCGGATCC	0.687	

-	5	706	_Splice_Site|PTTG	NM_004339	NP_004330	P53801	PTTG_HUMAN		1	TCCTTACCATAT	0.502	
-	14	2352	nk.1_Missense_M	NM_015241	NP_056056	Q7RTP6	MICA3_HUMAN		0	CTTGGGAGAAC	0.502	
-	4	672	ol.3_Missense_Mu	NM_016335	NP_057419	O43272	PROD_HUMAN		1	GGCTTCGATGC	0.612	
-	31	4855	_p.L1573M|CLTCL	NM_007098	NP_009029	P53675	CLH2_HUMAN	zation (By similarity).|Heav	5	GGCCAAGTCCA	0.617	
+	2	329	e_Mutation_p.R75	NM_013373	NP_037505	Q9ULC8	ZDHC8_HUMAN	lasmic (Potential).	2	TCCCCCGAGGT	0.562	
+	5	2391	CR_uc011aiy.1_Mi	NM_004327	NP_004318	P11274	BCR_HUMAN	DH.	12	AACTACGGAGTT	0.577	
+	4	2128	FH_uc003afp.2_5'U	NM_021076	NP_066554	P12036	NFH_HUMAN	ats of K-S-P-[AEPV]-[EAK]-	0	GAAGGCAGAAG	0.562	
-	1	729	ense_Mutation_p.	NM_014323	NP_055138	Q9HBE1	PATZ1_HUMAN		2	CCGTGCTGTGT	0.672	
+	4	539	aqc.3_Missense_M	NM_000395	NP_000386	P32927	IL3RB_HUMAN	ellular (Potential).	3	ACTGACGTTGAC	0.627	
-	2	388	rb.2_Nonsense_M	NM_001051	NP_001042	P32745	SSR3_HUMAN	ellular (Potential).	1	AGGGCCAGTAG	0.617	
+	7	2067	atq.1_Missense_M	NM_001039141	NP_001034230	Q9H2D6	TARA_HUMAN		1	ACCCCACAACAT	0.582	
+	1	783_784	_5'Flank|GCAT_u	NM_005318	NP_005309	P07305	H10_HUMAN		0	ATCAAGAAGGTA	0.564	
-	6	523		NM_025045	NP_079321	Q6UXY1	BI2L2_HUMAN	IMD.	1	GTGGCGGTACT	0.632	
+	3	291	gzn.2_Missense_	NM_013327	NP_037459	Q9HBI1	PARVB_HUMAN		0	CACTTCCAAGG	0.572	
-	2	564	aa.2_Missense_M	NM_058238	NP_478679	P56706	WNT7B_HUMAN		1	CCCCTCCCCAA	0.627	
-	13	5828	arc.1_Missense_M	NM_014246	NP_055061	Q9NYQ6	CELR1_HUMAN	ial).|EGF-like 6; calcium-bi	11	AGTACGGCCCG	0.612	
-	35	5441	.R571W|PLXNB2_	NM_012401	NP_036533	O15031	PLXB2_HUMAN	lasmic (Potential).	6	TACCCGGGAAA	0.617	
-	19	2389	_p.R396C|SBF1_u	NM_002972	NP_002963	O95248	MTMR5_HUMAN		0	CAAGCGCCGCT	0.642	
+	2	200	_p.R29Q|MIOX_u	NM_017584	NP_060054	Q9UGB7	MIOX_HUMAN		0	CTTCCGGAACT	0.612	rs151151350
+	9	1294	.G271R|CNTN6_	NM_014461	NP_055276	Q9UQ52	CNTN6_HUMAN	like C2-type 4.	8	CTAGTGGAAAG	0.398	
-	2	143	auj.1_Intron|GHR	NM_016362	NP_057446	Q9UBU3	GHRL_HUMAN		1	CTGGGGAGGGC	0.652	
+	2	1079	lt.2_Missense_Mu	NM_001098213	NP_001091683	P35367	HRH1_HUMAN	lasmic (Potential).	2	CAAGGGGGATG	0.532	
+	10	1809	xj.2_Missense_Mu	NM_001162499	NP_001155971	O75155	CAND2_HUMAN	HEAT 12.	4	GGAGGTGAAGG	0.632	
+	5	2377	wd.1_Missense_M	NM_001144382	NP_001137854	Q9UPR0	PLCL2_HUMAN	C2.	4	AGAACTTTCCC	0.473	rs138785787
+	2	674	cdq.2_Missense_	NM_052953	NP_443185	Q96PB8	LRC3B_HUMAN		4	GCTTTCATTCTG	0.443	
-	9	1329	_Mutation_p.Q37	NM_198056	NP_932173	Q14524	SCN5A_HUMAN		9	CTGCTGATAGA	0.612	
-	11	1645		NM_006514	NP_006505	Q9Y5Y9	SCNAA_HUMAN		10	AGGGAGGGGGC	0.612	
+	4	290	03ckr.2_Missense	NM_001904	NP_001895	P35222	CTNB1_HUMAN	0del(1)|p.M1_A87del(1)|p.	3166	TCCTTCTCTGA	0.498	rs121913409
+	2	968	al.1_Intron|CXCR	NM_006564	NP_006555	O00574	CXCR6_HUMAN	lasmic (Potential).	1	GTTTCGAAAGA	0.473	rs141955108
+	4	1373	k.1_Missense_Mu	NM_178329	NP_847899	P51677	CCR3_HUMAN	ellular (Potential).	8	GAGCAAGCATC	0.498	
-	3	419	.1_5'UTR|SCAP_u	NM_012235	NP_036367	Q12770	SCAP_HUMAN	nal (By similarity).	1	ATTCCACAGGT	0.537	
-	14	3272	.2_Missense_Muta	NM_002673	NP_002664	O43157	PLXB1_HUMAN	ellular (Potential).	5	GACGCAGAAAC	0.662	
-	11	2819	csx.2_Missense_M	NM_002673	NP_002664	O43157	PLXB1_HUMAN	ellular (Potential).	5	CCTCGGGCAGC	0.687	
-	1	1957	uf.1_Missense_M	NM_001407	NP_001398	Q9NYQ7	CELR3_HUMAN	(Potential).|Cadherin 3.	11	GGGGGCGCACA	0.602	rs140226738
-	16	2332	wf.1_Missense_M	NM_002292	NP_002283	P55268	LAMB2_HUMAN	ninin IV type B.	3	GGATTAGGAAAT	0.572	
+	1	166	yl.2_Missense_M	NM_144499	NP_653082	P11488	GNAT1_HUMAN		3	GGAAAAGAAGC	0.612	
+	46	4804		NM_004947	NP_004938	Q8IZD9	DOCK3_HUMAN	DHR-2.	0	CCTTGGAGTTG	0.488	
+	53	5707_5708		NM_004947	NP_004938	Q8IZD9	DOCK3_HUMAN		0	GTCCTCCTTGA	0.614	
+	26	3380	p.R1073C|CACNA	NM_001128840	NP_001122312	Q01668	CAC1D_HUMAN	llular (Potential).|III.	11	TGGTCCGTGAA	0.527	
+	9	977	_p.G216E|CACNA	NM_018398	NP_060868	Q8IZS8	CA2D3_HUMAN	lar (Potential).|VWFA.	7	GAATGGAACTT	0.453	
+	18	1655	TR|PXK_uc010hn	NM_017771	NP_060241	Q7Z7A4	PXK_HUMAN		1	TCCTCCACCTC	0.612	
-	21	2985		NM_020872	NP_065923	Q9P232	CNTN3_HUMAN	nectin type-III 4.	5	GTAGTCCTCTTT	0.408	
-	6	822	_p.C30G|PROS1_	NM_000313	NP_000304	P07225	PROS_HUMAN	alcium-binding (Potential).	1	CTTTGCATTCAT	0.348	
+	9	1318	x.2_Missense_Mu	NM_198196	NP_937839	P40200	TACT_HUMAN	otential).|Pro/Ser/Thr-rich.	3	AAATTTCCTCAA	0.358	
+	16	3180		NM_032242	NP_115618	Q9UIW2	PLXA1_HUMAN	r (Potential).|IPT/TIG 3.	3	AATCCGGGCCA	0.632	
-	3	921	_Mutation_p.G24	NM_003925	NP_003916	O95243	MBD4_HUMAN		2	TACATCCTTTTTT	0.363	
-	4	1790		NM_015103	NP_055918	Q9Y4D7	PLXD1_HUMAN	ellular (Potential).	1	GTAGGCGTCCG	0.692	

-	2	230	.R27G|NMNAT3_	NM_178177	NP_835471	Q96T66	NMNA3_HUMAN		0	CACTCGGTGAT	0.572	
+	5	1184	hvn.2_Missense_	NM_207365	NP_997248	Q6P093	ADCL2_HUMAN		0	ACTTCGAAATG	0.358	
+	5	545_546	_p.P125F|FNDC3	NM_022763	NP_073600	Q53EP0	FND3B_HUMAN		3	TCCCTCCCTATC	0.535	
+	26	3581	hz.3_Missense_M	NM_022763	NP_073600	Q53EP0	FND3B_HUMAN	nectin type-III 9.	3	CTCAGGAGCTA	0.517	
+	9	1118	my.2_Missense_M	NM_004068	NP_004059	Q96CW1	AP2M1_HUMAN	MHD.	0	AGATCGAGGTG	0.542	
+	17	1770	p.R540Q|ABCF3_	NM_018358	NP_060828	Q9NUQ8	ABCF3_HUMAN	C transporter 2.	4	TGTTCGGGGCA	0.577	
+	10	2109	G1_uc003fqr.2_Int	NM_001102416	NP_001095886	P01042	KNG1_HUMAN		1	ATGAAAGAATCT	0.368	
-	2	1351		NM_178496	NP_848591	Q8IYB1	M21D2_HUMAN		0	GGCAGGAAGTC	0.532	
-	3	3308	tron|ABCA11P_uc	NM_133474	NP_597731	D9N162	D9N162_HUMAN		1	TAAAGGTTTTGC	0.418	
-	3	2433	ron|ABCA11P_uc0	NM_133474	NP_597731	D9N162	D9N162_HUMAN		1	TTCTCTCCAGTA	0.398	
-	3	1628	tron|ABCA11P_uc	NM_133474	NP_597731	D9N162	D9N162_HUMAN		1	TAAAGGCTTTGC	0.403	
-	27	3894	AK_uc010ibi.2_Mi	NM_005255	NP_005246	O14976	GAK_HUMAN		4	GGGCCCGGATG	0.687	
-	9	816	_p.A239T|CRMP1_	NM_001313	NP_001304	Q14194	DPYL1_HUMAN		2	GATGGCCCGGA	0.557	
-	9	1669	p.D465N|JAKMIP1	NM_144720	NP_653321	Q96N16	JKIP1_HUMAN	tion with TYK2 and GABBR	4	TCCTGTCTGTCC	0.537	
-	16	2384	_Mutation_p.S788	NM_198595	NP_940997	Q8N556	AFAP1_HUMAN		0	CCTGGCTCTTC	0.677	
-	10	6442	r.1_Missense_Mut	NM_148894	NP_683692	Q8NFC6	BOD1L_HUMAN		6	TTACTCTGGTAC	0.483	
+	10	1556	l.1_Missense_Mu	NM_182485	NP_872291	Q7Z5Q1	CPEB2_HUMAN	RRM 2.	1	TTTCTCCAATC	0.433	
+	10	1170	.P312S|RBPJ_uc	NM_005349	NP_005340	Q06330	SUH_HUMAN		3	CCACTCCATGT	0.338	
+	11	1414		NM_021927	NP_068746	Q8N442	GUF1_HUMAN		1	GGCTAGGATTT	0.373	
+	4	3067	_p.P907L|REST_u	NM_005612	NP_005603	Q13127	REST_HUMAN		9	CCTACCTGGTC	0.428	
+	1	135	0ihr.2_Missense_	NM_053039	NP_444267	Q9BY64	UDB28_HUMAN		1	TGAAAGAGCTT	0.443	
+	1	331	ihr.2_Missense_	NM_053039	NP_444267	Q9BY64	UDB28_HUMAN		1	TTTTTCACAAGA	0.294	
+	13	1793	B_uc003hgu.3_M	NM_000477	NP_000468	P02768	ALBU_HUMAN	Albumin 3.	6	TGGATGATTTCG	0.413	
-	9	1237		NM_001042784	NP_001036249	Q5M9N0	CD158_HUMAN	Potential.	6	TGTCCGGGCTT	0.388	
+	27	3909	w.2_Missense_Mu	NM_025074	NP_079350	Q86XX4	FRAS1_HUMAN	xtracellular (Potential).	5	GAAATGGAAAA	0.478	
+	2	993		NM_001201	NP_001192	P12645	BMP3_HUMAN		5	CCAAGGGACGC	0.438	
-	8	1087	H1B_uc011ceh.1	NM_000668	NP_000659	P00325	ADH1B_HUMAN		2	TAAAATCAGCCA	0.368	
-	3	269		NM_000673	NP_000664	P40394	ADH7_HUMAN		3	AGATTCCTGTG	0.393	
+	8	1722	_p.P382S|EGF_uc	NM_001963	NP_001954	P01133	EGF_HUMAN	Extracellular (Potential).	4	TCTGTCCTGAA	0.398	rs146224376
+	9	1865_1866	p.D430N|EGF_uc	NM_001963	NP_001954	P01133	EGF_HUMAN	Extracellular (Potential).	4	CAACTGGATGAA	0.441	
+	6	879	a.2_Missense_Mu	NM_016648	NP_057732	Q4G0J3	LARP7_HUMAN	RRM.	3	ATATTTCCTAAA	0.279	
-	8	1705		NM_015130	NP_055945	Q6ZT07	TBCD9_HUMAN		1	CCAATTTCGGG	0.463	
+	1	1787	t.3_Intron|LRBA_u	NM_006439	NP_006430	Q9Y586	MB212_HUMAN		1	AGAGCGACGCC	0.652	
+	3	1301	_p.S361L|TLR2_uc	NM_003264	NP_003255	O60603	TLR2_HUMAN	tracellular (Potential).	3	TAAAATCATTAG	0.323	
+	3	696	_p.P175S|RBM46_	NM_144979	NP_659416	Q8TBY0	RBM46_HUMAN	RRM 2.	2	TTTATCCAAGTG	0.353	
+	4	636	3_uc003iox.2_Mis	NM_000856	NP_000847	Q02108	GCYA3_HUMAN		4	AGGCAGCAGGA	0.488	
+	15	2993	_Mutation_p.R798	NM_001083619	NP_001077088	P42262	GRIA2_HUMAN	lasmic (Potential).	4	GAAACGAATGA	0.448	
+	11	1977	p.R444C|TLL1_uc	NM_012464	NP_036596	O43897	TLL1_HUMAN	CUB 1.	7	AGTTTCGTAGC	0.368	
-	9	1223	e.1_Missense_Mu	NM_012224	NP_036356	Q96PY6	NEK1_HUMAN	rotein kinase.	6	CTATCCCTAGGA	0.368	
+	8	949	e_Mutation_p.R25	NM_021942	NP_068761	Q7Z392	CD041_HUMAN		0	ATTGAGAGCCC	0.318	
-	10	6595		NM_005245	NP_005236	Q14517	FAT1_HUMAN	(Potential).|Cadherin 19.	12	TCAGTGAAATTT	0.428	
+	18	2891	3jdk.1_Missense_	NM_139056	NP_620687	Q8TE57	ATS16_HUMAN	SP type-1 2.	8	CACGGGGCTGG	0.527	
-	7	2121	se_Mutation_p.E3	NM_024091	NP_076996	Q14CZ7	FAKD3_HUMAN		4	TTCATTCTTGCA	0.333	
+	11	1523	RR_uc003jef.3_R	NM_024010	NP_076915	Q9UBK8	MTRR_HUMAN	-binding FR-type.	1	CTTCAACATTGT	0.443	
-	78	13601	c.2_Nonsense_Mu	NM_001369	NP_001360	Q8TE73	DYH5_HUMAN		31	TTCATCCATTTG	0.478	
+	11	1984		NM_020227	NP_064612	Q9NQV7	PRDM9_HUMAN	2H2-type 4.	6	GAGGACACACA	0.597	
+	11	2068		NM_020227	NP_064612	Q9NQV7	PRDM9_HUMAN	2H2-type 5.	6	GAGGAGACACA	0.612	rs112192848

-	4	959		NM_022130	NP_071413	Q9H4A6	GOLP3_HUMAN			1	TTCACCCATTTGT	0.502
-	12	1928	0iuq.1_Missense_	NM_030955	NP_112217	P58397	ATS12_HUMAN	TSP type-1 1.		9	ACAAGCGATAGC	0.458
-	7	960		NM_001737	NP_001728	P02748	CO9_HUMAN	MACPF.		0	TTTTTTCCTGTGT	0.328
+	19	2486	GA1_uc003jow.2_M	NM_181501	NP_852478	P56199	ITA1_HUMAN	cellular (Potential).		3	AATAAGGAAAAT	0.398
+	20	1971	h.3_Missense_Mu	NM_001136034	NP_001129506	Q9NQI0	DDX4_HUMAN	case C-terminal.		2	ACTGGTCGTTGTC	0.388
+	2	330		NM_005242	NP_005233	P55085	PAR2_HUMAN	cellular (Potential).		1	GAAAAGGAGTTAC	0.433
+	33	8017	p.G347R|GPR98_	NM_032119	NP_115495	Q8WXG9	GPR98_HUMAN	.|Extracellular (Potential).		16	GTGCTGGAGAG	0.423
-	17	2333	_p.F511C|MCTP1_	NM_024717	NP_078993	Q6DN14	MCTP1_HUMAN			2	CTGATAAAGTTTC	0.353
+	8	1045	R36_uc010jbu.2_F	NM_139281	NP_644810	Q8NI36	WDR36_HUMAN	WD 3.		2	GGAAGCCCATGTC	0.373
-	13	1452	03kpp.1_Splice_Si	NM_022140	NP_071423	Q9HCS5	E41LA_HUMAN			1	CACTGACCTTTTT	0.313
+	3	513	ksn.2_Missense_M	NM_182761	NP_877438	A1A519	F170A_HUMAN			1	ACAACATGTCTCC	0.493
+	1	580		NM_177478	NP_803431	Q8N4E7	FTMT_HUMAN	rritin-like diiron.		1	TGTGCGATTTCC	0.507
-	7	1289	wk.2_Missense_M	NM_004199	NP_004190	O15460	P4HA2_HUMAN			0	CAGCTCGTTCGT	0.433
-	13	1850	_p.E551K|KIF3A_	NM_007054	NP_008985	Q9Y496	KIF3A_HUMAN	Potential.		1	GATGTTCTTGTTG	0.398
-	2	445	f20_uc003lav.2_5'F	NM_001099221	NP_001092691	Q6ZNK6	TIFAB_HUMAN	FHA.		0	ACAGCCCTTGCC	0.647
-	10	1614_1615	L3_uc011cyd.1_In	NM_017415	NP_059111	Q9UH77	KLHL3_HUMAN	Kelch 2.		0	GAGCACCGCTGC	0.599
+	26	5064	_p.R386Q|ANKHD	NM_020690	NP_065741	Q8IWZ2	Q8IWZ2_HUMAN			6	AGACACGGTAAA	0.363
+	1	563	03lhc.1_Missense_	NM_018905	NP_061728	Q9Y5H9	PCDA2_HUMAN	cellular (Potential).		4	GGTTTCCTCTAG	0.448
+	1	1966	lhd.2_Intron|PCDH	NM_018906	NP_061729	Q9Y5H8	PCDA3_HUMAN	|Extracellular (Potential).		8	CACGGTGAACCC	0.697
+	1	1050	03lhf.2_Intron|PCD	NM_018907	NP_061730	Q9UN74	PCDA4_HUMAN	|Extracellular (Potential).		6	TCCTATGAAATTA	0.358
+	1	1475	003lhi.2_Intron|PC	NM_018908	NP_061731	Q9Y5H7	PCDA5_HUMAN	r (Potential).|Cadherin 5.		3	CTACTCGCTGGT	0.662
+	1	1922	l.2_Intron|PCDHA6	NM_018901	NP_061724	Q9Y5I2	PCDAA_HUMAN	r (Potential).|Cadherin 6.		5	CTGACTCGCCACC	0.647
+	1	871	dah.1_Missense_M	NM_018939	NP_061762	Q9Y5E3	PCDB6_HUMAN	|Extracellular (Potential).		1	CCCTTCGAAATAA	0.458
+	1	1948	dah.1_Missense_M	NM_018939	NP_061762	Q9Y5E3	PCDB6_HUMAN	|Extracellular (Potential).		1	CTCCGCGCTCG	0.706
+	1	1463	o.1_Intron|PCDHG	NM_018923	NP_061746	Q9Y5G2	PCDGE_HUMAN	r (Potential).|Cadherin 5.		0	AAGTTTCCTACTC	0.592
+	1	610	3ljo.1_Intron|PCDH	NM_018924	NP_061747	Q9Y5G1	PCDGF_HUMAN	r (Potential).|Cadherin 2.		0	GGGAAGAGCAG	0.552
+	11	1093	p.S353L|ARHGAP	NM_015071	NP_055886	Q9UNA1	RHG26_HUMAN	PH.		1	CTTTGTCGGAAGA	0.498
+	3	326	_p.R69Q|FBXO38_	NM_205836	NP_995308	Q6PIJ6	FBX38_HUMAN	KLF7 (By similarity).|F-box		6	TCTGCGAGTTGT	0.468
-	8	1034	3lua.2_Missense_M	NM_181776	NP_861441	Q495M3	S36A2_HUMAN	ical; (Potent	p.G302V(1)	2	ACATTCCCAAAGA	0.453
-	2	1445	o.Q463R|PWWP2A	NM_001130864	NP_001124336	Q96N64	PWP2A_HUMAN			0	GGATTCTGATATC	0.403
+	2	397	C99_uc011deq.1_5	NM_017785	NP_060255	Q96EA4	SPDLY_HUMAN	Potential.		2	CAGAATCAATTGC	0.413
+	4	389	ndf.1_Missense_M	NM_006650	NP_006641	Q6PUV4	CPLX2_HUMAN			1	ACAAAGGACATGC	0.413
+	4	1334	SD1_uc011dfx.1_I	NM_022455	NP_071900	Q96L73	NSD1_HUMAN			3	TCCTTAGGAGAAC	0.418
-	5	760	_p.G196D|DOK3_u	NM_024872	NP_079148	Q7L591	DOK3_HUMAN	RS-type PTB.		0	TGGGTGCCCTTG	0.687
+	3	648		NM_197975	NP_932079	Q6UXE8	BTNL3_HUMAN	.|Extracellular (Potential).		0	GGACAGGATTTGT	0.502
+	8	1245	p.2_Missense_Mu	NM_197975	NP_932079	Q6UXE8	BTNL3_HUMAN	.|Cytoplasmic (Potential).		0	TTGTCTCCCAACA	0.498
-	5	734	nj.1_Missense_Mu	NM_006098	NP_006089	P63244	GBLP_HUMAN	WD 5.		0	TGCCTCCAGAAGC	0.512
-	13	1483	_p.A450V|EXOC2_	NM_018303	NP_060773	Q96KP1	EXOC2_HUMAN			7	CAAAGGCCACCC	0.428
-	11	1776_1777	nba.2_Missense_M	NM_005493	NP_005484	Q96S59	RANB9_HUMAN			2	GTTTCTCCAACTC	0.356
-	3	711	_p.D171N|NUP153	NM_005124	NP_005115	P49790	NU153_HUMAN			9	GTAGAATCTTTAAT	0.398
-	20	2045		NM_001503	NP_001494	P80108	PHLD_HUMAN	FG-GAP 5.		3	AGTTTCCCCATTC	0.493
-	1	236	nk|HIST1H2AC_uc	NM_003526	NP_003517	P62807	H2B1C_HUMAN			1	TGCGCTCAAATAT	0.577
+	5	658	p.G118R|BTN3A3_	NM_006994	NP_008925	O00478	BT3A3_HUMAN	Potential).|Ig-like V-type 2.		0	AGGATGGAGGGA	0.468
+	1	699	2_5'Flank|TRIM10_	NM_033229	NP_150232	Q9C019	TRI15_HUMAN			0	CTGTGCCCCTGC	0.632
-	5	1046	dnk.1_RNA|HLA-E	NM_005514	NP_005505	P01889	1B07_HUMAN	ical; (Potential).		0	CTACACATCACAC	0.597
+	18	1739	SH5_uc003nwx.1_I	NM_172166	NP_751898	O43196	MSH5_HUMAN			3	CAAGTCCTTGGGC	0.572
-	12	1907_1908	xd.2_Missense_M	NM_025258	NP_079534	Q9Y334	G7C_HUMAN			3	CTAGAGGACCCC	0.584

+	11	3661	cp.3_Missense_M	NM_005104	NP_005095	P25440	BRD2_HUMAN	ET.		5	CTGGACATCAAC	0.517	
-	4	1457	318_uc003ouw.2_	NM_014345	NP_055160	Q5VUA4	ZN318_HUMAN			7	TCTTTGGGAATC	0.478	
+	9	999	11_uc011dvn.1_5	NM_007058	NP_008989	Q9UMQ6	CAN11_HUMAN	alpain catalytic.		2	GGAATCCCTGG	0.597	
-	3	650	_p.S158L|RCAN2_	NM_005822	NP_005813	Q14206	RCAN2_HUMAN			0	GGGGCGAGATG	0.532	
+	1	501	se_Mutation_p.G11	NM_014464	NP_055279	Q9UJW2	TINAG_HUMAN			4	CAGAAGGTAGG	0.353	
-	83	14940	.R4822Q|DST_uc	NM_001144769	NP_001138241	Q03001	DYST_HUMAN	Spectrin 19.		14	GTTCTCGGGCTC	0.478	
+	7	1671	k.2_Missense_Mu	NM_001704	NP_001695	O60242	BAI3_HUMAN	.|Extracellular (Potential).		50	GAGTTCGTGGA	0.527	
+	14	3788	e_Mutation_p.P88	NM_001162529	NP_001156001	Q9P2D6	F135A_HUMAN			1	AACTTCCTGGG	0.393	
+	19	4409	135A_uc003pfn.2_	NM_001162529	NP_001156001	Q9P2D6	F135A_HUMAN			1	CAGGATCGCTAT	0.328	
-	5	3300	p.R877Q|FILIP1_	NM_015687	NP_056502	Q7Z7B0	FLIP1_HUMAN			4	ATGGCTCGTTCT	0.443	
+	2	1331	bm.2_Missense_M	NM_153362	NP_699193	Q8N3Z0	PRS35_HUMAN	eptidase S1.		1	GCTGTTCGCATC	0.507	
-	15	2148	_p.M606I|LAMA4_	NM_001105206	NP_001098676	Q16363	LAMA4_HUMAN	al.|Domain II and I.		9	CCCGTTCATATC	0.358	
-	30	5123	1_Intron|GOPC_u	NM_002944	NP_002935	P08922	ROS_HUMAN	III 7.|Extracellular (Potentia		25	ACATTTCCTCAG	0.398	
-	14	3238	184A_uc003pyl.3_	NM_024581	NP_078857	Q8NB25	F184A_HUMAN			7	TTATTTCCTTGAG	0.358	
-	2	232	nse_Mutation_p.R	NM_004665	NP_004656	O95498	VNN2_HUMAN	N hydrolase.		0	ATGATTCGAGCA	0.448	
-	4	1101	.R281Q|BCLAF1_	NM_014739	NP_055554	Q9NYF8	BCLF1_HUMAN			1	CTGTATCGACTA	0.443	rs145724464
-	2	598	.H67Y|SHPRH_uc	NM_001042683	NP_001036148	Q149N8	SHPRH_HUMAN			3	TCTGTGAGCCA	0.388	
-	3	652		NM_020861	NP_065912	Q8N680	ZBTB2_HUMAN			1	GGCCTCAGGGA	0.557	
+	13	4101	.P4_uc003qrg.2_Ir	NM_020245	NP_064630	Q9NRJ4	TULP4_HUMAN			1	GTACACCCTCC	0.662	
-	30	4833		NM_005577	NP_005568	P08519	APOA_HUMAN	Kringle 36.		6	GTACTCCCACCT	0.493	
-	21	3334		NM_005577	NP_005568	P08519	APOA_HUMAN	Kringle 32.		6	TTCTTCCTGTGA	0.483	
+	10	1246		NM_000301	NP_000292	P00747	PLMN_HUMAN	Kringle 4.		4	CCACAGGAAAG	0.488	
-	11	1339	sh.1_Missense_M	NM_001013836	NP_001013858	Q9Y6D9	MD1L1_HUMAN	Potential.		2	GTCTACCTGCTG	0.582	
+	2	659	e_Mutation_p.P10	NM_133463	NP_597720	Q400G9	AMZ1_HUMAN			0	CTACAGCCGATA	0.642	
+	8	1050	p.P297S|SLC29A	NM_153247	NP_694979	Q7RTT9	S29A4_HUMAN	lasmic (Potential).		1	AGCACCCAGCC	0.682	
+	2	270	yb.1_Missense_M	NM_058176	NP_478056	Q9UKV0	HDAC9_HUMAN			5	TGACACGGCAG	0.483	
-	5	698	ug.2_Missense_M	NM_182762	NP_877439	Q6ZN28	MACC1_HUMAN			3	TTGAGGAAGTC	0.383	
+	41	6681		NM_003777	NP_003768	Q96DT5	DYH11_HUMAN	2 (By similarity).		15	TGACAACAGATG	0.393	
+	5	1138	kwe.2_Missense_	NM_032222	NP_115598	Q4G0A6	F188B_HUMAN			0	CCAGCCCGCAC	0.547	
+	11	2499	_p.M353I|CCDC12	NM_194300	NP_919276	Q6ZRS4	CC129_HUMAN			0	GTGATGGAGGA	0.537	
-	10	1458	_p.R390Q|PDE1C_	NM_005020	NP_005011	Q14123	PDE1C_HUMAN	ytic (By similarity).		4	AGGTTCGAAAC	0.388	
+	10	1133		NM_133468	NP_597725	Q8N8U9	BMPER_HUMAN	VWFC 5.		3	CATCAGTAGCT	0.483	
+	4	2353	_p.K691*|CDK13_	NM_003718	NP_003709	Q14004	CDK13_HUMAN			5	GAAACCAAAGAA	0.343	
+	2	91	_p.S31L|MRPS17	NM_182633	NP_872439	Q8N859	ZN713_HUMAN			2	GGAATCACTGA	0.517	
+	7	2086	te.2_Missense_Mu	NM_016220	NP_057304	Q9UII5	ZN107_HUMAN	2H2-type 13.		1	AAAATTCATACTG	0.353	
+	6	906		NM_001099435	NP_001092905	A6NIY4	SPDE5_HUMAN	Arg-rich.		0	GAACCCGAGGG	0.592	
+	6	981		NM_001099435	NP_001092905	A6NIY4	SPDE5_HUMAN	Arg-rich.		0	GAACCTGAGGG	0.577	
-	19	1899	.1_Nonsense_Mu	NM_005338	NP_005329	O00291	HIP1_HUMAN	Potential.	p.D620G(1)	8	TTTTTCGTTGGT	0.537	
-	2	1134	.1_Intron|CCDC14	NM_006682	NP_006673	Q14314	FGL2_HUMAN	nogen C-terminal.		2	GGATATCGATCA	0.398	
-	5	7208	_Mutation_p.E230	NM_033026	NP_149015	Q9Y6V0	PCLO_HUMAN			7	CAGTTTCCTTCTT	0.418	
-	5	4875	v.2_Missense_Mut	NM_033026	NP_149015	Q9Y6V0	PCLO_HUMAN			7	GTTCTTCGTTTT	0.398	
-	16	2195	nc.1_Missense_Mu	NM_000927	NP_000918	P08183	MDR1_HUMAN	r 1.|Cytoplasmic (Potential)		7	CATTACGAACTG	0.393	rs28381914
+	8	881	R260S|CYP3A43_	NM_057095	NP_476436	Q9HB55	CP343_HUMAN			2	GAAAGTCGCCTC	0.204	
+	14	2378	ZAN_uc003uwl.2_F	NM_003386	NP_003377	Q9Y493	ZAN_HUMAN	ate) (mucin-like domain).|E		11	AAAAACCCACCA	0.522	
-	33	4973	.2_Missense_Muta	NM_005045	NP_005036	P78509	RELN_HUMAN			19	GAAATCCAGTTTG	0.413	
-	4	1349		NM_002711	NP_002702	Q16821	PPR3A_HUMAN		p.D440N(1)	34	CATTATCATCCAG	0.418	rs145814266
+	9	1536	OXP2_uc011kmv.1	NM_014491	NP_055306	O15409	FOXP2_HUMAN	eucine-zipper.		8	AGGTGGTGCAA	0.408	

+	14	2219	nq.1_Missense_Mu	NM_000492	NP_000483	P13569	CFTR_HUMAN	lasmic (Potential).	5	GGAAAAAAGGA	0.378	
-	13	1461	lks.2_Missense_M	NM_022444	NP_071889	Q9BZW2	S13A1_HUMAN	ical; (Potential).	2	ACCATCAAAGAA	0.363	
-	5	1827	vly.1_Missense_M	NM_176814	NP_789784	Q2TB10	ZN800_HUMAN	C2H2-type 6.	1	AAAGAGGACACT	0.358	
+	6	705	N33_uc003voq.1_	NM_178562	NP_848657	Q86UF1	TSN33_HUMAN	cellular (Potential).	1	GTGGAGGGATTT	0.512	
-	15	1860		NM_004333	NP_004324	P15056	BRAF_HUMAN	rotein kinas_R603>I(2)|p.T	18290	GATTTCACTGTAC	0.368	
-	14	1711_1712		NM_000420	NP_000411	P23276	KELL_HUMAN	cellular (Potential).	4	CTCGATCCAAGCT	0.545	
+	1	757	uc003wda.2_Intror	NM_176883	NP_795364	P59536	T2R41_HUMAN	Name=6; (Potential).	2	ATCATTGATGCCC	0.498	
+	1	1267		NM_001008747	NP_001008747	A4D2H0	A4D2H0_HUMAN		0	GAGAAGCTTTCTA	0.378	
-	6	2513		NM_015694	NP_056509	Q9ULD5	ZN777_HUMAN		1	GCTTGCCGCACTC	0.687	
+	4	656	p.A113V|REPIN1_	NM_013400	NP_037532	Q9BWE0	REPI1_HUMAN		1	GCAGGGCCCATC	0.701	
-	36	5881	zz.2_Missense_Mu	NM_170606	NP_733751	Q8NEZ4	MLL3_HUMAN	Pro-rich.	63	GTGAGTTAGAGGA	0.527	
-	22	3673	zz.2_Missense_Mu	NM_170606	NP_733751	Q8NEZ4	MLL3_HUMAN		63	AAGATTCACAGCA	0.269	
-	58	9334	e_Mutation_p.P23	NM_033225	NP_150094	Q96PZ7	CSMD1_HUMAN	ar (Potential).|Sushi 23.	25	TGCCAGGGTTGC	0.522	
-	28	4819	p.E869K|CSMD1_	NM_033225	NP_150094	Q96PZ7	CSMD1_HUMAN	lar (Potential).|CUB 9.	25	CACATTCCTTCCC	0.458	
+	24	2749	p.Y892D|XPO7_uc	NM_015024	NP_055839	Q9UIA9	XPO7_HUMAN		5	CAGGATTACCCCA	0.458	
-	1	408	k|LGI3_uc010ltu.2_	NM_139278	NP_644807	Q8N145	LGI3_HUMAN	LRRNT.	1	TGGGCGGGCAG	0.597	
-	10	1281		NM_003844	NP_003835	O00220	TR10A_HUMAN	mic (Potential).|Death.	6	GGCATCCCCTGC	0.537	
+	6	619	ea.1_Missense_M	NM_003817	NP_003808	Q9H2U9	ADAM7_HUMAN	cellular (Potential).	5	ATTATTCCTGTAC	0.373	
+	3	756	HD2_uc003xlc.2_M	NM_015214	NP_056029	O94830	DDHD2_HUMAN		2	TATGTTCCCTACT	0.398	
+	13	903	_p.Q235*|POLB_u	NM_002690	NP_002681	P06746	DPOLB_HUMAN		2	AAAGATCAGTATT	0.343	
-	2	461		NM_003068	NP_003059	O43623	SNAI2_HUMAN		2	GCCACTGTGGTC	0.517	
-	17	3318	DNL_uc003xqt.3_F	NM_144651	NP_653252	A1KZ92	PXDNL_HUMAN		2	AAATTTCACCTAA	0.473	
+	4	1262_1263	P1_uc011ldy.1_Intr	NM_006269	NP_006260	P56715	RP1_HUMAN		12	CAGGAAGAACAG	0.396	
+	4	3056	P1_uc011ldy.1_Intr	NM_006269	NP_006260	P56715	RP1_HUMAN		12	GTTATGGAAAGTA	0.328	
-	4	1216		NM_004820	NP_004811	O75881	CP7B1_HUMAN		3	GGATGGGAAATC	0.443	
-	9	1280	A6_uc003xxr.3_Int	NM_020361	NP_065094	Q8N4T0	CBPA6_HUMAN		2	AATTGGGAATTGT	0.378	rs140734555
+	26	3317		NM_024870	NP_079146	Q70Z35	PREX2_HUMAN		17	AAGATTCTGGTCA	0.393	
+	8	1009	ar.2_Missense_Mu	NM_004133	NP_004124	Q14541	HNF4G_HUMAN		1	TTTTTTGATCCAG	0.318	
+	2	927		NM_173549	NP_775820	Q6P6B1	CH047_HUMAN	Glu-rich.	0	TAGAAAGAATTCC	0.433	
-	6	817	_Mutation_p.P254	NM_006281	NP_006272	Q13188	STK3_HUMAN	rotein kinase.	4	TCATTGGATGTAT	0.348	
+	14	2460	ylq.2_Missense_Mu	NM_014677	NP_055492	Q9UQ26	RIMS2_HUMAN		15	TTATAGGAAGGAC	0.388	
+	28	4156	lq.2_Missense_Mu	NM_014677	NP_055492	Q9UQ26	RIMS2_HUMAN	C2 2.	15	CCGCATGGATCAC	0.393	
-	5	2822	83H_uc010mfk.1_	NM_198488	NP_940890	Q6ZRV2	FA83H_HUMAN		3	GCACGGGGGGC	0.692	
-	6	716	AH_uc003zat.1_5'	NM_017570	NP_060040	O14841	OPLA_HUMAN		0	TGAAGCCCAGCTC	0.682	
+	6	675	p.A173V|GPT_uc0	NM_005309	NP_005300	P24298	ALAT1_HUMAN		2	GGTGGCCGGCGA	0.692	
-	12	835	zkl.2_Missense_Mu	NM_002839	NP_002830	P23468	PTPRD_HUMAN	1.|Extracellular (Potential).	22	TGAAAGAGGCAAC	0.418	
-	8	1257	n_p.L400F|MPDZ_	NM_003829	NP_003820	O75970	MPDZ_HUMAN	PDZ 3.	6	ATTACCCAATTTT	0.303	
-	2	417	zuv.2_Missense_M	NM_148179	NP_680545	Q8N5L8	CI023_HUMAN		0	CAACCGACCCAC	0.622	
-	2	1376		NM_003028	NP_003019	Q15464	SHB_HUMAN	with LAT, FAK1, JAK1 and	3	GGGCTCCATGTA	0.557	
+	1	526	42421_uc004aed.1_RNA						0	GAGCCCAATCTGC	0.607	rs141617852
-	17	2002	e_Mutation_p.P582	NM_013417	NP_038203	P41252	SYIC_HUMAN		2	AAGGCGGTTGTC	0.438	rs45474891
+	23	5299	.R1730W|WNK2_u	NM_006648	NP_006639	Q9Y3S1	WNK2_HUMAN		12	TCCCCTCGGAAA	0.662	
-	4	679	axx.1_Missense_M	NM_016481	NP_057565	Q9BU70	NAP1_HUMAN		0	AGCTGTCGCTGG	0.458	
+	8	849	sx.2_RNA|STX17_	NM_017919	NP_060389	P56962	STX17_HUMAN	e IV membrane protein; (Po	1	GTGCACTCATCGC	0.493	
-	1	779		NM_012363	NP_036495	Q8NGS0	OR1N1_HUMAN	cellular (Potential).	3	AGGGAGGACAC	0.527	
+	8	1166	_p.A374V|SLC2A8	NM_014580	NP_055395	Q9NY64	GTR8_HUMAN	Name=10; (Potential).	2	GCTGGCCGTGG	0.701	
-	5	374	n_p.S26L|C9orf78_	NM_016520	NP_057604	Q9NZ63	CI078_HUMAN		0	GAAAACGATGTCC	0.507	

-	6	1233	cc.1_Missense_M	NM_032843	NP_116232	Q8N539	FBCD1_HUMAN	inal.|Extracellular (Potenti	0	CAGCTCGTAGG	0.627	
-	5	668	mzn.2_Missense_	NM_005312	NP_005303	Q13905	RPGF1_HUMAN		7	GTCTTCTGAGT	0.557	
+	2	593		NM_000093	NP_000084	P20908	CO5A1_HUMAN	P N-terminal.	11	AAGGCCCGGAT	0.557	
-	3	2147	_p.P613L|SEC16A	NM_014866	NP_055681	O15027	SC16A_HUMAN		0	TTACCGGTTCG	0.522	
+	1	1328	T1_uc004cjp.2_5'	NM_001080482	NP_001073951	C9J069	CI172_HUMAN		0	CAGCCGCCACT	0.741	
-	6	983	_p.R26C|FBXW5_	NM_018998	NP_061871	Q969U6	FBXW5_HUMAN		0	GATGCGGCAGG	0.697	
-	2	1609	u.2_Missense_Mu	NM_173691	NP_775962	Q4KMQ1	TPRN_HUMAN	Glu-rich.	0	ctgctcTAGGGAG	0.348	
+	4	1016_1017	mg.1_Missense_	NM_006088	NP_006079	P68371	TBB2C_HUMAN		1	GACCCCCGCC	0.604	
-	6	2812	ndi.2_Missense_	NM_181332	NP_851849	Q8N0W4	NLGNX_HUMAN	lasmic (Potential).	4	TGGGATGTCAT	0.557	
-	6	934		NM_000216	NP_000207	P23352	KALM_HUMAN	nectin type-III 1.	4	CACTCGAAACT	0.512	rs137852516
+	3	317		NM_016562	NP_057646	Q9NYK1	TLR7_HUMAN	lar (Potential).|LRR 1.	5	AAATTCCTGGA	0.493	
+	2	769	e_Mutation_p.L1	NM_152634	NP_689847	Q8N8B7	TEANC_HUMAN	FIIS central.	1	TAGAGCTTCTTTA	0.428	
-	3	569		NM_030624	NP_085127	Q96M94	KLH15_HUMAN		2	CTGAAGAATCT	0.388	
+	1	1487		NM_001136533	NP_001130005				2	GACACAGAAATA	0.448	
+	4	1179	_p.E287K|MAGEB	NM_002363	NP_002354	P43366	MAGB1_HUMAN	MAGE.	0	TCCTCGAGTTT	0.512	
-	40	5918	_Mutation_p.C176	NM_004006	NP_003997	P11532	DMD_HUMAN	tion with SYNM (By simila	6	CAAGCATTTCAG	0.383	
+	8	1437	rf22_uc010ngv.2_	NM_152632	NP_689845	Q6ZTR5	CX022_HUMAN		3	ATCCTGAAAAG	0.373	
+	1	687		NM_001013736	NP_001013758	Q5HY64	FA47C_HUMAN		3	GCCCACAGCCT	0.647	
+	1	281		NM_000531	NP_000522	P00480	OTC_HUMAN		2	TGGTTCGAAAT	0.378	rs72552300
-	27	4003	ey.1_Missense_M	NM_004229	NP_004220	O60244	MED14_HUMAN		4	CATACTCTTGTT	0.343	
+	22	2876	_p.P832A|RBM10_	NM_005676	NP_005667	P98175	RBM10_HUMAN		5	CAGAGCCCAAG	0.612	
-	33	4204	dsn.2_Nonsense_	NM_031407	NP_113584	Q7Z6Z7	HUWE1_HUMAN		17	CCATTCGTCCAC	0.458	
-	2	164		NM_198510	NP_940912	Q6UXX5	ITH5L_HUMAN	VIT.	6	CCACCGTGGAG	0.493	
+	3	582	H159Y|TRO_uc00	NM_001039705	NP_001034794	Q12816	TROP_HUMAN		1	CTGGCCATGAG	0.507	
-	1	999		NM_001012968	NP_001012986	Q56A73	SPIN4_HUMAN		2	GAACAGGATCT	0.448	
-	2	1620	g.2_Missense_Mu	NM_145119	NP_660095	Q8NG27	PJA1_HUMAN		0	GTTCTCGAACT	0.572	
+	2	1512	XO4_uc004dyt.1_	NM_005938	NP_005929	P98177	FOXO4_HUMAN		3	AGGTAGATCCC	0.632	
+	8	1294	N1_uc011mpt.1_	NM_052957	NP_443189	Q96QF7	ACRC_HUMAN	sp/Ser-rich.	3	AAGCTCCCGAC	0.557	
+	8	1324	N1_uc011mpt.1_	NM_052957	NP_443189	Q96QF7	ACRC_HUMAN	sp/Ser-rich.	3	AAGCTCCCGAC	0.557	
+	8	1334_1335	N1_uc011mpt.1_	NM_052957	NP_443189	Q96QF7	ACRC_HUMAN	sp/Ser-rich.	3	CGACAGCAGTG	0.55	
-	16	2144	_p.T681A|ABCB7	NM_004299	NP_004290	O75027	ABCB7_HUMAN		1	TCTGTGTATGCC	0.408	
+	1	712		NM_020932	NP_065983	Q9HCI5	MAGE1_HUMAN	Pro-rich.	6	CCCCTGGTGAG	0.687	
-	15	4565	.E1407K|ATRX_u	NM_000489	NP_000480	P46100	ATRX_HUMAN	Poly-Glu.	30	ctcctcttcttcctcAGA	0.199	
+	1	392	_Mutation_p.H74	NM_053281	NP_444511	Q96NX9	DACH2_HUMAN	ACHbox-N.	5	ATGCACGGGAT	0.547	
-	3	1172		NM_080879	NP_543155	Q8WXH6	RB40A_HUMAN		0	CTTAAGAAATTT	0.483	
+	13	1481	c.1_Missense_Mu	NM_198465	NP_940867	Q7Z2Y5	NRK_HUMAN		14	GCCAAGGTGGC	0.557	
+	32	2967	_p.K922I|COL4A5	NM_033380	NP_203699	P29400	CO4A5_HUMAN	e-helical region.	4	GTCTTAAAGGTA	0.408	
+	13	1753		NM_007231	NP_009162	Q9UN76	S6A14_HUMAN		3	TTCATAGACCTA	0.358	
-	11	1931		NM_020721	NP_065772	Q9ULL0	K1210_HUMAN		5	CCATGGAATTG	0.458	
-	10	1456		NM_020721	NP_065772	Q9ULL0	K1210_HUMAN		5	TCTTTTCGTTGA	0.433	
-	16	1707	uh.1_Missense_M	NM_001081550	NP_001075019	Q8NI27	THOC2_HUMAN		3	ATTTTCCTTGG	0.388	
-	31	8096	.E2684K|ODZ1_u	NM_014253	NP_055068	Q9UKZ4	TEN1_HUMAN	ellular (Potential).	23	CCCTTCTGTCC	0.517	
-	6	2931	vf.1_Missense_M	NM_031907	NP_114113	Q9BXU7	UBP26_HUMAN		8	TATGATCTCCCT	0.383	
-	6	2929	vf.1_Missense_M	NM_031907	NP_114113	Q9BXU7	UBP26_HUMAN		8	TGATCTCCCTTA	0.383	
+	6	5036	.S1377F|GPR112	NM_153834	NP_722576	Q8IZF6	GP112_HUMAN	ellular (Potential).	12	CACTTCCACAA	0.428	
-	14	1540	P11C_uc004fba.2_	NM_173694	NP_775965	Q8NB49	AT11C_HUMAN	lasmic (Potential).	8	AGCATCGTTTG	0.353	
-	2	1145		NM_001009615	NP_001009615	Q5MJ10	SPXN2_HUMAN		1	TTCAGATGAGT	0.527	

-	2	1106		NM_001009615	NP_001009615	Q5MJ10	SPXN2_HUMAN		1	TTCAGATGAGT	0.522	
+	2	124		NM_001009614	NP_001009614	Q5VSR9	SPXN1_HUMAN		0	TTGAAAAAGATG	0.408	
-	3	913	.D187N|CSAG1_	NM_005367	NP_005358	P43365	MAGAC_HUMAN	MAGE.	1	GCCATCGTAGG	0.582	
-	9	998	p.R265C|MPP1_u	NM_002436	NP_002427	Q00013	EM55_HUMAN	-like.|Interaction with MPP	3	GCTGCGACCCA	0.527	
-	2	680		NM_171998	NP_741995	Q96DA2	RB39B_HUMAN		0	GGCGAGTCACT	0.498	
+	11	1728	1akj.2_Missense_	NM_014448	NP_055263	Q5VV41	ARHGG_HUMAN		1	TCCCTCCCACTG	0.627	
+	8	937		NM_015215	NP_056030	Q9Y6Y1	CMTA1_HUMAN		9	AGCTGGTGCAG	0.662	
-	4	1279	pa.1_Missense_M	NM_018948	NP_061821	Q9UJM3	ERRFI_HUMAN	RBB2 and regulation of EG	1	TGACCCCATTGA	0.537	
-	1	138	|PEX14_uc010oar	NM_004401	NP_004392	O00273	DFFA_HUMAN		0	GATCTCGCCAG	0.667	
+	4	253		NM_001010980	NP_001010980	Q5T1S8	CA130_HUMAN		0	GGCGGGAACTA	0.587	
+	1	131	.1_5'UTR|CATSP	NM_198137	NP_937770	Q7RTX7	CTSR4_HUMAN	lasmic (Potential).	1	CTCTCCCCTGC	0.617	
-	6	3478	sz.1_Missense_M	NM_001029882	NP_001025053	Q5TGY3	AHDC1_HUMAN		1	GCCGGTGAAGA	0.632	
-	7	1372	p.V411M|PHC2_u	NM_198040	NP_932157	Q8IXK0	PHC2_HUMAN		1	GGGCACGCCCT	0.602	rs146737581
-	2	1646	zw.1_Missense_	NM_005202	NP_005193	P25067	CO8A2_HUMAN	lical region (NC1).	1	GTTGGGCAGGT	0.716	
-	1	1058		NM_002699	NP_002690	Q03052	PO3F1_HUMAN	Homeobox.	0	CGCTTCTTGCG	0.652	
+	47	15372	s.1_Nonsense_M	NM_033044	NP_149033	Q9UPN3	MACF1_HUMAN		16	TTGTCCAGCGA	0.443	
+	6	867	.2_Missense_Mut	NM_005424	NP_005415	P35590	TIE1_HUMAN	r (Potential).|EGF-like 2.	7	GGGCCGTTTTG	0.642	
-	3	556		NM_032027	NP_114416	Q9BX74	TM2D1_HUMAN		1	GGGTGCTGGAA	0.353	
+	3	401	e_Mutation_p.P63	NM_144701	NP_653302	Q5VWK5	IL23R_HUMAN	ellular (Potential).	0	AATGTCCCAAA	0.358	
-	6	1066	IQ3_uc001dfz.3_	NM_001105659	NP_001099129	A6PVS8	LRIQ3_HUMAN		2	GATAATATATATT	0.169	
+	10	1685	q.2_Nonsense_M	NM_001001933	NP_001001933	Q68G74	LHX8_HUMAN		3	GACTCCAGCCC	0.328	
+	16	2229		NM_002440	NP_002431	O15457	MSH4_HUMAN		5	ATATCGAAACA	0.289	
+	6	716	HN2_uc001div.2_	NM_012302	NP_036434	O95490	LPHN2_HUMAN	otential).|Olfactomedin-like	9	CCTATCGTACC	0.398	
+	7	776		NM_033055	NP_149044	Q96MC6	HIAT1_HUMAN	Name=7; (Potential).	0	CCTACCGGAGG	0.383	
-	8	1480	_p.E400K|COL11A	NM_001854	NP_001845	P12107	COBA1_HUMAN	nhelical region.	12	CATATTCTTTATA	0.363	
+	3	216	M5_uc010ovu.1_5	NM_000851	NP_000842	P46439	GSTM5_HUMAN	(By similarity).|GST N-ter	6	CTGAATGAAAAA	0.572	
-	4	430	ff.1_Nonsense_M	NM_000036	NP_000027	P23109	AMPD1_HUMAN		4	TCTCTGAAAAT	0.463	
-	3	435		NM_002524	NP_002515	P01111	RASN_HUMAN	GTP.)|p.Q61P(21)|	2607	TTCTTGTCCAG	0.458	rs121913254
+	4	488	hr.1_Missense_M	NM_001005783	NP_001005783	Q9NYQ3	HAOX2_HUMAN	xy acid dehydrogenase.	4	GAATTCGCCTC	0.552	
+	19	2193	tion_p.E30G|NBP	NM_001037675	NP_001032764	Q3BBV1	NBPFK_HUMAN	NBPF 5.	0	GAAAGAGCCTG	0.483	
+	4	2006	10_uc001emp.3_	NM_001039888	NP_001034977	Q69YU3	AN34A_HUMAN	Pro-rich.	0	CCATCCCCCAA	0.612	
+	12	1506	kt.1_Missense_M	NM_001102663	NP_001096133				0	AGGACTCACTG	0.468	
+	12	1525	kt.1_Missense_M	NM_001102663	NP_001096133				0	TTATTCGACTC	0.478	
-	2	991	e.1_Missense_M	NM_007113	NP_009044	Q07283	TRHY_HUMAN	-E-Q-E-E- E-R-R-E-Q-Q-L	5	tctcctcctgctgctcgc	0	
-	3	1734		NM_001009931	NP_001009931	Q86YZ3	HORN_HUMAN	5	3	ACTGCCTGGAA	0.592	
-	3	2699	c001ezv.2_5'Flan	NM_002016	NP_002007	P20930	FILA_HUMAN	Ser-rich.	16	TGGATCCTGAC	0.562	
-	2	65		NM_002964	NP_002955	P05109	S10A8_HUMAN		0	CAGCTCGGTCA	0.512	
-	3	317	1fcd.1_Missense_	NM_080388	NP_525127	Q96FQ6	S10AG_HUMAN	EF-hand 2.	0	GATGAGCTTAT	0.587	
+	7	1821	ite_p.D213_splic	NM_000906	NP_000897	P16066	ANPRA_HUMAN		7	ctGCAGATCACC	0.348	
-	13	4253		NM_000130	NP_000121	P12259	FA5_HUMAN	ndem repeats of [TNP]-L-S	6	GCTGAGGTCTA	0.517	
-	13	4214		NM_000130	NP_000121	P12259	FA5_HUMAN	ndem repeats of [TNP]-L-S	6	AGAAAGGGGCA	0.517	
+	1	97	he.2_Missense_M	NM_022716	NP_073207	P54821	PRRX1_HUMAN		1	GGGCGGCCGCT	0.657	
+	7	1183	b.1_Missense_M	NM_001002294	NP_001002294	P31513	FMO3_HUMAN		1	GTATTTCCTCCT	0.453	
-	4	1339_1340	_Mutation_p.G42	NM_003285	NP_003276	Q92752	TENR_HUMAN	nectin type-III 2.	11	TAGCCCTTGAG	0.495	
+	8	1485		NM_014864	NP_055679	O75063	XYLK_HUMAN	enal (Potential).	3	ACACAGTACTG	0.498	
+	31	6580	50_uc001gnv.2_	NM_014810	NP_055625	Q5VT06	CE350_HUMAN	Potential.	4	AAAATCAGTTG	0.393	
+	12	1783	_Mutation_p.E570	NM_002826	NP_002817	O00391	QSOX1_HUMAN		2	CCCTGGAGCTG	0.622	

+	38	5392	1gox.1_Missense_	NM_000721	NP_000712	Q15878	CAC1E_HUMAN	Cytoplasmic (Potential).	6	TGGACGAGTTT	0.607	
+	6	1103	tm.2_Missense_M	NM_002113	NP_002104	Q03591	FHR1_HUMAN		0	CAAAAAGATAGA	0.323	
+	5	748		NM_030787	NP_110414	Q9BXR6	FHR5_HUMAN	Sushi 4.	2	TACGATCATGTG	0.318	
+	12	2092	p.G597S|CAMSAF	NM_203459	NP_982284	Q08AD1	CAMP2_HUMAN		4	CGAAAGGTGCC	0.353	
+	20	2717	01gyb.1_Missense_	NM_002481	NP_002472	O60237	MYPT2_HUMAN		3	AAGAGCCCGTC	0.473	
-	8	1369	gyr.3_Missense_M	NM_015999	NP_057083	Q96A54	ADR1_HUMAN	cellular (Potential).	0	TACAGCCGCCTT	0.512	
-	12	3208		NM_025179	NP_079455	O75051	PLXA2_HUMAN	cellular (Potential).	3	GGTCGGCCTTG	0.627	
-	7	1162	se_Mutation_p.R25	NM_001017402	NP_001017402	Q13751	LAMB3_HUMAN	ninin EGF-like 1.	6	CGCAGCGATCAG	0.677	rs145575474
+	20	2278	p.G607E|CAPN2_	NM_001748	NP_001739	P17655	CAN2_HUMAN	ain IV.|EF-hand 3.	5	ATACTGGAACAA	0.502	
-	4	1014	e_Mutation_p.G278	NM_003240	NP_003231	O00292	LFTY2_HUMAN		0	CGGCCCCAGAA	0.657	
-	7	1796	9xes.2_Missense_	NM_003607	NP_003598	Q5VT25	MRCKA_HUMAN	rotein kinase.	11	GCGATTCTGCAT	0.368	
+	1	200		NM_003272	NP_003263	O60478	G137B_HUMAN	cellular (Potential).	0	CGGCCGTGCCC	0.562	
+	10	1335	0pyl.1_Missense_	NM_006642	NP_006633	Q86SQ7	SDCG8_HUMAN	r homodimerization (By sim	0	CATGATGAAAAA	0.433	
+	17	2212	nse_Mutation_p.Q	NM_006642	NP_006633	Q86SQ7	SDCG8_HUMAN	Potential.|Sufficient for hom	0	CAGAACCAGCTT	0.617	
-	8	858_859	z.1_Missense_Mu	NM_005465	NP_005456	Q9Y243	AKT3_HUMAN	rotein kinase.	4	ATAGTCCAAGGC	0.416	
+	1	548		NM_001004690	NP_001004690	A3KFT3	OR2M5_HUMAN	cellular (Potential).	3	TCCCTTCCCTAC	0.418	
-	1	548		NM_001004691	NP_001004691	Q8NG81	OR2M7_HUMAN	cellular (Potential).	2	GTAGGGAAGGG	0.428	
-	8	959	2C_uc009xhj.1_5'U	NM_014974	NP_055789	Q9Y2E4	DIP2C_HUMAN		7	GGATCCGGTTGT	0.512	
+	10	1321	g.2_Nonsense_Mu	NM_005180	NP_005171	P35226	BMI1_HUMAN	action with E4F1.	2	GAGTTCGACCT	0.373	
+	6	1742	se_Mutation_p.E29	NM_019590	NP_062536	Q5T5P2	SKT_HUMAN		7	CATATGGAACAAT	0.512	
-	7	1310	t.2_Missense_Mut	NM_025209	NP_079485	Q9H2F5	EPC1_HUMAN		4	GCAGACGATGGT	0.443	
+	7	1016		NM_052997	NP_443723	Q9BXX3	AN30A_HUMAN		9	AAATTACGAGTC	0.433	
+	7	1156		NM_052997	NP_443723	Q9BXX3	AN30A_HUMAN		9	CGTGGGCAGCA	0.408	
-	1	634		NM_002900	NP_002891	P10745	RET3_HUMAN	nate tandem repeats.|1.	2	GCCTCCTGTGC	0.607	
-	10	1432	.2_Missense_Muta	NM_138932	NP_620310	Q9NQ94	A1CF_HUMAN		1	TGTCTCCTTTGA	0.498	
-	33	6235	sense_Mutation_p	NM_033056	NP_149045	Q96QU1	PCD15_HUMAN	lasmic (Potential).	13	TGAGATTGTTTTT	0.353	
-	37	6532	K3_uc010qih.1_In	NM_020987	NP_066267	Q12955	ANK3_HUMAN		19	AAAGTCATCAG	0.433	
-	4	311	kan.3_Missense_M	NM_006926	NP_008857	Q8IWL1	SFPA2_HUMAN	Collagen-like.	0	CATTATTCCCAG	0.622	
+	3	582	l4_uc010qmk.1_M	NM_033282	NP_150598	Q9UHM6	OPN4_HUMAN	Name=2; (Potential).	1	TTCCTCATGTCC	0.567	
+	29	4997	F20B_uc001kgt.1_	NM_016195	NP_057279	Q96Q89	KI20B_HUMAN	action with PIN1.	3	CTGGTTGTACCA	0.383	
-	13	1324	ip.3_Missense_Mu	NM_013451	NP_038479	Q9NZM1	MYOF_HUMAN	mic (Potential).|C2 3.	4	AGGAAACTTCTA	0.373	
+	4	562	_p.D53N|CYP2C1	NM_000769	NP_000760	P33261	CP2CJ_HUMAN		6	CGTTTCGATTATA	0.403	
-	10	1501	po.1_Missense_M	NM_021828	NP_068600	Q8WWQ2	HPSE2_HUMAN		1	GAGCATAAATCC	0.572	
-	2	835	_p.S150*|CALHM2	NM_015916	NP_057000	Q9HA72	CAHM2_HUMAN		1	GGGCTGATGGG	0.592	
+	12	1186	_p.P405S|ACSL5_	NM_203379	NP_976313	Q9ULC5	ACSL5_HUMAN	lasmic (Potential).	3	TGTTTCCCGCG	0.507	
+	16	2264	R11_uc001lfd.1_M	NM_018117	NP_060587	Q9BZH6	WDR11_HUMAN		0	CTGCCCGGGAA	0.408	
-	17	2730	e_Mutation_p.E57	NM_000141	NP_000132	P21802	FGFR2_HUMAN	Potential).|Protein kinase.	96	AGATCTCCCACA	0.517	
+	49	6119	04_splice|DMBT1_	NM_007329	NP_015568	Q9UGM3	DMBT1_HUMAN		7	ACAGCAGATTAT	0.448	
+	35	3521	p.L1174F|DOCK1_	NM_001380	NP_001371	Q14185	DOCK1_HUMAN	DHR-2.	9	TCAGCCTTCTG	0.343	
+	11	1799	_p.A535T|KNDC1_	NM_152643	NP_689856	Q76NI1	VKIND_HUMAN	KIND 2.	2	CTCAGAGCTTCC	0.662	
+	8	1288	p.G220R|CYP2E1	NM_000773	NP_000764	P05181	CP2E1_HUMAN		3	GAAAATGGAAAG	0.448	
-	13	1831	9ycc.2_Missense_	NM_021924	NP_068743	Q9HBB8	CDHR5_HUMAN	dem repeats.|2.|Extracellula	0	TTCCTGGCTCTG	0.667	rs139058512
+	35	13223		NM_002457	NP_002448	Q02817	MUC2_HUMAN		2	GTCCACGCCCT	0.647	
-	1	505		NM_001005237	NP_001005237	Q8NGK1	O51G1_HUMAN	cellular (Potential).	2	AGTATTGGAAGC	0.512	
-	1	482		NM_001005160	NP_001005160	Q9H2C5	O52A5_HUMAN	Name=4; (Potential).	4	CCTAAGGAAGGT	0.458	
-	1	641	.1_Intron|HBE1_u	NM_033179	NP_149419	Q9Y5P0	O51B4_HUMAN	Name=5; (Potential).	2	ATATAAGAAAAG	0.378	
-	1	78	.1_Intron|HBE1_u	NM_033180	NP_149420	Q9Y5P1	O51B2_HUMAN	cellular (Potential).	3	AAGGGGCTGCA	0.488	

+	1	418	mbs.1_Missense_	NM_001005180	NP_001005180	Q8NGI3	O56B1_HUMAN	lasmic (Potential).	2	CTCTTCGCTAT	0.443	rs150132590
+	1	842	.1_Intron|TRIM22_	NM_001005180	NP_001005180	Q8NGI3	O56B1_HUMAN	ellular (Potential).	2	TGATTCCAGTTC	0.428	
+	5	750	_p.M217I|SWAP70	NM_015055	NP_055870	Q9UH65	SWP70_HUMAN	PH.	3	TTACATGATGAA	0.343	
-	11	1461_1462	rcv.1_Missense_M	NM_175058	NP_778228	Q6IQ23	PKHA7_HUMAN		3	GGAGCCCCCCG	0.629	
-	30	3781		NM_000352	NP_000343	Q09428	ABCC8_HUMAN	ype-1 2.|Cytoplasmic (By si	1	GGCCTCATACC	0.567	
-	2	816		NM_054030	NP_473371	Q96LB1	MRGX2_HUMAN	Name=6; (Potential).	1	GGAACCACTGA	0.507	
+	5	1074	p.R219C|RCN1_u	NM_002901	NP_002892	Q15293	RCN1_HUMAN	EF-hand 5.	1	AGATTCGCCAC	0.473	
+	3	486	go.3_Missense_M	NM_002843	NP_002834	Q12913	PTPRJ_HUMAN	ellular (Potential).	8	AATTCCTGACC	0.418	
-	1	782		NM_001004700	NP_001004700	Q6IEV9	OR4CB_HUMAN	ellular (Potential).	1	AAGTGGTCGGG	0.433	
+	3	712_713	ik.1_Missense_Mu	NM_001004704	NP_001004704	Q8NH72	OR4C6_HUMAN	Name=4; (Potential).	2	GTGGGGGGATT	0.465	
+	1	449		NM_001001967	NP_001001967	Q8NGL4	OR5DD_HUMAN	Name=4; (Potential).	3	TGGGTCCTATA	0.418	
-	1	865		NM_006637	NP_006628	Q13606	OR5I1_HUMAN	Name=7; (Potential).	1	CAACGGATTCA	0.368	
-	1	241		NM_001004742	NP_001004742	Q8NGP4	OR5M3_HUMAN	ellular (Potential).	2	GGTTTTCCAACA	0.368	
+	4	1670	_p.T446I|FAM111	NM_198947	NP_945185	Q6SJ93	F111B_HUMAN		2	ATGCTACTTGCT	0.388	
-	2	620		NM_004778	NP_004769	Q9Y5Y4	GPR44_HUMAN	ellular (Potential).	1	GTCCCGGAACA	0.642	
+	3	982	N3_uc001nxp.2_Ir	NM_201428	NP_958831	O95197	RTN3_HUMAN		1	TCATATAAGGA	0.363	
+	3	406	_5'Flank|ESRRA_	NM_001039496	NP_001034585	Q9NTU4	CK020_HUMAN		0	TATTGCGAAGC	0.552	
+	18	3039	_Missense_Mutat	NM_032251	NP_115627	A6NC98	CC88B_HUMAN	Potential.	4	TGCAGGGGCAG	0.682	
-	16	1921		NM_017525	NP_059995	Q6DT37	MRCKG_HUMAN	Potential.	4	GTTTTCCTCCT	0.667	
+	8	1711	5_uc009ysg.2_5'U	NM_002335	NP_002326	O75197	LRP5_HUMAN	ta-propeller 2.|Extracellula	7	AGCTCCCGCAC	0.602	
+	10	2873	sp.1_Missense_M	NM_020798	NP_065849	Q9P2H5	UBP35_HUMAN		3	TGCCGCTTCTC	0.587	
+	5	1393	u.1_Missense_Mu	NM_015885	NP_056969	O94913	PCF11_HUMAN	Lys-rich.	1	CAGGTGAAAAA	0.303	
+	2	986		NM_000372	NP_000363	P14679	TYRO_HUMAN	elanosome (Potential).	3	ATCCTGGAAAC	0.473	
-	4	959	p.R190Q|GUCY1A	NM_000855	NP_000846	P33402	GCYA2_HUMAN		8	CAGCTCGAAGG	0.398	
-	2	2609	.2_RNA|C11orf93_	NM_207429	NP_997312				1	GATCCTTGCTG	0.547	
-	7	784	SP28_uc001poj.3_	NM_020886	NP_065937	Q96RU2	UBP28_HUMAN		7	CTGTTCCTCAG	0.423	
+	6	629	09yzm.2_Intron|PA	NM_002572	NP_002563	P68402	PA1B2_HUMAN		1	TACCGACGGGG	0.542	
+	6	670	09yzm.2_Intron|PA	NM_002572	NP_002563	P68402	PA1B2_HUMAN		1	GCCACGACATG	0.537	
+	6	1123		NM_005422	NP_005413	O75443	TECTA_HUMAN	VWFD 1.	10	CAGCCGTCTCC	0.537	
-	5	472	9zcq.1_Missense_	NM_001142685	NP_001136157	A7KAX9	RHG32_HUMAN	PX; atypical.	5	CTGCACGAGGT	0.343	
-	15	2383	ln.1_Missense_Mu	NM_001042603	NP_001036068	P29375	KDM5A_HUMAN		3	CTGCCGCTCAT	0.418	
+	14	1321	_Mutation_p.E344	NM_173593	NP_775864	Q6L9W6	B4GN3_HUMAN	enal (Potential).	2	CAGAGGAGACC	0.517	
+	49	6572	|CACNA1C_uc00	NM_199460	NP_955630	Q13936	CAC1C_HUMAN	ytoplasmic (Potential).	11	GCGGGGGCAGC	0.701	
+	6	857	_p.P138L|CD9_uc	NM_001769	NP_001760	P21926	CD9_HUMAN	ellular (Potential).	1	TGAGCCCCAGC	0.542	
+	2	272_273	G6_uc010sew.1_	NM_018173	NP_060643	Q3KR16	PKHG6_HUMAN		2	CCGAGGATACC	0.619	
-	3	792	sense_Mutation_p	NM_001038	NP_001029	P37088	SCNNA_HUMAN	llular (By similarity).	0	GAGTGGTGAAG	0.662	
-	2	178	nse_Mutation_p.G	NM_014231	NP_055046	P23763	VAMP1_HUMAN	lasmic (Potential).	0	CTGTCCCTTCA	0.502	
-	3	673	B4_uc001qzf.1_Int	NM_006249	NP_006240	Q04118	PRB3_HUMAN	[PQS]-P-[PS]-Q-[GE]-G-N-[	1	TGGTTTCCTCCT	0.622	
-	3	239	_p.P68S|PRB1_u	NM_005039	NP_005030	P04280	PRP1_HUMAN	-[PAQ]-Q-[GE]-[GD]- [NKS]	0	CTTGAGGTTTGT	0.607	
+	6	769	1C1_uc009zip.2_	NM_017435	NP_059131	Q9NYB5	SO1C1_HUMAN	ellular (Potential).	7	CAAATATGAGAG	0.373	rs145524055
-	18	2332	_p.T771I|ABCC9_	NM_005691	NP_005682	O60706	ABCC9_HUMAN	tential).|ABC transporter 1	6	CCAAAAGTAATAT	0.328	
-	14	1985		NM_025003	NP_079279	P59510	ATS20_HUMAN	Cys-rich.	19	TGGTTCCAGCAA	0.348	
+	15	4175	_p.P848L|ARID2_u	NM_152641	NP_689854	Q68CP9	ARID2_HUMAN		10	TATCTCCAATGG	0.358	
-	34	9272		NM_003482	NP_003473	O14686	MLL2_HUMAN		41	GTCCTGGCTCC	0.627	
+	6	1219		NM_006262	NP_006253	P41219	PERI_HUMAN	Coil 2.|Rod.	0	AGGAGCTCCTC	0.637	
+	15	2967	mj.1_Missense_M	NM_012284	NP_036416	Q9ULD8	KCNH3_HUMAN	lasmic (Potential).	0	CACTTCGCCAG	0.662	rs148404630
-	7	1472		NM_005555	NP_005546	P04259	K2C6B_HUMAN		2	TACCCACCTGC	0.567	

-	7	1472		NM_173086	NP_775109	P48668	K2C6C_HUMAN		2	TTACCTACCTGC	0.567
-	9	1291	e_Mutation_p.S40	NM_000889	NP_000880	P26010	ITB7_HUMAN	ellular (Potential).	8	TCGTAAGAAATG	0.552
+	1	341		NM_017409	NP_059105	Q9NYD6	HXC10_HUMAN		1	GGCGACCCCAA	0.637
-	5	709	w.1_RNA|ITGA5_	NM_002205	NP_002196	P08648	ITA5_HUMAN	r (Potential).|FG-GAP 3.	2	CCTTGGTGAAC	0.582
+	1	460		NM_001005280	NP_001005280	Q8NGE5	O10A7_HUMAN	Name=4; (Potential).	4	GGTGTTCCTGTG	0.488
+	1	812		NM_054105	NP_473446	Q9NZP2	OR6C2_HUMAN	Name=7; (Potential).	2	TAAAGGAGTTT	0.423
-	5	743		NM_001686	NP_001677	P06576	ATPB_HUMAN	(By similarity).	1	GTACAGTCTTG	0.408
+	8	1450		NM_032230	NP_115606	Q8N6Q8	CL026_HUMAN		0	TTCTATCGTGCT	0.284
-	1	1178_1179	sun.1_Intron|GAL	NM_003774	NP_003765	Q8N4A0	GALT4_HUMAN	main B.|Lumenal (Potential	0	TCCAAGGTACTG	0.49
+	32	3649		NM_017564	NP_060034	Q8WWQ8	STAB2_HUMAN	lar (Potential).|FAS1 4.	14	TCCGGGGCTAC	0.507
+	2	122	tkm.1_Missense_	NM_001093771	NP_001087240	Q16881	TRXR1_HUMAN		0	AAGATCATCAC	0.428
-	4	487	PL2_uc010swu.1_	NM_018171	NP_060641	Q8NEU8	DP13B_HUMAN	B5A binding (By similarity)	1	CTTTGGAAAAA	0.343
-	3	705	1_Missense_Muta	NM_001145374	NP_001138846	Q6NS38	ALKB2_HUMAN	bstrate binding.	0	GTGCCACTTCCC	0.572
+	10	1147	e.1_Missense_Mu	NM_001143854	NP_001137326	Q9Y2J0	RP3A_HUMAN	Pro-rich.	7	CAGCCGGAGCC	0.532
-	15	2643		NM_015335	NP_056150	Q71F56	MD13L_HUMAN		8	AACATCCTTTGC	0.403
-	7	1227		NM_173598	NP_775869	Q6VAB6	KSR2_HUMAN	ol-ester/DAG-type.	15	GACATCCAGTAC	0.458
-	11	1476	.G427R|KDM2B_	NM_032590	NP_115979	Q8NHM5	KDM2B_HUMAN		2	CTTCCCGAGGG	0.562
-	4	526	SRC2_uc001ucs.	NM_023012	NP_075388	Q7L4I2	RSRC2_HUMAN	Ser-rich.	1	TAGATCTTGAG	0.378
+	16	2447	p.P350S|DNAH10_	NM_207437	NP_997320	Q8IVF4	DYH10_HUMAN	n (By similarity).	6	GAACTCCCAGGT	0.299
+	6	2218	_p.L130I|ZNF664_	NM_152437	NP_689650	Q8N3J9	ZN664_HUMAN	2H2-type 5.	0	TCAAACCTTTGC	0.468
+	1	1954	_5'Flank|uc001ui	NM_007197	NP_009128	Q9ULW2	FZD10_HUMAN	ellular (Potential).	5	TCCCCGCCGTG	0.552
-	11	2244	_p.E602K|RIMBP2	NM_015347	NP_056162	O15034	RIMB2_HUMAN		11	TTCTCTCTAGGA	0.587
+	6	720		NM_003565	NP_003556	O75385	ULK1_HUMAN	rotein kinase.	4	CGCCGGCCGCC	0.468
-	10	14105	A4359T|SACS_uc	NM_014363	NP_055178	Q9NZJ4	SACS_HUMAN	HEPN.	12	CTGAGCAAGTG	0.388
-	13	1683	T3_uc010tdn.1_M	NM_004119	NP_004110	P36888	FLT3_HUMAN	ellular (Potential).	8549	GGAAGGGGCCT	0.393
+	1	132	0tdr.1_Missense_	NM_001629	NP_001620	P20292	AL5AP_HUMAN	l.|Inhibitor binding.	0	TCAGCGTGGTC	0.493
-	8	2140	_Mutation_p.W63	NM_016179	NP_057263	Q9UBN4	TRPC4_HUMAN	and ITPR3.|Cytoplasmic (P	6	AAATTTCCATTC	0.428
+	7	6406	ww.2_Missense_	NM_207361	NP_997244	Q5SZK8	FREM2_HUMAN	(Potential).|Calx-beta 3.	11	GGAGAACGGGC	0.493
-	8	1597	.D384E|ELF1_uc	NM_172373	NP_758961	P32519	ELF1_HUMAN		1	GTTTCATCCTGC	0.428
+	1	1542		NR_003268					0	ATTATATACCATG	0.383
+	1	61	hk.1_Missense_M	NM_006418	NP_006409	Q6UX06	OLFM4_HUMAN		1	CAGGGGATTTG	0.478
-	1	632	h.2_Missense_Mu	NM_001922	NP_001913	P40126	TYRP2_HUMAN	elanosome (Potential).	5	GGGCCTTGTGT	0.607
-	19	2858	nse_Mutation_p.P	NM_198968	NP_945319	Q86YF9	DZIP1_HUMAN		2	TTTCTGGGAAAA	0.279
-	3	1121		NM_000452	NP_000443	Q12908	NTCP2_HUMAN	ical; (Potential).	4	AAACAGGAACA	0.393
-	5	707		NM_004093	NP_004084	P52799	EFNB2_HUMAN	ellular (Potential).	1	TGCAAATAAGG	0.493
+	2	670	0agj.2_Missense_	NM_006573	NP_006564	Q9Y275	TN13B_HUMAN	ellular (Potential).	0	GTGCCGTTCAG	0.453
+	1	686		NM_001004717	NP_001004717	Q8NH43	OR4L1_HUMAN	lasmic (Potential).	5	AAAATCATCACA	0.438
-	5	1021	se_Mutation_p.S1	NM_019852	NP_062826	Q86U44	MTA70_HUMAN		2	CTAAAGACTCA	0.398
-	22	2813		NM_002471	NP_002462	P13533	MYH6_HUMAN	Potential.	4	CCAGCTGAATCT	0.517
-	12	1878	p.S496F|RALGAP	NM_014990	NP_055805	Q6GYQ0	RGPA1_HUMAN		4	AACTGGAATTT	0.413
-	4	1179	.1_Missense_Mut	NM_007361	NP_031387	Q14112	NID2_HUMAN		7	GTAATCCAAATTG	0.498
-	1	238	_p.D23N|OTX2_u	NM_172337	NP_758840	P32243	OTX2_HUMAN		1	GCAAGTCCATAC	0.587
-	1	1133	135_uc001xed.2_	NM_022571	NP_072093	Q8IZ08	GP135_HUMAN	lasmic (Potential).	0	GATGACGAAGA	0.697
+	7	2579	_p.P744L|SIPA1L1	NM_015556	NP_056371	O43166	SI1L1_HUMAN	Rap-GAP.	4	CAATCCGTGCT	0.512
+	10	1314	.R369Q|RBM25_	NM_021239	NP_067062	P49756	RBM25_HUMAN	eckle localization.|Glu-rich	4	TGACCGGGATA	0.234
+	2	1779		NM_018228	NP_060698	Q9H8Y1	VRTN_HUMAN		0	GCTTCCGCCTC	0.652
+	2	1509		NM_022054	NP_071337	Q9HB14	KCNKD_HUMAN	lasmic (Potential).	1	AGCCAACAAGG	0.602

-	5	831	6KA5_uc001xyt.2_	NM_004755	NP_004746	O75582	KS6A5_HUMAN	otein kinase 1.	1	CACTTCATCAGC	0.343	
-	15	1978_1979		NM_001080414	NP_001073883	Q9P219	DAPLE_HUMAN	Potential.	3	GCTCCCCCTTCT	0.629	
-	10	2698	o.1_Missense_M	NM_001002860	NP_001002860	Q9P203	BTBD7_HUMAN	Pro-rich.	1	ATGAACGTGAA	0.552	
+	2	334	_p.W55*|PPP2R5	NM_002719	NP_002710	Q13362	2A5G_HUMAN		2	TAAAGTGGAAGG	0.408	
+	1	122	727924_uc001yu	NM_001004719	NP_001004719	Q8NGB6	OR4M2_HUMAN	Name=1; (Potential).	1	TACCAGGAAATAT	0.413	
-	23	4569	.2_Missense_Mut	NM_003257	NP_003248	Q07157	ZO1_HUMAN		6	AAACTTCTTCGG	0.428	
+	3	1328		NM_152260	NP_689473	Q8IZ73	RUSD2_HUMAN		1	ACTCTACGGCCC	0.597	rs148617479
-	3	1115	FAF1_uc010bcf.2_	NM_016013	NP_057097	Q9Y375	CIA30_HUMAN		1	TCCCCCGCGGG	0.383	
+	15	5207	GA_uc010uda.1_	NM_001164273	NP_001157745	Q8IWI9	MGAP_HUMAN	Thr-rich.	12	GCTTTTCCTAAG	0.478	
-	4	558		NM_052955	NP_443187	Q96PF1	TGM7_HUMAN		2	CTGCCCGTAGT	0.493	
-	12	2495	_p.D788N|TP53BP	NM_005657	NP_005648	Q12888	TP53B_HUMAN		7	GGAATCTGAGC	0.433	
+	4	243		NM_004212	NP_004203	O43868	S28A2_HUMAN		4	GGAGTCGGTGG	0.408	rs144302819
-	5	2140	D4_uc010ugj.1_	NM_198400	NP_006145	P46934	NEDD4_HUMAN	raction with TNIK (By simil	4	CCCTGGAGGTA	0.473	
-	5	487	_5'Flank|RFX7_u	NM_022841	NP_073752	Q2KHR2	RFX7_HUMAN	type winged-helix.	0	GACGTGCCTTCA	0.378	
-	7	780	DH1A2_uc010ug	NM_003888	NP_003879	O94788	AL1A2_HUMAN		1	CCATATCCTGGC	0.473	
+	48	6604	.3_Missense_Mut	NM_015059	NP_055874	Q9Y4G6	TLN2_HUMAN		11	GAGGACGTGATT	0.498	
+	11	1526	xp.2_Missense_	NM_025055	NP_079331	Q8N5R6	CCD33_HUMAN		5	GCAAGGCTCTT	0.398	
+	4	895	.3_RNA|IL16_uc0	NM_172217	NP_757366	Q14005	IL16_HUMAN		4	TAACAGGAAGTC	0.498	
+	3	1422		NM_001080435	NP_001073904	Q8TF30	WHAMM_HUMAN		0	AGGAGACAGTAA	0.308	
+	9	1047	_p.Q275*|ADAMTS	NM_207517	NP_997400	P82987	ATL3_HUMAN		27	CACTTCAAGGA	0.333	
+	2	202		NM_152336	NP_689549	Q96MI9	CBPC4_HUMAN		0	GCCTAAGAGGTA	0.522	
+	2	256	_p.S52F|WDR93_	NM_020212	NP_064597	Q6P2C0	WDR93_HUMAN		2	TGGATTCCTTGC	0.502	
+	6	1220	vg.1_Missense_M	NM_016111	NP_057195	Q9Y4R8	TELO2_HUMAN		0	CCGGCTCACGG	0.597	
-	9	1305	dbg.1_Missense_	NM_015914	NP_056998	Q6PKC3	TXD11_HUMAN		0	GAGACGCTCCA	0.612	
-	20	2752	H7A_uc002dbl.2_	NM_014153	NP_054872	Q8IWR0	Z3H7A_HUMAN	p.E852Q(1)	4	TAACTTCAGCAT	0.328	rs150604583
-	4	1033		NM_001012991	NP_001013009	Q1ED39	CP088_HUMAN	th ZFP106 (By similarity).	0	CGCGATCGATCT	0.557	
-	2	862	_5'Flank|IQCK_uc	NM_001012991	NP_001013009	Q1ED39	CP088_HUMAN	Lys-rich.	0	CTGGCTCCTCGA	0.473	
+	4	629	hd.1_Missense_M	NM_017888	NP_060358	Q6NUN0	ACSM5_HUMAN		2	GGCGTCCAGGG	0.562	
-	49	7777	bd.1_Nonsense_	NM_017539	NP_060009	Q8TD57	DYH3_HUMAN	4 (By similarity).	18	AGGACTGGAACC	0.473	
+	2	1746		NM_006040	NP_006031	Q9Y661	HS3S4_HUMAN	enal (Potential).	2	GAACAGGAAGAG	0.463	
-	2	153	uc010vct.1_Intron	NM_145659	NP_663634	Q8NEV9	IL27A_HUMAN		0	CCTCCGCAGCT	0.647	
+	9	1235	51N|ATP2A1_uc0	NM_173201	NP_775293	O14983	AT2A1_HUMAN	smic (By similarity).	4	GTTCCGACAAG	0.582	
+	9	1480	P_uc002duj.2_Mis	NM_005115	NP_005106	Q14764	MVP_HUMAN	MVP 9.	4	CACAACGCTGCG	0.657	
+	2	1179	tron|ASPHD1_uc0	NM_181718	NP_859069	Q5U4P2	ASPH1_HUMAN	enal (Potential).	0	GTGGACGACTCT	0.512	
+	10	1021	_p.P315L|TGFB1I1	NM_001042454	NP_001035919	O43294	TGFI1_HUMAN	zinc-binding 2.	0	GCCGCCCCTACT	0.682	
+	4	2252		NM_003414	NP_003405	Q14586	ZN267_HUMAN	2H2-type 13.	4	GAGAAGACATACT	0.448	
-	2	3356	_Mutation_p.P101	NM_002968	NP_002959	Q9NSC2	SALL1_HUMAN		8	AGACGGGACGT	0.562	
+	8	772	kj.2_Missense_Mu	NM_000078	NP_000069	P11597	CETP_HUMAN		2	GATCCCGTCATC	0.572	
+	6	596	C29_uc002esg.2_	NM_014187	NP_054906	Q9BTX3	TM208_HUMAN		0	AGCGCCGACAG	0.632	
-	14	2228	HOD1_uc010ced.	NM_013241	NP_037373	Q9Y613	FHOD1_HUMAN	n with ROCK1.|FH2.	3	TTAGGCCGATGT	0.562	
+	13	2519	eti.1_Missense_M	NM_024519	NP_078795	Q6ZS17	FA65A_HUMAN		3	GGACAGGAGCC	0.662	
-	11	1504	_p.P437L|RANBP	NM_020850	NP_065901	Q6VN20	RBP10_HUMAN		1	CCGTTGGGGTAG	0.602	
+	10	3360_3361	n_p.Q572*|NFATC	NM_173165	NP_775188	Q12968	NFAC3_HUMAN		3	GTTTCCCAAGGA	0.49	
-	3	2426	ej.1_Missense_Mu	NM_024533	NP_078809	Q9GZS9	CHST5_HUMAN	enal (Potential).	0	CTAGACGAAGTAT	0.657	
+	5	1095		NM_012213	NP_036345	O95822	DCMC_HUMAN		0	GATTCGGAATGTA	0.522	
+	3	898	hl.2_Missense_Mu	NM_024731	NP_079007	Q8N4N3	KLH36_HUMAN		2	CGGCCGTGTGC	0.677	
-	15	2189	.1_RNA|TRPV3_u	NM_145068	NP_659505	Q8NET8	TRPV3_HUMAN		4	GCTGCCGTAGG	0.537	

-	10	1448		NM_002558	NP_002549	P51575	P2RX1_HUMAN	al).|Pore-forming motif (Pot	2	CAGAGCCGATG	0.587	
+	21	2702	sn.1_Missense_M	NM_153827	NP_722549	Q8N4C8	MINK1_HUMAN		6	AGGACGACGAG	0.657	
-	2	397		NM_001212	NP_001203	Q07021	C1QBP_HUMAN		1	AACCTCCAGACA	0.448	
-	9	1191	e_Mutation_p.T31	NM_031220	NP_112497	Q9BZ71	PITM3_HUMAN		4	TCATAGGTGGAG	0.582	
+	71	10969	nm.1_Missense_M	NM_020877	NP_065928	Q9P225	DYH2_HUMAN		13	ACCGCAGCAATA	0.542	
+	14	2331	p.G737E|ARHGEF	NM_173728	NP_776089	O94989	ARHGF_HUMAN		3	GCTGGGAGCCT	0.582	
+	5	701	_p.K134N|MYOCD	NM_153604	NP_705832	Q8IZQ8	MYCD_HUMAN		5	TGTGAAAGAGGC	0.488	
+	3	5781	n.1_Missense_Mut	NM_030665	NP_109590	Q7Z5J4	RAI1_HUMAN		2	GCGCACCAGTG	0.701	
+	11	1086	_p.G234D|LGALS	NM_009587	NP_033665	O00182	LEG9_HUMAN	Galectin 2.	0	GGATGGTCAGC	0.552	rs145626584
+	3	365	ag.1_5'Flank|TME	NM_152464	NP_689677	Q6SZW1	SARM1_HUMAN		0	ATCACCCGCAAC	0.468	
-	5	1562	_p.G374R|SLFN11_	NM_001104588	NP_001098058	Q7Z7L1	SLN11_HUMAN		3	GAGGCCCACTAG	0.383	
+	2	383		NM_033315	NP_201572	Q96S79	RSLAB_HUMAN	all GTPase-like.	4	CTACCGGGTGG	0.697	
-	1	403		NM_139285	NP_644814	Q8NHY3	GA2L2_HUMAN	CH.	2	GATGCCCATCTC	0.592	
-	4	1144		NM_001004334	NP_001004334	Q6PRD1	GP179_HUMAN	cellular (Potential).	3	CCTCTTCCACCA	0.652	
+	5	792	_p.G76R|PPP1R1	NM_032192	NP_115568	Q9UD71	PPR1B_HUMAN		0	AGCTGGGGGAG	0.418	
-	14	2203		NM_133373	NP_588614	Q8N3E9	PLCD3_HUMAN	C2.	3	GTCTGCGGGCA	0.627	
+	4	1438		NM_014726	NP_055541	A7MCY6	TBKB1_HUMAN		0	GATTTAGACCTG	0.597	
+	2	421	.1_Intron|DHX40_	NM_024612	NP_078888	Q8IX18	DHX40_HUMAN	ase ATP-binding.	0	TATATGAAGCAG	0.323	
-	2	643	ddt.2_Missense_M	NM_001915	NP_001906	P49447	CY561_HUMAN	tochrome b561.	1	GGTGCGTTTAG	0.647	
-	16	2065	n.2_Missense_Mu	NM_001144952	NP_001138424	Q58EX2	SDK2_HUMAN	cellular (Potential).	2	GGGGGGCTCCT	0.577	
+	9	1346	1_5'Flank|LLGL2_	NM_207346	NP_997229	Q7Z6J9	SEN54_HUMAN		1	GTGCCCGGTAAG	0.537	
+	14	4319	uf.2_Missense_M	NM_018996	NP_061869	Q9HCJ0	TNR6C_HUMAN	Pro-rich.	2	CCCCTCGCACC	0.647	
-	3	795		NM_178520	NP_848615	Q8N8V8	TM105_HUMAN		1	TGTCTTCGCCTT	0.662	rs75774881
+	2	246_247	1WG>*R|USP14_	NM_005151	NP_005142	P54578	UBP14_HUMAN	biquitin-like.	2	AAATGGGGAAAG	0.371	
-	6	392	dkt.2_Missense_	NM_173464	NP_775735	Q8NA19	LMBL4_HUMAN	MBT 1.	3	CTCTGGAAAGG	0.343	
-	23	3438	wzj.1_Missense_M	NM_005559	NP_005550	P25391	LAMA1_HUMAN	inin EGF-like 13.	21	GCCCCGGTTTCC	0.572	
+	17	2503	.2_Missense_Mut	NM_020774	NP_065825	Q86YT6	MIB1_HUMAN	RING-type 1.	4	CCATGTGGACAT	0.383	
+	7	1446	kub.2_Intron|CABL	NM_001100619	NP_001094089	Q8TDN4	CABL1_HUMAN	th CDK3 (By similarity).	1	TACATGGTGAG	0.567	
+	5	589	vr.2_Missense_Mu	NM_177986	NP_817123	Q86SJ6	DSG4_HUMAN	|Extracellular (Potential).	8	ATAAATGATAACG	0.408	
+	3	557	lfp.1_Missense_M	NM_173629	NP_775900	Q8N1N2	CR026_HUMAN		0	TGTCCACCTACA	0.468	
+	5	959	if.2_Missense_Mu	NM_031891	NP_114097	Q9HBT6	CAD20_HUMAN	(Potential).|Cadherin 3.	5	GGATGGAGATG	0.423	
-	2	641	km.3_Missense_M	NM_006566	NP_006557	Q15762	CD226_HUMAN	1.|Extracellular (Potential).	0	TGAGTAGGGCTG	0.448	
-	8	1251	_p.E322K|NETO1_	NM_138966	NP_620416	Q8TDF5	NETO1_HUMAN	ss A.|Extracellular (Potenti	4	GATTTTCATCCC	0.378	
-	9	1486		NM_152769	NP_689982	Q8N350	DOS_HUMAN		0	CCCTGGGCCGC	0.711	
-	2	333	_p.V27M|SLC39A	NM_144564	NP_653165	Q9BRY0	S39A3_HUMAN	lasmic (Potential).	0	CTTCACGGGGA	0.547	
+	3	654		NM_002067	NP_002058	P29992	GNA11_HUMAN		86	GGGAGGACCCG	0.652	
+	8	1561_1562		NM_005483	NP_005474	Q13111	CAF1A_HUMAN		2	GCTTTCCATCCA	0.594	
-	2	234	N5_uc002mat.1_In	NM_052972	NP_443204	P02750	A2GL_HUMAN		1	TTCCACGGCCA	0.607	
-	22	3935	w.2_Missense_Mu	NM_002850	NP_002841	Q13332	PTPRS_HUMAN	cellular (Potential).	4	GGCCCCGGTTA	0.622	
-	2	792	dj.2_Missense_M	NM_001097641	NP_001091110	P21217	FUT3_HUMAN	nenal (Potential).	0	TGGTCCCCTTG	0.607	
-	1	181	A41_uc010dut.2_	NM_173637	NP_775908	Q8N5S1	S2541_HUMAN	Pro-rich.	0	ttgggggggaggcgg	0.423	rs113229271
-	26	3094		NM_012335	NP_036467	O00160	MYO1F_HUMAN		3	GGGTCGTCTGC	0.697	
-	5	36158		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).	57	CAGTGGGACTG	0.498	
-	5	35792		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).	57	GAAGTTGGAATC	0.488	
-	5	32182		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).	57	TGTCCCCGAAA	0.498	
-	3	30874		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	h.|Extracellular (Potential).	57	CACTGGAATTT	0.458	
-	3	26695		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	h.|Extracellular (Potential).	57	TCATAGGAGTGG	0.527	

-	3	24100		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	ch.|Extracellular (Potential).	57	TTTTTCCAGAAG	0.468	
-	1	9503		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).	57	CTGCAATGGTCT	0.478	
-	1	4672		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).	57	TAGGTGGAAAAT	0.423	
+	1	946		NM_175883	NP_787079	Q96RA2	OR7D2_HUMAN	Name=6; (Potential).	3	TTATGGGACAGC	0.498	
+	4	1932	e_Mutation_p.S62	NM_144566	NP_653167	Q9H0M5	ZN700_HUMAN	:2H2-type 14.	0	CTTCAGTTGTGC	0.483	
+	4	1934	e_Mutation_p.C62	NM_144566	NP_653167	Q9H0M5	ZN700_HUMAN	:2H2-type 14.	0	TCAGTTGTGCCT	0.483	
-	5	1075		NM_001080404	NP_001073873	C9JN71	ZN878_HUMAN	C2H2-type 8.	0	TACACTCATAGG	0.398	
-	4	1042		NM_005815	NP_005806	Q9Y2A4	ZN443_HUMAN	C2H2-type 6.	1	TACATTTATATGG	0.383	
+	1	905		NM_012377	NP_036509	O60412	OR7C2_HUMAN	lasmic (Potential).	3	GGGGAGACTCC	0.542	
-	9	1546	_p.S435L|SLC1A6_	NM_005071	NP_005062	P48664	EAA4_HUMAN		6	CCAATTGAGTCC	0.567	
-	4	558		NM_022904	NP_075055	Q86YV0	RASL3_HUMAN		0	GCCTTCGAGGAC	0.537	
-	1	501		NM_013940	NP_039228	Q9Y4A9	O10H1_HUMAN	lasmic (Potential).	0	CCGCGGGCTCA	0.647	
-	23	2976		NM_015692	NP_056507	Q8IZJ3	CPMD8_HUMAN		13	GGGGACTCCTT	0.602	
-	4	1316		NM_021030	NP_066358	P17017	ZNF14_HUMAN		3	GTTTCTCTCCAG	0.378	
+	4	1601		NM_031218	NP_112495	P35789	ZNF93_HUMAN	:2H2-type 13.	1	CCCTTACTAAAC	0.358	
+	4	1624		NM_031218	NP_112495	P35789	ZNF93_HUMAN		1	ATACTGGAGAG	0.353	
+	4	1693	429_uc010ecu.1_I	NM_001001415	NP_001001415	Q86V71	ZN429_HUMAN	:2H2-type 14.	2	CTTTTATCCTGTC	0.378	
+	4	1696	429_uc010ecu.1_I	NM_001001415	NP_001001415	Q86V71	ZN429_HUMAN	:2H2-type 14.	2	TTATCCTGTCCTC	0.378	
-	6	2775	208_uc002nqo.1_I	NM_007153	NP_009084				7	ATTCTTCACATTT	0.368	
-	5	1789	208_uc002nqo.1_I	NM_007153	NP_009084				7	ACCTTAATAAAG	0.398	
-	4	822	1_Intron|ZNF208_	NM_007153	NP_009084				7	TCTCTCCAGTATG	0.353	
-	5	1066		NM_001080409	NP_001073878				2	CAGTATGAATTAT	0.368	rs34442493
-	4	1170	rj.1_Missense_Mu	NM_003430	NP_003421	Q05481	ZNF91_HUMAN	C2H2-type 8.	0	ATTCTTTACATTT	0.373	
-	4	1111	rj.1_Missense_Mu	NM_003430	NP_003421	Q05481	ZNF91_HUMAN	C2H2-type 7.	0	GAAGAACGGCTA	0.393	rs410211
+	4	2677	dd.1_Missense_M	NM_014717	NP_055532	O15090	ZN536_HUMAN		11	CTCCCTGGAATC	0.572	
-	15	2117	p.S533F|RHPN2_	NM_033103	NP_149094	Q8IUC4	RHPN2_HUMAN		6	ACCAAGAACTGT	0.502	
-	7	1102	2nul.2_Missense_	NM_019849	NP_062823	Q9NS82	AAA1_HUMAN	ical; (Potential).	2	GACAGGCATGA	0.612	
+	5	754	_p.T131I|KIRREL2	NM_199180	NP_954649	Q6UWL6	KIRR2_HUMAN	2.|Extracellular (Potential).	3	AGGGACCCCTG	0.458	
+	5	1902		NM_144689	NP_653290	Q8TAQ5	ZN420_HUMAN	:2H2-type 16.	0	GTAAGGAATGTG	0.428	
+	7	775	NF383_uc002ofu.1	NM_152604	NP_689817	Q8NA42	ZN383_HUMAN	KRAB.	2	CCCTGGATGGT	0.493	
+	4	284	xtq.1_RNA|ZNF52	NM_032453	NP_115829	Q8NB42	ZN527_HUMAN	KRAB.	2	CCATTTCTAAGC	0.483	
+	14	4222		NM_015073	NP_055888	O60292	SI1L3_HUMAN		2	CGGAAGCAGCG	0.612	
+	1	851		NM_002446	NP_002437	Q02779	M3K10_HUMAN	rotein kinase.	6	GGCAGGTCGCC	0.637	
-	7	4471	_Mutation_p.S126	NM_181882	NP_870998	Q9BXM0	PRAX_HUMAN		2	CGGGGGACTTG	0.692	
+	27	3449	se_Mutation_p.P2	NM_001042544	NP_001036009	Q8N2S1	LTBP4_HUMAN	Pro-rich.	1	GGCACCTGCTA	0.697	
+	2	894	sk.3_Missense_M	NM_022752	NP_073589	Q6ZN55	ZN574_HUMAN		0	CTGTACCCGAGT	0.617	
+	3	1277	.2_Missense_Muta	NM_199285	NP_954979	A6NJB7	PRR19_HUMAN	Pro-rich.	0	TCGGCCCTGGG	0.647	
-	1	707	g.1_Intron|DMPK_	NM_001081563	NP_001075032	Q09013	DMPK_HUMAN		3	GAACCGAGGGT	0.602	
-	16	2371	p.R709H|SYMPK_	NM_004819	NP_004810	Q92797	SYMPK_HUMAN		1	ACTGGCGGGAC	0.597	rs145063068
-	1	1352	uc002peu.1_5'UTF	NM_020709	NP_065760	Q9ULN7	PNML2_HUMAN		1	CGTCCGGGGTG	0.572	
-	6	705	xt.2_Missense_Mu	NM_001190	NP_001181	O15382	BCAT2_HUMAN		1	CCCCGCCCACC	0.647	
+	22	3108	.E794K|PPFIA3_u	NM_003660	NP_003651	O75145	LIPA3_HUMAN		1	ACGAGGAGATG	0.647	
-	1	77	K1_uc010ycg.1_R	NM_002257	NP_002248	P06870	KLK1_HUMAN		0	TCCCCCCCAGG	0.642	
+	2	219	se_Mutation_p.V6	NM_001030047	NP_001025218	P07288	KLK3_HUMAN	eptidase S1.	3	AGTGGGTCCTC	0.632	
+	3	642	D33_uc010eot.1_M	NM_001772	NP_001763	P20138	CD33_HUMAN	Potential).|Ig-like C2-type.	0	CACCCCACGGC	0.612	
-	2	1102		NM_002029	NP_002020	P21462	FPR1_HUMAN	lasmic (Potential).	3	GAATTGGTAGCT	0.582	
-	5	1038	77_uc010ydf.1_5'	NM_023074	NP_075562	Q9BS31	ZN649_HUMAN		3	CTCCTTTGTGA	0.507	

-	5	1531	.2_Intron|uc002py	NM_021632	NP_067645	Q9GZX5	ZN350_HUMAN		1	GATTTTCCACCT	0.493
+	5	649	sense_Mutation_p	NM_144684	NP_653285	Q8WV37	ZN480_HUMAN		1	CAAGAACAGAA	0.358
-	6	848	n.1_Missense_Mu	NM_002287	NP_002278	Q6GTX8	LAIR1_HUMAN	ical; (Potential).	4	CAGGAGGAGGA	0.542
+	10	1540	fw.2_Missense_Mutation_p.P503S			Q96PV6	LENG8_HUMAN		2	AGGACCCGGAG	0.667
+	8	2341	.R728Q|NLRP2_	NM_017852	NP_060322	Q9NX02	NALP2_HUMAN		2	TCTTCGAGGTC	0.453
+	10	2787	p.T877P|NLRP2_	NM_017852	NP_060322	Q9NX02	NALP2_HUMAN	LRR 4.	2	TGCAGACCTTG	0.552
-	5	1369	b.2_Missense_Mu	NM_145007	NP_659444	P59045	NAL11_HUMAN	NACHT.	6	GGGATCAGACA	0.478
+	7	1604	mi.2_Missense_M	NM_153447	NP_703148	P59047	NALP5_HUMAN	NACHT.	7	TATGGCTGTGG	0.557
+	6	397	LP_uc010eti.2_3'U	NM_033106	NP_149097	Q9UBC7	GALP_HUMAN		0	AGCATGAAAATT	0.368
-	5	1758		NM_052882	NP_443114	Q96PE6	ZIM3_HUMAN	2H2-type 11.	2	CCTGTCAGCGA	0.408
-	5	499		NM_001012729	NP_001012747	A6NLW8	DUXA_HUMAN	omeobox 2.	1	TCTTCGATTTTG	0.383
-	19	3912		NM_012293	NP_036425	Q92626	PXDN_HUMAN		8	GCACCCGGGTG	0.627
-	10	1533	e_Mutation_p.D23	NM_015025	NP_055840	Q9UL68	MYT1L_HUMAN		6	ACTATCGTCTTC	0.443
+	7	671	.G127S|COLEC1	NM_024027	NP_076932	Q9BWP8	COL11_HUMAN	-type lectin.	0	GCGGGGGCACG	0.667
-	2	229	BP1_uc002qzm.2	NM_004763	NP_004754	O14713	ITBP1_HUMAN	Ser/Thr-rich.	0	TGATTTCGCTACT	0.398
-	8	1338	da.2_Missense_M	NM_001002006	NP_001002006	Q96P26	5NT1B_HUMAN		3	TTTTCCCCCGG	0.393
-	26	10625		NM_000384	NP_000375	P04114	APOB_HUMAN	parin-binding.	27	TTGACATCTCC	0.458
-	26	8053		NM_000384	NP_000375	P04114	APOB_HUMAN		27	CTGGATGGGATT	0.358
+	4	454	p.G146E|KRTCAP	NM_173853	NP_776252	Q53RY4	KCP3_HUMAN		0	TGAGGGGCCGG	0.547
-	18	2644		NM_019024	NP_061897	Q9P2D3	HTR5B_HUMAN	HEAT 1.	8	ATTTACGAACTT	0.398
+	8	932	nk.1_Missense_M	NM_144736	NP_653337	Q7L592	MIDA_HUMAN		1	AACTTTCTCAAC	0.413
+	8	934	nk.1_Nonsense_	NM_144736	NP_653337	Q7L592	MIDA_HUMAN		1	TTTCTCAACGC	0.413
+	8	955	sff.2_Missense_M	NM_032208	NP_115584	Q9H6X2	ANTR1_HUMAN	lar (Potential).|VWFA.	4	GTTTCCCGTGA	0.488
+	11	1204	V1B1_uc010fdw.2	NM_001692	NP_001683	P15313	VATB1_HUMAN		1	TCTACGTGGAC	0.552
+	2	1034	10feb.1_Missense_	NM_005791	NP_005782	O00566	MPP10_HUMAN	Potential.	3	ATAATGATGAG	0.323
+	51	6134	YSF_uc010fej.2_M	NM_003494	NP_003485	O75923	DYSF_HUMAN	lasmic (Potential).	7	TTTGATGATTTTC	0.522
+	7	706	uq.2_Missense_M	NM_013434	NP_038462	Q9Y2W7	CSEN_HUMAN	EF-hand 3.	3	GACATGATGGG	0.667
+	7	1083		NM_004804	NP_004795	O76071	CIAO1_HUMAN		0	CTTCTCCCTGA	0.612
-	29	3934	RNP200_uc002s	NM_014014	NP_054733	O75643	U520_HUMAN	SEC63 1.	10	AGACAGGCAGC	0.552
+	7	794	e_Mutation_p.G13	NM_001134224	NP_001127696	Q96PE3	INP4A_HUMAN	C2.	1	ACTGGGCTCTG	0.458
-	1	791	LL_uc010fju.2_R	NM_005434	NP_005425	Q13021	MALL_HUMAN		2	CGGGCGGGTCG	0.706
-	22	2922		NM_022662	NP_073153	Q9H1A4	APC1_HUMAN		2	GTGAGGATTCA	0.289
+	3	408	LI2_uc002tmu.3_	NM_005270	NP_005261	P10070	GLI2_HUMAN		13	CACATGGAGCA	0.647
+	2	468	0flu.2_Missense_	NM_130773	NP_570129	Q8WYK1	CNTP5_HUMAN	|Extracellular (Potential).	10	ACTAGCATCCC	0.458
-	3	387	IMS2_uc010yzm.1	NM_001161403	NP_001154875	Q7Z4I7	LIMS2_HUMAN	zinc-binding 1.	0	AGCACGGAGCA	0.602
-	14	3243	AP5_uc002ttq.2_I	NM_207363	NP_997246	O14513	NCKP5_HUMAN		0	GGTTTCGGACT	0.567
-	14	2946	AP5_uc002ttq.2_I	NM_207363	NP_997246	O14513	NCKP5_HUMAN		0	TAATTCAAAGAG	0.532
-	6	1158		NM_002299	NP_002290	P09848	LPH_HUMAN	tial).|4 X approximate repe	13	TTCAGGGAAAG	0.602
+	27	4684		NM_001080427	NP_001073896				7	CACCTCCCCAA	0.418
-	89	14518		NM_018557	NP_061027	Q9NZR2	LRP1B_HUMAN	lasmic (Potential).	50	GGTCTATCATAA	0.373
+	1	1118		NR_026904					0	AGACAGCTATG	0.388
+	9	1616	foc.1_Missense_M	NM_052917	NP_443149	Q8IUC8	GLT13_HUMAN	enal (Potential).	6	CAACTCCATACA	0.413
+	3	387	o.2_Missense_Mu	NM_173355	NP_775491	O95045	UPP2_HUMAN		0	GTGTCGGTGGG	0.418
-	12	2539		NM_022168	NP_071451	Q9BYX4	IFIH1_HUMAN	case C-terminal.	1	TGACTTCTTTTTG	0.294
-	16	3400	p.E1008K|SCN1A	NM_006920	NP_008851	P35498	SCN1A_HUMAN		13	TTTCTTCCAGAT	0.284
+	8	2470	udy.2_Missense_	NM_152381	NP_689594	A4UGR9	XIRP2_HUMAN	Xin 8.	14	CTTTGGAGAAA	0.378
+	2	910		NM_020981	NP_066191	Q9Y5Z6	B3GT1_HUMAN	enal (Potential).	4	GACAATCTTATT	0.408

-	2	229		NM_020675	NP_065726	Q9HBM1	SPC25_HUMAN	omplex.|Interaction with the		1	GTATCTCTTAGTC	0.373	
-	36	6052		NM_004525	NP_004516	P98164	LRP2_HUMAN	B 18.|Extracellular (Potent		29	CCACGTTTCCTCT	0.343	
-	4	405	.2_Intron|SLC25A	NM_003705	NP_003696	O75746	CMC1_HUMAN	2.|EF-hand 2.		0	ATGTCACCTCTC	0.363	
-	254	55829	2230I|TTN_uc010z	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN			153	TGGTCTCATTTCC	0.453	
-	253	54483	782K|TTN_uc010z	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN			153	TTGTTTCGATGGT	0.393	
-	250	52053	072C|TTN_uc010z	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN			153	CATTACGAATTTC	0.388	
-	238	48717	860F|TTN_uc010z	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN			153	CATAGAGAACAG	0.433	
-	65	16329	N_uc010zfj.1_Intro	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN			153	CAAGTTCCACAT	0.408	
-	65	16228	N_uc010zfj.1_Intro	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN			153	CCAGGTTTCACTA	0.338	
-	47	11075	N_uc010zfj.1_Intro	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN			153	TCCTCTATCTTGA	0.408	
+	3	884		NM_194250	NP_919226	Q7Z570	Z804A_HUMAN		p.R97Q(1)	11	TTGCTCGAAATGT	0.368	rs145158210
-	7	911	frt.2_Nonsense_M	NM_005795	NP_005786	Q16602	CALRL_HUMAN	cellular (Potential).		4	ATTTGTCCATGTT	0.333	
+	22	1721		NM_000090	NP_000081	P02461	CO3A1_HUMAN	le-helical region.		13	CAGGAATGAGGG	0.488	
-	44	8356		NM_018897	NP_061720	Q8WXX0	DYH7_HUMAN	k (By similarity).		12	CATGAAGTGACT	0.373	
-	41	7050		NM_018897	NP_061720	Q8WXX0	DYH7_HUMAN	4 (By similarity).		12	CAAATCGAAACA	0.443	rs115474479
-	36	6037		NM_018897	NP_061720	Q8WXX0	DYH7_HUMAN	milarity).|ATP (Potential).		12	CCAGTTCCTGTTG	0.368	
+	11	2709	tr.2_Missense_Mu	NM_001204	NP_001195	Q13873	BMPR2_HUMAN	lasmic (Potential).		9	AATCCAATGTCTA	0.423	
+	3	285	010ziu.1_5'Flank|E	NM_001037663	NP_001032752	P24534	EF1B_HUMAN	ST C-terminal.		0	GTGTCCAGCCCA	0.468	
+	5	4256		NM_020923	NP_065974	Q9HCK1	ZDBF2_HUMAN			3	AATATCCCTCTTC	0.378	
-	2	323	zjg.1_Missense_M	NM_001608	NP_001599	P28330	ACADL_HUMAN			0	TCTTCCCCTCCG	0.348	
-	7	979	_p.P294L|ERBB4_	NM_005235	NP_005226	Q15303	ERBB4_HUMAN	Extracellular (Potential).		33	TTACGTGGACATT	0.318	
-	13	1071	S1_uc010fvj.1_Mis	NM_022648	NP_072174	Q9HBL0	TENS1_HUMAN	2 tensin-type.		4	CTCCTGGGATGT	0.582	
+	4	392	_p.P131L|RQCD1_	NM_005444	NP_005435	Q92600	RCD1_HUMAN			2	CACGTCCCTTTGA	0.423	
-	1	1032_1033	e_Mutation_p.G32	NM_015311	NP_056126	O75147	OBSL1_HUMAN	Ig-like 3.		0	CTGGCCCGCCGA	0.683	
+	28	2285	utation_p.K708R|C	NM_000091	NP_000082	Q01955	CO4A3_HUMAN	le-helical region.		3	GACCTAAGGGTA	0.373	
-	10	1868	p.R555W|ECEL1_	NM_004826	NP_004817	O95672	ECEL1_HUMAN	nenal (Potential).		2	CCTGCCGAATCT	0.567	
+	12	1227	YF2_uc002vtk.3_M	NM_015575	NP_056390	Q6Y7W6	PERQ2_HUMAN			7	AAGAAATGGGTA	0.448	
+	4	671		NM_001080437	NP_001073906	Q8TER0	SNED1_HUMAN	NIDO.		2	GGCAGCGTTACT	0.657	
+	3	469		NM_032515	NP_115904	Q9UMX3	BOK_HUMAN	BH3.		1	CAGGCGATGAG	0.647	
-	2	471		NM_015963	NP_057047	Q8WY91	THAP4_HUMAN	THAP-type.		0	AGATGGATGGCA	0.582	
+	4	582	al.1_Missense_Mu	NM_198994	NP_945345	O95932	TGM3L_HUMAN			4	ACGAGCCCAGG	0.622	
+	11	1051	f.2_Intron|VPS16_	NM_022575	NP_072097	Q9H269	VPS16_HUMAN			4	GCCAGCGAGGAA	0.602	
-	3	921	mp.2_Missense_M	NM_152611	NP_689824	Q8WUT4	LRRN4_HUMAN	lar (Potential).|LRR 8.		3	GGTAGAGGGATG	0.572	
-	5	1408	nj.2_Missense_Mu	NM_020341	NP_065074	Q9P286	PAK7_HUMAN	Linker.		23	GAGCCTGACCTG	0.552	
-	5	1064	nj.2_Missense_Mu	NM_020341	NP_065074	Q9P286	PAK7_HUMAN	Linker.		23	CATTTTCATTACG	0.463	
+	3	302	OLR3F_uc002wqx	NM_006466	NP_006457	Q9H1D9	RPC6_HUMAN			0	TAGGGTCAGTTG	0.303	
+	15	2497	lv.1_Missense_Mu	NM_012112	NP_036244	Q9ULW0	TPX2_HUMAN			2	CAGAAGAGGTG	0.488	
+	6	991	eb.2_Missense_Mu	NM_015338	NP_056153	Q8IXJ9	ASXL1_HUMAN			248	GCATCAGGTATGT	0.507	
+	3	228_229		NM_182519	NP_872325	P59827	LPLC4_HUMAN			0	GGACCCCCCCCA	0.485	rs145261889
+	15	2212	v.2_Nonsense_Mu	NM_012156	NP_036288	Q9H4G0	E41L1_HUMAN			3	CGGATCGAGGG	0.652	
+	5	501	_p.E72K|MYBL2_	NM_002466	NP_002457	P10244	MYBB_HUMAN	TH myb-type 2.		5	GTCATCGAGCTG	0.587	
+	8	1203	p.E350K|HNF4A_	NM_000457	NP_000448	P41235	HNF4A_HUMAN			3	TTGCAGGAGATG	0.383	
-	6	680	gu.2_Missense_M	NM_182970	NP_892015	Q9H426	RIMS4_HUMAN			5	GCCAGGGTGGTC	0.657	
+	6	869	e_Mutation_p.G21	NM_001164116	NP_001157588	Q9NQ75	CASS4_HUMAN			3	ACAGGGGCAGG	0.502	
+	18	2599	np.2_Missense_Mu	NM_012469	NP_036601	O94906	PRP6_HUMAN			2	ACTCCGGTAAG	0.642	
+	18	2522	P25_uc002yjz.1_M	NM_013396	NP_037528	Q9UHP3	UBP25_HUMAN			5	GAGCATGAAGATA	0.378	
-	2	276	orf59_uc010glx.2_	NM_021254	NP_067077	P57076	CU059_HUMAN			0	ATATGCCATGTTC	0.328	

-	29	3637	2yqg.2_Missense	NM_003895	NP_003886	O43426	SYNJ1_HUMAN	Pro-rich.	5	ACTGCGTCCTG	0.299	
+	4	476	yri.1_Missense_M	NM_000628	NP_000619	Q08334	I10R2_HUMAN	-III.|Extracellular (Potential	0	CTGATTCTTTAC	0.348	
+	4	1278	p.D326N|KCNJ15	NM_002243	NP_002234	Q99712	IRK15_HUMAN	smic (By similarity).	6	TGGCTGATTTC	0.443	
-	6	1522	AM_uc002yyr.1_	NM_001389	NP_001380	O60469	DSCAM_HUMAN	otential).|Ig-like C2-type 4.	11	TTTTTCCAGGG	0.507	
+	21	3495	1afa.1_Missense_	NM_003274	NP_003265	P48553	TPC10_HUMAN		2	ATTTTTCGACAA	0.299	
-	5	706	Splice_Site|PTTG	NM_004339	NP_004330	P53801	PTTG_HUMAN		1	TCCTTACCATAT	0.502	
-	7	939	.R299W|FTCD_uc	NM_006657	NP_006648	O95954	FTCD_HUMAN	se C-subdomain (By simila	2	GATCCGCTGCT	0.697	
-	14	2352	nk.1_Missense_M	NM_015241	NP_056056	Q7RTP6	MICA3_HUMAN		0	CTTGGGAGAAC	0.502	
-	5	831	GCR2_uc011agr.1_	NM_005137	NP_005128	P98153	IDD_HUMAN	(Potential).|C-type lectin.	1	GGTTCCGGCCAG	0.562	
-	3	556	GCR2_uc011agr.1	NM_005137	NP_005128	P98153	IDD_HUMAN	ellular (Potential).	1	GCTGCGCCACG	0.647	
-	31	4855	p.L1573M|CLTCL	NM_007098	NP_009029	P53675	CLH2_HUMAN	zation (By similarity).|Heav	5	GGCCAAGTCCA	0.617	
+	5	2391	R_uc011aiy.1_Mi	NM_004327	NP_004318	P11274	BCR_HUMAN	DH.	12	ACTACGGAGTT	0.577	
-	2	276	70_uc002zxs.2_5'	NM_013378	NP_037510	Q9UKI3	VPRE3_HUMAN	Ig-like.	0	ATATCGAGGGG	0.622	
-	11	1188_1189	n_p.K416E|CHEK	NM_007194	NP_009125	O96017	CHK2_HUMAN	rotein kinas73E(2)|p.S372	20	AATCTTGGAGTG	0.416	470496;rs146546850
+	12	2752	sense_Mutation_p	NM_001017437	NP_001017437	Q569K6	CC157_HUMAN		1	CCCCATCTCGG	0.667	
-	6	907	p.G250R|SYN3_u	NM_003490	NP_003481	O14994	SYN3_HUMAN	and synaptic-vesicle bindin	1	ATGTCCCAGCT	0.542	
-	6	727	_Mutation_p.G12	NM_006860	NP_006851	Q9BW83	IFT27_HUMAN		0	TGTTCCCAACTA	0.542	
-	2	388_389	rb.2_Nonsense_M	NM_001051	NP_001042	P32745	SSR3_HUMAN	ellular (Potential).	1	AGGGCCAGTAG	0.619	
+	7	1998	atq.1_Missense_M	NM_001039141	NP_001034230	Q9H2D6	TARA_HUMAN		1	CCCCAGAACAT	0.587	
+	1	783_784	_5'Flank|GCAT_u	NM_005318	NP_005309	P07305	H10_HUMAN		0	ATCAAGAAGGTA	0.564	
+	31	6228		NM_001429	NP_001420	Q09472	EP300_HUMAN		64	GCCCACGTGCAA	0.597	
+	4	358	e_Mutation_p.R4	NM_017590	NP_060060	Q9UGR2	Z3H7B_HUMAN	TPR 1.	1	TGTTCCGGGAG	0.602	rs139726421
+	3	291	gzn.2_Missense_	NM_013327	NP_037459	Q9HBI1	PARVB_HUMAN		0	CACTTCCAAGG	0.572	
-	2	564	aa.2_Missense_	NM_058238	NP_478679	P56706	WNT7B_HUMAN		1	CCCCCTCCCCAA	0.627	
-	13	5828	arc.1_Missense_M	NM_014246	NP_055061	Q9NYQ6	CELR1_HUMAN	ial).|EGF-like 6; calcium-bi	11	AGTACGGCCCG	0.612	
-	35	5441	.R571W|PLXNB2_	NM_012401	NP_036533	O15031	PLXB2_HUMAN	lasmic (Potential).	6	TTACCCGGGAAA	0.617	
+	9	1294	.G271R|CNTN6_	NM_014461	NP_055276	Q9UQ52	CNTN6_HUMAN	like C2-type 4.	8	CTAGTGGAAAG	0.398	
+	2	1079	lt.2_Missense_Mu	NM_001098213	NP_001091683	P35367	HRH1_HUMAN	lasmic (Potential).	2	CAAGGGGGATG	0.532	
+	10	1809	xj.2_Missense_Mu	NM_001162499	NP_001155971	O75155	CAND2_HUMAN	HEAT 12.	4	GGAGGTGAAGG	0.632	
-	1	241		NM_024923	NP_079199	Q8TEM1	PO210_HUMAN	enal (Probable).	11	GGTAGCAGCCC	0.582	
+	5	2377	wd.1_Missense_M	NM_001144382	NP_001137854	Q9UPR0	PLCL2_HUMAN	C2.	4	AGAACTTTCCC	0.473	rs138785787
+	2	674	cdq.2_Missense_	NM_052953	NP_443185	Q96PB8	LRC3B_HUMAN		4	TGCTTTCATTCT	0.443	
-	11	1307	axh.1_Nonsense_	NM_016141	NP_057225	Q9Y6G9	DC1L1_HUMAN		1	TGTTCGTGGGG	0.378	
-	10	1084	j.1_Missense_Mut	NM_000404	NP_000395	P16278	BGAL_HUMAN		1	ATAGGGTGAGT	0.502	
-	9	1329	_Mutation_p.Q37	NM_198056	NP_932173	Q14524	SCN5A_HUMAN		9	CTGCTGATAGA	0.612	
-	11	1645		NM_006514	NP_006505	Q9Y5Y9	SCNAA_HUMAN		10	AGGGAGGGGGC	0.612	
+	4	290	03ckr.2_Missense	NM_001904	NP_001895	P35222	CTNB1_HUMAN	0del(1)|p.M1_A87del(1)|p.	3166	TCCTTCTCTGA	0.498	rs121913409
+	2	968	al.1_Intron|CXCR	NM_006564	NP_006555	O00574	CXCR6_HUMAN	lasmic (Potential).	1	AGTTTCGAAAGA	0.473	rs141955108
+	4	1373	k.1_Missense_Mu	NM_178329	NP_847899	P51677	CCR3_HUMAN	ellular (Potential).	8	GAGCAAGCATC	0.498	
+	7	639	qn.2_Nonsense_M	NM_000316	NP_000307	Q03431	PTH1R_HUMAN	ellular (Potential).	1	CCTACCGACGC	0.607	rs143863124
-	3	419	.1_5'UTR|SCAP_u	NM_012235	NP_036367	Q12770	SCAP_HUMAN	nal (By similarity).	1	ATTCCACAGGT	0.537	
-	14	3272	.2_Missense_Muta	NM_002673	NP_002664	O43157	PLXB1_HUMAN	ellular (Potential).	5	GACGCAGAAAC	0.662	
-	3	368	NB1_uc003csx.2_	NM_002673	NP_002664	O43157	PLXB1_HUMAN	lar (Potential).|Sema.	5	GATACGTGCCA	0.647	
-	16	2332	wf.1_Missense_M	NM_002292	NP_002283	P55268	LAMB2_HUMAN	ninin IV type B.	3	GGATTAGGAAAT	0.572	
+	46	4804		NM_004947	NP_004938	Q8IZD9	DOCK3_HUMAN	DHR-2.	0	CCTTGGAGTTG	0.488	
+	53	5707_5708		NM_004947	NP_004938	Q8IZD9	DOCK3_HUMAN		0	GTCCTCCTTGAG	0.614	
-	21	2413	.W588R|ITIH4_uc	NM_002218	NP_002209	Q14624	ITIH4_HUMAN		3	AACCCATACCA	0.567	

-	9	1261	_p.P384L|TKT_uc0	NM_001135055	NP_001128527	P29401	TKT_HUMAN		2	AGAAGGGCACC	0.652	
+	26	3380	p.R1073C|CACNA	NM_001128840	NP_001122312	Q01668	CAC1D_HUMAN	llular (Potential).|III.	11	TGGTCCGTGAA	0.527	
+	9	977	_p.G216E|CACNA	NM_018398	NP_060868	Q8IZS8	CA2D3_HUMAN	lar (Potential).|VWFA.	7	GAATGGAACTT	0.453	
-	14	2161	_p.L291S|C3orf63_	NM_015224	NP_056039	Q9UK61	CC063_HUMAN		5	TGAATTAAATTA	0.363	
+	18	1655	TR|PXK_uc010hn	NM_017771	NP_060241	Q7Z7A4	PXK_HUMAN		1	TCCTCCACCTC	0.612	
-	21	2985		NM_020872	NP_065923	Q9P232	CNTN3_HUMAN	nectin type-III 4.	5	GTAGTCCTCTT	0.408	
-	6	822	_p.C30G|PROS1_	NM_000313	NP_000304	P07225	PROS_HUMAN	lcium-binding (Potential).	1	CTTTGCATTCAT	0.348	
-	13	2919	e.1_Nonsense_M	NM_016247	NP_057331	Q9BZV3	IMPG2_HUMAN	lar (Potential).|SEA 2.	3	CACTCGGAGGC	0.423	
+	9	1318	x.2_Missense_Mu	NM_198196	NP_937839	P40200	TACT_HUMAN	otential).|Pro/Ser/Thr-rich.	3	AATTTCCTCAA	0.358	
-	3	921	_Mutation_p.G24	NM_003925	NP_003916	O95243	MBD4_HUMAN		2	TACATCCTTTTTT	0.363	
-	2	230	.R27G|NMNAT3_	NM_178177	NP_835471	Q96T66	NMNA3_HUMAN		0	CACTCGGTGAT	0.572	
+	5	1184	hvn.2_Missense_	NM_207365	NP_997248	Q6P093	ADCL2_HUMAN		0	ACTTCGAAATG	0.358	
-	2	3118	fek.2_Missense_M	NM_014926	NP_055741	O94933	SLIK3_HUMAN	lasmic (Potential).	10	GGCAGGCTGTG	0.552	
+	5	545_546	_p.P125F|FNDC3	NM_022763	NP_073600	Q53EP0	FND3B_HUMAN		3	TCCCTCCCTATC	0.535	
+	26	3581	hz.3_Missense_M	NM_022763	NP_073600	Q53EP0	FND3B_HUMAN	nectin type-III 9.	3	CTCAGGAGCTA	0.517	
-	1	320	HL6_uc003flt.1_	NM_130446	NP_569713	Q8WZ60	KLHL6_HUMAN	BTB.	3	CACCACGCGGT	0.507	
+	17	1770	p.R540Q|ABCF3_	NM_018358	NP_060828	Q9NUQ8	ABCF3_HUMAN	C transporter 2.	4	TGTTCGGGGCA	0.577	
-	2	1351		NM_178496	NP_848591	Q8IYB1	M21D2_HUMAN		0	GGCAGGAAGTC	0.532	
-	2	610		NM_178496	NP_848591	Q8IYB1	M21D2_HUMAN		0	CACCACGCCTT	0.493	
-	3	2433	ron|ABCA11P_uc0	NM_133474	NP_597731	D9N162	D9N162_HUMAN		1	TTCTCTCCAGTA	0.398	
-	3	2289	ron|ABCA11P_uc	NM_133474	NP_597731	D9N162	D9N162_HUMAN		1	CCACATACTTCA	0.398	
+	5	1035	.P211L|PIGG_uc	NM_001127178	NP_001120650	Q5H8A4	PIGG_HUMAN	enal (Potential).	4	GAAACCCGGTG	0.393	
+	15	2719	812N|FAM193A_	NM_003704	NP_003695	P78312	F193A_HUMAN		3	ACTGCGACTGC	0.577	
+	10	1351	D1_uc003gfq.2_	NM_001119	NP_001110	P35611	ADDA_HUMAN		1	CTAGGGCTACA	0.358	
+	45	6167		NM_002111	NP_002102	P42858	HD_HUMAN		4	TGGCTCGCATG	0.502	
-	14	2350	_p.R206S|EVC2_u	NM_147127	NP_667338	Q86UK5	LBN_HUMAN	Potential.	5	CCCACGCTTGA	0.647	
-	9	816	_p.A239T|CRMP1_	NM_001313	NP_001304	Q14194	DPYL1_HUMAN		2	GATGGCCCGGA	0.557	
-	9	1669	p.D465N|JAKMIP1	NM_144720	NP_653321	Q96N16	JKIP1_HUMAN	tion with TYK2 and GABBR	4	TCCTGTCTGTCC	0.537	
+	8	2122	_p.Y652*|WFS1_u	NM_001145853	NP_001139325	O76024	WFS1_HUMAN	ical; (Potential).	2	GTGTACCGCTC	0.607	
-	16	2384	Mutation_p.S788	NM_198595	NP_940997	Q8N556	AFAP1_HUMAN		0	CCTGGCTCTTC	0.677	
+	10	1556	l.1_Missense_Mu	NM_182485	NP_872291	Q7Z5Q1	CPEB2_HUMAN	RRM 2.	1	TTTCTCCAATC	0.433	
+	10	1170	.P312S|RBPJ_uc	NM_005349	NP_005340	Q06330	SUH_HUMAN		3	CCACTCCATGT	0.338	
+	11	1414		NM_021927	NP_068746	Q8N442	GUF1_HUMAN		1	GGCTAGGATTT	0.373	
+	1	135	0ihr.2_Missense_	NM_053039	NP_444267	Q9BY64	UDB28_HUMAN		1	TGAAAGAGCTT	0.443	
+	1	331	ihr.2_Missense_	NM_053039	NP_444267	Q9BY64	UDB28_HUMAN		1	TTTTTCACAAGA	0.294	
+	13	1793	B_uc003hgu.3_M	NM_000477	NP_000468	P02768	ALBU_HUMAN	Albumin 3.	6	TGGATGATTTCG	0.413	
+	27	3909	w.2_Missense_Mu	NM_025074	NP_079350	Q86XX4	FRAS1_HUMAN	xtracellular (Potential).	5	GAAATGGAAAA	0.478	
+	16	3326	PAQR3_uc003hln.	NM_198892	NP_942595	Q9NSY1	BMP2K_HUMAN		1	GGAAAGATAGG	0.507	
+	2	993		NM_001201	NP_001192	P12645	BMP3_HUMAN		5	CCAAGGGACGC	0.438	
-	3	349	EF1B_uc010ijq.1_	NM_152545	NP_689758	Q0VAM2	RGF1B_HUMAN	rminal Ras-GEF.	0	AGAACTGAGTA	0.368	
-	7	1006	s.1_Missense_Mu	NM_001098540	NP_001092010	Q9Y251	HPSE_HUMAN		1	AGTCCGTCCAT	0.299	
-	8	1087	H1B_uc011ceh.1	NM_000668	NP_000659	P00325	ADH1B_HUMAN		2	AAAATCAGCCA	0.368	
-	3	269		NM_000673	NP_000664	P40394	ADH7_HUMAN		3	AGATTCCTGTG	0.393	
-	26	3328	hxc.1_Splice_Site_	NM_001813	NP_001804	Q02224	CENPE_HUMAN		9	ATGGTCTAGAA	0.318	
+	8	1722	_p.P382S|EGF_uc	NM_001963	NP_001954	P01133	EGF_HUMAN	Extracellular (Potential).	4	TCTGTCCTGAA	0.398	rs146224376
+	9	1865_1866	p.D430N|EGF_uc	NM_001963	NP_001954	P01133	EGF_HUMAN	Extracellular (Potential).	4	CAACTGGATGAA	0.441	
+	6	879	a.2_Missense_Mu	NM_016648	NP_057732	Q4G0J3	LARP7_HUMAN	RRM.	3	ATATTTCCTAAA	0.279	

+	6	951	.D212G|PHF17_u	NM_199320	NP_955352	Q6IE81	JADE1_HUMAN	PHD-type 1.	0	TCTGTGACAAAT	0.532	
-	8	1705		NM_015130	NP_055945	Q6ZT07	TBCD9_HUMAN		1	ACCAATTTCGGG	0.463	
+	1	1787	t.3_Intron|LRBA_u	NM_006439	NP_006430	Q9Y586	MB212_HUMAN		1	AGAGCGACGCC	0.652	
+	3	1301	_p.S361L|TLR2_uc	NM_003264	NP_003255	O60603	TLR2_HUMAN	xtracellular (Potential).	3	TAAAATCATTAG	0.323	
+	3	696	_p.P175S|RBM46_	NM_144979	NP_659416	Q8TBY0	RBM46_HUMAN	RRM 2.	2	TTTATCCAAGT	0.353	
+	4	636	3_uc003iox.2_Mis	NM_000856	NP_000847	Q02108	GCYA3_HUMAN		4	AGGCAGCAGG	0.488	
+	15	2993	_Mutation_p.R798	NM_001083619	NP_001077088	P42262	GRIA2_HUMAN	lasmic (Potential).	4	GAAACGAATG	0.448	
+	11	1977	p.R444C|TLL1_uc	NM_012464	NP_036596	O43897	TLL1_HUMAN	CUB 1.	7	AGTTTCGTAGC	0.368	
-	5	685		NM_017631	NP_060101	Q8IY21	DDX60_HUMAN		3	ACTTCCCCACTC	0.368	
+	9	1725	_p.T505N|PALLD_	NM_016081	NP_057165	Q8WX93	PALLD_HUMAN	-like C2-type 2.	1	TTTGCACCCTAG	0.443	
-	9	1223	e.1_Missense_Mu	NM_012224	NP_036356	Q96PY6	NEK1_HUMAN	rotein kinase.	6	CTATCCCTAGGA	0.368	
+	8	949	e_Mutation_p.R25	NM_021942	NP_068761	Q7Z392	CD041_HUMAN		0	AATTGAGAGCCC	0.318	
-	10	6595		NM_005245	NP_005236	Q14517	FAT1_HUMAN	(Potential).|Cadherin 19.	12	TTCAGTGAAATTT	0.428	
+	11	1176	e_Mutation_p.L35	NM_020731	NP_065782	A9YTQ3	AHRR_HUMAN		2	TGTGCCTCCGG	0.662	
+	18	2891	3jdk.1_Missense_	NM_139056	NP_620687	Q8TE57	ATS16_HUMAN	TSP type-1 2.	8	CACGGGGCTGG	0.527	
-	7	2121	se_Mutation_p.E3	NM_024091	NP_076996	Q14CZ7	FAKD3_HUMAN		4	TTCATTCTTGCA	0.333	
+	11	1523	RR_uc003jef.3_R	NM_024010	NP_076915	Q9UBK8	MTRR_HUMAN	-binding FR-type.	1	TCTTCAACATTGT	0.443	
-	78	13601	c.2_Nonsense_Mu	NM_001369	NP_001360	Q8TE73	DYH5_HUMAN		31	TTCATCCATTTG	0.478	
-	40	6628		NM_001369	NP_001360	Q8TE73	DYH5_HUMAN		31	CATCCTCATCAA	0.368	
-	4	959		NM_022130	NP_071413	Q9H4A6	GOLP3_HUMAN		1	TTCACCCATTTG	0.502	
-	7	960		NM_001737	NP_001728	P02748	CO9_HUMAN	MACPF.	0	TTTTTTCCTGTG	0.328	
+	19	2486	A1_uc003jow.2_	NM_181501	NP_852478	P56199	ITA1_HUMAN	ellular (Potential).	3	AATAAGGAAAAA	0.398	
+	20	1971	h.3_Missense_Mu	NM_001136034	NP_001129506	Q9NQI0	DDX4_HUMAN	case C-terminal.	2	CTGGTCGTTGT	0.388	
+	2	330		NM_005242	NP_005233	P55085	PAR2_HUMAN	ellular (Potential).	1	AAAAGGAGTTA	0.433	
+	33	8017	p.G347R|GPR98_	NM_032119	NP_115495	Q8WXG9	GPR98_HUMAN	.|Extracellular (Potential).	16	GTGCTGGAGAG	0.423	
-	17	2333	_p.F511C|MCTP1_	NM_024717	NP_078993	Q6DN14	MCTP1_HUMAN		2	TGATAAAGTTT	0.353	
-	13	1452	03kpp.1_Splice_S	NM_022140	NP_071423	Q9HCS5	E41LA_HUMAN		1	ACTGACCTTTT	0.313	
-	1	514		NM_001085377	NP_001078846	P23508	CRCM_HUMAN		1	CGGTGCTGGAC	0.383	
+	3	513	ksn.2_Missense_	NM_182761	NP_877438	A1A519	F170A_HUMAN		1	ACAACATGTCTC	0.493	
+	1	580		NM_177478	NP_803431	Q8N4E7	FTMT_HUMAN	rritin-like diiron.	1	TGTGCGATTTC	0.507	
-	7	1289	wk.2_Missense_M	NM_004199	NP_004190	O15460	P4HA2_HUMAN		0	CAGCTCGTTCG	0.433	
-	13	1850	_p.E551K|KIF3A_	NM_007054	NP_008985	Q9Y496	KIF3A_HUMAN	Potential.	1	ATGTTCTTGTT	0.398	
-	2	445	f20_uc003lav.2_5'	NM_001099221	NP_001092691	Q6ZNK6	TIFAB_HUMAN	FHA.	0	ACAGCCCTTGC	0.647	
-	10	1614_1615	L3_uc011cyd.1_In	NM_017415	NP_059111	Q9UH77	KLHL3_HUMAN	Kelch 2.	0	AGCACCGCTGC	0.599	
+	1	563	03lhc.1_Missense	NM_018905	NP_061728	Q9Y5H9	PCDA2_HUMAN	ellular (Potential).	4	GGTTTCCTCTAG	0.448	
+	1	1966	lhd.2_Intron|PCDH	NM_018906	NP_061729	Q9Y5H8	PCDA3_HUMAN	|Extracellular (Potential).	8	ACGGTGAACCC	0.697	
+	1	1050	03lhf.2_Intron|PC	NM_018907	NP_061730	Q9UN74	PCDA4_HUMAN	|Extracellular (Potential).	6	TCCTATGAAATT	0.358	
+	1	1475	03lhi.2_Intron|PC	NM_018908	NP_061731	Q9Y5H7	PCDA5_HUMAN	r (Potential).|Cadherin 5.	3	CTACTCGCTGG	0.662	
+	1	1922	.2_Intron|PCDHA	NM_018901	NP_061724	Q9Y5I2	PCDAA_HUMAN	r (Potential).|Cadherin 6.	5	TGACTCGCCAC	0.647	
+	1	871	ah.1_Missense_	NM_018939	NP_061762	Q9Y5E3	PCDB6_HUMAN	|Extracellular (Potential).	1	CCTTCGAAATA	0.458	
+	1	1948	ah.1_Missense_	NM_018939	NP_061762	Q9Y5E3	PCDB6_HUMAN	|Extracellular (Potential).	1	CTCCGCGCTCG	0.706	
+	1	1463	.1_Intron|PCDHG	NM_018923	NP_061746	Q9Y5G2	PCDGE_HUMAN	r (Potential).|Cadherin 5.	0	AAGTTTCCTACT	0.592	
+	1	610	ljo.1_Intron|PCD	NM_018924	NP_061747	Q9Y5G1	PCDGF_HUMAN	r (Potential).|Cadherin 2.	0	GGGAAGAGCAG	0.552	
+	1	2213	ljs.1_Intron|PCDH	NM_032088	NP_114477	Q9Y5G5	PCDG8_HUMAN	|Extracellular (Potential).	0	AAATCGCTCTG	0.468	
+	1	967	_Intron|PCDHGB	NM_018929	NP_061752	Q9Y5F6	PCDGM_HUMAN	r (Potential).|Cadherin 3.	3	GAGCCCGTGAC	0.542	rs142098675
+	11	1093	p.S353L|ARHGA	NM_015071	NP_055886	Q9UNA1	RHG26_HUMAN	PH.	1	TTTGTCGGAAG	0.498	
+	3	326	_p.R69Q|FBXO38	NM_205836	NP_995308	Q6PIJ6	FBX38_HUMAN	KLF7 (By similarity).|F-box	6	TCTGCGAGTTGT	0.468	

-	2	433	on_p.G80R|CSF1	NM_005211	NP_005202	P07333	CSF1R_HUMAN	1.|Extracellular (Potential).	54	GGTCCCCGTGT	0.612	
-	8	1034	lua.2_Missense_	NM_181776	NP_861441	Q495M3	S36A2_HUMAN	ical; (Potent p.G302V(1)	2	CATTCCCAAAG	0.453	
-	26	3239	.2_Missense_Mut	NM_003062	NP_003053	O75094	SLIT3_HUMAN	EGF-like 1.	4	CACAGCGGTAC	0.622	
+	2	397	99_uc011deq.1_5	NM_017785	NP_060255	Q96EA4	SPDLY_HUMAN	Potential.	2	AGAATCAATTG	0.413	
+	35	3589	CK2_uc010jjm.2_	NM_004946	NP_004937	Q92608	DOCK2_HUMAN	teraction with CRKL.	7	CAAGTCGGTGG	0.577	rs137955744
+	4	389	ndf.1_Missense_M	NM_006650	NP_006641	Q6PUV4	CPLX2_HUMAN		1	CAAAGGACATG	0.413	
+	4	1334	SD1_uc011dfx.1_	NM_022455	NP_071900	Q96L73	NSD1_HUMAN		3	CCTTAGGAGAA	0.418	
-	5	760	p.G196D|DOK3_u	NM_024872	NP_079148	Q7L591	DOK3_HUMAN	S-type PTB.	0	GGGTGCCCTTG	0.687	
+	8	1246	jll.2_3'UTR|BTNL	NM_001040462	NP_001035552	Q6UX41	BTNL8_HUMAN	.|Cytoplasmic (Potential).	2	TCCAAGCAGGG	0.507	
+	3	648		NM_197975	NP_932079	Q6UXE8	BTNL3_HUMAN	.|Extracellular (Potential).	0	GACAGGATTTG	0.502	
+	8	1245	p.2_Missense_Mu	NM_197975	NP_932079	Q6UXE8	BTNL3_HUMAN	.|Cytoplasmic (Potential).	0	TGTCTCCCAAC	0.498	
-	5	734	j.1_Missense_Mu	NM_006098	NP_006089	P63244	GBLP_HUMAN	WD 5.	0	GCCTCCAGAAG	0.512	
-	13	1483	_p.A450V|EXOC2_	NM_018303	NP_060773	Q96KP1	EXOC2_HUMAN		7	CAAAGGCCACC	0.428	
+	1	885	ua.2_Missense_	NM_020135	NP_064520	Q96S55	WRIP1_HUMAN		2	CGATGCGTCCT	0.547	
-	11	1776_1777	ba.2_Missense_	NM_005493	NP_005484	Q96S59	RANB9_HUMAN		2	TTTCTCCAACTC	0.356	
-	3	711	p.D171N|NUP153	NM_005124	NP_005115	P49790	NU153_HUMAN		9	TAGAATCTTTAA	0.398	
+	15	1712	.1_Missense_Mu	NM_017774	NP_060244	Q5VV42	CDKAL_HUMAN		2	CTCGGGTTTGA	0.453	
-	20	2045		NM_001503	NP_001494	P80108	PHLD_HUMAN	FG-GAP 5.	3	GTTTCCCCATT	0.493	
-	1	236	nk|HIST1H2AC_u	NM_003526	NP_003517	P62807	H2B1C_HUMAN		1	TGCGCTCAAATA	0.577	
-	1	233		NM_030876	NP_110503	Q9UGF6	OR5V1_HUMAN	lasmic (Potential).	4	ATCAGTCACAG	0.393	
-	3	199	se_Mutation_p.R1	NM_019052	NP_061925	Q8TD31	CCHCR_HUMAN		1	CATTCTTGGCA	0.547	
-	5	1046	dnk.1_RNA|HLA-	NM_005514	NP_005505	P01889	1B07_HUMAN	ical; (Potential).	0	TACACATCACA	0.597	
+	18	1739	H5_uc003nwx.1_	NM_172166	NP_751898	O43196	MSH5_HUMAN		3	AAGTCCTTGGG	0.572	
-	12	1907_1908	xd.2_Missense_M	NM_025258	NP_079534	Q9Y334	G7C_HUMAN		3	CTAGAGGACCC	0.584	
-	1	341	w.2_Missense_M	NM_002586	NP_002577	P40425	PBX2_HUMAN		1	AGGCTCCCCAC	0.592	
-	4	1457	318_uc003ouw.2_	NM_014345	NP_055160	Q5VUA4	ZN318_HUMAN		7	CTTTGGGAATC	0.478	
+	9	999	11_uc011dvn.1_5	NM_007058	NP_008989	Q9UMQ6	CAN11_HUMAN	lpain catalytic.	2	GGAATCCCTGG	0.597	
-	3	650	p.S158L|RCAN2_	NM_005822	NP_005813	Q14206	RCAN2_HUMAN		0	GGGGCGAGATG	0.532	
-	17	2787	oyp.3_Missense_	NM_001098518	NP_001091988	Q8IZF2	GP116_HUMAN	ellular (Potential).	2	CTTGGGAAAAT	0.463	
-	5	484		NM_145740	NP_665683	P08263	GSTA1_HUMAN	ST C-terminal.	1	TCTTTGATCAAG	0.398	
+	1	501	e_Mutation_p.G11	NM_014464	NP_055279	Q9UJW2	TINAG_HUMAN		4	CAGAAGGTAGG	0.353	
+	7	1671	k.2_Missense_Mu	NM_001704	NP_001695	O60242	BAI3_HUMAN	.|Extracellular (Potential).	50	GAGTTCGTGGA	0.527	
+	14	3788	e_Mutation_p.P88	NM_001162529	NP_001156001	Q9P2D6	F135A_HUMAN		1	AACTTCCTGGG	0.393	
+	19	4409	135A_uc003pfn.2_	NM_001162529	NP_001156001	Q9P2D6	F135A_HUMAN		1	AGGATCGCTAT	0.328	
-	51	8038	ht.2_Missense_M	NM_004370	NP_004361	Q99715	COCA1_HUMAN	l.|Nonhelical region (NC3).	9	TGTATCCTTGTTA	0.279	
-	5	3300	p.R877Q|FILIP1_	NM_015687	NP_056502	Q7Z7B0	FLIP1_HUMAN		4	TGGCTCGTTCT	0.443	
+	2	1331	bm.2_Missense_	NM_153362	NP_699193	Q8N3Z0	PRS35_HUMAN	eptidase S1.	1	CTGTTCGCATC	0.507	
+	15	2676	p.S809R|GRIK2_	NM_021956	NP_068775	Q13002	GRIK2_HUMAN	ellular (Potential).	5	GAGAGCAAAGA	0.483	
-	15	2148	_p.M606I|LAMA4_	NM_001105206	NP_001098676	Q16363	LAMA4_HUMAN	al.|Domain II and I.	9	CCCGTTCATATC	0.358	
-	30	5123	1_Intron|GOPC_u	NM_002944	NP_002935	P08922	ROS_HUMAN	III 7.|Extracellular (Potentia	25	CATTTCCTCAG	0.398	
-	14	3238	184A_uc003pyl.3_	NM_024581	NP_078857	Q8NB25	F184A_HUMAN		7	TTATTTCCTTGA	0.358	
-	2	232	nse_Mutation_p.R	NM_004665	NP_004656	O95498	VNN2_HUMAN	N hydrolase.	0	TGATTCGAGCA	0.448	
-	4	1101	.R281Q|BCLAF1_	NM_014739	NP_055554	Q9NYF8	BCLF1_HUMAN		1	CTGTATCGACTA	0.443	rs145724464
-	11	1526	v.2_Missense_Mu	NM_003980	NP_003971	Q14244	MAP7_HUMAN	Pro-rich.	0	atggctggagcAGC	0.214	
-	2	598	.H67Y|SHPRH_u	NM_001042683	NP_001036148	Q149N8	SHPRH_HUMAN		3	TCTGTGAGCCA	0.388	
-	3	652		NM_020861	NP_065912	Q8N680	ZBTB2_HUMAN		1	GGCCTCAGGGA	0.557	
+	13	4101	.P4_uc003qrg.2_I	NM_020245	NP_064630	Q9NRJ4	TULP4_HUMAN		1	GTACACCCTCC	0.662	

+	10	1394		NM_000876	NP_000867	P11717	MPRI_HUMAN	enal (Potential).|3.		3	TATTTTGGAGGT	0.423	
+	44	6746		NM_000876	NP_000867	P11717	MPRI_HUMAN	umenal (Potential).		3	CCCAACGATCAG	0.498	
-	30	4833		NM_005577	NP_005568	P08519	APOA_HUMAN	Kringle 36.		6	GTACTCCCACCT	0.493	
-	21	3334		NM_005577	NP_005568	P08519	APOA_HUMAN	Kringle 32.		6	TTCTTCCTGTGA	0.483	
+	10	1246		NM_000301	NP_000292	P00747	PLMN_HUMAN	Kringle 4.		4	ACCACAGGAAAG	0.488	
-	15	2490		NM_003247	NP_003238	P35442	TSP2_HUMAN	TSP type-3 2.		5	TCACACCGTCAT	0.562	
+	2	659	e_Mutation_p.P10	NM_133463	NP_597720	Q400G9	AMZ1_HUMAN			0	CTACAGCCGATA	0.642	
+	18	3226	e_Mutation_p.E64	NM_001007157	NP_001007158	O94880	PHF14_HUMAN			3	GAAGCTGAAAGA	0.274	
+	4	681	03ssh.2_Missense	NM_018374	NP_060844	Q9NUM4	T106B_HUMAN			0	GAAGAACGTAAG	0.279	
-	5	698	ug.2_Missense_M	NM_182762	NP_877439	Q6ZN28	MACC1_HUMAN			3	CTTGAGGAAGTC	0.383	
+	41	6681		NM_003777	NP_003768	Q96DT5	DYH11_HUMAN	2 (By similarity).		15	TGACAACAGATG	0.393	
+	5	1138	kwe.2_Missense_	NM_032222	NP_115598	Q4G0A6	F188B_HUMAN			0	GCCAGCCCGCAC	0.547	
+	11	2499	_p.M353I|CCDC12	NM_194300	NP_919276	Q6ZRS4	CC129_HUMAN			0	GTGATGGAGGA	0.537	
-	10	1458	_p.R390Q|PDE1C_	NM_005020	NP_005011	Q14123	PDE1C_HUMAN	ytic (By similarity).		4	AAGGTTCGAAAC	0.388	
+	10	1133		NM_133468	NP_597725	Q8N8U9	BMPER_HUMAN	VWFC 5.		3	CCATCAGTAGCT	0.483	
+	4	2353	_p.K691*|CDK13_	NM_003718	NP_003709	Q14004	CDK13_HUMAN			5	GAAACCAAAGAA	0.343	
+	2	91	_p.S31L|MRPS17	NM_182633	NP_872439	Q8N859	ZN713_HUMAN			2	AGGAATCACTGA	0.517	
-	5	1605		NM_033273	NP_150376	Q96JC4	ZN479_HUMAN	C2H2-type 10.		4	CTAAAGGCTTTG	0.443	
+	7	2086	te.2_Missense_M	NM_016220	NP_057304	Q9UII5	ZN107_HUMAN	C2H2-type 13.		1	AAAATTCATACTG	0.353	
-	14	1282	z.1_Missense_Mut	NM_005338	NP_005329	O00291	HIP1_HUMAN	otential.|pDED.		8	AGATCTGCTTCC	0.677	
-	2	1134	.1_Intron|CCDC14	NM_006682	NP_006673	Q14314	FGL2_HUMAN	nogen C-terminal.		2	GGATATCGATCA	0.398	
-	5	7208	_Mutation_p.E230	NM_033026	NP_149015	Q9Y6V0	PCLO_HUMAN			7	CAGTTTCCTTCT	0.418	
-	5	4875	v.2_Missense_Mut	NM_033026	NP_149015	Q9Y6V0	PCLO_HUMAN			7	GTTCTTCGTTTT	0.398	
-	22	3032	nc.1_Missense_M	NM_000927	NP_000918	P08183	MDR1_HUMAN	ne type-1 2.|Helical; (Poten		7	CAACTCCTGCTA	0.353	
-	16	2195	nc.1_Missense_M	NM_000927	NP_000918	P08183	MDR1_HUMAN	r 1.|Cytoplasmic (Potential)		7	CATTACGAACTG	0.393	rs28381914
+	14	2378	ZAN_uc003uwl.2_	NM_003386	NP_003377	Q9Y493	ZAN_HUMAN	ate) (mucin-like domain).|E		11	AAAAACCCACCA	0.522	
-	33	4973_4974	.2_Missense_Mut	NM_005045	NP_005036	P78509	RELN_HUMAN			19	GAAATCCAGTTT	0.411	
-	4	1349		NM_002711	NP_002702	Q16821	PPR3A_HUMAN		p.D440N(1)	34	CATTATCATCCAG	0.418	rs145814266
+	9	1536	OXP2_uc011kmv.1	NM_014491	NP_055306	O15409	FOXP2_HUMAN	eucine-zipper.		8	CAGGTGGTGCAA	0.408	
+	14	2219	nq.1_Missense_M	NM_000492	NP_000483	P13569	CFTR_HUMAN	lasmic (Potential).		5	GGGAAAAAAGGA	0.378	
-	13	1461	lks.2_Missense_M	NM_022444	NP_071889	Q9BZW2	S13A1_HUMAN	ical; (Potential).		2	ACCATCAAAGAA	0.363	
-	5	1827	vly.1_Missense_M	NM_176814	NP_789784	Q2TB10	ZN800_HUMAN	C2H2-type 6.		1	AAAGAGGACACT	0.358	
+	6	705	N33_uc003voq.1_	NM_178562	NP_848657	Q86UF1	TSN33_HUMAN	cellular (Potential).		1	GTGGAGGGATTT	0.512	
-	33	2983	vtu.2_Splice_Site_	NM_004717	NP_004708	O75912	DGKI_HUMAN			3	CACCCCTAAATC	0.572	
-	15	1860		NM_004333	NP_004324	P15056	BRAF_HUMAN	rotein kinas	_R603>I(2)|p.T	18290	GATTTCACTGTA	0.368	
-	14	1711_1712		NM_000420	NP_000411	P23276	KELL_HUMAN	cellular (Potential).		4	CTCGATCCAAGC	0.545	
+	1	757	uc003wda.2_Intro	NM_176883	NP_795364	P59536	T2R41_HUMAN	Name=6; (Potential).		2	ATCATTGATGCC	0.498	
+	1	1267		NM_001008747	NP_001008747	A4D2H0	A4D2H0_HUMAN			0	GAGAAGCTTTCT	0.378	
+	2	493	3wfn.2_Missense_	NM_003575	NP_003566	Q9UDV7	ZN282_HUMAN			0	ACAGCCGAGAAG	0.632	
-	2	965		NM_015694	NP_056509	Q9ULD5	ZN777_HUMAN			1	GGATCCAGAAAT	0.562	
+	1	566	C61_uc003wgx.2_	NM_138434	NP_612443	Q96FA7	CG029_HUMAN			1	TGGTCCGCGAG	0.632	
-	36	5881	kz.2_Missense_Mu	NM_170606	NP_733751	Q8NEZ4	MLL3_HUMAN	Pro-rich.		63	GTGAGTTAGAGG	0.527	
-	22	3673	kz.2_Missense_Mu	NM_170606	NP_733751	Q8NEZ4	MLL3_HUMAN			63	AAGATTCACAGC	0.269	
-	58	9334	e_Mutation_p.P23	NM_033225	NP_150094	Q96PZ7	CSMD1_HUMAN	ar (Potential).|Sushi 23.		25	TGCCAGGGTTGC	0.522	
-	28	4819	p.E869K|CSMD1_	NM_033225	NP_150094	Q96PZ7	CSMD1_HUMAN	lar (Potential).|CUB 9.		25	CACATTCCTTCC	0.458	
-	20	3332	p.S373F|CSMD1_	NM_033225	NP_150094	Q96PZ7	CSMD1_HUMAN	lar (Potential).|CUB 6.		25	CGTGGGAACTC	0.478	
+	24	2749	p.Y892D|XPO7_u	NM_015024	NP_055839	Q9UIA9	XPO7_HUMAN			5	CAGGATTACCCC	0.458	

-	10	1281		NM_003844	NP_003835	O00220	TR10A_HUMAN	nic (Potential).|Death.		6	GGCATCCCCTG	0.537	
+	6	619	ea.1_Missense_M	NM_003817	NP_003808	Q9H2U9	ADAM7_HUMAN	ellular (Potential).		5	ATTATTCCTGTAC	0.373	
+	3	2501	p.R605K|NEFM_u	NM_005382	NP_005373	P07197	NFM_HUMAN	Tail.		1	agtgggagggaagag	0.214	
+	3	756	HD2_uc003xlc.2_M	NM_015214	NP_056029	O94830	DDHD2_HUMAN			2	TATGTTCCCTACT	0.398	
-	2	461		NM_003068	NP_003059	O43623	SNAI2_HUMAN			2	CCACTGTGGTC	0.517	
-	17	3318	DNL_uc003xqt.3_F	NM_144651	NP_653252	A1KZ92	PXDNL_HUMAN			2	AAATTTCACCTA	0.473	
+	4	1262_1263	P1_uc011ldy.1_Intr	NM_006269	NP_006260	P56715	RP1_HUMAN			12	CAGGAAGAACAG	0.396	
+	4	3056	P1_uc011ldy.1_Intr	NM_006269	NP_006260	P56715	RP1_HUMAN			12	GTTATGGAAAGT	0.328	
+	4	6432	P1_uc011ldy.1_Intr	NM_006269	NP_006260	P56715	RP1_HUMAN			12	GTCATTACTTCTT	0.323	
-	4	1216		NM_004820	NP_004811	O75881	CP7B1_HUMAN			3	GATGGGAAATC	0.443	
-	1	292	_5'Flank|C8orf44_	NM_025054	NP_079330	Q96JH7	VCIP1_HUMAN	Pro-rich.		8	gcggcggcaacggag	0.527	
-	9	1280	A6_uc003xxr.3_Int	NM_020361	NP_065094	Q8N4T0	CBPA6_HUMAN			2	ATTGGGAATTG	0.378	rs140734555
+	26	3317		NM_024870	NP_079146	Q70Z35	PREX2_HUMAN			17	AAGATTCTGGTC	0.393	
-	6	732	h.1_Missense_Mu	NM_000971	NP_000962	P18124	RL7_HUMAN			0	GGTCCTCCCTG	0.433	
+	8	1009	ar.2_Missense_Mu	NM_004133	NP_004124	Q14541	HNF4G_HUMAN			1	TTTTTTGATCCAG	0.318	
-	5	833_834	_p.E93K|HEY1_uc	NM_012258	NP_036390	Q9Y5J3	HEY1_HUMAN			3	CGGTTCCGTGGG	0.713	
+	2	927		NM_173549	NP_775820	Q6P6B1	CH047_HUMAN	Glu-rich.		0	TAGAAAGAATTCC	0.433	
-	6	817	_Mutation_p.P254	NM_006281	NP_006272	Q13188	STK3_HUMAN	rotein kinase.		4	TCATTGGATGTA	0.348	
+	14	2460	lq.2_Missense_M	NM_014677	NP_055492	Q9UQ26	RIMS2_HUMAN			15	TTATAGGAAGGA	0.388	
+	28	4156	lq.2_Missense_Mu	NM_014677	NP_055492	Q9UQ26	RIMS2_HUMAN	C2 2.		15	CCGCATGGATCA	0.393	
-	10	924	ank|NRBP2_uc01	NM_178564	NP_848659	Q9NSY0	NRBP2_HUMAN	rotein kinase.		2	TGTGACCCGGG	0.647	
-	12	835	zkl.2_Missense_M	NM_002839	NP_002830	P23468	PTPRD_HUMAN	1.|Extracellular (Potential).		22	GAAAGAGGCAA	0.418	
-	8	1257	_p.L400F|MPDZ_	NM_003829	NP_003820	O75970	MPDZ_HUMAN	PDZ 3.		6	ATTACCCAATTT	0.303	
+	10	1439	_p.V383F|UNC13B	NM_006377	NP_006368	O14795	UN13B_HUMAN			5	CCAAGGTTCGA	0.433	
-	2	1376		NM_003028	NP_003019	Q15464	SHB_HUMAN	with LAT, FAK1, JAK1 and		3	GGGCTCCATGT	0.557	
+	1	526	42421_uc004aed.1_RNA							0	AGCCCAATCTG	0.607	rs141617852
+	6	1181	_p.P102L|CENPF	NM_001012267	NP_001012267	Q6IPU0	CENPP_HUMAN			2	CCGGCCAGGGT	0.567	
+	2	371		NM_001012994	NP_001013012	Q5VWJ9	SNX30_HUMAN			0	CCCTTCTCAAC	0.403	
-	1	779		NM_012363	NP_036495	Q8NGS0	OR1N1_HUMAN	ellular (Potential).		3	AGGGAGGACAC	0.527	
-	2	494		NM_005347	NP_005338	P11021	GRP78_HUMAN			4	CTTGGCGGCAT	0.607	
-	3	1359	PS1_uc011mac.1_	NM_012098	NP_036230	Q9UKU9	ANGL2_HUMAN	ogen C-terminal.		0	GGTGTCGTGGC	0.632	
+	8	1166	_p.A374V|SLC2A8	NM_014580	NP_055395	Q9NY64	GTR8_HUMAN	ame=10; (Potential).		2	GCTGGCCGTGG	0.701	
+	13	1160	e_Mutation_p.R27	NM_001005373	NP_001005373	Q6UWE0	LRSM1_HUMAN	Potential.		0	TGAACGGCGCC	0.582	
-	5	374	_p.S26L|C9orf78_	NM_016520	NP_057604	Q9NZ63	CI078_HUMAN			0	AAAACGATGTC	0.507	
-	5	668	mzn.2_Missense_	NM_005312	NP_005303	Q13905	RPGF1_HUMAN			7	GTCTTCTGAGT	0.557	
+	6	598	ez.2_Missense_Mu	NM_017588	NP_060058	P61964	WDR5_HUMAN	WD 3.		0	TCCAACCTTATT	0.473	
+	2	593		NM_000093	NP_000084	P20908	CO5A1_HUMAN	SP N-terminal.		11	AAGGCCCGGAT	0.557	
-	6	929		NM_017617	NP_060087	P46531	NOTC1_HUMAN	GF-like 8; c	p.G310R(1)	856	AGGTCCCGCCG	0.627	
-	2	1609	u.2_Missense_Mu	NM_173691	NP_775962	Q4KMQ1	TPRN_HUMAN	Glu-rich.		0	ctgctcTAGGGAG	0.348	
+	4	1016_1017	mg.1_Missense_	NM_006088	NP_006079	P68371	TBB2C_HUMAN			1	CGACCCCCGCC	0.604	
-	6	2812	ndi.2_Missense_	NM_181332	NP_851849	Q8N0W4	NLGNX_HUMAN	lasmic (Potential).		4	TGGGATGTCAT	0.557	
+	3	317		NM_016562	NP_057646	Q9NYK1	TLR7_HUMAN	lar (Potential).|LRR 1.		5	GAAATTCCTGGA	0.493	
+	2	769	se_Mutation_p.L18	NM_152634	NP_689847	Q8N8B7	TEANC_HUMAN	FIIS central.		1	TAGAGCTTCTTTA	0.428	
-	3	569		NM_030624	NP_085127	Q96M94	KLH15_HUMAN			2	CCTGAAGAATCT	0.388	
+	1	1487		NM_001136533	NP_001130005					2	GACACAGAAATA	0.448	
+	4	1179	p.E287K|MAGEB	NM_002363	NP_002354	P43366	MAGB1_HUMAN	MAGE.		0	TCCTCGAGTTT	0.512	
-	40	5918	Mutation_p.C176	NM_004006	NP_003997	P11532	DMD_HUMAN	ction with SYNM (By simila		6	CAAGCATTTCAG	0.383	

+	8	1437	rf22_uc010ngv.2_	NM_152632	NP_689845	Q6ZTR5	CX022_HUMAN		3	ATCCTGAAAAG	0.373	
+	1	281		NM_000531	NP_000522	P00480	OTC_HUMAN		2	ATGGTTCGAAAT	0.378	rs72552300
-	27	4003	ey.1_Missense_M	NM_004229	NP_004220	O60244	MED14_HUMAN		4	CATACTCTTGTT	0.343	
+	22	2876	_p.P832A|RBM10_	NM_005676	NP_005667	P98175	RBM10_HUMAN		5	CAGAGCCCAAG	0.612	
+	1	132_133	tron|LOC100133	NR_027444					0	TTGGCCTCACA	0.653	
+	6	822		NM_007137	NP_009068	P51508	ZNF81_HUMAN		0	TGAGTCGCACT	0.333	
-	41	4908	nip.2_Missense_M	NM_005183	NP_005174	O60840	CAC1F_HUMAN	lasmic (Potential).	6	AAGGGCGGAAG	0.512	
-	2	164		NM_198510	NP_940912	Q6UXX5	ITH5L_HUMAN	VIT.	6	CCACCGTGGAG	0.493	
+	3	582	H159Y|TRO_uc00	NM_001039705	NP_001034794	Q12816	TROP_HUMAN		1	CTGGCCATGAG	0.507	
-	1	999		NM_001012968	NP_001012986	Q56A73	SPIN4_HUMAN		2	GAACAGGATCT	0.448	
-	2	1620	g.2_Missense_Mu	NM_145119	NP_660095	Q8NG27	PJA1_HUMAN		0	GTTCTCGAACT	0.572	
+	8	1294	N1_uc011mpt.1_	NM_052957	NP_443189	Q96QF7	ACRC_HUMAN	sp/Ser-rich.	3	AAGCTCCCGAC	0.557	
-	3	1196		NM_001008537	NP_001008537	Q5QGS0	K2022_HUMAN		15	ATATTTCATATTT	0.453	
-	16	2144	_p.T681A|ABCB7	NM_004299	NP_004290	O75027	ABCB7_HUMAN		1	TCTGTGTATGCC	0.408	
+	1	392	_Mutation_p.H74	NM_053281	NP_444511	Q96NX9	DACH2_HUMAN	ACHbox-N.	5	ATGCACGGGAT	0.547	
-	3	1172		NM_080879	NP_543155	Q8WXH6	RB40A_HUMAN		0	CCTTAAGAAATT	0.483	
+	13	1481	c.1_Missense_Mu	NM_198465	NP_940867	Q7Z2Y5	NRK_HUMAN		14	GCCAAGGTGGC	0.557	
+	32	2967	_p.K922I|COL4A5	NM_033380	NP_203699	P29400	CO4A5_HUMAN	le-helical region.	4	GTCTTAAAGGTA	0.408	
+	13	1753		NM_007231	NP_009162	Q9UN76	S6A14_HUMAN		3	TTCATAGACCTA	0.358	
-	11	1931		NM_020721	NP_065772	Q9ULL0	K1210_HUMAN		5	CCATGGAATTG	0.458	
-	10	1456		NM_020721	NP_065772	Q9ULL0	K1210_HUMAN		5	TCTTTTCGTTGA	0.433	
-	16	1707	uh.1_Missense_M	NM_001081550	NP_001075019	Q8NI27	THOC2_HUMAN		3	ATTTTCCTTGG	0.388	
-	31	8096	.E2684K|ODZ1_u	NM_014253	NP_055068	Q9UKZ4	TEN1_HUMAN	ellular (Potential).	23	CCCTTCTGTCC	0.517	
-	6	2931	vf.1_Missense_M	NM_031907	NP_114113	Q9BXU7	UBP26_HUMAN		8	TATGATCTCCCT	0.383	
-	6	2929	vf.1_Missense_M	NM_031907	NP_114113	Q9BXU7	UBP26_HUMAN		8	TGATCTCCCTTA	0.383	
+	6	5036	.S1377F|GPR112	NM_153834	NP_722576	Q8IZF6	GP112_HUMAN	ellular (Potential).	12	CACTTCCACAA	0.428	
-	14	1540	P11C_uc004fba.2_	NM_173694	NP_775965	Q8NB49	AT11C_HUMAN	lasmic (Potential).	8	AGCATCGTTTG	0.353	
+	4	1679	EC1_uc010nsl.1_	NM_005462	NP_005453	O60732	MAGC1_HUMAN		4	CTGAGAGAACT	0.478	
+	4	1681	EC1_uc010nsl.1_	NM_005462	NP_005453	O60732	MAGC1_HUMAN		4	TGAGAGAACTCA	0.483	
+	2	124		NM_001009614	NP_001009614	Q5VSR9	SPXN1_HUMAN		0	TTGAAAAAGATG	0.408	
-	3	913	.D187N|CSAG1_	NM_005367	NP_005358	P43365	MAGAC_HUMAN	MAGE.	1	GCCATCGTAGG	0.582	
+	9	813	p.G218S|SRPK3_	NM_014370	NP_055185	Q9UPE1	SRPK3_HUMAN	rotein kinase.	3	AGACCGGTAAG	0.627	
-	9	998	p.R265C|MPP1_u	NM_002436	NP_002427	Q00013	EM55_HUMAN	-like.|Interaction with MPP	3	GCTGCGACCCA	0.527	
-	2	680		NM_171998	NP_741995	Q96DA2	RB39B_HUMAN		0	GGCGAGTCACT	0.498	
-	39	5751	_Mutation_p.R74	NM_015557	NP_056372	Q8TDI0	CHD5_HUMAN		12	GGATGCGGGAC	0.647	
+	3	509	nv.2_Intron|TAS1	NM_138697	NP_619642	Q7RTX1	TS1R1_HUMAN	ellular (Potential).	3	CTATGCGGCCA	0.378	
-	9	1151	i.1_Missense_Mu	NM_001428	NP_001419	P06733	ENOA_HUMAN		4	CTTCTCGTTCA	0.572	
+	27	6673	13D_uc001atx.2_	NM_015378	NP_056193	Q5THJ4	VP13D_HUMAN		5	CGAAGGCACCA	0.502	
-	3	415	ca.1_Missense_M	NM_004431	NP_004422	P29317	EPHA2_HUMAN	ellular (Potential).	10	AGATACGCTCA	0.542	
-	8	956	1_Intron|MST1P9_	NR_002729					0	CGTCGAGGTTC	0.667	rs1057378
-	14	1741	_p.V429I|ALDH4A	NM_170726	NP_733844	P30038	AL4A1_HUMAN		0	CACGACGTCCC	0.458	rs150916561
-	39	4949	d.2_Missense_Mu	NM_005529	NP_005520	P98160	PGBM_HUMAN	inin EGF-like 11.	9	GCAGCGGTACC	0.597	rs142149919
-	2	1042		NM_152365	NP_689578	Q8NAX2	CA172_HUMAN		2	AACGACCCTCC	0.642	
+	4	945	B2_uc001bzd.1_I	NM_178548	NP_848643	Q6VUC0	AP2E_HUMAN		0	ACTCTCGCCTC	0.642	
+	1	4631	.1_Intron|MACF1_	NM_015038	NP_055853	O94854	K0754_HUMAN	Ala-rich.	0	CAACCTAGAGG	0.667	
+	1	4642	.1_Intron|MACF1_	NM_015038	NP_055853	O94854	K0754_HUMAN	Ala-rich.	0	AGCCCGCCTCC	0.672	
+	9	1238	ym.2_Missense_M	NM_000779	NP_000770	P13584	CP4B1_HUMAN		2	GTACCGCCAGC	0.572	

+	2	416	_p.V67I|ELAVL4_	NM_021952	NP_068771	P26378	ELAV4_HUMAN	RRM 1.	2	CTCATCGTCAAC	0.448	rs116391279
-	2	548	105L|ZCCHC11_	NM_015269	NP_056084	Q5TAX3	TUT4_HUMAN		3	TCACCGGTGAA	0.403	
-	4	2334	_p.R25C|KANK4_	NM_181712	NP_859063	Q5T7N3	KANK4_HUMAN		6	TGCACGGAAGC	0.468	rs139344628
-	14	2230	_Mutation_p.V64	NM_002227	NP_002218	P23458	JAK1_HUMAN	otein kinase 1.	61	CTCCACGTCGC	0.592	
+	2	344	se_Mutation_p.H6	NM_152996	NP_694541	Q8NDV1	SIA7C_HUMAN	enal (Potential).	5	GAACTCACTAT	0.438	
+	22	7065		NM_001408	NP_001399	Q9HCU4	CELR2_HUMAN	ular (Potential).|GPS.	8	CTGGTCGGCCA	0.617	
-	3	192	A5_uc010ovj.1_5'	NM_002790	NP_002781	P28066	PSA5_HUMAN		0	TGGCTGTAGAA	0.418	
+	7	990	ense_Mutation_p.	NM_004425	NP_004416	Q16610	ECM1_HUMAN	roximate repeats.|1.	3	GGGGGAGGCTC	0.632	
-	3	5928	uc001ezv.2_Intron	NM_001014342	NP_001014364	Q5D862	FILA2_HUMAN	Filaggrin 8.	17	CAGATCCCCTT	0.527	
+	8	947_948	_Missense_Mutat	NM_023015	NP_075391	Q68E01	INT3_HUMAN		3	GGGAACGGGTG	0.515	
-	6	1289	MUC1_uc001fin.2_Missense_Mutation_p.R104W|MUC			P15941	MUC1_HUMAN	tential).|Interaction with P5	4	ATCCCGGGCTG	0.587	
-	1	437	S59L|C1orf66_uc0	NM_030980	NP_112242	Q9H9L3	I20L2_HUMAN		2	TCTTTGAAGGT	0.507	
+	1	68		NM_001004473	NP_001004473	Q8NGX5	O10K1_HUMAN	ellular (Potential).	1	CAGGCTGCAGC	0.512	
-	24	3672		NM_003126	NP_003117	P02549	SPTA1_HUMAN	Spectrin 11.	8	CCTGCCGGATT	0.463	
+	2	506	tp.3_Missense_Mu	NM_002036	NP_002027	Q16570	DUFFY_HUMAN	lasmic (Potential).	2	CTTCCGCTGGC	0.602	
-	2	301_302	Site_p.G66_splice	NM_000567	NP_000558	P02741	CRP_HUMAN	Pentaxin.	1	TGTACCCACGG	0.455	
+	12	1792	c001fym.2_5'Flan	NM_001014443	NP_001014443	Q9UK80	UBP21_HUMAN		5	AGGCTCCATCA	0.517	
+	6	650	10ppg.1_Missense	NM_002838	NP_002829	P08575	PTPRC_HUMAN	ellular (Potential).	12	CTTTCCTACAG	0.552	
+	15	2234	97L|PPP1R12B_u	NM_002481	NP_002472	O60237	MYPT2_HUMAN		3	AGTTCCAGCAA	0.582	
+	20	3030	_p.S805*|ZC3H11	NM_014827	NP_055642	O75152	ZC11A_HUMAN		2	AGCTATCAGAAA	0.378	
+	16	2119	0pyl.1_Missense_	NM_006642	NP_006633	Q86SQ7	SDCG8_HUMAN	otential.|Sufficient for hom	0	GGAGAGTACAT	0.408	
-	2	245	C_uc009xhk.1_5'	NM_014974	NP_055789	Q9Y2E4	DIP2C_HUMAN		7	TACTCGGAGGC	0.478	
-	4	288	_p.E42K|A1CF_uc	NM_138932	NP_620310	Q9NQ94	A1CF_HUMAN		1	ATTTTCCTGCA	0.413	
-	7	1082	_p.T320M|CTNNA	NM_001127384	NP_001120856	Q9UI47	CTNA3_HUMAN		8	CCCTCGTACAT	0.502	rs139460414
+	3	456		NM_012339	NP_036471	O95858	TSN15_HUMAN	ical; (Potential).	0	GTGGCGTGGTG	0.388	rs150067289
-	16	3510	_p.P562L|DLG5_u	NM_004747	NP_004738	Q8TDM6	DLG5_HUMAN		8	GCTCCGGGGAG	0.557	
-	42	4760	_Mutation_p.P15	NM_013451	NP_038479	Q9NZM1	MYOF_HUMAN	mic (Potential).|C2 5.	4	TGTCAGGTAAT	0.552	
-	1	2175		NR_002319					0	CCAGTGTCTGG	0.537	
-	4	517	se_Mutation_p.R1	NM_022362	NP_071757	Q96T76	MMS19_HUMAN		0	CAGCCGGTTCT	0.463	rs29001280
-	9	2959	nse_Mutation_p.A	NM_015221	NP_056036	Q6XZF7	DNMBP_HUMAN	DH.	6	TGACCGCAAGG	0.443	
-	8	2130	.2_Missense_Mut	NM_013274	NP_037406	Q9UGP5	DPOLL_HUMAN		0	GGAACCCTGGC	0.607	
-	2	210	C2_uc001kvm.2_	NM_024040	NP_076945	Q9H467	CUED2_HUMAN		0	CCTCCGGGAGG	0.602	
-	1	441	C2_uc009xxx.2_I	NR_026715					0	CCAGGTGCCCC	0.537	
+	4	1204	se_Mutation_p.A	NM_206862	NP_996744	O95359	TACC2_HUMAN		10	ATCCAGCCCCA	0.602	
-	5	1030	10qty.1_Intron|CU	NM_022034	NP_071317	Q86UP6	CUZD1_HUMAN	lar (Potential).|CUB 2.	2	TGGGAGTCACA	0.453	
+	18	2788		NM_178537	NP_848632	Q76KP1	B4GN4_HUMAN	enal (Potential).	1	TGGACGGCATC	0.711	
-	2	1538	sense_Mutation_p	NM_203389	NP_976323	P13489	RINI_HUMAN	LRR 1.	0	GCACCGTGCTT	0.632	rs149360262
-	30	4076		NM_005961	NP_005952	Q6W4X9	MUC6_HUMAN	-rich.|Thr-rich.	1	GCAGCGTGGGG	0.612	
-	29	3697		NM_005961	NP_005952	Q6W4X9	MUC6_HUMAN		1	GGGCCGTGAGC	0.672	
+	51	14903	b.2_Missense_Mu	NM_017511	NP_059981	Q9HC84	MUC5B_HUMAN	em repeats, Ser/Thr- rich.|	0	AGAGCCGAGCA	0.662	
+	51	14906	b.2_Missense_Mu	NM_017511	NP_059981	Q9HC84	MUC5B_HUMAN	em repeats, Ser/Thr- rich.|	0	GCCGAGCACTA	0.662	
+	52	15536	b.2_Missense_Mu	NM_017511	NP_059981	Q9HC84	MUC5B_HUMAN	em repeats, Ser/Thr- rich.|	0	GGGGACGACCC	0.622	
-	1	626	2_uc001mak.1_I	NM_145053	NP_659490	Q8IYU4	UBQLN_HUMAN		3	GGTCCCGGAAG	0.542	
+	1	277	5_uc001mbq.1_I	NM_001005165	NP_001005165	Q8NGH9	O52E4_HUMAN	ellular (Potential).	2	TCCAAGAGATC	0.463	
-	6	932	PPED2_uc009yji.	NM_001584	NP_001575	Q15777	MPPD2_HUMAN		1	ACGTCGAGGCA	0.448	
+	7	1533	go.3_Missense_M	NM_002843	NP_002834	Q12913	PTPRJ_HUMAN	tential).|Fibronectin type-III	8	CGAGTCGTCAT	0.512	
-	14	1144	obi.2_Missense_M	NM_004579	NP_004570	Q12851	M4K2_HUMAN		2	TCACCGGCTCA	0.602	

-	4	758	nk.2_Missense_Mu	NM_001277	NP_001268	P35790	CHKA_HUMAN		2	ACATAACGCTCT	0.393	rs143460799
+	62	9311	1_Intron|C11orf65	NM_000051	NP_000042	Q13315	ATM_HUMAN		240	CCGGAAGATGAA	0.403	
-	6	3093	al.2_Missense_Mu	NM_182557	NP_872363	Q86UU0	BCL9L_HUMAN	Met-rich.	2	TCATCCGCTCCA	0.657	
-	10	1571	p.R404C|KIRREL	NM_032531	NP_115920	Q8IZU9	KIRR3_HUMAN	otential).|Ig-like C2-type 4.	3	CACACGGGGCA	0.632	
+	24	6250	.P1667S|WNK1_	NM_018979	NP_061852	Q9H4A3	WNK1_HUMAN		23	ACCATCCCTGGT	0.498	
-	3	552	_5'Flank|NCAPD2_	NM_016497	NP_057581	Q4U2R6	RM51_HUMAN		0	TTCTATCGAAAC	0.433	
+	7	1347	3_uc001qrs.2_Intr	NM_001135217	NP_001128689	Q53EV4	LRC23_HUMAN	Potential.	1	TGATTCGACAG	0.547	
+	12	1635		NM_006446	NP_006437	Q9Y6L6	SO1B1_HUMAN	cellular (Potential).	8	GTAACTGGTCTC	0.363	
-	53	7882	g.1_Missense_Mu	NM_002223	NP_002214	Q14571	ITPR2_HUMAN	cellular (Pote p.V2489G(1)	14	CAGCACGGTGA	0.413	
+	5	751	_Mutation_p.R167	NM_152438	NP_689651	Q96FC9	DDX11_HUMAN	Helicase ATP-binding.	3	AGAAAGAGAGA	0.612	
+	26	2889	.1_Missense_Muta	NM_152438	NP_689651	Q96FC9	DDX11_HUMAN		3	GCCCGTGTGGA	0.597	
-	4	583	e_Mutation_p.K17	NM_004719	NP_004710	Q99590	SCAFB_HUMAN		0	CTTACCTTAACA	0.299	
+	11	2257	mj.1_Missense_Mu	NM_012284	NP_036416	Q9ULD8	KCNH3_HUMAN	toplasmic (Potential).	0	GCTGACGTACT	0.662	
+	34	4204	lt.2_Missense_Mu	NM_173602	NP_775873	Q9P265	DIP2B_HUMAN		6	GGGTTCGTCTC	0.502	
+	3	997	1_uc009zmb.1_M	NM_002135	NP_002126	P22736	NR4A1_HUMAN		0	GCCTACGGCCT	0.667	rs150018506
-	8	1392		NM_175068	NP_778238	Q86Y46	K2C73_HUMAN	Tail.	6	GCTCACGGAGT	0.507	rs145362309
+	3	314	CKAP1L_uc010sc	NM_005337	NP_005328	P55160	NCKPL_HUMAN		4	TACATCGTGAA	0.378	
+	20	2171	p.V240M|NCKAP1	NM_005337	NP_005328	P55160	NCKPL_HUMAN		4	TTCTCCGTGTTT	0.453	
+	1	209		NM_001005182	NP_001005182	Q96RD1	OR6C1_HUMAN	Name=2; (Potential).	2	AATTTCGTTCA	0.378	
-	24	5077	.G434D|BAZ2A_	NM_013449	NP_038477	Q9UIF9	BAZ2A_HUMAN		0	TGGTGCCCTCA	0.547	
+	11	1293	1snj.1_Missense_	NM_005412	NP_005403	P34897	GLYM_HUMAN		2	AGGGGCCCCAG	0.557	
-	10	1670		NM_020700	NP_065751	Q9ULR3	PPM1H_HUMAN	PP2C-like.	4	ATGTATTAAAGG	0.527	
+	2	397		NM_032230	NP_115606	Q8N6Q8	CL026_HUMAN		0	CTCCTTTTGAA	0.378	
-	16	1991	p.P501L|CDK17_	NM_002595	NP_002586	Q00537	CDK17_HUMAN		7	AACCCGGGTCC	0.353	
-	26	3086		NM_006836	NP_006827	Q92616	GCN1L_HUMAN		4	CCGCCCGGGTG	0.602	
-	2	304	2B_uc001uau.2_5	NM_032590	NP_115979	Q8NHM5	KDM2B_HUMAN		2	TGAAGCCGCGG	0.672	
-	4	578	p.P154L|NCOR2_	NM_001077261	NP_001070729	Q9Y618	NCOR2_HUMAN		4	TGTGCGGGGGG	0.642	
+	1	132	_p.N33H|EP400_	NM_015409	NP_056224	Q96L91	EP400_HUMAN		12	ACCCCAACCCA	0.657	
-	14	1970		NM_175066	NP_778236	Q8N8A6	DDX51_HUMAN		2	ACCGAGGAACC	0.617	
+	3	862	PH8_uc001umg.	NM_017520	NP_059990	Q99549	MPP8_HUMAN		0	ATTCCGACAGC	0.443	
+	4	925		NM_206827	NP_996563	Q6T310	RSLBA_HUMAN	all GTPase-like.	1	AATGCGTGCAG	0.517	
-	4	365	e_Mutation_p.M1	NM_001010875	NP_001010875	Q5SVS4	KMCP1_HUMAN	e=2; (Potential).|Solcar 1.	1	CGTAACATCGC	0.478	
+	19	2171	1A_uc001vsm.1_	NM_015205	NP_056020	P98196	AT11A_HUMAN	lasmic (Potential).	4	CGGCCGCGGC	0.622	rs146012121
+	12	1625	p.E482Q|MCF2L_	NM_001112732	NP_001106203	O15068	MCF2L_HUMAN	Potential.	2	GGTGCGGAAAA	0.532	
-	1	265	4P_uc001vwb.3_	NM_001145442	NP_001138914	A6NI47	POTEM_HUMAN		0	CTGCACCAGGG	0.587	
-	1	260	4P_uc001vwb.3_	NM_001145442	NP_001138914	A6NI47	POTEM_HUMAN		0	CCAGGGGAAGC	0.592	
-	33	4896		NM_002471	NP_002462	P13533	MYH6_HUMAN	Potential.	4	CGTTGCGGCTG	0.607	
+	11	1107	sense_Mutation_	NM_004086	NP_004077	O43405	COCH_HUMAN	VWFA 1.	3	AAATACGTAAAG	0.438	
-	13	1904	se_Mutation_p.P4	NM_001083893	NP_001077362	Q13033	STRN3_HUMAN	WD 2.	0	GGACTCGGCATA	0.368	
-	6	1492		NM_015382	NP_056197	Q9ULT8	HECD1_HUMAN		5	CTTTTCGTCCTT	0.458	
+	2	134	xsg.2_Missense_	NM_001102564	NP_001096034	Q96FT9	IFT43_HUMAN		0	AGGCCGAGAAT	0.473	rs140366557
+	9	1738	e_Mutation_p.F53	NM_014844	NP_055659	O15040	TCPR2_HUMAN		3	AGCTTCAATGG	0.512	
-	8	1296		NM_006035	NP_006026	Q9Y5S2	MRCKB_HUMAN	kinase C-terminal.	11	AAGGTGCTTCTA	0.463	
-	4	807	T1_uc001ypm.2_	NM_005163	NP_005154	P31749	AKT1_HUMAN	PH.	134	GCGTTCGATGA	0.657	
-	7	1676	px.2_Missense_	NM_138420	NP_612429	Q8IVF2	AHNK2_HUMAN		1	AGGACGCATCC	0.537	
+	8	945	qv.2_Missense_Mu	NM_015197	NP_056012	Q86VP3	PACS2_HUMAN		1	GGTAGCGCTGC	0.657	
-	1363								0	CGTGCTCAGTG	0.647	rs76812739

-	80	12471		NM_004667	NP_004658	O95714	HERC2_HUMAN	RCC1 16.	13	CCAGCCGGCCG	0.647	
+	3	915	_p.T282A|C15orf5	NM_175741	NP_786883	Q86Y26	NUT_HUMAN		30	AGCCCACTATG	0.547	
-	17	1707		NM_014691	NP_055506	O60306	AQR_HUMAN		1	CCATTCGCGCC	0.443	
+	8	1207	cl.1_Missense_Mu	NM_001211	NP_001202	O60566	BUB1B_HUMAN		4	GATAGCTGTAC	0.418	
-	2	330	3_uc002ayv.2_Mi	NM_001099436	NP_001092906	Q6PHR2	ULK3_HUMAN	rotein kinase.	2	GCTGCACAATG	0.552	
+	4	496	bmt.1_Missense_	NM_207517	NP_997400	P82987	ATL3_HUMAN	SP type-1 1.	27	GACCTGTGGGG	0.512	
-	21	3725	r.3_Missense_Mut	NM_002693	NP_002684	P54098	DPOG1_HUMAN		2	CAGCGCGGTAG	0.602	rs145004638
-	18	3110	r.3_Missense_Mu	NM_002693	NP_002684	P54098	DPOG1_HUMAN		2	GCTCACGGCTG	0.557	
-	6	538	ense_Mutation_p.	NM_001077350	NP_001070818	Q12980	NPRL3_HUMAN		1	ACGACGGGACA	0.607	
-	3	202		NM_001025190	NP_001020361	Q96KJ4	MSLNL_HUMAN		4	ACGGGTAGGTG	0.592	
-	5	985	010uus.1_5'Flank|	NM_058192	NP_478072	Q9UJJ7	RUSD1_HUMAN		0	CTGCACGAGCT	0.721	
-	2	451		NM_001013658	NP_001013680	Q96A99	PTX4_HUMAN		0	CAGGCGTGCCA	0.741	
-	8	1458	_p.P249L|ABCA3_	NM_001089	NP_001080	Q99758	ABCA3_HUMAN		16	TGAACGGCGGG	0.627	
+	1	990	2_5'Flank|TBC1D2	NM_006181	NP_006172	O00634	NET3_HUMAN	inin EGF-like 1.	1	CCTCACGGTGC	0.672	
-	14	1395	407_splice|CORO	NM_024535	NP_078811	P57737	CORO7_HUMAN		0	TACTTACGCTTG	0.587	
+	12	1094	h.2_Missense_Mu	NM_020686	NP_065737	P80404	GABT_HUMAN		1	TCTTTCGGAAG	0.557	
-	5	1157	_p.S343L|UMOD_	NM_003361	NP_003352	P07911	UROM_HUMAN	ZP.	2	CCAGCGACACC	0.552	
+	17	3613	e_Mutation_p.E82	NM_006910	NP_008841	Q7Z6E9	RBBP6_HUMAN		4	ATAGAGAGAACT	0.428	
+	11	2500	y.2_Missense_Mu	NM_000418	NP_000409	P24394	IL4RA_HUMAN	lasmic (Potential).	2	GTCCTCGCCCC	0.662	
+	4	2329		NM_003414	NP_003405	Q14586	ZN267_HUMAN	2H2-type 14.	4	ACATCGGAGAA	0.433	rs146914846
+	4	2341		NM_003414	NP_003405	Q14586	ZN267_HUMAN		4	TCATAGTGGAG	0.418	
-	5	440	A10P_uc002edi.1_RNA						0	GTGTTTTTGTA	0.512	
-	6	3854	n.1_Missense_Mu	NM_015069	NP_055884	Q2M1K9	ZN423_HUMAN	2H2-type 27.	4	AACGTGGATTT	0.423	
+	4	1271	c010cbm.1_Misse	NM_022162	NP_071445	Q9HC29	NOD2_HUMAN	NACHT.	4	GTTCACGGATC	0.547	
+	4	473	.2_5'UTR|NUP93_	NM_014669	NP_055484	Q8N1F7	NUP93_HUMAN		2	AGTCCCGGAAG	0.308	
-	5	678	q.2_Intron|NQO1_	NM_000903	NP_000894	P15559	NQO1_HUMAN		0	GTCCCCGTGGA	0.333	
+	8	1179	.M239V|WWOX_u	NM_016373	NP_057457	Q9NZC7	WWOX_HUMAN	ith MAPT (By similarity).	0	AGTCCATGGTA	0.517	
-	29	4861	1L2_uc002fgg.1_	NM_052892	NP_443124	Q7Z442	PK1L2_HUMAN	lasmic (Potential).	3	GACCCGGGGAC	0.587	
+	9	1583		NM_022041	NP_071324	Q9H2C0	GAN_HUMAN	Kelch 5.	2	GAAGTCGTGAG	0.498	
+	3	393	chl.2_Missense_M	NM_024731	NP_079007	Q8N4N3	KLH36_HUMAN	BTB.	2	TTCCAGAAGGA	0.612	
-	9	1179	jf.2_Intron|PRDM	NM_001098173	NP_001091643	Q9NQW5	PRDM7_HUMAN		1	CCCCATACCAG	0.522	
-	2	765	d.1_Missense_Mu	NM_017575	NP_060045	Q86US8	EST1A_HUMAN	n with telomeric DNA.	4	CCGGCCTCCCG	0.627	
-	23	3316	.R1094Q|ANKFY1_	NM_016376	NP_057460	Q9P2R3	ANFY1_HUMAN		3	GCAGTCGGAAC	0.562	
+	8	1523	he.2_Missense_M	NM_000937	NP_000928	P24928	RPB1_HUMAN		1	CTTGCGTTTCC	0.552	
-	8	993	n_p.R135G|TP53_	NM_001126112	NP_001119584	P04637	P53_HUMAN	K1 (By simil.GRNS(2)|p.G	22245	GTTCCGTCCCA	0.522	rs55832599
+	6	1222	LK_uc010cri.1_R	NM_016231	NP_057315	Q9UBE8	NLK_HUMAN	rotein kinase.	3	TAGGACGAAGAA	0.413	
-	7	877	_p.R58Q|CORO6_	NM_032854	NP_116243	Q6QEF8	CORO6_HUMAN	WD 5.	0	AGTACCGAATG	0.607	
+	3	230	_p.G73R|MLLT6_	NM_005937	NP_005928	P55198	AF17_HUMAN		6	AAGACGGGGCA	0.597	
-	5	926		NM_181535	NP_853513	Q7Z3Y7	K1C28_HUMAN	Rod.|Coil 2.	1	GCAGCGAGGCG	0.652	
-	1	296_297		NM_033059	NP_149048	Q9BYQ6	KR411_HUMAN	C-[GIKRQVHEL]- [SPTR]-[	0	TGGGGCTTGCA	0.446	375721;rs425755
-	2	1043	_p.R215W|HOXB	NM_002146	NP_002137	P14651	HXB3_HUMAN	Homeobox.	0	AGGCCGGCACA	0.632	
-	5	639		NM_018509	NP_060979	Q96AG4	LRC59_HUMAN	ytoplasmic (Potential).	1	CCAGCCGCCGC	0.532	
-	8	3841	_p.A629T|RNF43_	NM_017763	NP_060233	Q68DV7	RNF43_HUMAN	ytoplasmic (Potential).	1	GGAGGCGTCAA	0.632	
+	4	2468	p.S623N|TNRC6C	NM_018996	NP_061869	Q9HCJ0	TNR6C_HUMAN	on with argonaute family pr	2	TGACAGTAATA	0.532	
+	30	4379	_p.V1034I|RPTO	NM_020761	NP_065812	Q8N122	RPTOR_HUMAN	WD 4.	6	TCCGCGTCTAC	0.617	
+	3	569		NM_032048	NP_114437	Q9BXX0	EMIL2_HUMAN		3	GCCTCGAAACA	0.512	rs147386217
-	1	458	DLGAP1_uc002kn	NM_004746	NP_004737	O14490	DLGP1_HUMAN		4	GCTGCGGTGCT	0.677	

+	19	3394	192_uc002kru.2_F	NM_032142	NP_115518	E9PF99	E9PF99_HUMAN		5	CATTATCATCTAT	0.373	
+	7	716	L3_uc002kxq.2_5'	NM_030632	NP_085135	Q9C0F0	ASXL3_HUMAN		3	AATCTCCCACT	0.318	
-	2	1410	p.R474H|ZBTB7C_	NM_001039360	NP_001034449	A1YPR0	ZBT7C_HUMAN	ype 4; degenerate.	1	TGTGGCGGTGC	0.607	rs141739519
-	10	1423	ec.1_Missense_M	NM_001080467	NP_001073936	Q9ULV0	MYO5B_HUMAN	osin head-like.	5	CTTGCGATGAC	0.577	
+	13	2986	1_3'UTR|CTDP1_	NM_004715	NP_004706	Q9Y5B0	CTDP1_HUMAN		0	AGGCCGACGAG	0.652	
+	4	452	wq.2_Missense_M	NM_024967	NP_079243	Q9HAH1	ZN556_HUMAN		3	TAAACGTGGAA	0.373	
+	14	1775	j.1_RNA|NCLN_u	NM_020170	NP_064555	Q969V3	NCLN_HUMAN	ical; (Potential).	0	CCTACGTGGCT	0.672	
-	10	998	p.P301S|STAP2_	NM_001013841	NP_001013863	Q9UGK3	STAP2_HUMAN	Pro-rich.	1	TGGGGGCAGTG	0.597	rs139216713
-	3	2836	N4_uc010dub.1_5'	NM_001080400	NP_001073869	Q96Q06	PLIN4_HUMAN	roximate tandem repeat.|26	0	CTTAGCGCCAC	0.592	
+	7	1026	mgu.3_Missense_	NM_020902	NP_065953	Q9P1Y5	CAMP3_HUMAN	CH.	1	TGGCCGAGTTG	0.662	
-	5	36092		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).	57	TTGGACTCACT	0.478	
-	1	7184		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	h.|Extracellular (Potential).	57	TGGGGGAAGTG	0.473	
-	4	725	709_uc002mtx.3_	NM_144976	NP_659413	Q8TBZ8	ZN564_HUMAN	2H2-type 3.	1	ATTCCGGACAT	0.433	
-	3	590	nse_Mutation_p.T	NM_032301	NP_115677	Q5XUX1	FBXW9_HUMAN	WD 1.	1	ACTCCGTCCCC	0.557	
+	8	2081	p.E617K|SYDE1_	NM_033025	NP_149014	Q6ZW31	SYDE1_HUMAN		2	ACAGCGAGGAC	0.642	
-	10	1285	p.G29E|ILVBL_uc	NM_006844	NP_006835	A1L0T0	ILVBL_HUMAN		2	GGCTTCCAGAA	0.557	
+	3	468		NM_024074	NP_076979	Q9H6F2	TM38A_HUMAN	lasmic (Potential).	3	GGTGCGAGTCC	0.527	
+	12	1636	se_Mutation_p.A2	NM_173544	NP_775815	Q86XR2	NIBL2_HUMAN		0	ACCAGGCTGCC	0.637	
-	4	827	pc.1_Missense_M	NM_001076675	NP_001070143	Q68DY1	ZN626_HUMAN		1	GGTTTCTCTCCA	0.393	
+	2	903	_p.P336L|ZNF493_	NM_175910	NP_787106	Q6ZR52	ZN493_HUMAN	ype 7; degenerate.	1	AACCCCTACTA	0.348	rs142651314
-	4	1111	rj.1_Missense_Mu	NM_003430	NP_003421	Q05481	ZNF91_HUMAN	2H2-type 7.	0	AAGAACGGCTA	0.393	rs410211
+	14	1298		NM_015302	NP_056117	O94927	HAUS5_HUMAN		0	GTGCCGGAGCC	0.632	
-	2	233	u.1_Missense_M	NM_172139	NP_742151	Q8IZI9	IL28B_HUMAN		0	CCTGGGGAAGA	0.637	
-	5	1534	mv.2_Missense_	NM_001005851	NP_001005851	Q9Y6R6	Z780B_HUMAN	2H2-type 12.	2	TATGTCGAGCA	0.408	
+	5	1053	2F1_uc010xvw.1_	NM_052848	NP_443080	Q96F63	CCD97_HUMAN		0	ACCCCGACTTC	0.612	
-	4	842	g.1_Intron|PSG3_	NM_021016	NP_066296	Q16557	PSG3_HUMAN		2	GCTTCGCTGTG	0.502	
-	2	472	e_Mutation_p.R11	NM_002781	NP_002772	Q15238	PSG5_HUMAN	g-like V-type.	3	CTTCCCGGGTG	0.433	
-	11	1552	dp.1_Missense_M	NM_004819	NP_004810	Q92797	SYMPK_HUMAN		1	CCACGGGGGTG	0.607	
+	3	410	X_uc010elm.1_R	NM_000554	NP_000545	O43186	CRX_HUMAN	Homeobox.	2	TGCCCGTGAGG	0.632	
+	11	1602	p.D348N|PPFIA3_	NM_003660	NP_003651	O75145	LIPA3_HUMAN	Potential.	1	TGAACGATGAC	0.642	
+	1	248	2A1_uc002ppo.2_	NM_014203	NP_055018	O95782	AP2A1_HUMAN		2	GGGGGCTCGCG	0.697	
-	5	921	77_uc010ydf.1_5'	NM_023074	NP_075562	Q9BS31	ZN649_HUMAN	2H2-type 2.	3	CTGTACTTCTTG	0.483	
+	6	1161		NM_001099694	NP_001093164	Q96N58	ZN578_HUMAN	2H2-type 3.	0	CCATCGTAGAT	0.433	
+	4	2891	dw.1_Missense_M	NM_138374	NP_612383	Q96IR2	ZN845_HUMAN	2H2-type 26.	0	CTTCCGTCACA	0.363	rs150688663
+	4	2950	dw.1_Missense_M	NM_138374	NP_612383	Q96IR2	ZN845_HUMAN	2H2-type 27.	0	TACAAGTGTAAT	0.348	
-	6	1060	ILRA3_uc010erk.2	NM_006865	NP_006856	Q8N6C8	LIRA3_HUMAN	like C2-type 4.	1	GGCCCGGCCGC	0.627	
-	2	908	_p.R206*|ZBTB45_	NM_032792	NP_116181	Q96K62	ZBT45_HUMAN		0	ACCTCGGTCAT	0.677	
-	2	194	_p.G71V|PDIA6_u	NM_005742	NP_005733	Q15084	PDIA6_HUMAN		0	TACAGACCATTC	0.413	
-	1	1274	F3C_uc010ykr.1_	NM_002254	NP_002245	O14782	KIF3C_HUMAN	inesin-motor.	4	GGGTGCTGCCC	0.567	
-	7	1105	R113_uc010eyk.1_	NM_001145168	NP_001138640	Q8IZF5	GP113_HUMAN	ellular (Potential).	4	CCAGGCCGCGG	0.632	
+	5	641	R144Q|SEMA4F_u	NM_004263	NP_004254	O95754	SEM4F_HUMAN	tracellular (Potential).	4	TCAGCGGTCAG	0.512	
+	20	2975	nse_Mutation_p.K2	NM_144992	NP_659429	Q502W6	VWA3B_HUMAN		6	CAAATAAGATGA	0.418	
+	21	2481	ion_p.T805M|MAP	NM_145687	NP_663720	O95819	M4K4_HUMAN		4	TGAAACGGAAT	0.478	
+	12	3257		NM_198581	NP_940983	P61129	ZC3H6_HUMAN		4	CACACGGTTCA	0.393	
+	15	3701	p.2_Missense_Mu	NM_019014	NP_061887	Q9H9Y6	RPA2_HUMAN		1	AGATGGAACGG	0.507	
+	2	1254	_p.R261C|TMEM1	NM_001105198	NP_001098668	Q53S58	TM177_HUMAN		1	CCCTGCGCAGT	0.592	rs114786834
-	3	687		NM_001099771	NP_001093241	A5A3E0	POTEF_HUMAN		5	TCTTGTTCCTG	0.607	

-	81	12516	.2_Missense_Muta	NM_004543	NP_004534	P20929	NEBU_HUMAN	Nebulin 112.	20	TCACATCGCTCT	0.493	
-	27	3766	.P1233S|LY75_uc	NM_002349	NP_002340	O60449	LY75_HUMAN	cellular (Potential).	0	AACTGGTTTGA	0.328	
+	48	3770		NM_000090	NP_000081	P02461	CO3A1_HUMAN		13	TTGCCCCGTATT	0.498	
-	20	3226		NM_018897	NP_061720	Q8WXX0	DYH7_HUMAN	n (By similarity).	12	TCAGCCTTTCC	0.299	
-	40	6658	vfh.2_Intron|FN1_	NM_212482	NP_997647	P02751	FINC_HUMAN	trand 3 (CS-3) (V region).	13	GACCAGAAGTG	0.527	
-	14	2212		NM_005381	NP_005372	P19338	NUCL_HUMAN	g/Gly/Phe-rich.	3	TCCTCGGAAGC	0.517	
+	5	755	P_uc002vsr.2_5'F	NM_001632	NP_001623	P05187	PPB1_HUMAN		1	CGTGCCTGCCT	0.672	
-	41	9262	znj.1_Missense_M	NM_004369	NP_004360	P12111	CO6A3_HUMAN	ype-III.|Nonhelical region.	18	TTCACGGGACA	0.473	rs148318789
-	2	762_763	oc.1_Missense_M	NM_001005853	NP_001005853	Q6IFH4	OR6B2_HUMAN	Name=6; (Potential).	0	CAGGTAGAGAA	0.579	
+	7	637	gca.1_Missense_	NM_130811	NP_570824	P60880	SNP25_HUMAN	coiled-coil homology 2.	2	TGCCCGAGAAA	0.458	
-	5	635	wtu.2_Missense_	NM_178312	NP_842564	Q9BX51	GGTL1_HUMAN		1	CGTGACGTTGG	0.622	
-	17	2820	_p.T898M|PTPRT_	NM_007050	NP_008981	O14522	PTPRT_HUMAN	lasmic (Potential).	20	TCTGCGTGATG	0.572	
-	5	776		NM_005560	NP_005551	O15230	LAMA5_HUMAN	inin N-terminal.	3	ACGTCCGTTCA	0.498	
-	3	721	lv.1_Missense_Mu	NM_033081	NP_149072	Q9BTC0	DIDO1_HUMAN		6	ACTATCGGAGG	0.572	
+	2	734	.1_Intron|C21orf29	NM_198689	NP_941962	P60409	KR107_HUMAN	epeats of C-C-X(3).|18.	0	AGCCCGTCTGC	0.662	
-	2	1274	f57_uc002ziw.2_5'	NM_003906	NP_003897	O60318	MCM3A_HUMAN		5	GCGCCGGAGTT	0.507	rs17182566
-	36	4259	y.3_Missense_Mu	NM_058004	NP_477352	P42356	PI4KA_HUMAN		4	CTTCACGCAGC	0.512	
-	2	1458	70_uc002zxr.1_5'F	NM_021916	NP_068735	Q9UC06	ZNF70_HUMAN		2	CTTCTCGCCAG	0.572	
+	11	1367	C2A11_uc011ajc.	NM_001024938	NP_001020109	Q9BYW1	GTR11_HUMAN	lame=11; (Potential).	1	GGTCGGCCTGG	0.642	
-	2	1018	rb.2_Missense_Mu	NM_001051	NP_001042	P32745	SSR3_HUMAN	lasmic (Potential).	1	TGAAGCGGTAG	0.617	
+	2	1222	xy.2_Missense_M	NM_002409	NP_002400	Q09327	MGAT3_HUMAN	enal (Potential).	0	CGTCCTTTTCC	0.642	
+	21	2663	issense_Mutation_	NM_152513	NP_689726	Q5TIA1	MEI1_HUMAN		2	TGGGCGGTCTT	0.567	
+	2	1940		NM_001137674	NP_001131146	A6NHJ4	ZN860_HUMAN	2H2-type 9.	1	CCTTCCATCACA	0.418	rs1808125
-	13	7315		NM_014831	NP_055646	O15050	TRNK1_HUMAN		2	TTAAGCGGGTC	0.512	
-	1	643	_p.P127S|MST1R_	NM_002447	NP_002438	Q04912	RON_HUMAN	lar (Potential).|Sema.	6	CGCGGGATCCA	0.687	
+	5	669	lg.1_Missense_Mu	NM_002070	NP_002061	P04899	GNAI2_HUMAN		3	GACCACGGGGA	0.592	
+	4	1536	.3_5'UTR|GRM2_	NM_000839	NP_000830	Q14416	GRM2_HUMAN	cellular (Potential).	1	CCTTTCGCCCA	0.542	
-	4	428	d.2_Missense_Mu	NM_017442	NP_059138	Q9NR96	TLR9_HUMAN		4	GCATTCGCTCC	0.607	
-	1	774	_p.R83H|MAGI1_	NM_001033057	NP_001028229	Q96QZ7	MAGI1_HUMAN	PDZ 1.	6	CATAGCGGGGC	0.716	
-	9	609	bfy.1_Missense_M	NM_003968	NP_003959	Q8TBC4	UBA3_HUMAN	with UBE2M N-terminus.	1	CAAAGGGACAAT	0.423	
-	6	843	AM86D_uc003dpc	NR_024241					0	ACCTGCTGCAA	0.597	
-	29	2496	l.2_Missense_Mu	NM_015429	NP_056244	Q7Z7G0	TARSH_HUMAN	p.R805Q(1)	4	TGTATCGCACAT	0.458	
-	16	3329		NM_015103	NP_055918	Q9Y4D7	PLXD1_HUMAN	r (Potential).|IPT/TIG 3.	1	GCGGCGGGGA	0.667	
-	7	2195	olc.1_Missense_M	NM_001017395	NP_001017395	O94876	TMCC1_HUMAN	Potential.	1	GCTGCTGCAGC	0.572	
-	3	866		NM_001040100	NP_001035189	Q8NFR3	SSPTB_HUMAN	enal (Potential).	0	TAGATCGCTCC	0.428	
+	4	546	_p.A83T|ACTL6A_	NM_004301	NP_004292	O96019	ACL6A_HUMAN		1	CAGAGGCACCG	0.323	
-	6	866	_p.L223F|ALG3_u	NM_005787	NP_005778	Q92685	ALG3_HUMAN		0	TGGGAGGAAGC	0.637	
+	18	2833	Mutation_p.R839C	NM_198241	NP_937884	Q04637	IF4G1_HUMAN	3/EIF4A-binding.	7	GAGGACGCCTG	0.488	
+	13	2946		NM_004443	NP_004434	P54753	EPHB3_HUMAN	Potential).|Protein kinase.	11	GAGAGCGACCC	0.567	
+	13	2058	.T380M|TBC1D14	NM_001113361	NP_001106832	Q9P2M4	TBC14_HUMAN		2	CGCCACGATCC	0.607	
+	19	2545	wi.1_Missense_M	NM_020777	NP_065828	Q96PQ0	SORC2_HUMAN	umenal (Potential).	2	TCTACCGCGTG	0.522	
+	1	4105	p.A986T|PCDH7_	NM_002589	NP_002580	O60245	PCDH7_HUMAN	lasmic (Potential).	4	TGGGAGCAGGA	0.443	
+	21	2686	p.G718R|LIMCH1_	NM_014988	NP_055803	Q9UPQ0	LIMC1_HUMAN		4	TCCAGGGAGAT	0.403	
+	4	805	P|MUC7_uc003hfj.	NM_001145006	NP_001138478	Q8TAX7	MUC7_HUMAN	1.|Thr-rich.	4	CACCTTCTGCA	0.522	
+	32	5357	iek.2_Missense_M	NM_015312	NP_056127	Q2LD37	K1109_HUMAN		12	TGAACAGGTAAG	0.373	
+	9	2193	.G642R|GAB1_uc	NM_002039	NP_002030	Q13480	GAB1_HUMAN		4	ATGGAGGAAGC	0.438	
-	2	1113		NM_145720	NP_663772	Q8IY51	TIGD4_HUMAN	e.|H-T-H motif (By similarity	1	TTAGACGTAACAT	0.383	

+	12	2001	p.E154K|ETFDH_	NM_004453	NP_004444	Q16134	ETFD_HUMAN		3	GGCCCGAGCAG	0.363	
-	10	5068		NM_005245	NP_005236	Q14517	FAT1_HUMAN	(Potential).|Cadherin 14.	12	TTACTTCGATCT	0.368	
+	17	2767	3jdk.1_Missense_	NM_139056	NP_620687	Q8TE57	ATS16_HUMAN	SP type-1 2.	8	CCATCGTGCGC	0.627	
-	4	441		NM_032286	NP_115662	Q9BTT4	MED10_HUMAN		1	AAGGCGGGTGA	0.517	
+	11	2068		NM_020227	NP_064612	Q9NQV7	PRDM9_HUMAN	2H2-type 5.	6	GAGGAGACACA	0.612	rs112192848
+	4	923		NM_002439	NP_002430	P20585	MSH3_HUMAN	action with EXO1.	4	ACAAACGGTCC	0.378	
-	2	1288		NM_203406	NP_981951	Q68D91	MBLC2_HUMAN		0	TTACACGTAGA	0.323	rs138820203
+	64	12971	_Mutation_p.S199	NM_032119	NP_115495	Q8WXG9	GPR98_HUMAN	ellular (Potential).	16	TTCCAGTGGAG	0.438	
+	74	15724	p.V2916I|GPR98_	NM_032119	NP_115495	Q8WXG9	GPR98_HUMAN	ellular (Potential).	16	CCACTGTAACT	0.463	
-	2	550	cxc.1_Missense_	NM_178450	NP_848545	Q86UD3	MARH3_HUMAN		1	CTAGGCTGCCA	0.587	
-	15	2417	v.2_Missense_Mu	NM_001999	NP_001990	P35556	FBN2_HUMAN	10; calcium-binding.	15	ATTCATCAACAT	0.502	
-	8	1479	v.2_Missense_Mu	NM_001999	NP_001990	P35556	FBN2_HUMAN	5; calcium-binding.	15	ATCCACGTGGA	0.438	rs112428886
-	5	766		NM_015082	NP_055897	Q6MZW2	FSTL4_HUMAN	EF-hand.	2	CCCTGAACAGA	0.557	
-	4	624	lbp.2_Missense_M	NM_004598	NP_004589	Q08629	TICN1_HUMAN	Kazal-like.	1	CATGGCTGACT	0.473	
+	3	2887	826R|PCDHA7_u	NM_018899	NP_061722	Q9Y5I4	PCDC2_HUMAN	-X-X-P.|Cytoplasmic (Pote	4	AGGCTGGCATT	0.498	
+	1	1103	DHGA4_uc003ljq.	NM_018919	NP_061742	Q9Y5G7	PCDG6_HUMAN	|Extracellular (Potential).	1	CGCCCTTTTTC	0.428	
-	3	349	3mbs.1_Missense_	NM_001017995	NP_001017995	A1X283	SPD2B_HUMAN	PX.	4	CATGGGAAATT	0.463	
-	11	1546	p.R528W|CCHCR	NM_019052	NP_061925	Q8TD31	CCHCR_HUMAN		1	ACCCCGAATGG	0.612	
+	4	835	_p.R208H|MICB_u	NM_005931	NP_005922	Q29980	MICB_HUMAN	.|Extracellular (Potential).	0	CTGGCGTCAGG	0.582	
-	9	3776		NM_019105	NP_061978	P22105	TENX_HUMAN	nectin type-III 5.	0	GTACTGGACCA	0.582	
+	7	1403	rf.1_Missense_Mu	NM_002263	NP_002254	Q9BW19	KIFC1_HUMAN	inesin-motor.	0	GGTCCGCCCTG	0.647	
-	3	554	_Intron|TMEM151	NM_182539	NP_872345	Q5JU00	TCTE1_HUMAN		4	AGCAGCGGAGC	0.607	rs151164597
+	16	2846	k.2_Missense_Mut	NM_001704	NP_001695	O60242	BAI3_HUMAN	ellular (Potential).	50	CAACCGATTCG	0.363	
+	7	793	f165_uc010kbv.1_	NM_001031743	NP_001026913	Q8IYR0	CF165_HUMAN		1	TGCCCGGAGCC	0.488	rs142943998
+	2	327	_p.M45V|DSE_uc	NM_001080976	NP_001074445	Q9UL01	DSE_HUMAN		1	CATCCCATGCTG	0.542	
-	12	1705	.1_Missense_Mut	NM_003379	NP_003370	P15311	EZRI_HUMAN	ction with SCYL3.	1	AGCCCGTGGGC	0.647	
+	5	457	e_Mutation_p.R7	NM_004906	NP_004897	Q15007	FL2D_HUMAN		0	TAATGCGACTA	0.378	
+	2	427	e_Mutation_p.K10	NM_032448	NP_115824	Q96EK7	F120B_HUMAN		1	GGCTCAAGAAC	0.433	
-	3	270	kq.2_Missense_M	NM_001080453	NP_001073922	Q8N201	INT1_HUMAN		0	CTTGCGCTCAG	0.647	
+	11	1382	p.A119T|TTYH3_	NM_025250	NP_079526	Q9C0H2	TTYH3_HUMAN	Name=5; (Potential).	0	TCACAGCCCTC	0.637	
+	15	2606	wq.1_Missense_M	NM_032172	NP_115548	Q9H9J4	UBP42_HUMAN	Pro-rich.	5	CGATGCGAGCC	0.716	
+	9	1215	.2_Missense_Mut	NM_001134388	NP_001127860	Q9NPG8	ZDHC4_HUMAN		2	CCAGACTACTA	0.577	
-	6	791_792		NM_001004320	NP_001004320	Q6ZNB7	ALKMO_HUMAN		0	ACCAAGGTTATT	0.307	
+	18	2722	_Mutation_p.V490	NM_031449	NP_113637	Q8NF64	ZMIZ2_HUMAN	Pro-rich.	5	CAGGCGTGATG	0.677	
+	4	1558		NM_001159522	NP_001152994	A8MUV8	ZN727_HUMAN	2H2-type 11.	0	CAAAACCTTTA	0.428	
+	9	1211	ldp.2_Nonsense_	NM_020879	NP_065930	Q8IYE0	CC146_HUMAN		2	GATTTTCGAAAT	0.423	
-	19	2402	ll.2_RNA|POT1_u	NM_015450	NP_056265	Q9NUX5	POTE1_HUMAN		1	CCACGGATATG	0.323	
+	4	535	_p.R32C|UBE3C_	NM_014671	NP_055486	Q15386	UBE3C_HUMAN		5	TTGATCGCTGT	0.388	
+	9	1227	oz.2_Missense_M	NM_183421	NP_904357	Q8TCJ0	FBX25_HUMAN		1	TCTGTCGGCAC	0.383	
+	7	1422	p.Q235*|MTMR9_	NM_015458	NP_056273	Q96QG7	MTMR9_HUMAN	ularin phosphatase.	0	CACTCCAGGTG	0.483	
+	11	1292	_p.L279F|ADAMD	NM_014479	NP_055294	O15204	ADEC1_HUMAN	ptidase M12B.	2	CATGTCCTTGG	0.388	
-	1	806	RG_uc003xim.1_	NM_013357	NP_037489	Q9UJV8	PURG_HUMAN	By similarity.	0	CCCCTCTGGGA	0.448	
+	29	6304		NM_017780	NP_060250	Q9P2D1	CHD7_HUMAN	Poly-Arg.	9	GACGGCGGCCT	0.537	
-	1	52		NM_001010893	NP_001010893	Q5PT55	NTCP5_HUMAN		0	TTGCTTCTTCTAT	0.299	
-	2	742_743		NM_005328	NP_005319	Q92819	HAS2_HUMAN	lasmic (Potential).	15	TTTTCGGTGCTC	0.401	
-	5	829	_p.A99T|MTSS1_	NM_014751	NP_055566	O43312	MTSS1_HUMAN	IMD.	1	TAAAGCGCTTT	0.403	
-	14	3611	M135B_uc003yva	NM_015912	NP_056996	Q49AJ0	F135B_HUMAN		9	CCAGGCCATGG	0.348	

-	5	623	104N|TOP1MT_uc	NM_052963	NP_443195	Q969P6	TOP1M_HUMAN		1	ATGGTCGCCAC	0.547	
-	9	805	zb.2_Missense_M	NM_003313	NP_003304	Q13630	FCL_HUMAN		1	CGCCTCGGCTG	0.667	
-	3	280		NM_006664	NP_006655	Q9Y4X3	CCL27_HUMAN		0	TGCTGCGTTGA	0.527	
-	18	3692	M2_uc010mos.2_	NM_013390	NP_037522	Q9UHN6	TMEM2_HUMAN		2	GTGCCGGCCC	0.443	
+	4	1872	apq.3_Missense_	NM_001145124	NP_001138596				0	TTTCCCGTATCC	0.547	
-	5	1173	p.M306I|LPAR1_	NM_057159	NP_476500	Q92633	LPAR1_HUMAN	Name=7; (Potential).	2	GGGTTCATGGC	0.522	
+	3	2650	p.R747C|TLR4_uc	NM_138554	NP_612564	O00206	TLR4_HUMAN	smic (Potential).|TIR.	16	CTGTACCGCCTT	0.557	
-	1	722		NM_012363	NP_036495	Q8NGS0	OR1N1_HUMAN	Name=6; (Potential).	3	GGTGGGAACTG	0.547	
+	6	861	nse_Mutation_p.E	NM_002540	NP_002531	Q5BJF6	ODFP2_HUMAN	Potential.	1	ACATCGAGCGC	0.582	
-	7	694	50A|GBGT1_uc01	NM_021996	NP_068836	Q8N5D6	GBGT1_HUMAN	enal (Potential).	0	TACCCACGCATG	0.597	
+	3	791		NM_000093	NP_000084	P20908	CO5A1_HUMAN	minal.|Laminin G-like.	11	TCTCCCGTCTTC	0.592	rs145757313
-	9	1190	mez.1_Missense_	NM_001130969	NP_001124441	Q6X4W1	NELF_HUMAN		0	GGCCTCGTCCA	0.657	
-	7	898	B11_uc010nes.1_	NM_080873	NP_543149	Q8WXH4	ASB11_HUMAN	SOCS box.	3	TCGACCGAGAC	0.512	
+	8	5209	.R1468H|NHS_uc	NM_198270	NP_938011	Q6T4R5	NHS_HUMAN		7	CGACCGTTCCT	0.562	
-	11	1592	p.E473K|MAP7D	NM_152780	NP_689993	Q96T17	MA7D2_HUMAN		3	TCTCTCGAGAC	0.458	
-	5	482	KA6_uc011mqu.1	NM_014496	NP_055311	Q9UK32	KS6A6_HUMAN	otein kinase 1.	8	TTTGACAATAAAT	0.269	
-	2	212		NM_001012755	NP_001012773	Q5H9E4	MCAR6_HUMAN		0	AAGCTCCTTCC	0.517	
+	2	510		NM_198576	NP_940978	O00468	AGRIN_HUMAN	NtA.	3	GTGTGGAAGGT	0.652	
-	5	1021	p.R231Q|SDF4_u	NM_016176	NP_057260	Q9BRK5	CAB45_HUMAN	EF-hand 3.	2	TTCCCCGGCTG	0.672	
+	4	1348		NM_152228	NP_689414	Q7RTX0	TS1R3_HUMAN	ellular (Potential).	0	GAAACGTGGAC	0.667	
+	6	2033		NM_152228	NP_689414	Q7RTX0	TS1R3_HUMAN	lasmic (Potential).	0	GCGGGGGCCCT	0.682	
-	11	1383	1_Missense_Muta	NM_030937	NP_112199	Q96S94	CCNL2_HUMAN		3	GCAGTCCTTGG	0.627	
+	4	719	2_uc001agl.1_Mis	NM_080875	NP_543151	Q96AX9	MIB2_HUMAN		0	CGCGCCCGTGA	0.687	
+	12	1727	Mutation_p.G490	NM_080875	NP_543151	Q96AX9	MIB2_HUMAN	ANK 1.	0	ACCTGGGCCAG	0.662	
-	5	251	.S47F|CDK11A_uc	NM_033486	NP_277021	P21127	CD11B_HUMAN		1	cctcaagggaatcccg	0.179	
+	5	778	1ajt.1_Missense_	NM_003820	NP_003811	Q92956	TNR14_HUMAN	.|Extracellular (Potential).	1	GGACACCCTGT	0.647	
+	4	433	vlk.1_Missense_M	NM_005427	NP_005418	O15350	P73_HUMAN		2	CGACACCATGT	0.677	
-	2	1041		NM_020710	NP_065761	Q8N1G4	LRC47_HUMAN		2	CGGCCCCCACA	0.652	
-	8	1170	AA0562_uc001ak	NM_014704	NP_055519	O60308	CE104_HUMAN	Potential.	0	CTTCTCCTTGG	0.552	
-	3	543	IAA0562_uc001ak	NM_014704	NP_055519	O60308	CE104_HUMAN		0	AGCAAGTAACT	0.368	
+	2	496	aln.2_Missense_M	NM_001042478	NP_001035943	Q9UKB5	AJAP1_HUMAN	ellular (Potential).	1	ACCTGCCCGCC	0.572	
+	2	523	aln.2_Missense_M	NM_001042478	NP_001035943	Q9UKB5	AJAP1_HUMAN	ellular (Potential).	1	CGGGGCCGGA	0.602	
-	3	167	me.2_Nonsense_	NM_000983	NP_000974	P35268	RL22_HUMAN		0	AAACTGCTCCT	0.408	
+	6	1301		NM_031475	NP_113663	B1AK53	ESPN_HUMAN		0	CCTCTCCAACT	0.612	
+	3	1186	nv.2_Intron|TAS1	NM_138697	NP_619642	Q7RTX1	TS1R1_HUMAN	ellular (Potential).	3	ATGCGGTGGCC	0.607	
+	2	131	_p.G3D|ZBTB48_	NM_005341	NP_005332	P10074	ZBT48_HUMAN		0	GGACGGCTCCT	0.622	
+	3	898		NM_153812	NP_722519	Q86YI8	PHF13_HUMAN		0	TACTCCCTCGA	0.587	
+	17	2442	p.G757D|PER3_u	NM_016831	NP_058515	P56645	PER3_HUMAN		3	CACCGGCTCTG	0.682	
+	17	2459	p.G763R|PER3_u	NM_016831	NP_058515	P56645	PER3_HUMAN		3	GCAGGGGAGCG	0.706	
+	17	2858	p.P896S|PER3_u	NM_016831	NP_058515	P56645	PER3_HUMAN	Pro-rich.	3	CACCCCCTTCA	0.547	
-	2	351	FI1_uc001apa.1_5	NM_018948	NP_061821	Q9UJM3	ERRFI_HUMAN		1	CTGCTCCAGTA	0.433	
-	20	4250	p.T1147I|RERE_u	NM_012102	NP_036234	Q9P2R6	RERE_HUMAN		2	GGTCTGTCCGG	0.617	
-	14	2209	E_uc010nzx.1_Mi	NM_012102	NP_036234	Q9P2R6	RERE_HUMAN		2	GGACGCGGTGC	0.602	rs140945349
-	7	1483	p.R225*|RERE_u	NM_012102	NP_036234	Q9P2R6	RERE_HUMAN	BAH.	2	GCTCTCGGTTCT	0.408	
-	5	1223	p.A138V|RERE_u	NM_012102	NP_036234	Q9P2R6	RERE_HUMAN	BAH.	2	AACAGGCCTGG	0.547	
-	7	705	i.1_Missense_Mut	NM_001428	NP_001419	P06733	ENOA_HUMAN	sion of c-myc promoter act	4	TCTGCTCCAATG	0.522	
+	17	2952	BE4B_uc010oaj.1_	NM_001105562	NP_001099032	O95155	UBE4B_HUMAN		4	AGCCTCCATTT	0.418	

+	21	2181	_p.T634I|KIF1B_	NM_015074	NP_055889	O60333	KIF1B_HUMAN		3	ACTGGACATTTG	0.478
+	25	2601	qz.2_Missense_M	NM_015074	NP_055889	O60333	KIF1B_HUMAN		3	TGTACTCCCCTT	0.448
+	1	98	_Splice_Site_p.Q3	NM_002631	NP_002622	P52209	6PGD_HUMAN		1	GCCCAGTGAGT	0.701
+	3	247	_Missense_Mutati	NM_002631	NP_002622	P52209	6PGD_HUMAN		1	AAGTGGTGGGT	0.507
+	1	192	.2_Intron|APITD1_	NM_001302	NP_001293	O00230	CORT_HUMAN		0	GATTGGGCTTAA	0.522
-	8	1043	p.W328*|C1orf127	NM_173507	NP_775778	B7ZLG7	B7ZLG7_HUMAN		1	GGCCGCCAGGG	0.687
-	9	1027	_p.T326I|EXOSC1	NM_001001998	NP_001001998	Q01780	EXOSX_HUMAN		1	GGCAGGTCAGT	0.453
-	1	103	_p.T18N|EXOSC1	NM_001001998	NP_001001998	Q01780	EXOSX_HUMAN		1	ATTTGGTTGCG	0.672
-	55	7536	sc.2_Missense_M	NM_004958	NP_004949	P42345	MTOR_HUMAN	PI3K/PI4K.	29	TGGTCCCCGTT	0.423
+	4	946	R_uc001asd.2_In	NM_021146	NP_066969	O43827	ANGL7_HUMAN	ogen C-terminal.	0	AGTATAGCCACT	0.522
-	26	4061		NM_004958	NP_004949	P42345	MTOR_HUMAN		29	CCTGGCCATCG	0.517
+	13	2795	asi.1_Missense_M	NM_020780	NP_065831	Q9P2K9	PTHD2_HUMAN	ellular (Potential).	7	TGACCGCTTGTA	0.587
+	17	3460		NM_020780	NP_065831	Q9P2K9	PTHD2_HUMAN	ellular (Potential).	7	ACGGGGCAGTG	0.672
+	20	3940		NM_020780	NP_065831	Q9P2K9	PTHD2_HUMAN	ellular (Potential).	7	TGCCCCCCCAC	0.652
+	17	1864	p.G300D|CLCN6_	NM_001286	NP_001277	P51797	CLCN6_HUMAN	smic (By similarity).	0	GCGAGGCGTGC	0.468
-	2	1474	1atl.1_Missense_M	NM_138346	NP_612355	Q8IYS2	K2013_HUMAN	ellular (Potential).	1	GGTCAGAGAGC	0.647
+	17	1943	bb.1_Missense_M	NM_000302	NP_000293	Q02809	PLOD1_HUMAN		3	TGCTGGAGTAC	0.597
+	9	1388	i.2_Missense_Mu	NM_014874	NP_055689	O95140	MFN2_HUMAN	lasmic (Potential).	1	CAACGCCAGGA	0.537
+	13	1756	i.2_Missense_Mu	NM_014874	NP_055689	O95140	MFN2_HUMAN	lasmic (Potential).	1	CAATGGCCGAG	0.502
+	15	1807_1808	01atr.2_Missense_	NM_001243	NP_001234	P28908	TNR8_HUMAN	lasmic (Potential).	5	TGGGGACCGTG	0.649
+	19	3527	p.S1129F|VPS13D	NM_015378	NP_056193	Q5THJ4	VP13D_HUMAN		5	AAAATCCTTTCC	0.353
+	19	4379	p.G1413E|VPS13D	NM_015378	NP_056193	Q5THJ4	VP13D_HUMAN		5	GGCGGGAGATG	0.473
+	57	11282	13D_uc001atx.2_	NM_015378	NP_056193	Q5THJ4	VP13D_HUMAN		5	GTGGAGTTTCC	0.502
-	2	110		NM_001009611	NP_001009611	O60810	PRAM4_HUMAN		1	GCAAGCTCCAG	0.562
-	4	1241		NM_001099854	NP_001093324	Q5SWL7	PRA14_HUMAN		0	CACTGGTGTGG	0.552
+	8	2100	od.1_Missense_M	NM_012231	NP_036363	Q13029	PRDM2_HUMAN		1	AGCAGGGTTAA	0.498
+	7	681		NM_033440	NP_254275	P08217	CEL2A_HUMAN	eptidase S1.	2	GCGGGCCACTG	0.577
+	3	161		NM_015849	NP_056933	P08218	CEL2B_HUMAN	eptidase S1.	1	TCTCCCTGCAG	0.527
+	4	662	e_Mutation_p.W18	NM_015291	NP_056106	Q9Y2G8	DJC16_HUMAN	(Potential).|Thioredoxin.	3	TGTGTGGAAAG	0.328
+	6	914	_Mutation_p.G26	NM_015291	NP_056106	Q9Y2G8	DJC16_HUMAN	lasmic (Potential).	3	CTCTGGCTGGC	0.343
+	15	2164	e_Mutation_p.P37	NM_015291	NP_056106	Q9Y2G8	DJC16_HUMAN	ellular (Potential).	3	CAATCCCAAAC	0.438
+	4	616	nse_Mutation_p.G	NM_017556	NP_060026	Q8WUP2	FBLI1_HUMAN	-binding.|Pro-rich.	1	GGCGGGGAGGC	0.677
+	10	1491	LIM1_uc001axh.1_	NM_017556	NP_060026	Q8WUP2	FBLI1_HUMAN	ding.|LIM zinc-binding 3.	1	ACCAAGGCTGC	0.637
+	2	533	N_uc010obp.1_5'	NM_015001	NP_055816	Q96T58	MINT_HUMAN	By similarity.	15	AGGAGGTGGTG	0.517
-	1	865	101K|HSPB7_uc	NM_014424	NP_055239	Q9UBY9	HSPB7_HUMAN	ation to SC35 splicing spe	0	AACTTCTCTCCC	0.567
+	19	2052	.V657M|CLCNKA_	NM_004070	NP_004061	P51800	CLCKA_HUMAN	CBS 2.	1	TCTTCGTGACA	0.612
+	7	821	cd.1_Missense_M	NM_018090	NP_060560	Q9NVZ3	NECP2_HUMAN		0	ACTTTACCAAAT	0.572
+	22	3365	p.A698V|CROCC_	NM_014675	NP_055490	Q5TZA2	CROCC_HUMAN	Potential.	5	AGATGCCCAGA	0.642
-	7	459	zy.2_Missense_M	NM_002403	NP_002394	P55001	MFAP2_HUMAN		0	GTATGGAGTAG	0.622
-	20	2403	ense_Mutation_p.	NM_022089	NP_071372	Q9NQ11	AT132_HUMAN	lasmic (Potential).	4	GCAGAGCCTGG	0.627
-	3	315	_p.G42D|ATP13A	NM_022089	NP_071372	Q9NQ11	AT132_HUMAN	ellular (Potential).	4	GACTGCCACAG	0.652
-	2	222	_p.S11N|ATP13A	NM_022089	NP_071372	Q9NQ11	AT132_HUMAN	lasmic (Potential).	4	GCGTGCTGCCC	0.522
-	15	1811	m.1_Missense_M	NM_007365	NP_031391	Q9Y2J8	PADI2_HUMAN		6	GTCCTCGTCCA	0.597
-	12	1491	m.1_Missense_M	NM_007365	NP_031391	Q9Y2J8	PADI2_HUMAN		6	CGTGGCCCACA	0.582
+	12	1478		NM_016233	NP_057317	Q9ULW8	PADI3_HUMAN		2	TCCCTGCCCCC	0.607
+	6	1416	p.R271H|PAX7_u	NM_002584	NP_002575	P23759	PAX7_HUMAN	Homeobox.	203	TTGGCGTAAGC	0.652
-	3	313	090_uc001bbq.2_	NM_015047	NP_055862	Q8N766	K0090_HUMAN	ellular (Potential).	1	AGCAGCATGGC	0.552

-	8	847	cy.1_Missense_Mu	NM_201252	NP_957704				0	CGCGTCCCCGT	0.637	
-	4	735	pk.2_Missense_M	NM_004930	NP_004921	P47756	CAPZB_HUMAN		0	CCATGGTGACCT	0.542	
+	3	1455		NM_000871	NP_000862	P50406	5HT6R_HUMAN	smic (By similarity).	1	AGCGGGCGCTG	0.652	
+	2	444		NM_015207	NP_056022	Q5T2D3	OTUD3_HUMAN	OTU.	0	GGGAAGATTTT	0.438	
+	3	523		NM_015207	NP_056022	Q5T2D3	OTUD3_HUMAN	OTU.	0	TGCTGGCAATG	0.388	
+	2	680		NM_032409	NP_115785	Q9BXM7	PINK1_HUMAN	.|Cytoplasmic (Potential).	3	GAGGCCCAGGT	0.602	rs35802484
+	7	1458	n.2_Missense_Mu	NM_032409	NP_115785	Q9BXM7	PINK1_HUMAN	.|Cytoplasmic (Potential).	3	CTACGGCCAGG	0.602	
-	8	1662	KIF17_uc009vpx.2	NM_020816	NP_065867	Q9P2E2	KIF17_HUMAN		4	CCTGAGTCTTG	0.542	
-	15	2592	.G499E|EIF4G3_	NM_003760	NP_003751	O43432	IF4G3_HUMAN	(By similarity).|MIF4G.|HE	1	TAAGTCCTGAC	0.413	
-	11	1841	p.L249F|EIF4G3_	NM_003760	NP_003751	O43432	IF4G3_HUMAN		1	CTTTAAGCTAAA	0.358	
+	5	868	b.2_Missense_Mu	NM_032264	NP_115640	Q9H094	NBPF3_HUMAN	Potential.	2	AGGGAGAGATG	0.527	
+	1	240		NM_001013693	NP_001013715	Q5SZI1	LRAD2_HUMAN		0	GGGGGCAGCCG	0.577	
-	26	3394_3395	d.2_Missense_Mu	NM_005529	NP_005520	P98160	PGBM_HUMAN	inin IV type A 2.	9	GCGGGGTCCTG	0.569	
-	7	662	tation_p.S208G|H	NM_005529	NP_005520	P98160	PGBM_HUMAN	eceptor class A 1.	9	GTAGCTGTGGC	0.627	
+	6	602	p.H104Y|CDC42_	NM_001039802	NP_001034891	P60953	CDC42_HUMAN		1	CTCACCACTGT	0.378	
+	4	1340	p.E277K|ZBTB40_	NM_001083621	NP_001077090	Q9NUA8	ZBT40_HUMAN		1	AGAAGGAGGTA	0.383	
+	8	1997	qi.1_Missense_M	NM_001083621	NP_001077090	Q9NUA8	ZBT40_HUMAN		1	GCCCCTGgagaa	0.239	
+	11	2036	gf.2_Missense_Mu	NM_017449	NP_059145	P29323	EPHB2_HUMAN	.|ATP (By similarity).|Protei	5	CAGGGGAGTTT	0.582	
-	3	1658	gu.2_Missense_M	NM_030634	NP_085137	Q9C0F3	ZN436_HUMAN	2H2-type 11.	1	TGAAACCTTTC	0.473	
-	3	896	gu.2_Missense_M	NM_030634	NP_085137	Q9C0F3	ZN436_HUMAN	2H2-type 2.	1	CCTTTTCCACAT	0.438	
-	3	832		NM_004091	NP_004082	Q14209	E2F2_HUMAN	Potential.	4	GCAGCCCCAGC	0.627	
+	9	660	A2_uc001bhs.1_3	NM_007260	NP_009191	O95372	LYPA2_HUMAN		2	GGTGCCCGTAC	0.617	
+	2	127		NM_001010980	NP_001010980	Q5T1S8	CA130_HUMAN		0	CCAGGGGAGAA	0.428	
+	10	1943	p.D354N|TMEM57	NM_018202	NP_060672	Q8N5G2	MACOI_HUMAN		0	AGCTGGACCTG	0.542	
+	5	1210	vry.1_Missense_M	NM_020379	NP_065112	Q9NR34	MA1C1_HUMAN	enal (Potential).	1	TGCCGGCGTTC	0.592	
+	9	1727	_Mutation_p.A286	NM_020379	NP_065112	Q9NR34	MA1C1_HUMAN	enal (Potential).	1	GGATGCCAAGG	0.617	
-	3	905		NM_024037	NP_076942	Q9H7T9	CA135_HUMAN		0	CTCTAGTGTTG	0.478	
+	3	466		NM_015871	NP_056955	O00488	ZN593_HUMAN		0	CTGAGGTCCCT	0.622	
+	21	2121	on_p.S423F|CNK	NM_006314	NP_006305	Q969H4	CNKR1_HUMAN		2	TGACTCCACAG	0.637	
-	4	368	_5'UTR|UBXN11_	NM_183008	NP_892120	Q5T124	UBX11_HUMAN		1	CATCTCCATAG	0.552	
-	2	851		NM_021969	NP_068804	Q15466	NR0B2_HUMAN		0	GATAGGGCGAA	0.612	
-	2	1042		NM_152365	NP_689578	Q8NAX2	CA172_HUMAN		2	AACGACCCTCC	0.642	
-	3	546	.2_Missense_Mut	NM_005248	NP_005239	P09769	FGR_HUMAN	SH3.	2	AGGGGCCACGT	0.557	
+	9	949		NM_177424	NP_803173	Q86Y82	STX12_HUMAN	cular (Potential).	2	TAAAACGAAGT	0.418	
+	4	370	x.1_Intron|PPP1R	NM_014110	NP_054829	Q12972	PP1R8_HUMAN	CDC5L, SF3B1 and MELK	0	ACAAGCCTCAG	0.493	
+	6	1934	10ofn.1_Missense	NM_001105556	NP_001099026	Q5TEJ8	THMS2_HUMAN	sp/Glu-rich.	1	AAATACTTGAG	0.358	
+	7	1063	10ofq.1_Splice_Si	NM_014474	NP_055289	Q92485	ASM3B_HUMAN		3	TGACAGGTGTC	0.567	
+	3	594		NM_018053	NP_060523	Q9H6D3	XKR8_HUMAN	ical; (Potential).	0	TCCTGGGCATCT	0.642	
+	3	812		NM_018053	NP_060523	Q9H6D3	XKR8_HUMAN		0	GTCTGGCTTCA	0.637	
-	6	520	.P119S|EYA3_uc	NM_001990	NP_001981	Q99504	EYA3_HUMAN		3	AAAAGGAGGTA	0.423	
+	9	1035	C1_uc001bqc.1_	NM_001269	NP_001260	P18754	RCC1_HUMAN	RCC1 6.	1	ATACAGCCTGG	0.602	
+	11	1775	tk.1_Missense_Mu	NM_203342	NP_976217	P11171	41_HUMAN	Hydrophilic.	1	AGAAGGAAACA	0.512	
-	6	757	CR_uc001brs.1_	NM_016011	NP_057095	Q9BV79	MECR_HUMAN		1	TTAGCTCCTCTT	0.493	
+	27	3859	RU_uc009vtq.2_	NM_005704	NP_005695	Q92729	PTPRU_HUMAN	hatase 2.|Cytoplasmic (Po	7	CGTGACCCTGC	0.647	
-	8	791		NM_006762	NP_006753	Q13571	LAPM5_HUMAN		0	GACCACCTGGG	0.592	
-	12	1777	1_uc001bsj.1_Mi	NM_014676	NP_055491	Q14671	PUM1_HUMAN	Ala-rich.	3	CAGCAGGAGCC	0.458	
-	11	1754	utation_p.M548I|	NM_014676	NP_055491	Q14671	PUM1_HUMAN	Ala-rich.	3	CCTGGCATGCC	0.532	

-	8	1356	j.1_Missense_Mut	NM_014676	NP_055491	Q14671	PUM1_HUMAN	Ala-rich.	3	GTGCGGCTGAT	0.493	
-	2	282	oge.1_Missense_	NM_004814	NP_004805	Q96DI7	SNR40_HUMAN	WD 1.	0	AGGTGGATCCG	0.443	
-	37	2847	p.V657M|COL16A	NM_001856	NP_001847	Q07092	COGA1_HUMAN	5 (COL5) with 3 imperfect	8	TTTCACCCCTG	0.557	
-	23	1950	_p.P358S|COL16A	NM_001856	NP_001847	Q07092	COGA1_HUMAN	8 (COL8) with 1 imperfec	8	TTTGGGCCCTG	0.572	
-	17	1570	p.G231D|COL16A	NM_001856	NP_001847	Q07092	COGA1_HUMAN	9 (COL9) with 3 imperfect	8	TCTCGCCTTTC	0.647	
-	29	4690	_Missense_Mutat	NM_001703	NP_001694	O60241	BAI2_HUMAN	lasmic (Potential).	13	GCGAGGCATGG	0.637	
+	4	469	_uc001bum.2_5'F	NM_024296	NP_077272	Q9BUN5	CC28B_HUMAN		0	GGAAGGAATGC	0.527	
+	8	886	_Mutation_p.R25	NM_005356	NP_005347	P06239	LCK_HUMAN	rotein kinase.	6	TGGAGCGGCTG	0.672	
+	4	395	ohe.1_Missense_	NM_004964	NP_004955	Q13547	HDAC1_HUMAN	ne deacetylase.	3	TCTGTCAGTTGT	0.438	
+	6	2067	522_uc010ohm.1_	NM_020888	NP_065939	Q9P206	K1522_HUMAN	Pro-rich.	0	CGCCAGTCCTC	0.627	
+	6	2474	522_uc010ohm.1_	NM_020888	NP_065939	Q9P206	K1522_HUMAN	Pro-rich.	0	CAGCTCCGCCA	0.657	
-	9	1755	1_5'Flank|YARS_u	NM_003680	NP_003671	P54577	SYYC_HUMAN		2	GATTGGATCCA	0.498	
+	5	580		NM_152493	NP_689706	Q5T0B9	ZN362_HUMAN		0	CGCGGGCACGG	0.701	
+	5	682		NM_152493	NP_689706	Q5T0B9	ZN362_HUMAN		0	CCCCCCTCTCC	0.672	
-	6	718	uh.1_Missense_M	NM_198040	NP_932157	Q8IXK0	PHC2_HUMAN		1	CTGTACCTGGA	0.582	
-	15	2252	m.1_Nonsense_	NM_052896	NP_443128	Q7Z408	CSMD2_HUMAN	xtracellular (Potential).	12	CTGTTCCAGAC	0.632	
-	4	520	xm.1_Missense_M	NM_052896	NP_443128	Q7Z408	CSMD2_HUMAN	xtracellular (Potential).	12	TGCAGCTGTAG	0.622	
-	3	1376		NM_001080418	NP_001073887	O95886	DLGP3_HUMAN		3	CAGTGGTGAGG	0.567	
+	10	1286	n_p.I361V|ZMYM1	NM_024772	NP_079048	Q5SVZ6	ZMYM1_HUMAN		0	GATGTCATTGTG	0.214	
+	11	1347	_p.T381M|ZMYM1	NM_024772	NP_079048	Q5SVZ6	ZMYM1_HUMAN	Ser-rich.	0	TAGTACGGAAC	0.353	
+	9	1480	yu.2_Missense_M	NM_005095	NP_005086	Q5VZL5	ZMYM4_HUMAN	MYM-type 3.	5	ACTTTGCAGTG	0.418	
+	8	2018	_p.A631T|NCDN_u	NM_001014839	NP_001014839	Q9UBB6	NCDN_HUMAN		3	TCTGGGCCGAC	0.692	
-	11	2115	ux.2_Missense_M	NM_022111	NP_071394	Q9HAW4	CLSPN_HUMAN	Potential.	8	GGAATTCTGCAG	0.343	
-	8	1659	vux.2_Splice_Site_	NM_022111	NP_071394	Q9HAW4	CLSPN_HUMAN		8	GATTACCTCTG	0.438	
+	15	2104	se_Mutation_p.R5	NM_012199	NP_036331	Q9UL18	AGO1_HUMAN	Piwi.	3	TACAGCGACCA	0.522	
+	3	456	HL2_uc001bzu.2_	NM_017825	NP_060295	Q9NX46	ARHL2_HUMAN		1	GCGATGTCTTT	0.557	
+	2	308	D1_uc001cab.2_	NM_018067	NP_060537	Q3KQU3	MA7D1_HUMAN	Pro-rich.	5	AGAAGGTGACC	0.597	
+	2	90	_p.R76W|MACF1_	NM_012090	NP_036222	Q9UPN3	MACF1_HUMAN		16	ATGAACGGGAC	0.507	
+	16	1754	da.1_Missense_M	NM_012090	NP_036222	Q9UPN3	MACF1_HUMAN		16	AGCTGGTCACC	0.393	
+	27	3474	p.R177K|MACF1_	NM_012090	NP_036222	Q9UPN3	MACF1_HUMAN		16	ATTAAGGATTGC	0.502	
+	4	6004	.1_Intron|MACF1_	NM_033044	NP_149033	Q9UPN3	MACF1_HUMAN		16	TGACAGCCTGA	0.413	
+	13	8013	.G2034S|MACF1_	NM_033044	NP_149033	Q9UPN3	MACF1_HUMAN		16	TGCAGGGCAAA	0.552	
+	1	3841	.1_Intron|MACF1_	NM_015038	NP_055853	O94854	K0754_HUMAN	Ala-rich.|2.	0	AGCCCACCTCC	0.721	
+	1	4075	.1_Intron|MACF1_	NM_015038	NP_055853	O94854	K0754_HUMAN	Ala-rich.|8.	0	AGCCCACCTCC	0.726	rs783822
+	31	12879	a.1_Nonsense_M	NM_033044	NP_149033	Q9UPN3	MACF1_HUMAN	23.|Spectrin 9.	16	AGGACCAGACC	0.478	
+	38	14020	s.1_Missense_Mu	NM_033044	NP_149033	Q9UPN3	MACF1_HUMAN		16	GAAGAGCATTG	0.438	
-	4	1440	4_uc001cdm.2_M	NM_003819	NP_003810	Q13310	PABP4_HUMAN		0	GCTCAGCTTCC	0.423	
-	1	881	tart_Site|PABPC4_	NM_003819	NP_003810	Q13310	PABP4_HUMAN		0	CACCACCCCGA	0.721	
+	3	186	dv.2_Missense_Mu	NM_006112	NP_006103	Q9UNP9	PPIE_HUMAN	RRM.	0	ACCGAGGATTTG	0.383	
-	2	519	_p.A101V|MYCL1_	NM_001033082	NP_001028254	P12524	MYCL1_HUMAN		2	CCCGGGCCGAG	0.706	
+	6	905	T229A|MFSD2A_u	NM_001136493	NP_001129965	Q8NA29	MFS2A_HUMAN		2	ACCATACACAT	0.547	
-	8	1030	_Splice_Site_p.Q	NM_000310	NP_000301	P50897	PPT1_HUMAN		1	AGTTACCTGTG	0.488	
+	8	2423	.3_Missense_Mut	NM_012421	NP_036553	Q13129	RLF_HUMAN		3	TTTAGGGATGCA	0.363	
+	5	1120		NM_152373	NP_689586	Q5T5D7	ZN684_HUMAN	2H2-type 5.	0	ACATTCCAGATT	0.378	
-	8	6887	e_Mutation_p.A18	NM_024503	NP_078779	Q5T1R4	ZEP3_HUMAN		6	GTCTGCCCGCA	0.672	
-	8	883	J3_uc001chg.2_M	NM_014947	NP_055762	Q9UPW0	FOXJ3_HUMAN		2	ACACTCCATTCC	0.323	
+	3	887	k.2_Missense_Mu	NM_024664	NP_078940	Q9HAB8	PPCS_HUMAN		0	ACTCGGAAACC	0.408	

-	1	165	RE1_uc001chy.3_	NM_022356	NP_071751	Q32P28	P3H1_HUMAN			4	GGCAGCGGCCA	0.692	
+	12	1301	se_Mutation_p.S	NM_001017922	NP_001017922	Q96PL5	ERMAP_HUMAN	(Potential).|B30.2/SPRY.		1	CACATCCCCGC	0.527	
-	9	1732		NM_006516	NP_006507	P11166	GTR1_HUMAN	lame=11; (Potential).		5	AATGGCAGCTG	0.547	
-	8	1036	1cim.2_Missense_	NM_006824	NP_006815	Q99848	EBP2_HUMAN			0	TGAGGCCTCTG	0.557	
+	10	1738	ense_Mutation_p.	NM_152498	NP_689711	Q96MR6	WDR65_HUMAN	WD 8.		1	GAATGGAATCT	0.458	
+	11	2147	0ojz.1_Intron|WD	NM_152498	NP_689711	Q96MR6	WDR65_HUMAN			1	CTCCTTCTTCTC	0.363	
+	4	1033	TMEM125_uc001c	NM_144626	NP_653227	Q96AQ2	TM125_HUMAN	ical; (Potential).		1	CTCTGGCTGCC	0.687	
+	4	542	p.R166K|MPL_uc	NM_005373	NP_005364	P40238	TPOR_HUMAN	tential).|Fibronectin type-III		363	CCTGAGGTACG	0.587	
+	44	5947		NM_015284	NP_056099	Q5T011	SZT2_HUMAN			0	CCATGGAAGTG	0.617	
+	44	6026		NM_015284	NP_056099	Q5T011	SZT2_HUMAN			0	TGGTGGGGGTC	0.642	
+	9	1830	_p.G68D|PTPRF_	NM_002840	NP_002831	P10586	PTPRF_HUMAN	tential).|Fibronectin type-III		10	CGATGGCCCTC	0.677	
+	16	3200	se_Mutation_p.V5	NM_002840	NP_002831	P10586	PTPRF_HUMAN	III 7.|Extracellular (Potentia		10	CCGTGGTGTTC	0.567	
+	27	4839	wt.2_Missense_M	NM_002840	NP_002831	P10586	PTPRF_HUMAN	hatase 1.|Cytoplasmic (Po		10	TGGCTCCAGTG	0.587	
-	5	892	d.2_RNA|SLC6A9	NM_201649	NP_964012	P48067	SC6A9_HUMAN	ellular (Potential).		0	GGCGTCCAGTA	0.622	
-	1	218	d.2_RNA|SLC6A	NM_201649	NP_964012	P48067	SC6A9_HUMAN	lasmic (Potential).		0	CGATCGCAGCC	0.667	
+	3	1172		NM_173484	NP_775755	Q5JT82	KLF17_HUMAN			2	CAGACCCACAG	0.493	
+	5	558	F|DMAP1_uc001c	NM_001034024	NP_001029196	Q9NPF5	DMAP1_HUMAN	SANT.		0	ACCACCTCTTT	0.517	
+	2	258	lb.1_Missense_M	NM_006845	NP_006836	Q99661	KIF2C_HUMAN	ular (Potential).		1	AGAAGGAGGTG	0.413	
+	7	945	3_uc001cmo.2_R	NM_004073	NP_004064	Q9H4B4	PLK3_HUMAN	rotein kinase.		0	TGCCAGCCTCT	0.622	
+	13	1664	3_uc001cmo.2_In	NM_004073	NP_004064	Q9H4B4	PLK3_HUMAN	OLO box 1.		0	CTGTGCCCCGG	0.597	
-	18	2843	lg.1_Missense_M	NM_003738	NP_003729	Q9Y6C5	PTC2_HUMAN	ellular (Potential).		18	GGTAGGCGTGC	0.672	
-	9	2300		NM_020883	NP_065934	Q9P217	ZSWM5_HUMAN			0	GGAGCTGCTCC	0.512	
+	1	791		NM_032756	NP_116145	Q96IR7	HPDL_HUMAN			0	CGGCAGCTCCC	0.682	
+	29	5651	e_Mutation_p.V17	NM_015112	NP_055927	Q6P0Q8	MAST2_HUMAN			11	CATTGGTTCCA	0.502	
-	10	2117	pc.3_Missense_M	NM_003629	NP_003620	Q92569	P55G_HUMAN			0	ATCTGTGCATGA	0.483	
+	3	541	pw.2_Missense_M	NM_147192	NP_671725	Q8NFW5	DMBX1_HUMAN			1	ACCCCCCTGCT	0.677	
-	3	719	BKL2C_uc001cqe	NM_201403	NP_958805	Q70IA8	MOL2C_HUMAN			1	CATGGACAAAG	0.557	
+	9	1187		NM_178134	NP_835235	Q86W10	CP4Z1_HUMAN	enal (Potential).		1	AGATGGACGCT	0.423	
+	1	638		NM_012186	NP_036318	Q13461	FOXE3_HUMAN	Fork-head.		0	TCAAGGTGCCC	0.652	
+	9	1122	ense_Mutation_p.	NM_001011547	NP_001011547	Q2M3M2	SC5A9_HUMAN	ellular (Potential).		3	CCAAAGAATCT	0.557	
+	10	1325	ense_Mutation_p.	NM_001011547	NP_001011547	Q2M3M2	SC5A9_HUMAN	lasmic (Potential).		3	AGCAGGAGCTG	0.587	
-	13	1595	p.A461V|SPATA6_	NM_019073	NP_061946	Q9NWH7	SPAT6_HUMAN			1	CTACAGGCCTTT	0.423	
-	7	602	F1_uc001cse.1_	NM_007051	NP_008982	Q9UNN5	FAF1_HUMAN		p.0?(1)	2	TGACTAGATGAT	0.338	
+	2	1232	1csg.2_Missense_	NM_001262	NP_001253	P42773	CDN2C_HUMAN	ANK 1.	p.0?(4)	17	CTTGGGGGAAC	0.468	
+	12	912	SBPL9_uc001csw	NM_024586	NP_078862	Q96SU4	OSBL9_HUMAN			1	TGATGCTGATG	0.398	
-	4	490		NM_002867	NP_002858	P20337	RAB3B_HUMAN			1	AGTAGGTCTTG	0.353	
-	1	736	C12_uc001cti.2_	NM_138417	NP_612426	Q96EK9	KTI12_HUMAN			2	GCCCACCAAAG	0.637	
-	1	575	C12_uc001cti.2_	NM_138417	NP_612426	Q96EK9	KTI12_HUMAN			2	CCCCGGATTCT	0.587	
+	4	935	p.D255N|ZFYVE9	NM_004799	NP_004790	O95405	ZFYV9_HUMAN			8	GTAGAGACCCC	0.433	
+	3	482	.1_Intron|FAM159	NM_001042693	NP_001036158	Q6UWV7	F159A_HUMAN			0	AAGTGCCAAAA	0.562	
+	3	1073	G11B_uc010onj.1	NM_024646	NP_078922	Q9C0D3	ZY11B_HUMAN			4	GTCCAAGCATGC	0.403	
+	7	914	nr.1_Missense_M	NM_153703	NP_714914	Q7Z5L7	PODN_HUMAN	LRR 7.		2	TCCCCCCGGGG	0.617	
-	4	271	C1orf123_uc001c	NM_017887	NP_060357	Q9NWV4	CA123_HUMAN			2	ACCTACCGATG	0.562	rs112803850
-	13	2107	j.1_Missense_Mu	NM_004631	NP_004622	Q14114	LRP8_HUMAN	s B 5.|Extracellular (Potenti		0	AGCCGATTTGC	0.512	
-	4	2131		NM_201546	NP_963840	Q5VXM1	CDCP2_HUMAN			1	TTAGGGGTCCC	0.582	
+	3	496	orf175_uc010oof.1	NM_001039464	NP_001034553	Q68CQ1	HEAT8_HUMAN			0	CTCTCGTTCCA	0.572	
-	48	5585		NM_015306	NP_056121	Q9UPU5	UBP24_HUMAN			13	TATGGGTTTGCT	0.373	

+	1	145		NM_006252	NP_006243	P54646	AAPK2_HUMAN	ase.|ATP (By similarity).	6	CGTCGGCACCT	0.647
-	18	2472	rf168_uc001cyl.2_	NM_001004303	NP_001004303	Q5VWT5	CA168_HUMAN		5	ATTCTTCTCCAG	0.323
+	8	1307		NM_000562	NP_000553	P07357	CO8A_HUMAN	MACPF.	3	TTGGTGGAGGTT	0.413
-	14	1849	r.1_Missense_Mut	NM_021080	NP_066566	O75553	DAB1_HUMAN		3	TCGTGCCTGGG	0.592
-	12	1432	r.1_Missense_Mut	NM_021080	NP_066566	O75553	DAB1_HUMAN		3	GGTGTGGACATG	0.438
-	9	1363	SM1_uc001czc.2_	NM_001085487	NP_001078956	Q5VVJ2	MYSM1_HUMAN	SWIRM.	1	ATCCGTCCAATA	0.348
+	16	1591	OK1_uc001czp.2_	NM_015888	NP_056972	Q9UJC3	HOOK1_HUMAN	tion with microtubules.|Pote	2	CAGCTAGAACAG	0.403
+	19	1846	OK1_uc001czp.2_	NM_015888	NP_056972	Q9UJC3	HOOK1_HUMAN		2	AAAATGGTAGGT	0.353
-	5	739		NM_152377	NP_689590	Q8N0U7	CA087_HUMAN		2	GCTGAGATTGG	0.423
+	8	1007	DL_uc001daa.2_M	NM_176877	NP_795352	Q8NI35	INADL_HUMAN	PDZ 2.	4	TGGTGGCACAA	0.438
+	27	3743	dbq.1_Missense_	NM_020925	NP_065976	Q5VU97	CAHD1_HUMAN	lasmic (Potential).	2	GGCGGCCGTCA	0.517
+	13	1923	_p.P574S|DNAJC6	NM_014787	NP_055602	O75061	AUXI_HUMAN	Pro-rich.	3	GGAGCACCTTCT	0.443
+	16	2387	_p.M728I|DNAJC6	NM_014787	NP_055602	O75061	AUXI_HUMAN	Pro-rich.	3	CAGCATGCCCCA	0.612
+	3	333	DE4B_uc001dco.2	NM_001037341	NP_001032418	Q07343	PDE4B_HUMAN		3	TGCTCAGGAAAC	0.458
+	3	253	u.2_RNA|TCTEX1	NM_152665	NP_689878	Q8N7M0	TC1D1_HUMAN		0	TTAGTTCTATGAG	0.318
-	12	1861	se_Mutation_p.G3	NM_024763	NP_079039	Q5VTH9	WDR78_HUMAN	WD 2.	2	CCATCTCCTGTT	0.348
-	12	1816	se_Mutation_p.P3	NM_024763	NP_079039	Q5VTH9	WDR78_HUMAN	WD 2.	2	CATACAGGTCCC	0.328
+	7	813	df.2_Missense_M	NM_001077700	NP_001071168	Q8N108	MIER1_HUMAN	Glu-rich.	1	TATATTCCATCAG	0.249
-	12	1435		NM_015139	NP_055954	Q9NTN3	S35D1_HUMAN		0	CTTTCCCCTTAAT	0.453
-	1	499	D1_uc010oph.1_	NM_015139	NP_055954	Q9NTN3	S35D1_HUMAN	ical; (Potential).	0	AAACACGGTCA	0.557
+	11	1325	0opt.1_Splice_Sit	NM_144701	NP_653302	Q5VWK5	IL23R_HUMAN		0	TCCTAGGAAAAT	0.318
-	7	1246	ldy.2_Missense_M	NM_001018067	NP_001018077	Q8NC51	PAIRB_HUMAN		1	CCCTGCCGCCA	0.517
-	8	1820	DC1_uc001dek.3_	NM_001114120	NP_001107592	Q5TB30	DEP1A_HUMAN		0	TCTATTGTACTTT	0.388
+	4	737	dge.1_Intron|FPG	NM_003838	NP_003829	O14772	FPGT_HUMAN		1	AGCATAGAAAAG	0.388
+	2	109	dgd.2_Missense_	NM_015978	NP_057062	Q59H18	TNI3K_HUMAN		10	AAAAAAGTCAGT	0.308
-	14	4553		NM_001002912	NP_001002912	Q5RHP9	CA173_HUMAN	Glu-rich.	5	CCTGTCCTAGC	0.592
-	14	3809		NM_001002912	NP_001002912	Q5RHP9	CA173_HUMAN	Glu-rich.	5	CTGCTGGACAGC	0.557
-	14	3013		NM_001002912	NP_001002912	Q5RHP9	CA173_HUMAN	Glu-rich.	5	CAGCCTCTCCCT	0.537
-	24	2207	10oqz.1_Intron|SL	NM_152697	NP_689910	Q8NCS7	CTL5_HUMAN	lasmic (Potential).	4	TCATTTCTTTCCA	0.418
+	14	1828		NM_002440	NP_002431	O15457	MSH4_HUMAN		5	GATAGTGTGCA	0.323
+	2	344	se_Mutation_p.H6	NM_152996	NP_694541	Q8NDV1	SIA7C_HUMAN	enal (Potential).	5	CGAACTCACTAT	0.438
-	8	754	x.2_Missense_Mu	NM_005482	NP_005473	Q92643	GPI8_HUMAN	enal (Potential).	3	GATCAGGTTGAT	0.308
-	1	141	n.1_Missense_Mut	NM_003902	NP_003893	Q96AE4	FUBP1_HUMAN	Gly-rich.	3	ccaccaccgccacca	0.488
+	6	1104		NM_017655	NP_060125	Q8TF65	GIPC2_HUMAN		1	TTGGGGAGTCA	0.403
+	5	928	1_5'UTR|IFI44L_u	NM_006820	NP_006811	Q53G44	IF44L_HUMAN		0	AGATGGAAAAA	0.373
-	9	1285		NM_022159	NP_071442	Q9HBW9	ELTD1_HUMAN	tracellular (Potential).	2	TATCAGGTGAGT	0.403
+	11	2268	se_Mutation_p.R6	NM_012302	NP_036434	O95490	LPHN2_HUMAN	cellular (Potential).	9	ACAGCAGGAATG	0.358
-	1	216	S_uc001dkd.2_5'	NM_004388	NP_004379	Q01459	DIAC_HUMAN		0	AATCGGGCGGC	0.542
-	7	948	A225_splice|SSX2I	NM_014021	NP_054740	Q9Y2D8	ADIP_HUMAN		2	TGTTTACCTATT	0.303
-	2	256	LN3_uc001dkr.2_	NM_018298	NP_060768	Q8TDD5	MCLN3_HUMAN		1	TCGAGCCCAGA	0.398
-	6	949	_uc010osb.1_Mis	NM_012137	NP_036269	O94760	DDAH1_HUMAN		0	GTTCAGACATG	0.473
-	39	3406	_Mutation_p.G422	NM_152890	NP_690850	Q17RW2	COOA1_HUMAN	llagen-like 11.	5	TTTGTCCTTTATC	0.403
+	14	2764		NM_001285	NP_001276	A8K7I4	CLCA1_HUMAN		1	CTGATGAAACG	0.423
+	14	2771		NM_001285	NP_001276	A8K7I4	CLCA1_HUMAN		1	AACGTCTGCTC	0.418
-	7	1109		NM_002053	NP_002044	P32455	GBP1_HUMAN		2	CAGCACCAGGC	0.473
-	7	1340	P2_uc001dmy.1_	NM_004120	NP_004111	P32456	GBP2_HUMAN		1	ACTGTCCCTGT	0.512
-	8	1413	P2_uc001dmy.1_	NM_207398	NP_997281	Q8N8V2	GBP7_HUMAN		2	AGAAAGTTCCT	0.428

+	5	713	st.1_Missense_Mu	NM_198460	NP_940862	Q6ZN66	GBP6_HUMAN		2	TGACGGAGCTC	0.403	
+	7	1487	_p.G327D|LRRC8	NM_001134476	NP_001127948	Q6P9F7	LRC8B_HUMAN	ical; (Potential).	2	TTTATGGTCTGAC	0.428	
-	4	3614	.2_Intron|ZNF644_	NM_201269	NP_958357	Q9H582	ZN644_HUMAN		3	GTTCTGGTTTTG	0.383	
+	6	1051	BD8_uc010otc.1_	NM_183242	NP_899065	Q5XKL5	BTBD8_HUMAN	BTB 2.	1	ATGATGCATTTT	0.279	
+	6	1067	BD8_uc010otc.1_	NM_183242	NP_899065	Q5XKL5	BTBD8_HUMAN	BTB 2.	1	TGGAGGAACTCT	0.299	
+	11	1392	e_Mutation_p.G26	NM_007358	NP_031384	Q9Y483	MTF2_HUMAN		2	CTGAAGGAACAT	0.378	
+	11	1419	se_Mutation_p.G2	NM_007358	NP_031384	Q9Y483	MTF2_HUMAN		2	TAAAGGCAGAA	0.353	
+	1	229	ED5_uc001dpo.2_	NM_206886	NP_996769	Q5T9S5	CCD18_HUMAN		5	GGCGGGCTCCG	0.726	
+	4	281	dpv.2_Missense_	NM_001024948	NP_001020119	Q5T0N5	FBP1L_HUMAN	rane tubulation (By similari	0	AATGGCGCACA	0.348	
-	25	3804		NM_000350	NP_000341	P78363	ABCA4_HUMAN	Cytoplasmic.	12	ATTTGGAAGAAG	0.473	
-	23	3431	AP29_uc009wdq.1	NM_004815	NP_004806	Q52LW3	RHG29_HUMAN		11	CTACAGGCAAA	0.398	
+	2	438	e_Mutation_p.G12	NM_015485	NP_056300	Q9Y3V2	RWDD3_HUMAN		1	AACTGGCAGTG	0.448	
-	20	2759		NM_000110	NP_000101	Q12882	DPYD_HUMAN		8	CACATACCTTGT	0.413	
-	5	1135	sc.2_Missense_Mu	NM_001037317	NP_001032394	Q32ZL2	LPPR5_HUMAN		0	CCTTTTCCAAAG	0.353	
+	4	708	ue.1_Missense_Mu	NM_014839	NP_055654	Q7Z2D5	LPPR4_HUMAN		3	CCACAGGATATC	0.368	
-	7	1324		NM_001013660	NP_001013682	Q6ZNA5	FRRS1_HUMAN	DOMON.	1	AAATAGCCTTTAC	0.413	
+	3	472	_p.G92E|SLC35A	NM_012243	NP_036375	Q9Y2D2	S35A3_HUMAN		0	CATCAGGGATCT	0.299	
+	8	1149	LC35A3_uc001ds	NM_012243	NP_036375	Q9Y2D2	S35A3_HUMAN		0	CCAAACCTGCA	0.363	
-	7	740	vdz.2_Missense_	NM_194292	NP_919268	Q6UVJ0	SAS6_HUMAN	Potential.	2	GTGACGCCCAT	0.328	
-	9	1090	g.1_Missense_Mut	NM_001918	NP_001909	P11182	ODB2_HUMAN		1	CAAACCCTGCT	0.393	
-	17	1747	vl.1_Missense_Mu	NM_006113	NP_006104	Q9UKW4	VAV3_HUMAN		9	AATTAACTCTGC	0.343	
-	7	992	_p.A252T|C1orf59_	NM_001102592	NP_001096062	Q5T8I9	HENMT_HUMAN		0	TCACAGCTTTATA	0.403	
-	13	2720	lwi.2_Missense_M	NM_001142551	NP_001136023	O94967	WDR47_HUMAN	WD 4.	1	GAAGATCCCAAA	0.353	
+	3	399	1324_uc009wey.2_	NM_020775	NP_065826	Q6UXG2	K1324_HUMAN	ellular (Potential).	5	CAAGGGCACCG	0.632	
+	1	1247		NM_001408	NP_001399	Q9HCU4	CELR2_HUMAN	|Extracellular (Potential).	8	GATAATGCCCCC	0.587	
+	3	4107		NM_001408	NP_001399	Q9HCU4	CELR2_HUMAN	ial).|EGF-like 3; calcium-bi	8	GGTGGGCGGTT	0.617	
+	4	4284		NM_001408	NP_001399	Q9HCU4	CELR2_HUMAN	otential).|Laminin G-like 1.	8	ACAATGGGCGTT	0.582	
+	21	6920		NM_001408	NP_001399	Q9HCU4	CELR2_HUMAN	ellular (Potential).	8	ATCAGCGTCCAT	0.612	rs141489111
+	27	7857		NM_001408	NP_001399	Q9HCU4	CELR2_HUMAN	Name=7; (Potential).	8	GCAATTGCATCC	0.617	
-	2	819		NM_020703	NP_065754	Q86WK6	AMGO1_HUMAN	tracellular (Potential).	2	GCCATGATGTGG	0.557	
+	8	666	TM2_uc009wfk.2_	NM_001142368	NP_001135840	P28161	GSTM2_HUMAN		0	AGCATTCCTGAT	0.443	
-	5	509	9wfm.1_Missense_	NM_133181	NP_573444	Q8TE67	ES8L3_HUMAN		3	GCCTGGCAGGC	0.587	
+	7	734	_p.A144T|FAM40	NM_033088	NP_149079	Q5VSL9	FA40A_HUMAN		4	ACAAGGCTGAG	0.582	
+	10	2005		NM_001010898	NP_001010898	Q9H1V8	S6A17_HUMAN	ellular (Potential).	2	GCGCTCCGGAA	0.572	
+	1	2211	sense_Mutation_p.	NM_022768	NP_073605	Q96T37	RBM15_HUMAN	Arg-rich.	3	GTTTGGAGAAG	0.517	
-	7	1419	ovy.1_Missense_	NM_004696	NP_004687	O15374	MOT5_HUMAN	ical; (Potential).	3	CCAGTACAGGCA	0.388	rs140070822
-	6	928	ovy.1_Missense_	NM_004696	NP_004687	O15374	MOT5_HUMAN	lasmic (Potential).	3	TTTTGCTAGGTA	0.423	
-	1	1682		NM_005549	NP_005540	Q16322	KCA10_HUMAN		4	CCCTGGGGTGG	0.552	
-	1	1494		NM_002232	NP_002223	P22001	KCNA3_HUMAN		5	AGTGGGGTCGT	0.567	
-	3	1959	eab.2_Missense_	NM_018372	NP_060842	Q5T3J3	LRIF1_HUMAN		0	AATTCAGCATCA	0.388	
-	2	456	f103_uc001eab.2_	NM_018372	NP_060842	Q5T3J3	LRIF1_HUMAN		0	TTCAAAGCATCA	0.393	
+	3	626	ai.1_Missense_M	NM_001007794	NP_001007795	Q9Y6K0	CEPT1_HUMAN		0	AACAGGCAAGA	0.378	
+	7	696	ao.2_Missense_M	NM_004000	NP_003991	Q15782	CH3L2_HUMAN		1	ATCAACCTCCTG	0.473	
+	8	753	eat.2_Missense_	NM_201653	NP_970615	Q9BZP6	CHIA_HUMAN		1	TGGCTCCTGGG	0.532	
-	11	1233	_p.P355S|OVGP1_	NM_002557	NP_002548	Q12889	OVGP1_HUMAN		5	ATTGTGGTAAAG	0.423	
-	5	412	1_uc010owb.1_5'	NM_002557	NP_002548	Q12889	OVGP1_HUMAN		5	ATAAACTTTTCAC	0.448	
+	6	951	e_Mutation_p.A32	NM_001688	NP_001679	P24539	AT5F1_HUMAN		0	CTATGGCTTTGG	0.373	

+	11	2171	p.G367E|DDX20_	NM_007204	NP_009135	Q9UHI6	DDX20_HUMAN			2	AGAGGGGTTAG	0.408	
+	3	428	2_Missense_Mutat	NM_001130079	NP_001123551	Q9HCE1	MOV10_HUMAN			5	CCCCTGGCTTCT	0.627	
+	4	793	p.P175S|MOV10_	NM_001130079	NP_001123551	Q9HCE1	MOV10_HUMAN			5	GGACACCCCAG	0.577	rs146126921
+	4	841	.G191S|MOV10_	NM_001130079	NP_001123551	Q9HCE1	MOV10_HUMAN			5	CACTGGCCCC	0.562	
-	9	1349	M1J_uc001ecs.1_	NM_005167	NP_005158	Q5JR12	PPM1J_HUMAN	PP2C-like.		3	CAGTGGCAGCT	0.547	
+	4	386	G129R|FAM19A3_	NM_182759	NP_877436	Q7Z5A8	F19A3_HUMAN			0	GCCGGGGGAGG	0.622	
+	7	1800	p.H547Y|HIPK1_u	NM_198268	NP_938009	Q86Z02	HIPK1_HUMAN			4	AGGGTTCACATG	0.398	
+	9	2232	1_uc001eeo.2_Mi	NM_198268	NP_938009	Q86Z02	HIPK1_HUMAN			4	GCTCAGCCACTA	0.438	
+	11	2508	eo.2_Missense_M	NM_198268	NP_938009	Q86Z02	HIPK1_HUMAN			4	CAGAGGCCATG	0.552	
-	15	2774	_p.G529E|TRIM33	NM_015906	NP_056990	Q9UPN9	TRI33_HUMAN	PHD-type.		11	AGATCTCCTCCG	0.433	
-	16	2210	|AMPD1_uc001eff	NM_000036	NP_000027	P23109	AMPD1_HUMAN			4	CAGGGCCTTCC	0.428	
-	14	2058	1eff.1_Splice_Site_	NM_000036	NP_000027	P23109	AMPD1_HUMAN			4	ACTATACCTTGG	0.368	rs145328844
-	3	436		NM_002524	NP_002515	P01111	RASN_HUMAN	GTP.	)|p.Q61P(21)|	2607	TCTTCTTGTCCAC	0.458	rs11554290
-	3	427		NM_002524	NP_002515	P01111	RASN_HUMAN	GTP.	p.T58I(2)	2607	CCAGCTGTATCC	0.478	
-	19	2799	p.G747E|CSDE1_	NM_001007553	NP_001007554	O75534	CSDE1_HUMAN			1	CTGGTCCCCTTG	0.478	
-	17	2393	E1_uc001efm.2_	NM_001007553	NP_001007554	O75534	CSDE1_HUMAN	CSD 8.		1	ATCCCCTTTGTT	0.483	
+	4	503	_p.A76T|VANGL1	NM_138959	NP_620409	Q8TAA9	VANG1_HUMAN	lasmic (Potential).		1	CCACGGCCATC	0.542	
+	4	665	_p.L130F|VANGL1	NM_138959	NP_620409	Q8TAA9	VANG1_HUMAN	Name=1; (Potential).		1	TTCATCCTTTTAC	0.522	
+	6	1236	wgy.1_Missense_	NM_138959	NP_620409	Q8TAA9	VANG1_HUMAN	lasmic (Potential).		1	TGCCACTGGCC	0.517	
-	6	2254	p.V537M|IGSF3_	NM_001007237	NP_001007238	O75054	IGSF3_HUMAN	4.|Extracellular (Potential).		2	CCGCACCCATT	0.607	
-	3	842	gq.1_Missense_M	NM_001007237	NP_001007238	O75054	IGSF3_HUMAN	1.|Extracellular (Potential).		2	TGGTAGCCACTC	0.572	
+	4	1091	xc.1_Missense_M	NM_004258	NP_004249	Q93033	IGSF2_HUMAN	3.|Extracellular (Potential).		4	AGAGAGCAAGT	0.498	
+	5	413	x.1_Missense_Mu	NM_003594	NP_003585	Q9UNY4	TTF2_HUMAN			1	GACAAGAATCA	0.408	
+	15	2563		NM_003594	NP_003585	Q9UNY4	TTF2_HUMAN			1	GCTTTCTGAAG	0.358	
-	6	2285	p.G548D|TRIM45_	NM_025188	NP_079464	Q9H8W5	TRI45_HUMAN			1	GCCCACCTGTC	0.527	
-	2	1787	RIM45_uc001eha.	NM_025188	NP_079464	Q9H8W5	TRI45_HUMAN	Filamin.		1	CATTTGGCTGGA	0.473	
-	1	662	e_Mutation_p.G2	NM_025188	NP_079464	Q9H8W5	TRI45_HUMAN			1	TCTTGCCTGAG	0.522	
-	36	5422		NM_206996	NP_996879	Q6Q759	SPG17_HUMAN		p.S1785S(1)	6	TAAGGGAAACC	0.443	
-	5	702		NM_206996	NP_996879	Q6Q759	SPG17_HUMAN			6	TACTGACCAATG	0.478	
-	8	1684	hj.1_Missense_M	NM_152380	NP_689593	Q96SF7	TBX15_HUMAN			2	GTGCTCCATCC	0.552	
-	8	1223	hj.1_Missense_M	NM_152380	NP_689593	Q96SF7	TBX15_HUMAN			2	GCAAGGCAGCC	0.547	
-	2	272	RS2_uc010oxg.1_	NM_015836	NP_056651	Q9UGM6	SYWM_HUMAN			0	TTGGGGGACAG	0.493	rs142739265
-	5	917	_p.P247L|HMGCS	NM_005518	NP_005509	P54868	HMCS2_HUMAN			2	TGAAGGGTCGA	0.502	rs146296049
-	34	6636		NM_024408	NP_077719	Q04721	NOTC2_HUMAN	lasmic (Potential).		27	TACCCTTGGCAT	0.507	
-	27	4180	4DIP_uc001elm.3	NM_014644	NP_055459	Q5VU43	MYOME_HUMAN			5	CTCACACTCTG	0.502	
-	23	3397	E4DIP_uc001elm.	NM_014644	NP_055459	Q5VU43	MYOME_HUMAN	Potential.		5	CTGCTTCCTCAA	0.532	
-	22	3121	1elo.2_Intron|PDE	NM_014644	NP_055459	Q5VU43	MYOME_HUMAN			5	TGTCATCCCCTG	0.488	
-	19	2833	001elx.3_Missens	NM_014644	NP_055459	Q5VU43	MYOME_HUMAN	Potential.		5	TTGACCCTGGG	0.353	
-	12	1896	1elx.3_Splice_Site	NM_014644	NP_055459	Q5VU43	MYOME_HUMAN			5	CTCTTACTTGCA	0.473	
+	3	565	10_uc001emp.3_	NM_153713	NP_714924	Q8IVB5	LIX1L_HUMAN			1	GAGTGCTGCAA	0.473	
+	5	409	nu.1_Missense_M	NM_005105	NP_005096	Q9Y5S9	RBM8A_HUMAN	RRM.		0	GGAAGCCCAGG	0.478	
-	5	772	_p.S217L|POLR3	NM_006468	NP_006459	Q9BUI4	RPC3_HUMAN			1	TCAGATGATCTC	0.428	
-	4	681	k|POLR3C_uc001	NM_006468	NP_006459	Q9BUI4	RPC3_HUMAN			1	TGGTGGTGGCC	0.478	
-	2	91		NR_024442						0	CAGAATCTAGGG	0.532	
+	1	498		NR_002305						0	ATAGTCCCATTAC	0.473	
+	9	3760	r.1_Missense_Mu	NM_004326	NP_004317	O00512	BCL9_HUMAN	Pro-rich.		6	CACTCTCTATTAT	0.512	
-	2	964	t.1_Missense_Mu	NM_181703	NP_859054	P36382	CXA5_HUMAN	lasmic (Potential).		1	CCCAGGGCCAT	0.552	

-	8	882	tron|NBPF14_uc01	NM_015383	NP_056198	Q5TI25	NBPFE_HUMAN	NBPF 3.	1	CTTCAGGCCCTT	0.478	
-	4	598	P188L|uc001erc.3_	NM_017940	NP_060410	Q86T75	NBPFB_HUMAN	NBPF 1.	0	ACCTGGGGGCA	0.428	
-	1	244	_p.S65F|HIST2H2	NM_001024599	NP_001019770	Q5QNW6	H2B2F_HUMAN		0	ACGAAGGAGTTC	0.617	
-	2	519	th.2_Missense_Mu	NM_014849	NP_055664	Q7L0J3	SV2A_HUMAN	Interaction with SYT1 (By s	7	GAAAGCTGCCC	0.542	
-	12	2329		NM_020205	NP_064590	Q6GQQ9	OTU7B_HUMAN		3	CCACCCCCTATT	0.562	
-	12	1716		NM_020205	NP_064590	Q6GQQ9	OTU7B_HUMAN		3	TCCAGCTGAGG	0.627	
+	14	2096	PS45_uc010pbs.1_	NM_007259	NP_009190	Q9NRW7	VPS45_HUMAN		2	AATTGGAGGAG	0.428	
+	6	984	_p.P195L|C1orf51_	NM_144697	NP_653298	Q8N365	CA051_HUMAN		0	ATGGTCCTTTAG	0.552	
+	11	2953	_p.V892I|RPRD2_	NM_015203	NP_056018	Q5VT52	RPRD2_HUMAN	Ser-rich.	1	TCAGCGTAAGA	0.507	
+	11	3664	PRD2_uc001eup.3_	NM_015203	NP_056018	Q5VT52	RPRD2_HUMAN	Poly-Gly.	1	GTGGGGGCAGC	0.532	
+	9	998	.2_Intron|TARS2_	NM_025150	NP_079426	Q9BW92	SYTM_HUMAN		1	ACAAGGGTGTAT	0.527	
+	3	365	CM1_uc001euu.2_	NM_004425	NP_004416	Q16610	ECM1_HUMAN		3	AGCCTCCCCATG	0.607	
-	3	1145	p.A229T|MCL1_u	NM_021960	NP_068779	Q07820	MCL1_HUMAN	ical; (Potential).	0	TCCAGCAACAC	0.433	
+	13	1382		NM_003568	NP_003559	O76027	ANXA9_HUMAN	Annexin 4.	0	GACTGACCTTCT	0.483	
+	2	1136		NM_006818	NP_006809	Q13015	AF1Q_HUMAN		0	TCCACTCCTTCG	0.527	
-	15	1846	eww.2_Missense_	NM_030913	NP_112175	Q9H3T2	SEM6C_HUMAN	ılar (Potential).|Sema.	2	GCTGAGAGGGA	0.617	
-	3	1297	pcr.1_Missense_M	NM_212551	NP_997716	Q96S90	LYSM1_HUMAN		0	ATCCTCCTGGT	0.562	
+	10	1662	P5K1A_uc001exk.	NM_001135638	NP_001129110	Q99755	PI51A_HUMAN	PIPK.	3	ATCATTGACATT	0.428	
-	6	663	_Mutation_p.A144	NM_003944	NP_003935	Q13228	SBP1_HUMAN		0	GGGAGCTGCCC	0.587	
-	4	337	_Intron|SELENBP	NM_003944	NP_003935	Q13228	SBP1_HUMAN		0	GACTGGGCAGC	0.607	
-	6	1081	Z_uc010pdc.1_Mi	NM_015100	NP_055915	Q7Z3K3	POGZ_HUMAN		3	CAGTGGGAGTGG	0.577	
+	19	3394	de.1_Missense_Mu	NM_020770	NP_065821	Q9P2M7	CING_HUMAN	Potential.	3	GTTAAAGAACTA	0.493	
+	20	3469	e.1_Missense_Mu	NM_020770	NP_065821	Q9P2M7	CING_HUMAN	Potential.	3	GTGAAGGCTTTG	0.542	
+	2	348	e_Mutation_p.G18	NM_030918	NP_112180	Q96L92	SNX27_HUMAN	PDZ.	3	TGAGGGGGCGA	0.493	
+	3	729	_p.G145E|SNX27_	NM_030918	NP_112180	Q96L92	SNX27_HUMAN	PX.	3	GTCGGGGATTGG	0.408	
-	4	567	DRKH_uc001eza.3	NM_006862	NP_006853	Q9Y2W6	TDRKH_HUMAN	KH 2.	2	CTGAAAGCTGCT	0.483	
-	2	1958		NM_001004432	NP_001004432	Q6UY18	LIGO4_HUMAN	lasmic (Potential).	1	CTTGGCAGTGA	0.542	
-	2	1436		NM_001004432	NP_001004432	Q6UY18	LIGO4_HUMAN	Potential).|Ig-like C2-type.	1	ACTTTCGGATCA	0.612	rs140280186
-	2	1313		NM_001004432	NP_001004432	Q6UY18	LIGO4_HUMAN	lar (Potential).|LRRCT.	1	CAGGTGGCGGC	0.612	
-	2	452		NM_001004432	NP_001004432	Q6UY18	LIGO4_HUMAN	ılar (Potential).|LRR 2.	1	CCAATTCCTGGA	0.622	
-	3	412	uc001ezm.1_Intron	NM_005620	NP_005611	P31949	S10AB_HUMAN		0	GGACAGCCTTGA	0.532	
-	2	4600	ne.1_Missense_Mu	NM_007113	NP_009044	Q07283	TRHY_HUMAN	proximate tandem repeats.	5	CCTGGAGGAATT	0.597	
-	2	1528	ne.1_Missense_Mu	NM_007113	NP_009044	Q07283	TRHY_HUMAN	roximate tandem repeats.	5	CTTGCTCCCGCC	0.577	
-	3	2184		NM_001122965	NP_001116437	Q6XPR3	RPTN_HUMAN	Gln-rich.	0	GCTCTTCCTCTG	0.562	
-	3	6564		NM_001009931	NP_001009931	Q86YZ3	HORN_HUMAN	24	3	CCAGACCCATGC	0.622	
-	3	10606		NM_002016	NP_002007	P20930	FILA_HUMAN	rich.|Filaggrin 21.	16	ATTGTCCCTGGC	0.567	
-	3	10301		NM_002016	NP_002007	P20930	FILA_HUMAN	Ser-rich.	16	GCCTGGAGCTG	0.597	
-	3	3494	uc001ezv.2_5'Flan	NM_002016	NP_002007	P20930	FILA_HUMAN	Ser-rich.	16	GCCTGGAGCTG	0.602	
-	3	2450	uc001ezv.2_5'Flan	NM_002016	NP_002007	P20930	FILA_HUMAN	Ser-rich.	16	GGGAGGACTCA	0.572	rs72698904
-	3	1807	uc001ezv.2_5'Flan	NM_002016	NP_002007	P20930	FILA_HUMAN	ggrin 3.|Ser-rich.	16	AGGAAGCTTCAT	0.557	
-	3	4899	uc001ezv.2_Intron	NM_001014342	NP_001014364	Q5D862	FILA2_HUMAN	Filaggrin 6.	17	AATTCTGGCTCT	0.522	
-	3	4470	uc001ezv.2_Intron	NM_001014342	NP_001014364	Q5D862	FILA2_HUMAN	Filaggrin 5.	17	GTAGTTCCGTGT	0.502	
-	3	2586	uc001ezv.2_Intron	NM_001014342	NP_001014364	Q5D862	FILA2_HUMAN	Ser-rich.	17	GATCTAGACTCAT	0.512	
-	3	1140	uc001ezv.2_Intron	NM_001014342	NP_001014364	Q5D862	FILA2_HUMAN	Ser-rich.	17	CTAGCTCCATAT	0.522	
-	2	129		NM_016190	NP_057274	Q9UBG3	CRNN_HUMAN		3	TCCTTGCATAGC	0.522	
+	2	119		NM_001025231	NP_001020402	Q5T749	KPRP_HUMAN	Gln-rich.	5	AGGGTCCCTCC	0.582	
+	2	299	R1B_uc009wnx.1_	NM_003125	NP_003116	P22528	SPR1B_HUMAN		1	TCACTCCAGCA	0.617	

-	2	251		NM_001014291	NP_001014313	Q9BYE4	SPR2G_HUMAN	proximate tandem repeats.	0	ATGCTCAGGTG	0.597	
+	3	356		NM_176823	NP_789793	Q86SG5	S1A7A_HUMAN		1	GGGAAGCCAGT	0.532	
+	2	307	.G29E|INTS3_uc0	NM_023015	NP_075391	Q68E01	INT3_HUMAN	Ala/Gly-rich.	3	ggagcaggagcccca	0.413	rs140871791
+	8	947_948	_Missense_Mutati	NM_023015	NP_075391	Q68E01	INT3_HUMAN		3	GGGAACGGGT	0.515	
+	16	1841	p.E334D|INTS3_u	NM_023015	NP_075391	Q68E01	INT3_HUMAN		3	GAAGAGGATCT	0.512	
-	7	1389		NM_020699	NP_065750	Q8WXI9	P66B_HUMAN	CR2.	0	CTGCACTAGGC	0.478	
-	32	4510	p.H389Y|NUP210L	NM_207308	NP_997191	Q5VU65	P210L_HUMAN		11	GGCATGCTCTA	0.493	
-	10	1355	_Site|NUP210L_u	NM_207308	NP_997191	Q5VU65	P210L_HUMAN		11	CAACACCATCT	0.403	
-	4	638	0peh.1_Splice_Sit	NM_207308	NP_997191	Q5VU65	P210L_HUMAN		11	AGTTTACCTAATT	0.418	
+	6	646	pel.1_Missense_	NM_014847	NP_055662	Q14157	UBP2L_HUMAN		2	TGGCACCAAGA	0.448	
+	5	816	.P227S|HAX1_uc	NM_006118	NP_006109	O00165	HAX1_HUMAN	calization in sarcoplasmic r	0	CTAAACCAGAT	0.483	
-	3	1012	HE_uc001ffc.2_R	NM_001010846	NP_001010846	Q5VZ18	SHE_HUMAN		6	TGGGGGCCGCG	0.667	
-	1	629	_uc001ffd.2_5'Flan	NM_001010846	NP_001010846	Q5VZ18	SHE_HUMAN	Ser-rich.	6	CCCAGggaggaa	0.433	rs138829106
-	9	1068		NM_017582	NP_060052	Q7Z7E8	UB2Q1_HUMAN		0	TCAAAGGGAAAG	0.597	
-	2	544	115D|ADAR_uc0	NM_001111	NP_001102	P55265	DSRAD_HUMAN		6	TCCTGCCACGT	0.532	
-	2	1278	_p.L17F|KCNN3_u	NM_002249	NP_002240	Q9UGI6	KCNN3_HUMAN	=Segment S2; (Potential).	1	TGATAAGGCATT	0.542	
-	10	1944	p.A600T|PBXIP1_	NM_020524	NP_065385	Q96AQ6	PBIP1_HUMAN		1	CCCAGCCCAGG	0.602	
-	10	972	.G276R|PBXIP1_	NM_020524	NP_065385	Q96AQ6	PBIP1_HUMAN	Potential.	1	TAGCCCTTTGG	0.592	
-	9	1431	se_Mutation_p.P4	NM_183001	NP_892113	P29353	SHC1_HUMAN	CH1.	2	TTCTGGATCTC	0.592	
+	3	1511	e_Mutation_p.T28	NM_025207	NP_079483	Q8NFF5	FAD1_HUMAN		3	TACAGACCATTG	0.562	
+	11	1216	72L|ADAM15_uc0	NM_207197	NP_997080	Q13444	ADA15_HUMAN	B.|Extracellular (Potential).	6	AGCCCCAGCCA	0.637	
+	2	229	6_uc001fht.1_RN	NM_025058	NP_079334	Q7Z4K8	TRI46_HUMAN	ype 1; degenerate.	3	CTGTACCCACA	0.612	
-	22	2727	ense_Mutation_p.	NM_007112	NP_009043	P49746	TSP3_HUMAN	P C-terminal.	5	ATCCGCCACAA	0.537	
-	13	1695	MP3_uc001fjt.2_	NM_003993	NP_003984	P49760	CLK2_HUMAN	rotein kinase.	0	CAAGGTCAGCC	0.567	
-	5	586	PKLR_uc001fka.3	NM_000298	NP_000289	P30613	KPYR_HUMAN		5	CAGCACCTGGG	0.677	
-	25	8872	SH1L_uc001fkt.2	NM_018489	NP_060959	Q9NR48	ASH1L_HUMAN	BAH.	11	TCCGGTGGATCT	0.473	
-	3	5000	.S1507F|ASH1L_	NM_018489	NP_060959	Q9NR48	ASH1L_HUMAN		11	ATCGGGAAGAG	0.483	
-	3	4157	.S1226F|ASH1L_	NM_018489	NP_060959	Q9NR48	ASH1L_HUMAN		11	TCAAAAGAATGC	0.403	
-	3	2998	p.E840K|ASH1L_	NM_018489	NP_060959	Q9NR48	ASH1L_HUMAN		11	CCCTTCCAGTT	0.398	
-	2	539	_p.R20K|ASH1L_	NM_018489	NP_060959	Q9NR48	ASH1L_HUMAN		11	CTCTTTCTTGAA	0.403	
+	9	914	ld.3_Missense_M	NM_018116	NP_060586	Q9BUK6	MSTO1_HUMAN		0	TCACAGCTCTC	0.522	
-	21	3836	N4L_uc001fmb.3	NM_001037533	NP_001032622	Q3T8J9	GON4L_HUMAN		3	TTTGGGTTCTAG	0.512	
-	21	2868	p.S889F|ARHGEF	NM_001162383	NP_001155855	Q92974	ARHG2_HUMAN		1	GGACAGAGCGA	0.592	
-	4	408	mu.2_Missense_	NM_001162383	NP_001155855	Q92974	ARHG2_HUMAN		1	GCAGGGCCGCT	0.572	
-	7	1235	gx.1_Missense_	NM_020131	NP_064516	Q9NRR5	UBQL4_HUMAN		2	TGTAGGGTGCT	0.532	
+	6	1406	pgz.1_Splice_Site_	NM_170707	NP_733821	P02545	LMNA_HUMAN		2	GAGAGGTGGGC	0.642	
-	3	173	_uc001fnx.1_5'UT	NM_198406	NP_940798	Q6TCH4	PAQR6_HUMAN	lasmic (Potential).	0	CAAAGCCGAGC	0.622	
+	6	875	utation_p.P196L|	NM_144772	NP_658985	Q8NCW5	AIBP_HUMAN		1	CTACCCTGACA	0.532	
-	8	839	PATCH4_uc001fp	NM_015590	NP_056405	Q5T3I0	GPTC4_HUMAN		1	TCATTCCCTTTA	0.463	
-	1	437	S59L|C1orf66_uc0	NM_030980	NP_112242	Q9H9L3	I20L2_HUMAN		2	TTCTTTGAAGGT	0.507	
-	4	467	fpx.1_Missense_M	NM_024540	NP_078816	Q96A35	RM24_HUMAN		0	ACTAGGGATCA	0.572	
-	2	293	fpx.1_Missense_	NM_024540	NP_078816	Q96A35	RM24_HUMAN		0	GTCTTCATCAG	0.582	
-	2	817	si.1_Intron|INSRR	NM_014215	NP_055030	P14616	INSRR_HUMAN		20	GCTCACCAGCA	0.627	
+	12	1443	p.A162T|NTRK1_	NM_002529	NP_002520	P04629	NTRK1_HUMAN	lasmic (Potential).	17	GGCTGGCCATG	0.627	
+	8	1014	fql.2_Missense_M	NM_144702	NP_653303	Q8N4P6	LRC71_HUMAN	LRR 5.	0	CCGTTCCCTGC	0.716	
-	4	656	t.2_Missense_Mut	NM_001145312	NP_001138784	P41162	ETV3_HUMAN		0	GTTGGGCATCA	0.313	
-	6	1014	RL4_uc010phy.1_	NM_031282	NP_112572	Q96PJ5	FCRL4_HUMAN	4.|Extracellular (Potential).	4	GCTGGGTCTCC	0.617	

-	9	1399	L2_uc010phz.1_In	NM_030764	NP_110391	Q96LA5	FCRL2_HUMAN	(Potential).|ITIM motif 1.	2	GAATAGGTGAAC	0.512	
-	6	1002	e_Mutation_p.P29	NM_052938	NP_443170	Q96LA6	FCRL1_HUMAN	ellular (Potential).	7	AGTAGGCACTA	0.557	
+	9	1449	wsq.2_Missense_	NM_018240	NP_060710	Q96J84	KIRR1_HUMAN	otential).|Ig-like C2-type 4.	1	GCCCAGGTCCTG	0.642	
+	11	1714	wsq.2_Missense_	NM_018240	NP_060710	Q96J84	KIRR1_HUMAN	5.|Extracellular (Potential).	1	GGGGACCCTGG	0.572	
+	1	68		NM_001004473	NP_001004473	Q8NGX5	O10K1_HUMAN	ellular (Potential).	1	CAGGCTGCAGC	0.512	
+	1	169	uc001fso.1_RNA	NM_001004472	NP_001004472	Q8NGX6	O10R2_HUMAN	Name=1; (Potential).	3	TATCTAGTCATT	0.433	
-	51	7196		NM_003126	NP_003117	P02549	SPTA1_HUMAN	nd 2.|2 (Potential).	8	AGACATAGCCCT	0.468	
-	4	669		NM_003126	NP_003117	P02549	SPTA1_HUMAN		8	TCAGGGCCCGC	0.527	
-	2	387		NM_004833	NP_004824	O14862	AIM2_HUMAN	DAPIN.	3	TAGCTACTTGTA	0.388	
+	2	1027	p.3_Missense_Mu	NM_002036	NP_002027	Q16570	DUFFY_HUMAN	Name=6; (Potential).	2	GACTGGATTTC	0.562	
-	2	301_302	Site_p.G66_splice	NM_000567	NP_000558	P02741	CRP_HUMAN	Pentaxin.	1	CTGTACCCACGG	0.455	
-	4	615	_5'Flank|C1orf204	NM_001013661	NP_001013683	Q5VU13	VSIG8_HUMAN	Potential).|Ig-like V-type 2.	1	TCGTTGCCATAT	0.592	
-	2	137	k.2_5'UTR|CCDC	NM_012337	NP_036469	Q9UL16	CCD19_HUMAN		1	ATATCTCCAAAG	0.517	
-	30	3620	.3_Missense_Mut	NM_004371	NP_004362	P53621	COPA_HUMAN		2	AGTCTCTTTGG	0.512	
+	17	2235	p.P566L|NCSTN_	NM_015331	NP_056146	Q92542	NICA_HUMAN	lasmic (Potential).	2	GGAGCCAGGAG	0.527	
+	5	1242	Y9_uc001fwx.2_In	NM_002348	NP_002339	Q9HBG7	LY9_HUMAN	otential).|Ig-like C2-type 2.	1	GGACCCCGCTG	0.552	
-	9	815	STD1_uc009wtw.	NM_007122	NP_009053	P22415	USF1_HUMAN		3	GCTCCACTGTGG	0.537	
-	3	226	F1_uc001fxj.2_5'U	NM_007122	NP_009053	P22415	USF1_HUMAN		3	CCTCTTCCGTTT	0.488	
-	10	1445	_p.A213T|ARHGA	NM_001025598	NP_001020769	Q7Z6I6	RHG30_HUMAN		3	CTGCTGCCTCTA	0.637	
+	2	780	HDC9_uc001fxs.	NM_152366	NP_689579	Q8NEP7	KLDC9_HUMAN		0	ATCCAGGTCATC	0.512	
+	13	1681	_Mutation_p.R302	NM_001122764	NP_001116236	P50336	PPOX_HUMAN		1	TGGGCGCCAGG	0.522	rs145559645
-	3	413	uc001fyr.1_Missen	NM_003779	NP_003770	O60512	B4GT3_HUMAN	enal (Potential).	0	ACGAGGGTGAG	0.572	
-	3	315	uc001fyr.1_Missen	NM_003779	NP_003770	O60512	B4GT3_HUMAN	type II membrane protein;	0	GCTGGGAGCCC	0.602	
+	13	1727	376S|NDUFS2_uc	NM_004550	NP_004541	O75306	NDUS2_HUMAN		1	AGGCTCCTGGT	0.453	
+	3	408		NM_001102566	NP_001096036	A6NKN8	PC4L1_HUMAN	IQ.	0	TTCAGGGCAAG	0.527	
-	1	11		NM_001013625	NP_001013647	Q5VTH2	CA192_HUMAN		0	TTAGTGGCCATG	0.458	
+	3	174	se_Mutation_p.A4	NM_001136219	NP_001129691	P12318	FCG2A_HUMAN	otential).|Ig-like C2-type 1.	1	CAAAGGCTGTG	0.587	
+	5	763	e_Mutation_p.A2	NM_001136219	NP_001129691	P12318	FCG2A_HUMAN	ical; (Potential).	1	TAGTGGCCTTGA	0.517	
+	8	967		NM_201563	NP_963857				0	AACAGCTGACG	0.254	
+	3	319	gba.1_Missense_	NM_004001	NP_003992	P31994	FCG2B_HUMAN	1.|Extracellular (Potential).	0	CTCACAGCCCTG	0.587	
+	5	988	p.A161T|PBX1_u	NM_002585	NP_002576	P40424	PBX1_HUMAN	eobox; TALE-type.	5	AGCAAGCGACA	0.398	
-	6	858		NM_199351	NP_955383	Q71H61	ILDR2_HUMAN	lasmic (Potential).	1	TGAGGGGGCTC	0.592	
+	6	637	e_Mutation_p.G1	NM_032858	NP_116247	Q96JY0	MAEL_HUMAN		1	ACGTGGGCATA	0.373	
+	6	448	_p.A96T|POU2F1_	NM_002697	NP_002688	P14859	PO2F1_HUMAN		5	CAGGCAGCCATT	0.493	
-	23	3438	sense_Mutation_p	NM_018417	NP_060887	Q96PN6	ADCYA_HUMAN		3	TCAGATGTCTTC	0.373	
-	3	1076	1ggf.3_Missense_	NM_006996	NP_008927	O60779	S19A2_HUMAN	ical; (Potential).	0	CGAGAGGAGTAG	0.483	
-	20	6009		NM_000130	NP_000121	P12259	FA5_HUMAN	5/8 type C 1.	6	AATTCTGCTGCA	0.338	
-	13	3576		NM_000130	NP_000121	P12259	FA5_HUMAN	B.	6	GACTGGGGTCT	0.483	
-	13	2709		NM_000130	NP_000121	P12259	FA5_HUMAN	B.	6	ATTCTCCAGCA	0.453	
-	10	1718	f112_uc001ggj.2_	NM_000450	NP_000441	P16581	LYAM2_HUMAN	ar (Potential).|Sushi 6.	5	TTCAGGACAGG	0.537	
+	17	1849	e|C1orf112_uc009	NM_018186	NP_060656	Q9NSG2	CA112_HUMAN		0	ATCAGGCAAGG	0.388	
-	14	2384	YL3_uc001ggt.2_	NM_181093	NP_851607	Q8IZE3	PACE1_HUMAN	action with EZR.	2	CTTCCCAGCCT	0.363	
+	16	3790	mh.1_Missense_M	NM_015172	NP_055987	Q9Y520	PRC2C_HUMAN		0	AGCTAGAGAGA	0.468	
+	16	4767	mh.1_Missense_M	NM_015172	NP_055987	Q9Y520	PRC2C_HUMAN		0	CTTCTGAAAGC	0.398	
+	19	6207	e_Mutation_p.P9	NM_015172	NP_055987	Q9Y520	PRC2C_HUMAN		0	AGACCCCACAG	0.453	
-	5	1230	gjg.3_Missense_M	NM_033319	NP_201576	Q8N0S6	CENPL_HUMAN		0	AAAATTGCCAGT	0.308	
+	15	1977		NM_018122	NP_060592	Q6PI48	SYDM_HUMAN		2	AGGCCCGTAGC	0.388	

-	6	1296		NM_000488	NP_000479	P01008	ANT3_HUMAN		1	GAGGTCATCTC	0.473
-	5	981		NM_000488	NP_000479	P01008	ANT3_HUMAN		1	ACTTGCCTTCCT	0.527
-	10	1825	jv.2_Missense_Mu	NM_172071	NP_742068	Q5TC82	RC3H1_HUMAN	Pro-rich.	2	AGAACCTCGAG	0.488
+	7	1165	AP1L_uc001gjw.2	NM_014857	NP_055672	Q5R372	RBG1L_HUMAN		4	AACAAAGAATTA	0.363
+	4	840	gki.1_Missense_	NM_014412	NP_055227	Q9HB71	CYBP_HUMAN	tion with SKP1.|CS.	0	CTGTGGAAGGC	0.363
-	18	3664	.1_Missense_Mut	NM_003285	NP_003276	Q92752	TENR_HUMAN	ogen C-terminal.	11	AATCAGCCCATT	0.398
-	16	3370	.1_Missense_Mut	NM_003285	NP_003276	Q92752	TENR_HUMAN	nectin type-III 9.	11	GCCCTCCAGTC	0.557
+	2	1673	_Mutation_p.A17	NM_020318	NP_064714	Q9BXP8	PAPP2_HUMAN		16	GGCTGCCACTA	0.557
+	3	2357	_Mutation_p.P39	NM_020318	NP_064714	Q9BXP8	PAPP2_HUMAN		16	CAGCCCCTTCA	0.587
+	8	4283	A2_uc009www.2_	NM_020318	NP_064714	Q9BXP8	PAPP2_HUMAN		16	TCAGCCCCACA	0.557
-	12	2236	d.1_Missense_Mu	NM_004319	NP_004310	O14525	ASTN1_HUMAN	EGF-like 3.	15	AGGTGGGGTCG	0.532
+	16	3538	_Mutation_p.S127	NM_004841	NP_004832	Q9UJF2	NGAP_HUMAN		5	CAGCAGCTGCT	0.522
-	6	1838	GPS2_uc010pnb.	NM_004673	NP_004664	O95841	ANGL1_HUMAN	ogen C-terminal.	0	TCTGTACCATAC	0.438
+	5	557	1orf125_uc010pn	NM_144696	NP_653297	Q5T1B0	AXDN1_HUMAN		0	AGAAGGCAGTT	0.363
+	10	1026	_p.R88Q|C1orf125	NM_144696	NP_653297	Q5T1B0	AXDN1_HUMAN		0	TGCTCGGCAGA	0.299
+	9	1745	_p.L499F|TDRD5_	NM_173533	NP_775804	Q8NAT2	TDRD5_HUMAN		5	AGTTACTCGAA	0.348
+	5	2452	_Mutation_p.W41	NM_020950	NP_066001	Q5VZ46	K1614_HUMAN		4	GCCTGGCAGCC	0.612
-	2	1674	SEL_uc001gpk.2_	NM_021133	NP_066956	Q05823	RN5A_HUMAN	rotein kinase.	5	AAAATCTGCCAG	0.378
-	5	719		NM_002928	NP_002919	O15492	RGS16_HUMAN		1	AGTGGCAGAGG	0.632
-	5	400	_p.E48K|RGS8_u	NM_001102450	NP_001095920	P57771	RGS8_HUMAN		1	CTTCTTCTGTCG	0.383
+	11	865	L_uc009wyc.2_In	NM_030769	NP_110396	Q9BXD5	NPL_HUMAN		3	TTTAGCCCTGA	0.413
+	4	416	_uc001gps.2_Splic	NM_001357	NP_001348	Q08211	DHX9_HUMAN		2	TTGCAGGTAGC	0.458
+	17	2581	h.2_Missense_Mu	NM_173156	NP_775179	Q92540	SMG7_HUMAN	Gln/Pro-rich.	3	GCCCTACTACC	0.463
+	22	3508	G7_uc001gqi.2_	NM_173156	NP_775179	Q92540	SMG7_HUMAN		3	ACGGGGACAAG	0.527
+	3	429	sense_Mutation_p	NM_015149	NP_055964	Q9NZL6	RGL1_HUMAN	rminal Ras-GEF.	11	ACTTTACCTATAT	0.443
-	5	966	1ABP_uc009wyj.2_	NM_006469	NP_006460	Q9Y6Y0	NS1BP_HUMAN		5	TCGATCCATCTT	0.303
+	15	2510	rr.1_Missense_Mu	NM_031935	NP_114141	Q96RW7	HMCN1_HUMAN	like C2-type 4.	23	ATTCAAGAAACA	0.443
+	18	2939	rr.1_Missense_Mu	NM_031935	NP_114141	Q96RW7	HMCN1_HUMAN	like C2-type 6.	23	TTGAAGGACAG	0.418
+	30	4718		NM_031935	NP_114141	Q96RW7	HMCN1_HUMAN	ike C2-type 12.	23	TTTTGGGCGAT	0.353
+	58	9195		NM_031935	NP_114141	Q96RW7	HMCN1_HUMAN	ike C2-type 28.	23	GGTCTCTGGTT	0.398
+	64	10028		NM_031935	NP_114141	Q96RW7	HMCN1_HUMAN	ike C2-type 31.	23	AGCTGGTCTGC	0.393
+	107	16820	rs.1_Missense_M	NM_031935	NP_114141	Q96RW7	HMCN1_HUMAN		23	TTGAGCCCATAT	0.443
+	3	128	Site_p.D26_splice|	NM_005807	NP_005798	Q92954	PRG4_HUMAN		1	ATTTTAGATTTAT	0.428
+	7	2279	_Mutation_p.S650	NM_005807	NP_005798	Q92954	PRG4_HUMAN	-X-P-X-P-T-T-X.|46; appro	1	CACATCCACCA	0.592
+	7	3160	_Mutation_p.P944	NM_005807	NP_005798	Q92954	PRG4_HUMAN		1	AAAAGCCAAAA	0.423
+	2	256	oy.1_Missense_M	NM_021023	NP_066303	Q02985	FHR3_HUMAN	Sushi 1.	0	GTGATGAACATT	0.388
+	2	136	R2_uc001gtr.1_In	NM_005666	NP_005657	P36980	FHR2_HUMAN		3	TCCCAGCAATG	0.269
-	21	9382	.G1457E|ASPM_	NM_018136	NP_060606	Q8IZT6	ASPM_HUMAN	IQ 36.	6	TTATATCCTCTAT	0.378
+	4	304	.1_Intron|PTPRC_	NM_002838	NP_002829	P08575	PTPRC_HUMAN	ellular (Potential).	12	AGTGTTCCACTT	0.418
+	6	650	10ppg.1_Missense	NM_002838	NP_002829	P08575	PTPRC_HUMAN	ellular (Potential).	12	CTTTCCTACAG	0.552
+	29	3295	_p.E991K|PTPRC_	NM_002838	NP_002829	P08575	PTPRC_HUMAN	hatase 2.|Cytoplasmic (Po	12	TGAAGGAGACC	0.418
+	1	173		NM_001105517	NP_001098987	P0C7Q3	FA58B_HUMAN		0	GCTAGGGATGC	0.498
-	2	849	Mutation_p.D248	NM_012482	NP_036614	Q9Y2X9	ZN281_HUMAN		2	TCCATCTCCAA	0.483
-	16	3237	j.1_Missense_Mu	NM_014875	NP_055690	Q15058	KIF14_HUMAN	equired for CIT-binding.	7	GTGCCATGAGC	0.383
-	6	2012	pj.1_Missense_Mu	NM_014875	NP_055690	Q15058	KIF14_HUMAN	inesin-motor.	7	AACAGGATGTT	0.368
+	1	101		NM_018265	NP_060735	Q3KP66	CA106_HUMAN		3	GGAGGGAAGAT	0.612
-	30	4359	l.1_Missense_Mu	NM_017596	NP_060066	O75037	KI21B_HUMAN	WD 2.	6	GTTGGGGTGGC	0.577

-	7	1272	p.H319Y|KIF21B_	NM_017596	NP_060066	O75037	KI21B_HUMAN		6	AACGTGCACCA	0.612	
+	20	4611	x.2_Missense_Mut	NM_020443	NP_065176	Q8NEY1	NAV1_HUMAN		4	TGGTGGTGAGG	0.493	
+	26	5521	x.2_Missense_Mu	NM_020443	NP_065176	Q8NEY1	NAV1_HUMAN		4	CCACACCTTCC	0.567	
+	2	582	NPEP_uc001gxf.	NM_020216	NP_064601	Q9H4A4	AMPB_HUMAN		1	ACACGCCTGCT	0.502	
+	2	3488	_p.G99D|ELF3_uc	NM_004433	NP_004424	P78545	ELF3_HUMAN	PNT.	0	GGATGGCGCCA	0.572	
+	18	1817	R6_uc009xab.2_R	NM_001017403	NP_001017403	Q9HBX8	LGR6_HUMAN	Name=2; (Potential).	10	TGCAGGCGCCA	0.617	
+	15	2234	97L|PPP1R12B_u	NM_002481	NP_002472	O60237	MYPT2_HUMAN		3	AGTTCCAGCAA	0.582	
-	7	1110	_p.S306L|SYT2_u	NM_001136504	NP_001129976	Q8N9I0	SYT2_HUMAN	imilarity).|C2 2.|Cytoplasmi	3	TACCTGAAAGG	0.587	
-	3	253	5R1_uc010pqe.1_	NM_016243	NP_057327	Q9UHQ9	NB5R1_HUMAN	-binding FR-type.	1	TCTTGGTGTTG	0.612	
-	9	1135	p.G58S|CHI3L1_u	NM_001276	NP_001267	P36222	CH3L1_HUMAN		1	GTTGCCCTTGG	0.567	
-	2	956	OD_uc010pqi.1_R	NM_002023	NP_002014	Q06828	FMOD_HUMAN	LRR 8.	3	CAGCCGCACAT	0.567	
-	2	263	OD_uc010pqi.1_R	NM_002023	NP_002014	Q06828	FMOD_HUMAN		3	AGGGTCATAGG	0.597	
+	8	1890	p.E336K|ATP2B4_	NM_001684	NP_001675	P23634	AT2B4_HUMAN	lasmic (Potential).	3	ATGAGGAAAAG	0.532	
+	14	3126	p.P748S|ATP2B4_	NM_001684	NP_001675	P23634	AT2B4_HUMAN	lasmic (Potential).	3	TCTGGCCTAAG	0.512	
+	15	3226	p.A781V|ATP2B4_	NM_001684	NP_001675	P23634	AT2B4_HUMAN	lasmic (Potential).	3	CGTGGCTGTCA	0.537	
+	17	3588	2_Missense_Mutat	NM_001684	NP_001675	P23634	AT2B4_HUMAN	lasmic (Potential).	3	TGAAGCGGCGC	0.488	
+	4	964	13_uc010pqp.1_N	NM_005686	NP_005677	Q9UN79	SOX13_HUMAN		2	GACTGGAAGGA	0.527	
-	15	2790	qv.1_Missense_	NM_002646	NP_002637	O00750	P3C2B_HUMAN		7	ATTAGGTGCAC	0.547	
+	2	272	p.P18L|CDK18_uc	NM_212503	NP_997668	Q07002	CDK18_HUMAN		2	AGTGCCCCGCA	0.552	
+	10	1587	.1_RNA|MFSD4_	NM_181644	NP_857595	Q8N468	MFSD4_HUMAN		3	CCCAAGACAGA	0.443	
-	5	1919	ro.1_Intron|SLC45	NM_033102	NP_149093	Q96JT2	S45A3_HUMAN	ame=11; (Potential).	4	CTGCGGCAGAC	0.527	
-	7	1804	1hdg.1_5'Flank|uc	NM_173854	NP_776253	Q8IVJ1	S41A1_HUMAN		2	TTGTGGCTGGA	0.592	
-	4	1269	xcb.1_Missense_	NM_023938	NP_076427	Q9BW04	SARG_HUMAN		4	AACAGGAGATC	0.542	
+	2	544	55_uc010psf.1_R	NM_000574	NP_000565	P08174	DAF_HUMAN	Sushi 1.	1	TTAAGGGCAGT	0.368	
+	5	848	2_uc009xch.2_Mis	NM_001877	NP_001868	P20023	CR2_HUMAN	xtracellular (Potential).	8	GCCCACCTTCT	0.473	
-	20	4492		NM_025179	NP_079455	O75051	PLXA2_HUMAN	ical; (Potential).	3	TGCCGCCGGCC	0.587	
-	2	1344	ha.3_Missense_	NM_025179	NP_079455	O75051	PLXA2_HUMAN	lar (Potential).|Sema.	3	GGTCGGGAAGT	0.577	
-	14	2461	_Missense_Mutati	NM_001017402	NP_001017402	Q13751	LAMB3_HUMAN	Domain II.	6	GAGACCATTGA	0.547	rs144538210
-	8	1796	iv.2_Missense_M	NM_014873	NP_055688	Q92604	LGAT1_HUMAN		2	TATGGCCCTTG	0.378	
-	8	1063	pte.1_Missense_	NM_018252	NP_060722	Q9H813	TM206_HUMAN	ellular (Potential).	1	AGTGACTATCT	0.313	
-	8	1534	e_Mutation_p.P33	NM_144567	NP_653168	Q5VTE6	ANGE2_HUMAN		0	TGTCAGGAAAG	0.378	
-	1	183	EL2_uc001hka.2_	NM_144567	NP_653168	Q5VTE6	ANGE2_HUMAN		0	GTAGCCCTTCC	0.667	
+	11	2915	p.A707V|RPS6KC	NM_012424	NP_036556	Q96S38	KS6C1_HUMAN	otein kinase 2.	8	TTGATGCTTTAC	0.413	
+	2	179		NM_016343	NP_057427	P49454	CENPF_HUMAN	d for localization to the cyt	13	AATGAGCTGGG	0.393	
+	6	869		NM_016343	NP_057427	P49454	CENPF_HUMAN	d for localization to the cyt	13	TAATTCTCAAAG	0.448	
+	13	5314		NM_016343	NP_057427	P49454	CENPF_HUMAN		13	CTGGTGCAGTG	0.448	
+	20	9337		NM_016343	NP_057427	P49454	CENPF_HUMAN		13	GGAGCCCAGTA	0.478	
-	47	9746		NM_206933	NP_996816	O75445	USH2A_HUMAN	ential).|Fibronectin type-III	26	TGATGCCACGA	0.388	
-	39	7759		NM_206933	NP_996816	O75445	USH2A_HUMAN	ential).|Fibronectin type-III	26	AGCTGGTGTAG	0.512	
-	29	6239		NM_206933	NP_996816	O75445	USH2A_HUMAN	ellular (Potential).	26	CTGCTCCTGTT	0.388	rs111598839
-	24	5341		NM_206933	NP_996816	O75445	USH2A_HUMAN	1.|Extracellular (Potential).	26	TCGCGGGAGCC	0.408	
-	23	5201		NM_206933	NP_996816	O75445	USH2A_HUMAN	1.|Extracellular (Potential).	26	CATTTTCCATCA	0.338	
-	19	4532	v.2_Nonsense_M	NM_206933	NP_996816	O75445	USH2A_HUMAN	tential).|Fibronectin type-III	26	TTCTCCCAGGAG	0.403	
-	16	3616	v.2_Missense_Mu	NM_206933	NP_996816	O75445	USH2A_HUMAN	tential).|Fibronectin type-III	26	ATCAGGTGGAC	0.428	
-	6	1348	kv.2_Missense_M	NM_206933	NP_996816	O75445	USH2A_HUMAN	nal.|Extracellular (Potential	26	ATTAGGAATGC	0.498	
-	2	796	hlg.3_Missense_	NM_018040	NP_060510	Q9NW75	GPTC2_HUMAN		1	TCGTTTCCTCAC	0.328	
-	2	153	1hlg.3_Nonsense_	NM_018040	NP_060510	Q9NW75	GPTC2_HUMAN		1	GAAATGCCTTCA	0.383	

-	29	4354		NM_004446	NP_004437	P07814	SYEP_HUMAN	-tRNA synthetase.	2	GAACTCCCTATA	0.358	
-	11	1700	lz.1_Missense_Mu	NM_004446	NP_004437	P07814	SYEP_HUMAN	yl-tRNA synthetase.	2	ACCTGAGCAGCA	0.383	
+	9	1399	un.1_Nonsense_M	NM_018650	NP_061120	Q9P0L2	MARK1_HUMAN	rotein kinase.	10	GAGAGCGAGTT	0.348	
+	16	2512	un.1_Missense_Mu	NM_018650	NP_061120	Q9P0L2	MARK1_HUMAN		10	AAACGGGTGCA	0.502	
-	5	1635		NM_024746	NP_079022	Q6UWX4	HIPL2_HUMAN		1	CTTACCCACTC	0.323	
+	5	3257	ea.1_Missense_Mu	NM_198551	NP_940953	Q5JRA6	MIA3_HUMAN	cellular (Potential).	5	ACCCACCCACT	0.468	
+	17	4411	p.E1245K|MIA3_uc	NM_198551	NP_940953	Q5JRA6	MIA3_HUMAN	lasmic (Potential).	5	TAGTTGAAGAG	0.378	
+	5	792	uu.1_Missense_M	NM_144695	NP_653296	Q5VW32	BROX_HUMAN	BRO1.	0	GAAAAGAAAAG	0.328	
+	2	181		NM_032890	NP_116279	Q96F81	DISP1_HUMAN		0	TTGTGGTTCTG	0.488	
+	6	999		NM_032890	NP_116279	Q96F81	DISP1_HUMAN		0	GACTGGAACTT	0.398	rs79910153
+	8	4522		NM_032890	NP_116279	Q96F81	DISP1_HUMAN		0	AGAATGAACCA	0.448	
+	1	780		NM_152610	NP_689823	Q8N715	CA065_HUMAN		2	GGACTCCCAGC	0.602	
+	3	568	puy.1_Missense_M	NM_001748	NP_001739	P17655	CAN2_HUMAN	alpain catalytic.	5	CCTCACCTTGA	0.493	
-	9	1331	96_splice|LBR_uc	NM_002296	NP_002287	Q14739	LBR_HUMAN		2	GACATACCCATC	0.353	
-	7	1379	e_Mutation_p.G30	NM_001008493	NP_001008493	Q8N8S7	ENAH_HUMAN		2	GTGGTCCCAAG	0.224	
-	2	598	pd.1_Missense_M	NM_001008493	NP_001008493	Q8N8S7	ENAH_HUMAN	WH1.	2	GCCCACCACTC	0.398	
-	2	288	2_Missense_Mutation_p.L45F|PYCR2_uc001hpr.2_Intr			O75610	LFTY1_HUMAN		0	CCTGAGCGCGG	0.617	
-	6	1126	pv.2_Missense_M	NM_152608	NP_689821	Q6IQ49	CA055_HUMAN		1	CAGGTGCTACC	0.483	
-	2	423		NM_022735	NP_073572	Q9H3P7	GCP60_HUMAN	ACB.	0	TGTCTGGATTAT	0.373	
-	3	2363		NM_002221	NP_002212	P27987	IP3KB_HUMAN		5	GTGTCCTGCCA	0.537	
-	26	4381	10pvs.1_Missense	NM_003607	NP_003598	Q5VT25	MRCKA_HUMAN	PH.	11	CAGGGTATATCT	0.328	
+	3	1213	hrd.2_Missense_M	NM_053052	NP_444280	Q5SQN1	SNP47_HUMAN		1	GAACAGAGTCT	0.463	
+	14	4089	sn.2_Missense_Mu	NM_001098623	NP_001092093	Q5VST9	OBSCN_HUMAN	Ig-like 14.	28	AGGCGGTGTTT	0.647	
+	64	16536	p.G5498R|OBSCN	NM_001098623	NP_001092093	Q5VST9	OBSCN_HUMAN		28	CACAGGGGTTG	0.587	
-	1	394		NM_003493	NP_003484	Q16695	H31T_HUMAN		0	CCCGCGGATAC	0.587	
-	4	757	orf96_uc009xfc.2_	NM_145257	NP_660300	Q6IQ19	CA096_HUMAN		0	TTTTTTCCACCT	0.423	
-	2	199	orf96_uc009xfc.2_	NM_145257	NP_660300	Q6IQ19	CA096_HUMAN		0	CTGCTCCAGCA	0.632	
-	6	985		NM_001100	NP_001091	P68133	ACTS_HUMAN		0	CAGGTCCTTCC	0.602	
-	5	621		NM_018230	NP_060700	Q8WUM0	NU133_HUMAN		7	GGCAACCATGA	0.443	
+	4	3110	d.1_Missense_Mu	NM_014777	NP_055592	Q14146	URB2_HUMAN		3	ATGATCCCGCT	0.428	
-	3	674	tv.2_Missense_Mu	NM_024554	NP_078830	Q8N414	PGBD5_HUMAN		4	TGAAGCCAGTG	0.562	
+	18	2079	_p.V593I|CAPN9_	NM_006615	NP_006606	O14815	CAN9_HUMAN	Domain IV.	1	GCCTGGTCCGG	0.592	rs150802007
-	3	454	198_uc001huc.1_I	NM_032800	NP_116189	Q9H425	CA198_HUMAN		0	ATAGGGCGGAG	0.577	
+	4	1402		NM_001004342	NP_001004342	Q6ZTA4	TRI67_HUMAN	COS.	4	ACCCCTCCGGG	0.547	
+	2	408	.1_5'UTR|GNPAT_	NM_014236	NP_055051	O15228	GNPAT_HUMAN		4	TGTAAACCAATT	0.353	
-	19	4999	hvf.2_Missense_M	NM_020808	NP_065859	Q9P2F8	SI1L2_HUMAN		6	TCAGGGTGCAG	0.517	
-	15	4450	hvf.2_Missense_M	NM_020808	NP_065859	Q9P2F8	SI1L2_HUMAN		6	GCTGAGTTGCT	0.408	
-	14	4236	vf.2_Missense_M	NM_020808	NP_065859	Q9P2F8	SI1L2_HUMAN	Ser-rich.	6	ACCCACTACTTT	0.498	
+	1	1531		NM_019090	NP_061963	Q9P2G4	K1383_HUMAN		1	ATTGAGCCTCAA	0.448	
+	1	1621		NM_019090	NP_061963	Q9P2G4	K1383_HUMAN		1	AGCATCCAAGT	0.423	
-	33	6068	e_Mutation_p.A59	NM_014801	NP_055616	A6NKB5	PCX2_HUMAN	Ser-rich.	2	TAGCGCTGAGT	0.567	
-	30	5495	e_Mutation_p.D40	NM_014801	NP_055616	A6NKB5	PCX2_HUMAN		2	CTCGTCCACCA	0.607	
+	6	1892	hvs.1_Missense_	NM_032435	NP_115811	Q5TCX8	M3KL4_HUMAN		8	CAGTCCCCCGA	0.567	
+	1	511		NM_002245	NP_002236	O00180	KCNK1_HUMAN		1	CCGTGCTCTCC	0.582	
-	2	1403	_p.P68S|IRF2BP2_	NM_182972	NP_892017	Q7Z5L9	I2BP2_HUMAN		0	GGGCGGACTGT	0.592	
-	20	3113	e_Mutation_p.K78	NM_016374	NP_057458	Q4LE39	ARI4B_HUMAN		3	GTCATCTTTGCT	0.383	
-	13	1495	hws.3_Missense_	NM_016374	NP_057458	Q4LE39	ARI4B_HUMAN	RID.|Glu-rich.	3	TCCAAGTACAG	0.289	

-	45	10443	ki.2_Missense_Mut	NM_000081	NP_000072	Q99698	LYST_HUMAN		12	GCTCCAGGTCTG	0.522	
-	44	10199	i.2_Missense_Mut	NM_000081	NP_000072	Q99698	LYST_HUMAN	BEACH.	12	CCTGCCGATGGA	0.483	
-	31	8405	ja.1_Missense_Mu	NM_000081	NP_000072	Q99698	LYST_HUMAN		12	TCCCAAGCTGCA	0.413	
-	23	6854	b.1_RNA|LYST_uc	NM_000081	NP_000072	Q99698	LYST_HUMAN		12	ATCAGGTCGGC	0.532	
-	21	6296	_Intron|LYST_uc01	NM_000081	NP_000072	Q99698	LYST_HUMAN		12	TACCTACCTATGT	0.348	
-	6	2681	xs.1_RNA|LYST_u	NM_000081	NP_000072	Q99698	LYST_HUMAN		12	TGGAACTGAGG	0.378	
+	6	484	lhxv.1_Missense_I	NM_145861	NP_665860	Q8WWZ3	EDAD_HUMAN	Death.	0	ACTGGAGGAATT	0.522	
+	37	5161		NM_001035	NP_001026	Q92736	RYR2_HUMAN	ilarity).|4 X approximate rep	33	CATGTGGATGAA	0.537	
+	38	5996		NM_001035	NP_001026	Q92736	RYR2_HUMAN	ilarity).|4 X approximate rep	33	TCACAGCCAGGA	0.403	
-	10	1334	130331_uc010pyc	NM_021186	NP_067009	Q12836	ZP4_HUMAN	acellular (Potential).	3	CAGACTGACACG	0.498	
+	5	3203	ye.1_Missense_Mu	NM_020066	NP_064450	Q9NZ56	FMN2_HUMAN	Pro-rich.|FH1.	12	ACTTCCCGGAG	0.711	
+	7	4378	MN2_uc010pyf.1_S	NM_020066	NP_064450	Q9NZ56	FMN2_HUMAN		12	AACATGGTAAGT	0.323	
-	2	277		NM_000143	NP_000134	P07954	FUMH_HUMAN		5	ACACCTCCAATC	0.398	
-	3	235		NM_001004343	NP_001004343	Q9BXW4	MLP3C_HUMAN		1	TTTGTCCAGCGG	0.592	
-	13	3718	zu.2_Missense_M	NM_014812	NP_055627	Q5SW79	CE170_HUMAN	ng to microtubules.	2	CTCTGCGCAAGA	0.458	
+	3	222	_p.E55K|C1orf101_	NM_001130957	NP_001124429	Q5SY80	CA101_HUMAN	cellular (Potential).	2	GTGCCAGAAACT	0.279	
+	16	2249	)_splice|C1orf101_	NM_001130957	NP_001124429	Q5SY80	CA101_HUMAN		2	TTCACAGGTCAT	0.323	
-	4	1158	ation_p.E38K|HNR	NM_031844	NP_114032	Q00839	HNRPU_HUMAN	B30.2/SPRY.	0	AACTCTCCATTG	0.343	
+	6	1963	_p.A508V|KIF26B_	NM_018012	NP_060482	Q2KJY2	KI26B_HUMAN	Kinesin-motor.	3	TGTTTGCCTTCG	0.502	
+	14	6472		NM_018012	NP_060482	Q2KJY2	KI26B_HUMAN		3	GGAGGCCATGT	0.577	
-	10	1057	ibi.2_Missense_M	NM_022743	NP_073580	Q9H7B4	SMYD3_HUMAN		0	ATATCGGGAAGC	0.498	
-	1	393	ST_uc001ibp.2_5'F	NM_022366	NP_071761	Q9H5Q4	TFB2M_HUMAN		1	GTTTTCCCAAAT	0.463	rs150011053
-	32	5966	CTF1_uc009xgs.1_	NM_015446	NP_056261	Q8WYP5	ELYS_HUMAN	lear localization (By similar	7	TAGATCCTACAT	0.408	
-	1	605		NM_001005487	NP_001005487	Q8NGZ3	O13G1_HUMAN	Name=5; (Potential).	1	GCCAGGGTAATAT	0.458	
-	1	874		NM_001005286	NP_001005286	Q8NGZ6	OR6F1_HUMAN	Name=7; (Potential).	0	TACGAAGCGTATA	0.438	
+	1	47		NM_001004690	NP_001004690	A3KFT3	OR2M5_HUMAN	cellular (Potential).	3	TCCTGGGAATCT	0.443	
+	1	538		NM_017504	NP_059974	Q96R27	OR2M4_HUMAN	cellular (Potential).	2	TCTGTGATGTTG	0.428	
+	1	556		NM_017504	NP_059974	Q96R27	OR2M4_HUMAN	cellular (Potential).	2	CTTTTACCTCTAT	0.398	
+	1	26		NM_001004696	NP_001004696	Q8NH00	OR2T4_HUMAN	cellular (Potential).	1	GGCCAGCCACA	0.483	rs140989725
+	1	343		NM_001005495	NP_001005495	Q8NH03	OR2T3_HUMAN	Name=3; (Potential).	1	GCTGGAGCTGAG	0.557	
+	1	515		NM_001013355	NP_001013373	Q5TZ20	OR2G6_HUMAN	cellular (Potential).	3	GTCATCGCACAC	0.552	
-	20	2481	_p.M183I|DIP2C_u	NM_014974	NP_055789	Q9Y2E4	DIP2C_HUMAN		7	GACCACCATGAG	0.612	
-	1	352	LF6_uc010qal.1_M	NM_001300	NP_001291	Q99612	KLF6_HUMAN		4	CTCCTCCAGAG	0.557	
+	2	274		NM_053049	NP_444277	Q969E3	UCN3_HUMAN		0	GGGGGGCCCCA	0.632	
+	8	862	o.2_Missense_Mut	NM_001047160	NP_001040625	Q7Z628	ARHG8_HUMAN	DH.	1	ACCAAGCCTGAT	0.398	
+	19	7632	iik.2_Missense_Mu	NM_017782	NP_060252	Q5VWN6	CJ018_HUMAN		2	CAACTGCACATA	0.328	
-	15	1852	iks.1_Missense_M	NM_014688	NP_055503	Q92738	US6NL_HUMAN		0	GGTGCGCTGCTC	0.567	
-	15	1573	iks.1_Missense_M	NM_014688	NP_055503	Q92738	US6NL_HUMAN		0	CTGGGGGTGCG	0.657	
-	2	1201	c.2_Missense_Mut	NM_080599	NP_542166	Q9HAU5	RENT2_HUMAN	MIF4G 1.	3	CCAGACCTGAA	0.413	
+	13	1269	1ilm.2_Splice_Site	NM_006023	NP_006014	O75794	CD123_HUMAN		1	TGACAGAAGAG	0.507	
-	4	555	nse_Mutation_p.E	NM_031453	NP_113641	Q9H098	F107B_HUMAN	Potential.	4	CTTGCTCTTCTTG	0.443	
+	5	1095	e_Mutation_p.G347	NM_024670	NP_078946	Q9H5I1	SUV92_HUMAN	Post-SET.	3	TGCAGAGGTTAC	0.348	
-	8	717	no.2_Missense_M	NM_001033855	NP_001029027	Q96SD1	DCR1C_HUMAN		1	CATAGCCATAAG	0.398	
-	7	988	o.G229V|RSU1_uc	NM_152724	NP_689937	Q15404	RSU1_HUMAN		1	GACACGCCAAGC	0.428	
-	40	6014		NM_001081	NP_001072	O60494	CUBN_HUMAN	CUB 14.	19	ACACGGGTGCAT	0.512	rs142570571
-	12	1371		NM_001081	NP_001072	O60494	CUBN_HUMAN	alcium-binding (Potential).	19	AACAGGGGTTG	0.453	
-	3	281	'L|TRDMT1_uc009	NM_004412	NP_004403	O14717	TRDMT_HUMAN		1	GGCAGGGAGGG	0.264	

+	2	894	_Missense_Mutatic	NM_003380	NP_003371	P08670	VIME_HUMAN	Rod.|Coil 1B.	4	GGCAGGTGGAC	0.652
+	8	1570	ipp.2_Missense_	NM_001145195	NP_001138667	Q504Y0	S39AC_HUMAN	lasmic (Potential).	2	AAGCCCCAGAA	0.343
+	3	311	NB2_uc001ipx.2_	NM_201596	NP_963890	Q08289	CACB2_HUMAN		3	CGATTCCGATG	0.502
-	17	2129	BL_uc001iqk.2_Int	NM_006393	NP_006384	O76041	NEBL_HUMAN	Nebulin 16.	2	TTCAGGAGTAT	0.313
+	18	2330	2_splice|ARMC3_	NM_173081	NP_775104	Q5W041	ARMC3_HUMAN		0	ACACAGGTATG	0.328
+	6	1478	nse_Mutation_p.P	NM_019590	NP_062536	Q5T5P2	SKT_HUMAN	Pro-rich.	7	CCAGACCCATC	0.517
+	1	580	10qde.1_Missens	NM_020752	NP_065803	Q5T848	GP158_HUMAN	ellular (Potential).	8	CCCGGGCGGCC	0.652
+	26	3236	Q959R|MYO3A_u	NM_017433	NP_059129	Q8NEV4	MYO3A_HUMAN	osin head-like.	18	GCGTCAGGCAA	0.408
-	32	4950	S1280N|ANKRD2	NM_014915	NP_055730	Q9UPS8	ANR26_HUMAN		4	ATCTGCTCTGC	0.408
-	1	198	9xku.1_Missense_	NM_014915	NP_055730	Q9UPS8	ANR26_HUMAN		4	GACTCGCCCTTC	0.657
-	20	2472	1L1_uc010qdl.1_	NM_139312	NP_647473	Q96TA2	YMEL1_HUMAN		1	AAGAACAATTT	0.378
-	1	2190		NR_003525					0	TGGGAGGTTCT	0.542
-	1	192		NM_001034842	NP_001030014	Q3KNS1	PTHD3_HUMAN		4	GCCCGGTGGCA	0.652
+	5	599		NM_032517	NP_115906	Q6UWQ5	LYZL1_HUMAN		0	TGAGGGCAGAG	0.502
-	6	1243	b.3_Missense_M	NM_018109	NP_060579	Q9NVV4	PAPD1_HUMAN		1	AATAGGGGGTG	0.368
-	3	354		NM_183058	NP_898881	Q7Z4W2	LYZL2_HUMAN		0	TGCTGCCGTCA	0.587
-	7	1530	1iwc.1_Nonsense_	NM_018287	NP_060757	Q8IWW6	RHG12_HUMAN		0	ATGTCTCCACTT	0.363
-	18	2520		NM_004521	NP_004512	P33176	KINH_HUMAN		5	CTTTTCCATTT	0.313
-	14	2356	p.G623S|EPC1_u	NM_025209	NP_079485	Q9H2F5	EPC1_HUMAN		4	GTAAGCCCTTGT	0.343
-	25	4058	nse_Mutation_p.	NM_019619	NP_062565	Q8TEW0	PARD3_HUMAN		1	AGAAGGGCCTC	0.502
+	7	1054		NM_052997	NP_443723	Q9BXX3	AN30A_HUMAN		9	CGTGGCCAGCA	0.423
+	34	3425		NM_052997	NP_443723	Q9BXX3	AN30A_HUMAN	Potential.	9	ATATAGTGGGC	0.343
+	5	1289	33A_uc010qev.1_	NM_006974	NP_008905	Q06730	ZN33A_HUMAN	2H2-type 2.	3	CAAACCTCACT	0.438
-	5	791	NF33B_uc001jag.	NM_006955	NP_008886	Q06732	ZN33B_HUMAN		0	GGGTTTCCTGAC	0.368
-	9	1093	1jao.1_Missense_	NM_145313	NP_660356	Q8N9B8	RGF1A_HUMAN	Ras-GEF.	0	CTTGGCTGTCT	0.617
-	2	1303	j.2_Missense_M	NM_005674	NP_005665	Q16600	ZN239_HUMAN	2H2-type 1.	0	TTTGACTGAAG	0.443
-	2	1206		NM_016204	NP_057288	Q9UK05	GDF2_HUMAN		3	CCTTGGGTGCA	0.597
-	5	847	P22_uc010qgl.1_	NM_021226	NP_067049	Q7Z5H3	RHG22_HUMAN	Rho-GAP.	1	CTCCCGGATGA	0.647
+	3	838		NM_199459	NP_955629	Q711Q0	CJ071_HUMAN		0	GCAAGCCTCCG	0.507
-	4	288	_p.E42K|A1CF_uc	NM_138932	NP_620310	Q9NQ94	A1CF_HUMAN		1	ATTTTCCTGCA	0.413
+	1	162	_5'Flank|uc009xo	NM_012242	NP_036374	O94907	DKK1_HUMAN		3	GATGGCTCTGG	0.612
-	27	3954	se_Mutation_p.P1	NM_033056	NP_149045	Q96QU1	PCD15_HUMAN	|Extracellular (Potential).	13	TAATTGGTGGTA	0.368
-	6	599	a.1_Missense_Mu	NM_007057	NP_008988	O95229	ZWINT_HUMAN	Potential.	0	AAACACCCTGT	0.557
+	10	1361	kj.1_Missense_M	NM_001080512	NP_001073981	Q9H694	BICC1_HUMAN		4	TCACTGGACTAG	0.507
-	37	4640	.1_Intron|ANK3_u	NM_020987	NP_066267	Q12955	ANK3_HUMAN		19	TTGCTCCTGTA	0.403
-	11	1441	se_Mutation_p.E4	NM_020987	NP_066267	Q12955	ANK3_HUMAN	ANK 11.	19	GGAGTTCCATTA	0.423
+	5	795	_p.P257S|ARID5B	NM_032199	NP_115575	Q14865	ARI5B_HUMAN		4	AGAAACCATGC	0.413
+	1	944		NM_032804	NP_116193	Q96SZ5	AEDO_HUMAN		0	ACGACCCGGAC	0.692
-	2	312	p.G53E|EGR2_uc	NM_001136177	NP_001129649	P11161	EGR2_HUMAN		2	CCACTCCGTTC	0.652
-	4	511	e_Mutation_p.A13	NM_001127384	NP_001120856	Q9UI47	CTNA3_HUMAN		8	CGCAGCCAGCA	0.483
-	2	316	1jnc.2_Missense_	NM_021800	NP_068572	Q9UKB3	DJC12_HUMAN	J.	1	TTTGGGGTTTT	0.343
+	12	2568	PN_uc009xpt.2_	NM_032578	NP_115967	Q86TC9	MYPN_HUMAN	Pro-rich.	5	CACCACCACCA	0.547
-	19	3119	e_Mutation_p.L71	NM_001080449	NP_001073918	P51530	DNA2L_HUMAN		0	CGTGCCAATAAA	0.353
+	15	2091	50_uc010qjc.1_In	NM_024045	NP_076950	Q9BQ39	DDX50_HUMAN		1	AAATTACCTGAA	0.448
+	4	536	C1_uc010qje.1_5'	NM_025130	NP_079406	Q2TB90	HKDC1_HUMAN		5	TGTCTGGCAGAT	0.468
+	10	1508	je.1_Missense_M	NM_025130	NP_079406	Q2TB90	HKDC1_HUMAN		5	CCGCGGTGGCC	0.647
+	9	1183	p.V365A|HK1_uc	NM_000188	NP_000179	P19367	HXK1_HUMAN	Regulatory.	1	GGGAGTGGAGC	0.537

+	15	2203	i.3_Missense_Mut	NM_000188	NP_000179	P19367	HXK1_HUMAN	Catalytic.	1	CCAGGGGCAG	0.577	
+	17	1507	1jqc.1_Missense_	NM_005203	NP_005194	Q5TAT6	CODA1_HUMAN	al).|Triple-helical region 2 (	1	GCCAGGGATGC	0.617	
-	3	956		NM_018055	NP_060525	Q96S42	NODAL_HUMAN		2	GGTGGGGCTGG	0.473	
-	2	503	p.G118D|DNAJB1	NM_017626	NP_060096	Q9NXW2	DJB12_HUMAN		0	CTTCACCGTTG	0.612	
+	6	603	uc001jtk.2_Missen	NM_015901	NP_056985	Q86X67	NUD13_HUMAN		0	CTCTTCTCCGC	0.522	
-	18	3913	p.R387K|USP54_	NM_152586	NP_689799	Q70EL1	UBP54_HUMAN		6	TGATTTCTCTCT	0.483	rs150112870
-	5	966		NM_021245	NP_067068	Q9NP98	MYOZ1_HUMAN		2	CAAGTTCCATTT	0.512	
-	4	835		NM_021245	NP_067068	Q9NP98	MYOZ1_HUMAN	Gly-rich.	2	TGCCAGCAGCT	0.592	
+	9	1017	n_p.P205S|PLAU_	NM_002658	NP_002649	P00749	UROK_HUMAN	eptidase S1.	3	CGCAGCCATCC	0.542	
-	5	1053	wh.2_Missense_M	NM_207012	NP_996895	Q9Y2T2	AP3M1_HUMAN	MHD.	0	TGCAAGCATCA	0.368	
+	3	1056	wo.1_Missense_M	NM_012330	NP_036462	Q8WYB5	MYST4_HUMAN		16	AGTATCCCAGTG	0.527	
-	1	156	5'UTR|DUSP13_u	NM_001007271	NP_001007272	Q6B8I1	MDSP_HUMAN		0	CTGCAAGAAGAC	0.617	
+	5	417	a.2_Nonsense_M	NM_003375	NP_003366	P45880	VDAC2_HUMAN	nded; (By similarity).	3	AAAGTGGAACAC	0.343	
-	20	2778		NM_007055	NP_008986	O14802	RPC1_HUMAN		0	ATATCGCCAGTAG	0.438	
+	7	1334	_p.P215L|NRG3_	NM_001010848	NP_001010848	P56975	NRG3_HUMAN	lasmic (Potential).	6	GGCATCCTGTGA	0.483	
+	2	399	n_p.V58I|OPN4_u	NM_033282	NP_150598	Q9UHM6	OPN4_HUMAN	ellular (Potential).	1	CCTGGGTCCCC	0.478	
+	5	690	t.1_Missense_Mut	NM_004190	NP_004181	P07098	LIPG_HUMAN		0	GGGCACCACCA	0.378	
+	7	1326	ite|STAMBPL1_uc	NM_020799	NP_065850	Q96FJ0	STALP_HUMAN		1	AAACTGGTATGA	0.318	
-	9	1162		NM_014391	NP_055206	Q15327	ANKR1_HUMAN	ANK 5.	0	CTGAGGCTGTCG	0.453	
+	6	675	.1_RNA|BTAF1_u	NM_003972	NP_003963	O14981	BTAF1_HUMAN	lization signal (Potential).	3	CAGGCAGCTGAA	0.368	
+	32	4614		NM_003972	NP_003963	O14981	BTAF1_HUMAN		3	ATGAAAGAAGAT	0.373	
-	1	2320		NR_002319					0	CACCGGGTTTC	0.478	
-	10	1104	1_uc001kks.2_Mis	NM_001034954	NP_001030126	Q9BX66	SRBS1_HUMAN		1	ATAGCCTTGCCA	0.502	
-	4	767	qot.1_Missense_	NM_020123	NP_064508	Q9HD45	TM9S3_HUMAN		0	TGGAACCAGTTT	0.318	
-	20	2317	h.1_Missense_Mu	NM_003061	NP_003052	O75093	SLIT1_HUMAN	LRRCT 3.	4	TCTTGCGCTTCC	0.612	
-	16	1856	h.1_Missense_Mu	NM_003061	NP_003052	O75093	SLIT1_HUMAN	LRRNT 3.	4	GCTCAGGGATC	0.637	
+	12	1439	HC16_uc001knn.2	NM_198046	NP_932163	Q969W1	ZDH16_HUMAN	lasmic (Potential).	1	AGCCCCCTCCC	0.532	rs12259677
-	10	1599	p.D404N|CRTAC1	NM_018058	NP_060528	Q9NQ79	CRAC1_HUMAN	GAP 4; atypical.	5	CCCGTCTCCGT	0.582	
-	8	914	_Mutation_p.G276	NM_018294	NP_060764	Q69YN2	C19L1_HUMAN		0	GCTTTCCTATGG	0.398	
-	2	93	1S2_uc001kqv.1_	NM_173809	NP_776170	Q6QNY1	BL1S2_HUMAN		1	TGTCTCCACGG	0.572	
+	2	659		NM_005063	NP_005054	O00767	ACOD_HUMAN	lasmic (Potential).	0	ATGACCCCACCT	0.483	
+	5	503		NM_003393	NP_003384	Q93098	WNT8B_HUMAN		4	GTGGGGAGGCT	0.587	
-	1	77	31B_uc010qpq.1_	NM_005004	NP_004995	O95169	NDUB8_HUMAN		0	GGATGCCCTTT	0.627	
+	3	582		NM_017902	NP_060372	Q9NWT6	HIF1N_HUMAN	ith HIF1A.|Interaction with	0	GAACTGGATTAA	0.418	
-	9	1590	sn.2_Missense_M	NM_024895	NP_079171	Q9H5P4	PDZD7_HUMAN		3	GGCACCCTTCT	0.557	
-	8	2130	.2_Missense_Mut	NM_013274	NP_037406	Q9UGP5	DPOLL_HUMAN		0	GGAACCCTGGC	0.607	
-	16	3159	se_Mutation_p.P8	NM_012215	NP_036347	O60502	NCOAT_HUMAN	sferase activity (By similari	3	CTTTGGAAATC	0.413	
-	9	1761	se_Mutation_p.Q	NM_012215	NP_036347	O60502	NCOAT_HUMAN		3	CTCCCTGGCTCA	0.463	
-	4	621	KCNIP2_uc001kue	NM_173191	NP_775283	Q9NS61	KCIP2_HUMAN	nd 1; degenerate.	0	CCTCAGGCCGG	0.617	
+	1	1425		NM_024747	NP_079023	Q86YV9	HPS6_HUMAN		0	ACCTGCCCCCAT	0.627	
+	9	4382	S1328F|PPRC1_u	NM_015062	NP_055877	Q5VV67	PPRC1_HUMAN	raction with CREB1 and NF	3	CATCGTCTTCCT	0.597	
+	1	191		NM_152310	NP_689523	Q9HB03	ELOV3_HUMAN		2	TCACATGAAGTA	0.517	
+	6	655	uy.1_Missense_M	NM_004193	NP_004184	Q92538	GBF1_HUMAN		2	TGATAGGTTCTAC	0.468	
+	40	5630	.P1793L|GBF1_u	NM_004193	NP_004184	Q92538	GBF1_HUMAN	Pro-rich.	2	CACCCCCGACG	0.672	
+	5	465	_p.G67D|NFKB2_	NM_001077494	NP_001070962	Q00653	NFKB2_HUMAN	RHD.	3	GCCCGGTGCCT	0.582	
+	12	1356	p.A364V|NFKB2_	NM_001077494	NP_001070962	Q00653	NFKB2_HUMAN	RR.|Gly-rich.	3	TGCAGCCGGGG	0.607	
-	2	1056	.P177S|PSD_uc0	NM_002779	NP_002770	A5PKW4	PSD1_HUMAN	Pro-rich.	3	CTGGCGGCCCAT	0.662	

-	15	1280	vq.2_Missense_M	NM_012229	NP_036361	P49902	5NTC_HUMAN		0	GCCACCCTTGC	0.398	
+	19	2905	CS3_uc010qqz.1_	NM_014978	NP_055793	Q9UPU3	SORC3_HUMAN	umenal (Potential).	10	TGACAGCCTATG	0.532	
-	1	343	p.G112E|SORCS1	NM_052918	NP_443150	Q8WY21	SORC1_HUMAN	enal (Potential).	2	CCGCTCCGCTC	0.716	
+	5	649	p.S112N|ADD3_u	NM_016824	NP_058432	Q9UEY8	ADDG_HUMAN		5	TTTTAGGTCTTG	0.468	
+	17	1870		NM_005445	NP_005436	Q9UQE7	SMC3_HUMAN	lexible hinge.	3	ATCTTCCTGGA	0.343	
+	3	485	_p.G70E|PDCD4_	NM_014456	NP_055271	Q53EL6	PDCD4_HUMAN		3	CAGTGGGAGTG	0.512	
+	6	576	e_Mutation_p.W20	NM_203379	NP_976313	Q9ULC5	ACSL5_HUMAN	lasmic (Potential).	3	CAGTGGATCAT	0.448	rs151027490
-	22	2336	qsi.1_Missense_M	NM_002313	NP_002304	O14639	ABLM1_HUMAN	HP.	1	CTTCAGGGGCT	0.433	
-	4	589	0qss.1_Splice_Site	NM_022063	NP_071346	Q9H8W3	F204A_HUMAN		0	AAACACCTTTT	0.323	
+	2	117	_uc010qsw.1_5'U	NM_207009	NP_996892	Q8TCE6	FA45A_HUMAN		1	ATGGAGAAGTT	0.443	
-	7	424	XN4_uc001ldz.2_	NM_213649	NP_998814	Q6P4A7	SFXN4_HUMAN	ical; (Potential).	1	CAGTGGCGTCA	0.413	
+	13	1623	h.2_Missense_Mu	NM_005308	NP_005299	P34947	GRK5_HUMAN	kinase C-terminal.	3	ACCCTCCCTTC	0.632	
+	20	2478	ep.2_Missense_M	NM_014937	NP_055752	Q9Y2H2	SAC2_HUMAN		2	TTTGGCCCAGG	0.373	
+	20	2397	zz.1_Missense_M	NM_007329	NP_015568	Q9UGM3	DMBT1_HUMAN	SRCR 6.	7	GGATACCAATG	0.607	
+	20	2463	zz.1_Missense_M	NM_007329	NP_015568	Q9UGM3	DMBT1_HUMAN	SRCR 6.	7	AAATGCCCGGT	0.622	
-	5	1030	10qty.1_Intron|CU	NM_022034	NP_071317	Q86UP6	CUZD1_HUMAN	lar (Potential).|CUB 2.	2	TGGGAGTCACA	0.453	
+	2	289	n_p.I90T|LHPP_u	NM_022126	NP_071409	Q9H008	LHPP_HUMAN		0	CCAGATCCTGA	0.632	
-	11	2587	.1_Missense_Mut	NM_018180	NP_060650	Q7L7V1	DHX32_HUMAN		4	AGATTACTGAAA	0.398	
-	8	2035	.1_Splice_Site_p.	NM_018180	NP_060650	Q7L7V1	DHX32_HUMAN		4	TGGAGCTTCAA	0.443	
-	4	739	_p.A109V|ADAM1	NM_003474	NP_003465	O43184	ADA12_HUMAN		9	TTCGAGCGAGG	0.438	
+	35	3599	p.E1200K|DOCK1_	NM_001380	NP_001371	Q14185	DOCK1_HUMAN	DHR-2.	9	TTAATGGAAAGG	0.423	
+	47	4901	.G1634S|DOCK1_	NM_001380	NP_001371	Q14185	DOCK1_HUMAN	DHR-2.	9	AGTACGGCGTC	0.532	
-	7	1040	67_uc009yav.1_Int	NM_002417	NP_002408	P46013	KI67_HUMAN		7	TCTCCCCCTGT	0.458	
-	1	156	27_uc010quv.1_5'	NM_173575	NP_775846	Q86UX6	ST32C_HUMAN		5	CCCGCCCGCCC	0.587	
-	1	91		NM_001080998	NP_001074467	Q96QU4	FRG2B_HUMAN		0	TGGAGGAGCAG	0.502	
+	2	162	3_uc010qvk.1_5'	NM_145651	NP_663626	Q8TD33	SG1C1_HUMAN		1	ATGAGGGGACC	0.542	
+	9	809		NM_178537	NP_848632	Q76KP1	B4GN4_HUMAN	enal (Potential).	1	CCTGCCCGGCC	0.672	
-	3	1823	w.1_RNA|RNH1_u	NM_203389	NP_976323	P13489	RINI_HUMAN	LRR 5.	0	GGGGTCCAGGA	0.657	
-	2	1538	sense_Mutation_p	NM_203389	NP_976323	P13489	RINI_HUMAN	LRR 1.	0	GCACCGTGCTT	0.632	rs149360262
+	8	979	_p.R282K|PHRF1_	NM_020901	NP_065952	Q9P1Y6	PHRF1_HUMAN	Arg-rich.	0	AGTGAGAGCAA	0.652	
+	14	2380	RF1_uc010qwe.1_	NM_020901	NP_065952	Q9P1Y6	PHRF1_HUMAN		0	CCGGCCCCCAG	0.692	
-	13	1897	ycc.2_Missense_	NM_021924	NP_068743	Q9HBB8	CDHR5_HUMAN	em repeats.|2.|Extracellul	0	CCCACCGGGTG	0.672	rs139590704
+	4	1138		NM_000797	NP_000788	P21917	DRD4_HUMAN	Name=7; (Potential).	0	CCCCGCGGCTG	0.672	
+	5	673	ra.2_Missense_M	NM_006755	NP_006746	P37837	TALDO_HUMAN		0	TGAGCCCCTGG	0.607	
+	8	1403	uc001lrx.2_5'Flank|CD151_uc001lry.2_5'Flank|CD151_			Q8N4Y2	EFC4A_HUMAN		0	CTCAGGTACGG	0.592	
+	4	421	_p.G71D|TSPAN4_	NM_003271	NP_003262	O14817	TSN4_HUMAN	ical; (Potential).	1	CGTGGGCTGCC	0.657	
-	31	4942		NM_005961	NP_005952	Q6W4X9	MUC6_HUMAN	truncated.|Approximate re	1	TGATGACTGTGT	0.557	
-	30	3947		NM_005961	NP_005952	Q6W4X9	MUC6_HUMAN	-rich.|Thr-rich.	1	CTGTGGGTTTT	0.622	
+	20	2380	5B_uc001ltb.2_M	NM_017511	NP_059981	Q9HC84	MUC5B_HUMAN	VWFD 1.	0	GCTTCCCTGGC	0.647	
+	51	14903	b.2_Missense_Mu	NM_017511	NP_059981	Q9HC84	MUC5B_HUMAN	em repeats, Ser/Thr- rich.|	0	AGAGCCGAGCA	0.662	
+	6	754	Missense_Mutatio	NM_138567	NP_612634	Q8NBV8	SYT8_HUMAN	toplasmic (Potential).	1	CTCGGGGCATG	0.672	
+	8	1016	p.P219S|LSP1_uc	NM_002339	NP_002330	P33241	LSP1_HUMAN		1	AGACTCCGTCC	0.622	
-	6	1861	_uc010qxr.1_Non	NM_001130520	NP_001123992	O14628	ZN195_HUMAN	2H2-type 8.	0	GAGAACCACAT	0.393	
-	4	782	_p.A31V|CHRNA1	NM_020402	NP_065135	Q9GZZ6	ACH10_HUMAN	ellular (Potential).	1	AGGCGGCGGCG	0.716	
-	27	4571	.R1427K|NUP98_	NM_016320	NP_057404	P52948	NUP98_HUMAN		12	GCGCCCTAGAA	0.443	
-	5	698	_p.T136I|NUP98_	NM_016320	NP_057404	P52948	NUP98_HUMAN	Gly/Thr-rich.	12	TTAGAGGTGGTA	0.378	
+	9	1706	p.A380T|STIM1_u	NM_003156	NP_003147	Q13586	STIM1_HUMAN	ic (Potential).|Potential.	1	TGCAGGCTGAG	0.483	

+	1	881		NM_001005169	NP_001005169	Q8NGK6	O52I1_HUMAN	Name=7; (Potential).	2	TAAATCCCATCAT	0.498	rs150466381
+	1	940		NM_001005169	NP_001005169	Q8NGK6	O52I1_HUMAN	lasmic (Potential).	2	CTGATGCACTTCC	0.458	
+	2	241		NM_021801	NP_068573	Q9NRE1	MMP26_HUMAN		0	ATGCATGCTCTG	0.537	
-	1	149		NM_001004760	NP_001004760	Q9H2C8	O51V1_HUMAN	Name=1; (Potential).	1	CAATTGCCCAAAA	0.507	
+	1	559	_uc001mam.1_Int	NM_001004757	NP_001004757	Q8NH59	O51Q1_HUMAN	cellular (Potential).	1	GATATGATCCGCC	0.512	
-	2	1482	uc001mam.1_5'Fla	NM_017481	NP_059509	Q9H347	UBQL3_HUMAN		3	GGCTGCCGTGG	0.542	
+	1	277	M5_uc001mbq.1_In	NM_001005165	NP_001005165	Q8NGH9	O52E4_HUMAN	cellular (Potential).	2	CTCCAAGAGATCA	0.463	
-	1	970		NM_001005179	NP_001005179	Q8NGH8	O56A4_HUMAN	cellular (Potential).	2	CTGGAGGAATTCT	0.532	
+	42	13927	sense_Mutation_p.	NM_144666	NP_653267	Q96M86	DNHD1_HUMAN	Potential.	2	CTGCAGGATCTG	0.637	
+	3	341	_Mutation_p.T69I|	NM_001014794	NP_001014794	Q13418	ILK_HUMAN	n with LIMS1.|ANK 3.	1	ATGACACCCCCC	0.557	
-	21	10186	P1_uc001mel.1_5'	NM_003737	NP_003728	Q96JQ0	PCD16_HUMAN	lasmic (Potential).	5	GAGGAGACAGA	0.642	
-	21	9978	P1_uc001mel.1_5'	NM_003737	NP_003728	Q96JQ0	PCD16_HUMAN	lasmic (Potential).	5	GCCGAGCTTCAT	0.622	
+	1	290		NM_178168	NP_835462	Q9H207	O10A5_HUMAN	cellular (Potential).	3	TCCTTGGCTGTG	0.507	
+	1	889		NM_001004684	NP_001004684	Q8NGH3	OR2D3_HUMAN	Name=7; (Potential).	0	CAGCGGTGACT	0.418	
+	4	2230		NM_176822	NP_789792	Q86W24	NAL14_HUMAN		8	CTGTAACTGTGG	0.438	
+	11	1355	0rbd.1_Missense_M	NM_003621	NP_003612	Q8ND30	LIPB2_HUMAN		4	CAGGGCCTTCG	0.383	
-	1	761		NM_153445	NP_703146	Q8WZ94	OR5P3_HUMAN	Name=6; (Potential).	1	GTAATGGTCCCAT	0.527	
-	22	3000	_p.E946K|SCUBE2	NM_020974	NP_066025	Q9NQ36	SCUB2_HUMAN		2	GGACTCCTGGG	0.448	
-	16	2034	CUBE2_uc001mhj.	NM_020974	NP_066025	Q9NQ36	SCUB2_HUMAN		2	AGCGTTCTCGTG	0.488	
+	10	1519	nhx.2_Missense_M	NM_015055	NP_055870	Q9UH65	SWP70_HUMAN	Potential.	3	CAGCAGGCCATT	0.547	
-	3	383	f.3_5'UTR|SBF2_u	NM_030962	NP_112224	Q86WG5	MTMRD_HUMAN	UDENN.	3	GTTAGGCATGAG	0.448	
+	4	831	x.1_Missense_Mu	NM_001025389	NP_001020560	Q01432	AMPD3_HUMAN		2	AAGTATGCGCGG	0.567	
+	21	3175	njs.2_Missense_M	NM_017944	NP_060414	Q96K76	UBP47_HUMAN		2	CAGATGGCCTTT	0.363	
-	4	585	6_splice|DKK3_uc	NM_001018057	NP_001018067	Q9UBP4	DKK3_HUMAN		1	TACTCACCATCCT	0.642	
+	4	679	_p.P131S|MICAL2_	NM_014632	NP_055447	O94851	MICA2_HUMAN		2	CTCTGGCCTTTCA	0.552	
+	11	1702	L2_uc001mkb.2_M	NM_014632	NP_055447	O94851	MICA2_HUMAN		2	CGGTACCCAAAC	0.552	
+	23	3173	41V|MICAL2_uc00	NM_014632	NP_055447	O94851	MICA2_HUMAN		2	GGCTGCAGCTGA	0.562	
+	14	1492	_uc001mkt.2_Miss	NM_001178	NP_001169	O00327	BMAL1_HUMAN	PAS 2.	0	ATTTTGGCATATT	0.368	
-	9	1384	e_Mutation_p.T36	NM_032320	NP_115696	Q9BSF8	BTBDA_HUMAN		0	TTGTAGGTAGGAT	0.413	
+	5	1769	0rcr.1_Splice_Site_	NM_000922	NP_000913	Q13370	PDE3B_HUMAN		0	CTTTTAGTCAAGC	0.333	
-	4	1462	nmr.3_RNA|PIK3C	NM_002645	NP_002636	O00443	P3C2A_HUMAN		10	CAACATCTACTTC	0.348	
-	24	2993		NM_000352	NP_000343	Q09428	ABCC8_HUMAN	smic (By similarity).	1	GCACGAGATAGG	0.542	rs72559721
-	12	1841	cy.1_Missense_Mu	NM_000352	NP_000343	Q09428	ABCC8_HUMAN	rity).|ABC transmembrane t	1	AGGGCGAGAAG	0.597	
-	3	266	se_Mutation_p.P53	NM_005709	NP_005700	Q9Y6N9	USH1C_HUMAN		1	GGCTGGGTTCAT	0.617	
-	18	2892	_p.P758S|HPS5_u	NM_181507	NP_852608	Q9UPZ3	HPS5_HUMAN		3	TGGATGGAAAGA	0.368	
-	9	1140	0rdf.1_Splice_Site_	NM_001040697	NP_001035787	Q8IX04	UEVLD_HUMAN		0	TTCTTACCTTTGT	0.219	
+	3	574		NM_153347	NP_699178	Q8N2M4	TM86A_HUMAN		1	GGCAGGGCTGC	0.607	
+	17	1964	mpj.2_Missense_M	NM_019028	NP_061901	Q8IUH4	ZDH13_HUMAN		0	TTCTTCGCTCAG	0.428	
+	8	1443	_p.T274I|NAV2_u	NM_145117	NP_660093	Q8IVL1	NAV2_HUMAN		6	GCTCCACCCCTA	0.602	
+	36	7212	hz.2_Missense_M	NM_182964	NP_892009	Q8IVL1	NAV2_HUMAN		6	TCCAGGCCCCC	0.557	
+	8	1609	yic.2_Missense_M	NM_004211	NP_004202	Q9Y345	SC6A5_HUMAN		4	CTGGAGCTGGA	0.562	
+	13	1547	_p.G493E|NELL1_u	NM_006157	NP_006148	Q92832	NELL1_HUMAN	alcium-binding (Potential).	3	TCCCAGGATACAT	0.418	
+	7	862	qj.2_Missense_Mu	NM_213599	NP_998764	Q75V66	ANO5_HUMAN	lasmic (Potential).	4	AGTATCCCCATC	0.453	
+	1	447		NM_020346	NP_065079	Q9P2U8	VGLU2_HUMAN	lasmic (Potential).	4	CCCCAGGAAAA	0.433	
-	1	794		NM_022725	NP_073562	Q9NPI8	FANCF_HUMAN		1	TGGGAGGGCGC	0.562	
+	4	508	_p.E6K|LUZP2_u	NM_001009909	NP_001009909	Q86TE4	LUZP2_HUMAN	Potential.	2	TTCAGGAGGCC	0.368	
-	18	2770	rk.3_Missense_Mu	NM_018490	NP_060960	Q9BXB1	LGR4_HUMAN	Name=6; (Potential).	1	CCACAGGGCAG	0.408	

-	13	2080		NM_031217	NP_112494	Q8NI77	KI18A_HUMAN		2	GAACAGAAATCC	0.378
-	3	556		NM_031217	NP_112494	Q8NI77	KI18A_HUMAN	Kinesin-motor.	2	GCTGATCCTAGC	0.378
-	3	541	_p.V141M|MPPE	NM_001584	NP_001575	Q15777	MPPD2_HUMAN		1	GGACACAGAGG	0.393
-	3	243	P1L_uc009yjo.2_	NM_144981	NP_659418	Q96LU5	IMP1L_HUMAN		0	GAATAGTATAGC	0.363
+	4	2024	_p.S347F|QSER1_	NM_001076786	NP_001070254	Q2KHR3	QSER1_HUMAN		6	GGCTATCTGATG	0.398
+	2	186	reh.1_Missense_	NM_001077242	NP_001070710	Q96QD5	DEPD7_HUMAN		2	AGAAGCCATTT	0.393
+	2	488	ense_Mutation_p.	NM_018393	NP_060863	Q9NUJ3	T11L1_HUMAN		0	CTGTGGAAGGT	0.413
-	21	2118	1L1_uc001muf.1_	NM_001326	NP_001317	Q12996	CSTF3_HUMAN		0	TCAACAGCTATT	0.428
-	14	1347	1L1_uc001muf.1_	NM_001326	NP_001317	Q12996	CSTF3_HUMAN		0	ATTCTTCCAGATT	0.343
+	12	2603	n.1_Intron|HIPK3_	NM_005734	NP_005725	Q9H422	HIPK3_HUMAN	with AR (By similarity).	5	GGAATGGGAGC	0.353
+	1	302	mun.1_Missense_	NM_012194	NP_036326	Q6ZVL6	CK041_HUMAN	Poly-Pro.	2	CTCCCCCTCCC	0.562
-	1	294		NM_145804	NP_665803	Q8N961	ABTB2_HUMAN		2	GCGACCCACTG	0.672
-	11	2256	we.2_Missense_	NM_004171	NP_004162	P43004	EAA2_HUMAN		3	TGGCTGCCAGA	0.433
-	9	1929	_p.G437E|SLC1A	NM_004171	NP_004162	P43004	EAA2_HUMAN	ical; (Potential).	3	CCAGCCCGGCA	0.572
-	11	1946	ew.1_Nonsense_	NM_001001991	NP_001001991	Q6UXH9	PAMR1_HUMAN	eptidase S1.	2	GTCCTCATGCT	0.572
-	2	180	OMMD9_uc010rfb	NM_014186	NP_054905	Q9P000	COMD9_HUMAN		1	AGCTGGAACAT	0.463
+	2	542	G1_uc001mwt.2_	NM_000448	NP_000439	P15918	RAG1_HUMAN	with importin alpha-1.	5	TAGGCCTTTTA	0.502
+	2	2834	G1_uc001mwt.2_	NM_000448	NP_000439	P15918	RAG1_HUMAN		5	CTAAAGAGTGC	0.468
-	2	1735	_uc001mwx.1_5'	NM_000536	NP_000527	P55895	RAG2_HUMAN		5	TGGCAGGAGTC	0.368
-	2	3681	nxd.1_Missense_	NM_020929	NP_065980	Q9HCJ2	LRC4C_HUMAN		8	TCTCATCATCCA	0.468
+	23	3243	xl.2_Missense_Mu	NM_018259	NP_060729	Q96AE7	TTC17_HUMAN	TPR 5.	5	CCATGGCAGTA	0.522
+	1	1247	6_splice|SLC35C	NM_018389	NP_060859	Q96A29	FUCT1_HUMAN		0	CATCGGTGAGT	0.493
+	10	1634	ncg.2_Missense_	NM_052854	NP_443086	Q96BA8	CR3L1_HUMAN	enal (Potential).	8	CTCCGGCTCCC	0.637
-	7	2425	p.L599F|AMBRA1_	NM_017749	NP_060219	Q9C0C7	AMRA1_HUMAN		3	CCTGAGTGAAT	0.483
-	7	1448	BRA1_uc001ncv.	NM_017749	NP_060219	Q9C0C7	AMRA1_HUMAN		3	GGAGGCCCTGG	0.627
-	7	1039	MBRA1_uc001ncv.	NM_017749	NP_060219	Q9C0C7	AMRA1_HUMAN		3	GAGGGCACGCT	0.582
-	8	1006	p.A185V|CKAP5_	NM_001008938	NP_001008938	Q14008	CKAP5_HUMAN		2	TCCAGGGCCTCT	0.373
+	8	1627	.1_Missense_Mut	NM_003682	NP_003673	Q8WXG6	MADD_HUMAN		11	TCTATGGCAATG	0.458
-	32	3783		NM_000256	NP_000247	Q14896	MYPC3_HUMAN	like C2-type 7.	3	GGCAGGGCTTT	0.602
-	32	3683		NM_000256	NP_000247	Q14896	MYPC3_HUMAN	like C2-type 7.	3	TCTTGGGCTATA	0.557
+	6	824	C39A13_uc001nff	NM_001128225	NP_001121697	Q96H72	S39AD_HUMAN	ellular (Potential).	0	TCAGCGGCTACC	0.642
-	12	1434	lr.1_Missense_Mu	NM_002804	NP_002795	P17980	PRS6A_HUMAN		4	GAGCTCCGTGG	0.607
-	6	687	lr.1_Missense_Mu	NM_002804	NP_002795	P17980	PRS6A_HUMAN		4	TGTGGGCAGCG	0.562
-	9	1487	se_Mutation_p.P4	NM_024783	NP_079059	Q5U5Z8	CBPC2_HUMAN		2	TCCAGGGTGAA	0.488
-	2	382	.2_5'UTR|FNBP4_	NM_015308	NP_056123	Q8N3X1	FNBP4_HUMAN		1	CGCTTCCTGTT	0.348
-	1	224	P160_uc001ngn.	NM_015231	NP_056046	Q12769	NU160_HUMAN		7	TTAGCTCCACGA	0.657
-	7	1118	_Mutation_p.A271	NM_004476	NP_004467	Q04609	FOLH1_HUMAN	.|Extracellular (Probable).	3	CAACAGCCTCT	0.368
+	1	406		NM_001001955	NP_001001955	Q8NGP0	OR4CD_HUMAN	lasmic (Potential).	4	TGAAGCAGCAT	0.468
-	1	355		NM_001004700	NP_001004700	Q6IEV9	OR4CB_HUMAN	lasmic (Potential).	1	GCGATCAACAG	0.433
+	1	356		NM_001005200	NP_001005200	Q8N162	OR8H2_HUMAN	Name=3; (Potential).	2	AATGGCCCATG	0.468
+	1	400		NM_001005202	NP_001005202	Q8NH51	OR8K3_HUMAN	lasmic (Potential).	4	TACACAGTAATC	0.408
-	1	653		NM_001005245	NP_001005245	Q96RB7	OR5MB_HUMAN	lasmic (Potential).	0	TGAAGGCATAG	0.483
-	5	3626	.G1105E|TNKS1B	NM_033396	NP_203754	Q9C0C2	TB182_HUMAN	ly-rich.|Acidic.	1	GCTGCCCTGGG	0.592
-	2	548	_Mutation_p.R79	NM_033396	NP_203754	Q9C0C2	TB182_HUMAN	ys/Pro-rich (charged).	1	TCTTCCTGGCA	0.667
-	9	1020	nkl.2_Missense_	NM_003627	NP_003618	O75387	LAT3_HUMAN		0	TGGGGGAGCAG	0.602
-	3	296	nko.1_Missense_	NM_004223	NP_004214	O14933	UB2L6_HUMAN		1	TGATCATGGGA	0.537
+	3	1157	p.P276S|CLP1_uc	NM_006831	NP_006822	Q92989	CLP1_HUMAN		1	TGTTTACCTTTG	0.493

+	9	2211	p.D266N|ZDHHC5	NM_015457	NP_056272	Q9C0B5	ZDHC5_HUMAN		1	AGCCAGACCTG	0.512	
+	8	2096	sense_Mutation_p	NM_001085458	NP_001078927	O60716	CTND1_HUMAN	ARM 4.	6	GTTGGGAGCGG	0.488	
+	1	607	Q1_uc001nmj.2_I	NM_001005186	NP_001005186	Q8NGQ2	OR6Q1_HUMAN	Name=5; (Potential).	1	ACTGTGGATTTC	0.517	
-	1	544		NM_001005566	NP_001005566	Q96R09	OR5B2_HUMAN	ellular (Potential).	3	CATGACTGCTG	0.388	
+	5	1372	no.2_Missense_	NM_001142521	NP_001135993	Q96PZ2	F111A_HUMAN		3	TTTAACTTGTCG	0.423	
-	1	874		NM_001039396	NP_001034485	Q2M385	MPEG1_HUMAN	xtracellular (Potential).	2	TCCAGCAGAGG	0.537	
-	1	458		NM_001001954	NP_001001954	Q8NGI9	OR5A2_HUMAN	Name=4; (Potential).	0	GGAATCCACCC	0.458	
+	3	465	_uc001nqe.2_5'F	NM_207341	NP_997224	P60852	ZP1_HUMAN	ellular (Potential).	0	AGCTGGCACCA	0.607	
+	9	1480	e.2_Missense_Mu	NM_207341	NP_997224	P60852	ZP1_HUMAN	llular (Potential).|ZP.	0	ACAGAACCCAAA	0.592	
+	4	737	0D|TMEM132A_u	NM_024092	NP_076997	Q9BVC6	TM109_HUMAN		0	CCAGGGCCTGA	0.622	
+	6	1170		NM_014207	NP_055022	P06127	CD5_HUMAN	ar (Potential).|SRCR 3.	1	GGAGAGAAATT	0.552	
+	4	524	se.1_Missense_M	NM_001127392	NP_001120864	Q9Y2G1	MRF_HUMAN	Pro-rich.	1	CTCGGGCTCCG	0.672	
+	27	3538	_p.R1108C|C11orf	NM_001127392	NP_001120864	Q9Y2G1	MRF_HUMAN		1	TTCTACCGCCTG	0.627	
-	5	15023	AK_uc001ntk.1_I	NM_001620	NP_001611	Q09666	AHNK_HUMAN		19	CCAGCGATGGC	0.463	rs146517943
-	5	14611	AK_uc001ntk.1_I	NM_001620	NP_001611	Q09666	AHNK_HUMAN		19	CATGAACATCCA	0.522	rs143263481
-	5	8109	AK_uc001ntk.1_I	NM_001620	NP_001611	Q09666	AHNK_HUMAN		19	TCCACTTTGGG	0.522	
-	5	7862	AK_uc001ntk.1_I	NM_001620	NP_001611	Q09666	AHNK_HUMAN		19	AGCCAGGCATG	0.517	rs143391519
-	5	7514	AK_uc001ntk.1_I	NM_001620	NP_001611	Q09666	AHNK_HUMAN		19	TCTACATCCACC	0.483	
-	5	6706	AK_uc001ntk.1_I	NM_001620	NP_001611	Q09666	AHNK_HUMAN		19	ACACATCCACAT	0.507	
-	5	1325	AK_uc001ntk.1_I	NM_001620	NP_001611	Q09666	AHNK_HUMAN		19	TGCCGCCCTTG	0.577	
-	5	1219	AK_uc001ntk.1_I	NM_001620	NP_001611	Q09666	AHNK_HUMAN		19	TGGTGGGAAATT	0.527	
+	1	607	_5'Flank|EML3_u	NM_000327	NP_000318	Q03395	ROM1_HUMAN	ical; (Potential).	3	CTCTGGCTCCT	0.662	
-	9	931	p.P203S|GANAB_	NM_198334	NP_938148	Q14697	GANAB_HUMAN		5	CACAGGCACAG	0.537	
-	5	503	_p.R60H|GANAB_	NM_198334	NP_938148	Q14697	GANAB_HUMAN		5	CAAGGCGGAAT	0.522	
-	2	2766	AB_uc001nuc.2_5'	NM_030628	NP_085131	Q6P9B9	INT5_HUMAN		2	TGCCTCCAGGT	0.617	
+	4	397	R2G_uc001nvb.2_	NM_002696	NP_002687	P62487	RPB7_HUMAN		0	GGTTGGACTCT	0.299	
+	4	463	p.G121D|TAF6L_	NM_006473	NP_006464	Q9Y6J9	TAF6L_HUMAN		3	CAAAGGCTGTG	0.627	
+	12	1899	we.2_Nonsense_	NM_002394	NP_002385	P08195	4F2_HUMAN	ellular (Potential).	0	GGGACCAGAAT	0.617	
-	8	1149	ense_Mutation_p.	NM_004254	NP_004245	Q8TCC7	S22A8_HUMAN	ical; (Potential).	3	CAAAACCGGTA	0.493	
-	3	580	C22A25_uc001nw	NM_199352	NP_955384	Q6T423	S22AP_HUMAN	Name=3; (Potential).	4	GGTGGGAGCAA	0.468	
+	3	436		NM_004585	NP_004576	Q9UL19	TIG3_HUMAN		1	ATATGGCAAGT	0.522	
-	13	1823	uc001nxj.1_5'Flan	NM_015459	NP_056274	Q6DD88	ATLA3_HUMAN	Cytoplasmic.	1	TATGAGAAGAA	0.368	
-	11	1345	_p.A339T|ATL3_u	NM_015459	NP_056274	Q6DD88	ATLA3_HUMAN	Cytoplasmic.	1	AGAGGCTGCAG	0.403	
+	4	2817	TN3_uc001nxp.2_	NM_201428	NP_958831	O95197	RTN3_HUMAN	Potential).|Reticulon.	1	TCATCAGTGTGG	0.488	
+	5	1150		NM_138471	NP_612480	Q9BUA3	CK084_HUMAN		0	TCCCCGGGCGG	0.652	
+	16	2513	nxv.3_Splice_Site	NM_001039469	NP_001034558	Q7KZI7	MARK2_HUMAN		3	CGCAGGTAAGC	0.627	
-	8	1115		NM_173587	NP_775858	Q8IZ40	RCOR2_HUMAN		2	CTGGACCTCCT	0.637	
+	11	1016	ph.1_Missense_M	NM_000932	NP_000923	Q01970	PLCB3_HUMAN	I-PLC X-box.	2	AGCGGGGCAGC	0.697	
+	17	1914	yph.1_Splice_Site	NM_000932	NP_000923	Q01970	PLCB3_HUMAN		2	TCTCAGATACA	0.642	
+	2	328	nse_Mutation_p.G	NM_012094	NP_036226	P30044	PRDX5_HUMAN	Thioredoxin.	1	TGAAGGGGAGC	0.597	
-	7	1458	_p.S316F|NRXN2_	NM_015080	NP_055895	P58401	NRX2B_HUMAN		10	TGAGGGACAGG	0.587	
-	2	519	.1_Nonsense_Mu	NM_004630	NP_004621	Q15637	SF01_HUMAN		3	TTTCTTGTTCTC	0.408	
-	2	501	.1_Missense_Mut	NM_004630	NP_004621	Q15637	SF01_HUMAN		3	TCCAGGGGGAA	0.423	
-	26	2977		NM_017525	NP_059995	Q6DT37	MRCKG_HUMAN	PH.	4	GGCCCCACTGG	0.657	
-	2	238		NM_017525	NP_059995	Q6DT37	MRCKG_HUMAN	nilarity).|Protein kinase.	4	GGCTCCTCGGC	0.493	
-	1	587	p.G111D|EHD1_u	NM_006795	NP_006786	Q9H4M9	EHD1_HUMAN		0	CGTTGCCCGGC	0.687	
-	30	4272	bw.2_Missense_M	NM_015104	NP_055919	Q2TAZ0	ATG2A_HUMAN		2	GGCCGGGATGC	0.657	

+	2	1015	rnv.1_Missense_M	NM_013299	NP_037431				0	GCGCGCCTGCC	0.652	
-	5	638		NM_080668	NP_542399	Q96FF9	CDCA5_HUMAN		0	GGGTGGAGGTA	0.617	
+	5	1038	cs.1_Missense_M	NM_013265	NP_037397	Q9UID3	FFR_HUMAN		0	AGCAGGTGCCG	0.687	
-	6	1161	odr.1_Missense_	NM_001077241	NP_001070709	Q8N413	S2545_HUMAN	Solcar 3.	0	GCTCACCATGC	0.592	
-	5	1017	odr.1_Missense_	NM_001077241	NP_001070709	Q8N413	S2545_HUMAN	Solcar 3.	0	ACTGGGATTCT	0.607	
+	14	3021	_p.P850S|SIPA1_	NM_006747	NP_006738	Q96FS4	SIPA1_HUMAN		0	GACAGCCCATC	0.617	
+	15	3138	_p.D889N|SIPA1_	NM_006747	NP_006738	Q96FS4	SIPA1_HUMAN	Potential.	0	AGGAGGACCTG	0.637	
-	10	1116	e_Mutation_p.P27	NM_021975	NP_068810	Q04206	TF65_HUMAN		4	TGGAGGCCGGG	0.627	
+	9	1149	_p.S333F|KAT5_u	NM_006388	NP_006379	Q92993	KAT5_HUMAN		0	CCATCTCCTTCT	0.507	
-	1	2014		NM_138368	NP_612377	Q2VPB7	YK046_HUMAN		0	AGGGCGGCCAG	0.667	
+	10	1061		NM_006842	NP_006833	Q13435	SF3B2_HUMAN		3	TGCGAGGGGTG	0.552	
+	10	1374		NM_018026	NP_060496	Q6VY07	PACS1_HUMAN		6	AGACGGAGATT	0.627	
+	2	282		NM_153266	NP_694998	Q8N4L1	T151A_HUMAN	ical; (Potential).	1	CGGGGCCGTGG	0.741	
-	1	798		NM_020404	NP_065137	Q9HCU0	CD248_HUMAN	ellular (Potential).	3	GAAGCCCTCAG	0.682	
-	1	878	_5'Flank|BRMS1_	NM_006876	NP_006867	O43505	B3GN1_HUMAN	enal (Potential).	0	TCTGATCCAGCA	0.622	
+	2	277	I3_uc001oid.3_Mi	NM_145065	NP_659502	Q8N2H9	PELI3_HUMAN		1	GCCAGGCGAGG	0.617	
+	17	1978	pe.1_Missense_M	NM_005700	NP_005691	Q9NY33	DPP3_HUMAN		2	GCGGGCCCTGT	0.602	
-	1	195	S_uc001oir.2_5'Fl	NM_018219	NP_060689	Q9NVE4	CCD87_HUMAN		2	AATCCGGCCCT	0.682	
+	3	1192	.1_Intron|RBM4_	NM_002896	NP_002887	Q9BWF3	RBM4_HUMAN	with TNPO3.|Poly-Ala.	1	AGTGGCAGCTG	0.567	
-	35	6940	_uc001ojc.1_Silent	NM_006946	NP_008877	O15020	SPTN2_HUMAN	PH.	4	CTTTCGGTAAT	0.587	
+	5	558	11orf80_uc001oji.	NM_024650	NP_078926	Q8N6T0	CK080_HUMAN		0	AATCTCTGCAA	0.433	
+	9	945	_p.G80D|C11orf80	NM_024650	NP_078926	Q8N6T0	CK080_HUMAN		0	GGCTGGCATGG	0.478	
+	8	868	jl.1_Missense_Mu	NM_005133	NP_005124	Q9Y256	FACE2_HUMAN		2	CGCGGCCTTGG	0.612	
-	19	3053	ojp.1_Missense_	NM_022172	NP_071504	P11498	PYC_HUMAN		4	CGTCACCTCCT	0.617	
+	4	574	rm.1_Missense_	NM_001619	NP_001610	P25098	ARBK1_HUMAN	S.|N-terminal.	1	TGTGGCCCGCA	0.597	rs67452775
+	3	239	9A_uc001oks.2_5'	NM_004584	NP_004575	Q99638	RAD9A_HUMAN		0	CTATGCCTGCT	0.632	
-	5	935	ense_Mutation_p.	NM_004910	NP_004901	O00562	PITM1_HUMAN		3	TGCGAGCAGTC	0.692	
-	4	1074	ns.2_Missense_	NM_022338	NP_071733	Q96F05	CK024_HUMAN	ellular (Potential).	0	GTGTGGCCAAT	0.602	
+	9	2092	g.2_Missense_M	NM_002335	NP_002326	O75197	LRP5_HUMAN	3.|Extracellular (Potential).	7	TCACGGGCGTC	0.587	
+	20	2309	onu.2_Missense_	NM_001164161	NP_001157633	Q5H9R7	PP6R3_HUMAN		0	AGCACCCAACT	0.448	
+	3	466	BP2_uc001ooj.1_	NM_002180	NP_002171	P38935	SMBP2_HUMAN		0	AGTCCCACGAT	0.527	
+	5	648	nse_Mutation_p.L	NM_139075	NP_620714	Q8NHX9	TPC2_HUMAN	ellular (Potential).	0	TGAGTCTCGTG	0.612	
+	24	2805	nse_Mutation_p.T	NM_018043	NP_060513	Q5XXA6	ANO1_HUMAN	ellular (Potential).	2	ACCACACCCTC	0.577	
+	16	2252	.P685L|PPFIA1_u	NM_003626	NP_003617	Q13136	LIPA1_HUMAN		3	CTACCCTGCTT	0.582	
-	21	4939	1opz.2_Missense_	NM_012309	NP_036441	Q9UPX8	SHAN2_HUMAN		5	GTTTGCCTTTG	0.522	
-	21	4312	1opz.2_Missense_	NM_012309	NP_036441	Q9UPX8	SHAN2_HUMAN		5	AGGAGGCAATG	0.522	
-	14	2090	sense_Mutation_	NM_012309	NP_036441	Q9UPX8	SHAN2_HUMAN	PDZ.	5	CCCCACCTTCA	0.567	
+	3	337	.2_RNA|NADSYN	NM_018161	NP_060631	Q6IA69	NADE_HUMAN	N hydrolase.	2	TCCTAGCGGCC	0.542	
-	25	6216	se_Mutation_p.T1	NM_006185	NP_006176	Q14980	NUMA1_HUMAN		8	GGGGAGTCATG	0.557	
-	24	6006	e_Mutation_p.S15	NM_006185	NP_006176	Q14980	NUMA1_HUMAN		8	TCAGGGAAGGC	0.592	
+	26	3274	sg.2_Missense_M	NM_001567	NP_001558	O15357	SHIP2_HUMAN	Pro-rich.	4	ATGAGGAGTCT	0.612	
-	5	739	1_Intron|CLPB_uc	NM_030813	NP_110440	Q9H078	CLPB_HUMAN		1	CTTGTCCACTGG	0.592	
-	23	3373	ss.2_Missense_	NM_001040118	NP_001035207	Q96P48	ARAP1_HUMAN	Rho-GAP.	1	CTTCTCCTCCT	0.592	
+	1	2959		NM_014786	NP_055601	Q96PE2	ARHGH_HUMAN	Pro-rich.	0	TTGGTCCCCCT	0.612	
-	15	2865		NM_015531	NP_056346	Q4AC94	C2CD3_HUMAN		7	CAATTACCATCA	0.433	rs146497546
-	11	1665		NM_173582	NP_775853	Q6PCE3	PGM2L_HUMAN		1	AGCAACCACAA	0.378	
-	9	1046	sense_Mutation_p	NM_030792	NP_110419	Q8WTR4	GDPD5_HUMAN	ical; (Potential).	1	CTGCTGCCACA	0.632	

-	4	2200		NM_033063	NP_149052	Q96JE9	MAP6_HUMAN	Pro-rich.	0	TCACGGACTCGC	0.498
+	14	1590	nse_Mutation_p.T7	NM_003369	NP_003360	Q9P2Y5	UVRAG_HUMAN		6	GGCAAACCCTTC	0.408
-	5	1061	rrz.1_Missense_M	NM_004705	NP_004696	O43422	P52K_HUMAN		3	TAGATAGCTTGG	0.393
+	8	1213	rsb.1_Missense_M	NM_020193	NP_064578	Q7Z589	EMSY_HUMAN	nteraction with BRCA2.	6	TGGTGTCCTCTA	0.433
-	3	1925	_p.T561I|LRRC32	NM_005512	NP_005503	Q14392	LRC32_HUMAN	cellular (Potential).	0	GGCTGGTCTCC	0.667
+	1	576	P11_uc009yuu.2_In	NM_173039	NP_766627	Q8NBQ7	AQP11_HUMAN		0	CCCCGCGCACC	0.642
-	6	1048	ym.2_Missense_M	NM_016578	NP_057662	Q96T23	RSF1_HUMAN	Glu-rich.	4	TTTCTTCTTTGAT	0.353
+	6	1366	P35_uc010rsp.1_In	NM_020798	NP_065849	Q9P2H5	UBP35_HUMAN		3	CAGCTGGCGGAG	0.637
-	4	952	zg.2_Missense_Mu	NM_080491	NP_536739	Q9UQC2	GAB2_HUMAN		6	GGTGGCCGGAA	0.552
+	6	2415	rf82_uc010rss.1_M	NM_145018	NP_659455	Q8IXT1	NOXIN_HUMAN		2	CACTTTCTGAAG	0.383
+	9	4034		NM_015885	NP_056969	O94913	PCF11_HUMAN		1	CAGTAGCTTTTG	0.333
-	15	2051	_p.R583K|DLG2_u	NM_001364	NP_001355	Q15700	DLG2_HUMAN	SH3.	6	ATGACTCTCCTG	0.473
-	1	1054	c.1_RNA|CREBZF	NM_001039618	NP_001034707	Q9NS37	ZHANG_HUMAN	eucine-zipper.	1	TAGCGACTCTCC	0.657
+	7	1172	DC83_uc001pbi.1_	NM_173556	NP_775827	Q8IWF9	CCD83_HUMAN	Potential.	1	TGACTGGCTCAA	0.353
-	10	1180	e|PICALM_uc010rt	NM_007166	NP_009097	Q13492	PICAL_HUMAN		2	GTTGCCCTAGGA	0.443
+	2	698	PRSS23_uc010rts.	NM_007173	NP_009104	O95084	PRS23_HUMAN		2	GCTGCACCGGCA	0.517
-	2	1078	S23_uc001pcc.1_	NM_012193	NP_036325	Q9ULV1	FZD4_HUMAN	Name=2; (Potential).	1	TACTGAGAAATAT	0.458
+	5	1541		NM_000372	NP_000363	P14679	TYRO_HUMAN	ical; (Potential).	3	GGGCCGTCCTC	0.527
-	14	1480	X4_uc001pcv.2_In	NM_016931	NP_058627	Q9NPH5	NOX4_HUMAN	ar (Potential).|Mediates inte	2	GACTTCCAAAA	0.398
+	1	2697		NM_001008781	NP_001008781	Q8TDW7	FAT3_HUMAN	|Extracellular (Potential).	5	TGGACCGGGAA	0.423
+	1	3264		NM_001008781	NP_001008781	Q8TDW7	FAT3_HUMAN	.|Extracellular (Potential).	5	CCATCAGGGATG	0.468
+	9	5290		NM_001008781	NP_001008781	Q8TDW7	FAT3_HUMAN	.|Extracellular (Potential).	5	ATATTCAGATTGT	0.438
+	23	12829	di.3_Missense_Mu	NM_001008781	NP_001008781	Q8TDW7	FAT3_HUMAN	lasmic (Potential).	5	GTCGCCCCGCA	0.657
+	25	13665	i.3_Nonsense_Mut	NM_001008781	NP_001008781	Q8TDW7	FAT3_HUMAN	lasmic (Potential).	5	TTGTGGAGACTC	0.517
-	7	734	82_splice|MRE11A	NM_005591	NP_005582	P49959	MRE11_HUMAN		5	TGGATCCTGAAAT	0.299
+	3	1795		NM_018039	NP_060509	Q6B0I6	KDM4D_HUMAN		0	TCCATGGATGCC	0.567
+	1	748	S2B_uc001pfg.1_5	NM_032102	NP_115285	Q9BRL6	SRSF8_HUMAN	Arg-rich.	0	CCGGGGTCCCA	0.716
-	4	668	ESN3_uc001pfl.2_	NM_144665	NP_653266	P58005	SESN3_HUMAN		0	CTTTGTGGCACA	0.368
-	9	1225	76B_uc001pfm.2_	NM_144664	NP_653265	Q5HYJ3	FA76B_HUMAN	Potential.	0	CCACAGTTTCTTT	0.348
-	7	969	76B_uc001pfm.2_	NM_144664	NP_653265	Q5HYJ3	FA76B_HUMAN		0	TTTGGGCTTTTTC	0.313
+	2	1765	|CCDC82_uc009y	NM_003772	NP_003763	Q9Y4A0	JERKL_HUMAN		0	AGACTGGTAATA	0.353
+	17	2347	N5_uc001pgb.2_M	NM_014361	NP_055176	O94779	CNTN5_HUMAN	onectin type-III 1.	8	TAGGACCCCCA	0.448
+	21	3062	gb.2_Missense_Mu	NM_014361	NP_055176	O94779	CNTN5_HUMAN	onectin type-III 3.	8	CACAGGGATTTG	0.423
-	5	3034	e_Mutation_p.G66	NM_000926	NP_000917	P06401	PRGR_HUMAN	teroid-binding.	4	CTCCATCCTAGA	0.328
+	5	1221	_p.P246L|YAP1_u	NM_001130145	NP_001123617	P46937	YAP1_HUMAN		3	CACCACCCCTGG	0.507
+	3	442		NM_182962	NP_892007	Q13489	BIRC3_HUMAN	BIR 1.	4	ATGCTGGATAACT	0.443
-	2	292	MP8_uc010ruu.1_	NM_002424	NP_002415	P22894	MMP8_HUMAN		4	GCATTTCTTTAA	0.448
-	6	842		NM_002427	NP_002418	P45452	MMP13_HUMAN		3	TGGGGTCTTCAT	0.448
+	17	2699	e_Mutation_p.A85	NM_001080463	NP_001073932	Q8NCM8	DYHC2_HUMAN	n (By similarity).	0	TGTCAGCTGTTTT	0.294
+	49	8104	e_Mutation_p.A26	NM_001080463	NP_001073932	Q8NCM8	DYHC2_HUMAN	4 (By similarity).	0	CTATTAGCAGGA	0.433
-	6	1283	hp.2_Missense_M	NM_025208	NP_079484	Q9GZP0	PDGFD_HUMAN		2	CAATTTCCTCCA	0.463
-	3	249	Mutation_p.E15K|	NM_004347	NP_004338	P51878	CASP5_HUMAN	CARD.	3	GGTATTCCAACA	0.348
-	8	1069	SP1_uc010rvi.1_M	NM_033292	NP_150634	P29466	CASP1_HUMAN		2	AGTCTTCCAATAA	0.398
-	2	74	ASP1_uc010rvh.1_	NM_001017534	NP_001017534	Q5EG05	CAR16_HUMAN	CARD.	1	CCCATGGAATGG	0.413
+	13	2374	iw.2_Missense_Mu	NM_000829	NP_000820	P48058	GRIA4_HUMAN	ical; (Potential).	8	ACCTCGCTGCTT	0.403
+	3	582	.1_Intron|AASDHP	NM_015423	NP_056238	Q9NRN7	ADPPT_HUMAN		0	TTCTTTCATATTA	0.299
-	6	2181	_p.M618I|GUCY1A	NM_000855	NP_000846	P33402	GCYA2_HUMAN	anylate cyclase.	8	AAGTTCCATCAT	0.483

-	16	2440	n.3_RNA|CWF19L	NM_152434	NP_689647	Q2TBE0	C19L2_HUMAN		0	AGAGATCTATCA	0.313
-	2	558	LC35F2_uc001pjs	NM_017515	NP_059985	Q8IXU6	S35F2_HUMAN	ical; (Potential).	1	ATCTGACCCAGG	0.348
-	17	3404	v.1_Missense_Mu	NM_002519	NP_002510	Q14207	NPAT_HUMAN		2	ACATTGGGTGAG	0.438
+	62	9311	1_Intron|C11orf65	NM_000051	NP_000042	Q13315	ATM_HUMAN		240	CCGGAAGATGAA	0.403
-	6	3299	z.1_Missense_Mu	NM_015065	NP_055880	Q8NEV8	EXPH5_HUMAN		5	TAGTTCCCCATTG	0.443
-	4	407	.V33M|RDX_uc00	NM_002906	NP_002897	P35241	RADI_HUMAN	FERM.	0	TCACCACCTAAA	0.348
-	5	738		NM_017589	NP_060059	Q9NY30	BTG4_HUMAN		0	GCGGGGGATTT	0.443
+	6	505	e_Mutation_p.D19	NM_001100388	NP_001093858	Q6PI97	CK088_HUMAN		0	ACTTTGGACTAAT	0.408
-	5	2158	XACB1_uc009yyi.2	NM_138378	NP_612387	Q9BRP7	FDXA1_HUMAN	FDX-ACB.	0	GTATAACATATAG	0.458
+	8	1789	_p.G272E|DLAT_u	NM_001931	NP_001922	P10515	ODP2_HUMAN	ng site (By similarity).	0	TACAGGGACAG	0.418
+	12	2229	_p.P419S|DLAT_u	NM_001931	NP_001922	P10515	ODP2_HUMAN	ytic (By similarity).	0	ATCACACCTATTG	0.338
-	4	475	mp.3_Missense_M	NM_138789	NP_620144	Q8WWB5	PIHD2_HUMAN		1	CATGGCCATCTG	0.368
-	4	364	3_5'UTR|TMPRSS	NM_030770	NP_110397	Q9H3S3	TMPS5_HUMAN	cellular (Potential).	1	GTCCCGGAAATG	0.542
-	10	1060	e_Mutation_p.P21	NM_020886	NP_065937	Q96RU2	UBP28_HUMAN		7	GGAGGGAAGAA	0.493
+	2	206	ool.2_Missense_M	NM_006028	NP_006019	O95264	5HT3B_HUMAN	cellular (Potential).	0	AAGAAGTGAGA	0.443
+	7	2096	oq.2_Missense_M	NM_006006	NP_005997	Q05516	ZBT16_HUMAN	C2H2-type 8.	2	GCGCTCCCGGG	0.622
-	3	508	M55A_uc001ppb.	NM_152315	NP_689528	Q8N323	FA55A_HUMAN		0	GCCCTCCCAGA	0.557
-	5	716	_p.S196L|CADM1_	NM_014333	NP_055148	Q9BY67	CADM1_HUMAN	1.|Extracellular (Potential).	2	ATGTCTGACCAC	0.527
-	8	1568	po.2_Missense_M	NM_032725	NP_116114	Q9BRD0	BUD13_HUMAN	Potential.	2	CATCCTCCACAT	0.478
-	2	213	_p.A60V|BUD13_	NM_032725	NP_116114	Q9BRD0	BUD13_HUMAN		2	GAGATAGCTGTC	0.388
-	22	3590	_p.S1125N|SIK3_u	NM_025164	NP_079440	Q9Y2K2	SIK3_HUMAN		12	GCAGAGCTAAGT	0.507
-	20	3311	w.2_Missense_Mu	NM_025164	NP_079440	Q9Y2K2	SIK3_HUMAN		12	TGTATCCCCAAT	0.517
-	19	2155	w.2_Missense_Mu	NM_025164	NP_079440	Q9Y2K2	SIK3_HUMAN	Gln-rich.	12	GGAAGAAGATG	0.522
-	13	1498	_p.L387F|SIK3_uc	NM_025164	NP_079440	Q9Y2K2	SIK3_HUMAN		12	GCCAAGGGGGC	0.622
+	19	1881	e_Mutation_p.A63	NM_001040455	NP_001035545	Q8NBJ9	SIDT2_HUMAN	ical; (Potential).	0	TGCCTGGCCATT	0.572
-	11	1548		NM_004716	NP_004707	Q16549	PCSK7_HUMAN	Extracellular (Potential).	0	GTGACCCACTC	0.557
-	3	503		NM_004716	NP_004707	Q16549	PCSK7_HUMAN		0	CAGCAGGCTGG	0.657
+	3	421	se_Mutation_p.E12	NM_207343	NP_997226	Q8ND24	RN214_HUMAN		0	TTCGGGAGAGC	0.542
-	6	1333	7D|BACE1_uc010	NM_012104	NP_036236	P56817	BACE1_HUMAN	cellular (Potential).	1	TGGTGCCACTG	0.483
+	19	2512	.V763I|CEP164_u	NM_014956	NP_055771	Q9UPV0	CE164_HUMAN	Glu-rich.	2	AGGTGGTCTCC	0.582
+	30	4136	rf.2_RNA|CEP164	NM_014956	NP_055771	Q9UPV0	CE164_HUMAN		2	ACCCACGTCCA	0.627
+	32	4426	.P1422S|CEP164_	NM_014956	NP_055771	Q9UPV0	CE164_HUMAN		2	AATGACCCCAGG	0.582
-	27	4933		NM_020693	NP_065744	Q8TD84	DSCL1_HUMAN	cellular (Potential).	8	CTTCACCTTGA	0.522
-	2	526	1prt.1_5'UTR|TM	NM_001077263	NP_001070731	Q9BYE2	TMPSD_HUMAN	lasmic (Potential).	1	GGTGGCCCTGG	0.597
-	4	407	ense_Mutation_p.	NM_001098526	NP_001091996	Q86YT9	JAML1_HUMAN	1.|Extracellular (Potential).	1	GCACACTGAGA	0.502
-	2	337	st.1_Missense_M	NM_000732	NP_000723	P04234	CD3D_HUMAN	cellular (Potential).	1	CTCGTGGGTCC	0.458
+	19	3112	sv.2_Missense_Mu	NM_004788	NP_004779	Q14139	UBE4A_HUMAN	U-box.	5	CTGGATCCCATT	0.473
+	3	2955	L_uc001psz.1_Mis	NM_005933	NP_005924	Q03164	MLL1_HUMAN		25	TCGGCCCAACT	0.458
+	5	3373	.2_Missense_Mut	NM_005933	NP_005924	Q03164	MLL1_HUMAN		25	AATTGCTGGCT	0.408
+	27	6979	.2_Missense_Mut	NM_005933	NP_005924	Q03164	MLL1_HUMAN		25	AGGGATCTGCAC	0.458
-	7	733	_p.V170I|IFT46_u	NM_020153	NP_064538	Q9NQC8	IFT46_HUMAN		0	GTGGGACCTGGT	0.408
+	1	122	11_uc010ryy.1_5'	NM_021729	NP_068375	Q9H270	VPS11_HUMAN		3	TGGGGCCGCTC	0.637
+	4	394	LRX1_uc001pvw.2	NM_024618	NP_078894	Q86UT6	NLRX1_HUMAN		2	TAGCGCTCCCC	0.632
+	6	1495	.R427Q|NLRX1_	NM_024618	NP_078894	Q86UT6	NLRX1_HUMAN	eraction with MAVS.|NACH	2	AGCCCGAACCA	0.577
-	9	1129	M_uc001pwg.1_5'	NM_006500	NP_006491	P43121	MUC18_HUMAN	2.|Extracellular (Potential).	4	CTCTCTGCCTCA	0.632
+	1	1080		NM_032015	NP_114404	Q9BY78	RNF26_HUMAN	Leu-rich.	1	CAGAACCTCTTT	0.582
-	4	1304	_p.P133S|TRIM2	NM_012101	NP_036233	Q14134	TRI29_HUMAN		4	GGTGGGCAGGG	0.522

+	10	3095		NM_005422	NP_005413	O75443	TECTA_HUMAN	TIL 2.	10	TGTCACGCGGA	0.577
+	11	3559		NM_005422	NP_005413	O75443	TECTA_HUMAN	VWFD 3.	10	AACGGCTCTAT	0.478
+	3	479	nse_Mutation_p.E	NM_006918	NP_008849	O75845	SC5D_HUMAN		1	TAGGAGAGTTT	0.378
-	1	607	9959_uc009zba.2	NM_001001786	NP_001001786	Q8IZY5	BLID_HUMAN		0	CCTCAGCAGAG	0.448
+	11	1875		NM_032873	NP_116262	Q8TF42	UBS3B_HUMAN	phosphatase (By similarity	1	AAATGGGTTGC	0.458
+	12	1990		NM_032873	NP_116262	Q8TF42	UBS3B_HUMAN	phosphatase (By similarity	1	GTTTCAGAATCC	0.299
-	2	269	sense_Mutation_p	NM_006597	NP_006588	P11142	HSP7C_HUMAN		8	TGTTGGTGGGG	0.428
+	5	765	_p.E106K|GRAMD	NM_020716	NP_065767	Q3KR37	GRM1B_HUMAN	GRAM.	1	GCTGGGAAACT	0.507
-	1	554		NM_001005325	NP_001005325	Q8NGM8	OR6M1_HUMAN	ellular (Potential).	2	TACAGGCCACC	0.438
+	1	419		NM_001004462	NP_001004462	Q8NGN3	O10G4_HUMAN	Name=4; (Potential).	4	CAGGTGTGCCC	0.557
-	1	47		NM_001002918	NP_001002918	Q9GZM6	OR8D2_HUMAN	ellular (Potential).	3	TCAAGCCTGCC	0.423
-	12	1848	_p.P460S|ROBO4	NM_019055	NP_061928	Q8WZ75	ROBO4_HUMAN		2	GCCGGGGCTTC	0.597
+	8	952	_Mutation_p.P184	NM_022062	NP_071345	Q96KN3	PKNX2_HUMAN		3	TAACCCCCAGG	0.562
+	4	916		NM_014026	NP_054745	Q96C86	DCPS_HUMAN		0	AGATCCCTCTG	0.502
-	15	2067	_Mutation_p.G55	NM_032531	NP_115920	Q8IZU9	KIRR3_HUMAN	lasmic (Potential).	3	CAACACCTTTG	0.488
+	9	1248	v.1_Missense_Mut	NM_002017	NP_002008	Q01543	FLI1_HUMAN	ETS.	2273	CCTGGGAGGGG	0.617
+	9	1305	v.1_Missense_Mut	NM_002017	NP_002008	Q01543	FLI1_HUMAN	ETS.	2273	GCTGGGGCGAG	0.562
+	2	1003	p.V230G|KCNJ5_	NM_000890	NP_000881	P48544	IRK5_HUMAN	smic (By similarity).	1	CATCGTGGAGG	0.597
-	20	2516	AP32_uc009zco.2_	NM_001142685	NP_001136157	A7KAX9	RHG32_HUMAN		5	TACTACCTGTTT	0.468
+	5	654	1qff.1_Missense_	NM_138788	NP_620143	Q96B21	TM45B_HUMAN	ical; (Potential).	0	TCCCACCTTTTG	0.537
-	19	2104	_Mutation_p.D65	NM_001143835	NP_001137307	Q6P4R8	NFRKB_HUMAN		3	AGGGATCTTTTT	0.448
-	7	904	fh.2_Missense_Mu	NM_001143835	NP_001137307	Q6P4R8	NFRKB_HUMAN		3	CACCACCCGCA	0.527
+	4	564	0sbz.1_Translatio	NM_001642	NP_001633	Q06481	APLP2_HUMAN	ellular (Potential).	3	AGTGGGTGAAT	0.458
-	7	2895	se_Mutation_p.P22	NM_014758	NP_055573	Q92543	SNX19_HUMAN		4	TTCTGGGGCTT	0.478
+	9	1057	z.1_Missense_Mu	NM_032801	NP_116190	Q9BX67	JAM3_HUMAN	lasmic (Potential).	1	TGCAGGGCGAC	0.517
-	2	145	YN1_uc009zdb.2_	NM_001037305	NP_001032382	Q9P016	THYN1_HUMAN		0	CTCACCTGAAC	0.512
+	11	1254	1L2_uc009zdg.1_	NM_138342	NP_612351	Q8IW92	GLBL2_HUMAN		3	TACACGGCCAAG	0.552
+	13	1453	1L2_uc009zdg.1_	NM_138342	NP_612351	Q8IW92	GLBL2_HUMAN		3	CAATGGGGGAA	0.562
+	4	1399	hu.1_Missense_M	NM_015232	NP_056047	Q9UPP2	IQEC3_HUMAN	SEC7.	4	ACCCCGAAGTG	0.622
-	4	723	se_Mutation_p.W6	NM_003044	NP_003035	P48065	S6A12_HUMAN	Name=1; (Potential).	1	AAACCTCCAGAC	0.562
-	8	1363	5A_uc010sdn.1_	NM_001042603	NP_001036068	P29375	KDM5A_HUMAN	PHD-type 1.	3	CCAGTCTCCTT	0.383
+	15	2335	1qik.1_Missense_	NM_173593	NP_775864	Q6L9W6	B4GN3_HUMAN	enal (Potential).	2	CTCAGGGTTTC	0.642
+	11	3109	.3_Intron|WNK1_	NM_018979	NP_061852	Q9H4A3	WNK1_HUMAN		23	CAGCTGGCATT	0.527
+	17	4183	_p.E979K|WNK1_	NM_018979	NP_061852	Q9H4A3	WNK1_HUMAN		23	AAGGAGAGTTC	0.343
+	18	4307	.R1020Q|WNK1_	NM_018979	NP_061852	Q9H4A3	WNK1_HUMAN		23	AAAGCCGATTAC	0.408
+	24	6250	.P1667S|WNK1_	NM_018979	NP_061852	Q9H4A3	WNK1_HUMAN		23	ACCATCCCTGGT	0.498
+	5	744	1qjn.2_Missense_	NM_024551	NP_078827	Q86V24	ADR2_HUMAN	Name=2; (Potential).	0	AAGGTGGTCTTT	0.468
+	4	1005	lr.1_Intron|LRTM2_	NM_001039029	NP_001034118	Q8N967	LRTM2_HUMAN	xtracellular (Potential).	1	ACGTGCCCGCA	0.647
-	2	356	issense_Mutation	NM_021953	NP_068772	Q08050	FOXM1_HUMAN		2	TAGGTTCCTCCT	0.507
+	11	1309	ULP3_uc001qlj.2_	NM_003324	NP_003315	O75386	TULP3_HUMAN		0	GTGTGGCAGAT	0.408
-	5	650	mt.2_Nonsense_	NM_020374	NP_065107	Q9NQ89	CL004_HUMAN		0	ATCTTGATCTGT	0.338
+	1	1755		NM_002234	NP_002225	P22460	KCNA5_HUMAN	=Segment S6; (Potential).	4	CATTGCCCTGC	0.607
-	13	1450		NM_020373	NP_065106	Q9NQ90	ANO2_HUMAN	lasmic (Potential).	7	CAGTCGCATCT	0.413
-	6	792	_p.T181I|VWF_uc	NM_000552	NP_000543	P04275	VWF_HUMAN	VWFD 1.	12	CCGAGGTCAAG	0.507
+	2	449	ev.1_Missense_Mu	NM_001769	NP_001760	P21926	CD9_HUMAN	lasmic (Potential).	1	CATGCCGGTCA	0.637
-	3	933	ense_Mutation_p.	NM_001038	NP_001029	P37088	SCNNA_HUMAN	llular (By similarity).	0	CCTGGGGGTTG	0.507
+	7	893	_p.T223I|LTBR_uc	NM_002342	NP_002333	P36941	TNR3_HUMAN	ical; (Potential).	2	TTGCCACCGTCT	0.582

+	30	4005	sfd.1_Missense_Mu	NM_014865	NP_055680	Q15021	CND1_HUMAN		5	AACCATCCACTG	0.532	
-	10	1605	_p.P474S|CHD4_u	NM_001273	NP_001264	Q14839	CHD4_HUMAN	PHD-type 2.	2	CTCTGGAAGTG	0.522	
-	6	744	_p.P187S|CHD4_u	NM_001273	NP_001264	Q14839	CHD4_HUMAN		2	TCTTGGGATTTTT	0.448	
-	5	603	_p.E140K|CHD4_u	NM_001273	NP_001264	Q14839	CHD4_HUMAN		2	AGGCTCCTGCA	0.468	
-	2	1314	_p.D345N|LPAR5_	NM_001142961	NP_001136433	Q9H1C0	LPAR5_HUMAN	lasmic (Potential).	2	GGCATCCGGCC	0.682	
-	2	1107	_p.R276C|LPAR5_	NM_001142961	NP_001136433	Q9H1C0	LPAR5_HUMAN	cellular (Potential).	2	CCCGCGCACGC	0.682	
-	3	488	qqg.1_Missense_M	NM_153685	NP_710152	Q8IYJ0	CL053_HUMAN	cellular (Potential).	0	TGCGAGCCCAT	0.612	
+	6	820	PS7A_uc001qqi.2	NM_001164094	NP_001157566	Q9UBW8	CSN7A_HUMAN	Potential.	1	TGAGCCGTGCCA	0.602	rs146030026
+	2	524	e_Mutation_p.A59	NM_002286	NP_002277	P18627	LAG3_HUMAN	.|Extracellular (Potential).	0	GAAGAGCAGGG	0.652	
+	8	892	_p.D119N|GNB3_u	NM_002075	NP_002066	P16520	GBB3_HUMAN	WD 3.	0	CGGGGGACACC	0.587	
+	1	132	1qrg.2_5'Flank|US	NM_001098536	NP_001092006	P45974	UBP5_HUMAN		4	GACCGGGTCCAC	0.627	
+	9	1183	rh.3_Missense_Mu	NM_001098536	NP_001092006	P45974	UBP5_HUMAN		4	TCAGCACCCAGG	0.537	
+	14	1805	h.3_Nonsense_Mu	NM_001098536	NP_001092006	P45974	UBP5_HUMAN		4	GACTGGGTGCC	0.473	
+	7	994	_p.L212S|PTPN6_	NM_002831	NP_002822	P29350	PTN6_HUMAN	protein phosphatase.	1	GAGTTTGCAGA	0.582	
-	6	838	Flank|PHB2_uc001	NM_001144831	NP_001138303	Q99623	PHB2_HUMAN	Potential.	3	TTGGGCCCGCT	0.592	
-	2	290	01_splice|C1R_uc0	NM_001733	NP_001724	P00736	C1R_HUMAN		0	CCCCTACCTTGA	0.572	
-	13	3235	ge.1_Missense_M	NM_174941	NP_777601	Q9NR16	C163B_HUMAN	Extracellular (Potential).	11	CGTGGGCATCG	0.617	
-	2	447		NM_004054	NP_004045	Q16581	C3AR_HUMAN	lasmic (Potential).	1	AGCGATCCAGGC	0.512	
+	24	3037	_p.P560L|A2ML1_u	NM_144670	NP_653271	A8K2U0	A2ML1_HUMAN		3	TTGCTCCCATCA	0.552	
+	29	3745	_p.A796V|A2ML1_u	NM_144670	NP_653271	A8K2U0	A2ML1_HUMAN		3	AGATAGCGAAGG	0.532	
-	23	2564	_p.G12D|DDX12_	NM_004400	NP_004391				0	ACCGGCCTAGG	0.602	
-	23	2500	.3_5'UTR|DDX12_	NM_004400	NP_004391				0	GCAGGGCCCCTG	0.567	
+	1	33	D_uc009zgs.1_RN	NM_013269	NP_037401	Q9UHP7	CLC2D_HUMAN	lasmic (Potential).	0	ATGACAGTAACA	0.418	
-	1	27	ion_p.T7I|KLRC2_	NM_002261	NP_002252	Q07444	NKG2E_HUMAN	lasmic (Potential).	3	GAGAAGGTTCCT	0.433	rs149277235
-	3	530		NM_018423	NP_060893	Q6J9G0	STYK1_HUMAN		8	CCGTGTCATGCC	0.478	
-	9	1327	vu.2_Missense_Mu	NM_003651	NP_003642	P16989	DBPA_HUMAN		4	GAGCAGGGTTCT	0.512	
-	5	652	RH1_uc001qzb.3_F	NM_006250	NP_006241	P02810	PRPC_HUMAN	tion, binds to hydroxyapatit	0	TCTTACCTTCATT	0.483	
-	1	521	RH1_uc001qzc.2_Ir	NM_176890	NP_795371	P59544	T2R50_HUMAN	cellular (Potential).	2	CATATTCTTCTGC	0.393	
-	3	375	B4_uc001qzf.1_Int	NM_006249	NP_006240	Q04118	PRB3_HUMAN	[PQS]-P-[PS]-Q-[GE]-G-N-[	1	GTGGGGGACCTT	0.642	
-	3	456	.1_Intron|PRB1_u	NM_005039	NP_005030	P04280	PRP1_HUMAN	-[PAQ]-Q-[GE]-[GD]- [NKS]	0	GGTGGTCCTTGT	0.617	
+	3	697	rad.2_Missense_M	NM_138723	NP_620049	Q9BZR8	B2L14_HUMAN		1	GGCCACCACCA	0.517	
-	13	3085	LRP6_uc010shl.1_	NM_002336	NP_002327	O75581	LRP6_HUMAN	xtracellular (Potential).|Beta	12	GTCAATCCAATA	0.463	
-	12	2694	LRP6_uc010shl.1_	NM_002336	NP_002327	O75581	LRP6_HUMAN	ta-propeller 3.|LDL-recepto	12	CGTCGGCTCCAG	0.468	
-	11	2544	LRP6_uc010shl.1_	NM_002336	NP_002327	O75581	LRP6_HUMAN	L-receptor class B 13.|Beta	12	CTTTTAGCATAAT	0.398	
-	3	568	01raj.1_Missense_I	NM_018050	NP_060520	Q9H8J5	MANS1_HUMAN	Extracellular (Potential).	0	AGGCTTCCTCGT	0.378	
-	2	243	raq.2_Missense_M	NM_006143	NP_006134	Q15760	GPR19_HUMAN	cellular (Potential).	1	AGTGTAGGAATA	0.448	
-	3	709		NM_000834	NP_000825	Q13224	NMDE2_HUMAN	cellular (Potential).	12	TAGCCAGGGAAA	0.478	
+	2	733	7IP_uc010sht.1_M	NM_018179	NP_060649	Q6VMQ6	MCAF1_HUMAN		5	CCTCTGGTGATG	0.572	
-	10	1566		NM_024829	NP_079105	Q6P4A8	PLBL1_HUMAN		0	ACAGGGGTCAC	0.433	
+	4	1036	_p.A337V|AEBP2_	NM_001114176	NP_001107648	Q6ZN18	AEBP2_HUMAN	C2H2-type 3.	1	GCAATGCCAGCT	0.448	
+	9	1325	zip.2_Missense_M	NM_017435	NP_059131	Q9NYB5	SO1C1_HUMAN	lasmic (Potential).	7	CACACAGACTAC	0.333	
-	14	2053	_p.Y469C|SLCO1A	NM_021094	NP_066580	P46721	SO1A2_HUMAN	cellular (Potential).	4	CCGAGGTAGATG	0.318	
-	34	4129	_p.I1370N|ABCC9_	NM_005691	NP_005682	O60706	ABCC9_HUMAN	otential).|ABC transporter 2	6	ATGACAATTTTTC	0.328	
+	8	1308	IAS_uc001rfn.2_R	NM_018686	NP_061156	Q8NFW8	NEUA_HUMAN		3	TGGTGGCCGTG	0.433	
-	5	1143	9zix.2_Missense_M	NM_003034	NP_003025	Q92185	SIA8A_HUMAN	nenal (Potential).	3	AGGCAGGCATGT	0.388	
-	22	2761	0sit.1_Missense_M	NM_014802	NP_055617	Q86YS7	K0528_HUMAN		4	ACCAACCTTTAGC	0.378	
-	3	381	IAA0528_uc010siu	NM_014802	NP_055617	Q86YS7	K0528_HUMAN	C2.	4	CGAGTTCCACTGA	0.323	

+	19	2166	MP_uc001rgi.2_Int	NM_006152	NP_006143	Q12912	LRMP_HUMAN	lasmic (Potential).	2	GAAGAAGAAAAT	0.398	
-	7	668	_p.D156N|CASC1	NM_001082973	NP_001076442	Q6TDU7	CASC1_HUMAN		2	CCAGATCTGCCA	0.363	
+	3	686	_p.L93F|SSPN_uc	NM_005086	NP_005077	Q14714	SSPN_HUMAN	ical; (Potential).	0	TTCTTACTCATCC	0.512	
+	3	779	p.G124S|SSPN_uc	NM_005086	NP_005077	Q14714	SSPN_HUMAN	lasmic (Potential).	0	ATGTGGGTGTC	0.478	
-	57	8515		NM_002223	NP_002214	Q14571	ITPR2_HUMAN	lasmic (Potential).	14	GTGTGGTGGCA	0.498	
+	6	876	FAR2_uc009zjm.2_	NM_018099	NP_060569	Q96K12	FACR2_HUMAN		0	GGTTGGGTTGA	0.289	
-	5	416	GIC2_uc001riw.2_	NM_016570	NP_057654	Q96RQ1	ERGI2_HUMAN	enal (Potential).	1	CTAAATCCAATAC	0.363	
-	15	2342	rja.2_Missense_M	NM_175861	NP_787057	Q8IUR5	TMTC1_HUMAN		0	TCTGACCCATCA	0.453	
-	17	3377	e_Mutation_p.P10	NM_144973	NP_659410	Q6ZUT9	DEN5B_HUMAN		2	GCTGGGGTGGA	0.428	
-	3	631	_p.A68T|DENND	NM_144973	NP_659410	Q6ZUT9	DEN5B_HUMAN		2	ATGAAGCATACA	0.408	
-	20	1694	lr.1_Missense_Mu	NM_153634	NP_705898	Q86YQ8	CPNE8_HUMAN		1	ATATAGGAGAGA	0.478	
-	5	389		NM_153634	NP_705898	Q86YQ8	CPNE8_HUMAN	C2 1.	1	CTCTTTGAATCA	0.234	
-	27	3670	.2_Missense_Mut	NM_017641	NP_060111	Q7Z4S6	KI21A_HUMAN		7	GTACTAGTGTCTG	0.483	
-	1	1042		NM_005164	NP_005155	Q9UBJ2	ABCD2_HUMAN	e type-1.|Interaction with PE	6	GTCAGGGTTTG	0.413	
+	10	1861	9zjz.2_Missense_M	NM_013377	NP_037509	Q6ZMN7	PZRN4_HUMAN		11	CCAAAACCACTG	0.498	
+	6	631	6S|PPHLN1_uc00	NM_016488	NP_057572	Q8NEY8	PPHLN_HUMAN	Ser-rich.	2	CGTCCTGGTGCC	0.498	
+	11	1163	t.1_Missense_Mut	NM_016488	NP_057572	Q8NEY8	PPHLN_HUMAN		2	ggtaccccctgtgagga	0.01	
-	23	3269	_p.T244I|ADAMTS	NM_025003	NP_079279	P59510	ATS20_HUMAN	TSP type-1 6.	19	CATGTGGTTGTG	0.368	
-	2	751	7L_uc001rns.3_M	NM_001098615	NP_001092085	Q9H0K6	PUS7L_HUMAN		1	TATGAACTTCTTG	0.333	
-	11	2585	p.K451N|SFRS2I	NM_004719	NP_004710	Q99590	SCAFB_HUMAN		0	TTCAACCTTTTC	0.358	
-	4	583	e_Mutation_p.K17	NM_004719	NP_004710	Q99590	SCAFB_HUMAN		0	CTTACCTTAACAT	0.299	
-	6	921	SLC38A2_uc001r	NM_018976	NP_061849	Q96QD8	S38A2_HUMAN		2	TTCTTACCTCCA	0.383	
-	3	612	8A2_uc001rph.2_	NM_018976	NP_061849	Q96QD8	S38A2_HUMAN	turnover upon amino acid	2	TCTTCCCCAAATT	0.284	
-	3	765	ssense_Mutation_	NM_001143668	NP_001137140	Q86SJ2	AMGO2_HUMAN		2	CAGAGGCACCA	0.587	
-	13	1642	50_splice|RPAP3_	NM_024604	NP_078880	Q9H6T3	RPAP3_HUMAN		1	ACTCACTGCAG	0.358	
-	11	900	qv.2_Missense_M	NM_001844	NP_001835	P02458	CO2A1_HUMAN	le-helical region.	2	GGGGACCCATG	0.483	
-	9	794	qv.2_Missense_M	NM_001844	NP_001835	P02458	CO2A1_HUMAN	le-helical region.	2	CATGGGGCCCT	0.552	
-	2	360	2A1_uc001rqv.2_I	NM_001844	NP_001835	P02458	CO2A1_HUMAN	VWFC.	2	ACAGTCCCAGTG	0.577	
+	10	1017	KM_uc001rrd.2_Tr	NM_000289	NP_000280	P08237	K6PF_HUMAN		4	AGCTGGTGGTT	0.527	
-	6	1361	p.P385L|ZNF641_	NM_152320	NP_689533	Q96N77	ZN641_HUMAN		2	GGAAGGGCTTC	0.592	
-	6	844	p.D213N|ZNF641_	NM_152320	NP_689533	Q96N77	ZN641_HUMAN	ransactivation.	2	TGGAATCCCAGC	0.522	
-	1	109		NM_002289	NP_002280	P00709	LALBA_HUMAN		0	AGCTGGGACAGC	0.502	
-	3	609	T1_uc009zkz.1_5'	NM_001240	NP_001231	O60563	CCNT1_HUMAN		6	GCTGCTCCTCCA	0.393	
-	6	2104	Y6_uc001rsi.3_Mi	NM_015270	NP_056085	O43306	ADCY6_HUMAN	lasmic (Potential).	0	GCCGCAGTGCA	0.627	
+	6	1219		NM_033124	NP_149115	Q8IXS2	CCD65_HUMAN		2	GTAATGCCACCC	0.488	
-	4	319	AG1_uc001rsz.2_	NM_002733	NP_002724	P54619	AAKG1_HUMAN		1	GCTTACCCACA	0.458	
-	34	10052		NM_003482	NP_003473	O14686	MLL2_HUMAN	Gln-rich.	41	TGATTGGACACC	0.622	
-	2	322	se_Mutation_p.V3	NM_144593	NP_653194	Q8TAI7	REBL1_HUMAN	region (By similarity).	2	CTCCACTGTAG	0.507	
-	9	1076	BR1L_uc001rtj.1_	NM_018113	NP_060583	Q6UX01	LMBRL_HUMAN	lasmic (Potential).	1	CAAAGGCTGAG	0.592	
+	2	228	p.G8E|TUBA1C_	NM_032704	NP_116093	Q9BQE3	TBA1C_HUMAN		0	CATTGGGGGAG	0.567	rs139215369
+	4	796		NM_006262	NP_006253	P41219	PERI_HUMAN	inker 2.|Rod.	0	TGCAGGTGAGT	0.642	
+	4	631	e_Mutation_p.G15	NM_005480	NP_005471	Q12815	TROAP_HUMAN		1	TCGAGGAAGTC	0.607	
+	13	2223	ATS2_uc001ruf.2_	NM_023071	NP_075559	Q86XZ4	SPAS2_HUMAN	Ser-rich.	1	CCAGCCTTACA	0.537	
-	4	1210	smk.1_Missense_	NM_032130	NP_115506	Q8IYM0	F186B_HUMAN		1	GGAGGGTCTCT	0.542	
-	8	2678	p.V30M|NCKAP5	NM_001037806	NP_001032895	Q9HCH0	NCK5L_HUMAN	Pro-rich.	1	GCACCACCTTGG	0.627	
+	1	746		NM_001651	NP_001642	P55064	AQP5_HUMAN	lasmic (Potential).	0	CCTGGCCCTCT	0.682	
+	2	1037		NM_001651	NP_001642	P55064	AQP5_HUMAN	ical; (Potential).	0	CCTGGGCCACC	0.637	

-	17	2003	1rvs.2_Missense_	NM_013277	NP_037409	Q9H0H5	RGAP1_HUMAN		1	TCTGTGGTGTTG	0.438
+	7	1275	ln.2_Missense_M	NM_001095	NP_001086	P78348	ACCN2_HUMAN	llular (By similarity).	1	ATCCTGCTCTGG	0.587
-	11	1523	i.3_Missense_Mut	NM_016357	NP_057441	Q9UHB6	LIMA1_HUMAN		1	TAGTTGCCCTTA	0.383
-	3	304	p.A44T|LIMA1_uc	NM_016357	NP_057441	Q9UHB6	LIMA1_HUMAN		1	AGCTGCTTTCT	0.333
+	21	2608	lt.2_Missense_Mu	NM_173602	NP_775873	Q9P265	DIP2B_HUMAN		6	TGATGGTTAGT	0.373
+	3	372	1_uc010smu.1_In	NM_005171	NP_005162	P18846	ATF1_HUMAN	KID.	329	TTTTAGGTATCAT	0.443
-	7	695	nse_Mutation_p.D	NM_000617	NP_000608	P49281	NRAM2_HUMAN	ical; (Potential).	1	TTTGTCCAAGA	0.488
+	1	177	.2_Missense_Mut	NM_015416	NP_056231	Q6P1Q0	LTMD1_HUMAN	ired and sufficient for mitoc	2	CCCCTCGGTGA	0.582
-	4	902	_p.R148K|TFCP2_	NM_005653	NP_005644	Q12800	TFCP2_HUMAN	NA-binding.	1	GAATTCTGTCT	0.438
-	4	885	_p.W142*|TFCP2_	NM_005653	NP_005644	Q12800	TFCP2_HUMAN	NA-binding.	1	CGGTTCCACCT	0.433
-	3	457	_p.P89S|POU6F1	NM_002702	NP_002693	Q14863	PO6F1_HUMAN	Gln/Pro-rich.	1	TGTGGGCTGGA	0.602
+	2	380		NM_014191	NP_055006	Q9UQD0	SCN8A_HUMAN		7	CTTTCATCTACG	0.557
+	7	1030	p.W149*|SCN8A_	NM_014191	NP_055006	Q9UQD0	SCN8A_HUMAN	I.	7	TGTGTGGCCCAT	0.448
+	2	207	A1_uc001rzr.2_5'	NM_173157	NP_775180	P22736	NR4A1_HUMAN		0	CCAAGGCCTGT	0.637
+	3	913	1_uc009zmb.1_M	NM_002135	NP_002126	P22736	NR4A1_HUMAN		0	CAGCCCCAGCC	0.652
+	6	1638	uc001rzt.2_Misse	NM_002135	NP_002126	P22736	NR4A1_HUMAN	-binding (Potential).	0	AGTCGGCCTTC	0.617
-	7	1158	_p.Q389*|KRT80_	NM_182507	NP_872313	Q6KB66	K2C80_HUMAN	Rod.|Coil 2.	0	GGCCTGCTGCA	0.617
-	6	985	86_uc009zmg.2_I	NM_002281	NP_002272	Q14533	KRT81_HUMAN	Rod.|Coil 2.	0	TCTCCCCGTGC	0.592
+	2	198	T81_uc001sac.2_I	NM_002284	NP_002275	O43790	KRT86_HUMAN	Head.	1	CCGGCCCGGCC	0.672
-	2	607		NM_002282	NP_002273	P78385	KRT83_HUMAN	Rod.|Coil 1B.	1	TGAGGCCAGCC	0.627
-	1	347		NM_002282	NP_002273	P78385	KRT83_HUMAN	Head.	1	TGAGGGGCGTG	0.642
-	3	829		NM_033045	NP_149034	Q9NSB2	KRT84_HUMAN	Rod.|Coil 1B.	1	ATTGGCCCGAC	0.507
-	9	1515		NM_004693	NP_004684	O95678	K2C75_HUMAN	Tail.	0	TGCCCCCACCG	0.632
-	1	617	h.2_Missense_M	NM_000424	NP_000415	P13647	K2C5_HUMAN	Head.	0	GAGGGGAGTCA	0.498
-	4	884	sns.1_Splice_Site	NM_001146225	NP_001139697	Q14CN4	K2C72_HUMAN		6	TCCTTACCCCTT	0.498
-	7	1185		NM_175068	NP_778238	Q86Y46	K2C73_HUMAN	Rod.|Coil 2.	6	CCCCCGCTGCT	0.662
+	12	989	uc001sbo.1_Miss	NM_170754	NP_736610	Q63HR2	TENC1_HUMAN	hatase tensin-type.	2	TATCAGCTACTT	0.517
+	20	3404	.2_Missense_Mut	NM_170754	NP_736610	Q63HR2	TENC1_HUMAN	Pro-rich.	2	CTGGGGCCCAG	0.622
+	6	1538	cj.2_Missense_M	NM_012291	NP_036423	Q14674	ESPL1_HUMAN		3	AGCCGCTCTGT	0.522
+	18	4068	_Mutation_p.A100	NM_012291	NP_036423	Q14674	ESPL1_HUMAN		3	CTCTGCTCCCC	0.557
+	3	806	.1_Missense_Mut	NM_138473	NP_612482	P08047	SP1_HUMAN	tion domain A (Gln-rich).	3	CTGTCCCCCTC	0.483
-	12	1641	sdn.1_Missense_	NM_006301	NP_006292	Q12852	M3K12_HUMAN		5	AGGGAGCAAAG	0.552
-	11	1324	ion_p.P424S|ATF7	NM_001130059	NP_001123531	P17544	ATF7_HUMAN	binding adenovirus 2 E1A.	2	GGCTGGAGAAC	0.557
-	6	714	plice_Site_p.S220	NM_001130059	NP_001123531	P17544	ATF7_HUMAN		2	AGCTCACCGATA	0.532
+	9	1093	RNPA1_uc009zni.	NM_031157	NP_112420	P09651	ROA1_HUMAN	ar targeting sequence (M9)	3	TGAAGGGAGGA	0.433
-	3	455	F385A_uc001sfx.	NM_015481	NP_056296	Q96PM9	Z385A_HUMAN		1	TGCCTCTGGTC	0.592
-	26	2748		NM_002205	NP_002196	P08648	ITA5_HUMAN	ellular (Potential).	2	TTCCCGTTTTT	0.532
-	17	1732		NM_002205	NP_002196	P08648	ITA5_HUMAN	ellular (Potential).	2	CCCCTCCCTTC	0.552
+	1	209		NM_001005182	NP_001005182	Q96RD1	OR6C1_HUMAN	Name=2; (Potential).	2	AATTTCGTTCAC	0.378
+	1	469		NM_054104	NP_473445	Q9NZP0	OR6C3_HUMAN	Name=4; (Potential).	1	CACCCCTTATG	0.458
+	1	782		NM_054104	NP_473445	Q9NZP0	OR6C3_HUMAN	ellular (Potential).	1	ATCTGCAAAAG	0.388
+	1	506		NM_001005518	NP_001005518	A6NJZ3	O6C65_HUMAN	ellular (Potential).	0	TGACTCCAGCA	0.438
+	1	235		NM_206899	NP_996782	Q8NGE3	O10P1_HUMAN	ellular (Potential).	2	TCGTGCCCAGG	0.602
-	5	1945	p.G581S|DNAJC1	NM_032364	NP_115740	Q6Y2X3	DJC14_HUMAN		4	GAGGCCCAACA	0.473
+	6	1960	iz.2_Missense_Mu	NM_000456	NP_000447	P51687	SUOX_HUMAN	terin domain (By similarity).	0	CTCCCCATGAG	0.522
+	1	360	jr.2_Missense_Mu	NM_015292	NP_056107	Q9BSJ8	ESYT1_HUMAN	Potential.	5	TTCGAGCAGCG	0.642
+	8	940	jr.2_Missense_Mu	NM_015292	NP_056107	Q9BSJ8	ESYT1_HUMAN		5	GGACTCCATTG	0.527

-	12	1247	81_splice|SMARC	NM_003075	NP_003066	Q8TAQ2	SMRC2_HUMAN		6	TCTTACCCAGG	0.552	
+	7	1009	p.A142V|SLC39A	NM_173596	NP_775867	Q6ZMH5	S39A5_HUMAN	ical; (Potential).	2	GGGGGCCCTGG	0.617	rs144269176
-	6	598	RD52_uc001skn.1_	NM_173595	NP_775866	Q8NB46	ANR52_HUMAN		2	TTTTGTCACAGA	0.493	
-	6	1083	p.G237E|PAN2_u	NM_001127460	NP_001120932	Q504Q3	PAN2_HUMAN		6	GACTTCCTGAG	0.478	
-	4	725	S2_uc001slk.2_Int	NM_013267	NP_037399	Q9UI32	GLSL_HUMAN		2	TTCTTTCGGAAT	0.512	rs148320432
-	19	3544	AZ2A_uc009zov.1_	NM_013449	NP_038477	Q9UIF9	BAZ2A_HUMAN		0	CCTGACCCAGG	0.498	
-	7	1127		NM_001686	NP_001677	P06576	ATPB_HUMAN		1	TGCATAGTACCC	0.403	
-	12	1482	p.V301M|STAT6_u	NM_003153	NP_003144	P42226	STAT6_HUMAN		4	GACCACCAGGG	0.398	
+	32	5812		NM_002332	NP_002323	Q07954	LRP1_HUMAN	ntial).|LDL-receptor class B	22	GCCATGCGGAG	0.612	
+	61	10224		NM_002332	NP_002323	Q07954	LRP1_HUMAN	B 30.|Extracellular (Potent	22	AAAGTCCATTA	0.592	
+	64	10682		NM_002332	NP_002323	Q07954	LRP1_HUMAN	ntial).|LDL-receptor class A	22	ACGAGGCCAAC	0.607	
+	8	896	001snj.1_Missens	NM_005412	NP_005403	P34897	GLYM_HUMAN		2	AAGGGGTGAAG	0.562	
+	10	1159	q.2_Missense_Mu	NM_005269	NP_005260	P08151	GLI1_HUMAN		15	AGAAGCCGTAT	0.517	
+	1	288	rr.1_Missense_Mu	NM_004984	NP_004975	Q12840	KIF5A_HUMAN	inesin-motor.	3	GCGGGGAGACA	0.602	
+	6	1295	3R|GEFT_uc009z	NM_178502	NP_848597	Q8N9I9	DTX3_HUMAN		2	CAGGGGGACCC	0.587	
-	2	1194	_p.W398*|AGAP2	NM_001122772	NP_001116244	Q99490	AGAP2_HUMAN		5	AAAGTCCATTC	0.572	
+	2	305	e_Mutation_p.A51	NM_005981	NP_005972	Q12999	TSN31_HUMAN	ical; (Potential).	0	TCATTGCTGTG	0.542	
-	5	793	n_p.S69F|CDK4_	NM_000075	NP_000066	P11802	CDK4_HUMAN	rotein kinase.	3	ATGTGGACTGC	0.478	
+	3	947	1spy.2_Missense_	NM_138396	NP_612405	Q86YJ5	MARH9_HUMAN		0	TGACGGTCATC	0.592	
+	6	597		NM_033276	NP_150592	Q9Y6H3	ATP23_HUMAN		1	ACAGAGCCACTC	0.328	
-	13	1966	e_Mutation_p.A51	NM_153377	NP_700356	Q6UXM1	LRIG3_HUMAN	like C2-type 1.	4	ACTGGCAAATT	0.473	
+	3	312	.2_Missense_Mut	NM_004731	NP_004722	O60669	MOT2_HUMAN	lasmic (Potential).	1	CAATGCCAAGT	0.413	
+	11	1261	rb.1_Missense_M	NM_006313	NP_006304	Q9Y4E8	UBP15_HUMAN		3	AGGTGGTTGCC	0.348	
+	13	1642	rb.1_Missense_Mu	NM_006313	NP_006304	Q9Y4E8	UBP15_HUMAN		3	TTATGGAACGG	0.259	
+	24	3498	n.1_Missense_Mu	NM_015026	NP_055841	Q7Z3U7	MON2_HUMAN		2	GGATCCCCGTC	0.458	
-	6	1128		NM_020700	NP_065751	Q9ULR3	PPM1H_HUMAN	PP2C-like.	4	ATTTCCCAGCA	0.378	
-	3	798		NM_020700	NP_065751	Q9ULR3	PPM1H_HUMAN	PP2C-like.	4	GGCCCCCACCC	0.677	
+	9	1323	p.P423S|SRGAP1	NM_020762	NP_065813	Q7Z6B7	SRGP1_HUMAN		4	GTAAACCCAGC	0.493	
+	4	309		NM_013254	NP_037386	Q9UHD2	TBK1_HUMAN	rotein kinase.	5	CATAAAGTACTT	0.279	
+	8	924		NM_013254	NP_037386	Q9UHD2	TBK1_HUMAN	rotein kinase.	5	AAGCAGATCAG	0.368	
+	3	1633	zqo.1_Splice_Site_	NM_014319	NP_055134	Q9Y2U8	MAN1_HUMAN		4	TTGCAGGTAATT	0.279	
+	12	2530	qo.1_Missense_M	NM_014319	NP_055134	Q9Y2U8	MAN1_HUMAN	1, SMAD2, SMAD3 and S	4	TCTCCAGAATATG	0.289	
+	6	569	p.D163N|MSRB3_	NM_198080	NP_932346	Q8IXL7	MSRB3_HUMAN		2	CTGCGGATAGC	0.547	
-	3	332	p.A133T|TMBIM4_	NM_016056	NP_057140	Q9HC24	TMBI4_HUMAN	ical; (Potential).	2	TCAACGCAAAAA	0.353	
-	19	2673	p.S593N|GRIP1_u	NM_021150	NP_066973	Q9Y3R0	GRIP1_HUMAN		2	TCATAACTCAGC	0.502	
+	9	1815	D1_uc001sto.2_I	NM_018448	NP_060918	Q86VP6	CAND1_HUMAN	HEAT 10.	2	TTAACTGAGCTG	0.373	
+	14	3880	to.2_Missense_M	NM_018448	NP_060918	Q86VP6	CAND1_HUMAN	HEAT 27.	2	TTGAGCCATTAC	0.403	
+	3	712	sts.3_Missense_M	NM_006482	NP_006473	Q92630	DYRK2_HUMAN		4	ACAGTGCTCACG	0.537	
+	25	2416	_p.M526I|NUP107	NM_020401	NP_065134	P57740	NU107_HUMAN		1	CATATGAATTCA	0.294	
+	3	423		NM_000239	NP_000230	P61626	LYSC_HUMAN		0	ACAAGGCATTA	0.373	
+	6	1331	3IP_uc001svo.2_	NM_175623	NP_783322	Q96QF0	RAB3I_HUMAN		1	GAGTGGCAGTC	0.448	rs61758771
+	6	1064	rp.2_Missense_M	NM_014515	NP_055330	Q9NZN8	CNOT2_HUMAN		0	TTCAGGGTTAG	0.458	
-	6	1324	p.V152A|PTPRR_	NM_002849	NP_002840	Q15256	PTPRR_HUMAN	lasmic (Potential).	3	GGTCCACGACA	0.537	
+	7	1010	y.2_Missense_Mu	NM_173353	NP_775489	Q8IWU9	TPH2_HUMAN		4	GGCAGGACTGG	0.522	
+	3	1189		NM_013381	NP_037513	Q9UKU6	TRHDE_HUMAN	ellular (Potential).	3	AAGTGCCCTATT	0.358	
-	1	769		NM_007350	NP_031376	Q8WV24	PHLA1_HUMAN	PH.	0	CCTTGCGCTCC	0.612	
-	2	1589		NM_024685	NP_078961	Q8TAM1	BBS10_HUMAN		2	ATATATGTTTCT	0.353	

+	9	1091	HC17_uc001syj.2_	NM_015336	NP_056151	Q8IUH5	ZDH17_HUMAN	ical; (Potential).	0	GGAACTCCTTTC	0.353	
+	28	5535	V3_uc010sub.1_In	NM_014903	NP_055718	Q8IVL0	NAV3_HUMAN		17	GATCTCGGTAA	0.413	
-	14	2111	R12A_uc010sud.1	NM_002480	NP_002471	O14974	MYPT1_HUMAN	Ser/Thr-rich.	7	CCTCAGCCCAC	0.423	
-	24	2886	ce_Site|PPFIA2_u	NM_003625	NP_003616	B7Z663	B7Z663_HUMAN		6	CCAAAGCTGTTA	0.313	
+	2	397		NM_032230	NP_115606	Q8N6Q8	CL026_HUMAN		0	ACTCCTTTTGAA	0.378	
-	2	503		NM_005447	NP_005438	O75901	RASF9_HUMAN	as-associating.	1	GCAAAGCCTGG	0.483	
-	1	837	C1B_uc010sun.1_	NM_003774	NP_003765	Q8N4A0	GALT4_HUMAN	tial).|Catalytic subdomain A	0	ACGGGCCCTAA	0.488	
-	18	3345	31055D|ATP2B1_u	NM_001682	NP_001673	P20020	AT2B1_HUMAN	ical; (Potential).	3	CCTGGCCCCAG	0.313	
-	11	2042	_p.A621T|ATP2B1	NM_001682	NP_001673	P20020	AT2B1_HUMAN	lasmic (Potential).	3	CTTTTGCCTCAC	0.353	
-	5	1011	bg.2_Missense_M	NM_001682	NP_001673	P20020	AT2B1_HUMAN	lasmic (Potential).	3	CCTACAGCTGTA	0.289	
-	3	680	bg.2_Missense_M	NM_001682	NP_001673	P20020	AT2B1_HUMAN	ical; (Potential).	3	CTAACACCACAC	0.443	
-	2	1280		NM_007035	NP_008966	O60938	KERA_HUMAN	LRR 7.	1	TGTTGTCTAAAA	0.373	
-	5	798	.2_Intron|DCN_uc	NM_133503	NP_598010	P07585	PGS2_HUMAN	LRR 8.	4	TCAACTCTGCTG	0.348	
-	26	4016		NM_003566	NP_003557	Q15075	EEA1_HUMAN	Potential.	3	CAGTGCCTAAGT	0.393	
+	3	615	n_p.V21I|NUDT4_	NM_019094	NP_061967	Q9NZJ9	NUDT4_HUMAN	dix hydrolase.	0	CTGGAGTCAAA	0.284	
+	1	1228		NM_005761	NP_005752	O60486	PLXC1_HUMAN	ılar (Potential).|Sema.	3	CCACGGCGCTC	0.687	
+	5	1689		NM_005761	NP_005752	O60486	PLXC1_HUMAN		3	TTTTTAGGTGCA	0.393	
-	17	1605	.L475F|LTA4H_uc	NM_000895	NP_000886	P09960	LKHA4_HUMAN		1	ATGGAAGAGGTG	0.388	
+	2	289		NM_005230	NP_005221	P41970	ELK3_HUMAN		1	AGAGTGCAATC	0.547	
+	2	628	e_Mutation_p.P13	NM_001032283	NP_001027454	P42167	LAP2B_HUMAN	smic (Potential).|LEM.	2	GTGAATCCTGGT	0.353	
+	13	2469	AF1_uc001tgb.2_M	NM_181861	NP_863651	O14727	APAF_HUMAN	WD 1.	3	GAATAGCTTCTT	0.403	
-	1	527	NKS1B_uc009ztt.	NM_152788	NP_690001	Q7Z6G8	ANS1B_HUMAN		0	GCAGGGGTCCG	0.587	
-	6	898	001tgr.2_Splice_Si	NM_015054	NP_055869	A0JNW5	UH1BL_HUMAN		2	GACTCACCCTTC	0.328	
+	50	6724		NM_014503	NP_055318	O75691	UTP20_HUMAN		4	ACCATACTTGTC	0.423	
+	18	1990	vr.1_Missense_M	NM_206820	NP_996556	Q00872	MYPC1_HUMAN	nectin type-III 1.	4	TGACAGAGGTG	0.458	
-	13	2341		NM_024312	NP_077288	Q3T906	GNPTA_HUMAN		2	ATGTCTCCATGT	0.398	
-	13	2236		NM_024312	NP_077288	Q3T906	GNPTA_HUMAN		2	CTCCTTGTTGAG	0.428	
-	5	563	svy.1_RNA|CCDC	NM_016053	NP_057137	Q9Y3C0	CCD53_HUMAN		0	GCATATCTTGGA	0.403	
+	8	1218	88I|C12orf48_uc0	NM_017915	NP_060385	Q9NWS1	PR1BP_HUMAN		0	CTCCTACCAAAA	0.373	
-	3	578	n.2_Missense_Mu	NM_001111285	NP_001104755	P05019	IGF1_HUMAN		2	GGACAGAGCGA	0.592	
+	57	6218	AB2_uc009zug.2_F	NM_017564	NP_060034	Q8WWQ8	STAB2_HUMAN	tential).|Laminin EGF-like	14	TACAGCCTGTG	0.557	
+	13	1859	e_Mutation_p.G2	NM_003299	NP_003290	P14625	ENPL_HUMAN		3	TGATGGGAAGA	0.433	
+	3	597	.2_Missense_Mut	NM_003211	NP_003202	Q13569	TDG_HUMAN		6	CTCTCCCCGATA	0.343	
+	7	545	_Mutation_p.R15	NM_015275	NP_056090	Q2M389	WAHS7_HUMAN		2	TTACGAGGTGCT	0.338	
-	1	1466		NM_014840	NP_055655	O60285	NUAK1_HUMAN		2	TCGCCCCCGCC	0.736	
-	2	926		NM_006825	NP_006816	Q07065	CKAP4_HUMAN	Potential.	0	TTGTTCCCCTCA	0.498	
+	10	1537		NM_152772	NP_689985	Q8N4U5	T11L2_HUMAN		3	CAAGCCCTCAA	0.393	rs150377812
+	24	2936	tlq.2_Missense_M	NM_018082	NP_060552	Q9NW08	RPC2_HUMAN		2	CCCAGGTGTTT	0.483	
+	14	1522	t.2_Missense_Mut	NM_213594	NP_998759	Q33E94	RFX4_HUMAN	ary for dimerization.	1	TGAAGGGAGAA	0.433	
+	16	1834	p.P599S|RFX4_uc	NM_213594	NP_998759	Q33E94	RFX4_HUMAN		1	AGGATACCAGTT	0.453	
-	7	1218	ART3_uc010swy.	NM_014706	NP_055521	Q15020	SART3_HUMAN	HAT 5.	1	GAATGCGAGCA	0.453	
+	3	419	nc.3_Missense_M	NM_213595	NP_998760	Q9H1K1	ISCU_HUMAN		0	CATTAGCCACTG	0.368	rs145206633
+	13	1638	p.E481K|USP30_	NM_032663	NP_116052	Q70CQ3	UBP30_HUMAN	lasmic (Potential).	1	GCCAGGAGTGC	0.562	
+	35	4867	d.1_RNA|ACACB_	NM_001093	NP_001084	O00763	ACACB_HUMAN		8	TAACACCAGCGT	0.602	
+	11	1396	HP_uc001tpp.2_M	NM_001143852	NP_001137324	Q9BT92	TCHP_HUMAN	Glu-rich.|Potential.|Interact	1	AGGAGGTGAGA	0.537	
-	4	549	qp.3_Missense_M	NM_016238	NP_057322	Q9UJX3	APC7_HUMAN	TPR 2.	0	TCCTGACCAGCC	0.438	
+	9	952	_p.I203V|RAD9B_	NM_152442	NP_689655	Q6WBX8	RAD9B_HUMAN		2	AACTTTATTTTGG	0.378	

+	18	2928	e_Mutation_p.A94	NM_025247	NP_079523	Q6JQN1	ACD10_HUMAN		2	AGATCGCCCAG	0.607	
+	10	1643	_p.T354I|ALDH2_	NM_000690	NP_000681	P05091	ALDH2_HUMAN		4	GCCCACTGTGT	0.567	
+	10	1632	tto.2_Missense_M	NM_006700	NP_006691	O14545	TRAD1_HUMAN		0	ATTCGCCCTCCT	0.562	
+	19	1858	p.G593R|TPCN1_	NM_017901	NP_060371	Q9ULQ1	TPC1_HUMAN	S3 of repeat II; (Potential).	3	TCCTGGGACTG	0.642	
+	28	2656	e_Mutation_p.E85	NM_017901	NP_060371	Q9ULQ1	TPC1_HUMAN	ic (Potential).|Potential.	3	CCAGGGAGCAA	0.687	
-	12	1402	24A6_uc001tva.2_	NM_024959	NP_079235	Q6J4K2	NCKX6_HUMAN	Name=8; (Potential).	1	CTGTGCCTGCGA	0.592	
-	8	1121	p.R326K|RBM19_	NM_001146699	NP_001140171	Q9Y4C8	RBM19_HUMAN	RRM 2.	6	GCGTTTCTCACA	0.433	
-	19	4268		NM_015335	NP_056150	Q71F56	MD13L_HUMAN		8	CCTCTCCCAAA	0.522	
+	7	1209	e_Mutation_p.S31	NM_153348	NP_699179	Q8N3Y1	FBXW8_HUMAN		3	AGACTCCGCCA	0.542	
-	3	327	SC_uc001twi.2_R	NM_017899	NP_060369	Q96BS2	TESC_HUMAN		0	GTTGAGCTCCA	0.517	
-	8	1232	plice|FBXO21_uc	NM_033624	NP_296373	O94952	FBX21_HUMAN		1	ACCTTACCGCTT	0.463	
-	21	3792		NM_000620	NP_000611	P29475	NOS1_HUMAN	R-type.|FAD (By similarity).	7	GTGGTCCCCAG	0.597	
-	6	867	b.1_Missense_Mu	NM_018639	NP_061109	Q9NYS7	WSB2_HUMAN	WD 4.	1	AGAAGCCGTGA	0.512	
+	3	668	uc001txf.2_Intron	NM_178499	NP_848594	Q8IWA6	CCD60_HUMAN		3	GCCGTGGATATT	0.428	
+	3	770	249K|CCDC64_uc	NM_207311	NP_997194	Q6ZP65	BICR1_HUMAN	Potential.	2	GGCTGGAGAGC	0.527	
-	44	5711		NM_006836	NP_006827	Q92616	GCN1L_HUMAN		4	CCGCACCACCA	0.617	
-	43	5619		NM_006836	NP_006827	Q92616	GCN1L_HUMAN		4	TGTTGGACTGG	0.537	
-	42	5481		NM_006836	NP_006827	Q92616	GCN1L_HUMAN	HEAT 14.	4	AGAGGCCTTGC	0.473	
-	24	2634		NM_006836	NP_006827	Q92616	GCN1L_HUMAN		4	ACTGGGTCAGG	0.592	
-	21	2294		NM_006836	NP_006827	Q92616	GCN1L_HUMAN		4	CTCCTCCCGCG	0.597	
+	5	1303	F10_uc001tyq.3_	NM_014868	NP_055683	Q8N5U6	RNF10_HUMAN		2	AGAAGGATCTC	0.448	
-	3	217	P5_uc001tyt.2_Int	NM_015918	NP_057002	Q969H6	POP5_HUMAN		0	ATTCCAGTATAG	0.323	
+	10	1329	zb.3_Missense_Mu	NM_000017	NP_000008	P16219	ACADS_HUMAN		2	CGCCGGGCATC	0.697	
-	6	1303	SL_uc001tzk.1_3'U	NM_003733	NP_003724	Q15646	OASL_HUMAN	biquitin-like 1.	1	GATCTCGGAGG	0.537	
+	7	766	.2_RNA|P2RX7_	NM_002562	NP_002553	Q99572	P2RX7_HUMAN		5	AGAATCCACAG	0.418	rs146402035
-	10	1154	y.2_Missense_Mu	NM_006549	NP_006540	Q96RR4	KKCC2_HUMAN	rotein kinase.	3	GGAGAGGAGCG	0.582	
-	2	306	y.2_Missense_Mu	NM_006549	NP_006540	Q96RR4	KKCC2_HUMAN		3	CACAGCCCGGC	0.682	
-	4	546	uah.2_Missense_	NM_016237	NP_057321	Q9UJX4	APC5_HUMAN		6	GTAGGCCAAGA	0.443	
-	16	2457	s.2_Missense_Mu	NM_032590	NP_115979	Q8NHM5	KDM2B_HUMAN		2	CGGCACCTTCT	0.622	
-	8	455	bk.2_Splice_Site_	NM_002150	NP_002141	P32754	HPPD_HUMAN		0	CCATACTACGG	0.448	
-	6	364	bk.2_Splice_Site_	NM_002150	NP_002141	P32754	HPPD_HUMAN		0	TTCTTACCTGCA	0.577	
+	1	127	zxj.2_RNA|PSMD	NM_002813	NP_002804	O00233	PSMD9_HUMAN		0	CCGACGAGGAA	0.682	
-	8	1107	33A_uc001ucc.2_	NM_022916	NP_075067	Q96AX1	VP33A_HUMAN		1	CTCCCCCACGG	0.403	
-	14	1662	p.D273N|ZCCHC	NM_017612	NP_060082	Q6NZY4	ZCHC8_HUMAN		0	CCTCATCCACAG	0.602	
-	2	498	_Mutation_p.G63	NM_019625	NP_062571	Q9NP78	ABCB9_HUMAN	ical; (Potential).	0	TGGCTCCCAGC	0.647	
-	13	1695	NO1_uc001ueu.2_	NM_018183	NP_060653	A3KN83	SBNO1_HUMAN		9	GATGACCCACTG	0.403	
-	5	573	_p.A144T|EIF2B1_	NM_001414	NP_001405	Q14232	EI2BA_HUMAN		0	CTTGGCCGCCA	0.502	
+	17	2588	p.P397S|DNAH10	NM_207437	NP_997320	Q8IVF4	DYH10_HUMAN	n (By similarity).	6	AGGCCCCCAAG	0.502	
+	41	6905		NM_207437	NP_997320	Q8IVF4	DYH10_HUMAN	2 (By similarity).	6	ATAGTGGAAGGA	0.388	
-	3	235	ufx.1_Missense_	NM_025140	NP_079416	Q53HC0	CCD92_HUMAN	Potential.	0	CTGTGCGCTGT	0.612	rs150024637
-	6	863	p.G249E|NCOR2_	NM_001077261	NP_001070729	Q9Y618	NCOR2_HUMAN		4	GGGGCCCCAGG	0.587	
-	5	728	p.A204V|NCOR2_	NM_001077261	NP_001070729	Q9Y618	NCOR2_HUMAN	Potential.	4	TTGGCAGCCTCC	0.682	
-	2	350	|NCOR2_uc010tb	NM_001077261	NP_001070729	Q9Y618	NCOR2_HUMAN		4	TCCTCACCGTTC	0.652	
-	7	1176		NM_032656	NP_116045	Q8IY37	DHX37_HUMAN		1	ACCAACCTTCT	0.547	
+	2	864		NM_052907	NP_443139	Q14DG7	T132B_HUMAN	ellular (Potential).	19	TCTCGGTACCT	0.537	
+	8	1375	jb.1_Missense_Mu	NM_004592	NP_004583	Q12872	SFSWA_HUMAN		0	CACCGCCCCAC	0.647	
+	8	1384	jb.1_Missense_Mu	NM_004592	NP_004583	Q12872	SFSWA_HUMAN	Poly-Pro.	0	ACCACCTCCTG	0.647	

-	14	1970		NM_175066	NP_778236	Q8N8A6	DDX51_HUMAN		2	ACCGAGGAACC	0.617
-	35	4492	_p.S287N|POLE_	NM_006231	NP_006222	Q07864	DPOE1_HUMAN		8	GGATACTCCCT	0.587
-	30	3757	.E_uc010tbq.1_RN	NM_006231	NP_006222	Q07864	DPOE1_HUMAN		8	CCTGGCTCTCC	0.627
-	26	3213	q.1_RNA|POLE_	NM_006231	NP_006222	Q07864	DPOE1_HUMAN		8	CTTTGCTGTGC	0.577
-	24	2751	.1_Splice_Site|PC	NM_006231	NP_006222	Q07864	DPOE1_HUMAN		8	CCTTCCTGAGA	0.333
+	3	403	AM5_uc001uku.2_	NM_138575	NP_612642	Q96HS1	PGAM5_HUMAN		0	GTCGGGAGCAG	0.353
-	4	1014	ky.3_Missense_M	NM_015114	NP_055929	Q86XL3	ANKL2_HUMAN		0	CCACAGCTTTC	0.527
-	17	3843	la.1_Missense_M	NM_005895	NP_005886	Q08378	GOGA3_HUMAN	Potential.	6	TAAAGCCTCTG	0.448
-	4	668		NM_006001	NP_005992	Q13748	TBA3C_HUMAN		5	GGCTTCATTGT	0.582
-	1	236	j.1_RNA|PSPC1_	NM_001042414	NP_001035879	Q8WXF1	PSPC1_HUMAN		1	GGCGGGCCGG	0.647
-	6	1191	M5_uc001umn.2_	NM_001142684	NP_001136156	Q9UJ78	ZMYM5_HUMAN		0	GGAAGGATTTG	0.318
-	3	311	sense_Mutation_p.	NM_001142684	NP_001136156	Q9UJ78	ZMYM5_HUMAN		0	AGCAGGAGTCT	0.403
+	5	1230	_p.P311L|ZMYM2_	NM_003453	NP_003444	Q9UBW7	ZMYM2_HUMAN		6	CACTTCCTAAAC	0.448
-	1	56	O4_uc010tcr.1_5'U	NM_022459	NP_071904	Q9C0E2	XPO4_HUMAN		3	GGGGCCCCAGC	0.711
+	7	834	_p.L227F|SGCG_u	NM_000231	NP_000222	Q13326	SGCG_HUMAN	ellular (Potential).	0	GATATTCTTTTTC	0.443
-	10	13514	E4162K|SACS_uc	NM_014363	NP_055178	Q9NZJ4	SACS_HUMAN	J.	12	TCACTTCTTTTA	0.408
-	10	12953	A3975T|SACS_uc	NM_014363	NP_055178	Q9NZJ4	SACS_HUMAN		12	GCATAGCAATTA	0.353
-	10	9521	V2831M|SACS_uc	NM_014363	NP_055178	Q9NZJ4	SACS_HUMAN		12	CTTTCACTAGAC	0.388
-	10	8178	S2383N|SACS_uc	NM_014363	NP_055178	Q9NZJ4	SACS_HUMAN		12	ATTCTGCTGGTC	0.393
-	10	7536	.T2169I|SACS_uc	NM_014363	NP_055178	Q9NZJ4	SACS_HUMAN		12	GCATTGGTGATA	0.343
-	13	1524		NM_005932	NP_005923	Q99797	MIPEP_HUMAN		1	AACGGGGAAGA	0.428
-	25	3220		NM_006437	NP_006428	Q9UKK3	PARP4_HUMAN		4	AACATACCTGTT	0.353
+	8	1086	aa.2_Missense_M	NM_001676	NP_001667	P54707	AT12A_HUMAN	lasmic (Potential).	6	CCATTGCCATTG	0.517
-	7	2471	.2_RNA|CENPJ_u	NM_018451	NP_060921	Q9HC77	CENPJ_HUMAN		2	TAAAAGGCCCCT	0.443
+	1	194		NM_030979	NP_112241	Q9H361	PABP3_HUMAN	RRM 1.	4	GCAGGGACTTG	0.567
-	1	1731	p.G425D|FAM123	NM_152704	NP_689917	Q8N7J2	F123A_HUMAN		4	GGATGCCCGC	0.637
-	1	1667_1668	p.G404N|FAM123	NM_152704	NP_689917	Q8N7J2	F123A_HUMAN		4	AGTAGCCCTCGT	0.658
+	9	866	8A2_uc010tdj.1_	NM_016529	NP_057613	Q9NTI2	AT8A2_HUMAN	lasmic (Potential).	4	GTGAAGGGCCC	0.393
-	5	1307	p.2_Missense_M	NM_183044	NP_898865	Q9Y252	RNF6_HUMAN	Arg-rich.	2	CAGATCTTCTAG	0.433
+	10	981	_p.D319N|CDK8_u	NM_001260	NP_001251	P49336	CDK8_HUMAN	rotein kinase.	5	CCATGGACCCA	0.413
-	8	1957	m.1_Missense_M	NM_153371	NP_699202	Q8N448	LNX2_HUMAN	PDZ 3.	6	TTTAAGGGCAA	0.502
+	2	216	se_Mutation_p.G	NM_152705	NP_689918	Q9Y2S0	RPAC2_HUMAN		0	CATGGGTTGGT	0.254
-	3	1001		NM_001265	NP_001256	Q99626	CDX2_HUMAN		1	CACTTCTCAGA	0.552
-	20	2520	.2_RNA|FLT3_uc	NM_004119	NP_004110	P36888	FLT3_HUMAN	.|Cytoplasmic (Potential).	8549	TGGCGGCCAGG	0.458
-	7	933	T3_uc010tdn.1_	NM_004119	NP_004110	P36888	FLT3_HUMAN	Potential).|Ig-like C2-type.	8549	CCCAGGTGAGC	0.393
-	30	4210	q.2_Missense_Mu	NM_002019	NP_002010	P17948	VGFR1_HUMAN	lasmic (Potential).	24	GTCGTAGGTGA	0.577
+	1	1538		NM_001033602	NP_001028774	Q5JR59	MTUS2_HUMAN		0	AGGTGCCTGAG	0.512
+	1	1886		NM_001033602	NP_001028774	Q5JR59	MTUS2_HUMAN		0	CCAAGCCTGTC	0.522
+	4	718	.2_5'UTR|USPL1_	NM_005800	NP_005791	Q5W0Q7	USPL1_HUMAN		3	TGGAAGAATGT	0.318
+	4	1143	.W56*|USPL1_uc	NM_005800	NP_005791	Q5W0Q7	USPL1_HUMAN		3	TGTTGGTTAGA	0.448
+	9	1972	_p.L185F|USPL1_	NM_005800	NP_005791	Q5W0Q7	USPL1_HUMAN		3	CTTCCACTTAAA	0.408
-	11	1941	_p.E474K|HSPH1_	NM_006644	NP_006635	Q92598	HS105_HUMAN		0	ACACTCCATGT	0.433
-	9	1567	_p.R349K|HSPH1_	NM_006644	NP_006635	Q92598	HS105_HUMAN		0	AATTCTCTAACT	0.338
+	9	874	ALTL_uc001utn.3_	NM_194318	NP_919299	Q6Y288	B3GLT_HUMAN	enal (Potential).	2	TCCATTCTTTTCT	0.438
+	29	4188	Y_uc010tdw.1_R	NM_023037	NP_075463	Q5TBA9	FRY_HUMAN		7	CAGGTTCCTACC	0.428
+	42	6024	uc010tdw.1_Splic	NM_023037	NP_075463	Q5TBA9	FRY_HUMAN		7	CCCTAGGCTTC	0.507
+	19	8649		NM_000059	NP_000050	P51587	BRCA2_HUMAN		64	CATCGCTTTTCA	0.398

+	21	8925		NM_000059	NP_000050	P51587	BRCA2_HUMAN			64	TGCAAGATGGT	0.383
+	3	267	_uc001uuo.2_Spli	NM_015032	NP_055847	Q9NTI5	PDS5B_HUMAN			4	GTATAGATGGTT	0.299
+	3	1407	.1_Missense_Muta	NM_004795	NP_004786	Q9UEF7	KLOT_HUMAN	e-1 1.|Extracellular (Potenti		3	AGTGGCACAGA	0.502
-	10	2650	se_Mutation_p.P7	NM_178006	NP_821074	Q9Y3M8	STA13_HUMAN	Rho-GAP.		4	ATCTGGCTTCC	0.483
+	5	630	_p.P174S|RFC3_u	NM_002915	NP_002906	P40938	RFC3_HUMAN			0	ATCCCACCTATT	0.428
-	1	1146	A_uc010tee.1_Int	NM_005584	NP_005575	Q13394	MB211_HUMAN			2	GTTGGGTCCCG	0.637
+	45	7180	_p.T118I|NBEA_u	NM_015678	NP_056493	Q8NFP9	NBEA_HUMAN	BEACH.		11	TGTTAACCAACT	0.348
-	5	1120	uc001uvi.1_Intron	NM_004734	NP_004725	O15075	DCLK1_HUMAN	Pro/Ser-rich.		9	TCTTGGTGGTG	0.507
-	3	919		NM_004734	NP_004725	O15075	DCLK1_HUMAN	oublecortin 2.		9	CCACTCCCGAG	0.498
+	3	742	A1_uc010abp.2_	NM_003914	NP_003905	P78396	CCNA1_HUMAN			5	GCCCCCCAAGC	0.502
+	8	1650	A1_uc010abp.2_	NM_003914	NP_003905	P78396	CCNA1_HUMAN			5	ATATACCCCATC	0.398
-	2	495	e_Mutation_p.A51	NM_001127217	NP_001120689	O15198	SMAD9_HUMAN	MH1.		0	TCCATGGCTCCC	0.592
-	11	3138	_p.T827I|TRPC4_	NM_016179	NP_057263	Q9UBN4	TRPC4_HUMAN	and ITPR3.|Cytoplasmic (P		6	CGTGGGTGACT	0.448
+	1	4609		NM_207361	NP_997244	Q5SZK8	FREM2_HUMAN	r (Potential).|CSPG 10.		11	AAGAAGGTGGC	0.443
+	10	6986	ww.2_Missense_M	NM_207361	NP_997244	Q5SZK8	FREM2_HUMAN	ellular (Potential).		11	CAACTCTCCCT	0.458
+	13	1269	.G338D|COG6_u	NM_020751	NP_065802	Q9Y2V7	COG6_HUMAN			2	TAGTGGTATTGT	0.308
+	3	636	10tfb.1_Splice_Si	NM_014252	NP_055067	Q9Y619	ORNT1_HUMAN			0	CTGAGGTGAGT	0.363
-	1	2221	010tfe.1_Nonsens	NM_152903	NP_690867	Q86V97	KBTB6_HUMAN	Kelch 6.		2	TAAGTCCCATTC	0.458
-	44	5664		NM_015058	NP_055873	A3KMH1	K0564_HUMAN	VWFA.		6	GATCACCTAAA	0.413
-	19	2327	uyk.2_Missense_	NM_015058	NP_055873	A3KMH1	K0564_HUMAN			6	GAAAAGAACATC	0.363
-	18	2178	uyk.2_Missense_	NM_015058	NP_055873	A3KMH1	K0564_HUMAN			6	CATCTGCCAGA	0.373
-	8	960	uyk.2_Missense_	NM_015058	NP_055873	A3KMH1	K0564_HUMAN			6	TTGTGGCAAAG	0.313
+	9	1073	.R106H|DGKH_u	NM_178009	NP_821077	Q86XP1	DGKH_HUMAN	DAGKc.		2	TCCTCCGTCGCT	0.368
+	22	2692	.A646T|DGKH_u	NM_178009	NP_821077	Q86XP1	DGKH_HUMAN			2	AAATGGCAGTT	0.423
+	2	462	uyt.2_Missense_	NM_003701	NP_003692	O14788	TNF11_HUMAN	ellular (Potential).		0	CTCTGGAGAGT	0.383
+	2	311	P2_uc001uzk.2_	NM_001010897	NP_001010897	Q8N6R1	SERP2_HUMAN	IV membrane protein; (P		0	TGTTGGCACTG	0.383
-	1	80	_5'Flank|KIAA170	NM_012345	NP_036477	Q9UHK0	NUFP1_HUMAN			0	GCCACCCGATA	0.627
-	2	195	_p.V35M|LOC100	NM_003295	NP_003286	P13693	TCTP_HUMAN			0	ACTCACCTTCC	0.672
-	2	191	_p.G33E|LOC100	NM_003295	NP_003286	P13693	TCTP_HUMAN			0	CCTTCCCCTCC	0.672
-	2	181	_p.E30K|LOC100	NM_003295	NP_003286	P13693	TCTP_HUMAN			0	CACCTCCAGGC	0.672
+	1	267	_p.P56S|COG3_u	NM_031431	NP_113619	Q96JB2	COG3_HUMAN			2	CGGTGCCAGCT	0.701
-	14	3842	3H13_uc001vas.1	NM_015070	NP_055885	Q5T200	ZC3HD_HUMAN	Ser-rich.		2	TCTGGAGAACTT	0.343
-	13	3310	nse_Mutation_p.P	NM_015070	NP_055885	Q5T200	ZC3HD_HUMAN			2	AGGAGGAAGAA	0.313
-	15	1811	y.3_Missense_Mu	NM_002298	NP_002289	P13796	PLSL_HUMAN	-binding 2.|CH 4.		7	TGGAACCTGGT	0.428
-	3	982	issense_Mutation_	NM_025113	NP_079389	Q9H714	CM018_HUMAN	Ser-rich.		0	AGAAGCTGCTA	0.572
+	2	402		NM_021999	NP_068839	Q9Y287	ITM2B_HUMAN	type II membrane protein;		0	CTTTGGACTAG	0.378
-	1	1618	ce.2_Missense_M	NM_001162498	NP_001155970	P43657	LPAR6_HUMAN	ellular (Pot	p.?(4)	4	TCCATGtggcttctgg	0.333
-	10	1269	76S|RCBTB2_uc	NM_001268	NP_001259	O95199	RCBT2_HUMAN	RCC1 5.		5	AGTAGGATAGG	0.458
+	5	633	C3A_uc001vco.2_	NM_001079673	NP_001073141	Q9Y2H6	FND3A_HUMAN	Pro-rich.		2	ACACAGTTCTC	0.488
+	21	2661	C3A_uc001vco.2_	NM_001079673	NP_001073141	Q9Y2H6	FND3A_HUMAN	nectin type-III 6.		2	GTAATGGAACA	0.383
-	9	1342	_p.A282T|CAB39L_	NM_030925	NP_112187	Q9H9S4	CB39L_HUMAN			0	ACTGGCCACAA	0.478
+	10	1287	e_Mutation_p.R27	NM_001040443	NP_001035533	Q9UIL8	PHF11_HUMAN			0	AAAATAGAGATC	0.373
-	17	3800	.D1150N|ATP7B_	NM_000053	NP_000044	P35670	ATP7B_HUMAN	lasmic (Potential).		3	CACGTCCACAC	0.562
+	2	590	.2_3'UTR|UTP14	NM_021645	NP_067677	Q5TAP6	UT14C_HUMAN			5	AACTAGTGGAT	0.463
+	2	1815	14C_uc001vgc.2_	NM_021645	NP_067677	Q5TAP6	UT14C_HUMAN			5	GCAATCCCTTA	0.478
-	21	1978		NM_199289	NP_954983	Q6P3R8	NEK5_HUMAN			1	TCATGCCATCC	0.348
-	6	875	_p.A255V|LECT1_	NM_007015	NP_008946	O75829	LECT1_HUMAN			2	TGAAGGCTTGT	0.408

-	1	325	vhj.2_Missense_M	NM_002590	NP_002581	O95206	PCDH8_HUMAN	(Potential).|Cadherin 1.	1	CGGGGGCATCC	0.592	
-	2	812	thj.1_Missense_M	NM_022843	NP_073754	Q8N6Y1	PCD20_HUMAN	|Extracellular (Potential).	6	GGCCTCCCTGT	0.602	
-	10	2428	_p.V521I|DACH1_	NM_080759	NP_542937	Q9UI36	DACH1_HUMAN		1	TAAGACCCTGA	0.388	
+	2	1214	d.2_Missense_Mu	NM_001730	NP_001721	Q13887	KLF5_HUMAN		3	AACAGGCCACTT	0.517	
-	21	4101	.E409K|TBC1D4_	NM_014832	NP_055647	O60343	TBCD4_HUMAN		6	TTGTTCCAGGG	0.458	
-	6	1840	p.R498K|TBC1D4	NM_014832	NP_055647	O60343	TBCD4_HUMAN		6	TGAACTCTTTCA	0.403	
+	6	1142	1_Intron|LMO7_uc	NM_015842	NP_056667	Q8WWI1	LMO7_HUMAN		5	CAAACCCAGGG	0.398	
+	11	2606	.R515W|LMO7_uc	NM_015842	NP_056667	Q8WWI1	LMO7_HUMAN		5	AGTTACCGGAAA	0.483	
+	26	4763	7_uc010thw.1_Mi	NM_015842	NP_056667	Q8WWI1	LMO7_HUMAN		5	CTCAGGAGCTG	0.443	
-	65	11105	.D3076N|MYCBP	NM_015057	NP_055872	O75592	MYCB2_HUMAN		14	CATCATCTGACT	0.398	
-	57	9158	vkg.1_Missense_	NM_015057	NP_055872	O75592	MYCB2_HUMAN		14	GGAAAGTTCAG	0.388	
-	43	6408	ev.2_Missense_M	NM_015057	NP_055872	O75592	MYCB2_HUMAN		14	TCATATCCAATTG	0.343	
-	16	2358	aev.2_Missense_M	NM_015057	NP_055872	O75592	MYCB2_HUMAN	Cys-rich.	14	CTTACCCTCCG	0.438	
+	10	771	_p.P201S|SCEL_u	NM_144777	NP_659001	O95171	SCEL_HUMAN		5	TCTTCTCCTAAC	0.428	rs17854490
-	2	2830	afe.1_Missense_M	NM_032229	NP_115605	Q9H5Y7	SLIK6_HUMAN	lasmic (Potential).	3	TCCAGGATAAT	0.388	
+	2	961	RK5_uc010tic.1_I	NM_015567	NP_056382	O94991	SLIK5_HUMAN	xtracellular (Potential).	5	TAAAGGATTGG	0.517	
+	2	1343	tic.1_Missense_M	NM_015567	NP_056382	O94991	SLIK5_HUMAN	lar (Potential).|LRRNT.	5	GTGTCCCACCG	0.597	
-	31	4069	_p.T108I|ABCC4_	NM_005845	NP_005836	O15439	MRP4_HUMAN		4	TTAAGGTCGAG	0.388	
-	24	3058	fk.2_Missense_Mu	NM_005845	NP_005836	O15439	MRP4_HUMAN	|ABC transmembrane type	4	CCAAACCAACC	0.473	
-	27	3297	mu.1_Missense_M	NM_020121	NP_064506	Q9NYU1	UGGG2_HUMAN		3	ATTCAGGAATAT	0.408	
-	9	1170	se_Mutation_p.D	NM_020121	NP_064506	Q9NYU1	UGGG2_HUMAN		3	AAATGTCTTTCA	0.313	
-	4	1128	afr.1_Missense_M	NM_080818	NP_543008	Q96P68	OXGR1_HUMAN	Name=7; (Potential).	2	CAAAGGTGTTC	0.458	
-	4	1028	afr.1_Missense_M	NM_080818	NP_543008	Q96P68	OXGR1_HUMAN	Name=6; (Potential).	2	GAATGACCCTCA	0.433	
+	22	2801	nh.2_Missense_M	NM_005766	NP_005757	Q9Y4F1	FARP1_HUMAN	PH 1.	2	GGTGCCCCACT	0.617	
-	23	2528	ce|DOCK9_uc010	NM_015296	NP_056111	Q9BZ29	DOCK9_HUMAN		1	TGATCCTGAGG	0.358	
-	21	2328	OCK9_uc010tis.1_	NM_015296	NP_056111	Q9BZ29	DOCK9_HUMAN	DHR-1.	1	GCCAGGAGTAG	0.478	
-	13	1502	OCK9_uc010tis.1_	NM_015296	NP_056111	Q9BZ29	DOCK9_HUMAN		1	CTGAAGGACTT	0.403	
-	8	842	OCK9_uc010tis.1	NM_015296	NP_056111	Q9BZ29	DOCK9_HUMAN	PH.	1	GTCTGCTGCCA	0.393	
+	1	644		NM_007129	NP_009060	O95409	ZIC2_HUMAN	transcriptional activation o	0	GTACGGCCCCA	0.562	
-	14	1865	.A458T|TMTC4_u	NM_001079669	NP_001073137	Q5T4D3	TMTC4_HUMAN	TPR 4.	3	CTCTGCTGCTT	0.493	
-	11	1502	.G337R|TMTC4_u	NM_001079669	NP_001073137	Q5T4D3	TMTC4_HUMAN	|Helical; (Potential).	3	GATTCCCAGCA	0.507	
-	8	1038	_p.T182M|TMTC4_	NM_001079669	NP_001073137	Q5T4D3	TMTC4_HUMAN		3	GGCCCGTGCC	0.637	
+	24	3089		NM_003291	NP_003282	P29144	TPP2_HUMAN		2	TACCTCCACCA	0.313	
-	3	313	vpk.2_Missense_	NM_001010977	NP_001010977	Q5VZV1	MT21C_HUMAN		0	GTTCCTCCAAGT	0.403	
-	1	795		NM_000452	NP_000443	Q12908	NTCP2_HUMAN	lasmic (Potential).	4	ATGCCCCACGG	0.532	
-	1	619		NM_001080396	NP_001073865	B1AL88	F155A_HUMAN		1	CTGAGCCCTCT	0.562	
-	29	2227	4A1_uc010agl.2_I	NM_001845	NP_001836	P02462	CO4A1_HUMAN	le-helical region.	6	GTAAGCCGTCA	0.498	
-	22	1419	4A1_uc010agl.2_I	NM_001845	NP_001836	P02462	CO4A1_HUMAN	le-helical region.	6	GACATTCCACAA	0.413	
-	8	590	agl.2_Splice_Site	NM_001845	NP_001836	P02462	CO4A1_HUMAN		6	AATGTACCTTCAT	0.328	
+	1	824	1_uc001vrf.2_Intr	NM_005537	NP_005528	Q9UK53	ING1_HUMAN		1	GCTCAGCCCGG	0.736	
+	12	1625	p.E482Q|MCF2L_	NM_001112732	NP_001106203	O15068	MCF2L_HUMAN	Potential.	2	GGTGCGGAAAT	0.532	
+	17	1763	agu.2_Splice_Site	NM_001008895	NP_001008895	Q13619	CUL4A_HUMAN		3	AAGAAGTAAGT	0.289	
+	8	788		NM_182614	NP_872420	Q8WV15	FA70B_HUMAN		0	CTTCCGCCTGA	0.677	
-	11	1460	_p.P137L|GAS6_u	NM_000820	NP_000811	Q14393	GAS6_HUMAN	minin G-like 1.	4	TCACAGGCTGC	0.587	
+	1	167	a.1_RNA|POTEG_	NM_001005356	NP_001005356	Q6S5H5	POTEG_HUMAN		1	GGAGCGGCAAG	0.592	
-	1	265	4P_uc001vwb.3_	NM_001145442	NP_001138914	A6NI47	POTEM_HUMAN		0	CTGCACCAGGG	0.587	
-	1	689		NM_001004714	NP_001004714	Q8NH42	OR4KD_HUMAN	lasmic (Potential).	2	GACTAGCAGCA	0.502	

-	1	170		NM_001004714	NP_001004714	Q8NH42	OR4KD_HUMAN	lasmic (Potential).	2	TTGGTGTGTGA	0.438	
-	50	7251	EP1_uc010tlf.1_R	NM_007110	NP_009041	Q99973	TEP1_HUMAN	WD 18.	5	ATTTCAGATGGA	0.458	
-	14	2255	EP1_uc010tlf.1_R	NM_007110	NP_009041	Q99973	TEP1_HUMAN		5	GATGCCTTCTT	0.532	
-	14	2198	EP1_uc010tlf.1_R	NM_007110	NP_009041	Q99973	TEP1_HUMAN		5	GACGTCCACCT	0.547	
-	2	279	P1_uc010tlg.1_Mi	NM_007110	NP_009041	Q99973	TEP1_HUMAN	1 N-terminal 3.	5	GGCACTGGTTC	0.542	
-	2	223	EP1_uc010tlg.1_M	NM_007110	NP_009041	Q99973	TEP1_HUMAN	1 N-terminal 3.	5	TTTTTCCATGGT	0.507	
+	4	654	APEX1_uc001vxi.	NM_001641	NP_001632	P27695	APEX1_HUMAN		4	CTGAACTTCAG	0.502	
+	4	455	.2_3'UTR|PNP_uc	NM_000270	NP_000261	P00491	PNPH_HUMAN		2	TCCACCTTCTG	0.443	
-	4	721	ahr.2_Missense_	NM_001110357	NP_001103827	P60153	RNAS9_HUMAN		2	AGGTGGCTCCA	0.433	
+	2	973	IASE4_uc001vya.	NM_002937	NP_002928	P34096	RNAS4_HUMAN		1	TGAGGGTAACC	0.512	
+	3	484	6N|METT11D1_u	NM_022734	NP_073571	Q9H7H0	MET17_HUMAN		0	CTGGAGCAGAC	0.473	
+	14	1510	p.2_Missense_Mu	NM_022734	NP_073571	Q9H7H0	MET17_HUMAN		0	TTTTACCTGTGC	0.522	
+	4	582	RG2_uc010tll.1_In	NM_173846	NP_776245	P59282	TPPP2_HUMAN		0	ACAAGGAGCGC	0.542	
+	12	2512	10aij.2_RNA|FLJ1	NM_018071	NP_060541	Q8TER5	ARH40_HUMAN	Potential.	0	TTTCAGCGCTG	0.637	
+	7	1325	OX4_uc010tlu.1_	NM_014828	NP_055643	O94842	TOX4_HUMAN	Gln/Pro-rich.	1	AGTACAGCTACT	0.552	
+	1	620		NM_001001912	NP_001001912	Q8NGC2	OR4E2_HUMAN	Name=5; (Potential).	4	CATCTCCCTCT	0.493	
-	8	1361	_p.P408L|SLC7A7_	NM_003982	NP_003973	Q9UM01	YLAT1_HUMAN		2	GATCAGGCTCC	0.498	
+	1	405		NM_001099780	NP_001093250	A5LHX3	PSB11_HUMAN		0	TTCGGGAACTG	0.612	
-	17	3675	IN1_uc001wir.3_	NM_014977	NP_055792	Q9UKV3	ACINU_HUMAN	Pro-rich.	4	GCAGGGGCCG	0.662	
-	8	2586	_p.T435I|ACIN1_u	NM_014977	NP_055792	Q9UKV3	ACINU_HUMAN		4	GAGAGGTCTGA	0.493	
-	6	1253	nse_Mutation_p.E	NM_014977	NP_055792	Q9UKV3	ACINU_HUMAN	Glu-rich.	4	TCTCTTCCCCTT	0.373	
-	4	1261	_Mutation_p.A12	NM_005864	NP_005855	O43281	EFS_HUMAN	Pro-rich.	1	GGGCAGCATAG	0.622	
-	28	3936	R208A_hsa-mir-20	NM_002471	NP_002462	P13533	MYH6_HUMAN	Potential.	4	GCCGGGCCAAC	0.582	
+	2	669	e_Mutation_p.G1	NM_001126339	NP_001119811	Q9BU02	THTPA_HUMAN		0	TGACGGCCTGG	0.592	
+	2	263	4L1_uc010tnu.1_	NM_001082488	NP_001075957	P0CG22	DR4L1_HUMAN		0	TGTGTGCCATG	0.652	
+	34	3671	16B_uc001wlk.2_	NM_138360	NP_612369	Q8ND23	LR16B_HUMAN		5	TCGATGGGAAA	0.602	
+	4	617	_uc010tny.1_Trans	NM_001163484	NP_001156956	Q8TEB1	DCA11_HUMAN		0	CACAAGTGGAA	0.582	
+	14	1752	.1_Nonsense_Mut	NM_001163484	NP_001156956	Q8TEB1	DCA11_HUMAN	WD 7.	0	TCAGTTGGCACC	0.562	
-	2	216		NM_016049	NP_057133	Q9Y3B6	F158A_HUMAN		0	GGGCAGCATGC	0.647	
+	7	1271	1_uc010alg.1_Mis	NM_017999	NP_060469	Q96EP0	RNF31_HUMAN	ubiquitin-binding.	2	CCAAGGAACTG	0.587	
+	16	1595	ns.2_Missense_M	NM_005132	NP_005123	O95072	REC8_HUMAN	Glu-rich.	0	AGGAGGAAAGG	0.597	
-	26	2869	_p.P777L|IPO4_uc	NM_024658	NP_078934	Q8TEX9	IPO4_HUMAN	HEAT 5.	1	CCTCGGGGTCT	0.647	
-	21	2232	_p.E565K|IPO4_uc	NM_024658	NP_078934	Q8TEX9	IPO4_HUMAN		1	TACTTCTTCAAA	0.577	
-	11	1137	wmy.1_Missense_	NM_024658	NP_078934	Q8TEX9	IPO4_HUMAN		1	CACAACCTGAG	0.587	
-	2	209	M1_uc010tog.1_5'	NM_000359	NP_000350	P22735	TGM1_HUMAN	e anchorage region.	3	CTCTGGCTCTG	0.637	
-	15	1944	e_Mutation_p.P5	NM_004581	NP_004572	Q92696	PGTA_HUMAN	LRR 3.	0	CCGGGGTAGGT	0.617	
-	2	296	tation_p.E58K|LT	NM_014430	NP_055245	Q9UHD4	CIDEB_HUMAN	CIDE-N.	0	CAGCTCCTGGC	0.592	rs138292688
+	1	2660	_p.G317D|LTB4R2	NM_019839	NP_062813	Q9NPC1	LT4R2_HUMAN	lasmic (Potential).	0	AGGGGGCGGC	0.682	
+	9	3932		NM_025081	NP_079357	Q9P2P1	NYNRI_HUMAN		3	GTCAGGGGGTG	0.622	
-	4	526	e_Mutation_p.G14	NM_004131	NP_004122	P10144	GRAB_HUMAN	eptidase S1.	0	TTTTCCCAGGG	0.557	
-	5	896	_p.T169I|NOVA1_	NM_002515	NP_002506	P51513	NOVA1_HUMAN	KH 2.	5	TTCACAGTAGCA	0.433	
+	9	779	amf.1_Splice_Site	NM_016106	NP_057190	Q8WVM8	SCFD1_HUMAN		0	ATTCAGGTATTA	0.294	
+	16	1423	nf.1_Missense_M	NM_016106	NP_057190	Q8WVM8	SCFD1_HUMAN		0	AGCAAGCACCT	0.343	
-	20	3174	ami.2_Missense_	NM_015473	NP_056288	Q86XA9	HTR5A_HUMAN		1	CGCTGCTCCTA	0.358	
+	3	673	ml.2_Missense_M	NM_004274	NP_004265	Q13023	AKAP6_HUMAN		21	GCAAGGTCTGC	0.512	
+	11	3342		NM_004274	NP_004265	Q13023	AKAP6_HUMAN	Spectrin 2.	21	TCCAGGACACA	0.358	
+	13	6720		NM_004274	NP_004265	Q13023	AKAP6_HUMAN		21	CCAGCGAAGCT	0.458	

+	3	299	e_Mutation_p.P49	NM_173159	NP_071406	Q8IXF0	NPAS3_HUMAN	-loop-helix motif.	2	TTGTTGCCTCTTC	0.478
-	1	444	nse_Mutation_p.G	NM_022073	NP_071356	Q9H6Z9	EGLN3_HUMAN		0	GTCGCCCACCA	0.677
-	3	746	_p.P60S|BAZ1A_u	NM_013448	NP_038476	Q9NRL2	BAZ1A_HUMAN	C1/POLE3 complex.|Requi	7	GTCCAGGTCTAC	0.373
+	4	697	wsq.2_Missense_	NM_001079519	NP_001072987	Q8N128	F177A_HUMAN		0	GCCTGGAGAAG	0.378
-	6	773	_Mutation_p.G128	NM_014990	NP_055805	Q6GYQ0	RGPA1_HUMAN		4	GAACACCTTCCC	0.333
-	2	792	on_p.K181E|NKX2	NM_003317	NP_003308	P43699	NKX21_HUMAN		1	TGTTCTTGCTCA	0.667
+	3	1229	9_uc010amq.2_5'F	NM_006194	NP_006185	P55771	PAX9_HUMAN	ction with KDM5B.	3	GGCCGCCAAGG	0.682
-	7	798		NM_030631	NP_085134	Q9BQT8	ODC_HUMAN	Solcar 2.	1	AGTCCCCAGCCT	0.438
+	24	2653	_p.P744S|CTAGE	NM_005930	NP_005921	O15320	CTGE5_HUMAN	Pro-rich.	0	CCCCACCCCCA	0.463
+	9	3546	e_Mutation_p.G11	NM_015091	NP_055906	Q9Y4F4	F179B_HUMAN	Ser-rich.	3	GTATTTGGAAGT	0.224
+	11	2029	nf.2_Missense_M	NM_020937	NP_065988	Q8IYD8	FANCM_HUMAN		7	ATCACACATGGT	0.393
-	14	3602		NM_018353	NP_060823	Q6P0N0	M18BP_HUMAN		0	TTTATAGAACCTA	0.363
-	14	2613	wi.3_Missense_M	NM_001113498	NP_001106970	Q7Z553	MDGA2_HUMAN	MAM.	6	ATCTGGGTCGT	0.378
-	2	389	j.1_Intron|MGAT2_	NM_001001	NP_000992	Q969Q0	RL36L_HUMAN		0	TATCTCCTCCCA	0.418
-	2	307	1wxp.1_Missense_	NM_024558	NP_078834	Q9H867	MT21D_HUMAN		0	CGGTGACTACAA	0.468
-	23	4087	138_uc001wxn.1_	NM_006939	NP_008870	Q07890	SOS2_HUMAN		2	GGGGAGTTTCT	0.378
-	18	3552	.2_Intron|NIN_uc0	NM_182946	NP_891991	Q8N4C6	NIN_HUMAN		6	TTTGTTCCGCAG	0.448
-	16	2019	se_Mutation_p.V61	NM_182946	NP_891991	Q8N4C6	NIN_HUMAN		6	AATGACCAGCT	0.438
-	2	1660	p.R299C|TRIM9_u	NM_015163	NP_055978	Q9C026	TRIM9_HUMAN	Potential.	3	GTTGCGCAGCT	0.552
+	7	989	zc.2_Missense_M	NM_152330	NP_689543	Q96NE9	FRMD6_HUMAN	FERM.	3	ACTACAGATTGTA	0.388
+	1	493		NM_000956	NP_000947	P43116	PE2R2_HUMAN	Name=2; (Potential).	2	GCTCGGGACCT	0.692
-	3	410		NM_198066	NP_932332	Q96EK6	GNA1_HUMAN	cetyltransferase.	0	AAAAAACCTAGTT	0.338
-	7	1929	_Mutation_p.P567	NM_001160148	NP_001153620	Q8NEL9	DDHD1_HUMAN		2	CATCAGGCAACT	0.368
-	3	665	ao.3_Missense_M	NM_130851	NP_570912	P12644	BMP4_HUMAN		0	GAAGAGCCGAA	0.542
+	12	2145	p.S627F|SAMD4A	NM_015589	NP_056404	Q9UPU9	SMAG1_HUMAN		0	GGACCTCCACCA	0.582
-	4	419	1_uc001xbn.1_Spl	NM_007086	NP_009017	O75717	WDHD1_HUMAN		1	GCCTTACCTAGAT	0.383
-	3	181	D1_uc001xbn.1_5	NM_007086	NP_009017	O75717	WDHD1_HUMAN	WD 1.	1	CATCACCATCACT	0.274
-	7	1031	AA0831_uc001xb	NM_014924	NP_055739	Q6ZNE5	BAKOR_HUMAN		0	ACTTGCCTGTTG	0.368
+	2	236	1_Intron|NAA30_u	NM_001011713	NP_001011713	Q147X3	NAA30_HUMAN	Pro-rich.	1	GCTGTCCCTTC	0.741
-	4	606	e_Mutation_p.Q66	NM_018168	NP_060638	Q9NVL8	CN105_HUMAN		0	GCACTTGCATCTT	0.363
-	1	330	1_5'UTR|C14orf10	NM_018168	NP_060638	Q9NVL8	CN105_HUMAN		0	TAAAGGTGGCA	0.408
+	15	1593	dq.2_Missense_M	NM_002892	NP_002883	P29374	ARI4A_HUMAN		6	GTGAACCTGAG	0.333
+	3	745	1xeq.2_Missense_	NM_022495	NP_071940	Q63HM2	CN135_HUMAN	ical; (Potential).	2	TCATTCCAAGCA	0.333
-	8	706	rf39_uc010apo.2_	NM_174978	NP_777638	Q08AQ4	Q08AQ4_HUMAN		4	TTGCTGGCATGTT	0.244
-	2	963		NM_005982	NP_005973	Q15475	SIX1_HUMAN		0	CGTGGCCCATATT	0.587
+	6	725	AT1_uc001xfe.2_Ir	NM_002431	NP_002422	P51948	MAT1_HUMAN		2	ATAGATCTACCCA	0.368
-	4	1497		NM_020810	NP_065861	Q32P41	TRMT5_HUMAN		3	GAGGCAGGAATC	0.453
-	2	317	2_5'Flank|SLC38A	NM_020810	NP_065861	Q32P41	TRMT5_HUMAN		3	AGAAGGTGGTGA	0.373
+	13	1120	38A6_uc001xfj.1_	NM_153811	NP_722518	Q8IZM9	S38A6_HUMAN	ical; (Potential).	3	AGTTATGCATACT	0.348
+	7	1194	sa.1_Missense_M	NM_006255	NP_006246	P24723	KPCL_HUMAN		6	GTGGGGTAAATG	0.468
-	1	10	B5_uc001xgc.2_5	NM_145171	NP_660154	Q86YW7	GPHB5_HUMAN		1	GGAATGCCAGCT	0.567
+	48	8269	gl.2_Missense_Mu	NM_015180	NP_055995	Q8WXH0	SYNE2_HUMAN	lasmic (Potential).	14	GATTTTCTGTTTT	0.428
+	61	12306	py.2_Missense_M	NM_015180	NP_055995	Q8WXH0	SYNE2_HUMAN	ytoplasmic (Potential).	14	TGTCACCAGACC	0.338
+	102	18637	.R1098H|SYNE2_	NM_015180	NP_055995	Q8WXH0	SYNE2_HUMAN	Cytoplasmic (Potential).	14	GTGGCGCCTGT	0.527
+	12	1567	p.V430M|MTHFD	NM_005956	NP_005947	P11586	C1TC_HUMAN	hydrofolate synthetase.	2	GGCTAGTGCAA	0.463
+	2	1529	hk.3_Missense_M	NM_021979	NP_068814	P54652	HSP72_HUMAN		1	ATTGACGCCAAT	0.547
+	3	231		NM_172365	NP_758953	Q96LQ0	CN050_HUMAN		1	TCTCAGGTTTGC	0.383

+	11	997	xhm.1_Missense_	NM_172365	NP_758953	Q96LQ0	CN050_HUMAN		1	TGATGGCAAAA	0.363
+	16	2308	p.S801N|PLEKHG	NM_015549	NP_056364	A1L390	PKHG3_HUMAN		1	GGACAGCCCTT	0.627
-	29	6265	p.P2071S|SPTB_u	NM_000347	NP_000338	P11277	SPTB1_HUMAN	Spectrin 17.	11	GGTGGGCTTCT	0.592
-	10	1259	s.2_Missense_Mu	NM_000347	NP_000338	P11277	SPTB1_HUMAN	Spectrin 2.	11	ACTCAGCTTCC	0.577
+	18	2928	_p.P649S|GPHN_	NM_001024218	NP_001019389	Q9NQX3	GEPH_HUMAN	denylyltransferase.	2	TGAAACCAGGG	0.338
+	22	3315	_p.V778I|GPHN_	NM_001024218	NP_001019389	Q9NQX3	GEPH_HUMAN	denylyltransferase.	2	TCATGGTCATT	0.488
+	8	1016		NM_152443	NP_689656	Q96NR8	RDH12_HUMAN		1	CCCAGGCGTCG	0.632
-	32	5970	VE26_uc001xkc.	NM_015346	NP_056161	Q68DK2	ZFY26_HUMAN		11	CCCGGTGCAGA	0.627
-	16	2943	YVE26_uc001xkc	NM_015346	NP_056161	Q68DK2	ZFY26_HUMAN		11	CAGAGGTGTTG	0.512
-	6	1094	nse_Mutation_p.A	NM_015346	NP_056161	Q68DK2	ZFY26_HUMAN		11	CCAAGCCTCGG	0.488
+	5	479	_p.V20M|RAD51L1	NM_133509	NP_598193	O15315	RA51B_HUMAN		0	CTGTGGTGTAC	0.358
-	2	954	xki.1_Missense_	NM_004926	NP_004917	Q07352	TISB_HUMAN		1	AGGTGGTCGGG	0.637
+	2	410	p.R106Q|GALNTL	NM_020692	NP_065743	Q8N428	GLTL1_HUMAN	enal (Potential).	2	CATCCGGGACA	0.547
+	1	497		NM_003813	NP_003804	Q9UKJ8	ADA21_HUMAN		2	TGAGACACAAT	0.418
-	3	968	mk.2_Missense_M	NM_033141	NP_149132	P80192	M3K9_HUMAN	rotein kinase.	5	TGGAGGCCCGG	0.552
+	6	1320	_p.A292T|PCNX_	NM_014982	NP_055797	Q96RV3	PCX1_HUMAN		1	CTGTGGCTTTT	0.458
+	14	3730	e_Mutation_p.T98	NM_014982	NP_055797	Q96RV3	PCX1_HUMAN		1	TGCAACCAAGT	0.373
+	34	6748	rf.1_Missense_Mu	NM_014982	NP_055797	Q96RV3	PCX1_HUMAN		1	CCTAGGCACTA	0.507
+	14	4121	xmv.2_Missense_	NM_015556	NP_056371	O43166	SI1L1_HUMAN		4	CAGTGGGAGAT	0.453
+	15	4355	xmv.2_Missense_	NM_015556	NP_056371	O43166	SI1L1_HUMAN	Ser-rich.	4	CCCCAGCCACG	0.587
+	15	4378	xmv.2_Missense_	NM_015556	NP_056371	O43166	SI1L1_HUMAN	Ser-rich.	4	CGCTGGGGGCT	0.572
+	8	1024	ny.3_Nonsense_	NM_004296	NP_004287	P49758	RGS6_HUMAN		3	AAGTGGGAATT	0.403
-	12	2960	_p.P359S|ZFYVE1	NM_021260	NP_067083	Q9HBF4	ZFYV1_HUMAN	YVE-type 2.	1	ACCGGGCTTTT	0.572
-	11	2735	_p.P284S|ZFYVE1	NM_021260	NP_067083	Q9HBF4	ZFYV1_HUMAN		1	CTAGTGGTATGT	0.587
+	14	1752	.G515E|RBM25_	NM_021239	NP_067062	P49756	RBM25_HUMAN	eckle localization.|Glu-rich	4	CAGAGGAAGTG	0.408
+	2	794	COT1_uc010tuc.1	NM_001037161	NP_001032238	Q86TX2	ACOT1_HUMAN		0	CAAGACCATGG	0.498
-	4	2621	n_p.T613I|C14orf	NM_194278	NP_919254	Q6PJG2	CN043_HUMAN		5	CCTTGGTGGG	0.627
-	7	1715		NM_152445	NP_689658				1	TTCCTCCAGTT	0.348
+	4	761		NM_182894	NP_878314	P58304	VSX2_HUMAN	CVC.	1	CGGGGCCATGG	0.637
+	1	424		NM_019589	NP_062535	P49750	YLPM1_HUMAN	Pro-rich.	3	GACTGGCAGCC	0.682
+	14	5936	PM1_uc001xqm.1_	NM_019589	NP_062535	P49750	YLPM1_HUMAN		3	ACAGAGTTAGG	0.398
-	1	971	X2_uc001xqq.1_I	NM_001080408	NP_001073877	Q3B8N5	PROX2_HUMAN		0	GACAGGGTTTG	0.507
+	9	735	_uc010tuw.1_Splic	NM_001933	NP_001924	P36957	ODO2_HUMAN		1	ATCGGGTAAGC	0.517
+	3	426		NM_014239	NP_055054	P49770	EI2BB_HUMAN		1	GACATCCGGAG	0.527
-	19	2514	_p.G6E|NEK9_uc	NM_033116	NP_149107	Q8TD19	NEK9_HUMAN	ch.|Interaction with NEK6.	5	CCATTCCTCGG	0.562
+	3	615		NM_006399	NP_006390	Q16520	BATF_HUMAN		1	TTCCAGCCCTGA	0.697
+	10	1935	vd.1_Missense_M	NM_017791	NP_060261	Q9UPI3	FLVC2_HUMAN		0	CACTGCTGTGT	0.527
+	6	1075	3_uc001xsj.1_3'U	NM_017926	NP_060396	Q9NWQ4	CN118_HUMAN		3	GGAGACCAGCA	0.413
+	4	892	xtc.1_Missense_	NM_033426	NP_219494	Q9C0C6	K1737_HUMAN		0	AGGTGGAAGTC	0.627
-	8	1336		NM_004863	NP_004854	O15270	SPTC2_HUMAN		2	CAGAAGCACCA	0.517
+	2	181	_5'Flank|ALKBH1	NM_031210	NP_112487	Q9GZT3	SLIRP_HUMAN	RRM.	0	ATTTTACCTTTT	0.224
-	11	1072	su.2_Missense_M	NM_012245	NP_036377	Q13573	SNW1_HUMAN		1	ACGTGCCTCCC	0.408
+	9	2116	XN3_uc010asv.1_	NM_004796	NP_004787	Q9Y4C0	NRX3A_HUMAN	otential).|Laminin G-like 5.	10	TGATGGCAATG	0.463
-	3	600	k.1_Nonsense_M	NM_033104	NP_149095	Q8WXE9	STON2_HUMAN		5	CATGTCCAGCA	0.468
-	15	2119	LC_uc010tvy.1_M	NM_000153	NP_000144	P54803	GALC_HUMAN		0	ACCTCCTGTGT	0.373
-	3	727	7_splice|GALC_uc	NM_000153	NP_000144	P54803	GALC_HUMAN		0	TCCTACCTGTT	0.368
-	13	1521	wc.1_Missense_M	NM_007039	NP_008970	Q16825	PTN21_HUMAN		4	TGTGTGCACTG	0.542

+	9	1313	P1_uc001xya.2_N	NM_018319	NP_060789	Q9NUW8	TYDP1_HUMAN		2	GGAGTGGATAGA	0.428
-	4	512	.1_5'UTR|C14orf1	NM_017970	NP_060440	Q9H7Z3	CN102_HUMAN	Potential.	3	AGGTTTCTCCCG	0.478
-	4	509	.1_5'UTR|C14orf1	NM_017970	NP_060440	Q9H7Z3	CN102_HUMAN	Potential.	3	TTTCTCCCGTCA	0.483
-	15	1479	PERB_uc010aub.1	NM_024764	NP_079040	Q9H7T0	CTSRB_HUMAN		5	CATCATGAAAGTT	0.353
-	9	1225	2N_uc010auc.2_In	NM_001128595	NP_001122067	Q8N9U0	TAC2N_HUMAN		1	TTTGAAGGTGGT	0.373
-	9	1357	p.R300K|FBLN5_	NM_006329	NP_006320	Q9UBX5	FBLN5_HUMAN	alcium-binding (Potential).	6	TGGTTCCTGTGC	0.552
-	7	1812	uf.1_Missense_Mu	NM_004239	NP_004230	Q15643	TRIPB_HUMAN	Potential.	13	TCTTTTCCACATT	0.313
-	11	1063	p.D277N|ATXN3_	NM_004993	NP_004984	P54252	ATX3_HUMAN	UIM 3.	0	TAGCATCACCTGT	0.343
+	14	1421	p.G447E|SLC24A	NM_153646	NP_705932	Q8NFF2	NCKX4_HUMAN	ical; (Potential).	3	CACTTGGGATCC	0.468
+	8	2619	q.2_Missense_Mu	NM_024832	NP_079108	Q8TB24	RIN3_HUMAN	VPS9.	3	GGGAGGGTGAG	0.547
+	9	1347	p.E295K|UBR7_u	NM_175748	NP_786924	Q8N806	UBR7_HUMAN		0	CAAGTGGAACTC	0.393
+	23	3196	bs.1_Missense_M	NM_020818	NP_065869	Q9P2D8	UNC79_HUMAN		17	GAGCTCGCTTTG	0.522
+	36	5935	bs.1_Missense_M	NM_020818	NP_065869	Q9P2D8	UNC79_HUMAN		17	CAGATGGGACTT	0.483
-	2	668	_p.P108L|ASB2_	NM_016150	NP_057234	Q96Q27	ASB2_HUMAN	ANK 1.	2	TCAAGGGGTCC	0.597
-	3	1199	p.G324E|DDX24_	NM_020414	NP_065147	Q9GZR7	DDX24_HUMAN	ase ATP-binding.	4	AGATTTCCAGTCT	0.493
+	23	2571		NM_058237	NP_478144	Q6NUP7	PP4R4_HUMAN		4	CTCAGGGTTAG	0.308
-	5	1185	PINA6_uc010auv.2	NM_001756	NP_001747	P08185	CBG_HUMAN		5	AGCCAGCTGTGT	0.522
-	2	270	PINA6_uc010auv.2	NM_001756	NP_001747	P08185	CBG_HUMAN		5	TCAAGGCCACTA	0.537
-	2	94		NM_001080451	NP_001073920	Q86U17	SPA11_HUMAN		1	GGATCCCTGTTC	0.522
-	22	3868	p.P1219L|DICER1	NM_030621	NP_085124	Q9UPY3	DICER_HUMAN		5	GGCTGGGGCTGG	0.423
-	22	3523	.S1104F|DICER1_	NM_030621	NP_085124	Q9UPY3	DICER_HUMAN		5	GCTGAAGAGGAG	0.363
-	2	348	fb.3_Missense_M	NM_001098725	NP_001092195	P56279	TCL1A_HUMAN		1	ATGATAGGCAGC	0.552
-	23	4007		NM_018036	NP_060506	Q96BY7	ATG2B_HUMAN		3	CTCTTACCTGCT	0.274
+	3	225	1yfl.2_Missense_	NM_016472	NP_057556	Q9P0R6	GSKIP_HUMAN		0	TGAAGGAACTG	0.413
+	12	1326		NM_152327	NP_689540	Q96M32	KAD7_HUMAN	nase.|Potential.|Poly-Glu.	1	cgaagaggaagagga	0.403
+	6	677	OLA_uc001yfr.2_M	NM_032632	NP_116021	P51003	PAPOA_HUMAN		0	TACCAGTTATTAA	0.343
-	7	847	_p.T226I|SETD3_	NM_032233	NP_115609	Q86TU7	SETD3_HUMAN	SET.	0	GGATGGGTCTGG	0.423
+	6	768	yhd.2_Nonsense_	NM_207117	NP_997000	Q6Q0C1	S2547_HUMAN	e=5; (Potential).|Solcar 3.	0	GGCCTGGGCTG	0.682
+	23	5013		NM_001376	NP_001367	Q14204	DYHC1_HUMAN	n (By similarity).	10	TTGGGAGAATAT	0.458
+	35	7344	C1H1_uc001ykt.1_	NM_001376	NP_001367	Q14204	DYHC1_HUMAN	2 (By similarity).	10	GATGAGGCACAG	0.612
-	11	2375	1ykv.3_Missense_	NM_005348	NP_005339	P07900	HS90A_HUMAN	|Required for homodimeriz	7	CTTCTTCCATGC	0.403
+	9	2268	e_Mutation_p.G70	NM_014844	NP_055659	O15040	TCPR2_HUMAN		3	ACACAGGTCAGA	0.567
+	12	1794	md.1_Missense_M	NM_145725	NP_663777	Q13114	TRAF3_HUMAN	MATH.	3	CGTGGAGAATAT	0.517
-	36	5213		NM_006035	NP_006026	Q9Y5S2	MRCKB_HUMAN		11	GGTCTGGATCAG	0.532
-	2	505	uc001ynj.1_Misse	NM_004873	NP_004864	Q9UL15	BAG5_HUMAN		2	AATCCGGTGTG	0.453
+	2	240	14orf153_uc010ty	NM_005552	NP_005543	Q07866	KLC1_HUMAN		0	TTCGACCTGTTC	0.368
+	5	558	_Mutation_p.G17	NM_024071	NP_076976	Q9BQ24	ZFY21_HUMAN		0	CTCCTGGAGGTA	0.502
-	7	16304	px.2_Missense_M	NM_138420	NP_612429	Q8IVF2	AHNK2_HUMAN		1	GGAAGGAGAAC	0.468
-	7	10274	px.2_Missense_M	NM_138420	NP_612429	Q8IVF2	AHNK2_HUMAN		1	GGCCAGCTCCC	0.627
-	7	7434	px.2_Missense_M	NM_138420	NP_612429	Q8IVF2	AHNK2_HUMAN		1	GGGGCCATCAC	0.627
-	7	7372	px.2_Missense_Mu	NM_138420	NP_612429	Q8IVF2	AHNK2_HUMAN		1	GGGGCCCTTGA	0.632
-	7	7144	px.2_Missense_Mu	NM_138420	NP_612429	Q8IVF2	AHNK2_HUMAN		1	ACACATCCGCTG	0.587
-	7	4588	px.2_Missense_Mu	NM_138420	NP_612429	Q8IVF2	AHNK2_HUMAN		1	TGCTGTCTTTGG	0.602
-	2	179	qb.2_Missense_M	NM_145701	NP_663747	Q9BXL8	CDCA4_HUMAN		1	TATGAGGACACT	0.572
-	4	340	DT14_uc001yqi.2_	NM_177533	NP_803877	O95848	NUD14_HUMAN	udix hydrolase.	1	GGACCCTGGGA	0.667
+	10	1190	qv.2_Missense_Mu	NM_015197	NP_056012	Q86VP3	PACS2_HUMAN		1	AGCATCCACAGC	0.632
+	1	40	727924_uc001yu	NM_001004719	NP_001004719	Q8NGB6	OR4M2_HUMAN	cellular (Potential).	1	TTTGTTCTCACTG	0.333

+	9	962	_Mutation_p.L278	NM_052903	NP_443135	Q96RT8	GCP5_HUMAN		1	GGTTACTTTCAG	0.274
+	9	1108	_uc001ywv.1_Miss	NM_022807	NP_073718	P63162	RSMN_HUMAN		1	GCTGCGTGGGG	0.448
+	11	1320	_uc001ywv.1_Mis	NM_022807	NP_073718	P63162	RSMN_HUMAN		1	TGACTCCACAG	0.512
-	3	804		NM_024490	NP_077816	O60312	AT10A_HUMAN	lasmic (Potential).	5	TTCTCGCATTCG	0.498
-	16	1772	v.2_Nonsense_Mu	NM_000275	NP_000266	Q04671	P_HUMAN	lasmic (Potential).	5	AGGCGCCAGAC	0.627
-	61	9444		NM_004667	NP_004658	O95714	HERC2_HUMAN	RCC1 8.	13	TGAGGGCTGCG	0.552
-	32	5054		NM_004667	NP_004658	O95714	HERC2_HUMAN		13	CACATCCACTG	0.393
+	3	478	_p.P91S|APBA2_	NM_005503	NP_005494	Q99767	APBA2_HUMAN		0	GCCTCCCTGAG	0.607
+	3	682	p.D159N|APBA2_	NM_005503	NP_005494	Q99767	APBA2_HUMAN		0	GCCAGGACTAC	0.647
-	19	2897	.2_Missense_Mu	NM_003257	NP_003248	Q07157	ZO1_HUMAN		6	TGTAGCACCAT	0.398
-	16	1867	MR10_uc001zfg.1	NM_017762	NP_060232	Q9NXD2	MTMRA_HUMAN	ularin phosphatase.	1	TTAAGGCAGAC	0.403
+	1	805	_p.G28E|ARHGA	NM_014783	NP_055598	Q6P4F7	RHGBA_HUMAN		6	CCGTGGGCAGT	0.507
+	10	957	r.2_Missense_Mu	NM_001036	NP_001027	Q15413	RYR3_HUMAN	c (By similarity).|MIR 4.	10	CCTGGCCTTGA	0.522
+	11	1100	ar.2_Missense_Mu	NM_001036	NP_001027	Q15413	RYR3_HUMAN	c (By similarity).|MIR 5.	10	GAGTTCCAGAA	0.448
+	20	2589	ar.2_Missense_Mu	NM_001036	NP_001027	Q15413	RYR3_HUMAN	ats.|1.|Cytoplasmic (By sim	10	GGGTACCACCC	0.478
+	20	2600	ar.2_Missense_Mu	NM_001036	NP_001027	Q15413	RYR3_HUMAN	ats.|1.|Cytoplasmic (By sim	10	AGTTCCTCTCC	0.453
+	90	13049	r.2_Missense_Mut	NM_001036	NP_001027	Q15413	RYR3_HUMAN		10	TCTAGGCAGCA	0.393
+	3	388	hs.2_Missense_M	NM_016454	NP_057538	Q5J8M3	TMM85_HUMAN		0	GATGGCCTGGC	0.418
-	17	2355	nse_Mutation_p.R	NM_133647	NP_598408	Q9UHW9	S12A6_HUMAN		7	CCCACGGATAC	0.393
+	3	891	p.R274C|C15orf5	NM_175741	NP_786883	Q86Y26	NUT_HUMAN		30	TGCTTCGTTCC	0.557
+	3	915	_p.T282A|C15orf5	NM_175741	NP_786883	Q86Y26	NUT_HUMAN		30	AGCCCACTATG	0.547
+	7	1689	_p.P540S|C15orf5	NM_175741	NP_786883	Q86Y26	NUT_HUMAN		30	CCTCACCTGGG	0.587
+	7	2782	_p.S904F|C15orf5	NM_175741	NP_786883	Q86Y26	NUT_HUMAN		30	CTCCTCCTTGC	0.488
+	3	339	kc.2_Missense_M	NM_001042429	NP_001035894	Q52LJ0	FA98B_HUMAN		1	CAGGAGATATTA	0.308
+	11	1767	_p.A573T|EIF2AK4	NM_001013703	NP_001013725	Q9P2K8	E2AK4_HUMAN		4	CCAGTGCTGCC	0.418
+	14	1846	cl.1_Missense_Mu	NM_001211	NP_001202	O60566	BUB1B_HUMAN		4	TCCTCCTGCAG	0.378
+	15	2073	cl.1_Missense_Mu	NM_001211	NP_001202	O60566	BUB1B_HUMAN		4	CCACTCCTTTT	0.453
+	20	2776		NM_001211	NP_001202	O60566	BUB1B_HUMAN	rotein kinase.	4	ATATTACCCATG	0.368
+	5	940	_p.R167Q|PAK6_u	NM_001128628	NP_001122100	Q9NQU5	PAK6_HUMAN	Linker.	8	CCCACGGGTCC	0.687
+	8	1377		NM_033510	NP_277045	A7MBM2	DISP2_HUMAN		2	ACCAGGTGCCT	0.597
+	8	4282		NM_033510	NP_277045	A7MBM2	DISP2_HUMAN		2	GTCAGGCTATA	0.652
+	1	1089		NM_130468	NP_569735	Q8NCH0	CHSTE_HUMAN	enal (Potential).	0	TTGTGGGCTCC	0.597
+	11	4587	ne.2_Missense_M	NM_170589	NP_733468	Q8NG31	CASC5_HUMAN		5	ACCAACCTCCA	0.328
-	10	1551	p.E252K|EXD1_u	NM_152596	NP_689809	Q8NHP7	EXD1_HUMAN		1	TGTTTTCCACCA	0.388
-	7	733	cv.1_Missense_Mu	NM_152596	NP_689809	Q8NHP7	EXD1_HUMAN		1	CCTGTGTGTCA	0.398
+	8	1199		NM_015138	NP_055953	Q92541	RTF1_HUMAN	Plus3.	2	CAACAGCAAAC	0.448
-	20	2942	P1_uc001zoc.2_5'	NM_015540	NP_056355	Q9BWH6	RPAP1_HUMAN	Leu-rich.	1	TGTGAGGTGTG	0.587
-	8	1068		NM_015540	NP_056355	Q9BWH6	RPAP1_HUMAN		1	CAGAGCTGGGG	0.582
+	9	1446		NM_006293	NP_006284	Q06418	TYRO3_HUMAN	III 2.|Extracellular (Potentia	6	GTCAGCCACTG	0.577
+	8	2783	_p.A898T|MGA_uc	NM_001080541	NP_001074010	Q8IWI9	MGAP_HUMAN		12	GAAAGGCAAAG	0.393
+	8	990	_Mutation_p.T235	NM_001128608	NP_001122080	O60336	MABP1_HUMAN		10	TATTCACTGATGT	0.572
+	12	1003	n_p.A532V|JMJD	NM_001114633	NP_001108105	P0C869	PA24B_HUMAN	PLA2c.	1	TATGGCCACTG	0.587
-	25	5030		NM_016642	NP_057726	Q9NRC6	SPTN5_HUMAN	Spectrin 12.	2	CCTGGCACTGC	0.637
-	17	2069	_p.A162V|PLA2G4	NM_001080490	NP_001073959	Q3MJ16	PA24E_HUMAN	PLA2c.	0	GGTCGGCTTTT	0.607
-	12	1223	zpf.3_Missense_	NM_015497	NP_056312	Q8NBN3	TM87A_HUMAN		1	TCTGGGCCTGC	0.448
-	4	451	bcu.1_Missense_	NM_015497	NP_056312	Q8NBN3	TM87A_HUMAN		1	TTCTGCCTGGA	0.358
-	9	4861	pv.2_Missense_M	NM_022473	NP_071918	Q9H2Y7	ZF106_HUMAN		3	CTGAAGAATTC	0.338

-	2	2526	|ZFP106_uc010ud	NM_022473	NP_071918	Q9H2Y7	ZF106_HUMAN		3	TTAGATCCCTCT(	0.512	
-	2	671	CDAN1_uc010bcx.	NM_138477	NP_612486	Q8IWY9	CDAN1_HUMAN		2	CGGGGGGAACC	0.652	
-	12	1384	dk.1_Missense_Mu	NM_174916	NP_777576	Q8IWV7	UBR1_HUMAN		1	TAATGACAGAGA	0.353	
-	8	955	ik.1_Missense_Mu	NM_174916	NP_777576	Q8IWV7	UBR1_HUMAN		1	AAGTGGATGTT(	0.328	
-	4	529	ik.1_Missense_Mu	NM_174916	NP_777576	Q8IWV7	UBR1_HUMAN	UBR-type.	1	ATGCCTCTGTGT(	0.363	
-	13	2874	_p.P914L|TP53BP	NM_005657	NP_005648	Q12888	TP53B_HUMAN		7	TCTTTAGGCAAA(	0.323	rs2256238
-	28	5204	_p.T936I|STRC_u	NM_153700	NP_714544	Q7RTU9	STRC_HUMAN		0	CACTGGTGAGA	0.567	
+	1	212	on|CATSPER2P1_	NM_005313	NP_005304	P30101	PDIA3_HUMAN		2	GCCTCGCCGCT	0.706	
+	7	918	_p.G237D|PDIA3_	NM_005313	NP_005304	P30101	PDIA3_HUMAN		2	ACAGGGCAAGG	0.358	
-	4	607	tc.1_RNA|SERIN(	NM_001033517	NP_001028689	A6NH21	SERC4_HUMAN	ical; (Potential).	0	AGAAGCTTGTA(	0.493	
+	1	349	C4_uc001ztd.1_5'F	NM_016400	NP_057484	Q9NX55	HYPK_HUMAN		0	GAGTTCCAATCT	0.632	
-	9	1364		NM_005926	NP_005917	P55081	MFAP1_HUMAN		1	CACAAGGTGAG	0.408	
-	32	6122	Duei.1_Nonsense_	NM_025137	NP_079413	Q96JI7	SPTCS_HUMAN	cellular (Potential).	5	GCATCGGTCAG(	0.547	rs147713329
-	3	629	ei.1_Missense_Mu	NM_025137	NP_079413	Q96JI7	SPTCS_HUMAN	cellular (Potential).	5	GTCCACTGCCT(	0.403	
-	5	580	26V|DUOXA2_uc0	NM_014080	NP_054799	Q9NRD8	DUOX2_HUMAN	-like; mediates peroxidase	5	ACTCGGCGGGG	0.662	
+	29	3953	).A1203T|DUOX1_	NM_017434	NP_059130	Q9NRD9	DUOX1_HUMAN	TXNDC11 (By similarity).|F	8	ATCCTGGCCATC.	0.562	
-	8	1029	_p.P302L|MYEF2_	NM_016132	NP_057216	Q9P2K5	MYEF2_HUMAN	RRM 2.	3	TGCATAGGTCTA	0.338	
+	12	1750	_p.L512F|SLC12A	NM_000338	NP_000329	Q13621	S12A1_HUMAN	lasmic (Potential).	2	CCTCCCTTGTC/	0.498	
-	61	7869	N1_uc010beo.1_R	NM_000138	NP_000129	P35555	FBN1_HUMAN	43; calcium-binding.	3	TAAATCCGGGA(	0.423	
-	11	1536		NM_000138	NP_000129	P35555	FBN1_HUMAN	Pro-rich.	3	GTGGGGGAGG/	0.498	
-	26	4856	wz.2_Missense_M	NM_014985	NP_055800	O94986	CE152_HUMAN		2	TATCAGCCTTATG	0.408	
-	18	2321	_p.E763K|CEP152	NM_014985	NP_055800	O94986	CE152_HUMAN	Potential.	2	GTTTTTCTTTGAT	0.353	
-	11	1972	p.P272S|SHC4_u	NM_203349	NP_976224	Q6S5L8	SHC4_HUMAN	CH1.	5	GTGTGGCAAAG/	0.527	
-	14	2070	p.P601S|SECISBI	NM_014701	NP_055516	Q93073	SBP2L_HUMAN		2	ACACAGGTGTCA	0.433	
-	5	640		NM_032802	NP_116191	Q8TCT8	PSL2_HUMAN	lasmic (Potential).	0	TGTTATCTCCTAG	0.363	
+	7	808	p.P260S|AP4E1_u	NM_007347	NP_031373	Q9UPM8	AP4E1_HUMAN		0	AGCTCCCAGTA	0.398	
+	14	1735		NM_007347	NP_031373	Q9UPM8	AP4E1_HUMAN		0	TCTTCTAATACA(	0.358	
-	11	1645	zza.3_Missense_M	NM_031226	NP_112503	P11511	CP19A_HUMAN		3	CACTGTCCTTGC.	0.473	
-	10	1362	p.D371N|CYP19A	NM_031226	NP_112503	P11511	CP19A_HUMAN		3	CAAGTCCACGA(	0.408	
+	9	1295	bb.2_Missense_M	NM_181789	NP_861454	Q6ZMI3	GLDN_HUMAN	otential).|Olfactomedin-like	2	CACGTTGTTTAC/	0.493	
+	8	955	p.A209V|TMOD2_	NM_014548	NP_055363	Q9NZR1	TMOD2_HUMAN		2	ATAAGGCTTTTG(	0.348	
+	10	1255	p.R309K|TMOD2_	NM_014548	NP_055363	Q9NZR1	TMOD2_HUMAN		2	GAAGAGAGTTG/	0.368	
-	33	4179	O5C_uc010uga.1_l	NM_018728	NP_061198	Q9NQX4	MYO5C_HUMAN	Potential.	14	TCTTACCTTTTC(	0.343	
-	25	3283	a.1_RNA|MYO5C_	NM_018728	NP_061198	Q9NQX4	MYO5C_HUMAN	Potential.	14	GCTCCCCCTCC.	0.517	
-	1	1033		NM_004498	NP_004489	Q9UBC0	HNF6_HUMAN	CUT.	0	TCGGTGGTGATA(	0.617	
+	6	3397		NM_001080534	NP_001074003	Q8NB66	UN13C_HUMAN	ol-ester/DAG-type.	7	TGTGGAGTGAAA	0.507	
-	3	1063	adf.1_Missense_M	NM_015617	NP_056432	Q9Y3Y4	PYGO1_HUMAN		2	CAGAAGACGAA	0.473	
-	14	1659	R481K|ZNF280D_	NM_017661	NP_060131	Q6N043	Z280D_HUMAN		3	TGCAGCCTGCAT	0.348	
-	4	540	_p.T140I|ALDH1A	NM_003888	NP_003879	O94788	AL1A2_HUMAN		1	GAATGGTCATC(	0.448	
+	4	417	bge.2_Missense_M	NM_004701	NP_004692	O95067	CCNB2_HUMAN		0	GTAGGGTCCTT(	0.428	
-	2	215	ARG2_uc010bgk.2	NM_024611	NP_078887	Q659A1	NARG2_HUMAN		2	CTTCACTCTAG(	0.473	
-	41	4611	ahb.1_Splice_Site	NM_020821	NP_065872	Q709C8	VP13C_HUMAN		2	GTCTGCCTACAA.	0.313	
-	35	3975	hb.1_Missense_M	NM_020821	NP_065872	Q709C8	VP13C_HUMAN		2	TATAAAGTGTAA(	0.313	
-	29	3054	ahb.1_Missense_M	NM_020821	NP_065872	Q709C8	VP13C_HUMAN		2	TATACTCCACTTT	0.328	
+	8	910		NM_015059	NP_055874	Q9Y4G6	TLN2_HUMAN	FERM.	11	TCAAACTCGCA(	0.512	
+	55	7500	93_splice|TLN2_u	NM_015059	NP_055874	Q9Y4G6	TLN2_HUMAN		11	CTCAGGTTTGT/	0.343	
-	77	14505	C1_uc002amo.2_5	NM_003922	NP_003913	Q15751	HERC1_HUMAN	HECT.	19	CAGCAGTGTTG(	0.438	

-	29	5628		NM_003922	NP_003913	Q15751	HERC1_HUMAN		19	ACTTACCCAGTAC	0.453	
-	10	2321	RC1_uc010uil.1_In	NM_003922	NP_003913	Q15751	HERC1_HUMAN	RCC1 7.	19	TTCCAGCCGAAA	0.413	
-	10	890	_uc010uim.1_Spli	NM_014326	NP_055141	Q9UIK4	DAPK2_HUMAN		2	ACCGGCTGAGA	0.617	
-	8	728	PK2_uc010uim.1_	NM_014326	NP_055141	Q9UIK4	DAPK2_HUMAN	rotein kinase.	2	TTTCCTGCTTCG	0.478	
+	2	883		NM_015042	NP_055857	O15014	ZN609_HUMAN		3	ATGTGGCTCTG	0.517	
+	8	4169		NM_015042	NP_055857	O15014	ZN609_HUMAN		3	GGCTTTCTTCTAC	0.403	
-	8	1399	lice_Site_p.G136_	NM_025049	NP_079325	Q9H611	PIF1_HUMAN		0	GCTCACCTGGC	0.637	
-	6	558	bhb.2_Missense_	NM_001127889	NP_001121361	Q9NZD8	SPG21_HUMAN		0	GCAGGCATCAG	0.318	
+	4	465	aoh.2_Missense_	NM_178859	NP_849190	Q86UW2	OSTB_HUMAN	lasmic (Potential).	0	CATTTGGATGAG	0.478	
-	11	1465	PX_uc010uiu.1_R	NM_006660	NP_006651	O76031	CLPX_HUMAN		0	CGATTCCCCAC	0.453	
-	9	1822	aot.1_Missense_M	NM_020962	NP_066013	Q8TDY8	IGDC4_HUMAN	III 2.|Extracellular (Potentia	3	GTTGGGGCTGG	0.468	
-	2	433		NM_020962	NP_066013	Q8TDY8	IGDC4_HUMAN	1.|Extracellular (Potential).	3	CCCATCCTTGC	0.632	
-	2	352	.V6I|C15orf44_uc	NM_030800	NP_110427	Q96SY0	CO044_HUMAN	VWFA.	1	CATTACCACCA	0.453	
-	20	3157	_p.Q970*|DENND	NM_005848	NP_005839	Q7Z401	MYCPP_HUMAN	localization signal (Potentia	4	CTTCTTGAATGT	0.303	
-	16	2132	p.A589V|MEGF11_	NM_032445	NP_115821	A6BM72	MEG11_HUMAN	EGF-like 11.	1	GCTGGGCACAG	0.607	
+	2	654	ujp.1_Missense_	NM_002755	NP_002746	Q02750	MP2K1_HUMAN		0	GAAGGTGGGAG	0.557	
+	1	401		NM_005902	NP_005893	P84022	SMAD3_HUMAN	MH1.	5	AGGCGGTCAAG	0.597	
+	7	685	lice_Site_p.A40_s	NM_001031715	NP_001026885	Q86VS3	IQCH_HUMAN		4	CCACAGCCACT	0.428	
+	9	1168	1_uc002ara.2_5'	NM_016166	NP_057250	O75925	PIAS1_HUMAN	P-RING-type.	2	GTTTTGACGCA	0.378	
+	2	2152	rh.2_Missense_M	NM_015322	NP_056137	Q9UK73	FEM1B_HUMAN	ANK 7.	0	AATGCACTTGTC	0.483	
+	7	805	_p.S254F|CORO2	NM_006091	NP_006082	Q9UQ03	COR2B_HUMAN	WD 4.	6	ACCTCTCCATGC	0.557	
+	7	822	_p.E260K|CORO2	NM_006091	NP_006082	Q9UQ03	COR2B_HUMAN	WD 5.	6	ATCGAAGAGGAA	0.592	
-	10	1877	E3_uc010bil.1_Mi	NM_005078	NP_005069	Q04726	TLE3_HUMAN	CCN domain.	2	TCATTGGAAACAT	0.527	
+	4	644	D4_uc002atd.1_5'	NM_024817	NP_079093	Q6ZMP0	THSD4_HUMAN	TSP type-1 1.	2	AGAGGCTCCGG	0.582	
+	11	2046	te.2_Missense_Mu	NM_024817	NP_079093	Q6ZMP0	THSD4_HUMAN		2	CTGAGAGTTACT	0.542	
+	14	2577	_p.G473D|THSD4_	NM_024817	NP_079093	Q6ZMP0	THSD4_HUMAN	TSP type-1 4.	2	GGAGGGCTGTG	0.662	
-	33	6483	atk.2_Missense_M	NM_006901	NP_008832	B2RTY4	MYO9A_HUMAN	bol-ester/DAG-type 1.	3	GGTGGCTTTAA	0.378	
-	25	4882	p.G1451E|MYO9A	NM_006901	NP_008832	B2RTY4	MYO9A_HUMAN	Tail.	3	TCTTTTCCTGAG	0.383	rs112823141
-	23	3559	_Nonsense_Mutati	NM_006901	NP_008832	B2RTY4	MYO9A_HUMAN	or regulatory domain.	3	CTGAACCATCGC	0.453	
-	17	2902	p.R430K|MYO9A_	NM_006901	NP_008832	B2RTY4	MYO9A_HUMAN		3	ATAGTCTGCTCT	0.398	
-	2	1293	se_Mutation_p.G	NM_006901	NP_008832	B2RTY4	MYO9A_HUMAN	sin head-like 1.	3	CAGCTCCAAGAA	0.343	
-	2	273	M2_uc002aty.1_M	NM_182471	NP_872271	P14618	KPYM_HUMAN		1	TGAAGGCAGTC	0.542	
-	9	1172	ARP6_uc002aud.	NM_020214	NP_064599	Q2NL67	PARP6_HUMAN		0	GCTGAGGGCAC	0.607	
-	3	567	e_Mutation_p.G1	NM_031284	NP_112574	Q9BRR6	ADPGK_HUMAN	ADPK.	0	GCATTTCCTCCT	0.303	
+	27	4214	p.P1305S|NEO1_	NM_002499	NP_002490	Q92859	NEO1_HUMAN	lasmic (Potential).	1	CCCACCCATTG	0.582	
+	8	1747	276_uc002avw.1_	NM_001024736	NP_001019907	Q5ZPR3	CD276_HUMAN	lasmic (Potential).	1	CTGAGGACCAG	0.527	
+	9	2154	_p.P624S|PML_uc	NM_033238	NP_150241	P29590	PML_HUMAN		5	GCCGCCCTATC	0.602	
-	11	1071	A6_uc002axl.2_M	NM_022369	NP_071764	Q9BX79	STRA6_HUMAN	lasmic (Potential).	1	AAGCACCAGCT	0.602	
-	14	1921	_p.W462*|SEMA7	NM_003612	NP_003603	O75326	SEM7A_HUMAN	-like C2-type.	2	AGCTGCCAGTG	0.662	
+	2	404	_p.P68L|ARID3B_	NM_006465	NP_006456	Q8IVW6	ARI3B_HUMAN		0	TAGGTCCCTTAG	0.562	rs139778598
-	2	330	3_uc002ayv.2_Mi	NM_001099436	NP_001092906	Q6PHR2	ULK3_HUMAN	rotein kinase.	2	GCTGCACAATGT	0.552	
+	2	828	e.2_Missense_Mu	NM_024608	NP_078884	Q96FI4	NEIL1_HUMAN		1	CTGGCCCCCGG	0.687	
-	22	2586	pah.2_Missense_	NM_006715	NP_006706	Q9NTJ4	MA2C1_HUMAN		0	ACAGATCCATCC	0.607	
-	10	6202		NM_001897	NP_001888	Q6UVK1	CSPG4_HUMAN	ntaining.|Neurite growth in	3	TACGGCTGATG	0.612	
-	9	5217		NM_001897	NP_001888	Q6UVK1	CSPG4_HUMAN	ing.|CSPG 12.|Neurite grov	3	TTCTTCCAGAGC	0.642	
+	8	808	34_splice|C15orf2	NM_152335	NP_689548	Q2M3C6	CO027_HUMAN		0	CTTCCAGCCTAC	0.582	
-	8	764	p.G179E|ETFA_uc	NM_000126	NP_000117	P13804	ETFA_HUMAN		0	TTCTCTCCACTC	0.313	

+	5	826	p.G274D|RCN2_u	NM_002902	NP_002893	Q14257	RCN2_HUMAN	ential).|EF-hand 4.	0	AAAATGGTGATG	0.343
+	3	224	on_p.S8F|HMG20A	NM_018200	NP_060670	Q9NP66	HM20A_HUMAN		3	CTAGCTCCACCC	0.418
-	2	1007	cu.1_Missense_M	NM_032808	NP_116197	Q96FE5	LIGO1_HUMAN	ar (Potential).|LRR 10.	2	CGCCCACCAGCT	0.612
-	9	2183	_p.T728I|TBC1D2I	NM_144572	NP_653173	Q9UPU7	TBD2B_HUMAN	ab-GAP TBC.	3	CTGAGGTGGGG	0.542
-	4	526	BG1_uc010umx.1_	NM_015162	NP_055977	Q96GR2	ACBG1_HUMAN		1	CTGTGGGCCTGC	0.662
+	4	424	_Intron|MORF4L1_	NM_206839	NP_996670	Q9UBU8	MO4L1_HUMAN		0	CTGAAGGAGCTC	0.428
+	5	434	fn.1_Missense_Mu	NM_000137	NP_000128	P16930	FAAA_HUMAN		0	CACCTTCCAGCC	0.567
+	25	3732	nn.1_Missense_M	NM_018689	NP_061159	Q8WUJ3	K1199_HUMAN		3	TGAAAGGCTGT	0.502
+	7	754		NM_173528	NP_775799	Q6P656	CO026_HUMAN		0	GAAAGGAGGCT	0.418
+	11	1767	1_Missense_Mutat	NM_172217	NP_757366	Q14005	IL16_HUMAN		4	GTTTGGAAAGG	0.408
+	14	2792	e_Mutation_p.P19	NM_172217	NP_757366	Q14005	IL16_HUMAN		4	CAGACCCAAGA	0.517
+	15	3615	nse_Mutation_p.S	NM_172217	NP_757366	Q14005	IL16_HUMAN	ion with HTLV-1 tax.	4	GTCAGTCCGTTA	0.458
+	19	4259	se_Mutation_p.L12	NM_172217	NP_757366	Q14005	IL16_HUMAN	PDZ 4.	4	AGGGCCTCACA	0.522
-	3	362	RD5_uc002bgn.2_	NM_181900	NP_871629	Q9NSY2	STAR5_HUMAN	START.	1	ACGTCAGTGATG	0.483
+	1	73	1_5'Flank|FAM154	NM_001008226	NP_001008227	Q658L1	F154B_HUMAN		2	GCATGGGAGCC	0.627
+	3	335	se_Mutation_p.A7	NM_001008226	NP_001008227	Q658L1	F154B_HUMAN		2	TAGAGCTTGGG	0.328
-	3	831	jo.2_Missense_Mu	NM_025238	NP_079514	Q9H0C5	BTBD1_HUMAN		2	TTATTGCATCCAT	0.328
+	4	974	592_uc010upb.1_	NM_014630	NP_055445	Q92610	ZN592_HUMAN		6	CTTGGGGAGCC	0.537
+	12	5395	upc.1_Missense_M	NM_020778	NP_065829	Q96L96	ALPK3_HUMAN	type protein kinase.	12	AGGCTCCGACAG	0.552
+	19	2182	on_p.V418I|PDE8A	NM_002605	NP_002596	O60658	PDE8A_HUMAN	ytic (By similarity).	4	GACATGGTCTTAG	0.433
+	7	2253	13_uc002blu.1_Mi	NM_007200	NP_009131	Q12802	AKP13_HUMAN		9	CCACAGCAAGG	0.512
+	7	4123	13_uc002blu.1_Mi	NM_007200	NP_009131	Q12802	AKP13_HUMAN		9	GGAAGCCACGG	0.517
+	11	4818	0bnf.1_Missense_	NM_007200	NP_009131	Q12802	AKP13_HUMAN		9	GCTCTGTCCTAA	0.587
-	2	672		NM_022480	NP_071925	Q9H0H3	ENC2_HUMAN		2	GGCGTCCGAGA	0.607
-	16	2249	_p.G696E|NTRK3_	NM_001012338	NP_001012338	Q16288	NTRK3_HUMAN	Potential).|Protein kinase.	281	AAGTCCCCAATC	0.552
-	5	1659	ik.2_RNA|DET1_u	NM_001144074	NP_001137546	Q7L5Y6	DET1_HUMAN		2	CCCCGCCTGGA	0.517
+	2	549	p.S133F|AEN_uc0	NM_022767	NP_073604	Q8WTP8	AEN_HUMAN	Exonuclease.	0	GCTGTTCCATTG	0.607
+	5	379	Splice_Site|FANCI	NM_001113378	NP_001106849	Q9NVI1	FANCI_HUMAN		2	CTTTTAGGCTCA	0.353
+	13	1282	.1_RNA|FANCI_u	NM_001113378	NP_001106849	Q9NVI1	FANCI_HUMAN		2	AAGAAGGTTCTT	0.418
+	17	2998		NM_152259	NP_689472	Q7Z2Z1	TICRR_HUMAN		7	GTTGAAGAGTCC	0.398
+	20	3614	orf42_uc010upv.1_	NM_152259	NP_689472	Q7Z2Z1	TICRR_HUMAN	Pro-rich.	7	CGCCTGGGTTTT	0.517
+	20	4889	orf42_uc010upv.1_	NM_152259	NP_689472	Q7Z2Z1	TICRR_HUMAN		7	GCCTCTCCCACA	0.607
-	3	911		NM_001150	NP_001141	P15144	AMPN_HUMAN	ular.|Metalloprotease.	4	GGCCACCACCC	0.602
-	5	749	qc.1_Missense_Mu	NM_002168	NP_002159	P48735	IDHP_HUMAN		711	GTTGTACATGCC	0.478
+	8	929		NM_003870	NP_003861	P46940	IQGA1_HUMAN		8	ACAGGGTAAAA	0.299
+	12	1285		NM_003870	NP_003861	P46940	IQGA1_HUMAN		8	CACTGATTAATG	0.507
+	13	2105	NC45A_uc010uqr.	NM_018671	NP_061141	Q9H3U1	UN45A_HUMAN		2	TTGCGGTGGCC	0.592
+	5	1385	2B_uc010uqv.1_M	NM_014848	NP_055663	Q7L1I2	SV2B_HUMAN	lasmic (Potential).	8	ACCCCAGAGAAA	0.458
+	26	3877	o.1_Missense_Mu	NM_001271	NP_001262	O14647	CHD2_HUMAN		2	CTGCTTCTGAGA	0.517
+	37	5481	o.1_Missense_Mut	NM_001271	NP_001262	O14647	CHD2_HUMAN		2	AATGCAGGTAGG	0.443
+	10	2077	on.2_Missense_Mu	NM_000875	NP_000866	P08069	IGF1R_HUMAN	onectin type-III 2.	8	CGACGGCACCA	0.498
+	16	3086	e_Mutation_p.M10	NM_000875	NP_000866	P08069	IGF1R_HUMAN	tein kinase.|Cytoplasmic (P	8	GGGATGGTCTA	0.522
+	6	1976	e_Mutation_p.R61	NM_145728	NP_663780	O15061	SYNEM_HUMAN	Tail.	4	GTTCAGGTTGG	0.537
+	6	4093	.2_Intron|SYNM_u	NM_145728	NP_663780	O15061	SYNEM_HUMAN	d UTRN.|Interaction with T	4	CAGATAGTTTAC	0.562
-	15	2111	2bvx.1_Missense_	NM_139057	NP_620688	Q8TE56	ATS17_HUMAN	Cys-rich.	3	GATGCCGTCAC	0.557
+	6	671	10bpb.2_Intron|uc	NM_000693	NP_000684	P47895	AL1A3_HUMAN		4	GTGTGGAAGCT	0.602
+	10	1715	b.1_RNA|LRRK1_	NM_024652	NP_078928	Q38SD2	LRRK1_HUMAN	LRR 8.	12	GAAGTTCCCCTG	0.428

+	17	2561	b.1_RNA|LRRK1_	NM_024652	NP_078928	Q38SD2	LRRK1_HUMAN	Roc.	12	AGGCCCCAAAC	0.582
+	32	5732	K1_uc010usc.1_	NM_024652	NP_078928	Q38SD2	LRRK1_HUMAN		12	CCAACCCAAAG	0.637
-	11	1131	.3_uc010uub.1_Sp	NM_001077350	NP_001070818	Q12980	NPRL3_HUMAN		1	AGTACCTGCAG	0.597
-	3	592	02cgv.3_Translati	NM_021259	NP_067082	Q9HCN3	TMM8A_HUMAN	ellular (Potential).	3	GGCCACGAACC	0.677
+	10	1846	0uui.1_3'UTR|PIG	NM_148920	NP_683721	Q9BRB3	PIGQ_HUMAN		1	TGCCAGGGTGG	0.632
+	3	236	R90_uc002cih.1_	NM_145294	NP_660337	Q96KV7	WDR90_HUMAN		1	GAGCAGCACCC	0.607
+	24	2960	90_uc002cil.1_R	NM_145294	NP_660337	Q96KV7	WDR90_HUMAN	WD 11.	1	CATCGGCCACT	0.672
+	36	4598	_uc002cio.1_Miss	NM_145294	NP_660337	Q96KV7	WDR90_HUMAN	WD 18.	1	CCGCACGGCCA	0.677
-	11	1220	3_3'UTR|CCDC78	NM_001031737	NP_001026907	A2IDD5	CCD78_HUMAN		1	TCCCCCCTGGG	0.637
+	14	1544	_p.S489F|MSLN_	NM_013404	NP_037536	Q13421	MSLN_HUMAN		1	CGGGTCCGAAT	0.632
+	1	182		NM_001013638	NP_001013660	Q96S07	PRR25_HUMAN		1	AATAAGCCTGG	0.627
-	3	476		NM_207419	NP_997302	P60827	C1QT8_HUMAN		1	TTTGAGGATTT	0.677
+	32	3200	.R1032K|BAIAP3_	NM_003933	NP_003924	O94812	BAIP3_HUMAN	C2 2.	1	CCAGAGGACCC	0.552
+	6	1090	ense_Mutation_p.	NM_015133	NP_055948	Q9UPT6	JIP3_HUMAN		3	CCCAGGAGATG	0.622
+	6	869	|MRPS34_uc002c	NM_001010865	NP_001010865	A4GXA9	EME2_HUMAN		3	GGCCTCTTGGC	0.642
+	8	1300	w.1_Missense_M	NM_001010865	NP_001010865	A4GXA9	EME2_HUMAN		3	CCACAGCCAAC	0.692
+	4	492	UBP2_uc010brx.	NM_012225	NP_036357	Q9Y5Y2	NUBP2_HUMAN		0	CGCCCCCGGG	0.682
-	3	684	_p.V93M|HAGH_	NM_005326	NP_005317	Q16775	GLO2_HUMAN		1	TTTCACCCCGT	0.632
-	11	1139	_p.V341I|C16orf7	NM_152764	NP_689977	Q8N635	CP073_HUMAN		0	TTCGAACTACTTT	0.323
-	9	1096	X1_uc010uvs.1_5'	NM_005061	NP_005052	Q92901	RL3L_HUMAN		0	GGAGGGACTGG	0.552
+	6	937	p.S273F|SLC9A3	NM_001130012	NP_001123484	Q15599	NHRF2_HUMAN		1	CTCGTCCCGAA	0.572
+	7	1100	p.W316*|SLC9A3	NM_001130012	NP_001123484	Q15599	NHRF2_HUMAN		1	GACTGGAACAG	0.662
+	7	771	_Mutation_p.A21	NM_022372	NP_071767	Q9BVC4	LST8_HUMAN	WD 6.	0	TCCCTGCCCAC	0.652
-	7	1346	S1_uc002cpw.2_	NM_080594	NP_542161	Q15287	RNPS1_HUMAN	uclear localization and exc	1	GTGGGGGAGAC	0.582
+	4	1194	346N|TBC1D24_u	NM_020705	NP_065756	Q9ULP9	TBC24_HUMAN		0	ATGAGAGACATC	0.627
+	11	6034	.1_Missense_Mut	NM_016333	NP_057417	Q9UQ35	SRRM2_HUMAN	-rich.|Ser-rich.	4	GGCAGGAAAGT	0.652
+	12	8518		NM_016333	NP_057417	Q9UQ35	SRRM2_HUMAN	Ser-rich.	4	GCCCTCAGGCC	0.373
-	4	389	m.2_Missense_M	NM_007108	NP_009039	Q15370	ELOB_HUMAN		0	TGGCACTGCTT	0.582
-	3	296	2crz.1_Splice_Sit	NM_022119	NP_071402	Q9GZN4	BSSP4_HUMAN	eptidase S1.	1	GAGAACCTGCG	0.612
+	5	1567	2csc.2_Nonsense_	NM_032296	NP_115672	Q4VC44	FWCH1_HUMAN		0	CAACCCAGCCC	0.652
+	3	725	sl.3_Missense_M	NM_152341	NP_689554	Q8N4S7	PAQR4_HUMAN	ical; (Potential).	0	CAGGGGCCCTG	0.672
-	5	811	2cte.3_Missense_	NM_001103175	NP_001096645	A1A5D9	BICR2_HUMAN	Potential.	0	GCGTTCCAGCT	0.736
+	3	263	|MGC3771_uc002	NM_001042428	NP_001035893	O95201	ZN205_HUMAN		0	GGACACTCAGG	0.597
+	1	191		NM_012360	NP_036492	O43749	OR1F1_HUMAN	Name=2; (Potential).	0	CCTCAGCAACC	0.537
-	2	654	2cuk.2_Missense_	NM_003454	NP_003445	P98182	ZN200_HUMAN		0	GCATAGGAACCA	0.552
-	1	1006	r.2_3'UTR|TIGD7_	NM_033208	NP_149985	Q6NT04	TIGD7_HUMAN	H CENPB-type.	0	GGCTCCCGTTG	0.453
+	2	1218	5_splice|ZNF174_	NM_003450	NP_003441	Q15697	ZN174_HUMAN		0	TCCTAGGTGGC	0.483
+	6	806	_Mutation_p.P187	NM_001083601	NP_001077070	Q9H7X0	NAT15_HUMAN		0	ACCCTCCCTGGA	0.537
-	5	763		NM_178844	NP_849172	Q7RTR2	NLRC3_HUMAN		6	GGCGGGGTGCC	0.706
-	30	5161	vw.2_Missense_M	NM_004380	NP_004371	Q92793	CBP_HUMAN	tion with TRERF1.	127	GGGGTCGGGGT	0.632
-	14	2858	vw.2_Missense_	NM_004380	NP_004371	Q92793	CBP_HUMAN		127	GAGTGGGAGCT	0.637
-	4	1226	vw.2_Missense_	NM_004380	NP_004371	Q92793	CBP_HUMAN	ction with SRCAP.	127	CCTGTTGCAATT	0.418
-	11	4161		NM_001116	NP_001107	O60503	ADCY9_HUMAN	lasmic (Potential).	6	GCTCACCTGGA	0.587
+	1	112		NM_032575	NP_115964	Q9BZE0	GLIS2_HUMAN		0	TCCGGGCGGCA	0.677
-	6	986	wo.2_Missense_	NM_020677	NP_065728	Q9HBL8	NMRL1_HUMAN		1	TTGAGTCTCAGG	0.617
+	4	544	ws.3_Missense_	NM_001127206	NP_001120678	P30519	HMOX2_HUMAN		0	AGCAGGTGCAG	0.577
+	13	1430	N1_uc002cxb.2_	NM_001142290	NP_001135762	O60291	MGRN1_HUMAN		2	TCGCGGCTATC	0.662

+	16	1704	RN1_uc002cxb.2_M	NM_001142290	NP_001135762	O60291	MGRN1_HUMAN		2	GGACAGCAGCC	0.662	
-	8	1146	xl.2_Missense_Mu	NM_133450	NP_597707	Q6ZW76	ANKS3_HUMAN		0	GTGGGGCTCTG	0.602	
-	5	786	plice|ANKS3_uc00	NM_133450	NP_597707	Q6ZW76	ANKS3_HUMAN		0	AATCACCTCAC	0.577	
-	5	680	S3_uc002cxl.2_In	NM_133450	NP_597707	Q6ZW76	ANKS3_HUMAN	ANK 3.	0	TCATTTCTAGCTC	0.592	
-	14	1484	YR1_uc002cya.2_	NM_032569	NP_115958	Q49A26	GLYR1_HUMAN		0	CTGGTCCAGGA	0.527	
+	15	3269	_p.S977F|UBN1_u	NM_001079514	NP_001072982	Q9NPG3	UBN1_HUMAN	Ser-rich.	2	AGATTCCAGTG	0.567	
-	22	3766		NM_002705	NP_002696	O60437	PEPL_HUMAN	Potential.	6	TTCCACCTGGG	0.592	
-	21	2608		NM_002705	NP_002696	O60437	PEPL_HUMAN	Spectrin 4.	6	TGCTGCTTCCT	0.493	
+	5	1223	yv.1_Missense_M	NM_018723	NP_061193	Q9NWB1	RFOX1_HUMAN		0	CGGCGGACACG	0.652	
+	12	1094	h.2_Missense_Mu	NM_020686	NP_065737	P80404	GABT_HUMAN		1	TCTTTCGGAAG	0.557	
-	15	1881	j.1_Missense_Mu	NM_003470	NP_003461	Q93009	UBP7_HUMAN		3	GATGGGCTTCC	0.572	
-	3	1012	N2A_uc010uyn.1_	NM_001134407	NP_001127879	Q12879	NMDE1_HUMAN	ellular (Potential).	45	CCGTGGCTTGC	0.498	
+	3	463	IP2_uc010uyp.1_I	NM_024997	NP_079273	Q5U623	MCAF2_HUMAN		0	TGGACTCTAATA	0.348	
+	7	478	_p.M17T|NUBP1_	NM_002484	NP_002475	P53384	NUBP1_HUMAN		2	AGGCATGATCA	0.438	
+	3	344	g.2_Missense_Mu	NM_000246	NP_000237	P33076	C2TA_HUMAN	Glu-rich (acidic).	1	ACACAGACACC	0.552	
+	9	975	g.2_Missense_Mu	NM_000246	NP_000237	P33076	C2TA_HUMAN		1	ATCTCCAGACC	0.617	
+	11	1812	g.2_Missense_Mu	NM_000246	NP_000237	P33076	C2TA_HUMAN	NACHT.	1	CAAGGCCGACG	0.637	
+	11	1309	dan.3_Missense_	NM_015226	NP_056041	Q2KHT3	CL16A_HUMAN		2	CAAGCCCAGCA	0.448	
+	23	2884	16A_uc002dap.2_	NM_015226	NP_056041	Q2KHT3	CL16A_HUMAN		2	CGTGGCCCAGT	0.622	
-	5	461	lbt.2_Missense_M	NM_001130007	NP_001123479	P15170	ERF3A_HUMAN		3	AATAGGCACGA	0.398	
+	8	1511	yz.1_Missense_M	NM_005236	NP_005227	Q92889	XPF_HUMAN		10	AAAACCTGAAG	0.423	
+	9	1894	yz.1_Missense_M	NM_005236	NP_005227	Q92889	XPF_HUMAN	with EME1 and ERCC1.	10	AGGAAGCTTTT	0.398	
+	17	3028	_p.P908L|MKL2_u	NM_014048	NP_054767	Q9ULH7	MKL2_HUMAN		5	ACCACCCCAAG	0.478	
-	14	3009	uzv.1_Missense_	NM_014647	NP_055462	Q9Y4F3	LKAP_HUMAN		0	TGCTGGGTAGG	0.493	
+	3	429	p.R129H|NDE1_u	NM_017668	NP_060138	Q9NXR1	NDE1_HUMAN	AH1B1 (By similarity).|Pote	1	CAAGCGGTATG	0.418	
+	7	951	p.R303K|NDE1_u	NM_017668	NP_060138	Q9NXR1	NDE1_HUMAN		1	GGAGAGACGGC	0.607	
+	5	686	_p.R171C|ABCC1_	NM_004996	NP_004987	P33527	MRP1_HUMAN	Extracellular.	4	TGTTTCGTGAC	0.398	
+	23	3255	l.2_Missense_Mut	NM_004996	NP_004987	P33527	MRP1_HUMAN	ne type-1 2.|Helical; Name	4	TGCAGGGATCG	0.622	
-	3	750		NM_022166	NP_071449	Q86Y38	XYLT1_HUMAN	enal (Potential).	4	CGGCTCTGTCC	0.597	
+	7	1065	p.2_Missense_Mu	NM_024847	NP_079123	Q7Z402	TMC7_HUMAN	lasmic (Potential).	3	TGCCGGCTGGG	0.527	
+	4	603	dfy.2_Missense_M	NM_016524	NP_057608	Q9BSW7	SYT17_HUMAN		1	GGATGGAAGAC	0.582	
+	11	2656	se_Mutation_p.A3	NM_001105248	NP_001098718	Q6UXY8	TMC5_HUMAN	ical; (Potential).	1	TGCAGCCGTTT	0.542	
+	12	986	_p.G74E|C16orf62	NM_020314	NP_064710	Q7Z3J2	CP062_HUMAN		1	CAGAGGGATCG	0.572	rs138304472
+	6	1211	_p.T171I|IQCK_u	NM_153208	NP_694940	Q8N0W5	IQCK_HUMAN		1	TCTGACTGAGT	0.289	
-	5	1261	p.V378M|UMOD_	NM_003361	NP_003352	P07911	UROM_HUMAN	ZP.	2	AGACACCCAGT	0.532	
-	2	132	RI2_uc002dhs.2_M	NM_001142725	NP_001136197	A8K979	ERI2_HUMAN		1	TCACTGGATTTG	0.378	
-	2	359	I2_uc002dht.3_Int	NM_173475	NP_775746	Q8IWE4	DCNL3_HUMAN		2	CATCTCCCGAG	0.577	
-	62	12071	d.1_Missense_Mu	NM_017539	NP_060009	Q8TD57	DYH3_HUMAN		18	GGGCACCTTCT	0.502	
-	38	5504		NM_017539	NP_060009	Q8TD57	DYH3_HUMAN	2 (By similarity).	18	GGTCGGCGGGC	0.567	
-	4	245	p.G121D|ZP2_uc0	NM_003460	NP_003451	Q05996	ZP2_HUMAN	ellular (Potential).	3	CGAGACCAAGA	0.488	
+	2	296	M_uc010bwq.1_I	NM_145865	NP_665872	Q8N8V4	ANS4B_HUMAN	ANK 2.	2	TCCTGGTCAAC	0.517	
+	28	3377	A_uc002dji.2_Miss	NM_144672	NP_653273	Q7RTW8	OTOAN_HUMAN		3	TTTGGCTTGGT	0.517	
-	5	894		NM_173806	NP_776167	Q8IXQ8	PDZD9_HUMAN		1	CTTTACCCTCTT	0.448	
+	2	408		NM_000336	NP_000327	P51168	SCNNB_HUMAN	llular (By similarity).	7	GCTGGGAGGTC	0.607	
+	9	1486		NM_000336	NP_000327	P51168	SCNNB_HUMAN	llular (By similarity).	7	GCAGAGAGAGA	0.607	
-	1	135	lu.2_Missense_M	NM_001083614	NP_001077083	Q5JPH6	SYEM_HUMAN		0	CGCAACCCCGG	0.721	
+	3	654		NM_005030	NP_005021	P53350	PLK1_HUMAN	loop.|Protein kinase.	2	ACCAAAGTCGAA	0.507	

+	12	2505	Site_p.G489_splic	NM_006910	NP_008841	Q7Z6E9	RBBP6_HUMAN		4	CAACTGGTGAGT	0.358
+	15	2955	e_Mutation_p.E63	NM_006910	NP_008841	Q7Z6E9	RBBP6_HUMAN		4	TCCAGGGAAGAA	0.368
+	17	3613	e_Mutation_p.E82	NM_006910	NP_008841	Q7Z6E9	RBBP6_HUMAN		4	ATAGAGAGAACT	0.428
+	17	4746	_Mutation_p.E120	NM_006910	NP_008841	Q7Z6E9	RBBP6_HUMAN		4	AAATTGGAGTCA	0.383
+	6	1607	.G245D|TNRC6A_	NM_014494	NP_055309	Q8NDV7	TNR6A_HUMAN	with EIF2C1, EIF2C3 and	2	CATCAGGTATGA	0.483
+	6	2686	.G605R|TNRC6A_	NM_014494	NP_055309	Q8NDV7	TNR6A_HUMAN	ction with EIF2C1 and EIF	2	ACTGGGGAGAA	0.488
+	11	3766	mn.2_Missense_M	NM_014494	NP_055309	Q8NDV7	TNR6A_HUMAN	ction with EIF2C1 and EIF	2	GACTCACCAGAG	0.338
+	20	4958	nn.2_Missense_Mu	NM_014494	NP_055309	Q8NDV7	TNR6A_HUMAN		2	TCCTGGTGAGC	0.358
+	25	5789	p.S1590F|TNRC6	NM_014494	NP_055309	Q8NDV7	TNR6A_HUMAN	interaction with EIF2C2.	2	CATTCTCCAGCC	0.597
+	2	98		NM_001169	NP_001160	O94778	AQP8_HUMAN	lasmic (Potential).	3	CAGATAGCCATG	0.572
+	5	740		NM_001169	NP_001160	O94778	AQP8_HUMAN	cellular (Potential).	3	CGGTGGTGGCC	0.607
-	5	1251	p.E78K|ZKSCAN	NM_001012981	NP_001012999	Q63HK3	ZKSC2_HUMAN	KRAB.	4	CTGTTCCAACC	0.403
+	1	366		NM_001145545	NP_001139017	Q7Z2V1	TNT_HUMAN		0	GCAGCGGGTAC	0.642
+	6	1044	.D326N|JMJD5_uc	NM_024773	NP_079049	Q8N371	KDM8_HUMAN	JmjC.	3	AGCAGGACATC	0.602
+	9	1324	|IL21R_uc002dos.	NM_181078	NP_851564	Q9HBE5	IL21R_HUMAN	lasmic (Potential).	4	TTACAGTGAGG	0.612
-	16	2747	lou.2_Missense_M	NM_001520	NP_001511	Q12789	TF3C1_HUMAN		5	GAGAGCCCAGC	0.547
+	19	3736		NM_015202	NP_056017	O60303	K0556_HUMAN		8	AGGAGGGCCAG	0.597
+	3	533	Missense_Mutatio	NM_007245	NP_009176	Q8WWM7	ATX2L_HUMAN		2	ATTCCAGAATGC	0.408
+	11	1529	ation_p.A454V|AT	NM_007245	NP_009176	Q8WWM7	ATX2L_HUMAN		2	TGCTGCCCCTG	0.587
+	15	2173	_Missense_Mutati	NM_007245	NP_009176	Q8WWM7	ATX2L_HUMAN		2	AATCCTACAAAG	0.473
-	4	575	ntron|SH2B1_uc00	NM_003321	NP_003312	P49411	EFTU_HUMAN		1	GAGGGGTGCAG	0.537
+	11	2361	_uc002drl.2_Misse	NM_001145795	NP_001139267	Q9NRF2	SH2B1_HUMAN		2	CCCACCCCAGC	0.637
-	5	593	2_uc010byn.2_Mis	NM_024816	NP_079092	Q9H5N1	RABE2_HUMAN	Potential.	3	GGACGTCTCTAG	0.706
+	11	1468	_uc010byo.1_Mis	NM_001770	NP_001761	P15391	CD19_HUMAN	lasmic (Potential).	3	AGCTGACCCAGC	0.572
+	3	885	0bzh.1_5'Flank|M	NM_024516	NP_078792	Q9BTK6	PA1_HUMAN		0	CTCCAGGAAGC	0.493
+	7	758	P_uc010vdz.1_RN	NM_005115	NP_005106	Q14764	MVP_HUMAN	MVP 5.	4	GCAGACAGCCC	0.612
-	13	2491	681N|SEZ6L2_uc	NM_201575	NP_963869	Q6UXD5	SE6L2_HUMAN	xtracellular (Potential).	2	CTGTGTCCCGGC	0.687
+	13	2107	1_Missense_Muta	NM_016151	NP_057235	Q9UL54	TAOK2_HUMAN		1	AGCCGCCTGCA	0.627
+	10	1248	e_Mutation_p.L27	NM_002209	NP_002200	P20701	ITAL_HUMAN	Extracellular (Potential).	10	CTGACCTCAGC	0.607
-	2	742	ation_p.T182I|ZNF	NM_023931	NP_076420	Q9BV97	ZN747_HUMAN		0	CACAGGGTCGGG	0.632
-	3	1214	Mutation_p.S364L	NM_152458	NP_689671	A8K8V0	ZN785_HUMAN		1	GCTCTGAACGC	0.602
+	34	8778	CAP_uc002dzg.1_	NM_006662	NP_006653	Q6ZRS2	SRCAP_HUMAN	Pro-rich.	4	GTCAGGGCCAG	0.662
+	2	525		NM_152288	NP_689501	Q9BRQ5	ORAI3_HUMAN	ical; (Potential).	0	CTGGTGGCTGTG	0.607
+	6	1389	ae.1_Missense_M	NM_014712	NP_055527	O15047	SET1A_HUMAN		3	CGGTGGGCACT	0.627
+	2	5481		NM_014699	NP_055514	O15015	ZN646_HUMAN		2	CAAGCGCCACT	0.652
+	2	503	KDK_uc010cah.2_	NM_005881	NP_005872	O14874	BCKD_HUMAN		2	CGGCAGCGGAG	0.657
-	13	1969	fg.1_Missense_M	NM_173502	NP_775773	Q5K4E3	POLS2_HUMAN	eptidase S1 3.	1	TTGTAGAGCCT	0.592
+	13	1527	_p.T487I|ITGAX_	NM_000887	NP_000878	P20702	ITAX_HUMAN	Extracellular (Potential).	4	GCAGACCCGAG	0.687
+	18	2343	bt.2_Missense_Mu	NM_000887	NP_000878	P20702	ITAX_HUMAN	cellular (Potential).	4	CTCAGAGATACT	0.627
-	3	246	A10P_uc002edi.1_RNA						0	CCAGAGCAGGG	0.632
-	2	227		NM_024745	NP_079021	Q8NEM2	SHCBP_HUMAN		2	TTTTTCCTTCTG	0.333
-	6	805	_p.E57K|VPS35_u	NM_018206	NP_060676	Q96QK1	VPS35_HUMAN		0	AACGTTCCACAT	0.323
+	2	217	02eeg.1_Missens	NM_014321	NP_055136	Q9Y5N6	ORC6_HUMAN		0	GCCTGGACCTT	0.532
-	6	717	gh.1_Splice_Site_	NM_030790	NP_110417	Q8TB96	TIP_HUMAN		2	AACTCACCTGCT	0.328
+	7	744	p.S224N|PHKB_u	NM_000293	NP_000284	Q93100	KPBB_HUMAN		3	TGGCAGCACAG	0.338
-	25	3837	C12_uc002efa.1_	NM_033226	NP_150229	Q96J65	MRP9_HUMAN	C transporter 2.	3	GCCATTCCTAAC	0.418
-	6	3854	gn.1_Missense_Mu	NM_015069	NP_055884	Q2M1K9	ZN423_HUMAN	2H2-type 27.	4	CAACGTGGATTT	0.423

-	5	896	vgn.1_Missense_M	NM_015069	NP_055884	Q2M1K9	ZN423_HUMAN	2H2-type 4.	4	TGCCTCGCACT	0.597	
-	2	314		NM_015069	NP_055884	Q2M1K9	ZN423_HUMAN		4	TGCTCACCCCTC	0.478	
+	4	631	efx.2_Missense_M	NM_182922	NP_891552	Q7Z4Q2	HEAT3_HUMAN		2	TCTATTGAGAAC	0.428	
-	9	1056	ge.1_Missense_Mu	NM_013263	NP_037395	Q9NPI1	BRD7_HUMAN		0	GCCTGGTCAGC	0.413	
+	3	301		NM_033119	NP_149110	Q969G9	NKD1_HUMAN		0	CGTGAGCGCTG	0.682	
+	9	1787	gq.1_Missense_Mu	NM_015247	NP_056062	Q9NQC7	CYLD_HUMAN	RAF2.|Interaction with TRI	28	AGAGTCCACCC	0.507	
+	12	2354	gq.1_Missense_Mu	NM_015247	NP_056062	Q9NQC7	CYLD_HUMAN		28	TTAATCCTCTG	0.333	
-	4	793	p.A203T|TOX3_uc	NM_001080430	NP_001073899	O15405	TOX3_HUMAN		0	AGTGGCTGATT	0.517	
+	38	8358	p.T2717A|CHD9_	NM_025134	NP_079410	Q3L8U1	CHD9_HUMAN		7	TCCTGACAAAG	0.478	
+	2	250	p.G136_splice|IR	NM_005853	NP_005844	P78411	IRX5_HUMAN		0	CCGCAGGGCTC	0.667	
+	43	5249	LRC5_uc002ekq.1	NM_032206	NP_115582	Q86WI3	NLRC5_HUMAN	LRR 22.	7	CCTGGGGGATC	0.677	
+	2	400	eld.2_Missense_M	NM_133368	NP_588609	Q96DX4	RSPRY_HUMAN		1	CATGGGTAATT	0.537	
+	5	536	0vhl.1_Splice_Site	NM_012106	NP_036238	Q9Y2Y0	AR2BP_HUMAN		0	TTTGCAGGCACC	0.463	
-	9	1745		NM_033212	NP_149989	Q96A19	C102A_HUMAN	Potential.	1	GCTGCCTGCGG	0.637	
+	3	360	_p.E91K|CCDC13	NM_032269	NP_115645	Q8IY82	CC135_HUMAN		1	CCAAGGAGGAA	0.572	
+	6	810	p.V241M|CCDC13	NM_032269	NP_115645	Q8IY82	CC135_HUMAN		1	AAAAGGTGCTG	0.547	rs144863089
-	17	2536	se_Mutation_p.G6	NM_005550	NP_005541	Q9BVG8	KIFC3_HUMAN		3	AGGACCCAAGC	0.617	
-	13	1945	FC3_uc002emo.3_	NM_005550	NP_005541	Q9BVG8	KIFC3_HUMAN	inesin-motor.	3	TCCCACCTGAGG	0.652	
-	8	583	p.P173L|CNGB1_	NM_001297	NP_001288	Q14028	CNGB1_HUMAN	Pro-rich.	4	TGGGGGGCTGA	0.632	
-	5	435_436	p.D124S|CNGB1_	NM_001297	NP_001288	Q14028	CNGB1_HUMAN		4	CCGGGTCCTCC	0.644	
-	32	4764	se_Mutation_p.A1	NM_016284	NP_057368	A5YKK6	CNOT1_HUMAN		6	AGCTGCCTGAT	0.463	
-	32	4737	se_Mutation_p.P1	NM_016284	NP_057368	A5YKK6	CNOT1_HUMAN		6	TTGTGGGGAAG	0.423	
-	8	1181	LC38A7_uc010vil.	NM_018231	NP_060701	Q9NVC3	S38A7_HUMAN		1	AGACGGGCACA	0.572	
-	2	251	m.1_Missense_Mu	NM_002080	NP_002071	P00505	AATM_HUMAN		2	TGACTCCCAGA	0.473	
-	12	2518		NM_001796	NP_001787	P55286	CADH8_HUMAN	lasmic (Potential).	9	GCCAGCCACTG	0.512	
-	13	2715	oj.2_3'UTR|CDH11	NM_001797	NP_001788	P55287	CAD11_HUMAN	lasmic (Potential).	14	GGTGGCCGACT	0.493	
-	6	1078	plice_Site_p.G21	NM_001797	NP_001788	P55287	CAD11_HUMAN		14	GATACCTGGAC	0.478	
+	12	2381		NM_001795	NP_001786	P33151	CADH5_HUMAN	ic (Potential).|Ser-rich.	6	CGAGTCCCTCA	0.617	
+	4	626	15L|CMTM1_uc0	NM_181269	NP_851786	Q8IZ96	CKLF1_HUMAN		0	GAGGCCCGCCT	0.642	
-	3	562	qa.2_Missense_M	NM_178818	NP_848933	Q8IZR5	CKLF4_HUMAN	.|Helical; (Potential).	1	TGAGTCCAGTG	0.408	
-	4	402	ense_Mutation_p.	NM_006141	NP_006132	O43237	DC1L2_HUMAN		4	CAGCAGAAACT	0.458	
+	11	913	erd.2_Missense_M	NM_025187	NP_079463	Q9BSU1	CP070_HUMAN		2	AACAAGTTCCAT	0.368	
-	13	2393	_p.S553N|KCTD1	NM_001100915	NP_001094385	Q17RG1	KCD19_HUMAN		1	TGATGCTGTCC	0.617	
-	3	1323	p.A163V|TPPP3_	NM_016140	NP_057224	Q9BW30	TPPP3_HUMAN		1	TGTAGGCGCTC	0.627	
+	13	1786	eti.1_Missense_M	NM_024519	NP_078795	Q6ZS17	FA65A_HUMAN	Pro-rich.	3	CAGGCCCCACT	0.557	
+	13	1916	eti.1_Missense_M	NM_024519	NP_078795	Q6ZS17	FA65A_HUMAN	Pro-rich.	3	AGGCCCTACCC	0.542	
+	19	3543	32_splice|FAM65A	NM_024519	NP_078795	Q6ZS17	FA65A_HUMAN		3	AGAGGGTGAGT	0.647	
+	26	2732	PR_uc010vjr.1_Mi	NM_001013838	NP_001013860	Q6F5E8	LR16C_HUMAN		1	CACGGGGACCT	0.473	
-	4	673	tion_p.G69D|RAN	NM_020850	NP_065901	Q6VN20	RBP10_HUMAN	30.2/SPRY.	1	TGTGGCCATTC	0.577	
+	1	70	4_uc002eut.1_3'	NM_198443	NP_940845	Q496H8	NRN1L_HUMAN		1	ACCACCCCATG	0.706	
-	4	438		NM_002801	NP_002792	P40306	PSB10_HUMAN		0	GCGGGGCTCGC	0.682	
-	2	171		NM_002801	NP_002792	P40306	PSB10_HUMAN		0	GCGTTCCAATG	0.632	
-	17	2315	e_Mutation_p.T72	NM_005072	NP_005063	Q9UP95	S12A4_HUMAN		1	CAATGGTCAGG	0.627	
-	1	2238	2L_uc002evj.2_5'	NM_018380	NP_060850	Q9NUL7	DDX28_HUMAN	case C-terminal.	1	GCTGTCCAGGC	0.562	
+	5	1964	_p.A106V|NFATC	NM_173165	NP_775188	Q12968	NFAC3_HUMAN	RHD.	3	AGATAGCCTCTA	0.383	
-	3	562	SRP2_uc002evq.	NM_024939	NP_079215	Q9H6T0	ESRP2_HUMAN		1	TGTAGGGGCCC	0.607	
-	3	528	SRP2_uc002evq.1	NM_024939	NP_079215	Q9H6T0	ESRP2_HUMAN		1	GTTCACCAGCT	0.607	

+	12	1850	p.T514I|SLC7A6_u	NM_001076785	NP_001070253	Q92536	YLAT2_HUMAN	lasmic (Potential).	1	GGAAAACTGACT	0.473	
-	1	162	IT7_uc002evy.1_5'	NM_032178	NP_115554	Q96CW6	S7A6O_HUMAN		1	GCCGCTCTCTCC	0.637	
+	9	1067	/lg.1_Missense_Mu	NM_019023	NP_061896	Q9NVM4	ANM7_HUMAN		0	GCCATAGCAGGC	0.493	
+	8	1079	_p.R245Q|CIRH1	NM_032830	NP_116219	Q969X6	CIR1A_HUMAN	WD 8.	0	CTCTCCGAAAAA	0.537	
-	3	409		NM_144676	NP_653277	Q8WW62	TMED6_HUMAN	l (Potential).|GOLD.	1	CGAAGTGATTAT	0.413	
+	3	405	e_Mutation_p.P10	NM_030579	NP_085056	O43169	CYB5B_HUMAN		0	CTTAAACCTGAA	0.323	
+	12	4254	_Mutation_p.D940	NM_006599	NP_006590	O94916	NFAT5_HUMAN		0	GTGGGGACAAT	0.403	
+	4	237	_p.P50S|WWP2_u	NM_007014	NP_008945	O00308	WWP2_HUMAN	C2.	6	GGACTCCCCAGT	0.493	rs150059700
+	4	428	_p.T103I|CLEC18	NM_001136214	NP_001129686	A5D8T8	CL18A_HUMAN	SCP.	0	GCGCACCCTGC	0.662	
+	14	2564	PR_uc002eyg.1_M	NM_017990	NP_060460	Q8NCN5	PDPR_HUMAN		1	TGCAGTCCACTG	0.522	
+	9	871	nse_Mutation_p.C1	NM_018332	NP_060802	Q9NUU7	DD19A_HUMAN	ase ATP-binding.	0	GGAACTGCCAGA	0.577	
-	3	2719	eyx.2_Missense_M	NM_006927	NP_008858	Q16842	SIA4B_HUMAN	nenal (Potential).	1	TGGCACTCTCAC	0.597	
+	5	347	JK_uc010cft.2_Nor	NM_145059	NP_659496	Q8N0W3	FUK_HUMAN		1	AGGGTCGAGAC	0.622	
+	8	677	_Mutation_p.A239	NM_145059	NP_659496	Q8N0W3	FUK_HUMAN		1	ACTGAGGCAGAG	0.602	
+	3	341	111B_uc010cfv.1_	NM_012426	NP_036558	Q15393	SF3B3_HUMAN		1	GCCCAGACCCC	0.453	
-	13	1750	C14_uc002ezn.2_	NM_018052	NP_060522	Q08AM6	VAC14_HUMAN		2	GGTGGGCACCT	0.647	
-	86	15115	DIN_uc010cfy.2_R	NM_032821	NP_116210	Q4G0P3	HYDIN_HUMAN		2	TCTCACCCAGG	0.557	
-	64	11070		NM_032821	NP_116210	Q4G0P3	HYDIN_HUMAN		2	CACCTGCCACCA	0.463	
+	2	234	ALB2_uc002fac.3_	NM_001740	NP_001731	P22676	CALB2_HUMAN		0	AAGGCTCTGGCA	0.448	
-	5	725	NF19_uc002fal.1_	NM_006961	NP_008892	P17023	ZNF19_HUMAN	KRAB.	0	AGGCCCCAAGC	0.483	
-	19	2215	bb.2_Missense_M	NM_001128	NP_001119	O43747	AP1G1_HUMAN		2	TCATTTCCTCCC	0.383	
-	15	1783	G1_uc002fbb.2_Mi	NM_001128	NP_001119	O43747	AP1G1_HUMAN		2	ACTGGCCAGAT	0.418	
-	4	554	_p.G18S|ZNF821	NM_017530	NP_060000	O75541	ZN821_HUMAN		1	CATCACCCTCAC	0.453	
+	5	420	V|KIAA0174_uc002fbl.1_Missense_Mutation_p.A33V|K			P53990	IST1_HUMAN	h CHMP1A and CHMP1B.	1	AACTGGCCCAGA	0.542	
-	9	10040	l.2_Missense_Mut	NM_006885	NP_008816	Q15911	ZFHX3_HUMAN		4	CACAGGAGGAA	0.562	
-	9	9585	l.2_Missense_Mut	NM_006885	NP_008816	Q15911	ZFHX3_HUMAN	Homeobox 4.	4	ATAGTGGGTGTC	0.507	
-	7	4505	cl.2_Missense_Mu	NM_006885	NP_008816	Q15911	ZFHX3_HUMAN		4	AGGTGCCACGC	0.587	
-	11	1438	C18B_uc002fcu.2_	NM_001011880	NP_001011880	Q6UXF7	CL18B_HUMAN	C-type lectin.	0	GCCTACCCCATG	0.637	rs149961754
-	6	1044	G1_uc002fcw.3_M	NM_001145667	NP_001139139	Q92896	GSLG1_HUMAN	4.|Extracellular (Potential).	2	CTCTGCCCTCAC	0.299	
-	4	439	ln.2_Missense_Mu	NM_153486	NP_705690	Q86WU2	LDHD_HUMAN	inding PCMH-type.	0	CCACAGAGAAG	0.622	
-	5	1861	b.1_Missense_Mu	NM_014567	NP_055382	P56945	BCAR1_HUMAN	Ser-rich.	8	GGCCACCAGCC	0.682	
-	7	553	fep.1_Missense_	NM_012091	NP_036223	Q9BUB4	ADAT1_HUMAN	A to I editase.	2	ACTCAAGCATCG	0.363	
-	8	1701	MTS18_uc002ffe.1_	NM_199355	NP_955387	Q8TE60	ATS18_HUMAN	eptidase M12B.	18	GGCCAAGTCCTG	0.448	
+	8	1179	.M239V|WWOX_u	NM_016373	NP_057457	Q9NZC7	WWOX_HUMAN	with MAPT (By similarity).	0	AAGTCCATGGTA	0.517	
-	2	181		NM_152342	NP_689555	Q8N8U2	CDYL2_HUMAN	Chromo.	1	GGATAAGATACT	0.478	
-	4	1149	_p.R297H|C16orf4	NM_152337	NP_689550	Q6P387	CP046_HUMAN		0	GGCAGCGCTGC	0.602	
-	45	7310	e_Mutation_p.S23	NM_052892	NP_443124	Q7Z442	PK1L2_HUMAN	.|Interaction with GNAS an	3	TCCCTGCTGCTT	0.547	
-	15	2459	fgj.2_Missense_M	NM_052892	NP_443124	Q7Z442	PK1L2_HUMAN	racellular (Potential).	3	GGTTCAGGGCCA	0.547	
+	1	262	e_Mutation_p.P15	NM_017429	NP_059125	Q9HAY6	BCDO1_HUMAN		0	GGAGCCTGTGA	0.368	
+	9	1530		NM_022041	NP_071324	Q9H2C0	GAN_HUMAN	Kelch 4.	2	TGGAGCGGTGG	0.542	
+	31	3710		NM_002661	NP_002652	P16885	PLCG2_HUMAN		8	GAGATGCGGCC	0.522	
-	3	876		NM_145168	NP_660151	Q8WUS8	D42E1_HUMAN		0	GGGCTGCCCAG	0.572	
+	2	259	e_Mutation_p.D94	NM_001257	NP_001248	P55290	CAD13_HUMAN		1	ATTGAGGACCAG	0.398	
-	4	807	nv.1_Missense_Mu	NM_031463	NP_113651	Q3SXM5	HSDL1_HUMAN		0	TGCAGCAGGAG	0.463	
+	8	1251	nw.1_Missense_M	NM_178452	NP_848547	Q8NEP3	DAAF1_HUMAN		0	GCCCGCCAGTG	0.527	
+	9	1725	nw.1_Missense_M	NM_178452	NP_848547	Q8NEP3	DAAF1_HUMAN		0	CCAGGCTGTGG	0.478	
+	3	506	sense_Mutation_p.	NM_031476	NP_113664	Q9H0B8	CRLD2_HUMAN		0	GCGTGGGCCAG	0.612	

-	8	1209	se_Mutation_p.P32	NM_017740	NP_060210	Q9NXF8	ZDHC7_HUMAN		1	CAAAGGGATTCAT	0.582	
+	7	821	F8_uc010chp.2_Int	NM_002163	NP_002154	Q02556	IRF8_HUMAN		3	GCCGGCCGACG	0.731	
-	7	643	vop.1_Missense_M	NM_001159377	NP_001152849	Q2M296	MTHSD_HUMAN		0	TGATGTCGTGCTC	0.582	
-	3	528	rt_Site|FBXO31_u	NM_024735	NP_079011	Q5XUX0	FBX31_HUMAN		1	CACCACGTTCAC	0.552	
-	10	1184	CHC14_uc002fkb.	NM_015144	NP_055959	Q8WYQ9	ZCH14_HUMAN		2	CGGGCCCGACG	0.662	
-	7	723	e_Mutation_p.E21	NM_000512	NP_000503	P34059	GALNS_HUMAN		2	GGCTTCCTATGC	0.637	
-	9	1249	cjf.2_Intron|PRDM	NM_001098173	NP_001091643	Q9NQW5	PRDM7_HUMAN		1	ACCTCTCCCTGC	0.458	
-	9	1179	cjf.2_Intron|PRDM	NM_001098173	NP_001091643	Q9NQW5	PRDM7_HUMAN		1	TCCCCATACCAGA	0.522	
+	4	956		NM_018146	NP_060616	Q9HC36	RMTL1_HUMAN		1	ACTCGGGTCTATC	0.517	
+	4	965		NM_018146	NP_060616	Q9HC36	RMTL1_HUMAN		1	TATGTGGCTGACA	0.512	rs139632363
-	11	1642	jr.2_Missense_Mu	NM_016532	NP_057616	Q9BT40	INP5K_HUMAN	for ruffle localization.	0	CGCAGACTGTTG	0.383	
-	6	1008	P5K_uc010cjr.2_M	NM_016532	NP_057616	Q9BT40	INP5K_HUMAN	alytic (Potential).	0	GGATTCCCGAAC	0.542	
-	6	689	_p.D29N|PITPNA_	NM_006224	NP_006215	Q00169	PIPNA_HUMAN		1	TTCGATCTGCAAT	0.488	
-	38	6265		NM_006445	NP_006436	Q6P2Q9	PRP8_HUMAN		6	CATCGCCATGCTT	0.567	
+	1	443		NM_012352	NP_036484	Q9Y585	OR1A2_HUMAN	Name=4; (Potential).	2	CTGGGTCTTGGG	0.493	
-	1	958		NM_003554	NP_003545	P47887	OR1E2_HUMAN	lasmic (Potential).	1	GGAAGGGATTTT	0.378	
-	9	2041	n_p.T503I|TRPV1_	NM_080706	NP_542437	Q8NER1	TRPV1_HUMAN	lasmic (Potential).	1	AACAGGGTCTTCA	0.498	
-	20	2567		NM_002208	NP_002199	P38570	ITAE_HUMAN	cellular (Potential).	4	TCTTGCAGGCCT	0.547	
-	18	2885	kk.1_Missense_Mu	NM_015113	NP_055928	O43149	ZZEF1_HUMAN		4	TCGAGCAGCAAC	0.547	
-	20	2954	BP1A_uc002fya.3_	NM_014520	NP_055335	Q9BQG0	MBB1A_HUMAN		2	GCTCACCTGCGC	0.652	
-	15	2035	_Mutation_p.L658	NM_014520	NP_055335	Q9BQG0	MBB1A_HUMAN		2	GCCAACAGGGCC	0.672	
+	2	497	NL2_uc002fye.2_5	NM_001114974	NP_001108446	Q2TAL5	SMTL2_HUMAN		0	GAGTCGGAGATG.	0.592	
-	3	528	O1_uc010vsi.1_3'	NM_182566	NP_872372	Q7Z5L0	VMO1_HUMAN		1	TCCTCGCCGTCTC	0.647	
-	2	124	rf107_uc002fzl.3_3	NM_000080	NP_000071	Q04844	ACHE_HUMAN	cellular (Potential).	0	CGGCTTCCTGGG	0.552	
-	2	347	'Flank|RNF167_uc	NM_003562	NP_003553	Q02978	M2OM_HUMAN	Solcar 1.	0	ATGCCCCTCAGC	0.572	
+	11	1230		NM_006612	NP_006603	O43896	KIF1C_HUMAN		2	TACAGGGACTCTC	0.512	
+	20	2190		NM_006612	NP_006603	O43896	KIF1C_HUMAN		2	AGCCAGTCGACT	0.612	
-	5	1661	_p.P321S|ZNF232_	NM_014519	NP_055334	Q9UNY5	ZN232_HUMAN		2	TATAGGGTTTCTC	0.413	
-	2	423	cle.1_Missense_M	NM_002532	NP_002523	Q99567	NUP88_HUMAN		1	CTAATACCATAAG	0.333	
-	15	2709	0clo.2_Missense_M	NM_014804	NP_055619	Q2KHM9	K0753_HUMAN		0	CCATCTCTTCCAT	0.552	
-	3	1032	2_5'UTR|KIAA075	NM_014804	NP_055619	Q2KHM9	K0753_HUMAN		0	TCAGTTCTTTCTG	0.428	
+	9	1255	uc002gdy.1_Intron	NM_000697	NP_000688	P18054	LOX12_HUMAN	ipoxygenase.	1	CAACACCCGGGC	0.562	
+	1	382		NM_201566	NP_963860	Q7RTY0	MOT13_HUMAN	ical; (Potential).	2	AGTCGGCGCTTG	0.647	
-	4	1365	o.1_Missense_Mu	NM_001365	NP_001356	P78352	DLG4_HUMAN		2	TAGCGGTATTTCT	0.692	
-	5	673		NM_015982	NP_057066	Q9Y2T7	YBOX2_HUMAN	Pro-rich.	0	GCCAGGTCCTGT	0.672	
-	7	1373	e_Mutation_p.G45	NM_032442	NP_115818	Q96JN8	NEUL4_HUMAN	NHR 2.	2	CCTTACCCTGATC	0.552	
+	3	316	_p.P97S|TMEM95	NM_198154	NP_937797	Q3KNT9	TMM95_HUMAN	cellular (Potential).	0	AAGCTCCCTGAG	0.557	
+	2	548		NM_020795	NP_065846	Q8NFZ4	NLGN2_HUMAN	cellular (Potential).	1	AAAAACGTGACC	0.383	
+	3	503	F11_uc010vtw.1_In	NM_175734	NP_783861	Q0P670	CQ074_HUMAN		0	AGCAGCGGCCG	0.393	
+	3	1258	F11_uc010vtw.1_In	NM_175734	NP_783861	Q0P670	CQ074_HUMAN		0	CGCCTGGCGTCC	0.677	
+	4	321	e_Mutation_p.E22	NM_000747	NP_000738	P11230	ACHB_HUMAN	cellular (Potential).	2	CTGCGGAGCAC	0.622	
-	3	948	hd.3_Missense_M	NM_001128833	NP_001122305	Q9P1Z0	ZBTB4_HUMAN		4	GGAGGGGCCGC	0.697	
-	8	993	n_p.R135G|TP53_	NM_001126112	NP_001119584	P04637	P53_HUMAN	K1 (By simil.GRNS(2)|p.G2	22245	TGTTCCGTCCCAC	0.522	rs55832599
+	2	647		NM_001406	NP_001397	Q15768	EFNB3_HUMAN	cellular (Potential).	1	ACCTGGTAGGGC	0.622	
-	3	439	62M|CYB5D1_uc010cnn.1_5'Flank|CYB5D1_uc002gjb.			Q9BRA0	LSMD1_HUMAN		1	TCTGCACCTCAAT	0.562	
+	9	1994		NM_000180	NP_000171	Q02846	GUC2D_HUMAN	e.|Cytoplasmic (Potential).	1	GGACTGGATGTTC	0.617	
+	9	1138	AS_uc010vuv.1_5'U	NM_012393	NP_036525	O15067	PUR4_HUMAN	TP (Potential).	5	ATTCGAGATGTCC	0.587	

-	31	4300	.E1433K|MYH10_	NM_005964	NP_005955	P35580	MYH10_HUMAN	Potential.	2	GGCCTCCGCGT	0.537	
-	1	489		NM_152599	NP_689812	Q8IWD5	MFS6L_HUMAN		1	TCAGGCCGCTG	0.632	
+	5	607		NM_004246	NP_004237	O95838	GLP2R_HUMAN	lasmic (Potential).	3	TTGTTTCTTCGG	0.368	
-	30	4091		NM_003802	NP_003793	Q9UKX3	MYH13_HUMAN	Potential.	6	CGTGCGCCATG	0.527	
-	8	786	uc002gml.1_Intron	NM_002472	NP_002463	P13535	MYH8_HUMAN	osin head-like.	11	GGCCTCCAGTA	0.507	
-	22	2703	uc002gml.1_Intron	NM_005963	NP_005954	P12882	MYH1_HUMAN	Potential.	21	CCTCGGTCTTA	0.423	
-	20	2346	uc002gml.1_Intron	NM_005963	NP_005954	P12882	MYH1_HUMAN	osin head-like.	21	TGGACCCCAGG	0.403	
-	34	5202		NM_002470	NP_002461	P11055	MYH3_HUMAN	Potential.	7	GGAGTCCAGGA	0.647	
+	36	7152	o.2_Missense_Mu	NM_001372	NP_001363	Q9NYC9	DYH9_HUMAN		20	ACATCCCTGCA	0.483	
+	52	10129	o.2_Missense_Mu	NM_001372	NP_001363	Q9NYC9	DYH9_HUMAN		20	TGGAGGACTCG	0.498	
-	4	969	_p.D122N|ZNF18_	NM_144680	NP_653281	P17022	ZNF18_HUMAN	SCAN box.	1	GGGGTCCCCCT	0.522	rs148878294
+	4	755	V2_uc002gpz.2_5'	NM_016113	NP_057197	Q9Y5S1	TRPV2_HUMAN	interaction with SLC50A1	1	AGGACGGAGTC	0.572	
-	6	1012		NM_020787	NP_065838	Q9P2J8	ZN624_HUMAN	2H2-type 2.	2	GTTTTCCCACAT	0.353	
-	14	2207	6_uc010cpn.2_In	NM_144997	NP_659434	Q8NFG4	FLCN_HUMAN		3	GGACCGTGGAC	0.597	
-	1	376		NM_016084	NP_057168	Q9Y272	RASD1_HUMAN	region (By similarity).	0	TGGTAGGCGTG	0.627	
-	5	1054	n_p.G263D|SREB	NM_004176	NP_004167	P36956	SRBP1_HUMAN	Interaction with LMNA (By	1	TTCCGCCACTC	0.632	
-	6	693	_Mutation_p.P134	NM_001082968	NP_001076437	Q6ZVM7	TM1L2_HUMAN		0	ACCTGGGCATG	0.597	
-	7	634	se_Mutation_p.P1	NM_002018	NP_002009	Q13045	FLII_HUMAN	RRFIP1 and LRRFIP2.|LRF	2	CGCTGGGAGCT	0.672	
+	2	288	_p.A26V|SMCR7_	NM_139162	NP_631901	Q96C03	SMCR7_HUMAN	ical; (Potential).	0	CCTGGCCAATG	0.662	
+	3	1226		NM_021012	NP_066292	Q14500	IRK12_HUMAN	me=M2; (By similarity).	4	TCGACTCCTTCA	0.637	
+	6	1156	LK_uc010cri.1_RN	NM_016231	NP_057315	Q9UBE8	NLK_HUMAN	rotein kinase.	3	GGGCAGCCGTC	0.443	
-	2	208	_Mutation_p.V52I|IFT20_uc010wae.1_Missense_Mutat			Q8IY31	IFT20_HUMAN		0	GGTAACCTCTG	0.502	
-	2	429	e_Mutation_p.A11	NM_033198	NP_149975	Q96S52	PIGS_HUMAN	ical; (Potential).	4	GGGCGGCGCGC	0.677	
-	24	3670	2_5'Flank|ALDOC_	NM_006461	NP_006452	Q96R06	SPAG5_HUMAN		1	TCTTAGCTCAGA	0.483	
-	16	3038		NM_014680	NP_055495	Q14667	K0100_HUMAN		4	GGAAGGAGGCA	0.547	
+	7	1405	cq.1_Missense_Mu	NM_004295	NP_004286	Q9BUZ4	TRAF4_HUMAN	MATH.	2	TCTCTGGGCTTT	0.547	
-	8	1870	cry.1_Missense_M	NM_178860	NP_849191	Q53EL9	SEZ6_HUMAN	ar (Potential).|Sushi 2.	2	GGTCGCAGCTG	0.592	
-	2	2048	IP2_uc002hdx.3_I	NM_020772	NP_065823	Q7Z417	NUFP2_HUMAN		4	GAACCCCAGCT	0.388	
-	19	2270	g.1_Missense_Mu	NM_014030	NP_054749	Q9Y2X7	GIT1_HUMAN	N and TGFB1I1 (By similar	0	GGAGGCCATCT	0.612	
-	9	1046	g.1_Missense_Mu	NM_014030	NP_054749	Q9Y2X7	GIT1_HUMAN	milarity).|PTK2-binding (By	0	GAGTTCCTCAA	0.592	
+	19	3656	e_Mutation_p.G96	NM_001304	NP_001295	O75976	CBPD_HUMAN	ntial).|Carboxypeptidase-lik	2	CAAGGGAGTTC	0.353	
-	2	259	orf79_uc010css.2_	NM_018405	NP_060875	Q9NQ92	COPR5_HUMAN		0	CATAGCCTTCT	0.488	
-	1	140		NM_002981	NP_002972	P22362	CCL1_HUMAN		0	TCTTGCTGTCC	0.572	
+	3	773		NM_017559	NP_060029	Q8TC99	FNDC8_HUMAN	onectin type-III.	2	AAGAATCGTCCA	0.532	
-	5	516	.1_5'UTR|NLE1_u	NM_018096	NP_060566	Q9NVX2	NLE1_HUMAN	WD 2.	4	GACCAGGATATA	0.408	
+	20	2774	hjc.2_Missense_M	NM_173167	NP_775259	Q8IWX7	UN45B_HUMAN		6	TGCTGGAGATC	0.552	
-	2	1290		NM_000286	NP_000277	O00623	PEX12_HUMAN	nal matrix (Potential).	0	TCCTGGCTGGT	0.458	
-	2	1241		NM_000286	NP_000277	O00623	PEX12_HUMAN	nal matrix (Potential).	0	GAGCTTGTATAT	0.468	rs61752106
+	3	588		NM_033315	NP_201572	Q96S79	RSLAB_HUMAN	all GTPase-like.	4	GAGTGGGCAGA	0.602	
-	42	5376	_Mutation_p.E172	NM_198836	NP_942133	Q13085	ACACA_HUMAN	oxyltransferase.	2	GAATTTCTTCTG	0.448	
+	3	354	ACA_uc002hnq.2_	NM_173625	NP_775896	Q8N4C9	CQ078_HUMAN		0	TTGCTGCTCCC	0.458	
-	5	1279		NM_001004334	NP_001004334	Q6PRD1	GP179_HUMAN	Name=2; (Potential).	3	AGTTTCCAGCA	0.552	
-	3	495		NM_001008777	NP_001008777	Q5MNV8	FBX47_HUMAN		0	GCTCAAGGTTAT	0.398	
+	1	93	T_uc002hsi.1_5'F	NM_003673	NP_003664	O15273	TELT_HUMAN		0	GGAAGGATCTG	0.617	
-	6	663	ZF3_uc002hsx.2_	NM_012481	NP_036613	Q9UKT9	IKZF3_HUMAN		6	GTAGGGTTTCT	0.502	
-	2	150	RMDL3_uc002htk.	NM_139280	NP_644809	Q8N138	ORML3_HUMAN	lasmic (Potential).	0	TGTGCCCACAT	0.612	
-	16	1824	491V|MED24_uc0	NM_014815	NP_055630	O75448	MED24_HUMAN		1	TCTGGGCCACA	0.647	

-	1	169	39_uc010wfm.1_5	NM_213656	NP_998821	Q6A163	K1C39_HUMAN	Head.	0	CTGGTTGACAGT	0.498	
-	1	208		NM_031957	NP_114163	Q9BYS1	KRA15_HUMAN	-C-[QEPVRC]- [TPIVLE]-[S	0	CAGGTCCCACTG	0.632	
+	1	409		NM_001146041	NP_001139513	Q9BYQ8	KRA49_HUMAN	RQVHIEK]- [SPTR]-[VSTC	0	gctgcaagccccagtg	0.149	
-	1	163		NM_033188	NP_149445	Q9BYR2	KRA45_HUMAN	[GRQVCHIEK]- [SPTR]-[V	0	ACTGGGGCTTG	0.448	
-	1	491		NM_033187	NP_149443	Q9BYR4	KRA43_HUMAN	C-C-[GIKRQVH]-[SPT]- [S	0	CACAGCAGCTG	0.627	
-	7	1186	31_uc010cxn.2_3'	NM_002277	NP_002268	Q15323	K1H1_HUMAN	Tail.	0	TTGCTGCACGCG	0.567	
-	1	159	uc002hwo.1_RNA	NM_003770	NP_003761	O76014	KRT37_HUMAN	Head.	1	CATTGGCCTCTG	0.622	
-	7	1362		NM_002278	NP_002269	Q14532	K1H2_HUMAN	Tail.	0	ACAGTGCGTGGC	0.637	rs139528234
-	6	1148		NM_002278	NP_002269	Q14532	K1H2_HUMAN	Coil 2.|Rod.	0	CTGGGCCTCAA	0.627	
-	6	1430	xu.2_Splice_Site_	NM_006455	NP_006446	Q92791	SC65_HUMAN		0	CACTCACCTCAT	0.607	
-	5	663	X58_uc010wgf.1_	NM_024119	NP_077024	Q96C10	DHX58_HUMAN	ase ATP-binding.	0	TACTGGCTCATG	0.602	
-	1	329	B9_uc002hyy.2_5'	NM_021078	NP_066564	Q92830	KAT2A_HUMAN		2	GCCTTCCTCTGA	0.726	
-	6	801	xx.2_Missense_M	NM_201434	NP_958842	P51148	RAB5C_HUMAN		2	ATGTCTCCATGA	0.527	
-	10	1954		NM_012285	NP_036417	Q9UQ05	KCNH4_HUMAN	lasmic (Potential).	1	GTCAGCTCTCA	0.572	
-	1	150	1_5'UTR|FAM134	NM_178126	NP_835227	Q86VR2	F134C_HUMAN		2	TCGACCCCGAA	0.692	
+	10	1373	_p.V220I|TUBG2_	NM_016437	NP_057521	Q9NRH3	TBG2_HUMAN		1	ACCGGGTCAGC	0.597	
+	18	2992	AP1_uc010wgs.1	NM_003632	NP_003623	P78357	CNTP1_HUMAN	3.|Extracellular (Potential).	8	GACGCCCCTTT	0.468	
+	15	2300	p.P652S|DHX8_u	NM_004941	NP_004932	Q14562	DHX8_HUMAN		4	ACATATCCAGTG	0.443	
-	13	1724	o.1_Missense_Mu	NM_005374	NP_005365	Q14168	MPP2_HUMAN	ylate kinase-like.	0	CGTAGCCCCGC	0.632	
+	1	862		NM_001466	NP_001457	Q14332	FZD2_HUMAN	ellular (Potential).	3	GTTTCGCGCGC	0.597	
-	1	271	e_Mutation_p.A71	NM_002055	NP_002046	P14136	GFAP_HUMAN	Head.	2	CTCTGCCCGCT	0.607	
+	6	1381	PT_uc002ijx.3_Int	NM_016835	NP_058519	P10636	TAU_HUMAN		1	AGAGCCCTCTG	0.632	
+	10	1968	APT_uc002ijt.3_M	NM_016835	NP_058519	P10636	TAU_HUMAN		1	CTCCACCCAAG	0.672	
+	16	1932	kf.1_Splice_Site_	NM_006178	NP_006169	P46459	NSF_HUMAN		1	GCTTGGTGAGT	0.343	
+	12	1711	ill.1_Missense_Mu	NM_152347	NP_689560	Q8IY85	CQ057_HUMAN		3	AGAAGCCAGCT	0.383	
+	5	875	_p.G35E|KPNB1_	NM_002265	NP_002256	Q14974	IMB1_HUMAN	HEAT 2.	3	CCAGGGGATGA	0.388	
+	21	2818	_p.A683T|KPNB1_	NM_002265	NP_002256	Q14974	IMB1_HUMAN		3	GTACAGCATTTG	0.428	
+	3	975		NM_013351	NP_037483	Q9UL17	TBX21_HUMAN	T-box.	0	TGTGACCCAGG	0.587	
-	12	560		NM_016429	NP_057513	Q9P299	COPZ2_HUMAN		0	ATCTGCCTGTAA	0.597	
-	2	1081		NM_002145	NP_002136	P14652	HXB2_HUMAN		0	AGAGGCCTCCGG	0.592	
-	2	1506	_p.S369F|HOXB3	NM_002146	NP_002137	P14651	HXB3_HUMAN		0	AGAGGGAGGGG	0.716	
+	10	1047	_p.A251V|CALCO	NM_005831	NP_005822	Q13137	CACO2_HUMAN	Potential.	1	TAATGCTCTGCA	0.383	
+	8	1167	dbj.2_Missense_M	NM_006546	NP_006537	Q9NZI8	IF2B1_HUMAN	4 and binding to TAU mRN	1	AGGTTCCCCTGA	0.493	
-	2	871	e_Mutation_p.G13	NM_001145365	NP_001138837	Q9Y2D9	ZN652_HUMAN	Glu-rich.	1	AGACACCCTTT	0.428	
-	4	482		NM_000088	NP_000079	P02452	CO1A1_HUMAN		382	CTCGGGGGCCA	0.687	
+	2	243	e_Mutation_p.P63	NM_018346	NP_060816	Q9HA92	RSAD1_HUMAN		0	ACATCCCTCGC	0.632	
+	18	2852	BPAP_uc002iqz.2_	NM_032133	NP_115509	Q8TBZ2	MYBPP_HUMAN		6	CCGTCCCAACA	0.532	
+	9	1904	n_p.A518V|EPN3_	NM_017957	NP_060427	Q9H201	EPN3_HUMAN		1	AGAGGCCCGAG	0.607	
+	20	2775		NM_003786	NP_003777	O15438	MRP3_HUMAN	smic (By similarity).	4	ATGTGGTCCAG	0.562	
-	3	676		NM_052855	NP_443087	Q6AI12	ANR40_HUMAN		0	CTGGGCTGAAT	0.582	
+	2	2076	dbu.2_Missense_M	NM_175575	NP_783165	Q8TEU8	WFKN2_HUMAN	NTR.	3	TCGCAGCGACT	0.627	
-	5	817	n_p.S38L|SPAG9_	NM_001130528	NP_001124000	O60271	JIP4_HUMAN		5	CTAATGATATAG	0.393	
+	2	255	_Missense_Mutati	NM_002512	NP_002503	P22392	NDKB_HUMAN		0	AGAGATGGTGC	0.308	
+	13	1306	cd.1_Missense_M	NM_178509	NP_848604	Q6ZWJ1	STXB4_HUMAN	Potential.	1	GAATGGAAATG	0.433	
+	5	603	R11_uc002ixg.1_	NM_018304	NP_060774	Q96HE9	PRR11_HUMAN	Pro-rich.	2	TCCTCCCACAC	0.423	
-	2	586	RH2_uc002ixs.2_	NM_016077	NP_057161	Q9Y3E5	PTH2_HUMAN		0	GAGAGCCTGGT	0.448	
+	3	383	_p.L41F|RPS6KB	NM_003161	NP_003152	P23443	KS6B1_HUMAN	rotein kinase.	1	AGCTACTTCGG	0.403	

+	11	1119	p.G286D|RPS6KB	NM_003161	NP_003152	P23443	KS6B1_HUMAN	rotein kinase.	1	AGCTGGTCCTG	0.393
+	13	1305	p.S348N|RPS6KB	NM_003161	NP_003152	P23443	KS6B1_HUMAN	kinase C-terminal.	1	TCTCAGTGAAA	0.393
-	2	578	T1_uc010wop.1_	NM_016125	NP_057209	Q5M7Z0	RNFT1_HUMAN	ical; (Potential).	0	TGACGCTCAGA	0.358
+	6	1774	1D_uc010ddm.1_	NM_003620	NP_003611	O15297	PPM1D_HUMAN		1	CAACTCCTGGC	0.393
+	24	2601	3_uc002iyz.3_Mis	NM_001099432	NP_001092902	Q9H6U6	BCAS3_HUMAN		5	CGTGACCCTGC	0.642
+	1	407		NM_203425	NP_982249	Q86X59	CQ082_HUMAN		0	CGCTCCCTGCT	0.736
-	6	849	m.2_Missense_M	NM_020748	NP_065799	Q9H0H0	INT2_HUMAN		3	TGAGAAGGATTC	0.443
+	9	1082	izw.2_Missense_	NM_181725	NP_859076	Q96IZ6	MTL2A_HUMAN		0	CCGAGGAAAGC	0.512
+	7	996	AF7_uc010wpn.1	NM_005828	NP_005819	P61962	DCAF7_HUMAN		1	TGTCGCCAGGT	0.473
-	9	1034		NM_001433	NP_001424	O75460	ERN1_HUMAN		9	ACTTACCACGA	0.483
-	4	720	.1_5'UTR|SMURF	NM_022739	NP_073576	Q9HAU4	SMUF2_HUMAN		4	CACAACCAGTG	0.284
-	7	1979	1P_uc002jev.3_S	NR_024386					0	ACTTACCGGGC	0.557
-	11	5113	_p.L505F|LRRC37	NM_199340	NP_955372	O60309	L37A3_HUMAN	ellular (Potential).	0	ACTGAGAAGCT	0.517
-	2	494	jfh.2_Missense_	NM_004655	NP_004646	Q9Y2T1	AXIN2_HUMAN		2	AGATGCCCGCC	0.607
+	4	991		NM_014405	NP_055220	Q9UBN1	CCG4_HUMAN	lasmic (Potential).	1	CGACCCCTGTG	0.582
+	1	147		NM_000727	NP_000718	Q06432	CCG1_HUMAN	ical; (Potential).	0	TGACAGCCGTG	0.632
+	9	1131	C1_uc002jgb.2_	NM_012417	NP_036549	Q9UKF7	PITC1_HUMAN		1	GCATCCCCCTG	0.537
+	12	1295	_p.T249I|NOL11_	NM_015462	NP_056277	Q9H8H0	NOL11_HUMAN		0	TTCATACTGTCAT	0.413
+	11	5145	.2_Missense_Mut	NM_182641	NP_872579	Q12830	BPTF_HUMAN		4	TTCAAGACCAA	0.423
+	9	1787	b.1_Missense_Mu	NM_014960	NP_055775	Q96EG1	ARSG_HUMAN		1	GAAGTCCAGCC	0.562
-	7	747	o.1_Missense_M	NM_017983	NP_060453	Q5MNZ9	WIPI1_HUMAN	WD 1.	0	TTTGCCCATCA	0.498
+	9	1037	.G286E|PRKAR1	NM_212471	NP_997636	P10644	KAP0_HUMAN	cAMP 2.	12	GCAGGGAGAAC	0.388
-	22	3067	ez.2_Missense_M	NM_080283	NP_525022	Q8IUA7	ABCA9_HUMAN		6	GTATTACATGCTA	0.348
-	39	5393	qs.1_Missense_	NM_080282	NP_525021	Q8WWZ4	ABCAA_HUMAN		4	CCTGAGAGAGG	0.433
+	5	535	p.R83W|MAP2K6_	NM_002758	NP_002749	P52564	MP2K6_HUMAN	rotein kinase.	5	TTCAGCGGATC	0.458
+	11	1546	0dfp.2_RNA|uc00	NM_023036	NP_075462	Q9GZS0	DNAI2_HUMAN		3	TCTCGCCTGGG	0.642
+	3	1243	nse_Mutation_p.G	NM_018653	NP_061123	Q9NQ84	GPC5C_HUMAN	lasmic (Potential).	5	TGATGGGCAGT	0.617
+	1	511	_p.G14D|RAB37_	NM_175738	NP_783865	Q96AX2	RAB37_HUMAN		1	AGCTGGCCCTG	0.597
+	10	1439	wrg.1_Intron|TME	NM_017728	NP_060198	Q8NE00	TM104_HUMAN	ical; (Potential).	0	CACAGGGGCCT	0.667
-	12	2636	RIN2C_uc002jlu.1	NM_000835	NP_000826	Q14957	NMDE3_HUMAN	ical; (Potential).	4	CCAGCCCCATG	0.597
-	6	616	k.1_Missense_Mu	NM_024417	NP_077728	P22570	ADRO_HUMAN		0	TGTGTCACAGC	0.632
+	7	1177		NM_178160	NP_835454	Q7RTS6	OTOP2_HUMAN		4	GAACCCCACGC	0.612
+	3	553	_p.A61T|SLC16A	NM_004695	NP_004686	O15375	MOT6_HUMAN	ical; (Potential).	1	TCACGGCTGTG	0.602
+	4	572	_p.G67E|SLC16A	NM_004695	NP_004686	O15375	MOT6_HUMAN	ical; (Potential).	1	CACAGGGCCCC	0.627
-	2	130	1_5'UTR|GGA3_u	NM_138619	NP_619525	Q9NZ52	GGA3_HUMAN	o ARF1 (in long isoform).	2	CCCTTCCAGCT	0.552
+	15	1938	_p.A595V|LLGL2_	NM_001031803	NP_001026973	Q6P1M3	L2GL2_HUMAN	WD 10.	2	CTTGGCCCTGC	0.657
-	16	2543	_Mutation_p.G7	NM_004259	NP_004250	O94762	RECQ5_HUMAN		3	GGGGTCCCTGA	0.657
+	2	79	n.2_RNA|UNK_uc	NM_001080419	NP_001073888	Q9C0B0	UNK_HUMAN		0	AGCCGGACATA	0.647
-	26	2893	vsk.1_Missense_	NM_199242	NP_954712	Q70J99	UN13D_HUMAN	MHD2.	2	ATGAGCTGCGC	0.652
-	6	1381	pv.2_Missense_M	NM_033452	NP_258411	Q96LD4	TRI47_HUMAN	B30.2/SPRY.	5	CAGCACCCTCT	0.562
-	26	3237	_p.Y979C|FBF1_u	NM_001080542	NP_001074011	Q8TES7	FBF1_HUMAN		0	TCCTCGTACTTC	0.463
-	6	479	se_Mutation_p.A	NM_001080542	NP_001074011	Q8TES7	FBF1_HUMAN		0	GTCTGCCTCTG	0.527
-	19	2664	_p.Q834H|EVPL_u	NM_001988	NP_001979	Q92817	EVPL_HUMAN	Globular 1.	4	AGGGCCTGGGA	0.637
-	17	2016	w.1_Missense_M	NM_001145297	NP_001138769	Q9UPT5	EXOC7_HUMAN		0	GACTCCCGGCT	0.547
-	3	379	n_p.S95N|EXOC7	NM_001145297	NP_001138769	Q9UPT5	EXOC7_HUMAN		0	TGTCACTGGCC	0.522
-	2	637	ense_Mutation_p.	NM_001454	NP_001445	Q92949	FOXJ1_HUMAN	Fork-head.	1	CCGAGGCACTT	0.597
-	17	1867	ense_Mutation_p.	NM_052916	NP_443148	Q96PX1	RN157_HUMAN		1	CGTGGGTGATC	0.438

+	3	519		NM_182565	NP_872371	Q8IYN6	F100B_HUMAN		1	GCCGCCCAACT	0.682	
-	18	5087	8Q|QRICH2_uc01	NM_032134	NP_115510	Q9H0J4	QRIC2_HUMAN		5	GCGGCCTGTGC	0.667	
-	4	2786	_Mutation_p.G79	NM_032134	NP_115510	Q9H0J4	QRIC2_HUMAN		5	CTATACCAGGT	0.488	
-	13	2121	_p.V686I|UBE2O_	NM_022066	NP_071349	Q9C0C9	UBE2O_HUMAN		5	GCTGACGTCCA	0.632	
-	19	2680	e_Mutation_p.S76	NM_024599	NP_078875	Q6PJF5	RHDF2_HUMAN	lasmic (Potential).	0	TGTCGCTGGTG	0.622	
+	4	1242	_p.M214I|TNRC6C	NM_018996	NP_061869	Q9HCJ0	TNR6C_HUMAN	ith argonaute family protei	2	GGTATGGGGGC	0.512	
+	12	1764	38*|TMC8_uc010	NM_152468	NP_689681	Q8IU68	TMC8_HUMAN	enal (Potential).	0	GTTCTGGGCCT	0.637	
-	2	964		NM_003955	NP_003946	O14543	SOCS3_HUMAN	SOCS box.	1	TGGAGGAGAGG	0.632	
-	11	1840	.2_5'Flank|DNAH17_uc002jvs.2_RNA						9	CTCTGGCTTGT	0.562	
-	2	286	H17_uc002jvs.2_RNA						9	CTGCTCCAGAA	0.522	
-	16	2813	_Mutation_p.P44	NM_025090	NP_079366	Q9P275	UBP36_HUMAN		5	CTGTGGGAGGC	0.597	
-	12	1507	wb.1_Nonsense_	NM_025090	NP_079366	Q9P275	UBP36_HUMAN		5	TGGTACCACTG	0.443	
-	4	785	2_Missense_Muta	NM_001159772	NP_001153244	Q8WVQ1	CANT1_HUMAN	enal (Potential).	0	TGACTCTGTGT	0.562	
+	3	591		NM_178543	NP_848638	Q6UWV6	ENPP7_HUMAN		3	ATCTGGTCACA	0.617	
-	5	1619		NM_003655	NP_003646	O00257	CBX4_HUMAN	action with BMI1.	2	CGGCTCCCCGG	0.557	
+	6	891	_p.M288I|CCDC4	NM_017950	NP_060420	Q4G0X9	CCD40_HUMAN		3	CTGATGGTAAG	0.567	
+	6	896	_p.R290K|CCDC4	NM_017950	NP_060420	Q4G0X9	CCD40_HUMAN		3	GGTAAGATTCC	0.562	
+	18	2789	ug.1_Missense_M	NM_020761	NP_065812	Q8N122	RPTOR_HUMAN		6	GGCAGGAGCTG	0.488	
+	23	3537	ug.1_Missense_M	NM_020761	NP_065812	Q8N122	RPTOR_HUMAN		6	AGGCCCCGCTG	0.692	
+	13	1643	.S512N|BAIAP2_	NM_017451	NP_059345	Q9UQB8	BAIP2_HUMAN		0	GAGCAGGTAAG	0.652	
-	7	931	.1_Missense_Mut	NM_014984	NP_055799	Q9UPN4	AZI1_HUMAN		4	CCCCAGTATTG	0.637	
-	3	890		NM_178520	NP_848615	Q8N8V8	TM105_HUMAN	ical; (Potential).	1	CCTCACCACCCC	0.602	
-	3	636	_Mutation_p.A20	NM_001614	NP_001605	P63261	ACTG_HUMAN		2	GCTCGGCCGTG	0.632	rs11549225
+	11	994		NM_004712	NP_004703	O14964	HGS_HUMAN	ith SNX1 (By similarity).	1	CAGCAGCCTGT	0.637	
+	13	1060_1061		NM_004712	NP_004703	O14964	HGS_HUMAN	ith SNX1 (By similarity).	1	CGCACGGTATCT	0.639	
-	7	1161	_5'UTR|P4HB_uc	NM_000918	NP_000909	P07237	PDIA1_HUMAN		0	CTCCTCCTCCA	0.587	
-	5	656		NM_005782	NP_005773	Q86V81	THOC4_HUMAN	a/Arg/Gly-rich.	0	CACCACCAAAA	0.612	
+	3	249	sense_Mutation_p	NM_016476	NP_057560	Q9NYG5	APC11_HUMAN		0	GCGTGGCCACT	0.562	
-	4	627	vd.1_Missense_	NM_006907	NP_008838	P32322	P5CR1_HUMAN		0	GATGACCCTGG	0.642	
+	4	608	se_Mutation_p.A1	NM_004127	NP_004118	Q13098	CSN1_HUMAN		1	CGGGCCCGGG	0.642	
-	3	723	p.D109N|SECTM1	NM_003004	NP_002995	Q8WVN6	SCTM1_HUMAN	ellular (Potential).	0	GGAGTCCCGGG	0.532	
+	7	791	e_Mutation_p.P247L|HEXDC_uc010wvm.1_RNA|HEX			Q8WVB3	HEXDC_HUMAN		2	CTTTCCGCAGC	0.667	
+	8	967	_Mutation_p.V306M|HEXDC_uc010wvm.1_RNA|HEX			Q8WVB3	HEXDC_HUMAN		2	ACTCTGTGCTG	0.687	
+	8	930	_p.E310K|NARF_	NM_012336	NP_036468	Q9UHQ1	NARF_HUMAN		1	TAATGGAGCAA	0.522	
+	1	157	RP_uc010wvr.1_	NM_024619	NP_078895	Q9HA64	KT3K_HUMAN		0	TCAAGGACGAG	0.706	
+	2	679	kgi.2_Missense_	NM_001004431	NP_001004431	Q641Q3	METRL_HUMAN		0	GCTGTCTGGTG	0.657	
+	4	796	kgi.2_Missense_	NM_001004431	NP_001004431	Q641Q3	METRL_HUMAN		0	CTCAGCCATCC	0.647	
+	5	689	p.D234N|CLUL1_	NM_014410	NP_055225	Q15846	CLUL1_HUMAN		2	TGGAGGATGTG	0.388	
-	4	1535	dkj.2_Missense_	NM_022840	NP_073751	Q8N3J2	METL4_HUMAN		2	TCTGTCCCATTA	0.328	
+	4	450		NM_006101	NP_006092	O14777	NDC80_HUMAN	inus of CDCA1.|Nuclear l	1	ACAAAGCATTC	0.358	
+	3	569		NM_032048	NP_114437	Q9BXX0	EMIL2_HUMAN		3	GCCTCGAAACA	0.512	rs147386217
+	4	1709		NM_032048	NP_114437	Q9BXX0	EMIL2_HUMAN		3	GCTCAGTCCCC	0.512	
-	9	1512	lq.2_Missense_M	NM_003803	NP_003794	P52179	MYOM1_HUMAN		5	TCACACCAACT	0.388	
-	1	458	DLGAP1_uc002k	NM_004746	NP_004737	O14490	DLGP1_HUMAN		4	GCTGCGGTGCT	0.677	
-	7	826	dkq.1_Missense_	NM_012307	NP_036439	Q9Y2J2	E41L3_HUMAN	FERM.	5	AATCGCTCCCA	0.527	
+	5	482	_p.P100S|ARHGAP28_uc002kne.2_Missense_Mutatio			B4DXL2	B4DXL2_HUMAN		1	GATCACCGGAG	0.458	
-	62	8939	knl.2_Splice_Site_	NM_005559	NP_005550	P25391	LAMA1_HUMAN		21	AAGACCTAAAA	0.403	

-	58	8491	knl.2_Splice_Site_	NM_005559	NP_005550	P25391	LAMA1_HUMAN		21	TCGTACCGTGT	0.532	
+	13	3066	e_Mutation_p.V93	NM_015210	NP_056025	Q9Y4B5	CC165_HUMAN		0	CAACGTTCGCC	0.532	
+	9	3985	knx.2_Missense_	NM_015208	NP_056023	Q6UB98	ANR12_HUMAN		3	AATGTCCTTTT	0.463	
+	5	771	j.2_Missense_Mu	NM_194434	NP_919415	Q9P0L0	VAPA_HUMAN	lasmic (Potential).	0	ATGGACCTATG	0.373	
+	16	2503	_p.T333I|CEP192_	NM_032142	NP_115518	E9PF99	E9PF99_HUMAN		5	TGATACTTGGG	0.383	rs146445120
+	18	3112	192_uc002kru.2_R	NM_032142	NP_115518	E9PF99	E9PF99_HUMAN		5	TAGAGTCCTTTG	0.522	
+	19	3394	192_uc002kru.2_	NM_032142	NP_115518	E9PF99	E9PF99_HUMAN		5	CATTATCATCTA	0.373	
-	3	824	e_Mutation_p.R13	NM_001098801	NP_001092271	Q96ND0	CR019_HUMAN	DUF1279.	2	TACTGTCTAAAT	0.383	
+	6	860	se_Mutation_p.E2	NM_003799	NP_003790	O43148	MCES_HUMAN		0	TTTCAGGAACTT	0.333	
-	1	810	TEC_uc010xaj.1_	NM_001137671	NP_001131143	B2RU33	POTEC_HUMAN		3	CCCAAGCGCCC	0.597	
+	2	491	D30B_uc010xak.1	NM_001145029	NP_001138501	Q9BXX2	AN30B_HUMAN		2	TGATGGCGAAG	0.423	
-	7	1755		NM_005406	NP_005397	Q13464	ROCK1_HUMAN	rotein kinase.	5	CTACAAGCATTT	0.343	
-	1	1570		NM_172241	NP_758441	Q96RT6	CTGE2_HUMAN		1	AGGGACCATAT	0.413	
-	1	1533		NM_172241	NP_758441	Q96RT6	CTGE2_HUMAN		1	TATTTGGAACAT	0.368	
+	3	1007	ABLES1_uc002ku	NM_001100619	NP_001094089	Q8TDN4	CABL1_HUMAN	th CDK3 (By similarity).	1	GAATGGCAGGT	0.468	
+	10	1791	xas.1_Splice_Site_	NM_003831	NP_003822	O14730	RIOK3_HUMAN		3	TCACAGTTGAT	0.363	
-	20	3272	z.1_Missense_Mu	NM_000271	NP_000262	O15118	NPC1_HUMAN		2	CATGGGCAGGA	0.537	
-	8	1475	p.P202S|NPC1_u	NM_000271	NP_000262	O15118	NPC1_HUMAN		2	GAAAGGCCCAA	0.567	
-	2	390	1_uc010xba.1_In	NM_000271	NP_000262	O15118	NPC1_HUMAN		2	TGTACCTCTTGT	0.428	
+	4	820	kuu.2_Missense_	NM_001135993	NP_001129465	Q8N584	TT39C_HUMAN		1	CGCCCCCTCTA	0.443	
-	4	3069	nse_Mutation_p.S	NM_015461	NP_056276	Q96K83	ZN521_HUMAN	2H2-type 22.	7	TTTCGGAGAAG	0.488	
-	4	1766	nse_Mutation_p.A	NM_015461	NP_056276	Q96K83	ZN521_HUMAN		7	TTTAGCTGCAG	0.443	
-	2	670	p.G645D|KCTD1_	NM_001136205	NP_001129677	Q719H9	KCTD1_HUMAN	BTB.	1	GGCCGCCCACA	0.502	
-	5	1052	n.1_Missense_M	NM_001792	NP_001783	P19022	CADH2_HUMAN	|Extracellular (Potential).	4	GCCCAGTTACA	0.478	
-	11	2097	k.3_Missense_M	NM_024422	NP_077740	Q02487	DSC2_HUMAN	(Potential).|Cadherin 4.	3	AGGACTGTAATA	0.383	
-	5	998	k.3_Missense_Mu	NM_024422	NP_077740	Q02487	DSC2_HUMAN	|Extracellular (Potential).	3	CCGAGGTTCTT	0.373	
+	5	729		NM_001942	NP_001933	Q02413	DSG1_HUMAN		7	TGCAAGTAAGT	0.388	
+	1	119		NM_001944	NP_001935	P32926	DSG3_HUMAN		9	TGGGGCTCTTC	0.483	
+	4	509		NM_000371	NP_000362	P02766	TTHY_HUMAN		1	GCCGCTACACC	0.562	
+	7	1080	xh.2_Missense_M	NM_016271	NP_057355	Q8WVD3	RN138_HUMAN		0	TCAGAGACATC	0.308	
+	7	716	L3_uc002kxq.2_5'	NM_030632	NP_085135	Q9C0F0	ASXL3_HUMAN		3	AATCTCCCACT	0.318	
+	12	5868	q.2_Missense_Mu	NM_030632	NP_085135	Q9C0F0	ASXL3_HUMAN		3	GGCTGCCAGGG	0.522	
+	2	95	e_Mutation_p.L32	NM_001390	NP_001381	Q9Y4J8	DTNA_HUMAN	h MAGEE1 (By similarity).	0	TCCGACTCTCC	0.403	
-	4	983	ys.2_Missense_M	NM_006965	NP_008896	P17028	ZNF24_HUMAN		0	TTTCTCCCCAC	0.428	
+	8	1164	p.E311K|GALNT1	NM_020474	NP_065207	Q10472	GALT1_HUMAN	enal (Potential).	2	TTGCAGAAGTG	0.398	
+	4	711		NM_017947	NP_060417	Q96EN8	MOCOS_HUMAN		1	GCACGCCTGGG	0.562	
+	10	1287	LC14A1_uc002lbh	NM_001146036	NP_001139508	Q13336	UT1_HUMAN	ical; (Potential).	2	TCTTGGAGTCG	0.423	
-	2	1053	lbo.1_Missense_	NM_020964	NP_066015	Q9HCE0	EPG5_HUMAN		0	TTTTGGCAATCA	0.448	
-	4	444	lct.2_Missense_M	NM_032124	NP_115500	Q9H0R4	HDHD2_HUMAN		0	GTATTCCTGGG	0.343	
-	31	4387	ea.2_Missense_M	NM_001080467	NP_001073936	Q9ULV0	MYO5B_HUMAN	Potential.	5	CAGGGCCTCGA	0.607	
-	6	1187		NM_145020	NP_659457	Q96M91	CCD11_HUMAN	Potential.	3	TGTCTTCCTCTA	0.408	
-	15	2199	e_Mutation_p.A48	NM_015846	NP_056671	Q9UIS9	MBD1_HUMAN	TRD.	2	GACTGCTGTAT	0.542	
-	10	2055	nk|MBD1_uc010x	NM_014593	NP_055408	Q9P0U4	CXXC1_HUMAN	Potential.	2	GAGTGCGGGCA	0.602	
-	8	1671	p.S313F|CXXC1_	NM_014593	NP_055408	Q9P0U4	CXXC1_HUMAN	Glu-rich (acidic).	2	ATGGGGACTCT	0.483	
+	2	1095	APK4_uc010doz.	NM_002747	NP_002738	P31152	MK04_HUMAN	se.|ATP (By similarity).	6	TCAATGGTTTGG	0.612	
+	4	1781	se_Mutation_p.P5	NM_002747	NP_002738	P31152	MK04_HUMAN	rotein kinase.	6	GTGATGCCTTCC	0.597	
-	6	836	O_uc010dpb.2_In	NM_031939	NP_114145	Q9BYG7	MSTRO_HUMAN		0	GGAGGGAATCT	0.463	

+	7	1755	_p.V238M|DCC_uc	NM_005215	NP_005206	P43146	DCC_HUMAN	otential).|Ig-like C2-type 4.	17	TTGGGGTGGTG	0.428
+	27	4576	of.1_Missense_Mu	NM_005215	NP_005206	P43146	DCC_HUMAN	lasmic (Potential).	17	GCAGAACCATCC	0.537
+	3	451	lfo.3_Missense_M	NM_173529	NP_775800	Q8IYD9	CR054_HUMAN		2	GTAGAAGACACA	0.338
-	4	815	4_uc010xdy.1_Mis	NM_003199	NP_003190	P15884	ITF2_HUMAN	OD1 inhibition (By similarity	2	CCCTGGACGGG	0.383
-	6	979	2lgi.2_Missense_	NM_004786	NP_004777	O43396	TXNL1_HUMAN	PITH.	0	CAGTTACACTGT	0.333
+	12	1718	DR7_uc002lgl.1_	NM_015285	NP_056100	Q9Y4E6	WDR7_HUMAN	WD 6.	3	CTGGAGAAATG	0.353
+	14	2200	te|WDR7_uc002lg	NM_015285	NP_056100	Q9Y4E6	WDR7_HUMAN		3	GACAAGGTAAGT	0.393
+	19	3318	DR7_uc002lgl.1_M	NM_015285	NP_056100	Q9Y4E6	WDR7_HUMAN		3	AACTGAGAAGAA	0.493
-	2	275	RS_uc010xeb.1_R	NM_004539	NP_004530	O43776	SYNC_HUMAN		0	CCGTGGCATCG	0.413
-	5	3507	k.1_Missense_Mu	NM_052947	NP_443179	Q86TB3	ALPK2_HUMAN		14	GGGAATTACTG	0.493
-	5	2555	k.1_Missense_Mu	NM_052947	NP_443179	Q86TB3	ALPK2_HUMAN		14	TGTGGGTTCAG	0.537
-	4	1139		NM_052947	NP_443179	Q86TB3	ALPK2_HUMAN		14	AAAGTTCATAGT	0.478
+	4	674	n_p.Q41*|ZNF532	NM_018181	NP_060651	Q9HCE3	ZN532_HUMAN		2	ATGAAGCAGAAT	0.493
+	4	2019	_p.S489N|ZNF532	NM_018181	NP_060651	Q9HCE3	ZN532_HUMAN		2	CCAGCAGCGCC	0.547
+	6	3149	_p.V866I|ZNF532	NM_018181	NP_060651	Q9HCE3	ZN532_HUMAN		2	TGTGAAGTCTTC	0.453
-	1	217	ek.1_Missense_M	NM_005570	NP_005561	P49257	LMAN1_HUMAN	tential).|L-type lectin-like.	1	ACGGTCCCGTCG	0.687
-	5	582		NM_133459	NP_597716	Q6UXH8	CCBE1_HUMAN	lcium-binding (Potential).	3	GTCTTCCCATCA	0.453
-	1	1281		NM_005912	NP_005903	P32245	MC4R_HUMAN	Name=7; (Potential).	1	GTATGAGATACA	0.408
+	3	560	lif.2_Missense_Mu	NM_031891	NP_114097	Q9HBT6	CAD20_HUMAN	(Potential).|Cadherin 2.	5	GTACCTCCGTCA	0.498
+	8	1508	.2_RNA|ZCCHC2_	NM_017742	NP_060212	Q9C0B9	ZCHC2_HUMAN		2	AGCATGCCATAA	0.318
+	3	376	e_Mutation_p.A70	NM_012397	NP_036529	Q9UIV8	SPB13_HUMAN		1	ATAAAGGCTGAA	0.408
+	7	929	_p.G263D|SERPIN	NM_012397	NP_036529	Q9UIV8	SPB13_HUMAN		1	CGATGGCCTGG	0.468
+	9	1716	p.G464E|CDH7_u	NM_033646	NP_387450	Q9ULB5	CADH7_HUMAN	(Potential).|Cadherin 4.	4	AGTAGGAAGAG	0.413
-	12	2120	.1_RNA|CDH19_u	NM_021153	NP_066976	Q9H159	CAD19_HUMAN	lasmic (Potential).	2	GTACTACTCCTC	0.468
-	2	1766		NM_032160	NP_115536	Q8IZU8	DSEL_HUMAN		6	GAATGGCCAATT	0.373
-	12	952	ez.1_Missense_Mu	NM_019022	NP_061895	Q96JJ7	TMX3_HUMAN	nenal (Potential).	1	TTGCAACTTCCT	0.308
-	2	349	lky.1_Missense_M	NM_138966	NP_620416	Q8TDF5	NETO1_HUMAN		4	TGGTTGCCCCA	0.328
+	1	314	dqu.1_Missense_	NM_017757	NP_060227	Q9C0G0	ZN407_HUMAN		2	TTAAATCTGGAA	0.408
+	4	4980	qu.1_Nonsense_M	NM_017757	NP_060227	Q9C0G0	ZN407_HUMAN	2H2-type 17.	2	GAAGTGGGCCCT	0.468
+	18	3206	236_uc002lmj.2_	NM_007345	NP_031371	Q9UL36	ZN236_HUMAN	2H2-type 19.	4	GACGCGGCTTTG	0.478
+	2	1544	ra.2_Missense_Mu	NM_171999	NP_741996	Q9BXA9	SALL3_HUMAN		4	GGACAGCAAGC	0.711
+	3	586		NM_014913	NP_055728	Q6IQ32	ADNP2_HUMAN		8	ATCCAGGAGAGA	0.318
-	5	712	_p.A226T|PPAP2C	NM_003712	NP_003703	O43688	LPP2_HUMAN	ical; (Potential).	1	CAAAGGCCACCA	0.607
+	9	1060	p.G245E|PALM_u	NM_002579	NP_002570	O75781	PALM_HUMAN		0	GCCGGGGATCC	0.692
-	5	663	3_uc002lpw.1_Spli	NM_024888	NP_079164	Q6T4P5	LPPR3_HUMAN		0	GGCTCACCGTGC	0.642
-	2	79		NM_006830	NP_006821	O14957	QCR10_HUMAN	ical; (Potential).	2	CCGTCGGGACC	0.662
-	18	2201	e_Mutation_p.C60	NM_138813	NP_620168	O60423	AT8B3_HUMAN	lasmic (Potential).	0	ACAGGCAGATG	0.657
-	14	1503	NK2_uc010xgv.1_	NM_199054	NP_951009	Q9HBH9	MKNK2_HUMAN		2	CTGCCCCGCGG	0.687
+	5	1561	wl.2_Missense_M	NM_001102651	NP_001096121	Q86TJ5	ZN554_HUMAN	2H2-type 6.	1	AGCACGAGCGA	0.542
-	12	1567	04_splice|PIP5K1	NM_012398	NP_036530	O60331	PI51C_HUMAN		4	CCCTCACCTTCG	0.711
+	13	2499		NM_005483	NP_005474	Q13111	CAF1A_HUMAN	Binds to p60.	2	TCAAGCGGCTCA	0.637
-	8	1305		NM_001013706	NP_001013728	Q00G26	PLIN5_HUMAN		0	CCAGGCTCTCT	0.716
-	5	449		NM_019107	NP_061980	Q969H8	CS010_HUMAN		0	TCAAATGCGGCT	0.453
+	1	854	uc002mbg.1_RNA	NM_018708	NP_061178	Q9BSK4	FEM1A_HUMAN	ANK 7.	0	AGCAGCCCGGC	0.697
-	14	2258	bw.2_Missense_M	NM_002850	NP_002841	Q13332	PTPRS_HUMAN	tential).|Fibronectin type-III	4	GTCGGGGGGATG	0.672
-	21	2989		NM_014649	NP_055464	Q14151	SAFB2_HUMAN	with SAFB1.|Gly-rich.	0	GCCACTCCGCCA	0.502
-	4	467		NM_133492	NP_597999	Q8TDN7	ACER1_HUMAN	ical; (Potential).	0	GTGCTGACCACA	0.597

+	3	430		NM_006012	NP_006003	Q16740	CLPP_HUMAN		1	CACAGCTCCTC	0.582	
-	2	313		NM_000064	NP_000055	P01024	CO3_HUMAN		5	CGTTGCCCATG	0.488	
+	11	1271	e_Mutation_p.R34	NM_004240	NP_004231	Q15642	CIP4_HUMAN	nteraction with PDE6G (By	1	AAAACGGCTTC	0.532	
-	3	765	_p.C219Y|INSR_u	NM_000208	NP_000199	P06213	INSR_HUMAN	Cys-rich.	12	TCGGGCAAACT	0.393	
+	3	386	_p.G16E|PNPLA6_	NM_006702	NP_006693	Q8IY17	PLPL6_HUMAN	ical; (Potential).	3	GATCGGGGCCG	0.701	
-	4	384	q.2_Missense_Mu	NM_021155	NP_066978	Q9NNX6	CD209_HUMAN	e).|7 X approximate tande	1	TCAGCTGGGTC	0.562	
-	46	5926		NM_032447	NP_115823	Q75N90	FBN3_HUMAN		11	ACTCACCAATG	0.438	
-	8	997		NM_032447	NP_115823	Q75N90	FBN3_HUMAN	TB 2.	11	AGCTGCCCAGC	0.682	
+	4	704	_p.A88V|MARCH	NM_016496	NP_057580	Q9P0N8	MARH2_HUMAN	ING-CH-type.	2	GGGTGCCGTGC	0.597	
+	12	1200	dwd.2_Splice_Sit	NM_005968	NP_005959	P52272	HNRPM_HUMAN		0	TAAATGGTAAGC	0.493	
+	1	136		NM_001004699	NP_001004699	Q8NG97	OR2Z1_HUMAN	Name=1; (Potential).	2	GTTCTTCTCTTC	0.557	
+	1	802		NM_001004699	NP_001004699	Q8NG97	OR2Z1_HUMAN	ellular (Potential).	2	ACAGTCCACAG	0.542	
-	39	39220	16_uc010dwj.2_	NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	ellular (Potential).	57	AACAGCTGCTG	0.448	
-	3	26086		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	h.|Extracellular (Potential).	57	ACGTGGCTAATA	0.458	
-	3	21859		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	h.|Extracellular (Potential).	57	ATCCTCCTGGG	0.483	
-	3	18095		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).	57	TCCTGCCAGAG	0.483	
-	1	9388		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).	57	CCTTGCCATGG	0.483	
-	1	8536		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	h.|Extracellular (Potential).	57	CCCAGCTGATG	0.512	
-	1	7184		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	h.|Extracellular (Potential).	57	TGGGGGAAGTG	0.473	
-	1	7145		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	h.|Extracellular (Potential).	57	TCTCTCCCAGT	0.483	
-	1	541		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).	57	AGAGGGAGTTC	0.517	
+	7	1740	p.R457W|ZNF317_	NM_020933	NP_065984	Q96PQ6	ZN317_HUMAN	2H2-type 10.	0	TATCCCGGCGG	0.552	
+	7	2155	_uc002mle.3_Mis	NM_032497	NP_115886	Q9BR84	ZN559_HUMAN	2H2-type 13.	1	CTTTACTCGGT	0.438	
-	10	1793	wr.1_Missense_M	NM_152476	NP_689689	Q96MR9	ZN560_HUMAN	2H2-type 7.	6	AGGCAGAAGAG	0.383	
-	10	1135	wr.1_Missense_M	NM_152476	NP_689689	Q96MR9	ZN560_HUMAN	ype 1; degenerate.	6	GTGTGCTTCAA	0.403	
-	3	571	_RNA|ZNF846_u	NM_001077624	NP_001071092	Q147U1	ZN846_HUMAN	KRAB.	1	CACAGCCACAT	0.423	
-	26	2143		NM_015719	NP_056534	P25940	CO5A3_HUMAN	e-helical region.	10	CATGTCCTGGG	0.592	
-	5	788	K2_uc002mod.2_	NM_003331	NP_003322	P29597	TYK2_HUMAN	FERM.	9	GTGCTGTCTGA	0.557	rs149044054
-	6	936	_Mutation_p.A111	NM_007065	NP_008996	Q16543	CDC37_HUMAN		0	CATGGCCTTCT	0.662	
+	14	1892	om.2_Missense_	NM_001111307	NP_001104777	P27815	PDE4A_HUMAN	Catalytic.	3	CAACCCCACCA	0.617	
+	4	589	F3_uc002mpk.2_	NM_012218	NP_036350	Q12906	ILF3_HUMAN		3	GCGGGGAGTGA	0.602	
-	3	570		NM_006858	NP_006849	Q13445	TMED1_HUMAN	ellular (Potential).	4	GTCCTCCATTT	0.592	
+	25	3670	_p.T1129I|SMAR	NM_003072	NP_003063	P51532	SMCA4_HUMAN	case C-terminal.	67	AGGAACCACGA	0.627	
+	6	754	2mqu.1_RNA|uc0	NM_012466	NP_036598	Q9UKR8	TSN16_HUMAN	lasmic (Potential).	1	CTCAGGGCTGT	0.507	
-	3	435	RGL3_uc002mro.	NM_001035223	NP_001030300	Q3MIN7	RGL3_HUMAN		1	ACTGACCCGGG	0.627	
+	4	1932	e_Mutation_p.S62	NM_144566	NP_653167	Q9H0M5	ZN700_HUMAN	2H2-type 14.	0	TTCAGTTGTGC	0.483	
+	2	204	63_uc002msv.2_	NM_001012753	NP_001012771	Q0D2J5	ZN763_HUMAN	KRAB.	1	AGGAGGAGTGG	0.512	
-	4	1619		NM_145276	NP_660319	Q8TA94	ZN563_HUMAN	2H2-type 12.	0	ACTGGGATAAA	0.378	
+	4	1477	u.1_Missense_M	NM_153358	NP_699189	Q3KP31	ZN791_HUMAN		2	GACGGACCTTAT	0.418	
+	9	1041	vk.2_Missense_M	NM_014975	NP_055790	Q9Y2H9	MAST1_HUMAN		7	TGGAGGCGGCC	0.642	
+	1	171		NM_004343	NP_004334	P27797	CALR_HUMAN	N-domain.	1	ACGGAGGTAAC	0.677	
+	6	1603		NM_052876	NP_443108	Q96RE7	NACC1_HUMAN		0	CCAAGGTCAAG	0.597	
-	22	4021	nwy.3_Missense_	NM_001127221	NP_001120693	O00555	CAC1A_HUMAN	llular (Potential).|III.	2	CGGCGGCCAGG	0.602	
+	7	1385	ng.1_Missense_M	NM_023072	NP_075560	Q9H7M6	ZSWM4_HUMAN		2	GAAGGGCTCCA	0.627	
+	11	2087	ng.1_Missense_	NM_023072	NP_075560	Q9H7M6	ZSWM4_HUMAN		2	GGGCTCCATCC	0.647	
+	1	288		NM_001098622	NP_001092092	P60323	NANO3_HUMAN		1	TGCCGGGACCC	0.657	
-	6	1047	_Mutation_p.G21	NM_024323	NP_077299	Q0VDD7	CS057_HUMAN		3	GCATCCCAGGC	0.662	

+	8	1213	.2_Missense_Muta	NM_017721	NP_060191	Q6P1N0	C2D1A_HUMAN	Pro-rich.	0	TGAGCCCGTGG	0.597
+	14	1893	dzh.2_Missense_M	NM_017721	NP_060191	Q6P1N0	C2D1A_HUMAN		0	TGGAGCCTATG	0.627
+	25	2882	60_splice|CC2D1A	NM_017721	NP_060191	Q6P1N0	C2D1A_HUMAN		0	GGAAGGTGGGT	0.612
-	3	672	i.2_Missense_Mut	NM_002918	NP_002909	P22670	RFX1_HUMAN		2	AACCACCTGAG	0.726
+	3	647		NM_004843	NP_004834	Q6UWB1	I27RA_HUMAN	ellular (Potential).	0	CCGTTCCAACA	0.557
+	3	676		NM_004843	NP_004834	Q6UWB1	I27RA_HUMAN	ellular (Potential).	0	TGGCAGCCGGA	0.617
+	7	1366		NM_004843	NP_004834	Q6UWB1	I27RA_HUMAN	ellular (Potential).	0	CTTTGGTCTGC	0.597
+	8	1391		NM_004843	NP_004834	Q6UWB1	I27RA_HUMAN	tential).|Fibronectin type-III	0	TGCCCCCCGTA	0.632
-	2	360	xnr.1_Missense_M	NM_006145	NP_006136	P25685	DNJB1_HUMAN		0	TGCCACCGAAG	0.567
-	20	2891	p.A752V|EMR2_u	NM_013447	NP_038475	Q9UHX3	EMR2_HUMAN	lasmic (Potential).	4	CCTTAGCACTG	0.522
-	1	920		NM_198944	NP_945182	O76099	OR7C1_HUMAN	lasmic (Potential).	2	TTGCCCTACTGA	0.502
+	8	2007	p.G592E|SYDE1_	NM_033025	NP_149014	Q6ZW31	SYDE1_HUMAN		2	TTGCGGGCGGG	0.706
-	10	1285	p.G29E|ILVBL_uc	NM_006844	NP_006835	A1L0T0	ILVBL_HUMAN		2	GGCTTCCAGAA	0.557
-	11	1857	ao.1_Missense_M	NM_000435	NP_000426	Q9UM47	NOTC3_HUMAN	GF-like 15; calcium-binding	21	TGCCGCCATGG	0.657
-	5	565	KAP8L_uc002nay.	NM_014371	NP_055186	Q9ULX6	AKP8L_HUMAN		1	CATAGGCCATTT	0.622
-	7	808	L3_uc010eaa.1_5	NM_022904	NP_075055	Q86YV0	RASL3_HUMAN	PH.	0	CGGCACCCAGG	0.637
+	12	1419		NM_023944	NP_076433				7	GGGGAGGTCAC	0.557
+	1	520		NM_013939	NP_039227	O60403	O10H2_HUMAN	ellular (Potential).	3	ACTGACTTTCTG	0.577
+	1	841		NM_001004466	NP_001004466	Q8NGA6	O10H5_HUMAN	Name=7; (Potential).	1	ACACGGTCCTC	0.537
-	7	762	_p.E89K|CYP4F2_	NM_001082	NP_001073	P78329	CP4F2_HUMAN		2	GGATCTCATGGT	0.512
+	6	785	_p.E218K|TPM4_u	NM_003290	NP_003281	P67936	TPM4_HUMAN	By similarity.	13	AAAAGGAGGAC	0.353
-	3	121	33_uc010eaf.2_Int	NM_054113	NP_473454	Q96Q77	CIB3_HUMAN		1	CACGAGCTGTG	0.592
+	5	646	p.S158F|AP1M1_	NM_032493	NP_115882	Q9BXS5	AP1M1_HUMAN		4	GGTGTCCTGGC	0.572
-	20	2156	S15L1_uc010xpf.	NM_021235	NP_067058	Q9UBC2	EP15R_HUMAN	A repeats of D-P-F.	5	TTGAGGAGACA	0.473
-	12	2122	HERP_uc010xpg.1	NM_006387	NP_006378	Q8IWX8	CHERP_HUMAN		2	TCTCGCTGGGC	0.652
-	9	1317	2_Intron|CHERP_	NM_006387	NP_006378	Q8IWX8	CHERP_HUMAN	Pro-rich.	2	TGGTGGGATCT	0.537
-	9	1216	2_Intron|CHERP_	NM_006387	NP_006378	Q8IWX8	CHERP_HUMAN	Pro-rich.	2	ATGGGAGGCTTG	0.512
-	6	1166	026_uc002nee.2_I	NM_024881	NP_079157	Q96K37	S35E1_HUMAN		2	TTGCGGCCGTAC	0.567
-	31	4242	ID8_uc002nfd.1_5	NM_015692	NP_056507	Q8IZJ3	CPMD8_HUMAN		13	CTTGTCCACGT	0.582
-	8	785		NM_015692	NP_056507	Q8IZJ3	CPMD8_HUMAN		13	ATGAACCATTCT	0.413
-	9	1545	BP1_uc002nft.1_F	NM_031941	NP_114147	Q8N6Y0	USBP1_HUMAN	Potential.	1	CTTCTCCAGTCC	0.602
+	2	612	1_Intron|SLC27A1	NM_198580	NP_940982	Q6PCB7	S27A1_HUMAN	lasmic (Potential).	0	TGGCGGGTGAG	0.731
+	7	1065	A1_uc010xpp.1_M	NM_198580	NP_940982	Q6PCB7	S27A1_HUMAN	(By similarity).|Cytoplasm	0	TCGGGGAGATC	0.701
-	11	1613	.2_Nonsense_Mu	NM_000215	NP_000206	P52333	JAK3_HUMAN		56	GGTATTGGGATTG	0.542
+	5	1002		NM_000453	NP_000444	Q92911	SC5A5_HUMAN	ellular (Potential).	4	GCCAGGTGCTC	0.577
+	6	1159		NM_000453	NP_000444	Q92911	SC5A5_HUMAN	lasmic (Potential).	4	CGTGGCTTGCC	0.617
+	5	855	hu.2_Missense_M	NM_015683	NP_056498	Q8TBH0	ARRD2_HUMAN		1	AACGGGCAGTG	0.711
+	5	885	hu.2_Missense_M	NM_015683	NP_056498	Q8TBH0	ARRD2_HUMAN		1	AGCCGGTGGGC	0.711
+	6	1012	hu.2_Missense_M	NM_015683	NP_056498	Q8TBH0	ARRD2_HUMAN		1	CCCAGGAACGT	0.632
+	17	1829		NM_015016	NP_055831	O60307	MAST3_HUMAN	rotein kinase.	5	AGACGCCCAGG	0.602
+	27	3877		NM_015016	NP_055831	O60307	MAST3_HUMAN		5	TCGCCGTGGAG	0.622
+	2	272	ebj.2_Missense_	NM_032683	NP_116072	Q567V2	M17L2_HUMAN	ical; (Potential).	0	ATGGGTCCCTTC	0.592
-	1	1397	ix.2_Missense_M	NM_145256	NP_660299	Q8N386	LRC25_HUMAN	lasmic (Potential).	0	GCTCGGCTGCT	0.473
-	6	906	P8_uc002njl.1_Mi	NM_012181	NP_036313	Q14318	FKBP8_HUMAN		1	CTGTGCCTCCT	0.647
+	14	1886	bw.2_Missense_M	NM_015321	NP_056136	Q6UUV9	CRTC1_HUMAN		519	ACGAACTCAAG	0.637
-	7	2597	p.W817*|SFRS14_	NM_014884	NP_055699	Q8IX01	SUGP2_HUMAN	URP motif 2.	0	AGAAACCTGGG	0.413
-	3	1644	p.E500K|SFRS14_	NM_014884	NP_055699	Q8IX01	SUGP2_HUMAN		0	CAGCTTCTAAGA	0.507

+	2	515	xqv.1_Missense_	NM_017660	NP_060130	Q86YP4	P66A_HUMAN		0	CACGGCCATGG	0.627	
+	4	790	ense_Mutation_p.	NM_017660	NP_060130	Q86YP4	P66A_HUMAN	Potential.	0	AACTCGTGTTG	0.522	
-	6	500	p.S128N|GMIP_u	NM_016573	NP_057657	Q9P107	GMIP_HUMAN		1	TGGTGCTCTTA	0.607	
+	2	213	.2_Intron|ZNF253	NM_021047	NP_066385	O75346	ZN253_HUMAN	KRAB.	0	ACTTGGTCTTC	0.358	
+	4	955		NM_031218	NP_112495	P35789	ZNF93_HUMAN		1	CTGGAGAGAAA	0.368	
+	4	1624		NM_031218	NP_112495	P35789	ZNF93_HUMAN		1	ATACTGGAGAG	0.353	
+	4	1801		NM_031218	NP_112495	P35789	ZNF93_HUMAN		1	GAGAAACCTTAT	0.378	
+	4	1740	.1_Intron|ZNF90_	NM_007138	NP_009069	Q03938	ZNF90_HUMAN		2	TGGAGCGAAAC	0.408	
-	4	1010		NM_001159293	NP_001152765	C9JHM3	C9JHM3_HUMAN		1	TGAATTATCTTAT	0.413	
-	4	1127	pc.1_Missense_M	NM_001076675	NP_001070143	Q68DY1	ZN626_HUMAN	2H2-type 6.	1	GGGTATAGGAG	0.383	
+	6	1631	714_uc010ecp.1_	NM_182515	NP_872321	Q96N38	ZN714_HUMAN		0	AGAAACTCTACA	0.368	
+	2	291	_p.C132Y|ZNF49	NM_175910	NP_787106	Q6ZR52	ZN493_HUMAN		1	TGAGTGTAATGT	0.294	
+	2	1311	p.R472Q|ZNF493_	NM_175910	NP_787106	Q6ZR52	ZN493_HUMAN	2H2-type 12.	1	TTAAACGATCTTC	0.333	
+	2	1423	_p.I509M|ZNF493_	NM_175910	NP_787106	Q6ZR52	ZN493_HUMAN	2H2-type 13.	1	TAAAATAATTCAT	0.323	
-	4	1778	p.F544I|ZNF43_u	NM_003423	NP_003414	P17038	ZNF43_HUMAN	2H2-type 14.	2	TTGAGAAATGGT	0.383	
-	5	2059	208_uc002nqo.1_	NM_007153	NP_009084				7	GTTTAGTAAGGA	0.368	
-	5	1794	208_uc002nqo.1_	NM_007153	NP_009084				7	TTGAGACCTTAA	0.388	
-	5	1710	208_uc002nqo.1_	NM_007153	NP_009084				7	TTGAGACCTTAC	0.368	
-	5	1651	208_uc002nqo.1_	NM_007153	NP_009084				7	TGAATTCTCTTAT	0.353	
-	3	325	e_Mutation_p.G5	NM_007153	NP_009084				7	TCTTTTCCTTCC	0.413	
-	4	1483		NM_001098626	NP_001092096	A6NK75	ZNF98_HUMAN	2H2-type 10.	2	TGAATTATCTTAT	0.363	
-	7	2699		NM_001080409	NP_001073878				2	GTCGAGAAATTG	0.353	rs55891931
-	4	1821	NF91_uc010xrj.1_	NM_003430	NP_003421	Q05481	ZNF91_HUMAN		0	TCTTTCCAGCAT	0.323	
-	4	1567		NM_138330	NP_612203	Q8TD23	ZN675_HUMAN	2H2-type 12.	2	GATTGGATAAAA	0.368	
-	4	1655	p.S436P|ZNF681_	NM_138286	NP_612143	Q96N22	ZN681_HUMAN		0	TGTAGGATTTCTC	0.373	
-	4	1313	p.E322K|ZNF681_	NM_138286	NP_612143	Q96N22	ZN681_HUMAN		0	TTTCTCTCCAG	0.408	
+	3	2333	dd.1_Missense_M	NM_014717	NP_055532	O15090	ZN536_HUMAN		11	GAGATCTGCCG	0.567	
+	3	1207	rn.1_Missense_M	NM_001136156	NP_001129628	Q8TCN5	ZN507_HUMAN		5	AGAGAGTGAAC	0.478	
+	4	417	nth.1_Missense_	NM_207325	NP_997208	Q6ZPD9	D19L3_HUMAN		4	AGGAAGTGGAG	0.403	
-	6	607	e_Mutation_p.V3	NM_033103	NP_149094	Q8IUC4	RHPN2_HUMAN	BRO1.	6	CTCGACAAAGC	0.587	
+	5	740		NM_173479	NP_775750	Q6ZMY6	WDR88_HUMAN	WD 3.	3	CACCACCGTTT	0.502	
+	3	605	_p.P34S|CHST8_	NM_001127895	NP_001121367	Q9H2A9	CHST8_HUMAN	enal (Potential).	4	AGGACCCTACG	0.632	
+	5	563	n_p.Q99*|KCTD1	NM_001129994	NP_001123466	Q96SI1	KCD15_HUMAN	BTB.	1	TTGAAGCAACAT	0.537	
+	5	648	_p.D127V|KCTD1	NM_001129994	NP_001123466	Q96SI1	KCD15_HUMAN		1	GGATGACTTTA	0.532	
+	10	2883		NM_014686	NP_055501	O15063	K0355_HUMAN		1	TGCTGCCACAG	0.577	
+	10	2997		NM_014686	NP_055501	O15063	K0355_HUMAN		1	GACACCCCAGC	0.632	
+	10	3293		NM_014686	NP_055501	O15063	K0355_HUMAN		1	CGCAGGGACCT	0.502	
+	4	689		NM_032346	NP_115722	Q9BRP1	PDD2L_HUMAN		1	AGAAGGCATTG	0.507	
+	10	977	p.P176S|UBA2_u	NM_005499	NP_005490	Q9UBT2	SAE2_HUMAN		1	ATGAACCCCAG	0.358	
-	4	1872	dm.1_Missense_	NM_001007248	NP_001007249	Q96NL3	ZN599_HUMAN	2H2-type 11.	2	GTCGAGTGAAG	0.423	
+	5	1741	dq.1_Missense_M	NM_194325	NP_919306	P17039	ZNF30_HUMAN		2	AGAAACCCTAT	0.443	
+	10	1198	2_Missense_Muta	NM_020895	NP_065946	Q96CP6	GRM1A_HUMAN		0	CACTGGGGAGG	0.607	
+	3	242	_uc002nys.1_5'UT	NM_003367	NP_003358	Q15853	USF2_HUMAN		0	CGGAGGAGCAG	0.517	
+	5	991	.G305E|CD22_uc	NM_001771	NP_001762	P20273	CD22_HUMAN	otential).|Ig-like C2-type 2.	9	GAGTGGGAAGT	0.582	
-	3	714	d.1_Missense_Mu	NM_198538	NP_940940	Q6UWP8	SBSN_HUMAN	a/Gly/His-rich.	1	CCCCTCCTTGA	0.602	
+	2	464	/2_uc002oat.2_Int	NM_014209	NP_055024	O00321	ETV2_HUMAN		0	ATGAGGCATCC	0.602	
+	18	1854	p.S454N|ARHGA	NM_052948	NP_443180	O14559	RHG33_HUMAN		4	CAGCAGCTGGA	0.672	

+	21	2900	AP33_uc010eel.2_	NM_052948	NP_443180	O14559	RHG33_HUMAN		4	CTGGCCCCACC	0.647
-	29	3615		NM_004646	NP_004637	O60500	NPHN_HUMAN	2.|Cytoplasmic (Potential).	5	TCAGGCCAGTG	0.547
-	18	2425		NM_004646	NP_004637	O60500	NPHN_HUMAN	7.|Extracellular (Potential).	5	CTGGGCCAGTT	0.597
-	5	621		NM_133466	NP_597723	Q8N141	ZFP82_HUMAN		2	TCCTGTCCTTCA	0.388
-	4	1442	ey.1_Missense_M	NM_001012756	NP_001012774	Q3ZCT1	ZN260_HUMAN	C2H2-type 6.	0	TAAAAGCTTTTC	0.398
-	6	1714	_p.P465S|ZNF461	NM_153257	NP_694989	Q8TAF7	ZN461_HUMAN		0	ATAGGGTTTCT	0.393
-	5	1324	uc002oev.1_Intron	NM_206894	NP_996777	Q6PG37	ZN790_HUMAN	C2H2-type 8.	2	ATATAGGCTTTC	0.413
+	3	1330	e_Mutation_p.E31	NM_003419	NP_003410	Q14585	ZN345_HUMAN	2H2-type 10.	1	GTAAGGAGTGT	0.403
-	3	129	0_uc002ogq.2_Intr	NM_016536	NP_057620	Q7Z3V5	ZN571_HUMAN	KRAB.	0	CACATCCCTGA	0.443
-	5	1396	hb.1_Missense_M	NM_032689	NP_116078	Q96SK3	ZN607_HUMAN	C2H2-type 6.	0	TAAGGCCTGCT	0.428
-	2	158	e_Mutation_p.D44	NM_152360	NP_689573	Q86YE8	ZN573_HUMAN	KRAB.	1	AGGGTCCAGGT	0.403
-	6	705	ty.1_Missense_M	NM_001039672	NP_001034761	Q5BJH7	YIF1B_HUMAN	lasmic (Potential).	0	CGATGGTGGTG	0.637
+	8	941	_p.L226F|FAM98C	NM_174905	NP_777565	Q17RN3	FA98C_HUMAN		1	AGGTGCTTATG	0.557
+	5	542	u.2_Missense_Mu	NM_000540	NP_000531	P21817	RYR1_HUMAN	plasmic.|MIR 1.	12	TGCAGGAGGAC	0.612
+	25	3408	.2_Missense_Mut	NM_000540	NP_000531	P21817	RYR1_HUMAN	ats.|Cytoplasmic.|B30.2/S	12	TGAAGCAGTCA	0.607
+	39	6446	_Mutation_p.A210	NM_000540	NP_000531	P21817	RYR1_HUMAN	|6 X approximate repeats.	12	GCTGGGCCCAA	0.672
+	57	8849	_Mutation_p.P290	NM_000540	NP_000531	P21817	RYR1_HUMAN	te repeats.|Cytoplasmic.|6.	12	TGGTCCCCTAC	0.602
+	6	655	_p.W156*|EIF3K_	NM_013234	NP_037366	Q9UBQ5	EIF3K_HUMAN		2	CGCTGGCTGCT	0.612
+	20	2571	jb.1_Missense_Mu	NM_004924	NP_004915	O43707	ACTN4_HUMAN	EF-hand 2.	0	CGCGGGAGACC	0.607
-	8	785	h.2_Missense_Mu	NM_001398	NP_001389	Q13011	ECH1_HUMAN		1	GTCAGCCATCA	0.687
-	6	485	NL_uc010xuo.1_M	NM_198445	NP_940847	Q6ZS11	RINL_HUMAN		1	TTCATCTCTGG	0.567
-	4	397	_p.G46E|SIRT2_	NM_012237	NP_036369	Q8IXJ6	SIRT2_HUMAN	tylase sirtuin-type.	0	CCACCCCTTCC	0.617
+	2	343	63_splice|NFKBIB_	NM_002503	NP_002494	Q15653	IKBB_HUMAN		2	GCCAGGTGAGC	0.587
+	5	824	PL_uc010egl.2_Int	NM_001004318	NP_001004318	Q6ZNF0	PAPL_HUMAN		0	TTGGGGATAGG	0.607
-	2	233	uu.1_Missense_Mu	NM_172139	NP_742151	Q8IZI9	IL28B_HUMAN		0	CCTGGGGAAGA	0.637
+	1	102		NM_172140	NP_742152	Q8IU54	IL29_HUMAN		0	CATGGCTGCAG	0.557
+	8	1178	2olj.2_Missense_M	NM_022835	NP_073746	Q9H7P9	PKHG2_HUMAN		4	TGAAGCGCAAG	0.667
+	19	3006	HG2_uc002olj.2_	NM_022835	NP_073746	Q9H7P9	PKHG2_HUMAN		4	CCTGGGTCCTG	0.562
+	9	1160	MM50_uc002olv.1_	NM_001001563	NP_001001563	Q3ZCQ8	TIM50_HUMAN	brane (Potential).|FCP1 h	1	ATCGGGACCCA	0.532
-	34	15561		NM_003890	NP_003881	Q9Y6R7	FCGBP_HUMAN	Cys-rich.	9	AGTTTACCTGTG	0.388
-	21	9553		NM_003890	NP_003881	Q9Y6R7	FCGBP_HUMAN	TIL 7.	9	AGGGGCCCTCA	0.647
-	4	2223		NM_003890	NP_003881	Q9Y6R7	FCGBP_HUMAN		9	AGTTGGCTGGTG	0.567
+	7	1274	mt.2_Missense_M	NM_178544	NP_848639	Q86UE3	ZN546_HUMAN	C2H2-type 5.	3	TTTAGACTTCAT	0.398
-	6	800	sense_Mutation_p.	NM_001010880	NP_001010880	O75290	Z780A_HUMAN		0	CAAAGGGTTTC	0.368
-	7	623	_p.E67K|C19orf47	NM_178830	NP_849152	Q8N9M1	CS047_HUMAN		2	CCCCTCCATCT	0.647
+	11	1453	p.A352V|PLD3_u	NM_001031696	NP_001026866	Q8IV08	PLD3_HUMAN	enal (Potential).	3	GCGGGCCACCT	0.662
-	3	1519		NM_144685	NP_653286	Q8NE63	HIPK4_HUMAN		2	GAAGGGGCTGC	0.647
-	3	1394		NM_144685	NP_653286	Q8NE63	HIPK4_HUMAN		2	AGAGGCGGTAG	0.672
-	2	836		NM_144685	NP_653286	Q8NE63	HIPK4_HUMAN	rotein kinase.	2	TCTCAGGGGCC	0.647
+	33	7158	.N2358D|SPTBN4	NM_020971	NP_066022	Q9H254	SPTN4_HUMAN		5	TGCCCAACGGG	0.483
+	6	1831		NM_025194	NP_079470	Q96DU7	IP3KC_HUMAN		0	TGCCTAGAAGAA	0.572
-	8	1207		NM_000762	NP_000753	P11509	CP2A6_HUMAN		2	AGAGCCCAGCA	0.552
-	6	1395	p.E285K|CYP2A7	NM_000764	NP_000755	P20853	CP2A7_HUMAN		3	GAACTCCGTGT	0.552
-	4	1093	p.S184F|CYP2A7	NM_000764	NP_000755	P20853	CP2A7_HUMAN		3	CAATGGAGCTG	0.547
+	3	431	YP2B6_uc010xvu.	NM_000767	NP_000758	P20813	CP2B6_HUMAN		2	GGAGTGTGGAG	0.532
+	3	353		NM_000766	NP_000757	Q16696	CP2AD_HUMAN		3	CCCCAGGCGTG	0.697
+	3	477	.1_Intron|CYP2S1	NM_030622	NP_085125	Q96SQ9	CP2S1_HUMAN		1	CATGGGGAAGC	0.622

+	6	970	YP2S1_uc010xvx	NM_030622	NP_085125	Q96SQ9	CP2S1_HUMAN		1	ACGATGACGGT	0.493	
+	20	2753	02oqa.3_5'Flank|	NM_021913	NP_068713	P30530	UFO_HUMAN	lasmic (Potential).	13	GCTGCCTCACT	0.627	
-	2	230	91_uc002oqi.2_In	NM_030578	NP_085055	Q9BPU9	B9D2_HUMAN	B9.	1	GTGCACCTCAG	0.373	
+	2	409	ense_Mutation_p.E	NM_000709	NP_000700	P12694	ODBA_HUMAN		0	AATGTGAGACC	0.602	
+	7	1824	_p.A567V|CEACA	NM_004363	NP_004354	P06731	CEAM5_HUMAN	Ig-like 6.	2	CAAGAGCCTATG	0.522	
-	17	2562	p.G773D|ATP1A3_	NM_152296	NP_689509	P13637	AT1A3_HUMAN	ical; (Potential).	2	CAGTGCCCAGA	0.647	
-	16	2158	si.1_Missense_Mu	NM_002088	NP_002079	Q16478	GRIK5_HUMAN	ellular (Potential).	0	GCAATGCCCTCT	0.587	
-	15	2046	si.1_Missense_Mu	NM_002088	NP_002079	Q16478	GRIK5_HUMAN	ellular (Potential).	0	GCCGGCGTGGA	0.627	
+	2	1310	sk.3_Missense_M	NM_022752	NP_073589	Q6ZN55	ZN574_HUMAN	2H2-type 7.	0	TCCTGGCCCAC	0.582	
-	12	1221	_p.G158E|POU2F2	NM_002698	NP_002689	P09086	PO2F2_HUMAN		2	AGGTCCCCGCG	0.617	
-	8	632	OU2F2_uc002osq	NM_002698	NP_002689	P09086	PO2F2_HUMAN		2	TGGCTCCAAGC	0.682	
+	3	508		NM_133444	NP_597701	Q8TF50	ZN526_HUMAN	2H2-type 2.	0	TCATCCTCTCC	0.632	
-	2	226	F_uc002otd.3_5'U	NM_006494	NP_006485	P50548	ERF_HUMAN		4	TTGAGCCAGGG	0.637	
+	10	2639		NM_015125	NP_055940	Q96RK0	CIC_HUMAN	Pro-rich.	11	CCCTCCCACCG	0.682	
+	12	1014		NM_173633	NP_775904	Q8NBT3	TM145_HUMAN	ical; (Potential).	0	TCATTGGACTGC	0.582	
+	13	1230		NM_173633	NP_775904	Q8NBT3	TM145_HUMAN	ical; (Potential).	0	GTACGCCCATG	0.592	
-	5	1124	uc010eig.1_Intron|	NM_001816	NP_001807	P31997	CEAM8_HUMAN		1	AGTACTCCAATC	0.463	
-	4	1066	x.2_Missense_Mu	NM_002781	NP_002772	Q15238	PSG5_HUMAN	like C2-type 2.	3	TGGAGCTTTCC	0.458	
-	2	472	e_Mutation_p.R11	NM_002781	NP_002772	Q15238	PSG5_HUMAN	g-like V-type.	3	TCTTCCCGGGTG	0.433	
-	12	1510	wp.1_Missense_M	NM_006297	NP_006288	P18887	XRCC1_HUMAN		7	CTGGAGCACTG	0.408	
-	5	1306	iz.2_Missense_Mu	NM_002250	NP_002241	O15554	KCNN4_HUMAN	modulin-binding.	2	GATATCCATCAT	0.552	
-	3	364	xn.3_Missense_M	NM_001031749	NP_001026919	Q6UWN5	LYPD5_HUMAN		0	GTCTGGCGGCA	0.692	
+	7	1091	xp.3_Missense_M	NM_181845	NP_862828	Q8N7M2	ZN283_HUMAN	2H2-type 3.	0	GCTGGGGATCA	0.418	
-	2	1442		NM_001033719	NP_001028891	Q494X3	ZN404_HUMAN	2H2-type 13.	0	AAAGACCTGAG	0.343	
-	4	698	_p.A200V|ZNF45_	NM_003425	NP_003416	Q02386	ZNF45_HUMAN	2H2-type 2.	1	GGAAGGCATTA	0.418	
+	4	658	nse_Mutation_p.A	NM_013360	NP_037492	Q9UK12	ZN222_HUMAN	2H2-type 1.	3	TCTCAGCCCTT	0.423	rs139230139
+	4	1447	nse_Mutation_p.E	NM_013360	NP_037492	Q9UK12	ZN222_HUMAN		3	GTGGAGAAAAC	0.378	
+	5	1976	_p.S495N|ZNF225_	NM_013362	NP_037494	Q9UK10	ZN225_HUMAN	2H2-type 15.	0	CTTTAGCCGGG	0.428	
+	6	2190	226_uc010ejg.2_3	NM_001032373	NP_001027545	Q9NYT6	ZN226_HUMAN	2H2-type 16.	0	AAGTGGAGCTT	0.473	
-	7	1385	0ejp.1_Missense_	NM_001102597	NP_001096067	Q6UY09	CEA20_HUMAN	ical; (Potential).	2	GACAGCCAGGA	0.567	
-	6	1076	54K|CEACAM20_	NM_001102597	NP_001096067	Q6UY09	CEA20_HUMAN	4.|Extracellular (Potential).	2	CGACTCCCTGG	0.567	
+	3	668	jt.2_Missense_Mu	NM_012116	NP_036248	Q9ULV8	CBLC_HUMAN	F-hand-like.|Cbl-PTB.	6	CACCTGCAGCG	0.522	
+	7	1156	jt.2_Missense_Mu	NM_012116	NP_036248	Q9ULV8	CBLC_HUMAN	RING-type.	6	TTGAGCCGTGC	0.607	
+	12	1662	ozt.1_Splice_Site_	NM_005581	NP_005572	P50895	BCAM_HUMAN		1	CACCGGTGAGT	0.647	rs113739218
-	5	556		NM_001824	NP_001815	P06732	KCRM_HUMAN	en kinase C-terminal.	1	TGAGAGCTATG	0.602	
-	4	424		NM_001824	NP_001815	P06732	KCRM_HUMAN		1	CTCCACCCTGG	0.657	
+	4	674	.G186S|KLC3_uc	NM_177417	NP_803136	Q6P597	KLC3_HUMAN		1	GGAAAGGTGGG	0.657	
+	8	1238	p.A374T|KLC3_uc	NM_177417	NP_803136	Q6P597	KLC3_HUMAN	TPR 5.	1	ACGTGGCCAAG	0.642	
-	9	1926	_p.P196S|PPP1R1	NM_006663	NP_006654	Q8WUF5	IASPP_HUMAN		1	GCGCGGGGAGC	0.602	
+	3	1464	2pbp.2_5'Flank|C	NM_012099	NP_036231	O15446	RPA34_HUMAN		4	TGCCCCCTACG	0.587	
-	2	1964	A3_uc010xxk.1_In	NM_005282	NP_005273	P46093	GPR4_HUMAN	lasmic (Potential).	2	AGCTGCCAGTC	0.627	
-	15	1459	xl.1_Missense_Mu	NM_012155	NP_036287	O95834	EMAL2_HUMAN	WD 8.	2	CGGCCAGGTAC	0.692	
-	22	3127	_p.S961F|SYMPK_	NM_004819	NP_004810	Q92797	SYMPK_HUMAN		1	TGATGGATTTC	0.602	
-	14	2155	p.G637D|SYMPK_	NM_004819	NP_004810	Q92797	SYMPK_HUMAN		1	GGGAGCCCGAG	0.642	
-	11	1513	dp.1_Missense_M	NM_004819	NP_004810	Q92797	SYMPK_HUMAN		1	CCTCGGGTAGG	0.488	
-	8	975	dp.1_Missense_M	NM_004819	NP_004810	Q92797	SYMPK_HUMAN		1	GTGCACCATGA	0.572	
+	2	583		NM_004497	NP_004488	P55318	FOXA3_HUMAN	Fork-head.	1	CATGGCCATCC	0.597	

-	4	1417		NM_002516	NP_002507	Q9UNW9	NOVA2_HUMAN	KH 3.	0	GGTGACCCGCC	0.652	
+	1	164	PP5C_uc002pen.	NM_006247	NP_006238	P53041	PPP5_HUMAN	TPR 1.	2	TCAGGCCAATG	0.682	
-	1	1902_1903		NM_032040	NP_114429	Q9H0W5	CCDC8_HUMAN	Potential.	3	CCCTCCTCAGC	0.609	
-	5	718	p.L229F|STRN4_u	NM_013403	NP_037535	Q9NRL3	STRN4_HUMAN		0	ACTGAGCCCTG	0.652	
+	1	650		NM_004491	NP_004482	Q9NRY4	RHG35_HUMAN		1	TTTTGCCTTAAG	0.438	
-	4	775	ky.2_Missense_Mu	NM_014417	NP_055232	Q9BXH1	BBC3_HUMAN		0	GTGAGGGGCGG	0.612	
+	2	596		NM_001736	NP_001727	P21730	C5AR_HUMAN	ellular (Potential).	4	TACTTTCCACCA	0.637	
+	11	2785	34_uc010xyo.1_5'	NM_014681	NP_055496	Q14147	DHX34_HUMAN		5	CGTCCCCGACG	0.562	
-	7	2241	xyr.1_Missense_M	NM_015063	NP_055878	Q9UPR5	NAC2_HUMAN	lasmic (Potential).	4	AGTTCTCCCCAA	0.572	
+	3	726	yu.1_Missense_M	NM_014601	NP_055416	Q9NZN4	EHD2_HUMAN		2	CCTGTCGGGTG	0.408	
+	4	1097	e_Mutation_p.Q14	NM_014601	NP_055416	Q9NZN4	EHD2_HUMAN		2	ACATCCAGGGC	0.677	
+	3	409	e_Mutation_p.P12	NM_015710	NP_056525	Q9NZM5	GSCR2_HUMAN		1	AAGTCCCTGCC	0.557	
-	16	1978	_splice|PLA2G4C	NM_003706	NP_003697	Q9UP65	PA24C_HUMAN		2	ACCTACCCGGC	0.333	
-	7	1131	n_p.S298F|CARD	NM_014959	NP_055774	Q9Y2G2	CARD8_HUMAN		0	TTAGCAGAATTA	0.433	
-	3	490	2pja.1_Missense_	NM_006801	NP_006792	P24390	ERD21_HUMAN	ical; (Potential).	0	GAACGACCAGGA	0.522	
+	7	1301	_Mutation_p.G10	NM_020126	NP_064511	Q9NRA0	SPHK2_HUMAN	DAGKc.	1	GGGTGGTGGCC	0.617	
-	5	1088	C1_uc010ema.2_	NM_001217	NP_001208	O75493	CAH11_HUMAN		0	GCCGCGGGAGG	0.483	
-	4	1163		NM_000148	NP_000139	P19526	FUT1_HUMAN	enal (Potential).	1	TGGGGCCCATC	0.622	
-	1	738		NM_002152	NP_002143	P23327	SRCH_HUMAN	.|1-1.|6 X approximate tand	1	CATGGCCTCGG	0.463	
+	4	395	_Intron|TRPM4_u	NM_017636	NP_060106	Q8TD43	TRPM4_HUMAN	lasmic (Potential).	2	CACACGCACAT	0.657	
+	4	404	_Intron|TRPM4_u	NM_017636	NP_060106	Q8TD43	TRPM4_HUMAN	lasmic (Potential).	2	ATGGGGCTTCC	0.667	
+	10	1318	e_Mutation_p.G24	NM_017636	NP_060106	Q8TD43	TRPM4_HUMAN	lasmic (Potential).	2	TTCGGGGGGAC	0.572	
+	13	1820	e_Mutation_p.S40	NM_017636	NP_060106	Q8TD43	TRPM4_HUMAN	lasmic (Potential).	2	GGGTTCCAATG	0.582	
-	3	597	p.R135K|PIH1D1_	NM_017916	NP_060386	Q9NWS0	PIHD1_HUMAN		0	AGGCTCTCCCA	0.393	
+	4	213	n_p.T54I|SNORD3	NM_012423	NP_036555	P40429	RL13A_HUMAN		0	GAACACCAACC	0.642	
+	4	449		NM_020719	NP_065770	Q9ULL5	PRR12_HUMAN		2	GTCGGCTTACC	0.662	
+	3	308	ense_Mutation_p.	NM_007121	NP_009052	P55055	NR1H2_HUMAN		0	GGATACCCCCC	0.567	
+	8	1145	rz.3_Intron|NR1H2	NM_007121	NP_009052	P55055	NR1H2_HUMAN	-binding (Potential).	0	AGTGCCTGGTT	0.602	
+	1	331		NM_001506	NP_001497	O75388	GPR32_HUMAN	ellular (Potential).	1	TCGGAGAGTGG	0.527	
-	4	352	_p.P91S|KLK10_	NM_145888	NP_665895	O43240	KLK10_HUMAN	eptidase S1.	2	CAGTGGCCTGG	0.607	
+	7	1382	345V|SIGLEC7_	NM_014385	NP_055200	Q9Y286	SIGL7_HUMAN	c (Potential).|ITIM motif.	1	GTATGCACCCC	0.527	
+	5	923	19orf75_uc010ycw	NM_173635	NP_775906	Q8N7X8	CS075_HUMAN		2	TAGTCGCCACAT	0.458	
-	5	1155	EC8_uc002pwu.2_	NM_014442	NP_055257	Q9NYZ4	SIGL8_HUMAN	ellular (Potential).	5	CGACTGCTGCC	0.567	
+	5	1045		NM_007147	NP_009078	Q9Y473	ZN175_HUMAN		0	AACAGCTTGAT	0.413	
-	5	1580	2_5'Flank|ZNF577	NM_023074	NP_075562	Q9BS31	ZN649_HUMAN	2H2-type 10.	3	GTAAGCTTTCT	0.448	
-	5	1244	77_uc010ydf.1_5'	NM_023074	NP_075562	Q9BS31	ZN649_HUMAN	2H2-type 6.	3	GAAGCCTTTTC	0.463	
-	5	954	77_uc010ydf.1_5'	NM_023074	NP_075562	Q9BS31	ZN649_HUMAN		3	CTCCTCTGTGA	0.488	
-	4	423		NM_023074	NP_075562	Q9BS31	ZN649_HUMAN	KRAB.	3	GTTTGCCGGCT	0.498	
-	5	1115	.2_Intron|uc002py	NM_021632	NP_067645	Q9GZX5	ZN350_HUMAN	2H2-type 4.	1	CCTTTTCCACAT	0.408	
-	6	1047	yh.1_Missense_M	NM_198480	NP_940882	Q8N8J6	ZN615_HUMAN	2H2-type 2.	5	GAGTTCTCTGAT	0.388	
+	2	131	880_uc002pzb.3_	NM_001145434	NP_001138906	Q6PDB4	ZN880_HUMAN	KRAB.	0	CTGCTCAGAGG	0.483	
+	4	643		NM_001145434	NP_001138906	Q6PDB4	ZN880_HUMAN	ype 1; degenerate.	0	TTCAAGACTTGC	0.373	rs8104808
+	7	1816	zi.2_Missense_M	NM_032423	NP_115799	Q3MIS6	ZN528_HUMAN		2	AGAAACCTTAT	0.378	
+	4	1778	po.1_Intron|ZNF5	NM_001143939	NP_001137411	Q76KX8	ZN534_HUMAN	2H2-type 14.	0	TCTTCAGTCGG	0.453	
+	5	1117	.2_RNA|ZNF808_	NM_001039886	NP_001034975	Q8N4W9	ZN808_HUMAN		0	TAAAACCTTACA	0.393	
+	5	2522	.2_RNA|ZNF808_	NM_001039886	NP_001034975	Q8N4W9	ZN808_HUMAN	2H2-type 20.	0	CCATCGTAGAC	0.428	
+	4	1353	dn.1_Missense_M	NM_018260	NP_060730	Q9NV72	ZN701_HUMAN		0	GAAACGTTACA	0.373	

-	2	2553	pv.2_Missense_Mu	NM_018300	NP_060770	P51522	ZNF83_HUMAN	2H2-type 13.	1	GAAGACCTTCC	0.373	
-	5	1219	p.A385T|ZNF347_	NM_032584	NP_115973	Q96SE7	ZN347_HUMAN	2H2-type 5.	0	ACGAGCTCTAA	0.423	
-	5	994	p.V310M|ZNF347_	NM_032584	NP_115973	Q96SE7	ZN347_HUMAN	2H2-type 2.	0	GATCACCTGAT	0.393	
-	5	592	p.A176T|ZNF347_	NM_032584	NP_115973	Q96SE7	ZN347_HUMAN		0	TTCTTGCATCTC	0.368	
-	4	1748		NM_024733	NP_079009	Q9H7R5	ZN665_HUMAN	2H2-type 14.	2	GAAGACCTTGC	0.383	
-	4	651		NM_024733	NP_079009	Q9H7R5	ZN665_HUMAN	2H2-type 1.	2	ACCTTGCCACAT	0.368	
-	1	1399		NM_033341	NP_203127	Q96P09	BIRC8_HUMAN	BIR.	1	CTTGGGCTTCC	0.423	
+	4	2858	dw.1_Missense_M	NM_138374	NP_612383	Q96IR2	ZN845_HUMAN		0	AGAAACCTTACA	0.363	
+	4	2891	dw.1_Missense_M	NM_138374	NP_612383	Q96IR2	ZN845_HUMAN	2H2-type 26.	0	CTTCCGTCACA	0.363	rs150688663
+	4	2950	dw.1_Missense_M	NM_138374	NP_612383	Q96IR2	ZN845_HUMAN	2H2-type 27.	0	TACAAGTGTAAT	0.348	
+	7	1062	_p.L148F|ZNF761_	NM_001008401	NP_001008401	Q86XN6	ZN761_HUMAN		1	TCATTACTCACAC	0.373	
+	7	2551	_p.N644T|ZNF761_	NM_001008401	NP_001008401	Q86XN6	ZN761_HUMAN	2H2-type 18.	1	CAAGAACTTTA	0.393	
+	4	679	313_uc010eqq.1_	NM_001004301	NP_001004301	Q6ZN06	ZN813_HUMAN		1	TAGGCCCAAAA	0.383	
+	4	1746_1747	313_uc010eqq.1_	NM_001004301	NP_001004301	Q6ZN06	ZN813_HUMAN	2H2-type 12.	1	TTGCACATCATC	0.376	
-	3	1940	2qcj.3_Missense_	NM_144687	NP_653288	P59046	NAL12_HUMAN		7	CAGGTGGCTCC	0.577	rs149697517
+	3	630	_p.R161Q|MYADM_	NM_001020820	NP_001018656	Q96S97	MYADM_HUMAN	MARVEL 1.	1	GGCCCGGCCCG	0.662	
+	14	1857	25_splice|PRKCG_	NM_002739	NP_002730	P05129	KPCG_HUMAN		9	CGGAGGTAACC	0.572	
+	16	2292	OT3_uc002qdk.1_	NM_014516	NP_055331	O75175	CNOT3_HUMAN		3	ACTGTGGAATTC	0.642	
-	4	467	uc002qel.1_Intron|	NM_006864	NP_006855	O75022	LIRB3_HUMAN		3	GGCTCCTAGGA	0.622	
-	4	603	.1_Intron|LILRA3_	NM_006865	NP_006856	Q8N6C8	LIRA3_HUMAN	like C2-type 2.	1	GATGGCCCGGG	0.567	
+	4	409	fw.2_Missense_Mutation_p.W89R			Q96PV6	LENG8_HUMAN	Tyr-rich.	2	ACCAGTGGTAC	0.463	
+	7	1200	_p.L321F|LILRB4_	NM_006847	NP_006838	Q8NHJ6	LIRB4_HUMAN	ical; (Potential).	3	cctcctcctccAACAC	0.478	
+	3	161	_Mutation_p.V41M	NM_002255	NP_002246	Q99706	KI2L4_HUMAN	ellular (Potential).	1	CTGTGGTGCCT	0.577	
-	6	874	e_Mutation_p.P15	NM_001145971	NP_001139443	Q8NBN7	RDH13_HUMAN		3	CGCCGGGGTGC	0.647	
+	5	764	kf.2_Missense_Mu	NM_032430	NP_115806	Q8TDC3	BRSK1_HUMAN	rotein kinase.	6	AACCTGCTTTTG	0.612	
-	3	1009		NM_001101401	NP_001094871	P0C263	SBK2_HUMAN		0	TGCCTCCGCCT	0.726	
+	2	277	_5'Flank|FIZ1_uc	NM_153219	NP_694951	Q96C55	ZN524_HUMAN		0	GCCCCCACTGG	0.672	
-	5	1855	b.2_Missense_Mu	NM_145007	NP_659444	P59045	NAL11_HUMAN	NACHT.	6	TCCAGCCTCTG	0.522	
-	5	525	my.2_Nonsense_M	NM_144690	NP_653291	Q96NG8	ZN582_HUMAN		4	GCATTCCCAATC	0.418	
+	5	622	_p.V153I|ZNF583_	NM_001159860	NP_001153332	Q96ND8	ZN583_HUMAN		1	CCAGAAGTTCAA	0.358	
+	5	1875		NM_020813	NP_065864	Q9BX82	ZN471_HUMAN	2H2-type 14.	2	CTTTTAGTGATA	0.428	
+	3	1011		NM_021216	NP_067039	Q9NQZ8	ZNF71_HUMAN	2H2-type 5.	1	CCTCATCGTGC	0.657	
+	3	1014		NM_021216	NP_067039	Q9NQZ8	ZNF71_HUMAN	2H2-type 5.	1	CATCGTGCACC	0.662	
-	7	1975	_p.E513K|PEG3_	NM_001146186	NP_001139658	Q9GZU2	PEG3_HUMAN		12	GGCTTCCTCAC	0.453	
+	3	328	qod.2_Missense_	NM_001015878	NP_001015878	Q9UQB9	AURKC_HUMAN	rotein kinase.	6	TCGGGCGTCCC	0.542	
+	3	1718	_p.A491T|ZNF304_	NM_020657	NP_065708	Q9HCX3	ZN304_HUMAN		1	ACAGGAGCAAGA	0.468	
+	3	389	ZNF17_uc002qop.	NM_006959	NP_008890	P17021	ZNF17_HUMAN	KRAB.	1	TGGAGCCAAGG	0.493	
+	5	647	ense_Mutation_p.	NM_024691	NP_078967	Q96HQ0	ZN419_HUMAN		0	GAAACCCTTAA	0.522	
-	4	1073	47_uc002qpm.3_	NM_017879	NP_060349	Q9BWM5	ZN416_HUMAN	2H2-type 3.	0	ACTGACCACAC	0.453	
+	3	1351	e_Mutation_p.H24	NM_003435	NP_003426	P52741	ZN134_HUMAN	2H2-type 11.	0	ATCGGCACCAG	0.463	
+	3	1043		NM_152677	NP_689890	Q8NAM6	ZSCA4_HUMAN	SCAN box.	1	ACTTGGAGAGA	0.413	
+	2	264	.3_Intron|ZNF776_	NM_138347	NP_612356	Q7Z340	ZN551_HUMAN	KRAB.	1	GTATGACCTTTG	0.502	
-	2	313	671_uc010eug.2_	NM_024833	NP_079109	Q8TAW3	ZN671_HUMAN	KRAB.	1	CAAAAGTCTCT	0.463	
+	3	1094	NF776_uc002qqa.	NM_173632	NP_775903	Q68DI1	ZN776_HUMAN		1	GAAAGACCTTAT	0.423	
+	3	1610	NF776_uc002qqa.	NM_173632	NP_775903	Q68DI1	ZN776_HUMAN	ype 10; degenerate.	1	AGTGTGGAGAA	0.448	
+	3	833	_p.L174F|ZNF586_	NM_017652	NP_060122	Q9NXT0	ZN586_HUMAN	2H2-type 5.	2	CCTTTGCTTATA	0.438	
-	4	2157	F418_uc010yho.1	NM_133460	NP_597717	Q8TF45	ZN418_HUMAN	2H2-type 15.	0	ATTCGCTGCAC	0.438	

-	4	1830	IF418_uc010yho.1	NM_133460	NP_597717	Q8TF45	ZN418_HUMAN	C2H2-type 12.	0	CATTCACTACACT	0.433
+	7	1493	ation_p.S312F|ZNF	NM_014480	NP_055295	Q6NX49	ZN544_HUMAN		1	CCTCATCTTTTTC	0.468
+	3	1235	N22_uc010yhz.1_	NM_181846	NP_862829	P10073	ZSC22_HUMAN	C2H2-type 4.	1	CAGCCGCAGCA	0.592
-	2	1032	_p.A247V|ZBTB45	NM_032792	NP_116181	Q96K62	ZBT45_HUMAN		0	GCAGCAGCAGTG	0.652
+	8	1479	_p.A315V|TRIM28	NM_005762	NP_005753	Q13263	TIF1B_HUMAN		3	TCAATGCCTGGA	0.537
-	5	1006	Flank|CHMP2A_uc	NM_003969	NP_003960	P61081	UBC12_HUMAN		2	ACTCACCAAGA	0.552
-	7	640	Dewe.2_Missense_	NM_015677	NP_056492	Q96HL8	SH3Y1_HUMAN		1	CATAAGCTCGGA	0.318
+	14	2508	k.2_Missense_Muta	NM_000547	NP_000538	P07202	PERT_HUMAN	EGF-like; calcium-binding (	20	CCCACCCCCCCT	0.642
-	10	1305	p.A414V|PXDN_u	NM_012293	NP_036425	Q92626	PXDN_HUMAN	-like C2-type 2.	8	TGGTCGCAGAG	0.592
-	3	1058	p.E317*|CMPK2_	NM_207315	NP_997198	Q5EBM0	CMPK2_HUMAN		0	CTATTTCGGAGG	0.373
-	25	3667	0yiw.1_Intron|KIDIN	NM_020738	NP_065789	Q9ULH0	KDIS_HUMAN	lasmic (Potential).	4	CTGATGGACGT	0.388
-	16	2002	2qzd.2_Missense_	NM_020738	NP_065789	Q9ULH0	KDIS_HUMAN	(Potential).|KAP NTPase.	4	CCTACACTGGAC	0.358
+	10	1274	qzi.2_Missense_Mu	NM_003887	NP_003878	O43150	ASAP2_HUMAN	PH.	0	GGCAGCCTCTAC	0.463
+	4	405	H1_uc002qzt.2_N	NM_001039613	NP_001034702	Q2TAA2	IAH1_HUMAN		0	GAGAATCGAGTC	0.512
+	6	555	utation_p.S152N|T	NM_005680	NP_005671	Q53T94	TAF1B_HUMAN		3	TGCTAAGTGATG	0.408
-	2	194	_p.G71V|PDIA6_u	NM_005742	NP_005733	Q15084	PDIA6_HUMAN		0	TACAGACCATTC	0.413
-	6	1091	_uc002rbg.2_Splic	NM_198256	NP_937987	O75461	E2F6_HUMAN		1	TATTTACCTTCCT	0.393
+	3	547	B1_uc002rbm.2_5'	NM_014668	NP_055483	Q4ZG55	GREB1_HUMAN		1	CTGCACCCTCTG	0.622
+	7	1075	m.2_Missense_Mu	NM_014668	NP_055483	Q4ZG55	GREB1_HUMAN		1	CAGGACCAGCT	0.483
+	10	1549	n_p.V417I|GREB1_	NM_014668	NP_055483	Q4ZG55	GREB1_HUMAN		1	AGTCTGTCTCAC	0.582
+	12	2081	bo.1_Missense_Mu	NM_014668	NP_055483	Q4ZG55	GREB1_HUMAN		1	TACGGGGAAGG	0.418
+	21	3692	bp.1_Missense_Mu	NM_014668	NP_055483	Q4ZG55	GREB1_HUMAN	Ser-rich.	1	CCTCATCCCTCT	0.527
+	2	429	84A_uc002rca.1_5'	NM_145175	NP_660158	Q96KN4	FA84A_HUMAN		1	GCACCCCCTGC	0.647
-	45	5875	exl.1_Missense_Mu	NM_015909	NP_056993	A2RRP1	NBAS_HUMAN		4	GCATAGGTAACT	0.403
-	36	4317	e_Mutation_p.A50	NM_015909	NP_056993	A2RRP1	NBAS_HUMAN		4	GACGGCCTGCA	0.483
+	3	1550	jr.1_Missense_Mu	NM_005378	NP_005369	P04198	MYCN_HUMAN	-loop-helix motif.	5	GAAGGCCGCCA	0.547
-	1	389	0exn.1_Missense_	NM_001099218	NP_001092688	Q09MP3	R51A2_HUMAN		1	CAGGACTTTGTG	0.478
-	27	3444	p.P1050S|SMC6_u	NM_001142286	NP_001135758	Q96SB8	SMC6_HUMAN		6	TTGAGGTGTGA	0.318
-	3	1088		NM_145260	NP_660303	Q8TAX0	OSR1_HUMAN		1	ATCTTGGAGGTTT	0.557
-	14	2249	02_splice|PUM2_u	NM_015317	NP_056132	Q8TB72	PUM2_HUMAN		1	ATGAATCTACATA	0.338
-	3	196	jy.1_Missense_Mu	NM_015317	NP_056132	Q8TB72	PUM2_HUMAN	ction with SNAPIN.	1	GCTGGGACATT	0.343
-	29	13392		NM_000384	NP_000375	P04114	APOB_HUMAN		27	CAGAATGGAAGT	0.363
-	25	4261		NM_000384	NP_000375	P04114	APOB_HUMAN		27	GTGCTGGTGTTG	0.517
-	24	3891		NM_000384	NP_000375	P04114	APOB_HUMAN		27	TATTGAGGTGGT	0.443
-	11	1582		NM_000384	NP_000375	P04114	APOB_HUMAN	Vitellogenin.	27	AAATAGGTGTAAT	0.433
-	24	3581	nse_Mutation_p.P3	NM_017552	NP_060022	Q9ULI0	ATD2B_HUMAN		1	CTATGAGGATTTA	0.373
-	19	2926	nse_Mutation_p.P1	NM_017552	NP_060022	Q9ULI0	ATD2B_HUMAN		1	CTTCAGGCAGTT	0.294
-	15	2023	i.1_RNA|ATAD2B_	NM_017552	NP_060022	Q9ULI0	ATD2B_HUMAN		1	TTCTTGCCTAAGA	0.348
-	35	4538	ff.2_Missense_Mut	NM_006277	NP_006268	Q9NZM3	ITSN2_HUMAN		4	CAGTTGGTGAGA	0.478
+	3	260	NCOA1_uc002rfj.2	NM_003743	NP_003734	Q15788	NCOA1_HUMAN		11	CAACATGAGTGG	0.478
+	14	3035	_p.R775K|NCOA1	NM_003743	NP_003734	Q15788	NCOA1_HUMAN	ction with CREBBP.	11	AGGGAGAAATGA	0.428
+	18	3974	rfj.2_Missense_Mu	NM_003743	NP_003734	Q15788	NCOA1_HUMAN		11	GGTTCCCCAAG	0.418
-	4	1265	CY3_uc010ykm.1	NM_004036	NP_004027	O60266	ADCY3_HUMAN		4	TTACAGCTGCCA	0.632
-	7	809	G182D|DNAJC27_	NM_016544	NP_057628	Q9NZQ0	DJC27_HUMAN	J.	1	CACTGCCAGGT	0.438
-	19	2542	MT3A_uc010eyi.2_	NM_022552	NP_072046	Q9Y6K1	DNM3A_HUMAN		140	CTAACGCCCATG	0.547
-	12	4451	gt.1_Nonsense_Mu	NM_018263	NP_060733	Q76L83	ASXL2_HUMAN	D-type; atypical.	1	GCCTTTGCACAT	0.522
-	8	1146	gt.1_Missense_Mu	NM_018263	NP_060733	Q76L83	ASXL2_HUMAN		1	CTACCTCTGGGA	0.393

-	7	943	L2_uc002rgt.1_5'	NM_018263	NP_060733	Q76L83	ASXL2_HUMAN		1	AGTAAAGTATTTT	0.413
-	5	688	L2_uc002rgt.1_5'	NM_018263	NP_060733	Q76L83	ASXL2_HUMAN	Ser-rich.	1	ATGGAGAAATG	0.428
-	1	1012	F3C_uc010ykr.1_	NM_002254	NP_002245	O14782	KIF3C_HUMAN	inesin-motor.	4	GATGACCCCGC	0.592
+	13	1393	_p.A366V|HADHB_	NM_000183	NP_000174	P55084	ECHB_HUMAN		2	TGAAGCTTTCT	0.348
-	11	1745	113_uc010eyk.1_	NM_001145168	NP_001138640	Q8IZF5	GP113_HUMAN	ellular (Potential).	4	GGAGAGTCGAG	0.607
-	7	740	OF_uc010ylb.1_R	NM_194248	NP_919224	Q9HC10	OTOF_HUMAN	lasmic (Potential).	7	GTCAAGGTCTT	0.502
+	8	1014	hv.3_Nonsense_	NM_020134	NP_064519	Q9BPU6	DPYL5_HUMAN		2	ACCACCAGGAC	0.577
+	6	907	EM214_uc002rib.	NM_017727	NP_060197	Q6NUQ4	TM214_HUMAN		0	AGCAGGTTTTG	0.567
-	8	1344	EB_uc002riz.1_R	NM_013388	NP_037520	Q9HCU5	PREB_HUMAN	lasmic (Potential).	1	CATGGGACCCA	0.602
+	3	464	w.2_Missense_Mu	NM_004341	NP_004332	P27708	PYR1_HUMAN	amine amidotransferase).	10	TGCCACCCGCA	0.572
+	9	1387	v.2_Missense_Mu	NM_004341	NP_004332	P27708	PYR1_HUMAN	phosphate synthase).|CPS	10	GCCAAGCTGGA	0.592
+	41	6496	.2_Missense_Mut	NM_004341	NP_004332	P27708	PYR1_HUMAN	artate transcarbamylase).	10	GCATGCCACCC	0.652
+	10	1172	e_Mutation_p.R10	NM_014748	NP_055563	Q15036	SNX17_HUMAN		1	TCACCCGCATGC	0.657
+	19	2417	002rkr.2_Missense	NM_013392	NP_037524	Q9UHY1	NRBP_HUMAN		3	ACTCAGCCGCT	0.592
-	32	3533	72_uc010ezb.2_5'	NM_015662	NP_056477	Q9UG01	IF172_HUMAN	TPR 9.	2	CTTCAGCCTCT	0.527
-	4	855	R_uc010ezd.2_5'	NM_022823	NP_073734	Q9H6D8	FNDC4_HUMAN	ellular (Potential).	0	CTGGGCTTGAA	0.557
+	19	1844	_p.A591V|GCKR_	NM_001486	NP_001477	Q14397	GCKR_HUMAN		2	GGCTGCAGCTC	0.607
+	1	4679	1_5'Flank|ZNF512_	NM_032266	NP_115642	Q68DN1	CB016_HUMAN		1	ACCCCAGCTTCT	0.537
+	1	5482	1_5'Flank|ZNF512_	NM_032266	NP_115642	Q68DN1	CB016_HUMAN	dem repeat of P-S-E-R-S-H	1	CCTTGGAGAGG	0.537
+	4	436	F512_uc010ylx.1_	NM_032434	NP_115810	Q96ME7	ZN512_HUMAN		1	AATTTCCTCAG	0.413
-	5	1175	_p.E143K|SUPT7L_	NM_014860	NP_055675	O94864	ST65G_HUMAN		2	AGGTTCCTCCT	0.502
+	22	1478	nc.2_Missense_M	NM_153021	NP_694566	Q6P1J6	PLB1_HUMAN	ate repeats.|2.|Extracellular	9	GAAGAATGACA	0.582
+	39	2674	LB1_uc002rme.1_	NM_153021	NP_694566	Q6P1J6	PLB1_HUMAN	ate repeats.|Extracellular (	9	CTTAGGTGCCC	0.587
+	46	3265	B1_uc002rme.1_	NM_153021	NP_694566	Q6P1J6	PLB1_HUMAN	ate repeats.|Extracellular (	9	ACCAGCTCCGA	0.552
+	2	282	P4_uc010ezm.1_	NM_024692	NP_078968	Q8N3C7	CLIP4_HUMAN		1	GAAATCCTTTG	0.358
+	3	433	se_Mutation_p.T6	NM_024692	NP_078968	Q8N3C7	CLIP4_HUMAN	ANK 1.	1	CAAAACTTCAG	0.294
-	29	5261	o.1_Missense_Mu	NM_004304	NP_004295	Q9UM73	ALK_HUMAN	lasmic (Potential).	1218	TGCAGCCTTGC	0.607
-	20	4094	_uc010ymo.1_5'	NM_004304	NP_004295	Q9UM73	ALK_HUMAN	lasmic (Potential).	1218	CTGGTGCTTCC	0.597
-	3	1707		NM_004304	NP_004295	Q9UM73	ALK_HUMAN	xtracellular (Potential).	1218	CAAAGCTGCAC	0.567
-	7	963	q.2_Missense_Mu	NM_015955	NP_057039	Q9Y316	MEMO1_HUMAN		2	TTTGACCTTGA	0.338
-	4	2306	_Mutation_p.A68	NM_021209	NP_067032	Q9NPP4	NLRC4_HUMAN		6	TTGTGGCAGAG	0.463
-	4	1642	_Mutation_p.E46	NM_021209	NP_067032	Q9NPP4	NLRC4_HUMAN	NACHT.	6	CACCTCCTCTG	0.458
+	10	2905		NM_016252	NP_057336	Q9NR09	BIRC6_HUMAN		14	TTTGGCCAAAG	0.423
+	43	8275		NM_016252	NP_057336	Q9NR09	BIRC6_HUMAN		14	CAATACTTTGCT	0.348
+	3	613		NM_206943	NP_996826	Q14766	LTBP1_HUMAN	EGF-like 1.	8	GGCCACAACTC	0.527
+	4	991		NM_206943	NP_996826	Q14766	LTBP1_HUMAN		8	TCTTTCCCTTTA	0.468
+	5	1091	v.2_Missense_M	NM_206943	NP_996826	Q14766	LTBP1_HUMAN		8	AGTGACCTGCA	0.532
-	8	1297	nd.1_Missense_	NM_015475	NP_056290	Q8NCA5	FA98A_HUMAN	Gly-rich.	1	GATAGCCACCT	0.527
-	3	282	8A_uc010yne.1_	NM_015475	NP_056290	Q8NCA5	FA98A_HUMAN		1	TTCACTCGGAC	0.353
+	5	540	.2_Missense_Mut	NM_053276	NP_444506	Q6UXI7	VITRN_HUMAN	LCCL.	2	GGAAGGTTGCT	0.398
-	7	2341		NM_005760	NP_005751	Q03701	CEBPZ_HUMAN		1	GCATACCTTTG	0.318
-	2	1717		NM_006449	NP_006440	Q9UKI2	BORG2_HUMAN		0	CAAAAGTGAGG	0.453
-	2	1354		NM_006449	NP_006440	Q9UKI2	BORG2_HUMAN		0	TAAGGGCAACA	0.542
-	23	3729	j.3_Missense_Mut	NM_005633	NP_005624	Q07889	SOS1_HUMAN		10	TAGTGGTGAGC	0.507
-	19	3102	j.3_Missense_Mut	NM_005633	NP_005624	Q07889	SOS1_HUMAN		10	CTTAGGGTTTC	0.353
-	9	659	_Mutation_p.G190	NM_003618	NP_003609	Q8IVH8	M4K3_HUMAN	rotein kinase.	8	GTAACCCCCCT	0.433
-	7	2104	utation_p.E681K|	NM_021097	NP_066920	P32418	NAC1_HUMAN	ytoplasmic (Potential).	4	TCTCCTCTTCCT	0.478

-	1	1373	rsd.3_Missense_M	NM_021097	NP_066920	P32418	NAC1_HUMAN	|Cytoplasmic (Potential).	4	TTTGCTGTGCCAT	0.448	
+	7	957	p.2_Missense_Mu	NM_019063	NP_061936	Q9HC35	EMAL4_HUMAN		250	TATGCGCGGTCC	0.388	rs149615272
-	1	523	KHH2_uc002rtf.3_I	NM_001101330	NP_001094800				0	CGAGGTCTCCAA	0.428	
+	15	2535	LEKHH2_uc002rtf	NM_172069	NP_742066	Q8IVE3	PKHH2_HUMAN	PH 2.	3	GGATTGCTCACTA	0.478	
-	16	1785	vob.1_Missense_M	NM_133259	NP_573566	P42704	LPPRC_HUMAN		3	GTCGGTCCTCGA	0.403	
+	2	925	M1B_uc002rtv.2_In	NM_002706	NP_002697	O75688	PPM1B_HUMAN		2	TTTCTACCCAGGA	0.428	
+	9	1612	p.D512N|SLC3A1_	NM_000341	NP_000332	Q07837	SLC31_HUMAN	cellular (Potential).	0	CAGTGGGACAATA	0.393	
-	10	1684	_p.P550L|PREPL_	NM_006036	NP_006027	Q4J6C6	PPCEL_HUMAN		1	GACTTGGCTGA	0.507	
+	13	1938		NM_005400	NP_005391	Q02156	KPCE_HUMAN	rotein kinase.	10	CTGCAGGAGTTG	0.582	
+	1	395	71E2_uc002ruz.2_	NM_012249	NP_036381	P17081	RHOQ_HUMAN		2	TGCCTACTCATGA	0.677	
+	6	1081	vz.2_Missense_Mu	NM_000251	NP_000242	P43246	MSH2_HUMAN		55	CTCAAGGACAAA	0.368	
-	2	880	H2_uc002rvz.2_In	NM_022055	NP_071338	Q9HB15	KCNKC_HUMAN	ical; (Potential).	1	TGAAGAGCGAGT	0.642	
+	2	413	10fbj.2_Splice_Site	NM_000179	NP_000170	P52701	MSH6_HUMAN		168	GCAACAGTTGTGA	0.408	
+	6	1084		NM_002158	NP_002149	P32314	FOXN2_HUMAN		0	ATTTTAGAATGTA	0.254	
+	7	804	wl.2_Missense_Mu	NM_001135629	NP_001129101	Q6ZMI0	KLRAQ_HUMAN	Potential.	1	AAGACTCTTCATG	0.308	
+	1	930	GTF2A1L_uc002rw	NM_006873	NP_006864	B7ZL16	B7ZL16_HUMAN		5	CAATGGGGACCA	0.413	
-	11	1133	2A1L_uc002rwt.2_	NM_000233	NP_000224	P22888	LSHR_HUMAN	cellular (Potential).	8	TAATATCTTCACA	0.443	
-	10	1017	_p.A253T|FSHR_u	NM_000145	NP_000136	P23945	FSHR_HUMAN	cellular (Potential).	8	CTTCTGCCAGAGA	0.433	
+	1	216	.1_Intron|ASB3_u	NM_001008708	NP_001008708	Q8WUX2	CHAC2_HUMAN		0	ACCGCGGGGTC	0.632	
+	11	1392	se_Mutation_p.S37	NM_015701	NP_056516	Q96DZ1	ERLEC_HUMAN	PRKCSH 2.	2	AGGATAGTGGGA	0.398	
+	16	3245	rxx.2_Missense_M	NM_003128	NP_003119	Q01082	SPTB2_HUMAN	Spectrin 7.	8	GCTGACCGGCAT	0.622	
+	27	6058	_p.Q1924*|SPTBN	NM_003128	NP_003119	Q01082	SPTB2_HUMAN	.|Interaction with ANK2.	8	AGGCCCAGGAG	0.547	
-	32	6436	_p.R156K|CCDC8	NM_001135597	NP_001129069	Q3V6T2	GRDN_HUMAN		4	TGCTCCCTAGAC	0.358	
-	31	6358	_p.A341V|CCDC8	NM_001135597	NP_001129069	Q3V6T2	GRDN_HUMAN		4	GCAGCAGCTGGT	0.458	
-	31	6321	_p.D329N|CCDC8	NM_001135597	NP_001129069	Q3V6T2	GRDN_HUMAN		4	TACTGTCCTTGGT	0.473	
+	15	1538	DLG_uc002sak.2_	NM_022894	NP_075045	Q9BWT3	PAPOG_HUMAN		2	CAATGTGGTTCCT	0.279	
+	21	2299	sak.2_Missense_M	NM_022894	NP_075045	Q9BWT3	PAPOG_HUMAN		2	ATTGGAGGAGAA	0.328	
+	11	1771	n.1_Missense_Mut	NM_002908	NP_002899	Q04864	REL_HUMAN		3	TTCTGAGCATGA	0.438	
-	16	1453	_p.E465K|PUS10_	NM_144709	NP_653310	Q3MIT2	PUS10_HUMAN		4	GTGTCTCCATGAA	0.542	
-	30	4207		NM_014709	NP_055524	Q70CQ2	UBP34_HUMAN		19	AGCTCCCAGAC	0.368	
+	2	480		NM_006577	NP_006568	Q9NY97	B3GN2_HUMAN	nenal (Potential).	1	CCAGACGGGGG	0.557	
+	2	611		NM_006577	NP_006568	Q9NY97	B3GN2_HUMAN	nenal (Potential).	1	TTGAGATGCCGC	0.458	
+	14	2842	oz.2_Missense_Mu	NM_015252	NP_056067	Q8NDI1	EHBP1_HUMAN		2	CGGAGTCTGATC	0.348	
-	9	1197	2scg.2_Missense_	NM_015910	NP_056994	O95876	FRITZ_HUMAN		0	CCCAAGGCCAAG	0.458	
+	8	1579	p.P414S|UGP2_u	NM_006759	NP_006750	Q16851	UGPA_HUMAN		0	GAATTTCCTACA	0.358	
+	5	2426	sda.2_Splice_Site_	NM_203437	NP_982261	Q6ULP2	AFTIN_HUMAN		2	GTTCCAGGTAAAA	0.279	
-	1	199	se_Mutation_p.A40	NM_138458	NP_612467	Q96MX6	WDR92_HUMAN		0	CCCGTGCGAAGT	0.602	
+	2	414	1_5'Flank|WDR92_	NM_020143	NP_064528	Q9NRX1	PNO1_HUMAN		0	GTAGAAATCAGG	0.368	
+	5	640		NM_020143	NP_064528	Q9NRX1	PNO1_HUMAN	KH.	0	AATTCACCATAGA	0.363	
+	10	1791	2sew.2_Missense_	NM_001007231	NP_001007232	P42331	RHG25_HUMAN		4	AGAGGCTAAGG	0.502	
+	1	814	sgb.1_5'Flank|uc0	NM_006196	NP_006187	Q15365	PCBP1_HUMAN		0	CTCCGCAAGGG	0.652	
-	11	1044	se_Mutation_p.G26	NM_022173	NP_071505	P31483	TIA1_HUMAN	RRM 3.	0	ACATGACCTTCAA	0.368	
-	4	477	vqv.1_Nonsense_M	NM_173535	NP_775806	Q8N1N0	CLC4F_HUMAN	cellular (Potential).	5	GGAGCTGCGAAT	0.468	
-	1	163	261_uc010fdy.2_5'	NM_144582	NP_653183	Q6UWH6	TX261_HUMAN	ical; (Potential).	0	TGAAGGCCACCT	0.582	
+	2	692	OSPH10_uc010fe	NM_005791	NP_005782	O00566	MPP10_HUMAN	Potential.	3	GAACAGGAACGT	0.408	
+	7	1679		NM_005791	NP_005782	O00566	MPP10_HUMAN		3	GTAGTACGTAAA	0.338	
+	2	401	sense_Mutation_p	NM_014497	NP_055312	Q14966	ZN638_HUMAN		4	GGCCTCCAGGA	0.502	

+	11	2706	›.G796E|ZNF638_	NM_014497	NP_055312	Q14966	ZN638_HUMAN		4	‹AACTGGACAAG‹	0.274	
+	14	2925	p.T869I|ZNF638_u	NM_014497	NP_055312	Q14966	ZN638_HUMAN		4	TAAAGACCAGTAT	0.284	
-	3	1349	)2sit.3_Missense_I	NM_015470	NP_056285	Q9BXF6	RFIP5_HUMAN		0	‹GACAGCTTGCA/	0.612	
+	3	322	.2_Missense_Muta	NM_006429	NP_006420	Q99832	TCPH_HUMAN		0	;TCCATCCTGCA(	0.383	
-	8	2107		NM_001080410	NP_001073879	Q8TF61	FBX41_HUMAN		3	‹GCAGCCCCTGG	0.617	
+	14	10021	90_splice|ALMS1_	NM_015120	NP_055935	Q8TCU4	ALMS1_HUMAN		9	ATTCAGGTATTAT	0.353	
+	18	11291	g.2_Missense_Mut	NM_015120	NP_055935	Q8TCU4	ALMS1_HUMAN		9	AGCCAGGTTTTA.	0.393	
-	9	1088		NM_003584	NP_003575	O75319	DUS11_HUMAN		1	;GACTGGCATTG(	0.507	
+	5	571	_p.T150I|ACTG2_	NM_001615	NP_001606	P63267	ACTH_HUMAN		0	;CACGACAGGTG	0.493	
+	1	1576	z.1_Missense_Mut	NM_144993	NP_659430	O43151	TET3_HUMAN		0	;CCCCAGAACCT	0.642	
-	1	28	ɜnse_Mutation_p.(	NM_021196	NP_067019	Q9BY07	S4A5_HUMAN	lasmic (Potential).	9	;CTACCCCAGCC	0.343	
-	28	3625	ɜ_Mutation_p.S966	NM_004082	NP_004073	Q14203	DCTN1_HUMAN		5	‹GCTGGGAGATG	0.592	
-	12	1593	;kw.1_Missense_M	NM_004082	NP_004073	Q14203	DCTN1_HUMAN	Potential.	5	;CTGCTCCTTGA(	0.567	
-	7	896	_p.A247V|RTKN_u	NM_001015055	NP_001015055	Q9BST9	RTKN_HUMAN		1	;TGTGAGCCAAG/	0.557	
+	4	442	1_RNA|INO80B_u	NM_031288	NP_112578	Q9C086	IN80B_HUMAN		1	;CCTCTCCACTT(	0.512	
-	12	2122	_p.V628M|LOXL3_	NM_032603	NP_115992	P58215	LOXL3_HUMAN	;yl-oxidase like.	0	;CTTCACATCCG	0.522	
-	8	1382	)XL3_uc002smq.1	NM_032603	NP_115992	P58215	LOXL3_HUMAN	SRCR 4.	0	;GCCCAGGTCCC	0.632	
+	5	1260	ssense_Mutation_	NM_001381	NP_001372	Q99704	DOK1_HUMAN	Pro-rich.	0	'GCCACCCCCTC(	0.617	
+	3	2189		NM_000189	NP_000180	P52789	HXK2_HUMAN	ıtory.|Glucose-6-phosphate	2	;AGGGACCAACT	0.507	
-	2	1479	;OLN2_uc002spb.2	NM_006464	NP_006455	O43493	TGON2_HUMAN	ical; (Potential).	0	‹GGACAGCCACA/	0.557	
-	4	904	sm.1_Missense_M	NM_017750	NP_060220	Q6NUM9	RETST_HUMAN		2	'GGGTGGATGCT	0.597	
+	4	476	;e_Mutation_p.G14	NM_006590	NP_006581	Q53GS9	SNUT2_HUMAN	UBP-type.	1	;CCGGGGTTTGA	0.453	
-	13	2058		NM_015425	NP_056240	O95602	RPA1_HUMAN		3	'GGATGGAGGGT	0.577	
+	12	2129	p.G601D|KDM3A_	NM_018433	NP_060903	Q9Y4C1	KDM3A_HUMAN		5	;AATTGGCTTGT(	0.418	
+	16	2723	p.G799D|KDM3A_	NM_018433	NP_060903	Q9Y4C1	KDM3A_HUMAN		5	;TGTGGGTGGGG	0.562	
-	3	292	ɜnse_Mutation_p.G	NM_016079	NP_057163	Q9Y3E7	CHMP3_HUMAN	nteraction with C- terminus	1	'CTGGCCCTTCTT	0.433	
-	1	169	2srl.2_Missense_M	NM_016079	NP_057163	Q9Y3E7	CHMP3_HUMAN	nteraction with C- terminus	1	;CAGTTCTTTGGG	0.607	
-	4	2176	)02srm.2_Missens	NM_005667	NP_005658	O00237	RN103_HUMAN		1	‹TGAAGCCAGTG	0.393	
+	4	931	Intron|TEKT4_uc0	NM_144705	NP_653306	Q8WW24	TEKT4_HUMAN		3	CCGAGGACCTG(	0.672	
-	3	454	ud.1_Missense_M	NM_032788	NP_116177	Q96K75	ZN514_HUMAN	KRAB.	0	‹CCTCCCTGTAG/	0.517	
+	2	186	2sus.2_Missense_I	NM_016044	NP_057128	Q96GK7	FAH2A_HUMAN		1	‹TGCTGGTGTCT(	0.542	
+	52	6106	;wt.3_Missense_M	NM_001113382	NP_001106853	A0AVI2	FR1L5_HUMAN		1	;TATCCTCCCATT/	0.463	
-	13	1703	;xe.2_Missense_M	NM_017789	NP_060259	Q9C0C4	SEM4C_HUMAN	racellular (Potential).	2	‹ATAGGGGTCCC(	0.647	
+	20	2975	ıse_Mutation_p.K2	NM_144992	NP_659429	Q502W6	VWA3B_HUMAN		6	CAAATAAGATGA(	0.418	
+	4	648	ınse_Mutation_p.P	NM_014044	NP_054763	Q53HI1	UNC50_HUMAN	ical; (Potential).	0	TTTTATCCACTCC	0.368	
-	4	651	‹T4A_uc010fil.2_5'	NM_012214	NP_036346	Q9UM21	MGT4A_HUMAN	ıenal (Potential).	1	‹ATGAGGCAAAT(	0.328	
-	15	2163	2szi.3_Missense_M	NM_182911	NP_878915	Q9BZW7	TSG10_HUMAN		2	‹GTTCCCTAGTA(	0.338	
+	6	1466		NM_015904	NP_056988	O60841	IF2P_HUMAN		3	;TACAAGCTCAG(	0.398	
+	12	2214		NM_015904	NP_056988	O60841	IF2P_HUMAN		3	TTGAAGCTATTA/	0.343	
-	4	394	;1_splice|REV1_u	NM_016316	NP_057400	Q9UBZ9	REV1_HUMAN		2	GAAGGATCTGCa	0.308	
-	2	558		NM_153836	NP_722578	Q8IUH2	CREG2_HUMAN		1	‹AGAAAGGAATC(	0.517	
+	11	1463	bt.2_Missense_Mu	NM_003854	NP_003845	Q9HB29	ILRL2_HUMAN	oplasmic (Potential).	2	'GTGCAGGAGGC	0.493	
+	10	1674	fiz.2_Missense_M	NM_003853	NP_003844	O95256	I18RA_HUMAN	lasmic (Potential).	5	‹CCAGAGCAAGG.	0.557	
+	2	690		NM_003048	NP_003039	Q9UBY0	SL9A2_HUMAN	ame=E/M5; (Potential).	8	;CATTGGCATTGG	0.498	rs140049116
+	12	2408		NM_003048	NP_003039	Q9UBY0	SL9A2_HUMAN	lasmic (Potential).	8	;AAAAGGGCACC	0.542	
+	2	347	e_Mutation_p.G11	NM_144632	NP_653233	Q6ZP80	TM182_HUMAN	;ellular (Potential).	0	;ATGAAGGGTTC	0.353	
+	3	674	)fjd.1_Splice_Site_	NM_024093	NP_076998	Q9BVC5	ASHWN_HUMAN		0	;CCATGGTAAGT/	0.512	

-	9	842	3_splice|UXS1_uc	NM_025076	NP_079352	Q8NBZ7	UXS1_HUMAN		2	AAATACCTGCT	0.498	
-	20	3299		NM_001144013	NP_001137485	A6NKT7	RGPD3_HUMAN	RanBD1 1.	1	CCAAGCCCCTT	0.378	
-	2	1006	p.C296Y|ST6GAL	NM_001142351	NP_001135823	Q96JF0	SIAT2_HUMAN	enal (Potential).	11	CAGCGCAGCTG	0.687	
-	2	539	p.W140*|ST6GAL	NM_001142351	NP_001135823	Q96JF0	SIAT2_HUMAN	enal (Potential).	11	CTGTGCCACCC	0.572	
+	20	3830	_Mutation_p.D43	NM_182588	NP_872394	Q7Z3J3	RGPD4_HUMAN		2	AATGGGATAACT	0.443	
+	20	3896	_Mutation_p.P45	NM_182588	NP_872394	Q7Z3J3	RGPD4_HUMAN		2	CTTCTCCATTG	0.403	
+	5	577		NM_001008743	NP_001008743	Q6IMI6	ST1C3_HUMAN		1	CAAAAGACATG	0.468	rs140068346
+	6	1169	d.2_Missense_Mu	NM_181453	NP_852118	Q8IWJ2	GCC2_HUMAN	Potential.	1	TTAGAAGATACC	0.294	
+	6	2048	d.2_Missense_Mu	NM_181453	NP_852118	Q8IWJ2	GCC2_HUMAN	Potential.	1	AAGTAGAGCAA	0.313	rs145077426
+	20	6187		NM_006267	NP_006258	P49792	RBP2_HUMAN	RanBD1 2.	18	TGCCCGAAAAA	0.388	
+	20	7676		NM_006267	NP_006258	P49792	RBP2_HUMAN		18	ATTTGGTTCAG	0.383	
+	28	9431		NM_006267	NP_006258	P49792	RBP2_HUMAN	e cyclophilin-type.	18	CACTGGAGAGA	0.403	
+	2	203	T48I|CCDC138_uc	NM_144978	NP_659415	Q96M89	CC138_HUMAN		0	TCTAACCTCCC	0.194	
-	6	617	tfo.3_Splice_Site_	NM_207181	NP_997064	O15259	NPHP1_HUMAN		2	CCTTTCTTAAAG	0.323	
-	11	1590		NM_022662	NP_073153	Q9H1A4	APC1_HUMAN		2	GCTGGGACTCT	0.313	
+	9	1525	hl.1_Missense_Mu	NM_006343	NP_006334	Q12866	MERTK_HUMAN	III 2.|Extracellular (Potentia	9	AGGGGGAGTTG	0.537	
+	9	1214		NM_032824	NP_116213	Q96K49	TM87B_HUMAN		0	CCCAAGGCTTAT	0.418	
+	3	929	117N|POLR1B_uc	NM_019014	NP_061887	Q9H9Y6	RPA2_HUMAN		1	AGGCTGATATC	0.343	
+	9	1932	kp.2_Intron|POLR	NM_019014	NP_061887	Q9H9Y6	RPA2_HUMAN		1	AGATTCTGGAC	0.438	
+	15	3701	p.2_Missense_Mu	NM_019014	NP_061887	Q9H9Y6	RPA2_HUMAN		1	AGATGGAACGG	0.507	
+	4	1391	e.2_Missense_Mu	NM_012455	NP_036587	Q8NDX1	PSD4_HUMAN		2	AGGAGGTCCTT	0.488	
+	13	2570	_Splice_Site_p.T4	NM_012455	NP_036587	Q8NDX1	PSD4_HUMAN		2	GAACAGCGCCA	0.552	
+	26	2769	_p.S767N|DPP10_	NM_020868	NP_065919	Q8N608	DPP10_HUMAN	ellular (Potential).	10	CTACAGCACAA	0.368	
+	10	1574		NM_006773	NP_006764	Q9NVP1	DDX18_HUMAN	case C-terminal.	4	CATTCCTGAAG	0.438	
+	12	1177	yf.1_Missense_Mu	NM_006770	NP_006761	Q9UEW3	MARCO_HUMAN	.|Extracellul p.G349R(1)	6	TGAAAGGAAGC	0.567	rs137938144
+	2	87		NM_183240	NP_899063	Q8WXS4	CCGL_HUMAN		1	GCCCCGCCGGT	0.617	
+	2	537		NM_183240	NP_899063	Q8WXS4	CCGL_HUMAN	ical; (Potential).	1	CACTGCCTCCT	0.557	
-	2	300		NM_002980	NP_002971	P47872	SCTR_HUMAN	ellular (Potential).	3	CTCCAGTCTGC	0.532	
+	2	621	TMEM177_uc002tr	NM_001105198	NP_001098668	Q53S58	TM177_HUMAN		1	ACTGGCCTCAG	0.587	
+	9	1441	PN4_uc010flj.1_5'	NM_002830	NP_002821	P29074	PTN4_HUMAN	FERM.	2	ACTATGCAAGG	0.333	
+	2	181	fll.2_Missense_M	NM_020909	NP_065960	Q9HCM4	E41L5_HUMAN		1	ATGCAGAGAAG	0.478	
+	2	306	10fll.2_Splice_Site_	NM_020909	NP_065960	Q9HCM4	E41L5_HUMAN		1	TTGCCAGTAAGT	0.438	
+	13	3892	t.3_Missense_Mu	NM_005270	NP_005261	P10070	GLI2_HUMAN		13	CAGAAGTGGCA	0.637	
-	4	428	flr.2_Missense_M	NM_014553	NP_055368	Q9NZI6	TF2L1_HUMAN		3	TGCTCCGTATAC	0.662	
-	2	277	0flr.2_Missense_M	NM_014553	NP_055368	Q9NZI6	TF2L1_HUMAN		3	TTCATGCAGCT	0.622	
-	6	747	uc002tnj.1_RNA	NM_032390	NP_115766	Q9BYG3	MK67I_HUMAN		0	CTCAGGAGTGT	0.338	
+	3	704	flu.2_Missense_M	NM_130773	NP_570129	Q8WYK1	CNTP5_HUMAN	|Extracellular (Potential).	10	ACACAGGACGC	0.473	
+	4	401	se_Mutation_p.R6	NM_002101	NP_002092	P04921	GLPC_HUMAN	Cytoplasmic.	1	GCTGCGCTACA	0.607	rs149400883
-	1	380	w.1_Missense_Mu	NM_139343	NP_647593	O00499	BIN1_HUMAN	action with BIN2.	7	TCTTTCCCGCC	0.726	
-	4	566		NM_001001665	NP_001001665	Q4G0S4	C27C1_HUMAN		0	TCGGTCCATTTG	0.483	
-	8	1189	p.G301D|ERCC3_	NM_000122	NP_000113	P19447	ERCC3_HUMAN	ase ATP-binding.	7	AGTTGCCCAGC	0.542	
-	9	2194	S1_uc010yzl.1_R	NM_017969	NP_060439	Q96ST2	IWS1_HUMAN	IIS N-terminal.	1	CTTGAGTGCAG	0.438	
+	31	4230	_p.R246*|MYO7B_	NM_001080527	NP_001073996	Q6PIF6	MYO7B_HUMAN	FERM 1.	2	CCGTGCGAGAG	0.617	
-	16	1942		NM_018383	NP_060853	Q9C0J8	WDR33_HUMAN		0	AAAAGGCTGGG	0.493	
+	1	857	c002tpw.1_5'Flan	NM_032144	NP_115520	Q9H0N0	RAB6C_HUMAN		1	AGAGGCAAGTG	0.428	
-	3	707		NM_001099771	NP_001093241	A5A3E0	POTEF_HUMAN		5	GTGGCAGCACC	0.617	
+	9	1703	_p.L395F|ARHGE	NM_015320	NP_056135	Q9NR80	ARHG4_HUMAN	DH.	6	CCAAGCTCAGC	0.572	

+	5	870	HB2_uc010zao.1_	NM_001100623	NP_001094093	Q96CS7	PKHB2_HUMAN	PH.	2	TTTACACTCCAA	0.214
+	4	679		NM_080386	NP_525125	Q13748	TBA3C_HUMAN		0	GACCACCCACA	0.542
+	1	704		NM_001508	NP_001499	O43194	GPR39_HUMAN	Name=2; (Potential).	0	TGCTCGGACATC	0.557
-	2	1074	se_Mutation_p.L49	NM_144586	NP_653187	Q8N2G4	LYPD1_HUMAN	UPAR/Ly6.	0	TTGTTCAGCTGG	0.552
-	18	5924	ttq.2_Nonsense_M	NM_207363	NP_997246	O14513	NCKP5_HUMAN		0	CTCCCCCAGTC	0.542
-	9	3842	_Mutation_p.D115	NM_025052	NP_079328	Q56UN5	YSK4_HUMAN	rotein kinase.	5	CCTGTCCATGG	0.507
+	1	39	tion_p.S5N|RAB3	NM_012233	NP_036365	Q15042	RB3GP_HUMAN		2	CGACAGTGAGG	0.428
-	15	1590	j.1_Missense_Mu	NM_001349	NP_001340	P14868	SYDC_HUMAN		1	TGCCTCCACCA	0.313
+	3	982	SD7B_uc002tvb.2	NM_001080427	NP_001073896				7	TCTTGCCAGGA	0.532
+	9	1327	_p.A245V|ACVR2A	NM_001616	NP_001607	P27037	AVR2A_HUMAN	Potential).|Protein kinase.	13	GTCTGCAGGCG	0.388
+	12	4221	BD5_uc002two.2_	NM_018328	NP_060798	Q9P267	MBD5_HUMAN		5	TGTGGGTGGCC	0.498
+	6	907		NM_015630	NP_056445	Q52LR7	EPC2_HUMAN		3	GAAAAAGAGTTA	0.333
+	5	501	1_uc002txn.2_Mis	NM_018151	NP_060621	Q5UIP0	RIF1_HUMAN		15	TGATATCTAAGC	0.338
+	30	6557	_Mutation_p.A21	NM_018151	NP_060621	Q5UIP0	RIF1_HUMAN	nsed chromosomes in telo	15	AATAATGCATCT	0.443
-	100	14833	.2_Missense_Muta	NM_004543	NP_004534	P20929	NEBU_HUMAN	Nebulin 133.	20	ATGTGAGCTTTA	0.428
-	81	12516	.2_Missense_Mut	NM_004543	NP_004534	P20929	NEBU_HUMAN	Nebulin 112.	20	TCACATCGCTCT	0.493
-	3	294	_p.E58K|CACNB4	NM_000726	NP_000717	O00305	CACB4_HUMAN		2	TCTCTCCTGTC	0.502
-	7	594	n_p.S114F|PRPF4	NM_017892	NP_060362	O75400	PR40A_HUMAN	WW 2.	0	TTTCCAGAATCT	0.323
+	9	1465	D2_uc002tzd.3_	NM_001083112	NP_001076581	P43304	GPDM_HUMAN		1	CTTCAGAAGAA	0.403
-	10	1555	_p.A406T|ACVR1_	NM_001111067	NP_001104537	Q04771	ACVR1_HUMAN	Potential).|Protein kinase.	3	AAAGGCCCAAA	0.453
+	3	205		NM_001017920	NP_001017920	A0PJW8	DAPL1_HUMAN		0	CAGTGCCATTG	0.448
+	18	3375	C1_uc010fom.1_	NM_033394	NP_203752	Q9C0D5	TANC1_HUMAN		3	AGGCACCCTGA	0.672
+	22	3827	fom.1_Missense_	NM_033394	NP_203752	Q9C0D5	TANC1_HUMAN	ANK 9.	3	GCTGGGCTTGT	0.498
-	2	294	_p.P49S|WDSUB1	NM_152528	NP_689741	Q8N9V3	WSDU1_HUMAN		0	CAATGGAGAAT	0.463
+	3	316	zcn.1_Missense_	NM_022826	NP_073737	Q9H992	MARH7_HUMAN	Ser-rich.	0	ATCTGCATGGT	0.393
-	34	5054	_Mutation_p.P16	NM_002349	NP_002340	O60449	LY75_HUMAN	ellular (Potential).	0	CCAGAGGCAC	0.368
-	27	3766	.P1233S|LY75_u	NM_002349	NP_002340	O60449	LY75_HUMAN	ellular (Potential).	0	AACTGGTTTGA	0.328
-	15	2370	TGB6_uc010zcq.1	NM_000888	NP_000879	P18564	ITB6_HUMAN	lasmic (Potential).	3	TCTGTGGAAAGG	0.308
-	11	2349		NM_022168	NP_071451	Q9BYX4	IFIH1_HUMAN	case C-terminal.	1	TTGCTCCATTATG	0.338
-	7	1685		NM_022168	NP_071451	Q9BYX4	IFIH1_HUMAN	ase ATP-binding.	1	GAAGCTGTTAGT	0.383
-	15	3438	zcx.1_Missense_	NM_014900	NP_055715	Q53SF7	COBL1_HUMAN		3	TCTTTACTGAAA	0.463
-	12	1345	p.V248M|SLC38A	NM_173512	NP_775783	Q08AI6	S38AB_HUMAN	ellular (Potential).	1	AAAACACATTGG	0.388
-	15	2771	_p.P711L|SCN3A_	NM_006922	NP_008853	Q9NY46	SCN3A_HUMAN	S1 of repeat II; (Potential).	10	CAAATGGATCC	0.403
-	14	2588	_p.S650F|SCN3A_	NM_006922	NP_008853	Q9NY46	SCN3A_HUMAN		10	CAGAGGAATCC	0.473
+	9	1387	_p.S366N|SCN2A_	NM_001040142	NP_001035232	Q99250	SCN2A_HUMAN	I.	8	CACGAGCTTTG	0.408
+	12	2254	_p.S655F|SCN2A_	NM_001040142	NP_001035232	Q99250	SCN2A_HUMAN		8	GGTCTCCCTGG	0.577
+	27	5924	.Q1878H|SCN2A_	NM_001040142	NP_001035232	Q99250	SCN2A_HUMAN		8	ATACAGATGGA	0.463
+	7	1272	dg.2_Missense_	NM_024969	NP_079245	Q8WYN3	CSRN3_HUMAN		5	CTCACAGTAGTT	0.488
-	2	329	3_5'Flank|SCN1A_	NM_006920	NP_008851	P35498	SCN1A_HUMAN		13	GAGGTGGCACTG	0.343
-	27	5235	uc002udp.2_RNA	NM_002977	NP_002968	Q15858	SCN9A_HUMAN	IV.	13	CAACGCAGGAA	0.483
+	11	954	_Mutation_p.S289	NM_001039724	NP_001034813	Q8IVI9	NOSTN_HUMAN		0	AGCCTCAAAAG	0.388
-	2	131		NM_003742	NP_003733	O95342	ABCBB_HUMAN	lasmic (Potential).	5	GAGTCAGACATG	0.343
-	60	11689		NM_004525	NP_004516	P98164	LRP2_HUMAN	ntial).|LDL-receptor class A	29	AGACGCATCCA	0.453
-	26	4381		NM_004525	NP_004516	P98164	LRP2_HUMAN	g (Potential).|Extracellular	29	TATGTCTTCACA	0.438
+	25	3730	se_Mutation_p.P	NM_172070	NP_742067	Q6ZT12	UBR3_HUMAN		0	GTGGCCCCTCC	0.428
+	27	3370	3B_uc002ufz.2_M	NM_138995	NP_620482	Q8WXR4	MYO3B_HUMAN	IQ 1.	19	GCTTGGAGCCA	0.458
+	27	3382	3B_uc002ufz.2_Mi	NM_138995	NP_620482	Q8WXR4	MYO3B_HUMAN	IQ 1.	19	GGAGATACAAAA	0.468

+	2	271	)_uc010zdw.1_Spli	NM_199227	NP_954697	Q6UB28	AMP1D_HUMAN		0	CCTAAGGTACTG	0.388
+	6	749	dw.1_Missense_M	NM_199227	NP_954697	Q6UB28	AMP1D_HUMAN		0	GGGGCTCCCTTC	0.448
-	3	1171		NM_004405	NP_004396	Q07687	DLX2_HUMAN		1	CCGGGGCGCCC	0.672
-	4	1372	f.2_Missense_Muta	NM_003111	NP_003102	Q02447	SP3_HUMAN	ation domain (Gln-rich).	6	TGCTGAGACTCT	0.448
-	13	2403	uiv.2_Missense_M	NM_001033045	NP_001028217	Q7Z3F1	GP155_HUMAN	ical; (Potential).	1	ATTACAGCGAACA	0.423
-	6	1469	;uiv.2_Missense_M	NM_001033045	NP_001028217	Q7Z3F1	GP155_HUMAN	ical; (Potential).	1	CAGAAACGTACA	0.408
+	4	372	kw.2_Missense_Mu	NM_006554	NP_006545	O75431	MTX2_HUMAN		2	TACAGGCCTTTTT	0.318
+	1	201		NM_152945	NP_694453	Q8IUH3	RBM45_HUMAN	RRM 1.	0	TACACACCTGAG	0.627
+	12	1369	fe.1_Missense_Mu	NM_032523	NP_115912	Q9BZF3	OSBL6_HUMAN		1	CAGGTTCCTTTCA	0.433
+	5	931	umj.3_Missense_M	NM_001042702	NP_001036167	Q0ZLH3	PJVK_HUMAN		0	AGAATCCCAAGG	0.338
-	307	97509	010zfi.1_Missense	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	GGTGAGGACTC	0.473
-	307	94366	5076I|TTN_uc010z	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	CTTCTGGTTTGG	0.388
-	300	90516	23793S|TTN_uc01	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	CCTGAGGTAGGT	0.468
-	275	77689	517F|TTN_uc010z	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	GCCCAGGAAATTA	0.403
-	275	72214	592V|TTN_uc010z	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	TGAGGGCACAGA	0.418
-	275	62287	_uc010zfi.1_Misser	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	GAAGCAGATTTCT	0.428
-	201	39732	i.1_Missense_Muta	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	TGCCAACTCTGT	0.418
-	187	36641	1_Nonsense_Muta	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	GAGTTTCCAGTTC	0.463
-	161	32394	TTN_uc010fre.1_I	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	GGGCACCTCGG	0.423
-	137	30006	I_Missense_Mutat	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	TGTACTCTTCTTC	0.428
-	94	24580	N_uc010zfj.1_Intrc	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	CGGTCAGTTTTA	0.443
-	89	23212	N_uc010zfj.1_Intro	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	CAACAGGGTTCT	0.403
-	75	19221	N_uc010zfj.1_Intrc	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	TGCCTACTTTAAC	0.423
-	60	14995	N_uc010zfj.1_Intro	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	ACCCTGGCACCA	0.453
-	46	15571	TN_uc010zfi.1_Intr	NM_133379	NP_596870	Q8WZ42	TITIN_HUMAN		153	GAATATCTCTCTA	0.473
-	32	7603	p.T2414I|TTN_uc0	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	GCCTTGGTGCCT	0.408
-	24	4404	TTN_uc010zfj.1_M	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	GTGTGGGAATGTA	0.383
-	22	3885	.E1175K|TTN_uc0	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	GGCTTGTtctttttca	0.323
+	12	2072		NM_000885	NP_000876	P13612	ITA4_HUMAN	Extracellular (Potential).	6	CAGGACAAATTG	0.313
-	29	3563	pb.2_Missense_M	NM_013436	NP_038464	Q9Y2A7	NCKP1_HUMAN		2	TTAAGACGGTCTT	0.333
-	21	2671	upb.2_Missense_M	NM_013436	NP_038464	Q9Y2A7	NCKP1_HUMAN		2	TCTGCACATAGTT	0.353
+	16	1840	36_splice|ITGAV_u	NM_002210	NP_002201	P06756	ITAV_HUMAN		4	AACTTAGTAAGTC	0.264
+	8	2126	_p.A639T|FAM171I	NM_177454	NP_803237	Q6P995	F171B_HUMAN	lasmic (Potential).	10	CCCAGAGCCTGG	0.493
+	2	277		NM_000090	NP_000081	P02461	CO3A1_HUMAN	VWFC.	13	ATATGTGTCTGTG	0.443
+	37	2674		NM_000090	NP_000081	P02461	CO3A1_HUMAN	le-helical region.	13	AGGGTCCTCCTG	0.383
-	5	794		NM_014585	NP_055400	Q9NP59	S40A1_HUMAN		1	GTAGCAGTACTGC	0.239
+	5	2038		NM_019048	NP_061921	Q9NWL6	ASND1_HUMAN	agine synthetase.	3	ATCTTGGTCGTGA	0.383
+	13	2768	uqx.1_RNA|ANKAI	NM_144708	NP_653309	Q7Z5J8	ANKAR_HUMAN		4	GATACAGCTTTAT	0.284
+	7	1407	_p.T236I|INPP1_u	NM_001128928	NP_001122400	P49441	INPP_HUMAN		2	AGCTCACCATCTC	0.448
-	20	2054	sk.2_Missense_Mu	NM_007315	NP_009330	P42224	STAT1_HUMAN		10	CCAAAGCCAGAA	0.358
+	19	2284	O1B_uc002usr.2_M	NM_001130158	NP_001123630	O43795	MYO1B_HUMAN	yosin head-like.	8	GTGGAAGAATACT	0.323
+	5	887	sy.2_RNA|OBFC2A	NM_001031716	NP_001026886	Q96AH0	SOSB2_HUMAN		0	ATTCCATGAATAG	0.299
-	1	745		NM_004657	NP_004648	O95810	SDPR_HUMAN	Potential.	2	GCTTCACCTGTGC	0.612
-	6	972		NM_016192	NP_057276	Q9UIK5	TEFF2_HUMAN	|Extracellular (Potential).	5	CAGAGGGGATTG	0.358
-	42	7614		NM_018897	NP_061720	Q8WXX0	DYH7_HUMAN	.4 (By similarity).	12	CTTCAGGCCATGA	0.408
-	14	1833		NM_018897	NP_061720	Q8WXX0	DYH7_HUMAN	n (By similarity).	12	GATGATCTCTGAA	0.348
-	8	789		NM_018897	NP_061720	Q8WXX0	DYH7_HUMAN	n (By similarity).	12	CTCGAGGATCTTT	0.318

-	9	1300	2utu.2_Missense_I	NM_012086	NP_036218	Q9Y5Q9	TF3C3_HUMAN			7	TAAGTGGTTCAAC	0.393	
-	6	855	_p.W255*|GTF3C3	NM_012086	NP_036218	Q9Y5Q9	TF3C3_HUMAN	TPR 4.		7	TCGCTCCCACAG	0.393	
+	4	288	.2_Missense_Muta	NM_015387	NP_056202	Q9Y3A3	MOBL3_HUMAN			0	TAAATGGACTTGC	0.284	
-	9	1889		NM_144629	NP_653230	Q52LD8	RFTN2_HUMAN			0	ACCTGAGTCACTC	0.468	
+	1	1100	uc002uup.2_Intron	NM_138395	NP_612404	Q96GW9	SYMM_HUMAN			3	GCTTGGGCAACC	0.582	
+	2	718	uuv.3_Missense_M	NM_001114661	NP_001108133	Q15111	PLCL1_HUMAN	raction with PPP1C.		2	CTTCAAGCTCTTC	0.448	
+	6	703	hd.1_Missense_M	NM_152524	NP_689737	Q562F6	SGOL2_HUMAN			4	CACAACCTTTATC	0.294	
+	7	1543	_p.T477I|SGOL2_	NM_152524	NP_689737	Q562F6	SGOL2_HUMAN			4	TTCAAACTGGCTT	0.378	
+	17	1878	e_Mutation_p.A14	NM_001159	NP_001150	Q06278	ADO_HUMAN			6	AGCATGCCACGC	0.448	
+	21	2410	p.D326G|AOX1_u	NM_001159	NP_001150	Q06278	ADO_HUMAN			6	AAATGGATGTCTA	0.413	
-	8	744	hj.1_Missense_Mu	NM_006190	NP_006181	Q13416	ORC2_HUMAN			0	TACGAGGTGCTGT	0.274	
+	8	1292	e_Mutation_p.H24	NM_032974	NP_116756	Q92851	CASPA_HUMAN			6	AACAACCACAGC	0.428	
-	5	921	yc.2_Missense_Mu	NM_015049	NP_055864	O60296	TRAK2_HUMAN	Potential.		0	CTTGATCAAAGGC	0.408	
-	4	739	uyc.2_Missense_M	NM_015049	NP_055864	O60296	TRAK2_HUMAN			0	TCTGTGCCTAGA	0.333	
-	10	1069	e_Mutation_p.W24	NM_033066	NP_149055	Q96JB8	MPP4_HUMAN	SH3.		0	GCCTGCCACCAC	0.587	
-	27	4506	LS2_uc010ftl.2_RN	NM_020919	NP_065970	Q96Q42	ALS2_HUMAN			7	CCTGCCCAGGG	0.478	
-	18	3515	se_Mutation_p.W1	NM_020919	NP_065970	Q96Q42	ALS2_HUMAN	MORN 1.		7	TGAAAGCCAGCG	0.433	
-	9	2325	S2_uc002uyq.2_M	NM_020919	NP_065970	Q96Q42	ALS2_HUMAN			7	GAGTCTTAGAACC	0.418	
+	5	498	n_p.A99V|CDK15_	NM_139158	NP_631897	Q96Q40	CDK15_HUMAN	rotein kinase.		5	TTCTAGCTTCTCT	0.338	
+	8	882	_p.S227F|CDK15_	NM_139158	NP_631897	Q96Q40	CDK15_HUMAN	rotein kinase.		5	AATATTCCTCTGA	0.473	
+	1	393		NM_003507	NP_003498	O75084	FZD7_HUMAN	acellular (Potential).		4	TGTGCACCGTGC	0.637	
+	1	407		NM_003507	NP_003498	O75084	FZD7_HUMAN	acellular (Potential).		4	GATCAGGCCATCC	0.637	
+	1	527		NM_003507	NP_003498	O75084	FZD7_HUMAN	acellular (Potential).		4	ACGGTGCGGGC	0.726	
+	12	2812	PR2_uc010ftr.2_In	NM_001204	NP_001195	Q13873	BMPR2_HUMAN	lasmic (Potential).		9	AAGACTCTATCCA	0.373	
+	7	1415		NM_173511	NP_775782	Q6P1L5	F117B_HUMAN			1	AAAGGGAACCTC	0.393	
+	14	1893	p.G462D|ALS2CR	NM_001104586	NP_001098056	Q8N187	AL2S8_HUMAN			2	CCAGGGGTTCTT	0.353	
+	15	2112	p.G535D|ALS2CR	NM_001104586	NP_001098056	Q8N187	AL2S8_HUMAN			2	TGCTTGGTCAAAC	0.418	
-	14	2833		NM_213589	NP_998754	Q70E73	RAPH1_HUMAN			10	GGGTGGAAACT	0.572	rs143283518
-	14	2456		NM_213589	NP_998754	Q70E73	RAPH1_HUMAN			10	GAGGAGGCGGG	0.517	
+	9	1426	p.P407S|PARD3B	NM_152526	NP_689739	Q8TEW8	PAR3L_HUMAN	PDZ 2.		4	ATGGTCCCGGTC	0.413	
+	9	2086	_p.A432V|NRP2_u	NM_201266	NP_957718	O60462	NRP2_HUMAN	cellular (Potential).		4	AGATGCTCCCTC	0.572	
-	3	940	n_p.T185I|GPR1_u	NM_005279	NP_005270	P46091	GPR1_HUMAN	cellular (Potential).		0	CAAAGAGTATGAT	0.418	
+	2	440		NM_001102659	NP_001096129					0	CATGGAGCACTG	0.483	
+	20	3631	p.R839K|PIKFYVE	NM_015040	NP_055855	Q9Y2I7	FYV1_HUMAN			10	AGCCAGAGGAGC	0.463	
+	13	1496	e_Mutation_p.W43	NM_005048	NP_005039	P49190	PTH2R_HUMAN	lasmic (Potential).		3	GATGTGGAGTCC	0.557	
+	7	2238	.1_Intron|MAP2_u	NM_002374	NP_002365	P11137	MAP2_HUMAN			17	ATTGATCCAAAAC	0.438	
+	12	5178	lg.1_Missense_Mu	NM_002374	NP_002365	P11137	MAP2_HUMAN			17	AAGAAGGTCGCC	0.532	
-	2	1077	vdy.1_Missense_M	NM_152519	NP_689732	A0AUZ9	CB067_HUMAN			3	ATTTCAGTGCATT	0.378	
+	14	1492	460_splice|CPS1_u	NM_001875	NP_001866	P31327	CPSM_HUMAN			13	CTTTCAGGAAGA	0.373	
+	20	2672	p.S853N|CPS1_u	NM_001875	NP_001866	P31327	CPSM_HUMAN		p.S847T(1)	13	ACCAAGCAGCAC	0.438	
+	16	1908	.1_Missense_Muta	NM_024532	NP_078808	Q8N0X2	SPG16_HUMAN	WD 7.		2	ACGAGGCACAC	0.507	
-	1	214	D1_uc010zjm.1_5	NM_000465	NP_000456	Q99728	BARD1_HUMAN	ction with BRCA1.		2	CGGTTCCATGGC	0.682	
-	40	6807	i.2_Intron|FN1_uc	NM_212482	NP_997647	P02751	FINC_HUMAN	trand 3 (CS-3) (V region).		13	CCTGGGGATGTC	0.532	
-	40	6658	vfh.2_Intron|FN1_u	NM_212482	NP_997647	P02751	FINC_HUMAN	trand 3 (CS-3) (V region).		13	GACCAGAAGTGC	0.527	
-	25	4206	2_Intron|FN1_uc0	NM_212482	NP_997647	P02751	FINC_HUMAN	ype-III 8.|Cell-attachment.		13	CAAAATCTTCAA	0.498	
+	7	827	q.2_Missense_Mu	NM_015488	NP_056303	Q8N490	PNKD_HUMAN			0	ACCTGGCCACAC	0.602	
+	12	1554	02vhu.1_Missens	NM_000578	NP_000569	P49279	NRAM1_HUMAN	ical; (Potential).		4	CACCCGCTCCTC	0.647	

-	22	2938	_p.E829K|USP37_	NM_020935	NP_065986	Q86T82	UBP37_HUMAN	UIM 3.	5	ATCTTCTTTCTG	0.284	
-	4	523	P37_uc002vif.2_Mi	NM_020935	NP_065986	Q86T82	UBP37_HUMAN		5	ATCCTTCTTTCC	0.343	
-	8	4428	t.2_Missense_Mu	NM_001105537	NP_001099007	P52746	ZN142_HUMAN	2H2-type 21.	4	AGCGGGAACAG	0.657	
+	20	2622	786N|STK36_uc0	NM_015690	NP_056505	Q9NRP7	STK36_HUMAN		11	GCAGTGACGTT	0.488	
+	26	3987	iw.2_Missense_M	NM_015690	NP_056505	Q9NRP7	STK36_HUMAN		11	AAATGGCATGT	0.572	
+	3	801	TLL4_uc010fvx.2_	NM_014640	NP_055455	Q14679	TTLL4_HUMAN		3	AAAAAGCCCTT	0.537	
+	3	1239	_p.A125V|TTLL4_u	NM_014640	NP_055455	Q14679	TTLL4_HUMAN		3	TACCGCTAGCT	0.552	
-	10	1088	RNA|PRKAG3_uc0	NM_017431	NP_059127	Q9UGI9	AAKG3_HUMAN	CBS 3.	2	GTCTCGGAATG	0.592	
+	2	725		NM_025216	NP_079492	Q9GZT5	WN10A_HUMAN		2	TACAGGGCATC	0.582	
-	8	1079	ense_Mutation_p.	NM_194302	NP_919278	Q6ZU64	CC108_HUMAN		4	GGATGCTGCTC	0.662	
-	16	2480	we.1_Missense_M	NM_005689	NP_005680	Q9NP58	ABCB6_HUMAN	C transporter.	2	GGCGACGCGCT	0.612	
-	12	2174	|ATG9A_uc002vkd	NM_001077198	NP_001070666	Q7Z3C6	ATG9A_HUMAN	smic (By similarity).	1	TGGGCGCCTGC	0.687	rs35171882
+	2	257	F1_uc010zkw.1_I	NM_018089	NP_060559	Q9H8Y5	ANKZ1_HUMAN		2	TCAGGGCCTGA	0.622	
-	21	2883	42_splice|PTPRN_	NM_002846	NP_002837	Q16849	PTPRN_HUMAN		4	TCCCTACCTTTT	0.587	
-	9	1401	_p.P348S|PTPRN_	NM_002846	NP_002837	Q16849	PTPRN_HUMAN	ellular (Potential).	4	AGGGGGTCTGG	0.637	
+	18	4300		NM_005876	NP_005867	Q15772	SPEG_HUMAN	Ig-like 7.	14	CACGGGCCGGT	0.677	
+	31	7637		NM_005876	NP_005867	Q15772	SPEG_HUMAN		14	GCTCCGCTGGG	0.617	
+	40	9563		NM_005876	NP_005867	Q15772	SPEG_HUMAN	otein kinase 2.	14	TACATCCCAGA	0.607	
+	1	964	4_uc002vly.1_Mi	NM_182847	NP_878267	Q96FT7	ACCN4_HUMAN	ellular (Potential).	2	CGCCAGCAACT	0.612	
-	13	4264	zli.1_Missense_M	NM_015311	NP_056126	O75147	OBSL1_HUMAN	Ig-like 12.	0	CTGGGGCCCTG	0.632	
+	2	259		NM_022915	NP_075066	Q9H9J2	RM44_HUMAN		1	AGAAGCCGAAC	0.343	
-	2	314	0zlr.1_Missense_	NM_006216	NP_006207	P07093	GDN_HUMAN		4	ACAGAGGATTG	0.537	
-	45	5341	voa.2_Missense_	NM_014689	NP_055504	Q96BY6	DOC10_HUMAN	DHR-2.	2	GCCAGGTCCTG	0.498	
-	23	2863	ob.2_Missense_	NM_014689	NP_055504	Q96BY6	DOC10_HUMAN	DHR-1.	2	GACTGAGACATA	0.368	
-	1	1839		NM_005544	NP_005535	P35568	IRS1_HUMAN		12	GCCCCCCCCGA	0.687	
-	22	2207		NM_000092	NP_000083	P53420	CO4A4_HUMAN	e-helical region.	11	GGAGCCCCAAG	0.597	
-	7	1118		NM_000092	NP_000083	P53420	CO4A4_HUMAN	e-helical region.	11	GAGCTCCTCTT	0.438	
+	6	496	utation_p.G112S|	NM_000091	NP_000082	Q01955	CO4A3_HUMAN	e-helical region.	3	CCCCAGGCAAT	0.388	
+	51	5021	.1_Intron|uc002vo	NM_000091	NP_000082	Q01955	CO4A3_HUMAN	ell activity of tumstatin.|Col	3	AAGAGGAACGT	0.483	
+	3	516	pe.2_Missense_	NM_004504	NP_004495	P52594	AGFG1_HUMAN	Arf-GAP.	4	GGTCTGTAAAC	0.308	
+	7	1116	pe.2_Missense_	NM_004504	NP_004495	P52594	AGFG1_HUMAN		4	CTTCCCCAAAT	0.383	
-	3	867	C19A3_uc010zlv.	NM_025243	NP_079519	Q9BZV2	S19A3_HUMAN	lasmic (Potential).	2	AACGTCCACAG	0.473	
-	3	741	C19A3_uc010zlv.	NM_025243	NP_079519	Q9BZV2	S19A3_HUMAN	lasmic (Potential).	2	TTTCCTCTAATAC	0.443	
+	2	165	e_Mutation_p.S1	NM_178821	NP_849143	Q8N136	WDR69_HUMAN		1	CTAAGTCCATAG	0.353	
-	35	5211	.G1749E|TRIP12_	NM_004238	NP_004229	Q14669	TRIPC_HUMAN		9	ATTTTCCTAAGA	0.418	
-	28	4269	.A1435V|TRIP12_	NM_004238	NP_004229	Q14669	TRIPC_HUMAN		9	TACCAGCTCTG	0.373	
-	6	965	qi.3_Missense_M	NM_004509	NP_004500	Q9HB58	SP110_HUMAN		4	AGTGGGGCATC	0.448	
+	2	233	_Mutation_p.S31N|	NM_003113	NP_003104	P23497	SP100_HUMAN		5	tgcacacagccacgat	0	
+	3	536	_p.G139D|ITM2C_	NM_030926	NP_112188	Q9NQX7	ITM2C_HUMAN	BRICHOS.	0	CGGCGGTGACC	0.637	
+	14	1430	se_Mutation_p.Q4	NM_025139	NP_079415	Q7Z3E5	ARMC9_HUMAN		1	CCCTGCAGAAG	0.433	
-	3	575		NR_024079					0	GAACCCCCTAC	0.507	
-	3	509		NR_024079					0	CTCCTGGTGGC	0.507	
+	8	1147	n.3_RNA|DIS3L2_	NM_152383	NP_689596	Q8IYB7	DI3L2_HUMAN		3	TTGTGGCACGG	0.507	
+	11	1355	yc.2_Missense_M	NM_000751	NP_000742	Q07001	ACHD_HUMAN	lasmic (Potential).	3	TGAGGGACCAG	0.507	
+	27	3494	.3_Missense_Muta	NM_015575	NP_056390	Q6Y7W6	PERQ2_HUMAN		7	CTGGTCCTCCT	0.413	
-	2	430		NM_019850	NP_062824	Q8N5V2	NGEF_HUMAN	toward RHOA, RAC1 and	7	GAATTTCTCTTA	0.498	
+	28	3374	e_Mutation_p.T10	NM_152879	NP_690618	Q16760	DGKD_HUMAN		5	TCGTGACCAAGT	0.517	

-	5	612	mr.1_Missense_Mutation_p.T177I			Q9NVE5	UBP40_HUMAN		3	ACAATGGTTCCAT	0.388	
+	1	873	UGT1A9_uc002vu	NM_001072	NP_001063	P19224	UD16_HUMAN		0	TAATCACCTTATA	0.398	
+	1	165	UGT1A7_uc002vu	NM_007120	NP_009051	P22310	UD14_HUMAN		1	TGCGGGAGGCC	0.607	
+	1	641	zmy.1_Intron|UGT	NM_000463	NP_000454	P22309	UD11_HUMAN		2	GCAGCGGGTGA	0.527	
-	8	1063	p.G272R|HJURP_	NM_018410	NP_060880	Q8NCD3	HJURP_HUMAN		1	CTGTCCCTTTCA	0.433	
-	43	9697	znj.1_Missense_M	NM_004369	NP_004360	P12111	CO6A3_HUMAN	gion.|BPTI/Kunitz inhibitor.	18	ATCTTGCACAGC	0.378	
-	36	7649	_Mutation_p.T184	NM_004369	NP_004360	P12111	CO6A3_HUMAN	1.|Nonhelical region.	18	CCGTGGTCACC	0.552	
-	9	4439	p.P778L|COL6A3_	NM_004369	NP_004360	P12111	CO6A3_HUMAN	.|Nonhelical region.	18	ATTCGGGGCTC	0.617	
+	10	1095	_p.T212I|LRRFIP	NM_001137552	NP_001131024	Q32MZ4	LRRF1_HUMAN		3	CCGACACCCTCA	0.398	
+	4	855		NM_001040445	NP_001035535	Q9Y576	ASB1_HUMAN	ANK 6.	0	CTGCTGGTAGAA	0.562	
-	15	2807	zb.1_Missense_M	NM_016552	NP_057636	Q9P2S6	ANKY1_HUMAN		1	GCTGGGGCCCT	0.617	
+	29	4075	p.E561K|SNED1_	NM_001080437	NP_001073906	Q8TER0	SNED1_HUMAN		2	TCTCCGAGACA	0.582	
-	10	2715	.P875S|PASK_uc	NM_015148	NP_055963	Q96RG2	PASK_HUMAN		6	CACGGGCGTGG	0.627	
+	5	642		NM_001001891	NP_001001891	Q6IWH7	ANO7_HUMAN	lasmic (Potential).	3	TGCTCTGCTACT	0.662	
+	22	2635		NM_001001891	NP_001001891	Q6IWH7	ANO7_HUMAN	ical; (Potential).	3	CTACTGGAATCT	0.587	
-	28	3949	.A1241T|HDLBP_	NM_203346	NP_976221	Q00341	VIGLN_HUMAN		4	AGGAGCCTGTG	0.597	
+	6	758	g.2_Missense_M	NM_001008491	NP_001008491	Q15019	SEPT2_HUMAN		1	TGCAGAGATTGG	0.423	
+	16	1921	_p.A602T|FARP2_	NM_014808	NP_055623	O94887	FARP2_HUMAN	DH.	3	AGGCTGGCACTC	0.557	
-	2	504		NM_015963	NP_057047	Q8WY91	THAP4_HUMAN		0	CTCCAGCCCCC	0.637	
-	3	595	.2_Intron|PDCD1_	NM_005018	NP_005009	Q15116	PDCD1_HUMAN	ical; (Potential).	1	GCAGGCCGCCC	0.697	
+	2	388		NM_080831	NP_543021	Q9H1M3	DB129_HUMAN		1	CTCTGCCACCAT	0.438	
+	2	221	SMF1_uc010zpp.	NM_178578	NP_848693	Q92530	PSMF1_HUMAN		0	CTGCAGGCAGG	0.662	
+	7	929	pp.1_Missense_M	NM_178578	NP_848693	Q92530	PSMF1_HUMAN	Pro-rich.	0	CCCACCCGGGT	0.498	
+	6	658	et.2_Missense_Mu	NM_014723	NP_055538	O15079	SNPH_HUMAN	Potential.	2	AAAGGAGATCA	0.562	
-	4	920	SIRPG_uc002wfo.	NM_018556	NP_061026	Q9P1W8	SIRPG_HUMAN	otential).|Ig-like C1-type 2.	1	TCCGACCAGGT	0.537	
-	4	832	SIRPG_uc002wfo.	NM_018556	NP_061026	Q9P1W8	SIRPG_HUMAN	otential).|Ig-like C1-type 2.	1	GAGTAACCTCC	0.547	
+	3	610	_p.E84K|SIRPA_	NM_001040022	NP_001035111	P78324	SHPS1_HUMAN	.|Extracellular (Potential).	1	AAAAAGAAGGC	0.542	
+	12	1547	w.1_Missense_Mu	NM_080751	NP_542789	Q8TDI7	TMC2_HUMAN	ical; (Potential).	3	TCTTTGCACTCT	0.537	
-	6	517	E170K|IDH3B_uc	NM_006899	NP_008830	O43837	IDH3B_HUMAN		0	TGTACTCCCCTT	0.522	
+	21	2113	PS16_uc002whd.2	NM_022575	NP_072097	Q9H269	VPS16_HUMAN		4	TGGGGGGCCAG	0.592	
-	31	2921	.G696D|C20orf19	NM_001009984	NP_001009984	Q5TEA3	CT194_HUMAN		0	GCCAGCCAGGA	0.318	
-	18	1547	p.S238F|C20orf19	NM_001009984	NP_001009984	Q5TEA3	CT194_HUMAN		0	ACTACGGAGCTG	0.532	
+	10	1799	il.2_Missense_Mu	NM_139321	NP_647537	O75882	ATRN_HUMAN	ar (Potential).|Kelch 5.	2	GTTTGGAGGAA	0.413	
-	5	609	0orf27_uc002wjh.	NM_001039140	NP_001034229	Q9GZN8	CT027_HUMAN		0	CAGTGCCACCT	0.612	
-	1	1682	5B_uc010zql.1_5'	NM_001810	NP_001801	P07199	CENPB_HUMAN		0	CCTGGGCACCA	0.537	
+	15	2318	5B_uc002wjm.2_	NM_021873	NP_068659	P30305	MPIP2_HUMAN	Rhodanese.	5	CCAGCCTCTAC	0.592	
+	3	534	2_uc002wlu.2_Mis	NM_003818	NP_003809	O95674	CDS2_HUMAN	ical; (Potential).	0	CCAATGGTTTTG	0.453	
+	18	2626	nl.2_Missense_Mu	NM_032485	NP_115874	Q9UJA3	MCM8_HUMAN		1	TGCTAGGAACTT	0.393	
+	3	1369		NM_001200	NP_001191	P12643	BMP2_HUMAN		2	ACACCAGGTTGG	0.478	
+	9	711	_p.P192L|PLCB4_	NM_182797	NP_877949	Q15147	PLCB4_HUMAN		15	TCTTCCCAGTG	0.313	
+	17	1541	_p.V469I|PLCB4_	NM_182797	NP_877949	Q15147	PLCB4_HUMAN		15	CCTGAAGTTGAA	0.368	
-	7	2064	nj.2_Missense_Mu	NM_020341	NP_065074	Q9P286	PAK7_HUMAN	rotein kinase.	23	GTCAACCACATT	0.478	
+	7	637	gca.1_Missense_M	NM_130811	NP_570824	P60880	SNP25_HUMAN	oiled-coil homology 2.	2	ATGCCCGAGAAA	0.458	
-	5	1261		NM_000214	NP_000205	P78504	JAG1_HUMAN	r (Potential).|EGF-like 1.	9	AGTCACCTGGGA	0.433	rs6077865
+	8	1302		NM_018327	NP_060797	Q9NUV7	SPTC3_HUMAN		0	ATGAAGCTCACA	0.507	
-	13	1268	P1_uc002woh.2_	NM_017714	NP_060184	Q9H6P5	TASP1_HUMAN		0	TCCTGGGCTGAC	0.458	
-	3	295	_p.E60K|TASP1_	NM_017714	NP_060184	Q9H6P5	TASP1_HUMAN		0	TATACTCCTTGG	0.323	

-	3	2089	02wou.2_Intron|F	NM_198391	NP_938205	Q9NZU0	FLRT3_HUMAN	ical; (Potential).		1	CAATGGTAACC	0.468	
+	15	1409	p.G147D|MACRO	NM_080676	NP_542407	A1Z1Q3	MACD2_HUMAN	Glu-rich.		0	AGAAGGTGAAA	0.378	rs147212262
-	19	3174	h.1_Missense_Mu	NM_024704	NP_078980	Q96L93	KI16B_HUMAN	-rich.|Potential.		8	CCGCTCCAGCG	0.542	
-	3	366	p.Q417Q|RRBP1_uc002wpw.1_Silent_p.Q417Q|RRBP			Q9P2E9	RRBP1_HUMAN			1	CGCTGCTGCTC	0.617	
-	6	675	NX5_uc002wqe.2	NM_014426	NP_055241	Q9Y5X3	SNX5_HUMAN			1	AAGGACTTCAT	0.363	
-	3	637		NM_021220	NP_067043	Q9BRP0	OVOL2_HUMAN	2H2-type 1.		1	CATGCGCTGCA	0.597	
+	13	1373	20orf26_uc010zsf.	NM_015585	NP_056400	Q8NHU2	CT026_HUMAN			4	TTCTTCCTCATC	0.453	
-	3	413		NM_001900	NP_001891	P28325	CYTD_HUMAN			0	CTCTTCCTGTG	0.453	
-	2	240	_p.A47T|C20orf3_	NM_020531	NP_065392	Q9HDC9	APMAP_HUMAN	type II membrane protein;		1	AACAGCCAGCA	0.522	
+	3	521		NM_002862	NP_002853	P11216	PYGB_HUMAN			2	GCCTGGGGAGG	0.552	
+	11	1349		NM_002862	NP_002853	P11216	PYGB_HUMAN			2	CACCAGCACGT	0.647	
-	20	3561	n.1_Missense_Mu	NM_025176	NP_079452	Q9Y2I6	NINL_HUMAN	Potential.		5	TAGAAGCCTCCT	0.478	
-	9	1212	o.1_Missense_M	NM_025176	NP_079452	Q9Y2I6	NINL_HUMAN			5	GCAGGCCAGGG	0.642	
+	2	153		NM_153324	NP_697019	Q8N688	DB123_HUMAN			0	AGGTGGCACCC	0.413	
-	2	575	L2L1_uc002wwn	NM_138578	NP_612815	Q07817	B2CL1_HUMAN			2	TGTGGCCAGTG	0.632	
+	10	1711	v.1_Missense_M	NM_012112	NP_036244	Q9ULW0	TPX2_HUMAN			2	ACGAACCCCTA	0.413	
+	4	832		NM_033118	NP_149109	Q9H1R3	MYLK2_HUMAN			6	AGGCCCTCTGT	0.662	
+	6	963	160_uc002wxg.2_	NM_080625	NP_542192	Q9NUG4	CT160_HUMAN			4	GGAGTCCTGCG	0.552	
+	5	690	p.S59N|TM9SF4_	NM_014742	NP_055557	Q92544	TM9S4_HUMAN			2	AGACAGCGATG	0.562	
+	7	2062	w.1_Missense_Mu	NM_004798	NP_004789	O15066	KIF3B_HUMAN	Globular.		5	TCTCAGCCGTGG	0.512	
+	12	2933	eb.2_Missense_M	NM_015338	NP_056153	Q8IXJ9	ASXL1_HUMAN		p.T836fs*2(2)	248	TCCCACTATGA	0.493	
+	12	3271	b.2_Missense_M	NM_015338	NP_056153	Q8IXJ9	ASXL1_HUMAN		p.G949fs*5(1)	248	AGGAGGGTCTA	0.532	
+	9	1274	10gef.2_RNA|DN	NM_006892	NP_008823	Q9UBC3	DNM3B_HUMAN			5	CTTCCCCAGCA	0.627	
-	13	1661	0gel.2_Missense_	NM_016408	NP_057492	Q96SZ6	CK5P1_HUMAN	K5R1-binding.		5	ATTGGCTTTTG	0.453	
+	2	491		NM_176812	NP_789782	Q9H444	CHM4B_HUMAN	Potential.		2	CTATGCCGCCA	0.612	
+	4	664		NM_176812	NP_789782	Q9H444	CHM4B_HUMAN	Potential.		2	TTAGAAGAACTA	0.488	
-	4	527	j.2_Missense_Mu	NM_000687	NP_000678	P23526	SAHH_HUMAN			0	GTCGTCCAGAA	0.632	
-	12	6625	w.2_Missense_M	NM_014071	NP_054790	Q14686	NCOA6_HUMAN			7	TTTAGGGGCTT	0.522	
+	15	1484	a-mir-499|MI0003	NM_020884	NP_065935	A7E2Y1	MYH7B_HUMAN			2	AGCAGGTGAGC	0.657	
+	17	1683	a-mir-499|MI0003	NM_020884	NP_065935	A7E2Y1	MYH7B_HUMAN	osin head-like.		2	AATTGCAGCAG	0.552	
+	28	3477		NM_020884	NP_065935	A7E2Y1	MYH7B_HUMAN	Potential.		2	AGAAGCTCAAG	0.612	
+	13	1866	slation_Start_Site|	NM_007186	NP_009117	Q9BV73	CP250_HUMAN	Potential.		5	GGAGACGCCAG	0.512	
+	2	521	zvi.1_Missense_M	NM_003116	NP_003107	Q9NPE6	SPAG4_HUMAN	ical; (Potential).		0	GAGCTTTCTGA	0.637	
-	5	590	_Mutation_p.L116	NM_021100	NP_066923	Q9Y697	NFS1_HUMAN			2	TGGGAGGTAGG	0.507	
-	7	795	.2_Missense_Mut	NM_184234	NP_909122	Q14498	RBM39_HUMAN			2	TTGCATCTCTTT	0.299	
+	16	2543		NM_016436	NP_057520	Q9BVI0	PHF20_HUMAN			1	TAGAACTTTGAA	0.567	
+	10	1415	e_Mutation_p.G420E|C20orf152_uc010gfp.1_RNA			Q96M20	CT152_HUMAN			0	GCAGGGAGAA	0.483	
+	3	409	xew.2_Missense_	NM_012156	NP_036288	Q9H4G0	E41L1_HUMAN			3	CCACGCCCAGC	0.542	
+	3	610	zvp.1_Missense_	NM_014902	NP_055717	Q9Y2H0	DLGP4_HUMAN			3	TCTTTCCCCTC	0.677	
-	7	1013	u.2_Missense_Mu	NM_032214	NP_115590	Q9H6Q3	SLAP2_HUMAN	LA C-terminal.		0	TCTTTCCAGTT	0.572	rs139719845
-	7	959		NM_015474	NP_056289	Q9Y3Z3	SAMH1_HUMAN	HD.		0	TGATTCAAGTG	0.348	
-	6	828	j.1_Missense_Mu	NM_002895	NP_002886	P28749	RBL1_HUMAN			10	GTACAGCAATG	0.413	
-	18	2225	xgk.2_Missense_	NM_152503	NP_689716	Q9H579	CT132_HUMAN			0	AAGGAGAAATA	0.433	
-	12	1274	gm.2_Missense_	NM_152503	NP_689716	Q9H579	CT132_HUMAN			0	CTCAGCCACCT	0.532	
-	7	3031	hm.2_Missense_	NM_014657	NP_055472	O43156	TTI1_HUMAN			0	AGTCACCACAC	0.542	
-	5	2766	xhm.2_Missense_	NM_014657	NP_055472	O43156	TTI1_HUMAN			0	TGGCTCCACAT	0.493	
+	4	874		NM_021215	NP_067038	Q9NQG5	RPR1B_HUMAN			1	AGGAGGATGAC	0.458	

-	6	945	s.1_Missense_Mu	NM_004613	NP_004604	P21980	TGM2_HUMAN		3	CCACGGCGGCG	0.517	
-	14	3814	xhw.1_Missense_	NM_001029864	NP_001025035	Q5JYT7	K1755_HUMAN		5	CTGTCCCCTCT	0.647	
-	13	3004	xhw.1_5'UTR|KIA	NM_001029864	NP_001025035	Q5JYT7	K1755_HUMAN		5	CTGTAGCTCCC	0.672	
+	1	129		NM_004139	NP_004130	P18428	LBP_HUMAN		2	TGGTCGCCAGG	0.617	rs140031031
+	11	1959	ense_Mutation_p.	NM_020336	NP_065069	Q86X10	RLGPB_HUMAN		2	ACTCTCCTCCT	0.378	
+	7	1334		NM_024855	NP_079131	Q9H9F9	ARP5_HUMAN		0	ACTTGGCAGCA	0.398	
+	8	1526		NM_024855	NP_079131	Q9H9F9	ARP5_HUMAN		0	ATGTATCCTGGC	0.433	
+	12	1104	wb.1_Missense_M	NM_021931	NP_068750	Q9H5Z1	DHX35_HUMAN	case C-terminal.	3	TGAAACTCCGA	0.527	
+	15	1443	wb.1_Missense_M	NM_021931	NP_068750	Q9H5Z1	DHX35_HUMAN		3	CTGAACCGCTT	0.443	
+	16	1890	1_uc010zwe.1_M	NM_182811	NP_877963	P19174	PLCG1_HUMAN	SH2 1.	8	TGAGACCTTCG	0.572	
-	3	2742	e_Mutation_p.W78	NM_015035	NP_055850	Q9H4I2	ZHX3_HUMAN	omeobox 4.	3	CTTGGCCACTG	0.577	
-	3	1606	e_Mutation_p.L41	NM_015035	NP_055850	Q9H4I2	ZHX3_HUMAN	eraction with NFYA.|Requir	3	TGGAAGAGCGG	0.557	
+	18	2378	se_Mutation_p.A76	NM_022896	NP_075047	Q9BQK8	LPIN3_HUMAN	C-LIP.	4	ATGCTGCCTTTG	0.597	
-	4	2403		NM_052846	NP_443078	Q9NT22	EMIL3_HUMAN	Potential.	1	CACATGGCTCC	0.677	
-	14	2159	d.2_Missense_Mu	NM_032221	NP_115597	Q8TD26	CHD6_HUMAN		14	TCAGATCTCCAA	0.453	
-	25	3624	.G1166D|PTPRT_	NM_007050	NP_008981	O14522	PTPRT_HUMAN	lasmic (Potential).	20	TGTTGCCACAG	0.512	
-	8	1352	gj.2_Missense_Mu	NM_007050	NP_008981	O14522	PTPRT_HUMAN	tential).|Fibronectin type-III	20	CTGTGGGCCAT	0.562	
-	7	1307	gj.2_Missense_Mu	NM_007050	NP_008981	O14522	PTPRT_HUMAN	tential).|Fibronectin type-III	20	GGGAGGCCCTG	0.547	
+	6	1051	e_Mutation_p.R16	NM_006275	NP_006266	Q13247	SRSF6_HUMAN	r-rich (RS domain).	0	ATCCAGATCAAG	0.493	rs142261798
+	1	361	.2_Intron|SGK2_u	NM_016276	NP_057360	Q9HBY8	SGK2_HUMAN		6	TGCTCCTCCCT	0.617	
+	1	371	.2_Intron|SGK2_u	NM_016276	NP_057360	Q9HBY8	SGK2_HUMAN		6	TGTCCCCCCAG	0.617	
+	6	784	se_Mutation_p.R12	NM_016276	NP_057360	Q9HBY8	SGK2_HUMAN	rotein kinase.	6	GGGAGCGCCGG	0.642	
+	14	2304	wj.1_Missense_Mu	NM_002466	NP_002457	P10244	MYBB_HUMAN		5	GGACCCTCATC	0.602	
-	4	2705		NM_020433	NP_065166	Q9BR39	JPH2_HUMAN	ytoplasmic (Potential).	0	CGGGGCCTCGG	0.746	
+	6	1129	zwm.1_Missense_	NM_024034	NP_076939	Q96MZ0	GD1L1_HUMAN		1	TGGGATGGGCTA	0.587	
-	1	160	9F|SERINC3_uc	NM_198941	NP_945179	Q13530	SERC3_HUMAN	ellular (Potential).	3	CGAGGGAGAAG	0.647	
-	3	337	A_uc010ggt.2_R	NM_000022	NP_000013	P00813	ADA_HUMAN		3	ATAGCAGGCATG	0.542	
-	6	692	u.2_Missense_Mu	NM_182970	NP_892015	Q9H426	RIMS4_HUMAN		5	ACCAGCCCACG	0.667	
+	8	1175	_RNA|PABPC1L_	NM_001124756	NP_001118228	Q4VXU2	PAP1L_HUMAN	RRM 4.	1	TCTACGTGGCA	0.607	
-	2	115	j.1_Intron|WFDC3	NM_080614	NP_542181	Q8IUB2	WFDC3_HUMAN		0	AAGTGCCTTCA	0.483	
-	5	431		NM_003279	NP_003270	P02585	TNNC2_HUMAN	EF-hand 3.	1	CGGAGGCCCTG	0.632	
+	2	1827	zxg.1_Missense_	NM_080752	NP_542790	Q96MP5	ZSWM3_HUMAN	SWIM-type.	2	ACCAGGTTAGC	0.562	
-	1	752	j.3_5'Flank|CTSA_	NM_080749	NP_542787	Q9BR09	NEUL2_HUMAN	NHR.	0	GCGGCCCACCA	0.677	
+	16	2041	_p.P156L|PCIF1_	NM_022104	NP_071387	Q9H4Z3	PCIF1_HUMAN		1	CTCACCGGAGC	0.622	
-	5	895	qx.1_Missense_M	NM_022095	NP_071378	Q9H4Z2	ZN335_HUMAN	2H2-type 1.	4	TGTGGCCTTGG	0.627	
+	7	672	se_Mutation_p.P21	NM_001250	NP_001241	P25942	TNR5_HUMAN	ical; (Potential).	2	GTGATCCCCATC	0.587	
-	14	1351	xr.1_Missense_Mu	NM_133171	NP_573403	Q96JJ3	ELMO2_HUMAN	ELMO.	1	TTTAGCCAAGT	0.512	
-	5	1385	p.G363R|ZNF334_	NM_018102	NP_060572	Q9HCZ1	ZN334_HUMAN		2	TTTCCCCTGTGT	0.433	
+	2	707		NM_030777	NP_110404	O95528	GTR10_HUMAN	lasmic (Potential).	1	AGGGAGGTGAG	0.637	
+	2	483	so.2_Missense_Mu	NM_005244	NP_005235	O00167	EYA2_HUMAN		1	GACAAGGTAGG	0.493	
-	11	1194	MYND8_uc002xtb.	NM_012408	NP_036540	Q9ULU4	PKCB1_HUMAN	PWWP.	5	CCAGGCCCTAG	0.373	
-	2	279	on_p.D29N|ZMYN	NM_012408	NP_036540	Q9ULU4	PKCB1_HUMAN		5	CTCACCTTTGGA	0.398	
+	17	3330	m.2_Missense_Mu	NM_181659	NP_858045	Q9Y6Q9	NCOA3_HUMAN	tion with CREBBP.	5	ACCTTCCAACC	0.448	
-	30	3832	tv.1_Missense_Mu	NM_020820	NP_065871	Q8TCU6	PREX1_HUMAN		6	TCCGGCCACGG	0.547	
-	7	940		NM_020820	NP_065871	Q8TCU6	PREX1_HUMAN		6	ACTCACCTGGA	0.418	
+	29	4134	zyf.1_Missense_	NM_006420	NP_006411	Q9Y6D5	BIG2_HUMAN		4	TCCGAGGCTGG	0.458	
+	5	515	E1L_uc010ghx.2_	NM_001316	NP_001307	P55060	XPO2_HUMAN		2	AAATGGCCTGA	0.388	

+	12	1392	ı_p.P364S|CSE1L_	NM_001316	NP_001307	P55060	XPO2_HUMAN		2	AAAAATCCATCTC	0.393	
+	4	612		NM_017895	NP_060365	Q96GQ7	DDX27_HUMAN	p/Glu/Lys-rich.	2	'CCTCACCAAAGC	0.498	
-	14	5306		NM_021035	NP_066363	Q9P2E3	ZNFX1_HUMAN		2	GCTTCTCCTTTA/	0.532	
+	8	1173	ys.1_Nonsense_M	NM_002827	NP_002818	P18031	PTN1_HUMAN		0	CAGTGGGTGAA(	0.542	
-	14	1984	65C_uc010zyu.1_I	NM_080829	NP_543019	Q96MK2	FA65C_HUMAN		2	'GTGCTCCTGCC	0.667	
-	5	1038	vm.2_Missense_M	NM_018197	NP_060667	Q9NPA5	ZF64A_HUMAN		2	TGAAGGGCCGC	0.607	
-	3	2172	)gij.1_Missense_M	NM_006526	NP_006517	O75362	ZN217_HUMAN		6	;CCTGAGTTTCA/	0.443	
-	1	1205	gij.1_Missense_Mu	NM_006526	NP_006517	O75362	ZN217_HUMAN		6	TCACTTCTTGGC/	0.537	
-	1	460	)gij.1_Missense_M	NM_006526	NP_006517	O75362	ZN217_HUMAN		6	CAAGGGCATATAC	0.473	
-	8	1390	_p.T189I|CYP24A	NM_000782	NP_000773	Q07973	CP24A_HUMAN		3	TTGCTGTCTGC/	0.368	
-	1	984		NM_080617	NP_542184	Q9NTU7	CBLN4_HUMAN	C1q.	4	.GTTGGCCGCCC(	0.627	
+	1	162		NM_019888	NP_063941	P41968	MC3R_HUMAN	cellular (Potential).	4	CTAATGGCTCGG/	0.582	
+	6	1461	xn.1_Missense_M	NM_001033521	NP_001028693	Q05048	CSTF1_HUMAN	WD 6.	1	TCAGAGCGCGG	0.582	
+	9	975	ı.2_Missense_Mut	NM_016407	NP_057491	Q9BY42	CT043_HUMAN		1	;CCAAGCGCTCC.	0.587	
+	5	532	yf.2_Nonsense_Mı	NM_012444	NP_036576	Q9Y5K1	SPO11_HUMAN		3	;GTAACCAGACT(	0.274	
+	4	558	N|RAE1_uc002xyh	NM_003610	NP_003601	P78406	RAE1L_HUMAN		0	3TTCAAGACAGT(	0.448	
-	9	2480	_p.W606*|CTCFL_	NM_080618	NP_542185	Q8NI51	CTCFL_HUMAN		4	TTCCTTCCATCC(	0.498	
-	9	2475	_p.G605R|CTCFL_	NM_080618	NP_542185	Q8NI51	CTCFL_HUMAN		4	'CCATCCCTTCG(	0.507	
-	1	780	nse_Mutation_p.D	NM_080618	NP_542185	Q8NI51	CTCFL_HUMAN		4	GATGGTCTTTCT(	0.562	
-	7	1182	_p.A300T|ZBP1_uc	NM_030776	NP_110403	Q9H171	ZBP1_HUMAN		2	.CGAAGCTTCTG(	0.607	
-	4	883	kys.2_Missense_M	NM_020182	NP_064567	Q969W9	PMEPA_HUMAN	lasmic (Potential).	1	'GCAGGGGCCCT	0.652	
+	1	841	xzm.2_Missense_I	NM_001001433	NP_001001433	O14662	STX16_HUMAN	lasmic (Potential).	1	TCCAGCCCTCTG	0.498	rs142560013
+	4	2491	_p.Q19*|GNAS_uc	NM_080425	NP_536350	P63092	GNAS2_HUMAN		292	AAGTGCAGGAC	0.478	
+	6	676	I1L_uc002yaf.1_RI	NM_198976	NP_945327	Q8IXH7	NELFD_HUMAN		3	;GAGGAGAAGAA	0.463	
+	1	1312		NM_178457	NP_848552	Q5JPB2	ZN831_HUMAN		14	AACAGGGCAGC	0.682	
+	2	720	_p.W117*|EDN3_u	NM_000114	NP_000105	P14138	EDN3_HUMAN		1	CATTTGGATCAA(	0.597	
-	1	836	177_uc010zzx.1_5	NM_006242	NP_006233	O95685	PPR3D_HUMAN		0	AATCGGGCACC.	0.677	
+	13	2029	ıp.1_Missense_Mu	NM_001794	NP_001785	P55283	CADH4_HUMAN	r (Potential).|Cadherin 5.	6	ACTATGCCCAAC'	0.542	
-	3	846	ırf200_uc002ycy.2_	NM_152757	NP_689970				0	CCACGGCTGTG(	0.652	
-	3	655	ırf200_uc002ycy.2_	NM_152757	NP_689970				0	.GCCCCCTCCGC.	0.682	
+	5	1218	)4A1_uc002ydc.1_	NM_016354	NP_057438	Q96BD0	SO4A1_HUMAN	lasmic (Potential).	1	;AGGCTCCCAGC	0.662	
-	16	6118	ls.1_Missense_Mu	NM_033081	NP_149072	Q9BTC0	DIDO1_HUMAN	Pro-rich.	6	'AGGCGCTTGGC(	0.582	
+	8	1028	_p.P276S|SLC17A	NM_022082	NP_071365	Q9BYT1	S17A9_HUMAN	ical; (Potential).	2	3TGGTTCCTTGG'	0.612	
+	4	374	n_p.W8*|ARFGAP	NM_018209	NP_060679	Q8N6T3	ARFG1_HUMAN	Arf-GAP.	1	TCCTGGAGTCT(	0.512	
-	1	142	_p.G14D|EEF1A2_	NM_001958	NP_001949	Q05639	EF1A2_HUMAN	' (By similarity).	0	ACGTGGCCGATG.	0.602	
+	4	476	ıb.2_Intron|TPD52I	NM_003288	NP_003279	O43399	TPD54_HUMAN		2	;AGAGTGGAATG.	0.463	
-	15	1646	:L1_uc011abm.1_I	NM_017859	NP_060329	Q9NWZ5	UCKL1_HUMAN		0	GGGGACCGCGT	0.667	
-	5	733		NM_020713	NP_065764	Q96KM6	Z512B_HUMAN		0	;GATGGCCTTGG	0.587	
+	3	874	gks.2_Missense_M	NM_003195	NP_003186	Q15560	TCEA2_HUMAN	'IIS N-terminal.	0	CTCTCATCAAGT(	0.607	
+	5	1223	_p.G274D|OPRL1_	NM_182647	NP_872588	P41146	OPRX_HUMAN	Name=6; (Potential).	2	CGTGGGCTGCT(	0.682	
+	7	1485	MYT1_uc002yij.2_	NM_004535	NP_004526	Q01538	MYT1_HUMAN		2	'GATGACCCGGG(	0.627	
+	2	258	2yim.3_Missense_I	NM_018257	NP_060727	Q9NV79	PCMD2_HUMAN		0	TGAAAGAAGCA(	0.373	
-	22	1746	TE_uc002yir.1_Mi	NM_199261	NP_954870	P56180	TPTE_HUMAN	2 tensin-type.	5	TTTTGTCTGTTGT	0.338	
-	17	1387	TE_uc002yir.1_Mi	NM_199261	NP_954870	P56180	TPTE_HUMAN	hatase tensin-type.	5	3TGCCTCCTTTA(	0.328	
-	6	837	v.1_Missense_Mut	NM_198996	NP_945347	Q6XZB0	LIPI_HUMAN		2	ACTGCTCTCTGG'	0.318	
-	28	5054		NM_015565	NP_056380	O94822	LTN1_HUMAN		0	CCATTACCTCTC(	0.348	
+	2	275	C21orf7_uc010gln.	NM_020152	NP_064537	P57077	TAK1L_HUMAN		2	TAGATGGTTCAG(	0.443	

+	5	2160	e_Mutation_p.P68	NM_001186	NP_001177	O14867	BACH1_HUMAN			2	TGCCTCCCTGTG	0.522	
-	12	2098	_p.S545F|GRIK1_	NM_000830	NP_000821	P39086	GRIK1_HUMAN	ellular (Potential).		3	GGTTTGGAGAAG	0.502	
-	1	173		NM_181610	NP_853641	Q3LI73	KR194_HUMAN			2	GAGAATCCATATC	0.463	rs139592933
-	13	2024	glu.2_Missense_M	NM_020706	NP_065757	O95104	SFR15_HUMAN	RRM.		0	CAATTGGACCA	0.269	
+	2	718	0glw.1_Missense_	NM_058187	NP_478067	P58658	CU063_HUMAN	n 1.|Extracellular (Potential		3	GCCTGCCTCCC	0.468	
-	24	3227	.G1037D|SYNJ1_	NM_003895	NP_003886	O43426	SYNJ1_HUMAN	Pro-rich.		5	CAAGGCCGGAA	0.512	
-	13	2349	e_Mutation_p.S21	NM_016631	NP_057715	Q9Y5B6	GCFC1_HUMAN		p.S720A(1)	2	ACTACTGAAGGA	0.318	rs149793516
-	13	2275	e_Mutation_p.M1	NM_016631	NP_057715	Q9Y5B6	GCFC1_HUMAN			2	GTCCCACATATT	0.328	
-	4	1001	nse_Mutation_p.R	NM_016631	NP_057715	Q9Y5B6	GCFC1_HUMAN			2	CCGGCGTTTCT	0.343	
-	14	1793	nd.2_Missense_M	NM_000819	NP_000810	P22102	PUR2_HUMAN	AIRS.		1	ATTCCAGCAACA	0.408	
-	9	1016	t_Site|GART_uc0	NM_000819	NP_000810	P22102	PUR2_HUMAN	ATP-grasp.		1	GATCACCAAAA	0.318	
-	7	1199	sl.2_Missense_Mu	NM_017613	NP_060083	Q9NYP3	DONS_HUMAN			2	GTATGTCTGGCT	0.363	
-	3	638	NSON_uc002ysl.2	NM_017613	NP_060083	Q9NYP3	DONS_HUMAN			2	TGCCCTACAATG	0.388	
-	8	710	se_Mutation_p.C2	NM_145858	NP_665857	O95825	QORL1_HUMAN			0	GGCTGCATGCT	0.383	
+	8	945	on_p.R226K|ITSN	NM_003024	NP_003015	Q15811	ITSN1_HUMAN	EH 2.		4	AATACAGGCAAT	0.368	
+	21	2777	|ITSN1_uc002ysx.	NM_003024	NP_003015	Q15811	ITSN1_HUMAN			4	CTTTGGCAGTA	0.542	
+	36	4847	tj.2_Missense_Mu	NM_003024	NP_003015	Q15811	ITSN1_HUMAN	PH.		4	GTTCTAGTAAAA	0.493	
-	5	1827	TD4_uc002yuy.2_	NM_017438	NP_059134	Q9NVD3	SETD4_HUMAN	SET.		2	TTTGGGAAGAA	0.502	
+	13	1592	eb.1_Missense_M	NM_005128	NP_005119	Q9Y3R5	DOP2_HUMAN			2	CTCAGGTGCTC	0.483	
+	6	810		NM_015358	NP_056173	Q14149	MORC3_HUMAN			2	TGCCCCTGAGA	0.418	
+	12	1394		NM_005441	NP_005432	Q13112	CAF1B_HUMAN			2	GGGAACCCCTG	0.597	
+	4	736	_p.S62S|DSCR6_	NM_018962	NP_061835	P57055	DSCR6_HUMAN			1	CGCTCCCTCAA	0.617	
+	27	2649	_p.W848*|TTC3_u	NM_001001894	NP_001001894	P53804	TTC3_HUMAN			9	TTCTTGGAAAGT	0.358	
+	33	3890	p.S1262F|TTC3_u	NM_001001894	NP_001001894	P53804	TTC3_HUMAN			9	ATTCTTCTAGAC	0.458	
+	33	3946	p.P1281S|TTC3_u	NM_001001894	NP_001001894	P53804	TTC3_HUMAN			9	CTAAACCAGGC	0.458	
-	4	480	R3_uc010gnl.2_M	NM_006052	NP_006043	O14972	DSCR3_HUMAN			0	CCCCGGCTTCA	0.418	
-	4	1098	wo.2_Missense_M	NM_002240	NP_002231	P48051	IRK6_HUMAN	smic (By similarity).		1	GTCAACTTCGTA	0.567	
-	12	1388	_p.P242S|ERG_uc	NM_001136155	NP_001129627	P11308	ERG_HUMAN	ETS.		2828	GTTGGGTTTGC	0.572	
-	40	5457	p.A416V|BRWD1_	NM_018963	NP_061836	Q9NSI6	BRWD1_HUMAN			4	GGCCAGCAGTT	0.413	
-	28	3395	_Missense_Mutati	NM_018963	NP_061836	Q9NSI6	BRWD1_HUMAN			4	TTAACACTGTTC	0.373	
-	29	5416	CAM_uc002yyr.1_	NM_001389	NP_001380	O60469	DSCAM_HUMAN	lasmic (Potential).		11	GCAGGGTCTGC	0.443	
-	11	2647	CAM_uc002yyr.1_	NM_001389	NP_001380	O60469	DSCAM_HUMAN	otential).|Ig-like C2-type 8.		11	ACTGGGGAACC	0.483	
+	2	123	X2_uc011aer.1_R	NM_002463	NP_002454	P20592	MX2_HUMAN			2	CACAAGCCTTGG	0.512	
+	15	2109	p.A388T|MX1_uc0	NM_001144925	NP_001138397	P20591	MX1_HUMAN			1	ATCACTGCTCTC	0.418	
-	1	193		NM_020639	NP_065690	P57078	RIPK4_HUMAN			7	GATGGCCAGCC	0.488	
-	30	4130	zp.2_Missense_M	NM_022115	NP_071398	P57071	PRD15_HUMAN			0	CTGCGGAATTG	0.547	
-	12	1570	zp.2_Missense_M	NM_022115	NP_071398	P57071	PRD15_HUMAN	SET.		0	TGGCCGCACCA	0.637	
-	9	1072	yzp.2_Missense_	NM_022115	NP_071398	P57071	PRD15_HUMAN			0	GTCGTGGTACT	0.582	
-	14	2323	_p.P310L|C2CD2_	NM_015500	NP_056315	Q9Y426	CU025_HUMAN			1	TGCAGGGCTCC	0.592	
-	3	893	aa.3_Missense_M	NM_001098402	NP_001091872	Q9ULJ3	ZN295_HUMAN			3	GATCATCCAAAG	0.398	
-	3	780	aa.3_Missense_M	NM_001098402	NP_001091872	Q9ULJ3	ZN295_HUMAN			3	ACATGTGGCTTA	0.423	
-	12	1514	_p.T311I|TMPRSS	NM_024022	NP_076927	P57727	TMPS3_HUMAN	.|Extracellular (Potential).		3	AGGAGGTGACA	0.597	
+	6	762	2zbj.2_Splice_Site	NM_018964	NP_061837	P57057	GLPT_HUMAN			0	CTCAGGTAGGT	0.542	
-	11	1232	g.1_Nonsense_Mu	NM_033661	NP_387510	P57081	WDR4_HUMAN			1	GCCGCTGCTTCT	0.612	
-	12	1608		NM_173354	NP_775490	P57059	SIK1_HUMAN			7	TGGTGGAGGGG	0.632	
-	3	400		NM_173354	NP_775490	P57059	SIK1_HUMAN			7	CCCTTACCTGGT	0.398	
+	8	1241	0gpo.2_Missense_	NM_003274	NP_003265	P48553	TPC10_HUMAN			2	TGCTGGGTGTTT	0.572	

+	18	2246		NM_005049	NP_005040	Q15269	PWP2_HUMAN	WD 14.	1	GGCGGCCACCA	0.507
+	3	307	zed.3_Missense_	NM_004649	NP_004640	P30042	ES1_HUMAN		1	TGGAGGGGCTG	0.552
+	13	1680	se_Mutation_p.S32	NM_000383	NP_000374	O43918	AIRE_HUMAN	XXLL motif 4.	1	GGAGTCCCTTC	0.657
+	1	65	.1_Intron|C21orf2	NM_198687	NP_941960	P60372	KR104_HUMAN		0	CAGCAGCCGCG	0.662
+	1	83	.1_Intron|C21orf2	NM_198687	NP_941960	P60372	KR104_HUMAN		0	TTCCTGGTTCCT	0.687
+	1	1100	.1_Intron|C21orf2	NM_198687	NP_941960	P60372	KR104_HUMAN	epeats of C-C-X(3).|34.	0	CAGACCCTCCT	0.657
-	1	923	.1_Intron|C21orf2	NM_198688	NP_941961	P60371	KR106_HUMAN	ts of C-C-X(3).|27.|Poly-Se	0	AGGAGGAGGGT	0.677
-	3	421	j.1_RNA|PTTG1IP_	NM_004339	NP_004330	P53801	PTTG_HUMAN	racellular (Potential).	1	TTGTAACTGGGT	0.438
+	10	2210	B1_uc002zgv.2_R	NM_015833	NP_056648	P78563	RED1_HUMAN	to I editase.	1	TTACCACGGGG	0.562
-	7	933	hb.2_RNA|POFU	NM_133635	NP_598368	Q9Y2G5	OFUT2_HUMAN		0	CCTGTCTGTGA	0.572
+	15	1175		NM_001848	NP_001839	P12109	CO6A1_HUMAN	le-helical region.	1	ACCCCCTGGCC	0.647
-	27	5737	MCM3AP_uc002zi	NM_003906	NP_003897	O60318	MCM3A_HUMAN		5	GAGGGGAAGGG	0.383
-	7	1780	se_Mutation_p.P1	NM_058180	NP_478060	P58505	CU058_HUMAN		1	CTGAGGGAGCT	0.488
+	11	1825	j.2_Missense_Mut	NM_006031	NP_006022	O95613	PCNT_HUMAN	Glu-rich.	8	GAAAGGAAGAA	0.483
+	13	2142	j.2_Missense_Mut	NM_006031	NP_006022	O95613	PCNT_HUMAN	-rich.|Potential.	8	ACAAGGTGCAA	0.493
+	19	3926	j.2_Missense_Mut	NM_006031	NP_006022	O95613	PCNT_HUMAN		8	GAGATGGCCCT	0.617
+	22	2759	z.1_Missense_Mu	NM_015151	NP_055966	Q14689	DIP2A_HUMAN		2	GGTGGCTGAGC	0.627
-	3	250	jv.1_Missense_Mu	NM_006272	NP_006263	P04271	S100B_HUMAN	EF-hand 1.	0	GATTTCCTAAGA	0.408
+	6	705	ga.1_Nonsense_	NM_206962	NP_996845	P55345	ANM2_HUMAN	with RB1 (By similarity).	1	TCCTGCAGAAT	0.502
-	1	167		NM_001005239	NP_001005239	Q8NG94	O11H1_HUMAN	Name=1; (Potential).	0	CCATTCCCTGTT	0.408
-	5	1114	4_uc010gqs.1_3'	NM_001037814	NP_001032903	Q2WGN9	GAB4_HUMAN		2	GACTCCCTCAT	0.557
+	16	3751	R2_uc002zml.2_	NM_031413	NP_113601	Q9BXF3	CECR2_HUMAN	Poly-Pro.	2	AGCCTCCCCCA	0.562
-	31	6168	AL3_uc010grd.1_	NM_015241	NP_056056	Q7RTP6	MICA3_HUMAN	Potential.	0	CACTGCCATGC	0.627
-	3	744	nk.1_Missense_M	NM_015241	NP_056056	Q7RTP6	MICA3_HUMAN		0	GAATGGCCAGA	0.488
-	4	462	_Mutation_p.S81N|	NM_003325	NP_003316	P54198	HIRA_HUMAN	WD 2.	1	TCCCACTGTTTG	0.403
+	6	1737	_p.E463K|DGCR8_	NM_022720	NP_073557	Q8WYQ5	DGCR8_HUMAN	inding and pri-miRNA proc	0	GGGCTGAGCGG	0.488
+	8	1990	GCR8_uc002zrj.2	NM_022720	NP_073557	Q8WYQ5	DGCR8_HUMAN	sary for heme-binding and	0	GGTGACCATTG	0.428
+	4	635	_Mutation_p.G17	NM_013373	NP_037505	Q9ULC8	ZDHC8_HUMAN	enal (Potential).	2	CTGAGGGGCTG	0.597
+	4	642	_Mutation_p.G17	NM_013373	NP_037505	Q9ULC8	ZDHC8_HUMAN	enal (Potential).	2	GCTGGGAGCCG	0.602
-	4	542	CR6L_uc010gsc.	NM_033257	NP_150282	Q9BY27	DGC6L_HUMAN	Potential.	0	AGCCACCTTCC	0.677
-	41	4951	y.3_Missense_Mu	NM_058004	NP_477352	P42356	PI4KA_HUMAN		4	GAGAGGGTGCG	0.667
-	23	2821		NM_058004	NP_477352	P42356	PI4KA_HUMAN		4	TTTATCCTCAAA	0.373
+	2	185	RPIND1_uc002ztc.	NM_000185	NP_000176	P05546	HEP2_HUMAN		0	CAGATCCCCAG	0.527
+	3	595		NM_004782	NP_004773	O95721	SNP29_HUMAN		0	GGCCAGCCACC	0.413
+	3	673	aih.1_Missense_	NM_152612	NP_689825	Q8IYX3	CC116_HUMAN		2	TGCTGGAGAAG	0.642
+	4	1902	1aiz.1_Intron|LOC	NM_153615	NP_705843	Q8IZJ4	RGDSR_HUMAN	Ras-GEF.	1	TGCTTGGGCTG	0.572
+	12	1468	RNA|SLC2A11_uc	NM_001024938	NP_001020109	Q9BYW1	GTR11_HUMAN	lasmic (Potential).	1	TTCCTTCCTGAG	0.562
+	3	204	_p.T26I|CABIN1_	NM_012295	NP_036427	Q9Y6J0	CABIN_HUMAN		5	CAAAACCCAGA	0.433
+	16	2291	p.D672N|CABIN1_	NM_012295	NP_036427	Q9Y6J0	CABIN_HUMAN		5	GGTTTGACCGG	0.582
+	5	1922	_p.E539K|CYTSA_	NM_015330	NP_056145	Q69YQ0	CYTSA_HUMAN	Potential.	0	TCAAAGAACGC	0.463
+	18	3587	uz.1_Missense_	NM_032608	NP_115997	Q8IUG5	MY18B_HUMAN	osin head-like.	12	CCCTGGATGCA	0.602
+	43	7568	18B_uc011aka.1_	NM_032608	NP_115997	Q8IUG5	MY18B_HUMAN		12	AAGTGGACTTC	0.562
-	10	1462	9_splice|HPS4_u	NM_022081	NP_071364	Q9NQG7	HPS4_HUMAN		0	CCATTACCTTGT	0.493
-	10	1449	_Mutation_p.E55	NM_022081	NP_071364	Q9NQG7	HPS4_HUMAN		0	CTGTTCCACCG	0.488
+	4	602	p.3_Missense_Mu	NM_001013694	NP_001013716	Q9UH36	SRR1L_HUMAN		0	CTGTTCTCAGT	0.473
+	2	405	akj.1_Missense_	NM_173510	NP_775781	Q8IWD4	CC117_HUMAN		1	AGGAGGAGGAT	0.373
+	8	1115	h.1_Missense_Mu	NM_032173	NP_115549	Q9ULT6	ZNRF3_HUMAN	lasmic (Potential).	1	CATCCGCAGCT	0.692

+	7	1043	.3_Intron|NF2_uc0	NM_000268	NP_000259	P35240	MERL_HUMAN		p.?(4)	728	CCACAGGGATG	0.507	
-	17	2020	se_Mutation_p.R6	NM_032204	NP_115580	Q9H1I8	ASCC2_HUMAN			0	CCTGCGGCTGA	0.527	
-	14	2305		NM_005877	NP_005868	Q15459	SF3A1_HUMAN	biquitin-like.		5	CACCTGCCCAT	0.532	rs11550685
-	6	902		NM_005877	NP_005868	Q15459	SF3A1_HUMAN			5	cttcttcctctCACGT	0.443	
-	4	526		NM_005877	NP_005868	Q15459	SF3A1_HUMAN			5	TTGGACCTAAG	0.493	
+	3	856	1akv.1_Missense_	NM_001017437	NP_001017437	Q569K6	CC157_HUMAN			1	GTGACCCCGAG	0.637	
-	20	3162		NM_014941	NP_055756	Q9Y6X9	MORC2_HUMAN			2	GCTGGCCTCCT	0.622	
+	13	2646	P5J_uc003ajw.2_	NM_001002837	NP_001002837	Q15735	PI5PA_HUMAN	Ser-rich.		1	GCACAGACAGC	0.647	
-	5	2406	ATZ1_uc003akr.2_	NM_014323	NP_055138	Q9HBE1	PATZ1_HUMAN			2	CATTGGCACTC	0.532	
-	14	2121	ala.1_Missense_	NM_019843	NP_062817	Q9NRA8	4ET_HUMAN			1	GTCCACCTGTG	0.448	
+	3	503	1_uc003alg.2_Intr	NM_001007467	NP_001007468	A8K8P3	SFI1_HUMAN			1	TGGTGCAGTTA	0.393	
+	8	1081	se_Mutation_p.R1	NM_001007467	NP_001007468	A8K8P3	SFI1_HUMAN			1	GGCAGCGACTA	0.562	
-	10	1351		NM_014306	NP_055121	Q9Y3I0	RTCB_HUMAN			0	TACAGGTTCCC	0.428	
+	3	923	ms.2_Missense_	NM_012179	NP_036311	Q9Y3I1	FBX7_HUMAN			1	TACATACCTCAG	0.313	
-	4	709	e_Mutation_p.P44	NM_004737	NP_004728	O95461	LARGE_HUMAN	enal (Potential).		3	CAGCGGTGACA	0.632	
+	3	978	ny.2_Missense_M	NM_014310	NP_055125	Q96D21	RHES_HUMAN			3	GGCCCGTGAGA	0.647	
-	2	381	p.P101S|MB_uc0	NM_005368	NP_005359	P02144	MYG_HUMAN			0	CACGGGGATCT	0.348	
-	3	343	n_p.P115S|APOL2	NM_030882	NP_112092	Q9BQE5	APOL2_HUMAN			0	TACCTGGGTTCA	0.562	
-	34	5131		NM_002473	NP_002464	P35579	MYH9_HUMAN	Potential.		11	TTCGTCCCGGT	0.637	
-	5	490		NM_000878	NP_000869	P14784	IL2RB_HUMAN	ellular (Potential).		0	GGATGGCCATC	0.617	
+	9	897	nw.1_Missense_M	NM_013385	NP_037517	Q9UIA0	CYH4_HUMAN	PH.		2	ATCCAGACCGG	0.572	rs55891452
+	7	1920	atq.1_Missense_M	NM_001039141	NP_001034230	Q9H2D6	TARA_HUMAN			1	CCCCACAACAT	0.597	
+	7	1998	atq.1_Missense_M	NM_001039141	NP_001034230	Q9H2D6	TARA_HUMAN			1	CCCCAGAACAT	0.587	
+	7	2004	atq.1_Missense_M	NM_001039141	NP_001034230	Q9H2D6	TARA_HUMAN			1	AACATCCTGTG	0.597	
+	7	3126	atq.1_Missense_M	NM_001039141	NP_001034230	Q9H2D6	TARA_HUMAN			1	CTCTCCCAGCA	0.642	
+	1	144		NM_003614	NP_003605	O60755	GALR3_HUMAN	Name=1; (Potential).		0	GCTGGCAGTGC	0.637	
+	9	1052	s.2_Missense_M	NM_012407	NP_036539	Q9NRD5	PICK1_HUMAN	AH.		0	GTTCGGCATTC	0.522	
-	2	76	03avt.1_Translatio	NM_004981	NP_004972	P48050	IRK4_HUMAN			0	GGTCACCTGGG	0.687	
+	5	624	_uc003awq.1_Intr	NM_004900	NP_004891	Q9UH17	ABC3B_HUMAN			1	CCACAGATACC	0.532	
-	6	1591	xe.2_Missense_M	NM_002608	NP_002599	P01127	PDGFB_HUMAN			373	TTTTGGCTGCA	0.592	
+	23	3979	aye.2_Missense_	NM_021096	NP_066919	Q9P0X4	CAC1I_HUMAN	llular (Potential).|III.		2	CCCAGCTCTTC	0.577	
+	23	4006	aye.2_Missense_	NM_021096	NP_066919	Q9P0X4	CAC1I_HUMAN	llular (Potential).|III.		2	ACTGTCTGGGC	0.582	
+	20	4969	n.3_Nonsense_M	NM_001162501	NP_001155973	Q9UPQ9	TNR6B_HUMAN			0	ATGTGGAAAAA	0.507	
+	12	1251	DSL_uc003ayr.3_	NM_000026	NP_000017	P30566	PUR8_HUMAN			1	CCCAGGATTGC	0.463	
-	9	1301	ye.1_Missense_M	NM_020831	NP_065882	Q969V6	MKL1_HUMAN	SAP.		5	AGACAGGCAGT	0.617	
+	9	1331	aq.1_Missense_M	NM_001469	NP_001460	P12956	XRCC6_HUMAN	Ku.		5	AGTTGGATGAC	0.368	
-	1	49	.2_5'Flank|CENP	NM_024053	NP_076958	Q9NSP4	CENPM_HUMAN			0	CAACCGTTGCT	0.677	
+	9	1036	sense_Mutation_p.	NM_145733	NP_663786	Q9UH03	SEPT3_HUMAN			0	CCCTGCTTCGA	0.423	
-	1	4104	.D1324N|TCF20_	NM_005650	NP_005641	Q9UGU0	TCF20_HUMAN			5	ACTATCTGGACT	0.468	
-	15	1668	gzf.2_Missense_	NM_014570	NP_055385	Q9NP61	ARFG3_HUMAN			1	TGTCGGGGGCG	0.567	
-	5	678	_Mutation_p.A10	NM_014570	NP_055385	Q9NP61	ARFG3_HUMAN			1	GAGAGGCAAAA	0.398	
-	24	3136	gzi.1_Missense_	NM_022785	NP_073622	Q5THR3	EFCB6_HUMAN	EF-hand 11.		7	TTTTGGTGAAT	0.418	
-	5	860	p.Q183*|PHF21B_	NM_138415	NP_612424	Q96EK2	PF21B_HUMAN			3	CACTTGAGGCT	0.398	
+	4	456	E1_uc011aqz.1_5'	NM_016426	NP_057510	Q9NYZ3	GTSE1_HUMAN			1	CGTTGCCCACA	0.493	
+	11	2163	|GTSE1_uc003bh	NM_016426	NP_057510	Q9NYZ3	GTSE1_HUMAN			1	AACTGGAACCA	0.512	
-	3	4247		NM_014246	NP_055061	Q9NYQ6	CELR1_HUMAN	ial).|EGF-like 3; calcium-bi		11	AGGTGCCCCC	0.647	
-	1	1768		NM_014246	NP_055061	Q9NYQ6	CELR1_HUMAN	r (Potential).|Cadherin 4.		11	GTCCACCGCCT	0.642	

-	1	1396		NM_014246	NP_055061	Q9NYQ6	CELR1_HUMAN	(Potential).|Cadherin 3.		11	CTGGACCACGT	0.657	
+	6	854	e.2_Missense_Mu	NM_014346	NP_055161	Q8WUA7	TB22A_HUMAN	ab-GAP TBC.		1	ACCTTCCCGCCA	0.378	
-	9	3198	.A953V|BRD1_uc	NM_014577	NP_055392	O95696	BRD1_HUMAN			1	TGGCCGCCTTG	0.647	
-	1	687	RD1_uc011arh.1_	NM_014577	NP_055392	O95696	BRD1_HUMAN			1	CTTGAGCAGTG	0.448	
-	2	287		NM_024105	NP_077010	Q9BV10	ALG12_HUMAN			0	ATGACCCCTTTC	0.592	
+	10	1159	ak.2_Missense_M	NM_024324	NP_077300	Q6UXH1	CREL2_HUMAN			0	AAGGAGAAAGC	0.547	
+	5	1244	bjy.2_Missense_M	NM_031454	NP_113642	Q9BVL4	SELO_HUMAN			0	AGCCGGAACTG	0.657	
-	16	3186	_p.D884N|TUBG	NM_020461	NP_065194	Q96RT7	GCP6_HUMAN			4	GCTGTCAGAGA	0.667	
-	1	733	CP6_uc010has.1_	NM_020461	NP_065194	Q96RT7	GCP6_HUMAN			4	CAAAGGACAAC	0.522	
-	11	938	.D116N|MAPK11_	NM_002751	NP_002742	Q15759	MK11_HUMAN	rotein kinase.		2	CTGGTCACTGT	0.617	
-	8	687	|MAPK11_uc010h	NM_002751	NP_002742	Q15759	MK11_HUMAN	rotein kinase.		2	TGCAGCCCACG	0.647	
-	32	5123	p.E465K|PLXNB2_	NM_012401	NP_036533	O15031	PLXB2_HUMAN	lasmic (Potential).		6	TGTCTTCATCCT	0.632	
-	28	4604	p.R292C|PLXNB2_	NM_012401	NP_036533	O15031	PLXB2_HUMAN	lasmic (Potential).		6	CCCACGGTACA	0.652	
-	18	3003	_5'Flank|PLXNB2_	NM_012401	NP_036533	O15031	PLXB2_HUMAN	r (Potential).|IPT/TIG 2.		6	ACCCCCCGTAG	0.662	
+	19	2266	lc.2_Missense_M	NM_014678	NP_055493	O75170	PP6R2_HUMAN			0	GCCCAGCGCAG	0.597	
-	24	3280	x.1_Missense_Mu	NM_002972	NP_002963	O95248	MTMR5_HUMAN			0	AGAGCCCAAGG	0.647	
-	20	2609	_p.A469V|SBF1_u	NM_002972	NP_002963	O95248	MTMR5_HUMAN			0	TCTCGGCCACA	0.652	
+	10	898	_p.A257V|MIOX_u	NM_017584	NP_060054	Q9UGB7	MIOX_HUMAN			0	ACCTGCCGGAC	0.652	
-	7	888	YMP_uc003bme.3	NM_001014440	NP_001014440	A8MYP8	ODF3B_HUMAN			0	GTCCGCGTCGG	0.687	
-	6	877	.1_Missense_Muta	NM_001145137	NP_001138609	Q92523	CPT1B_HUMAN	lasmic (Potential).		2	CTCTTCCCACC	0.582	rs111267458
-	2	377	_uc011asa.1_Miss	NM_001145137	NP_001138609	Q92523	CPT1B_HUMAN	ical; (Potential).		2	AGGAGGAACCC	0.597	
+	14	1543	R1_uc011asu.1_In	NM_001099952	NP_001093422	Q14643	ITPR1_HUMAN	toplasmic (Potential).		21	CCTGGGTTCAC	0.423	
+	16	1820	R1_uc011asu.1_In	NM_001099952	NP_001093422	Q14643	ITPR1_HUMAN	lasmic (Pote	p.R491W(1)	21	ATTCTGGTCAAG	0.453	
+	26	3428	1_Intron|ITPR1_u	NM_001099952	NP_001093422	Q14643	ITPR1_HUMAN			21	TTTTCAGGTGCT	0.418	
+	5	1002	asw.1_Missense_	NM_003670	NP_003661	O14503	BHE40_HUMAN			1	GAGTGGGGAGC	0.577	
+	8	1081	_uc003brv.2_Nons	NM_001080517	NP_001073986	Q9C0A6	SETD5_HUMAN			2	ACTGACCAGTAT	0.413	
-	2	738	|ARPC4_uc003bs	NM_006354	NP_006345	O75528	TADA3_HUMAN	Potential.		0	CTCAAGCACAC	0.602	
-	4	378	ation_p.P90S|CID	NM_022094	NP_071377	Q96AQ7	CIDEC_HUMAN	CIDE-N.		1	GAAGGGCTTGT	0.547	
+	2	365	EC_uc003bto.2_In	NM_032492	NP_115881	Q8N5M9	JAGN1_HUMAN	ical; (Potent	p.P77P(1)	1	GAATACCCGTAT	0.522	
-	2	1015	k.2_RNA|PRRT3_	NM_207351	NP_997234	Q5FWE3	PRRT3_HUMAN	ar (Potential).|Pro-rich.		0	GACACCTCAGC	0.657	
+	4	1893	tr.1_Missense_Mu	NM_014760	NP_055575	Q93075	TATD2_HUMAN			2	CCTCAGAGGAA	0.527	
-	18	3098	vw.2_Missense_M	NM_001001331	NP_001001331	Q01814	AT2B2_HUMAN	ical; (Potential).		6	CACCACGTTGA	0.597	
+	8	1396	_p.P311S|TSEN2_	NM_025265	NP_079541	Q8NCE0	SEN2_HUMAN			1	TTCAGCCCACG	0.418	
+	11	1664	_p.P400L|TSEN2_	NM_025265	NP_079541	Q8NCE0	SEN2_HUMAN			1	TTAAACCCTCTA	0.358	
-	23	3295		NM_024923	NP_079199	Q8TEM1	PO210_HUMAN	enal (Probable).		11	GTGGGGCTGAG	0.512	
-	5	693		NM_024923	NP_079199	Q8TEM1	PO210_HUMAN	enal (Probable).		11	GGTGTCCCCTT	0.557	
-	5	1012	s.2_Missense_M	NM_015150	NP_055965	Q14699	RFTN1_HUMAN			4	ATCTCCCTCTC	0.627	
+	5	787	_Mutation_p.A19	NM_144633	NP_653234	Q96L42	KCNH8_HUMAN	lasmic (Potential).		5	AACCAGCATTTC	0.363	
+	2	690	AB5A_uc011awg.1	NM_004162	NP_004153	P20339	RAB5A_HUMAN	region (By similarity).		0	GAGTACCATTG	0.378	
-	6	867	OL1_uc003cbx.2_	NM_001012410	NP_001012410	Q5FBB7	SGOL1_HUMAN			0	AAAAATCCAACT	0.358	
+	5	616	_p.V131I|UBE2E1_	NM_003341	NP_003332	P51965	UB2E1_HUMAN			0	TCTAAAGTCCTC	0.333	
-	4	520	ccl.2_Missense_	NM_020345	NP_065078	Q9NYS0	KBRS1_HUMAN	ffector region.		0	ATCTTCCATTGT	0.403	
+	2	336	.2_RNA|NR1D2_u	NM_005126	NP_005117	Q14995	NR1D2_HUMAN			3	TCTAGGAGGTG	0.388	
-	15	2241	nse_Mutation_p.	NM_003615	NP_003606	Q9Y6M7	S4A7_HUMAN	lasmic (Potential).		5	CCTCTTCTGTAA	0.378	
+	2	2024		NM_001137674	NP_001131146	A6NHJ4	ZN860_HUMAN	2H2-type 10.		1	CCTTCCGTCACA	0.403	rs143925165
+	4	736	ez.1_Missense_M	NM_138410	NP_612419	Q96FZ5	CKLF7_HUMAN			0	GTGTGTAACCC	0.512	
-	7	992	axh.1_Nonsense_	NM_016141	NP_057225	Q9Y6G9	DC1L1_HUMAN			1	TTTCTGAACGA	0.279	

-	3	847	p.P106L|UBP1_uc	NM_014517	NP_055332	Q9NZI7	UBIP1_HUMAN		2	ATCTCAGGCATAT	0.299
-	2	685	_p.S52N|UBP1_uc	NM_014517	NP_055332	Q9NZI7	UBIP1_HUMAN		2	GAAGGCTGGAA	0.428
-	2	660	_p.P44S|UBP1_uc	NM_014517	NP_055332	Q9NZI7	UBIP1_HUMAN		2	AATGGGCAATG	0.433
+	12	1753	p.A538V|PDCD6IF	NM_013374	NP_037506	Q8WUM4	PDC6I_HUMAN	EIAV p9.|Self-association.	2	ATGCTGCCATCC	0.473
+	4	440	H1_uc003cgn.3_5	NM_000249	NP_000240	P40692	MLH1_HUMAN		77	CATACAGGTATA	0.368
+	14	1690	_Nonsense_Mutati	NM_000249	NP_000240	P40692	MLH1_HUMAN	action with E p.0?(1)	77	CAGCATCAAACC	0.463
-	8	959	_p.S210N|ACAA1_	NM_001607	NP_001598	P09110	THIK_HUMAN		1	TGGTGCTGGGG	0.562
-	5	653	.2_Intron|ACAA1_	NM_001607	NP_001598	P09110	THIK_HUMAN		1	TCTTACCCACA	0.423
+	3	644	LC22A13_uc011ay	NM_004256	NP_004247	Q9Y226	S22AD_HUMAN	ical; (Potential).	1	CTTTGCTGTGG	0.617
-	27	4834	i.2_Missense_Mut	NM_198056	NP_932173	Q14524	SCN5A_HUMAN	S1 of repeat IV; (Potential)	9	TCTCCACCATC	0.468
-	16	2899	_p.T902I|SCN5A_	NM_198056	NP_932173	Q14524	SCN5A_HUMAN		9	ACATGGTCTCG	0.552
-	27	5732		NM_006514	NP_006505	Q9Y5Y9	SCNAA_HUMAN		10	GAAGCAGTTTCA	0.453
+	2	143	_uc011ayu.1_5'U	NM_020839	NP_065890	Q8TAF3	WDR48_HUMAN	WD 1.	2	AATAGACTTTTCA	0.418
-	9	1338	ORASP1_uc011a	NM_031899	NP_114105	Q9BQQ3	GORS1_HUMAN		3	TGGTTCCTCCT	0.602
-	5	1856	cjh.2_Missense_M	NM_033027	NP_149016	Q96S65	CSRN1_HUMAN		5	GCTGGCATCCC	0.592
+	6	913	zc.1_Missense_M	NM_001145082	NP_001138554	E9PCD9	E9PCD9_HUMAN		1	TTCCACCACTG	0.413
+	4	354	03ckr.2_Nonsens	NM_001904	NP_001895	P35222	CTNB1_HUMAN	_K133del(1)|p.D6_K133del	3166	GAGTGGGAACA	0.443
-	4	548	_p.G116D|ULK4_u	NM_017886	NP_060356	Q96C45	ULK4_HUMAN	rotein kinase.	0	AGAATGCCAAGT	0.338
+	8	628	n_p.A51T|NKTR_	NM_005385	NP_005376	P30414	NKTR_HUMAN	e cyclophilin-type.	3	ATGCTGCAAGC	0.368
-	7	724	lx.2_Missense_Mu	NM_020707	NP_065758	Q9HCP6	HHATL_HUMAN		3	GCTCTCCAGTG	0.542
-	9	1108		NM_144719	NP_653320	Q8IYE1	CCD13_HUMAN	Potential.	1	TTCAAGCTCTC	0.527
-	2	652	mr.1_Missense_M	NM_032806	NP_116195	Q8NAT1	AGO61_HUMAN		2	CAGGTCGTCAT	0.632
-	8	2657	p.A758V|ZNF445_	NM_181489	NP_852466	P59923	ZN445_HUMAN	2H2-type 8.	1	GGAAGGCCTTG	0.532
-	8	1581	p.E399D|ZNF445_	NM_181489	NP_852466	P59923	ZN445_HUMAN		1	AGGGATTCCTT	0.408
+	6	1853	se_Mutation_p.H3	NM_018651	NP_061121	Q9P0L1	ZN167_HUMAN	2H2-type 4.	2	GAACCCATACT	0.458
+	3	463	cnv.1_Missense_M	NM_145044	NP_659481	Q96CX3	ZN501_HUMAN		0	GAAACCTTCAA	0.403
+	1	23	ion_Start_Site|KIA	NM_020242	NP_064627	Q9NS87	KIF15_HUMAN		1	CGTCAACGTCCG	0.637
+	5	481	iq.2_Missense_M	NM_020242	NP_064627	Q9NS87	KIF15_HUMAN	tor.|ATP (By similarity).	1	ACAGACTGGCT	0.308
+	9	1006	_Mutation_p.G189	NM_020242	NP_064627	Q9NS87	KIF15_HUMAN	inesin-motor.	1	AAGCAGGTAACA	0.393
-	3	641	on.2_Missense_M	NM_022842	NP_073753	Q9H5V8	CDCP1_HUMAN	ellular (Potential).	3	CGGTGGCATCG	0.572
+	5	574	hit.1_Missense_M	NM_015340	NP_056155	Q15031	SYLM_HUMAN		2	GGATGCTTTTG	0.438
+	1	675		NM_014240	NP_055055	Q9UGP4	LIMD1_HUMAN		1	GTGGCCTAGCT	0.602
-	14	4143	l.1_Missense_Mu	NM_024513	NP_078789	Q9BQS8	FYCO1_HUMAN		1	TTCAGCCGCATT	0.493
+	2	823	m.3_Missense_M	NM_001123041	NP_001116513	P41597	CCR2_HUMAN	ellular (Potential).	2	CAATGTGCAAAT	0.453
+	8	832	qn.2_Missense_M	NM_000316	NP_000307	Q03431	PTH1R_HUMAN	Name=1; (Potential).	1	CCTGGCCTACT	0.493
-	12	5647	_Mutation_p.S19	NM_014159	NP_054878	Q9BYW2	SETD2_HUMAN		32	CTGTGCTCAGC	0.458
-	7	4963	qv.2_Missense_M	NM_014159	NP_054878	Q9BYW2	SETD2_HUMAN	SET.	32	TTTGGGTTTCA	0.353
-	3	3117	v.2_Missense_Mu	NM_014159	NP_054878	Q9BYW2	SETD2_HUMAN		32	TACTGTCACACT	0.363
+	8	1322	av.1_Missense_M	NM_025010	NP_079286	O94889	KLH18_HUMAN	Kelch 3.	0	CAGCTCCGTGG	0.522
+	22	4177	11bay.1_Missens	NM_015466	NP_056281	Q9H3S7	PTN23_HUMAN	protein phosphatase.	3	GCCTGCCCGAC	0.617
+	4	1051	_uc003csn.2_RN	NM_016089	NP_057173	Q86UQ0	ZN589_HUMAN		1	CAAGGGAGAAA	0.502
-	27	3578		NM_000094	NP_000085	Q02388	CO7A1_HUMAN	region (NC1).|VWFA 2.	11	TCCAGCCATTC	0.607
-	34	9579	kf.2_Missense_M	NM_001407	NP_001398	Q9NYQ7	CELR3_HUMAN	lasmic (Potential).	11	GGACCCTGGCC	0.662
-	14	1300	QARS_uc003cvy.2	NM_005051	NP_005042	P47897	SYQ_HUMAN		1	ACCCACCATTT	0.607
-	4	381	te|QARS_uc011bc	NM_005051	NP_005042	P47897	SYQ_HUMAN		1	CTCCACCTGCA	0.562
-	26	4407	2_5'Flank|USP19_	NM_002292	NP_002283	P55268	LAMB2_HUMAN	Domain II.	3	CAGTGCCTCTG	0.587
+	4	777	3cwi.1_Missense_	NM_173546	NP_775817	Q8IXV7	KLD8B_HUMAN	Kelch 5.	0	ATCTGGAGGCC	0.637

-	1	43		NM_001080528	NP_001073997				0	GCTGGGATGATG	0.537
+	3	1338		NM_004393	NP_004384	Q14118	DAG1_HUMAN	for laminin recognition.	2	CTCTTCCCAAAC	0.612
+	15	1829	w.1_Missense_Mu	NM_001640	NP_001631	P13798	ACPH_HUMAN		1	GAGAATGTGCAG	0.612
+	20	1810	se_Mutation_p.S23	NM_022064	NP_071347	Q5XPI4	RN123_HUMAN		7	AGGCTTCCAATC	0.572
-	1	809	.2_Intron|RNF123	NM_198722	NP_942015	Q86WK7	AMGO3_HUMAN	cellular (Potential).	1	CGCGCGCAGGC	0.637
-	20	4354	dc.1_Missense_Mu	NM_002447	NP_002438	Q04912	RON_HUMAN	lasmic (Potential).	6	TGGGGCCCAAGT	0.597
-	1	643	_p.P127S|MST1R_	NM_002447	NP_002438	Q04912	RON_HUMAN	lar (Potential).|Sema.	6	GCGCGGGATCCA	0.687
-	3	853	.2_Intron|MON1A_	NM_032355	NP_115731	Q86VX9	MON1A_HUMAN		2	TGGCATCCTCCT	0.637
+	5	545	cyk.2_Missense_M	NM_004186	NP_004177	Q13275	SEM3F_HUMAN	Sema.	2	AGTGTGGGAACT	0.637
+	13	1402	0hli.2_Missense_	NM_004636	NP_004627	Q13214	SEM3B_HUMAN	Sema.	6	TTGGCACCTTCA	0.602
-	33	2785	_Mutation_p.S909	NM_006030	NP_006021	Q9NY47	CA2D2_HUMAN	cellular (Potential).	1	ACCTCACTGAAG	0.547
+	5	865	03dba.1_Missense	NM_004635	NP_004626	Q16644	MAPK3_HUMAN	rotein kinase.	2	CTGGCAGGCTT	0.542
+	9	717		NM_004947	NP_004938	Q8IZD9	DOCK3_HUMAN		0	GGGAAGATACC	0.458
+	1	1428		NM_013286	NP_037418	Q8NDT2	RB15B_HUMAN	RRM 3.	0	TGGGAGCATTC	0.572
+	1	1461		NM_013286	NP_037418	Q8NDT2	RB15B_HUMAN	RRM 3.	0	GAGATAGCTTTG	0.587
-	14	2789	lbf.1_Missense_Mu	NM_014703	NP_055518	Q9Y4B6	VPRBP_HUMAN	LisH.	2	AGGTCAGCCTCT	0.502
+	3	1483	.3_Intron|GRM2_	NM_000839	NP_000830	Q14416	GRM2_HUMAN	cellular (Potential).	1	TAACGGGCGCC	0.592
+	4	2269	se_Mutation_p.A5	NM_000839	NP_000830	Q14416	GRM2_HUMAN	lasmic (Potential).	1	TCCTGCCTCAC	0.652
+	5	511	CF3_uc010hlw.1_	NM_001085479	NP_001078948	P0C7M6	IQCF3_HUMAN		1	TGCTGCCCTCA	0.622
-	9	1070	91L|PCBP4_uc00	NM_033010	NP_127503	P57723	PCBP4_HUMAN		0	CAAAGGGGACC	0.632
-	7	1087	p.D219N|POC1A_	NM_015426	NP_056241	Q8NBT0	POC1A_HUMAN	WD 6.	0	CAGGTCCAGGA	0.597
+	6	1059	_p.T241I|ALAS1_	NM_000688	NP_000679	P13196	HEM1_HUMAN		3	TCATCACCAAAA	0.478
-	2	1910	b.2_Missense_Mu	NM_017442	NP_059138	Q9NR96	TLR9_HUMAN	xtracellular (Potential).	4	TGATGCGGTTGT	0.642
+	65	10643	dv.2_Missense_M	NM_015512	NP_056327	Q9P2D7	DYH1_HUMAN		3	TGTGTCCGACC	0.562
+	23	2532		NM_015136	NP_055951	Q9NY15	STAB1_HUMAN	Extracellular (Potential).	9	CCATGGGGGAC	0.662
+	34	3661		NM_015136	NP_055951	Q9NY15	STAB1_HUMAN	xtracellular (Potential).	9	GGAGGCCCTCT	0.627
+	54	5755	1_5'UTR|STAB1_	NM_015136	NP_055951	Q9NY15	STAB1_HUMAN	cellular (Potential).	9	GCCACCCTGTC	0.637
-	24	4018	_p.V1351I|PBRM1_	NM_181042	NP_060635	Q86U86	PB1_HUMAN		140	CAATGACCTCAC	0.498
-	20	3316	lew.2_Missense_M	NM_181042	NP_060635	Q86U86	PB1_HUMAN		140	CATTTGCAAATAC	0.443
-	9	1037	.D300N|GLT8D1_	NM_152932	NP_690909	Q68CQ7	GL8D1_HUMAN	enal (Potential).	0	AGGATCGATGG	0.453
-	12	1607	.S388F|ITIH4_uc	NM_002218	NP_002209	Q14624	ITIH4_HUMAN		3	ACACTGGACTCC	0.577
+	13	1295	p.G322E|CACNA2	NM_018398	NP_060868	Q8IZS8	CA2D3_HUMAN	lar (Potential).|VWFA.	7	TGACAGGATTTT	0.483
-	3	972	A2D3_uc003dhg.1_	NM_020678	NP_065729	Q9HBL6	LRTM1_HUMAN	cellular (Potential).	0	GTTGGCCGGCC	0.597
+	36	3119	se_Mutation_p.P93	NM_018398	NP_060868	Q8IZS8	CA2D3_HUMAN	cellular (Potential).	7	GGCCCCCATCA	0.512
+	13	1930	_Splice_Site_p.D5	NM_001141947	NP_001135419	A2RUB6	CCD66_HUMAN		1	AAACAGGTATTT	0.274
-	17	3436	dic.3_Missense_Mu	NM_015224	NP_056039	Q9UK61	CC063_HUMAN		5	TCAGAAGTCACC	0.433
-	12	1749	na.2_Missense_Mu	NM_017563	NP_060033	Q8NFM7	I17RD_HUMAN	lasmic (Potential).	0	CCTCGTCAATAA	0.572
+	22	2219	.1_Intron|ASB14_	NM_012096	NP_036228	Q9UKG1	DP13A_HUMAN		1	GCAGTAGCCAGT	0.443
+	7	1229	nf.2_Missense_Mu	NM_001457	NP_001448	O75369	FLNB_HUMAN	Filamin 2.	19	ATGCCAGTAAAG	0.507
+	19	3010	nf.2_Missense_Mu	NM_001457	NP_001448	O75369	FLNB_HUMAN	Filamin 8.	19	ATAAAACTCAATG	0.502
+	22	4052	nf.2_Missense_Mu	NM_001457	NP_001448	O75369	FLNB_HUMAN	Interaction with FBLP1.	19	ACACACCCTTTG	0.597
+	17	1576	c.1_Missense_Mut	NM_017771	NP_060241	Q7Z7A4	PXK_HUMAN		1	CTGGGGCCAGC	0.532
-	3	988	_p.V210I|CADPS_	NM_003716	NP_003707	Q9ULU8	CAPS1_HUMAN		3	GAAGACCTCCC	0.567
+	9	1893	nv.2_Missense_Mu	NM_000333	NP_000324	O15265	ATX7_HUMAN	Pro-rich.	0	CTAAACCTCACA	0.507
-	6	969	_p.T368I|PSMD6_	NM_014814	NP_055629	Q15008	PSMD6_HUMAN	PCI.	2	CCAAGGGTTAAT	0.368
-	25	3763	dmh.1_Missense_	NM_182920	NP_891550	Q9P2N4	ATS9_HUMAN	TSP type-1 8.	4	TCCAAGGCCTTC	0.552
-	20	2992	_Mutation_p.S81	NM_182920	NP_891550	Q9P2N4	ATS9_HUMAN	TSP type-1 3.	4	GGTTGCTTGGT	0.493

-	14	2757	_p.S744N|MAGI1_	NM_001033057	NP_001028229	Q96QZ7	MAGI1_HUMAN		6	TGAGAACTATTCT	0.517
-	2	1482	nt.2_Missense_Mu	NM_198271	NP_938012	Q0VAK6	LMOD3_HUMAN	Potential.	1	GCAGCCCCAACC	0.542
-	2	459	sense_Mutation_p	NM_015123	NP_055938	Q9Y2L6	FRM4B_HUMAN		4	TGCCTTCTGTCAT	0.522
-	14	1938	doq.1_Intron|FOXI	NM_032682	NP_116071	Q9H334	FOXP1_HUMAN	Fork-head.	2	ATTCTACTTCATC	0.413
-	11	1707	d.2_Missense_Mu	NM_018130	NP_060600	Q6PI26	SHQ1_HUMAN		3	AGACACTCCAA	0.512
+	1	1154	.1_Intron|PPP4R2	NM_018029	NP_060499	Q6P2I7	EBLN2_HUMAN		0	GATCAGCTCAA	0.438
-	10	3004	_p.G668R|PDZRN3	NM_015009	NP_055824	Q9UPQ7	PZRN3_HUMAN		7	AGCGCCCCATCT	0.662
+	3	1182	BO2_uc011bgj.1_F	NM_002942	NP_002933	Q9HCK4	ROBO2_HUMAN	2.|Extracellular (Potential).	11	AAGAAAGAATAA	0.383
-	28	4643	3dqd.2_Splice_Site	NM_002941	NP_002932	Q9Y6N7	ROBO1_HUMAN		2	GACTCACCATCT	0.463
-	27	4100	dqd.2_Missense_M	NM_002941	NP_002932	Q9Y6N7	ROBO1_HUMAN	lasmic (Potential).	2	AGGAGGACTCA	0.473
-	25	3740	dqd.2_Missense_M	NM_002941	NP_002932	Q9Y6N7	ROBO1_HUMAN	lasmic (Potential).	2	GCCACCCTGTTT	0.473
-	6	939	oj.1_Missense_M	NM_000306	NP_000297	P28069	PIT1_HUMAN	Homeobox.	2	TTTTCACCCGTT	0.378
+	2	1170		NM_000866	NP_000857	P30939	5HT1F_HUMAN	ame=7; (By similarity).	3	GGTATCTCAATT	0.318
-	7	948	_p.D72N|PROS1_	NM_000313	NP_000304	P07225	PROS_HUMAN	alcium-binding (Potential).	1	ATTCATCCACAT	0.378
+	10	1554	dre.2_Missense_M	NM_182896	NP_878899	Q3SXY8	AR13B_HUMAN		0	GTGATGCTCATG	0.413
-	2	236	P24S|NSUN3_uc0	NM_176815	NP_789785	Q86XF0	DYRL1_HUMAN	DHFR.	0	CCTGGGCAGGT	0.498
+	14	2726	drr.3_Missense_M	NM_001080448	NP_001073917	Q9UF33	EPHA6_HUMAN	e.|Cytoplasmic (Potential).	16	TAGCGGCTCGG	0.453
+	8	859	3dtb.2_Missense_M	NM_006100	NP_006091	Q9Y274	SIA10_HUMAN	enal (Potential).	1	AGAACACTAATG	0.333
-	16	2597	dte.2_Missense_M	NM_080927	NP_563615	Q96PD2	DCBD2_HUMAN	lasmic (Potential).	3	CGTCTGGGGCA	0.507
+	8	754		NM_032359	NP_115735	Q9BQ75	CC026_HUMAN		1	GAAGCGTGTGG	0.458
+	10	1201	dts.2_Missense_M	NM_018309	NP_060779	Q9NUY8	TBC23_HUMAN	Rhodanese.	2	TGGTGGATTGC	0.373
+	7	606	011bha.1_Silent_	NM_020202	NP_064587	Q9NQR4	NIT2_HUMAN	N hydrolase.	1	CAGGAGCTTTT	0.493
+	9	813		NM_020202	NP_064587	Q9NQR4	NIT2_HUMAN	N hydrolase.	1	GACATAGGTAAG	0.483
-	3	426	_p.S107L|ABI3BP_	NM_015429	NP_056244	Q7Z7G0	TARSH_HUMAN		4	GAACATGACTTC	0.393
-	24	3251	uw.2_Missense_M	NM_020654	NP_065705	Q9BQF6	SENP7_HUMAN	Protease.	5	TGCTGCCCTTC	0.413
-	4	367	_p.P53S|SENP7_	NM_020654	NP_065705	Q9BQF6	SENP7_HUMAN		5	AACAGGACACC	0.294
+	1	58	97_uc011bhf.1_M	NM_024548	NP_078824	Q8IW35	CEP97_HUMAN		2	CTTTGCCTCCC	0.537
+	4	602	po.2_Missense_M	NM_031419	NP_113607	Q9BYH8	IKBZ_HUMAN		2	ACAGTGGGAAA	0.388
+	5	1010	_Mutation_p.C15	NM_001627	NP_001618	Q13740	CD166_HUMAN	Potential).|Ig-like V-type 2.	3	GTGACTGCATTT	0.443
-	19	3054	_p.R126H|CBLB_u	NM_170662	NP_733762	Q13191	CBLB_HUMAN	eraction with SH3KBP1.	9	TCCTGCGCGGT	0.453
-	7	1293	e_Mutation_p.S32	NM_170662	NP_733762	Q13191	CBLB_HUMAN	-PTB.|SH2-like.	9	TCCCTGCTGCCA	0.418
-	40	5653		NM_014981	NP_055796	Q9Y2K3	MYH15_HUMAN	Potential.	7	CTCTGCCTGCA	0.448
-	32	4400		NM_014981	NP_055796	Q9Y2K3	MYH15_HUMAN	Potential.	7	CAGAGCGGACC	0.652
-	9	1242	ense_Mutation_p.	NM_020890	NP_065941	Q8TCG1	CIP2A_HUMAN		3	AGGTGGAGACT	0.458
+	9	1354	xx.2_Missense_Mu	NM_198196	NP_937839	P40200	TACT_HUMAN	otential).|Pro/Ser/Thr-rich.	3	AATCTACCCTTG	0.368
+	3	626	dyn.2_Missense_M	NM_001008272	NP_001008273	Q9UI15	TAGL3_HUMAN	CH.	0	AGAGTCAAAGAT	0.473
-	20	2692	_p.A87T|SLC9A10	NM_183061	NP_898884	Q4G0N8	S9A10_HUMAN		5	CAAAAGCCTTAA	0.308
-	7	841	LC9A10_uc010hqc	NM_183061	NP_898884	Q4G0N8	S9A10_HUMAN	ical; (Potential).	5	CGATCTCTTCAG	0.303
-	3	311	te|SLC9A10_uc01	NM_183061	NP_898884	Q4G0N8	S9A10_HUMAN		5	AAATGCTGCAA	0.318
-	3	2115	dzg.2_Missense_M	NM_199512	NP_955806	Q76M96	CCD80_HUMAN		2	CTCAGCCTTGG	0.423
-	2	2040	dzg.2_Missense_M	NM_199512	NP_955806	Q76M96	CCD80_HUMAN	Lys-rich.	2	CTTGGGACTCT	0.413
+	4	890	z.2_Missense_Mu	NM_033254	NP_150279	Q9BWV1	BOC_HUMAN	otential).|Ig-like C2-type 1.	6	CGGGACCCTCG	0.602
-	14	2044	DC52_uc003eah.	NM_144718	NP_653319	Q8N0Z3	SPICE_HUMAN		0	CAATAGGTAAGG	0.408
-	5	607	CDC52_uc003eah	NM_144718	NP_653319	Q8N0Z3	SPICE_HUMAN		0	CATCTTGCATCT	0.333
-	7	5885	eal.2_Missense_M	NM_001009899	NP_001009899	Q68DE3	K2018_HUMAN		3	GAGGGGCAAGT	0.448
-	7	5156	eal.2_Missense_M	NM_001009899	NP_001009899	Q68DE3	K2018_HUMAN	Gln-rich.	3	GTTGAAGGGTTT	0.498
-	7	1379	eal.2_Missense_M	NM_001009899	NP_001009899	Q68DE3	K2018_HUMAN		3	GTATGCTCAGG	0.473

-	1	155	_p.L3P|QTRTD1_	NM_020817	NP_065868	Q8NCU4	K1407_HUMAN		2	GCGCCAGGAG	0.587	rs140131124
-	7	1223	y.2_Missense_M	NM_001015887	NP_001015887	Q5DX21	IGS11_HUMAN	lasmic (Potential).	0	TTTTGGATTGT	0.448	
+	12	2660		NM_020754	NP_065805	Q2M1Z3	RHG31_HUMAN	Pro-rich.	2	CTGCTCCAGTC	0.592	
-	2	431	39A_uc003ecl.1_	NM_018266	NP_060736	Q9NV64	TM39A_HUMAN		2	CCAAAGTCTGC	0.473	
+	4	959		NM_005513	NP_005504	P29083	T2EA_HUMAN		1	GTTGAGAGAAA	0.408	
+	5	1010		NM_005513	NP_005504	P29083	T2EA_HUMAN		1	AGGGGGCATAG	0.393	
-	10	820	e_Mutation_p.S19	NM_005335	NP_005326	P14317	HCLS1_HUMAN		0	CACTAGAAGCT	0.522	
-	13	4417	.E1397K|GOLGB1	NM_004487	NP_004478	Q14789	GOGB1_HUMAN	ic (Potential).|Potential.	10	CTTGTTCTATTAT	0.383	
+	3	815	w.3_Missense_M	NM_000388	NP_000379	P41180	CASR_HUMAN	ellular (Potential).	7	CTCAGGCGTCT	0.527	
+	1	244	_uc011bjs.1_5'Fla	NM_138287	NP_612144	Q8TDB6	DTX3L_HUMAN		4	CCCGGGCACCT	0.687	
+	14	4350	e_Mutation_p.V11	NM_017554	NP_060024	Q460N5	PAR14_HUMAN		6	TTCGGGTGTGT	0.388	
-	13	2485	p.R462W|ADCY5_	NM_183357	NP_899200	O95622	ADCY5_HUMAN		4	GGACCGCACGA	0.403	
-	1	993		NM_183357	NP_899200	O95622	ADCY5_HUMAN	ical; (Potential).	4	ACGGTCCACCA	0.687	
+	27	4312	95_splice|KALRN_	NM_001024660	NP_001019831	O60229	KALRN_HUMAN		6	TTTGATGTAAGC	0.408	
+	35	5405	ehk.2_Missense_	NM_001024660	NP_001019831	O60229	KALRN_HUMAN		6	CGGGTCCCAAG	0.557	
+	60	9054	k.2_Missense_M	NM_001024660	NP_001019831	O60229	KALRN_HUMAN		6	TCAAGAGCTACA	0.527	
-	5	1040		NM_002213	NP_002204	P18084	ITB5_HUMAN	tracellular (Potential).	2	AGCCCCCCTCA	0.572	
-	6	2806	.1_Missense_Mut	NM_020733	NP_065784	Q9ULI3	HEG1_HUMAN	ellular (Potential).	2	TCAATCCAGTG	0.493	
-	10	1688	_p.A327V|SLC12A	NM_024628	NP_078904	A0AV02	S12A8_HUMAN		0	AGGAGGCAGCG	0.557	
-	9	2330	hsa.2_Missense_	NM_021964	NP_068799	Q9UQR1	ZN148_HUMAN		4	TAGTTCTGTCC	0.463	
+	11	1169	sg.1_Missense_M	NM_182628	NP_872434	Q494V2	CCD37_HUMAN		2	CGGTGGCGACT	0.642	
+	13	1304	sg.1_Missense_	NM_182628	NP_872434	Q494V2	CCD37_HUMAN	Potential.	2	GAACCTGTCGC	0.597	
+	28	5057	jh.2_Missense_M	NM_032242	NP_115618	Q9UIW2	PLXA1_HUMAN	lasmic (Potential).	3	ACCGGGGCTCA	0.627	
-	1	144	UVBL1_uc010hss.	NM_003707	NP_003698	Q9Y265	RUVB1_HUMAN		1	GATGCGCTGCG	0.627	
+	5	1221	ekj.2_Missense_M	NM_021937	NP_068756	P57772	SELB_HUMAN		1	AGGCCGACAAG	0.567	
+	4	429	_p.G66E|RAB7A_	NM_004637	NP_004628	P51149	RAB7A_HUMAN	(By similarity).	0	AGCAGGACAGG	0.502	
+	10	1179	9_uc003elb.2_Mis	NM_014049	NP_054768	Q9H845	ACAD9_HUMAN		3	GTACGCCTGCA	0.264	
-	3	346	e_Mutation_p.S40	NM_003418	NP_003409	P62633	CNBP_HUMAN		0	ACGAGGAAACA	0.383	
+	6	495	tb.2_Missense_M	NM_016128	NP_057212	Q9Y678	COPG_HUMAN		4	AGATCACTGATG	0.562	
+	17	1808	tb.2_Missense_M	NM_016128	NP_057212	Q9Y678	COPG_HUMAN		4	AACCATCAGAA	0.512	
+	24	2604	lank|C3orf37_uc0	NM_016128	NP_057212	Q9Y678	COPG_HUMAN	ith ZNF289/ARFGAP2.	4	GTTCCGGGGTG	0.517	
-	7	1798	D4_uc003emk.1_	NM_003925	NP_003916	O95243	MBD4_HUMAN		2	TCGTTGCCATAT	0.418	
+	19	2544	mq.2_Missense_	NM_052989	NP_443715	Q9HBG6	IF122_HUMAN		2	TCAAGGCCATC	0.522	rs141746785
+	24	3139	_p.S769F|IFT122	NM_052989	NP_443715	Q9HBG6	IF122_HUMAN		2	CATCTCCAGGT	0.522	
+	4	792		NM_000539	NP_000530	P08100	OPSD_HUMAN	Cytoplasmic.	0	TGCAGGCCGCT	0.652	
-	32	5342	PLXND1_uc011blb	NM_015103	NP_055918	Q9Y4D7	PLXD1_HUMAN	lasmic (Potential).	1	CTCAGCCTGCT	0.577	
-	16	3318		NM_015103	NP_055918	Q9Y4D7	PLXD1_HUMAN	r (Potential).|IPT/TIG 3.	1	TGATGGCCGTG	0.672	
-	5	1908		NM_015103	NP_055918	Q9Y4D7	PLXD1_HUMAN	ellular (Potential).	1	CGGTCATGGCA	0.657	
+	2	410		NM_001102608	NP_001096078	A6NMZ7	CO6A6_HUMAN	cal region.|VWFA 1.	8	GGAGAGACAAG	0.502	
+	8	3725	A6_uc003eni.3_5'	NM_001102608	NP_001096078	A6NMZ7	CO6A6_HUMAN	.|Nonhelical region.	8	AGGTGGGCACA	0.458	
-	4	1906		NM_014602	NP_055417	Q99570	PI3R4_HUMAN	HEAT 1.	12	CTTTGGTCAAC	0.428	
+	16	1463	no.2_Missense_M	NM_014382	NP_055197	P98194	AT2C1_HUMAN	smic (By similarity).	1	ATGATGCTGTAA	0.373	
+	43	5133		NM_015268	NP_056083	O75165	DJC13_HUMAN		2	TAGGGGAGATT	0.338	
-	24	3601	_p.S54F|NPHP3_	NM_153240	NP_694972	Q7Z494	NPHP3_HUMAN		1	CCAAAGAAGGG	0.358	
-	21	3147	pd.1_Missense_M	NM_153240	NP_694972	Q7Z494	NPHP3_HUMAN		1	TATATGGATGGT	0.393	
-	10	1659	PHP3_uc003epf.1	NM_153240	NP_694972	Q7Z494	NPHP3_HUMAN		1	AGACACGAGAA	0.388	
-	8	1369	pf.1_Missense_M	NM_153240	NP_694972	Q7Z494	NPHP3_HUMAN		1	GATCTCCTGAG	0.269	

-	7	1236	pf.1_Missense_Mu	NM_153240	NP_694972	Q7Z494	NPHP3_HUMAN		1	TTCAGGGTTTT	0.373
+	1	368		NM_003571	NP_003562	Q13515	BFSP2_HUMAN	Head.	0	CCGGGCCCTCG	0.647
+	6	1375		NM_003571	NP_003562	Q13515	BFSP2_HUMAN	Tail.	0	GGGAGGAGAGC	0.532
+	4	1027	_p.S191N|CDV3_	NM_017548	NP_060018	Q9UKY7	CDV3_HUMAN		0	TCTACAGTGATA	0.463
+	3	342		NM_021203	NP_067026	Q9Y5M8	SRPRB_HUMAN		1	TAACAGGGTAA	0.393
-	10	1646	_p.V382I|SLCO2	NM_005630	NP_005621	Q92959	SO2A1_HUMAN	r (Potential).|Kazal-like.	1	ACAGACCGGGT	0.562
-	9	2471	_Mutation_p.S72	NM_016201	NP_057285	Q9Y2J4	AMOL2_HUMAN		1	GGGTGCTCCCA	0.637
+	3	867	z.1_RNA|EPHB1_	NM_004441	NP_004432	P54762	EPHB1_HUMAN	ar (Potential).|Cys-rich.	30	GAGCACATCTC	0.507
-	2	1596	b.1_Missense_Mu	NM_018133	NP_060603	Q9HCI7	MSL2_HUMAN		1	AATTAGGGCAA	0.433
-	1	807	2_uc011bmb.1_5'	NM_018133	NP_060603	Q9HCI7	MSL2_HUMAN		1	CCTTGGGGTCT	0.517
+	9	976	c.1_Missense_Mu	NM_000532	NP_000523	P05166	PCCB_HUMAN	oxyltransferase.	0	CTTTGGAATCA	0.463
-	23	2573	p.D761N|STAG1_	NM_005862	NP_005853	Q8WVM7	STAG1_HUMAN		2	CAAATCCTCCT	0.368
+	5	800	20RB_uc010hud.1	NM_144717	NP_653318	Q6UXL0	I20RB_HUMAN	tential).|Fibronectin type-III	1	GGTGAGGAGTG	0.378
-	2	557	err.1_Missense_M	NM_173543	NP_775814	Q8IYY4	DZI1L_HUMAN		2	AGTTGCAGAAG	0.612
+	13	1581	T3_uc010hug.2_	NM_031913	NP_114119	A0FGR9	ESYT3_HUMAN	C2 2.	0	GGAGAGTGCCT	0.532
+	15	1729	_uc010hug.2_Spli	NM_031913	NP_114119	A0FGR9	ESYT3_HUMAN		0	GTAAGGTAAGA	0.438
-	18	1945	nl.1_Missense_Mu	NM_024491	NP_077817	Q8NHQ1	CEP70_HUMAN		1	GGCATCCAAGT	0.279
+	5	651	q.2_Missense_Mu	NM_001033032	NP_001028204	Q9NVQ4	FAIM1_HUMAN		0	TCCAGGGTGAG	0.398
+	5	718	q.2_Missense_Mu	NM_001033032	NP_001028204	Q9NVQ4	FAIM1_HUMAN		0	AAAGGCTGTCA	0.398
-	22	3190	se_Mutation_p.V5	NM_006219	NP_006210	P42338	PK3CB_HUMAN	PI3K/PI4K.	5	CCGAACTGTGT	0.408
-	1	858		NM_001013650	NP_001013672	Q6ZRT6	PR23B_HUMAN	Pro-rich.	1	GAGCACAGGGT	0.622
-	4	623	AT3_uc003etl.2_	NM_178177	NP_835471	Q96T66	NMNA3_HUMAN		0	CACAGGCTCCT	0.542
+	2	294	_Mutation_p.G20	NM_001104647	NP_001098117	Q96CQ1	S2536_HUMAN	ical; Name=1; (Potential).	0	AGTGGGAGCTA	0.383
+	8	3521	_p.A847T|ZBTB38	NM_001080412	NP_001073881	Q8NAP3	ZBT38_HUMAN		3	ACGAAGCCATT	0.423
+	4	1507		NM_139209	NP_631948	Q8WTQ7	GRK7_HUMAN	kinase C-terminal.	5	CAGACCCTTCA	0.428
-	36	4184	.2_Missense_Mut	NM_019001	NP_061874	Q8IZH2	XRN1_HUMAN		3	CTTATGGTCCA	0.358
-	2	203	_Mutation_p.P46	NM_019001	NP_061874	Q8IZH2	XRN1_HUMAN		3	ATTAGGATGGG	0.318
-	40	6949	y.1_Missense_Mu	NM_001184	NP_001175	Q13535	ATR_HUMAN		20	CATGGGTACCC	0.373
-	34	5861		NM_001184	NP_001175	Q13535	ATR_HUMAN		20	CTGGTCTAAAG	0.408
-	8	1155		NM_013363	NP_037495	Q9UKZ9	PCOC2_HUMAN	NTR.	3	CAGTGCCGGCT	0.438
-	12	1546		NM_173653	NP_775924	Q8IVB4	SL9A9_HUMAN		3	GCTGAGATTCT	0.463
-	18	2487	m.1_Missense_M	NM_000935	NP_000926	O00469	PLOD2_HUMAN	G dioxygenase.	2	AGAACGCTGTC	0.348
-	17	2388	m.1_Missense_M	NM_000935	NP_000926	O00469	PLOD2_HUMAN		2	GAACTCCCGGA	0.423
-	3	886	_p.P135S|ZIC4_uc	NM_032153	NP_115529	Q8N9L1	ZIC4_HUMAN	2H2-type 3.	2	ACAAGGGAAGG	0.517
+	2	149		NM_001870	NP_001861	P15088	CBPA3_HUMAN		2	CCCAGGATGAA	0.383
+	17	3066	.1_Missense_Mut	NM_032383	NP_115759	Q969F9	HPS3_HUMAN		6	TGAAGGATTTC	0.338
-	6	1410	_uc003ewz.2_Mis	NM_000096	NP_000087	P00450	CERU_HUMAN	in-like 3.|F5/8 type A 2.	1	AGGGAGCATAG	0.413
+	3	581		NM_004617	NP_004608	P48230	T4S4_HUMAN	ellular (Potential).	0	CAAGGGTCCTA	0.517
+	8	585	IF2A_uc011bnv.1_	NM_032025	NP_114414	Q9BY44	EIF2A_HUMAN		0	TCCAGGAAGTA	0.328
-	4	667	eyh.2_Missense_	NM_152394	NP_689607	Q7L0X2	F194A_HUMAN		3	ATTTACCTCTTAA	0.418
-	1	710		NM_005067	NP_005058	O43255	SIAH2_HUMAN		2	CCGGGGACGGA	0.697
-	3	932	y.1_Intron|CLRN1	NM_174878	NP_777367	P58418	CLRN1_HUMAN		0	CAAAAGGGAAC	0.363
+	4	492	_p.P152S|MED12L	NM_053002	NP_443728	Q86YW9	MD12L_HUMAN		7	CTGTGCCAATG	0.343
+	4	541	_p.S168F|MED12L	NM_053002	NP_443728	Q86YW9	MD12L_HUMAN		7	ATTATTCTGCTA	0.358
+	14	2059	yn.2_Missense_M	NM_053002	NP_443728	Q86YW9	MD12L_HUMAN		7	GTTGGGCAGAA	0.388
+	35	5191	p.P1578L|MED12	NM_053002	NP_443728	Q86YW9	MD12L_HUMAN		7	CATGCCCAAGC	0.577
+	39	5968	12L_uc011bnz.1_	NM_053002	NP_443728	Q86YW9	MD12L_HUMAN	Gln-rich.	7	ACATTCCAACC	0.582

-	5	5518	_5'Flank|IGSF10_	NM_178822	NP_849144	Q6WRI0	IGS10_HUMAN		13	TGGTGCTGCAA	0.473	
-	4	4523		NM_178822	NP_849144	Q6WRI0	IGS10_HUMAN		13	TTGAGGATTCG	0.493	
-	3	613		NM_178822	NP_849144	Q6WRI0	IGS10_HUMAN	LRR 6.	13	GGAGACCATCT	0.433	
-	22	3215	_p.A980T|PLCH1_	NM_001130960	NP_001124432	Q4KWH8	PLCH1_HUMAN		4	CAAAGCTCCCA	0.473	
+	3	1242	H1_uc003fbk.1_In	NM_002852	NP_002843	P26022	PTX3_HUMAN	Pentaxin.	1	GGTGGGGAGTC	0.448	
+	3	534	uc003fcw.1_Intron	NM_000882	NP_000873	P29459	IL12A_HUMAN		0	ATGAAGATATC	0.368	
+	4	573	lj.2_Missense_Mut	NM_001002800	NP_001002800	Q9NTJ3	SMC4_HUMAN		2	ACAAGGACATT	0.303	
-	3	866		NM_001040100	NP_001035189	Q8NFR3	SSPTB_HUMAN	enal (Potential).	0	TAGATCGCTCC	0.428	
-	3	309		NM_001041	NP_001032	P14410	SUIS_HUMAN	nenal.|P-type 1.	14	TGTTGGGAATT	0.289	
-	7	1672	fk.2_Missense_Mu	NM_005241	NP_005232	Q03112	EVI1_HUMAN		14	CAGCTCCTGAC	0.398	
-	7	1746	11bpt.1_Intron|uc0	NM_020949	NP_066000	Q8TBB6	S7A14_HUMAN		5	TGGTGGCTGGG	0.507	
-	16	2089	.P582S|TNIK_uc0	NM_015028	NP_055843	Q9UKE5	TNIK_HUMAN	nteraction with NEDD4.	5	GGGGGGTGTTC	0.527	rs148174466
+	4	986	n_p.T228I|NLGN1_	NM_014932	NP_055747	Q8N2Q7	NLGN1_HUMAN	ellular (Potential).	7	AAGGTACTGGAA	0.433	
-	5	484	XR1_uc011bpz.1_	NM_024665	NP_078941	Q9BZK7	TBL1R_HUMAN	F-box-like.	1	GTCGACCATCA	0.363	
-	1	120	33E|NDUFB5_uc0	NM_020409	NP_065142	Q9HD33	RM47_HUMAN		0	CTTACCCTGTG	0.507	
+	5	468	DUFB5_uc003fke.	NM_002492	NP_002483	O43674	NDUB5_HUMAN		1	AAAAGGCTGAA	0.383	
+	14	1346	p.P356S|FXR1_uc	NM_005087	NP_005078	P51114	FXR1_HUMAN	binding RGG-box.	1	GACGCCCAGGA	0.532	
+	3	311	n_p.G6R|KLHL24_	NM_017644	NP_060114	Q6TFL4	KLH24_HUMAN		1	TATTGGGACGC	0.378	
+	3	426	.P96S|DVL3_uc0	NM_004423	NP_004414	Q92997	DVL3_HUMAN		3	ATAACCCATCG	0.602	
+	1	1549	131A_uc003foc.2_	NM_144635	NP_653236	Q6UXB0	F131A_HUMAN		1	GTGCTCCCTGG	0.582	
+	3	2173	foc.2_Missense_	NM_144635	NP_653236	Q6UXB0	F131A_HUMAN		1	GGAGGCCCAGG	0.692	
-	2	248	_p.R42C|CLCN2_	NM_004366	NP_004357	P51788	CLCN2_HUMAN	smic (By similarity).	0	CAGGCGAATCC	0.627	
+	10	2296		NM_004443	NP_004434	P54753	EPHB3_HUMAN	lasmic (Potential).	11	TGAGGCTGTTC	0.542	
+	7	1277	1bru.1_Splice_Sit	NM_004721	NP_004712	O43283	M3K13_HUMAN		3	CTGTAGGTCTT	0.418	
-	10	1381	c.2_Missense_Mu	NM_001346	NP_001337	P49619	DGKG_HUMAN	l-ester/DAG-type 1.	5	GGTTGGTTTCT	0.567	
+	4	644	se_Mutation_p.R2	NM_014375	NP_055190	Q9UGM5	FETUB_HUMAN	tin fetuin-B-type 1.	2	CAAGTAGAGTTC	0.333	
+	4	292	c011bsb.1_5'Flan	NM_001967	NP_001958	Q14240	IF4A2_HUMAN	ase ATP-binding.	4	AGACAGCCACA	0.443	
-	1	365		NM_021101	NP_066924	O95832	CLD1_HUMAN	ellular (Potential).	1	CAGCCCCTCGT	0.607	
-	1	1022	12_uc003fsy.2_In	NM_021032	NP_066360	P61328	FGF12_HUMAN		4	ACCTGGTCTCC	0.662	
-	5	641	e_p.R178_splice|	NM_032279	NP_115655	Q4VNC1	AT134_HUMAN		2	TGGTACCTAAT	0.318	
-	2	96		NM_004488	NP_004479	P40197	GPV_HUMAN	xtracellular (Potential).	3	CTGGCGGACAG	0.662	
-	15	2072	ftz.1_Missense_M	NM_024524	NP_078800	Q9H7F0	AT133_HUMAN		1	GATCACCAGAG	0.318	
+	3	961	se_Mutation_p.V24	NM_152673	NP_689886	Q8N307	MUC20_HUMAN	d in oligomerization.	0	AAGGGGTGAAG	0.542	
-	19	2489	zy.2_Missense_Mu	NM_003234	NP_003225	P02786	TFR1_HUMAN	Potential).|Ligand-binding.	3	TAGAGCCAACT	0.463	
-	4	1182	iah.2_Missense_M	NM_152617	NP_689830	Q8IYW5	RN168_HUMAN		0	TTCTTACTTTTCT	0.363	
+	3	1233		NM_198565	NP_940967	Q86YC3	LRC33_HUMAN	ar (Potential).|LRR 13.	3	CCGGAGCGCTC	0.642	
+	3	1750		NM_198565	NP_940967	Q86YC3	LRC33_HUMAN	ar (Potential).|LRR 19.	3	CTTGACCACCT	0.572	
+	3	2047		NM_198565	NP_940967	Q86YC3	LRC33_HUMAN	ellular (Potential).	3	GGACCTGGGCC	0.627	
+	2	439	bty.1_Missense_M	NM_152699	NP_689912	Q96HI0	SENP5_HUMAN		3	AAAGCTCTTCAA	0.403	
+	2	1750	ty.1_Missense_Mu	NM_152699	NP_689912	Q96HI0	SENP5_HUMAN		3	CTGTCAGTCTGT	0.438	
-	20	2927	ation_p.C870Y|MI	NM_014687	NP_055502	Q92622	RUBIC_HUMAN	Cys-rich.	0	GCTTTACACTCT	0.582	
-	16	2435	p.H706R|KIAA022	NM_014687	NP_055502	Q92622	RUBIC_HUMAN		0	TCTCGTGGCAG	0.522	
-	14	2216	_p.A633V|KIAA022	NM_014687	NP_055502	Q92622	RUBIC_HUMAN		0	TGTCAGCGTGC	0.577	
+	9	1243	n.1_Intron|LRCH3	NM_032773	NP_116162	Q96II8	LRCH3_HUMAN		1	GCGGCGAATCT	0.428	
+	6	1591	1bus.1_Missense_	NM_182524	NP_872330	Q7Z3I0	Q7Z3I0_HUMAN		0	GAGAAACCCTAC	0.393	
+	5	1197	141_uc003gab.2_	NM_003441	NP_003432	Q15928	ZN141_HUMAN	C2H2-type 7.	0	CTACACATGTG	0.408	
-	5	828	d.2_RNA|ABCA11P_uc011buv.1_3'UTR|ABCA11P_uc010ibd.1_Missense_Mutation_p.T98I						0	TTGGAGTAGTG	0.413	

-	3	1617	ron|ABCA11P_uc	NM_133474	NP_597731	D9N162	D9N162_HUMAN		1	CCACATACTTCA	0.388	
+	7	1361	_Mutation_p.L320	NM_001127178	NP_001120650	Q5H8A4	PIGG_HUMAN	enal (Potential).	4	AGGTTCTCAGG	0.493	
+	11	2707	te|PIGG_uc010ibf.	NM_001127178	NP_001120650	Q5H8A4	PIGG_HUMAN		4	TTCAGGTAGGT	0.343	
-	6	890	az.2_Missense_Mu	NM_032219	NP_115595	Q6UXD7	MFSD7_HUMAN		0	AGTGGCCGCTT	0.637	
-	16	2055	bk.1_Splice_Site_	NM_005255	NP_005246	O14976	GAK_HUMAN		4	ACTCACCGCAT	0.647	
-	16	1960	n.2_Missense_Mu	NM_001347	NP_001338	P52824	DGKQ_HUMAN	DAGKc.	1	CTCACCCGGGA	0.662	
-	4	2175	z.2_Intron|IDUA_u	NM_213613	NP_998778	Q9H2B4	S26A1_HUMAN	STAS.	1	GCAGCCCTGGT	0.711	
-	3	887	ETM1_uc011bvg.1	NM_012318	NP_036450	O95202	LETM1_HUMAN	membrane (Potential).|LET	1	CCTGCCTGCGC	0.393	
-	21	2354	e_Mutation_p.T23	NM_181808	NP_861524	Q7Z5Q5	DPOLN_HUMAN		4	ACTGCAGTGAAG	0.607	
-	2	471	nse_Mutation_p.L	NM_024511	NP_078787	Q68CZ6	HAUS3_HUMAN		4	TTTTAAGAGCTT	0.388	
+	15	2317	.2_3'UTR|ADD1_	NM_001119	NP_001110	P35611	ADDA_HUMAN		1	TGGGTCTCCAG	0.637	
+	10	1292		NM_002111	NP_002102	P42858	HD_HUMAN		4	CTGTTGCAGCAG	0.557	
+	10	1376		NM_002111	NP_002102	P42858	HD_HUMAN		4	GCTAAGGAGGAG	0.527	
+	21	2843		NM_002111	NP_002102	P42858	HD_HUMAN		4	CATTATACAGGG	0.383	
+	40	5234		NM_002111	NP_002102	P42858	HD_HUMAN		4	CTTTCTCGTATTC	0.423	
+	54	7472		NM_002111	NP_002102	P42858	HD_HUMAN		4	TTCCTCCAGGAA	0.522	
+	56	7679		NM_002111	NP_002102	P42858	HD_HUMAN		4	CACTGGTGCTC	0.587	rs3025814
+	7	1581	.P366L|DOK7_uc	NM_173660	NP_775931	Q18PE1	DOK7_HUMAN		1	CCCTCCTTGAG	0.662	
-	2	451		NM_177998	NP_819056	Q7RTM1	OTOP1_HUMAN	ical; (Potential).	3	GACTGCAAACA	0.373	
+	3	929	TB49_uc010icy.2_	NM_145291	NP_660334	Q6ZSB9	ZBT49_HUMAN		2	CCACGGTAGAG	0.522	
+	6	1634	B49_uc010icy.2_	NM_145291	NP_660334	Q6ZSB9	ZBT49_HUMAN		2	TCGAGGTACAG	0.413	
-	3	251		NM_018659	NP_061129	Q9NRR1	CYTL1_HUMAN		1	AAAGTCCCGCA	0.552	
-	14	2317	_p.Q195*|EVC2_u	NM_147127	NP_667338	Q86UK5	LBN_HUMAN	Potential.	5	GTTCTGCAGGC	0.652	
+	9	1407	1_RNA|CRMP1_u	NM_153717	NP_714928	P57679	EVC_HUMAN		2	GCTGGCTGGTG	0.652	
+	14	2181	1_RNA|CRMP1_u	NM_153717	NP_714928	P57679	EVC_HUMAN		2	ATCGGGGAAGA	0.677	
+	8	1181	p.G382E|MAN2B2	NM_015274	NP_056089	Q9Y2E5	MA2B2_HUMAN		2	TGCCGGGGAGT	0.677	
+	7	1743	gjq.3_Missense_	NM_014743	NP_055558	Q92628	K0232_HUMAN		2	AAACAGACAGG	0.408	
+	7	1883	gjq.3_Missense_	NM_014743	NP_055558	Q92628	K0232_HUMAN		2	AAATGCCTGCA	0.368	
-	1	1085	3_5'Flank|TADA2B	NM_153376	NP_699207	Q2M329	CCD96_HUMAN	Potential.	0	CCATGGCCTGC	0.627	
+	8	957	e_Mutation_p.P21	NM_018986	NP_061859	Q8TE82	S3TC1_HUMAN		3	GGATCCCCCAG	0.582	
-	2	1179		NM_005114	NP_005105	O14792	HS3S1_HUMAN		1	TTCGTGCAGTT	0.493	
-	2	493		NM_005114	NP_005105	O14792	HS3S1_HUMAN		1	TGATGGTCTGC	0.677	
-	5	710	_uc011bwz.1_Spli	NM_001017979	NP_001017979	P51157	RAB28_HUMAN		2	ACTTACAGAGTC	0.338	
-	10	4339	dr.1_Missense_Mu	NM_148894	NP_683692	Q8NFC6	BOD1L_HUMAN		6	CATGTCCACTA	0.398	
-	3	529	.1_5'UTR|BOD1L_	NM_148894	NP_683692	Q8NFC6	BOD1L_HUMAN		6	CACAACCTGAG	0.378	
+	32	4300	S1244N|CC2D2A_	NM_001080522	NP_001073991	Q9P2K1	C2D2A_HUMAN		3	TCTGGAGCACAT	0.378	
+	1	67	D28_uc003gpj.2_	NM_025205	NP_079481	Q9H204	MED28_HUMAN		0	CTCAGGCCCCG	0.627	
+	18	2895	xj.1_Missense_Mu	NM_022346	NP_071741	Q9BPX3	CND3_HUMAN	HEAT 10.	1	CTGAAGCAGCA	0.338	
+	27	3047	s.1_Missense_Mu	NM_004787	NP_004778	O94813	SLIT2_HUMAN	EGF-like 1.	11	CATATGGTTTCA	0.388	
-	19	3456	p.G920E|GPR125	NM_145290	NP_660333	Q8IWK6	GP125_HUMAN	lasmic (Potential).	1	TCCGTCCTGGG	0.517	
-	17	2838	_Mutation_p.A71	NM_145290	NP_660333	Q8IWK6	GP125_HUMAN	lasmic (Potential).	1	CTTTTAGCTTTTT	0.403	rs145912220
-	3	355	1A_uc011bxp.1_S	NM_013261	NP_037393	Q9UBK2	PRGC1_HUMAN		8	ATCTTCTGCAGA	0.448	
-	8	1403		NM_018176	NP_060646	Q8N0V4	LGI2_HUMAN	EAR 5.	0	TAAGGGAAAGG	0.532	
+	1	3272	_p.P708L|PCDH7_	NM_002589	NP_002580	O60245	PCDH7_HUMAN	(Potential).|Cadherin 7.	4	GCCACCTTCGA	0.458	
+	2	4367	w.1_Missense_Mu	NM_002589	NP_002580	O60245	PCDH7_HUMAN		4	GGATGGCAGTG	0.517	
+	3	4538	w.1_Missense_Mu	NM_002589	NP_002580	O60245	PCDH7_HUMAN		4	AGGAAGCCAGG	0.547	
+	9	1863	ifd.2_Missense_M	NM_015173	NP_055988	Q86TI0	TBCD1_HUMAN		1	AGAGTCTTTAG	0.363	

-	2	971	p.P198S|TLR10_u	NM_030956	NP_112218	Q9BXR5	TLR10_HUMAN	ellular (Potential).	2	CATTGGTAAAA	0.348	
+	3	502	M114A1_uc011by	NM_138389	NP_612398	Q8IWE2	NXP20_HUMAN		1	AAATACCCCTGC	0.483	
+	8	1753	_p.E373K|KLHL5_	NM_015990	NP_057074	Q96PQ7	KLHL5_HUMAN	Kelch 2.	1	TACTGGAAGGT	0.448	
+	1	160	3gtu.1_Splice_Sit	NM_025132	NP_079408	Q8NEZ3	WDR19_HUMAN		1	ATGAAGGTAAAT	0.572	
+	11	1187	_Mutation_p.V34	NM_025132	NP_079408	Q8NEZ3	WDR19_HUMAN	WD 6.	1	TTCATGTTTTCC	0.483	
+	18	2268	.G545D|WDR19_	NM_025132	NP_079408	Q8NEZ3	WDR19_HUMAN		1	ATGTTGGCATAG	0.358	
+	30	3416	p.D928N|WDR19_	NM_025132	NP_079408	Q8NEZ3	WDR19_HUMAN		1	GTCAGGATGCC	0.428	
-	15	2185	x.1_Missense_Mu	NM_002913	NP_002904	P35251	RFC1_HUMAN		4	AAACTGCTCTTA	0.408	
-	5	818	_p.A71T|UGDH_u	NM_003359	NP_003350	O60701	UGDH_HUMAN		4	GATGGCTGTTC	0.473	
+	15	2113	_Mutation_p.D52	NM_014988	NP_055803	Q9UPQ0	LIMC1_HUMAN		4	AAGAATGATGTG	0.478	
+	21	2686	p.G718R|LIMCH1_	NM_014988	NP_055803	Q9UPQ0	LIMC1_HUMAN		4	TCCAGGGAGAT	0.403	
+	1	205	0A9_uc011byx.1_	NM_006345	NP_006336	Q6PML9	ZNT9_HUMAN		3	GTGCCGGCTCC	0.706	
+	2	694		NM_001080505	NP_001073974	A0PJX4	SHSA3_HUMAN	lasmic (Potential).	2	ACCCTCCCGGC	0.672	
-	9	1455		NM_173536	NP_775807	Q8N1C3	GBRG1_HUMAN	lasmic (Probable).	2	CAATGCGTATGT	0.403	
-	7	952		NM_173536	NP_775807	Q8N1C3	GBRG1_HUMAN	ellular (Probable).	2	TTCTGCTCAGG	0.308	
+	8	1236	P10D_uc003gxj.3	NM_020453	NP_065186	Q9P241	AT10D_HUMAN	ellular (Potential).	3	CCGAGCCTGAT	0.353	
+	12	2317	10D_uc003gxl.1_I	NM_020453	NP_065186	Q9P241	AT10D_HUMAN	lasmic (Potential).	3	ATTGGCCTGCA	0.572	
-	23	2872	se_Mutation_p.V8	NM_152995	NP_694540	Q6ZNB6	NFXL1_HUMAN	ical; (Potential).	3	TACAACCACAA	0.353	
+	2	136		NM_207330	NP_997213	Q6NVV3	NIPA3_HUMAN	ellular (Potential).	0	TCTGTCCAAAC	0.463	
+	5	643		NM_207330	NP_997213	Q6NVV3	NIPA3_HUMAN	ellular (Potential).	0	AAGAGGAAGTC	0.408	
-	62	9087	.1_Missense_Mut	NM_015030	NP_055845	O94915	FRYL_HUMAN		1	CCAATTCCTAGA	0.294	
-	55	8160	RYL_uc003gyi.1_	NM_015030	NP_055845	O94915	FRYL_HUMAN		1	GGTCTGGTATTG	0.408	
-	48	7114	i.1_Missense_Mut	NM_015030	NP_055845	O94915	FRYL_HUMAN		1	GCAGGTATCTG	0.348	
+	8	910	D1_uc003gys.2_	NM_017830	NP_060300	Q9NX40	OCAD1_HUMAN		0	AAAAGACTGACC	0.348	
+	11	1578	zl.1_Missense_M	NM_025087	NP_079363	Q9H720	PG2IP_HUMAN		3	TTTTGGAGAGT	0.388	
-	4	1713		NM_001024611	NP_001019782	Q68CR7	LRC66_HUMAN		3	TTGAGCCAGAG	0.502	
-	4	1488		NM_001024611	NP_001019782	Q68CR7	LRC66_HUMAN		3	TGTCCCCGCAC	0.557	
-	8	1743	haf.3_Missense_	NM_001126328	NP_001119800	Q8TBB1	LNX1_HUMAN		4	GGAGGGGCTGA	0.433	
-	6	1391	haf.3_Missense_	NM_001126328	NP_001119800	Q8TBB1	LNX1_HUMAN	p.A379A(1)	4	AAAGCTGTCAT	0.542	
+	3	564	e_Mutation_p.S7	NM_006206	NP_006197	P16234	PGFRA_HUMAN	1.|Extracellular (Potential).	674	CAACAGCGGCC	0.493	
+	5	552	c011bzz.1_5'Flan	NM_020722	NP_065773	Q6ZU35	K1211_HUMAN		2	GTCACCCAATG	0.478	
+	8	2492	zz.1_Missense_M	NM_020722	NP_065773	Q6ZU35	K1211_HUMAN		2	CCAGGGGCCGG	0.582	
+	11	4001	ha.2_Missense_M	NM_020722	NP_065773	Q6ZU35	K1211_HUMAN		2	CCCCGGATGCT	0.512	
-	7	957		NM_002703	NP_002694	Q06203	PUR1_HUMAN	midotransferase type-2.	0	CTCCAGGCAAG	0.328	
+	4	545	_p.T112I|PAICS_u	NM_006452	NP_006443	P22234	PUR6_HUMAN	AR synthetase.	0	TAGCAACTGGTT	0.393	
-	6	1871		NM_032313	NP_115689	Q8NC60	CD014_HUMAN		2	GAAATCCTGCC	0.373	
-	29	2760		NM_018227	NP_060697	A0AVT1	UBA6_HUMAN		0	CCAAGCCAGAA	0.418	
+	3	954	hq.2_Missense_M	NM_001074	NP_001065	P16662	UD2B7_HUMAN		2	AAAATGGTGTTG	0.443	
+	5	240	ev.1_Missense_M	NM_003154	NP_003145	P02808	STAT_HUMAN	cipitation of calcium phosp	1	CAGTTCCAGAA	0.378	
+	4	845	|MUC7_uc003hfj.	NM_001145006	NP_001138478	Q8TAX7	MUC7_HUMAN	1.|Thr-rich.	4	TCCACCAGAGA	0.582	
+	13	976		NM_016519	NP_057603	Q9NP70	AMBN_HUMAN		4	GCGGTGACTTC	0.587	
+	9	2730		NM_031889	NP_114095	Q9NRM1	ENAM_HUMAN		3	CTGGGCTTCAG	0.433	
-	4	855	_p.P140S|GRSF1_	NM_002092	NP_002083	Q12849	GRSF1_HUMAN	RRM 2.	0	TATAAGGAAGTC	0.398	
-	11	1546	.2_Missense_Mut	NM_000583	NP_000574	P02774	VTDB_HUMAN	Albumin 3.	3	TACCTCTGAAT	0.428	
-	2	111		NM_014243	NP_055058	O15072	ATS3_HUMAN		2	CATTACCAGCCT	0.368	rs143125991
-	29	6748	hgq.2_Missense_	NM_032217	NP_115593	O75179	ANR17_HUMAN		10	TGTGAGGTCTTT	0.448	
+	3	347	id.2_Missense_M	NM_001432	NP_001423	O14944	EREG_HUMAN	ellular (Potential).	2	GTGTGGCTCAA	0.398	

+	12	1541	p.E291K|USO1_u	NM_003715	NP_003706	O60763	USO1_HUMAN	ular head.|ARM 9.	3	CAGAAAGAACAG	0.433	
+	22	2916	p.A756V|USO1_u	NM_003715	NP_003706	O60763	USO1_HUMAN	Potential.	3	TCTTGGCCGATC	0.323	
-	11	1600	EF2_uc003hiz.1_	NM_006239	NP_006230	O14830	PPE2_HUMAN	Catalytic.	4	AGGGCTCCTCTT	0.677	
-	16	1420	_p.T337I|SDAD1_	NM_018115	NP_060585	Q9NVU7	SDA1_HUMAN		1	ATCAAAGTTCTAC	0.383	
-	2	310	DAD1_uc011cbr.1_	NM_018115	NP_060585	Q9NVU7	SDA1_HUMAN		1	ACCTGTGCCATA	0.353	
+	2	1232	ov.1_3'UTR|STBD1	NM_003943	NP_003934	O95210	STBD1_HUMAN	ytoplasmic (Potential).	1	GAATGGGGGAG	0.478	
+	11	1525	hky.1_Missense_M	NM_025074	NP_079350	Q86XX4	FRAS1_HUMAN	Extracellular (Potential).	5	CAAATGCTAGTGA	0.299	
+	18	2566	p.G413D|FRAS1_	NM_025074	NP_079350	Q86XX4	FRAS1_HUMAN	tracellular (Potential).	5	GCACTGGCATAT	0.522	
+	4	623	IP2K_uc003hlj.2_M	NM_198892	NP_942595	Q9NSY1	BMP2K_HUMAN	rotein kinase.	1	CAGAACCAGAA	0.363	
+	10	1365	IP2K_uc003hlj.2_M	NM_198892	NP_942595	Q9NSY1	BMP2K_HUMAN		1	CCTTGCTCCTG	0.433	
-	1	640		NM_032693	NP_116082	Q9BSU3	NAA11_HUMAN		2	ACCCGCCCTTC	0.532	
-	1	1631		NM_033214	NP_149991	Q14410	GLPK2_HUMAN		4	ATGCTACTCACT	0.403	
-	4	401	p.M79I|SEC31A_	NM_001077207	NP_001070675	O94979	SC31A_HUMAN	WD 1.	8	GGAATCCATTTTA	0.333	
-	9	1147	ense_Mutation_p.R	NM_139076	NP_620775	Q6UWZ7	F175A_HUMAN		1	ACAACCGAGAT	0.393	
-	67	10771	pc.2_Missense_M	NM_014991	NP_055806	Q8IZQ1	WDFY3_HUMAN	FYVE-type.	3	CACCTTCATCCT	0.542	
-	60	9469	pe.1_Missense_M	NM_014991	NP_055806	Q8IZQ1	WDFY3_HUMAN		3	CTACAGGTTCTT	0.348	
-	53	8587	pe.1_Missense_M	NM_014991	NP_055806	Q8IZQ1	WDFY3_HUMAN	BEACH.	3	AGACAGGATACT	0.343	
-	32	5408		NM_014991	NP_055806	Q8IZQ1	WDFY3_HUMAN		3	TCAAAACCCAGT	0.343	
-	21	3808		NM_014991	NP_055806	Q8IZQ1	WDFY3_HUMAN		3	ATGTTGCTCAGA	0.398	
-	15	2837		NM_014991	NP_055806	Q8IZQ1	WDFY3_HUMAN		3	CAGTACCTTTTCC	0.413	
+	3	1434	e_Mutation_p.Q35	NM_005935	NP_005926	P51825	AFF1_HUMAN		1	CCTTCTCAGTCA	0.483	
+	11	2800	k.3_Missense_Mu	NM_005935	NP_005926	P51825	AFF1_HUMAN		1	GCACAGCTCTGA	0.582	
+	15	3290	qk.3_Splice_Site_	NM_005935	NP_005926	P51825	AFF1_HUMAN		1	TTTCAGACAACA	0.358	
-	5	635	0ikk.2_Missense_	NM_178135	NP_835236	Q7Z5P4	DHB13_HUMAN		0	ACAGCGGCAAAT	0.438	rs80182459
-	6	1011		NM_016245	NP_057329	Q8NBQ5	DHB11_HUMAN		2	AAGATGGAATAA	0.363	
-	4	744		NM_016245	NP_057329	Q8NBQ5	DHB11_HUMAN		2	CGAAGCCACAG	0.403	
+	6	1267	w.2_Missense_Mu	NM_004407	NP_004398	Q13316	DMP1_HUMAN		2	GGACAGCTCGC	0.542	
+	4	1532	n.2_Missense_Mu	NM_020203	NP_064588	Q9NQ76	MEPE_HUMAN		3	CCATTCCAACA	0.478	
+	23	3082	p.V931I|HERC6_u	NM_017912	NP_060382	Q8IVU3	HERC6_HUMAN	HECT.	5	GAAATAGTATTTC	0.353	
+	14	1982	dm.1_Missense_M	NM_016323	NP_057407	Q9UII4	HERC5_HUMAN		9	CAGAAGGTACTT	0.343	
+	1	901	3A_uc003hsh.1_5	NM_145715	NP_663761	Q4W5G0	TIGD2_HUMAN	DDE.	0	CTGTGACATATTA	0.423	
+	9	1369	e_Mutation_p.E372	NM_020159	NP_064544	Q9H4L7	SMRCD_HUMAN		4	CTAGATGAGGAC	0.358	
-	6	892		NM_000673	NP_000664	P40394	ADH7_HUMAN		3	ACAGCACCTCAC	0.448	
-	12	2014	3hvt.2_Splice_Site	NM_000944	NP_000935	Q08209	PP2BA_HUMAN		2	TGCTTACCGCTT	0.517	
+	4	1037	0ill.2_Splice_Site_	NM_017935	NP_060405	Q8NDB2	BANK1_HUMAN		3	CTTTAGGTAAGA	0.318	
+	12	2387	ll.2_Nonsense_Mu	NM_017935	NP_060405	Q8NDB2	BANK1_HUMAN		3	ACTGGCAGATG	0.438	
+	23	3135	_p.A891T|NFKB1_	NM_003998	NP_003989	P19838	NFKB1_HUMAN	teraction with CFLAR.	5	ATCCAGGCAGCC	0.537	
+	24	3318	_p.L952F|NFKB1_	NM_003998	NP_003989	P19838	NFKB1_HUMAN	ction with CFLAR.	5	CTAACTCTCAAC	0.507	
-	3	311	ilr.2_Missense_Mu	NM_020395	NP_065128	Q96CB8	INT12_HUMAN		0	AAGAAACCTAGT	0.403	
+	4	1196	se_Mutation_p.R28	NM_001031720	NP_001026890	Q8NEC7	GSTCD_HUMAN		2	GACCAAGACCAA	0.358	
-	9	1208	SS1_uc011cfh.1_	NM_005443	NP_005434	O43252	PAPS1_HUMAN	ylyl-sulfate kinase.	1	ATCAGCCAATCT	0.333	
+	2	465	nh.1_Missense_M	NM_018983	NP_061856	Q9NY12	GAR1_HUMAN	RGG-box 1.	0	AGGGGGTGGCC	0.284	
+	12	2174		NM_001977	NP_001968	Q07075	AMPE_HUMAN	cellular (Potential).	5	CTAATCCTAGTGC	0.398	
-	12	3649	orf21_uc003iav.2_	NM_018392	NP_060862	Q6ZU11	YD002_HUMAN		0	TTCAGCCACTTC	0.413	
-	6	1888	aw.2_Nonsense_M	NM_018392	NP_060862	Q6ZU11	YD002_HUMAN		0	CTTTACCCAACTC	0.373	
+	4	624	ba.2_Missense_M	NM_016648	NP_057732	Q4G0J3	LARP7_HUMAN	a-type RNA-binding.	3	CTCTGGGGGAA	0.348	
+	12	1923	ba.2_Missense_Mu	NM_016648	NP_057732	Q4G0J3	LARP7_HUMAN		3	CTCGGGAAAAG	0.353	

+	38	4856	3_Intron|ANK2_uc	NM_001148	NP_001139	Q01484	ANK2_HUMAN		14	GAGAGAGGATTA	0.413	
+	38	8331	NK2_uc003ibh.3_I	NM_001148	NP_001139	Q01484	ANK2_HUMAN		14	ATTTAGCTGAAGA	0.418	
+	38	9150	NK2_uc003ibh.3_I	NM_001148	NP_001139	Q01484	ANK2_HUMAN		14	TCGAGCCTACTAT	0.398	
-	17	2224	p.W489*|CAMK2D	NM_001221	NP_001212	Q13557	KCC2D_HUMAN		1	GCGGTGCCACAC	0.488	
-	2	571		NM_003619	NP_003610	P56730	NETR_HUMAN	SRCR 1.	1	TTTTGCCGCCAC	0.423	rs72677056
-	11	1676	e_Mutation_p.M46	NM_014822	NP_055637	O94855	SC24D_HUMAN		0	TCCAGCATGGT	0.363	rs143804876
-	10	1455	e_Mutation_p.P39	NM_014822	NP_055637	O94855	SC24D_HUMAN		0	ATGGTGGAACTA	0.318	
-	5	700	4D_uc003icl.2_RN	NM_014822	NP_055637	O94855	SC24D_HUMAN	Pro-rich.	0	CAGGGGGTCCC	0.537	
+	6	905		NM_016599	NP_057683	Q9NPC6	MYOZ2_HUMAN		0	GACGGTCCTTTA	0.398	
-	8	1460	p.W393*|PDE5A_	NM_001083	NP_001074	O76074	PDE5A_HUMAN	GAF 2.	0	ACTGTCCAGGG	0.358	
-	4	1049	RFPR_uc003ids.2_	NM_198179	NP_937822	Q96P65	QRFPR_HUMAN	Name=5; (Potential).	0	GCAGGAGGAAGA	0.428	
-	5	1537	ef.2_Missense_Mu	NM_001130698	NP_001124170	Q13507	TRPC3_HUMAN	lasmic (Potential).	2	ATATTGGGCAGC	0.448	
+	71	12544	_p.A523T|KIAA110	NM_015312	NP_056127	Q2LD37	K1109_HUMAN		12	ATGGAGCAGGG	0.418	
+	82	14549	em.2_Missense_M	NM_015312	NP_056127	Q2LD37	K1109_HUMAN		12	AGATGCCAGCC	0.358	
+	10	1277	_p.A338T|ADAD1_	NM_139243	NP_640336	Q96M93	ADAD1_HUMAN	A to I editase.	0	ATATCTGCATTTG	0.363	
+	12	2181		NM_145207	NP_660208	Q8NB90	SPAT5_HUMAN		0	ATGTTGGTGAATC	0.378	
-	1	756	NKRD50_uc010inw	NM_020337	NP_065070	Q9ULJ7	ANR50_HUMAN		1	CTGGGTTTCTCT	0.408	
+	9	10967	_p.T1954I|FAT4_u	NM_024582	NP_078858	Q6V0I7	FAT4_HUMAN	cellular (Potential).	18	GAGTTACCAGCC	0.478	
+	9	11464	p.A2120T|FAT4_u	NM_024582	NP_078858	Q6V0I7	FAT4_HUMAN	r (Potential).|EGF-like 1.	18	AGATTGGCTGTG	0.502	
+	9	11722	p.P2206S|FAT4_u	NM_024582	NP_078858	Q6V0I7	FAT4_HUMAN	ng (Potential).|Extracellular	18	CAGAGTCCTTGC	0.463	
+	4	584	SPA4L_uc011cgr.1	NM_014278	NP_055093	O95757	HS74L_HUMAN		4	GAGAGACCTTTT	0.318	
-	6	880	e_Mutation_p.A12	NM_144643	NP_653244	Q96NL6	SCLT1_HUMAN	Potential.	5	TCATCTGCATATA	0.353	
-	4	593		NM_032623	NP_116012	Q8TDB4	CD049_HUMAN		2	GGACAGGCAGAT	0.547	
-	10	1161	ii.2_Missense_Mut	NM_001130675	NP_001124147	O14967	CLGN_HUMAN	umenal (Potential).	3	CATCAAGCCAGC	0.353	
-	8	1687		NM_015130	NP_055945	Q6ZT07	TBCD9_HUMAN		1	CCTCGGGAGAC	0.473	
-	8	1630		NM_015130	NP_055945	Q6ZT07	TBCD9_HUMAN		1	CTGTTGCCATTTA	0.572	
-	8	902	P103S|INPP4B_u	NM_003866	NP_003857	O15327	INP4B_HUMAN	C2.	2	AGATGGGATACT	0.408	
+	8	2082	se_Mutation_p.W5	NM_032557	NP_115946	Q8NB14	UBP38_HUMAN		5	TCCATGGTTTACT	0.383	
+	9	2662	se_Mutation_p.P71	NM_032557	NP_115946	Q8NB14	UBP38_HUMAN		5	CAGAAACCAGGA	0.368	
+	5	1595		NM_022475	NP_071920	Q96QV1	HHIP_HUMAN		6	ATCGGGCCTCAT	0.418	
+	6	1715		NM_022475	NP_071920	Q96QV1	HHIP_HUMAN		6	CATCTGGGAGGA	0.418	
+	2	396	p.A104V|MMAA_u	NM_172250	NP_758454	Q8IVH4	MMAA_HUMAN		1	CAGAGGCCATAA	0.393	
-	8	2426	F827_uc010iox.2_	NM_178835	NP_849157	Q17R98	ZN827_HUMAN		0	CCTGGAGCTGATA	0.403	
-	6	698	se_Mutation_p.W1	NM_031956	NP_114162	Q8NA56	TTC29_HUMAN		0	CCTTACCCACTT	0.408	
-	7	1158	RMT10_uc003ild.2	NM_138364	NP_612373	Q6P2P2	ANM10_HUMAN		2	GAATAAGCCGGA	0.413	
-	51	7993	.D402N|LRBA_uc	NM_006726	NP_006717	P50851	LRBA_HUMAN		7	TAACATCCTGCTG	0.473	
-	23	3362	.3_Missense_Mut	NM_006726	NP_006717	P50851	LRBA_HUMAN		7	ATATCCCTTCTAA	0.398	
-	7	1286	p.G271E|LRBA_u	NM_006726	NP_006717	P50851	LRBA_HUMAN		7	CAGCCTCCAACA	0.338	
-	11	2307	p.G370E|SH3D19_	NM_001009555	NP_001009555	Q5HYK7	SH319_HUMAN		2	GGGTGTCCTGGT	0.388	
-	4	524	mm.3_Missense_	NM_004564	NP_004555	O75879	GATB_HUMAN		0	TCCCTGCACAGA	0.512	
-	2	266	imm.3_Missense_	NM_004564	NP_004555	O75879	GATB_HUMAN		0	ACTTGAGATCCA	0.388	
+	2	590		NM_033393	NP_203751	Q9C0D6	FHDC1_HUMAN	FH2.	2	GGATGCAAAACG	0.303	
+	11	1811		NM_033393	NP_203751	Q9C0D6	FHDC1_HUMAN		2	GCAGGCCCGGC	0.677	
+	11	2089		NM_033393	NP_203751	Q9C0D6	FHDC1_HUMAN		2	ATTAAGGAGCAT	0.617	
+	6	459		NM_032117	NP_115493	Q9BWT6	MND1_HUMAN	Potential.	0	AGGCTAGCAAAA	0.353	
+	33	4419	.S1457N|KIAA092	NM_015196	NP_056011	A2VDJ0	T131L_HUMAN	lasmic (Potential).	2	TTTCCAGCGCATA	0.408	
+	35	4845	.P1599L|KIAA092	NM_015196	NP_056011	A2VDJ0	T131L_HUMAN	lasmic (Potential).	2	ATTTCCCACTGT	0.423	

-	9	1370	x.2_Missense_Mu	NM_017639	NP_060109	Q6V1P9	PCD23_HUMAN	Cadherin 3.	4	GGGCGCTGCCG	0.602
-	2	202	HS2_uc003inx.2_Ir	NM_017639	NP_060109	Q6V1P9	PCD23_HUMAN	Cadherin 1.	4	gcgttctcttcctggcttct	0.01
+	4	646	e_Mutation_p.E141	NM_005141	NP_005132	P02675	FIBB_HUMAN	Potential.	3	TCCTGGAAAAC	0.403
-	5	915	se_Mutation_p.P28	NM_000508	NP_000499	P02671	FIBA_HUMAN	By similarity.	3	TTCCTGGGGCTT	0.557
-	8	1121	_p.D155V|FGG_u	NM_021870	NP_068656	P02679	FIBG_HUMAN	ogen C-terminal.	0	AACTTGTCACTA	0.473
-	2	252		NM_001334	NP_001325	P43234	CATO_HUMAN		0	TTTATTCCATAGA	0.328
+	5	708		NM_000824	NP_000815	P48167	GLRB_HUMAN	ellular (Probable).	2	GTGATGGAGATG	0.308
+	13	2704	ciu.1_Missense_M	NM_001083619	NP_001077088	P42262	GRIA2_HUMAN	ellular (Potential).	4	ACCTGGATTCC	0.438
+	17	1896	jd.1_Missense_Mu	NM_021634	NP_067647	Q9HBX9	RXFP1_HUMAN	lasmic (Potential).	0	TTTATAGTGTTCA	0.299
+	5	897	TFDH_uc011cjh.1_	NM_004453	NP_004444	Q16134	ETFD_HUMAN		3	CAGAAGCCCTT	0.358
-	4	581		NM_005038	NP_005029	Q08752	PPID_HUMAN	e cyclophilin-type.	0	CCACTCCTATTC	0.373
-	4	608	rf45_uc010iqt.1_F	NM_152543	NP_689756	Q96LM5	CD045_HUMAN		0	CTTCGGCAGCT	0.408
+	2	485		NM_014247	NP_055062	Q9Y4G8	RPGF2_HUMAN		4	AGCAGTCTTTCT	0.398
-	1	434	.1_Intron|KLHL2_	NM_000167	NP_000158				0	TGGTGCCTTGG	0.517
+	13	1830	rc.2_Missense_Mu	NM_007246	NP_009177	O95198	KLHL2_HUMAN	Kelch 5.	0	ATGGAGACAGG	0.363
+	2	188		NM_007193	NP_009124	Q9UJ72	ANX10_HUMAN		0	CAGCTCCCAAT	0.338
+	11	936	rn.2_Missense_Mu	NM_007193	NP_009124	Q9UJ72	ANX10_HUMAN	Annexin 4.	0	ACTTTGGTTTCC	0.393
+	3	1227	e_Mutation_p.T33	NM_016081	NP_057165	Q8WX93	PALLD_HUMAN	like C2-type 1.	1	CGACACAGGTC	0.522
-	8	1780	rc.1_Nonsense_M	NM_020870	NP_065921	Q7Z6J0	SH3R1_HUMAN	on with AKT2 (By similarity	3	TGAACCAGCCA	0.438
+	8	1664		NM_001034845	NP_001030017	Q49A17	GLTL6_HUMAN	main B.|Lumenal (Potential	4	GGTCTCCTGTT	0.388
-	2	368	itb.2_Missense_M	NM_001130689	NP_001124161	P26583	HMGB2_HUMAN		0	TATCACCTTTGG	0.408
+	2	561		NM_003864	NP_003855	O75446	SAP30_HUMAN	COR1 (By similarity).|Atypi	1	GGCAAGGCATC	0.328
-	2	1537	uc003itg.1_Silent_	NM_021973	NP_068808	P61296	HAND2_HUMAN		1	CCTTTGGTTTTC	0.488
-	1	520		NM_006792	NP_006783				0	GAGATGTGGCA	0.448
+	6	911	se_Mutation_p.T1	NM_001040157	NP_001035247	Q9C0F1	CEP44_HUMAN		0	TTATGACCTCAG	0.373
-	2	919	ug.2_Missense_M	NM_201591	NP_963885	P51674	GPM6A_HUMAN	ical; (Potential).	0	AACACCCGCAT	0.502
+	29	3754	se_Mutation_p.P11	NM_170710	NP_733828	Q8IZU2	WDR17_HUMAN		6	TCAGTACCTTTA	0.363
+	23	5297		NM_001080477	NP_001073946	Q9P273	TEN3_HUMAN	ellular (Potential).	0	GAAAAGAGCAA	0.527
-	9	1198		NM_002199	NP_002190	P14316	IRF2_HUMAN		1	TGACGCTGGCC	0.582
-	4	552		NM_002199	NP_002190	P14316	IRF2_HUMAN		1	AGAAGGCCGTT	0.393
+	4	671	a.3_Missense_Mu	NM_001029887	NP_001025058	A6NFD8	HELT_HUMAN	Pro-rich.	0	GGGTTCGCTCC	0.687
-	7	1621	_p.A244V|LRP2BP	NM_018409	NP_060879	Q9P2M1	LR2BP_HUMAN	Sel1-like 5.	0	AGTCAGCGATC	0.498
-	5	586	SP2_uc003ixq.2_M	NM_018359	NP_060829	Q9NUQ7	UFSP2_HUMAN		0	TGGAGCAACAG	0.438
-	13	1808	1ckv.1_Missense_	NM_021069	NP_066547	O94875	SRBS2_HUMAN		1	AAAGGGATGGA	0.473
-	10	7054		NM_005245	NP_005236	Q14517	FAT1_HUMAN	(Potential).| p.A2289T(1)	12	TCACCGCATAA	0.463
-	10	6219		NM_005245	NP_005236	Q14517	FAT1_HUMAN	(Potential).|Cadherin 18.	12	CAAAGGCTCAT	0.463
-	3	3541		NM_005245	NP_005236	Q14517	FAT1_HUMAN	(Potential).|Cadherin 9.	12	AAAGAGGCACG	0.443
+	7	894	e_Mutation_p.G21	NM_004168	NP_004159	P31040	DHSA_HUMAN		0	CTACGGGCGCA	0.597
+	7	709	RR_uc010isz.2_Mi	NM_020731	NP_065782	A9YTQ3	AHRR_HUMAN		2	CCTGACCCGCT	0.667
+	12	1509	_p.P467S|AHRR_	NM_020731	NP_065782	A9YTQ3	AHRR_HUMAN		2	GCAGACCCATG	0.667
-	5	971	lx.1_Missense_M	NM_004174	NP_004165	P48764	SL9A3_HUMAN	lasmic (Potential).	0	GCCGGGCTCGA	0.622
-	2	488	lx.1_Missense_M	NM_004174	NP_004165	P48764	SL9A3_HUMAN	ame=D/M4; (Potential).	0	GGCGTCCAGCA	0.657
+	10	1633		NM_018140	NP_060610	Q9P209	CEP72_HUMAN	Potential.	1	CATTTAGATAAAT	0.363
-	3	1368	h.3_Missense_Mu	NM_007030	NP_008961	O94811	TPPP_HUMAN		0	TGCCCCCTTGC	0.627
-	6	2240	ERT_uc003jcc.1_	NM_198253	NP_937983	O14746	TERT_HUMAN	rse transcriptase.	12	GATGACCTCCG	0.622
-	4	606	nf.1_Missense_Mu	NM_016358	NP_057442	P78413	IRX4_HUMAN	obox; TALE-type.	0	GTGCTCCTGCA	0.622
-	2	846	|C5orf38_uc011c	NM_001134222	NP_001127694	Q9BZI1	IRX2_HUMAN		1	ACTCTCGTCCT	0.652

+	7	1286	_p.A383V|ADAMT	NM_139056	NP_620687	Q8TE57	ATS16_HUMAN	ptidase M12B.		8	CCACGCCATCT	0.522	
-	13	1458	SUN2_uc011cmk.1	NM_017755	NP_060225	Q08J23	NSUN2_HUMAN			1	TGTGGGTTTCC	0.448	
-	3	667		NM_138809	NP_620164	Q96DG6	CMBL_HUMAN			1	ATGGTTCTGCAA	0.438	
+	8	978	CH6_uc003jeu.1_	NM_005885	NP_005876	O60337	MARH6_HUMAN	lasmic (Potential).		2	GAATGGGACCG	0.289	
-	21	3534	ND2_uc011cmz.1_	NM_001332	NP_001323	Q9UQB3	CTND2_HUMAN			8	CGGGCGCACCA	0.343	
+	5	910	.1_Missense_Mut	NM_007118	NP_009049	O75962	TRIO_HUMAN			18	GCAATGCGGAC	0.557	
+	43	6304	IO_uc003jfh.1_Mis	NM_007118	NP_009049	O75962	TRIO_HUMAN	DH 2.		18	TCAAACCAGTG	0.443	
+	46	6634	IO_uc003jfh.1_Mis	NM_007118	NP_009049	O75962	TRIO_HUMAN	PH 2.		18	CCATGCCGGGA	0.488	
+	7	951		NM_019018	NP_061891	Q9NUU6	F105A_HUMAN			1	TCTGATCCTTTG	0.423	
-	3	645		NM_054027	NP_473368	Q9HCJ1	ANKH_HUMAN	ical; (Potential).		1	TATAAGCTGCA	0.368	
-	1	374		NM_033414	NP_219482	Q969S3	ZN622_HUMAN	U1-type 2.		1	TTGAGGTGGTTC	0.572	
-	9	1179	jfr.2_Missense_M	NM_001034850	NP_001030022	Q9H6L5	F134B_HUMAN			3	ACTGTCCAACT	0.468	
+	6	1192	d.1_Missense_Mu	NM_004932	NP_004923	P55285	CADH6_HUMAN	|Extracellular (Potential).		7	TGGCAGAATCA	0.453	
-	10	1822	a-mir-579|MI0003	NM_016107	NP_057191	Q96KR1	ZFR_HUMAN			0	TGGAACCGAATT	0.343	
-	22	4490	0iuq.1_Missense_	NM_030955	NP_112217	P58397	ATS12_HUMAN	SP type-1 7.		9	CTGAACTCCAC	0.488	
-	19	3057	0iuq.1_Missense_	NM_030955	NP_112217	P58397	ATS12_HUMAN	SP type-1 4.		9	GAATCCGCACT	0.493	
+	8	1005	.2_3'UTR|TTC23L_	NM_144725	NP_653326	Q6PF05	TT23L_HUMAN			1	GAGTGCGTTAC	0.468	
-	3	281	se_Mutation_p.E6	NM_031900	NP_114106	Q9BYV1	AGT2_HUMAN			4	GATTTCCAGGA	0.473	
-	10	1530	i.1_Intron|PRLR_u	NM_000949	NP_000940	P16471	PRLR_HUMAN	lasmic (Potential).		3	ACTTGGGTGTT	0.483	
-	10	1467	i.1_Intron|PRLR_u	NM_000949	NP_000940	P16471	PRLR_HUMAN	lasmic (Potential).		3	ATACTCCACCAG	0.443	
+	32	4700	p.S1016F|SPEF2_	NM_024867	NP_079143	Q9C093	SPEF2_HUMAN			4	CAACTCCGAGT	0.428	
+	4	915	_p.P40S|SLC1A3_	NM_004172	NP_004163	P43003	EAA1_HUMAN	ellular (Potential).		0	TCCATCCTGGG	0.458	
+	10	3017	_p.V840I|NIPBL_u	NM_133433	NP_597677	Q6KC79	NIPBL_HUMAN			9	CTAGGGTTCGA	0.408	
+	37	6993	.3_Missense_Mut	NM_133433	NP_597677	Q6KC79	NIPBL_HUMAN			9	CAACAGCAAGG	0.383	
-	22	4126	se_Mutation_p.A3	NM_023073	NP_075561	E9PH94	E9PH94_HUMAN			7	TCTTGCTTTCT	0.353	
+	6	578	va.1_Missense_M	NM_018034	NP_060504	Q9NW82	WDR70_HUMAN			2	ACTCGCATGAG	0.363	
-	18	2853	.2_Missense_Mut	NM_001127671	NP_001121143	P42702	LIFR_HUMAN	ical; (Potential).		4	GGATGAGAATGG	0.383	
-	7	1236	.2_Missense_Mut	NM_001127671	NP_001121143	P42702	LIFR_HUMAN	ellular (Pot	p.R302H(1)	4	TATTACGAATCTT	0.353	rs61751714
-	37	5059	.D1703N|RICTOR	NM_152756	NP_689969	Q6R327	RICTR_HUMAN			10	GTACATCTTGAA	0.318	
+	3	1460		NM_000958	NP_000949	P35408	PE2R4_HUMAN			2	TATGCAGGTGCG	0.393	
-	6	984		NM_000436	NP_000427	P55809	SCOT1_HUMAN			3	TTCCTGCTCGG	0.413	
+	7	1768	E544K|ZNF131_u	NM_003432	NP_003423	P52739	ZN131_HUMAN			0	AGAGAGAGTCT	0.483	
-	7	1114	MGCS1_uc003jnq.	NM_001098272	NP_001091742	Q01581	HMCS1_HUMAN			0	TAACATCCCTGA	0.328	
+	8	679	o.2_Missense_Mu	NM_024615	NP_078891	Q8N3A8	PARP8_HUMAN			5	TATATGGGCCAC	0.358	
+	2	1443	A1_uc003jou.2_I	NM_015946	NP_057030	Q9BRX2	PELO_HUMAN			0	AGTCACTCCCA	0.592	
+	4	520	qc.1_Missense_M	NM_002203	NP_002194	P17301	ITA2_HUMAN	r (Potential).|FG-GAP 2.		1	AACTGGAGGTT	0.408	
+	13	1717	c.1_Missense_Mu	NM_002203	NP_002194	P17301	ITA2_HUMAN	Extracellular (Potential).		1	GGAAGGAAGAG	0.353	
+	18	2446	c.1_Missense_Mu	NM_002203	NP_002194	P17301	ITA2_HUMAN	ellular (Potential).		1	CACTAGCCCTG	0.473	
+	1	287		NM_006308	NP_006299	Q12988	HSPB3_HUMAN			0	CACTGCCTGGG	0.547	
+	2	1892	18_uc011cqg.1_3'	NM_001102575	NP_001096045	Q96RF0	SNX18_HUMAN			0	ATTCAGGATCGC	0.433	
-	23	3623	X29_uc010ivw.2_	NM_019030	NP_061903	Q7Z478	DHX29_HUMAN			4	GATGTTCTATTAA	0.323	
-	22	3511	X29_uc010ivw.2_	NM_019030	NP_061903	Q7Z478	DHX29_HUMAN			4	ATCCGCCATGG	0.403	
-	15	2654	X29_uc010ivw.2_	NM_019030	NP_061903	Q7Z478	DHX29_HUMAN			4	GGTTGATTTTAT	0.368	
-	3	457	X29_uc010ivw.2_	NM_019030	NP_061903	Q7Z478	DHX29_HUMAN			4	TCATTCCTTTGT	0.328	
-	10	977	e_Mutation_p.G2	NM_173514	NP_775785	Q8NBW4	S38A9_HUMAN			0	CACTCCCGGCA	0.408	
-	17	2722	T_uc010iwd.2_Mis	NM_002184	NP_002175	P40189	IL6RB_HUMAN	lasmic (Potential).		2	TGGATTCATGCT	0.398	
+	19	4829		NM_005921	NP_005912	Q13233	M3K1_HUMAN	rotein kinase.		2	AATGGCTTGTG	0.348	

-	3	519	rf43_uc010iwl.1_F	NM_001048249	NP_001041714	Q7Z3B0	CE043_HUMAN	ical; (Potential).	0	GTGGAGTAAGG	0.463
+	5	803	p.E236K|PPWD1_	NM_015342	NP_056157	Q96BP3	PPWD1_HUMAN		1	AACTGGGAATAT	0.388
+	4	562	juc.3_Missense_M	NM_024941	NP_079217	A5PLN9	CE044_HUMAN		1	TGGGAGAGACC	0.229
-	2	288	2_5'Flank|NLN_uc	NM_019072	NP_061945	Q96EQ0	SGTB_HUMAN	TPR 1.	0	GTGTAAGTGTCC	0.353
+	20	2226	32IP_uc011cqy.1_	NM_018695	NP_061165	Q96RT1	LAP2_HUMAN		7	AGGAAACAGAT	0.313
+	5	832	_p.P174S|SFRS12	NM_139168	NP_631907	Q8WXA9	SREK1_HUMAN		0	GTGGATCCTTCC	0.423
+	5	884	_p.S191F|SFRS12	NM_139168	NP_631907	Q8WXA9	SREK1_HUMAN	RRM.	0	GAATTCCCAGG	0.358
+	10	977	p.D225N|CDK7_u	NM_001799	NP_001790	P50613	CDK7_HUMAN	rotein kinase.	1	CAGGAGACGAC	0.363
+	7	879	_p.P262S|RAD17_	NM_133339	NP_579917	O75943	RAD17_HUMAN		0	TTGTTTCCCAAA	0.289
+	11	1318	17_uc003jwk.2_Mi	NM_133339	NP_579917	O75943	RAD17_HUMAN		0	TCGGTTGCCCT	0.313
+	2	136	ELD2_uc003jwr.1_	NM_001038603	NP_001033692	Q8N4S9	MALD2_HUMAN	lasmic (Potential).	0	AGATACCACCAT	0.547
+	11	822	cre.1_Missense_	NM_001098728	NP_001092198	Q6P1K8	T2H2L_HUMAN		0	CTTATTCGTATG	0.303
+	25	5651	_p.S1796_splice|	NM_018429	NP_060899	A6H8Y1	BDP1_HUMAN		2	ATCTAGCTGTCC	0.338
+	5	6132	yx.1_Missense_M	NM_005909	NP_005900	P46821	MAP1B_HUMAN	MAP1B 6.	5	GACCACCAGCC	0.473
+	17	2117	p.S649N|TNPO1_	NM_002270	NP_002261	Q92973	TNPO1_HUMAN		7	ACTGAGTGGCC	0.413
+	6	845	_p.S157F|BTF3_u	NM_001037637	NP_001032726	P20290	BTF3_HUMAN		0	GGCTTCCAAGA	0.318
+	10	1194	_p.G395R|RGNE	NM_001080479	NP_001073948	Q8N1W1	RGNEF_HUMAN		0	TAGAGGGAATC	0.448
+	3	322	CR_uc003kdq.2_M	NM_000859	NP_000850	P04035	HMDH_HUMAN		1	TATTAGGATGTTT	0.294
-	15	1924	3kdt.2_Missense_	NM_005713	NP_005704	Q9Y5P4	C43BP_HUMAN	START.	1	GAGAAGCAGGC	0.368
-	5	979	3kdt.2_Missense_	NM_005713	NP_005704	Q9Y5P4	C43BP_HUMAN		1	CATCAGCACAG	0.383
+	2	84	LK_uc010izq.2_5	NM_016218	NP_057302	Q9UBT6	POLK_HUMAN		4	TTTTCAGATAAG	0.244
+	8	1109	OLK_uc010izr.2_	NM_016218	NP_057302	Q9UBT6	POLK_HUMAN	UmuC.	4	TCCCAATAGAC	0.318
+	13	1627	csv.1_Missense_	NM_006633	NP_006624	Q13576	IQGA2_HUMAN		7	GGAATCCTTTG	0.398
+	27	3601	P2_uc003kel.2_	NM_006633	NP_006624	Q13576	IQGA2_HUMAN	Ras-GAP.	7	CAGCTGGAGGT	0.463
+	2	921		NM_005242	NP_005233	P55085	PAR2_HUMAN	Name=5; (Potential).	1	CATTGGGGTCT	0.488
+	12	2165		NM_018046	NP_060516	Q8N302	AGGF1_HUMAN		3	TGAAGGAACTT	0.368
-	17	2035		NM_003664	NP_003655	O00203	AP3B1_HUMAN		1	CAATTAGATAATT	0.378
+	4	461	MT_uc011cti.1_Int	NM_001713	NP_001704	Q93088	BHMT1_HUMAN	Hcy-binding.	1	GGTAGCAGGAG	0.443
+	2	6635		NM_153610	NP_705838	Q8N3K9	CMYA5_HUMAN		9	TTTTGGATCGA	0.443
+	2	7513		NM_153610	NP_705838	Q8N3K9	CMYA5_HUMAN		9	CTGTGGCCCCA	0.393
-	9	868	TX3_uc003kge.3_	NM_001010891	NP_001010891	Q5HYI7	MTX3_HUMAN		0	GCGAAGATTGT	0.463
-	4	547	RINC5_uc003kgm	NM_178276	NP_840060	Q86VE9	SERC5_HUMAN	ical; (Potential).	1	AGCTCCTGAGC	0.388
+	4	1381	p.S360F|ZFYVE1	NM_001105251	NP_001098721	Q7Z3T8	ZFY16_HUMAN		0	AGATTCCTCTTC	0.383
-	4	1884	_p.V512I|ANKRD	NM_001004441	NP_001004441	A5PLL1	AN34B_HUMAN		1	AGTTTACTAATTG	0.299
+	8	1244	SGRF2_uc003khb	NM_006909	NP_008840	O14827	RGRF2_HUMAN	DH.	12	GTTTGCCAAAT	0.463
-	6	593	5E_uc011cto.1_Ir	NM_130767	NP_570123	Q8WYK0	ACO12_HUMAN	zyme A hydrolase 2.	2	GGTGCCCCTTG	0.507
-	13	1005	nse_Mutation_p.G	NM_012446	NP_036578	P81877	SSBP2_HUMAN	-rich.|Pro-rich.	5	TATCACCAGAG	0.289
+	9	1486	3khw.2_Missense_	NM_001017971	NP_001017971	Q52LC2	VAS1L_HUMAN		0	GTTGTCCATCC	0.418
+	7	2752	u.2_Missense_Mu	NM_004385	NP_004376	P13611	CSPG2_HUMAN	minoglycan attachment do	16	AGCCACTGTAT	0.408
+	8	6322	u.2_Intron|VCAN_	NM_004385	NP_004376	P13611	CSPG2_HUMAN	GAG-beta.	16	AGGACCCAGTA	0.512
-	3	959	ilent_p.E112E|LYS	NM_198273	NP_938014	Q7Z3D4	LYSM3_HUMAN	lasmic (Potential).	0	CATTTCTCTCTG	0.373
+	13	2507	98_uc003kjt.2_5'	NM_032119	NP_115495	Q8WXG9	GPR98_HUMAN	ellular (Potential).	16	GGGGTCCCTTG	0.408
+	37	8515	p.A513T|GPR98_	NM_032119	NP_115495	Q8WXG9	GPR98_HUMAN	ellular (Potential).	16	TTGATGCTCAA	0.438
+	59	12293	t.2_Missense_Mut	NM_032119	NP_115495	Q8WXG9	GPR98_HUMAN	ellular (Potential).	16	AGGAGGAAAAG	0.438
+	64	12971	_Mutation_p.S199	NM_032119	NP_115495	Q8WXG9	GPR98_HUMAN	ellular (Potential).	16	TTCCAGTGGAG	0.438
+	66	13469	p.T2164I|GPR98_	NM_032119	NP_115495	Q8WXG9	GPR98_HUMAN	(Potential).|Calx-beta 30.	16	AGTCACCTTTC	0.393
+	74	15724	p.V2916I|GPR98_	NM_032119	NP_115495	Q8WXG9	GPR98_HUMAN	ellular (Potential).	16	CCACTGTAACT	0.463

+	87	18453	w.2_Nonsense_Mu	NM_032119	NP_115495	Q8WXG9	GPR98_HUMAN	ical; (Potential).		16	ACATGGCTTTG	0.383	
-	5	1176	kp.2_Missense_M	NM_001145678	NP_001139150	Q8IV33	K0825_HUMAN			0	TTTTAACCACACC	0.343	
-	10	1986		NM_012081	NP_036213	O00472	ELL2_HUMAN			1	AGTCATCCTTATA	0.383	
-	8	1462		NM_012081	NP_036213	O00472	ELL2_HUMAN			1	GGATGGCAGCA	0.542	
-	2	703	P1_uc010jbm.1_Ir	NM_001040458	NP_001035548	Q9NZ08	ERAP1_HUMAN	enal (Potential).		2	TGCAGGGGTTCT	0.592	
+	2	774	mw.1_Missense_M	NM_005575	NP_005566	Q9UIQ6	LCAP_HUMAN	lasmic (Potential).		4	CTCAGGCCTTC	0.527	
-	29	4235	on.2_Missense_Mu	NM_001270	NP_001261	O14646	CHD1_HUMAN			5	ATCAGACTTCT	0.323	
-	9	1367		NM_001270	NP_001261	O14646	CHD1_HUMAN	Chromo 2.		5	ATCAGGATAACC	0.358	
+	20	2887	ense_Mutation_p.I	NM_015216	NP_056031	O43314	VIP2_HUMAN			2	CAGACCTTCAG	0.363	
-	3	514	vb.1_Missense_M	NM_031438	NP_113626	Q9BQG2	NUD12_HUMAN			0	TTTAGCTAGCAG	0.373	
-	3	1588	17_uc003kon.3_5	NM_001163315	NP_001156787	Q9UF56	FXL17_HUMAN			0	CAATCAGAAATG	0.338	
+	4	700	1_RNA|FER_uc00	NM_005246	NP_005237	P16591	FER_HUMAN	embranes containing pho		5	ATTAGGACAAG	0.398	
-	6	1701		NM_014819	NP_055634	O43164	PJA2_HUMAN			2	TCCAAGGATGTC	0.363	rs149837114
-	4	531		NM_014819	NP_055634	O43164	PJA2_HUMAN			2	CACAAGTGGGA	0.383	
+	2	260	te_p.R54_splice|C	NM_001744	NP_001735	Q16566	KCC4_HUMAN			5	GGACGGTAAGG	0.706	
+	16	2584	y.3_Missense_Mu	NM_001127511	NP_001120983	P25054	APC_HUMAN	r-rich.|ARM	p.?(1)	2515	GCCTGCGAAGT	0.443	rs147655929
+	1	343	e_Mutation_p.E54	NM_022828	NP_073739	Q9H6S0	YTDC2_HUMAN	R3H.		3	CGCTGGAGCGC	0.672	
+	8	2108	ion_p.V203I|KCNN	NM_021614	NP_067627	Q9H2S1	KCNN2_HUMAN			2	AGCACGTCACT	0.552	
-	5	633	1_splice|PGGT1B	NM_005023	NP_005014	P53609	PGTB1_HUMAN			0	AACTCACCATA	0.338	
-	5	566	_p.C59Y|PGGT1B	NM_005023	NP_005014	P53609	PGTB1_HUMAN	PFTB 1.		0	ATATAGCAAATAC	0.343	
-	4	1571	tion_p.L358F|TIC	NM_021649	NP_067681	Q86XR7	TCAM2_HUMAN	TIR.		0	TTGGAGGGCAA	0.443	
-	1	415		NM_001801	NP_001792	Q16878	CDO1_HUMAN			2	TGATGGCCTGC	0.607	
-	19	2975	krv.3_Missense_M	NM_020796	NP_065847	Q9H2E6	SEM6A_HUMAN	lasmic (Potential).		2	GGTGGGGAGGG	0.627	
-	3	344		NM_173666	NP_775937	Q8NBA8	DTWD2_HUMAN			0	TGTTTTCCTTTA	0.328	
+	18	3626	l.1_Missense_Mut	NM_005509	NP_005500	Q9Y485	DMXL1_HUMAN	WD 9.		2	GAGAAGACGGT	0.383	rs144768533
+	18	3822	l.1_Missense_Mu	NM_005509	NP_005500	Q9Y485	DMXL1_HUMAN	WD 10.		2	CCCACCTTTTC	0.453	
+	43	9183	XL1_uc010jcm.1_	NM_005509	NP_005500	Q9Y485	DMXL1_HUMAN	WD 16.		2	CTGATGGAACAA	0.363	
+	18	1685	17B4_uc003ksk.3_	NM_000414	NP_000405	P51659	DHB4_HUMAN	Enoyl-CoA hydratase 2.		2	ACTTTGCTAGTC	0.353	
+	2	882	_p.P217L|PRR16_	NM_016644	NP_057728	Q569H4	PRR16_HUMAN	Pro-rich.		3	CCACCCACCGG	0.488	
+	2	216	2_uc011cwn.1_5'	NM_003100	NP_003091	O60749	SNX2_HUMAN			1	AAACTCCAATG	0.353	
-	21	2876	wq.1_Missense_M	NM_153223	NP_694955	Q8N960	CE120_HUMAN			1	ATGGGGGGCCAT	0.428	
-	9	1214	_p.P187S|CEP120	NM_153223	NP_694955	Q8N960	CE120_HUMAN			1	TTTTGGCCCAG	0.388	
+	4	1063	NB1_uc010jdb.1_	NM_005573	NP_005564	P20700	LMNB1_HUMAN	Rod.|Linker 2.		2	TGGATTCTGGGC	0.488	
-	2	483	cxc.1_Missense_	NM_178450	NP_848545	Q86UD3	MARH3_HUMAN			1	TTCGGGCAGGT	0.527	
+	2	242	uj.3_Missense_M	NM_130809	NP_570721	Q96M27	PRRC1_HUMAN	Pro-rich.		0	TGCAGGGCTGG	0.403	
+	25	3570	12A2_uc010jdg.2	NM_001046	NP_001037	P55011	S12A2_HUMAN	lasmic (Potential).		3	ATAACAGATAATG	0.308	
-	15	2417	v.2_Missense_Mu	NM_001999	NP_001990	P35556	FBN2_HUMAN	10; calcium-binding.		15	ATTCATCAACAT	0.502	
+	17	2513	TS19_uc010jdh.1	NM_133638	NP_598377	Q8TE59	ATS19_HUMAN	Spacer.		9	AACAGTCTATTA	0.393	
+	22	3388	TS19_uc010jdh.1	NM_133638	NP_598377	Q8TE59	ATS19_HUMAN	TSP type-1 5.		9	CCTCAGAAAAC	0.418	rs2840016
+	3	1141		NM_175856	NP_787052	Q70JA7	CHSS3_HUMAN	enal (Potential).		3	TCCAAGACCTT	0.358	
+	3	1859		NM_175856	NP_787052	Q70JA7	CHSS3_HUMAN	enal (Potential).		3	AAAGAAAGTAC	0.348	
+	3	2050		NM_175856	NP_787052	Q70JA7	CHSS3_HUMAN	enal (Potential).		3	CCAAAGCAGAA	0.438	
-	25	4036	0jdi.1_Missense_	NM_016340	NP_057424	Q8TEU7	RPGF6_HUMAN	Ser-rich.		3	AATTGCTCACG	0.478	
-	7	812	0jdm.1_Missense_	NM_133372	NP_588613	Q8TF40	FNIP1_HUMAN			2	GAGCGGACCCT	0.517	
+	4	351		NM_000588	NP_000579	P08700	IL3_HUMAN			3	AGAATCTCCTG	0.428	
+	5	1215	ite_p.E341_splice|	NM_003060	NP_003051	O76082	S22A5_HUMAN			0	TGAGGTAAGCA	0.562	
+	6	1267	e_Mutation_p.L35	NM_003060	NP_003051	O76082	S22A5_HUMAN	lasmic (Potential).		0	ATCTGCTTCGA	0.468	

+	4	289	orf56_uc010jds.1_	NM_001013717	NP_001013739	Q8N8D9	CE056_HUMAN		0	ataatgcttcctgccatc	0.05	
-	8	926	kxb.2_Missense_M	NM_002198	NP_002189	P10914	IRF1_HUMAN		0	AATTTCCCTTCCT	0.532	
+	1	434	l.1_Missense_Mut	NM_000589	NP_000580	P05112	IL4_HUMAN		0	ACTTTGTCCAC	0.493	
-	4	772	1cxi.1_Splice_Site_	NM_001098811	NP_001092281	Q92599	SEPT8_HUMAN		2	GGATACCTTGC	0.547	
-	11	2497	p.E375K|AFF4_uc	NM_014423	NP_055238	Q9UHB7	AFF4_HUMAN		5	CTCTTCCATAGG	0.453	
-	10	1396	L4_uc003kym.1_5'	NM_015082	NP_055897	Q6MZW2	FSTL4_HUMAN	Ig-like 2.	2	CATTGGCTGCA	0.547	
-	5	766		NM_015082	NP_055897	Q6MZW2	FSTL4_HUMAN	EF-hand.	2	CCCTGAACAGA	0.557	
-	13	1860	.2_Intron|CDKL3_	NM_001113575	NP_001107047	Q8IVW4	CDKL3_HUMAN		1	CTTCCCCTCGC	0.348	
+	5	501	l.2_Missense_Mut	NM_015288	NP_056103	Q9NQC1	JADE2_HUMAN		0	TCCCACCACTG	0.637	
+	22	3412	xu.1_Missense_M	NM_021982	NP_068817	O95486	SC24A_HUMAN		0	CTTGGCTTAGA	0.358	
+	4	913	LG_uc003kzu.2_3	NM_001745	NP_001736	P49069	CAMLG_HUMAN	lasmic (Potential).	0	GCGAAGTCTTC	0.403	
+	15	2065	X46_uc003kzv.1_F	NM_014829	NP_055644	Q7L014	DDX46_HUMAN	case C-terminal.	1	CATGCTGATGGT	0.343	
-	2	794	_uc011cxy.1_Miss	NM_002653	NP_002644	P78337	PITX1_HUMAN	Homeobox.	1	TCACCCGCACG	0.652	
-	1	945		NM_006161	NP_006152	Q92886	NGN1_HUMAN		0	GCGTTGTGTGG	0.592	
+	4	565	3lba.2_Missense_Mutation_p.L131F			Q6ZT89	S2548_HUMAN	Solcar 2.	0	CGGTTGCAGAT	0.642	
+	3	268	lbw.1_Missense_M	NM_014386	NP_055201	Q9NZM6	PK2L2_HUMAN	ellular (Potential).	0	TGTGCCTGGTG	0.358	
-	12	1604	D8_uc003lch.2_Mi	NM_139199	NP_631938	Q9H0E9	BRD8_HUMAN		1	GACTGGCTCTG	0.507	
+	6	1038	yo.1_Missense_M	NM_005733	NP_005724	O95235	KI20A_HUMAN	inesin-motor.	0	TCTCCCCCGGT	0.522	
-	11	1230		NM_004661	NP_004652	Q9UJX2	CDC23_HUMAN	TPR 7.	0	AAGCTCTGTAGT	0.468	
-	11	1223		NM_004661	NP_004652	Q9UJX2	CDC23_HUMAN	TPR 6.	0	TGTAGTCCCGTT	0.463	
+	4	1246	53C_uc011cyq.1_	NM_001135647	NP_001129119	Q9NYF3	FA53C_HUMAN		1	GCTGCCCTGGC	0.672	rs138917148
+	7	691	_p.P192L|REEP2_	NM_016606	NP_057690	Q9BRK0	REEP2_HUMAN		0	TGACCCTGCCC	0.607	
+	12	1683	3ldi.2_Missense_M	NM_001903	NP_001894	P35221	CTNA1_HUMAN		11	TTGCTCTCCAA	0.488	
-	3	370	do.2_Splice_Site_	NM_022464	NP_071909	Q9H173	SIL1_HUMAN		0	ACTGTACCTTTT	0.403	
-	6	825		NM_198282	NP_938023	Q86WV6	TM173_HUMAN	lasmic (Potential).	1	TGCACCCCGTA	0.527	
+	12	1998	HD1_uc003lft.1_M	NM_020690	NP_065741	Q8IWZ2	Q8IWZ2_HUMAN		6	AGGTGCCAATG	0.373	
+	29	6876	3lfw.2_Missense_M	NM_020690	NP_065741	Q8IWZ2	Q8IWZ2_HUMAN		6	CCTGGGTAACT	0.522	
-	11	1446	3lge.1_Missense_	NM_133172	NP_573418	O95704	APBB3_HUMAN	PID 2.	2	CACAGGGCACT	0.602	
-	11	1431	3lge.1_Missense_	NM_133172	NP_573418	O95704	APBB3_HUMAN	PID 2.	2	ACAATGGCTCCT	0.597	
+	10	988	.1_Missense_Muta	NM_006083	NP_006074	Q13123	RED_HUMAN		1	GGGAACCCGTA	0.463	
+	1	214		NM_017706	NP_060176	Q9H6Y2	WDR55_HUMAN		1	CGGAAGACATC	0.657	
-	4	1071		NM_194249	NP_919225	Q8IYX4	DND1_HUMAN		0	CCCAGCAGACC	0.602	
-	10	1145	_p.G295S|HARS_	NM_002109	NP_002100	P12081	SYHC_HUMAN		2	ACTGCCCACAC	0.627	
+	8	1009	_p.A121T|HARS2	NM_012208	NP_036340	P49590	SYHM_HUMAN		0	AGGTGGCTGAT	0.488	
+	1	1970	.2_Intron|PCDHA6	NM_018903	NP_061726	Q9UN75	PCDAC_HUMAN	|Extracellular (Potential).	0	CGGCGGCGGTC	0.687	
+	3	2887	826R|PCDHA7_u	NM_018899	NP_061722	Q9Y5I4	PCDC2_HUMAN	-X-X-P.|Cytoplasmic (Pote	4	AGGCTGGCATT	0.498	
+	1	740		NM_018938	NP_061761	Q9Y5E5	PCDB4_HUMAN	|Extracellular (Potential).	3	ATATGGGGTGC	0.493	
+	1	868		NM_018940	NP_061763	Q9Y5E2	PCDB7_HUMAN	(Potential).|Cadherin 2.	6	ATTCTGGTTCTA	0.552	
+	1	962		NM_018940	NP_061763	Q9Y5E2	PCDB7_HUMAN	(Potential).|Cadherin 3.	6	TGTCTCCGTGT	0.458	
+	1	631	B16_uc003liv.2_5	NM_019120	NP_061993	Q9UN66	PCDB8_HUMAN	|Extracellular (Potential).	4	GTCCTCCTGGG	0.418	
+	3	1442		NM_019119	NP_061992	Q9Y5E1	PCDB9_HUMAN	(Potential).|Cadherin 5.	0	CTCAGGCACCA	0.652	
+	1	1181	B12_uc011dak.1_	NM_018932	NP_061755	Q9Y5F1	PCDBC_HUMAN	(Potential).|Cadherin 3.	3	AAAATCTACAGT	0.413	
-	1	865		NM_031947	NP_114153	Q9BXI2	ORNT2_HUMAN	ical; Name=5; (Potential).	1	CACTGGGAACA	0.418	
+	1	1309	dan.1_Missense_	NM_018912	NP_061735	Q9Y5H4	PCDG1_HUMAN	|Extracellular (Potential).	3	AAACTCACATTT	0.443	
+	1	2287	x.1_5'Flank|PCDH	NM_018915	NP_061738	Q9Y5H1	PCDG2_HUMAN	ical; (Potential).	3	GGTCTCCTGCG	0.662	
+	1	688	_uc010jfx.1_Transl	NM_018916	NP_061739	Q9Y5H0	PCDG3_HUMAN	(Potential).|Cadherin 2.	1	TCCAAGTGATA	0.547	
+	1	1409	10jfx.1_Missense	NM_018916	NP_061739	Q9Y5H0	PCDG3_HUMAN	(Potential).|Cadherin 5.	1	AGCCTCCATCT	0.547	

+	1	962	jfx.1_Intron|PCDH	NM_018923	NP_061746	Q9Y5G2	PCDGE_HUMAN	r (Potential).|Cadherin 3.	0	CGAAGCAAAAG	0.378	
+	1	1156	DHGB2_uc003ljs.	NM_003736	NP_003727	Q9UN71	PCDGG_HUMAN	|Extracellular (Potential).	0	TGGAAGGTGAT	0.403	
+	1	1778	1_Intron|PCDHGA	NM_018913	NP_061736	Q9Y5H3	PCDGA_HUMAN	|Extracellular (Potential).	0	GGTGACCAAGG	0.687	
+	1	2165	Intron|PCDHGB4_	NM_018927	NP_061750	Q9Y5F8	PCDGJ_HUMAN	r (Potential).|Cadherin 6.	2	TGCCGGATTTC	0.577	
+	1	1851	on|PCDHGB4_uc	NR_001297					0	GCCTGGGGCTG	0.652	
+	1	367	GA8_uc003lkd.1_	NM_018928	NP_061751	Q9Y5F7	PCDGL_HUMAN	|Extracellular (Potential).	4	TAGAGATCGTA	0.567	
+	1	688	1_Intron|PCDHGB	NM_018929	NP_061752	Q9Y5F6	PCDGM_HUMAN	r (Potential).|Cadherin 2.	3	TCTCTGTCATC	0.557	
-	3	1603	p.V496M|PCDH1_	NM_002587	NP_002578	Q08174	PCDH1_HUMAN	r (Potential).|Cadherin 4.	5	CACCACCTGCA	0.537	
-	1	2884		NM_016580	NP_057664	Q9NPG4	PCD12_HUMAN	r (Potential).|Cadherin 5.	3	CATTGGCATCCA	0.582	
-	1	2736		NM_016580	NP_057664	Q9NPG4	PCD12_HUMAN	r (Potential).|Cadherin 5.	3	CAATAGCTACTA	0.507	
-	1	2556		NM_016580	NP_057664	Q9NPG4	PCD12_HUMAN	|Extracellular (Potential).	3	GATCTGAATGC	0.488	
-	3	986	0jgh.2_Splice_Sit	NM_005471	NP_005462	P46926	GNPI1_HUMAN		0	AAGGCCTGTGG	0.547	
-	2	1295	nse_Mutation_p.	NM_000176	NP_000167	P04150	GCR_HUMAN	Modulating.	2	TACTGGGGCTT	0.428	
-	3	596	e_Mutation_p.P52	NM_001024947	NP_001020118	Q969M3	YIPF5_HUMAN	lasmic (Potential).	2	CTGGAGGGACA	0.428	
+	4	1530	nn.1_Missense_M	NM_020768	NP_065819	Q68DU8	KCD16_HUMAN		4	AAGAAGGGGAG	0.547	
-	23	2558	ARS_uc011dbr.1_	NM_020117	NP_064502	Q9P2J5	SYLC_HUMAN		0	TTTCACCCACT	0.478	
-	20	2328	r.1_Missense_Mu	NM_020117	NP_064502	Q9P2J5	SYLC_HUMAN		0	TTCACCTTTGTT	0.383	
-	5	582	nse_Mutation_p.P	NM_020117	NP_064502	Q9P2J5	SYLC_HUMAN		0	AATCAGGGGGG	0.348	
+	7	1284	_p.P394L|TCERG1	NM_006706	NP_006697	O14776	TCRG1_HUMAN		2	ACATCCCCAGG	0.388	
-	1	753		NM_194251	NP_919227	Q8TDV0	GP151_HUMAN	lasmic (Potential).	2	AGCAGCATCAC	0.498	
-	6	700	0jgx.2_Missense_	NM_024577	NP_078853	Q8TF17	S3TC2_HUMAN		2	ACAGGGCTCTG	0.473	
+	16	1603	lqc.1_Splice_Site	NM_014945	NP_055760	O94929	ABLM3_HUMAN		3	TCTGCAGGTGAT	0.532	
-	2	622	ation_p.E48K|CS	NM_001892	NP_001883	P48729	KC1A_HUMAN	rotein kinase.	1	AGATTCTAGCT	0.507	
+	3	458	_p.A139V|PPARG	NM_133263	NP_573570	Q86YN6	PRGC2_HUMAN		0	CCCTGCCCCGG	0.617	
+	5	653	_p.P165L|PPARG	NM_133263	NP_573570	Q86YN6	PRGC2_HUMAN		0	GGCTCCCATGA	0.582	
+	8	2332	_p.L725F|PPARG	NM_133263	NP_573570	Q86YN6	PRGC2_HUMAN		0	CCAGCCTCACC	0.607	
-	21	3080	jhc.2_RNA|CSF1	NM_005211	NP_005202	P07333	CSF1R_HUMAN	lasmic (Potential).	54	GCAAGGGCTGG	0.478	
-	9	1615	F1R_uc010jhc.2_	NM_005211	NP_005202	P07333	CSF1R_HUMAN	5.|Extracellular (Potential).	54	CTCAACAGTCA	0.597	
-	3	627	DGFRB_uc011dc	NM_002609	NP_002600	P09619	PGFRB_HUMAN	otential).|Ig-like C2-type 1.	17	AGCAGGTCAGA	0.607	
-	17	1426	_p.S115F|CAMK2	NM_171825	NP_741960	Q9UQM7	KCC2A_HUMAN		1	TCCGGGACCAC	0.607	
-	2	1485		NM_001012301	NP_001012301	Q5FYB1	ARSI_HUMAN		2	TGGCCACCATTG	0.587	
+	12	1997	_p.A630V|TCOF1_	NM_001135243	NP_001128715	Q13428	TCOF_HUMAN		3	TGCAGCTCAGG	0.622	
+	16	2671	e_Mutation_p.A85	NM_001135243	NP_001128715	Q13428	TCOF_HUMAN		3	CCGTGGCTACA	0.627	
-	7	783		NM_018047	NP_060517	Q9NW64	RBM22_HUMAN		0	CCGAGGCATTG	0.438	
-	7	771		NM_018047	NP_060517	Q9NW64	RBM22_HUMAN		0	TGAAGCCCGCT	0.443	
+	4	468	c.2_RNA|GPX3_u	NM_002084	NP_002075	P22352	GPX3_HUMAN		0	TGAATGCACTAC	0.552	
-	20	1713	_p.E521K|ANXA6_	NM_001155	NP_001146	P08133	ANXA6_HUMAN		0	ATCTTCCCGTG	0.607	
-	6	471	.1_Splice_Site_p.	NM_001155	NP_001146	P08133	ANXA6_HUMAN		0	ATGCCCTGGGG	0.547	rs36089400
-	22	12465	AT2_uc003lud.3_	NM_001447	NP_001438	Q9NYQ8	FAT2_HUMAN	lasmic (Potential).	6	CCGCAGCTGGC	0.557	
-	18	11189	AT2_uc003lud.3_	NM_001447	NP_001438	Q9NYQ8	FAT2_HUMAN	ellular (Potential).	6	GCAGGGCACCA	0.577	
-	9	7217	2A_uc011dcs.1_In	NM_001447	NP_001438	Q9NYQ8	FAT2_HUMAN	(Potential).|Cadherin 21.	6	AGCCTGGACTT	0.488	
-	1	1271	AT2_uc010jhx.1_	NM_001447	NP_001438	Q9NYQ8	FAT2_HUMAN	r (Potential).|Cadherin 3.	6	CATGAGCTTTG	0.507	
+	2	194	n_p.P8L|G3BP1_	NM_005754	NP_005745	Q13283	G3BP1_HUMAN		4	TAGTCCCCTGC	0.483	
+	10	1728	IA1_uc011dcx.1_	NM_001114183	NP_001107655	P42261	GRIA1_HUMAN	ellular (Potential).	6	CCTACCGTCTG	0.542	
-	10	1586	p.R333K|FAM114	NM_018691	NP_061161	Q9NRY5	F1142_HUMAN		0	GTATTTCTTGCC	0.408	
-	5	1003	e_Mutation_p.A13	NM_018691	NP_061161	Q9NRY5	F1142_HUMAN		0	TTTGGCATTTG	0.428	
+	9	1399	tation_p.Q264*|uc	NM_198321	NP_938080	Q86SR1	GLT10_HUMAN	enal (Potential).	2	cgcagtccagaaaa	0.323	

+	14	2944	'o.2_Missense_Mu	NM_033551	NP_291029	Q6PKG0	LARP1_HUMAN		4	GATTCCCGTGAG(	0.557	
-	20	2812	ldk.1_Missense_M	NM_015465	NP_056280	Q8TEQ6	GEMI5_HUMAN		3	CCTTTTCCTGTTT	0.413	
+	1	684		NM_001099293	NP_001092763	Q2VIQ3	KIF4B_HUMAN	Kinesin-motor.	1	TGTGGGACTCA(	0.438	
+	1	3426		NM_001099293	NP_001092763	Q2VIQ3	KIF4B_HUMAN	3y similarity).|Globular (By s	1	GGTGTTCCTGCA/	0.453	
+	1	581		NR_002168					0	AATACGGAAGAAT	0.343	
-	4	774	vi.2_Missense_Mu	NM_001099414	NP_001092884	Q96D42	HAVR1_HUMAN	pproximate tandem repeats	2	TTGTTGGAATGCT	0.458	
+	23	2453	_p.S772F|CYFIP2_	NM_001037333	NP_001032410	Q96F07	CYFP2_HUMAN		0	GCATCTCTGCCG(	0.448	
-	3	299	ADAM19_uc011ddr	NM_033274	NP_150377	Q9H013	ADA19_HUMAN		8	CAGGTCCAGGAT	0.478	
-	1	958	e_Mutation_p.A20(	NM_178424	NP_848511	O94993	SOX30_HUMAN		2	GATGGCTGCCG(	0.652	
-	2	401	ddz.1_Missense_M	NM_144726	NP_653327	Q96MT1	RN145_HUMAN		5	TGACATCCCATCT	0.423	
-	7	1376	se_Mutation_p.G32	NM_024565	NP_078841	Q8IV13	CCNJL_HUMAN		0	GATGAGCCTGTA(	0.622	
-	25	4692	jit.1_Missense_Mu	NM_025153	NP_079429	O94823	AT10B_HUMAN	cellular (Potential).	5	TGGTGGGGCTG	0.532	
+	7	1128	3lyy.3_Splice_Site_	NM_000816	NP_000807	P18507	GBRG2_HUMAN		5	GTTCCAGGAGAT	0.378	
+	5	1130	_p.A256V|ODZ2_u	NM_001122679	NP_001116151				10	TGCTGCCCTCT(	0.557	
+	23	5002	zt.3_Missense_Mu	NM_001122679	NP_001116151				10	CTGGAGCTTGGT	0.537	
+	25	5424	t.3_Missense_Muta	NM_001122679	NP_001116151				10	CTTAAACTCCATT	0.532	
+	18	2682	_p.E863D|WWC1_	NM_015238	NP_056053	Q8IX03	KIBRA_HUMAN	eraction with histone H3.	5	tggaggaggaggagg	0.403	
+	19	2830	_p.P913S|WWC1_	NM_015238	NP_056053	Q8IX03	KIBRA_HUMAN	ion with histone H3.	5	GCACCCCGTCC(	0.622	
-	27	3320	g.2_Missense_Mut	NM_003062	NP_003053	O75094	SLIT3_HUMAN	EGF-like 2.	4	GTGCCTCCATGC	0.498	
+	47	4849	e_Mutation_p.R10	NM_004946	NP_004937	Q92608	DOCK2_HUMAN	DHR-2.	7	AGAAAAGGGTGT(	0.517	
+	2	710	c003mbe.1_5'Flan	NM_021025	NP_066305	O43711	TLX3_HUMAN	Homeobox.	1	GCGCAGGTCAAG	0.642	
+	3	766		NM_003862	NP_003853	O76093	FGF18_HUMAN		0	CCCGCGGCGAG	0.527	
-	3	646		NM_005990	NP_005981	O94804	STK10_HUMAN	rotein kinase.	8	GGCTCCCCCTG(	0.572	
-	12	1328		NM_001017995	NP_001017995	A1X283	SPD2B_HUMAN	SH3 3.	4	CTGATGCCGTCT(	0.582	
-	3	349	3mbs.1_Missense_	NM_001017995	NP_001017995	A1X283	SPD2B_HUMAN	PX.	4	CCATGGGAAATTT	0.463	
+	5	1710	fd.1_Missense_Mu	NM_153607	NP_705835	Q8IUR6	CE041_HUMAN		0	AAAATGGCTTAC/	0.398	
+	1	2352	16N|CPEB4_uc01	NM_030627	NP_085130	Q17RY0	CPEB4_HUMAN		0	GCCGAGATCAC(	0.557	
-	9	1151	se_Mutation_p.A26	NM_020444	NP_065177	Q96A73	K1191_HUMAN		1	GGTTGGCCTGG(	0.532	
+	2	234	.2_5'Flank|NOP16	NM_138820	NP_620175	Q9BW72	HIG2A_HUMAN	Helical; (Potential).	0	TCTACTCCTTCC/	0.667	
-	2	344		NM_052899	NP_443131	Q7Z2K8	GRIN1_HUMAN		2	CCTGGGGGGTG	0.657	rs142576280
-	6	652	3_uc003mez.2_5'F	NM_002115	NP_002106	P52790	HXK3_HUMAN	ng (Potential).|Regulatory.	7	CTAAAACCTTTG(	0.602	
-	15	2170	_p.S545F|UIMC1_u	NM_016290	NP_057374	Q96RL1	UIMC1_HUMAN		4	GTGAAAGAACTCT	0.398	
+	5	3751	's.1_Missense_Mu	NM_022455	NP_071900	Q96L73	NSD1_HUMAN		3	TTTCCAGAGCAT/	0.463	
+	23	6787	).E1948K|NSD1_u	NM_022455	NP_071900	Q96L73	NSD1_HUMAN	Pro-rich.	3	CTGGGGAGATC	0.557	
-	12	770	3mib.1_RNA|FAM1	NM_173663	NP_775934	Q9UHL3	F153A_HUMAN		1	GCTCCTCCAGGT(	0.522	
+	2	531	P3_uc003mil.1_5'F	NM_015111	NP_055926	O15049	N4BP3_HUMAN		0	CGCGGGTGACT	0.612	
-	5	427	orf45_uc011dgu.1_	NM_016175	NP_057259	Q6NTE8	CE045_HUMAN		0	TGTTTGCTGAAA(	0.537	
+	3	649	TNL8_uc010jll.2_M	NM_001040462	NP_001035552	Q6UX41	BTNL8_HUMAN	2.|Extracellular (Potential).	2	GTTCCTCTCATTT	0.532	
+	9	1178		NM_152547	NP_689760	Q6UXG8	BTNL9_HUMAN	(Potential).|B30.2/SPRY.	2	CTGAAGGCCAGG	0.517	
+	6	2552	RIM41_uc003mnf.	NM_033549	NP_291027	Q8WV44	TRI41_HUMAN	B30.2/SPRY.	0	GGGTGCTCTCC/	0.647	
-	1	880	c003mnq.2_5'Flan	NM_032765	NP_116154	Q96A61	TRI52_HUMAN		0	CTGCGACGTGTA/	0.567	
-	1	519	c003mnq.2_5'Flan	NM_032765	NP_116154	Q96A61	TRI52_HUMAN	Glu-rich.	0	GCCCCCACCGCT	0.393	
-	21	2224	_p.G697E|EXOC2_	NM_018303	NP_060773	Q96KP1	EXOC2_HUMAN		7	ATACTTCCAAAC/	0.353	
-	11	1274	e_Mutation_p.W3	NM_018303	NP_060773	Q96KP1	EXOC2_HUMAN		7	AAGGATCCACTT(	0.478	
-	2	204	se_Mutation_p.V2	NM_018303	NP_060773	Q96KP1	EXOC2_HUMAN	IPT/TIG.	7	TTGTGACCTTCGT	0.542	
+	1	605	tn.2_Missense_Mu	NM_001452	NP_001443	Q12947	FOXF2_HUMAN	Fork-head.	0	TAAGGGCCTCG(	0.677	
-	9	1094	K4_uc003mtx.3_5'	NM_001012418	NP_001012418	Q86YV6	MYLK4_HUMAN	rotein kinase.	4	CTGGGGTTCCA/	0.443	

-	6	756	3muc.2_Missense_	NM_030666	NP_109591	P30740	ILEU_HUMAN		5	ACTCGTCCTCAAT	0.542
-	5	576	3muc.2_Missense_	NM_030666	NP_109591	P30740	ILEU_HUMAN		5	TGGCTTCTTTCAT	0.413
-	6	794	NB9_uc003muf.2_I	NM_004155	NP_004146	P50453	SPB9_HUMAN		0	TCAGCTCCTTCCT	0.652
-	6	2990	RPINB6_uc003mur	NM_004568	NP_004559	P35237	SPB6_HUMAN		0	TGGCGGCTGCA	0.567
-	10	1798	9Y|SLC22A23_uc	NM_015482	NP_056297	A1A5C7	S22AN_HUMAN	ical; (Potential).	1	gatgtggtgcaggaagt	0.458
-	3	483	.1_Intron|C6orf146	NM_173563	NP_775834	Q8IXS0	CF146_HUMAN		1	TACCACCTGCTG	0.328
+	5	492	36_uc003mwz.1_R	NM_004271	NP_004262	O95711	LY86_HUMAN		0	CGTGGCCTGTG	0.517
+	15	1606	xo.2_Missense_Mu	NM_031480	NP_113668	Q9BRS2	RIOK1_HUMAN	rotein kinase.	4	TGTCAGGAGTT	0.264
+	24	8528	q.1_Missense_Mut	NM_004415	NP_004406	P15924	DESP_HUMAN	in 16.|Globular 2.	9	AGAAGCCATCC	0.557
+	24	8822	q.1_Missense_Mut	NM_004415	NP_004406	P15924	DESP_HUMAN	Globular 2.	9	GAGAGGAAGCT	0.368
+	8	907	NRNP48_uc003mx	NM_152551	NP_689764	Q6IEG0	SNR48_HUMAN		0	GCAGTCTGGTG	0.393
+	4	2880	EP1_uc011diq.1_F	NM_002114	NP_002105	P15822	ZEP1_HUMAN		6	CAAGCAGCCATA	0.498
+	6	6453	EP1_uc011diq.1_F	NM_002114	NP_002105	P15822	ZEP1_HUMAN	C2H2-type 4.	6	TGTGAAGAATGT	0.373
+	8	7009	EP1_uc011diq.1_F	NM_002114	NP_002105	P15822	ZEP1_HUMAN		6	GAAGGCCAGGC	0.552
-	4	393	TBC1D7_uc003nac	NM_016495	NP_057579	Q9P0N9	TBCD7_HUMAN	ab-GAP TBC.	1	GGTGTGGCATCA	0.502
-	2	567	D1_uc003nat.1_Ir	NM_033069	NP_149060				0	GAAGGGCAATT	0.567
+	3	824	p.V136M|RNF182_	NM_152737	NP_689950	Q8N6D2	RN182_HUMAN		3	TGGAGGTGCAG	0.557
+	6	1062	liv.1_Missense_Mu	NM_004973	NP_004964	Q92833	JARD2_HUMAN		4	AGCGGCCCCCT	0.632
-	8	731	nbo.2_RNA|DTNB	NM_032122	NP_115498	Q96EV8	DTBP1_HUMAN	Dysbindin.	0	GCTGGGTGTGC	0.517
-	9	2938	e_Mutation_p.G65	NM_000332	NP_000323	P54253	ATX1_HUMAN	USP7.|RNA-binding.|AXH.	4	GACCAGCCCTGT	0.488
-	19	3861	p.P1252S|NUP153	NM_005124	NP_005115	P49790	NU153_HUMAN		9	CAGGTGGATTGG	0.478
-	18	3187	_p.T1027I|NUP15	NM_005124	NP_005115	P49790	NU153_HUMAN		9	AATGGAGTTAAA	0.358
+	4	601	cn.1_Missense_Mu	NM_153042	NP_694587	Q8NB78	KDM1B_HUMAN		1	CCTAAGGACTAC	0.428
+	3	188	CDKAL1_uc010jpc	NM_017774	NP_060244	Q5VV42	CDKAL_HUMAN		2	CTGCATCCTGTG	0.313
-	3	1025	_p.S263N|KIAA03	NM_014809	NP_055624	Q5VV43	K0319_HUMAN	cellular (Potential).	2	CAGAGCTGTTG	0.557
+	3	817	nfn.2_Missense_M	NM_006355	NP_006346	O00635	TRI38_HUMAN	B box-type.	0	ACAGCTCTTGTT	0.572
-	1	601		NM_005325	NP_005316	Q02539	H11_HUMAN		2	TTTACAGTTTTG	0.493
-	2	720	H2BF_uc003ngx.2_	NM_003530	NP_003521	P68431	H31_HUMAN		0	GGTTGGTGTCC	0.582
+	9	1118	e_Mutation_p.G14	NM_005865	NP_005856	Q9NQE7	TSSP_HUMAN		5	TGTGGGTGACC	0.507
+	3	1584		NM_001076781	NP_001070249	Q9UJN7	ZN391_HUMAN		3	CTTCATACTAAA	0.358
-	1	23	H2BN_uc003nju.1_	NM_003510	NP_003501	P0C0S8	H2A1_HUMAN		1	TGCCGCCCTGC	0.552
-	1	404		NM_005322	NP_005313	P16401	H15_HUMAN		3	GGCTTCCCCGG	0.617
+	2	710	kz.2_Missense_M	NM_032507	NP_115896	Q96JS3	PGBD1_HUMAN	SCAN box.	4	GAGAGGAGGCA	0.537
+	7	2550	kz.2_Missense_M	NM_032507	NP_115896	Q96JS3	PGBD1_HUMAN		4	AACCATCCATAG	0.393
-	2	403	p.M1I|ZNF323_uc	NM_001135216	NP_001128688	Q96LW9	ZN323_HUMAN		2	GAAGCCATTCCT	0.423
+	6	998	ZKSCAN3_uc003r	NM_024493	NP_077819	Q9BRR0	ZKSC3_HUMAN	KRAB.	2	GAGCAGGGACT	0.488
-	7	2041	p.D418N|ZNF311_	NM_001010877	NP_001010877	Q5JNZ3	ZN311_HUMAN	C2H2-type 10.	0	GCTTATCTTGGA	0.468
+	3	978	n_p.V179I|OR2H1_	NM_030883	NP_112145	Q9GZK4	OR2H1_HUMAN	cellular (Potential).	0	GTGAGGTCCCAT	0.507
-	15	2117	BR1_uc003nmu.3	NM_001470	NP_001461	Q9UBS5	GABR1_HUMAN	Name=1; (Potential).	7	GAGACGGAGATA	0.468
-	11	1619	3nmu.3_Missense_	NM_001470	NP_001461	Q9UBS5	GABR1_HUMAN	cellular (Potential).	7	AGCATGACAATCT	0.537
-	6	955	3nmu.3_Missense_	NM_001470	NP_001461	Q9UBS5	GABR1_HUMAN	cellular (Potential).	7	GTCCGGCAGGAT	0.687
+	2	221	se_Mutation_p.G1	NM_002127	NP_002118	P17693	HLAG_HUMAN		4	TCTCGGGGGCC	0.592
+	3	333	p.1_Intron|HLA-H_uc003nod.2_RNA						0	GGGGCCCGACG	0.701
-	7	1181	npn.2_Splice_Site	NM_006778	NP_006769	Q9UDY6	TRI10_HUMAN	B30.2/SPRY.	0	ACTCACCACCCA	0.637
+	1	840		NM_033229	NP_150232	Q9C019	TRI15_HUMAN		0	CTGGACGAGGCC	0.582
+	6	1111	_p.E267K|TRIM39_	NM_021253	NP_067076	Q9HCM9	TRI39_HUMAN		3	ACCCTGGAAAAG	0.473
+	8	1255	_p.E285K|TRIM39_	NM_021253	NP_067076	Q9HCM9	TRI39_HUMAN		3	GAGCTGGAAAAG	0.448

+	9	1582	e_Mutation_p.P39	NM_021253	NP_067076	Q9HCM9	TRI39_HUMAN	B30.2/SPRY.	3	CACTCCCTGAG	0.592	
+	2	470	_Mutation_p.E27	NM_001109938	NP_001103408	Q5SQH8	CF136_HUMAN		0	GGGAGGAGGGA	0.612	
-	1	318	16_uc011dmo.1_I	NM_003587	NP_003578	O60231	DHX16_HUMAN		4	GCAGCGCTGTG	0.652	
-	10	4807	C1_uc011dmp.1_	NM_014641	NP_055456	Q14676	MDC1_HUMAN	on with the PRKDC compl	4	AAGGCTGGAGC	0.562	
-	3	748	MDC1_uc003nrh.1	NM_014641	NP_055456	Q14676	MDC1_HUMAN	omplex.|FHA.|Interaction w	4	TAGGAGGTCTC	0.502	
+	4	384	_Mutation_p.I60T	NM_013993	NP_054699	Q08345	DDR1_HUMAN	(Potential).|F5/8 type C.	9	GACCATCCCAG	0.597	
+	9	1194	1_Missense_Muta	NM_013993	NP_054699	Q08345	DDR1_HUMAN	ellular (Potential).	9	CATGGCCTGGG	0.687	
+	8	944	011dmw.1_Missen	NM_001517	NP_001508	Q92759	TF2H4_HUMAN		3	TCTGGGCAAGG	0.507	
+	25	3262	_p.A875V|VARS2_	NM_020442	NP_065175	Q5ST30	SYVM_HUMAN		4	CCCTGCCCCCA	0.682	
-	2	896		NM_014070	NP_054789	Q6UXA7	CF015_HUMAN	Pro-rich.	0	GGACTCCAGGA	0.542	
-	6	922	_p.E320K|CCHCR	NM_019052	NP_061925	Q8TD31	CCHCR_HUMAN	Potential.	1	CAGTTCCCATG	0.532	
+	3	765	st.2_Missense_M	NM_001077511	NP_001070979	Q9Y242	TCF19_HUMAN	FHA.	0	CAGGTACTTTG	0.507	
+	4	918	_p.V236M|MICB_u	NM_005931	NP_005922	Q29980	MICB_HUMAN	.|Extracellular (Potential).	0	CCTGGGTGGCC	0.592	
+	4	976	_p.S255N|MICB_u	NM_005931	NP_005922	Q29980	MICB_HUMAN	.|Extracellular (Potential).	0	ACACAGCGGGA	0.617	
+	3	323	anslation_Start_Si	NM_001159740	NP_001153212	P01374	TNFB_HUMAN		0	TCCCTGGTGTTG	0.612	
+	3	329	_uc003nuh.2_5'UT	NM_001159740	NP_001153212	P01374	TNFB_HUMAN		0	TGTTGGCCTCA	0.607	
+	12	2014	T2_uc003nvc.3_	NM_080686	NP_542417	P48634	PRC2A_HUMAN	AA type A repeats.	0	GCCCAGGTATG	0.547	
+	16	2824	T2_uc003nvc.3_	NM_080686	NP_542417	P48634	PRC2A_HUMAN	AA type A repeats.	0	AGGAACCAGGG	0.607	
-	7	954	_p.V208I|BAT3_uc	NM_004639	NP_004630	P46379	BAG6_HUMAN	Pro-rich.	0	GGCTACTGGCT	0.622	
-	1	1336		NM_021184	NP_067007	O95873	CF047_HUMAN		1	TGGGCCCCCCA	0.657	
-	4	302	_uc003nvz.1_5'U	NM_021160	NP_066983	O95870	ABHGA_HUMAN		0	CTTTGGACAAA	0.557	
+	5	806	_Intron|LY6G6F_u	NM_001003693	NP_001003693	Q5SQ64	LY66F_HUMAN	lasmic (Potential).	2	AGATGCCTCGA	0.537	
-	5	1352	wq.2_Missense_M	NM_013974	NP_039268	O95865	DDAH2_HUMAN		0	CAGATCCCCAC	0.587	
-	5	1292	wq.2_Missense_M	NM_013974	NP_039268	O95865	DDAH2_HUMAN		0	AAAGAGACAGT	0.587	
-	4	1037	RS_uc011doi.1_R	NM_006295	NP_006286	P26640	SYVC_HUMAN	ST C-terminal.	3	CTTCTCCTAGC	0.592	
+	1	1880	_Missense_Mutati	NM_005345	NP_005336	P08107	HSP71_HUMAN		1	CTACGCCTTCA	0.597	
-	2	322	U1_uc010jth.2_In	NM_000434	NP_000425	Q99519	NEUR1_HUMAN		1	CAGCGGCTGCA	0.592	
-	20	2005	1_uc003nxr.3_5'	NM_025257	NP_079533	Q53GD3	CTL4_HUMAN	ical; (Potential).	4	GGCCCCCAGGA	0.602	
+	9	1467	p.D899Y|CFB_uc	NM_001710	NP_001701	P00751	CFAB_HUMAN	VWFA.	1	GCGGGGACCC	0.498	
-	7	676	se_Mutation_p.A9	NM_002904	NP_002895	P18615	NELFE_HUMAN		0	ACCAGCCCCTG	0.607	
-	19	6959		NM_019105	NP_061978	P22105	TENX_HUMAN	nectin type-III 15.	0	TGGCTCCAGGC	0.602	
-	17	6156		NM_019105	NP_061978	P22105	TENX_HUMAN		0	TGATGGGGGGC	0.632	
-	9	3776		NM_019105	NP_061978	P22105	TENX_HUMAN	nectin type-III 5.	0	GTACTGGACCA	0.582	
-	3	2040		NM_019105	NP_061978	P22105	TENX_HUMAN	EGF-like 15.	0	TCCTCACTCACG	0.657	
-	4	760	oax.3_Missense_	NM_022107	NP_071390	Q9Y4H4	GPSM3_HUMAN	GoLoco 2.	0	TGACCGCTGGG	0.627	
-	12	2113	_p.D20N|HLA-DO	NM_018833	NP_061313	Q03519	TAP2_HUMAN		0	GGAATCCAGTC	0.483	
-	5	785	AP2_uc003ocd.2_	NM_148919	NP_683720	P28062	PSB8_HUMAN		1	CTCTTACTATTG	0.468	
-	4	551	_Mutation_p.G16	NM_148919	NP_683720	P28062	PSB8_HUMAN		1	ACTGCCCATAGA	0.512	
-	4	711	juk.2_Missense_	NM_033554	NP_291032	P20036	DPA1_HUMAN	ical; (Potential).	1	CCAGGGCACAG	0.617	
-	66	5401	y.1_Missense_Mu	NM_080680	NP_542411	P13942	COBA2_HUMAN	lar collagen NC1.	5	CCCTCCCCGCC	0.637	
-	26	2314	nse_Mutation_p.E	NM_080680	NP_542411	P13942	COBA2_HUMAN	le-helical region.	5	ACCTTCCTTCC	0.537	
-	4	999	s.1_Missense_Mu	NM_021976	NP_068811	P28702	RXRB_HUMAN	Hinge.	3	CCTTACCCTCCC	0.592	
-	3	757	ation_p.P57L|RXR	NM_021976	NP_068811	P28702	RXRB_HUMAN	(By similarity).|Pro-rich.	3	GAGGGGGTGGA	0.607	
+	2	355	_5'Flank|RXRB_u	NM_001077516	NP_001070984	Q92504	S39A7_HUMAN	His-rich.	1	ATCACGACCAT	0.537	
-	7	886	p.V151M|VPS52_	NM_022553	NP_072047	Q8N1B4	VPS52_HUMAN		5	GAGCACGCCTC	0.587	rs149498990
-	6	1384	APBP_uc003odz.2	NM_003190	NP_003181	O15533	TPSN_HUMAN	enal (Potential).	1	TGAAAGACCTG	0.597	
-	4	1455	011dre.1_Splice_	NM_001350	NP_001341	Q9UER7	DAXX_HUMAN		23	CCACACCTCAC	0.562	

-	3	1079	nse_Mutation_p.A	NM_001350	NP_001341	Q9UER7	DAXX_HUMAN		23	CTACAGCCCGA	0.602	
+	6	721	.2_Missense_Mut	NM_024165	NP_077084	O43189	PHF1_HUMAN		0	GCTGGGTATGA	0.597	
+	25	3367		NM_002224	NP_002215	Q14573	ITPR3_HUMAN	lasmic (Potential).	19	ATGACGAGGGC	0.637	
+	33	4682		NM_002224	NP_002215	Q14573	ITPR3_HUMAN	lasmic (Potential).	19	GAACAGCACTT	0.458	
+	40	5689	3_uc003oey.2_5'	NM_002224	NP_002215	Q14573	ITPR3_HUMAN	lasmic (Potential).	19	TCGACCCCACC	0.657	
-	1	96	_5'Flank|LEMD2_	NM_181336	NP_851853	Q8NC56	LEMD2_HUMAN	LEM.	1	CATCCCGGGTG	0.716	
+	5	726	ojp.2_Missense_	NM_020804	NP_065855	Q9BY11	PACN1_HUMAN		0	CACGGGAGATG	0.542	
+	14	3074	1BP1_uc010jvn.2	NM_017754	NP_060224	Q6BDS2	URFB1_HUMAN		3	GGAGAGGCCAC	0.552	
+	22	3ojw.1_Silent_p.L84L|TAF11_	NM_017754		Q6BDS2	URFB1_HUMAN		3	TTTTCAGTTTTTT	0.368	
-	9	1407	c.2_Missense_M	NM_001093728	NP_001087197	Q8WWU5	TCP11_HUMAN		5	ACAAGGCCCATA	0.448	
-	7	936	kc.2_Splice_Site_	NM_001093728	NP_001087197	Q8WWU5	TCP11_HUMAN		5	GAGACCTATGA	0.473	
+	11	1286	_p.L426P|SCUBE	NM_152753	NP_689966	Q8IX30	SCUB3_HUMAN		1	TGCCCTGACCT	0.597	
+	11	1888	_p.A592T|DEF6_u	NM_022047	NP_071330	Q9H4E7	DEFI6_HUMAN		0	CCCCGGCTTCC	0.592	
+	6	1339	vw.1_Missense_M	NM_021922	NP_068741	Q9HB96	FANCE_HUMAN		3	TACAACTGCCC	0.498	
-	7	880	e_Mutation_p.G47	NM_001145776	NP_001139248	Q13451	FKBP5_HUMAN	se FKBP-type 2.	1	CCTCTCCAAAA	0.368	
+	1	502		NM_182548	NP_872354	Q8TAF8	TMHS_HUMAN	ical; (Potential).	1	TCATGGCCCTCT	0.592	
-	11	1177	lh.2_Missense_M	NM_003137	NP_003128	Q96SB4	SRPK1_HUMAN	rotein kinase.	1	TTCTGCTGCAC	0.353	
-	3	357	_p.W82*|SLC26A	NM_052961	NP_443193	Q96RN1	S26A8_HUMAN	lasmic (Potential).	2	CACATCCATTCT	0.458	
+	4	798	3olq.2_Missense_	NM_001315	NP_001306	Q16539	MK14_HUMAN	rotein kinase.	6	GGTGACCCATC	0.353	
+	9	829	K13_uc003olt.2_I	NM_002754	NP_002745	O15264	MK13_HUMAN	rotein kinase.	3	TGGCACGGAGT	0.607	rs146698142
+	6	2386	tj.1_RNA|BRPF3_	NM_015695	NP_056510	Q9ULD4	BRPF3_HUMAN		2	TTTACCGCTTCT	0.622	
+	8	2782	j.1_Intron|BRPF3_	NM_015695	NP_056510	Q9ULD4	BRPF3_HUMAN		2	ATCCCCCCCGG	0.502	
+	6	1153	_p.P290S|PNPLA1	NM_001145717	NP_001139189	Q8N8W4	PLPL1_HUMAN	Pro-rich.	4	TCCACACCTGGT	0.577	
-	6	1132	_p.D182N|STK38_	NM_007271	NP_009202	Q15208	STK38_HUMAN	rotein kinase.	6	GAGTGTCTTTTT	0.328	
+	2	256	ml.2_Missense_	NM_000389	NP_000380	P38936	CDN1A_HUMAN		2	GGAGGCCCGTG	0.657	
+	6	1691	b.2_Missense_M	NM_153370	NP_699201	Q6UXB8	PI16_HUMAN	ical; (Potential).	0	TCCTGCCTCCT	0.617	
+	4	603	D22B_uc010jwt.2_	NM_017772	NP_060242	Q9NU19	TB22B_HUMAN		0	AACAGCAATCA	0.542	
+	20	2331		NM_015050	NP_055865	Q8N1G2	MTR1_HUMAN		5	CAAGCCTAGTC	0.547	
-	12	2401	_Mutation_p.R57	NM_052893	NP_443125	Q96Q07	BTBD9_HUMAN		0	CTGCCGGTTGG	0.662	
+	64	9799	uc003oof.1_Intron	NM_001371	NP_001362				21	GAACGTATGAAT	0.279	
+	65	9910	uc003oof.1_Intron	NM_001371	NP_001362				21	CAGACGAAGTG	0.368	
+	68	10402	uc003oof.1_Intron	NM_001371	NP_001362				21	ATGTGGCTGGT	0.378	
+	82	12592	og.1_Missense_M	NM_001371	NP_001362				21	CTACGGAGCCC	0.393	
+	91	13985		NM_001371	NP_001362				21	ATTTGACCTTCAT	0.473	
+	91	14053		NM_001371	NP_001362				21	TGGCCCTTTTG	0.468	
+	8	914	h.2_RNA|GLP1R_	NM_002062	NP_002053	P43220	GLP1R_HUMAN	Name=4; (Potential).	5	CTGGGGCATTG	0.602	
+	10	1051	h.2_RNA|GLP1R_	NM_002062	NP_002053	P43220	GLP1R_HUMAN	lasmic (Potential).	5	GCATCGTGGTA	0.562	
-	3	343	0jwy.2_Splice_Site	NM_032115	NP_115491	Q96T55	KCNKG_HUMAN		3	ATATCCTGCAA	0.562	
+	11	1333	p.G393S|DAAM2_	NM_015345	NP_056160	Q86T65	DAAM2_HUMAN	GBD/FH3.	3	ACGGTGGCTAC	0.592	
-	2	451	_p.E105K|MOCS1	NM_005942	NP_005933	Q9NZB8	MOCS1_HUMAN	factor biosynthesis protein	3	CTCCTCTGTGG	0.607	
+	9	1125	p.G287E|NFYA_u	NM_002505	NP_002496	P23511	NFYA_HUMAN	YA/HAP2-type.	0	AAGGTGGACGAT	0.393	
-	5	775	.2_Intron|TRERF1	NM_033502	NP_277037	Q96PN7	TREF1_HUMAN		5	TTTTGGAGCCA	0.582	
-	2	891		NM_000322	NP_000313	P23942	PRPH2_HUMAN	enal (Potential).	5	TACCGCCCATCC	0.577	
+	13	3333	.G1061D|KIAA024	NM_015349	NP_056164	Q6AI39	K0240_HUMAN		1	TGAAGGTGTTG	0.507	
-	11	2713	.1_Nonsense_Mut	NM_014780	NP_055595	Q14999	CUL7_HUMAN		4	GATCTGGCCCA	0.552	
-	4	1051	p.L334F|CUL7_uc	NM_014780	NP_055595	Q14999	CUL7_HUMAN		4	GAAGAGCACCC	0.552	
+	2	317	_p.S40F|PTK7_uc	NM_002821	NP_002812	Q13308	PTK7_HUMAN	1.|Extracellular (Potential).	3	GTCCTCCCAGG	0.632	

+	14	2287	se_Mutation_p.P56	NM_002821	NP_002812	Q13308	PTK7_HUMAN	cellular (Potential).	3	GCCCTCCCCCC	0.602
+	18	2920	03ouf.1_Splice_Sit	NM_002821	NP_002812	Q13308	PTK7_HUMAN		3	CTCCAGGTGGC	0.557
+	19	3943	_p.V1290I|CUL9_u	NM_015089	NP_055904	Q8IWT3	CUL9_HUMAN	DOC.	12	CCCGGGTTCGG	0.582
+	3	508		NM_032538	NP_115927	Q5TCY1	TTBK1_HUMAN	rotein kinase.	9	AGATGGAGGTG	0.587
+	11	1426		NM_032538	NP_115927	Q5TCY1	TTBK1_HUMAN		9	GGCTGGGCCCC	0.632
-	10	4702	318_uc003ouw.2_I	NM_014345	NP_055160	Q5VUA4	ZN318_HUMAN		7	TGAGAGGGGTG	0.483
-	10	4309	318_uc003ouw.2_I	NM_014345	NP_055160	Q5VUA4	ZN318_HUMAN		7	CCCCTCCAAATG	0.423
-	6	3150	3_uc003ouw.2_Spl	NM_014345	NP_055160	Q5VUA4	ZN318_HUMAN		7	TTGTTACCTTGTT	0.368
+	3	575	ouz.1_Nonsense_I	NM_033450	NP_258261	Q5T3U5	MRP7_HUMAN	ical; (Potential).	7	CCTGTGGGTGTT	0.657
-	3	501	0jys.1_5'UTR|YIPF	NM_015388	NP_056203	Q9GZM5	YIPF3_HUMAN		0	ATGTCGATGTTG	0.522
+	8	1312	_uc011dvl.1_Splic	NM_006502	NP_006493	Q9Y253	POLH_HUMAN		2	GAACAGGTAAGC	0.443
+	11	2084	p.G667D|HSP90AI	NM_007355	NP_031381	P08238	HS90B_HUMAN		4	CTTCTGGCTTTTC	0.522
-	6	1032	2_RNA|TMEM151E	NM_020745	NP_065796	Q5JTZ9	SYAM_HUMAN		1	ACCTGACATCCC	0.632
+	4	1551		NM_014936	NP_055751	Q9Y6X5	ENPP4_HUMAN	lasmic (Potential).	4	AGAATAGACTTTC	0.418
-	2	625	dvz.1_Nonsense_N	NM_021572	NP_067547	Q9UJA9	ENPP5_HUMAN		0	CCGGGCCACATC	0.398
+	1	1652	ze.2_Missense_Mu	NM_001010870	NP_001010870	O60522	TDRD6_HUMAN	Tudor 3.	6	AAAATGGTTATTA	0.428
-	3	412	2G7_uc011dwd.1_I	NM_005084	NP_005075	Q13093	PAFA_HUMAN		0	CTTGCAGCAGCC	0.368
-	17	3350	oyp.3_Missense_M	NM_001098518	NP_001091988	Q8IZF2	GP116_HUMAN	Name=1; (Potential).	2	AAAGCCCACCC	0.493
-	17	3160	oyp.3_Nonsense_N	NM_001098518	NP_001091988	Q8IZF2	GP116_HUMAN	tracellular (Potential).	2	GAAGTTCCAGAA	0.483
-	12	1743	nse_Mutation_p.G	NM_001098518	NP_001091988	Q8IZF2	GP116_HUMAN	xtracellular (Potential).	2	TTTTGTCCCTCAC	0.338
-	2	1181		NM_014452	NP_055267	O75509	TNR21_HUMAN	cellular (Potential).	0	GTTACCTTTGGC	0.478
+	4	374	se_Mutation_p.P57	NM_153839	NP_722581	Q8IZF7	GP111_HUMAN	cellular (Potential).	1	GCCCTCCAGAC	0.488
-	6	519	_p.R88H|CRISP2_	NM_001142408	NP_001135880	P16562	CRIS2_HUMAN		1	ctggttttgcggtcctctg	0.264
+	8	1680	P2D_uc011dwt.1_	NM_172238	NP_758438	Q7Z6R9	AP2D_HUMAN	span-helix), dimerization.	7	ACTCCGGCAATA	0.433
-	58	9973	.P1216S|PKHD1_	NM_138694	NP_619639	P08F94	PKHD1_HUMAN	cellular (Potential).	44	GGAGGGAGCTC	0.488
-	35	5887	ai.2_Missense_Mu	NM_138694	NP_619639	P08F94	PKHD1_HUMAN	cellular (Potential).	44	CTCTTTCCAATTT	0.398
-	32	5365	ai.2_Missense_Mu	NM_138694	NP_619639	P08F94	PKHD1_HUMAN	ical.|Extracellular (Potentia	44	GGTTACCAGAGA	0.537
-	23	2665	ai.2_Missense_Mu	NM_138694	NP_619639	P08F94	PKHD1_HUMAN	cellular (Potential).	44	TATTAGGAAGCTC	0.498
-	16	1655	ai.2_Missense_Mu	NM_138694	NP_619639	P08F94	PKHD1_HUMAN	cellular (Potential).	44	GCTATCCCATGA	0.547
-	15	1456	ai.2_Missense_Mu	NM_138694	NP_619639	P08F94	PKHD1_HUMAN	cellular (Potential).	44	TATCTGCCTGAA	0.438
-	9	1420	vu.1_Missense_Mu	NM_002388	NP_002379	P25205	MCM3_HUMAN	MCM.	3	GGATGCCAGCC	0.542
+	5	1047	_p.V187I|EFHC1_	NM_018100	NP_060570	Q5JVL4	EFHC1_HUMAN	DM10 2.	3	GAGAGGTCCAC	0.438
-	7	747	1_Intron|TRAM2_	NM_012288	NP_036420	Q15035	TRAM2_HUMAN	Helical; (Potential).	0	ATGCACCAGGT	0.448
-	3	213	A3_uc010jzq.2_5'	NM_000847	NP_000838	Q16772	GSTA3_HUMAN	ST N-terminal.	0	CCATTTCTTAACT	0.333
-	3	570	_p.G27E|ICK_uc0	NM_016513	NP_057597	Q9UPZ9	ICK_HUMAN	rotein kinase.	5	GCTCCCCAGAC	0.478
-	9	1067	dxc.1_Missense_N	NM_019036	NP_061909	Q8TB92	HMGC2_HUMAN		4	CTGCGGAGTCC	0.423
-	97	16908	cy.3_Missense_Mu	NM_001144769	NP_001138241	Q03001	DYST_HUMAN		14	ACACGGACTGG	0.587
-	73	13277	.E4268K|DST_uc	NM_001144769	NP_001138241	Q03001	DYST_HUMAN	Spectrin 14.	14	GTCTTTCCATTTC	0.323
-	52	8073	.P2533L|DST_uc	NM_001144769	NP_001138241	Q03001	DYST_HUMAN	Spectrin 4.	14	GCCTCAGGAGTA	0.408
+	4	682	dxm.1_Missense_N	NM_020931	NP_065982	Q9HCI6	K1586_HUMAN		0	ATTTGGGATCGA	0.363
+	2	400	.S37F|PHF3_uc0	NM_015153	NP_055968	Q92576	PHF3_HUMAN		5	TGAGATCTCCAA	0.378
+	15	5250	.D1654N|PHF3_u	NM_015153	NP_055968	Q92576	PHF3_HUMAN		5	CAGGAGGATATT	0.383
+	36	2477	kam.1_Missense_N	NM_001858	NP_001849	Q14993	COJA1_HUMAN	lical region 4 (COL4).	4	GGGAAGAACTG	0.423
+	36	2492	kam.1_Missense_N	NM_001858	NP_001849	Q14993	COJA1_HUMAN	lical region 4 (COL4).	4	ATCCTGGTCCCA	0.443
+	47	3002		NM_001858	NP_001849	Q14993	COJA1_HUMAN	lical region 5 (COL5).	4	CAGAGGCTCAC	0.468
-	34	2360	_p.P283L|COL9A1	NM_001851	NP_001842	P20849	CO9A1_HUMAN	elical region (COL2).	4	CCCGGGGTCCA	0.637
-	15	1340	OL9A1_uc003pff.3	NM_001851	NP_001842	P20849	CO9A1_HUMAN	elical region (COL3).	4	GGGGGCCAGGG	0.443

+	10	1317	ao.2_Missense_Mu	NM_001044305	NP_001037770	Q8IYB5	SMAP1_HUMAN		0	CTTATAGGAAAT	0.512
+	29	4318	e_Mutation_p.S41	NM_014989	NP_055804	Q86UR5	RIMS1_HUMAN		10	CGGCAGCCAGT	0.517
+	7	1393	p.G349D|KCNQ5_	NM_019842	NP_062816	Q9NR82	KCNQ5_HUMAN		7	GCTCAGGTTTTG	0.348
-	38	6492	pht.2_Missense_M	NM_004370	NP_004361	Q99715	COCA1_HUMAN	nectin type-III 16.	9	CCATTTCCTGTTA	0.343
-	10	1722	OL12A1_uc003ph	NM_004370	NP_004361	Q99715	COCA1_HUMAN	VWFA 2.	9	TTGCCAGTATTT	0.388
-	5	1169	_p.Q167*|FILIP1_	NM_015687	NP_056502	Q7Z7B0	FLIP1_HUMAN	Potential.	4	CTTTCTGGCTTTG	0.403
+	24	3758	e_Mutation_p.L10	NM_015571	NP_056386	Q9GZR1	SENP6_HUMAN	Protease.	6	CCAATTCTCAGT	0.308
+	4	477	n_p.M66I|MYO6_	NM_004999	NP_004990	Q9UM54	MYO6_HUMAN	osin head-like.	2	ACTAATGTATTTA	0.274
+	16	1867	p.D530N|MYO6_	NM_004999	NP_004990	Q9UM54	MYO6_HUMAN	osin head-like.	2	ATTTTGGATGAA	0.343
+	32	3586	p.E1080K|MYO6_	NM_004999	NP_004990	Q9UM54	MYO6_HUMAN		2	TGCAGAGAAGAA	0.323
-	2	218	_p.D14N|HMGN3_	NM_004242	NP_004233	Q15651	HMGN3_HUMAN		0	ATCCATCTTTGCC	0.279
+	5	644	pje.2_Missense_M	NM_000056	NP_000047	P21953	ODBB_HUMAN		0	CATGGGGCTCTC	0.433
-	18	3208	se_Mutation_p.S6	NM_015525	NP_056340	Q9P2D0	IBTK_HUMAN		4	AACAAGACAGT	0.343
+	3	1436	p.A167V|TPBG_u	NM_006670	NP_006661	Q13641	TPBG_HUMAN	ellular (Potential).	1	GCAATGCCAGCG	0.657
+	3	930	M3_uc011dyz.1_5'	NM_033411	NP_219479	Q9UIY3	RWD2A_HUMAN		0	ACATTTCCTGTA	0.468
-	23	2559	kc.2_Missense_M	NM_014841	NP_055656	O60641	AP180_HUMAN		1	TGGCTGCCATTG	0.453
+	8	7350		NM_015021	NP_055836	O60281	ZN292_HUMAN		4	GTAAAGGAAACG	0.358
-	3	461		NM_198568	NP_940970	Q6PEY0	CXB7_HUMAN	ical; (Potential).	0	CTGCTGCCACCA	0.478
+	13	1906	plw.2_Missense_M	NM_001031743	NP_001026913	Q8IYR0	CF165_HUMAN		1	GAAAGAGCGAAA	0.458
+	2	191	SLC35A1_uc003pl	NM_006416	NP_006407	P78382	S35A1_HUMAN	enal (Potential).	0	ACATCAGACAAA	0.368
-	3	214	onc.2_Missense_M	NM_016021	NP_057105	Q9Y385	UB2J1_HUMAN	lasmic (Potential).	0	ATTAAACGTTTAA	0.313
-	97	16258		NM_014611	NP_055426	Q9NU22	MDN1_HUMAN		10	TACTGGCGTTTA	0.423
-	97	16232		NM_014611	NP_055426	Q9NU22	MDN1_HUMAN		10	TCGAAGCCAAAT	0.408
-	92	15505		NM_014611	NP_055426	Q9NU22	MDN1_HUMAN		10	TGCTCGGCATGG	0.552
-	14	2733	p.S826F|EPHA7_	NM_004440	NP_004431	Q15375	EPHA7_HUMAN	Potential).|Protein kinase.	28	CCATAAGACATA	0.403
+	3	1225		NM_006581	NP_006572	Q9Y231	FUT9_HUMAN	enal (Potential).	5	CTCTCCCAGTG	0.393
-	14	2058	eaf.1_Missense_M	NM_198468	NP_940870	Q6ZRQ5	MMS22_HUMAN		0	GGAAAGCACATG	0.438
-	12	1697	_splice|USP45_uc	NM_001080481	NP_001073950	Q70EL2	UBP45_HUMAN		2	TCCTTACCCTTT	0.294
-	11	2228	u.2_Missense_Mu	NM_005068	NP_005059	P81133	SIM1_HUMAN	minded C-terminal.	4	TCTTTAGCTAGG	0.463
-	8	1119	u.2_Nonsense_Mu	NM_005068	NP_005059	P81133	SIM1_HUMAN	PAC.	4	CCATACCCAGCC	0.582
+	16	5049	i.2_Missense_Mut	NM_001624	NP_001615	Q9Y4K1	AIM1_HUMAN	crystallin 'Greek key' 11.	9	TTAATGCAGAAA	0.358
+	7	876	rl.2_Missense_Mu	NM_018292	NP_060762	Q9H0R6	QRSL1_HUMAN		0	CCCAGGGACTCT	0.388
+	6	2099		NM_018013	NP_060483	A7XYQ1	SOBP_HUMAN	Pro-rich.	1	TCGTGCCCCTAC	0.667
-	2	202	su.2_Missense_M	NM_014454	NP_055269	Q9Y6P5	SESN1_HUMAN		1	CTAATGCCAAGTT	0.418
-	2	399	_p.S92N|SLC22A1	NM_033125	NP_149116	Q86VW1	S22AG_HUMAN		1	CCCAAACTCGAT	0.468
-	12	1317	p.G355E|CDK19_	NM_015076	NP_055891	Q9BWU1	CDK19_HUMAN		4	CGACCCCGGCC	0.692
-	20	7650	V3L_uc003puz.3_	NM_002912	NP_002903	O60673	DPOLZ_HUMAN		6	TTTCAGCTGCAA	0.348
-	7	1174	_p.P206L|REV3L_	NM_002912	NP_002903	O60673	DPOLZ_HUMAN		6	GACTCAGGTTGG	0.363
-	3	1348	p.P245S|TRAF3IP	NM_147686	NP_679211	O43734	CIKS_HUMAN		3	ATGCTGGATACC	0.562
-	16	2270	_p.A647V|LAMA4_	NM_001105206	NP_001098676	Q16363	LAMA4_HUMAN	omain II and I.	9	CTCACCGCCTAC	0.388
+	2	327	_p.M45V|DSE_uc	NM_001080976	NP_001074445	Q9UL01	DSE_HUMAN		1	CATCCCATGCTG	0.542
+	4	435	.2_5'UTR|RWDD1_	NM_015952	NP_057036	Q9H446	RWDD1_HUMAN	RWD.	3	CACAGGCTGAAG	0.269
+	7	863	_p.P138S|RWDD1_	NM_015952	NP_057036	Q9H446	RWDD1_HUMAN		3	TATAATCCTGCTG	0.493
+	18	2665		NM_173560	NP_775831	Q8HWS3	RFX6_HUMAN		3	GAACTCCAGTC	0.398
-	21	2532	kej.1_5'UTR|C6orf	NM_152730	NP_689943	Q96NH3	BROMI_HUMAN		3	TGGGACTTCAC	0.313
+	2	428	1_5'UTR|GJA1_uc	NM_000165	NP_000156	P17302	CXA1_HUMAN	ellular (Potential).	2	CAACCTGGTTGT	0.488
+	9	1131	v.2_Missense_Mu	NM_004506	NP_004497	Q03933	HSF2_HUMAN		0	GTTCAGGCAGTG	0.473

+	14	2737	qai.2_Missense_M	NM_181782	NP_861447	Q8NI08	NCOA7_HUMAN			3	CATGCAGCTACT	0.507	
-	13	1816	AP18_uc011ebw.1	NM_033515	NP_277050	Q8N392	RHG18_HUMAN			3	CTCCCTGAGGA	0.448	
-	12	2010	ation_p.G610R|EPI	NM_001431	NP_001422	O43491	E41L2_HUMAN	Hydrophilic.		2	CCTTTCCTTCAAT	0.413	
-	10	1591	3qci.2_Missense_	NM_001431	NP_001422	O43491	E41L2_HUMAN	FERM.		2	CCAATGGTACTCT	0.403	
+	3	403	se_Mutation_p.A2	NM_138633	NP_619539	O43687	AKA7A_HUMAN			2	CTCAAGGCTGTC	0.507	
-	14	1738	e_Mutation_p.P16	NM_004830	NP_004821	Q9ULK4	MED23_HUMAN			3	GTAAGGGGGTAA	0.398	
-	12	1342	a.1_Intron|MED23_	NM_004830	NP_004821	Q9ULK4	MED23_HUMAN			3	AATCAGCTAGTG	0.373	
+	21	2295	PP3_uc003qcv.2_	NM_005021	NP_005012	O14638	ENPP3_HUMAN	ar (Potential).|Nuclease.		4	GTCCCCCAGTTG	0.418	
-	2	629	fr.1_Missense_Mu	NM_001033080	NP_001028252	Q9P1P5	TAAR2_HUMAN	Name=5; (Potential).		1	GTGGTCCCCCAT	0.478	
-	6	1297	N1_uc003qdn.2_R	NM_004666	NP_004657	O95497	VNN1_HUMAN			3	CTGAGGGAGAAC	0.423	
+	20	2334	on_p.D626N|EYA4_	NM_004100	NP_004091	O95677	EYA4_HUMAN			2	CACTCAGACCTC	0.308	
+	1	590	21_uc003qej.2_Mi	NM_003206	NP_003197	O43680	TCF21_HUMAN	-loop-helix motif.		0	GACCACCCTGC	0.662	
-	6	910	S1L_uc011ecz.1_	NM_006620	NP_006611	Q9Y450	HBS1L_HUMAN			2	TTTCACCGGTG	0.493	
+	8	1145	_uc003qfe.2_RNA	NM_005375	NP_005366	P10242	MYB_HUMAN	onal activation domain.		1	GTGCTACCAGTA	0.423	
-	12	2960	y.1_Missense_Mu	NM_014739	NP_055554	Q9NYF8	BCLF1_HUMAN			1	TGGTCTCTTCTT	0.373	rs141900019
-	2	356	_Mutation_p.S59N|	NM_003980	NP_003971	Q14244	MAP7_HUMAN			0	GGCGGCTGGAG	0.378	
-	16	2634	_p.P5L|MAP3K5_	NM_005923	NP_005914	Q99683	M3K5_HUMAN	rotein kinase.		5	CTCCAGGGACC	0.378	
-	5	759	_p.T121I|IL22RA2	NM_052962	NP_443194	Q969J5	I22R2_HUMAN	nectin type-III 2.		0	AGGGAGTGAAC	0.532	
-	4	561	.2_Intron|IL22RA2	NM_052962	NP_443194	Q969J5	I22R2_HUMAN			0	agttacaagaaatgtg	0	
-	1	648		NM_175747	NP_786923	Q7RTU3	OLIG3_HUMAN			0	CTCCTCCAGGG	0.657	
+	4	605	qhs.2_Missense_M	NM_006290	NP_006281	P21580	TNAP3_HUMAN	F-binding.|C	p.0?(22)	137	CACACCCATGG	0.443	
+	12	2036		NM_020340	NP_065073	Q5TH69	BIG3_HUMAN	SEC7.		2	ACAGTCCCTGG	0.577	
+	3	629	n_p.A73V|GPR126	NM_020455	NP_065188	Q86SQ4	GP126_HUMAN	tracellular (Potential).		1	CCGAGCCCCCA	0.468	
-	6	6085		NM_006734	NP_006725	P31629	ZEP2_HUMAN			6	TCCTTACCCTCC	0.363	
-	5	2523		NM_006734	NP_006725	P31629	ZEP2_HUMAN			6	ATGCCGCTTGTC	0.522	
+	2	260	G1_uc011edw.1_M	NM_016108	NP_057192	Q9NVV5	AIG1_HUMAN			0	ACCAGGAGCAA	0.517	
+	5	647	0khi.2_Missense_	NM_014721	NP_055536	O75167	PHAR2_HUMAN			2	AATCACCTGTG	0.522	
+	5	737	0khi.2_Nonsense_	NM_014721	NP_055536	O75167	PHAR2_HUMAN			2	GTAAGCAGGCC	0.582	
-	2	989	PRH_uc003qlg.1_	NM_001042683	NP_001036148	Q149N8	SHPRH_HUMAN			3	TTTATTCTTCTCT	0.378	
-	2	602	.R68K|SHPRH_uc	NM_001042683	NP_001036148	Q149N8	SHPRH_HUMAN			3	TTATCTCTGTGAG	0.383	
+	2	735		NM_015278	NP_056093	O94885	SASH1_HUMAN			1	GAAACGGCGGG	0.542	
+	6	659	_p.A174V|PCMT1_	NM_005389	NP_005380					1	AAGAAGCCCCTT	0.418	
+	4	1327	e_Mutation_p.E26	NM_005100	NP_005091	Q02952	AKA12_HUMAN	PKC-binding (Probable).		8	CGGCAGAAAGT	0.557	
-	2	257	ense_Mutation_p.	NM_017909	NP_060379	Q9NWS8	RMND1_HUMAN			0	GATGACCGATTC	0.408	
-	130	24138	on_p.A7846T|SYN	NM_182961	NP_892006	Q8NF91	SYNE1_HUMAN	|Cytoplasmic (Potential).		45	GCTGGCTTTAG	0.443	
-	119	22437	ot.3_Missense_Mu	NM_182961	NP_892006	Q8NF91	SYNE1_HUMAN	lasmic (Potential).		45	TGGCAACCTCAT	0.483	
-	78	15021	ou.3_Missense_M	NM_182961	NP_892006	Q8NF91	SYNE1_HUMAN	lasmic (Potential).		45	GCGTTTCCTCAT	0.478	
-	46	7327	ou.3_Missense_Mu	NM_182961	NP_892006	Q8NF91	SYNE1_HUMAN	ytoplasmic (Potential).		45	CTTCAGACTGC	0.338	
-	6	731	1M_uc003qqk.2_In	NM_016020	NP_057104	Q8WVM0	TFB1M_HUMAN			1	GTCCACCTTCGT	0.453	
+	12	3297	qqp.2_Missense_	NM_017519	NP_059989	Q8NFD5	ARI1B_HUMAN	ARID.		2	AATGAGCCAGAG	0.577	
+	12	3369	qqp.2_Missense_M	NM_017519	NP_059989	Q8NFD5	ARI1B_HUMAN	ARID.		2	GTCTGCCTGCC	0.577	
+	17	4152	.P1294S|ARID1B_	NM_017519	NP_059989	Q8NFD5	ARI1B_HUMAN			2	GCCCTCCCTCG	0.557	
+	20	5520	.R1750C|ARID1B_	NM_017519	NP_059989	Q8NFD5	ARI1B_HUMAN			2	TGGGGCGTGTG	0.498	
-	4	395	AC1_uc003qrb.2_	NM_032861	NP_116250	Q96JX3	SRAC1_HUMAN			0	TTTCTCCTTTGTC	0.328	
+	9	1226	10kjr.1_Splice_Site	NM_020823	NP_065874	Q9P2C4	TM181_HUMAN			3	TCCAGGTGAGC	0.607	
+	16	1776	_p.P443L|SYTL3_	NM_001009991	NP_001009991	Q4VX76	SYTL3_HUMAN	C2 2.		0	CTCTGCCAGACC	0.552	
+	6	795	fw.1_Missense_Mu	NM_005891	NP_005882	Q9BWD1	THIC_HUMAN			2	AGTTTCCTCGC	0.438	

+	17	1468	qsy.1_Missense_M	NM_173516	NP_775787	Q8NA58	PNDC1_HUMAN	lasmic (Potential).	0	CTGGGGTCAGC	0.453	
+	27	4010		NM_000876	NP_000867	P11717	MPRI_HUMAN	menal (Potential).	3	GGGAACCGCAG	0.428	
-	28	4591		NM_005577	NP_005568	P08519	APOA_HUMAN		6	TTCTTACCTTGTT	0.478	
+	3	1097	LL2_uc011egr.1_R	NM_031949	NP_114155	Q9BWV7	TTLL2_HUMAN	TTL.	3	GATGTGGACGAT	0.458	
+	2	263	IF25_uc003qwl.1_	NM_030615	NP_085118	Q9UIL4	KIF25_HUMAN	Kinesin-motor.	2	TCCCAGATGACA	0.582	
-	7	1280		NM_003247	NP_003238	P35442	TSP2_HUMAN		5	GCCTCACCTTGC	0.562	
-	10	1616	wy.2_Missense_Mutation_p.N239D|WDR27_uc003qwz			A2RRH5	WDR27_HUMAN		1	CAGGTTTGCCA	0.403	
+	3	297	ehf.1_Missense_Mu	NM_003194	NP_003185	P20226	TBP_HUMAN		1	CCATGACTCCCG	0.483	
+	7	1139	_p.L303F|TBP_uc	NM_003194	NP_003185	P20226	TBP_HUMAN	2	1	GTTCTCCTTATTT	0.333	
-	5	908	p.D244N|PDCD2_	NM_002598	NP_002589	Q16342	PDCD2_HUMAN		0	GAATATCCTTTTC	0.358	
+	2	1015		NM_020223	NP_064608	Q8IXL6	DMP4_HUMAN		0	GCGTGGGTAGGT	0.617	
-	5	564	se_Mutation_p.A1	NM_032350	NP_115726	Q9BRJ6	CG050_HUMAN		0	ATCAGGGCTTCC	0.677	
-	43	6079	m.1_Missense_Mu	NM_001080453	NP_001073922	Q8N201	INT1_HUMAN		0	AGGTCACTGTTG	0.622	
-	9	1342	p.P321L|TMEM18	NM_001097620	NP_001091089	Q6ZMB5	T184A_HUMAN		0	GCATGGGTGCCC	0.667	
-	13	1522	ksh.1_Missense_M	NM_001013836	NP_001013858	Q9Y6D9	MD1L1_HUMAN	eraction with NEK2.|Potenti	2	TCGCTGTCGTAG	0.657	
+	10	1522	.A480V|EIF3B_uc	NM_003751	NP_003742	P55884	EIF3B_HUMAN		0	TAATCGCCTTCTG	0.463	
+	3	555	_5'Flank|TTYH3_u	NM_025250	NP_079526	Q9C0H2	TTYH3_HUMAN	cellular (Potential).	0	GCTCCGCCACG	0.697	
+	13	1687	20_splice|TTYH3_u	NM_025250	NP_079526	Q9C0H2	TTYH3_HUMAN		0	CCCTCAGTAAGT	0.642	
-	16	2365		NM_032415	NP_115791	Q9BXL7	CAR11_HUMAN		50	CAGAGGTGACC	0.647	
-	6	1125		NM_032415	NP_115791	Q9BXL7	CAR11_HUMAN	Potential.	50	ATTCCTCCTCCA	0.483	
+	29	4519	e_Mutation_p.W73	NM_152744	NP_689957	Q7Z5N4	SDK1_HUMAN	onectin type-III 8.	6	GGCTGGGGGGA	0.642	
+	10	1302	.2_RNA|KIAA041	NM_014855	NP_055670	O43299	K0415_HUMAN		1	ATGCTGGCCTTT	0.572	
-	7	1828	_p.S57N|RADIL_u	NM_018059	NP_060529	Q96JH8	RADIL_HUMAN	Dilute.	7	TCCTCGCTGGCC	0.632	
-	25	7163		NM_001080495	NP_001073964	O15417	TNC18_HUMAN		0	GGGGATCCTGC	0.617	
-	17	2693	_p.P457S|RNF216	NM_207116	NP_996999	Q9NWF9	RN216_HUMAN	Pro-rich.	5	GTTGGGCAGAG	0.642	
-	5	484	MS2_uc010ktg.2_5	NM_000535	NP_000526	P54278	PMS2_HUMAN		2	GTCGAGTTCCAA	0.517	
-	4	356	0ktg.2_5'UTR|PM	NM_000535	NP_000526	P54278	PMS2_HUMAN		2	ATCTTAGATGTGT	0.383	
-	2	143	0ktg.2_5'UTR|PM	NM_000535	NP_000526	P54278	PMS2_HUMAN		2	TTCCGATCAATA	0.413	
+	13	2102	_p.A660V|USP42_	NM_032172	NP_115548	Q9H9J4	UBP42_HUMAN		5	ACGGTGCTAATA	0.572	
+	15	2572	vq.1_Missense_Mu	NM_032172	NP_115548	Q9H9J4	UBP42_HUMAN	Pro-rich.	5	CCCCCTGACCTG	0.706	
+	16	3950	.G1276D|USP42_	NM_032172	NP_115548	Q9H9J4	UBP42_HUMAN		5	AGGGTGGCTTTC	0.537	
-	2	863		NM_001037163	NP_001032240	Q7Z4H9	SIPAR_HUMAN		0	CCTCCTCCCAGC	0.622	
-	15	2065	e_Mutation_p.G50	NM_139179	NP_631918	Q8NCG7	DGLB_HUMAN	lasmic (Potential).	3	TTCGGACCTATG	0.567	
-	4	742	LB_uc003sqc.2_In	NM_139179	NP_631918	Q8NCG7	DGLB_HUMAN	lasmic (Potential).	3	CACACGCTTGTA	0.507	
+	4	1266	p.1_Missense_Mu	NM_019005	NP_061878	Q9NXC5	MIO_HUMAN		0	GTGCAACCTTGT	0.388	rs141631713
-	13	1317	e_Mutation_p.P41	NM_022307	NP_071682	Q05084	ICA69_HUMAN		1	GCCTTGGGGTCT	0.552	
+	9	2252	rz.2_Missense_Mu	NM_014660	NP_055475	O94880	PHF14_HUMAN		3	TGGATGGAAGGA	0.393	
+	16	3025	rz.2_Missense_Mu	NM_014660	NP_055475	O94880	PHF14_HUMAN		3	CCCAAGGCTGAA	0.383	
-	25	4936	7A_uc003ssd.3_M	NM_015204	NP_056019	Q9UPZ6	THS7A_HUMAN	cellular (Potential).	3	TGGTGGGTAATA	0.507	
-	2	832		NM_015204	NP_056019	Q9UPZ6	THS7A_HUMAN	(Potential).|TSP type-1 2.	3	TGCAATCTTGCT	0.567	
-	6	791_792		NM_001004320	NP_001004320	Q6ZNB7	ALKMO_HUMAN		0	GACCAAGGTTATT	0.307	
-	9	1250	MY2_uc010ktz.2_	NM_020319	NP_064715	Q8IV38	ANKY2_HUMAN	MYND-type.	1	AGTAAACCAGTG	0.358	
+	11	3047	HR_uc003stt.3_R	NM_001621	NP_001612	P35869	AHR_HUMAN		3	ACATATCCAGCT	0.353	
+	11	1669	e_Mutation_p.G4	NM_058176	NP_478056	Q9UKV0	HDAC9_HUMAN		5	AGTTGGGGCTG	0.542	
+	3	1042	GB8_uc003sut.2_	NM_002214	NP_002205	P26012	ITB8_HUMAN	cellular (Potential).	3	GAAAATGAAATT	0.358	
+	39	6440		NM_003777	NP_003768	Q96DT5	DYH11_HUMAN		15	GGAGGAGGAAG	0.517	
+	53	8646		NM_003777	NP_003768	Q96DT5	DYH11_HUMAN	4 (By similarity).	15	GCTTGTCCAGGC	0.582	

+	76	12358		NM_003777	NP_003768	Q96DT5	DYH11_HUMAN	6 (By similarity).	15	GGCTGGAGCCG	0.478	
-	17	1521	1jyl.1_Missense_M	NM_012294	NP_036426	Q92565	RPGF5_HUMAN		1	ACATAGGAGTGC	0.428	
+	7	1424	yw.1_RNA|NUPL2_	NM_007342	NP_031368	O15504	NUPL2_HUMAN	action with GLE1.	3	TCACACCCAGA	0.383	
+	7	1479	jyw.1_RNA|NUPL2	NM_007342	NP_031368	O15504	NUPL2_HUMAN	action with GLE1.	3	AATTTACTCTGG	0.333	
-	15	1908	swf.2_Missense_M	NM_006547	NP_006538	O00425	IF2B3_HUMAN	KH 4.	2	GGCAACCTAGA	0.388	
-	12	1644	swf.2_Missense_M	NM_006547	NP_006538	O00425	IF2B3_HUMAN	KH 3.	2	CTCTGGTGGTC	0.453	
-	1	1230		NR_002711					0	TCTCATCCCAATC	0.512	
+	4	631	r.3_Missense_Mut	NM_199136	NP_954587	A4D161	CG046_HUMAN		0	AAAACCAGTGG	0.493	
+	5	798	r.3_Intron|C7orf46_	NM_199136	NP_954587	A4D161	CG046_HUMAN		0	TTTCAAGCATCAT	0.348	
+	6	917	lice_Site_p.R182_	NM_199136	NP_954587	A4D161	CG046_HUMAN		0	GAAAGGGTAGGT	0.338	
-	10	1276	ation_p.V260I|OSB	NM_015550	NP_056365	Q9H4L5	OSBL3_HUMAN		1	CGGGACCTGAA	0.353	
+	5	472	utation_p.L121F|C	NM_007276	NP_009207	Q13185	CBX3_HUMAN	2; shadow subtype.	1	AGAGGTCTTGAT	0.358	
-	9	957	_p.E50K|SKAP2_u	NM_003930	NP_003921	O75563	SKAP2_HUMAN		1	CAGATTCCATATC	0.303	
-	1	465	syd.2_Intron|uc00	NM_005522	NP_005513	P49639	HXA1_HUMAN		3	ACTGGGGGTAC	0.577	
-	1	331		NM_006735	NP_006726	O43364	HXA2_HUMAN		2	ACTCAGCGAGC	0.473	
-	2	473	syn.1_5'Flank|uc0	NM_024014	NP_076919	P31267	HXA6_HUMAN	Homeobox.	2	GGCGGCCTCGG	0.662	
-	8	1099	_p.L253F|HIBADH_	NM_152740	NP_689953	P31937	3HIDH_HUMAN		2	GCCAAGAAGGA	0.502	
+	4	572	on_p.T28I|CREB5_	NM_182898	NP_878901	Q02930	CREB5_HUMAN		2	TCCGACCCCAA	0.527	
-	12	1404	_p.A429T|CPVL_u	NM_031311	NP_112601	Q9H3G5	CPVL_HUMAN		2	ACCAGCCACTTC	0.493	
+	9	1191	N2_uc010kvh.2_In	NM_004067	NP_004058	P52757	CHIO_HUMAN	ol-ester/DAG-type.	2	TTGAACGTACAC	0.418	rs140638672
+	6	1315		NM_001080529	NP_001073998	A6NGB9	WIPF3_HUMAN		1	TATAAACCATGCC	0.468	
+	1	317	c.1_Missense_Mu	NM_198098	NP_932766	P29972	AQP1_HUMAN	Cytoplasmic.	0	CAGCTGCCAGA	0.657	
-	7	1162	_p.M291I|PDE1C_	NM_005020	NP_005011	Q14123	PDE1C_HUMAN	ytic (By similarity).	4	AGCGTGCATTAA	0.458	
+	5	963	_p.S314F|FKBP9_	NM_007270	NP_009201	O95302	FKBP9_HUMAN		14	GCATTTCCATTG	0.468	
+	2	821		NM_030636	NP_085139	Q7L9B9	EEPD1_HUMAN	HhH.	0	CCGTGGCACGC	0.577	
+	2	1466		NM_030636	NP_085139	Q7L9B9	EEPD1_HUMAN		0	AGAAGGCCAAC	0.617	
+	3	653	.2_Missense_Mut	NM_018685	NP_061155	Q9NQW6	ANLN_HUMAN	tion.|Interaction with CD2AI	3	ACTTGCAGAGC	0.463	
+	6	1491	tfg.2_Splice_Site_	NM_018685	NP_061155	Q9NQW6	ANLN_HUMAN		3	AGCAGGTATGG	0.383	
-	12	1256	p.D221N|ELMO1_	NM_014800	NP_055615	Q92556	ELMO1_HUMAN		6	CTGGTCCTGGG	0.488	
+	6	683	_p.E179K|STARD3	NM_032016	NP_114405	O95772	MENTO_HUMAN	ic (Potential).|MENTAL.	1	CTCAAGAAGCA	0.473	
+	3	310	kxo.2_Missense_M	NM_007252	NP_009183	P78424	PO6F2_HUMAN		1	CCATTTCCAGTT	0.453	rs148094915
+	3	562		NM_005402	NP_005393	P11233	RALA_HUMAN		2	GGGAGGGGTTC	0.458	
+	13	1135	_p.V360I|C7orf10_	NM_024728	NP_079004	Q9HAC7	CG010_HUMAN		2	TTTCAGGTATTAC	0.393	
+	14	1247	rf10_uc003tho.1_	NM_024728	NP_079004	Q9HAC7	CG010_HUMAN		2	GCCGCCCCCGC	0.572	
-	10	1448	g.1_Missense_Mut	NM_000168	NP_000159	P10071	GLI3_HUMAN		19	CTGTTCCTGAA	0.483	
-	8	1146	g.1_Missense_Mut	NM_000168	NP_000159	P10071	GLI3_HUMAN		19	GCGCGGAAGAG	0.537	
-	2	1494	hx.3_Missense_M	NM_024054	NP_076959	Q9BPX7	CG025_HUMAN		1	GGCACGCTCAG	0.448	
-	2	826	hx.3_Missense_M	NM_024054	NP_076959	Q9BPX7	CG025_HUMAN		1	TTCCGGCCAATG	0.478	
-	4	937	kya.2_Missense_M	NM_006230	NP_006221	P49005	DPOD2_HUMAN		2	ACAGAGTGCCC	0.627	
-	4	494	TMED4_uc003tlk.2	NM_182547	NP_872353	Q7Z7H5	TMED4_HUMAN	enal (Potential).	0	CGCGGAGCTGTA	0.517	
+	18	2764	_Mutation_p.E504K	NM_031449	NP_113637	Q8NF64	ZMIZ2_HUMAN	Pro-rich.	5	GCCCCAGAACCA	0.652	
-	1	804		NM_033224	NP_150093	Q96QR8	PURB_HUMAN		0	CCCAGGCTTTG	0.557	
-	11	1601	sense_Mutation_p	NM_033054	NP_149043	B0I1T2	MYO1G_HUMAN	osin head-like.	4	CCAGGGTCTGC	0.657	
+	1	386	Y1_uc003tnd.2_5'	NM_021116	NP_066939	Q08828	ADCY1_HUMAN		6	GGTCGGCCAGC	0.522	
-	30	4834		NM_138295	NP_612152	Q8TDX9	PK1L1_HUMAN	ellular (Potential).	11	GAAATGCCCTTG	0.393	
+	14	1832	yr.2_Missense_M	NM_152701	NP_689914	Q86UQ4	ABCAD_HUMAN		10	GCTGATCCCTCT	0.453	
-	12	1323	zb.2_Missense_Mu	NM_005311	NP_005302	Q13322	GRB10_HUMAN		6	CGAGGGAGTTC	0.547	

-	10	2032	p.3_Missense_Mu	NM_015198	NP_056013	O75128	COBL_HUMAN		5	ATGTTAGATAAG	0.502
+	6	929	e_Mutation_p.P22	NM_005228	NP_005219	P00533	EGFR_HUMAN	.|ExtracellulV30_R297>G(	9571	GTCCCCCAGTG	0.622
-	5	1707		NM_033273	NP_150376	Q96JC4	ZN479_HUMAN	2H2-type 11.	4	TAAGGGTTGAG	0.403
+	4	1013		NM_001159279	NP_001152751				2	AAGAATGTGGC	0.423
+	5	1442		NM_153363	NP_699194	Q8IYX0	ZN679_HUMAN	2H2-type 9.	1	AAGTGGTCCTC	0.383
+	9	719	.2_Missense_Mut	NM_000048	NP_000039	P04424	ARLY_HUMAN		2	TGGGGCCATTG	0.512
+	11	3143	.G783D|POM121	NM_172020	NP_742017	Q96HA1	P121A_HUMAN	side (Potential).	0	CTTCGGCGCTC	0.652
+	3	200	CF1B_uc011ker.1	NM_000265	NP_000256				0	ACCAGGGCACA	0.632
-	7	1595		NM_032408	NP_115784	Q9UIG0	BAZ1B_HUMAN	Lys-rich.	7	CTGTGGATTTC	0.458
-	7	503	sense_Mutation_	NM_004603	NP_004594	Q16623	STX1A_HUMAN	lasmic (Potential).	0	TCGTGGTCCTG	0.597
+	3	482	an.2_Missense_M	NM_003388	NP_003379	Q9UDT6	CLIP2_HUMAN		3	ACCCTCCTCCT	0.677
+	21	2605	uap.2_Missense_	NM_016328	NP_057412	Q9UHL9	GT2D1_HUMAN	TF2I-like 4.	4	GTAACCCCGGC	0.622
+	4	926	p.W242*|TRIM74_	NM_198924	NP_944606	Q86UV6	TRI74_HUMAN		0	ATCTGGGTGAG	0.627
+	9	914	_Mutation_p.P177	NM_000941	NP_000932	P16435	NCPR_HUMAN		1	CCAGCCCCTTT	0.582
+	1	307	_p.L28M|UPK3B_	NM_030570	NP_085047	Q9BT76	UPK3B_HUMAN		1	TGAGCCTGGGT	0.697
+	3	976	_p.M222I|UPK3B_	NM_030570	NP_085047	Q9BT76	UPK3B_HUMAN	ical; (Potential).	1	ACCATGCGCTT	0.627
-	17	3193	p.G966D|MAGI2_	NM_012301	NP_036433	Q86UL8	MAGI2_HUMAN	PDZ 5.	11	ACTGGCCATTC	0.502
+	5	830	gt.1_Missense_Mu	NM_002069	NP_002060	P63096	GNAI1_HUMAN		3	CTCAACCAAAT	0.308
-	15	2121	gw.1_Missense_	NM_006379	NP_006370	Q99985	SEM3C_HUMAN		1	CACAGGCTGTA	0.498
-	20	15077	ht.1_Missense_Mu	NM_033026	NP_149015	Q9Y6V0	PCLO_HUMAN		7	ACTTGGTTGAAT	0.488
-	6	11192	p.A3635T|PCLO_	NM_033026	NP_149015	Q9Y6V0	PCLO_HUMAN		7	TAAGGCTTTGC	0.493
-	16	2202		NM_012431	NP_036563	O15041	SEM3E_HUMAN		3	ATCCCCTACAA	0.353
+	17	2424	e_Mutation_p.P61	NM_001142327	NP_001135799	Q9Y222	DMTF1_HUMAN	similarity).|Required for trar	2	TCGTTCCTTCA	0.328
-	3	424		NM_024315	NP_077291	Q9BU79	CG023_HUMAN	ical; (Potential).	0	ATACTACTCAAA	0.373
-	3	342		NM_024315	NP_077291	Q9BU79	CG023_HUMAN		0	GTTACCTGTAT	0.378
+	11	1231	iu.2_Missense_Mu	NM_021151	NP_066974	Q9UKG9	OCTC_HUMAN		3	ATGCTCCTTTTG	0.303
-	10	1371	hc.1_Missense_M	NM_000927	NP_000918	P08183	MDR1_HUMAN	smembrane type-1 1.	7	AGGTGGTCCCA	0.388
-	4	524	khc.1_Missense_	NM_000927	NP_000918	P08183	MDR1_HUMAN	lasmic (Potential).	7	AAATACACTGA	0.274
+	3	748	F4_uc003ujg.1_5'	NM_006716	NP_006707	Q9UBU7	DBF4A_HUMAN	BRCT 1.	2	GCAAAGATATC	0.264
+	4	417	jl.1_Missense_Mu	NM_021723	NP_068369	Q9P0K1	ADA22_HUMAN		8	TGTCCTCTGAAT	0.348
+	22	1935	jm.2_Missense_M	NM_021723	NP_068369	Q9P0K1	ADA22_HUMAN	xtracellular (Potential).	8	TCGATGGTGAAA	0.373
-	6	554	_p.A153T|SRI_uc0	NM_003130	NP_003121	P30626	SORCN_HUMAN	EF-hand 4.	1	TAAGAGCCCTCA	0.443
+	9	1114	kg.2_Intron|C7orf6	NM_001039706	NP_001034795	A5D8W1	CG063_HUMAN		1	TAGGGCTTTGA	0.194
+	10	1126	o.1_Missense_Mu	NM_033107	NP_149098	A4D1E9	GTPBA_HUMAN		0	ATGCACTTCATA	0.368
+	5	1091	_p.I152N|CLDN12	NM_012129	NP_036261	P56749	CLD12_HUMAN	ical; (Potential).	0	CATCTATCTGGG	0.478
+	17	4840	lf.2_Missense_Mu	NM_005751	NP_005742	Q99996	AKAP9_HUMAN		26	GATATACCAGAAT	0.318
+	21	5453	.A1743V|AKAP9_	NM_005751	NP_005742	Q99996	AKAP9_HUMAN		26	AACAGCAGCTG	0.388
+	23	5900	.S1892F|AKAP9_	NM_005751	NP_005742	Q99996	AKAP9_HUMAN	ential.|Glu-rich.	26	AGAGTCCCTTA	0.468
+	48	11681	.G3442E|AKAP9_	NM_005751	NP_005742	Q99996	AKAP9_HUMAN		26	TGGTGGGCTGG	0.348
-	5	572	e_Mutation_p.A15	NM_000466	NP_000457	O43933	PEX1_HUMAN		2	ATTAGTGCAACT	0.388
-	3	4535	g.2_Nonsense_M	NM_017654	NP_060124	Q5K651	SAMD9_HUMAN		7	AAAACTGATAAG	0.383
-	3	2663	mg.2_Missense_M	NM_017654	NP_060124	Q5K651	SAMD9_HUMAN		7	TTGTTCTTCAA	0.353
-	5	4374	D9L_uc003umk.1	NM_152703	NP_689916	Q8IVG5	SAM9L_HUMAN		4	ACAGAGTGTCT	0.373
+	18	1722	_p.D502N|CCDC1	NM_017667	NP_060137	Q96JG6	CC132_HUMAN		0	ACAAAGATGAA	0.368
+	20	1942	_p.P575L|CCDC1	NM_017667	NP_060137	Q96JG6	CC132_HUMAN		0	ATGCACCTATCT	0.313
-	9	904	ALCR_uc003umu	NM_001742	NP_001733	P30988	CALCR_HUMAN	Name=2; (Potential).	9	GGTTACCCTTT	0.393
-	2	245	T1_uc003une.3_R	NM_005868	NP_005859	O15155	BET1_HUMAN	l).|t-SNARE coiled-coil hon	0	TCTTCACAGGCA	0.378

+	14	1157	1A2_uc011kib.1_I	NM_000089	NP_000080	P08123	CO1A2_HUMAN		9	CCCTGGCCCAG	0.398
-	4	341	ih.1_Missense_Mu	NM_000446	NP_000437	P27169	PON1_HUMAN		1	TCCAGGACTGTT	0.378
+	1	187	unx.2_Splice_Site_	NM_016116	NP_057200	Q9Y574	ASB4_HUMAN		1	ACAAGGTAAAA	0.308
+	11	3037		NM_014916	NP_055731	Q8IWU2	LMTK2_HUMAN		16	TGTAGGGAGTA	0.532
+	11	3087		NM_014916	NP_055731	Q8IWU2	LMTK2_HUMAN		16	TTTCGGAAGAC	0.473
-	23	3276		NM_015395	NP_056210	Q7Z6L1	TCPR1_HUMAN	TECPR 7.	1	ACCAGCAGTCA	0.637
-	11	1640	ph.1_Missense_M	NM_015395	NP_056210	Q7Z6L1	TCPR1_HUMAN		1	GGGGGCCGGGC	0.692
+	20	2619	p.D804N|TRRAP_	NM_003496	NP_003487	Q9Y4A5	TRRAP_HUMAN		37	TGAAGGACCTC	0.587
+	24	3499	.A1097V|TRRAP_	NM_003496	NP_003487	Q9Y4A5	TRRAP_HUMAN		37	CAATTGCTATTT	0.478
+	49	7411	p.T2383I|TRRAP_	NM_003496	NP_003487	Q9Y4A5	TRRAP_HUMAN		37	TGATGACTTACA	0.363
+	69	10972	.P3559L|TRRAP_	NM_003496	NP_003487	Q9Y4A5	TRRAP_HUMAN	PI3K/PI4K.	37	ACAACCCCTCTT	0.617
-	12	1645	p.G416D|SMURF	NM_020429	NP_065162	Q9HCE7	SMUF1_HUMAN	HECT.	4	CCACACCACCG	0.483
-	11	1455	_p.V353I|SMURF	NM_020429	NP_065162	Q9HCE7	SMUF1_HUMAN		4	TCTGGACTAGAT	0.562
-	5	712	p.G131D|SMURF	NM_020429	NP_065162	Q9HCE7	SMUF1_HUMAN		4	TCTGGCCACGA	0.433
+	5	565	upy.1_Missense_M	NM_006409	NP_006400	Q92747	ARC1A_HUMAN	WD 3.	1	AAAAGCCGATTC	0.478
+	7	932	upy.1_Missense_	NM_006409	NP_006400	Q92747	ARC1A_HUMAN	WD 5.	1	CGTGGCTGCTG	0.493
-	3	679	iw.1_Missense_Mu	NM_015545	NP_056360	O75127	PTCD1_HUMAN	PPR 2.	1	GCCCGCAGCCC	0.423
+	3	289	se_Mutation_p.E2	NM_213603	NP_998768	Q5FWF6	ZN789_HUMAN	KRAB.	0	GAGAGGAGTGG	0.453
-	12	1366	YP3A5_uc011kiy.	NM_000777	NP_000768	P20815	CP3A5_HUMAN		0	AGGATCTATGCT	0.383
-	8	863	_Mutation_p.S146	NM_000777	NP_000768	P20815	CP3A5_HUMAN		0	GGCGACTTTTC	0.308
-	6	595	3A5_uc003urs.2_I	NM_000765	NP_000756	P24462	CP3A7_HUMAN		1	CTCTGCTTCCC	0.512
+	5	510	utation_p.A136V|	NM_057095	NP_476436	Q9HB55	CP343_HUMAN		2	TCCAGCTTTCA	0.348
+	7	633	G177E|CYP3A43_	NM_057095	NP_476436	Q9HB55	CP343_HUMAN		2	CTTTGGGGCCT	0.403
-	1	125		NM_181538	NP_853516	Q8NFK1	CXG3_HUMAN	ical; (Potential).	1	AGACTCCAGGC	0.667
-	1	88		NM_181538	NP_853516	Q8NFK1	CXG3_HUMAN	ical; (Potential).	1	GAATCCCAGGA	0.657
-	2	381		NM_001185	NP_001176	P25311	ZA2G_HUMAN		2	ACTGACCGTTA	0.522
+	6	1187	_p.T287I|ZKSCAN	NM_003439	NP_003430	P17029	ZKSC1_HUMAN		3	GAAAACCAGGA	0.488
-	6	1114	|AP4M1_uc010lgl	NM_005916	NP_005907	P33993	MCM7_HUMAN		0	CAGAGGCATGA	0.507
+	2	284	M1_uc003utc.3_M	NM_004722	NP_004713	O00189	AP4M1_HUMAN		0	GTGGCGGCCGG	0.701
+	5	560	nse_Mutation_p.D	NM_004722	NP_004713	O00189	AP4M1_HUMAN		0	ACTAGGACTAT	0.433
-	3	754	96T|STAG3_uc01	NM_152742	NP_689955	Q8N158	GPC2_HUMAN		2	TGAGGCCAAGC	0.627
+	19	2086	S_uc003uty.3_RN	NM_012447	NP_036579	Q9UJ98	STAG3_HUMAN		8	TGAGGCTGGGG	0.577
+	30	3400	.3_Intron|GATS_u	NM_012447	NP_036579	Q9UJ98	STAG3_HUMAN		8	GCCTGCCAAGC	0.577
+	1	897	.1_5'Flank|ZCWP	NM_019606	NP_062552	Q7L2J0	MEPCE_HUMAN		1	GGAAGCGGCAT	0.592
-	2	1512	p.G14R|TSC22D4_	NM_030935	NP_112197	Q9Y3Q8	T22D4_HUMAN		2	CTGCCCCATCT	0.507
+	6	939	GFG2_uc010lgy.2_	NM_006076	NP_006067	O95081	AGFG2_HUMAN		1	CAGTGGCCCCA	0.493
-	2	316	H4_uc003uvi.2_	NM_002319	NP_002310	O75427	LRCH4_HUMAN	LRR 2.	2	GCTGGCACGCC	0.637
-	5	703	FR2_uc003uvu.1_	NM_003227	NP_003218	Q9UP52	TFR2_HUMAN	ellular (Potential).	2	GCTCTCCGACC	0.582
-	7	1565		NM_022574	NP_072096	O75420	PERQ1_HUMAN		2	CCTTGGGCCAG	0.552
+	14	3143	AN_uc003uwl.2_	NM_003386	NP_003377	Q9Y493	ZAN_HUMAN	ate) (mucin-like domain).|E	11	CATTCCCACAG	0.567
+	9	1331	_Mutation_p.A133	NM_020246	NP_064631	Q9BXP2	S12A9_HUMAN	ical; (Potential).	0	TGGGCAGCTGTA	0.592
+	3	4558	C17_uc010lho.1_	NM_001040105	NP_001035194	Q685J3	MUC17_HUMAN	ch.|59 X approximate tand	27	AGGTACCAGCA	0.468
+	3	6355	C17_uc010lho.1_	NM_001040105	NP_001035194	Q685J3	MUC17_HUMAN	X approximate tandem re	27	AGGAAGTCCTC	0.507
+	3	8110	C17_uc010lho.1_	NM_001040105	NP_001035194	Q685J3	MUC17_HUMAN	X approximate tandem re	27	CTCAACTCCTG	0.483
+	3	8427	C17_uc010lho.1_	NM_001040105	NP_001035194	Q685J3	MUC17_HUMAN	ch.|59 X approximate tand	27	TCCTCTCCTACA	0.512
+	3	8779	C17_uc010lho.1_	NM_001040105	NP_001035194	Q685J3	MUC17_HUMAN	X approximate tandem re	27	GTTCTTCTCCTA	0.507
+	9	13102	C17_uc010lho.1_	NM_001040105	NP_001035194	Q685J3	MUC17_HUMAN	ellular (Potential).	27	TGTCTCCAAGA	0.572

+	3	1961	M56_uc003uxr.2_Ir	NM_030961	NP_112223	Q9BRZ2	TRI56_HUMAN		3	CAACGGCGAAG	0.721	
-	11	1633	D3_uc010lhs.2_5'	NM_001084	NP_001075	O60568	PLOD3_HUMAN		2	GTCGGCGTCCA	0.657	
+	4	785	HIT1_uc003uyf.2_F	NM_006349	NP_006340	O43257	ZNHI1_HUMAN		1	CCGAGGGCCCTA	0.672	
+	17	2100	_uc011kkn.1_Intror	NM_181552	NP_853530	P39880	CUX1_HUMAN		8	AAACTGGTACAG	0.433	
+	3	460	H4_uc003uzm.2_	NM_152892	NP_690852	Q9UFC0	LRWD1_HUMAN	LRR 4.	1	GTCAATGACAAC	0.567	
-	11	1386	_uc003var.2_RNA|	NM_145032	NP_659469	Q8NEE6	FXL13_HUMAN	LRR 4.	0	CCATTCCCCAAG	0.473	
-	20	3245	og.3_RNA|DPY19L	NR_003561					0	AGACAGCTTGAC	0.388	
+	3	327	_p.E6K|PMPCB_	NM_004279	NP_004270	O75439	MPPB_HUMAN		4	ACAATGGAACAG	0.328	
-	18	2047	C26A5_uc003vbw.	NM_198999	NP_945350	P58743	S26A5_HUMAN	nic (Potential).|STAS.	1	TTGGTAGCATCC	0.393	
-	5	707	z.2_Missense_Mut	NM_005045	NP_005036	P78509	RELN_HUMAN	Reelin.	19	CTGTTGGAGCTG	0.368	
-	10	1069	lp.1_Missense_Mu	NM_002553	NP_002544	O43913	ORC5_HUMAN		0	TTGCTGGATTGT	0.323	
+	1	504	vcf.2_Missense_M	NM_199000	NP_945351	Q86UP9	LHPL3_HUMAN	ical; (Potential).	0	GCTTTACCCTCTT	0.577	
+	16	2408	e_Mutation_p.A62	NM_182931	NP_891847	Q8IZD2	MLL5_HUMAN		3	GTGATGCTGAAG	0.294	
+	27	5458	LL5_uc010ljf.1_Int	NM_182931	NP_891847	Q8IZD2	MLL5_HUMAN	Pro-rich.	3	CTTGTACAACAG	0.542	
-	5	805	y.2_Missense_Mut	NM_019042	NP_061915	Q96PZ0	PUS7_HUMAN		1	CGATAACCTATTA	0.358	
-	4	742	.2_Missense_Mut	NM_019042	NP_061915	Q96PZ0	PUS7_HUMAN		1	GCTTTTCTTCAG	0.333	
-	2	173	do.2_Missense_M	NM_006754	NP_006745	Q16563	SYPL1_HUMAN	c (Potential).|MARVEL.	0	TGGCTCCTTGA	0.498	
+	2	795	_p.P237L|PIK3CG_	NM_002649	NP_002640	P48736	PK3CG_HUMAN		38	CTCACCCGACG	0.532	
+	2	1400	_p.P439S|PIK3CG_	NM_002649	NP_002640	P48736	PK3CG_HUMAN		38	AAGCTCCAGCA	0.512	
-	4	943	_p.A140T|COG5_u	NM_181733	NP_859422	Q9UP83	COG5_HUMAN		4	GTAAAGCCCCAA	0.328	
+	6	784	DUS4L_uc011klx.1	NM_181581	NP_853559	O95620	DUS4L_HUMAN		0	GAAACCCCTGGA	0.348	
+	5	757		NM_000441	NP_000432	O43511	S26A4_HUMAN	cellular (Potential).	7	AGACACTGCAG	0.428	
+	6	838		NM_000441	NP_000432	O43511	S26A4_HUMAN	ical; (Potential).	7	TGGTGGCTTGC	0.403	
+	6	952	_p.P87S|CBLL1_u	NM_024814	NP_079090	Q75N03	HAKAI_HUMAN	Pro-rich.	5	CATCCTCCTATTG	0.458	
+	6	1423	_p.P244S|CBLL1_	NM_024814	NP_079090	Q75N03	HAKAI_HUMAN	Pro-rich.	5	GGTACTCCTCAC	0.527	
-	10	1407	ves.2_Missense_M	NM_000111	NP_000102	P40879	S26A3_HUMAN		4	CTGATCTGGAG	0.478	
-	4	549	ves.2_Missense_	NM_000111	NP_000102	P40879	S26A3_HUMAN	ical; (Potential).	4	ATTATGGCTGGG	0.433	
-	12	1765	ex.2_Missense_M	NM_002291	NP_002282	P07942	LAMB1_HUMAN	ninin EGF-like 4.	8	CAGTGACCTGTC	0.483	
-	25	3785	_p.P1234L|LAMB4	NM_007356	NP_031382	A4D0S4	LAMB4_HUMAN	Domain II.	8	AAAACAGGATGT	0.408	
-	3	905	fl.2_Missense_Mu	NM_001130475	NP_001123947	Q7Z6K1	THAP5_HUMAN		0	AGAATGGATTTTC	0.323	
+	3	642		NM_012328	NP_036460	Q9UBS3	DNJB9_HUMAN		0	AGGATGGTGGTT	0.348	
+	4	2517	LRRN3_uc003vfu.	NM_001099660	NP_001093130	Q9H3W5	LRRN3_HUMAN	Potential).|Ig-like C2-type.	8	AAAGAAGGGGG	0.408	
-	48	5443	vfw.2_Missense_M	NM_014705	NP_055520	Q8N1I0	DOCK4_HUMAN	Ser-rich.	4	AGATGGCACTG	0.468	
-	46	5279	K4_uc003vfw.2_M	NM_014705	NP_055520	Q8N1I0	DOCK4_HUMAN	Ser-rich.	4	TACCTGCATGTTA	0.403	
-	25	2886	_p.E314K|DOCK4_	NM_014705	NP_055520	Q8N1I0	DOCK4_HUMAN		4	TTCCTCCAGCA	0.403	
-	8	970	ce_Site|DOCK4_u	NM_014705	NP_055520	Q8N1I0	DOCK4_HUMAN		4	CAGGTACCTGAT	0.423	
+	8	1187	e_Mutation_p.W2	NM_001007245	NP_001007246	O00458	IFRD1_HUMAN		2	GCATGGACACT	0.348	
-	5	572	l.3_Missense_Mut	NM_012252	NP_036384	O14948	TFEC_HUMAN	Basic motif.	1	TAGTGTCAGTTT	0.318	
-	3	707	ja.2_Missense_Mu	NM_003391	NP_003382	P09544	WNT2_HUMAN		7	TCACAGGAACAG	0.483	rs148782147
+	21	3521	q.1_Missense_Mu	NM_000492	NP_000483	P13569	CFTR_HUMAN	ntial).|ABC transmembrane	5	GAGTTGGTATTA	0.383	
-	4	914		NM_033427	NP_219499	Q8WZ74	CTTB2_HUMAN	Potential.	5	TTTGCTGTCACT	0.478	
+	5	783		NM_019644	NP_062618	Q92527	ANKR7_HUMAN	ANK 5.	0	GAACCACCATGT	0.368	
+	1	1174		NM_012281	NP_036413	Q9NZV8	KCND2_HUMAN	lasmic (Potential).	5	GCAGTTCTGAGA	0.527	
+	1	1321		NM_012281	NP_036413	Q9NZV8	KCND2_HUMAN	lasmic (Potential).	5	AAGAACTGGCCT	0.572	
+	8	820	2_Missense_Muta	NM_019071	NP_061944	Q9NXR8	ING3_HUMAN		1	GGCAGCTGCTC	0.423	
+	23	3497		NM_024913	NP_079189	A4D0V7	CG058_HUMAN		9	TCTCAGCAGGA	0.458	
+	12	5109	.2_Intron|PTPRZ1	NM_002851	NP_002842	P23471	PTPRZ_HUMAN	cellular (Potential).	9	TTTGCAGACACT	0.453	

+	12	5142	.2_Intron|PTPRZ1_	NM_002851	NP_002842	P23471	PTPRZ_HUMAN	cellular (Potential).	9	TCCTGGCAGCA	0.458
+	24	6517	p.S1174F|PTPRZ1	NM_002851	NP_002842	P23471	PTPRZ_HUMAN	).|Tyrosine-protein phospha	9	ACTATTCTGCAG	0.338
-	18	2224	b.2_Missense_Mu	NM_005763	NP_005754	Q9UDR5	AASS_HUMAN	pine dehydrogenase.	2	AAATCTCAGCAT	0.428
-	4	1281	ense_Mutation_p.	NM_001024613	NP_001019784	A0PJY2	FEZF1_HUMAN	C2H2-type 6.	3	CGTGGGGCAGG	0.567
-	1	566		NM_016945	NP_058641	Q9NYV7	T2R16_HUMAN	cellular (Potential).	2	TTGTCAGTTACA	0.398
-	12	2666	JB_uc003vko.2_M	NM_178827	NP_849149	Q8NA54	IQUB_HUMAN		4	CCATGACCAGAT	0.473
-	6	1533	.2_RNA|IQUB_uc0	NM_178827	NP_849149	Q8NA54	IQUB_HUMAN		4	TTATCAGTCATAT	0.328
+	2	1302		NM_207163	NP_997046	Q6P5Q4	LMOD2_HUMAN		0	GCAAAGAGGAA	0.488
+	4	769	PAM1_uc003vlf.3_	NM_153189	NP_694859	P38567	HYALP_HUMAN		4	AAGACCATCTG	0.393
+	5	1421	PAM1_uc003vlf.3_	NM_153189	NP_694859	P38567	HYALP_HUMAN		4	ATGGGGAACCC	0.318
-	8	935	T1_uc003vll.2_RN	NM_015450	NP_056265	Q9NUX5	POTE1_HUMAN		1	AGGGGCTCCCA	0.428
-	1	699	RM8_uc003vlt.2_M	NM_000845	NP_000836	O00222	GRM8_HUMAN	cellular (Potential).	23	TCACATCCGAAG	0.512
-	5	2205	vly.1_Missense_M	NM_176814	NP_789784	Q2TB10	ZN800_HUMAN		1	CTTCAGGTGAATT	0.393
-	4	690	g.1_Missense_Mu	NM_006193	NP_006184	O43316	PAX4_HUMAN	Homeobox.	1	GTGGCCGGTCC	0.582
+	15	1820	e.2_Missense_Mut	NM_014390	NP_055205	Q7KZF4	SND1_HUMAN	TNase-like 4.	3	GTGGTGGAATAC	0.438
-	17	1959	_p.P157L|RBM28_	NM_018077	NP_060547	Q9NW13	RBM28_HUMAN		2	TTGCAGGCTCT	0.512
-	5	455	p.D192N|IMPDH1_	NM_001142573	NP_001136045	P20839	IMDH1_HUMAN	CBS 1.	4	AGGGTCCGTGA	0.602
+	4	589	_p.G146E|CALU_u	NM_001130674	NP_001124146	O43852	CALU_HUMAN		0	ATGATGGATTTA	0.388
-	2	516		NM_001708	NP_001699	P03999	OPSB_HUMAN	Name=4; (Potential).	0	CGGCTCCAGCC	0.542
+	10	1803	a.3_Missense_Mu	NM_001458	NP_001449	Q14315	FLNC_HUMAN	Filamin 3.	12	ATGGTGTGTTC	0.617
+	13	2272	a.3_Missense_Mu	NM_001458	NP_001449	Q14315	FLNC_HUMAN	Filamin 5.	12	GCCCGCTGAGT	0.602
+	18	2901	a.3_Missense_Mu	NM_001458	NP_001449	Q14315	FLNC_HUMAN	Filamin 7.	12	GAGCCGGCAAG	0.592
+	44	7566	a.3_Missense_Mut	NM_001458	NP_001449	Q14315	FLNC_HUMAN	Interaction with INPPL1.	12	TGGAGGAGTGC	0.667
+	3	461	_p.P114S|IRF5_uc	NM_002200	NP_002191	Q13568	IRF5_HUMAN	phan pentad repeat.	0	CCTCAGCCCTAC	0.637
-	1	378	n_p.E2K|TNPO3_	NM_012470	NP_036602	Q9Y5L0	TNPO3_HUMAN		5	TCCTTCCATGG	0.617
+	11	2148	s.2_Missense_Mu	NM_005631	NP_005622	Q99835	SMO_HUMAN	lasmic (Potential).	37	TGTCACCAAGA	0.557
+	16	1883	7_splice|AHCYL2_	NM_015328	NP_056143	Q96HN2	SAHH3_HUMAN		2	TACAGGTGCCTT	0.507
-	10	1510	_p.Q339*|ZC3HC1	NM_016478	NP_057562	Q86WB0	NIPA_HUMAN		0	CCACTGCCGAA	0.398
+	9	1204	_p.P328S|KLHDC1	NM_014997	NP_055812	Q6PID8	KLD10_HUMAN	Kelch 5.	0	AGCTCCCAGCT	0.398
-	5	664	p.V181M|TMEM20	NM_032842	NP_116231	Q96SK2	TM209_HUMAN	Ser-rich.	3	GGTCACTCCAG	0.458
+	5	496	_p.G117E|CPA4_u	NM_016352	NP_057436	Q9UI42	CBPA4_HUMAN		1	AGATTGGACATT	0.517
+	6	758	_Mutation_p.T141	NM_001868	NP_001859	P15085	CBPA1_HUMAN		1	CTTCACGCACA	0.562
-	2	615	_p.A129V|PLXNA4_	NM_020911	NP_065962	Q9HCM2	PLXA4_HUMAN	lar (Potential).|Sema.	1	CACAGGCAATC	0.542
+	10	1252		NM_020299	NP_064695	O60218	AK1BA_HUMAN		5	ACTATCCCTTCA	0.393
+	6	804	kps.1_Missense_	NM_001080538	NP_001074007	C9JRZ8	AK1BF_HUMAN		1	TGGATGCCTGG	0.423
+	3	671	n_p.Q44*|BPGM_	NM_199186	NP_954655	P07738	PMGE_HUMAN		0	GGAAGCAACTC	0.478
-	11	2181	pz.1_Missense_M	NM_001008225	NP_001008226	O95628	CNOT4_HUMAN		0	GCTGGGGGGTC	0.537
-	15	2392	e_Mutation_p.A56	NM_012450	NP_036582	Q9UKG4	S13A4_HUMAN		0	CGATGGCATTA	0.557
-	4	690	ZP6_uc010lmv.2_	NM_145808	NP_665807	Q538Z0	LUZP6_HUMAN		0	TGATTGCCTGGT	0.512
-	13	1361	u.2_Missense_Mut	NM_004717	NP_004708	O75912	DGKI_HUMAN	DAGKc.	3	AGGAGGCTGAG	0.542
+	6	730	1D1_uc011kqf.1_	NM_005989	NP_005980	P51857	AK1D1_HUMAN	NADP.	1	ATAGCCCTTTGG	0.418
-	12	1482	p.G415E|ATP6V0	NM_130841	NP_570856	Q9HBG4	VPP4_HUMAN	ical; (Potential).	1	CGGTTCCATGA	0.547
-	10	1133	p.V299M|ATP6V0	NM_130841	NP_570856	Q9HBG4	VPP4_HUMAN	lasmic (Potential).	1	CTGCACCTTGAT	0.537
-	2	875	_p.G226S|KIAA15	NM_020910	NP_065961	Q9HCM3	K1549_HUMAN		230	CACACCCTCTG	0.502
-	3	858	vup.2_Missense_	NM_020119	NP_064504	Q7Z2W4	ZCCHV_HUMAN	C3H1-type 3.	1	GCCGACCCTCT	0.483
+	15	3605		NM_173569	NP_775840	Q6ZU65	UBN2_HUMAN	Ser-rich.	2	CAAACCATTGT	0.483
+	2	409	7orf55_uc003vuw.	NM_016019	NP_057103	Q9Y383	LC7L2_HUMAN		0	CATGAGCTTCAT	0.498

+	9	1264	.R363Q|LUC7L2_	NM_016019	NP_057103	Q9Y383	LC7L2_HUMAN	Arg/Ser-rich.	0	ATCTCGGGAGA	0.552
-	17	2292	M1D_uc010lng.2_	NM_030647	NP_085150	Q6ZMT4	KDM7_HUMAN		1	GAGTTTCTTTCA	0.458
-	11	1343	M1D_uc010lng.2_	NM_030647	NP_085150	Q6ZMT4	KDM7_HUMAN		1	ATACAAGCTGTAT	0.294
-	17	2117		NM_004333	NP_004324	P15056	BRAF_HUMAN	rotein kinase.	18290	CTTTTGGACAGT	0.403
-	15	1860		NM_004333	NP_004324	P15056	BRAF_HUMAN	rotein kinas_R603>I(2)|p.T	18290	GATTTCACTGTAC	0.368
-	13	1752		NM_004333	NP_004324	P15056	BRAF_HUMAN	rotein kinase.	18290	ACTCCATGCCCT	0.373
-	2	188	vwe.3_Missense_	NM_016071	NP_057155	Q9Y291	RT33_HUMAN		0	GAGACATGCGG	0.443
+	2	884	852_uc010lnn.2_F	NM_001105558	NP_001099028	P0C1S8	WEE2_HUMAN		2	TTCACTCCAGAG	0.428
+	6	1311	852_uc010lnn.2_I	NM_001105558	NP_001099028	P0C1S8	WEE2_HUMAN	rotein kinase.	2	CTATATCTGAAA	0.383
+	10	1827	52_uc010lnn.2_In	NM_001105558	NP_001099028	P0C1S8	WEE2_HUMAN	rotein kinase.	2	ACAGAGACCTT	0.458
+	1	670		NM_016944	NP_058640	Q9NYW5	TA2R4_HUMAN	lasmic (Potential).	0	CGGAAGCTCAT	0.443
-	1	395	11krl.1_Missense_	NM_001008270	NP_001008271	A4D1T9	PRS37_HUMAN		1	AGGACACCCAAA	0.478
+	48	5617		NM_004668	NP_004659	O43451	MGA_HUMAN	enal (Potential).	2	TGGATAAGCACT	0.333
+	2	237	.2_Intron|uc003wa	NR_001296					0	GGCTCCCTCATC	0.567
+	3	427	10loj.1_Intron|uc0	NR_001296					0	CTCCACACCTG	0.542
+	18	3481	bt.2_Nonsense_M	NM_004445	NP_004436	O15197	EPHB6_HUMAN	Potential).|Protein kinase.	19	ACTTGGCAGAA	0.587
-	7	1070	_p.S71F|TRPV6_	NM_018646	NP_061116	Q9H1D0	TRPV6_HUMAN	lasmic (Potential).	2	CTGAGGAGTCG	0.562
+	1	105		NM_178829	NP_849151	Q96L11	CG034_HUMAN		0	AGTGGGTGGGC	0.647
+	1	386		NM_001001667	NP_001001667	Q8N148	OR6V1_HUMAN	lasmic (Potential).	1	ACTGCGCTATG	0.592
+	1	733		NM_001001667	NP_001001667	Q8N148	OR6V1_HUMAN	Name=6; (Potential).	1	TCACACTGGTC	0.547
+	1	433		NM_176881	NP_795362	P59534	T2R39_HUMAN	lasmic (Potential).	1	TCCTACCCCCTT	0.408
+	1	856		NM_176882	NP_795363	P59535	T2R40_HUMAN	Name=7; (Potential).	1	ATCATGGCTGCC	0.463
+	8	719	cj.2_Missense_M	NM_015917	NP_057001	Q9Y2Q3	GSTK1_HUMAN		0	CAGGAGAGAAG	0.488
+	13	1535	tc.1_Missense_M	NM_000083	NP_000074	P35523	CLCN1_HUMAN	electivity filter part_3 (By s	5	CGGAGGCTTCA	0.512
-	4	1953	nse_Mutation_p.A	NM_014690	NP_055505	Q86XD5	F131B_HUMAN		0	GTGGGCCACCC	0.587
+	8	1539	_p.A462T|ZYX_uc	NM_001010972	NP_001010972	Q15942	ZYX_HUMAN	zinc-binding 2.	0	GCAAGGCCTAT	0.667
+	7	2476	.1_Intron|uc011kt	NM_001130025	NP_001123497	A6NFQ2	F115C_HUMAN		0	TCAGGCCCACG	0.602
-	2	194	M115A_uc003wd	NM_014719	NP_055534	Q9Y4C2	F115A_HUMAN		0	TTCGGGTACAT	0.512
+	1	472		NM_001004685	NP_001004685	O95006	OR2F2_HUMAN	Name=4; (Potential).	4	CTCTTGTGCAG	0.532
+	1	942		NM_012369	NP_036501	Q13607	OR2F1_HUMAN	lasmic (Potential).	3	AGGGGGCCTGG	0.423
+	14	4754	3wem.2_Splice_Si	NM_005435	NP_005426	Q12774	ARHG5_HUMAN		2	TGACGGTAAGC	0.483
+	2	474	tart_Site|CUL1_u	NM_003592	NP_003583	Q13616	CUL1_HUMAN		1	AACTAGCTGTAC	0.433
+	4	939	_p.A138V|CUL1_u	NM_003592	NP_003583	Q13616	CUL1_HUMAN		1	TTTGTGCCTACC	0.363
-	13	1697	p.D516N|EZH2_u	NM_004456	NP_004447	Q15910	EZH2_HUMAN		183	GCTAACCCTTTTT	0.363
-	2	170	nse_Mutation_p.G	NM_004456	NP_004447	Q15910	EZH2_HUMAN	MT1, DNMT3A and DNMT	183	TCTGGCCCATGA	0.423
-	4	954		NM_001001661	NP_001001661	Q6IV72	ZN425_HUMAN	2H2-type 3.	3	TGTAGACACAGG	0.662
-	3	321		NM_001001661	NP_001001661	Q6IV72	ZN425_HUMAN		3	GAGGGCTAGTT	0.363
-	2	182		NM_001001661	NP_001001661	Q6IV72	ZN425_HUMAN	KRAB.	3	TCATCTCTTGCT	0.433
+	2	417	NF398_uc011kum.	NM_170686	NP_733787	Q8TD17	ZN398_HUMAN		1	TGGTGGCCGCC	0.592
-	5	1415		NM_015694	NP_056509	Q9ULD5	ZN777_HUMAN	Glu-rich.	1	CTCTGGCTCCT	0.622
+	6	1368	62_uc003wgm.2_	NM_001099220	NP_001092690	O60290	ZN862_HUMAN	KRAB 2.	1	CCCTGGATCAA	0.562
+	3	1547_1548	3743_uc003whg.2_	NM_173680	NP_775951	Q96BV0	ZN775_HUMAN	2H2-type 10.	0	CCCTACCCGTGC	0.703
+	3	998		NM_175571	NP_783161	Q8ND71	GIMA8_HUMAN		7	AGAGGGAGACA	0.373
+	3	414	IMAP4_uc011kuv.	NM_018326	NP_060796	Q9NUV9	GIMA4_HUMAN		1	GACCTCCCCAG	0.507
+	3	427	hp.2_Missense_M	NM_130759	NP_570115	Q8WWP7	GIMA1_HUMAN	lasmic (Potential).	3	CCCACGCGCTG	0.622
+	16	2131	y.1_Missense_Mu	NM_000603	NP_000594	P29474	NOS3_HUMAN	avodoxin-like.	8	GATCCGCTTCAA	0.607
+	3	1135	N3_uc003wip.2_	NM_004769	NP_004760	Q9UHC3	ACCN3_HUMAN	ellular (Potential).	2	CTTGGGGGTGT	0.617

+	4	551	_p.P90S|SLC4A2_	NM_003040	NP_003031	P04920	B3A2_HUMAN	ic (Potential).|Pro-rich.	0	AGACACCCCAG	0.677
+	7	1104	p.G274E|SLC4A2_	NM_003040	NP_003031	P04920	B3A2_HUMAN	ic (Potential).|Pro-rich.	0	TCCTGGGGTGC	0.672
-	3	437	jo.1_Missense_Mu	NM_007189	NP_009120	Q9UG63	ABCF2_HUMAN	C transporter 1.	1	CCTGAGTTTAAT	0.488
-	5	600	p.P154S|SMARCD	NM_001003801	NP_001003801	Q6STE5	SMRD3_HUMAN		2	CGCAGGGTTAA	0.577
-	3	601		NM_005614	NP_005605	Q15382	RHEB_HUMAN		2	CTTGCCCGGCT	0.363
-	47	12358	vkx.2_Splice_Site_	NM_170606	NP_733751	Q8NEZ4	MLL3_HUMAN		63	TTCTTACTTTTCC	0.398
-	36	5659	z.2_Missense_Mu	NM_170606	NP_733751	Q8NEZ4	MLL3_HUMAN		63	GCCAGGCTGAG	0.408
-	32	5012	kz.2_Splice_Site_	NM_170606	NP_733751	Q8NEZ4	MLL3_HUMAN		63	TTGTACCTGGC	0.353
+	14	1547	n.2_Missense_Mu	NM_130797	NP_570629	P42658	DPP6_HUMAN	ellular (Potential).	4	CAGCAGCAACG	0.562
+	3	744	.1_Intron|INSIG1_	NM_005542	NP_005533	O15503	INSI1_HUMAN	enal (Potential).	0	CGCCAGTGCTG	0.418
+	5	900	me.2_Missense_M	NM_053043	NP_444271	Q96EV2	RBM33_HUMAN	Glu-rich.	1	TGTTAGACATC	0.433
+	3	1235		NM_138400	NP_612409	Q5C9Z4	NOM1_HUMAN	MIF4G.	0	GGGTGCCTGCG	0.547
+	5	1648	1_uc010lqp.1_5'F	NM_138400	NP_612409	Q5C9Z4	NOM1_HUMAN		0	TTGAAGATTCG	0.463
+	13	2059	ng.2_Missense_M	NM_014671	NP_055486	Q15386	UBE3C_HUMAN		5	GTTACTACTAGC	0.363
+	22	3313	ni.3_Missense_Mu	NM_014671	NP_055486	Q15386	UBE3C_HUMAN	HECT.	5	TTGTGGAAGGG	0.438
-	14	1719	CAPG2_uc011kw	NM_017760	NP_060230	Q86XI2	CNDG2_HUMAN		3	AGGAAAGAATTA	0.547
+	6	1252	ov.2_Missense_M	NM_173539	NP_775810	Q8TC21	ZN596_HUMAN	C2H2-type 5.	0	TCTTACCTTAGA	0.398
+	16	1910	3wpt.2_Missense_	NM_014629	NP_055444	O15013	ARHGA_HUMAN	DH.	1	TAGCAGAGAAG	0.483
+	17	2036	_p.D582N|ARHGE	NM_014629	NP_055444	O15013	ARHGA_HUMAN		1	CGATCAGATGAT	0.433
+	5	665	M2_uc011kwi.1_I	NM_003970	NP_003961	P54296	MYOM2_HUMAN	-like C2-type 1.	6	CTTCACCGTGC	0.557
+	34	4103	kwi.1_Splice_Site	NM_003970	NP_003961	P54296	MYOM2_HUMAN		6	TCACAGCTTTT	0.348
-	57	9160	p.P2253S|CSMD1	NM_033225	NP_150094	Q96PZ7	CSMD1_HUMAN	r (Potential).|Sushi 22.	25	TCCCCGGATCAC	0.478
-	24	4138	p.A642T|CSMD1_	NM_033225	NP_150094	Q96PZ7	CSMD1_HUMAN	ar (Potential).|Sushi 7.	25	CATGGCGTACC	0.522
-	4	812		NM_033225	NP_150094	Q96PZ7	CSMD1_HUMAN	ellular (Potential).	25	TGGCTAGGTAAA	0.383
+	8	1572	_p.A502T|MCPH1_	NM_024596	NP_078872	Q8NEM0	MCPH1_HUMAN		2	CTTCTGCCCCT	0.498
-	5	3142		NM_001080826	NP_001074295	Q86YV5	SG223_HUMAN	rotein kinase.	0	GCAGTCCTGCT	0.627
-	2	1169		NM_001080826	NP_001074295	Q86YV5	SG223_HUMAN		0	TCAGCCCAAGG	0.652
+	25	3634	w.1_Missense_Mu	NM_003747	NP_003738	O95271	TNKS1_HUMAN	ARP catalytic.	7	TGGGGCCGGG	0.408
-	4	5201		NM_178857	NP_849188	Q8IWN7	RP1L1_HUMAN		8	GCAGGGACAGA	0.662
-	4	3632		NM_178857	NP_849188	Q8IWN7	RP1L1_HUMAN		8	GGCAGGAGACC	0.582
+	7	1422	p.Q235*|MTMR9_	NM_015458	NP_056273	Q96QG7	MTMR9_HUMAN	ularin phosphatase.	0	CACTCCAGGTG	0.483
+	1	624		NM_054028	NP_473369	Q96KT7	AMCL2_HUMAN	.|Helical; (Potential).	0	TCCTAGGACTAA	0.582
-	2	742	3wtw.2_Missense_	NM_053279	NP_444509	Q96KS9	F167A_HUMAN		0	TGCGGGTCTCC	0.682
+	2	670	K_uc003wtz.2_Int	NM_001715	NP_001706	P51451	BLK_HUMAN		3	CAGCGCCCAAG	0.473
+	6	1641	_p.P157S|GATA4_	NM_002052	NP_002043	P43694	GATA4_HUMAN		1	ATGCGTCCCATC	0.642
+	1	231	M|FDFT1_uc011k	NM_004462	NP_004453	P37268	FDFT_HUMAN		0	GGAAGGTGATG	0.701
-	1	1454	.1_Intron|FAM66D	NM_201402	NP_958804	Q6R6M4	U17L2_HUMAN		3	GCAGGGAGCTT	0.512
+	9	1159	Mutation_p.V317	NM_006765	NP_006756	Q13454	TUSC3_HUMAN	ical; (Potential).	3	GCCTAGTGGGA	0.328
+	11	1187		NM_181723	NP_859074	Q86XE3	EFHA2_HUMAN		1	AAATGGAATGA	0.284
+	8	1394	ye.1_Missense_	NM_001008539	NP_001008539	P52569	CTR2_HUMAN	ellular (Potential).	3	TGAAGGCGCTT	0.502
+	4	767		NM_006207	NP_006198	Q15198	PGFRL_HUMAN		0	TGCAACCTCATT	0.567
-	4	2774	0lsy.2_RNA|MTUS	NM_001001924	NP_001001924	Q9ULD2	MTUS1_HUMAN		2	TCAAGGATGTA	0.443
+	7	1323	yg.2_Missense_Mu	NM_006197	NP_006188	Q15154	PCM1_HUMAN	Potential.	36	GGCAGGCTGC	0.403
+	12	2217	yj.3_Missense_Mu	NM_006197	NP_006188	Q15154	PCM1_HUMAN		36	ATGCCTCCTTCT	0.353
-	10	1029	AH1_uc003wyn.2_	NM_177924	NP_808592	Q13510	ASAH1_HUMAN		0	AGAATCCATTC	0.418
+	2	559		NM_000015	NP_000006	P11245	ARY2_HUMAN		2	TTTTCTGCTTGA	0.443
-	3	1424	g.1_Missense_Mu	NM_021020	NP_066300	Q9Y250	LZTS1_HUMAN		1	GGGCGCCCTCC	0.647

-	4	706	wzz.1_Missense_	NM_003974	NP_003965	O60496	DOK2_HUMAN	RS-type PTB.	0	CTTGTCCCGCC	0.502
+	8	693	.G130D|EPB49_u	NM_001114136	NP_001107608	Q08495	DEMA_HUMAN		1	GGGAGGCAGCC	0.612
-	8	2752	.2_Missense_Mut	NM_005144	NP_005135	O43593	HAIR_HUMAN		2	CCCGGGCATCA	0.627
-	3	1726	.2_Missense_Mut	NM_005144	NP_005135	O43593	HAIR_HUMAN		2	TGGCTCCACTG	0.652
+	5	465	e_Mutation_p.D12	NM_001722	NP_001713	P05423	RPC4_HUMAN		0	CAGTGGATGTG	0.463
+	9	1371	xbt.2_Nonsense_	NM_005605	NP_005596	P48454	PP2BC_HUMAN		1	ACATGGTCTTT	0.408
+	14	1475	RBS3_uc003xbw.	NM_005775	NP_005766	O60504	VINEX_HUMAN		0	GGGAAGAGAAG	0.627
-	1	491	_5'Flank|EGR3_u	NM_004430	NP_004421	Q06889	EGR3_HUMAN		0	GTAATGGACTAC	0.373
+	7	2171	|RHOBTB2_uc011	NM_015178	NP_055993	Q9BYZ6	RHBT2_HUMAN	BTB 2.	2	TCCCTACACAA	0.547
+	3	1103	HMP7_uc003xdd.	NM_152272	NP_689485	Q8WUX9	CHMP7_HUMAN		0	TGTCGCTGTGG	0.532
-	13	2552	XL2_uc010lty.1_In	NM_002318	NP_002309	Q9Y4K0	LOXL2_HUMAN	yl-oxidase like.	3	GGTGGCCGTCA	0.557
-	2	439		NM_002318	NP_002309	Q9Y4K0	LOXL2_HUMAN		3	CTCGGGGTAAT	0.642
+	4	1043	10ltz.2_RNA|SLC	NM_016612	NP_057696	Q9NYZ2	MFRN1_HUMAN	Solcar 3.	0	TGGCCGGCTACT	0.587
+	21	2323	AM28_uc010lua.2	NM_014265	NP_055080	Q9UKQ2	ADA28_HUMAN	lasmic (Potential).	5	AGCCTCTTTTG	0.408
-	3	1412		NM_006158	NP_006149	P07196	NFL_HUMAN	ail, subdomain A.	2	AGGAGCGGGT	0.577
+	14	1567	se_Mutation_p.G	NM_024940	NP_079216	Q9H7D0	DOCK5_HUMAN	DHR-1.	3	GGAGGGCAAGC	0.478
+	6	898	PP2R2A_uc011laf.	NM_002717	NP_002708	P63151	2ABA_HUMAN	WD 3.	2	ATTTGCGGATTA	0.353
-	3	1464		NM_007257	NP_009188	Q9UL42	PNMA2_HUMAN		0	caaacactcttctacac	0
+	5	867	e_Mutation_p.R17	NM_001386	NP_001377	Q16555	DPYL2_HUMAN		1	AAGATCGCTTC	0.453
+	12	1686	SL2_uc010luk.1_	NM_001386	NP_001377	Q16555	DPYL2_HUMAN		1	TGGTGGTCATC	0.552
+	13	1963	SL2_uc010luk.1_	NM_001386	NP_001377	Q16555	DPYL2_HUMAN		1	AGTCTGGATTCA	0.607
-	3	468	U_uc003xfy.1_Mi	NM_203339	NP_976084	P10909	CLUS_HUMAN		2	GGCGGCCAACC	0.562
+	3	340	xgb.1_Missense_	NM_016240	NP_057324	Q6AZY7	SCAR3_HUMAN	type II membrane protein;	4	TCCTGGTGGCC	0.647
+	3	271	SCO2_uc003xgh.2	NM_001017420	NP_001017420	Q56NI9	ESCO2_HUMAN		1	AAACAACTGAAA	0.353
-	3	461	gr.2_Missense_M	NM_018660	NP_061130	Q9H8N7	ZN395_HUMAN		0	CTCTGCCAGCC	0.667
+	5	969	.2_Nonsense_Mu	NM_017412	NP_059108	Q9NPG1	FZD3_HUMAN	ellular (Potential).	2	TTTTTGGTGTCC	0.448
-	13	1648	se_Mutation_p.T4	NM_018250	NP_060720	Q9NV88	INT9_HUMAN		2	GCCGGGTGTCG	0.512
-	2	302	M66_uc003xhu.2_	NM_016127	NP_057211	Q96BY9	TMM66_HUMAN		0	ATCCCGCAGCA	0.478
+	5	927	.1_RNA|RBPMS_	NM_006867	NP_006858	Q93062	RBPMS_HUMAN	RRM.	1	TTCGATCCTGAA	0.448
-	1	79	c.1_Missense_M	NM_031271	NP_112561	Q9BXT5	TEX15_HUMAN		7	CATTAAGACCAC	0.368
-	1	806	RG_uc003xim.1_	NM_013357	NP_037489	Q9UJV8	PURG_HUMAN	By similarity.	0	CCCCTCTGGGA	0.448
+	7	578	8024_uc010lvx.1_	NM_007175	NP_009106	O94905	ERLN2_HUMAN	enal (Potential).	0	AACAGGACCTG	0.493
+	9	1464	vy.2_Nonsense_M	NM_032777	NP_116166	Q96PE1	GP124_HUMAN	ellular (Potential).	5	AGGTGGCCCCG	0.662
+	19	3154	lvy.2_Missense_M	NM_032777	NP_116166	Q96PE1	GP124_HUMAN	Name=5; (Potential).	5	TACATCCCTGTG	0.612
-	4	1686	FIP1_uc003xkl.1_	NM_001002814	NP_001002814	Q6WKZ4	RFIP1_HUMAN		3	TTGCGCCTCTG	0.498
+	10	1147	u.3_Nonsense_M	NM_004674	NP_004665	Q9UBL3	ASH2L_HUMAN	B30.2/SPRY.	2	TGCTGGGCAGG	0.488
+	5	1576	z.1_Missense_Mu	NM_004874	NP_004865	O95429	BAG4_HUMAN	BAG.	1	GCCAGGACTCT	0.403
-	4	356	xlg.3_Missense_	NM_001102559	NP_001096029	Q8NEB5	PPC1B_HUMAN	ase sequence motif I.	0	ACCTCCCTACG	0.493
-	17	3598	p.A1027V|WHSC1	NM_023034	NP_075447	Q9BZ95	NSD3_HUMAN		1	CTTCAGCAAAG	0.443
-	16	2920	e_Mutation_p.G5	NM_023110	NP_075598	P11362	FGFR1_HUMAN	Potential).|Protein kinase.	15	TCGGCCCTGAA	0.602
-	1	341		NR_003129					0	GGCGGGGTGG	0.567
+	1	194		NM_153692	NP_710159	P83105	HTRA4_HUMAN		0	CCGTCCTCTGG	0.706
+	7	1235		NM_153692	NP_710159	P83105	HTRA4_HUMAN		0	GAAAGGCGTTT	0.423
+	11	1170	1_Intron|ADAM32_	NM_145004	NP_659441	Q8TC27	ADA32_HUMAN	B.|Extracellular (Potential).	3	CCAAGGAGATA	0.318
+	4	1273		NM_178819	NP_848934	Q86UL3	GPAT4_HUMAN		0	TTCGAGCTCTCT	0.448
+	4	718	P3M2_uc003xoq.1	NM_001134296	NP_001127768	P53677	AP3M2_HUMAN		0	GAACGGTTGTC	0.463
-	4	369	t.2_Intron|PLAT_u	NM_000930	NP_000921	P00750	TPA_HUMAN	ronectin type-I.	2	ATGACTGATGTT	0.483

-	7	1463	xpe.2_Missense_	NM_006749	NP_006740	Q08357	S20A2_HUMAN	lasmic (Potential).	2	TTTCGTCAGATA	0.423	
+	5	1111		NM_000749	NP_000740	Q05901	ACHB3_HUMAN	lasmic (Potential).	1	CACGTACCACC	0.453	
-	7	1235	nse_Mutation_p.T	NM_001160223	NP_001153695	Q96K19	RN170_HUMAN		0	TTTGGGTTATC	0.353	
+	9	1081	TA_uc003xpu.2_M	NM_002027	NP_002018	P49354	FNTA_HUMAN		1	TCCTAGCTAAA	0.308	
+	13	1915	A0146_uc003xqf.2	NM_001080394	NP_001073863	Q14159	K0146_HUMAN		0	TTAAGAGACATT	0.418	
+	15	2140	186T|KIAA0146_	NM_001080394	NP_001073863	Q14159	K0146_HUMAN		0	TGGAGGCACTC	0.607	
+	16	2233	qf.2_RNA|KIAA01	NM_001080394	NP_001073863	Q14159	K0146_HUMAN		0	TCTTGCTTCAG	0.517	
+	16	2321	qf.2_RNA|KIAA01	NM_001080394	NP_001073863	Q14159	K0146_HUMAN		0	TGCAACACCTG	0.468	
-	85	11990	_Mutation_p.G39	NM_006904	NP_008835	P78527	PRKDC_HUMAN	PI3K/PI4K.	34	TAAGGCCCGTT	0.493	
-	6	613	_p.P186S|PRKDC_	NM_006904	NP_008835	P78527	PRKDC_HUMAN		34	ACTAGGATGAA	0.353	
-	15	4291	rf.3_Missense_M	NM_014781	NP_055596	Q8TDY2	RBCC1_HUMAN	Potential.	11	TAGGGCAGTCT	0.338	
-	8	815	_p.M168I|LYPLA1_	NM_006330	NP_006321	O75608	LYPA1_HUMAN		1	ACTGTGCATCAT	0.388	
-	5	435	_p.D76N|LYPLA1_	NM_006330	NP_006321	O75608	LYPA1_HUMAN		1	TGAATCTGGTG	0.294	
+	3	472		NM_014175	NP_054894	Q9P015	RM15_HUMAN		0	ATTATGGTGTC	0.343	
+	4	494		NM_014175	NP_054894	Q9P015	RM15_HUMAN		0	TCAGGGTGCTG	0.378	
+	4	4992	1_uc011ldy.1_Intr	NM_006269	NP_006260	P56715	RP1_HUMAN		12	CAGTGGCGAAC	0.393	
+	3	623	1_uc010lyh.2_5'	NM_024831	NP_079107	Q96RS0	TGS1_HUMAN		3	CAAAGGCATAG	0.418	
-	3	1944	lyi.2_Missense_M	NM_001114635	NP_001108107	Q6DJT9	PLAG1_HUMAN	lack of NLS and KPNA2 in	129	GAAAAGCTTGA	0.433	
-	3	1502	lyi.2_Missense_M	NM_001114635	NP_001108107	Q6DJT9	PLAG1_HUMAN	tion.|Repression domain; c	129	TTAATGGCTGTT	0.428	
-	4	1126	_p.A163V|SDR16	NM_138969	NP_620419	Q8N3Y7	RDHE2_HUMAN		3	TCATAGCAGGT	0.328	
-	2	892	_p.R85Q|SDR16	NM_138969	NP_620419	Q8N3Y7	RDHE2_HUMAN		3	CTTCCCGAGCC	0.502	rs141509977
-	4	990		NM_017813	NP_060283	Q9NX62	IMPA3_HUMAN		1	TTGGGGTCTTC	0.458	
-	2	160		NM_000780	NP_000771	P22680	CP7A1_HUMAN		1	TAGAGGTGGTT	0.413	
-	27	2449	e.1_Missense_M	NM_003580	NP_003571	Q92636	FAN_HUMAN		1	GGCATCTCTGC	0.418	
-	6	889		NM_003878	NP_003869	Q92820	GGH_HUMAN		0	TGATACCTTCA	0.343	
-	4	643		NM_003878	NP_003869	Q92820	GGH_HUMAN		0	TATTTACCTGTAT	0.368	
+	5	1875	p.R464H|YTHDF3	NM_152758	NP_689971	Q7Z739	YTHD3_HUMAN	YTH.	0	ATATTCGCTTAG	0.393	
+	6	866	JC5B_uc003xvt.1_	NM_033105	NP_149096	Q9UF47	DNJ5B_HUMAN		0	AGGATCTCGAA	0.428	
+	2	500	xvw.2_Missense_	NM_184085	NP_908973	Q9BYV6	TRI55_HUMAN		5	ATGGGGTATAT	0.502	
-	1	1247	_5'Flank|C8orf44_	NM_025054	NP_079330	Q96JH7	VCIP1_HUMAN	OTU.	8	CTTCTCTGCAG	0.458	
+	9	1115	SPP1_uc003xxj.2_	NM_001077204	NP_001070672	Q1MSJ5	CSPP1_HUMAN		5	AATATGCCTCCT	0.348	
+	15	1772	PP1_uc003xxj.2_	NM_001077204	NP_001070672	Q1MSJ5	CSPP1_HUMAN		5	CTGCAGCTTAT	0.284	
+	31	3695	_p.E1187K|CSPP1	NM_001077204	NP_001070672	Q1MSJ5	CSPP1_HUMAN		5	CTTCAGAAACG	0.532	
-	31	4838	p.A937V|ARFGEF	NM_006421	NP_006412	Q9Y6D6	BIG1_HUMAN		8	GCTGAGCAAAA	0.378	
-	31	4790	_p.T921I|ARFGEF	NM_006421	NP_006412	Q9Y6D6	BIG1_HUMAN		8	TACTGAGTGAAT	0.393	
-	11	2027	EF1_uc003xxl.1_	NM_006421	NP_006412	Q9Y6D6	BIG1_HUMAN		8	CCATCCATTTGT	0.289	
-	10	1371	A6_uc003xxr.3_Int	NM_020361	NP_065094	Q8N4T0	CBPA6_HUMAN		2	TTGTGGAGGCT	0.413	
+	5	742	ion_p.V9I|SULF1_	NM_015170	NP_055985	Q8IWU6	SULF1_HUMAN		7	CTCTGGTTTTG	0.483	
+	8	1382	_p.A222V|SULF1_	NM_015170	NP_055985	Q8IWU6	SULF1_HUMAN		7	CCACGCTGCGC	0.483	
-	6	2316	CO5A1_uc003xyk	NM_030958	NP_112220	Q9H2Y9	SO5A1_HUMAN	ellular (Potential).	4	TATAAGGGATGT	0.443	
-	2	656		NM_024504	NP_078780	Q9GZV8	PRD14_HUMAN		3	GGGCGGTGGA	0.577	
-	2	636		NM_024504	NP_078780	Q9GZV8	PRD14_HUMAN		3	CAGGTCCACAA	0.587	
-	7	919	yp.2_Missense_M	NM_016027	NP_057111	Q53H82	LACB2_HUMAN		1	TGTTGCTAACT	0.294	
+	5	1390	_p.P286S|XKR9_u	NM_001011720	NP_001011720	Q5GH70	XKR9_HUMAN		2	AGTGTCCAATG	0.323	
-	16	1950	.G482R|EYA1_uc	NM_172058	NP_742055	Q99502	EYA1_HUMAN		5	CATCTCCTATAA	0.343	
-	7	1111		NM_007332	NP_015628	O75762	TRPA1_HUMAN	ytoplasmic (Potential).	6	TGAAGCATGGT	0.423	
-	7	996		NM_007332	NP_015628	O75762	TRPA1_HUMAN	nic (Potential).|ANK 7.	6	TGGCTGTGCAC	0.398	

+	2	820		NM_004770	NP_004761	Q92953	KCNB2_HUMAN	lasmic (Potential).	7	GTGTGCGACGAC	0.522	
-	4	381	zh.1_Missense_Mu	NM_000971	NP_000962	P18124	RL7_HUMAN		0	AAGGTTCCATTG	0.428	
-	5	432	lfi.1_Missense_Mu	NM_014393	NP_055208	Q9NUL3	STAU2_HUMAN	DRBM 1.	0	TATTGGCAACAG	0.443	
+	2	362	yac.2_Missense_M	NM_017866	NP_060336	Q9BUB7	TMM70_HUMAN		1	AAGATGGAAGGC	0.358	
+	2	2144	au.1_Missense_Mu	NM_024721	NP_078997	Q86UP3	ZFHX4_HUMAN		15	GTTCAGCCACTC	0.587	
+	10	4865	.S1538F|ZFHX4_	NM_024721	NP_078997	Q86UP3	ZFHX4_HUMAN		15	ATCCATCTCGTC	0.388	
+	10	8090	p.T2613I|ZFHX4_	NM_024721	NP_078997	Q86UP3	ZFHX4_HUMAN	Homeobox 3.	15	CGATCACCCCGG	0.423	
-	6	1008		NM_001033723	NP_001028895	Q6ZNC4	ZN704_HUMAN		0	GACTGGGAAGGT	0.537	rs147777181
-	7	1142		NM_018440	NP_060910	Q9NWQ8	PAG1_HUMAN	lasmic (Potential).	0	AGCATGGTATCC	0.592	
-	2	109	P12_uc003ycg.3_	NM_001105281	NP_001098751	A6NFH5	FBP12_HUMAN		0	GTTTTGCCAAAC	0.368	
-	1	52		NM_001010893	NP_001010893	Q5PT55	NTCP5_HUMAN		0	TTGCTTCTTCTAT	0.299	
-	7	651	ce_Site_p.V151_s	NM_001738	NP_001729	P00915	CAH1_HUMAN		2	ACCAACCTGGAG	0.333	
+	10	1404	nai.2_Missense_M	NM_007013	NP_008944	Q9H0M0	WWP1_HUMAN	WW 1.	2	GAACTACCACATG	0.318	
-	10	1149	naj.2_Missense_M	NM_019098	NP_061971	Q9NQW8	CNGB3_HUMAN	Name=H4; (Potential).	3	ACACAGGCATTA	0.378	
-	1	1100		NM_152418	NP_689631	Q8NA75	DC4L2_HUMAN	WD 2.	1	GCAGTCCTGGC	0.562	
-	1	988		NM_152418	NP_689631	Q8NA75	DC4L2_HUMAN	WD 1.	1	CAAGTCCCACAG	0.498	
-	2	481	yec.2_Missense_M	NM_005941	NP_005932	P51512	MMP16_HUMAN		8	GGTCTCTGCAG	0.458	
-	1	326		NM_018710	NP_061180	Q8N4L2	TM55A_HUMAN		0	CTCTGGGGCTGC	0.562	
+	6	861	ense_Mutation_p.	NM_052832	NP_439897	Q8TE54	S26A7_HUMAN	cellular (Potential).	2	TCACAAGTCAAA	0.438	
-	10	1528	_p.E455K|RUNX1T	NM_175634	NP_783552	Q06455	MTG8_HUMAN		16	CCCTCTCTGTTG	0.622	
-	10	1495	_p.A444T|RUNX1	NM_175634	NP_783552	Q06455	MTG8_HUMAN		16	GCTCCGCCTCAG	0.627	
-	3	2229		NM_203390	NP_976324	Q8IXT5	RB12B_HUMAN		0	TCCTCTGGGGGC	0.627	
-	3	1466		NM_203390	NP_976324	Q8IXT5	RB12B_HUMAN	RRM 3.	0	CAGCAAGAAGAA	0.373	
+	13	1423	naw.2_Missense_M	NM_153704	NP_714915	Q5HYA8	MKS3_HUMAN		2	GTGGACGAGAAA	0.348	rs75165625
+	13	1450	naw.2_Missense_M	NM_153704	NP_714915	Q5HYA8	MKS3_HUMAN		2	AGCCAAGAGTAA	0.368	
-	13	3080	_Mutation_p.G10	NM_015496	NP_056311	Q69YN4	VIR_HUMAN		2	ATCCACCTCTCA	0.458	
-	5	464	ygp.2_Missense_M	NM_015496	NP_056311	Q69YN4	VIR_HUMAN	Pro-rich.	2	GTTGTGGCTGG	0.299	
+	9	1184	q.1_RNA|INTS8_u	NM_017864	NP_060334	Q75QN2	INT8_HUMAN	TPR 2.	0	CCTTGAGTTTAC	0.333	
-	6	947	.S169N|MTERFD	NM_015942	NP_057026	Q96E29	MTER1_HUMAN		1	TCCAGACTTCCA	0.373	
+	8	1574		NM_016134	NP_057218	Q9Y646	PGCP_HUMAN		1	ATGCTGCCTAGG	0.438	
-	3	267		NM_005836	NP_005827	P52758	UK114_HUMAN		1	TAAGAGCCTGT	0.333	
+	8	1166	_p.A356T|POP1_u	NM_001145860	NP_001139332	Q99575	POP1_HUMAN		2	AAATCAGCTGTC	0.363	
-	4	439	.E128K|STK3_uc	NM_006281	NP_006272	Q13188	STK3_HUMAN	rotein kinase.	4	AGTACTCCATAA	0.303	
+	25	3952	yiu.1_Missense_M	NM_017890	NP_060360	Q7Z7G8	VP13B_HUMAN		20	GCAGCCCATCT	0.443	
+	57	11087	iw.2_Missense_M	NM_017890	NP_060360	Q7Z7G8	VP13B_HUMAN		20	TGGCAGCCCTG	0.557	
+	57	11188	iw.2_Missense_M	NM_017890	NP_060360	Q7Z7G8	VP13B_HUMAN		20	GTGGCGTCTCC	0.542	
-	9	1650	.1_Nonsense_Mu	NM_015668	NP_056483	Q8NE09	RGS22_HUMAN		7	TTCATTCCACTG	0.308	
-	2	2005	_p.T397I|FBXO43_	NM_001029860	NP_001025031	Q4G163	FBX43_HUMAN		2	CTAAAGGTCAAAT	0.438	
-	11	2322	yjk.1_Missense_M	NM_015435	NP_056250	Q9NV58	RN19A_HUMAN	action with CASR.	4	TCCCTGCTGTTG	0.458	
-	7	1466	se_Mutation_p.T2	NM_002568	NP_002559	P11940	PABP1_HUMAN	RRM 4.	0	GCACTAGTGATT	0.294	
-	3	459	ykb.2_Missense_M	NM_001042510	NP_001035975	Q9Y5V0	ZN706_HUMAN		2	TTTTTGGCATTTT	0.413	
+	2	524	_p.G65D|GRHL2_	NM_024915	NP_079191	Q6ISB3	GRHL2_HUMAN	cription activation.	3	CCCTCGGCCTGC	0.527	
-	2	724	yki.2_Missense_M	NM_032041	NP_114430	P61601	NCALD_HUMAN	nd 3.|2 (Potential).	0	TCTCTGCCTTGC	0.488	
-	5	726	109I|RRM2B_uc0	NM_015713	NP_056528	Q7LG56	RIR2B_HUMAN		2	GGCATGGTTTCA	0.274	rs72554098
-	52	7396	_Mutation_p.E245	NM_015902	NP_056986	O95071	UBR5_HUMAN		28	CATTTTCCCTAA	0.328	
-	40	5630	s.1_Missense_Mut	NM_015902	NP_056986	O95071	UBR5_HUMAN		28	GATGTCCAGGA	0.458	
-	16	2029	s.1_Missense_Mu	NM_015902	NP_056986	O95071	UBR5_HUMAN		28	CAACAGGAACAT	0.398	

+	2	366	03yla.2_Missense_	NM_001695	NP_001686	P21283	VATC1_HUMAN		0	AATATTCCTGACT	0.428
+	5	1764	n.1_Missense_Mut	NM_003506	NP_003497	O60353	FZD6_HUMAN	Name=7; (Potential).	2	TCTGGGTTGGA	0.353
-	2	556	5A32_uc011lhr.1_	NM_030780	NP_110407	Q9H2D1	MFTC_HUMAN	Solcar 1.	1	GGGTTACTCCTT	0.368
+	10	1914	ylo.2_Missense_Mu	NM_015420	NP_056235	Q9NV06	DCA13_HUMAN		1	GTCATCGACATC	0.388
+	17	2694	_p.P892L|RIMS2_	NM_014677	NP_055492	Q9UQ26	RIMS2_HUMAN		15	CTCATCCTCGTA	0.418
-	7	2329	_p.G726E|LRP12_	NM_013437	NP_038465	Q9Y561	LRP12_HUMAN	lasmic (Potential).	0	GATCGTCCTAAT	0.463
-	5	712	e_Mutation_p.P18	NM_013437	NP_038465	Q9Y561	LRP12_HUMAN	cellular (Potential).	0	GTTGGAGGATTT	0.418
+	3	285		NM_012082	NP_036214	Q8WW38	FOG2_HUMAN		5	AACCGGGGCAA	0.443
+	21	2407		NM_177531	NP_803875	Q86WI1	PKHL1_HUMAN	cellular (Potential).	14	ACAATAGCAAGA	0.294
+	38	5323		NM_177531	NP_803875	Q86WI1	PKHL1_HUMAN	Extracellular (Potential).	14	ACTGCACCTTTT	0.448
+	49	8149		NM_177531	NP_803875	Q86WI1	PKHL1_HUMAN	ar (Potential).|PbH1 3.	14	GGCTGGAATTG	0.438
+	5	606	AG9_uc003yng.2_	NM_198120	NP_936056	O00559	RCAS1_HUMAN	lasmic (Potential).	0	ATGGGAGCACAG	0.343
-	6	3679	y.2_Missense_Mut	NM_014112	NP_054831	Q9UHF7	TRPS1_HUMAN	ion with RNF4 (By similarit	7	CGCAGGTCTCA	0.438
-	6	3544	y.2_Missense_Mut	NM_014112	NP_054831	Q9UHF7	TRPS1_HUMAN	ion with RNF4 (By similarit	7	TTTTGTGAATATC	0.448
-	5	674	b.2_Nonsense_Mu	NM_003756	NP_003747	O15372	EIF3H_HUMAN		3	AGTTCCCACATT	0.388
-	2	294	_p.D104N|EIF3H_	NM_003756	NP_003747	O15372	EIF3H_HUMAN	MPN.	3	CATCATCCTCTGT	0.428
-	11	1744		NM_006265	NP_006256	O60216	RAD21_HUMAN	Pro-rich.	2	AGGCTCTGGGT	0.448
+	2	400	11lia.1_Missense_	NM_173851	NP_776250	Q8IWU4	ZNT8_HUMAN	lasmic (Potential).	4	TGGCTCCAAGC	0.507
+	7	1189	lia.1_Missense_M	NM_173851	NP_776250	Q8IWU4	ZNT8_HUMAN	lasmic (Potential).	4	ATGTTGCTACAG	0.428
-	1	1183		NM_000127	NP_000118	Q16394	EXT1_HUMAN	nenal (Potential).	4	TCGATGGCCGCT	0.493
-	2	199	_p.G38E|ENPP2_	NM_001040092	NP_001035181	Q13822	ENPP2_HUMAN		7	TCCCATCCTTCT	0.353
-	16	2131		NM_003184	NP_003175	Q6P1X5	TAF2_HUMAN		6	AATCAGCACTGC	0.299
-	8	1286		NM_003184	NP_003175	Q6P1X5	TAF2_HUMAN		6	AAAGGTGTCTCA	0.353
-	7	1024		NM_024094	NP_076999	Q9BVC3	DCC1_HUMAN		1	TTCAGGAACACT	0.403
+	10	1392	_p.A54V|COL14A	NM_021110	NP_066933	Q05707	COEA1_HUMAN	nectin type-III 2.	12	CTCATGCCCCAG	0.428
+	2	172	ank|MTBP_uc003y	NM_022045	NP_071328	Q96DY7	MTBP_HUMAN		3	TTCACAGCAGCA	0.353
+	22	2733		NM_022045	NP_071328	Q96DY7	MTBP_HUMAN	ith MDM2 (By similarity).	3	TGACTGGGTATT	0.284
-	4	1688		NM_005328	NP_005319	Q92819	HAS2_HUMAN	Name=3; (Potential).	15	AGAATCCAGTGA	0.448
-	2	742_743		NM_005328	NP_005319	Q92819	HAS2_HUMAN	lasmic (Potential).	15	TTTTCGGTGCTC	0.401
-	2	539		NM_005328	NP_005319	Q92819	HAS2_HUMAN		15	ATGCATCTGTAA	0.313
+	3	2788		NM_014943	NP_055758	Q9Y6X8	ZHX2_HUMAN		2	GAAGAGGACTTG	0.537
+	7	1055	.1_RNA|WDR67_	NM_145647	NP_663622	Q96DN5	WDR67_HUMAN	WD 5.	1	ACATTGCATCTA	0.348
+	13	1205	_p.F382I|FAM91A	NM_144963	NP_659400	Q658Y4	F91A1_HUMAN		2	TTCCTGTTTGAC	0.383
+	2	692		NM_007218	NP_009149	Q8WU17	RN139_HUMAN		1	GAATTGAGCTG	0.433
+	2	1817		NM_007218	NP_009149	Q8WU17	RN139_HUMAN		1	AGTCGGGAAGT	0.368
+	3	480	im.1_Missense_M	NM_005005	NP_004996	Q9Y6M9	NDUB9_HUMAN		2	GGAAAGCTGGG	0.483
+	3	442		NM_152412	NP_689625	Q7Z3I7	ZN572_HUMAN		2	ATTGGGGAAATT	0.423
+	3	762		NM_152412	NP_689625	Q7Z3I7	ZN572_HUMAN	C2H2-type 3.	2	TCCCATCTTATTA	0.468
-	9	1477	1lir.1_Missense_M	NM_014846	NP_055661	Q12768	STRUM_HUMAN		2	TTACCTGAGTCT	0.473
+	2	1108		NM_002467	NP_002458	P01106	MYC_HUMAN		6	TGCAGGATCTG	0.667
-	11	1148	_p.T54I|FAM49B_	NM_016623	NP_057707	Q9NUQ9	FA49B_HUMAN		0	CTCAAGGTTTTC	0.393
-	28	3221	76_splice|ASAP1_	NM_018482	NP_060952	Q9ULH1	ASAP1_HUMAN		4	TTCCCCTTAAAG	0.363
-	9	2379	Y8_uc010mds.2_	NM_001115	NP_001106	P40145	ADCY8_HUMAN	lasmic (Potential).	6	TCATCCCTCATTT	0.363
+	8	1021		NM_015137	NP_055952	Q14156	EFR3A_HUMAN		5	TTTGCAGTTCAC	0.284
+	21	2469		NM_015137	NP_055952	Q14156	EFR3A_HUMAN		5	ATTTCAGAAAGC	0.378
+	10	1419	20L1_uc011lja.1_	NM_016018	NP_057102	A8MW92	P20L1_HUMAN		2	TAAAACCCCCTA	0.413
+	44	7687	b.1_Missense_Mu	NM_003235	NP_003226	P01266	THYG_HUMAN		15	GGGTGGCGAGG	0.507

+	4	696	_Mutation_p.G35D	NM_003882	NP_003873	O95388	WISP1_HUMAN		2	TGTGGGTGAGG	0.592	
-	7	1418	um.2_Missense_	NM_173344	NP_775479	Q11201	SIA4A_HUMAN	nenal (Potential).	0	CAGCTCCCGGA	0.582	
-	11	3101	_uc010meh.2_Mis	NM_020863	NP_065914	Q9P243	ZFAT_HUMAN	2H2-type 17.	1	CTGGGCCGCTG	0.542	
-	63	4883	ljo.1_Missense_M	NM_152888	NP_690848	Q8NFW1	COMA1_HUMAN	-rich.|Gly-rich.	13	CGAGTCTGGCT	0.557	
-	36	3203	ljo.1_Missense_M	NM_152888	NP_690848	Q8NFW1	COMA1_HUMAN	ly-rich.|Collagen-like 7.	13	GAGCACCCTGT	0.547	
-	2	519	_p.R227C|TRAPP	NM_001160372	NP_001153844	Q96Q05	TPPC9_HUMAN		2	GGTGCGCGGCT	0.567	
-	25	2552	e_Mutation_p.W3	NM_153831	NP_722560	Q05397	FAK1_HUMAN	tion with TGFB1I1.	6	ATGATTCCATGA	0.458	
+	2	247	yvx.2_Missense_	NM_014957	NP_055772	A2RUS2	DEND3_HUMAN		1	GGCCGGTGCCA	0.532	
+	12	1791	66_splice|DENND	NM_014957	NP_055772	A2RUS2	DEND3_HUMAN		1	CGCAGGTGAGG	0.617	
-	4	615	RE1_uc003ywj.2_	NM_145003	NP_659440	Q96NA8	TSNA1_HUMAN		0	GGATGCGGCTC	0.662	
-	3	249	RE1_uc003ywj.2_	NM_145003	NP_659440	Q96NA8	TSNA1_HUMAN		0	GGCAGGGGAAA	0.617	
+	20	3317		NM_001702	NP_001693	O14514	BAI1_HUMAN	lasmic (Potential).	8	CCTCCGGAACC	0.657	
+	2	94		NM_002066	NP_002057	Q99445	GML_HUMAN		2	TGATGCTCCTC	0.577	
-	1	93	_p.A29V|CYP11B1	NM_000497	NP_000488	P15538	C11B1_HUMAN		3	CCCGGGCGGCT	0.647	
+	4	849	41_uc003yxv.2_R	NM_138465	NP_612474	P10075	GLI4_HUMAN	2H2-type 3.	0	CTTCACGCAGC	0.682	
-	5	3344	83H_uc010mfk.1_	NM_198488	NP_940890	Q6ZRV2	FA83H_HUMAN		3	AGATGGCTGAA	0.711	
-	1	4365		NM_031308	NP_112598	P58107	EPIPL_HUMAN		2	TGGCCCTCAGA	0.627	
-	32	13597	e.1_Missense_Mu	NM_201380	NP_958782	Q15149	PLEC_HUMAN	ular 2.|Plectin 30.	9	CCAGGCCCTTG	0.667	
-	31	6903	.1_Missense_Mut	NM_201380	NP_958782	Q15149	PLEC_HUMAN	us rod domain.|Potential.	9	CCGCCGGGACT	0.756	
-	2	735	ae.1_Missense_	NM_201380	NP_958782	Q15149	PLEC_HUMAN	bular 1.|Actin-binding.	9	GTTGACCCACT	0.642	
+	2	539	_p.P125S|GRINA_	NM_001009184	NP_001009184	Q7Z429	GRINA_HUMAN	Pro-rich.	1	AAGACCCTGAC	0.677	
-	14	2001	H_uc003zas.1_5'	NM_017570	NP_060040	O14841	OPLA_HUMAN		0	TGCGGCCGGTG	0.672	
-	14	1995	H_uc003zas.1_5'	NM_017570	NP_060040	O14841	OPLA_HUMAN		0	CGGTGCCCCGC	0.667	
+	7	1110	p.A212T|GPAA1_	NM_003801	NP_003792	O43292	GPAA1_HUMAN	nenal (Potential).	0	TGGTGGCAGTG	0.637	
-	6	1335	PIN_uc003zbb.2_	NM_030974	NP_112236	Q9H0F6	SHRPN_HUMAN	tion with SHANK1 (By simi	1	AAGAGGCAAGG	0.637	
+	8	938	3zbi.3_Missense_	NM_032450	NP_115826	Q8NDA8	HTR7A_HUMAN		0	GCAGAGTCGAG	0.612	
+	10	1118	3zbi.3_Missense_	NM_032450	NP_115826	Q8NDA8	HTR7A_HUMAN		0	GGCAGCTGTGA	0.657	
+	11	1474	F1_uc003zbu.3_R	NM_005526	NP_005517	Q00613	HSF1_HUMAN	activation domain.	0	CAGCAGCCTGG	0.622	
-	9	1040	T1_uc010mfv.2_I	NM_012079	NP_036211	O75907	DGAT1_HUMAN	nenal (Potential).	0	GGGGGCGAAGA	0.622	rs144983092
-	5	797	Splice_Site_p.V19	NM_012162	NP_036294	Q8N531	FBXL6_HUMAN		2	TCCACCTGGGG	0.622	
+	5	401	Splice_Site|ADCK	NM_174922	NP_777582	Q3MIX3	ADCK5_HUMAN		1	GAACAGCCCAG	0.657	
-	18	1781		NM_013291	NP_037423	Q10570	CPSF1_HUMAN		1	TGCGGCCGTCG	0.682	
-	14	1438		NM_013291	NP_037423	Q10570	CPSF1_HUMAN		1	TGTTCCCGACT	0.662	
-	16	1985	uc011llh.1_Intron	NM_013432	NP_038460	Q96HA7	TONSL_HUMAN		0	CCCTGGCCTTC	0.672	
-	11	1352		NM_013432	NP_038460	Q96HA7	TONSL_HUMAN		0	CCTGGGGCTGC	0.507	
+	4	431	p.P92S|GPT_uc0	NM_005309	NP_005300	P24298	ALAT1_HUMAN		2	GTTAACCCTGAT	0.647	
+	4	1218	_Mutation_p.G358	NM_014665	NP_055480	Q15048	LRC14_HUMAN	LRR 3.	0	TCCAGGGTCTG	0.597	
-	4	236	NF34_uc003zdx.	NM_030580	NP_085057	Q8IZ26	ZNF34_HUMAN	KRAB.	0	CCCGGGAGAGG	0.652	
+	5	1333	303N|ZNF7_uc00	NM_003416	NP_003407	P17097	ZNF7_HUMAN		4	TCCAAGCCTTG	0.493	
+	5	2094	Q557*|ZNF7_uc00	NM_003416	NP_003407	P17097	ZNF7_HUMAN	2H2-type 14.	4	TACACCAGAGA	0.408	
-	6	1408	nse_Mutation_p.A	NM_021061	NP_066405	P15622	ZN250_HUMAN	2H2-type 9.	0	GAAGGCCTTCC	0.572	
-	1	479		NM_207305	NP_997188	Q12950	FOXD4_HUMAN		1	CCCGCCCCACC	0.697	
+	35	4488	gv.2_Missense_M	NM_203447	NP_982272	Q8NF50	DOCK8_HUMAN	DHR-2.	6	GCTGGGAGGTG	0.527	
+	7	907	_Mutation_p.W86*|	NM_015158	NP_055973	Q14678	KANK1_HUMAN		4	TATATGGACTTC	0.493	
+	12	4083	mgx.1_Missense_	NM_015158	NP_055973	Q14678	KANK1_HUMAN		4	TGAGGCCATTT	0.552	
-	3	218	_p.A40V|KIAA002	NM_014878	NP_055693	Q15397	K0020_HUMAN		1	TCTTTAGCAACT	0.363	
-	4	481	_p.V57M|RFX3_u	NM_134428	NP_602304	P48380	RFX3_HUMAN		4	CTGCACCTGAG	0.418	

+	7	1066	hk.1_Missense_M	NM_005772	NP_005763	Q9Y2P8	RCL1_HUMAN		0	GCAGCAGTACTT	0.592	
-	8	1459	RMP1_uc010mhs.	NM_024896	NP_079172	Q7Z2K6	ERMP1_HUMAN	ical; (Potential).	1	TAATGAGAACGG	0.413	
-	1	780		NM_001017969	NP_001017969	Q5HYC2	K2026_HUMAN		3	CTCCAGCATCAT	0.597	
+	18	3048	M4C_uc011lmk.1_	NM_015061	NP_055876	Q9H3R0	KDM4C_HUMAN	PHD-type 2.	1	TGGAGCCTGCA	0.522	
-	23	2662	3zkl.2_Missense_	NM_002839	NP_002830	P23468	PTPRD_HUMAN	III 4.|Extracellular (Potentia	22	CACTGCAGTGT	0.448	
-	6	859	_p.G268R|MPDZ_	NM_003829	NP_003820	O75970	MPDZ_HUMAN	PDZ 2.	6	CAAATCCCAAAC	0.388	
+	10	1456	me.2_Missense_	NM_173550	NP_775821	Q6TFL3	CI093_HUMAN	Potential.	0	AAGAAAGTAATT	0.313	
+	24	4364	p.P732L|DENND4	NM_017925	NP_060395	Q5VZ89	DEN4C_HUMAN		2	CCAATCCTCCCC	0.353	
+	6	903	ER2_uc003znz.1_	NM_001010887	NP_001010887	Q5QJU3	ACER2_HUMAN	lasmic (Potential).	2	TTCTGGCCCAAT	0.517	
-	1	505	zob.1_Missense_	NM_020344	NP_065077	Q9UI40	NCKX2_HUMAN	ical; (Potential).	3	GCTAAGGCTATG	0.458	
-	7	1547	nf.1_Missense_Mu	NM_004529	NP_004520	P42568	AF9_HUMAN		3	CCATTTCAGAGT	0.453	
-	1	497	14_uc003zoo.1_I	NM_002173	NP_002164	P05015	IFN16_HUMAN		1	CCTCCCAGGCA	0.408	
+	2	931		NM_022160	NP_071443	Q5VZB9	DMRTA_HUMAN		2	AATGGACAAGAA	0.408	
-	4	650	zqr.1_Missense_M	NM_018325	NP_060795	Q96LT7	CI072_HUMAN		4	GCAGTTCCATTA	0.348	
-	2	443	zqr.1_Missense_M	NM_018325	NP_060795	Q96LT7	CI072_HUMAN		4	GTGGAAGTATAAT	0.363	
-	6	960	ense_Mutation_p.	NM_022917	NP_075068	Q9H6R4	NOL6_HUMAN		2	ACCATCCCCTG	0.612	
-	29	3438	_p.P864S|UBAP2_	NM_018449	NP_060919	Q5T6F2	UBAP2_HUMAN		3	GGCAGGTTTGG	0.597	
-	7	1231		NM_015397	NP_056212	Q5T6F0	DCA12_HUMAN		0	CTCACGGCAAT	0.488	
+	7	1876	RA_uc003zvk.2_	NM_004512	NP_004503	Q14626	I11RA_HUMAN	III 1.|Extracellular (Potentia	1	AGGATCCCCTA	0.602	
+	2	558	zvv.2_Missense_	NM_203299	NP_976044	Q5VYM1	CI131_HUMAN		0	GCTTTCCTGTG	0.562	
+	2	1141	zvv.2_Missense_	NM_203299	NP_976044	Q5VYM1	CI131_HUMAN		0	GGGAACCGTGG	0.557	
+	2	1608	zvv.2_Missense_	NM_203299	NP_976044	Q5VYM1	CI131_HUMAN		0	TGGAACCACAC	0.507	rs147472233
+	2	1719	zvv.2_Missense_	NM_203299	NP_976044	Q5VYM1	CI131_HUMAN		0	TCAGCCCACCC	0.522	
-	7	1074	2_splice|CD72_u	NM_001782	NP_001773	P21854	CD72_HUMAN		0	AACTTACCTAGT	0.443	
+	11	1370	p.3_Missense_Mu	NM_001216	NP_001207	Q16790	CAH9_HUMAN	Cytoplasmic.	5	GGGAACCAAAG	0.552	
+	4	1115	lb.2_Missense_Mu	NM_003995	NP_003986	P20594	ANPRB_HUMAN	ellular (Potential).	3	GACGAAGATATC	0.493	rs144675513
+	3	517	se_Mutation_p.E1	NM_007096	NP_009027	P09496	CLCA_HUMAN	ding clathrin heavy chain.	1	AAATGGAACGC	0.428	
+	11	1634	POLR1E_uc011lqk	NM_022490	NP_071935	Q9GZS1	RPA49_HUMAN		0	TGTGGCCGCCG	0.552	
+	9	1155	e_Mutation_p.E28	NM_003558	NP_003549	O14986	PI51B_HUMAN	PIPK.	1	AGAAAGAGGAG	0.468	
+	47	6584	p.W2108*|VPS13	NM_033305	NP_150648	Q96RL7	VP13A_HUMAN		10	TTTGTGGCCACC	0.333	
+	6	1100	pp.2_Missense_M	NM_032171	NP_115547	Q5JTW2	CEP78_HUMAN		1	CAAAGGCTTTGC	0.388	
+	16	2294	_p.G94D|TLE4_uc	NM_007005	NP_008936	O60756	BCE1_HUMAN		5	AGATGGTCAGA	0.512	
-	16	2342		NM_152573	NP_689786	Q8IZ41	RASEF_HUMAN		3	TTAGAACCATCTT	0.373	
-	3	942	mw.2_Missense_	NM_013438	NP_038466	Q9UMX0	UBQL1_HUMAN		0	CTTCCAGCTGTA	0.373	
-	8	1200	z.2_Intron|GKAP1	NM_025211	NP_079487	Q5VSY0	GKAP1_HUMAN		0	TCTGTTCCATTAT	0.294	
-	18	4207	.P1289S|KIF27_u	NM_017576	NP_060046	Q86VH2	KIF27_HUMAN		5	TACAGGTGTGA	0.423	
-	1	435	f64_uc004anc.2_	NM_032307	NP_115683	Q5T6V5	CI064_HUMAN		0	CGCGGCCTCGT	0.627	
+	3	1420	p.3_Missense_Mu	NM_024945	NP_079221	Q9H9A7	RMI1_HUMAN		0	TTGCAACCATTG	0.353	
+	15	1549	1ltg.1_Missense_	NM_004938	NP_004929	P53355	DAPK1_HUMAN	ANK 3.	2	TCAAATCCCAAT	0.547	
+	5	581		NR_027917					1	AAGTGGTGGGG	0.478	
+	5	736	e_Mutation_p.T21	NM_024077	NP_076982	Q96T21	SEBP2_HUMAN		3	AATTTACCACACT	0.408	
-	12	1347	lice_Site|SEMA4D	NM_006378	NP_006369	Q92854	SEM4D_HUMAN		2	GTCCCCCTAAAA	0.612	
+	10	1550	|SYK_uc004arc.2_	NM_003177	NP_003168	P43405	KSYK_HUMAN	rotein kinase.	5	GTTATGGAGATG	0.527	
-	9	2768	R2_uc004ari.1_Int	NM_004560	NP_004551	Q01974	ROR2_HUMAN	ic (Potential).|Pro-rich.	20	GCTTGGGGACCA	0.652	
-	3	432	t_Site|ROR2_uc0	NM_004560	NP_004551	Q01974	ROR2_HUMAN	Potential).|Ig-like C2-type.	20	ATTGCCGTCTGG	0.547	
-	14	1366	1ltv.1_Splice_Site_	NM_006415	NP_006406	O15269	SPTC1_HUMAN		2	ACTGACCTGGG	0.388	
+	3	1037	_Mutation_p.A346	NM_006648	NP_006639	Q9Y3S1	WNK2_HUMAN	rotein kinase.	12	GCCTGGCCACTC	0.537	

+	3	175	_p.T24A|ZNF169_	NM_194320	NP_919301	Q14929	ZN169_HUMAN	KRAB.	2	CCTTCACCCAG	0.547
+	1	496	rf3_uc004auy.2_	NM_032823	NP_116212	Q8N6M6	AMPO_HUMAN		1	AGGAACATGCT	0.388
-	23	4267	rq.2_Missense_M	NM_000264	NP_000255	Q13635	PTC1_HUMAN	lasmic (Potential).	379	GCACGGAGCTG	0.697
-	2	640	14B_uc004awl.2_	NM_033331	NP_201588	O60729	CC14B_HUMAN	A.	1	GTCTGCTGTAG	0.323
+	2	287	D7_uc011lux.1_In	NM_014290	NP_055105	Q8NHU6	TDRD7_HUMAN	us/OST-HTH 1.	3	GAATGGAGTAG	0.448
+	7	1171	ux.1_Missense_M	NM_014290	NP_055105	Q8NHU6	TDRD7_HUMAN	us/OST-HTH 2.	3	AGAAAGTACCT	0.443
-	11	2588	_p.S803N|TBC1D2	NM_018421	NP_060891	Q9BYX2	TBD2A_HUMAN	ab-GAP TBC.	3	ATGTTGCTAATG	0.552
-	2	835	S6_uc004ayy.1_	NM_173551	NP_775822	Q68DC2	ANKS6_HUMAN	ANK 7.	2	AAGGTCCCTGT	0.607
+	8	992	x.2_RNA|STX17_	NM_017919	NP_060389	P56962	STX17_HUMAN	cular (Potential).	1	AGAAGCTCACT	0.438
+	6	1172	c.2_Missense_M	NM_207299	NP_997182	Q8TBJ4	LPPR1_HUMAN	ical; (Potential).	0	CGTGATTGCTG	0.552
-	2	172	lvj.1_Missense_M	NM_019051	NP_061924	Q8N5N7	RM50_HUMAN		0	CTCTTCTACTGT	0.408
+	25	3775	_Mutation_p.D116	NM_001042551	NP_001036016	O95347	SMC2_HUMAN		9	TTGTGGATGGT	0.348
-	1	440		NM_001001956	NP_001001956	Q8NGT0	O13C9_HUMAN	Name=4; (Potential).	0	AGGACCCAACA	0.453
-	36	5172		NM_005502	NP_005493	O95477	ABCA1_HUMAN	xtracellular.	17	CTCCCTTTTGC	0.473
+	11	7428	sense_Mutation_	NM_021224	NP_067047	Q96JM2	ZN462_HUMAN		5	CAGCAGCGATG	0.498
-	16	1936	p.A632T|CTNNAL	NM_003798	NP_003789	Q9UBT7	CTNL1_HUMAN		1	CTCTGCAGCAA	0.353
-	11	1672	orf5_uc004bdr.3_	NM_032012	NP_114401	Q9H330	CI005_HUMAN		1	TTATCTCCTAGA	0.333
-	34	5868	1_uc010mty.2_5'	NM_153366	NP_699197	Q4LDE5	SVEP1_HUMAN		7	AACAGCTTAAC	0.338
-	5	1173	_p.M306I|LPAR1_	NM_057159	NP_476500	Q92633	LPAR1_HUMAN	Name=7; (Potential).	2	GGGTTCATGGC	0.522
-	43	5009		NM_001080398	NP_001073867				0	TTTTCGGATTTCT	0.423
+	9	1324		NM_003358	NP_003349	Q16739	CEGT_HUMAN	enal (Potential).	1	GTTTTTCAAAAC	0.353
-	2	273	e_Mutation_p.T24	NM_000031	NP_000022	P13716	HEM2_HUMAN		0	GGGTGGTGGTG	0.552
+	7	908	hp.2_Missense_M	NM_152786	NP_689999	Q8TAL5	CI043_HUMAN		0	CTCTGGAAATC	0.448
+	3	315	_5'Flank|RGS3_u	NM_144488	NP_652759	P49796	RGS3_HUMAN		3	CCTTTGCCCAAT	0.512
-	2	444	e_Mutation_p.D2	NM_001633	NP_001624	P02760	AMBP_HUMAN		1	CCTGTCCATGA	0.602
+	8	2146	2_RNA|COL27A1_	NM_032888	NP_116277	Q8IZC6	CORA1_HUMAN	ro-rich.|Triple-helical regio	4	CTGGACCGGCA	0.672
+	19	2711	27A1_uc004bii.2_	NM_032888	NP_116277	Q8IZC6	CORA1_HUMAN	ro-rich.|Triple-helical regio	4	TCCCGGGCCCC	0.527
+	51	4676	27A1_uc004bii.2_	NM_032888	NP_116277	Q8IZC6	CORA1_HUMAN	Pro-rich.|Triple-helical regi	4	CCAGGGCCCTC	0.627
-	18	3797	_splice|AKNA_uc	NM_030767	NP_110394	Q7Z591	AKNA_HUMAN		6	GTGGCCTGGGG	0.507
-	10	2901	biy.3_Missense_M	NM_015404	NP_056219	Q9P202	WHRN_HUMAN		6	GGTGGGAGAGC	0.483
-	17	3097	n_p.S51N|ASTN	NM_198187	NP_937830	O75129	ASTN2_HUMAN	ellular (Potential).	9	TGGGGCTCAGC	0.582
+	2	178	STN2_uc004bjt.1_	NM_001099679	NP_001093149	Q13049	TRI32_HUMAN		3	AGCTTCTCACC	0.537
-	29	3775		NM_001735	NP_001726	P01031	CO5_HUMAN		2	TTGTTTCTACCA	0.403
-	18	2378	m.1_Splice_Site_	NM_001735	NP_001726	P01031	CO5_HUMAN		2	TAATACCTTCTG	0.388
-	16	2060	_p.R677K|C5_uc0	NM_001735	NP_001726	P01031	CO5_HUMAN		2	GCGTTCTTCTT	0.289
-	15	1979	_p.G650E|C5_uc0	NM_001735	NP_001726	P01031	CO5_HUMAN		2	TAAGTCCAGCT	0.448
+	28	4748	110_uc004blb.1_	NM_007018	NP_008949	Q7Z7A1	CNTRL_HUMAN	Potential.	0	CTGAGGTGCTT	0.443
-	1	523	J2_uc004bmj.1_I	NM_001004451	NP_001004451	Q8NGS3	OR1J1_HUMAN	ellular (Potential).	2	GTGAGGGATGA	0.527
-	1	722		NM_012363	NP_036495	Q8NGS0	OR1N1_HUMAN	Name=6; (Potential).	3	GGTGGGAACTG	0.547
+	1	9		NM_001005234	NP_001005234	Q8NH93	OR1L3_HUMAN	ellular (Potential).	1	GGAATGTCCAA	0.413
+	1	701		NM_001005235	NP_001005235	Q8NGR5	OR1L4_HUMAN	lasmic (Potential).	0	AGCCGGGAAGT	0.512
+	1	604		NM_001001923	NP_001001923	Q8NGR4	OR5C1_HUMAN	Name=5; (Potential).	1	AACTCCTTCTC	0.557
-	17	1705	e_Mutation_p.T56	NM_001144877	NP_001138349	Q8N9R8	SCAI_HUMAN		5	TCTTGTGAGGA	0.343
-	2	516		NM_005347	NP_005338	P11021	GRP78_HUMAN		4	CGGGGTTGGAG	0.592
+	3	371	mac.1_Missense_	NM_014636	NP_055451	Q5JS13	RGPS1_HUMAN		1	CTATGCCAGCA	0.547
+	11	1057	brc.1_Missense_	NM_001005373	NP_001005373	Q6UWE0	LRSM1_HUMAN		0	ATGGGCCCACG	0.458
-	5	626	_p.T129S|FAM129	NM_022833	NP_073744	Q96TA1	NIBL1_HUMAN	PH.	0	CGTGGTCCCTG	0.582

-	5	742	_p.P208L|ST6GAL	NM_013443	NP_038471	Q969X2	SIA7F_HUMAN	enal (Potential).	0	TGTTGGGGAAC	0.637	
-	5	986	04bst.2_Missense	NM_175039	NP_778204	Q9H4F1	SIA7D_HUMAN	enal (Potential).	0	AGTAGCTGTCG	0.647	
-	2	669		NM_003863	NP_003854	O94777	DPM2_HUMAN		0	CCGTGGCCTGG	0.582	
-	4	1158	_p.A36V|PTGES2	NM_025072	NP_079348	Q9H7Z7	PGES2_HUMAN	lasmic (Potential).	0	TCCTGGCCTCC	0.612	
-	14	2417	.D672N|CIZ1_uc	NM_001131016	NP_001124488	Q9ULV3	CIZ1_HUMAN	Glu-rich.	4	cttcttcatcctcatcatc	0.403	
-	18	1799	OLGA2_uc004bul	NM_004486	NP_004477	Q08379	GOGA2_HUMAN	Potential.	1	CGTTTCCTTCA	0.647	
+	7	1306	nxz.2_Missense_	NM_016174	NP_057258	Q5T4B2	GT253_HUMAN		1	GCAGGCCTCAG	0.617	
-	1	1185	1_5'Flank|NUP18	NM_014908	NP_055723	Q9UPQ8	DOLK_HUMAN	lasmic (Potential).	0	CCCAGGTGCCT	0.577	
-	11	1736	_p.S464F|CRAT_u	NM_000755	NP_000746	P43155	CACP_HUMAN		1	CGCTGGAGTCA	0.517	
+	7	1390		NM_006059	NP_006050	Q9Y6N6	LAMC3_HUMAN	inin EGF-like 4.	3	CTGCACTTGCA	0.557	
+	29	5053	ense_Mutation_p.	NM_005085	NP_005076	P35658	NU214_HUMAN	1 X 5 AA approximate repe	16	CTCAGCCTCCT	0.602	
+	16	4565	ao.3_Missense_M	NM_013318	NP_037450	Q5JSZ5	PRC2B_HUMAN		0	ACCTTCCCGAA	0.607	
+	26	5952	p.S1323F|BAT2L1	NM_013318	NP_037450	Q5JSZ5	PRC2B_HUMAN		0	CACATCTCTGC	0.607	
-	22	3005	cbb.2_Missense_	NM_005312	NP_005303	Q13905	RPGF1_HUMAN	Ras-GEF.	7	CAGTGTGCAGT	0.577	
-	10	4939	.P1205S|SETX_u	NM_015046	NP_055861	Q7Z333	SETX_HUMAN		3	AGGAGGAGGCA	0.408	
-	4	449	dd.2_Missense_M	NM_133640	NP_598395	Q15528	MED22_HUMAN		1	ACTCGCCGGCT	0.493	
-	4	322	1_5'Flank|SURF2_	NM_003172	NP_003163	Q15526	SURF1_HUMAN		2	GAACTCTGGAC	0.582	
-	13	1789	e_Mutation_p.P55	NM_001134707	NP_001128179	Q9UL12	SARDH_HUMAN		0	GGTGGGGCGGG	0.677	
-	3	552	H_uc011mdn.1_	NM_001134707	NP_001128179	Q9UL12	SARDH_HUMAN		0	CGTCTCCTCCT	0.672	
-	6	1079	x.2_Missense_Mu	NM_007371	NP_031397	Q15059	BRD3_HUMAN		8	GGCACCTCGCC	0.657	
-	6	991	x.2_Missense_Mu	NM_007371	NP_031397	Q15059	BRD3_HUMAN		8	GGTCTGACAAC	0.657	
+	2	242	ez.2_Missense_	NM_017588	NP_060058	P61964	WDR5_HUMAN		0	CGCCACTCAGA	0.612	
+	38	3388		NM_000093	NP_000084	P20908	CO5A1_HUMAN		11	CTCAGGTAAGC	0.647	
+	11	960	bf.2_Missense_M	NM_020822	NP_065873	Q5JUK3	KCNT1_HUMAN		4	GGGCGGGCGA	0.677	
-	11	3676	p.P1116S|CAMSA	NM_015447	NP_056262	Q5T5Y3	CAMP1_HUMAN		3	CAGAGGCTCCT	0.617	
-	9	1274	p.R315K|CAMSA	NM_015447	NP_056262	Q5T5Y3	CAMP1_HUMAN		3	TCTGTCTCAGT	0.388	
-	3	3148	C16A_uc010nbn.	NM_014866	NP_055681	O15027	SC16A_HUMAN		0	TTCCTGCCTTAC	0.493	
-	3	1594	.P429S|SEC16A_	NM_014866	NP_055681	O15027	SC16A_HUMAN		0	GCCTGGGAGAA	0.632	
-	34	6235		NM_017617	NP_060087	P46531	NOTC1_HUMAN	ytoplasmic (Potential).	856	CAGCACCTTGG	0.677	
+	18	2346	mej.1_Missense_	NM_206920	NP_996803	Q6UXC1	AEGP_HUMAN	xtracellular (Potential).	7	GCCCCCCAACA	0.662	
-	9	1133	se_Mutation_p.E3	NM_015392	NP_056207	Q9NQX5	NPDC1_HUMAN		0	CACCTCCATTT	0.682	
-	11	1282		NM_013379	NP_037511	Q9UHL4	DPP2_HUMAN		0	GGGGTCCAGGT	0.493	
-	6	1328	lq.1_Missense_M	NM_013366	NP_037498	Q9UJX6	ANC2_HUMAN		1	GGCCACCTCCA	0.632	
-	26	3309	nse_Mutation_p.T	NM_152286	NP_689499	Q6ZV29	PLPL7_HUMAN	Patatin.	1	AGGACGTCATG	0.602	rs151043513
+	4	361	np.1_Missense_M	NM_152285	NP_689498	Q8N5I2	ARRD1_HUMAN		0	CACTGCACCCA	0.627	
+	7	1275	np.1_Missense_M	NM_152285	NP_689498	Q8N5I2	ARRD1_HUMAN	Pro-rich.	0	TTGATTCTTCCT	0.617	
+	3	624	uc004cof.1_Intron	NM_000718	NP_000709	Q00975	CAC1B_HUMAN	asmic (Potential).|I.	6	GGGCTCTTACC	0.592	
+	13	1391	.P357S|CSF2RA_	NM_001161529	NP_001155001	P15509	CSF2R_HUMAN	(Potential).|Box 1 motif.	2	TGTTCCCGCCA	0.547	
-	2	406	5A6_uc004cpu.2_	NM_001636	NP_001627	P12236	ADT3_HUMAN		0	CTTGTCCACGC	0.612	
-	2	1099	ED1_uc004cqh.1_	NM_004729	NP_004720	O96006	ZBED1_HUMAN		0	CTGCTGGATGC	0.632	
+	7	506	99_uc004cqn.2_R	NM_002414	NP_002405	P14209	CD99_HUMAN	ellular (Potential).	1	TGGTGGAGGCA	0.527	
+	3	293		NM_001011719	NP_001011719	Q5FYA8	ARSH_HUMAN		1	AACGACTTTTG	0.552	
+	9	1342	f.1_Missense_Mu	NM_004042	NP_004033	P54793	ARSF_HUMAN		2	GGGGGGCTGGG	0.413	
+	11	1786	f.1_Missense_Mu	NM_004042	NP_004033	P54793	ARSF_HUMAN		2	ACCTGCCACAG	0.532	
-	5	5073		NM_015419	NP_056234	Q9NR99	MXRA5_HUMAN		8	GACGAGGTGAC	0.458	
-	5	5045		NM_015419	NP_056234	Q9NR99	MXRA5_HUMAN		8	TCTGGAAGCGC	0.473	
+	4	674		NM_001649	NP_001640	Q13796	SHRM2_HUMAN		8	CAACAGCAGCA	0.617	

+	4	1563		NM_001649	NP_001640	Q13796	SHRM2_HUMAN		8	CTCTGGGCGGG	0.677	
+	11	1363	se_Mutation_p.V5	NM_015691	NP_056506	Q9ULE0	WWC3_HUMAN	Ser-rich.	4	GCTCGGTCAGC	0.672	
+	11	1493	se_Mutation_p.G9	NM_015691	NP_056506	Q9ULE0	WWC3_HUMAN	Ser-rich.	4	CCCAGGCCCCT	0.662	
+	5	354	ntron|ARHGAP6_	NM_001142	NP_001133	Q99217	AMELX_HUMAN		0	TGATCCCCCAG	0.632	
+	13	1654	_p.P368S|MSL3_u	NM_078629	NP_523353	Q8N5Y2	MS3L1_HUMAN		1	AGAACCCCCGG	0.458	
-	1	566		NM_001135995	NP_001129467	Q9H3M9	ATX3L_HUMAN	Josephin.	6	ATTGAGGCTAAT	0.423	
+	4	679	ion_p.T106I|OFD1	NM_003611	NP_003602	O75665	OFD1_HUMAN		0	TATTTACTATGCA	0.284	
+	9	1380	_p.R350C|GLRA2_	NM_001118885	NP_001112357	P23416	GLRA2_HUMAN	lasmic (Probable).	2	TCCTGCGCCTC	0.483	
-	4	511	wv.2_Splice_Site_	NM_003662	NP_003653	O00625	PIR_HUMAN		1	CCATACCTGCA	0.378	
-	17	2353	b.2_Missense_Mu	NM_021804	NP_068576	Q9BYF1	ACE2_HUMAN	cellular (Potential).	3	TGTTGGCTGTA	0.468	
-	13	1946	xb.2_Missense_Mu	NM_021804	NP_068576	Q9BYF1	ACE2_HUMAN	cellular (Potential).	3	GCCAGGTAAATA	0.448	rs140857723
+	11	1106		NM_005089	NP_005080	Q15696	U2AFM_HUMAN		3	GACTGGCTCCT	0.512	
+	4	1323	_p.E173K|NHS_uc	NM_198270	NP_938011	Q6T4R5	NHS_HUMAN		7	CAGAGGAGAAG	0.473	
+	6	3864	p.D1020N|NHS_u	NM_198270	NP_938011	Q6T4R5	NHS_HUMAN		7	ACTGAAGACACC	0.403	
+	8	5091	.A1429T|NHS_uc	NM_198270	NP_938011	Q6T4R5	NHS_HUMAN		7	CTCGGGCCCCT	0.582	
-	3	874	_p.P102S|RAI2_u	NM_021785	NP_068557	Q9Y5P3	RAI2_HUMAN		2	CTCTGGTGCGG	0.622	
-	4	260	fd.1_Missense_Mu	NM_006089	NP_006080	Q9UQR0	SCML2_HUMAN	MBT 1.	0	CTCCCAGTGGA	0.348	
+	12	2124	yn.2_Missense_Mu	NM_003159	NP_003150	O76039	CDKL5_HUMAN		6	CAAGGGCTTGG	0.512	
-	7	408	n_p.L58F|GPR64_	NM_001079858	NP_001073327	Q8IZP9	GPR64_HUMAN	cellular (Potential).	0	AGGGAGTAAGC	0.353	
-	9	1786	jg.1_Intron|CXorf2	NM_198279	NP_938020	A2AJT9	CX023_HUMAN		2	TCTCTGCGTAG	0.323	
-	9	706	_p.A224T|RPS6KA	NM_004586	NP_004577	P51812	KS6A3_HUMAN	otein kinase 1.	8	CTGGAGCCATAT	0.388	
+	3	397	mjn.1_Missense_	NM_014927	NP_055742	Q8WXI2	CNKR2_HUMAN	CRIC.	2	AAATTGCCAAAC	0.453	
+	11	1412	_p.W403*|PHEX_u	NM_000444	NP_000435	P78562	PHEX_HUMAN	cellular (Potential).	3	TCAATGGGACAA	0.393	
+	7	1327	se_Mutation_p.P3	NM_003410	NP_003401	P17010	ZFX_HUMAN		2	TTCATGCCGATT	0.483	
+	9	2581	se_Mutation_p.P8	NM_003410	NP_003401	P17010	ZFX_HUMAN		2	ACTATCCTCAC	0.453	
-	1	757		NM_001136233	NP_001129705	P0C7V6	F48B2_HUMAN		0	AGACTGCTCCT	0.498	
+	9	756	_p.G251R|POLA1_	NM_016937	NP_058633	P09884	DPOLA_HUMAN		3	AGTCAGGGGCA	0.463	
+	22	2371	A23_uc004dbo.1_	NM_016937	NP_058633	P09884	DPOLA_HUMAN		3	GGGTGGACGAT	0.378	
+	2	229	EB6_uc010ngc.1_	NM_173523	NP_775794	Q8N7X4	MAGB6_HUMAN		3	CACGGGTCCCC	0.567	
-	1	1110		NM_001017930	NP_001017930	A6NGE4	DC8L1_HUMAN	WD 4.	4	TTCTTATCATTTT	0.423	
-	3	712		NM_025159	NP_079435	Q9HAI6	CX021_HUMAN		1	TCTCAGAGGGAA	0.428	
-	3	338		NM_025159	NP_079435	Q9HAI6	CX021_HUMAN		1	AAGAGGCACAA	0.443	
-	35	5253	_Mutation_p.W154	NM_004006	NP_003997	P11532	DMD_HUMAN	ction with SYNM (By simila	6	TTTAACCACTCTT	0.413	
+	9	1250		NM_173695	NP_775966	Q8N9S7	CX059_HUMAN		1	TGAGAGATGGA	0.338	
+	1	1438		NM_001013736	NP_001013758	Q5HY64	FA47C_HUMAN		3	TCTCTGCCCGG	0.627	
+	1	1665		NM_001013736	NP_001013758	Q5HY64	FA47C_HUMAN		3	AGCCTCCTGAG	0.617	
+	1	2193		NM_001013736	NP_001013758	Q5HY64	FA47C_HUMAN		3	ATCTCTGCCCG	0.637	
+	1	2239		NM_001013736	NP_001013758	Q5HY64	FA47C_HUMAN		3	AGAGCCTCCCA	0.632	
+	1	375	ddp.1_Missense_	NM_198511	NP_940913	Q6ZV70	LANC3_HUMAN		0	GTGAGGAGGCG	0.716	
-	4	650	_p.P120S|BCOR_u	NM_001123385	NP_001116857	Q6W2J9	BCOR_HUMAN		4	TCTCTGGATTTC	0.507	
+	3	349	6AP2_uc011mkm.	NM_005765	NP_005756	O75787	RENR_HUMAN	cellular (Potential).	0	AGGGAGTGAAC	0.443	
+	10	1852	fc.2_Missense_Mu	NM_001039590	NP_001034679	Q93008	USP9X_HUMAN		6	ATCAGCCACAG	0.353	
+	18	3086	lfc.2_Missense_Mu	NM_001039590	NP_001034679	Q93008	USP9X_HUMAN		6	TTCAGTCTTGTTT	0.353	
+	9	1672	_Mutation_p.A257	NM_001356	NP_001347	O00571	DDX3X_HUMAN	n with XPO1.|Helicase AT	6	TATTAGCACCA	0.368	
+	14	2356	485T|DDX3X_uc0	NM_001356	NP_001347	O00571	DDX3X_HUMAN	ecessary for interaction wit	6	AGGTAGCAGCA	0.343	
+	3	838	se_Mutation_p.G1	NM_001097579	NP_001091048	Q9UPC5	GPR34_HUMAN	Name=4; (Potential).	1	TTGGTGGATTCC	0.353	
+	15	1626	kw.1_Missense_M	NM_000240	NP_000231	P21397	AOFA_HUMAN	Cytoplasmic.	3	CGTTCCAGCGG	0.493	

-	4	661	lgv.1_Missense_M	NM_032591	NP_115980	Q96T83	SL9A7_HUMAN	ical; (Potential).		2	CAGTCCCCAAG	0.388
+	2	724		NM_006915	NP_008846	O75695	XRP2_HUMAN	P/cofactor C-like.		0	TTACACCTGTG	0.423
+	4	460		NM_003446	NP_003437	P51786	ZN157_HUMAN			0	CATTGGATCAA	0.348
-	4	1842	w.3_Missense_M	NM_153380	NP_700359	P51814	ZNF41_HUMAN			3	TTATAGGGTTTC	0.418
-	4	673	.1_Missense_Mut	NM_001145252	NP_001138724	P27918	PROP_HUMAN	SP type-1 2.		3	ACAGGCCTCTG	0.642
-	5	1136	K1_uc010nhw.2_	NM_001114123	NP_001107595	P19419	ELK1_HUMAN			2	CTCGGCCTTGG	0.657
-	4	278	8A5_uc004djk.3_5	NM_033518	NP_277053	Q8WUX1	S38A5_HUMAN	lasmic (Potential).		3	CCCAGGAGCAG	0.592
+	9	915	jn.1_Missense_M	NM_012280	NP_036412	Q9UET6	RRMJ1_HUMAN			0	GTCAGGGCTAT	0.642
+	6	1829	.P319L|TBC1D25_	NM_002536	NP_002527	Q3MII6	TBC25_HUMAN			1	CTCTCCCACTG	0.577
+	8	1301	5_splice|WDR13_	NM_017883	NP_060353	Q9H1Z4	WDR13_HUMAN			2	TACAGGTGGGT	0.597
+	1	91		NM_000377	NP_000368	P42768	WASP_HUMAN			1	CCGGGGGCCGA	0.592
+	3	796	e_Mutation_p.D26	NM_003173	NP_003164	O43463	SUV91_HUMAN	SET.		0	GCACGGATGAT	0.597
+	5	520	_Mutation_p.D111	NM_001032382	NP_001027554	O60828	PQBP1_HUMAN	tandem repeats of D- R-[S		1	AGTCGGACAGG	0.587
+	4	647	_Mutation_p.S47	NM_033626	NP_296375	Q96HB5	CC120_HUMAN			1	CCTGAGCCTGA	0.667
-	5	565	_p.T99I|PRICKLE	NM_006150	NP_006141	O43900	PRIC3_HUMAN	PET.		1	TGATGGTCACC	0.612
-	6	734	_p.P122S|SYP_uc	NM_003179	NP_003170	P08247	SYPH_HUMAN	lasmic (Potential).		3	TCGGGGGCGC	0.711
-	4	592	_p.T135N|FOXP3_	NM_014009	NP_054728	Q9BZS1	FOXP3_HUMAN			0	CGGTGGTGGGT	0.672
+	4	1610	dni.2_Missense_	NM_033215	NP_149992	Q6ZSY5	PPR3F_HUMAN	ellular (Potential).		3	CGGACCGCGAC	0.692
+	3	282	.1_Intron|GAGE1_	NM_001127212	NP_001120684	Q6NT46	GAG2A_HUMAN			0	TGAGGGAGCAT	0.403
+	6	2256	.S653F|CCNB3_u	NM_033031	NP_149020	Q8WWL7	CCNB3_HUMAN			9	AGTGTCCCTCT	0.433
+	4	1015	p.G363D|MAGED	NM_001005332	NP_001005332	Q9Y5V3	MAGD1_HUMAN	dem repeats of W-[PQ]-X-		3	CTCAGGCTGGC	0.632
+	2	93		NM_130775	NP_570131	Q8WWM1	GAGD5_HUMAN			1	ATAGACCAAGA	0.308
-	26	4954	n|KDM5C_uc004	NM_004187	NP_004178	P41229	KDM5C_HUMAN			18	CCTCTCGGGCT	0.706
-	15	2635	nse_Mutation_p.P	NM_004187	NP_004178	P41229	KDM5C_HUMAN			18	CATCTGGGAGC	0.522
-	24	3659	e.1_Missense_M	NM_006306	NP_006297	Q14683	SMC1A_HUMAN			6	TCTCGGCCTTG	0.572
-	10	1741	_p.Q536*|SMC1A_	NM_006306	NP_006297	Q14683	SMC1A_HUMAN	lexible hinge.		6	TATACTGAATACA	0.517
+	5	622	_Mutation_p.Q15	NM_001031745	NP_001026915	Q8N443	RIBC1_HUMAN			0	TGCAGCAGGGG	0.522
-	82	13220	sn.2_Missense_M	NM_031407	NP_113584	Q7Z6Z7	HUWE1_HUMAN	HECT.		17	AGTTGGACTGG	0.463
-	75	11935	p.P2653S|HUWE1	NM_031407	NP_113584	Q7Z6Z7	HUWE1_HUMAN			17	CAGGGGTAACT	0.537
-	11	2419	noh.1_Missense_	NM_017848	NP_060318	Q9NX05	F120C_HUMAN			2	TTCGGCCACCA	0.393
-	23	5663	nse_Mutation_p.P	NM_001002838	NP_001002838	Q9BYP7	WNK3_HUMAN			11	TTTAGGACCAG	0.438
-	5	1478	tc.1_Missense_Mu	NM_001002838	NP_001002838	Q9BYP7	WNK3_HUMAN	rotein kinase.		11	AATAAGGATACT	0.373
+	12	1232	L3L_uc004dti.2_R	NM_019067	NP_061940	Q9NVN8	GNL3L_HUMAN			1	TGACGGCAGTG	0.547
-	8	1355		NM_198510	NP_940912	Q6UXX5	ITH5L_HUMAN	VWFA.	p.S442S(1)	6	CCAGGGACAGG	0.577
+	7	1108		NM_174912	NP_777572	Q6GMR7	FAAH2_HUMAN			3	AATGTCCAAAGT	0.303
-	9	1122	_p.A352T|MTMR8_	NM_017677	NP_060147	Q96EF0	MTMR8_HUMAN	ularin phosphatase.		4	GCTAGCCACTG	0.443
-	10	1292	_p.P390L|LAS1L_	NM_031206	NP_112483	Q9Y4W2	LAS1L_HUMAN			4	AGGCTGGCAGT	0.592
+	4	523		NM_002444	NP_002435	P26038	MOES_HUMAN	FERM.		10	AAAGAGGGCATT	0.498
-	2	345	_Mutation_p.S73	NM_007268	NP_009199	Q9Y279	VSIG4_HUMAN	xtracellular (Potential).		0	CTCCAGAAGAG	0.552
-	9	1061	_p.A256D|OPHN1_	NM_002547	NP_002538	O60890	OPHN1_HUMAN			2	TGGGGAGCTTCT	0.378
-	2	1710	g.2_Missense_Mu	NM_145119	NP_660095	Q8NG27	PJA1_HUMAN			0	TTATCCCCCTCA	0.478
-	2	852	g.2_Intron|PJA1_	NM_145119	NP_660095	Q8NG27	PJA1_HUMAN			0	AGCATCTTGCT	0.537
+	2	206	1_5'Flank|PDZD11	NM_012310	NP_036442	O95239	KIF4A_HUMAN	inesin-motor.		4	GCGAGGGCTGC	0.582
+	12	1436	_p.L437F|KIF4A_	NM_012310	NP_036442	O95239	KIF4A_HUMAN	Potential.		4	AAGAGCTCAGG	0.458
+	15	2199	9_splice|DLG3_uc	NM_021120	NP_066943	Q92796	DLG3_HUMAN			2	TCTCTAGTTCAC	0.532
+	2	1426	XO4_uc004dyt.1_	NM_005938	NP_005929	P98177	FOXO4_HUMAN			3	AGAAGGGTGCT	0.612
-	4	333	mpp.1_Splice_Sit	NM_001025265	NP_001020436	A6NEN9	CX065_HUMAN			1	TTCTTACCAAGC	0.502

+	37	5226	p.G1676D|MED12	NM_005120	NP_005111	Q93074	MED12_HUMAN	with CTNNB1 and GLI3.		4	GCAGGGTCTAC	0.463
+	7	2390	ps.1_Missense_M	NM_018977	NP_061850	Q9NZ94	NLGN3_HUMAN	ical; (Potential).		1	TGGGGGCCTCC	0.637
-	13	2236	ense_Mutation_p.A	NM_201599	NP_963893	Q14202	ZMYM3_HUMAN	MYM-type 9.		1	GGCAGCCTGAG	0.597
+	10	844	B1BP2_uc004dzs	NM_012278	NP_036410	Q9UKP3	ITBP2_HUMAN	CS.		1	CTGGGGGGTAA	0.493
+	24	3751	nse_Mutation_p.L	NM_138923	NP_620278	P21675	TAF1_HUMAN	HMG box.		17	GGCGGCTTAAG	0.468
+	36	5248	0nle.1_RNA|TAF1_	NM_138923	NP_620278	P21675	TAF1_HUMAN	cidic tail).|P	p.E1733D(1)	17	ATGAAGAAGGA	0.473
+	5	753	n_p.C169Y|OGT_	NM_181672	NP_858058	O15294	OGT1_HUMAN	TPR 4.		5	GGCATGTTATTT	0.428
+	8	1232	n_p.E329K|OGT_	NM_181672	NP_858058	O15294	OGT1_HUMAN	TPR 9.		5	AACGAGAACAG	0.438
+	8	1294	RN1_uc011mpt.1_	NM_052957	NP_443189	Q96QF7	ACRC_HUMAN	Asp/Ser-rich.		3	AAGCTCCCGAC	0.557
+	8	1324	RN1_uc011mpt.1_	NM_052957	NP_443189	Q96QF7	ACRC_HUMAN	Asp/Ser-rich.		3	AAGCTCCCGAC	0.557
+	8	1334_1335	RN1_uc011mpt.1_	NM_052957	NP_443189	Q96QF7	ACRC_HUMAN	Asp/Ser-rich.		3	CGACAGCAGTG	0.55
+	11	2151	RN1_uc011mpt.1_	NM_052957	NP_443189	Q96QF7	ACRC_HUMAN			3	AAGATGGTGAA	0.443
-	2	121	CXCR3_uc011mpx.	NM_001504	NP_001495	P49682	CXCR3_HUMAN	ellular (Potential).		3	GGAGGGCGGCA	0.572
-	2	3222	C6L_uc004eap.1_	NM_017669	NP_060139	Q2NKX8	ERC6L_HUMAN			3	TTTATGCTTGAG	0.358
-	7	808		NM_001007	NP_000998	P62701	RS4X_HUMAN			0	GGGAAGAGAAA	0.502
-	19	2364	e_Mutation_p.R68	NM_002637	NP_002628	P46020	KPB1_HUMAN			4	GGAACCGATCT	0.517
+	1	1813		NM_020932	NP_065983	Q9HCI5	MAGE1_HUMAN	MAGE 1.		6	GGCGAGCAGCA	0.473
-	1	518	.2_Intron|ATP7A_	NM_001029891	NP_001025062	Q8N0Y7	PGAM4_HUMAN			0	TCTGGGGAACT	0.522
+	2	1439		NM_005296	NP_005287	Q99677	LPAR4_HUMAN	lasmic (Potential).		3	GCCTTCCCTTC	0.408
+	2	1462		NM_005296	NP_005287	Q99677	LPAR4_HUMAN	lasmic (Potential).		3	AGGAAGTGAGT	0.403
-	8	1066	uc004edu.2_5'UT	NM_153252	NP_694984	Q6RI45	BRWD3_HUMAN	WD 4.		4	TGGAAGTAATAG	0.383
+	2	582	10nmm.2_Missen	NM_003022	NP_003013	O75368	SH3L1_HUMAN	inding (Potential).		1	CACAGGTTACC	0.393
-	5	482	KA6_uc011mqu.1	NM_014496	NP_055311	Q9UK32	KS6A6_HUMAN	otein kinase 1.		8	TTTGACAATAAAT	0.269
-	3	1253	_p.A382T|HDX_uc	NM_144657	NP_653258	Q7Z353	HDX_HUMAN			2	TAGATGCTGTAT	0.338
-	6	844	es.2_Missense_M	NM_024921	NP_079197	Q8WVV4	POF1B_HUMAN			0	ATCCACTATGG	0.413
+	6	1258	_p.G196D|DACH	NM_053281	NP_444511	Q96NX9	DACH2_HUMAN			5	AGCTGGTACCT	0.403
+	1	870	H2_uc004efu.3_I	NM_013347	NP_037479	Q13156	RFA4_HUMAN			0	TGCTGGGGATA	0.493
-	6	4594	_p.P925L|PCDH1	NM_020766	NP_001098713	Q8TAB3	PCD19_HUMAN	lasmic (Pot	p.P973P(1)	7	TCCGGGGCATC	0.488
-	6	751	Mutation_p.T182I|	NM_007052	NP_008983	Q9Y5S8	NOX1_HUMAN	tial).|Ferric oxidoreductase.		1	GCTATTGTCATG	0.433
+	19	2236	rg.1_Missense_M	NM_006733	NP_006724	Q92674	CENPI_HUMAN			1	TCCAAACCCTTT	0.358
+	22	2885	h.1_Missense_Mu	NM_001939	NP_001930	Q13474	DRP2_HUMAN			2	CCGAGGCCCGTA	0.607
-	8	796	p.E176K|TAF7L_	NM_024885	NP_079161	Q5H9L4	TAF7L_HUMAN			1	ATTTTCCACGT	0.448
-	15	1655	TK_uc010nnm.2_	NM_000061	NP_000052	Q06187	BTK_HUMAN	rotein kinase.		6	CATCTCCCTCA	0.542
-	3	1475	p.P374S|ARMCX2	NM_177949	NP_808818	Q7L311	ARMX2_HUMAN			6	AAAGGGGCGCT	0.542
-	3	626	_p.D91N|ARMCX2	NM_177949	NP_808818	Q7L311	ARMX2_HUMAN	Ala-rich.		6	TGTGTCCAGAG	0.627
-	2	4741	in.2_Missense_Mu	NM_032441	NP_115817	Q5H9K5	ZMAT1_HUMAN			1	CTTGACTCTAT	0.383
+	6	1618	ejh.2_Missense_M	NM_022838	NP_073749	Q6P1M9	ARMX5_HUMAN			1	AGAAGGAAACT	0.473
+	6	2007	ejh.2_Missense_M	NM_022838	NP_073749	Q6P1M9	ARMX5_HUMAN			1	GTATGGTGGAT	0.378
+	5	3376	.G859R|GPRASP	NM_014710	NP_055525	Q5JY77	GASP1_HUMAN	Glu-rich.		2	TGGCAGGAGTC	0.532
+	4	1447	P2_uc004ejm.2_	NM_138437	NP_612446	Q96D09	GASP2_HUMAN			1	CAGACCCAAGG	0.572
+	4	1640	mrt.1_Missense_	NM_001142526	NP_001135998	Q6PI77	BHLH9_HUMAN			2	CATTTGCCCAA	0.363
+	4	2036	mrt.1_Missense_	NM_001142526	NP_001135998	Q6PI77	BHLH9_HUMAN			2	TTGGCAGCATTA	0.353
-	3	794		NM_001012979	NP_001012997	Q5H9L2	TCAL5_HUMAN			2	AAAACCACCCA	0.517
-	5	989	ou.2_Missense_M	NM_001024452	NP_001019623	Q5JXX5	GLRA4_HUMAN	ellular (Potential).		0	TCTCAAGCTGCA	0.303
-	2	212		NM_001012755	NP_001012773	Q5H9E4	MCAR6_HUMAN			0	AAGCTCCTTCC	0.517
+	4	960	mg.1_Missense_	NM_152423	NP_689636	Q5H9M0	MUML1_HUMAN			4	TTTGAGTCAAG	0.438
+	5	842	nse_Mutation_p.G	NM_017752	NP_060222	Q0IIM8	TBC8B_HUMAN			4	CCAAGGAGAGA	0.358

-	4	539	my.1_Missense_M	NM_018301	NP_060771	Q96IZ5	RBM41_HUMAN		1	AAGAGCCTTAAG	0.408	
-	8	790	L_uc004enb.2_Sp	NM_017681	NP_060151	Q9H1M0	N62CL_HUMAN		0	GTGGAGCTAAAA	0.353	
-	3	438	e_Mutation_p.A11	NM_002814	NP_002805	O75832	PSD10_HUMAN	nteraction with RELA.	1	TCGAAGCTGCAT	0.433	
-	30	2970	nsn.1_Missense_M	NM_001847	NP_001838	Q14031	CO4A6_HUMAN	le-helical region.	8	GGACTAGGTATTC	0.547	
-	23	1988	nsn.1_Missense_M	NM_001847	NP_001838	Q14031	CO4A6_HUMAN	le-helical region.	8	ACGGGGTCCAG	0.547	
+	45	4227	p.G1339E|COL4A	NM_033380	NP_203699	P29400	CO4A5_HUMAN	le-helical region.	4	GAAAGGACCCA	0.473	
-	1	125		NM_003604	NP_003595	O14654	IRS4_HUMAN		10	GGGTGGTCACC	0.637	
-	17	3383	Y2F_uc011msq.1_	NM_001522	NP_001513	P51841	GUC2F_HUMAN	lasmic (Potential).	8	CCTCACTCAGA	0.428	
-	4	675	ok.2_Missense_M	NM_022977	NP_075266	O60488	ACSL4_HUMAN	lasmic (Potential).	3	TATGGACTTCCA	0.403	
+	3	1559	nsr.1_Missense_M	NM_020769	NP_065820	Q8NET4	RGAG1_HUMAN		4	CATGACCACCT	0.502	
-	5	668	.2_Missense_Mut	NM_001143981	NP_001137453	Q9BU40	CRDL1_HUMAN		0	GTTCACTGGGG	0.473	
+	17	2124	19_splice|ALG13_uc011mta.1_Splice_Site_p.R593_spli			Q9NP73	ALG13_HUMAN		1	ATCTCGGTAAGT	0.368	
-	2	426	PL1_uc010nqa.2_	NM_178175	NP_835469	Q86WI0	LHPL1_HUMAN		0	AGCCAGTAAGG	0.557	
+	3	535	S3_uc004eqe.2_	NM_005032	NP_005023	P13797	PLST_HUMAN		2	CATTACCAGGA	0.343	
+	3	511_512		NM_000686	NP_000677	P50052	AGTR2_HUMAN	Name=2; (Potential).	3	GGGCAACCTATT	0.381	
-	5	732	.P218S|KLHL13_	NM_033495	NP_277030	Q9P2N7	KLH13_HUMAN	BACK.	2	ATGCAGGAAAT	0.438	
+	18	2924	ntr.1_Nonsense_M	NM_019045	NP_061918	Q5JSH3	WDR44_HUMAN		5	TTCTGGGAAGG	0.333	
+	8	898	eqq.2_Missense_	NM_144658	NP_653259	Q5JSL3	DOC11_HUMAN		3	AGTTTAGTTCAA	0.358	
+	12	1400	eqq.2_Missense_M	NM_144658	NP_653259	Q5JSL3	DOC11_HUMAN		3	TTCACCCGAAT	0.473	
+	47	5344	qq.2_Missense_M	NM_144658	NP_653259	Q5JSL3	DOC11_HUMAN	DHR-2.	3	CTTTTAGGCACT	0.299	
+	10	2036	RF3_uc004eqy.2_	NM_001031855	NP_001027026	Q496Y0	LONF3_HUMAN	Lon.	2	CTCATGGGATTA	0.438	
+	2	330	1B4_uc011mtx.1_	NM_001142447	NP_001135919	Q9UN42	AT1B4_HUMAN	lear (Potential).	2	GCCTGGTGGCA	0.343	
-	3	855	4esz.2_Missense_	NM_152692	NP_689905	Q96EU7	C1GLC_HUMAN	enal (Potential).	0	GTGGCCTAGAT	0.373	
+	14	2425	e_Mutation_p.P71	NM_007325	NP_015564	P42263	GRIA3_HUMAN	ellular (Potential).	5	GGAGCCATCTG	0.453	
+	32	3959	c.2_Missense_Mu	NM_006603	NP_006594	Q8N3U4	STAG2_HUMAN		5	AGAGAGAACAG	0.338	
-	29	7299	.Y2418C|ODZ1_u	NM_014253	NP_055068	Q9UKZ4	TEN1_HUMAN	ellular (Potential).	23	ACTGGGTAGTTA	0.358	
-	23	4332	.S1429F|ODZ1_u	NM_014253	NP_055068	Q9UKZ4	TEN1_HUMAN	tracellular (Potential).	23	GAGTGGAGTGA	0.532	
-	5	974	p.A304T|ODZ1_u	NM_014253	NP_055068	Q9UKZ4	TEN1_HUMAN	inal.|Cytoplasmic (Potential	23	AAAGGCAGGTC	0.522	
-	1	1055		NM_001013628	NP_001013650	Q5VW00	DC122_HUMAN		7	ACAGGGGCCGG	0.617	
-	1	1084		NM_138289	NP_612146	Q8TDG2	ACTT1_HUMAN		5	ATGTCTGCATAA	0.522	rs141475882
-	1	969		NM_138289	NP_612146	Q8TDG2	ACTT1_HUMAN		5	GGGCACTTGGT	0.547	
-	19	2445	muk.1_Missense_	NM_003069	NP_003060	P28370	SMCA1_HUMAN		4	CCGTGGAGCCT	0.338	
-	2	509	HC9_uc004eux.1_	NM_001008222	NP_001008223	Q9Y397	ZDHC9_HUMAN	ical; (Potential).	1	ATGTCCCCAGG	0.512	
-	9	1613	e.3_Missense_Mu	NM_001421	NP_001412	Q99607	ELF4_HUMAN		1	CACGGGGGCCA	0.592	
+	9	955	T|SLC25A14_uc0	NM_003951	NP_003942	O95258	UCP5_HUMAN	ical; Name=5; (Potential).	1	GTTTGGCTGGG	0.488	
+	6	656		NM_016024	NP_057108	Q9Y388	RBMX2_HUMAN	Lys-rich.	4	AAAAGGATGAC	0.483	
-	8	1142	evy.2_Missense_M	NM_182314	NP_872114	Q16206	ENOX2_HUMAN		1	TGGGGGTGGAG	0.438	
-	6	938	p.P223S|IGSF1_	NM_001555	NP_001546	Q8N6C5	IGSF1_HUMAN	3.|Extracellular (Potential).	5	CCCAGGATGGG	0.473	
-	1	358		NM_016521	NP_057605	Q5H9I0	TFDP3_HUMAN		1	AGTAGGAATGC	0.557	
-	1	327	27B_uc004eyg.3_	NM_001078172	NP_001071640	Q9BWD3	F127B_HUMAN		0	GTAGGGGATCA	0.602	
-	1	165	eyg.3_Missense_	NM_001078172	NP_001071640	Q9BWD3	F127B_HUMAN		0	AAAGGGAATCG	0.662	
+	3	1107		NM_001727	NP_001718	P32247	BRS3_HUMAN	Name=7; (Potential).	1	TTGGCTTTCAGC	0.458	
-	6	1138	_p.P99S|ARHGEF	NM_004840	NP_004831	Q15052	ARHG6_HUMAN		0	TTTTGGGGAGA	0.318	
-	1	1168		NM_054021	NP_473362	Q96P66	GP101_HUMAN	lasmic (Potential).	5	CCTGGGCAGAG	0.527	rs41310741
-	1	1051		NM_054021	NP_473362	Q96P66	GP101_HUMAN	lasmic (Potential).	5	GTCATCTTCACC	0.527	
+	1	1218		NM_003413	NP_003404	O60481	ZIC3_HUMAN		3	CGGCGCCTTCT	0.642	
-	1	196		NM_004065	NP_004056	P51861	CDR1_HUMAN		0	ACCAAGCCATGT	0.428	

+	4	3068	EC1_uc010nsl.1_	NM_005462	NP_005453	O60732	MAGC1_HUMAN	MAGE.	4	AAGCAGCCTATC	0.473	
+	5	781		NM_152578	NP_689791	Q8N0W7	FMR1N_HUMAN	lasmic (Potential).	1	GCGAAAGAGGA	0.413	
+	3	1362	.2_Nonsense_Mut	NM_002025	NP_002016	P51816	AFF2_HUMAN		5	ATGGCCAGGAC	0.483	
+	13	3219	.1_Missense_Mut	NM_002025	NP_002016	P51816	AFF2_HUMAN		5	TATTTCCTCCT	0.433	
-	9	1409	.1_Missense_Mut	NM_000202	NP_000193	P22304	IDS_HUMAN		0	GAGACACAAGT	0.532	
+	5	541	|CXorf40A_uc004f	NM_178124	NP_835225	Q8TE69	CX04A_HUMAN		0	CATTGGGGAAA	0.468	
-	4	581	f40B_uc011mxs.1_	NM_001013845	NP_001013867	Q96DE9	CX04B_HUMAN		0	TCCACAGTCTTG	0.607	
+	5	648	MGB3_uc004fer.2	NM_005342	NP_005333	O15347	HMGB3_HUMAN	Glu-rich (acidic).	0	agatgaagaagagga	0.299	
-	3	1574	tx.2_Missense_M	NM_001103151	NP_001096621	Q96PV4	PNMA5_HUMAN		2	CCTTGGGATAC	0.617	
-	3	266		NM_004988	NP_004979	P43355	MAGA1_HUMAN		10	CTCAAGGGCTT	0.632	
+	4	469	_p.E98K|ZNF275_uc011myn.1_Missense_Mutation_p.			A6NFS0	A6NFS0_HUMAN		1	CCCATAGAACAT	0.552	
+	7	1001	N_uc004fhq.1_R	NM_001711	NP_001702	P21810	PGS1_HUMAN	LRR 9.	2	TCCTGCCCACC	0.607	
+	8	1199	N_uc004fhq.1_R	NM_001711	NP_001702	P21810	PGS1_HUMAN	LRR 12.	2	CCGTGCCCTAC	0.592	
+	15	2624	_Mutation_p.T83	NM_001001344	NP_001001344	Q16720	AT2B3_HUMAN	lasmic (Potential).	1	CTTCACCAGCA	0.562	
+	20	3553	nse_Mutation_p.	NM_001001344	NP_001001344	Q16720	AT2B3_HUMAN	lasmic (Potential).	1	TCATGGCCACG	0.592	
+	3	917	hy.3_Missense_M	NM_001395	NP_001386	Q99956	DUS9_HUMAN	protein phosphatase.	2	CACCCCCAACC	0.562	
+	7	1798	.G224S|PLXNB3_	NM_005393	NP_005384	Q9ULL4	PLXB3_HUMAN	ellular (Potential).	1	AGCAGGGCCAG	0.677	
+	25	4466	zd.1_Missense_M	NM_005393	NP_005384	Q9ULL4	PLXB3_HUMAN	lasmic (Potential).	1	CCTGGCGGCCC	0.642	
+	27	4831	NB3_uc011mzd.1_	NM_005393	NP_005384	Q9ULL4	PLXB3_HUMAN	lasmic (Potential).	1	TCAAGGAGAAG	0.682	
+	34	5702	3_uc004fik.2_5'UT	NM_005393	NP_005384	Q9ULL4	PLXB3_HUMAN	lasmic (Potential).	1	GAACTCTGCTT	0.647	
+	14	1479	p.E407K|SRPK3_	NM_014370	NP_055185	Q9UPE1	SRPK3_HUMAN	rotein kinase.	3	TAGTGGAGCTT	0.667	
-	23	3155	G1016E|L1CAM_	NM_000425	NP_000416	P32004	L1CAM_HUMAN	III 5.|Extracellular (Potentia	9	AGATCCCTGGG	0.612	
-	22	2983	.D959N|L1CAM_	NM_000425	NP_000416	P32004	L1CAM_HUMAN	tential).|Fibronectin type-III	9	CTCATCCACTG	0.682	
-	11	1457	uo.2_Missense_M	NM_000425	NP_000416	P32004	L1CAM_HUMAN	otential).|Ig-like C2-type 5.	9	CGAAGGCCTTG	0.622	
-	4	490	GAP4_uc004fjl.1_	NM_001666	NP_001657	P98171	RHG04_HUMAN	Potential.	1	CTGCTCCAGAT	0.652	
-	17	3433		NM_005334	NP_005325	P51610	HCFC1_HUMAN		2	CTCCACCCCAC	0.637	
-	9	2099		NM_005334	NP_005325	P51610	HCFC1_HUMAN		2	CCATCCGCACT	0.597	
+	2	640	3202-2|MI001425	NM_003492	NP_003483	Q14656	TM187_HUMAN		0	AAGTGGGCTAT	0.652	
-	4	1480	jw.2_Missense_M	NM_004992	NP_004983	P51608	MECP2_HUMAN		0	TCTGGGCATCTT	0.667	
+	5	826		NM_020061	NP_064445	P04000	OPSR_HUMAN	Cytoplasmic.	0	AGAAGGAAGTG	0.572	
+	13	1879	zm.1_Missense_M	NM_012253	NP_036385	P51854	TKTL1_HUMAN		4	TGTCGGGAGTG	0.522	
-	37	6142	.1_Missense_Mut	NM_001110556	NP_001104026	P21333	FLNA_HUMAN	Filamin 18.	6	GCCGACCTTTA	0.642	
-	8	1330	u.1_Missense_Mu	NM_001110556	NP_001104026	P21333	FLNA_HUMAN	Filamin 1.	6	GCCAGCAAAGA	0.647	
+	3	261	S|RPL10_uc004fk	NM_006013	NP_006004	P27635	RL10_HUMAN		0	GCCGAGGTGTC	0.537	
+	3	330	|DNASE1L1_uc0	NM_006013	NP_006004	P27635	RL10_HUMAN		0	TGGGAGACCTC	0.607	
+	4	1455		NM_017514	NP_059984	P51805	PLXA3_HUMAN	tracellular (Potential).	3	TCTGTGGTCTTC	0.662	
-	2	412	nh.1_Missense_M	NM_020994	NP_066274	O75638	CTAG2_HUMAN		1	CCGCCCCTGGT	0.642	
-	6	659	nq.1_Missense_M	NM_002436	NP_002427	Q00013	EM55_HUMAN	SH3.	3	TCCCGCCTCCT	0.493	
-	13	2252		NM_000132	NP_000123	P00451	FA8_HUMAN	2.|Plastocyanin-like 4.	11	TTTCTCCTGAG	0.403	
-	3	527	.1_Missense_Mut	NM_000132	NP_000123	P00451	FA8_HUMAN	in-like 1.|F5/8 type A 1.	11	CAACAGCATGA	0.433	
-	3	503	.1_Missense_Mut	NM_000132	NP_000123	P00451	FA8_HUMAN	in-like 1.|F5/8 type A 1.	11	GGGAAGCCATG	0.443	
+	2	551	vl.1_Missense_M	NM_005840	NP_005831	O43610	SPY3_HUMAN		0	CTCCAGCCCCC	0.517	
+	17	4502	_p.T475I|CAMTA	NM_015215	NP_056030	Q9Y6Y1	CMTA1_HUMAN		9	TGCCACCATTA	0.512	
-	2	357		NM_001009611	NP_001009611	O60810	PRAM4_HUMAN		1	GGGACGAACCC	0.622	rs76269416
-	78	11600	4_uc001bbj.1_3'	NM_020765	NP_065816	Q5T4S7	UBR4_HUMAN		25	TGTGTGGCCAC	0.592	
-	14	2598	.1_RNA|EPHA10_	NM_001099439	NP_001092909	Q5JZY3	EPHAA_HUMAN	Potential).|Protein kinase.	8	TCACCTCCCACA	0.612	
-	6	701	H2_uc010olg.1_I	NM_003738	NP_003729	Q9Y6C5	PTC2_HUMAN	ellular (Potential).	18	CAAGGAGGCA	0.637	

-	14	1740	r.1_Missense_Mut	NM_021080	NP_066566	O75553	DAB1_HUMAN		3	CACAGTTGGCC	0.652	
+	7	1151	va.1_Missense_M	NM_001144937	NP_001138409	Q5VTL7	FNDC7_HUMAN	nectin type-III 5.	2	GGTGTCCAGTG	0.517	
+	15	1680	_p.P459L|FAM40A	NM_033088	NP_149079	Q5VSL9	FA40A_HUMAN		4	AGATGCCGTGAG	0.502	
-	14	2609	ENND2C_uc001ef	NM_198459	NP_940861	Q68D51	DEN2C_HUMAN	DENN.	3	GTCCAGGAGCT	0.443	
-	12	2659		NM_020205	NP_064590	Q6GQQ9	OTU7B_HUMAN		3	GGTAGGGGGGT	0.612	
-	3	4628	uc001ezv.2_Intron	NM_001014342	NP_001014364	Q5D862	FILA2_HUMAN		17	TGTGTCCTGAAT	0.502	
-	8	1539	sn.2_RNA|FCRL3_	NM_052939	NP_443171	Q96P31	FCRL3_HUMAN	5.|Extracellular (Potential).	4	TAAAATCGGTAC	0.587	
+	15	2581	sense_Mutation_p	NM_018240	NP_060710	Q96J84	KIRR1_HUMAN	lasmic (Potential).	1	ATGACCCCATTG	0.642	
+	2	557	1C_uc001frv.2_5'F	NM_001765	NP_001756	P29017	CD1C_HUMAN	cellular (Pote p.R89C(1)	4	TTATTTCGTTTCT	0.398	rs145638725
+	2	220	_Mutation_p.G57	NM_002348	NP_002339	Q9HBG7	LY9_HUMAN	Potential).|Ig-like V-type 1.	1	GTCAGGGATCC	0.517	
+	18	1989	orf112_uc009wvu.	NM_018186	NP_060656	Q9NSG2	CA112_HUMAN		0	ATGCAGGAAAT	0.378	
-	1	142	_p.L21F|TNR_uc	NM_003285	NP_003276	Q92752	TENR_HUMAN		11	CAGAAGGATCA	0.552	
+	6	584	_p.V42A|FAM163	NM_173509	NP_775780	Q96GL9	F163A_HUMAN		1	CGAGGTTGCAG	0.632	
-	1	303	gpk.2_Missense_	NM_021133	NP_066956	Q05823	RN5A_HUMAN	ANK 1.	5	CACCTTCCAGCA	0.502	
-	4	1533	ense_Mutation_p.	NM_018713	NP_061183	Q6XR72	ZNT10_HUMAN	lasmic (Potential).	0	TCACTTCCGTAT	0.532	
-	4	1462	695_uc009xgt.1_I	NM_020394	NP_065127	Q8IW36	ZN695_HUMAN	2H2-type 11.	0	ACATTCATCACA	0.368	
-	18	2171	p.P732L|PRKCQ_	NM_006257	NP_006248	Q04759	KPCT_HUMAN	kinase C-terminal.	6	ATCCCGGGGTTC	0.498	
+	3	992	DC2_uc001iqh.1_I	NM_032812	NP_116201	Q6UX71	PXDC2_HUMAN	cellular (Potential).	4	ATATCTCGAATAT	0.333	
+	11	1796	e_Mutation_p.E33	NM_032812	NP_116201	Q6UX71	PXDC2_HUMAN	ar (Potential).|Thr-rich.	4	CAGTGGAAACT	0.423	
-	16	2001	BL_uc001iqk.2_Int	NM_006393	NP_006384	O76041	NEBL_HUMAN	Nebulin 15.	2	TGCATTCCTTTC	0.368	
+	7	1156		NM_052997	NP_443723	Q9BXX3	AN30A_HUMAN		9	CGTGGGCAGCA	0.408	
-	7	1429	GMS1_uc009xou.	NM_147156	NP_671512	Q86VZ5	SMS1_HUMAN		2	GTACTCGTTCGT	0.483	
+	5	1284		NM_000314	NP_000305	P60484	PTEN_HUMAN	hatase tensi.Y27fs*1(2)|p.	2334	GCAGAGGTAGG	0.318	
+	1	41		NM_001102469	NP_001095939	Q5VXI9	LIPN_HUMAN		0	TCTGTGGAACTT	0.333	
-	13	1831	9ycc.2_Missense_	NM_021924	NP_068743	Q9HBB8	CDHR5_HUMAN	dem repeats.|2.|Extracellul	0	TTCCTGGCTCTG	0.667	rs139058512
+	9	1050		NM_001003678	NP_001003678	Q9H6J7	CK049_HUMAN		0	GGTACCGACGC	0.632	
+	3	738		NM_004268	NP_004259	Q9NVC6	MED17_HUMAN		1	TTGCTGGAGCA	0.373	
-	1	650		NM_001002917	NP_001002917	Q8WZ84	OR8D1_HUMAN	Name=5; (Potential).	3	GCATAGGAGACA	0.512	
-	2	940		NM_004054	NP_004045	Q16581	C3AR_HUMAN	cellular (Potential).	1	TTATCCAGTGGG	0.423	
-	3	252		NM_006248	NP_006239				0	AGGAGGTGGGG	0.607	
-	4	364	_p.R75Q|RERG_u	NM_032918	NP_116307	Q96A58	RERG_HUMAN		1	CCCATCGCATG	0.463	
-	4	1278	p.R388Q|PKP2_uc	NM_004572	NP_004563	Q99959	PKP2_HUMAN	ARM 2.	2	CTCTTCCGAGCT	0.448	
-	6	1015	.R290K|KIF21A_u	NM_017641	NP_060111	Q7Z4S6	KI21A_HUMAN	inesin-motor.	7	TTGCCCTCTCG	0.403	
-	6	1081		NM_002282	NP_002273	P78385	KRT83_HUMAN	Rod.|Coil 2.	1	CACCTCGGCTG	0.597	
-	9	1338	sense_Mutation_p.	NM_032496	NP_115885	Q9BRR9	RHG09_HUMAN		1	GAGGTCGAGGG	0.617	
+	10	2635	to.2_Missense_M	NM_018448	NP_060918	Q86VP6	CAND1_HUMAN	HEAT 17.	2	GTGGATCCATTC	0.428	
-	2	611	di.2_Missense_Mu	NM_020698	NP_065749	Q9ULS5	TMCC3_HUMAN		2	AAGAGCGATGTA	0.498	
+	4	420	ion_p.V122I|ACTR	NM_022496	NP_071941	Q9GZN1	ARP6_HUMAN		1	CAAGCAGTATTA	0.279	
-	9	2757	1uia.2_Missense_	NM_133448	NP_597705	Q14C87	T132D_HUMAN	cellular (Potential).	14	GTGTGTCTGCTG	0.498	
+	1	1360	_5'Flank|uc001ui	NM_007197	NP_009128	Q9ULW2	FZD10_HUMAN	cellular (Potential).	5	TCCAGGAGGGA	0.647	
+	7	703	UGT1_uc010thb.1	NM_001130912	NP_001124384	Q9Y2Z0	SUGT1_HUMAN		0	GAATGGTATGTG	0.308	
-	1	359	4P_uc001vwb.3_	NM_001145442	NP_001138914	A6NI47	POTEM_HUMAN		0	GTGGCAGCACC	0.632	
+	1	193		NM_001001912	NP_001001912	Q8NGC2	OR4E2_HUMAN	Name=2; (Potential).	4	CTGAGCAATCTG	0.423	
+	28	4473	bs.1_Missense_	NM_020818	NP_065869	Q9P2D8	UNC79_HUMAN		17	GGCCTGAAAAA	0.473	
+	4	595	L_uc001ygu.2_Mi	NM_016337	NP_057421	Q9UI08	EVL_HUMAN		3	AGGCCCCTCCA	0.592	
-	7	3074	px.2_Missense_	NM_138420	NP_612429	Q8IVF2	AHNK2_HUMAN		1	CCAGGGACAGG	0.612	
+	1	566	727924_uc001yu	NM_001004719	NP_001004719	Q8NGB6	OR4M2_HUMAN	cellular (Potential).	1	TTGCCTGTGCCA	0.468	

-	19	2629	un.2_Missense_M	NM_014080	NP_054799	Q9NRD8	DUOX2_HUMAN	lasmic (Potential).	5	ACTCGGCCCTG	0.632	
-	6	834		NM_003613	NP_003604	O75339	CILP1_HUMAN		7	ATGCAGGCATCA	0.582	
+	2	828	e_Mutation_p.A17	NM_015492	NP_056307	Q6ZRI6	CO039_HUMAN		0	CCTCAGCTGAC	0.622	
+	3	312	bmt.1_Missense_	NM_207517	NP_997400	P82987	ATL3_HUMAN		27	AATCTCCTGGA	0.478	
+	21	3132	p.H970Y|ADAMTS	NM_207517	NP_997400	P82987	ATL3_HUMAN	-like C2-type 1.	27	AAATCCATGGT	0.542	
-	4	1434	p.V279M|RGMA_	NM_020211	NP_064596	Q96B86	RGMA_HUMAN		0	GTTCACGTCGC	0.582	
+	1	705		NM_012360	NP_036492	O43749	OR1F1_HUMAN	lasmic (Potential).	0	AAGGTGGAAAGC	0.517	
+	5	1068	yv.1_Missense_Mu	NM_018723	NP_061193	Q9NWB1	RFOX1_HUMAN		0	CGCTTCGGCCC	0.607	
+	3	937	lgb.3_Missense_M	NM_001105248	NP_001098718	Q6UXY8	TMC5_HUMAN	cellular (Potential).	1	CACGTCCAGACT	0.483	
-	4	869	Mutation_p.P140L|	NM_201575	NP_963869	Q6UXD5	SE6L2_HUMAN	xtracellular (Potential).	2	TAGCCAGGGTAG	0.592	
-	4	541	eiz.2_Nonsense_	NM_007006	NP_008937	O43809	CPSF5_HUMAN	with PAPOLA and PABPN1	0	CATCCTGACGAC	0.403	
+	3	278	RG4_uc010vig.1_	NM_022910	NP_075061	Q9ULP0	NDRG4_HUMAN		1	ATGCAGGAGATC	0.567	
-	7	1120	ep.1_Missense_Mu	NM_012091	NP_036223	Q9BUB4	ADAT1_HUMAN	to I editase.	2	CATGGCTTCCT	0.378	
+	1	266		NM_020927	NP_065978	Q9HCJ6	VAT1L_HUMAN		1	AGCTGCGGCTC	0.687	
-	7	1203	fgj.2_Missense_Mu	NM_052892	NP_443124	Q7Z442	PK1L2_HUMAN	cellular (Potential).	3	GAGCCCTTTTG	0.522	
+	2	103	.2_Intron|KIAA018	NM_014615	NP_055430	Q14687	GSE1_HUMAN		5	CCAAGTCCCCTT	0.662	
-	9	1179	cjf.2_Intron|PRDM	NM_001098173	NP_001091643	Q9NQW5	PRDM7_HUMAN		1	CCCCATACCAG	0.522	
-	9	1090	cjf.2_Intron|PRDM	NM_001098173	NP_001091643	Q9NQW5	PRDM7_HUMAN	SET.	1	CCCCAGACCAG	0.532	
+	56	8725	H2_uc010cnm.1_5	NM_020877	NP_065928	Q9P225	DYH2_HUMAN	4 (By similarity).	13	GATCCGCCAGT	0.557	rs2309808
-	19	2837	2_5'Flank|PER1_u	NM_002616	NP_002607	O15534	PER1_HUMAN	Pro-rich.	9	CCAGGGGGTGG	0.677	
-	21	2453	uc002gml.1_Intron	NM_017533	NP_060003	Q9Y623	MYH4_HUMAN	osin head-like.	13	TCATCTCGCATTT	0.433	
+	6	859	hhr.2_Missense_M	NM_015544	NP_056359	Q9Y2Y6	TMM98_HUMAN		0	CAAGCGGATCA	0.587	rs147119833
-	1	110		NM_033185	NP_149441	Q9BYR6	KRA33_HUMAN	repeats of C-C-X(3).	0	GGCAGGATTTG	0.587	
-	1	107		NM_031959	NP_114165	Q9BYR7	KRA32_HUMAN	repeats of C-C-X(3).	0	GGCAGGATTTG	0.602	
-	1	225		NM_032524	NP_115913	Q9BYR3	KRA44_HUMAN	f C-C-[GRQVCH]-[SPT]- [V	0	TGGGGTGGCAG	0.662	
+	1	1312		NM_001466	NP_001457	Q14332	FZD2_HUMAN	cellular (Potential).	3	AGATCGACGGC	0.667	
+	2	356	0_uc002ird.2_Miss	NM_022827	NP_073738	Q8TB22	SPT20_HUMAN		0	ACCATACCTCC	0.612	
+	1	526	uc010wna.1_RNA	NM_032559	NP_115948	Q8N4N8	KIF2B_HUMAN		8	AAAACCAAACA	0.592	
+	2	523	ac.2_Missense_Mu	NM_006039	NP_006030	Q9UBG0	MRC2_HUMAN	otential).|Ricin B-type lectin	3	CAGAACCCAAC	0.557	
-	1	476	issense_Mutation_	NM_001039360	NP_001034449	A1YPR0	ZBT7C_HUMAN	-rich.|Asp-rich.	1	cctcctcttcgtcctcctc	0.284	
-	8	1143	p.E332K|SERPIN	NM_002974	NP_002965	P48594	SPB4_HUMAN		3	ATAATTCGACTA	0.463	
+	4	876	wq.2_Missense_M	NM_024967	NP_079243	Q9HAH1	ZN556_HUMAN	C2H2-type 5.	3	AAGCACTGTGG	0.537	
+	5	841	e_Mutation_p.E13	NM_016496	NP_057580	Q9P0N8	MARH2_HUMAN		2	GGACGGAGAAG	0.662	
-	3	15707		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).	57	GCATTGATGTG	0.493	
-	3	10927		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).	57	AGAAGTTGTGC	0.517	
-	5	600		NM_001080404	NP_001073873	C9JN71	ZN878_HUMAN	C2H2-type 2.	0	GGAAACCTGAA	0.423	
-	4	1916	799_uc002mts.3_I	NM_001080821	NP_001074290	Q96GE5	ZN799_HUMAN	C2H2-type 17.	6	TTACATTCATACG	0.413	
-	13	1897	O8_uc010eap.2_R	NM_020959	NP_066010	Q9HCE9	ANO8_HUMAN	ch.|Cytoplasmic (Potential).	3	tTGCCCCCTGG	0.134	
+	4	1280		NM_031218	NP_112495	P35789	ZNF93_HUMAN	C2H2-type 9.	1	GAGAGTTCATA	0.393	
-	4	827	pc.1_Missense_M	NM_001076675	NP_001070143	Q68DY1	ZN626_HUMAN		1	GGTTTCTCTCCA	0.393	
+	4	983	ecy.2_Missense_M	NM_033468	NP_258429	Q9Y2Q1	ZN257_HUMAN	C2H2-type 4.	0	TCACACATTACT	0.393	
-	4	1567		NM_138330	NP_612203	Q8TD23	ZN675_HUMAN	C2H2-type 12.	2	GATTGGATAAAA	0.368	
+	3	442	_p.E37G|ZNF540_	NM_152606	NP_689819	Q8NDQ6	ZN540_HUMAN	KRAB.	1	TGTTGGAGAATT	0.418	
+	44	7172	_Mutation_p.E234	NM_000540	NP_000531	P21817	RYR1_HUMAN	6 X approximate repeats.	12	TGGAGGAGAAC	0.672	
-	6	2022	ense_Mutation_p.	NM_001010880	NP_001010880	O75290	Z780A_HUMAN	C2H2-type 16.	0	AATAAGTTGCAT	0.403	
-	6	1350	wb.2_Nonsense_M	NM_002780	NP_002771	Q00888	PSG4_HUMAN		1	ggtaatatccagtctac	0	
+	8	1151		NM_005178	NP_005169	P20749	BCL3_HUMAN	ANK 7.	2	GGGGGAAGGCC	0.642	

-	1	1961		NM_032040	NP_114429	Q9H0W5	CCDC8_HUMAN		3	GGGCCTCTGCC	0.607	
-	8	1014	H2_uc002prv.3_I	NR_002798					1	GTAATCCTGGG	0.537	
+	7	1007	se_Mutation_p.S2	NM_007121	NP_009052	P55055	NR1H2_HUMAN	-binding (Potential).	0	CTTCTCCGACC	0.607	
-	5	1005	77_uc010ydf.1_5'	NM_023074	NP_075562	Q9BS31	ZN649_HUMAN	2H2-type 3.	3	CTGTACCTCTTG	0.502	
-	4	495	qeo.1_Missense_	NM_024318	NP_077294	Q6PI73	LIRA6_HUMAN	ellular (Potential).	2	GGGTGGGTTTG	0.577	
+	7	1351	_p.A388V|LILRA1_	NM_006863	NP_006854	O75019	LIRA1_HUMAN	4.|Extracellular (Potential).	3	CTCAGCCCACT	0.587	
-	4	628	se_Mutation_p.L7	NM_001145971	NP_001139443	Q8NBN7	RDH13_HUMAN		3	TCACCCAGGTGG	0.418	
-	6	337	ft.1_Missense_Mu	NM_000363	NP_000354	P19429	TNNI3_HUMAN		2	CTATGTCGTATC	0.567	rs35173650
-	4	2485	F3C_uc010ykr.1_	NM_002254	NP_002245	O14782	KIF3C_HUMAN	Potential.	4	CGCGGATATACT	0.632	
+	1	5089	1_5'Flank|ZNF512_	NM_032266	NP_115642	Q68DN1	CB016_HUMAN	em repeat of P-S-E-R-S-H	1	ATCGCGGTCCC	0.572	rs112465116
-	6	2475	rxe.3_Missense_	NM_001135659	NP_001129131	P58400	NRX1B_HUMAN		2	GAATGGGGTTT	0.378	
+	1	170	LR1A_uc002sqv.2_	NM_017952	NP_060422	Q96EY7	PTCD3_HUMAN		1	CTGCAGGTAAG	0.602	
-	5	847	AT4A_uc010fil.2_5	NM_012214	NP_036346	Q9UM21	MGT4A_HUMAN	enal (Potential).	1	CCTCTCCTATGA	0.294	
+	13	2579	2_Missense_Mutat	NM_012455	NP_036587	Q8NDX1	PSD4_HUMAN	PH.	2	ATGGGGCAAGC	0.547	
-	3	707		NM_001099771	NP_001093241	A5A3E0	POTEF_HUMAN		5	GTGGCAGCACC	0.617	
-	67	11390		NM_018557	NP_061027	Q9NZR2	LRP1B_HUMAN	ellular (Potential).	50	GTCTTTTTATCT	0.408	
-	2	496	fof.2_Missense_M	NM_145259	NP_660302	Q8NER5	ACV1C_HUMAN	ellular (Potential).	7	GCATTCGGTTTT	0.403	
-	7	1190	_p.E278K|BAZ2B_	NM_013450	NP_038478	Q9UIF8	BAZ2B_HUMAN		4	TTTCTTCAATACT	0.313	
-	26	5722		NM_006920	NP_008851	P35498	SCN1A_HUMAN		13	CTTGTTTTCGTT	0.408	
-	275	66166	676L|TTN_uc010z	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	ATTTTTGAACCT	0.453	
-	225	45513	_uc010zfi.1_Miss	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	TGGTTCAGCCA	0.423	
-	200	39450	.1_Missense_Muta	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	CTTTTCCATGTTT	0.363	
-	38	9351	.G2997R|TTN_uc0	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	TTTTCCAGCCA	0.388	
-	15	1255	frx.2_Missense_M	NM_000393	NP_000384	P05997	CO5A2_HUMAN		2	TTGGACCAGTG	0.373	
+	1	353		NM_003507	NP_003498	O75084	FZD7_HUMAN	acellular (Potential).	4	CCGAACTCCGC	0.637	
+	2	230	_Mutation_p.S27N|	NM_015934	NP_057018	Q9Y2X3	NOP58_HUMAN		0	TTGATAGTTTAT	0.289	
+	3	1073		NM_025216	NP_079492	Q9GZT5	WN10A_HUMAN		2	GCCCAGGCCTG	0.652	
+	3	798		NM_001927	NP_001918	P17661	DESM_HUMAN	od.|Coil 1B.	2	ATCGCGTTCCTT	0.562	
+	4	539	mp.1_Missense_	NM_001017915	NP_001017915	Q92835	SHIP1_HUMAN	H3-binding 1.	2	CCCAAGAAACA	0.607	
+	4	625		NM_003245	NP_003236	Q08188	TGM3_HUMAN		9	GGCTGGAACTT	0.493	
+	32	4146		NM_020884	NP_065935	A7E2Y1	MYH7B_HUMAN	Potential.	2	TGAGCCGTGGA	0.637	
+	13	3355	02xfh.2_Missens	NM_014902	NP_055717	Q9Y2H0	DLGP4_HUMAN		3	CCGAGAGCGCA	0.567	
-	2	1860	us.1_Missense_M	NM_004975	NP_004966	Q14721	KCNB1_HUMAN	lasmic (Potential).	2	GCTGGGGATAC	0.502	
+	10	1244	_p.A325T|RTEL1_	NM_016434	NP_057518	Q9NZ71	RTEL1_HUMAN		0	TCAGCGCGGAC	0.662	rs144255879
+	9	2006	31_uc002zgv.2_R	NM_015833	NP_056648	P78563	RED1_HUMAN	to I editase.	1	CAAAATAGAGT	0.517	
-	17	1594	NRD2_uc002zqp.	NM_006440	NP_006431	Q9NNW7	TRXR2_HUMAN		2	GCAGCCTGTCA	0.672	
+	17	3621		NM_001429	NP_001420	Q09472	EP300_HUMAN	Bromo.	64	CCTTTCGTCAA	0.348	
-	8	1132	.1_Splice_Site_p.	NM_001145137	NP_001138609	Q92523	CPT1B_HUMAN		2	AGTTACCTGTG	0.607	
+	2	245	HUMPD3_uc003	NM_001114092	NP_001107564	Q9BV44	THUM3_HUMAN		1	GAAGTGAATCT	0.443	
+	3	355		NM_001570	NP_001561	O43187	IRAK2_HUMAN	Death.	8	TCAGGGAAACC	0.328	
-	2	149	auj.1_Intron|GHRL	NM_016362	NP_057446	Q9UBU3	GHRL_HUMAN		1	CGGTCCCTGGG	0.647	
+	6	557	21_uc011axy.1_	NM_016300	NP_057384	Q9UBL0	ARP21_HUMAN		3	TTTTTCCAGCC	0.358	
-	8	973		NM_003335	NP_003326	P41226	UBA7_HUMAN	roximate repeats.	2	TGTGTCCAGGG	0.602	
-	8	2984		NM_198859	NP_942559	Q7Z3G6	PRIC2_HUMAN		5	AGGCGCGCTG	0.557	
-	34	5269	_p.K1718I|ADAMT	NM_182920	NP_891550	Q9P2N4	ATS9_HUMAN	GON.	4	GCACCTTTAAGT	0.383	
+	4	1017_1018	p.G140K|CADM2_	NM_153184	NP_694854	Q8N3J6	CADM2_HUMAN	1.|Extracellular (Potential).	4	TTAGTGGATTCT	0.381	
+	14	1659	K11_uc010htn.2_	NM_024800	NP_079076	Q8NG66	NEK11_HUMAN		6	CTATTCCTTCC	0.428	

-	5	5231	_5'Flank|IGSF10_	NM_178822	NP_849144	Q6WRI0	IGS10_HUMAN		13	TGGGAGGATAG	0.517	
-	11	1412	_p.G298E|UBXN7_	NM_015562	NP_056377	O94888	UBXN7_HUMAN	UBX.	3	GGTATCCTTTAG	0.383	
-	3	324	X1_uc003gbj.2_In	NM_006651	NP_006642	O14810	CPLX1_HUMAN	Potential.	0	CTCCTCCGCCT	0.612	
+	1	223		NM_152679	NP_689892	Q96EP9	NTCP4_HUMAN	ellular (Potential).	1	CCATGGACGGC	0.627	
+	6	720	LB_uc003hgu.3_	NM_000477	NP_000468	P02768	ALBU_HUMAN	Albumin 2.	6	GGCTTCGTCTG	0.373	
+	6	774	_p.P241L|AIMP1_	NM_001142415	NP_001135887	Q12904	AIMP1_HUMAN	RNA-binding.	0	GGCTCCTCCAA	0.378	
-	19	5144		NM_017639	NP_060109	Q6V1P9	PCD23_HUMAN	Cadherin 15.	4	TGTCCTGAATT	0.333	
+	22	3587		NM_139056	NP_620687	Q8TE57	ATS16_HUMAN	SP type-1 6.	8	GAGGTCCGTGC	0.657	
+	11	2152		NM_020227	NP_064612	Q9NQV7	PRDM9_HUMAN	2H2-type 6.	6	GAGGAGACACA	0.607	rs112679149
-	4	1452	_p.H368Y|ANKRD	NM_001004441	NP_001004441	A5PLL1	AN34B_HUMAN		1	TGTAGTGATTTG	0.448	
+	7	1504	xu.1_Missense_M	NM_021982	NP_068817	O95486	SC24A_HUMAN		0	AACTTCCTTTG	0.299	
+	1	2119		NM_018940	NP_061763	Q9Y5E2	PCDB7_HUMAN	|Extracellular (Potential).	6	ATGGCGAGCCT	0.716	
+	1	2963	B9_uc003liw.1_5'	NM_020957	NP_066008	Q9NRJ7	PCDBG_HUMAN	|Extracellular (Potential).	2	GCTGTCGTACC	0.721	
-	8	1103	b.1_Missense_Mu	NM_000129	NP_000120	P00488	F13A_HUMAN		6	GGCATCGTAAA	0.408	rs121913072
-	3	1688		NM_052923	NP_443155	Q6R2W3	SCND3_HUMAN		1	AGTTTTGAATTTT	0.368	
-	3	589	ron|uc010jub.1_5'	NM_002124	NP_002115	P01911	2B1F_HUMAN	ta-2.|Extracellular (Potenti	1	AAGGTCCAGTC	0.557	
+	9	3112	D2_uc003ocp.3_	NM_005104	NP_005095	P25440	BRD2_HUMAN		5	TGCCCCCTGGC	0.408	
+	89	13586		NM_001371	NP_001362				21	GGAAAGAAATG	0.443	
-	4	1526	p.P492L|CUL7_uc	NM_014780	NP_055595	Q14999	CUL7_HUMAN	action with TP53.	4	CAGGAGGCACA	0.602	
-	4	1577	P5_uc011dvz.1_	NM_021572	NP_067547	Q9UJA9	ENPP5_HUMAN		0	ACTGTGAATTA	0.348	
-	3	1079	lvz.1_Missense_M	NM_021572	NP_067547	Q9UJA9	ENPP5_HUMAN		0	ATTAGGATGAG	0.408	
-	3	240	zx.2_Missense_	NM_001131	NP_001122	P54107	CRIS1_HUMAN		0	CTACTCTTCTC	0.378	
+	3	284	RMT11_uc010kev.	NM_001031712	NP_001026882	Q7Z4G4	TRM11_HUMAN		1	GCATTCCCTCT	0.348	
+	23	2389		NM_006208	NP_006199	P22413	ENPP1_HUMAN	xtracellular (Potential).	4	AAATGGTGTCA	0.393	
-	11	1526		NM_015718	NP_056533	Q9HBY0	NOX3_HUMAN	lasmic (Potential).	1	ATATATGATAACT	0.413	
+	24	3578	o.2_Nonsense_M	NM_152744	NP_689957	Q7Z5N4	SDK1_HUMAN	nectin type-III 5.	6	GATTTCGAATG	0.537	
-	5	615	_p.S143F|DGKB_u	NM_004080	NP_004071	Q9Y6T7	DGKB_HUMAN		12	GCAGAGACAGG	0.443	
+	72	11549		NM_003777	NP_003768	Q96DT5	DYH11_HUMAN		15	TACAGGCAATT	0.403	
+	4	955_956	zu.2_Missense_M	NM_152626	NP_689839	Q03936	ZNF92_HUMAN	2H2-type 5.	0	CTCAACCCTTA	0.351	
-	4	4152	v.2_Missense_Mut	NM_033026	NP_149015	Q9Y6V0	PCLO_HUMAN		7	TGTTTCCCTTCT	0.413	
+	2	772		NM_002523	NP_002514	P47972	NPTX2_HUMAN		3	AGACCGAGAGC	0.622	
+	5	1441		NM_002523	NP_002514	P47972	NPTX2_HUMAN	Pentaxin.	3	CCGTGGAGACG	0.587	
-	13	2475		NM_022574	NP_072096	O75420	PERQ1_HUMAN	GYF.	2	TGAAGGGGCCT	0.637	
+	3	2812	C17_uc010lho.1_	NM_001040105	NP_001035194	Q685J3	MUC17_HUMAN	ch.|59 X approximate tand	27	TCCTGGGGAAG	0.512	
+	3	9661	C17_uc010lho.1_	NM_001040105	NP_001035194	Q685J3	MUC17_HUMAN	ch.|59 X approximate tand	27	CCACTTCATCTA	0.507	
+	8	1366	nse_Mutation_p.S	NM_014491	NP_055306	O15409	FOXP2_HUMAN		8	CAGCTCGTCAC	0.468	
-	9	1054	_p.L108F|SLC35B	NM_032826	NP_116215	Q969S0	S35B4_HUMAN	ical; (Potential).	1	CATGAGGAGGT	0.433	
-	13	4473	.P1425L|KIAA154	NM_020910	NP_065961	Q9HCM3	K1549_HUMAN		230	CCGGGGGGCGG	0.642	
+	9	1603	v.2_Missense_Mu	NM_173569	NP_775840	Q6ZU65	UBN2_HUMAN		2	ATGATCGTTTAA	0.363	
-	15	1860		NM_004333	NP_004324	P15056	BRAF_HUMAN	rotein kinas_R603>I(2)|p.T	18290	ATTTCACTGTA	0.368	
+	3	313	76B_uc003whv.3_	NM_018487	NP_060957	Q96HP8	T176A_HUMAN		2	TCCGCGACTAC	0.572	
-	27	4454	z.2_Missense_Mu	NM_170606	NP_733751	Q8NEZ4	MLL3_HUMAN		63	AACTAAGTAGT	0.343	
-	4	5778		NM_178857	NP_849188	Q8IWN7	RP1L1_HUMAN		8	TCTACACCTTCT	0.642	
-	10	2959	t.2_Missense_Mut	NM_005144	NP_005135	O43593	HAIR_HUMAN		2	CCGCGGTAGAA	0.647	
+	9	920	z.1_Nonsense_Mu	NM_014265	NP_055080	Q9UKQ2	ADA28_HUMAN	B.|Extracellular (Potential).	5	AAATGGAGGGG	0.398	
-	4	732	a.1_Missense_Mut	NM_004056	NP_004047	P35219	CAH8_HUMAN		0	GATTCCGTGCG	0.428	
+	9	1011	_p.W328*|PREX2_	NM_024870	NP_079146	Q70Z35	PREX2_HUMAN	PH.	17	GGATGGAAGAT	0.318	

+	12	1340	;xyb.2_Splice_Site	NM_052958	NP_443190	Q49A92	CH034_HUMAN		1	AGAAACGTGAGTA	0.358	
+	1	372	AP1_uc010mbs.1_	NR_002182					0	ATACCTACATGGT	0.423	
+	7	888	ense_Mutation_p.D	NM_012082	NP_036214	Q8WW38	FOG2_HUMAN		5	AATGAAGACAGTC	0.517	
-	15	2593	nt.2_Nonsense_M	NM_198123	NP_937756	Q7Z407	CSMD3_HUMAN	lar (Potential).|CUB 4.	63	CAGCCTGAAATTC	0.393	
+	7	678		NM_139021	NP_620590	Q8TD08	MK15_HUMAN	rotein kinase.	2	ATGCTGCGGGGG	0.647	
-	15	1928	_p.S539F|RFX3_u	NM_134428	NP_602304	P48380	RFX3_HUMAN		4	ACCCAGGAAGCC	0.478	
-	44	6331	).Q1467*|PTPRD_	NM_002839	NP_002830	P23468	PTPRD_HUMAN	l).|Tyrosine-protein phospha	22	CAGTCTGGAAGA	0.418	
-	2	841	p.M216R|LINGO2_	NM_152570	NP_689783	Q7L985	LIGO2_HUMAN	xtracellular (Potential).	3	ACAGGCATATTGT	0.468	
+	1	321	f79_uc004apo.1_I	NM_178828	NP_849150	Q6ZUB1	CI079_HUMAN		3	CGCCCGGGAGG	0.557	rs146303708
-	2	191	/I18_uc010mvy.2_I	NM_033117	NP_149108	Q96H35	RBM18_HUMAN		0	CAGGGGAAGAG	0.448	
-	7	1499		NM_006336	NP_006327	Q7Z7L7	ZER1_HUMAN		1	TCAGCACCTGCTC	0.592	
-	1	154		NM_031297	NP_112587	Q9H0X6	RN208_HUMAN		0	GAGGCCCGGCC	0.652	
-	2	97		NM_001009616	NP_001009616	Q5MJ07	SPXN5_HUMAN		0	CTAAGTCCCTGTT	0.398	
-	25	2201	).R355Q|TEX11_u	NM_001003811	NP_001003811	Q8IYF3	TEX11_HUMAN		5	GTTTTCCGTGCAA	0.393	
+	8	1290	RN1_uc011mpt.1_I	NM_052957	NP_443189	Q96QF7	ACRC_HUMAN	Asp/Ser-rich.	3	TCGGAAGCTCCC	0.552	
+	8	1292	RN1_uc011mpt.1_I	NM_052957	NP_443189	Q96QF7	ACRC_HUMAN	Asp/Ser-rich.	3	GGAAGCTCCCGA	0.557	
+	4	725	eh.1_Missense_M	NM_021118	NP_066941	P35663	CYLC1_HUMAN	p.S234*(1)	5	CCATATCAGAGAT	0.333	
-	1	611	en.2_Missense_Mu	NM_001163541	NP_001157013	Q86VE3	SATL1_HUMAN	Gln-rich.	2	TGCTGGCTGATGC	0.567	
+	8	1441		NM_014467	NP_055282	O60687	SRPX2_HUMAN		2	TGCTCGTGAGTGA	0.547	
+	4	1483	;P2_uc004ejm.2_M	NM_138437	NP_612446	Q96D09	GASP2_HUMAN		1	CAAGGCCCAAAA	0.567	
-	2	1074		NM_001009615	NP_001009615	Q5MJ10	SPXN2_HUMAN		1	GAAGATCCTTCAC	0.527	
+	2	733	0_uc011myc.1_Mi	NM_004224	NP_004215	Q13585	MTR1L_HUMAN	Name=5; (Potential).	4	GTCCTCCCTCTCC	0.547	
-	3	476		NM_004988	NP_004979	P43355	MAGA1_HUMAN		10	GCCCCTCCTCTTC	0.542	
+	6	1318	Y_uc011nan.1_Mi	NM_003411	NP_003402	P08048	ZFY_HUMAN		0	TTGCAGCAGCAC	0.403	
-	15	1762	_1_uc009vka.2_Mi	NM_004421	NP_004412	O14640	DVL1_HUMAN		0	CCCCAGCTCCCC	0.711	
+	14	1600	'207_uc010nzp.1_	NM_207396	NP_997279	Q6ZRF8	RN207_HUMAN		0	CTGGACGTGCAG	0.617	
-	5	516		NM_001561	NP_001552	Q07011	TNR9_HUMAN	(Potential).|TNFR-Cys 4.	4	TGCCACGTTTCTC	0.323	
+	5	1883		NM_004285	NP_004276	O95479	G6PE_HUMAN	Linker.	0	GCCGGCCCCAA	0.622	
-	4	1183	p.V132M|CLSTN1_	NM_001009566	NP_001009566	O94985	CSTN1_HUMAN	|Extracellular (Potential).	1	TTTTCACGTTGGT	0.458	
+	2	333	'_uc010oap.1_Sile	NM_007375	NP_031401	Q13148	TADBP_HUMAN		2	GATGCTGGCTGG	0.488	
-	4	1319		NM_152232	NP_689418	Q8TE23	TS1R2_HUMAN	cellular (Potential).	4	TTGCGGGTCGA	0.592	
+	11	2218		NM_020526	NP_065387	P29322	EPHA8_HUMAN	Potential).|Protein kinase.	13	CATCCGCCTCGA	0.642	
+	4	841	).R237Q|CCDC21_	NM_022778	NP_073615	Q6P2H3	CEP85_HUMAN		0	TGAGCGGAATGC	0.597	
+	9	1403	E290K|WDTC1_uc	NM_015023	NP_055838	Q8N5D0	WDTC1_HUMAN	WD 5.	2	GGGGGGAACAG	0.527	
+	5	553	M222_uc001bnt.3_	NM_032125	NP_115501	Q9H0R3	TM222_HUMAN	ical; (Potential).	0	GGTGACGCTCTC	0.582	
-	2	748		NM_001003682	NP_001003682	Q69YZ2	T200B_HUMAN	Pro-rich.	0	GCAGCCCGGGGC	0.617	
-	65	4410	DL16A1_uc001btj.1	NM_001856	NP_001847	Q07092	COGA1_HUMAN	2 (COL2) with 2 imperfect	8	TGCCAGCTGCACC	0.522	
-	10	2258	).R454C|PABPC4_	NM_003819	NP_003810	Q13310	PABP4_HUMAN		0	ACTGGCGTATAGC	0.547	
+	4	481		NM_152373	NP_689586	Q5T5D7	ZN684_HUMAN	KRAB.	0	ACGAGAGCTCTCC	0.493	
+	47	6394	)467_uc001cjl.1_5	NM_015284	NP_056099	Q5T011	SZT2_HUMAN		0	AGCGGCGCCATC	0.607	
-	14	3370		NM_020883	NP_065934	Q9P217	ZSWM5_HUMAN		0	GGCTGAGAGCAC	0.552	
+	22	3964	of.1_RNA|C1orf17	NM_001039464	NP_001034553	Q68CQ1	HEAT8_HUMAN		0	GCCTCCCTCCGG	0.557	
+	41	5308	ADL_uc009wag.2_	NM_176877	NP_795352	Q8NI35	INADL_HUMAN	PDZ 10.	4	ATTAACGGGCAAC	0.433	
+	14	1002	SGIP1_uc001dct.2	NM_032291	NP_115667	Q9BQI5	SGIP1_HUMAN	Pro-rich.	3	CACCCCGAACAG	0.468	
+	5	1208	<.1_RNA|IL12RB2_	NM_001559	NP_001550	Q99665	I12R2_HUMAN	tential).|Fibronectin type-III	3	ACCCCTGAATCAC	0.403	
+	6	939	PHN2_uc001div.2_	NM_012302	NP_036434	O95490	LPHN2_HUMAN	otential).|Olfactomedin-like	9	ATGATACCTCACC	0.388	
-	5	540	PYD_uc001drw.2_I	NM_000110	NP_000101	Q12882	DPYD_HUMAN		8	CACAAAGATCAGA	0.388	

-	10	1993	tation_p.A617V|A	NM_006594	NP_006585	Q9Y6B7	AP4B1_HUMAN		4	TGAGGGCTCCA	0.453	
-	3	188	eff.1_Missense_M	NM_000036	NP_000027	P23109	AMPD1_HUMAN		4	CCTGACGACCT	0.423	rs147972392
+	4	953	5'UTR|NOTCH2N	NM_203458	NP_982283	Q7Z3S9	NT2NL_HUMAN	EGF-like 6.	1	ATGGAGGCACC	0.572	
-	2	3473	e.1_Missense_Mu	NM_007113	NP_009044	Q07283	TRHY_HUMAN	0 AA tandem repeats.	5	TTCTCCGGTTCC	0.174	rs113946258
-	3	759		NM_016190	NP_057274	Q9UBG3	CRNN_HUMAN	Gln-rich.	3	AGATCCAGTCA	0.577	
+	2	728		NM_001025231	NP_001020402	Q5T749	KPRP_HUMAN		5	GGTCCCGGACT	0.582	
+	3	756	ey.1_Intron|HCN3_	NM_020897	NP_065948	Q9P1Z3	HCN3_HUMAN	lasmic (Potential).	2	TGGTTCGCATC	0.572	
-	6	754	q.2_Missense_Mu	NM_001135050	NP_001128522	Q9P2J2	TUTLA_HUMAN	xtracellular (Potential).	5	CTGCACCTAGG	0.662	
+	6	1196	p.A230V|PBX1_u	NM_002585	NP_002576	P40424	PBX1_HUMAN		5	TCACTGCTACCA	0.448	
-	13	3902		NM_000130	NP_000121	P12259	FA5_HUMAN	dem repeats of [TNP]-L-S-	6	GCTGAGGTCTA	0.527	
-	3	1121	nk.1_Missense_M	NM_000261	NP_000252	Q99972	MYOC_HUMAN	actomedin-like.	1	CTGTCCGTGGT	0.532	rs74315334
+	3	800	_p.R175Q|ZBTB3	NM_001122770	NP_001116242	Q5TC79	ZBT37_HUMAN		0	CCGGCGAGGTC	0.522	
+	31	5106		NM_031935	NP_114141	Q96RW7	HMCN1_HUMAN	ike C2-type 13.	23	TGGAACTGCTG	0.363	
+	7	1474	_Mutation_p.A382	NM_005807	NP_005798	Q92954	PRG4_HUMAN	ats of K-X-P-X-P-T-T-X.|17	1	AGCCTGCACCC	0.657	rs138528418
+	2	188	_p.R39H|CFHR4_	NM_006684	NP_006675	Q92496	FHR4_HUMAN	Sushi 1.	3	GTTTGCGTAGAC	0.323	
-	8	2173	pj.1_Missense_M	NM_014875	NP_055690	Q15058	KIF14_HUMAN	inesin-motor.	7	TGGGTCATCAC	0.388	rs144936292
+	11	1511	p.S403F|CAMSA	NM_203459	NP_982284	Q08AD1	CAMP2_HUMAN		4	AAGGTCTTCAT	0.308	
-	34	5058	l.1_Missense_Mu	NM_017596	NP_060066	O75037	KI21B_HUMAN	WD 6.	6	CTCACCGATGG	0.612	
-	27	4050	l.1_Missense_Mut	NM_017596	NP_060066	O75037	KI21B_HUMAN		6	GGGCCGAGTGG	0.622	
-	11	1746		NM_000069	NP_000060	Q13698	CAC1S_HUMAN	3 of repeat II; (Potential).|	5	GATACCGCTAC	0.572	
+	4	413	.2_RNA|LGR6_uc	NM_001017403	NP_001017403	Q9HBX8	LGR6_HUMAN	ellular (Potential).	10	GCTGCCGAGCC	0.607	
+	12	1727	gxz.1_Missense_	NM_002481	NP_002472	O60237	MYPT2_HUMAN		3	TACCCGGCAGC	0.438	
+	20	2777	gyb.1_Missense_	NM_002481	NP_002472	O60237	MYPT2_HUMAN		3	AGACAGCAACA	0.512	
-	2	394	1gyr.3_5'UTR|ADI	NM_015999	NP_057083	Q96A54	ADR1_HUMAN	lasmic (Potential).	0	GTTGGCGATTA	0.522	
+	9	1418	.2_RNA|CR1L_uc	NM_175710	NP_783641	Q2VPA4	CR1L_HUMAN	Sushi 7.	0	ATGTTGGATCC	0.453	
-	2	464	kv.2_Missense_M	NM_206933	NP_996816	O75445	USH2A_HUMAN		26	TTGAAGCAAAA	0.438	
-	6	811	pv.2_Missense_M	NM_152608	NP_689821	Q6IQ49	CA055_HUMAN		1	CCATTGCTACCA	0.493	
+	2	894		NM_020435	NP_065168	Q5T442	CXG2_HUMAN	ellular (Potential).	0	GGTGCGACCGT	0.642	
+	83	19162	sr.1_Missense_Mu	NM_001098623	NP_001092093	Q5VST9	OBSCN_HUMAN	Ig-like 54.	28	CGGAACGGCC	0.632	
-	1	128		NM_003493	NP_003484	Q16695	H31T_HUMAN		0	CGGGCCGGTAG	0.667	
+	7	682	e_Mutation_p.L16	NM_004481	NP_004472	Q10471	GALT2_HUMAN	tial).|Catalytic subdomain	2	CAGGCCTCATG	0.647	
+	6	682	hxv.1_Missense_	NM_145861	NP_665860	Q8WWZ3	EDAD_HUMAN		0	CAAGCGGGAGC	0.587	
-	2	440	_p.S11N|CEP170_	NM_014812	NP_055627	Q5SW79	CE170_HUMAN		2	CTCCACTGCTC	0.423	
+	3	217	1iai.2_Missense_	NM_001012970	NP_001012988	Q5SVJ3	CA100_HUMAN		0	CCCTGGGCAGC	0.453	
+	5	1732	_p.A431V|KIF26B	NM_018012	NP_060482	Q2KJY2	KI26B_HUMAN		3	CCCAGCCCCAC	0.607	
+	1	373		NM_001001915	NP_001001915	Q8NGZ5	OR2G2_HUMAN	lasmic (Potential).	0	GTGACCGCTAT	0.527	
+	1	26		NM_001004696	NP_001004696	Q8NH00	OR2T4_HUMAN	ellular (Potential).	1	GGCCAGCCACA	0.483	rs140989725
+	1	55		NM_001004696	NP_001004696	Q8NH00	OR2T4_HUMAN	ellular (Potential).	1	TCCTGATGGGA	0.488	
+	3	1399	.V167M|PGBD2_	NM_170725	NP_733843	Q6P3X8	PGBD2_HUMAN		1	GCAGCGTGGTC	0.507	
+	15	3984	rf18_uc001iik.2_I	NM_017782	NP_060252	Q5VWN6	CJ018_HUMAN		2	GAAGGGCACTA	0.502	
-	6	649	25_splice|PRKCQ_	NM_006257	NP_006248	Q04759	KPCT_HUMAN		6	ACTTACGTCGG	0.378	
+	3	581	C3_uc009xix.2_5	NM_024693	NP_078969	Q96DC8	ECHD3_HUMAN		0	ATTACCATGCC	0.453	
-	3	502	mo.3_Missense_	NM_152751	NP_689964	Q8N7W2	BEND7_HUMAN		2	GGGCGGTAGCT	0.582	
-	7	962	KRD26_uc009xk	NM_014915	NP_055730	Q9UPS8	ANR26_HUMAN		4	GTCTTCGTCAT	0.328	
-	7	1229	.3_Missense_Mut	NM_173576	NP_775847	Q8IYA7	MKX_HUMAN		1	GGGACGACTTC	0.463	
-	21	4595	iuu.1_Splice_Site_	NM_021738	NP_068506	O95425	SVIL_HUMAN		6	CCAACTATCAA	0.403	
-	2	1708	nse_Mutation_p.S	NM_020848	NP_065899	Q9P266	K1462_HUMAN		4	AGGTGCTCTCG	0.498	

+	7	860		NM_052997	NP_443723	Q9BXX3	AN30A_HUMAN		9	CTTGGTGGAAA	0.502	
-	1	737		NM_145178	NP_660161	Q8N100	ATOH7_HUMAN		0	GTCCCGCTCCG	0.647	
-	15	2651	g.1_Intron|DNA2_u	NM_001080449	NP_001073918	P51530	DNA2L_HUMAN		0	GCTTCACGGTTT	0.398	
+	12	1936	w.1_Missense_Mu	NM_004728	NP_004719	Q9NR30	DDX21_HUMAN		3	GCACTGGCCCAT	0.502	
+	8	1064	qjd.1_Missense_M	NM_003171	NP_003162	Q8IYB8	SUV3_HUMAN		2	CAACGGGGGAG	0.478	
-	14	2385	RID1_uc010qmf.1_	NM_017551	NP_060021	Q9ULK0	GRID1_HUMAN	ellular (Potential).	10	TGTTGCCGATGA	0.582	
-	5	816	nse_Mutation_p.R	NM_000770	NP_000761	P10632	CP2C8_HUMAN		0	ACTTCGTGTAAG	0.373	
-	17	3540	.R374W|PSD_uc0	NM_002779	NP_002770	A5PKW4	PSD1_HUMAN		3	AGCCCGGGGCT	0.682	
-	9	2092	67_uc009yav.1_N	NM_002417	NP_002408	P46013	KI67_HUMAN		7	GACTTCGGCTGA	0.423	
+	26	4551		NM_152643	NP_689856	Q76NI1	VKIND_HUMAN	Ras-GEF.	2	CTCTTTCGGCCA	0.552	
+	14	2212	RF1_uc010qwe.1_	NM_020901	NP_065952	Q9P1Y6	PHRF1_HUMAN		0	CAGACGGGATG	0.657	
-	11	1295	_p.S397L|CDHR5_	NM_021924	NP_068743	Q9HBB8	CDHR5_HUMAN	|Extracellular (Potential).	0	TGGCCGAGTTG	0.607	
-	1	377	.1_Intron|HBE1_u	NM_033179	NP_149419	Q9Y5P0	O51B4_HUMAN	lasmic (Potential).	2	TCAGTGGTGTG	0.443	
-	3	625	rdi.1_Missense_M	NM_194285	NP_919261	Q68D10	SPT2_HUMAN	Potential.	1	ACTCTGCGTGAT	0.478	rs144792493
-	2	459		NM_054030	NP_473371	Q96LB1	MRGX2_HUMAN	lasmic (Potential).	1	CGGTGCTGACG	0.597	
+	8	1405		NM_020229	NP_064614	Q9NQV5	PRD11_HUMAN		1	CCCATGGTGTG	0.582	
+	6	539	2_uc001ndg.3_RN	NM_000506	NP_000497	P00734	THRB_HUMAN	Kringle 1.	3	CCACGGGACCC	0.612	
-	26	2867		NM_000256	NP_000247	Q14896	MYPC3_HUMAN	nectin type-III 2.	3	CCGGGCCCCCG	0.662	
+	2	646	-CNTF_uc010rkm.	NM_000614	NP_000605	P26441	CNTF_HUMAN		1	AGCACGTGGGA	0.478	
+	18	1929	K_uc009ynm.1_3'	NM_015533	NP_056348	Q3LXA3	DHAK_HUMAN	ATP (By similarity).	0	ACCCCGGGGCG	0.627	
+	8	1139	b.1_Missense_Mu	NM_006819	NP_006810	P31948	STIP1_HUMAN	TPR 6.	3	GCACCGAACCC	0.403	
+	5	434	B2_uc009yrq.2_Int	NM_003952	NP_003943	Q9UBS0	KS6B2_HUMAN	rotein kinase.	7	CACGGGCTGAG	0.458	
-	11	2100	onn.1_Missense_	NM_017635	NP_060105	Q4FZB7	SV421_HUMAN		3	CTTGTCGTGAC	0.478	
-	1	949	c.1_RNA|CREBZF	NM_001039618	NP_001034707	Q9NS37	ZHANG_HUMAN	eucine-zipper.	1	CCCATCACGTAC	0.413	
+	1	3048		NM_001008781	NP_001008781	Q8TDW7	FAT3_HUMAN	|Extracellular (Potential).	5	CTGTGCGGGCC	0.453	
-	3	420		NM_022122	NP_071405	Q9H306	MMP27_HUMAN		3	ACCTTCTTGGA	0.388	
+	39	6316	e_Mutation_p.I205	NM_001080463	NP_001073932	Q8NCM8	DYHC2_HUMAN	2 (By similarity).	0	GGTGATATTGAC	0.348	
-	2	274	Mutation_p.T86M|	NM_033292	NP_150634	P29466	CASP1_HUMAN	CARD.	2	CCAGCGTCCCT	0.463	
-	4	677		NM_006235	NP_006226	Q16633	OBF1_HUMAN		1	GCATAGGTCAAC	0.572	
-	2	769	2_Missense_Muta	NM_012104	NP_036236	P56817	BACE1_HUMAN	ellular (Potential).	1	GGGCAGCACCC	0.562	
-	13	2551	_p.S185L|CDON_u	NM_016952	NP_058648	Q4KMG0	CDON_HUMAN	III 2.|Extracellular (Potentia	6	GATGCTGAACTC	0.393	
+	2	530	C1_uc001qja.2_R	NM_178040	NP_829884	Q8IUD2	RB6I2_HUMAN		5	GGGGACGTCTG	0.507	
+	5	1271	se_Mutation_p.A2	NM_018009	NP_060479	Q9BX59	TPSNR_HUMAN	tential).|Ig-like C1-type.	0	CCCCAGCCCAA	0.607	
-	12	1332	l.2_Missense_Muta	NM_002864	NP_002855				5	GGTCTTCTGCTA	0.458	
-	3	269	zt.2_Missense_Mu	NM_002723	NP_002714	P10163	PRB4_HUMAN	R]-[PR]-P-Q-G-G-N-Q-[PS	1	GTCCTTCTGGCT	0.622	
+	14	1933		NM_006446	NP_006437	Q9Y6L6	SO1B1_HUMAN	ellular (Potential).	8	GCACACGTGGGT	0.333	
-	5	1638	_Intron|CAPRIN2_	NM_001002259	NP_001002259	Q6IMN6	CAPR2_HUMAN		2	CATGTCGTTCCT	0.408	
-	7	2084		NM_005164	NP_005155	Q9UBJ2	ABCD2_HUMAN	BC transporter.	6	CCAAGAGACATA	0.393	
-	5	1220	.C2A13_uc001rme	NM_052885	NP_443117	Q96QE2	MYCT_HUMAN	lasmic (Potential).	1	TTCTGCGGCCC	0.383	
+	2	122	1rnf.2_Missense_M	NM_016488	NP_057572	Q8NEY8	PPHLN_HUMAN		2	AGGGACGATATG	0.383	
-	36	5393		NM_025003	NP_079279	P59510	ATS20_HUMAN	GON.	19	GTGTATCCAGCA	0.338	
-	1	272	h.2_Missense_Mu	NM_000424	NP_000415	P13647	K2C5_HUMAN	Head.	0	GGACCGGGACA	0.677	
+	2	333	_p.E43K|EIF4B_u	NM_001417	NP_001408	P23588	IF4B_HUMAN		2	GCTGATGAAACG	0.418	
-	11	1454	ion_p.P467L|ATF7	NM_001130059	NP_001123531	P17544	ATF7_HUMAN	inding adenovirus 2 E1A.	2	TGTATCGGCATG	0.592	
-	1	358		NM_001005499	NP_001005499	A6NIJ9	O6C70_HUMAN	lasmic (Potential).	1	CATAGCGATCAT	0.393	
-	5	894	s.1_Missense_Mu	NM_001144996	NP_001138468	Q13683	ITA7_HUMAN	Extracellular (Potential).	5	TGGCCGTGCCT	0.677	
+	57	9552		NM_002332	NP_002323	Q07954	LRP1_HUMAN	ellular (Potential).	22	AGGAACCGTTTC	0.597	

+	12	1449	r.1_Missense_Mu	NM_004984	NP_004975	Q12840	KIF5A_HUMAN			3	GGAGCGGCAG	0.642	
-	18	2232	ui.1_RNA|PPFIA2	NM_003625	NP_003616	B7Z663	B7Z663_HUMAN			6	GCCTTCGAGGC	0.463	
-	3	1569		NM_007035	NP_008966	O60938	KERA_HUMAN			1	CATAACTGAAG	0.453	
+	20	2767	e_Mutation_p.E14	NM_130466	NP_569733	Q7Z3V4	UBE3B_HUMAN	HECT.		4	TGGACGAAGCA	0.507	
-	6	1454	_p.A382T|ABCB9	NM_019625	NP_062571	Q9NP78	ABCB9_HUMAN	nsmembrane type-1.		0	ATTGGCGAAGC	0.587	
-	3	697	AP1_uc001uep.2_	NM_004642	NP_004633	O14519	CDKA1_HUMAN			0	TTGGGGCACCT	0.408	
-	40	6245	.R2014Q|NCOR2_	NM_006312	NP_006303	Q9Y618	NCOR2_HUMAN			4	TTCCCGGTGC	0.637	
+	10	1612	jd.1_Missense_M	NM_016155	NP_057239	Q9ULZ9	MMP17_HUMAN	mopexin-like 4.		0	ATGGCGAGCTG	0.657	
-	7	847	e_Mutation_p.P2	NM_001161344	NP_001154816	Q96EP1	CHFR_HUMAN			1	CACGGGCTCC	0.562	
-	12	1464	uyk.2_Missense_	NM_015058	NP_055873	A3KMH1	K0564_HUMAN			6	TTGTATCCTAAG	0.368	
-	9	1047	ron|CPB2_uc001v	NM_001872	NP_001863	Q96IY4	CBPB2_HUMAN			2	TCTTTGCTTTTA	0.318	
-	16	3713	.G1121S|ATP7B_	NM_000053	NP_000044	P35670	ATP7B_HUMAN	lasmic (Potential).		3	GATACCGTCAA	0.463	
+	7	722	_p.A212T|ATP11A_	NM_015205	NP_056020	P98196	AT11A_HUMAN	lasmic (Potential).		4	TTCACGCCACC	0.527	
+	13	1347	p.T420K|ATP11A_	NM_015205	NP_056020	P98196	AT11A_HUMAN	lasmic (Potential).		4	CCTCACGGAA	0.607	
+	1	365		NM_001005500	NP_001005500	Q8NGD0	OR4M1_HUMAN	lasmic (Potential).		0	TGACCGCTATG	0.502	rs143164519
-	1	184		NM_001005466	NP_001005466	Q8NGC3	O10G2_HUMAN	Name=2; (Potential).		1	GGGCGAGCAC	0.512	
+	14	1385	s.2_Nonsense_M	NM_005132	NP_005123	O95072	REC8_HUMAN	Glu-rich.		0	AATTCCAGGAA	0.632	
-	3	277	uc001wnj.2_5'UTR	NM_138476	NP_612485	Q86V88	MGDP1_HUMAN			0	CAGCCGCACCG	0.547	rs17101962
-	8	1314	M1_uc010tog.1_In	NM_000359	NP_000350	P22735	TGM1_HUMAN			3	TGACAGTACGG	0.572	
-	15	3440	1_Missense_Muta	NM_007361	NP_031387	Q14112	NID2_HUMAN	globulin type-1 2.		7	CCTCTCTGCCA	0.632	
-	10	1294	A0831_uc001xbw.	NM_014924	NP_055739	Q6ZNE5	BAKOR_HUMAN			0	ATCTCCGCTCT	0.537	
-	7	2333	.R779Q|C14orf37	NM_001001872	NP_001001872	Q86TY3	CN037_HUMAN	ytoplasmic (Potential).		0	TCCTTCGGCGA	0.433	rs141152358
+	20	3133	_p.G1015S|KIAA0	NM_014749	NP_055564	E9PGW8	E9PGW8_HUMAN			1	AGCAAGGTCCT	0.398	
-	5	2236	se_Mutation_p.T1	NM_021136	NP_066959	Q16799	RTN1_HUMAN	Reticulon.		4	AGTCCGTGTAC	0.478	
-	26	5647	p.A1865T|SPTB_u	NM_000347	NP_000338	P11277	SPTB1_HUMAN	Spectrin 15.		11	ATATGCTGTCT	0.627	
+	5	3369	M1_uc001xql.3_	NM_019589	NP_062535	P49750	YLPM1_HUMAN	Arg-rich.	p.L888fs*0(1)	3	CAGAGGGTTGG	0.562	
+	2	613		NM_003608	NP_003599	Q8IYL9	PSYR_HUMAN	Name=1; (Potential).		0	AGTCAGCATTCC	0.363	
-	4	2417	gb.2_Missense_M	NM_138576	NP_612808	Q9C0K0	BC11B_HUMAN			10	GCGACGCCGCG	0.677	
-	2	653	gb.2_Missense_M	NM_138576	NP_612808	Q9C0K0	BC11B_HUMAN			10	TGGGTGAGAGC	0.617	
-	11	1370	GE_uc001ylh.2_I	NM_014226	NP_055041	Q9UQ07	MOK_HUMAN			4	CAGCACCGGCA	0.587	
+	46	7061	r.2_Missense_Mut	NM_001036	NP_001027	Q15413	RYR3_HUMAN	eats.|Cytoplasmic (By simil		10	TGGTTGGGATC	0.592	
-	15	2004	.G436E|RASGRP	NM_005739	NP_005730	O95267	GRP1_HUMAN			2	CTGGCCCCACA	0.478	
+	13	2190	bi.2_Missense_M	NM_003246	NP_003237	P07996	TSP1_HUMAN	EGF-like 3.		6	TATAGCGACCCC	0.602	
+	2	329	_p.D80N|MGA_uc	NM_001080541	NP_001074010	Q8IWI9	MGAP_HUMAN			12	CCCTCGATAAC	0.428	
-	6	1577		NM_139265	NP_644670	Q9H223	EHD4_HUMAN	F-hand.|EH	p.A505V(1)	2	CCAGCGCGAAC	0.642	
-	13	1361	pc.2_Missense_M	NM_015289	NP_056104	Q96JC1	VPS39_HUMAN			3	GGAGAGCACAG	0.512	
-	17	2111		NM_004998	NP_004989	Q12965	MYO1E_HUMAN	osin head-like.		3	GGGGCGTACAT	0.483	
+	2	226		NM_015059	NP_055874	Q9Y4G6	TLN2_HUMAN			11	TGTTGCGGAAT	0.478	
+	13	1534		NM_015059	NP_055874	Q9Y4G6	TLN2_HUMAN			11	AGCAGGCCCAG	0.562	
+	5	512	P3_uc010uij.1_Mi	NM_006537	NP_006528	Q9Y6I4	UBP3_HUMAN			1	CACAGCTGACA	0.308	
-	2	778		NM_001039614	NP_001034703	Q2T9L4	CO059_HUMAN			1	CGTGCCACCAT	0.662	
+	3	1116	n.1_Missense_Mu	NM_001130028	NP_001123500	P49761	CLK3_HUMAN	Arg-rich.		2	CATACCGGTGT	0.632	
-	2	814	CYP1A1_uc002ay	NM_000499	NP_000490	P04798	CP1A1_HUMAN			5	GGTTTCCAGAG	0.493	
-	3	1405	k.2_Intron|DET1_u	NM_001144074	NP_001137546	Q7L5Y6	DET1_HUMAN			2	GCCTTGCAAAA	0.453	
-	3	367	5orf38_uc002bou.	NM_182616	NP_872422	P59780	AP3S2_HUMAN			0	TACGGCGATGG	0.567	
+	6	746	_p.A72T|C16orf5	NM_025108	NP_079384	Q7L2K0	CP059_HUMAN			0	CCGCTGCCAA	0.612	
+	2	415	d.2_Missense_Mu	NM_024339	NP_077315	Q86W42	THOC6_HUMAN	WD 1.		2	TCTGGCGGCTG	0.587	

-	5	1235	ctw.1_Missense_M	NM_032805	NP_116194	Q96SZ4	ZSC10_HUMAN	C2H2-type 4.		1	GCGGCCGCACT	0.711	
+	8	1052	p.G343S|DNAJA3_	NM_005147	NP_005138	Q96EY1	DNJA3_HUMAN			4	AGGGACGGCGCA	0.542	
+	7	780	yam.1_Missense_M	NR_003569						0	GTTTCCCGGCTTC	0.532	
+	2	295	dfs.2_Missense_M	NM_016138	NP_057222	Q99807	COQ7_HUMAN	ximate tandem repeats.		1	CCAGCGTCGGG	0.547	rs138449068
-	6	1441	_p.A438T|UMOD_u	NM_003361	NP_003352	P07911	UROM_HUMAN	ZP.		2	GTAGGGCGGTCT	0.542	
-	4	751	SM1_uc010bwg.1_	NM_052956	NP_443188	Q08AH1	ACSM1_HUMAN	P (By similarity).		2	GTGGTCCCACTG	0.517	rs150786519
-	5	1024	_uc002dqm.2_Mis	NM_177534	NP_803878	P50225	ST1A1_HUMAN			0	TGGGTGCGGCTC	0.592	rs145721404
-	3	980		NM_001080417	NP_001073886	Q9UEG4	ZN629_HUMAN			0	TCTCGCCGGTGT	0.627	
+	4	737	C1_uc002ebo.2_5'	NM_001008274	NP_001008275	Q6ZMU5	TRI72_HUMAN			0	TCCGGGGGGCC	0.652	
+	6	676	6L_uc010cbe.1_3	NM_014321	NP_055136	Q9Y5N6	ORC6_HUMAN			0	GTGGTTGAAGCC	0.443	
-	14	2453	CC12_uc002efa.1_	NM_033226	NP_150229	Q96J65	MRP9_HUMAN			3	ATCCTCGCAGGT	0.483	rs146815895
-	49	7390	NOT1_uc002ent.2	NM_016284	NP_057368	A5YKK6	CNOT1_HUMAN			6	GCTGGGCCTGC	0.478	
-	12	2552		NM_001796	NP_001787	P55286	CADH8_HUMAN	lasmic (Potential).		9	GAGTCTGATGTG	0.517	
-	13	2664	bj.2_3'UTR|CDH11	NM_001797	NP_001788	P55287	CAD11_HUMAN	lasmic (Potential).		14	CATAACCGTAGAT	0.537	
+	34	3931	jr.1_Missense_Mut	NM_001013838	NP_001013860	Q6F5E8	LR16C_HUMAN			1	GTGTCTGCTGGT	0.592	
-	12	1348		NM_000353	NP_000344	P17735	ATTY_HUMAN			2	CCACTCGGATGA	0.522	rs118203916
-	7	1035	FBP1_uc002fce.2_	NM_031293	NP_112583	Q8TBY8	PMFBP_HUMAN			2	GTGGCTGTACAG	0.468	
+	5	542	ymr.1_Missense_M	NM_002811	NP_002802	P51665	PSD7_HUMAN			0	CAGAAGCGTACAT	0.433	
+	5	1091		NM_002153	NP_002144	P37059	DHB2_HUMAN			2	GAATTTCCTCCTAT	0.532	
-	9	1179	cjf.2_Intron|PRDM7	NM_001098173	NP_001091643	Q9NQW5	PRDM7_HUMAN			1	TCCCCATACCAGA	0.522	
-	2	501		NM_182705	NP_874364	Q8N5W9	F101B_HUMAN			0	AGTTGCGCCACC	0.657	
+	10	1209	0vqr.1_Missense_M	NM_000934	NP_000925	P08697	A2AP_HUMAN			0	TCCGGCGTGCAG	0.672	
+	1	991		NR_024128						1	TCCTCCGATGCTC	0.587	
-	8	1121	p.R324W|ATP2A3_	NM_174955	NP_777615	Q93084	AT2A3_HUMAN	smic (By similarity).		5	GCGCCGCGTGC	0.667	
-	5	596	_p.D149N|ATP2A3	NM_174955	NP_777615	Q93084	AT2A3_HUMAN	smic (By similarity).		5	AATGTCCCCTGG	0.438	
-	6	1044	X33_uc002gcb.2_M	NM_020162	NP_064547	Q9H6R0	DHX33_HUMAN	case C-terminal.		2	CTTTGCGATAGCC	0.383	
+	4	300	nse_Mutation_p.E6	NM_203415	NP_981960	Q8TE02	DERP6_HUMAN			0	GTGAGCGAGGAA	0.458	
-	4	500	_Intron|SAT2_uc00	NM_133491	NP_597998	Q96F10	SAT2_HUMAN	cetyltransfer	p.?(1)	0	TGGTGCGTCCCT	0.542	
-	14	1397	uc002gml.1_Intron	NM_017533	NP_060003	Q9Y623	MYH4_HUMAN	yosin head-like.		13	CCAGAGCACCCA	0.473	
-	3	655		NM_031898	NP_114104	Q9BXF9	TEKT3_HUMAN			2	AGATTTCCAAAAC	0.403	
+	3	742		NM_021012	NP_066292	Q14500	IRK12_HUMAN	smic (By similarity).		4	AGCATCGTGTCAT	0.706	
+	20	2949	_p.G771R|TAOK1_	NM_020791	NP_065842	Q7L7X3	TAOK1_HUMAN			4	GGTCCAGGACCT	0.577	
-	2	897	ht.2_Missense_Mu	NM_001094	NP_001085	Q16515	ACCN1_HUMAN	llular (By similarity).		4	TTGACCGTGGTGA	0.537	
-	3	1736	_p.T469I|SLFN13_	NM_144682	NP_653283	Q68D06	SLN13_HUMAN			2	ATGGGGGTGCTG	0.537	
-	26	3628	p.S679N|MYO19_u	NM_001163735	NP_001157207	Q96H55	MYO19_HUMAN	hondrial targeting.		1	TGAAAGCTGCCTA	0.617	
-	44	5574	e_Mutation_p.E179	NM_198836	NP_942133	Q13085	ACACA_HUMAN	boxyltransferase.		2	GGTTCTCGGGTC	0.388	
-	3	436	T40_uc002hvq.1_F	NM_182497	NP_872303	Q6A162	K1C40_HUMAN	Rod.|Coil 1A.		0	TGCATCGTCTCCT	0.532	
-	10	1264	p.G342S|STAT3_u	NM_139276	NP_644805	P40763	STAT3_HUMAN			4	GGACGCCGGTCT	0.567	
+	1	1075	t.2_Missense_Mut	NM_009590	NP_033720	O75106	AOC2_HUMAN			2	ATGTTCGGTTCCA	0.507	
+	1	182		NM_003734	NP_003725	Q16853	AOC3_HUMAN	type II membrane protein;		4	ATCCTCGTGCTC	0.552	
-	21	5634	CA1_uc002icu.2_In	NM_007294	NP_009225	P38398	BRCA1_HUMAN	BRCT 2.		52	CTGTGCCAAGG	0.473	
-	19	5484	A1_uc002icu.2_M	NM_007294	NP_009225	P38398	BRCA1_HUMAN		p.R1751*(1)	52	CTTGCTCGCTTTG	0.468	rs80357442
-	9	930	gg.3_Missense_M	NM_000342	NP_000333	P02730	B3AT_HUMAN	Cytoplasmic.		3	GTATAGGCACCG	0.647	
+	4	509	ne.2_5'UTR|DBF4B	NM_145663	NP_663696	Q8NFT6	DBF4B_HUMAN	BRCT.		0	CAGAGAGCAGTG	0.522	
-	23	2643	lw.1_Missense_Mu	NM_145798	NP_665741	Q9BZF2	OSBL7_HUMAN			0	CTTTCCCGCTGC	0.637	
+	13	1702	wmn.1_Missense_	NM_025149	NP_079425	Q96CM8	ACSF2_HUMAN			0	CACACCCGAAGG	0.537	
+	18	1920	nse_Mutation_p.P6	NM_003835	NP_003826	O75916	RGS9_HUMAN			4	AAGTGCCCTGCT	0.617	

-	2	872	wro.1_Missense_M	NM_173477	NP_775748	Q495M9	USH1G_HUMAN		2	TGAAGGTGCCT	0.672	
-	18	3459	wsc.1_Missense_M	NM_020753	NP_065804	Q8WXE0	CSKI2_HUMAN	Pro-rich.	1	GGGGCGGGGGG	0.667	
-	10	1476	wtb.1_Missense_	NM_002766	NP_002757	Q14558	KPRA_HUMAN		1	CTGAACCTCATG	0.453	
+	8	1630	sense_Mutation_p.	NM_001142602	NP_001136074	Q9NYA1	SPHK1_HUMAN		1	TGTTTGCTGCAC	0.632	
-	9	1476	p.E247K|RHBDF2_	NM_024599	NP_078875	Q6PJF5	RHDF2_HUMAN	lasmic (Potential).	0	GCTCTCCAGCT	0.637	
+	9	1359	jth.2_Missense_M	NM_198955	NP_945193	Q3V5L5	MGT5B_HUMAN	enal (Potential).	3	CGCCACGCTGC	0.637	rs140999399
+	30	8034	_uc010dhw.1_Mis	NM_020914	NP_065965	Q9HCF4	ALO17_HUMAN		21	TGCGCCGATTG	0.507	rs143904490
+	20	3167	ug.1_Missense_M	NM_020761	NP_065812	Q8N122	RPTOR_HUMAN		6	AGATGCGCCGC	0.652	
-	26	3436	_uc002jzo.1_Miss	NM_014984	NP_055799	Q9UPN4	AZI1_HUMAN		4	TTGGCGTGGGC	0.677	
-	6	569	n_p.P30L|SIRT7_u	NM_016538	NP_057622	Q9NRC8	SIRT7_HUMAN	tylase sirtuin-type.	0	TGCGCGGCAGC	0.637	
+	1	665		NM_018949	NP_061822	Q9UKP6	UR2R_HUMAN	Name=5; (Potential).	1	CGCGGGGCCCG	0.672	
-	15	1415	.D419N|L3MBTL4	NM_173464	NP_775735	Q8NA19	LMBL4_HUMAN		3	ACGATCGTGAA	0.378	
-	19	2663	zj.1_Missense_Mu	NM_005559	NP_005550	P25391	LAMA1_HUMAN	inin EGF-like 8.	21	CGAGGGGTCCA	0.552	
+	3	614		NM_001025300	NP_001020471	Q6IQ22	RAB12_HUMAN		0	TCAGCTTATTACA	0.403	
+	9	5629	knx.2_Missense_M	NM_015208	NP_056023	Q6UB98	ANR12_HUMAN		3	GTCACGTGTAC	0.418	
-	12	1792	oq.2_Missense_M	NM_022068	NP_071351	Q9H5I5	PIEZ2_HUMAN		1	TCACTAGGTGCT	0.274	
-	8	1363	_p.T242M|MPPE1_	NM_023075	NP_075563	Q53F39	MPPE1_HUMAN		0	CAGACGTGGGC	0.622	
+	5	946	_p.T56M|C18orf1_	NM_181481	NP_852146	O15165	CR001_HUMAN	lasmic (Potential).	3	CTCCACGCGGT	0.642	
+	2	93	e_Mutation_p.R31	NM_001390	NP_001381	Q9Y4J8	DTNA_HUMAN	h MAGEE1 (By similarity).	0	CATCCGACTCT	0.403	
+	3	317	e_Mutation_p.Q10	NM_001390	NP_001381	Q9Y4J8	DTNA_HUMAN	h MAGEE1 (By similarity).	0	TGGAGCAGTCC	0.488	rs140768365
-	16	2222	ec.1_Missense_Mu	NM_001080467	NP_001073936	Q9ULV0	MYO5B_HUMAN	e.|Actin-binding (Potential)	5	GGGTCTCCATG	0.488	
-	2	906	.1_Missense_Mut	NM_003927	NP_003918	Q9UBB5	MBD2_HUMAN		0	TCGTTTCGCAGT	0.363	
-	4	488	e_Mutation_p.R13	NM_000140	NP_000131	P22830	HEMH_HUMAN		1	TCCTGCGGTAC	0.493	
+	1	342	lik.1_Missense_M	NM_020854	NP_065905	Q9P260	K1468_HUMAN		6	TGGGCGCCGGA	0.647	
-	31	4305	TN_uc010xfb.1_M	NM_173630	NP_775901	Q86VV8	RTTN_HUMAN		8	GAGCCCACCGG	0.483	
+	1	4703	qu.1_Missense_M	NM_017757	NP_060227	Q9C0G0	ZN407_HUMAN	ype 14; degenerate.	2	AAGCAGCAACT	0.502	
+	5	2135	FATC1_uc010xfi.1	NM_006162	NP_006153	O95644	NFAC1_HUMAN	RHD.	2	GGTACGGCTGG	0.597	
-	2	503	2_uc002lop.3_5'F	NM_012435	NP_036567	P98077	SHC2_HUMAN	PID.	0	GGGAGCGCATA	0.637	
+	6	1764		NM_001194	NP_001185	Q9UL51	HCN2_HUMAN	toplasmic (Potential).	0	GACTACATCATC	0.592	
-	5	598	2_uc002lqi.2_Silen	NM_138774	NP_620129	Q96D70	CS022_HUMAN	Arg-rich.	1	CGGCTCGCAGA	0.647	
+	4	295	_p.E77K|MUM1_uc002lsb.2_Missense_Mutation_p.E8			Q2TAK8	MUM1_HUMAN		0	AGAATGAGGTT	0.567	
-	10	809	_uc002ltq.2_Miss	NM_003200	NP_003191	P15923	TFE2_HUMAN		7	GAGGGGCAGCG	0.726	
+	1	1059		NM_003775	NP_003766	O95977	S1PR4_HUMAN	smic (By similarity).	2	GGCTCACTCCG	0.692	
+	5	824	_Mutation_p.G13	NM_033064	NP_149053	Q86WG3	ATCAY_HUMAN		1	TGCCCGGGGAC	0.667	
+	8	1180	_p.S239N|ZNF557_	NM_001044388	NP_001037853	Q8N988	ZN557_HUMAN	2H2-type 4.	2	ATGCAGTGACT	0.438	
-	3	26930		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	h.|Extracellular (Potential).	57	TGGGAGGTGAA	0.493	
+	12	1318	p.D169N|ZNF177_	NM_003451	NP_003442	Q13360	ZN177_HUMAN	2H2-type 4.	1	TTCATCGATCAG	0.468	
-	5	664		NM_001080404	NP_001073873	C9JN71	ZN878_HUMAN	2H2-type 3.	0	ACACTGCTTAC	0.408	
+	8	970		NM_017682	NP_060152	Q8NFU1	BEST2_HUMAN	lasmic (Potential).	2	TGGACGAGATG	0.627	
+	2	333	_p.E78K|NFIX_uc002mwf.2_Missense_Mutation_p.E8			Q14938	NFIX_HUMAN	CTF/NF-I.	2	GGCCCGAGTTC	0.657	
+	4	639	naf.2_Missense_M	NM_012114	NP_036246	P31944	CASPE_HUMAN		4	TCGAGGCCCTG	0.567	
-	7	2583	_p.R721C|WIZ_uc0	NM_021241	NP_067064	O95785	WIZ_HUMAN		0	TCGGCGTTCAA	0.617	
-	1	117	nhx.1_Missense_	NM_005535	NP_005526	P42701	I12R1_HUMAN		1	GCCTGGACAGC	0.582	
-	4	827	pc.1_Missense_M	NM_001076675	NP_001070143	Q68DY1	ZN626_HUMAN		1	GGTTTCTCTCCA	0.393	
-	7	2771		NM_001080409	NP_001073878				2	TTAAAAGCTTTG	0.368	
+	3	2081		NM_014727	NP_055542	Q9UMN6	MLL4_HUMAN	Pro-rich.	11	GCCTCGGGCAG	0.642	
-	2	512		NM_001864	NP_001855	P24310	CX7A1_HUMAN		0	GGGCGGTGGAG	0.697	

+	74	11027	iv.1_Missense_Mu	NM_000540	NP_000531	P21817	RYR1_HUMAN		12	GCAGTCGTGGCC	0.607	
-	11	1301	j.1_Missense_Mut	NM_001626	NP_001617	P31751	AKT2_HUMAN	rotein kinase.	2	CAGGCGGCCGC	0.622	rs145305228
+	8	978	p.G298R|SPTBN4	NM_020971	NP_066022	Q9H254	SPTN4_HUMAN		5	CGTATCGGGAAG	0.567	
-	4	679	.F_uc002otd.3_5'U	NM_006494	NP_006485	P50548	ERF_HUMAN		4	CAGCCGAGAAG	0.662	
+	6	892	wk.2_Missense_M	NM_001130011	NP_001123483	Q9BY14	TX101_HUMAN		1	TTTGGGGGTTA	0.507	
+	3	1737	2pbp.2_5'Flank|C	NM_012099	NP_036231	O15446	RPA34_HUMAN		4	AGGCAGCTCCC	0.493	
-	8	870	ise_Mutation_p.V1	NM_001983	NP_001974	P07992	ERCC1_HUMAN		2	CTTCACGGTGG	0.458	
-	9	1137	dp.1_Missense_M	NM_004819	NP_004810	Q92797	SYMPK_HUMAN		1	CTTACGCACAC	0.592	
-	8	1394	e_Mutation_p.V32	NM_002103	NP_002094	P13807	GYS1_HUMAN		2	GCGCACAGCTT	0.567	
-	1	1839		NM_002152	NP_002143	P23327	SRCH_HUMAN		1	CTTCcctcctctcctc	0.308	
+	2	195	se_Mutation_p.G5	NM_001030047	NP_001025218	P07288	KLK3_HUMAN	eptidase S1.	3	GCGGCGGTGTT	0.642	
+	2	355	p.V104M|FPR2_u	NM_001005738	NP_001005738	P25090	FPR2_HUMAN	Name=3; (Potential).	4	ACATCGTGGTG	0.483	rs117415514
-	5	888	77_uc010ydf.1_5'	NM_023074	NP_075562	Q9BS31	ZN649_HUMAN	2H2-type 2.	3	TACACACGTGG	0.488	
+	4	1578	po.1_Intron|ZNF5	NM_001143939	NP_001137411	Q76KX8	ZN534_HUMAN		0	AGAAGCTTTACA	0.398	
+	4	1695	po.1_Intron|ZNF5	NM_001143939	NP_001137411	Q76KX8	ZN534_HUMAN	2H2-type 13.	0	TCTTCCGTCGGA	0.443	
-	5	976	LRA3_uc010erk.2	NM_006865	NP_006856	Q8N6C8	LIRA3_HUMAN	like C2-type 3.	1	CGGAGGAGAGG	0.677	
+	3	366	_p.G93R|LILRA2_	NM_001130917	NP_001124389	Q8N149	LIRA2_HUMAN	otential).|Ig-like C2-type 1.	1	ACGCAGGGCGC	0.532	
+	3	1653	IF776_uc002qqa.2	NM_173632	NP_775903	Q68DI1	ZN776_HUMAN	ype 10; degenerate.	1	TCATTCGACATCA	0.448	
-	2	604	_p.R60C|CHMP2A	NM_198426	NP_940818	O43633	CHM2A_HUMAN	ction with VPS4B.	0	GATGCGAACAG	0.522	
+	7	1028	2qyt.2_Missense_	NM_014746	NP_055561	P50876	R144A_HUMAN	ype 2; degenerate.	2	GAGACGAAGGC	0.567	
-	2	646	n_p.L4F|LAPTM4	NM_014713	NP_055528	Q15012	LAP4A_HUMAN	ical; (Potential).	1	GTCAGCAAAAT	0.398	
-	23	3083	N2_uc002rfg.2_M	NM_006277	NP_006268	Q9NZM3	ITSN2_HUMAN	SH3 2.	4	CTCTTCCTCCA	0.408	
+	2	331	ENPA_uc002rhs.2_	NM_001809	NP_001800	P49450	CENPA_HUMAN	H3-like.	0	TAAAGGAGATC	0.547	
+	2	253	se_Mutation_p.W1	NM_182551	NP_872357	Q6UWP7	LCLT1_HUMAN		2	ACCCATGGTCAA	0.423	
+	61	12279	a-mir-558|MI0003	NM_016252	NP_057336	Q9NR09	BIRC6_HUMAN		14	CTCCAGGTGAT	0.403	
+	6	1027	a.1_Missense_M	NM_022437	NP_071882	Q9H221	ABCG8_HUMAN	er.|Cytoplasmic (Potential).	4	TGTCCTCGCTAC	0.597	
-	68	8081		NM_014709	NP_055524	Q70CQ2	UBP34_HUMAN		19	CAGAAGATAAG	0.423	
-	42	5558	34_uc002sbf.2_5'	NM_014709	NP_055524	Q70CQ2	UBP34_HUMAN		19	CAAATCGTAAGC	0.413	
-	13	1347		NM_002056	NP_002047	Q06210	GFPT1_HUMAN	SIS 1.	1	CAGCTCCTCAA	0.413	
+	26	3095	YSF_uc010fek.2_	NM_003494	NP_003485	O75923	DYSF_HUMAN	lasmic (Potential).	7	CTGACGTCACG	0.592	
-	7	501	1_5'UTR|SFXN5_	NM_144579	NP_653180	Q8TD22	SFXN5_HUMAN		1	CAAGAGAAGAC	0.478	
-	7	1168	_p.M213I|IMMT_u	NM_006839	NP_006830	Q16891	IMMT_HUMAN	intermembrane (Potential).	1	TTGTCCATGGC	0.468	
-	19	2487	fhz.2_Missense_	NM_001115016	NP_001108488	Q9P2N6	K1310_HUMAN		0	CACAGGAATGG	0.627	
+	10	2081		NM_198581	NP_940983	P61129	ZC3H6_HUMAN		4	TGAAAGTACCC	0.483	
-	3	707		NM_001099771	NP_001093241	A5A3E0	POTEF_HUMAN		5	GTGGCAGCACC	0.617	
+	12	1069	18_uc002trb.2_M	NM_014369	NP_055184	Q99952	PTN18_HUMAN		4	GACTCCCCAGG	0.612	
+	1	1124		NM_001508	NP_001499	O43194	GPR39_HUMAN	ellular (Potential).	0	GGACCGTGTTC	0.597	
-	18	5911	ttq.2_Missense_M	NM_207363	NP_997246	O14513	NCKP5_HUMAN		0	GAAGCGGCTGG	0.537	
-	10	1535		NM_005915	NP_005906	Q14566	MCM6_HUMAN	MCM.	0	TCCTGCTTTAG	0.403	
+	9	1336		NM_015630	NP_056445	Q52LR7	EPC2_HUMAN		3	ATTGCCTTACA	0.398	
-	7	682		NM_004543	NP_004534	P20929	NEBU_HUMAN	Nebulin 3.	20	TGCTGCGACACT	0.418	
-	14	2861	aq.1_Missense_M	NM_013450	NP_038478	Q9UIF8	BAZ2B_HUMAN	Arg-rich.	4	TGATACGAGGAA	0.403	
-	11	1441	n.2_Missense_Mu	NM_016836	NP_058520	P29558	RBMS1_HUMAN		0	TGCGGGCTGTA	0.493	
+	6	673	.1_Missense_Mut	NM_012198	NP_036330	P28676	GRAN_HUMAN	ential).|EF-hand 4.	0	TTAAACGTTATAG	0.313	
-	28	3928	.R686W|ABCB11_	NM_003742	NP_003733	O95342	ABCBB_HUMAN	tential).|ABC transporter 2	5	GGTCCGACCCT	0.522	
-	206	40825	1_Nonsense_Mut	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	TTAGTCCATGTTT	0.438	
-	48	11692	N_uc010zfj.1_Intr	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	TTTCAGTACTGC	0.358	

-	8	758		NM_178123	NP_835224	Q86VW0	SESD1_HUMAN		1	TCAACCGATGGA	0.294	
+	51	4411		NM_000090	NP_000081	P02461	CO3A1_HUMAN	lar collagen NC1.	13	GAATATCGAACAC	0.408	
-	35	2613	frx.2_Missense_M	NM_000393	NP_000384	P05997	CO5A2_HUMAN		2	GCCACCCTGGG	0.264	rs147911170
-	4	626	so.2_Splice_Site_	NM_003151	NP_003142	Q14765	STAT4_HUMAN		9	ATATTACCTGGAC	0.269	
-	7	1703	_p.G296S|SATB2_	NM_015265	NP_056080	Q9UPW6	SATB2_HUMAN		1	GAAGACCAGGGC	0.512	
+	5	2441		NM_020923	NP_065974	Q9HCK1	ZDBF2_HUMAN		3	GTAAATCTTAAAG	0.423	
+	15	1641	M23_uc010ziv.1_	NM_003812	NP_003803	O75077	ADA23_HUMAN	B.|Extracellular (Potential).	3	AATTTTCAAAGTG	0.363	
+	13	1987		NM_032726	NP_116115	Q9BRC7	PLCD4_HUMAN	I-PLC Y-box.	3	ATGGCGGCTGT	0.517	
-	8	3561	fvt.2_Missense_M	NM_001105537	NP_001099007	P52746	ZN142_HUMAN		4	TGAGAGGTAATA	0.607	
+	20	2655	V797I|STK36_uc0	NM_015690	NP_056505	Q9NRP7	STK36_HUMAN		11	CATGTCGTCTCT	0.463	rs148974664
-	16	2462	ve.1_Missense_M	NM_005689	NP_005680	Q9NP58	ABCB6_HUMAN	C transporter.	2	CCCGCCGCTCA	0.622	
+	26	2363	xp.1_Missense_M	NM_001080391	NP_001073860	P23497	SP100_HUMAN		5	CGTGGAGTTGCA	0.493	
-	7	1308	_p.R77C|NGEF_	NM_019850	NP_062824	Q8N5V2	NGEF_HUMAN	DH.	7	CATAACGGTACA	0.567	
+	10	970	p.G276R|PPP1R7	NM_002712	NP_002703	Q15435	PP1R7_HUMAN		3	TGAAGGGAGCC	0.612	
-	4	817	SIRPG_uc002wfo.	NM_018556	NP_061026	Q9P1W8	SIRPG_HUMAN	ellular (Potential).	1	TGGGTGGAACT	0.552	
+	19	3401	l.2_Missense_Mut	NM_139321	NP_647537	O75882	ATRN_HUMAN	tential).|Laminin EGF-like	2	TGGAGGGAAAT	0.468	
+	20	3484	il.2_Missense_Mut	NM_139321	NP_647537	O75882	ATRN_HUMAN	tential).|Laminin EGF-like	2	AGGGCGTCAAG	0.592	
+	3	636	_p.R87*|PCSK2_	NM_002594	NP_002585	P16519	NEC2_HUMAN		7	TTGACCGAAAA	0.393	
+	9	1733	T2_uc002wzf.1_R	NM_005093	NP_005084	O43439	MTG8R_HUMAN		2	GAAAACGGGGA	0.517	
-	5	474	S_uc010zup.1_Mi	NM_000178	NP_000169	P48637	GSHB_HUMAN		3	GCTGCGCTGGA	0.597	
+	3	720	OCR_uc010zuw.1	NM_006404	NP_006395	Q9UNN8	EPCR_HUMAN	ellular (Potential).	0	ACTGCGGGAAT	0.577	
-	4	828	p.T195M|CHD6_u	NM_032221	NP_115597	Q8TD26	CHD6_HUMAN		14	GGTTCGTCAGG	0.532	
+	20	2406		NM_017895	NP_060365	Q96GQ7	DDX27_HUMAN		2	GAGACGAGGAG	0.433	
+	8	1100	ys.1_Missense_M	NM_002827	NP_002818	P18031	PTN1_HUMAN		0	CCCACCTCCCC	0.552	
-	15	2113	e_Mutation_p.P60	NM_080829	NP_543019	Q96MK2	FA65C_HUMAN		2	TGGGGGCAGGG	0.587	
-	7	1326	.R168W|CYP24A	NM_000782	NP_000773	Q07973	CP24A_HUMAN		3	AAGCCGATTCT	0.458	
+	5	1237	zm.2_Missense_	NM_001001433	NP_001001433	O14662	STX16_HUMAN	lasmic (Potential).	1	CGCAGGCCCTG	0.672	
-	1	440	CFL5_uc002ydq.2	NM_006602	NP_006593	Q9UL49	TCFL5_HUMAN	Ala-rich.	1	CGTCGGCCGCC	0.488	
-	13	1649	fa.1_Missense_M	NM_172107	NP_742105	O43526	KCNQ2_HUMAN	lasmic (Potential).	2	GTGCCCGGCTG	0.682	
-	6	794	ia.2_Missense_M	NM_005873	NP_005864	P49795	RGS19_HUMAN	RGS.	1	CGAACGTGTGT	0.647	
-	10	1014	.1_5'Flank|MRPL3	NM_017446	NP_059142	Q9NYK5	RM39_HUMAN		0	TACATTCCTCTG	0.259	
+	5	2159	e_Mutation_p.P68	NM_001186	NP_001177	O14867	BACH1_HUMAN		2	TGCCTCCCTGT	0.522	
-	3	432	wo.2_Missense_M	NM_002240	NP_002231	P48051	IRK6_HUMAN	llular (By similarity).	1	GGAGGGGTCCT	0.458	
+	23	3804	_p.S923L|TRAPP	NM_003274	NP_003265	P48553	TPC10_HUMAN		2	GCATTCGGCCT	0.632	
-	1	871	.1_Intron|C21orf2	NM_198691	NP_941964	P60331	KR101_HUMAN		1	GCACGCGGGGC	0.726	
-	1	581	.1_Intron|C21orf2	NM_198696	NP_941969	P60369	KR103_HUMAN	A repeats of C-C-X(3).	1	CAGGGGCACAG	0.721	
+	1	644	.1_Intron|C21orf2	NM_198687	NP_941960	P60372	KR104_HUMAN	repeats of C-C-X(3).	0	CTGCACGCCCT	0.662	
-	6	671	_Mutation_p.V15	NM_003325	NP_003316	P54198	HIRA_HUMAN	WD 3.	1	TATCCACGCTGC	0.522	
+	6	411	_p.G99R|PPIL2_u	NM_148175	NP_680480	Q13356	PPIL2_HUMAN	U-box.	2	GTGAGGGTGAG	0.458	
-	2	733	gwa.1_Intron|DUS	NM_152511	NP_689724	Q8NEJ0	DUS18_HUMAN		0	GAGACGTGAGT	0.522	
+	10	1398	kj.2_Missense_Mu	NM_005569	NP_005560	P53671	LIMK2_HUMAN	rotein kinase.	2	TCTGCGCAGTA	0.532	rs147975203
+	25	2894	.R740K|SFI1_uc0	NM_001007467	NP_001007468	A8K8P3	SFI1_HUMAN		1	AGCCAGGAGGC	0.632	
-	2	280	arb.2_Missense_M	NM_001051	NP_001042	P32745	SSR3_HUMAN	lasmic (Potential).	1	TGGCCGTGTGC	0.647	
-	3	1169		NM_052906	NP_443138	Q5R3F8	LRFN6_HUMAN	tracellular (Potential).	2	GCAGGCGGCTC	0.632	
+	7	1998	atq.1_Missense_M	NM_001039141	NP_001034230	Q9H2D6	TARA_HUMAN		1	CCCCAGAACAT	0.587	
+	7	2067	atq.1_Missense_M	NM_001039141	NP_001034230	Q9H2D6	TARA_HUMAN		1	CCCCACAACAT	0.582	
+	7	2304	atq.1_Missense_M	NM_001039141	NP_001034230	Q9H2D6	TARA_HUMAN		1	TGCCCTACGGG	0.582	

+	12	1321	DSL_uc003ayr.3_	NM_000026	NP_000017	P30566	PUR8_HUMAN		1	GTGACAATGACC	0.488	rs145750778
-	9	1110		NM_173050	NP_766638	Q8IWY4	SCUB1_HUMAN	alcium-binding (Potential).	5	TGCCCGGGGAG	0.647	
+	6	1046	_p.V117I|MPPED	NM_001044370	NP_001037835	O15442	MPPD1_HUMAN		0	GGCGCGTCCAG	0.622	
+	4	604		NM_015653	NP_056468	Q9H4K1	RIBC2_HUMAN		0	ATGTTCGGAATA	0.448	
+	8	867	_p.V261I|TRABD_	NM_025204	NP_079480	Q9H4I3	TRABD_HUMAN		0	GCGACGTCTAC	0.672	
-	16	4134	CP6_uc010har.1_	NM_020461	NP_065194	Q96RT7	GCP6_HUMAN	AA tandem repeats.	4	CCGGGTGGGAG	0.622	rs145066767
-	9	876	bkl.1_Missense_	NM_002969	NP_002960	P53778	MK12_HUMAN	rotein kinase.	0	GTCCCCGTCACC	0.672	
-	13	1826	_p.L421F|LMF2_u	NM_033200	NP_149977	Q9BU23	LMF2_HUMAN		1	CCTGAGCAGCG	0.657	
+	9	1244	w.1_Missense_M	NM_006614	NP_006605	O00533	CHL1_HUMAN	3.|Extracellular (Potential).	12	TTTCACGTTATAG	0.398	
-	19	3002	rg.1_Missense_M	NM_014850	NP_055665	O43295	SRGP2_HUMAN	SH3.	9	GGCGCGGTGGT	0.587	
+	4	406		NM_153635	NP_705899	Q8IYJ1	CPNE9_HUMAN	C2 1.	2	TTGAGGAAAAG	0.597	
+	6	755	h.2_Splice_Site_p.	NM_001077415	NP_001070883	Q96HD1	CREL1_HUMAN		1	TTCGGGTAGGT	0.622	
+	1	200	se_Mutation_p.P2	NM_144633	NP_653234	Q96L42	KCNH8_HUMAN	lasmic (Potential).	5	AAATGCCGGTTA	0.493	
+	2	301	awp.1_5'UTR|OXS	NM_017897	NP_060367	Q9NWU1	OXSM_HUMAN		2	GGATCGTCTTAT	0.463	
-	2	1618		NM_033403	NP_208382	Q9C098	DCLK3_HUMAN	rotein kinase.	9	TCTCGCGGTGT	0.547	
+	4	525	c.2_Missense_Mu	NM_002207	NP_002198	Q13797	ITA9_HUMAN	r (Potential).|FG-GAP 2.	6	ATCCTACCCCAT	0.512	
+	18	2626	.1_Missense_Mut	NM_007335	NP_031361	Q9Y238	DLEC1_HUMAN		9	AGTTTGGTCTG	0.627	
-	15	1900	.2_Missense_Muta	NM_002343	NP_002334	P02788	TRFL_HUMAN	ansferrin-like 2.	4	CCATCCGAGAC	0.552	rs142148325
-	17	3703	003csx.2_Missens	NM_002673	NP_002664	O43157	PLXB1_HUMAN	Extracellular (Potential).	5	CGGCACCTCCA	0.667	
-	63	5429		NM_000094	NP_000085	Q02388	CO7A1_HUMAN	le-helical region.	11	TGGAAGCCCCT	0.552	
+	5	6893		NM_003458	NP_003449	Q9UPA5	BSN_HUMAN		8	TGTACCGCTATC	0.592	
-	5	728	MPPB_uc003cxl.	NM_021971	NP_068806	Q9Y5P6	GMPPB_HUMAN		0	TTATTGGACACA	0.592	
+	2	894		NM_203370	NP_976248	Q96EL1	CC054_HUMAN		0	CCCACCTCGCC	0.632	
-	5	573	.1_5'UTR|CAMKV	NM_024046	NP_076951	Q8NCB2	CAMKV_HUMAN	rotein kinase.	7	ACTTGCCGTACC	0.602	
-	2	1610	T449I|MST1R_uc	NM_002447	NP_002438	Q04912	RON_HUMAN	lar (Potential).|Sema.	6	ATGCAGTGACC	0.572	
+	8	961	3cyk.2_Splice_Site	NM_004186	NP_004177	Q13275	SEM3F_HUMAN		2	GAACGGTAAGC	0.567	
+	7	1132	1bdu.1_Missense_	NM_015106	NP_055921	Q9Y4B4	ARIP4_HUMAN	ase ATP-binding.	3	TGTGCCGGTAA	0.512	
+	5	561	ei.1_Missense_Mu	NM_015136	NP_055951	Q9NY15	STAB1_HUMAN	Extracellular (Potential).	9	AATCGGGTGAG	0.632	
+	19	2335	gm.2_Missense_M	NM_006254	NP_006245	Q05655	KPCD_HUMAN	kinase C-terminal.	9	ATTCGCTGGCT	0.557	
+	9	1276	66_uc003dhu.2_	NM_001141947	NP_001135419	A2RUB6	CCD66_HUMAN		1	CTCCTGACACT	0.453	
+	9	1116	_Mutation_p.A30	NM_007159	NP_009090	Q14BN4	SLMAP_HUMAN	ytoplasmic (Potential).	0	AATTAGCCAACA	0.323	
-	8	1903	m.2_Nonsense_M	NM_003716	NP_003707	Q9ULU8	CAPS1_HUMAN		3	CATTCGGACAG	0.448	
-	35	5335	p.A1740V|ADAMT	NM_182920	NP_891550	Q9P2N4	ATS9_HUMAN	GON.	4	ATCCCCGCACAG	0.463	
-	2	821	fx.1_Missense_Mu	NM_007114	NP_009045	P82094	TMF1_HUMAN		0	ACTTACAGTTGG	0.388	
-	16	2130	p.R603W|FOXP1_	NM_032682	NP_116071	Q9H334	FOXP1_HUMAN	p.R603Q(1)	2	TTCCCGTATTG	0.512	
-	5	1590	ense_Mutation_p.A	NM_019895	NP_063948	Q9NY35	CLDN1_HUMAN		1	TGTGAGCAGCC	0.448	
-	10	1335	e.1_Missense_Mu	NM_016247	NP_057331	Q9BZV3	IMPG2_HUMAN	ellular (Potential).	3	GGAATCAGGAT	0.378	
-	2	347	egb.1_Missense_	NM_001031702	NP_001026872	Q9P283	SEM5B_HUMAN	ellular (Potential).	7	AGGGACGAGGT	0.612	
-	21	3718	gg.1_Missense_M	NM_183357	NP_899200	O95622	ADCY5_HUMAN	lasmic (Potential).	4	GACCACGCCCC	0.612	
-	2	274		NM_033049	NP_149038	Q9H3R2	MUC13_HUMAN	xtracellular (Potential).	0	GAGCAGGTGTAG	0.453	
+	10	911	tb.2_Missense_Mu	NM_016128	NP_057212	Q9Y678	COPG_HUMAN		4	AAGCCGCCTCG	0.557	
+	11	1364	p.R402Q|PLS1_uc	NM_001145319	NP_001138791	Q14651	PLSI_HUMAN	.|Actin-binding 2.	1	ATTTCGGAACT	0.398	rs138340155
-	2	147		NM_138786	NP_620141	Q96CE8	T4S18_HUMAN	lasmic (Potential).	1	ACTTCCGAGACC	0.413	
+	4	1215	wq.2_Nonsense_	NM_014373	NP_055188	Q9UJ42	GP160_HUMAN	lasmic (Potential).	0	TGGTACAGGCT	0.328	
+	1	72	fkb.2_5'Flank|ND	NM_002492	NP_002483	O43674	NDUB5_HUMAN		1	CTGCGGTGGCA	0.632	
-	11	1244	j.1_Missense_Mu	NM_016559	NP_057643	Q8IYB4	PEX5R_HUMAN	TPR 1.	4	ATTCTCCGCCTG	0.443	
-	8	934	L2_uc003flp.1_Mi	NM_015078	NP_055893	Q86YR7	MF2L2_HUMAN		5	GGTTGAGATTGA	0.428	

+	10	1456	ns.2_Missense_M	NM_198241	NP_937884	Q04637	IF4G1_HUMAN		7	TCAGTGAGCCA	0.622	
-	6	730	brs.1_Missense_M	NM_001966	NP_001957	Q08426	ECHP_HUMAN	hydratase / isomerase.	3	TGCACGGACAC	0.537	rs141664962
-	2	7133	C4_uc003fvp.2_Int	NM_018406	NP_060876	Q99102	MUC4_HUMAN		0	AAGAAGAGGGA	0.597	
+	3	436	se_Mutation_p.P5	NM_017861	NP_060331	Q8TBF5	PIGX_HUMAN	enal (Potential).	0	GGATCCGTATG	0.408	
+	44	6002		NM_002111	NP_002102	P42858	HD_HUMAN		4	CCAGCGGCCTG	0.488	
-	1	1528	3_5'Flank|TADA2B	NM_153376	NP_699207	Q2M329	CCD96_HUMAN		0	CGTCCGCAGCC	0.557	
+	3	1423	PZ_uc003gll.2_Intr	NM_080819	NP_543009	Q96P69	GPR78_HUMAN	lasmic (Potential).	6	GCACCAGCTGC	0.647	rs149989249
+	31	3466	s.1_Missense_Mut	NM_004787	NP_004778	O94813	SLIT2_HUMAN	alcium-binding (Potential).	11	AAAACGGAGCC	0.413	rs144073473
-	46	6465	i.1_Missense_Mut	NM_015030	NP_055845	O94915	FRYL_HUMAN		1	CCGCCGGTCAC	0.418	rs140338334
-	26	3805	.1_Missense_Mut	NM_002253	NP_002244	P35968	VGFR2_HUMAN	lasmic (Potential).	33	TGCTGAGCATTA	0.502	
-	6	1491	e_Mutation_p.D34	NM_021139	NP_066962	P06133	UD2B4_HUMAN		2	GAGGTCGTGGG	0.493	
+	3	194		NM_001133	NP_001124	P43652	AFAM_HUMAN	Albumin 1.	3	AGTATGTTCAG	0.413	
-	3	600		NM_001729	NP_001720	P35070	BTC_HUMAN	ar (Potential).|EGF-like.	2	CACCACGAAGC	0.557	
+	8	2802	_p.E655K|PRDM8_	NM_020226	NP_064611	Q9NQV8	PRDM8_HUMAN		1	CGATGGAGCCC	0.597	
-	9	1217	SE_uc011ccs.1_M	NM_001098540	NP_001092010	Q9Y251	HPSE_HUMAN		1	TTCGGGCTGAC	0.443	
+	1	157		NM_005390	NP_005381	P29803	ODPAT_HUMAN		1	AATGACGCTACA	0.502	
+	2	847	ifb.2_Missense_M	NM_199327	NP_955359	O43609	SPY1_HUMAN	ys-rich.|SPR.	3	TGGAACCTGCA	0.512	
+	5	1381	_p.S347F|PLK4_u	NM_014264	NP_055079	O00444	PLK4_HUMAN		0	ATTCCTCTGATA	0.413	
+	12	2514		NM_022475	NP_071920	Q96QV1	HHIP_HUMAN	EGF-like 1.	6	CCCCACGGGAA	0.537	
-	2	1646	e_Mutation_p.G43	NM_000901	NP_000892	P08235	MCR_HUMAN	Modulating.	1	GGTGCCTGAAC	0.373	
-	7	1157	P9_uc010iqa.1_R	NM_001039580	NP_001034669	Q49MG5	MAP9_HUMAN	Potential.	2	CAACTGCAGTA	0.368	
+	20	3563	nse_Mutation_p.V	NM_016081	NP_057165	Q8WX93	PALLD_HUMAN	action with EZR.	1	TGGACGTTTAC	0.423	
+	7	1306	_p.T249I|CLCN3_	NM_001829	NP_001820	P51790	CLCN3_HUMAN	al; (By similarity).	3	TTAAAACCATCA	0.398	
-	10	6931		NM_005245	NP_005236	Q14517	FAT1_HUMAN	(Potential).|Cadherin 20.	12	ATGCCGGGTGG	0.473	
+	7	989	P72_uc011clz.1_R	NM_018140	NP_060610	Q9P209	CEP72_HUMAN		1	GGATACCGAGG	0.527	
+	10	1333	D2_uc010itf.1_3'U	NM_033120	NP_149111	Q969F2	NKD2_HUMAN	His-rich.	0	caccaccaccacca	0.522	
+	20	3214	jdk.1_Missense_	NM_139056	NP_620687	Q8TE57	ATS16_HUMAN	SP type-1 4.	8	TGCTGCCCGAC	0.637	
-	18	3125		NM_003966	NP_003957	Q13591	SEM5A_HUMAN	.|Extracellular (Potential).	2	GTTCCGAATGC	0.582	
-	18	3204	D2_uc011cmz.1_	NM_001332	NP_001323	Q9UQB3	CTND2_HUMAN		8	GATCTCGGTAC	0.532	
-	17	2948	D2_uc011cmz.1_	NM_001332	NP_001323	Q9UQB3	CTND2_HUMAN		8	GTCTCGCATGG	0.512	
-	66	11419	H5_uc003jfc.2_In	NM_001369	NP_001360	Q8TE73	DYH5_HUMAN	|AAA 5 (By similarity).	31	CTCCTCGGCTG	0.458	
+	12	2420	_p.L678F|PDZD2_	NM_178140	NP_835260	O15018	PDZD2_HUMAN		9	CCAGCCTCACA	0.532	
-	2	261		NM_001737	NP_001728	P02748	CO9_HUMAN	TSP type-1.	0	TCTGAGACAAG	0.478	
+	3	371		NM_006144	NP_006135	P12544	GRAA_HUMAN	eptidase S1.	4	CACGCGAAGGT	0.438	
+	29	3894	NEF_uc011csr.1_	NM_001080479	NP_001073948	Q8N1W1	RGNEF_HUMAN	of axonal branching and sy	0	TGGGCGCCGTG	0.428	
+	35	4819	.V1029M|IQGAP2_	NM_006633	NP_006624	Q13576	IQGA2_HUMAN		7	AAAAGGTGCAA	0.368	
-	8	2787		NM_000046	NP_000037	P15848	ARSB_HUMAN		1	TAGGCGGGACA	0.542	
-	7	1036	DH_uc011ctf.1_N	NM_013391	NP_037523	Q9UI17	M2GD_HUMAN		4	TGATTCGATCTA	0.423	rs143021634
+	20	2679	uc003kgi.3_Intron	NM_003248	NP_003239	P35443	TSP4_HUMAN	P C-terminal.	0	ACCTTCCATGTG	0.453	
-	4	610		NM_000439	NP_000430	P29120	NEC1_HUMAN	Catalytic.	2	ATCCTGGTATCT	0.443	
+	3	550	uj.3_Missense_M	NM_130809	NP_570721	Q96M27	PRRC1_HUMAN	Pro-rich.	0	CTGCACCCCCT	0.517	rs149336967
+	1	653	DHA5_uc003lhk.	NM_018911	NP_061734	Q9Y5H6	PCDA8_HUMAN	|Extracellular (Potential).	2	TGGGGGCAAAC	0.473	
+	19	2869	_p.R926C|WWC1_	NM_015238	NP_056053	Q8IX03	KIBRA_HUMAN	ion with histone H3.	5	ATCATCCGCTCT	0.647	
-	9	1820		NM_005990	NP_005981	O94804	STK10_HUMAN		8	TCAGCGACAGG	0.572	
+	4	2680	408Q|CPEB4_uc0	NM_030627	NP_085130	Q17RY0	CPEB4_HUMAN		0	TGGGCGAAGGA	0.353	
+	8	1128	p.R321W|FGFR4_	NM_002011	NP_002002	P22455	FGFR4_HUMAN	otential).|Ig-like C2-type 3.	16	ACCTGCGGAAC	0.632	
-	3	387	P2_uc003mis.2_In	NM_017838	NP_060308	Q9NX24	NHP2_HUMAN		0	TCCTGCCAAAA	0.483	

-	15	1212	jkt.2_Missense_M	NM_173465	NP_775736	Q86Y22	CONA1_HUMAN	ntial).|Collagen-like 2.|Gly-	2	TGCCTCGGTGG	0.652	
-	7	1017	tron|C5orf45_uc01	NM_016175	NP_057259	Q6NTE8	CE045_HUMAN		0	GGGTCGAGGAT	0.547	
-	10	1199	ntx.3_Missense_M	NM_001012418	NP_001012418	Q86YV6	MYLK4_HUMAN	rotein kinase.	4	AAGGCGACAAA	0.498	
-	2	212	P2L_uc011dim.1_	NM_004752	NP_004743	O75603	GCM2_HUMAN	GCM.	3	TGAAGCGCACA	0.562	rs104893959
-	1	59	_5'UTR|HIST1H2	NM_021065	NP_066409	P20671	H2A1D_HUMAN		0	CCCGCGAAGAG	0.587	
+	7	997		NM_001732	NP_001723	Q13410	BT1A1_HUMAN	.|Cytoplasmic (Potential).	2	TGTTCGACTGG	0.488	
-	10	5112	C1_uc011dmp.1_	NM_014641	NP_055456	Q14676	MDC1_HUMAN	ith the PRKDC complex.	4	CCTGCCCCTAG	0.582	
-	9	1676	p.R349*|BAT1_uc	NM_004640	NP_004631	Q13838	DX39B_HUMAN	case C-terminal.	0	GCCTCGGCCAA	0.428	
+	9	1182	|SKIV2L_uc011do	NM_006929	NP_008860	Q15477	SKIV2_HUMAN		4	AGGAAGCGTCC	0.557	
+	17	2316	_p.L485F|SKIV2L_	NM_006929	NP_008860	Q15477	SKIV2_HUMAN	case C-terminal.	4	CCATCCTCAAG	0.602	
+	6	563	L8_uc003oac.1_	NM_030652	NP_085155	Q99944	EGFL8_HUMAN	alcium-binding (Potential).	0	CCTGCGGCTGC	0.597	
-	2	178	dqm.1_Missense_	NM_006120	NP_006111	Q31604	Q31604_HUMAN		0	GAGTAGGAGCT	0.478	
-	2	387	_uc010jvx.2_Silent	NM_003214	NP_003205	Q99594	TEAD3_HUMAN	TEA.	1	GGGCGGGTAGA	0.706	
-	5	838	17_uc003oop.2_	NM_031460	NP_113648	Q96T54	KCNKH_HUMAN		2	GGGAGGGGTTC	0.517	
-	6	1143		NM_173561	NP_775832	Q8IV45	UN5CL_HUMAN	.|Interaction with RELA and	2	TCTCATCGGCTA	0.517	
-	2	344	_p.S111N|TREM2_	NM_018965	NP_061838	Q9NZC2	TREM2_HUMAN	.|Extracellular (Potential).	1	CTGTGCTCCCA	0.602	
-	16	2815	5'Flank|PEX6_uc0	NM_000287	NP_000278	Q13608	PEX6_HUMAN		1	CAGCTGGGGAG	0.562	
+	5	701		NM_032538	NP_115927	Q5TCY1	TTBK1_HUMAN	rotein kinase.	9	GGAGTCCATCG	0.642	
-	3	850	_Intron|TMEM151	NM_182539	NP_872345	Q5JU00	TCTE1_HUMAN		4	CAGATCGCCCA	0.627	
-	2	446		NM_000255	NP_000246	P22033	MUTA_HUMAN		0	CTTCCGGGGTG	0.488	
-	6	563	zq.2_Missense_M	NM_000847	NP_000838	Q16772	GSTA3_HUMAN	ST C-terminal.	0	AAGTTCCACCA	0.502	
-	3	471	zr.2_Missense_M	NM_003643	NP_003634	Q9NP62	GCM1_HUMAN	GCM.	1	CTCTGCGAGAC	0.597	rs150847762
+	5	1555		NM_001010872	NP_001010872	Q5T0W9	FA83B_HUMAN		6	ACAACGAATGC	0.413	
+	34	5037	gg.2_Missense_M	NM_014989	NP_055804	Q86UR5	RIMS1_HUMAN		10	TGATCGGATGG	0.542	
-	32	5633	pht.2_Missense_	NM_004370	NP_004361	Q99715	COCA1_HUMAN	nectin type-III 13.	9	GGATACGGTGA	0.468	
-	3	860	cc.2_Missense_M	NM_021244	NP_067067	Q9NQL2	RRAGD_HUMAN		3	TCTTTGGGTTT	0.433	
-	5	2790		NM_001080450	NP_001073919	Q5T5X7	BEND3_HUMAN		3	CACCGGGAAGT	0.652	
-	17	7264	/3L_uc003puz.3_	NM_002912	NP_002903	O60673	DPOLZ_HUMAN		6	GATCCGGTTCT	0.378	
+	2	523	_p.A110V|DSE_uc	NM_001080976	NP_001074445	Q9UL01	DSE_HUMAN		1	CTTGGCAATGT	0.512	
+	12	1437	nse_Mutation_p.	NM_004100	NP_004091	O95677	EYA4_HUMAN		2	AGTTCGATACC	0.388	rs144415484
-	16	2227	gv.2_Missense_M	NM_003980	NP_003971	Q14244	MAP7_HUMAN		0	GGTAACCACAT	0.463	rs140358034
-	3	2186	kg.2_Missense_M	NM_002656	NP_002647	Q9UM63	PLAL1_HUMAN		1	AGGTAGAAGTG	0.552	
+	2	597	ll.2_Missense_Mu	NM_000838	NP_000829	Q13255	GRM1_HUMAN	ellular (Potential).	19	TGGACGGAGAT	0.597	
+	9	3576	_3'UTR|GRM1_u	NM_000838	NP_000829	Q13255	GRM1_HUMAN	lasmic (Potential).	19	TCCAGGGAGTG	0.672	
+	2	653		NM_015278	NP_056093	O94885	SASH1_HUMAN		1	ACATCGATGAC	0.572	
-	6	844	P43_uc011eee.1_	NM_198887	NP_942590	Q8NFH3	NUP43_HUMAN	WD 6.	1	ACTTTCAGCTT	0.373	
+	18	2090	nse_Mutation_p.V	NM_015440	NP_056255	Q6UB35	C1TM_HUMAN	hydrofolate synthetase.	4	TCGCAGTGGCC	0.607	
+	7	2627	e_Mutation_p.D45	NM_012454	NP_036586	Q8IVF5	TIAM2_HUMAN		4	GCAGCGATCCC	0.502	
-	15	1800	qrb.2_Missense_M	NM_032861	NP_116250	Q96JX3	SRAC1_HUMAN		0	CCAACGAGGGG	0.353	
-	8	1650	ju.2_Missense_M	NM_031924	NP_114130	Q86UC2	RSPH3_HUMAN		2	CACCAGGCTCA	0.507	
+	2	822	sense_Mutation_	NM_001098201	NP_001091671	Q99527	GPER_HUMAN	Name=3; (Potential).	1	GCAGCGTCTTC	0.607	
+	6	1072	IN_uc003sso.3_M	NM_001112706	NP_001106177	Q9Y6U3	ADSV_HUMAN	.|Actin-severing (Potential).	2	ACCACGGGGCT	0.393	
+	13	1864	_p.R885C|ABCB5_	NM_178559	NP_848654	Q2M3G0	ABCB5_HUMAN	ial).|ABC tra p.R440H(1)	6	AATATACGTACT	0.323	
+	6	1179		NM_003777	NP_003768	Q96DT5	DYH11_HUMAN	(By similarity).	15	AGCTCGGGTTA	0.388	
-	3	429	1_5'UTR|TRA2A_	NM_013293	NP_037425	Q13595	TRA2A_HUMAN	-rich (RS1 domain).	1	GGGATCTGGAT	0.448	
-	18	1955	.1_RNA|DPY19L2P1_uc010kwz.1_RNA						0	CCTGTCGAGAG	0.363	
+	2	753	_p.A154T|IGFBP1_	NM_000596	NP_000587	P08833	IBP1_HUMAN		1	GGGACGCCATC	0.527	

-	7	770		NM_138295	NP_612152	Q8TDX9	PK1L1_HUMAN	ellular (Potential).	11	TGGGGGTGCGA	0.577	
+	4	893		NM_001159524	NP_001152996	P0CB33	ZN735_HUMAN	C2H2-type 6.	0	CCTACAAATGTG	0.458	
+	3	661	7orf42_uc003tvl.2_	NM_017994	NP_060464	Q9NWD8	CG042_HUMAN		1	CGCAACGTCACC	0.547	
+	4	506	P120L|FKBP6_uc0	NM_003602	NP_003593	O75344	FKBP6_HUMAN	ase FKBP-type.	0	GCCCTCCCTTGA	0.552	
+	4	515	P123L|FKBP6_uc0	NM_003602	NP_003593	O75344	FKBP6_HUMAN	ase FKBP-type.	0	TGATCCCCCCAA	0.542	
+	9	980	e_Mutation_p.E19	NM_000941	NP_000932	P16435	NCPR_HUMAN	-binding FR-type.	1	GAACCGAGCGC	0.602	rs11540674
+	10	2100	j.3_Missense_Mut	NM_020892	NP_065943	Q86UW9	DTX2_HUMAN		2	CCCATGGTATCCA	0.607	
-	22	3044	nc.1_Missense_Mu	NM_000927	NP_000918	P08183	MDR1_HUMAN	smembrane type-1 2.	7	TTTTCATTTCAAC	0.353	
-	3	967	TEAP4_uc003ujt.2	NM_024636	NP_078912	Q687X5	STEA4_HUMAN	oxidoreductase.	0	GCAAAGCATCC	0.473	
+	8	1046	_p.G220S|DYNC1	NM_004411	NP_004402	O14576	DC1I1_HUMAN		4	ACAGCGGCCGA	0.373	
+	3	473	I3_uc011kip.1_Int	NM_015379	NP_056194	O95415	BRI3_HUMAN		0	GAAGCGACGAT	0.522	rs137943501
+	4	894	A_uc003uup.1_M	NM_013439	NP_038467	Q9UKJ1	PILRA_HUMAN	lasmic (Potential).	1	AGCAGCGGACT	0.637	rs145267648
+	22	4300	uwl.2_RNA|ZAN_u	NM_003386	NP_003377	Q9Y493	ZAN_HUMAN	ellular (Potential).	11	TTCTTCGACAGC	0.612	
-	14	2975	735_splice|EPHB4	NM_004444	NP_004435	P54760	EPHB4_HUMAN		15	CACTTACGTCCT	0.542	
+	11	1125	SLC26A5_uc003v	NM_002803	NP_002794	P35998	PRS7_HUMAN		0	GTCGGACCCACA	0.333	
+	8	1037	tion_p.T297I|CDH	NM_152750	NP_689963	Q6ZTQ4	CDHR3_HUMAN	|Extracellular (Potential).	1	ATCCCACCATTT	0.478	
-	13	1603	ey.2_Missense_Mu	NM_007356	NP_031382	A4D0S4	LAMB4_HUMAN	EGF-like 5; truncated.	8	ACAGTCACAGG	0.388	
+	5	1400	PAM1_uc003vlf.3_	NM_153189	NP_694859	P38567	HYALP_HUMAN		4	TGGGTGCTTCTG	0.343	
+	9	1340	p.E315K|IRF5_uc	NM_002200	NP_002191	Q13568	IRF5_HUMAN		0	TTGGGGAAGAA	0.522	
-	28	5105	A4_uc003vqz.3_5	NM_020911	NP_065962	Q9HCM2	PLXA4_HUMAN	lasmic (Potential).	1	TGTACCGGATCA	0.572	
+	7	1283	ub.2_Missense_M	NM_015905	NP_056989	O15164	TIF1A_HUMAN	Potential.	8	CAATTGGAGCA	0.373	
+	19	3352	ub.2_Missense_Mu	NM_015905	NP_056989	O15164	TIF1A_HUMAN		8	AGAACGCCAGT	0.343	
-	2	503	_p.V102I|KIAA154	NM_020910	NP_065961	Q9HCM3	K1549_HUMAN		230	ATTGACGGCCA	0.468	
+	5	652	Intron|uc003wad.2	NM_002769	NP_002760	P07477	TRY1_HUMAN	eptidase S1.	2	TCCAAGGAGTTG	0.507	
+	1	466		NM_001001667	NP_001001667	Q8N148	OR6V1_HUMAN	Name=4; (Potential).	1	ATGGTACCCACT	0.572	
+	7	1312	_p.R386Q|ZYX_uc	NM_001010972	NP_001010972	Q15942	ZYX_HUMAN	zinc-binding 1.	0	CGGCCGATGCC	0.617	
-	4	2130	_p.E628K|ZNF786_	NM_152411	NP_689624	Q8N393	ZN786_HUMAN	2H2-type 13.	4	TGTGCTCGATGA	0.577	
-	4	1275	R86_uc011kvk.1_	NM_198285	NP_938026	Q86TI4	WDR86_HUMAN	WD 7.	0	GTTGCGTCTGT	0.627	
+	2	342	wpm.2_Missense_	NM_004745	NP_004736	Q9P1A6	DLGP2_HUMAN		0	CTTCCCGCGGA	0.706	
-	3	708	.1_RNA|FGF20_u	NM_019851	NP_062825	Q9NP95	FGF20_HUMAN		1	GGTCTAGGTAAG	0.458	
+	18	2134	p.V687M|XPO7_u	NM_015024	NP_055839	Q9UIA9	XPO7_HUMAN		5	CTCATGGTGGAT	0.453	
-	8	1752	.2_Missense_Mut	NM_139278	NP_644807	Q8N145	LGI3_HUMAN	EAR 6.	1	GTGAAGGAGAAA	0.642	
+	19	2933	p.E646K|BMP1_u	NM_006129	NP_006120	P13497	BMP1_HUMAN	CUB 5.	3	TGGCCGAGGAA	0.592	
+	5	1036	|RHOBTB2_uc011	NM_015178	NP_055993	Q9BYZ6	RHBT2_HUMAN	Rho-like.	2	CCTAATGAAATC	0.577	
+	34	3541	xfp.1_Splice_Site_	NM_173174	NP_775266	Q14289	FAK2_HUMAN		5	TGAAGGTGAGA	0.632	
+	9	1461	0lvy.2_Splice_Site_	NM_032777	NP_116166	Q96PE1	GP124_HUMAN		5	CCCCAGGTGGC	0.657	
-	4	1515	p.A492V|JPH1_uc	NM_020647	NP_065698	Q9HDC5	JPH1_HUMAN	lasmic (Potential).	1	GTCTCGCCCCT	0.572	
+	23	2876		NM_007013	NP_008944	Q9H0M0	WWP1_HUMAN	HECT.	2	CTCATGGGTAAA	0.378	
-	3	339		NM_203390	NP_976324	Q8IXT5	RB12B_HUMAN		0	TCATCTGTTGCA	0.428	
+	5	582	M67_uc010maw.2_	NM_153704	NP_714915	Q5HYA8	MKS3_HUMAN		2	GGTGCGTCCGA	0.284	
+	1	344	ion_p.S5L|GRHL2_	NM_024915	NP_079191	Q6ISB3	GRHL2_HUMAN	cription activation.	3	AGAGTCGGACA	0.438	
-	18	3130	ynt.2_Missense_M	NM_198123	NP_937756	Q7Z407	CSMD3_HUMAN	lar (Potential).|CUB 5.	63	GGAACGACTGT	0.328	
-	18	3059	ynt.2_Missense_M	NM_198123	NP_937756	Q7Z407	CSMD3_HUMAN	lar (Potential).|CUB 5.	63	TGGGTGCCATTG	0.363	
+	1	123		NM_006438	NP_006429	Q9Y6Z7	COL10_HUMAN		3	TGCTTCGAAGAA	0.423	
-	1	37	90_uc011lix.1_Int	NM_001080399	NP_001073868	Q02509	OC90_HUMAN		3	ATGGCTGTAATG	0.413	
+	10	2662		NM_003235	NP_003226	P01266	THYG_HUMAN	globulin type-1 7.	15	AAATGGCCAACT	0.542	
-	12	1371	se_Mutation_p.S1	NM_001135242	NP_001128714	Q92597	NDRG1_HUMAN		4	GCGAGCTGTCC	0.517	

+	19	3122		NM_001702	NP_001693	O14514	BAI1_HUMAN	lasmic (Potential).		8	CAGAGCGTTCTG	0.587	
-	1	6591		NM_031308	NP_112598	P58107	EPIPL_HUMAN			2	TCCTCCGTGATTA	0.552	
-	1	4283		NM_031308	NP_112598	P58107	EPIPL_HUMAN	Plectin 25.		2	GGAGTCGCACA	0.612	
-	8	3913	mht.2_Missense_M	NM_001017969	NP_001017969	Q5HYC2	K2026_HUMAN			3	GCTGACCTGTGG	0.463	
+	16	2645	z.2_RNA|UHRF2_	NM_152896	NP_690856	Q96PU4	UHRF2_HUMAN	RING-type.		3	CCTGCCCTGCTT	0.443	
-	19	2423		NM_000170	NP_000161	P23378	GCSP_HUMAN			2	CAGACCCGAAGT	0.562	
-	1	669		NM_019897	NP_063950	Q9NQN1	OR2S1_HUMAN	Name=5; (Potential).		1	AGATCACATTCGT	0.478	
-	7	1334	1_Missense_Mutat	NM_016734	NP_057953	Q02548	PAX5_HUMAN		p.?(23)	147	CTGCGGGCCTG	0.617	
+	6	688	MTD3_uc011lqq.1_	NM_144964	NP_659401	Q6PF06	RG9D3_HUMAN			0	TATTTCCCTTGGA	0.353	
+	68	9399	akq.3_Missense_M	NM_033305	NP_150648	Q96RL7	VP13A_HUMAN			10	GATGGAGTTATCA	0.333	
+	26	4180	p.G1282R|DAPK1_	NM_004938	NP_004929	P53355	DAPK1_HUMAN	Death.		2	AGTAACGGGGCT	0.632	
-	5	678	n.1_RNA|SEMA4D	NM_006378	NP_006369	Q92854	SEM4D_HUMAN	tracellular (Potential).		2	ACTCACCTCTGT	0.627	
-	8	1150	C14B_uc004awl.2_	NM_033331	NP_201588	O60729	CC14B_HUMAN	B.		1	CTGGCTCTTGAAT	0.353	
+	19	2312		NM_002486	NP_002477	Q09161	NCBP1_HUMAN			1	GTGCTGCCGTAG	0.338	
-	11	2573	_p.A798V|TBC1D2	NM_018421	NP_060891	Q9BYX2	TBD2A_HUMAN	ab-GAP TBC.		3	CTGTCCGCAAAG	0.602	
+	10	7332	sense_Mutation_p	NM_021224	NP_067047	Q96JM2	ZN462_HUMAN	C2H2-type 26.		5	ACCTTCGGGATG	0.527	
+	5	884	p.R173W|RAD23B	NM_002874	NP_002865	P54727	RD23B_HUMAN			1	TCTTCTCGGTCA	0.294	
+	6	1764	483_uc004bfg.2_I	NM_133464	NP_597721	Q8TF39	ZN483_HUMAN	C2H2-type 3.		1	AAACATCAGAGA	0.403	
+	2	368	xo.1_Missense_Mu	NM_000607	NP_000598	P02763	A1AG1_HUMAN			0	GACCCGGTGAG	0.537	rs1126866
-	4	1219	e_Mutation_p.P37	NM_198187	NP_937830	O75129	ASTN2_HUMAN	lasmic (Potential).		9	GCAGGGGTGGT	0.597	rs139454684
-	36	4499		NM_001735	NP_001726	P01031	CO5_HUMAN			2	GTGGCAGGACTG	0.373	
-	16	1654	e_p.D548_splice|S	NM_001144877	NP_001138349	Q8N9R8	SCAI_HUMAN			5	AGGGTACCTATT	0.368	
+	6	746		NM_001261	NP_001252	P50750	CDK9_HUMAN	rotein kinase.		1	CGGCCCCCCCA	0.667	
-	11	2081	.R560W|CIZ1_uc0	NM_001131016	NP_001124488	Q9ULV3	CIZ1_HUMAN			4	GTCCCGGGGCA	0.632	
-	17	4549	.R1407C|CAMSAF	NM_015447	NP_056262	Q5T5Y3	CAMP1_HUMAN	CKK.		3	CATCACGAAACA	0.493	
-	4	1159	p.E139K|CTPS2_u	NM_001144002	NP_001137474	Q9NRF8	PYRG2_HUMAN			1	GGGGCTCTTCCT	0.373	
+	1	634	YY2_uc010nfq.2_I	NM_206923	NP_996806	O15391	TYY2_HUMAN			2	TATTCCGAGTACT	0.493	
-	1	956		NM_001017930	NP_001017930	A6NGE4	DC8L1_HUMAN			4	CCACACGCTTAG	0.502	
-	4	941	lv.2_Missense_Mu	NM_017602	NP_060072	Q96G74	OTUD5_HUMAN	OTU.		1	CAGGACGGTTGT	0.522	
-	7	628	FKFB1_uc011mol.1	NM_002625	NP_002616	P16118	F261_HUMAN	phofructo-2-kinase.		1	TTTTCCCGGTCA	0.378	
-	3	376		NM_080879	NP_543155	Q8WXH6	RB40A_HUMAN			0	GGAAGTCATAGG	0.682	
-	3	370		NM_080879	NP_543155	Q8WXH6	RB40A_HUMAN			0	CATAGGCCTGGT	0.672	
+	3	555	a-mir-934|MI0005	NM_016267	NP_057351	Q99990	VGLL1_HUMAN			0	CCTGGGGAGCTG	0.627	
+	4	1679	EC1_uc010nsl.1_I	NM_005462	NP_005453	O60732	MAGC1_HUMAN			4	CCTGAGAGAACT	0.478	
+	4	2019	EC1_uc010nsl.1_I	NM_005462	NP_005453	O60732	MAGC1_HUMAN			4	CTCCTCACTACTT	0.582	
-	2	1145		NM_001009615	NP_001009615	Q5MJ10	SPXN2_HUMAN			1	CTTCAGATGAGT	0.527	
+	15	1743	TM1_uc011mxz.1_	NM_000252	NP_000243	Q13496	MTM1_HUMAN			3	AGCAGCGTTACAT	0.522	
+	9	1579	6A8_uc011myx.1_I	NM_005629	NP_005620	P48029	SC6A8_HUMAN	lasmic (Potential).		1	TCCTCCCGGCCT	0.607	
+	29	5140	P9Y_uc010nwu.1_I	NM_004654	NP_004645	O00507	USP9Y_HUMAN			0	AATGCTGAAGTT	0.343	
+	2	412		NM_198576	NP_940978	O00468	AGRIN_HUMAN	NtA.		3	CTGCACCCCCATA	0.587	
-	4	460	DK_uc001aie.2_Mi	NM_023018	NP_075394	O95544	NADK_HUMAN			0	ATCTCTCATCTT	0.602	
-	4	360	D1_uc009vmi.1_Int	NM_001428	NP_001419	P06733	ENOA_HUMAN			4	GTTTTATTGATGT	0.463	
-	46	6594	sc.2_Missense_Mu	NM_004958	NP_004949	P42345	MTOR_HUMAN			29	AAGACGGTGCT	0.498	
-	1	678		NM_001136561	NP_001130033	B2RXH8	B2RXH8_HUMAN			0	GAGAATCCACTT	0.443	
+	4	615	ense_Mutation_p.G	NM_017556	NP_060026	Q8WUP2	FBLI1_HUMAN	n-binding.|Pro-rich.		1	TGGCGGGGAGG	0.677	
+	11	8440	p.1_Missense_Mu	NM_015001	NP_055816	Q96T58	MINT_HUMAN	h RBPSUH (By similarity).		15	GGTGCGGTTACT	0.607	
-	7	952	p.E162G|ZBTB17_	NM_003443	NP_003434	Q13105	ZBT17_HUMAN			0	ctcttgctcctcttgctcct	0.498	

+	3	246	LCNKB_uc001ax	NM_000085	NP_000076	P51801	CLCKB_HUMAN	ical; (Potential).	1	TGACCCTCGGG	0.647
-	14	2515		NM_004431	NP_004422	P29317	EPHA2_HUMAN	nd ELMO2.|Protein kinase.	10	TGAACTTCCGG	0.642
-	10	1580	_p.S173F|FBXO42	NM_018994	NP_061867	Q6P3S6	FBX42_HUMAN		2	CCAAAGAAGAG	0.557
-	5	585	DI2_uc001bag.1_	NM_007365	NP_031391	Q9Y2J8	PADI2_HUMAN		6	CATCACGGCAG	0.627
+	3	438		NM_013358	NP_037490	Q9ULC6	PADI1_HUMAN		0	GCGTCGGTAAG	0.577
-	104	15279	n_p.S726F|UBR4_	NM_020765	NP_065816	Q5T4S7	UBR4_HUMAN		25	GGGAAGAACGG	0.468
-	51	7611	k.1_Missense_Mu	NM_020765	NP_065816	Q5T4S7	UBR4_HUMAN		25	CCGAGCGGCTG	0.532
-	19	2558	m.1_Missense_M	NM_020765	NP_065816	Q5T4S7	UBR4_HUMAN	ical; (Potential).	25	AAGCGGCACGA	0.502
-	1	307		NM_019062	NP_061935	Q9NXI6	RN186_HUMAN	RING-type.	0	CTCCCGGCACA	0.647
-	2	580		NM_020317	NP_064713	Q9BUV0	CA063_HUMAN	Arg-rich.	1	GTACCGCGAAG	0.672
+	6	688	DLRAP1_uc009vr	NM_015627	NP_056442	Q5SW96	ARH_HUMAN	PID.	1	GGGACGTCCTG	0.617
+	4	859		NM_031459	NP_113647	P58004	SESN2_HUMAN		7	GCATCGGCCAT	0.632
+	8	2222	vui.2_Nonsense_	NM_145238	NP_660281	P17040	ZSC20_HUMAN		4	CAGTGGCAAGA	0.453
-	59	9228	m.1_Missense_M	NM_052896	NP_443128	Q7Z408	CSMD2_HUMAN	xtracellular (Potential).	12	CTTACGGAAAC	0.577
+	4	671	e_Mutation_p.P78	NM_012199	NP_036331	Q9UL18	AGO1_HUMAN		3	TGTTCCCTTGG	0.542
+	1	4642	.1_Intron|MACF1_	NM_015038	NP_055853	O94854	K0754_HUMAN	Ala-rich.	0	AGCCCGCCTCC	0.672
+	2	890	.R253Q|ZNF691_	NM_015911	NP_056995	Q5VV52	ZN691_HUMAN	ype 7; degenerate.	2	CTACCGGTGCA	0.567
-	7	1184	T11_uc001cxm.1_	NM_176782	NP_788954	Q8WW52	F151A_HUMAN		0	CGCTGCCCTGG	0.592
-	40	4553		NM_015306	NP_056121	Q9UPU5	UBP24_HUMAN		13	CTGGGGGAAGG	0.453
-	32	3620		NM_015306	NP_056121	Q9UPU5	UBP24_HUMAN		13	TGTTTCGAATT	0.438
+	3	2983	dnn.2_Missense_	NM_001134479	NP_001127951	Q7L1W4	LRC8D_HUMAN		2	ATATTCCCTTTGC	0.393
+	3	185	f146_uc010ote.1_	NM_001012425	NP_001012425	Q5VVC0	CA146_HUMAN		1	AAGTTCGATATT	0.299
+	15	2185	.R566Q|CDC14A_	NM_003672	NP_003663	Q9UNH5	CC14A_HUMAN		1	CCTCCGACCCT	0.572
-	13	1533	vi.1_Missense_M	NM_002959	NP_002950	Q99523	SORT_HUMAN	ellular (Potential).	1	CATCCCCCACG	0.438
+	1	811	ense_Mutation_p.	NM_022768	NP_073605	Q96T37	RBM15_HUMAN	RRM 1.	3	TGACCGGCCTC	0.627
+	8	2335		NM_020440	NP_065173	Q9P2B2	FPRP_HUMAN	6.|Extracellular (Potential).	1	GTTTGCGGTGC	0.552
+	76	9461	BPF10_uc010oyl.1	NM_001039703	NP_001034792	A6NDV3	A6NDV3_HUMAN		0	CTGGATGAGAA	0.488
+	8	748	NKRD35_uc010oy	NM_144698	NP_653299	Q8N283	ANR35_HUMAN	ANK 5.	5	CGGGGGCTGTG	0.617
-	3	278	_p.R49C|CTSS_u	NM_004079	NP_004070	P25774	CATS_HUMAN		0	GAGACGTCGTA	0.388
+	2	1800	no.2_Missense_M	NM_020832	NP_065883	Q8N1G0	ZN687_HUMAN		4	GCGCCCGCCGC	0.597
-	3	811		NM_016190	NP_057274	Q9UBG3	CRNN_HUMAN	Gln-rich.	3	GGCTGCTGTCC	0.602
-	12	2073		NM_014856	NP_055671	O75064	DEN4B_HUMAN		1	CCTGCGGCCAC	0.637
-	7	985	_p.R165*|C1orf43_	NM_001098616	NP_001092086	Q9BWL3	CA043_HUMAN		0	ATGTCGCTGAG	0.512
+	6	891	.E252K|HAX1_uc	NM_006118	NP_006109	O00165	HAX1_HUMAN	.|Involved in GNA13 bindin	0	GACACGAAGCA	0.498
-	12	1827	md.3_Missense_	NM_001037533	NP_001032622	Q3T8J9	GON4L_HUMAN		3	CTGCCCGGTCA	0.423
-	8	1932	.1_Intron|NTRK1_	NM_014215	NP_055030	P14616	INSRR_HUMAN	nectin type-III 1.	20	GGTCACCCCTG	0.617
-	6	1087	phw.1_Missense_	NM_031281	NP_112571	Q96RD9	FCRL5_HUMAN	otential).|Ig-like C2-type 3.	6	CCTGGGTTTCA	0.502
-	2	165	RL1_uc001fri.2_	NM_052938	NP_443170	Q96LA6	FCRL1_HUMAN	otential).|Ig-like C2-type 1.	7	CTCACCGGCAG	0.483
-	1	515		NM_001004475	NP_001004475	Q8NGX3	O10T2_HUMAN	ellular (Potential).	3	TGTTGGGGCCA	0.473
-	2	307	1_Intron|CRP_uc0	NM_000567	NP_000558	P02741	CRP_HUMAN	Pentaxin.	1	AAAATACTGTAC	0.443
-	10	1514	_p.R236*|ARHGA	NM_001025598	NP_001020769	Q7Z6I6	RHG30_HUMAN		3	AGCTCGTGGTG	0.602
-	4	617	S5_uc009wvb.2_	NM_003617	NP_003608	O15539	RGS5_HUMAN	RGS.	0	AGCCTCCGTTT	0.478
+	5	2239		NM_001080426	NP_001073895	Q5VZP5	DUS27_HUMAN		3	TGTCCCGCTCA	0.537
-	19	3484_3485	jv.2_Missense_Mu	NM_172071	NP_742068	Q5TC82	RC3H1_HUMAN		2	TTTAAGGAGCAG	0.45
+	11	2656		NM_022093	NP_071376	Q9UQP3	TENN_HUMAN	nectin type-III 7.	9	GCAGAGCAGCA	0.632
-	19	3354	.P1048S|ASTN1_	NM_004319	NP_004310	O14525	ASTN1_HUMAN	nectin type-III 1.	15	TGGTGGCTCTG	0.542
+	16	2129	wxs.2_Missense_	NM_000721	NP_000712	Q15878	CAC1E_HUMAN	llular (Potential).|II.	6	CCTGACGGGTG	0.537

-	1	832	pk.2_Missense_M	NM_021133	NP_066956	Q05823	RN5A_HUMAN	ANK 6.	p.T222S(1)	5	AGATGCGTAATA	0.527	
-	10	1450	yh.1_Missense_	NM_052966	NP_443198	Q9BZQ8	NIBAN_HUMAN			4	GCAGGCGCTCG	0.522	rs141805525
-	22	2208	D1B_uc010ppf.1_	NM_001142795	NP_001136267	Q6P3S1	DEN1B_HUMAN			0	TGGAGGGAGGT	0.493	
+	4	617		NM_198149	NP_937792	Q96DD7	SHSA4_HUMAN	ic (Potential).|Pro-rich.		0	CTGGGCCCCCA	0.612	
+	10	988	e_Mutation_p.I22	NM_002393	NP_002384	O15151	MDM4_HUMAN	|Asp/Glu-rich (acidic).		3	AGGTGATTGAA	0.358	
-	2	554	bx.2_Missense_M	NM_015375	NP_056190	Q6XUX3	DUSTY_HUMAN			1	CAGGCTGACCC	0.602	
+	25	4167	.G893R|CR1_uc0	NM_000573	NP_000564	P17927	CR1_HUMAN	r (Potential).|Sushi 21.		3	CCTATGGAAAA	0.468	
+	11	1562	.R523C|RCOR3_	NM_018254	NP_060724	Q9P2K3	RCOR3_HUMAN	Pro-rich.		1	CACCCCGTCTA	0.527	
-	16	1689		NM_014698	NP_055513	O94886	TM63A_HUMAN	ical; (Potential).		2	TGGAGGGGAGC	0.597	
-	1	327	_p.R83*|LEFTY2_	NM_003240	NP_003231	O00292	LFTY2_HUMAN			0	ACCTCGGAAGC	0.687	
+	4	1357		NM_001004342	NP_001004342	Q6ZTA4	TRI67_HUMAN			4	CCACCGGACTG	0.517	
-	13	2773	_Mutation_p.G75	NM_002508	NP_002499	P14543	NID1_HUMAN	oglobulin type-1.		2	GCTGCCGTGGC	0.716	
+	1	37		NM_001013355	NP_001013373	Q5TZ20	OR2G6_HUMAN	ellular (Potential).		3	GATTTCTTCTC	0.423	
-	3	284	uc009xhk.1_Silent	NM_014974	NP_055789	Q9Y2E4	DIP2C_HUMAN			7	TGACAGGAGCC	0.567	
-	3	380	ihz.2_Missense_M	NM_024803	NP_079079	A6NHL2	TBAL3_HUMAN			1	GTAACGGCCTC	0.632	
+	13	2355	rf18_uc001iik.2_I	NM_017782	NP_060252	Q5VWN6	CJ018_HUMAN			2	TTTGCGAGGTA	0.383	
+	15	3554	A1217_uc010qda	NM_019590	NP_062536	Q5T5P2	SKT_HUMAN			7	CGCCACCTCCT	0.547	
-	9	2120	p.A565V|ARHGA	NM_021226	NP_067049	Q7Z5H3	RHG22_HUMAN	Potential.		1	GCTCGGCCCTG	0.692	
-	4	546	jlk.2_Nonsense_M	NM_014836	NP_055651	O94844	RHBT1_HUMAN	Rho-like.		1	GTGTTGCACGC	0.562	
+	10	2532		NM_032199	NP_115575	Q14865	ARI5B_HUMAN			4	TCCCCTCATCTC	0.493	
+	2	600	2K|CYP2C19_uc	NM_000772	NP_000763	P33260	CP2CI_HUMAN			5	ATGGAGAGGAG	0.433	
-	7	1239	nse_Mutation_p.P	NM_000770	NP_000761	P10632	CP2C8_HUMAN			0	CTTGGGGATGA	0.453	
+	1	695	nk|MRPL43_uc00	NM_021830	NP_068602	Q96RR1	PEO1_HUMAN			1	CCGAAGTGGGT	0.587	
+	6	1265		NM_030912	NP_112174	Q9BZR9	TRIM8_HUMAN			1	CTCAACGGCCT	0.687	
+	2	67		NM_004832	NP_004823	P78417	GSTO1_HUMAN			0	CGGTCCCGGAG	0.682	
+	2	190		NM_001008723	NP_001008723	Q5T655	CC147_HUMAN			5	AGAAATGGAAA	0.388	
+	22	3173	i.1_Missense_Mu	NM_198795	NP_942090	Q9BXT4	TDRD1_HUMAN	Tudor 4.		0	ATTTTTGGTATCG	0.403	
+	2	796		NM_153442	NP_703143	Q8NDV2	GPR26_HUMAN	Name=6; (Potential).		1	TCATAGGGACCT	0.572	
+	4	1085		NM_007183	NP_009114	Q9Y446	PKP3_HUMAN	ARM 1.		1	TGCAGGTGCTG	0.607	
+	2	202	n_p.P25L|SYT8_u	NM_138567	NP_612634	Q8NBV8	SYT8_HUMAN	ellular (Potential).		1	TGCCCCGGCCC	0.642	
-	9	1165	_p.P268L|OSBPL	NM_020896	NP_065947	Q9H0X9	OSBL5_HUMAN			3	GCACCGGGGCC	0.667	
-	7	1075	lyj.1_Splice_Site_	NM_016320	NP_057404	P52948	NUP98_HUMAN			12	tgcttACTAGTTCC	0.254	
-	1	49		NM_001004052	NP_001004052	Q96RD2	O52B2_HUMAN	ellular (Potential).		0	GCCAGGAAGGA	0.453	
+	6	1681	mcx.2_Missense_	NM_000543	NP_000534	P17405	ASM_HUMAN			0	AAATAGATGGA	0.567	
-	7	1340	d.2_Missense_Mu	NM_006458	NP_006449	O75382	TRIM3_HUMAN	Filamin.		5	CGCTCGTGGTG	0.647	
+	3	536	_p.S83L|MICAL2_	NM_014632	NP_055447	O94851	MICA2_HUMAN			2	GAAGTCGTGCA	0.502	
-	6	1018	cy.1_Missense_M	NM_000352	NP_000343	Q09428	ABCC8_HUMAN	smic (By similarity).		1	CAGGCGCCTCC	0.632	rs144705160
-	11	1542	22_uc001mpa.2_	NM_173588	NP_775859	Q8N9C0	IGS22_HUMAN	Ig-like 3.		7	TCTTCCAGCGC	0.517	
+	2	323	S2_uc001mqn.2_	NM_001143830	NP_001137302	O43903	GAS2_HUMAN			2	TCTGAGCCCAA	0.408	
-	1	429	LC5A12_uc001mr	NM_178498	NP_848593	Q1EHB4	SC5AC_HUMAN	lasmic (Potential).		2	ACTCTCGGGAA	0.498	
+	11	1363	mvi.2_Missense_	NM_005898	NP_005889	Q14444	CAPR1_HUMAN			1	TATCTGCACAG	0.383	
+	8	1042	T_uc009ykc.1_R	NM_001752	NP_001743	P04040	CATA_HUMAN			3	AAACCGGAATC	0.458	rs139421991
+	2	1712	p.S321P|SLC35C	NM_018389	NP_060859	Q96A29	FUCT1_HUMAN			0	GCGGCTCCTCC	0.637	
+	24	4085		NM_002843	NP_002834	Q12913	PTPRJ_HUMAN	ate binding (By similarity).|		8	GGGTCGGAAGG	0.453	
-	1	547_548		NM_001004740	NP_001004740	Q8NGP8	OR5M1_HUMAN	ellular (Pot	p.P183P(1)	1	TAAGAGGAGGAT	0.446	
+	1	461		NM_001013358	NP_001013376	P0C7N8	OR9G9_HUMAN	Name=4; (Potential).		0	TTATTAACTCTT	0.463	
-	8	1268		NM_003146	NP_003137	Q08945	SSRP1_HUMAN			2	TCTCACCCTTGG	0.567	

+	6	1407	Missense_Mutatio	NM_001085458	NP_001078927	O60716	CTND1_HUMAN		6	AGAGCCTTATG	0.557	
-	1	272		NM_001005489	NP_001005489	Q8NGF7	OR5BH_HUMAN	ellular (Potential).	3	TGTAGGAGATG	0.463	
-	4	674	A2_uc010rlx.1_5'U	NM_004739	NP_004730	O94776	MTA2_HUMAN	BAH.	2	TGGCTGGTAAT	0.517	
-	9	992	m.1_Missense_M	NM_015853	NP_056937	Q04323	UBXN1_HUMAN	raction with BRCA1.	0	GAACAGCAGAA	0.478	
+	4	421	_p.R137*|DPF2_u	NM_006268	NP_006259	Q92785	REQU_HUMAN		1	ATCCCCGAGTT	0.562	
+	3	1958	ri.2_Silent_p.G15	NM_006328	NP_006319	Q96PK6	RBM14_HUMAN		3	ACCGGCGTTTA	0.572	
+	4	511	ju.2_Missense_M	NM_177963	NP_808878	Q8IV01	SYT12_HUMAN	lasmic (Potential).	1	CAGCCGCAAAG	0.637	rs34985365
-	8	1123		NM_080658	NP_542389	Q96HD9	ACY3_HUMAN		0	GGAAGCTGGGC	0.597	
-	4	815	k.2_Missense_M	NM_001277	NP_001268	P35790	CHKA_HUMAN		2	TTGGGGAAAGA	0.488	
+	20	5938		NM_014786	NP_055601	Q96PE2	ARHGH_HUMAN		0	GCCACGTCCGC	0.652	
+	3	226	.L21F|RELT_uc00	NM_152222	NP_689408	Q969Z4	TR19L_HUMAN		1	GGCCTCTCGCC	0.602	
+	10	1259	e_Mutation_p.S3	NM_152222	NP_689408	Q969Z4	TR19L_HUMAN	lasmic (Potential).	1	GGTGTCTGAGG	0.408	
-	5	448	wf.1_Missense_M	NM_004041	NP_004032	P49407	ARRB1_HUMAN	ilarity).|Interaction with SR	2	CTTGCGAAAGG	0.642	
+	5	996	uc001pen.1_RNA	NM_001098672	NP_001092142	Q6MZM0	HPHL1_HUMAN	e 2.|Extracellular (Potential	3	CTTCCCGGAGC	0.468	rs141998596
+	5	654	3A_uc009yyx.2_	NM_213621	NP_998786	P46098	5HT3A_HUMAN	ellular (Potential).	0	AATATCCCGTAC	0.532	
+	3	390	1_Missense_Muta	NM_001558	NP_001549	Q13651	I10R1_HUMAN	ellular (Potential).	1	TGGACGGCAGC	0.577	
+	10	1716	vn.2_Nonsense_	NM_014807	NP_055622	O14523	C2C2L_HUMAN		0	CTGTCCAGTCC	0.597	
+	2	545	pyl.1_Missense_	NM_024806	NP_079082	Q6NUN7	CK063_HUMAN		3	ATGGGGAAGCC	0.542	
+	18	2364	pzt.2_Splice_Site	NM_001130142	NP_001123614	O00534	VMA5A_HUMAN		2	GTGCAGCTTGT	0.507	
-	1	361		NM_001005468	NP_001005468	Q96RD0	OR8B2_HUMAN	lasmic (Potential).	0	GCGATCATATG	0.403	
-	2	189	at.2_Missense_M	NM_014312	NP_055127	Q96IQ7	VSIG2_HUMAN	(Potential).|Ig-like V-type.	4	TCTTCCCCAGG	0.642	
+	8	2007		NM_025004	NP_079280	Q0P6D6	CCD15_HUMAN		2	GGACCAGGATT	0.438	
+	7	2234	_p.R576Q|WNK1_	NM_018979	NP_061852	Q9H4A3	WNK1_HUMAN		23	GGTACGGGAGG	0.463	
+	7	2333	_p.A609V|WNK1_	NM_018979	NP_061852	Q9H4A3	WNK1_HUMAN		23	TTCTGCTAGCA	0.473	
-	31	3059_3060	1qjs.1_Missense_	NM_172364	NP_758952	Q7Z3S7	CA2D4_HUMAN	ellular (Potential).	1	CTCGAGGGTTT	0.614	
-	4	866	_p.P144S|PRB1_u	NM_005039	NP_005030	P04280	PRP1_HUMAN	-P-[PAQ]-Q-[GE]-[GD]- [N	0	TGGAGGAGATC	0.607	
-	3	852		NM_006248	NP_006239				0	AGGTTTGTTGC	0.607	
+	23	3187	p.V1023D|PLEKH	NM_019012	NP_061885	Q9HAU0	PKHA5_HUMAN		3	GGATGTTACAT	0.269	
+	15	3113		NM_000921	NP_000912	Q14432	PDE3A_HUMAN	ytic (By similarity).	4	ACAGCGATGAG	0.468	
+	9	1117	Mutation_p.S331	NM_019844	NP_062818	Q9NPD5	SO1B3_HUMAN	lasmic (Potential).	4	TTGAAAAGCATC	0.234	
-	11	2367	_p.S707L|PKP2_u	NM_004572	NP_004563	Q99959	PKP2_HUMAN	ARM 6.	2	GCAGCGAGATG	0.463	
-	4	1275	p.A387V|PKP2_u	NM_004572	NP_004563	Q99959	PKP2_HUMAN	ARM 2.	2	TTCCGAGCTTCA	0.458	
+	4	1836	rpq.2_Missense_	NM_138371	NP_612380	Q96HM7	F113B_HUMAN	Pro-rich.	5	TTCTTCGTCGAA	0.527	
-	33	2357	L2A1_uc001rqv.2	NM_001844	NP_001835	P02458	CO2A1_HUMAN	e-helical region.	2	AGTGCCAGGAG	0.647	
+	9	1756	ATS2_uc001ruf.2_	NM_023071	NP_075559	Q86XZ4	SPAS2_HUMAN		1	GGTATCGAGTTG	0.363	
+	14	2404	ATS2_uc001ruf.2_	NM_023071	NP_075559	Q86XZ4	SPAS2_HUMAN		1	ATGACAGTATGG	0.507	
-	3	473	_p.P94L|POU6F1	NM_002702	NP_002693	Q14863	PO6F1_HUMAN	Gln/Pro-rich.	1	GCTGGGGCACG	0.612	
+	2	189		NM_014191	NP_055006	Q9UQD0	SCN8A_HUMAN		7	AGCGCGGCTGC	0.517	
-	27	3525	.2_Intron|SMARC	NM_003075	NP_003066	Q8TAQ2	SMRC2_HUMAN	Pro-rich.	6	GGTTCGCCATG	0.637	
-	11	1148	_p.P348S|SMARC	NM_003075	NP_003066	Q8TAQ2	SMRC2_HUMAN		6	GACTGGTGAGG	0.552	
-	25	3771	tion_p.T281I|PAN	NM_001127460	NP_001120932	Q504Q3	PAN2_HUMAN	xonuclease.	6	CATGGGTTTCC	0.512	
-	10	1129	1slg.2_Missense_	NM_003920	NP_003911	Q9UNS1	TIM_HUMAN		8	GCGACGTTTAG	0.517	
-	7	810		NM_001031701	NP_001026871	Q86UY8	NT5D3_HUMAN	e binding (Potential).	3	GTGGACGTCTC	0.393	
-	7	2261		NM_014840	NP_055655	O60285	NUAK1_HUMAN	rotein kinase.	2	TGGCCCGGCGA	0.547	
-	16	2177	vx.1_Missense_M	NM_014706	NP_055521	Q15020	SART3_HUMAN	or nuclear localization.	1	GTTCTCGACCC	0.502	
+	2	157	_p.R2C|DAO_uc0	NM_001917	NP_001908	P14920	OXDA_HUMAN		2	CAATGCGTGTG	0.493	
+	12	2008	c.2_Missense_M	NM_001093	NP_001084	O00763	ACACB_HUMAN	in carboxylation.	8	GGGAGTGACTC	0.552	

+	20	3508	e_Mutation_p.T95	NM_170665	NP_733765	P16615	AT2A2_HUMAN	me=10; (By similarity).	4	TGAGACGCTCA	0.542	rs149024535
-	2	672	u.2_Missense_Mu	NM_138451	NP_612460	Q96DY2	IQCD_HUMAN		1	CTCCCCCAGCA	0.532	
+	3	353	n_p.L79F|ACADS_	NM_000017	NP_000008	P16219	ACADS_HUMAN		2	CTTGGGCTTCTG	0.682	
-	19	2872	.2_Missense_Mut	NM_032590	NP_115979	Q8NHM5	KDM2B_HUMAN		2	CGGCCCCTTCG	0.577	
-	4	460	S33A_uc001uce.2	NM_022916	NP_075067	Q96AX1	VP33A_HUMAN		1	CTACGGCGTGGC	0.413	
-	2	386		NM_024667	NP_078943	Q9H9H4	VP37B_HUMAN	inal.|Interaction with IST1.	0	AGTTACCTAATTT	0.413	
-	8	1225		NM_032656	NP_116045	Q8IY37	DHX37_HUMAN	ase ATP-binding.	1	CCTCTCGTGGG	0.667	
-	1	1328	rj.2_Missense_Mu	NM_152912	NP_690876	Q9H2K0	IF3M_HUMAN		2	ACTGTGCTGGT	0.413	
+	3	252	se_Mutation_p.R	NM_152705	NP_689918	Q9Y2S0	RPAC2_HUMAN		0	ATAAAAGATTTC	0.433	
-	5	589	D13_uc001uux.2_	NM_178006	NP_821074	Q9Y3M8	STA13_HUMAN		4	CACACGAGACC	0.557	
+	1	2869		NM_207361	NP_997244	Q5SZK8	FREM2_HUMAN	xtracellular (Potential).	11	TTGCACGTGAAT	0.507	
-	22	2197		NM_199289	NP_954983	Q6P3R8	NEK5_HUMAN		1	GCACAGACTCA	0.567	
-	1	561	h.2_Missense_Mu	NM_001922	NP_001913	P40126	TYRP2_HUMAN	elanosome (Potential).	5	CTGCACCCAGG	0.627	
-	3	956	AC2_uc001vod.2_	NM_005292	NP_005283	Q14330	GPR18_HUMAN	Name=4; (Potential).	0	TGGTCGTGGTC	0.493	
-	4	1304		NM_000452	NP_000443	Q12908	NTCP2_HUMAN	ical; (Potential).	4	TAACCCGCCACA	0.433	
+	32	5174_5175	k.1_Missense_Mu	NM_015011	NP_055826	Q9Y6X6	MYO16_HUMAN		10	GGGAGGAGTG	0.649	
-	25	1822	4A1_uc010agl.2_	NM_001845	NP_001836	P02462	CO4A1_HUMAN	le-helical region.	6	GACCCGGATGG	0.517	
-	1	59		NM_001004712	NP_001004712	Q8NGD5	OR4KE_HUMAN	ellular (Potential).	3	GTCGTGAAGTG	0.373	
-	2	755	ahw.2_Missense_	NM_145250	NP_660293	Q8TAA1	RNS11_HUMAN		3	CAGCTCATCAG	0.423	
-	17	3734	N1_uc001wir.3_M	NM_014977	NP_055792	Q9UKV3	ACINU_HUMAN	sp/Glu/Lys-rich.	4	CTCCCGCTGCT	0.662	
-	1	1385		NM_032135	NP_115511	Q5H9T9	FSCB_HUMAN	Pro-rich.	9	CTGAAGGGGAC	0.493	rs17857204
-	5	431	_Intron|POLE2_u	NM_002692	NP_002683	P56282	DPOE2_HUMAN		2	ACTTACCTGGT	0.418	
-	5	363	nj.1_Intron|POLE2	NM_002692	NP_002683	P56282	DPOE2_HUMAN		2	ATTTGGTGCAG	0.418	
+	4	2374	dx.2_Missense_M	NM_016651	NP_057735	Q9NYF0	DACT1_HUMAN		5	CTCCACCGTGG	0.647	
-	3	250	xgc.2_Missense_	NM_145171	NP_660154	Q86YW7	GPHB5_HUMAN		1	TAGGTACAGACT	0.483	
+	67	13140	py.2_Missense_M	NM_015180	NP_055995	Q8WXH0	SYNE2_HUMAN	lasmic (Potential).	14	CTGGGAGATAAT	0.413	
+	11	1457	lt.1_Missense_Mu	NM_022137	NP_071420	Q9H4F8	SMOC1_HUMAN	EF-hand 2.	2	GTGCCCGGCGT	0.527	
+	20	2065	asq.1_Missense_	NM_020431	NP_065164	Q9P1W3	TM63C_HUMAN	ical; (Potential).	0	CTTGCCCCATCA	0.547	
-	4	512	.1_5'UTR|C14orf1	NM_017970	NP_060440	Q9H7Z3	CN102_HUMAN	Potential.	3	AGGTTTCTCCCG	0.478	
-	10	978		NM_024764	NP_079040	Q9H7T0	CTSRB_HUMAN		5	CTGCCCTGGAAA	0.333	
-	3	534	_5'Flank|C14orf10	NM_022151	NP_071434	Q96BY2	MOAP1_HUMAN		3	ctcctgaacatccttcca	0	
-	42	6562		NM_018036	NP_060506	Q96BY7	ATG2B_HUMAN		3	CTTGCCGGACA	0.537	
+	10	1612	_p.L316F|MARK3_	NM_001128918	NP_001122390	P27448	MARK3_HUMAN		4	GATGAACTCAAA	0.363	
-	7	8482	px.2_Missense_M	NM_138420	NP_612429	Q8IVF2	AHNK2_HUMAN		1	CTTTGCTCTCGC	0.612	
+	1	2347		NM_018958	NP_061831	Q9NZP6	CO002_HUMAN		8	CCACTTCCATTT	0.493	
-	3	489	.2_Intron|BMF_uc	NM_033503	NP_277038	Q96LC9	BMF_HUMAN	BH3.	1	CTTTCGGGCAA	0.597	
+	4	2040	bp.1_Missense_M	NM_014952	NP_055767	Q8TBE0	BAHD1_HUMAN	BAH.	0	ACCCCGAGTCA	0.602	
-	41	7330		NM_016642	NP_057726	Q9NRC6	SPTN5_HUMAN	Spectrin 21.	2	ACAACACGTGTA	0.592	
-	21	3650	11_uc010uei.1_	NM_025137	NP_079413	Q96JI7	SPTCS_HUMAN	ellular (Potential).	5	TGGCCGCCCAT	0.363	
+	11	1522	_p.F445I|SQRDL_	NM_021199	NP_067022	Q9Y6N5	SQRD_HUMAN		1	AAGTTGTTTCAT	0.488	
-	11	1202	xm.2_Nonsense_	NM_152647	NP_689860	Q96M60	CO033_HUMAN		1	GTTTCCAGTGG	0.318	
-	5	594	_p.R115*|CYP19A	NM_031226	NP_112503	P11511	CP19A_HUMAN		3	CGAATCGAGAGC	0.438	
+	4	585		NM_152450	NP_689663	Q8TBF8	FA81A_HUMAN		1	TCTTCGAGGAA	0.463	
-	81	10893	hb.1_Missense_M	NM_020821	NP_065872	Q709C8	VP13C_HUMAN		2	AGGACGAATGA	0.443	rs149574145
+	9	1029_1030	se_Mutation_p.C2	NM_006537	NP_006528	Q9Y6I4	UBP3_HUMAN		1	AACAAGTGTTGC	0.431	
+	9	1171	1_uc002ara.2_5'	NM_016166	NP_057250	O75925	PIAS1_HUMAN	P-RING-type.	2	TTTGACGCAACT	0.378	
-	17	1837	b.2_RNA|PARP6_	NM_020214	NP_064599	Q2NL67	PARP6_HUMAN	ARP catalytic.	0	GGTCCGGAACC	0.632	

-	2	696	ı|CYP1A1_uc002a	NM_000499	NP_000490	P04798	CP1A1_HUMAN		5	CTGATACCACCA(	0.517	
+	2	1771	av.2_Missense_Mu	NM_153271	NP_695003	Q8WV41	SNX33_HUMAN	BAR.	1	ACCAGCGGGTG(	0.622	
-	11	985		NR_027024					0	CCTGGGATTGG/	0.567	
+	3	2585	unk.1_Missense_M	NM_015206	NP_056021	Q9UPX6	K1024_HUMAN		4	TGCACGGAATG(	0.627	
+	1	153	SSF1_uc002bjq.2_	NM_023003	NP_075379	Q9BZW5	TM6S1_HUMAN	ical; (Potential).	1	CCTCTCGGCCA'	0.567	
-	4	1761	s.1_Missense_Mu	NM_001717	NP_001708	Q01954	BNC1_HUMAN		3	TTGTGTCTTTTC'	0.468	
+	14	1753	p.G510E|ADAMTS	NM_207517	NP_997400	P82987	ATL3_HUMAN	TSP type-1 3.	27	CCGCGGAGAGC	0.458	
+	12	5113	e_Mutation_p.A158	NM_013227	NP_037359	E7EX88	E7EX88_HUMAN		3	CTTCAGCTTCTG(	0.537	
-	6	810	nn.2_Missense_M	NM_005928	NP_005919	Q08431	MFGM_HUMAN	F5/8 type C 2.	1	CCAGGGGATTGG	0.577	
+	10	1604	L13_uc002bpe.1_I	NM_001029964	NP_001025135	A6NNM8	TTL13_HUMAN		0	GGAACGGCTTT'	0.488	
+	9	1943	p.2_Missense_Mut	NR_003659					0	GGCATCGGCAAG	0.652	
-	1	123	cgs.1_Missense_M	NM_006428	NP_006419	Q13084	RM28_HUMAN		0	GGCGTCCGCTCC	0.647	
+	4	985	ıh.1_Missense_Mu	NM_005632	NP_005623	O75808	CAN15_HUMAN		2	GGGAAGGTGCC	0.736	
+	2	252	2cnj.2_Missense_M	NM_004548	NP_004539	O96000	NDUBA_HUMAN		0	AGAGCGGCAGC/	0.483	
-	6	1512	ot.1_Missense_Mut	NM_001009944	NP_001009944	P98161	PKD1_HUMAN	.|Extracellular (Potential).	3	GACACTGCTCCT(	0.721	
+	4	421	2ctz.3_5'Flank|ZN	NM_001042428	NP_001035893	O95201	ZN205_HUMAN		0	TCCCCCCGGATC(	0.672	rs140013925
+	2	191	n_p.T29I|CLUAP1	NM_015041	NP_055856	Q96AJ1	CLUA1_HUMAN		3	TCCGTACACCCA/	0.393	
+	5	516	AP1_uc002cvl.1_M	NM_015041	NP_055856	Q96AJ1	CLUA1_HUMAN		3	GATTTGAAGGC/	0.353	
-	3	588	_p.P131L|KIAA043	NM_014647	NP_055462	Q9Y4F3	LKAP_HUMAN		0	GCGCCCGGGTGA	0.547	
-	34	5837	ou.2_Missense_Mu	NM_001520	NP_001511	Q12789	TF3C1_HUMAN		5	CTCACCGACAC(	0.627	
+	7	1656		NM_014712	NP_055527	O15047	SET1A_HUMAN	Ser-rich.	3	CCGCCTCCACG	0.413	
+	2	269		NM_014669	NP_055484	Q8N1F7	NUP93_HUMAN		2	CTAACACGCACG'	0.577	
+	26	3859	.1_RNA|NLRC5_u	NM_032206	NP_115582	Q86WI3	NLRC5_HUMAN		7	CCAACGAGGAG(	0.602	
-	5	1031	oh.2_Missense_Mu	NM_001796	NP_001787	P55286	CADH8_HUMAN	r (Potential).|Cadherin 2.	9	GTGTCGTGGTC(	0.458	
+	3	1493	ı_p.A165T|CES2_u	NM_003869	NP_003860	O00748	EST2_HUMAN		0	CTCACCGCAGTG	0.567	
+	2	404	C50_uc010chi.1_I	NM_178452	NP_848547	Q8NEP3	DAAF1_HUMAN		0	CACTTCGCACAC(	0.413	
-	2	268	n_p.S7L|ABR_uc0	NM_021962	NP_068781	Q12979	ABR_HUMAN		1	GTGGGCGACTCA'	0.672	
+	8	1323	AFAH1B1_uc010v	NM_000430	NP_000421	P43034	LIS1_HUMAN	on with dynein and dynactin	1	CCAGCTGTTCCA/	0.473	rs140360173
-	1	79		NM_002550	NP_002541	P47881	OR3A1_HUMAN	cellular (Potential).	3	TGGCTGCAGCC(	0.567	
+	1	493		NM_012373	NP_036505	P47888	OR3A3_HUMAN	Name=4; (Potential).	0	CCAACGCACTG/	0.587	
+	3	587	F11_uc010vtw.1_In	NM_175734	NP_783861	Q0P670	CQ074_HUMAN		0	CTACACCGAGTG(	0.567	
-	17	2276	58_splice|MYH10_	NM_005964	NP_005955	P35580	MYH10_HUMAN		2	GCAATACCTCTGT	0.393	
-	22	2694	uc002gml.1_Intron	NM_002472	NP_002463	P13535	MYH8_HUMAN	Potential.	11	ACTTGGCGAGTT(	0.443	
-	17	1753	T313M|ELAC2_uc0	NM_018127	NP_060597	Q9BQ52	RNZ2_HUMAN		0	CTCACCGTGTGG'	0.597	
-	2	873	1_Intron|NF1_uc0	NM_006495	NP_006486	P34910	EVI2B_HUMAN	lasmic (Potential).	2	ATCTACCTGCCC	0.348	
+	13	1771	_p.R471C|AP2B1_	NM_001282	NP_001273	P63010	AP2B1_HUMAN		1	TATTGGCGCCTTC	0.463	
+	14	2300	S11_uc002hnd.2_5	NM_024835	NP_079111	Q9H3C7	GGNB2_HUMAN		2	ACAAGAGGCCCA	0.388	
-	10	1014	2huy.2_Missense_M	NM_003079	NP_003070	Q969G3	SMCE1_HUMAN	Potential.	0	CTTTTGCGGGCC	0.507	
-	2	863	0cxg.2_Missense_	NM_015515	NP_056330	Q9C075	K1C23_HUMAN	Rod.|Coil 1A.	1	CAGGGCGCGAA	0.547	
-	6	1014		NM_004138	NP_004129	O76009	KT33A_HUMAN	Coil 2.|Rod.	0	ATCTCCGCCAGC'	0.627	
-	6	1068	kd.3_Missense_Mu	NM_021991	NP_068831	P14923	PLAK_HUMAN		5	GCTCATCCAGCA(	0.577	
-	7	1367		NM_012285	NP_036417	Q9UQ05	KCNH4_HUMAN	or; Name=Segment S4; (Po	1	gcagccgcagcagccg	0.537	
-	4	899		NM_012285	NP_036417	Q9UQ05	KCNH4_HUMAN	lasmic (Potential).	1	TGCCTCCCTGG(	0.602	
-	13	4631	e_Mutation_p.Q14	NM_007294	NP_009225	P38398	BRCA1_HUMAN		52	GATTCTGGCTTAT	0.358	
-	12	1649	_Mutation_p.A507T	NM_001256	NP_001247	P30260	CDC27_HUMAN	TPR 3.	5	AATAGGCCCTTC(	0.348	
+	18	2468	_p.P566L|KPNB1_	NM_002265	NP_002256	Q14974	IMB1_HUMAN	HEAT 8.	3	TGAAGCCGCAGA'	0.388	
-	3	734	ıe.3_Missense_Mu	NM_006807	NP_006798	P83916	CBX1_HUMAN		0	CTTTGCGCTTGC(	0.328	

+	11	1755	p.A480T|B4GALN	NM_153446	NP_703147	Q8NHY0	B4GN2_HUMAN	enal (Potential).	2	GTGCCGCATAA	0.512	
+	4	404	4_uc010wou.1_Int	NM_000717	NP_000708	P22748	CAH4_HUMAN		0	GAGGAGGACTG	0.582	
+	11	1335	se_Mutation_p.V9	NM_007372	NP_031398	Q86XP3	DDX42_HUMAN	ase ATP-binding.	5	TGGCCGTATATG	0.438	
-	4	200	nse_Mutation_p.R	NM_014877	NP_055692				2	AGCTCTTCTGT	0.418	
+	4	613	_p.Q118R|NUP85_	NM_024844	NP_079120	Q9BW27	NUP85_HUMAN		1	GCACCAGGTTG	0.254	
-	22	3968	p.T1269M|EVPL_	NM_001988	NP_001979	Q92817	EVPL_HUMAN	fibrous rod domain.	4	CCACCGTGGGC	0.647	rs145713300
-	3	468	e_Mutation_p.Q80	NM_001988	NP_001979	Q92817	EVPL_HUMAN	Globular 1.	4	TCCTGCTGGTG	0.692	
+	6	1121	ud.1_RNA|CARD	NM_024110	NP_077015	Q9BXL6	CAR14_HUMAN	Potential.	5	GCTGCGGGAGC	0.687	
+	8	758	2jyl.1_Nonsense_	NM_173627	NP_775898	Q8N8Q3	ENDOV_HUMAN		0	GCTCCCGAGAG	0.637	
-	5	1784	yw.1_Missense_M	NM_004746	NP_004737	O14490	DLGP1_HUMAN		4	CTGTCCGTCCA	0.557	
+	6	1310	ub.2_Intron|CABL	NM_001100619	NP_001094089	Q8TDN4	CABL1_HUMAN	th CDK3 (By similarity).	1	AGGCCGGGCAA	0.592	
-	17	2770	e_Mutation_p.E74	NM_014939	NP_055754	Q9Y2L5	TPPC8_HUMAN		0	AATCATTTCAGG	0.274	
+	1	10	se_Mutation_p.E3	NM_001390	NP_001381	Q9Y4J8	DTNA_HUMAN	h MAGEE1 (By similarity).	0	ATTGAAGATAGT	0.383	
+	8	1244	p.A308V|SLC14A	NM_007163	NP_009094	Q15849	UT2_HUMAN	ical; (Potential).	4	GGTGGCTCTGT	0.557	
-	7	575	lbq.3_Missense_M	NM_024430	NP_077748	Q9H939	PPIP2_HUMAN	Potential.	1	CACTCCGGCTG	0.468	
-	19	2533		NM_001080467	NP_001073936	Q9ULV0	MYO5B_HUMAN	osin head-like.	5	TGCTCGAAAGA	0.557	
-	4	1077		NM_052947	NP_443179	Q86TB3	ALPK2_HUMAN		14	CGGCACTGTCA	0.498	
+	7	1442	p.E373K|CDH7_u	NM_033646	NP_387450	Q9ULB5	CADH7_HUMAN	(Potential).|Cadherin 3.	4	TAGATGAGCCC	0.498	
-	4	902	v.2_Missense_Mu	NM_182511	NP_872317	Q8IUK8	CBLN2_HUMAN	C1q.	0	TAGAGGAAACA	0.507	
-	7	1111	p.R275Q|NETO1_	NM_138966	NP_620416	Q8TDF5	NETO1_HUMAN	xtracellular (Potential).	4	TGTTTCGACTG	0.463	
+	10	1324	_Mutation_p.D304	NM_018235	NP_060705	Q96KP4	CNDP2_HUMAN		3	TCTCCGACTTC	0.557	
-	2	430		NM_017797	NP_060267	Q9BX70	BTBD2_HUMAN	BTB.	2	GACGGCGCTGC	0.652	
-	14	1711	p.R552C|PIP5K1	NM_012398	NP_036530	O60331	PI51C_HUMAN		4	TGTGCGCCGCC	0.468	
+	3	614		NM_005483	NP_005474	Q13111	CAF1A_HUMAN	1 chromo shadow domain.	2	CATTTCCTGGA	0.557	
-	2	497	F14_uc002mfj.1_	NM_003807	NP_003798	O43557	TNF14_HUMAN	type II membrane protein;	1	CAGACCCACCC	0.642	
-	18	3455	e.1_Missense_Mu	NM_000208	NP_000199	P06213	INSR_HUMAN	e.|Cytoplasmic (Potential).	12	AGAACGGAGGT	0.662	
-	9	924		NM_198492	NP_940894	Q6UXB4	CLC4G_HUMAN	(Potential).|C-type lectin.	0	CAGATCCAGCC	0.637	
-	8	2011		NM_198471	NP_940873	Q6NY19	KANK3_HUMAN	ANK 1.	0	GACCTCGCAGG	0.647	
-	3	18804		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).	57	TTGTTCATGACA	0.473	
-	8	1730	ws.2_Missense_M	NM_024106	NP_077011	Q9BUY5	ZN426_HUMAN	2H2-type 10.	1	ATGAACTGGAA	0.413	
-	4	454	dyn.1_RNA|ZNF62	NM_145233	NP_660276	Q96I27	ZN625_HUMAN	ype 1; degenerate.	0	CACATGATTTTA	0.453	
+	11	1873		NM_004843	NP_004834	Q6UWB1	I27RA_HUMAN	tential).|Fibronectin type-III	0	GGGGTCCCTGT	0.542	
+	15	2015	p.S582N|CD97_u	NM_078481	NP_510966	P48960	CD97_HUMAN	Name=3; (Potential).	4	GATGAGCCTCG	0.687	rs140048136
+	1	536	.2_Intron|GIPC1_u	NM_001146693	NP_001140165	F5H5R7	F5H5R7_HUMAN		0	ATATTGCGGGGA	0.398	
+	2	661	p.L196F|C19orf44	NM_032207	NP_115583	Q9H6X5	CS044_HUMAN		0	ACTTTGCAAAC	0.428	
+	14	3483	p.D886N|NWD1_uc002nev.3_Missense_Mutation_p.D8			Q149M9	NWD1_HUMAN	WD 5.	7	CCAGGGATGGT	0.547	
+	16	3774	p.R983C|NWD1_uc002nev.3_Missense_Mutation_p.R9			Q149M9	NWD1_HUMAN	WD 7.	7	GGCTTTCGCCGA	0.537	
+	3	464		NM_024656	NP_078932	Q8NBJ5	GT251_HUMAN		0	AGCCCTGAAAT	0.562	
+	5	1684	p.A559T|MAP1S_	NM_018174	NP_060644	Q66K74	MAP1S_HUMAN	tubule-organizing center lo	1	AGGCGGCACCC	0.677	
-	14	2195	.G287E|PDE4C_	NM_001098819	NP_001092289	Q08493	PDE4C_HUMAN		5	GGTCTCCCTGC	0.627	
+	1	825		NR_003128					0	TAGTACGAAATT	0.378	
+	2	1423	p.I509M|ZNF493	NM_175910	NP_787106	Q6ZR52	ZN493_HUMAN	2H2-type 13.	1	TAAAATAATTCAT	0.323	
-	5	2403	208_uc002nqo.1_	NM_007153	NP_009084				7	TTACCTTATGTTT	0.373	
+	1	1372	_5'Flank|ANKRD2	NM_207391	NP_997274	Q6ZS82	R9BP_HUMAN	ilarity).|Cytoplasmic (Pote	1	GCCCCGCTGGA	0.706	
+	2	202	se_Mutation_p.R2	NM_020895	NP_065946	Q96CP6	GRM1A_HUMAN		0	GAAACGGCTGC	0.622	
+	7	2169	nse_Mutation_p.H	NM_198539	NP_940941	Q3ZCX4	ZN568_HUMAN	2H2-type 12.	2	AAAATTCATACTG	0.383	
+	12	1286	u.2_Missense_Mu	NM_000540	NP_000531	P21817	RYR1_HUMAN	plasmic.|MIR 5.	12	ACGACGCACTG	0.637	

-	6	453	kx.3_Missense_Mu	NM_004877	NP_004868	O60234	GMFG_HUMAN	ADF-H.		1	GCTCTGCTGTCT	0.557
-	2	321	RB_uc010egw.1_	NM_000713	NP_000704	P30043	BLVRB_HUMAN			0	GCCACGGTCTTG	0.662
-	4	449	oo.2_Missense_M	NM_004756	NP_004747	Q9Y6R0	NUMBL_HUMAN	PID.	p.R94W(1)	5	ATTCCCCGGGAC	0.557
+	4	551	.1_Intron|CYP2S1	NM_030622	NP_085125	Q96SQ9	CP2S1_HUMAN			1	CCAGGACGCCCA	0.627
+	21	2060	osb.2_Missense_	NM_004706	NP_004697	Q92888	ARHG1_HUMAN	PH.		4	TCCACGAGGGC	0.627
+	5	1181	284_uc010ejd.2_	NM_013361	NP_037493	Q9UK11	ZN223_HUMAN	2H2-type 5.		1	TGGTCCACACA	0.448
+	2	108		NM_000483	NP_000474	P02655	APOC2_HUMAN			1	CTATGGGCACAC	0.612
+	13	1467	p.P488S|MARK4_uc002pbc.1_Missense_Mutation_p.P			Q96L34	MARK4_HUMAN			3	GAGATCCCAGAG	0.711
+	1	2749		NM_004491	NP_004482	Q9NRY4	RHG35_HUMAN			1	ATTGACGGAAGG	0.453
+	2	688	lc.1_Missense_Mu	NM_014681	NP_055496	Q14147	DHX34_HUMAN			5	CACGCGGGGCT	0.632
+	6	1260	phi.3_Missense_M	NM_015711	NP_056526	Q9NZM4	GSCR1_HUMAN			3	AGCCCGCGGGG	0.746
-	2	710	e.2_RNA|IZUMO1	NM_182575	NP_872381	Q8IYV9	IZUM1_HUMAN	ellular (Potential).		1	CCTTTCCATCATG	0.552
-	2	419	UVBL2_uc002plq.	NM_002103	NP_002094	P13807	GYS1_HUMAN			2	GTTGTCGCCCC	0.667
+	6	4646		NM_020719	NP_065770	Q9ULL5	PRR12_HUMAN			2	ATCTGGCCAAAA	0.672
-	6	1152	ybi.1_Missense_M	NM_052884	NP_443116	Q96RL6	SIG11_HUMAN	ellular (Potential).		6	TCTGGAGGATCT	0.582
+	23	2834		NM_004533	NP_004524	Q14324	MYPC2_HUMAN	like C2-type 6.		1	CATCCGCGTTG	0.632
-	4	626	LK15_uc002pto.2_	NM_017509	NP_059979	Q9H2R5	KLK15_HUMAN	eptidase S1.		2	CTCTGCCCTCCG	0.572
-	3	801	AS1_uc002pxn.1_	NM_001523	NP_001514	Q92839	HAS1_HUMAN	lasmic (Potential).		2	GGTCCTCGTCCA	0.622
-	4	1901	616_uc002pyn.2_	NM_178523	NP_848618	Q08AN1	ZN616_HUMAN	2H2-type 13.		0	TCTCCGATGCC	0.443
-	4	422_423	qar.3_Missense_	NM_001102603	NP_001096073	Q9HCG1	ZN160_HUMAN			1	AGTAAGGGCCAT	0.416
+	3	568		NM_001012728	NP_001012746	A6NFQ7	DPRX_HUMAN			0	GTTTGCGCTCCA	0.428
+	3	376	era.1_Missense_M	NM_031896	NP_114102	P62955	CCG7_HUMAN	ical; (Potential).		1	ACATCGGCCAC	0.597
+	5	505	.2_Missense_Mut	NM_001013	NP_001004	P46781	RS9_HUMAN	RNA-binding.		1	TGTCCGCCTGG	0.612
+	5	705	LRA1_uc010yfh.1_	NM_006863	NP_006854	O75019	LIRA1_HUMAN	2.|Extracellular (Potential).		3	CGTACCCATGGG	0.567
+	13	1925	e_Mutation_p.E53	NM_006669	NP_006660	Q8NHL6	LIRB1_HUMAN	lasmic (Potential).		3	CCCAGGAAGAA	0.612
+	6	735	_Intron|KIR2DS4_	NM_012314	NP_036446	P43632	KI2S4_HUMAN	ellular (Potential).		0	GCCTTCACCCA	0.493
+	4	690	kf.2_Missense_Mu	NM_032430	NP_115806	Q8TDC3	BRSK1_HUMAN	rotein kinase.		6	TCTTCCGCCAGA	0.602
+	2	746	2qls.2_Missense_	NM_013301	NP_037433	Q9BWC9	CC106_HUMAN			0	TGACCGGAGCA	0.662
-	8	2981	b.2_Missense_Mu	NM_145007	NP_659444	P59045	NAL11_HUMAN	LRR 3.		6	CTCAGCGGATTG	0.498
+	2	534		NM_134444	NP_604393	Q96MN2	NALP4_HUMAN	DAPIN.		15	CAGCTTGAACTC	0.413
+	4	2365	_p.S573N|NLRP4_	NM_134444	NP_604393	Q96MN2	NALP4_HUMAN	LRR 1.		15	GGACAGCACCC	0.562
+	7	1648	mi.2_Missense_Mu	NM_153447	NP_703148	P59047	NALP5_HUMAN	NACHT.		7	GGTGACGACCTC	0.537
-	12	1353	qzd.2_Missense_	NM_020738	NP_065789	Q9ULH0	KDIS_HUMAN	ic (Potential).|ANK 12.		4	CTTTGGGATTTC	0.393
+	25	4681	bp.1_Missense_M	NM_014668	NP_055483	Q4ZG55	GREB1_HUMAN			1	AAGTACGCAGCG	0.577
+	18	2456	t.2_Missense_Mu	NM_145693	NP_663731	Q14693	LPIN1_HUMAN	C-LIP.		4	CCATCGGGATG	0.537
-	2	562	xu.1_Nonsense_M	NM_002381	NP_002372	O15232	MATN3_HUMAN	VWFA.		0	TGTCTGGATGG	0.567
-	25	3850	nse_Mutation_p.V	NM_017552	NP_060022	Q9ULI0	ATD2B_HUMAN			1	TGCTTACCTCAA	0.398
+	17	3623	rfj.2_Missense_Mu	NM_003743	NP_003734	Q15788	NCOA1_HUMAN	Gln-rich.		11	GCACCGACAGA	0.473
+	3	428		NM_001105519	NP_001098989	A6NJV1	CB070_HUMAN			1	CGTGAGGGAGC	0.592
+	2	216	rhv.3_Missense_M	NM_020134	NP_064519	Q9BPU6	DPYL5_HUMAN			2	GTGAACGATGAC	0.567
+	5	761	u.2_RNA|ABHD1_	NM_032604	NP_115993	Q96SE0	ABHD1_HUMAN			0	GCCGTGGGCATC	0.522
+	1	3620	1_5'Flank|ZNF512_	NM_032266	NP_115642	Q68DN1	CB016_HUMAN			1	TCATACGGAGAA	0.453
+	8	1874		NM_018158	NP_060628	Q9BWU0	NADAP_HUMAN			0	AGTCTCCATCTC	0.363
+	3	1202	k.3_Nonsense_M	NM_015147	NP_055962	Q76N32	CEP68_HUMAN			1	TCCTGCAGGAC	0.557
+	10	1358	p.R28K|SEMA4F_	NM_004263	NP_004254	O95754	SEM4F_HUMAN	tracellular (Potential).		4	GGACAGGCCAG	0.577
+	3		010fhg.2_Splice_Site|FLJ40330_uc010fhh.2_Splice_Site							0	AGAAGGTAATTA	0.323
-	6	592		NM_001002036	NP_001002036	Q6HA08	ASTL_HUMAN			0	CCGGTCGGCCC	0.657

-	2	574	p.S152F|ST6GAL	NM_001142351	NP_001135823	Q96JF0	SIAT2_HUMAN	nenal (Potential).		11	CGGGGGAAGGG	0.612	
+	15	1991	POTEE_uc002tsl.2	NM_001083538	NP_001077007	Q6S8J3	POTEE_HUMAN	Potential.		0	TTGCATGAAAATA	0.353	
+	1	533		NM_001508	NP_001499	O43194	GPR39_HUMAN	cellular (Potential).		0	TCCCCGAGTTT	0.542	
-	9	1127	nse_Mutation_p.D	NM_032143	NP_115519	Q5FWF4	ZRAB3_HUMAN	case C-terminal.		2	GCGAATCATTCT	0.303	
-	3	225	_p.D35N|CACNB4	NM_000726	NP_000717	O00305	CACB4_HUMAN			2	GGAATCCGCTG	0.458	
+	13	1129	p.Q347H|NOSTRI	NM_001039724	NP_001034813	Q8IVI9	NOSTN_HUMAN			0	GAGCAAAGACC	0.428	
-	39	7472		NM_004525	NP_004516	P98164	LRP2_HUMAN	cellular (Potential).		29	ATGACAGTTCTT	0.403	
-	3	803	uiv.2_Missense_M	NM_001033045	NP_001028217	Q7Z3F1	GP155_HUMAN	ical; (Potential).		1	AAATAGGGAATA	0.289	
-	245	50368	0410I|TTN_uc010z	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN			153	GGTACAGCTGCG	0.353	
-	229	46588	50Q|TTN_uc010z	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN			153	TCACTTCGGGAT	0.468	
-	46	13096	N_uc010zfi.1_Intr	NM_133379	NP_596870	Q8WZ42	TITIN_HUMAN			153	GGACCAGCTGGA	0.383	
-	5	787	_Intron|CERKL_u	NM_001030311	NP_001025482	Q49MI3	CERKL_HUMAN	DAGKc.		4	GGTTTCCGATGC	0.313	
+	4	930	p.A120S|NAB1_uc	NM_005966	NP_005957	Q13506	NAB1_HUMAN			0	GCAATGCCCGG	0.498	
-	2	913		NM_004657	NP_004648	O95810	SDPR_HUMAN			2	GGTTTCCTCCA	0.557	
+	31	3567_3568	p.G712N|AOX1_u	NM_001159	NP_001150	Q06278	ADO_HUMAN			6	GCGAAGGCCAG	0.475	
+	5	509	hv.1_Missense_M	NM_015934	NP_057018	Q9Y2X3	NOP58_HUMAN			0	GAATTCGTTCAC	0.363	
-	7	749		NM_001093730	NP_001087199	A2CJ06	DYTN_HUMAN		p.P211L(1)	2	AGGTCGGGAGC	0.527	
-	18	2555	e_Mutation_p.P46	NM_173076	NP_775099	Q86UK0	ABCAC_HUMAN			11	AAATGGTGCTG	0.363	
+	4	932	p.R236H|CXCR2_	NM_001557	NP_001548	P25025	CXCR2_HUMAN	lasmic (Potential).		2	CCTGCGTACGC	0.567	rs144013681
-	11	1315		NM_000092	NP_000083	P53420	CO4A4_HUMAN	le-helical region.		11	CGGAGGTCCCT	0.423	
+	14	1768	p.R546H|PSMD1_	NM_002807	NP_002798	Q99460	PSMD1_HUMAN			2	TCTGCGTGGTC	0.463	
-	17	3037	za.2_Missense_M	NM_006037	NP_006028	P56524	HDAC4_HUMAN	one deacetylase.		6	AGGGAGCCGGA	0.602	
+	3	224	.1_5'UTR|ATG4B_	NM_013325	NP_037457	Q9Y4P1	ATG4B_HUMAN			0	AAGGACGAGATC	0.383	
+	3	1021_1022	dn.2_Missense_M	NM_021158	NP_066981	Q96RU7	TRIB3_HUMAN	rotein kinase.		2	GGCGCACTGTCA	0.639	
-	3	813	250_splice|SIRPG_	NM_018556	NP_061026	Q9P1W8	SIRPG_HUMAN			1	CCTCTACCTCGG	0.612	
-	2	2301	ntron|UBOX5_uc0	NM_021826	NP_068598	Q7L8L6	FAKD5_HUMAN			0	CCAGAGGTACAG	0.532	
-	9	1727	1_uc010gcd.1_5'	NM_000214	NP_000205	P78504	JAG1_HUMAN	GF-like 5; calcium-binding		9	CAGTCCACTGTG	0.478	
-	1	1449		NM_012072	NP_036204	Q9NPY3	C1QR1_HUMAN	GF-like 5; calcium-binding		2	CCCCCCGGGCCC	0.637	rs41520247
+	6	683	p.D205N|PLUNC_	NM_130852	NP_570913	Q9NP55	PLUNC_HUMAN			0	CTTCTGGACAGC	0.537	
-	10	4861	aw.2_Missense_M	NM_014071	NP_054790	Q14686	NCOA6_HUMAN	binding region.|Gln-rich.|C		7	TCTGTCCTGACA	0.557	
+	4	657	e_Mutation_p.G13	NM_020336	NP_065069	Q86X10	RLGPB_HUMAN			2	GAACAGGGTTCC	0.498	
-	4	430	DA_uc010ggt.2_R	NM_000022	NP_000013	P00813	ADA_HUMAN			3	CTGTACCGCACC	0.587	rs121908714
-	2	629	_Missense_Mutat	NM_173179	NP_775271	Q9NQQ7	S35C2_HUMAN	ical; (Potential).		1	GATGCCGATGG	0.612	
+	2	593	02yav.2_Missense	NM_080672	NP_542403	Q96KR7	PHAR3_HUMAN			3	GAGATGGACCA	0.582	
+	5	1035	TR3_uc002yav.2_	NM_080672	NP_542403	Q96KR7	PHAR3_HUMAN			3	GTGGTGAAGAA	0.542	
-	16	6805	s.1_Missense_Mu	NM_033081	NP_149072	Q9BTC0	DIDO1_HUMAN	Arg-rich.		6	ctcgctcgcgctctcggt	0.194	
-	22	4070	p.L1200F|TIAM1_	NM_003253	NP_003244	Q13009	TIAM1_HUMAN	DH.		10	CCTGAGCAGAA	0.622	
-	9	2426	dl.1_Missense_Mu	NM_003253	NP_003244	Q13009	TIAM1_HUMAN			10	GCGGCCCATGG	0.478	
+	2	121	|DYRK1A_uc002y	NM_001396	NP_001387	Q13627	DYR1A_HUMAN			4	CTGTTCGGCTT	0.438	
-	36	4193	se_Mutation_p.D1	NM_018963	NP_061836	Q9NSI6	BRWD1_HUMAN	Bromo 2.		4	TAATATCTCTGTA	0.343	
+	40	4784	1353L|SLC19A1_	NM_130444	NP_569711	P39060	COIA1_HUMAN	cal region 11 (NC11).		1	CCTGTCAGGCG	0.756	
+	3	519	e_Mutation_p.H20	NM_006031	NP_006022	O95613	PCNT_HUMAN			8	GGTGACCACCCA	0.552	
-	1	1457	sense_Mutation_p.	NM_031890	NP_114096	Q9BXQ6	CECR6_HUMAN			0	CGCGGGCAGCG	0.706	
-	5	572	02zmg.2_Missens	NM_033070	NP_149061	Q9BXW7	CECR5_HUMAN			0	CCTCGGGAGGG	0.572	
+	9	1217	K1_uc002zqc.2_In	NM_080646	NP_542377	O43435	TBX1_HUMAN			2	TCTGAGGGATG	0.592	
+	8	1113	.G336D|ZDHHC8	NM_013373	NP_037505	Q9ULC8	ZDHC8_HUMAN	lasmic (Potential).		2	GCCCAGGCAGTG	0.637	
-	7	1119		NM_014433	NP_055248	Q9UHP6	RTDR1_HUMAN			1	CTCCACCTCCAT	0.622	

+	13	3283	y.1_Missense_Mut	NM_004327	NP_004318	P11274	BCR_HUMAN	C2.		12	GCATTCCGCTGA	0.577	
-	2	1402	70_uc002zxr.1_5'F	NM_021916	NP_068735	Q9UC06	ZNF70_HUMAN	C2H2-type 7.		2	GCCTTCCCGCAC	0.552	
+	42	6583	utation_p.M1991I|M	NM_032608	NP_115997	Q8IUG5	MY18B_HUMAN			12	TTCTAGGGATAAC	0.398	
+	2	638	uc011akd.1_Misse	NM_021115	NP_066938	Q9BYH1	SE6L1_HUMAN	cellular (Pote	p.T161M(1)	6	CTCCACGGAGA	0.677	
-	12	2434	k.2_Missense_Mut	NM_022081	NP_071364	Q9NQG7	HPS4_HUMAN			0	TCATCCCTGGGC	0.587	
+	9	1280	p.R406C|KREMEN	NM_032045	NP_114434	Q96MU8	KREM1_HUMAN	lasmic (Potential).		5	TCCCATCGTGTT	0.433	
-	10	1439	e_Mutation_p.R41	NM_001127	NP_001118	Q10567	AP1B1_HUMAN			2	ACTTGCGGAAGA	0.597	
+	9	2026	ja.1_Nonsense_M	NM_030758	NP_110385	Q969R2	OSBP2_HUMAN			2	ATGGCTGGAGCC	0.602	
+	6	928	se_Mutation_p.E9	NM_001007467	NP_001007468	A8K8P3	SFI1_HUMAN	HAT 2.		1	GAGCCGAGGTT	0.453	
-	11	1381	oh.1_Missense_Mu	NM_002473	NP_002464	P35579	MYH9_HUMAN	yosin head-like.		11	TGAAATCGGTCA	0.502	
-	15	1936	3aqt.1_Missense_M	NM_153609	NP_705837	Q8IU80	TMPS6_HUMAN	.|Extracellular (Potential).		6	GGTCAGCGATGA	0.652	
+	3	348	31_uc011aok.1_5'U	NM_006116	NP_006107	Q15750	TAB1_HUMAN	PP2C-like.		1	CGAGGCCGATG	0.647	
+	4	778	_p.Q27H|MPPED1_	NM_001044370	NP_001037835	O15442	MPPD1_HUMAN			0	GTGCAGTCGCT	0.562	
+	4	577	K3A_uc010gzy.2_In	NM_006953	NP_008884	O75631	UPK3A_HUMAN			0	CCAGCGTAAGT	0.612	rs145723454
-	1	5032		NM_006071	NP_006062	Q9NTG1	PKDRE_HUMAN	lasmic (Potential).		5	TTCGGACGATCT	0.418	rs141502138
+	2	504	EC_uc003bto.2_In	NM_032492	NP_115881	Q8N5M9	JAGN1_HUMAN	nenal (Potential).		1	AGATGTTCCCTG	0.522	
-	6	1954	_p.P527S|IQSEC1_	NM_014869	NP_055684	Q6DN90	IQEC1_HUMAN	SEC7.		1	GTCTGGGTTCC	0.607	
+	9	3448	vd.1_Missense_Mu	NM_001144382	NP_001137854	Q9UPR0	PLCL2_HUMAN			4	GCAAACGATGAA	0.423	rs144964120
+	30	4213	G1401R|DLEC1_u	NM_007335	NP_031361	Q9Y238	DLEC1_HUMAN			9	CTGCTGGGGGC	0.597	
-	97	7441		NM_000094	NP_000085	Q02388	CO7A1_HUMAN			11	TACGTACCCGGA	0.592	
-	24	2299	T218I|QARS_uc01	NM_005051	NP_005042	P47897	SYQ_HUMAN			1	GTGACAGTTCGG	0.572	
-	2	310	cm.1_Missense_M	NM_000581	NP_000572	P07203	GPX1_HUMAN			1	TGCACGGGAAG	0.617	
+	3	1536		NM_004393	NP_004384	Q14118	DAG1_HUMAN	minin recognition.|Mucin-lik		2	GGACTCGAGGCG	0.597	
+	25	2537	|RBM5_uc003cyh.	NM_005778	NP_005769	P52756	RBM5_HUMAN	interaction with U2AF2.		1	GGCGCCGATTCC	0.478	
-	2	3642	p.2_Missense_Mut	NM_017442	NP_059138	Q9NR96	TLR9_HUMAN	oplasmic (Potential).		4	AAGCTGCGCTGA	0.682	
-	5	623	c.1_5'Flank|TWF2_	NM_007284	NP_009215	Q6IBS0	TWF2_HUMAN			3	TAATGCGGATCT	0.637	
+	8	957	e_Mutation_p.D20	NM_006254	NP_006245	Q05655	KPCD_HUMAN	l-ester/DAG-type 1.		9	TGCATCGACAAG	0.617	rs149165175
+	21	3328	anf.2_Missense_Mu	NM_001457	NP_001448	O75369	FLNB_HUMAN	Filamin 9.		19	GGTCTCGTGGGC	0.562	rs9813235
+	12	2897	nv.2_Missense_Mu	NM_000333	NP_000324	O15265	ATX7_HUMAN	Ser-rich.		0	CCACCGGGAGC	0.532	rs148498434
-	1	919		NM_183357	NP_899200	O95622	ADCY5_HUMAN	ical; (Potential).		4	CACGGCGATGA	0.662	
-	3	299	se_Mutation_p.G9	NM_024628	NP_078904	A0AV02	S12A8_HUMAN			0	GCCAGCCAGTC	0.562	
+	5	880	CM2_uc010hsl.2_F	NM_004526	NP_004517	P49736	MCM2_HUMAN			4	AAGTACGACCGC	0.627	rs144753488
+	8	3024	_p.A681V|ZBTB38	NM_001080412	NP_001073881	Q8NAP3	ZBT38_HUMAN			3	AAAATGCTGTCA	0.463	
+	6	1193	7_splice|RNF13_u	NM_007282	NP_009213	O43567	RNF13_HUMAN			1	ACGACAGTAAGT	0.363	
-	3	1409	.1_Intron|MED12L	NM_023915	NP_076404	Q9BY21	GPR87_HUMAN	lasmic (Potential).		1	ATATGCGAACTTC	0.348	
+	3	329	orf55_uc011bot.1_F	NM_001130002	NP_001123474	A1A4F0	CC055_HUMAN			0	AGGTGGAGACC	0.423	
-	2	581		NM_032487	NP_115876	Q9BYD9	ARPM1_HUMAN			0	TCCACTGGGTAA	0.418	
-	6	1144	c011bro.1_Intron|T	NM_000460	NP_000451	P40225	TPO_HUMAN	Pro-rich.		1	TGGGTGGAAGA	0.592	
-	2	252		NM_004488	NP_004479	P40197	GPV_HUMAN	cellular (Potential).		3	GGACGGTCATG	0.637	
-	2	6794	C4_uc003fvp.2_Int	NM_018406	NP_060876	Q99102	MUC4_HUMAN	Ser-rich.		0	AAGAGCGGTGG	0.567	
-	10	1165	IA_uc003fwh.2_Mi	NM_005017	NP_005008	P49585	PCY1A_HUMAN	ximate.|3 X repeats.		0	AGGGGGAGGGG	0.607	
+	8	1293	on_p.G346E|FGFR	NM_000142	NP_000133	P22607	FGFR3_HUMAN	3.|Extracellular (Potential).		2600	CTATTGGGTTTT	0.617	
+	5	2958	e_Mutation_p.S37	NM_198229	NP_937872	O14924	RGS12_HUMAN			1	GCGTCAGCAACA	0.692	
+	2	164	icw.2_Missense_M	NM_001528	NP_001519	Q04756	HGFA_HUMAN			2	CCCCTGCGATCC	0.632	
+	8	1985	.E87K|ZBTB49_uc	NM_145291	NP_660334	Q6ZSB9	ZBT49_HUMAN			2	GCCATCGAGACC	0.577	
-	1	1295	).3_Intron|SORCS	NM_001085382	NP_001078851	Q6NUJ1	SAPL1_HUMAN	posin B-type 4.		0	GCAGCCTCTTGC	0.637	
-	4	2381		NM_003263	NP_003254	Q15399	TLR1_HUMAN	smic (Potential).|TIR.		5	CACTCTGGACAA	0.413	

-	22	3055	x.1_Missense_Mu	NM_002913	NP_002904	P35251	RFC1_HUMAN		4	ACAATACGATCAT	0.488	
-	30	3101	p.W183R|ATP8A1_	NM_006095	NP_006086	Q9Y2Q0	AT8A1_HUMAN	ical; (Potential).	3	GAAACCAAAACA	0.348	
-	6	706	0iik.1_Missense_M	NM_201431	NP_958834	Q6ZTQ3	RASF6_HUMAN		2	TCATCCTTTTTCT	0.413	
-	6	1579	ijt.2_Missense_Mu	NM_194282	NP_919258	Q6MZP7	LIN54_HUMAN		0	CATCCGCACTG	0.328	
-	2	816	_p.M142I|PPM1K_	NM_152542	NP_689755	Q8N3J5	PPM1K_HUMAN	PP2C-like.	0	TTTCTCCATGTG	0.453	
+	6	1931	cgf.1_Missense_M	NM_004784	NP_004775	O95803	NDST3_HUMAN	Heparan sulfate N-deacetyl	1	CTGTCGTCCTC	0.428	
+	1	2495		NM_024582	NP_078858	Q6V0I7	FAT4_HUMAN	r (Potential).|Cadherin 8.	18	TTACTACTGGGG	0.443	
+	10	1646		NM_000824	NP_000815	P48167	GLRB_HUMAN	ical; (Probable).	2	TTGTTTCCTTTCT	0.353	
+	4	933		NM_006174	NP_006165	Q15761	NPY5R_HUMAN	lasmic (Potential).	7	CTTGAAGAAAAT	0.378	
-	1	698	CH1_uc003iqs.1_I	NM_012403	NP_036535	O43423	AN32C_HUMAN		0	ttctcattttcgcttctgac	0.085	
-	1	1327	.1_Intron|KLHL2_	NM_000167	NP_000158				0	CCAAAGCGTAAT	0.393	
+	4	1111	e_Mutation_p.R15	NM_012464	NP_036596	O43897	TLL1_HUMAN	otease (By similarity).	7	CGGAAAGAATAT	0.393	
+	12	1853	_p.S425N|FAM149	NM_015398	NP_056213	A5PLN7	F149A_HUMAN		1	GCCCAGCACAA	0.448	
+	4	734		NM_207352	NP_997235	Q6ZWL3	CP4V2_HUMAN		0	AATGGCGCTCC	0.323	
+	10	1191	D2_uc010itf.1_3'U	NM_033120	NP_149111	Q969F2	NKD2_HUMAN		0	CGCCACTCAAG	0.716	
-	3	1661	ERT_uc003jcc.1_M	NM_198253	NP_937983	O14746	TERT_HUMAN	ization.|RNA-interacting do	12	CAGACGGTGCT	0.582	
-	12	1658		NM_001044	NP_001035	Q01959	SC6A3_HUMAN		6	CTGCCCGGTCA	0.647	
-	9	1704	ND2_uc011cmz.1	NM_001332	NP_001323	Q9UQB3	CTND2_HUMAN		8	CAGGGCCGGAT	0.562	
+	11	1984		NM_020227	NP_064612	Q9NQV7	PRDM9_HUMAN	2H2-type 4.	6	GAGGACACACA	0.597	
-	12	1997	1_Missense_Muta	NM_000065	NP_000056	P13671	CO6_HUMAN	SP type-1 3.	7	CTCCTCGTTGG	0.502	rs148521858
+	24	5592	e_Mutation_p.V17	NM_018429	NP_060899	A6H8Y1	BDP1_HUMAN		2	AAACTGTAGGA	0.338	
+	2	10093		NM_153610	NP_705838	Q8N3K9	CMYA5_HUMAN		9	CGGTTCCATTT	0.493	
+	8	6465	.2_Intron|VCAN_	NM_004385	NP_004376	P13611	CSPG2_HUMAN	GAG-beta.	16	GTACAGCTTCC	0.473	
-	3	797	knp.2_Missense_	NM_173488	NP_775759	Q86UG4	SO6A1_HUMAN	ellular (Potential).	7	TTTCTTCGCAAAT	0.323	
-	8	2209	se_Mutation_p.A	NM_020389	NP_065122	Q9HCX4	TRPC7_HUMAN	lasmic (Potential).	0	TTTTGGCCTTAG	0.413	
+	1	1915	DHA4_uc003lhh.1	NM_018909	NP_061732	Q9UN73	PCDA6_HUMAN	|Extracellular (Potential).	2	CGGGCGAGATC	0.662	
+	1	2389	1dan.1_Missense_	NM_018912	NP_061735	Q9Y5H4	PCDG1_HUMAN	lasmic (Potential).	3	AGTCTTTACTT	0.418	
-	6	538	C3_uc010jgd.1_	NM_003883	NP_003874	O15379	HDAC3_HUMAN	ne deacetylase.	1	CTTGAGCAGCT	0.537	
-	16	1594	se_Mutation_p.E1	NM_033449	NP_258260	Q86WN1	FCSD1_HUMAN	SH3 1.	4	TACCTCGCCGT	0.572	
-	3	3184	.R1023C|PCDH1_	NM_002587	NP_002578	Q08174	PCDH1_HUMAN	lasmic (Potential).	5	GGTGCGGTAGC	0.632	rs147327566
+	9	1814	RF2_uc003lnu.2_	NM_152550	NP_689763	Q8TEC5	SH3R2_HUMAN		2	GACCCCTCCAG	0.612	rs146976434
-	9	1066	oo.2_Missense_M	NM_001387	NP_001378	Q14195	DPYL3_HUMAN		1	AGCAAGGAGTTG	0.557	
+	15	2066	_Mutation_p.R64	NM_205836	NP_995308	Q6PIJ6	FBX38_HUMAN		6	ACTTCGAAAGA	0.458	
+	5	1211	_p.S351L|PPARG	NM_133263	NP_573570	Q86YN6	PRGC2_HUMAN		0	GTCCTCGGTGG	0.662	
-	9	8780	2A_uc011dcs.1_In	NM_001447	NP_001438	Q9NYQ8	FAT2_HUMAN	(Potential).|Cadherin 26.	6	CAGTTCGCCAG	0.512	
-	2	136	jii.2_Missense_M	NM_138379	NP_612388	Q96H15	TIMD4_HUMAN	.|Extracellular (Potential).	2	TCACAACAGTCT	0.478	
-	12	1266	M19_uc003lwy.2_	NM_033274	NP_150377	Q9H013	ADA19_HUMAN	B.|Extracellular (Potential).	8	ACATTCCACCA	0.542	
+	9	885	K2_uc011der.1_	NM_004946	NP_004937	Q92608	DOCK2_HUMAN		7	CTAAGGAGATT	0.507	
+	11	1731	p.R461K|CNOT6_	NM_015455	NP_056270	Q9ULM6	CNOT6_HUMAN		0	TGGAAGGATCA	0.413	
+	1	824	C5_uc003mxw.2_	NR_027712					0	CTATGCGCCGG	0.522	
-	1	903	_5'Flank|C6orf114	NM_018988	NP_061861	Q9NXC2	GFOD1_HUMAN		2	GACAGCGATCT	0.602	
+	8	2321	.R521W|JARID2_	NM_004973	NP_004964	Q92833	JARD2_HUMAN	ARID.	4	AGGACCGGCTG	0.587	
+	12	1499	e_Mutation_p.C35	NM_006366	NP_006357	P40123	CAP2_HUMAN	P/cofactor C-like.	1	AAGGTTGCCACA	0.398	
-	10	1725	p.V475M|DCDC2_	NM_016356	NP_057440	Q9UHG0	DCDC2_HUMAN		1	AGCCACGGCAG	0.368	rs145154884
-	3	172	ense_Mutation_p.	NM_005074	NP_005065	Q14916	NPT1_HUMAN		4	CATAGCGAAAG	0.408	
+	1	905		NM_013936	NP_039224	P58182	O12D2_HUMAN	Name=7; (Potential).	1	GTCACTCCTGTA	0.448	
+	2	3595_3596		NM_080870	NP_543146	Q3MIW9	DPCR1_HUMAN	ar (Potential).|Thr-rich.	0	CCAAAGGGAAA	0.48	

+	5	395	1C1_uc003nsn.1_	NM_014068	NP_054787	Q9UIG5	PS1C1_HUMAN		1	CCCACGTTAAT	0.562	
+	7	1151	_uc011dqu.1_5'F	NM_001077516	NP_001070984	Q92504	S39A7_HUMAN		1	GGGCCGGGGA	0.567	
+	8	2198	f.1_Missense_Mu	NM_002263	NP_002254	Q9BW19	KIFC1_HUMAN	inesin-motor.	0	GGAGCGGGAA	0.657	
-	3	724	f106_uc003ojs.2_	NM_024294	NP_077270	Q9H6K1	CF106_HUMAN		3	ACATCCGCCAC	0.512	
+	1	123	L4_uc003oqd.2_5	NM_198153	NP_937796	Q6UXN2	TRML4_HUMAN		1	GGGTCCACACC	0.587	
-	1	585		NM_000322	NP_000313	P23942	PRPH2_HUMAN	ical; (Potential).	5	GGTACGGCTTC	0.577	
-	3	565	_Intron|TMEM151	NM_182539	NP_872345	Q5JU00	TCTE1_HUMAN		4	GCGATGCATGC	0.597	
-	4	884	YS_uc003per.1_M	NM_001142800	NP_001136272	Q5T1H1	EYS_HUMAN		6	TATTTTGCACAC	0.353	
-	11	1296		NM_001563	NP_001554	Q17R60	IMPG1_HUMAN		3	TGTCAGGACCA	0.388	
-	4	564	_p.R136H|BVES_u	NM_147147	NP_671488	Q8NE79	POPD1_HUMAN	lasmic (Potential).	0	GCACACGGAGT	0.438	rs143510978
+	1	335	.2_Intron|BET3L_	NM_153711	NP_714922	Q8N5C1	FA26E_HUMAN		0	AGCTGCCGTTTC	0.502	
-	6	651	.1_RNA|GOPC_uc	NM_002944	NP_002935	P08922	ROS_HUMAN	III 1.|Extracellular (Potentia	25	AGGACGGTCTG	0.478	
-	4	872	2_Missense_Muta	NM_014432	NP_055247	Q9UHF4	I20RA_HUMAN	tential).|Fibronectin type-III	4	TCTCATCTGTAG	0.428	
-	30	4338	jb.1_Missense_M	NM_182961	NP_892006	Q8NF91	SYNE1_HUMAN	lasmic (Potential).	45	TTCTTCGAGAG	0.348	rs138915528
-	2	525	.2_5'UTR|RNASE	NM_003730	NP_003721	O00584	RNT2_HUMAN		0	GCTGAACCATAA	0.418	
-	7	1772	ski.3_Missense_	NM_182924	NP_891554	Q8IY33	MILK2_HUMAN		1	CTGAGGATTCC	0.657	
-	11	1673	e_Mutation_p.S39	NM_000535	NP_000526	P54278	PMS2_HUMAN		2	CCTGCGAGCCC	0.552	
+	3	1979		NM_017560	NP_060030	P0CG23	ZN853_HUMAN		0	GGAGCGACCCT	0.697	
+	3	1213	H1_uc011jxh.1_5'	NM_152745	NP_689958	P58417	NXPH1_HUMAN	III.	2	GCCTCGGCCCA	0.473	
-	4	687	_p.R57Q|TRA2A_	NM_013293	NP_037425	Q13595	TRA2A_HUMAN	RRM.	1	GAGATCGCCCA	0.393	
-	1	1009		NR_002711					0	GTGCTCGGTAA	0.532	
-	2	844	11_uc003syy.2_R	NM_005523	NP_005514	P31270	HXA11_HUMAN	Homeobox.	2	CTCCCGTTCCA	0.532	
-	7	690	_p.P191S|CPVL_u	NM_031311	NP_112601	Q9H3G5	CPVL_HUMAN		2	TTCAGGAAATAT	0.333	
+	8	1105	tion_p.R87L|CHN2	NM_004067	NP_004058	P52757	CHIO_HUMAN	l-ester/DAG-type.	2	GTTCCGAGGCC	0.478	
-	8	755		NM_015283	NP_056098	Q2PZI1	D19L1_HUMAN	ical; (Potential).	0	TACACGGGTAC	0.299	
-	21	2920	ng.2_Missense_M	NM_033054	NP_149043	B0I1T2	MYO1G_HUMAN		4	CTGGTCTCCTC	0.721	
-	2	734	se_Mutation_p.S2	NM_000598	NP_000589	P17936	IBP3_HUMAN	Ser/Thr-rich.	3	CGGAGGAGAAG	0.493	
-	16	1944	33_splice|TYW1B_	NM_001145440	NP_001138912	Q6NUM6	TYW1B_HUMAN		0	TTCTTACCTTTCT	0.428	
+	9	546	tzr.2_RNA|ELN_u	NM_000501	NP_001075224	P15502	ELN_HUMAN		5	CCCAGGTGGCG	0.478	
+	9	549	tzr.2_RNA|ELN_u	NM_000501	NP_001075224	P15502	ELN_HUMAN		5	AGGTGGCGTGC	0.463	
+	8	1189	b.2_Missense_Mu	NM_002314	NP_002305	P53667	LIMK1_HUMAN	rotein kinase.	3	TCCACGGGGAG	0.677	
-	22	15232		NM_033026	NP_149015	Q9Y6V0	PCLO_HUMAN		7	CTGTCCCATCTT	0.323	
-	5	6233	v.2_Missense_Mut	NM_033026	NP_149015	Q9Y6V0	PCLO_HUMAN		7	TAAATCCATTTT	0.363	
-	25	3345	.A1090V|ABCB4_	NM_018849	NP_061337	P21439	MDR3_HUMAN	2.|Cytoplasmic (By similarit	6	TCCCCGCCAAG	0.498	rs143392573
-	3	257	54_splice|SRI_uc0	NM_003130	NP_003121	P30626	SORCN_HUMAN		1	AACTTACGTTTG	0.383	
+	2	675	_p.H94Q|STEAP2	NM_152999	NP_694544	Q8NFT2	STEA2_HUMAN		2	TATACACAGAGA	0.378	
+	6	695	tion_p.K170E|AP4	NM_004722	NP_004713	O00189	AP4M1_HUMAN		0	AGAGCAAAGTG	0.572	
+	3	9234	C17_uc010lho.1_	NM_001040105	NP_001035194	Q685J3	MUC17_HUMAN	ch.|59 X approximate tand	27	CCATTCCTGAG	0.493	
-	23	3189	.2_Missense_Mut	NM_005045	NP_005036	P78509	RELN_HUMAN		19	TCCAGCGGAAA	0.488	
+	9	903	D_uc011kmh.1_M	NM_000108	NP_000099	P09622	DLDH_HUMAN		1	GCATCCTTCAA	0.353	
+	3	483	p.C121Y|IRF5_uc	NM_002200	NP_002191	Q13568	IRF5_HUMAN	phan pentad repeat.	0	GGTCTGCTCCA	0.637	
-	15	1860		NM_004333	NP_004324	P15056	BRAF_HUMAN	rotein kinas_R603>I(2)|p.T	18290	GATTTCACTGTA	0.368	
+	5	1198		NM_014141	NP_054860	Q9UHC6	CNTP2_HUMAN	1.|Extracellular (Potential).	11	TGCACGGAGAA	0.388	
+	13	1753	PO_uc010lpl.1_Int	NM_198455	NP_940857	A2VEC9	SSPO_HUMAN	VWFD 2.	0	GGGGTGGTCAA	0.677	
+	53	7813		NM_198455	NP_940857	A2VEC9	SSPO_HUMAN	SP type-1 5.	0	CCTGCGGCTTG	0.701	
+	2	365	kr.2_RNA|GALNT	NM_145292	NP_660335	Q7Z4T8	GLTL5_HUMAN	enal (Potential).	2	GGTCCCCTGGA	0.413	
-	2	268	x.2_RNA|VIPR2_	NM_003382	NP_003373	P41587	VIPR2_HUMAN	ellular (Potential).	2	CAGATGAAATC	0.383	

-	2	104		NM_001925	NP_001916	P12838	DEF4_HUMAN		1	CTGCCCGGACC	0.597	
-	6	488	.1_Intron|PINX1_	NM_017884	NP_060354	Q96BK5	PINX1_HUMAN		3	TTCTTACTCTGT	0.403	
+	8	1370	_p.A300V|SH2D4A	NM_022071	NP_071354	Q9H788	SH24A_HUMAN		0	CATAGCCCCCT	0.517	
-	7	1012	_uc010ltt.1_Silent_	NM_025232	NP_079508	Q9H6H4	REEP4_HUMAN		1	GGCCCGGTACC	0.652	
-	12	2371	y.1_Missense_Mu	NM_002318	NP_002309	Q9Y4K0	LOXL2_HUMAN	yl-oxidase like.	3	CTGATCGCCGA	0.592	
-	1	503		NM_006158	NP_006149	P07196	NFL_HUMAN	od.|Linker 1.	2	GGAAGCGGGAT	0.672	
+	26	2643	_p.A612V|PTK2B_	NM_173174	NP_775266	Q14289	FAK2_HUMAN	otein kinase.	5	CCCAGCCGTGT	0.617	
-	6	1925	e_Mutation_p.R4	NM_025115	NP_079391	Q6NXR4	CH041_HUMAN		0	AACAGCGGTCC	0.448	
+	13	2345	124_uc010lvy.2_I	NM_032777	NP_116166	Q96PE1	GP124_HUMAN	ellular (Potential).	5	CACCTCCCGCC	0.682	
-	1	262		NM_000025	NP_000016	P13945	ADRB3_HUMAN	llular (By similarity).	2	TATTGGGCGCC	0.716	
-	19	4006	.R1163K|WHSC1	NM_023034	NP_075447	Q9BZ95	NSD3_HUMAN	SET.	1	TGCTCCTTTTG	0.498	
+	16	1849	_p.G279R|IKBKB_	NM_001556	NP_001547	O14920	IKKB_HUMAN		7	AGGGGGGAACG	0.602	
-	60	8158	_Mutation_p.G270	NM_006904	NP_008835	P78527	PRKDC_HUMAN	KIP-binding.	34	TTTCCCAAAATC	0.502	
-	6	1249	1_Missense_Muta	NM_014682	NP_055497	O60284	ST18_HUMAN	2HC-type 1.	5	GGTCTCCCTCT	0.527	
-	3	718	sh.1_Missense_	NM_152417	NP_689630	Q96MH6	TMM68_HUMAN		1	TCTGCGATGAC	0.368	
-	4	1216		NM_004820	NP_004811	O75881	CP7B1_HUMAN		3	GATGGGAAATC	0.443	
+	9	1175	yhu.1_Splice_Site	NM_014754	NP_055569	P48651	PTSS1_HUMAN		1	TTTGGGTGAGT	0.403	
-	22	3523	p.E929K|RGS22_	NM_015668	NP_056483	Q8NE09	RGS22_HUMAN	RGS 2.	7	TAACTCCTTCC	0.358	
-	3	1437	_p.R336H|ZHX1_	NM_007222	NP_009153	Q9UKY1	ZHX1_HUMAN	obox 1.|Required for inter	1	TTAAACGTTGG	0.403	
+	3	409		NM_152412	NP_689625	Q7Z3I7	ZN572_HUMAN		2	TGATTCCTATG	0.403	
+	8	1972		NM_001702	NP_001693	O14514	BAI1_HUMAN	ellular (Potential).	8	CAGCGGGAGAG	0.637	
+	10	1074		NM_145754	NP_665697	Q96AC6	KIFC2_HUMAN	Potential.	3	GACTTCGGGCA	0.652	
+	5	1231		NM_138431	NP_612440	Q96ES6	MFSD3_HUMAN		2	CCCTCAGGCCA	0.672	
-	1	485		NM_005454	NP_005445	O95813	CER1_HUMAN		0	TGACCCCCTGA	0.498	
-	25	5055	lk.2_5'Flank|FRE	NM_144966	NP_659403	Q5H8C1	FREM1_HUMAN	CSPG 11.	5	GGTCCGCAGTC	0.522	
-	4	1132	M1_uc010mic.2_	NM_144966	NP_659403	Q5H8C1	FREM1_HUMAN		5	GCAGCCGAGTT	0.522	
+	7	1076	p.R161Q|C9orf93_	NM_173550	NP_775821	Q6TFL3	CI093_HUMAN	ential.|Glu-rich.	0	ACGGCGACAAA	0.348	
-	4	890	mkj.1_Intron|FAN	NM_004629	NP_004620	O15287	FANCG_HUMAN		4	GCTCCGGCAGA	0.627	
+	11	1158	lqm.1_Nonsense_	NM_014907	NP_055722	Q5SYB0	FRPD1_HUMAN	FERM.	9	AACCCCGACAG	0.438	
+	4	2479	1_Intron|uc004am	NM_001145197	NP_001138669	Q6ZUB0	YI020_HUMAN		0	TAACTCTGAGA	0.468	
-	11	1174	p.P281L|SLC28A3	NM_022127	NP_071410	Q9HAS3	S28A3_HUMAN	ellular (Potential).	4	AATATGGTCGG	0.507	
-	7	1010	t.2_Missense_Mu	NM_001039803	NP_001034892	Q8IZL9	CDK20_HUMAN	otein kinase.	1	AGTCCGGCAGC	0.572	
+	3	461	s.2_RNA|ANKRD19_uc004asr.3_RNA						0	CAACACTGCTC	0.433	
-	1	520		NM_205859	NP_995581	Q8NGT1	OR2K2_HUMAN	ellular (Potential).	1	AGTGATCGATGA	0.537	
-	8	785	se_Mutation_p.G2	NM_012212	NP_036344	Q14914	PTGR1_HUMAN		0	CTGGCCGATAA	0.403	rs146199919
-	1	25	J2_uc004bmj.1_I	NM_001004451	NP_001004451	Q8NGS3	OR1J1_HUMAN	ellular (Potential).	2	GGACACGCTGC	0.532	
-	4	289		NM_000476	NP_000467	P00568	KAD1_HUMAN		0	GACCTCGGACC	0.632	
+	10	911		NM_015354	NP_056169	Q5SRE5	NU188_HUMAN		7	AGTTTGCGCAG	0.428	
+	2	496_497		NM_001012715	NP_001012733	Q8NAJ2	CI106_HUMAN		0	CTCATGGGTGG	0.609	
-	5	754	x.2_Missense_M	NM_007371	NP_031397	Q15059	BRD3_HUMAN		8	AGACGGTGGGG	0.637	
+	3	210		NM_183241	NP_899064	Q9BUH6	CI142_HUMAN		0	AGAAAGCCCGT	0.657	
-	30	5226	_Mutation_p.R162	NM_001606	NP_001597	Q9BZC7	ABCA2_HUMAN		0	CTCACCGGTGC	0.652	
+	6	1010	XD1_uc011mgx.1_	NM_018390	NP_060860	Q9NUJ7	PLCX1_HUMAN		0	CATCCGATACC	0.657	
+	6	693	f.1_Missense_Mut	NM_004042	NP_004033	P54793	ARSF_HUMAN		2	ATTATGGGTTTG	0.498	
+	4	1126		NM_001649	NP_001640	Q13796	SHRM2_HUMAN	Poly-Ala.	8	CTGCGGCACAG	0.677	
-	14	1715	_Mutation_p.D22	NM_031892	NP_114098	Q96B97	SH3K1_HUMAN		0	GGAGTCAAAAC	0.433	
-	1	649		NM_153270	NP_695002	Q8N239	KLH34_HUMAN	BTB.	1	TGCCCTCGGTC	0.657	

+	1	1488		NM_001013736	NP_001013758	Q5HY64	FA47C_HUMAN		3	CTCCCGACACT	0.622
+	18	2585	34_splice|SYTL5_	NM_001163335	NP_001156807	Q8TDW5	SYTL5_HUMAN		1	TCTTCAGGTGTG	0.507
-	1	338		NM_001013742	NP_001013764	Q5KSL6	DGKK_HUMAN	te tandem repeats of E-P-A	2	ctgggccggttctgag	0.174
+	1	660		NM_018094	NP_060564	Q8IYD1	ERF3B_HUMAN		1	AAATGGCCCTAG	0.517
+	2	806		NM_018969	NP_061842	Q9NS66	GP173_HUMAN	ellular (Potential).	1	CAAGGCCAATG	0.547
-	13	1414	p.R256Q|PFKFB1	NM_002625	NP_002616	P16118	F261_HUMAN	-2,6-bisphosphatase.	1	TTCTCCCGGTGT	0.557
+	6	1135	ense_Mutation_p.	NM_001145408	NP_001138880	Q15233	NONO_HUMAN	DBHS.	4	TGTGCGCTTTG	0.512
+	4	781	edf.2_Missense_M	NM_014499	NP_055314	O00398	P2Y10_HUMAN	lasmic (Potential).	5	TCAAGCCCTTC	0.512
+	4	2453	mg.1_Missense_	NM_152423	NP_689636	Q5H9M0	MUML1_HUMAN		4	TTGAGGATGAA	0.338
+	3	3433	sr.1_Missense_Mu	NM_020769	NP_065820	Q8NET4	RGAG1_HUMAN		4	TGACAGCCACA	0.532
+	1	132	1mts.1_Missense_	NM_006667	NP_006658	O00264	PGRC1_HUMAN	enal (Potential).	0	AGGATGTGGTG	0.637
-	1	401	uc004fbf.1_RNA	NM_004065	NP_004056	P51861	CDR1_HUMAN	pproximate repeats.|12.	0	CTTCCGAAAAAT	0.453
+	4	1259	EC1_uc010nsl.1_	NM_005462	NP_005453	O60732	MAGC1_HUMAN		4	CTGAGAGAACT	0.468
-	2	2723	fby.2_Missense_M	NM_173078	NP_775101	Q8IW52	SLIK4_HUMAN	lasmic (Potential).	2	TTTTTCTGGATA	0.383
+	7	1338		NM_005140	NP_005131	Q16280	CNGA2_HUMAN	ellular (Potential).	3	AATGTGGGCTCC	0.517
+	8	1129		NM_018558	NP_061028	Q9UN88	GBRT_HUMAN		3	CCGAAGAGTCA	0.522
+	11	2308	XNB3_uc010nuk.	NM_005393	NP_005384	Q9ULL4	PLXB3_HUMAN	ellular (Potential).	1	ATTTCCGAGTG	0.642
+	9	1009	vf.2_Missense_Mu	NM_001363	NP_001354	O60832	DKC1_HUMAN		0	ATGTGCTTGAT	0.433
+	2	367	4ftf.2_5'UTR|NLG	NM_014893	NP_055708	Q8NFZ3	NLGNY_HUMAN		0	CCCTCATTGAC	0.463
-	9	913	se_Mutation_p.W	NM_017871	NP_060341	Q5TA45	INT11_HUMAN		0	TTGGTCCAGGG	0.562
-	13	1314	a.2_Missense_Mu	NM_004421	NP_004412	O14640	DVL1_HUMAN	DEP.	0	GTCCGCCCCTG	0.697
-	4	460	K_uc001aie.2_Mi	NM_023018	NP_075394	O95544	NADK_HUMAN		0	ATCTCTCATCTT	0.602
-	2	860		NM_020710	NP_065761	Q8N1G4	LRC47_HUMAN		2	gctctcttccttctccGA	0.413
-	29	4390	P4_uc001alr.1_3'	NM_015102	NP_055917	O75161	NPHP4_HUMAN		1	TCCTCTCTGAAC	0.612
-	21	3362	a.1_RNA|CHD5_	NM_015557	NP_056372	Q8TDI0	CHD5_HUMAN	case C-terminal.	12	GGTACCATTGA	0.567
-	4	602	l.2_Missense_M	NM_012405	NP_036537	O60725	ICMT_HUMAN		0	CATGGCCGCCT	0.502
+	10	2963	A1_uc010nzv.1_5	NM_015215	NP_056030	Q9Y6Y1	CMTA1_HUMAN	IPT/TIG.	9	GCCTGGGGTGC	0.607
-	21	4459	p.L1217F|RERE_	NM_012102	NP_036234	Q9P2R6	RERE_HUMAN		2	ACTGAGGCGAC	0.642
-	14	2165	E_uc010nzx.1_Mi	NM_012102	NP_036234	Q9P2R6	RERE_HUMAN		2	GGTGCCTACGA	0.592
-	11	1467	7_splice|SLC2A5_	NM_003039	NP_003030	P22732	GTR5_HUMAN		3	GGGACCTGTAG	0.647
-	20	2277	asb.2_Missense_	NM_001001998	NP_001001998	Q01780	EXOSX_HUMAN		1	AGCTGCCTTCT	0.453
-	3	325	_p.G92E|EXOSC1	NM_001001998	NP_001001998	Q01780	EXOSX_HUMAN		1	GACACCCATGG	0.398
-	7	1350	atb.1_Splice_Site_	NM_005957	NP_005948	P42898	MTHR_HUMAN		0	CCTCACCAGCG	0.562
-	1	678		NM_001136561	NP_001130033	B2RXH8	B2RXH8_HUMAN		0	GAGAATCCACTT	0.443
+	8	3981	j.2_Intron|PRDM2	NM_012231	NP_036363	Q13029	PRDM2_HUMAN	g (Potential).|Pro-rich.	1	TGATGTCTGCCG	0.403
+	9	5916	.D179N|PRDM2_	NM_012231	NP_036363	Q13029	PRDM2_HUMAN		1	GTCCCGATGCT	0.587
+	6	530		NM_015849	NP_056933	P08218	CEL2B_HUMAN	eptidase S1.	1	GGGCTCTCCCT	0.567
+	11	7379	p.1_Missense_Mu	NM_015001	NP_055816	Q96T58	MINT_HUMAN	with MSX2 (By similarity).	15	CCATTCCACTC	0.502
-	6	886	m.2_Missense_M	NM_001136204	NP_001129676	Q9P258	RCC2_HUMAN	RCC1 4.	0	CAGGGCACCCA	0.418
-	6	1887		NM_152232	NP_689418	Q8TE23	TS1R2_HUMAN	ellular (Potential).	4	GGCAGGTGGAG	0.622
-	104	15279	n_p.S726F|UBR4_	NM_020765	NP_065816	Q5T4S7	UBR4_HUMAN		25	GGGAAGAACGG	0.468
-	35	4934	m.1_Missense_M	NM_020765	NP_065816	Q5T4S7	UBR4_HUMAN		25	TTCCTCTTCCAC	0.502
-	1	508	.2_Intron|CAPZB_	NM_004930	NP_004921	P47756	CAPZB_HUMAN		0	CCGAGGGACTT	0.552
-	8	1875	IF17_uc009vpx.2	NM_020816	NP_065867	Q9P2E2	KIF17_HUMAN		4	GCCCAGCGGCC	0.652
-	2	169	_p.V29M|ECE1_u	NM_001397	NP_001388	P42892	ECE1_HUMAN	lasmic (Potential).	3	GTCCACCAGGT	0.706
-	77	10668	d.2_Missense_Mu	NM_005529	NP_005520	P98160	PGBM_HUMAN	ike C2-type 21.	9	CGTGGGCGATC	0.622
-	57	7343	qd.2_Missense_M	NM_005529	NP_005520	P98160	PGBM_HUMAN	like C2-type 9.	9	GGTGACCCCAA	0.637

-	9	1065	nf.3_Missense_Mu	NM_001039775	NP_001034864	Q8N1P7	AIM1L_HUMAN		1	TTACCGTCCGG	0.597	
+	2	679		NM_000911	NP_000902	P41143	OPRD_HUMAN	lasmic (Potential).	2	TTGACCGCTACA	0.572	
-	6	1653	S4_uc010ofy.1_3'	NM_005626	NP_005617	Q08170	SRSF4_HUMAN	r-rich (RS domain).	0	CTCGACCTTCC	0.542	
-	4	1011	d.2_Missense_Mu	NM_014654	NP_055469	O75056	SDC3_HUMAN	ellular (Potential).	2	TCTCTTCTTCTG	0.617	
+	6	546	_p.A150V|KPNA6_	NM_012316	NP_036448	O60684	IMA7_HUMAN	(major) (By similarity).|ARM	0	ATATTGCCTCTG	0.453	
+	11	1292	hj.1_Missense_Mu	NM_005610	NP_005601	Q09028	RBBP4_HUMAN	WD 6.	1	AGATATCTGATT	0.363	
+	6	2076	522_uc010ohm.1_	NM_020888	NP_065939	Q9P206	K1522_HUMAN	Pro-rich.	0	TCAGTCCCCTC	0.617	
-	5	1243	_p.V414I|RNF19B	NM_153341	NP_699172	Q6ZMZ0	RN19B_HUMAN	ical; (Potential).	0	AATAACTGGGG	0.463	
-	13	2207	p.G719D|PHC2_u	NM_198040	NP_932157	Q8IXK0	PHC2_HUMAN		1	ACAGTGCCTGTT	0.498	
-	12	2058	69_splice|PHC2_	NM_198040	NP_932157	Q8IXK0	PHC2_HUMAN		1	TTGTACCTTCAG	0.567	
+	10	1334		NM_017629	NP_060099	Q9HCK5	AGO4_HUMAN		1	GGTGGACCTGAT	0.443	
+	4	671	e_Mutation_p.P78	NM_012199	NP_036331	Q9UL18	AGO1_HUMAN		3	TGTTCCCTTGG	0.542	
+	5	1659	p.P479S|THRAP3	NM_005119	NP_005110	Q9Y2W1	TR150_HUMAN		9	CACCTCCAGGG	0.483	
-	14	2093		NM_013285	NP_037417	Q13823	NOG2_HUMAN		2	TTCTTCCAGTG	0.333	
-	2	368	_p.D82N|RRAGC	NM_022157	NP_071440	Q9HB90	RRAGC_HUMAN	(By similarity).	1	GAAAATCCCATA	0.408	
+	10	1584		NM_005857	NP_005848	O75844	FACE1_HUMAN		0	ATTATTCTCATCC	0.388	
+	55	7748	1cjl.1_Missense_	NM_015284	NP_056099	Q5T011	SZT2_HUMAN		0	TCCTATCCATGA	0.572	
+	10	1529	oki.1_Splice_Site_	NM_014663	NP_055478	O75164	KDM4A_HUMAN		1	TCCCAGGTTAGT	0.502	
+	6	478	76S|ATP6V0B_u	NM_004047	NP_004038	Q99437	VATO_HUMAN	lasmic (Potential).	1	CAGACCCCAAG	0.517	
-	22	3524	lg.1_Missense_Mu	NM_003738	NP_003729	Q9Y6C5	PTC2_HUMAN	lasmic (Potential).	18	AGGCACCAGGC	0.657	
+	7	1410	uc010oll.1_5'Flan	NM_025077	NP_079353	Q96GM8	TOE1_HUMAN		1	TTCCAGCATGA	0.577	rs142271220
-	6	633	T1_uc001cpg.2_M	NM_017739	NP_060209	Q8WZA1	PMGT1_HUMAN	enal (Potential).	1	CTCATCCTCAT	0.547	
+	2	351	UN4_uc009vyg.1_	NM_199044	NP_950245	Q96CB9	NSUN4_HUMAN		0	CTTTGCTGCCT	0.493	
-	8	1027	STIL_uc001crd.1_	NM_003035	NP_003026	Q15468	STIL_HUMAN		3	CTTGCCTTTCTT	0.348	
+	10	1126	ctw.3_Missense_	NM_032864	NP_116253	Q8NAV1	PR38A_HUMAN		0	GAGCCGGAGAG	0.348	
+	3	668	.1_Intron|FAM159	NM_001042693	NP_001036158	Q6UWV7	F159A_HUMAN		0	CCAGTCCCATAA	0.498	
+	16	3071	1orf175_uc010oog	NM_001039464	NP_001034553	Q68CQ1	HEAT8_HUMAN		0	ACTGAGGATGG	0.597	
+	8	1064	ya.3_Missense_	NM_001110533	NP_001104003	Q3ZCV2	CA177_HUMAN		0	CAAGGGGTCAG	0.552	
-	5	669	p.S139F|C8B_uc	NM_000066	NP_000057	P07358	CO8B_HUMAN	MACPF.	4	GCGGGGAGCAT	0.398	
-	5	1043	se_Mutation_p.H3	NM_145243	NP_660286	Q96E52	OMA1_HUMAN		1	GTTGATGAATAT	0.338	
-	3	594	3_Intron|KANK4_u	NM_181712	NP_859063	Q5T7N3	KANK4_HUMAN		6	GCTGAAGTTTC	0.562	
-	10	1110	p.A251V|DOCK7_	NM_033407	NP_212132	Q96N67	DOCK7_HUMAN		2	GTTCTGCACAC	0.328	
+	20	2740	dbq.1_Missense_	NM_020925	NP_065976	Q5VU97	CAHD1_HUMAN	ellular (Potential).	2	GGATCCCAGGA	0.498	
+	7	832	pc.1_Missense_	NM_014787	NP_055602	O75061	AUXI_HUMAN		3	CAAGCCCTACC	0.478	
-	11	1246		NM_000329	NP_000320	Q16518	RPE65_HUMAN		1	CTCGTCACTGC	0.473	
-	12	2338	73_uc001dgi.3_Mi	NM_001002912	NP_001002912	Q5RHP9	CA173_HUMAN	Glu-rich.	5	TGCTTTCTTCCC	0.478	
-	3	1251	BL2_uc001dmr.2_	NM_001162536	NP_001156008	Q96E39	RBMXL_HUMAN		0	CTCTTCCTCCCA	0.517	
-	3	1011	CBL2_uc001dmr.2	NM_001162536	NP_001156008	Q96E39	RBMXL_HUMAN		0	TGGAGGTGGGG	0.512	
+	11	2046	st.1_Missense_Mu	NM_198460	NP_940862	Q6ZN66	GBP6_HUMAN		2	ATACTCCCTGGA	0.393	
+	3	2983	dnn.2_Missense_	NM_001134479	NP_001127951	Q7L1W4	LRC8D_HUMAN		2	ATATTCCCTTTGC	0.393	
-	4	3318	.2_Intron|ZNF644_	NM_201269	NP_958357	Q9H582	ZN644_HUMAN	2H2-type 7.	3	AGTGGCCTCTA	0.363	
+	3	185	f146_uc010ote.1_	NM_001012425	NP_001012425	Q5VVC0	CA146_HUMAN		1	AAGTTCGATATT	0.299	
-	45	3760	.P1160S|COL11A1	NM_001854	NP_001845	P12107	COBA1_HUMAN	le-helical region.	12	GGGAGGGCCCT	0.448	
-	18	2156	OL11A1_uc001du	NM_001854	NP_001845	P12107	COBA1_HUMAN	le-helical region.	12	TGTGACCTTTG	0.299	
-	5	602	e_Mutation_p.W1	NM_001048210	NP_001041675	Q96S66	CLCC1_HUMAN		1	CCACTTCCATGT	0.368	
+	3	575	dxw.2_3'UTR|CY	NM_182580	NP_872386	Q8N8Q1	C56D1_HUMAN	b561.|Helical; (Potential).	0	GACTGGTGGTC	0.592	
-	1	1830		NM_002232	NP_002223	P22001	KCNA3_HUMAN		5	TCATACCCCCCT	0.517	

-	2	694	ebp.1_Missense_M	NM_019099	NP_061972	Q9NTI7	CA183_HUMAN		2	TTCTCCCCACCC	0.592
+	8	1156	ww.1_Missense_M	NM_000701	NP_000692	P05023	AT1A1_HUMAN	lasmic (Potential).	1	CCACACTTGCTT	0.498
-	2	1130	_p.G181D|TRIM45	NM_025188	NP_079464	Q9H8W5	TRI45_HUMAN		1	CTGTAGCCTTTC	0.512
-	5	818	_p.S154N|VTCN1_	NM_024626	NP_078902	Q7Z7D3	VTCN1_HUMAN	ellular (Potential).	0	GGTGACTCCGC	0.453
-	15	2148		NM_206996	NP_996879	Q6Q759	SPG17_HUMAN		6	ACTAGGATCTG	0.373
+	14	1459		NM_003568	NP_003559	O76027	ANXA9_HUMAN	Annexin 4.	0	GAAAGGGGATT	0.552
+	7	1047	.1_Missense_Mut	NM_021222	NP_067045	Q86TP1	PRUNE_HUMAN		1	CTGTCCCCATGT	0.502
+	9	3715	_Mutation_p.G120	NM_020832	NP_065883	Q8N1G0	ZN687_HUMAN	2H2-type 10.	4	CTGTGGCAAGA	0.617
-	6	1157	Z_uc010pdc.1_Mi	NM_015100	NP_055915	Q7Z3K3	POGZ_HUMAN		3	GCTTGGGATTC	0.557
-	2	371	0pdc.1_Missense_	NM_015100	NP_055915	Q7Z3K3	POGZ_HUMAN		3	ACATCACTGATTT	0.388
-	2	1127		NM_001004432	NP_001004432	Q6UY18	LIGO4_HUMAN	ar (Potential).|LRR 10.	1	GGAGGTGAGGC	0.602
-	2	2866	e.1_Missense_Mu	NM_007113	NP_009044	Q07283	TRHY_HUMAN	30 AA tandem repeats.	5	TTCCCGCTCCT	0.333
-	3	6755		NM_002016	NP_002007	P20930	FILA_HUMAN	ich.|Filaggrin 13.	16	TGGATCCCCGG	0.582
-	3	7173	uc001ezv.2_Intron	NM_001014342	NP_001014364	Q5D862	FILA2_HUMAN		17	TTCTGCTGCCA	0.453
-	4	956		NM_006694	NP_006685	O76095	JTB_HUMAN	ellular (Potential).	0	CATATCCTGTGG	0.443
-	3	464	nse_Mutation_p.A	NM_152263	NP_689476	P06753	TPM3_HUMAN	By similarity.	34	TTTCAGCTTCTTC	0.498
+	21	2251		NM_020452	NP_065185	P98198	AT8B2_HUMAN	lasmic (Potential).	2	CCCGGGAGAAG	0.542
-	2	411	_uc001ffk.2_5'UT	NM_001111	NP_001102	P55265	DSRAD_HUMAN		6	CCGGAGTCCTG	0.562
-	3	456		NM_138300	NP_612157	Q9BRQ0	PYGO2_HUMAN	Pro-rich.	1	GGGGGCTCCGA	0.617
+	10	2224	nse_Mutation_p.L	NM_025058	NP_079334	Q7Z4K8	TRI46_HUMAN	B30.2/SPRY.	3	GCTCTTGGAGT	0.657
-	9	984	_p.A321T|THBS3_	NM_007112	NP_009043	P49746	TSP3_HUMAN	alcium-binding (Potential).	5	GTGAGCACACT	0.617
-	4	608	tion_p.E119K|SCA	NM_005698	NP_005689	O14828	SCAM3_HUMAN	lasmic (Potential).	3	CAGCTCTCGCT	0.577
+	2	329	.2_Missense_Muta	NM_014655	NP_055470	Q96H78	S2544_HUMAN		1	TGGAGGACAAA	0.512
-	18	2776	G5_uc009wrv.2_In	NM_015327	NP_056142	Q9UPR3	SMG5_HUMAN	PINc.	5	CACTGGTGGCC	0.502
-	4	767	n_p.E252K|C1orf8	NM_144580	NP_653181	Q8WWB7	NCUG1_HUMAN	enal (Potential).	2	CTGCTCCTGCA	0.607
-	3	179	1fpl.2_Missense_M	NM_015590	NP_056405	Q5T3I0	GPTC4_HUMAN	G-patch.	1	TCACCCTGAGA	0.572
-	2	165	RL1_uc001fri.2_M	NM_052938	NP_443170	Q96LA6	FCRL1_HUMAN	otential).|Ig-like C2-type 1.	7	CTCACCGGCAG	0.483
+	3	650	D_uc009wss.2_M	NM_001766	NP_001757	P15813	CD1D_HUMAN	ellular (Potential).	1	GGCTGGGGGAG	0.647
-	2	307	1_Intron|CRP_uc0	NM_000567	NP_000558	P02741	CRP_HUMAN	Pentaxin.	1	AAAATACTGTACC	0.443
+	17	2476	_p.P782S|ATP1A2_	NM_000702	NP_000693	P50993	AT1A2_HUMAN	ical; (Potential).	7	AACATCCCCGAG	0.552
+	10	1239	_p.T234I|NCSTN_	NM_015331	NP_056146	Q92542	NICA_HUMAN	ellular (Potential).	2	TAAGAACTTCATT	0.483
-	4	561	p.A130T|DEDD_u	NM_001039712	NP_001034801	O75618	DEDD_HUMAN		0	GAGGGCTCTGG	0.473
+	3	940	kd.1_Missense_M	NM_001014443	NP_001014443	Q9UK80	UBP21_HUMAN		5	ATCCGCCCGGT	0.577
+	6	843	POX_uc001fyh.2_	NM_001122764	NP_001116236	P50336	PPOX_HUMAN		1	TGCTTTCCCAGT	0.542
-	4	617	S5_uc009wvb.2_F	NM_003617	NP_003608	O15539	RGS5_HUMAN	RGS.	0	AGCCTCCGTTT	0.478
-	2	412		NM_199351	NP_955383	Q71H61	ILDR2_HUMAN	.|Extracellular (Potential).	1	CTCTGCCCCTG	0.463
+	15	1700	e_Mutation_p.P45	NM_002697	NP_002688	P14859	PO2F1_HUMAN		5	AGCGCCTCCAG	0.532
+	5	893	ZL1_uc001geq.2_I	NM_003953	NP_003944	O95297	MPZL1_HUMAN	lasmic (Potential).	2	AGTCTGCCTTCT	0.507
-	13	3902		NM_000130	NP_000121	P12259	FA5_HUMAN	dem repeats of [TNP]-L-S-	6	GCTGAGGTCTA	0.527
+	7	1209	_p.P358L|FMO1_u	NM_002021	NP_002012	Q01740	FMO1_HUMAN		1	CTTCCCTGCACA	0.483
+	4	1524	gib.2_Missense_M	NM_015935	NP_057019	Q8N6R0	MTL13_HUMAN		1	GCAGCCCCTTG	0.547
+	2	202	c009wwf.2_Intron|	NM_014458	NP_055273	Q9Y2M5	KLH20_HUMAN		1	GCGCAGGTAGG	0.348
-	11	1979	gjv.2_Missense_Mu	NM_172071	NP_742068	Q5TC82	RC3H1_HUMAN	Pro-rich.	2	CAGGAGCAGAT	0.488
+	10	1264		NM_015602	NP_056417	Q5JTV8	TOIP1_HUMAN	ical; (Potential).	2	TTGCCTCTGGGA	0.433
+	10	1830		NM_015602	NP_056417	Q5JTV8	TOIP1_HUMAN	enal (Potential).	2	CTTAAAGTCAAGT	0.418
+	38	9655	.G1226E|CEP350	NM_014810	NP_055625	Q5VT06	CE350_HUMAN		4	CGACGGGATCT	0.443
+	28	5050		NM_002293	NP_002284	P11047	LAMC1_HUMAN	al.|Domain II and I.	5	TACCATCTGGCT	0.537

+	68	10733		NM_031935	NP_114141	Q96RW7	HMCN1_HUMAN	ike C2-type 33.	23	GATTCGGGAAAG	0.483
+	12	1582	_p.V427I|CAMSAF	NM_203459	NP_982284	Q08AD1	CAMP2_HUMAN		4	CATGGCGTATCA	0.294
+	28	5835	vx.2_Missense_Mu	NM_020443	NP_065176	Q8NEY1	NAV1_HUMAN		4	GGACAGTCAAA	0.502
+	4	617		NM_198149	NP_937792	Q96DD7	SHSA4_HUMAN	ic (Potential).|Pro-rich.	0	GCTGGGCCCCCA	0.612
+	5	382		NM_006335	NP_006326	Q99595	TI17A_HUMAN	ical; (Potential).	0	GGTCAGCCGCA	0.398
+	3	709	RNPEP_uc001gxf.2	NM_020216	NP_064601	Q9H4A4	AMPB_HUMAN		1	CCATCCCCTCCT	0.527
+	15	1304	R6_uc009xab.2_R	NM_001017403	NP_001017403	Q9HBX8	LGR6_HUMAN	xtracellular (Potential).	10	GCTGACCACAC	0.572
+	20	3011	p.D799N|ZC3H11	NM_014827	NP_055642	O75152	ZC11A_HUMAN		2	GAAGATGACCTT	0.403
-	3	2183	p.V599M|LRRN2_	NM_006338	NP_006329	O75325	LRRN2_HUMAN	cellular (Potential).	2	GGCCACTTGCA	0.637
-	2	554	bx.2_Missense_Mu	NM_015375	NP_056190	Q6XUX3	DUSTY_HUMAN		1	CAGGCTGACCC	0.602
-	17	1891	_p.V261I|SLC26A	NM_052934	NP_443166	Q7LBE3	S26A9_HUMAN	STAS.	2	GGAGACAGTCT	0.612
+	25	4167	p.G893R|CR1_uc0	NM_000573	NP_000564	P17927	CR1_HUMAN	ar (Potential).|Sushi 21.	3	CCTATGGAAAA	0.468
-	13	2317	_Missense_Mutatic	NM_001017402	NP_001017402	Q13751	LAMB3_HUMAN	Domain II.	6	TGTGACTGCGG	0.587
+	16	1849	_p.P500L|TRAF3I	NM_025228	NP_079504	Q9Y228	T3JAM_HUMAN	lasmic (Potential).	2	TGCCTCCCAGAG	0.498
+	11	1562	.R523C|RCOR3_	NM_018254	NP_060724	Q9P2K3	RCOR3_HUMAN	Pro-rich.	1	CACCCCGTCTA	0.527
+	7	924	e_Mutation_p.Q16	NM_016448	NP_057532	Q9NZJ0	DTL_HUMAN		0	AAGAAACAGAAT	0.388
-	7	653	uh.1_Missense_Mu	NM_006085	NP_006076	O95861	BPNT1_HUMAN		1	CATCTGGTCCTG	0.428
+	11	1714	un.1_Missense_Mu	NM_018650	NP_061120	Q9P0L2	MARK1_HUMAN		10	AACCACCTGAA	0.299
-	9	1008	DA_uc010pus.1_M	NM_022831	NP_073742	Q96BJ3	AIDA_HUMAN		0	GGCCCAGGTTTA	0.358
+	3	679		NM_032890	NP_116279	Q96F81	DISP1_HUMAN		0	AGTTGCCAAAA	0.318
-	3	218	/L_uc010pve.1_5'U	NM_002533	NP_002524	O15381	NVL_HUMAN		2	TTTCTACCTGAAT	0.294
-	7	1095	nse_Mutation_p.A	NM_013328	NP_037460	Q96C36	P5CR2_HUMAN		0	CAGGGCCAGGC	0.612
-	1	327	n_p.R83*|LEFTY2_	NM_003240	NP_003231	O00292	LFTY2_HUMAN		0	ACCTCGGAAGC	0.687
-	7	1396		NM_022735	NP_073572	Q9H3P7	GCP60_HUMAN	GOLD.	0	CGCTGGACTCA	0.473
-	4	874	47_uc001hrf.2_5'F	NM_023007	NP_075383	Q9H9V9	JMJD4_HUMAN	JmjC.	0	CAGCAAGCTGGT	0.647
+	55	14734	sn.2_Missense_Mu	NM_001098623	NP_001092093	Q5VST9	OBSCN_HUMAN	IQ.	28	GGAAGGGCCCA	0.602
-	2	435	M17_uc001hsw.2_I	NM_016102	NP_057186	Q9Y577	TRI17_HUMAN	RING-type.	1	CAGATGGAGCAC	0.403
+	4	2114	d.1_Missense_Mu	NM_014777	NP_055592	Q14146	URB2_HUMAN		3	AAGATAGAGAAG	0.443
+	4	989	p.G181S|C1orf12	NM_032018	NP_114407	Q9H040	CA124_HUMAN		0	TATTACGGCTAT	0.517
+	1	1829		NM_019090	NP_061963	Q9P2G4	K1383_HUMAN		1	ACCTAGCCTGGT	0.448
-	5	795	u.2_RNA|PCNXL2	NM_014801	NP_055616	A6NKB5	PCX2_HUMAN		2	GAGGTAGATGAC	0.438
-	9	895	o.2_RNA|ARID4B_	NM_015014	NP_055829	P42696	RBM34_HUMAN	RRM 2.	1	CAAAAACCGATC	0.338
-	6	773	hws.3_Splice_Site	NM_016374	NP_057458	Q4LE39	ARI4B_HUMAN		3	CAAAAACTATGAG	0.368
-	5	2142	ks.1_RNA|LYST_u	NM_000081	NP_000072	Q99698	LYST_HUMAN		12	AGTTTCCCTGCA	0.408
-	3	311	se_Mutation_p.L4	NM_000081	NP_000072	Q99698	LYST_HUMAN		12	GGACAAGGTACT	0.428
-	13	2773	e_Mutation_p.G75	NM_002508	NP_002499	P14543	NID1_HUMAN	oglobulin type-1.	2	TGCTGCCGTGGC	0.716
+	79	11187	ya.1_Missense_M	NM_001035	NP_001026	Q92736	RYR2_HUMAN		33	ATATATGGCCTAT	0.358
+	1	811	ye.1_Missense_Mu	NM_020066	NP_064450	Q9NZ56	FMN2_HUMAN	Potential.	12	GATTTGCTTTCA	0.408
-	5	505	ibk.2_Missense_M	NM_022743	NP_073580	Q9H7B4	SMYD3_HUMAN	SET.	0	TCTTCAGTCAGT	0.368
+	1	340		NM_001004136	NP_001004136	Q6IF00	OR2T2_HUMAN	Name=3; (Potential).	1	GAATTCTTCCTG	0.537
+	1	37		NM_001013355	NP_001013373	Q5TZ20	OR2G6_HUMAN	cellular (Potential).	3	GGATTTCTTCTC	0.423
-	3	380	ihz.2_Missense_M	NM_024803	NP_079079	A6NHL2	TBAL3_HUMAN		1	GTAACGGCCTC	0.632
-	1	367	107B_uc010qbu.1_	NM_031453	NP_113641	Q9H098	F107B_HUMAN		4	AGCCACGCCGG	0.552
+	2	558	ense_Mutation_p.E	NM_024670	NP_078946	Q9H5I1	SUV92_HUMAN	Pre-SET.	3	ATCTATGAATGCA	0.403
+	6	1420	e_p.E212_splice|P	NM_032812	NP_116201	Q6UX71	PXDC2_HUMAN		4	AAGAAGTAAGT	0.438
-	1	608		NM_001034842	NP_001030014	Q3KNS1	PTHD3_HUMAN		4	CTTCCTCTTCGT	0.657
-	7	1067	p.H211L|ZNF438_	NM_182755	NP_877432	Q7Z4V0	ZN438_HUMAN		2	CTGCCATGGGTG	0.557

+	7	860		NM_052997	NP_443723	Q9BXX3	AN30A_HUMAN		9	CCTTGGTGGAAA	0.502	
+	9	1532		NM_014753	NP_055568	Q14692	BMS1_HUMAN		3	GTCGAGTGACG	0.438	
+	6	1416	p.S409F|RET_uc0	NM_020975	NP_066124	P07949	RET_HUMAN	cellular (Potential).	451	CCTACTCCCTCT	0.617	
+	7	787	_p.G211D|NCOA4_	NM_001145263	NP_001138735	Q13772	NCOA4_HUMAN		2	CATCCGGTATTG	0.348	
-	2	176	n_p.D8N|EGR2_u	NM_001136177	NP_001129649	P11161	EGR2_HUMAN		2	TTTTGTCTACGG	0.557	
-	15	2158	mw.2_Missense_M	NM_001127384	NP_001120856	Q9UI47	CTNA3_HUMAN		8	TGAAATCAGCAA	0.378	
-	3	728	41_splice|RUFY2_	NM_017987	NP_060457	Q8WXA3	RUFY2_HUMAN		1	TCCTTACTTCAG	0.463	
+	2	1640		NM_030625	NP_085128	Q8NFU7	TET1_HUMAN		9	GAACTTCCTGGT	0.507	
+	5	804	p.D233N|DDX50_u	NM_024045	NP_076950	Q9BQ39	DDX50_HUMAN	ase ATP-binding.	1	TTCAAAGATATA	0.373	
+	2	187	G21R|VPS26A_uc	NM_004896	NP_004887	O75436	VP26A_HUMAN		0	ATGATGGGGAA	0.348	
+	2	369		NM_019058	NP_061931	Q9NX09	DDIT4_HUMAN		1	GCGAGTCCCTGG	0.726	
-	18	3667	p.G305D|USP54_u	NM_152586	NP_689799	Q70EL1	UBP54_HUMAN		6	GTTTCACCATTAG	0.512	
-	30	5525	p.D574N|DLG5_uc	NM_004747	NP_004738	Q8TDM6	DLG5_HUMAN	ylate kinase-like.	8	CAATGTCCAGGA	0.612	
-	8	1035	1P_uc001kbf.2_In	NM_003019	NP_003010	P35247	SFTPD_HUMAN	C-type lectin.	1	CCAGGGACTCT	0.567	
+	2	575		NM_002729	NP_002720	Q03014	HHEX_HUMAN	Homeobox.	1	GTCTGGCCAAGA	0.637	
+	2	600	92K|CYP2C19_uc	NM_000772	NP_000763	P33260	CP2CI_HUMAN		5	CATGGAGAGGAG	0.433	
-	7	1239	nse_Mutation_p.P	NM_000770	NP_000761	P10632	CP2C8_HUMAN		0	CCTTGGGGATGA	0.453	
-	28	3425	m.2_Missense_Mu	NM_015179	NP_055994	Q5JTH9	RRP12_HUMAN		3	GCTGCTCCTTGC	0.587	
-	14	1715	ou.1_Missense_M	NM_015179	NP_055994	Q5JTH9	RRP12_HUMAN		3	TGTGGGGGAAAT	0.597	
-	20	2147	knr.2_Missense_M	NM_022362	NP_071757	Q96T76	MMS19_HUMAN		0	ACTGAGGGCTCC	0.478	
+	13	2059	A4G_uc001krx.2_I	NM_017893	NP_060363	Q9NTN9	SEM4G_HUMAN	lular (Potential).|PSI.	1	CCACCACCATAG	0.627	
+	6	1519		NM_030912	NP_112174	Q9BZR9	TRIM8_HUMAN		1	AAGATTCTCGTC	0.637	
-	4	435	0qqu.1_Missense_	NM_014631	NP_055446	Q5TCZ1	SPD2A_HUMAN	PX.	0	AGTATTCATCGAT	0.592	
+	9	1071	p.1_Missense_Mut	NM_014720	NP_055535	Q9H2G2	SLK_HUMAN	Glu-rich.	8	GTATCGCCAGCT	0.353	
+	2	190		NM_001008723	NP_001008723	Q5T655	CC147_HUMAN		5	AAGAAATGGAAA	0.388	
+	3	1151	el.2_Missense_Mut	NM_004281	NP_004272	O95817	BAG3_HUMAN		2	AGCCAGGAGCA	0.657	
+	20	2453	ep.2_Missense_Mu	NM_014937	NP_055752	Q9Y2H2	SAC2_HUMAN		2	GGTATCAGGTCT	0.358	
-	7	1005	1les.1_Missense_	NM_024834	NP_079110	Q9BTE3	MCMBP_HUMAN		0	GCAGGGCCCTTC	0.398	
-	9	2256	.1_Missense_Muta	NM_018180	NP_060650	Q7L7V1	DHX32_HUMAN		4	GTTCAGCTCGAA	0.423	
-	19	2578	qul.1_Missense_M	NM_003474	NP_003465	O43184	ADA12_HUMAN	ical; (Potential).	9	CGGCAGCAAGA	0.418	
-	13	2828	av.1_Missense_Mu	NM_002417	NP_002408	P46013	KI67_HUMAN		7	TCTGTAGACCTT	0.413	
-	3	359	BNIP3_uc010qut.1_	NM_004052	NP_004043	Q12983	BNIP3_HUMAN		2	GAAGCTCTGTTG	0.423	rs143231747
+	17	2119	yba.1_Missense_M	NM_001105521	NP_001098991				1	ATGGTGGATCTG	0.617	
+	18	2203	yba.1_Nonsense_	NM_001105521	NP_001098991				1	TTGGACCAGGCC	0.632	
+	3	886	se_Mutation_p.S2	NM_152911	NP_690875	Q6QHF9	PAOX_HUMAN		0	CAGTGTCGGTAG	0.582	rs139393085
+	2	432	ybv.1_Missense_M	NM_030783	NP_110410	Q9BVG9	PTSS2_HUMAN	cellular (Potential).	0	GAAACACCTCAG	0.562	
+	9	1193		NM_002457	NP_002448	Q02817	MUC2_HUMAN		2	GCCCCGGCACCT	0.652	
+	16	1990		NM_017511	NP_059981	Q9HC84	MUC5B_HUMAN	VWFD 2.	0	AGCGTGGAGAAT	0.657	
+	1	240	uc001lwe.2_Intron	NM_004356	NP_004347	P60033	CD81_HUMAN	lasmic (Potential).	0	TGGGAGTGGAGG	0.338	
+	1	353		NM_001004759	NP_001004759	Q8NGJ9	O51T1_HUMAN	cellular (Potential).	3	TTCATGCCCGGG	0.493	
+	1	847		NM_001004749	NP_001004749	Q8NH64	O51A7_HUMAN	Name=7; (Potential).	2	TTGGTGCCGCCC	0.458	
+	1	583	_uc001mam.1_Int	NM_001004756	NP_001004756	B2RNI9	B2RNI9_HUMAN		0	CACCAGGAAGTG	0.517	
-	1	49		NM_001004052	NP_001004052	Q96RD2	O52B2_HUMAN	cellular (Potential).	0	TGCCAGGAAGGA	0.453	
-	4	508	f.3_5'UTR|SBF2_u	NM_030962	NP_112224	Q86WG5	MTMRD_HUMAN	DENN.	3	TGGATACCAACA	0.358	
-	15	2146	5A12_uc001mrb.2_	NM_178498	NP_848593	Q1EHB4	SC5AC_HUMAN	lasmic (Potential).	2	AAATGCCATATTG	0.358	
+	3	720	e_Mutation_p.P101	NM_002901	NP_002892	Q15293	RCN1_HUMAN		1	GGAAACCCCGCA	0.453	
+	4	570	e_Mutation_p.G10	NM_021117	NP_066940	Q49AN0	CRY2_HUMAN	A photolyase.	1	TGAATGGGCAGA	0.567	

+	3	753	0652_uc001ncz.2_	NM_001142673	NP_001136145	O75143	ATG13_HUMAN		0	CTCAAGGTAATG	0.383	
+	9	1687	n.1_Missense_Mu	NM_003682	NP_003673	Q8WXG6	MADD_HUMAN	dDENN.	11	CAATTCCGCCA	0.522	
-	1	269		NM_001005245	NP_001005245	Q96RB7	OR5MB_HUMAN	ellular (Potential).	0	GAAATGGTCTTC	0.443	
-	3	344	nko.1_Missense_M	NM_004223	NP_004214	O14933	UB2L6_HUMAN		1	ATCTGTCCGTTC	0.547	
+	6	1173	lissense_Mutation	NM_001085458	NP_001078927	O60716	CTND1_HUMAN		6	CTGCTACCCTTC	0.507	
+	4	948	.14_uc001npk.2_M	NM_032597	NP_115986	Q96JA4	M4A14_HUMAN	ical; (Potential).	1	CTTTCACCATTCT	0.368	
+	3	457	yna.2_Missense_M	NM_152866	NP_690605	P11836	CD20_HUMAN	lasmic (Potential).	5	CCCGGCAGAGC	0.438	
+	12	2144	6_uc001nqs.2_Int	NM_006725	NP_006716	P30203	CD6_HUMAN	lasmic (Potential).	1	CCTTCGGAGGAG	0.612	
-	5	10006	AK_uc001ntk.1_Ir	NM_001620	NP_001611	Q09666	AHNK_HUMAN		19	CCACCTCTCCTT	0.403	
-	19	1402	AP4K2_uc001obi	NM_004579	NP_004570	Q12851	M4K2_HUMAN		2	GGGAGCTGTTG	0.672	
-	5	800		NM_080668	NP_542399	Q96FF9	CDCA5_HUMAN		0	TCTCGGGTGGT	0.572	
+	9	1223	p.G288D|FRMD8_	NM_031904	NP_114110	Q9BZ67	FRMD8_HUMAN	FERM.	2	CGAGGGCACAC	0.667	
+	19	3831	M2A_uc001ojz.1_	NM_012308	NP_036440	Q9Y2K7	KDM2A_HUMAN	LRR 2.	9	CTCCTGGTCTGC	0.532	
+	23	4804	g.2_Missense_Mu	NM_002335	NP_002326	O75197	LRP5_HUMAN	toplasmic (Potential).|Pro-	7	CCCCACCCACG	0.662	
-	22	5384	ation_p.L1174Q|uc	NM_012309	NP_036441	Q9UPX8	SHAN2_HUMAN		5	GTTGCAGTATC	0.512	
+	1	2762		NM_014786	NP_055601	Q96PE2	ARHGH_HUMAN		0	TCTGTCCCCGA	0.632	
+	3	226	.L21F|RELT_uc00	NM_152222	NP_689408	Q969Z4	TR19L_HUMAN		1	GGCCTCTCGCC	0.602	
+	5	986	s.1_Missense_Mu	NM_007256	NP_009187	O94956	SO2B1_HUMAN	Name=4; (Potential).	2	GCTGGGCGTGG	0.607	
-	5	548	TS4_uc001oyu.1_	NM_033547	NP_291025	Q96HW7	INT4_HUMAN	HEAT 2.	2	GCCAAGTAACT	0.353	
+	6	2302	su.1_Missense_Mu	NM_015885	NP_056969	O94913	PCF11_HUMAN		1	CAGATTCCTAAA	0.388	
+	8	2515	su.1_Missense_Mu	NM_015885	NP_056969	O94913	PCF11_HUMAN	Gly-rich.	1	GATAAACCATTT	0.403	
+	8	2965	u.1_Missense_Mu	NM_015885	NP_056969	O94913	PCF11_HUMAN	Gly-rich.	1	CTGTGGGTGGT	0.542	
+	4	755	to.1_RNA|C11orf7	NM_016401	NP_057485	Q53FT3	CK073_HUMAN		0	TTCATTCCGGCA	0.358	
+	4	3946		NM_001008781	NP_001008781	Q8TDW7	FAT3_HUMAN	.|Extracellular (Potential).	5	CTAAAACTGGGA	0.458	
+	9	5593		NM_001008781	NP_001008781	Q8TDW7	FAT3_HUMAN	.|Extracellular (Potential).	5	GTAGCCCCCAAC	0.463	
+	5	996	uc001pen.1_RNA	NM_001098672	NP_001092142	Q6MZM0	HPHL1_HUMAN	e 2.|Extracellular (Potential	3	ACTTCCCGGAGC	0.468	rs141998596
+	2	1072		NM_015036	NP_055851	O94919	ENDD1_HUMAN		0	CTCATGGGCTTC	0.428	
-	2	253	1piz.2_Missense_	NM_032424	NP_115800	Q8NCY6	K1826_HUMAN		1	TCTTTCCTTTTC	0.348	
-	6	865	z.1_Missense_Mu	NM_015065	NP_055880	Q8NEV8	EXPH5_HUMAN		5	ACCATGTCTGTT	0.403	
+	2	825	pns.2_3'UTR|uc010rwu.1_5'Flank			P13591	NCAM1_HUMAN	lasmic (Potential).	1	CACAGACAAAGG	0.502	
+	3	1317	L_uc001psz.1_Mi	NM_005933	NP_005924	Q03164	MLL1_HUMAN		25	AGGATGAGGAT	0.458	
-	2	1260	zal.2_Missense_M	NM_182557	NP_872363	Q86UU0	BCL9L_HUMAN		2	CCCTGCCTGGG	0.642	
+	4	846	PC4_uc001pup.2_	NM_016146	NP_057230	Q9Y296	TPPC4_HUMAN		0	CTATCAGGTAAGT	0.428	
-	4	1259	_p.E118K|TRIM2	NM_012101	NP_036233	Q14134	TRI29_HUMAN		4	CAAATTCCTACC	0.557	
-	1	681	M29_uc001pxa.2_	NM_012101	NP_036233	Q14134	TRI29_HUMAN		4	GGCAGGACTTG	0.662	
+	7	1667		NM_005422	NP_005413	O75443	TECTA_HUMAN		10	GTGCAGTGTGA	0.577	
+	8	1965		NM_025004	NP_079280	Q0P6D6	CCD15_HUMAN		2	AAGGTGTTCTTC	0.423	
+	8	2007		NM_025004	NP_079280	Q0P6D6	CCD15_HUMAN		2	AGGACCAGGATT	0.438	
+	1	596	1_5'Flank|NCAPD	NM_052875	NP_443107	Q4G0F5	VP26B_HUMAN		0	GGTCTCCGGGA	0.587	
+	14	2015	p.E575G|B4GALN	NM_173593	NP_775864	Q6L9W6	B4GN3_HUMAN	enal (Potential).	2	CTCTGGAGGTCA	0.597	
-	9	857	issense_Mutation_	NM_134424	NP_602296	P43351	RAD52_HUMAN		1	CCACGGCGGAT	0.463	
-	31	3059_3060	1qjs.1_Missense_	NM_172364	NP_758952	Q7Z3S7	CA2D4_HUMAN	ellular (Potential).	1	CTCGAGGGTTT	0.614	
-	4	751	sense_Mutation_p	NM_001065	NP_001056	P19438	TNR1A_HUMAN	.|Extracellular (Potential).	3	CACAGGAGAGG	0.587	
-	5	570	_p.E118K|KLRC1_	NM_002259	NP_002250	P26715	NKG2A_HUMAN	.|Extracellular (Potential).	0	TTCTTTCCTTAC	0.373	
-	4	866	_p.P144S|PRB1_u	NM_005039	NP_005030	P04280	PRP1_HUMAN	-P-[PAQ]-Q-[GE]-[GD]- [N	0	TGGAGGAGATC	0.607	
-	18	3878	af.1_Intron|LRP6_	NM_002336	NP_002327	O75581	LRP6_HUMAN	ellular (Potential).	12	TTGGAGGTTCTT	0.428	
-	11	2367	_p.S707L|PKP2_u	NM_004572	NP_004563	Q99959	PKP2_HUMAN	ARM 6.	2	GCAGCGAGATG	0.463	

+	12	1431	p.S310N|IRAK4_u	NM_001114182	NP_001107654	Q9NWZ3	IRAK4_HUMAN	rotein kinase.		0	TTGCTAGTCAAT	0.313
-	15	4315		NM_003482	NP_003473	O14686	MLL2_HUMAN	rich.|PHD-type 4.		41	TGAGGGGTCGG	0.582
+	13	1843	_p.C559Y|TROAP_	NM_005480	NP_005471	Q12815	TROAP_HUMAN	ate tandem repeats.|Cys-ri		1	GTCCTGCTGTAC	0.597
+	13	1852	_p.S562I|TROAP_	NM_005480	NP_005471	Q12815	TROAP_HUMAN	ate tandem repeats.|Cys-ri		1	TAGGAGTGAGC	0.592
-	3	473	_p.P94L|POU6F1	NM_002702	NP_002693	Q14863	PO6F1_HUMAN	Gln/Pro-rich.		1	GCTGGGGCACG	0.612
+	3	873	1_uc009zmb.1_M	NM_002135	NP_002126	P22736	NR4A1_HUMAN			0	AGCCTCCAGCC	0.667
+	13	1367	CKAP1L_uc010so	NM_005337	NP_005328	P55160	NCKPL_HUMAN			4	TACCACCTTCAG	0.393
-	1	475		NM_001005493	NP_001005493	A6NF89	OR6C6_HUMAN	Name=4; (Potential).		2	CATGACCAATG	0.413
+	13	1330	sil.2_Missense_M	NM_001345	NP_001336	P23743	DGKA_HUMAN			4	ACCATGGATGAT	0.507
+	7	726	lank|MYL6_uc001	NM_002475	NP_002466	P14649	MYL6B_HUMAN	EF-hand 3.		0	TGCAGCCTTCT	0.597
+	15	1954	se_Mutation_p.S4	NM_004990	NP_004981	P56192	SYMC_HUMAN			5	ATAATTCTGAGC	0.542
+	9	1288	srs.1_Missense_	NM_001146258	NP_001139730	Q8TBX8	PI42C_HUMAN	PIPK.		3	AGCAGCTCATG	0.478
-	2	810		NR_026825						0	CAGCAGCAGCC	0.473
+	2	715		NM_018656	NP_061126	Q7Z769	S35E3_HUMAN	ical; (Potential).		0	GTTTTAGTTACAT	0.308
+	3	949	uc001svy.1_5'Flan	NM_014505	NP_055320	Q86W47	KCMB4_HUMAN	ellular (Potential).		0	ACTCATGATGAG	0.493
+	16	3975	V3_uc010sub.1_	NM_014903	NP_055718	Q8IVL0	NAV3_HUMAN	Ser-rich.		17	CTGAGGGTGTG	0.498
-	4	706		NM_014167	NP_054886	Q9P031	TAP26_HUMAN			0	TGGCCCTTTTTA	0.343
-	1	569	az.2_Missense_M	NM_001946	NP_001937	Q16828	DUS6_HUMAN	Rhodanese.		0	CGTTGCCCAGC	0.632
+	2	415		NM_005230	NP_005221	P41970	ELK3_HUMAN	ETS.		1	TGTGGGGACTC	0.473
-	4	314	k.1_Missense_M	NM_006166	NP_006157	P25208	NFYB_HUMAN	A domain.		1	TCATGCTGTCC	0.299
+	12	2008	c.2_Missense_M	NM_001093	NP_001084	O00763	ACACB_HUMAN	in carboxylation.		8	GGGAGTGACTC	0.552
+	7	1118	e_Mutation_p.Q2	NM_153348	NP_699179	Q8N3Y1	FBXW8_HUMAN			3	AGGTTCAGTAC	0.408
-	8	2126		NM_000620	NP_000611	P29475	NOS1_HUMAN			7	GAGTTCCAGAC	0.622
-	10	1536		NM_173598	NP_775869	Q6VAB6	KSR2_HUMAN	Pro-rich.		15	TCGTGGAGGAG	0.642
+	4	1791	_p.A586T|EP400_	NM_015409	NP_056224	Q96L91	EP400_HUMAN			12	TAGAGGCCCAG	0.667
-	30	3693	E_uc010tbq.1_RN	NM_006231	NP_006222	Q07864	DPOE1_HUMAN			8	TACGAGGCCGA	0.592
+	3	252	se_Mutation_p.R	NM_152705	NP_689918	Q9Y2S0	RPAC2_HUMAN			0	ATAAAAGATTTC	0.433
+	7	694	ALTL_uc001utn.3_	NM_194318	NP_919299	Q6Y288	B3GLT_HUMAN	enal (Potential).		2	TATTCCACTTGT	0.403
+	9	1401		NM_015678	NP_056493	Q8NFP9	NBEA_HUMAN			11	TCAACCCAGCA	0.378
-	1	1376		NM_145203	NP_660204	Q8N752	KC1AL_HUMAN			1	TGCCTGTCTGG	0.453
-	1	1349		NM_145203	NP_660204	Q8N752	KC1AL_HUMAN			1	CCTGCCCACTG	0.458
+	1	4519		NM_207361	NP_997244	Q5SZK8	FREM2_HUMAN	r (Potential).|CSPG 10.		11	ATAAATCCCCTC	0.418
+	11	1477	.3_Missense_Mut	NM_024561	NP_078837	Q6N069	NAA16_HUMAN	TPR 5.		1	ACTTTGATAAA	0.343
-	13	1257	TI1_uc001uyx.1_3	NM_001002264	NP_001002264	Q96J88	ESIP1_HUMAN			1	GTTCAGGAATC	0.403
+	8	1010	uzs.2_Missense_	NM_018559	NP_061029	Q8IXQ4	K1704_HUMAN			2	TTTGACCGTGAT	0.348
-	1	1154	lvce.2_Nonsense_	NM_001162498	NP_001155970	P43657	LPAR6_HUMAN	Name=1; (P	p.?(4)	4	CACCCATACAA	0.403
+	10	2267	adh.2_Missense_	NM_031915	NP_114121	Q96T68	SETB2_HUMAN	SET.		2	TAGAACTGCTA	0.338
+	1	769	177I|TRIM13_uc0	NM_173605	NP_775876	Q8N5I3	KCNRG_HUMAN			0	ACCTGGTTTTC	0.438
+	9	2077	_p.R626H|CKAP2_	NM_001098525	NP_001091995	Q8WWK9	CKAP2_HUMAN			2	GAGACGTTCTC	0.363
-	11	2500	_p.I545V|DACH1_	NM_080759	NP_542937	Q9UI36	DACH1_HUMAN			1	CTTGTATTGTCC	0.438
+	2	390	_Mutation_p.V29I|	NM_006346	NP_006337	Q8WXW3	PIBF1_HUMAN			2	CAACAGTTCCT	0.343
-	15	2962	1D4_uc010aer.2_	NM_014832	NP_055647	O60343	TBCD4_HUMAN			6	TTCTGGACTGG	0.323
+	19	1299	_Mutation_p.D35	NM_144777	NP_659001	O95171	SCEL_HUMAN	imate tandem repeats.|7.		5	AAGTGGATCCT	0.333
-	1	2685		NM_052910	NP_443142	Q96PX8	SLIK1_HUMAN	ellular (Potential).		5	TCTCCGCCAAC	0.567
-	2	2755	afe.1_Missense_	NM_032229	NP_115605	Q9H5Y7	SLIK6_HUMAN	lasmic (Potential).		3	CTGAAGTTCCC	0.403
+	5	1589		NM_004466	NP_004457	P78333	GPC5_HUMAN			5	TGCTAATGAAT	0.373
+	3	1006	nse_Mutation_p.E	NM_144778	NP_659002	Q5VZF2	MBNL2_HUMAN	3H1-type 2.		0	CGAGAGAGAAC	0.393

-	4	1304		NM_000452	NP_000443	Q12908	NTCP2_HUMAN	ical; (Potential).	4	TAACCCGCCACA	0.433	
-	4	1222		NM_000452	NP_000443	Q12908	NTCP2_HUMAN	ical; (Potential).	4	CACAGCTATGA	0.458	
+	1	781		NM_002929	NP_002920	Q15835	RK_HUMAN	rotein kinase.	2	AGAAGCGGCTG	0.657	
+	1	439		NM_172194	NP_751944	Q8NH05	OR4Q3_HUMAN	Name=4; (Potential).	3	TGGTTCTTGCC	0.493	
-	22	3198	.1_RNA|TEP1_uc	NM_007110	NP_009041	Q99973	TEP1_HUMAN		5	GTGCGGCCTCT	0.537	
-	1	457		NM_001001968	NP_001001968	Q8NH40	OR6S1_HUMAN	Name=4; (Potential).	2	TCCCCCCACCC	0.607	rs150354315
-	7	1225	war.1_Splice_Site_	NM_020920	NP_065971	Q9HCK8	CHD8_HUMAN		10	CCTCACCTCCT	0.254	
+	7	1095	OX4_uc010tlu.1_	NM_014828	NP_055643	O94842	TOX4_HUMAN		1	AGCTTCAATAG	0.537	
+	2	497	se_Mutation_p.A1	NM_182908	NP_878912	Q13268	DHRS2_HUMAN		2	CTGTGCTAGGC	0.597	
+	3	1526	on_p.A94V|NFAT	NM_004554	NP_004545	Q14934	NFAC4_HUMAN	RHD.	3	CTCTGCCCTAC	0.612	
+	2	2631	.2_Missense_Mut	NM_001173	NP_001025226	Q13017	RHG05_HUMAN		5	TTTCACCCTTC	0.418	
-	1	1385		NM_032135	NP_115511	Q5H9T9	FSCB_HUMAN	Pro-rich.	9	CTGAAGGGGAC	0.493	rs17857204
+	11	2029	nf.2_Missense_M	NM_020937	NP_065988	Q8IYD8	FANCM_HUMAN		7	ATCACACATGGT	0.393	
+	20	5224	we.3_Missense_M	NM_020937	NP_065988	Q8IYD8	FANCM_HUMAN		7	CAGTGCCTTCT	0.393	
-	5	363	nj.1_Intron|POLE2	NM_002692	NP_002683	P56282	DPOE2_HUMAN		2	ATTTGGTGCAG	0.418	
+	2	594	sense_Mutation_p	NM_014315	NP_055130	Q9Y2U9	KLDC2_HUMAN	Kelch 1.	1	GCCTAGAGAAG	0.279	
+	2	1103		NM_001663	NP_001654	P62330	ARF6_HUMAN		0	GGACGGACTCT	0.522	
-	18	2524	xz.2_Missense_M	NM_004196	NP_004187	Q00532	CDKL1_HUMAN	rotein kinase.	2	CTCAGGGGAGC	0.587	
-	12	2899	e_Mutation_p.Q8	NM_007361	NP_031387	Q14112	NID2_HUMAN	EGF-like 4.	7	GCACTGGTGCC	0.567	
-	14	1718	e_Mutation_p.M41	NM_020784	NP_065835	Q9P2K2	TXD16_HUMAN	Thioredoxin.	0	AATGCCATGGA	0.318	
-	2	529		NM_021136	NP_066959	Q16799	RTN1_HUMAN		4	ATGAGAGATGTG	0.458	
-	2	450	2_5'Flank|SLC38A	NM_020810	NP_065861	Q32P41	TRMT5_HUMAN		3	CTGGGCGCTGC	0.378	
+	49	10131	p.E3301K|SYNE2	NM_015180	NP_055995	Q8WXH0	SYNE2_HUMAN	ic (Potential).|Potential.	14	AACAAGAGGAA	0.448	
-	2	191	on_p.T3I|ZBTB25_	NM_006977	NP_008908	P24278	ZBT25_HUMAN	BTB.	2	TGGCAGTGTCC	0.368	
-	1	502	'UTR|VTI1B_uc00	NM_006370	NP_006361	Q9UEU0	VTI1B_HUMAN	ytoplasmic (Potential).	0	CCCCGCCGTCC	0.701	
+	3	1320		NM_152331	NP_689544	Q8N9L9	ACOT4_HUMAN		0	GTTACCCTGGG	0.507	
+	2	1432		NM_018228	NP_060698	Q9H8Y1	VRTN_HUMAN		0	CATCTCCCTGA	0.572	
-	2	3182	e_Mutation_p.R9	NM_001040108	NP_001035197	Q9UHC1	MLH3_HUMAN		2	AGGCTCTGATA	0.388	
+	2	456	1xrh.2_Missense_	NM_001042430	NP_001035895	Q53FD0	F164C_HUMAN		1	AGCAAGATCCA	0.473	
-	21	2816	p.P107S|NEK9_u	NM_033116	NP_149107	Q8TD19	NEK9_HUMAN	ch.|Interaction with NEK6.	5	CGCAGGAGGAG	0.537	
+	20	2065	asq.1_Missense_	NM_020431	NP_065164	Q9P1W3	TM63C_HUMAN	ical; (Potential).	0	TTGCCCCATCA	0.547	
-	7	1728	p.R429H|KCNK1	NM_021161	NP_066984	P57789	KCNKA_HUMAN	lasmic (Potential).	5	TCAGGCGCAGG	0.602	
+	8	1325	se_Mutation_p.G1	NM_001102366	NP_001095836	Q7Z3D6	CN159_HUMAN		3	CGGAGGTGAGC	0.612	
-	10	978		NM_024764	NP_079040	Q9H7T0	CTSRB_HUMAN		5	TGCCCTGGAAA	0.333	
-	21	6616	uf.1_Missense_Mu	NM_004239	NP_004230	Q15643	TRIPB_HUMAN		13	GCCCGGGCCCA	0.507	
-	3	821	ion_p.S198N|DDX	NM_020414	NP_065147	Q9GZR7	DDX24_HUMAN	inding.|ATP (By similarity).	4	TTCCCACTTCCT	0.408	
-	20	3519		NM_018036	NP_060506	Q96BY7	ATG2B_HUMAN		3	TGAGAGAAAAC	0.363	
+	1	234	|PPP2R5C_uc001	NM_002719	NP_002710	Q13362	2A5G_HUMAN		2	ATTCGAGGTAAG	0.468	
+	36	7593	1H1_uc001ykt.1_	NM_001376	NP_001367	Q14204	DYHC1_HUMAN		10	ACCATCCCGAC	0.622	
-	11	1379	GE_uc001ylh.2_Ir	NM_014226	NP_055041	Q9UQ07	MOK_HUMAN		4	CAAGGGTCTCA	0.577	
-	12	2651	P1R13B_uc001yo	NM_015316	NP_056131	Q96KQ4	ASPP1_HUMAN	Pro-rich.	1	GGCATCTGATGA	0.572	
+	1	2347		NM_018958	NP_061831	Q9NZP6	CO002_HUMAN		8	CCACTTCCATTT	0.493	
-	18	2672	bl.1_Missense_Mu	NM_004667	NP_004658	O95714	HERC2_HUMAN		13	CAGACCTAAAC	0.542	
+	63	9078	r.2_Missense_Mut	NM_001036	NP_001027	Q15413	RYR3_HUMAN	lame=M'; (Potential).	10	GACGTCCATCT	0.473	
+	7	2622	p.E851K|C15orf5	NM_175741	NP_786883	Q86Y26	NUT_HUMAN		30	ATCAAGAACAG	0.517	
+	2	333	uc001zmk.3_RNA|	NM_002875	NP_002866	Q06609	RAD51_HUMAN		0	AATGCAGATACT	0.378	
+	4	869		NM_020857	NP_065908	Q9P253	VPS18_HUMAN		3	AGCCAGCGAAG	0.602	

-	7	1051	80_uc010ucu.1_F	NM_017553	NP_060023	Q9ULG1	INO80_HUMAN	f conserved components A	4	CCATACTTTCCT	0.468	
-	23	4537	_p.D714N|STRC_	NM_153700	NP_714544	Q7RTU9	STRC_HUMAN		0	AAAGTCTGAGA	0.547	rs149597053
+	11	1522	_p.F445I|SQRDL_	NM_021199	NP_067022	Q9Y6N5	SQRD_HUMAN		1	AAGTTGTTTCAT	0.488	
-	64	8358	N1_uc010beo.1_R	NM_000138	NP_000129	P35555	FBN1_HUMAN	47; calcium-binding.	3	AAGTAACCAGGT	0.493	
-	11	1202	xm.2_Nonsense_	NM_152647	NP_689860	Q96M60	CO033_HUMAN		1	GTTTCCAGTGG	0.318	
+	8	1075	D3_uc010bfc.1_	NM_014547	NP_055362	Q9NYL9	TMOD3_HUMAN		1	CCCTGGCAGAG	0.463	
-	18	2717	p.P859S|SLTM_u	NM_024755	NP_079031	Q9NWH9	SLTM_HUMAN	Arg/Glu-rich.	1	GGAAGGATTGG	0.502	
-	4	263	A2_uc002agm.2_	NM_001136015	NP_001129487	P07355	ANXA2_HUMAN		1	CTCAGCATCAA	0.403	
+	9	1029_1030	se_Mutation_p.C2	NM_006537	NP_006528	Q9Y6I4	UBP3_HUMAN		1	AACAAGTGTTGC	0.431	
-	8	1042	PX_uc010bhg.1_N	NM_006660	NP_006651	O76031	CLPX_HUMAN		0	AGCCTGAGTCA	0.393	
-	9	2447		NM_003613	NP_003604	O75339	CILP1_HUMAN		7	CCTCACCTTAA	0.522	
-	4	553	_p.D41N|AAGAB_	NM_024666	NP_078942	Q6PD74	AAGAB_HUMAN		0	ACCATCCTCCTC	0.353	
-	1	669	uc002ard.2_RNA|	NM_033429	NP_219501	Q96GE6	CALL4_HUMAN		0	CGCCACCTGGG	0.597	
-	3	463	02aud.3_RNA|PA	NM_020214	NP_064599	Q2NL67	PARP6_HUMAN		0	GATGTCCTAGTG	0.453	
+	12	1171	_p.V330I|CSK_uc	NM_001127190	NP_001120662	P41240	CSK_HUMAN	rotein kinase.	3	CCAAGGTCAGC	0.602	
+	14	1388	p.G402D|CSK_uc	NM_001127190	NP_001120662	P41240	CSK_HUMAN	rotein kinase.	3	GAAGGGCTACA	0.657	
-	9	1056	2C1_uc010bkk.2_	NM_006715	NP_006706	Q9NTJ4	MA2C1_HUMAN		0	CCTCACCATGG	0.612	
-	11	985		NR_027024					0	CCTGGGATTGG	0.567	
-	6	557	bgu.1_Missense_	NM_024580	NP_078856	Q7Z2Z2	ETUD1_HUMAN		1	CAGAACTGCCT	0.363	
-	4	1761	s.1_Missense_Mu	NM_001717	NP_001708	Q01954	BNC1_HUMAN		3	TTGTGTCTTTTC	0.468	
+	14	1753	p.G510E|ADAMTS	NM_207517	NP_997400	P82987	ATL3_HUMAN	SP type-1 3.	27	CCGCGGAGAGC	0.458	
+	12	5113	e_Mutation_p.A15	NM_013227	NP_037359	E7EX88	E7EX88_HUMAN		3	TTCAGCTTCTG	0.537	
-	6	810	nn.2_Missense_M	NM_005928	NP_005919	Q08431	MFGM_HUMAN	5/8 type C 2.	1	CAGGGGATTGG	0.577	
+	10	1544	lutation_p.V477M|	NM_006122	NP_006113	P49641	MA2A2_HUMAN	enal (Potential).	3	CAGGGGTGGAG	0.557	
+	6	1063	p.G163D|CHD2_	NM_001271	NP_001262	O14647	CHD2_HUMAN		2	ACAAGGCACCA	0.398	
+	26	3951	.1_Missense_Mu	NM_001271	NP_001262	O14647	CHD2_HUMAN		2	GGAAGGACCTC	0.532	
+	2	1951	urj.1_Missense_M	NM_021005	NP_066285	P24468	COT2_HUMAN	similarity).|Ligand-binding (	3	AGGTGGCCCTG	0.667	
+	1	736		NM_001001674	NP_001001674	Q8NGB8	O4F15_HUMAN	Name=6; (Potential).	0	TCACTGTGGTC	0.428	
+	9	1943	p.2_Missense_Mu	NR_003659					0	GCATCGGCAAG	0.652	
+	2	196	.3_5'UTR|NUBP2_	NM_012225	NP_036357	Q9Y5Y2	NUBP2_HUMAN		0	GCTGGCCCTGG	0.687	
+	3	641	c.2_Missense_Mu	NM_005262	NP_005253	P55789	ALR_HUMAN	R sulfhydryl oxidase.	0	CAAAAGTGGAT	0.607	
+	12	1352	e.1_Missense_Mu	NM_001761	NP_001752	P41002	CCNF_HUMAN		2	TAGTCCCTGTG	0.672	
+	14	1623	e.1_Missense_Mu	NM_001761	NP_001752	P41002	CCNF_HUMAN		2	GACCGCCGTGA	0.597	
-	4	1376		NM_000243	NP_000234	O15553	MEFV_HUMAN		6	CTTCTCCTCCC	0.532	
+	6	1136	75A_uc002cuv.3_	NM_153028	NP_694573	Q96N20	ZN75A_HUMAN	2H2-type 2.	1	TCAGATCTTAATA	0.353	
-	22	4261		NM_002705	NP_002696	O60437	PEPL_HUMAN	Potential.	6	CAGCCGCCGCA	0.706	rs34645685
+	9	1207	za.2_Missense_	NM_024109	NP_077014	Q9BUU2	MET22_HUMAN		0	TTGACTGATGCT	0.483	
-	13	4596	1350N|GRIN2A_	NM_001134407	NP_001127879	Q12879	NMDE1_HUMAN	lasmic (Potential).	45	GCTGTCCTCCA	0.537	
-	6	1160		NM_144674	NP_653275	Q96M29	TEKT5_HUMAN	Potential.	2	GCAGCGTCTGC	0.632	rs142647849
+	15	2800	_p.P832L|MKL2_u	NM_014048	NP_054767	Q9ULH7	MKL2_HUMAN		5	AGATCCCCCCC	0.562	
-	3	990		NM_022166	NP_071449	Q86Y38	XYLT1_HUMAN	enal (Potential).	4	CGAGGGGGCAG	0.602	
+	17	3313	gd.1_Missense_M	NM_001105248	NP_001098718	Q6UXY8	TMC5_HUMAN	ical; (Potential).	1	CATCACCATCT	0.453	rs138670843
+	20	3624	p.D959N|TMC5_u	NM_001105248	NP_001098718	Q6UXY8	TMC5_HUMAN	ellular (Potential).	1	TGCAGGATATG	0.448	
-	7	1138	SM1_uc010bwg.1	NM_052956	NP_443188	Q08AH1	ACSM1_HUMAN		2	TCCGTCTTTTC	0.448	
-	42	6092		NM_017539	NP_060009	Q8TD57	DYH3_HUMAN		18	TCTTTGGTGATAT	0.393	
-	1	702	KSCAN2_uc002do	NM_001012981	NP_001012999	Q63HK3	ZKSC2_HUMAN	SCAN box.	4	TCTTCTCGGGTA	0.512	
+	4	241		NM_015202	NP_056017	O60303	K0556_HUMAN		8	TCTATGTCAAC	0.502	

-	18	2977	_p.P812S|XPO6_u	NM_015171	NP_055986	Q96QU8	XPO6_HUMAN		2	AGCTGGAAAGAC	0.527	
-	6	1122	_uc002dqm.2_Mis	NM_177534	NP_803878	P50225	ST1A1_HUMAN	PAPS.	0	CTCCTCTGGCA	0.552	
+	10	1315	10bzr.2_Intron|COI	NM_007074	NP_009005	P31146	COR1A_HUMAN		0	CGTACCCCCAA	0.706	
+	34	8972	CAP_uc002dzg.1_	NM_006662	NP_006653	Q6ZRS2	SRCAP_HUMAN	hook 1.|Pro-rich.	4	GGAGGCCCCCC	0.612	
+	14	4998		NM_014712	NP_055527	O15047	SET1A_HUMAN	action with CFP1.	3	ACTCAGAGGAC	0.458	
+	3	1224	C5_uc002eca.3_M	NM_001105247	NP_001098717	Q96C12	ARMC5_HUMAN	ARM 3.	1	CCTGGCCTTGG	0.667	
-	4	701	ETO2_uc002ees.1_	NM_018092	NP_060562	Q8NC67	NETO2_HUMAN	lar (Potential).|CUB 1.	0	AACTTCCAAGT	0.393	
+	3	903	e_Mutation_p.Y12	NM_024335	NP_077311	P78412	IRX6_HUMAN		6	GGAGCCTATTAT	0.498	
-	10	1420	iq.2_Missense_Mu	NM_001143685	NP_001137157	Q6NT32	EST5A_HUMAN		0	TCACCTCTGTGAT	0.532	
+	2	255	ho.1_Missense_M	NM_020312	NP_064708	O75208	COQ9_HUMAN		1	ACCCCCCAGGT	0.493	
+	2	290	0vid.1_Missense_	NM_014157	NP_054876	Q9H0I3	CC113_HUMAN		0	TATCAGCAGCA	0.403	
+	6	533	0vig.1_Missense_	NM_022910	NP_075061	Q9ULP0	NDRG4_HUMAN		1	CCAATGGCAAA	0.657	
-	12	1394	vis.1_Missense_M	NM_006141	NP_006132	O43237	DC1L2_HUMAN		4	GGCTGTGCTCT	0.547	
-	8	1059	vis.1_Missense_M	NM_006141	NP_006132	O43237	DC1L2_HUMAN		4	CGGGAGGTTTC	0.279	
-	3	1236	_p.S134F|TPPP3_	NM_016140	NP_057224	Q9BW30	TPPP3_HUMAN		1	TGTGGGAGCCC	0.597	
-	2	1160	_p.A109T|TPPP3_	NM_016140	NP_057224	Q9BW30	TPPP3_HUMAN		1	ATTGGCTGGCT	0.622	
+	3	255	2L_uc010vkk.1_M	NM_017803	NP_060273	Q9NX74	DUS2L_HUMAN		0	ATGGAGCGGAC	0.498	
+	5	473	.A66V|PRMT7_uc	NM_019023	NP_061896	Q9NVM4	ANM7_HUMAN		0	GAAGGCCTTGG	0.522	
-	16	2396	vlu.1_Splice_Site_	NM_001605	NP_001596	P49588	SYAC_HUMAN		1	GCTCACCTTCT	0.557	
+	9	1611	p.1_Intron|DHX38_	NM_014003	NP_054722	Q92620	PRP16_HUMAN		1	GGATGGGCGCA	0.502	
-	7	1534	fgj.2_Missense_Mu	NM_052892	NP_443124	Q7Z442	PK1L2_HUMAN	racellular (Potential).	3	AACCGGAACAG	0.577	
-	6	1116	gj.2_Nonsense_M	NM_052892	NP_443124	Q7Z442	PK1L2_HUMAN	ellular (Potential).	3	TGAATCCACAG	0.542	
+	3	653		NM_022041	NP_071324	Q9H2C0	GAN_HUMAN	BACK.	2	ACGGAAGAATTC	0.423	rs119485095
+	13	2182	nt.1_Missense_Mu	NM_001257	NP_001248	P55290	CAD13_HUMAN	Cadherin 5.	1	AAGTGGACTGC	0.542	
-	2	852	hu.1_Missense_M	NM_172347	NP_758857	Q8TDN1	KCNG4_HUMAN		3	GGTCGGGCATG	0.522	
-	12	1721	CHC14_uc002fkb	NM_015144	NP_055959	Q8WYQ9	ZCH14_HUMAN		2	CGGACGCGGGC	0.557	rs147152692
+	6	772	_p.S191N|BANP_	NM_079837	NP_524576	Q8N9N5	BANP_HUMAN	X1 and HDAC1 (By similar	0	GGCCAGCGACT	0.647	
-	5	655	_Site_p.R195_splic	NM_000512	NP_000503	P34059	GALNS_HUMAN		2	CCATTACCTGCC	0.607	
-	9	2020	fnc.1_Missense_M	NM_013275	NP_037407	Q6UB99	ANR11_HUMAN	Ser-rich.	6	AGGAGGCAGAG	0.632	
+	4	577	i.2_Missense_Mut	NM_003119	NP_003110	Q9UQ90	SPG7_HUMAN	intermembrane (Potential).	0	AGGTGGTGCCT	0.637	
+	5	752	i.2_Missense_Mut	NM_003119	NP_003110	Q9UQ90	SPG7_HUMAN	intermembrane (Potential).	0	AGTTTCCTACA	0.408	
-	18	1727	pn.1_Missense_Mu	NM_000135	NP_000126	O15360	FANCA_HUMAN		6	ATGTTCCCCGTA	0.557	
+	3	300	.1_5'UTR|TUBB3_	NM_006086	NP_006077	Q13509	TBB3_HUMAN		3	GCTCAGGGGCC	0.582	
-	15	1704	|VPS53_uc002frm	NM_018289	NP_060759	Q5VIR6	VPS53_HUMAN		0	TGGTTCTGAAG	0.453	
+	5	583	_p.G149E|FAM57	NM_024792	NP_079068	Q8TBR7	FA57A_HUMAN	elical; (Potential).	0	TGAATGGAATCC	0.542	
-	4	382	ru.2_Missense_Mu	NM_016080	NP_057164	Q9HC38	GLOD4_HUMAN		0	ATTTACCATAAA	0.269	
-	8	1333	z.2_Missense_Mut	NM_022463	NP_071908	Q6DKJ4	NXN_HUMAN		4	CGGGGGTGATC	0.572	
-	3	317	NA_uc010cju.2_5	NM_006224	NP_006215	Q00169	PIPNA_HUMAN		1	CTGCCCCACTT	0.507	
+	8	1056	M2_uc010vqw.1_M	NM_001098509	NP_001091979	O43147	SGSM2_HUMAN		0	GTGGACCCCCA	0.607	
+	17	2237	.1_Missense_Muta	NM_001098509	NP_001091979	O43147	SGSM2_HUMAN	ab-GAP TBC.	0	CTCCGGGCACC	0.612	
-	5	1535	_p.Q279*|ZNF232_	NM_014519	NP_055334	Q9UNY5	ZN232_HUMAN		2	CATCTGCCTGA	0.453	
+	3	451	e_Mutation_p.S84	NM_001042	NP_001033	P14672	GTR4_HUMAN	Name=2; (Potential).	0	CCTCTCCGTGG	0.617	
-	4	3066	nd.3_Missense_Mu	NM_001128833	NP_001122305	Q9P1Z0	ZBTB4_HUMAN		4	AAGTTACTGAAG	0.602	
+	60	9346	nm.1_Missense_M	NM_020877	NP_065928	Q9P225	DYH2_HUMAN	k (By similarity).	13	ATATAGGAGAGA	0.537	
+	2	1067	2gjp.2_Missense_	NM_053051	NP_444279	Q8N137	CNTRB_HUMAN		2	CGGAGGCCACG	0.582	
+	16	1975	S_uc010cnw.1_Mi	NM_012393	NP_036525	O15067	PUR4_HUMAN		5	GAAATGGCCAG	0.597	
-	4	758	5A35_uc002gkt.2_	NM_201520	NP_958928	Q3KQZ1	S2535_HUMAN	Solcar 3.	0	CATCTGTGGGC	0.582	

-	1	704		NM_152599	NP_689812	Q8IWD5	MFS6L_HUMAN		1	GAGGAGAGCTT	0.552	
-	19	2285	uc002gml.1_Intron	NM_017533	NP_060003	Q9Y623	MYH4_HUMAN	osin head-like.	13	ACAAACCTCTGT	0.403	
-	12	1169	_Mutation_p.E347	NM_001100112	NP_001093582	Q9UKX2	MYH2_HUMAN	osin head-like.	14	CTTTTCTTCATT	0.418	
-	4	480	_p.P144L|PMP22_	NM_153322	NP_696997	Q01453	PMP22_HUMAN	al; (By similarity).	0	CCAGGGGGAAG	0.592	
-	6	972	2gps.1_Splice_Sit	NM_006311	NP_006302	O75376	NCOR1_HUMAN		5	AGCTTACCCGAT	0.448	
+	3	5003	.1_Missense_Mut	NM_030665	NP_109590	Q7Z5J4	RAI1_HUMAN		2	CCCCGGAGGGC	0.657	
-	7	873	_p.S194F|TOM1L2	NM_001082968	NP_001076437	Q6ZVM7	TM1L2_HUMAN	GAT.	0	ATCTCAGACATG	0.527	
-	6	2473	5A10_uc002gut.1_	NM_001039999	NP_001035088	A6ND36	FA83G_HUMAN		2	TCATGGGGCGG	0.652	
-	2	948	M11_uc002gyq.2_	NM_003876	NP_003867	P17152	TMM11_HUMAN		0	CAGTCTCTTTCT	0.542	
-	22	2935		NM_000625	NP_000616	P35228	NOS2_HUMAN	-binding FR-type.	4	AGACACCCGCA	0.577	
-	28	5341	2hbt.2_Splice_Sit	NM_014680	NP_055495	Q14667	K0100_HUMAN		4	TGAATACCTTCC	0.398	
-	6	828	_p.P42S|CORO6_	NM_032854	NP_116243	Q6QEF8	CORO6_HUMAN	WD 5.	0	AGTCGGGATCGT	0.627	
+	15	3305	e_Mutation_p.G85	NM_001304	NP_001295	O75976	CBPD_HUMAN	ntial).|Carboxypeptidase-lik	2	TAGATGGTGGTT	0.368	
-	16	3262	_p.F885L|SRCIN1_	NM_025248	NP_079524	Q9C0H9	SRCN1_HUMAN	Pro-rich.	0	GGGGAAGCTCC	0.657	
+	6	556	_p.F181L|MLLT6_	NM_005937	NP_005928	P55198	AF17_HUMAN		6	CACTTCAGCAA	0.443	
+	3	377	e_Mutation_p.E85	NM_006804	NP_006795	Q14849	STAR3_HUMAN	ar (Potential).|MENTAL.	0	AGCAGGAGATC	0.557	
-	1	229	ssense_Mutation_	NM_001042471	NP_001035936	Q8TAX9	GSDMB_HUMAN		2	AGCCCAGAATCC	0.502	
-	1	355		NM_031960	NP_114166	Q9BYQ9	KRA48_HUMAN	IKRQVHEC]- [SPRT]-[STC	0	gctggacacacagcag	0.204	
-	5	841		NM_002279	NP_002270	Q14525	KT33B_HUMAN	Coil 2.|Rod.	0	GGACTGCAGCT	0.607	
-	6	1068	xd.3_Missense_M	NM_021991	NP_068831	P14923	PLAK_HUMAN		5	CTCATCCAGCA	0.577	
-	4	899		NM_012285	NP_036417	Q9UQ05	KCNH4_HUMAN	lasmic (Potential).	1	TGCCTCCCTGG	0.602	
-	17	2036	_p.E591K|EZH1_u	NM_001991	NP_001982	Q92800	EZH1_HUMAN	SET.	3	CAGACTCCTTTAT	0.532	
+	2	1768	_Mutation_p.P578	NM_009590	NP_033720	O75106	AOC2_HUMAN		2	AAGCCCCCTAC	0.617	
+	4	995	s.2_Missense_Mu	NM_001076674	NP_001070142	Q71RG4	TMUB2_HUMAN	ical; (Potential).	1	TTGTGGTGCTG	0.587	
+	1	389		NM_001466	NP_001457	Q14332	FZD2_HUMAN	acellular (Potential).	3	CTCGCCCGAAC	0.632	
-	11	1563	p.A488T|KIF18B_	NM_001080443	NP_001073912				2	CAGTGCATGTG	0.572	
-	43	3287		NM_000088	NP_000079	P02452	CO1A1_HUMAN	le-helical region.	382	GGGGccagggca	0.552	
+	8	1054	_Mutation_p.S325	NM_003786	NP_003777	O15438	MRP3_HUMAN	rity).|ABC transmembrane	4	TGCTCTCCTTCA	0.617	
+	17	2193		NM_003786	NP_003777	O15438	MRP3_HUMAN	1.|Cytoplasmic (By similarit	4	TGCACTCTTCAG	0.607	
-	1	1001	CA10_uc002ity.3_	NM_020178	NP_064563	Q9NS85	CAH10_HUMAN		2	CACCTCCCAGAC	0.517	
+	8	2668	p.D813N|AKAP1_	NM_003488	NP_003479	Q92667	AKAP1_HUMAN	Tudor.	1	AGGTCTGACTTT	0.517	
-	10	1845	ive.1_Missense_M	NM_017949	NP_060419	Q9NWM3	CUED1_HUMAN		2	CTTGGGTGCCT	0.627	
+	11	2032		NM_000502	NP_000493	P11678	PERE_HUMAN		2	AGACAGGTAAGT	0.498	
-	10	992	_p.T103I|MKS1_	NM_017777	NP_060247	Q9NXB0	MKS1_HUMAN		1	GGACAGTCTAA	0.532	
-	9	1195	R257K|SEPT4_uc	NM_004574	NP_004565	O43236	SEPT4_HUMAN		0	CGCCCTCTGGCC	0.572	
-	8	1007	vs.1_Missense_M	NM_198393	NP_938207	Q8IWB6	TEX14_HUMAN	rotein kinase.	17	GTGTTCCTGCT	0.572	
-	7	823		NM_032043	NP_114432	Q9BX63	FANCJ_HUMAN	ase ATP-binding.	1	ATGACTCTTGAC	0.393	
-	4	527	dds.2_Missense_	NM_001100875	NP_001094345	Q8NA82	MARHA_HUMAN		0	TGCTGGAAGTTT	0.428	
-	5	994	198S|CYB561_uc	NM_001915	NP_001906	P49447	CY561_HUMAN	tochrome b561.	1	GACACCCTCGG	0.632	
-	11	1708	dea.1_Missense_	NM_001098426	NP_001091896	Q92925	SMRD2_HUMAN		0	CCTGGGGGTCG	0.527	
-	10	1128		NM_001433	NP_001424	O75460	ERN1_HUMAN	enal (Potential).	9	GACGTCCGTGC	0.557	
-	4	602	.1_5'UTR|SMURF	NM_022739	NP_073576	Q9HAU4	SMUF2_HUMAN	C2.	4	AATCAGACTTTC	0.363	
+	3	1574	.D505N|BPTF_uc	NM_182641	NP_872579	Q12830	BPTF_HUMAN		4	TTAATTGACTGT	0.363	rs140629327
+	11	4628	.2_Missense_Mut	NM_182641	NP_872579	Q12830	BPTF_HUMAN		4	CTTGTCCAGAA	0.413	
-	25	3570	.P1171T|ABCA8_	NM_007168	NP_009099	O94911	ABCA8_HUMAN	ical; (Potential).	3	GGCAGGTGGTA	0.388	
-	5	409	jlr.2_Splice_Site_	NM_015654	NP_056469	Q9BTE0	NAT9_HUMAN		0	GGGCTCTAGGA	0.358	
-	9	1111	13D_uc002jpq.1_	NM_199242	NP_954712	Q70J99	UN13D_HUMAN	ction with RAB27A.	2	CGTTCCCCAGA	0.617	

-	4	465	_p.E43K|SRP68_	NM_014230	NP_055045	Q9UHB9	SRP68_HUMAN			1	TGGCTTCCTGTT	0.502	
-	4	539		NM_001008528	NP_001008528	P84157	MXRA7_HUMAN			0	CTGTTCCTTCT	0.572	rs147040032
-	10	1748	H17_uc002jvs.2_RNA							9	CACTTTCCCTTT	0.557	
+	27	7712	_uc010dhw.1_Mis	NM_020914	NP_065965	Q9HCF4	ALO17_HUMAN			21	TCGTGGACAAT	0.498	
+	29	4176	66_splice|RPTOR	NM_020761	NP_065812	Q8N122	RPTOR_HUMAN			6	CTCCAGGAGCT	0.612	
+	24	7343	ae.2_Missense_M	NM_001080519	NP_001073988	Q9P281	BAHC1_HUMAN			1	CCTGCCCGCCC	0.652	
-	42	7372	SN_uc002kdv.1_R	NM_004104	NP_004095	P49327	FAS_HUMAN	rase (By similarity).		1	GGCCGCAAAGC	0.647	
+	2	667	_p.E166K|FOXK2_	NM_004514	NP_004505	Q01167	FOXK2_HUMAN			0	AGCAGGAGGCG	0.552	
+	9	983	_p.L268F|TBCD_u	NM_005993	NP_005984	Q9BTW9	TBCD_HUMAN			0	GCAGACTCCCT	0.602	
-	10	1200	e_Mutation_p.A37	NM_012307	NP_036439	Q9Y2J2	E41L3_HUMAN	FERM.		5	GGCAGCTCGAT	0.299	
+	2	477	p.P131S|LAMA3_	NM_198129	NP_937762	Q16787	LAMA3_HUMAN	inin N-terminal.		11	GCCCTCCCCTG	0.507	
+	4	1107	YR_uc002kva.2_	NM_012189	NP_036321	O75952	CABYR_HUMAN			0	TTATCCCTTTTA	0.383	
+	7	1492	F4B_uc002kvt.3_	NM_005640	NP_005631	Q92750	TAF4B_HUMAN	TAFH.		3	TTCTGCCTAAC	0.428	
+	5	824	kyf.2_Missense_M	NM_014268	NP_055083	Q15555	MARE2_HUMAN	TN1-binding.		1	ACCAGGATCCA	0.398	
+	5	4306		NM_015559	NP_056374	Q9Y6X0	SETBP_HUMAN			3	TGCCAAGTCCCC	0.468	
-	10	1481	bs.1_Missense_M	NM_004046	NP_004037	P25705	ATPA_HUMAN			0	GCACGCCACGA	0.483	
-	5	718	b.2_Missense_Mu	NM_031939	NP_114145	Q9BYG7	MSTRO_HUMAN	HEAT.		0	GTCATCTAATAA	0.343	
-	2	1130		NM_016626	NP_057710	Q5U5Q3	MEX3C_HUMAN	KH 2.		4	TTTCAGGCATC	0.418	
+	5	700	p.A108V|POLI_uc	NM_007195	NP_009126	Q9UNA4	POLI_HUMAN	UmuC.		3	GGAAGCCATGT	0.408	
-	4	1077		NM_052947	NP_443179	Q86TB3	ALPK2_HUMAN			14	CGGCACTGTCA	0.498	
-	4	902	v.2_Missense_M	NM_182511	NP_872317	Q8IUK8	CBLN2_HUMAN	C1q.		0	TAGAGGAAACA	0.507	
-	3	264		NM_005035	NP_005026	O00411	RPOM_HUMAN			2	CCGCACCCGCG	0.667	
+	2	226	L3_uc010drt.1_5'	NM_005860	NP_005851	O95633	FSTL3_HUMAN	TB.		0	TGCCTCCGGCA	0.652	
-	2	225	ES_uc002lxb.1_	NM_001130	NP_001121	Q08117	AES_HUMAN	rich (Q domain).		0	TTTGAGTTGCT	0.657	
-	2	357		NM_030662	NP_109587	P36507	MP2K2_HUMAN			0	GTCCACCAGGT	0.597	
+	3	614		NM_005483	NP_005474	Q13111	CAF1A_HUMAN	1 chromo shadow domain.		2	CATTTCCTGGA	0.557	
+	1	2105	uc002mbg.1_RNA	NM_018708	NP_061178	Q9BSK4	FEM1A_HUMAN			0	ACAAGGGCTTC	0.602	
+	4	677	uf.2_RNA|UHRF1_	NM_001048201	NP_001041666	Q96T88	UHRF1_HUMAN			2	GCCCTGCAGCT	0.642	
-	5	763	e_Mutation_p.G1	NM_014649	NP_055464	Q14151	SAFB2_HUMAN			0	CTTCCCCATCC	0.438	
-	20	1539	_p.A33T|DENND1	NM_024898	NP_079174	Q8IV53	DEN1C_HUMAN			1	TGGGGCCCTCA	0.637	
-	2	497	F14_uc002mfj.1_	NM_003807	NP_003798	O43557	TNF14_HUMAN	type II membrane protein;		1	CAGACCCACCC	0.642	
+	18	2412	_p.D773N|EMR1_	NM_001974	NP_001965	Q14246	EMR1_HUMAN	lasmic (Potential).		5	TAAAAGACACC	0.483	
+	11	1606	_Mutation_p.P529	NM_020902	NP_065953	Q9P1Y5	CAMP3_HUMAN	Pro-rich.		1	CCTGCCCGAGG	0.682	
-	9	924		NM_198492	NP_940894	Q6UXB4	CLC4G_HUMAN	(Potential).|C-type lectin.		0	CAGATCCAGCC	0.637	
+	5	608	4M_uc010dvs.2_	NM_001144910	NP_001138382	Q9H2X3	CLC4M_HUMAN	|7 X approximate tandem r		1	TGACCCGGCTG	0.582	
-	11	1403		NM_032447	NP_115823	Q75N90	FBN3_HUMAN	4; calcium-binding.		11	AGTCACCGTGG	0.667	
-	21	2299		NM_012335	NP_036467	O00160	MYO1F_HUMAN			3	TCCGCTCCTTCT	0.652	
+	1	214		NM_145208	NP_660209	Q8WWY6	MB3L1_HUMAN	cription repressor.		0	GAATTACACCCC	0.512	
-	5	33913		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).		57	CCATGAGTCTA	0.483	
-	3	27518		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	h.|Extracellular (Potential).		57	TGGGTCCCTGAC	0.478	
-	3	27337		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	h.|Extracellular (Potential).		57	TAGGTCCTCTGC	0.498	
-	3	21724		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	h.|Extracellular (Potential).		57	GCACAGCTTCTG	0.502	
-	3	18804		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).		57	TTGTTCATGACA	0.473	
-	16	1638		NM_015719	NP_056534	P25940	CO5A3_HUMAN	le-helical re	p.G518E(1)	10	AGGTCCCTGCA	0.493	
-	6	395		NM_003755	NP_003746	O75821	EIF3G_HUMAN			0	GGGGTCAAACT	0.602	
-	33	4215	lq.1_Missense_M	NM_020812	NP_065863	Q96HP0	DOCK6_HUMAN			3	CAGAACCACTA	0.572	
+	4	1293	yf.2_Missense_M	NM_145295	NP_660338	Q7L945	ZN627_HUMAN			1	AGAAACCCTATG	0.413	

-	4	407	3_uc002msz.1_M	NM_001080411	NP_001073880	Q8N7K0	ZN433_HUMAN	KRAB.	0	TGATGACCTTCT	0.363	
-	4	454	dyn.1_RNA|ZNF62	NM_145233	NP_660276	Q96I27	ZN625_HUMAN	type 1; degenerate.	0	CCACATGATTTTA	0.453	
-	17	1776	.1_Intron|HOOK2_	NM_013312	NP_037444	Q96ED9	HOOK2_HUMAN		3	TACTTACAATGG	0.607	
+	12	1201	nzk.3_Missense_M	NM_032433	NP_115809	Q96JL9	ZN333_HUMAN		3	TGTGCCCGAGA	0.428	
+	5	715	.2_5'UTR|HSH2D_	NM_032855	NP_116244	Q96JZ2	HSH2D_HUMAN	SH2.	0	GTCAGTCACAGC	0.587	
+	11	1487	se_Mutation_p.G1	NM_173544	NP_775815	Q86XR2	NIBL2_HUMAN		0	CTTGGGGCAGC	0.627	
+	4	890		NM_000453	NP_000444	Q92911	SC5A5_HUMAN		4	CTGTGGTGAGT	0.602	
-	14	2195	.G287E|PDE4C_	NM_001098819	NP_001092289	Q08493	PDE4C_HUMAN		5	GGTCTCCCTGC	0.627	
+	3	410		NM_004386	NP_004377	O14594	NCAN_HUMAN	g-like V-type.	4	GGTGGCCAAAA	0.647	
+	13	1339	892_uc010ecd.2_	NM_015329	NP_056144	Q9Y6X3	SCC4_HUMAN		0	GACACCAAGAG	0.532	
-	16	1708	_p.E505K|GMIP_u	NM_016573	NP_057657	Q9P107	GMIP_HUMAN	ol-ester/DAG-type.	1	AGTCTCCAGGC	0.597	
+	1	825		NR_003128					0	TAGTACGAAATT	0.378	
-	5	1871		NM_001080409	NP_001073878				2	GACTGGCTAAAA	0.373	
-	25	2654		NM_032139	NP_115515	Q96NW4	ANR27_HUMAN	ANK 10.	5	AGGCCCCGTGC	0.398	
+	1	103		NM_173479	NP_775750	Q6ZMY6	WDR88_HUMAN		3	GCTCCCCGACA	0.612	
+	21	2730	AP33_uc010eel.2_	NM_052948	NP_443180	O14559	RHG33_HUMAN		4	GCCACCCTTCC	0.687	
-	26	3337	S1_uc010eem.1_	NM_004646	NP_004637	O60500	NPHN_HUMAN	lasmic (Potential).	5	CATATTCGTTCCT	0.632	
-	3	1095	_Missense_Mutati	NM_152658	NP_689871	Q8NA92	THAP8_HUMAN		0	CCGCACCCGGC	0.711	
-	5	1413	ti.1_Missense_Mu	NM_020951	NP_066002	Q6P280	ZN529_HUMAN	C2H2-type 7.	1	CTATTTCTAAAGA	0.388	
-	10	1000	PF1_uc010xtu.1_	NM_004647	NP_004638	Q92782	DPF1_HUMAN	PHD-type 2.	0	ACCCGCCCAGC	0.682	
+	2	795	gn.1_Missense_Mu	NM_003407	NP_003398	P26651	TTP_HUMAN		1	CCCCACCCCAG	0.672	
-	7	2463	_Mutation_p.V593	NM_181882	NP_870998	Q9BXM0	PRAX_HUMAN	L]-[LIVMAP]- [AQKHRPE];	2	AGGCACCTTGG	0.577	
-	2	321	RB_uc010egw.1_	NM_000713	NP_000704	P30043	BLVRB_HUMAN		0	CCACGGTCTTG	0.662	
+	8	1743	ph.2_Missense_M	NM_080732	NP_542770	Q96KS0	EGLN2_HUMAN		2	ATGAACCAGGC	0.672	
-	1	706	YP2A7_uc002opn	NM_000764	NP_000755	P20853	CP2A7_HUMAN		3	GAGTCACATATG	0.592	
+	2	354	.1_Intron|CYP2S1_	NM_030622	NP_085125	Q96SQ9	CP2S1_HUMAN		1	CAGCGGCCGGG	0.587	
+	3	688		NM_133444	NP_597701	Q8TF50	ZN526_HUMAN		0	CTTTGCCTCCC	0.622	
-	4	612	2otd.3_Translation	NM_006494	NP_006485	P50548	ERF_HUMAN		4	CAGCACCTCGG	0.687	
+	5	1181	284_uc010ejd.2_	NM_013361	NP_037493	Q9UK11	ZN223_HUMAN	C2H2-type 5.	1	TGGTCCACACA	0.448	
-	4	856	NF285_uc010xxa.1	NM_152354	NP_689567	Q96NJ3	ZN285_HUMAN		4	ATTTTTCTCCTAG	0.428	
-	6	1086	NF229_uc010ejl.1_	NM_014518	NP_055333	Q9UJW7	ZN229_HUMAN		4	CATCATCCCAGT	0.393	rs146515421
+	4	1168	zv.2_Missense_Mu	NM_001042724	NP_001036189	Q92692	PVRL2_HUMAN	cellular (Potential).	0	CCAGACCCTCCT	0.587	
-	3	183	_p.A36T|PPP1R1	NM_006663	NP_006654	Q8WUF5	IASPP_HUMAN		1	GGCCGCCGCCG	0.652	
-	9	1270	dp.1_Missense_M	NM_004819	NP_004810	Q92797	SYMPK_HUMAN		1	TCCTTGCTGCTC	0.652	
-	1	318		NM_001029861	NP_001025032	P60321	NANO2_HUMAN	os-type.|C2HC 1.	0	GGTGTGAGGAG	0.677	
-	3	349		NM_002516	NP_002507	Q9UNW9	NOVA2_HUMAN		0	CCTTCTCGGCAA	0.562	
-	6	860	.S276N|STRN4_	NM_013403	NP_037535	Q9NRL3	STRN4_HUMAN		0	TCGTCGCTGTCT	0.622	
+	15	3417	yo.1_Missense_M	NM_014681	NP_055496	Q14147	DHX34_HUMAN		5	CTGGCCTCTTT	0.587	
-	6	760	issense_Mutation_	NM_003827	NP_003818	P54920	SNAA_HUMAN		0	CCTCGCCTTTGT	0.652	
-	18	1768	b.1_RNA|LIG1_uc	NM_000234	NP_000225	P18858	DNLI1_HUMAN		3	GATGCCCCGGG	0.562	
-	2	735	e.2_Intron|IZUMO	NM_182575	NP_872381	Q8IYV9	IZUM1_HUMAN	cellular (Potential).	1	GAAATCCTTCA	0.562	rs147003407
+	10	1586	tation_p.R374W|S	NM_003089	NP_003080	P08621	RU17_HUMAN	lu-rich (mixed charge).	0	gggggagcggggca	0.139	
-	1	166		NM_178449	NP_848544	Q96A98	TIP39_HUMAN		0	ACCACcagcagca	0.597	
+	6	4646		NM_020719	NP_065770	Q9ULL5	PRR12_HUMAN		2	TCTGGCCAAAA	0.672	
+	5	1678	_p.H481N|ZNF473_	NM_001006656	NP_001006657	Q8WTR7	ZN473_HUMAN	pre-mRNA complex.|C2H2	2	CCATTCACACC	0.502	
-	3	801	AS1_uc002pxn.1_	NM_001523	NP_001514	Q92839	HAS1_HUMAN	lasmic (Potential).	2	GGTCCTCGTCCA	0.622	
-	5	1005	77_uc010ydf.1_5'	NM_023074	NP_075562	Q9BS31	ZN649_HUMAN	C2H2-type 3.	3	CTGTACCTCTTG	0.502	

-	4	422_423	2qar.3_Missense_	NM_001102603	NP_001096073	Q9HCG1	ZN160_HUMAN		1	AGTAAGGGCCAT	0.416	
-	1	478	se_Mutation_p.W8	NM_144687	NP_653288	P59046	NAL12_HUMAN	DAPIN.	7	TCTCTCCCACAG	0.507	
+	6	892	yek.1_Missense_	NM_015629	NP_056444	Q8WWY3	PRP31_HUMAN		1	ATCATGGTCGTC	0.607	
+	5	705	LRA1_uc010yfh.1_	NM_006863	NP_006854	O75019	LIRA1_HUMAN	2.|Extracellular (Potential).	3	CGTACCCATGGG	0.567	
+	13	1925	e_Mutation_p.E53	NM_006669	NP_006660	Q8NHL6	LIRB1_HUMAN	lasmic (Potential).	3	GCCCAGGAAGAA	0.612	
+	6	735	_Intron|KIR2DS4_	NM_012314	NP_036446	P43632	KI2S4_HUMAN	cellular (Potential).	0	GGCCTTCACCCA	0.493	
+	6	621	p.S155G|NLRP2_	NM_017852	NP_060322	Q9NX02	NALP2_HUMAN		2	GGAGATAGCAAA	0.507	
-	5	834	e_Mutation_p.R14	NM_001145971	NP_001139443	Q8NBN7	RDH13_HUMAN		3	CAGCCGCCGGC	0.592	
-	2	1389		NM_176820	NP_789790	Q7RTR0	NALP9_HUMAN	NACHT.	7	ACATGGCGGCA	0.502	
+	2	534		NM_134444	NP_604393	Q96MN2	NALP4_HUMAN	DAPIN.	15	CAGCTTGAACTC	0.413	
-	2	218	sense_Mutation_p.	NM_024303	NP_077279	Q9BUG6	ZSA5A_HUMAN		3	CCCAGGTCTGT	0.468	rs112550672
+	3	166	2_5'UTR|ZNF211_	NM_003435	NP_003426	P52741	ZN134_HUMAN		0	GATGAAGAGTCA	0.448	
+	3	1979	e_Mutation_p.L52	NM_138347	NP_612356	Q7Z340	ZN551_HUMAN	C2H2-type 12.	1	TCTAGCCTCATT	0.458	
-	5	922	0yhp.1_Splice_Site	NM_025027	NP_079303	Q8WXB4	ZN606_HUMAN		2	GCCTTACCCACA	0.552	
-	10	1025	we.2_Missense_	NM_015677	NP_056492	Q96HL8	SH3Y1_HUMAN	SH3.	1	GTTTTTGATATAA	0.388	
+	1	657		NM_003108	NP_003099	P35716	SOX11_HUMAN		3	GCTGGGCAGCC	0.483	
-	10	1304	e_Mutation_p.G37	NM_003183	NP_003174	P78536	ADA17_HUMAN	B.|Extracellular (Potential).	2	TCTTCCCAACTG	0.289	
+	13	1394	se_Mutation_p.E4	NM_182625	NP_872431	Q17RS7	GEN_HUMAN		8	ATTGAGGAAGAA	0.308	
-	26	10384		NM_000384	NP_000375	P04114	APOB_HUMAN	eparin-binding.	27	ATATTTTTCGTGG	0.388	
-	11	1889	R113_uc010eyk.1_	NM_001145168	NP_001138640	Q8IZF5	GP113_HUMAN	cellular (Potential).	4	GGGGCCGAGTA	0.557	
+	3	501	u.2_RNA|ABHD1_	NM_032604	NP_115993	Q96SE0	ABHD1_HUMAN		0	CAGCAGCCAAG	0.532	
+	1	3620	1_5'Flank|ZNF512	NM_032266	NP_115642	Q68DN1	CB016_HUMAN		1	TCATACGGAGAA	0.453	
+	6	710	e_Mutation_p.Q15	NM_206876	NP_996759	P62140	PP1B_HUMAN		1	TGGAGCAGATTC	0.323	
+	7	1171	nl.2_Missense_Mu	NM_182551	NP_872357	Q6UWP7	LCLT1_HUMAN		2	TCAAGGGGAGA	0.473	
-	3	431	_p.G62D|NLRC4_	NM_021209	NP_067032	Q9NPP4	NLRC4_HUMAN	CARD.	6	TCTGAACCCTTT	0.403	
-	10	1226	x.2_Missense_Mu	NM_003162	NP_003153	O43815	STRN_HUMAN		1	ACTTTCCAGAA	0.438	
-	32	5300	se_Mutation_p.S4	NM_019024	NP_061897	Q9P2D3	HTR5B_HUMAN		8	GAGTCTGACACC	0.453	
-	2	161	2_5'Flank|CCDC7	NM_019024	NP_061897	Q9P2D3	HTR5B_HUMAN		8	ACTGGTCTTTTT	0.378	
+	4	403	orf56_uc010ynk.1_	NM_144736	NP_653337	Q7L592	MIDA_HUMAN		1	AATGGATGGCC	0.378	
-	2	94	k|DHX57_uc002rr	NM_198963	NP_945314	Q6P158	DHX57_HUMAN		3	TTTCACCTGCA	0.388	
-	6	865	SOS1_uc002rrl.2_	NM_005633	NP_005624	Q07889	SOS1_HUMAN	DH.	10	GATGGGGACTG	0.353	
-	10	2831	utation_p.E923G|	NM_021097	NP_066920	P32418	NAC1_HUMAN	cellular (Potential).	4	CCAGCTCACCT	0.557	
-	13	1760	yoc.1_Missense_	NM_018079	NP_060549	Q8N5C6	SRBD1_HUMAN		1	TATGAAGTATCTG	0.318	
+	7	1253		NM_002158	NP_002149	P32314	FOXN2_HUMAN		0	CACAGCGTTGTG	0.458	
+	13	1684	p.D315N|KIAA184	NM_001129993	NP_001123465	Q6NSI8	K1841_HUMAN		0	TGAGGGACCAC	0.418	
-	3	446	cp.2_Missense_M	NM_016516	NP_057600	Q9P1Q0	VPS54_HUMAN		0	CCAATCCCCATG	0.383	
+	3	1496	dk.3_Missense_Mu	NM_015147	NP_055962	Q76N32	CEP68_HUMAN		1	ACTATAGGCAAG	0.642	
-	11	1704	uc010yqm.1_Misse	NM_014911	NP_055726	Q2M2I8	AAK1_HUMAN	Gln-rich.	0	CCTGAGGTGGG	0.532	
-	3	881	sns.2_Missense_	NM_001134745	NP_001128217	Q86VH4	LRRT4_HUMAN	cellular (Potential).	4	TCCGAAGGCCTT	0.393	
-	6	697	.1_Intron|MRPL30	NM_138798	NP_620153	Q8WV92	MITD1_HUMAN		2	CCTGTGGTTTCT	0.303	
+	10	1908		NM_015904	NP_056988	O60841	IF2P_HUMAN		3	GGATTCAGGGA	0.303	
-	17	2974	c.2_Missense_Mu	NM_016316	NP_057400	Q9UBZ9	REV1_HUMAN		2	GCACACTGACA	0.428	rs3087396
-	14	2386	c.2_Missense_Mu	NM_016316	NP_057400	Q9UBZ9	REV1_HUMAN		2	TCTTTTGGCTATG	0.353	
-	22	5170		NM_001144013	NP_001137485	A6NKT7	RGPD3_HUMAN	GRIP.	1	CAGACACCTCTT	0.388	rs114550867
-	8	1326	PT10_uc010ywv.1	NM_144710	NP_653311	Q9P0V9	SEP10_HUMAN		0	GCCTGGTATGG	0.483	
+	11	2445	fkp.2_Missense_	NM_019014	NP_061887	Q9H9Y6	RPA2_HUMAN		1	ACGGCCTGTGC	0.433	
+	19	2108	_p.L547F|DPP10_	NM_020868	NP_065919	Q8N608	DPP10_HUMAN	cellular (Potential).	10	TTGTCCCTTCCC	0.294	

+	2	447		NM_183240	NP_899063	Q8WXS4	CCGL_HUMAN	ical; (Potent p.S138F(1)	1	CCTCTCCTCCGC	0.557	
+	3	464	.2_Missense_Muta	NM_002881	NP_002872	P11234	RALB_HUMAN		3	CTTCTTGTGTTCT	0.458	
+	24	2874	GAP1_uc010fng.2_	NM_012233	NP_036365	Q15042	RB3GP_HUMAN		2	CTGCTCCCTACT	0.542	
-	9	1127	nse_Mutation_p.D3	NM_032143	NP_115519	Q5FWF4	ZRAB3_HUMAN	case C-terminal.	2	AGCGAATCATTCT	0.303	
-	50	9038		NM_018557	NP_061027	Q9NZR2	LRP1B_HUMAN	ntial).|LDL-receptor class A	50	CTAGGACAACTA	0.328	
-	2	430	_p.S27N|STAM2_	NM_005843	NP_005834	O75886	STAM2_HUMAN	VHS.	1	ATAAGACTCCAAT	0.368	
+	14	2784	NC1_uc010fom.1_	NM_033394	NP_203752	Q9C0D5	TANC1_HUMAN		3	CCCAGGTACGG	0.542	
-	30	4428	.W1453*|LY75_uc	NM_002349	NP_002340	O60449	LY75_HUMAN	Potential).|C-type lectin 9.	0	CCCAACCCATAG	0.393	
+	13	1129	p.Q347H|NOSTRI	NM_001039724	NP_001034813	Q8IVI9	NOSTN_HUMAN		0	GAGCAAAGACC	0.428	
-	17	2633	lf.1_Missense_Mut	NM_004525	NP_004516	P98164	LRP2_HUMAN	s B 7.|Extracellular (Potenti	29	CTGATACTCTTG	0.418	
+	4	558	p.D152N|GORASI	NM_015530	NP_056345	Q9H8Y8	GORS2_HUMAN		2	GAGCAGATACA	0.358	
-	11	1625	.K1_uc002ugq.2_F	NM_012290	NP_036422	Q9UKI8	TLK1_HUMAN		1	AATTTGGTCTAAC	0.343	
+	25	3108	.W879*|OSBPL6_	NM_032523	NP_115912	Q9BZF3	OSBL6_HUMAN		1	AGCCTGGGTTTC	0.423	
-	307	98608	010zfi.1_Missense_	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	CCTTCACCAGAA	0.368	
-	284	82572	45S|TTN_uc010z	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	CACAGGGTTCCC	0.428	
-	275	73650	171*|TTN_uc010z	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	AAACTGGTACTC	0.413	
-	275	73296	3053I|TTN_uc010z	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	CGTTTACTCTTGT	0.393	
-	244	50211	58R|TTN_uc010zf	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	GGTCCATGCTCT	0.443	
-	46	13096	N_uc010zfi.1_Intr	NM_133379	NP_596870	Q8WZ42	TITIN_HUMAN		153	GGACCAGCTGGA	0.383	
-	9	1378		NM_173648	NP_775919	Q6ZP82	CC141_HUMAN		10	CACCTCCTGGA	0.363	
+	3	388	n_p.A57T|UBE2E3	NM_182678	NP_872619	Q969T4	UB2E3_HUMAN		1	ACCACTGCTAAG	0.463	
-	9	1142	_p.P252S|STAT1_	NM_007315	NP_009330	P42224	STAT1_HUMAN		10	ATTGGGCGGCC	0.483	
-	14	1483	gk.1_Missense_Mu	NM_003151	NP_003142	Q14765	STAT4_HUMAN		9	CCAGCACTGGAC	0.328	
-	19	2001	utz.3_Missense_M	NM_153697	NP_710181	Q8N8A2	ANR44_HUMAN		5	TGGCATCTTTCA	0.458	
+	31	3567_3568	p.G712N|AOX1_u	NM_001159	NP_001150	Q06278	ADO_HUMAN		6	GCGAAGGCCAG	0.475	
-	3	571	2uwf.2_Splice_Site	NM_004071	NP_004062	P49759	CLK1_HUMAN		2	GTTCATACCCCAT	0.343	
+	5	557	hv.1_Missense_Mu	NM_015934	NP_057018	Q9Y2X3	NOP58_HUMAN		0	AAATGGCAGCTA	0.318	
-	4	671	_p.A149V|RAPH1_	NM_213589	NP_998754	Q70E73	RAPH1_HUMAN		10	AGCTGGCATGG	0.433	
+	5	2502		NM_020923	NP_065974	Q9HCK1	ZDBF2_HUMAN		3	AGTTGACTTTTG	0.438	
+	4	522	YVE_uc002vcv.2_	NM_015040	NP_055855	Q9Y2I7	FYV1_HUMAN		10	CATGACCCTCGT	0.438	
+	21	3859	cy.1_Missense_M	NM_015040	NP_055855	Q9Y2I7	FYV1_HUMAN		10	CTCCTAGTGCCT	0.418	
-	32	5325	|FN1_uc002vfh.2_	NM_212482	NP_997647	P02751	FINC_HUMAN		13	TCATTTCTGTTTG	0.458	
+	10	1050	02vhs.2_RNA|uc0	NM_198559	NP_940961	Q7Z7H3	CB062_HUMAN		0	AGCCGGAGGAC	0.701	rs137997315
+	6	940	_p.V201M|CTDSP1	NM_021198	NP_067021	Q9GZU7	CTDS1_HUMAN	CP1 homology.	1	GGCGGGTGCTC	0.627	
-	2	371		NM_002181	NP_002172	Q14623	IHH_HUMAN		1	TCACACCGGGC	0.622	
-	4	887	w.1_Missense_Mu	NM_181457	NP_852122	P23760	PAX3_HUMAN		766	TCCTTCCTCTCC	0.602	
-	12	1140	_p.A389T|FARSB_	NM_005687	NP_005678	Q9NSD9	SYFB_HUMAN	B5.	1	CAATAGCTGCAT	0.368	
-	1	770		NM_005544	NP_005535	P35568	IRS1_HUMAN	RS-type PTB.	12	CATCCACCTGCAT	0.612	
-	4	699		NM_024795	NP_079071	Q53R12	T4S20_HUMAN	lasmic (Potential).	0	AGAGACTCCAC	0.378	
-	3	750	y.1_Intron|TRIP12	NM_004238	NP_004229	Q14669	TRIPC_HUMAN		9	CAGTGGAGGAG	0.552	
+	4	273	.W75*|CHRND_uc	NM_000751	NP_000742	Q07001	ACHD_HUMAN	ellular (Potential).	3	TGAAGTGGAATG	0.582	
-	2	436		NM_019850	NP_062824	Q8N5V2	NGEF_HUMAN	toward RHOA, RAC1 and	7	AAGATGGAATTT	0.498	
+	1	678	JGT1A7_uc002vu	NM_007120	NP_009051	P22310	UD14_HUMAN		1	CTCTACCCTCTG	0.473	
-	11	2062	se_Mutation_p.P42	NM_006037	NP_006028	P56524	HDAC4_HUMAN		6	TGCCGGCGGCT	0.672	
-	5	1034	Intron|ANKMY1_u	NM_016552	NP_057636	Q9P2S6	ANKY1_HUMAN		1	TCCCTTCCTCAG	0.562	
+	3	1021_1022	dn.2_Missense_Mu	NM_021158	NP_066981	Q96RU7	TRIB3_HUMAN	rotein kinase.	2	GGCGCACTGTCA	0.639	
+	5	478	qd.1_Missense_Mutation_p.V40I|PTPRA_uc002whl.2_			P18433	PTPRA_HUMAN	ellular (Potential).	1	CCTTCTGTAGGA	0.383	

-	1	821	5B_uc010zql.1_5'	NM_001810	NP_001801	P07199	CENPB_HUMAN		0	GGTCGGGCAGG	0.711
+	20	1763	p.E555K|PLCB4_	NM_182797	NP_877949	Q15147	PLCB4_HUMAN		15	CTGTAGAAGAT	0.423
-	11	2652	nj.2_Missense_M	NM_020341	NP_065074	Q9P286	PAK7_HUMAN		23	ACCTGCTAGTT	0.512
+	10	1515	p.E380K|PCSK2_	NM_002594	NP_002585	P16519	NEC2_HUMAN	Catalytic.	7	CTCTGGAGGCT	0.572
+	2	454	_p.P50S|DSTN_u	NM_006870	NP_006861	P60981	DEST_HUMAN	ADF-H.	2	CTGATCCTTTC	0.383
+	7	2006	_p.P334S|CSRP2	NM_020536	NP_065397	Q9H8E8	CSR2B_HUMAN		6	TATACTCCCGTG	0.512
-	2	138	2wtu.2_Missense_	NM_178312	NP_842564	Q9BX51	GGTL1_HUMAN		1	CGGAGGTCATG	0.647
+	2	260	F4_uc010zts.1_5'	NM_014742	NP_055557	Q92544	TM9S4_HUMAN		2	GGTTGCCGTGG	0.502
+	3	405	FUT1_uc010ztt.1_	NM_015352	NP_056167	Q9H488	OFUT1_HUMAN		1	GCCCCCTGAGA	0.597
+	2	310	_p.G48E|KIF3B_u	NM_004798	NP_004789	O15066	KIF3B_HUMAN	inesin-motor.	5	CAAAGGGACGG	0.517
+	12	2929	eb.2_Missense_M	NM_015338	NP_056153	Q8IXJ9	ASXL1_HUMAN		248	AGTCATCCCACT	0.498
+	6	683	p.D205N|PLUNC_	NM_130852	NP_570913	Q9NP55	PLUNC_HUMAN		0	TTCTGGACAGC	0.537
+	9	1332	341_uc010geq.2_	NM_032819	NP_116208	Q9BYN7	ZN341_HUMAN		2	AGCAGGTGGTC	0.592
+	4	652		NM_176812	NP_789782	Q9H444	CHM4B_HUMAN	Potential.	2	TCATGGCGGAA	0.493
+	3	240	se_Mutation_p.M1	NM_031483	NP_113671	Q96J02	ITCH_HUMAN	C2.	6	ACCATGAAATC	0.383
+	25	2720		NM_020884	NP_065935	A7E2Y1	MYH7B_HUMAN		2	AACTGGTCATG	0.622
-	19	2391	PC4AP_uc002xb	NM_015638	NP_056453	Q8TEL6	TP4AP_HUMAN		2	TGTAGGGCTCC	0.587
+	2	372	OCR_uc010zuw.	NM_006404	NP_006395	Q9UNN8	EPCR_HUMAN	ellular (Potential).	0	AGACACCAACA	0.637
+	9	1024	vi.1_Missense_M	NM_003116	NP_003107	Q9NPE6	SPAG4_HUMAN	SUN.	0	TCCTGGAGGTG	0.617
+	2	415	p.V108M|C20orf4_	NM_015511	NP_056326	Q9Y312	CT004_HUMAN		0	CTGAGGTGGAG	0.592
-	13	1727	L1_uc002xgj.1_M	NM_002895	NP_002886	P28749	RBL1_HUMAN	ocket; binds T and E1A.	10	CATGTCCCTTG	0.478
-	10	1532	p.R418C|TGM2_u	NM_004613	NP_004604	P21980	TGM2_HUMAN		3	CACACGGATCC	0.592
-	5	1742	nd.2_Missense_M	NM_002251	NP_002242	Q96KK3	KCNS1_HUMAN	=Segment S6; (Potential).	0	TGCTACCACCA	0.602
+	5	862	2xqi.2_RNA|CTS	NM_001127695	NP_001121167	P10619	PPGB_HUMAN		1	CCCCAGCTGGG	0.552
-	18	2791	_p.E2K|ZNF335_	NM_022095	NP_071378	Q9H4Z2	ZN335_HUMAN		4	CTCCTCCATAG	0.592
+	1	426	ND8_uc002xtb.1_	NR_024594					0	GGCAGGGAACG	0.532
+	16	3257	m.2_Missense_M	NM_181659	NP_858045	Q9Y6Q9	NCOA3_HUMAN		5	TCCATGGAACAA	0.483
-	14	4772		NM_021035	NP_066363	Q9P2E3	ZNFX1_HUMAN		2	GCAGGGACTAC	0.587
+	5	607	zyk.1_Missense_	NM_015266	NP_056081	Q9Y2E8	SL9A8_HUMAN	ical; (Potential).	1	CTTCCCCCTATT	0.393
+	2	340		NM_032521	NP_115910	Q9BYG5	PAR6B_HUMAN	OPR.	1	CGCTGGAAAGA	0.338
-	4	2855	p.M481I|SALL4_u	NM_020436	NP_065169	Q9UJQ4	SALL4_HUMAN	2H2-type 7.	2	TGTGTCATGTA	0.458
+	4	358	1L_uc002yaf.1_R	NM_198976	NP_945327	Q8IXH7	NELFD_HUMAN		3	TGCAGGTTCAG	0.413
+	2	593	2yav.2_Missense	NM_080672	NP_542403	Q96KR7	PHAR3_HUMAN		3	GAGATGGACCA	0.582
+	5	1035	TR3_uc002yav.2_	NM_080672	NP_542403	Q96KR7	PHAR3_HUMAN		3	GTGGTGAAGAA	0.542
-	16	6310	s.1_Missense_Mu	NM_033081	NP_149072	Q9BTC0	DIDO1_HUMAN	Pro-rich.	6	CTGCGGGGCCT	0.687
-	4	761	D10_uc002yhn.2_	NM_080621	NP_542188	Q9BYL1	SAM10_HUMAN		0	CTGACCTTGGC	0.682
+	3	383	se_Mutation_p.G8	NM_001338	NP_001329	P78310	CXAR_HUMAN	otential).|Ig-like C2-type 1.	1	TGAAAGGCCGA	0.333
-	2	1251		NM_006988	NP_008919	Q9UHI8	ATS1_HUMAN	ptidase M12B.	6	GTCTGCCACAA	0.463
-	10	1535	160_uc010gll.1_	NM_015565	NP_056380	O94822	LTN1_HUMAN		0	AGTTTCTGCTA	0.388
-	2	275	160_uc010gll.1_	NM_015565	NP_056380	O94822	LTN1_HUMAN		0	ACTCTGAGATG	0.438
-	1	259		NM_001077711	NP_001071179	Q3LI81	KR271_HUMAN		2	AGTTACTTTGC	0.478
+	1	339		NM_181599	NP_853630	Q8IUC0	KR131_HUMAN		1	CCGCTCCCTGG	0.597
-	9	2426	l.1_Missense_Mu	NM_003253	NP_003244	Q13009	TIAM1_HUMAN		10	GCGGCCCATGG	0.478
+	3	368	tion_p.P34S|ITSN	NM_003024	NP_003015	Q15811	ITSN1_HUMAN	EH 1.	4	TTAAAGCCAATAT	0.383
+	2	160		NM_015358	NP_056173	Q14149	MORC3_HUMAN		2	ACCTGGCCATT	0.294
-	3	841	o.2_Missense_M	NM_002240	NP_002231	P48051	IRK6_HUMAN	smic (By similarity).	1	TAATACCCTACG	0.502
-	36	4193	se_Mutation_p.D1	NM_018963	NP_061836	Q9NSI6	BRWD1_HUMAN	Bromo 2.	4	TAATATCTCTGTA	0.343

-	28	5369	CAM_uc002yyr.1_F	NM_001389	NP_001380	O60469	DSCAM_HUMAN	lasmic (Potential).	11	TTACCTCATGAG	0.333	
-	12	1408	p.G276R|TMPRSS	NM_024022	NP_076927	P57727	TMPS3_HUMAN	.|Extracellular (Potential).	3	GGGCCCCCCGC	0.607	
+	13	1314	zem.2_Missense_	NM_002626	NP_002617	P17858	K6PL_HUMAN		0	CCGTGCGCTCG	0.652	
-	8	1127	afl.1_Splice_Site_	NM_001127491	NP_001120963	P05107	ITB2_HUMAN		9	AGACTCACATTG	0.587	rs149804560
-	1	1009	f57_uc002ziw.2_5'	NM_003906	NP_003897	O60318	MCM3A_HUMAN		5	CAGGTCGTTTGT	0.542	
+	5	638	qt.2_Missense_Mu	NM_014339	NP_055154	Q96F46	I17RA_HUMAN	cellular (Potential).	2	CCCATCCCTGAT	0.542	
-	5	572	02zmg.2_Missens	NM_033070	NP_149061	Q9BXW7	CECR5_HUMAN		0	CCTCGGGAGGG	0.572	
+	5	1023	znq.3_Splice_Site_	NM_017929	NP_060399	Q7Z412	PEX26_HUMAN		1	TCCAGGTAAGAG	0.567	
-	4	666	GCR2_uc011agr.1	NM_005137	NP_005128	P98153	IDD_HUMAN	(Potential).|C-type lectin.	1	CGGCATCCCAGT	0.627	
+	1	1503	R14_uc002zou.2_	NM_053006	NP_443732	Q96PF2	TSSK2_HUMAN		1	GACAGGCTTGA	0.637	rs17853776
+	7	750	Missense_Mutation	NM_152906	NP_690870	Q6ICL3	CV025_HUMAN		0	CTATGGGAACC	0.587	
-	3	452	GCR6L_uc010gsc.	NM_033257	NP_150282	Q9BY27	DGC6L_HUMAN	Potential.	0	CTGCTGAGCCG	0.687	
-	5	767	uc002ztt.1_5'Flank	NM_001008695	NP_001008695	Q9BT49	THAP7_HUMAN		0	GGGCTGCCTCG	0.667	
+	13	3283	y.1_Missense_Mut	NM_004327	NP_004318	P11274	BCR_HUMAN	C2.	12	GCATTCCGCTGA	0.577	
+	6	572	p.E149K|CABIN1_	NM_012295	NP_036427	Q9Y6J0	CABIN_HUMAN	TPR 3.	5	TTGAGGAAGGG	0.532	
+	42	6583	utation_p.M1991I|	NM_032608	NP_115997	Q8IUG5	MY18B_HUMAN		12	TCTAGGGATAAC	0.398	
+	13	1145	eo.2_Missense_M	NM_133455	NP_597712	Q96A84	EMID1_HUMAN	Collagen-like.	0	GCAGGGGGAAC	0.333	
-	13	1752	_p.G523D|AP1B1_	NM_001127	NP_001118	Q10567	AP1B1_HUMAN		2	TGTAGCCACGG	0.592	
-	9	948	n.1_Missense_Mu	NM_014303	NP_055118	O00541	PESC_HUMAN		0	CTCCTCTGTGG	0.662	
-	6	5798		NM_173566	NP_775837	Q5THK1	PR14L_HUMAN		0	CCTCCTCCAATA	0.582	
-	2	995	3_5'UTR|RFPL2_	NM_001098527	NP_001091997	O75678	RFPL2_HUMAN		1	cagcacatagacagat	0.03	
-	3	970	aos.2_Missense_M	NM_145640	NP_663615	O95236	APOL3_HUMAN		0	GCCAGGTGGTC	0.562	
+	7	582	H4_uc011amw.1_	NM_013385	NP_037517	Q9UIA0	CYH4_HUMAN	SEC7.	2	CGGGCGAGGCC	0.672	
-	3	2096		NM_052906	NP_443138	Q5R3F8	LRFN6_HUMAN	lasmic (Potential).	2	AGGATGGTCTTC	0.612	
+	9	1269	a.1_Missense_Mu	NM_014291	NP_055106	O75600	KBL_HUMAN		0	ACGGGGCACTG	0.617	
+	10	1090	_p.V287I|EIF3L_u	NM_016091	NP_057175	Q9Y262	EIF3L_HUMAN		1	TCCGGGTCTTC	0.512	
-	7	998	e|CSNK1E_uc003	NM_152221	NP_689407	P49674	KC1E_HUMAN		3	TTCGGCTGGAG	0.582	
+	3	348	1_uc011aok.1_5'U	NM_006116	NP_006107	Q15750	TAB1_HUMAN	PP2C-like.	1	CGAGGCCGATG	0.647	
+	17	3655		NM_001429	NP_001420	Q09472	EP300_HUMAN	Bromo.	64	GAATCCCTGTAA	0.308	
+	28	4924		NM_001429	NP_001420	Q09472	EP300_HUMAN		64	CTGGCCCAATG	0.393	
-	8	1225	dr.1_Missense_M	NM_015140	NP_055955	Q14166	TTL12_HUMAN	TTL.	1	ACTGGGGCAGC	0.662	
+	8	865	_p.S13N|SAMM5	NM_015380	NP_056195	Q9Y512	SAM50_HUMAN		1	GACCAGCCACA	0.468	
-	4	473		NM_001099294	NP_001092764	Q3SXP7	K1644_HUMAN	ical; (Potential).	1	CCAGAACCAGCA	0.522	
-	3	390	e_Mutation_p.S11	NM_148674	NP_683515	Q8NDV3	SMC1B_HUMAN		2	GAACGACTCACA	0.303	
-	1	6124		NM_006071	NP_006062	Q9NTG1	PKDRE_HUMAN	cellular (Potential).	5	AAACTGCATGAA	0.393	
-	32	8524		NM_014246	NP_055061	Q9NYQ6	CELR1_HUMAN	lasmic (Potential).	11	CCCTGGCCGGGT	0.652	
+	5	607	nad.2_Missense_M	NM_015124	NP_055939	Q6IC98	GRAM4_HUMAN		1	AACACTGTGGAG	0.687	
+	3	457	ie.2_Missense_Mu	NM_014346	NP_055161	Q8WUA7	TB22A_HUMAN		1	GCCAGCGGCAG	0.711	
+	11	1464	plice_Site_p.Q365_	NM_014346	NP_055161	Q8WUA7	TB22A_HUMAN		1	TACCAGGTGAGC	0.607	
+	8	1795	jy.2_Nonsense_Mu	NM_031454	NP_113642	Q9BVL4	SELO_HUMAN		0	GCCTGGCAGGC	0.647	
-	8	2137	_uc010has.1_RNA	NM_020461	NP_065194	Q96RT7	GCP6_HUMAN		4	ACCCCGCTGTAC	0.488	
-	20	2761	_p.P520S|SBF1_u	NM_002972	NP_002963	O95248	MTMR5_HUMAN		0	TACCTGGCACCA	0.597	
+	19	1686	ls.3_RNA|NCAPH	NM_152299	NP_689512	Q6IBW4	CNDH2_HUMAN		2	TATGGGGACCAG	0.637	
+	1	1576		NM_138433	NP_612442	Q96G42	KLD7B_HUMAN	Kelch 4.	1	TGCCAGCCACC	0.657	
+	2	241	IP2_uc003bmy.2_	NM_012324	NP_036456	Q13387	JIP2_HUMAN		3	ATCACTGATGACT	0.557	
-	5	945	A_uc003bnd.3_M	NM_001085426	NP_001078895	P15289	ARSA_HUMAN		2	ACTGAGGGTAG	0.612	
+	2	504	EC_uc003bto.2_In	NM_032492	NP_115881	Q8N5M9	JAGN1_HUMAN	nenal (Potential).	1	AGATGTTCCCTG	0.522	

+	14	1394	otx.2_Missense_Mu	NM_153483	NP_705616	Q8NFR9	I17RE_HUMAN	cellular (Potential).	1	CCTGAGGCCAG	0.552	
-	3	1287	uk.2_RNA|PRRT3_	NM_207351	NP_997234	Q5FWE3	PRRT3_HUMAN	ar (Potential).|Pro-rich.	0	GGGCCCCCATG	0.637	
+	11	1502		NM_014229	NP_055044	P48066	S6A11_HUMAN	Name=10; (Potential).	4	GCTGGGTGTAT	0.587	
+	9	1236	zi.2_Missense_Mu	NM_003298	NP_003289	P49116	NR2C2_HUMAN		0	TGGAGGAGGGA	0.493	
-	11	3951	_p.T771I|SATB1_	NM_002971	NP_002962	Q01826	SATB1_HUMAN		4	AAAAGGGTGTTA	0.378	
+	8	2025	1D2_uc011awk.1_	NM_005126	NP_005117	Q14995	NR1D2_HUMAN		3	GCACTCTGAGG	0.348	
+	2	830		NM_001137674	NP_001131146	A6NHJ4	ZN860_HUMAN	KRAB.	1	ATGAAAGTCATC	0.383	
+	2	427		NM_005508	NP_005499	P51679	CCR4_HUMAN	Name=2; (Potential).	1	GATCTGCTCTTC	0.502	
+	2	970		NM_005508	NP_005499	P51679	CCR4_HUMAN	cellular (Potential).	1	CCCTGGTGGAG	0.493	
-	5	2297		NM_015551	NP_056366	O60279	SUSD5_HUMAN	lasmic (Potential).	2	CTTCTCCATCT	0.537	
+	2	431	on_p.T72I|TRAK1_	NM_001042646	NP_001036111	Q9UPV9	TRAK1_HUMAN	AP1 N-terminal.	1	TCCATACACCTC	0.478	
-	2	360	_p.D51N|CCK_uc	NM_000729	NP_000720	P06307	CCKN_HUMAN		1	GCCATCCGTTC	0.687	
-	2	301_302	S42_uc003cqj.2_I	NM_182702	NP_874361	Q7Z5A4	PRS42_HUMAN	Peptidase S1.	1	GCCTGCCTTTGG	0.683	
+	15	1378	N23_uc011bax.1_	NM_015466	NP_056281	Q9H3S7	PTN23_HUMAN		3	CGGCTCTCAGC	0.577	
+	12	2152	010hjy.2_5'UTR|T	NM_130384	NP_569055	Q8WXE1	ATRIP_HUMAN		1	GGGACCCCCAA	0.647	
-	2	310	cm.1_Missense_M	NM_000581	NP_000572	P07203	GPX1_HUMAN		1	TGCACGGGAAG	0.617	
-	1	619	_p.D119N|MST1R_	NM_002447	NP_002438	Q04912	RON_HUMAN	ular (Potential).|Sema.	6	TGTGTCTGTGT	0.677	
+	8	1823	M6_uc003cye.2_M	NM_005777	NP_005768	P78332	RBM6_HUMAN		2	CAAGAGAAGGT	0.388	
-	7	805	af.1_5'Flank|RAS	NM_015896	NP_056980	O75800	ZMY10_HUMAN		5	GTTCCACCAGG	0.597	
-	14	3359	bf.1_Missense_Mu	NM_014703	NP_055518	Q9Y4B6	VPRBP_HUMAN		2	ACCCCTCCATAC	0.463	
-	2	136	2_5'Flank|PARP3_	NM_004704	NP_004695	O43818	U3IP2_HUMAN	lization signal (Potential).	3	CCCCGCAGAGT	0.587	
+	5	1589	K_uc003ddp.1_Sile	NM_145262	NP_660305	Q8IVS8	GLCTK_HUMAN		0	CCAGGGTGGGG	0.582	
-	20	2236	H4_uc011bem.1_M	NM_002218	NP_002209	Q14624	ITIH4_HUMAN		3	GATGGCAGAGG	0.677	
-	9	1141	.E233K|ITIH4_uc0	NM_002218	NP_002209	Q14624	ITIH4_HUMAN	VWFA.	3	GCTCCTCCTGGT	0.617	
+	1	946	iv.2_Missense_Mu	NM_177966	NP_808881	Q6L8Q7	PDE12_HUMAN		0	CTGGGCCTGGC	0.582	
-	8	2256		NM_198859	NP_942559	Q7Z3G6	PRIC2_HUMAN		5	CATCAGCAGAG	0.493	
-	11	1609	od.2_Missense_Mu	NM_018130	NP_060600	Q6PI26	SHQ1_HUMAN		3	GAAAGGCACTG	0.478	
+	5	1415		NM_153605	NP_705833				0	CTGACCCAGCC	0.423	
+	11	2191		NM_153605	NP_705833				0	AACTGGTGAGT	0.348	
-	11	1120	p.S338R|ABI3BP_	NM_015429	NP_056244	Q7Z7G0	TARSH_HUMAN		4	TTTAGTGCTTCT	0.348	
-	4	1034	BTB20_uc003ebl.	NM_015642	NP_056457	Q9HC78	ZBT20_HUMAN		5	AGCTGGGGTCT	0.662	
+	3	178	PK1B_uc003ecd.	NM_006952	NP_008883	O75841	UPK1B_HUMAN	ical; (Potential).	0	CCTGACTGCGG	0.557	
+	5	1976		NM_001102608	NP_001096078	A6NMZ7	CO6A6_HUMAN	cal region.|VWFA 4.	8	ACCTGGTGAGC	0.418	
-	20	2942	Site_p.R432_splic	NM_006219	NP_006210	P42338	PK3CB_HUMAN		5	TACTCACCGGCC	0.413	
+	2	619	e_Mutation_p.S16	NM_032383	NP_115759	Q969F9	HPS3_HUMAN		6	TATTTAGTTTGAA	0.378	
+	1	2101	SC22D2_uc003ex	NM_014779	NP_055594	O75157	T22D2_HUMAN		1	CTCAGACCCAGC	0.498	
-	6	982	.Q46_splice|IFT80	NM_020800	NP_065851	Q9P2H3	IFT80_HUMAN		1	GAAGTACCTGCA	0.423	
+	8	1080	_p.S303F|FNDC3	NM_022763	NP_073600	Q53EP0	FND3B_HUMAN	onectin type-III 1.	3	GACTTTCCTGTG	0.443	
+	24	3228	hz.3_Missense_Mu	NM_022763	NP_073600	Q53EP0	FND3B_HUMAN	onectin type-III 8.	3	CCAGAGACTGA	0.468	
+	10	1121	e_Mutation_p.A36	NM_033540	NP_284941	Q8IWA4	MFN1_HUMAN	lasmic (Potential).	3	GTCAGCAGTGA	0.408	
-	1	148	C39_uc003fkn.2_	NM_181426	NP_852091	Q9UFE4	CCD39_HUMAN		4	TCCTCCCAGTG	0.552	
+	15	1911	nt.2_Missense_Mu	NM_004423	NP_004414	Q92997	DVL3_HUMAN		3	AGGACCCGAAG	0.726	
+	11	1481	foy.2_Missense_M	NM_003741	NP_003732	Q9H2X0	CHRD_HUMAN	CHRD 3.	3	TTGTGGGGCTG	0.607	
+	3	444	bru.1_Intron|MAP	NM_004721	NP_004712	O43283	M3K13_HUMAN		3	AGAGCGTGCAC	0.532	rs147690863
+	20	2095	j.2_Nonsense_Mu	NM_015560	NP_056375	O60313	OPA1_HUMAN	termembrane (By similarity	0	ATCCTTCAACAA	0.289	
-	2	1494		NM_001080513	NP_001073982	P22792	CPN2_HUMAN	p.W468R(1)	5	CAGATCCCAGCT	0.667	
-	2	252		NM_004488	NP_004479	P40197	GPV_HUMAN	cellular (Potential).	3	GGACGGTCATG	0.637	

-	13	1876	3ftz.1_Missense_M	NM_024524	NP_078800	Q9H7F0	AT133_HUMAN		1	GATTGAGCTGTC	0.343	
-	3	8372	C4_uc003fvp.2_Int	NM_018406	NP_060876	Q99102	MUC4_HUMAN		0	GGGTGGCGTGAC	0.572	
-	3	8369	C4_uc003fvp.2_Int	NM_018406	NP_060876	Q99102	MUC4_HUMAN		0	TGGCGTGACCTG	0.572	
-	2	6305	C4_uc003fvp.2_Int	NM_018406	NP_060876	Q99102	MUC4_HUMAN		0	TGGTGTGACCTG	0.597	
-	2	5153	C4_uc003fvp.2_Int	NM_018406	NP_060876	Q99102	MUC4_HUMAN		0	TGGTGTGACCTG	0.572	
-	10	1165	IA_uc003fwh.2_Mi	NM_005017	NP_005008	P49585	PCY1A_HUMAN	ximate.|3 X repeats.	0	AGGGGGAGGGG	0.607	
+	1	4077		NM_175918	NP_787114	Q8N1N5	CRPAK_HUMAN	action with PAK1.	0	GAGTGCCCGCCT	0.657	
+	8	1293	on_p.G346E|FGFR	NM_000142	NP_000133	P22607	FGFR3_HUMAN	3.|Extracellular (Potential).	2600	CTATTGGGTTTTC	0.617	
-	14	1666	N_uc010ich.1_Intr	NM_181808	NP_861524	Q7Z5Q5	DPOLN_HUMAN		4	TGGAGCCCTTTAT	0.433	
+	19	3014	IAN2B2_uc011bwf	NM_015274	NP_056089	Q9Y2E5	MA2B2_HUMAN		2	TCATCACCGTCCA	0.612	
-	2	373	.1_Intron|TAPT1_u	NM_153365	NP_699196	Q6NXT6	TAPT1_HUMAN		0	TGTATACTCTTTC	0.348	
-	3	636	gqo.2_Missense_M	NM_145290	NP_660333	Q8IWK6	GP125_HUMAN	lar (Potential).|LRR 2.	1	CAGAAGGCACCT	0.338	
-	8	1576	GC1A_uc011bxp.1	NM_013261	NP_037393	Q9UBK2	PRGC1_HUMAN		8	CACTGTCCCTCAC	0.463	
+	8	695	A74V|ANAPC4_uc	NM_013367	NP_037499	Q9UJX5	APC4_HUMAN		5	TTTATGCTTATGC	0.338	
-	4	2381		NM_003263	NP_003254	Q15399	TLR1_HUMAN	smic (Potential).|TIR.	5	CACTCTGGACAAA	0.413	
+	4	2012	j.1_Missense_Mut	NM_175737	NP_783864	Q86Z14	KLOTB_HUMAN	ential).|Glycosyl hydrolase-1	1	GCGATGGTCACC	0.647	rs144804057
-	1	463	gm.2_Missense_M	NM_152540	NP_689753	Q8WU76	SCFD2_HUMAN		3	TGGACAGCGTGG	0.612	
+	2	568	ST_uc003hcj.1_Mi	NM_005612	NP_005603	Q13127	REST_HUMAN	action with SIN3A.	9	AGATGGCAGAAC	0.473	
-	2	392	.1_Missense_Muta	NM_004439	NP_004430	P54756	EPHA5_HUMAN	cellular (Potential).	24	CAGTGCGTGAATC	0.308	
+	9	1209	LB_uc003hgu.3_M	NM_000477	NP_000468	P02768	ALBU_HUMAN	Albumin 2.	6	ATGAAACCACTCT	0.383	
+	11	1549	.2_Missense_Muta	NM_198892	NP_942595	Q9NSY1	BMP2K_HUMAN	Gln/His-rich.	1	CACcagcagcagcag	0.244	
+	12	1657	e.1_Missense_Mu	NM_001263	NP_001254	Q92903	CDS1_HUMAN		4	GATTTTGCAAATA	0.338	
-	3	778		NM_145244	NP_660287	Q96D03	DDT4L_HUMAN		1	TAGGACCCTTCAA	0.393	
-	39	6313	e_Mutation_p.V19	NM_001813	NP_001804	Q02224	CENPE_HUMAN	Potential.	9	GTTTTACTTGGTC	0.368	
+	1	153		NM_021227	NP_067050	Q9NRP0	OSTC_HUMAN	lasmic (Potential).	1	CACATGCCGTCGC	0.587	
-	4	3488	_p.S245F|PCDH18	NM_019035	NP_061908	Q9HCL0	PCD18_HUMAN	y similarity).|Cytoplasmic (P	5	TCCAGGGAGTTG	0.562	
-	3	1226	_p.M393T|ZNF827	NM_178835	NP_849157	Q17R98	ZN827_HUMAN	C2H2-type 1.	0	ATCACCATGTGCC	0.458	
+	10	1646		NM_000824	NP_000815	P48167	GLRB_HUMAN	ical; (Probable).	2	TTGTTTCCTTTCT	0.353	
+	4	933		NM_006174	NP_006165	Q15761	NPY5R_HUMAN	lasmic (Potential).	7	CTTGAAGAAAATC	0.378	
+	9	1489	R17_uc003ium.3_M	NM_170710	NP_733828	Q8IZU2	WDR17_HUMAN	WD 7.	6	TCTTGGGCTCCAC	0.338	
-	12	1318	.G342R|ACSL1_uc	NM_001995	NP_001986	P33121	ACSL1_HUMAN	lasmic (Potential).	2	AAAATCCGATTTT	0.448	
-	15	3269	p.Q1059*|TERT_uc	NM_198253	NP_937983	O14746	TERT_HUMAN	CTE.	12	GCCACTGCACGG	0.667	
+	13	1891		NM_015325	NP_056140	Q9Y2F5	K0947_HUMAN		2	ATGATGGGATCGC	0.423	
-	2	870	ee.3_5'Flank|MTRF	NM_024091	NP_076996	Q14CZ7	FAKD3_HUMAN		4	TTTCACCTTGAAG	0.383	
-	3	856	P255L|SLC45A2_u	NM_016180	NP_057264	Q9UMX9	S45A2_HUMAN	lasmic (Potential).	3	TCCTGAGGGGTT	0.468	
-	12	2461	v.2_Missense_Mut	NM_001343	NP_001334	P98082	DAB2_HUMAN		3	TATCCCCAAGTGC	0.557	
-	12	1997	1_Missense_Muta	NM_000065	NP_000056	P13671	CO6_HUMAN	TSP type-1 3.	7	CTCCTCGTTGGC	0.502	rs148521858
-	3	737	se_Mutation_p.D85	NM_006451	NP_006442	Q9H074	PAIP1_HUMAN	MIF4G.	1	AAAAATCCTGAAC	0.368	
+	1	1670	_p.A494T|SNX18_	NM_052870	NP_443102	Q96RF0	SNX18_HUMAN	BAR.	0	GCTATCGCCTTCA	0.612	
-	10	1010	se_Mutation_p.S33	NM_015084	NP_055899	Q92552	RT27_HUMAN		0	AGCTTGGACTGC	0.473	
+	2	10093		NM_153610	NP_705838	Q8N3K9	CMYA5_HUMAN		9	GCGGTTCCATTTG	0.493	
+	7	1546	u.2_Missense_Mu	NM_004385	NP_004376	P13611	CSPG2_HUMAN	minoglycan attachment dor	16	TCCCTCCCGTGG	0.433	
-	6	889	kip.1_Splice_Site_	NM_005711	NP_005702	O43854	EDIL3_HUMAN		2	AGCATTCTGGAA	0.348	
+	2	306	cuc.1_Missense_M	NM_006467	NP_006458	O15318	RPC7_HUMAN		0	CCACCCCCACTAT	0.348	
-	10	1636		NM_001270	NP_001261	O14646	CHD1_HUMAN	ase ATP-binding.	5	CTTGCACCAAGAA	0.333	
-	4	1241	ation_p.L248F|TICA	NM_021649	NP_067681	Q86XR7	TCAM2_HUMAN	TIR.	0	ATTTGAGGAACAC	0.458	
+	36	8384	l.1_Missense_Mut	NM_005509	NP_005500	Q9Y485	DMXL1_HUMAN		2	GGCAGAGGAGCA	0.343	

-	1	976	se_Mutation_p.E2	NM_020747	NP_065798	Q9ULD9	ZN608_HUMAN	Potential.		6	CTCTTCCTTCTT	0.542	
-	11	1422	e_Mutation_p.D40	NM_016340	NP_057424	Q8TEU7	RPGF6_HUMAN			3	CCGGTCTAGTT	0.373	
-	4	1754	kxy.1_Missense_	NM_133456	NP_597713	Q2M3G4	SHRM1_HUMAN			1	TGATCCTCCCC	0.577	
+	5	564	l.2_Missense_Mu	NM_015288	NP_056103	Q9NQC1	JADE2_HUMAN			0	CCCAGCCTGAT	0.582	
+	10	1844	cxu.1_Missense_	NM_021982	NP_068817	O95486	SC24A_HUMAN			0	TCGAAACTGGAT	0.328	
-	9	761	_p.V169I|BRD8_	NM_139199	NP_631938	Q9H0E9	BRD8_HUMAN			1	GCCTACCTCCA	0.522	
-	2	514	RNA|APBB3_uc01	NM_133172	NP_573418	O95704	APBB3_HUMAN	WW.		2	TGCTACCGCTG	0.612	
-	3	293	ARS_uc010jfu.2_	NM_002109	NP_002100	P12081	SYHC_HUMAN			2	AACTGCCATCT	0.448	
+	1	2389	1dan.1_Missense_	NM_018912	NP_061735	Q9Y5H4	PCDG1_HUMAN	lasmic (Potential).		3	AGTCTTTACTT	0.418	
+	1	2038	_Intron|PCDHGA	NM_018913	NP_061736	Q9Y5H3	PCDGA_HUMAN	|Extracellular (Potential).		0	ACCTCGGCAG	0.652	
-	3	3184	.R1023C|PCDH1_	NM_002587	NP_002578	Q08174	PCDH1_HUMAN	lasmic (Potential).		5	GGTGCGGTAGC	0.632	rs147327566
-	6	809	r.1_Missense_Mu	NM_020117	NP_064502	Q9P2J5	SYLC_HUMAN			0	TAAATCCTGAAT	0.323	
+	7	1362	p.A420V|TCERG1	NM_006706	NP_006697	O14776	TCRG1_HUMAN	WW 2.		2	AACAGCAGATGG	0.383	
-	9	1066	oo.2_Missense_M	NM_001387	NP_001378	Q14195	DPYL3_HUMAN			1	GCAAGGAGTTG	0.557	
+	8	991	_p.T287I|AFAP1L	NM_152406	NP_689619	Q8TED9	AF1L1_HUMAN	PH 1.		2	TTTCACCCAGG	0.627	
+	2	289	dca.1_Missense_	NM_152407	NP_689620	Q8TAA5	GRPE2_HUMAN			1	TTGGGCCCCCT	0.483	
-	10	1869	jhd.2_Missense_M	NM_002609	NP_002600	P09619	PGFRB_HUMAN	otential).|Ig-like C2-type 5.		17	TGTTCCCCAGC	0.617	
+	11	1985	IA1_uc011dcx.1_	NM_001114183	NP_001107655	P42261	GRIA1_HUMAN	ical; (Potential).		6	ATTTGGATGTG	0.448	
+	11	2294	_p.T545I|LARP1_	NM_033551	NP_291029	Q6PKG0	LARP1_HUMAN			4	GAACACCTTCA	0.507	
-	12	1266	M19_uc003lwy.2_	NM_033274	NP_150377	Q9H013	ADA19_HUMAN	B.|Extracellular (Potential).		8	ACATTCCACCA	0.542	
+	5	1126	_p.A255S|ODZ2_u	NM_001122679	NP_001116151					10	AATGTGCTGCC	0.562	
+	9	885	CK2_uc011der.1_	NM_004946	NP_004937	Q92608	DOCK2_HUMAN			7	CTAAGGAGATT	0.507	
-	2	1116		NM_004387	NP_004378	P52952	NKX25_HUMAN			1	CACTCCCGAGT	0.657	
-	5	493	_p.K134K|NOP16_	NM_016391	NP_057475	Q9Y3C1	NOP16_HUMAN			2	GAAGTCTTGCC	0.512	
-	3	280	_uc003mez.2_5'F	NM_002115	NP_002106	P52790	HXK3_HUMAN	Regulatory.		7	GTCCCCTCAGC	0.622	
+	3	695	P3_uc003mil.1_5'	NM_015111	NP_055926	O15049	N4BP3_HUMAN			0	GCCTGCACACG	0.682	
+	5	1209	kz.1_Missense_M	NM_182594	NP_872400	Q8N9F8	ZN454_HUMAN	2H2-type 5.		3	CAGGGCACACC	0.383	
-	22	3436	c003mjv.3_5'Flan	NM_014244	NP_055059	O95450	ATS2_HUMAN			4	GGAGGCATTGA	0.567	
-	6	788	.A173T|MAPK9_	NM_002752	NP_002743	P45984	MK09_HUMAN	rotein kinase.		4	CCGGGCCAGGC	0.488	
-	18	2029		NM_005110	NP_005101	O94808	GFPT2_HUMAN	SIS 2.		2	GGAGGCAGTCC	0.532	
+	4	1448	mua.2_Splice_Sit	NM_020135	NP_064520	Q96S55	WRIP1_HUMAN			2	TTTCAGGCCCG	0.522	
+	23	5347	P_uc003mxq.1_In	NM_004415	NP_004406	P15924	DESP_HUMAN	us rod domain.|Potential.		9	CGATAGAAGAT	0.458	
-	10	1172	myb.2_Missense_	NM_001142541	NP_001136013	Q9H1N7	S35B3_HUMAN	ical; (Potential).		0	TGGTCATTGCTT	0.259	
+	10	1689	ag.1_Missense_	NM_030948	NP_112210	Q9C0D0	PHAR1_HUMAN			0	GGCTGGAGCTG	0.572	
+	5	487		NM_016167	NP_057251	Q9UMY1	NOL7_HUMAN			0	AAAAGGAAATG	0.294	
-	9	1411	_p.C404Y|NUP153	NM_005124	NP_005115	P49790	NU153_HUMAN			9	CACTGCACTTG	0.308	
-	39	5003	_p.T1598I|KIF13A_	NM_022113	NP_071396	Q9H1H9	KI13A_HUMAN			4	GCTCGGTGGAG	0.507	
-	23	3029	ch.3_Missense_M	NM_022113	NP_071396	Q9H1H9	KI13A_HUMAN			4	GTTCTTGTCTTA	0.418	
-	4	529	1_uc011dji.1_Spli	NM_001080480	NP_001073949	Q6ZNC8	MBOA1_HUMAN			0	GAATATCTGAAA	0.368	
+	1	35	H2BL_uc003njl.2_	NM_003536	NP_003527	P68431	H31_HUMAN		p.R9G(1)	1	CTGCTCGCAAG	0.587	
-	4	2803		NM_052923	NP_443155	Q6R2W3	SCND3_HUMAN			1	tagcatgaactcttttgg	0	
+	1	905		NM_013936	NP_039224	P58182	O12D2_HUMAN	Name=7; (Potential).		1	GTCACTCCTGTA	0.448	
+	3	484	se_Mutation_p.G1	NM_030883	NP_112145	Q9GZK4	OR2H1_HUMAN	ellular (Potential).		0	TCTGGGCTTCT	0.527	
-	4	631	nl.3_Missense_M	NM_001109809	NP_001103279	Q9NU63	ZFP57_HUMAN			5	CTGTCCATAGT	0.577	
-	4	1159	39_uc003npd.2_I	NM_025236	NP_079512	Q9H2S5	RNF39_HUMAN	B30.2/SPRY.		0	CCACGCGAATG	0.761	
-	10	3795	C1_uc011dmp.1_	NM_014641	NP_055456	Q14676	MDC1_HUMAN	Pro-rich.		4	AGCTGGAAAGG	0.572	
+	2	3595_3596		NM_080870	NP_543146	Q3MIW9	DPCR1_HUMAN	ar (Potential).|Thr-rich.		0	CAAAGGGAAA	0.48	

-	1	1031		NM_021184	NP_067007	O95873	CF047_HUMAN			1	AAGCAGCCCCA	0.542	
+	3	543	_5'Flank|RDBP_uc	NM_006929	NP_008860	Q15477	SKIV2_HUMAN			4	GTGCCCCAGAT	0.542	
+	3	160	0jtu.1_3'UTR|EG	NM_030652	NP_085155	Q99944	EGFL8_HUMAN			0	ACGCAGTCAGG	0.617	rs143726348
+	6	627	FL8_uc003oac.1_	NM_030652	NP_085155	Q99944	EGFL8_HUMAN			0	AGAGCCCCCAA	0.667	
-	66	5387	y.1_Missense_Mu	NM_080680	NP_542411	P13942	COBA2_HUMAN	lar collagen NC1.		5	GTGGGGCTCCC	0.647	
+	41	5714	3_uc003oey.2_5'	NM_002224	NP_002215	Q14573	ITPR3_HUMAN	lasmic (Potential).		19	TGGCCTCCTTCT	0.682	
+	6	470		NM_003093	NP_003084	P09234	RU1C_HUMAN			1	TCGGCCCGGAA	0.552	
+	12	1535	K14_uc003olr.2_	NM_001315	NP_001306	Q16539	MK14_HUMAN			6	CACCACCCCTT	0.478	
-	4	320		NM_138493	NP_612502	Q9P0B6	CF129_HUMAN	ical; (Potential).		0	TCAGGAGGATAA	0.537	
+	14	2116	51_splice|FOXP4_	NM_001012426	NP_001012426	Q8IVH2	FOXP4_HUMAN			1	ACAGGGTATGT	0.622	
-	5	498		NM_006653	NP_006644	O43559	FRS3_HUMAN	S-type PTB.		2	ATATTCCTGGA	0.488	
+	13	2931	_p.P927L|KIAA024	NM_015349	NP_056164	Q6AI39	K0240_HUMAN			1	AGAGCCTCTGA	0.527	
-	3	473	k|KLHDC3_uc00	NM_014623	NP_055438	Q16626	MEA1_HUMAN			2	TTTTACCTGGG	0.433	rs113749803
+	8	1322	.G409E|SLC22A7	NM_153320	NP_696961	Q9Y694	S22A7_HUMAN	ical; (Potential).		0	AGCTGGGACAC	0.647	
+	11	2022	LH_uc011dvl.1_R	NM_006502	NP_006493	Q9Y253	POLH_HUMAN			2	TCCAGGGTGTG	0.463	
+	5	670	dvq.1_Missense_	NM_004955	NP_004946	Q99808	S29A1_HUMAN	ical; (Potential).		3	CCTGGGCAGCC	0.602	
-	11	1085	_p.T93I|SUPT3H_	NM_181356	NP_852001	O75486	SUPT3_HUMAN		p.T256T(1)	3	CCTTGGTTACC	0.413	
-	2	157		NM_001037499	NP_001032588	Q30KQ6	DB114_HUMAN			1	TCTTGGTAAGG	0.388	
-	33	5522	i.2_Missense_Mu	NM_138694	NP_619639	P08F94	PKHD1_HUMAN	ellular (Potential).		44	TTCCACCCAGG	0.483	
-	22	2486	ai.2_Missense_M	NM_138694	NP_619639	P08F94	PKHD1_HUMAN	ellular (Potential).		44	GAGGGGATCCC	0.557	
-	1	860	xf.1_Missense_M	NM_021073	NP_066551	P22003	BMP5_HUMAN			2	TATTTCCCGTC	0.453	
-	4	465	23_uc010kac.2_	NM_183227	NP_899050	Q9ULC3	RAB23_HUMAN			1	CACGAGCACAC	0.353	
-	1	1005	GAT2_uc003pfw.2	NM_080742	NP_542780	Q9NPZ5	B3GA2_HUMAN	enal (Potential).		3	GTCCTCCACCA	0.726	
+	1	543	3_5'Flank|DDX43_	NM_018665	NP_061135	Q9NXZ2	DDX43_HUMAN	KH.		4	ACGAGGAACTG	0.622	
+	17	1994	_p.R572K|MYO6_	NM_004999	NP_004990	Q9UM54	MYO6_HUMAN	osin head-like.		2	TATCAGAGACG	0.338	
-	3	557	bq.1_Missense_M	NM_001080508	NP_001073977	O95935	TBX18_HUMAN	T-box.		5	GCAATGTAATATT	0.383	
+	6	690	_Missense_Mutat	NM_006416	NP_006407	P78382	S35A1_HUMAN	lasmic (Potential).		0	AGATACTTCTC	0.294	
-	63	10189		NM_014611	NP_055426	Q9NU22	MDN1_HUMAN			10	GTGGCCCATCT	0.602	
-	34	4900		NM_014611	NP_055426	Q9NU22	MDN1_HUMAN			10	TTCTGCCAAAC	0.448	
+	7	1544	ense_Mutation_p.	NM_001137667	NP_001131139	Q9UKL3	C8AP2_HUMAN			2	CTAAGGAAGTT	0.348	
-	3	933	c.1_Missense_M	NM_004440	NP_004431	Q15375	EPHA7_HUMAN	ar (Potential).|Cys-rich.		28	TCCCTCGAACC	0.463	
+	3	1086		NM_006581	NP_006572	Q9Y231	FUT9_HUMAN	enal (Potential).		5	CAATCCACAAG	0.363	
-	6	1280	qi.1_Missense_M	NM_001040179	NP_001035269	Q969V1	MCHR2_HUMAN	lasmic (Potential).		8	CTCTTCTTTGG	0.423	
-	6	1307	ef.1_Missense_M	NM_145062	NP_659499	Q96AP4	ZUFSP_HUMAN			1	TGTCGCCTAAA	0.383	
+	1	275		NM_173560	NP_775831	Q8HWS3	RFX6_HUMAN			3	GGGGGCAGTG	0.607	
-	18	3003	.1_RNA|GOPC_u	NM_002944	NP_002935	P08922	ROS_HUMAN	ellular (Potential).		25	GCAGGGGCTTA	0.363	
-	12	2483	u.1_Missense_M	NM_002844	NP_002835	Q15262	PTPRK_HUMAN	ellular (Potential).		8	GTATCCTTTGC	0.512	
-	3	830	e_Mutation_p.A15	NM_002844	NP_002835	Q15262	PTPRK_HUMAN	lar (Potential).|MAM.		8	CACTGCTAGCT	0.408	
+	41	6001	o.2_Missense_Mu	NM_000426	NP_000417	P24043	LAMA2_HUMAN	II and I.|Potential.		10	AGGAAGATGCC	0.338	
+	3	1920	0kfi.2_Missense_	NM_052913	NP_443145	Q86VY9	T200A_HUMAN	lasmic (Potential).		1	TAATTCCATTG	0.522	
-	9	1569	3qci.2_Missense_	NM_001431	NP_001422	O43491	E41L2_HUMAN	FERM.		2	TACCTCTGCCG	0.308	
-	7	1154	de.2_Missense_M	NM_015529	NP_056344	Q6UVY6	MOXD1_HUMAN	enal (Potential).		1	CTGGAGGGATG	0.498	
-	11	1201	u.1_Missense_Mu	NM_005627	NP_005618	O00141	SGK1_HUMAN	kinase C-terminal.		6	TTAAAAGGGGA	0.373	
-	3	431	_p.E82K|IFNGR1_	NM_000416	NP_000407	P15260	INGR1_HUMAN	ellular (Potential).		1	CAGATTCTTTTT	0.343	
+	3	512	hs.2_Missense_	NM_006290	NP_006281	P21580	TNAP3_HUMAN	F-binding.|	p.0?(22)	137	TCAAATCTCAGG	0.488	
-	5	2901		NM_006734	NP_006725	P31629	ZEP2_HUMAN			6	CACAGGAGTGC	0.512	
-	5	1902		NM_006734	NP_006725	P31629	ZEP2_HUMAN			6	TCAGAAGGTTGA	0.438	

+	8	868	hq.1_Missense_M	NM_007124	NP_009055	P46939	UTRO_HUMAN	Spectrin 1.	5	AGTCACCATAG	0.363	
-	2	1680	uc003qky.1_Intron	NM_032145	NP_115521	Q8TB52	FBX30_HUMAN		3	ACGGACTTGGA	0.428	
-	2	1469	uc003qky.1_Intron	NM_032145	NP_115521	Q8TB52	FBX30_HUMAN		3	TCAGATCTATTC	0.413	
-	8	995	ee.1_RNA|NUP4	NM_198887	NP_942590	Q8NFH3	NUP43_HUMAN		1	TATGAGACAAA	0.358	
-	76	13116	e_Mutation_p.V41	NM_182961	NP_892006	Q8NF91	SYNE1_HUMAN	|Cytoplasmic (Potential).	45	TGAAACCATGT	0.438	
-	69	11855	qou.3_Splice_Site	NM_182961	NP_892006	Q8NF91	SYNE1_HUMAN		45	GCCTACCTCCA	0.428	
-	57	9715	NE1_uc010kja.1_	NM_182961	NP_892006	Q8NF91	SYNE1_HUMAN	lasmic (Potential).	45	CTTTTCCACTG	0.358	
-	55	9204	u.3_Missense_Mu	NM_182961	NP_892006	Q8NF91	SYNE1_HUMAN	lasmic (Potential).	45	CATATCTGACC	0.403	
-	37	5484	p.E1628K|SYNE1_	NM_182961	NP_892006	Q8NF91	SYNE1_HUMAN	lasmic (Potential).	45	AGCCTCCTGAA	0.582	
+	6	1605	qe.2_Nonsense_M	NM_012454	NP_036586	Q8IVF5	TIAM2_HUMAN		4	CTTTCTCAACTG	0.557	
+	13	4068	.P4_uc003qrg.2_I	NM_020245	NP_064630	Q9NRJ4	TULP4_HUMAN		1	GCCCCGCACCC	0.652	
-	2	743	_p.P185S|RSPH3_	NM_031924	NP_114130	Q86UC2	RSPH3_HUMAN		2	CATAGGTTCTT	0.338	
+	8	1070	o.2_Missense_Mu	NM_004906	NP_004897	Q15007	FL2D_HUMAN		0	CTCCTCCCGCC	0.512	
+	1	74	22A3_uc011efx.1_	NM_021977	NP_068812	O75751	S22A3_HUMAN		4	CGGGCGCTTCC	0.567	
+	2	204		NM_000301	NP_000292	P00747	PLMN_HUMAN	PAN.	4	TATAGAAGAATG	0.473	
+	2	333	.2_Missense_Mut	NM_005922	NP_005913	Q9Y6R4	M3K4_HUMAN		9	GAGTCCTGAAT	0.428	
-	2	525	.2_5'UTR|RNASE	NM_003730	NP_003721	O00584	RNT2_HUMAN		0	GCTGAACCATAA	0.418	
-	9	1476		NM_003247	NP_003238	P35442	TSP2_HUMAN	SP type-1 1.	5	GGTGACGTCAC	0.657	rs144973525
+	2	928	e_Mutation_p.V27	NM_032448	NP_115824	Q96EK7	F120B_HUMAN		1	CGAAAGTTCTT	0.338	
+	2	1497	ense_Mutation_p.	NM_001098201	NP_001091671	Q99527	GPER_HUMAN	lasmic (Potential).	1	ATGTGAGGTTC	0.602	
-	7	1772	ski.3_Missense_	NM_182924	NP_891554	Q8IY33	MILK2_HUMAN		1	CTGAGGATTCC	0.657	
-	3	450	q.2_Missense_Mu	NM_001080453	NP_001073922	Q8N201	INT1_HUMAN		0	CATTACCTTCAAT	0.592	
-	14	2146	mh.3_Missense_M	NM_152743	NP_689956	Q6PJG6	BRAT1_HUMAN		0	GAAGTCAAAGA	0.622	
+	18	2793	o.2_Missense_Mu	NM_152744	NP_689957	Q7Z5N4	SDK1_HUMAN	nectin type-III 3.	6	CACCACCATTC	0.592	
-	15	5147	18_uc003soj.2_5'	NM_001080495	NP_001073964	O15417	TNC18_HUMAN		0	TTCATCCCAAG	0.537	
-	2	221	e_Mutation_p.R62	NM_001101	NP_001092	P60709	ACTB_HUMAN		0	TGCCTCTCTTG	0.582	
-	2	646		NM_001037163	NP_001032240	Q7Z4H9	SIPAR_HUMAN		0	ATAATGCCTCAC	0.507	
+	1	608		NM_138426	NP_612435	Q86VQ1	GLCI1_HUMAN		0	CCCCTCATCCC	0.388	
+	13	1957	p.P642L|HDAC9_	NM_058176	NP_478056	Q9UKV0	HDAC9_HUMAN	ne deacetylase.	5	TGACCCCTTGA	0.438	
-	5	547	ug.2_Missense_	NM_182762	NP_877439	Q6ZN28	MACC1_HUMAN		3	TTATGTCATCCA	0.348	
+	3	704	4_uc003svb.2_5'U	NM_003112	NP_003103	Q02446	SP4_HUMAN		5	CAGTGGAAGGT	0.383	
+	3	1358	b.2_Missense_Mu	NM_003112	NP_003103	Q02446	SP4_HUMAN		5	ATTCTCTTCAG	0.468	
+	80	13095		NM_003777	NP_003768	Q96DT5	DYH11_HUMAN		15	CCTAGCCCAGT	0.512	
+	7	1493	yw.1_RNA|NUPL2_	NM_007342	NP_031368	O15504	NUPL2_HUMAN	action with GLE1.	3	AAAATTCCATTA	0.318	
-	4	687	_p.R57Q|TRA2A_	NM_013293	NP_037425	Q13595	TRA2A_HUMAN	RRM.	1	GAGATCGCCCA	0.393	
-	15	2137	n_p.P547S|OSBP	NM_015550	NP_056365	Q9H4L5	OSBL3_HUMAN		1	CAGGGGGCTGG	0.647	
-	3	760	_p.G29E|HOXA3_	NM_030661	NP_109377	O43365	HXA3_HUMAN		2	CCTGCCCCGGC	0.711	
-	7	690	_p.P191S|CPVL_u	NM_031311	NP_112601	Q9H3G5	CPVL_HUMAN		2	TTCAGGAAATAT	0.333	
-	11	1655	_p.E456K|PDE1C_	NM_005020	NP_005011	Q14123	PDE1C_HUMAN	tic (By similarity).	4	CTCCTCCAGGA	0.433	
-	22	2044	19L1_uc003tel.1_	NM_015283	NP_056098	Q2PZI1	D19L1_HUMAN		0	TACATCCCAAATT	0.398	
-	6	1426	_p.D356N|KIAA08	NM_001100425	NP_001093895	Q8NCT3	K0895_HUMAN		0	GGAAGTCTATGG	0.463	
+	11	2098	g.2_Missense_Mu	NM_018685	NP_061155	Q9NQW6	ANLN_HUMAN	ction with F-actin.	3	GACTGGAATTG	0.388	
-	5	988	i.1_RNA|TARP_uc003tgf.1_RNA|TARP_uc003tgj.1_RN			A2JGV3	A2JGV3_HUMAN		0	TTCATGGTGTTC	0.398	
-	5	978	i.1_RNA|TARP_uc003tgf.1_RNA|TARP_uc003tgj.1_RN			A2JGV3	A2JGV3_HUMAN		0	CCCCTCCTGGG	0.418	
-	21	2061	_p.W622*|AMPH_	NM_001635	NP_001626	P49418	AMPH_HUMAN	SH3.	5	ACCAGCCAGCC	0.458	
+	2	198	.2_5'Flank|PSMA2	NM_031903	NP_114109	Q9BYC8	RM32_HUMAN		0	TACAGGGCCCA	0.378	
+	16	3660	bi.1_Missense_M	NM_015052	NP_055867	Q76N89	HECW1_HUMAN	WW 2.	23	GGCTGGAACTG	0.552	

+	7	589	xv.2_Missense_Mu	NM_000712	NP_000703	P53004	BIEA_HUMAN		1	CAGCGGCATCT	0.517
+	3	354	ov.1_Missense_Mu	NM_006555	NP_006546	O15498	YKT6_HUMAN	Longin.	0	TCTGTGCCACG	0.478
-	4	1800	bw.1_Missense_M	NM_013389	NP_037521	Q9UHC9	NPCL1_HUMAN	ellular (Potential).	5	GTCCCCGGCAG	0.577
+	6	842	oy.1_Intron|OGDH_	NM_002541	NP_002532	Q02218	ODO1_HUMAN		2	ATCATGCAGTTC	0.577
-	16	2230	e_Mutation_p.P45	NM_033054	NP_149043	B0I1T2	MYO1G_HUMAN		4	CCGGGGTGAGC	0.647
-	16	2143	e_Mutation_p.D42	NM_033054	NP_149043	B0I1T2	MYO1G_HUMAN	osin head-like.	4	CTTGTCGGAGC	0.632
+	2	327	on_p.D61N|CCM2_	NM_031443	NP_113631	Q9BSQ5	CCM2_HUMAN	PID.	0	CTGAGCGACTAT	0.532
-	3	680	lissense_Mutation_	NM_004749	NP_004740	Q969Z0	TBRG4_HUMAN		0	GGAAGGCCAGG	0.612
-	2	734	nse_Mutation_p.S2	NM_000598	NP_000589	P17936	IBP3_HUMAN	Ser/Thr-rich.	3	CGGAGGAGAAG	0.493
+	4	1099	p.P102S|POM121_	NM_172020	NP_742017	Q96HA1	P121A_HUMAN	side (Potential).	0	TTGTGCCTAAG	0.468
+	32	2228	zs.2_Missense_Mu	NM_000501	NP_001075224	P15502	ELN_HUMAN		5	TTGTCTCCCATT	0.602
+	3	935	_p.A209T|UPK3B_	NM_030570	NP_085047	Q9BT76	UPK3B_HUMAN	enal (Potential).	1	CTCTGGCCGGC	0.622
-	18	2194	m.2_Missense_Mu	NM_000601	NP_000592	P14210	HGF_HUMAN	eptidase S1.	4	AACAAGTGGGC	0.373
-	5	6233	v.2_Missense_Mut	NM_033026	NP_149015	Q9Y6V0	PCLO_HUMAN		7	TAAATCCATTTTC	0.363
+	4	3116		NM_181646	NP_857597	A4D1E1	Z804B_HUMAN		11	TCAATAGAGAAA	0.408
+	2	675	_p.H94Q|STEAP2_	NM_152999	NP_694544	Q8NFT2	STEA2_HUMAN		2	TATACACAGAGA	0.378
+	21	5416	.L1731F|AKAP9_	NM_005751	NP_005742	Q99996	AKAP9_HUMAN		26	ATAGACTTTTGA	0.348
+	10	928	1_Intron|COL1A2_	NM_000089	NP_000080	P08123	CO1A2_HUMAN		9	GACGACCTGGT	0.413
+	43	3286	1A2_uc011kib.1_I	NM_000089	NP_000080	P08123	CO1A2_HUMAN		9	GTCGCGATGGT	0.478
-	6	741		NM_018842	NP_061330	Q9UHR4	BI2L1_HUMAN	IMD.	1	CAATTTCTTTGT	0.318
+	51	7741	p.T2493I|TRRAP_	NM_003496	NP_003487	Q9Y4A5	TRRAP_HUMAN		37	TGGCACCAGCT	0.612
+	6	695	tion_p.K170E|AP4	NM_004722	NP_004713	O00189	AP4M1_HUMAN		0	AGAGCAAAGTG	0.572
-	7	1297	C2_uc010lgr.2_R	NM_152742	NP_689955	Q8N158	GPC2_HUMAN		2	CCGCTCCTCCT	0.632
+	5	541	.1_5'UTR|STAG3_	NM_012447	NP_036579	Q9UJ98	STAG3_HUMAN		8	TGCAGGATTTC	0.358
-	5	1434	B4_uc011kkf.1_	NM_004444	NP_004435	P54760	EPHB4_HUMAN	ar (Potential).|Cys-rich.	15	CCGGGGGTCTG	0.637
+	16	2184	a.2_Missense_Mut	NM_015908	NP_056992	Q9BXP5	SRRT_HUMAN		2	CAATCGCTGTG	0.587
-	2	376	uya.1_Missense_	NM_198571	NP_940973	Q8N8M0	CG052_HUMAN		1	CCTCAGGCCCC	0.647
-	5	529	k|CLDN15_uc003	NM_016068	NP_057152	Q9Y3D6	FIS1_HUMAN	intermembrane (Potential).	0	ACTTGGACACA	0.647
+	9	903	D_uc011kmh.1_M	NM_000108	NP_000099	P09622	DLDH_HUMAN		1	GCATCCTTCAA	0.353
-	11	1325	_p.G280E|NRCAM	NM_001037132	NP_001032209	Q92823	NRCAM_HUMAN	xtracellular (Potential).	5	ACATTTCCTCTT	0.378
-	1	1004		NM_024523	NP_078799	Q96CN9	GCC1_HUMAN	Potential.	2	TAAGTCCTGTT	0.527
+	13	1680	lle.2_Splice_Site_	NM_014390	NP_055205	Q7KZF4	SND1_HUMAN		3	GCCAGGTAAGA	0.458
-	3	365	2_5'UTR|ZC3HC1	NM_016478	NP_057562	Q86WB0	NIPA_HUMAN	C3HC-type.	0	AGCATATCACATT	0.408
+	1	98	ense_Mutation_p.	NM_013255	NP_037387	Q9UL63	MKLN1_HUMAN		1	CGCCCGAGTGC	0.697
-	2	186	2_5'Flank|WDR91_	NM_014149	NP_054868	A4D1P6	WDR91_HUMAN		4	ATCCACCTGGC	0.507
-	11	2548	d.3_Missense_Mu	NM_022740	NP_073577	Q9H2X6	HIPK2_HUMAN	1.|Interaction with POU4F	7	CTGCCGCATCA	0.562
-	13	1425	7A3_uc003vvp.2_	NM_207113	NP_996996	Q8NCC5	SPX3_HUMAN		3	CTTCACTGCTC	0.498
-	15	1860		NM_004333	NP_004324	P15056	BRAF_HUMAN	rotein kinas_R603>I(2)|p.T	18290	GATTTCACTGTA	0.368
+	1	290		NM_176881	NP_795362	P59534	T2R39_HUMAN	ellular (Potential).	1	CATCAGCTCAA	0.383
+	5	1198		NM_014141	NP_054860	Q9UHC6	CNTP2_HUMAN	1.|Extracellular (Potential).	11	TGCACGGAGAA	0.388
+	6	1267	.S160N|ZNF398_	NM_170686	NP_733787	Q8TD17	ZN398_HUMAN		1	TGGGTAGCTATC	0.527
+	21	3704	sense_Mutation_	NM_003040	NP_003031	P04920	B3A2_HUMAN	ne (anion exchange).	0	ACCACCCAGAT	0.582
-	2	414	3wiz.1_Missense_	NM_006712	NP_006703	Q14296	FASTK_HUMAN		4	GCTGGGGTTCT	0.677
-	12	1417	p.G426D|SMARC	NM_001003801	NP_001003801	Q6STE5	SMRD3_HUMAN		2	GGTTGCCGGCT	0.617
-	11	1692		NM_170606	NP_733751	Q8NEZ4	MLL3_HUMAN	PHD-type 3.	63	TGAACCCACCT	0.378
+	16	3607	p.R890H|RBM33_	NM_053043	NP_444271	Q96EV2	RBM33_HUMAN		1	GGGGCGCCTG	0.617
-	16	1587	n_p.L306F|LMBR1	NM_022458	NP_071903	Q8WVP7	LMBR1_HUMAN	lasmic (Potential).	0	TGAAAAGTTCTT	0.338

+	13	1800	DR60_uc010lqw.2_	NM_018051	NP_060521	Q8WVS4	WDR60_HUMAN		4	CGGAGGAAATA	0.403
-	2	268	x.2_RNA|VIPR2_	NM_003382	NP_003373	P41587	VIPR2_HUMAN	ellular (Potential).	2	CAGATGAAATC	0.383
-	24	4060	p.P616S|CSMD1_	NM_033225	NP_150094	Q96PZ7	CSMD1_HUMAN	ar (Potential).|Sushi 7.	25	GTTAGGGATGC	0.493
+	3	441	se_Mutation_p.L92	NM_001081552	NP_001075021	Q6PDA7	SG11A_HUMAN		0	TGCAGACTTTTT	0.413
+	7	1511	4_splice|MTMR9_	NM_015458	NP_056273	Q96QG7	MTMR9_HUMAN		0	TGCAGGTGAGA	0.458
+	7	1128	.2_Missense_Mut	NM_001715	NP_001706	P51451	BLK_HUMAN	SH2.	3	GCCTGGATGAA	0.592
+	18	2433	p.G766S|KIAA196	NM_199205	NP_954675	Q8N163	K1967_HUMAN		3	AGGAGGGCCTG	0.632
+	5	776	SF10C_uc011kzr.1	NM_003841	NP_003832	O14798	TR10C_HUMAN	TAPE 3.	0	TGCCCCAGCTG	0.627
-	12	2371	y.1_Missense_Mu	NM_002318	NP_002309	Q9Y4K0	LOXL2_HUMAN	yl-oxidase like.	3	CTGATCGCCGA	0.592
-	8	1021	S9_uc011lax.1_M	NM_018250	NP_060720	Q9NV88	INT9_HUMAN		2	GCAAGGAGGAT	0.468
+	4	865	.1_RNA|RBPMS_	NM_006867	NP_006858	Q93062	RBPMS_HUMAN	RRM.	1	TTGTCAGTTTTG	0.383
+	12	2087	se_Mutation_p.E2	NM_013964	NP_039258	Q02297	NRG1_HUMAN	lasmic (Potential).	0	GATGAGGAGTAT	0.557
+	16	1724	NU1_uc003xjw.2_	NM_001031836	NP_001027006	A8MYU2	KCNU1_HUMAN	.|Cytoplasmic (Potential).	1	GCTCTGCTTTC	0.463
-	6	1249	1_Missense_Muta	NM_014682	NP_055497	O60284	ST18_HUMAN	2HC-type 1.	5	TGGTCTCCCTCT	0.527
-	1	85		NM_000780	NP_000771	P22680	CP7A1_HUMAN		1	TCCCCCAAATCA	0.373
+	1	735	e.3_5'Flank|ADHF	NM_015169	NP_055984	Q15050	RRS1_HUMAN		0	CTACCGGACAC	0.657
-	10	1209	zp.2_Missense_M	NM_014393	NP_055208	Q9NUL3	STAU2_HUMAN	DRBM 4.	0	ATAATCCGGCT	0.403
-	1	162	TPD52_uc003ybt.1	NM_001025253	NP_001020424	P55327	TPD52_HUMAN		1	GCGGTCCATGT	0.532
-	7	1066		NM_018440	NP_060910	Q9NWQ8	PAG1_HUMAN	lasmic (Potential).	0	GTCCTGGGAAT	0.537
+	3	428		NM_000067	NP_000058	P00918	CAH2_HUMAN		1	AGGACCCCTGG	0.264
-	1	444	ydr.1_Missense_M	NM_138817	NP_620172	Q8TCU3	S7A13_HUMAN	ellular (Potential).	1	CTCAGCAAGGA	0.483
+	6	702	P1_uc010mai.2_5'	NM_007013	NP_008944	Q9H0M0	WWP1_HUMAN		2	TTGATGGATTGG	0.338
+	22	2770		NM_007013	NP_008944	Q9H0M0	WWP1_HUMAN	HECT.	2	ATTTGGTTTGG	0.333
-	11	1824	p.P490S|NBN_uc	NM_002485	NP_002476	O60934	NBN_HUMAN		7	CTCTGGTTTTGT	0.353
-	14	2485		NM_012415	NP_036547	O95073	FSBP_HUMAN		4	TCTTGGTGAGG	0.353
-	12	2786	e_Mutation_p.P92	NM_015496	NP_056311	Q69YN4	VIR_HUMAN		2	TTCTGGGGTCA	0.383
+	2	305	be.2_Missense_M	NM_016134	NP_057218	Q9Y646	PGCP_HUMAN		1	GATGTTGCTAAA	0.433
+	54	9946	iw.2_Missense_M	NM_017890	NP_060360	Q7Z7G8	VP13B_HUMAN		20	TTTGAGGTTTATT	0.383
-	22	3523	p.E929K|RGS22_	NM_015668	NP_056483	Q8NE09	RGS22_HUMAN	RGS 2.	7	TAACTCCTTCC	0.358
-	37	4933	.1_Missense_Mut	NM_015902	NP_056986	O95071	UBR5_HUMAN		28	ATTATCTTGGTT	0.423
+	1	289		NM_003301	NP_003292	P34981	TRFR_HUMAN	ellular (Potential).	3	TTCCTGGGTCTA	0.493
-	14	2201	nse_Mutation_p.S	NM_198123	NP_937756	Q7Z407	CSMD3_HUMAN	ar (Potential).|Sushi 3.	63	GATTAGAAAT	0.358
+	3	585		NM_032334	NP_115710	Q9BRU9	UTP23_HUMAN		0	CAGTGGAGTCA	0.378
+	2	312		NM_006438	NP_006429	Q9Y6Z7	COL10_HUMAN	ollagen-like.	3	GGGGCCGAAAG	0.413
+	37	5008	uc003yqy.1_Intron	NM_001039112	NP_001034201	Q2WGJ9	FR1L6_HUMAN	toplasmic (Potential).	11	AGTGACCATCT	0.413
-	14	2374	nse_Mutation_p.P	NM_014751	NP_055566	O43312	MTSS1_HUMAN	Pro-rich.	1	TCACGGGTGTCT	0.632
+	3	409		NM_152412	NP_689625	Q7Z3I7	ZN572_HUMAN		2	ATGATTCCTATGA	0.403
-	12	1043	.1_Missense_Mut	NM_001080399	NP_001073868	Q02509	OC90_HUMAN	holipase A2-like 2.	3	GATGGGACAAG	0.552
+	2	109		NM_003235	NP_003226	P01266	THYG_HUMAN		15	TCCTAGAGTACC	0.542
+	29	5520	.1_Missense_Muta	NM_003235	NP_003226	P01266	THYG_HUMAN	Type IIIB.	15	ACATGGGGTCT	0.463
+	2	417	P1_uc010mec.2_	NM_003882	NP_003873	O95388	WISP1_HUMAN	FBP N-terminal.	2	AGGAGTGTGTG	0.627
-	3	382	se_Mutation_p.T7	NM_153831	NP_722560	Q05397	FAK1_HUMAN	FERM.	6	CCCAGGTGGTT	0.408
-	32	13300	e.1_Missense_Mu	NM_201380	NP_958782	Q15149	PLEC_HUMAN	Globular 2.	9	CACCGGCGTTG	0.672
+	7	976	y.2_Nonsense_Mu	NM_001916	NP_001907	P08574	CY1_HUMAN		0	AAGTGGTCAGT	0.582
+	10	1086		NM_145754	NP_665697	Q96AC6	KIFC2_HUMAN	Potential.	3	GGATGGCCAGC	0.657
+	3	1066		NM_138431	NP_612440	Q96ES6	MFSD3_HUMAN	.|Helical; (Potential).	2	CCTTGGTCTTC	0.637
+	19	2927	p.R943K|SMARCA	NM_003070	NP_003061	P51531	SMCA2_HUMAN		3	TGTTAAGACCAT	0.348

+	2	571		NM_017913	NP_060383	Q7L3B6	CD37L_HUMAN	al.|Self-association.	0	AAAGAGAGAAG	0.438
+	13	2396	DM4C_uc003zkg.2_	NM_015061	NP_055876	Q9H3R0	KDM4C_HUMAN		1	AGGAGGAAGTG	0.483
-	1	485		NM_005454	NP_005445	O95813	CER1_HUMAN		0	ATGACCCCCTGA	0.498
+	15	2008	me.2_Missense_M	NM_173550	NP_775821	Q6TFL3	CI093_HUMAN		0	TGCAGGAGAAG	0.338
+	15	2545	p.G840D|CNTLN_	NM_017738	NP_060208	Q9NXG0	CNTLN_HUMAN		1	TGTGGGTCGTC	0.443
+	11	1334	p.C386R|ADAMTS	NM_001040272	NP_001035362	Q8N6G6	ATL1_HUMAN	TSP type-1 2.	5	GTTTCCTGTGTG	0.597
+	24	4452	3znf.3_Missense_	NM_001040272	NP_001035362	Q8N6G6	ATL1_HUMAN	-like C2-type 4.	5	CCACAGGACTGA	0.512
+	21	2590	zoh.1_Missense_M	NM_017794	NP_060264	Q5VW36	K1797_HUMAN		10	TTAGATGACGAT	0.383
+	2	606	|NFX1_uc003zsp.1	NM_002504	NP_002495	Q12986	NFX1_HUMAN		1	GAGGACCAAAAG	0.478
+	5	775	Mutation_p.G216S	NM_007343	NP_031369	P35030	TRY3_HUMAN	Peptidase S1.	0	CTGGTGGCCCT	0.512
+	8	2053	RA_uc003zvk.2_M	NM_004512	NP_004503	Q14626	I11RA_HUMAN	tential).|Fibronectin type-III	1	GGTTACCCCCGA	0.627
+	2	1038	zvv.2_Missense_M	NM_203299	NP_976044	Q5VYM1	CI131_HUMAN		0	GCTTTTGAGCCT	0.537
-	12	2125	.1_5'Flank|FANCG	NM_004629	NP_004620	O15287	FANCG_HUMAN	TPR 4.	4	ACCTGGGCACAT	0.532
-	8	1679	2_Missense_Mutat	NM_025182	NP_079458	Q7L5A3	K1539_HUMAN		2	AGCAGGCATGT	0.547
-	1	150	T1_uc003zxf.1_RN	NM_014450	NP_055265	Q9Y3P8	SIT1_HUMAN		0	GCTGCAGATGTG	0.627
+	21	3038	_Mutation_p.G989	NM_003995	NP_003986	P20594	ANPRB_HUMAN	lasmic (Potential).	3	GCTAGGATGCT	0.537
+	7	772	MTD3_uc011lqq.1_	NM_144964	NP_659401	Q6PF06	RG9D3_HUMAN		0	CGGTGGGCTTG	0.343
-	4	1023		NM_001145196	NP_001138668	Q5VVP1	F75A6_HUMAN		0	CTGTGACTTGTAT	0.453
+	8	1481	e_Mutation_p.G31	NM_006200	NP_006191	Q92824	PCSK5_HUMAN	Catalytic.	3	ATGGTGGAAGG	0.488
+	17	2588	p.S192N|TLE4_uc	NM_007005	NP_008936	O60756	BCE1_HUMAN		5	AAGCCAGTACTT	0.557
+	4	2479	1_Intron|uc004amj	NM_001145197	NP_001138669	Q6ZUB0	YI020_HUMAN		0	CTAACTCTGAGA	0.468
-	13	3052	e_Mutation_p.E90	NM_017576	NP_060046	Q86VH2	KIF27_HUMAN	Potential.	5	TATTTTCCAGGTG	0.333
-	11	1173_1174	p.P281L|SLC28A3	NM_022127	NP_071410	Q9HAS3	S28A3_HUMAN	cellular (Potential).	4	AATATGGTCGGA	0.51
-	11	1710	CCHC6_uc004aot	NM_024617	NP_078893	Q5VYS8	TUT7_HUMAN		2	CTTGAAGGTTGA	0.373
+	5	592		NR_027917					1	GATGAGGATCAC	0.483
+	4	1926	apq.3_Missense_M	NM_001145124	NP_001138596				0	GGAAAGCCTGT	0.537
+	2	452	ense_Mutation_p.A	NM_003177	NP_003168	P43405	KSYK_HUMAN	SH2 1.	5	CCCATGCCAGC	0.662
-	5	701	.P147S|FANCC_u	NM_000136	NP_000127	Q00597	FANCC_HUMAN		1	AACCAGGATAGT	0.313
-	4	892	ayr.2_Missense_M	NM_018421	NP_060891	Q9BYX2	TBD2A_HUMAN		3	AATCTTCCCCTG	0.597
-	15	2952	p.V752M|TEX10_u	NM_017746	NP_060216	Q9NXF1	TEX10_HUMAN		2	TATACACGTTGAA	0.448
-	3	607	p.A134V|TEX10_u	NM_017746	NP_060216	Q9NXF1	TEX10_HUMAN	HEAT.	2	TGTTCAGCTCGT	0.388
+	5	724	218K|NIPSNAP3B_	NM_018376	NP_060846	Q9BS92	NPS3B_HUMAN		2	ATCCCAGAGTTG	0.408
+	8	1045	_p.T275I|SLC44A	NM_080546	NP_536856	Q8WWI5	CTL1_HUMAN	intermembrane (Potential).	4	CTGTTACTCCTG	0.453
-	8	1206	wc.1_Missense_M	NM_003640	NP_003631	O95163	ELP1_HUMAN		7	GCAAAGCAAAC	0.488
-	25	4178	_Mutation_p.S130	NM_173521	NP_775792	Q5VXU9	CI084_HUMAN		2	TTTGAACTTTCAC	0.373
-	4	593	CL_uc004bna.2_3'U	NM_005388	NP_005379	Q13371	PHLP_HUMAN		0	TCTCCACTGGAG	0.458
-	17	3197	se_Mutation_p.D9	NM_001100588	NP_001094058	Q9HBD1	RC3H2_HUMAN		4	AAGGTCCCCAG	0.348
-	18	1840	e_Mutation_p.E61	NM_001144877	NP_001138349	Q8N9R8	SCAI_HUMAN		5	CTAATTCCAAAAT	0.388
+	3	495	p.E149K|LMX1B_u	NM_002316	NP_002307	O60663	LMX1B_HUMAN		0	AGAAGGAGAAG	0.657
+	3	1162	p.T303M|LRRC8A	NM_019594	NP_062540	Q8IWT6	LRC8A_HUMAN		0	CCTGACGGGCT	0.547
+	4	2502	p.V750M|LRRC8A	NM_019594	NP_062540	Q8IWT6	LRC8A_HUMAN	LRR 16.	0	CCAGGGTGGGC	0.677
+	4	1072	HD1_uc004bwm.2_	NM_001100876	NP_001094346	Q5SRE7	PHYD1_HUMAN		0	GTTCCTCTCCACT	0.547
+	2	496_497		NM_001012715	NP_001012733	Q8NAJ2	CI106_HUMAN		0	CTCATGGGTGG	0.609
+	20	2400	_p.T730I|USP20_u	NM_001110303	NP_001103773	Q9Y2K6	UBP20_HUMAN	DUSP 1.	2	CCATCACCAACC	0.672
-	1	389		NM_198180	NP_937823	P83859	OX26_HUMAN		0	GGAAGCTGAAG	0.622
-	7	916	.S263F|UCK1_uc	NM_031432	NP_113620	Q9HA47	UCK1_HUMAN		0	CTGCTGGACTCC	0.652
-	8	980	RAPGEF1_uc010m	NM_005312	NP_005303	Q13905	RPGF1_HUMAN	SH3-binding.	7	ATGCTGGTGGAG	0.572

+	11	1633		NM_015456	NP_056271	Q8WX92	NELFB_HUMAN		0	AATTTGCCCTTGA	0.612	
-	5	1019		NM_015419	NP_056234	Q9NR99	MXRA5_HUMAN		8	TGCTCCTGTTCTC	0.478	
+	3	730	mij.1_Missense_M	NM_014728	NP_055543	Q14CM0	FRPD4_HUMAN		13	TCCGGCTCCTCC	0.527	
+	3	184		NM_021109	NP_066932				0	GCGATTGAACAGC	0.393	
+	10	1120	_p.R311K|BMX_uc	NM_203281	NP_975010	P51813	BMX_HUMAN	SH2.	5	TACTCAGACAAAA	0.363	
-	6	1101	ID2_uc010nfb.2_Ir	NM_153346	NP_699177	Q8NDZ0	BEND2_HUMAN		5	GTCTCAGTGCTG	0.289	
-	2	564	ı.1_RNA|PHKA2_u	NM_000292	NP_000283	P46019	KPB2_HUMAN		2	TATCCCGCACCC	0.572	
-	3	948		NM_030624	NP_085127	Q96M94	KLH15_HUMAN	BACK.	2	AAACGCTGGTTC	0.423	
-	4	1412		NM_139058	NP_620689	Q96QS3	ARX_HUMAN	Pro-rich.	0	CCCCGGGAAGG	0.692	
+	1	215	2_5'Flank|MAGEB1	NM_002367	NP_002358	O15481	MAGB4_HUMAN		1	CCTCATCTGTTTT	0.572	
-	1	149		NM_000475	NP_000466	P51843	NR0B1_HUMAN	A tandem repeats.|1.	2	GGCTCATCGCCG	0.662	
-	18	2423	D_uc004ddb.1_Mi	NM_004006	NP_003997	P11532	DMD_HUMAN	Spectrin 4.	6	TTATATCAACATC	0.333	
+	1	1488		NM_001013736	NP_001013758	Q5HY64	FA47C_HUMAN		3	CCTCCCGACACTC	0.622	
+	18	2585	34_splice|SYTL5_u	NM_001163335	NP_001156807	Q8TDW5	SYTL5_HUMAN		1	TCTTCAGGTGTGA	0.507	
-	4	473	z.1_RNA|ZNF630_	NM_001037735	NP_001032824	Q2M218	ZN630_HUMAN	KRAB.	2	CACCTTGACAACT	0.418	
+	5	426	se_Mutation_p.R1	NM_006044	NP_006035	Q9UBN7	HDAC6_HUMAN	ne deacetylase 1.	4	CCTGAGCGGCTC	0.592	
+	6	1530	.K411T|CCNB3_uc	NM_033031	NP_149020	Q8WWL7	CCNB3_HUMAN		9	GAGAGAAGTCGC	0.463	
-	18	2931	moe.1_Splice_Site	NM_006306	NP_006297	Q14683	SMC1A_HUMAN		6	TACTCACCTCTTC	0.502	
-	13	2177	_p.S681F|SMC1A_	NM_006306	NP_006297	Q14683	SMC1A_HUMAN	Potential.	6	GCCTGAGACTGCA	0.562	
-	1	421		NM_002565	NP_002556	P51582	P2RY4_HUMAN	Name=2; (Potential).	1	AGGTGTCTGACAA	0.567	
+	15	1101	345S|RAB41_uc0	NM_004312	NP_004303	P36575	ARRC_HUMAN		4	GAGCTACCCTTGC	0.547	rs151266240
+	6	1135	ense_Mutation_p.I	NM_001145408	NP_001138880	Q15233	NONO_HUMAN	DBHS.	4	GTGTGCGCTTTGC	0.512	
-	2	376	AGT1_uc004ect.3_	NM_032121	NP_115497	Q9H0U3	MAGT1_HUMAN		1	ATAACGGAGTAAT	0.408	
+	4	781	edf.2_Missense_M	NM_014499	NP_055314	O00398	P2Y10_HUMAN	lasmic (Potential).	5	TCAAGCCCTTCA	0.512	
+	2	1329	eff.1_Missense_Mu	NM_080832	NP_543022	Q96DU9	PABP5_HUMAN		3	AAAAAAGTCGGC	0.443	
+	1	669	PH2_uc004efu.3_Ir	NM_013347	NP_037479	Q13156	RFA4_HUMAN		0	GAGTATATGTCAA	0.448	
-	2	508	_p.P70Q|TRMT2B	NM_024917	NP_079193	Q96GJ1	TRM2_HUMAN		1	TGGCTTGGTTTCT	0.478	
+	5	682	4eib.1_Missense_M	NM_016607	NP_057691	Q9UH62	ARMX3_HUMAN		2	ATGCTGGGGACTC	0.502	
-	3	534	_p.T161I|TSC22D3	NM_004089	NP_004080	Q99576	T22D3_HUMAN	eucine-zipper.	0	ACAGGGTGTTCT	0.567	
+	4	576	msz.1_Missense_Mutation_p.T103I|ALG13_uc011mta.1			Q9NP73	ALG13_HUMAN		1	ATCCTACCTGCAC	0.502	
-	5	585	ıqd.1_Missense_M	NM_000640	NP_000631	Q14627	I13R2_HUMAN	tential).|Fibronectin type-III	3	AACAGAGTAAATA	0.318	
+	8	1727	RF3_uc004eqy.2_	NM_001031855	NP_001027026	Q496Y0	LONF3_HUMAN	Lon.	2	GCCTATCCCACCC	0.458	
-	1	394		NM_178471	NP_848566	Q8TDV5	GP119_HUMAN	Name=4; (Potential).	2	AGACACTAACCA	0.542	
-	6	636	ın_p.I44T|ENOX2_	NM_182314	NP_872114	Q16206	ENOX2_HUMAN	Pro-rich.	1	GGTGGAATTCCAC	0.398	
-	1	407		NM_054021	NP_473362	Q96P66	GP101_HUMAN	lasmic (Potential).	5	GAGAGAGGGTGG	0.597	
+	8	1910	2_3'UTR|MAGEC3	NM_138702	NP_619647	Q8TD91	MAGC3_HUMAN	MAGE 2.	3	TCATGTCCACCA	0.522	
-	2	2723	fby.2_Missense_M	NM_173078	NP_775101	Q8IW52	SLIK4_HUMAN	lasmic (Potential).	2	GTTTTTCTGGATA	0.383	
+	14	1597	).G449S|FMR1_uc	NM_002024	NP_002015	Q06787	FMR1_HUMAN	ction with RANBP9.	3	GGAATGGGTCGAC	0.438	
+	7	1338		NM_005140	NP_005131	Q16280	CNGA2_HUMAN	cellular (Potential).	3	AATGTGGGCTCC	0.517	
+	8	1129		NM_018558	NP_061028	Q9UN88	GBRT_HUMAN		3	CCCGAAGAGTCAT	0.522	
+	12	911	j.1_Intron|ZNF185_	NM_007150	NP_009081	O15231	ZN185_HUMAN		3	CCAGGGCAGGA	0.602	
-	16	3352		NM_005334	NP_005325	P51610	HCFC1_HUMAN		2	GCCCGCCTGCCG	0.647	
-	7	679	u.1_Missense_Mu	NM_021806	NP_068578	P98173	FAM3A_HUMAN		1	AACTTCAACAGC	0.597	
-	8	977	flx.1_Splice_Site_	NM_001042351	NP_001035810	P11413	G6PD_HUMAN		4	CCCCTACCTTCTC	0.622	
+	2	583	KBKG_uc004fmc.3	NM_001099857	NP_001093327	Q9Y6K9	NEMO_HUMAN	h CHUK/IKBKB.|Potential.	0	CTGGAGGAGAATC	0.627	
+	2	586	4ftf.2_5'UTR|NLGN	NM_014893	NP_055708	Q8NFZ3	NLGNY_HUMAN	cellular (Potential).	0	TGCCCCCAGCACC	0.493	
-	36	4659	qd.2_Missense_Mu	NM_005529	NP_005520	P98160	PGBM_HUMAN	GF-like 9; second part.	9	TGGCAGGACAGA	0.657	

+	2	779	|GJB3_uc001bxz.	NM_024009	NP_076872	O75712	CXB3_HUMAN	ellular (Potential).	0	CAACACCAAGC	0.607	
+	34	4365	10_uc010oyl.1_Int	NM_001039703	NP_001034792	A6NDV3	A6NDV3_HUMAN		0	TCACTGAATAGA	0.473	
-	3	8411		NM_002016	NP_002007	P20930	FILA_HUMAN	Ser-rich.	16	TGCTTGACCCC	0.587	
-	1	43		NM_001004467	NP_001004467	Q5JRS4	O10J3_HUMAN	ellular (Potential).	2	ACCTTCAAAGA	0.428	
+	6	877	POX_uc001fyh.2_	NM_001122764	NP_001116236	P50336	PPOX_HUMAN		1	ATCGTTCCATAT	0.547	
+	7	624	sk.2_Missense_M	NM_002927	NP_002918	O14921	RGS13_HUMAN	RGS.	0	TTCAGGAACCC	0.348	
+	8	2362_2363	N1_uc001gwb.2_	NM_178275	NP_840059				3	GGAGAGGGCTA	0.614	
+	7	1349_1350	2_uc009xch.2_Mis	NM_001877	NP_001868	P20023	CR2_HUMAN	xtracellular (Potential).	8	TCAATGGGCAAA	0.421	
-	1	538		NM_001001959	NP_001001959	Q8NGX0	O11L1_HUMAN	ellular (Potential).	3	GAGGTCGCAGA	0.507	
+	1	103		NM_001004688	NP_001004688	Q96R28	OR2M2_HUMAN	Name=1; (Potential).	4	GCATCTTTTTA	0.522	
-	1	352	LF6_uc010qal.1_	NM_001300	NP_001291	Q99612	KLF6_HUMAN		4	CTCCTCCAGAG	0.557	
+	1	575		NM_001005181	NP_001005181	Q8NH76	O56B4_HUMAN	ellular (Potential).	1	TTATCAGCCTGG	0.488	
+	1	427		NM_001005323	NP_001005323	Q8NH90	O5AK2_HUMAN	Name=4; (Potential).	3	GCATCCGTTTG	0.443	
+	8	4653		NM_001008781	NP_001008781	Q8TDW7	FAT3_HUMAN	|Extracellular (Potential).	5	CTTATCGAAGA	0.358	
+	20	2806	gb.2_Missense_	NM_014361	NP_055176	O94779	CNTN5_HUMAN	nectin type-III 2.	8	GGAAGGAAAAA	0.408	
-	21	2696	_p.F793L|HYOU1_	NM_006389	NP_006380	Q9Y4L1	HYOU1_HUMAN		0	GAGGAACATGC	0.567	
-	8	1220	.R287W|KIRREL	NM_032531	NP_115920	Q8IZU9	KIRR3_HUMAN	otential).|Ig-like C2-type 3.	3	GCCCCGCTTGG	0.592	
-	1	373		NM_175068	NP_778238	Q86Y46	K2C73_HUMAN	Head.	6	CCAGGAGGCTC	0.602	
-	9	1066		NM_182496	NP_872302	Q502W7	CCD38_HUMAN		1	AAGGACAGCTG	0.438	rs139965944
+	15	1422	_p.L446F|KIAA103	NM_015275	NP_056090	Q2M389	WAHS7_HUMAN		2	CTTCTTGTATGC	0.299	
-	10	1429	_p.G239R|FOXN4_	NM_213596	NP_998761	Q96NZ1	FOXN4_HUMAN		2	TGAATCCCTCAT	0.572	
+	4	2801		NM_001033602	NP_001028774	Q5JR59	MTUS2_HUMAN	microtubules.|Mediates int	0	CCAAGGGGGCC	0.562	
-	2	3185	hl.1_Missense_M	NM_203487	NP_982354	Q9HC56	PCDH9_HUMAN	ical; (Potential).	6	GTGACGAAGAT	0.512	
+	10	2368		NM_000369	NP_000360	P16473	TSHR_HUMAN	lasmic (Potential).	299	AAGATGTCTAT	0.453	
-	6	1183	uc001zit.1_Intron	NM_005159	NP_005150	P68032	ACTC_HUMAN		2	CATACGATCAG	0.438	
+	18	2237	_Mutation_p.K645	NM_001128608	NP_001122080	O60336	MABP1_HUMAN	WD 10.	10	AGCAGAAGAAG	0.527	
-	16	2257	_p.E665K|TRPM7_	NM_017672	NP_060142	Q96QT4	TRPM7_HUMAN	lasmic (Potential).	10	TTGCTTCATATG	0.358	
-	14	1982	_p.R614*|SLTM_u	NM_024755	NP_079031	Q9NWH9	SLTM_HUMAN	lu-rich.|Potential.	1	ACCTTCGAAGTT	0.363	
-	10	1877	E3_uc010bil.1_Mi	NM_005078	NP_005069	Q04726	TLE3_HUMAN	CN domain.	2	TCATTGGAAACAT	0.527	
-	4	2370	s.1_Missense_M	NM_001717	NP_001708	Q01954	BNC1_HUMAN	2H2-type 4.	3	TGCGGGAGGGA	0.323	
+	25	2886	v.1_Missense_M	NM_000548	NP_000539	P49815	TSC2_HUMAN		10	TGACACCCCCG	0.637	rs144329595
+	2	610	F213_uc010bth.2_	NM_004220	NP_004211	O14771	ZN213_HUMAN	SCAN box.	0	ACGGGGATGTG	0.622	
-	5	2188		NM_024675	NP_078951	Q86YC2	PALB2_HUMAN		11	CCATGCGTTTA	0.433	
-	5	440	A10P_uc002edi.1_RNA						0	GTGTTTTTGTA	0.512	
+	15	2022	nl.2_Missense_M	NM_003119	NP_003110	Q9UQ90	SPG7_HUMAN	drial matrix (Potential).	0	GGGATGGCACC	0.657	
-	1	896		NM_002548	NP_002539	P34982	OR1D2_HUMAN	lasmic (Potential).	1	CCAGAGCCCCA	0.463	
+	4	595	CA3_uc010cte.1_	NM_173847	NP_776246	Q8IXA5	SACA3_HUMAN	ellular (Potential).	2	CTAATCTCAAG	0.413	
-	1	457		NM_033059	NP_149048	Q9BYQ6	KR411_HUMAN	-[GIKRQVHEL]- [SPTR]-[S	0	gagatgctgcagctgg	0.129	
-	1	103		NM_025237	NP_079513	Q9BQB4	SOST_HUMAN		0	CTACACGGAAG	0.627	
+	6	893	.2_RNA|DCAF7_u	NM_005828	NP_005819	P61962	DCAF7_HUMAN		1	TGCTTCGCCTC	0.572	
-	1	69	nse_Mutation_p.A	NM_002059	NP_002050	P01242	SOM2_HUMAN		3	TACCTGCAGCCA	0.597	rs148779841
-	11	1400	_p.S448F|PIP5K1	NM_012398	NP_036530	O60331	PI51C_HUMAN		4	TTACAGGAGTTC	0.652	
-	3	21493		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	h.|Extracellular (Potential).	57	GGAAGGGAGAG	0.507	
-	3	15005		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).	57	TAGAGGAAGTG	0.517	
-	4	1258		NM_031310	NP_112600	Q9BX97	PLVAP_HUMAN	ellular (Potential).	0	CCATGGGCCTT	0.597	
+	5	1465		NM_144689	NP_653290	Q8TAQ5	ZN420_HUMAN		0	TGAGAAACCCT	0.403	
-	5	629	10xuc.1_Missense	NM_170604	NP_733749	Q8TDF6	GRP4_HUMAN	rminal Ras-GEF.	3	GGGATCCTGGT	0.582	

-	1	310	)02ozg.3_Missens	NM_013256	NP_037388	Q9UJW8	ZN180_HUMAN		2	AGCTTCCCGCG	0.667	
-	1	166		NM_178449	NP_848544	Q96A98	TIP39_HUMAN		0	ACCACcagcagca	0.597	
+	4	1011	)221E|SIGLEC7_	NM_014385	NP_055200	Q9Y286	SIGL7_HUMAN	2.|Extracellular (Potential).	1	GGGGATGAAGG	0.597	
+	8	1498	_p.A453V|LILRA2_	NM_001130917	NP_001124389	Q8N149	LIRA2_HUMAN	ical; (Potential).	1	TGAGGCTCAGC	0.567	
+	5	1578		NM_152677	NP_689890	Q8NAM6	ZSCA4_HUMAN		1	ATGAGGGAAATT	0.473	
+	5	494	F512_uc010ylx.1_	NM_032434	NP_115810	Q96ME7	ZN512_HUMAN		1	CCAATCCCAAAT	0.468	
+	9	1831	v.2_Missense_Mut	NM_206943	NP_996826	Q14766	LTBP1_HUMAN		8	ATGATGGAATGC	0.368	
-	9	3464	_Mutation_p.G103	NM_025052	NP_079328	Q56UN5	YSK4_HUMAN	rotein kinase.	5	GCCACCAGGAA	0.408	
-	3	581		NM_019850	NP_062824	Q8N5V2	NGEF_HUMAN	toward RHOA, RAC1 and	7	GGAGGCATTCT	0.468	
-	2	235	nk|C20orf7_uc002	NM_016649	NP_057733	Q9H501	ESF1_HUMAN		1	GTCATGAAACAT	0.443	
+	2	63	tj.1_RNA|FRG1B_uc010gdr.1_RNA|FRG1B_uc010ztk.1_Intron						0	AGAATCGCCCTG	0.353	rs7266938
-	2	143		NM_003225	NP_003216	P04155	TFF1_HUMAN	P-type.	0	ACGGGGGGCCA	0.522	
-	2	301	oa.2_Missense_M	NM_001351	NP_001342	Q92904	DAZL_HUMAN		0	TTGCAGTAGACT	0.343	
-	7	3619	eal.2_Missense_M	NM_001009899	NP_001009899	Q68DE3	K2018_HUMAN		3	TTGATCAGGGA	0.423	
-	7	2195	olc.1_Missense_M	NM_001017395	NP_001017395	O94876	TMCC1_HUMAN	Potential.	1	GCTGCTGCAGC	0.572	
+	14	2124	eyn.2_Missense_M	NM_053002	NP_443728	Q86YW9	MD12L_HUMAN		7	ATTTTTCCATCTA	0.388	
+	7	932	.S218L|FAM193A_	NM_003704	NP_003695	P78312	F193A_HUMAN		3	GTTATCGTCCC	0.488	
+	11	1864	_p.I443L|CPZ_uc	NM_001014447	NP_001014447	Q66K79	CBPZ_HUMAN		3	GACTTCATTCTG	0.587	rs149680311
-	1	675	_p.R74W|UGT2B4_	NM_021139	NP_066962	P06133	UD2B4_HUMAN		2	TTACCCTCTCTAT	0.373	
+	13	2363		NM_020840	NP_065891	Q9P278	FNIP2_HUMAN	tion with PRKAA1.	0	ATCTCCAGAGT	0.552	
-	19	2230	_p.R608C|NEK1_u	NM_012224	NP_036356	Q96PY6	NEK1_HUMAN		6	ACCACGAAGTT	0.338	
+	15	2141	7_uc011cpn.1_RN	NM_000587	NP_000578	P10643	CO7_HUMAN	Sushi 2.	0	GCTCCAGCCTTA	0.493	
-	13	2318	knp.2_Missense_	NM_173488	NP_775759	Q86UG4	SO6A1_HUMAN	lasmic (Potential).	7	CAGTTTCTTCTT	0.269	
+	10	1954	011cwm.1_Missen	NM_005460	NP_005451	Q9Y6H5	SNCAP_HUMAN		2	ATGATTCTGTAG	0.473	
+	2	282	dix.1_Missense_M	NM_001143942	NP_001137414	Q9BX46	RBM24_HUMAN		2	AACCAAGGATCA	0.517	
-	5	1065	_uc003ntw.2_Miss	NM_004640	NP_004631	Q13838	DX39B_HUMAN	ase ATP-binding.	0	CAGCAACCTGC	0.498	
-	10	6683	318_uc003ouw.2_	NM_014345	NP_055160	Q5VUA4	ZN318_HUMAN		7	TCCAGGGAACTA	0.473	
-	5	756	p.P232S|RHAG_u	NM_000324	NP_000315	Q02094	RHAG_HUMAN	cellular (Potential).	2	TCCAGGTTCAG	0.502	
+	2	581	bm.2_Missense_	NM_153362	NP_699193	Q8N3Z0	PRS35_HUMAN	eptidase S1.	1	TTCTTAACCAATT	0.478	
+	5	1098	.R243L|ESR1_uc0	NM_001122742	NP_001116214	P03372	ESR1_HUMAN	tor.|Mediates interaction wi	5	GGCTCCGTAAAT	0.542	
+	3	1262	.2_Missense_Mut	NM_005922	NP_005913	Q9Y6R4	M3K4_HUMAN		9	AGGCTCTTCAG	0.423	
-	6	669	)2_uc003snn.3_Int	NM_001100600	NP_001094070	Q8IY49	PAQRA_HUMAN	lasmic (Potential).	1	AGCTCCCTGTT	0.552	
+	19	2202	S_uc003uty.3_RN	NM_012447	NP_036579	Q9UJ98	STAG3_HUMAN		8	GAGCTTGAAGAG	0.572	
-	8	1420	_p.V342A|CREB3L	NM_194071	NP_919047	Q70SY1	CR3L2_HUMAN	Potential).|Leucine-zipper.	160	TCTAGAACCTCT	0.438	
-	15	1860		NM_004333	NP_004324	P15056	BRAF_HUMAN	rotein kinas_R603>I(2)|p.T	18290	GATTTCACTGTA	0.368	
-	4	2553		NM_178857	NP_849188	Q8IWN7	RP1L1_HUMAN		8	GTATGGGGGCC	0.657	
+	4	1335	1_uc011ldy.1_Intr	NM_006269	NP_006260	P56715	RP1_HUMAN		12	GGAGCGAAGCA	0.433	rs141279458
-	6	1422	_p.K262*|SDR16	NM_138969	NP_620419	Q8N3Y7	RDHE2_HUMAN		3	ACATTTTTTCTTG	0.318	
+	8	879	P1_uc010mai.2_I	NM_007013	NP_008944	Q9H0M0	WWP1_HUMAN		2	TAGTCCAAAACT	0.403	
-	14	1651	s.1_Missense_Mu	NM_015902	NP_056986	O95071	UBR5_HUMAN		28	AAAGAGGATTATT	0.323	
-	6	1753	s.2_Intron|TMEM2	NM_013390	NP_037522	Q9UHN6	TMEM2_HUMAN		2	TGAAAGAGAAA	0.368	
+	4	805		NM_001001670	NP_001001670	Q6ZQQ2	F75D1_HUMAN		0	ATCACATTGAGA	0.527	
-	4	3084	bq.1_Missense_M	NM_133445	NP_597702	Q8TCU5	NMD3A_HUMAN	cellular (Potential).	7	CCACTCCATCAG	0.418	
-	7	1012	GBGT1_uc011mcx.	NM_021996	NP_068836	Q8N5D6	GBGT1_HUMAN	enal (Potential).	0	ACACGCCTGCGC	0.597	
+	46	6986	coi.2_Missense_M	NM_000718	NP_000709	Q00975	CAC1B_HUMAN	lasmic (Potential).	6	CTTTCGAGGAG	0.647	
-	5	4056		NM_015419	NP_056234	Q9NR99	MXRA5_HUMAN		8	TTTTTCTGGTGG	0.368	
+	3	354	IB3_uc004doz.2_	NM_033031	NP_149020	Q8WWL7	CCNB3_HUMAN		9	TCAGTCCAGCA	0.483	

-	13	1152	i.1_Nonsense_Mu	NM_022052	NP_071335	Q9H4D5	NXF3_HUMAN	NTF2.	3	CTGTCGATCTC	0.522	
-	105	15336	e_Mutation_p.P76	NM_020765	NP_065816	Q5T4S7	UBR4_HUMAN		25	TGGTAGGCACC	0.542	
-	13	2891	p.D203N|KIF17_u	NM_020816	NP_065867	Q9P2E2	KIF17_HUMAN		4	ATTGTCTGCTG	0.582	
+	19	2184	ation_p.D27A|NBP	NM_001037675	NP_001032764	Q3BBV1	NBPFK_HUMAN	NBPF 5.	0	GCTGGATGAGA	0.483	
-	11	1575	nr.1_Missense_Mu	NM_001025603	NP_001020774	P48382	RFX5_HUMAN		1	TCTATATCCTGCT	0.532	
-	2	3389	e.1_Missense_Mu	NM_007113	NP_009044	Q07283	TRHY_HUMAN	0 AA tandem repeats.	5	cgccttctcttctcccgtt	0.239	
-	3	4292	uc001ezv.2_Intron	NM_001014342	NP_001014364	Q5D862	FILA2_HUMAN		17	CTGTCCATGAC	0.527	
-	3	1113		NM_016190	NP_057274	Q9UBG3	CRNN_HUMAN	Gln-rich.	3	CTGAGTGTGTC	0.592	
-	2	900	HDC8A_uc001hc	NM_018203	NP_060673	Q8IYD2	KLD8A_HUMAN	Kelch 3.	1	GCATGCTCCTC	0.622	
+	1	494		NM_001004690	NP_001004690	A3KFT3	OR2M5_HUMAN	ellular (Potential).	3	CATTTTCCTTCT	0.443	
-	2	885	2_Intron|RASSF4_	NM_007021	NP_008952	Q9NTK1	DEPP_HUMAN		0	TCTGAGGACAC	0.607	
-	21	2892	qul.1_Missense_M	NM_003474	NP_003465	O43184	ADA12_HUMAN	lasmic (Potential).	9	TGCACGTGGAG	0.552	
+	52	5620_1562	b.2_Missense_Mu	NM_017511	NP_059981	Q9HC84	MUC5B_HUMAN	em repeats, Ser/Thr- rich.|	0	CCAGGGACCA	0.639	
-	3	560		NM_001012709	NP_001012727	Q6L8H1	KRA54_HUMAN	repeats of C-C-X-P.	0	AGGAGCCACAG	0.677	
+	32	6648	p.R1157Q|NAV2_	NM_182964	NP_892009	Q8IVL1	NAV2_HUMAN		6	CCGTCGGATCA	0.582	
-	1	444		NM_001039396	NP_001034485	Q2M385	MPEG1_HUMAN	xtracellular (Potential).	2	GAGTTCATCTCC	0.438	
-	2	570	nsense_Mutation_	NM_013402	NP_037534	O60427	FADS1_HUMAN	l).|Cytochrome b5 heme-b	1	TTCTCCAATCA	0.507	
-	5	6119	AK_uc001ntk.1_I	NM_001620	NP_001611	Q09666	AHNK_HUMAN		19	ACATCCACATCC	0.502	
+	3	423		NM_004585	NP_004576	Q9UL19	TIG3_HUMAN		1	TCACCCAGCTG	0.542	
-	3	897		NM_006248	NP_006239				0	TTGTGGGGGTG	0.617	
-	3	584	_p.G11W|GJB6_uc	NM_006783	NP_006774	O95452	CXB6_HUMAN	lasmic (Potential).	1	ACCCCCGATGA	0.507	rs104894415
+	1	461		NM_030979	NP_112241	Q9H361	PABP3_HUMAN	RRM 2.	4	TGTGATGAAAAT	0.363	
+	1	2205		NR_003268					0	ATGTGCCTGATT	0.428	rs57976037
+	2	409	_p.R5W|TSSK4_	NM_174944	NP_777604	Q6SA08	TSSK4_HUMAN	rotein kinase.	0	TCTTGCGGCAC	0.517	
+	2	367	.1_5'UTR|SRP54_	NM_003136	NP_003127	P61011	SRP54_HUMAN	G-domain.	1	CAGACCTTGGA	0.328	
-	7	8020	px.2_Missense_M	NM_138420	NP_612429	Q8IVF2	AHNK2_HUMAN		1	GGACAGGTCCC	0.597	
-	187								0	CTGACCTCCCC	0.587	rs7146961
+	1	109		NM_001080841	NP_001074310				0	TTGTTGTGATG	0.498	
+	2	87		NM_000761	NP_000752	P05177	CP1A2_HUMAN		4	TGTTCCCTTCT	0.532	
-	5	785	HRNB4_uc010blh	NM_000750	NP_000741	P30926	ACHB4_HUMAN	ellular (Potential).	0	GAAGTCGTAAG	0.552	
+	4	2161		NM_003414	NP_003405	Q14586	ZN267_HUMAN	2H2-type 12.	4	ACATCAGAGAA	0.438	
+	2	199	2_uc010cbk.1_M	NM_022162	NP_071445	Q9HC29	NOD2_HUMAN	CARD 1.	4	CGCAGGAGGCT	0.607	
+	1	213	P9-9_uc010wfq.1_	NM_031963	NP_114169	Q9BYQ0	KRA98_HUMAN	C-C-[RQVSGE]- [SPSNQ]-	1	GCCCATCTGTG	0.637	
-	9	1241	zi.3_Missense_Mu	NM_012448	NP_036580	P51692	STA5B_HUMAN		6	CTTCCCGCCCA	0.587	
+	4	279	iky.2_Missense_M	NM_004287	NP_004278	O14653	GOSR2_HUMAN	ic (Potential).|Potential.	2	CAGTCGGGTTG	0.527	
+	4	1858	e_Mutation_p.H59	NM_144566	NP_653167	Q9H0M5	ZN700_HUMAN	2H2-type 13.	0	CCTCACACCTT	0.463	
+	4	1651	ym.1_Missense_M	NM_001136501	NP_001129973	Q08AG5	ZN844_HUMAN		0	AAACCCTATGA	0.413	
-	4	1523		NM_145276	NP_660319	Q8TA94	ZN563_HUMAN	2H2-type 11.	0	TAACGCTTTCC	0.428	
-	4	1355		NM_145276	NP_660319	Q8TA94	ZN563_HUMAN	2H2-type 9.	0	TAACGTTTTCC	0.413	
-	4	901		NM_005815	NP_005806	Q9Y2A4	ZN443_HUMAN	2H2-type 4.	1	AAAAGAAAAGG	0.378	
-	4	1409	709_uc002mtx.3_I	NM_144976	NP_659413	Q8TBZ8	ZN564_HUMAN	2H2-type 11.	1	AGGCTCTACCA	0.433	
+	4	1543		NM_031218	NP_112495	P35789	ZNF93_HUMAN		1	CTGGAGAGAAA	0.373	
-	7	1908	_Mutation_p.Q40	NM_181882	NP_870998	Q9BXM0	PRAX_HUMAN	L]-[LIVMAP]- [AQKHRPE];	2	CAGCTGTACCT	0.587	
-	4	2233	p.N652Y|ZNF28_	NM_006969	NP_008900	P17035	ZNF28_HUMAN	2H2-type 18.	1	AAGGTTTGACAT	0.408	
-	5	1439	k.1_Intron|ZNF81	NM_001031665	NP_001026835	Q0VGE8	ZN816_HUMAN	2H2-type 6.	0	TTTCTGACTGA	0.398	
+	4	1386	dw.1_Missense_M	NM_138374	NP_612383	Q96IR2	ZN845_HUMAN	2H2-type 8.	0	TCAGATGTCATC	0.413	
+	7	1834	_p.R405L|ZNF761_	NM_001008401	NP_001008401	Q86XN6	ZN761_HUMAN	2H2-type 9.	1	TAGACGTCATA	0.393	

+	5		010fhg.2_Splice_Site|FLJ40330_uc010fhh.2_Splice_Site						0	TTTTCAGTGTCTT	0.313	
-	38	6659		NM_004525	NP_004516	P98164	LRP2_HUMAN	B 20.|Extracellular (Potent	29	GCAATACCCCGG	0.393	
+	3	195	RG1B_uc010gdr.1_RNA|FRG1B_uc010ztk.1_Missense_Mutation_p.N7D						0	GCCTCAAATAGC	0.358	
+	3	222	RG1B_uc010gdr.1_RNA|FRG1B_uc010ztk.1_Missense_Mutation_p.A16T						0	ATGAAGCAGGG	0.373	
+	3	243_244	RG1B_uc010gdr.1_RNA|FRG1B_uc010ztk.1_Missense_Mutation_p.S23D						0	CAAAAAGTAAAA	0.361	
-	12	1120	N_uc002ysl.2_5'	NM_145858	NP_665857	O95825	QORL1_HUMAN		0	AAACACCAGTTG	0.378	
+	5	1146	A2A_uc010guq.2_	NM_000675	NP_000666	P29274	AA2AR_HUMAN	lical; Name=4.	0	CATCTGCTGGG	0.587	
+	4	2181	H_uc003afp.2_5'	NM_021076	NP_066554	P12036	NFH_HUMAN	S-P-[AEPV]-[EAK]- [AEVK]	0	GCAAAGTCCCCT	0.557	
+	7	3960	tq.1_Missense_M	NM_001039141	NP_001034230	Q9H2D6	TARA_HUMAN		1	CCCACCCCGCC	0.706	
-	3	753		NM_198560	NP_940962	Q7Z7J7	LHPL4_HUMAN		3	ATGTCCCGGATG	0.627	
-	34	10131	kf.2_Missense_M	NM_001407	NP_001398	Q9NYQ7	CELR3_HUMAN	lasmic (Potential).	11	GGGCCCAAGCA	0.597	
-	8	1164		NM_003500	NP_003491	Q99424	ACOX2_HUMAN		0	GCCTGGGCCGG	0.637	
+	11	1887	tm.2_Missense_	NM_022131	NP_071414	Q9H4D0	CSTN2_HUMAN	ellular (Potential).	7	GCAGTCCATCC	0.502	
+	5	1146	141_uc003gab.2_	NM_003441	NP_003432	Q15928	ZN141_HUMAN	2H2-type 6.	0	TAGGTCCACAA	0.378	
-	3	3308	tron|ABCA11P_uc	NM_133474	NP_597731	D9N162	D9N162_HUMAN		1	TAAAGGTTTTGC	0.418	
+	1	1599	t.3_Intron|LRBA_u	NM_006439	NP_006430	Q9Y586	MB212_HUMAN		1	GGAGCGCTATG	0.627	
+	31	4597	p.D982N|SPEF2_	NM_024867	NP_079143	Q9C093	SPEF2_HUMAN		4	TGATCGATTTG	0.358	
+	20	3831	|ANKHD1_uc003lf	NM_020690	NP_065741	Q8IWZ2	Q8IWZ2_HUMAN		6	GGGCCGAGCAG	0.448	
-	8	1174		NM_005990	NP_005981	O94804	STK10_HUMAN	rotein kinase.	8	GAAGGGATGCT	0.632	
-	5	698	_Missense_Mutati	NM_002020	NP_002011	P35916	VGFR3_HUMAN	2.|Extracellular (Potential).	15	GGTCTCGCACT	0.642	
-	10	4192	C1_uc011dmp.1_	NM_014641	NP_055456	Q14676	MDC1_HUMAN	on with the PRKDC compl	4	AAGGCTGGAGC	0.527	
-	5	1864	.M535I|BCLAF1_	NM_014739	NP_055554	Q9NYF8	BCLF1_HUMAN		1	CGCTATCATTTT	0.423	
+	9	1437	p.V278M|HECW1_	NM_015052	NP_055867	Q76N89	HECW1_HUMAN	C2.	23	CTGACGTGCTG	0.493	
-	5	1584		NM_033273	NP_150376	Q96JC4	ZN479_HUMAN	2H2-type 10.	4	CACATTTGTAGG	0.453	
-	6	763	_p.S148L|SMURF	NM_020429	NP_065162	Q9HCE7	SMUF1_HUMAN		4	CCACCGAGCCG	0.473	
+	2	349	tron|uc011kjy.1_R	NM_033506	NP_277041	O75426	FBX24_HUMAN		4	CTGCCCTTCTT	0.562	
+	14	2798	AN_uc003uwl.2_	NM_003386	NP_003377	Q9Y493	ZAN_HUMAN	ate) (mucin-like domain).|E	11	AAAAACTCACCA	0.502	
+	3	7450	C17_uc010lho.1_	NM_001040105	NP_001035194	Q685J3	MUC17_HUMAN	ch.|59 X approximate tand	27	CACCACGCCGG	0.522	
+	3	7512	C17_uc010lho.1_	NM_001040105	NP_001035194	Q685J3	MUC17_HUMAN	X approximate tandem re	27	ACACCTATGACC	0.493	rs139444589
+	3	7514	C17_uc010lho.1_	NM_001040105	NP_001035194	Q685J3	MUC17_HUMAN	X approximate tandem re	27	ACCTATGACCAC	0.493	rs147944556
+	10	1173		NM_001868	NP_001859	P15085	CBPA1_HUMAN		1	GACTGGACCTA	0.532	
+	10	1791	ub.2_Missense_M	NM_015905	NP_056989	O15164	TIF1A_HUMAN		8	CCAAACCCAAT	0.408	
-	14	1960	p.S208N|MTMR7_	NM_004686	NP_004677	Q9Y216	MTMR7_HUMAN		1	GCTATGCTGTTG	0.453	
-	1	327	14_uc003zoo.1_	NM_002172	NP_002163	P01570	IFN14_HUMAN		0	ATGAGTTCTTTG	0.468	
+	1	604_605	42421_uc004aed.1_RNA						0	AGTCGCGCAAG	0.589	
+	17	2060	b.1_RNA|TMC1_u	NM_138691	NP_619636	Q8TDI8	TMC1_HUMAN	lasmic (Potential).	1	TTCACCCTGCAG	0.433	
+	4	906	mij.1_Missense_M	NM_014728	NP_055543	Q14CM0	FRPD4_HUMAN	PDZ.	13	CCAGAGAGCGG	0.512	
-	4	399	K_uc001aie.2_Mis	NM_023018	NP_075394	O95544	NADK_HUMAN		0	TCGCGGGGTCC	0.502	
-	3	801	tart_Site|RERE_u	NM_012102	NP_036234	Q9P2R6	RERE_HUMAN		2	CGCCACGTGCC	0.343	
+	8	3062	d.1_Missense_M	NM_012231	NP_036363	Q13029	PRDM2_HUMAN		1	AGAGGCGGACC	0.522	
+	8	3807	.2_Intron|PRDM2_	NM_012231	NP_036363	Q13029	PRDM2_HUMAN	Pro-rich.	1	TGCCACTCCGC	0.612	
+	8	4719	.2_Intron|PRDM2_	NM_012231	NP_036363	Q13029	PRDM2_HUMAN		1	TGTTCGATTGG	0.408	
-	13	1971	br.1_Missense_M	NM_003443	NP_003434	Q13105	ZBT17_HUMAN	2H2-type 10.	0	GGTGGCGAATAT	0.587	
-	105	15336	e_Mutation_p.P76	NM_020765	NP_065816	Q5T4S7	UBR4_HUMAN		25	TGGTAGGCACC	0.542	
-	13	2891	p.D203N|KIF17_u	NM_020816	NP_065867	Q9P2E2	KIF17_HUMAN		4	ATTGTCTGCTG	0.582	
+	12	2328	gf.2_Missense_M	NM_017449	NP_059145	P29323	EPHB2_HUMAN	Potential).|Protein kinase.	5	GCTTCGGGGCA	0.542	
-	5	541	ce_Site_p.G141_s	NM_000191	NP_000182	P35914	HMGCL_HUMAN		1	ACTCACCCCCG	0.488	

-	6	1420	_p.R151*|AHDC1_	NM_001029882	NP_001025053	Q5TGY3	AHDC1_HUMAN	Pro-rich.	1	CAGTCGGAGCC	0.632
+	5	930		NM_031459	NP_113647	P58004	SESN2_HUMAN		7	CTGGCCGAGCTC	0.642
-	3	615	_p.R164K|RRAGC_	NM_022157	NP_071440	Q9HB90	RRAGC_HUMAN		1	TTGGCCCTTTGAT	0.378
+	59	17196	cde.1_Missense_I	NM_033044	NP_149033	Q9UPN3	MACF1_HUMAN	tail (By similarity).|GAR.	16	CAGATCGGAGAG	0.443
-	4	359	iw.1_Missense_Mu	NM_014571	NP_055386	Q9NQ87	HEYL_HUMAN	eraction with NCOR1 and S	1	CTGTCCCACCAC	0.363
-	12	2022	nse_Mutation_p.A	NM_003035	NP_003026	Q15468	STIL_HUMAN	nding (By similarity).	3	TGTTTGCTCCTTC	0.438
-	7	871	mv.1_Missense_M	NM_019073	NP_061946	Q9NWH7	SPAT6_HUMAN		1	CAGCCGCCGCC	0.408
+	1	456	ation_p.C9Y|ACAD	NM_000016	NP_000007	P11310	ACADM_HUMAN		4	GATGCTGCAGGG	0.652
+	2	692	orn.1_Missense_M	NM_007034	NP_008965	Q9UDY4	DNJB4_HUMAN		0	CCAAACGGATGA	0.413
+	3	210	09wda.1_Missens	NM_182976	NP_892021	Q5BKZ1	ZN326_HUMAN	al activation (By similarity).|	1	TGGATCGTGATTA	0.353
+	7	1876	p.G494R|VCAM1_	NM_001078	NP_001069	P19320	VCAM1_HUMAN	6.|Extracellular (Potential).	1	AGGCTGGAAGA	0.383
-	2	1848		NM_020703	NP_065754	Q86WK6	AMGO1_HUMAN	lasmic (Potential).	2	ATGGGCGTATCAC	0.587
-	7	2048	bv.1_Missense_Mu	NM_004980	NP_004971	Q9UK17	KCND3_HUMAN	lasmic (Potential).	3	ATTGAACTCTCCA	0.522
+	10	1618	p.L479F|MAGI3_u	NM_001142782	NP_001136254	Q5TCQ9	MAGI3_HUMAN	on with PTEN.|PDZ 2.	6	TCAATTGGTACCT	0.423
-	10	1414	eff.1_Missense_Mu	NM_000036	NP_000027	P23109	AMPD1_HUMAN		4	GCAGACGAACCA	0.567
+	19	2184	ation_p.D27A|NBP	NM_001037675	NP_001032764	Q3BBV1	NBPFK_HUMAN	NBPF 5.	0	GCTGGATGAGA	0.483
+	19	2193	ation_p.E30G|NBP	NM_001037675	NP_001032764	Q3BBV1	NBPFK_HUMAN	NBPF 5.	0	GAAAGAGCCTG	0.483
+	6	892	1_Intron|NBPF10_	NM_001039703	NP_001034792	A6NDV3	A6NDV3_HUMAN		0	CAGAGATGAACA	0.498
+	14	2035	oyk.1_Translation_	NM_001039703	NP_001034792	A6NDV3	A6NDV3_HUMAN		0	ACAGCGTGTTG	0.453
+	6	1189	zr.1_Missense_Mu	NM_004326	NP_004317	O00512	BCL9_HUMAN		6	TACAGCCCCCAC	0.498
-	17	1995	uc010pab.1_Intron|	NM_015383	NP_056198	Q5TI25	NBPFE_HUMAN	NBPF 7.	1	CTTCTTGGTACT	0.438
-	7	1140	NP32E_uc010pbv.1	NM_030920	NP_112182	Q9BTT0	AN32E_HUMAN	u-rich (highly acidic).	0	GCATCTCGTTTCC	0.383
+	2	303	1orf51_uc001euj.2	NM_144697	NP_653298	Q8N365	CA051_HUMAN		0	GTTCACGGCCCA	0.602
-	11	1575	nr.1_Missense_Mu	NM_001025603	NP_001020774	P48382	RFX5_HUMAN		1	TCTATATCCTGCT	0.532
-	4	761	OGZ_uc010pdc.1_	NM_015100	NP_055915	Q7Z3K3	POGZ_HUMAN		3	ACCTGCGTAGTG	0.448
+	10	1798	R_uc001ffa.1_3'U	NM_000565	NP_000556	P08887	IL6RA_HUMAN	lasmic (Potential).	4	ACCCACGGAGCC	0.582
-	2	990	2_Missense_Muta	NM_001111	NP_001102	P55265	DSRAD_HUMAN		6	TATGACTGTCTG	0.488
-	5	1024	se_Mutation_p.P2	NM_183001	NP_892113	P29353	SHC1_HUMAN	PID.	2	TCACCGGATCC	0.532
+	5	490	e_Mutation_p.R12	NM_022367	NP_071762	Q9H3S1	SEM4A_HUMAN	tracellular (Potential).	2	TCATCCGTGTCCT	0.542
-	5	437	hj.1_Nonsense_M	NM_005998	NP_005989	P49368	TCPG_HUMAN		2	GATGCTGGACTT	0.443
-	5	485	wsb.1_Missense_M	NM_178229	NP_839943	Q86VI3	IQGA3_HUMAN	CH.	6	ACTACCCGGGGC	0.478
-	4	949	c010pjc.1_Missens	NM_015726	NP_056541	Q5TAQ9	DCAF8_HUMAN	WD 1.	2	GGTCATCGCTGC	0.582
+	5	723	gbp.2_Missense_M	NM_007240	NP_009171	Q9UNI6	DUS12_HUMAN		1	GATCACCGTGAA	0.413
+	7	1189	p.R148Q|KLHL20_	NM_014458	NP_055273	Q9Y2M5	KLH20_HUMAN	Kelch 1.	1	TTGAACGATATGA	0.438
-	11	2777	u.1_Missense_Mu	NM_003285	NP_003276	Q92752	TENR_HUMAN	onectin type-III 7.	11	GTGGGTCGATAT	0.453
+	7	1244	_Mutation_p.P305	NM_005807	NP_005798	Q92954	PRG4_HUMAN	eats of K-X-P-X-P-T-T-X.|7.	1	CTGCACCCACCA	0.647
-	6	317	NNI1_uc001gwp.2_	NM_003281	NP_003272	P19237	TNNI1_HUMAN		0	CCACCACCTCCA	0.587
+	8	1371	_p.R149*|RNPEP_	NM_020216	NP_064601	Q9H4A4	AMPB_HUMAN		1	AAATTCCGAAGCA	0.493
-	3	2085	z.2_Missense_Mu	NM_001973	NP_001964	P28324	ELK4_HUMAN		0	TGTGTCGATGTC	0.488
-	9	1500	BP2_uc010puz.1_	NM_001031685	NP_001026855	Q13625	ASPP2_HUMAN		3	AAGCAGCCCCA	0.468
+	15	1840	zg.1_Missense_M	NM_144625	NP_653226	B1ANS9	WDR64_HUMAN		1	GTTTTCGGCTCTC	0.458
+	1	494		NM_001004690	NP_001004690	A3KFT3	OR2M5_HUMAN	cellular (Potential).	3	CATTTTCCTTCTC	0.443
+	19	2017	p.V623M|PFKP_uc	NM_002627	NP_002618	Q01813	K6PP_HUMAN		3	AAAGGCGTGTTT	0.493
+	8	929	qbc.1_Missense_M	NM_001001973	NP_001001973	P36542	ATPG_HUMAN		0	TCATCACAAAAGA	0.378
+	2	646	g.2_Nonsense_Mu	NM_005180	NP_005171	P35226	BMI1_HUMAN		2	ATGCATCGAACAA	0.393
-	14	3316	SVIL_uc001iuu.1_I	NM_021738	NP_068506	O95425	SVIL_HUMAN		6	GTGTGACTGGCT	0.473
-	10	1970	t.2_Missense_Muta	NM_025209	NP_079485	Q9H2F5	EPC1_HUMAN		4	GAGGTACTGCAT	0.418

-	12	1844	iwr.3_Splice_Site_	NM_133376	NP_596867	P05556	ITB1_HUMAN		2	TACTTACCTCCAC	0.383	
-	20	2544	.3_Intron|TTC18_u	NM_145170	NP_660153	Q5T0N1	TTC18_HUMAN		3	ATTGCTGTTGCAC	0.383	
+	18	2623	ig.2_Missense_Mu	NM_020338	NP_065071	Q9ULJ6	ZMIZ1_HUMAN		4	TACACCGGCCCT	0.642	
+	9	1218	1_uc001kef.2_Spli	NM_133447	NP_597704	Q8TF27	AGA11_HUMAN		0	AATATCGTGAGTA	0.388	
+	9	1421	_p.R425H|PI4K2A_	NM_018425	NP_060895	Q9BTU6	P4K2A_HUMAN		2	CGGCCCGTTCCC	0.537	
-	8	1118	n_p.T274M|ABLIM	NM_002313	NP_002304	O14639	ABLM1_HUMAN	l zinc-binding 4.	1	GTCTTCGTAGAT	0.483	
-	4	734	qsk.1_Missense_M	NM_002313	NP_002304	O14639	ABLM1_HUMAN	l zinc-binding 2.	1	GACATCGGCTGT	0.567	
-	13	5167	v.1_Missense_Mut	NM_002417	NP_002408	P46013	KI67_HUMAN	AA approximate repeats.	7	TAGTCTCTCCTGA	0.502	
+	14	2213	ou.3_Missense_Mu	NM_025092	NP_079368	Q32M88	ATHL1_HUMAN		3	AGCTCCGAGTTCC	0.622	
-	8	1058	ense_Mutation_p.A	NM_024698	NP_078974	Q9H936	GHC1_HUMAN	e=5; (Potential).|Solcar 3.	0	ACAGCGGCGGCA	0.682	
-	31	5260		NM_005961	NP_005952	Q6W4X9	MUC6_HUMAN	cated.|Approximate repeats	1	AGCTTCGGGATTC	0.532	
+	47	8276	tb.2_Missense_Mu	NM_017511	NP_059981	Q9HC84	MUC5B_HUMAN	approximate tandem repeat	0	TGCTTACCGCCAC	0.637	
+	52	15620_1562	b.2_Missense_Mu	NM_017511	NP_059981	Q9HC84	MUC5B_HUMAN	em repeats, Ser/Thr- rich.|	0	CCCAGGGACCAC	0.639	
-	3	560		NM_001012709	NP_001012727	Q6L8H1	KRA54_HUMAN	repeats of C-C-X-P.	0	CAGGAGCCACAG	0.677	
-	8	1479	ol.1_RNA|TRIM5_u	NM_033034	NP_149023	Q9C035	TRIM5_HUMAN	B30.2/SPRY.	1	ATTTAACTCCTTC	0.398	
-	10	953	p.R285Q|ARFGAP	NM_032389	NP_115765	Q8N6H7	ARFG2_HUMAN	interaction with coatomer.	1	CACCTTCGGGATA	0.522	
+	1	374		NM_001005201	NP_001005201	Q8N146	OR8H3_HUMAN	lasmic (Potential).	2	ATGCAGCGATCTC	0.473	
-	1	877		NM_001004741	NP_001004741	Q6IEU7	OR5MA_HUMAN	lasmic (Potential).	0	TGTTCCGTAGGC	0.393	
+	4	1602	se_Mutation_p.R63	NM_015457	NP_056272	Q9C0B5	ZDHC5_HUMAN	DHHC-type.	1	CCCCCTCGATGT	0.507	
-	1	444		NM_001039396	NP_001034485	Q2M385	MPEG1_HUMAN	xtracellular (Potential).	2	TGAGTTCATCTCC	0.438	
+	1	754		NM_001004705	NP_001004705	Q8NGI6	OR4DA_HUMAN	Name=6; (Potential).	3	CATTTCGTGCCC	0.547	
-	12	1900	nse_Mutation_p.P5	NM_004630	NP_004621	Q15637	SF01_HUMAN	Pro-rich.	3	GGTGGCGGAGGC	0.657	
-	4	782	_p.R237C|MEN1_u	NM_130800	NP_570712	O00255	MEN1_HUMAN	ction with FANCD2.	238	CTTGCGGTCACA	0.483	
+	8	1091	e_Mutation_p.P42	NM_002689	NP_002680	Q14181	DPOA2_HUMAN		0	AGGAGCCTGTCAC	0.493	
-	1	977	ojb.2_Missense_Mu	NM_031492	NP_113680	Q9BQ04	RBM4B_HUMAN	RRM 2.	0	ATGACCGGACCA	0.498	
+	24	3374	c001opr.2_Nonser	NM_003626	NP_003617	Q13136	LIPA1_HUMAN	SAM 3.	3	TTCGCTGGATCC	0.413	
+	15	1557	Missense_Mutatio	NM_033388	NP_203746	Q8NAA4	A16L2_HUMAN	WD 5.	0	GGGTCACCTCCC	0.622	
+	7	914	e_Mutation_p.R24	NM_015517	NP_056332	Q9BQA5	HINFP_HUMAN	C2H2-type 5.	4	CAGAGCGGCTAT	0.592	
+	1	832		NM_032015	NP_114404	Q9BY78	RNF26_HUMAN	Leu-rich.	1	TGGGGGCTTGCA	0.602	
+	8	783	ion_p.V225M|STT3	NM_152713	NP_689926	P46977	STT3A_HUMAN	ical; (Potential).	0	GTCCTCGTGCTG	0.478	
+	6	560	p.S114_splice|ST3	NM_006278	NP_006269	Q11206	SIA4C_HUMAN		0	CAGAGGTAAGGC	0.602	
+	6	724	h.3_Missense_Mu	NM_001098536	NP_001092006	P45974	UBP5_HUMAN	e binding.|UBP-type.	4	GGCGACGCTACT	0.567	
+	18	2319	e_Mutation_p.R73	NM_001098536	NP_001092006	P45974	UBP5_HUMAN	UBA 2.	4	TAGAACGGGCTC	0.363	
-	2	493		NM_004054	NP_004045	Q16581	C3AR_HUMAN	lasmic (Potential).	1	ACATTGCGATGAT	0.478	
-	3	897		NM_006248	NP_006239				0	CTTGTGGGGGTG	0.617	
+	19	2103	1ria.2_Missense_M	NM_003622	NP_003613	Q86W92	LIPB1_HUMAN		5	CAGATACCGCCTC	0.453	
-	21	2454	_p.V251I|IPO8_uc	NM_006390	NP_006381	O15397	IPO8_HUMAN		3	GTTGAACGAAGAC	0.418	
+	11	1192	t.1_Missense_Mut	NM_016488	NP_057572	Q8NEY8	PPHLN_HUMAN		2	atcacgacggaacccc	0.01	
+	10	1292	4A8_uc001ryp.1_3	NM_001039960	NP_001035049	Q2Y0W8	S4A8_HUMAN	cellular (Potential).	5	CATGACGTAGCAT	0.438	
-	11	1187	cs.3_Nonsense_Mu	NM_015665	NP_056480	Q9NRG9	AAAS_HUMAN		1	GCAGTCGGCTGC	0.522	
+	3	315	RNPA1_uc009zni.2	NM_031157	NP_112420	P09651	ROA1_HUMAN	r A domain.|RRM 1.	3	GATGCAGCTATGA	0.458	
+	6	1911	z.2_Nonsense_Mu	NM_000456	NP_000447	P51687	SUOX_HUMAN	terin domain (By similarity).	0	AACCTGCGAGGT	0.542	
+	4	629	RBB3_uc010sqc.1_	NM_001982	NP_001973	P21860	ERBB3_HUMAN	cellular (Potential).	8	TCAGGGGGTGTT	0.502	
-	17	1661	_p.R519*|SMARC	NM_003075	NP_003066	Q8TAQ2	SMRC2_HUMAN	SWIRM.	6	TTGGTCGACTCT	0.577	
-	6	762	p.R125Q|CS_uc00	NM_004077	NP_004068	O75390	CISY_HUMAN		0	TTGGTTCGGCTG	0.488	
+	10	1150	se_Mutation_p.R24	NM_004990	NP_004981	P56192	SYMC_HUMAN		5	TGAAACGAGGTT	0.572	rs150428018
-	12	2401	p.R800W|AGAP2_	NM_001122772	NP_001116244	Q99490	AGAP2_HUMAN	PH.	5	AATTCCGGTCTGC	0.572	

+	1	419	1_Missense_Mutat	NM_015026	NP_055841	Q7Z3U7	MON2_HUMAN			2	AGGCGGTGAAG	0.562	
+	4	496	_p.G41D|C12orf23	NM_152261	NP_689474	Q8WUH6	CL023_HUMAN	ical; (Potential).		0	CTGGGGGTATCT	0.458	
+	2	444	oc.2_Missense_Mu	NM_001093	NP_001084	O00763	ACACB_HUMAN			8	GTGACGCAGCA	0.632	
+	6	1532	sf.2_Missense_Mut	NM_005475	NP_005466	Q9UQQ2	SH2B3_HUMAN	SH2.		1	GGTGCGGCAGA	0.527	
-	16	2299	1tts.2_Missense_M	NM_001109662	NP_001103132					2	CTGAGCGCGAA	0.463	
-	46	6084		NM_006836	NP_006827	Q92616	GCN1L_HUMAN	HEAT 17.		4	CTGCCGCCTCT	0.542	
+	39	7248	R2404C|EP400_u	NM_015409	NP_056224	Q96L91	EP400_HUMAN			12	ACAACCGTCCT	0.512	
+	1	461		NM_030979	NP_112241	Q9H361	PABP3_HUMAN	RRM 2.		4	TGTGATGAAAAT	0.363	
+	1	4006		NM_207361	NP_997244	Q5SZK8	FREM2_HUMAN	xtracellular (Potential).		11	CAATTCCCCACT	0.428	
+	15	1771	v.1_Missense_Mut	NM_031431	NP_113619	Q96JB2	COG3_HUMAN			2	ATCCTACGGTTC	0.393	
+	20	2148		NM_000321	NP_000312	P06400	RB_HUMAN	ls T and E1A	(3)|p.L660fs*2(	358	ATCTCCGGCTAA	0.388	
-	64	10907	p.E3010K|MYCBP	NM_015057	NP_055872	O75592	MYCB2_HUMAN			14	CAGCTTCCCCGG	0.468	
+	9	2571	se_Mutation_p.V7	NM_000123	NP_000114	P28715	ERCC5_HUMAN			7	ACGACGTGGAT	0.512	
-	2	305	vsf.2_Missense_M	NM_006322	NP_006313	Q96CW5	GCP3_HUMAN			1	GCTGCCAATCA	0.428	
+	1	167	a.1_RNA|POTEG_	NM_001005356	NP_001005356	Q6S5H5	POTEG_HUMAN			1	GGAGCGGCAAG	0.592	
+	1	314	a.1_RNA|POTEG_	NM_001005356	NP_001005356	Q6S5H5	POTEG_HUMAN			1	CACGACGACTCT	0.617	
+	2	952	ASE4_uc001vya.	NM_002937	NP_002928	P34096	RNAS4_HUMAN			1	CTAGACGTGTTG	0.522	
-	7	687	uc010tne.1_Trans	NM_001077351	NP_001070819	Q86U06	RBM23_HUMAN			1	GCATCACGCTCC	0.517	
-	6	1162	p.G301E|CDH24_	NM_022478	NP_071923	Q86UP0	CAD24_HUMAN	(Potential).|Cadherin 3.		1	CCCTCCCCATCC	0.627	
+	2	367	.1_5'UTR|SRP54_	NM_003136	NP_003127	P61011	SRP54_HUMAN	G-domain.		1	CAGACCTTGGA	0.328	
+	5	2923	179B_uc010anc.2_	NM_015091	NP_055906	Q9Y4F4	F179B_HUMAN			3	CCCGACGAGGTC	0.423	
-	17	3688	.R1104W|NID2_uc	NM_007361	NP_031387	Q14112	NID2_HUMAN			7	CTCCCGGCAGT	0.488	rs138581322
+	6	1199	_Mutation_p.R31	NM_015589	NP_056404	Q9UPU9	SMAG1_HUMAN			0	AGCCTGCGCATC	0.657	
+	8	1039	p.R305H|DAAM1_	NM_014992	NP_055807	Q9Y4D1	DAAM1_HUMAN	GBD/FH3.		1	ATCTTCGCTATG	0.289	
+	8	1018		NM_152443	NP_689656	Q96NR8	RDH12_HUMAN			1	CCAGGCGTCGTC	0.632	
+	7	1404	.A219T|SLC39A9_	NM_018375	NP_060845	Q9NUM3	S39A9_HUMAN			0	TGAACGCCACG	0.493	
+	11	1458	lt.1_Missense_Mu	NM_022137	NP_071420	Q9H4F8	SMOC1_HUMAN	EF-hand 2.		2	TGCCCGGCGTT	0.527	
-	35	5635		NM_000428	NP_000419	Q14767	LTBP2_HUMAN	alcium-binding (Potential).		2	CACGCGCACAC	0.617	
+	6	386	p.V118M|C14orf17	NM_001102564	NP_001096034	Q96FT9	IFT43_HUMAN			0	TGCAGGTGGCA	0.458	
-	12	1184	su.2_Missense_Mu	NM_012245	NP_036377	Q13573	SNW1_HUMAN			1	ATATCCCGATTT	0.373	
+	9	1045	_p.R260*|PSMC1_	NM_002802	NP_002793	P62191	PRS4_HUMAN			0	ACAAACCGAATA	0.388	
+	4	389		NM_023112	NP_075601	Q96DC9	OTUB2_HUMAN	OTU.		0	AAGAACGCGTA	0.532	
+	14	1405	vv.1_Nonsense_M	NM_032632	NP_116021	P51003	PAPOA_HUMAN			0	AAAATCCGAATC	0.373	
-	7	8498	px.2_Missense_M	NM_138420	NP_612429	Q8IVF2	AHNK2_HUMAN			1	GCCGCGCACCA	0.602	
-	7	1739	px.2_Missense_M	NM_138420	NP_612429	Q8IVF2	AHNK2_HUMAN			1	CCCTGCCCGGC	0.592	
-	187									0	ACTGACCTCCCC	0.587	rs7146961
-	9	1301	zba.2_Missense_M	NM_000814	NP_000805	P28472	GBRB3_HUMAN	lasmic (Pro	p.D387N(1)	5	GGTATCGCCAAT	0.478	
-	77	11897		NM_004667	NP_004658	O95714	HERC2_HUMAN	WD 5.		13	GTTGTTCGTCTT	0.408	
+	3	634	ct.1_Missense_Mu	NM_024111	NP_077016	Q9BUX1	CHAC1_HUMAN			0	TGCCACGCAGA	0.622	
+	15	1980		NM_006293	NP_006284	Q06418	TYRO3_HUMAN	.|Cytoplasmic (Potential).		6	CAGGGGTAAGC	0.602	
+	5	679		NM_024908	NP_079184	Q9H967	WDR76_HUMAN			0	CAATGCGATTAC	0.373	
-	13	1340	ense_Mutation_p.	NM_016132	NP_057216	Q9P2K5	MYEF2_HUMAN	Gly-rich.		3	CACCACGGTACA	0.383	
-	9	3277	X7_uc002adn.1_M	NM_022841	NP_073752	Q2KHR2	RFX7_HUMAN			0	GAAACGGTCTT	0.443	
-	18	2696	p.P852S|SLTM_uc	NM_024755	NP_079031	Q9NWH9	SLTM_HUMAN	Arg/Glu-rich.		1	CTCGAGGATGTC	0.498	
-	78	10614	hb.1_Nonsense_M	NM_020821	NP_065872	Q709C8	VP13C_HUMAN			2	TGTCTCCAAAAT	0.423	
+	23	3482	_p.V1114I|NEO1_	NM_002499	NP_002490	Q92859	NEO1_HUMAN	ical; (Potential).		1	GTTGGCGTCATC	0.493	
+	2	87		NM_000761	NP_000752	P05177	CP1A2_HUMAN			4	CTGTTCCCTTCT	0.532	

-	5	785	HRNB4_uc010blh	NM_000750	NP_000741	P30926	ACHB4_HUMAN	ellular (Potential).	0	GAAGTCGTAAG	0.552	
-	6	646	bgn.2_Missense_	NM_181900	NP_871629	Q9NSY2	STAR5_HUMAN	START.	1	CACCACGTTCT	0.512	
+	9	2170		NM_001080435	NP_001073904	Q8TF30	WHAMM_HUMAN		0	TGTCCGAAACA	0.473	
+	7	1066	_p.P299L|AKAP13_	NM_007200	NP_009131	Q12802	AKP13_HUMAN		9	TTATGCCCTTAAT	0.483	
+	3	1753		NM_198526	NP_940928	Q8N1W2	ZN710_HUMAN		1	CGCCCGTGAAG	0.592	
+	12	1256	v.1_Missense_Mu	NM_000548	NP_000539	P49815	TSC2_HUMAN	r interaction with TSC1.	10	ACCATCGTCCAT	0.587	
+	7	1579	ua.2_Missense_M	NM_001042428	NP_001035893	O95201	ZN205_HUMAN	2H2-type 7.	0	ACTGCGGCAAG	0.672	
+	4	471	_p.V144M|ALG1_u	NM_019109	NP_061982	Q9BT22	ALG1_HUMAN	enal (Potential).	2	GGTTCGTGGGC	0.542	
+	5	640	_p.R200Q|ALG1_u	NM_019109	NP_061982	Q9BT22	ALG1_HUMAN	enal (Potential).	2	TATGCGAGAAG	0.592	
+	16	1318	.R369W|C16orf62	NM_020314	NP_064710	Q7Z3J2	CP062_HUMAN		1	CCTTCCGGGCT	0.453	
+	2	522	S2_uc002dlt.3_5'F	NM_019116	NP_061989	O14562	UBFD1_HUMAN	biquitin-like.	0	CACAGGCTCCG	0.602	
-	3	462	ep.2_Missense_	NM_005880	NP_005871	O60884	DNJA2_HUMAN		1	CATTTCGACTT	0.428	rs143994918
+	3	485	efx.2_Missense_	NM_182922	NP_891552	Q7Z4Q2	HEAT3_HUMAN	HEAT 2.	2	CAGTGCTTGTG	0.378	
+	2	199	2_uc010cbk.1_M	NM_022162	NP_071445	Q9HC29	NOD2_HUMAN	CARD 1.	4	CGCAGGAGGCT	0.607	
-	6	739	.R42H|KIFC3_uc	NM_005550	NP_005541	Q9BVG8	KIFC3_HUMAN	Potential.	3	TGTCACGGAGC	0.627	
+	7	1163	n.1_Missense_M	NM_001795	NP_001786	P33151	CADH5_HUMAN	|Extracellular (Potential).	6	CTTCATCGTCG	0.423	
-	6	1739	_p.E251K|ZNF23_	NM_145911	NP_666016	P17027	ZNF23_HUMAN	2H2-type 6.	0	ACACTCGTAAG	0.408	
-	6	1270	F19_uc002fal.1_	NM_006961	NP_008892	P17023	ZNF19_HUMAN	2H2-type 4.	0	CTACTCGTGAAA	0.443	
-	4	722	nv.1_Missense_M	NM_031463	NP_113651	Q3SXM5	HSDL1_HUMAN		0	AGCGGCGGCAA	0.498	
+	14	1596	RISPLD2_uc002fi	NM_031476	NP_113664	Q9H0B8	CRLD2_HUMAN	LCCL 2.	0	GTGACGTGGAC	0.567	
-	31	3074	_p.R1011H|FANCA	NM_000135	NP_000126	O15360	FANCA_HUMAN		6	CTGTGCGGCCA	0.408	
-	16	1934	|VPS53_uc002fr	NM_018289	NP_060759	Q5VIR6	VPS53_HUMAN		0	ACATACGTGCT	0.493	
-	8	1335	r.2_Missense_Mu	NM_016532	NP_057616	Q9BT40	INP5K_HUMAN	lytic (Potential).	0	CGTGCCGGAGA	0.587	
+	19	2412	R336K|EIF4A1_uc	NM_001416	NP_001407	P60842	IF4A1_HUMAN	case C-terminal.	1	GTCGAGGTGGA	0.502	
+	1	235	sense_Mutation_p	NM_004870	NP_004861	O75352	MPU1_HUMAN		1	CGGACGGACC	0.567	
+	3	682	a.2_5'Flank|CYB5	NM_144607	NP_653208	Q6P9G0	CB5D1_HUMAN	me b5 heme-binding.	1	GCGGGGCCGCT	0.622	
+	39	5912	_p.P1887L|CHD3_	NM_001005273	NP_001005273	Q12873	CHD3_HUMAN	r interaction with PCNT.	1	CTACCCGCCGG	0.607	
-	4	524	_p.R159C|PMP22_	NM_153322	NP_696997	Q01453	PMP22_HUMAN		0	TTCGCGTTTCC	0.547	
+	2	1302		NM_000676	NP_000667	P29275	AA2BR_HUMAN	smic (By similarity).	2	CTGGGGTACAG	0.498	
+	3	370	_uc002gsi.1_Spli	NM_001388	NP_001379	P55039	DRG2_HUMAN		1	TTGAAGTAAGT	0.557	
+	39	8100	5A_uc010vxj.1_5'	NM_016239	NP_057323	Q9UKN7	MYO15_HUMAN	Tail.	9	CGTTCCGGGGA	0.632	
+	14	1670	1_uc002gzm.2_	NM_014238	NP_055053	Q8IVT5	KSR1_HUMAN		4	GGCTCGATGAC	0.552	
+	9	706	_p.R225Q|GOSR1_	NM_004871	NP_004862	O95249	GOSR1_HUMAN	lasmic (Potential).	0	GAAGCGGCGGG	0.493	
-	3	436	rf79_uc010css.2_	NM_018405	NP_060875	Q9NQ92	COPR5_HUMAN		0	AAGATCGCCAG	0.517	
+	15	1756	c.2_Missense_Mu	NM_139215	NP_631961	Q92804	RBP56_HUMAN	tandem repeats of D-R- [S	35	TGGCGGCTATG	0.562	
-	39	4668	n.2_Missense_M	NM_198836	NP_942133	Q13085	ACACA_HUMAN		2	GCTCCGCACGG	0.453	
+	6	570	rr.1_Missense_Mu	NM_000981	NP_000972	P84098	RL19_HUMAN		0	AAGCACGCAAG	0.527	
+	2	291	wc.2_Missense_M	NM_005310	NP_005301	Q14451	GRB7_HUMAN		5	CTCTCCGGAAG	0.617	
-	2	351		NM_033060	NP_149049	Q9BYQ7	KRA41_HUMAN	s of C-C-[GRQC]-[SPT]- [	0	TGGACGGCAGC	0.597	
-	4	890	P_uc010wfs.1_Int	NM_000422	NP_000413	Q04695	K1C17_HUMAN	Coil 2.|Rod.	2	GTCACGCATCT	0.592	
+	3	394	.1_Intron|EIF1_uc	NM_005801	NP_005792	P41567	EIF1_HUMAN		0	GCATCCGGAAT	0.463	
-	13	2045	8_uc002hyw.3_5'	NM_021078	NP_066564	Q92830	KAT2A_HUMAN		2	GCTCCGTGTAG	0.557	
+	9	1906	02ibk.1_Missense_	NM_032387	NP_115763	Q96J92	WNK4_HUMAN		7	TTCCACGTTCTG	0.547	rs61755600
-	4	483	_uc002icg.2_RNA	NM_025267	NP_079543	Q9BTE6	AASD1_HUMAN		0	TCCATCGGCAT	0.512	rs147796875
+	10	1327	T1_uc010dad.1_	NM_021079	NP_066565	P30419	NMT1_HUMAN		0	TGAGCGACGCC	0.567	
-	48	3775		NM_000088	NP_000079	P02452	CO1A1_HUMAN	l region (C-terminal).	382	AGCCCGGTAGT	0.622	
-	6	762	m.2_Missense_M	NM_020748	NP_065799	Q9H0H0	INT2_HUMAN		3	TTATCAGGCCC	0.358	

-	13	2344		NM_000334	NP_000325	P35499	SCN4A_HUMAN	II.		3	GGATGCGGAAG	0.587	
+	2	1194	.R378Q|BPTF_uc	NM_182641	NP_872579	Q12830	BPTF_HUMAN			4	TGCTCGAGAGG	0.423	
-	4	461	_p.S102L|RECQL5	NM_004259	NP_004250	O94762	RECQ5_HUMAN	ase ATP-bin	p.T102T(1)	3	GCTTCGAGTTC	0.512	
-	6	929	H17_uc002jvs.2_RNA							9	CGGCCGTGGAC	0.542	
-	2	1031		NM_022840	NP_073751	Q8N3J2	METL4_HUMAN			2	AATTTTCGTGTG	0.393	
+	9	5853	knx.2_Missense_M	NM_015208	NP_056023	Q6UB98	ANR12_HUMAN			3	TATGACGAATAT	0.358	
+	2	1434	XNDC2_uc002koh	NM_001098529	NP_001091999	Q86VQ3	TXND2_HUMAN	repeat of Q-P-K-X-G-D-I-P		2	GGTGACATCCCC	0.592	
-	3	972		NM_003927	NP_003918	Q9UBB5	MBD2_HUMAN			0	GATGCTGTTTGT	0.318	
-	11	6288		NM_052947	NP_443179	Q86TB3	ALPK2_HUMAN	ype protein kinase.		14	GCATACGGGATA	0.458	
+	4	1041	_p.T163M|ZNF532	NM_018181	NP_060651	Q9HCE3	ZN532_HUMAN			2	GTTGACGGGGT	0.527	
+	5	525	_p.V150I|C19orf36	NM_001039846	NP_001034935	Q1ZYL8	IZUM4_HUMAN			0	CGCACGTCGCC	0.632	
+	2	219	xp.2_Missense_M	NM_205843	NP_995315	P08651	NFIC_HUMAN	CTF/NF-I.		0	AGGACGAGGAG	0.647	
+	3	320	_p.V32M|KDM4B_	NM_015015	NP_055830	O94953	KDM4B_HUMAN	JmjN.		1	AAATACGTGGCC	0.622	
-	4	453	vq.2_Missense_M	NM_021155	NP_066978	Q9NNX6	CD209_HUMAN	|2.|7 X approximate tanden		1	TCAGCCGGGTC	0.567	
+	9	1310	_p.S305L|LPPR2_	NM_022737	NP_073574	Q96GM1	LPPR2_HUMAN			1	GCATTCGACAC	0.647	
+	4	1307		NM_152357	NP_689570	Q8IYI8	ZN440_HUMAN	2H2-type 9.		0	CCCTTCGATATC	0.433	
+	4	1683	ym.1_Missense_M	NM_001136501	NP_001129973	Q08AG5	ZN844_HUMAN			0	CCTTCACATCTG	0.408	
+	3	699	_p.G200R|NFIX_uc002mwf.2_Missense_Mutation_p.G2			Q14938	NFIX_HUMAN			2	CCAACGGTCAG	0.572	
-	6	716	e_Mutation_p.D13	NM_032571	NP_115960	Q9BY15	EMR3_HUMAN	ellular (Pote	p.D190N(1)	6	CACTATCGTTTT	0.413	
-	7	695	hx.1_Nonsense_	NM_005535	NP_005526	P42701	I12R1_HUMAN	tential).|Fibronectin type-III		1	TCGTCGGAGCT	0.602	
-	14	2191	.Q286K|PDE4C_	NM_001098819	NP_001092289	Q08493	PDE4C_HUMAN			5	TCCCTGCTGGA	0.627	
-	4	1390		NM_001159293	NP_001152765	C9JHM3	C9JHM3_HUMAN			1	GGCTTCGCCAC	0.423	
-	4	1655	_p.S436P|ZNF681_	NM_138286	NP_612143	Q96N22	ZN681_HUMAN			0	TGTAGGATTTCT	0.373	
+	7	1374	22_uc010edv.2_N	NM_001771	NP_001762	P20273	CD22_HUMAN	otential).|Ig-like C2-type 4.		9	CGATTCGAGAA	0.512	
+	9	1027	ai.1_5'Flank|TMEM	NM_014364	NP_055179	O14556	G3PT_HUMAN			0	GATGGCGTTCC	0.617	
-	14	2041	4A_uc010eee.1_5'	NM_000704	NP_000695	P20648	ATP4A_HUMAN	lasmic (Potential).		1	CACGGGCATCC	0.637	
+	19	2376	dd.2_Missense_M	NM_173636	NP_775907	O43379	WDR62_HUMAN			0	CCACCGGCAGC	0.572	
-	6	2022	ense_Mutation_p.	NM_001010880	NP_001010880	O75290	Z780A_HUMAN	2H2-type 16.		0	AATAAGTTGCAT	0.403	
-	3	670	11_uc002oty.2_Mis	NM_001712	NP_001703	P13688	CEAM1_HUMAN	1.|Extracellular (Potential).		2	TGACCGGGAGG	0.527	rs144709978
-	17	1948	wp.1_Nonsense_M	NM_006297	NP_006288	P18887	XRCC1_HUMAN	BRCT 2.		7	CCATCGGGGAC	0.527	
+	8	1838	2D_uc010elx.2_5	NM_000836	NP_000827	O15399	NMDE4_HUMAN	ical; (Potential).		6	GCCCCGCCGTG	0.488	
-	9	963	i.2_Missense_Mu	NM_003598	NP_003589	Q15562	TEAD2_HUMAN	al activation (Potential).		3	GGGCCACGATC	0.572	
+	10	1230	D1_uc010enx.2_	NM_002691	NP_002682	P28340	DPOD1_HUMAN			2	CCGACGTGATC	0.607	
-	4	1361		NM_024733	NP_079009	Q9H7R5	ZN665_HUMAN	2H2-type 9.		2	TTCTTCGATGATT	0.408	
+	7	1576	p.H319R|ZNF761_	NM_001008401	NP_001008401	Q86XN6	ZN761_HUMAN	2H2-type 6.		1	GCCATCATAGAC	0.428	rs147132093
+	7	1972	p.R451Q|ZNF761_	NM_001008401	NP_001008401	Q86XN6	ZN761_HUMAN	2H2-type 11.		1	TTAGTCGGAAGT	0.418	
-	6	1246	fi.2_Missense_Mu	NM_012276	NP_036408	P59901	LIRA4_HUMAN	4.|Extracellular (Potential).		2	TGAGCCGTAGC	0.607	rs142697594
+	5	1487	se_Mutation_p.R4	NM_024691	NP_078967	Q96HQ0	ZN419_HUMAN	2H2-type 8.		0	TAGTTAGACATC	0.428	
-	17	3606		NM_012293	NP_036425	Q92626	PXDN_HUMAN			8	TGTGCCGCCGAT	0.572	
-	19	2197	R35_uc002rdh.2_	NM_001006657	NP_001006658	Q9P2L0	WDR35_HUMAN			1	AAGTCGGGGGT	0.438	
+	4	572	NPA_uc002rhs.2_	NM_001809	NP_001800	P49450	CENPA_HUMAN	H3-like.		0	GGCCCGGAGGA	0.552	
-	37	4147	172_uc010ezb.2_	NM_015662	NP_056477	Q9UG01	IF172_HUMAN	TPR 11.		2	AGCATCGATTG	0.507	
+	15	1857	q.2_Missense_Mu	NM_020744	NP_065795	Q9BTC8	MTA3_HUMAN			2	AGTCCGAAACA	0.478	
+	2	495	1B_uc002rtv.2_In	NM_002706	NP_002697	O75688	PPM1B_HUMAN			2	GGTTTACGTTAT	0.413	
+	19	2056	sak.2_Missense_	NM_022894	NP_075045	Q9BWT3	PAPOG_HUMAN			2	CTACCGTAGTAG	0.383	
-	16	2522	D2_uc002sha.2_	NM_001617	NP_001608	P35612	ADDB_HUMAN			3	GTGACCGACTCG	0.537	
-	2	338	Intron|LMAN2L_uc	NM_030805	NP_110432	Q9H0V9	LMA2L_HUMAN	like.|Lumenal (Potential).		0	CCACCCGGTTC	0.478	

+	8	1697	_p.R409H|CNGA3	NM_001298	NP_001289	Q16281	CNGA3_HUMAN		6	GTTCCGCAAGG	0.532
+	4	993		NM_017546	NP_060016	Q9UKZ1	CB029_HUMAN		5	CCCCACGGAGC	0.493
-	2	401	2_uc010fje.2_5'U	NM_201557	NP_963851	Q14192	FHL2_HUMAN	type (Potential).	1	CTCCCGCAGGA	0.532
-	17	2492		NM_001144013	NP_001137485	A6NKT7	RGPD3_HUMAN	Potential.	1	ATTTTCAGTAAA	0.348
-	2	528	_p.Q137*|ST6GAL	NM_001142351	NP_001135823	Q96JF0	SIAT2_HUMAN	enal (Potential).	11	TGGCTGACCAG	0.557
+	3	670	lonsense_Mutatio	NM_001056	NP_001047	O00338	ST1C2_HUMAN		1	GCCAGCGAGCC	0.443
-	3	371	10fnj.1_Translatio	NM_001349	NP_001340	P14868	SYDC_HUMAN		1	TGCACGTACCC	0.343
+	10	1407		NM_001001664	NP_001001664	Q6IQ16	SPOPL_HUMAN		3	TGGGTGTAAAG	0.358
-	6	832	_p.S161L|STAM2_	NM_005843	NP_005834	O75886	STAM2_HUMAN		1	TGTTCGATGAC	0.323
-	11	1677	q.1_Missense_Mu	NM_000888	NP_000879	P18564	ITB6_HUMAN	).|III.|Cysteine-rich tandem	3	CCGTTACCTGTA	0.522
+	4	673	gh.2_Missense_Mu	NM_000817	NP_000808	Q99259	DCE1_HUMAN		1	CGACCGGGATG	0.547
-	17	2786	uiv.2_Missense_M	NM_001033045	NP_001028217	Q7Z3F1	GP155_HUMAN	DEP.	1	ACCACGGTCGG	0.493
-	17	2771	uiv.2_Missense_M	NM_001033045	NP_001028217	Q7Z3F1	GP155_HUMAN	DEP.	1	AAGGCCGACTT	0.493
-	5	437	2_uc002ujr.2_RN	NM_001880	NP_001871	P15336	ATF2_HUMAN		3	ATTACGTGCTG	0.348
-	277	79894	252I|TTN_uc010z	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	TGGTTGTACCA	0.428
-	275	73074	79C|TTN_uc010z	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	GACACGGAACT	0.418
-	205	40639	.1_Missense_Muta	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	TCACACGGTTT	0.368
+	3	468	n_p.R3C|GULP1_	NM_016315	NP_057399	Q9UBP9	GULP1_HUMAN		1	TGAACCGTGCT	0.363
+	6	660	_p.P138S|MAP2_u	NM_002374	NP_002365	P11137	MAP2_HUMAN		17	CTCCACCCCCA	0.413
+	17	3429	.2_Missense_Mut	NM_014640	NP_055455	Q14679	TTLL4_HUMAN		3	TCGCCGTGGTC	0.463
-	11	1645	p.R429Q|PTPRN_	NM_002846	NP_002837	Q16849	PTPRN_HUMAN	ellular (Potential).	4	TGTGCCGGATG	0.557
-	3	446	zlm.1_Missense_M	NM_004438	NP_004429	P54764	EPHA4_HUMAN	ellular (Potential).	12	TGAAACGCTCT	0.458
+	21	2494	KD_uc010fyh.1_	NM_152879	NP_690618	Q16760	DGKD_HUMAN		5	ACGGGCGACCC	0.547
-	7	1219		NM_016652	NP_057736	Q9BZJ0	CRNL1_HUMAN	HAT 6.	3	CTTTCCGTGCAT	0.418
-	4	943	_uc002wvb.2_Mi	NM_015655	NP_056470	Q9Y3M9	ZN337_HUMAN		0	AGCTTACTGCAT	0.423
+	3	187	RG1B_uc010gdr.1_RNA|FRG1B_uc010ztk.1_Missense_Mutation_p.L4S						0	CTTTGTTGGCCT	0.353
+	3	189	RG1B_uc010gdr.1_RNA|FRG1B_uc010ztk.1_Missense_Mutation_p.A5T						0	TTGTTGGCCTCA	0.353
+	3	195	RG1B_uc010gdr.1_RNA|FRG1B_uc010ztk.1_Missense_Mutation_p.N7D						0	CCTCAAATAGC	0.358
+	3	222	RG1B_uc010gdr.1_RNA|FRG1B_uc010ztk.1_Missense_Mutation_p.A16T						0	ATGAAGCAGGG	0.373
+	3	243_244	RG1B_uc010gdr.1_RNA|FRG1B_uc010ztk.1_Missense_Mutation_p.S23D						0	CAAAAAGTAAAA	0.361
-	3	2028	dk.2_Intron|CPNE	NM_152838	NP_690051	Q9NTZ6	RBM12_HUMAN		3	ACTTACGTGCA	0.398
+	14	2179		NM_016436	NP_057520	Q9BVI0	PHF20_HUMAN	PHD-type.	1	TGCCCGAGAAA	0.453
+	4	639	EPL1_uc010gjo.	NM_024663	NP_078939	Q8NDH3	PEPL1_HUMAN		0	TAGCAGCCCGC	0.617
-	7	600	ju.1_Missense_M	NM_014258	NP_055073	Q9BX26	SYCP2_HUMAN		5	AAATGCGAGGT	0.303
-	5	748	_p.R211*|SYNJ1_	NM_003895	NP_003886	O43426	SYNJ1_HUMAN	SAC.	5	AGCTCGTTCAC	0.383
-	21	2938	d.2_Missense_Mu	NM_000819	NP_000810	P22102	PUR2_HUMAN	GART.	1	GACTCCGGTTT	0.398
+	22	5184	.R1651H|DOPEY	NM_005128	NP_005119	Q9Y3R5	DOP2_HUMAN		2	CCAGCGTCACA	0.423
-	3	2549	zy.3_Missense_M	NM_001098402	NP_001091872	Q9ULJ3	ZN295_HUMAN	2H2-type 5.	3	GCACTCGAGGC	0.532
+	20	3673	DL1_uc002zag.1	NM_001004416	NP_001004416	Q5DID0	UROL1_HUMAN	llular (Potential).|ZP.	3	CCCCCGGAGCC	0.453
+	26	2453	_Mutation_p.D79	NM_001849	NP_001840	P12110	CO6A2_HUMAN	.|Nonhelical region.	8	TCTCCGACCTG	0.632
+	3	534	e_Mutation_p.R25	NM_006031	NP_006022	O95613	PCNT_HUMAN		8	AACAGCGTGGG	0.542
+	2	356	2_uc002zml.2_5'	NM_031413	NP_113601	Q9BXF3	CECR2_HUMAN		2	GCACCGACTCT	0.537
-	15	1935	e_Mutation_p.R57	NM_003325	NP_003316	P54198	HIRA_HUMAN	ction with CCNA1.	1	TGGACCGCTCT	0.562
+	26	4199	BIN1_uc002zzl.1_	NM_012295	NP_036427	Q9Y6J0	CABIN_HUMAN		5	ACCACGATTAC	0.622
+	4	2128	H_uc003afp.2_5'	NM_021076	NP_066554	P12036	NFH_HUMAN	ats of K-S-P-[AEPV]-[EAK]-	0	GAAGGCAGAAG	0.562
-	4	567	aii.1_Missense_M	NM_004861	NP_004852	Q99999	G3ST1_HUMAN	enal (Potential).	0	GAAGCGCATGT	0.627
-	3	2375		NM_052906	NP_443138	Q5R3F8	LRFN6_HUMAN	lasmic (Potential).	2	CAGCCGAGCCC	0.607

+	7	2384	atq.1_Missense_M	NM_001039141	NP_001034230	Q9H2D6	TARA_HUMAN		1	GGGACGATCCC	0.582	
+	7	2415	atq.1_Missense_M	NM_001039141	NP_001034230	Q9H2D6	TARA_HUMAN		1	AACCACCCAAC	0.577	
+	7	1310		NM_004286	NP_004277	O00178	GTPB1_HUMAN		1	CCCCCCGCACC	0.567	
+	12	1531	ot.1_Missense_Mu	NM_015705	NP_056520	Q96HU1	SGSM3_HUMAN		2	CCTGCGCGTGG	0.617	
-	14	2580	hek.1_Missense_M	NM_022340	NP_071735	Q9H1K0	RBNS5_HUMAN	AB5A.|Necessary for the ir	2	GATGCGGGCTG	0.562	
+	6	812		NM_015141	NP_055956	Q8N335	GPD1L_HUMAN		0	TGTCTACAGCCA	0.607	
+	7	1260		NM_017875	NP_060345	Q96DW6	S2538_HUMAN	ical; Name=6; (Potential).	0	TGGCAGCAATG	0.532	
-	50	11780	cuk.2_Missense_	NM_001407	NP_001398	Q9NYQ7	CELR3_HUMAN		11	TATCCGTGTCTG	0.552	
-	18	1756	p.A439V|QARS_u	NM_005051	NP_005042	P47897	SYQ_HUMAN		1	TGGCAGCAGGA	0.552	
+	10	2150	ck.1_Missense_M	NM_178173	NP_835467	Q8IYA8	CCD36_HUMAN		2	TTGATAGCAGTG	0.473	
+	5	3415		NM_003458	NP_003449	Q9UPA5	BSN_HUMAN		8	CCATCGAGGAT	0.662	
+	20	1735	se_Mutation_p.P2	NM_022064	NP_071347	Q5XPI4	RN123_HUMAN		7	CTGCCCCCCTG	0.547	
+	8	1086	ense_Mutation_p.T	NM_002070	NP_002061	P04899	GNAI2_HUMAN		3	TCTACACGCACT	0.527	
-	8	1164		NM_003500	NP_003491	Q99424	ACOX2_HUMAN		0	GCCTGGGCCGG	0.637	
-	2	780	p.R92W|MINA_uc	NM_001042533	NP_001035998	Q8IUF8	MINA_HUMAN		1	CCCCCGGCTGC	0.488	
+	7	1480	C_uc003dzz.2_Mis	NM_033254	NP_150279	Q9BWV1	BOC_HUMAN	3.|Extracellular (Potential).	6	TCATCGACACC	0.632	
-	4	605	R1_uc003eer.2_S	NM_175924	NP_787120	Q86SU0	ILDR1_HUMAN		1	ACTTACGTAGG	0.453	
-	7	2440	lc.1_Missense_Mu	NM_001017395	NP_001017395	O94876	TMCC1_HUMAN		1	GAACCGTTCCA	0.498	
+	17	3145	_uc003epw.1_Intr	NM_001063	NP_001054	P02787	TRFE_HUMAN	ansferrin-like 2.	2	CGGCAGTTGGC	0.493	
-	13	1957	mo.1_Missense_M	NM_006219	NP_006210	P42338	PK3CB_HUMAN	PI3K helical.	5	ACAATCAAGAA	0.353	
+	11	1887	tm.2_Missense_M	NM_022131	NP_071414	Q9H4D0	CSTN2_HUMAN	ellular (Potential).	7	GCAGTCCATCC	0.502	
+	2	396	e_Mutation_p.A54	NM_001104647	NP_001098117	Q96CQ1	S2536_HUMAN	e=2; (Potential).|Solcar 1.	0	TGGAGCCAGTG	0.443	
+	5	790	om.1_Missense_M	NM_003875	NP_003866	P49915	GUAA_HUMAN	midotransferase type-1.	3	TGCTTACACATG	0.343	
-	5	1245	_p.R10C|CCNL1_	NM_020307	NP_064703	Q9UK58	CCNL1_HUMAN	Cyclin-like 2.	5	GATTACGTTCAC	0.358	
+	19	2318	fhz.3_Missense_M	NM_022763	NP_073600	Q53EP0	FND3B_HUMAN	nectin type-III 5.	3	AAGACGTAGCC	0.542	
+	17	2734	_Mutation_p.R806	NM_198241	NP_937884	Q04637	IF4G1_HUMAN	/EIF4A-binding.	7	TTGAATCGATGT	0.438	
-	22	2585	c.2_Missense_Mu	NM_001346	NP_001337	P49619	DGKG_HUMAN		5	TTCCTGCTTTCC	0.493	
-	6	985	c.2_Missense_Mu	NM_001346	NP_001337	P49619	DGKG_HUMAN		5	AGACCGAGGGA	0.547	rs137931929
+	1	49	003fqv.2_5'UTR|E	NM_001967	NP_001958	Q14240	IF4A2_HUMAN		4	CTGGTGGCTCC	0.572	
-	6	1967	ense_Mutation_p.	NM_152617	NP_689830	Q8IYW5	RN168_HUMAN		0	TAGCGCGTAAGT	0.463	
+	9	1062	.R347H|LMLN_uc	NM_033029	NP_149018	Q96KR4	LMLN_HUMAN		1	GCCTCGTGTTG	0.368	
-	3	3294	ron|ABCA11P_uc0	NM_133474	NP_597731	D9N162	D9N162_HUMAN		1	CATTCTCCACAT	0.418	
-	9	1657		NM_012318	NP_036450	O95202	LETM1_HUMAN	rial matrix (Potential).	1	CACCTCGGCCA	0.627	
-	17	2485	C4orf10_uc003ggi	NM_003703	NP_003694	P78316	NOP14_HUMAN		1	TTCTCGAACGG	0.498	
+	26	3431		NM_002111	NP_002102	P42858	HD_HUMAN		4	TGGCCGGAAAC	0.512	
+	2	371		NM_005980	NP_005971	P25815	S100P_HUMAN		0	AGGCAGGACTC	0.522	
+	10	1627	l.1_Missense_Mu	NM_182485	NP_872291	Q7Z5Q1	CPEB2_HUMAN	RRM 2.	1	ATAAACGTGTAA	0.398	
+	8	878	s.1_Missense_Mu	NM_004787	NP_004778	O94813	SLIT2_HUMAN	LRRCT 1.	11	GCTTCGCCAAA	0.493	
-	12	2165	_p.R72Q|DHX15_	NM_001358	NP_001349	O43143	DHX15_HUMAN		1	ATAATTCGAGATA	0.383	
+	12	2215	x.2_Nonsense_M	NM_020860	NP_065911	Q9P246	STIM2_HUMAN	lasmic (Potential).	2	CTTTATCGAAATG	0.522	
+	3	825	1D1_uc010ifd.2_	NM_015173	NP_055988	Q86TI0	TBCD1_HUMAN		1	GCACTGCCCGT	0.617	
-	1	1943	.1_Missense_Mut	NM_006068	NP_006059	Q9Y2C9	TLR6_HUMAN	lasmic (Potential).	2	CCCTGCGCCGA	0.502	
+	4	888		NM_017581	NP_060051	Q9UGM1	ACHA9_HUMAN		7	CATGCCGGCCT	0.512	
+	2	721	_p.R76W|NSUN7_	NM_024677	NP_078953				0	CCCTGCGGTCC	0.478	
+	13	1956	ay.1_Missense_Mu	NM_001037442	NP_001032519	Q7L099	RUFY3_HUMAN		0	AAGCCGCCAAT	0.507	
-	2	196	0ijq.1_Nonsense_	NM_152545	NP_689758	Q0VAM2	RGF1B_HUMAN		0	GTTTCGATTGT	0.428	
+	46	7634	qa.2_Missense_M	NM_080683	NP_542414	Q12923	PTN13_HUMAN	protein phosphatase.	6	TCAACCAGATG	0.463	

-	5	462		NM_014485	NP_055300	O60760	HPGDS_HUMAN	ST C-terminal.		1	TGAGGCGCATTAT	0.368	
+	2	450	7_uc003hux.2_Spli	NM_032149	NP_115525	Q53FE4	CD017_HUMAN			0	TCAAAGGTAAGGT	0.413	
-	10	1699	itz.1_Missense_Mu	NM_006529	NP_006520	O75311	GLRA3_HUMAN	lasmic (Probable).		3	TTTGGAGTCATGC	0.478	
+	8	920	n_p.A255V|PAPD7	NM_006999	NP_008930	Q5XG87	PAPD7_HUMAN			1	GCCATGCTGTGTC	0.552	
+	24	2603	jeu.1_Missense_M	NM_005885	NP_005876	O60337	MARH6_HUMAN	lasmic (Potential).		2	TGTTCGTAAACT	0.418	
+	15	2231	j.2_RNA|SLC30A5	NM_022902	NP_075053	Q8TAD4	ZNT5_HUMAN	lasmic (Potential).		1	CATACCGAGACCC	0.373	
-	3	1609		NM_152625	NP_689838	Q8N895	ZN366_HUMAN			2	AGGCGCGGATGTT	0.552	
-	9	1369	on_p.R190C|MCT	NM_024717	NP_078993	Q6DN14	MCTP1_HUMAN	C2 2.		2	ATAGGCGTAAACT	0.413	
-	6	689	ARD4_uc010jbx.1_	NM_139164	NP_631903	Q96DR4	STAR4_HUMAN	START.		1	GCTTTTCGTAAAT	0.403	
-	6	1236		NM_002715	NP_002706	P67775	PP2AA_HUMAN			4	GAGTATCGTCAAG	0.328	
+	4	339	zl.2_Missense_Mut	NM_015288	NP_056103	Q9NQC1	JADE2_HUMAN			0	GTTTTCCGGACAC	0.557	
+	5	894	sleq.2_Nonsense_N	NM_003339	NP_003330	P62837	UB2D2_HUMAN		p.R90*(1)	1	ATTCTACGATCAC	0.328	
+	1	1670		NM_018933	NP_061756	Q9Y5F0	PCDBD_HUMAN	r (Potential).|Cadherin 5.		3	CCCCAGGACCCG	0.657	
+	1	1330	o.1_Intron|PCDHG	NM_018923	NP_061746	Q9Y5G2	PCDGE_HUMAN	r (Potential).|Cadherin 4.		0	ATCTCCGACGTCA	0.557	
+	1	1718	CDHGB1_uc003ljo.	NM_018918	NP_061741	Q9Y5G8	PCDG5_HUMAN	|Extracellular (Potential).		4	GTTCCACGGGCG	0.617	
-	8	932	llc.3_Missense_Mu	NM_005219	NP_005210	O60610	DIAP1_HUMAN	GBD/FH3.		1	AGAGCAGAAAGCA	0.418	
-	3	385	3llc.3_Nonsense_M	NM_005219	NP_005210	O60610	DIAP1_HUMAN			1	ATGACTGTGCTGT	0.418	
-	5	373	g.2_5'Flank|FCHSD	NM_033449	NP_258260	Q86WN1	FCSD1_HUMAN			4	GGTCACGGTATCC	0.637	
+	5	699	ny.2_Missense_Mu	NM_018989	NP_061862	Q9P2N5	RBM27_HUMAN	Arg-rich.		3	TGAGTCGCAGTAC	0.423	
+	5	1140	p.R367H|TCERG1	NM_006706	NP_006697	O14776	TCRG1_HUMAN	Pro-rich.		2	CGTTTCGTGTTCC	0.463	
-	10	1901	nsense_Mutation_p	NM_014790	NP_055605	Q96AA8	JKIP2_HUMAN	Potential.		2	CTTCTCGTTCAGC	0.443	
+	1	615	TC2_uc003lpp.1_I	NM_000024	NP_000015	P07550	ADRB2_HUMAN	elical; Name=3.		1	CTGTGCGTGATCC	0.488	
-	5	925	se_Mutation_p.L24	NM_005211	NP_005202	P07333	CSF1R_HUMAN	Potential).|Ig-like C2-type 3.		54	TGCGAGCTGCAC	0.308	
-	23	12797	AT2_uc003lud.3_M	NM_001447	NP_001438	Q9NYQ8	FAT2_HUMAN	lasmic (Potential).		6	CAGGCGCTCCCC	0.647	
+	16	1636	p.R500W|CYFIP2_	NM_001037333	NP_001032410	Q96F07	CYFP2_HUMAN			0	GCGGTACGGAAG	0.562	
+	23	4438	zt.3_Missense_Mu	NM_001122679	NP_001116151					10	GTCCTCTACATCA	0.532	
+	23	4738	zt.3_Missense_Mu	NM_001122679	NP_001116151					10	CCCCCGGAGAGC	0.463	
+	16	1615	ense_Mutation_p.D	NM_004946	NP_004937	Q92608	DOCK2_HUMAN	DHR-1.		7	TGTTTCGACATCG	0.498	
+	16	1620	2_Silent_p.I40I|DC	NM_004946	NP_004937	Q92608	DOCK2_HUMAN	DHR-1.		7	CGACATCGGTCAT	0.483	
-	8	1174		NM_005990	NP_005981	O94804	STK10_HUMAN	rotein kinase.		8	GAAGGGATGCTC	0.632	
+	5	613	ndb.1_Missense_M	NM_022754	NP_073591	Q9H9B4	SFXN1_HUMAN	ical; (Potential).		1	GGTGCCGTAGCA	0.428	
+	3	2095	akn.1_Missense_M	NM_014757	NP_055572	Q92585	MAML1_HUMAN			6	CCCCCTATCTCAC	0.572	
+	5	2352	IL1_uc003mkn.1_I	NM_014757	NP_055572	Q92585	MAML1_HUMAN			6	GTGCCCGGCATG	0.592	
+	24	8833	q.1_Missense_Mut	NM_004415	NP_004406	P15924	DESP_HUMAN	Globular 2.		9	TTTGACGCCACAC	0.358	
-	3	728	on.2_Missense_Mu	NM_006778	NP_006769	Q9UDY6	TRI10_HUMAN			0	CATCCCGTTGCCT	0.502	rs138056642
+	5	537	_Mutation_p.R111C	NM_013993	NP_054699	Q08345	DDR1_HUMAN	(Potential).|F5/8 type C.		9	TACAACGACTGCA	0.652	
+	10	1680	/380I|VARS2_uc01	NM_020442	NP_065175	Q5ST30	SYVM_HUMAN			4	GTGGCCGTTCATC	0.527	
+	11	1720	R393Q|VARS2_uc	NM_020442	NP_065175	Q5ST30	SYVM_HUMAN			4	CGGGCGACAGC	0.592	
-	11	1829	xd.2_Missense_Mu	NM_025258	NP_079534	Q9Y334	G7C_HUMAN			3	GGATCCGGACTG	0.577	
-	2	1739	te.2_Missense_Mu	NM_005527	NP_005518	P34931	HS71L_HUMAN			6	ACCATGCGCTCA	0.473	
-	5	472	dpg.1_Missense_M	NM_004381	NP_004372	Q99941	ATF6B_HUMAN	lasmic (Potential).		0	TCTGGACGGTTTC	0.527	
+	7	1399		NM_004053	NP_004044	Q13895	BYST_HUMAN			0	CCTTACCGGGTGC	0.562	
-	5	1030	2_5'UTR|TRERF1	NM_033502	NP_277037	Q96PN7	TREF1_HUMAN			5	TGAATTCGCAGG	0.567	
-	5	1003	.2_5'UTR|TRERF1	NM_033502	NP_277037	Q96PN7	TREF1_HUMAN			5	ACCTGGGTGAAAC	0.552	
+	4	861	_p.R125*|EFHC1_u	NM_018100	NP_060570	Q5JVL4	EFHC1_HUMAN			3	GAACTCCGAAAAC	0.378	
+	5	1266		NM_024641	NP_078917	Q5SRI9	MANEA_HUMAN	able).|Lumenal (Potential).		3	CGGAACCGAATCA	0.418	
+	2	1146	_p.R200L|GJA1_u	NM_000165	NP_000156	P17302	CXA1_HUMAN	lasmic (Potential).		2	CTTGCCGCAATTA	0.502	

+	6	891	e_Mutation_p.R24	NM_152553	NP_689766	Q8TC41	RN217_HUMAN			0	AAATATCGCTACC	0.438	
+	5	618	1_uc010kfm.1_Sp	NM_000045	NP_000036	P05089	ARGI1_HUMAN			1	GGAACAGTAAGC	0.423	
+	1	482		NM_053278	NP_444508	Q969N4	TAAR8_HUMAN	Name=4; (Potential).		1	CTCTCACGTACAC	0.488	rs140382740
-	5	1864	.M535I|BCLAF1_u	NM_014739	NP_055554	Q9NYF8	BCLF1_HUMAN			1	CGCTATCATTTTG	0.423	
-	4	918	.S220N|BCLAF1_u	NM_014739	NP_055554	Q9NYF8	BCLF1_HUMAN			1	CTAGGACTATTAT	0.433	
-	93	18156	E1_uc003qot.3_Mis	NM_182961	NP_892006	Q8NF91	SYNE1_HUMAN	lasmic (Potential).		45	ACAGCGACCTG	0.502	
+	1	282		NM_002377	NP_002368	P04201	MAS_HUMAN	cellular (Potential).		4	TCTATCGACTATG	0.433	
-	7	1381	qte.1_Missense_M	NM_003058	NP_003049	O15244	S22A2_HUMAN	lasmic (Potential).		2	GGTAACGGCGT	0.502	
-	8	1237	p.T197M|AGPAT4_	NM_020133	NP_064518	Q9NRZ5	PLCD_HUMAN			0	CCAGCGTCAGG	0.622	
+	24	3350	vc.1_Missense_Mu	NM_001040001	NP_001035090	P55196	AFAD_HUMAN	PDZ.		5	CTCTCTCAGGAA	0.403	
+	7	2115	e_Mutation_p.D13	NM_019005	NP_061878	Q9NXC5	MIO_HUMAN			0	TCTTACGATGGA	0.338	
-	1	226		NM_175886	NP_787082	P21108	PRPS3_HUMAN		p.R49C(1)	1	CTCCACGCACAC	0.488	rs112075478
+	83	13362	.2_3'UTR|CDCA7L	NM_003777	NP_003768	Q96DT5	DYH11_HUMAN			15	CGCCCGCTGGG	0.488	
-	5	726	g.1_Missense_Mut	NM_000168	NP_000159	P10071	GLI3_HUMAN			19	AGAGCGATGGG	0.572	
-	4	874	ya.2_Missense_M	NM_006230	NP_006221	P49005	DPOD2_HUMAN			2	CTCCACTGCCTC	0.617	
-	2	220	_p.A45V|DDC_uc	NM_000790	NP_000781	P20711	DDC_HUMAN			2	GGGCAGCGGCA	0.562	
-	10	2154	.3_Missense_Mut	NM_015198	NP_056013	O75128	COBL_HUMAN			5	CTCCCCGTCAG	0.483	
-	5	1668		NM_033273	NP_150376	Q96JC4	ZN479_HUMAN	C2H2-type 11.		4	CACATGTGTAGC	0.428	
+	4	871_872	zu.2_Missense_Mu	NM_152626	NP_689839	Q03936	ZNF92_HUMAN	C2H2-type 4.		0	CCTCAAATCTTAC	0.351	
+	4	946	zu.2_Missense_Mu	NM_152626	NP_689839	Q03936	ZNF92_HUMAN	C2H2-type 5.		0	TAACCGGTCCTC	0.368	
+	4	907	udv.1_Missense_M	NM_001040456	NP_001035546	Q6NTF9	RHBD2_HUMAN			0	CAGCACGCCAGT	0.652	
+	4	1101		NM_181646	NP_857597	A4D1E1	Z804B_HUMAN			11	CAAATCGACACC	0.413	
+	5	634	1khj.1_Missense_	NM_001039706	NP_001034795	A5D8W1	CG063_HUMAN			1	AAGTGTCGGATG	0.328	
-	14	2480	e_Mutation_p.R73	NM_000466	NP_000457	O43933	PEX1_HUMAN			2	GAGAGTCGAGAA	0.393	
+	13	1683	_p.R432H|DYNC1	NM_004411	NP_004402	O14576	DC1I1_HUMAN	WD 4.		4	CTTGTCGTCATGC	0.443	
-	7	2008	iw.1_Missense_Mu	NM_015545	NP_056360	O75127	PTCD1_HUMAN			1	GCTGGCGGATG	0.562	
-	2	538	iw.1_Missense_Mu	NM_015545	NP_056360	O75127	PTCD1_HUMAN	PPR 1.		1	CAGTACGGGGTG	0.557	
+	2	349	tron|uc011kjy.1_R	NM_033506	NP_277041	O75426	FBX24_HUMAN			4	GCTGCCCTTCTTC	0.562	
-	6	1496		NM_022574	NP_072096	O75420	PERQ1_HUMAN			2	GCCTCTCGCCTCT	0.657	
+	14	2315	ZAN_uc003uwl.2_F	NM_003386	NP_003377	Q9Y493	ZAN_HUMAN	ate) (mucin-like domain).|E		11	AAAAACCCACCAT	0.507	
-	19	2376	_p.S296N|RBM28_	NM_018077	NP_060547	Q9NW13	RBM28_HUMAN			2	CATTTGCTCCTCT	0.498	
+	16	1793	_p.T477I|AHCYL2_	NM_015328	NP_056143	Q96HN2	SAHH3_HUMAN			2	TGCCTACCTTTGA	0.498	
+	10	1173		NM_001868	NP_001859	P15085	CBPA1_HUMAN			1	GACTGGACCTAC	0.532	
+	10	1152	h.2_Missense_Mu	NM_013255	NP_037387	Q9UL63	MKLN1_HUMAN	Kelch 2.		1	TCTATCGTTATGA	0.413	
-	27	5048	A4_uc003vqz.3_5	NM_020911	NP_065962	Q9HCM2	PLXA4_HUMAN	lasmic (Potential).		1	TCACTGCGTTATA	0.552	
+	34	4875	205_uc003vsx.2_	NM_015135	NP_055950	Q92621	NU205_HUMAN			6	GGATCGCTACCC	0.507	rs144088473
-	4	1081	vtb.2_Missense_M	NM_012450	NP_036582	Q9UKG4	S13A4_HUMAN	ical; (Potential).		0	AACGTGGTACAG	0.632	
+	10	1791	ub.2_Missense_M	NM_015905	NP_056989	O15164	TIF1A_HUMAN			8	CCCAAACCCAATC	0.408	
-	2	1250	NND2A_uc003vvv	NM_015689	NP_056504	Q9ULE3	DEN2A_HUMAN			4	CATAGACGTTCTC	0.527	
+	7	1079	p.A213V|UBE3C_	NM_014671	NP_055486	Q15386	UBE3C_HUMAN			5	AGGTGCGAGGT	0.333	
-	4	5778		NM_178857	NP_849188	Q8IWN7	RP1L1_HUMAN			8	TCTACACCTTCTC	0.642	
+	6	918	e_Mutation_p.V24	NM_004462	NP_004453	P37268	FDFT_HUMAN			0	TGGCCGTGCAG	0.448	
-	3	258	tion_p.R32C|ENTF	NM_004901	NP_004892	Q9Y227	ENTP4_HUMAN	lasmic (Potential).		2	TTGGCGTAAATT	0.398	
-	8	813	k.2_Intron|KCTD9_	NM_017634	NP_060104	Q7L273	KCTD9_HUMAN			0	GCATCGCAGTTC	0.358	
+	5	2914		NM_001440	NP_001431	O43909	EXTL3_HUMAN	enal (Potential).		2	TGGCCGTTACCA	0.542	
-	15	2878	e_Mutation_p.R55	NM_023110	NP_075598	P11362	FGFR1_HUMAN	Potential).|Protein kinase.		15	GTCCCGTGCGAC	0.493	
+	6	827		NM_152565	NP_689778	Q8N8Y2	VA0D2_HUMAN			0	GGTTGCGGCTGT	0.468	

+	3	1028	.1_Intron|DCAF13_	NM_015420	NP_056235	Q9NV06	DCA13_HUMAN	WD 1.	1	ACTCAGCGGAAT	0.353	
+	10	1931	_Mutation_p.S603	NM_018002	NP_060472	Q8N573	OXR1_HUMAN		0	AGTGGAGTCCAG	0.348	
-	10	1038	3E_uc003ymv.2_M	NM_001568	NP_001559	P60228	EIF3E_HUMAN	PCI.	3	AGAGACGGGCA	0.368	
-	2	983		NM_031415	NP_113603	Q9BYG8	GSDMC_HUMAN		3	AACTGACGTAATT	0.403	
-	5	984	ae.1_Missense_Mu	NM_201380	NP_958782	Q15149	PLEC_HUMAN	bular 1.|Actin-binding.	9	GAGGCCAAGGG	0.622	
+	4	747	p.R194Q|GRINA_u	NM_001009184	NP_001009184	Q7Z429	GRINA_HUMAN		1	TTGTCCGGGAGA	0.552	
+	3	1244	kx.1_Missense_Mu	NM_198572	NP_940974	Q76KD6	SPERI_HUMAN		2	CCCACTGTCCTCC	0.617	
+	2	312	F1_uc003zbu.3_R	NM_005526	NP_005517	Q00613	HSF1_HUMAN	By similarity.	0	GTGTTCGACCAGC	0.622	
-	17	1703		NM_013291	NP_037423	Q10570	CPSF1_HUMAN		1	TCCTTACGCACCC	0.647	
-	5	440	sense_Mutation_p.	NM_021061	NP_066405	P15622	ZN250_HUMAN		0	CAGGCTGTAGTGT	0.353	
-	1	327	A14_uc003zoo.1_	NM_002172	NP_002163	P01570	IFN14_HUMAN		0	ATGAGTTCTTTGT	0.468	
-	1	450		NM_000605	NP_000596	P01563	IFNA2_HUMAN		1	CTGTCACCCCCAC	0.493	
-	2	156	uw.1_Missense_M	NM_007234	NP_009165	O75935	DCTN3_HUMAN		0	CCACCTGCACCT	0.498	
+	12	2540	e_Mutation_p.R39	NM_004512	NP_004503	Q14626	I11RA_HUMAN	lasmic (Potential).	1	GAGACGGGGTG	0.537	
+	9	1136	_p.E282K|UNC13B	NM_006377	NP_006368	O14795	UN13B_HUMAN		5	TATCACGAACAAC	0.502	
+	5	599	2_Intron|CCDC107	NM_174923	NP_777583	Q8WV48	CC107_HUMAN		0	AGGCTCGGGAG	0.547	
-	10	2745	15_splice|FBXO10_	NM_012166	NP_036298	Q9UK96	FBX10_HUMAN		5	GCACTCACTTTTT	0.522	
-	21	3648	1056T|CNTNAP3_	NM_033655	NP_387504	Q9BZ76	CNTP3_HUMAN	4.|Extracellular (Potential).	1	TGACGGCGTTGA	0.393	
+	1	604_605	42421_uc004aed.1_RNA						0	AGTCGCGCAAGC	0.589	
-	5	1661		NM_001163	NP_001154	Q02410	APBA1_HUMAN	PID.	1	TGGCGGCAAAA	0.552	
-	5	1762	NF484_uc010mrb.	NM_031486	NP_113674	Q5JVG2	ZN484_HUMAN	C2H2-type 10.	0	TGAGCCGAGACT	0.398	
-	1	443		NM_001004482	NP_001004482	Q8NGS8	O13C5_HUMAN	Name=4; (Potential).	4	TCCAGGACCCAC	0.463	
+	1	389		NM_001004484	NP_001004484	Q8NGV5	O13D1_HUMAN	cellular (Potential).	2	GCTGTGCTCTGCA	0.483	
+	1	721	lzh.1_Intron|RABG	NM_005294	NP_005285	Q99679	GPR21_HUMAN	lasmic (Potential).	1	ACTGGGGAAGTG	0.488	
-	10	1649	_Mutation_p.A247	NM_001006617	NP_001006618	Q9BPZ7	SIN1_HUMAN		4	TCACAGGCACAGA	0.468	
+	8	1066	n_p.S200N|GARNL	NM_032293	NP_115669	Q5VVW2	GARL3_HUMAN	Rap-GAP.	3	TGTTCAGCAATGC	0.468	
+	2	263	_p.R59Q|DNM1_u	NM_004408	NP_004399	Q05193	DYN1_HUMAN		2	GCCTCGAGGATC	0.617	
+	7	977	p.R297Q|DNM1_u	NM_004408	NP_004399	Q05193	DYN1_HUMAN		2	GGCTGCGGAACA	0.587	
+	14	1852	_p.R592H|SPTAN1	NM_003127	NP_003118	Q13813	SPTA2_HUMAN	Spectrin 7.	10	TTTTCCGTGATTC	0.493	
+	11	1037	p.R276W|USP20_u	NM_001110303	NP_001103773	Q9Y2K6	UBP20_HUMAN		2	GGTGACCGGAGC	0.662	
+	3	501	11mbx.1_Missense	NM_001136557	NP_001130029	Q5VW38	GP107_HUMAN		1	CTAGACCGTACAA	0.393	
+	10	1341	nzj.1_Missense_M	NM_013318	NP_037450	Q5JSZ5	PRC2B_HUMAN		0	GACTCGAGAGG	0.592	
+	9	998	0ncu.2_RNA|CSF2	NM_001161529	NP_001155001	P15509	CSF2R_HUMAN	cellular (Potential).	2	GTCACCGTACGTT	0.582	
-	2	1660	BED1_uc004cqh.1_	NM_004729	NP_004720	O96006	ZBED1_HUMAN		0	GAAGGCGGAGA	0.622	
+	4	906	mij.1_Missense_M	NM_014728	NP_055543	Q14CM0	FRPD4_HUMAN	PDZ.	13	CCAGAGAGCGG	0.512	
+	7	1026	p.R304Q|PRPS2_	NM_002765	NP_002756	P11908	PRPS2_HUMAN		0	CAATCCGAAGGA	0.458	
-	15	2104	GR_uc004dea.2_In	NM_001034853	NP_001030025	Q92834	RPGR_HUMAN	Glu-rich.	1	CTGCTTCTCCCAC	0.373	
-	3	567	j.1_Missense_Muta	NM_000169	NP_000160	P06280	AGAL_HUMAN		0	CAATGTCGTAGTA	0.438	
+	4	204	se_Mutation_p.R59	NM_006649	NP_006640	Q9BVJ6	UT14A_HUMAN	Potential.	2	CAGGCGGAAATT	0.428	rs143564742
+	7	898	gs.1_Missense_Mu	NM_001129765	NP_001123237	Q15738	NSDHL_HUMAN		0	TTGGTACCCATC	0.582	
+	5	829	vlj.2_Missense_Mu	NM_182752	NP_877429	Q5T0D9	TPRGL_HUMAN		0	TACGTGGGACTC	0.547	
-	4	953	pa.1_Missense_M	NM_018948	NP_061821	Q9UJM3	ERRFI_HUMAN		1	GGATTTGGATCTC	0.483	
-	2	253	p.S46R|MTHFR_u	NM_005957	NP_005948	P42898	MTHR_HUMAN		0	GCTCTCACTGCCA	0.612	
-	2	1354	atl.1_Missense_M	NM_138346	NP_612355	Q8IYS2	K2013_HUMAN	cellular (Potential).	1	GGTCTCGCTCCC	0.642	
+	11	9704	p.1_Missense_Mu	NM_015001	NP_055816	Q96T58	MINT_HUMAN		15	CTGTCGCTCGAGC	0.617	
+	20	2284	se_Mutation_p.A46	NM_018125	NP_060595	Q9HCE6	ARGAL_HUMAN		3	CACTCGGCCAACA	0.607	
-	12	1224	ense_Mutation_p.	NM_017707	NP_060177	Q8TDY4	ASAP3_HUMAN	PH.	3	TCACGGGTCACCA	0.607	

+	4	328	hm.2_Missense_M	NM_000975	NP_000966	P62913	RL11_HUMAN		1	ATACTGGAAACT	0.428	
-	3	612	blg.1_Missense_M	NM_032513	NP_115902	Q9BRI3	ZNT2_HUMAN	ical; (Potential).	0	CCGACGTGATC	0.607	rs148861822
-	3	316	2_Intron|UBXN11_	NM_183008	NP_892120	Q5T124	UBX11_HUMAN		1	GCAGGGGCACTT	0.547	
+	2	759		NM_005281	NP_005272	P46089	GPR3_HUMAN	lasmic (Potential).	1	GTCTGCCGCCAT	0.597	
+	10	1834	p.V556M|GMEB1_	NM_006582	NP_006573	Q9Y692	GMEB1_HUMAN		0	CACAATGTGGAG	0.413	
+	12	2965	_Mutation_p.R914	NM_005119	NP_005110	Q9Y2W1	TR150_HUMAN		9	TGTTCCGGAAAT	0.607	
-	6	692	CH2_uc010olg.1_In	NM_003738	NP_003729	Q9Y6C5	PTC2_HUMAN	cellular (Potential).	18	GCAAAGGGACCC	0.642	
+	5	589	vym.2_Missense_M	NM_000779	NP_000770	P13584	CP4B1_HUMAN		2	AGTGGGAAGAG	0.567	
+	3	1514	orf175_uc010oof.1	NM_001039464	NP_001034553	Q68CQ1	HEAT8_HUMAN		0	CAACCCCGCAG	0.597	
-	5	985	RIQ3_uc001dfz.3_F	NM_001105659	NP_001099129	A6PVS8	LRIQ3_HUMAN		2	TATCTTCATACCC	0.299	
+	3	551	.1_Intron|ST6GALI	NM_030965	NP_112227	Q9BVH7	SIA7E_HUMAN	nenal (Potential).	2	ATGACGCCCCCA	0.622	rs144853725
+	5	656	se_Mutation_p.R84	NM_182976	NP_892021	Q5BKZ1	ZN326_HUMAN	Gly-rich.	1	GCTCTCGGGGGA	0.502	
+	6	730	td.2_Missense_Mu	NM_003729	NP_003720	O00442	RTC1_HUMAN		0	TTGTTCGAATGTC	0.378	rs139397880
+	12	2283		NM_001010898	NP_001010898	Q9H1V8	S6A17_HUMAN	cellular (Potential).	2	GCTGCCGAGCGC	0.662	
+	5	1008	e_Mutation_p.T276	NM_001142782	NP_001136254	Q5TCQ9	MAGI3_HUMAN	nylate kinase-like.	6	ACCAAACAAATAG	0.428	
-	2	96		NM_005621	NP_005612	P80511	S10AC_HUMAN		0	CAATTCCCTCCAC	0.473	
+	3	584		NM_020387	NP_065120	P57735	RAB25_HUMAN		0	ATCGTCGTCATG	0.597	
+	5	1565		NM_001080426	NP_001073895	Q5VZP5	DUS27_HUMAN		3	GGACAGCGTGG	0.562	
-	1	443	_p.P121L|TNR_uc	NM_003285	NP_003276	Q92752	TENR_HUMAN		11	TTTTTGGGGAAG	0.592	
+	2	1333	se_Mutation_p.R57	NM_020318	NP_064714	Q9BXP8	PAPP2_HUMAN		16	AAGGTTCGAAGA	0.567	
-	13	2350	d.1_Missense_Mu	NM_004319	NP_004310	O14525	ASTN1_HUMAN		15	CTTTCCCCACAG	0.542	
-	7	841	_p.R21*|CHI3L1_u	NM_001276	NP_001267	P36222	CH3L1_HUMAN		1	ACCTCGGAACAC	0.572	rs151205460
-	3	381	bz.2_Missense_M	NM_002644	NP_002635	P01833	PIGR_HUMAN	1.|Extracellular (Potential).	3	ATGAGGGTTATG	0.577	
-	8	1732	kv.2_Missense_Mu	NM_206933	NP_996816	O75445	USH2A_HUMAN	nal.|Extracellular (Potential	26	TGCCACGGGAATA	0.348	
+	3	445		NM_183062	NP_898885	A1L453	PRS38_HUMAN	Peptidase S1.	2	TCGGAGGTGAC	0.572	
+	6	1832	hvs.1_Missense_	NM_032435	NP_115811	Q5TCX8	M3KL4_HUMAN		8	GATAACCGTGCA	0.502	
-	2	732		NM_022469	NP_071914	Q9H772	GREM2_HUMAN	CTCK.	0	TTCACCTTCTGG	0.577	
+	1	376		NM_001004698	NP_001004698	A6NFC9	OR2W5_HUMAN		3	TGGCCGTCTGCC	0.587	
+	11	1650	010qct.1_Missense	NM_012443	NP_036575	O75602	SPAG6_HUMAN		1	TGGACAGCTATCA	0.353	
+	10	987	DSS1_uc010qdf.1	NM_014317	NP_055132	Q5T2R2	DPS1_HUMAN		0	TCACCTCGTGTTC	0.478	
-	1	852		NM_001034842	NP_001030014	Q3KNS1	PTHD3_HUMAN		4	CTTCCCTTTTCCC	0.627	
+	3	530	_Mutation_p.R114	NM_020975	NP_066124	P07949	RET_HUMAN	cellular (Potential).	451	CAGACCGCGGC	0.627	
-	4	718	GAP22_uc010qgl.1	NM_021226	NP_067049	Q7Z5H3	RHG22_HUMAN	PH.	1	TCGGCGGATGG	0.677	rs140701623
-	5	1942	T2_uc001jvl.1_5'F	NM_003635	NP_003626	P52849	NDST2_HUMAN	Heparan sulfate N-deacetyl	1	CTTTGCGGTGCT	0.577	
+	6	1414		NM_000314	NP_000305	P60484	PTEN_HUMAN	hatase tensi).Y27_N212>Y	2334	CTGGAAAGGGAC	0.413	
+	2	1004	nx.1_Missense_Mu	NM_016341	NP_057425	Q9P212	PLCE1_HUMAN		3	TTTTATGAAATGT	0.398	
+	6	571	_p.S17N|LCOR_u	NM_015652	NP_056467	Q8N655	CJ012_HUMAN		2	AAAATAGCTCTAC	0.522	
+	38	5350	.R1700C|GBF1_u	NM_004193	NP_004184	Q92538	GBF1_HUMAN		2	TGGGAACGCATT	0.552	
-	13	1670	09ycc.2_Missense_	NM_021924	NP_068743	Q9HBB8	CDHR5_HUMAN	cellular (Potential).	0	CACCCGGGGGC	0.677	
+	6	761		NM_002457	NP_002448	Q02817	MUC2_HUMAN		2	TGGAGCCGTATC	0.706	
+	1	451		NM_001001480	NP_001001480	Q701N2	KRA55_HUMAN	repeats of C-C-X-P.	1	GGGGGGCTGTG	0.692	
-	1	478		NM_001004052	NP_001004052	Q96RD2	O52B2_HUMAN	Name=4; (Potential).	0	GACTGGGAAGAT	0.517	
-	10	1641	ew.1_Missense_M	NM_001001991	NP_001001991	Q6UXH9	PAMR1_HUMAN	Peptidase S1.	2	TCATCCCGGTCAT	0.527	
-	1	280		NM_001005282	NP_001005282	Q8NGP6	OR5M8_HUMAN	cellular (Potential).	1	AGGCAGGATAGG	0.463	
-	5	2828	p.A839G|TNKS1BF	NM_033396	NP_203754	Q9C0C2	TB182_HUMAN	Acidic.	1	ACATCTGCCTCCT	0.577	
+	12	1236		NM_002559	NP_002550	P56373	P2RX3_HUMAN	lasmic (Potential).	0	AGCAGTCCACCG	0.612	
+	1	340		NM_001005283	NP_001005283	Q8NGE9	OR9Q2_HUMAN	Name=3; (Potential).	4	TGCTACCTTCTG	0.592	

+	1	845		NM_001004728	NP_001004728	Q8NGJ0	OR5A1_HUMAN	Name=7; (Potential).	2	TCTATTCATTGGT	0.483	
-	5	6754	IAK_uc001ntk.1_Ir	NM_001620	NP_001611	Q09666	AHNK_HUMAN		19	CACATCCACACT	0.498	
+	4	483	18BP_uc001orh.1_	NM_001039659	NP_001034748	O95998	I18BP_HUMAN	j-like C2-type.	0	TGGAAGTGACCT	0.607	
+	7	1168	_uc009yyx.2_Spli	NM_213621	NP_998786	P46098	5HT3A_HUMAN		0	TCATTGGTAAGG	0.597	
+	13	4675		NM_005422	NP_005413	O75443	TECTA_HUMAN	VWFD 4.	10	ACGACCGGAAC	0.537	
+	14	1950		NM_003105	NP_003096	Q92673	SORL_HUMAN	cellular (Potential).	15	GAGTTCCCTGC	0.537	
+	2	517	2CR1_uc009zhu.2_	NM_058169	NP_477517	Q969J3	L12R1_HUMAN		1	AACGATCCCGAT	0.473	
+	7	891	.172M|PPFIBP1_u	NM_003622	NP_003613	Q86W92	LIPB1_HUMAN	Potential.	5	TTGGATCTGATG	0.358	
+	5	1094	e_Mutation_p.R33	NM_001714	NP_001705	Q96G01	BICD1_HUMAN	Potential.	2	AGAGCGGGAAA	0.502	
+	19	2303	mn.1_Missense_M	NM_001843	NP_001834	Q12860	CNTN1_HUMAN	onectin type-III 2.	9	GCCTTTGTCAAG	0.373	
+	8	1073	e_Mutation_p.P232	NM_032256	NP_115632	Q9H0C3	TM117_HUMAN		0	CGGCCCGGGGC	0.378	rs141562455
-	13	1742	p.P410L|CALCOC	NM_020898	NP_065949	Q9P1Z2	CACO1_HUMAN	NB1 binding site) (By simila	1	CTGCCGGGCAG	0.557	
+	3	1253		NM_032786	NP_116175	Q96K80	ZC3HA_HUMAN	Pro-rich.	0	CCCCACCCCCAC	0.627	
+	11	1023	n_p.T150I|NUP107	NM_020401	NP_065134	P57740	NU107_HUMAN		1	TGCATACCTTAA	0.318	
-	16	1764	se_Mutation_p.I55	NM_024953	NP_079229	Q14CX7	NAA25_HUMAN		3	CTTGAATAATATA	0.383	
-	55	7518		NM_006836	NP_006827	Q92616	GCN1L_HUMAN		4	TGCCGGCACAA	0.587	
+	12	2036	ot.2_Missense_Mu	NM_014938	NP_055753	Q9HAP2	MLXIP_HUMAN		2	AGGTCGGGACT	0.627	
-	1	469	R81_uc001ucw.1_Ir	NM_177551	NP_808219	Q8TDS4	HCAR2_HUMAN	lasmic (Potential).	0	GGTGGGGATGG	0.567	
-	1	550	R81_uc001ucw.1_Ir	NM_006018	NP_006009	P49019	HCAR3_HUMAN	lasmic (Potential).	2	GGTGGGGATGG	0.562	
+	21	4426	G1463D|EP400_u	NM_015409	NP_056224	Q96L91	EP400_HUMAN		12	ACAGGGCCCGC	0.647	
-	2	140		NM_006001	NP_005992	Q13748	TBA3C_HUMAN		5	CGGGCTGAATTC	0.547	
+	2	1349		NM_153456	NP_703157	Q8IZP7	H6ST3_HUMAN	nenal (Potential).	2	GCAGCGAGAGC	0.612	
+	1	327	_p.D26A|ARHGEF	NM_001113511	NP_001106983	Q14155	ARHG7_HUMAN	CH.	7	CTCGGACCCGG	0.617	
-	1	1937		NM_032135	NP_115511	Q5H9T9	FSCB_HUMAN	Ala-rich.	9	GAGACTGAGCT	0.498	
+	3	835	tsa.1_Missense_M	NM_006255	NP_006246	P24723	KPCL_HUMAN	l-ester/DAG-type 1.	6	GGCCACGTATCT	0.512	
+	9	1132	p.G285R|MTHFD1	NM_005956	NP_005947	P11586	C1TC_HUMAN	e dehydrogenase and cyclo	2	CAAATGGGAGA	0.478	
-	3	265	MA1_uc001ybx.1_	NM_178013	NP_821092	Q86XR5	PRIMA_HUMAN	cellular (Potential).	2	CCTggggcggagag	0.373	
+	8	994	e_Mutation_p.G18	NM_001112726	NP_001106197	Q9Y4F5	K0284_HUMAN		1	TGGGGGCGGAG	0.622	
+	6	529	p.R142H|CYFIP1_	NM_014608	NP_055423	Q7L576	CYFP1_HUMAN		9	GAGGCGCCTGT	0.562	
+	1	3007		NM_018958	NP_061831	Q9NZP6	CO002_HUMAN		8	GGAAGGAGGAG	0.498	
-	20	2408		NM_178034	NP_828848	Q86XP0	PA24D_HUMAN	PLA2c.	2	GTAGGTCATGTT	0.657	
-	7	872	lk.1_Missense_Mu	NM_174916	NP_777576	Q8IWV7	UBR1_HUMAN		1	CAGCCCGACGA	0.383	
+	4	3279		NM_002373	NP_002364	P78559	MAP1A_HUMAN		9	GAGCTGTGGAA	0.507	
-	3	454	01zsj.2_Missense_	NM_172095	NP_742093	Q96P56	CTSR2_HUMAN	lasmic (Potential).	1	CTCTGGGCATGT	0.498	
-	12	1195	ef.1_Missense_Mu	NM_032892	NP_116281	Q7Z6J6	FRMD5_HUMAN		1	GTATTTCCGGTG	0.488	
+	13	1657	vz.2_Missense_Mu	NM_153618	NP_705871	Q8NFY4	SEM6D_HUMAN	tracellular (Potential).	4	GGACCCTACCAG	0.512	
+	9	1999	on.2_Missense_Mu	NM_000875	NP_000866	P08069	IGF1R_HUMAN	onectin type-III 2.	8	GCAGCGGCAGC	0.557	rs61731172
-	8	2014	p.H575Y|LINS1_u	NM_001040614	NP_001035704	Q8NG48	LINES_HUMAN		0	AACGATGGGGTA	0.473	
+	6	554	yh.1_Missense_M	NM_000303	NP_000294	O15305	PMM2_HUMAN		1	GATCTACGGAAA	0.358	rs104894526
+	8	1079	p.V302I|ABCC1_u	NM_004996	NP_004987	P33527	MRP1_HUMAN	Cytoplasmic.	4	TTGATCGTCAAG	0.527	
-	4	398	_p.R63Q|ACSM2E	NM_182617	NP_872423	Q68CK6	ACS2B_HUMAN		5	GGAGTCGCTTG	0.512	
-	32	4567		NM_017539	NP_060009	Q8TD57	DYH3_HUMAN	.1 (By similarity).	18	GGTTGGGTTCA	0.517	
-	11	1030	uc002diq.3_Intron	NR_003370					0	CTCTGAGGATACT	0.338	rs141895991
-	6	982	41K|RABEP2_uc0	NM_024816	NP_079092	Q9H5N1	RABE2_HUMAN	Potential.	3	CCGCTCGCGACT	0.562	
+	14	4932		NM_014712	NP_055527	O15047	SET1A_HUMAN	n with CFP1.|Pro-rich.	3	ccTACGAGCCAC	0.398	
+	4	2173		NM_003414	NP_003405	Q14586	ZN267_HUMAN		4	GTCATACTGGAG	0.453	
-	2	503	_RNA|SIAH1_uc00	NM_003031	NP_003022	Q8IUQ4	SIAH1_HUMAN	AH-type.|SBD.	1	GGCACGGACAG	0.478	

+	9	937		NM_033119	NP_149110	Q969G9	NKD1_HUMAN		0	CAGCCGCCTGG	0.562	rs142743935
-	29	4778	1L2_uc002fgg.1_	NM_052892	NP_443124	Q7Z442	PK1L2_HUMAN	ellular (Potential).	3	TCACCTCCTGC	0.572	
+	7	1007	voj.1_Missense_	NM_014732	NP_055547	O60268	K0513_HUMAN		1	GGGAAGACGAG	0.582	
-	6	1841	tn.1_Missense_Mu	NM_052928	NP_443160	Q8IYR2	SMYD4_HUMAN	SET.	5	ACGCCCGGATG	0.577	
-	2	741	d.1_Missense_Mu	NM_017575	NP_060045	Q86US8	EST1A_HUMAN	n with telomeric DNA.	4	TCGTGGGTTTCC	0.612	
-	36	5871	xi.2_Missense_Mu	NM_015113	NP_055928	O43149	ZZEF1_HUMAN		4	GGCTCCGCAGG	0.597	
+	7	1053	_Mutation_p.R28	NM_001042	NP_001033	P14672	GTR4_HUMAN	lasmic (Potential).	0	CCCACCGGCAG	0.637	rs140743598
-	37	5569	uc002gml.1_Intron	NM_017533	NP_060003	Q9Y623	MYH4_HUMAN	Potential.	13	GGCCTCCAGTT	0.527	
-	26	3396	_Missense_Mutat	NM_001100112	NP_001093582	Q9UKX2	MYH2_HUMAN	Potential.	14	AAACTCTTTCC	0.328	
-	4	821		NM_031898	NP_114104	Q9BXF9	TEKT3_HUMAN		2	ATCGTGAACTA	0.398	
-	6	2088		NM_020787	NP_065838	Q9P2J8	ZN624_HUMAN	2H2-type 15.	2	TACATTTATATGG	0.393	
+	1	615	ul.2_Missense_M	NM_031456	NP_113644	Q5XX13	FBW10_HUMAN		1	GAACAGCACCC	0.448	
+	16	2007	OK1_uc010wbf.1_	NM_020791	NP_065842	Q7L7X3	TAOK1_HUMAN	Potential.	4	TTCTTCGACGT	0.443	
-	11	4123		NM_001004334	NP_001004334	Q6PRD1	GP179_HUMAN	lasmic (Potential).	3	TTCTGGGCCAG	0.607	
-	14	1622	LXDC1_uc002hrh	NM_020405	NP_065138	Q8IUK5	PXDC1_HUMAN	lasmic (Potential).	3	AACTTCATGGC	0.627	
-	1	150		NM_032524	NP_115913	Q9BYR3	KRA44_HUMAN	-C-[GRQVCH]-[SPT]- [VS	0	TGGGGCGGCAG	0.652	
+	12	3079	c002irv.1_Missens	NM_018896	NP_061496	O43497	CAC1G_HUMAN	llular (Potential).|II.	1	CAGACCGGAAG	0.607	
-	2	1041		NM_004645	NP_004636	P38432	COIL_HUMAN		1	CCGCAGCACAC	0.552	
+	2	1375	ir.2_Missense_Mu	NM_000891	NP_000882	P63252	IRK2_HUMAN	smic (By similarity).	0	CCACCGCTATG	0.493	
+	3	1747		NM_000346	NP_000337	P48436	SOX9_HUMAN		0	GCCAGGGCACC	0.647	
-	2	88	1_5'UTR|GGA3_u	NM_138619	NP_619525	Q9NZ52	GGA3_HUMAN	o ARF1 (in long isoform).	2	GTATTCCCAGTC	0.512	
+	16	2317	195_uc010wsb.1_	NM_014738	NP_055553	Q12767	K0195_HUMAN		1	GCCTCCCCTCA	0.612	
+	4	595		NM_001080419	NP_001073888	Q9C0B0	UNK_HUMAN		0	ACCTTCGTTAC	0.567	
-	19	2165	F1_uc002jqd.1_Mi	NM_001080542	NP_001074011	Q8TES7	FBF1_HUMAN		0	GATGCGGCTTC	0.612	
-	11	1352	_p.S258P|PPP4R1	NM_001042388	NP_001035847	Q8TF05	PP4R1_HUMAN		1	ATTCTGAGGACA	0.443	
-	4	3359	se_Mutation_p.H1	NM_015461	NP_056276	Q96K83	ZN521_HUMAN	2H2-type 24.	7	TCCCATGGATTT	0.532	
-	9	1251	vi.3_Missense_Mu	NM_001941	NP_001932	Q14574	DSC3_HUMAN	|Extracellular (Potential).	4	CATTTTCCTCTA	0.274	
+	14	2147	3_uc002kwt.2_5'	NM_001944	NP_001935	P32926	DSG3_HUMAN	lasmic (Potential).	9	TGCAGGAAATC	0.353	
+	3	1195	_p.S68F|ZNF271_	NR_024565					0	CTCAGTCCTTAT	0.383	
+	23	2522	D4L_uc002lhb.2_	NM_001144967	NP_001138439	Q96PU5	NED4L_HUMAN	HECT.	4	ACATGGAATCT	0.428	
+	11	1972	if.2_Missense_Mu	NM_031891	NP_114097	Q9HBT6	CAD20_HUMAN	lasmic (Potential).	5	TCGACGACGAG	0.577	
+	13	2068	CHC2_uc002liq.2_	NM_017742	NP_060212	Q9C0B9	ZCHC2_HUMAN		2	AGCCACCTGTT	0.403	
+	7	1487	_p.E388K|CDH7_u	NM_033646	NP_387450	Q9ULB5	CADH7_HUMAN	(Potential).|Cadherin 4.	4	TGTCGGAAGCT	0.473	
+	15	2824	236_uc002lmj.2_	NM_007345	NP_031371	Q9UL36	ZN236_HUMAN		4	CCTTCGAACCA	0.473	
+	4	577	P_uc002men.1_5'	NM_006012	NP_006003	Q16740	CLPP_HUMAN		1	AGGCCGCCAGC	0.687	
+	9	1019	.G227D|PNPLA6_	NM_006702	NP_006693	Q8IY17	PLPL6_HUMAN	ytoplasmic (Potential).	3	CCAGGGTCACC	0.687	
-	1	311		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).	57	TGGCTCCTGTC	0.522	
+	9	1005	2_uc010dxk.2_5'	NM_031209	NP_112486	Q9BXR0	TGT_HUMAN		1	CAGCCGCGCCT	0.672	
+	11	1343		NM_023944	NP_076433				7	GGGTCCATCAC	0.552	
+	13	2217	.R689W|MYO9B_	NM_004145	NP_004136	Q13459	MYO9B_HUMAN	osin head-like.	1	TGCTCCGGGCT	0.711	
+	10	1554		NM_000453	NP_000444	Q92911	SC5A5_HUMAN	ical; (Potential).	4	TGGCAGCCCTG	0.542	
+	5	553	hs.2_Missense_	NM_001136203	NP_001129675	Q96CT7	CC124_HUMAN		0	GCATGCGGGCA	0.652	
+	5	1407	_p.M329I|ZNF431_	NM_133473	NP_597730	Q8TF32	ZN431_HUMAN	2H2-type 9.	2	TAAGATGATTCAT	0.378	
-	6	3079	208_uc002nqo.1_	NM_007153	NP_009084				7	TGAATTCTCTTAT	0.393	
-	5	2181	hb.1_Missense_M	NM_032689	NP_116078	Q96SK3	ZN607_HUMAN		0	TCTTACCACTGT	0.413	
+	89	12368	_p.V4075I|RYR1_	NM_000540	NP_000531	P21817	RYR1_HUMAN		12	ACTACGTAACG	0.493	
-	5	546	u.1_Missense_Mu	NM_172139	NP_742151	Q8IZI9	IL28B_HUMAN		0	TGAGGAGGCGG	0.577	

+	8	2009	p.N629D|CEACAN	NM_004363	NP_004354	P06731	CEAM5_HUMAN	Ig-like 7.	2	CGTATCAATGGG	0.507	
-	4	1311	.3_Missense_Mut	NM_006494	NP_006485	P50548	ERF_HUMAN		4	GCGTCCGAGTG	0.692	
+	5	805		NM_015125	NP_055940	Q96RK0	CIC_HUMAN		11	TTCCAGGTAACG	0.617	
-	5	1938	uc010eif.1_Intron	NM_005357	NP_005348	Q05469	LIPS_HUMAN		2	TGGCCAGAGAC	0.642	
-	4	992	ense_Mutation_p.F	NM_002782	NP_002773	Q00889	PSG6_HUMAN	like C2-type 2.	2	CATATCGGTCCC	0.502	
-	2	479	vf.3_Missense_Mu	NM_002784	NP_002775	Q00887	PSG9_HUMAN	site (Potential).|Ig-like V-typ	2	TCACCTCGCTTT	0.468	
+	12	1637	S1_uc002pfy.2_M	NM_002517	NP_002508	Q99742	NPAS1_HUMAN		0	GCGACGAGGAT	0.692	
+	5	734		NM_014475	NP_055290	Q9UQ10	DHDH_HUMAN		0	TCACCGTGCAG	0.592	
+	3	411		NM_014419	NP_055234	Q9UK85	DKKL1_HUMAN		0	GCTTCGGGGCA	0.612	
-	3	426	se_Mutation_p.P13	NM_017509	NP_059979	Q9H2R5	KLK15_HUMAN	eptidase S1.	2	GGTGGGGGCAA	0.697	
+	4	672	5'Flank|TSEN34_u	NM_024075	NP_076980	Q9BSV6	SEN34_HUMAN		0	GCTGGCCACTG	0.657	
+	1	52	b.1_RNA|KIR3DX1_uc010yfc.1_RNA|KIR3DX1_uc010yfd.1_RNA						1	AGCTCTGAAATC	0.517	
-	3	123	rf51_uc002qjk.1_5'UTR|C19orf51_uc002qjl.1_Missense			Q8N9W5	CS051_HUMAN		0	CAGGAGGACCT	0.592	
-	7	5032	3_uc002qnv.2_Mis	NM_001146186	NP_001139658	Q9GZU2	PEG3_HUMAN		12	ACTTCTCATCAG	0.537	
-	3	961	N3_uc010exu.1_I	NM_002381	NP_002372	O15232	MATN3_HUMAN	EGF-like 1.	0	CTTGTCGGCAT	0.532	
-	6	1280	TF3C2_uc002rjw.	NM_001521	NP_001512	Q8WUA4	TF3C2_HUMAN		2	AAACAGGAGCC	0.483	
-	2	1386	sm.2_Missense_M	NM_133329	NP_579875	Q8TAE7	KCNG3_HUMAN	=Segment S3; (Potential).	1	ATACGGCGTGA	0.453	
-	8	1239		NM_018079	NP_060549	Q8N5C6	SRBD1_HUMAN		1	AGTTCCGAATG	0.378	
+	2	2135	z.1_Missense_Mut	NM_144993	NP_659430	O43151	TET3_HUMAN		0	CTTGGGATCTG	0.423	
+	2	243	sq.1_Missense_M	NM_198274	NP_938015	Q8NB12	SMYD1_HUMAN	MYND-type.	4	AGAAGGATGCT	0.532	
+	23	5204	ense_Mutation_p.F	NM_181453	NP_852118	Q8IWJ2	GCC2_HUMAN	teraction with RAB9A.	1	GACTTCGATAG	0.308	
-	5	632	_Mutation_p.G15	NM_003466	NP_003457	Q06710	PAX8_HUMAN		2	GTGTCCGGGAC	0.458	
+	18	3287	flu.2_Missense_M	NM_130773	NP_570129	Q8WYK1	CNTP5_HUMAN	Extracellular (Potential).	10	GTGTGGAGAAG	0.562	
+	2	334	_p.R15H|SCN2A_	NM_001040142	NP_001035232	Q99250	SCN2A_HUMAN		8	CTTCCGCTTCT	0.468	
-	119	28287	_uc002umz.1_Mis	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	TCTTTTCTTCAG	0.393	
-	46	16178	N_uc010zfi.1_Intr	NM_133379	NP_596870	Q8WZ42	TITIN_HUMAN		153	GTCTTTTTCACT	0.378	
-	46	16176	N_uc010zfi.1_Intr	NM_133379	NP_596870	Q8WZ42	TITIN_HUMAN		153	CTTTTTCACTTA	0.383	
-	46	10722	N_uc010zfi.1_Intr	NM_133379	NP_596870	Q8WZ42	TITIN_HUMAN		153	ATATTCAGGCCA	0.383	
-	3	211	zfq.1_Missense_M	NM_001003683	NP_001003683	P54750	PDE1A_HUMAN	-binding (By similarity).	3	TCTTTCCAGCT	0.353	
+	3	431	usr.2_Missense_M	NM_001130158	NP_001123630	O43795	MYO1B_HUMAN	osin head-like.	8	ATACCGGTCTT	0.353	rs146816421
+	12	2712	p.P641S|NRP2_u	NM_201266	NP_957718	O60462	NRP2_HUMAN	ellular (Potential).	4	AGCTCCCTTCG	0.493	
-	2	201	A4_uc010zlm.1_I	NM_004438	NP_004429	P54764	EPHA4_HUMAN		12	ACTTACCCCTC	0.423	rs67977689
-	6	1388	.R395W|ECEL1_	NM_004826	NP_004817	O95672	ECEL1_HUMAN	enal (Potential).	2	ATACCGGTGGG	0.587	
-	1	468	T1A6_uc002vuu.2_	NM_001001394	NP_001001394	Q8WWF6	DNJB3_HUMAN		0	CCCCCCCAAAAT	0.547	rs61744897
-	2	246	A1_uc002vwa.1_	NM_024726	NP_079002	Q86XH1	IQCA1_HUMAN		1	CTTTATCGAGTA	0.373	
+	4	477	_p.A52T|XRN2_u	NM_012255	NP_036387	Q9H0D6	XRN2_HUMAN		1	TGGAAGCAGCA	0.408	
+	5	628	_p.W114*|MYBL2_	NM_002466	NP_002457	P10244	MYBB_HUMAN	H myb-type 3.	5	TTGCTGGACCG	0.612	
+	13	1181	244K|ARFGAP1_	NM_018209	NP_060679	Q8N6T3	ARFG1_HUMAN		1	CCACCGAGAGG	0.662	
+	13	1881	_p.R316*|MX2_uc	NM_002463	NP_002454	P20592	MX2_HUMAN		2	AAGTCCGAGAA	0.403	
-	1	75		NM_020639	NP_065690	P57078	RIPK4_HUMAN		7	AGGGCCCATGG	0.726	
+	19	3814	j.2_Missense_Mut	NM_006031	NP_006022	O95613	PCNT_HUMAN		8	TAGCAGCCACAT	0.587	
-	22	2693		NM_058004	NP_477352	P42356	PI4KA_HUMAN		4	GTGCGGACACC	0.587	
+	9	1115	_p.R264C|UPB1_	NM_016327	NP_057411	Q9UBR1	BUP1_HUMAN	N hydrolase.	2	TGTCCCGTAGC	0.542	
-	15	2582	wp.2_Missense_M	NM_004737	NP_004728	O95461	LARGE_HUMAN	enal (Potential).	3	ACTCCGGGCAG	0.567	
+	5	885		NM_002133	NP_002124	P09601	HMOX1_HUMAN		1	TTCTCCGATGG	0.562	
-	3	283	qa.1_5'UTR|EFC	NM_022785	NP_073622	Q5THR3	EFCB6_HUMAN		7	GGTCTTGAATGT	0.373	
-	14	1763	1axu.1_Missense_	NM_015097	NP_055912	B2RTR1	B2RTR1_HUMAN		4	AATAAATCTAAA	0.323	

+	6	820	KOG_uc010hhe.2_	NM_005107	NP_005098	Q9Y2C4	EXOG_HUMAN			0	CTACCGAACCAC	0.517	
+	3	281	se_Mutation_p.D8	NM_015004	NP_055819	Q15024	EXOS7_HUMAN			0	GTTGACTGGTCA	0.413	
-	3	1900	qv.2_Missense_Mu	NM_014159	NP_054878	Q9BYW2	SETD2_HUMAN			32	ATGGAGCTGGAC	0.318	
-	11	1496		NM_000094	NP_000085	Q02388	CO7A1_HUMAN	(NC1).|Fibronectin type-III		11	AACCACGGTTG	0.652	
+	4	2380	se_Mutation_p.R9	NM_000839	NP_000830	Q14416	GRM2_HUMAN	cellular (Potential).		1	ACGGCGGGAGG	0.637	
-	3	1112		NM_015576	NP_056391	O15083	ERC2_HUMAN	Potential.		2	CCATTTCCTCTA	0.473	
-	15	2845	_p.V582M|ADCY5_	NM_183357	NP_899200	O95622	ADCY5_HUMAN	ical; (Potential).		4	TGGCACCTCCA	0.622	rs151227955
+	20	3500	.R1125W|KALRN_	NM_001024660	NP_001019831	O60229	KALRN_HUMAN			6	AGCGGCGGTTA	0.547	
+	3	962		NM_007117	NP_009048	P20396	TRH_HUMAN			1	CAAGCGGCAGC	0.567	
+	3	799	11L_uc003fdt.2_Mi	NM_139245	NP_640338	Q5SGD2	PPM1L_HUMAN	c (Potential).|PP2C-like.		1	CAAGCCTTACCA	0.498	
-	5	566	_p.W49*|B3GALN	NM_033169	NP_149359	O75752	B3GL1_HUMAN	nenal (Potential).		1	GTACATCCAGTTC	0.453	
-	3	8618	C4_uc003fvp.2_Int	NM_018406	NP_060876	Q99102	MUC4_HUMAN			0	AAGAGGGGTGG	0.587	
-	3	390	iad.1_Missense_M	NM_138461	NP_612470	Q96DZ7	T4S19_HUMAN	lasmic (Potential).		0	AGAGCCCACTCT	0.423	
-	3	2904	tron|ABCA11P_uc	NM_133474	NP_597731	D9N162	D9N162_HUMAN			1	AGGTTTGTGGAC	0.393	
-	12	2134		NM_012318	NP_036450	O95202	LETM1_HUMAN	natrix (Potential).|Potential.		1	TTTGCTGCACCC	0.517	
+	51	7061		NM_002111	NP_002102	P42858	HD_HUMAN			4	CCCACGCCTGC	0.587	
+	3	1368	PZ_uc003gll.2_Intr	NM_080819	NP_543009	Q96P69	GPR78_HUMAN	lasmic (Potential).		6	GAACCCCGCGC	0.672	
+	2	455	xs.1_Missense_M	NM_018323	NP_060793	Q8TCG2	P4K2B_HUMAN			4	TTTGCCGATATTA	0.388	
+	11	1635	zl.1_Missense_Mu	NM_025087	NP_079363	Q9H720	PG2IP_HUMAN			3	CTAGGGGAAAAG	0.418	
-	1	16		NM_006168	NP_006159	P78426	NKX61_HUMAN			0	CCCCCACCGCTA	0.721	
+	24	3935	F_uc011cfv.1_Mis	NM_001963	NP_001954	P01133	EGF_HUMAN	lasmic (Potential).		4	GGTAATGGAGCG	0.527	
-	13	1495	e.1_Missense_Mu	NM_176824	NP_789794	Q8IWZ6	BBS7_HUMAN			1	CAAGAAGGAAGT	0.323	
-	7	1202		NM_030648	NP_085151	Q8WTS6	SETD7_HUMAN	SET.	p.D306N(1)	2	ACATATCGTAGAT	0.502	
+	10	1623		NM_018241	NP_060711	Q9NVA4	T184C_HUMAN			0	AAGGACGGACAC	0.368	
-	8	1379	AP9_uc010iqa.1_R	NM_001039580	NP_001034669	Q49MG5	MAP9_HUMAN			2	TGGCAGATGCAC	0.274	
-	11	1157	_p.P336L|SPOCK3	NM_016950	NP_058646	Q9BQ16	TICN3_HUMAN	oglobulin type-1.		3	CACAGGGGGATA	0.433	
+	11	2037		NM_020227	NP_064612	Q9NQV7	PRDM9_HUMAN	C2H2-type 5.		6	TTTAGCCGGCAG	0.622	rs111393391
+	7	903	jc.1_Missense_Mu	NM_002203	NP_002194	P17301	ITA2_HUMAN	lar (Potential).|VWFA.		1	ACATTCGGAGCA	0.323	
-	7	1132	GDH_uc011ctf.1_M	NM_013391	NP_037523	Q9UI17	M2GD_HUMAN			4	TGTCAGGAGAATA	0.438	
+	5	2126	v.1_Nonsense_Mu	NM_152405	NP_689618	Q8N9B5	JMY_HUMAN	/EP300 (By similarity).|Pot		0	CAACTTCAGTTGT	0.383	
+	8	1761	11cwm.1_Missens	NM_005460	NP_005451	Q9Y6H5	SNCAP_HUMAN	Potential.		2	TCGCTGGCCTCTC	0.552	
+	1	922	HA6_uc003lhn.2_I	NM_018902	NP_061725	Q9Y5I1	PCDAB_HUMAN			1	CTCCTCGAATTCT	0.577	
+	1	2267		NM_018938	NP_061761	Q9Y5E5	PCDB4_HUMAN	lasmic (Potential).		3	GACAGGAGACTC	0.567	
+	1	974		NM_015669	NP_056484	Q9Y5E4	PCDB5_HUMAN	|Extracellular (Potential).		5	TGCCCGAGAAC	0.498	
+	1	1940		NM_015669	NP_056484	Q9Y5E4	PCDB5_HUMAN	|Extracellular (Potential).		5	AGCTGGTGCCC	0.701	
+	1	410		NM_018940	NP_061763	Q9Y5E2	PCDB7_HUMAN	r (Potential).|Cadherin 1.		6	TCAGTTCGCTTAC	0.473	
-	6	580	K2A_uc010jhe.2_M	NM_171825	NP_741960	Q9UQM7	KCC2A_HUMAN	rotein kinase.		1	GCACAGCCTCC	0.632	
-	24	3517_3518	dk.1_Missense_M	NM_015465	NP_056280	Q8TEQ6	GEMI5_HUMAN			3	GTGTGGTAAGAG	0.545	
+	1	1595		NM_001099293	NP_001092763	Q2VIQ3	KIF4B_HUMAN	Potential.		1	CAGATGAAACTG	0.438	
-	2	615	FIP2_uc003lwr.2_I	NM_001001343	NP_001001343	Q8TBE3	FNDC9_HUMAN			0	ATCGCGGCTCATC	0.602	
+	4	799	_p.A146T|ODZ2_u	NM_001122679	NP_001116151					10	TCGTCCGCCAAC	0.622	
-	1	578		NM_001001657	NP_001001657	Q8NGV0	OR2Y1_HUMAN	cellular (Potential).		1	TCTGTTCCTTCTC	0.517	
+	21	2038	ow.2_Missense_M	NM_001040274	NP_001035364	Q5T4T6	SYC2L_HUMAN			2	CATCTCCAAAGA	0.333	
-	5	1101	no.1_Missense_M	NM_003587	NP_003578	O60231	DHX16_HUMAN			4	GTAGCGATTGGT	0.627	
+	2	1246	C21_uc003nsi.1_F	NM_001010909	NP_001010909	Q5SSG8	MUC21_HUMAN	tandem repeats.|21.|Extra		2	CCACCAACTCTGA	0.622	rs144550410
+	2	229	CA_uc003rxz.1_5'UTR							0	CAGAAATGCAGG	0.552	rs17200172
-	22	7907_7908		NM_019105	NP_061978	P22105	TENX_HUMAN	nectin type-III 18.		0	GGCCCCCAACAC	0.683	

+	49	7225		NM_001371	NP_001362					21	TGGATGCCATC	0.353	
+	13	1807	vg.1_Missense_M	NM_032538	NP_115927	Q5TCY1	TTBK1_HUMAN		p.G510G(2)	9	CCAGTGGCCGC	0.657	
+	1	1572	ze.2_Nonsense_M	NM_001010870	NP_001010870	O60522	TDRD6_HUMAN			6	TTTCTATTCCTCT	0.413	
+	8	920	pje.2_Nonsense_	NM_000056	NP_000047	P21953	ODBB_HUMAN			0	TGATCCGAGAG	0.388	
+	2	306	pll.1_Nonsense_	NM_015021	NP_055836	O60281	ZN292_HUMAN			4	AAGCCCGACCT	0.378	
+	8	3600		NM_015021	NP_055836	O60281	ZN292_HUMAN			4	AGCATGTCTCG	0.418	
+	4	799	o.3_Missense_M	NM_021956	NP_068775	Q13002	GRIK2_HUMAN	ellular (Potential).		5	CTCATTCGTTTG	0.313	
+	8	1003	r.1_Missense_Mu	NM_173674	NP_775945	Q8N8Z6	DCBD1_HUMAN	|Extracellular (Potential).		1	ACTTCAGGACC	0.522	
+	2	379	CT1_uc003qpc.3_	NM_025107	NP_079383	Q8N699	MYCT1_HUMAN			1	GAACTGGATTTT	0.517	
-	13	1573	sh.1_Missense_M	NM_001013836	NP_001013858	Q9Y6D9	MD1L1_HUMAN	eraction with NEK2.|Potent		2	CCTCCCGCATG	0.687	rs140460596
+	9	1547	zr.2_Missense_M	NM_182898	NP_878901	Q02930	CREB5_HUMAN	Basic motif.		2	GAACCGGGCAG	0.592	
-	2	1008		NM_022728	NP_073565	Q96NK8	NDF6_HUMAN			2	TGGGGGAGTGG	0.527	
-	14	1893	_p.S535L|PDE1C_	NM_005020	NP_005011	Q14123	PDE1C_HUMAN	tic (By similarity).		4	CTGACGAGCTG	0.443	
-	7	668	R2J4_uc003tjc.2_RNA							0	TTACTCGTCAT	0.667	
-	3	302	.R36Q|PHKG1_u	NM_006213	NP_006204	Q16816	PHKG1_HUMAN	rotein kinase.		1	TGCATCGCCTG	0.657	
+	4	1558		NM_001159522	NP_001152994	A8MUV8	ZN727_HUMAN	2H2-type 11.		0	GCAAAACCTTTA	0.428	
+	4	1576		NM_001159522	NP_001152994	A8MUV8	ZN727_HUMAN	2H2-type 11.		0	CCTCAAGCCTTA	0.418	
-	2	602	z.2_Missense_M	NM_001259	NP_001250	Q00534	CDK6_HUMAN	rotein kinase.		2	CAGCACCGCCA	0.711	
+	2	198	X6AS_uc003uol.2_	NM_005222	NP_005213	P56179	DLX6_HUMAN			2	agcaccaccaccacG	0.612	
-	5	1128	.R208W|ASNS_u	NM_133436	NP_597680	P08243	ASNS_HUMAN			1	ATCCCGACAGT	0.448	
+	11	1686		NM_014916	NP_055731	Q8IWU2	LMTK2_HUMAN			16	TCACCGTGACC	0.587	
+	5	564	is.1_Missense_M	NM_003496	NP_003487	Q9Y4A5	TRRAP_HUMAN		p.R119C(1)	37	ATGTTTCGCTTT	0.348	
-	2	482		NM_001004323	NP_001004323	Q8IZ16	CG061_HUMAN			0	CGCAGGGATCT	0.592	
+	3	9003	C17_uc010lho.1_	NM_001040105	NP_001035194	Q685J3	MUC17_HUMAN	ch.|48.|59 X approximate t		27	CTGGCGAAAGA	0.512	
+	7	1058		NM_014390	NP_055205	Q7KZF4	SND1_HUMAN	Nase-like 2.		3	ACCATCCTTCAT	0.473	
-	4	1455	C3HAV1_uc003vu	NM_020119	NP_064504	Q7Z2W4	ZCCHV_HUMAN			1	TGGGGGCTGAT	0.552	
-	15	1860		NM_004333	NP_004324	P15056	BRAF_HUMAN	rotein kinas	R603>I(2)|p.T	18290	GATTTCACTGTA	0.368	
-	1	293		NM_001001658	NP_001001658	Q8NGT5	OR9A2_HUMAN	ellular (Potential).		1	TTGAGCGATACA	0.473	
+	103	14390	.2_Intron|SSPO_	NM_198455	NP_940857	A2VEC9	SSPO_HUMAN	SP type-1 24.		0	GGTGGCACCAT	0.657	
+	6	1787	pm.2_Missense_	NM_004745	NP_004736	Q9P1A6	DLGP2_HUMAN			0	ACCAGGACAGC	0.662	
+	2	795		NM_000015	NP_000006	P11245	ARY2_HUMAN			2	CAGAAGGGGTT	0.388	
+	16	2381	bf.2_3'UTR|BMP1_	NM_006129	NP_006120	P13497	BMP1_HUMAN	lcium-binding (Potential).		3	ACGGCGGCTGC	0.587	rs148687489
+	3	1153		NM_001440	NP_001431	O43909	EXTL3_HUMAN	enal (Potential).		2	TTCTCGTTGCC	0.592	
+	14	1032	_p.A278T|POLB_	NM_002690	NP_002681	P06746	DPOLB_HUMAN			2	GAGTTGCAGGA	0.438	
+	10	1760	lissense_Mutation_	NM_184085	NP_908973	Q9BYV6	TRI55_HUMAN			5	GATTTGAGGCT	0.468	
-	3	219	ense_Mutation_p.	NM_001738	NP_001729	P00915	CAH1_HUMAN			2	ATATCCCCAGT	0.328	
-	8	2186	p.D729N|FBXO10	NM_012166	NP_036298	Q9UK96	FBX10_HUMAN			5	TGGGTCGTCCT	0.567	
-	5	701	a.1_Missense_Mu	NM_005077	NP_005068	Q04724	TLE1_HUMAN	Gln-rich.		2	CAAATCGTATTC	0.353	rs149694150
+	3	489	e_Mutation_p.Q13	NM_024077	NP_076982	Q96T21	SEBP2_HUMAN			3	TCCCACAAGAA	0.383	
-	11	1447	ask.1_Splice_Site_	NM_022755	NP_073592	Q9H8X2	IPPK_HUMAN			2	TGCCCACCTTCG	0.428	
-	22	2523		NM_019114	NP_061987	Q9H329	E41LB_HUMAN			3	CAGAGGGGCTC	0.512	
-	11	1585	e_Mutation_p.D44	NM_173521	NP_775792	Q5VXU9	CI084_HUMAN			2	AGTGATCGTTAT	0.328	rs41316510
+	7	2985	e_Mutation_p.M56	NM_002581	NP_002572	Q13219	PAPP1_HUMAN			9	GCCATGTTGAC	0.567	
-	11	1700	_Mutation_p.T264	NM_001006617	NP_001006618	Q9BPZ7	SIN1_HUMAN			4	AGATACGTGAGT	0.448	
+	11	1803	f.1_Missense_Mut	NM_004042	NP_004033	P54793	ARSF_HUMAN			2	CTCCATGATTTT	0.557	
-	4	636		NM_015419	NP_056234	Q9NR99	MXRA5_HUMAN	LRR 5.		8	AGATTTCCTTCC	0.468	
-	1	290		NM_203408	NP_981953	Q5JRC9	FA47A_HUMAN			5	CTTGGGGACCT	0.552	

+	5	1028	e_Mutation_p.P33	NM_003173	NP_003164	O43463	SUV91_HUMAN	with MECOM (By similarity	0	TGACCCCAACC	0.627	
-	20	2517	nip.2_Missense_	NM_005183	NP_005174	O60840	CAC1F_HUMAN	ytoplasmic (Potential).	6	tcttcctcttcttcctcttct	0.289	
-	4	538	E3_uc011mon.1_	NM_001017931	NP_001017931				0	TGACCGAGTCA	0.373	
+	15	2082	OGT_uc004eac.2_	NM_181672	NP_858058	O15294	OGT1_HUMAN		5	CAATGGAAAAG	0.348	
-	3	3678		NM_001008537	NP_001008537	Q5QGS0	K2022_HUMAN		15	TGATATCATCATC	0.478	
+	2	790		NM_005296	NP_005287	Q99677	LPAR4_HUMAN	Name=3; (Potential).	3	CTCTTTCTCACC	0.453	
+	3	903	efc.3_Missense_M	NM_033048	NP_149037	Q8N123	CPXCR_HUMAN		3	ATCAGGAAAAT	0.413	
+	38	4112	qq.2_Missense_M	NM_144658	NP_653259	Q5JSL3	DOC11_HUMAN		3	AAAATCGCAAA	0.413	
-	2	527	uc004esi.1_Intron	NM_032498	NP_115887	P0C7M4	RHF2B_HUMAN		0	AGGTTCCTTCT	0.677	
+	2	1196	qm.1_Missense_	NM_006777	NP_006768	Q86T24	KAISO_HUMAN		3	AACAGGAAACA	0.418	
-	29	7047	.S2334N|ODZ1_u	NM_014253	NP_055068	Q9UKZ4	TEN1_HUMAN	lar (Potential).|YD 23.	23	GGCTGCTGAAC	0.418	
-	9	1261	RE_uc011myd.1_	NM_004961	NP_004952	P78334	GBRE_HUMAN	lasmic (Probable).	2	AGCTTCCTGAT	0.587	
-	3	396				Q8N1B3	FA58A_HUMAN		0	GCCAGCTGTGG	0.647	
-	8	697	jn.1_Missense_Mu	NM_003491	NP_003482	P41227	NAA10_HUMAN		1	CTCCTCGCGAC	0.602	
-	7	804	q.1_Missense_Mu	NM_002436	NP_002427	Q00013	EM55_HUMAN		3	CCATACTTGCC	0.552	
+	6	625	n.2_Missense_Mu	NM_001215	NP_001206	P23280	CAH6_HUMAN		2	TTGACGTTCAG	0.582	rs140314132
+	24	4029	1_RNA|UBE4B_u	NM_001105562	NP_001099032	O95155	UBE4B_HUMAN		4	TCCAGAAGCCC	0.537	
-	1	780	0obf.1_Missense_	NM_001146181	NP_001139653	B7ZW38	B7ZW38_HUMAN		0	CTTCATGGAGC	0.458	
-	6	853	F1_uc010oce.1_I	NM_017940	NP_060410	Q3BBV0	NBPF1_HUMAN		0	ACTTACTGTTGT	0.418	
-	8	949	1_Intron|MST1P9_	NR_002729					0	GTTCCAGCAGA	0.662	rs1806514
+	15	2179	_p.A467T|CROC	NM_014675	NP_055490	Q5TZA2	CROCC_HUMAN	Potential.	5	AGAAGGCCGAG	0.657	rs2781608
+	4	328	hm.2_Missense_	NM_000975	NP_000966	P62913	RL11_HUMAN		1	TACTGGAAACT	0.428	
-	4	461	.1_Missense_Muta	NM_001127621	NP_001121093	Q14376	GALE_HUMAN		0	TGACCGCCATA	0.557	
-	6	692	H2_uc010olg.1_I	NM_003738	NP_003729	Q9Y6C5	PTC2_HUMAN	ellular (Potential).	18	CAAAGGGACCC	0.642	
+	5	589	ym.2_Missense_	NM_000779	NP_000770	P13584	CP4B1_HUMAN		2	AGTGGGAAGAG	0.567	
-	2	96		NM_005621	NP_005612	P80511	S10AC_HUMAN		0	AATTCCCTCCA	0.473	
+	4	675	FDPS_uc001fke.2	NM_002004	NP_001995	P14324	FPPS_HUMAN		0	GCCTGGACTGT	0.582	
-	4	760	_5'Flank|C1orf204	NM_001013661	NP_001013683	Q5VU13	VSIG8_HUMAN	Potential).|Ig-like V-type 2.	1	GACTCCTGGTA	0.582	
+	5	1565		NM_001080426	NP_001073895	Q5VZP5	DUS27_HUMAN		3	GGACAGCGTGG	0.562	
-	1	443	_p.P121L|TNR_uc	NM_003285	NP_003276	Q92752	TENR_HUMAN		11	TTTTTGGGGAAG	0.592	
+	2	1333	se_Mutation_p.R5	NM_020318	NP_064714	Q9BXP8	PAPP2_HUMAN		16	AGGTTCGAAGA	0.567	
-	13	2350	d.1_Missense_Mu	NM_004319	NP_004310	O14525	ASTN1_HUMAN		15	TTTCCCCACAG	0.542	
+	28	6121	p.E1912V|CEP35	NM_014810	NP_055625	Q5VT06	CE350_HUMAN		4	GAAAGAACTGG	0.353	
-	3	381	bz.2_Missense_M	NM_002644	NP_002635	P01833	PIGR_HUMAN	1.|Extracellular (Potential).	3	TGAGGGTTATG	0.577	
-	1	52		NM_003493	NP_003484	Q16695	H31T_HUMAN		0	CTTGCGCGGCG	0.687	
+	6	1832	hvs.1_Missense_	NM_032435	NP_115811	Q5TCX8	M3KL4_HUMAN		8	GATAACCGTGC	0.502	
+	3	530	_Mutation_p.R114	NM_020975	NP_066124	P07949	RET_HUMAN	ellular (Potential).	451	CAGACCGCGGC	0.627	
-	6	741		NM_002778	NP_002769	P07602	SAP_HUMAN	posin B-type 2.	1	GGTCCGTACAG	0.537	rs150521779
+	6	1414		NM_000314	NP_000305	P60484	PTEN_HUMAN	hatase tensi.Y27_N212>Y	2334	TGGAAAGGGAC	0.413	
+	2	1004	nx.1_Missense_M	NM_016341	NP_057425	Q9P212	PLCE1_HUMAN		3	TTTTATGAAATGT	0.398	
-	9	1175	se_Mutation_p.A3	NM_024928	NP_079204	Q9H668	STN1_HUMAN		1	AGAACGCTGTG	0.567	rs140449924
-	1	776		NM_001005164	NP_001005164	Q8NGJ4	O52E2_HUMAN	Name=6; (Potential).	3	TAAAGGAAAAG	0.473	
+	2	717	uc001mbe.2_Tran	NM_001003819	NP_001003819	B2RNG4	B2RNG4_HUMAN		1	CCACACGTTCC	0.532	
-	1	478		NM_001004052	NP_001004052	Q96RD2	O52B2_HUMAN	Name=4; (Potential).	0	GACTGGGAAGA	0.517	
-	1	710		NM_001004461	NP_001004461	Q8NH74	O10A6_HUMAN	lasmic (Potential).	2	GAAAAGGCCTTT	0.443	
+	1	876		NM_001005274	NP_001005274	Q8NH70	O4A16_HUMAN	lasmic (Potential).	3	GAGATGAAAAA	0.318	
-	1	280		NM_001005282	NP_001005282	Q8NGP6	OR5M8_HUMAN	ellular (Potential).	1	GGCAGGATAGG	0.463	

+	12	1236		NM_002559	NP_002550	P56373	P2RX3_HUMAN	lasmic (Potential).		0	GCAGTCCACCG	0.612	
+	1	340		NM_001005283	NP_001005283	Q8NGE9	OR9Q2_HUMAN	Name=3; (Potential).		4	GCTACCTTCTG	0.592	
+	1	845		NM_001004728	NP_001004728	Q8NGJ0	OR5A1_HUMAN	Name=7; (Potential).		2	CTATTCATTGGT	0.483	
-	4	365		NM_017525	NP_059995	Q6DT37	MRCKG_HUMAN	rotein kinase.		4	CGAGCACATCC	0.602	
+	8	1062	_p.R304H|KAT5_u	NM_006388	NP_006379	Q92993	KAT5_HUMAN	C2HC-type.		0	CGGCCGTAGTC	0.592	
-	3	785	n|CLCF1_uc010r	NM_013246	NP_037378	Q9UBD9	CLCF1_HUMAN			0	CGAGCGCCACA	0.597	rs76654399
+	2	433		NM_153696	NP_710163	Q9HBA9	FOH1B_HUMAN			6	GAATACGCTTAT	0.328	
+	7	923	fz.2_Missense_M	NM_014361	NP_055176	O94779	CNTN5_HUMAN		p.G195E(1)	8	ATCTGGGAAATT	0.423	
+	19	2656_2657	gb.2_Missense_M	NM_014361	NP_055176	O94779	CNTN5_HUMAN	nectin type-III 2.		8	CAGTTCCGAAGA	0.426	
+	7	1168	_uc009yyx.2_Spli	NM_213621	NP_998786	P46098	5HT3A_HUMAN			0	CATTGGTAAGG	0.597	
-	2	1003	_p.E299K|KCNJ1_	NM_000220	NP_000211	P48048	IRK1_HUMAN	smic (By similarity).		4	CACCTCCTCTG	0.493	
+	8	1085		NM_207345	NP_997228	Q6UXN8	CLC9A_HUMAN	(Potential).|C-type lectin.		1	TCATAGGATTTT	0.398	rs148583174
-	3	1038		NM_006248	NP_006239					0	AGGTTTGTTGC	0.612	
+	2	517	CR1_uc009zhu.2	NM_058169	NP_477517	Q969J3	L12R1_HUMAN			1	ACGATCCCGAT	0.473	
+	7	891	.172M|PPFIBP1_u	NM_003622	NP_003613	Q86W92	LIPB1_HUMAN	Potential.		5	TGGATCTGATG	0.358	
+	19	2303	nn.1_Missense_M	NM_001843	NP_001834	Q12860	CNTN1_HUMAN	nectin type-III 2.		9	CCTTTGTCAAG	0.373	
+	11	1023	_p.T150I|NUP107	NM_020401	NP_065134	P57740	NU107_HUMAN			1	TGCATACCTTAA	0.318	
+	2	874	tmt.2_Missense_	NM_014653	NP_055468	Q2TBF2	WSCD2_HUMAN			3	AGCCCGCTGTC	0.612	
-	11	1302		NM_018711	NP_061181	Q8N4V2	SVOP_HUMAN	ical; (Potential).		0	TCCACAGCAAG	0.552	
-	16	1764	se_Mutation_p.I5	NM_024953	NP_079229	Q14CX7	NAA25_HUMAN			3	CTTGAATAATATA	0.383	
-	1	550	81_uc001ucw.1_I	NM_006018	NP_006009	P49019	HCAR3_HUMAN	lasmic (Potential).		2	GGTGGGGATGG	0.562	
-	2	140		NM_006001	NP_005992	Q13748	TBA3C_HUMAN			5	GGGCTGAATTC	0.547	
+	2	1349		NM_153456	NP_703157	Q8IZP7	H6ST3_HUMAN	enal (Potential).		2	GCAGCGAGAGC	0.612	
+	1	327	_p.D26A|ARHGE	NM_001113511	NP_001106983	Q14155	ARHG7_HUMAN	CH.		7	CTCGGACCCGG	0.617	
+	9	1151	n_p.E257*|GMPR	NM_001002001	NP_001002001	Q9P2T1	GMPR2_HUMAN			3	TCATCGAGAGG	0.552	
-	8	1710	mk.2_Missense_M	NM_033141	NP_149132	P80192	M3K9_HUMAN			5	ccaggttttgctgctttca	0.333	
-	15	2626		NM_001080414	NP_001073883	Q9P219	DAPLE_HUMAN	Potential.		3	CAGCCGCTTGG	0.612	
+	3	639	m.1_Missense_M	NM_182923	NP_891553	Q07866	KLC1_HUMAN			0	AGGTTCGTCGT	0.537	
+	1	3007		NM_018958	NP_061831	Q9NZP6	CO002_HUMAN			8	GGAAGGAGGA	0.498	
-	11	1570	zfr.2_Missense_M	NM_130901	NP_570971	Q8TE49	OTU7A_HUMAN			2	cttGCCGTTCTTG	0.507	
-	20	2408		NM_178034	NP_828848	Q86XP0	PA24D_HUMAN	PLA2c.		2	TAGGTCATGTT	0.657	
-	5	475		NM_020764	NP_065815	Q8WXD9	CSKI1_HUMAN	ANK 4.		2	TCTTCCCCGAG	0.632	
+	3	1109	l.3_Missense_Mu	NM_152341	NP_689554	Q8N4S7	PAQR4_HUMAN	ical; (Potential).		0	GCGTCGTGCCC	0.672	
+	4	427	ense_Mutation_p.	NM_001010845	NP_001010845	Q08AH3	ACS2A_HUMAN			3	CAAGCGACTCC	0.522	
-	4	398	_p.R63Q|ACSM2	NM_182617	NP_872423	Q68CK6	ACS2B_HUMAN			5	GGAGTCGCTTG	0.512	
-	32	4567		NM_017539	NP_060009	Q8TD57	DYH3_HUMAN	1 (By similarity).		18	GGTTGGGTTCA	0.517	
-	11	1030	uc002diq.3_Intron	NR_003370						0	CTCTGAGGATAC	0.338	rs141895991
+	11	1473	_uc010byo.1_Miss	NM_001770	NP_001761	P15391	CD19_HUMAN	lasmic (Potential).		3	CCCAGCCGGTC	0.577	
+	4	1324	iu.3_Missense_M	NM_138736	NP_620073	P09471	GNAO_HUMAN			2	TCAACCGGTCC	0.607	
-	2	1122	|KIAA0895L_uc00	NM_001040715	NP_001035805	Q68EN5	K895L_HUMAN			0	AGGCTGCAGGC	0.642	
+	3	1006	_5'Flank|PARD6A_	NM_016948	NP_058644	Q9NPB6	PAR6A_HUMAN			1	TGCTGGGACCT	0.642	
+	13	1868	p.E477K|TSNAXI	NM_018430	NP_060900	Q2TAA8	TXIP1_HUMAN			0	AGAACGAGGGG	0.517	
-	1	76	p.A2V|NIP7_uc00	NM_032382	NP_115758	Q96MW5	COG8_HUMAN			1	CGGTCGCCATC	0.622	rs151318611
+	12	1926	p.G441E|CNTNA	NM_033401	NP_207837	Q9C0A0	CNTP4_HUMAN	otential).|Laminin G-like 2.		2	TCAGGGATGTAT	0.423	
-	29	4778	1L2_uc002fgg.1_	NM_052892	NP_443124	Q7Z442	PK1L2_HUMAN	ellular (Potential).		3	TCACCTCCTGC	0.572	
+	7	1007	voj.1_Missense_	NM_014732	NP_055547	O60268	K0513_HUMAN			1	GGGAAGACGAG	0.582	
-	12	1608	M3_uc010clm.2_	NM_031220	NP_112497	Q9BZ71	PITM3_HUMAN	DDHD.		4	GGAAGAGGGGG	0.662	

-	37	5569	uc002gml.1_Intron	NM_017533	NP_060003	Q9Y623	MYH4_HUMAN	Potential.	13	GGCCTCCAGTT	0.527	
-	26	3396	_Missense_Mutat	NM_001100112	NP_001093582	Q9UKX2	MYH2_HUMAN	Potential.	14	AAACTCTTTCC	0.328	
-	4	821		NM_031898	NP_114104	Q9BXF9	TEKT3_HUMAN		2	ATCGTGAACTA	0.398	
+	4	1327	_p.P175Q|MAPK	NM_139033	NP_620602	Q13164	MK07_HUMAN	zation (By similarity).|Prote	9	GTACCCAGGTG	0.647	
-	14	2195	6A4_uc010csg.2_	NM_001045	NP_001036	P31645	SC6A4_HUMAN	lame=11; (Potential).	4	TGATGAACTAAA	0.368	
-	14	1622	LXDC1_uc002hrh	NM_020405	NP_065138	Q8IUK5	PXDC1_HUMAN	lasmic (Potential).	3	AACTTCATGGC	0.627	
-	1	150		NM_032524	NP_115913	Q9BYR3	KRA44_HUMAN	-C-[GRQVCH]-[SPT]- [VS	0	TGGGGCGGCAG	0.652	
+	3	1747		NM_000346	NP_000337	P48436	SOX9_HUMAN		0	GCCAGGGCACC	0.647	
-	2	88	1_5'UTR|GGA3_u	NM_138619	NP_619525	Q9NZ52	GGA3_HUMAN	o ARF1 (in long isoform).	2	GTATTCCCAGTC	0.512	
+	16	2317	195_uc010wsb.1_	NM_014738	NP_055553	Q12767	K0195_HUMAN		1	GCCTCCCCTCA	0.612	
+	4	293	g.3_Missense_Mu	NM_001258	NP_001249	Q00526	CDK3_HUMAN	rotein kinase.	1	ACAACGAGAGG	0.572	rs140567861
+	5	1033		NM_005189	NP_005180	Q14781	CBX2_HUMAN		0	ACACCCATGGT	0.662	
+	27	4342	.C1293Y|PTPRM_	NM_002845	NP_002836	P28827	PTPRM_HUMAN	hatase 2.|Cytoplasmic (Po	6	TCACTGCACATC	0.458	
-	10	1985	TEC_uc010xaj.1_	NM_001137671	NP_001131143	B2RU33	POTEC_HUMAN	Potential.	3	ATACCTCAGAAT	0.269	
-	4	3359	se_Mutation_p.H1	NM_015461	NP_056276	Q96K83	ZN521_HUMAN	2H2-type 24.	7	TCCCATGGATTT	0.532	
-	9	1251	vi.3_Missense_Mu	NM_001941	NP_001932	Q14574	DSC3_HUMAN	|Extracellular (Potential).	4	CATTTTCCTCTA	0.274	
+	14	2147	3_uc002kwt.2_5'	NM_001944	NP_001935	P32926	DSG3_HUMAN	lasmic (Potential).	9	TTGCAGGAAATC	0.353	
+	3	1195	_p.S68F|ZNF271_	NR_024565					0	CTCAGTCCTTAT	0.383	
+	23	2522	D4L_uc002lhb.2_	NM_001144967	NP_001138439	Q96PU5	NED4L_HUMAN	HECT.	4	ACATGGAATCT	0.428	
+	11	1972	if.2_Missense_Mu	NM_031891	NP_114097	Q9HBT6	CAD20_HUMAN	lasmic (Potential).	5	TCGACGACGAG	0.577	
+	7	1487	p.E388K|CDH7_u	NM_033646	NP_387450	Q9ULB5	CADH7_HUMAN	(Potential).|Cadherin 4.	4	TGTCGGAAGCT	0.473	
+	2	1025	2_Intron|SCAMP4_	NM_138422	NP_612431	Q96EY9	ADAT3_HUMAN		2	CGTGCGTAAAC	0.731	
+	22	2611	c002lvd.1_5'Flan	NM_032482	NP_115871	Q8TEK3	DOT1L_HUMAN		4	GCAGCGGGGAG	0.672	
-	3	12038		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).	57	AAGGGTGAATT	0.488	
-	1	311		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).	57	TGGCTCCTGTC	0.522	
-	1	500		NM_001005191	NP_001005191	Q8NG98	OR7D4_HUMAN	ellular (Potential).	4	AGAAGGTCAAC	0.493	
+	11	1343		NM_023944	NP_076433				7	GGGTCCATCAC	0.552	
-	2	645		NM_138454	NP_612463	Q96CM4	NXNL1_HUMAN	Poly-Gly.	0	accccctcccccgggg	0.448	
+	4	1014	.1_Intron|ZNF90_	NM_007138	NP_009069	Q03938	ZNF90_HUMAN	2H2-type 5.	2	TGGCAGAGCAT	0.383	
-	4	1319		NM_001159293	NP_001152765	C9JHM3	C9JHM3_HUMAN		1	AGGACCAGTTG	0.418	
-	6	3079	208_uc002nqo.1_	NM_007153	NP_009084				7	TGAATTCTCTTAT	0.393	
+	8	2009	p.N629D|CEACA	NM_004363	NP_004354	P06731	CEAM5_HUMAN	Ig-like 7.	2	GTATCAATGGG	0.507	
-	2	479	vf.3_Missense_Mu	NM_002784	NP_002775	Q00887	PSG9_HUMAN	site (Potential).|Ig-like V-typ	2	TCACCTCGCTTT	0.468	
+	12	1637	S1_uc002pfy.2_M	NM_002517	NP_002508	Q99742	NPAS1_HUMAN		0	GCGACGAGGAT	0.692	
+	3	331	X_uc010elm.1_R	NM_000554	NP_000545	O43186	CRX_HUMAN	Homeobox.	2	GGGAGCGCACC	0.642	
-	3	426	se_Mutation_p.P13	NM_017509	NP_059979	Q9H2R5	KLK15_HUMAN	eptidase S1.	2	GGTGGGGGCAA	0.697	
-	9	3289	S966R|NLRP12_u	NM_144687	NP_653288	P59046	NAL12_HUMAN		7	GGATGGCTCAG	0.557	
+	4	672	5'Flank|TSEN34_u	NM_024075	NP_076980	Q9BSV6	SEN34_HUMAN		0	GCTGGCCACTG	0.657	
+	1	52	b.1_RNA|KIR3DX1_uc010yfc.1_RNA|KIR3DX1_uc010yfd.1_RNA						1	AGCTCTGAAATC	0.517	
-	7	5032	3_uc002qnv.2_Mis	NM_001146186	NP_001139658	Q9GZU2	PEG3_HUMAN		12	CTTCTCATCAG	0.537	
+	3	1623	47_uc002qpm.3_	NM_001023561	NP_001018855	O43361	ZN749_HUMAN	2H2-type 10.	0	AGCACCAGAAA	0.423	
-	2	521		NM_001037160	NP_001032237	Q717R9	CYS1_HUMAN		0	GTGCTCTGCTC	0.527	
-	1	232		NM_018263	NP_060733	Q76L83	ASXL2_HUMAN		1	GTCCCTTTTCC	0.667	
-	6	1280	TF3C2_uc002rjw.	NM_001521	NP_001512	Q8WUA4	TF3C2_HUMAN		2	AAACAGGAGCC	0.483	
+	1	174	qh.2_Missense_M	NM_012413	NP_036545	Q16769	QPCT_HUMAN		1	TGCTGCTGGTG	0.682	
-	2	1386	sm.2_Missense_M	NM_133329	NP_579875	Q8TAE7	KCNG3_HUMAN	=Segment S3; (Potential).	1	ATACGGCGTGAT	0.453	
+	2	2135	z.1_Missense_Mut	NM_144993	NP_659430	O43151	TET3_HUMAN		0	CTTGGGATCTG	0.423	

-	6	937	se_Mutation_p.A27	NM_138804	NP_620159	Q8TC57	CB065_HUMAN		2	GCCAGCGAGTA	0.483	
+	2	243	sq.1_Missense_M	NM_198274	NP_938015	Q8NB12	SMYD1_HUMAN	MYND-type.	4	AGAAGGATGCT	0.532	
-	41	5887	e_Mutation_p.G54	NM_014014	NP_054733	O75643	U520_HUMAN	SEC63 2.	10	GCCACCCATTG	0.552	
+	23	5204	ense_Mutation_p.	NM_181453	NP_852118	Q8IWJ2	GCC2_HUMAN	nteraction with RAB9A.	1	GACTTCGATAG	0.308	
+	18	3287	flu.2_Missense_	NM_130773	NP_570129	Q8WYK1	CNTP5_HUMAN	Extracellular (Potential).	10	GTGTGGAGAAG	0.562	
-	78	13088		NM_018557	NP_061027	Q9NZR2	LRP1B_HUMAN		50	ACCTACCCTCT	0.368	
-	26	3627	21B_uc002udj.1_	NM_024753	NP_079029	Q7Z4L5	TT21B_HUMAN		5	AAGCCGTTGCC	0.393	
-	16	2884	uc002udp.2_Intron	NM_002977	NP_002968	Q15858	SCN9A_HUMAN	II.	13	TTACCAATGATC	0.408	rs80356474
-	119	28287	_uc002umz.1_Mi	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	TCTTTTCTTCAG	0.393	
-	46	16178	N_uc010zfi.1_Intr	NM_133379	NP_596870	Q8WZ42	TITIN_HUMAN		153	GTCTTTTTCACT	0.378	
-	46	16176	N_uc010zfi.1_Intr	NM_133379	NP_596870	Q8WZ42	TITIN_HUMAN		153	CTTTTTCACTTA	0.383	
-	46	10722	N_uc010zfi.1_Intr	NM_133379	NP_596870	Q8WZ42	TITIN_HUMAN		153	ATATTCAGGCCA	0.383	
-	3	211	zfq.1_Missense_	NM_001003683	NP_001003683	P54750	PDE1A_HUMAN	-binding (By similarity).	3	TCTTTCCAGCT	0.353	
+	3	542	o.2_Missense_M	NM_001136039	NP_001129511	Q9GZT8	NIF3L_HUMAN		1	CCTCCAGGCCC	0.418	
+	12	2712	_p.P641S|NRP2_u	NM_201266	NP_957718	O60462	NRP2_HUMAN	ellular (Potential).	4	AGCTCCCTTCG	0.493	
-	1	468	T1A6_uc002vuu.2_	NM_001001394	NP_001001394	Q8WWF6	DNJB3_HUMAN		0	CCCCCCCAAAT	0.547	rs61744897
-	2	246	A1_uc002vwa.1_	NM_024726	NP_079002	Q86XH1	IQCA1_HUMAN		1	CTTTATCGAGTA	0.373	
-	5	651	fu.2_Nonsense_M	NM_032214	NP_115590	Q9H6Q3	SLAP2_HUMAN	SH2.	0	GCCCTCATACA	0.328	
-	17	2678	d.2_Missense_Mu	NM_032221	NP_115597	Q8TD26	CHD6_HUMAN	case C-terminal.	14	TCCCCGTACTC	0.532	
-	3	248	n_p.S2P|CHD6_u	NM_032221	NP_115597	Q8TD26	CHD6_HUMAN		14	ATCAGACATTG	0.383	
-	1	87	GE_uc002yix.2_R	NM_182482	NP_872288				0	acgagccacggtgtta	0	
-	26	5163	AM_uc002yyr.1_I	NM_001389	NP_001380	O60469	DSCAM_HUMAN		11	AGCTTACTGCC	0.582	
+	13	1881	_p.R316*|MX2_uc	NM_002463	NP_002454	P20592	MX2_HUMAN		2	AAGTCCGAGAA	0.403	
-	1	75		NM_020639	NP_065690	P57078	RIPK4_HUMAN		7	AGGGCCCATGG	0.726	
-	11	1253	se_Mutation_p.V34	NM_003325	NP_003316	P54198	HIRA_HUMAN	WD 7.	1	GCATACCAAGAT	0.587	
-	22	2693		NM_058004	NP_477352	P42356	PI4KA_HUMAN		4	GTGCGGACACC	0.587	
+	23	3423	.R1049Q|CABIN1_	NM_012295	NP_036427	Q9Y6J0	CABIN_HUMAN		5	GGCCCGGGCCA	0.537	
+	5	885		NM_002133	NP_002124	P09601	HMOX1_HUMAN		1	TTCTCCGATGG	0.562	
-	5	604	_p.R202G|APOL2_	NM_030882	NP_112092	Q9BQE5	APOL2_HUMAN		0	CTCCCTTTTCA	0.507	
-	7	1038	e.1_Missense_Mu	NM_020831	NP_065882	Q969V6	MKL1_HUMAN	Gln-rich.	5	TGCTGCTGGTT	0.657	
-	2	410	uk.2_RNA|PRRT3	NM_207351	NP_997234	Q5FWE3	PRRT3_HUMAN	ellular (Potential).	0	GGCTGGGCCAA	0.602	
+	16	1360	e_Mutation_p.V35	NM_001134367	NP_001127839	P31641	SC6A6_HUMAN		1	AAGGGGTGGAC	0.537	
-	9	1055	lx.2_Missense_Mu	NM_020707	NP_065758	Q9HCP6	HHATL_HUMAN	ical; (Potential).	3	CGGCCGCCTTC	0.617	
+	6	780	2_uc003cpu.3_5'	NM_003212	NP_003203	P13385	TDGF1_HUMAN		0	ACTACCACCGT	0.448	
-	3	1112		NM_015576	NP_056391	O15083	ERC2_HUMAN	Potential.	2	CCATTTCCTCTA	0.473	
-	15	2677	_p.S463F|C3orf63_	NM_015224	NP_056039	Q9UK61	CC063_HUMAN		5	TGGTAGAAATA	0.403	
+	3	799	1L_uc003fdt.2_Mi	NM_139245	NP_640338	Q5SGD2	PPM1L_HUMAN	c (Potential).|PP2C-like.	1	CAAGCCTTACC	0.498	
+	12	2344	p.G549D|MAP3K1	NM_004721	NP_004712	O43283	M3K13_HUMAN		3	GCCCGGCTCGA	0.622	
-	3	2904	tron|ABCA11P_uc	NM_133474	NP_597731	D9N162	D9N162_HUMAN		1	GGTTTGTGGAC	0.393	
-	4	832	0_uc003ggb.1_Mi	NM_001120	NP_001111	Q14728	MFS10_HUMAN		0	GACTGCGGGCC	0.632	
+	6	739	p.V235M|MAN2B2	NM_015274	NP_056089	Q9Y2E5	MA2B2_HUMAN		2	ATGGCGTGGCT	0.383	
-	4	540	EL1_uc003gjz.1_3	NM_025196	NP_079472	Q9HAV7	GRPE1_HUMAN		0	GGCTCCGACAG	0.527	
+	3	1368	Z_uc003gll.2_Intr	NM_080819	NP_543009	Q96P69	GPR78_HUMAN	lasmic (Potential).	6	GAACCCCGCGC	0.672	
+	11	1635	zl.1_Missense_M	NM_025087	NP_079363	Q9H720	PG2IP_HUMAN		3	TAGGGGAAAAG	0.418	
+	11	1546	.2_Missense_Mut	NM_198892	NP_942595	Q9NSY1	BMP2K_HUMAN	Gln/His-rich.	1	CTCACcagcagcag	0.254	
-	1	220	_p.M22I|UNC5C_	NM_003728	NP_003719	O95185	UNC5C_HUMAN		4	ACGAGCATTTG	0.652	
+	24	3935	F_uc011cfv.1_Mis	NM_001963	NP_001954	P01133	EGF_HUMAN	lasmic (Potential).	4	GTAATGGAGCG	0.527	

-	13	1495	e.1_Missense_Mu	NM_176824	NP_789794	Q8IWZ6	BBS7_HUMAN		1	CAAGAAGGAAGT	0.323
-	8	1379	AP9_uc010iqa.1_R	NM_001039580	NP_001034669	Q49MG5	MAP9_HUMAN		2	TGGCAGATGCA	0.274
+	12	1995		NM_014247	NP_055062	Q9Y4G8	RPGF2_HUMAN		4	ATGACAGCATAG	0.368
-	11	1157	_p.P336L|SPOCK3	NM_016950	NP_058646	Q9BQ16	TICN3_HUMAN	oglobulin type-1.	3	CACAGGGGGATA	0.433
+	3	561		NM_003248	NP_003239	P35443	TSP4_HUMAN	SP N-terminal.	0	TACTCTTCAACTG	0.393
+	1	922	HA6_uc003lhn.2_	NM_018902	NP_061725	Q9Y5I1	PCDAB_HUMAN		1	CTCCTCGAATTCT	0.577
+	1	2267		NM_018938	NP_061761	Q9Y5E5	PCDB4_HUMAN	lasmic (Potential).	3	GACAGGAGACT	0.567
+	1	410		NM_018940	NP_061763	Q9Y5E2	PCDB7_HUMAN	r (Potential).|Cadherin 1.	6	TCAGTTCGCTTA	0.473
+	3	2013	_p.R303*|SYNPO_	NM_001109974	NP_001103444	Q8N3V7	SYNPO_HUMAN		1	GGCAGCGAAGC	0.652
+	1	1595		NM_001099293	NP_001092763	Q2VIQ3	KIF4B_HUMAN	Potential.	1	TCAGATGAAACTG	0.438
-	2	615	FIP2_uc003lwr.2_	NM_001001343	NP_001001343	Q8TBE3	FNDC9_HUMAN		0	ATCGCGGCTCAT	0.602
-	1	578		NM_001001657	NP_001001657	Q8NGV0	OR2Y1_HUMAN	cellular (Potential).	1	TCTGTTCCTTCT	0.517
+	21	2038	ow.2_Missense_M	NM_001040274	NP_001035364	Q5T4T6	SYC2L_HUMAN		2	CATCTCCAAAGA	0.333
-	5	1101	no.1_Missense_M	NM_003587	NP_003578	O60231	DHX16_HUMAN		4	GTAGCGATTGGT	0.627
+	49	7225		NM_001371	NP_001362				21	GTGGATGCCATC	0.353
+	11	1693	_p.P410L|FOXP4_	NM_001012426	NP_001012426	Q8IVH2	FOXP4_HUMAN		1	CCCCCCGACCT	0.677
+	1	1572	ze.2_Nonsense_M	NM_001010870	NP_001010870	O60522	TDRD6_HUMAN		6	TTTCTATTCCTCT	0.413
+	2	306	pll.1_Nonsense_M	NM_015021	NP_055836	O60281	ZN292_HUMAN		4	AAGCCCGACCT	0.378
+	8	3600		NM_015021	NP_055836	O60281	ZN292_HUMAN		4	CAGCATGTCTCG	0.418
+	8	6765		NM_015021	NP_055836	O60281	ZN292_HUMAN		4	GACCACGGGATT	0.423
+	4	799	qo.3_Missense_Mu	NM_021956	NP_068775	Q13002	GRIK2_HUMAN	cellular (Potential).	5	CTCATTCGTTTG	0.313
-	5	547	D23_uc003qct.1_M	NM_004830	NP_004821	Q9ULK4	MED23_HUMAN		3	CAATTATTTTCCG	0.353
+	2	379	YCT1_uc003qpc.3_	NM_025107	NP_079383	Q8N699	MYCT1_HUMAN		1	GAACTGGATTTTA	0.517
+	18	2598	wc.1_Missense_Mu	NM_001040001	NP_001035090	P55196	AFAD_HUMAN	Dilute.	5	TTATCCGTCAGC	0.547
+	39	5810	p.Q1147K|SDK1_u	NM_152744	NP_689957	Q7Z5N4	SDK1_HUMAN	nectin type-III 12.	6	GAGCTCCAAGC	0.597
-	1	272	ntron|HOXA6_uc0	NM_024014	NP_076919	P31267	HXA6_HUMAN		2	TGCCCGAGGGC	0.622
-	2	1008		NM_022728	NP_073565	Q96NK8	NDF6_HUMAN		2	TGGGGGAGTGG	0.527
-	14	1893	_p.S535L|PDE1C_	NM_005020	NP_005011	Q14123	PDE1C_HUMAN	ytic (By similarity).	4	TCTGACGAGCTG	0.443
+	17	1973		NM_016616	NP_057700	Q8N427	TXND3_HUMAN	NDK 3.	3	GAGACGATTGAT	0.458
-	3	226		NM_032014	NP_114403	Q96EL2	RT24_HUMAN		0	GTGCGGCGCGT	0.587
+	1	1130		NR_003595					0	GGCTGGAAGGG	0.507
-	3	302	p.R36Q|PHKG1_u	NM_006213	NP_006204	Q16816	PHKG1_HUMAN	rotein kinase.	1	ATGCATCGCCTG	0.657
+	4	1558		NM_001159522	NP_001152994	A8MUV8	ZN727_HUMAN	C2H2-type 11.	0	GCAAAACCTTTA	0.428
+	4	1576		NM_001159522	NP_001152994	A8MUV8	ZN727_HUMAN	C2H2-type 11.	0	CCTCAAGCCTTA	0.418
-	13	2690	og.3_RNA|DPY19L	NR_003561					0	ACATGGGAAATA	0.249
+	1	39	03vbm.2_5'UTR|P	NM_004279	NP_004270	O75439	MPPB_HUMAN		4	AATGGCGGCTG	0.652
+	15	2273	n_p.L709*|CDHR3	NM_152750	NP_689963	Q6ZTQ4	CDHR3_HUMAN	ical; (Potential).	1	CCATATTGCTTCT	0.512
-	6	894	lmc.1_Missense_M	NM_032842	NP_116231	Q96SK2	TM209_HUMAN		3	ACCCAGCTTAAC	0.343
+	8	768		NM_001869	NP_001860	P48052	CBPA2_HUMAN		1	GTGTTGGTGTGG	0.547
-	8	2048	yd.3_Missense_Mu	NM_022740	NP_073577	Q9H2X6	HIPK2_HUMAN	with SKI and SMAD1.	7	TGGATGCCGCT	0.572
-	15	1860		NM_004333	NP_004324	P15056	BRAF_HUMAN	rotein kinas_R603>I(2)|p.T	18290	GATTTCACTGTA	0.368
+	6	1787	ypm.2_Missense_M	NM_004745	NP_004736	Q9P1A6	DLGP2_HUMAN		0	ACCAGGACAGC	0.662
+	24	3544	yw.1_Missense_Mu	NM_003747	NP_003738	O95271	TNKS1_HUMAN	ARP catalytic.	7	ATGAGCGCATGT	0.473
+	10	1760	lissense_Mutation_	NM_184085	NP_908973	Q9BYV6	TRI55_HUMAN		5	GATTTGAGGCT	0.468
-	3	219	ense_Mutation_p.	NM_001738	NP_001729	P00915	CAH1_HUMAN		2	CATATCCCCAGTC	0.328
+	3	649		NM_002514	NP_002505	P48745	NOV_HUMAN	VWFC.	5	GCCCCGCTGTC	0.542
+	3	409	w.2_Missense_Mu	NM_004972	NP_004963	O60674	JAK2_HUMAN	growth hormone receptors (	28641	CACCCAACCATG	0.348

-	8	2186	p.D729N|FBXO10	NM_012166	NP_036298	Q9UK96	FBX10_HUMAN		5	3TGGGTCGTCCT	0.567	
+	4	498	se_Mutation_p.P37	NM_001010940	NP_001010940	Q5VTT2	CI135_HUMAN	lasmic (Potential).	1	CATCCACCGGATT	0.413	
-	22	2523		NM_019114	NP_061987	Q9H329	E41LB_HUMAN		3	TCAGAGGGGCTC	0.512	
+	14	2463	ez.1_Missense_Mu	NM_005592	NP_005583	O15146	MUSK_HUMAN	e.|Cytoplasmic (Potential).	6	3CCTATGGCGTG	0.507	
-	11	1585	se_Mutation_p.D44	NM_173521	NP_775792	Q5VXU9	CI084_HUMAN		2	AGTGATCGTTATT	0.328	rs41316510
+	11	3313	v.2_Missense_Mut	NM_005157	NP_005148	P00519	ABL1_HUMAN	-actin-binding.	817	CGACAGCAGGC	0.542	
-	2	218		NM_002003	NP_001994	O00602	FCN1_HUMAN		2	GAGCCCTCCAG	0.642	
-	13	1997	A2_uc004ckm.1_M	NM_001606	NP_001597	Q9BZC7	ABCA2_HUMAN		0	CGGGAGCGAGC	0.453	
+	11	1803	f.1_Missense_Mut	NM_004042	NP_004033	P54793	ARSF_HUMAN		2	CTCCATGATTTT	0.557	
-	4	636		NM_015419	NP_056234	Q9NR99	MXRA5_HUMAN	LRR 5.	8	AGATTTCCTTCC	0.468	
-	11	1730		NM_000216	NP_000207	P23352	KALM_HUMAN		4	TTCCCCTTAAGA	0.502	
+	6	3209	OM2_uc011mic.1_	NM_001649	NP_001640	Q13796	SHRM2_HUMAN		8	3CTCACCCCTGC	0.672	
-	1	290		NM_203408	NP_981953	Q5JRC9	FA47A_HUMAN		5	CTTGGGGACCT	0.552	
+	5	1028	e_Mutation_p.P33	NM_003173	NP_003164	O43463	SUV91_HUMAN	with MECOM (By similarity)	0	3TGACCCCAACC	0.627	
+	7	974	se_Mutation_p.G27	NM_014008	NP_054727	O60826	CCD22_HUMAN		1	ACCTGGGAGAAC	0.647	
+	6	3092	A932T|CCNB3_uc	NM_033031	NP_149020	Q8WWL7	CCNB3_HUMAN		9	ATGATAGCTCTGA	0.463	
+	1	1371	R_uc011mpe.1_RN	NM_000044	NP_000035	P10275	ANDR_HUMAN	|Modulating.|Gln-rich.	8	ccccaggcagcagca	0.289	
+	15	2082	OGT_uc004eac.2_	NM_181672	NP_858058	O15294	OGT1_HUMAN		5	3CAATGGAAAAG	0.348	
-	3	3678		NM_001008537	NP_001008537	Q5QGS0	K2022_HUMAN		15	TGATATCATCATC	0.478	
+	3	903	efc.3_Missense_M	NM_033048	NP_149037	Q8N123	CPXCR_HUMAN		3	CATCAGGAAAATT	0.413	
+	1	303	128_uc004emk.2_	NM_194463	NP_919445	Q8TEB7	RN128_HUMAN		2	3CTTTTCCAGATT	0.721	
+	38	4112	qq.2_Missense_M	NM_144658	NP_653259	Q5JSL3	DOC11_HUMAN		3	3AAAATCGCAAA	0.413	
-	2	527	uc004esi.1_Intron	NM_032498	NP_115887	P0C7M4	RHF2B_HUMAN		0	CAGGTTCCTTCT	0.677	
+	2	1196	qm.1_Missense_M	NM_006777	NP_006768	Q86T24	KAISO_HUMAN		3	AACAGGAAACAA	0.418	
-	9	1261	3RE_uc011myd.1_	NM_004961	NP_004952	P78334	GBRE_HUMAN	lasmic (Probable).	2	AAGCTTCCTGAT	0.587	
-	15	1814	za.1_Missense_Mu	NM_018216	NP_060686	Q9NVE7	PANK4_HUMAN		3	CTGTAGGAATCC	0.617	
-	14	2304	a.1_RNA|CHD5_u	NM_015557	NP_056372	Q8TDI0	CHD5_HUMAN	ase ATP-binding.	12	ACGATGGTCTGC	0.652	
+	2	307	ww.2_Missense_M	NM_032341	NP_115717	Q5TDH0	DDI2_HUMAN	Jbiquitin-like.	0	3GGGACGTTGTG	0.468	
+	11	6232	p.1_Missense_Mut	NM_015001	NP_055816	Q96T58	MINT_HUMAN		15	3CTACACGTCCT	0.582	
-	61	8925	k.1_Missense_Mu	NM_020765	NP_065816	Q5T4S7	UBR4_HUMAN		25	ATTAGACGGACC	0.512	
-	16	3374	OCD1_uc001btu.2	NM_144569	NP_653170	Q6ZMY3	SPOC1_HUMAN		6	3CCCAGGATGCT	0.647	
-	9	1755	1_5'Flank|YARS_u	NM_003680	NP_003671	P54577	SYYC_HUMAN		2	3GATTGGATCCA	0.498	
-	11	1943	631_splice|PHC2_	NM_198040	NP_932157	Q8IXK0	PHC2_HUMAN		1	3GATTCTGAAAA	0.547	
-	24	3762	.R1285W|CSMD2	NM_052896	NP_443128	Q7Z408	CSMD2_HUMAN	xtracellular (Potential).	12	TACCCCGCAGGC	0.602	
-	6	912	km.1_Missense_M	NM_052896	NP_443128	Q7Z408	CSMD2_HUMAN	xtracellular (Potential).	12	3CTGCCGGTGGT	0.607	
+	6	902		NM_004559	NP_004550	P67809	YBOX1_HUMAN		5	ACCACGATTCCG	0.443	rs150137463
+	18	3383	ky.2_Missense_Mu	NM_014652	NP_055467	O94829	IPO13_HUMAN		1	ACGGTCGTATGC	0.612	
+	7	911	AH_uc001cpv.2_In	NM_001441	NP_001432	O00519	FAAH1_HUMAN	smic (By similarity).	2	ACAGTGCGTCTC	0.657	
+	6	794	e_Mutation_p.A24	NM_001010969	NP_001010969	Q5TCH4	CP4AM_HUMAN		4	CTCTGCTGGCC	0.547	
+	1	403		NM_012183	NP_036315	Q9UJU5	FOXD3_HUMAN		0	AGCAAGCCCAAG	0.373	
+	4	477	aq.2_Missense_M	NM_002303	NP_002294	P48357	LEPR_HUMAN	cellular (Potential).	1	3CTTTCGGAGTGA	0.348	
+	1	223		NM_032291	NP_115667	Q9BQI5	SGIP1_HUMAN		3	CATGATGGAAGG	0.488	
+	16	1730	C7_uc009wbg.2_I	NM_020794	NP_065845	Q96NW7	LRRC7_HUMAN		14	TAAAACGATATC	0.323	
-	12	1991	73_uc001dgi.3_Mi	NM_001002912	NP_001002912	Q5RHP9	CA173_HUMAN	Glu-rich.	5	TCACTAGAATAAG	0.423	
-	16	1331	p.A354V|SLC44A	NM_152697	NP_689910	Q8NCS7	CTL5_HUMAN	lasmic (Potential).	4	3ATGTCGCCAAG	0.393	rs148437935
-	46	6421		NM_000350	NP_000341	P78363	ABCA4_HUMAN	porter 2.|Cytoplasmic.	12	TGCGGCGTGCC	0.632	
-	6	774	eal.1_Nonsense_	NM_024901	NP_079177	Q9H6A0	DEN2D_HUMAN	DENN.	1	CTCTCGGAGGC	0.567	

-	12	1938	dm.2_Missense_M	NM_006608	NP_006599	Q9UMS5	PHTF1_HUMAN		1	GAAAAGTCGAT	0.403	
-	20	2460	edt.2_Missense_M	NM_015967	NP_057051	Q9Y2R2	PTN22_HUMAN		4	TTATTTGACTGA	0.318	
-	1	94	VTCN1_uc009whf.	NM_024626	NP_078902	Q7Z7D3	VTCN1_HUMAN		0	GAAGAGGATCT	0.557	
-	3	667	MGCS2_uc001eie.	NM_005518	NP_005509	P54868	HMCS2_HUMAN		2	GGGACGAGCAT	0.512	
-	25	4523		NM_024408	NP_077719	Q04721	NOTC2_HUMAN	ellular (Potential).	27	GGTGGCAGGAG	0.622	
+	19	2193	tion_p.E30G|NBP	NM_001037675	NP_001032764	Q3BBV1	NBPFK_HUMAN	NBPF 5.	0	GAAAGAGCCTG	0.483	
-	11	2037	p.R414*|CELF3_u	NM_007185	NP_009116	Q5SZQ8	CELF3_HUMAN	RRM 3.	2	GGCTCGGTCAA	0.433	
-	2	5696	e.1_Missense_Mu	NM_007113	NP_009044	Q07283	TRHY_HUMAN		5	TCTCCCCGACTT	0.582	
-	3	1749		NM_001122965	NP_001116437	Q6XPR3	RPTN_HUMAN	Gln-rich.	0	GTCTGTCTGAC	0.498	
-	2	196	R2D_uc009wnz.2_	NM_006945	NP_008876	P22532	SPR2D_HUMAN	eats of P-K-C-P-[EQ]- P-C	0	AGGTGGGCAGG	0.602	
-	10	6742	ASH1L_uc001fkt.2	NM_018489	NP_060959	Q9NR48	ASH1L_HUMAN		11	AGAAAGGGGTT	0.413	
-	1	1219		NM_145167	NP_660150	Q9H3S5	PIGM_HUMAN	ical; (Potential).	3	AAATGGACGTA	0.443	
+	2	478		NM_004983	NP_004974	Q92806	IRK9_HUMAN	me=M1; (By similarity).	2	CATCTGGTGGC	0.662	
-	5	620	_p.L187F|ITLN2_u	NM_080878	NP_543154	Q8WWU7	ITLN2_HUMAN	ogen C-terminal.	1	CTGGAGGAAGC	0.572	
-	3	440		NM_182581	NP_872387	Q5T0L3	CA111_HUMAN		1	GTCCCACTTGC	0.567	
+	1	279	_uc001gev.2_Misse	NM_001017977	NP_001017977	Q58WW2	DCAF6_HUMAN		3	TGTGGGACGTG	0.726	
+	1	435	sense_Mutation_p	NM_015935	NP_057019	Q8N6R0	MTL13_HUMAN		1	CTTTCGAGTGG	0.512	
+	20	2460	mp.2_Missense_	NM_144696	NP_653297	Q5T1B0	AXDN1_HUMAN		0	GTAAATCCACTA	0.368	
+	11	1616	e_Mutation_p.P47	NM_004736	NP_004727	Q9UBH6	XPR1_HUMAN	l; (Potential).|EXS.	0	CCTTTCCTCATT	0.458	
-	1	742	pk.2_Missense_M	NM_021133	NP_066956	Q05823	RN5A_HUMAN	ANK 5.	5	CTGCCCCCATC	0.517	
+	1	995		NM_005298	NP_005289	O00155	GPR25_HUMAN	lasmic (Potential).	1	GCGAAGGATCA	0.711	
-	3	275	HI3L1_uc001gzj.2_	NM_001276	NP_001267	P36222	CH3L1_HUMAN		1	CTTCCCGGTAC	0.562	rs146010120
-	57	11618		NM_206933	NP_996816	O75445	USH2A_HUMAN		26	AGTTTACCTGCT	0.371	rs111033382
+	1	1475		NM_152610	NP_689823	Q8N715	CA065_HUMAN	Potential.	2	TCCAGCGGTCC	0.617	
+	4	821	.1_Intron|ZNF678_	NM_178549	NP_848644	F5GXA7	F5GXA7_HUMAN		1	AATGTGGCAAAG	0.333	rs145397350
+	4	938	.1_Intron|ZNF678_	NM_178549	NP_848644	F5GXA7	F5GXA7_HUMAN		1	TAACTAGCCATA	0.363	
-	4	625	tr.2_Missense_Mu	NM_014409	NP_055224	O75529	TAF5L_HUMAN		1	AAGCTTGAAGTT	0.473	
-	17	5555	b.1_RNA|LYST_uc	NM_000081	NP_000072	Q99698	LYST_HUMAN		12	TAGGTTGGAGAT	0.373	
-	2	202	130331_uc010pyc	NM_021186	NP_067009	Q12836	ZP4_HUMAN	ellular (Potential).	3	ATTCTGCAGCT	0.562	
-	8	1228		NM_000143	NP_000134	P07954	FUMH_HUMAN		5	CATTGCTGCCT	0.413	
+	12	3249	p.D555N|KIF26B_	NM_018012	NP_060482	Q2KJY2	KI26B_HUMAN		3	GCATCGACGGC	0.637	
-	3	249	qay.1_Missense_	NM_001029880	NP_001025051	Q5VUG0	SMBT2_HUMAN	MBT 1.	8	CTCCTGTCTCT	0.438	
-	15	1867	iks.1_Missense_M	NM_014688	NP_055503	Q92738	US6NL_HUMAN		0	AACTGCGAGCG	0.592	
+	4	473	ct.1_Missense_Mu	NM_012443	NP_036575	O75602	SPAG6_HUMAN	ARM 2.	1	GCAGTTGGTAA	0.448	
+	11	2688	e_Mutation_p.G5	NM_019590	NP_062536	Q5T5P2	SKT_HUMAN		7	AGTGGGAGAGG	0.517	
-	6	518	_uc001jka.1_Splic	NM_007057	NP_008988	O95229	ZWINT_HUMAN		0	TTCTCCTGCCA	0.537	
+	2	269		NM_003338	NP_003329	P51668	UB2D1_HUMAN		2	AGCGCGATCCA	0.388	
+	4	569	q.1_Missense_Mu	NM_018344	NP_060814	Q9BZD2	S29A3_HUMAN	ical; (Potential).	0	TGTCTGCATGG	0.547	
-	15	2777	LG5_uc009xru.1_	NM_004747	NP_004738	Q8TDM6	DLG5_HUMAN		8	GCCACGGTCCC	0.682	
-	2	758	nc.1_Nonsense_M	NM_001017924	NP_001017924	A6NDA9	LRIT2_HUMAN	LRRCT.	2	CTTCATGCAAGC	0.547	
+	12	1863	P11_uc001kef.2_I	NM_133447	NP_597704	Q8TF27	AGA11_HUMAN	PH.	0	GCTGGGTGACT	0.542	
+	2	703	.3_Intron|LIPA_uc	NM_001010987	NP_001010987	Q5T764	IFT1B_HUMAN	TPR 4.	0	AAAACGAGCTG	0.438	
-	1	641		NR_002319					0	TGTGGGTAATG	0.502	
-	3	145	Intron|SORBS1_u	NM_001034954	NP_001030126	Q9BX66	SRBS1_HUMAN		1	AGAGCGTGCGC	0.478	
-	5	827	f.1_Missense_Mut	NM_012465	NP_036597	Q9Y6L7	TLL2_HUMAN	otease (By similarity).	3	TTTCCTCATCCG	0.483	
+	5	1136	RC1_uc010qqj.1_	NM_015062	NP_055877	Q5VV67	PPRC1_HUMAN		3	GGTGCGACAGG	0.587	
-	1	441	C2_uc009xxx.2_Ir	NR_026715					0	CCAGGTGCCCC	0.537	

+	12	1327		NM_000936	NP_000927	P16233	LIPP_HUMAN	PLAT.	3	AACTTTACCTAGA	0.368	
+	3	182	PRP1_uc001lcn.2_	NM_006229	NP_006220	P54315	LIPR1_HUMAN		2	GCACCCGCTTCCT	0.542	rs115887041
-	13	946	KN4_uc001ldz.2_M	NM_213649	NP_998814	Q6P4A7	SFXN4_HUMAN	ical; (Potential).	1	AAAATGGCACCAT	0.393	
+	15	1927		NM_014937	NP_055752	Q9Y2H2	SAC2_HUMAN		2	AGCTTTGCATAAG	0.393	
-	9	1547	XM2_uc001lhj.2_F	NM_198148	NP_937791	Q8N436	CPXM2_HUMAN		2	GTGGACGATGC	0.652	
+	8	1009	_p.T292M|PHRF1_	NM_020901	NP_065952	Q9P1Y6	PHRF1_HUMAN	Arg-rich.	0	CTCCACGGCCA	0.667	
-	21	2666		NM_005961	NP_005952	Q6W4X9	MUC6_HUMAN	VWFD 3.	1	CCCTCCCCGTAG	0.662	
-	2	790		NM_030774	NP_110401	Q9H255	O51E2_HUMAN	cellular (Potential).	5	CATTACATCCTGG	0.512	rs146553571
+	5	1385	BR_uc001mcr.2_I	NM_176875	NP_795344	P32239	GASR_HUMAN	lasmic (Potential).	8	CGCTTTCGCCAG	0.642	
+	12	3149	p.R843W|NAV2_u	NM_145117	NP_660093	Q8IVL1	NAV2_HUMAN		6	GTGGTACGGGAG	0.567	
-	18	2971	rk.3_Missense_Mu	NM_018490	NP_060960	Q9BXB1	LGR4_HUMAN	lasmic (Potential).	1	CTGATGGAAACT	0.448	
+	14	1701	en.1_Missense_Mu	NM_024662	NP_078938	Q9H0A0	NAT10_HUMAN		2	TGCTGTGCCTGG	0.557	
-	10	1314		NM_002334	NP_002325	O75096	LRP4_HUMAN	GF-like 1; calcium-binding	4	TGTGCCCATCCT	0.552	
-	3	253		NM_006093	NP_006084	Q9Y2Y8	PRG3_HUMAN		0	AAGTCTCTCTCCT	0.547	
+	2	234	_p.S32L|CLP1_uc	NM_006831	NP_006822	Q92989	CLP1_HUMAN		1	CTCAGTCAGTTCA	0.473	
+	8	1284	.2_Missense_Muta	NM_207341	NP_997224	P60852	ZP1_HUMAN	llular (Potential).|ZP.	0	TACTATGGGGAG	0.602	
+	12	2131	M2A_uc001ojy.2_	NM_012308	NP_036440	Q9Y2K7	KDM2A_HUMAN		9	TGGCTGGGGAC	0.527	
-	21	3328	1opz.2_Missense_	NM_012309	NP_036441	Q9UPX8	SHAN2_HUMAN		5	GGCTCCGGCGA	0.701	
+	1	363		NM_001012710	NP_001012728	Q6L8G5	KR510_HUMAN	repeats of C-C-X-P.	1	GGGGGGCTGTG	0.657	
+	15	1751	n_p.R132*|UVRAG	NM_003369	NP_003360	Q9P2Y5	UVRAG_HUMAN		6	GACATCGAAAA	0.532	
+	2	433		NM_153696	NP_710163	Q9HBA9	FOH1B_HUMAN		6	AGAATACGCTTAT	0.328	
+	11	1343	AD2_uc009yvy.2_	NM_005467	NP_005458	Q9Y3Q0	NALD2_HUMAN	(Potential).|NAALADase.	2	GCTGGGATGCA	0.378	
+	9	1350	e.1_RNA|PIWIL4_	NM_152431	NP_689644	Q7Z3Z4	PIWL4_HUMAN	PAZ.	1	AGCTCTGCTTTCT	0.473	
-	15	2165	ofs.2_Missense_M	NM_016156	NP_057240	Q13614	MTMR2_HUMAN		1	GACAGGAGTGA	0.443	
+	31	5075	M_uc001pke.1_M	NM_000051	NP_000042	Q13315	ATM_HUMAN		240	TTAGATCCTTTTC	0.294	
+	7	1201	.2_Missense_Muta	NM_015157	NP_055972	Q86UU1	PHLB1_HUMAN		0	GCCCCCGCTGG	0.627	rs141040260
-	5	1559	0rzi.1_Missense_M	NM_012101	NP_036233	Q14134	TRI29_HUMAN		4	TCTTACCTTTGG	0.572	
+	23	3417		NM_003105	NP_003096	Q92673	SORL_HUMAN		15	ACTGCCGTGAGT	0.532	
-	7	1130	oze.1_Missense_M	NM_003455	NP_003446	O95125	ZN202_HUMAN	KRAB.	1	AGCATACGGCCA	0.458	rs140595866
-	7	1000	SD4_uc009zbz.2_	NM_032795	NP_116184	Q96CM3	RUSD4_HUMAN		1	GTAGCGGGCCT	0.582	
+	11	1637	p.R282W|APLP2_	NM_001642	NP_001633	Q06481	APLP2_HUMAN	cellular (Potential).	3	GCCTTACGGCGT	0.443	
-	1	226		NM_020996	NP_066276	P10767	FGF6_HUMAN		3	CGCGAGACCTG	0.647	
+	15	3043	e.2_Missense_Mu	NM_004426	NP_004417	P78364	PHC1_HUMAN	SAM.	2	GAATTTCGCTCA	0.453	
-	2	372	hl.1_Missense_Mu	NM_002336	NP_002327	O75581	LRP6_HUMAN	tracellular (Potential).|Beta	12	TCTGTTCGTTTAA	0.443	rs74887171
+	1	149	_p.A43P|ETNK1_	NM_018638	NP_061108	Q9HBU6	EKI1_HUMAN		0	CTGCCGCTCGC	0.632	
-	4	788	rjc.1_Missense_M	NM_175861	NP_787057	Q8IUR5	TMTC1_HUMAN	ical; (Potential).	0	CACAGGTCCCC	0.498	
-	25	3240	PO8_uc010sjt.1_M	NM_006390	NP_006381	O15397	IPO8_HUMAN		3	AGAGGACTCCTT	0.403	
-	5	766	qj.3_Missense_Mutation_p.P223L|HDAC7_uc001rqk.3_			Q8WUI4	HDAC7_HUMAN	epression 1 (By similarity).	2	GGCTGGGGGGC	0.647	
-	6	2123	Y6_uc001rsi.3_Mis	NM_015270	NP_056085	O43306	ADCY6_HUMAN	lasmic (Potential).	0	CATTTCCGCAAG	0.637	
-	11	1270	L3_uc001rut.1_5'F	NM_175736	NP_783863	Q8IVF7	FMNL3_HUMAN	GBD/FH3.	4	TAAACTCATACTG	0.542	
+	1	377	smv.1_Nonsense_	NM_014033	NP_054752	Q9H8H3	MET7A_HUMAN		0	GGAGCTGGATAT	0.473	
-	2	622		NM_175053	NP_778223	Q7RTS7	K2C74_HUMAN	Rod.|Linker 1.	2	GCCCTCAAGGAT	0.572	
-	3	660	e.1_Missense_Mut	NM_032345	NP_115721	Q9BRP8	WIBG_HUMAN	ential.|eIF2A-like.	0	GGATCCGCTGCT	0.537	
+	11	2096		NM_002332	NP_002323	Q07954	LRP1_HUMAN	cellular (Potential).	22	GATATGGGGGCC	0.592	
+	2	628		NM_031435	NP_113623	Q9H0W7	THAP2_HUMAN	THAP-type.	1	TTAGGCGCAAAA	0.368	
-	3	479	tdo.3_Missense_M	NM_003297	NP_003288	P13056	NR2C1_HUMAN	ction with KAT2B (By simila	1	CTGCATCTGGAG	0.433	
-	2	388		NM_001031701	NP_001026871	Q86UY8	NT5D3_HUMAN		3	TCAGCGTGTGGA	0.433	

+	4	471_472	0LA>FS|TCP11L2	NM_152772	NP_689985	Q8N4U5	T11L2_HUMAN		3	AGTTTGGCTGGT	0.292	
+	20	2689	se_Mutation_p.E12	NM_130466	NP_569733	Q7Z3V4	UBE3B_HUMAN		4	GGCTACGAGCAG	0.562	rs145812083
+	24	2151	af.1_Missense_Mu	NM_014708	NP_055523	P50748	KNTC1_HUMAN		10	AGTTGGGATTGG	0.368	
+	19	2871	p.E491G|DNAH10	NM_207437	NP_997320	Q8IVF4	DYH10_HUMAN	similarity).|Poly-Glu.	6	GGGGGAGGAAG	0.388	
+	2	294	AM5_uc010tbr.1_F	NM_018663	NP_061133	Q9NR77	PXMP2_HUMAN	ical; (Potential).	0	TATGCCGTTTACG	0.498	
-	3	434		NM_003045	NP_003036	P30825	CTR1_HUMAN	lasmic (Potential).	0	ACCTTCCGCCGC	0.567	
-	1	268	RD13_uc010tec.1_	NM_178006	NP_821074	Q9Y3M8	STA13_HUMAN		4	GCTGATGGCGTG	0.473	
-	1	1876	uc001uxv.1_Intron	NM_032138	NP_115514	Q8WVZ9	KBTB7_HUMAN	Kelch 3.	1	TTTCATCATTGAA	0.433	
+	12	1642	A16_uc010tfg.1_R	NM_024561	NP_078837	Q6N069	NAA16_HUMAN	TPR 6.	1	GACACAGCTGAT	0.358	
-	9	1459	_p.E321K|CAB39L	NM_030925	NP_112187	Q9H9S4	CB39L_HUMAN		0	CTTCTCGTCAG	0.468	
+	12	2512	dh.2_Missense_M	NM_031915	NP_114121	Q96T68	SETB2_HUMAN	SET.	2	AGGGAGCACAA	0.403	
+	7	1881		NM_005708	NP_005699	Q9Y625	GPC6_HUMAN		0	GCACGTCCAAC	0.537	
+	5	966	a.1_Missense_Mu	NM_005561	NP_005552	P11279	LAMP1_HUMAN	ial).|Second lumenal domai	2	ACCAACGGGACC	0.677	
-	1	260	4P_uc001vwb.3_F	NM_001145442	NP_001138914	A6NI47	POTEM_HUMAN		0	CCAGGGGAAGC	0.592	
+	3	443	9A2_uc001vys.2_	NM_014579	NP_055394	Q9NP94	S39A2_HUMAN	ellular (Potential).	3	GATCAGCAAGT	0.463	
-	2	428	_p.E56D|CDH24_	NM_022478	NP_071923	Q86UP0	CAD24_HUMAN	|Extracellular (Potential).	1	AGCATATTCCTC	0.602	
-	2	675	wjb.2_Missense_M	NM_020834	NP_065885	Q8IX15	HOMEZ_HUMAN	Pro-rich.	0	TCTGGGTAGGC	0.562	
+	19	1701	16B_uc001wlk.2_	NM_138360	NP_612369	Q8ND23	LR16B_HUMAN	LRR 10.	5	TGTTTTTGGGCA	0.562	
-	27	3003	p.R822C|IPO4_uc	NM_024658	NP_078934	Q8TEX9	IPO4_HUMAN	HEAT 6.	1	GTCACGGACAC	0.617	
-	9	1257	S2_uc010tqm.1_F	NM_006939	NP_008870	Q07890	SOS2_HUMAN	DH.	2	AAATTCGGTCCAT	0.418	
+	49	10122	_p.R3298*|SYNE2	NM_015180	NP_055995	Q8WXH0	SYNE2_HUMAN	ic (Potential).|Potential.	14	CCTCTTCGAAAA	0.463	
-	19	4301	p.R1416Q|SPTB_	NM_000347	NP_000338	P11277	SPTB1_HUMAN	Spectrin 11.	11	AACATCCGATTG	0.522	
-	32	5972	VE26_uc001xkc.3	NM_015346	NP_056161	Q68DK2	ZFY26_HUMAN	p.R1945Q(1)	11	GTCCCGGTGCA	0.627	
+	6	1576	_p.R377Q|PCNX_	NM_014982	NP_055797	Q96RV3	PCX1_HUMAN		1	CACACGGAGTA	0.478	
-	24	3934		NM_000428	NP_000419	Q14767	LTBP2_HUMAN	12; calcium-binding (Poten	2	GCTCCTCCCCCAT	0.642	
-	4	1407		NM_000428	NP_000419	Q14767	LTBP2_HUMAN		2	TTACCCCAGGG	0.617	
+	8	1028		NM_014239	NP_055054	P49770	EI2BB_HUMAN		1	ACTACGTTCCC	0.488	
+	6	665	_p.P154S|TTLL5_u	NM_015072	NP_055887	Q6EMB2	TTLL5_HUMAN	TTL.	3	ATCCTCCCCCAG	0.463	
+	8	823	LL5_uc010ask.1_M	NM_015072	NP_055887	Q6EMB2	TTLL5_HUMAN	TTL.	3	CATTTTGGTCTC	0.393	
+	15	3276	_p.R297C|NRXN3	NM_004796	NP_004787	Q9Y4C0	NRX3A_HUMAN	ellular (Potential).	10	AAGAATCGCTCT	0.418	
-	4	794	xvg.1_Missense_M	NM_015859	NP_056943	P52655	TF2AA_HUMAN		1	GAATCTGGAACA	0.353	
-	4	368	14orf143_uc001xx	NM_145231	NP_660274	Q9BUY7	EFC11_HUMAN	EF-hand 2.	0	TTACTTCGTTCC	0.333	
+	1	624		NM_003403	NP_003394	P25490	TYY1_HUMAN	Glu-rich (acidic).	0	aggaggacgacgacg	0.289	
-	2	410	qb.2_Missense_M	NM_145701	NP_663747	Q9BXL8	CDCA4_HUMAN		1	CCCACGCTGCA	0.667	
+	15	1710	P1_uc010aya.1_M	NM_014608	NP_055423	Q7L576	CYFP1_HUMAN		9	GGGGCGAGAAG	0.627	
-	9	1170	C2P2_uc010ayf.1_Intron						0	GATGACAGGAG	0.388	
+	68	9948	r.2_Missense_Mut	NM_001036	NP_001027	Q15413	RYR3_HUMAN		10	TCTTCCGCATGG	0.418	
-	3	2346	uck.1_Missense_M	NM_007223	NP_009154	Q14439	GP176_HUMAN	lasmic (Potential).	6	TGCCTACCTTGG	0.527	
-	22	2682	nse_Mutation_p.A7	NM_004573	NP_004564	Q00722	PLCB2_HUMAN		8	AGAGCGCAGGC	0.607	
-	5	1036		NM_013309	NP_037441	O14863	ZNT4_HUMAN	ic (Potential).|His-rich.	0	GTGACGGTGAC	0.438	
-	26	3775_3776	'Flank|MYO5A_uc	NM_000259	NP_000250	Q9Y4I1	MYO5A_HUMAN	Potential.	4	CTTGCGGTCCAG	0.569	
-	82	10955	ha.2_Missense_M	NM_020821	NP_065872	Q709C8	VP13C_HUMAN		2	TCCTTCCAACTTT	0.343	
+	6	3854		NM_015042	NP_055857	O15014	ZN609_HUMAN		3	AGCCAGCCCCA	0.517	
+	4	686	x.1_Missense_Mu	NM_016166	NP_057250	O75925	PIAS1_HUMAN	PINIT.	2	AGTACAGGTCC	0.353	
+	10	1862	_p.D235N|THSD4_	NM_024817	NP_079093	Q6ZMP0	THSD4_HUMAN		2	CATCCAGACAGA	0.587	
-	5	334	bis.2_Missense_M	NM_001012642	NP_001012660	Q8IUY3	GRAM2_HUMAN	GRAM.	0	GAGCCGGCCCT	0.567	
-	10	6608		NM_001897	NP_001888	Q6UVK1	CSPG4_HUMAN	ntaining.|Neurite growth inl	3	CCACGCTGTAG	0.682	

-	7	545	bdo.2_Splice_Site	NM_025234	NP_079510	Q9GZS3	WDR61_HUMAN		2	GGACTCTGTTC	0.418	
+	9	845	2bem.2_Splice_Si	NM_206839	NP_996670	Q9UBU8	MO4L1_HUMAN		0	AACAGGTAACT	0.333	
+	2	941	qa.1_Missense_M	NM_001039958	NP_001035047	Q0VG99	MESP2_HUMAN		0	GTCTCCAGAGC	0.587	
-	7	1049	o.2_Nonsense_Mu	NM_003981	NP_003972	O43663	PRC1_HUMAN	tial.|Dimerization.	2	CACTCGAATTG	0.448	
+	38	4931	_uc002cio.1_Misse	NM_145294	NP_660337	Q96KV7	WDR90_HUMAN		1	TGCCACCACGG	0.652	
-	13	1346	3_3'UTR|CCDC78	NM_001031737	NP_001026907	A2IDD5	CCD78_HUMAN		1	CCATCGTGGCC	0.657	
-	1	130		NM_001010878	NP_001010878	Q4G0I0	CSMT1_HUMAN		0	GGCTCGGCTTC	0.652	
+	1	1027	010uwy.1_5'Flank	NM_003450	NP_003441	Q15697	ZN174_HUMAN	SCAN box.	0	GCTCTGCCGTC	0.582	
-	2	1495		NM_001116	NP_001107	O60503	ADCY9_HUMAN	lasmic (Potential).	6	TTCCCGTGCATA	0.542	
-	11	2556	uzv.1_Missense_M	NM_014647	NP_055462	Q9Y4F3	LKAP_HUMAN		0	CATTTGCAAATG	0.498	
-	16	2113	dx.2_Missense_Mu	NM_002474	NP_002465	P35749	MYH11_HUMAN	.|Actin-binding (By similarit	15	TGTTGCGTAGC	0.647	
-	6	651	A2_uc010bxo.1_F	NM_015044	NP_055859	Q9UJY4	GGA2_HUMAN	GAT.	2	CCTTGGACTTT	0.458	
-	6	1169	240D|SEZ6L2_uc	NM_201575	NP_963869	Q6UXD5	SE6L2_HUMAN	xtracellular (Potential).	2	CAGTGCCCCCA	0.652	
-	5	410	PT1_uc010veq.1_	NM_052838	NP_443070	Q8WYJ6	SEPT1_HUMAN		1	AATCTCTACGCC	0.582	
+	19	3288	se_Mutation_p.R8	NM_006662	NP_006653	Q6ZRS2	SRCAP_HUMAN		4	GCACCGCCTCT	0.557	
+	6	644	ag.2_Intron|HSD3	NM_025193	NP_079469	Q9H2F3	3BHS7_HUMAN		0	TCCGTGGGGGG	0.677	
+	7	665	p.1_Missense_Mu	NM_005353	NP_005344	Q13349	ITAD_HUMAN	lar (Potential).|VWFA.	1	AATTCCGGACC	0.587	rs145982469
+	2	569	M2_uc010cdu.2_I	NM_144673	NP_653274	Q8TAZ6	CKLF2_HUMAN	MARVEL.	1	GCCATTCATAGA	0.488	
+	7	2160	_p.P387L|CES2_u	NM_003869	NP_003860	O00748	EST2_HUMAN		0	GCACCCCCAGG	0.572	
+	3	628	Start_Site|SLC9A	NM_004594	NP_004585	Q14940	SL9A5_HUMAN	ical; (Potential).	2	TGGCCGTGCTA	0.572	
+	3	1495	utation_p.G429*|N	NM_173165	NP_775188	Q12968	NFAC3_HUMAN	RHD.	3	ATTTTGGACAA	0.428	
-	4	634		NM_144676	NP_653277	Q8WW62	TMED6_HUMAN	ical; (Potential).	1	AGTTCACGTAG	0.418	
-	3	1605	_p.A400V|FTSJD1_	NM_001099642	NP_001093112	Q8IYT2	FTSJ1_HUMAN		1	GTATAGCACAAT	0.303	
-	4	742	NF23_uc002fag.2_	NM_145911	NP_666016	P17027	ZNF23_HUMAN		0	GCCACGTCCTC	0.557	
-	14	2225	.2_Intron|PMFBP1	NM_031293	NP_112583	Q8TBY8	PMFBP_HUMAN	Potential.	2	GTTGAGAGAGG	0.448	
+	2	167	FP1_uc010cgs.2_	NM_153688	NP_710155	Q6P2D0	ZFP1_HUMAN		2	AAAATGAACAA	0.368	
+	11	1077	g.1_Missense_Mu	NM_002661	NP_002652	P16885	PLCG2_HUMAN		8	ACGCGGTGGAC	0.493	
+	8	1566	nw.1_Missense_M	NM_178452	NP_848547	Q8NEP3	DAAF1_HUMAN	Pro-rich.	0	AGATCAAGAGC	0.612	
-	9	894	LHDC4_uc002fkk.	NM_017566	NP_060036	Q8TBB5	KLDC4_HUMAN	Kelch 4.	2	GAGTCCAAACC	0.587	
+	8	1208		NM_030928	NP_112190	Q9H211	CDT1_HUMAN		1	CCTGCGCTCTG	0.672	rs143840572
-	9	2020	fnc.1_Missense_M	NM_013275	NP_037407	Q6UB99	ANR11_HUMAN	Ser-rich.	6	AGGAGGCAGAG	0.632	
+	4	550	fpi.1_Missense_M	NM_006086	NP_006077	Q13509	TBB3_HUMAN		3	CGACCGCATCA	0.642	
-	42	6910	P_uc002ftd.2_5'Fl	NM_006445	NP_006436	Q6P2Q9	PRP8_HUMAN		6	GAAACGGTCCG	0.572	
+	6	999	.1_Intron|PAFAH1	NM_000430	NP_000421	P43034	LIS1_HUMAN	n with dynein and dynactin	1	TTGAACGAACTC	0.423	
-	1	79		NM_002550	NP_002541	P47881	OR3A1_HUMAN	ellular (Potential).	3	TGGCTGCAGCC	0.567	
-	33	5339	F1_uc002fxi.2_Int	NM_015113	NP_055928	O43149	ZZEF1_HUMAN		4	TGGATCTTCCT	0.473	
+	3	343	utation_p.D39N|A	NM_004313	NP_004304	P32121	ARRB2_HUMAN		0	CCTGTAGGTAAG	0.577	
-	16	2842	_p.A911S|CAMTA	NM_015099	NP_055914	O94983	CMTA2_HUMAN		1	GAGGGCAGGAA	0.592	
+	5	451	e_Mutation_p.G65	NM_000747	NP_000738	P11230	ACHB_HUMAN	ellular (Potential).	2	CGACGGCTCCG	0.522	
+	2	292	1_5'Flank|CYB5D1	NM_203411	NP_981956	Q6PEY1	TMM88_HUMAN	ical; (Potential).	0	TCACCGGATTC	0.692	
+	16	2609	_p.G830*|ARHGEF	NM_173728	NP_776089	O94989	ARHGF_HUMAN		3	GCTGTTGGATCT	0.602	
+	49	9345	o.2_Missense_Mu	NM_001372	NP_001363	Q9NYC9	DYH9_HUMAN	similarity).|Potential.	20	CTGCCCAGGAA	0.507	
-	2	195	02gqt.1_Intron|TN	NM_012452	NP_036584	O14836	TR13B_HUMAN	.|Extracellular (Potential).	2	CACAGGTGCGC	0.597	
+	14	2031	_p.V659I|MPRIP_	NM_201274	NP_958431	Q6WCQ1	MPRIP_HUMAN	ction with RHOA.	0	CCCCCGTCCAC	0.602	
-	12	1473	n.1_Missense_Mu	NM_000386	NP_000377	Q13867	BLMH_HUMAN		1	CACTCATCTGT	0.473	
-	2	982	.2_Intron|NF1_uc	NM_002544	NP_002535	P23515	OMGP_HUMAN	Ser/Thr-rich.	2	ATATTTGGGTAG	0.398	
+	12	1940	j.2_Missense_Mut	NM_013975	NP_039269	P49916	DNLI3_HUMAN		9	TCTGTGTGAGC	0.478	

+	18	2378	jc.2_Missense_M	NM_173167	NP_775259	Q8IWX7	UN45B_HUMAN	ARM 3.	6	AGGAGAGGGCC	0.547	
+	8	1208	cwb.2_Missense_	NM_004448	NP_004439	P04626	ERBB2_HUMAN	ellular (Potential).	143	TGACAGCAGAG	0.592	
-	4	963		NM_019016	NP_061889	Q2M2I5	K1C24_HUMAN	od.|Linker 12.	0	AGCATTCATTTC	0.507	
-	3	693		NM_181535	NP_853513	Q7Z3Y7	K1C28_HUMAN	Rod.|Coil 1B.	1	TCCTGGTCGGT	0.502	
-	1	394		NM_031854	NP_114060	Q9BQ66	KR412_HUMAN	-[GRQVIL]-[SPTR]- [VST	0	ctggggcggcagcaA	0.313	
-	1	120		NM_002278	NP_002269	Q14532	K1H2_HUMAN	Head.	0	CAGGCCGGGG	0.622	
-	8	1479	e_Mutation_p.S40	NM_021991	NP_068831	P14923	PLAK_HUMAN	ARM 5.	5	TCCACACTCAGC	0.582	
-	14	1601	e_Mutation_p.P53	NM_001096	NP_001087	P53396	ACLY_HUMAN		3	ACTTGGGACTG	0.562	
-	11	1224	n_p.R221H|EZH1_	NM_001991	NP_001982	Q92800	EZH1_HUMAN		3	GGCGACGACCA	0.557	
+	5	679	f.1_Missense_Mu	NM_000151	NP_000142	P35575	G6PC_HUMAN	ical; (Potential).	4	CACAGCATCTA	0.468	
-	2	544	dab.1_Missense_	NM_024819	NP_079095	Q8WVC6	DCAKD_HUMAN	DPCK.	0	CTCCTTCATCAT	0.617	
+	5	1630		NM_014726	NP_055541	A7MCY6	TBKB1_HUMAN	Potential.	0	GGGAGCTGAAG	0.697	
+	4	427	_p.H28N|LUC7L3_	NM_006107	NP_006098	O95232	LC7L3_HUMAN		0	GAGGCCATGCT	0.433	
+	1	383		NM_203425	NP_982249	Q86X59	CQ082_HUMAN		0	GGCGGGATCCC	0.721	
+	12	2157	_p.V622M|TANC2_	NM_025185	NP_079461	Q9HCD6	TANC2_HUMAN		2	TGGCAGTGGCC	0.493	
-	3	716	Mutation_p.G162	NM_000873	NP_000864	P13598	ICAM2_HUMAN	2.|Extracellular (Potential).	1	CTTCCCGAAGG	0.617	rs149059683
-	6	1224	KHM1P_uc010wc	NR_024386					0	CTGCTGAGGCC	0.667	
+	13	992	nse_Mutation_p.M	NM_003835	NP_003826	O75916	RGS9_HUMAN		4	AAGATGCGAGT	0.522	
+	10	1270	wrg.1_Intron|TME	NM_017728	NP_060198	Q8NE00	TM104_HUMAN	ical; (Potential).	0	ACTTCCCCATC	0.622	
-	4	1114	e_Mutation_p.P23	NM_032134	NP_115510	Q9H0J4	QRIC2_HUMAN		5	TGCCAGGAAATG	0.498	
+	4	1781	_p.T394I|TNRC6C	NM_018996	NP_061869	Q9HCJ0	TNR6C_HUMAN	ith argonaute family protei	2	AACTACAGCAA	0.532	
+	2	133	R2_uc002juv.1_	NM_004710	NP_004701	O43760	SNG2_HUMAN	.|Helical; (Potential).	0	TCTTCGCCTTG	0.622	
-	4	1387	TL4_uc010dkj.2_5	NM_022840	NP_073751	Q8N3J2	METL4_HUMAN		2	CCATTTCACATA	0.378	
-	11	1997	se_Mutation_p.R4	NM_024899	NP_079175	Q8TAP6	CEP76_HUMAN		0	CTTACCGAAGA	0.348	
-	1	581	TEC_uc010xaj.1_	NM_001137671	NP_001131143	B2RU33	POTEC_HUMAN		3	TGCCCATGTTGC	0.587	
-	2	217		NM_145756	NP_665699	Q96N95	ZN396_HUMAN		0	CTTCCTCTTCCA	0.483	
+	5	448	ATNAL2_uc002lc	NM_031303	NP_112593	Q8IYT4	KATL2_HUMAN		4	CACTCGCCTGG	0.483	rs148023825
-	2	1271		NM_016626	NP_057710	Q5U5Q3	MEX3C_HUMAN	p.A424D(1)	4	GCCACGCAGAG	0.448	
+	3	1209	r.1_Missense_Mu	NM_005215	NP_005206	P43146	DCC_HUMAN	otential).|Ig-like C2-type 2.	17	GACATTGGAATT	0.498	
-	3	593	se_Mutation_p.P1	NM_021153	NP_066976	Q9H159	CAD19_HUMAN	|Extracellular (Potential).	2	TCATAAGGTTCA	0.363	
+	1	1564	qu.1_Nonsense_	NM_017757	NP_060227	Q9C0G0	ZN407_HUMAN		2	AGGGCCAGGGG	0.577	
+	2	1679	ra.2_Missense_M	NM_171999	NP_741996	Q9BXA9	SALL3_HUMAN		4	CGCCTCCAGCG	0.756	
-	2	369	_p.R39C|SLC39A	NM_144564	NP_653165	Q9BRY0	S39A3_HUMAN	lasmic (Potential).	0	CGAGCGATGGG	0.547	
-	6	736	.R160W|DPP9_u	NM_139159	NP_631898	Q86TI2	DPP9_HUMAN		1	TTTCCGCTCCC	0.632	
-	12	1622	_p.T267I|GTF2F1	NM_002096	NP_002087	P35269	T2FA_HUMAN		0	TGGGTGTTGTC	0.637	
+	6	806	_Mutation_p.V218	NM_145245	NP_660288	Q96CN4	EVI5L_HUMAN	ab-GAP TBC.	1	TTCTGTGTGTTC	0.652	
+	5	1298	c002mnr.1_5'Flan	NM_000201	NP_000192	P05362	ICAM1_HUMAN	4.|Extracellular (Potential).	1	GGACCGAGGTG	0.642	rs143008699
+	4	1932	e_Mutation_p.S62	NM_144566	NP_653167	Q9H0M5	ZN700_HUMAN	2H2-type 14.	0	TTCAGTTGTGC	0.483	
+	4	1934	e_Mutation_p.C62	NM_144566	NP_653167	Q9H0M5	ZN700_HUMAN	2H2-type 14.	0	TCAGTTGTGCCT	0.483	
+	5	1163	ng.1_Missense_M	NM_023072	NP_075560	Q9H7M6	ZSWM4_HUMAN		2	CGCGGGCATGA	0.692	
+	7	994	15_uc002mxu.2_5	NM_138353	NP_612362	Q66K64	DCA15_HUMAN		1	TCCGCCGGGCC	0.687	
-	13	1231	S15L1_uc002nea.	NM_021235	NP_067058	Q9UBC2	EP15R_HUMAN		5	CTTTTCTCGAAT	0.403	
+	7	1309		NM_000453	NP_000444	Q92911	SC5A5_HUMAN	ellular (Pote21L(1)|p.P321	4	TGCCCCAGACC	0.468	rs149570759
-	13	1397	p.G427D|GMIP_u	NM_016573	NP_057657	Q9P107	GMIP_HUMAN		1	CGCCACCCACG	0.642	
+	4	1708		NM_031218	NP_112495	P35789	ZNF93_HUMAN		1	ATACTAGAGAG	0.358	
-	4	1447	p.K353E|ZNF708_	NM_021269	NP_067092	P17019	ZN708_HUMAN		6	GTTTCTTTCCAG	0.343	
+	4	1693	429_uc010ecu.1_	NM_001001415	NP_001001415	Q86V71	ZN429_HUMAN	2H2-type 14.	2	CTTTTATCCTGT	0.378	

+	4	1578	cy.2_Missense_M	NM_033468	NP_258429	Q9Y2Q1	ZN257_HUMAN	2H2-type 11.	0	TTAACCAGTCTT	0.408	
-	3	1913		NM_001001411	NP_001001411	Q8N7Q3	ZN676_HUMAN		0	TTGTAGGGTTTC	0.418	
-	7	2699		NM_001080409	NP_001073878				2	GTCGAGAAATTG	0.353	rs55891931
-	4	1027	rj.1_Missense_Mu	NM_003430	NP_003421	Q05481	ZNF91_HUMAN	2H2-type 6.	0	AAGAATGGCTA	0.413	
-	4	1655	_p.S436P|ZNF681_	NM_138286	NP_612143	Q96N22	ZN681_HUMAN		0	TGTAGGATTTCT	0.373	
+	1	133	Intron|C19orf2_uc	NM_003796	NP_003787	O94763	RMP_HUMAN		2	TGCGCGAGGAG	0.781	
-	2	2575		NM_020856	NP_065907	Q63HK5	TSH3_HUMAN		8	GCGGCGAGTTT	0.532	
-	1	217	xrq.1_Missense_	NM_019849	NP_062823	Q9NS82	AAA1_HUMAN		2	CCCTGGGACTG	0.751	
+	4	690	165V|LSM14A_u	NM_001114093	NP_001107565	Q8ND56	LS14A_HUMAN		1	TTCTGCCTTTA	0.358	
+	15	1773	D1A_uc010xsf.1_	NM_020895	NP_065946	Q96CP6	GRM1A_HUMAN		0	ATGCCCGGGG	0.692	
+	3	576		NM_015073	NP_055888	O60292	SI1L3_HUMAN		2	GGGTGGGCGAT	0.647	
-	2	519	e_Mutation_p.R13	NM_002781	NP_002772	Q15238	PSG5_HUMAN	g-like V-type.	3	TAGTCCTATCAC	0.473	
-	2	1433	iv.2_Missense_Mu	NM_001007561	NP_001007562	Q8WZA9	IRGQ_HUMAN		2	TGGGAGTCCGC	0.716	
-	4	719	_p.P126S|C19orf6	NM_019108	NP_061981	Q9H0W8	SMG9_HUMAN	Pro-rich.	0	AGGGGGTGGTG	0.682	
+	5	1748	_p.H419L|ZNF225_	NM_013362	NP_037494	Q9UK10	ZN225_HUMAN	2H2-type 12.	0	TACCCATCGTA	0.373	
+	6	985	yl.3_Missense_Mu	NM_006630	NP_006621	Q14588	ZN234_HUMAN	2H2-type 3.	0	GTCCACACTGT	0.413	
-	1	1902_1903		NM_032040	NP_114429	Q9H0W5	CCDC8_HUMAN	Potential.	3	CCCTCCTCAGC	0.609	
+	3	409	X_uc010elm.1_R	NM_000554	NP_000545	O43186	CRX_HUMAN	Homeobox.	2	ATGCCCGTGAG	0.632	
+	12	2549	elx.2_Missense_M	NM_000836	NP_000827	O15399	NMDE4_HUMAN	ellular (Potential).	6	TGGAGCGGCTG	0.507	
-	4	943	A4_uc002pjo.2_5	NM_017708	NP_060178	Q2M2I3	FA83E_HUMAN		1	GCGCAGGTGG	0.721	
-	10	2685	kh.2_Missense_M	NM_017805	NP_060275	Q5U651	RAIN_HUMAN	Dilute.	1	TTTCCGGAAGA	0.572	
+	4	255	BL2_uc002pls.1_	NM_006666	NP_006657	Q9Y230	RUVB2_HUMAN	ATP.	0	GGGCACGGGGA	0.562	
-	3	498	_p.L102P|PIH1D1_	NM_017916	NP_060386	Q9NWS0	PIHD1_HUMAN		0	GGGGGAGTGGC	0.542	rs146926384
+	3	512	pvy.3_Missense_Mutation_p.D168N|SIGLECP3_uc002pvz.3_Missense_Mutation_p.D168N						0	GGCCCGACATC	0.622	
-	5	1819		NM_014650	NP_055465	O94892	ZN432_HUMAN	2H2-type 11.	3	TAACATCAGTC	0.433	
+	6	1245		NM_001099694	NP_001093164	Q96N58	ZN578_HUMAN	2H2-type 4.	0	CCATCATAGGT	0.428	
+	4	2549	dw.1_Missense_M	NM_138374	NP_612383	Q96IR2	ZN845_HUMAN	2H2-type 22.	0	CAAGAACTTCC	0.418	
-	2	299	.2_Intron|ZNF154	NM_001085384	NP_001078853	Q13106	ZN154_HUMAN	KRAB.	0	TGTACGGCCACA	0.512	
-	6	1006	hp.1_Missense_	NM_025027	NP_079303	Q8WXB4	ZN606_HUMAN	KRAB.	2	AGTGCGTTGAG	0.532	
+	7	540	G2_uc010ewi.2_I	NM_018968	NP_061841	Q9NY99	SNTG2_HUMAN		3	TGACAGGTGCA	0.428	
+	1	417_418		NM_080657	NP_542388	Q8WXG1	RSAD2_HUMAN		0	CACAGCCAAAA	0.51	
+	3	482	yjc.1_Missense_M	NM_003597	NP_003588	O14901	KLF11_HUMAN		2	CATAACTCCTC	0.408	
+	15	2460	bo.1_Missense_M	NM_014668	NP_055483	Q4ZG55	GREB1_HUMAN		1	GTTTTGCTGGA	0.363	
-	6	723		NM_000384	NP_000375	P04114	APOB_HUMAN	Vitellogenin.	27	TGCCACATTGC	0.507	
-	2	1508	ya.2_Missense_M	NM_025203	NP_079479	Q9H6R7	CB044_HUMAN		2	TTTTCTATTTGC	0.373	
-	6	836	REF1_uc010eyr.	NM_006569	NP_006560	Q99674	CGRE1_HUMAN		1	TCCTTTAGCCT	0.677	rs11889832
+	1	5330	1_5'Flank|ZNF512_	NM_032266	NP_115642	Q68DN1	CB016_HUMAN	m repeat of P-S-E-R-S-H-	1	TTGCAGTCCCT	0.537	
+	49	3508	B1_uc002rme.1_	NM_153021	NP_694566	Q6P1J6	PLB1_HUMAN	ate repeats.|Extracellular (	9	TGGCAGCGGAA	0.567	
-	10	959		NM_000379	NP_000370	P47989	XDH_HUMAN	inding PCMH-type.	8	GTCGGGTCCAT	0.517	
-	4	1270	qf.1_Missense_M	NM_005813	NP_005804	O94806	KPCD3_HUMAN		4	TACCTCTTCACT	0.408	
-	32	5144	DA_uc002rsx.3_	NM_001083953	NP_001077422	Q6YHU6	THADA_HUMAN		3	GATTTTCCTTCAT	0.493	
-	1	219	P2_uc002rxq.3_I	NM_001003937	NP_001003937	Q8N831	TSYL6_HUMAN		0	CCTCTGTCGCC	0.617	
+	5	1808		NM_019002	NP_061875	Q9NY74	ETAA1_HUMAN		4	ATCTAGGCAGT	0.338	
-	17	1894	sij.2_Nonsense_	NM_015189	NP_056004	Q9Y2D4	EXC6B_HUMAN		2	TGTCTCTGGAA	0.418	
+	2	260		NM_001080474	NP_001073943	A6NCI8	CB078_HUMAN	Ser-rich.	2	ATTCTCGGCAG	0.438	
-	1	194	ense_Mutation_p.	NM_001015055	NP_001015055	Q9BST9	RTKN_HUMAN		1	GGAAGCGGCCG	0.701	
+	13	1947	p.D648Y|CTNNA	NM_004389	NP_004380	P26232	CTNA2_HUMAN		9	GATTATGATGTG	0.458	

-	8	1106		NM_005735	NP_005726	P42025	ACTY_HUMAN		1	TGAGAGCACGA	0.592	
-	5	604	se_Mutation_p.P	NM_175735	NP_783862	Q86SG7	LYG2_HUMAN		1	ACGTGGGGAAT	0.478	
+	2	674		NM_001099289	NP_001092759	Q8TEJ3	SH3R3_HUMAN	SH3 1.	1	GCGGCGCAAGG	0.607	
+	3	1315	e.2_Missense_Mu	NM_012455	NP_036587	Q8NDX1	PSD4_HUMAN		2	ggatgtgtcggatctgat	0.139	
-	35	4352	y.1_RNA|CLASP1	NM_015282	NP_056097	Q7Z460	CLAP1_HUMAN	B2 and RSN.|Potential.|In	2	CCTTCCGTTCC	0.567	
-	3	707		NM_001099771	NP_001093241	A5A3E0	POTEF_HUMAN		5	GTGGCAGCACC	0.617	
-	11	1628	_p.P430L|ACVR1_	NM_001111067	NP_001104537	Q04771	ACVR1_HUMAN	Potential).|Protein kinase.	3	AGAACGGTGGC	0.458	
-	26	3656	21B_uc002udj.1_	NM_024753	NP_079029	Q7Z4L5	TT21B_HUMAN		5	GGCTCGTGGAG	0.403	
-	27	5786	uc002udp.2_Intro	NM_002977	NP_002968	Q15858	SCN9A_HUMAN		13	AGATCCATGGC	0.463	
-	66	12371		NM_004525	NP_004516	P98164	LRP2_HUMAN	ellular (Potential).	29	AAGGAGAGCTA	0.363	
-	47	8966		NM_004525	NP_004516	P98164	LRP2_HUMAN	A 21.|Extracellular (Potent	29	GGATGCACCTC	0.448	
+	31	3748	_Mutation_p.G117	NM_138995	NP_620482	Q8WXR4	MYO3B_HUMAN		19	AAAAGGGTGCG	0.358	
+	6	808	zdm.1_Missense_	NM_015530	NP_056345	Q9H8Y8	GORS2_HUMAN		2	GTACACCTATTA	0.403	
-	10	1562		NM_173648	NP_775919	Q6ZP82	CC141_HUMAN		10	GCTGAGCAAGG	0.433	
-	10	1327	p.2_Missense_M	NM_020943	NP_065994	Q9HCG8	CWC22_HUMAN	MIF4G.	0	TTTCCGTACAG	0.388	
-	2	1044	KL_uc002uod.1_I	NM_002500	NP_002491	Q13562	NDF1_HUMAN		1	TCCATCAAAGG	0.547	
+	13	3176	d.1_Missense_M	NM_000534	NP_000525	P54277	PMS1_HUMAN		4	CAGTGCGTCTA	0.393	rs142159998
-	11	958	rv.2_Missense_M	NM_014362	NP_055177	Q6NVY1	HIBCH_HUMAN		0	CTAGGGCAAAA	0.398	
-	38	6274		NM_018897	NP_061720	Q8WXX0	DYH7_HUMAN	3 (By similarity).	12	TGGGAGGTTGA	0.403	
-	11	2764	tl.1_Missense_Mu	NM_020760	NP_065811	Q9P2P5	HECW2_HUMAN	with TP73.|Potential.	18	CCGCCGGTTCA	0.493	
+	3	341	0fsl.1_Missense_	NM_025147	NP_079423	Q9H8M1	CQ10B_HUMAN		0	AGTATCGGGAG	0.279	
+	23	3484	nse_Mutation_p.	NM_152526	NP_689739	Q8TEW8	PAR3L_HUMAN		4	CAGATCCTGTA	0.433	
+	3	493	2vfw.2_Missense_	NM_001142310	NP_001135782	Q96HH4	TM169_HUMAN	ellular (Pot p.R56H(1)	1	CTACCGCTCAG	0.517	rs143856543
-	4	908	269K|TUBA4B_uc	NM_006000	NP_005991	P68366	TBA4A_HUMAN		3	CTGCTCGTGGT	0.582	
+	2	228		NM_080671	NP_542402	Q8WWG9	KCNE4_HUMAN		1	CCGTGCGGCCG	0.612	
-	4	1338	SMD1_uc002vrn.	NM_000867	NP_000858	P41595	5HT2B_HUMAN	smic (By similarity).	0	TTTCCGGTGAC	0.463	
+	14	1956_1957	.3_RNA|DIS3L2_	NM_152383	NP_689596	Q8IYB7	DI3L2_HUMAN		3	CTCTGGACCAC	0.426	
+	10	2079	_Missense_Mutati	NM_023083	NP_075571	Q9HC96	CAN10_HUMAN	Domain III 2.	6	CCTGCCGGACA	0.672	
+	2	1199	110A_uc002weh.1	NM_001042353	NP_001035812	Q9BQ89	F110A_HUMAN		0	GGCTCGGGAGA	0.627	
+	4	688	B_uc010zqz.1_In	NM_001819	NP_001810	P05060	SCG1_HUMAN		6	GAGGCGGGCAC	0.617	
-	2	223	uc002wqu.1_RNA	NM_001099407	NP_001092877	Q9NVP4	CT012_HUMAN		1	ACACTGAACCA	0.323	
+	22	2774	e_Mutation_p.D88	NM_015585	NP_056400	Q8NHU2	CT026_HUMAN		4	ACCGGGATGCG	0.642	
-	11	905		NM_080675	NP_542406	Q8TC36	SUN5_HUMAN	SUN.	1	TTGGACAGGTAA	0.572	
-	7	491		NM_080675	NP_542406	Q8TC36	SUN5_HUMAN		1	TTTATGCTGTCAT	0.413	
+	21	2408	98_splice|ITCH_u	NM_031483	NP_113671	Q96J02	ITCH_HUMAN		6	TCAGGTGAGAG	0.333	
+	10	1027	zvi.1_Splice_Site_	NM_003116	NP_003107	Q9NPE6	SPAG4_HUMAN		0	CTGCAGCCCCA	0.502	
+	17	1728	NBL1_uc002xhi.2_	NM_030877	NP_110517	Q8WYA6	CTBL1_HUMAN		2	GAGCCCGGAGT	0.602	
-	3	1821	xhm.2_Missense_	NM_014657	NP_055472	O43156	TTI1_HUMAN		0	CTCAACCTCCA	0.408	
+	4	609	jo.1_Missense_M	NM_182811	NP_877963	P19174	PLCG1_HUMAN	EF-hand.	8	TTACTCAGTGG	0.567	
+	19	2315	we.1_Missense_M	NM_182811	NP_877963	P19174	PLCG1_HUMAN	SH2 2.	8	AGTTCGACAGC	0.527	
-	31	6087		NM_032221	NP_115597	Q8TD26	CHD6_HUMAN		14	TTTTACTTTTGA	0.433	
+	2	343	xlv.2_Missense_M	NM_000457	NP_000448	P41235	HNF4A_HUMAN	clear receptor.	3	CTTCCGGAGGA	0.542	
-	2	280	j.3_Missense_Mu	NM_001336	NP_001327	Q9UBR2	CATZ_HUMAN		1	AGGCCGGGGGT	0.642	
+	6	876	H26_uc010zzy.1_	NM_177980	NP_817089	Q8IXH8	CAD26_HUMAN	|Extracellular (Potential).	4	GATTTGGATGA	0.373	
+	28	1510	A3_uc002ydn.2_5	NM_001853	NP_001844	Q14050	CO9A3_HUMAN	lical region 3 (COL3).	0	AGGGCGTCCCG	0.657	
-	16	6390_6391	s.1_Missense_Mu	NM_033081	NP_149072	Q9BTC0	DIDO1_HUMAN		6	GGCCTCCTCCC	0.738	
+	10	1901	_p.A215S|MYT1_u	NM_004535	NP_004526	Q01538	MYT1_HUMAN		2	CCATTGCTGCC	0.547	

-	8	2514		NM_006988	NP_008919	Q9UHI8	ATS1_HUMAN	Cys-rich.	6	AGGTGGAATCTG	0.423	
-	1	1107		NM_006988	NP_008919	Q9UHI8	ATS1_HUMAN		6	TCCCTTCGTCCT	0.677	
+	2	834		NM_030891	NP_112153	Q9BY71	LRRC3_HUMAN		0	GAGTTTGTGGGG	0.652	
+	3	530		NM_001848	NP_001839	P12109	CO6A1_HUMAN	erminal globular domain.	1	CGTGGGGTGAG	0.662	
+	4	1755	FH_uc003afp.2_In	NM_021076	NP_066554	P12036	NFH_HUMAN	-S-P-[AEPV]-[EAK]- [AEVK	0	CACCGCCTGAG	0.567	
+	12	1378	uc003aht.2_RNA|S	NM_012429	NP_036561	O76054	S14L2_HUMAN		0	GCACCCCGAAAT	0.512	
-	7	800	RP7A_uc003bcp.2	NM_015703	NP_056518	Q9Y3A4	RRP7A_HUMAN		2	CCTCCTCGAACT	0.662	
-	1	2837		NM_014246	NP_055061	Q9NYQ6	CELR1_HUMAN	r (Potential).|Cadherin 7.	11	CGGACGTGGGC	0.647	
+	4	664	e.2_Intron|TBC1D2	NM_014346	NP_055161	Q8WUA7	TB22A_HUMAN		1	ACGCTGGGTGGC	0.642	
-	11	1481		NM_001080447	NP_001073916				2	TCCTGGGCCACC	0.627	
-	7	623	K11_uc010hay.1_F	NM_002751	NP_002742	Q15759	MK11_HUMAN	rotein kinase.	2	GTGCCCGGTACC	0.632	
-	1	296	_uc011asa.1_Miss	NM_001145137	NP_001138609	Q92523	CPT1B_HUMAN	lasmic (Potential).	2	TGATGCGGATC	0.607	
+	10	1736	n_p.C443Y|TTLL3_	NM_001025930	NP_001021100	Q9Y4R7	TTLL3_HUMAN	TTL.	2	GCAACTGTGACA	0.607	
-	2	590	vw.2_Missense_M	NM_001001331	NP_001001331	Q01814	AT2B2_HUMAN	lasmic (Potential).	6	TGTCCCCATAAG	0.597	
-	12	1620	xx.2_Missense_M	NM_024923	NP_079199	Q8TEM1	PO210_HUMAN	ienal (Probable).	11	GGATCACACTGA	0.572	
+	13	1833	zi.2_Missense_Mu	NM_003298	NP_003289	P49116	NR2C2_HUMAN	inding (By similarity).	0	CCTACCGGTGAG	0.448	
-	5	822	n_p.R70*|ZFYVE2	NM_022340	NP_071735	Q9H1K0	RBNS5_HUMAN		2	CTGCTCGATCAT	0.423	
+	2	298	TAC_uc011aya.1_I	NM_003149	NP_003140	Q99469	STAC_HUMAN		4	CCACTCCCTGCT	0.557	rs149439391
+	10	1348	sense_Mutation_p	NM_001248	NP_001239	O75355	ENTP3_HUMAN	cellular (Potential).	1	ATGCCCGCTCTTA	0.438	rs144319630
-	10	1394		NM_144719	NP_653320	Q8IYE1	CCD13_HUMAN	Potential.	1	TCAGCTACCATG	0.597	
-	1	1541	mg.2_Intron|CYP8	NM_004391	NP_004382	Q9UNU6	CP8B1_HUMAN		2	AGCGATCGTACT	0.557	
+	4	361	_p.R111Q|EXOSC	NM_015004	NP_055819	Q15024	EXOS7_HUMAN		0	TCTATCGGATAT	0.453	
-	8	1112	MT_uc003cwy.2_M	NM_000481	NP_000472	P48728	GCST_HUMAN		1	ATGGGGGCCCCC	0.622	
+	2	558	o.3_Intron|GRM2_	NM_000839	NP_000830	Q14416	GRM2_HUMAN	cellular (Potential).	1	TTTGTGCGTGCC	0.622	
-	1	36	CH_uc003ded.3_5'I	NM_003280	NP_003271	P63316	TNNC1_HUMAN		0	TGTAGATGTCAT	0.607	
+	18	2044	H3_uc011bek.1_Int	NM_002217	NP_002208	Q06033	ITIH3_HUMAN		3	AACATCGATGAA	0.592	
-	11	2459	nt.1_Missense_Mu	NM_015576	NP_056391	O15083	ERC2_HUMAN	Potential.	2	CCACCTCCTTGA	0.468	
+	21	3780	se_Mutation_p.Y2	NM_002841	NP_002832	P23470	PTPRG_HUMAN	).|Tyrosine-protein phosph	7	ATCCAGTATCAC	0.507	
-	7	1691	_p.G444V|CADPS_	NM_003716	NP_003707	Q9ULU8	CAPS1_HUMAN	C2.	3	GGGTGCCCCAG	0.517	
-	9	1074	LG2_uc010hob.2_	NM_003848	NP_003839	Q96I99	SUCB2_HUMAN		2	GCTGTGAGCAAT	0.413	
-	8	1051	AM86D_uc003dpq.	NR_024241					0	CCATAGGGAAAC	0.527	
+	5	1410	apn.2_Missense_M	NM_145037	NP_659474	Q969Y0	FA55C_HUMAN		3	CTTGCAGCAGCA	0.493	
-	3	1321	dn.2_Missense_M	NM_001146156	NP_001139628	P49841	GSK3B_HUMAN	rotein kinase.	2	AAATAACGCAAT	0.343	
-	9	2136		NM_022776	NP_073613	Q9BXB4	OSB11_HUMAN		5	CTACCTCGCTTT	0.453	
+	3	881		NM_007117	NP_009048	P20396	TRH_HUMAN		1	ggggggCTGTGGG	0.428	
-	3	1166	TL2_uc003eqh.1_M	NM_016201	NP_057285	Q9Y2J4	AMOL2_HUMAN		1	CCACAGCAGGT	0.672	
-	14	1587	RN1_uc003euu.2_	NM_019001	NP_061874	Q8IZH2	XRN1_HUMAN		3	TTAAAAGGTTTT	0.358	
+	1	1602		NM_003412	NP_003403	Q15915	ZIC1_HUMAN	2-type 2; atypical.	2	ATCCGCGTGCAC	0.577	
-	2	551	ECOM_uc010hwn.	NM_004991	NP_004982	Q03112	EVI1_HUMAN		14	ATGTGGCAGGAG	0.483	
+	8	782	_p.E168*|FXR1_uc	NM_005087	NP_005078	P51114	FXR1_HUMAN		1	GCCATTGAGCTA	0.418	
-	16	1859	_p.R562C|CLCN2_	NM_004366	NP_004357	P51788	CLCN2_HUMAN	ısmic (By similarity).	0	CACACGCACCC	0.642	
-	12	1466	y.2_Missense_Mut	NM_004454	NP_004445	P41161	ETV5_HUMAN	ETS.	5	CCAGCGCCGAG	0.542	
+	6	984	11bus.1_Missense	NM_182524	NP_872330	Q7Z3I0	Q7Z3I0_HUMAN		0	CAAGAAAATTCA	0.378	
+	5	1197	141_uc003gab.2_I	NM_003441	NP_003432	Q15928	ZN141_HUMAN	C2H2-type 7.	0	CCTACACATGTG	0.408	
-	8	1056	k.1_Missense_Mut	NM_005255	NP_005246	O14976	GAK_HUMAN	rotein kinase.	4	AAGACCGTGTAC	0.607	
-	5	909	bwe.1_Missense_	NM_020416	NP_065149	Q9Y2T4	2ABG_HUMAN	WD 3.	4	TGACGGAGATG	0.572	
+	15	2419	p.R795W|MAN2B2	NM_015274	NP_056089	Q9Y2E5	MA2B2_HUMAN		2	TCCACCGGCGG	0.647	

-	7	842	2_Missense_Mutat	NM_000320	NP_000311	P09417	DHPR_HUMAN			1	CTCGGTCGGTTTT	0.458	
-	3	416		NM_018176	NP_060646	Q8N0V4	LGI2_HUMAN	LRR 1.		0	AGTCCAGCAAAAC	0.388	
+	3	271	PC4_uc003grp.2_5	NM_013367	NP_037499	Q9UJX5	APC4_HUMAN			5	CTTCATCGACTGG	0.348	
-	9	1426		NM_173536	NP_775807	Q8N1C3	GBRG1_HUMAN	lasmic (Probable).		2	CAAGATCCTGTTC	0.408	rs75184362
+	12	2443	3gxl.1_Missense_M	NM_020453	NP_065186	Q9P241	AT10D_HUMAN	lasmic (Potential).		3	CTTTGGGACCATT	0.502	
-	4	2304		NM_001024611	NP_001019782	Q68CR7	LRC66_HUMAN			3	CATTTCCCTGGA	0.468	
+	2	1090	FRA_uc003haa.2_	NM_133267	NP_573574	Q9BZM3	GSX2_HUMAN			0	GCGTCGGGAGC	0.612	
-	15	2180	3hgl.2_Missense_I	NM_014243	NP_055058	O15072	ATS3_HUMAN	Spacer.		2	CCTTCACGGTTCC	0.433	
+	62	9831	ulc.1_Missense_Mu	NM_025074	NP_079350	Q86XX4	FRAS1_HUMAN	|Extracellular (Potential).		5	TCACTAGTCCTTG	0.488	
-	8	748	_Mutation_p.S177	NM_016242	NP_057326	Q9ULC0	MUCEN_HUMAN	cellular (Potential).		0	ATAATACCTAAAA	0.398	
-	4	511	_p.T111I|EMCN_u	NM_016242	NP_057326	Q9ULC0	MUCEN_HUMAN	xtracellular (Potential).		0	GGAAGTGTAACAC	0.363	
+	2	542	3ihk.1_Missense_M	NM_012118	NP_036250	Q9UK39	NOCT_HUMAN			1	GGGCCGTCCTG	0.557	
+	3	1382	p.S388F|TLR2_uc	NM_003264	NP_003255	O60603	TLR2_HUMAN	xtracellular (Potential).		3	GGCCCTCTCTACA	0.348	
+	7	1129	p.E302K|FGB_uc0	NM_005141	NP_005132	P02675	FIBB_HUMAN	nogen C-terminal.		3	CAGAATGAAGCCA	0.463	
+	17	2042	jd.1_Nonsense_M	NM_021634	NP_067647	Q9HBX9	RXFP1_HUMAN	Name=7; (Potential).		0	CTGCTTCAGGTAC	0.274	
+	5	2981	irr.2_Missense_Mu	NM_014269	NP_055084	Q9UKF5	ADA29_HUMAN	).|4.|9 X 9 AA approximate		16	CAACCTCGGGTG	0.577	rs144239698
-	10	1094	mk.1_Missense_M	NM_017755	NP_060225	Q08J23	NSUN2_HUMAN			1	AAGCTCCAAAGCA	0.333	
+	19	2391	p.R720H|TARS_u	NM_152295	NP_689508	P26639	SYTC_HUMAN			2	GGGAACGCACCA	0.423	
-	32	6402	te|C5orf42_uc011c	NM_023073	NP_075561	E9PH94	E9PH94_HUMAN			7	TGCTTACCTGAAC	0.343	
-	32	4252	R1434W|RICTOR	NM_152756	NP_689969	Q6R327	RICTR_HUMAN			10	GGACCGCACTGA	0.383	
-	26	2587	p.R855W|RICTOR	NM_152756	NP_689969	Q6R327	RICTR_HUMAN			10	GCTTCCGGTAAG	0.343	rs140964083
-	10	1543	v.2_Missense_Mut	NM_001343	NP_001334	P98082	DAB2_HUMAN			3	CATCACCATTCAG	0.483	
-	1	774	34_uc003jng.2_5'F	NM_001014279	NP_001014301	Q3ZCQ2	AX2R_HUMAN			0	CGGGAGGTGGC	0.612	
-	7	921	p.Q125K|POC5_u	NM_001099271	NP_001092741	Q8NA72	POC5_HUMAN	n-binding (CBR) 2.		1	CCTTTTGCTTGCC	0.398	
+	2	8668		NM_153610	NP_705838	Q8N3K9	CMYA5_HUMAN			9	CAATCTGTTCTTG	0.398	
+	1	676	uc011ctk.1_Intron	NM_032567	NP_115956	Q9BXG8	SPZ1_HUMAN			1	AGGAGATGATATT	0.358	
+	10	1749	3khw.2_Missense_	NM_001017971	NP_001017971	Q52LC2	VAS1L_HUMAN			0	GACTGCGCCTCC	0.547	
-	3	786_787	kin.2_Missense_M	NM_001884	NP_001875	P10915	HPLN1_HUMAN	Link 1.	p.G239E(1)	5	AAAATCCGTAGT	0.455	rs139074313
-	1	305	129716_uc003kka	NM_020801	NP_065852	Q96B67	ARRD3_HUMAN			2	TACACAGGGACAT	0.368	
-	8	707	bf.1_Missense_Mu	NM_014639	NP_055454	Q6PGP7	TTC37_HUMAN			4	TCCTGCCGTGTT	0.353	
-	8	1290	SK1_uc010jbi.1_In	NM_000439	NP_000430	P29120	NEC1_HUMAN	Catalytic.		2	TCTGGTCGGTGTA	0.517	
+	4	838	_Intron|SNCAIP_u	NM_005460	NP_005451	Q9Y6H5	SNCAP_HUMAN			2	TTCTTTCTCCCGT	0.483	
-	3	564	cxi.1_Missense_M	NM_001098811	NP_001092281	Q92599	SEPT8_HUMAN			2	ATCTGATCCCCAA	0.617	
-	2	1479	TNNA1_uc003ldj.2	NM_015564	NP_056379	O43300	LRRT2_HUMAN	lar (Potential).|LRRCT.		0	TCAGGACTGTGG	0.522	
+	12	1738	3ldi.2_Missense_M	NM_001903	NP_001894	P35221	CTNA1_HUMAN			11	AGGCCGGGCAGC	0.522	rs143060269
+	1	2396		NM_015669	NP_056484	Q9Y5E4	PCDB5_HUMAN	lasmic (Potential).		5	CGGTGCCCGAGC	0.667	
+	1	2915	HB9_uc003liw.1_5'	NM_020957	NP_066008	Q9NRJ7	PCDBG_HUMAN	|Extracellular (Potential).		2	GGTGACCAAGGT	0.701	
+	1	2357	x.1_Intron|PCDHG	NM_018922	NP_061745	Q9Y5G3	PCDGD_HUMAN	lasmic (Potential).		0	TTGTATGTGCCAC	0.403	
+	5	1271	p.R371H|PPARGC	NM_133263	NP_573570	Q86YN6	PRGC2_HUMAN			0	CCTGCGCCCACT	0.532	
-	1	541		NM_000440	NP_000431	P16499	PDE6A_HUMAN	GAF 1.		2	GCCCACGATGCC	0.547	
+	19	2916	41_splice|WWC1_	NM_015238	NP_056053	Q8IX03	KIBRA_HUMAN			5	GCCGGGTAAGTC	0.478	
+	5	1033		NM_003862	NP_003853	O76093	FGF18_HUMAN			0	AGACCCGGGAG	0.617	
-	6	799	se_Mutation_p.Y11	NM_001001502	NP_001001502	Q16143	SYUB_HUMAN			1	TCCTCATAACTCT	0.612	
-	7	799	3_uc003mez.2_5'F	NM_002115	NP_002106	P52790	HXK3_HUMAN	Regulatory.		7	CACACGGCCTGA	0.582	rs147991837
-	3	265	se_Mutation_p.C44	NM_018303	NP_060773	Q96KP1	EXOC2_HUMAN	IPT/TIG.		7	GTCCACAAATGG	0.368	
+	3	354_355		NM_004271	NP_004262	O95711	LY86_HUMAN			0	CTCTGCCCAAGTT	0.46	
-	8	1545	e_Mutation_p.G19	NM_000332	NP_000323	P54253	ATX1_HUMAN			4	GTGTCCCGGCG	0.378	

+	6	700	.G127C|CAP2_uc	NM_006366	NP_006357	P40123	CAP2_HUMAN		1	AACCTGGTCCT	0.408	
+	15	1909	cp.1_Missense_M	NM_153042	NP_694587	Q8NB78	KDM1B_HUMAN		1	TTCGAGAAGCA	0.398	
-	1	313	H3B_uc003nfs.1_	NM_003513	NP_003504	P04908	H2A1B_HUMAN		0	ACCCTGCGCGA	0.537	
+	5	1131	_p.E155K|BTN2A1	NM_007049	NP_008980	Q7KYR7	BT2A1_HUMAN	lasmic (Potential).	2	AGGAAGAACTT	0.229	
+	6	1300	ZKSCAN3_uc003r	NM_024493	NP_077819	Q9BRR0	ZKSC3_HUMAN	2H2-type 2.	2	ATCAGAGAGTC	0.488	
+	26	3702	003nyt.2_5'Flank|	NM_006929	NP_008860	Q15477	SKIV2_HUMAN		4	TGCGGCCTGAG	0.617	
-	20	7337		NM_019105	NP_061978	P22105	TENX_HUMAN	nectin type-III 16.	0	CACACGCTGGC	0.627	
-	11	1326	ra.1_Missense_M	NM_005452	NP_005443	O15213	WDR46_HUMAN	WD 6.	0	CTGCCCTGCCC	0.637	
+	13	1530	i.2_Intron|PHF1_u	NM_024165	NP_077084	O43189	PHF1_HUMAN		0	GCAGCGGCTAC	0.572	
-	4	272		NM_138493	NP_612502	Q9P0B6	CF129_HUMAN	Potential.	0	TTGCCGAAGAA	0.542	
-	8	3449	18_uc003ouw.2_	NM_014345	NP_055160	Q5VUA4	ZN318_HUMAN		7	CTTTTGCAGGA	0.453	
-	5	749		NM_152688	NP_689901	Q5VWX1	KHDR2_HUMAN		11	CTGACGAATTT	0.403	
-	8	2450	y.2_Nonsense_M	NM_001122769	NP_001116241	Q86VQ0	LCA5_HUMAN		0	GTTTTAATCGGT	0.383	
+	5	644	_p.L128F|DOPEY	NM_015018	NP_055833	Q5JWR5	DOP1_HUMAN		4	CAGTTTGTATGA	0.378	
-	50	7800		NM_014611	NP_055426	Q9NU22	MDN1_HUMAN		10	AGATGCAGCAC	0.328	
-	7	2535	p.R576W|BACH2_	NM_021813	NP_068585	Q9BYV9	BACH2_HUMAN		6	GGGCCGCACTT	0.537	
-	10	1260	_p.S106G|C6orf16	NM_198468	NP_940870	Q6ZRQ5	MMS22_HUMAN		0	GGTCACTTGATT	0.343	
-	6	782	CE1_uc010kcz.1_	NM_020771	NP_065822	Q8IYU2	HACE1_HUMAN	ANK 4.	7	AACATGCAGTG	0.458	
-	5	2779		NM_001080450	NP_001073919	Q5T5X7	BEND3_HUMAN		3	CAGGCGAGGGG	0.647	
+	4	684	_5'Flank|PPIL6_u	NM_003080	NP_003071	O60906	NSMA_HUMAN		0	GCACATCTACA	0.512	
+	1	577		NM_175067	NP_778237	Q96RI8	TAAR6_HUMAN	ellular (Potential).	3	AGACCGTTGTA	0.418	
-	3	427	010kgh.2_Transla	NM_022568	NP_072090	Q9H2A2	AL8A1_HUMAN		4	CTGACGTGTGG	0.592	
-	1	303	244_uc003qhu.2_	NM_021635	NP_067648	Q9GZY1	PBOV1_HUMAN		0	AATAATCAATGA	0.284	
-	3	614		NM_020861	NP_065912	Q8N680	ZBTB2_HUMAN		1	GTGGCCGTGGA	0.522	
+	8	1713	L46P|ESR1_uc01	NM_001122742	NP_001116214	P03372	ESR1_HUMAN	.|Interaction with AKAP13.	5	TGTGCCTCAAAT	0.413	
+	2	1352_1353	_Mutation_p.M41	NM_032448	NP_115824	Q96EK7	F120B_HUMAN		1	TCCCATGTGTAC	0.53	
-	8	1898	MICALL2_uc003s	NM_182924	NP_891554	Q8IY33	MILK2_HUMAN		1	CTGCCGGCCCG	0.542	rs139452103
-	12	1978		NM_032415	NP_115791	Q9BXL7	CAR11_HUMAN		50	GCCCCTTGGCT	0.363	
+	4	953	_Mutation_p.V15	NM_001037165	NP_001032242	P85037	FOXK1_HUMAN	Fork-head.	2	TGATCGTGCAG	0.627	
-	11	1069	s.1_Missense_M	NM_004227	NP_004218	O43739	CYH3_HUMAN	PH.	0	GTTTCCGGGGG	0.617	
+	5	584	w.2_Missense_M	NM_006908	NP_008839	P63000	RAC1_HUMAN	(By similarity).	2	TGGGAACTAAA	0.493	
-	2	308	y.1_Missense_M	NM_006408	NP_006399	O95994	AGR2_HUMAN		0	CTGGGGCAGTT	0.498	
+	8	1837	DC129_uc011ka	NM_194300	NP_919276	Q6ZRS4	CC129_HUMAN		0	AAGGATGAAGTT	0.438	
+	14	4106	e_Mutation_p.K88	NM_194300	NP_919276	Q6ZRS4	CC129_HUMAN		0	AGAAAAGGATG	0.443	
+	12	1288		NM_016616	NP_057700	Q8N427	TXND3_HUMAN		3	TTCCCCGATTTT	0.358	
+	21	3159	p.R527C|AEBP1_	NM_001129	NP_001120	Q8IUX7	AEBP1_HUMAN	equired for transcriptional r	0	AGTACCGCGTG	0.557	
+	17	5082	yr.2_Missense_M	NM_152701	NP_689914	Q86UQ4	ABCAD_HUMAN		10	AAGTTAGTGTAA	0.388	
+	6	953		NM_001099435	NP_001092905	A6NIY4	SPDE5_HUMAN	Arg-rich.	0	AGCGTCGGTTC	0.562	
+	6	969		NM_001099435	NP_001092905	A6NIY4	SPDE5_HUMAN	Arg-rich.	0	AGGCCGTTCCA	0.572	
+	5	1200	_p.R215H|DTX2_u	NM_020892	NP_065943	Q86UW9	DTX2_HUMAN		2	CTACCGCCACT	0.657	
-	18	2795	gw.1_Missense_	NM_006379	NP_006370	Q99985	SEM3C_HUMAN	Lys-rich (basic).	1	ATTCCTCCTGT	0.403	
-	14	2044	kgz.1_Missense_	NM_001142749	NP_001136221	A8MWY0	K132L_HUMAN	ellular (Potential).	7	GGCAGGGGACA	0.522	
+	2	721	ujh.1_5'UTR|DBF4	NM_006716	NP_006707	Q9UBU7	DBF4A_HUMAN	BRCT 1.	2	TGGGAGGGGTA	0.343	
-	6	952	p.R159W|CYP51A	NM_000786	NP_000777	Q16850	CP51A_HUMAN		0	TTCCCGATGAG	0.348	
-	6	661	mu.1_Missense_	NM_001742	NP_001733	P30988	CALCR_HUMAN	ellular (Potential).	9	AAACACCTTTTT	0.323	
+	47	3577	1A2_uc011kib.1_	NM_000089	NP_000080	P08123	CO1A2_HUMAN		9	CTTTAAAGGGTC	0.423	rs112557463
+	14	2378	AN_uc003uwl.2_	NM_003386	NP_003377	Q9Y493	ZAN_HUMAN	ate) (mucin-like domain).|E	11	AAAACCCACCA	0.522	

+	3	302	C17_uc010lho.1_F	NM_001040105	NP_001035194	Q685J3	MUC17_HUMAN	cellular (Potential).	27	GTATTTGAGTTGC	0.448	
+	3	1291	KL13_uc003var.2_	NM_001031692	NP_001026862	Q8N6Y2	LRC17_HUMAN	LRR 5.	1	TCAGCAGCAATG	0.383	
-	9	1138	_Mutation_p.T301I	NM_198999	NP_945350	P58743	S26A5_HUMAN	Name=7; (Potential).	1	ATGCCAGTTCCC	0.373	
+	14	2560_2561	q.1_Missense_Mu	NM_000492	NP_000483	P13569	CFTR_HUMAN	lasmic (Potential).	5	ATTCAAGAAGGT	0.416	
-	18	2165	_p.R226W|RBM28_	NM_018077	NP_060547	Q9NW13	RBM28_HUMAN		2	GTCCCGCAACC	0.493	
+	10	1019	qf.2_Missense_Mu	NM_002402	NP_002393	Q5EB52	MEST_HUMAN	ical; (Potential).	2	GTGGGAGCTCTT	0.408	
-	15	1860		NM_004333	NP_004324	P15056	BRAF_HUMAN	rotein kinas_R603>I(2)|p.T	18290	GATTTCACTGTAC	0.368	
-	1	654		NM_001098834	NP_001092304	Q14549	GBX1_HUMAN	Pro-rich.	0	GTCGGCCGCCT	0.562	
+	1	757		NM_138400	NP_612409	Q5C9Z4	NOM1_HUMAN	ization and for targeting PF	0	CTCCCCGAAAGT	0.338	rs151324588
+	11	2788	vpm.2_Missense_M	NM_004745	NP_004736	Q9P1A6	DLGP2_HUMAN		0	GATGATGGAGTC	0.582	
-	4	936	xbj.3_Missense_M	NM_001099335	NP_001092805	Q92561	PHYIP_HUMAN	onectin type-III.	0	CCGTGCGGGGG	0.637	
-	8	603	_p.R121Q|BIN3_uc	NM_018688	NP_061158	Q9NQY0	BIN3_HUMAN	BAR.	0	CCTCCCGCACAC	0.617	
+	19	2039	fq.1_Nonsense_M	NM_173174	NP_775266	Q14289	FAK2_HUMAN		5	CCCTGCGAAGG	0.582	
-	10	1936	xrf.3_Missense_M	NM_014781	NP_055596	Q8TDY2	RBCC1_HUMAN		11	CATGAAGCATTAC	0.358	
+	11	1217	yb.2_Missense_Mu	NM_052958	NP_443190	Q49A92	CH034_HUMAN		1	GGAGTAGGACAC	0.408	
+	2	934	au.1_Missense_Mu	NM_024721	NP_078997	Q86UP3	ZFHX4_HUMAN		15	GCTTCTGCACCT	0.488	
-	1	755	be.2_Missense_Mu	NM_021021	NP_066301	Q13884	SNTB1_HUMAN	PH 1.|PDZ.	5	CTGCACCGCCT	0.592	
+	16	2393	lja.1_Missense_M	NM_016018	NP_057102	A8MW92	P20L1_HUMAN	PHD-type.	2	ATGGATGAGGAG	0.388	
-	4	842	SLC39A4_uc003zc	NM_130849	NP_570901	Q6P5W5	S39A4_HUMAN	cellular (Potential).	0	GCTGGCTCCCC	0.667	
+	11	2168	_p.P419S|GPT_uc	NM_032902	NP_116291	Q96I34	PP16A_HUMAN		0	GGCTCCCCAGTG	0.657	
-	5	1126	1_5'Flank|LRRC14	NM_004260	NP_004251	O94761	RECQ4_HUMAN		4	GGCCCCGCACG	0.632	
+	15	2565	LR_uc003zhm.1_F	NM_003383	NP_003374	P98155	VLDLR_HUMAN	r (Potential).|EGF-like 3.	3	CAGCACCACAGA	0.403	
-	3	1315	if.1_Missense_Mu	NM_152629	NP_689842	Q8NEA6	GLIS3_HUMAN		1	CCTTTGCGCTGG	0.592	
-	20	2177	_p.S479F|PTPRD_	NM_002839	NP_002830	P23468	PTPRD_HUMAN	III 2.|Extracellular (Potentia	22	TTGACAGAATATC	0.433	
+	27	5064	_p.S347*|ADAMTS	NM_001040272	NP_001035362	Q8N6G6	ATL1_HUMAN		5	ACCATCAGAGCA	0.522	
-	1	424	zob.1_Missense_M	NM_020344	NP_065077	Q9UI40	NCKX2_HUMAN	cellular (Potential).	3	TCTTTCGGGTAG	0.423	
-	1	2752	uc003zrh.1_5'Flank	NM_153809	NP_722516	Q8IZX4	TAF1L_HUMAN		26	GTAAACGAAAATC	0.478	
+	8	1661	|NFX1_uc003zsp.1	NM_002504	NP_002495	Q12986	NFX1_HUMAN		1	ATTGCGGCAGCA	0.358	
+	6	1061	zvr.2_Missense_M	NM_015297	NP_056112	Q9UPV7	K1045_HUMAN		1	AGGAGCGGGAG	0.567	
-	38	5395		NM_006289	NP_006280	Q9Y490	TLN1_HUMAN	action with SYNM.	13	TGCAGCGAGGG	0.537	
-	9	2173		NM_001163	NP_001154	Q02410	APBA1_HUMAN	PID.	1	GCAGGTCACTATA	0.493	
-	8	1156	C14B_uc004awl.2_	NM_033331	NP_201588	O60729	CC14B_HUMAN	B.	1	TCAAGTCTGGCTC	0.358	
+	15	2284	566_splice|SMC2_	NM_001042551	NP_001036016	O95347	SMC2_HUMAN		9	GTGGAGGTAAGT	0.383	
-	1	318		NM_006686	NP_006677	Q9Y614	ACL7B_HUMAN		1	CGCCTCGGGGC	0.652	
-	13	4282	F.2_Missense_Muta	NM_002160	NP_002151	P24821	TENA_HUMAN	onectin type-III 8.	7	GCAGGCTGCCA	0.587	
-	5	797	_p.Q259*|LHX6_uc	NM_014368	NP_055183	Q9UPM6	LHX6_HUMAN	Homeobox.	0	CAGCTGTTCCGC	0.602	
-	1	300		NM_001004450	NP_001004450	Q8NGR6	OR1B1_HUMAN	Name=3; (Potential).	0	TGAGCCAAGCAC	0.517	
+	6	1325	_p.G205S|GTF3C5	NM_012087	NP_036219	Q9Y5Q8	TF3C5_HUMAN		0	AAACACGGTAAA	0.403	
-	3	234	1_5'Flank|SURF2_	NM_003172	NP_003163	Q15526	SURF1_HUMAN	ical; (Potential).	2	GATGAGGAGCA	0.577	
+	22	2471		NM_000093	NP_000084	P20908	CO5A1_HUMAN	le-helical region.	11	CACAGGGTGTCA	0.542	
-	2	204	ZBED1_uc004cqh.	NM_004729	NP_004720	O96006	ZBED1_HUMAN		0	ATTCTCCATTGCT	0.597	
+	2	352	on_p.V87I|SYAP1_	NM_032796	NP_116185	Q96A49	SYAP1_HUMAN		1	AATCCGTAGAAC	0.308	
-	9	1325	_p.H367Y|RBBP7_	NM_002893	NP_002884	Q16576	RBBP7_HUMAN	WD 6.	2	ACCAGTGGACCT	0.398	
+	9	2221	nse_Mutation_p.V6	NM_003410	NP_003401	P17010	ZFX_HUMAN	C2H2-type 8.	2	ATTTCAGTTCACA	0.443	
+	1	1990		NM_001136234	NP_001129706				1	GCAGTGCAGGCA	0.617	
+	1	47		NM_004651	NP_004642	P51784	UBP11_HUMAN		3	GTTTCCGGGACC	0.512	
+	20	3013	nse_Mutation_p.V1	NM_138923	NP_620278	P21675	TAF1_HUMAN		17	AGACAGTGACAC	0.433	

+	8	1304_1305	RN1_uc011mpt.1_	NM_052957	NP_443189	Q96QF7	ACRC_HUMAN	Asp/Ser-rich.	3	CGACAGCAGTG	0.554
-	17	4932	29_splice|ATRX_u	NM_000489	NP_000480	P46100	ATRX_HUMAN		30	AACACCTAAAA	0.351
-	5	572	o.2_Missense_Mu	NM_000061	NP_000052	Q06187	BTK_HUMAN	PH.	6	GAGCTGGTGAA	0.328
-	5	413	isn.1_Missense_M	NM_001847	NP_001838	Q14031	CO4A6_HUMAN	le-helical region.	8	GATGCCAAGAA	0.433
+	4	843	EC1_uc010nsl.1_	NM_005462	NP_005453	O60732	MAGC1_HUMAN		4	AGAGTACTCAAA	0.502
-	9	1525	g.1_Nonsense_Mu	NM_000202	NP_000193	P22304	IDS_HUMAN		0	GGAATCGAAAAT	0.542
-	6	976	u.1_Intron|IDS_uc	NM_000202	NP_000193	P22304	IDS_HUMAN		0	AGGGGGTAGGC	0.527
-	3	808	vp.1_Nonsense_M	NM_080701	NP_542432	Q9BQ50	TREX2_HUMAN		1	CGGCTGAGTGG	0.726
+	3	553		NM_020061	NP_064445	P04000	OPSR_HUMAN	Name=4; (Potential).	0	GGCATTGCCTTC	0.577
-	3	758		NM_006014	NP_006005	Q14657	LAGE3_HUMAN		0	CGGGGGGCCCA	0.592
+	8	2600	p.R569Q|ZFY_uc0	NM_003411	NP_003402	P08048	ZFY_HUMAN	2H2-type 12.	0	TTAAACGGCACG	0.413
-	4	334	_uc001aeh.1_Intro	NM_017871	NP_060341	Q5TA45	INT11_HUMAN		0	GTGAGTCATGTA	0.617
-	9	972	y.2_Nonsense_Mu	NM_002074	NP_002065	P62873	GBB1_HUMAN		0	TTCTCGCACAT	0.567
-	15	1814	za.1_Missense_M	NM_018216	NP_060686	Q9NVE7	PANK4_HUMAN		3	TGTAGGAATCC	0.617
-	2	376	IAA0562_uc001ak	NM_014704	NP_055519	O60308	CE104_HUMAN		0	ACAAATCCAATC	0.483
-	5	719	.2_RNA|ACOT7_	NM_181864	NP_863654	O00154	BACH_HUMAN		0	CCTCCTCCTCCT	0.642
+	2	481		NM_004285	NP_004276	O95479	G6PE_HUMAN	1-dehydrogenase.	0	CAGCCCCCAAG	0.572
+	46	5180	z.2_Missense_Mu	NM_015074	NP_055889	O60333	KIF1B_HUMAN		3	TCTAGTCCCTGC	0.423
-	2	381	.2_5'UTR|CASP9	NM_001229	NP_001220	P55211	CASP9_HUMAN		2	ACTTTGCTGCTT	0.532
+	6	1310	dn.2_Missense_M	NM_032409	NP_115785	Q9BXM7	PINK1_HUMAN	.|Cytoplasmic (Potential).	3	ACGTGGATCGG	0.627
-	23	3048	qc.2_Missense_M	NM_032236	NP_115612	Q86UV5	UBP48_HUMAN	biquitin-like.	2	TATGTCGCATAC	0.373
+	15	2533	_p.P782L|SRRM1_	NM_005839	NP_005830	Q8IYB3	SRRM1_HUMAN	Pro-rich.	3	ATCCCCCGTCC	0.577
-	3	263	YF2_uc010oeo.1_	NM_015484	NP_056299	O95926	SYF2_HUMAN	Potential.	0	TTTTGGCTTCCC	0.353
+	8	872	es.1_Missense_Mu	NM_020451	NP_065184	Q9NZV5	SELN_HUMAN		2	CTCAGGGAGCT	0.637
-	2	764		NM_021969	NP_068804	Q15466	NR0B2_HUMAN	inding (By similarity).	0	TTGGGCTGCTG	0.632
+	4	1300	ofx.1_Missense_M	NM_016258	NP_057342	Q9Y5A9	YTHD2_HUMAN		2	ACCCCCGATAA	0.488
-	42	3111	p.G729S|COL16A	NM_001856	NP_001847	Q07092	COGA1_HUMAN	4 (COL4) with 2 imperfect	8	GGGGCCTGGTG	0.622
+	4	446		NM_001099434	NP_001092904	A2VCK2	DCD2B_HUMAN	oublecortin 2.	0	GCTGTCCCAGG	0.552
+	6	1653	522_uc010ohm.1_	NM_020888	NP_065939	Q9P206	K1522_HUMAN	Pro-rich.	0	TCCGGGTGGTT	0.677
-	9	1755	1_5'Flank|YARS_u	NM_003680	NP_003671	P54577	SYYC_HUMAN		2	GATTGGATCCA	0.498
+	8	1881	p.A585V|NCDN_u	NM_001014839	NP_001014839	Q9UBB6	NCDN_HUMAN		3	TGCAGCTCTTC	0.597
-	9	1357	vj.1_Missense_Mu	NM_005955	NP_005946	Q14872	MTF1_HUMAN		2	GAACATCACTGA	0.458
-	2	302	RAGC_uc001ccr.	NM_022157	NP_071440	Q9HB90	RRAGC_HUMAN		1	TACTTTCCAAAA	0.343
+	29	12558	a.1_Missense_Mu	NM_033044	NP_149033	Q9UPN3	MACF1_HUMAN		16	CAGATACCCCAG	0.478
-	5	582	5'UTR|TRIT1_uc0	NM_017646	NP_060116	Q9H3H1	MOD5_HUMAN		1	AACTTGCAAGC	0.408
-	8	7217	e_Mutation_p.E20	NM_024503	NP_078779	Q5T1R4	ZEP3_HUMAN		6	TGGTTCTCGGG	0.632
-	8	935	J3_uc001chg.2_M	NM_014947	NP_055762	Q9UPW0	FOXJ3_HUMAN		2	TGTTAGTCACA	0.328
+	3	216	H_uc009vwl.2_5'U	NM_006347	NP_006338	O43447	PPIH_HUMAN	e cyclophilin-type.	0	CACCGGAGAAT	0.483
+	9	1215	T2_uc001coz.1_M	NM_015112	NP_055927	Q6P0Q8	MAST2_HUMAN		11	TTGACAGTGAAA	0.408
-	4	1515	p.R70W|TAL1_uc	NM_003189	NP_003180	P17542	TAL1_HUMAN		1	GGGCCGTGTGT	0.687
-	16	2146	_uc001cte.2_Splic	NM_002525	NP_002516	O43847	NRDC_HUMAN		0	AAATTCTGTGAA	0.214
-	17	2667	tu.2_Missense_Mu	NM_004153	NP_004144	Q13415	ORC1_HUMAN	ient for ORC complex asse	0	TCTGACATGGT	0.537
-	2	722	163E|ZCCHC11_u	NM_015269	NP_056084	Q5TAX3	TUT4_HUMAN		3	TGGGTCCCTTT	0.373
+	4	1146		NM_000098	NP_000089	P23786	CPT2_HUMAN	ial matrix (By similarity).	0	GCGTATCCCCTG	0.493
-	6	692	w.2_RNA|YIPF1_u	NM_018982	NP_061855	Q9Y548	YIPF1_HUMAN	lasmic (Potential).	2	GAGATCTGGAT	0.403
+	9	1226	ya.3_Missense_M	NM_001110533	NP_001104003	Q3ZCV2	CA177_HUMAN		0	CCGGGACATGC	0.602
-	46	5449		NM_015306	NP_056121	Q9UPU5	UBP24_HUMAN		13	CCTGTCCTTAA	0.517

-	10	1619	p.G456R|C8B_uc(	NM_000066	NP_000057	P07358	CO8B_HUMAN	EGF-like.	4	TGGTACCTTTCAC	0.537	
-	2	544	se_Mutation_p.M1	NM_145243	NP_660286	Q96E52	OMA1_HUMAN		1	AAGAATCATCAAC	0.343	
+	4	517	au.2_Missense_M	NM_178221	NP_835739	Q96DT6	ATG4C_HUMAN		1	CAGATGCTCTTG(	0.388	
+	3	472	plice_Site|ALG6_u	NM_013339	NP_037471	Q9Y672	ALG6_HUMAN		0	ACAATGGTATGAT	0.328	
-	12	1991	73_uc001dgi.3_Mi	NM_001002912	NP_001002912	Q5RHP9	CA173_HUMAN	Glu-rich.	5	TCACTAGAATAAG	0.423	
+	10	1659	q.2_Missense_Mu	NM_001001933	NP_001001933	Q68G74	LHX8_HUMAN		3	TTGTAGCTCATTC	0.358	
-	16	1331	p.A354V|SLC44A5	NM_152697	NP_689910	Q8NCS7	CTL5_HUMAN	lasmic (Potential).	4	GATGTCGCCAAG	0.393	rs148437935
+	6	677	PHN2_uc001div.2_	NM_012302	NP_036434	O95490	LPHN2_HUMAN	otential).|Olfactomedin-like	9	CTTCAGGCTGCA	0.418	
-	4	3579	.2_Intron|ZNF644_	NM_201269	NP_958357	Q9H582	ZN644_HUMAN		3	TTCAGCCCTTCTT	0.363	
+	12	1525	p.P426S|CDC7_u	NM_003503	NP_003494	O00311	CDC7_HUMAN	rotein kinase.	5	GAAGTTCCAGCA(	0.353	
-	7	1302	p.V237A|TGFBR3	NM_003243	NP_003234	Q03167	TGBR3_HUMAN	cellular (Potential).	3	CAGTTGACAGAC	0.353	
-	5	786	sense_Mutation_p.	NM_003567	NP_003558	O75815	BCAR3_HUMAN	SH2.	3	CACCATCTCGCT(	0.483	
+	4	546	_p.V110I|RTCD1_	NM_003729	NP_003720	O00442	RTC1_HUMAN		0	CCGTGTGTTCTCT	0.418	
-	61	4838	G1519D|COL11A1	NM_001854	NP_001845	P12107	COBA1_HUMAN	le-helical region.	12	TGAGGACCCTAC	0.338	
-	12	1938	dm.2_Missense_M	NM_006608	NP_006599	Q9UMS5	PHTF1_HUMAN		1	GGAAAAGTCGAT(	0.403	
-	1	94	VTCN1_uc009whf.	NM_024626	NP_078902	Q7Z7D3	VTCN1_HUMAN		0	AGAAGAGGATCT(	0.557	
-	2	177	oxg.1_Missense_M	NM_015836	NP_056651	Q9UGM6	SYWM_HUMAN		0	TAATTGCCCAGGT	0.453	
+	8	872	TGA10_uc009wiw.2	NM_003637	NP_003628	O75578	ITA10_HUMAN	xtracellular (Potential).	8	CGACCCGAGGCT	0.502	
-	7	786	p.P215S|ARNT_u	NM_001668	NP_001659	P27540	ARNT_HUMAN	PAS 1.	9	CATCTGGGTGCA(	0.473	
-	4	1150	mx.1_Missense_M	NM_007185	NP_009116	Q5SZQ8	CELF3_HUMAN	RRM 2.	2	ATGGTCCCGAAG(	0.617	
-	4	687	EM4_uc001ezk.1_	NM_053055	NP_444283	Q5T1C6	THEM4_HUMAN		0	CAGCCATCATTG(	0.373	
-	2	196	R2D_uc009wnz.2_	NM_006945	NP_008876	P22532	SPR2D_HUMAN	peats of P-K-C-P-[EQ]- P-C	0	AGGTGGGCAGG	0.602	
+	23	2919	p.P928S|UBAP2L	NM_014847	NP_055662	Q14157	UBP2L_HUMAN		2	GGGTCCCGGGC	0.587	
+	5	593	_Mutation_p.V185	NM_080429	NP_536354	Q96PS8	AQP10_HUMAN	lasmic (Potential).	1	AGGGAGTCCCT(	0.617	
-	8	2340	fo.2_Missense_Mu	NM_002249	NP_002240	Q9UGI6	KCNN3_HUMAN		1	CGATGAGCAGCG(	0.632	
+	1	173	sense_Mutation_p.	NM_018845	NP_061333	Q9BRV3	SWET1_HUMAN	MtN3/slv 1.	0	TCTCCGCCGGC(	0.637	
-	23	8566	ASH1L_uc001fkt.2_	NM_018489	NP_060959	Q9NR48	ASH1L_HUMAN	BAH.	11	TATCTCGGTTAAT	0.502	
-	10	6742	ASH1L_uc001fkt.2	NM_018489	NP_060959	Q9NR48	ASH1L_HUMAN		11	CAGAAAGGGGTTT	0.413	
-	3	684	N4L_uc001fmc.2_M	NM_001037533	NP_001032622	Q3T8J9	GON4L_HUMAN		3	GATTTCCTGGGCT	0.478	
-	13	2176	rv.2_Missense_Mu	NM_015327	NP_056142	Q9UPR3	SMG5_HUMAN		5	ACCTGCGCACAC	0.607	
-	5	756	L3_uc009wsn.2_R	NM_052939	NP_443171	Q96P31	FCRL3_HUMAN	2.|Extracellular (Potential).	4	CCCTGGAGACT(	0.333	
+	2	886	p.3_Missense_Mu	NM_002036	NP_002027	Q16570	DUFFY_HUMAN	Name=5; (Potential).	2	TGTCTTGCCATCT	0.567	
-	1	1219		NM_145167	NP_660150	Q9H3S5	PIGM_HUMAN	ical; (Potential).	3	AAAATGGACGTAT	0.443	
+	2	478		NM_004983	NP_004974	Q92806	IRK9_HUMAN	me=M1; (By similarity).	2	CCATCTGGTGGC	0.662	
+	9	1632	wc.1_Missense_M	NM_020335	NP_065068	Q9ULK5	VANG2_HUMAN	lasmic (Potential).	1	GCGGCTGGACCT	0.547	
-	4	369	p.G103E|ITLN2_	NM_080878	NP_543154	Q8WWU7	ITLN2_HUMAN	nogen C-terminal.	1	CACTTCCCACGC	0.582	
+	4	1199	e_Mutation_p.V10	NM_152366	NP_689579	Q8NEP7	KLDC9_HUMAN	Kelch 3.	0	CCACAGGTTTGC	0.478	
-	5	845	pkz.1_Missense_M	NM_000696	NP_000687	P49189	AL9A1_HUMAN		0	ACATCGGGATGCT	0.532	
+	2	139	.1_5'UTR|POGK_u	NM_017542	NP_060012	Q9P215	POGK_HUMAN		1	GCCTACCCTCTC	0.527	
-	21	6084		NM_000130	NP_000121	P12259	FA5_HUMAN	F5/8 type C 1.	6	TTGGCACCTTGG(	0.458	
-	18	5836		NM_000130	NP_000121	P12259	FA5_HUMAN	A 3.|Plastocyanin-like 6.	6	TGGCGTTTGCAT(	0.403	
+	3	256	ense_Mutation_p.E	NM_001002294	NP_001002294	P31513	FMO3_HUMAN		1	CAGAGGAGGGCA	0.408	
+	6	863	nd.1_Missense_M	NM_001460	NP_001451	Q99518	FMO2_HUMAN		1	TGCCACGAACAG	0.453	rs147029269
+	18	2589	d.2_Missense_Mut	NM_014283	NP_055098	Q9UBS9	OSPT_HUMAN		2	AGGCAGGACATAT	0.378	
-	23	3170	vwe.2_Missense_M	NM_178527	NP_848622	Q5TAH2	S9A11_HUMAN	cNMP.	2	GATAAACTATGCA	0.388	
+	9	1521	e_Mutation_p.Q61	NM_004841	NP_004832	Q9UJF2	NGAP_HUMAN	Ras-GAP.	5	GGCAAGCAAGAC	0.463	
+	5	856	p.A138S|CACNA1	NM_000721	NP_000712	Q15878	CAC1E_HUMAN	Name=S5 of repeat I.	6	TTCTTTGCCATC(	0.458	

-	1	742	gpk.2_Missense_M	NM_021133	NP_066956	Q05823	RN5A_HUMAN	ANK 5.	5	TCTGCCCCCATCT	0.517	
-	6	795	_p.G149R|NMNAT	NM_015039	NP_055854	Q9BZQ4	NMNA2_HUMAN		1	CCTTCCCCAAGA	0.582	
+	5	918	se_Mutation_p.V15	NM_007212	NP_009143	Q99496	RING2_HUMAN		1	GAATTAGTATTCA	0.383	
+	7	1460	_Mutation_p.T377	NM_005807	NP_005798	Q92954	PRG4_HUMAN	8 AA repeats of K-X-P-X-F	1	CACCCACCACCA	0.662	
+	6	871	_p.P514S|CFHR4_	NM_006684	NP_006675	Q92496	FHR4_HUMAN	Sushi 5.	3	TCAGATCCATGT	0.259	
+	1	172		NM_030787	NP_110414	Q9BXR6	FHR5_HUMAN		2	TATCCACTGTTG	0.343	
+	8	2936	p.P822L|CRB1_uc	NM_201253	NP_957705	P82279	CRUM1_HUMAN	(Potential).|EGF-like 14.	9	CGTGTCCTCACG	0.527	
+	12	4241	se_Mutation_p.T1	NM_201253	NP_957705	P82279	CRUM1_HUMAN	lasmic (Potential).	9	TTGTCACCTCCA	0.527	
-	23	3954	.D1316N|KDM5B_	NM_006618	NP_006609	Q9UGL1	KDM5B_HUMAN		5	CTCGATCTTGCA	0.473	
-	5	2529		NM_001973	NP_001964	P28324	ELK4_HUMAN		0	GTAGGTCTGGGG	0.453	
-	4	754	xca.1_Missense_M	NM_001122980	NP_001116452	Q8WWV6	FCAMR_HUMAN	cellular (Potential).	1	CCATGGCCCGG	0.597	
-	5	753	_p.P69S|IRF6_uc	NM_006147	NP_006138	O14896	IRF6_HUMAN		2	GAAGGGGAAGG	0.498	
+	4	392	_p.S111N|TRAF5_	NM_004619	NP_004610	O00463	TRAF5_HUMAN		5	ATTGCAGCAATG	0.373	rs143951452
-	13	2750	pty.1_Missense_M	NM_005401	NP_005392	Q15678	PTN14_HUMAN		5	GTCTCTCCTTCA	0.547	
-	30	6398		NM_206933	NP_996816	O75445	USH2A_HUMAN	tential).|Fibronectin type-III	26	TGGCAGAGGGC	0.433	
-	21	4796	kv.2_Missense_Mu	NM_206933	NP_996816	O75445	USH2A_HUMAN	cellular (Potential).	26	GGCCTCAGTTGT	0.383	
-	33	3859	sense_Mutation_p	NM_012414	NP_036546	Q9H2M9	RBGPR_HUMAN		1	ACCTTTGTGGCT	0.443	
-	2	1997	gh.2_Missense_Mu	NM_002221	NP_002212	P27987	IP3KB_HUMAN		5	GCTTGTCCGGAT	0.607	
+	4	821	.1_Intron|ZNF678_	NM_178549	NP_848644	F5GXA7	F5GXA7_HUMAN		1	AATGTGGCAAAG	0.333	rs145397350
+	4	938	.1_Intron|ZNF678_	NM_178549	NP_848644	F5GXA7	F5GXA7_HUMAN		1	TAACTAGCCATA	0.363	
+	3	1124	hrd.2_Missense_M	NM_053052	NP_444280	Q5SQN1	SNP47_HUMAN		1	CAAAGCCCAGGG	0.458	
-	1	386		NM_003493	NP_003484	Q16695	H31T_HUMAN		0	ATACGGCGTGCC	0.602	
-	23	6543	b.1_RNA|LYST_uc	NM_000081	NP_000072	Q99698	LYST_HUMAN		12	AAACTTCCAGTC	0.418	
+	1	454	pxx.1_Missense_M	NM_000254	NP_000245	Q99707	METH_HUMAN		3	TCGCAACCCGGT	0.627	
+	1	421	L13_uc001ids.2_I	NM_001004686	NP_001004686	Q8NH16	OR2L2_HUMAN	Name=3; (Potential).	3	CAGTTGCAGAA	0.313	
-	22	3273	9xjf.1_Missense_M	NM_018027	NP_060497	Q9P2Q2	FRM4A_HUMAN	Ser-rich.	3	ATCCTGGTGACC	0.667	
-	6	880	m.2_Missense_Mu	NM_152724	NP_689937	Q15404	RSU1_HUMAN	LRR 7.	1	AGAACGGTGAGG	0.468	
-	40	6140		NM_001081	NP_001072	O60494	CUBN_HUMAN	CUB 14.	19	ACGTTCGGTGAG	0.448	
+	3	364		NM_012228	NP_036360	Q9Y3D2	MSRB2_HUMAN		0	AGGAAGCAGGA	0.433	
+	2	563	AA1217_uc010qcy	NM_019590	NP_062536	Q5T5P2	SKT_HUMAN		7	AGTCGTGGTTCA	0.483	
+	11	2688	e_Mutation_p.G57	NM_019590	NP_062536	Q5T5P2	SKT_HUMAN		7	AGTGGGAGAGG	0.517	
+	15	3560	AA1217_uc010qda	NM_019590	NP_062536	Q5T5P2	SKT_HUMAN		7	CCTCCTCGTCGA	0.557	
-	4	730	vb.3_Missense_Mu	NM_018109	NP_060579	Q9NVV4	PAPD1_HUMAN		1	AGTCTGGAAAATA	0.453	
-	23	2935		NM_004521	NP_004512	P33176	KINH_HUMAN		5	CCTCCGGTGTCA	0.343	
+	9	1461		NM_014753	NP_055568	Q14692	BMS1_HUMAN		3	TGGGGCCCACCC	0.498	
-	1	2092		NM_002900	NP_002891	P10745	RET3_HUMAN	nate tandem repeats.|3.	2	CACTGGTCTGCC	0.667	
-	3	174	NT_uc001jka.1_Mi	NM_007057	NP_008988	O95229	ZWINT_HUMAN		0	TCTGAGAGTCCT	0.542	
-	4	733	FY2_uc001jod.1_M	NM_017987	NP_060457	Q8WXA3	RUFY2_HUMAN	RUN.	1	CCAGAGGGGTCC	0.428	
-	11	1372	orf27_uc009xqh.1_	NM_152710	NP_689923	Q96M53	SPATL_HUMAN		1	GAGCTTCTCCAAT	0.587	
+	8	837	M|HECTD2_uc001	NM_182765	NP_877497	Q5U5R9	HECD2_HUMAN		1	CATCTACGTATGT	0.323	
-	1	2107		NR_002319					0	CTCAGGGTTGCT	0.522	
-	5	827	f.1_Missense_Mut	NM_012465	NP_036597	Q9Y6L7	TLL2_HUMAN	otease (By similarity).	3	TTTCCTCATCCG	0.483	
+	4	928	OPSL_uc001knz.2_	NM_138413	NP_612422	Q86XE5	HOGA1_HUMAN		0	AGCACCCGAATA	0.587	
+	4	2362	e_Mutation_p.D10	NM_021830	NP_068602	Q96RR1	PEO1_HUMAN	SF4 helicase.	1	AAAGAGGATGAT	0.502	
-	1	777	001ktk.1_5'UTR|PC	NM_013274	NP_037406	Q9UGP5	DPOLL_HUMAN		0	ATACCCCTGGGA	0.512	
+	9	2007	q.1_Missense_Mu	NM_006951	NP_008882	Q15542	TAF5_HUMAN	WD 4.	2	AACTGTGTAAGG	0.388	
-	11	1605	ih.3_Missense_Mu	NM_001329	NP_001320	P56545	CTBP2_HUMAN		0	GGTGCTCTCGAT	0.512	

+	13	1233	un.1_Missense_M	NM_001380	NP_001371	Q14185	DOCK1_HUMAN		9	TTCCTGGAGATAT	0.413	
-	1	684	_p.P215S|FAM19	NM_001039762	NP_001034851	Q6ZSG2	F196A_HUMAN		2	TGGAGGCCGAG	0.637	
+	12	1158	p.E304K|INPP5A_	NM_005539	NP_005530	Q14642	I5P1_HUMAN		1	CTCTTGGAGTTT	0.488	
+	10	1418	_Mutation_p.E41	NM_012305	NP_036437	O94973	AP2A2_HUMAN		0	TATCTGGAGACA	0.617	rs11538724
+	51	14906	b.2_Missense_Mu	NM_017511	NP_059981	Q9HC84	MUC5B_HUMAN	em repeats, Ser/Thr- rich.|	0	GCCGAGCACTA	0.662	
+	51	14909	tb.2_Missense_Mu	NM_017511	NP_059981	Q9HC84	MUC5B_HUMAN	em repeats, Ser/Thr- rich.|	0	GAGCACTACAG	0.667	
-	3	557		NM_001012709	NP_001012727	Q6L8H1	KRA54_HUMAN	repeats of C-C-X-P.	0	AGCCACAGCCC	0.672	
-	7	1581	se_Mutation_p.T2	NM_018073	NP_060543	Q6AZZ1	TRI68_HUMAN	B30.2/SPRY.	1	GGAAAGTGAAG	0.552	
+	1	688		NM_001004755	NP_001004755	Q8NGJ5	O51L1_HUMAN	lasmic (Potential).	1	CTGGATATTGCAT	0.408	
+	1	146	_uc001mam.1_Int	NM_001004757	NP_001004757	Q8NH59	O51Q1_HUMAN	lasmic (Potential).	1	TCCTCACTGTCAT	0.567	
+	18	2009	NTL_uc001mkt.2_	NM_001178	NP_001169	O00327	BMAL1_HUMAN		0	CTCTTCTCCAG	0.493	
+	6	946	p.A193V|BBOX1_	NM_003986	NP_003977	O75936	BODG_HUMAN		1	ATGTGGCTTACA	0.418	
-	25	3286	5_uc001ndj.1_Mis	NM_001008938	NP_001008938	Q14008	CKAP5_HUMAN		2	AGTTTCCCAGTA	0.323	
-	7	918	lr.1_Missense_Mu	NM_002804	NP_002795	P17980	PRS6A_HUMAN		4	CTGTGCGGCAC	0.587	rs139347167
+	1	418		NM_001004703	NP_001004703	A6NHA9	O4C46_HUMAN	lasmic (Potential).	1	GTGTGTGCCCTG	0.478	
+	1	152		NM_001005274	NP_001005274	Q8NH70	O4A16_HUMAN	lasmic (Potential).	3	CAGCCCCTCCT	0.413	
+	1	668		NM_001005200	NP_001005200	Q8N162	OR8H2_HUMAN	lasmic (Potential).	2	TTCTCTTTACCAT	0.393	
-	1	893		NM_001004740	NP_001004740	Q8NGP8	OR5M1_HUMAN	lasmic (Potential).	1	GCAAGGATTACAT	0.388	
-	3	253		NM_006093	NP_006084	Q9Y2Y8	PRG3_HUMAN		0	AAGTCTCTCTCC	0.547	
-	11	1357	S329N|SLC43A3_	NM_014096	NP_054815	Q8NBI5	S43A3_HUMAN		1	AGGTGCTGACT	0.527	
-	1	572		NM_001001954	NP_001001954	Q8NGI9	OR5A2_HUMAN	ellular (Potential).	0	GTATCAGAGCAG	0.463	
-	18	2224	TA2_uc010rlx.1_	NM_004739	NP_004730	O94776	MTA2_HUMAN		2	TAGGGCCCTGG	0.567	
-	10	1286	x.1_Missense_Mut	NM_004739	NP_004730	O94776	MTA2_HUMAN	SANT.	2	ACTATGCTGGCA	0.547	
-	14	1666	nse_Mutation_p.E	NM_198334	NP_938148	Q14697	GANAB_HUMAN		5	ATGGTTCGTTCAT	0.527	
-	4	772	L12_uc001nuh.2_	NM_024099	NP_077004	Q9BQE6	CK048_HUMAN		0	TCTAGGGTCCT	0.423	
+	11	1897	79B_uc001nvd.3_	NM_006473	NP_006464	Q9Y6J9	TAF6L_HUMAN		3	ACTGCCCATGAT	0.697	
-	2	447		NM_014067	NP_054786	Q9BQ69	MACD1_HUMAN		0	CTCCCGCTGCT	0.607	rs140541432
+	2	223	nk|NUDT22_uc00	NM_032344	NP_115720	Q9BRQ3	NUD22_HUMAN		0	GCGGGGGCCTG	0.692	
+	10	1540	obz.2_Missense_	NM_006244	NP_006235	Q15173	2A5B_HUMAN		2	ATCCGGGGGCTG	0.597	
-	5	840	1odr.1_Missense_	NM_001077241	NP_001070709	Q8N413	S2545_HUMAN	Solcar 2.	0	TGGGGGGCTCC	0.647	
+	7	1557	_p.H464Y|SIPA1_	NM_006747	NP_006738	Q96FS4	SIPA1_HUMAN	Rap-GAP.	0	GGGCACACACA	0.647	
-	4	694	_Mutation_p.G154	NM_005507	NP_005498	P23528	COF1_HUMAN		0	TGCCCCCCAGCT	0.597	
-	6	777	EMP2_uc001oga.	NM_016938	NP_058634	O95967	FBLN4_HUMAN	alcium-binding (Potential).	1	AGGCCCCAGCT	0.667	
-	4	954	s.1_Missense_Mu	NM_005438	NP_005429	P15407	FOSL1_HUMAN		0	GGTCTCCGCTG	0.612	
-	29	6082	N2_uc001ojc.1_5'	NM_006946	NP_008877	O15020	SPTN2_HUMAN	Spectrin 16.	4	TCTTCTCCTGCC	0.632	
-	1	1165	lank|CABP4_uc0	NM_206997	NP_996880	Q8TDT2	GP152_HUMAN	lasmic (Potential).	0	GGGCTGTGGGA	0.637	
-	3	266	11orf51_uc001orv	NM_014042	NP_054761	P60006	CK051_HUMAN		0	ACAGAGTCTCA	0.507	
-	2	504		NM_173582	NP_775853	Q6PCE3	PGM2L_HUMAN		1	GTCCTGCAGTCC	0.413	
-	1	806		NM_001005285	NP_001005285	A6NND4	O2AT4_HUMAN	ellular (Potential).	1	AGGTCAGCCCTG	0.522	
-	1	262	LM_uc001pbn.2_	NM_007166	NP_009097	Q13492	PICAL_HUMAN		2	CCCCACCCGCT	0.716	
+	11	1343	AD2_uc009yvy.2_	NM_005467	NP_005458	Q9Y3Q0	NALD2_HUMAN	(Potential).|NAALADase.	2	GCTGGGATGCA	0.378	
-	9	1243	R1B_uc010rwj.1_	NM_002716	NP_002707	P30154	2AAB_HUMAN	HEAT 10.	0	CCTCATCCTTTA	0.343	
+	7	1260	2_Missense_Muta	NM_015157	NP_055972	Q86UU1	PHLB1_HUMAN		0	CCCGCCCAAGT	0.672	
-	5	1559	0rzi.1_Missense_	NM_012101	NP_036233	Q14134	TRI29_HUMAN		4	TCTTACCTTTGG	0.572	
-	1	731		NM_001005188	NP_001005188	Q8NH79	OR6X1_HUMAN	Name=6; (Potential).	3	ACAACTGTCAGG	0.448	
+	1	802		NM_001004464	NP_001004464	Q8NGN5	O10G8_HUMAN	ellular (Potential).	2	CTGTGGATGGA	0.527	
+	8	1965		NM_025004	NP_079280	Q0P6D6	CCD15_HUMAN		2	AGGTGTTCTTC	0.423	

-	1	91		NM_001142685	NP_001136157	A7KAX9	RHG32_HUMAN		5	TTCCTCTTCAC	0.463
-	11	3516	_p.V370I|SNX19_	NM_014758	NP_055573	Q92543	SNX19_HUMAN		4	GGAGACACCCA	0.537
-	23	4000	ie.1_Missense_Mu	NM_001042603	NP_001036068	P29375	KDM5A_HUMAN	PHD-type 2.	3	AAGAGGGCAAA	0.483
+	19	5714	_p.T1489I|WNK1_	NM_018979	NP_061852	Q9H4A3	WNK1_HUMAN		23	TTTCTACCCCAG	0.448
-	13	2163	qnw.2_Missense_	NM_001038	NP_001029	P37088	SCNNA_HUMAN	smic (By similarity).	0	ggacaaggacagaga	0.214
+	8	1453	.1_Missense_Muta	NM_000616	NP_000607	P01730	CD4_HUMAN	ical; (Potential).	0	GCTGGGGGGCG	0.622
+	9	1248	X5_uc001qsu.2_In	NM_001131026	NP_001124498	P50542	PEX5_HUMAN		1	GATTGGCGAAG	0.582
-	16	3487	.3_Intron|CD163_	NM_004244	NP_004235	Q86VB7	C163A_HUMAN	lasmic (Potential).	8	CAGCTGACTCA	0.388
-	10	2497	p.G790E|CD163_	NM_004244	NP_004235	Q86VB7	C163A_HUMAN	xtracellular (Potential).	8	TCTTTTCCATTG	0.522
-	6	1372	ran.1_Missense_	NM_030640	NP_085143	Q9BY84	DUS16_HUMAN	protein phosphatase.	0	GAGATCCCAGCT	0.448
+	2	151		NM_006205	NP_006196	Q13956	CNCG_HUMAN	Lys-rich (basic).	2	AAGGCCCTCCC	0.483
+	19	2493	_Mutation_p.D79	NM_019012	NP_061885	Q9HAU0	PKHA5_HUMAN		3	GGTCCAGATTAT	0.333
-	22	2758	_p.P352L|IPO8_uc	NM_006390	NP_006381	O15397	IPO8_HUMAN		3	TTGAGGGAACA	0.443
-	15	1839	_p.D46Y|IPO8_uc	NM_006390	NP_006381	O15397	IPO8_HUMAN		3	CATCATCATTTTC	0.383
+	26	2889	.1_Missense_Muta	NM_152438	NP_689651	Q96FC9	DDX11_HUMAN		3	GCCCGTGTGGA	0.597
-	11	2836	_p.S535F|SFRS2I	NM_004719	NP_004710	Q99590	SCAFB_HUMAN	Arg-rich.	0	TTGGGGACTGA	0.468
+	2	241	rd.2_Translation_S	NM_000289	NP_000280	P08237	K6PF_HUMAN		4	CTCTGGTGGAG	0.453
+	13	1843	_p.C559Y|TROAP_	NM_005480	NP_005471	Q12815	TROAP_HUMAN	ate tandem repeats.|Cys-ri	1	GTCCTGCTGTA	0.597
-	10	1120	IL3_uc001rut.1_5'	NM_175736	NP_783863	Q8IVF7	FMNL3_HUMAN	GBD/FH3.	4	GCATACCTGAAT	0.517
+	5	425	uy.2_Missense_M	NM_003217	NP_003208	P55061	BI1_HUMAN	ical; (Potential).	0	AGTTGGCCTGG	0.408
+	22	3172	yo.2_Missense_M	NM_001039960	NP_001035049	Q2Y0W8	S4A8_HUMAN	lasmic (Potential).	5	TCTAAGCGAGA	0.408
+	2	1455	ch.1_Missense_M	NM_032889	NP_116278	Q6N075	MFSD5_HUMAN	ical; (Potential).	3	TGCTGGCAGTG	0.557
-	16	1685	s.3_Missense_Mu	NM_015665	NP_056480	Q9NRG9	AAAS_HUMAN		1	TCCACCCCCAG	0.612
-	9	1548	se_Mutation_p.Q2	NM_001098815	NP_001092285	A2RU30	K0748_HUMAN		2	TGGCTGCTGGC	0.517
+	1	841		NM_001005490	NP_001005490	A6NCV1	O6C74_HUMAN	Name=7; (Potential).	1	TTGCCCCCATG	0.358
+	7	934	_p.P117L|SLC39A	NM_173596	NP_775867	Q6ZMH5	S39A5_HUMAN	ical; (Potential).	2	CCTCCCTTCTC	0.642
+	2	666	H4_uc009zpj.2_5'	NM_007224	NP_009155	O95158	NXPH4_HUMAN	(linker domain).	0	GTTCGGAGGAG	0.657
-	2	229	_p.G23C|TSPAN8	NM_004616	NP_004607	P19075	TSN8_HUMAN	ical; (Potential).	4	GATACCACATAG	0.373
-	5	862	n.2_Nonsense_Mu	NM_203394	NP_976328	Q96AV8	E2F7_HUMAN	Potential.	3	CATGCCAGCCA	0.502
-	4	769	n.2_Missense_Mu	NM_203394	NP_976328	Q96AV8	E2F7_HUMAN	Potential.	3	CAAGACTGACA	0.473
-	3	479	do.3_Missense_M	NM_003297	NP_003288	P13056	NR2C1_HUMAN	ction with KAT2B (By simila	1	TGCATCTGGAG	0.433
+	10	1574	_p.P323L|NEDD1_	NM_152905	NP_690869	Q8NHV4	NEDD1_HUMAN		0	TCTCACCTATCA	0.373
+	27	3425		NM_014503	NP_055318	O75691	UTP20_HUMAN		4	TTCTTCCTTTAG	0.418
+	8	928		NM_017564	NP_060034	Q8WWQ8	STAB2_HUMAN	r (Potential).|EGF-like 4.	14	GCCACCCTCAT	0.507
+	3	314	utation_p.R70K|L	NM_003299	NP_003290	P14625	ENPL_HUMAN		3	ACTTAGAGAGA	0.353
-	14	1952	g.1_Missense_Mu	NM_018984	NP_061857	Q8WYL5	SSH1_HUMAN		4	TCTTGCTGTTG	0.567
+	17	2558		NM_015267	NP_056082	O14529	CUX2_HUMAN	Poly-Ser.	6	CGCCTCCGTGT	0.721
-	11	1499	1tts.2_Missense_	NM_001109662	NP_001103132				2	GGGTGGCAAGA	0.403
-	20	2561	DDX54_uc001tuq.	NM_024072	NP_076977	Q8TDD1	DDX54_HUMAN		3	GCCACCACGCT	0.701
-	4	417	wy.3_Missense_M	NM_016281	NP_057365	Q9H2K8	TAOK3_HUMAN	rotein kinase.	6	TTTGTAGCCTGT	0.348
+	28	4796		NM_207437	NP_997320	Q8IVF4	DYH10_HUMAN	n (By similarity).	6	AGGAGCACATG	0.542
+	40	7387	.P2450L|EP400_u	NM_015409	NP_056224	Q96L91	EP400_HUMAN		12	TGAATCCCTTTC	0.388
-	3	317	ice_Site_p.S78_s	NM_001161344	NP_001154816	Q96EP1	CHFR_HUMAN		1	TACTCACCTGGT	0.468
+	4	783	_p.R162K|ZMYM2	NM_003453	NP_003444	Q9UBW7	ZMYM2_HUMAN		6	TTTCAAGAAGTA	0.383
-	10	4401	R1124K|SACS_uc	NM_014363	NP_055178	Q9NZJ4	SACS_HUMAN		12	AGGCTCTAAAA	0.373
-	15	3956	_uc010aae.2_Spli	NM_018451	NP_060921	Q9HC77	CENPJ_HUMAN		2	TTTGTACCTATTT	0.398
-	1	1301	_p.P282S|FAM123	NM_152704	NP_689917	Q8N7J2	F123A_HUMAN		4	CCCGGGGACAT	0.577

+	2	461	n_p.P72L|NUPL1_	NM_014089	NP_054808	Q9BVL2	NUPL1_HUMAN	AA repeats of F-G.	0	TAAACCTGCCA	0.453	
-	30	4148	q.2_Missense_Mu	NM_002019	NP_002010	P17948	VGFR1_HUMAN	lasmic (Potential).	24	GCCTGCTGACA	0.473	
+	6	3060		NM_001033602	NP_001028774	Q5JR59	MTUS2_HUMAN	g distal tip of microtubules	0	GGCCCGTGAGG	0.632	
+	14	1206	ba.2_Missense_M	NM_130806	NP_570718	Q8WXD0	RXFP2_HUMAN	cellular (Potential).	0	AAGAATCTTTCT	0.358	
+	6	1073	Y_uc010tdw.1_R	NM_023037	NP_075463	Q5TBA9	FRY_HUMAN		7	GTAATAGACAGT	0.313	
+	26	3659	Y_uc010tdw.1_R	NM_023037	NP_075463	Q5TBA9	FRY_HUMAN		7	CCCTAGAGCGG	0.383	
+	11	4524		NM_000059	NP_000050	P51587	BRCA2_HUMAN	BRCA2 3.	64	CAAGTGGGAA	0.289	
-	5	641	D13_uc001uux.2_	NM_178006	NP_821074	Q9Y3M8	STA13_HUMAN		4	CTCCCGGTGAC	0.577	
-	5	1328	vo.2_Missense_M	NM_001142296	NP_001135768	Q8N0X7	SPG20_HUMAN		0	TAGTTCTTCCA	0.408	
+	17	2064	_p.V645I|LRCH1_	NM_015116	NP_055931	Q9Y2L9	LRCH1_HUMAN	CH.	2	ATGGTGTCGTC	0.512	
-	1	484	TR2A_uc010acr.2_	NM_000621	NP_000612	P28223	5HT2A_HUMAN	ame=2; (By similarity).	6	CTATGGCAAGT	0.453	
+	8	1164	se_Mutation_p.R2	NM_052950	NP_443182	Q96P53	WDFY2_HUMAN	WD 6.	0	GGAGAGGCAGG	0.547	
-	18	3954	.G1201E|ATP7B_	NM_000053	NP_000044	P35670	ATP7B_HUMAN	lasmic (Potential).	3	CATCCCCCACC	0.597	
+	4	4151	p.D1086N|PCDH1	NM_001040429	NP_001035519	O14917	PCD17_HUMAN	lasmic (Potential).	7	CAAGAGACCCT	0.532	
-	2	971	_p.P183L|DACH1_	NM_080759	NP_542937	Q9UI36	DACH1_HUMAN		1	TCTGAGGGGTG	0.483	
+	4	391	_p.R74K|SCEL_u	NM_144777	NP_659001	O95171	SCEL_HUMAN		5	GGACAGGTGGG	0.408	
-	14	1599	OCK9_uc010tis.1_	NM_015296	NP_056111	Q9BZ29	DOCK9_HUMAN		1	TTTGGCATGCC	0.438	
-	43	3990	4A1_uc010agl.2_	NM_001845	NP_001836	P02462	CO4A1_HUMAN	le-helical region.	6	CATGCCCTGGA	0.413	
-	6	854	vsf.2_Missense_	NM_006322	NP_006313	Q96CW5	GCP3_HUMAN		1	ACTGGGGACAC	0.493	
-	10	972	.G249S|RASA3_u	NM_007368	NP_031394	Q14644	RASA3_HUMAN		4	GGAGCCCAGGT	0.582	
-	3	384	p.V53I|RASA3_uc	NM_007368	NP_031394	Q14644	RASA3_HUMAN	C2 1.	4	GAAAACGTCTC	0.448	
-	1	260	4P_uc001vwb.3_	NM_001145442	NP_001138914	A6NI47	POTEM_HUMAN		0	CCAGGGGAAGC	0.592	
-	4	1298	_Missense_Mutati	NM_012244	NP_036376	Q9UHI5	LAT2_HUMAN	ical; (Potential).	1	CAGCTGTGAAG	0.527	
-	33	4927		NM_002471	NP_002462	P13533	MYH6_HUMAN	Potential.	4	TCCTTCCATCTT	0.607	
+	4	1045	SSK4_uc001wnf.2	NM_174944	NP_777604	Q6SA08	TSSK4_HUMAN	rotein kinase.	0	CCTGGGTGCTC	0.542	
+	5	447	_p.C52Y|G2E3_u	NM_017769	NP_060239	Q7L622	G2E3_HUMAN	PHD-type 1.	3	CCGATGTAAAC	0.353	
-	9	1243	L1_uc001wxz.2_I	NM_004196	NP_004187	Q00532	CDKL1_HUMAN		2	tataataggatgaggtt	0	
+	9	1212	p.G324D|ATL1_uc	NM_015915	NP_056999	Q8WXF7	ATLA1_HUMAN	Cytoplasmic.	4	CCGGGGTCTGG	0.368	
+	5	985	wzt.3_Nonsense_	NM_001099652	NP_001093122	Q8N3F9	G137C_HUMAN	lasmic (Potential).	0	TTAAACCAGAAT	0.363	
+	2	678	se_Mutation_p.T2	NM_015589	NP_056404	Q9UPU9	SMAG1_HUMAN		0	TCCCCACCACAA	0.507	
-	7	600	bn.1_Nonsense_	NM_007086	NP_009017	O75717	WDHD1_HUMAN		1	AGTGGCCAACT	0.333	
-	1	539		NM_030791	NP_110418	Q9BX95	SGPP1_HUMAN	ical; (Potential).	1	GAAGGGGAAGA	0.622	
+	35	5298	l.2_Missense_Mu	NM_015180	NP_055995	Q8WXH0	SYNE2_HUMAN	ic (Potential).|Potential.	14	TCCATGAACAA	0.284	
+	8	1171	HG3_uc001xhp.2_	NM_015549	NP_056364	A1L390	PKHG3_HUMAN	PH.	1	CTACGGGGAGC	0.577	
-	19	4301	p.R1416Q|SPTB_	NM_000347	NP_000338	P11277	SPTB1_HUMAN	Spectrin 11.	11	ACATCCGATTG	0.522	
+	5	548		NM_020715	NP_065766	Q9ULM0	PKHH1_HUMAN	Potential.	0	GGGTGACACTC	0.532	
-	2	2073	e_Mutation_p.A44	NM_183002	NP_892114	P57103	NAC3_HUMAN	|Cytoplasmic (Potential).	7	CATTGGCAGAA	0.522	
-	6	2043	_p.R53Q|ZFYVE1_	NM_021260	NP_067083	Q9HBF4	ZFYV1_HUMAN		1	TACACTCGGTTG	0.517	rs143773668
-	24	3934		NM_000428	NP_000419	Q14767	LTBP2_HUMAN	12; calcium-binding (Poten	2	CTCCTCCCCCA	0.642	
-	4	1407		NM_000428	NP_000419	Q14767	LTBP2_HUMAN		2	TTACCCCAGGG	0.617	
-	12	1941	_p.T318I|KIAA031	NM_001039479	NP_001034568	O15033	K0317_HUMAN		5	TCCGAGTGGCT	0.403	
+	5	299	se_Mutation_p.Q8	NM_001102564	NP_001096034	Q96FT9	IFT43_HUMAN		0	GACCACAGAGC	0.453	
+	9	1297	se_Mutation_p.A3	NM_020421	NP_065154	Q86TW2	ADCK1_HUMAN	rotein kinase.	3	TCACTGCCACT	0.617	
+	15	3276	_p.R297C|NRXN	NM_004796	NP_004787	Q9Y4C0	NRX3A_HUMAN	cellular (Potential).	10	AGAATCGCTCT	0.418	
-	4	368	4orf143_uc001xx	NM_145231	NP_660274	Q9BUY7	EFC11_HUMAN	EF-hand 2.	0	TTACTTCGTTCC	0.333	
+	11	1693	se_Mutation_p.R	NM_001102366	NP_001095836	Q7Z3D6	CN159_HUMAN		3	GGAACCGGGGG	0.363	
-	9	873		NM_024764	NP_079040	Q9H7T0	CTSRB_HUMAN	ical; (Potential).	5	ATCCACCAATG	0.343	

+	3	215	0twm.1_Splice_Si	NM_153646	NP_705932	Q8NFF2	NCKX4_HUMAN		3	TTCCAGCGATT	0.532	
-	1	35	7_uc001ybn.3_5'	NM_032490	NP_115879	Q9BXV9	CN142_HUMAN		0	CGCCACCCGGA	0.632	
+	17	4000		NM_001376	NP_001367	Q14204	DYHC1_HUMAN	(By similarity).	10	TTCAGGCTCTCA	0.502	
+	68	12558		NM_001376	NP_001367	Q14204	DYHC1_HUMAN	6 (By similarity).	10	TCAACCCCAAG	0.597	
+	3	378	e.2_Missense_Mu	NM_152328	NP_689541	Q8N142	PURA1_HUMAN		2	ACGGGGTGGTC	0.488	
-	7	12965	px.2_Missense_M	NM_138420	NP_612429	Q8IVF2	AHNK2_HUMAN		1	GGTCACCCTCC	0.612	
-	7	9176	px.2_Missense_M	NM_138420	NP_612429	Q8IVF2	AHNK2_HUMAN		1	GGTCCCCCTGC	0.647	
+	5	1451	1_uc010axg.1_Intr	NM_033271	NP_150374	Q96KE9	BTBD6_HUMAN		0	GGAGGGGATGA	0.612	
-	3	2346	uck.1_Missense_	NM_007223	NP_009154	Q14439	GP176_HUMAN	lasmic (Potential).	6	GCCTACCTTGG	0.527	
-	5	427	zkr.2_3'UTR|uc00	NM_003134	NP_003125	P37108	SRP14_HUMAN	Ala/Thr-rich.	0	tgctgctgcggcaggtg	0.234	
-	22	3290	oc.2_Missense_M	NM_015540	NP_056355	Q9BWH6	RPAP1_HUMAN	Leu-rich.	1	GTTGCGGATGC	0.642	
+	30	4496	PKBP1_uc010ud	NM_001128608	NP_001122080	O60336	MABP1_HUMAN		10	CAGGGGCAGCC	0.622	
-	3	1316	389V|ZSCAN29_	NM_152455	NP_689668	Q8IWY8	ZSC29_HUMAN		1	GGGTCGCCTCT	0.552	
+	13	1608	_p.P467L|PDIA3_u	NM_005313	NP_005304	P30101	PDIA3_HUMAN		2	AAACCCCCCTG	0.383	
+	1	210	4_uc001ztd.1_5'F	NM_016400	NP_057484	Q9NX55	HYPK_HUMAN		0	CGACCGAGGGG	0.657	
+	14	1842	_Mutation_p.T49	NM_017434	NP_059130	Q9NRD9	DUOX1_HUMAN	roxidase activity.|Extracellu	8	TCAGCACCATCG	0.607	
-	26	3775_3776	'Flank|MYO5A_uc	NM_000259	NP_000250	Q9Y4I1	MYO5A_HUMAN	Potential.	4	CTTGCGGTCCA	0.569	
+	13	3198	w.2_Missense_Mu	NM_032866	NP_116255	Q0VF96	CGNL1_HUMAN	Potential.	11	GCAGACGCTGA	0.547	
-	3	1456	M10_uc010ugz.1_	NR_002927					0	TGTCACCCGCT	0.468	
-	8	1130		NM_004998	NP_004989	Q12965	MYO1E_HUMAN	osin head-like.	3	ACTCCCGCCTG	0.527	rs143368771
+	19	2620		NM_015059	NP_055874	Q9Y4G6	TLN2_HUMAN	Ala-rich.	11	GCATGGTGGAA	0.448	
+	10	1862	_p.D235N|THSD4_	NM_024817	NP_079093	Q6ZMP0	THSD4_HUMAN		2	CATCCAGACAGA	0.587	
-	6	1306	se_Mutation_p.S1	NM_000499	NP_000490	P04798	CP1A1_HUMAN		5	TTCAAACTTGTG	0.517	
-	5	1558	RNA3_uc002beb.	NM_000743	NP_000734	P32297	ACHA3_HUMAN	lasmic (Potential).	4	CATTTTGTGCTT	0.368	
+	22	3141		NM_152336	NP_689549	Q96MI9	CBPC4_HUMAN		0	AGGACGCTCTG	0.532	
-	11	2352	bnr.3_Splice_Site_	NM_002693	NP_002684	P54098	DPOG1_HUMAN		2	CCTCACCGTTT	0.617	
+	10	1038		NM_003870	NP_003861	P46940	IQGA1_HUMAN		8	AATATCGACCTG	0.473	
+	9	1388	qd.2_Missense_M	NM_018671	NP_061141	Q9H3U1	UN45A_HUMAN		2	TGGAAGTGGGG	0.507	
+	2	373	p.G108D|IGF1R_u	NM_000875	NP_000866	P08069	IGF1R_HUMAN		8	CCGCGGCTGGA	0.552	
-	2	643	q.1_Missense_M	NM_003502	NP_003493	O15169	AXIN1_HUMAN	RGS.	2	GGACACGATGC	0.537	
-	1	9	se_Mutation_p.A2	NM_172168	NP_751908	Q8NFA2	NOXO1_HUMAN	PX.	0	GGCCTGCCATG	0.617	
-	15	6879	t.1_Missense_Mut	NM_001009944	NP_001009944	P98161	PKD1_HUMAN	ular (Potential).|REJ.	3	CACAGGCAGCG	0.706	
-	4	805	e_Mutation_p.E47	NM_001103175	NP_001096645	A1A5D9	BICR2_HUMAN	Potential.	0	CACCTCCAGGC	0.657	
+	7	1538	ua.2_Missense_M	NM_001042428	NP_001035893	O95201	ZN205_HUMAN	2H2-type 6.	0	CAACCGCACAC	0.657	
-	2	2169		NM_001116	NP_001107	O60503	ADCY9_HUMAN	lasmic (Potential).	6	CATTTCGTACC	0.532	
+	3	1023	IP2_uc010uyp.1_	NM_024997	NP_079273	Q5U623	MCAF2_HUMAN		0	GTGCAGACTCA	0.328	
-	1	199	rf75_uc002daq.1_	NM_005425	NP_005416	Q05952	STP2_HUMAN		0	TGGCCGGGCTC	0.627	
-	42	7308	wa.2_Splice_Site	NM_015092	NP_055907	Q96Q15	SMG1_HUMAN		16	ACATACCTGCG	0.463	
-	6	651	A2_uc010bxo.1_	NM_015044	NP_055859	Q9UJY4	GGA2_HUMAN	GAT.	2	CCTTGGACTTT	0.458	
-	8	2967		NM_024675	NP_078951	Q86YC2	PALB2_HUMAN	n with RAD51 and BRCA2	11	CTGGAACTATCT	0.343	
+	6	2880	.W669*|TNRC6A_	NM_014494	NP_055309	Q8NDV7	TNR6A_HUMAN	ction with EIF2C1 and EIF	2	GGATGGGGAGA	0.433	
+	2	587		NM_152288	NP_689501	Q9BRQ5	ORAI3_HUMAN		0	TGTGAGCAACAT	0.607	
-	44	6726	NOT1_uc002ent.	NM_016284	NP_057368	A5YKK6	CNOT1_HUMAN		6	GAATGGGTCGG	0.388	
-	42	6421	.S2038F|CNOT1_	NM_016284	NP_057368	A5YKK6	CNOT1_HUMAN		6	GATGGGAAATC	0.443	
+	5	1125	p.G84R|ZFP90_u	NM_133458	NP_597715	Q8TF47	ZFP90_HUMAN		1	CACTGGGGAGA	0.453	
-	2	746	8_uc002ewy.2_3'	NM_022341	NP_071736	Q9HBH1	DEFM_HUMAN		0	ATTCACCTTCAT	0.498	
+	16	2617	38_uc010vmp.1_I	NM_014003	NP_054722	Q92620	PRP16_HUMAN		1	TTGAGGTGCGT	0.577	

+	8	1566	nw.1_Missense_M	NM_178452	NP_848547	Q8NEP3	DAAF1_HUMAN	Pro-rich.	0	AGATCAAGAGC	0.612	
+	6	980	voj.1_Missense_	NM_014732	NP_055547	O60268	K0513_HUMAN		1	TGAAGGGGCCC	0.657	
+	3	494	E7_uc002fnq.2_Ir	NM_014427	NP_055242	Q9UBL6	CPNE7_HUMAN		0	CAGCCCAAAAG	0.527	
-	8	996	p.V303M|SLC43A	NM_152346	NP_689559	Q8N370	LAT4_HUMAN		0	CTTCACCTCCA	0.687	
-	2	790		NM_020310	NP_064706	Q99583	MNT_HUMAN		1	TCCAGGGTGTG	0.642	
+	1	716	3_Intron|ITGAE_u	NM_031965	NP_114171	Q8TF76	HASP_HUMAN		0	AGGAGCCAAGG	0.617	
-	12	1642	_p.T535I|ANKFY1	NM_016376	NP_057460	Q9P2R3	ANFY1_HUMAN		3	AGCTGGTCAGG	0.612	
-	24	3313	2fya.3_Missense_	NM_014520	NP_055335	Q9BQG0	MBB1A_HUMAN		2	GGGAGGACAGT	0.647	
+	23	4099		NM_000937	NP_000928	P24928	RPB1_HUMAN		1	TGCATCGAGTCC	0.572	
+	2	550	ja.2_5'Flank|CYB5	NM_144607	NP_653208	Q6P9G0	CB5D1_HUMAN	me b5 heme-binding.	1	TCAAGGGAACC	0.572	
-	6	1177	16_uc002gow.2_	NM_006470	NP_006461	O95361	TRI16_HUMAN		3	ACACCGACACC	0.512	
-	28	4030	OR1_uc010vwb.1	NM_006311	NP_006302	O75376	NCOR1_HUMAN	action with ETO.	5	TACAGGAGACT	0.348	
+	2	487		NM_018019	NP_060489	Q9NWA0	MED9_HUMAN		0	AATCCCCAAGG	0.562	
-	11	1392	P3A_uc002gsw.1	NM_004618	NP_004609	Q13472	TOP3A_HUMAN		3	CCCAGCGTGGA	0.547	
-	3	382	cqw.1_Missense_	NM_007202	NP_009133	O43572	AKA10_HUMAN		1	AAAAGGAGTCC	0.453	
+	7	1127	p.A313T|CCDC55_	NM_032141	NP_115517	Q9H0G5	NSRP1_HUMAN		0	CAAGGGCGAGG	0.323	
-	1	922		NM_152462	NP_689675	Q8N808	AMAC1_HUMAN	DUF6 2.	0	GGGCAGGGTGG	0.577	
+	4	749	2_5'Flank|MRM1_	NM_024308	NP_077284	Q6UWP2	DHR11_HUMAN		0	CAGAGGGACTG	0.642	
+	4	1033	TF_uc002hnj.2_R	NM_012138	NP_036270	Q9NY61	AATF_HUMAN		0	TTTTCCCATTGTT	0.423	
+	6	507	7I|TBC1D3_uc002	NM_032258	NP_115634	Q8IZP1	TBC3A_HUMAN	ab-GAP TBC.	0	GAACACTGAGG	0.557	rs143321126
-	17	3990	_Mutation_p.P10	NM_004774	NP_004765	Q15648	MED1_HUMAN	Interaction with TP53.	8	TGGGGGAGTTT	0.478	
-	17	3907	_Mutation_p.S10	NM_004774	NP_004765	Q15648	MED1_HUMAN	Ser-rich.	8	TATGAGAACCA	0.502	
-	21	2708		NM_001067	NP_001058	P11388	TOP2A_HUMAN		7	TGCAGGACCAC	0.423	
-	4	963		NM_019016	NP_061889	Q2M2I5	K1C24_HUMAN	od.|Linker 12.	0	AGCATTCATTTC	0.507	
-	25	3014	.D1005N|ACLY_u	NM_001096	NP_001087	P53396	ACLY_HUMAN		3	ACTGTCAAAGG	0.498	
+	5	485	iky.2_Missense_M	NM_004287	NP_004278	O14653	GOSR2_HUMAN	lasmic (Potential).	2	GCATGGATGAC	0.502	
-	22	3075	d.2_Missense_Mu	NM_001130528	NP_001124000	O60271	JIP4_HUMAN		5	CCAAGTCTTGTT	0.388	
-	6	776		NM_012329	NP_036461	Q15546	PAQRB_HUMAN	ical; (Potential).	0	CTGGAGAGAAT	0.333	
-	1	318		NM_003916	NP_003907				0	cgatagtgggacatac	0.249	
+	4	323	ense_Mutation_p.	NM_001099432	NP_001092902	Q9H6U6	BCAS3_HUMAN	WD 1.	5	TTAAATGGTATG	0.348	
+	5	430	ice_Site_p.P107_s	NM_001099432	NP_001092902	Q9H6U6	BCAS3_HUMAN		5	ATCCCTGTAAGT	0.333	
-	27	6088		NM_005121	NP_005112	Q9UHV7	MED13_HUMAN		2	TCATCTCCTGTG	0.408	
+	8	1158	AF7_uc010wpn.1_	NM_005828	NP_005819	P61962	DCAF7_HUMAN		1	TGAAGGAGAGA	0.547	
+	10	1270	wrg.1_Intron|TME	NM_017728	NP_060198	Q8NE00	TM104_HUMAN	ical; (Potential).	0	ACTTCCCCATC	0.622	
-	18	3922	jrl.3_Missense_Mu	NM_022066	NP_071349	Q9C0C9	UBE2O_HUMAN		5	ACTCCGGCATG	0.632	
-	10	971	xs.2_Missense_Mu	NM_014740	NP_055555	P38919	IF4A3_HUMAN	case C-terminal.	1	GTTGGCTTCCC	0.512	
+	9	1237	jyd.1_Missense_	NM_173626	NP_775897	Q86WA9	S2611_HUMAN	ical; (Potential).	0	CATTGCGGTGG	0.632	
-	5	458	_p.P137L|C17orf6	NM_001100407	NP_001093877	Q9BQA9	CQ062_HUMAN		0	TGAGGGGGTGG	0.622	
+	4	496	wvr.1_Missense_	NM_024619	NP_078895	Q9HA64	KT3K_HUMAN		0	GGTGACGTGCT	0.547	rs139863997
+	4	1051		NM_032048	NP_114437	Q9BXX0	EMIL2_HUMAN	Potential.	3	AGCTCCAGGAA	0.512	
-	23	3384	zj.1_Missense_Mu	NM_005559	NP_005550	P25391	LAMA1_HUMAN	inin EGF-like 13.	21	CCGACGTCCCC	0.582	
+	6	1110	p.G323D|KIAA080	NM_015210	NP_056025	Q9Y4B5	CC165_HUMAN	Potential.	0	AGAGGGTGCAA	0.632	
+	2	1161	NDC2_uc002koh.	NM_001098529	NP_001091999	Q86VQ3	TXND2_HUMAN	repeat of Q-P-K-X-G-D-I-P	2	AGAGTGATATC	0.557	
-	9	1492	PPE1_uc002kqk.2	NM_023075	NP_075563	Q53F39	MPPE1_HUMAN		0	CCTCCCGTGAA	0.502	rs145870573
-	17	2374	B6_uc002kqy.2_3'	NM_006796	NP_006787	Q9Y4W6	AFG32_HUMAN		0	TAGGTAGATTTTT	0.423	
-	9	1228	_p.P310L|ABHD3_	NM_138340	NP_612213	Q8WU67	ABHD3_HUMAN		1	ACATTAGGATTT	0.378	
+	4	1462	YR_uc002kva.2_	NM_012189	NP_036321	O75952	CABYR_HUMAN		0	GTCTGGGGAAA	0.488	

-	11	1021	2kvf.3_Missense_I	NM_080597	NP_542164	Q9BXW6	OSBL1_HUMAN	PH.	4	TCAGGTGTTTGC	0.363	
+	1	797	AF4B_uc002kvt.3_	NM_005640	NP_005631	Q92750	TAF4B_HUMAN		3	CCACGACAATCC	0.577	
+	10	1558		NM_001942	NP_001933	Q02413	DSG1_HUMAN	r (Potential).|Cadherin 4.	7	AGTTACCAAGGA	0.338	
+	15	2249	33_uc002kwt.2_5'U	NM_001944	NP_001935	P32926	DSG3_HUMAN	lasmic (Potential).	9	CGGTGGAAGGC	0.443	
+	11	1311		NM_005925	NP_005916	Q16820	MEP1B_HUMAN	ılar (Potential).|MAM.	2	ATCAATCTTTCGC	0.438	
-	15	1790	rf34_uc010dmf.1_I	NM_001105528	NP_001098998	Q5BJE1	CR034_HUMAN		1	GAAGCACCATTC	0.318	
-	4	1342	2_Intron|ZNF397C	NM_001112734	NP_001106205	Q86W11	ZSC30_HUMAN	C2H2-type 3.	0	TGATGAGCTCTG	0.468	
+	9	866	.P2_uc010xch.1_M	NM_018255	NP_060725	Q6IA86	ELP2_HUMAN	WD 6.	4	AACTGGGTAAATC	0.398	
+	3	1209	dr.1_Missense_Mu	NM_005215	NP_005206	P43146	DCC_HUMAN	Potential).|Ig-like C2-type 2.	17	GACATTGGAATT	0.498	
-	11	1397	).R389Q|NARS_uc	NM_004539	NP_004530	O43776	SYNC_HUMAN		0	TCATCCGTTTGA	0.323	
+	8	1442	if.2_Missense_Mu	NM_031891	NP_114097	Q9HBT6	CAD20_HUMAN	|Extracellular (Potential).	5	TTGGAAGTGTTC	0.413	
-	3	593	ıse_Mutation_p.P1	NM_021153	NP_066976	Q9H159	CAD19_HUMAN	|Extracellular (Potential).	2	TCATAAGGTTCA	0.363	
+	5	983	_p.V254I|CCDC10	NM_001093729	NP_001087198	Q68D86	C102B_HUMAN		3	AATGAAGTAACT	0.378	
+	1	1564	dqu.1_Nonsense_N	NM_017757	NP_060227	Q9C0G0	ZN407_HUMAN		2	AGGGCCAGGGG	0.577	
-	8	1109	).G164D|MBP_uc0	NM_001025101	NP_001020272	P02686	MBP_HUMAN		1	GCGTGCCCTGG	0.552	
+	14	1948	R413C|HMHA1_uc	NM_012292	NP_036424	Q92619	HMHA1_HUMAN		1	TCATGCGTGCC	0.647	
-	6	829	.2_RNA|ATP8B3_u	NM_138813	NP_620168	O60423	AT8B3_HUMAN	lasmic (Potential).	0	GTCCCGGGTGG	0.657	
+	4	1228	wn.3_Missense_M	NM_152791	NP_690004	Q8NEP9	ZN555_HUMAN	C2H2-type 8.	1	TTTATCCCCAGTC	0.463	
+	4	1395	wn.3_Missense_M	NM_152791	NP_690004	Q8NEP9	ZN555_HUMAN	C2H2-type 10.	1	AATTGGCCCATA	0.453	
+	1	338	CLN_uc002lxh.1_R	NM_020170	NP_064555	Q969V3	NCLN_HUMAN	ıenal (Potential).	0	CCTACGGTGCG	0.756	
-	2	282	lye.1_Missense_M	NM_001060	NP_001051	P21731	TA2R_HUMAN	cellular (Potential).	0	ATCAGCCGTCTC	0.697	
-	2	240	RD37_uc002lzf.1_5	NM_001961	NP_001952	P13639	EF2_HUMAN		0	TGTCTCCCCGG	0.632	
+	13	2433		NM_005483	NP_005474	Q13111	CAF1A_HUMAN	Binds to p60.	2	CCTCCACCACCT	0.647	
+	1	1647	uc002mbg.1_RNA	NM_018708	NP_061178	Q9BSK4	FEM1A_HUMAN		0	TGCTCTACCTGCT	0.652	
+	8	1180	p.S239N|ZNF557_	NM_001044388	NP_001037853	Q8N988	ZN557_HUMAN	C2H2-type 4.	2	ATGCAGTGACTC	0.438	
-	4	658_659	q.2_Missense_Mut	NM_021155	NP_066978	Q9NNX6	CD209_HUMAN	|5.|7 X approximate tanden	1	CAGCCGGGTCAC	0.564	rs141131967
+	3	395	2_uc002mix.1_Spl	NM_003083	NP_003074	Q13487	SNPC2_HUMAN		0	CGCAGGTACCG	0.363	
-	33	4279		NM_032447	NP_115823	Q75N90	FBN3_HUMAN	22; calcium-binding.	11	GGTTCTCACAGC	0.617	
-	1	2462		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).	57	CCTGTGGTAATAC	0.473	
-	2	80	nou.1_Missense_I	NM_030760	NP_110387	Q9H228	S1PR5_HUMAN	llular (By similarity).	2	GCGCCGGCCGC	0.716	
+	5	805	nse_Mutation_p.T	NM_001005361	NP_001005361	P50570	DYN2_HUMAN		6	GGGCACCGACG	0.567	
+	4	1932	e_Mutation_p.S62	NM_144566	NP_653167	Q9H0M5	ZN700_HUMAN	C2H2-type 14.	0	CTTCAGTTGTGC	0.483	
+	4	1934	e_Mutation_p.C62	NM_144566	NP_653167	Q9H0M5	ZN700_HUMAN	C2H2-type 14.	0	TCAGTTGTGCCT	0.483	
-	4	1148	799_uc002mts.3_I	NM_001080821	NP_001074290	Q96GE5	ZN799_HUMAN		6	CCATCTCTCGTG	0.413	
+	4	1289	yu.1_Missense_Mu	NM_153358	NP_699189	Q3KP31	ZN791_HUMAN	C2H2-type 10.	2	TGAAAGGACTC	0.378	
+	5	532	)2mvf.1_Missense_	NM_006397	NP_006388	O75792	RNH2A_HUMAN		3	AGTTTTCCCGGG	0.537	
-	6	1128	kmr.1_Missense_M	NM_001375	NP_001366	O00115	DNS2A_HUMAN		0	GCTGGGCACACA	0.597	
+	3	210	ı_p.W29*|CD97_u	NM_078481	NP_510966	P48960	CD97_HUMAN	r (Potential).|EGF-like 1.	4	CGGTGGTGCCC	0.597	
-	19	2687	IR2_uc002mzr.1_M	NM_013447	NP_038475	Q9UHX3	EMR2_HUMAN	Name=6; (Potential).	4	ACCACGTGCAG	0.552	
-	12	1603	_Missense_Mutati	NM_013447	NP_038475	Q9UHX3	EMR2_HUMAN	cellular (Potential).	4	GCATCACTGCCT	0.502	
-	3	1963	)26_uc002nee.2_I	NM_004831	NP_004822	O95402	MED26_HUMAN		2	GTGTGTCCTGAC	0.617	
+	9	1440	_p.E438K|GTPBP3	NM_032620	NP_116009	Q969Y2	GTPB3_HUMAN		1	CGGCAGAGGCG	0.657	
+	3	320	I29C_uc010xps.1_	NM_173544	NP_775815	Q86XR2	NIBL2_HUMAN		0	CCTGCCTTGCT	0.622	
+	16	2574	_p.E756K|UPF1_u	NM_002911	NP_002902	Q92900	RENT1_HUMAN		2	CAAGAGGAGATT	0.582	
+	10	1018	3_5'Flank|KIAA089	NM_015329	NP_056144	Q9Y6X3	SCC4_HUMAN		0	TGCTGGACTGC	0.637	
+	8	2367	ıw.3_Missense_Mu	NM_153221	NP_694953	Q8IUL8	CILP2_HUMAN		1	TGGTCACGCTGG	0.701	
+	4	1601		NM_031218	NP_112495	P35789	ZNF93_HUMAN	C2H2-type 13.	1	CCCTTACTAAAC	0.358	

+	4	1708		NM_031218	NP_112495	P35789	ZNF93_HUMAN		1	ATACTAGAGAG	0.358	
-	4	1673		NM_001159293	NP_001152765	C9JHM3	C9JHM3_HUMAN		1	TTATGTCTAGTAA	0.408	rs151059862
-	4	1447	p.K353E|ZNF708_	NM_021269	NP_067092	P17019	ZN708_HUMAN		6	GTTTCTTTCCAG	0.343	
+	4	1693	429_uc010ecu.1_I	NM_001001415	NP_001001415	Q86V71	ZN429_HUMAN	2H2-type 14.	2	CTTTTATCCTGT	0.378	
+	4	1696	429_uc010ecu.1_I	NM_001001415	NP_001001415	Q86V71	ZN429_HUMAN	2H2-type 14.	2	TTATCCTGTCCT	0.378	
-	5	1579	qh.2_Missense_M	NM_173531	NP_775802	Q8IYN0	ZN100_HUMAN	2H2-type 11.	0	ACATTCGTCACA	0.408	
-	5	1789	208_uc002nqo.1_I	NM_007153	NP_009084				7	ACCTTAATAAAG	0.398	
-	4	762	1_Intron|ZNF208_	NM_007153	NP_009084				7	ACCTTCTTCAC	0.363	
+	4	1578	cy.2_Missense_M	NM_033468	NP_258429	Q9Y2Q1	ZN257_HUMAN	2H2-type 11.	0	TTAACCAGTCTT	0.408	
-	3	1913		NM_001001411	NP_001001411	Q8N7Q3	ZN676_HUMAN		0	TTGTAGGGTTTC	0.418	
-	7	2699		NM_001080409	NP_001073878				2	GTCGAGAAATTG	0.353	rs55891931
-	4	1027	rj.1_Missense_Mu	NM_003430	NP_003421	Q05481	ZNF91_HUMAN	C2H2-type 6.	0	GAAGAATGGCTA	0.413	
+	3	1819	rn.1_Missense_M	NM_001136156	NP_001129628	Q8TCN5	ZN507_HUMAN		5	CCTGGGGCACT	0.423	
+	3	1827	rn.1_Nonsense_M	NM_001136156	NP_001129628	Q8TCN5	ZN507_HUMAN		5	CACTATGGAGAT	0.418	
+	10	2834		NM_014686	NP_055501	O15063	K0355_HUMAN		1	ACATGGGCCAG	0.517	
+	10	1082	p.D211N|UBA2_u	NM_005499	NP_005490	Q9UBT2	SAE2_HUMAN		1	AGGGGGATGGA	0.408	
+	3	432	e_Mutation_p.E81	NM_001037	NP_001028	Q07699	SCN1B_HUMAN	Potential).|Ig-like C2-type.	2	AGCTGGAGGAG	0.577	
+	10	2335	efi.2_Missense_Mutation_p.T411I|uc010efj.2_Missens			Q3ZCX4	ZN568_HUMAN		2	ACTCACACATC	0.463	
-	5	899	_p.F168Y|ZNF585	NM_199126	NP_954577	Q6P3V2	Z585A_HUMAN	C2H2-type 3.	3	AAGAGAAGCCT	0.423	
+	9	3018		NM_015073	NP_055888	O60292	SI1L3_HUMAN		2	ACACCCCCATC	0.582	
+	2	996	gn.1_Missense_M	NM_003407	NP_003398	P26651	TTP_HUMAN		1	AGCCCCCCGGC	0.617	
+	10	911	nse_Mutation_p.V	NM_138392	NP_612401	Q8TBC3	SHKB1_HUMAN	WD 2.	2	TGGGGGTGCCT	0.602	
+	6	935		NM_000766	NP_000757	Q16696	CP2AD_HUMAN		3	GCACCACCCTGC	0.562	
+	3	1127	.2_Missense_Muta	NM_199285	NP_954979	A6NJB7	PRR19_HUMAN	Pro-rich.	0	CACTGCGCACA	0.587	
-	2	519	e_Mutation_p.R13	NM_002781	NP_002772	Q15238	PSG5_HUMAN	g-like V-type.	3	TAGTCCTATCAC	0.473	
-	2	754	v.2_Nonsense_Mu	NM_001007561	NP_001007562	Q8WZA9	IRGQ_HUMAN		2	CGCACCCACGA	0.672	
-	4	719	_p.P126S|C19orf6	NM_019108	NP_061981	Q9H0W8	SMG9_HUMAN	Pro-rich.	0	AGGGGGTGGTG	0.682	
-	2	602	.2_5'Flank|KCNN4	NM_002250	NP_002241	O15554	KCNN4_HUMAN	=Segment S2; (Potential).	2	AGAAGGTGGAA	0.607	
-	4	1994	_p.R632K|ZNF45_	NM_003425	NP_003416	Q02386	ZNF45_HUMAN	2H2-type 17.	1	TGAACTCTTTGA	0.483	
+	5	971	p.G256R|ZNF155_	NM_003445	NP_003436	Q12901	ZN155_HUMAN		2	ACACAGGAGAG	0.423	
+	3	518	y.1_Missense_Mu	NM_177417	NP_803136	Q6P597	KLC3_HUMAN	Potential.	1	GCGAGGAGTCC	0.721	
+	8	1004	e_Site|SAE1_uc0	NM_016402	NP_057486	Q9UBE0	SAE1_HUMAN		1	TGAAGGTAAAA	0.453	
+	3	409	X_uc010elm.1_R	NM_000554	NP_000545	O43186	CRX_HUMAN	Homeobox.	2	ATGCCCGTGAG	0.632	
-	4	943	A4_uc002pjo.2_5	NM_017708	NP_060178	Q2M2I3	FA83E_HUMAN		1	GCGCAGGTGGG	0.721	
-	2	498	UVBL2_uc002plq.	NM_002103	NP_002094	P13807	GYS1_HUMAN		2	TCAGGGCCGGG	0.667	
-	3	325		NM_000894	NP_000885	P01229	LSHB_HUMAN		0	GCTGAGAGCCA	0.662	
-	2	214	H2_uc002prv.3_Ir	NM_004851	NP_004842	O96009	NAPSA_HUMAN		0	ACTTGGGGAGC	0.587	
-	5	944	ydc.1_Missense_	NM_001245	NP_001236	O43699	SIGL6_HUMAN	2.|Extracellular (Potential).	1	GGAGGGACGAG	0.602	
+	4	1894	po.1_Intron|ZNF5	NM_001143939	NP_001137411	Q76KX8	ZN534_HUMAN	2H2-type 15.	0	TAGGAAAATTCA	0.423	
+	6	1245		NM_001099694	NP_001093164	Q96N58	ZN578_HUMAN	C2H2-type 4.	0	CCATCATAGGT	0.428	
-	7	2083	p.S520N|ZNF611_	NM_030972	NP_112234	Q8N823	ZN611_HUMAN		1	TCACCACTATGA	0.433	
-	7	1479	au.2_Missense_	NR_028343		Q09FC8	ZN415_HUMAN	C2H2-type 5.	1	TTACATGTGTAA	0.403	rs147077991
+	3	178	dw.1_Missense_	NM_138374	NP_612383	Q96IR2	ZN845_HUMAN	KRAB.	0	AGGAAGAGTGG	0.463	
+	11	1218	fr.2_Missense_Mu	NM_020659	NP_065710	Q9H313	TTYH1_HUMAN	ellular (Potential).	0	CTCAGGACTAT	0.587	
+	6	1237	e_Mutation_p.G38	NM_001130917	NP_001124389	Q8N149	LIRA2_HUMAN	4.|Extracellular (Potential).	1	CATGGGTCCTG	0.597	
-	7	823	0_splice|C19orf51_uc002qjk.1_Splice_Site_p.Y209_spl			Q8N9W5	CS051_HUMAN		0	ACGCACGTAGC	0.652	
+	2	1207	_Mutation_p.S164	NM_016535	NP_057619	Q9P0T4	ZN581_HUMAN	C2H2-type 3.	0	GCACAGCCGGG	0.667	

-	3	239		NM_001002836	NP_001002836	Q6DD87	ZN787_HUMAN	Pro-rich.		1	GGAGGCCAGCT	0.463	
-	3	228		NM_001002836	NP_001002836	Q6DD87	ZN787_HUMAN			1	GGGGACGTCGT	0.468	
+	4	1463	gu.1_Missense_M	NM_001023563	NP_001018857	Q5CZA5	ZN805_HUMAN	2H2-type 8.		0	CCAGCGGATTC	0.512	
+	4	1342	ud.1_Intron|ZNF5	NM_153263	NP_694995	Q6P9A3	ZN549_HUMAN	2H2-type 6.		1	GTATGGAATGT	0.443	
-	2	299	.2_Intron|ZNF154	NM_001085384	NP_001078853	Q13106	ZN154_HUMAN	KRAB.		0	GTACGGCCACA	0.512	
+	7	540	G2_uc010ewi.2_I	NM_018968	NP_061841	Q9NY99	SNTG2_HUMAN			3	TGACAGGTGCA	0.428	
+	9	727	wi.2_Missense_	NM_018968	NP_061841	Q9NY99	SNTG2_HUMAN		p.S200L(1)	3	CCCATCGTCAC	0.567	rs6751090
+	20	2748	t.2_Missense_Mu	NM_145693	NP_663731	Q14693	LPIN1_HUMAN	C-LIP.		4	TAAAGGAGAGC	0.348	
-	17	1918	R35_uc002rdh.2_	NM_001006657	NP_001006658	Q9P2L0	WDR35_HUMAN			1	ATTATCTTTGG	0.398	
-	37	4927	f.2_Missense_Mut	NM_006277	NP_006268	Q9NZM3	ITSN2_HUMAN	C2.		4	GTAAGCTTTCT	0.617	
-	33	4307	f.2_Missense_Mut	NM_006277	NP_006268	Q9NZM3	ITSN2_HUMAN	DH.		4	GCATGGGTTTC	0.577	
-	3	314		NM_194248	NP_919224	Q9HC10	OTOF_HUMAN	lasmic (Potential).		7	AATCTCCAGCA	0.577	
-	10	959		NM_000379	NP_000370	P47989	XDH_HUMAN	inding PCMH-type.		8	GTCGGGTCCAT	0.517	
-	8	1074	zq.2_Missense_M	NM_015955	NP_057039	Q9Y316	MEMO1_HUMAN			2	TAAAAGATACA	0.249	
+	46	9054		NM_016252	NP_057336	Q9NR09	BIRC6_HUMAN			14	GTGTTCAAGGA	0.453	
+	13	2405	.2_Missense_Mut	NM_206943	NP_996826	Q14766	LTBP1_HUMAN			8	AACTGCACCCC	0.289	
-	12	2082	A_uc010fat.1_5'F	NM_001083953	NP_001077422	Q6YHU6	THADA_HUMAN			3	TTGTCCTGAAA	0.383	
+	4	2601	p.D515N|MSH6_u	NM_000179	NP_000170	P52701	MSH6_HUMAN			168	TTCCAGATCTT	0.413	
+	16	3491	xx.2_Missense_M	NM_003128	NP_003119	Q01082	SPTB2_HUMAN	Spectrin 8.		8	TAGGACCCAGA	0.582	
-	3	1136	p.A74T|RTN4_uc	NM_020532	NP_065393	Q9NQC3	RTN4_HUMAN	lasmic (Potential).		3	TTTTTGCCTTCT	0.373	
-	12	1426	p.G276D|CCT4_u	NM_006430	NP_006421	P50991	TCPD_HUMAN			2	GAGCACCACCT	0.328	
+	6	1034	.G232D|UGP2_u	NM_006759	NP_006750	Q16851	UGPA_HUMAN			0	AGAAGGCAAAG	0.403	
+	3	945	LC1A4_uc010fcv.	NM_003038	NP_003029	P43007	SATT_HUMAN	ellular (Potential).		1	TGTAACCCATG	0.378	
+	11	1009	e_Mutation_p.P2	NM_006062	NP_006053	Q6GMV2	SMYD5_HUMAN	SET.		0	CTTTCCAGAAA	0.478	
+	7	1421	jf.1_Missense_Mu	NM_015120	NP_055935	Q8TCU4	ALMS1_HUMAN			9	TTGTATGCAGTG	0.388	
-	16	2251	se_Mutation_p.L7	NM_021196	NP_067019	Q9BY07	S4A5_HUMAN	ical; (Potential).		9	AGAAAAGGATG	0.532	
-	25	4083	p.G601D|POLR1A	NM_015425	NP_056240	O95602	RPA1_HUMAN			3	CTCTGCCTGCA	0.632	
-	5	1073		NM_004836	NP_004827	Q9NZJ5	E2AK3_HUMAN	enal (Potential).		3	AGACTCTTCTGT	0.403	
+	23	2615	M2_uc002suk.2_	NM_144707	NP_653308	Q8N271	PROM2_HUMAN	lasmic (Potential).		1	TCCCCCGGGTT	0.592	
-	27	3195		NM_015348	NP_056163	Q92545	TM131_HUMAN			6	GTAAGGAGCTT	0.423	
+	4	969		NM_015904	NP_056988	O60841	IF2P_HUMAN			3	AACAGGTAAAA	0.388	
-	6	1086	SD9_uc010fja.2_	NM_032718	NP_116107	Q8NBP5	MFSD9_HUMAN	ical; (Potential).		4	TGGCCCCAGGG	0.632	
-	22	5171		NM_001144013	NP_001137485	A6NKT7	RGPD3_HUMAN	GRIP.		1	CAGACACCTCT	0.393	rs143574937
+	11	3499	ed.2_Splice_Site_	NM_181453	NP_852118	Q8IWJ2	GCC2_HUMAN			1	ATAAAGGTAAAA	0.294	
+	20	6923		NM_006267	NP_006258	P49792	RBP2_HUMAN			18	AACAGGATTTA	0.413	
+	9	1531	hl.1_Missense_M	NM_006343	NP_006334	Q12866	MERTK_HUMAN	III 2.|Extracellular (Potentia		9	AGTTGGGCCCT	0.532	
+	1	597	R6Q|POLR1B_uc0	NM_019014	NP_061887	Q9H9Y6	RPA2_HUMAN			1	CAGCCGGTGGC	0.642	
+	15	3942	kp.2_Missense_M	NM_019014	NP_061887	Q9H9Y6	RPA2_HUMAN			1	TGTAGCTGAACT	0.383	
-	8	1254	35F5_uc002tkt.2_	NM_025181	NP_079457	Q8WV83	S35F5_HUMAN	Helical; (Potential).		0	TACCGGAAGTT	0.284	
+	16	1393	yf.1_Missense_M	NM_006770	NP_006761	Q9UEW3	MARCO_HUMAN	ellular (Potential).		6	AAAACTCAGTG	0.512	
-	3	707		NM_001099771	NP_001093241	A5A3E0	POTEF_HUMAN			5	GTGGCAGCACC	0.617	
+	5	377	tua.2_Missense_	NM_138326	NP_612199	Q8TDX5	ACMSD_HUMAN			1	GCACCGTTGTG	0.562	
-	28	5578	l.1_Missense_Mu	NM_018557	NP_061027	Q9NZR2	LRP1B_HUMAN	ellular (Potential).		50	CTTTGCCATCAT	0.468	
-	8	3358	e_Mutation_p.G93	NM_014795	NP_055610	O60315	ZEB2_HUMAN			9	AAATCCTTGTTT	0.388	
+	6	834		NM_004522	NP_004513	O60282	KIF5C_HUMAN	inesin-motor.		1	TGGCTGTTCAT	0.333	
+	13	1707	.1_RNA|KIF5C_u	NM_004522	NP_004513	O60282	KIF5C_HUMAN			1	TGAAGCAACAG	0.343	
+	5	653	z.2_RNA|LYPD6_	NM_194317	NP_919298	Q86Y78	LYPD6_HUMAN			0	GCACCCACGCT	0.473	

+	18	3266	C1_uc010fom.1_M	NM_033394	NP_203752	Q9C0D5	TANC1_HUMAN		3	CACTTGGATAAGA	0.587	
+	3	1248	y.2_Missense_Mu	NM_006593	NP_006584	Q16650	TBR1_HUMAN	T-box.	2	AACAAAGGAGCT	0.478	
-	27	5786	uc002udp.2_Intron	NM_002977	NP_002968	Q15858	SCN9A_HUMAN		13	CAGATCCATGGC	0.463	
+	8	4081	e_Mutation_p.E11	NM_152381	NP_689594	A4UGR9	XIRP2_HUMAN	Xin 23.	14	CTTTTTGAAACA	0.378	
+	1	758	D10_uc010zdh.1_	NM_006063	NP_006054	O60662	KBTBA_HUMAN		0	CCTTATGACAGA	0.358	
-	2	464	ufp.2_Missense_M	NM_014168	NP_054887	Q9NRN9	METL5_HUMAN		1	CCTGCTCCTAAC	0.378	
+	27	3926	.C130Y|UBR3_uc	NM_172070	NP_742067	Q6ZT12	UBR3_HUMAN	-type; degenerate.	0	GTTCATGTCTCTT	0.303	
+	2	153	_Missense_Mutati	NM_138995	NP_620482	Q8WXR4	MYO3B_HUMAN		19	AAACATCTGTAT	0.393	
+	3	456	.2_Missense_Muta	NM_138995	NP_620482	Q8WXR4	MYO3B_HUMAN	rotein kinase.	19	GGCTGGTCCTG	0.448	
+	31	3748	_Mutation_p.G117	NM_138995	NP_620482	Q8WXR4	MYO3B_HUMAN		19	CAAAAGGGTGCG	0.358	
-	10	1092	0fqh.2_Missense_	NM_003705	NP_003696	O75746	CMC1_HUMAN	ical; Name=1; (Potential).	0	AGCAACTGAGC	0.473	
+	22	3027	o.1_Missense_Mu	NM_001079818	NP_001073286	P23229	ITA6_HUMAN	cellular (Potential).	2	CGCTGCGGGGG	0.473	
+	6	845	2uld.2_Missense_	NM_194247	NP_919223	P51991	ROA3_HUMAN	Gly-rich.	2	GGAAGAGGTAGG	0.408	
-	112	27716	_uc002umz.1_Mis	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	TGGAACTTTTCT	0.343	
-	56	13947	N_uc010zfj.1_Intro	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	CTTTTACTGAGA	0.423	
-	30	7137	TN_uc010zfj.1_Mi	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	TAAGCTCCACAT	0.403	
+	4	839	P19_uc010zfr.1_F	NM_080876	NP_543152	Q8WTR2	DUS19_HUMAN	protein phosphatase.	5	GCGTTTCCAGGG	0.338	
-	4	639	se_Mutation_p.R84	NM_007315	NP_009330	P42224	STAT1_HUMAN		10	CTTTTCCTTATGT	0.373	
-	22	1934	lissense_Mutation_	NM_033066	NP_149055	Q96JB8	MPP4_HUMAN	kinase-like.|Potential.	0	GTAGGTCTTCAT	0.358	
-	17	1490	P4_uc010zhs.1_M	NM_033066	NP_149055	Q96JB8	MPP4_HUMAN	ylate kinase-like.	0	GAGGCGGTACT	0.557	
+	23	3484	ense_Mutation_p.F	NM_152526	NP_689739	Q8TEW8	PAR3L_HUMAN		4	GCAGATCCTGTA	0.433	
-	11	1520	_p.E488K|MDH1B_	NM_001039845	NP_001034934	Q5I0G3	MDH1B_HUMAN		4	GAAACTCTGCTG	0.343	
-	2	1287		NM_003468	NP_003459	Q13467	FZD5_HUMAN	cellular (Potential).	3	GGCATGGCCCA	0.627	
+	32	5185		NM_015040	NP_055855	Q9Y2I7	FYV1_HUMAN		10	CTCTCAGGTATTA	0.353	
-	3	376	eb.2_Missense_Mu	NM_079420	NP_524144	P05976	MYL1_HUMAN	EF-hand 1.	1	TGTGCCCAGAG	0.468	
+	11	1179	_p.Q61*|VIL1_uc	NM_007127	NP_009058	P09327	VILI_HUMAN	Core.	1	GTGGAACAGGTG	0.443	
+	11	1537		NM_031313	NP_112603	P10696	PPBN_HUMAN		1	CGACCTGGCGC	0.736	
+	5	598	yh.1_Missense_M	NM_152879	NP_690618	Q16760	DGKD_HUMAN	l-ester/DAG-type 1.	5	GCGAGGGTACG	0.537	
+	4	2098	p.V569M|SH3BP4	NM_014521	NP_055336	Q9P0V3	SH3B4_HUMAN		4	GCAAGGTGAGC	0.562	
+	7	1041	_p.D124N|COPS8_	NM_006710	NP_006701	Q99627	CSN8_HUMAN		1	GCCCTGGATGTT	0.299	
-	36	7540	_Mutation_p.G181	NM_004369	NP_004360	P12111	CO6A3_HUMAN	1.|Nonhelical region.	18	CCGGCCGAAAG	0.567	
+	7	1041	Missense_Mutatio	NM_024101	NP_077006	Q9BV36	MELPH_HUMAN		1	ACGGCGCCCTG	0.667	
+	10	2079	_Missense_Mutati	NM_023083	NP_075571	Q9HC96	CAN10_HUMAN	Domain III 2.	6	CCTGCCGGACA	0.672	
-	7	1694	se_Mutation_p.A2	NM_016143	NP_057227	Q9UNZ2	NSF1C_HUMAN		0	TGAAGGCTCCT	0.577	
+	14	1869	w.1_Nonsense_M	NM_080751	NP_542789	Q8TDI7	TMC2_HUMAN	lasmic (Potential).	3	GTGCTGGGACTT	0.493	
+	5	1174	wkp.2_Missense_	NM_175839	NP_787033	Q9NWM0	SMOX_HUMAN		1	ATCCCGGCGGAC	0.637	
+	2	991	_p.V210I|PRNP_	NM_001080122	NP_001073591	P04156	PRIO_HUMAN	2, ERI3 and SYN1 (By simi	1	CGCGTGGTTGAG	0.537	rs74315407
+	1	660	Mutation_p.G40S|	NM_014962	NP_055777	Q9Y2F9	BTBD3_HUMAN		3	TGGCAGGGTCTT	0.483	
+	4	1293	zrf.1_Missense_M	NM_014962	NP_055777	Q9Y2F9	BTBD3_HUMAN		3	GCAAGGTTCTA	0.458	
-	8	1720	zrn.1_Nonsense_M	NM_001195	NP_001186	Q12934	BFSP1_HUMAN	Tail.	1	CACCCTCACGTT	0.557	
-	8	1597	zrn.1_Missense_M	NM_001195	NP_001186	Q12934	BFSP1_HUMAN	Tail.	1	TAAAGGGGGCT	0.542	
+	7	1111	N2_uc010gcv.1_M	NM_018993	NP_061866	Q8WYP3	RIN2_HUMAN		5	CTCCACCCCGG	0.612	
+	22	2774	e_Mutation_p.D88	NM_015585	NP_056400	Q8NHU2	CT026_HUMAN		4	ACCGGGATGCG	0.642	
+	10	1633	lv.1_Missense_Mu	NM_012112	NP_036244	Q9ULW0	TPX2_HUMAN		2	CCAAGGAAAGA	0.423	
+	11	1804	eb.2_Missense_Mu	NM_015338	NP_056153	Q8IXJ9	ASXL1_HUMAN		248	CAGCAGGGCTG	0.567	
+	15	2442	se_Mutation_p.A7	NM_032819	NP_116208	Q9BYN7	ZN341_HUMAN		2	GTGGTGCGGTG	0.706	
+	17	1884	23_splice|ITCH_u	NM_031483	NP_113671	Q96J02	ITCH_HUMAN		6	CAACAGGTACTG	0.408	

-	12	6301	aw.2_Missense_M	NM_014071	NP_054790	Q14686	NCOA6_HUMAN	1-binding region.		7	CATTGAGTCTTT	0.483	
+	27	4273	APB_uc002xiy.1_	NM_020336	NP_065069	Q86X10	RLGPB_HUMAN	Rap-GAP.		2	TGGACCTGAGA	0.458	
+	2	798		NM_080552	NP_542119	Q9H598	VIAAT_HUMAN	l, vesicle (Potential).		0	GCGAGGTGGTG	0.627	
+	7	866	tm.2_Missense_M	NM_181659	NP_858045	Q9Y6Q9	NCOA3_HUMAN			5	CAGAGATATGAA	0.408	
+	15	1846	_p.E246K|SLC9A8	NM_015266	NP_056081	Q9Y2E8	SL9A8_HUMAN			1	CGCAGGAGGTG	0.647	
-	9	754	e_Mutation_p.G18	NM_003859	NP_003850	O60762	DPM1_HUMAN			1	ATAATCCTTTCAA	0.308	
+	7	1448	zzi.1_Missense_M	NM_003222	NP_003213	Q92754	AP2C_HUMAN	span-helix), dimerization.		1	TGGCAGCCAGG	0.552	
-	3	691	xys.2_Missense_	NM_020182	NP_064567	Q969W9	PMEPA_HUMAN	lasmic (Potential).		1	GCCTGACACTG	0.642	
+	6	819	p.1_Missense_Mu	NM_001794	NP_001785	P55283	CADH4_HUMAN	|Extracellular (Potential).		6	TCATCGACATG	0.567	
+	7	921	p.1_Missense_Mu	NM_001794	NP_001785	P55283	CADH4_HUMAN	(Potential).|Cadherin 2.		6	CCAACGATGCT	0.632	
-	1	283	CFL5_uc002ydq.	NM_006602	NP_006593	Q9UL49	TCFL5_HUMAN			1	CATGTGCGAGC	0.443	
-	16	6390_6391	s.1_Missense_Mu	NM_033081	NP_149072	Q9BTC0	DIDO1_HUMAN			6	GGCCTCCTCCC	0.738	
+	18	2580	cm.1_Nonsense_	NM_006447	NP_006438	Q9Y5T5	UBP16_HUMAN			4	GCAGTGGTTTC	0.343	
-	5	834	M1_uc011adl.1_M	NM_003253	NP_003244	Q13009	TIAM1_HUMAN			10	CAGAGGCTGCT	0.562	
-	3	578	_p.P34L|RCAN1_	NM_004414	NP_004405	P53805	RCAN1_HUMAN			0	CCACTGGCGGA	0.542	
-	3	432	wo.2_Missense_M	NM_002240	NP_002231	P48051	IRK6_HUMAN	llular (By similarity).		1	GGAGGGGTCCT	0.458	
-	22	4408	CAM_uc002yyr.1_	NM_001389	NP_001380	O60469	DSCAM_HUMAN	otential).|Ig-like C2-type 10		11	TTCATCCATTTGA	0.458	
+	3	456	2_5'UTR|PCNT_u	NM_006031	NP_006022	O95613	PCNT_HUMAN			8	AGCAGTGTGGG	0.547	
+	5	674	qt.2_Missense_M	NM_014339	NP_055154	Q96F46	I17RA_HUMAN	ellular (Potential).		2	AATTTCCTTGTG	0.572	
-	3	687	issense_Mutation_	NM_015241	NP_056056	Q7RTP6	MICA3_HUMAN	D (Potential).		0	AACCACCTTGG	0.527	
+	3	353	1_5'UTR|MYO18	NM_032608	NP_115997	Q8IUG5	MY18B_HUMAN			12	TCCCAGGGGGC	0.542	
+	4	1755	FH_uc003afp.2_In	NM_021076	NP_066554	P12036	NFH_HUMAN	-S-P-[AEPV]-[EAK]- [AEVK		0	CACCGCCTGAG	0.567	
-	3	231	14L3_uc003aia.2_	NM_174975	NP_777635	Q9UDX4	S14L3_HUMAN			5	CAAGTCAAAATT	0.532	
+	5	633	se_Mutation_p.R1	NM_005569	NP_005560	P53671	LIMK2_HUMAN	PDZ.		2	CAGGCGGGGCT	0.562	
-	2	182	03alb.1_Missense_	NM_019843	NP_062817	Q9NRA8	4ET_HUMAN			1	TTCACCCATACTT	0.443	
+	22	1854	3alt.2_Missense_	NM_014662	NP_055477	O75140	DEPD5_HUMAN			8	CAGTGCACCAG	0.522	
+	2	1207	g.1_Missense_Mu	NM_001008494	NP_001008494	Q2M1V0	ISX_HUMAN	Homeobox.		5	AGGGTTCGTACC	0.557	
-	13	1853	xp.2_Missense_M	NM_001098504	NP_001091974	Q92841	DDX17_HUMAN			4	ACTCATCCTGAT	0.473	
-	10	1194	p.R304W|SUN2_u	NM_015374	NP_056189	Q9UH99	SUN2_HUMAN	inuclear space.		2	CAGCCGCATGG	0.642	
+	30	5431		NM_001429	NP_001420	Q09472	EP300_HUMAN	or E1A adenovirus.|ZZ-typ		64	GGAGACACGCT	0.582	
+	4	722		NM_014460	NP_055275	Q9Y534	CSDC2_HUMAN			0	CACTCCCCACG	0.652	
-	8	956	p.W273*|NAGA_u	NM_000262	NP_000253	P17050	NAGAB_HUMAN			1	ACCGTCCACAG	0.557	rs144669656
-	2	363		NM_002490	NP_002481	P56556	NDUA6_HUMAN			0	GGGGTCTGTGA	0.438	
-	19	2436	se_Mutation_p.E5	NM_022785	NP_073622	Q5THR3	EFCB6_HUMAN	EF-hand 8.		7	TGACTCCTTCA	0.562	
-	13	1149		NM_001001694	NP_001001694	Q6ZVW7	I17EL_HUMAN			1	CTGTGACTTCCT	0.647	
+	16	2201	e_Mutation_p.R68	NM_018995	NP_061868	Q9BXT6	M10L1_HUMAN			3	GAGAGGCGTGT	0.473	
+	5	496	NTN4_uc003bpd.	NM_175607	NP_783200	Q8IWV2	CNTN4_HUMAN	like C2-type	p.K92N(1)	7	TAAAACCCAAG	0.413	
+	2	298	TAC_uc011aya.1_	NM_003149	NP_003140	Q99469	STAC_HUMAN			4	CACTCCCTGCT	0.557	rs149439391
-	8	3747		NM_014831	NP_055646	O15050	TRNK1_HUMAN	TPR 3.		2	CGCAGGAGTTG	0.458	
-	10	1394		NM_144719	NP_653320	Q8IYE1	CCD13_HUMAN	Potential.		1	TCAGCTACCATG	0.597	
-	1	1541	mg.2_Intron|CYP8	NM_004391	NP_004382	Q9UNU6	CP8B1_HUMAN			2	AGCGATCGTACT	0.557	
-	1	715	_5'Flank|ARIH2_	NM_001123040	NP_001116512	Q8N7S6	CC071_HUMAN			0	GAATAGTGGCT	0.592	
+	2	1640	hkn.2_Missense_	NM_018031	NP_060501	Q9NNW5	WDR6_HUMAN	WD 7.		1	CGCACCCTCTG	0.607	
-	5	588	r.2_Missense_Mu	NM_003363	NP_003354	Q13107	UBP4_HUMAN			4	GCTTCCGCATC	0.488	rs117411669
+	6	483	1_5'Flank|RNF123	NM_022064	NP_071347	Q5XPI4	RN123_HUMAN			7	CAAAGGTGAGA	0.557	
-	18	3916	dc.1_Missense_M	NM_002447	NP_002438	Q04912	RON_HUMAN	Potential).|Protein kinase.		6	TGACTCGTCCA	0.517	
-	11	2459	t.1_Missense_Mu	NM_015576	NP_056391	O15083	ERC2_HUMAN	Potential.		2	CACCTCCTTGA	0.468	

-	12	1617	7_uc003dkv.1_Mis	NM_198463	NP_940865	Q6ZVT6	CC067_HUMAN			0	CACTGCTGTCG	0.423	
+	28	4692	se_Mutation_p.P5	NM_002841	NP_002832	P23470	PTPRG_HUMAN	).|Tyrosine-protein phosph		7	ATGCCCCCATA	0.423	
-	15	2192	m.1_Nonsense_M	NM_000158	NP_000149	Q04446	GLGB_HUMAN			3	AACTCGGTAGT	0.363	
-	16	3441	e_Mutation_p.R94	NM_016247	NP_057331	Q9BZV3	IMPG2_HUMAN	ing motif involved in chon		3	CACCCGGCACC	0.507	
-	2	89		NM_018338	NP_060808	Q96MT7	WDR52_HUMAN			1	ATGTAACTGATTT	0.328	
+	2	314	ce|PLA1A_uc003	NM_015900	NP_056984	Q53H76	PLA1A_HUMAN			3	ATTCAGGTGGGA	0.433	
-	3	598		NM_001039783	NP_001034872	Q6F5E7	TR3N_HUMAN			0	CAGTGGTGTGG	0.552	
-	9	1610	q.1_Missense_Mu	NM_002950	NP_002941	P04843	RPN1_HUMAN	lasmic (Potential).		3	GTTGAGGGTGG	0.532	
+	37	4406		NM_015268	NP_056083	O75165	DJC13_HUMAN			2	TAGAGGTAATA	0.418	
-	6	1787	eqh.1_Missense_	NM_016201	NP_057285	Q9Y2J4	AMOL2_HUMAN	Potential.		1	CACAGGCTGCC	0.657	
+	5	666	A36_uc003etq.2_	NM_001104647	NP_001098117	Q96CQ1	S2536_HUMAN	Solcar 2.		0	AAAGACTCGGT	0.303	
+	3	1915		NM_003412	NP_003403	Q15915	ZIC1_HUMAN	Ser-rich.	p.S399C(1)	2	CCAGCTCTGGCT	0.617	
+	6	2032	aw.2_Missense_M	NM_015508	NP_056323	Q7Z3E1	PARPT_HUMAN	ARP catalytic.		2	GGGCAGATACA	0.353	
+	7	960	.W238*|CHRD_uc	NM_003741	NP_003732	Q9H2X0	CHRD_HUMAN	CHRD 1.		3	GTGTGGCGGGC	0.597	
+	7	832		NM_000412	NP_000403	P04196	HRG_HUMAN			2	ATGAGCGTTCTT	0.512	
-	2	303	_p.G27E|RFC4_u	NM_002916	NP_002907	P35249	RFC4_HUMAN			5	TACTTCCCGCA	0.443	
-	17	14793	_p.A470V|MUC4_	NM_018406	NP_060876	Q99102	MUC4_HUMAN	VWFD.		0	GTTCAGCCCAG	0.522	
-	15	14553	n_p.P390L|MUC4_	NM_018406	NP_060876	Q99102	MUC4_HUMAN	VWFD.		0	GGGCGGGAGG	0.721	
-	6	758	e.1_Intron|DLG1_	NM_001098424	NP_001091894	Q12959	DLG1_HUMAN	n with SH3 domains.		3	GGTGGGTAGGA	0.383	
+	12	2783	GG_uc010ibf.2_M	NM_001127178	NP_001120650	Q5H8A4	PIGG_HUMAN	ical; (Potential).		4	TCCCAGCCGTG	0.587	
-	4	410	ense_Mutation_p.	NM_006527	NP_006518	Q14493	SLBP_HUMAN	calization signal NLS2.		0	TGAGGAGTTTCC	0.353	
+	8	1079	fk.3_Missense_M	NM_001122681	NP_001116153	P78314	3BP2_HUMAN			1	CAGTGCTGCCA	0.667	
-	5	909	bwe.1_Missense_	NM_020416	NP_065149	Q9Y2T4	2ABG_HUMAN	WD 3.		4	TGACGGAGATG	0.572	
+	11	1696	p.E554K|MAN2B2	NM_015274	NP_056089	Q9Y2E5	MA2B2_HUMAN			2	CCCAGGAGCCG	0.612	
+	12	2734	R802Q|SH3TC1_u	NM_018986	NP_061859	Q8TE82	S3TC1_HUMAN	TPR 5.		3	GGGCCGGACGA	0.677	
-	24	4242		NM_015230	NP_056045	Q8WZ64	ARAP2_HUMAN			3	CTTGATCTTCTT	0.303	
-	9	1426		NM_173536	NP_775807	Q8N1C3	GBRG1_HUMAN	lasmic (Probable).		2	AAGATCCTGTT	0.408	rs75184362
+	12	1798	zl.1_Missense_Mu	NM_025087	NP_079363	Q9H720	PG2IP_HUMAN			3	TTCGGGCAAGC	0.458	
-	4	1506		NM_001024611	NP_001019782	Q68CR7	LRC66_HUMAN			3	CACTTCCTGCC	0.542	
-	7	868		NM_005420	NP_005411	P49888	ST1E1_HUMAN			1	AGGGCGACAAT	0.398	
+	7	1379	p.D280N|RUFY3_	NM_014961	NP_055776	Q7L099	RUFY3_HUMAN			0	TTCTGGACCAG	0.378	
+	19	2738	ce_Site_p.R874_s	NM_001098484	NP_001091954	Q9Y6R1	S4A4_HUMAN			5	GTGAGGTGTGT	0.468	
+	7	5643	hkg.2_Missense_	NM_020859	NP_065910	Q8TF72	SHRM3_HUMAN			3	AGGATCCCGAG	0.622	
+	62	9831	lc.1_Missense_Mu	NM_025074	NP_079350	Q86XX4	FRAS1_HUMAN	|Extracellular (Potential).		5	CACTAGTCCTTG	0.488	
+	16	3425	PAQR3_uc003hln.	NM_198892	NP_942595	Q9NSY1	BMP2K_HUMAN			1	ATCAGGGCCTG	0.522	
+	2	397	.2_5'UTR|ENOPH	NM_021204	NP_067027	Q9UHY7	ENOPH_HUMAN			0	ACATTGGGAAG	0.383	
-	8	976	j.2_Missense_Mut	NM_001077207	NP_001070675	O94979	SC31A_HUMAN	n with SEC13.|WD 5.		8	GATCTGCCATG	0.398	
-	9	1227	ense_Mutation_p.	NM_139076	NP_620775	Q6UWZ7	F175A_HUMAN			1	TTTCTGGGCTGC	0.358	
-	60	9460	pe.1_Missense_M	NM_014991	NP_055806	Q8IZQ1	WDFY3_HUMAN			3	CTTTGAGTTCTA	0.338	
-	3	516	N5_uc011cdz.1_5	NM_005723	NP_005714	P62079	TSN5_HUMAN	ellular (Potential).		0	GCCGAGATCGG	0.502	
-	8	748	_Mutation_p.S177	NM_016242	NP_057326	Q9ULC0	MUCEN_HUMAN	ellular (Potential).		0	ATAATACCTAAAA	0.398	
+	38	7859	.3_Intron|ANK2_u	NM_001148	NP_001139	Q01484	ANK2_HUMAN			14	GAAGAGGAGATG	0.383	
-	3	712		NM_003619	NP_003610	P56730	NETR_HUMAN	SRCR 1.		1	ACGGGGTTTGT	0.373	
+	19	2293	0ins.1_Missense_	NM_015312	NP_056127	Q2LD37	K1109_HUMAN			12	TTATAGGAAAACT	0.343	
+	4	963	LK2_uc003ilo.3_	NM_001040260	NP_001035350	Q8N568	DCLK2_HUMAN			3	AGAATGTCGTG	0.408	
+	9	944	98_splice|KIAA092	NM_015196	NP_056011	A2VDJ0	T131L_HUMAN			2	CTCAGGTAAGG	0.303	
+	3	1382	p.S388F|TLR2_uc	NM_003264	NP_003255	O60603	TLR2_HUMAN	tracellular (Potential).		3	GCCCTCTCTAC	0.348	

+	7	1129	p.E302K|FGB_uc	NM_005141	NP_005132	P02675	FIBB_HUMAN	ogen C-terminal.		3	AGAATGAAGCC	0.463	
+	17	2042	jd.1_Nonsense_M	NM_021634	NP_067647	Q9HBX9	RXFP1_HUMAN	Name=7; (Potential).		0	TGCTTCAGGTA	0.274	
-	2	625	e_Mutation_p.S14	NM_138386	NP_612395	Q96HR8	NAF1_HUMAN	Ser-rich.		2	ACaagaggaagaag	0.249	
-	4	553		NM_001100389	NP_001093859	Q8IY95	TM192_HUMAN	ical; (Potential).		1	GAGGAGAAGCA	0.408	
+	12	2038	p.G464D|TLL1_uc	NM_012464	NP_036596	O43897	TLL1_HUMAN	CUB 2.		7	TGGAGGTGAGA	0.388	
+	31	4096	e_Mutation_p.G12	NM_170710	NP_733828	Q8IZU2	WDR17_HUMAN			6	CTTTAGGGACT	0.393	
+	12	1560	5_splice|KLKB1_	NM_000892	NP_000883	P03952	KLKB1_HUMAN			1	ACTGGTATGTA	0.383	
+	5	736	.2_Missense_Mut	NM_000128	NP_000119	P03951	FA11_HUMAN	Apple 2.		0	CTCAAGAATGC	0.478	rs121965063
+	20	4872	k.3_Missense_Mu	NM_133433	NP_597677	Q6KC79	NIPBL_HUMAN			9	TTTTTACTTCACT	0.289	
-	7	1208	mb.2_Missense_M	NM_006251	NP_006242	Q13131	AAPK1_HUMAN			1	TTACACCTTGG	0.403	
+	3	2483		NM_032587	NP_115976	Q9BX69	CARD6_HUMAN			5	ATTTTCCAGAG	0.468	
+	24	2777	p.W869*|TNPO1_	NM_002270	NP_002261	Q92973	TNPO1_HUMAN			7	AAATTGGAGGC	0.353	
+	11	1522	p.E476K|HMGCR_	NM_000859	NP_000850	P04035	HMDH_HUMAN	Catalytic.		1	ATGCAGAGGTG	0.348	
+	1	292	uc011ctk.1_RNA	NM_032567	NP_115956	Q9BXG8	SPZ1_HUMAN			1	CAAAACCGTTA	0.483	
-	3	786_787	in.2_Missense_M	NM_001884	NP_001875	P10915	HPLN1_HUMAN	Link 1.	p.G239E(1)	5	AAAATCCGTAGT	0.455	rs139074313
-	8	1290	K1_uc010jbi.1_In	NM_000439	NP_000430	P29120	NEC1_HUMAN	Catalytic.		2	CTGGTCGGTGT	0.517	
-	6	953	e_Mutation_p.R14	NM_017676	NP_060146	Q9NXP7	GIN1_HUMAN	grase catalytic.		2	ATTTCGACTAA	0.299	
+	13	1672	R36_uc010jbu.2_	NM_139281	NP_644810	Q8NI36	WDR36_HUMAN	WD 6.		2	ACTGTAGATGTA	0.338	
+	7	638	_Mutation_p.P18	NM_001744	NP_001735	Q16566	KCC4_HUMAN	rotein kinase.		5	TGCACCACTCA	0.373	
+	16	4317	y.3_Missense_Mu	NM_001127511	NP_001120983	P25054	APC_HUMAN	through a	)|p.T1313fs*8(	2515	TTGGAACTAGG	0.428	
-	6	1064	p.G267E|CCDC11	NM_152549	NP_689762	Q8NEF3	CC112_HUMAN			0	GCTTCCCTTTA	0.388	
+	2	109		NM_016144	NP_057228	Q9Y6G5	COMDA_HUMAN			1	AGGAAGATTTC	0.348	
+	4	1125	_Intron|SNCAIP_u	NM_005460	NP_005451	Q9Y6H5	SNCAP_HUMAN			2	GCTCCCAAGGC	0.473	
-	6	642	EP120_uc010jcz.	NM_153223	NP_694955	Q8N960	CE120_HUMAN			1	AGTCAGTACAG	0.448	
-	6	4414	F608_uc003ktp.1_	NM_020747	NP_065798	Q9ULD9	ZN608_HUMAN			6	AGCAGGAGACT	0.428	
-	1	317	ense_Mutation_p.	NM_001182	NP_001173	P49419	AL7A1_HUMAN			3	TCTTTCAGCCAC	0.607	
+	5	1250	xu.1_Missense_	NM_021982	NP_068817	O95486	SC24A_HUMAN			0	TGGGCCACAAG	0.403	
-	1	529	_Intron|HNRNPA0	NM_006805	NP_006796	Q13151	ROA0_HUMAN	RRM 1.		0	ACACCGCCCGC	0.652	
-	2	1479	NNA1_uc003ldj.2_	NM_015564	NP_056379	O43300	LRRT2_HUMAN	lar (Potential).|LRRCT.		0	TCAGGACTGTGG	0.522	
+	1	1706	lhk.1_Intron|PCD	NM_031857	NP_114063	Q9Y5H5	PCDA9_HUMAN	|Extracellular (Potential).		5	GCTTCCCACCC	0.463	
-	20	3066	be.1_Missense_M	NM_022481	NP_071926	Q8WWN8	ARAP3_HUMAN	Rho-GAP.		7	GGCAGCAACCG	0.577	
+	2	936		NM_002700	NP_002691	Q15319	PO4F3_HUMAN	Homeobox.		0	TCGCGGCGCCG	0.587	
+	1	278	aj.3_Missense_M	NM_012188	NP_036320	Q12951	FOXI1_HUMAN	Pro-rich.		4	GCCCGGCCCCA	0.731	
-	7	799	_uc003mez.2_5'F	NM_002115	NP_002106	P52790	HXK3_HUMAN	Regulatory.		7	CACACGGCCTG	0.582	rs147991837
+	23	8074	.A2377T|NSD1_u	NM_022455	NP_071900	Q96L73	NSD1_HUMAN			3	CACTGGCACAG	0.547	
+	1	868	nua.2_Missense_	NM_020135	NP_064520	Q96S55	WRIP1_HUMAN			2	CAAGCCGCTGG	0.572	
+	9	1650	p.G408D|RIPK1_	NM_003804	NP_003795	Q13546	RIPK1_HUMAN	tion with SQSTM1.		5	ACATGGCTTTG	0.498	
-	4	1480	ense_Mutation_p.	NM_178012	NP_821080	Q9BVA1	TBB2B_HUMAN			1	CGTCGGCCGTG	0.642	
+	3	354_355		NM_004271	NP_004262	O95711	LY86_HUMAN			0	TCTGCCCAAGT	0.46	
+	4	845	q.1_Missense_Mu	NM_004415	NP_004406	P15924	DESP_HUMAN	plakophilin 1 and junction		9	TCACCAGTGAAT	0.572	
+	26	2460	jow.2_Splice_Site	NM_001040274	NP_001035364	Q5T4T6	SYC2L_HUMAN			2	ATTTAGCTTAGG	0.323	
+	8	1209	ag.1_Missense_	NM_030948	NP_112210	Q9C0D0	PHAR1_HUMAN			0	GCCACGGCCAG	0.642	
+	2	939		NM_016255	NP_057339	Q9UBU6	FA8A1_HUMAN	Helical; (Potential).		0	ATTATGCACCT	0.353	
+	36	4317	.S1269N|LRRC16	NM_017640	NP_060110	Q5VZK9	LR16A_HUMAN			4	CCAGAGTAGCC	0.483	
-	1	312	2AE_uc003nha.1_	NM_003518	NP_003509	P62807	H2B1C_HUMAN			1	CTCCGGGAAGC	0.557	
+	6	1498	2A3_uc011dkm.1_RNA							0	GAGCAGGGACC	0.557	
-	1	65	2BM_uc003njo.2_	NM_021066	NP_066544	Q99878	H2A1J_HUMAN			0	GCCCGGCCCGA	0.622	

+	2	1594	C21_uc003nsi.1_F	NM_001010909	NP_001010909	Q5SSG8	MUC21_HUMAN	acellular (Potential).		2	GCTCTGGAACAG	0.582	
+	3	659	obi.2_Nonsense_M	NM_019111	NP_061984	P01903	DRA_HUMAN	tracellular (Potential).|Alpha		2	AGCACTGGGGCT	0.522	
+	12	3549	wc.2_Intron|BRPF3	NM_015695	NP_056510	Q9ULD4	BRPF3_HUMAN	PWWP.		2	AATGGCGTTCCC.	0.587	
+	24	2968	ooox.2_Splice_Site	NM_015345	NP_056160	Q86T65	DAAM2_HUMAN			3	TGACAGTTCGCC	0.562	
-	2	326	oqg.1_Missense_M	NM_018643	NP_061113	Q9NP99	TREM1_HUMAN	(Potential).|Ig-like V-type.		1	AGTCTTCTAGTAT	0.498	
-	7	1583		NM_006653	NP_006644	O43559	FRS3_HUMAN			2	AGGGTGGGTGG	0.637	
+	11	2364	OLH_uc011dvl.1_R	NM_006502	NP_006493	Q9Y253	POLH_HUMAN			2	CAAGAGCCCTTT	0.473	
+	14	1220	M63B_uc003ows.2	NM_018426	NP_060896	Q5T3F8	TM63B_HUMAN			3	GCCAGGGCTGCA	0.592	
+	14	1557	dvn.1_Missense_M	NM_007058	NP_008989	Q9UMQ6	CAN11_HUMAN	Domain III.		2	CACGGGAGGTGA	0.498	
-	11	2514	dwl.1_Missense_M	NM_153840	NP_722582	Q5T601	GP110_HUMAN	lasmic (Potential).		3	CAGTCGGCCTCC	0.562	rs143941431
-	8	942	110_uc011dwl.1_5	NM_153840	NP_722582	Q5T601	GP110_HUMAN	tracellular (Potential).		3	CTGAAAGAGCCG	0.458	rs61740071
+	1	383		NM_018214	NP_060684	Q9BTT6	LRRC1_HUMAN	LRR 2.		1	TATGCCCGGAGCC	0.667	
-	5	749		NM_152688	NP_689901	Q5VWX1	KHDR2_HUMAN			11	CCTGACGAATTTC	0.403	
-	11	1329		NM_001563	NP_001554	Q17R60	IMPG1_HUMAN			3	ATAACAGCAAAAC	0.383	
+	8	992	pje.2_Missense_M	NM_000056	NP_000047	P21953	ODBB_HUMAN			0	ATAATACCTTGGC	0.363	
-	6	1055	n_p.D74N|SYNCRI	NM_006372	NP_006363	O60506	HNRPQ_HUMAN	RRM 1.		2	ATAGATCTCTTGG	0.358	
+	14	1430	nse_Mutation_p.M	NM_012381	NP_036513	Q9UBD5	ORC3_HUMAN			0	TAGGATGTTGGCA	0.328	
-	17	2706	P45_uc003ppw.2_	NM_001080481	NP_001073950	Q70EL2	UBP45_HUMAN			2	TATCTCCCACACT	0.358	
+	4	684	2_5'Flank|PPIL6_u	NM_003080	NP_003071	O60906	NSMA_HUMAN			0	AGCACATCTACAC	0.512	
+	7	948	G4_uc011eau.1_Int	NM_014845	NP_055660	Q92562	FIG4_HUMAN	SAC.		1	CATCGTGACTGG	0.328	
+	4	950		NM_138459	NP_612468	Q96E22	NGBR_HUMAN	lasmic (Potential).		1	AGTTCGGTCCTC	0.378	
+	3	582		NM_014034	NP_054753	Q9Y294	ASF1A_HUMAN	stone H3, CHAF1B, and HII		0	ATCCAGGACTCAT	0.383	
-	21	1349	ON_uc003pzl.1_Mis	NM_006073	NP_006064	Q13061	TRDN_HUMAN	Lumenal.		1	TCCAGGTACAGC	0.363	
+	7	1913	qhs.2_Missense_M	NM_006290	NP_006281	P21580	TNAP3_HUMAN	AF1 (By simi	p.0?(22)	137	ATTTTGGGACTCC	0.547	
+	9	2326	qhs.2_Missense_M	NM_006290	NP_006281	P21580	TNAP3_HUMAN	with NAF1 (B	p.0?(22)	137	CTGCCCCCGAAC	0.627	
+	14	2417	khe.2_Missense_M	NM_020455	NP_065188	Q86SQ4	GP126_HUMAN	cellular (Potential).		1	ATAGCACATCACA	0.348	
-	3	421		NM_020861	NP_065912	Q8N680	ZBTB2_HUMAN			1	CCTGTTCTAATCG	0.537	
+	21	3374	k.1_Missense_Mut	NM_014892	NP_055707	Q9UPN6	SCAF8_HUMAN	Pro-rich.		0	GAGAAGGTCCTC	0.483	
+	20	2897	wc.1_Missense_Mu	NM_001040001	NP_001035090	P55196	AFAD_HUMAN			5	GAAGGGAAGTG	0.433	
+	29	4269	vc.1_Missense_Mu	NM_001040001	NP_001035090	P55196	AFAD_HUMAN	Pro-rich.		5	ATGCCGGTGATTT	0.627	
-	9	1873		NM_005618	NP_005609	O00548	DLL1_HUMAN	EGF-like 7; calcium-binding		5	GGCAGGTGCAG	0.692	
+	5	1071	siz.2_Missense_M	NM_017802	NP_060272	Q86Y56	HEAT2_HUMAN			1	TGCCGGGAGCTC	0.572	
-	14	2042	smh.3_Missense_M	NM_152743	NP_689956	Q6PJG6	BRAT1_HUMAN			0	GGCGGCCCCAAA	0.716	
-	11	1430	e_Mutation_p.G31	NM_000535	NP_000526	P54278	PMS2_HUMAN			2	TCTGTCCTAGAG	0.527	
-	3	337	_uc010ktg.2_Splice	NM_000535	NP_000526	P54278	PMS2_HUMAN			2	AACTTACTTAAGC	0.328	
-	1	203	LB_uc003sqc.2_5'U	NM_139179	NP_631918	Q8NCG7	DGLB_HUMAN	lasmic (Potential).		3	GATGGCCCAGCGC	0.677	
-	5	840	NF12_uc003sqs.1_	NM_016265	NP_057349	P17014	ZNF12_HUMAN			0	TATTTTCCTCTTC	0.358	
+	7	1208	kuh.2_Missense_M	NM_178559	NP_848654	Q2M3G0	ABCB5_HUMAN	cellular (Potential).		6	AATCCACCCAATC	0.353	
-	6	856	n_p.E151K|OSBPI	NM_015550	NP_056365	Q9H4L5	OSBL3_HUMAN			1	CAATTTCATTCTG	0.403	
+	8	1837	CDC129_uc011kae	NM_194300	NP_919276	Q6ZRS4	CC129_HUMAN			0	AAGGATGAAGTT	0.438	
-	4	1170	3tes.3_Missense_I	NM_022373	NP_071768	Q9BSE4	HERP2_HUMAN	Ser-rich.		3	GATGGAGTTGTTC	0.373	
-	9	932	p.V113M|ELMO1_	NM_014800	NP_055615	Q92556	ELMO1_HUMAN			6	TGAGCACCATCGA	0.507	
+	12	1288		NM_016616	NP_057700	Q8N427	TXND3_HUMAN			3	TTCCCCGATTTTA	0.358	
-	9	730	e_Mutation_p.G21	NM_014396	NP_055211	P49754	VPS41_HUMAN			4	GAAGTCCCCCAG	0.473	
-	17	2247	w.2_Missense_Mu	NM_022748	NP_073585	Q68CZ2	TENS3_HUMAN			4	CTCTGGGCTGGC	0.657	
+	13	1605	kyr.2_Missense_M	NM_152701	NP_689914	Q86UQ4	ABCAD_HUMAN			10	GGGTGGTCTCCA	0.453	
-	3	218		NM_207366	NP_997249	Q6ZU15	SEP14_HUMAN			0	TCAAAACCAAAAT	0.303	

-	5	1598		NM_033273	NP_150376	Q96JC4	ZN479_HUMAN	2H2-type 10.	4	CTTTGCCACATT	0.433
+	6	953		NM_001099435	NP_001092905	A6NIY4	SPDE5_HUMAN	Arg-rich.	0	AGCGTCGGTTC	0.562
+	6	969		NM_001099435	NP_001092905	A6NIY4	SPDE5_HUMAN	Arg-rich.	0	TAGGCCGTTCCA	0.572
-	31	2624	p.A170T|PION_uc	NM_017439	NP_059135	A4D1B5	GSAP_HUMAN		1	CATCGCGGTGT	0.413
-	18	2627	gw.1_Missense_	NM_006379	NP_006370	Q99985	SEM3C_HUMAN		1	CGGGTGGAAGG	0.488
-	5	7736	_Mutation_p.P248	NM_033026	NP_149015	Q9Y6V0	PCLO_HUMAN	Pro-rich.	7	AGGAGGTGCAG	0.463
-	14	2044	kgz.1_Missense_	NM_001142749	NP_001136221	A8MWY0	K132L_HUMAN	ellular (Potential).	7	GGCAGGGGACA	0.522
+	12	2236	g.1_Missense_Mu	NM_006716	NP_006707	Q9UBU7	DBF4A_HUMAN		2	GAAAAGTGAAA	0.333
-	2	223	te_p.W31_splice|F	NM_152789	NP_690002	Q5BKY9	F133B_HUMAN		1	AAATACCAGGT	0.368
-	6	661	mu.1_Missense_	NM_001742	NP_001733	P30988	CALCR_HUMAN	ellular (Potential).	9	AAACACCTTTTT	0.323
+	20	1535	1A2_uc011kib.1_I	NM_000089	NP_000080	P08123	CO1A2_HUMAN		9	CAAAGGAGAGA	0.433
-	13	1699		NM_018842	NP_061330	Q9UHR4	BI2L1_HUMAN		1	CAGTCCCGTTG	0.418
+	39	5719	.T1819M|TRRAP_	NM_003496	NP_003487	Q9Y4A5	TRRAP_HUMAN		37	CGCCACGCTGC	0.627
+	7	1766	p.P548S|ZKSCAN	NM_145102	NP_659570	Q9Y2L8	ZKSC5_HUMAN		1	GAGAGACCACA	0.423
+	14	2378	AN_uc003uwl.2_	NM_003386	NP_003377	Q9Y493	ZAN_HUMAN	ate) (mucin-like domain).|E	11	AAAACCCACCA	0.522
+	18	2546	a.2_Missense_Mut	NM_015908	NP_056992	Q9BXP5	SRRT_HUMAN	Pro-rich.	2	AGCGCCCAGCT	0.507
-	1	583	c010lhm.1_5'Flan	NM_001015072	NP_001015072	Q6NVU6	UFSP1_HUMAN		0	CAGCTCCCCGT	0.692
+	18	2872	_uc011kkn.1_Intro	NM_181552	NP_853530	P39880	CUX1_HUMAN	CUT 2.	8	TGGACACCATCG	0.612
+	27	5336	LL5_uc010ljf.1_Int	NM_182931	NP_891847	Q8IZD2	MLL5_HUMAN	Pro-rich.	3	TCCAGGACACC	0.498
-	10	1639	_p.V372I|COG5_u	NM_181733	NP_859422	Q9UP83	COG5_HUMAN		4	CCTTAACTATTTC	0.313
-	21	2882	_Mutation_p.S93	NM_007356	NP_031382	A4D0S4	LAMB4_HUMAN	inin EGF-like 9.	8	CTGAGCTCCAC	0.423
-	5	515	_Mutation_p.T15	NM_130768	NP_570124	Q8WWH4	ASZ1_HUMAN	ANK 4.	3	ATTGGGGTCATA	0.418
+	14	2560_2561	q.1_Missense_Mu	NM_000492	NP_000483	P13569	CFTR_HUMAN	lasmic (Potential).	5	ATTCAAGAAGGT	0.416
+	27	4438	q.1_Missense_Mu	NM_000492	NP_000483	P13569	CFTR_HUMAN	tential).|ABC transporter 2	5	GGAGCCTCTTC	0.527
-	2	2174		NM_024523	NP_078799	Q96CN9	GCC1_HUMAN	Potential.	2	CTTGTGCAGCT	0.647
+	3	460		NM_014390	NP_055205	Q7KZF4	SND1_HUMAN	TNase-like 1.	3	CCCTGGGCATT	0.403
+	2	616	a.3_Missense_Mu	NM_001458	NP_001449	Q14315	FLNC_HUMAN	1.|Actin-binding.	12	CTGGACGCTGA	0.622
+	11	2202	s.2_Missense_Mu	NM_005631	NP_005622	Q99835	SMO_HUMAN	lasmic (Potential).	37	CACCCCTGTGG	0.597
+	12	1658	|CPA5_uc010lme.	NM_001127441	NP_001120913	Q8WXQ8	CBPA5_HUMAN		2	AGTTGGTGAGA	0.517
-	4	1223	qx.3_Missense_M	NM_001018111	NP_001018121	O00592	PODXL_HUMAN	xtracellular (Potential).	3	TAGTTGATGCT	0.597
+	5	848	1_uc011kpt.1_Intro	NM_033138	NP_149129	Q05682	CALD1_HUMAN	odulin-binding (By similarity	0	AAGTCTGTCGC	0.498
-	13	2931		NM_020119	NP_064504	Q7Z2W4	ZCCHV_HUMAN	ARP catalytic.	1	ACTTTCCAACC	0.423
-	15	1860		NM_004333	NP_004324	P15056	BRAF_HUMAN	rotein kinas R603>I(2)|p.T	18290	GATTTCACTGTA	0.368
-	12	1575		NM_004333	NP_004324	P15056	BRAF_HUMAN	rotein kinase.	18290	ACCTGAGTACT	0.393
+	4	313	GK_uc011krg.1_R	NM_018238	NP_060708	Q53H12	AGK_HUMAN		2	TTTTAGGTGTTTG	0.368
+	18	3435	bt.2_Missense_Mu	NM_004445	NP_004436	O15197	EPHB6_HUMAN	mic (Potential).|Protein kin	19	CCCGCCTCCAG	0.532
+	7	931	_p.P146S|CASP2	NM_032982	NP_116764	P42575	CASP2_HUMAN		3	AGTTACCTGCA	0.493
-	7	1962	pi.2_Missense_Mu	NM_152557	NP_689770	Q6NUN9	ZN746_HUMAN		3	AGGGCCGCACG	0.667
+	13	1727	wjj.1_Missense_M	NM_031946	NP_114152	Q96P47	AGAP3_HUMAN	PH.	3	ATCTCCCCACT	0.507
-	3	445	YGN_uc003wkg.2_	NM_144727	NP_653328	Q8WXF5	CRGN_HUMAN	crystallin 'Greek key' 3.	0	GAAGGGGCTGT	0.587
-	14	2109		NM_170606	NP_733751	Q8NEZ4	MLL3_HUMAN		63	GAAGACATTTTC	0.348
+	14	2221	ng.2_Missense_M	NM_014671	NP_055486	Q15386	UBE3C_HUMAN		5	AAGCAGATAAG	0.318
-	21	3632	p.A473V|CSMD1_	NM_033225	NP_150094	Q96PZ7	CSMD1_HUMAN	xtracellular (Potential).	25	TTGGTGGCACCT	0.542
+	3	388	tron|PRSS55_uc0	NM_198464	NP_940866	Q6UWB4	PRS55_HUMAN	(Potential).|Peptidase S1.	1	TGCTGGGGACC	0.512
-	1	632		NM_173683	NP_775954	Q5GH73	XKR6_HUMAN		2	GGCCCCGGCTG	0.766
-	2	1903	nse_Mutation_p.P4	NM_001001924	NP_001001924	Q9ULD2	MTUS1_HUMAN		2	ACTGGGTTTAC	0.403
+	9	934	_Mutation_p.A26	NM_199205	NP_954675	Q8N163	K1967_HUMAN		3	TATCAGCCTTCC	0.577

-	9	1080		NM_003844	NP_003835	O00220	TR10A_HUMAN	lasmic (Potential).	6	CGGTCCCTGTA	0.368	
-	13	1834	ITPD4_uc003xdm.	NM_004901	NP_004892	Q9Y227	ENTP4_HUMAN	enal (Potential).	2	AAACGCCCCGC	0.587	
-	5	640	.1_Missense_Mut	NM_018492	NP_060962	Q96KB5	TOPK_HUMAN	rotein kinase.	0	CAAAGCAACTTT	0.313	
-	1	4231		NM_031271	NP_112561	Q9BXT5	TEX15_HUMAN		7	CTACATCCAACT	0.358	
+	3	303	_p.Q63R|ERLIN2_	NM_007175	NP_009106	O94905	ERLN2_HUMAN	enal (Potential).	0	TGTGCAGGTAT	0.502	
-	3	1006	21E|RAB11FIP1_u	NM_001002814	NP_001002814	Q6WKZ4	RFIP1_HUMAN		3	GGTTCCCATTG	0.512	
+	2	569	G4_uc003xkz.1_In	NM_004874	NP_004865	O95429	BAG4_HUMAN		1	CATATCCTAGCT	0.363	
+	6	625	D1_uc003xnn.2_R	NM_002164	NP_002155	P14902	I23O1_HUMAN		2	TGGTGGAAATAG	0.408	
-	14	1490	se_Mutation_p.D4	NM_020476	NP_065209	P16157	ANK1_HUMAN	4.|89 kDa domain.	9	GGTCATCCTGG	0.363	rs78606390
+	21	2215		NM_032410	NP_115786	Q86VS8	HOOK3_HUMAN	ith MSR1.|Required for as	2	GTCAGAGAGAGA	0.244	
+	2	209		NM_152419	NP_689632	Q68CP4	HGNAT_HUMAN	l, vesicle (Potential).	0	ATCAGGCTTTGC	0.378	
-	85	12096	e_Mutation_p.W39	NM_006904	NP_008835	P78527	PRKDC_HUMAN	PI3K/PI4K.	34	TACTTTCCAATC	0.493	
+	9	1041	_p.E316K|MCM4_	NM_182746	NP_877423	P33991	MCM4_HUMAN		4	GGGTGGAGATG	0.617	
-	8	1013		NM_003878	NP_003869	Q92820	GGH_HUMAN	-glutamyl hydrolase.	0	TGGATGCCACT	0.343	
+	5	615	vt.2_Missense_Mu	NM_001033578	NP_001028750	Q96BR1	SGK3_HUMAN	PX.	4	TATCCAGAACTT	0.289	
+	11	1217	yb.2_Missense_M	NM_052958	NP_443190	Q49A92	CH034_HUMAN		1	GAGTAGGACAC	0.408	
-	2	545	p.E169Q|JPH1_u	NM_020647	NP_065698	Q9HDC5	JPH1_HUMAN	lasmic (Potential).	1	CTGCTCGCTGC	0.711	
+	6	641	P1_uc010mai.2_5'	NM_007013	NP_008944	Q9H0M0	WWP1_HUMAN		2	TTAAAACTTTCCT	0.333	
+	4	496	M67_uc010maw.2_	NM_153704	NP_714915	Q5HYA8	MKS3_HUMAN		2	TTAATGGAACATT	0.333	
-	24	5321	1429_uc010maz.1	NM_015496	NP_056311	Q69YN4	VIR_HUMAN		2	AGCACGGTCCC	0.468	
-	3	526	hf.2_Intron|TP53IN	NM_033285	NP_150601	Q96A56	T53I1_HUMAN	Glu-rich.	0	CTTCTTCTTCTTC	0.458	
-	59	8365	.S2777P|UBR5_u	NM_015902	NP_056986	O95071	UBR5_HUMAN	HECT.	28	AGAGGAATAGA	0.378	
+	2	592	_p.L147F|RIMS2_	NM_014677	NP_055492	Q9UQ26	RIMS2_HUMAN		15	GAATTTGGCCCG	0.458	
-	7	704	nv.2_Missense_Mu	NM_001568	NP_001559	P60228	EIF3E_HUMAN		3	CTTTGGGGTGAT	0.358	
-	2	510	F11B_uc010mdc.	NM_002546	NP_002537	O00300	TR11B_HUMAN		2	AGGGGCGCACA	0.517	rs116321565
+	4	903		NM_002514	NP_002505	P48745	NOV_HUMAN	TSP type-1.	5	CCCGGGTCACC	0.532	
-	5	791		NM_003184	NP_003175	Q6P1X5	TAF2_HUMAN		6	GAGCACCTCTC	0.338	
+	2	155	se_Mutation_p.E32	NM_144963	NP_659400	Q658Y4	F91A1_HUMAN		2	CAGAGAGAATAT	0.338	
-	20	2096		NM_013291	NP_037423	Q10570	CPSF1_HUMAN		1	CCGTAGGAGTCA	0.692	
-	20	2177	p.S479F|PTPRD_	NM_002839	NP_002830	P23468	PTPRD_HUMAN	III 2.|Extracellular (Potentia	22	TTGACAGAATAT	0.433	
-	3	2056		NM_020702	NP_065753	Q6NSJ0	K1161_HUMAN	ellular (Potential).	3	GGTCACCCGTG	0.662	
-	41	5830		NM_006289	NP_006280	Q9Y490	TLN1_HUMAN	action with SYNM.	13	CATGCCACCCA	0.617	
-	5	537	ZNF484_uc010mrl	NM_031486	NP_113674	Q5JVG2	ZN484_HUMAN		0	GGTTTTCTCCAC	0.343	
+	9	2144	e_Mutation_p.T71	NM_006648	NP_006639	Q9Y3S1	WNK2_HUMAN		12	CAGCACCCCCA	0.741	
+	2	292	p.R63W|NIPSNA	NM_015469	NP_056284	Q9UFN0	NPS3A_HUMAN		0	ATCTTCGGACA	0.373	
+	7	959	hp.2_Missense_M	NM_152786	NP_689999	Q8TAL5	CI043_HUMAN		0	GCCTCCCCCAA	0.478	
-	3	1932	f.2_Missense_Mut	NM_002160	NP_002151	P24821	TENA_HUMAN	EGF-like 12.	7	AGGGCCGGTGA	0.597	
+	4	908	yv.1_Missense_M	NM_054107	NP_473448	Q8NGS2	OR1J2_HUMAN	ellular (Potential).	5	CCTCCCCATCC	0.562	
+	19	2457	ABGAP1_uc011lzj.	NM_012197	NP_036329	Q9Y3P9	RBGP1_HUMAN		5	TTGACAGACTTT	0.358	
+	33	3611	wu.2_Missense_M	NM_015354	NP_056169	Q5SRE5	NU188_HUMAN		7	GACCAGCAACTC	0.507	
-	11	1687	p.R448C|CRAT_u	NM_000755	NP_000746	P43155	CACP_HUMAN		1	CGAGCGGATGG	0.612	
-	8	1045	_5'Flank|SETX_uc	NM_015046	NP_055861	Q7Z333	SETX_HUMAN		3	CGCTGGCCAGA	0.368	
+	22	2471		NM_000093	NP_000084	P20908	CO5A1_HUMAN	le-helical region.	11	CACAGGGTGTC	0.542	
-	4	632	z.2_Missense_Mu	NM_178138	NP_835258	Q9UBR4	LHX3_HUMAN	Homeobox.	1	GGGCGAGGTGT	0.726	
-	22	4388	1_5'Flank|CARD9_	NM_003086	NP_003077	Q5SXM2	SNPC4_HUMAN		0	GTGTGCCTGGCA	0.612	
-	6	837	V51I|WDR85_uc0	NM_138778	NP_620133	Q9BTV6	WDR85_HUMAN	WD 1.	0	GGGTACCCTGG	0.587	
+	5	1010	MT1_uc004cob.1_	NM_024757	NP_079033	Q9H9B1	EHMT1_HUMAN		3	CTGTGGGTTCC	0.443	

-	2	622	11mha.1_Transla	NM_013239	NP_037371	Q9Y5P8	P2R3B_HUMAN		0	ATCCACGTTGA	0.617
-	5	2694		NM_015419	NP_056234	Q9NR99	MXRA5_HUMAN		8	GTAGAGGTACA	0.473
-	6	962		NM_000216	NP_000207	P23352	KALM_HUMAN	nectin type-III 1.	4	CTCGAGTTCCA	0.517
+	14	1563	_p.Q459*|BMX_uc	NM_203281	NP_975010	P51813	BMX_HUMAN	rotein kinase.	5	TCTTTCAGGAG	0.433
+	9	1276	ey.1_Missense_M	NM_018360	NP_060830	Q9NUQ3	TXLNG_HUMAN	Potential.	1	ATAAAGCACTTC	0.398
+	1	264	nfu.1_Missense_	NM_173495	NP_775766	Q96NR3	PTHD1_HUMAN		6	ACTCGGACCTG	0.622
+	1	1665		NM_001013736	NP_001013758	Q5HY64	FA47C_HUMAN		3	AGCCTCCTGAG	0.617
-	4	606	rf38_uc004dev.1_	NM_144970	NP_659407	Q8TB03	CX038_HUMAN		1	AGTATACTGCCA	0.358
+	19	3221	_p.R904L|KDM6A	NM_021140	NP_066963	O15550	KDM6A_HUMAN		84	ATAAACGTGATG	0.323
+	7	760	gy.2_Missense_M	NM_001077445	NP_001070913	Q92613	JADE3_HUMAN	PHD-type.	0	TCAAGGTCCCA	0.537
-	2	221		NM_015698	NP_056513	Q92917	GPKOW_HUMAN		2	CAAAGGGATGA	0.632
-	7	930	nip.2_Missense_	NM_005183	NP_005174	O60840	CAC1F_HUMAN	cellular (Potential).	6	CGCACGCCCTG	0.617
+	6	2210	E638K|CCNB3_u	NM_033031	NP_149020	Q8WWL7	CCNB3_HUMAN		9	CCCAGGAACCA	0.453
-	11	2470	noh.1_Missense_	NM_017848	NP_060318	Q9NX05	F120C_HUMAN		2	GGGTAGACACT	0.448
-	21	2200	N1_uc011mpg.1_	NM_002547	NP_002538	O60890	OPHN1_HUMAN	Pro-rich.	2	TTTGGGGTGTT	0.517
-	12	1462	z.1_Missense_Mu	NM_000390	NP_000381	P24386	RAE1_HUMAN		1	TGCTGGCACTG	0.368
+	1	1360	efm.1_Missense_	NM_032968	NP_116750	Q9BZA7	PC11X_HUMAN	(Potential).|Cadherin 2.	2	AAACGGAGTTC	0.323
+	8	1717		NM_017416	NP_059112	Q9NP60	IRPL2_HUMAN	3.|Extracellular (Potential).	3	ACTCAGTTGTG	0.403
+	2	208	5'UTR|ATG4A_uc	NM_052936	NP_443168	Q8WYN0	ATG4A_HUMAN		1	AGCTGGTATGG	0.388
+	15	1745	_p.G493S|ALG13_uc011mta.1_Missense_Mutation_p.G			Q9NP73	ALG13_HUMAN		1	CTGGGGGTTAT	0.418
-	9	2426	_uc011mtc.1_Miss	NM_001113490	NP_001106962	Q4VCS5	AMOT_HUMAN		1	TGATGGGGGAG	0.517
+	5	561	p.C173Y|IL13RA1	NM_001560	NP_001551	P78552	I13R1_HUMAN	ellular (Potential).	0	ATCAATGTGAAA	0.343
-	16	3315	_p.T1020I|IGSF1_	NM_001555	NP_001546	Q8N6C5	IGSF1_HUMAN	otential).|Ig-like C2-type 10	5	TATTGGTGATGG	0.517
-	3	758		NM_006014	NP_006005	Q14657	LAGE3_HUMAN		0	CGGGGGGCCCA	0.592
-	2	532		NM_171998	NP_741995	Q96DA2	RB39B_HUMAN		0	AAGACCACCTA	0.433
-	2	913	_uc009vno.2_Sile	NM_001013631	NP_001013653	O60812	HNRCL_HUMAN		0	TTTCTTCATGGA	0.468
-	3	765	_5'Flank|ARHGE	NM_153213	NP_694945	Q8IW93	ARHGJ_HUMAN		3	CAGGCGCAGAG	0.672
-	18	2279	1bbm.1_Translatio	NM_020765	NP_065816	Q5T4S7	UBR4_HUMAN		25	GAGGCGTGAAA	0.507
-	2	1170		NM_052943	NP_443175	Q96A09	FA46B_HUMAN		1	CTGCCCCACCG	0.657
+	7	1093	_p.R328H|PTPRU_	NM_005704	NP_005695	Q92729	PTPRU_HUMAN	III 1.|Extracellular (Potentia	7	GGCGCGCGGGC	0.632
-	9	1432	j.1_Missense_Mu	NM_005955	NP_005946	Q14872	MTF1_HUMAN	Pro-rich.	2	CTGGGGTGGCT	0.572
+	15	2736	wt.2_Missense_M	NM_002840	NP_002831	P10586	PTPRF_HUMAN	III 5.|Extracellular (Potentia	10	TTGCTGCCTATA	0.592
-	2	522	F53L|CCDC163P_	NM_001102601	NP_001096071				0	CAAGAAGATAC	0.483
+	17	1964	p.Y617S|RAD54L_	NM_001142548	NP_001136020	Q92698	RAD54_HUMAN	case C-terminal.	3	CTTGCTATATCTA	0.522
-	12	1803	b.1_RNA|uc001de	NM_001002292	NP_001002292	Q5T9L3	WLS_HUMAN		0	tcttccctcgatttacatg	0
+	3	4043		NM_001408	NP_001399	Q9HCU4	CELR2_HUMAN	ial).|EGF-like 3; calcium-bi	8	GTGCTCGCTCA	0.592
+	3	515	dxw.2_3'UTR|CYB	NM_182580	NP_872386	Q8N8Q1	C56D1_HUMAN	tochrome b561.	0	GTCCCCGGGCA	0.612
+	4	1338		NM_020440	NP_065173	Q9P2B2	FPRP_HUMAN	ellular (Potential).	1	TGGGTGTGACC	0.562
+	13	2317	_Mutation_p.R71	NM_019032	NP_061905	Q6UY14	ATL4_HUMAN		2	CTCCCGTGAGT	0.657
+	3	406	_p.G117E|ZBTB7B	NM_015872	NP_056956	O15156	ZBT7B_HUMAN	BTB.	0	TGGGGGAGCAG	0.632
-	4	1220	p.R392Q|IGSF8_	NM_052868	NP_443100	Q969P0	IGSF8_HUMAN	3.|Extracellular (Potential).	0	TCTAGCCGTAGC	0.642
+	11	3021	N1_uc001gwb.2_	NM_178275	NP_840059				3	CTGGTGCATCC	0.662
+	6	1122	_p.A66T|RNPEP_	NM_020216	NP_064601	Q9H4A4	AMPB_HUMAN		1	CAGGCGCTGCG	0.562
-	17	3115	pqv.1_Missense_	NM_002646	NP_002637	O00750	P3C2B_HUMAN		7	TGTGGGTCCAC	0.597
-	6	1180	vx.1_Missense_M	NM_145214	NP_660215	Q96F44	TRI11_HUMAN	330.2/SPRY.	4	CTGCACGCTCC	0.697
-	4	818	tv.2_Missense_M	NM_024554	NP_078830	Q8N414	PGBD5_HUMAN		4	GCCCCGTGAAA	0.587
+	15	5870	iik.2_Missense_	NM_017782	NP_060252	Q5VWN6	CJ018_HUMAN		2	TCGGGGTTTCC	0.458

-	4	718	e_Mutation_p.R15	NM_001080449	NP_001073918	P51530	DNA2L_HUMAN		0	TTGGCGTGTGG(	0.353	
+	20	2584	p.R352Q|CDH23_	NM_022124	NP_071407	Q9H251	CAD23_HUMAN	.|Extracellular (Potential).	11	TGACCGAGAGA(	0.527	
+	9	863	_Mutation_p.G129	NM_018063	NP_060533	Q9NRZ9	HELLS_HUMAN	rity).|Helicase ATP-binding.	2	GATTGGGTAAGA(	0.378	
-	28	2983	kkr.2_Intron|SORE	NM_001034954	NP_001030126	Q9BX66	SRBS1_HUMAN		1	CATCTCGGGGG.	0.562	
-	3	462	74M|ALDH18A1_u	NM_002860	NP_002851	P54886	P5CS_HUMAN	:amate 5-kinase.	3	TCACCACGATTC	0.562	rs143330350
+	6	1114	RRC27_uc001lli.2_	NM_030626	NP_085129	Q9C0I9	LRC27_HUMAN		1	AGACACGTTTTC/	0.403	
-	8	1175	7_uc010qwg.1_5'U	NM_001572	NP_001563	Q92985	IRF7_HUMAN		0	GGTACGGCTCTG(	0.697	
+	31	12230		NM_002457	NP_002448	Q02817	MUC2_HUMAN		2	caccactacggtgacc(	0.015	rs147438840
+	51	14906	b.2_Missense_Mu	NM_017511	NP_059981	Q9HC84	MUC5B_HUMAN	em repeats, Ser/Thr- rich.|	0	GCCGAGCACTA(	0.662	
-	6	621	w.2_Intron|OSBPL!	NM_020896	NP_065947	Q9H0X9	OSBL5_HUMAN	PH.	3	GATGAGCAGCA(	0.657	
+	11	2844	_p.P741L|NAV2_u	NM_145117	NP_660093	Q8IVL1	NAV2_HUMAN		6	GGTATCCCCCTC(	0.632	
+	11	2903	_p.A761T|NAV2_u	NM_145117	NP_660093	Q8IVL1	NAV2_HUMAN		6	ACTCCGCCCCT(	0.597	
+	14	3557	mpt.2_Missense_M	NM_145117	NP_660093	Q8IVL1	NAV2_HUMAN		6	ATGACAGCTCAG(	0.602	
-	6	853	_p.S198L|ELF5_u	NM_198381	NP_938195	Q9UKW6	ELF5_HUMAN	ETS.	1	GCTTCCGATTTA/	0.418	
-	8	1113	ADL1_uc010rnw.1_	NM_005468	NP_005459	Q9UQQ1	NALDL_HUMAN	.|Extracellular (Potential).	0	TGGTTCCCATAC/	0.662	
-	7	706	e_Mutation_p.P13	NM_021975	NP_068810	Q04206	TF65_HUMAN	RHD.	4	GTGTTGGGGGCA	0.592	
+	6	942	gz.1_Missense_Mu	NM_018026	NP_060496	Q6VY07	PACS1_HUMAN		6	GCAGATCGTTCT(	0.443	
+	6	619	TN3_uc010rpi.1_R	NM_001104	NP_001095	Q08043	ACTN3_HUMAN	n-binding.|CH 2.	0	GACACCGCCCT	0.647	
-	9	1451	ense_Mutation_p./	NM_004910	NP_004901	O00562	PITM1_HUMAN		3	CCTCAGCCCCA.	0.647	
+	13	1714	.A506T|PPFIA1_u	NM_003626	NP_003617	Q13136	LIPA1_HUMAN	Potential.	3	TTGAAGCACTGA	0.413	
-	7	1339	uv.2_Missense_Mu	NM_015531	NP_056346	Q4AC94	C2CD3_HUMAN	p.R371P(1)	7	TTAAACCGATTC(	0.388	
-	12	2631		NM_020693	NP_065744	Q8TD84	DSCL1_HUMAN	otential).|Ig-like C2-type 9.	8	GATGGGCCGCT(	0.642	
-	6	2184	al.2_Missense_Mu	NM_182557	NP_872363	Q86UU0	BCL9L_HUMAN	teraction with CTNNB1 (By	2	GTTCCCGATGCT(	0.687	
-	6	948	p.P153L|PRDM10_	NM_020228	NP_064613	Q9NQV6	PRD10_HUMAN	SET.	1	CGAGAGGCCCC	0.567	
+	14	2340	ATS2_uc001ruf.2_	NM_023071	NP_075559	Q86XZ4	SPAS2_HUMAN		1	GAGGAGGACAG	0.473	
+	24	3113	lt.2_Missense_Mu	NM_173602	NP_775873	Q9P265	DIP2B_HUMAN		6	GGTGAGGAAGG	0.458	
-	8	923	s.3_Missense_Mu	NM_015665	NP_056480	Q9NRG9	AAAS_HUMAN	WD 3.	1	ACTGGGGGCCC	0.607	
-	1	31	nse_Mutation_p.D	NM_001130059	NP_001123531	P17544	ATF7_HUMAN	activation domain.	2	GTCTGTCGTCTC	0.418	
-	3	525	e.1_Missense_Mu	NM_032345	NP_115721	Q9BRP8	WIBG_HUMAN		0	ACTGGGGAGTT	0.567	
-	18	3991		NM_144982	NP_659419	O60293	ZC3H1_HUMAN		5	TGTTTTCGGCTA/	0.323	
-	7	898	syg.1_Missense_M	NM_020841	NP_065892	Q9BZF1	OSBL8_HUMAN		1	ACTGAGCAGCT(	0.338	
+	7	705	sxn.1_Missense_Mutation_p.V953I			Q8N1T3	MYO1H_HUMAN		0	GATGCCGTTTG(	0.453	
+	11	1659	tw.1_Missense_Mu	NM_002834	NP_002825	Q06124	PTN11_HUMAN	protein phos p.G427G(1)	392	ACCACGGCGTG	0.567	
-	1	257	_p.W73*|FBXO21_	NM_033624	NP_296373	O94952	FBX21_HUMAN	F-box.	1	TCCTTCCACACC	0.443	
+	77	13281	ufu.3_Missense_M	NM_207437	NP_997320	Q8IVF4	DYH10_HUMAN		6	CCATCGCCTCA/	0.532	
-	35	4498	_p.R289H|POLE_u	NM_006231	NP_006222	Q07864	DPOE1_HUMAN		8	ATATGGCGGATA(	0.592	
-	5	1489	n.1_Missense_Mu	NM_153371	NP_699202	Q8N448	LNX2_HUMAN	PDZ 2.	6	CAGGTCGTGCC(	0.522	rs144420848
+	1	649		NM_207361	NP_997244	Q5SZK8	FREM2_HUMAN	cellular (Potential).	11	ACGACGCACTG(	0.687	
-	5	2461	gz.1_Missense_Mu	NM_018676	NP_061146	Q9NS62	THSD1_HUMAN	lasmic (Potential).	4	CGGACGGGCCC	0.607	
-	1	447	RP1_uc001vni.2_Ir	NM_178861	NP_849192	Q8IZP6	R113B_HUMAN		3	GACCCCGCAGT	0.642	
-	5	966		NM_004093	NP_004084	P52799	EFNB2_HUMAN	lasmic (Potential).	1	ACACCGGGTGC(	0.592	
-	2	239	P1_uc010tlg.1_Mi	NM_007110	NP_009041	Q99973	TEP1_HUMAN	1 N-terminal 3.	5	ACACATATCCAT(	0.502	
-	26	3407	a-mir-208b|MI000!	NM_000257	NP_000248	P12883	MYH7_HUMAN	Potential.	4	GCTGCCGAGGG	0.592	
+	10	752	mh.2_Missense_M	NM_006263	NP_006254	Q06323	PSME1_HUMAN		1	GAGATCCGCAAT(	0.627	
-	1	664	on_p.A138V|NKX2	NM_003317	NP_003308	P43699	NKX21_HUMAN		1	CCAGAGGCGCTG	0.706	
-	8	3419	e_Mutation_p.G88	NM_183002	NP_892114	P57103	NAC3_HUMAN	cellular (Potential).	7	CTCCCCTCCCA(	0.597	
+	3	1353	TR4_uc010tua.1_I	NM_024644	NP_078920	Q9H6W3	NO66_HUMAN	JmjC.	0	CCAGCGCAATA(	0.542	

-	3	536	Mutation_p.E63K|P	NM_002632	NP_002623	P49763	PLGF_HUMAN		1	GTACTCGGACA	0.657	
+	6	1471	e_Mutation_p.R46	NM_001161476	NP_001154948	Q64LD2	WDR25_HUMAN	WD 5.	0	CCTACCGGATG	0.632	
-	1	2323	a-mir-432|MI0003	NM_001134888	NP_001128360	A6NKG5	RTL1_HUMAN		1	GGAAGCGGACC	0.562	
-	23	3324	se_Mutation_p.T3	NM_002226	NP_002217	Q9Y219	JAG2_HUMAN	ellular (Potential).	5	CAAGGTGAGGC	0.662	
-	4	897	h.2_Nonsense_Mu	NM_002226	NP_002217	Q9Y219	JAG2_HUMAN	ellular (Potential).	5	CACTCGCTCGA	0.667	
-	27	3907	e_Mutation_p.R11	NM_002420	NP_002411	Q7Z4N2	TRPM1_HUMAN	lasmic (Potential).	4	TTTGCCGGAGA	0.473	
-	15	2193	nse_Mutation_p.R	NM_133647	NP_598408	Q9UHW9	S12A6_HUMAN	lasmic (Potential).	7	GTAGCGGAATC	0.413	
-	31	3847	_Mutation_p.A11	NM_001130858	NP_001124330	Q6PFW1	VIP1_HUMAN		0	TTGTGCTCCAC	0.532	
-	2	491	ABPB1_uc001zyd	NM_005254	NP_005245	Q06547	GABP1_HUMAN	ANK 1.	1	AATACGAACTT	0.368	rs139444439
-	13	1549	ib.2_Missense_Mu	NM_001004439	NP_001004439	Q9UKX5	ITA11_HUMAN	ntial.|Extracellular (Potentia	3	GATGTCCACCG	0.612	
+	2	109	bic.2_Missense_M	NM_006091	NP_006082	Q9UQ03	COR2B_HUMAN		6	CAACCGGGAGC	0.602	
-	24	3751	_Missense_Mutati	NM_006901	NP_008832	B2RTY4	MYO9A_HUMAN	or regulatory domain.	3	AGTACCGCTGC	0.507	
-	26	3034	3L|MAN2C1_uc0	NM_006715	NP_006706	Q9NTJ4	MA2C1_HUMAN		0	GGTCTGGTCGC	0.632	
-	5	507	1_uc010bkk.2_Mi	NM_006715	NP_006706	Q9NTJ4	MA2C1_HUMAN		0	AGGGGCTGCAA	0.597	
+	5	1331	j.2_Missense_Mu	NM_198243	NP_937886	Q9H672	ASB7_HUMAN	ANK 6.	1	TACGCCGTGATC	0.478	
-	3	461		NM_001025190	NP_001020361	Q96KJ4	MSLNL_HUMAN		4	TGCACGGGTAG	0.557	
-	3	1318		NM_001013658	NP_001013680	Q96A99	PTX4_HUMAN	Pentaxin.	0	TTTCCCGATGG	0.627	
-	15	2079	lz.2_Missense_Mu	NM_014714	NP_055529	Q96RY7	IF140_HUMAN		5	AGAAGCGATGC	0.672	
-	22	2893	p.A929V|MYH11_	NM_002474	NP_002465	P35749	MYH11_HUMAN	Potential.	15	GGCGGGCCTCC	0.622	
-	16	2189	p.2_Missense_Mu	NM_033266	NP_150296	Q76MJ5	ERN2_HUMAN	.|Cytoplasmic (Potential).	6	GTGGGCCAGGC	0.617	
-	7	1100	FR_uc002eix.2_5'	NM_001144	NP_001135	Q9UKV5	AMFR2_HUMAN		2	GGTAACGCAGCT	0.458	
+	3	467	p.V106M|CPNE2_	NM_152727	NP_689940	Q96FN4	CPNE2_HUMAN	C2 1.	2	AGTTCGTGCTT	0.542	
+	5	438	ALB2_uc002fac.3_	NM_001740	NP_001731	P22676	CALB2_HUMAN	nd 3.|3 (Probable).	0	AGACAGGAGTG	0.542	
+	19	2922	np.1_Missense_M	NM_014003	NP_054722	Q92620	PRP16_HUMAN	case C-terminal.	1	AGGGCGAGCCG	0.637	
+	1	1055	fdl.1_Missense_M	NM_032268	NP_115644	Q8ND25	ZNRF1_HUMAN		0	TCGCACCCAGG	0.677	
+	2	1528	p.A491T|HIC1_uc	NM_001098202	NP_001091672	Q14526	HIC1_HUMAN	2H2-type 2.	1	GCTGCGCGTCG	0.716	
+	3	672	fye.2_Missense_M	NM_001114974	NP_001108446	Q2TAL5	SMTL2_HUMAN		0	CACCCGAGTCT	0.637	
+	12	1995		NM_020877	NP_065928	Q9P225	DYH2_HUMAN	n (By similarity).	13	TGAACGTAGCT	0.542	
+	19	2536	_Mutation_p.V375	NM_012393	NP_036525	O15067	PUR4_HUMAN		5	TGGCAGTGGAT	0.667	
+	6	1420	_uc002gvg.1_Splic	NM_014964	NP_055779	O95208	EPN2_HUMAN		1	AGAGGTAAGAG	0.507	
-	2	1229		NM_198147	NP_937790	Q6UXT9	ABH15_HUMAN		0	GCCTCCGTGGC	0.607	
+	1	239		NM_001146041	NP_001139513	Q9BYQ8	KRA49_HUMAN	-[RQVHIEK]- [SPTR]-[VST	0	CTGCTACCGCC	0.657	
-	1	611		NM_031854	NP_114060	Q9BQ66	KR412_HUMAN		0	GGCAGGTGGA	0.468	
-	5	1192	P_uc010wfs.1_Int	NM_000226	NP_000217	P35527	K1C9_HUMAN	Rod.|Coil 2.	3	GACACCGTGCC	0.547	
+	11	1813	391K|STAT5A_uc	NM_003152	NP_003143	P42229	STA5A_HUMAN		1	GCAGCGAGTGC	0.642	
+	1	1066		NM_001466	NP_001457	Q14332	FZD2_HUMAN	ellular (Potential).	3	TTCTCCGAGGAC	0.597	
+	7	1330	.1_Missense_Mut	NM_016428	NP_057512	Q9P2A4	ABI3_HUMAN	Pro-rich.	0	ACCTGCCTCCT	0.592	
+	6	548	_p.D103E|MSI2_u	NM_138962	NP_620412	Q96DH6	MSI2H_HUMAN	RRM 2.	2	GAAGATGTAAA	0.458	
-	3	607	137_uc002ixa.3_5'	NM_001005207	NP_001005207	O94972	TRI37_HUMAN	-type; degenerate.	7	TTACCGGCAAT	0.373	
-	19	3010	e|ABCA10_uc010	NM_080282	NP_525021	Q8WWZ4	ABCAA_HUMAN		4	TTTATACCTGGTT	0.323	
+	3	303	jpi.3_Missense_Mu	NM_000213	NP_000204	P16144	ITB4_HUMAN	racellular (Potential).	4	CTGCACGGAGT	0.607	
-	18	3376	rl.3_Missense_Mu	NM_022066	NP_071349	Q9C0C9	UBE2O_HUMAN		5	ATCAGCGCCATC	0.577	
+	19	2746	p.G855E|GAA_uc	NM_001079803	NP_001073271	P10253	LYAG_HUMAN		1	CCGAGGGGAG	0.652	
+	2	1425	NDC2_uc002koh.	NM_001098529	NP_001091999	Q86VQ3	TXND2_HUMAN	repeat of Q-P-K-X-G-D-I-P	2	CCAAGGAGGGT	0.592	
+	16	2324	p.2_Missense_Mu	NM_020774	NP_065825	Q86YT6	MIB1_HUMAN		4	GTCAATCGCCAC	0.433	
+	4	1290	YR_uc002kva.2_	NM_012189	NP_036321	O75952	CABYR_HUMAN		0	ATATGGAGGCAG	0.438	
-	5	796	_Mutation_p.R12	NM_004775	NP_004766	Q9UBX8	B4GT6_HUMAN	enal (Potential).	0	ATGGCGATTAC	0.358	

-	8	1010	p.R304Q|FECH_u	NM_000140	NP_000131	P22830	HEMH_HUMAN		1	CCAGTCGGTAG	0.493	rs141888884
-	3	978		NM_001044369	NP_001037834	Q0P6D2	FA69C_HUMAN	enal (Potential).	0	TCAAAGAAATT	0.468	
+	11	1235	BP1_uc002lps.2_	NM_031991	NP_114368	P26599	PTBP1_HUMAN	RRM 3.	2	AGAACGCCCTA	0.677	
-	2	394	dsr.1_Missense_M	NM_020695	NP_065746	Q8N1G1	REXO1_HUMAN	Potential.	0	CCTCACTGCGC	0.607	
+	4	1228	wn.3_Missense_M	NM_152791	NP_690004	Q8NEP9	ZN555_HUMAN	2H2-type 8.	1	TTATCCCCAGT	0.463	
+	10	1158	_Mutation_p.A34	NM_021938	NP_068757	Q8N6W0	CELF5_HUMAN		2	CGCGGCCATCA	0.766	
+	10	1362	3L3_uc010xib.1_	NM_032607	NP_115996	Q68CJ9	CR3L3_HUMAN	enal (Potential).	2	CGACGGAGGAG	0.672	
-	8	2029		NM_198471	NP_940873	Q6NY19	KANK3_HUMAN		0	GGCTCGGTTCT	0.627	
-	1	689		NM_178525	NP_848620	Q8TC94	ACTL9_HUMAN		3	GACACGACCGT	0.652	
-	16	1603	p.R151C|KRI1_uc	NM_023008	NP_075384	Q8N9T8	KRI1_HUMAN		1	TGTGCGGTACT	0.617	
+	4	1932	e_Mutation_p.S62	NM_144566	NP_653167	Q9H0M5	ZN700_HUMAN	2H2-type 14.	0	TTCAGTTGTGC	0.483	
+	1	286		NM_001098622	NP_001092092	P60323	NANO3_HUMAN		1	AGTGCCGGGAC	0.662	
+	10	774	_p.R61Q|TECR_	NM_138501	NP_612510	Q9NZ01	TECR_HUMAN		0	CCTGCGGGACC	0.677	
-	10	1518	2_5'Flank|RASAL	NM_022904	NP_075055	Q86YV0	RASL3_HUMAN	Ras-GAP.	0	CAGCGCCTAGG	0.632	
+	8	1011	p.E292K|AP1M1_	NM_032493	NP_115882	Q9BXS5	AP1M1_HUMAN	MHD.	4	GGATCGAGTCG	0.587	
+	40	6220	2_3'UTR|MYO9B_	NM_004145	NP_004136	Q13459	MYO9B_HUMAN	Tail.	1	CCCTGCGCCTG	0.711	
-	4	935		NM_001159293	NP_001152765	C9JHM3	C9JHM3_HUMAN		1	TCTCCACTATGA	0.403	
-	4	984	p.N198K|ZNF708_	NM_021269	NP_067092	P17019	ZN708_HUMAN	2H2-type 5.	6	GACCGGTTAAA	0.368	
+	2	1395	p.Q500R|ZNF493	NM_175910	NP_787106	Q6ZR52	ZN493_HUMAN	2H2-type 13.	1	TTAACCAATCTT	0.343	
+	4	1693	429_uc010ecu.1_	NM_001001415	NP_001001415	Q86V71	ZN429_HUMAN	2H2-type 14.	2	CTTTTATCCTGT	0.378	
+	4	1696	429_uc010ecu.1_	NM_001001415	NP_001001415	Q86V71	ZN429_HUMAN	2H2-type 14.	2	TTATCCTGTCCT	0.378	
-	3	1694		NM_001001411	NP_001001411	Q8N7Q3	ZN676_HUMAN	2H2-type 11.	0	ACCAGGTGAAG	0.433	
+	4	1398		NM_020855	NP_065906	Q9P255	ZN492_HUMAN	2H2-type 9.	0	ATAAGAGAATTC	0.378	
-	4	1876		NM_175872	NP_787068	Q3KQV3	ZN792_HUMAN	2H2-type 10.	0	TCTCCGATGGC	0.493	
+	2	618	a.2_Missense_M	NM_005306	NP_005297	O15552	FFAR2_HUMAN	Name=5; (Potential).	1	CCGTGCGGCTG	0.542	
+	3	1828		NM_014727	NP_055542	Q9UMN6	MLL4_HUMAN	Pro-rich.	11	CATTTCGCTGG	0.408	
+	2	505	9A_uc002oru.2_I	NM_001783	NP_001774	P11912	CD79A_HUMAN	.|Extracellular (Potential).	3	GTGCCGGGTCC	0.642	rs143511203
-	2	155	tq.3_Missense_M	NM_032488	NP_115877	Q9BYD5	CNFN_HUMAN	Cys-rich.	0	CATGTCGTTGC	0.612	
-	1	1961		NM_032040	NP_114429	Q9H0W5	CCDC8_HUMAN		3	GGGCCTCTGCC	0.607	
-	3	1092	C10_uc010ycy.1_	NM_033130	NP_149121	Q96LC7	SIG10_HUMAN	otential).|Ig-like C2-type 1.	1	TCACCGGCTGC	0.607	rs143118289
-	5	1005	77_uc010ydf.1_5'	NM_023074	NP_075562	Q9BS31	ZN649_HUMAN	2H2-type 3.	3	CTGTACCTCTTG	0.502	
-	5	785	.2_Intron|uc002py	NM_021632	NP_067645	Q9GZX5	ZN350_HUMAN		1	TTAGTGCTGATG	0.408	
-	4	2192	p.Y638C|ZNF28_	NM_006969	NP_008900	P17035	ZNF28_HUMAN	2H2-type 18.	1	ACTTGTAAGGT	0.403	
+	4	2549	dw.1_Missense_M	NM_138374	NP_612383	Q96IR2	ZN845_HUMAN	2H2-type 22.	0	CAAGAACTTCC	0.418	
+	7	2551	p.N644T|ZNF761_	NM_001008401	NP_001008401	Q86XN6	ZN761_HUMAN	2H2-type 18.	1	CAAGAACTTTA	0.393	
+	3	1110		NM_021216	NP_067039	Q9NQZ8	ZNF71_HUMAN	2H2-type 6.	1	GCGCACGCACA	0.657	
+	6	861		NM_182572	NP_872378	Q8NBB4	ZSCA1_HUMAN		2	CCGGGCCCGCT	0.662	
+	14	1725	zp.1_Missense_M	NM_016207	NP_057291	Q9UKF6	CPSF3_HUMAN		2	ATGGTGGTATTA	0.313	
-	34	4364	f.2_Missense_Mut	NM_006277	NP_006268	Q9NZM3	ITSN2_HUMAN	DH.	4	TCTCCGGGGTG	0.597	
-	3	490	rkj.2_Missense_M	NM_144631	NP_653232	Q8N8E2	ZN513_HUMAN	Gly-rich.	1	TCTCCGCACTT	0.662	rs35554630
+	1	5038	1_5'Flank|ZNF512	NM_032266	NP_115642	Q68DN1	CB016_HUMAN	m repeat of P-S-E-R-S-H-	1	GCCATCGCAGT	0.577	
+	3	1197	mi.1_Missense_M	NM_005253	NP_005244	P15408	FOSL2_HUMAN	Basic motif.	3	GCATCCGGCGG	0.557	rs139808662
-	2	353	e_Mutation_p.P10	NM_019885	NP_063938	Q9NR63	CP26B_HUMAN		2	TGCGAGGCCAC	0.562	
+	2	662	Intron|TEKT4_uc0	NM_144705	NP_653306	Q8WW24	TEKT4_HUMAN		3	GATCCGGTGGG	0.597	
-	16	2457		NM_018383	NP_060853	Q9C0J8	WDR33_HUMAN	ollagen-like.	0	CCTTGGATCCC	0.622	
+	29	3290	r.2_Missense_Mu	NM_020120	NP_064505	Q9NYU2	UGGG1_HUMAN		1	TTTTACCGTTAT	0.383	
-	3	687		NM_001099771	NP_001093241	A5A3E0	POTEF_HUMAN		5	ATCTTGTTCCTG	0.607	

+	8	9907	dy.2_Missense_Mu	NM_152381	NP_689594	A4UGR9	XIRP2_HUMAN		14	ATCATCCGCAAG	0.458	
-	214	42435	_uc010zfi.1_Misse	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	CACTGGGTTCAC	0.483	
+	2	941		NM_005383	NP_005374	Q9Y3R4	NEUR2_HUMAN		0	CCCGCGACCTC	0.692	
-	28	7111	znj.1_Missense_M	NM_004369	NP_004360	P12111	CO6A3_HUMAN	l region.|Collagen-like 4.	18	GCTCTCCGGGCT	0.597	
+	2	93	ense_Mutation_p.V	NM_080741	NP_542779	Q8WWR8	NEUR4_HUMAN		0	ATGGGGGTCCCT	0.697	
+	4	639	0zrc.1_Missense_	NM_012261	NP_036393	Q9UJQ1	CT103_HUMAN	cellular (Potential).	3	CTTGGAGGCTGA	0.577	
+	5	781		NM_080820	NP_543010	Q8TEA8	DTD1_HUMAN		2	TGAACGGGAGC	0.537	
+	2	273	se_Mutation_p.R6	NM_022896	NP_075047	Q9BQK8	LPIN3_HUMAN	N-LIP.	4	GTCGCGGGAGA	0.642	
-	37	7689	jz.1_Missense_Mu	NM_032221	NP_115597	Q8TD26	CHD6_HUMAN		14	GCATCGTGGCA	0.572	rs150243429
+	4	496	gp.2_Missense_M	NM_001098798	NP_001092268	Q96NM4	TOX2_HUMAN		1	TGACTCGGGCC	0.627	rs139062099
-	4	376	ih.1_Nonsense_M	NM_006045	NP_006036	O75110	ATP9A_HUMAN	lasmic (Potential).	4	AGCATCGGATCT	0.612	
+	3	497		NM_080821	NP_543011	Q96KR6	CT108_HUMAN	DUF1279.	0	CTGGTACAGTCA	0.483	
+	1	566		NM_174981	NP_778146	Q86YR6	POTED_HUMAN	ANK 1.	6	GACAAGGAAAAG	0.577	
-	4	452	p.W143*|TMPRSS	NM_005656	NP_005647	O15393	TMPS2_HUMAN	cellular (Potential).	2524	AACTTCCAGAG	0.592	
+	14	2652	j.2_Missense_Mut	NM_006031	NP_006022	O95613	PCNT_HUMAN		8	AGGACGGGGAG	0.667	
+	14	1836	_p.Q520*|MED15_	NM_001003891	NP_001003891	Q96RN5	MED15_HUMAN		1	ACCTTGCAAAAG	0.562	
+	5	1661		NM_152612	NP_689825	Q8IYX3	CC116_HUMAN		2	CAGAGACACCCT	0.667	
-	3	573	s.1_3'UTR|uc003a	NM_002309	NP_002300	P15018	LIF_HUMAN		0	ACAGGCGGCAC	0.612	
+	4	515	oz.3_Missense_Mu	NM_000631	NP_000622	Q15080	NCF4_HUMAN	PX.	1	CTCAACGCCTAC	0.582	
+	7	1164		NM_015653	NP_056468	Q9H4K1	RIBC2_HUMAN		0	GCTCGCGCCACC	0.647	
-	15	6058	arc.1_Missense_M	NM_014246	NP_055061	Q9NYQ6	CELR1_HUMAN	otential).|Laminin EGF-like	11	ACTGCCCGGTGG	0.642	
-	16	4300	CP6_uc010har.1_	NM_020461	NP_065194	Q96RT7	GCP6_HUMAN	A tandem repeats.|9.	4	GTGGCCGGGTG	0.647	rs145170543
+	10	1391	_p.R328Q|TTLL3_	NM_001025930	NP_001021100	Q9Y4R7	TTLL3_HUMAN	TTL.	2	GCCATCGGCATC	0.572	rs141771643
+	3	1207	tr.1_Missense_Mu	NM_014760	NP_055575	Q93075	TATD2_HUMAN		2	CCACTCGGGCAA	0.567	
+	8	1149	zi.2_Missense_Mu	NM_003298	NP_003289	P49116	NR2C2_HUMAN		0	TAACTCGGTACG	0.502	
+	1	140		NM_145166	NP_660149	Q9UFB7	ZBT47_HUMAN		0	GCCGGGGTACCC	0.721	
-	8	2376	al.1_Missense_Mu	NM_024513	NP_078789	Q9BQS8	FYCO1_HUMAN	Potential.	1	GGCTTCTGCCA	0.602	
-	5	783	31_splice|PRKAR2	NM_004157	NP_004148	P13861	KAP2_HUMAN		1	CTCCTACCGTTC	0.428	
-	8	1123	MT_uc003cwy.2_M	NM_000481	NP_000472	P48728	GCST_HUMAN		1	GTGTGCCCGCA	0.617	
+	10	1335	w.1_Missense_Mu	NM_001640	NP_001631	P13798	ACPH_HUMAN		1	ACCAATGTCGCA	0.612	
-	6	847		NM_003335	NP_003326	P41226	UBA7_HUMAN	roximate repeats.	2	AGACCGGGGAT	0.562	
+	12	1177	o.S321N|SLC38A3	NM_006841	NP_006832	Q99624	S38A3_HUMAN		1	CTACAGTACGG	0.602	
+	5	2400	_p.P719S|COL8A1	NM_001850	NP_001841	P27658	CO8A1_HUMAN	helical region (NC1).	0	CAGATGCCCTCA	0.502	
+	8	735	_Mutation_p.A191	NM_172027	NP_742024	Q969K4	ABTB1_HUMAN		0	AGTGGCGTCTA	0.667	
-	3	1205	1blk.1_5'Flank|NE	NM_014065	NP_054784	Q2TB18	ASTE1_HUMAN		0	GGATTCGGTGGT	0.433	
+	2	626	esi.3_Missense_Mu	NM_012219	NP_036351	O14807	RASM_HUMAN	P (By similarity).	4	GGATGGGGGTG	0.552	
+	2	810		NM_152616	NP_689829	Q8IWZ5	TRI42_HUMAN		7	CTGCCCGAGAAC	0.617	
-	5	1197	e_Mutation_p.V26	NM_033169	NP_149359	O75752	B3GL1_HUMAN	enal (Potential).	1	GTTTTACGTGAC	0.378	
+	8	2148		NM_004443	NP_004434	P54753	EPHB3_HUMAN	ical; (Potential).	11	TCTTCGTGGTG	0.627	rs147361564
-	3	1712	tron|ABCA11P_uc	NM_133474	NP_597731	D9N162	D9N162_HUMAN		1	TAAAGGTTTTGC	0.433	
-	3	1698	ron|ABCA11P_uc0	NM_133474	NP_597731	D9N162	D9N162_HUMAN		1	CATTCTCCACAT	0.428	
+	17	3319	3gee.3_RNA|WHS	NM_001042424	NP_001035889	O96028	NSD2_HUMAN	AWS.	9	TCCCGCGGGCG	0.562	
+	27	3453		NM_002111	NP_002102	P42858	HD_HUMAN		4	CCAGTGCTCCCA	0.542	
-	3	557	.1_Missense_Mut	NM_001290	NP_001281	O43679	LDB2_HUMAN		0	TCCTGCCGATAG	0.478	
+	4	472	D28_uc003gpj.2_F	NM_025205	NP_079481	Q9H204	MED28_HUMAN		0	AGCCCGCCGAC	0.567	rs139145192
+	4	370	_p.G96R|SLC34A	NM_006424	NP_006415	O95436	NPT2B_HUMAN	lasmic (Potential).	5	TCCAAGGGATTG	0.473	
-	13	1732	XL1_uc003gxq.3_	NM_152995	NP_694540	Q6ZNB6	NFXL1_HUMAN	NF-X1-type 7.	3	GGCAGGGATAGC	0.333	

-	42	5691	YL_uc003gyi.1_Mi	NM_015030	NP_055845	O94915	FRYL_HUMAN		1	TAAAATCGTTAAT	0.388	
+	9	1589	du.1_Missense_Mu	NM_001510	NP_001501	O43424	GRID2_HUMAN	cellular (Potential).	6	TTCTACGTGTAG	0.388	
-	13	2132	1ckv.1_Missense_I	NM_021069	NP_066547	O94875	SRBS2_HUMAN		1	CGTAGGGGGAC	0.597	
+	10	1715	_p.A526D|ADAMTS	NM_139056	NP_620687	Q8TE57	ATS16_HUMAN	Disintegrin.	8	AGAAAGCCAAGC	0.408	
+	4	1361		NM_012304	NP_036436	Q9UJT9	FBXL7_HUMAN	LRR 5.	3	CCATCGCGGCG	0.607	
-	14	2067		NM_198566	NP_940968	Q96MH7	CE034_HUMAN		1	AAATCTGGTTTAC	0.308	
+	4	948		NM_014979	NP_055794	Q496J9	SV2C_HUMAN	lasmic (Potential).	1	TGGCCCGGGAA	0.562	
-	1	473	_uc011cxy.1_Miss	NM_002653	NP_002644	P78337	PITX1_HUMAN		1	GGCCCCATGTCAT	0.706	
+	4	1152		NM_032289	NP_115665	Q9BQI7	PSD2_HUMAN	SEC7.	1	CTCATCGGCTGG	0.647	
+	1	1930	1daj.1_Missense_M	NM_018931	NP_061754	Q9Y5F2	PCDBB_HUMAN	r (Potential).|Cadherin 6.	6	GTGCTGGTCAAG	0.711	
+	1	1880	dak.1_Missense_M	NM_018932	NP_061755	Q9Y5F1	PCDBC_HUMAN	cellular (Potential).	3	TGTACCCGCTGCA	0.716	
+	1	694	DHGA3_uc010jfx.	NM_018916	NP_061739	Q9Y5H0	PCDG3_HUMAN	r (Potential).|Cadherin 2.	1	GTGATAGTCCTGC	0.537	
+	4	776	ncf.2_Missense_M	NM_153607	NP_705835	Q8IUR6	CE041_HUMAN		0	TACCCCGATTCAC	0.403	
-	3	748	D1_uc003mcr.2_In	NM_138369	NP_612378	Q96IK1	BOD1_HUMAN		2	TCCTGGCCTTCG	0.512	
-	18	3045	1djq.1_Nonsense_	NM_014809	NP_055624	Q5VV43	K0319_HUMAN	cellular (Potential).	2	CTCCATCCATAAC	0.522	
-	3	755	w.2_Missense_Mu	NM_002586	NP_002577	P40425	PBX2_HUMAN		1	TGCTGCGATAGTC	0.602	
-	7	1094	p.R319Q|MOCS1_	NM_005942	NP_005933	Q9NZB8	MOCS1_HUMAN	factor biosynthesis protein A	3	GTGATTCGCAGG	0.572	rs104893969
-	6	587	RPS18A_uc003ow	NM_018135	NP_060605	Q9NVS2	RT18A_HUMAN		0	AGCTTCCAAGGTC	0.567	
+	26	1918	kam.1_Missense_M	NM_001858	NP_001849	Q14993	COJA1_HUMAN	lical region 3 (COL3).	4	CTGGTCCACGTC	0.308	
-	26	2843	okc.2_Missense_M	NM_014841	NP_055656	O60641	AP180_HUMAN	Pro-rich.	1	ACTCACCATTCCA	0.313	
+	7	1916	5E_uc010kbr.2_Int	NM_002526	NP_002517	P21589	5NTD_HUMAN		4	GTGGGCGGTAAG	0.373	
-	8	1383	dzv.1_Missense_M	NM_002042	NP_002033	P24046	GBRR1_HUMAN	ical; (Probable).	1	AGGCACGGCTC	0.478	
+	3	710	e_Mutation_p.G179	NM_018593	NP_061063	Q8TF71	MOT10_HUMAN	ical; (Potential).	0	CCTGCGGCTGC	0.448	
+	1	204	ense_Mutation_p.A	NM_001127715	NP_001121187	Q5T5C0	STXB5_HUMAN		0	CTGACCGCCGGC	0.682	
+	1	51		NM_025218	NP_079494	Q9BZM6	N2DL1_HUMAN		1	GGCAGCGGCCG	0.652	
-	14	1483	p.G333R|RPS6KA2	NM_021135	NP_066958	Q15349	KS6A2_HUMAN	ilarity).|Protein kinase 2.	8	CCACCCCGATGT	0.557	
+	16	2290	h.2_Missense_Mu	NM_178559	NP_848654	Q2M3G0	ABCB5_HUMAN	otential).|ABC transporter 2	6	CATGTCGCCCAC	0.468	
-	5	1584		NM_033273	NP_150376	Q96JC4	ZN479_HUMAN	C2H2-type 10.	4	TCACATTTGTAGG	0.453	
-	10	1604	dt.1_Missense_Mu	NM_000181	NP_000172	P08236	BGLR_HUMAN		0	CGTAGTCGTGATA	0.507	rs146011906
+	7	1142	3tvz.2_Missense_I	NM_022479	NP_071924	Q6IS24	GLTL3_HUMAN	main B.|Lumenal (Potential	7	TGAGCGGAAGA	0.488	
+	6	894		NM_001099435	NP_001092905	A6NIY4	SPDE5_HUMAN	Arg-rich.	0	TAGGCCGTTCCAT	0.592	
-	15	1860		NM_004333	NP_004324	P15056	BRAF_HUMAN	rotein kinase_R603>I(2)|p.T	18290	GATTTCACTGTAC	0.368	
-	4	1707		NM_001001661	NP_001001661	Q6IV72	ZN425_HUMAN	C2H2-type 12.	3	AGCCTCGTGTGC	0.637	
+	11	1287	on_p.V404M|NUB1	NM_016118	NP_057202	Q9Y5A7	NUB1_HUMAN	UBA 1.	0	GGAACGTGGAT	0.478	
+	2	2554	au.1_Missense_Mu	NM_024721	NP_078997	Q86UP3	ZFHX4_HUMAN	C2H2-type 3.	15	GACAAGCACCTG	0.507	
+	6	1055	_p.A297T|GRINA_u	NM_001009184	NP_001009184	Q7Z429	GRINA_HUMAN	ical; (Potential).	1	ATCTTCGCCATTC	0.612	
-	6	397	_p.P115L|VPS28_	NM_016208	NP_057292	Q9UK41	VPS28_HUMAN	S28 N-terminal.	0	GTGATGGGCCGG	0.667	
+	2	675		NM_212558	NP_997723	Q68D42	TM215_HUMAN		0	AATCCGGCAAGC	0.602	
+	10	1634	SK1_uc010mks.2_	NM_006285	NP_006276	Q15569	TESK1_HUMAN		7	TGCCCGCCGCTC	0.672	
+	6	668	omf.1_Missense_M	NM_000962	NP_000953	P23219	PGH1_HUMAN		2	GGCCCGCCGCT	0.552	
-	4	1121	_p.E24K|PTGES2_	NM_025072	NP_079348	Q9H7Z7	PGES2_HUMAN	lasmic (Potential).	0	CCTTCTCGTTGAC	0.597	
+	33	4338	p.G1409R|SPTAN1	NM_003127	NP_003118	Q13813	SPTA2_HUMAN	Spectrin 15.	10	GCTCACGGACAC	0.547	
-	2	1981	BED1_uc004cqh.1_	NM_004729	NP_004720	O96006	ZBED1_HUMAN		0	CAGGCGGTCTG	0.642	
-	6	3690	OOM4_uc004dpd.3	NM_020717	NP_065768	Q9ULL8	SHRM4_HUMAN	ASD2.	1	CCAAGTGACCCC	0.547	
+	3	2072	2_Intron|ZCCHC18	NM_001143978	NP_001137450	P0CG32	ZCC18_HUMAN		0	CGCCCAGCCAATA	0.493	
+	4	1679	EC1_uc010nsl.1_I	NM_005462	NP_005453	O60732	MAGC1_HUMAN		4	CTGAGAGAACTC	0.478	
+	4	2019	EC1_uc010nsl.1_I	NM_005462	NP_005453	O60732	MAGC1_HUMAN		4	CTCCTCACTACTT	0.582	

-	2	122	V22I|CPSF3L_uc	NM_017871	NP_060341	Q5TA45	INT11_HUMAN		0	GGAGACCAGGA	0.647	
-	3	689	vkg.1_Splice_Site_	NM_014188	NP_054907	Q9NP77	SSU72_HUMAN		0	TCCTCACCTTCC	0.582	
-	9	935	FRSF25_uc009vl	NM_003790	NP_003781	Q93038	TNR25_HUMAN	lasmic (Potential).	3	GCCAGGGGTCC	0.617	
-	13	1550	0nzr.1_Splice_Site	NM_001042663	NP_001036128	O94827	PKHG5_HUMAN		1	CCGTACCATCT	0.721	
+	7	1942	apc.2_Missense_	NM_001080397	NP_001073866	Q9Y2W3	S45A1_HUMAN		4	ACCTTGCCTTAC	0.547	
-	21	4732		NM_001079843	NP_001073312	Q86V15	CASZ1_HUMAN	2H2-type 6.	1	GCGTGCGCCCG	0.607	
-	35	5057		NM_004958	NP_004949	P42345	MTOR_HUMAN	FAT.	29	ATGAGGGCTGA	0.537	
+	1	72	_Translation_Start	NM_018090	NP_060560	Q9NVZ3	NECP2_HUMAN		0	GTTCGGTGGGC	0.662	
+	8	911		NM_207421	NP_997304	Q6TGC4	PADI6_HUMAN		1	TGGCTCCCTGTG	0.537	
-	6	825	m.2_Missense_M	NM_001136204	NP_001129676	Q9P258	RCC2_HUMAN	RCC1 3.	0	ACAGGCCATTT	0.403	
+	4	959		NM_032409	NP_115785	Q9BXM7	PINK1_HUMAN	.|Cytoplasmic (Potential).	3	TGCTGCCAGGG	0.602	
+	8	1783		NM_020526	NP_065387	P29322	EPHA8_HUMAN	ical; (Potential).	13	CACGGGCCTGG	0.647	
-	11	1793	bgs.3_Missense_	NM_005826	NP_005817	O43390	HNRPR_HUMAN	binding RGG-box.	2	CTCTGCCACCC	0.622	
+	9	1195	_uc009vrc.2_Miss	NM_020448	NP_065181	Q6P499	NPAL3_HUMAN		0	TCAAGCCTCAC	0.463	
+	12	1785	_Mutation_p.R48	NM_005839	NP_005830	Q8IYB3	SRRM1_HUMAN	d matrix localization.|Arg-ri	3	GGCGGCGGAG	0.483	
+	12	1164	nse_Mutation_p.G	NM_006314	NP_006305	Q969H4	CNKR1_HUMAN	Pro-rich.	2	TCCAGGGCTCC	0.632	
+	3	800	_p.L157F|PIGV_u	NM_017837	NP_060307	Q9NUD9	PIGV_HUMAN	ical; (Potential).	1	TCTGTCTCAGC	0.527	
-	12	2869	_p.P252L|SLC9A1_	NM_003047	NP_003038	P19634	SL9A1_HUMAN	lasmic (Potential).	2	TTGCAGGATCC	0.607	
+	7	977	gj.1_Missense_M	NM_022164	NP_071447	Q9GZM7	TINAL_HUMAN		0	GCGTCGCCGAG	0.637	
-	6	1410		NM_003680	NP_003671	P54577	SYYC_HUMAN		2	ATGGACCCGTT	0.433	
-	9	1682	se_Mutation_p.S5	NM_198040	NP_932157	Q8IXK0	PHC2_HUMAN		1	AGGCAGAGTTT	0.552	
+	6	1101	_p.Y258H|ZSCAN	NM_145238	NP_660281	P17040	ZSC20_HUMAN		4	AACAATACCAG	0.483	
-	11	2131	ux.2_Missense_M	NM_022111	NP_071394	Q9HAW4	CLSPN_HUMAN		8	CTTCACTACTAA	0.353	
+	3	630	IRIN1_uc010oiq.	NM_024595	NP_078871	Q9H9L7	AKIR1_HUMAN		0	AACTAGCAGGT	0.403	
+	1	1293	.1_Intron|MACF1_	NM_033044	NP_149033	Q9UPN3	MACF1_HUMAN		16	TACCGTGCAGC	0.448	
+	8	3743	.3_Missense_Mut	NM_012421	NP_036553	Q13129	RLF_HUMAN		3	GTAGTAACTCT	0.373	
+	8	1061	ki.1_Missense_M	NM_014663	NP_055478	O75164	KDM4A_HUMAN	JmjC.	1	TTGAGTACGGC	0.428	
+	21	2228	.1_Missense_Mut	NM_006845	NP_006836	Q99661	KIF2C_HUMAN		1	CCTTGCGCCTG	0.527	
+	26	3744	_Mutation_p.G11	NM_015112	NP_055927	Q6P0Q8	MAST2_HUMAN	PDZ.	11	TCAAGGTGACC	0.592	
+	17	1964	p.Y617S|RAD54L_	NM_001142548	NP_001136020	Q92698	RAD54_HUMAN	case C-terminal.	3	CTTGCTATATCTA	0.522	
-	13	1517	p.A435V|SPATA6_	NM_019073	NP_061946	Q9NWH7	SPAT6_HUMAN		1	AAGAGGCTGCC	0.428	
-	6	1120	tu.2_Missense_M	NM_004153	NP_004144	Q13415	ORC1_HUMAN		0	AGAGAGTCCAG	0.463	rs140388455
-	57	6659		NM_015306	NP_056121	Q9UPU5	UBP24_HUMAN		13	GGAGGGGCAAC	0.453	
-	1	1323	_5'Flank|uc010oo	NM_002228	NP_002219	P05412	JUN_HUMAN		0	GGTGGGGGTCG	0.667	
+	5	576	ddf.2_Missense_	NM_001077700	NP_001071168	Q8N108	MIER1_HUMAN	Glu-rich.	1	agaagaaggtgaag	0.269	
-	12	1851	ron|WLS_uc001d	NM_024911	NP_079187	Q5T9L3	WLS_HUMAN	lasmic (Potential).	0	TGGGTCCGTCC	0.572	
+	6	1073	ls.1_Missense_M	NM_001285	NP_001276	A8K7I4	CLCA1_HUMAN	VWFA.	1	ATCTGGAAGCA	0.433	
+	4	877	p.A253T|VCAM1_	NM_001078	NP_001069	P19320	VCAM1_HUMAN	3.|Extracellular (Potential).	1	TACCAGCTCCA	0.433	
-	6	1317	FM3_uc001dui.2_	NM_058170	NP_477518	Q96PB7	NOE3_HUMAN	actomedin-like.	3	ATACACCTTGG	0.453	
-	1	467	M3_uc001dui.2_R	NM_058170	NP_477518	Q96PB7	NOE3_HUMAN		3	TCCGGCAAACA	0.398	
-	6	1204	OL11A1_uc001du	NM_001854	NP_001845	P12107	COBA1_HUMAN	nhelical region.	12	TCTGTGCTATTG	0.443	
+	12	2142	1dur.2_Missense_	NM_020978	NP_066188	P19961	AMY2B_HUMAN		0	GCTGAATCtaatt	0.279	
+	14	1789	_p.W464*|KIAA13	NM_020775	NP_065826	Q6UXG2	K1324_HUMAN	ellular (Potential).	5	ACCTGGGCCTT	0.522	
+	12	1618	gn.1_Missense_M	NM_014813	NP_055628	O94898	LRIG2_HUMAN	xtracellular (Potential).	3	CACACCCTGAA	0.363	
-	1	1650		NM_021794	NP_068566	Q9UKF2	ADA30_HUMAN	xtracellular (Potential).	3	TGCACCCCTTC	0.468	
+	1	601	bs.1_Intron|VPS4	NM_007259	NP_009190	Q9NRW7	VPS45_HUMAN		2	AAGCAGTACATT	0.478	
+	4	321	_p.P95S|C1orf54_	NM_024579	NP_078855	Q8WWF1	CA054_HUMAN		0	TGAAACCAGTA	0.498	

-	2	942	e_Mutation_p.G16	NM_021960	NP_068779	Q07820	MCL1_HUMAN	BH1.	0	AGGCACCAAAA	0.443
-	6	885	vq.1_Missense_Mu	NM_000396	NP_000387	P43235	CATK_HUMAN		1	AGGAGGTCAGG	0.502
+	2	224	NE_uc010pco.1_5	NM_021222	NP_067045	Q86TP1	PRUNE_HUMAN		1	ATTTGGACTCC	0.343
-	3	589	dc.1_Intron|POGZ	NM_015100	NP_055915	Q7Z3K3	POGZ_HUMAN		3	ACTTACCATTG	0.468
-	3	2954		NM_001009931	NP_001009931	Q86YZ3	HORN_HUMAN	10	3	GCCGTGTTGTT	0.547
-	3	1743	c001ezv.2_5'Flan	NM_002016	NP_002007	P20930	FILA_HUMAN	Ser-rich.	16	GTTTGTCTGCT	0.537
-	6	457	k.2_Missense_Mu	NM_004515	NP_004506	Q12905	ILF2_HUMAN	DZF.	0	TCTTGAGTATCA	0.413
+	1	693	7A3_uc009won.2_	NM_024330	NP_077306	Q5K4L6	S27A3_HUMAN		1	CCGCCCCTCTG	0.726
-	5	403	G86E|PBXIP1_uc	NM_020524	NP_065385	Q96AQ6	PBIP1_HUMAN		1	CTGGTCCCAGG	0.612
-	3	1360	1_uc001ffs.2_5'F	NM_138300	NP_612157	Q9BRQ0	PYGO2_HUMAN	PHD-type.	1	CCTTGGTCTTG	0.587
+	15	2008	636D|ADAM15_u	NM_207197	NP_997080	Q13444	ADA15_HUMAN	ar (Potential).|Cys-rich.	6	CTGTGGCCCTG	0.587
+	10	2139	nse_Mutation_p.	NM_025058	NP_079334	Q7Z4K8	TRI46_HUMAN	30.2/SPRY.	3	CAGTGCCCCTG	0.647
-	11	1885	e_Mutation_p.P49	NM_005920	NP_005911	Q14814	MEF2D_HUMAN		1	GGCTGGGCGCA	0.652
+	4	777	hq.1_Missense_M	NM_021817	NP_068589	Q9GZV7	HPLN2_HUMAN	g-like V-type.	0	ACGAGGGCCGG	0.711
-	4	3356		NM_006617	NP_006608	P48681	NEST_HUMAN	Tail.	6	GTCACCCCCTG	0.682
+	2	137	1fza.1_Missense_	NM_004106	NP_004097	P30273	FCERG_HUMAN	ical; (Potential).	0	GAATTGTCCTC	0.592
-	2	204		NM_182581	NP_872387	Q5T0L3	CA111_HUMAN		1	CTGGGCTGGAT	0.547
+	2	790	0794_uc001gdd.2	NM_001005214	NP_001005214	Q8N7C0	LRC52_HUMAN	ical; (Potential).	1	AAGACTACATCT	0.607
-	3	910	1_RNA|FAM78B_	NM_001017961	NP_001017961	Q5VT40	FA78B_HUMAN		2	CATCTGAGTCA	0.522
-	16	5521		NM_000130	NP_000121	P12259	FA5_HUMAN	3.|Plastocyanin-like 6.	6	AGTCTCCAAGA	0.383
+	29	7813	0pmi.1_Missense_	NM_015172	NP_055987	Q9Y520	PRC2C_HUMAN	Gln-rich.	0	AAATACTCAGC	0.478
+	8	1399	p.G218D|KLHL20_	NM_014458	NP_055273	Q9Y2M5	KLH20_HUMAN	Kelch 2.	1	TGTTGGTGTAG	0.458
+	18	2368	wxs.2_Missense_	NM_000721	NP_000712	Q15878	CAC1E_HUMAN	lasmic (Potential).	6	AGGAGGTCAGC	0.522
+	37	5218	1gox.1_Missense_	NM_000721	NP_000712	Q15878	CAC1E_HUMAN	llular (Potential).|IV.	6	CCGCACCATCA	0.552
+	8	942	ps.2_Missense_M	NM_001357	NP_001348	Q08211	DHX9_HUMAN	ction with BRCA1.	2	TTACTCCGGAC	0.413
+	25	4014		NM_031935	NP_114141	Q96RW7	HMCN1_HUMAN	ike C2-type 10.	23	ACCACCCACAG	0.393
+	5	1208	w.2_Missense_Mu	NM_004600	NP_004591	P10155	RO60_HUMAN	TROVE.	0	GGCGCCCTGAT	0.333
+	7	1427	sw.2_Missense_M	NM_004600	NP_004591	P10155	RO60_HUMAN		0	CCGATGAAATG	0.343
+	11	1856		NM_000186	NP_000177	P08603	CFAH_HUMAN	Sushi 9.	6	ATGATGGTTATG	0.289
+	8	1333		NM_030787	NP_110414	Q9BXR6	FHR5_HUMAN	Sushi 7.	2	ATATGACAACCA	0.333
+	6	2263	pb.1_Splice_Site_	NM_201253	NP_957705	P82279	CRUM1_HUMAN		9	GAGAGGTGAGA	0.512
+	9	1354	p.P351S|CAMSAF	NM_203459	NP_982284	Q08AD1	CAMP2_HUMAN		4	TCAATTCCTGTC	0.328
-	5	609	RP1_uc010ppr.1_	NM_004078	NP_004069	P21291	CSRP1_HUMAN	zinc-binding 2.	1	CTTATGCCAGG	0.527
+	3	658	NPEP_uc001gxf.2	NM_020216	NP_064601	Q9H4A4	AMPB_HUMAN		1	CACCTGGGAGA	0.473
-	2	489	OD_uc010pqi.1_R	NM_002023	NP_002014	Q06828	FMOD_HUMAN	LRR 1.	3	ATGGAGGTGATC	0.537
+	2	1047	zt.2_Missense_Mu	NM_002725	NP_002716	P51888	PRELP_HUMAN	LRR 9.	3	GGGGACTCCCC	0.498
+	2	595	plice_Site|SOX13	NM_005686	NP_005677	Q9UN79	SOX13_HUMAN		2	CCCCAGGATGT	0.597
-	2	2421		NM_032833	NP_116222	Q5SWA1	PR15B_HUMAN		2	TTCTGGAACCT	0.393
-	22	3728	pqv.1_Splice_Site	NM_002646	NP_002637	O00750	P3C2B_HUMAN		7	TCTCACCTTGA	0.522
-	6	1836	_p.T591I|DSTYK_	NM_015375	NP_056190	Q6XUX3	DUSTY_HUMAN		1	GCCGAGTCCGG	0.542
-	3	1917	z.2_Missense_Mu	NM_001973	NP_001964	P28324	ELK4_HUMAN		0	AAGCTTGGATAG	0.478
-	5	938		NM_001007544	NP_001007545	Q6ZWK4	CA186_HUMAN		0	GCGAACTGCAG	0.507
-	3	572	bz.2_Splice_Site_	NM_002644	NP_002635	P01833	PIGR_HUMAN		3	CCTTACCCTGG	0.562
-	4	739	xca.1_Missense_	NM_001122980	NP_001116452	Q8WWV6	FCAMR_HUMAN	ellular (Potential).	1	GGGTCCTGGAG	0.592
+	11	1801		NM_000715	NP_000706	P04003	C4BPA_HUMAN	Sushi 8.	3	GGTGCCCAAGT	0.507
+	9	898	p.Y266H|CAMK1G	NM_020439	NP_065172	Q96NX5	KCC1G_HUMAN	rotein kinase.	1	AGCGGTACACC	0.493
+	5	630	OR3_uc010psw.1	NM_018254	NP_060724	Q9P2K3	RCOR3_HUMAN		1	TCAGGGTGACA	0.383

-	5	1297	hiv.2_Missense_M	NM_014873	NP_055688	Q92604	LGAT1_HUMAN		2	GAGAAGCAGCA	0.393	
-	13	2612	0puz.1_Missense_	NM_001031685	NP_001026855	Q13625	ASPP2_HUMAN		3	ATGATGGGACAG	0.478	
-	14	1413		NM_014698	NP_055513	O94886	TM63A_HUMAN		2	GCTCCCTGCTAT	0.547	
-	2	1025	jh.2_Nonsense_M	NM_002221	NP_002212	P27987	IP3KB_HUMAN		5	CACCTGCGAGG	0.607	
-	2	651	jh.2_Missense_Mu	NM_002221	NP_002212	P27987	IP3KB_HUMAN		5	GGCGACCAGCC	0.587	
+	20	5844	_Mutation_p.D193	NM_001098623	NP_001092093	Q5VST9	OBSCN_HUMAN	Ig-like 19.	28	TCCGGGACGGT	0.642	
+	45	12178	sn.2_Missense_Mu	NM_001098623	NP_001092093	Q5VST9	OBSCN_HUMAN	Ig-like 41.	28	AGGATGCGGGTG	0.632	
-	1	1477		NM_020808	NP_065859	Q9P2F8	SI1L2_HUMAN		6	AAGAGCAGCTT	0.507	
-	1	137	RF2BP2_uc001hw	NM_182972	NP_892017	Q7Z5L9	I2BP2_HUMAN		0	GCAGACGGGTT	0.726	
+	14	1417	xr.1_Missense_Mu	NM_003193	NP_003184	Q15813	TBCE_HUMAN		0	GATTGGGAACTC	0.333	
+	22	2767	x.1_Missense_Mu	NM_000254	NP_000245	Q99707	METH_HUMAN	B12-binding.	3	GTTAAAGGCGAC	0.507	
-	3	980	b.2_RNA|OPN3_u	NM_014322	NP_055137	Q9H1Y3	OPN3_HUMAN	Name=6; (Potential).	0	CATTAACCACCA	0.368	
+	2	133	e_Mutation_p.T25	NM_001130957	NP_001124429	Q5SY80	CA101_HUMAN	cellular (Potential).	2	ATTCCACTAACAG	0.323	
-	7	1032		NM_022366	NP_071761	Q9H5Q4	TFB2M_HUMAN		1	GACGAGGAATCA	0.323	
-	32	5951	CTF1_uc009xgs.1_	NM_015446	NP_056261	Q8WYP5	ELYS_HUMAN	r nuclear localization (By si	7	CAGATGGATTGA	0.428	
-	1	538		NM_001001959	NP_001001959	Q8NGX0	O11L1_HUMAN	cellular (Potential).	3	GGAGGTCGCAGA	0.507	
+	1	795	L13_uc001ids.2_I	NR_002145					0	CCTGCGATCTC	0.522	
-	4	925	0pzq.1_Missense_	NM_030645	NP_085148	Q7L8J4	3BP5L_HUMAN	Potential.	0	ATACCTCCTTAG	0.512	
+	6	670	ib.2_Splice_Site_	NM_001047160	NP_001040625	Q7Z628	ARHG8_HUMAN		1	GTTTTTAGGCAA	0.244	rs12219587
-	9	1073	_p.R229*|PHYH_u	NM_006214	NP_006205	O14832	PAHX_HUMAN		0	AAGTCGAGCTC	0.363	
-	64	10414		NM_001081	NP_001072	O60494	CUBN_HUMAN		19	ATATCACCTCCA	0.373	
-	3	280	'S|TRDMT1_uc00	NM_004412	NP_004403	O14717	TRDMT_HUMAN		1	GCAGGGAGGG	0.264	
+	10	1782	se_Mutation_p.E37	NM_003380	NP_003371	P08670	VIME_HUMAN	Tail.	4	ATCAACGAAACT	0.303	
+	1	356	128811_uc010qde.	NM_020752	NP_065803	Q5T848	GP158_HUMAN	cellular (Potential).	8	CCAACTGCTCCG	0.682	
-	8	1128		NM_004521	NP_004512	P33176	KINH_HUMAN	Kinesin-motor.	5	TTTGTTCCGTTT	0.313	
+	7	860		NM_052997	NP_443723	Q9BXX3	AN30A_HUMAN		9	CCTTGGTGGAAA	0.502	
-	3	1061	p.A303T|EGR2_u	NM_001136177	NP_001129649	P11161	EGR2_HUMAN	Poly-Ala.	2	CGGCTGCTGCTG	0.687	
-	1	202	on_p.A23T|PPP3C	NM_021132	NP_066955	P16298	PP2BB_HUMAN	Catalytic.	1	GTCAGCCCCGG	0.662	
-	6	680	an.3_Missense_M	NM_006926	NP_008857	Q8IWL1	SFPA2_HUMAN	C-type lectin.	0	TCCAGGGCTGG	0.532	
+	9	1199	p.R263Q|GHITM_	NM_014394	NP_055209	Q9H3K2	GHITM_HUMAN	intermembrane (Potential).	0	TATGCGAGTTGC	0.358	
+	1	478	lkny.2_Missense_	NM_018425	NP_060895	Q9BTU6	P4K2A_HUMAN		2	CTACCCCCCTG	0.592	
+	10	1515	A4G_uc001krx.2_	NM_017893	NP_060363	Q9NTN9	SEM4G_HUMAN	ılar (Potential).|Sema.	1	AGGATGGTTCC	0.632	
+	29	3765	.W1175*|GBF1_u	NM_004193	NP_004184	Q92538	GBF1_HUMAN		2	GTGTGGCAGAC	0.552	
-	11	913	wq.2_Missense_M	NM_012229	NP_036361	P49902	5NTC_HUMAN		0	CTTTCCCTACTTC	0.343	
+	2	326	XI1_uc010qrc.1_M	NM_005962	NP_005953	P50539	MXI1_HUMAN		0	GAGCCCCCGAC	0.532	
+	6	434		NM_005445	NP_005436	Q9UQE7	SMC3_HUMAN		3	TTATTGGTGCCA	0.264	
+	6	1047	1lcc.2_Missense_	NM_020940	NP_065991	Q5W0V3	F16B1_HUMAN		1	TCCACAAGCTTG	0.453	
-	4	490		NM_006793	NP_006784	P30048	PRDX3_HUMAN		0	GCCATACCTTTCT	0.418	
+	4	1142	qtc.1_Missense_M	NM_007190	NP_009121	Q9Y6Y8	S23IP_HUMAN	ction with SEC23A.	3	TTATTCCCTATAC	0.418	
+	1	860	jug.1_Nonsense_M	NM_017580	NP_060050	Q9UGI0	ZRAN1_HUMAN	anBP2-type 3.	2	AACTGGGCCAA	0.383	
+	2	162		NM_002412	NP_002403	P16455	MGMT_HUMAN		2	GACAGCCCTTTG	0.473	
-	16	2799	c001lrl.1_Missens	NM_145886	NP_665893	Q9HB75	PIDD_HUMAN		0	CCCATGCGTCGG	0.687	rs147404421
+	2	928	RTAP5-2_uc001ltv.	NR_021489					0	CAGCTGGACTGG	0.622	
+	4	975	wk.2_Missense_Mu	NM_005706	NP_005697	Q9Y5U2	TSSC4_HUMAN		0	AGGATCCCTCCA	0.647	
-	3	306	3PL5_uc001lxl.2_M	NM_020896	NP_065947	Q9H0X9	OSBL5_HUMAN		3	TGGGCTCCATGT	0.657	
+	1	946		NM_001005169	NP_001005169	Q8NGK6	O52I1_HUMAN	lasmic (Potential).	2	CACTTCCTCTTT	0.458	
+	1	674	M5_uc001mbq.1_I	NM_001005165	NP_001005165	Q8NGH9	O52E4_HUMAN	lasmic (Potential).	2	TTAGAGCTGTTTT	0.403	

+	1	520		NM_001004684	NP_001004684	Q8NGH3	OR2D3_HUMAN	Name=4; (Potential).	0	TCTTTAGTAGATA	0.502	
+	2	592		NM_176822	NP_789792	Q86W24	NAL14_HUMAN	DAPIN.	8	TGAGAGAGCGA	0.473	
-	18	2491	_p.C776Y|SCUBE2	NM_020974	NP_066025	Q9NQ36	SCUB2_HUMAN		2	CTTTTACACTGG	0.483	
-	21	2955	_p.A883V|COPB1_	NM_016451	NP_057535	P53618	COPB_HUMAN		2	AAAGGGCCTGG	0.358	
-	25	4132	cw.1_Missense_M	NM_002645	NP_002636	O00443	P3C2A_HUMAN	PI3K/PI4K.	10	GTGCATCTCTAA	0.313	
+	5	660	DHC_uc001moo.3	NM_017448	NP_059144	P07864	LDHC_HUMAN		0	CCCCACAAGCT	0.318	
+	2	363	reh.1_Missense_M	NM_001077242	NP_001070710	Q96QD5	DEPD7_HUMAN	DEP.	2	ATATTCCTCGAG	0.378	
+	17	3859	_p.P1176S|HIPK3_	NM_005734	NP_005725	Q9H422	HIPK3_HUMAN		5	GCATCACCTGCA	0.423	
-	1	369		NM_145804	NP_665803	Q8N961	ABTB2_HUMAN		2	GCAGGCGGTGA	0.667	
+	5	628		NM_020229	NP_064614	Q9NQV5	PRD11_HUMAN		1	GCCCCCCGGTG	0.612	
+	5	709		NM_020229	NP_064614	Q9NQV5	PRD11_HUMAN	SET.	1	AGGTGGTCAAG	0.622	
+	10	1722	_p.S485N|CRY2_u	NM_021117	NP_066940	Q49AN0	CRY2_HUMAN		1	GAGCAGTGCAG	0.547	
+	5	1839	gw.1_Missense_M	NM_024741	NP_079017	Q9H9D4	ZN408_HUMAN	C2H2-type 7.	0	AGCTGCCTGAA	0.672	
-	4	492	lh.1_Missense_Mu	NM_002334	NP_002325	O75096	LRP4_HUMAN	ential).|LDL-receptor class	4	GCAGGGAAACT	0.617	rs35025381
-	3	368	rhi.1_5'UTR|ACP2	NM_001610	NP_001601	P11117	PPAL_HUMAN	enal (Potential).	1	GCTGCCGCAGG	0.582	
+	4	963	n.1_Missense_Mut	NM_003682	NP_003673	Q8WXG6	MADD_HUMAN	DENN.	11	GCTCCCCAGTA	0.557	
+	6	623		NM_002559	NP_002550	P56373	P2RX3_HUMAN	cellular (Potential).	0	TTCCCCCTCTTC	0.537	
-	7	734	nkl.2_Missense_M	NM_003627	NP_003618	O75387	LAT3_HUMAN	ical; (Potential).	0	GCAGGCCAGGC	0.602	
-	1	700		NM_001001954	NP_001001954	Q8NGI9	OR5A2_HUMAN	lasmic (Potential).	0	CCTACCTGTAGC	0.478	
+	18	1957	K_uc009ynm.1_3'U	NM_015533	NP_056348	Q3LXA3	DHAK_HUMAN	DhaL.	0	CCTCCGGGCCA	0.602	
-	3	246	nuk.2_Nonsense_	NM_015853	NP_056937	Q04323	UBXN1_HUMAN	UBA.	0	ATCAGCCTGGC	0.642	
+	2	1207	OD1_uc001nyh.2_	NM_013280	NP_037412	Q9NZU1	FLRT1_HUMAN	xtracellular (Potential).	0	CAACACGCTGG	0.652	
-	10	1460		NM_015104	NP_055919	Q2TAZ0	ATG2A_HUMAN		2	GTCAGGTGGTC	0.612	
+	2	684	_p.G173S|SIPA1_u	NM_006747	NP_006738	Q96FS4	SIPA1_HUMAN		0	GTGAGGGTGAG	0.677	
-	11	1642	p.T512I|RELA_uc	NM_021975	NP_068810	Q04206	TF65_HUMAN		4	GGCGAGTTATA	0.627	
+	2	432		NM_153266	NP_694998	Q8N4L1	T151A_HUMAN	ical; (Potential).	1	TCGTCTCCCTCC	0.721	
-	2	520	HC24_uc001oim.	NM_207340	NP_997223	Q6UX98	ZDH24_HUMAN	DHHC-type.	0	AGTGTCCGCTG	0.647	
+	2	392	P5_uc009ysg.2_5'U	NM_002335	NP_002326	O75197	LRP5_HUMAN	ptor class B 1.|Extracellular	7	CTCCGGCCTGG	0.637	
+	2	531	se_Mutation_p.N4	NM_018043	NP_060513	Q5XXA6	ANO1_HUMAN	lasmic (Potential).	2	CGGGCAACCGG	0.662	
+	1	544		NM_003824	NP_003815	Q13158	FADD_HUMAN		3	CGACTTCgaggcg	0.498	
+	2	208		NM_001002035	NP_001002035	Q8NET1	D108B_HUMAN		0	ACTACACCCAAA	0.338	
+	11	2132	rs.1_Missense_Mu	NM_007256	NP_009187	O94956	SO2B1_HUMAN	Name=10; (Potential).	2	CACCCTCCTTCA	0.617	
-	5	1042		NM_001039548	NP_001034637	Q6PF15	KLH35_HUMAN	Kelch 5.	0	ACCCCCCATGA	0.592	
-	3	555	.2_RNA|TAF1D_u	NM_024116	NP_077021	Q9H5J8	TAF1D_HUMAN		0	ATTAGTGAGTATA	0.368	
-	7	886	vi.1_Intron|CASP1	NM_033292	NP_150634	P29466	CASP1_HUMAN		2	CACCAGGGCTG	0.388	
-	16	3106	_p.P905S|ARHGA	NM_020809	NP_065860	Q9P2F6	RHG20_HUMAN	Ser-rich.	5	GCCTGGGGAGG	0.493	
+	4	835		NM_198498	NP_940900	Q8IXP5	CK053_HUMAN		0	GGTCATATGAAT	0.512	
+	13	2439	_p.E489K|DLAT_u	NM_001931	NP_001922	P10515	ODP2_HUMAN	ytic (By similarity).	0	CTTCAGAGGAT	0.348	
-	1	44	/10_uc009yyv.2_R	NM_004724	NP_004715	O43264	ZW10_HUMAN	INT1.|Interaction with ZWI	2	GAACGAGGCCA	0.662	
-	3	855		NM_000482	NP_000473				0	GAGCTCCTCGG	0.662	
+	5	862	ar.2_Missense_Mu	NM_022169	NP_071452	Q9H172	ABCG4_HUMAN	otential).|ABC transporter.	2	AGGAGGTGAAG	0.592	
-	6	1343	yp.2_Missense_M	NM_006597	NP_006588	P11142	HSP7C_HUMAN		8	GCTTGGTAGGA	0.448	
+	11	2956	.3_Intron|WNK1_u	NM_018979	NP_061852	Q9H4A3	WNK1_HUMAN		23	TTGTTCCAGTC	0.522	
+	19	5291	_p.P1348L|WNK1_	NM_018979	NP_061852	Q9H4A3	WNK1_HUMAN		23	TATTACCCCAAG	0.498	
+	23	6053	.S1601N|WNK1_u	NM_018979	NP_061852	Q9H4A3	WNK1_HUMAN		23	AACTAGTTCAG	0.393	
+	13	2648	f.2_Missense_Mut	NM_178040	NP_829884	Q8IUD2	RB6I2_HUMAN	Potential.	5	AGGTGGAAAAA	0.433	
+	6	729	se_Mutation_p.P4	NM_018463	NP_060933	Q969R8	ITFG2_HUMAN		0	CCCTCCTGCCT	0.577	rs150956987

-	4	1026	p.R254K|FOXM1_	NM_021953	NP_068772	Q08050	FOXM1_HUMAN	Fork-head.	2	GCTTCCTCTCA	0.507	
-	38	7048	VF_uc010set.1_Int	NM_000552	NP_000543	P04275	VWF_HUMAN		12	CTCCTACCTGGT	0.552	rs61750624
-	16	2318	VF_uc010set.1_Int	NM_000552	NP_000543	P04275	VWF_HUMAN	TIL 2.	12	TGGGGGGCAGA	0.612	
+	4	935	se_Mutation_p.G9	NM_018009	NP_060479	Q9BX59	TPSNR_HUMAN	otential).|Ig-like V-type.	0	ACAAGGGCAGG	0.652	
-	5	539	RBP_uc010sfg.1_Ir	NM_032489	NP_115878	Q8NEB7	ACRBP_HUMAN		1	GGAAGGTCTGG	0.562	
+	7	3136	x.1_Missense_Mut	NM_001007026	NP_001007027	P54259	ATN1_HUMAN		6	GGCCGGGCTTG	0.667	
-	15	3858	ge.1_Missense_M	NM_174941	NP_777601	Q9NR16	C163B_HUMAN	Extracellular (Potential).	11	CTCGGCCAGGT	0.612	
-	10	695	_p.P151L|MFAP5_	NM_003480	NP_003471	Q13361	MFAP5_HUMAN		1	CACAGGGAGGA	0.473	
+	26	3213	p.A619T|A2ML1_	NM_144670	NP_653271	A8K2U0	A2ML1_HUMAN		3	CTGACAGCGTTT	0.438	
-	4	526	e_Mutation_p.P14	NM_001781	NP_001772	Q07108	CD69_HUMAN	.|Extracellular (Potential).	0	GACCAGGTTCCT	0.418	
-	1	218	H1_uc001qzc.2_Ir	NM_176885	NP_795366	P59538	T2R31_HUMAN	lasmic (Potential).	0	AGAGCAGTGAGA	0.373	
-	3	747		NM_006248	NP_006239				0	TGGAGGAGATC	0.612	
+	15	2211	zip.2_Nonsense_M	NM_017435	NP_059131	Q9NYB5	SO1C1_HUMAN	cellular (Potential).	7	TCAAATGGGGAT	0.373	
-	7	958	_p.V314I|LDHB_u	NM_002300	NP_002291	P07195	LDHB_HUMAN		3	GAGCAACCTCAT	0.448	
-	2	429		NM_004982	NP_004973	Q15842	IRK8_HUMAN	smic (By similarity).	0	GGGGAGGCGGT	0.597	
-	10	1402	_p.P48S|SOX5_uc	NM_006940	NP_008871	P35711	SOX5_HUMAN		6	TGCTGGGACAG	0.483	
+	4	1303	_p.T361I|RASSF8	NM_007211	NP_009142	Q8NHQ8	RASF8_HUMAN		0	AAGTTACCGTTTT	0.438	
-	55	8206	jg.1_Missense_Mu	NM_002223	NP_002214	Q14571	ITPR2_HUMAN	lasmic (Potential).	14	CAGGACTATGA	0.368	
-	53	7919	g.1_Missense_Mu	NM_002223	NP_002214	Q14571	ITPR2_HUMAN	cellular (Potential).	14	CATCCCCCACA	0.428	
+	4	3778	rf35_uc001rkt.2_5'	NM_018169	NP_060639	Q9HCM1	CL035_HUMAN		2	GAACAGGATGAT	0.428	
-	1	425_426	10_uc009zju.1_5'U	NM_198992	NP_945343	Q6XYQ8	SYT10_HUMAN	cular (Potential).	2	TGGCTGCCCCTC	0.683	
+	10	1879	zjz.2_Missense_M	NM_013377	NP_037509	Q6ZMN7	PZRN4_HUMAN		11	GTTGTAGCGCTG	0.512	
-	53	16433		NM_003482	NP_003473	O14686	MLL2_HUMAN	SET.	41	TAGGGGCACAG	0.502	
+	13	2074	_p.C636Y|TROAP_	NM_005480	NP_005471	Q12815	TROAP_HUMAN	A approximate tandem rep	1	GCCCTGCCCTA	0.647	
-	9	1822		NM_005554	NP_005545	P02538	K2C6A_HUMAN	Tail.	5	CTGAGGCCACCC	0.577	
-	7	1459		NM_057088	NP_476429	P12035	K2C3_HUMAN	Rod.|Coil 2.	0	GCTCTTGGAGCT	0.612	
+	5	507	AT2_uc009zms.2_	NM_003578	NP_003569	O75908	SOAT2_HUMAN	ical; (Potential).	1	CCCTGGCCATCG	0.587	
-	3	426	cs.3_Missense_Mu	NM_015665	NP_056480	Q9NRG9	AAAS_HUMAN		1	AAAGGCCCACA	0.423	
+	6	898	my.1_Missense_M	NM_020547	NP_065434	Q16671	AMHR2_HUMAN	Potential).|Protein kinase.	2	CTCTCTGGGCCC	0.493	
+	8	1398	E160K|TARBP2_u	NM_134323	NP_599150	Q15633	TRBP2_HUMAN	l.|DRBM 3.|Sufficient for int	1	CTGAGGAGCAG	0.627	
-	6	784	_p.E214K|CALCO	NM_020898	NP_065949	Q9P1Z2	CACO1_HUMAN		1	TCTCTTCTGTGA	0.527	
+	1	203	C13_uc010sop.1_	NM_017410	NP_059106	P31276	HXC13_HUMAN	Gly-rich.	1	gcatcggcggcggcgg	0.493	
+	23	2888	ERBB3_uc009zok.	NM_001982	NP_001973	P21860	ERBB3_HUMAN	Potential).|Protein kinase.	8	CAGGTGTGACA	0.507	
-	3	577		NM_012064	NP_036196	P30301	MIP_HUMAN		1	TTCATGCCTGCA	0.537	
-	4	601	nq.2_Missense_M	NM_145064	NP_659501	Q96MF2	STAC3_HUMAN	ol-ester/DAG-type.	3	GCATTTCCACATA	0.373	
+	5	1165		NM_032230	NP_115606	Q8N6Q8	CL026_HUMAN		0	TGATGGTGGGT	0.308	
+	25	4011	G1091E|APAF1_u	NM_181861	NP_863651	O14727	APAF_HUMAN	WD 12.	3	CAACGGGAGATG	0.522	
+	42	5674		NM_014503	NP_055318	O75691	UTP20_HUMAN		4	GTTATGGAAGCT	0.368	
+	3	398	VP1_uc009zuu.1_	NM_007062	NP_008993	Q13610	PWP1_HUMAN		0	GGAAGGTGACC	0.438	
-	2	551	)_splice|SELPLG_	NM_003006	NP_002997	Q14242	SELPL_HUMAN	ntial).|12 X 10 AA tandem re	0	CTGTGCCTCCG	0.612	
+	10	1157	_p.N271I|RAD9B_	NM_152442	NP_689655	Q6WBX8	RAD9B_HUMAN		2	GGAAAACTGTG	0.453	
-	6	1084		NM_002710	NP_002701	P36873	PP1G_HUMAN		3	ATGGCACCTGCA	0.393	
+	2	539	b.2_Missense_Mu	NM_016816	NP_058132	P00973	OAS1_HUMAN	for binding to dsRNA.	2	AGGGGGTGGA	0.572	
-	7	893	zy.2_Missense_Mu	NM_006549	NP_006540	Q96RR4	KKCC2_HUMAN	rotein kinase.	3	GGGGTCATCCA	0.572	
-	18	3264		NM_015347	NP_056162	O15034	RIMB2_HUMAN	p.Q1034E(1)	11	TATCTTGAGAGT	0.448	
-	7	753	_Mutation_p.G10	NM_015347	NP_056162	O15034	RIMB2_HUMAN	SH3 1.	11	TTTTCCCGCCG	0.547	
-	2	303		NM_152726	NP_689939	Q8IYU8	EFHA1_HUMAN		0	AGTGAAGAAAAC	0.348	

-	8	1272	p.1_Missense_Mu	NM_014363	NP_055178	Q9NZJ4	SACS_HUMAN		12	CATTGGCCTGAT	0.383	
-	8	2221	se_Mutation_p.R5	NM_178006	NP_821074	Q9Y3M8	STA13_HUMAN	Rho-GAP.	4	ATTTGCGAAAAA	0.498	
-	1	2179	uc001uxv.1_Intron	NM_032138	NP_115514	Q8WVZ9	KBTB7_HUMAN		1	AGGTTCAAGGC	0.443	
+	7	767		NM_016248	NP_057332	Q9UKA4	AKA11_HUMAN		2	GAGGAAGAGACT	0.358	
-	7	904		NM_012345	NP_036477	Q9UHK0	NUFP1_HUMAN		0	TCTTTGCCATTT	0.388	
-	13	2593	ense_Mutation_p.	NM_015070	NP_055885	Q5T200	ZC3HD_HUMAN		2	TCAAGAGTCTGT	0.393	
-	1	92	_p.R29K|ZC3H13	NM_015070	NP_055885	Q5T200	ZC3HD_HUMAN		2	CCAAGCCTCTCA	0.398	
+	3	509		NM_021999	NP_068839	Q9Y287	ITM2B_HUMAN	enal (Potential).	0	ATCAAAGATGAT	0.363	
+	4	857	_Splice_Site|PIBF1	NM_006346	NP_006337	Q8WXW3	PIBF1_HUMAN		2	GTATCTGTAAGTA	0.289	
-	57	9506	vkg.1_Missense_	NM_015057	NP_055872	O75592	MYCB2_HUMAN		14	AAGCAGCTTTGA	0.299	
-	55	7910	_p.V2011I|MYCB	NM_015057	NP_055872	O75592	MYCB2_HUMAN		14	ACTCTACCATGC	0.458	rs141701958
-	2	1956		NM_033132	NP_149123	Q96T25	ZIC5_HUMAN	C2H2-type 4.	0	TGCTTCCTCAG	0.557	
+	7	723	p.A212V|ATP11A_	NM_015205	NP_056020	P98196	AT11A_HUMAN	lasmic (Potential).	4	TTCACGCCACCA	0.527	
+	1	728		NM_001004479	NP_001004479	Q8NGC9	O11H4_HUMAN	lasmic (Potential).	1	AGCTGGTCGGA	0.423	
+	6	489	41_splice|PARP2_	NM_005484	NP_005475	Q9UGN5	PARP2_HUMAN		2	TTGCAGTTGGG	0.463	
+	3	537	APEX1_uc001vxi.	NM_001641	NP_001632	P27695	APEX1_HUMAN	export signal (NES).	4	GGAATGTGGAT	0.483	
-	4	501	_p.A86V|HNRNP	NM_031314	NP_112604	P07910	HNRPC_HUMAN	RRM.	0	GCTCTGCAGCC	0.388	
-	23	2786		NM_000257	NP_000248	P12883	MYH7_HUMAN	Potential.	4	TTGTTCCTGAA	0.522	
-	13	1347		NM_000257	NP_000248	P12883	MYH7_HUMAN	osin head-like.	4	TCTGCCCCTTG	0.567	
+	2	711		NM_203402	NP_981947	A5D6W6	FITM1_HUMAN	ical; (Potential).	0	GTGTTCGCCAAG	0.637	
-	4	238	1_uc001wmm.1_	NM_002818	NP_002809	Q9UL46	PSME2_HUMAN		0	AGGGAAGTCAAG	0.577	
+	11	2209	lg.1_Missense_Mu	NM_017999	NP_060469	Q96EP0	RNF31_HUMAN		2	CACTCCCCAGC	0.607	
+	6	848	e|GMPR2_uc010a	NM_001002001	NP_001002001	Q9P2T1	GMPR2_HUMAN		3	TCTCAGGCAGG	0.463	
-	3	335	B_uc001wop.2_Mi	NM_014430	NP_055245	Q9UHD4	CIDEB_HUMAN	CIDE-N.	0	GCACTCCATTCA	0.547	
+	1	1820	ense_Mutation_p.	NM_019839	NP_062813	Q9NPC1	LT4R2_HUMAN	Name=1; (Potential).	0	TGCCTGGCAACG	0.721	
+	16	1372	nf.1_Missense_Mu	NM_016106	NP_057190	Q8WVM8	SCFD1_HUMAN		0	GGAACTCCAGAA	0.343	
-	22	3627	ami.2_Missense_	NM_015473	NP_056288	Q86XA9	HTR5A_HUMAN		1	AGGAAGTTGGG	0.328	
-	2	326	EC23A_uc010tqb.	NM_006364	NP_006355	Q15436	SC23A_HUMAN		5	GAACAACCATTC	0.443	
+	2	212		NM_002687	NP_002678	Q9H307	PININ_HUMAN	ternative 5' splicing.|Neces	1	ACAGGCCCATC	0.423	
-	1	1271		NM_032135	NP_115511	Q5H9T9	FSCB_HUMAN	Pro-rich.	9	CTTCAGCAGGT	0.507	
-	1	412		NM_080746	NP_542784	Q96L21	RL10L_HUMAN		1	TGTCAGCCCCA	0.542	
-	20	2836	L1_uc001wxz.2_I	NM_004196	NP_004187	Q00532	CDKL1_HUMAN		2	GTGATACGCTGG	0.542	
+	44	4266	_p.E1294K|KTN1_	NM_182926	NP_891556	Q86UP2	KTN1_HUMAN	(Potential).|Potential.	7	AGAAGGAGACA	0.388	
+	15	2306	_p.T739I|KIAA05	NM_014749	NP_055564	E9PGW8	E9PGW8_HUMAN		1	GACAAACCCAAA	0.378	
+	15	2091	ea.1_Nonsense_M	NM_014992	NP_055807	Q9Y4D1	DAAM1_HUMAN	FH2.	1	GACAGCAGGTA	0.438	
-	11	1654	R5E_uc001xge.2_	NM_006246	NP_006237	Q16537	2A5E_HUMAN		1	AATGGGGGCTA	0.368	
+	42	6555	gl.2_Missense_Mu	NM_015180	NP_055995	Q8WXH0	SYNE2_HUMAN	lasmic (Potential).	14	GCGAGGCCCCG	0.473	
+	109	19975	|SYNE2_uc001xg	NM_015180	NP_055995	Q8WXH0	SYNE2_HUMAN	(Potential).|Spectrin 9.	14	CAAAGCCTCCCT	0.438	
+	2	1114	325_uc001xhc.2_	NM_004857	NP_004848	P24588	AKAP5_HUMAN		0	CCCAGCAAGCA	0.408	
+	11	2026	_p.R456H|EXD2_	NM_018199	NP_060669	Q9NVH0	EXD2_HUMAN		0	GAGCCGCTGGC	0.587	
+	2	966	COT2_uc001xom.	NM_006821	NP_006812	P49753	ACOT2_HUMAN		1	GAGACGCTCCAT	0.478	
+	11	1486	nse_Mutation_p.S	NM_021188	NP_067011	Q86VK4	ZN410_HUMAN		1	CCCTGTCTTCAG	0.438	
+	3	1328	tvd.1_Splice_Site	NM_017791	NP_060261	Q9UPI3	FLVC2_HUMAN		0	CCTATGGTAAGG	0.443	
+	10	1392	E431*|C14orf118_	NM_017926	NP_060396	Q9NWQ4	CN118_HUMAN		3	CAGTGGAGCCA	0.463	
-	3	202_203	su.2_Intron|SNW	NM_012245	NP_036377	Q13573	SNW1_HUMAN		1	CATCTCCAAAAT	0.317	
+	6	806	se_Mutation_p.V1	NM_020421	NP_065154	Q86TW2	ADCK1_HUMAN	rotein kinase.	3	GAAGGTGTCCC	0.507	
+	13	2691	n_p.A102T|NRXN	NM_004796	NP_004787	Q9Y4C0	NRX3A_HUMAN	otential).|Laminin G-like 6.	10	GGCCAGCCAAT	0.572	

-	3	388	1xva.1_Missense_	NM_152446	NP_689659	Q6ZU80	CE128_HUMAN		0	CACCCGCCTGTC	0.438	
+	2	1918	td.2_Missense_Mu	NM_013231	NP_037363	O43155	FLRT2_HUMAN	cellular (Potential).	4	AGCCTCCCACCC	0.542	
-	13	1823	ALC_uc010tvy.1_M	NM_000153	NP_000144	P54803	GALC_HUMAN		0	TAGCTGCCTTTG	0.463	
-	13	1604	wc.1_Missense_M	NM_007039	NP_008970	Q16825	PTN21_HUMAN		4	GACGTCACTCC	0.587	
-	9	1183	30_splice|PTPN21_	NM_007039	NP_008970	Q16825	PTN21_HUMAN		4	TACTCACAGTTT	0.413	
-	15	1846	tion_p.A2V|TTC7B	NM_001010854	NP_001010854	Q86TV6	TTC7B_HUMAN	TPR 7.	2	CTCAGGGCCATG	0.473	
-	3	802		NM_173850	NP_776249	Q8IW75	SPA12_HUMAN		4	TGTGGGGTTCAT	0.453	
+	17	2146		NM_152327	NP_689540	Q96M32	KAD7_HUMAN	DPY-30.	1	TTGCAACGTCC	0.318	
+	8	1269	se_Mutation_p.N2	NM_001128918	NP_001122390	P27448	MARK3_HUMAN	rotein kinase.	4	TAGCAATGAATTT	0.423	
+	5	975	m.1_Missense_Mu	NM_182923	NP_891553	Q07866	KLC1_HUMAN	TPR 1.	0	ATCCAGTACGCC	0.682	
+	6	554	e_Mutation_p.P16	NM_001312	NP_001303	P52943	CRIP2_HUMAN	l zinc-binding 2.	0	GACCCCCGGCG	0.716	
-	4	503	te|NIPA1_uc001yv	NM_144599	NP_653200	Q7RTP0	NIPA1_HUMAN		0	GGAATTACCTGG	0.498	
-	1	150	1_5'UTR|MTMR1	NM_017762	NP_060232	Q9NXD2	MTMRA_HUMAN		1	GGGCGGTGGCA	0.701	
-	7	1003	zfr.2_Missense_M	NM_130901	NP_570971	Q8TE49	OTU7A_HUMAN	larity).|TRAF-binding (By si	2	ACTCTTCCAGGC	0.483	
+	2	1227	bp.1_Missense_Mu	NM_014952	NP_055767	Q8TBE0	BAHD1_HUMAN		0	GCCAAGAGGGG	0.647	
+	7	2320	op.1_Missense_Mu	NM_014952	NP_055767	Q8TBE0	BAHD1_HUMAN	BAH.	0	CCACCGCACAG	0.617	
+	2	588	p.G166D|MGA_uc	NM_001080541	NP_001074010	Q8IWI9	MGAP_HUMAN	T-box.	12	CCACAGGTCATT	0.433	
-	4	614		NM_139265	NP_644670	Q9H223	EHD4_HUMAN		2	TCCACCCTCTCG	0.562	
-	36	5440	yr.2_Missense_Mu	NM_017672	NP_060142	Q96QT4	TRPM7_HUMAN	tial).|Alpha-type protein kin	10	TAAATTCTCCAGT	0.348	
-	5	702	51_splice|CYP19A	NM_031226	NP_112503	P11511	CP19A_HUMAN		3	TGCTTACCTTTC	0.313	
-	8	1357	ofd.2_Splice_Site_	NM_138792	NP_620147	Q8WVC0	LEO1_HUMAN		0	GACATGCTGGAA	0.348	
+	4	1166	|FAM63B_uc002af	NM_001040450	NP_001035540	Q8NBR6	FA63B_HUMAN		1	TTTTCAGAATATG	0.328	
-	18	2755	_p.M871I|SLTM_uc	NM_024755	NP_079031	Q9NWH9	SLTM_HUMAN	Arg/Glu-rich.	1	AGTGGACATGCT	0.443	
-	27	3482		NM_004998	NP_004989	Q12965	MYO1E_HUMAN		3	CTGGGGGAGGC	0.622	
+	6	670	NX1_uc002amx.2_	NM_003099	NP_003090	Q13596	SNX1_HUMAN	PX.	0	CGCCCCCGGAG	0.433	
-	9	2228		NM_003613	NP_003604	O75339	CILP1_HUMAN		7	TCGAGTCAAGGT	0.507	
-	4	667	0ujb.1_Missense_M	NM_030800	NP_110427	Q96SY0	CO044_HUMAN	VWFA.	1	GGACAACCTGTT	0.448	
+	4	2011	IAD6_uc002aqg.2_	NM_005585	NP_005576	O43541	SMAD6_HUMAN	MH2.	1	TCAGGGCAGCG	0.667	
+	3	1096		NM_001031807	NP_001026977	P84550	SKOR1_HUMAN		0	AAAAGGACGAC	0.478	
+	2	965	arh.2_Missense_M	NM_015322	NP_056137	Q9UK73	FEM1B_HUMAN		0	ACCATACCACAG	0.463	
-	38	7128	p.R132C|MYO9A_u	NM_006901	NP_008832	B2RTY4	MYO9A_HUMAN	ail.|Rho-GAP.	3	GCAGCGGAGAA	0.453	
-	16	1763	ib.2_RNA|PARP6_	NM_020214	NP_064599	Q2NL67	PARP6_HUMAN	ARP catalytic.	0	CCCTGCTGAGA	0.418	
+	14	1958	axq.2_Missense_M	NM_025055	NP_079331	Q8N5R6	CCD33_HUMAN	Potential.	5	AGAAGGAGCTG	0.612	
+	9	1763	se_Mutation_p.T52	NM_006465	NP_006456	Q8IVW6	ARI3B_HUMAN		0	TCATCACGGGGT	0.547	
-	5	490	n_p.M1R|EDC3_uc	NM_001142443	NP_001135915	Q96F86	EDC3_HUMAN	and interaction with DCP1A	1	GTAGCCATGTTTC	0.443	
-	4	553		NM_004255	NP_004246	P20674	COX5A_HUMAN		0	GAGATTCCCAGT	0.458	rs1803317
+	9	1591	tion_p.G448E|MIR	NM_024608	NP_078884	Q96FI4	NEIL1_HUMAN		1	GAAGGGGCGAC	0.617	
-	8	952	N2C1_uc010bkk.2_	NM_006715	NP_006706	Q9NTJ4	MA2C1_HUMAN		0	ACAGGCCAGGG	0.632	
-	25	3289	bbx.2_Missense_M	NM_020843	NP_065894	Q9BY12	SCAPE_HUMAN		3	TTGGGGTAGCTG	0.438	
-	5	742	_p.D98N|CIB2_uc0	NM_006383	NP_006374	O75838	CIB2_HUMAN		0	CCTCATCCAGCT	0.562	
-	25	3898	0blm.1_Missense_	NM_002891	NP_002882	Q13972	RGRF1_HUMAN	Ras-GEF.	6	CTCTGAGATTCT	0.433	
+	7	606	n.1_Missense_Mut	NM_000137	NP_000128	P16930	FAAA_HUMAN		0	CCGAAGGCCCA	0.582	
-	2	369	.2_RNA|MESDC2_	NM_015154	NP_055969	Q14696	MESD_HUMAN	domain (By similarity).	0	GGCTTGCTTGGG	0.423	
+	3	1376	Mutation_p.H234Y	NM_181877	NP_870992	Q7Z7L9	ZSCA2_HUMAN	C2H2-type 6.	2	AGAATCCACACA	0.507	
+	14	5865	oc.1_Missense_Mu	NM_020778	NP_065829	Q96L96	ALPK3_HUMAN		12	AGGAGGGCTCC	0.632	
+	14	1538	LC28A1_uc010upf	NM_004213	NP_004204	O00337	S28A1_HUMAN	ical; (Potential).	3	CTGCCCTCTCC	0.602	
+	2	788		NM_152259	NP_689472	Q7Z2Z1	TICRR_HUMAN		7	GGAGTGGAATAA	0.473	

+	2	500	L13_uc002bpe.1_	NM_001029964	NP_001025135	A6NNM8	TTL13_HUMAN		0	TTGACACAGGCG	0.502	
-	8	769	x.2_RNA|SNRPA1	NM_003090	NP_003081	P09661	RU2A_HUMAN		1	CTCTGCCAGGG	0.468	
-	1	878		NM_001004195	NP_001004195	Q96R69	OR4F4_HUMAN	lasmic (Potential).	0	TCAGCCGTCTT	0.343	rs149105772
-	7	450	DF1_uc010utz.1_	NM_022450	NP_071895	Q96CC6	RHDF1_HUMAN	lasmic (Potential).	2	GCTGCCATTTC	0.657	rs11547503
+	37	4675	_uc002cio.1_Miss	NM_145294	NP_660337	Q96KV7	WDR90_HUMAN	WD 19.	1	CTGTCCTCTCT	0.637	
-	7	1718		NM_001025190	NP_001020361	Q96KJ4	MSLNL_HUMAN	ellular (Potential).	4	TCCCACCGGCC	0.701	
+	27	3431	.S1098F|MAPK8	NM_015133	NP_055948	Q9UPT6	JIP3_HUMAN		3	GGTGTCCATCC	0.617	
+	11	7405	.1_Missense_Mut	NM_016333	NP_057417	Q9UQ35	SRRM2_HUMAN	-rich.|Ser-rich.	4	TGGCTGACCCT	0.637	
+	1	166	RSF12A_uc002c	NM_016639	NP_057723	Q9NP84	TNR12_HUMAN		0	GGCCGGGGAGC	0.746	
+	4	757	ws.3_Nonsense_	NM_001127206	NP_001120678	P30519	HMOX2_HUMAN		0	ATGCCCAGCAG	0.572	
-	22	4887		NM_002705	NP_002696	O60437	PEPL_HUMAN	Potential.	6	ACGGTCATGTT	0.557	
+	8	807	g.2_Missense_Mut	NM_000246	NP_000237	P33076	C2TA_HUMAN		1	TGAGGGACCCA	0.537	
+	17	3426	p.P1041S|MKL2_	NM_014048	NP_054767	Q9ULH7	MKL2_HUMAN		5	TAGACCCACAG	0.478	
-	26	5163	uzv.1_Missense_	NM_014647	NP_055462	Q9Y4F3	LKAP_HUMAN		0	CTTGAGGGCGC	0.527	
-	12	2676	uzv.1_Missense_	NM_014647	NP_055462	Q9Y4F3	LKAP_HUMAN	RRM.	0	TATGGGGGCTG	0.448	
-	9	2282	uzv.1_Missense_	NM_014647	NP_055462	Q9Y4F3	LKAP_HUMAN		0	AACGGGTTCTG	0.483	
+	9	1435		NM_001039	NP_001030	P51170	SCNNG_HUMAN	llular (By similarity).	6	CTCAGTGTATTG	0.567	
-	17	1857		NM_015044	NP_055859	Q9UJY4	GGA2_HUMAN	GAE.	2	TGAAAGGCTGT	0.498	
-	5	2386		NM_024675	NP_078951	Q86YC2	PALB2_HUMAN		11	AGATGGGGAAA	0.468	
+	15	2723	1_Missense_Muta	NM_016151	NP_057235	Q9UL54	TAOK2_HUMAN		1	GTACAAGCGCA	0.647	
-	4	1129	lank|INO80E_uc0	NM_003609	NP_003600	Q9BW71	HIRP3_HUMAN	Glu-rich.	1	TGTTCACTTTCC	0.373	
-	1	296	dxs.2_Missense_	NM_006110	NP_006101	O95400	CD2B2_HUMAN		1	ATCCTCCTCAT	0.532	
+	11	1321	_Mutation_p.A29	NM_002209	NP_002200	P20701	ITAL_HUMAN	Extracellular (Potential).	10	GAAGGCAGACC	0.547	
-	3	1798	ao.2_Missense_M	NM_024706	NP_078982	Q96K58	ZN668_HUMAN		4	CTCCACCGTCA	0.692	
+	8	2836	10cbo.1_RNA|NO	NM_022162	NP_071445	Q9HC29	NOD2_HUMAN	LRR 5.	4	ACAGAGTGGGT	0.522	
-	3	425	m.2_Missense_M	NM_001012398	NP_001012398	Q9H8T0	AKTIP_HUMAN		0	GAAGGGTCCAT	0.408	
+	5	1113	p.D192N|MMP2_	NM_004530	NP_004521	P08253	MMP2_HUMAN	pe-II 1.|Collagen-binding.	11	AGAAGGATGGC	0.567	
-	5	376	_p.T104I|CNGB1_	NM_001297	NP_001288	Q14028	CNGB1_HUMAN		4	GCCAGGTCAGT	0.632	
-	2	1086	n_p.T84I|TPPP3_	NM_016140	NP_057224	Q9BW30	TPPP3_HUMAN		1	TCTTGGTCGCC	0.577	
-	3	424		NM_000229	NP_000220	P04180	LCAT_HUMAN		0	TTGCTGCTGTCC	0.652	
-	12	1758	RP2_uc002evq.1_	NM_024939	NP_079215	Q9H6T0	ESRP2_HUMAN	RRM 3.	1	TCATCTGAATGA	0.552	
-	9	2323	_p.S617F|SMPD3_	NM_018667	NP_061137	Q9NY59	NSMA2_HUMAN	enal (Potential).	1	GGCCGGACAGC	0.622	rs147387314
+	3	267		NM_013245	NP_037377	Q9UN37	VPS4A_HUMAN	n with CHMP1B.|MIT.	0	ATGAGGCCCAC	0.607	
+	9	818	_Mutation_p.D286	NM_145059	NP_659496	Q8N0W3	FUK_HUMAN		1	GCTTGGACTCC	0.582	
+	2	1155	o.2_Missense_M	NM_005769	NP_005760	Q8NCG5	CHST4_HUMAN	enal (Potential).	0	TGCCAGGGATG	0.532	
+	2	116	DH_uc010cgk.2_	NM_001361	NP_001352	Q02127	PYRD_HUMAN	termembrane (By similarity	0	CACGGGAGATG	0.597	
-	9	7358	l.2_Missense_Mut	NM_006885	NP_008816	Q15911	ZFHX3_HUMAN		4	CGAAGGGGGCC	0.527	
-	3	1357	ST6_uc002feh.1_	NM_021615	NP_067628	Q9GZX3	CHST6_HUMAN	enal (Potential).	0	TCGGGGGTGCG	0.637	
+	3	479	hl.2_Missense_M	NM_024731	NP_079007	Q8N4N3	KLH36_HUMAN	BTB.	2	GGATGGCGGCA	0.612	
+	10	1542		NM_004933	NP_004924	P55291	CAD15_HUMAN	|Extracellular (Potential).	1	CGCCGGGCAGC	0.726	
+	13	2106		NM_004933	NP_004924	P55291	CAD15_HUMAN	lasmic (Potential).	1	CGACAGCGCTG	0.706	
-	1	118		NM_002550	NP_002541	P47881	OR3A1_HUMAN	Name=1; (Potential).	3	CGTGACCAGGT	0.577	
-	3	367	2fxz.3_Missense_	NM_014520	NP_055335	Q9BQG0	MBB1A_HUMAN	with MYB (By similarity).	2	TCAAAAGACTGT	0.527	
+	5	956	ye.2_Missense_M	NM_001114974	NP_001108446	Q2TAL5	SMTL2_HUMAN		0	AGCGTCGCAGG	0.677	rs142209104
-	5	732	.A172V|SLC13A5	NM_177550	NP_808218	Q86YT5	S13A5_HUMAN	ical; (Potential).	0	TGGCCGCGTAG	0.617	
-	5	1276	HF23_uc010vtt.1_	NM_024297	NP_077273	Q9BUL5	PHF23_HUMAN	PHD-type.	0	GCCGCCCTGCA	0.493	
+	5	1128		NM_001406	NP_001397	Q15768	EFNB3_HUMAN	ical; (Potential).	1	GGCAGGGGCTG	0.726	

+	24	4012	e_Mutation_p.V12	NM_001005273	NP_001005273	Q12873	CHD3_HUMAN			1	TCAAGGTGGCA	0.517	
-	2	219	rf68_uc010cnv.2_	NM_025099	NP_079375	Q2NKJ3	CTC1_HUMAN			0	CCTTCCCTGGG	0.517	
+	7	1425	p.S435F|ARHGEF	NM_173728	NP_776089	O94989	ARHGF_HUMAN	DH.		3	GCGCTCCCTGC	0.607	
-	8	847	uc002gml.1_Intron	NM_017533	NP_060003	Q9Y623	MYH4_HUMAN	osin head-like.		13	AAAGCGAGAGG	0.448	
+	64	12284	p.W3290*|DNAH9_	NM_001372	NP_001363	Q9NYC9	DYH9_HUMAN	6 (By similarity).		20	GGATGGAATCG	0.493	
+	1	420		NM_014695	NP_055510	A2RUR9	C144A_HUMAN			0	AAGAGGTAATG	0.652	
-	13	1703	_p.P22S|TOP3A_u	NM_004618	NP_004609	Q13472	TOP3A_HUMAN			3	GACAGGGAGGA	0.552	
+	3	1028	ul.2_Missense_M	NM_031456	NP_113644	Q5XX13	FBW10_HUMAN			1	TCAGAGACCTG	0.468	
+	5	476	gun.2_Missense_	NM_016078	NP_057162	Q9NYZ1	F18B1_HUMAN			0	TTCAGAGTAAAG	0.393	
+	2	395	_Intron|WSB1_uc	NM_015626	NP_056441	Q9Y6I7	WSB1_HUMAN			0	CTGCAGCTCCT	0.378	
+	4	521	wan.1_Missense_	NM_003984	NP_003975	Q13183	S13A2_HUMAN			0	CCATCGCACAT	0.612	
-	3	1015	ay.1_Missense_	NM_018182	NP_060652	Q8WU58	CQ063_HUMAN			1	AAGGGGGATAG	0.602	
+	2	490	AP2_uc002hfy.2_	NM_018404	NP_060874	Q9NPF8	ADAP2_HUMAN	Arf-GAP.	p.?(1)	1	GGGACGACAGT	0.507	
+	15	2106	hjc.2_Missense_	NM_173167	NP_775259	Q8IWX7	UN45B_HUMAN			6	CACCATTGTGG	0.537	
-	2	628	_p.S84N|SLFN12_	NM_018042	NP_060512	Q8IYM2	SLN12_HUMAN			1	ATGTTACTAAAA	0.373	
-	11	5687		NM_001004334	NP_001004334	Q6PRD1	GP179_HUMAN	lasmic (Potential).		3	TCTTGGGGGCC	0.498	
+	6	933	002hsc.2_Missen	NM_032192	NP_115568	Q9UD71	PPR1B_HUMAN			0	CCTGTGGCCAG	0.582	rs142405059
+	8	869	htm.1_Splice_Site	NM_178171	NP_835465	Q96QA5	GSDMA_HUMAN			0	TGTTGGTAAGG	0.438	
-	14	1658	e_Mutation_p.D4	NM_014815	NP_055630	O75448	MED24_HUMAN	XXLL motif 3.		1	CAAGTCCAGAC	0.607	
+	2	389	tart_Site|RARA_u	NM_000964	NP_000955	P10276	RARA_HUMAN			3	GAGGGGTGGTC	0.662	
-	11	1241	ion_p.G338R|SMA	NM_003079	NP_003070	Q969G3	SMCE1_HUMAN	Glu-rich.		0	GACCCCCTCCT	0.522	
-	2	659	cxg.2_Missense_	NM_015515	NP_056330	Q9C075	K1C23_HUMAN	Head.		1	GGGCCGGCCCC	0.706	
-	1	62	39_uc010wfm.1_5	NM_213656	NP_998821	Q6A163	K1C39_HUMAN	Head.		0	GAATTGGTTGTT	0.473	
+	1	271		NM_033061	NP_149050					0	agctgctgtatgtccagc	0.189	rs148949542
-	1	150		NM_032524	NP_115913	Q9BYR3	KRA44_HUMAN	-C-[GRQVCH]-[SPT]- [VS		0	TGGGGCGGCAG	0.652	
-	1	628	EKHH3_uc010cy	NM_024927	NP_079203	Q7Z736	PKHH3_HUMAN			2	TTACCCTCCCG	0.687	
+	13	2080	AP1_uc010wgs.1	NM_003632	NP_003623	P78357	CNTP1_HUMAN	ential).|Fibrinogen C-termi		8	ACCGAGCGTGG	0.587	
-	10	2624	tron|BRCA1_uc01	NM_007294	NP_009225	P38398	BRCA1_HUMAN			52	TATTTGGTTCTG	0.398	
+	1	215	HX8_uc010wig.1_	NM_004941	NP_004932	Q14562	DHX8_HUMAN			4	ACAAGGACCTT	0.557	
+	14	2132	p.A596T|DHX8_u	NM_004941	NP_004932	Q14562	DHX8_HUMAN	.|Helicase ATP-binding.		4	ACGAGGCACAT	0.448	
-	4	330	n_p.A29T|ETV4_u	NM_001986	NP_001977	P43268	ETV4_HUMAN	Glu-rich (acidic).		7	CTCACCTTCAG	0.527	
+	5	1346	e_Mutation_p.P28	NM_001145080	NP_001138552	A2RUB1	CQ104_HUMAN			1	TGATCCCCCAC	0.368	
+	15	2083	_p.I462V|C17orf57	NM_152347	NP_689560	Q8IY85	CQ057_HUMAN	EF-hand 2.		3	TTTGGTATTTAC	0.338	
+	19	2669	p.G633E|KPNB1_	NM_002265	NP_002256	Q14974	IMB1_HUMAN			3	AAAGGGGGATC	0.483	
+	7	1535	T2_uc010dbo.2_	NM_022167	NP_071450	Q9H1B5	XYLT2_HUMAN	enal (Potential).		1	TTGTGGACTGG	0.627	
+	6	548	_p.D103E|MSI2_u	NM_138962	NP_620412	Q96DH6	MSI2H_HUMAN	RRM 2.		2	GAAGATGTAAA	0.458	
-	6	713	14_uc002iws.1_M	NM_198393	NP_938207	Q8IWB6	TEX14_HUMAN			17	AAATGACTCCAG	0.413	
+	7	2256	dd.2_Missense_M	NM_014906	NP_055721	Q8WY54	PPM1E_HUMAN			5	TGGAAGTGGGA	0.413	
-	12	1515	yn.1_Missense_M	NM_032582	NP_115971	Q8NFA0	UBP32_HUMAN	DUSP.		5	TTGACATATTCTT	0.423	
-	9	1498	izp.2_Missense_	NM_005121	NP_005112	Q9UHV7	MED13_HUMAN			2	AAGGAGTCAAG	0.468	
-	17	2320		NM_001433	NP_001424	O75460	ERN1_HUMAN	Potential).|Protein kinase.		9	TCCAGCCTTCT	0.537	
-	27	3939	LZ_uc002jfx.3_Mi	NM_014877	NP_055692					2	CATAAGGAATA	0.453	
+	2	604	jir.2_Missense_M	NM_000891	NP_000882	P63252	IRK2_HUMAN	smic (By similarity).		0	ACGGTACCTCG	0.517	
+	14	1608	_p.R505K|TTYH2_	NM_032646	NP_116035	Q9BSA4	TTYH2_HUMAN	lasmic (Potential).		4	CCTGAGGCACT	0.517	
+	6	550	wrg.1_Missense_	NM_017728	NP_060198	Q8NE00	TM104_HUMAN	lasmic (Potential).		0	ACCGGGTGGAA	0.532	
+	8	1714	1_5'Flank|OTOP3_	NM_178160	NP_835454	Q7RTS6	OTOP2_HUMAN	ical; (Potential).		4	CCTCCCTTTCG	0.607	
-	6	480	fz.2_Intron|ATP5H	NM_006356	NP_006347	O75947	ATP5H_HUMAN			0	GGAAAGCTTCA	0.388	

-	15	2054	e_Mutation_p.P60	NM_004259	NP_004250	O94762	RECQ5_HUMAN		3	TCCGGGGGCTCA	0.607
-	4	1984	e_Mutation_p.Q52	NM_032134	NP_115510	Q9H0J4	QRIC2_HUMAN	Gln-rich.	5	ATGCTGATCTG	0.413
+	12	1737	jth.2_Missense_M	NM_198955	NP_945193	Q3V5L5	MGT5B_HUMAN	enal (Potential).	3	CTTCCCCTACG	0.652
+	8	1007	_p.Y247C|SEC14L	NM_003003	NP_002994	Q92503	S14L1_HUMAN		2	GAGATACCTGG	0.498
-	16	2583	.1_Intron|USP36_	NM_025090	NP_079366	Q9P275	UBP36_HUMAN		5	AGGGGGGTTGC	0.632
+	3	517	.2_Missense_Mut	NM_024110	NP_077015	Q9BXL6	CAR14_HUMAN		5	TGCAGCCTGAT	0.577
-	2	157	6G_uc002kaz.3_I	NM_002602	NP_002593	P18545	CNRG_HUMAN		0	GGGCGGTTCCA	0.657
-	9	1428	_p.G88R|P4HB_uc	NM_000918	NP_000909	P07237	PDIA1_HUMAN	hioredoxin 2.	0	TCTCTCCCAGTT	0.527
-	4	275	2kfb.3_Missense_	NM_001100407	NP_001093877	Q9BQA9	CQ062_HUMAN		0	CCTTCCCTGTG	0.602
-	8	1499	lq.2_Missense_M	NM_003803	NP_003794	P52179	MYOM1_HUMAN		5	GAGGGGCATGG	0.398
+	2	979	NDC2_uc002koh.	NM_001098529	NP_001091999	Q86VQ3	TXND2_HUMAN	eat of Q-P-K-X-G-D-I-P-K-	2	GGAGGGTGACA	0.567
+	6	1029_1030	j.2_Nonsense_Mu	NM_194434	NP_919415	Q9P0L0	VAPA_HUMAN	IV membrane protein; (Po	0	TCTTTCTAGGGA	0.371
+	2	478	_p.P131L|LAMA3_	NM_198129	NP_937762	Q16787	LAMA3_HUMAN	inin N-terminal.	11	CCCTCCCCTGT	0.512
+	31	3918	r.2_Missense_Mu	NM_198129	NP_937762	Q16787	LAMA3_HUMAN	F-like 9.|Domain III B.	11	CTCACTGCAGC	0.652
-	2	864		NM_020805	NP_065856	Q9P2G3	KLH14_HUMAN		1	TGACCGACAGC	0.612
+	17	1779	_p.S533F|DTNA_u	NM_001390	NP_001381	Q9Y4J8	DTNA_HUMAN		0	GGACTCCCTCA	0.557
-	3	438	eb.1_RNA|NARS_	NM_004539	NP_004530	O43776	SYNC_HUMAN		0	CCTATGCCACAT	0.388
-	4	702		NM_052947	NP_443179	Q86TB3	ALPK2_HUMAN		14	GGGAGGAGTCA	0.473
+	13	2018	CHC2_uc002liq.2	NM_017742	NP_060212	Q9C0B9	ZCHC2_HUMAN		2	AACAACTAGGT	0.398
+	13	3059	CHC2_uc002liq.2_	NM_017742	NP_060212	Q9C0B9	ZCHC2_HUMAN		2	GTGCAGCTGTG	0.502
-	18	2466	.2_RNA|RTTN_uc	NM_173630	NP_775901	Q86VV8	RTTN_HUMAN		8	GAGAACTCTGG	0.413
-	3	978		NM_001044369	NP_001037834	Q0P6D2	FA69C_HUMAN	enal (Potential).	0	TCAAAGAAATT	0.468
-	3	505	XNL4A_uc010drf.2	NM_006701	NP_006692	P83876	TXN4A_HUMAN		0	GGGCCCCGCGG	0.587
+	4	883		NM_014913	NP_055728	Q6IQ32	ADNP2_HUMAN		8	TTTTAGGTGAAA	0.398
+	4	269	p.G55S|PTBP1_u	NM_031991	NP_114368	P26599	PTBP1_HUMAN		2	GTGCAGGCGTC	0.582
-	16	1457	F3_uc002ltq.2_Mi	NM_003200	NP_003191	P15923	TFE2_HUMAN		7	GAGGGCCGCGT	0.682
-	6	2490	_uc010xgs.1_Spli	NM_020695	NP_065746	Q8N1G1	REXO1_HUMAN		0	AAACTCTAGAGG	0.572
+	6	903	gz.1_Missense_M	NM_003249	NP_003240	P52888	THOP1_HUMAN		3	GCAAGGAGGTG	0.612
+	6	764	_Mutation_p.P24	NM_021938	NP_068757	Q8N6W0	CELF5_HUMAN		2	TTCAGCCCCTAC	0.647
-	4	361	p.V102M|PIP5K1	NM_012398	NP_036530	O60331	PI51C_HUMAN	PIPK.	4	GAGCACGTCGC	0.657
-	3	627		NM_030662	NP_109587	P36507	MP2K2_HUMAN	rotein kinase.	0	AGTTGCATTCGT	0.612
-	7	683	_p.D136G|SIRT6_	NM_016539	NP_057623	Q8N6T7	SIRT6_HUMAN	tylase sirtuin-type.	1	ACAGGTCGGCG	0.692
+	3	209		NM_018074	NP_060544	Q9BW85	CCD94_HUMAN		0	TGCTCGGAAGG	0.557
+	6	2310	.2_Missense_Mut	NM_020209	NP_064594	Q96IW2	SHD_HUMAN	SH2.	0	GCCAGGGCTTC	0.657
-	7	757	20_splice|STAP2_	NM_001013841	NP_001013863	Q9UGK3	STAP2_HUMAN		1	GCTCACCGGCT	0.622
-	2	435		NM_182919	NP_891549	Q8IUC6	TCAM1_HUMAN		1	TGCCTCTAGAG	0.662
-	6	1199	nse_Mutation_p.G	NM_020175	NP_064560	Q96G46	DUS3L_HUMAN		0	GGCGCCCTCCA	0.652
-	20	2595		NM_000064	NP_000055	P01024	CO3_HUMAN		5	TTTCCACCTGCT	0.577
+	8	1285	p.R274H|ZNF557_	NM_001044388	NP_001037853	Q8N988	ZN557_HUMAN	2H2-type 5.	2	GTTCCGCACTC	0.458
+	11	1484	mgp.2_Splice_Sit	NM_020533	NP_065394	Q9GZU1	MCLN1_HUMAN		1	TGAAGGTACAT	0.582
+	14	1842	PLA6_uc010xjq.1	NM_020533	NP_065394	Q9GZU1	MCLN1_HUMAN		1	CCTCGGAGGAG	0.592
+	10	999	.G268R|HNRNP	NM_005968	NP_005959	P52272	HNRPM_HUMAN		0	GCATGGGGTTA	0.468
-	19	2041		NM_012335	NP_036467	O00160	MYO1F_HUMAN	osin head-like.	3	CCGCGGCCACG	0.652
-	4	385	_p.D91N|MYO1F_	NM_012335	NP_036467	O00160	MYO1F_HUMAN	osin head-like.	3	GTTGTCCGTGA	0.582
-	3	19939		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).	57	TAATGTCTTCTG	0.458
-	6	2027	F846_uc010dww.	NM_001077624	NP_001071092	Q147U1	ZN846_HUMAN	2H2-type 13.	1	TGTGAGTTCGT	0.398
-	55	4062		NM_015719	NP_056534	P25940	CO5A3_HUMAN	e-helical region.	10	TTTCTCCCCTT	0.607

-	43	3235		NM_015719	NP_056534	P25940	CO5A3_HUMAN	le-helical region.	10	CAGTGGGGCCAC	0.657
+	5	893		NM_015725	NP_056540	Q9NYR8	RDH8_HUMAN		4	TGCACTACTTCCC	0.612
+	3	454	mnv.3_Missense_M	NM_003259	NP_003250	Q9UMF0	ICAM5_HUMAN	Potential).|Ig-like C2-type 1.	3	TGCCTCCCTGGC	0.682
-	3	543	Site|CDC37_uc00	NM_007065	NP_008996	Q16543	CDC37_HUMAN		0	CCCTCACCTCCTC	0.577
+	4	753	plice_Site_p.G197	NM_001005361	NP_001005361	P50570	DYN2_HUMAN		6	CCCAAGGTAACCC	0.592
-	3	420		NM_006858	NP_006849	Q13445	TMED1_HUMAN	xtracellular (I p.D102N(1)	4	TGTAGTCCCCGGC	0.592
+	4	979	nsn.3_Missense_M	NM_152355	NP_689568	Q8N8Z8	ZN441_HUMAN	type 4; degenerate.	1	CCTTCAGTTGTTC	0.393
-	10	1112	ise_Mutation_p.R3	NM_004461	NP_004452	Q9Y285	SYFA_HUMAN		1	AATACGCGGTCG	0.602
-	3	551	xnj.1_Missense_M	NM_024825	NP_079101	Q6PEZ8	PONL1_HUMAN	eu-rich.|LRR 1.	1	ACAGCTCATTGTA	0.607
+	10	1588	yq.2_Missense_Mu	NM_002741	NP_002732	Q16512	PKN1_HUMAN		8	CCCCAGGTCACCT	0.597
-	11	1469	p.G389S|EMR3_u	NM_032571	NP_115960	Q9BY15	EMR3_HUMAN	lasmic (Potential).	6	GCACACCCTCCAC	0.557
+	10	1177		NM_023944	NP_076433				7	CTTAGGGACGAC	0.517
+	9	1521	312_splice|SLC27A	NM_198580	NP_940982	Q6PCB7	S27A1_HUMAN		0	CTCAGGTGCGCA	0.647
+	5	975	nhu.2_Missense_M	NM_015683	NP_056498	Q8TBH0	ARRD2_HUMAN		1	CTACACGTGGACT	0.677
-	8	800	nhx.1_Missense_M	NM_005535	NP_005526	P42701	I12R1_HUMAN	tential).|Fibronectin type-III	1	GCTGCTCCACCG	0.478
-	4	935		NM_001159293	NP_001152765	C9JHM3	C9JHM3_HUMAN		1	TCTCCACTATGAA	0.403
-	4	1480	pc.1_Missense_M	NM_001076675	NP_001070143	Q68DY1	ZN626_HUMAN	C2H2-type 10.	1	TTCTCCTATGTGT	0.373
-	5	1723	208_uc002nqo.1_I	NM_007153	NP_009084				7	TGTGTAGTAAGGC	0.368
-	4	1395	1_Intron|ZNF208_	NM_007153	NP_009084				7	TGACCTCATGTTT	0.368
-	3	503		NM_001001411	NP_001001411	Q8N7Q3	ZN676_HUMAN		0	TGGAAAGAATCTT	0.308
-	7	2771		NM_001080409	NP_001073878				2	TTAAAAGCTTTGC	0.368
-	5	905		NM_001080409	NP_001073878				2	TTCTGTCCAGTAT	0.363
+	4	3808	dd.1_Missense_Mu	NM_014717	NP_055532	O15090	ZN536_HUMAN		11	GTCTCACCTTTAT	0.667
+	3	2256	xrn.1_Missense_M	NM_001136156	NP_001129628	Q8TCN5	ZN507_HUMAN	C2H2-type 4.	5	TTACGAGTCCATC	0.502
+	7	1018		NM_018025	NP_060495	Q9BRR8	GPTC1_HUMAN		1	TGCATGGTCTAGC	0.463
+	5	1147	dq.1_Missense_Mu	NM_194325	NP_919306	P17039	ZNF30_HUMAN		2	ACTGGTGAAAAAC	0.448
+	5	1301	dq.1_Missense_Mu	NM_194325	NP_919306	P17039	ZNF30_HUMAN	C2H2-type 7.	2	ATCAGAGAATTCA	0.448
+	9	1711	s.1_Missense_Mut	NM_002361	NP_002352	P20916	MAG_HUMAN	ical; (Potential).	7	CCGTGGTCGCCT	0.592
+	9	1125	ai.1_5'Flank|TMEM	NM_014364	NP_055179	O14556	G3PT_HUMAN		0	AAGCAGCAGCCA	0.642
+	2	1312		NM_024509	NP_078785	Q9BTN0	LRFN3_HUMAN	xtracellular (Potential).	0	GGTGGGCGAGG	0.726
-	6	1279	345_uc002oez.2_I	NM_001037232	NP_001032309	Q3KNS6	ZN829_HUMAN	C2H2-type 6.	0	TGTTGAGTAAAGC	0.383
-	2	210	2_Missense_Mutat	NM_152360	NP_689573	Q86YE8	ZN573_HUMAN	KRAB.	1	ACCAGGTTTCTAT	0.408
+	3	1812		NM_015073	NP_055888	O60292	SI1L3_HUMAN		2	AGATCGGGGGCC	0.657
+	17	4978		NM_015073	NP_055888	O60292	SI1L3_HUMAN		2	GCAACCGAGGTT	0.537
+	3	509	p.P119S|NFKBIB_	NM_002503	NP_002494	Q15653	IKBB_HUMAN	ANK 3.	2	CCCGCCCCCGG	0.721
+	3	458		NM_172140	NP_742152	Q8IU54	IL29_HUMAN		0	CACACCCTGCACC	0.682
+	2	186	2olq.3_Missense_	NM_001111020	NP_001104490	O00267	SPT5H_HUMAN		4	ATGTCGGACAGCC	0.657
-	7	836	p.D130N|AKT2_uc	NM_001626	NP_001617	P31751	AKT2_HUMAN	rotein kinase.	2	CTTCATCCTGCAC	0.617
-	7	1728	e_Mutation_p.P348	NM_181882	NP_870998	Q9BXM0	PRAX_HUMAN	DKL]-[LIVMAP]- [AQKHRP	2	CCTCCGGCACAG	0.592
+	1	70	P4_uc002oog.1_Ir	NM_001042544	NP_001036009	Q8N2S1	LTBP4_HUMAN		1	CAGCCGCCACCT	0.672
+	1	728	K4_uc002oor.2_5'I	NM_025194	NP_079470	Q96DU7	IP3KC_HUMAN		0	GCTCCAGGACAC	0.512
+	1	775		NM_001410	NP_001401	Q7Z7M0	MEGF8_HUMAN	lar (Potential).|CUB 1.	1	GGATGGTGCGG	0.667
+	6	593	227_uc010xww.1_I	NM_182490	NP_872296	Q86WZ6	ZN227_HUMAN		1	CCAGGTGTCTTC	0.373
+	5	550	xf.1_Missense_Mu	NM_001294	NP_001285	O96005	CLPT1_HUMAN	cellular (Potential).	1	CAGACCCCCGG	0.622
+	7	1225	kn.2_Missense_Mu	NM_017659	NP_060129	Q9NXS2	QPCTL_HUMAN		1	CTTCAGGGGTACC	0.597
-	2	582	dk.1_Missense_M	NM_004943	NP_004934	Q09019	DMWD_HUMAN		0	GAGATGGTCTCGC	0.542
+	4	369		NM_022142	NP_071425	Q96BH3	ESPB1_HUMAN	onectin type-II 2.	0	GATTACCCACGCT	0.463

+	2	563	c.2_Missense_Mu	NM_001097638	NP_001091107	Q10981	FUT2_HUMAN	enal (Potential).		1	CTACCCCTGCT	0.647	
-	4	452	u.1_Missense_Mu	NM_025129	NP_079405	Q9BT04	FUZZY_HUMAN			0	ATATTGGTCAGT	0.458	
-	8	1615	p.D521N|IL4I1_uc	NM_152899	NP_690863	Q96RQ9	OXLA_HUMAN			3	CGTGTCCGATG	0.692	
-	3	300	_uc002puj.2_Intro	NM_001012964	NP_001012982	Q92876	KLK6_HUMAN			0	CCCACCTGCAG	0.423	
+	2	725		NM_002030	NP_002021	P25089	FPR3_HUMAN	ellular (Potential).		6	ACTTTGCATTCT	0.433	
+	5	2096	.2_RNA|ZNF808_	NM_001039886	NP_001034975	Q8N4W9	ZN808_HUMAN	2H2-type 15.		0	TGGCACGACATA	0.408	
-	3	2019		NM_198457	NP_940859	Q6ZNG1	ZN600_HUMAN			0	TTCTCTCCAGTAT	0.433	
-	4	527	ae.2_Missense_	NM_001008801	NP_001008801	Q5VIY5	ZN468_HUMAN			2	ATCATGTTGGC	0.438	
+	7	1151	_p.A271T|LILRB1_	NM_006669	NP_006660	Q8NHL6	LIRB1_HUMAN	3.|Extracellular (Potential).		3	CTGGCGCACAG	0.607	
-	1	159		NM_176820	NP_789790	Q7RTR0	NALP9_HUMAN	DAPIN.		7	CAGCCCAGGGG	0.453	
+	4	1907	ud.1_Intron|ZNF5	NM_153263	NP_694995	Q6P9A3	ZN549_HUMAN			1	CACTGGCGAAA	0.448	
-	2	247	F550_uc002qpc.2	NM_001039654	NP_001034743	Q7Z398	ZN550_HUMAN			0	TCTCCCCAACC	0.532	
+	3	1601	F776_uc002qqa.	NM_173632	NP_775903	Q68DI1	ZN776_HUMAN	ype 10; degenerate.		1	GGCCACATGAG	0.453	
+	12	1385	zi.2_Missense_Mu	NM_003887	NP_003878	O43150	ASAP2_HUMAN	PH.		0	CAAAGCTCAAC	0.483	
-	17	2646	_p.V735I|PUM2_u	NM_015317	NP_056132	Q8TB72	PUM2_HUMAN	ilio 5.|PUM-HD.		1	AAATACCTGAG	0.363	
+	10	836	_p.S257F|GCKR_	NM_001486	NP_001477	Q14397	GCKR_HUMAN	SIS 1.		2	CGGCTCCTCCC	0.552	
+	5	247	zj.1_Missense_Mu	NM_153021	NP_694566	Q6P1J6	PLB1_HUMAN	ate repeats.|Extracellular (		9	AGCCTCCAGAC	0.408	
-	1	3247		NM_001029883	NP_001025054	A6NGG8	CB071_HUMAN	Pro-rich.		1	GAAAGGGGGGC	0.607	
-	8	3028	p.G928S|NLRC4_	NM_021209	NP_067032	Q9NPP4	NLRC4_HUMAN	LRR 11.		6	ACCTACCTAAAA	0.413	
-	36	6263	_p.P368L|HEATR5	NM_019024	NP_061897	Q9P2D3	HTR5B_HUMAN			8	TGGCGGGGGCT	0.423	
+	5	638	k.1_Intron|C2orf5	NM_144736	NP_653337	Q7L592	MIDA_HUMAN			1	GAAAGGTGTCA	0.403	
-	7	960	UMPD2_uc010ynt	NM_025264	NP_079540	Q9BTF0	THUM2_HUMAN			1	CAAGTCCACAC	0.323	
-	16	2785	se_Mutation_p.M	NM_001083953	NP_001077422	Q6YHU6	THADA_HUMAN			3	TAACTTCATCAG	0.343	
-	37	4044		NM_133259	NP_573566	P42704	LPPRC_HUMAN			3	TGAGACTGACA	0.368	
-	7	1069	REPL_uc002rui.3_	NM_006036	NP_006027	Q4J6C6	PPCEL_HUMAN			1	GTATTTCTCTTC	0.363	
+	2	578	6_uc010fbj.2_5'U	NM_000179	NP_000170	P52701	MSH6_HUMAN	PWWP.		168	GGCTGGGTTAG	0.373	
+	4	1714	_p.T219I|MSH6_u	NM_000179	NP_000170	P52701	MSH6_HUMAN			168	GGGTACACAGA	0.438	rs149159527
+	4	2346	_p.R430*|MSH6_u	NM_000179	NP_000170	P52701	MSH6_HUMAN			168	ATCAACGAATG	0.398	rs63751127
+	8	3808	i.1_Missense_Mu	NM_000179	NP_000170	P52701	MSH6_HUMAN		p.T1219I(4)	168	AGGTACTGCAA	0.323	rs63750949
+	1	753	TF2A1L_uc002r	NM_006873	NP_006864	B7ZL16	B7ZL16_HUMAN			5	AACATCTCCAG	0.408	
+	14	1719	se_Mutation_p.S4	NM_015701	NP_056516	Q96DZ1	ERLEC_HUMAN			2	TTCTTTCTCTCC	0.358	
-	80	10083	d.2_Missense_M	NM_014709	NP_055524	Q70CQ2	UBP34_HUMAN			19	GCCGCCTTTTA	0.488	
-	3	1171	se_Mutation_p.A1	NM_032180	NP_115556	Q3B820	F161A_HUMAN			3	TCTGGCTTTAA	0.418	
-	3	1610	2sit.3_Missense_	NM_015470	NP_056285	Q9BXF6	RFIP5_HUMAN			0	GCGTTCCTCCT	0.652	
+	10	1276	p.A350S|CCT7_u	NM_006429	NP_006420	Q99832	TCPH_HUMAN			0	CATGATGCCATC	0.542	
-	12	1832	p.G392R|GGCX_	NM_000821	NP_000812	P38435	VKGC_HUMAN	enal (Potential).		1	TTCTCCCTCTC	0.353	
-	4	2210	02srm.2_Missens	NM_005667	NP_005658	O00237	RN103_HUMAN	ical; (Potential).		1	TGTGAAGAGTAA	0.388	
-	39	5584	e_Mutation_p.S44	NM_014014	NP_054733	O75643	U520_HUMAN	SEC63 2.		10	ACATGCTGAAG	0.517	
+	8	1137	_p.W222*|CNGA3	NM_001298	NP_001289	Q16281	CNGA3_HUMAN			6	CTGTGGCAGC	0.483	
+	6	535	zt.1_RNA|MRPL3	NM_145213	NP_660214	Q8TCC3	RM30_HUMAN			1	AGTTGCCACAA	0.343	
+	10	857	e_Mutation_p.G2	NM_145687	NP_663720	O95819	M4K4_HUMAN	rotein kinase.		4	TAGAAGGGTGC	0.373	
+	13	2579	2_Missense_Mutat	NM_012455	NP_036587	Q8NDX1	PSD4_HUMAN	PH.		2	ATGGGGCAAGC	0.547	
+	2	269	fll.2_Missense_M	NM_020909	NP_065960	Q9HCM4	E41L5_HUMAN	FERM.		1	GGTGTCCCTTC	0.473	
-	79	13097		NM_018557	NP_061027	Q9NZR2	LRP1B_HUMAN	ntial).|LDL-receptor class B		50	TCCAGTACATC	0.388	
+	1	1684	.NT5_uc010zci.1_	NM_014568	NP_055383	Q7Z7M9	GALT5_HUMAN	enal (Potential).		4	ATAGAGCCATT	0.443	
+	15	2766	nse_Mutation_p.E	NM_003628	NP_003619	Q99569	PKP4_HUMAN	ARM 7.		7	TAGCAGAAAGT	0.527	
-	6	1278	_p.Y357*|PLA2R1	NM_007366	NP_031392	Q13018	PLA2R_HUMAN	ellular (Potential).		3	GTTTAGATATTT	0.343	

+	22	4285	.G1332E|SCN2A_	NM_001040142	NP_001035232	Q99250	SCN2A_HUMAN	III.	8	TTTTAGGAGCCAT	0.333	
-	4	629		NM_013233	NP_037365	Q9UEW8	STK39_HUMAN	rotein kinase.	2	GTTCTCCTCGGTT	0.363	
-	55	10880		NM_004525	NP_004516	P98164	LRP2_HUMAN	s A 27.|Extracellular (Potent	29	ACTGTCCCAGTC	0.532	
-	8	1055	df.1_Missense_Mu	NM_004525	NP_004516	P98164	LRP2_HUMAN	s A 7.|Extracellular (Potenti	29	AAATGGAGATGC	0.423	
+	4	512	L23_uc002ufh.1_I	NM_001008489	NP_001008489	Q8TCD6	PHOP2_HUMAN		1	GAAAAGGATTTT	0.368	
-	272	61110	uc010zfi.1_Misser	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	AGGTTCAGTCCA	0.388	
-	207	40893	.1_Missense_Muta	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	ATAAGTACTCTTT	0.368	
-	46	15496	N_uc010zfi.1_Intr	NM_133379	NP_596870	Q8WZ42	TITIN_HUMAN		153	CCAGAGTCTCTC	0.527	
-	46	15409	N_uc010zfi.1_Intr	NM_133379	NP_596870	Q8WZ42	TITIN_HUMAN		153	GTGGAGTATCTC	0.512	
+	8	1140	NAJC10_uc002uo	NM_018981	NP_061854	Q8IXB1	DJC10_HUMAN		4	TTTGGACAGGTA	0.328	
+	8	1738	AR_uc002uqu.2_I	NM_144708	NP_653309	Q7Z5J8	ANKAR_HUMAN	ANK 4.	4	CAGGAGCACTG	0.333	
+	10	2666	d.1_Nonsense_Mu	NM_000534	NP_000525	P54277	PMS1_HUMAN		4	AGAAACAAAACA	0.333	
-	16	1656	_p.P423L|STAT1_	NM_007315	NP_009330	P42224	STAT1_HUMAN		10	ATGAGAGGACCC	0.408	
-	41	7132		NM_018897	NP_061720	Q8WXX0	DYH7_HUMAN	al).|AAA 4 (By similarity).	12	CACTCCCTCCAA	0.473	
+	4	699	D1_uc002uuk.2_5'	NM_002157	NP_002148	P61604	CH10_HUMAN		0	TTGCAGGATTATT	0.333	
-	6	590	L3_uc002uwj.2_3'U	NM_130906	NP_570981	Q9H2H8	PPIL3_HUMAN	e cyclophilin-type.	0	CAAATACGGTGTA	0.383	rs61730410
+	4	619	CASP8_uc010ftd.1	NM_033355	NP_203519	Q14790	CASP8_HUMAN	DED 2.	5	ATGACATGGTAAC	0.413	
+	8	904	uxv.1_Missense_M	NM_033355	NP_203519	Q14790	CASP8_HUMAN		5	GCAAACCTCGGG	0.428	
+	10	1175	_Mutation_p.G354	NM_001875	NP_001866	P31327	CPSM_HUMAN	midotransferase type-1.	13	TGCTGGCTGGA	0.423	
+	12	1481	ver.2_Nonsense_M	NM_024532	NP_078808	Q8N0X2	SPG16_HUMAN	WD 3.	2	AATTTGGGATGT	0.413	
-	40	6675	fh.2_Intron|FN1_u	NM_212482	NP_997647	P02751	FINC_HUMAN	trand 3 (CS-3) (V region).	13	CCCAACACTGG	0.532	
-	31	5281	|FN1_uc002vfh.2_	NM_212482	NP_997647	P02751	FINC_HUMAN	ype-III 12; extra domain.	13	CCTGGTCCATTTT	0.358	
-	22	3781	f.2_Missense_Mut	NM_212482	NP_997647	P02751	FINC_HUMAN	onectin type-III 6.	13	TTACGTGTCACCA	0.383	
-	9	755	fvw.2_Splice_Site_	NM_022453	NP_071898	Q96BH1	RNF25_HUMAN		2	AGCTCCTGGAAC	0.562	
-	8	894	te|PRKAG3_uc010	NM_017431	NP_059127	Q9UGI9	AAKG3_HUMAN		2	CACCCACCTATC	0.582	
-	15	1712	zkx.1_Splice_Site_	NM_024506	NP_078782	Q6UWU2	GLB1L_HUMAN		0	AGCTCACCTTGA	0.443	
-	4	458	119S|TUBA4B_uc	NM_006000	NP_005991	P68366	TBA4A_HUMAN		3	GAAGCCCTGAA	0.542	
-	7	1197	p.G280S|PTPRN_	NM_002846	NP_002837	Q16849	PTPRN_HUMAN	ellular (Potential).	4	TGCACCCTTGG	0.627	
+	18	2228		NM_052902	NP_443134	Q8N1F8	S11IP_HUMAN		1	GTTCTCCTCGCT	0.622	
+	21	2587	SMD1_uc010fxu.1	NM_002807	NP_002798	Q99460	PSMD1_HUMAN		2	GGAAGTACCAA	0.343	
-	12	5932	p.P1677S|COL6A3	NM_004369	NP_004360	P12111	CO6A3_HUMAN	0.|Nonhelical region.	18	GGTGGGCGAGC	0.602	
+	11	1484	002vxd.2_Missens	NM_001137552	NP_001131024	Q32MZ4	LRRF1_HUMAN		3	GCACCAGATGAC	0.498	
-	3	401	se_Mutation_p.E1	NM_016552	NP_057636	Q9P2S6	ANKY1_HUMAN		1	GCCTTCTCGGTC	0.562	
+	10	1080	ab.3_Missense_M	NM_000030	NP_000021	P21549	SPYA_HUMAN		0	TTCCCACAGTCA	0.622	
-	10	1602	p.A504T|PASK_uc	NM_015148	NP_055963	Q96RG2	PASK_HUMAN		6	CAGCGCCTGTT	0.562	
-	7	1077	Mutation_p.A329T	NM_015148	NP_055963	Q96RG2	PASK_HUMAN		6	GGCCGCCTCAC	0.612	
-	16	2131	p.N635Y|HDLBP_	NM_203346	NP_976221	Q00341	VIGLN_HUMAN	KH 7.	4	GCAGTTGGCTC	0.458	
-	2	422	wee.2_Missense_	NM_033409	NP_212134	Q9NQ40	RFT2_HUMAN		2	GCAGGGGCAGC	0.647	
+	3	1154	K35_uc002wfw.3_	NM_080836	NP_543026	Q8TDR2	STK35_HUMAN	rotein kinase.	1	ACTAAGCAAGG	0.527	
+	15	1897	gg.1_Missense_Mu	NM_080751	NP_542789	Q8TDI7	TMC2_HUMAN	lasmic (Potential).	3	TCATATGCTGAG	0.343	
-	4	730	_p.L244F|SIGLEC	NM_023068	NP_075556	Q9BZZ2	SN_HUMAN	2.|Extracellular (Potential).	10	TGAGGAGGATCT	0.577	
-	37	8249	z.1_Missense_Mu	NM_032221	NP_115597	Q8TD26	CHD6_HUMAN		14	CAAAGGGGCAC	0.542	
-	36	7410	D6_uc002xjz.1_5'U	NM_032221	NP_115597	Q8TD26	CHD6_HUMAN		14	CCTTGGGGATG	0.537	
-	4	398	UTR|SYS1-DBNDI	NM_014477	NP_055292	Q9Y2B4	T53G5_HUMAN		1	TCTCGGAGCAC	0.493	
-	2	2548	us.1_Missense_Mu	NM_004975	NP_004966	Q14721	KCNB1_HUMAN	lasmic (Potential).	2	AGTGGTTTTTCT	0.537	
+	7	2228	ze.1_Missense_Mu	NM_001164116	NP_001157588	Q9NQ75	CASS4_HUMAN		3	TGAGAGGAAAC	0.532	
-	3	1181	p.A218T|BMP7_u	NM_001719	NP_001710	P18075	BMP7_HUMAN		1	CGAGGCCCAGA	0.632	

+	6	708	L1_uc002ybz.1_R	NM_198935	NP_945173	O75177	CREST_HUMAN	intra-molecular domain (By	2	GATGGGGCAGG	0.706
+	4	936		NM_178463	NP_848558	Q9H1L0	CT166_HUMAN		0	AAAAGGAAAAT	0.483
+	2	255	_p.S46N|CXADR_	NM_001338	NP_001329	P78310	CXAR_HUMAN	otential).|Ig-like C2-type 1.	1	GCTTAGTCCCG	0.458
+	3	399	se_Mutation_p.T94	NM_001338	NP_001329	P78310	CXAR_HUMAN	otential).|Ig-like C2-type 1.	1	ATTTTACGAGTA	0.343
-	3	1593		NM_006988	NP_008919	Q9UHI8	ATS1_HUMAN	ptidase M12B.	6	TCGGATCACACA	0.443
+	14	2116	cm.1_Nonsense_	NM_006447	NP_006438	Q9Y5T5	UBP16_HUMAN		4	TTTATATCAGTTC	0.378
+	5	564	e_Mutation_p.G12	NM_000454	NP_000445	P00441	SODC_HUMAN		0	GACAGGAAACG	0.418
+	11	1559	gpo.2_Missense_	NM_003274	NP_003265	P48553	TPC10_HUMAN		2	CCCATGCCACC	0.348
-	6	997	p.P308S|CLTCL1_	NM_007098	NP_009029	P53675	CLH2_HUMAN	ar terminal domain.	5	GTGTGGAGCAG	0.428
-	2	1399	2zqh.2_Missense_	NM_024627	NP_078903	Q7L3V2	CV029_HUMAN	Pro-rich.	0	CCTTGGGCCCA	0.617
-	17	1508	NRD2_uc002zqp.	NM_006440	NP_006431	Q9NNW7	TRXR2_HUMAN		2	CGGTCCGCATC	0.657
+	2	852	e_Mutation_p.V16	NM_022720	NP_073557	Q8WYQ5	DGCR8_HUMAN	nd retention.|Necessary for	0	GGAGTGTTGGT	0.582
-	3	715	67Q|TRMT2A_uc	NM_182984	NP_892029	Q8IZ69	TRM2A_HUMAN		1	CCACTCGTGTT	0.642
-	3	385	57L|TRMT2A_uc0	NM_182984	NP_892029	Q8IZ69	TRM2A_HUMAN		1	GCCCGGGCTGA	0.652
+	6	763	_p.P184L|ZNF74_	NM_003426	NP_003417	Q16587	ZNF74_HUMAN		1	GTGTCCCCTCT	0.677
-	3	1176	ue.2_Missense_M	NM_004173	NP_004164	O43246	CTR4_HUMAN	ical; (Potential).	2	GGTGCCCGCCA	0.642
-	2	879	6610_uc011aim.1_	NM_080740	NP_542778	P59817	Z280A_HUMAN		1	TGTGAGGGTGTA	0.433
+	366		uc002zws.2_Intron						0	TCTTCTCCCCTC	0.542
-	7	1363	T5_uc002zzq.3_	NM_004121	NP_004112	P36269	GGT5_HUMAN	ellular (Potential).	3	GTTCACCCTCC	0.572
+	10	1224	p.G246D|GGT1_u	NM_013430	NP_038347	P19440	GGT1_HUMAN	ellular (Potential).	0	AGGGGGCATTG	0.612
-	3	748	S4_uc003acn.2_	NM_022081	NP_071364	Q9NQG7	HPS4_HUMAN		0	GGATCGCCTTCT	0.443
-	6	945	p.G191R|TFIP11_	NM_012143	NP_036275	Q9UBB9	TFP11_HUMAN	G-patch.	0	AGCCCCCACAG	0.468
-	5	418	3aia.2_Missense_	NM_174975	NP_777635	Q9UDX4	S14L3_HUMAN	CRAL-TRIO.	5	GCAACCCCTTG	0.577
+	16	2054	k.2_Missense_Mu	NM_005569	NP_005560	P53671	LIMK2_HUMAN		2	ACTCACCTCCC	0.672
-	6	945	lo.1_3'UTR|PIK3IF	NM_052880	NP_443112	Q96FE7	P3IP1_HUMAN	lasmic (Potential).	1	GGGGGTGGTG	0.642
-	1	1637	ense_Mutation_p.L	NM_014323	NP_055138	Q9HBE1	PATZ1_HUMAN		2	AGGAAGGTCGA	0.622
-	3	1145	_p.S346F|FOXRED	NM_024955	NP_079231	Q8IWF2	FXRD2_HUMAN		2	AAATGGAGAAG	0.577
+	13	1569	te.2_Missense_Mu	NM_013365	NP_037497	Q9UJY5	GGA1_HUMAN	tructured hinge.	3	AGGCCCCCAGT	0.647
+	9	5170	tu.2_Nonsense_M	NM_001039141	NP_001034230	Q9H2D6	TARA_HUMAN		1	GGCTGGGCCGA	0.662
+	2	424	us.2_Missense_M	NM_012407	NP_036539	Q9NRD5	PICK1_HUMAN		0	AAGAGGATAAA	0.517
-	6	976	NK1E_uc003avo.	NM_152221	NP_689407	P49674	KC1E_HUMAN	rotein kinase.	3	GAGGACCTCGA	0.597
-	2	831	vt.1_Missense_Mu	NM_004981	NP_004972	P48050	IRK4_HUMAN	smic (By similarity).	0	TCATAGCCCACG	0.622
-	13	2046	xp.2_Missense_M	NM_001098504	NP_001091974	Q92841	DDX17_HUMAN		4	TGGTGCCATAA	0.498
+	2	413		NM_004286	NP_004277	O00178	GTPB1_HUMAN		1	GGATGGACGAG	0.423
+	3	299	EC3D_uc011aoe.1	NM_014508	NP_055323	Q9NRW3	ABC3C_HUMAN		0	ATTGTCATGCA	0.572
-	2	272		NM_194326	NP_919307	Q86WX3	AROS_HUMAN		0	CGAGTTCCGCA	0.662
+	8	988	_p.P193L|SGSM3_	NM_015705	NP_056520	Q96HU1	SGSM3_HUMAN	ab-GAP TBC.	2	CCTGCCTCGCC	0.632
+	9	1368	e_Mutation_p.L34	NM_022098	NP_071381	Q9NQH7	XPP3_HUMAN		0	ACTACCTCGGG	0.502
+	2	897		NM_001429	NP_001420	Q09472	EP300_HUMAN		64	ACACAGGGATG	0.507
+	14	2934		NM_001429	NP_001420	Q09472	EP300_HUMAN		64	CTCCCCCAAGC	0.592
-	2	108	OLR3H_uc003bai.	NM_138338	NP_612211	Q9Y535	RPC8_HUMAN		1	AACTGCCAAGG	0.637
+	8	1058	aq.1_Missense_M	NM_001469	NP_001460	P12956	XRCC6_HUMAN	lu-rich (acidic).|Ku.	5	TACTGGAGAAA	0.438
+	11	1541	aq.1_Missense_M	NM_001469	NP_001460	P12956	XRCC6_HUMAN		5	ACCTGGAGGCC	0.443
+	12	1436	ron|MEI1_uc003ba	NM_152513	NP_689726	Q5TIA1	MEI1_HUMAN		2	GTGCGGAGTTT	0.512
-	1	5433	.E1767K|TCF20_	NM_005650	NP_005641	Q9UGU0	TCF20_HUMAN		5	TTCCTCCTCCT	0.582
-	1	3778	.P1215L|TCF20_	NM_005650	NP_005641	Q9UGU0	TCF20_HUMAN		5	CATGGGGCGGC	0.498
-	1	2347	p.G738D|TCF20_	NM_005650	NP_005641	Q9UGU0	TCF20_HUMAN		5	CATGGCCAGTG	0.493

-	4	667		NM_145912	NP_666017	Q8NET5	NFAM1_HUMAN	mic (Potential).|ITAM.	0	TGGGGCTGCTG	0.592	
-	4	401	RP7A_uc003bcp.2	NM_015703	NP_056518	Q9Y3A4	RRP7A_HUMAN		2	CTGACACCCCAC	0.597	
+	5	924	|uc011aqp.1_5'Fla	NM_001104595	NP_001098065	Q9NWS6	F118A_HUMAN		0	CACAGGCGATG	0.423	
-	11	1859	_p.P603S|SMC1B_	NM_148674	NP_683515	Q8NDV3	SMC1B_HUMAN	lexible hinge.	2	CTGAGGAAACT	0.378	
+	4	499	_p.A118T|FBLN1_	NM_006486	NP_006477	P23142	FBLN1_HUMAN	phylatoxin-like 3.	2	GGAGGGCGGCC	0.647	
-	1	1922		NM_006071	NP_006062	Q9NTG1	PKDRE_HUMAN	ular (Potential).|REJ.	5	TATTGACTAGCC	0.483	
+	21	2359	onf.1_Missense_M	NM_001080420	NP_001073889	F2Z3L0	F2Z3L0_HUMAN		1	TGCCGGGCTCC	0.667	
+	4	580		NM_001097	NP_001088	P10323	ACRO_HUMAN	eptidase S1.	0	TAGCCCCCAGG	0.567	
+	19	2527	_p.P441L|CNTN4_	NM_175607	NP_783200	Q8IWV2	CNTN4_HUMAN	nectin type-III 2.	7	TGCACCCCTTCT	0.517	
+	7	1453	_p.F219L|EDEM1_	NM_014674	NP_055489	Q92611	EDEM1_HUMAN	enal (Potential).	3	AGGCCTTTTTC	0.463	
+	19	3512	_p.S915F|SETD5_	NM_001080517	NP_001073986	Q9C0A6	SETD5_HUMAN		2	GATTTTCCAGCA	0.512	
+	13	2465	C4_uc003btc.1_Ir	NM_001025930	NP_001021100	Q9Y4R7	TTLL3_HUMAN		2	TTGACTCCATTG	0.557	
+	11	1446	e_Mutation_p.P31	NM_153461	NP_703191	Q8NAC3	I17RC_HUMAN	cellular (Potential).	2	GGGCTCCGGGT	0.682	
+	19	2473	_p.G645E|IL17RC_	NM_153461	NP_703191	Q8NAC3	I17RC_HUMAN	lasmic (Potential).	2	TTCCGGGCGGC	0.711	
-	5	615	EM111_uc003buo.	NM_018447	NP_060917	Q9P0I2	TM111_HUMAN		0	ACGGAGGGTCA	0.383	
+	9	902	_p.S262F|ATG7_u	NM_006395	NP_006386	O95352	ATG7_HUMAN		1	CCAGTCTGTTG	0.423	
-	14	2956	hek.1_Missense_	NM_022340	NP_071735	Q9H1K0	RBNS5_HUMAN	AB5A.|Necessary for the i	2	TGCCCCCCTTC	0.622	
-	4	683	ssense_Mutation_	NM_004844	NP_004835	O60239	3BP5_HUMAN		0	ATACCCTCTGA	0.642	
+	9	3328	vd.1_Missense_M	NM_001144382	NP_001137854	Q9UPR0	PLCL2_HUMAN		4	CATTGGAGAAC	0.383	
-	9	1724	_p.G205E|OSBPL1	NM_017784	NP_060254	Q9BXB5	OSB10_HUMAN		1	TGGCCCCAGCG	0.552	
+	2	1606		NM_001137674	NP_001131146	A6NHJ4	ZN860_HUMAN	2H2-type 5.	1	TTCAGGCGTGAT	0.393	
+	3	469	e_Mutation_p.F72	NM_015442	NP_056257	Q9H9A5	CNOTA_HUMAN		2	CTGAGTTTTTT	0.289	
-	6	686	_uc003cgr.2_Intro	NM_006309	NP_006300	Q9Y608	LRRF2_HUMAN	VL3-binding.	1	GACTGGACCGG	0.403	
+	14	4619	_Mutation_p.S146	NM_002078	NP_002069	Q13439	GOGA4_HUMAN	ential.|Glu-rich.	4	ACTGGTCCAAT	0.353	
+	14	6233	_Mutation_p.E199	NM_002078	NP_002069	Q13439	GOGA4_HUMAN	ential.|Glu-rich.	4	GGGAAGAGAAA	0.308	
+	28	3114	uc003che.2_Intron	NM_002207	NP_002198	Q13797	ITA9_HUMAN	lasmic (Potential).	6	AGAACCGGAAA	0.463	
+	19	2615	I.2_Missense_Mut	NM_015873	NP_056957	O15195	VILL_HUMAN		0	AGTCGGCTGGC	0.662	
-	4	557	.2_Intron|ACAA1_	NM_001607	NP_001598	P09110	THIK_HUMAN		1	CAGTGGACAAA	0.532	
+	12	2041	_Splice_Site_p.K5	NM_015460	NP_056275	Q8NFW9	MYRIP_HUMAN		5	CAAACAGAAGTT	0.438	
+	11	1774	.540F|CTNNB1_uc	NM_001904	NP_001895	P35222	CTNB1_HUMAN	ARM 10.	3166	AGTTGCTTGTT	0.488	
-	3	534	pu.3_Missense_M	NM_024512	NP_078788	Q9BYS8	LRRC2_HUMAN		1	GGATGCCCTTC	0.532	
+	11	1239	qn.2_Missense_M	NM_000316	NP_000307	Q03431	PTH1R_HUMAN	cellular (Potential).	1	CTACCCTGGCC	0.622	
-	12	6063	e_Mutation_p.D20	NM_014159	NP_054878	Q9BYW2	SETD2_HUMAN		32	TTATATCCACTG	0.413	
-	3	1555	ro.3_Missense_M	NM_006574	NP_006565	O95196	CSPG5_HUMAN	OPC.|Cytoplasmic (Potenti	2	ACTTGGTCCTA	0.592	
-	26	3504		NM_000094	NP_000085	Q02388	CO7A1_HUMAN	region (NC1).|VWFA 2.	11	TCAAGGGTTCA	0.587	
-	3	479	uq.2_Missense_M	NM_001005909	NP_001005909	Q9UHH9	IP6K2_HUMAN		0	TCCTGTCTTCAT	0.408	
-	9	1190	MT_uc003cwy.2_	NM_000481	NP_000472	P48728	GCST_HUMAN		1	AGAGGGGGAG	0.597	
-	28	2372	_Mutation_p.W77	NM_006030	NP_006021	Q9NY47	CA2D2_HUMAN	cellular (Potential).	1	TCTGTCCAGTC	0.607	
+	7	1133	11bdu.1_Splice_Si	NM_015106	NP_055921	Q9Y4B4	ARIP4_HUMAN		3	GCCGGTAAGAG	0.502	
+	5	362	|ACY1_uc011beb.	NM_000666	NP_000657	Q03154	ACY1_HUMAN		2	TTCAAGGATTCT	0.547	
+	5	980	ddn.2_Intron|GLYC	NM_145262	NP_660305	Q8IVS8	GLCTK_HUMAN		0	TGACCCCCATG	0.602	rs75893100
-	15	2047	dgg.2_Missense_	NM_001005159	NP_001005159	Q9UHJ3	SMBT1_HUMAN		1	TACCTGACTCTG	0.383	
+	6	883	C66_uc003dhx.2_	NM_001141947	NP_001135419	A2RUB6	CCD66_HUMAN	Potential.	1	AAGCCCAGTGG	0.313	
-	14	2182	_p.S298N|C3orf63_	NM_015224	NP_056039	Q9UK61	CC063_HUMAN		5	CCCACACTCTTT	0.378	
+	2	968	EF3_uc003dih.2_	NM_181727	NP_859078	Q7Z6I5	SPT12_HUMAN		0	TATCCCAAATAA	0.398	
-	13	2199	p.E680K|IL17RD_	NM_017563	NP_060033	Q8NFM7	I17RD_HUMAN	lasmic (Potential).	0	CTCCTCACCTA	0.537	
-	7	1404		NM_198859	NP_942559	Q7Z3G6	PRIC2_HUMAN	zinc-binding 3.	5	TGTTGGCCATCA	0.522	

-	15	2220	lmh.1_Missense_M	NM_182920	NP_891550	Q9P2N4	ATS9_HUMAN	Cys-rich.	4	CATGATCGCATCC	0.338	
+	2	305	19A1_uc003dng.2_	NM_213609	NP_998774	Q7Z5A9	F19A1_HUMAN		1	AGCACACTTTCCA	0.498	
+	8	714	dpi.1_Missense_M	NM_174907	NP_777567	Q9NY27	PP4R2_HUMAN		1	GTGACTCTTCGAC	0.343	
-	30	5010	p.P1501L|ROBO1_	NM_002941	NP_002932	Q9Y6N7	ROBO1_HUMAN	lasmic (Potential).	2	GAACTGGGATCTC	0.383	
-	16	2300	e_Mutation_p.D66	NM_002941	NP_002932	Q9Y6N7	ROBO1_HUMAN	tential).|Fibronectin type-III	2	GTTGATCTACCTA	0.318	
+	4	1229	rp.1_Missense_Mu	NM_001080448	NP_001073917	Q9UF33	EPHA6_HUMAN	cellular (Potential).	16	AGTTTAACATACA	0.373	
-	3	931		NM_014820	NP_055635	O94826	TOM70_HUMAN	nic (Potential).|TPR 2.	1	ATTTTTGCTGTAA	0.328	
-	11	1396	ne.1_Missense_Mu	NM_016247	NP_057331	Q9BZV3	IMPG2_HUMAN	cellular (Potential).	3	GTGTTCCAAACTA	0.398	
-	24	3251	uw.2_Missense_M	NM_020654	NP_065705	Q9BQF6	SENP7_HUMAN	Protease.	5	CTGCTGCCCTTCT	0.413	
-	5	846		NM_018010	NP_060480	Q9NWB7	IFT57_HUMAN		3	CATTATCTGTCTC	0.274	
-	14	2079	524_uc010hpv.1_	NM_020890	NP_065941	Q8TCG1	CIP2A_HUMAN		3	ACTGAAGTTTCT	0.333	
-	1	216	lzb.3_Missense_M	NM_181780	NP_861445	Q7Z6A9	BTLA_HUMAN		0	TGGCAGGCAATG	0.438	
-	15	2461	CDC52_uc003eah.1	NM_144718	NP_653319	Q8N0Z3	SPICE_HUMAN		0	TACCTGGTGTTAG	0.373	
+	14	1599	AMD1C_uc003eas	NM_017577	NP_060047	Q8IYS0	GRM1C_HUMAN		3	TTACTGGCCTACG	0.403	
+	6	1390	ise_Mutation_p.S1	NM_017554	NP_060024	Q460N5	PAR14_HUMAN		6	TCCAAAGCATTGA	0.368	
+	4	518	ehf.1_Missense_Mu	NM_001024660	NP_001019831	O60229	KALRN_HUMAN	CRAL-TRIO.	6	ATTAAACCCGACA	0.507	
+	6	644	G1L2_uc010hth.2_I	NM_001136152	NP_001129624	C9J202	AG1L2_HUMAN		0	ACACGTCCTCCAC	0.602	
+	30	3471		NM_015268	NP_056083	O75165	DJC13_HUMAN		2	TCCAATGTGCTTC	0.328	
+	20	3574	v.1_Missense_Mut	NM_001063	NP_001054	P02787	TRFE_HUMAN	ansferrin-like 2.	2	GCTTGCGTCCAC	0.527	rs146055081
-	8	1152		NM_013363	NP_037495	Q9UKZ9	PCOC2_HUMAN	NTR.	3	GTGCCGGCTAATA	0.433	
-	3	456	se_Mutation_p.L15	NM_021105	NP_066928	O15162	PLS1_HUMAN	1 (Potential).|WW-binding 1	2	TACTGAGGAGGAT	0.313	
-	5	5731	l_5'Flank|IGSF10_	NM_178822	NP_849144	Q6WRI0	IGS10_HUMAN	-like C2-type 5.	13	CCCTGTCTGAAGA	0.438	
-	1	397	.2_Intron|MBNL1_	NM_001123228	NP_001116700	Q6UXP3	TM14E_HUMAN		0	ATACTTCCAAGTT	0.388	
-	9	851	76_splice|ZBBX_u	NM_024687	NP_078963	A8MT70	ZBBX_HUMAN		2	GCCATACCTGCAA	0.343	
-	2	638	ECOM_uc010hwn.	NM_004991	NP_004982	Q03112	EVI1_HUMAN		14	CAAACTCAGCAGC	0.488	
+	3	1292		NM_001080460	NP_001073929	A6NIV6	LRIQ4_HUMAN	LRR 18.	0	GGCACAATTTGCT	0.458	
+	16	2489		NM_006218	NP_006209	P42336	PK3CA_HUMAN		3553	AAAGGCCACTGT	0.348	
+	12	2063	e_Mutation_p.E288	NM_003907	NP_003898	Q13144	EI2BE_HUMAN	W2.	5	AAAGAGGAGAAC	0.473	
+	8	928	'L3_uc003fmt.2_5'	NM_004423	NP_004414	Q92997	DVL3_HUMAN	PDZ.	3	GCATCTCCATTGT	0.507	
+	6	755	n_p.P170L|LPP_u	NM_005578	NP_005569	Q93052	LPP_HUMAN	Pro-rich.	165	ACCAACCCCCTC	0.517	
-	4	771		NM_021101	NP_066924	O95832	CLD1_HUMAN	ical; (Potential).	1	CAGGAACAGCAA	0.522	
-	8	1089	RC_uc010hzy.2_M	NM_003234	NP_003225	P02786	TFR1_HUMAN	llular (Potential).|PA.	3	GCATTTGCAACCT	0.353	
-	23	2456	_p.D439N|DLG1_u	NM_001098424	NP_001091894	Q12959	DLG1_HUMAN	nylate kinase-like.	3	TTCCATCTACCTC	0.303	
+	5					Q7Z3I0	Q7Z3I0_HUMAN		0	TCTCTAGAAGCAA	0.383	
-	3	3298	ron|ABCA11P_uc0	NM_133474	NP_597731	D9N162	D9N162_HUMAN		1	GCCACATTCTCCA	0.413	
-	3	2373	tron|ABCA11P_uc0	NM_133474	NP_597731	D9N162	D9N162_HUMAN		1	CCACATTCTTCAC	0.413	
-	3	312	p.P66L|SLBP_uc00	NM_006527	NP_006518	Q14493	SLBP_HUMAN		0	GGTTTAGGGCCT	0.408	
+	8	1122	ADD1_uc003gfq.2_	NM_001119	NP_001110	P35611	ADDA_HUMAN		1	AGCGTTGAGGAG	0.512	
+	23	3093		NM_002111	NP_002102	P42858	HD_HUMAN		4	CAATAACCAGGTA	0.438	
+	4	453	K7_uc003ghe.2_5'U	NM_173660	NP_775931	Q18PE1	DOK7_HUMAN	RS-type PTB.	1	GCGGCCCGGCTA	0.488	
+	17	2640	1_RNA|CRMP1_u	NM_153717	NP_714928	P57679	EVC_HUMAN		2	GTGAGAGGATGG	0.567	
-	7	906	p.G255S|ABLIM2_u	NM_001130084	NP_001123556	Q6H8Q1	ABLM2_HUMAN	l zinc-binding 4.	3	TTGTACCTTGAAG	0.498	
+	5	541	ise_Mutation_p.T7	NM_018986	NP_061859	Q8TE82	S3TC1_HUMAN		3	TTAAGACTTTTGA	0.502	
-	1	207	2A9_uc003gmd.2_	NM_020041	NP_064425	Q9NRM0	GTR9_HUMAN	lasmic (Potential).	3	ACCTTTCTTCTCC	0.632	
-	11	694	np.2_Missense_Mu	NM_052964	NP_443196	Q7Z7G1	CLNK_HUMAN	Pro-rich.	1	GATAAAGGTGGCC	0.532	
+	16	1854	.1_RNA|CC2D2A_	NM_001080522	NP_001073991	Q9P2K1	C2D2A_HUMAN	Potential.	3	TAAAGGGAAAAAG	0.294	
-	3	1161	AF16_uc003gpo.2_	NM_017741	NP_060211	Q9NXF7	DCA16_HUMAN		1	AGGAATCCCACTC	0.438	

-	14	2402	eo.1_Missense_M	NM_145290	NP_660333	Q8IWK6	GP125_HUMAN	ular (Potential).|GPS.	1	GCCTCCTTGTC	0.458	
-	12	2268	HX15_uc003gqw.	NM_001358	NP_001349	O43143	DHX15_HUMAN		1	TACATACCTGCAT	0.328	
+	9	1121	_p.L211F|PGM2_u	NM_018290	NP_060760	Q96G03	PGM2_HUMAN		1	GGGCCCTCCTG	0.448	
+	3	423	tg.2_Missense_Mu	NM_016531	NP_057615	P57682	KLF3_HUMAN	sor domain.|Pro-rich.	2	TGAAGCCTAAC	0.418	
-	2	458	_p.E27K|TLR10_u	NM_030956	NP_112218	Q9BXR5	TLR10_HUMAN	ular (Potential).|LRR 1.	2	CCCTTTCTTCTG	0.433	
-	23	2874	k.2_Missense_Mu	NM_015030	NP_055845	O94915	FRYL_HUMAN		1	AATAGAGCAAAG	0.318	
-	9	2155	m.2_Missense_M	NM_152540	NP_689753	Q8WU76	SCFD2_HUMAN		3	TCAGTTGCAAAT	0.502	
-	15	2548	t.1_Missense_Mut	NM_002253	NP_002244	P35968	VGFR2_HUMAN	7.|Extracellular (Potential).	33	AATGCCTCCACT	0.328	
+	9	1234	p.G359D|EXOC1_	NM_018261	NP_060731	Q9NV70	EXOC1_HUMAN		6	TTTAGGGTCATG	0.373	
+	21	2941	bj.2_Missense_M	NM_025009	NP_079285	Q66GS9	CP135_HUMAN	Potential.	5	AGGGAGAAAGC	0.398	
+	14	2662	_p.G830D|LPHN3_	NM_015236	NP_056051	Q9HAR2	LPHN3_HUMAN	tracellular (Potential).	18	TGACAGGTTATT	0.398	
-	6	1024	ln.2_RNA|PAQR3	NM_001040202	NP_001035292	Q6TCH7	PAQR3_HUMAN	lasmic (Potential).	0	TTGGTGGCTTG	0.368	
-	6	314	1ccj.1_Missense_	NM_001080506	NP_001073975	B9EJG8	T150C_HUMAN	ical; (Potential).	1	CAAGGGCTAGG	0.388	
-	3	550	of.2_RNA|COQ2_	NM_015697	NP_056512	Q96H96	COQ2_HUMAN	ical; (Potential).	2	CCAGGGTTAGC	0.383	
-	4	549		NM_144645	NP_653246	Q96KX1	CD036_HUMAN		0	TACTCCCTTTCG	0.363	
-	11	940	p.S241F|EMCN_u	NM_016242	NP_057326	Q9ULC0	MUCEN_HUMAN	lasmic (Potential).	0	GTGCAGAGTGC	0.378	
-	5	1287	wa.1_Missense_	NM_022154	NP_071437	Q9C0K1	S39A8_HUMAN	cellular (Potential).	0	TCACACCATTG	0.373	
-	3	510	T6_uc003iex.2_5'	NM_007083	NP_009014	P53370	NUDT6_HUMAN	udix hydrolase.	0	GTACAACCAGTA	0.274	
+	1	3182	gz.2_Missense_M	NM_032961	NP_116586	Q9P2E7	PCD10_HUMAN	lasmic (Potential).	2	AAGTCAGACATC	0.622	
-	2	1918	L3_uc011chd.1_I	NM_018717	NP_061187	Q96JK9	MAML3_HUMAN		1	CCGTGGAGACA	0.567	
-	3	267	_Mutation_p.P38	NM_014885	NP_055700	Q9UM13	APC10_HUMAN	DOC.	0	ACCTGGTTTGC	0.368	
-	13	2480	_p.V405I|SH3D19	NM_001009555	NP_001009555	Q5HYK7	SH319_HUMAN	SH3 1.	2	GTGAACTCTGC	0.423	
+	13	2672		NM_020840	NP_065891	Q9P278	FNIP2_HUMAN	tion with PRKAA1.	0	AACGGGAGGGA	0.637	
+	11	1919		NM_014247	NP_055062	Q9Y4G8	RPGF2_HUMAN		4	AGATACTCGAC	0.368	
+	7	1555	_p.T303I|TLL1_uc	NM_012464	NP_036596	O43897	TLL1_HUMAN	otease (By similarity).	7	GAACACCTTCT	0.403	
+	15	2511	_p.L645F|TLL1_uc	NM_012464	NP_036596	O43897	TLL1_HUMAN	CUB 3.	7	GACTTCTTACC	0.458	
+	13	2196	uc003jbb.1_5'Flan	NM_007277	NP_009208	O60645	EXOC3_HUMAN		0	CCAGGGATGAC	0.642	
-	10	1496	c.2_RNA|ZDHHC1	NM_024786	NP_079062	Q9H8X9	ZDH11_HUMAN		2	CACGAGTGGAG	0.577	
+	10	1715	_p.A526D|ADAMT	NM_139056	NP_620687	Q8TE57	ATS16_HUMAN	Disintegrin.	8	GAAAGCCAAGC	0.408	
+	13	1636		NM_015325	NP_056140	Q9Y2F5	K0947_HUMAN		2	TCCATGAGTGAT	0.413	
-	1	238		NM_033414	NP_219482	Q969S3	ZN622_HUMAN		1	TGGGGCCATGC	0.687	
-	7	1569	jhi.2_Missense_	NM_013235	NP_037367	Q9NRR4	RNC_HUMAN		0	TTCTTCTTCCT	0.473	
+	1	535		NM_016568	NP_057652	Q9NSD7	RL3R1_HUMAN	cellular (Potential).	1	ACGGCGCGCCG	0.697	
+	8	1144	p.E345K|SPEF2_	NM_024867	NP_079143	Q9C093	SPEF2_HUMAN	Potential.	4	AGCAGGAGCGC	0.463	
+	10	2663	p.P722S|NIPBL_u	NM_133433	NP_597677	Q6KC79	NIPBL_HUMAN		9	GGCATCCTGAA	0.468	
+	17	4387	.3_Nonsense_Mu	NM_133433	NP_597677	Q6KC79	NIPBL_HUMAN		9	TTATGGAGAGA	0.313	
-	29	5999	rf42_uc003jks.2_	NM_023073	NP_075561	E9PH94	E9PH94_HUMAN		7	GACTTCTGAAA	0.338	
-	1	1045	2_Nonsense_Mut	NM_199335	NP_955367	O15117	FYB_HUMAN		2	TGGCCCCATGG	0.537	
-	9	1444	mb.2_Missense_	NM_006251	NP_006242	Q13131	AAPK1_HUMAN		1	TAATTTCATCTG	0.403	
+	20	3146	.2_Missense_Mut	NM_012343	NP_036475	Q13423	NNTM_HUMAN	chondrial matrix.	3	TCACCCAGTTG	0.458	
-	19	3083	X29_uc010ivw.2_	NM_019030	NP_061903	Q7Z478	DHX29_HUMAN	case C-terminal.	4	AGAAGCCATCT	0.438	
-	6	1174	PAP2A_uc003jpz.	NM_003711	NP_003702	O14494	LPP1_HUMAN	lasmic (Potential).	2	AAGTTCTTTCT	0.348	
-	2	165	_p.R31Q|DEPDC	NM_018369	NP_060839	Q8WUY9	DEP1B_HUMAN	DEP.	1	TGTTTCCGTAAC	0.453	rs148021233
-	5	1913		NM_152625	NP_689838	Q8N895	ZN366_HUMAN		2	TCTGTGCCAGG	0.597	
-	9	1353	3kdt.2_Missense_	NM_005713	NP_005704	Q9Y5P4	C43BP_HUMAN		1	GCCTTCCTATT	0.328	
+	22	3279		NM_002439	NP_002430	P20585	MSH3_HUMAN		4	TTGTCACCCATT	0.328	
+	5	754	_p.P109S|ATG10_	NM_001131028	NP_001124500	Q9H0Y0	ATG10_HUMAN		0	AAGTGCCTGTA	0.353	

+	8	8206	.2_Intron|VCAN_u	NM_004385	NP_004376	P13611	CSPG2_HUMAN	GAG-beta.		16	ACAGCACTCAAG	0.413	
-	1	481	ip.1_Missense_Mu	NM_005711	NP_005702	O43854	EDIL3_HUMAN			2	CTTTGCCGAACT	0.701	
+	54	11315	p.T1446I|GPR98_	NM_032119	NP_115495	Q8WXG9	GPR98_HUMAN	cellular (Pote	p.T3740T(1)	16	CCCTCACCCGTAT	0.408	
-	24	2842		NM_014639	NP_055454	Q6PGP7	TTC37_HUMAN	TPR 14.		4	CAATTTGTTCTGA	0.313	
-	16	2646	m.1_Missense_Mu	NM_001040458	NP_001035548	Q9NZ08	ERAP1_HUMAN	enal (Potential).		2	GGTCACGTCGA	0.453	
-	27	3992	jbn.2_Missense_M	NM_001270	NP_001261	O14646	CHD1_HUMAN			5	ACTGAGGTCAG	0.303	
-	6	1269	ense_Mutation_p.G	NM_173488	NP_775759	Q86UG4	SO6A1_HUMAN	lasmic (Potential).		7	TAGTTCCAAGTT	0.299	
+	12	1798	nse_Mutation_p.P	NM_015216	NP_056031	O43314	VIP2_HUMAN			2	AAAAAACCAAAA	0.224	
+	13	1694	R36_uc010jbu.2_F	NM_139281	NP_644810	Q8NI36	WDR36_HUMAN	WD 6.		2	AGTCTGGCATAC	0.353	
+	28	7308	cl.1_Missense_Mu	NM_005509	NP_005500	Q9Y485	DMXL1_HUMAN			2	CAAAAACTTTACC	0.338	
-	5	740		NM_000943	NP_000934	P45877	PPIC_HUMAN			1	TGTCACCAATCA	0.373	
+	12	1986	_p.V391I|CSNK1G	NM_004384	NP_004375	Q9Y6M4	KC1G3_HUMAN			0	ACTGAAGTAGAA	0.353	
-	1	602	se_Mutation_p.G1	NM_020747	NP_065798	Q9ULD9	ZN608_HUMAN			6	CTGCCGCCGCTG	0.612	
+	20	2836	kui.3_Missense_M	NM_032446	NP_115822	Q96KG7	MEG10_HUMAN	P2M1, self-assembly and f		4	GAAGGGAGCGA	0.373	
+	9	1309	C1_uc003kuj.3_3'	NM_130809	NP_570721	Q96M27	PRRC1_HUMAN			0	CACAGGCTCAA	0.363	
+	5	1258	C12A2_uc010jdg.2	NM_001046	NP_001037	P55011	S12A2_HUMAN	lasmic (Potential).		3	AATTTGGTGGTG	0.373	
-	13	1951	wk.2_Missense_M	NM_004199	NP_004190	O15460	P4HA2_HUMAN	G dioxygenase.		0	CACCAGCTTCTA	0.483	
+	3	189		NM_144723	NP_653324	Q96NC0	ZMAT2_HUMAN			0	GACTTGGAATCC	0.458	
+	1	761		NM_015669	NP_056484	Q9Y5E4	PCDB5_HUMAN	|Extracellular (Potential).		5	GTTGCTACGCATA	0.498	
+	1	1265	3lka.1_Intron|PCD	NM_018914	NP_061737	Q9Y5H2	PCDGB_HUMAN	(Potential).|Cadherin 3.		0	TGTTGATCACTGT	0.408	
-	1	1875		NM_016580	NP_057664	Q9NPG4	PCD12_HUMAN	(Potential).|Cadherin 2.		3	GGGGGGGTTCC	0.478	
+	13	1282	.C384W|SPINK5_	NM_006846	NP_006837	Q9NQ38	ISK5_HUMAN	Kazal-like 6.		4	CATGTGTGAGGT	0.413	
-	17	3987	ps.2_RNA|SH3TC	NM_024577	NP_078853	Q8TF17	S3TC2_HUMAN			2	CCACCGCGCCC	0.612	
-	17	3870	lps.2_RNA|SH3TC	NM_024577	NP_078853	Q8TF17	S3TC2_HUMAN	TPR 8.		2	CGCTGCTGCCA	0.592	
+	3	1308		NM_000112	NP_000103	P50443	S26A2_HUMAN	ical; (Potential).		0	TAGCCTCTCATTT	0.388	
-	1	274	_p.G20D|CAMK2A	NM_171825	NP_741960	Q9UQM7	KCC2A_HUMAN	ase.|ATP (By similarity).		1	CACTTGCCCAAT	0.632	
+	23	3793	.P1191S|TCOF1_	NM_001135243	NP_001128715	Q13428	TCOF_HUMAN			3	TCCAGCCCCTCA	0.547	
-	8	886	TN4_uc010jhi.2_M	NM_016221	NP_057305	Q9UJW0	DCTN4_HUMAN			1	GATAGAGCTGTG	0.463	rs140781660
-	6	1511	GM_uc011dcl.1_Int	NM_052860	NP_443092	Q96RE9	ZN300_HUMAN	2H2-type 6.		2	GCTTTCCCACAT	0.463	
-	7	973	_uc003lua.2_Splic	NM_181776	NP_861441	Q495M3	S36A2_HUMAN			2	ACCTTACCACAC	0.498	
-	1	2466	AT2_uc010jhx.1_M	NM_001447	NP_001438	Q9NYQ8	FAT2_HUMAN	(Potential).|Cadherin 6.		6	AATCTGGGTGCG	0.498	
+	22	2348	_p.I737T|CYFIP2_	NM_001037333	NP_001032410	Q96F07	CYFP2_HUMAN			0	TCATCATTCCGT	0.478	
+	3	280	yk.2_Missense_Mu	NM_004219	NP_004210	O95997	PTTG1_HUMAN			0	CCAAGGGACCC	0.413	
-	11	1477	2_Missense_Muta	NM_003062	NP_003053	O75094	SLIT3_HUMAN	LRR 8.		4	CAGGCCCTGGA	0.527	
+	49	5157	se_Mutation_p.V1	NM_004946	NP_004937	Q92608	DOCK2_HUMAN			7	CTGAGGTCAAG	0.587	
-	3	748	D1_uc003mcr.2_In	NM_138369	NP_612378	Q96IK1	BOD1_HUMAN			2	CCTGGCCTTCG	0.512	
+	1	1428	jjv.2_Missense_Mu	NM_030627	NP_085130	Q17RY0	CPEB4_HUMAN			0	TTTGGAGTGCTA	0.448	
+	14	1689	GRK6_uc003mgs.	NM_002082	NP_002073	P43250	GRK6_HUMAN	kinase C-terminal.		3	CATCCCCTGGC	0.632	
+	5	3142	IL1_uc003mkn.1_I	NM_014757	NP_055572	Q92585	MAML1_HUMAN			6	CCAGGCCTACC	0.687	
-	11	1711	ation_p.A223V|MG	NM_014275	NP_055090	Q9UQ53	MGT4B_HUMAN	enal (Potential).		0	CTGACCGCTCCA	0.552	rs149772768
+	4	1186	p.E284K|FARS2_	NM_006567	NP_006558	O95363	SYFM_HUMAN			0	ATGGAGAATGG	0.428	
+	1	692	C5_uc003mxw.2_	NR_027712						0	GGGGAGCCTGA	0.493	
+	1	809	C5_uc003mxw.2_	NR_027712						0	CTTCCGTTTCA	0.532	
+	3	587	n_p.L85F|EDN1_u	NM_001955	NP_001946	P05305	EDN1_HUMAN			1	ATGGACTTGGA	0.403	
+	9	1134	ax.2_Missense_M	NM_012241	NP_036373	Q9NXA8	SIRT5_HUMAN	tylase sirtuin-type.		3	ACCACCCCAGCT	0.562	
+	3	1055	_p.V213I|RNF182_	NM_152737	NP_689950	Q8N6D2	RN182_HUMAN	ical; (Potential).		3	CTTGGGGTCGTC	0.473	
+	26	2625	jpy.2_Missense_M	NM_017640	NP_060110	Q5VZK9	LR16A_HUMAN			4	CCAGTGGCTTAC	0.393	

+	1	344	03njt.1_RNA|HIST	NM_003520	NP_003511	Q99877	H2B1N_HUMAN			0	GGAGGGCACCA	0.647	
+	1	82	_5'Flank|HIST1H2	NM_003527	NP_003518	P23527	H2B1O_HUMAN			0	GGGCTCCAAGA	0.522	
-	1	589		NM_033057	NP_149046	Q9GZK3	OR2B2_HUMAN	Name=5; (Potential).		0	TTCAGCCTCATT	0.433	
-	1	904	uc003nlp.1_5'Flan	NM_052923	NP_443155	Q6R2W3	SCND3_HUMAN	SCAN box.		1	CAGCACCAACA	0.562	
+	5	551	RPS18B_uc010jsc	NM_014046	NP_054765	Q9Y676	RT18B_HUMAN		p.G132C(1)	1	ACACGGGTATC	0.502	
-	5	1133	dmo.1_Splice_Site	NM_003587	NP_003578	O60231	DHX16_HUMAN			4	CCTCACCTGTC	0.622	
+	4	1424	p.G426E|TUBB_uc	NM_178014	NP_821133	P07437	TBB5_HUMAN			1	AAGAGGAGGAG	0.577	
-	3	228	dmr.1_Missense_M	NM_005803	NP_005794	O75955	FLOT1_HUMAN			0	CATGACTGGGG	0.602	
+	2	229	A_uc003rxz.1_5'UTR							0	AGAAATGCAGG	0.552	rs17200172
+	3	409	.3_Missense_Mut	NM_080686	NP_542417	P48634	PRC2A_HUMAN	type A repeats.|1-1.		0	TTGCCCGGCGT	0.557	
+	14	2241	T2_uc003nvc.3_N	NM_080686	NP_542417	P48634	PRC2A_HUMAN	X 57 AA type A repeats.		0	caccagtggcagcagc	0.483	
-	3	519	l.2_5'UTR|C6orf27	NM_025258	NP_079534	Q9Y334	G7C_HUMAN			3	AACCAGGTCCA	0.597	
+	28	4095	lank|STK19_uc01	NM_006929	NP_008860	Q15477	SKIV2_HUMAN			4	GGCGGGACATC	0.567	
-	4	1368	TR|DOM3Z_uc010	NM_005510	NP_005501	O77932	DOM3Z_HUMAN			0	TGAGCCCACCA	0.542	
-	1	800	ation_p.P89L|STK	NM_005510	NP_005501	O77932	DOM3Z_HUMAN			0	GATCCGGGTAT	0.632	
-	25	8957		NM_019105	NP_061978	P22105	TENX_HUMAN	nectin type-III 21.		0	GCCCACGCGCT	0.637	
-	24	8474		NM_019105	NP_061978	P22105	TENX_HUMAN	nectin type-III 20.		0	GGGGATGGTCC	0.672	
-	7	3245		NM_019105	NP_061978	P22105	TENX_HUMAN	nectin type-III 3.		0	CAGAGCCTGGC	0.657	
-	9	1761	dpv.1_RNA|NOTC	NM_004557	NP_004548	Q99466	NOTC4_HUMAN	ng (Potential).|Extracellular		22	CACCAGGCAGG	0.597	
-	2	289	1_5'Flank|HLA-DM	NM_002118	NP_002109	P28068	DMB_HUMAN	Lumenal (Potential).		0	AGCCACCTAGA	0.403	
+	6	1171	dl.2_Missense_M	NM_002931	NP_002922	Q06587	RING1_HUMAN	nteraction with CBX2 (By s		2	TGACACCGGAG	0.677	
-	6	2083	tion_p.P552S|DA	NM_001350	NP_001341	Q9UER7	DAXX_HUMAN	action with SPOP.		23	GGGGGGACCA	0.512	
+	7	878	AP1_uc010juy.2_	NM_006772	NP_006763	Q96PV0	SYGP1_HUMAN	PH.		4	AGGAACAAAAT	0.517	
+	9	1354	RF1BP1_uc010jvr	NM_017754	NP_060224	Q6BDS2	URFB1_HUMAN			3	GGCAGGTTAGG	0.478	
-	3	461	.1_RNA|MTCH1_	NM_014341	NP_055156	Q9NZJ7	MTCH1_HUMAN	Solcar 1.		0	GCCGGGGACTC	0.557	
+	1	477	1_uc011dtw.1_5'F	NM_002648	NP_002639	P11309	PIM1_HUMAN			2	CGCGCCCTGCA	0.716	
+	35	5056		NM_001371	NP_001362					21	TCCTCAGATATA	0.363	
+	42	6238		NM_001371	NP_001362					21	TCAGAGGCCTA	0.353	
+	2	154	10jxx.1_Intron|PT	NM_138296	NP_612153	Q6ISU1	PTCRA_HUMAN	ellular (Potential).		2	GGCACACCCTTT	0.567	
+	11	2749	_p.E892K|CUL9_u	NM_015089	NP_055904	Q8IWT3	CUL9_HUMAN			12	CCCAAGAGCTG	0.512	
-	32	3797	1C_uc003ovo.1_	NM_020750	NP_065801	Q9HAV4	XPO5_HUMAN			4	GCCACCCCCAT	0.483	
+	7	1131	LH_uc011dvl.1_R	NM_006502	NP_006493	Q9Y253	POLH_HUMAN			2	CATGGGTGAAC	0.418	
+	10	1751	p.S556N|HSP90A	NM_007355	NP_031381	P08238	HS90B_HUMAN			4	AGAGAGCAAGG	0.458	
-	16	1774	ai.2_Missense_M	NM_138694	NP_619639	P08F94	PKHD1_HUMAN	ellular (Potential).		44	TGGAAGCCTCT	0.537	
+	2	260		NM_133367	NP_588608	Q8TEZ7	MPRB_HUMAN	lasmic (Potential).		0	GGATGGGCTTC	0.672	
+	2	393	FHC1_uc011dww.	NM_018100	NP_060570	Q5JVL4	EFHC1_HUMAN			3	CCCAGGCTGAG	0.537	
+	29	2047	am.1_Missense_	NM_001858	NP_001849	Q14993	COJA1_HUMAN	lical region 3 (COL3).		4	TCCAGGGTCCT	0.458	
+	3	617	ite|IRAK1BP1_uc0	NM_001010844	NP_001010844	Q5VVH5	IKBP1_HUMAN			0	TCTTCGGTAAGT	0.338	
+	8	2805		NM_015021	NP_055836	O60281	ZN292_HUMAN			4	GTTTGGAAAAC	0.443	
-	8	1383	dzv.1_Missense_M	NM_002042	NP_002033	P24046	GBRR1_HUMAN	ical; (Probable).		1	AGGCACGGCTC	0.478	
+	4	759	Intron|KLHL32_uc	NM_052904	NP_443136	Q96NJ5	KLH32_HUMAN	BTB.		4	GCAGGCTCTGG	0.423	
-	31	5208		NM_006828	NP_006819	Q8N3C0	HELC1_HUMAN	ase C-terminal 2.		6	TCGGTCCCTCT	0.373	
-	31	5161		NM_006828	NP_006819	Q8N3C0	HELC1_HUMAN	ase C-terminal 2.		6	CAAGGGTCAGC	0.368	
-	40	5506	as.1_Missense_M	NM_001145128	NP_001138600	Q5TCS8	AKD1_HUMAN			1	GAGAAGTTGCA	0.373	
+	2	587	_p.P151L|GPR6_u	NM_005284	NP_005275	P46095	GPR6_HUMAN	ellular (Potential).		0	GGTGCCCTCGG	0.637	
+	7	800	MT11_uc010kev.2	NM_001031712	NP_001026882	Q7Z4G4	TRM11_HUMAN			1	GGAACAGGTATT	0.289	
-	6	704	utation_p.A142V|	NM_001139510	NP_001132982	Q9NTX5	ECHD1_HUMAN			0	TTTAGAGCATTTT	0.443	

-	17	2979	41L2_uc011eby.1_	NM_001431	NP_001422	O43491	E41L2_HUMAN	xyl-terminal (CTD).	2	TGACACGGACT	0.453	rs145851233
-	17	2266	gv.2_Missense_Mu	NM_003980	NP_003971	Q14244	MAP7_HUMAN		0	ATCGGGAGTGC	0.264	
+	53	7902		NM_007124	NP_009055	P46939	UTRO_HUMAN		5	TGAAAGGCCCT	0.448	
-	2	745	_p.R66K|LATS1_u	NM_004690	NP_004681	O95835	LATS1_HUMAN		6	GGATTTCTGACT	0.408	
+	4	3826	_Mutation_p.E109	NM_005100	NP_005091	Q02952	AKA12_HUMAN		8	ATCCATGAGGAG	0.547	
+	24	5275	_p.W710*|TIAM2_	NM_012454	NP_036586	Q8IVF5	TIAM2_HUMAN		4	TTCCTGGTTGAA	0.433	
+	7	2486	e_Mutation_p.D78	NM_005922	NP_005913	Q9Y6R4	M3K4_HUMAN		9	GTGCGGATGAC	0.448	
+	6	1369	siz.2_Missense_M	NM_017802	NP_060272	Q86Y56	HEAT2_HUMAN		1	CTCTGCCTCCG	0.642	
+	16	1913	e_Mutation_p.G51	NM_001130965	NP_001124437	O94901	SUN1_HUMAN	inuclear space.	0	AGACCGGGATG	0.507	
+	5	1052	.1_Intron|AMZ1_u	NM_133463	NP_597720	Q400G9	AMZ1_HUMAN		0	CAGCAGCAGAC	0.687	
-	9	1021	_p.P71L|SKAP2_	NM_003930	NP_003921	O75563	SKAP2_HUMAN		1	GTAGAGGATGA	0.303	
-	1	86	A10_uc003syw.3_	NM_018951	NP_061824	P31260	HXA10_HUMAN		0	GAGCATGACATT	0.458	
+	7	712	HR_uc003tby.2_	NM_000823	NP_000814	Q02643	GHRHR_HUMAN	Name=3; (Potential).	5	TGTTGGCAGAA	0.627	
+	2	336	_Mutation_p.D64	NM_015060	NP_055875	Q8NBF6	AVL9_HUMAN		0	TACCAGATGGC	0.428	
-	3	274		NM_203288	NP_976033	Q8TA86	RP9_HUMAN	nding (By similarity).	0	TGCATGAGCCA	0.453	
+	2	248		NM_133468	NP_597725	Q8N8U9	BMPER_HUMAN		3	TTCAGGTTCTG	0.368	
+	4	925	g.2_Missense_Mu	NM_018685	NP_061155	Q9NQW6	ANLN_HUMAN	ction with F-actin.	3	CCTCTGCAAGT	0.428	
+	12	3436	.D1052N|CDK13_	NM_003718	NP_003709	Q14004	CDK13_HUMAN		5	GCTTGGATGAC	0.498	
-	7	915	ense_Mutation_p.	NM_032158	NP_115534				0	ACTCACCCTTGG	0.542	
-	15	2809	_p.G838E|MAGI2_	NM_012301	NP_036433	Q86UL8	MAGI2_HUMAN	PDZ 4.	11	CCTGCCCATTG	0.532	
+	32	8282	_Mutation_p.G230	NM_005751	NP_005742	Q99996	AKAP9_HUMAN	ential.|Glu-rich.	26	AAAGTGGATTTT	0.353	
-	15	2009	p.G613D|KRIT1_u	NM_194456	NP_919438	O00522	KRIT1_HUMAN	RAP1A binding.|FERM.	3	TGACACCTTCA	0.328	rs35311859
+	9	1760		NM_019004	NP_061877	Q9P2G1	AKIB1_HUMAN	ype; degenerate.	1	AAGGACACCTC	0.418	
-	5	622	mu.1_Missense_	NM_001742	NP_001733	P30988	CALCR_HUMAN	ellular (Potential).	9	ATGGATCAAAAT	0.403	
-	4	663		NM_001185	NP_001176	P25311	ZA2G_HUMAN	-like C1-type.	2	AGAGGGAGGAT	0.577	
+	2	243	TAG3_uc011kjk.1_	NM_012447	NP_036579	Q9UJ98	STAG3_HUMAN		8	TTGATGACAGG	0.527	
+	33	3816	a.3_Intron|GATS_	NM_012447	NP_036579	Q9UJ98	STAG3_HUMAN		8	AGCTGGATATT	0.502	
-	14	2849	_p.W693*|EPHB4	NM_004444	NP_004435	P54760	EPHB4_HUMAN	Potential).|Protein kinase.	15	GCAGTCCATCG	0.582	
+	9	13152	C17_uc010lho.1_	NM_001040105	NP_001035194	Q685J3	MUC17_HUMAN	ellular (Potential).	27	CTCAGTGCCTG	0.607	
+	27	5099	LL5_uc010ljf.1_Int	NM_182931	NP_891847	Q8IZD2	MLL5_HUMAN	Pro-rich.	3	ACAGACACCCT	0.493	
+	6	831		NM_002736	NP_002727	P31323	KAP3_HUMAN	cAMP 1.	1	TCGTGGGAGTT	0.423	
-	4	935	p.R137K|COG5_u	NM_181733	NP_859422	Q9UP83	COG5_HUMAN		4	CCAATTCTCGTC	0.323	
-	3	983	fl.2_Missense_Mu	NM_001130475	NP_001123947	Q7Z6K1	THAP5_HUMAN		0	AGCAGGTACAA	0.323	
+	4	2833	|LRRN3_uc003vfu	NM_001099660	NP_001093130	Q9H3W5	LRRN3_HUMAN	tential).|Fibronectin type-II	8	ATATTCCCACCA	0.348	
-	4	2793		NM_002711	NP_002702	Q16821	PPR3A_HUMAN		34	ATTTCAGTATGA	0.378	
-	5	1195	a.2_Missense_Mu	NM_003391	NP_003382	P09544	WNT2_HUMAN	p.N295_D302del	7	GCCCCGGGAAG	0.572	rs148046128
+	12	4192	.2_Intron|PTPRZ1	NM_002851	NP_002842	P23471	PTPRZ_HUMAN	ellular (Potential).	9	ATGCAAGTGAGA	0.403	
-	9	1157		NM_003941	NP_003932	O00401	WASL_HUMAN	Pro-rich.	0	TGGTGGTGCTG	0.279	
+	6	770	a.1_Missense_Mu	NM_005011	NP_005002	Q16656	NRF1_HUMAN		1	TACAGGTCGGG	0.527	
-	12	1495	lmc.1_Missense_	NM_032842	NP_116231	Q96SK2	TM209_HUMAN		3	AATCAAGGTAGG	0.373	
+	18	2784	.G527S|EXOC4_	NM_021807	NP_068579	Q96A65	EXOC4_HUMAN		9	ACCAGGGTGTG	0.582	
+	15	2231		NM_015135	NP_055950	Q92621	NU205_HUMAN		6	TTTGACCCTTATT	0.468	rs150179196
+	14	1881	AS1_uc003vvi.2_	NM_001130966	NP_001124438	P24557	THAS_HUMAN	lasmic (Potential).	3	AATGGTGTCTAT	0.398	
-	15	1860		NM_004333	NP_004324	P15056	BRAF_HUMAN	rotein kinas_R603>I(2)|p.T	18290	GATTTCACTGTA	0.368	
+	5	1230	852_uc010lnn.2_	NM_001105558	NP_001099028	P0C1S8	WEE2_HUMAN	rotein kinase.	2	TACGTTACTATT	0.408	
+	21	3898		NM_014141	NP_054860	Q9UHC6	CNTP2_HUMAN		11	CTGCAGCTCGA	0.458	
+	46	6680		NM_198455	NP_940857	A2VEC9	SSPO_HUMAN		0	CACAGGGTCCC	0.672	

-	58	14801	x.2_Missense_Mu	NM_170606	NP_733751	Q8NEZ4	MLL3_HUMAN	SET.	63	CAAAAGTCACC	0.433
-	36	6721	z.2_Missense_Mut	NM_170606	NP_733751	Q8NEZ4	MLL3_HUMAN	Pro-rich.	63	AGTAGGCCGGG	0.478
-	27	4439	z.2_Missense_Mu	NM_170606	NP_733751	Q8NEZ4	MLL3_HUMAN		63	CTAAGGAAGGA	0.343
+	6	633	r.2_Missense_Mut	NM_030936	NP_112198	Q9H0A6	RNF32_HUMAN	-type 1; atypical.	0	TTCAGGCATGT	0.358
+	9	2218		NM_138400	NP_612409	Q5C9Z4	NOM1_HUMAN	MI.	0	TTCGGGACTTG	0.383
-	7	1375		NM_033225	NP_150094	Q96PZ7	CSMD1_HUMAN	ellular (Potential).	25	TCCATCCTTGCT	0.453
+	5	840	e_Mutation_p.P13	NM_152415	NP_689628	Q8NEZ2	VP37A_HUMAN		0	ATCCTCCACAAG	0.413
+	20	2529	_p.G794D|PIWIL2_	NM_018068	NP_060538	Q8TC59	PIWL2_HUMAN	Piwi.	1	TCGTGGGCTCCT	0.403
+	6	1103	xbp.3_Missense_	NM_001128431	NP_001121903	Q15043	S39AE_HUMAN	lasmic (Potential).	0	GCTCGCTCTCT	0.602
+	18	2083	xbw.3_Splice_Sit	NM_005775	NP_005766	O60504	VINEX_HUMAN		0	CCAGGTGAGGT	0.662
+	2	1159	_Mutation_p.E37	NM_005382	NP_005373	P07197	NFM_HUMAN	Rod.|Coil 2B.	1	AGTGGGAAATG	0.507
-	6	1712	p.G353E|CHRNA2	NM_000742	NP_000733	Q15822	ACHA2_HUMAN	Cytoplasmic.	1	GGGCCCCCCGC	0.647
-	1	655		NM_031271	NP_112561	Q9BXT5	TEX15_HUMAN		7	AAAAACTGTAG	0.363
-	24	4627	lwe.2_Missense_	NM_023034	NP_075447	Q9BZ95	NSD3_HUMAN		1	TGCTGCACTCA	0.363
+	6	936	3M2_uc003xoq.1_	NM_001134296	NP_001127768	P53677	AP3M2_HUMAN	MHD.	0	GGCATGCCAGA	0.448
+	13	906	_p.Y236H|POLB_	NM_002690	NP_002681	P06746	DPOLB_HUMAN		2	ATCAGTATTACT	0.343
-	8	1790	xpe.2_Missense_	NM_006749	NP_006740	Q08357	S20A2_HUMAN	lasmic (Potential).	2	GGGGCCCCTGT	0.587
+	3	309	c003xql.1_Misse	NM_182746	NP_877423	P33991	MCM4_HUMAN		4	CCAGCCCTCCC	0.547
+	19	1656	p.A429T|SNTG1_	NM_018967	NP_061840	Q9NSN8	SNTG1_HUMAN		5	TTTAGGCTGTC	0.318
-	12	1485		NM_144651	NP_653252	A1KZ92	PXDNL_HUMAN	like C2-type 3.	2	GCCTTCCACAG	0.517
-	5	785	eo.1_Missense_M	NM_018120	NP_060590	Q9NVT9	ARMC1_HUMAN		1	CACCACACACC	0.333
-	13	1406	E7A_uc003xvp.2_	NM_002604	NP_002595	Q13946	PDE7A_HUMAN		0	CAGCATCAGTG	0.483
+	1	729	e.3_5'Flank|ADHF	NM_015169	NP_055984	Q15050	RRS1_HUMAN		0	TGCACCCTACC	0.662
+	2	2554	u.1_Missense_Mu	NM_024721	NP_078997	Q86UP3	ZFHX4_HUMAN	2H2-type 3.	15	ACAAGCACCTG	0.507
+	2	2578	u.1_Missense_Mu	NM_024721	NP_078997	Q86UP3	ZFHX4_HUMAN		15	ATCTCCAAAATG	0.517
+	6	1187	eh.2_Missense_M	NM_004337	NP_004328	Q9Y236	OSGI2_HUMAN		0	CTTTTGTGTTTC	0.463
-	2	162	D54B_uc003ygn.	NM_012415	NP_036547	O95073	FSBP_HUMAN		4	CTGGAGGTATAA	0.368
-	7	654	_Mutation_p.R214	NM_015496	NP_056311	Q69YN4	VIR_HUMAN	Glu-rich.	2	CTTCTCTATGAG	0.343
-	3	334	.1_RNA|UQCRB_	NM_006294	NP_006285	P14927	QCR7_HUMAN		1	CTTTAGGCAAG	0.408
+	7	1446	DH_uc010mbf.2_In	NM_178812	NP_848927	Q86UE4	LYRIC_HUMAN	lasmic (Potential).	2	ATCAACCCTATAT	0.348
+	10	1845	DH_uc010mbf.2_F	NM_178812	NP_848927	Q86UE4	LYRIC_HUMAN	lasmic (Potential).	2	AAAATAGCCAGG	0.239
+	7	1061	p.P321S|POP1_u	NM_001145860	NP_001139332	Q99575	POP1_HUMAN		2	GTGACCCTTCT	0.488
+	13	1979	p.G627S|POP1_u	NM_001145860	NP_001139332	Q99575	POP1_HUMAN		2	GCTGGGGCATG	0.408
-	2	1878	.E355K|FBXO43_	NM_001029860	NP_001025031	Q4G163	FBX43_HUMAN		2	TTGTTCCCGAA	0.493
+	9	979	03yla.2_Splice_S	NM_001695	NP_001686	P21283	VATC1_HUMAN		0	AACAAGTAAGAT	0.343
+	5	1416	03ylr.2_Missense_	NM_014677	NP_055492	Q9UQ26	RIMS2_HUMAN	PDZ.	15	ATCAGGTCGGC	0.338
+	47	7224		NM_177531	NP_803875	Q86WI1	PKHL1_HUMAN	ellular (Potential).	14	CACTCCCTGAT	0.358
-	13	1246	s.1_Missense_Mut	NM_001040092	NP_001035181	Q13822	ENPP2_HUMAN		7	TTCCAGGCACT	0.338
-	25	3529		NM_003184	NP_003175	Q6P1X5	TAF2_HUMAN		6	CTGGGGTATTA	0.438
+	2	215	ank|MTBP_uc003y	NM_022045	NP_071328	Q96DY7	MTBP_HUMAN		3	TGCTTCAATTAA	0.338
+	13	1465		NM_022045	NP_071328	Q96DY7	MTBP_HUMAN		3	ATGTTCAAGTT	0.323
+	16	2369	R67_uc003yps.1_	NM_145647	NP_663622	Q96DN5	WDR67_HUMAN	Potential.	1	TAGCTGCTGTGA	0.368
-	25	3650	_Mutation_p.R97	NM_014109	NP_054828	Q6PL18	ATAD2_HUMAN		2	ATCTTCCTTCGC	0.358
+	24	2471	1lil.1_Missense_M	NM_144963	NP_659400	Q658Y4	F91A1_HUMAN		2	ACATGGGTGTT	0.393
-	14	2648	nse_Mutation_p.A	NM_014751	NP_055566	O43312	MTSS1_HUMAN	Pro-rich.	1	CAGTGGCACTT	0.582
+	3	640	i.2_Missense_Mu	NM_002467	NP_002458	P01106	MYC_HUMAN		6	AGCCCCCGGCG	0.637
+	37	6445	.1_Missense_Mut	NM_003235	NP_003226	P01266	THYG_HUMAN	Type IIIA.	15	ATGTTCCCAAC	0.423

-	64	5065	ljo.1_Missense_M	NM_152888	NP_690848	Q8NFW1	COMA1_HUMAN	y-rich.|Collagen-like 15.	13	TCGCTCACCTG	0.612	
-	5	680	yvt.2_Splice_Site_	NM_153831	NP_722560	Q05397	FAK1_HUMAN		6	CTAATACCTGTT	0.274	
+	3	561	se_Mutation_p.P7	NM_032611	NP_116000	O75365	TP4A3_HUMAN		0	GCCCCCGCCCG	0.692	
-	15	1788	zo.1_Missense_M	NM_015356	NP_056171	Q14160	SCRIB_HUMAN	ens junction and to inhibit	5	GCAGGGTCCAG	0.642	
-	11	3578	003zdr.1_5'Flank|	NM_025251	NP_079527	Q9C0H5	RHG39_HUMAN	Rho-GAP.	0	CCATGCGGTTG	0.517	
-	16	2177	_p.S622F|RFX3_u	NM_134428	NP_602304	P48380	RFX3_HUMAN		4	GGAAGGAGCCA	0.438	
-	2	1008	zob.1_Missense_	NM_020344	NP_065077	Q9UI40	NCKX2_HUMAN	lasmic (Potential).	3	CTTGTCCCTGG	0.458	
-	1	2372	v.2_Intron|KLHL9_	NM_018847	NP_061335	Q9P2J3	KLHL9_HUMAN		4	ACCCAGGGTTTT	0.438	
+	4	363	TAP_uc011lnk.1_	NM_002451	NP_002442	Q13126	MTAP_HUMAN		1	AGGAAGAGGGC	0.483	
-	1	477	_5'UTR|CHMP5_u	NM_004323	NP_004314	Q99933	BAG1_HUMAN	lem repeat of E-E-X(4).|6.	1	GCTCCGGGTCG	0.662	
+	2	719	|NFX1_uc003zsp.	NM_002504	NP_002495	Q12986	NFX1_HUMAN		1	TCTTCAGAGGCA	0.512	
-	8	1134	ense_Mutation_p.	NM_022917	NP_075068	Q9H6R4	NOL6_HUMAN		2	CCCACCCTGGC	0.577	
-	30	4339		NM_006289	NP_006280	Q9Y490	TLN1_HUMAN	action with SYNM.	13	GTTAGGGGCAG	0.577	
-	5	1366	_p.P405L|ZNF658	NM_033160	NP_149350	Q5TYW1	ZN658_HUMAN	type 3; degenerate.	1	AGTGGGGCCTC	0.403	
+	15	1812	.1_Intron|PIP5K1B	NM_003558	NP_003549	O14986	PI51B_HUMAN		1	GCAAAGGGTTA	0.478	rs138893749
+	1	144	_Site|C9orf135_uc	NM_001010940	NP_001010940	Q5VTT2	CI135_HUMAN	cellular (Potential).	1	ACTTGGTGGAG	0.592	
-	2	829	4ail.2_Missense_	NM_001025780	NP_001020951	Q5VST6	F108B_HUMAN		0	TGTTGCCTTTAC	0.413	
+	12	1994	e_Mutation_p.R48	NM_006200	NP_006191	Q92824	PCSK5_HUMAN	Homo B/P.	3	CAGTGCGCTCC	0.542	
+	3	342	e_Mutation_p.H88	NM_024077	NP_076982	Q96T21	SEBP2_HUMAN		3	ACTCTTCATCCA	0.398	
-	10	1000	ltv.1_Missense_M	NM_006415	NP_006406	O15269	SPTC1_HUMAN	lasmic (Potential).	2	AAGACCTGCCA	0.378	
-	5	788	04asb.2_Missens	NM_014057	NP_054776	P20774	MIME_HUMAN	LRR 4.	0	AGGAAGAACTG	0.303	
+	10	1857	_p.G410D|FGD3_	NM_001083536	NP_001077005	Q5JSP0	FGD3_HUMAN	PH 1.	2	TCATGGGCCAGA	0.607	
-	3	441	th.3_Missense_M	NM_004148	NP_004139	Q92982	NINJ1_HUMAN	ical; (Potential).	1	CAGGCCCGTGG	0.587	
+	31	3706	1529_uc004axh.1	NM_020893	NP_065944				7	AGAGCATTGTA	0.428	
-	12	1757		NM_005502	NP_005493	O95477	ABCA1_HUMAN	Extracellular.	17	GGTGTACACAG	0.488	
-	4	311	q.1_Missense_Mu	NM_003329	NP_003320	P10599	THIO_HUMAN	Thioredoxin.	0	TTTTGTCCCTTC	0.393	
+	17	2810	10_uc004bla.1_M	NM_007018	NP_008949	Q7Z7A1	CNTRL_HUMAN	Potential.	0	GTATGGAGGAA	0.393	
+	8	1811	ow.2_Nonsense_	NM_182487	NP_872293	Q68BL7	OLM2A_HUMAN	actomedin-like.	0	ACGTGGAAGAC	0.657	
-	6	1019	AP1_uc004bpy.2_	NM_001006617	NP_001006618	Q9BPZ7	SIN1_HUMAN		4	AGTAGGCACTG	0.488	
+	3	277	mxf.2_Missense_	NM_014007	NP_054726	O43298	ZBT43_HUMAN		1	AAATGGAGCCT	0.398	
-	3	275		NM_015679	NP_056494	O95900	TRUB2_HUMAN		1	CTTGAGATGGG	0.512	
+	4	710		NM_014506	NP_055321	O14657	TOR1B_HUMAN		0	TGCAGGCGGGG	0.373	
+	3	361	n_p.V84I|NUP214	NM_005085	NP_005076	P35658	NU214_HUMAN		16	ATAAAGTCCAA	0.398	
+	2	341	am.1_Missense_	NM_013318	NP_037450	Q5JSZ5	PRC2B_HUMAN		0	AAGACCCAAAG	0.567	
+	13	2006	_p.P234S|BAT2L1	NM_013318	NP_037450	Q5JSZ5	PRC2B_HUMAN		0	TGTACCCCCCG	0.627	
+	2	1212	C4_uc010mzw.2_	NM_012204	NP_036336	Q9UKN8	TF3C4_HUMAN		2	TTTTGGTGGGA	0.433	
-	8	1180	e_Mutation_p.A32	NM_016172	NP_057256	Q9BSL1	UBAC1_HUMAN	UBA 2.	2	TCACCGCGGCA	0.313	
-	9	1285	85_uc004cnm.1_	NM_138778	NP_620133	Q9BTV6	WDR85_HUMAN		0	GACAGGGTGTT	0.582	
+	29	4466	p.D971N|CACNA	NM_000718	NP_000709	Q00975	CAC1B_HUMAN	lasmic (Potential).	6	TGCATTGACTTC	0.567	
+	12	1346	.L342F|CSF2RA_	NM_001161529	NP_001155001	P15509	CSF2R_HUMAN	ical; (Potential).	2	TCGTCCTCGGC	0.542	
+	7	1100		NM_001011719	NP_001011719	Q5FYA8	ARSH_HUMAN		1	GCCGTCAGTCT	0.517	
-	9	1325		NM_000292	NP_000283	P46019	KPB2_HUMAN		2	ACCATCTCGAAG	0.388	
+	3	353	njn.1_Missense_	NM_014927	NP_055742	Q8WXI2	CNKR2_HUMAN	CRIC.	2	AGGAAGGAGAA	0.408	
+	1	499		NM_152631	NP_689844	Q8NA70	FA47B_HUMAN		4	TGGAGGACGCT	0.582	
+	4	441	hl.2_Missense_M	NM_001129898	NP_001123370	Q5JUW0	ZN673_HUMAN	KRAB.	0	CCGTGGGTGAG	0.557	
-	47	5707	nip.2_Missense_M	NM_005183	NP_005174	O60840	CAC1F_HUMAN	lasmic (Potential).	6	GGGTTCCAGGC	0.637	
-	16	2239	nip.2_Missense_	NM_005183	NP_005174	O60840	CAC1F_HUMAN	llular (Potential).|II.	6	AGGGGCCACCA	0.522	

-	2	262	0nip.2_Missense_	NM_005183	NP_005174	O60840	CAC1F_HUMAN	lasmic (Potential).		6	GTGACCGCTGG	0.622	
-	2	187	OM4_uc004dpd.3	NM_020717	NP_065768	Q9ULL8	SHRM4_HUMAN	PDZ.		1	TCACCAGTCCTC	0.473	
-	17	3304		NM_004463	NP_004454	P98174	FGD1_HUMAN	PH 2.		6	GGGGCTCCGTAG	0.532	
+	15	1779	L3L_uc004dti.2_R	NM_019067	NP_061940	Q9NVN8	GNL3L_HUMAN			1	TGAAAAATAAGA	0.527	
-	2	2882		NM_152424	NP_689637	Q5JTC6	F123B_HUMAN		p.0?(40)	112	ATCGAGGGAGG	0.577	
+	5	2266		NM_001010888	NP_001010888	Q5HYM0	ZC12B_HUMAN			3	GGAGCGTGCCT	0.507	
-	21	2227	N1_uc011mpg.1_	NM_002547	NP_002538	O60890	OPHN1_HUMAN	Pro-rich.		2	AGTTTCCCCAC	0.532	
+	5	1640	xe.2_Missense_M	NM_004429	NP_004420	P98172	EFNB1_HUMAN	lasmic (Potential).		0	GGCCAGTCCCA	0.602	
+	35	5033	_p.A1612T|MED12	NM_005120	NP_005111	Q93074	MED12_HUMAN			4	AGCGTGCATAC	0.517	
+	3	284	o.1_Missense_M	NM_006223	NP_006214	Q9Y237	PIN4_HUMAN	PpiC.		0	AAGTTAAAGTC	0.383	
-	9	3951	cr.2_Missense_Mu	NM_000489	NP_000480	P46100	ATRX_HUMAN			30	AAAATCCAGTA	0.338	
-	1	713	.2_Intron|ATP7A_	NM_001029891	NP_001025062	Q8N0Y7	PGAM4_HUMAN			0	ACACCGTCTCT	0.557	
+	3	309	K1_uc011mqq.1_	NM_000291	NP_000282	P00558	PGK1_HUMAN			2	TCCCAAGCATCA	0.463	
-	9	2045	_p.E646K|HDX_uc	NM_144657	NP_653258	Q7Z353	HDX_HUMAN			2	GTTGTTCCTTAT	0.338	
-	1	318	h.2_Intron|TSC22	NM_004089	NP_004080	Q99576	T22D3_HUMAN	ding (By similarity).		0	AGAAGGAGATG	0.607	
-	12	2581	Y2F_uc011msq.1_	NM_001522	NP_001513	P51841	GUC2F_HUMAN	.|Cytoplasmic (Potential).		8	CACAGGAGGAG	0.463	
+	2	293	oz.2_Missense_M	NM_001128173	NP_001121645	O75914	PAK3_HUMAN	rity).|Linker.|GTPase-bindi		10	TCACCGGGGAAT	0.418	
+	23	2563	qq.2_Missense_	NM_144658	NP_653259	Q5JSL3	DOC11_HUMAN	DHR-1.		3	TTCCATCATTGCC	0.403	
-	1	223	uc004esi.1_Intron	NM_139282	NP_644811	Q8NHV9	RHXF1_HUMAN			0	CCTCAGGGTTC	0.617	rs140029775
+	15	1613		NM_003399	NP_003390	O43895	XPP2_HUMAN			0	ATAGGGACGGG	0.582	
+	20	1992		NM_003399	NP_003390	O43895	XPP2_HUMAN			0	CCCAGGGAGCT	0.577	
-	12	2201	uy.1_Missense_M	NM_194277	NP_919253	Q6ZUT3	FRMD7_HUMAN			1	TCTGGCCATGG	0.413	
-	2	2202	fby.2_Missense_M	NM_173078	NP_775101	Q8IW52	SLIK4_HUMAN	ellular (Potential).		2	GAGGACTTCGA	0.428	
+	5	1963	nwr.1_Missense_	NM_032539	NP_115928	Q9H156	SLIK2_HUMAN	ellular (Potential).		7	AGTTTTGGACCC	0.537	
+	5	3271	se_Mutation_p.E7	NM_032539	NP_115928	Q9H156	SLIK2_HUMAN	lasmic (Potential).		7	TTGCTGAGCGA	0.488	
-	22	5990		NM_005334	NP_005325	P51610	HCFC1_HUMAN			2	CATTGGTGCCC	0.542	
+	24	3945	1_RNA|UBE4B_u	NM_001105562	NP_001099032	O95155	UBE4B_HUMAN			4	TTGCTCAGGAT	0.587	
+	5	842	qb.2_Missense_M	NM_032264	NP_115640	Q9H094	NBPF3_HUMAN	Potential.		2	ACCCAGTTAAG	0.502	
-	51	6522	d.2_Missense_Mu	NM_005529	NP_005520	P98160	PGBM_HUMAN	like C2-type 7.		9	CGTGTGAGGAG	0.687	
+	5	1161	utation_p.S339F|	NM_017449	NP_059145	P29323	EPHB2_HUMAN	tential).|Fibronectin type-III		5	GACCTCCCTCA	0.657	
-	16	2416	xm.1_Missense_M	NM_052896	NP_443128	Q7Z408	CSMD2_HUMAN	tracellular (Potential).		12	AGCACCTGTCG	0.587	
-	5	6389	e_Mutation_p.E17	NM_024503	NP_078779	Q5T1R4	ZEP3_HUMAN			6	CGGCTCCCCTC	0.552	
+	8	883		NM_178134	NP_835235	Q86W10	CP4Z1_HUMAN	enal (Potential).		1	AGAGCGAAAAC	0.368	
+	3	655	orf175_uc010oof.1	NM_001039464	NP_001034553	Q68CQ1	HEAT8_HUMAN			0	CCAAGGATGTC	0.433	
-	10	731	_p.G154E|SLC44A	NM_152697	NP_689910	Q8NCS7	CTL5_HUMAN	ellular (Potential).		4	TTACTTCCTATTG	0.328	
+	13	2372		NM_006536	NP_006527	Q9UQC9	CLCA2_HUMAN	ellular (Potential).		3	GGAGCGAAAGT	0.448	
+	6	706	se_Mutation_p.T1	NM_001114106	NP_001107578	Q8N4M1	CTL3_HUMAN			1	TGACACCCTCC	0.388	
-	32	4743		NM_206996	NP_996879	Q6Q759	SPG17_HUMAN			6	GAAAAGGATAGT	0.438	
+	4	1005	hw.2_Missense_	NM_000862	NP_000853	P14060	3BHS1_HUMAN			2	GCTTTCCTTTAT	0.473	
+	12	1400	_RNA|NBPF9_uc	NM_001037675	NP_001032764	Q3BBV1	NBPFK_HUMAN	NBPF 2.		0	GATGACAATGAA	0.423	
+	76	9493	PF10_uc010oyl.1	NM_001039703	NP_001034792	A6NDV3	A6NDV3_HUMAN			0	ACTCACTGGATA	0.478	
-	2	3373	e.1_Missense_Mu	NM_007113	NP_009044	Q07283	TRHY_HUMAN	0 AA tandem repeats.		5	gttcctctctcagcagct	0.224	
-	3	883		NM_016190	NP_057274	Q9UBG3	CRNN_HUMAN	Gln-rich.		3	CGTGGGTCTCA	0.612	rs3814301
+	13	1163		NM_020452	NP_065185	P98198	AT8B2_HUMAN	lasmic (Potential).		2	ACAGCTACTTCA	0.597	
-	2	858	2_Missense_Muta	NM_001111	NP_001102	P55265	DSRAD_HUMAN			6	TGGGGCTCCTT	0.527	
-	2	843	2_Missense_Muta	NM_001111	NP_001102	P55265	DSRAD_HUMAN			6	TATGACCGTCTG	0.522	
-	9	1479	T2_uc009wpb.2_	NM_144622	NP_653223	Q5T1A1	DCST2_HUMAN	ellular (Potential).		3	GGTCACGATAAA	0.522	

-	1	260		NM_001004476	NP_001004476	Q6IF99	O10K2_HUMAN	ellular (Potential).	1	TCTGGGACAGC	0.488	
+	3	336	D1_uc010pli.1_In	NM_052862	NP_443094	Q6JBY9	CPZIP_HUMAN		5	CTGTTCCCTCC	0.567	
+	37	5233	1gox.1_Missense_	NM_000721	NP_000712	Q15878	CAC1E_HUMAN	llular (Potential).|IV.	6	AGAACGAGAAC	0.557	
-	7	587	.A176V|KCNT2_u	NM_198503	NP_940905	Q6UVM3	KCNT2_HUMAN	=Segment S4; (Potential).	7	CCAAGGCATGTT	0.284	
+	4	633	gtr.1_Missense_M	NM_005666	NP_005657	P36980	FHR2_HUMAN	Sushi 3.	3	TTGAGGGTAAC	0.383	
+	10	1704		NM_030787	NP_110414	Q9BXR6	FHR5_HUMAN	Sushi 9.	2	GAAACGATGGA	0.328	
+	6	1495	1_uc010ppb.1_M	NM_201253	NP_957705	P82279	CRUM1_HUMAN	(Potential).|EGF-like 11.	9	ATAATGGAACAT	0.468	
+	2	825	zt.2_Missense_Mu	NM_002725	NP_002716	P51888	PRELP_HUMAN	LRR 6.	3	TGAGCGACGGC	0.597	
+	6	1165	.3_Missense_Mut	NM_152609	NP_689822	Q6PJW8	CNST_HUMAN		0	TTGAACGGCTT	0.323	
-	2	304		NM_000242	NP_000233	P11226	MBL2_HUMAN	ollagen-like.	1	GATTTCCTGGA	0.542	
-	8	1175	_p.G351E|CTNNA	NM_001127384	NP_001120856	Q9UI47	CTNA3_HUMAN	Potential.	8	TTTTTCCAGCCT	0.358	
-	6	746	_p.R208Q|CTNNA	NM_001127384	NP_001120856	Q9UI47	CTNA3_HUMAN		8	AAGCTCGGGCT	0.418	
-	4	512	9xqi.1_RNA|C10o	NM_152710	NP_689923	Q96M53	SPATL_HUMAN		1	ATCACCAGTTCT	0.592	
+	4	512	89_splice|PCGF5_	NM_032373	NP_115749	Q86SE9	PCGF5_HUMAN		1	AGAACGTAAGT	0.338	
+	5	583	gd.1_Missense_M	NM_144587	NP_653188	Q32M84	BTBDG_HUMAN		1	GAAAGCCCTGG	0.607	
-	13	1831	9ycc.2_Missense_	NM_021924	NP_068743	Q9HBB8	CDHR5_HUMAN	em repeats.|2.|Extracellul	0	TCCTGGCTCTG	0.667	rs139058512
-	2	1485		NM_176821	NP_789791	Q86W26	NAL10_HUMAN		9	GGACTCCTTCC	0.498	
-	2	1171	p.R84S|STK33_uc	NM_030906	NP_112168	Q9BYT3	STK33_HUMAN		7	TGCTTTTCTCTC	0.353	
-	2	348	1_5'Flank|C11orf7	NM_000536	NP_000527	P55895	RAG2_HUMAN		5	TGACATGGTTAT	0.453	
-	14	1926		NM_002334	NP_002325	O75096	LRP4_HUMAN	ntial).|LDL-receptor class	4	GGTATCGGCAA	0.552	
-	1	66	A13_uc001nfd.2_	NM_000256	NP_000247	Q14896	MYPC3_HUMAN		3	TCCCCGGCTCA	0.582	
-	5	6868	AK_uc001ntk.1_I	NM_001620	NP_001611	Q09666	AHNK_HUMAN		19	TTAAGTTCACATC	0.473	rs1634804
-	5	6673	AK_uc001ntk.1_I	NM_001620	NP_001611	Q09666	AHNK_HUMAN		19	CAAGTGTAAGT	0.522	
-	5	6640	AK_uc001ntk.1_I	NM_001620	NP_001611	Q09666	AHNK_HUMAN		19	GGGGGCCTTGA	0.507	rs1298288
-	17	2066	yp.2_Intron|INTS4	NM_033547	NP_291025	Q96HW7	INT4_HUMAN		2	CTACATTCCACA	0.453	
-	2	976	_p.P184L|TRPC6_	NM_004621	NP_004612	Q9Y210	TRPC6_HUMAN	nic (Potential).|ANK 3.	4	AAGCCGGATGA	0.453	
+	13	2373	iw.2_Missense_Mu	NM_000829	NP_000820	P48058	GRIA4_HUMAN	ical; (Potential).	8	ACCTCGCTGCT	0.403	
-	1	942		NM_001005187	NP_001005187	Q8NGN1	OR6T1_HUMAN	lasmic (Potential).	1	AGTTTCATCAC	0.428	
+	8	1632		NM_025004	NP_079280	Q0P6D6	CCD15_HUMAN		2	TTCTCCACAAAG	0.418	rs113451248
-	6	1375	n.1_RNA|NCAPD	NM_015261	NP_056076	P42695	CNDD3_HUMAN		5	ATTCATGAAGAA	0.353	
+	18	3380	1_uc001qjd.2_R	NM_178040	NP_829884	Q8IUD2	RB6I2_HUMAN	FIP-RBD.	5	TCACTCCACCA	0.502	
+	7	1284	c001qkn.2_Misse	NM_199460	NP_955630	Q13936	CAC1C_HUMAN	cellular (Potential).	11	CGGGCGGCAGT	0.602	
+	2	997	DC5_uc009zjj.2_	NM_020782	NP_065833	Q9P2K6	KLDC5_HUMAN	Kelch 3.	2	CATCGGAGGGC	0.478	
-	1	705	h.2_Missense_Mu	NM_000424	NP_000415	P13647	K2C5_HUMAN	oil 1A.|Rod.	0	TGAAGGAGGCA	0.478	
-	1	351		NM_175068	NP_778238	Q86Y46	K2C73_HUMAN	Head.	6	GACCTGATGGA	0.627	
+	10	2283	p.R704C|NAV3_u	NM_014903	NP_055718	Q8IVL0	NAV3_HUMAN	Potential.	17	GTCTTCGTGGG	0.328	
+	9	1362	u.2_Missense_Mu	NM_001135805	NP_001129277	P21579	SYT1_HUMAN	hospholipid binding (Prob	6	GTATATGATTTTG	0.388	
+	1	604	S1B_uc001tgf.1_	NM_153364	NP_699195	Q8NEG0	FA71C_HUMAN		0	GATTGACGTGC	0.527	
+	38	4189		NM_017564	NP_060034	Q8WWQ8	STAB2_HUMAN	ellular (Potential).	14	CGAGAGAATGC	0.527	
+	11	1105	u.1_Nonsense_M	NM_007062	NP_008993	Q13610	PWP1_HUMAN		0	TGTGGCGATTC	0.423	
+	10	1036	A_uc009zwe.1_Mi	NM_001143854	NP_001137326	Q9Y2J0	RP3A_HUMAN	Pro-rich.	7	TCCCGGGCGAG	0.562	
-	8	1115	e_Mutation_p.W2	NM_015347	NP_056162	O15034	RIMB2_HUMAN	nectin type-III 1.	11	GGCTCCCAGCC	0.562	
-	4	621		NM_005932	NP_005923	Q99797	MIPEP_HUMAN		1	CAAGGGAATCC	0.279	
+	2	1012		NM_153456	NP_703157	Q8IZP7	H6ST3_HUMAN	enal (Potential).	2	TGAACGAGAGT	0.493	
+	1	803		NM_001005500	NP_001005500	Q8NGD0	OR4M1_HUMAN	ellular (Potential).	0	CATTTTCCCTAG	0.418	
+	1	449		NM_001004723	NP_001004723	Q8NGD1	OR4N2_HUMAN	Name=4; (Potential).	4	GTGGCTTGGGG	0.532	
-	2	734	wih.2_Missense_	NM_021944	NP_068763	Q9H972	CN093_HUMAN		1	CTCTTCCACGG	0.632	

+	4	387	IUBPL_uc010tpl.1_	NM_025152	NP_079428	Q8TB37	NUBPL_HUMAN		0	ATGGACCTTCAG	0.274	
+	3	896	op.2_Missense_Mu	NM_199421	NP_955453	Q8WXH5	SOCS4_HUMAN		2	AGTAGTCGGCAC	0.428	
-	4	1102	kmk.2_Missense_M	NM_033141	NP_149132	P80192	M3K9_HUMAN	rotein kinase.	5	AGGAAGGGCGA	0.512	
-	7	1513	_p.S437F|FOXN3_	NM_001085471	NP_001078940	O00409	FOXN3_HUMAN		3	GGAGGGACCCT	0.522	
+	1	124		NM_001080841	NP_001074310				0	TTTGACCGCTAC	0.498	rs267613
-	33	6106	-4310|MI0015840_	NM_016642	NP_057726	Q9NRC6	SPTN5_HUMAN	Spectrin 16.	2	GCGGGCTGCCC	0.682	
+	10	1585	p.R429Q|CKMT1A	NM_001015001	NP_001015001	P12532	KCRU_HUMAN	jen kinase C-terminal.	0	TGAACGGCGTC	0.493	
+	4	597	zxr.2_Missense_M	NM_020234	NP_064619	Q8N5C7	DTWD1_HUMAN		0	AAAGTACTGCTA	0.214	
+	5	1270	_p.W293*|SLC27A	NM_003645	NP_003636	O14975	S27A2_HUMAN	lasmic (Potential).	2	TGTGTGGAGACA	0.433	
-	11	1721	zza.3_Missense_M	NM_031226	NP_112503	P11511	CP19A_HUMAN		3	AAAGATCATTTC	0.448	
-	61	12014		NM_003922	NP_003913	Q15751	HERC1_HUMAN		19	CAGGTTCTAGAT	0.428	
+	18	2547		NM_152336	NP_689549	Q96MI9	CBPC4_HUMAN		0	CTTTCTCCCAGT	0.473	
-	9	2439	uyn.1_Missense_M	NM_001134407	NP_001127879	Q12879	NMDE1_HUMAN	lasmic (Potential).	45	CAGATACCATGAT	0.478	
+	2	299		NM_003498	NP_003489	O75324	SNN_HUMAN	Cytoplasmic.	0	CTGCAGCGCATC	0.647	
+	6	873	p.2_Missense_Mu	NM_024847	NP_079123	Q7Z402	TMC7_HUMAN	cellular (Potential).	3	TTTACGGACATTA	0.493	
-	5	1060		NM_020718	NP_065769	Q70CQ4	UBP31_HUMAN		10	CCATAGACACTG	0.443	
-	27	4125	CC12_uc002efa.1_	NM_033226	NP_150229	Q96J65	MRP9_HUMAN	C transporter 2.	3	CGTTCCCCTACT	0.413	
+	11	1346	IA|GPR114_uc002	NM_153837	NP_722579	Q8IZF4	GP114_HUMAN	Name=5; (Potential).	1	ACGGCGGCCTC	0.697	
+	4	2048	nn.1_Missense_Mu	NM_015251	NP_056066	O43313	ATMIN_HUMAN		0	ACTTCTTACTCG	0.458	
-	1	205	2fgj.2_Missense_M	NM_052892	NP_443124	Q7Z442	PK1L2_HUMAN	(Potential).|C-type lectin.	3	TGCCTTCGTCCT	0.562	
+	3	574	chl.2_Missense_Mu	NM_024731	NP_079007	Q8N4N3	KLH36_HUMAN		2	GTGAGCGAGGAC	0.577	
-	5	591	se_Mutation_p.G17	NM_000512	NP_000503	P34059	GALNS_HUMAN		2	AGGTCCAAAGTG	0.587	
-	5	669	.1_RNA|TRPV3_u	NM_145068	NP_659505	Q8NET8	TRPV3_HUMAN	lasmic (Potential).	4	CGCCTCTTTTTC	0.552	
-	12	1524	p.P211S|C17orf85	NM_001114118	NP_001107590	Q53F19	CQ085_HUMAN		1	TTTCCGGAGAAT	0.502	
-	4	626		NM_003342	NP_003333	P62253	UB2G1_HUMAN		0	AAATGCACACATC	0.368	
-	9	1206	p.E359K|ALOX15_	NM_001140	NP_001131	P16050	LOX15_HUMAN	ipoxygenase.	5	TAATTTCCAGGG	0.522	
+	33	5258	p.Q1010*|USP6_u	NM_004505	NP_004496	P35125	UBP6_HUMAN		5	CATCCCAGGAA	0.413	
-	14	1420	_Mutation_p.A431	NM_001100112	NP_001093582	Q9UKX2	MYH2_HUMAN	osin head-like.	14	GCTTTGGCCAGA	0.483	
+	9	2181	e_Mutation_p.R17	NM_014695	NP_055510	A2RUR9	C144A_HUMAN	Potential.	0	ATTTGAGGTATG	0.323	
+	8	1229	2hgo.2_Missense_	NM_032932	NP_116321	Q86YS3	RFIP4_HUMAN	11A, subcellular location, h	1	AGCATTGACTCT	0.602	
-	3	1568	_p.W413*|SLFN13	NM_144682	NP_653283	Q68D06	SLN13_HUMAN		2	CCTTCCAGAGG	0.423	
+	1	1130	p.E182K|CDK12_	NM_016507	NP_057591	Q9NYV4	CDK12_HUMAN		19	ACAAGGAGAAG	0.493	
-	1	183		NM_033059	NP_149048	Q9BYQ6	KR411_HUMAN	GIKRQVHEL]- [SPTR]-[ST	0	GCAGCAGCTGGA	0.672	
-	1	422		NM_031854	NP_114060	Q9BQ66	KR412_HUMAN	f C-C-[GRQVIL]-[SPTR]- [V	0	ggggtctgcagcagctg	0.219	
+	18	2053	2jyd.1_Missense_M	NM_173626	NP_775897	Q86WA9	S2611_HUMAN	cellular (Potential).	0	AAGACTCCATTCT	0.502	
+	2	187	_p.W66*|CLUL1_	NM_014410	NP_055225	Q15846	CLUL1_HUMAN		2	GCTGTGGTTGAA	0.443	
+	2	1128	XNDC2_uc002koh.	NM_001098529	NP_001091999	Q86VQ3	TXND2_HUMAN	repeat of Q-P-K-X-G-D-I-P	2	CCAAGACCTCAC	0.562	
-	2	1637		NM_016626	NP_057710	Q5U5Q3	MEX3C_HUMAN		4	AATGTAGGAGAC	0.498	
+	13	2640	p.G533R|DCC_uc	NM_005215	NP_005206	P43146	DCC_HUMAN	tential).|Fibronectin type-III	17	TCACAGGTCAG	0.403	
+	4	530	2liy.2_Missense_M	NM_002639	NP_002630	P36952	SPB5_HUMAN		1	ACGAAAGGTCAG	0.388	
-	2	359		NM_001080523	NP_001073992	A6NEK1	ARRD5_HUMAN		0	GTAGAAGGAAGC	0.448	
-	18	2353		NM_000064	NP_000055	P01024	CO3_HUMAN	p.R764Q(1)	5	TCACTTCGGGAA	0.478	rs143642234
-	5	33071		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).	57	TCACCAAGAGAA	0.498	
-	5	33064		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).	57	GAGAAAAAGTCA	0.483	
-	3	13802		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).	57	ATGGAAGGATGA	0.453	
-	10	2291	wr.1_Missense_M	NM_152476	NP_689689	Q96MR9	ZN560_HUMAN		6	GAATTTCGAAAG	0.378	rs148650284
+	4	1515	ym.1_Missense_M	NM_001136501	NP_001129973	Q08AG5	ZN844_HUMAN		0	CCTTCAGATCTG	0.423	

+	3	295	_p.P58S|CD97_u	NM_078481	NP_510966	P48960	CD97_HUMAN	r (Potential).|EGF-like 1.		4	CCACCCCGACG	0.592	
+	3	267	_p.P69L|CYP4F1	NM_023944	NP_076433					7	CACTCCTACAG	0.358	
+	1	169		NM_013939	NP_039227	O60403	O10H2_HUMAN	lasmic (Potential).		3	CGTCTGGAGCG	0.607	
-	6	3184	208_uc002nqo.1_	NM_007153	NP_009084					7	TGTAGGGTTTC	0.368	
-	3	325		NM_001098626	NP_001092096	A6NK75	ZNF98_HUMAN	KRAB.		2	TCTTTTCCTTGC	0.423	
-	4	1961	p.G538R|ZNF681_	NM_138286	NP_612143	Q96N22	ZN681_HUMAN	2H2-type 16.		0	TATGTCCAGTAA	0.338	
+	5	738	14A_uc010xru.1_	NM_001114093	NP_001107565	Q8ND56	LS14A_HUMAN			1	AGGTCGCTCAA	0.423	
+	4	702	p.G114R|KIRREL	NM_199180	NP_954649	Q6UWL6	KIRR2_HUMAN	2.|Extracellular (Potential).		3	GAGATGGGGTC	0.582	
-	7	1908	_Mutation_p.Q40	NM_181882	NP_870998	Q9BXM0	PRAX_HUMAN	L]-[LIVMAP]- [AQKHRPE];		2	CAGCTGTACCT	0.587	
+	7	1010	nse_Mutation_p.G	NM_021913	NP_068713	P30530	UFO_HUMAN	tential).|Fibronectin type-III		13	AGGCGGGAGAA	0.612	
+	14	1573	ba.1_Missense_Mutation_p.P523L			Q96L34	MARK4_HUMAN			3	GCGCCCGTCAC	0.587	
-	5	2254	ydj.1_Missense_M	NM_001102657	NP_001096127	Q6ZNA1	ZN836_HUMAN	2H2-type 15.		0	TTATGATTTGAAA	0.408	
-	5	2067	dj.1_Missense_M	NM_001102657	NP_001096127	Q6ZNA1	ZN836_HUMAN	2H2-type 13.		0	ACTGTAATTGAA	0.388	
-	5	1439	k.1_Intron|ZNF81	NM_001031665	NP_001026835	Q0VGE8	ZN816_HUMAN	2H2-type 6.		0	TTTCTGACTGA	0.398	
+	4	1386	dw.1_Missense_	NM_138374	NP_612383	Q96IR2	ZN845_HUMAN	2H2-type 8.		0	TCAGATGTCATC	0.413	
+	4	2950	dw.1_Missense_M	NM_138374	NP_612383	Q96IR2	ZN845_HUMAN	2H2-type 27.		0	TACAAGTGTAAT	0.348	
+	7	1834	_p.R405L|ZNF761_	NM_001008401	NP_001008401	Q86XN6	ZN761_HUMAN	2H2-type 9.		1	TAGACGTCATA	0.393	
+	7	1848	p.Q410K|ZNF761_	NM_001008401	NP_001008401	Q86XN6	ZN761_HUMAN			1	GAGAGCAACCT	0.393	rs146851069
-	3	976		NM_001101401	NP_001094871	P0C263	SBK2_HUMAN	rotein kinase.		0	GCGCCCCAGGT	0.731	
+	3	1610	F776_uc002qqa.	NM_173632	NP_775903	Q68DI1	ZN776_HUMAN	ype 10; degenerate.		1	AGTGTGGAGAA	0.448	
+	3	1653	F776_uc002qqa.	NM_173632	NP_775903	Q68DI1	ZN776_HUMAN	ype 10; degenerate.		1	TCATTCGACATC	0.448	
-	17	3650		NM_012293	NP_036425	Q92626	PXDN_HUMAN			8	GGATCTCAGGGT	0.527	
-	3	382	10yjv.1_Missense_	NM_001002006	NP_001002006	Q96P26	5NT1B_HUMAN			3	GCTGGCCCTGC	0.527	
-	6	836	REF1_uc010eyr.	NM_006569	NP_006560	Q99674	CGRE1_HUMAN			1	TCCTTTAGCCT	0.677	rs11889832
+	1	5246	1_5'Flank|ZNF512	NM_032266	NP_115642	Q68DN1	CB016_HUMAN	m repeat of P-S-E-R-S-H-		1	AGAGAGAAGCC	0.562	
-	27	3116		NM_000379	NP_000370	P47989	XDH_HUMAN			8	AAAAGGAACTG	0.388	
+	1	378_379	.2_Intron|SPTBN1	NR_002229						0	TGAGTTTGCCAT	0.48	
-	10	1288	2scg.2_Missense_	NM_015910	NP_056994	O95876	FRITZ_HUMAN			0	CTGTGCGGACA	0.428	rs3738877
-	6	1224	svl.2_Missense_	NM_020151	NP_064536	Q9NQZ5	STAR7_HUMAN	START.		0	GTGGGGACGGA	0.468	
+	12	2402		NM_003048	NP_003039	Q9UBY0	SL9A2_HUMAN	lasmic (Pot	p.E754K(1)	8	GCAGAGAAAAG	0.532	rs147224345
+	4	564	H2P_uc002tkd.2_	NM_182905	NP_878908					0	CATCCGCCAAG	0.522	
+	14	2558	flu.2_Nonsense_	NM_130773	NP_570129	Q8WYK1	CNTP5_HUMAN	ential).|Fibrinogen C-termi		10	ACATTCAGCAC	0.488	
-	3	279	_p.E53K|CACNB4	NM_000726	NP_000717	O00305	CACB4_HUMAN			2	TGCTTCCCGGT	0.483	
-	12	1858	e_Mutation_p.W3	NM_004490	NP_004481	Q14449	GRB14_HUMAN	SH2.		7	TGAAACCATGG	0.388	
-	58	11467		NM_004525	NP_004516	P98164	LRP2_HUMAN	A 31.|Extracellular (Potent		29	GTTTTCCTCAT	0.448	
-	46	13983	N_uc010zfi.1_Intr	NM_133379	NP_596870	Q8WZ42	TITIN_HUMAN			153	TCACATCTGTGT	0.318	rs149720053
-	40	2947	rx.2_Missense_M	NM_000393	NP_000384	P05997	CO5A2_HUMAN			2	GAACACCATTA	0.438	
-	2	237		NM_014617	NP_055432	P11844	CRGA_HUMAN	crystallin 'Greek key' 2.		0	CGAGTCGCTGA	0.517	
+	11	1286	_Mutation_p.I391	NM_001875	NP_001866	P31327	CPSM_HUMAN	midotransferase type-1.		13	GCCAATAGACA	0.423	
-	7	954	fuw.2_Missense_	NM_016260	NP_057344	Q9UKS7	IKZF2_HUMAN			0	CAGGTCTCTCA	0.388	
-	1	1392		NM_005544	NP_005535	P35568	IRS1_HUMAN			12	AATCCGGAGTG	0.627	
-	8	1375	_p.R376*|HJURP_	NM_018410	NP_060880	Q8NCD3	HJURP_HUMAN			1	AAATCGGATTT	0.488	
+	17	2342	M8_uc010fyj.2_In	NM_024080	NP_076985	Q7Z2W7	TRPM8_HUMAN	Name=3; (Potential).		4	CCCCCGAGCTG	0.572	
-	40	8938	znj.1_Missense_	NM_004369	NP_004360	P12111	CO6A3_HUMAN	ical region.|Thr-rich.		18	TGTGGTGGTCA	0.493	
-	6	2167	p.R560Q|ZNF343_	NM_024325	NP_077301	Q6P1L6	ZN343_HUMAN	2H2-type 11.		3	ATTTCCGGCTA	0.512	
-	14	1298	rf194_uc002wik.2_	NM_001009984	NP_001009984	Q5TEA3	CT194_HUMAN			0	TTAAACGGAATC	0.378	rs73577662
-	14	3758	GLEC1_uc002wiz.	NM_023068	NP_075556	Q9BZZ2	SN_HUMAN	ellular (Potential).		10	CCAGGGACGTG	0.692	

+	6	1239	_p.G216D|MAVS_	NM_020746	NP_065797	Q7Z434	MAVS_HUMAN	lasmic (Probable).	0	GTGCTGGCATGG	0.562	
+	26	2525	_p.R809*|PLCB4_	NM_182797	NP_877949	Q15147	PLCB4_HUMAN		15	GGATATCGACAC	0.448	
+	2	120	tj.1_RNA|FRG1B_uc010gdr.1_RNA|FRG1B_uc010ztk.1_Intron						0	GTTGGGCATTCA	0.338	
+	2	127	tj.1_RNA|FRG1B_uc010gdr.1_RNA|FRG1B_uc010ztk.1_Intron						0	ATTCAGATGCAA	0.333	
+	2	133	tj.1_RNA|FRG1B_uc010gdr.1_RNA|FRG1B_uc010ztk.1_Intron						0	ATGCAATTGGAC	0.343	
+	2	142	tj.1_RNA|FRG1B_uc010gdr.1_RNA|FRG1B_uc010ztk.1_Intron						0	GACCAAGAGAAC	0.338	rs147809085
+	3	187	FRG1B_uc010gdr.1_RNA|FRG1B_uc010ztk.1_Missense_Mutation_p.L4S						0	CTTTGTTGGCCT	0.353	
+	3	189	FRG1B_uc010gdr.1_RNA|FRG1B_uc010ztk.1_Missense_Mutation_p.A5T						0	TTGTTGGCCTCA	0.353	
+	3	240	RG1B_uc010gdr.1_RNA|FRG1B_uc010ztk.1_Nonsense_Mutation_p.K22*						0	GAAGCAAAAAGT	0.363	
+	11	1423	ggc.2_Missense_	NM_015568	NP_056383	Q96T49	PP16B_HUMAN		3	GAATTTCCTACC	0.567	
-	4	488		NM_182482	NP_872288				0	TCCTTCGCTATA	0.368	rs28441174
+	3	523	CAM2_uc011acc.1	NM_004540	NP_004531	O15394	NCAM2_HUMAN	1.|Extracellular (Potential).	4	ATATATCGTTGT	0.348	
+	21	3495	1afa.1_Missense_	NM_003274	NP_003265	P48553	TPC10_HUMAN		2	ATTTTTCGACAA	0.299	
-	1	1815		NM_014406	NP_055221	Q96SF2	TCPQM_HUMAN		1	CGATTTCATCTA	0.473	
+	14	1837	_p.Q520P|MED15_	NM_001003891	NP_001003891	Q96RN5	MED15_HUMAN		1	CCTTGCAAAAGT	0.557	
-	2	1461	6610_uc011aim.1_	NM_080740	NP_542778	P59817	Z280A_HUMAN		1	ACCGACGATCTG	0.408	
+	3	1474	R1_uc002zwt.2_I	NM_002073	NP_002064	P19086	GNAZ_HUMAN		2	CTGAACCGCAAC	0.567	
-	11	1188_1189	n_p.K416E|CHEK	NM_007194	NP_009125	O96017	CHK2_HUMAN	rotein kinas73E(2)|p.S372	20	AATCTTGGAGTG	0.416	470496;rs146546850
+	6	461	gyz.2_Missense_M	NM_014509	NP_055324	Q9H4I8	SEHL2_HUMAN		0	CTGTACCTTCCC	0.527	
-	11	1624	bde.3_Missense_	NM_007229	NP_009160	Q9UNF0	PACN2_HUMAN	SH3.	0	CCAAGCGTCCCT	0.617	
+	16	1945	_p.D610Y|ATG7_u	NM_006395	NP_006386	O95352	ATG7_HUMAN		1	AGTGACGATCGG	0.478	
-	3	873	_p.M166I|IQSEC1_	NM_014869	NP_055684	Q6DN90	IQEC1_HUMAN		1	GTGGTCCATGCC	0.667	
-	15	2844	1A_uc010hhn.1_	NM_014139	NP_054858	Q9UI33	SCNBA_HUMAN		9	ACCAGGGGAATG	0.507	
-	2	360	R3_uc003cpg.1_In	NM_001295	NP_001286	P32246	CCR1_HUMAN	cellular (Potential).	3	AGTCATCCTTCA	0.463	
-	83	6621		NM_000094	NP_000085	Q02388	CO7A1_HUMAN	le-helical region.	11	GGCTCCCCCTGC	0.607	
-	12	1414	ASSF1_uc003daf.	NM_015896	NP_056980	O75800	ZMY10_HUMAN	MYND-type.	5	TTTTCCCAGTGC	0.567	
-	5	619	KT_uc011beq.1_M	NM_001135055	NP_001128527	P29401	TKT_HUMAN		2	ATGCTGGCGAAG	0.577	
-	14	2663	RC2_uc003dht.1_	NM_015576	NP_056391	O15083	ERC2_HUMAN	Potential.	2	GTTCCTCTATCTG	0.488	
-	2	168	.3_Intron|THOC7_	NM_025075	NP_079351	Q6I9Y2	THOC7_HUMAN		3	GGAGACGCTTCC	0.433	
+	19	3398	OBO2_uc011bgk.1	NM_002942	NP_002933	Q9HCK4	ROBO2_HUMAN	lasmic (Potential).	11	GGTGATCCCAGC	0.458	
+	2	698		NM_017819	NP_060289	Q7L0Y3	MRRP1_HUMAN		1	CTTTGGGATAGG	0.408	
+	4	2218	dyg.2_Missense_	NM_001134438	NP_001127910	Q86SQ0	PHLB2_HUMAN	Potential.	6	CTCGAGGAACTT	0.408	
+	3	1940		NM_016298	NP_057382	Q9UH90	FBX40_HUMAN	F-box.	5	GCCTGCCCCTGG	0.522	
-	15	1919	p.G513E|CPNE4_	NM_130808	NP_570720	Q96A23	CPNE4_HUMAN	VWFA.	3	GGCTCTCCCTTG	0.517	
-	6	7502	_p.R528K|IGSF10_	NM_178822	NP_849144	Q6WRI0	IGS10_HUMAN	like C2-type 11.	13	TTTCCTCTGTCAT	0.393	
+	17	2651		NM_006218	NP_006209	P42336	PK3CA_HUMAN	PI3K/PI4K.	3553	GATCTTCGGTAG	0.308	
+	18	2333		NM_003940	NP_003931	Q92995	UBP13_HUMAN	UBA 2.	1	CACTACGAGCAA	0.368	
-	3	564	.2_Missense_Mut	NM_139248	NP_640341	Q8WWY8	LIPH_HUMAN		2	TTACTCCGATCA	0.443	
+	10	1401	c.1_RNA|SDHAP2_uc003fuv.2_RNA						0	CACGAATCTTGA	0.413	
-	3	1350	732_uc010ibb.1_I	NM_001137608	NP_001131080	B4DXR9	ZN732_HUMAN	C2H2-type 12.	0	CACATTTGTAAG	0.418	
+	1	1630		NM_000798	NP_000789	P21918	DRD5_HUMAN	lasmic (Potential).	1	TACATCCACATG	0.577	
-	18	2858	_p.S721F|APBB2_	NM_173075	NP_775098	Q92870	APBB2_HUMAN		3	ATGAGGGATAAG	0.488	
+	8	658		NM_016519	NP_057603	Q9NP70	AMBN_HUMAN	1	4	GGAATGGATTTT	0.194	
-	6	649	0iik.1_Missense_	NM_201431	NP_958834	Q6ZTQ3	RASF6_HUMAN		2	CTGGTTCATCCT	0.428	
-	1	142		NM_033214	NP_149991	Q14410	GLPK2_HUMAN		4	TTAATTCCACTTT	0.468	
+	14	3228	k.3_Missense_Mu	NM_005935	NP_005926	P51825	AFF1_HUMAN		1	CCTTTTCCAGTG	0.378	
-	34	2368	25A1_uc003hzd.2_	NM_198721	NP_942014	Q9BXS0	COPA1_HUMAN	Potential).|Collagen-like 7.	2	TTTCTCCCTTTT	0.438	

+	6	599	IRR_uc010isy.2_Ir	NM_013232	NP_037364	O75340	PDCD6_HUMAN	EF-hand 5.		1	TCAGACGTTACG	0.502	
+	2	437		NM_153610	NP_705838	Q8N3K9	CMYA5_HUMAN			9	ATGTTTCCTTTAT	0.423	
-	8	2244	on.3_Missense_Mu	NM_001163315	NP_001156787	Q9UF56	FXL17_HUMAN			0	ATCGCCCAATGG	0.458	
+	9	1582	MTS19_uc010jdh.1	NM_133638	NP_598377	Q8TE59	ATS19_HUMAN	eptidase M12B.		9	AGGAAGATTTG	0.363	
+	4	777	P103S|FAM53C_u	NM_001135647	NP_001129119	Q9NYF3	FA53C_HUMAN			1	CCAGATCCAGAG	0.657	
+	7	1485	e_Mutation_p.S85	NM_016604	NP_057688	Q7LBC6	KDM3B_HUMAN			11	GCCAGCTCCACC	0.587	
+	1	352	_p.H118Y|PCDHA1	NM_018900	NP_061723	Q9Y5I3	PCDA1_HUMAN	|Extracellular (Potential).		1	GTTTTCCATGTG	0.512	
+	5	1179	dbl.1_Missense_M	NM_152550	NP_689763	Q8TEC5	SH3R2_HUMAN			2	TCCATTCTCCTTC	0.572	
+	8	1873	_p.P572S|PPARG	NM_133263	NP_573570	Q86YN6	PRGC2_HUMAN			0	ACACCACCGTAC	0.522	
+	7	1264		NM_014228	NP_055043	Q99884	SC6A7_HUMAN	Name=6; (Potential).		0	TCTATTCCCTGGG	0.562	
+	12	1417	n_p.R234*|G3BP1_	NM_005754	NP_005745	Q13283	G3BP1_HUMAN			4	AGACTCGAGCT	0.572	
+	24	2689	_p.L851V|CYFIP2_	NM_001037333	NP_001032410	Q96F07	CYFP2_HUMAN			0	GACTTTCTCCCC	0.587	
-	12	1061	l_uc010jkt.2_Silen	NM_173465	NP_775736	Q86Y22	CONA1_HUMAN	ntial).|Collagen-like 1.|Gly-r		2	CTCACCCTGGG	0.607	
+	3	1184		NM_001718	NP_001709	P22004	BMP6_HUMAN			3	GGGATGGTAAGT	0.507	
+	26	2495	ow.2_Missense_M	NM_001040274	NP_001035364	Q5T4T6	SYC2L_HUMAN			2	GAAAATGCAAAG	0.343	
-	1	733		NM_030903	NP_112165	Q9Y3N9	OR2W1_HUMAN	Name=6; (Potential).		3	CAGTAAGATGAG	0.428	rs143534892
-	2	1136		NM_020737	NP_065788	Q9ULH4	LRFN2_HUMAN	cellular (Potential).		3	AAGCCGAAGCC	0.592	
-	2	228	oqg.1_Nonsense_M	NM_018643	NP_061113	Q9NP99	TREM1_HUMAN	(Potential).|Ig-like V-type.		1	TCTGCCAAGCTT	0.478	
-	7	1949	xf.1_Missense_Mu	NM_021073	NP_066551	P22003	BMP5_HUMAN			2	TACGTGGTCAG	0.308	
-	4	911	ohz.2_Missense_M	NM_015687	NP_056502	Q7Z7B0	FLIP1_HUMAN			4	CGTATACGGTGC	0.502	
+	5	824	3psx.3_Missense_	NM_001083535	NP_001077004	Q8IYX8	CE57L_HUMAN	Potential.		0	AACATTCTTTCCA	0.368	
+	64	9352	ense_Mutation_p.F	NM_000426	NP_000417	P24043	LAMA2_HUMAN	minin G-like 5.		10	AGTATTCCGTTCC	0.493	
-	5	906		NM_004666	NP_004657	O95497	VNN1_HUMAN	CN hydrolase.		3	TTCCCTCTTCTGT	0.438	
-	125	23307	ot.3_Missense_Mu	NM_182961	NP_892006	Q8NF91	SYNE1_HUMAN	ytoplasmic (Potential).		45	TCTCCCTATAGCG	0.527	
-	2	487	rf118_uc011egi.1_	NM_144980	NP_659417	Q5T5N4	CF118_HUMAN			0	GACAGCCTCCA	0.617	
+	3	1736	LL2_uc011egr.1_R	NM_031949	NP_114155	Q9BWV7	TTLL2_HUMAN			3	GCTCCAGATCCC	0.502	
-	6	747	1egt.1_Missense_	NM_024919	NP_079195	Q8N878	FRMD1_HUMAN	FERM.	p.R228W(1)	1	GTGCCGGAGGA	0.657	
+	75	12167		NM_003777	NP_003768	Q96DT5	DYH11_HUMAN	6 (By similarity).		15	CTCCTGGAAAAT	0.473	
+	12	1544	ze.1_Missense_Mu	NM_031414	NP_113602	Q9BXU1	STK31_HUMAN			9	TCTGATGAAATAC	0.368	
+	9	1723		NM_021116	NP_066939	Q08828	ADCY1_HUMAN	lasmic (Potential).		6	GGTACATCAGC	0.522	
-	25	4047	v.2_Missense_Mut	NM_022748	NP_073585	Q68CZ2	TENS3_HUMAN	SH2.		4	AAATCTCCAGCT	0.433	
+	4	1510		NM_001159522	NP_001152994	A8MUV8	ZN727_HUMAN	C2H2-type 10.		0	ATAAGAGAATTCA	0.393	
-	2	116		NM_002991	NP_002982	O00175	CCL24_HUMAN			0	CTCTTGGAAACA	0.557	
+	14	2315	ZAN_uc003uwl.2_F	NM_003386	NP_003377	Q9Y493	ZAN_HUMAN	ate) (mucin-like domain).|E		11	AAAAACCCACCA	0.507	
+	3	5881	C17_uc010lho.1_F	NM_001040105	NP_001035194	Q685J3	MUC17_HUMAN	9 X approximate tandem re		27	CTGAAATCAACA	0.498	
+	3	7512	C17_uc010lho.1_F	NM_001040105	NP_001035194	Q685J3	MUC17_HUMAN	9 X approximate tandem re		27	ACACCTATGACC	0.493	rs139444589
-	27	3731	kg.3_Nonsense_M	NM_017954	NP_060424	Q86UW7	CAPS2_HUMAN			2	TTTCTCGAAGAA	0.368	
-	18	2418	M1D_uc010lng.2_	NM_030647	NP_085150	Q6ZMT4	KDM7_HUMAN			1	AGGAGGAAGTC	0.318	
-	15	1860		NM_004333	NP_004324	P15056	BRAF_HUMAN	rotein kinas	_R603>I(2)|p.T	18290	GATTTCACTGTAC	0.368	
+	7	1371	_p.H406Y|ZYX_uc	NM_001010972	NP_001010972	Q15942	ZYX_HUMAN	I zinc-binding 1.		0	CTGTTCCACATC	0.642	
+	8	1391	kr.2_RNA|GALNTL	NM_145292	NP_660335	Q7Z4T8	GLTL5_HUMAN	nenal (Potential).		2	CTGGATGAATATA	0.468	
+	2	371	.2_5'UTR|ADAMD	NM_014479	NP_055294	O15204	ADEC1_HUMAN			2	AAACTTCACATTT	0.343	
-	8	877		NM_144651	NP_653252	A1KZ92	PXDNL_HUMAN	-like C2-type 1.		2	GGTTTCCTTCCC	0.443	
-	6	1140_1141	_p.G267K|PCMTD	NM_052937	NP_443169	Q96MG8	PCMD1_HUMAN			0	GAATCCCCTTGG	0.421	
+	39	7232	iw.2_Missense_Mu	NM_017890	NP_060360	Q7Z7G8	VP13B_HUMAN			20	ATGTGCTACAGG	0.378	
+	9	1781	_p.R235C|DCAF13	NM_015420	NP_056235	Q9NV06	DCA13_HUMAN	WD 7.		1	ACATTCGCCTGT	0.328	
+	69	11265		NM_177531	NP_803875	Q86WI1	PKHL1_HUMAN	cellular (Potential).		14	AGAATTCCTAAG	0.438	

+	35	4881	uc003yqy.1_Intron	NM_001039112	NP_001034201	Q2WGJ9	FR1L6_HUMAN	lasmic (Pot	p.D1559Y(1)	11	ACAAGGATAAG	0.428	
-	10	1733	yum.2_Missense_	NM_173344	NP_775479	Q11201	SIA4A_HUMAN	enal (Potential).		0	TGTTCTCCCAGT	0.572	
-	13	1991	M135B_uc003yva	NM_015912	NP_056996	Q49AJ0	F135B_HUMAN			9	TGTCTGAAGAG	0.468	
+	13	1390		NM_139021	NP_620590	Q8TD08	MK15_HUMAN			2	GAGGGGAGCTG	0.687	
+	9	1423	_p.S466F|CNTLN_	NM_017738	NP_060208	Q9NXG0	CNTLN_HUMAN			1	GAAGTCTGAAA	0.338	
-	1	3013	uc003zrh.1_5'Flan	NM_153809	NP_722516	Q8IZX4	TAF1L_HUMAN			26	TGTGGGATCTG	0.498	
+	3	307		NM_019592	NP_062538	Q5VTR2	BRE1A_HUMAN	Potential.		8	AACTTCGTGAG	0.453	
+	1	70		NM_001004485	NP_001004485	Q8NGS4	O13F1_HUMAN	ellular (Potential).		3	AAAGTTCAGGTC	0.418	
-	1	256		NM_001001956	NP_001001956	Q8NGT0	O13C9_HUMAN	ellular (Potential).		0	TGAAAGGAAGC	0.512	
-	2	167	lwl.1_Missense_	NM_001003936	NP_001003936	Q6A555	TXND8_HUMAN	Thioredoxin.		0	AAACAGGAAACA	0.353	
-	8	2383		NM_014618	NP_055433	O60477	DBC1_HUMAN			8	GGAGGGATCCG	0.562	
+	1	22	|GOLGA2_uc004b	NM_001040011	NP_001035100	Q1ZZU3	SWI5_HUMAN			0	AGAGGGACCTG	0.642	
+	61	5045	uc004cff.2_Intron	NM_000093	NP_000084	P20908	CO5A1_HUMAN	le-helical region.		11	CGAAGGGTGAG	0.592	
+	26	3954	_p.A800V|CACNA	NM_000718	NP_000709	Q00975	CAC1B_HUMAN	smic (Potential).|III.		6	GCAGGCTGTGT	0.562	
-	2	640	0ndi.2_Missense_	NM_181332	NP_851849	Q8N0W4	NLGNX_HUMAN	ellular (Potential).		4	TGACAACTGGAT	0.502	
+	13	1500	_p.D327N|TBL1X_	NM_001139466	NP_001132938	O60907	TBL1X_HUMAN	WD 4.		1	ATGTGGACTGG	0.527	
+	15	2667	mij.1_Missense_M	NM_014728	NP_055543	Q14CM0	FRPD4_HUMAN			13	TAGGCGATGTG	0.522	rs147167664
-	3	1112_1113	wh.1_Missense_M	NM_001018113	NP_001018123	Q8NB91	FANCB_HUMAN			1	GATCTCCAAATG	0.391	
-	3	357	wh.1_Missense_	NM_001018113	NP_001018123	Q8NB91	FANCB_HUMAN			1	AAATTTCCTTTA	0.368	
-	7	1013	9_uc004cwm.2_3	NM_001031739	NP_001026909	Q96DX5	ASB9_HUMAN	SOCS box.		0	AGAAGGGGGCC	0.393	
-	2	230	A9L_uc010nfp.2_	NM_001412	NP_001403	P47813	IF1AX_HUMAN			1	ACCTCCTTTACC	0.308	
-	27	3959	_Mutation_p.E123	NM_004006	NP_003997	P11532	DMD_HUMAN	Spectrin 8.		6	AAGTTCCTTTTT	0.433	
+	4	409	7S|ATP6AP2_uc0	NM_005765	NP_005756	O75787	RENR_HUMAN	ellular (Potential).		0	CAGTTCCTTTT	0.353	
-	19	1796	p.A220V|TEX11_u	NM_001003811	NP_001003811	Q8IYF3	TEX11_HUMAN			5	GGGCAGCTAAA	0.328	
-	1	457	_p.L147F|SERPIN	NM_000354	NP_000345	P05543	THBG_HUMAN			0	ATCATTCAAGAA	0.423	
+	2	939	mk.2_Missense_	NM_194463	NP_919445	Q8TEB7	RN128_HUMAN			2	TTATTCTGCTCG	0.363	
-	24	4657	.M1537I|ODZ1_u	NM_014253	NP_055068	Q9UKZ4	TEN1_HUMAN	ellular (Potential).		23	ATGTTCATGTC	0.483	
-	3	581	_p.Q173*|ODZ1_u	NM_014253	NP_055068	Q9UKZ4	TEN1_HUMAN	inal.|Cytoplasmic (Potential		23	AGCTTGAGCCT	0.413	
+	12	4813	vc.1_Missense_	NM_021946	NP_068765	Q5H9F3	BCORL_HUMAN			7	CAGAGGAAAAA	0.473	
-	6	921	n.1_Missense_Mu	NM_005369	NP_005360	P10911	MCF2_HUMAN			2	TGATGTTTTTCC	0.323	
+	7	1354		NM_005140	NP_005131	Q16280	CNGA2_HUMAN	ellular (Potential).		3	CTCCAACATGA	0.502	
-	4	470	011mye.1_RNA|M	NM_004961	NP_004952	P78334	GBRE_HUMAN	ellular (Probable).		2	CAAGAGACTCA	0.488	
+	4	363	se_Mutation_p.T1	NM_153478	NP_705611	Q6PB30	CSAG1_HUMAN			1	cttCACTGTCCTG	0.303	
-	10	973	4fir.2_Missense_M	NM_004135	NP_004126	P51553	IDH3G_HUMAN			0	GGGCCGGGACA	0.632	
-	51	6522	qd.2_Missense_Mu	NM_005529	NP_005520	P98160	PGBM_HUMAN	like C2-type 7.		9	CGTGTGAGGAG	0.687	
+	5	1161	utation_p.S339F|	NM_017449	NP_059145	P29323	EPHB2_HUMAN	tential).|Fibronectin type-III		5	GACCTCCCTCA	0.657	
-	16	2416	xm.1_Missense_M	NM_052896	NP_443128	Q7Z408	CSMD2_HUMAN	xtracellular (Potential).		12	AGCACCTGTCG	0.587	
-	10	731	_p.G154E|SLC44A	NM_152697	NP_689910	Q8NCS7	CTL5_HUMAN	ellular (Potential).		4	TTACTTCCTATT	0.328	
+	13	2372		NM_006536	NP_006527	Q9UQC9	CLCA2_HUMAN	ellular (Potential).		3	GGAGCGAAAGT	0.448	
-	3	437		NM_002524	NP_002515	P01111	RASN_HUMAN	GTP.	)|p.Q61P(21)|	2607	CTCTTCTTGTCC	0.463	rs121913255
-	32	4743		NM_206996	NP_996879	Q6Q759	SPG17_HUMAN			6	AAAAGGATAGT	0.438	
+	4	1005	hw.2_Missense_	NM_000862	NP_000853	P14060	3BHS1_HUMAN			2	GCTTTCCTTTAT	0.473	
+	74	9249	.1_Intron|NBPF10	NM_001039703	NP_001034792	A6NDV3	A6NDV3_HUMAN			0	GGCCTAAAGTC	0.473	
+	13	1163		NM_020452	NP_065185	P98198	AT8B2_HUMAN	lasmic (Potential).		2	ACAGCTACTTCA	0.597	
-	2	858	2_Missense_Muta	NM_001111	NP_001102	P55265	DSRAD_HUMAN			6	TGGGGCTCCTT	0.527	
-	2	843	2_Missense_Muta	NM_001111	NP_001102	P55265	DSRAD_HUMAN			6	TATGACCGTCTG	0.522	
-	9	1479	T2_uc009wpb.2_	NM_144622	NP_653223	Q5T1A1	DCST2_HUMAN	ellular (Potential).		3	GGTCACGATAAA	0.522	

-	1	260		NM_001004476	NP_001004476	Q6IF99	O10K2_HUMAN	cellular (Potential).	1	TCTGGGACAGC	0.488	
+	3	336	SD1_uc010pli.1_In	NM_052862	NP_443094	Q6JBY9	CPZIP_HUMAN		5	CCTGTTCCCTCC	0.567	
+	37	5233	1gox.1_Missense_	NM_000721	NP_000712	Q15878	CAC1E_HUMAN	llular (Potential).|IV.	6	CAGAACGAGAAC	0.557	
+	5	580	qh.2_Missense_Mu	NM_173156	NP_775179	Q92540	SMG7_HUMAN	TPR 1.	3	CCAGCACTGCC	0.443	
+	26	4229		NM_031935	NP_114141	Q96RW7	HMCN1_HUMAN	ike C2-type 10.	23	ACAATGGGGAG	0.423	
-	7	587	.A176V|KCNT2_u	NM_198503	NP_940905	Q6UVM3	KCNT2_HUMAN	=Segment S4; (Potential).	7	CCAAGGCATGTT	0.284	
+	4	633	gtr.1_Missense_Mu	NM_005666	NP_005657	P36980	FHR2_HUMAN	Sushi 3.	3	CTTGAGGGTAAC	0.383	
+	6	1495	31_uc010ppb.1_M	NM_201253	NP_957705	P82279	CRUM1_HUMAN	(Potential).|EGF-like 11.	9	AATAATGGAACAT	0.468	
-	2	304		NM_000242	NP_000233	P11226	MBL2_HUMAN	Collagen-like.	1	GATTTCCTGGA	0.542	
-	8	1175	_p.G351E|CTNNA	NM_001127384	NP_001120856	Q9UI47	CTNA3_HUMAN	Potential.	8	TTTTTTCCAGCCT	0.358	
-	6	746	_p.R208Q|CTNNA	NM_001127384	NP_001120856	Q9UI47	CTNA3_HUMAN		8	AAGCTCGGGCT	0.418	
-	4	512	9xqi.1_RNA|C10o	NM_152710	NP_689923	Q96M53	SPATL_HUMAN		1	ATCACCAGTTCT	0.592	
+	8	1728		NM_000314	NP_000305	P60484	PTEN_HUMAN	2 tensin-typ)|p.?(1)|p.R23	2334	CCACACGACGG	0.423	rs121909219
-	15	1986	10orf79_uc001kxx	NM_025145	NP_079421	Q8NDM7	WDR96_HUMAN		0	AGATACCGGTAT	0.383	
+	5	583	gd.1_Missense_M	NM_144587	NP_653188	Q32M84	BTBDG_HUMAN		1	GAAAGCCCTGG	0.607	
-	13	1831	9ycc.2_Missense_	NM_021924	NP_068743	Q9HBB8	CDHR5_HUMAN	dem repeats.|2.|Extracellul	0	TCCTGGCTCTG	0.667	rs139058512
+	1	793		NM_178168	NP_835462	Q9H207	O10A5_HUMAN	cellular (Potential).	3	CCTAAATCAAAT	0.418	
-	2	1485		NM_176821	NP_789791	Q86W26	NAL10_HUMAN		9	GGACTCCTTCC	0.498	
-	2	1171	p.R84S|STK33_uc	NM_030906	NP_112168	Q9BYT3	STK33_HUMAN		7	TGCTTTTCTCTC	0.353	
-	2	348	1_5'Flank|C11orf7	NM_000536	NP_000527	P55895	RAG2_HUMAN		5	TGACATGGTTAT	0.453	
-	14	1926		NM_002334	NP_002325	O75096	LRP4_HUMAN	ential).|LDL-receptor class	4	GGTATCGGCAA	0.552	
+	2	247	_p.S83A|C11orf8	NM_001100388	NP_001093858	Q6PI97	CK088_HUMAN		0	TCGCAGTCTTTT	0.338	
-	1	942		NM_001005187	NP_001005187	Q8NGN1	OR6T1_HUMAN	lasmic (Potential).	1	CAGTTTCATCAC	0.428	
+	1	19		NM_001001953	NP_001001953	Q8NGN4	O10G9_HUMAN	cellular (Potential).	2	GCCTCGTGACA	0.532	
+	8	1632		NM_025004	NP_079280	Q0P6D6	CCD15_HUMAN		2	TCTCCACAAAG	0.418	rs113451248
+	8	1722		NM_025004	NP_079280	Q0P6D6	CCD15_HUMAN		2	TCTCCCCAAAG	0.403	rs112861775
-	6	1375	n.1_RNA|NCAPD	NM_015261	NP_056076	P42695	CNDD3_HUMAN		5	ATTCATGAAGAA	0.353	
+	18	3380	C1_uc001qjd.2_R	NM_178040	NP_829884	Q8IUD2	RB6I2_HUMAN	FIP-RBD.	5	CTCACTCCACCA	0.502	
+	2	997	DC5_uc009zjj.2_	NM_020782	NP_065833	Q9P2K6	KLDC5_HUMAN	Kelch 3.	2	CATCGGAGGGC	0.478	
+	13	1852	_p.S562I|TROAP_	NM_005480	NP_005471	Q12815	TROAP_HUMAN	ate tandem repeats.|Cys-ri	1	TAGGAGTGAGC	0.592	
-	1	705	h.2_Missense_Mu	NM_000424	NP_000415	P13647	K2C5_HUMAN	Coil 1A.|Rod.	0	ATGAAGGAGGCA	0.478	
-	1	351		NM_175068	NP_778238	Q86Y46	K2C73_HUMAN	Head.	6	TGACCTGATGGA	0.627	
+	9	1362	u.2_Missense_Mu	NM_001135805	NP_001129277	P21579	SYT1_HUMAN	hospholipid binding (Prob	6	GTATATGATTTTG	0.388	
+	1	604	S1B_uc001tgf.1_	NM_153364	NP_699195	Q8NEG0	FA71C_HUMAN		0	TGATTGACGTGC	0.527	
+	38	4189		NM_017564	NP_060034	Q8WWQ8	STAB2_HUMAN	cellular (Potential).	14	CGAGAGAATGC	0.527	
+	10	1036	A_uc009zwe.1_Mi	NM_001143854	NP_001137326	Q9Y2J0	RP3A_HUMAN	Pro-rich.	7	TCCCGGGCGAG	0.562	
-	8	1115	e_Mutation_p.W2	NM_015347	NP_056162	O15034	RIMB2_HUMAN	onectin type-III 1.	11	GGCTCCCAGCC	0.562	
-	4	621		NM_005932	NP_005923	Q99797	MIPEP_HUMAN		1	CAAGGGAATCC	0.279	
+	2	1012		NM_153456	NP_703157	Q8IZP7	H6ST3_HUMAN	nenal (Potential).	2	TGAACGAGAGT	0.493	
+	1	803		NM_001005500	NP_001005500	Q8NGD0	OR4M1_HUMAN	cellular (Potential).	0	CATTTTCCCTAG	0.418	
+	1	449		NM_001004723	NP_001004723	Q8NGD1	OR4N2_HUMAN	Name=4; (Potential).	4	GTGGCTTGGGG	0.532	
-	2	734	wih.2_Missense_	NM_021944	NP_068763	Q9H972	CN093_HUMAN		1	CTCTTCCACGG	0.632	
-	12	1959		NM_002742	NP_002733	Q15139	KPCD1_HUMAN	nilarity).|Protein kinase.	8	CAAACTGTCCA	0.323	
+	4	387	UBPL_uc010tpl.1_	NM_025152	NP_079428	Q8TB37	NUBPL_HUMAN		0	ATGGACCTTCAG	0.274	
+	3	896	p.2_Missense_Mu	NM_199421	NP_955453	Q8WXH5	SOCS4_HUMAN		2	GTAGTCGGCAC	0.428	
-	4	1102	mk.2_Missense_	NM_033141	NP_149132	P80192	M3K9_HUMAN	rotein kinase.	5	AGGAAGGGCGA	0.512	
-	7	1513	_p.S437F|FOXN3_	NM_001085471	NP_001078940	O00409	FOXN3_HUMAN		3	GGAGGGACCCT	0.522	

+	8	988	e_Mutation_p.G18	NM_001112726	NP_001106197	Q9Y4F5	K0284_HUMAN		1	GGCAGGTGGGG	0.642	
+	1	124		NM_001080841	NP_001074310				0	TTTGACCGCTAC	0.498	rs267613
-	33	6106	-4310|MI0015840_	NM_016642	NP_057726	Q9NRC6	SPTN5_HUMAN	Spectrin 16.	2	GCGGGCTGCCC	0.682	
+	4	597	zxr.2_Missense_M	NM_020234	NP_064619	Q8N5C7	DTWD1_HUMAN		0	AAAGTACTGCTA	0.214	
+	5	1270	_p.W293*|SLC27A	NM_003645	NP_003636	O14975	S27A2_HUMAN	lasmic (Potential).	2	TGTGTGGAGACA	0.433	
-	11	1721	zza.3_Missense_M	NM_031226	NP_112503	P11511	CP19A_HUMAN		3	AAAGATCATTTC	0.448	
-	61	12014		NM_003922	NP_003913	Q15751	HERC1_HUMAN		19	CAGGTTCTAGAT	0.428	
+	18	2547		NM_152336	NP_689549	Q96MI9	CBPC4_HUMAN		0	CTTTCTCCCAGT	0.473	
-	9	2439	uyn.1_Missense_M	NM_001134407	NP_001127879	Q12879	NMDE1_HUMAN	lasmic (Potential).	45	CAGATACCATGAT	0.478	
+	6	873	p.2_Missense_Mu	NM_024847	NP_079123	Q7Z402	TMC7_HUMAN	cellular (Potential).	3	TTTACGGACATTA	0.493	
+	12	1647	lhg.3_Missense_M	NM_001010845	NP_001010845	Q08AH3	ACS2A_HUMAN	nzyme A binding.	3	CCAGCGGGTGA	0.498	
-	12	1618	p.G470R|ACSM2E	NM_182617	NP_872423	Q68CK6	ACS2B_HUMAN	A binding (By similarity).	5	CTCACCCGCTGG	0.507	rs150327444
-	5	1060		NM_020718	NP_065769	Q70CQ4	UBP31_HUMAN		10	CCATAGACACTG	0.443	
-	27	4125	CC12_uc002efa.1_	NM_033226	NP_150229	Q96J65	MRP9_HUMAN	C transporter 2.	3	CGTTCCCCTACT	0.413	
+	11	1346	1A|GPR114_uc002	NM_153837	NP_722579	Q8IZF4	GP114_HUMAN	Name=5; (Potential).	1	ACGGCGGCCTC	0.697	
+	4	2048	nn.1_Missense_Mu	NM_015251	NP_056066	O43313	ATMIN_HUMAN		0	ACTTCTTACTCG	0.458	
-	1	205	2fgj.2_Missense_M	NM_052892	NP_443124	Q7Z442	PK1L2_HUMAN	(Potential).|C-type lectin.	3	TGCCTTCGTCCT	0.562	
-	5	591	se_Mutation_p.G17	NM_000512	NP_000503	P34059	GALNS_HUMAN		2	AGGTCCAAAGT	0.587	
-	12	1524	p.P211S|C17orf85	NM_001114118	NP_001107590	Q53F19	CQ085_HUMAN		1	TTTCCGGAGAAT	0.502	
-	4	626		NM_003342	NP_003333	P62253	UB2G1_HUMAN		0	AATGCACACAT	0.368	
-	9	1206	p.E359K|ALOX15_	NM_001140	NP_001131	P16050	LOX15_HUMAN	ipoxygenase.	5	TAATTTCCAGGG	0.522	
+	33	5258	p.Q1010*|USP6_u	NM_004505	NP_004496	P35125	UBP6_HUMAN		5	CATCCCAGGAA	0.413	
+	11	2472	gix.2_Missense_M	NM_001080424	NP_001073893	O15054	KDM6B_HUMAN	Pro-rich.	2	ACATCATGAAGA	0.572	
-	14	1420	_Mutation_p.A431	NM_001100112	NP_001093582	Q9UKX2	MYH2_HUMAN	osin head-like.	14	CTTTGGCCAGA	0.483	
+	9	2181	e_Mutation_p.R17	NM_014695	NP_055510	A2RUR9	C144A_HUMAN	Potential.	0	ATTTGAGGTATG	0.323	
-	2	171	se_Mutation_p.A3	NM_001042685	NP_001036150	Q3B8N2	LEG9B_HUMAN	Galectin 1.	1	AACGGCCCCAT	0.562	rs144269928
-	3	1568	_p.W413*|SLFN1	NM_144682	NP_653283	Q68D06	SLN13_HUMAN		2	CCTTCCAGAGG	0.423	
+	1	1130	p.E182K|CDK12_	NM_016507	NP_057591	Q9NYV4	CDK12_HUMAN		19	ACAAGGAGAAG	0.493	
-	1	393		NM_033059	NP_149048	Q9BYQ6	KR411_HUMAN	GIKRQVHEL]- [SPTR]-[ST	0	tgcagcagctggaca	0.129	
-	1	183		NM_033059	NP_149048	Q9BYQ6	KR411_HUMAN	GIKRQVHEL]- [SPTR]-[ST	0	CAGCAGCTGGA	0.672	
+	18	2053	2jyd.1_Missense_M	NM_173626	NP_775897	Q86WA9	S2611_HUMAN	cellular (Potential).	0	AAGACTCCATTC	0.502	
+	2	187	_p.W66*|CLUL1_	NM_014410	NP_055225	Q15846	CLUL1_HUMAN		2	CTGTGGTTGAA	0.443	
-	2	1637		NM_016626	NP_057710	Q5U5Q3	MEX3C_HUMAN		4	ATGTAGGAGAC	0.498	
+	13	2640	p.G533R|DCC_uc	NM_005215	NP_005206	P43146	DCC_HUMAN	tential).|Fibronectin type-III	17	TCACAGGTCAG	0.403	
+	4	530	2liy.2_Missense_M	NM_002639	NP_002630	P36952	SPB5_HUMAN		1	CGAAAGGTCAG	0.388	
-	1	327	2luv.2_Missense_	NM_130807	NP_570719	Q96BX8	MOL2A_HUMAN		1	TTCAGGTCCTC	0.667	
-	2	359		NM_001080523	NP_001073992	A6NEK1	ARRD5_HUMAN		0	TAGAAGGAAGC	0.448	
-	18	2353		NM_000064	NP_000055	P01024	CO3_HUMAN	p.R764Q(1)	5	TCACTTCGGGAA	0.478	rs143642234
-	4	659	q.2_Missense_Mu	NM_021155	NP_066978	Q9NNX6	CD209_HUMAN	|5.|7 X approximate tanden	1	CAGCCGGGTCA	0.562	rs141131967
-	3	13802		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).	57	TGGAAGGATGA	0.453	
-	10	2291	wr.1_Missense_M	NM_152476	NP_689689	Q96MR9	ZN560_HUMAN		6	AATTTCGAAAG	0.378	rs148650284
+	4	1651	ym.1_Missense_M	NM_001136501	NP_001129973	Q08AG5	ZN844_HUMAN		0	AAACCCTATGA	0.413	
+	3	295	_p.P58S|CD97_u	NM_078481	NP_510966	P48960	CD97_HUMAN	r (Potential).|EGF-like 1.	4	CCACCCCGACG	0.592	
+	3	267	_p.P69L|CYP4F1	NM_023944	NP_076433				7	CACTCCTACAG	0.358	
+	1	169		NM_013939	NP_039227	O60403	O10H2_HUMAN	lasmic (Potential).	3	CGTCTGGAGCG	0.607	
-	4	935		NM_001159293	NP_001152765	C9JHM3	C9JHM3_HUMAN		1	TCTCCACTATGA	0.403	
-	3	325		NM_001098626	NP_001092096	A6NK75	ZNF98_HUMAN	KRAB.	2	TCTTTTCCTTGC	0.423	

+	4	1251	rk.1_Missense_M	NM_203282	NP_975011	O75437	ZN254_HUMAN			0	TTCATACTGGA	0.378	
+	4	702	p.G114R|KIRREL	NM_199180	NP_954649	Q6UWL6	KIRR2_HUMAN	2.|Extracellular (Potential).		3	GAGATGGGGTC	0.582	
-	4	529_530	8KN>NY|ZNF573_	NM_152360	NP_689573	Q86YE8	ZN573_HUMAN	2H2-type 2.		1	AAAGTTCTTCCC	0.366	
+	7	1010	se_Mutation_p.G	NM_021913	NP_068713	P30530	UFO_HUMAN	tential).|Fibronectin type-III		13	AGGCGGGAGAA	0.612	
+	14	1573	ba.1_Missense_Mutation_p.P523L			Q96L34	MARK4_HUMAN			3	GCGCCCGTCAC	0.587	
-	5	1038	77_uc010ydf.1_5'	NM_023074	NP_075562	Q9BS31	ZN649_HUMAN			3	CTCCTTTGTGA	0.507	
+	4	2950	dw.1_Missense_M	NM_138374	NP_612383	Q96IR2	ZN845_HUMAN	2H2-type 27.		0	ACAAGTGTAAT	0.348	
-	3	976		NM_001101401	NP_001094871	P0C263	SBK2_HUMAN	rotein kinase.		0	GCGCCCCAGGT	0.731	
-	9	1992	DH14_uc002rcx.3	NM_033253	NP_150278	Q96P26	5NT1B_HUMAN			3	ATCCATAGCTTT	0.423	
-	3	382	10yjv.1_Missense_	NM_001002006	NP_001002006	Q96P26	5NT1B_HUMAN			3	GCTGGCCCTGC	0.527	
+	1	378_379	.2_Intron|SPTBN1	NR_002229						0	TGAGTTTGCCAT	0.48	
-	6	1224	svl.2_Missense_	NM_020151	NP_064536	Q9NQZ5	STAR7_HUMAN	START.		0	GTGGGGACGG	0.468	
+	12	2402		NM_003048	NP_003039	Q9UBY0	SL9A2_HUMAN	lasmic (Pote	p.E754K(1)	8	GCAGAGAAAAG	0.532	rs147224345
+	4	564	H2P_uc002tkd.2_	NM_182905	NP_878908					0	CATCCGCCAAG	0.522	
-	34	4076	yy.1_RNA|CLASP	NM_015282	NP_056097	Q7Z460	CLAP1_HUMAN			2	CCCCCCGGCCC	0.637	
+	14	2558	flu.2_Nonsense_	NM_130773	NP_570129	Q8WYK1	CNTP5_HUMAN	ential).|Fibrinogen C-termi		10	ACATTCAGCAC	0.488	
-	3	279	_p.E53K|CACNB4	NM_000726	NP_000717	O00305	CACB4_HUMAN			2	TGCTTCCCGGT	0.483	
-	12	1858	e_Mutation_p.W3	NM_004490	NP_004481	Q14449	GRB14_HUMAN	SH2.		7	TGAAACCATGG	0.388	
-	58	11467		NM_004525	NP_004516	P98164	LRP2_HUMAN	A 31.|Extracellular (Potent		29	GTTTTCCTCAT	0.448	
-	46	13983	N_uc010zfi.1_Intr	NM_133379	NP_596870	Q8WZ42	TITIN_HUMAN			153	CACATCTGTGT	0.318	rs149720053
-	40	2947	rx.2_Missense_M	NM_000393	NP_000384	P05997	CO5A2_HUMAN			2	GAACACCATTA	0.438	
+	3	285	10ziu.1_5'Flank|E	NM_001037663	NP_001032752	P24534	EF1B_HUMAN	ST C-terminal.		0	TGTCCAGCCCA	0.468	
-	2	237		NM_014617	NP_055432	P11844	CRGA_HUMAN	crystallin 'Greek key' 2.		0	CGAGTCGCTGA	0.517	
-	7	954	fuw.2_Missense_	NM_016260	NP_057344	Q9UKS7	IKZF2_HUMAN			0	CAGGTCTCTCA	0.388	
-	8	1375	_p.R376*|HJURP_	NM_018410	NP_060880	Q8NCD3	HJURP_HUMAN			1	AAATCGGATTT	0.488	
+	17	2342	M8_uc010fyj.2_In	NM_024080	NP_076985	Q7Z2W7	TRPM8_HUMAN	Name=3; (Potential).		4	CCCCCGAGCTG	0.572	
-	40	8938	znj.1_Missense_	NM_004369	NP_004360	P12111	CO6A3_HUMAN	ical region.|Thr-rich.		18	TGTGGTGGTCA	0.493	
-	14	1298	rf194_uc002wik.2_	NM_001009984	NP_001009984	Q5TEA3	CT194_HUMAN			0	TAAACGGAATC	0.378	rs73577662
-	14	3758	GLEC1_uc002wiz.	NM_023068	NP_075556	Q9BZZ2	SN_HUMAN	ellular (Potential).		10	CCAGGGACGTG	0.692	
+	26	2525	_p.R809*|PLCB4_	NM_182797	NP_877949	Q15147	PLCB4_HUMAN			15	GGATATCGACAC	0.448	
+	2	120	tj.1_RNA|FRG1B_uc010gdr.1_RNA|FRG1B_uc010ztk.1_Intron							0	TTGGGCATTCA	0.338	
+	2	127	tj.1_RNA|FRG1B_uc010gdr.1_RNA|FRG1B_uc010ztk.1_Intron							0	ATTCAGATGCAA	0.333	
+	2	133	tj.1_RNA|FRG1B_uc010gdr.1_RNA|FRG1B_uc010ztk.1_Intron							0	TGCAATTGGAC	0.343	
+	3	187	RG1B_uc010gdr.1_RNA|FRG1B_uc010ztk.1_Missense_Mutation_p.L4S							0	TTTGTTGGCCT	0.353	
+	3	189	RG1B_uc010gdr.1_RNA|FRG1B_uc010ztk.1_Missense_Mutation_p.A5T							0	TGTTGGCCTCA	0.353	
+	11	1423	ggc.2_Missense_	NM_015568	NP_056383	Q96T49	PP16B_HUMAN			3	AATTTCCTACC	0.567	
-	4	488		NM_182482	NP_872288					0	TCCTTCGCTATA	0.368	rs28441174
-	4	488		NM_182482	NP_872288					0	CTTCGCTATAAT	0.368	rs28537865
-	2	297	GE_uc002yix.2_R	NM_182482	NP_872288					0	gctccaacctccagctc	0.09	
+	3	523	AM2_uc011acc.1	NM_004540	NP_004531	O15394	NCAM2_HUMAN	1.|Extracellular (Potential).		4	ATATATCGTTGT	0.348	
+	21	3495	1afa.1_Missense_	NM_003274	NP_003265	P48553	TPC10_HUMAN			2	ATTTTTCGACAA	0.299	
+	3	1474	R1_uc002zwt.2_I	NM_002073	NP_002064	P19086	GNAZ_HUMAN			2	TGAACCGCAAC	0.567	
-	11	1188_1189	n_p.K416E|CHEK	NM_007194	NP_009125	O96017	CHK2_HUMAN	rotein kinas	73E(2)|p.S372	20	AATCTTGGAGTG	0.416	470496;rs146546850
+	6	461	yz.2_Missense_M	NM_014509	NP_055324	Q9H4I8	SEHL2_HUMAN			0	CTGTACCTTCCC	0.527	
+	16	1945	p.D610Y|ATG7_u	NM_006395	NP_006386	O95352	ATG7_HUMAN			1	GTGACGATCGG	0.478	
-	3	873	_p.M166I|IQSEC1_	NM_014869	NP_055684	Q6DN90	IQEC1_HUMAN			1	TGGTCCATGCC	0.667	
-	15	2844	1A_uc010hhn.1_	NM_014139	NP_054858	Q9UI33	SCNBA_HUMAN			9	CCAGGGGAATG	0.507	

-	2	360	R3_uc003cpg.1_In	NM_001295	NP_001286	P32246	CCR1_HUMAN	ellular (Potential).	3	AGTCATCCTTCA	0.463	
-	83	6621		NM_000094	NP_000085	Q02388	CO7A1_HUMAN	le-helical region.	11	GCTCCCCCTGC	0.607	
-	12	1414	ASSF1_uc003daf.	NM_015896	NP_056980	O75800	ZMY10_HUMAN	MYND-type.	5	TTTTCCCAGTGC	0.567	
-	14	2663	RC2_uc003dht.1_	NM_015576	NP_056391	O15083	ERC2_HUMAN	Potential.	2	GTTCCTCTATCTG	0.488	
+	19	3398	OBO2_uc011bgk.1	NM_002942	NP_002933	Q9HCK4	ROBO2_HUMAN	lasmic (Potential).	11	GGTGATCCCAGC	0.458	
+	2	698		NM_017819	NP_060289	Q7L0Y3	MRRP1_HUMAN		1	CTTTGGGATAGG	0.408	
+	3	171	hpu.2_Missense_	NM_007072	NP_009003	Q9UM44	HHLA2_HUMAN		1	GACATGAAGGCA	0.303	
+	4	2218	dyg.2_Missense_	NM_001134438	NP_001127910	Q86SQ0	PHLB2_HUMAN	Potential.	6	CTCGAGGAACTT	0.408	
+	7	1310	C_uc003dzz.2_Mis	NM_033254	NP_150279	Q9BWV1	BOC_HUMAN	ellular (Potential).	6	CTGCCCGCATCA	0.622	
+	3	1940		NM_016298	NP_057382	Q9UH90	FBX40_HUMAN	F-box.	5	GCCTGCCCCTGG	0.522	
-	15	1919	p.G513E|CPNE4_	NM_130808	NP_570720	Q96A23	CPNE4_HUMAN	VWFA.	3	GGCTCTCCCTTG	0.517	
-	6	7502	p.R528K|IGSF10_	NM_178822	NP_849144	Q6WRI0	IGS10_HUMAN	like C2-type 11.	13	TTTCCTCTGTCAT	0.393	
-	3	564	.2_Missense_Mut	NM_139248	NP_640341	Q8WWY8	LIPH_HUMAN		2	TTACTCCGATCA	0.443	
+	1	119		NM_001083308	NP_001076777	Q56P42	PYDC2_HUMAN	DAPIN.	0	AGCTACAGACCG	0.542	
+	10	1401	c.1_RNA|SDHAP2_uc003fuv.2_RNA						0	CACGAATCTTGA	0.413	
+	1	1630		NM_000798	NP_000789	P21918	DRD5_HUMAN	lasmic (Potential).	1	TACATCCACATG	0.577	
-	18	2858	p.S721F|APBB2_	NM_173075	NP_775098	Q92870	APBB2_HUMAN		3	ATGAGGGATAAG	0.488	
+	8	658		NM_016519	NP_057603	Q9NP70	AMBN_HUMAN	1	4	GGAATGGATTTT	0.194	
-	6	649	0iik.1_Missense_	NM_201431	NP_958834	Q6ZTQ3	RASF6_HUMAN		2	CTGGTTCATCCT	0.428	
-	6	744	e_Mutation_p.S22	NM_014435	NP_055250	Q02083	NAAA_HUMAN		1	TTTTCCGACTCA	0.517	
-	1	142		NM_033214	NP_149991	Q14410	GLPK2_HUMAN		4	TTAATTCCACTTT	0.468	
+	14	3228	k.3_Missense_Mu	NM_005935	NP_005926	P51825	AFF1_HUMAN		1	CCTTTTCCAGTG	0.378	
-	34	2368	25A1_uc003hzd.2_	NM_198721	NP_942014	Q9BXS0	COPA1_HUMAN	Potential).|Collagen-like 7.	2	TTTCTCCCTTTT	0.438	
+	2	437		NM_153610	NP_705838	Q8N3K9	CMYA5_HUMAN		9	ATGTTTCCTTTAT	0.423	
+	9	1582	TS19_uc010jdh.1	NM_133638	NP_598377	Q8TE59	ATS19_HUMAN	ptidase M12B.	9	AGGAAGATTTG	0.363	
+	4	777	P103S|FAM53C_u	NM_001135647	NP_001129119	Q9NYF3	FA53C_HUMAN		1	CCAGATCCAGAG	0.657	
+	7	1485	e_Mutation_p.S85	NM_016604	NP_057688	Q7LBC6	KDM3B_HUMAN		11	GCCAGCTCCACC	0.587	
+	1	352	p.H118Y|PCDHA1	NM_018900	NP_061723	Q9Y5I3	PCDA1_HUMAN	|Extracellular (Potential).	1	GTTTTCCATGTG	0.512	
+	5	1179	dbl.1_Missense_M	NM_152550	NP_689763	Q8TEC5	SH3R2_HUMAN		2	TCCATTCTCCTTC	0.572	
+	8	1873	p.P572S|PPARG	NM_133263	NP_573570	Q86YN6	PRGC2_HUMAN		0	ACACCACCGTAC	0.522	
+	7	1264		NM_014228	NP_055043	Q99884	SC6A7_HUMAN	Name=6; (Potential).	0	CTATTCCCTGG	0.562	
+	12	1417	_p.R234*|G3BP1_	NM_005754	NP_005745	Q13283	G3BP1_HUMAN		4	AGACTCGAGCT	0.572	
+	24	2689	p.L851V|CYFIP2_	NM_001037333	NP_001032410	Q96F07	CYFP2_HUMAN		0	GACTTTCTCCCC	0.587	
-	12	1061	_uc010jkt.2_Silen	NM_173465	NP_775736	Q86Y22	CONA1_HUMAN	ntial).|Collagen-like 1.|Gly-	2	CTCACCCTGGG	0.607	
+	3	1184		NM_001718	NP_001709	P22004	BMP6_HUMAN		3	GGGATGGTAAGT	0.507	
+	26	2495	ow.2_Missense_M	NM_001040274	NP_001035364	Q5T4T6	SYC2L_HUMAN		2	GAAAATGCAAA	0.343	
-	1	733		NM_030903	NP_112165	Q9Y3N9	OR2W1_HUMAN	Name=6; (Potential).	3	CAGTAAGATGAG	0.428	rs143534892
+	25	3380		NM_002224	NP_002215	Q14573	ITPR3_HUMAN	lasmic (Potential).	19	GCCGCATGTTCC	0.647	
-	2	1136		NM_020737	NP_065788	Q9ULH4	LRFN2_HUMAN	ellular (Potential).	3	AAGCCGAAGCC	0.592	
-	2	228	qg.1_Nonsense_	NM_018643	NP_061113	Q9NP99	TREM1_HUMAN	(Potential).|Ig-like V-type.	1	TCTGCCAAGCTT	0.478	
-	7	1949	f.1_Missense_Mu	NM_021073	NP_066551	P22003	BMP5_HUMAN		2	TACGTGGTCAG	0.308	
+	5	824	3psx.3_Missense_	NM_001083535	NP_001077004	Q8IYX8	CE57L_HUMAN	Potential.	0	AACATTCTTTCC	0.368	
+	64	9352	ense_Mutation_p.	NM_000426	NP_000417	P24043	LAMA2_HUMAN	minin G-like 5.	10	AGTATTCCGTTC	0.493	
-	5	906		NM_004666	NP_004657	O95497	VNN1_HUMAN	N hydrolase.	3	TTCCCTCTTCTG	0.438	
+	2	1381		NM_016217	NP_057301	Q9UBI9	HDC_HUMAN		0	TCCACGTGCGC	0.602	
-	2	487	rf118_uc011egi.1_	NM_144980	NP_659417	Q5T5N4	CF118_HUMAN		0	GACAGCCTCCA	0.617	
+	3	1736	LL2_uc011egr.1_R	NM_031949	NP_114155	Q9BWV7	TTLL2_HUMAN		3	GCTCCAGATCCC	0.502	

+	75	12167		NM_003777	NP_003768	Q96DT5	DYH11_HUMAN	.6 (By similarity).	15	CTCCTGGAAAAT	0.473	
+	12	1544	:e.1_Missense_Mu	NM_031414	NP_113602	Q9BXU1	STK31_HUMAN		9	TCTGATGAAATAC	0.368	
+	9	1723		NM_021116	NP_066939	Q08828	ADCY1_HUMAN	lasmic (Potential).	6	GGTACATCAGC	0.522	
-	25	4047	v.2_Missense_Mut	NM_022748	NP_073585	Q68CZ2	TENS3_HUMAN	SH2.	4	AATCTCCAGCT	0.433	
+	4	1510		NM_001159522	NP_001152994	A8MUV8	ZN727_HUMAN	2H2-type 10.	0	ATAAGAGAATTCA	0.393	
-	2	116		NM_002991	NP_002982	O00175	CCL24_HUMAN		0	TCTTGGAAACA	0.557	
+	14	2315	AN_uc003uwl.2_F	NM_003386	NP_003377	Q9Y493	ZAN_HUMAN	ate) (mucin-like domain).|E	11	AAAAACCCACCA	0.507	
-	27	3731	kg.3_Nonsense_M	NM_017954	NP_060424	Q86UW7	CAPS2_HUMAN		2	TTTCTCGAAGAA	0.368	
-	18	2418	M1D_uc010lng.2_	NM_030647	NP_085150	Q6ZMT4	KDM7_HUMAN		1	AGGAGGAAGTC	0.318	
-	15	1860		NM_004333	NP_004324	P15056	BRAF_HUMAN	rotein kinas_R603>I(2)|p.T	18290	GATTTCACTGTA	0.368	
+	7	1371	_p.H406Y|ZYX_uc	NM_001010972	NP_001010972	Q15942	ZYX_HUMAN	zinc-binding 1.	0	CTGTTCCACATC	0.642	
+	8	1391	kr.2_RNA|GALNTL	NM_145292	NP_660335	Q7Z4T8	GLTL5_HUMAN	enal (Potential).	2	CTGGATGAATATA	0.468	
+	2	371	.2_5'UTR|ADAMD	NM_014479	NP_055294	O15204	ADEC1_HUMAN		2	AAACTTCACATTT	0.343	
-	8	877		NM_144651	NP_653252	A1KZ92	PXDNL_HUMAN	-like C2-type 1.	2	GGTTTCCTTCC	0.443	
-	6	1140_1141	_p.G267K|PCMTD	NM_052937	NP_443169	Q96MG8	PCMD1_HUMAN		0	GAATCCCCTTGG	0.421	
+	69	11265		NM_177531	NP_803875	Q86WI1	PKHL1_HUMAN	ellular (Potential).	14	GAATTCCTAAG	0.438	
-	4	835	x.1_Missense_Mu	NM_198123	NP_937756	Q7Z407	CSMD3_HUMAN	ar (Potential).|Sushi 1.	63	ACGAAGCTGTAT	0.423	
+	35	4881	uc003yqy.1_Intron	NM_001039112	NP_001034201	Q2WGJ9	FR1L6_HUMAN	lasmic (Pote p.D1559Y(1)	11	ACAAGGATAAG	0.428	
-	13	1991	M135B_uc003yva	NM_015912	NP_056996	Q49AJ0	F135B_HUMAN		9	TGTCTGAAGAG	0.468	
+	13	1390		NM_139021	NP_620590	Q8TD08	MK15_HUMAN		2	GAGGGGAGCTG	0.687	
+	9	1423	_p.S466F|CNTLN_	NM_017738	NP_060208	Q9NXG0	CNTLN_HUMAN		1	GAAGTCTGAAA	0.338	
-	1	3013	c003zrh.1_5'Flan	NM_153809	NP_722516	Q8IZX4	TAF1L_HUMAN		26	TGTGGGATCTG	0.498	
+	3	307		NM_019592	NP_062538	Q5VTR2	BRE1A_HUMAN	Potential.	8	AACTTCGTGAG	0.453	
+	1	70		NM_001004485	NP_001004485	Q8NGS4	O13F1_HUMAN	ellular (Potential).	3	AAAGTTCAGGTC	0.418	
-	1	256		NM_001001956	NP_001001956	Q8NGT0	O13C9_HUMAN	ellular (Potential).	0	TGAAAGGAAGC	0.512	
-	2	167	lwl.1_Missense_M	NM_001003936	NP_001003936	Q6A555	TXND8_HUMAN	Thioredoxin.	0	AAACAGGAAACA	0.353	
-	8	2383		NM_014618	NP_055433	O60477	DBC1_HUMAN		8	GGAGGGATCCG	0.562	
+	1	22	|GOLGA2_uc004b	NM_001040011	NP_001035100	Q1ZZU3	SWI5_HUMAN		0	AGAGGGACCTG	0.642	
+	61	5045	uc004cff.2_Intron	NM_000093	NP_000084	P20908	CO5A1_HUMAN	le-helical region.	11	CGAAGGGTGAG	0.592	
+	26	3954	_p.A800V|CACNA	NM_000718	NP_000709	Q00975	CAC1B_HUMAN	smic (Potential).|III.	6	GCAGGCTGTGT	0.562	
-	2	640	0ndi.2_Missense_	NM_181332	NP_851849	Q8N0W4	NLGNX_HUMAN	ellular (Potential).	4	TGACAACTGGAT	0.502	
+	13	1500	p.D327N|TBL1X_	NM_001139466	NP_001132938	O60907	TBL1X_HUMAN	WD 4.	1	ATGTGGACTGG	0.527	
+	15	2667	mij.1_Missense_M	NM_014728	NP_055543	Q14CM0	FRPD4_HUMAN		13	TAGGCGATGTG	0.522	rs147167664
-	3	1112_1113	wh.1_Missense_M	NM_001018113	NP_001018123	Q8NB91	FANCB_HUMAN		1	GATCTCCAAATG	0.391	
-	3	357	wh.1_Missense_M	NM_001018113	NP_001018123	Q8NB91	FANCB_HUMAN		1	AAATTTCCTTTAG	0.368	
-	7	1013	9_uc004cwm.2_3	NM_001031739	NP_001026909	Q96DX5	ASB9_HUMAN	SOCS box.	0	AGAAGGGGGCC	0.393	
-	2	230	A9L_uc010nfp.2_	NM_001412	NP_001403	P47813	IF1AX_HUMAN		1	TACCTCCTTTACC	0.308	
-	27	3959	_Mutation_p.E123	NM_004006	NP_003997	P11532	DMD_HUMAN	Spectrin 8.	6	CAAGTTCCTTTTT	0.433	
+	1	1956		NM_001013736	NP_001013758	Q5HY64	FA47C_HUMAN		3	CCTCCCAATACT	0.642	rs145580328
+	4	409	7S|ATP6AP2_uc0	NM_005765	NP_005756	O75787	RENR_HUMAN	ellular (Potential).	0	GCAGTTCCTTTT	0.353	
-	19	1796	p.A220V|TEX11_u	NM_001003811	NP_001003811	Q8IYF3	TEX11_HUMAN		5	TGGGCAGCTAAA	0.328	
-	1	457	_p.L147F|SERPIN	NM_000354	NP_000345	P05543	THBG_HUMAN		0	ATCATTCAAGAA	0.423	
+	2	939	mk.2_Missense_M	NM_194463	NP_919445	Q8TEB7	RN128_HUMAN		2	TTATTCTGCTCG	0.363	
-	24	4657	.M1537I|ODZ1_u	NM_014253	NP_055068	Q9UKZ4	TEN1_HUMAN	ellular (Potential).	23	AATGTTCATGTC	0.483	
-	3	581	_p.Q173*|ODZ1_u	NM_014253	NP_055068	Q9UKZ4	TEN1_HUMAN	inal.|Cytoplasmic (Potential	23	AGCTTGAGCCT	0.413	
+	12	4813	vc.1_Missense_M	NM_021946	NP_068765	Q5H9F3	BCORL_HUMAN		7	CAGAGGAAAAA	0.473	
+	4	1679	EC1_uc010nsl.1_	NM_005462	NP_005453	O60732	MAGC1_HUMAN		4	CTGAGAGAACT	0.478	

+	7	1354		NM_005140	NP_005131	Q16280	CNGA2_HUMAN	ellular (Potential).	3	CTCCAACATGA	0.502	
-	4	470	011mye.1_RNA|M	NM_004961	NP_004952	P78334	GBRE_HUMAN	ellular (Probable).	2	CAAGAGACTCA	0.488	
+	4	363	se_Mutation_p.T1	NM_153478	NP_705611	Q6PB30	CSAG1_HUMAN		1	cttCACTGTCCTG	0.303	
+	10	1079	k.1_Missense_Mu	NM_002631	NP_002622	P52209	6PGD_HUMAN		1	CGCTTCCAAGA	0.498	
-	11	2941	_p.S874L|CASZ1_	NM_001079843	NP_001073312	Q86V15	CASZ1_HUMAN		1	TGGGCGAGATG	0.662	
+	11	4450	p.1_Missense_Mu	NM_015001	NP_055816	Q96T58	MINT_HUMAN	Potential.	15	AGCTACGTGAG	0.398	
+	3	379		NM_016183	NP_057267	Q9UKD2	MRT4_HUMAN		0	CTTTTCATCTTCT	0.557	
+	13	1157	.R316C|RPS6KA	NM_002953	NP_002944	Q15418	KS6A1_HUMAN	kinase C-terminal.	1	ACCGTCGTGAG	0.597	
-	9	7977	e_Mutation_p.S22	NM_024503	NP_078779	Q5T1R4	ZEP3_HUMAN		6	CAGGCGACACG	0.687	rs146175722
+	49	6741_6742	1cjl.1_Missense_	NM_015284	NP_056099	Q5T011	SZT2_HUMAN		0	ATCATCCTCATG	0.574	
+	8	1227	_p.S325F|CYP4X1_	NM_178033	NP_828847	Q8N118	CP4X1_HUMAN		2	CATCTCCTGGA	0.512	
-	14	1723	_p.P69S|CC2D1B_	NM_032449	NP_115825	Q5T0F9	C2D1B_HUMAN		2	ACTCGGTGACT	0.632	
+	9	1175	ya.3_Missense_	NM_001110533	NP_001104003	Q3ZCV2	CA177_HUMAN		0	GATATCGATCCC	0.592	
-	5	769	_p.V76I|DHCR24_	NM_014762	NP_055577	Q15392	DHC24_HUMAN	inding PCMH-type.	1	GGGTACGGCAT	0.572	
+	3	484	_p.Q15*|RAVER2_	NM_018211	NP_060681	Q9HCJ3	RAVR2_HUMAN	RRM 1.	1	TAGTCCAGCTTC	0.368	
-	14	3346		NM_001002912	NP_001002912	Q5RHP9	CA173_HUMAN	Glu-rich.	5	ATCTTCCCTATT	0.468	
-	2	378	_p.A35T|BCAR3_	NM_003567	NP_003558	O75815	BCAR3_HUMAN		3	CTCAGCGAGAG	0.537	
+	8	727	53_uc010owa.1_M	NM_001040033	NP_001035122	P19397	CD53_HUMAN	ical; (Potential).	0	TATATCGGAATC	0.259	
+	5	279	F10_uc009wir.2_	NM_001037675	NP_001032764	Q3BBV1	NBPFK_HUMAN		0	TCATAAGATTTAT	0.537	
+	12	1400	_RNA|NBPF9_uc	NM_001037675	NP_001032764	Q3BBV1	NBPFK_HUMAN	NBPF 2.	0	ATGACAATGAA	0.423	
+	76	9469	PF10_uc010oyl.1	NM_001039703	NP_001034792	A6NDV3	A6NDV3_HUMAN		0	GAAAGGGCCTG	0.483	rs78186669
-	2	2983	e.1_Missense_M	NM_007113	NP_009044	Q07283	TRHY_HUMAN	tandem repeats.|4-3.	5	ctgcaactcctcttcctc	0.065	
-	3	5721		NM_001009931	NP_001009931	Q86YZ3	HORN_HUMAN	20	3	AACCAGAGGAC	0.557	
-	3	7594		NM_002016	NP_002007	P20930	FILA_HUMAN	Ser-rich.	16	TTCATCGTTAC	0.587	
-	3	883		NM_016190	NP_057274	Q9UBG3	CRNN_HUMAN	Gln-rich.	3	CGTGGGTCTCA	0.612	rs3814301
-	2	858	2_Missense_Muta	NM_001111	NP_001102	P55265	DSRAD_HUMAN		6	TGGGGCTCCTT	0.527	
-	2	843	2_Missense_Muta	NM_001111	NP_001102	P55265	DSRAD_HUMAN		6	TATGACCGTCTG	0.522	
-	11	1558	1fmd.3_Missense_	NM_001037533	NP_001032622	Q3T8J9	GON4L_HUMAN		3	CTGTCATCCAT	0.468	
+	2	234	1_Intron|MAEL_uc	NM_032858	NP_116247	Q96JY0	MAEL_HUMAN	HMG box.	1	AATACGCAGAA	0.527	
+	12	1273	e_Mutation_p.S37	NM_032858	NP_116247	Q96JY0	MAEL_HUMAN		1	GCATTTCCAATT	0.413	
-	10	1553	.2_5'UTR|SLC9A1	NM_178527	NP_848622	Q5TAH2	S9A11_HUMAN	ical; (Potential).	2	CAGACCACGTG	0.383	
+	6	1174	_p.H83R|RNPEP_	NM_020216	NP_064601	Q9H4A4	AMPB_HUMAN		1	TCAGCACATGG	0.577	
-	31	6282	gy.2_Missense_M	NM_025179	NP_079455	O75051	PLXA2_HUMAN	lasmic (Potential).	3	CTCCACGGCGT	0.562	rs139305640
-	21	4710		NM_025179	NP_079455	O75051	PLXA2_HUMAN	lasmic (Potential).	3	GGTACGATAGT	0.582	
-	8	1274	se_Mutation_p.P2	NM_001017402	NP_001017402	Q13751	LAMB3_HUMAN	inin EGF-like 1.	6	AGAAGGGTGCA	0.602	
-	2	812	.1_5'UTR|SUSD4_	NM_017982	NP_060452	Q5VX71	SUSD4_HUMAN	xtracellular (Potential).	0	GCCGGGGTCAG	0.507	
+	1	339		NR_002141					0	TGAGTTACCTTC	0.413	
-	1	492		NM_001004693	NP_001004693	Q8NGZ9	O2T10_HUMAN	ellular (Potential).	1	AAGCTCATGGC	0.512	
+	4	653		NM_018706	NP_061176	Q96HY7	DHTK1_HUMAN		2	GTTCTCGACAG	0.522	rs149544379
+	1	98		NM_032517	NP_115906	Q6UWQ5	LYZL1_HUMAN		0	TAAGTGGAGCA	0.512	
-	6	905	NF248_uc001izc.2	NM_021045	NP_066383	Q8NDW4	ZN248_HUMAN		1	TATAGGGATAATT	0.323	
-	3	460	103S|SYT15_uc	NM_031912	NP_114118	Q9BQS2	SYT15_HUMAN	lasmic (Potential).	0	GCAGGGGTCCC	0.682	
-	8	842	p.Q222K|ZWINT_	NM_007057	NP_008988	O95229	ZWINT_HUMAN		0	AGGTTGTAGAC	0.517	
+	3	479	_p.L152F|CYP2C9	NM_000771	NP_000762	P11712	CP2C9_HUMAN		6	GCTGCCTTGTG	0.498	
-	9	1393	P2C8_uc010qob.1	NM_000770	NP_000761	P10632	CP2C8_HUMAN		0	CAAATTCGTTTT	0.363	
-	2	746	c010qpy.1_5'Flan	NM_006562	NP_006553	P52954	LBX1_HUMAN		0	CTGCCCGCTGG	0.672	
-	27	3537	xq.2_Missense_	NM_025145	NP_079421	Q8NDM7	WDR96_HUMAN		0	TTGAGGAATCA	0.328	

-	2	464	BE1_uc001mam.1	NM_005330	NP_005321	P02100	HBE_HUMAN		0	AAAGGAAGTCA	0.512	
+	1	342	ense_Mutation_p.	NM_176875	NP_795344	P32239	GASR_HUMAN	ellular (Potential).	8	GACACGAGGTG	0.647	
+	1	164		NM_001001955	NP_001001955	Q8NGP0	OR4CD_HUMAN	lasmic (Potential).	4	TGAGATCCCCCA	0.428	
+	4	943	9F|TMEM132A_u	NM_024092	NP_076997	Q9BVC6	TM109_HUMAN	ical; (Potential).	0	TGCTACTCCTG	0.677	
-	5	6667	AK_uc001ntk.1_I	NM_001620	NP_001611	Q09666	AHNK_HUMAN		19	TAAGTCCACAT	0.522	
-	5	6640	AK_uc001ntk.1_I	NM_001620	NP_001611	Q09666	AHNK_HUMAN		19	GGGGGCCTTGA	0.507	rs1298288
-	5	6119	AK_uc001ntk.1_I	NM_001620	NP_001611	Q09666	AHNK_HUMAN		19	ACATCCACATCC	0.502	
-	5	6042	AK_uc001ntk.1_I	NM_001620	NP_001611	Q09666	AHNK_HUMAN		19	TGCATGTCTGG	0.507	rs147590412
-	9	1366	.G330D|SF1_uc0	NM_004630	NP_004621	Q15637	SF01_HUMAN	Pro-rich.	3	TGGAGCCCACA	0.612	
+	4	347	2_uc009yrq.2_5'U	NM_003952	NP_003943	Q9UBS0	KS6B2_HUMAN	rotein kinase.	7	TGCAAGGCACC	0.393	
+	59	8989_8990	1_Intron|C11orf65	NM_000051	NP_000042	Q13315	ATM_HUMAN	PI3K/PI4K.	240	GGACTTGGTGAT	0.302	
+	8	1115	_p.V166A|TMEM2	NM_032780	NP_116169	Q86YD3	TMM25_HUMAN	lasmic (Potential).	0	AGCAGTGAAAC	0.602	
+	31	4404	_p.R288*|SORL1_	NM_003105	NP_003096	Q92673	SORL_HUMAN	ential).|LDL-receptor class	15	GGTACCGAGAT	0.597	
+	9	908	p.R230Q|ST3GAL	NM_006278	NP_006269	Q11206	SIA4C_HUMAN	enal (Potential).	0	AGATTCGGATTC	0.512	
-	4	655		NM_020373	NP_065106	Q9NQ90	ANO2_HUMAN	lasmic (Potential).	7	TGCCTCTCTGG	0.468	
-	8	2008	p.G627E|CD163_	NM_004244	NP_004235	Q86VB7	C163A_HUMAN	xtracellular (Potential).	8	GCAACTCCACAT	0.517	
-	7	1735	p.G536E|CD163_	NM_004244	NP_004235	Q86VB7	C163A_HUMAN	xtracellular (Potential).	8	CCATTTCCCTCT	0.532	
-	4	352	3_5'UTR|PLCZ1_	NM_033123	NP_149114	Q86YW0	PLCZ1_HUMAN	EF-hand.	3	GTGATTCTTCCT	0.308	
-	38	4585	rfg.2_Missense_M	NM_020297	NP_064693	O60706	ABCC9_HUMAN	otential).|ABC transporter 2	6	ATATTTCCTCGC	0.408	
+	4	1816	rpq.2_Missense_	NM_138371	NP_612380	Q96HM7	F113B_HUMAN	Pro-rich.	5	CTCATCAGCCC	0.542	
-	33	8365		NM_003482	NP_003473	O14686	MLL2_HUMAN		41	TCACCGGCTGT	0.567	
-	3	314	_p.D85N|CPM_uc	NM_198320	NP_938079	P14384	CBPM_HUMAN		0	CCTCATCTCCAT	0.463	
+	15	1807		NM_017564	NP_060034	Q8WWQ8	STAB2_HUMAN	lar (Potential).|FAS1 2.	14	ATTTGGGACAT	0.388	
-	9	1094	tki.1_Missense_M	NM_031302	NP_112592	Q9H1C3	GL8D2_HUMAN	enal (Potential).	2	AATCACACCAG	0.488	
+	21	2563	tlq.2_Nonsense_	NM_018082	NP_060552	Q9NW08	RPC2_HUMAN		2	TTGAAACGATAC	0.408	
-	65	11164		NM_001109662	NP_001103132				2	CAGCGGGACGT	0.632	
-	31	3707		NM_006836	NP_006827	Q92616	GCN1L_HUMAN		4	GGCTTCCCACT	0.527	
+	6	885	p.E252G|ACADS_	NM_000017	NP_000008	P16219	ACADS_HUMAN		2	GGGGGAGCCAG	0.657	
+	6	892	_Mutation_p.P49	NM_014938	NP_055753	Q9HAP2	MLXIP_HUMAN	cytoplasmic localization.	2	CCTGGCCCAAT	0.602	
-	10	10625	P3199S|SACS_uc	NM_014363	NP_055178	Q9NZJ4	SACS_HUMAN		12	CAAAGGAACAA	0.383	
-	5	1684	se_Mutation_p.R4	NM_183044	NP_898865	Q9Y252	RNF6_HUMAN		2	CCTACGAAGAG	0.438	
-	20	3019	se_Mutation_p.G1	NM_198968	NP_945319	Q86YF9	DZIP1_HUMAN		2	GGTCCCGTCCG	0.552	
-	1	215	|RIPK3_uc010toi.1	NM_006871	NP_006862	Q9Y572	RIPK3_HUMAN		4	CGCACGACATC	0.582	
-	9	1244	L1_uc001wxz.2_I	NM_004196	NP_004187	Q00532	CDKL1_HUMAN		2	ctataataggatgagg	0	
+	8	951		NM_003082	NP_003073	Q16533	SNPC1_HUMAN		0	GGCATCGTCAA	0.358	
-	3	284	_p.G52E|RDH11_	NM_016026	NP_057110	Q8TC12	RDH11_HUMAN	lasmic (Potential).	1	GAGCTCCTGTC	0.423	
-	1	1313		NR_003951					0	CATGATCCCTGG	0.443	
+	15	1423	asq.1_Missense_	NM_020431	NP_065164	Q9P1W3	TM63C_HUMAN		0	CCGCTTCTTTT	0.512	
-	8	719	XN3_uc010auh.2_	NM_004993	NP_004984	P54252	ATX3_HUMAN		0	GAGCCATCATTT	0.423	rs75188275
+	11	1679		NM_017437	NP_059133	Q9P2I0	CPSF2_HUMAN		2	TATCAAGTATGTG	0.333	
-	8	1231	1_uc001yqo.2_Mi	NM_001519	NP_001510	Q92994	TF3B_HUMAN		4	GGGGTCGCACT	0.577	
+	32	4313	r.2_Missense_Mut	NM_001036	NP_001027	Q15413	RYR3_HUMAN	0.2/SPRY 3.|Cytoplasmic (	10	TGTCTCGTGGAT	0.562	
-	10	1383		NM_000138	NP_000129	P35555	FBN1_HUMAN	TB 2.	3	TTATGGACTGTG	0.542	
+	3	406		NM_014547	NP_055362	Q9NYL9	TMOD3_HUMAN		1	CAGGGCCATTT	0.453	
+	27	5951		NM_001080534	NP_001074003	Q8NB66	UN13C_HUMAN	MHD2.	7	TGGCTACCATCA	0.468	
+	8	1150		NM_152450	NP_689663	Q8TBF8	FA81A_HUMAN		1	GAAATGAAAGC	0.423	
-	4	530	22_uc002anc.1_3'	NM_000942	NP_000933	P23284	PPIB_HUMAN	e cyclophilin-type.	0	AGCGCTCACCGT	0.572	

+	12	5392	e_Mutation_p.S16	NM_013227	NP_037359	E7EX88	E7EX88_HUMAN			3	AGCCTCCACTG	0.537	
+	4	1059		NM_001013657	NP_001013679	Q6ZNW5	VTC2_HUMAN			0	CCCGGGGAGCT	0.557	
+	9	2564	.H_uc002chj.2_5'F	NM_005632	NP_005623	O75808	CAN15_HUMAN	alpain catalytic.		2	TCTGCGGCTCC	0.697	
+	11	1286	qe.1_Missense_M	NM_001761	NP_001752	P41002	CCNF_HUMAN	clin N-terminal.		2	TCTCCGCCTTG	0.527	
-	2	228	_p.R23K|PRSS33_	NM_152891	NP_690851	Q8NF86	PRS33_HUMAN			0	ACTTCCTTCCC	0.617	
+	7	1467	lfy.2_Missense_Mu	NM_016524	NP_057608	Q9BSW7	SYT17_HUMAN	C2 2.		1	GTCCTTCTTAAG	0.423	
-	3	218	_p.R30K|UMOD_	NM_003361	NP_003352	P07911	UROM_HUMAN	EGF-like 1.		2	ACCATCCTGTG	0.572	
-	5	831	SM1_uc010bwg.1_	NM_052956	NP_443188	Q08AH1	ACSM1_HUMAN			2	GGCTCCGTAATT	0.438	
+	19	2153	_uc002dji.2_Misse	NM_144672	NP_653273	Q7RTW8	OTOAN_HUMAN			3	GCCCAGACCTC	0.607	
-	37	6314	u.2_Missense_Mu	NM_001520	NP_001511	Q12789	TF3C1_HUMAN			5	CAGCCGGAGGG	0.637	
-	2	277	n.2_Missense_Mu	NM_024816	NP_079092	Q9H5N1	RABE2_HUMAN	Potential.		3	CTGCCGCTGCA	0.637	
+	3	1532	C5_uc002eca.3_M	NM_001105247	NP_001098717	Q96C12	ARMC5_HUMAN	ARM 5.	p.R335C(1)	1	AGCGCCGGGAT	0.652	
+	4	2329		NM_003414	NP_003405	Q14586	ZN267_HUMAN	2H2-type 14.		4	ACATCGGAGAA	0.433	rs146914846
-	5	605	VPS35_uc002eee.	NM_018206	NP_060676	Q96QK1	VPS35_HUMAN			0	ACTTACTCTGTT	0.358	
+	2	589	n_p.T17I|MMP2_	NM_004530	NP_004521	P08253	MMP2_HUMAN			11	GAATACCATCG	0.527	
-	5	652	n.1_Missense_Mu	NM_002080	NP_002071	P00505	AATM_HUMAN			2	ATACCGATAACC	0.473	
-	17	2466	w.3_Missense_Mu	NM_001145667	NP_001139139	Q92896	GSLG1_HUMAN	12.|Extracellular (Potential)		2	CACACGGAGCT	0.632	
-	3	373	HST6_uc002feh.1_	NM_021615	NP_067628	Q9GZX3	CHST6_HUMAN	enal (Potential).		0	GACGTCGGGGT	0.687	
-	9	4401	_Mutation_p.E131	NM_013275	NP_037407	Q6UB99	ANR11_HUMAN	Lys-rich.		6	CGGCTCCTGCC	0.567	
-	1	635		NM_002551	NP_002542	P47893	OR3A2_HUMAN	ellular (Pote	p.S199F(1)	1	TGCTGGAGCAG	0.552	rs140935076
-	4	1603	_p.A350T|NLRP1_	NM_033004	NP_127497	Q9C000	NALP1_HUMAN	NACHT.		9	CCAGGCTTCCT	0.582	
+	30	4848		NM_020877	NP_065928	Q9P225	DYH2_HUMAN	n (By similarity).		13	TTGGCGATGTG	0.607	
-	12	2052	rf68_uc010cnv.2_	NM_025099	NP_079375	Q2NKJ3	CTC1_HUMAN			0	TTCTCACGTCCC	0.547	
-	1	357		NM_152599	NP_689812	Q8IWD5	MFS6L_HUMAN	ical; (Potential).		1	TTTTGGCCAGG	0.627	
-	15	1701	_Mutation_p.E525	NM_001100112	NP_001093582	Q9UKX2	MYH2_HUMAN	osin head-like.		14	GAGCTCGATGC	0.433	
+	36	7170	o.2_Missense_Mu	NM_001372	NP_001363	Q9NYC9	DYH9_HUMAN		p.E2368K(1)	20	CCTAAGGAAATT	0.493	rs140313224
-	19	2408	pp.1_Missense_M	NM_006311	NP_006302	O75376	NCOR1_HUMAN			5	TCTTCTGGATTT	0.388	
-	1	111	10vyc.1_RNA|CCD	NM_182568	NP_872374					2	CTCCCCGCTTT	0.642	
-	21	2828		NM_000625	NP_000616	P35228	NOS2_HUMAN	-binding FR-type.		4	TGTCTCTCAGGC	0.637	
-	39	5913	p.Q1461*|MYO18	NM_078471	NP_510880	Q92614	MY18A_HUMAN	Potential.		0	AGCCTGCAGGC	0.562	
+	6	594	K1_uc010wbf.1_M	NM_020791	NP_065842	Q7L7X3	TAOK1_HUMAN	rotein kinase.		4	CACATGGTGCT	0.284	
+	20	3905	e_Mutation_p.P10	NM_001304	NP_001295	O75976	CBPD_HUMAN	ntial).|Carboxypeptidase-lik		2	TTTGCCAAGGG	0.378	
-	11	4189		NM_001004334	NP_001004334	Q6PRD1	GP179_HUMAN	lasmic (Potential).		3	ATCCTCGCCTC	0.562	
+	5	751	AP1_uc010wgs.1	NM_003632	NP_003623	P78357	CNTP1_HUMAN	ellular (Potential).		8	TCGACGGCGAC	0.627	
-	3	237	1_5'UTR|GPATCH	NM_001002909	NP_001002909	Q9UKJ3	GPTC8_HUMAN	G-patch.		4	CCAATCCCTGG	0.388	
+	10	777	fd.2_Missense_Mu	NM_003835	NP_003826	O75916	RGS9_HUMAN	rotein gamma.		4	CAGTCGTTGCT	0.353	
-	4	902	v.2_Missense_Mu	NM_182511	NP_872317	Q8IUK8	CBLN2_HUMAN	C1q.		0	TAGAGGAAACA	0.507	
-	8	772		NM_017550	NP_060020	Q8N344	MIER2_HUMAN	ELM2.		0	AGGCCCGGCCA	0.677	
+	17	3032	M13_uc002lvx.1_3	NM_182973	NP_892018	Q7Z410	TMPS9_HUMAN	Potential).|Peptidase S1 3.		2	TGGGGGACCCC	0.622	
+	4	1336	a.1_Missense_Mu	NM_173480	NP_775751	Q68EA5	ZNF57_HUMAN	2H2-type 9.		3	GAACAATGTGG	0.428	
+	4	1371	a.1_Missense_Mu	NM_173480	NP_775751	Q68EA5	ZNF57_HUMAN	2H2-type 9.		3	ATTCCGAGGTC	0.428	rs149690257
+	4	1386	a.1_Missense_Mu	NM_173480	NP_775751	Q68EA5	ZNF57_HUMAN	2H2-type 9.		3	GAGGACGCACA	0.438	rs148390269
-	5	533	_p.R146G|STAP2_	NM_001013841	NP_001013863	Q9UGK3	STAP2_HUMAN	SH2.		1	TGCACGGCGCG	0.647	rs143484969
+	1	998	uc002mbg.1_RNA	NM_018708	NP_061178	Q9BSK4	FEM1A_HUMAN			0	TCTTACGAAAGC	0.607	
-	32	5006	w.2_Missense_Mu	NM_002850	NP_002841	Q13332	PTPRS_HUMAN	lasmic (Potential).|Tyrosine		4	CACCGGCACTG	0.642	
-	5	738	C25A41_uc010du	NM_173637	NP_775908	Q8N5S1	S2541_HUMAN	Solcar 2.		0	CGTCCGACGCA	0.502	
-	40	4797	2_Missense_Muta	NM_000064	NP_000055	P01024	CO3_HUMAN	NTR.		5	CTGTCCAACCT	0.602	

+	18	2380	ı_p.S762F|EMR1_	NM_001974	NP_001965	Q14246	EMR1_HUMAN	lasmic (Potential).	5	GGCTTTCCAGTG	0.423
-	3	18371		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).	57	GGTGTTGATGTG	0.483
-	3	17651		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).	57	CTGTCCTGGAG	0.498
-	1	8092		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	ch.|Extracellular (Potential).	57	TACTTGGAAATT	0.473
+	4	511	_Mutation_p.R74C	NM_000527	NP_000518	P01130	LDLR_HUMAN	ential).|LDL-receptor class	4	GAGTTTCGCTGC	0.622
-	7	1560		NM_138783	NP_620138	Q96CK0	ZN653_HUMAN	C2H2-type 2.	0	GCCAGGATGAG	0.572
+	4	1300	dyf.2_Missense_M	NM_145295	NP_660338	Q7L945	ZN627_HUMAN	C2H2-type 9.	1	CTATGATTGTAA	0.413
+	4	1027	ym.1_Missense_M	NM_001136501	NP_001129973	Q08AG5	ZN844_HUMAN	C2H2-type 7.	0	TCCATTCCTTTC	0.398
+	4	1651	ym.1_Missense_M	NM_001136501	NP_001129973	Q08AG5	ZN844_HUMAN		0	GAAACCCTATGA	0.413
-	4	1382		NM_005815	NP_005806	Q9Y2A4	ZN443_HUMAN	C2H2-type 10.	1	TGCTTGCATTCAT	0.413
-	4	1409	709_uc002mtx.3_I	NM_144976	NP_659413	Q8TBZ8	ZN564_HUMAN	C2H2-type 11.	1	AAGGCTCTACCA	0.433
+	2	281_282	ı_p.P48S|MAST1_	NM_014975	NP_055790	Q9Y2H9	MAST1_HUMAN		7	CACTCCCCGCTG	0.644
+	12	1706	ızk.3_Missense_M	NM_032433	NP_115809	Q96JL9	ZN333_HUMAN	C2H2-type 6.	3	CGTGCACAAGAG	0.512
-	6	1134_1135	.C1A6_uc010xod.1	NM_005071	NP_005062	P48664	EAA4_HUMAN	ical; (Potential).	6	GCATGCCCCCAA	0.584
-	2	381	2nbg.3_Missense_	NM_052890	NP_443122	Q96PD5	PGRP2_HUMAN		3	GGCAGGGATCC	0.592
-	9	1083	_p.A196S|CYP4F2_	NM_001082	NP_001073	P78329	CP4F2_HUMAN		2	GCTTTGCAAGGT	0.597
-	9	1059	ıtation_p.L188F|CY	NM_001082	NP_001073	P78329	CP4F2_HUMAN		2	GGAGAGACCAC	0.602
+	3	428	ı_p.R69Q|RAB8A_	NM_005370	NP_005361	P61006	RAB8A_HUMAN		1	GGAACGGTTTC	0.458
+	9	1164	3B_uc002nez.1_M	NM_015260	NP_056075	O75182	SIN3B_HUMAN	ith NCOR1 (By similarity).	2	GGGACGGGATA	0.542
+	4	1003		NM_052852	NP_443084	Q96H40	ZN486_HUMAN	C2H2-type 5.	1	AAAATTCATACTG	0.378
-	4	1480	pc.1_Missense_M	NM_001076675	NP_001070143	Q68DY1	ZN626_HUMAN	C2H2-type 10.	1	TTCTCCTATGTG	0.373
-	7	2712		NM_001080409	NP_001073878				2	ATGTTTCATAAGG	0.353
-	5	689		NM_001080409	NP_001073878				2	TTAAAAGCTTTG	0.388
+	2	354	ı_p.R53H|LSM14A	NM_001114093	NP_001107565	Q8ND56	LS14A_HUMAN		1	CAGATCGTCCAA	0.428
-	13	1051	oiy.1_Missense_M	NM_007181	NP_009112	Q92918	M4K1_HUMAN		8	CCGAGGGATAG	0.617
+	4	561	.2_Intron|CYP2B6	NM_000767	NP_000758	P20813	CP2B6_HUMAN		2	TCTTTGGAAAAC	0.502
+	11	1535	nse_Mutation_p.P	NM_021913	NP_068713	P30530	UFO_HUMAN	cellular (Potential).	13	CGTGGCCCTGG	0.567
-	7	803	3_5'Flank|PHLDB3	NM_014297	NP_055112	O95571	ETHE1_HUMAN		0	CACAGCGCATGT	0.522
-	1	44	10ejp.1_Missense_	NM_001102597	NP_001096067	Q6UY09	CEA20_HUMAN		2	CCAGTGGTGTC	0.552
+	3	729	02pbp.2_5'Flank|C	NM_012099	NP_036231	O15446	RPA34_HUMAN		4	CGCTATCGAGTC	0.632
-	7	805	bu.1_Missense_M	NM_001983	NP_001974	P07992	ERCC1_HUMAN		2	AGGTCCGCTGGT	0.627
-	5	2086	ydj.1_Missense_M	NM_001102657	NP_001096127	Q6ZNA1	ZN836_HUMAN	C2H2-type 13.	0	TTATGAATTGAA	0.383
-	5	2067	ydj.1_Missense_M	NM_001102657	NP_001096127	Q6ZNA1	ZN836_HUMAN	C2H2-type 13.	0	CACTGTAATTGA	0.388
-	4	2233	_p.N652Y|ZNF28_	NM_006969	NP_008900	P17035	ZNF28_HUMAN	C2H2-type 18.	1	CAAGGTTTGACAT	0.408
-	5	1439	k.1_Intron|ZNF816	NM_001031665	NP_001026835	Q0VGE8	ZN816_HUMAN	C2H2-type 6.	0	ATTTCTGACTGA	0.398
+	7	1666	_p.L349R|ZNF761_	NM_001008401	NP_001008401	Q86XN6	ZN761_HUMAN	C2H2-type 7.	1	GTAGACTTCATA	0.373
+	7	1680	_p.K354Q|ZNF761_	NM_001008401	NP_001008401	Q86XN6	ZN761_HUMAN		1	GGAGAGAAACCT	0.368
+	7	1911	p.R431W|ZNF761_	NM_001008401	NP_001008401	Q86XN6	ZN761_HUMAN	C2H2-type 10.	1	AGACATAGGAGA	0.413
+	4	517	2qid.2_Missense_M	NM_004829	NP_004820	O76036	NCTR1_HUMAN	ar (Potential).|Ig-like 2.	2	AGGGAAGATCCA	0.582
+	7	2143	_p.P662L|NLRP2_	NM_017852	NP_060322	Q9NX02	NALP2_HUMAN		2	TGCTTCCTTTCTG	0.453
-	6	1176	_p.V190E|PTPRH_	NM_002842	NP_002833	Q9HD43	PTPRH_HUMAN	tential).|Fibronectin type-III	4	TCCCCACCCAC	0.512
-	7	2854	b.2_Missense_Mu	NM_145007	NP_659444	P59045	NAL11_HUMAN		6	GGGCTCGTGCA	0.498
-	6	2226		NM_004304	NP_004295	Q9UM73	ALK_HUMAN	ss A.|Extracellular (Potentia	1218	GTGAAGGAGCTC	0.587
-	23	4009	_p.P643S|DHX57_	NM_198963	NP_945314	Q6P158	DHX57_HUMAN		3	CAGCGGGTACA	0.493
-	1	521		NM_148962	NP_683765	Q8TDS5	OXER1_HUMAN	Name=2; (Potential).	1	GCGGAGGGGCA	0.617
-	17	4881	XN1_uc002rxe.3_M	NM_001135659	NP_001129131	P58400	NRX1B_HUMAN		2	ACACCTTGATTG	0.443
+	1	70	sda.2_Missense_M	NM_203437	NP_982261	Q6ULP2	AFTIN_HUMAN		2	CATCCCCACCAC	0.383

+	1	1831	z.1_Nonsense_Mu	NM_144993	NP_659430	O43151	TET3_HUMAN			0	GCCCCTGAGAGC	0.572	
-	8	1379	XL3_uc002smq.1_	NM_032603	NP_115992	P58215	LOXL3_HUMAN	SRCR 4.		0	CCAGGTCCCCCT	0.632	
+	5	494	_p.P137S|REG3G	NM_198448	NP_940850	Q6UW15	REG3G_HUMAN	C-type lectin.		0	AAAAATCCCTCC	0.517	
+	1	232	.2_Intron|SH2D6_	NM_198482	NP_940884	Q7Z4S9	SH2D6_HUMAN	Pro-rich.		1	cccaccccaccccacc	0.517	
+	6	1346	Intron|TEKT4_uc0	NM_144705	NP_653306	Q8WW24	TEKT4_HUMAN			3	AGAAGTGCATGG	0.612	
-	8	844	KRD23_uc002sxc	NM_144994	NP_659431	Q86SG2	ANR23_HUMAN			1	GCGTTCCGCACC	0.682	
-	10	3146		NM_207362	NP_997245	Q6NV74	CB055_HUMAN			0	GCTTGAGATTTCT	0.468	
+	5	1047	fiz.2_Missense_M	NM_003853	NP_003844	O95256	I18RA_HUMAN	1.|Extracellular (Potential).		5	GTCCAGCGGTAA	0.294	rs139554960
+	12	1775	.2_5'UTR|RGPD4_	NM_182588	NP_872394	Q7Z3J3	RGPD4_HUMAN			2	CTAAGAGCCCAG	0.333	
+	2	428		NM_002410	NP_002401	Q09328	MGT5A_HUMAN	enal (Potential).		3	ATTTTGCAGCGC	0.428	
-	6	1029	s.2_Missense_Mu	NM_002349	NP_002340	O60449	LY75_HUMAN	Potential).|C-type lectin 1.		0	AGCATCCATTCTT	0.453	
+	3	901	1_uc002uhm.2_3'	NM_178120	NP_835221	P56177	DLX1_HUMAN			0	TATATCCCCAGCT	0.632	
-	275	72987	50R|TTN_uc010z	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN			153	AGTTCCTTTGGG	0.463	
-	266	59479	_uc010zfi.1_Misse	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN			153	CACAGCGCAAG	0.398	
-	208	41052	.1_Missense_Muta	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN			153	AGGTGGATCCC	0.438	
-	46	13024	N_uc010zfi.1_Intr	NM_133379	NP_596870	Q8WZ42	TITIN_HUMAN			153	ATATTTTCCATAA	0.388	
+	10	2478	ftr.2_Missense_Mu	NM_001204	NP_001195	Q13873	BMPR2_HUMAN	.|Cytoplasmic (Potential).		9	AACCATCCCACT	0.413	
+	3	285	10ziu.1_5'Flank|E	NM_001037663	NP_001032752	P24534	EF1B_HUMAN	ST C-terminal.		0	GTGTCCAGCCCA	0.468	
+	8	653	_Mutation_p.G10	NM_015575	NP_056390	Q6Y7W6	PERQ2_HUMAN	Poly-Gly.		7	TGACAGGACGA	0.378	
-	7	700	ba.1_Intron|ADAM	NM_025220	NP_079496	Q9BZ11	ADA33_HUMAN	ellular (Potential).		4	GCGCGCTTCTC	0.622	
-	4	512	p.V120M|C20orf27	NM_001039140	NP_001034229	Q9GZN8	CT027_HUMAN			0	GCACCACGCTGA	0.617	rs148088379
-	7	619	02wmd.3_Translat	NM_019593	NP_062539	Q9NPB8	GPCP1_HUMAN			0	GCAAACGTAATCT	0.308	
+	25	2345	p.E749K|PLCB4_	NM_182797	NP_877949	Q15147	PLCB4_HUMAN	C2.	p.E737K(1)	15	CGTAAGGAATTCC	0.408	
-	3	1149	se_Mutation_p.F8	NM_018848	NP_061336	Q9NPJ1	MKKS_HUMAN			0	CACTGAAGCTTG	0.423	
+	4	1716	zrf.1_Missense_M	NM_014962	NP_055777	Q9Y2F9	BTBD3_HUMAN			3	TTTCCCGTATGGT	0.493	
-	10	1999		NM_016649	NP_057733	Q9H501	ESF1_HUMAN	Lys-rich.		1	CCCAAGGGGTCA	0.284	
+	2	63	tj.1_RNA|FRG1B_uc010gdr.1_RNA|FRG1B_uc010ztk.1_Intron							0	AGAATCGCCCTG	0.353	rs7266938
-	2	1748	_Missense_Mutati	NM_000557	NP_000548	P43026	GDF5_HUMAN			0	GAAGAGGATGCT	0.567	
+	16	2750		NM_016436	NP_057520	Q9BVI0	PHF20_HUMAN			1	CCTTTCCCCGCC	0.607	
-	4	635	s.1_Missense_Mut	NM_004613	NP_004604	P21980	TGM2_HUMAN			3	TCCAAGGTATGTT	0.582	
+	2	464		NM_030777	NP_110404	O95528	GTR10_HUMAN	Name=4; (Potential).		1	ATCTACGTGTCAG	0.642	
-	15	2491	ND8_uc002xtb.1_	NM_012408	NP_036540	Q9ULU4	PKCB1_HUMAN			5	GGTGGAGTTTTA	0.557	
+	18	3650	m.2_Missense_Mu	NM_181659	NP_858045	Q9Y6Q9	NCOA3_HUMAN	etyltransferase.		5	AATTTTCCTCTCC	0.517	
+	13	1298	283S|ARFGAP1_	NM_018209	NP_060679	Q8N6T3	ARFG1_HUMAN			1	GCCGTGCCCACT	0.697	
-	5	849	l.2_Nonsense_Mu	NM_006806	NP_006797	Q14201	BTG3_HUMAN			0	TCCCTCGATACAT	0.413	
+	3	1528	f.1_Missense_Mu	NM_053277	NP_444507	Q96NY7	CLIC6_HUMAN			2	CAGTGGACCTG	0.378	
+	3	397	X2_uc011aer.1_R	NM_002463	NP_002454	P20592	MX2_HUMAN			2	GGTGCGCCCCT	0.637	
+	19	1796	bx.2_Missense_M	NM_002606	NP_002597	O76083	PDE9A_HUMAN			2	GAAGTCCAGAG	0.502	
-	1	321		NM_014406	NP_055221	Q96SF2	TCPQM_HUMAN			1	GGCTCTCCCTTG	0.657	
+	16	3211	R2_uc002zml.2_	NM_031413	NP_113601	Q9BXF3	CECR2_HUMAN			2	GGGGCGCTCTA	0.622	
-	3	1594	ue.2_Missense_M	NM_004173	NP_004164	O43246	CTR4_HUMAN	ical; (Potential).		2	ATGTAACCCCAG	0.562	
+	43	7629	18B_uc011aka.1_	NM_032608	NP_115997	Q8IUG5	MY18B_HUMAN			12	CTGGATCAGCCA	0.527	
-	1	1710	nse_Mutation_p.	NM_014323	NP_055138	Q9HBE1	PATZ1_HUMAN			2	CTGGTCCGGCTC	0.597	
-	18	2529	aqt.1_Nonsense_	NM_153609	NP_705837	Q8IU80	TMPS6_HUMAN	.|Extracellular (Potential).		6	CTGGATCCAGCT	0.647	
+	10	1879	aye.2_Missense_	NM_021096	NP_066919	Q9P0X4	CAC1I_HUMAN	plasmic (Potential).		2	TGTGGCGGGAG	0.542	
+	5	2054_2055	nse_Mutation_p.	NM_001162501	NP_001155973	Q9UPQ9	TNR6B_HUMAN			0	GGACCCCAGGG	0.52	
+	7	789	k.1_Missense_Mut	NM_152613	NP_689826	Q6ICG8	WBP2L_HUMAN	eat of Y-G-X-P-P-X-G.|9.|		2	CTCTCGGATATG	0.612	

+	11	1444	e.2_Missense_Mu	NM_014346	NP_055161	Q8WUA7	TB22A_HUMAN	ab-GAP TBC.		1	CCATCCGCCTGT	0.637	
+	5	619	AC_uc011aya.1_M	NM_003149	NP_003140	Q99469	STAC_HUMAN			4	TGTGGCAATAAG	0.582	
+	11	1201	a.1_Missense_Mu	NM_003149	NP_003140	Q99469	STAC_HUMAN			4	CTCAGTGGAAAA	0.443	
+	10	1763_1764	e_Mutation_p.S57	NM_004803	NP_004794	Q9Y267	S22AE_HUMAN	lasmic (Potential).		0	CCACTCCTCACA	0.619	
+	6	777_778	se_Mutation_p.G6	NM_145755	NP_665698	Q8NDW8	TT21A_HUMAN	TPR 4.		1	GCCCTGGAGGT	0.559	
-	1	836	mg.2_Intron|CYP8	NM_004391	NP_004382	Q9UNU6	CP8B1_HUMAN			2	GAAGCGAAAGA	0.512	
+	1	642	vh.2_Missense_M	NM_177939	NP_808808	Q9NXG6	P4HTM_HUMAN	enal (Potential).		2	ACACCGTGCCC	0.687	
+	4	309	1_5'Flank|RNF123	NM_022064	NP_071347	Q5XPI4	RN123_HUMAN	B30.2/SPRY.		7	AGGTGGACAAT	0.582	
-	17	3501_3502	AGI1_uc003dmp.2	NM_001033057	NP_001028229	Q96QZ7	MAGI1_HUMAN	eraction with FCHSD2.		6	GCTTCGGGCCTG	0.569	
+	5	1062	pn.2_Missense_M	NM_145037	NP_659474	Q969Y0	FA55C_HUMAN			3	TGGAGACTACCT	0.498	
-	9	1426		NM_199420	NP_955452	O75417	DPOLQ_HUMAN	case C-terminal.		11	CTTGACGAAAGG	0.388	rs140193287
+	34	5232	ehi.2_Missense_M	NM_001024660	NP_001019831	O60229	KALRN_HUMAN	SH3 1.		6	GGTCCCCAGCA	0.652	
-	4	798	11blv.1_Intron|SLC	NM_005630	NP_005621	Q92959	SO2A1_HUMAN	Name=4; (Potential).		1	GGGCAACCACC	0.592	
-	5	1014	e_Mutation_p.H19	NM_033169	NP_149359	O75752	B3GL1_HUMAN	enal (Potential).		1	CTGAGTGGTTTA	0.348	
-	10	1546	R49_uc011bpd.1_M	NM_178824	NP_849146	Q8IV35	WDR49_HUMAN	WD 6.		3	AAAATTCAGCCA	0.383	
-	5	1030	w.1_Missense_Mu	NM_001146276	NP_001139748	Q6PIU2	NCEH1_HUMAN	enal (Potential).		0	GTTGCCTTTGAA	0.458	
-	6	798	O_uc003fop.2_Int	NM_000460	NP_000451	P40225	TPO_HUMAN		p.L195P(1)	1	TGGGAGCTCGT	0.567	
-	26	2984	13A4_uc010hzi.2_	NM_032279	NP_115655	Q4VNC1	AT134_HUMAN	cellular (Potential).		2	CTGAAAGGCACC	0.398	
-	2	7089	C4_uc003fvp.2_Int	NM_018406	NP_060876	Q99102	MUC4_HUMAN			0	TGACAGGAAGA	0.597	
-	2	6974	C4_uc003fvp.2_Int	NM_018406	NP_060876	Q99102	MUC4_HUMAN			0	CGTGACCTGTGG	0.577	
-	2	5443	C4_uc003fvp.2_Int	NM_018406	NP_060876	Q99102	MUC4_HUMAN			0	GGTGGCGTGACC	0.587	rs76596008
-	8	1549	GC1A_uc011bxp.	NM_013261	NP_037393	Q9UBK2	PRGC1_HUMAN			8	CTGCTTCGTCGT	0.473	
+	1	195	df.2_Missense_M	NM_012108	NP_036240	Q9ULZ2	STAP1_HUMAN	PH.		0	GGTCAGGATACC	0.378	
-	32	7607	hgq.2_Missense_M	NM_032217	NP_115593	O75179	ANR17_HUMAN			10	GCTTGATGTTGT	0.463	
+	6	816_817	p.A255V|AIMP1_	NM_001142415	NP_001135887	Q12904	AIMP1_HUMAN			0	TGATGCTTTCCC	0.366	
+	3	1147		NM_001977	NP_001968	Q07075	AMPE_HUMAN	cellular (Potential).		5	GTGGATGATAAAT	0.353	
+	27	4540	ins.1_Missense_M	NM_015312	NP_056127	Q2LD37	K1109_HUMAN			12	CAACCCGTGATG	0.393	
-	2	1085	e_Mutation_p.L34	NM_178835	NP_849157	Q17R98	ZN827_HUMAN	Pro-rich.		0	AATTCCAGGGAT	0.333	
+	2	907	e_Mutation_p.G87	NM_012464	NP_036596	O43897	TLL1_HUMAN			7	CCTTTGGAAACC	0.333	
+	9	1354		NM_000128	NP_000119	P03951	FA11_HUMAN	Apple 4.		0	GCAACGAAGGG	0.502	
+	17	2770	3jdk.1_Missense_	NM_139056	NP_620687	Q8TE57	ATS16_HUMAN	TSP type-1 2.		8	ATCGTGCGCTCT	0.637	
+	34	5027	p.P1125R|SPEF2_	NM_024867	NP_079143	Q9C093	SPEF2_HUMAN			4	CCACCCAGACA	0.463	
-	5	939		NM_173489	NP_775760	Q7Z745	HTRB2_HUMAN			8	CAGAAAGTCCCC	0.453	
+	1	2052	g.1_Intron|SNX18_	NM_052870	NP_443102	Q96RF0	SNX18_HUMAN	BAR.		0	GAGTACCTTTGAT	0.413	
+	6	1752	3jrj.3_Splice_Site_	NM_022913	NP_075064	Q86WP2	GPBP1_HUMAN			2	TGTGGGGTAAGT	0.328	
+	4	599	L21_uc003lbc.2_	NM_012159	NP_036291	Q9UKT6	FXL21_HUMAN	LRR 2.		1	ATGATCCTTCATT	0.358	
+	1	1678	CDHA1_uc003lgz.	NM_018900	NP_061723	Q9Y5I3	PCDA1_HUMAN	|Extracellular (Potential).		1	GAGAACGACAAC	0.672	
+	3	1945		NM_019119	NP_061992	Q9Y5E1	PCDB9_HUMAN	r (Potential).|Cadherin 6.		0	ATGGCGAGCCT	0.711	
+	1	397	B12_uc011dak.1_	NM_018932	NP_061755	Q9Y5F1	PCDBC_HUMAN	r (Potential).|Cadherin 1.		3	TCTAATGATAACA	0.527	
+	1	2216	DHGB2_uc003ljs.	NM_003736	NP_003727	Q9UN71	PCDGG_HUMAN	lasmic (Potential).		0	TTCCCCCCAACT	0.517	
-	5	1216	1_5'UTR|GRM6_u	NM_000843	NP_000834	O15303	GRM6_HUMAN	cellular (Potential).		8	AGGGATCGAGTC	0.532	
+	10	1055	e_Mutation_p.W9	NM_001040274	NP_001035364	Q5T4T6	SYC2L_HUMAN			2	TAAATGGTTTGAT	0.368	
+	4	740	p.E136K|EDN1_u	NM_001955	NP_001946	P05305	EDN1_HUMAN			1	ATTATGGAGAAA	0.353	
+	5	762	_3'UTR|MOG_uc	NM_206809	NP_996532	Q16653	MOG_HUMAN	lasmic (Potential).		1	CCACCGGACTT	0.443	
+	18	2370	_uc011dna.1_Miss	NM_020442	NP_065175	Q5ST30	SYVM_HUMAN			4	CCAGATCCTGAT	0.557	
-	6	874	wq.2_5'Flank|CLI	NM_001288	NP_001279	O00299	CLIC1_HUMAN	ST C-terminal.		2	TCCCCGGAAGG	0.577	
+	34	4792		NM_002224	NP_002215	Q14573	ITPR3_HUMAN	lasmic (Pote	p.C1525F(1)	19	GAGGCCTGCATC	0.652	

-	4	1063	ojs.2_Missense_M	NM_024294	NP_077270	Q9H6K1	CF106_HUMAN			3	TGCTGGGAGAC	0.502	
+	14	2891	1BP1_uc010jvn.2	NM_017754	NP_060224	Q6BDS2	URFB1_HUMAN			3	GCATCCTGCAC	0.512	
-	5	1502		NM_003740	NP_003731	O95279	KCNK5_HUMAN			2	AGGGGCCCGTG	0.617	
-	5	642		NM_002630	NP_002621	P20142	PEPC_HUMAN			0	CCATGCCCTGC	0.627	
+	2	162	u.2_Missense_Mu	NM_201521	NP_958929	Q9NSK0	KLC4_HUMAN			4	GGCTGGTCAGC	0.652	
-	4	1663	318_uc003ouw.2_	NM_014345	NP_055160	Q5VUA4	ZN318_HUMAN			7	GTCGGGAAAGC	0.488	
-	7	1333	p.1_Missense_Mu	NM_014611	NP_055426	Q9NU22	MDN1_HUMAN			10	AGGGGGCATAG	0.463	
-	1	307		NM_175747	NP_786923	Q7RTU3	OLIG3_HUMAN	Poly-His.		0	ggtggtggcggtggtgg	0.493	
-	2	517	_p.P118L|GNA12_	NM_007353	NP_031379	Q03113	GNA12_HUMAN			1	GCCAAGGAATG	0.483	
-	3	573		NM_001004320	NP_001004320	Q6ZNB7	ALKMO_HUMAN	istidine box-1.		0	ATGAGCCATAC	0.313	
-	2	328		NM_022150	NP_071433	Q9HCQ7	RFRP_HUMAN			1	CGTTCCTCCCA	0.448	
-	2	1326	hr.2_Missense_Mu	NM_002192	NP_002183	P08476	INHBA_HUMAN			6	GTGAGGACCCG	0.567	
+	3	1320		NM_198570	NP_940972	Q2TAL6	VWC2_HUMAN	VWFC 2.		0	GTGTCCCCAGA	0.567	
+	2	114	_p.V39M|MRPS17	NM_182633	NP_872439	Q8N859	ZN713_HUMAN	KRAB.		2	TGGCCGTGGAC	0.517	
-	4	1195	zr.2_Missense_Mu	NM_178558	NP_848653	Q8NEM1	ZN680_HUMAN	2H2-type 6.		1	ATTTTCTTATGTT	0.348	
-	4	1188	zr.2_Missense_M	NM_178558	NP_848653	Q8NEM1	ZN680_HUMAN	2H2-type 6.		1	TATGTTTAGTAAG	0.348	
+	4	533	urn.2_RNA|ZNF4	NM_145115	NP_660090	Q6NSZ9	ZN498_HUMAN	SCAN box.		2	TCGTCGGTGGC	0.612	
+	3	1893	C17_uc010lho.1_	NM_001040105	NP_001035194	Q685J3	MUC17_HUMAN	X approximate tandem re		27	CAACTGCTGAA	0.483	
+	3	7480	C17_uc010lho.1_	NM_001040105	NP_001035194	Q685J3	MUC17_HUMAN	ich.|59 X approximate tand		27	CACCCTTTCCA	0.522	
+	3	9432	C17_uc010lho.1_	NM_001040105	NP_001035194	Q685J3	MUC17_HUMAN	ich.|50.|59 X approximate t		27	TTTCAACAACT	0.498	
+	3	9658	C17_uc010lho.1_	NM_001040105	NP_001035194	Q685J3	MUC17_HUMAN	ich.|59 X approximate tand		27	AGCCACTTCAT	0.507	
+	5	1788	ET_uc011kng.1_M	NM_000245	NP_000236	P08581	MET_HUMAN	ellular (Potential).		159	CCCACCCTTTG	0.532	
-	15	1860		NM_004333	NP_004324	P15056	BRAF_HUMAN	rotein kinas	R603>I(2)|p.T	18290	GATTTCACTGTA	0.368	
-	52	13651	x.2_Nonsense_Mu	NM_170606	NP_733751	Q8NEZ4	MLL3_HUMAN			63	GCATCGAAATC	0.438	
-	42	6736	p.P1508S|CSMD1	NM_033225	NP_150094	Q96PZ7	CSMD1_HUMAN	r (Potential).|Sushi 12.		25	CCCAGGATAAC	0.448	
-	5	4018		NM_001080826	NP_001074295	Q86YV5	SG223_HUMAN			0	CTCCTCCGAGG	0.677	
-	3	1897		NM_173683	NP_775954	Q5GH73	XKR6_HUMAN			2	ATATCGAATGC	0.458	
+	1	348		NM_054028	NP_473369	Q96KT7	AMCL2_HUMAN	.|Helical; (Potential).		0	CTGTCGATGCC	0.637	
+	9	1530	ye.1_Missense_M	NM_001008539	NP_001008539	P52569	CTR2_HUMAN	lasmic (Potential).		3	GGGATCGTCTC	0.507	
-	3	617	_p.T55R|REEP4_	NM_025232	NP_079508	Q9H6H4	REEP4_HUMAN	ical; (Potential).		1	TGTCTGTAACG	0.597	
+	5	617	_p.E54K|ADAMD	NM_014479	NP_055294	O15204	ADEC1_HUMAN			2	TAAATGAAAAG	0.289	
+	6	520	CK5_uc003xef.2_	NM_024940	NP_079216	Q9H7D0	DOCK5_HUMAN			3	GTGGCGGTCCC	0.483	
+	2	689	.E58K|NRG1_uc	NM_013964	NP_039258	Q02297	NRG1_HUMAN	Potential).|Ig-like C2-type.		0	GGTGTGAAACC	0.383	
-	9	808	M2_uc011lck.1_	NM_001464	NP_001455	Q99965	ADAM2_HUMAN	otential).|Peptidase M12B.		2	ATAACTCATTAG	0.284	
-	6	984	xrf.3_Missense_M	NM_014781	NP_055596	Q8TDY2	RBCC1_HUMAN			11	ATGTTCATCATG	0.353	
+	12	1447	_p.E474K|PREX2_	NM_024870	NP_079146	Q70Z35	PREX2_HUMAN			17	GAAATGAGATG	0.348	
+	9	1099	ar.2_Missense_Mu	NM_004133	NP_004124	Q14541	HNF4G_HUMAN			1	ATGATCGGCAG	0.453	
+	27	4097	.E1275K|RIMS2_	NM_014677	NP_055492	Q9UQ26	RIMS2_HUMAN	C2 2.		15	CTTTCGAAGAG	0.368	
-	1	535		NM_015193	NP_056008	Q7LC44	ARC_HUMAN			1	CATCTCGCGCT	0.692	
-	2	310		NM_015117	NP_055932	Q8IXZ2	ZC3H3_HUMAN			1	GCAACGGCCGC	0.642	
-	4	1087		NM_001145196	NP_001138668	Q5VVP1	F75A6_HUMAN			0	GTCATTTGATTT	0.428	
-	4	1083		NM_001145196	NP_001138668	Q5VVP1	F75A6_HUMAN			0	TTTGATTTGTAA	0.418	
+	4	1135	tk.2_Missense_Mu	NM_006648	NP_006639	Q9Y3S1	WNK2_HUMAN	rotein kinase.		12	TGGACGTCTAT	0.602	
+	30	3580	_p.S121T|KIAA15	NM_020893	NP_065944					7	AGAGAGTTTAT	0.264	
+	1	698		NM_001004483	NP_001004483	Q8NGS7	O13C8_HUMAN	lasmic (Pot	p.G233E(1)	2	TGAAGGAAAAC	0.418	rs150858980
-	1	115		NM_001001956	NP_001001956	Q8NGT0	O13C9_HUMAN	Name=1; (Potential).		0	CAGAAGGATGA	0.433	rs150686997
-	2	696	f.2_Missense_Mut	NM_002160	NP_002151	P24821	TENA_HUMAN			7	ACAGCCACAGG	0.587	

+	17	2283	nvs.1_Missense_M	NM_000177	NP_000168	P06396	GELS_HUMAN	, Ca-sensitive (Potential).		3	ATCGGCGGACGC	0.572	rs141510612
+	11	1890	ouu.2_Missense_M	NM_005094	NP_005085	Q6P1M0	S27A4_HUMAN			0	GTGGCCGTGTATC	0.642	
-	1	446		NM_033387	NP_203745	Q5JUQ0	FA78A_HUMAN			1	TCCCTTCCCGGA	0.572	
-	2	769	1mdf.1_Missense_	NM_020385	NP_065118	Q9GZR2	REXO4_HUMAN			0	ACTCGGTGGGTG	0.542	
+	5	567	IA1_uc011mjd.1_M	NM_000284	NP_000275	P08559	ODPA_HUMAN			1	AGGACGAAAAGC	0.488	
+	2	373	_p.R59H|MBTPS2	NM_206923	NP_996806	O15391	TYY2_HUMAN			2	TCAATCGTGCCTT	0.403	
-	5	723	_Mutation_p.S189	NM_018684	NP_061154	Q9NQZ6	ZC4H2_HUMAN			1	TTCCGGGACCGA	0.488	
+	6	250	ya.2_Missense_Mu	NM_004312	NP_004303	P36575	ARRC_HUMAN			4	ATGGCCGTGATGA	0.542	
-	2	1104		NM_152694	NP_689907	Q8N8U3	ZCHC5_HUMAN			1	CAGTGGGATACAC	0.507	
+	5	1226	p.V142G|GPRASP	NM_014710	NP_055525	Q5JY77	GASP1_HUMAN			2	AACTGGTTAATAC	0.458	
-	5	820	4ffl.2_Missense_M	NM_001011543	NP_001011543	P43363	MAGAA_HUMAN	MAGE.		0	CAGTCACCTTTTC	0.458	
+	2	868	3202-2|MI0014253	NM_003492	NP_003483	Q14656	TM187_HUMAN			0	CGTGCCGCGGTG	0.687	
+	10	1079	k.1_Missense_Mu	NM_002631	NP_002622	P52209	6PGD_HUMAN			1	ACGCTTCCAAGAT	0.498	
-	11	2941	p.S874L|CASZ1_u	NM_001079843	NP_001073312	Q86V15	CASZ1_HUMAN			1	TGGGCGAGATGA	0.662	
-	6	853	PF1_uc010oce.1_Ir	NM_017940	NP_060410	Q3BBV0	NBPF1_HUMAN			0	AACTTACTGTTGT	0.418	
+	3	379		NM_016183	NP_057267	Q9UKD2	MRT4_HUMAN			0	CTTTTCATCTTCT	0.557	
+	13	1157	p.R316C|RPS6KA1	NM_002953	NP_002944	Q15418	KS6A1_HUMAN	kinase C-terminal.		1	TACCGTCGTGAGA	0.597	
+	49	6741_6742	01cjl.1_Missense_M	NM_015284	NP_056099	Q5T011	SZT2_HUMAN			0	CATCATCCTCATG	0.574	
+	8	1227	p.S325F|CYP4X1_	NM_178033	NP_828847	Q8N118	CP4X1_HUMAN			2	GCATCTCCTGGAT	0.512	
-	14	1723	_p.P69S|CC2D1B_	NM_032449	NP_115825	Q5T0F9	C2D1B_HUMAN			2	GACTCGGTGACT	0.632	
+	9	1175	cya.3_Missense_M	NM_001110533	NP_001104003	Q3ZCV2	CA177_HUMAN			0	GATATCGATCCCT	0.592	
+	3	484	n_p.Q15*|RAVER2_	NM_018211	NP_060681	Q9HCJ3	RAVR2_HUMAN	RRM 1.		1	ATAGTCCAGCTTC	0.368	
-	14	3346		NM_001002912	NP_001002912	Q5RHP9	CA173_HUMAN	Glu-rich.		5	CATCTTCCCTATT	0.468	
+	8	727	53_uc010owa.1_M	NM_001040033	NP_001035122	P19397	CD53_HUMAN	ical; (Potential).		0	TATATCGGAATCA	0.259	
-	3	435_436		NM_002524	NP_002515	P01111	RASN_HUMAN	GTP.	5)|p.Q61P(21)|p	2607	CTTCTTGTCCAG	0.46	554290;rs121913254
+	3	183	oyd.1_Intron|NBPF	NM_001037675	NP_001032764	Q3BBV1	NBPFK_HUMAN			0	AGTTCGTAAACCT	0.478	rs77154268
+	4	571	PF9_uc010oyg.1_Ir	NM_001039703	NP_001034792	A6NDV3	A6NDV3_HUMAN			0	AGGAGGCTGAGA	0.433	rs4068083
-	3	5721		NM_001009931	NP_001009931	Q86YZ3	HORN_HUMAN	20		3	TAACCAGAGGACT	0.557	
-	3	7594		NM_002016	NP_002007	P20930	FILA_HUMAN	Ser-rich.		16	GTTCATCGTTACG	0.587	
-	16	2228	nc.2_Missense_M	NM_001037533	NP_001032622	Q3T8J9	GON4L_HUMAN			3	GGTTGCAGGTGG	0.438	
-	11	1558	1fmd.3_Missense_	NM_001037533	NP_001032622	Q3T8J9	GON4L_HUMAN			3	ACTGTCATCCATG	0.468	
+	2	234	1_Intron|MAEL_uc	NM_032858	NP_116247	Q96JY0	MAEL_HUMAN	HMG box.		1	AAATACGCAGAAA	0.527	
+	12	1273	se_Mutation_p.S37	NM_032858	NP_116247	Q96JY0	MAEL_HUMAN			1	GCATTTCCAATTC	0.413	
-	10	1553	e.2_5'UTR|SLC9A1	NM_178527	NP_848622	Q5TAH2	S9A11_HUMAN	ical; (Potential).		2	CCAGACCACGTGA	0.383	
+	24	5463	xl.2_Missense_Mu	NM_014810	NP_055625	Q5VT06	CE350_HUMAN			4	GAAATGAGGGCA	0.428	
+	6	1174	_p.H83R|RNPEP_	NM_020216	NP_064601	Q9H4A4	AMPB_HUMAN			1	GTCAGCACATGG	0.577	
-	8	1274	se_Mutation_p.P29	NM_001017402	NP_001017402	Q13751	LAMB3_HUMAN	ninin EGF-like 1.		6	TAGAAGGGTGCAC	0.602	
-	1	492		NM_001004693	NP_001004693	Q8NGZ9	O2T10_HUMAN	cellular (Potential).		1	GAAGCTCATGGC	0.512	
+	1	98		NM_032517	NP_115906	Q6UWQ5	LYZL1_HUMAN			0	CTAAGTGGAGCAC	0.512	
-	6	905	NF248_uc001izc.2_	NM_021045	NP_066383	Q8NDW4	ZN248_HUMAN			1	TATAGGGATAATT	0.323	
+	3	479	_p.L152F|CYP2C9	NM_000771	NP_000762	P11712	CP2C9_HUMAN			6	CGCTGCCTTGTGC	0.498	
-	9	1393	P2C8_uc010qob.1	NM_000770	NP_000761	P10632	CP2C8_HUMAN			0	CAAATTCGTTTTC	0.363	
-	12	934		NM_024541	NP_078817	Q5T2E6	CJ076_HUMAN			0	CCCACCTGTGGA	0.458	
-	27	3537	xxq.2_Missense_M	NM_025145	NP_079421	Q8NDM7	WDR96_HUMAN			0	GTTGAGGAATCAC	0.328	
-	2	464	BE1_uc001mam.1	NM_005330	NP_005321	P02100	HBE_HUMAN			0	CAAAGGAAGTCAC	0.512	
+	1	342	ense_Mutation_p.F	NM_176875	NP_795344	P32239	GASR_HUMAN	cellular (Potential).		8	GGACACGAGGTG	0.647	
-	7	950	bt.2_Missense_Mu	NM_004813	NP_004804	Q9Y5Y5	PEX16_HUMAN	lasmic (Potential).		3	GCCCCAGGGGG	0.672	

+	1	164		NM_001001955	NP_001001955	Q8NGP0	OR4CD_HUMAN	lasmic (Potential).		4	TGAGATCCCCCAT	0.428	
+	59	8989_8990	1_Intron|C11orf65_	NM_000051	NP_000042	Q13315	ATM_HUMAN	PI3K/PI4K.		240	GGACTTGGTGAT	0.302	
-	4	655		NM_020373	NP_065106	Q9NQ90	ANO2_HUMAN	lasmic (Potential).		7	TGCCTCTCTGGC	0.468	
-	8	2008	p.G627E|CD163_u	NM_004244	NP_004235	Q86VB7	C163A_HUMAN	xtracellular (Potential).		8	GCAACTCCACAT	0.517	
-	7	1735	p.G536E|CD163_u	NM_004244	NP_004235	Q86VB7	C163A_HUMAN	xtracellular (Potential).		8	CCATTTCCCTCTC	0.532	
-	4	352	3_5'UTR|PLCZ1_u	NM_033123	NP_149114	Q86YW0	PLCZ1_HUMAN	EF-hand.		3	GTGATTCTTCCTT	0.308	
-	38	4585	rfg.2_Missense_M	NM_020297	NP_064693	O60706	ABCC9_HUMAN	otential).|ABC transporter 2		6	ATATTTCCTCGCT	0.408	
+	4	1816	rpq.2_Missense_M	NM_138371	NP_612380	Q96HM7	F113B_HUMAN	Pro-rich.		5	CCTCATCAGCCC	0.542	
+	15	1807		NM_017564	NP_060034	Q8WWQ8	STAB2_HUMAN	lar (Potential).|FAS1 2.		14	AATTTGGGACATC	0.388	
+	3	1119	01tpe.2_Intron|C1	NM_032829	NP_116218	Q5U5X8	CL034_HUMAN	Pro-rich.		1	GGGCCGGGGCC	0.741	
-	65	11164		NM_001109662	NP_001103132					2	CAGCGGGACGT	0.632	
+	6	885	p.E252G|ACADS_	NM_000017	NP_000008	P16219	ACADS_HUMAN			2	GGGGGAGCCAG	0.657	
+	6	892	e_Mutation_p.P49	NM_014938	NP_055753	Q9HAP2	MLXIP_HUMAN	cytoplasmic localization.		2	GCCTGGCCCAAT	0.602	
-	10	10625	P3199S|SACS_uc	NM_014363	NP_055178	Q9NZJ4	SACS_HUMAN			12	ACAAAGGAACAA	0.383	
+	7	1548	p.V159M|HNRNPA	NM_001011724	NP_001011724	Q32P51	RA1L2_HUMAN	r B domain.|RRM 2.		0	GACTCCGTGGAT	0.438	
+	2	338	_Mutation_p.T102	NM_021004	NP_066284	Q9BTZ2	DHRS4_HUMAN			1	GGCCACGGTGA	0.652	
-	9	1244	L1_uc001wxz.2_I	NM_004196	NP_004187	Q00532	CDKL1_HUMAN			2	ctataataggatgagg	0	
-	3	284	_p.G52E|RDH11_	NM_016026	NP_057110	Q8TC12	RDH11_HUMAN	lasmic (Potential).		1	GAGCTCCTGTCA	0.423	
-	1	1313		NR_003951						0	CATGATCCCTGG	0.443	
+	15	1423	asq.1_Missense_	NM_020431	NP_065164	Q9P1W3	TM63C_HUMAN			0	GCCGCTTCTTTTC	0.512	
-	8	719	XN3_uc010auh.2_	NM_004993	NP_004984	P54252	ATX3_HUMAN			0	GAGCCATCATTTC	0.423	rs75188275
+	11	1679		NM_017437	NP_059133	Q9P2I0	CPSF2_HUMAN			2	TATCAAGTATGTG	0.333	
-	111									0	CACTGCGTCTTTC	0.527	rs144392595
-	10	1383		NM_000138	NP_000129	P35555	FBN1_HUMAN	TB 2.		3	GTTATGGACTGTG	0.542	
+	12	5392	e_Mutation_p.S16	NM_013227	NP_037359	E7EX88	E7EX88_HUMAN			3	CAGCCTCCACTG	0.537	
+	4	1059		NM_001013657	NP_001013679	Q6ZNW5	VTC2_HUMAN			0	CCCGGGGAGCT	0.557	
-	2	228	_p.R23K|PRSS33_	NM_152891	NP_690851	Q8NF86	PRS33_HUMAN			0	GACTTCCTTCCC	0.617	
+	7	1467	lfy.2_Missense_Mu	NM_016524	NP_057608	Q9BSW7	SYT17_HUMAN	C2 2.		1	CGTCCTTCTTAAG	0.423	
-	3	218	_p.R30K|UMOD_u	NM_003361	NP_003352	P07911	UROM_HUMAN	EGF-like 1.		2	CACCATCCTGTG	0.572	
+	19	2153	_uc002dji.2_Misse	NM_144672	NP_653273	Q7RTW8	OTOAN_HUMAN			3	TGCCCAGACCTC	0.607	
+	2	4265		NM_014699	NP_055514	O15015	ZN646_HUMAN	2H2-type 24.		2	GGCCAGTACAGC	0.687	
-	5	605	VPS35_uc002eee.	NM_018206	NP_060676	Q96QK1	VPS35_HUMAN			0	CACTTACTCTGTT	0.358	
+	2	589	n_p.T17I|MMP2_u	NM_004530	NP_004521	P08253	MMP2_HUMAN			11	AGAATACCATCGA	0.527	
+	3	523	CF_uc010cek.2_In	NM_006565	NP_006556	P49711	CTCF_HUMAN			1	AGTAATGGAGG	0.498	
-	17	2466	w.3_Missense_Mu	NM_001145667	NP_001139139	Q92896	GSLG1_HUMAN	12.|Extracellular (Potential)		2	CACACGGAGCT	0.632	
-	9	4401	_Mutation_p.E131	NM_013275	NP_037407	Q6UB99	ANR11_HUMAN	Lys-rich.		6	CGGCTCCTGCC	0.567	
-	1	635		NM_002551	NP_002542	P47893	OR3A2_HUMAN	cellular (Pote	p.S199F(1)	1	TGCTGGAGCAG	0.552	rs140935076
-	4	1603	_p.A350T|NLRP1_	NM_033004	NP_127497	Q9C000	NALP1_HUMAN	NACHT.		9	CCAGGCTTCCT	0.582	
-	1	357		NM_152599	NP_689812	Q8IWD5	MFS6L_HUMAN	ical; (Potential).		1	TTTTGGCCAGG	0.627	
-	15	1701	_Mutation_p.E525	NM_001100112	NP_001093582	Q9UKX2	MYH2_HUMAN	osin head-like.		14	GAGCTCGATGC	0.433	
+	36	7170	o.2_Missense_Mu	NM_001372	NP_001363	Q9NYC9	DYH9_HUMAN		p.E2368K(1)	20	CCTAAGGAAATT	0.493	rs140313224
-	19	2408	pp.1_Missense_M	NM_006311	NP_006302	O75376	NCOR1_HUMAN			5	TCTTCTGGATTT	0.388	
-	1	401		NM_033059	NP_149048	Q9BYQ6	KR411_HUMAN	C-[GIKRQVHEL]- [SPTR]-[		0	actggggtctgcagca	0.1	rs79388709
-	1	436		NM_033188	NP_149445	Q9BYR2	KRA45_HUMAN	-C-[GRQVCHIEK]- [SPTR]		0	acagcaagaggggtg	0.313	
-	3	237	1_5'UTR|GPATCH	NM_001002909	NP_001002909	Q9UKJ3	GPTC8_HUMAN	G-patch.		4	CCAATCCCTGGC	0.388	
-	5	386	s.2_Missense_Mu	NM_014740	NP_055555	P38919	IF4A3_HUMAN	ase ATP-binding.		1	TTTCACGAACCTC	0.393	
-	5	860_861	_p.T80I|SLC38A1	NM_001037984	NP_001033073	Q9HBR0	S38AA_HUMAN	ical; (Potential).		2	AACACGGTGTAG	0.634	rs150309813

+	5	405	s.1_Missense_Mu	NM_004712	NP_004703	O14964	HGS_HUMAN	VHS.		1	ATCCTGTACCTG	0.597	
-	4	902	xv.2_Missense_Mu	NM_182511	NP_872317	Q8IUK8	CBLN2_HUMAN	C1q.		0	TAGAGGAAACAC	0.507	
-	5	533	_p.R146G|STAP2_	NM_001013841	NP_001013863	Q9UGK3	STAP2_HUMAN	SH2.		1	TGCACGGCGCG	0.647	rs143484969
-	40	4797	2_Missense_Muta	NM_000064	NP_000055	P01024	CO3_HUMAN	NTR.		5	CTGTCCAACCT	0.602	
+	18	2380	_p.S762F|EMR1_	NM_001974	NP_001965	Q14246	EMR1_HUMAN	lasmic (Potential).		5	GGCTTTCCAGTG	0.423	
-	3	18371		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).		57	GTGTTGATGTG	0.483	
-	3	17651		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).		57	CTGTCCTGGAG	0.498	
-	1	8092		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	ch.|Extracellular (Potential).		57	TACTTGGAAATT	0.473	
+	4	511	_Mutation_p.R74C	NM_000527	NP_000518	P01130	LDLR_HUMAN	ential).|LDL-receptor class		4	AGTTTCGCTGC	0.622	
-	7	1560		NM_138783	NP_620138	Q96CK0	ZN653_HUMAN	C2H2-type 2.		0	GCCAGGATGAG	0.572	
+	4	1027	ym.1_Missense_M	NM_001136501	NP_001129973	Q08AG5	ZN844_HUMAN	C2H2-type 7.		0	TCCATTCCTTTC	0.398	
-	4	1523		NM_145276	NP_660319	Q8TA94	ZN563_HUMAN	2H2-type 11.		0	ATAACGCTTTCC	0.428	
-	4	1382		NM_005815	NP_005806	Q9Y2A4	ZN443_HUMAN	2H2-type 10.		1	TGCTTGCATTCAT	0.413	
+	2	281_282	_p.P48S|MAST1_	NM_014975	NP_055790	Q9Y2H9	MAST1_HUMAN			7	CACTCCCCGCTG	0.644	
-	6	1134_1135	C1A6_uc010xod.1	NM_005071	NP_005062	P48664	EAA4_HUMAN	ical; (Potential).		6	GCATGCCCCCAA	0.584	
-	2	381	2nbg.3_Missense_	NM_052890	NP_443122	Q96PD5	PGRP2_HUMAN			3	GGCAGGGATCC	0.592	
-	9	1059	tation_p.L188F|CY	NM_001082	NP_001073	P78329	CP4F2_HUMAN			2	GGAGAGACCAC	0.602	
+	4	1003		NM_052852	NP_443084	Q96H40	ZN486_HUMAN	C2H2-type 5.		1	AAAATTCATACTG	0.378	
-	4	1319		NM_001159293	NP_001152765	C9JHM3	C9JHM3_HUMAN			1	AGGACCAGTTG	0.418	
-	5	2403	208_uc002nqo.1_I	NM_007153	NP_009084					7	TTACCTTATGTTT	0.373	
-	7	2712		NM_001080409	NP_001073878					2	ATGTTTCATAAGG	0.353	
-	5	689		NM_001080409	NP_001073878					2	TTAAAAGCTTTG	0.388	
-	13	1051	oiy.1_Missense_M	NM_007181	NP_009112	Q92918	M4K1_HUMAN			8	CCGAGGGATAG	0.617	
+	4	561	.2_Intron|CYP2B6	NM_000767	NP_000758	P20813	CP2B6_HUMAN			2	TCTTTGGAAAAC	0.502	
+	11	1535	nse_Mutation_p.P	NM_021913	NP_068713	P30530	UFO_HUMAN	ellular (Potential).		13	CGTGGCCCTGG	0.567	
-	1	44	10ejp.1_Missense_	NM_001102597	NP_001096067	Q6UY09	CEA20_HUMAN			2	CCAGTGGTGTC	0.552	
+	7	1911	.R431W|ZNF761_	NM_001008401	NP_001008401	Q86XN6	ZN761_HUMAN	2H2-type 10.		1	AGACATAGGAGA	0.413	
+	4	517	qid.2_Missense_M	NM_004829	NP_004820	O76036	NCTR1_HUMAN	ar (Potential).|Ig-like 2.		2	GGGAAGATCCA	0.582	
+	7	2143	_p.P662L|NLRP2_	NM_017852	NP_060322	Q9NX02	NALP2_HUMAN			2	GCTTCCTTTCTG	0.453	
-	6	1176	_p.V190E|PTPRH_	NM_002842	NP_002833	Q9HD43	PTPRH_HUMAN	tential).|Fibronectin type-III		4	TCCCCACCCAC	0.512	
-	7	2854	b.2_Missense_Mu	NM_145007	NP_659444	P59045	NAL11_HUMAN			6	GGGCTCGTGCA	0.498	
+	3	1841_1842	47_uc002qpm.3_I	NM_001023561	NP_001018855	O43361	ZN749_HUMAN	2H2-type 12.		0	CAGCATGAGAAA	0.45	
-	3	1484	.2_Intron|ZNF814_	NM_001144989	NP_001138461	B7Z6K7	ZN814_HUMAN			0	TTTTTTGTCAGTG	0.393	
-	6	2226		NM_004304	NP_004295	Q9UM73	ALK_HUMAN	ss A.|Extracellular (Potentia		1218	TGAAGGAGCTC	0.587	
-	17	4881	N1_uc002rxe.3_M	NM_001135659	NP_001129131	P58400	NRX1B_HUMAN			2	ACACCTTGATTG	0.443	
-	8	1379	XL3_uc002smq.1_	NM_032603	NP_115992	P58215	LOXL3_HUMAN	SRCR 4.		0	CCAGGTCCCCCT	0.632	
+	5	494	_p.P137S|REG3G	NM_198448	NP_940850	Q6UW15	REG3G_HUMAN	C-type lectin.		0	AAAAATCCCTCC	0.517	
-	10	3146		NM_207362	NP_997245	Q6NV74	CB055_HUMAN			0	GCTTGAGATTTC	0.468	
+	12	1775	.2_5'UTR|RGPD4_	NM_182588	NP_872394	Q7Z3J3	RGPD4_HUMAN			2	TAAGAGCCCAG	0.333	
-	3	709								0	ACTTCTAGTGAA	0.567	rs115341812
-	6	1029	s.2_Missense_Mu	NM_002349	NP_002340	O60449	LY75_HUMAN	Potential).|C-type lectin 1.		0	AGCATCCATTCTT	0.453	
+	3	901	1_uc002uhm.2_3'	NM_178120	NP_835221	P56177	DLX1_HUMAN			0	TATATCCCCAGC	0.632	
-	275	72987	50R|TTN_uc010z	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN			153	AGTTCCTTTGG	0.463	
-	208	41052	.1_Missense_Muta	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN			153	AGGTGGATCCC	0.438	
-	46	13024	N_uc010zfi.1_Intr	NM_133379	NP_596870	Q8WZ42	TITIN_HUMAN			153	ATATTTTCCATAA	0.388	
+	10	2478	ftr.2_Missense_Mu	NM_001204	NP_001195	Q13873	BMPR2_HUMAN	.|Cytoplasmic (Potential).		9	AACCATCCCACT	0.413	
+	25	2345	p.E749K|PLCB4_	NM_182797	NP_877949	Q15147	PLCB4_HUMAN	C2.	p.E737K(1)	15	GTAAGGAATTC	0.408	

-	3	1149	se_Mutation_p.F8	NM_018848	NP_061336	Q9NPJ1	MKKS_HUMAN		0	ACTGAAGCTTG	0.423	
-	10	1999		NM_016649	NP_057733	Q9H501	ESF1_HUMAN	Lys-rich.	1	CCAAGGGGTCA	0.284	
+	2	63	tj.1_RNA|FRG1B_uc010gdr.1_RNA|FRG1B_uc010ztk.1_Intron						0	AGAATCGCCCTG	0.353	rs7266938
-	2	1748	_Missense_Mutati	NM_000557	NP_000548	P43026	GDF5_HUMAN		0	GAAGAGGATGC	0.567	
+	16	2750		NM_016436	NP_057520	Q9BVI0	PHF20_HUMAN		1	CCTTTCCCCGC	0.607	
-	4	635	s.1_Missense_Mu	NM_004613	NP_004604	P21980	TGM2_HUMAN		3	TCCAAGGTATGT	0.582	
+	18	3650	m.2_Missense_Mu	NM_181659	NP_858045	Q9Y6Q9	NCOA3_HUMAN	etyltransferase.	5	AATTTTCCTCTC	0.517	
-	5	849	l.2_Nonsense_Mu	NM_006806	NP_006797	Q14201	BTG3_HUMAN		0	TCCCTCGATACA	0.413	
+	3	1528	uf.1_Missense_Mu	NM_053277	NP_444507	Q96NY7	CLIC6_HUMAN		2	CAGTGGACCTG	0.378	
+	19	1796	zbx.2_Missense_M	NM_002606	NP_002597	O76083	PDE9A_HUMAN		2	GAAGTCCAGAG	0.502	
-	1	321		NM_014406	NP_055221	Q96SF2	TCPQM_HUMAN		1	GCTCTCCCTTG	0.657	
+	43	7629	O18B_uc011aka.1_	NM_032608	NP_115997	Q8IUG5	MY18B_HUMAN		12	TGGATCAGCCA	0.527	
-	18	2529	aqt.1_Nonsense_	NM_153609	NP_705837	Q8IU80	TMPS6_HUMAN	.|Extracellular (Potential).	6	TGGATCCAGCT	0.647	
+	5	2054_2055	ense_Mutation_p.F	NM_001162501	NP_001155973	Q9UPQ9	TNR6B_HUMAN		0	GGACCCCAGGG	0.52	
+	7	789	.1_Missense_Mut	NM_152613	NP_689826	Q6ICG8	WBP2L_HUMAN	eat of Y-G-X-P-P-X-G.|9.|G	2	TCTCGGATATG	0.612	
+	21	2767	R1_uc011asu.1_In	NM_001099952	NP_001093422	Q14643	ITPR1_HUMAN	lasmic (Potential).	21	CCCGCCTCTGG	0.557	
+	11	1201	a.1_Missense_Mu	NM_003149	NP_003140	Q99469	STAC_HUMAN		4	TCAGTGGAAAA	0.443	
+	10	1763_1764	e_Mutation_p.S57	NM_004803	NP_004794	Q9Y267	S22AE_HUMAN	lasmic (Potential).	0	CCACTCCTCACA	0.619	
+	6	777_778	se_Mutation_p.G6	NM_145755	NP_665698	Q8NDW8	TT21A_HUMAN	TPR 4.	1	GCCCTGGAGGT	0.559	
-	1	836	mg.2_Intron|CYP8	NM_004391	NP_004382	Q9UNU6	CP8B1_HUMAN		2	GAAGCGAAAGA	0.512	
-	17	3501_3502	AGI1_uc003dmp.2	NM_001033057	NP_001028229	Q96QZ7	MAGI1_HUMAN	eraction with FCHSD2.	6	GCTTCGGGCCTG	0.569	
+	5	1062	pn.2_Missense_M	NM_145037	NP_659474	Q969Y0	FA55C_HUMAN		3	TGGAGACTACC	0.498	
-	9	1426		NM_199420	NP_955452	O75417	DPOLQ_HUMAN	case C-terminal.	11	TTGACGAAAGG	0.388	rs140193287
+	34	5232	ehi.2_Missense_M	NM_001024660	NP_001019831	O60229	KALRN_HUMAN	SH3 1.	6	GGTCCCCAGCA	0.652	
-	4	798	1blv.1_Intron|SLC	NM_005630	NP_005621	Q92959	SO2A1_HUMAN	Name=4; (Potential).	1	GGGCAACCACC	0.592	
-	5	1014	e_Mutation_p.H19	NM_033169	NP_149359	O75752	B3GL1_HUMAN	nenal (Potential).	1	TGAGTGGTTTA	0.348	
-	10	1546	R49_uc011bpd.1_	NM_178824	NP_849146	Q8IV35	WDR49_HUMAN	WD 6.	3	AAAATTCAGCCA	0.383	
-	26	2984	13A4_uc010hzi.2_	NM_032279	NP_115655	Q4VNC1	AT134_HUMAN	cellular (Potential).	2	TGAAAGGCACC	0.398	
-	2	6974	C4_uc003fvp.2_In	NM_018406	NP_060876	Q99102	MUC4_HUMAN		0	GTGACCTGTGG	0.577	
+	1	195	ndf.2_Missense_M	NM_012108	NP_036240	Q9ULZ2	STAP1_HUMAN	PH.	0	GTCAGGATACC	0.378	
-	32	7607	hgq.2_Missense_	NM_032217	NP_115593	O75179	ANR17_HUMAN		10	GCTTGATGTTGT	0.463	
+	6	816_817	p.A255V|AIMP1_	NM_001142415	NP_001135887	Q12904	AIMP1_HUMAN		0	TGATGCTTTCCC	0.366	
+	3	1147		NM_001977	NP_001968	Q07075	AMPE_HUMAN	cellular (Potential).	5	GTGGATGATAAA	0.353	
+	2	907	e_Mutation_p.G87	NM_012464	NP_036596	O43897	TLL1_HUMAN		7	CTTTGGAAACC	0.333	
+	34	5027	p.P1125R|SPEF2_	NM_024867	NP_079143	Q9C093	SPEF2_HUMAN		4	CCACCCAGACA	0.463	
-	5	939		NM_173489	NP_775760	Q7Z745	HTRB2_HUMAN		8	AGAAAGTCCCC	0.453	
+	1	2052	.1_Intron|SNX18_	NM_052870	NP_443102	Q96RF0	SNX18_HUMAN	BAR.	0	AGTACCTTTGA	0.413	
+	17	2272	uc003kgi.3_Intron	NM_003248	NP_003239	P35443	TSP4_HUMAN	TSP type-3 6.	0	CAGTGCCCAGC	0.547	
+	4	599	L21_uc003lbc.2_	NM_012159	NP_036291	Q9UKT6	FXL21_HUMAN	LRR 2.	1	ATGATCCTTCAT	0.358	
+	1	1678	CDHA1_uc003lgz.	NM_018900	NP_061723	Q9Y5I3	PCDA1_HUMAN	|Extracellular (Potential).	1	AGAACGACAAC	0.672	
+	1	397	B12_uc011dak.1_	NM_018932	NP_061755	Q9Y5F1	PCDBC_HUMAN	(Potential).|Cadherin 1.	3	TCTAATGATAACA	0.527	
+	1	2216	DHGB2_uc003ljs.	NM_003736	NP_003727	Q9UN71	PCDGG_HUMAN	lasmic (Potential).	0	TTCCCCCCAACT	0.517	
-	8	906	oo.2_Nonsense_M	NM_001387	NP_001378	Q14195	DPYL3_HUMAN		1	GGCTTGTGAGA	0.507	
-	5	1216	1_5'UTR|GRM6_u	NM_000843	NP_000834	O15303	GRM6_HUMAN	cellular (Potential).	8	AGGGATCGAGTC	0.532	
+	10	1055	e_Mutation_p.W9	NM_001040274	NP_001035364	Q5T4T6	SYC2L_HUMAN		2	TAAATGGTTTGA	0.368	
+	4	740	_p.E136K|EDN1_u	NM_001955	NP_001946	P05305	EDN1_HUMAN		1	ATTATGGAGAAA	0.353	
+	18	2370	_uc011dna.1_Miss	NM_020442	NP_065175	Q5ST30	SYVM_HUMAN		4	CAGATCCTGAT	0.557	

-	4	1063	ojs.2_Missense_M	NM_024294	NP_077270	Q9H6K1	CF106_HUMAN		3	TGCTGGGAGAC	0.502	
+	14	2891	1BP1_uc010jvn.2	NM_017754	NP_060224	Q6BDS2	URFB1_HUMAN		3	GCATCCTGCACC	0.512	
-	5	1502		NM_003740	NP_003731	O95279	KCNK5_HUMAN		2	AGGGGCCCGTG	0.617	
-	5	642		NM_002630	NP_002621	P20142	PEPC_HUMAN		0	ACCATGCCCTGC	0.627	
+	2	162	u.2_Missense_Mu	NM_201521	NP_958929	Q9NSK0	KLC4_HUMAN		4	GGCTGGTCAGC	0.652	
-	4	1663	318_uc003ouw.2_	NM_014345	NP_055160	Q5VUA4	ZN318_HUMAN		7	GTCGGGAAAGC	0.488	
-	2	517	_p.P118L|GNA12_	NM_007353	NP_031379	Q03113	GNA12_HUMAN		1	GCCAAGGAATG	0.483	
-	3	573		NM_001004320	NP_001004320	Q6ZNB7	ALKMO_HUMAN	istidine box-1.	0	ATGAGCCATAC	0.313	
-	2	328		NM_022150	NP_071433	Q9HCQ7	RFRP_HUMAN		1	ACGTTCCTCCCA	0.448	
-	2	1326	hr.2_Missense_Mu	NM_002192	NP_002183	P08476	INHBA_HUMAN		6	GTGAGGACCCG	0.567	
+	3	1320		NM_198570	NP_940972	Q2TAL6	VWC2_HUMAN	VWFC 2.	0	GTGTCCCCAGA	0.567	
+	5	1788	ET_uc011kng.1_M	NM_000245	NP_000236	P08581	MET_HUMAN	cellular (Potential).	159	CCCCACCCTTTG	0.532	
-	15	1860		NM_004333	NP_004324	P15056	BRAF_HUMAN	rotein kinas_R603>I(2)|p.T	18290	GATTTCACTGTA	0.368	
-	42	6736	p.P1508S|CSMD1	NM_033225	NP_150094	Q96PZ7	CSMD1_HUMAN	ar (Potential).|Sushi 12.	25	CCCAGGATAAC	0.448	
-	5	4018		NM_001080826	NP_001074295	Q86YV5	SG223_HUMAN		0	CTCCTCCGAGG	0.677	
-	3	1897		NM_173683	NP_775954	Q5GH73	XKR6_HUMAN		2	GATATCGAATGC	0.458	
+	9	1530	kye.1_Missense_M	NM_001008539	NP_001008539	P52569	CTR2_HUMAN	lasmic (Potential).	3	GGGATCGTCTC	0.507	
-	3	617	_p.T55R|REEP4_	NM_025232	NP_079508	Q9H6H4	REEP4_HUMAN	ical; (Potential).	1	ATGTCTGTAACG	0.597	
+	5	617	_p.E54K|ADAMD	NM_014479	NP_055294	O15204	ADEC1_HUMAN		2	CTAAATGAAAAG	0.289	
+	2	689	.E58K|NRG1_uc	NM_013964	NP_039258	Q02297	NRG1_HUMAN	Potential).|Ig-like C2-type.	0	GGTGTGAAACC	0.383	
-	9	808	AM2_uc011lck.1_M	NM_001464	NP_001455	Q99965	ADAM2_HUMAN	otential).|Peptidase M12B.	2	ATAACTCATTAGC	0.284	
+	12	1447	_p.E474K|PREX2_	NM_024870	NP_079146	Q70Z35	PREX2_HUMAN		17	GAAATGAGATG	0.348	
+	9	1099	ar.2_Missense_Mu	NM_004133	NP_004124	Q14541	HNF4G_HUMAN		1	AATGATCGGCAG	0.453	
+	27	4097	.E1275K|RIMS2_	NM_014677	NP_055492	Q9UQ26	RIMS2_HUMAN	C2 2.	15	CTTTCGAAGAGA	0.368	
-	1	535		NM_015193	NP_056008	Q7LC44	ARC_HUMAN		1	CATCTCGCGCT	0.692	
+	1	698		NM_001004483	NP_001004483	Q8NGS7	O13C8_HUMAN	lasmic (Pote p.G233E(1)	2	TGAAGGAAAAC	0.418	rs150858980
-	1	115		NM_001001956	NP_001001956	Q8NGT0	O13C9_HUMAN	Name=1; (Potential).	0	CAGAAGGATGA	0.433	rs150686997
-	2	696	f.2_Missense_Mut	NM_002160	NP_002151	P24821	TENA_HUMAN		7	ACAGCCACAGG	0.587	
+	24	2778	yt.1_Missense_Mu	NM_001110303	NP_001103773	Q9Y2K6	UBP20_HUMAN	DUSP 2.	2	CGGCCATGTCC	0.657	
-	1	446		NM_033387	NP_203745	Q5JUQ0	FA78A_HUMAN		1	CCCTTCCCGGA	0.572	
+	4	1084	P5_uc010ncq.2_3'UTR						0	TTCCCCGACAAC	0.512	rs147421666
-	5	723	_Mutation_p.S189	NM_018684	NP_061154	Q9NQZ6	ZC4H2_HUMAN		1	TTCCGGGACCGA	0.488	
-	2	1104		NM_152694	NP_689907	Q8N8U3	ZCHC5_HUMAN		1	AGTGGGATACA	0.507	
+	5	1226	.V142G|GPRASP	NM_014710	NP_055525	Q5JY77	GASP1_HUMAN		2	AACTGGTTAATA	0.458	
-	5	820	4ffl.2_Missense_M	NM_001011543	NP_001011543	P43363	MAGAA_HUMAN	MAGE.	0	AGTCACCTTTT	0.458	
-	2	319	5F|CASP9_uc001	NM_001229	NP_001220	P55211	CASP9_HUMAN	CARD.	2	AGCAGGAGATG	0.547	
-	6	707	_p.Y168H|ATP13A	NM_022089	NP_071372	Q9NQ11	AT132_HUMAN	lasmic (Potential).	4	GATATAGCGCTG	0.537	
-	17	2464	xm.1_Missense_M	NM_052896	NP_443128	Q7Z408	CSMD2_HUMAN	xtracellular (Potential).	12	AAGTCCGCCCA	0.502	
-	5	826	_p.P95S|DHCR24_	NM_014762	NP_055577	Q15392	DHC24_HUMAN	inding PCMH-type.	1	GGCAGGGATGA	0.582	
+	6	746	PR_uc009waq.2_In	NM_002303	NP_002294	P48357	LEPR_HUMAN	cellular (Potential).	1	AGTTTTCAGATG	0.368	
-	14	3116		NM_001002912	NP_001002912	Q5RHP9	CA173_HUMAN	Glu-rich.	5	TCCTCTCTCTTT	0.522	
+	9	1318	.2_Missense_Mut	NM_174858	NP_777283	Q9Y6K8	KAD5_HUMAN		1	ACAGGGTGATG	0.294	
+	21	2777	g.1_Missense_Mu	NM_020775	NP_065826	Q6UXG2	K1324_HUMAN	cellular (Potential).	5	CTTACGTGTGG	0.507	rs142358404
-	2	1046	_p.G72R|SLC16A	NM_003051	NP_003042	P53985	MOT1_HUMAN	ical; (Potential).	1	TACCTCCACCAT	0.378	
+	34	4365	10_uc010oyl.1_Int	NM_001039703	NP_001034792	A6NDV3	A6NDV3_HUMAN		0	TCACTGAATAGA	0.473	
+	13	2422	uc010ozk.1_5'UTR	NM_017940	NP_060410	A6NDV3	A6NDV3_HUMAN		0	CCGGACAAGTC	0.587	
-	3	400		NM_001008536	NP_001008536	Q5QJ38	TCHL1_HUMAN		2	GCCTGAACATCC	0.433	

-	24	8732_8733	ASH1L_uc001fkt.2	NM_018489	NP_060959	Q9NR48	ASH1L_HUMAN	BAH.	11	TCCAAGGGAATC	0.431	
-	41	5873		NM_003126	NP_003117	P02549	SPTA1_HUMAN	Spectrin 18.	8	TTTCCTCCTGCA	0.428	
-	5	609		NM_000537	NP_000528	P00797	RENI_HUMAN		4	AAACTCGGCCA	0.557	
-	8	1172	e_Mutation_p.L25	NM_025160	NP_079436	Q9H7D7	WDR26_HUMAN	WD 2.	0	GCAACAAGATAG	0.428	
-	12	1545	j.2_RNA|NEBL_uc	NM_006393	NP_006384	O76041	NEBL_HUMAN	Nebulin 10.	2	CCTTTAATCTCC	0.333	
-	7	1309	GMS1_uc009xou.	NM_147156	NP_671512	Q86VZ5	SMS1_HUMAN		2	GCATGGGGATCT	0.502	
+	1	144	uc001kwr.2_Intron	NM_001143909	NP_001137381	Q2QD12	Q2QD12_HUMAN		0	TCCATCCTCAAC	0.542	
+	14	2550	RF1_uc010qwe.1_	NM_020901	NP_065952	Q9P1Y6	PHRF1_HUMAN		0	GATAAGGAGCAG	0.577	
-	31	5326		NM_005961	NP_005952	Q6W4X9	MUC6_HUMAN	Approximate repeats.	1	CTTCAGGATGGT	0.562	
+	51	14903	b.2_Missense_Mu	NM_017511	NP_059981	Q9HC84	MUC5B_HUMAN	em repeats, Ser/Thr- rich.|	0	AGAGCCGAGCA	0.662	
-	1	488		NM_001005238	NP_001005238	Q8NGK0	O51G2_HUMAN	Name=4; (Potential).	2	GGTAATGGAAAA	0.473	
+	11	2849	_p.R743*|NAV2_u	NM_145117	NP_660093	Q8IVL1	NAV2_HUMAN		6	CCCCTCGAGCC	0.632	
+	29	3169	tation_p.L826P|D	NM_001105540	NP_001099010	Q13574	DGKZ_HUMAN	ANK 1.	3	GCACGCTCCTGC	0.692	
+	11	1281	RD13D_uc001okg.	NM_207354	NP_997237	Q6ZTN6	AN13D_HUMAN		1	AGTCACGGAACA	0.637	rs78983123
+	9	1346	_p.R376K|BCO2_	NM_031938	NP_114144	Q9BYV7	BCDO2_HUMAN		0	CTCGAAGGTTTG	0.413	
-	17	2565	e_Mutation_p.G72	NM_032531	NP_115920	Q8IZU9	KIRR3_HUMAN	ic (Potential).|Ser-rich.	3	GCTTGCCGCTG	0.607	
+	9	1468	v.1_Missense_Mu	NM_002017	NP_002008	Q01543	FLI1_HUMAN		2273	CCGAGTCGTCCA	0.493	
-	3	857	.R198C|FOXM1_	NM_021953	NP_068772	Q08050	FOXM1_HUMAN		2	GCTGCGGGAGC	0.493	
-	3	276		NM_006248	NP_006239				0	GGGTGGTCCTT	0.612	
+	11	2149	cw.1_Missense_M	NM_030667	NP_109592	Q16827	PTPRO_HUMAN	III 7.|Extracellular (Potentia	9	CAACGGACTTG	0.413	
-	4	444	3_5'UTR|PLCZ1_	NM_033123	NP_149114	Q86YW0	PLCZ1_HUMAN		3	GAATTTTCCGGT	0.333	
-	11	3652	p.S807F|SFRS2IP	NM_004719	NP_004710	Q99590	SCAFB_HUMAN		0	TTATAGGATTGC	0.428	
-	1	183		NM_012064	NP_036196	P30301	MIP_HUMAN	al; (By similarity).	1	CAGGGCCAAGC	0.582	
+	14	2031	ense_Mutation_p.	NM_182947	NP_891992	Q86VW2	ARHGP_HUMAN		0	CTCTCCCCTCTC	0.577	
-	2	1182	_p.V275I|ZFC3H1_	NM_144982	NP_659419	O60293	ZC3H1_HUMAN		5	TACTGACATTATC	0.358	
+	24	3023_3024	tlq.2_Missense_M	NM_018082	NP_060552	Q9NW08	RPC2_HUMAN		2	CGGCTTCCCATC	0.5	
+	12	1215	t.2_Missense_Mut	NM_213594	NP_998759	Q33E94	RFX4_HUMAN	ary for dimerization.	1	CAGGAGTTTGA	0.458	
-	8	2201_2202	_Mutation_p.P65	NM_016179	NP_057263	Q9UBN4	TRPC4_HUMAN	and ITPR3.| p.P656P(1)	6	TGAAGGGAGTAG	0.431	
+	2	2484	.2_Missense_Mut	NM_001173	NP_001025226	Q13017	RHG05_HUMAN		5	AGCAAGCTCTCA	0.413	
+	13	5940		NM_004274	NP_004265	Q13023	AKAP6_HUMAN		21	CACATGGGAAA	0.383	
-	2	538		NM_021136	NP_066959	Q16799	RTN1_HUMAN		4	ATGTCAGAAATG	0.458	
-	2	886	orf43_uc010tud.1_	NM_194278	NP_919254	Q6PJG2	CN043_HUMAN		5	CTGGGGGGGCT	0.662	
+	2	671	4orf109_uc001yb	NM_001098621	NP_001092091	Q8N6I4	CN109_HUMAN	ical; (Potential).	0	TCCTTGCCTTTTT	0.453	
+	23	2577		NM_058237	NP_478144	Q6NUP7	PP4R4_HUMAN		4	GGTTAGGAAAGA	0.303	rs150367623
+	4	538	p.R145C|EML1_u	NM_004434	NP_004425	O00423	EMAL1_HUMAN		5	GGAATCGCACA	0.507	
+	3	239	27924_uc001yua.2	NM_001005241	NP_001005241	Q8N0Y3	OR4N4_HUMAN		5	TTCTAACGTGACA	0.328	
+	1	2045		NM_018958	NP_061831	Q9NZP6	CO002_HUMAN	Pro-rich.	8	ATTCCCCTCCTC	0.547	
-	9	828	pc.2_Missense_M	NM_015289	NP_056104	Q96JC1	VPS39_HUMAN	CNH.	3	CCACGGTGAGA	0.527	
-	14	2239	RNA|CDAN1_uc00	NM_138477	NP_612486	Q8IWY9	CDAN1_HUMAN		2	CAAGGGAACAA	0.607	
-	3	560		NM_207381	NP_997264	Q5GJ75	TP8L3_HUMAN		0	TGTGCTCTTTGG	0.448	
+	1	1499		NM_001080534	NP_001074003	Q8NB66	UN13C_HUMAN		7	GCAGCAGAATTT	0.388	
+	9	1837	|IL21R_uc002dos.	NM_181078	NP_851564	Q9HBE5	IL21R_HUMAN	lasmic (Potential).	4	TGGACCCCAGG	0.642	
-	10	1091		NM_001896	NP_001887	P19784	CSK22_HUMAN	rotein kinase.	1	CTCTTTGGCAG	0.468	
+	3	704		NM_001124758	NP_001118230	Q8IVW8	SPNS2_HUMAN		0	GCGACCGCTTC	0.632	rs139404093
+	3	605	fye.2_Missense_	NM_001114974	NP_001108446	Q2TAL5	SMTL2_HUMAN		0	CAGATCCCCCC	0.632	
+	4	442	.R143H|DNAH2_	NM_020877	NP_065928	Q9P225	DYH2_HUMAN	n (By similarity).	13	CATTCGCCAAGC	0.587	
+	9	1020		NM_004140	NP_004131	Q15334	L2GL1_HUMAN	WD 6.	6	TGACCGCCACT	0.577	

+	6	544	splice|TBC1D3_uc	NM_032258	NP_115634	Q8IZP1	TBC3A_HUMAN		0	ACCAGGTACGC	0.587	
-	1	329		NM_030966	NP_112228	Q8IUG1	KRA13_HUMAN		0	CTCCACTGCTGC	0.652	
-	1	416		NM_031960	NP_114166	Q9BYQ9	KRA48_HUMAN	-C-[IKRQVHEC]- [SPRT]-[	0	agctggggcggcagc	0.09	rs144672535
-	19	2195	p.R610Q|EFTUD2	NM_004247	NP_004238	Q15029	U5S1_HUMAN		1	ATCTTCCGCAAA	0.517	
+	3	498	x.1_Missense_Mu	NM_003396	NP_003387	O14905	WNT9B_HUMAN		2	GAGCCGGCAGG	0.662	
+	2	664	F_uc002iuh.2_5'U	NM_002126	NP_002117	Q16534	HLF_HUMAN		2	ACAAGGAAAAG	0.433	
-	7	801	_p.F39L|MKS1_u	NM_017777	NP_060247	Q9NXB0	MKS1_HUMAN		1	CCCGTGAAGTC	0.473	
-	8	1079	xa.3_Missense_M	NM_001005207	NP_001005207	O94972	TRI37_HUMAN	Potential.	7	TCTTGGGTTAGA	0.328	
-	4	2132	_Mutation_p.V57	NM_032134	NP_115510	Q9H0J4	QRIC2_HUMAN	Gln-rich.	5	cacgctgaactgcacc	0.015	rs113162124
+	17	2812	p.G712S|CCDC4	NM_017950	NP_060420	Q4G0X9	CCD40_HUMAN	Potential.	3	AGATCGGCCAG	0.567	rs59896146
-	8	1464	_p.S383L|CSNK1	NM_001893	NP_001884	P48730	KC1D_HUMAN		2	TCGGACGAGGA	0.672	
+	2	1128	NDC2_uc002koh.	NM_001098529	NP_001091999	Q86VQ3	TXND2_HUMAN	repeat of Q-P-K-X-G-D-I-P	2	CCAAGACCTCA	0.562	
-	6	1782	md.1_Missense_M	NM_020805	NP_065856	Q9P2G3	KLH14_HUMAN	Kelch 3.	1	CTCCCGCATGA	0.463	
+	4	1322	a.1_Missense_Mu	NM_173480	NP_775751	Q68EA5	ZNF57_HUMAN	C2H2-type 9.	3	CAGCTCTATAAA	0.438	
+	4	1336	a.1_Missense_Mu	NM_173480	NP_775751	Q68EA5	ZNF57_HUMAN	C2H2-type 9.	3	GAACAATGTGG	0.428	
+	4	1371	a.1_Missense_Mu	NM_173480	NP_775751	Q68EA5	ZNF57_HUMAN	C2H2-type 9.	3	ATTCCGAGGTC	0.428	rs149690257
+	4	1386	a.1_Missense_Mu	NM_173480	NP_775751	Q68EA5	ZNF57_HUMAN	C2H2-type 9.	3	GAGGACGCACA	0.438	rs148390269
+	13	1292	g.2_Missense_Mut	NM_024760	NP_079036	Q9H808	TLE6_HUMAN	WD 4.	1	GGTTATCCTGAT	0.567	
+	6	2416	u.2_Missense_Mut	NM_020209	NP_064594	Q96IW2	SHD_HUMAN	SH2.	0	CAGTTCACGCC	0.662	
+	4	1515	ym.1_Missense_M	NM_001136501	NP_001129973	Q08AG5	ZN844_HUMAN		0	CCTTCAGATCTG	0.423	
-	4	1523		NM_145276	NP_660319	Q8TA94	ZN563_HUMAN	2H2-type 11.	0	ATAACGCTTTCC	0.428	
-	4	1355		NM_145276	NP_660319	Q8TA94	ZN563_HUMAN	C2H2-type 9.	0	ATAACGTTTTCC	0.413	
-	4	1409	709_uc002mtx.3_I	NM_144976	NP_659413	Q8TBZ8	ZN564_HUMAN	2H2-type 11.	1	AAGGCTCTACCA	0.433	
-	2	504	zi.2_Missense_Mu	NM_002918	NP_002909	P22670	RFX1_HUMAN		2	CGGGAGCTCCG	0.438	
+	8	2027	p.G599R|SYDE1_	NM_033025	NP_149014	Q6ZW31	SYDE1_HUMAN		2	CCTGTGGGCGG	0.697	
+	12	1425		NM_023944	NP_076433				7	GGTCACCTCTGG	0.557	
+	9	1057	2nkr.1_RNA|DDX	NM_019070	NP_061943	Q9Y6V7	DDX49_HUMAN	case C-terminal.	1	ACATCCACCGA	0.657	
-	2	468	_p.L110*|LPAR2_	NM_004720	NP_004711	Q9HBW0	LPAR2_HUMAN	Name=3; (Potential).	2	CCAGCAAGCCC	0.667	
+	2	1049	_p.A385T|ZNF493_	NM_175910	NP_787106	Q6ZR52	ZN493_HUMAN	C2H2-type 9.	1	GGCAAAGCCTTT	0.363	
-	4	1333	1_Intron|ZNF208_	NM_007153	NP_009084				7	AGGGTTTCTCT	0.383	
-	4	1187	p.Q280K|ZNF681_	NM_138286	NP_612143	Q96N22	ZN681_HUMAN	C2H2-type 7.	0	GGACTGGTTAA	0.433	
+	5	1060	.Q328L|CD22_uc	NM_001771	NP_001762	P20273	CD22_HUMAN	ellular (Potential).	9	AGTGCAGTGTG	0.652	
+	39	6573	_Mutation_p.S214	NM_000540	NP_000531	P21817	RYR1_HUMAN	6 X approximate repeats.	12	GTCCTCCGTGG	0.662	
-	7	1908	_Mutation_p.Q40	NM_181882	NP_870998	Q9BXM0	PRAX_HUMAN	L]-[LIVMAP]- [AQKHRPE];	2	GCAGCTGTACCT	0.587	
-	5	368	pjp.1_Missense_M	NM_000979	NP_000970	Q07020	RL18_HUMAN		0	GGATGCGGCTG	0.667	rs1804326
+	4	1553	dw.1_Missense_M	NM_138374	NP_612383	Q96IR2	ZN845_HUMAN	2H2-type 10.	0	GTCAGACATCAT	0.378	
-	5	979	LRA3_uc010erk.2	NM_006865	NP_006856	Q8N6C8	LIRA3_HUMAN	like C2-type 3.	1	ACTCGGAGGAG	0.677	
+	4	1330	|ZIK1_uc002qpi.2_	NM_001010879	NP_001010879	Q3SY52	ZIK1_HUMAN	C2H2-type 7.	2	GGTGACTGTGG	0.448	
+	4	1339	|ZIK1_uc002qpi.2_	NM_001010879	NP_001010879	Q3SY52	ZIK1_HUMAN	C2H2-type 7.	2	TGGGAAATCCTT	0.453	
+	1	5246	1_5'Flank|ZNF512	NM_032266	NP_115642	Q68DN1	CB016_HUMAN	m repeat of P-S-E-R-S-H-	1	AGAGAGAAGCC	0.562	
-	8	1027	sij.2_Nonsense_M	NM_015189	NP_056004	Q9Y2D4	EXC6B_HUMAN		2	GACATCGATAAA	0.368	
+	7	2842		NM_144993	NP_659430	O43151	TET3_HUMAN		0	CATAACCTCTAC	0.617	
-	2	782	OLN2_uc002spb.	NM_006464	NP_006455	O43493	TGON2_HUMAN	l).|8.|14 X 14 AA tandem r	0	TGCTAGGGCTGT	0.597	
+	4	1894	yuy.1_Missense_M	NM_020184	NP_064569	Q6P4Q7	CNNM4_HUMAN		3	CGCCCGCCATT	0.567	
-	2	531	e.1_RNA|ANKRD	NM_025190	NP_079466	Q8N2N9	AN36B_HUMAN		0	CTTCACGGTCG	0.463	
-	4	729	s.2_Nonsense_Mu	NM_002349	NP_002340	O60449	LY75_HUMAN	ellular (Potential).	0	CTTTTCCCAATT	0.353	
+	8	4574	e_Mutation_p.P13	NM_152381	NP_689594	A4UGR9	XIRP2_HUMAN		14	TCCCTCCTTCTG	0.358	

-	307	97342_9734	010zfi.1_Missense	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN			153	CGAGGGGCATGG	0.431	
-	41	7488		NM_018897	NP_061720	Q8WXX0	DYH7_HUMAN	.4 (By similarity).		12	AATGATCAATAA	0.468	
+	14	2159	p.A651V|PARD3B	NM_152526	NP_689739	Q8TEW8	PAR3L_HUMAN			4	ATGGGCCGAGA	0.438	
+	3	429	1486_uc010fxa.1_	NM_020864	NP_065915	Q9P242	K1486_HUMAN			3	ACGAAGGAAGTT	0.478	
+	21	1404	utation_p.M414I|C	NM_000091	NP_000082	Q01955	CO4A3_HUMAN	le-helical region.		3	GCCATGGGGAC	0.602	
+	2	61	tj.1_RNA|FRG1B_uc010gdr.1_RNA|FRG1B_uc010ztk.1_Intron							0	CAGAATCGCCC	0.353	rs143761036
-	3	1038	xdk.2_Intron|CPNE	NM_152838	NP_690051	Q9NTZ6	RBM12_HUMAN	Pro-rich.		3	TTATTGTTCAAAT	0.512	
+	6	1242	K2_uc010ggp.2_M	NM_001098798	NP_001092268	Q96NM4	TOX2_HUMAN	Pro-rich.		1	CAGCCCCCCAG	0.677	
+	10	1244	_p.A325T|RTEL1_	NM_016434	NP_057518	Q9NZ71	RTEL1_HUMAN			0	TCAGCGCGGAC	0.662	rs144255879
+	26	5528	eb.1_Missense_M	NM_005128	NP_005119	Q9Y3R5	DOP2_HUMAN			2	GAACTCCCAAC	0.403	
-	25	4734	CAM_uc002yyr.1_	NM_001389	NP_001380	O60469	DSCAM_HUMAN	III 5.|Extracellular (Potentia		11	TGATTGGAAAAC	0.488	
+	5	478	L12_uc003ato.1_	NM_001039141	NP_001034230	Q9H2D6	TARA_HUMAN			1	CATCCACGGAGA	0.627	
+	7	2403	atq.1_Missense_M	NM_001039141	NP_001034230	Q9H2D6	TARA_HUMAN			1	CCTCTCCTAACA	0.582	
+	2	379	R8_uc003cjm.2_In	NM_005201	NP_005192	P51685	CCR8_HUMAN	Name=2; (Potential).		2	CTGTCTGACCTG	0.488	
-	2	1226	ro.3_Missense_M	NM_006574	NP_006565	O95196	CSPG5_HUMAN	cellular (Potential).		2	GAGGCCAAGTC	0.637	
+	4	620	.S21L|ARIH2_uc0	NM_006321	NP_006312	O95376	ARI2_HUMAN			1	AAGTTTCAGAGA	0.363	
+	5	7708		NM_003458	NP_003449	Q9UPA5	BSN_HUMAN			8	GTCTCCCCAGC	0.632	
+	1	379		NM_001005482	NP_001005482	Q8NGV7	OR5H2_HUMAN	lasmic (Potential).		3	TATGATCGCTAT	0.378	
+	3	237	a.1_Missense_M	NM_020202	NP_064587	Q9NQR4	NIT2_HUMAN	N hydrolase.		1	TATTTTCCTGAAT	0.373	
+	8	1414		NM_020754	NP_065805	Q2M1Z3	RHG31_HUMAN			2	TCTTTTAGGCGA	0.378	
-	7	1562	er.2_Missense_M	NM_175924	NP_787120	Q86SU0	ILDR1_HUMAN	lasmic (Potential).		1	GCCTCTCCTTGT	0.672	
+	12	1699_1700		NM_001004316	NP_001004316	Q6ZMV7	LEKR1_HUMAN			0	TTAAGGAAGAAA	0.347	
-	10	1211	.1_3'UTR|LRRC34	NM_153353	NP_699184	Q8IZ02	LRC34_HUMAN			0	GATTCTCCATAAG	0.378	
+	4	467	e_Mutation_p.R67	NM_182610	NP_872416	Q7Z3H4	SAMD7_HUMAN		p.R67W(1)	1	CAGTCGGATCT	0.428	rs138236130
+	11	1911	w.1_Missense_M	NM_198485	NP_940887	Q6ZUI0	TPRG1_HUMAN			0	CCACAAGAATTC	0.408	
+	12	1714	se_Mutation_p.P44	NM_003722	NP_003713	Q9H3D4	P63_HUMAN	SAM.		12	CACCTCCGTATC	0.607	
-	11	2052	fsg.2_Missense_	NM_018192	NP_060662	Q8IVL5	P3H2_HUMAN			4	GTATAGGAAAAAT	0.433	
-	9	1067_1068	_p.S183F|UBXN7_	NM_015562	NP_056377	O94888	UBXN7_HUMAN			3	CAAACGGATATG	0.416	
-	1	668	168_uc010iah.2_5	NM_152617	NP_689830	Q8IYW5	RN168_HUMAN	RING-type.		0	TTCGACGGTCG	0.577	
+	5	978	141_uc003gab.2_	NM_003441	NP_003432	Q15928	ZN141_HUMAN	C2H2-type 4.		0	TAGGTTCACAAC	0.363	rs140024736
-	22	3199		NM_001042784	NP_001036249	Q5M9N0	CD158_HUMAN	Ser-rich.		6	TCTTAGGAGAAG	0.358	
-	12	1661	.1_Nonsense_Mut	NM_000204	NP_000195	P05156	CFAI_HUMAN	Peptidase S1.		0	CCCACTGAAGTG	0.333	
+	2	524	TU_uc011cgq.1_R	NM_015693	NP_056508	Q9ULD6	PDZD6_HUMAN			1	ACAGGAGTCATT	0.393	
+	1	2889	gz.2_Missense_M	NM_032961	NP_116586	Q9P2E7	PCD10_HUMAN	|Extracellular (Potential).		2	CAgggcgggggcgg	0.587	
-	1	1990	.1_Intron|PCDH18	NM_019035	NP_061908	Q9HCL0	PCD18_HUMAN	r (Potential).|Cadherin 5.		5	CTTCATGATCAA	0.418	
-	2	323	FS6_uc003jcy.2_5'	NM_032479	NP_115868	Q9P0J6	RM36_HUMAN			0	ACCACCGACCC	0.562	
-	28	4403		NM_001369	NP_001360	Q8TE73	DYH5_HUMAN	.|Stem (By similarity).		31	AGCTTTCGACAT	0.468	
+	1	672	uc011ctk.1_Intron	NM_032567	NP_115956	Q9BXG8	SPZ1_HUMAN			1	AAACAGGAGATG	0.358	
+	1	816	uc011ctk.1_RNA	NM_032567	NP_115956	Q9BXG8	SPZ1_HUMAN	notif (By similarity).		1	AAACAGCAGATG	0.353	
-	2	1200		NM_203406	NP_981951	Q68D91	MBLC2_HUMAN			0	CCAATCGAAAAA	0.408	
-	5	647	kpw.1_Nonsense_	NM_022140	NP_071423	Q9HCS5	E41LA_HUMAN	FERM.		1	GCCCTGAAGGA	0.468	
-	14	1547	lwy.2_Missense_	NM_033274	NP_150377	Q9H013	ADA19_HUMAN	Extracellular (Potential).		8	GGTAGGGCAGT	0.622	
+	9	7204	EP1_uc011diq.1_	NM_002114	NP_002105	P15822	ZEP1_HUMAN			6	CAGCCCCCAGA	0.512	
-	30	4190	27_uc003nxd.2_5'	NM_006295	NP_006286	P26640	SYVC_HUMAN			3	CGATGGCCTCA	0.572	
-	32	4462	ai.2_Missense_Mu	NM_138694	NP_619639	P08F94	PKHD1_HUMAN	Extracellular (Potential).		44	CGATGGGAAGA	0.507	
+	17	1964	Splice_Site|STXBP	NM_001127715	NP_001121187	Q5T5C0	STXB5_HUMAN			0	TTTTAGAGTTAA	0.313	
+	7	1005	G_uc003quc.2_Mis	NM_152410	NP_689623	Q96M98	PACRG_HUMAN			0	AACATTGGGGAC	0.507	

+	3	1358	LL2_uc011egr.1_R	NM_031949	NP_114155	Q9BWV7	TTLL2_HUMAN	TTL.		3	ATGAGGGGAGA	0.433	rs141172576
+	6	1057	.3_Missense_Muta	NM_000600	NP_000591	P05231	IL6_HUMAN			0	TTTAAGGAGTTC	0.527	
+	4	1320		NM_001159522	NP_001152994	A8MUV8	ZN727_HUMAN	2H2-type 8.		0	GGTTCTCAGAC	0.388	
+	4	1390		NM_001159522	NP_001152994	A8MUV8	ZN727_HUMAN	2H2-type 9.		0	CAAAAGCTTTA	0.388	
+	4	1488		NM_001159522	NP_001152994	A8MUV8	ZN727_HUMAN	2H2-type 10.		0	GGTTCCCAGAC	0.393	
+	4	1558		NM_001159522	NP_001152994	A8MUV8	ZN727_HUMAN	2H2-type 11.		0	CAAAACCTTTA	0.428	
-	9	1318	UN5_uc003txx.2_	NM_018044	NP_060514	Q96P11	NSUN5_HUMAN			0	CCTTGGCACCT	0.607	
+	14	2315	AN_uc003uwl.2_F	NM_003386	NP_003377	Q9Y493	ZAN_HUMAN	ate) (mucin-like domain).|E		11	AAAACCCACCA	0.507	
+	14	2903	AN_uc003uwl.2_F	NM_003386	NP_003377	Q9Y493	ZAN_HUMAN	ate) (mucin-like domain).|E		11	AAAACCCACCA	0.507	
+	14	2911	AN_uc003uwl.2_F	NM_003386	NP_003377	Q9Y493	ZAN_HUMAN	ate) (mucin-like domain).|E		11	CCATCTCCACG	0.502	
+	3	2023	C17_uc010lho.1_F	NM_001040105	NP_001035194	Q685J3	MUC17_HUMAN	X approximate tandem re		27	CTCCAACACTC	0.473	
+	3	6777	C17_uc010lho.1_F	NM_001040105	NP_001035194	Q685J3	MUC17_HUMAN	X approximate tandem re		27	TTTCAGCAACT	0.498	
+	3	6811	C17_uc010lho.1_F	NM_001040105	NP_001035194	Q685J3	MUC17_HUMAN	ch.|59 X approximate tand		27	TGACCACTTCTA	0.478	
+	3	7480	C17_uc010lho.1_F	NM_001040105	NP_001035194	Q685J3	MUC17_HUMAN	ch.|59 X approximate tand		27	CACCCTTTCCA	0.522	
+	3	9657_9658	C17_uc010lho.1_F	NM_001040105	NP_001035194	Q685J3	MUC17_HUMAN	ch.|59 X approximate tand		27	AAGCCACTTCAT	0.505	
-	2	257		NM_001024607	NP_001019778	A4D0T2	CG066_HUMAN			2	TGACGATATTGA	0.418	
-	2	476	T2_uc003vja.2_5'	NM_003391	NP_003382	P09544	WNT2_HUMAN			7	CATCTGGATGT	0.597	
-	15	1860		NM_004333	NP_004324	P15056	BRAF_HUMAN	rotein kinas	_R603>I(2)|p.T	18290	ATTTCACTGTA	0.368	
-	4	776	9B_uc003wig.3_F	NM_173681	NP_775952	Q674R7	ATG9B_HUMAN	nal (By similarity).		1	GCATCGAAGGA	0.537	
-	3	452		NM_014420	NP_055235	Q9UBT3	DKK4_HUMAN			1	TTGTTCCTTCT	0.458	
-	3	1741	CO5A1_uc003xyk	NM_030958	NP_112220	Q9H2Y9	SO5A1_HUMAN	Name=6; (Potential).		4	AGTTTCCAATG	0.348	
-	8	1926	M1_uc010mic.2_F	NM_144966	NP_659403	Q5H8C1	FREM1_HUMAN	CSPG 2.		5	AGCACCAATGT	0.488	
-	10	2369		NM_001163	NP_001154	Q02410	APBA1_HUMAN	PDZ 1.		1	GCTTCCCAGAT	0.527	
+	1	805		NM_001004484	NP_001004484	Q8NGV5	O13D1_HUMAN	lasmic (Potential).		2	AGAAAGCCTTC	0.383	
+	1	863		NM_001004484	NP_001004484	Q8NGV5	O13D1_HUMAN	Name=6; (Potential).		2	CAGCCCTTTTTA	0.413	
+	12	1648	p.R476Q|SLC44A	NM_080546	NP_536856	Q8WWI5	CTL1_HUMAN	membrane (Potential).|Cys-		4	TGCACGATGTG	0.289	
+	11	1721	mf.1_Missense_M	NM_000962	NP_000953	P23219	PGH1_HUMAN			2	CTTTTCCCTCA	0.512	
-	2	422	34_uc004bvr.1_M	NM_052844	NP_443076	Q96EX3	WDR34_HUMAN			3	GGACGGGGGCT	0.627	
-	28	7018	6A_uc004cht.2_M	NM_014866	NP_055681	O15027	SC16A_HUMAN	action with SEC23A.|Pro-ri		0	CTGTGGTTCTT	0.622	
+	4	859	P5_uc010ncq.2_3'UTR							0	TTGCCCCACTG	0.622	
-	2	231	A9L_uc010nfp.2_	NM_001412	NP_001403	P47813	IF1AX_HUMAN			1	TTACCTCCTTTAC	0.313	
+	19	2411	_p.F754L|UBA1_u	NM_153280	NP_695012	P22314	UBA1_HUMAN			1	CTCACCTTTGAT	0.557	
-	2	2186		NM_152424	NP_689637	Q5JTC6	F123B_HUMAN		p.0?(40)	112	ACTTGAGTCTCT	0.617	
-	25	2239	p.E368K|TEX11_u	NM_001003811	NP_001003811	Q8IYF3	TEX11_HUMAN			5	CTTGCTCTAGAT	0.393	
+	4	551	EC1_uc010nsl.1_I	NM_005462	NP_005453	O60732	MAGC1_HUMAN			4	CTGAGGGCGAC	0.582	
+	4	564	EC1_uc010nsl.1_I	NM_005462	NP_005453	O60732	MAGC1_HUMAN			4	ACACCCAGTCTC	0.582	rs141277731
-	2	319	5F|CASP9_uc001	NM_001229	NP_001220	P55211	CASP9_HUMAN	CARD.		2	AGCAGGAGATG	0.547	
-	6	707	_p.Y168H|ATP13A	NM_022089	NP_071372	Q9NQ11	AT132_HUMAN	lasmic (Potential).		4	GATATAGCGCTG	0.537	
-	17	2464	m.1_Missense_M	NM_052896	NP_443128	Q7Z408	CSMD2_HUMAN	tracellular (Potential).		12	AAGTCCGCCCA	0.502	
-	5	826	_p.P95S|DHCR24_	NM_014762	NP_055577	Q15392	DHC24_HUMAN	inding PCMH-type.		1	GGCAGGGATGA	0.582	
+	6	746	R_uc009waq.2_I	NM_002303	NP_002294	P48357	LEPR_HUMAN	ellular (Potential).		1	AGTTTTCAGATG	0.368	
-	14	3116		NM_001002912	NP_001002912	Q5RHP9	CA173_HUMAN	Glu-rich.		5	TCCTCTCTCTTT	0.522	
+	9	1318	.2_Missense_Mut	NM_174858	NP_777283	Q9Y6K8	KAD5_HUMAN			1	ACAGGGTGATG	0.294	
-	2	1046	_p.G72R|SLC16A	NM_003051	NP_003042	P53985	MOT1_HUMAN	ical; (Potential).		1	TACCTCCACCAT	0.378	
-	3	436		NM_002524	NP_002515	P01111	RASN_HUMAN	GTP.	)|p.Q61P(21)|	2607	TCTTCTTGTCCA	0.458	rs11554290
+	8	663	|NBPF9_uc010oy	NM_001037675	NP_001032764	Q3BBV1	NBPFK_HUMAN	NBPF 1.		0	TGAAGTGAGCA	0.512	rs71527379
+	3	405	F9_uc010oyg.1_I	NM_001039703	NP_001034792	A6NDV3	A6NDV3_HUMAN			0	TCATTGTATGAG	0.562	rs4996268

+	9	1402	.1_Missense_Muta	NM_001039703	NP_001034792	A6NDV3	A6NDV3_HUMAN		0	AGAAATCATCTGC	0.438	
-	3	400		NM_001008536	NP_001008536	Q5QJ38	TCHL1_HUMAN		2	GCCTGAACATCCA	0.433	
-	24	8732_8733	ASH1L_uc001fkt.2	NM_018489	NP_060959	Q9NR48	ASH1L_HUMAN	BAH.	11	TCCAAGGGAATC	0.431	
-	41	5873		NM_003126	NP_003117	P02549	SPTA1_HUMAN	Spectrin 18.	8	TTTCCTCCTGCAA	0.428	
-	8	1172	e_Mutation_p.L253	NM_025160	NP_079436	Q9H7D7	WDR26_HUMAN	WD 2.	0	GCAACAAGATAGT	0.428	
-	12	1545	j.2_RNA|NEBL_uc	NM_006393	NP_006384	O76041	NEBL_HUMAN	Nebulin 10.	2	CCTTTAATCTCCT	0.333	
+	5	599	)1izo.1_RNA|HSD17B7P2_uc001izp.1_Missense_Mutation_p.N173S						0	CTCGCAATGCAAC	0.453	rs2257765
-	7	1309	GMS1_uc009xou.1	NM_147156	NP_671512	Q86VZ5	SMS1_HUMAN		2	GCATGGGGATCT	0.502	
+	1	144	uc001kwr.2_Intron	NM_001143909	NP_001137381	Q2QD12	Q2QD12_HUMAN		0	TCCATCCTCAACA	0.542	
+	20	3052	CS3_uc010qqz.1_	NM_014978	NP_055793	Q9UPU3	SORC3_HUMAN	enal (Potential).	10	GTCAACTGGGGA	0.463	
-	1	441	C2_uc009xxx.2_Ir	NR_026715					0	GCCAGGTGCCCC	0.537	
+	14	2550	RF1_uc010qwe.1_	NM_020901	NP_065952	Q9P1Y6	PHRF1_HUMAN		0	GATAAGGAGCAGA	0.577	
-	1	488		NM_001005238	NP_001005238	Q8NGK0	O51G2_HUMAN	Name=4; (Potential).	2	GGTAATGGAAAAA	0.473	
-	11	1231	.2_RNA|SERGEF_	NM_012139	NP_036271	Q9UGK8	SRGEF_HUMAN	RCC1 7.	1	CCTGACGATGACA	0.617	
+	11	2849	_p.R743*|NAV2_u	NM_145117	NP_660093	Q8IVL1	NAV2_HUMAN		6	CCCCTCGAGCCA	0.632	
+	29	3169	utation_p.L826P|D	NM_001105540	NP_001099010	Q13574	DGKZ_HUMAN	ANK 1.	3	GCACGCTCCTGCA	0.692	
+	9	1346	_p.R376K|BCO2_u	NM_031938	NP_114144	Q9BYV7	BCDO2_HUMAN		0	CTCGAAGGTTTGT	0.413	
+	9	1468	v.1_Missense_Mut	NM_002017	NP_002008	Q01543	FLI1_HUMAN		2273	CCGAGTCGTCCA	0.493	
-	3	857	p.R198C|FOXM1_u	NM_021953	NP_068772	Q08050	FOXM1_HUMAN		2	GCTGCGGGAGCC	0.493	
+	11	2149	cw.1_Missense_Mu	NM_030667	NP_109592	Q16827	PTPRO_HUMAN	III 7.|Extracellular (Potentia	9	CAACGGACTTGT	0.413	
-	4	444	3_5'UTR|PLCZ1_u	NM_033123	NP_149114	Q86YW0	PLCZ1_HUMAN		3	GAATTTTCCGGT	0.333	
-	11	3652	p.S807F|SFRS2IP	NM_004719	NP_004710	Q99590	SCAFB_HUMAN		0	TTATAGGATTGCT	0.428	
-	1	183		NM_012064	NP_036196	P30301	MIP_HUMAN	al; (By similarity).	1	CCAGGGCCAAGC	0.582	
+	14	2031	ense_Mutation_p.F	NM_182947	NP_891992	Q86VW2	ARHGP_HUMAN		0	CTCTCCCCTCTCT	0.577	
-	2	1182	_p.V275I|ZFC3H1_	NM_144982	NP_659419	O60293	ZC3H1_HUMAN		5	TACTGACATTATC	0.358	
+	24	3023_3024	tlq.2_Missense_M	NM_018082	NP_060552	Q9NW08	RPC2_HUMAN		2	CGGCTTCCCATC	0.5	
+	12	1215	t.2_Missense_Mut	NM_213594	NP_998759	Q33E94	RFX4_HUMAN	ary for dimerization.	1	CAGGAGTTTGAC	0.458	
-	8	2201_2202	e_Mutation_p.P656	NM_016179	NP_057263	Q9UBN4	TRPC4_HUMAN	and ITPR3.| p.P656P(1)	6	TGAAGGGAGTAG	0.431	
+	2	2484	n.2_Missense_Muta	NM_001173	NP_001025226	Q13017	RHG05_HUMAN		5	AGCAAGCTCTCA	0.413	
+	13	5940		NM_004274	NP_004265	Q13023	AKAP6_HUMAN		21	TCACATGGGAAAC	0.383	
-	2	538		NM_021136	NP_066959	Q16799	RTN1_HUMAN		4	ATGTCAGAAATGA	0.458	
-	2	886	orf43_uc010tud.1_	NM_194278	NP_919254	Q6PJG2	CN043_HUMAN		5	CTGGGGGGGCT	0.662	
+	2	671	4orf109_uc001ybk	NM_001098621	NP_001092091	Q8N6I4	CN109_HUMAN	ical; (Potential).	0	TCCTTGCCTTTTT	0.453	
+	23	2577		NM_058237	NP_478144	Q6NUP7	PP4R4_HUMAN		4	GGTTAGGAAAGA	0.303	rs150367623
+	4	538	p.R145C|EML1_u	NM_004434	NP_004425	O00423	EMAL1_HUMAN		5	CGGAATCGCACAC	0.507	
+	1	2045		NM_018958	NP_061831	Q9NZP6	CO002_HUMAN	Pro-rich.	8	ATTCCCCTCCTCC	0.547	
-	9	828	pc.2_Missense_M	NM_015289	NP_056104	Q96JC1	VPS39_HUMAN	CNH.	3	ACCACGGTGAGA	0.527	
-	3	560		NM_207381	NP_997264	Q5GJ75	TP8L3_HUMAN		0	TGTGCTCTTTGGT	0.448	
+	1	1499		NM_001080534	NP_001074003	Q8NB66	UN13C_HUMAN		7	GCAGCAGAATTTC	0.388	
-	14	1581	Flank|uc002bcw.1	NR_027024					0	GATGTTCTCCTCC	0.627	rs56290535
-	10	1091		NM_001896	NP_001887	P19784	CSK22_HUMAN	rotein kinase.	1	CCTCTTTGGCAGT	0.468	
+	3	605	2fye.2_Missense_M	NM_001114974	NP_001108446	Q2TAL5	SMTL2_HUMAN		0	CCAGATCCCCCCA	0.632	
+	6	544	splice|TBC1D3_uc	NM_032258	NP_115634	Q8IZP1	TBC3A_HUMAN		0	ACCAGGTACGCT	0.587	
-	1	457		NM_033059	NP_149048	Q9BYQ6	KR411_HUMAN	-[GIKRQVHEL]- [SPTR]-[S	0	ggagatgctgcagctgg	0.129	
+	3	498	xx.1_Missense_Mu	NM_003396	NP_003387	O14905	WNT9B_HUMAN		2	GAGCCGGCAGG	0.662	
+	2	664	.F_uc002iuh.2_5'U	NM_002126	NP_002117	Q16534	HLF_HUMAN		2	ACAAGGAAAAGA	0.433	
-	8	1079	xa.3_Missense_M	NM_001005207	NP_001005207	O94972	TRI37_HUMAN	Potential.	7	TCTTGGGTTAGAC	0.328	

-	8	1464	_p.S383L|CSNK1	NM_001893	NP_001884	P48730	KC1D_HUMAN			2	TCGGACGAGGAG	0.672	
-	6	1782	md.1_Missense_M	NM_020805	NP_065856	Q9P2G3	KLH14_HUMAN	Kelch 3.		1	CTCCCGCATGA	0.463	
+	13	1292	g.2_Missense_Mut	NM_024760	NP_079036	Q9H808	TLE6_HUMAN	WD 4.		1	GGTTATCCTGAT	0.567	
+	6	2416	u.2_Missense_Mut	NM_020209	NP_064594	Q96IW2	SHD_HUMAN	SH2.		0	CAGTTCACGCC	0.662	
+	8	2027	p.G599R|SYDE1_	NM_033025	NP_149014	Q6ZW31	SYDE1_HUMAN			2	CCTGTGGGCGG	0.697	
+	12	1425		NM_023944	NP_076433					7	GGTCACCTCTGG	0.557	
-	2	468	_p.L110*|LPAR2_	NM_004720	NP_004711	Q9HBW0	LPAR2_HUMAN	Name=3; (Potential).		2	CCAGCAAGCCC	0.667	
+	5	1060	.Q328L|CD22_uc	NM_001771	NP_001762	P20273	CD22_HUMAN	ellular (Potential).		9	AGTGCAGTGTG	0.652	
+	39	6573	_Mutation_p.S214	NM_000540	NP_000531	P21817	RYR1_HUMAN	6 X approximate repeats.		12	GTCCTCCGTGG	0.662	
-	5	979	LRA3_uc010erk.2	NM_006865	NP_006856	Q8N6C8	LIRA3_HUMAN	like C2-type 3.		1	ACTCGGAGGAG	0.677	
-	8	1027	sij.2_Nonsense_M	NM_015189	NP_056004	Q9Y2D4	EXC6B_HUMAN			2	GACATCGATAAA	0.368	
+	7	2842		NM_144993	NP_659430	O43151	TET3_HUMAN			0	CATAACCTCTAC	0.617	
-	4	729	s.2_Nonsense_Mu	NM_002349	NP_002340	O60449	LY75_HUMAN	ellular (Potential).		0	CTTTTCCCAATT	0.353	
+	8	4574	e_Mutation_p.P13	NM_152381	NP_689594	A4UGR9	XIRP2_HUMAN			14	TCCCTCCTTCTG	0.358	
-	41	7488		NM_018897	NP_061720	Q8WXX0	DYH7_HUMAN	4 (By similarity).		12	AATGATCAATAA	0.468	
+	14	2159	p.A651V|PARD3B	NM_152526	NP_689739	Q8TEW8	PAR3L_HUMAN			4	ATGGGCCGAGA	0.438	
+	3	429	1486_uc010fxa.1_	NM_020864	NP_065915	Q9P242	K1486_HUMAN			3	ACGAAGGAAGTT	0.478	
+	21	1404	utation_p.M414I|C	NM_000091	NP_000082	Q01955	CO4A3_HUMAN	e-helical region.		3	GCCATGGGGAC	0.602	
-	2	225	wtu.2_Missense_M	NM_178312	NP_842564	Q9BX51	GGTL1_HUMAN			1	TCCGGCATGTAG	0.622	
+	2	61	tj.1_RNA|FRG1B_uc010gdr.1_RNA|FRG1B_uc010ztk.1_Intron							0	CAGAATCGCCC	0.353	rs143761036
+	6	1242	K2_uc010ggp.2_M	NM_001098798	NP_001092268	Q96NM4	TOX2_HUMAN	Pro-rich.		1	CAGCCCCCCAG	0.677	
+	26	5528	eb.1_Missense_M	NM_005128	NP_005119	Q9Y3R5	DOP2_HUMAN			2	GAACTCCCAAC	0.403	
-	25	4734	CAM_uc002yyr.1_	NM_001389	NP_001380	O60469	DSCAM_HUMAN	III 5.|Extracellular (Potentia		11	TGATTGGAAAAC	0.488	
-	1	4437		NM_015672	NP_056487					0	GGTGCCCATGT	0.557	
+	2	954	D221G|RFPL3S_u	NM_001098535	NP_001092005	O75679	RFPL3_HUMAN	B30.2/SPRY.		1	TCTGGATATGG	0.512	
+	7	2403	atq.1_Missense_M	NM_001039141	NP_001034230	Q9H2D6	TARA_HUMAN			1	CCTCTCCTAACA	0.582	
+	2	379	R8_uc003cjm.2_In	NM_005201	NP_005192	P51685	CCR8_HUMAN	Name=2; (Potential).		2	CTGTCTGACCTG	0.488	
+	4	620	.S21L|ARIH2_uc0	NM_006321	NP_006312	O95376	ARI2_HUMAN			1	AAGTTTCAGAGA	0.363	
+	5	7708		NM_003458	NP_003449	Q9UPA5	BSN_HUMAN			8	GGTCTCCCCAGC	0.632	
+	1	379		NM_001005482	NP_001005482	Q8NGV7	OR5H2_HUMAN	lasmic (Potential).		3	TATGATCGCTAT	0.378	
+	3	237	a.1_Missense_Mu	NM_020202	NP_064587	Q9NQR4	NIT2_HUMAN	N hydrolase.		1	TATTTTCCTGAAT	0.373	
+	8	1414		NM_020754	NP_065805	Q2M1Z3	RHG31_HUMAN			2	TCTTTTAGGCGA	0.378	
-	7	1562	er.2_Missense_Mu	NM_175924	NP_787120	Q86SU0	ILDR1_HUMAN	lasmic (Potential).		1	GCCTCTCCTTGT	0.672	
+	12	1699_1700		NM_001004316	NP_001004316	Q6ZMV7	LEKR1_HUMAN			0	TTAAGGAAGAAA	0.347	
-	10	1211	.1_3'UTR|LRRC34	NM_153353	NP_699184	Q8IZ02	LRC34_HUMAN			0	GATTCTCCATAAG	0.378	
+	4	467	e_Mutation_p.R67	NM_182610	NP_872416	Q7Z3H4	SAMD7_HUMAN		p.R67W(1)	1	CAGTCGGATCT	0.428	rs138236130
+	11	1911	w.1_Missense_Mu	NM_198485	NP_940887	Q6ZUI0	TPRG1_HUMAN			0	CCACAAGAATTC	0.408	
+	12	1714	se_Mutation_p.P44	NM_003722	NP_003713	Q9H3D4	P63_HUMAN	SAM.		12	CACCTCCGTATC	0.607	
-	11	2052	fsg.2_Missense_M	NM_018192	NP_060662	Q8IVL5	P3H2_HUMAN			4	GTATAGGAAAAT	0.433	
-	9	1067_1068	_p.S183F|UBXN7_	NM_015562	NP_056377	O94888	UBXN7_HUMAN			3	CAAACGGATATG	0.416	
-	22	3199		NM_001042784	NP_001036249	Q5M9N0	CD158_HUMAN	Ser-rich.		6	TCTTAGGAGAAG	0.358	
-	12	1661	.1_Nonsense_Muta	NM_000204	NP_000195	P05156	CFAI_HUMAN	eptidase S1.		0	CCACTGAAGTG	0.333	
+	2	524	TU_uc011cgq.1_R	NM_015693	NP_056508	Q9ULD6	PDZD6_HUMAN			1	ACAGGAGTCATT	0.393	
+	1	2889	gz.2_Missense_M	NM_032961	NP_116586	Q9P2E7	PCD10_HUMAN	|Extracellular (Potential).		2	CAgggcgggggcgg	0.587	
-	1	1990	.1_Intron|PCDH18	NM_019035	NP_061908	Q9HCL0	PCD18_HUMAN	(Potential).|Cadherin 5.		5	CTTCATGATCAA	0.418	
-	1	46	A|GYPE_uc003ijk.	NM_198682	NP_941391	P15421	GLPE_HUMAN			0	GATCACGAGCT	0.398	
-	28	4403		NM_001369	NP_001360	Q8TE73	DYH5_HUMAN	.|Stem (By similarity).		31	AGCTTTCGACAT	0.468	

-	2	1200		NM_203406	NP_981951	Q68D91	MBLC2_HUMAN		0	CCAATCGAAAAA	0.408	
-	14	1547	3lwy.2_Missense_	NM_033274	NP_150377	Q9H013	ADA19_HUMAN	Extracellular (Potential).	8	GGTAGGGCAGT	0.622	
+	9	7204	EP1_uc011diq.1_	NM_002114	NP_002105	P15822	ZEP1_HUMAN		6	CAGCCCCCAGA	0.512	
-	30	4190	27_uc003nxd.2_5'	NM_006295	NP_006286	P26640	SYVC_HUMAN		3	GCGATGGCCTCA	0.572	
-	32	4462	ai.2_Missense_Mu	NM_138694	NP_619639	P08F94	PKHD1_HUMAN	Extracellular (Potential).	44	GCGATGGGAAGA	0.507	
-	16	3591	I2A1_uc003pht.2_	NM_004370	NP_004361	Q99715	COCA1_HUMAN	onectin type-III 8.	9	AAAACAACTGTG	0.418	
+	17	1964	Splice_Site|STXBF	NM_001127715	NP_001121187	Q5T5C0	STXB5_HUMAN		0	ATTTTAGAGTTAA	0.313	
+	7	1005	G_uc003quc.2_Mis	NM_152410	NP_689623	Q96M98	PACRG_HUMAN		0	AACATTGGGGAC	0.507	
+	3	1358	LL2_uc011egr.1_R	NM_031949	NP_114155	Q9BWV7	TTLL2_HUMAN	TTL.	3	ATGAGGGGAGA	0.433	rs141172576
+	6	1057	.3_Missense_Muta	NM_000600	NP_000591	P05231	IL6_HUMAN		0	TTTAAGGAGTTC	0.527	
-	9	1318	SUN5_uc003txx.2_	NM_018044	NP_060514	Q96P11	NSUN5_HUMAN		0	CCTTGGCACCT	0.607	
-	2	257		NM_001024607	NP_001019778	A4D0T2	CG066_HUMAN		2	TGACGATATTGA	0.418	
+	14	1470	2_3'UTR|ST7_uc0	NM_021908	NP_068708	Q9NRC1	ST7_HUMAN		2	ACCTCACCCGC	0.507	
-	2	476	T2_uc003vja.2_5'	NM_003391	NP_003382	P09544	WNT2_HUMAN		7	CATCTGGATGTC	0.597	
+	5	634	_Mutation_p.S10	NM_001868	NP_001859	P15085	CBPA1_HUMAN		1	AGGCCAGTGGG	0.652	
-	15	1860		NM_004333	NP_004324	P15056	BRAF_HUMAN	rotein kinas _R603>I(2)|p.T	18290	GATTTCACTGTA	0.368	
-	4	776	39B_uc003wig.3_	NM_173681	NP_775952	Q674R7	ATG9B_HUMAN	nal (By similarity).	1	GCATCGAAGGA	0.537	
-	3	452		NM_014420	NP_055235	Q9UBT3	DKK4_HUMAN		1	GTTGTTCCTTCT	0.458	
-	3	1741	CO5A1_uc003xyk	NM_030958	NP_112220	Q9H2Y9	SO5A1_HUMAN	Name=6; (Potential).	4	CAGTTTCCAATG	0.348	
-	10	2369		NM_001163	NP_001154	Q02410	APBA1_HUMAN	PDZ 1.	1	AGCTTCCCAGAT	0.527	
+	1	805		NM_001004484	NP_001004484	Q8NGV5	O13D1_HUMAN	lasmic (Potential).	2	AAGAAAGCCTTC	0.383	
+	11	1721	omf.1_Missense_M	NM_000962	NP_000953	P23219	PGH1_HUMAN		2	CCTTTTCCCTCA	0.512	
-	2	422	R34_uc004bvr.1_M	NM_052844	NP_443076	Q96EX3	WDR34_HUMAN		3	GGACGGGGGCT	0.627	
-	28	7018	6A_uc004cht.2_M	NM_014866	NP_055681	O15027	SC16A_HUMAN	action with SEC23A.|Pro-ri	0	GCTGTGGTTCTT	0.622	
-	2	231	NA9L_uc010nfp.2_	NM_001412	NP_001403	P47813	IF1AX_HUMAN		1	TTACCTCCTTTAC	0.313	
-	2	2186		NM_152424	NP_689637	Q5JTC6	F123B_HUMAN	p.0?(40)	112	ACTTGAGTCTCT	0.617	
-	25	2239	p.E368K|TEX11_u	NM_001003811	NP_001003811	Q8IYF3	TEX11_HUMAN		5	CTTGCTCTAGAT	0.393	
+	25	4487		NM_198576	NP_940978	O00468	AGRIN_HUMAN	minin G-like 1.	3	GGCGAGAGTCC	0.692	
+	8	916	nse_Mutation_p.G	NM_153339	NP_699170	Q8N0Z8	PUSL1_HUMAN		1	TGCAGGGGCCA	0.662	
-	38	5594	_Mutation_p.V68	NM_015557	NP_056372	Q8TDI0	CHD5_HUMAN		12	ACTCCACTTCAG	0.652	
-	6	672		NM_001561	NP_001552	Q07011	TNR9_HUMAN	cellular (Potential).	4	AGTTACCTGGCT	0.537	
-	12	1431		NM_207420	NP_997303	Q6PXP3	GTR7_HUMAN	lasmic (Potential).	0	GCGGTTTATCTC	0.483	
+	35	3967	z.2_Nonsense_Mu	NM_015074	NP_055889	O60333	KIF1B_HUMAN		3	GGTTTGGTTTGA	0.373	
-	3	234	_p.L77F|C1orf127	NM_173507	NP_775778	B7ZLG7	B7ZLG7_HUMAN		1	GAAGAAGGCCTT	0.607	
+	8	2164	asi.1_Missense_M	NM_020780	NP_065831	Q9P2K9	PTHD2_HUMAN	lasmic (Potential).	7	AGGTCGAGGAA	0.632	
-	2	397	.1_Intron|CLCN6_	NM_006172	NP_006163	P01160	ANF_HUMAN		2	GGGGCCCCGCC	0.672	
+	1	307		NM_001080830	NP_001074299	O95522	PRA12_HUMAN		3	AGGTTCGCCCC	0.592	
-	1	317	10obf.1_Missense_	NM_001146181	NP_001139653	B7ZW38	B7ZW38_HUMAN		0	AGCAATCATTCT	0.502	
+	7	787		NM_033440	NP_254275	P08217	CEL2A_HUMAN	Peptidase S1.	2	TCACGCGGGTCT	0.622	
+	11	1654	JC16_uc001awt.2_	NM_015291	NP_056106	Q9Y2G8	DJC16_HUMAN	lasmic (Potential).	3	CTCCTTCGATGG	0.468	
+	1	408	C7A_uc009vpg.2_	NM_152375	NP_689588	Q5VTJ3	KLD7A_HUMAN		3	CCAGAGAAAAG	0.627	
+	1	1307	vpg.2_Missense_	NM_152375	NP_689588	Q5VTJ3	KLD7A_HUMAN		3	CATATCCCGCTC	0.647	
-	2	117	G2D_uc009vpo.2_	NM_012400	NP_036532	Q9UNK4	PA2GD_HUMAN		0	TTTTCCCAGTCA	0.552	
-	4	954		NM_024544	NP_078820	Q969V5	MUL1_HUMAN	lasmic (Potential).	0	TCCTGCCGCTGC	0.607	
-	8	964	ei.2_Nonsense_M	NM_001397	NP_001388	P42892	ECE1_HUMAN	cellular (Potential).	3	CTCCTCGTCCC	0.622	
-	15	1286	bew.2_Missense_	NM_002885	NP_002876	P47736	RPGP1_HUMAN	Rap-GAP.	3	AAGAAGGGCACA	0.647	
+	10	1997	ogf.2_Missense_M	NM_017449	NP_059145	P29323	EPHB2_HUMAN	lasmic (Potential).	5	ATTGACATCTCC	0.532	

+	10	1299	p.R413Q|GRHL3_	NM_021180	NP_067003	Q8TE85	GRHL3_HUMAN		1	CGAGCGGAAGC	0.627	
+	2	967	vry.1_Missense_	NM_020379	NP_065112	Q9NR34	MA1C1_HUMAN	enal (Potential).	1	TGTTCGGTGAG	0.502	
-	24	3586	w.1_Missense_M	NM_004672	NP_004663	O95382	M3K6_HUMAN		9	TGCCCGCACAG	0.662	rs143876994
-	17	2467	p.P732S|MAP3K6	NM_004672	NP_004663	O95382	M3K6_HUMAN	rotein kinase.	9	CAGGGGTCCCC	0.582	rs138197184
-	2	203		NM_207397	NP_997280	Q6UWJ8	C16L2_HUMAN	ellular (Potential).	0	AGGCGGATCA	0.622	
-	6	1602_1603	S4_uc010ofy.1_3'	NM_005626	NP_005617	Q08170	SRSF4_HUMAN	r-rich (RS domain).	0	ACACGGAGCG	0.446	rs146685214
+	31	4434	tq.2_Missense_M	NM_005704	NP_005695	Q92729	PTPRU_HUMAN	lasmic (Potential).	7	TGGAGGGGCTG	0.602	
-	1	126	lank|ZCCHC17_u	NM_004814	NP_004805	Q96DI7	SNR40_HUMAN		0	CCGCTCCCAAC	0.637	
-	4	529	to.2_Missense_M	NM_001703	NP_001694	O60241	BAI2_HUMAN	ellular (Potential).	13	GGTAGGAAAGA	0.677	
-	2	900	e_Mutation_p.G28	NM_144569	NP_653170	Q6ZMY3	SPOC1_HUMAN		6	CAGTCCCTGAG	0.637	
+	13	1540	z.2_Missense_Mut	NM_005356	NP_005347	P06239	LCK_HUMAN	rotein kinase.	6	CAGAGGAGCTG	0.597	
-	5	825	xm.1_Missense_	NM_052896	NP_443128	Q7Z408	CSMD2_HUMAN	tracellular (Potential).	12	CCAGAGGGAGG	0.542	
-	2	150	xm.1_Missense_	NM_052896	NP_443128	Q7Z408	CSMD2_HUMAN	tracellular (Potential).	12	GAACCCTGGGC	0.537	
+	5	796	_Mutation_p.E12	NM_012199	NP_036331	Q9UL18	AGO1_HUMAN		3	GGCGCGAGGT	0.632	
-	4	672	nse_Mutation_p.S	NM_017850	NP_060320	Q9NX04	CA109_HUMAN		0	TAGACGAAAG	0.438	
-	2	232	e_Mutation_p.H49	NM_004468	NP_004459	Q13643	FHL3_HUMAN	l zinc-binding 1.	0	GTCATGCCCGA	0.607	
+	1	3712	.1_Intron|MACF1_	NM_015038	NP_055853	O94854	K0754_HUMAN	Ala-rich.	0	ATGCTCCAGAG	0.617	
-	2	265		NM_032526	NP_115915	Q9BXI3	5NT1A_HUMAN		1	GGGTTCGTTCT	0.448	
-	3	305	AL4_uc010oix.1_	NM_016257	NP_057341	Q9UM19	HPCL4_HUMAN	EF-hand 2.	1	ACTTGGAGGCG	0.692	
+	9	770	E_uc001cdv.2_Mi	NM_006112	NP_006103	Q9UNP9	PPIE_HUMAN	e cyclophilin-type.	0	CAAACACCAAT	0.547	
+	4	385	001cfy.3_Missens	NM_001142588	NP_001136060	Q13952	NFYC_HUMAN		3	ACCTCCAAAGC	0.423	
-	5	6392	e_Mutation_p.P17	NM_024503	NP_078779	Q5T1R4	ZEP3_HUMAN		6	CGCCGGCTCCC	0.562	
-	9	1723		NM_006516	NP_006507	P11166	GTR1_HUMAN	lasmic (Potential).	5	TGGACGTGGAC	0.552	rs80359839
+	13	2096	q.2_Missense_Mu	NM_005424	NP_005415	P35590	TIE1_HUMAN	III 3.|Extracellular (Potentia	7	CTGGGCCAATA	0.637	
+	11	2137_2138	p.R171C|PTPRF_	NM_002840	NP_002831	P10586	PTPRF_HUMAN	tential).|Fibronectin type-III	10	AGGCCCGCAC	0.545	
+	7	936	s.1_Missense_Mu	NM_001034024	NP_001029196	Q9NPF5	DMAP1_HUMAN		0	CGGAACGCAAG	0.617	
+	10	1654	_Mutation_p.R148	NM_018150	NP_060620	Q5VTB9	RN220_HUMAN		2	CACTTCGGGGC	0.592	
-	2	557	s.3_Missense_Mu	NM_005897	NP_005888	Q9Y573	IPP_HUMAN	BTB.	1	TACCTGTGTAA	0.274	
+	5	842	AH_uc001cpv.2_R	NM_001441	NP_001432	O00519	FAAH1_HUMAN	smic (By similarity).	2	GCGGCCTCAAG	0.517	
-	3	429	e_Mutation_p.W12	NM_000778	NP_000769	Q02928	CP4AB_HUMAN		4	CCAATCCATGG	0.458	
+	7	854	A9_uc010omt.1_	NM_001011547	NP_001011547	Q2M3M2	SC5A9_HUMAN	ellular (Potential).	3	CTTTCCACATT	0.612	
-	5	461	A6_uc010omv.1_	NM_019073	NP_061946	Q9NWH7	SPAT6_HUMAN		1	ACGTAGACAGT	0.363	
-	3	808		NM_147193	NP_671726	Q8NBF1	GLIS1_HUMAN		1	GGCACAGGGTG	0.677	
-	9	1016	w.2_RNA|YIPF1_u	NM_018982	NP_061855	Q9Y548	YIPF1_HUMAN	enal (Potential).	2	CCAACGAACAG	0.483	rs77267196
+	5	553		NM_006252	NP_006243	P54646	AAPK2_HUMAN	rotein kinase.	6	GATTATCTAATAT	0.333	
-	2	1157	orf168_uc009vzv.	NM_001004303	NP_001004303	Q5VWT5	CA168_HUMAN		5	TGGGGCCTGAC	0.507	
-	2	1071	orf168_uc009vzv.	NM_001004303	NP_001004303	Q5VWT5	CA168_HUMAN		5	CTTTTTCTGATAT	0.512	
+	4	575		NM_000562	NP_000553	P07357	CO8A_HUMAN	MACPF.	3	TCCAGGATCAC	0.498	
-	11	1656	p.Q468R|C8B_uc	NM_000066	NP_000057	P07358	CO8B_HUMAN	EGF-like.	4	GGCCTTGGGAT	0.498	
-	2	286	8B_uc010ooo.1_	NM_000066	NP_000057	P07358	CO8B_HUMAN	SP type-1 1.	4	GTGGTCCAAGA	0.522	
-	14	1620	r.1_Missense_Mu	NM_021080	NP_066566	O75553	DAB1_HUMAN		3	GACGAGGGGCT	0.617	
+	8	1642_1643	uc001dbl.2_Intron	NM_005012	NP_005003	Q01973	ROR1_HUMAN	ical; (Potential).	19	CCATTCCCCTG	0.446	
+	9	3086	c001dbm.2_5'Fla	NM_005012	NP_005003	Q01973	ROR1_HUMAN	lasmic (Potential).	19	TGGTGGAATGG	0.428	
+	4	563	aq.2_Nonsense_M	NM_002303	NP_002294	P48357	LEPR_HUMAN	ellular (Potential).	1	TTTTTCAACAA	0.313	
+	3	1083	uc001dim.2_Silent	NM_000959	NP_000950	P43088	PF2R_HUMAN	ellular (Pot273*(1)|p.L296	6	AACATTGGAATA	0.343	
+	9	1814	se_Mutation_p.E5	NM_012302	NP_036434	O95490	LPHN2_HUMAN	ellular (Potential).	9	CCAATGAACTG	0.403	
+	14	2810	.L877F|LPHN2_uc	NM_012302	NP_036434	O95490	LPHN2_HUMAN	Name=2; (Potential).	9	TCAACCTTTTC	0.378	

-	5	1606	ose.1_RNA|COL2	NM_152890	NP_690850	Q17RW2	COOA1_HUMAN	ollagen-like 1.	5	GATTTCCATGTG	0.393	
+	7	1377	9524_uc001dme.1	NM_012262	NP_036394	Q7LGA3	HS2ST_HUMAN	enal (Potential).	1	CCCATGCCGTTC	0.383	
-	3	1761	BL2_uc001dmr.2_	NM_001162536	NP_001156008	Q96E39	RBMXL_HUMAN	Ser-rich.	0	AGGGGGAAGCC	0.537	
+	2	370	P6_uc010ost.1_In	NM_198460	NP_940862	Q6ZN66	GBP6_HUMAN		2	TCTTGAAAAGAT	0.468	
+	3	573	P6_uc010ost.1_In	NM_198460	NP_940862	Q6ZN66	GBP6_HUMAN	(By similarity).	2	CGAAGGTCTGG	0.507	
-	3	2255	lnx.2_Intron|ZNF6	NM_201269	NP_958357	Q9H582	ZN644_HUMAN		3	ATGAGGAGAGC	0.378	
+	6	614	w.1_Missense_Mu	NM_003503	NP_003494	O00311	CDC7_HUMAN	rotein kinase.	5	CTCTTTCCTTTCA	0.294	
+	7	986		NM_173567	NP_775838	Q8IUS5	EPHX4_HUMAN		1	CACATGGTGAC	0.413	
-	18	2304	f.1_Missense_Mut	NM_005665	NP_005656	O60447	EVI5_HUMAN	s.|Interaction with AURKB	2	GACATCGAACCA	0.458	
-	8	1144	tn.1_Missense_Mu	NM_000350	NP_000341	P78363	ABCA4_HUMAN	Extracellular.	12	AGAAAGGCCTTA	0.473	
-	5	567	tn.1_Missense_Mu	NM_000350	NP_000341	P78363	ABCA4_HUMAN	Extracellular.	12	AGATATCCCTTAT	0.408	
-	13	1775	RHGAP29_uc001c	NM_004815	NP_004806	Q52LW3	RHG29_HUMAN		11	TTGTGGCCTTG	0.373	
-	5	516	YD_uc001drw.2_	NM_000110	NP_000101	Q12882	DPYD_HUMAN		8	CATTCCACAAG	0.353	
+	7	775_776		NM_033055	NP_149044	Q96MC6	HIAT1_HUMAN	Name=7; (Potential).	0	ACCTACCGGAGG	0.386	
-	16	2055	e|COL11A1_uc00	NM_001854	NP_001845	P12107	COBA1_HUMAN		12	GCCATACCCTTT	0.353	
-	8	1555	_p.E425K|COL11A	NM_001854	NP_001845	P12107	COBA1_HUMAN	nhelical regi p.F413V(1)	12	TTGTTTCTGTAA	0.328	
+	7	1259	ense_Mutation_p.L	NM_013296	NP_037428	P81274	GPSM2_HUMAN	TPR 6.	1	ATATTTCTTGGTG	0.318	
+	1	698		NM_001408	NP_001399	Q9HCU4	CELR2_HUMAN	|Extracellular (Potential).	8	GGTGAGGCAGGT	0.627	
+	10	1702	561D1_uc001dxu.	NM_153340	NP_699171	Q5T6C5	AT7L2_HUMAN		2	ACGGGGTGGAG	0.602	rs148343235
+	2	1323		NM_031936	NP_114142	Q9BZJ8	GPR61_HUMAN	Name=5; (Potential).	2	TTTGCTGTCCTT	0.602	
+	2	1532	e_Mutation_p.R49	NM_004978	NP_004969	Q03721	KCNC4_HUMAN	lasmic (Potential).	3	GAAACGGAAGA	0.617	rs140378578
+	1	1834	sense_Mutation_p.	NM_022768	NP_073605	Q96T37	RBM15_HUMAN		3	TGACTCTGATTG	0.567	
-	11	1432	p.S421F|OVGP1_	NM_002557	NP_002548	Q12889	OVGP1_HUMAN		5	CAAGGGATACA	0.502	
-	2	571	ebv.1_Missense_M	NM_004980	NP_004971	Q9UK17	KCND3_HUMAN	lasmic (Potential).	3	GGCCGGGGCCA	0.677	
-	5	435		NM_005725	NP_005716	O60636	TSN2_HUMAN	ellular (Potential).	0	CCTCTTCATACAT	0.403	
+	10	2007	vhg.1_Missense_M	NM_006699	NP_006690	O60476	MA1A2_HUMAN	enal (Potential).	0	TGTAGGCTATAG	0.353	
-	11	1530	hg.2_Missense_M	NM_017686	NP_060156	Q9NXN4	GDAP2_HUMAN	CRAL-TRIO.	2	CAACATCGTAGA	0.363	
-	19	2687		NM_206996	NP_996879	Q6Q759	SPG17_HUMAN		6	CTCATTCATTTTA	0.328	
+	6	915	r.1_Missense_Mu	NM_001005783	NP_001005783	Q9NYQ3	HAOX2_HUMAN	xy acid dehydrogenase.	4	TATAGGGAAATG	0.418	
+	19	2193	tion_p.E30G|NBP	NM_001037675	NP_001032764	Q3BBV1	NBPFK_HUMAN	NBPF 5.	0	GAAAGAGCCTG	0.483	
+	10	4827	.1_Missense_Mut	NM_004326	NP_004317	O00512	BCL9_HUMAN	Pro-rich.	6	AGGATCGGGGG	0.597	
+	12	1536	vkt.1_Missense_M	NM_001102663	NP_001096133				0	CCTTCAGATTAT	0.483	
-	19	2487_2488	ww.2_Missense_	NM_030913	NP_112175	Q9H3T2	SEM6C_HUMAN	lasmic (Potential).	2	ACCCTCCTTGG	0.604	
-	3	205		NM_001122965	NP_001116437	Q6XPR3	RPTN_HUMAN	y similarity).|EF-hand 1.	0	TTTGGTCTCTGT	0.433	
-	3	8357		NM_002016	NP_002007	P20930	FILA_HUMAN	Ser-rich.	16	GCCTGGAGCTG	0.592	
-	3	2615	uc001ezv.2_5'Flan	NM_002016	NP_002007	P20930	FILA_HUMAN	Ser-rich.	16	CTACCGATTGC	0.592	
-	3	3984	uc001ezv.2_Intron	NM_001014342	NP_001014364	Q5D862	FILA2_HUMAN		17	TGGATCCTGAC	0.478	
+	2	175_176		NM_001025231	NP_001020402	Q5T749	KPRP_HUMAN	Gln-rich.	5	CAAGCCCCTTGT	0.574	
+	2	81		NM_005547	NP_005538	P07476	INVO_HUMAN		3	CCTCTCCCCTG	0.532	
-	2	444		NM_005978	NP_005969	P29034	S10A2_HUMAN	EF-hand 1.	1	GAAGTTCCTTCA	0.577	
+	25	2969		NM_020452	NP_065185	P98198	AT8B2_HUMAN	ical; (Potential).	2	CATCTGCATCG	0.572	
-	2	1302	_p.L25F|KCNN3_u	NM_002249	NP_002240	Q9UGI6	KCNN3_HUMAN	=Segment S2; (Potential).	1	CAAAAGGATGA	0.542	
+	7	842	p.S274C|DCST1_	NM_152494	NP_689707	Q5T197	DCST1_HUMAN	ellular (Potential).	2	TTGCTCCTGTG	0.617	rs56354873
+	17	2015	ADAM15_uc001fg	NM_152494	NP_689707	Q5T197	DCST1_HUMAN	lasmic (Potential).	2	GCGCCGCTGGC	0.721	
+	9	2666_2667	1fkq.2_Missense_	NM_001105203	NP_001098673	Q9BVN2	RUSC1_HUMAN		2	TGCCCCCGACA	0.579	
-	3	4601	.S1374F|ASH1L_	NM_018489	NP_060959	Q9NR48	ASH1L_HUMAN		11	TACTAGAAAGA	0.438	
+	3	939	b.2_Missense_Mu	NM_005973	NP_005964	Q92733	PRCC_HUMAN		27	CTAAGCCCTCC	0.562	

+	11	1371	p.L138F|NTRK1_	NM_002529	NP_002520	P04629	NTRK1_HUMAN	ical; (Potential).	17	CTTGTGCTCAAC	0.577	
+	20	2628	fqk.1_Splice_Site_	NM_001080471	NP_001073940	Q5VY43	PEAR1_HUMAN		3	TCTTAGGTTCC	0.642	
+	2	446	1C_uc001frv.2_5'F	NM_001765	NP_001756	P29017	CD1C_HUMAN	ellular (Potential).	4	TGGACGAGTTG	0.498	
-	1	509		NM_001005279	NP_001005279	Q8NGY2	OR6K2_HUMAN	ellular (Potential).	1	TGATTCGAACCA	0.483	
-	1	122		NM_001005279	NP_001005279	Q8NGY2	OR6K2_HUMAN	Name=1; (Potential).	1	AGGTTTCCAACA	0.428	
+	4	814	p.S181F|PYHIN1_	NM_152501	NP_689714	Q6K0P9	IFIX_HUMAN		4	ACACTTCCTCAA	0.502	
+	1	149	uc001fts.3_Intron	NM_012351	NP_036483	P30954	O10J1_HUMAN	Name=1; (Potential).	1	TAACCTTAGCAG	0.433	
+	1	568	uc001fts.3_Intron	NM_012351	NP_036483	P30954	O10J1_HUMAN	ellular (Potential).	1	TCTGTGACATCC	0.493	
+	9	1221	L6_uc009wsz.1_S	NM_001004310	NP_001004310	Q6DN72	FCRL6_HUMAN		3	AAAGGTGAGCT	0.542	
+	16	2249	p.G706E|ATP1A2_	NM_000702	NP_000693	P50993	AT1A2_HUMAN	lasmic (Potential).	7	CCAGGGAGCCA	0.612	
+	6	1150	1A4_uc001fvf.3_	NM_144699	NP_653300	Q13733	AT1A4_HUMAN	lasmic (Potential).	4	ACAACTCATCCT	0.498	
+	5	664	wc.1_Missense_M	NM_020335	NP_065068	Q9ULK5	VANG2_HUMAN	Name=1; (Potential).	1	CCTCACGCCTC	0.662	
+	11	1467	289F|NDUFS2_uc	NM_004550	NP_004541	O75306	NDUS2_HUMAN		1	CCAGTCCCTGA	0.522	
+	9	1469	_Mutation_p.G32	NM_002585	NP_002576	P40424	PBX1_HUMAN		5	TGGAGGTTGGC	0.458	
-	10	1553	p.G389E|ALDH9A	NM_000696	NP_000687	P49189	AL9A1_HUMAN		0	TTATATCCACCAA	0.448	
-	19	2651	plj.1_Missense_M	NM_018417	NP_060887	Q96PN6	ADCYA_HUMAN		3	ACTATGGAGAG	0.373	
-	13	3234		NM_000130	NP_000121	P12259	FA5_HUMAN	B.	6	TTTTTTCGTGTC	0.408	
-	14	2413	ELP_uc009wvr.2_	NM_003005	NP_002996	P16109	LYAM3_HUMAN	ical; (Potential).	4	GACCTATCGTAG	0.443	
-	2	399	nk|C1orf112_uc00	NM_033418	NP_219486	O95568	MET18_HUMAN		0	CTTCTCCTTTTT	0.423	
+	6	799	b.1_Missense_M	NM_001002294	NP_001002294	P31513	FMO3_HUMAN		1	GTTATCCTTGG	0.463	
-	8	632	hy.1_Missense_M	NM_003762	NP_003753	O75379	VAMP4_HUMAN	cular (Potential).	0	AGTACGGTATT	0.289	
-	2	693_694	p.P205S|TNR_uc	NM_003285	NP_003276	Q92752	TENR_HUMAN	Cys-rich.	11	AGCGGGCAGT	0.589	
-	1	97	n_p.E6K|TNR_uc	NM_003285	NP_003276	Q92752	TENR_HUMAN		11	TGTTTCCCCAT	0.532	
+	8	4135	A2_uc009www.2_	NM_020318	NP_064714	Q9BXP8	PAPP2_HUMAN		16	AAAACAAGGAG	0.552	
+	19	2275	orf125_uc001gmp.	NM_144696	NP_653297	Q5T1B0	AXDN1_HUMAN		0	TTTAATGATACCC	0.368	
+	24	5501	xl.2_Missense_M	NM_014810	NP_055625	Q5VT06	CE350_HUMAN		4	CGTGAAAAGGC	0.393	
+	14	2207	n.2_Missense_M	NM_004736	NP_004727	Q9UBH6	XPR1_HUMAN	lasmic (Potential).	0	CCGGCCTCGCC	0.463	
+	18	2323	wxs.2_Missense_	NM_000721	NP_000712	Q15878	CAC1E_HUMAN	ic (Potential).|Poly-Glu.	6	AGGAAGAAGAG	0.552	
+	7	1086	e_Mutation_p.L25	NM_005562	NP_005553	Q13753	LAMC2_HUMAN	inin IV type A.	3	AAATTTCTTGGG	0.463	
+	7	1118	_Mutation_p.S26	NM_005562	NP_005553	Q13753	LAMC2_HUMAN	inin IV type A.	3	TCAAAGCCTGTC	0.478	
-	2	1272	.2_Intron|RGL1_u	NM_203454	NP_982279	Q8WW27	ABEC4_HUMAN		0	CCTTCCAAGGT	0.438	
-	8	1150	yh.1_Nonsense_	NM_052966	NP_443198	Q9BZQ8	NIBAN_HUMAN		4	TTCTTTGAGTTC	0.418	
-	3	381	_Site_p.P63_splic	NM_052966	NP_443198	Q9BZQ8	NIBAN_HUMAN		4	GGTGGCTTAAA	0.343	
+	7	1474	_Mutation_p.A382	NM_005807	NP_005798	Q92954	PRG4_HUMAN	ats of K-X-P-X-P-T-T-X.|17	1	AGCCTGCACCC	0.657	rs138528418
+	15	1785	0pos.1_Splice_Sit	NM_024420	NP_077734	P47712	PA24A_HUMAN		3	TTTTAAGATCCT	0.308	
-	6	1055	ot.1_Missense_M	NM_199051	NP_950252	Q76B58	FAM5C_HUMAN		5	CATTTTCCTTGC	0.448	
+	7	1202	.2_Missense_Mu	NM_000186	NP_000177	P08603	CFAH_HUMAN	Sushi 5.	6	GATGTACCTGTA	0.358	
+	7	2615	B1_uc010ppb.1_In	NM_201253	NP_957705	P82279	CRUM1_HUMAN	otential).|Laminin G-like 2.	9	AAAGGGAGATG	0.373	
-	2	1445	14_uc010ppj.1_5'	NM_014875	NP_055690	Q15058	KIF14_HUMAN	d for PRC1-binding.	7	TTCGGGAAGAA	0.383	
-	2	1443	14_uc010ppj.1_5'	NM_014875	NP_055690	Q15058	KIF14_HUMAN	d for PRC1-binding.	7	TCGGGAAGAATT	0.383	
-	7	1202_1203		NM_000069	NP_000060	Q13698	CAC1S_HUMAN	=S6 of repeat I; (Potential)	5	GTTGAGGATGAA	0.401	
-	5	176	NNI1_uc001gwp.2	NM_003281	NP_003272	P19237	TNNI1_HUMAN	ed in binding TNC.	0	AGCATTCCTTG	0.667	
-	2	75	|TNNI1_uc001gw	NM_003281	NP_003272	P19237	TNNI1_HUMAN		0	CAGCACCTAGG	0.592	
+	14	3718	p.R725H|NAV1_u	NM_020443	NP_065176	Q8NEY1	NAV1_HUMAN	Potential.	4	ATCCCGCCTGC	0.582	
+	21	2850		NM_018085	NP_060555	Q96P70	IPO9_HUMAN		2	ATGCCGCTCGC	0.507	
+	17	1630	R6_uc009xab.2_R	NM_001017403	NP_001017403	Q9HBX8	LGR6_HUMAN	ellular (Potential).	10	GTGTCCAGTGT	0.562	
+	17	2530	1gyb.1_Nonsense	NM_002481	NP_002472	O60237	MYPT2_HUMAN		3	CCATCCGAGAG	0.463	

-	4	472	zk.1_5'Flank|CHI3L	NM_001276	NP_001267	P36222	CH3L1_HUMAN		1	ACCCAAAGTTCC	0.552	
+	17	2478	naf.2_Missense_M	NM_014827	NP_055642	O75152	ZC11A_HUMAN		2	GGTGGAGGTAG	0.478	
+	3	1150	orf.1_Missense_Mu	NM_014858	NP_055673	O75069	TMCC2_HUMAN		1	AGCAACGTGTAC	0.677	rs146720283
+	4	519	.P130L|C4BPB_u	NM_001017365	NP_001017365	P20851	C4BPB_HUMAN	Sushi 2.	1	CACCTCCCTTTC	0.453	
+	3	208	hhk.2_Missense_	NM_181755	NP_861420	P28845	DHI1_HUMAN	nenal (Potential).	1	TCCAAGGAAAGA	0.517	
-	8	1706_1707	ic.2_Missense_Mu	NM_172362	NP_758872	O95259	KCNH1_HUMAN	lasmic (Potential).	5	CTCATGGTATCT	0.465	
-	13	2672	oty.1_Missense_Mu	NM_005401	NP_005392	Q15678	PTN14_HUMAN		5	GGCCCCGTTGA	0.612	rs142432691
-	68	15292		NM_206933	NP_996816	O75445	USH2A_HUMAN	II 35.|Extracellular (Potenti	26	GCCCTCCGTCGG	0.542	
-	63	13471		NM_206933	NP_996816	O75445	USH2A_HUMAN	ential).|Fibronectin type-III	26	GATCTGGAGGGC	0.478	
-	27	3982		NM_004446	NP_004437	P07814	SYEP_HUMAN		2	TCCTCCCTAAAAT	0.318	
+	4	979	a.1_Missense_Mu	NM_198551	NP_940953	Q5JRA6	MIA3_HUMAN	cellular (Potential).	5	CAAGAAGACTTT	0.388	
+	8	2803		NM_032890	NP_116279	Q96F81	DISP1_HUMAN		0	GAGATTTTTGAA	0.483	
-	2	879	.1_5'UTR|SUSD4_	NM_017982	NP_060452	Q5VX71	SUSD4_HUMAN	xtracellular (Potential).	0	TGAAATCGGGCT	0.517	
-	5	1102	od.1_Missense_Mu	NM_001008493	NP_001008493	Q8N8S7	ENAH_HUMAN	Potential.	2	ctgccgctccaggcgtt	0.264	
-	33	5691	p.P1555L|CDC42	NM_003607	NP_003598	Q5VT25	MRCKA_HUMAN		11	CCATGGGCAGA	0.383	
+	39	10431	p.E3463K|OBSCN	NM_001098623	NP_001092093	Q5VST9	OBSCN_HUMAN	Ig-like 35.	28	CCGTGGAAGGG	0.582	
-	7	2566	1L2_uc001hvf.2_5'	NM_020808	NP_065859	Q9P2F8	SI1L2_HUMAN	Rap-GAP.	6	CTCGTTCGAGTG	0.483	
-	7	2451	1L2_uc001hvf.2_5'	NM_020808	NP_065859	Q9P2F8	SI1L2_HUMAN	Rap-GAP.	6	CTTTGGGAATCG	0.408	
+	2	1201	hvs.1_Missense_	NM_032435	NP_115811	Q5TCX8	M3KL4_HUMAN	rotein kinase.	8	GCCCCCGAAGTG	0.473	
-	4	1162	d.2_Missense_Mu	NM_002508	NP_002499	P14543	NID1_HUMAN		2	CAACTGGAAAG	0.557	
+	5	3190	ve.1_Missense_Mu	NM_020066	NP_064450	Q9NZ56	FMN2_HUMAN	Pro-rich.|FH1.	12	CCCCTCCTCCC	0.711	
+	5	3322	e.1_Missense_Mu	NM_020066	NP_064450	Q9NZ56	FMN2_HUMAN	Pro-rich.|FH1.	12	CCCCTCCGCCC	0.731	
-	7	710	z.1_Missense_Mu	NM_005465	NP_005456	Q9Y243	AKT3_HUMAN	rotein kinase.	4	TCAAGGACTTG	0.299	
+	2	118	01iai.2_Missense_	NM_001012970	NP_001012988	Q5SVJ3	CA100_HUMAN		0	CATGACTGCCAT	0.453	
-	4	1221	cf.2_Missense_Mu	NM_024804	NP_079080	Q96BR6	ZN669_HUMAN	C2H2-type 6.	0	GTAACGAAGGG	0.408	
+	1	784		NM_001004698	NP_001004698	A6NFC9	OR2W5_HUMAN		3	CTGAAGCCGGC	0.517	
+	3	423	ozb.1_Missense_M	NM_001001957	NP_001001957	Q7Z3T1	OR2W3_HUMAN	lasmic (Potential).	3	GGCTGGACCCC	0.592	
+	1	124	L13_uc001ids.2_I	NM_001004686	NP_001004686	Q8NH16	OR2L2_HUMAN	cellular (Potential).	3	TCAACTGATTTC	0.328	
+	1	519		NM_001004689	NP_001004689	Q8NG83	OR2M3_HUMAN	cellular (Potential).	2	TCGGGAAATAGC	0.423	
-	1	785		NM_001004695	NP_001004695	Q8NG76	O2T33_HUMAN	cellular (Potential).	2	CTATGGGATTTG	0.478	
-	1	166		NM_001004695	NP_001004695	Q8NG76	O2T33_HUMAN	Name=2; (Potential).	2	CATGGGCGTGT	0.522	
-	1	136		NM_001004734	NP_001004734	A6ND48	O14I1_HUMAN	Name=1; (Potential).	0	TGATGACTGCAA	0.507	
+	12	1266	PBP4_uc010qad.1	NM_012341	NP_036473	Q9BZE4	NOG1_HUMAN		2	CAGGAACGAGAT	0.388	
+	2	277	T1_uc010qar.1_5'U	NM_001047160	NP_001040625	Q7Z628	ARHG8_HUMAN	lear localization (By similar	1	CCCTTCGGAGA	0.358	
+	10	1095		NM_017782	NP_060252	Q5VWN6	CJ018_HUMAN		2	TATTTCGTTCACC	0.254	
+	15	4299	1iik.2_Missense_M	NM_017782	NP_060252	Q5VWN6	CJ018_HUMAN		2	GCATTTCGTCAG	0.438	
-	2	365	_p.G69E|IL2RA_u	NM_000417	NP_000408	P01589	IL2RA_HUMAN	xtracellular (Potential).	2	GAGTTTCCTGTA	0.463	
+	4	394		NM_002216	NP_002207	P19823	ITIH2_HUMAN	VIT.	3	AAAGTCCAGTCT	0.413	
+	6	662	qbc.1_Missense_M	NM_001001973	NP_001001973	P36542	ATPG_HUMAN		0	TCATCTCCTATAA	0.299	
-	10	1376	o.1_Missense_Mut	NM_004808	NP_004799	O60551	NMT2_HUMAN		1	GGGGCGTCTCT	0.547	
-	44	6813		NM_001081	NP_001072	O60494	CUBN_HUMAN	CUB 16.	19	CCGGTGGAGCC	0.458	
+	5	1208	se_Mutation_p.R1	NM_032812	NP_116201	Q6UX71	PXDC2_HUMAN	cellular (Potential).	4	GTACATCGAATG	0.333	
-	4	617		NM_213569	NP_998734	O76041	NEBL_HUMAN		2	AAATCTCTTTTG	0.488	
+	13	3251	se_Mutation_p.I76	NM_019590	NP_062536	Q5T5P2	SKT_HUMAN		7	TTGTTCATTGAA	0.517	
+	21	5758	6N|KIAA1217_uc0	NM_019590	NP_062536	Q5T5P2	SKT_HUMAN		7	TAAGAAATCTGG	0.507	
-	10	2925	ense_Mutation_p.	NM_020824	NP_065875	Q5T5U3	RHG21_HUMAN		8	TGCTAGGGCTA	0.393	
+	3	2284	UR_uc001ish.1_I	NM_024838	NP_079114	Q8IYQ7	THNS1_HUMAN		1	CAGATAGGGTGC	0.418	

+	11	1639	q.2_Nonsense_Mu	NM_001134366	NP_001127838	Q05329	DCE2_HUMAN			2	CAAGTGGAAAC	0.383	
+	16	2118	q.2_Missense_Mu	NM_001134366	NP_001127838	Q05329	DCE2_HUMAN			2	TGATGGAGTAT	0.502	
-	1	317_318		NM_001034842	NP_001030014	Q3KNS1	PTHD3_HUMAN			4	CAGGGGTGCA	0.703	
-	7	1310	t.2_Missense_Mut	NM_025209	NP_079485	Q9H2F5	EPC1_HUMAN			4	CAGACGATGGT	0.443	
+	10	1179_1180	e_Mutation_p.P21	NM_024688	NP_078964	Q9H943	CJ068_HUMAN			3	CGTTTCCTTTAG	0.322	
+	31	2746		NM_052997	NP_443723	Q9BXX3	AN30A_HUMAN			9	TGTGTGTACCC	0.299	
-	5	2139	NF33B_uc001jag.	NM_006955	NP_008886	Q06732	ZN33B_HUMAN	2H2-type 13.		0	TTCACACAGAAA	0.393	
+	17	3308		NM_014753	NP_055568	Q14692	BMS1_HUMAN			3	TTTGGGGTAAAA	0.398	
-	11	1408	1jao.1_Missense_	NM_145313	NP_660356	Q8N9B8	RGF1A_HUMAN	Ras-GEF.		0	GGCGCCGTGA	0.567	
-	9	1041	1jao.1_Missense_	NM_145313	NP_660356	Q8N9B8	RGF1A_HUMAN	Ras-GEF.		0	AGGTTCATGCC	0.607	
-	3	1691	ense_Mutation_p.	NM_001098208	NP_001091678	P52597	HNRPF_HUMAN			0	GGCCCCGTAAC	0.537	
-	7	1711	L1_uc009xmu.2_	NM_001128324	NP_001121796	Q86XD8	ANUB1_HUMAN			0	TCTCTGGTTTC	0.418	
-	5	901_902	T15_uc001jeb.2_	NM_031912	NP_114118	Q9BQS2	SYT15_HUMAN	lasmic (Potential).		0	CAAGGGGAAGA	0.604	
-	17	2334	_p.D711N|FRMPD	NM_001018071	NP_001018081	Q68DX3	FRPD2_HUMAN			1	AGAGTCCCAGG	0.577	
-	6	757		NM_001080520	NP_001073989	A6NNA5	DRGX_HUMAN			0	TCTTTTCCTGGC	0.672	
+	1	1416	_5'Flank|CHAT_uc	NM_003055	NP_003046	Q16572	VACHT_HUMAN	ical; (Potential).		2	AGTGGGAGATG	0.657	
+	3	278	.1_3'UTR|C10orf5	NM_001042427	NP_001035892	Q8N6V4	CJ053_HUMAN			0	CCTAGGAGGCG	0.438	
+	1	475		NM_001077665	NP_001071133	Q5VW22	AGAP6_HUMAN		p.P26L(1)	1	TGTGTCCCTCTG	0.597	rs148430930
-	2	200	os.2_Missense_M	NM_019893	NP_063946	Q9NR71	ASAH2_HUMAN	enal (Potential).		0	CTGTGGAGCGT	0.507	
-	2	179	os.2_Missense_M	NM_019893	NP_063946	Q9NR71	ASAH2_HUMAN	enal (Potential).		0	TGGAGCCCTGG	0.502	rs142364715
-	1	929	KG1_uc001jjn.2_I	NM_015235	NP_056050	Q9H0L4	CSTFT_HUMAN	Gly-rich.		1	GCCAACCCCTG	0.592	
-	27	3967	e_Mutation_p.G1	NM_033056	NP_149045	Q96QU1	PCD15_HUMAN	|Extracellular (Potential).		13	TCTTTTCCCTCT	0.368	
-	18	2368	_p.Q720K|ANK3_	NM_020987	NP_066267	Q12955	ANK3_HUMAN			19	TGTCTGGGCGT	0.498	
+	10	2161		NM_032199	NP_115575	Q14865	ARI5B_HUMAN			4	TGGCTCCCCAC	0.537	
+	2	1062	jmx.3_Intron|CTN	NM_178011	NP_821079	Q86VH5	LRRT3_HUMAN	lar (Potential).|LRR 5.		3	GAGAACCATCC	0.488	
-	7	1129	_p.R336C|CTNNA	NM_001127384	NP_001120856	Q9UI47	CTNA3_HUMAN	Potential.	p.R336C(1)	8	CTGGCGAATGG	0.512	
-	4	466	e_Mutation_p.A88	NM_022129	NP_071412	P30039	PBLD_HUMAN			3	GCACAGCTGCA	0.418	
-	3	697	5A16_uc010qiy.1_	NM_152707	NP_689920	P16260	GDC_HUMAN	Solcar 1.		0	GAACAGCACGC	0.338	
+	5	1083	p.2_Missense_Mu	NM_170744	NP_734465	Q8IZJ1	UNC5B_HUMAN	.|Extracellu	p.R213C(1)	3	CATCCGCCAGG	0.602	
+	10	1997	p.2_Missense_Mu	NM_170744	NP_734465	Q8IZJ1	UNC5B_HUMAN	lasmic (Potential).		3	CCCGGGACACC	0.687	
+	7	883	ense_Mutation_p.	NM_138357	NP_612366	Q8NE86	MCU_HUMAN	drial matrix (Potential).		0	TTTTAGGAATAT	0.328	
-	1	113	LA2G12B_uc010	NM_032562	NP_115951	Q9BX93	PG12B_HUMAN			1	GCCACCCCCAA	0.592	
-	21	2577	3_5'UTR|TTC18_	NM_145170	NP_660153	Q5T0N1	TTC18_HUMAN			3	CAGCTCCTGGT	0.328	
-	18	3886	p.S378F|USP54_	NM_152586	NP_689799	Q70EL1	UBP54_HUMAN			6	TATGGGAATCA	0.473	
-	12	2202	G5_uc009xru.1_R	NM_004747	NP_004738	Q8TDM6	DLG5_HUMAN	PDZ 2.		8	CCAGGGACTTC	0.607	
-	8	1022	1P_uc001kbf.2_I	NM_003019	NP_003010	P35247	SFTPD_HUMAN	-type lectin.		1	TGTGGGGTAGG	0.567	
-	6	1427	_p.E77K|MMRN2_	NM_024756	NP_079032	Q9H8L6	MMRN2_HUMAN	Potential.		1	CTCCTCCACCT	0.587	
+	5	561	F1_uc009xua.1_	NM_003972	NP_003963	O14981	BTAF1_HUMAN			3	TTGGCCTTAAT	0.373	
-	29	3143	e_Mutation_p.S99	NM_013451	NP_038479	Q9NZM1	MYOF_HUMAN	lasmic (Potential).		4	CCCAGGATTTG	0.478	
+	6	867	iq.3_Missense_M	NM_001127182	NP_001120654	Q53EZ4	CEP55_HUMAN	tion with TSG101.		0	GTTATCTTCAAG	0.328	
+	8	1623	I1_uc001kjd.3_Int	NM_005097	NP_005088	O95970	LGI1_HUMAN	EAR 5.		4	AACATGGAGGA	0.423	
-	1	1509_1510		NR_002319						0	GCCACCCATAT	0.515	
-	3	462	74M|ALDH18A1_u	NM_002860	NP_002851	P54886	P5CS_HUMAN	amate 5-kinase.		3	TCACCACGATTC	0.562	rs143330350
-	12	1599	p.G296E|TCTN3_	NM_015631	NP_056446	Q6NUS6	TECT3_HUMAN	ellular (Potential).		0	GCCTTCCATGA	0.488	
-	15	2202		NM_012465	NP_036597	Q9Y6L7	TLL2_HUMAN	CUB 3.		3	GAAGGGAGATC	0.517	
-	15	2141		NM_012465	NP_036597	Q9Y6L7	TLL2_HUMAN	CUB 3.		3	ATACTCCTTCG	0.527	
-	4	499	GAP19_uc009xvi.2	NM_032900	NP_116289	Q14CB8	RHG19_HUMAN	Rho-GAP.		0	TGAGAGCATCC	0.438	

+	1	564	sense_Mutation_p	NM_018121	NP_060591	Q8IX21	F178A_HUMAN			0	TGCCCGCTAGG	0.682	
-	8	2369_2370	se_Mutation_p.E2	NM_002779	NP_002770	A5PKW4	PSD1_HUMAN	SEC7.		3	CAGCTCCTTCAG	0.579	
+	6	1553		NM_030912	NP_112174	Q9BZR9	TRIM8_HUMAN			1	TTCTTCCGTGG	0.647	
-	14	2280	ense_Mutation_p.	NM_014631	NP_055446	Q5TCZ1	SPD2A_HUMAN			0	GTTCGCATCAG	0.592	
+	10	1206	P2_uc010qrz.1_	NM_004132	NP_004123	Q14520	HABP2_HUMAN	eptidase S1.		3	TAAAAACCAGAC	0.303	
+	2	573	10D|C10orf81_uc	NM_024889	NP_079165	Q5SXH7	CJ081_HUMAN			1	TATTAGGCAAAC	0.338	
+	5	1158	se_Mutation_p.H2	NM_207303	NP_997186	Q5VV63	ATRN1_HUMAN	ellular (Potential).		7	CAGATCACGGT	0.403	
+	20	3630_3631	e_Mutation_p.G2	NM_207303	NP_997186	Q5VV63	ATRN1_HUMAN	e 2.|Extracellular (Potential		7	CTAAAGGAATAA	0.322	
+	11	1417		NM_001011709	NP_001011709	Q17RR3	LIPR3_HUMAN	PLAT.		1	TGATAAATACATC	0.308	
-	19	3483	p.L1079M|EIF3A_	NM_003750	NP_003741	Q14152	EIF3A_HUMAN	-[DE]-R-[SEVGFPILV]-[HP		0	ATCCAACCCTC	0.607	
-	3	759	_p.P38S|FGFR2_	NM_000141	NP_000132	P21802	FGFR2_HUMAN	1.|Extracellular (Potential).		96	TGGTGGCTCTG	0.557	
+	16	8468	C2_uc001lfy.2_In	NM_206862	NP_996744	O95359	TACC2_HUMAN	Potential.		10	TTCCCGCAGCC	0.587	
+	20	2439	z.1_Nonsense_M	NM_007329	NP_015568	Q9UGM3	DMBT1_HUMAN	SRCR 6.		7	TGGCTGGGCCA	0.612	
+	52	6662	185_splice|DMBT1	NM_007329	NP_015568	Q9UGM3	DMBT1_HUMAN			7	TCCTAGGCAGA	0.522	
-	8	1756	p.G194E|CUZD1_	NM_022034	NP_071317	Q86UP6	CUZD1_HUMAN	llular (Potential).|ZP.		2	TAGTGTCCAAATA	0.363	
-	4	1649	_p.H379L|CHST15	NM_015892	NP_056976	Q7LFX5	CHSTF_HUMAN	enal (Potential).		1	AGGCGTGGATG	0.527	
-	1	709	_p.E66K|CHST15	NM_015892	NP_056976	Q7LFX5	CHSTF_HUMAN	lasmic (Potential).		1	AGTTTTCGTTCC	0.463	
+	22	2306	un.1_Missense_M	NM_001380	NP_001371	Q14185	DOCK1_HUMAN			9	TCAAGTTCATCG	0.473	
+	22	2312	un.1_Missense_M	NM_001380	NP_001371	Q14185	DOCK1_HUMAN			9	TCATCGTGCGC	0.458	
-	1	71	x.1_Intron|LOC33	NM_001005922	NP_001005922	Q6L8H4	KRA51_HUMAN			0	ACAGCTGGAGC	0.672	
+	16	983	q.3_Nonsense_M	NM_006757	NP_006748	P45378	TNNT3_HUMAN			1	CGCTGGAAGTA	0.647	
+	4	601_602	wk.2_Missense_M	NM_005706	NP_005697	Q9Y5U2	TSSC4_HUMAN			0	CCATTCCATCTG	0.658	
-	20	3005	.N999S|TRPM5_	NM_014555	NP_055370	Q9NZQ8	TRPM5_HUMAN	lasmic (Potential).		4	TCAGGTTGTAG	0.642	
-	6	1908	5_uc010qxr.1_Mis	NM_001130520	NP_001123992	O14628	ZN195_HUMAN			0	TGTAGGGTTTCT	0.398	
+	1	919_920		NM_001005172	NP_001005172	Q8NGK3	O52K2_HUMAN	lasmic (Potential).		2	TCTTGGGAGTAT	0.485	
+	2	665		NM_152430	NP_689643	Q8TCB6	O51E1_HUMAN	ellular (Potential).		4	CCGCTCCAATAT	0.537	rs148260821
+	2	797		NM_152430	NP_689643	Q8TCB6	O51E1_HUMAN	Name=5; (Potential).		4	TCATCTCCTTCT	0.498	
-	2	909		NM_030774	NP_110401	Q9H255	O51E2_HUMAN	lasmic (Potential).		5	ACCGTTCGTATT	0.488	
-	2	554		NM_030774	NP_110401	Q9H255	O51E2_HUMAN	Name=3; (Potential).		5	GGCATGAATAA	0.517	
-	1	1163		NM_001005177	NP_001005177	Q8NGF1	O52R1_HUMAN	lasmic (Potential).		1	AACATCCTTGG	0.448	
+	1	406		NM_001004753	NP_001004753	Q8NH61	O51F2_HUMAN	lasmic (Potential).		2	TTTGATCGTTTT	0.463	
+	1	478		NM_001001916	NP_001001916	Q8NH60	O52J3_HUMAN	Name=4; (Potential).		3	CACTTCCCATG	0.468	
-	2	649	BG2_uc001maj.1_	NM_000559	NP_000550	P69892	HBG2_HUMAN		p.S71F(1)	1	CCAAGGAAGTC	0.532	rs151258456
-	1	778	.1_Intron|HBE1_u	NM_001005567	NP_001005567	Q9H339	O51B5_HUMAN	ellular (Potential).		1	ACGATGAATCA	0.428	
-	1	908	.1_Intron|TRIM22_	NM_001001913	NP_001001913	Q8NH53	O52N1_HUMAN	lasmic (Potential).		1	TTTCTCGTACC	0.388	
-	1	758	.1_Intron|TRIM22_	NM_001001913	NP_001001913	Q8NH53	O52N1_HUMAN	Name=6; (Potential).		1	ACATAGGTGAGG	0.443	
-	1	685		NM_001004052	NP_001004052	Q96RD2	O52B2_HUMAN	lasmic (Potential).		0	CAAACGAAACA	0.478	
-	1	25		NM_001004490	NP_001004490	A6NM03	O2AG2_HUMAN	ellular (Potential).		4	GCTTCCCAAGG	0.438	
+	8	2899		NM_176822	NP_789792	Q86W24	NAL14_HUMAN	LRR 5.		8	TGGTGGAGTAA	0.413	
+	9	3096		NM_176822	NP_789792	Q86W24	NAL14_HUMAN			8	TCTTTCGGCAT	0.428	
-	8	643	rcu.1_Missense_	NM_175058	NP_778228	Q6IQ23	PKHA7_HUMAN	PH.		3	CAAGGGGATGC	0.537	
-	1	605	11_uc001mnb.3_	NM_000525	NP_000516	B4DWI4	B4DWI4_HUMAN			1	TCAGCACGTATT	0.677	rs139079635
-	5	759	cy.1_Missense_Mu	NM_000352	NP_000343	Q09428	ABCC8_HUMAN	smic (By similarity).		1	AGGTCTTGCAG	0.567	
-	2	699		NM_054030	NP_473371	Q96LB1	MRGX2_HUMAN	Name=5; (Potential).		1	GCAGGGCCAGA	0.532	
+	16	4397	n_p.V409M|NAV2	NM_145117	NP_660093	Q8IVL1	NAV2_HUMAN			6	ATTCGGTGGTC	0.527	
+	16	1740	s.1_Missense_Mu	NM_031418	NP_113606	Q9BYT9	ANO3_HUMAN	lasmic (Potential).		4	CACGGGAAAAC	0.398	
-	2	1297	_uc009yiz.2_Intro	NM_001143816	NP_001137288	P23560	BDNF_HUMAN			0	CTGCCGTTACC	0.547	

-	14	2331		NM_031217	NP_112494	Q8NI77	KI18A_HUMAN		2	TAGACGGATTTT	0.363	
+	4	616	_Mutation_p.R117	NM_001076786	NP_001070254	Q2KHR3	QSER1_HUMAN		6	TTGAGCGCCTG	0.423	
+	13	2851	_p.D840N|HIPK3_	NM_005734	NP_005725	Q9H422	HIPK3_HUMAN	n to nuclear speckles (By s	5	TTGCCGACTCCC	0.473	
-	11	1957		NM_145804	NP_665803	Q8N961	ABTB2_HUMAN		2	CCACCGAGTAC	0.612	
-	6	825	_p.E189K|ELF5_u	NM_198381	NP_938195	Q9UKW6	ELF5_HUMAN	ETS.	1	CTTGTTCCCTATC	0.428	
+	9	1219_1220	R5L_uc009ykk.2_	NM_001160167	NP_001153639	Q6MZQ0	PRR5L_HUMAN		1	GGAGGGGGAAG	0.629	
+	9	1326	R5L_uc009ykk.2_	NM_001160167	NP_001153639	Q6MZQ0	PRR5L_HUMAN		1	GCCTGGGGGAG	0.662	
+	2	1109	G1_uc001mwt.2_F	NM_000448	NP_000439	P15918	RAG1_HUMAN	RING-type.	5	TATTGTCCCTCTT	0.498	
+	8	898	18_uc001myg.2_Ir	NM_130783	NP_570139	Q96SJ8	TSN18_HUMAN	lasmic (Potential).	0	CCGGGGCATCC	0.597	
+	8	1667		NM_020229	NP_064614	Q9NQV5	PRD11_HUMAN		1	CTGAGCCCCCCG	0.522	
-	2	376	13_uc009yku.1_5'	NM_020826	NP_065877	Q7L8C5	SYT13_HUMAN	lasmic (Potential).	1	TGGGTCCATAGA	0.532	
+	10	1417	e_Mutation_p.A436	NM_152312	NP_689525	Q8N3Y3	LARG2_HUMAN	nenal (Potential).	3	CTTGTGGCCCAG	0.637	
+	8	1541	n.1_Missense_Mut	NM_003682	NP_003673	Q8WXG6	MADD_HUMAN		11	CATGAGGGCCAC	0.502	
+	9	1764	n.1_Missense_Mut	NM_003682	NP_003673	Q8WXG6	MADD_HUMAN	dDENN.	11	TTTCAAGCTGGC	0.557	
-	10	1739	se_Mutation_p.E5	NM_024783	NP_079059	Q5U5Z8	CBPC2_HUMAN		2	TTTCTTCAAGAAC	0.383	
+	3	491	go.3_Missense_M	NM_002843	NP_002834	Q12913	PTPRJ_HUMAN	cellular (Potential).	8	CTGACCCTTCAC	0.423	
+	1	520		NM_001004726	NP_001004726	Q8NH49	OR4X1_HUMAN	cellular (Potential).	3	ATGGACCACTAC	0.567	
+	1	245		NM_001004702	NP_001004702	Q8NH37	OR4C3_HUMAN	lasmic (Potential).	1	TGGCTTCCCCTG	0.458	
-	1	358		NM_001005272	NP_001005272	Q8NH83	OR4A5_HUMAN	lasmic (Potential).	3	CATAGCGATCAC	0.468	rs141762692
+	1	546		NM_001004703	NP_001004703	A6NHA9	O4C46_HUMAN	cellular (Potential).	1	CCCTTTGCTCAAC	0.458	
-	1	844		NM_001004700	NP_001004700	Q6IEV9	OR4CB_HUMAN	Name=7; (Potential).	1	GAGTGGATTGAC	0.413	
+	1	656		NM_001004735	NP_001004735	Q8NGL3	OR5DE_HUMAN	Name=5; (Potential).	3	TCACTTCCTATG	0.478	
+	1	545		NM_001005200	NP_001005200	Q8N162	OR8H2_HUMAN	cellular (Potential).	2	ACACTTCCCCAA	0.398	
+	1	586		NM_001005200	NP_001005200	Q8N162	OR8H2_HUMAN	cellular (Potential).	2	ACACCGAAATCC	0.388	
-	1	767		NM_001005199	NP_001005199	Q8NGG4	OR8H1_HUMAN	Name=6; (Potential).	3	TAAGTAAAAATCA	0.358	
+	1	797		NM_001005202	NP_001005202	Q8NH51	OR8K3_HUMAN	cellular (Potential).	4	GTCATTCCTTTGA	0.423	
+	1	364		NM_001004730	NP_001004730	Q8NGP9	O5AR1_HUMAN	lasmic (Potential).	0	TATGGTCGTTTTC	0.512	
-	6	905	jq.1_Missense_Mu	NM_003146	NP_003137	Q08945	SSRP1_HUMAN		2	CATAACGACCAC	0.527	
+	1	898		NM_001004458	NP_001004458	Q8NH92	OR1S1_HUMAN	Name=7; (Potential).	1	ATAAACCCCTTC	0.453	
-	5	515	ymq.2_Missense_	NM_145016	NP_659453	Q8WU03	GLYL2_HUMAN		2	GGTTTTCATGTA	0.388	
+	1	347		NM_001004705	NP_001004705	Q8NGI6	OR4DA_HUMAN	Name=3; (Potential).	3	CTCTTTCGGTGAT	0.478	
+	1	90	9ynx.2_Missense_	NM_002411	NP_002402	Q13296	SG2A2_HUMAN		1	TGGCGGCCCTC	0.612	
+	3	342	R2G_uc001nvb.2_	NM_002696	NP_002687	P62487	RPB7_HUMAN		0	GTTTTCCGGCCA	0.473	
-	2	778		NM_000738	NP_000729	P11229	ACM1_HUMAN	lasmic (Potential).	0	GTCACGGAGAAG	0.632	
+	6	1240	22A9_uc001nwx.2_	NM_080866	NP_543142	Q8IVM8	S22A9_HUMAN	lasmic (Potential).	3	CACCATGAAAAA	0.413	
+	9	1764	2A9_uc001nwx.2_	NM_080866	NP_543142	Q8IVM8	S22A9_HUMAN	ical; (Potential).	3	TGCCCTGGATCA	0.502	
-	3	288	T|MRPL49_uc001	NM_001997	NP_001988	P35544	UBIM_HUMAN		0	CAGGGCCTCCA	0.607	
+	2	1075		NM_006779	NP_006770	O14613	BORG1_HUMAN		0	CAGATCCCCACA	0.657	
-	5	1739	rol.1_Splice_Site_	NM_002419	NP_002410	Q16584	M3K11_HUMAN		6	AGTTCCTGCGCC	0.716	
+	4	588	rot.1_Missense_M	NM_005146	NP_005137	O43290	SNUT1_HUMAN	Potential.	1	GAGAGGAGCTG	0.657	
+	16	1991		NM_006842	NP_006833	O13435	SF3B2_HUMAN		3	AAAATCCCTGGG	0.498	
-	16	3206_3207		NM_006946	NP_008877	O15020	SPTN2_HUMAN	Spectrin 7.	4	CAGCCGGTCTGC	0.688	
-	2	313		NM_005995	NP_005986	O75333	TBX10_HUMAN	T-box.	0	TCCTCCCACAGA	0.642	
-	13	1707_1708	e_Mutation_p.P51	NM_001876	NP_001867	P50416	CPT1A_HUMAN	lasmic (Potential).	2	GGTACGGAATGT	0.495	rs146533704
-	1	45	21_uc001ooh.2_Tr	NM_181514	NP_852615	Q7Z2W9	RM21_HUMAN		0	TGACCGTCAGG	0.687	
+	1	284_285		NM_005553	NP_005544	P26371	KRA59_HUMAN		0	GTGGAGGCTGTC	0.639	
-	3	477	uq.1_Missense_M	NM_003355	NP_003346	P55851	UCP2_HUMAN	Solcar 1.	0	CAGAGGAAAGG	0.542	

-	10	1584		NM_173582	NP_775853	Q6PCE3	PGM2L_HUMAN		1	AAAAAGGACTT	0.323	
-	6	1172		NM_001039548	NP_001034637	Q6PF15	KLH35_HUMAN	Kelch 6.	0	CCCGCCCGCC	0.597	
+	1	470_471	.2_Intron|CAPN5_	NM_006189	NP_006180	P47874	OMP_HUMAN		0	GGCCTCCGTGG	0.604	rs2233550
+	5	1859	u.1_Missense_Mu	NM_015885	NP_056969	O94913	PCF11_HUMAN		1	CAAACGAAGGC	0.458	
-	14	1892	ak.2_Missense_M	NM_001364	NP_001355	Q15700	DLG2_HUMAN		6	GCAGGGATCCG	0.473	
-	3	1252	m.2_Missense_M	NM_001143831	NP_001137303	P41594	GRM5_HUMAN	ellular (Potential).	9	GGTTTCGGTGG	0.458	
+	1	699		NM_001008781	NP_001008781	Q8TDW7	FAT3_HUMAN	|Extracellular (Potential).	5	GGTATGATCTG	0.388	
+	1	1525		NM_001008781	NP_001008781	Q8TDW7	FAT3_HUMAN	|Extracellular (Potential).	5	AGGAGAAAATG	0.388	
+	15	10153		NM_001008781	NP_001008781	Q8TDW7	FAT3_HUMAN	(Potential).|Cadherin 31.	5	ATTTTTCCATTGT	0.408	
+	4	467	N5_uc001pfz.2_	NM_014361	NP_055176	O94779	CNTN5_HUMAN		8	CATCTTCATCTC	0.398	
+	5	777	KIAA1377_uc010r	NM_020802	NP_065853	Q9P2H0	K1377_HUMAN		4	TTCACAGAGCTA	0.318	
+	6	2075	run.1_Missense_	NM_020802	NP_065853	Q9P2H0	K1377_HUMAN		4	GTTTGGAAATC	0.294	
-	4	679	1_uc010ruv.1_Mis	NM_002421	NP_002412	P03956	MMP1_HUMAN	etalloprotease.	4	GATTTCCTCCA	0.438	
-	2	326		NM_002427	NP_002418	P45452	MMP13_HUMAN	switch (By s p.D100N(1)	3	CACATCAGGAA	0.408	rs148152034
+	26	4091	_Mutation_p.P13	NM_001080463	NP_001073932	Q8NCM8	DYHC2_HUMAN	(By similarity).	0	ATTCTCCTTATT	0.338	
-	7	1453	hp.2_Missense_M	NM_025208	NP_079484	Q9GZP0	PDGFD_HUMAN		2	TACAATCACATC	0.458	rs146343067
+	1	566	.2_Intron|PDGFD_	NM_001001711	NP_001001711	Q8WTU0	DDI1_HUMAN		5	CTCCCGTCCAC	0.672	rs138983347
-	6	4283	z.1_Missense_Mu	NM_015065	NP_055880	Q8NEV8	EXPH5_HUMAN		5	GTTTCACTTTGC	0.348	
+	16	2364	kl.1_Missense_M	NM_004398	NP_004389	Q13206	DDX10_HUMAN		4	GACAAGCAAAG	0.338	
+	2	348	.1_5'Flank|HSPB2	NM_001541	NP_001532	Q16082	HSPB2_HUMAN		3	TACCCCAGACG	0.657	
+	14	1320	qg.2_Splice_Site_	NM_001040455	NP_001035545	Q8NBJ9	SIDT2_HUMAN		0	CCCCAGCAATA	0.582	
+	3	434	se_Mutation_p.P1	NM_207343	NP_997226	Q8ND24	RN214_HUMAN		0	CCATCCAGTCA	0.542	
-	32	5563		NM_020693	NP_065744	Q8TD84	DSCL1_HUMAN	lasmic (Potential).	8	TTCCTTCCTTTG	0.597	
+	8	1012	_Mutation_p.L21	NM_019894	NP_063947	Q9NRS4	TMPS4_HUMAN	(Potential).|Peptidase S1.	2	GGGTCCTCACG	0.612	
+	7	3865	1281L|MLL_uc001	NM_005933	NP_005924	Q03164	MLL1_HUMAN		25	TGGGCCTGAAT	0.582	
+	7	1215	.2_Missense_Mut	NM_015157	NP_055972	Q86UU1	PHLB1_HUMAN		0	CTGCCCGTTCC	0.637	
+	7	1737	462S|PHLDB1_uc	NM_015157	NP_055972	Q86UU1	PHLB1_HUMAN		0	TTAAGTCCATCT	0.652	
+	2	348	uf.2_Missense_M	NM_001716	NP_001707	P32302	CXCR5_HUMAN	lasmic (Potential).	1	GGCACCGGCAG	0.647	
+	8	2200		NM_005422	NP_005413	O75443	TECTA_HUMAN	VWFD 2.	10	CCTCCGAGTTC	0.617	
+	9	2429		NM_005422	NP_005413	O75443	TECTA_HUMAN	VWFD 2.	10	TTTATCGAAACA	0.433	
+	16	5318		NM_005422	NP_005413	O75443	TECTA_HUMAN		10	CAACCGAACTT	0.542	
+	45	6148	_p.S869L|SORL1_	NM_003105	NP_003096	Q92673	SORL_HUMAN	tential).|Fibronectin type-III	15	AGTTTCATTATC	0.249	
-	9	1972	yp.2_Missense_M	NM_006597	NP_006588	P11142	HSP7C_HUMAN		8	AGAGGGAGGAG	0.512	
+	10	1374	D1B_uc010rzx.1_	NM_020716	NP_065767	Q3KR37	GRM1B_HUMAN		1	ACATCCCCACT	0.498	
-	1	899		NM_001005188	NP_001005188	Q8NH79	OR6X1_HUMAN	lasmic (Potential).	3	CCTTTCTTAAG	0.388	
+	1	47		NM_001001965	NP_001001965	Q8NGN0	OR4D5_HUMAN	ellular (Potential).	1	ACTGGGGCTCT	0.418	
+	1	86		NM_001001965	NP_001001965	Q8NGN0	OR4D5_HUMAN	Name=1; (Potential).	1	TCTTCACTGTTT	0.458	
+	3	237	_p.L10F|VWA5A_	NM_001130142	NP_001123614	O00534	VMA5A_HUMAN	VIT.	2	TCACCCTCCAC	0.448	
+	18	2427	zt.2_Missense_M	NM_001130142	NP_001123614	O00534	VMA5A_HUMAN		2	GTAAGGACTTG	0.562	
-	1	10		NM_001002917	NP_001002917	Q8WZ84	OR8D1_HUMAN	ellular (Potential).	3	AATTTTCCATGG	0.413	
-	1	535		NM_001005195	NP_001005195	Q8NGG6	OR8BC_HUMAN	ellular (Potential).	3	GGATGTCACACA	0.507	
+	5	481_482		NM_017425	NP_059121	Q15506	SP17_HUMAN	IQ.	0	GAAGAGGTTGCT	0.391	
+	13	1404	0sav.1_Missense_	NM_001145290	NP_001138762	Q8TED4	SPX2_HUMAN		2	GCCAGGACGGG	0.622	
+	7	1601	_p.P324S|NTM_u	NM_016522	NP_057606	Q9P121	NTRI_HUMAN		6	CAGGTCCAGGC	0.597	
-	1	122		NM_174927	NP_777587	Q7Z5L4	SPT19_HUMAN		0	AACTGGTTATT	0.433	
-	11	1543	on_p.G334R|SLC	NM_003044	NP_003035	P48065	S6A12_HUMAN	Name=7; (Potential).	1	AAACCCAGCCA	0.502	
+	5	1465_1466	1_Intron|LRTM2_u	NM_001039029	NP_001034118	Q8N967	LRTM2_HUMAN	xtracellular (Potential).	1	TGTAGGGGGAC	0.589	

+	7	1257	c001qkn.2_Misse	NM_199460	NP_955630	Q13936	CAC1C_HUMAN	cellular (Potential).	11	CTTCCCCTTGTG	0.592	
+	8	1447	A1C_uc001qkn.2_	NM_199460	NP_955630	Q13936	CAC1C_HUMAN	cellular (Potential).	11	GGAAGGGACTG	0.517	
+	2	210_211	ee.1_Missense_M	NR_027363					0	AAAGCCCCGCTC	0.559	
+	4	290	_p.L159F|DYRK4_	NM_003845	NP_003836	Q9NR20	DYRK4_HUMAN		3	CTAAAGCTTTTT	0.517	
+	1	1383		NM_002235	NP_002226	P17658	KCNA6_HUMAN		3	GGCCGGCCAGG	0.617	
+	1	615	k.3_Missense_Mu	NM_002527	NP_002518	P20783	NTF3_HUMAN		1	TGGGGGAGATC	0.522	
-	21	2228		NM_020373	NP_065106	Q9NQ90	ANO2_HUMAN	ellular (Potential).	7	GTTTCGAATGG	0.453	
-	5	788	quh.2_Missense_	NM_018088	NP_060558	Q86YD7	F90A1_HUMAN		1	TCCCTTCCTTTTC	0.552	
-	26	3205	.2_Missense_Mut	NM_002864	NP_002855				5	AGGATCGAGCC	0.488	
-	1	566		NM_023919	NP_076408	Q9NYW3	TA2R7_HUMAN	ellular (Potential).	1	AACTCCAAGTT	0.423	
-	3	285	_p.Q83P|PRB1_u	NM_005039	NP_005030	P04280	PRP1_HUMAN	-P-[PAQ]-Q-[GE]-[GD]- [N	0	CCCCTTGTGGG	0.622	
+	1	416		NR_003932					0	AGCCTGCAAGA	0.567	
-	13	4359		NM_000834	NP_000825	Q13224	NMDE2_HUMAN	lasmic (Potential).	12	CTGGTCGTCCC	0.612	
-	8	1856		NM_000834	NP_000825	Q13224	NMDE2_HUMAN	ical; (Potential).	12	ATCACCCATAC	0.463	
-	12	1868	0sio.1_Missense_	NM_021094	NP_066580	P46721	SO1A2_HUMAN	lasmic (Potential).	4	AGATTTCATACAC	0.299	
-	5	793	_p.S49F|SLCO1A	NM_021094	NP_066580	P46721	SO1A2_HUMAN	Name=4; (Potential).	4	TATAGGAAATAC	0.343	
-	5	530		NM_183378	NP_899234	Q7RTY7	OVCH1_HUMAN	ptidase S1 1.	10	CCCATCCACTG	0.413	
-	10	2696	rjj.1_Missense_M	NM_001002259	NP_001002259	Q6IMN6	CAPR2_HUMAN		2	CGTTGGAATTG	0.388	
-	26	3940	p.G432R|ADAMT	NM_025003	NP_079279	P59510	ATS20_HUMAN	SP type-1 9.	19	TGATCCCCATG	0.353	
-	4	1127_1128		NM_001004329	NP_001004329	Q6ZNG2	DBX2_HUMAN		0	GGCACCTTGCA	0.47	rs149681179
-	7	689	_p.T144I|SLC38A	NM_030674	NP_109599	Q9H2H9	S38A1_HUMAN	lasmic (Potential).	5	CTGTGGTGCCA	0.383	
+	4	753	AM113B_uc001rp	NM_138371	NP_612380	Q96HM7	F113B_HUMAN		5	CCTCCGAAGTG	0.587	
+	4	1128	_p.P13S|FAM113B	NM_138371	NP_612380	Q96HM7	F113B_HUMAN		5	TATGGTCCGAAC	0.592	
+	4	1393	p.A101V|FAM113	NM_138371	NP_612380	Q96HM7	F113B_HUMAN		5	CCACGCGAGGG	0.597	
-	14	1752	p.P387A|RPAP3_	NM_024604	NP_078880	Q9H6T3	RPAP3_HUMAN		1	TGCAGGAATTG	0.403	
-	23	2742	_Missense_Mutat	NM_001098532	NP_001092002	A8K2G5	A8K2G5_HUMAN		4	GACAGGAGGGG	0.413	
-	54	4613	A1_uc009zkw.2_	NM_001844	NP_001835	P02458	CO2A1_HUMAN	lar collagen NC1.	2	CACACCGAATT	0.517	
-	6	1270	_p.P355S|ZNF641_	NM_152320	NP_689533	Q96N77	ZN641_HUMAN		2	CTTTGGCACTG	0.592	
-	5	1970	Y6_uc001rsi.3_Mi	NM_015270	NP_056085	O43306	ADCY6_HUMAN	lasmic (Potential).	0	CCTCCGGCAGC	0.552	
-	48	15620		NM_003482	NP_003473	O14686	MLL2_HUMAN	R N-terminal.	41	CCACGGGATAG	0.607	
-	48	15358		NM_003482	NP_003473	O14686	MLL2_HUMAN	ype 4; degenerate.	41	GGCACGGATGG	0.537	
-	21	5117		NM_003482	NP_003473	O14686	MLL2_HUMAN		41	TGTGGGATTTC	0.637	
+	8	1669	ATS2_uc001ruf.2_	NM_023071	NP_075559	Q86XZ4	SPAS2_HUMAN		1	TGTTCCCCTCG	0.428	
-	3	606		NM_030809	NP_110436	Q9H175	CSRN2_HUMAN		0	AGCTCCGTACAC	0.537	
+	10	1380	4A8_uc001ryp.1_	NM_001039960	NP_001035049	Q2Y0W8	S4A8_HUMAN	ellular (Potential).	5	AGAGTGGGATC	0.493	
+	7	1744	zt.2_Missense_M	NM_002135	NP_002126	P22736	NR4A1_HUMAN		0	TGCCCGTGGCT	0.612	
-	7	1472		NM_033045	NP_149034	Q9NSB2	KRT84_HUMAN	Tail.	1	CTCACCGGCTC	0.557	
-	2	633		NM_005555	NP_005546	P04259	K2C6B_HUMAN	oil 1A.|Rod.	2	AGGGTCCACTT	0.542	
-	1	74		NM_005555	NP_005546	P04259	K2C6B_HUMAN	Head.	2	GGCTCCTGATG	0.632	
-	4	818		NM_173352	NP_775487	Q8N1N4	K2C78_HUMAN	oil 1B.|Rod.	2	TCACTTCTTCAT	0.547	
+	8	926	T2_uc009zms.2_	NM_003578	NP_003569	O75908	SOAT2_HUMAN	ical; (Potential).	1	CAACACTCATC	0.493	
+	29	3251	p.E600K|NCKAP1	NM_005337	NP_005328	P55160	NCKPL_HUMAN		4	TCAAGGAATTT	0.418	
-	1	184		NM_001005499	NP_001005499	A6NIJ9	O6C70_HUMAN	lasmic (Potential).	1	ATTACGGAGGA	0.403	
-	2	902	zob.1_Missense_	NM_032364	NP_115740	Q6Y2X3	DJC14_HUMAN		4	CCTTTGCGCTTA	0.567	
-	19	2410	10_splice|STAT6_	NM_003153	NP_003144	P42226	STAT6_HUMAN		4	ACTTACTCCTGG	0.522	
-	7	1002	ion_p.R199H|ARH	NM_032496	NP_115885	Q9BRR9	RHG09_HUMAN		1	GACAGCGGCGA	0.652	rs139154961
+	3	670	sts.3_Missense_M	NM_006482	NP_006473	Q92630	DYRK2_HUMAN		4	TCCAGGTTCAA	0.488	rs138020482

+	2	817		NM_014505	NP_055320	Q86W47	KCMB4_HUMAN	ellular (Potential).	0	AGAGAGAAAT	0.328	
-	14	1439	xi.3_Missense_Mu	NM_032606	NP_115995	Q9BXY5	CAYP2_HUMAN		2	TCATCCTCCTGT	0.333	
-	7	992		NM_004950	NP_004941	Q99645	EPYC_HUMAN	LRR 6.	1	TTAATAGGGTTT	0.393	
-	3	235	2_5'Flank|CLLU1_	NM_001025232	NP_001020403	Q5K130	CLU1O_HUMAN		0	TCACATTTCCT	0.438	
-	5	1132	NKS1B_uc009ztt.1	NM_152788	NP_690001	Q7Z6G8	ANS1B_HUMAN	ANK 7.	0	ATCCACCTTTC	0.378	
-	17	3801	1tgp.2_Missense_	NM_015054	NP_055869	A0JNW5	UH1BL_HUMAN		2	ACAACGGACATC	0.338	
+	26	2741	p.P886L|KIAA103	NM_015275	NP_056090	Q2M389	WAHS7_HUMAN		2	AGTATCCTTTTG	0.373	
-	10	2289	se_Mutation_p.H2	NM_012406	NP_036538	Q9UKN5	PRDM4_HUMAN	2H2-type 2.	2	CTTGTGGGGCT	0.473	
+	4	1355	mt.2_Missense_M	NM_014653	NP_055468	Q2TBF2	WSCD2_HUMAN	WSC 1.	3	GCGAGGCAGC	0.692	
-	2	968	M119_uc001tnf.2_	NM_181724	NP_859075	Q4V9L6	TM119_HUMAN	lasmic (Potential).	1	GGGGGGACCCA	0.667	
+	18	1877		NM_001101421	NP_001094891	Q8N1T3	MYO1H_HUMAN		0	CCGAAGGAAAT	0.443	
+	10	1454	p.K380R|CCDC6	NM_152591	NP_689804	Q8NA47	CCD63_HUMAN	Potential.	8	TCAAGAAGATAA	0.502	
+	16	2095		NM_015267	NP_056082	O14529	CUX2_HUMAN		6	GCTCAGACGAC	0.622	
-	16	2186_2187	orf51_uc001tts.2_	NM_001109662	NP_001103132				2	TTAAGGAAGGG	0.396	
+	19	2028	e.1_Missense_Mu	NM_001143854	NP_001137326	Q9Y2J0	RP3A_HUMAN	C2 2.	7	ATCCTGGTCTCC	0.592	
+	2	338_339	tux.2_Missense_	NM_017901	NP_060371	Q9ULQ1	TPC1_HUMAN	lasmic (Potential).	3	CTGACCTTGGA	0.569	
-	20	3727		NM_000620	NP_000611	P29475	NOS1_HUMAN	-binding FR-type.	7	CCTACCTGGAT	0.522	
-	2	1188		NM_000620	NP_000611	P29475	NOS1_HUMAN	arity).|PIN (nNOS-inhibiting	7	AGCCTCCTGCC	0.682	
-	3	363	_p.S75F|PITPNM	NM_020845	NP_065896	Q9BZ72	PITM2_HUMAN		3	GGATGGAGCGG	0.622	
+	2	717	P35_uc009zxz.2_	NM_022717	NP_073208	Q16560	U1SBP_HUMAN	Arg-rich.	0	GGGATCGAGAC	0.552	rs140144369
+	7	903	ya.2_Nonsense_M	NM_024809	NP_079085	Q96GX1	TECT2_HUMAN	ellular (Potential).	1	CCAAACAGGAC	0.323	
+	43	7252		NM_207437	NP_997320	Q8IVF4	DYH10_HUMAN		6	CCCATGGAGTAA	0.408	
-	3	1335		NM_133448	NP_597705	Q14C87	T132D_HUMAN	ellular (Potential).	14	TGGCTCGCACG	0.547	rs147819967
+	18	2451	o.2_Intron|GPR13	NM_198827	NP_942122	Q6QNK2	GP133_HUMAN	ellular (Potential).	10	GACCCCCTGCC	0.582	
-	12	995	2_uc001ume.2_N	NM_199254	NP_954863	Q6XPS3	TPTE2_HUMAN	hatase tensin-type.	0	GACTCGATAGT	0.338	
+	3	862	PH8_uc001umg.	NM_017520	NP_059990	Q99549	MPP8_HUMAN		0	ATTCCGACAGC	0.443	
-	9	1010	dc.1_Missense_M	NM_006437	NP_006428	Q9UKK3	PARP4_HUMAN	P alpha-helical.	4	TAGAAGGAGAAT	0.383	
+	15	2113	NF17_uc010tde.1_	NM_031277	NP_112567	Q9BXT8	RNF17_HUMAN		2	TCCTGGAGATT	0.284	
-	1	1359	p.G301E|FAM123	NM_152704	NP_689917	Q8N7J2	F123A_HUMAN		4	CGCCTCCTTGG	0.637	
+	1	1368		NM_001033602	NP_001028774	Q5JR59	MTUS2_HUMAN		0	GACATCCAGCA	0.507	
+	17	1910	ba.2_Missense_M	NM_130806	NP_570718	Q8WXD0	RXFP2_HUMAN	Name=5; (Potential).	0	TATGTTCTGTTC	0.393	rs139736966
+	61	9385	e_Mutation_p.Y4	NM_023037	NP_075463	Q5TBA9	FRY_HUMAN		7	TACTTATGCCCT	0.522	
+	11	2718		NM_000059	NP_000050	P51587	BRCA2_HUMAN	ction with NPM1.	64	AAAACGTTGAG	0.313	
+	1	4322		NM_207361	NP_997244	Q5SZK8	FREM2_HUMAN	ar (Potential).|CSPG 9.	11	ACAAATCTTTGG	0.343	
-	10	1233_1234	uyk.2_Missense_	NM_015058	NP_055873	A3KMH1	K0564_HUMAN		6	GCTTGGGACAC	0.366	
-	4	354	LC25A30_uc010t	NM_001010875	NP_001010875	Q5SVS4	KMCP1_HUMAN	=2; (Potential).|Solcar 1.	1	GGGGGCAATCC	0.473	
+	6	1062	p.Y127H|CYSLTR	NM_020377	NP_065110	Q9NS75	CLTR2_HUMAN	Name=3; (Potential).	2	AGTATTTATTTC	0.483	
-	11	2821_2822	p.H889Y|ATP7B_	NM_000053	NP_000044	P35670	ATP7B_HUMAN	lasmic (Potential).	3	CACGTGGGTAG	0.441	
+	5	748	M4_uc001vhk.1_I	NM_006418	NP_006409	Q6UX06	OLFM4_HUMAN	actomedin-like.	1	ATGGTGGTGTG	0.423	
-	6	1858	.1_Intron|DACH1_	NM_080759	NP_542937	Q9UI36	DACH1_HUMAN		1	ACCTACGGATTC	0.488	
-	15	2292	e_Mutation_p.H61	NM_014953	NP_055768	Q9Y2L1	RRP44_HUMAN		1	CATGTGGAATC	0.318	
-	1	1775		NM_052910	NP_443142	Q96PX8	SLIK1_HUMAN	ellular (Potential).	5	ATGATCCTCTT	0.557	
-	2	2890	afe.1_Missense_	NM_032229	NP_115605	Q9H5Y7	SLIK6_HUMAN	lasmic (Potential).	3	TAATACCTTCCT	0.403	
+	2	2528	tic.1_Missense_M	NM_015567	NP_056382	O94991	SLIK5_HUMAN	lasmic (Potential).	5	AGAGGGCAACT	0.493	
+	3	1004		NM_004466	NP_004457	P78333	GPC5_HUMAN		5	AATGGGACAGA	0.517	
-	12	1744	p.R467Q|ABCC4_	NM_005845	NP_005836	O15439	MRP4_HUMAN	C transporter 1.	4	TTTACCCGTGCT	0.493	
+	13	1113	CA_uc010tiz.1_M	NM_000282	NP_000273	P05165	PCCA_HUMAN	.|Biotin carboxylation.	2	AGCATCCTGTC	0.433	

-	39	3489	4A1_uc010agl.2_	NM_001845	NP_001836	P02462	CO4A1_HUMAN	le-helical region.		6	TCCTGGGAGGC	0.498	
+	41	4110		NM_001846	NP_001837	P08572	CO4A2_HUMAN	le-helical region.		6	CCCTTCCAACA	0.527	
+	20	2480	.3_Intron|ARHGE	NM_001113511	NP_001106983	Q14155	ARHG7_HUMAN			7	ATCACGTCTTG	0.587	
+	8	782	gr.1_Missense_Mu	NM_003891	NP_003882	P22891	PROZ_HUMAN	eptidase S1.		0	CGGGGGAGAAT	0.567	
+	13	2343		NM_017905	NP_060375	Q6UWJ1	TMCO3_HUMAN			0	GTGGAGAGCTG	0.597	
-	6	650	6_uc001vuf.2_5'F	NM_000820	NP_000811	Q14393	GAS6_HUMAN	alcium-binding (Potential).		4	GGCAGCCCCC	0.612	
+	1	343		NM_001005483	NP_001005483	Q8NGD3	OR4K5_HUMAN	Name=3; (Potential).		2	GTGCTACTTGTT	0.438	
+	1	650		NM_001004063	NP_001004063	Q8NGD4	OR4K1_HUMAN	Name=5; (Potential).		3	TTATTTCCTACAC	0.433	
-	8	966	_p.S241F|HNRN	NM_031314	NP_112604	P07910	HNRPC_HUMAN	Glu-rich (acidic).		0	TCACGGAGCTG	0.488	
-	1	238		NM_001005465	NP_001005465	Q8NGC4	O10G3_HUMAN	ellular (Potential).		2	GCGAGGGACAA	0.498	
+	6	1225		NM_004995	NP_004986	P50281	MMP14_HUMAN	1.|Extracellular (Potential)		0	TCCGAGGGGAG	0.433	
-	6	2591_2592	c010akt.2_5'Flank|	NM_032452	NP_115828	Q96JJ6	JPH4_HUMAN	lasmic (Potential).		2	CTGGGGCCCT	0.673	
+	2	558		NM_203402	NP_981947	A5D6W6	FITM1_HUMAN	ellular (Potential).		0	GCTTCGAGCCA	0.692	
+	8	1720	1_uc010alg.1_Mis	NM_017999	NP_060469	Q96EP0	RNF31_HUMAN			2	TCCAGCTAGTG	0.582	
-	4	578	.1_Intron|GZMH_	NM_033423	NP_219491	P20718	GRAH_HUMAN	eptidase S1.		2	TAATTGCCATGG	0.517	
-	5	749	e_Mutation_p.R21	NM_004131	NP_004122	P10144	GRAB_HUMAN	eptidase S1.		0	AGGCTCGTGGA	0.498	
+	11	1279	sense_Mutation_p	NM_004086	NP_004077	O43405	COCH_HUMAN	VWFA 2.	p.S400L(1)	3	AATCTCGGACA	0.433	
+	6	4320	_p.P1361S|ARHG	NM_001173	NP_001025226	Q13017	RHG05_HUMAN	Rho-GAP.		5	AAATCCCGGAT	0.294	
+	13	4483		NM_004274	NP_004265	Q13023	AKAP6_HUMAN			21	TAAATGGAAAAG	0.368	
-	37	6179	LGAPA1_uc010tp	NM_014990	NP_055805	Q6GYQ0	RGPA1_HUMAN	to TCF3/E12 (By similarity		4	AATAAGGACATC	0.343	
+	5	3308	a.2_Missense_M	NM_152447	NP_689660	Q96NI6	LRFN5_HUMAN	lasmic (Potential).		8	TTGCTGACTAAT	0.294	
+	7	3420	e_Mutation_p.H10	NM_015091	NP_055906	Q9Y4F4	F179B_HUMAN	Ser-rich.		3	ATTTCTCATATTG	0.299	
-	1	168		NM_080746	NP_542784	Q96L21	RL10L_HUMAN			1	ATCAGGAACCC	0.542	
-	14	1782	p.T518M|PYGL_u	NM_002863	NP_002854	P06737	PYGL_HUMAN			1	ACTCCGTCTCC	0.453	
+	2	1131		NM_000956	NP_000947	P43116	PE2R2_HUMAN	ellular (Potential).		2	GAAAGGAAAAA	0.398	
-	16	1869	trg.1_Missense_M	NM_006544	NP_006535	O00471	EXOC5_HUMAN			3	ATTTAATGTCCT	0.269	
-	2	945		NM_021136	NP_066959	Q16799	RTN1_HUMAN			4	TCCCTCCACAG	0.448	
-	11	2152	H5_uc001xfy.2_3'	NM_139318	NP_647479	Q8NCM2	KCNH5_HUMAN	lasmic (Potential).		9	CACGGGAATGC	0.532	
-	4	362	xfz.1_Missense_	NM_139318	NP_647479	Q8NCM2	KCNH5_HUMAN	toplasmic (Potential).		9	AAACAGGGGTT	0.443	
+	30	4263	gl.2_Missense_Mu	NM_015180	NP_055995	Q8WXH0	SYNE2_HUMAN	lasmic (Potential).		14	CAGACCTTTCA	0.443	
+	113	20571	SYNE2_uc001xgq.	NM_015180	NP_055995	Q8WXH0	SYNE2_HUMAN	lasmic (Potential).		14	GCTTCGACGAG	0.527	rs150644129
+	11	1507	p.V410M|MTHFD	NM_005956	NP_005947	P11586	C1TC_HUMAN	hydrofolate synthetase.		2	TGGTGGTGACT	0.458	
-	3	1123	TB25_uc001xhg.2	NM_006977	NP_008908	P24278	ZBT25_HUMAN			2	ACCCCGGTTGG	0.453	
-	15	2980	s.2_Missense_Mu	NM_000347	NP_000338	P11277	SPTB1_HUMAN	Spectrin 7.		11	CCACTACCTTTG	0.612	
-	31	5907	VE26_uc001xkc.	NM_015346	NP_056161	Q68DK2	ZFY26_HUMAN			11	CACTCCGCACC	0.408	
-	2	2510	e_Mutation_p.E58	NM_183002	NP_892114	P57103	NAC3_HUMAN	|Cytoplasmic (Potential).		7	CAACTCCCCAT	0.502	
-	2	327	2BP_uc010arc.2_	NM_018373	NP_060843	P57105	SYJ2B_HUMAN	toplasmic (Potential).		0	TCACCGAAAGG	0.542	
+	12	1603	N1_uc010ark.2_	NM_000021	NP_000012	P49768	PSN1_HUMAN	with CTNNB1.|Helical; (P		2	CATCACCTTTG	0.398	
-	31	4871		NM_000428	NP_000419	Q14767	LTBP2_HUMAN	alcium-binding (Potential).		2	AGAGACCAGGC	0.473	
+	5	2507	M1_uc001xql.3_	NM_019589	NP_062535	P49750	YLPM1_HUMAN			3	CAAGACCCAG	0.512	
+	2	188	e_Mutation_p.A4	NM_004452	NP_004443	A2VDJ2	A2VDJ2_HUMAN			2	CCGACGCCAGC	0.701	
-	4	885	se_Mutation_p.E1	NM_199296	NP_954993	Q6H9L7	ISM2_HUMAN			1	tcctcgtcttcctcctttcc	0.284	
+	2	2169	td.2_Missense_Mu	NM_013231	NP_037363	O43155	FLRT2_HUMAN	-III.|Extracellular (Potential		4	TTCAGGAGCGC	0.493	
-	43	6064	d.2_Missense_Mu	NM_183387	NP_899243	Q05BV3	EMAL5_HUMAN	WD 29.		3	TCCAGCACTAA	0.413	
-	18	3259		NM_001080414	NP_001073883	Q9P219	DAPLE_HUMAN	Potential.		3	CACTCGGAGAA	0.622	
-	12	1301		NM_001080414	NP_001073883	Q9P219	DAPLE_HUMAN	Potential.		3	TGTCCCGGTCC	0.542	
-	10	1552	5_uc010aue.2_M	NM_006329	NP_006320	Q9UBX5	FBLN5_HUMAN			6	GAACGGAGCGT	0.542	

+	12	2275	GA5_uc001yba.1_	NM_005113	NP_005104	Q8TBA6	GOGA5_HUMAN	lasmic (Potential).	3	TAGCGCGAGTTT	0.323	
-	11	3225	vo.1_Missense_Mu	NM_001002860	NP_001002860	Q9P203	BTBD7_HUMAN		1	CGAAGGGGAAG	0.493	
+	45	7110	bs.1_Nonsense_M	NM_020818	NP_065869	Q9P2D8	UNC79_HUMAN		17	CAAAATCAGAAT	0.493	
-	2	742	_uc010twr.1_Intro	NM_020414	NP_065147	Q9GZR7	DDX24_HUMAN	Q motif.	4	TGTGGGTGCAG	0.547	
-	5	1490	ense_Mutation_p.G	NM_000295	NP_000286	P01009	A1AT_HUMAN		1	ACTTTTCCCATG	0.498	
-	3	862	ydg.2_Missense_	NM_175739	NP_783866	Q86WD7	SPA9_HUMAN		2	GGTGAAAGGGC	0.428	
+	4	1113	ense_Mutation_p.G	NM_001085	NP_001076	P01011	AACT_HUMAN		6	GTCAGGGATCA	0.507	
+	2	784		NR_015340					2	GCCTGGGAGAA	0.577	
-	24	5116	p.P1635L|DICER1_	NM_030621	NP_085124	Q9UPY3	DICER_HUMAN		5	CTTGGTGGAATC	0.393	
+	3	741	ense_Mutation_p.W	NM_000623	NP_000614	P30411	BKRB2_HUMAN	Name=4; (Potential).	5	GATCTGGGGGT	0.607	
+	11	1199	twv.1_Missense_M	NM_032632	NP_116021	P51003	PAPOA_HUMAN		0	ATGTGTCCGTTT	0.408	
-	3	416	t_Site|SLC25A29_	NM_001039355	NP_001034444	Q8N8R3	MCATL_HUMAN	Solcar 1.	1	GCAACGTCCCG	0.632	
+	37	7753	1ykt.1_Missense_	NM_001376	NP_001367	Q14204	DYHC1_HUMAN		10	CTGCGCCCAACA	0.507	
-	12	1757		NM_006035	NP_006026	Q9Y5S2	MRCKB_HUMAN	Potential.	11	CTGTCGCTCGA	0.522	
+	12	2814_2815		NM_015656	NP_056471	Q9ULI4	KI26A_HUMAN		1	GAAAAGGCTGC	0.668	
+	8	1162	l.1_Missense_Mut	NM_138790	NP_620145	Q96BZ4	PLD4_HUMAN		2	GTGATGGAGTAT	0.687	
-	3164								0	CAGCAGGAGGG	0.592	
+	8	945	_Mutation_p.R272	NM_052903	NP_443135	Q96RT8	GCP5_HUMAN		1	TTATTCGGGAAA	0.353	
-	4	423	IPA1_uc001yve.2_	NM_144599	NP_653200	Q7RTP0	NIPA1_HUMAN	ical; (Potential).	0	CGACGGAGCCT	0.473	
+	1	2276		NM_018958	NP_061831	Q9NZP6	CO002_HUMAN		8	CTCTCCCAAATT	0.468	
-	1	479	89A1_uc010azk.1_	NM_138704	NP_619649	Q96MG7	MAGG1_HUMAN	MAGE.	0	GGTCGGGGAAG	0.532	
-	21	3722	.2_Missense_Mut	NM_003257	NP_003248	Q07157	ZO1_HUMAN		6	GGACGCGATCTT	0.483	rs35392254
-	14	2390	q.2_Nonsense_Mu	NM_003257	NP_003248	Q07157	ZO1_HUMAN	ylate kinase-like.	6	CTTCTCGAAGAA	0.363	
-	9	1199	lissense_Mutation_	NM_139320	NP_647536	Q494W8	CRFM7_HUMAN	ical; (Potential).	1	GATGATCATGGT	0.622	
+	10	1217	utation_p.G201E|	NM_000746	NP_000737	P36544	ACHA7_HUMAN	lasmic (Potential).	1	GCAACGGGAACC	0.721	
+	3	783	zhl.1_Missense_M	NM_012125	NP_036257	P08912	ACM5_HUMAN	ame=1; (By similarity).	2	TGACTGCTGTGG	0.493	
-	29	3597		NM_014691	NP_055506	O60306	AQR_HUMAN		1	GCTCTGGCTCTC	0.413	
+	20	3485	bi.2_Nonsense_M	NM_003246	NP_003237	P07996	TSP1_HUMAN	SP C-terminal.	6	GGCTGGAAAGA	0.468	
+	3	1626	bp.1_Missense_M	NM_014952	NP_055767	Q8TBE0	BAHD1_HUMAN		0	CCCGTCCCCCAT	0.657	
+	4	1965	bp.1_Missense_M	NM_014952	NP_055767	Q8TBE0	BAHD1_HUMAN	BAH.	0	GACACCGTCCTT	0.587	
+	3	1420		NM_152260	NP_689473	Q8IZ73	RUSD2_HUMAN		1	CCTCAGGAGTTG	0.562	
-	26	3266	O80_uc010ucu.1_F	NM_017553	NP_060023	Q9ULG1	INO80_HUMAN	nserved components INO8	4	ACTGCGGTAACC	0.453	
+	10	1188	e_Mutation_p.T29	NM_001128608	NP_001122080	O60336	MABP1_HUMAN	WD 4.	10	ATGGCACCGTGC	0.592	
-	2	349	uc010bcp.1_RNA	NM_016642	NP_057726	Q9NRC6	SPTN5_HUMAN	Actin-binding.	2	CCGTCTCGTACT	0.622	
-	15	1668		NM_178034	NP_828848	Q86XP0	PA24D_HUMAN		2	CCCTCACCTTCC	0.627	
-	2	1254	n|ZFP106_uc010u	NM_022473	NP_071918	Q9H2Y7	ZF106_HUMAN		3	CTGAAGGAAATT	0.418	
-	2	904	px.2_Intron|ZFP1	NM_022473	NP_071918	Q9H2Y7	ZF106_HUMAN		3	ACTGCTCCACTA	0.473	
-	10	1272	qp.2_Missense_M	NM_173500	NP_775771	Q6IQ55	TTBK2_HUMAN	rotein kinase.	7	AACACGGATGTA	0.378	
-	12	2078	_p.Q649*|TP53BP	NM_005657	NP_005648	Q12888	TP53B_HUMAN		7	CCTCCTGATCTA	0.478	
+	15	1928	_Mutation_p.E528	NM_017434	NP_059130	Q9NRD9	DUOX1_HUMAN	roxidase activity.|Extracellu	8	AGAAGGAGATT	0.527	
+	3	211		NM_004212	NP_004203	O43868	S28A2_HUMAN		4	GGATGGACTGG	0.522	
-	15	2332	fi.1_Missense_M	NM_182758	NP_877435	Q3MJ13	WDR72_HUMAN		2	TGCCATCATTTTC	0.408	
+	7	3667	acl.2_Missense_	NM_001080534	NP_001074003	Q8NB66	UN13C_HUMAN	C2 1.	7	AAAATAACCATTA	0.313	
+	31	6508	acm.2_Missense_	NM_001080534	NP_001074003	Q8NB66	UN13C_HUMAN		7	TGGTATCCTCTT	0.398	
-	7	948_949		NM_004998	NP_004989	Q12965	MYO1E_HUMAN	osin head-like.	3	CAGAAGGAAGTT	0.441	
-	81	10863_1086	hb.1_Missense_M	NM_020821	NP_065872	Q709C8	VP13C_HUMAN		2	GCGAGGGGGA	0.441	
+	1	167	nh.2_5'UTR|USP3	NM_006537	NP_006528	Q9Y6I4	UBP3_HUMAN		1	GCATTGCTCCGG	0.726	

-	31	5882		NM_003922	NP_003913	Q15751	HERC1_HUMAN		19	TCTGCGAAGAA	0.403	
+	7	4058		NM_015042	NP_055857	O15014	ZN609_HUMAN		3	TGACCGGCCCC	0.612	
-	10	1281_1282	PX_uc010uiu.1_R	NM_006660	NP_006651	O76031	CLPX_HUMAN		0	TCCACGGAGCTT	0.361	
-	9	2460		NM_003613	NP_003604	O75339	CILP1_HUMAN		7	CACTCCGGTAG	0.547	
-	9	2163		NM_003613	NP_003604	O75339	CILP1_HUMAN		7	TCCACAGAGAAC	0.522	
-	22	4148	.P1300L|DENND	NM_005848	NP_005839	Q7Z401	MYCPP_HUMAN		4	GCTTAGGAGAA	0.418	
-	10	1295_1296	p.W310*|MEGF11	NM_032445	NP_115821	A6BM72	MEG11_HUMAN		1	CCAGACCAGCC	0.584	
+	16	1644	qw.2_Missense_	NM_145160	NP_660143	Q13163	MP2K5_HUMAN	rotein kinase.	2	CAGGGGAGCAG	0.433	
+	2	340	.1_Intron|NOX5_u	NM_145658	NP_663633	Q6UW49	SPESP_HUMAN		0	CAAAGGGATCAA	0.393	
+	15	2163	se_Mutation_p.P6	NM_024505	NP_078781	Q96PH1	NOX5_HUMAN	ellular (Potential).	2	CCCAGCCTGGG	0.607	
+	5	705	C49_uc010ukf.1_	NM_017691	NP_060161	Q8IUZ0	LRC49_HUMAN	LRR 2.	1	GCTTTCGACTC	0.343	
+	2	268		NM_145805	NP_665804	Q96A47	ISL2_HUMAN	zinc-binding 1.	0	TGGACGAGACG	0.667	
-	2	366	T50M|TSPAN3_uc	NM_005724	NP_005715	O60637	TSN3_HUMAN	ellular (Potential).	0	ATGAGCGTGTAC	0.473	
-	8	1090	mx.1_Missense_	NM_015162	NP_055977	Q96GR2	ACBG1_HUMAN		1	GGGCCCCCCAC	0.622	
+	7	603	.1_Missense_Mut	NM_000137	NP_000128	P16930	FAAA_HUMAN		0	AATCCGAAGGC	0.582	
+	12	1711	unn.1_Missense_	NM_018689	NP_061159	Q8WUJ3	K1199_HUMAN		3	AGACGGCGTGG	0.552	
-	3	348	orf40_uc010uop.1_	NM_001160115	NP_001153587	Q8WUR7	CO040_HUMAN		1	AGATACCGACAG	0.388	
+	7	744	upe.1_Missense_	NM_004213	NP_004204	O00337	S28A1_HUMAN	ical; (Potential).	3	GGTGTCCTTCG	0.582	
+	7	1468	p.P433L|AKAP13_	NM_007200	NP_009131	Q12802	AKP13_HUMAN		9	AATGCCCACAG	0.522	
+	7	3951	13_uc002blu.1_Mi	NM_007200	NP_009131	Q12802	AKP13_HUMAN		9	TCATCGAACAA	0.572	rs114446918
-	2	1465		NM_022480	NP_071925	Q9H0H3	ENC2_HUMAN	Kelch 3.	2	TGTTGGCCCCA	0.587	
-	19	2639	_p.A804V|NTRK3_	NM_001012338	NP_001012338	Q16288	NTRK3_HUMAN	Potential).|Protein kinase.	281	CCAAAGCATGG	0.537	
-	2	1138	k.2_RNA|DET1_u	NM_001144074	NP_001137546	Q7L5Y6	DET1_HUMAN		2	TTCGCAGCTGC	0.488	
+	4	352		NM_001013657	NP_001013679	Q6ZNW5	VTC2_HUMAN		0	AATCTCCCTTTG	0.557	
+	5	997	2brb.2_Splice_Site	NM_006011	NP_006002	Q92186	SIA8B_HUMAN		0	CGCGGGTGAGC	0.547	
-	2	537	174B_uc002bsl.3_	NM_207446	NP_997329	Q3ZCQ3	F174B_HUMAN	lasmic (Potential).	0	CTGCTGGAGTG	0.473	
+	3	425	_5'Flank|uc002bu	NM_173499	NP_775770	Q6RVD6	SPAT8_HUMAN		2	TCACGGAAGGA	0.458	
-	16	2326		NM_139057	NP_620688	Q8TE56	ATS17_HUMAN	Spacer.	3	TTCTCCCACAG	0.552	
-	3	392	S1_uc002bwh.2_	NM_001040614	NP_001035704	Q8NG48	LINES_HUMAN		0	ACTGCTGGGTTG	0.433	
+	6	1214	DIA2_uc002cgo.1_	NM_006849	NP_006840	Q13087	PDIA2_HUMAN	hioredoxin 1.	2	CAGAGGAGGAA	0.657	
-	3	566	18A_uc002cgv.3_	NM_021259	NP_067082	Q9HCN3	TMM8A_HUMAN	ellular (Potential).	3	GGTGGGAAACG	0.687	
-	3	1614	D8_uc002cix.1_5'	NM_032259	NP_115635	Q96S15	WDR24_HUMAN	WD 5.	2	AGGGCCGGCGC	0.652	
+	8	758	va.1_Missense_M	NM_003933	NP_003924	O94812	BAIP3_HUMAN	C2 1.	1	TGGACCCCTGC	0.672	
-	2	654_655		NM_001009606	NP_001009606	C9JH64	C9JH64_HUMAN		0	ACGCTCCCCGC	0.663	
-	15	5785	t.1_Missense_Mut	NM_001009944	NP_001009944	P98161	PKD1_HUMAN	xtracellular (Potential).	3	TGCCAGCATCC	0.662	
+	9	1382	rl.1_Missense_Mu	NM_016333	NP_057417	Q9UQ35	SRRM2_HUMAN	Ser-rich.	4	CAGTCGGTAAG	0.433	
+	11	5350	.1_Missense_Mut	NM_016333	NP_057417	Q9UQ35	SRRM2_HUMAN	Ser-rich.	4	GTTCCTCCCCT	0.567	
-	5	736	rz.1_Missense_M	NM_022119	NP_071402	Q9GZN4	BSSP4_HUMAN	eptidase S1.	1	CATGTCCTCAG	0.642	
-	2	394		NM_021195	NP_067018	P56747	CLD6_HUMAN	lasmic (Potential).	0	TGGAATCCTTCT	0.612	
-	5	1898	ctw.1_Missense_	NM_032805	NP_116194	Q96SZ4	ZSC10_HUMAN		1	CTTCTCCCCTG	0.716	
-	10	2126		NM_000243	NP_000234	O15553	MEFV_HUMAN	330.2/SPRY.	6	CATTTTCCTTCAT	0.537	
-	7	2479	C3_uc010bto.1_5'	NM_178844	NP_849172	Q7RTR2	NLRC3_HUMAN		6	CAAGAGGGATC	0.502	
-	13	2500_2501	vw.2_Missense_	NM_004380	NP_004371	Q92793	CBP_HUMAN		127	GGAAGGAGAA	0.55	
-	8	877	e_Mutation_p.P20	NM_144605	NP_653206	Q8IYM1	SEP12_HUMAN		1	AAAAGGGATTC	0.587	
-	22	4303		NM_002705	NP_002696	O60437	PEPL_HUMAN	Potential.	6	TAGCTCCTCCA	0.706	
+	7	668	yh.1_Missense_	NM_000303	NP_000294	O15305	PMM2_HUMAN		1	AATGACGGTTAT	0.463	
-	13	3694	uyn.1_Missense_	NM_001134407	NP_001127879	Q12879	NMDE1_HUMAN	lasmic (Potential).	45	TACCTAGGGCTC	0.507	

-	9	2538	uyn.1_Missense_M	NM_001134407	NP_001127879	Q12879	NMDE1_HUMAN	ellular (Potential).	45	GAGGCCGGTCA	0.502	
+	3	675	NFRSF17_uc010b	NM_001192	NP_001183	Q02223	TNR17_HUMAN	lasmic (Potential).	0	AAGGCGCAACC	0.483	rs150352299
+	8	1262	C4_uc010uyz.1_5	NM_005236	NP_005227	Q92889	XPF_HUMAN		10	ATGTTCCCAGC	0.428	
+	21	2140	C1_uc002ddb.3_	NM_015027	NP_055842	Q6P996	PDXD1_HUMAN		1	TGTTGCGGCAG	0.597	
-	35	5100	H11_uc010bvg.2_	NM_002474	NP_002465	P35749	MYH11_HUMAN	Potential.	15	GGCACGGGCAT	0.517	
-	5	1241		NM_001012991	NP_001013009	Q1ED39	CP088_HUMAN	th ZFP106 (By similarity).	0	TGTCAGCCGCC	0.627	
-	6	1001		NM_174924	NP_777584	Q8N807	PDILT_HUMAN		1	TGTATTCGATCA	0.443	
-	4	516_517	_p.L103V|ACSM2	NM_182617	NP_872423	Q68CK6	ACS2B_HUMAN		5	TGCAGGCCAC	0.569	
-	3	224	n_p.R5Q|ACSM2	NM_182617	NP_872423	Q68CK6	ACS2B_HUMAN		5	CTTTTCGCAGC	0.498	rs144570025
-	8	1248	SM1_uc010bwg.1	NM_052956	NP_443188	Q08AH1	ACSM1_HUMAN		2	GGGTGGAGTGG	0.537	
-	2	432	SM1_uc010bwg.1	NM_052956	NP_443188	Q08AH1	ACSM1_HUMAN		2	CTCAGGAACTC	0.587	
-	62	12160	d.1_Missense_Mu	NM_017539	NP_060009	Q8TD57	DYH3_HUMAN		18	TCTCCCCAGGTT	0.517	
+	6	356	_uc010vbj.1_Mis	NM_144672	NP_653273	Q7RTW8	OTOAN_HUMAN		3	AGTTCCGCACT	0.587	
+	32	3593	nse_Mutation_p.S	NM_173615	NP_775886	A6NCI4	VWA3A_HUMAN		1	CCCAATCCTTCA	0.577	
+	8	1282	2K_uc002dkh.2_	NM_013302	NP_037434	O00418	EF2K_HUMAN	ype protein kinase.	1	GCGTTCCGGCC	0.572	
+	5	1467	p.D143N|RBBP6_	NM_006910	NP_008841	Q7Z6E9	RBBP6_HUMAN		4	AATACGACCCA	0.368	
+	15	2763	e_Mutation_p.P57	NM_006910	NP_008841	Q7Z6E9	RBBP6_HUMAN		4	cttcctctccctccgggt	0.308	
+	7	841	_p.R185Q|IL4R_u	NM_000418	NP_000409	P24394	IL4RA_HUMAN	tential).|Fibronectin type-II	2	GGCACGGGTGA	0.547	rs147547377
-	7	1213	_p.L224F|XPO6_u	NM_015171	NP_055986	Q96QU8	XPO6_HUMAN		2	ATCAAGGATGG	0.483	
+	9	2120	_uc002drl.2_Misse	NM_001145795	NP_001139267	Q9NRF2	SH2B1_HUMAN	SH2.	2	CAAGGCGGGGT	0.612	
+	4	527	_uc002dsc.2_Miss	NM_014387	NP_055202	O43561	LAT_HUMAN	lasmic (Potential).	0	TTGCCCCCTGG	0.612	
+	6	971	.P248L|KIF22_uc	NM_007317	NP_015556	Q14807	KIF22_HUMAN		0	CCTCCCTCGTG	0.582	
+	2	88	c010bzb.1_Intron|	NM_001109660	NP_001103130	Q96LL3	CP092_HUMAN		0	AGCTTCCGCCT	0.602	
+	10	1217_1218	tation_p.264_265	NM_002209	NP_002200	P20701	ITAL_HUMAN	Extracellular (Potential).	10	AACATGGAGCTG	0.569	
+	14	4653		NM_014712	NP_055527	O15047	SET1A_HUMAN		3	TGCCCGCACCC	0.706	
-	8	749	fd.1_Missense_Mu	NM_052874	NP_443106	P61266	STX1B_HUMAN	omology.|Cytoplasmic (Pot	0	CATATCGTGCA	0.562	
+	5	543	_p.Q105*|STX4_u	NM_004604	NP_004595	Q12846	STX4_HUMAN	ic (Potential).|Potential.	0	AGCCCCAGAAG	0.418	
-	3	2020	ao.2_Missense_M	NM_024706	NP_078982	Q96K58	ZN668_HUMAN	2H2-type 15.	4	CCGGTCAGAGA	0.652	
-	15	2569	fg.1_Missense_M	NM_173502	NP_775773	Q5K4E3	POLS2_HUMAN		1	ATCCCGAGGCC	0.642	
+	14	1524	_p.R276*|FUS_uc	NM_004960	NP_004951	P35637	FUS_HUMAN	Arg/Gly-rich.	958	TATGATCGAGGC	0.612	
+	13	1434	_p.S456F|ITGAX_	NM_000887	NP_000878	P20702	ITAX_HUMAN	Extracellular (Potential).	4	CGGCTCCTACT	0.677	
+	18	2252	bt.2_Missense_Mu	NM_000887	NP_000878	P20702	ITAX_HUMAN	ellular (Potential).	4	TGACCCCCATT	0.627	
-	20	3057	C12_uc002efa.1_	NM_033226	NP_150229	Q96J65	MRP9_HUMAN	smembrane type-1 2.	3	CAGTGGGAGTC	0.478	
+	7	1047	efx.2_Missense_M	NM_182922	NP_891552	Q7Z4Q2	HEAT3_HUMAN		2	CAAATGAAAGAG	0.368	
-	7	1177	p.E331K|TOX3_u	NM_001080430	NP_001073899	O15405	TOX3_HUMAN		0	GGCTTCTGCTG	0.423	
-	4	530	p.G142E|CES1_u	NM_001025194	NP_001020365	P23141	EST1_HUMAN		0	CCCCTCCGTGG	0.562	
-	14	2002		NM_031885	NP_114091	Q9BXC9	BBS2_HUMAN		1	CTCAAAATAGAC	0.368	
+	6	747	p.G199E|CPNE2_	NM_152727	NP_689940	Q96FN4	CPNE2_HUMAN	C2 2.	2	CTTTGGGAAGT	0.612	
-	10	1006		NM_001896	NP_001887	P19784	CSK22_HUMAN	rotein kinase.	1	GTTCTCACTATG	0.443	
+	2	232	on.1_Missense_M	NM_001795	NP_001786	P33151	CADH5_HUMAN		6	CAGCAGCAGGT	0.612	
+	4	509	_uc002eqj.2_Miss	NM_005182	NP_005173	P43166	CAH7_HUMAN		0	CTTTTGGGGAG	0.582	
+	4	846		NM_000196	NP_000187	P80365	DHI2_HUMAN		0	TCATGGACACA	0.502	
-	1	372	ex.2_Missense_M	NM_022357	NP_071752	Q9H4B8	DPEP3_HUMAN		3	TGAGGCCTGGG	0.711	
-	8	1075	RP2_uc002evq.1	NM_024939	NP_079215	Q9H6T0	ESRP2_HUMAN	RRM 1.	1	TTCTGCGGCCC	0.632	rs146812395
-	77	13320	DIN_uc010cfy.2_R	NM_032821	NP_116210	Q4G0P3	HYDIN_HUMAN		2	TGAGAGCCCAT	0.438	
-	3	276	nse_Mutation_p.E	NM_032821	NP_116210	Q4G0P3	HYDIN_HUMAN		2	GAACTCTGAGG	0.403	
-	16	2743	_p.R363Q|ADAMT	NM_199355	NP_955387	Q8TE60	ATS18_HUMAN	Spacer.	18	TGCTTCGGGCG	0.502	

-	15	2598	_p.H315Y|ADAMT	NM_199355	NP_955387	Q8TE60	ATS18_HUMAN	Cys-rich.		18	TTCATGATCAC	0.393	
+	7	1049		NM_020927	NP_065978	Q9HCJ6	VAT1L_HUMAN			1	TTTTCCCTTTT	0.507	
-	2	648		NM_152342	NP_689555	Q8N8U2	CDYL2_HUMAN			1	TCATTCAAATCC	0.502	
+	4	684	_p.E156K|BCMO1	NM_017429	NP_059125	Q9HAY6	BCDO1_HUMAN			0	CCCTGGAGAAG	0.507	
+	5	1005		NM_022041	NP_071324	Q9H2C0	GAN_HUMAN	Kelch 1.	p.R286Q(1)	2	TTCACGGAAAC	0.403	
+	25	2856		NM_002661	NP_002652	P16885	PLCG2_HUMAN			8	TTCAGAGCATC	0.582	
-	23	3651	fhh.2_Missense_M	NM_003791	NP_003782	Q14703	MBTP1_HUMAN	asic).|Cytoplasmic (Potent		2	CCGAAGGGGTC	0.627	
-	5	1178		NM_003791	NP_003782	Q14703	MBTP1_HUMAN	ase.|Lumenal (Potential).		2	GTGGGGATGCT	0.453	
+	8	1540	ense_Mutation_p.	NM_001145400	NP_001138872	Q8NCV1	ADAD2_HUMAN	to I editase.		0	CTTCCGAACCC	0.697	
+	8	720	fhy.2_Missense_M	NM_014861	NP_055676	O75185	AT2C2_HUMAN	lasmic (Potential).		2	TCACGGACCTC	0.532	
+	4	618	_p.P78S|KIAA018	NM_014615	NP_055430	Q14687	GSE1_HUMAN			5	CCTACCCCTTC	0.667	
+	9	1508		NM_030928	NP_112190	Q9H211	CDT1_HUMAN			1	GGGCAGCTGTT	0.647	
+	2	240	n_p.V13I|DPEP1_	NM_001128141	NP_001121613	P16444	DPEP1_HUMAN			1	TGGCCGTCTGC	0.637	
-	5	858_859	n_p.P7F|NXN_uc	NM_022463	NP_071908	Q6DKJ4	NXN_HUMAN	Thioredoxin.		4	GTAGGGGACGG	0.639	
-	14	1767	_p.T481I|MYO1C_	NM_001080779	NP_001074248	O00159	MYO1C_HUMAN	osin head-like.		0	TTGACAGTATCC	0.652	
-	1	859		NM_003553	NP_003544	P30953	OR1E1_HUMAN	Name=7; (Potential).		0	GAAGGGGTTCA	0.448	
+	15	2490	e_Mutation_p.G71	NM_004703	NP_004694	Q15276	RABE1_HUMAN	Potential.		2	AAAAAGGACAG	0.244	
+	11	1509	ron|ALOX12_uc00	NM_000697	NP_000688	P18054	LOX12_HUMAN	ipoxygenase.		1	AAAGGGATGAC	0.592	
+	3	437	11_uc010vtw.1_In	NM_175734	NP_783861	Q0P670	CQ074_HUMAN	Arg-rich.		0	CTTCTTCGCTGT	0.428	
-	41	5923	R1974W|MYH10_	NM_005964	NP_005955	P35580	MYH10_HUMAN	Potential.		2	GCGCCGGCCAG	0.577	
-	15	1563	vf.1_Missense_M	NM_003802	NP_003793	Q9UKX3	MYH13_HUMAN	osin head-like.		6	TGGTTGAAAAA	0.483	
-	37	5480	uc002gml.1_Intron	NM_005963	NP_005954	P12882	MYH1_HUMAN	Potential.		21	CAGGTCCTTCA	0.562	
-	26	3402	_Missense_Mutati	NM_001100112	NP_001093582	Q9UKX2	MYH2_HUMAN	Potential.		14	TGATTTCAAACT	0.328	
+	17	3183	oo.2_Missense_M	NM_001372	NP_001363	Q9NYC9	DYH9_HUMAN	n (By similarity).		20	CGGAAGAAATT	0.498	
-	7	1488	ow.2_Missense_M	NM_006470	NP_006461	O95361	TRI16_HUMAN			3	TTTGCGGATGCC	0.453	rs146392947
+	11	2459	e_Mutation_p.E26	NM_014695	NP_055510	A2RUR9	C144A_HUMAN	Potential.		0	AAAAGGAACTA	0.333	
+	65	10914	uc002gsl.2_3'UTR	NM_016239	NP_057323	Q9UKN7	MYO15_HUMAN	Tail.|FERM.		9	CCAGCGAGATC	0.423	
-	2	282	A10_uc002gut.1_	NM_001039999	NP_001035088	A6ND36	FA83G_HUMAN			2	GGCCACCAGGG	0.637	
+	10	1320	_p.P374L|RNF112_	NM_007148	NP_009079	Q7Z5V9	Q7Z5V9_HUMAN			2	AAGCCCTGGTG	0.642	
-	2	135	e_Mutation_p.G2	NM_001042685	NP_001036150	Q3B8N2	LEG9B_HUMAN	Galectin 1.		1	GAGACCCCCTT	0.582	
+	5	604	crt.2_Missense_M	NM_003170	NP_003161	Q7KZ85	SPT6H_HUMAN	sp/Glu-rich.		3	AGGAGGAGGAA	0.522	
+	8	1285	tv.2_Missense_M	NM_003250	NP_003241	P10827	THA_HUMAN	gand-binding.		0	GCTACGACCCT	0.632	
-	1	301	39_uc010wfm.1_5	NM_213656	NP_998821	Q6A163	K1C39_HUMAN	Head.		0	TTCACCATACC	0.498	
+	1	289		NM_001146041	NP_001139513	Q9BYQ8	KRA49_HUMAN	-C-[RQVHIEK]- [SPTR]-[V		0	GCCAGCCTGCG	0.542	
-	1	363_364		NM_032524	NP_115913	Q9BYR3	KRA44_HUMAN	-C-[GRQVCH]-[SPT]- [VST		0	CACTGGGGCCT	0.658	
-	1	281	T13_uc010wfr.1_I	NM_153490	NP_705694	P13646	K1C13_HUMAN	ly-rich.|Head.		5	cacctccatagccacct	0.179	
-	2	662	14_uc010cxp.1_	NM_000526	NP_000517	P02533	K1C14_HUMAN	oil 1B.|Rod.		1	GGTGCGGAAGT	0.517	
+	11	1882	_5'Flank|CNP_uc0	NM_031421	NP_113609	Q96NG3	TTC25_HUMAN			1	AGGCAGGAAGC	0.488	
+	14	2444	_p.G472E|WNK4_	NM_032387	NP_115763	Q96J92	WNK4_HUMAN			7	TCCTGGAACTC	0.577	rs147081637
+	4	2166	_Mutation_p.P684	NM_009590	NP_033720	O75106	AOC2_HUMAN			2	AGGACCCCTCC	0.572	
+	3	621	ifs.2_Intron|TMUB	NM_001076674	NP_001070142	Q71RG4	TMUB2_HUMAN			1	CAGTCCAGAGG	0.612	
-	7	2233	_p.S163F|PLEKH	NM_014798	NP_055613	Q9Y4G2	PKHM1_HUMAN	PH 2.		0	GCAGGGACTCC	0.552	
+	4	341	iky.2_Missense_M	NM_004287	NP_004278	O14653	GOSR2_HUMAN	ic (Potential).|Potential.		2	AGCATCGGCGC	0.542	
-	5	691	N2_uc002imf.2_	NM_138355	NP_612364	Q96FV2	SCRN2_HUMAN			1	GTTGCGGGCCC	0.438	
-	1	753	e_Mutation_p.G1	NM_002146	NP_002137	P14651	HXB3_HUMAN			0	CGGGACCGCAC	0.617	
+	15	3368	c002irv.1_Missen	NM_018896	NP_061496	O43497	CAC1G_HUMAN	lasmic (Potential).		1	CAAGTCCGAAT	0.597	
+	29	4246	n.2_Missense_M	NM_003786	NP_003777	O15438	MRP3_HUMAN	similarity).|ABC transporter		4	CGGCAGCTACT	0.622	

+	7	2606	.R792Q|AKAP1_	NM_003488	NP_003479	Q92667	AKAP1_HUMAN	Tudor.	1	GATTCGATACG	0.602	
+	18	1806	_p.P547L|BCAS3_	NM_001099432	NP_001092902	Q9H6U6	BCAS3_HUMAN		5	ACCTCCTCCAC	0.353	
+	10	1351	pc.1_Missense_	NM_173503	NP_775774	Q8N7B9	EFCB3_HUMAN		1	ACTCAGGAAGA	0.338	
-	6	1318	_Mutation_p.M398	NM_001100875	NP_001094345	Q8NA82	MARHA_HUMAN		0	GGCTCCATTGC	0.478	
+	13	1501	_uc010deu.1_Mis	NM_015462	NP_056277	Q9H8H0	NOL11_HUMAN		0	AATCAGTCACC	0.358	
-	23	3211	z.2_Missense_Mu	NM_080283	NP_525022	Q8IUA7	ABCA9_HUMAN		6	TTACTTCGGTAC	0.418	
-	20	2808	ez.2_Nonsense_	NM_080283	NP_525022	Q8IUA7	ABCA9_HUMAN		6	TTTCTGATATGA	0.368	
-	2	131	plice_Site|ABCA9_	NM_080283	NP_525022	Q8IUA7	ABCA9_HUMAN		6	TGTTTCCTTTAA	0.373	
+	3	1024	_p.S277F|C17orf	NM_017941	NP_060411	Q9BSJ5	CQ080_HUMAN	ellular (Potential).	1	CAGAATCCCTCA	0.423	
+	1	301	_p.G133R|GPRC5	NM_018653	NP_061123	Q9NQ84	GPC5C_HUMAN	Name=2; (Potential).	5	TGCTGGGGACC	0.622	
-	3	528		NM_181449	NP_852114	Q496F6	CLM2_HUMAN	ellular (Potential).	4	ATTTTGGGTCA	0.622	
+	11	1343	85_uc010wrv.1_M	NM_024844	NP_079120	Q9BW27	NUP85_HUMAN		1	GTAATCAAAGA	0.498	
-	13	1912	.D431N|SLC38A1	NM_001037984	NP_001033073	Q9HBR0	S38AA_HUMAN		2	TCGGTCTTGGC	0.647	
+	5	877_878	_5'Flank|STRA13_	NM_144999	NP_659436	Q96CN5	LRC45_HUMAN		1	ACATCCCTGGA	0.653	
-	2	418		NM_014646	NP_055461	Q92539	LPIN2_HUMAN	N-LIP.	2	CTTTGGATCTCA	0.478	
-	4	1194	_p.A345T|ZFP161_	NM_003409	NP_003400	O43829	ZF161_HUMAN	2H2-type 3.	1	TGGGGCACGG	0.448	
-	1	1717		NM_001080209	NP_001073678	A6NKL6	T200C_HUMAN		0	AGTCTCGCGTT	0.677	
+	2	1662	NDC2_uc002koh.	NM_001098529	NP_001091999	Q86VQ3	TXND2_HUMAN	eat of Q-P-K-X-G-D-I-P-K-	2	ACATCCCCAAG	0.552	
-	3	542	519_uc002ksr.1_I	NM_145287	NP_660330	Q8TB69	ZN519_HUMAN		0	ACAGAAACTGA	0.284	
-	1	872	TEC_uc010xaj.1_	NM_001137671	NP_001131143	B2RU33	POTEC_HUMAN	ANK 1.	3	GTCCAGATCTT	0.597	
+	36	3448	0xal.1_Missense_	NM_001145029	NP_001138501	Q9BXX2	AN30B_HUMAN	Potential.	2	AAAAGGAAATT	0.303	
+	57	7547	us.3_Missense_	NM_198129	NP_937762	Q16787	LAMA3_HUMAN	minin G-like 1.	11	GTTATGGATCG	0.493	
-	4	452		NM_080597	NP_542164	Q9BXW6	OSBL1_HUMAN	ANK 2.	4	CCTTTCGTCCT	0.418	
-	7	4153	lice_Site_p.Q130	NM_015461	NP_056276	Q96K83	ZN521_HUMAN		7	CATTACCTGCA	0.438	
-	6	833	_p.P200L|SS18_u	NM_001007559	NP_001007560	Q15532	SSXT_HUMAN	Gln-rich.	1884	TATAGGGAGGA	0.413	
-	5	1003	z.2_Missense_Mu	NM_001650	NP_001641	P55087	AQP4_HUMAN	lasmic (Potential).	0	TTGGTCTTTCC	0.478	
-	13	2540	n.1_Missense_M	NM_001792	NP_001783	P19022	CADH2_HUMAN	(Potential).|Cadherin 5.	4	GGATGGAAATA	0.463	
-	11	1866	m.2_Missense_M	NM_024421	NP_077739	Q08554	DSC1_HUMAN	(Potential).|Cadherin 4.	4	GATTCTCTATCTA	0.318	
-	1	887		NM_001034172	NP_001029344	Q3SY17	MCAR2_HUMAN	=5; (Potential).|Solcar 3.	1	ACATGGCACCC	0.443	
-	3	584	_p.L143F|ZNF24_	NM_006965	NP_008896	P17028	ZNF24_HUMAN		0	ACGGAGAGAAA	0.418	rs148053646
+	4	843		NM_015559	NP_056374	Q9Y6X0	SETBP_HUMAN		3	CTTACGAGAGG	0.408	
-	1	631_632	issense_Mutation_	NM_001039360	NP_001034449	A1YPR0	ZBT7C_HUMAN		1	AAGTCCCTGG	0.574	
+	2	1191	APK4_uc010doz.	NM_002747	NP_002738	P31152	MK04_HUMAN	rotein kinase.	6	GCTCCGAGAGA	0.602	
+	20	3649	p.R849Q|DCC_uc	NM_005215	NP_005206	P43146	DCC_HUMAN	tential).|Fibronectin type-III	17	CTTTCGAATTCA	0.373	
-	18	2137	.1_RNA|uc002lgv.	NM_005603	NP_005594	O43520	AT8B1_HUMAN	lasmic (Potential).	10	AACTCCATCCT	0.363	
+	2	135	10dpv.2_Missense_	NM_003839	NP_003830	Q9Y6Q6	TNR11_HUMAN	ellular (Potential).	3	CTCCTCCATGT	0.473	
-	6	652	_Mutation_p.S209F|SERPINB3_uc010dqa.2_Intron			P48594	SPB4_HUMAN	p.S209Y(1)	3	GTATGGACTTG	0.373	
+	7	950	n_p.G136E|SERP	NM_001143818	NP_001137290	P05120	PAI2_HUMAN		2	CAAAGGAAAGT	0.383	
+	12	2464	b.2_Missense_Mu	NM_033646	NP_387450	Q9ULB5	CADH7_HUMAN	lasmic (Potential).	4	TGGGAAAGATTA	0.438	
-	4	1210	m.3_Missense_M	NM_006566	NP_006557	Q15762	CD226_HUMAN	ical; (Potential).	0	CCCTCCAGCCA	0.363	
+	12	1706	ls.2_Missense_M	NM_032649	NP_116038	Q96KN2	CNDP1_HUMAN		0	CTGCCTTTTTC	0.408	
+	2	1720	ra.2_Missense_M	NM_171999	NP_741996	Q9BXA9	SALL3_HUMAN		4	ACGTGGAGTCC	0.741	
+	2	253	_p.R80K|ATP9B_	NM_198531	NP_940933	O43861	ATP9B_HUMAN	lasmic (Potential).	3	GCAAAGGAAAA	0.428	
+	2	502		NM_014913	NP_055728	Q6IQ32	ADNP2_HUMAN		8	GGTGCGAAAAA	0.368	
-	3	312	_p.T97M|MBD3_u	NM_003926	NP_003917	O95983	MBD3_HUMAN		3	GCGCCGTGTTC	0.597	
+	3	338_339	lvv.1_Missense_	NM_182973	NP_892018	Q7Z410	TMPS9_HUMAN	ellular (Potential).	2	CGAGGGATCC	0.624	
-	2	234		NM_145173	NP_660156	O95057	DIRA1_HUMAN		1	GAAGCGCAGCA	0.557	

-	5	481	_p.R142C|PIP5K1	NM_012398	NP_036530	O60331	PI51C_HUMAN	PIPK.		4	GTAGCGGAAGG	0.493	
+	2	240		NM_015897	NP_056981	Q8N2W9	PIAS4_HUMAN			1	ACAGCCGCACC	0.637	rs142623244
+	10	1270	3L3_uc010xib.1_	NM_032607	NP_115996	Q68CJ9	CR3L3_HUMAN	enal (Potential).		2	ACCCCGACCCG	0.647	rs138185635
+	18	2192	_p.G610E|ANKRD	NM_133475	NP_597732	Q8TF21	ANR24_HUMAN			0	CATGGGGGTGG	0.557	
+	19	3368		NM_133475	NP_597732	Q8TF21	ANR24_HUMAN	Potential.		0	GCTACGGACCG	0.667	
+	2	66		NM_018074	NP_060544	Q9BW85	CCD94_HUMAN			0	TACTACCCGCC	0.552	
-	2	284	dtv.1_Missense_	NM_144615	NP_653216	Q96BF3	TMIG2_HUMAN	lar (Potential).|Ig-like.		0	GCAGACCCCCA	0.657	
+	3	524_525		NM_005483	NP_005474	Q13111	CAF1A_HUMAN	1 chromo shadow domain.		2	CTCTCCCTCCA	0.5	rs150150583
-	5	1017	mfj.1_Missense_	NM_003807	NP_003798	O43557	TNF14_HUMAN	ellular (Potential).		1	TCTCCCCAGCC	0.627	
+	26	2509_2510	a.1_Missense_Mu	NM_005428	NP_005419	P15498	VAV_HUMAN	SH3 2.		16	CTCAAGGAGGG	0.569	
+	18	2335	_p.S747F|EMR1_	NM_001974	NP_001965	Q14246	EMR1_HUMAN	Name=5; (Potential).		5	TCAACTCCCTTC	0.323	
+	8	1194	_p.T244S|ZNF557_	NM_001044388	NP_001037853	Q8N988	ZN557_HUMAN	2H2-type 4.		2	GGAAAACCTTC	0.453	
+	7	802	S4_uc002mji.2_5'	NM_024552	NP_078828	Q9HA82	CERS4_HUMAN	TLC.		1	GCTGTGGGCAC	0.572	
+	4	686	_p.C82Y|MARCH	NM_016496	NP_057580	Q9P0N8	MARH2_HUMAN	ING-CH-typ	p.C82S(1)	2	TGGCTGCACCG	0.582	
-	3	542	42_splice|ZNF414	NM_032370	NP_115746	Q96IQ9	ZN414_HUMAN			0	GCCCTACCTTCC	0.632	
-	61	41292	wj.2_Missense_M	NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	lar (Potential).|SEA 11.		57	CCATCCTTTTCA	0.562	
-	21	37694		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	lar (Potential).|SEA 3.		57	TGTTCCTGTCC	0.517	
-	4	31574		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).		57	CAGGCGAAGTG	0.448	
-	3	29368		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	h.|Extracellular (Potential)		57	TGTTTCCACAA	0.488	
-	3	26554		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	h.|Extracellular (Potential)		57	TCATTTCTGCTG	0.507	
-	3	23335		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	h.|Extracellular (Potential)		57	GGGGGGGATAT	0.547	
-	3	19093		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).		57	AGAAGGATGCA	0.443	
-	3	11488		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).		57	GAGTTCCTGGG	0.532	
-	1	8251		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	h.|Extracell	p.E2683K(1)	57	TAGTCTCTGGGA	0.488	
+	1	251		NM_001004456	NP_001004456	Q8NGA1	OR1M1_HUMAN	ellular (Potential).		3	GGTGAGCCTTC	0.527	
-	1	158		NM_001005192	NP_001005192	Q8NGA0	OR7G1_HUMAN	lasmic (Potential).		2	GGTGGGAGTCA	0.488	
+	1	957		NM_175883	NP_787079	Q96RA2	OR7D2_HUMAN	Name=6; (Potential).		3	GCATTGGGGTC	0.498	
+	1	332		NM_001079935	NP_001073404	Q6IFN5	O7E24_HUMAN	ellular (Potential).		1	TCATCTCCTATG	0.493	
-	10	1276	wr.1_Missense_M	NM_152476	NP_689689	Q96MR9	ZN560_HUMAN	2H2-type 2.		6	TAAAATCTTTTCC	0.393	
-	8	689	dwr.1_Missense_	NM_152476	NP_689689	Q96MR9	ZN560_HUMAN	KRAB 2.		6	GCCAAGAGATC	0.468	
+	6	933	_Mutation_p.A17	NM_022737	NP_073574	Q96GM1	LPPR2_HUMAN			1	CGTGGCCGCCG	0.701	
-	6	933	mk.1_Missense_	NM_030824	NP_110451	Q9H7R0	ZN442_HUMAN	KRAB.		4	GTTTTTCATTCA	0.348	
-	6	665	se_Mutation_p.P	NM_004461	NP_004452	Q9Y285	SYFA_HUMAN			1	TGAAGGGCCGG	0.687	
+	1	207	yz.1_Missense_	NM_152654	NP_689867	Q8N907	DAND5_HUMAN			1	AGCTTCTGCCC	0.672	
+	3	867_868		NM_173482	NP_775753	Q8IYK2	CC105_HUMAN			1	GTTCTGGAGCAG	0.614	
-	13	1717	KAP8L_uc002nax.	NM_014371	NP_055186	Q9ULX6	AKP8L_HUMAN			1	GCGCTCCAGCT	0.627	
+	2	133	_Mutation_p.S28	NM_000896	NP_000887	Q08477	CP4F3_HUMAN	ical; (Potential).		3	GGCCTCCTGGC	0.637	
+	8	994_995		NM_023944	NP_076433					7	GGGAAGGCATTG	0.386	
+	1	28		NM_013939	NP_039227	O60403	O10H2_HUMAN	ellular (Potential).		3	GCTGGGGCTAA	0.557	
-	7	901	26_uc002nee.2_I	NM_006387	NP_006378	Q8IWX8	CHERP_HUMAN	CID.		2	TGATGGAGTCA	0.637	
+	6	975		NM_024074	NP_076979	Q9H6F2	TM38A_HUMAN	lasmic (Potential).		3	GAAGGCCAAGA	0.632	
-	22	2901		NM_015692	NP_056507	Q8IZJ3	CPMD8_HUMAN			13	ATTCTCCTCAG	0.562	
-	16	2054		NM_015692	NP_056507	Q8IZJ3	CPMD8_HUMAN			13	CCAGACCTGAG	0.607	
-	11	1246		NM_015692	NP_056507	Q8IZJ3	CPMD8_HUMAN			13	GGCCCGGCTTG	0.632	
+	39	6148	.S1999L|MYO9B_	NM_004145	NP_004136	Q13459	MYO9B_HUMAN	Tail.		1	GGACTCGGAGA	0.647	
-	1	55		NM_138454	NP_612463	Q96CM4	NXNL1_HUMAN	Thioredoxin.		0	ACAGGGAGGCC	0.602	
-	5	454		NM_001080421	NP_001073890	Q9UPW8	UN13A_HUMAN	C2 1.		3	CCACACCTCCA	0.517	

-	8	824	_p.G230E|COMP_	NM_000095	NP_000086	P49747	COMP_HUMAN	EGF-like 4.	0	GGATCCCGTTG	0.706	
-	5	2079	_p.R645*|SFRS14_	NM_014884	NP_055699	Q8IX01	SUGP2_HUMAN		0	TCCTCGCAAGT	0.498	
-	4	1452		NM_021030	NP_066358	P17017	ZNF14_HUMAN	2H2-type 12.	3	GAAGGGAACTT	0.383	
-	4	1562	op.2_Missense_M	NM_033196	NP_149973	O95780	ZN682_HUMAN		2	TGCAGGATTTCT	0.353	
+	3	315	s.1_RNA|ZNF90_	NM_007138	NP_009069	Q03938	ZNF90_HUMAN	KRAB.	2	GCAAGGAAAAA	0.398	
+	4	524	.1_Intron|ZNF90_	NM_007138	NP_009069	Q03938	ZNF90_HUMAN		2	AAAAGAGGTTAT	0.328	
-	4	1600	pc.1_Missense_M	NM_001076675	NP_001070143	Q68DY1	ZN626_HUMAN	ype 12; degenerate.	1	ATTCTTCACATTT	0.388	
-	4	1432	pc.1_Missense_M	NM_001076675	NP_001070143	Q68DY1	ZN626_HUMAN	2H2-type 10.	1	ATTCTTCACATTT	0.388	
-	3	2081		NM_001001411	NP_001001411	Q8N7Q3	ZN676_HUMAN		0	TTTTAGGGATTCT	0.348	
-	5	1966		NM_001080409	NP_001073878				2	TAAGTTTTGAGG	0.363	
+	4	2501	dd.1_Missense_M	NM_014717	NP_055532	O15090	ZN536_HUMAN	2H2-type 9.	11	TGCCGGCACGC	0.507	
+	4	3694	dd.1_Missense_M	NM_014717	NP_055532	O15090	ZN536_HUMAN		11	AAACCGAACCG	0.567	
-	4	448	1_Intron|RHPN2_	NM_033103	NP_149094	Q8IUC4	RHPN2_HUMAN	BRO1.	6	GAGGACGACTG	0.383	rs149250532
+	4	513	M42_uc002oap.2_	NM_024321	NP_077297	Q9BTD8	RBM42_HUMAN		0	GCGGCGGGCAG	0.562	
+	4	443	ense_Mutation_p.	NM_007000	NP_008931	O00322	UPK1A_HUMAN	ellular (Potential).	0	GACCCGCCTCT	0.647	
-	28	3542		NM_004646	NP_004637	O60500	NPHN_HUMAN	2.|Cytoplasmic (Potential).	5	TACGTTCTTTCT	0.547	
+	8	1431	_Mutation_p.R33	NM_001013659	NP_001013681	Q6ZN11	ZN793_HUMAN	2H2-type 4.	0	TACATCGAAAAAT	0.458	
+	5	666	_p.R112C|ZNF540	NM_152606	NP_689819	Q8NDQ6	ZN540_HUMAN		1	CTCTTCGTCTGA	0.333	
-	5	2218	hb.1_Missense_M	NM_032689	NP_116078	Q96SK3	ZN607_HUMAN	2H2-type 15.	0	TAAAAGACTTC	0.428	
+	53	8463	_Mutation_p.G277	NM_000540	NP_000531	P21817	RYR1_HUMAN	.|6 X approximate repeats.	12	CTATGGAGAGA	0.607	
+	73	10827	iv.1_Missense_M	NM_000540	NP_000531	P21817	RYR1_HUMAN		12	AGGCTCCCCGT	0.637	
+	89	12293	p.E4050K|RYR1_	NM_000540	NP_000531	P21817	RYR1_HUMAN		12	ATGTGGAGATG	0.567	
+	3	377	SARS2_uc010xur.	NM_033362	NP_203526	O15235	RT12_HUMAN		0	TTCCCCGGCTC	0.607	rs150096976
-	6	3019		NM_003890	NP_003881	Q9Y6R7	FCGBP_HUMAN	VWFD 2.	9	AGTTCCCACAG	0.597	
-	6	926	sense_Mutation_p	NM_001010880	NP_001010880	O75290	Z780A_HUMAN	2H2-type 3.	0	GCAGGGTAAGA	0.388	
+	16	3662_3663	N4_uc002onz.2_	NM_020971	NP_066022	Q9H254	SPTN4_HUMAN	Spectrin 9.	5	GCAGGGAGGC	0.658	
+	16	2230	10xvo.1_Intron|LT	NM_001042544	NP_001036009	Q8N2S1	LTBP4_HUMAN	n-binding (Potential).|Cys-r	1	GCTCCCGAGGG	0.657	
-	2	291	F_uc002otd.3_5'U	NM_006494	NP_006485	P50548	ERF_HUMAN	ETS.	4	AATGACGCCCT	0.602	
+	41	8208	p.V2133M|MEGF8	NM_001410	NP_001401	Q7Z7M0	MEGF8_HUMAN	ellular (Potential).	1	GCGGCGTGCGG	0.692	rs148860986
-	3	736	g.1_Intron|PSG3_	NM_021016	NP_066296	Q16557	PSG3_HUMAN	like C2-type 1.	2	AAAGAGGGTCC	0.507	
-	3	685	_Mutation_p.S74	NM_182707	NP_874366	Q9UQ74	PSG8_HUMAN	like C2-type 1.	0	TTTCAGACAAC	0.522	
-	4	894_895	sense_Mutation_p.	NM_006905	NP_008836	P11464	PSG1_HUMAN	like C2-type 2.	2	ATTCTCCCTGGG	0.49	
-	2	526	tion_p.G130R|PSG	NM_006905	NP_008836	P11464	PSG1_HUMAN	g-like V-type.	2	TAGTCCCATCAT	0.502	rs34055642
-	4	804_805	ense_Mutation_p.	NM_002782	NP_002773	Q00889	PSG6_HUMAN	like C2-type 2.	2	TTCTCCCTGGG	0.51	
+	6	2489	226_uc010ejg.2_3	NM_001032373	NP_001027545	Q9NYT6	ZN226_HUMAN		0	ATAAATCCTATAA	0.358	
-	4	884	F285_uc010xxa.1	NM_152354	NP_689567	Q96NJ3	ZN285_HUMAN	ype 2; degenerate.	4	TTCTTTCCATACT	0.433	
-	4	707	F285_uc010xxa.	NM_152354	NP_689567	Q96NJ3	ZN285_HUMAN		4	AGTTGGGATGT	0.468	
+	7	865	zt.1_Missense_M	NM_005581	NP_005572	P50895	BCAM_HUMAN	otential).|Ig-like C2-type 1.	1	CAGCCCGTCCA	0.647	
+	7	1636		NM_001042724	NP_001036189	Q92692	PVRL2_HUMAN	lasmic (Potential).	0	AGCTGGAGGCA	0.577	
+	10	1327		NM_006509	NP_006500	Q01201	RELB_HUMAN	RHD.	1	CTCGCGACCAT	0.552	
+	4	300	RS16_uc002pam.	NM_007056	NP_008987	Q8N2M8	CLASR_HUMAN		0	GGATGCCCTGG	0.587	
-	3	514	se_Mutation_p.P9	NM_005619	NP_005610	O75298	RTN2_HUMAN		3	TCGTGGTTCCG	0.677	
+	3	242	eb.2_Missense_M	NM_001135113	NP_001128585	Q6UWQ7	IGFL2_HUMAN		0	TCCCCCCTGCA	0.552	
-	2	950	per.3_Missense_M	NM_018215	NP_060685	Q86V59	PNML1_HUMAN		0	TGTTGGGGGTC	0.557	
-	3	1080		NM_000960	NP_000951	P43119	PI2R_HUMAN	lasmic (Potential).	0	GGAAAGGGGTG	0.657	
+	6	4412		NM_004491	NP_004482	Q9NRY4	RHG35_HUMAN	Pro-rich.	1	TCAGCCGTCGC	0.677	
-	8	1059	H4_uc002pgb.1_	NM_015168	NP_055983	Q9UPT8	ZC3H4_HUMAN	Gly-rich.	6	GCCCCGACCCA	0.627	

+	4	474		NM_022142	NP_071425	Q96BH3	ESPB1_HUMAN	onectin type-II 2.	0	GTCTTCGATGAG	0.517
+	9	2085	N2D_uc010elx.2_5	NM_000836	NP_000827	O15399	NMDE4_HUMAN	ical; (Potential).	6	TCTTCGCCGTCA	0.587
-	4	374		NM_001080434	NP_001073903				6	GCAGCGACTGT	0.622
+	2	287_288	2pjm.2_Missense_	NM_177973	NP_814444	O00204	ST2B1_HUMAN		1	CTACCCCAAGTC	0.644
+	4	1131	n.1_5'Flank|FGF21	NM_019113	NP_061986	Q9NSA1	FGF21_HUMAN		1	CCCCCCGATGTG	0.682
+	3	662	10yaf.1_Missense_	NM_033378	NP_203696				0	AGCCTTCCAAGC	0.642
-	5	938	_Mutation_p.P235L	NM_014037	NP_054756	Q9GZN6	S6A16_HUMAN	cellular (Potential).	4	CATTCAGGATCTG	0.388
+	7	814	7_uc002pqp.2_5'U	NM_024682	NP_078958	Q9HA65	TBC17_HUMAN		0	CCTACTCCACCA	0.692
-	3	116	_p.P21L|IL4I1_uc	NM_152899	NP_690863	Q96RQ9	OXLA_HUMAN		3	gaggatggggacgag	0.453
+	5	2132	_p.S632F|ZNF473_	NM_001006656	NP_001006657	Q8WTR7	ZN473_HUMAN		2	GTGCCTCCCTTA	0.478
-	7	734		NM_152358	NP_689571	Q6UXV1	IZUM2_HUMAN	lasmic (Potential).	0	AGTTTTCGGTTT	0.403
-	1	271		NM_152358	NP_689571	Q6UXV1	IZUM2_HUMAN	cellular (Potential).	0	AGGCCCCTCCA	0.677
+	13	1622	p.W533C|MYH14_	NM_024729	NP_079005	Q7Z406	MYH14_HUMAN	yosin head-like.	1	CCCCTGGACCTT	0.592
+	26	3412	p.A1163V|MYH14_	NM_024729	NP_079005	Q7Z406	MYH14_HUMAN	Potential.	1	TGGGGCCCGGG	0.652
-	3	249	o.2_Missense_Mu	NM_017509	NP_059979	Q9H2R5	KLK15_HUMAN	Peptidase S1.	2	GCTCTCCCAGG	0.622
-	2	601		NM_002029	NP_002020	P21462	FPR1_HUMAN	cellular (Potential).	3	GTTTTACCAGGT	0.537
+	6	1703	pya.1_Missense_M	NM_001031721	NP_001026891	Q6PF04	ZN613_HUMAN		1	AGAAACCCTATG	0.418
+	4	596	dn.1_Missense_M	NM_018260	NP_060730	Q9NV72	ZN701_HUMAN		0	ACCCCGAAGGG	0.413
+	4	1353	dn.1_Missense_M	NM_018260	NP_060730	Q9NV72	ZN701_HUMAN		0	AGAAACGTTACA	0.373
-	5	1222	p.R386C|ZNF347_	NM_032584	NP_115973	Q96SE7	ZN347_HUMAN	C2H2-type 5.	0	TTGAACGAGCTC	0.413
+	3	537	a-mir-935|MI0005	NM_031895	NP_114101	Q8WXS5	CCG8_HUMAN	ical; (Potential).	0	GTGTGTGCGTGG	0.637
-	4	473	j.2_RNA|LILRB2_	NM_005874	NP_005865	Q8N423	LIRB2_HUMAN	Potential).|Ig-like C2-type 1.	1	TGTAATCCAAGA	0.527
+	7	1141	18_splice|LILRA1_	NM_006863	NP_006854	O75019	LIRA1_HUMAN		3	CTCCAGGACAG	0.597
+	16	2261	RB1_uc002qgm.2_	NM_006669	NP_006660	Q8NHL6	LIRB1_HUMAN	lasmic (Potential).	3	GCTGTGCCCAGC	0.652
-	4	1537_1538	p.E488K|NLRP7_	NM_206828	NP_996611	Q8WX94	NALP7_HUMAN	NACHT.	3	GTCCTCCCCCTC	0.574
-	2	1151	nse_Mutation_p.A	NM_003180	NP_003171	O00445	SYT5_HUMAN	ical; (Potential).	0	CAGGGCCCAGG	0.602
-	4	504	TPRH_uc002qjs.2_	NM_002842	NP_002833	Q9HD43	PTPRH_HUMAN	III 2.|Extracellular (Potentia	4	CTGGGCCGTCG	0.597
-	2	361		NM_176820	NP_789790	Q7RTR0	NALP9_HUMAN		7	CTTCTCCCATATG	0.373
+	5	572	P5_uc002qmi.2_I	NM_153447	NP_703148	P59047	NALP5_HUMAN		7	AAATTTCACAAG	0.408
+	4	2057		NM_213598	NP_998763	Q08ER8	ZN543_HUMAN		2	GAAGACCTTTTA	0.418
+	3	1809	_p.P521L|ZNF304_	NM_020657	NP_065708	Q9HCX3	ZN304_HUMAN		1	CAAGGCCTTATG	0.488
+	3	1043		NM_152677	NP_689890	Q8NAM6	ZSCA4_HUMAN	SCAN box.	1	AACTTGGAGAGA	0.413
+	5	1853		NM_152677	NP_689890	Q8NAM6	ZSCA4_HUMAN	C2H2-type 3.	1	CGGTCTCATGAG	0.463
+	3	359	so.2_Missense_Mu	NM_001009	NP_001000	P46782	RS5_HUMAN		0	AGCATGCCTTCG	0.577
-	3	359		NM_003310	NP_003301	Q53HC9	TSSC1_HUMAN		0	TTTTATTTATAAT	0.413
+	8	1089	zi.2_Missense_Mu	NM_003887	NP_003878	O43150	ASAP2_HUMAN		0	TGTCTACGGATC	0.418
+	18	2077	.T258M|IAH1_uc0	NM_016207	NP_057291	Q9UKF6	CPSF3_HUMAN		2	CCCTGACGCCAG	0.458
+	19	3396	rbp.1_Missense_M	NM_014668	NP_055483	Q4ZG55	GREB1_HUMAN		1	GGGATGGACCC	0.592
-	14	2280	_p.P613S|PUM2_u	NM_015317	NP_056132	Q8TB72	PUM2_HUMAN	ilio 1.|PUM-HD.	1	CAGCTGGAGTAG	0.343
-	26	8008		NM_000384	NP_000375	P04114	APOB_HUMAN		27	ACTGATGGAATC	0.413
-	26	6802		NM_000384	NP_000375	P04114	APOB_HUMAN		27	TGGATTGTTTTTA	0.274
-	26	4512		NM_000384	NP_000375	P04114	APOB_HUMAN		27	GTGGTCCCCAGG	0.378
+	12	1641	hv.3_Missense_M	NM_020134	NP_064519	Q9BPU6	DPYL5_HUMAN		2	GTGGGGGATGTC	0.567
-	3	706		NM_178553	NP_848648	Q53SZ7	CB053_HUMAN	Pro-rich.	0	GAGGCCCTGATG	0.617
-	8	1307	p.R220W|SLC30A	NM_003459	NP_003450	Q99726	ZNT3_HUMAN	lasmic (Potential).	0	ATCTCCGGCTGA	0.667
-	11	1630	kk.2_5'Flank|PPM1	NM_002707	NP_002698	O15355	PPM1G_HUMAN		1	GTGTTTCGGGGC	0.527
+	27	1876	c.2_Missense_Mu	NM_153021	NP_694566	Q6P1J6	PLB1_HUMAN	ate repeats.|2.|Extracellular	9	CTGTGGTTGTGC	0.473

+	13	2065	_p.E517K|FAM17	NM_199280	NP_954974	Q6ZUX3	F179A_HUMAN		4	CCGAGGAGATC	0.587	
-	7	2357		NM_004304	NP_004295	Q9UM73	ALK_HUMAN	xtracellular (Potential).	1218	GCCATCTTCAA	0.522	
-	36	4070		NM_000379	NP_000370	P47989	XDH_HUMAN		8	CCTCACAGACC	0.498	
+	13	884	LC30A6_uc002ro	NM_017964	NP_060434	Q6NXT4	ZNT6_HUMAN	lasmic (Potential).	0	AAGTCCGAAAT	0.318	
-	7	849	ynd.1_Missense_	NM_015475	NP_056290	Q8NCA5	FA98A_HUMAN		1	TTTAGGGGATA	0.403	
-	29	2385	p.W744*|MAP4K3	NM_003618	NP_003609	Q8IVH8	M4K3_HUMAN	CNH.	8	TAAACCATGAA	0.348	
-	2	1930	002rrz.2_Intron|SL	NM_021097	NP_066920	P32418	NAC1_HUMAN	lasmic (Potential).	4	TCTTCTCACTCA	0.507	
+	4	428	oa.1_Missense_M	NM_022437	NP_071882	Q9H221	ABCG8_HUMAN	r.|Cytoplasmic (Potential).	4	AGCCTCCTTGC	0.607	
-	8	1197_1198	REPL_uc002rui.3	NM_006036	NP_006027	Q4J6C6	PPCEL_HUMAN		1	CCCAAGGAGGG	0.371	
+	3	755		NM_002158	NP_002149	P32314	FOXN2_HUMAN	Fork-head.	0	ATTTTCCATATTT	0.393	rs147349434
-	27	3073	SME4_uc010fbu.1	NM_014614	NP_055429	Q14997	PSME4_HUMAN	HEAT 2.	5	CCAAGGGAATG	0.338	
-	4	552	.2_Intron|C2orf63_	NM_152385	NP_689598	Q8NHS4	CB063_HUMAN		3	GAATGGATTTG	0.303	
-	11	1751	zj.2_Missense_M	NM_004105	NP_004096	Q12805	FBLN3_HUMAN	nteraction with TIMP3.	6	AAGGTCCCTATA	0.438	
+	6	2109		NM_001080433	NP_001073902	Q96PX6	CC85A_HUMAN		5	AGGTTCGTGTC	0.408	
-	3	274	e_Mutation_p.R7	NM_144709	NP_653310	Q3MIT2	PUS10_HUMAN	Potential.	4	CAGTCGAATTT	0.368	
+	3	461	le.2_Missense_M	NM_002664	NP_002655	P08567	PLEK_HUMAN	PH 1.	1	AGGCCATTAAAT	0.468	
-	4	828		NM_001024680	NP_001019851	Q5FWF7	FBX48_HUMAN		0	GCATCCATTGG	0.378	
-	3	370		NM_002056	NP_002047	Q06210	GFPT1_HUMAN	midotransferase type-2.	1	ACTTTTCCTTTC	0.413	
-	10	1907		NM_017880	NP_060350	Q9NWW7	CB042_HUMAN		0	GGGAAGGATAT	0.507	
+	4	626	p.G110E|PCYOX1	NM_016297	NP_057381	Q9UHG3	PCYOX_HUMAN		1	TCTAGGAGGAG	0.403	
+	13	1393	V1B1_uc010fdw.2	NM_001692	NP_001683	P15313	VATB1_HUMAN		1	GGGAGGAGGCG	0.607	
+	3	1184		NM_001080474	NP_001073943	A6NCI8	CB078_HUMAN		2	GCCAGGAAAAA	0.428	
+	14	1943	b.1_Missense_M	NM_004263	NP_004254	O95754	SEM4F_HUMAN	.|Extracellular (Potential).	4	CCGGCGGGATG	0.622	
+	11	3590		NM_000189	NP_000180	P52789	HXK2_HUMAN	Catalytic.	2	GGAGATGCACA	0.612	
+	13	1908	p.E635K|CTNNA2	NM_004389	NP_004380	P26232	CTNA2_HUMAN		9	CAGAAGAACTA	0.443	
+	8	1267	HNSL2_uc002sta.	NM_018271	NP_060741	Q86YJ6	THNS2_HUMAN		1	CGGATGAAGCC	0.562	
+	6	1603	e.1_Missense_Mu	NM_021088	NP_066574	Q9BSG1	ZNF2_HUMAN	2H2-type 8.	0	GCCAGCGGTGC	0.502	
-	5	633	M131_uc010yvg.1	NM_015348	NP_056163	Q92545	TM131_HUMAN		6	GAACTAGGATTA	0.289	
-	4	471	se_Mutation_p.G1	NM_175735	NP_783862	Q86SG7	LYG2_HUMAN		1	AAGTCCCCTGT	0.517	
+	7	821	vt.1_Missense_M	NM_002518	NP_002509	Q99743	NPAS2_HUMAN		4	TGAACCCAAAG	0.393	
-	2	494_495		NM_153836	NP_722578	Q8IUH2	CREG2_HUMAN		1	GCAGTCCTTGG	0.51	
+	11	1459	wd.1_Missense_	NM_003855	NP_003846	Q13478	IL18R_HUMAN	oplasmic (Potential).	3	AAAGCCGAAGA	0.348	
-	4	994	_p.G74R|TGFBRA	NM_004257	NP_004248	Q8WUH2	TGFA1_HUMAN		2	AACTCCTTTACT	0.418	
-	16	2320		NM_001144013	NP_001137485	A6NKT7	RGPD3_HUMAN		1	GTTTTCGAGTTC	0.368	
+	6	802		NM_001008743	NP_001008743	Q6IMI6	ST1C3_HUMAN	PAPS.	1	GGAAAGGTAGA	0.403	rs139414825
-	20	3464	_p.W989*|RGPD5_	NM_005054	NP_005045	Q99666	RGPD5_HUMAN	RanBD1 1.	0	CCACATCCATGC	0.438	
+	10	2312	nse_Mutation_p.L	NM_019014	NP_061887	Q9H9Y6	RPA2_HUMAN		1	GATTCTCTTCGT	0.512	
+	3	128		NM_014440	NP_055255	Q9UHA7	IL36A_HUMAN		0	AGTCACTATTG	0.498	
+	12	2525	_uc002tjf.2_Misse	NM_012455	NP_036587	Q8NDX1	PSD4_HUMAN	PH.	2	GCAGGGCATCC	0.612	
+	2	518	PP10_uc002tle.2	NM_020868	NP_065919	Q8N608	DPP10_HUMAN	KCND2.|Cytoplasmic (Pote	10	GGTAGGAACTG	0.388	
+	20	2158	_p.M563I|DPP10_	NM_020868	NP_065919	Q8N608	DPP10_HUMAN	ellular (Potential).	10	TGCAGGGATGA	0.388	
+	15	1555	yq.1_Missense_M	NM_001029996	NP_001025167	Q4G0U5	PCDP1_HUMAN		0	ATCAAGGAATTT	0.343	
+	2	954_955	_p.L161*|TMEM1	NM_001105198	NP_001098668	Q53S58	TM177_HUMAN		1	TGTACCTGGAAA	0.658	
+	13	4739	t.3_Missense_Mu	NM_005270	NP_005261	P10070	GLI2_HUMAN		13	GAGCTCCATGC	0.642	
-	8	953	0flr.2_Splice_Site	NM_014553	NP_055368	Q9NZI6	TF2L1_HUMAN		3	ACGTACCCTTC	0.552	
-	2	208	fls.2_Missense_M	NM_032390	NP_115766	Q9BYG3	MK67I_HUMAN		0	CTCCAGGAGTA	0.413	
+	6	1215	flu.2_Missense_M	NM_130773	NP_570129	Q8WYK1	CNTP5_HUMAN	1.|Extracellular (Potential).	10	CTTCACGGTGG	0.602	

+	13	1552		NM_001080527	NP_001073996	Q6PIF6	MYO7B_HUMAN	osin head-like.	2	GCTGGCCCTCA	0.602
+	15	1863		NM_001080527	NP_001073996	Q6PIF6	MYO7B_HUMAN	osin head-like.	2	TGGGCCATGGG	0.552
-	1	2051		NR_002826					0	TCTTTCCAAGA	0.428
-	7	1707	K4_uc010zbg.1_	NM_025052	NP_079328	Q56UN5	YSK4_HUMAN		5	TTAATGGACCT	0.418
-	8	3118		NM_002299	NP_002290	P09848	LPH_HUMAN	ential).|4 X approximate re	13	AGGCAGGATTC	0.488
+	6	653	f.2_Missense_Mu	NM_006895	NP_008826	P50135	HNMT_HUMAN		1	AAGATGCTCATT	0.353
-	60	10576		NM_018557	NP_061027	Q9NZR2	LRP1B_HUMAN	ntial).|LDL-receptor class B	50	ATCCATCCATGT	0.294
-	6	1672	1B_uc010fnl.1_In	NM_018557	NP_061027	Q9NZR2	LRP1B_HUMAN	ellular (Potential).	50	GAATTTCATTTC	0.294
+	2	206	_p.D26N|KYNU_u	NM_003937	NP_003928	Q16719	KYNU_HUMAN		2	CAACGGATGAG	0.488
+	8	830	p.P234S|KYNU_u	NM_003937	NP_003928	Q16719	KYNU_HUMAN		2	ATATTCCTGCC	0.418
+	2	231	0zbl.1_Missense_	NM_018460	NP_060930	Q53QZ3	RHG15_HUMAN		2	AAATGAGAATCA	0.443
+	23	2827	5C_uc002twu.1_	NM_004522	NP_004513	O60282	KIF5C_HUMAN		1	GTTGGACAACG	0.527
+	2	1843	NT5_uc010zci.1_	NM_014568	NP_055383	Q7Z7M9	GALT5_HUMAN	main A.|Lumenal (Potential	4	TCAAGGAGATT	0.448
+	19	2603	p.G777S|SLC4A1	NM_022058	NP_071341	Q6U841	S4A10_HUMAN	ellular (Potential).	5	CTTTAGGTCCA	0.373
-	13	2456	.2_Intron|SCN3A_	NM_006922	NP_008853	Q9NY46	SCN3A_HUMAN		10	CCAAGGAAACC	0.488
-	26	4821	uc002udp.2_Intro	NM_002977	NP_002968	Q15858	SCN9A_HUMAN		13	TCCTTGGATTTT	0.313
-	14	2235	7A_uc010fpm.1_	NM_002976	NP_002967	Q01118	SCN7A_HUMAN		1	ACCAGGATTGG	0.403
+	8	2000	udy.2_Missense_	NM_152381	NP_689594	A4UGR9	XIRP2_HUMAN	Xin 4.	14	AACAAGGCCAT	0.438
+	8	8534	_p.R2664K|XIRP2	NM_152381	NP_689594	A4UGR9	XIRP2_HUMAN		14	TGAAAGAAAAC	0.383
+	22	3030	o.1_Missense_Mu	NM_001079818	NP_001073286	P23229	ITA6_HUMAN	ellular (Potential).	2	TGCGGGGGCTG	0.468
+	9	1227	ej.1_Nonsense_M	NM_145810	NP_665809	Q9BWT1	CDCA7_HUMAN	transcriptional activity.	1	AAACAGGAATTT	0.323
+	9	1229	ej.1_Missense_Mu	NM_145810	NP_665809	Q9BWT1	CDCA7_HUMAN	transcriptional activity.	1	CAGGAATTTGA	0.323
-	12	1645	jj.2_Missense_Mu	NM_001822	NP_001813	P15882	CHIN_HUMAN	Rho-GAP.	3	TCATCCGGATCC	0.408
-	284	3277_8327	80K|TTN_uc010z	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	CTCCTCCATTAT	0.446
-	284	82243	35E|TTN_uc010z	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	TATTTTCCTGTAT	0.403
-	275	71598	87C|TTN_uc010z	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	TTATACGGAAAA	0.413
-	275	71377	13K|TTN_uc010z	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	CCTGGTCTATCT	0.413
-	200	39408	.1_Missense_Muta	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	TGTCTCCTTTCTT	0.358
-	124	28730	_Intron|TTN_uc00	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	CACACCTTCCTC	0.388
-	124	28701	_Intron|TTN_uc00	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	ATTCCTCCTCTG	0.398
-	80	20556	_uc010zfj.1_Intro	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	CATTTCCATCCTG	0.512
-	74	18751	_uc010zfj.1_Intro	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	CAAAAGAAGGT	0.408
-	67	16791	_uc010zfj.1_Intro	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	AGGAGGGAAGC	0.373
-	61	15172	_uc010zfj.1_Intro	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	CAAACGGAGGT	0.443
-	46	11885_1188	G3821S|TTN_uc0	NM_133437	NP_597681	Q8WZ42	TITIN_HUMAN		153	GGGACCCTTTAA	0.46
-	46	13152	N_uc010zfi.1_Intr	NM_133379	NP_596870	Q8WZ42	TITIN_HUMAN		153	GGCTTTGAAAAT	0.408
-	31	7306	TN_uc010zfj.1_Mi	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	CTAAGTCCTTGT	0.428
-	18	3066	p.G902S|TTN_uc0	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	TAAGCCCTGAAG	0.388
-	13	2455	une.1_Nonsense_	NM_173648	NP_775919	Q6ZP82	CC141_HUMAN		10	CTGATTGAAACC	0.488
-	9	1019	fq.1_Missense_M	NM_001003683	NP_001003683	P54750	PDE1A_HUMAN	tic (By similarity).	3	TCTTTGGATAAA	0.343
+	3	872_873		NM_194250	NP_919226	Q7Z570	Z804A_HUMAN		11	ACAAAGGGAATT	0.351
+	4	1154		NM_194250	NP_919226	Q7Z570	Z804A_HUMAN		11	AGATCCAGAAA	0.368
-	5	770		NM_182521	NP_872327	Q8NEG5	ZSWM2_HUMAN	ZZ-type.	3	CTTCCCCTCAAT	0.358
-	5	539		NM_182521	NP_872327	Q8NEG5	ZSWM2_HUMAN	ING-type 1.	3	CACAGCCAAACC	0.274
+	9	809	A1_uc010frw.1_5'	NM_000090	NP_000081	P02461	CO3A1_HUMAN	e-helical region.	13	CTAGGGAGAAT	0.403
+	22	2567	_Mutation_p.R77	NM_001130158	NP_001123630	O43795	MYO1B_HUMAN	IQ 3.	8	TCTGCGGGAAC	0.463
-	43	7902		NM_018897	NP_061720	Q8WXX0	DYH7_HUMAN	k (By similarity).	12	CTACTTGAGATG	0.363

-	41	6983		NM_018897	NP_061720	Q8WXX0	DYH7_HUMAN		12	TACTATCATTCGA	0.383	
-	31	5112		NM_018897	NP_061720	Q8WXX0	DYH7_HUMAN	2 (By similarity).	12	AGCAAGGACCC	0.378	
-	22	3992	utl.1_Missense_M	NM_020760	NP_065811	Q9P2P5	HECW2_HUMAN	HECT.	18	TCTCTGGATACC	0.358	
-	14	2056		NM_213589	NP_998754	Q70E73	RAPH1_HUMAN		10	TTGCGGGGATA	0.343	
+	5	4094		NM_020923	NP_065974	Q9HCK1	ZDBF2_HUMAN		3	CCTACAGATTCC	0.393	
+	5	659	jb.1_Missense_M	NM_005048	NP_005039	P49190	PTH2R_HUMAN	Name=1; (Potential).	3	TGTATACCGTTG	0.423	
+	8	925	r.2_Missense_Mu	NM_001875	NP_001866	P31327	CPSM_HUMAN	midotransferase type-1.	13	GAGGACCGGG	0.498	
-	32	5060_5061	p.G1296K|ABCA1	NM_173076	NP_775099	Q86UK0	ABCAC_HUMAN		11	GCTCTCCCCCA	0.5	
-	2	799		NM_000634	NP_000625	P25024	CXCR1_HUMAN	lasmic (Potential).	2	GTGTACGCAGG	0.547	rs140085060
-	8	1397	0zlr.1_Missense_	NM_006216	NP_006207	P07093	GDN_HUMAN		4	CTGTAGGATTAT	0.418	
-	1	690		NM_005544	NP_005535	P35568	IRS1_HUMAN	RS-type PTB.	12	CACAGCGCCTG	0.597	
-	46	5323		NM_000092	NP_000083	P53420	CO4A4_HUMAN	llagen IV NC1.	11	CGCCTCTTCAG	0.652	
+	37	3322	tation_p.G1054R|	NM_000091	NP_000082	Q01955	CO4A3_HUMAN	le-helical region.	3	ATAAGGGAGAG	0.493	
+	25	2336_2337	xp.1_Missense_M	NM_001080391	NP_001073860	P23497	SP100_HUMAN		5	CCCATCCGTGG	0.505	
+	1	374	UGT1A9_uc002vu	NM_001072	NP_001063	P19224	UD16_HUMAN		0	TCTATCCAGTG	0.423	
-	2	288	yp.1_Missense_M	NM_212556	NP_997721	Q6ZVZ8	ASB18_HUMAN		1	CCATTCCATCTC	0.488	
+	13	3010		NM_001080504	NP_001073973	Q6ZP01	RBM44_HUMAN		4	TTTTCCCTTCC	0.413	
-	13	2488	za.2_Missense_M	NM_006037	NP_006028	P56524	HDAC4_HUMAN		6	CTCATCGCTCT	0.701	
-	1	923		NM_001080835	NP_001074304	Q8WXC7	PRR21_HUMAN	Pro-rich.	2	CGTGGGTGAAG	0.622	
+	7	1293	_Mutation_p.F14	NM_018226	NP_060696	Q9HAU8	RNPL1_HUMAN		2	ATGACTTTCTC	0.642	
+	12	1699		NM_001080437	NP_001073906	Q8TER0	SNED1_HUMAN	EGF-like 7.	2	GCGAGTGCCCG	0.716	
-	14	2263	as.2_Missense_M	NM_019609	NP_062555	Q96SM3	CPXM1_HUMAN		4	TCAATCCTTCTGT	0.612	
-	7	936	as.2_Missense_M	NM_019609	NP_062555	Q96SM3	CPXM1_HUMAN		4	CAGAGGATCCC	0.537	
-	18	2536	4A11_uc002wih.2_	NM_032034	NP_114423	Q8NBS3	S4A11_HUMAN	bicarbonate transporter).	1	GTAGTGGATCT	0.617	
-	13	3475	GLEC1_uc002wiz	NM_023068	NP_075556	Q9BZZ2	SN_HUMAN	11.|Extracellular (Potential)	10	GAGGCGGGGTG	0.652	
-	18	1771	md.3_Missense_	NM_019593	NP_062539	Q9NPB8	GPCP1_HUMAN	GDPD.	0	TATCGGATATTT	0.363	
+	2	121	CB1_uc002wmz.1	NM_015192	NP_056007	Q9NQ66	PLCB1_HUMAN		12	GTTACTCCAATT	0.318	
+	5	388	mz.1_Splice_Site_	NM_015192	NP_056007	Q9NQ66	PLCB1_HUMAN		12	TTTCAGGAATG	0.388	
+	5	813	zrc.1_Missense_	NM_012261	NP_036393	Q9UJQ1	CT103_HUMAN	ellular (Potential).	3	TGATCCGCAGA	0.512	rs137866690
-	5	1093	nj.2_Missense_Mu	NM_020341	NP_065074	Q9P286	PAK7_HUMAN	Linker.	23	CCTCAGAATAG	0.458	
+	2	249	_uc010gca.1_Mis	NM_130811	NP_570824	P60880	SNP25_HUMAN	ith CENPF (By similarity).	2	TGGAGGAGATG	0.597	
-	18	1838	.H447Y|SEL1L2_	NM_025229	NP_079505	Q5TEA6	SE1L2_HUMAN	(Potential).|Sel1-like 10.	2	CGTTGTGGTATT	0.398	
+	2	448	n_p.A2V|SEC23B	NM_006363	NP_006354	Q15437	SC23B_HUMAN		1	TATGGCGACAT	0.418	
+	22	2757	e_Mutation_p.G87	NM_015585	NP_056400	Q8NHU2	CT026_HUMAN		4	CGCCGGAGTC	0.652	
+	28	2716	sk.1_Missense_M	NM_012255	NP_036387	Q9H0D6	XRN2_HUMAN		1	TCCTCCCCTTT	0.378	
-	3	813	sm.2_Missense_M	NM_153675	NP_710141	Q9Y261	FOXA2_HUMAN	Fork-head.	4	AGTGGCGGATG	0.617	
+	8	889	_p.A259S|HM13_	NM_030789	NP_110416	Q8TCT9	HM13_HUMAN	ical; (Potential).	1	ACTTTGCCATG	0.562	rs1044419
+	4	776		NM_033118	NP_149109	Q9H1R3	MYLK2_HUMAN		6	CACCTCGAGGG	0.577	
+	7	762	xb.1_RNA|TTLL9_	NM_001008409	NP_001008409	Q3SXZ7	TTLL9_HUMAN	TTL.	2	GGTAGCCCGGT	0.607	
+	9	1103	_p.T290I|HCK_uc	NM_002110	NP_002101	P08631	HCK_HUMAN	rotein kinase.	9	TGAAAACTCTGC	0.567	
+	14	1995	se_Mutation_p.G5	NM_032819	NP_116208	Q9BYN7	ZN341_HUMAN	2H2-type 11.	2	ACACAGGCTGC	0.597	
-	6	797	j.2_Missense_Mu	NM_000687	NP_000678	P23526	SAHH_HUMAN		0	ATAGCCTGCTA	0.602	
+	17	1874	_p.S520F|ITCH_u	NM_031483	NP_113671	Q96J02	ITCH_HUMAN		6	GGATTCCTTTC	0.403	
-	6	664	S_uc010zup.1_Mi	NM_000178	NP_000169	P48637	GSHB_HUMAN		3	TCCCAGGCTTTG	0.488	
-	4	1551	1_5'Flank|EIF6_uc	NM_178468	NP_848563	Q9BQN1	FA83C_HUMAN		2	GCAGGGGGCTG	0.642	
+	3	240	L_uc002xgw.2_R	NM_022077	NP_071360	Q9NQG1	MANBL_HUMAN		0	CACCTCCGGAG	0.557	
-	11	1841	p.D500N|TGM2_u	NM_004613	NP_004604	P21980	TGM2_HUMAN		3	GAGGTCCCTCT	0.597	

+	4	584	gp.2_Missense_M	NM_001098798	NP_001092268	Q96NM4	TOX2_HUMAN		1	CAGATGGGCAT	0.682	
-	2	1872		NM_020433	NP_065166	Q9BR39	JPH2_HUMAN	ytoplasmic (Potential).	0	TGGCCGTCGGG	0.667	
-	2	1870		NM_020433	NP_065166	Q9BR39	JPH2_HUMAN	ytoplasmic (Potential).	0	GCCGTCGGGCA	0.662	
+	9	1239	p.H362Y|HNF4A_	NM_000457	NP_000448	P41235	HNF4A_HUMAN		3	CACCCCATGCC	0.592	
+	2	427	_p.H124Y|SEMG2_	NM_003008	NP_002999	Q02383	SEMG2_HUMAN	at-rich region.|3-1.	1	CATTTTCACATG	0.398	
-	1	47		NM_080608	NP_542175	Q9BR10	CT165_HUMAN		0	GCAGAGGACCT	0.597	
+	8	1307		NM_004994	NP_004985	P14780	MMP9_HUMAN		2	GGCCCCCCTTG	0.632	
-	5	1817	_p.E507K|ZNF334_	NM_018102	NP_060572	Q9HCZ1	ZN334_HUMAN	2H2-type 10.	2	TGCATTCATATGG	0.453	
-	5	1232	_p.E312K|ZNF334_	NM_018102	NP_060572	Q9HCZ1	ZN334_HUMAN	2H2-type 5.	2	TGCATTCGTAAG	0.438	
+	34	4740	zyf.1_Missense_	NM_006420	NP_006411	Q9Y6D5	BIG2_HUMAN		4	TCTAACCCAACA	0.408	
-	2	1107	_Mutation_p.P33	NM_020436	NP_065169	Q9UJQ4	SALL4_HUMAN		2	CTGAGGAAGCA	0.647	
-	2	393	e_Mutation_p.P98	NM_020436	NP_065169	Q9UJQ4	SALL4_HUMAN		2	AGGTGGATTTT	0.537	
-	2	1147		NM_080617	NP_542184	Q9NTU7	CBLN4_HUMAN	C1q.	4	TGAAACTGTAA	0.343	
+	1	832_833		NM_019888	NP_063941	P41968	MC3R_HUMAN	lasmic (Potential).	4	AGGGGGCAGT	0.609	
+	5	969	xn.1_Missense_M	NM_001033521	NP_001028693	Q05048	CSTF1_HUMAN		1	GCAATCCTCAA	0.403	
+	6	1507	_Mutation_p.E42	NM_001164116	NP_001157588	Q9NQ75	CASS4_HUMAN	Ser-rich.	3	CGGAGGAGTCA	0.567	
+	8	2816	.R127H|GNAS_uc	NM_080425	NP_536350	P63092	GNAS2_HUMAN	(By similar7)|p.R201L(1)|	292	CTGCCGTGTCC	0.423	rs121913495
+	1	2711		NM_178457	NP_848552	Q5JPB2	ZN831_HUMAN		14	GGCTACCCCAC	0.652	
+	1	3649		NM_178457	NP_848552	Q5JPB2	ZN831_HUMAN		14	GCCTCCGAGAT	0.627	
+	2	3760		NM_178457	NP_848552	Q5JPB2	ZN831_HUMAN		14	TCCCAGGGGTG	0.507	
-	4	329	P2_uc010gju.1_5'	NM_014258	NP_055073	Q9BX26	SYCP2_HUMAN		5	CATTGTGGATAT	0.284	
+	7	964	p.1_Missense_Mu	NM_001794	NP_001785	P55283	CADH4_HUMAN	(Potential).|Cadherin 2.	6	GTACCGGATCG	0.612	rs147810745
-	16	4145	s.1_Missense_Mu	NM_033081	NP_149072	Q9BTC0	DIDO1_HUMAN		6	CTGCCGCTGCT	0.602	
-	1	192_193		NM_080823	NP_543013	Q9H3Y6	SRMS_HUMAN	SH3.	2	GAAGGGGCTG	0.708	
+	3	594	e_Mutation_p.R84	NM_016434	NP_057518	Q9NZ71	RTEL1_HUMAN	ase ATP-binding.	0	GGATCGGGCCT	0.642	
+	23	2294	_Mutation_p.R675	NM_016434	NP_057518	Q9NZ71	RTEL1_HUMAN		0	CCCCACGCATG	0.657	
-	23	1824	TE_uc002yir.1_Mi	NM_199261	NP_954870	P56180	TPTE_HUMAN	2 tensin-type.	5	TGTAGGAAGAT	0.264	
-	19	1506	TE_uc002yir.1_Mi	NM_199261	NP_954870	P56180	TPTE_HUMAN	hatase tensin-type.	5	TTTTTCGCTGTG	0.393	
+	5	818	p.S145N|RBM11_	NM_144770	NP_658983	P57052	RBM11_HUMAN		0	TAGTAGCACAG	0.378	
-	5	825	l.2_Missense_Mu	NM_006806	NP_006797	Q14201	BTG3_HUMAN		0	TCTGGGCAAAG	0.388	
+	3	523	AM2_uc011acc.1	NM_004540	NP_004531	O15394	NCAM2_HUMAN	1.|Extracellular (Potential).	4	ATATATCGTTGT	0.348	
+	4	909	_p.E86K|JAM2_u	NM_021219	NP_067042	P57087	JAM2_HUMAN	.|Extracellular (Potential).	0	ACCTGGAAGAG	0.478	
+	11	1925		NM_014586	NP_055401	P57058	HUNK_HUMAN		2	CATCCCCGTGC	0.552	
-	4	561	_p.V51M|C21orf5	NM_021254	NP_067077	P57076	CU059_HUMAN		0	CATCACCGCGC	0.498	
-	2	1091	yrw.2_Missense_	NM_017833	NP_060303	Q9NX36	DJC28_HUMAN		0	TCTCCTTTTGC	0.378	
+	2	847	S6_uc002ytp.2_I	NM_006933	NP_008864	P53794	SC5A3_HUMAN	ellular (Potential).	2	TGAATACTTGT	0.453	
+	2	874	S6_uc002ytp.2_I	NM_006933	NP_008864	P53794	SC5A3_HUMAN	ellular (Potential).	2	CCATAGGATTC	0.448	
-	4	1592	ETD4_uc002yuy.2	NM_017438	NP_059134	Q9NVD3	SETD4_HUMAN	SET.	2	AATAATCATCTG	0.463	
+	12	1548	aeb.1_Missense_	NM_005128	NP_005119	Q9Y3R5	DOP2_HUMAN		2	TCATTCCTTTGG	0.532	
+	6	543_544	e_Mutation_p.L14	NM_001001894	NP_001001894	P53804	TTC3_HUMAN		9	TCATTCCTTATT	0.337	
+	34	4556	f.2_Missense_Mu	NM_001001894	NP_001001894	P53804	TTC3_HUMAN		9	TAATCCTTTTGA	0.308	
-	3	430		NM_005867	NP_005858	P56555	DSCR4_HUMAN		1	CTTGTCCCTTC	0.328	
-	26	4996	AM_uc002yyr.1_	NM_001389	NP_001380	O60469	DSCAM_HUMAN	tential).|Fibronectin type-III	11	CAAAGGGCCTG	0.557	
-	24	4602	AM_uc002yyr.1_	NM_001389	NP_001380	O60469	DSCAM_HUMAN	III 5.|Extracellular (Potentia	11	AAGCCGAGGCT	0.428	
+	2	199	2yzd.1_Missense_	NM_058186	NP_478066	P58499	FAM3B_HUMAN		0	CGCCTCCTTGT	0.627	
-	10	1165	M15_uc002yzp.2_	NM_022115	NP_071398	P57071	PRD15_HUMAN		0	GTGCACGTGTC	0.637	
-	1	137	2yzp.2_Missense_	NM_022115	NP_071398	P57071	PRD15_HUMAN		0	GCACCGGAAgc	0.338	

-	10	1158	S_uc002zcw.3_Mis	NM_000071	NP_000062	P35520	CBS_HUMAN		0	CGATCCCTTCCAC	0.637	
+	2	362		NM_000394	NP_000385	P02489	CRYAA_HUMAN		2	TCCACGGAAAGC	0.647	
-	12	1820		NM_173354	NP_775490	P57059	SIK1_HUMAN		7	TGACAGGGAGCA	0.682	
+	7	679_680	n_p.P46F|RRP1_u	NM_003683	NP_003674	P56182	RRP1_HUMAN		0	TCGACCCCTTCT	0.614	
-	2	259	rf29_uc010gpv.1_5	NM_144991	NP_659428	Q8WU66	TSEAR_HUMAN		0	GGGGGCGGCTA	0.562	rs76207741
+	1	1166	.1_Intron|C21orf29	NM_198687	NP_941960	P60372	KR104_HUMAN	A repeats of C-C-X(3).	0	TCCCTTCCTGCT	0.711	
+	23	1660_1661	A1_uc010gqd.1_5	NM_001848	NP_001839	P12109	CO6A1_HUMAN	le-helical region.	1	CCGAGGGCTTCC	0.663	
+	31	2147	A1_uc002zhv.1_M	NM_001848	NP_001839	P12109	CO6A1_HUMAN	erminal globular domain.	1	GCATCCGGAACG	0.697	rs148962954
+	3	588	6A2_uc002zhz.1_I	NM_001849	NP_001840	P12110	CO6A2_HUMAN	I.|Nonhelical region.	8	CAGCCCCTGCG	0.711	
-	10	1101	l.2_Missense_Mut	NM_001001438	NP_001001438	P48449	ERG7_HUMAN		0	TTGATGGTTTTCC	0.602	
+	8	1315	e_p.R285_splice|P	NM_006031	NP_006022	O95613	PCNT_HUMAN		8	TTCTAGGGGCCC	0.52	
+	22	4415	j.2_Missense_Mut	NM_006031	NP_006022	O95613	PCNT_HUMAN	Potential.	8	CCAGATGAAGAT	0.572	
+	34	4219	P2A_uc002zjs.2_M	NM_015151	NP_055966	Q14689	DIP2A_HUMAN		2	GGGTTCGTTTGC	0.458	
-	9	1431	se_Mutation_p.G1	NM_001136213	NP_001129685	Q6S545	POTEH_HUMAN		1	GTACTTCCGTGC	0.358	
-	4	1053	ense_Mutation_p.N	NM_001136213	NP_001129685	Q6S545	POTEH_HUMAN	ANK 5.	1	TTTAAATTTGCTT	0.318	
-	1	703		NM_001005239	NP_001005239	Q8NG94	O11H1_HUMAN	Name=5; (Potential).	0	GGACAAGAGTATA	0.418	
-	7	1071		NM_014433	NP_055248	Q9UHP6	RTDR1_HUMAN		1	GCGGCCCTCGG	0.647	
+	5	555	tw.1_Missense_Mu	NM_004914	NP_004905	O95755	RAB36_HUMAN		2	TTCCCTATAGCCT	0.507	
+	7	1110	y.2_Intron|MMP11_	NM_005940	NP_005931	P24347	MMP11_HUMAN	mopexin-like 2.	3	ctcagtactgggtgtacg	0.453	
+	12	1508	T1_uc003aav.1_Sp	NM_013430	NP_038347	P19440	GGT1_HUMAN		0	CGGCAGGTGGT	0.637	
+	39	6259	_p.M1883I|MYO18	NM_032608	NP_115997	Q8IUG5	MY18B_HUMAN	Tail.	12	AAGATGGGGGAC	0.627	
+	2	702	L1S_uc003afm.1_	NM_021026	NP_066306	O75677	RFPL1_HUMAN	B30.2/SPRY.	0	TTTGACGTGTCC	0.572	
+	4	576		NM_182527	NP_872333	Q86V35	CABP7_HUMAN	lasmic (Potential).	0	AGTGTCCCGTGG	0.637	
-	6	564	aia.2_Missense_M	NM_174975	NP_777635	Q9UDX4	S14L3_HUMAN	CRAL-TRIO.	5	CAGTCCCAGGC	0.517	
+	3	354	oz.3_Missense_Mu	NM_000631	NP_000622	Q15080	NCF4_HUMAN	PX.	1	CTACCGCCGCTA	0.592	
-	2	181	_p.G14R|TMPRSS	NM_153609	NP_705837	Q8IU80	TMPS6_HUMAN	lasmic (Potential).	6	GTCCCCCTGCC	0.657	
+	7	1932	atq.1_Missense_M	NM_001039141	NP_001034230	Q9H2D6	TARA_HUMAN		1	CTGTGCCCAGC	0.607	
+	9	5253_5254	tu.2_Missense_Mu	NM_001039141	NP_001034230	Q9H2D6	TARA_HUMAN		1	CACCTCCACCCA	0.673	
+	9	1151	k.1_Missense_Mut	NM_006116	NP_006107	Q15750	TAB1_HUMAN	PP2C-like.	1	GCTACCCGCTG	0.657	
+	28	4765	aye.2_Missense_M	NM_021096	NP_066919	Q9P0X4	CAC1I_HUMAN	4 of repeat IV; (Potential).|I	2	TGAGGGTTCTG	0.597	
+	20	4066		NM_001429	NP_001420	Q09472	EP300_HUMAN	p.Y1198_L1243del(1)	64	TCAAACGTAAGTA	0.373	
+	16	2018	RNA|POLR3H_uc0	NM_001098	NP_001089	Q99798	ACON_HUMAN		4	ACTACGGCGAG	0.622	
+	10	1478	aq.1_Missense_M	NM_001469	NP_001460	P12956	XRCC6_HUMAN		5	AAGCTTCGCTTC	0.448	
-	2	637	naa.2_Missense_M	NM_058238	NP_478679	P56706	WNT7B_HUMAN		1	TCTCGCCGAGG	0.652	
+	17	2118	blc.2_Missense_M	NM_014678	NP_055493	O75170	PP6R2_HUMAN		0	TCTGACTACCAGA	0.453	
+	19	2442	e_Mutation_p.P41	NM_175607	NP_783200	Q8IWV2	CNTN4_HUMAN	onectin type-III 2.	7	TTCCGGCCCTAC	0.512	
-	8	1239	RA_uc011asm.1_	NM_000564	NP_000555	Q01344	IL5RA_HUMAN	cellular (Potential).	1	TCCTGGGAAACC	0.478	
+	33	4570	PR1_uc011asu.1_In	NM_001099952	NP_001093422	Q14643	ITPR1_HUMAN	lasmic (Potential).	21	TCGTTCGCGTG	0.597	
+	1	637	DEM1_uc003bqh.2	NM_014674	NP_055489	Q92611	EDEM1_HUMAN	nenal (Potential).	3	GCGGGGACCCG	0.612	
-	6	682	osn.2_Intron|OGG1	NM_003656	NP_003647	Q14012	KCC1A_HUMAN	rotein kinase.	2	GTCCTCCATCTT	0.602	
-	3	279	11atm.1_Missense	NM_173659	NP_775930	Q6P087	RUSD3_HUMAN		1	TCAACGTCACTA	0.512	
+	6	936	S254F|PPARG_uc	NM_015869	NP_056953	P37231	PPARG_HUMAN		2	TGAATTCCTTAAT	0.448	
-	27	3691		NM_024923	NP_079199	Q8TEM1	PO210_HUMAN	nenal (Probable).	11	ACGGCATTGCCA	0.617	rs147038229
-	10	1206	P2_uc011avh.1_5'	NM_001080423	NP_001073892	Q9C0E4	GRIP2_HUMAN	PDZ 3.	1	GTGTTCCATGCT	0.642	
+	1	1095	k.1_Missense_Mu	NM_152536	NP_689749	Q6ZNL6	FGD5_HUMAN		5	ATTGTCCCTTTT	0.552	
+	5	535	_p.V26I|PLCL2_u	NM_001144382	NP_001137854	Q9UPR0	PLCL2_HUMAN	PH.	4	AAAAGGTTCGC	0.418	rs141837634
-	1	710	B_uc003cbm.2_In	NM_144715	NP_653316	Q8N7U6	EFHB_HUMAN		0	CTTTTTCCATTTC	0.507	

-	36	4781	_p.R451Q|TOP2B_	NM_001068	NP_001059	Q02880	TOP2B_HUMAN		5	:CGGTTCGTGGC	0.413	
-	6	759	ɜnse_Mutation_p.L	NM_003615	NP_003606	Q9Y6M7	S4A7_HUMAN	:ellular (Potential).	5	GAACAAGAGGAA'	0.413	
-	9	1661	_p.S184C|OSBPL1	NM_017784	NP_060254	Q9BXB5	OSB10_HUMAN		1	AGCAAAGATCGC'	0.512	
+	12	1648	;e_Mutation_p.L46	NM_015442	NP_056257	Q9H9A5	CNOTA_HUMAN		2	ATATGTCTCAGA/	0.408	
-	4	560	B1_uc003cfj.1_Intr	NM_000404	NP_000395	P16278	BGAL_HUMAN		1	;AGGAGCGGAGA	0.368	
+	7	691	P21_uc011axy.1_M	NM_016300	NP_057384	Q9UBL0	ARP21_HUMAN		3	TACACGGATTCTA	0.388	
+	21	2352		NM_002207	NP_002198	Q13797	ITA9_HUMAN	:ellular (Potential).	6	:TGATGCACGAG(	0.562	
+	22	3195	;e_Mutation_p.M1(	NM_007335	NP_031361	Q9Y238	DLEC1_HUMAN		9	GGCATGAAGAA(	0.567	
-	28	5589	i.2_Missense_Mut	NM_198056	NP_932173	Q14524	SCN5A_HUMAN		9	ATTTCTCCCAGAT	0.532	
-	27	5218		NM_006514	NP_006505	Q9Y5Y9	SCNAA_HUMAN		10	:AAAGTCGTCCT(	0.493	
-	5	1334	cjh.2_Missense_M	NM_033027	NP_149016	Q96S65	CSRN1_HUMAN		5	TGGGTGGGTGG	0.582	
+	2	1129	m.2_Missense_Mu	NM_005201	NP_005192	P51685	CCR8_HUMAN	lasmic (Potential).	2	:AAATGCCTAGG(	0.393	rs146661016
-	2	358		NM_144634	NP_653235	Q96KX0	LYZL4_HUMAN		1	AATAATCCAGGC(	0.552	
+	1	227		NM_152393	NP_689606	Q2TBA0	KBTB5_HUMAN	BTB.	1	;AGCGCGAGTTC	0.682	
-	11	1388	lx.2_Missense_Mu	NM_020707	NP_065758	Q9HCP6	HHATL_HUMAN		3	TCAATTCGTGCTA	0.577	
+	7	2073	ik.2_Missense_Mu	NM_017719	NP_060189	Q9NRH2	SNRK_HUMAN		6	;ATGGCGGGGGC	0.662	
+	1	264		NM_014240	NP_055055	Q9UGP4	LIMD1_HUMAN	tes nuclear export.	1	GCCCAGGGGGA	0.632	
+	17	1659	ɔah.1_Missense_M	NM_014016	NP_054735	Q9NTJ5	SAC1_HUMAN		1	;AACAACTTTTCC	0.343	
+	17	1664_1665	ɔah.1_Missense_M	NM_014016	NP_054735	Q9NTJ5	SAC1_HUMAN		1	CTTTTCCGATGG	0.342	
-	13	1576	.2_Missense_Muta	NM_002343	NP_002334	P02788	TRFL_HUMAN	ansferrin-like 2.	4	:CAGGGGCACAG	0.517	
-	2	455	:pu.3_Missense_M	NM_024512	NP_078788	Q9BYS8	LRRC2_HUMAN		1	:CACCTCCTTCTT	0.458	
-	21	4292_4293	3csx.2_Missense_	NM_002673	NP_002664	O43157	PLXB1_HUMAN	ır (Potential).|IPT/TIG 3.	5	GGAGGGCAGG'	0.574	
-	4	980	ɜnse_Mutation_p.G	NM_024661	NP_078937	Q96ER9	CCD51_HUMAN		0	GACTACCTGCCT(	0.557	
-	34	9637	ıkf.2_Missense_M	NM_001407	NP_001398	Q9NYQ7	CELR3_HUMAN	lasmic (Potential).	11	GGGTGCTGCCC	0.682	
-	21	2055	_p.P539S|QARS_u	NM_005051	NP_005042	P47897	SYQ_HUMAN		1	'CAAAGGCTGTG/	0.567	
-	18	1674	_p.V412L|QARS_uc	NM_005051	NP_005042	P47897	SYQ_HUMAN		1	:ACGCACACAGG	0.547	
+	6	9236		NM_003458	NP_003449	Q9UPA5	BSN_HUMAN		8	:CGCTGCTCCTG(	0.642	
-	21	2854		NM_003335	NP_003326	P41226	UBA7_HUMAN		2	TATAGCGGATGA(	0.587	
+	23	2320		NM_004947	NP_004938	Q8IZD9	DOCK3_HUMAN		0	'CCAGTCCATCC(	0.468	
-	5	445		NM_003280	NP_003271	P63316	TNNC1_HUMAN	EF-hand 4.	0	TTGTCTCCGTCC'	0.577	
+	6	1047	A1D_uc003dgy.3_I	NM_001128840	NP_001122312	Q01668	CAC1D_HUMAN	ellular (Potential).|I.	11	TTATTGGAAAAAT	0.318	
+	42	5361	ɜ_Mutation_p.G17'	NM_001128840	NP_001122312	Q01668	CAC1D_HUMAN	lasmic (Potential).	11	:AGCAGGAAATT(	0.463	
+	25	2273	ɔn_p.G648E|CACN	NM_018398	NP_060868	Q8IZS8	CA2D3_HUMAN	:ellular (Potential).	7	TGTCGGGGCTG/	0.517	
-	15	2909	RC2_uc003dht.1_M	NM_015576	NP_056391	O15083	ERC2_HUMAN	Potential.	2	:TTCTTCCTGCG'	0.463	
-	13	2579	RC2_uc003dht.1_M	NM_015576	NP_056391	O15083	ERC2_HUMAN	Potential.	2	TCTTTTCCAACTG	0.443	
+	9	1234	:C66_uc003dhu.2_I	NM_001141947	NP_001135419	A2RUB6	CCD66_HUMAN		1	TTCTCTCAGTCA/	0.443	
-	3	740		NM_003865	NP_003856	Q9UBX0	HESX1_HUMAN	Homeobox.	1	TAATATCGATACC	0.289	
+	21	3814	ıf.2_Missense_Mut	NM_001457	NP_001448	O75369	FLNB_HUMAN	with FBLP1.|Filamin 10.	19	:ACTTCCCCGCC(	0.537	
-	3	398	;ense_Mutation_p.	NM_004944	NP_004935	Q13609	DNSL3_HUMAN		3	GCATATTGTTCTT'	0.363	
-	2	1636	dnt.2_Missense_M	NM_198271	NP_938012	Q0VAK6	LMOD3_HUMAN		1	'ACTTCGGGGCC'	0.557	
+	15	2726	HA3_uc010hon.1_F	NM_005233	NP_005224	P29320	EPHA3_HUMAN	Potential).|Protein kinase.	33	AGGTAATTAAAG(	0.478	
-	2	567	2_5'UTR|PROS1_	NM_000313	NP_000304	P07225	PROS_HUMAN	Gla.	1	TTTCCGGGTCAT	0.388	
+	1	331		NM_001005514	NP_001005514	A6NHG9	O5H14_HUMAN	Name=3; (Potential).	1	ACCACGGAATGT'	0.413	
+	1	728		NM_001005515	NP_001005515	A6NDH6	O5H15_HUMAN	Name=6; (Potential).	2	GTGGAGCCCATC	0.428	
+	3	563		NM_032787	NP_116176	Q96K78	GP128_HUMAN	:ellular (Potential).	4	AGATATGGACCA'	0.343	
-	2	436	G2_uc011bhe.1_5'	NM_016247	NP_057331	Q9BZV3	IMPG2_HUMAN	:ellular (Potential).	3	:GCCTTCTGATT/	0.428	
+	15	1807	_p.L325F|ZPLD1_u	NM_175056	NP_778226	Q8TCW7	ZPLD1_HUMAN	acellular (Potential).	5	:CCTTCCTTATG(	0.388	

+	1	676_677		NM_032600	NP_115989	Q8NEL0	CCD54_HUMAN	Potential.	0	GAACTGGAAATT	0.391	
-	38	5513		NM_014981	NP_055796	Q9Y2K3	MYH15_HUMAN	Potential.	7	TACTCCCCATCA	0.468	
-	27	3406		NM_014981	NP_055796	Q9Y2K3	MYH15_HUMAN	Potential.	7	TCTTCTGAAGCT	0.343	
-	6	625		NM_014981	NP_055796	Q9Y2K3	MYH15_HUMAN	osin head-like.	7	TAGACTGATTTTC	0.308	
+	2	294	xx.2_Missense_Mu	NM_198196	NP_937839	P40200	TACT_HUMAN	Potential).|Ig-like V-type 1.	3	ATGTCAACCTG	0.408	
+	12	1510	bhr.1_Missense_M	NM_001042575	NP_001036040	Q7RTY8	TMPS7_HUMAN	ntial).|LDL-receptor class	2	CTTTAGGAAAC	0.378	
-	2	1458	dzg.2_Missense_M	NM_199512	NP_955806	Q76M96	CCD80_HUMAN		2	GGTAAAGATTCT	0.607	
-	1	913	F80_uc003ebf.2_F	NM_007136	NP_009067	P51504	ZNF80_HUMAN	2H2-type 4.	0	ACACTCGCTGC	0.527	
-	5	665	D_uc003edv.2_5'F	NM_000187	NP_000178	Q93099	HGD_HUMAN		0	AAATGGTTTCC	0.378	
-	2	143		NM_173825	NP_776186	Q5HYI8	RABL3_HUMAN	all GTPase-like.	0	CCACAGTCCAT	0.363	
-	14	8470	.D2787N|GOLGB	NM_004487	NP_004478	Q14789	GOGB1_HUMAN	ic (Potential).|Potential.	10	AGCATCTCTCT	0.418	
+	6	1064	on_p.S80L|PARP1	NM_001113523	NP_001106995	Q460N3	PAR15_HUMAN	Macro 2.	5	GAAATCAGGTA	0.313	
-	10	1313	gq.2_Missense_Mu	NM_053025	NP_444253	Q15746	MYLK_HUMAN		9	TGATGGAGCTG	0.627	
+	9	1605	ehf.1_Missense_M	NM_001024660	NP_001019831	O60229	KALRN_HUMAN		6	CGAATCCCTCA	0.572	
-	3	188	se_Mutation_p.W5	NM_024628	NP_078904	A0AV02	S12A8_HUMAN		0	TCCACCAGGGC	0.572	
+	11	1913_1914	M2_uc010hsl.2_F	NM_004526	NP_004517	P49736	MCM2_HUMAN	MCM.	4	ACCTCCCTGCA	0.604	
-	3	1917	uc003ekl.1_5'Flan	NM_153330	NP_699161	Q8NHS0	DNJB8_HUMAN		0	GAAGGGGCTGT	0.592	
-	13	2362_2363		NM_007027	NP_008958	Q92547	TOPB1_HUMAN		7	AACCTTCTTTAG	0.361	
-	2	220	.1_Missense_Muta	NM_178554	NP_848649	Q8NBH2	KY_HUMAN		2	GGACTCCATTT	0.388	
+	3	650	HB1_uc011bly.1_	NM_004441	NP_004432	P54762	EPHB1_HUMAN	ellular (Potential).	30	CAGATGAGAGC	0.493	
+	2	741	R3A_uc011blz.1_	NM_002718	NP_002709	Q06190	P2R3A_HUMAN		7	CATCCCTGTGT	0.463	
+	3	471	ne.1_Missense_M	NM_006153	NP_006144	P16333	NCK1_HUMAN	SH3 2.	1	AGAGAGAGGAT	0.453	
-	4	476	ui.2_Missense_Mu	NM_004766	NP_004757	P35606	COPB2_HUMAN	WD 3.	2	TGCTAGTTAGAA	0.393	
+	2	690		NM_152616	NP_689829	Q8IWZ5	TRI42_HUMAN	RING-type.	7	TGTGCGAGAAG	0.602	
+	3	1413		NM_152616	NP_689829	Q8IWZ5	TRI42_HUMAN		7	AGAAGGAAATT	0.453	
-	21	3942		NM_001184	NP_001175	Q13535	ATR_HUMAN		20	GGTCTCCTATAT	0.368	
+	3	283	_p.E42K|PLS1_uc	NM_001145319	NP_001138791	Q14651	PLSI_HUMAN	EF-hand 1.	1	TTAAGGAAGCA	0.368	
+	10	1772	_p.L512F|TRPC1_	NM_003304	NP_003295	P48995	TRPC1_HUMAN	ical; (Potential).	2	TTTCTTCTTGTTT	0.348	
+	15	2226	L590F|P2RY12_uc	NM_053002	NP_443728	Q86YW9	MD12L_HUMAN		7	TCCTTCTCTATG	0.423	
-	5	5258	_5'Flank|IGSF10_	NM_178822	NP_849144	Q6WRI0	IGS10_HUMAN	like C2-type 4.	13	TCTCTTTGGTA	0.493	
-	9	1506	p.G410E|PLCH1_	NM_001130960	NP_001124432	Q4KWH8	PLCH1_HUMAN	I-PLC X-box.	4	AATATTCCTTTCA	0.438	
-	5	569	am.1_Missense_M	NM_173657	NP_775928	Q96NB5	Q96NB5_HUMAN		0	GTTGGAACCAT	0.403	
-	1	1123	fao.1_Nonsense_	NM_004733	NP_004724	O00400	ACATN_HUMAN	ellular (Potential).	4	AGGCTGAAACC	0.408	
+	4	1346		NM_001080440	NP_001073909	A6NHN0	OTOL1_HUMAN	C1q.	0	AGATTGGAATG	0.443	
-	1	220	n_p.L64F|SERPIN	NM_006217	NP_006208	O75830	SPI2_HUMAN		3	AGAACCAAAGT	0.393	
-	7	1215	fk.2_Missense_Mu	NM_005241	NP_005232	Q03112	EVI1_HUMAN		14	CAAAGGAGGCC	0.478	
-	7	1162	fk.2_Missense_Mu	NM_005241	NP_005232	Q03112	EVI1_HUMAN		14	AAAATCCAGGA	0.473	
-	2	768	COM_uc010hwn.2	NM_004991	NP_004982	Q03112	EVI1_HUMAN		14	ATCCATAACTG	0.393	
+	2	1422	.2_Missense_Mut	NM_005414	NP_005405	P12757	SKIL_HUMAN		3	GCCACGAACTT	0.443	
-	5	674	2_Missense_Muta	NM_015028	NP_055843	Q9UKE5	TNIK_HUMAN	rotein kinase.	5	AGCCAGCACCA	0.448	
+	19	2360	fhz.3_Missense_M	NM_022763	NP_073600	Q53EP0	FND3B_HUMAN	nectin type-III 5.	3	GCACCGTCGGC	0.557	rs138991587
+	10	1138	e_Mutation_p.E36	NM_033540	NP_284941	Q8IWA4	MFN1_HUMAN	lasmic (Potential).	3	AGTTCGAACAG	0.403	
+	10	1249		NM_018023	NP_060493	Q9ULM3	YETS2_HUMAN		4	ATGCCCCTCCA	0.488	
-	22	2498	LCN2_uc011brl.1_	NM_004366	NP_004357	P51788	CLCN2_HUMAN	oplasmic (By similarity).	0	AGCAGGATCAA	0.552	
-	9	1458	p.G376R|MASP1_	NM_001879	NP_001870	P48740	MASP1_HUMAN	Sushi 2.	4	CAGCCCGTGTT	0.478	rs139378189
-	4	1286	fsg.2_Missense_M	NM_018192	NP_060662	Q8IVL5	P3H2_HUMAN		4	GATGGGAGAGA	0.507	
-	30	3634	13A4_uc010hzi.2_	NM_032279	NP_115655	Q4VNC1	AT134_HUMAN	ellular (Potential).	2	CTCCGGCATGT	0.468	

-	21	2584	13A4_uc011bsr.1_	NM_032279	NP_115655	Q4VNC1	AT134_HUMAN	cellular (Potential).		2	GCCCAGGAGACA	0.428
-	8	1215	x.3_RNA|SDHAP1_uc011btp.1_RNA							0	CCTGCACGACTC	0.537
+	1	204	1btu.1_Missense_	NM_152672	NP_689885	Q86UW1	OSTA_HUMAN			1	GCGATGGAGCC	0.736
+	12	1524	_p.E491K|PDE6B_	NM_000283	NP_000274	P35913	PDE6B_HUMAN			0	AGAAGGAGGAG	0.562
+	7	489	n_p.V49M|TMEM1	NM_032326	NP_115702	Q9BSA9	TM175_HUMAN	ical; (Potential).		0	TTAATGGTGACCT	0.542
-	3	796	p.R100W|WHSC2_	NM_005663	NP_005654	Q9H3P2	NELFA_HUMAN			1	CGCCCGCAGCG	0.567
+	9	1195	p.G336E|ADD1_u	NM_001119	NP_001110	P35611	ADDA_HUMAN			1	GTGCAGGAGGAC	0.507
-	3	580		NM_177998	NP_819056	Q7RTM1	OTOP1_HUMAN	ical; (Potential).		3	CCCAAAGAAAATA	0.323
+	5	710	p.S225F|MAN2B2	NM_015274	NP_056089	Q9Y2E5	MA2B2_HUMAN			2	CTTTCTCCAACAC	0.537
-	14	2012_2013	_Mutation_p.A664I	NM_198595	NP_940997	Q8N556	AFAP1_HUMAN	Potential.		0	CGCAGGGCCTCT	0.559
-	10	6730	dr.1_Missense_Mu	NM_148894	NP_683692	Q8NFC6	BOD1L_HUMAN			6	AGGCAAGAGGAC	0.522
+	37	4781	s.1_Missense_Mut	NM_004787	NP_004778	O94813	SLIT2_HUMAN	CTCK.		11	GTACGAGGTGTG	0.498
-	10	2062	GC1A_uc003gqt.2	NM_013261	NP_037393	Q9UBK2	PRGC1_HUMAN			8	ATTCTTCCCTCTT	0.468
-	9	1756	15_uc003gqw.2_5'	NM_001358	NP_001349	O43143	DHX15_HUMAN			1	CTGGTGGATCCAT	0.299
-	2	695		NM_015187	NP_056002	Q68CR1	SE1L3_HUMAN			0	GCCACTGTATTTG	0.428
-	18	3348		NM_015230	NP_056045	Q8WZ64	ARAP2_HUMAN			3	ATAAGGGAACAA	0.358
+	3	835	g.2_Missense_Mut	NM_016531	NP_057615	P57682	KLF3_HUMAN	Pro-rich.		2	TGGTCTCCTTATC	0.567
-	4	1758	BM47_uc011bys.1_	NM_001098634	NP_001092104	A0AV96	RBM47_HUMAN			3	GGGGTCGCAGG	0.632
-	6	2160	D4_uc003gwm.2_3	NM_207406	NP_997289	Q6ZU67	BEND4_HUMAN			0	TGGGAACTTTTAT	0.517
-	13	1424	_p.E398K|ATP8A1_	NM_006095	NP_006086	Q9Y2Q0	AT8A1_HUMAN	lasmic (Potential).		3	GTTCCTCATTCA	0.358
-	4	1007	bzc.1_Nonsense_N	NM_001114175	NP_001107647	P47869	GBRA2_HUMAN	cellular (Probable).		4	TTAGTCGAAGGAT	0.289
+	6	942	oze.1_Missense_M	NM_000812	NP_000803	P18505	GBRB1_HUMAN	cellular (Probable).		2	GACATTGAATTTT	0.373
+	4	2856	_p.L837F|REST_u	NM_005612	NP_005603	Q13127	REST_HUMAN			9	CAAGTCCTTATTC	0.458
-	5	1205	T2A3_uc010ihp.1_	NM_024743	NP_079019	Q6UWM9	UD2A3_HUMAN	cellular (Potential).		2	ATATGGGAACTCC	0.408
-	1	581	uc003hei.1_Intron	NM_001073	NP_001064	O75310	UDB11_HUMAN			3	AGGAAGGAGGG	0.403
-	1	80	uc003hei.1_RNA	NM_001073	NP_001064	O75310	UDB11_HUMAN			3	ACTTTTCCACAAC	0.453
-	6	1625	_p.G521E|UGT2A1	NM_006798	NP_006789	Q9Y4X1	UD2A1_HUMAN	lasmic (Potential).		1	TTCTTTCCTATCT	0.323
+	5	667	4_splice|SLC4A4_	NM_001098484	NP_001091954	Q9Y6R1	S4A4_HUMAN			5	TGGTGGGTAAGTA	0.428
-	3	300		NM_014243	NP_055058	O15072	ATS3_HUMAN			2	TCTTTTCCAAATG	0.488
-	29	7073	hgq.2_Missense_M	NM_032217	NP_115593	O75179	ANR17_HUMAN			10	CTGAGGGACTTC	0.383
-	5	701	PEF2_uc003hiz.1_M	NM_006239	NP_006230	O14830	PPE2_HUMAN			4	GGCCCCGTGTAA	0.537
-	4	557	10ijq.1_Missense_	NM_152545	NP_689758	Q0VAM2	RGF1B_HUMAN	rminal Ras-GEF.		0	GGTGAGCCAGAT	0.473
+	4	525	p.G103R|AGPAT9_	NM_032717	NP_116106	Q53EU6	GPAT3_HUMAN			1	AGAAGGGATTGC	0.443
-	14	1881	n_p.S218F|FAM13	NM_014883	NP_055698	O94988	FA13A_HUMAN			2	ACTTCGGAGACA	0.483
+	6	1392	MRN1_uc011cds.1	NM_007351	NP_031377	Q13201	MMRN1_HUMAN			4	GCCCAGCAAAAG	0.398
+	10	1131	p.S286F|BMPR1B	NM_001203	NP_001194	O00238	BMR1B_HUMAN	Potential).|Protein kinase.		8	ATGGTTCCCTTTA	0.403
-	7	775	se_Mutation_p.S1	NM_181887	NP_871616	P61077	UB2D3_HUMAN			0	CAAATGGATAAAA	0.353
+	3	1453	ET2_uc010ilp.1_Mi	NM_001127208	NP_001120680	Q6N021	TET2_HUMAN		p.S356fs*18(1)	733	CAGGTTCCAGCA	0.418
+	3	2937	ET2_uc010ilp.1_Mi	NM_001127208	NP_001120680	Q6N021	TET2_HUMAN	Gln-rich.		733	ACACATCCTGAA	0.373
+	11	1676	se_Mutation_p.G4	NM_001033047	NP_001028219	Q6UXI9	NPNT_HUMAN	MAM.		1	GTGACGGGGCTG	0.602
-	10	1301	_p.D334N|AGXT2L	NM_031279	NP_112569	Q8TBG4	AT2L1_HUMAN			1	GATGGTCCTTCA	0.468
+	1	692		NM_001977	NP_001968	Q07075	AMPE_HUMAN	cellular (Potential).		5	CACGGGCACCG	0.627
+	31	3780	jc.1_Missense_Mu	NM_001148	NP_001139	Q01484	ANK2_HUMAN			14	GAAGAAGAAAATT	0.423
-	4	2157		NM_024574	NP_078850	Q8TB73	CD031_HUMAN	onectin type-III 2.		0	AACATCCAGCAC	0.388
+	60	10619	iel.1_Missense_Mu	NM_015312	NP_056127	Q2LD37	K1109_HUMAN			12	CATCTGCTAGCCA	0.408
+	1	3328		NM_024582	NP_078858	Q6V0I7	FAT4_HUMAN	|Extracellular (Potential).		18	ACTTCGAAGAAG	0.388
+	3	5545	p.1_Missense_Mut	NM_024582	NP_078858	Q6V0I7	FAT4_HUMAN	|Extracellular (Potential).		18	TCTTTTGACATTC	0.413

+	4	5612	.1_Missense_Mut	NM_024582	NP_078858	Q6V0I7	FAT4_HUMAN	.|Extracellular (Potential).		18	CTCTGGTGTGA	0.328	
+	13	2703_2704	_p.P788F|PLK4_u	NM_014264	NP_055079	O00444	PLK4_HUMAN			0	CTCCTCCTTCTG	0.347	
+	15	2186		NM_057175	NP_476516	Q9BXJ9	NAA15_HUMAN			2	TTATTCCAGAGA	0.179	
-	12	2401		NM_015130	NP_055945	Q6ZT07	TBCD9_HUMAN			1	CTAGGGCCAAC	0.438	
+	2	980	.1_Missense_Muta	NM_022475	NP_071920	Q96QV1	HHIP_HUMAN			6	TGGAGGAAATC	0.398	
+	4	419		NM_001080531	NP_001074000	C9J302	CD051_HUMAN			0	ATTATGGAAAAT	0.299	
-	11	1894	h.1_Missense_Mu	NM_033632	NP_361014	Q969H0	FBXW7_HUMAN	WD 6.	82L(6)|p.S582	308	TTAACGACTGG	0.413	
+	8	1120	_p.R250C|ARFIP1_	NM_001025595	NP_001020766	P53367	ARFP1_HUMAN	AH.		1	GACCACGTGAC	0.383	
+	11	2906		NM_033393	NP_203751	Q9C0D6	FHDC1_HUMAN			2	GAACTCCGTGC	0.711	
+	34	4500	.P1484L|KIAA092	NM_015196	NP_056011	A2VDJ0	T131L_HUMAN	lasmic (Potential).		2	CTGTCCTGCAG	0.448	
-	3	334	x.2_Missense_Mu	NM_017639	NP_060109	Q6V1P9	PCD23_HUMAN	Cadherin 1.		4	AGGGTCGATCC	0.463	
+	11	2463	e_Mutation_p.P4	NM_000856	NP_000847	Q02108	GCYA3_HUMAN			4	GAACTTCCACCA	0.398	
+	12	1767_1768	p.G462K|GUCY1	NM_000857	NP_000848	Q02153	GCYB1_HUMAN	anylate cyclase.		0	TCATAGGACAGC	0.386	
+	3	431		NM_000824	NP_000815	P48167	GLRB_HUMAN	ellular (Probable).		2	TCAAAGGTTTG	0.333	
+	5	710		NM_000824	NP_000815	P48167	GLRB_HUMAN	ellular (Probable).		2	ATGGAGATGTC	0.308	
-	34	4957_4958	ro.2_Missense_M	NM_017631	NP_060101	Q8IY21	DDX60_HUMAN			3	CAATGGGAGTT	0.327	
-	6	947		NM_017631	NP_060101	Q8IY21	DDX60_HUMAN			3	TCTTTCCAACT	0.249	
-	14	1996	_p.S592F|DDX60L_	NM_001012967	NP_001012985	Q5H9U9	DDX6L_HUMAN			1	CAATAGAAAAC	0.338	
-	1	478		NM_006792	NP_006783					0	GACAATCTGCAA	0.443	
-	1	290		NM_006792	NP_006783					0	CGGCAGGAAGA	0.378	
+	5	815	0irr.2_Missense_M	NM_014269	NP_055084	Q9UKF5	ADA29_HUMAN			16	CACCTCCAGGC	0.512	
+	7	1438	3_uc003ive.1_5'F	NM_001080477	NP_001073946	Q9P273	TEN3_HUMAN	ellular (Potential).		0	GAGAGAGCCGG	0.547	
+	25	7178		NM_001080477	NP_001073946	Q9P273	TEN3_HUMAN	ellular (Potential).		0	CCAGCTCCTTTT	0.403	
+	3	753	_p.E170K|ZFP42_	NM_174900	NP_777560	Q96MM3	ZFP42_HUMAN			2	TCGCAGAATTT	0.463	
+	1	450		NM_178556	NP_848651	Q8N9V2	TRIML_HUMAN			4	GGGTGGAAGC	0.622	
+	4	494	V127M|SDHA_uc	NM_004168	NP_004159	P31040	DHSA_HUMAN			0	ACACCGTGAAG	0.607	
-	15	1803	.2_RNA|BRD9_u	NM_023924	NP_076413	Q9H8M2	BRD9_HUMAN			0	CGACGGCCGAG	0.657	
-	72	12496	fc.2_Missense_Mu	NM_001369	NP_001360	Q8TE73	DYH5_HUMAN	.6 (By similarity).		31	AGGATCGTTGG	0.453	
-	14	1853		NM_001369	NP_001360	Q8TE73	DYH5_HUMAN	n (By similarity).		31	AGCTTTGAAATC	0.393	
+	50	7915	IO_uc003jfg.2_R	NM_007118	NP_009049	O75962	TRIO_HUMAN			18	CACTCCGTTTA	0.448	
-	2	578_579	8MG>IR|CDH18_	NM_004934	NP_004925	Q13634	CAD18_HUMAN	(Potential).|Cadherin 1.		7	TGGTCCCATAT	0.391	
+	4	277	.1_RNA|GUSBP1	NR_027028						0	GATCTCCGTCA	0.527	
+	3	612	d.1_Missense_M	NM_004932	NP_004923	P55285	CADH6_HUMAN	(Potential).|Cadherin 1.		7	GAGATGGAGCA	0.393	
-	4	876	_p.P74S|RAD1_u	NM_002853	NP_002844	O60671	RAD1_HUMAN			0	GTCAGGAGACA	0.393	rs79789213
-	10	1740	RLR_uc003jjj.1_In	NM_000949	NP_000940	P16471	PRLR_HUMAN	lasmic (Potential).		3	ATAGGGGATTT	0.493	
-	10	1707	RLR_uc003jjj.1_In	NM_000949	NP_000940	P16471	PRLR_HUMAN	lasmic (Potential).		3	GGGGTCCCAGG	0.507	
+	9	1321	_p.L404F|SPEF2_	NM_024867	NP_079143	Q9C093	SPEF2_HUMAN			4	CAATTCCTTAAA	0.303	
+	8	1337_1338	R_uc011cop.1_R	NM_002185	NP_002176	P16871	IL7RA_HUMAN	lasmic (Potential).		5	CTGCCCCCTCC	0.52	
-	2	188	_Intron|UGT3A2_u	NM_174914	NP_777574	Q3SY77	UD3A2_HUMAN			6	TTCCACCTAGG	0.431	
+	7	1066	FLAM_uc003jle.1_	NM_152403	NP_689616	Q63HQ2	EGFLA_HUMAN			7	GCTATGGACCC	0.483	
+	2	732		NM_000958	NP_000949	P35408	PE2R4_HUMAN	lasmic (Potential).		2	GCGCAAGGAGC	0.622	
+	4	338	7_uc011cpn.1_RN	NM_000587	NP_000578	P10643	CO7_HUMAN	SP type-1 1.		0	TGAACCTACAA	0.473	
-	39	4899	jmi.3_Missense_M	NM_173489	NP_775760	Q7Z745	HTRB2_HUMAN			8	ATACCCCATAG	0.502	
-	17	2767	1_Missense_Muta	NM_000065	NP_000056	P13671	CO6_HUMAN	-binding domain.		7	GGATGAAAGTC	0.428	
+	13	1110	o.2_Missense_Mu	NM_024615	NP_078891	Q8N3A8	PARP8_HUMAN			5	AGGACGGAATC	0.478	
+	1	1712	_p.A508T|SNX18_	NM_052870	NP_443102	Q96RF0	SNX18_HUMAN	BAR.		0	TCTTCGCGGAG	0.602	
+	7	873	e_Mutation_p.V16	NM_004520	NP_004511	O00139	KIF2A_HUMAN	ular (Potential).		0	AGGACGTTGAT	0.284	

-	19	3130	3jtq.2_RNA|ADAM	NM_197941	NP_922932	Q9UKP5	ATS6_HUMAN	Spacer.	0	ATAGTCCAGGC	0.373
-	16	2786_2787	3jtq.2_RNA|ADAM	NM_197941	NP_922932	Q9UKP5	ATS6_HUMAN		0	TATAACCTTCAG	0.446
+	3	425		NM_006633	NP_006624	Q13576	IQGA2_HUMAN	CH.	7	AGAAGGGCTCC	0.383
+	15	2849	R98_uc003kjt.2_5'	NM_032119	NP_115495	Q8WXG9	GPR98_HUMAN	ellular (Potential).	16	TAGTAAGAAATCG	0.343
+	74	15803	.G2942D|GPR98_	NM_032119	NP_115495	Q8WXG9	GPR98_HUMAN	ellular (Potential).	16	AGAATGGCACAT	0.428
-	12	1887	bi.1_Missense_Mu	NM_000439	NP_000430	P29120	NEC1_HUMAN		2	GTTCTCTCCCC	0.398
-	2	255	na.3_Missense_M	NM_018343	NP_060813	Q9BVS4	RIOK2_HUMAN		1	TATTACAGCCAC	0.358
-	9	1822		NM_180991	NP_851322	Q6ZQN7	SO4C1_HUMAN	Extracellular (Potential).	4	GGATAATAATATG	0.418
+	11	973	K4_uc010jbv.2_	NM_001744	NP_001735	Q16566	KCC4_HUMAN	rotein kinase.	5	ACTACATTTCAA	0.423
-	3	1995		NM_020177	NP_064562	Q96JP0	FEM1C_HUMAN		3	TTCCCCTTGGAT	0.388
+	3	485	ksn.2_Missense_	NM_182761	NP_877438	A1A519	F170A_HUMAN		1	GGAACGAGGAG	0.507
+	1	373		NM_177478	NP_803431	Q8N4E7	FTMT_HUMAN	rritin-like diiron.	1	GGGAGGAGACC	0.577
+	4	580	_Intron|SNCAIP_u	NM_005460	NP_005451	Q9Y6H5	SNCAP_HUMAN		2	AGATGGAGTGG	0.557
+	5	1254	_Intron|SNCAIP_	NM_005460	NP_005451	Q9Y6H5	SNCAP_HUMAN	ANK 1.	2	GAAAATGGAAAC	0.438
+	5	1356	_Intron|SNCAIP_	NM_005460	NP_005451	Q9Y6H5	SNCAP_HUMAN	ANK 2.	2	ACACTGAGAAG	0.483
+	7	1129	uj.3_Missense_M	NM_130809	NP_570721	Q96M27	PRRC1_HUMAN		0	GCTTGCGTCGA	0.378
-	50	6851		NM_001999	NP_001990	P35556	FBN2_HUMAN	TB 8.	15	GGGGTCCCCCC	0.458
+	15	2119	X46_uc003kzv.1_	NM_014829	NP_055644	Q7L014	DDX46_HUMAN	case C-terminal.	1	CTTCATGGAGGT	0.353
+	8	1281	p.D200N|TGFBI_u	NM_000358	NP_000349	Q15582	BGH3_HUMAN		4	TCCCAGACTCA	0.572
+	13	1941_1942	BI_uc011cyb.1_Mi	NM_000358	NP_000349	Q15582	BGH3_HUMAN	FAS1 4.	4	TCCAAGGTGACA	0.53
-	5	850	LHL3_uc010jem.1_	NM_017415	NP_059111	Q9UH77	KLHL3_HUMAN		0	TCTGCCGAACAT	0.547
-	2	1524	NNA1_uc003ldj.2_	NM_015564	NP_056379	O43300	LRRT2_HUMAN	lar (Potential).|LRRCT.	0	TGAAATCCATGG	0.473
-	3	1196	w.1_Missense_Mu	NM_004883	NP_004874	O14511	NRG2_HUMAN	e.|Extracellular (Potential).	6	GCCGGCCCCGG	0.632
+	20	2796	_p.V834I|SLC4A9	NM_031467	NP_113655	Q96Q91	B3A4_HUMAN	ne (anion exchange).	1	TGGGGGTCCGA	0.488
+	1	116_117	.2_Intron|PCDHA4	NM_018907	NP_061730	Q9UN74	PCDA4_HUMAN		6	CCTGGGGAAGC	0.515
+	1	1849	3lhf.2_Intron|PCD	NM_018907	NP_061730	Q9UN74	PCDA4_HUMAN	ellular (Potential).	6	GCCATGGTCGG	0.667
+	1	190	lhh.1_Intron|PCD	NM_018910	NP_061733	Q9UN72	PCDA7_HUMAN	|Extracellular (Potential).	4	GCCTGTTCCGG	0.612
+	1	1987	CDHA5_uc003lhk.	NM_018911	NP_061734	Q9Y5H6	PCDA8_HUMAN	|Extracellular (Potential).	2	CCACGGCCACG	0.647
+	1	1993	.2_Intron|PCDHA	NM_018901	NP_061724	Q9Y5I2	PCDAA_HUMAN	r (Potential).|Cadherin 6.	5	ACTGTGCTTGTG	0.672
+	1	1760	_Intron|PCDHA8_	NM_018899	NP_061722	Q9Y5I4	PCDC2_HUMAN	|Extracellular (Potential).	4	CTACTCCCTTCT	0.488
+	1	353	HB2_uc003lim.1_	NM_018936	NP_061759	Q9Y5E7	PCDB2_HUMAN	r (Potential).|Cadherin 1.	6	CAAAGGAAAAA	0.522
+	1	1496	uc003lin.2_RNA	NM_018937	NP_061760	Q9Y5E6	PCDB3_HUMAN	r (Potential).|Cadherin 5.	2	ACCTGCCCCTCT	0.667
+	1	454	dah.1_Missense_	NM_018939	NP_061762	Q9Y5E3	PCDB6_HUMAN	|Extracellular (Potential).	1	ATATTTCCTTTGA	0.478
+	1	2164	ah.1_Missense_M	NM_018939	NP_061762	Q9Y5E3	PCDB6_HUMAN	lasmic (Potential).	1	TGGGTCGCTAC	0.657
+	1	1804		NM_018940	NP_061763	Q9Y5E2	PCDB7_HUMAN	r (Potential).|Cadherin 5.	6	GCAGCGAGGCG	0.706
+	1	1585	HB16_uc010jfw.1_	NM_020957	NP_066008	Q9NRJ7	PCDBG_HUMAN	r (Potential).|Cadherin 2.	2	TACCGGAAAACA	0.388
+	1	1931	HB16_uc010jfw.1_	NM_020957	NP_066008	Q9NRJ7	PCDBG_HUMAN	r (Potential).|Cadherin 3.	2	TGGCTCCCTGG	0.488
+	1	511		NM_018930	NP_061753	Q9UN67	PCDBA_HUMAN	r (Potential).|Cadherin 1.	2	GATGATCCCTTT	0.418
+	1	2056	dan.1_Missense_	NM_018912	NP_061735	Q9Y5H4	PCDG1_HUMAN	ellular (Potential).	3	CCAACGATTCG	0.692
+	1	666	DHGA2_uc011da	NM_018915	NP_061738	Q9Y5H1	PCDG2_HUMAN	r (Potential).|Cadherin 2.	3	ATGCAGACGTA	0.512
+	1	373	ju.1_Intron|PCDH	NM_018921	NP_061744	Q9Y5G4	PCDG9_HUMAN	|Extracellular (Potential).	0	GTAACTGATATTA	0.478
-	20	2902	e.1_Missense_Mu	NM_022481	NP_071926	Q8WWN8	ARAP3_HUMAN	Rho-GAP.	7	CTTTCCGGTATA	0.657
+	5	1231	_p.A358T|PPARG	NM_133263	NP_573570	Q86YN6	PRGC2_HUMAN		0	GGATCGCAGCT	0.657
-	20	3179	jhd.2_Missense_M	NM_002609	NP_002600	P09619	PGFRB_HUMAN	Potential).|Protein kinase.	17	TGGGTAAGGGG	0.582
-	2	405	e_Mutation_p.D40	NM_001146040	NP_001139512	P23415	GLRA1_HUMAN	ellular (Probable).	2	GAAATCCGAGG	0.502
+	1	180		NM_001099293	NP_001092763	Q2VIQ3	KIF4B_HUMAN	inesin-motor.	1	TGAAGGGAATTC	0.592
+	1	2960		NM_001099293	NP_001092763	Q2VIQ3	KIF4B_HUMAN	RC1 (By similarity).|Potenti	1	CTATACCTTGTCA	0.463

+	33	3818	lws.2_Missense_M	NM_001037333	NP_001032410	Q96F07	CYFP2_HUMAN		0	GAAGTCCGTGG	0.522	
-	11	1542	p.R404W|GABRB	NM_021911	NP_068711	P47870	GBRB2_HUMAN	lasmic (Probable).	0	CTTTCCGATACT	0.517	
+	5	1011_1012	_p.P217S|ODZ2_u	NM_001122679	NP_001116151				10	GGATACCCTTTG	0.569	
+	5	650	idf.1_Missense_Mu	NM_006650	NP_006641	Q6PUV4	CPLX2_HUMAN		1	CCATCCCTGCG	0.622	
-	6	1002	Silent_p.L206L|MX	NM_031300	NP_112590	Q9BW11	MAD3_HUMAN		0	ACCCCCAAACA	0.701	
+	5	1242	kz.1_Missense_Mu	NM_182594	NP_872400	Q8N9F8	ZN454_HUMAN		3	CAGTGGAGAGA	0.388	
+	14	1727	kc.1_Missense_M	NM_025158	NP_079434	Q96T51	RUFY1_HUMAN	Potential.	5	ACTCAGGATGG	0.517	
-	20	2966	mlf.2_Missense_M	NM_198868	NP_942568	Q66K14	TBC9B_HUMAN		2	CTCTTCCTGTG	0.498	
-	8	1264	p.A323T|RASGEF	NM_175062	NP_778232	Q8N431	RGF1C_HUMAN	Ras-GEF.	1	CTTGGCCGTCC	0.617	
+	3	593	q.1_Missense_Mut	NM_004415	NP_004406	P15924	DESP_HUMAN	plakophilin 1 and junction p	9	GGAGTCGAGAAT	0.463	
+	12	1796	q.1_Missense_Mu	NM_004415	NP_004406	P15924	DESP_HUMAN	plakophilin 1 and junction p	9	TGTTCCCTCTGT	0.557	
-	13	1974	10jot.2_RNA|MAK	NM_005906	NP_005897	P20794	MAK_HUMAN		3	GCCCCCGACCA	0.403	
+	13	1625	_p.T397I|CAP2_u	NM_006366	NP_006357	P40123	CAP2_HUMAN		1	CAAGACAGCAT	0.403	
+	1	266		NM_138574	NP_612641	Q5TGJ6	HDGL1_HUMAN	PWWP.	0	CCCACGAGACG	0.602	
+	11	1565	p.G420E|BTN3A3_	NM_006994	NP_008925	O00478	BT3A3_HUMAN	.|Cytoplasmic (Potential).	0	AGTGGGGATCT	0.498	
-	3	1381		NM_052923	NP_443155	Q6R2W3	SCND3_HUMAN	Potential.	1	TCACTTCCTTTAT	0.353	
+	1	691		NM_030905	NP_112167	O76002	OR2J2_HUMAN	Name=5; (Potential).	0	CAAATGAGCTG	0.478	
+	3	852	_p.R137C|OR2H1	NM_030883	NP_112145	Q9GZK4	OR2H1_HUMAN	lasmic (Potential).	0	ACCCCCGCCTG	0.597	rs141663433
+	7	970		NR_027822					0	GTTCTGGTGTC	0.478	rs145231932
-	4	2060	nrb.3_Missense_M	NM_001134870	NP_001128342	Q6NYC8	PHTNS_HUMAN		0	GGCAGGACTCA	0.537	
-	2	262	1_5'Flank|PSORS	NM_014070	NP_054789	Q6UXA7	CF015_HUMAN		0	AGGTGGGAAGC	0.607	
+	16	3766	T2_uc003nvc.3_M	NM_080686	NP_542417	P48634	PRC2A_HUMAN	AA type A repeats.	0	GCCGAGGAGGA	0.672	
+	2	315_316	_uc003nwb.1_Miss	NM_001003693	NP_001003693	Q5SQ64	LY66F_HUMAN	(Potential).|Ig-like V-type.	2	TACTGGTGCGC	0.569	
-	6	1240	J1_uc010jth.2_No	NM_000434	NP_000425	Q99519	NEUR1_HUMAN		1	ATAGCTGGACTG	0.597	
+	23	3201	_p.E780*|SKIV2L_	NM_006929	NP_008860	Q15477	SKIV2_HUMAN		4	AATGGGGAGAAG	0.577	
+	25	3263	.1_Missense_Mut	NM_007293	NP_009224	P0C0L4	CO4A_HUMAN		0	GTTGTCACGGG	0.622	
-	15	2508	u.1_RNA|NOTCH	NM_004557	NP_004548	Q99466	NOTC4_HUMAN	|Extracellular (Potential).	22	GGCAGGAGAAG	0.632	
-	12	1644	f10_uc011dpx.1_I	NM_006781	NP_006772	Q5SRN2	CF010_HUMAN	Lys-rich.	1	AACTCTCCTTCT	0.244	
-	3	456_457	L2_uc010jtz.1_Int	NM_019602	NP_062548	Q9UIR0	BTNL2_HUMAN	2.|Extracellular (Potential).	1	TCCCTCCATGTG	0.604	
-	4	767	03obo.1_Intron|uc	NM_002124	NP_002115	P01911	2B1F_HUMAN	ical; (Potential).	1	CCCAAGGAAGA	0.547	
-	46	3631	se_Mutation_p.G1	NM_080680	NP_542411	P13942	COBA2_HUMAN	le-helical region.	5	GTGTCCCTGGG	0.592	
-	6	2099	ation_p.S557F|DA	NM_001350	NP_001341	Q9UER7	DAXX_HUMAN	al (Potential).|Interaction w	23	TTCCGAGATTTT	0.502	
+	3	472		NM_002224	NP_002215	Q14573	ITPR3_HUMAN	lasmic (Potential).	19	AAGATCGCTGAT	0.562	
+	49	6814	ey.2_Missense_Mu	NM_002224	NP_002215	Q14573	ITPR3_HUMAN	lasmic (Potential).	19	TCTCCCGCCGC	0.617	
-	6	565	w.3_Missense_M	NM_003322	NP_003313	O00294	TULP1_HUMAN		3	GAGCTTCCTTAT	0.582	
+	76	11600	sense_Mutation_p	NM_001371	NP_001362				21	TGTGGCTGCAG	0.502	
+	6	712	h.2_RNA|GLP1R_	NM_002062	NP_002053	P43220	GLP1R_HUMAN	cellular (Potential).	5	GGCTCCTCTCC	0.617	
-	4	627_628	se_Mutation_p.P21	NM_018965	NP_061838	Q9NZC2	TREM2_HUMAN	ical; (Potential).	1	GAGAAGGATGG	0.554	
-	3	613		NM_024807	NP_079083	Q5T2D2	TRML2_HUMAN	cellular (Potential).	2	ACAGTTCCACTC	0.527	
+	3	358	_Intron|PPP2R5D_	NM_006245	NP_006236	Q14738	2A5D_HUMAN		2	CTCCCGCTTCA	0.572	
+	5	529		NM_033112	NP_149103	Q96EU6	RRP36_HUMAN	Potential.	0	TCAGCGAATGG	0.433	
-	3	889	.R280W|CUL7_u	NM_014780	NP_055595	Q14999	CUL7_HUMAN		4	AGTCCGGGTCC	0.502	
+	14	2566		NM_032538	NP_115927	Q5TCY1	TTBK1_HUMAN	-rich.|Potential.	9	ggaagaagaggagga	0.259	
-	3	1046	318_uc003ouw.2_	NM_014345	NP_055160	Q5VUA4	ZN318_HUMAN	Potential.	7	GCTTTCGTCTG	0.517	
+	7	1103	e_Mutation_p.P34	NM_007355	NP_031381	P08238	HS90B_HUMAN		4	GGCTCCCTTTG	0.403	
-	5	1588	_Intron|TMEM151	NM_182539	NP_872345	Q5JU00	TCTE1_HUMAN		4	CTGGCGGGCTG	0.562	
-	2	416	_p.G80E|RCAN2_	NM_005822	NP_005813	Q14206	RCAN2_HUMAN		0	AACAGTCCCTCA	0.393	

-	7	918	e_Mutation_p.G21	NM_001098518	NP_001091988	Q8IZF2	GP116_HUMAN	tracellular (Potential).	2	AAATTCCGTAA	0.373	
+	5	689	e_Mutation_p.D16	NM_153839	NP_722581	Q8IZF7	GP111_HUMAN	cellular (Potential).	1	GGTGTTGATGAG	0.398	
+	6	1634	e_Mutation_p.Y47	NM_153839	NP_722581	Q8IZF7	GP111_HUMAN	Name=3; (Potential).	1	ATCCTCTATGGA	0.448	
+	7	2216	_p.T710I|GPR115_	NM_153838	NP_722580	Q8IZF3	GP115_HUMAN	Name=7; (Potential).	8	TTGGAACCATTA	0.398	
+	2	154	I5_uc003ozd.2_5'	NM_181744	NP_859528	Q6U736	OPN5_HUMAN	Name=1; (Potential).	1	CATTTGGAAATG	0.358	
-	61	10807_10808		NM_138694	NP_619639	P08F94	PKHD1_HUMAN	cellular (Potential).	44	TTTCCCCTAAGA	0.431	rs112030234
-	3	417_418	MGCLL1_uc011dx	NM_019036	NP_061909	Q8TB92	HMGC2_HUMAN		4	TCCATCCCTAGG	0.317	
-	4	891	se_Mutation_p.R2	NM_030820	NP_110447	Q96P44	COLA1_HUMAN		2	GGAATTCGTGTT	0.323	
+	3	282	586_uc011dxm.1_	NM_020931	NP_065982	Q9HCI6	K1586_HUMAN		0	AAGGACCATCG	0.348	
+	5	1359	k.2_Missense_Mu	NM_001704	NP_001695	O60242	BAI3_HUMAN	.|Extracellular (Potential).	50	CATGTTCGGTTA	0.468	
+	12	2423	k.2_Missense_Mu	NM_001704	NP_001695	O60242	BAI3_HUMAN	cellular (Potential).	50	ACAAGGAAAAA	0.289	
-	11	1166	COL9A1_uc003pff.	NM_001851	NP_001842	P20849	CO9A1_HUMAN	elical region (COL3).	4	CAATGGAGCCA	0.388	
-	6	725		NM_001563	NP_001554	Q17R60	IMPG1_HUMAN		3	AGTGAGAGGGA	0.398	
-	12	1382	p.G351R|ME1_uc	NM_002395	NP_002386	P48163	MAOX_HUMAN		2	CACGTCCCTACA	0.393	
-	4	695_696	bq.1_Missense_M	NM_001080508	NP_001073977	O95935	TBX18_HUMAN	T-box.	5	GTCTCCCCCGAG	0.51	
+	3	1119	_p.G188E|NT5E_u	NM_002526	NP_002517	P21589	5NTD_HUMAN		4	CCTTAGGGACAA	0.229	
-	16	3034	p.W926*|EPHA7_	NM_004440	NP_004431	Q15375	EPHA7_HUMAN	mic (Potential).|SAM.	28	TTGTAGCCATTC	0.373	
-	15	2925	p.R890Q|EPHA7_	NM_004440	NP_004431	Q15375	EPHA7_HUMAN	lasmic (Potential).	28	GGGTTTCGAATC	0.408	
+	18	2209	0776_uc010kck.2_	NM_015323	NP_056138	O94874	UFL1_HUMAN		1	AAAATTCCAGAG	0.368	
-	14	2248	eaf.1_Missense_M	NM_198468	NP_940870	Q6ZRQ5	MMS22_HUMAN		0	GATTCTCGACAT	0.378	
+	10	1684	qo.3_Missense_Mu	NM_021956	NP_068775	Q13002	GRIK2_HUMAN	cellular (Potential).	5	ACATATGAAATTA	0.388	
+	12	2023	_p.P592S|GRIK2_	NM_021956	NP_068775	Q13002	GRIK2_HUMAN	lasmic (Potential).	5	TATAATCCACAC	0.398	
+	4	839	pre.2_Missense_M	NM_001198	NP_001189	O75626	PRDM1_HUMAN	SET.	56	ATTGTCGGGACT	0.453	
+	3	788	rw.1_Missense_M	NM_018013	NP_060483	A7XYQ1	SOBP_HUMAN		1	TTTCACCATACA	0.403	
+	7	989	ao.1_Missense_M	NM_032131	NP_115507	Q8NEN0	ARMC2_HUMAN	ARM 1.	0	ATACAAGGATTG	0.343	
-	8	1952		NM_002031	NP_002022	P42685	FRK_HUMAN		6	ATGAAGTTATTTG	0.343	
+	6	2899	t.2_Missense_Mut	NM_001080976	NP_001074445	Q9UL01	DSE_HUMAN		1	ATACCAGGTTGTT	0.468	
+	11	1245		NM_173560	NP_775831	Q8HWS3	RFX6_HUMAN		3	GCCCAGGTATGT	0.302	
+	17	2273		NM_173560	NP_775831	Q8HWS3	RFX6_HUMAN		3	TTTCAAGAGACT	0.547	
-	4	1227	kei.1_Missense_M	NM_005907	NP_005898	P33908	MA1A1_HUMAN	enal (Potential).	4	ACCCATGATTTT	0.303	
-	24	2782	ense_Mutation_p.	NM_152730	NP_689943	Q96NH3	BROMI_HUMAN		3	GGATATGATGAA	0.303	
+	6	992		NM_001010905	NP_001010905	Q6P5S2	CF058_HUMAN		0	GTTATGGAAATA	0.264	
-	23	3630	c.2_Missense_Mu	NM_002844	NP_002835	Q15262	PTPRK_HUMAN	ine-protein phosphatase 1.|	8	CCAGTTCGTCCA	0.383	
+	54	7787	ense_Mutation_p.	NM_000426	NP_000417	P24043	LAMA2_HUMAN	minin G-like 3.	10	AGTCCGGCATCA	0.488	
-	2	175		NM_001010876	NP_001010876	Q5VVB8	CF191_HUMAN	ical; (Potential).	1	CTCAGGGACACA	0.373	
+	5	651	.1_RNA|ENPP3_	NM_005021	NP_005012	O14638	ENPP3_HUMAN	lar (Potential).|SMB 2.	4	AATTTCGTTGTG	0.378	
+	9	1035	o.1_RNA|ENPP3_	NM_005021	NP_005012	O14638	ENPP3_HUMAN	tential).|Phosphodiesteras	4	ATGTATGATGTAA	0.318	
+	1	943		NM_053278	NP_444508	Q969N4	TAAR8_HUMAN	lasmic (Potential).	1	TTTTATCCTTGGT	0.333	
-	16	2543	_p.S720F|AHI1_u	NM_001134831	NP_001128303	Q8N157	AHI1_HUMAN	WD 3.	3	ATCATGGAATCA	0.363	
-	4	582	.S108L|BCLAF1_	NM_014739	NP_055554	Q9NYF8	BCLF1_HUMAN		1	GAACGTGAACGA	0.468	
-	15	2153	gv.2_Missense_Mu	NM_003980	NP_003971	Q14244	MAP7_HUMAN		0	CTGTTCCTCCA	0.358	
-	13	2042	gv.2_Missense_Mu	NM_003980	NP_003971	Q14244	MAP7_HUMAN	Potential.	0	TCTTTCTCTCCA	0.542	
+	22	3664		NM_020340	NP_065073	Q5TH69	BIG3_HUMAN		2	CATAAGGAAAGA	0.473	
-	9	7098		NM_006734	NP_006725	P31629	ZEP2_HUMAN	ts of S-P-[RGMKC]- [RK].|	6	CCCAGGAGACA	0.463	
-	3	2135	kg.2_Missense_M	NM_002656	NP_002647	Q9UM63	PLAL1_HUMAN		1	CAGGGGATACC	0.602	
+	69	9780		NM_007124	NP_009055	P46939	UTRO_HUMAN		5	CTCATCCAGCAG	0.512	
-	3	1827	son.3_Missense_M	NM_024963	NP_079239	Q96ME1	FXL18_HUMAN	LRR 11.	3	GCGCGGGCATG	0.657	

-	3	1542	on.3_Missense_M	NM_024963	NP_079239	Q96ME1	FXL18_HUMAN	LRR 8.	3	GGAAGGGCAGG	0.657	
+	4	917	_p.T209I|C7orf26_	NM_024067	NP_076972	Q96N11	CG026_HUMAN		1	CCTGACCGAGA	0.587	
-	27	2224	p.P386S|COL28A	NM_001037763	NP_001032852	Q2UY09	COSA1_HUMAN		3	AGGGGGGCCAG	0.468	
-	9	1335	se_Mutation_p.P1	NM_004956	NP_004947	P50549	ETV1_HUMAN		35	GCAAAGGAGGA	0.478	
+	22	2966	p.N978K|HDAC9_	NM_058176	NP_478056	Q9UKV0	HDAC9_HUMAN	one deacetylase.	5	GGAAATGAGGT	0.413	
-	1	143		NM_001002926	NP_001002926	Q3B726	RPA43_HUMAN		1	CTGTTCACCAGC	0.647	
+	15	2906		NM_003777	NP_003768	Q96DT5	DYH11_HUMAN	n (By similarity).	15	TTTAAACCTTCC	0.408	
+	45	7295		NM_003777	NP_003768	Q96DT5	DYH11_HUMAN		15	GCTTTTGGAGGC	0.418	
-	3	422	1_5'UTR|TRA2A_	NM_013293	NP_037425	Q13595	TRA2A_HUMAN	-rich (RS1 domain).	1	GGATCGAGTGT	0.448	
+	21	2628	_p.S854L|STK31_	NM_031414	NP_113602	Q9BXU1	STK31_HUMAN	rotein kinase.	9	ATGGATCACTTC	0.353	
+	12	1489		NM_133468	NP_597725	Q8N8U9	BMPER_HUMAN	VWFD.	3	ACCTGGATGGC	0.652	
+	6	1024		NM_007252	NP_009183	P78424	PO6F2_HUMAN	Gln-rich.	1	CCAGTCTTCAG	0.517	
+	3	559		NM_020192	NP_064577	Q9NRH1	CG036_HUMAN		0	TATGTAGAATGTT	0.393	
-	8	1146	g.1_Missense_Mu	NM_000168	NP_000159	P10071	GLI3_HUMAN		19	GCGCGGAAGAG	0.537	
-	3	140	3tim.1_RNA|C7or	NM_018224	NP_060694	Q9GZY4	CG044_HUMAN	ical; (Potential).	1	TGCTCCCAGAG	0.488	
-	1	1		NM_000290	NP_000281	P15259	PGAM2_HUMAN		0	ACGGGGACGGC	0.617	
-	2	981	bw.1_Missense_M	NM_013389	NP_037521	Q9UHC9	NPCL1_HUMAN	lasmic (Potential).	5	GGCGGGGGCCA	0.592	
-	22	3604		NM_138295	NP_612152	Q8TDX9	PK1L1_HUMAN	ular (Potential).|REJ.	11	GTGGGGCTGCA	0.547	
+	5	580_581	_uc011kcg.1_Miss	NM_181597	NP_853628	Q16831	UPP1_HUMAN		0	GATTGCCCCGTC	0.416	
+	17	3722	yr.2_Missense_M	NM_152701	NP_689914	Q86UQ4	ABCAD_HUMAN		10	CTCAGGGATTTTT	0.383	
+	23	9342	ys.1_Missense_M	NM_152701	NP_689914	Q86UQ4	ABCAD_HUMAN		10	CCACTCCAAGG	0.448	rs139183809
-	7	990	.G233E|ZPBP_uc	NM_007009	NP_008940	Q9BS86	ZPBP1_HUMAN		0	TTCATTCCATATC	0.338	
+	4	1257	_Mutation_p.H42	NM_182633	NP_872439	Q8N859	ZN713_HUMAN	2H2-type 5.	2	AAATCCATACTC	0.393	
-	5	1641		NM_033273	NP_150376	Q96JC4	ZN479_HUMAN	2H2-type 10.	4	GAATTCTCTTGT	0.433	
+	4	1206		NM_001159522	NP_001152994	A8MUV8	ZN727_HUMAN	2H2-type 7.	0	TTTGTGAAGAAT	0.388	
+	7	2081	tte.2_Missense_M	NM_016220	NP_057304	Q9UII5	ZN107_HUMAN	2H2-type 13.	1	ATAAGAAAATTC	0.348	
-	5	1008	p.E203K|CALN1_	NM_001017440	NP_001017440	Q9BXU9	CABP8_HUMAN	lasmic (Potential).	1	TCTCTTCCTCAT	0.517	
+	2	186		NM_000941	NP_000932	P16435	NCPR_HUMAN		1	GTTTTCGCTCAT	0.502	
-	10	1977	dy.1_Missense_Mu	NM_012301	NP_036433	Q86UL8	MAGI2_HUMAN		11	ACCATCAGTTG	0.488	
-	20	15033	ht.1_Missense_Mu	NM_033026	NP_149015	Q9Y6V0	PCLO_HUMAN		7	GCTATGGCAGCC	0.498	
-	7	11487	p.S3733F|PCLO_	NM_033026	NP_149015	Q9Y6V0	PCLO_HUMAN		7	CTGTGGAAATC	0.443	
-	5	4487	v.2_Missense_Mu	NM_033026	NP_149015	Q9Y6V0	PCLO_HUMAN		7	TGCTTTCTTGTG	0.403	
-	3	3053	v.2_Missense_Mu	NM_033026	NP_149015	Q9Y6V0	PCLO_HUMAN	Pro-rich.	7	AGGAGTTGTAG	0.502	
-	3	2447	v.2_Missense_Mu	NM_033026	NP_149015	Q9Y6V0	PCLO_HUMAN	Pro-rich.	7	GCTTGGCCTTGG	0.542	
-	2	1064	v.2_Nonsense_Mu	NM_033026	NP_149015	Q9Y6V0	PCLO_HUMAN	-rich.|Pro-rich.	7	ACCCTGAATTG	0.473	rs10251512
-	29	4211	c.1_Missense_Mu	NM_000927	NP_000918	P08183	MDR1_HUMAN	tential).|ABC transporter 2	7	GATGCCTTTCTG	0.443	
-	2	234	n_p.Y43*|STEAP4	NM_024636	NP_078912	Q687X5	STEA4_HUMAN		0	ACAGAATAACC	0.433	
-	5	4383	D9L_uc003umk.1_	NM_152703	NP_689916	Q8IVG5	SAM9L_HUMAN		4	ATGGGGAAAAC	0.393	
+	20	1535	1A2_uc011kib.1_I	NM_000089	NP_000080	P08123	CO1A2_HUMAN		9	CAAAGGAGAGA	0.433	
+	11	1609	nj.3_Missense_Mu	NM_022900	NP_075051	Q96PB1	CASD1_HUMAN		2	ACATTCGAGTTC	0.353	
+	3	1060		NM_002523	NP_002514	P47972	NPTX2_HUMAN	Pentaxin.	3	TCAACGACAAG	0.667	
-	11	1357	_p.R377K|CYP3A4	NM_017460	NP_059488	P08684	CP3A4_HUMAN		4	TTGTACCTTTCAG	0.502	
-	4	441	uc003uuu.1_Misse	NM_017984	NP_060454	Q9H0M4	ZCPW1_HUMAN		0	CTTTTTCCTCTTT	0.468	
+	12	1586	ZAN_uc003uwl.2_	NM_003386	NP_003377	Q9Y493	ZAN_HUMAN	xtracellular (Potential).	11	TGCGGGGAGTC	0.617	
+	3	4275	C17_uc010lho.1_	NM_001040105	NP_001035194	Q685J3	MUC17_HUMAN	approximate tandem repea	27	CGCCGGTAGTC	0.507	
+	3	9154	C17_uc010lho.1_	NM_001040105	NP_001035194	Q685J3	MUC17_HUMAN	ch.|59 X approximate tand	27	AGGTACCGGCA	0.507	
+	3	12117	C17_uc010lho.1_	NM_001040105	NP_001035194	Q685J3	MUC17_HUMAN	ellular (Potential).	27	GGCTGCACTACT	0.532	

+	17	1470	_uc003uyv.2_Splic	NM_001913	NP_001904	P39880	CUX1_HUMAN		8	TGCTAGGACCT	0.657	
-	8	1086	_Mutation_p.E284I	NM_198999	NP_945350	P58743	S26A5_HUMAN	lasmic (Potential).	1	ATTTCTCTTTAA	0.448	
-	42	6594	.2_Missense_Muta	NM_005045	NP_005036	P78509	RELN_HUMAN	EGF-like 5.	19	TTGGTTCCATTG	0.458	
-	13	1631	z.2_Missense_Mut	NM_005045	NP_005036	P78509	RELN_HUMAN		19	CATTTTCATGAG	0.343	
-	9	998	z.2_Missense_Mut	NM_005045	NP_005036	P78509	RELN_HUMAN		19	GCTGGGGTCTG	0.323	
-	33	3738	_p.R64C|DOCK4_	NM_014705	NP_055520	Q8N1I0	DOCK4_HUMAN	DHR-2.	4	TTAGACGAGTTA	0.403	
+	4	706	D1_uc003vgj.2_M	NM_001007245	NP_001007246	O00458	IFRD1_HUMAN		2	GATTAATTGACC	0.368	
-	4	3051		NM_002711	NP_002702	Q16821	PPR3A_HUMAN		34	CCTAGAGATTTT	0.378	
+	17	2472	XP2_uc011kmu.1	NM_014491	NP_055306	O15409	FOXP2_HUMAN		8	AATTAGAAGAC	0.438	
+	3	1549_1550	455NL>KF|MET_u	NM_000245	NP_000236	P08581	MET_HUMAN	lar (Potential).|Sema.	159	GCTAATCTTGGG	0.431	
-	5	1351	a.2_Missense_Mu	NM_003391	NP_003382	P09544	WNT2_HUMAN		7	CTTGGGGGCCT	0.577	
+	14	2074	q.1_Missense_Mu	NM_000492	NP_000483	P13569	CFTR_HUMAN	lasmic (Potential).	5	GATGTGATTCT	0.383	
+	27	4465	q.1_Missense_Mu	NM_000492	NP_000483	P13569	CFTR_HUMAN	lasmic (Potential).	5	CCTCCGACAGG	0.522	rs148783445
-	8	1009	0lkj.2_Missense_	NM_012338	NP_036470	O95859	TSN12_HUMAN	ellular (Potential).	0	AAAAAGGAATAC	0.398	
-	1	638	PS2_uc010lkq.2_	NM_198085	NP_932351	Q8N7C7	RN148_HUMAN	PA.	0	ACATGGGAAATA	0.448	
-	7	1691	UB_uc010lkt.2_R	NM_178827	NP_849149	Q8NA54	IQUB_HUMAN		4	TGTTTCCCATT	0.343	
+	3	1175	_p.S185F|FSCN3_	NM_020369	NP_065102	Q9NQT6	FSCN3_HUMAN		1	CCTATCCCAGG	0.498	
+	2	401		NM_014390	NP_055205	Q7KZF4	SND1_HUMAN	Nase-like 1.	3	GAAATCTTGCT	0.582	
+	3	549	_p.C106Y|METTL	NM_018396	NP_060866	Q6P1Q9	MTL2B_HUMAN		1	AAATTTGTGCTG	0.423	
+	21	3442	.3_Missense_Mut	NM_001458	NP_001449	Q14315	FLNC_HUMAN	Filamin 9.	12	GGTAGGCACCC	0.652	
+	21	3834	.3_Missense_Mut	NM_001458	NP_001449	Q14315	FLNC_HUMAN	Filamin 10.	12	ACGCGGATGGC	0.602	
+	38	6427	.3_Missense_Mut	NM_001458	NP_001449	Q14315	FLNC_HUMAN	Filamin 19.	12	TGGGGGCTTGG	0.587	
-	28	5101	A4_uc003vqz.3_5	NM_020911	NP_065962	Q9HCM2	PLXA4_HUMAN	lasmic (Potential).	1	CGGATCATGTT	0.572	
-	22	4373		NM_020911	NP_065962	Q9HCM2	PLXA4_HUMAN	lasmic (Potential).	1	ACGGTCGCGCA	0.577	rs118107843
-	22	4337		NM_020911	NP_065962	Q9HCM2	PLXA4_HUMAN	lasmic (Potential).	1	CGTGCGGATGA	0.602	
-	2	818	p.P197S|PLXNA4	NM_020911	NP_065962	Q9HCM2	PLXA4_HUMAN	lar (Potential).|Sema.	1	GGTGGGAAAAT	0.537	
+	4	1416	HRM2_uc003vtm	NM_001006630	NP_001006631	P08172	ACM2_HUMAN	smic (By similarity).	5	GCAAAGCCCCC	0.493	
-	8	930	tu.2_Missense_Mu	NM_004717	NP_004708	O75912	DGKI_HUMAN		3	CCAGGGAGCAG	0.488	
-	15	4864_4865	.Q1556*|KIAA154	NM_020910	NP_065961	Q9HCM3	K1549_HUMAN		230	ACCTGGTGTTT	0.554	
-	7	2117	p.R38W|ZC3HAV1	NM_020119	NP_064504	Q7Z2W4	ZCCHV_HUMAN		1	TTACCCGAAAAT	0.423	rs144346512
-	2	830	d.3_Missense_Mu	NM_022740	NP_073577	Q9H2X6	HIPK2_HUMAN	pression (By similarity).|Int	7	TGCCCCGTTTC	0.557	
+	2	349	rc.1_Missense_Mu	NM_001008749	NP_001008749	A4D1S5	RAB19_HUMAN	region (By similarity).	0	CGATTGGAGTG	0.468	
+	3	518	rc.1_Missense_Mu	NM_001008749	NP_001008749	A4D1S5	RAB19_HUMAN		0	CGAGTCCATCC	0.502	
-	1	570	NND2A_uc003vvw	NM_015689	NP_056504	Q9ULE3	DEN2A_HUMAN		4	CTCGGCCTCGG	0.592	
+	1	947	vz.2_Missense_M	NM_052853	NP_443085	Q7Z695	ADCK2_HUMAN	rotein kinase.	0	GATACCTTGGA	0.562	
-	15	1860		NM_004333	NP_004324	P15056	BRAF_HUMAN	rotein kinas _R603>I(2)|p.T	18290	ATTTCACTGTA	0.368	
-	11	1461		NM_004333	NP_004324	P15056	BRAF_HUMAN	nilarity).|Pro p.S467L(1)	18290	CAAATGATCCA	0.383	
+	1	576	852_uc010lnn.2_	NM_001105558	NP_001099028	P0C1S8	WEE2_HUMAN		2	ACCTTGGACTC	0.493	
+	32	3903		NM_004668	NP_004659	O43451	MGA_HUMAN	se.|Lumenal (Potential).	2	TACATGGAGCG	0.562	
-	4	617	TRPV6_uc010lou.	NM_018646	NP_061116	Q9H1D0	TRPV6_HUMAN	ytoplasmic (Potential).	2	GGGCTCGCACC	0.572	rs150734746
-	8	1241	bz.2_Missense_M	NM_019841	NP_062815	Q9NQA5	TRPV5_HUMAN	lasmic (Potential).	6	TACGGCCGGCC	0.552	rs149241771
-	6	934	bz.2_Missense_M	NM_019841	NP_062815	Q9NQA5	TRPV5_HUMAN	lasmic (Potential).	6	ATGTCCATCGT	0.567	
+	1	82		NM_176881	NP_795362	P59534	T2R39_HUMAN	ellular (Potential).	1	AAAGTGAATTG	0.418	
+	1	701		NM_176881	NP_795362	P59534	T2R39_HUMAN	lasmic (Potential).	1	CCTCTCTCTCA	0.512	
+	20	2461	tc.1_Missense_Mu	NM_000083	NP_000074	P35523	CLCN1_HUMAN	smic (By similarity).	5	TCCACAGATTTA	0.428	
-	4	910		NM_005232	NP_005223	P21709	EPHA1_HUMAN	ar (Potential).|Cys-rich.	5	TGCTTCGCCAC	0.627	
+	1	575	uc003wda.2_Intro	NM_176883	NP_795364	P59536	T2R41_HUMAN	Name=5; (Potential).	2	CAATTCCTTTTT	0.408	

+	1	350		NM_012369	NP_036501	Q13607	OR2F1_HUMAN	Name=3; (Potential).	3	GTTATTTTTCTCC	0.527	
+	1	777		NM_001005480	NP_001005480	Q6IF42	OR2A2_HUMAN	ellular (Potential).	2	TACATGGTCCC	0.507	
+	2	680	wek.2_Missense_	NM_005435	NP_005426	Q12774	ARHG5_HUMAN		2	GCGAAGAGCAT	0.502	
+	2	2646	_Mutation_p.P843	NM_005435	NP_005426	Q12774	ARHG5_HUMAN		2	CACTACCCATCA	0.607	
+	7	1465		NM_014141	NP_054860	Q9UHC6	CNTP2_HUMAN	1.|Extracellular (Potential).	11	CCTTTGGAGGC	0.378	
+	2	601		NM_145304	NP_660347	Q8WU49	CG033_HUMAN		1	GGGATGGAATT	0.473	
-	4	1709_1710	_p.R488C|ZNF786_	NM_152411	NP_689624	Q8N393	ZN786_HUMAN	2H2-type 8.	4	CTCACGGAGCT	0.653	
+	6	1437	p.T217A|ZNF398_	NM_170686	NP_733787	Q8TD17	ZN398_HUMAN	ype 2; degenerate.	1	GCAGCACCTCC	0.567	
-	2	510		NM_015694	NP_056509	Q9ULD5	ZN777_HUMAN		1	GAAGGGAGACT	0.607	
+	1	31	467_uc003wgd.2_	NM_198455	NP_940857	A2VEC9	SSPO_HUMAN		0	GGATGGCGTGG	0.647	
+	43	6302		NM_198455	NP_940857	A2VEC9	SSPO_HUMAN	F5/8 type C.	0	CCAGGGGCCCA	0.682	
+	4	998	p.P227L|REPIN1_	NM_013400	NP_037532	Q9BWE0	REPI1_HUMAN		1	CCCTCCCGCCC	0.652	
+	5	1640		NM_175571	NP_783161	Q8ND71	GIMA8_HUMAN		7	TGACAGAAACC	0.498	
+	5	1846		NM_175571	NP_783161	Q8ND71	GIMA8_HUMAN		7	AAAAGGACCCA	0.537	
+	3	296	76B_uc003whv.3_	NM_018487	NP_060957	Q96HP8	T176A_HUMAN	ical; (Potential).	2	TAGGAGGATTTT	0.572	
-	14	2636		NM_170606	NP_733751	Q8NEZ4	MLL3_HUMAN	p.S806S(1)	63	CAGAGGAACTA	0.438	
-	3	584		NM_170606	NP_733751	Q8NEZ4	MLL3_HUMAN		63	CAACAGAGACC	0.423	
-	3	566		NM_170606	NP_733751	Q8NEZ4	MLL3_HUMAN		63	TTTGCCGATTCC	0.433	
+	1	87	.1_Intron|uc003wlt	NM_024012	NP_076917	P47898	5HT5A_HUMAN	llular (By similarity).	3	CCTAACCTCCT	0.612	
+	2	963		NM_024012	NP_076917	P47898	5HT5A_HUMAN	ame=6; (By similarity).	3	GATCCCCTTCT	0.592	
-	4	1019_1020	pe.1_Missense_	NM_207332	NP_997215	Q86X53	ERIC1_HUMAN	Glu-rich.	2	CTCCTCCCCGG	0.54	
-	68	10743	p.F2765L|CSMD1_	NM_033225	NP_150094	Q96PZ7	CSMD1_HUMAN	ellular (Potential).	25	CCTTGAAAAGT	0.333	
-	2	854		NM_001080826	NP_001074295	Q86YV5	SG223_HUMAN		0	TGGGTGAGCAG	0.682	
-	4	4169_4170		NM_178857	NP_849188	Q8IWN7	RP1L1_HUMAN		8	tcttgcagcccttctcctt	0.198	
-	3	1246	v.2_Intron|FAM16	NM_053279	NP_444509	Q96KS9	F167A_HUMAN		0	ACCTCCGAGAG	0.597	
-	7	1400	s.2_Missense_Mu	NM_139167	NP_631906	Q96LD1	SGCZ_HUMAN	ellular (Potential).	3	CCTCCCCTTCT	0.493	
-	13	1739	ya.1_Nonsense_	NM_004686	NP_004677	Q9Y216	MTMR7_HUMAN	ularin phosphatase.	1	CCACTCCAAAA	0.448	
+	7	847	O7_uc010ltj.1_R	NM_015024	NP_055839	Q9UIA9	XPO7_HUMAN		5	AGATTCCCACC	0.498	
-	2	580		NM_002318	NP_002309	Q9Y4K0	LOXL2_HUMAN	SRCR 1.	3	GGTGCCCCACT	0.657	
+	11	1101	se_Mutation_p.E1	NM_014265	NP_055080	Q9UKQ2	ADA28_HUMAN	B.|Extracellular (Potential).	5	CACATGAAATG	0.408	
+	6	567	ea.1_Missense_M	NM_003817	NP_003808	Q9H2U9	ADAM7_HUMAN	ellular (Potential).	5	AGGGAGAACAT	0.398	
+	14	2262	DCA2_uc003xeq.	NM_152562	NP_689775	Q69YH5	CDCA2_HUMAN		0	TTCCCGAGCTG	0.433	rs144313074
-	13	1348	ek.2_Intron|EBF2	NM_022659	NP_073150	Q9HAK2	COE2_HUMAN		4	TTATTTCCTTGTG	0.473	
+	14	2032	SL2_uc010luk.1_	NM_001386	NP_001377	Q16555	DPYL2_HUMAN		1	GGCGCCCCCG	0.642	
-	18	2312		NM_001010906	NP_001010906	Q68CJ6	SLIP_HUMAN		2	ACCTTCTCCAC	0.517	
-	2	186		NM_001010906	NP_001010906	Q68CJ6	SLIP_HUMAN		2	GTTACCTGGAT	0.423	
-	3	7453		NM_031271	NP_112561	Q9BXT5	TEX15_HUMAN		7	GATCTGGGGAAT	0.413	
+	13	2365	54_splice|WRN_u	NM_000553	NP_000544	Q14191	WRN_HUMAN		7	TTCCAGACTTTT	0.348	
+	33	4737	k.2_Missense_Mut	NM_000553	NP_000544	Q14191	WRN_HUMAN		7	ATTATTGCTGAT	0.488	
+	10	1221	u.3_Missense_Mu	NM_004674	NP_004665	Q9UBL3	ASH2L_HUMAN	B30.2/SPRY.	2	TGATCGAGGTA	0.458	
+	1	130	1_uc003xnn.2_R	NM_002164	NP_002155	P14902	I23O1_HUMAN		2	CTATGGAAAAC	0.458	
-	3	270	ns.2_Missense_	NM_024645	NP_078921	Q9H898	ZMAT4_HUMAN	atrin-type 1.	3	TCGGACTTTGC	0.473	
+	8	1833_1834		NM_178819	NP_848934	Q86UL3	GPAT4_HUMAN		0	ATCGCCACCTG	0.54	
-	29	3545	K1_uc003xoj.2_M	NM_020476	NP_065209	P16157	ANK1_HUMAN		9	TCCAGGAAGGA	0.657	
+	3	512	qa.1_Missense_M	NM_001005365	NP_001005365	Q6S8J7	POTEA_HUMAN	ANK 2.	1	GCACTGATCCA	0.393	
+	11	1489	_p.A465V|MCM4_	NM_182746	NP_877423	P33991	MCM4_HUMAN	MCM.	4	TTCAGCCTTGG	0.373	
+	4	407		NM_001007176	NP_001007177	Q8WWR9	PDPFL_HUMAN		0	TCTGTCTGCTA	0.393	

-	6	1180	_p.R280K|PCMTD	NM_052937	NP_443169	Q96MG8	PCMD1_HUMAN		0	TTAACTCTCTTT	0.343	
+	4	5198	1_uc011ldy.1_Intr	NM_006269	NP_006260	P56715	RP1_HUMAN		12	TCTTCTGAACAG	0.413	
+	4	5358	1_uc011ldy.1_Intr	NM_006269	NP_006260	P56715	RP1_HUMAN		12	AGAGGAAGGAG	0.413	
+	3	1918		NM_052898	NP_443130	Q5GH76	XKR4_HUMAN		2	ATCTCCTCCAA	0.458	
-	3	1742	lyi.2_Missense_Mu	NM_001114635	NP_001108107	Q6DJT9	PLAG1_HUMAN	lack of NLS and KPNA2 in	129	TATAGGGAGGAC	0.453	
-	3	571_572		NM_000780	NP_000771	P22680	CP7A1_HUMAN		1	ACATCCCTTCTG	0.46	
+	26	3299		NM_024870	NP_079146	Q70Z35	PREX2_HUMAN		17	AGCAGGAGATG	0.383	
+	6	686	p.D213Y|C8orf34_	NM_052958	NP_443190	Q49A92	CH034_HUMAN		1	AAAATGACCAAT	0.443	
+	4	760	.1_5'UTR|CRISPL	NM_031461	NP_113649	Q9H336	CRLD1_HUMAN		2	ATAGGCCCCCG	0.363	
-	6	890		NM_018440	NP_060910	Q9NWQ8	PAG1_HUMAN	lasmic (Potential).	0	TCTGAAGGCTG	0.418	
+	4	459_460	P1_uc010mai.2_5'	NM_007013	NP_008944	Q9H0M0	WWP1_HUMAN	C2.	2	TTCTTCTAATCC	0.332	
-	10	1109	aj.2_Nonsense_M	NM_019098	NP_061971	Q9NQW8	CNGB3_HUMAN	ellular (Potential).	3	TTGTTCGAATAA	0.363	
+	9	1191	nse_Mutation_p.L	NM_052832	NP_439897	Q8TE54	S26A7_HUMAN	lasmic (Potential).	2	ACATCCTCTCT	0.438	
+	4	554	p.P152S|POP1_u	NM_001145860	NP_001139332	Q99575	POP1_HUMAN		2	GCCTTCCCAGA	0.458	
+	13	1978	p.W626*|POP1_u	NM_001145860	NP_001139332	Q99575	POP1_HUMAN		2	GGCTGGGGCAT	0.408	
+	2	600	iq.2_Missense_M	NM_001142462	NP_001135934	Q8N2R0	OSR2_HUMAN		1	ATTACTCCTTCCT	0.647	
-	4	388	yjc.1_Missense_M	NM_015668	NP_056483	Q8NE09	RGS22_HUMAN		7	GTTTTTCCAGAA	0.323	
-	16	1945	s.1_Missense_Mu	NM_015902	NP_056986	O95071	UBR5_HUMAN		28	TGCAGGGGTTG	0.383	
+	3	753		NM_001100117	NP_001093587	Q9UQ26	RIMS2_HUMAN		15	AAAGTCGATCTC	0.453	
+	24	3741	p.G1156D|RIMS2	NM_014677	NP_055492	Q9UQ26	RIMS2_HUMAN		15	AGATGGTAGCA	0.493	
+	8	1278	nse_Mutation_p.E	NM_012082	NP_036214	Q8WW38	FOG2_HUMAN		5	GAAGCGAACTT	0.498	
-	6	1456	no.2_Missense_M	NM_001146	NP_001137	Q15389	ANGP1_HUMAN	ogen C-terminal.	7	CTTCACGATGTT	0.338	
+	2	998		NM_003301	NP_003292	P34981	TRFR_HUMAN	lasmic (Potential).	3	AAATTCCGTGCA	0.438	
+	38	5815		NM_177531	NP_803875	Q86WI1	PKHL1_HUMAN	r (Potential).|IPT/TIG 11.	14	CTTATCCACCTTT	0.403	
+	49	8241		NM_177531	NP_803875	Q86WI1	PKHL1_HUMAN	ellular (Potential).	14	GCCATCTTGAT	0.468	
-	69	10939	nt.2_Missense_Mu	NM_198123	NP_937756	Q7Z407	CSMD3_HUMAN	ellular (Potential).	63	TAAATCCTTGAA	0.353	
-	29	4972	t.2_Missense_Mu	NM_198123	NP_937756	Q7Z407	CSMD3_HUMAN	lar (Potential).|CUB 9.	63	ATGAGGGAAGT	0.373	
-	8	1529	p.R417K|CSMD3_	NM_198123	NP_937756	Q7Z407	CSMD3_HUMAN	ellular (Potential).	63	AATCCTCTAGATT	0.289	
-	6	595	p.S170F|ENPP2_	NM_001040092	NP_001035181	Q13822	ENPP2_HUMAN		7	CCACGGAGAAG	0.373	
+	3	560	DC6_uc011lid.1_I	NM_022783	NP_073620	Q8TB45	DPTOR_HUMAN		0	ACCTTCCCATTG	0.408	
+	10	1107		NM_001039112	NP_001034201	Q2WGJ9	FR1L6_HUMAN	toplasmic (Potential).	11	GTGCTGATCCT	0.502	
+	31	4245	uc003yqy.1_Intron	NM_001039112	NP_001034201	Q2WGJ9	FR1L6_HUMAN	toplasmic (Potential).	11	AGCAAGGGATT	0.488	
-	13	1928	M135B_uc003yva.	NM_015912	NP_056996	Q49AJ0	F135B_HUMAN		9	TCTAATCCATAC	0.448	
+	7	942	nep.2_Missense_	NM_014957	NP_055772	A2RUS2	DEND3_HUMAN	DENN.	1	CCTCGGACTGG	0.542	
+	3	837	.1_3'UTR|LY6K_u	NM_017527	NP_059997	Q17RY6	LY6K_HUMAN	UPAR/Ly6.	1	AGCATGGGTGA	0.547	
+	3	1031_1032	kx.1_Missense_M	NM_198572	NP_940974	Q76KD6	SPERI_HUMAN		2	CCAGCCCAGTG	0.396	
-	8	1526	MP1_uc010mhs.1	NM_024896	NP_079172	Q7Z2K6	ERMP1_HUMAN	ical; (Potential).	1	AAACGGAGACA	0.368	
-	20	1970	p.A410V|PTPRD_	NM_002839	NP_002830	P23468	PTPRD_HUMAN	III 2.|Extracellular (Potentia	22	TCGGGGCACTG	0.507	
-	16	2381	_p.P775L|MPDZ_	NM_003829	NP_003820	O75970	MPDZ_HUMAN	PDZ 5.	6	CTGACGGTGCT	0.428	
+	3	403	ite_p.K4_splice|S	NM_003026	NP_003017	Q99962	SH3G2_HUMAN		1	TTTCAGAAAGT	0.383	
-	14	1847	nl.1_Missense_Mu	NM_017645	NP_060115	Q7Z4H7	HAUS6_HUMAN		2	AAATGGATCAC	0.313	
+	18	2446	93S|DENND4C_u	NM_017925	NP_060395	Q5VZ89	DEN4C_HUMAN		2	ATTTTCCTGAG	0.393	
-	1	5395		NM_153809	NP_722516	Q8IZX4	TAF1L_HUMAN		26	CTTCTCCTTCAG	0.473	
+	8	815		NM_012144	NP_036276	Q9UI46	DNAI1_HUMAN		0	TCTTTAGGATCG	0.502	
-	4	1773		NM_003028	NP_003019	Q15464	SHB_HUMAN	with LAT, FAK1, JAK1 and	3	GGACGGCAGG	0.552	
+	1	526	42421_uc004aed.1_RNA						0	AGCCCAATCTG	0.607	rs141617852
+	2	521		NM_021965	NP_068800	Q15124	PGM5_HUMAN		2	ATGGCATCTTG	0.478	

+	8	1076	_p.R257_splice|P	NM_003558	NP_003549	O14986	PI51B_HUMAN		1	GCCGGGTAAGG	0.403	
+	10	1799	_Mutation_p.A421	NM_006200	NP_006191	Q92824	PCSK5_HUMAN	Catalytic.	3	CCCGTGCGGGA	0.398	
+	19	3029_3030	SK5_uc004akb.2_	NM_006200	NP_006191	Q92824	PCSK5_HUMAN	(Cys-rich motif).	3	AGAATGGATACA	0.426	
+	3	1168	akf.3_Missense_M	NM_001490	NP_001481	Q02742	GCNT1_HUMAN	tial).|Catalytic (By similarity	0	GCTTCCTCCAC	0.453	
-	8	4085		NM_015225	NP_056040	Q8WUY3	PRUN2_HUMAN		0	TCCATCGCCAT	0.542	
-	5	692	akn.2_Missense_M	NM_015225	NP_056040	Q8WUY3	PRUN2_HUMAN		0	GAATTTCCTCCT	0.433	
+	8	870	akq.3_Missense_M	NM_033305	NP_150648	Q96RL7	VP13A_HUMAN		10	TGGTTCGTAAG	0.323	
-	6	692	mr.1_Missense_M	NM_174938	NP_777598	A2A2Y4	FRMD3_HUMAN	FERM.	2	AGGATCGTAAT	0.388	
-	9	1916	mw.2_Missense_	NM_013438	NP_038466	Q9UMX0	UBQL1_HUMAN		0	TATCAGGATTCT	0.398	
-	6	466	ation_p.S81N|HNR	NM_031262	NP_112552	P61978	HNRPK_HUMAN	n with DDX1.|2 X 22 AA ap	1	CACTGCTGTCT	0.438	
+	15	2221	p.P575S|PHF2_u	NM_005392	NP_005383	O75151	PHF2_HUMAN		1	AGTTTCCCATC	0.597	
-	1	79	msc.1_Missense_	NM_000197	NP_000188	P37058	DHB3_HUMAN		0	TGTGAGGATGA	0.547	
-	2	252_253	uc004awu.2_5'UT	NM_001333	NP_001324	O60911	CATL2_HUMAN		0	ATTTTGGAACAG	0.431	
+	1	1060		NM_004473	NP_004464	O00358	FOXE1_HUMAN	Fork-head.	0	ACGCGGAGGA	0.647	
-	4	617_618	ion_p.P200L|TRIM	NM_033220	NP_150089	Q14142	TRI14_HUMAN		1	GCACGGGATG	0.594	
+	7	1282	c.2_Missense_Mu	NM_207299	NP_997182	Q8TBJ4	LPPR1_HUMAN		0	ATCCCCGTGGA	0.488	
-	2	1691	bq.1_Missense_M	NM_133445	NP_597702	Q8TCU5	NMD3A_HUMAN	ellular (Potential).	7	TCAGTTCCTCCA	0.512	
+	4	324		NM_001340	NP_001331	Q14093	CYLC2_HUMAN	A repeats of K-K-X.	1	AATTTCTGAGA	0.393	
+	5	644		NM_001340	NP_001331	Q14093	CYLC2_HUMAN	epeats.|31 X 3 AA repeats	1	caaaaaagataaaa	0.164	
+	1	578		NM_001004485	NP_001004485	Q8NGS4	O13F1_HUMAN	ellular (Potential).	3	CACCTCCCTGG	0.438	
-	1	842		NM_001001956	NP_001001956	Q8NGT0	O13C9_HUMAN	Name=7; (Potential).	0	AACATGGATATA	0.393	
-	14	2019	vc.1_Missense_M	NM_003640	NP_003631	O95163	ELP1_HUMAN		7	TCAGCGGGTTT	0.408	
-	2	167	lwl.1_Missense_M	NM_001003936	NP_001003936	Q6A555	TXND8_HUMAN	Thioredoxin.	0	AAACAGGAAACA	0.353	
-	3	245	_Mutation_p.P48	NM_012212	NP_036344	Q14914	PTGR1_HUMAN		0	GTAGGGATCCA	0.353	
-	3	359	LAD_uc004bhl.3_	NM_000031	NP_000022	P13716	HEM2_HUMAN		0	GGCCACTCCTG	0.522	
-	13	3005	A_uc004bir.3_Mis	NM_030767	NP_110394	Q7Z591	AKNA_HUMAN		6	CAAAGGGCTGG	0.622	
-	15	4867	C_uc010mvf.2_Int	NM_002160	NP_002151	P24821	TENA_HUMAN	nectin type-III 10.	7	AATCAGTACTAG	0.458	
-	9	1807	p.G569D|ASTN2_	NM_198187	NP_937830	O75129	ASTN2_HUMAN	ellular (Potential).	9	TCATAGCCCCTC	0.493	
-	8	1654	p.A239V|TRAF1_	NM_005658	NP_005649	Q13077	TRAF1_HUMAN	MATH.	3	GGAAGGCGTCA	0.602	
-	5	1118	_p.M60I|TRAF1_u	NM_005658	NP_005649	Q13077	TRAF1_HUMAN		3	TCCTTCATGAA	0.627	
-	1	510_511		NM_012363	NP_036495	Q8NGS0	OR1N1_HUMAN	ellular (Potential).	3	AATTTCCCCAGT	0.5	
+	15	2109	l.3_RNA|RABGAP	NM_012197	NP_036329	Q9Y3P9	RBGP1_HUMAN	ab-GAP TBC.	5	TGCTCCTTCTC	0.413	
+	3	414	.V122M|LMX1B_	NM_002316	NP_002307	O60663	LMX1B_HUMAN	zinc-binding 2.	0	GCTGCGTGTGT	0.632	
+	2	643		NM_006059	NP_006050	Q9Y6N6	LAMC3_HUMAN	inin N-terminal.	3	CCCCGGCGAGG	0.706	
+	2	870		NM_032536	NP_115925	Q96CW9	NTNG2_HUMAN		0	AGGGCCCCACC	0.617	
-	10	2516	.R397Q|SETX_u	NM_015046	NP_055861	Q7Z333	SETX_HUMAN		3	TTTTTCGTTTTG	0.348	
+	28	4493_4494	TS13_uc004cdz.3	NM_139025	NP_620594	Q76LX8	ATS13_HUMAN	CUB 2.	6	TGGGACCGAGG	0.624	
+	9	1443		NM_000787	NP_000778	P09172	DOPO_HUMAN		4	ACAGTGGTAAGT	0.587	rs75075472
+	36	3228		NM_000093	NP_000084	P20908	CO5A1_HUMAN	le-helical region.	11	CCAGGGACCCA	0.607	
-	15	4295	.P1322L|CAMSA	NM_015447	NP_056262	Q5T5Y3	CAMP1_HUMAN		3	GTATGGGCAGG	0.627	
-	3	443	SEC16A_uc010nb	NM_014866	NP_055681	O15027	SC16A_HUMAN		0	GGCAAGTTGTC	0.567	
-	34	6964		NM_017617	NP_060087	P46531	NOTC1_HUMAN	lasmic (Potential).	856	TGTATTGGTTCG	0.647	
-	12	2225	clq.1_Missense_M	NM_013366	NP_037498	Q9UJX6	ANC2_HUMAN		1	GCTCCTCCTCAA	0.662	
-	6	1308	clq.1_Missense_M	NM_013366	NP_037498	Q9UJX6	ANC2_HUMAN		1	TGGAAGGGTCC	0.622	
+	7	943	es.1_Missense_M	NM_014434	NP_055249	Q9UHB4	NDOR1_HUMAN	-binding FR-type.	0	TGCAGCCGCGG	0.697	
-	8	1332	.1_Intron|ENTPD	NM_001033113	NP_001028285	Q5MY95	ENTP8_HUMAN	ellular (Potential).	1	AGGGCCTCTGG	0.632	
+	2	782	pi.2_Missense_Mu	NM_000451	NP_000442	O15266	SHOX_HUMAN		0	AAGAAGGATTCC	0.617	

+	3	380	_p.G79R|ASMT_u	NM_004043	NP_004034	P46597	HIOM_HUMAN		1	CGAGGGGAGGA	0.493	
+	6	593	p.E150K|ASMT_u	NM_004043	NP_004034	P46597	HIOM_HUMAN		1	GGTCCGAGGGC	0.567	rs147969184
-	5	557	RSD_uc004cra.1_	NM_001669	NP_001660	P51689	ARSD_HUMAN		0	GCAGTGATCCC	0.557	
-	5	3806		NM_015419	NP_056234	Q9NR99	MXRA5_HUMAN		8	CATTTCCAACT	0.463	
-	2	743	ndi.2_Missense_	NM_181332	NP_851849	Q8N0W4	NLGNX_HUMAN	ellular (Potential).	4	TGGGGGGTGAG	0.567	
+	3	754		NM_013452	NP_038480	Q9H320	VCX1_HUMAN	of L-S-Q-E-S- [EQ]-V-E-E-	0	AGAGCGAGATG	0.577	
+	4	1637		NM_001649	NP_001640	Q13796	SHRM2_HUMAN		8	GAGCCCACGCC	0.682	
+	2	1482	d.2_Missense_Mu	NM_138636	NP_619542	Q9NR97	TLR8_HUMAN	ellular (Potential).	7	TTCACCCGTCCT	0.388	
+	2	2823	d.2_Missense_Mu	NM_138636	NP_619542	Q9NR97	TLR8_HUMAN	mic (Potential).|TIR.	7	TAGAGGAGAGG	0.438	
+	5	737	_p.A166V|EGFL6_	NM_015507	NP_056322	Q8IUX8	EGFL6_HUMAN	EGF-like 3.	2	CCTGGCCCCAA	0.493	
+	9	1212	p.E337K|PHEX_u	NM_000444	NP_000435	P78562	PHEX_HUMAN	ellular (Potential).	3	CCTCCGAGAAT	0.458	
+	17	1921	p.A573V|PHEX_u	NM_000444	NP_000435	P78562	PHEX_HUMAN	ellular (Potential).	3	TGGTGCTATAG	0.323	
+	4	714	h.2_Missense_Mu	NM_005391	NP_005382	Q15120	PDK3_HUMAN	stidine kinase.	6	TTTCCGCATGC	0.373	
+	3	201	e_Mutation_p.E6	NM_016937	NP_058633	P09884	DPOLA_HUMAN		3	TATGAAGAAGTT	0.443	
-	3	710		NM_025159	NP_079435	Q9HAI6	CX021_HUMAN		1	TCAGAGGGAAAA	0.428	
-	1	1742		NM_203408	NP_981953	Q5JRC9	FA47A_HUMAN		5	GGCTCCGAGAAT	0.522	
+	7	1011		NM_173695	NP_775966	Q8N9S7	CX059_HUMAN		1	GGCATGGACAGA	0.333	
-	4	550	X_uc011mkh.1_I	NM_006307	NP_006298	P78539	SRPX_HUMAN	Sushi 2.	0	GCTCCCCTTTC	0.527	
-	19	2489	a.2_RNA|RPGR_	NM_000328	NP_000319	Q92834	RPGR_HUMAN		1	CCTATGGATTTTA	0.368	
-	15	2004		NM_004229	NP_004220	O60244	MED14_HUMAN	tion with SREBF1.	4	TACTGGACATG	0.323	
+	3	1187	se_Mutation_p.W	NM_001097579	NP_001091048	Q9UPC5	GPR34_HUMAN	ellular (Potential).	1	TACTGGAAAGA	0.343	
+	10	1936	nil.2_Missense_M	NM_033626	NP_296375	Q96HB5	CC120_HUMAN	Pro-rich.	1	TCTCCCGCCGG	0.697	
-	4	491		NM_015698	NP_056513	Q92917	GPKOW_HUMAN		2	GGGGACCGCCT	0.582	
-	9	1380	mmw.1_Missense_	NM_006150	NP_006141	O43900	PRIC3_HUMAN		1	GGACTCTGGGG	0.682	
-	24	3302		NM_001013742	NP_001013764	Q5KSL6	DGKK_HUMAN		2	GAGCTAAGTGC	0.502	
-	2	224	w.2_Missense_M	NM_015107	NP_055922	Q9UPP1	PHF8_HUMAN	PHD-type.	3	TCACATCGTAAG	0.637	
+	1	222		NM_174912	NP_777572	Q6GMR7	FAAH2_HUMAN	ical; (Potential).	3	TAGTAGGCCGA	0.562	
+	6	900		NM_174912	NP_777572	Q6GMR7	FAAH2_HUMAN		3	TGGTTCCCAAC	0.463	
-	7	867	_p.R267C|MTMR8	NM_017677	NP_060147	Q96EF0	MTMR8_HUMAN	ularin phosphatase.	4	GAAGCGAATGT	0.488	
-	5	732	_Mutation_p.P192	NM_018684	NP_061154	Q9NQZ6	ZC4H2_HUMAN		1	TTTTGGGGTTC	0.502	
-	12	1816	n_p.E523K|LAS1L	NM_031206	NP_112483	Q9Y4W2	LAS1L_HUMAN		4	ttcttcctcctcctcTAC	0.338	
+	2	259	N_uc010nkp.1_R	NM_002444	NP_002435	P26038	MOES_HUMAN	FERM.	10	CCATCCAGCCC	0.517	
+	17	2908	kr.2_Missense_Mu	NM_138737	NP_620074	Q9BQS7	HEPH_HUMAN	tential).|Plastocyanin-like	9	CCCAGGATCCA	0.413	
+	3	2950	R_uc011mpf.1_Mi	NM_000044	NP_000035	P10275	ANDR_HUMAN	HIPK3 (By similarity).|Nuc	8	AAAATTGTCCAT	0.333	
+	1	846_847		NM_207320	NP_997203	Q7L8S5	OTU6A_HUMAN	OTU.	2	AACTCCGTGAC	0.678	
+	3	333		NM_198512	NP_940914	Q6ZPD8	DG2L6_HUMAN		1	CCCTATGGAAGT	0.552	
-	1	748		NM_002565	NP_002556	P51582	P2RY4_HUMAN	ellular (Potential).	1	AGGCCGAGTGG	0.572	
+	13	2066	yz.2_Missense_M	NM_005120	NP_005111	Q93074	MED12_HUMAN		4	GAGGGGACCTT	0.537	
+	18	2649	yz.2_Missense_M	NM_005120	NP_005111	Q93074	MED12_HUMAN		4	GCGACGCAACC	0.562	
+	1	193	|TAF1_uc004dzt.3_	NM_138923	NP_620278	P21675	TAF1_HUMAN	otein kinase 1.	17	TCAATGGAGCC	0.617	
+	6	978	TAF1_uc004dzt.3_	NM_138923	NP_620278	P21675	TAF1_HUMAN	otein kinase 1.	17	GATGATGAAGT	0.423	rs139324935
-	1	1205	G4_uc004eaj.1_	NM_001024455	NP_001019626	Q5HYW3	RGAG4_HUMAN		3	GAATTCCGACA	0.498	
-	22	2756	_p.E819K|PHKA1_	NM_002637	NP_002628	P46020	KPB1_HUMAN	in-binding (Potential).	4	GAATTTCTCCCA	0.413	
-	21	2538	_p.S746F|PHKA1_	NM_002637	NP_002628	P46020	KPB1_HUMAN		4	GAACAGAGGGA	0.388	
-	21	2534	_p.P745S|PHKA1_	NM_002637	NP_002628	P46020	KPB1_HUMAN		4	AGAGGGAACCT	0.388	
+	3	496	se_Mutation_p.P1	NM_001039840	NP_001034929	Q5VXU3	CHIC1_HUMAN		0	GGCCCCAGAAG	0.403	
+	1	331		NM_203303	NP_976048	Q8WW36	ZCH13_HUMAN		0	TAAACGAGAGA	0.502	rs142122114

-	9	1788	ecr.2_Missense_Mu	NM_000489	NP_000480	P46100	ATRX_HUMAN		30	GGAACAGACACA	0.398	
+	5	1611	cw.2_Missense_Mu	NM_000052	NP_000043	Q04656	ATP7A_HUMAN	lasmic (Potential).	0	AGGAAGGAAAGA	0.418	
+	5	380	edm.1_Missense_	NM_152630	NP_689843	Q8NEK8	FA46D_HUMAN		2	GTTATAACACTGC	0.358	
-	32	3981	ense_Mutation_p.R	NM_153252	NP_694984	Q6RI45	BRWD3_HUMAN		4	TAAATCGAAGTAA	0.289	
-	18	1821	p.P582S|RPS6KA	NM_014496	NP_055311	Q9UK32	KS6A6_HUMAN	otein kinase 2.	8	AGCATGGAGTTAA	0.363	
-	1	2116	_p.R147H|PCDH19	NM_020766	NP_001098713	Q8TAB3	PCD19_HUMAN	|Extracellular (Potential).	7	GGATGCGCGTG	0.597	
-	7	806	na.1_Missense_M	NM_003270	NP_003261	O43657	TSN6_HUMAN	lasmic (Potential).	1	GGCACGAGAGAC	0.388	rs149522304
+	5	733	rh.1_Missense_Mu	NM_001939	NP_001930	Q13474	DRP2_HUMAN	Spectrin 1.	2	CAAAAGGATGAG	0.537	
-	2	3817	n.2_Missense_Mut	NM_032441	NP_115817	Q5H9K5	ZMAT1_HUMAN		1	ATGTCCGGAAAG	0.403	
-	19	2476	eja.3_Missense_M	NM_001099686	NP_001093156	Q9GZY0	NXF2_HUMAN	RRM.	1	AGTAGGGCGCAG	0.483	
+	5	3170	p.R790K|GPRASP	NM_014710	NP_055525	Q5JY77	GASP1_HUMAN	Glu-rich.	2	AGGACAGACTAGA	0.512	
+	4	3118	SP2_uc004ejm.2_M	NM_138437	NP_612446	Q96D09	GASP2_HUMAN		1	TGGTTCTGAAGA	0.418	
-	2	356		NM_153448	NP_703149	Q8N693	ESX1_HUMAN		1	GCGGCTCCTCCT	0.716	
-	2	218_219		NM_153448	NP_703149	Q8N693	ESX1_HUMAN		1	CTGTTCCGTACT	0.594	rs76590545
+	23	4165	c.1_Missense_Mut	NM_198465	NP_940867	Q7Z2Y5	NRK_HUMAN	CNH.	14	AATAATGATCCAG	0.373	
+	4	2403	emg.1_Missense_M	NM_152423	NP_689636	Q5H9M0	MUML1_HUMAN		4	TGAAATCATTTTT	0.398	
-	16	2786	nse_Mutation_p.R	NM_024657	NP_078933	Q8TE76	MORC4_HUMAN	Potential.	1	TTGGTTCTTTCCA	0.488	
+	4	634	sk.1_Missense_Mu	NM_182607	NP_872413	Q86XK7	VSIG1_HUMAN	Potential).|Ig-like C2-type 2.	2	CTATTTCCCTTTC	0.438	
+	7	1165	sk.1_Missense_Mu	NM_182607	NP_872413	Q86XK7	VSIG1_HUMAN	lasmic (Potential).	2	ccccagGATCAGAG	0.378	
-	35	3519	sn.1_Missense_M	NM_001847	NP_001838	Q14031	CO4A6_HUMAN	le-helical region.	8	GGTTCTCCTCTCA	0.493	
-	23	1976	nsn.1_Missense_M	NM_001847	NP_001838	Q14031	CO4A6_HUMAN	le-helical region.	8	GAAGTCCTGGTA	0.547	
-	22	1791	nsn.1_Missense_M	NM_001847	NP_001838	Q14031	CO4A6_HUMAN	le-helical region.	8	GAGCCAGAATCAC	0.547	
+	7	588	nso.1_Missense_M	NM_033380	NP_203699	P29400	CO4A5_HUMAN	le-helical region.	4	CTAGGGAGAACC	0.363	
+	33	3029	_p.K943*|COL4A5	NM_033380	NP_203699	P29400	CO4A5_HUMAN	le-helical region.	4	GGTAGTAAAGGAC	0.478	
-	4	1315	Y2F_uc011msq.1_	NM_001522	NP_001513	P51841	GUC2F_HUMAN	cellular (Potential).	8	ACAACGGTGAAA	0.408	
-	4	1167_1168	_p.A251V|DCX_uc	NM_000555	NP_000546	O43602	DCX_HUMAN	oublecortin 2.	4	CCACAGGCAATA	0.401	
-	2	213	LHL13_uc011mtp.	NM_033495	NP_277030	Q9P2N7	KLH13_HUMAN		2	CCATTTCGCTGCC	0.433	
+	18	2910	ntr.1_Missense_M	NM_019045	NP_061918	Q5JSH3	WDR44_HUMAN		5	AGAGATCGTAATC	0.353	
+	2	270		NM_144658	NP_653259	Q5JSL3	DOC11_HUMAN	ctivated CDC42 (By similari	3	CCCAATGGAAGA	0.398	
+	28	3140	eqq.2_Missense_M	NM_144658	NP_653259	Q5JSL3	DOC11_HUMAN		3	ACTATAGTTTGGC	0.408	
+	4	1181	RF3_uc004eqy.2_	NM_001031855	NP_001027026	Q496Y0	LONF3_HUMAN		2	TGAAGGGGGATC	0.532	
-	3	446	sa.1_Missense_Mu	NM_080632	NP_542199	Q9BZI7	REN3B_HUMAN	C core.|Necessary for inter	3	CTCACCTTTATTC	0.358	
-	12	2297	_p.P744S|ODZ1_u	NM_014253	NP_055068	Q9UKZ4	TEN1_HUMAN	Extracellular (Potential).	23	ATCCAGGGCTACA	0.458	
-	1	846		NM_138289	NP_612146	Q8TDG2	ACTT1_HUMAN		5	ACTTCTCTTTGAT	0.537	
+	15	1759	ur.2_Missense_Mu	NM_000276	NP_000267	Q01968	OCRL_HUMAN		4	CTCTTCCATATTG	0.378	
-	4	719	4eux.1_Missense_	NM_001008222	NP_001008223	Q9Y397	ZDHC9_HUMAN	lasmic (Potential).	1	CCTGGGGCACC	0.468	
-	8	1484	e.3_Missense_Mut	NM_001421	NP_001412	Q99607	ELF4_HUMAN		1	ACGGTCCCAATTC	0.587	
+	5	1051	4ewb.2_Missense_	NM_144967	NP_659404	Q6ZRI8	RHG36_HUMAN	Rho-GAP.	3	CAAATCCCCCAGC	0.458	
-	16	3407	p.E1051K|IGSF1_u	NM_001555	NP_001546	Q8N6C5	IGSF1_HUMAN	otential).|Ig-like C2-type 10	5	GAGTTCCAGGGT	0.498	
-	1	107	0nrl.1_RNA|MBNL3	NM_018388	NP_060858	Q9NUK0	MBNL3_HUMAN		0	TATCACGAATCAG	0.398	
-	6	2148	vf.1_Missense_Mu	NM_031907	NP_114113	Q9BXU7	UBP26_HUMAN		8	CAAGGGAAGAGC	0.378	
-	4	611	nvw.1_Missense_M	NM_173470	NP_775741	Q8N4V1	MMGT1_HUMAN	lasmic (Potential).	0	GTATCCGAAGGCC	0.358	rs150859420
+	2	250	se_Mutation_p.H6	NM_000074	NP_000065	P29965	CD40L_HUMAN	cellular (Potential).	1	AATCTTCATGAAC	0.348	
+	4	416	EC1_uc010nsl.1_5	NM_005462	NP_005453	O60732	MAGC1_HUMAN		4	CTGAGAGCGACC	0.587	rs147626195
+	4	914	EC1_uc010nsl.1_I	NM_005462	NP_005453	O60732	MAGC1_HUMAN		4	TCCACTTTATTGA	0.502	
+	4	1517	EC1_uc010nsl.1_I	NM_005462	NP_005453	O60732	MAGC1_HUMAN		4	CAGATTCCTATGA	0.478	
+	4	2019	EC1_uc010nsl.1_I	NM_005462	NP_005453	O60732	MAGC1_HUMAN		4	CTCCTCACTACTT	0.582	

+	5	398	n.2_Intron|MAGEA	NM_005366	NP_005357	P43364	MAGAB_HUMAN		2	TATTTCCCACAGT	0.532	
+	5	1328_1329	.2_Intron|MAGEA	NM_005366	NP_005357	P43364	MAGAB_HUMAN	MAGE.	2	TGGGAGGGATCC	0.545	
+	2	988	|GPR50_uc011my	NM_004224	NP_004215	Q13585	MTR1L_HUMAN	Name=7; (Potential).	4	CCTACTTCAACA	0.502	
-	5	994	4ffl.2_Missense_M	NM_001011543	NP_001011543	P43363	MAGAA_HUMAN	MAGE.	0	AGTGGGATCCA	0.493	
+	9	1488_1489		NM_018558	NP_061028	Q9UN88	GBRT_HUMAN		3	CCCATGGCCATG	0.55	
+	3	567	e_Mutation_p.R12	NM_005363	NP_005354	P43360	MAGA6_HUMAN	MAGE.	0	AGTATCGAGCCA	0.527	
-	3	1057	AGEA12_uc004fg	NM_005367	NP_005358	P43365	MAGAC_HUMAN	MAGE.	1	TGTCCTCCCTCC	0.562	
-	5	531	fgr.2_Missense_M	NM_004344	NP_004335	P41208	CETN2_HUMAN	EF-hand 4.	0	CAGGAACTCTT	0.393	
-	1	662	hn.1_Missense_M	NM_017518	NP_059988	Q99871	HAUS7_HUMAN		0	CCCTGGACACG	0.736	
-	21	5897		NM_005334	NP_005325	P51610	HCFC1_HUMAN		2	CCAGGGACTCG	0.647	
-	9	1978		NM_005334	NP_005325	P51610	HCFC1_HUMAN		2	AGCAGGGACAC	0.607	
-	9	1510	u.1_Nonsense_M	NM_001110556	NP_001104026	P21333	FLNA_HUMAN	Filamin 2.	6	GTCCTGGATCA	0.682	
+	6	1686		NM_017514	NP_059984	P51805	PLXA3_HUMAN	ellular (Potential).	3	CCGGGGACCCG	0.711	
+	10	2196		NM_017514	NP_059984	P51805	PLXA3_HUMAN	ellular (Potential).	3	AGGAGGGCAGG	0.667	
+	21	3855		NM_017514	NP_059984	P51805	PLXA3_HUMAN	ical; (Potential).	3	CGGGGGGTGG	0.677	
+	25	4487		NM_198576	NP_940978	O00468	AGRIN_HUMAN	minin G-like 1.	3	GGCGAGAGTCC	0.692	
-	10	1151	K_uc001aie.2_Mi	NM_023018	NP_075394	O95544	NADK_HUMAN		0	TGATCATGATGG	0.672	
-	38	5594	_Mutation_p.V68	NM_015557	NP_056372	Q8TDI0	CHD5_HUMAN		12	CTCCACTTCAG	0.652	
-	12	1431		NM_207420	NP_997303	Q6PXP3	GTR7_HUMAN	lasmic (Potential).	0	CGGTTTATCTC	0.483	
+	35	3967	z.2_Nonsense_M	NM_015074	NP_055889	O60333	KIF1B_HUMAN		3	GTTTGGTTTGA	0.373	
-	3	234	_p.L77F|C1orf127	NM_173507	NP_775778	B7ZLG7	B7ZLG7_HUMAN		1	AAGAAGGCCTT	0.607	
+	8	2164	asi.1_Missense_M	NM_020780	NP_065831	Q9P2K9	PTHD2_HUMAN	lasmic (Potential).	7	AGGTCGAGGAA	0.632	
-	2	397	.1_Intron|CLCN6_	NM_006172	NP_006163	P01160	ANF_HUMAN		2	GGGGCCCCGCC	0.672	
+	1	307		NM_001080830	NP_001074299	O95522	PRA12_HUMAN		3	AGGTTCGCCCC	0.592	
-	1	317	10obf.1_Missense_	NM_001146181	NP_001139653	B7ZW38	B7ZW38_HUMAN		0	AGCAATCATTCT	0.502	
+	11	1654	C16_uc001awt.2_	NM_015291	NP_056106	Q9Y2G8	DJC16_HUMAN	lasmic (Potential).	3	TCCTTCGATGG	0.468	
-	7	844	1_Intron|MST1P9_	NR_002729					0	TGATGTGGGATT	0.647	
+	1	408	C7A_uc009vpg.2_	NM_152375	NP_689588	Q5VTJ3	KLD7A_HUMAN		3	CCAGAGAAAAG	0.627	
+	1	1307	vpg.2_Missense_	NM_152375	NP_689588	Q5VTJ3	KLD7A_HUMAN		3	ATATCCCGCTC	0.647	
-	2	117	G2D_uc009vpo.2_	NM_012400	NP_036532	Q9UNK4	PA2GD_HUMAN		0	TTTTCCCAGTCA	0.552	
-	8	964	ei.2_Nonsense_M	NM_001397	NP_001388	P42892	ECE1_HUMAN	ellular (Potential).	3	CTCCTCGTCCC	0.622	
-	15	1286	bew.2_Missense_	NM_002885	NP_002876	P47736	RPGP1_HUMAN	Rap-GAP.	3	AGAAGGGCACA	0.647	
+	10	1997	gf.2_Missense_M	NM_017449	NP_059145	P29323	EPHB2_HUMAN	lasmic (Potential).	5	ATTGACATCTCC	0.532	
+	10	1299	p.R413Q|GRHL3_	NM_021180	NP_067003	Q8TE85	GRHL3_HUMAN		1	CGAGCGGAAGC	0.627	
+	20	6860	_p.C1009R|ARID1	NM_006015	NP_006006	O14497	ARI1A_HUMAN		142	CGGTGTGCCGG	0.597	
-	17	2467	_p.P732S|MAP3K6	NM_004672	NP_004663	O95382	M3K6_HUMAN	rotein kinase.	9	CAGGGGTCCCC	0.582	rs138197184
-	2	203		NM_207397	NP_997280	Q6UWJ8	C16L2_HUMAN	ellular (Potential).	0	CAGGCGGATCA	0.622	
-	6	1602_1603	S4_uc010ofy.1_3'	NM_005626	NP_005617	Q08170	SRSF4_HUMAN	r-rich (RS domain).	0	ACACGGAGCGG	0.446	rs146685214
+	3	532	_p.R141H|PTPRU_	NM_005704	NP_005695	Q92729	PTPRU_HUMAN	lar (Potential).|MAM.	7	CGGCCGTCAGT	0.652	
+	31	4434	tq.2_Missense_M	NM_005704	NP_005695	Q92729	PTPRU_HUMAN	lasmic (Potential).	7	TGGAGGGGCTG	0.602	
-	2	900	e_Mutation_p.G28	NM_144569	NP_653170	Q6ZMY3	SPOC1_HUMAN		6	CAGTCCCTGAG	0.637	
+	13	1540	z.2_Missense_Mut	NM_005356	NP_005347	P06239	LCK_HUMAN	rotein kinase.	6	CAGAGGAGCTG	0.597	
-	5	825	xm.1_Missense_M	NM_052896	NP_443128	Q7Z408	CSMD2_HUMAN	tracellular (Potential).	12	CCAGAGGGAGG	0.542	
-	2	150	xm.1_Missense_M	NM_052896	NP_443128	Q7Z408	CSMD2_HUMAN	tracellular (Potential).	12	GAACCCTGGGC	0.537	
+	5	796	_Mutation_p.E12	NM_012199	NP_036331	Q9UL18	AGO1_HUMAN		3	GGCGCGAGGTC	0.632	
-	4	672	nse_Mutation_p.S	NM_017850	NP_060320	Q9NX04	CA109_HUMAN		0	ATAGACGAAAGA	0.438	
+	1	3712	.1_Intron|MACF1_	NM_015038	NP_055853	O94854	K0754_HUMAN	Ala-rich.	0	ATGCTCCAGAG	0.617	

-	2	265		NM_032526	NP_115915	Q9BXI3	5NT1A_HUMAN			1	AGGGTTCGTTCT	0.448	
-	3	305	AL4_uc010oix.1_	NM_016257	NP_057341	Q9UM19	HPCL4_HUMAN	EF-hand 2.		1	ACTTGGAGGCG	0.692	
+	9	770	IE_uc001cdv.2_Mi	NM_006112	NP_006103	Q9UNP9	PPIE_HUMAN	e cyclophilin-type.		0	CCAAACACCAAT	0.547	
+	4	385	c001cfy.3_Missens	NM_001142588	NP_001136060	Q13952	NFYC_HUMAN			3	ACCTCCAAAGC	0.423	
+	13	2096	q.2_Missense_Mu	NM_005424	NP_005415	P35590	TIE1_HUMAN	III 3.|Extracellular (Potentia		7	CCTGGGCCAATA	0.637	
+	11	2137_2138	p.R171C|PTPRF_	NM_002840	NP_002831	P10586	PTPRF_HUMAN	tential).|Fibronectin type-III		10	AGGCCCGCACA	0.545	
+	7	936	s.1_Missense_Mu	NM_001034024	NP_001029196	Q9NPF5	DMAP1_HUMAN			0	CGGAACGCAAG	0.617	
+	10	1654	_Mutation_p.R148	NM_018150	NP_060620	Q5VTB9	RN220_HUMAN			2	CACTTCGGGGC	0.592	
+	5	842	AH_uc001cpv.2_R	NM_001441	NP_001432	O00519	FAAH1_HUMAN	smic (By similarity).		2	GCGGCCTCAAG	0.517	
-	3	429	e_Mutation_p.W1	NM_000778	NP_000769	Q02928	CP4AB_HUMAN			4	CCAATCCATGG	0.458	
+	4	485		NM_178134	NP_835235	Q86W10	CP4Z1_HUMAN	nenal (Potential).		1	TGTTCGGATGA	0.483	
+	7	854	A9_uc010omt.1_	NM_001011547	NP_001011547	Q2M3M2	SC5A9_HUMAN	cellular (Potential).		3	CTTTCCACATT	0.612	
-	5	461	TA6_uc010omv.1_	NM_019073	NP_061946	Q9NWH7	SPAT6_HUMAN			1	TACGTAGACAGT	0.363	
-	3	808		NM_147193	NP_671726	Q8NBF1	GLIS1_HUMAN			1	GGCACAGGGTG	0.677	
-	9	1016	w.2_RNA|YIPF1_u	NM_018982	NP_061855	Q9Y548	YIPF1_HUMAN	nenal (Potential).		2	CCAACGAACAG	0.483	rs77267196
+	5	553		NM_006252	NP_006243	P54646	AAPK2_HUMAN	rotein kinase.		6	GATTATCTAATAT	0.333	
-	2	1071	orf168_uc009vzv.	NM_001004303	NP_001004303	Q5VWT5	CA168_HUMAN			5	CTTTTTCTGATAT	0.512	
+	4	575		NM_000562	NP_000553	P07357	CO8A_HUMAN	MACPF.		3	TCCAGGATCAC	0.498	
-	11	1656	p.Q468R|C8B_uc	NM_000066	NP_000057	P07358	CO8B_HUMAN	EGF-like.		4	GGCCTTGGGAT	0.498	
-	2	286	8B_uc010ooo.1_	NM_000066	NP_000057	P07358	CO8B_HUMAN	TSP type-1 1.		4	GTGGTCCAAGA	0.522	
-	14	1620	r.1_Missense_Mu	NM_021080	NP_066566	O75553	DAB1_HUMAN			3	GACGAGGGGCT	0.617	
-	9	1371		NM_000775	NP_000766	P51589	CP2J2_HUMAN			1	CTCAGTCCTGG	0.453	
+	8	1642_1643	uc001dbl.2_Intron	NM_005012	NP_005003	Q01973	ROR1_HUMAN	ical; (Potential).		19	CCATTCCCCTG	0.446	
+	9	3086	c001dbm.2_5'Flan	NM_005012	NP_005003	Q01973	ROR1_HUMAN	lasmic (Potential).		19	TGGTGGAATGG	0.428	
+	3	1083	uc001dim.2_Silent	NM_000959	NP_000950	P43088	PF2R_HUMAN	cellular (Pote	273*(1)|p.L296	6	AACATTGGAATA	0.343	
+	9	1814	se_Mutation_p.E5	NM_012302	NP_036434	O95490	LPHN2_HUMAN	cellular (Potential).		9	CCAATGAACTG	0.403	
+	14	2810	.L877F|LPHN2_uc	NM_012302	NP_036434	O95490	LPHN2_HUMAN	Name=2; (Potential).		9	TCAACCTTTTC	0.378	
-	5	1606	ose.1_RNA|COL2	NM_152890	NP_690850	Q17RW2	COOA1_HUMAN	ollagen-like 1.		5	ATTTCCATGTG	0.393	
+	7	1377	9524_uc001dme.1	NM_012262	NP_036394	Q7LGA3	HS2ST_HUMAN	nenal (Potential).		1	CCATGCCGTTC	0.383	
-	3	1761	BL2_uc001dmr.2_	NM_001162536	NP_001156008	Q96E39	RBMXL_HUMAN	Ser-rich.		0	AGGGGGAAGCC	0.537	
+	3	573	P6_uc010ost.1_In	NM_198460	NP_940862	Q6ZN66	GBP6_HUMAN	(By similarity).		2	CGAAGGTCTGG	0.507	
-	3	2255	lnx.2_Intron|ZNF6	NM_201269	NP_958357	Q9H582	ZN644_HUMAN			3	ATGAGGAGAGC	0.378	
+	6	614	w.1_Missense_Mu	NM_003503	NP_003494	O00311	CDC7_HUMAN	rotein kinase.		5	TCTTTCCTTTCA	0.294	
+	7	986		NM_173567	NP_775838	Q8IUS5	EPHX4_HUMAN			1	CACATGGTGAC	0.413	
-	18	2304	f.1_Missense_Mut	NM_005665	NP_005656	O60447	EVI5_HUMAN	s.|Interaction with AURKB		2	ACATCGAACCA	0.458	
-	8	1144	tn.1_Missense_M	NM_000350	NP_000341	P78363	ABCA4_HUMAN	Extracellular.		12	AGAAAGGCCTTA	0.473	
-	5	567	tn.1_Missense_M	NM_000350	NP_000341	P78363	ABCA4_HUMAN	Extracellular.		12	AGATATCCCTTAT	0.408	
-	13	1775	RHGAP29_uc001	NM_004815	NP_004806	Q52LW3	RHG29_HUMAN			11	TTGTGGCCTTG	0.373	
-	5	516	YD_uc001drw.2_	NM_000110	NP_000101	Q12882	DPYD_HUMAN			8	CATTCCACAAG	0.353	
+	7	775_776		NM_033055	NP_149044	Q96MC6	HIAT1_HUMAN	Name=7; (Potential).		0	ACCTACCGGAGG	0.386	
-	16	2055	e|COL11A1_uc00	NM_001854	NP_001845	P12107	COBA1_HUMAN			12	CCATACCCTTTT	0.353	
-	8	1555	_p.E425K|COL11A	NM_001854	NP_001845	P12107	COBA1_HUMAN	nhelical regi	p.F413V(1)	12	TTGTTTCTGTAA	0.328	
+	10	1702	561D1_uc001dxu.	NM_153340	NP_699171	Q5T6C5	AT7L2_HUMAN			2	ACGGGGTGGAG	0.602	rs148343235
+	1	1834	sense_Mutation_p.	NM_022768	NP_073605	Q96T37	RBM15_HUMAN			3	TGACTCTGATTG	0.567	
-	11	1432	p.S421F|OVGP1_	NM_002557	NP_002548	Q12889	OVGP1_HUMAN			5	CAAGGGATACA	0.502	
-	2	571	bv.1_Missense_M	NM_004980	NP_004971	Q9UK17	KCND3_HUMAN	lasmic (Potential).		3	GCCGGGGCCA	0.677	
-	5	435		NM_005725	NP_005716	O60636	TSN2_HUMAN	cellular (Potential).		0	CTCTTCATACAT	0.403	

+	10	2007	vhg.1_Missense_M	NM_006699	NP_006690	O60476	MA1A2_HUMAN	enal (Potential).	0	TGTAGGCTATAG	0.353
-	19	2687		NM_206996	NP_996879	Q6Q759	SPG17_HUMAN		6	CTCATTCATTTTA	0.328
+	6	915	r.1_Missense_Mu	NM_001005783	NP_001005783	Q9NYQ3	HAOX2_HUMAN	xy acid dehydrogenase.	4	TATAGGGAAATG	0.418
+	10	4827	.1_Missense_Muta	NM_004326	NP_004317	O00512	BCL9_HUMAN	Pro-rich.	6	AGGATCGGGGG	0.597
-	6	1182	jj.1_Missense_Mut	NM_016361	NP_057445	Q9NPH0	PPA6_HUMAN		4	AATGCCCATCC	0.468
+	12	1536	vkt.1_Missense_M	NM_001102663	NP_001096133				0	CCTTCAGATTAT	0.483
-	19	2487_2488	ww.2_Missense_	NM_030913	NP_112175	Q9H3T2	SEM6C_HUMAN	lasmic (Potential).	2	ACCCTCCTTGG	0.604
-	3	205		NM_001122965	NP_001116437	Q6XPR3	RPTN_HUMAN	y similarity).|EF-hand 1.	0	TTTGGTCTCTGT	0.433
-	3	8357		NM_002016	NP_002007	P20930	FILA_HUMAN	Ser-rich.	16	GCCTGGAGCTG	0.592
-	3	2615	uc001ezv.2_5'Flan	NM_002016	NP_002007	P20930	FILA_HUMAN	Ser-rich.	16	CTACCGATTGC	0.592
-	3	3984	uc001ezv.2_Intron	NM_001014342	NP_001014364	Q5D862	FILA2_HUMAN		17	TGGATCCTGAC	0.478
+	2	175_176		NM_001025231	NP_001020402	Q5T749	KPRP_HUMAN	Gln-rich.	5	CAAGCCCCTTGT	0.574
+	2	81		NM_005547	NP_005538	P07476	INVO_HUMAN		3	CCTCTCCCCTG	0.532
-	2	444		NM_005978	NP_005969	P29034	S10A2_HUMAN	EF-hand 1.	1	GAAGTTCCTTCA	0.577
-	2	1302	_p.L25F|KCNN3_u	NM_002249	NP_002240	Q9UGI6	KCNN3_HUMAN	=Segment S2; (Potential).	1	CAAAAGGATGA	0.542
+	9	2666_2667	1fkq.2_Missense_	NM_001105203	NP_001098673	Q9BVN2	RUSC1_HUMAN		2	TGCCCCCGACA	0.579
-	3	4601	.S1374F|ASH1L_	NM_018489	NP_060959	Q9NR48	ASH1L_HUMAN		11	TACTAGAAAGA	0.438
+	2	789	11_uc010pgq.1_I	NM_152280	NP_689493	Q9BT88	SYT11_HUMAN	mic (Potential).|C2 1.	2	TGGTGGTGACA	0.532
+	1	568		NM_181885	NP_871001	Q8TDU9	RL3R2_HUMAN	ellular (Potential).	0	TGGAGGGTGAG	0.662
-	22	2597		NM_178229	NP_839943	Q86VI3	IQGA3_HUMAN	IQ 4.	6	AATATCCTGTAGT	0.542
+	3	939	b.2_Missense_Mu	NM_005973	NP_005964	Q92733	PRCC_HUMAN		27	CTAAGCCCTCC	0.562
+	20	2628	fqk.1_Splice_Site_	NM_001080471	NP_001073940	Q5VY43	PEAR1_HUMAN		3	TCTTAGGTTCC	0.642
-	5	921	_p.H270Y|FCRL1_	NM_052938	NP_443170	Q96LA6	FCRL1_HUMAN	3.|Extracellular (Potential).	7	AGAATGTTCTT	0.557
+	2	446	1C_uc001frv.2_5'F	NM_001765	NP_001756	P29017	CD1C_HUMAN	ellular (Potential).	4	TGGACGAGTTG	0.498
-	1	509		NM_001005279	NP_001005279	Q8NGY2	OR6K2_HUMAN	ellular (Potential).	1	TGATTCGAACCA	0.483
-	1	122		NM_001005279	NP_001005279	Q8NGY2	OR6K2_HUMAN	Name=1; (Potential).	1	GGTTTCCAACA	0.428
+	1	1024_1025		NM_001005184	NP_001005184	Q8NGW6	OR6K6_HUMAN	lasmic (Potential).	1	GGGCTGGGAAA	0.416
+	4	814	_p.S181F|PYHIN1_	NM_152501	NP_689714	Q6K0P9	IFIX_HUMAN		4	CACTTCCTCAA	0.502
+	5	1113	_Mutation_p.P16	NM_005531	NP_005522	Q16666	IF16_HUMAN		1	ATCTCCCAAGA	0.532
+	1	149	uc001fts.3_Intron	NM_012351	NP_036483	P30954	O10J1_HUMAN	Name=1; (Potential).	1	AACCTTAGCAG	0.433
+	1	568	uc001fts.3_Intron	NM_012351	NP_036483	P30954	O10J1_HUMAN	ellular (Potential).	1	TCTGTGACATC	0.493
+	9	1221	L6_uc009wsz.1_S	NM_001004310	NP_001004310	Q6DN72	FCRL6_HUMAN		3	AAAGGTGAGCT	0.542
+	16	2249	p.G706E|ATP1A2_	NM_000702	NP_000693	P50993	AT1A2_HUMAN	lasmic (Potential).	7	CCAGGGAGCCA	0.612
+	6	1150	1A4_uc001fvf.3_	NM_144699	NP_653300	Q13733	AT1A4_HUMAN	lasmic (Potential).	4	ACAACTCATCCT	0.498
+	11	1467	289F|NDUFS2_uc	NM_004550	NP_004541	O75306	NDUS2_HUMAN		1	CCAGTCCCTGA	0.522
+	9	1469	_Mutation_p.G32	NM_002585	NP_002576	P40424	PBX1_HUMAN		5	TGGAGGTTGGC	0.458
-	10	1553	p.G389E|ALDH9A	NM_000696	NP_000687	P49189	AL9A1_HUMAN		0	TTATATCCACCAA	0.448
+	4	236	ense_Mutation_p.	NM_002697	NP_002688	P14859	PO2F1_HUMAN		5	CAATGGTCTGG	0.428
-	19	2651	plj.1_Missense_M	NM_018417	NP_060887	Q96PN6	ADCYA_HUMAN		3	ACTATGGAGAG	0.373
-	13	3234		NM_000130	NP_000121	P12259	FA5_HUMAN	B.	6	TTTTTTCGTGTC	0.408
-	14	2413	ELP_uc009wvr.2_	NM_003005	NP_002996	P16109	LYAM3_HUMAN	ical; (Potential).	4	GACCTATCGTAG	0.443
-	2	399	nk|C1orf112_uc00	NM_033418	NP_219486	O95568	MET18_HUMAN		0	CTTCTCCTTTTT	0.423
+	6	799	b.1_Missense_M	NM_001002294	NP_001002294	P31513	FMO3_HUMAN		1	GTTATCCTTGG	0.463
-	2	693_694	_p.P205S|TNR_uc	NM_003285	NP_003276	Q92752	TENR_HUMAN	Cys-rich.	11	AGCGGGCAGT	0.589
-	1	97	n_p.E6K|TNR_uc	NM_003285	NP_003276	Q92752	TENR_HUMAN		11	TGTTTCCCCAT	0.532
+	8	4135	A2_uc009www.2_	NM_020318	NP_064714	Q9BXP8	PAPP2_HUMAN		16	AAAACAAGGAG	0.552
+	19	2275	orf125_uc001gmp.	NM_144696	NP_653297	Q5T1B0	AXDN1_HUMAN		0	TTTAATGATACC	0.368

+	24	5501	xl.2_Missense_Mu	NM_014810	NP_055625	Q5VT06	CE350_HUMAN		4	CGTGAAAAGGC	0.393
+	14	2207	kn.2_Missense_Mu	NM_004736	NP_004727	Q9UBH6	XPR1_HUMAN	lasmic (Potential).	0	CCGGCCTCGCC	0.463
+	18	2323	wxs.2_Missense_I	NM_000721	NP_000712	Q15878	CAC1E_HUMAN	ic (Potential).|Poly-Glu.	6	AGGAAGAAGAG	0.552
+	7	1086	e_Mutation_p.L25	NM_005562	NP_005553	Q13753	LAMC2_HUMAN	ninin IV type A.	3	AAATTTCTTGGG	0.463
+	7	1118	_Mutation_p.S26	NM_005562	NP_005553	Q13753	LAMC2_HUMAN	ninin IV type A.	3	TCAAAGCCTGTC	0.478
-	2	1272	.2_Intron|RGL1_u	NM_203454	NP_982279	Q8WW27	ABEC4_HUMAN		0	GCCTTCCAAGGT	0.438
-	8	1150	vyh.1_Nonsense_	NM_052966	NP_443198	Q9BZQ8	NIBAN_HUMAN		4	TTCTTTGAGTTC	0.418
-	3	381	_Site_p.P63_splic	NM_052966	NP_443198	Q9BZQ8	NIBAN_HUMAN		4	GGTGGCTTAAA	0.343
+	15	1785	0pos.1_Splice_Sit	NM_024420	NP_077734	P47712	PA24A_HUMAN		3	TTTTAAGATCCTG	0.308
-	6	1055	ot.1_Missense_Mu	NM_199051	NP_950252	Q76B58	FAM5C_HUMAN		5	CATTTTCCTTGC	0.448
+	7	1202	w.2_Missense_Mut	NM_000186	NP_000177	P08603	CFAH_HUMAN	Sushi 5.	6	GATGTACCTGTA	0.358
+	2	345	R1_uc001gtm.2_I	NM_002113	NP_002104	Q03591	FHR1_HUMAN	Sushi 1.	0	GGATGGTCACC	0.388
+	7	2615	B1_uc010ppb.1_In	NM_201253	NP_957705	P82279	CRUM1_HUMAN	otential).|Laminin G-like 2.	9	AAAGGGAGATG	0.373
-	2	1445	14_uc010ppj.1_5'U	NM_014875	NP_055690	Q15058	KIF14_HUMAN	d for PRC1-binding.	7	TTCGGGAAGAA	0.383
-	2	1443	14_uc010ppj.1_5'U	NM_014875	NP_055690	Q15058	KIF14_HUMAN	d for PRC1-binding.	7	TCGGGAAGAATT	0.383
-	7	1202_1203		NM_000069	NP_000060	Q13698	CAC1S_HUMAN	=S6 of repeat I; (Potential)	5	GTTGAGGATGAA	0.401
-	5	176	NNI1_uc001gwp.2	NM_003281	NP_003272	P19237	TNNI1_HUMAN	ed in binding TNC.	0	AGCATTCCTTG	0.667
-	2	75	|TNNI1_uc001gwp	NM_003281	NP_003272	P19237	TNNI1_HUMAN		0	CAGCACCTAGG	0.592
+	17	1630	R6_uc009xab.2_R	NM_001017403	NP_001017403	Q9HBX8	LGR6_HUMAN	cellular (Potential).	10	GTGTCCAGTGT	0.562
+	17	2530	1gyb.1_Nonsense	NM_002481	NP_002472	O60237	MYPT2_HUMAN		3	CCATCCGAGAG	0.463
-	4	472	zk.1_5'Flank|CHI3L	NM_001276	NP_001267	P36222	CH3L1_HUMAN		1	ACCCAAAGTTCC	0.552
+	15	1488	_p.R362I|PFKFB2_	NM_001018053	NP_001018063	O60825	F262_HUMAN		1	GCGCAGACGCC	0.527
+	4	519	.P130L|C4BPB_u	NM_001017365	NP_001017365	P20851	C4BPB_HUMAN	Sushi 2.	1	ACCTCCCTTTC	0.453
+	3	208	hhk.2_Missense_I	NM_181755	NP_861420	P28845	DHI1_HUMAN	enal (Potential).	1	CCAAGGAAAGA	0.517
-	8	1706_1707	ic.2_Missense_Mu	NM_172362	NP_758872	O95259	KCNH1_HUMAN	lasmic (Potential).	5	CTCATGGTATCT	0.465
+	8	862	D3_uc010pub.1_M	NM_016121	NP_057205	Q9Y597	KCTD3_HUMAN		3	CTAATAGTAGCTG	0.323
-	63	13471		NM_206933	NP_996816	O75445	USH2A_HUMAN	ential).|Fibronectin type-III	26	ATCTGGAGGGC	0.478
-	27	3982		NM_004446	NP_004437	P07814	SYEP_HUMAN		2	TCCTCCCTAAAAT	0.318
-	6	812	p.Y208C|TAF1A_u	NM_139352	NP_647603	Q15573	TAF1A_HUMAN		0	GCATTGTAAGCA	0.333
+	4	979	a.1_Missense_Mu	NM_198551	NP_940953	Q5JRA6	MIA3_HUMAN	cellular (Potential).	5	AAGAAGACTTT	0.388
+	8	2803		NM_032890	NP_116279	Q96F81	DISP1_HUMAN		0	GAGATTTTTGAA	0.483
-	2	879	.1_5'UTR|SUSD4_	NM_017982	NP_060452	Q5VX71	SUSD4_HUMAN	xtracellular (Potential).	0	TGAAATCGGGCT	0.517
-	33	5691	p.P1555L|CDC42	NM_003607	NP_003598	Q5VT25	MRCKA_HUMAN		11	CCATGGGCAGA	0.383
+	39	10431	p.E3463K|OBSCN	NM_001098623	NP_001092093	Q5VST9	OBSCN_HUMAN	Ig-like 35.	28	CCGTGGAAGGG	0.582
-	7	2451	1L2_uc001hvf.2_5'	NM_020808	NP_065859	Q9P2F8	SI1L2_HUMAN	Rap-GAP.	6	TTTGGGAATCG	0.408
+	2	1201	hvs.1_Missense_	NM_032435	NP_115811	Q5TCX8	M3KL4_HUMAN	rotein kinase.	8	CCCCCGAAGTG	0.473
-	7	917		NM_018072	NP_060542	Q9H583	HEAT1_HUMAN		3	ACATATTATCATG	0.308
+	5	3190	e.1_Missense_Mu	NM_020066	NP_064450	Q9NZ56	FMN2_HUMAN	ro-rich.|FH1.	12	CCCCTCCTCCC	0.711
-	4	1221	cf.2_Missense_Mu	NM_024804	NP_079080	Q96BR6	ZN669_HUMAN	2H2-type 6.	0	GTAACGAAGGG	0.408
+	1	784		NM_001004698	NP_001004698	A6NFC9	OR2W5_HUMAN		3	CTGAAGCCGGC	0.517
+	3	423	zb.1_Missense_M	NM_001001957	NP_001001957	Q7Z3T1	OR2W3_HUMAN	lasmic (Potential).	3	GGCTGGACCCC	0.592
+	1	124	L13_uc001ids.2_I	NM_001004686	NP_001004686	Q8NH16	OR2L2_HUMAN	cellular (Potential).	3	TCAACTGATTTC	0.328
+	1	519		NM_001004689	NP_001004689	Q8NG83	OR2M3_HUMAN	cellular (Potential).	2	TCGGGAAATAGC	0.423
-	1	785		NM_001004695	NP_001004695	Q8NG76	O2T33_HUMAN	cellular (Potential).	2	CTATGGGATTTG	0.478
-	1	166		NM_001004695	NP_001004695	Q8NG76	O2T33_HUMAN	Name=2; (Potential).	2	CATGGGCGTGT	0.522
-	1	136		NM_001004734	NP_001004734	A6ND48	O14I1_HUMAN	Name=1; (Potential).	0	TGATGACTGCAA	0.507
+	12	1266	PBP4_uc010qad.1	NM_012341	NP_036473	Q9BZE4	NOG1_HUMAN		2	AGGAACGAGAT	0.388

-	6	750	.V165_splice|AKR	NM_205845	NP_995317	P52895	AK1C2_HUMAN			0	CCACCTGCAGA	0.373	
+	15	4299	1iik.2_Missense_	NM_017782	NP_060252	Q5VWN6	CJ018_HUMAN			2	CATTTCGTCAG	0.438	
-	2	365	_p.G69E|IL2RA_	NM_000417	NP_000408	P01589	IL2RA_HUMAN	xtracellular (Potential).		2	AGTTTCCTGTA	0.463	
+	4	394		NM_002216	NP_002207	P19823	ITIH2_HUMAN	VIT.		3	AAGTCCAGTCT	0.413	
+	6	662	qbc.1_Missense_	NM_001001973	NP_001001973	P36542	ATPG_HUMAN			0	TCATCTCCTATAA	0.299	
-	44	6813		NM_001081	NP_001072	O60494	CUBN_HUMAN	CUB 16.		19	CCGGTGGAGCC	0.458	
+	5	1208	se_Mutation_p.R1	NM_032812	NP_116201	Q6UX71	PXDC2_HUMAN	ellular (Potential).		4	TACATCGAATG	0.333	
-	4	617		NM_213569	NP_998734	O76041	NEBL_HUMAN			2	AAATCTCTTTTG	0.488	
+	21	5758	6N|KIAA1217_uc0	NM_019590	NP_062536	Q5T5P2	SKT_HUMAN			7	AAGAAATCTGG	0.507	
-	10	2925	ense_Mutation_p.	NM_020824	NP_065875	Q5T5U3	RHG21_HUMAN			8	TGCTAGGGCTA	0.393	
+	3	2284	UR_uc001ish.1_I	NM_024838	NP_079114	Q8IYQ7	THNS1_HUMAN			1	AGATAGGGTGC	0.418	
+	16	2118	q.2_Missense_Mu	NM_001134366	NP_001127838	Q05329	DCE2_HUMAN			2	TGATGGAGTAT	0.502	
-	1	317_318		NM_001034842	NP_001030014	Q3KNS1	PTHD3_HUMAN			4	CAGGGGTGCA	0.703	
-	19	3079	qdt.1_Missense_	NM_018076	NP_060546	Q5T2S8	ARMC4_HUMAN	ARM 10.		6	TTATCGGCGTCT	0.468	
+	10	1179_1180	e_Mutation_p.P21	NM_024688	NP_078964	Q9H943	CJ068_HUMAN			3	CGTTTCCTTTAG	0.322	
+	5	869	33A_uc010qev.1_	NM_006974	NP_008905	Q06730	ZN33A_HUMAN			3	AAAAGGCAGTA	0.383	
-	5	2139	NF33B_uc001jag.	NM_006955	NP_008886	Q06732	ZN33B_HUMAN	2H2-type 13.		0	TTCACACAGAAA	0.393	
-	11	1408	1jao.1_Missense_	NM_145313	NP_660356	Q8N9B8	RGF1A_HUMAN	Ras-GEF.		0	GGCGCCGTGA	0.567	
-	9	1041	1jao.1_Missense_	NM_145313	NP_660356	Q8N9B8	RGF1A_HUMAN	Ras-GEF.		0	AGGTTCATGCC	0.607	
-	5	901_902	T15_uc001jeb.2_	NM_031912	NP_114118	Q9BQS2	SYT15_HUMAN	lasmic (Potential).		0	CAAGGGGAAGA	0.604	
-	17	2334	_p.D711N|FRMPD	NM_001018071	NP_001018081	Q68DX3	FRPD2_HUMAN			1	AGAGTCCCAGG	0.577	
-	6	757		NM_001080520	NP_001073989	A6NNA5	DRGX_HUMAN			0	TCTTTTCCTGGC	0.672	
+	1	1416	_5'Flank|CHAT_uc	NM_003055	NP_003046	Q16572	VACHT_HUMAN	ical; (Potential).		2	AGTGGGAGATG	0.657	
+	3	278	.1_3'UTR|C10orf5	NM_001042427	NP_001035892	Q8N6V4	CJ053_HUMAN			0	CCTAGGAGGCG	0.438	
+	1	475		NM_001077665	NP_001071133	Q5VW22	AGAP6_HUMAN		p.P26L(1)	1	TGTGTCCCTCTG	0.597	rs148430930
-	2	200	os.2_Missense_M	NM_019893	NP_063946	Q9NR71	ASAH2_HUMAN	enal (Potential).		0	CTGTGGAGCGT	0.507	
-	1	929	KG1_uc001jjn.2_I	NM_015235	NP_056050	Q9H0L4	CSTFT_HUMAN	Gly-rich.		1	GCCAACCCCTG	0.592	
-	27	3967	e_Mutation_p.G1	NM_033056	NP_149045	Q96QU1	PCD15_HUMAN	|Extracellular (Potential).		13	TCTTTTCCCTCT	0.368	
-	18	2368	_p.Q720K|ANK3_	NM_020987	NP_066267	Q12955	ANK3_HUMAN			19	TGTCTGGGCGT	0.498	
+	10	2161		NM_032199	NP_115575	Q14865	ARI5B_HUMAN			4	TGGCTCCCCAC	0.537	
+	2	1062	jmx.3_Intron|CTN	NM_178011	NP_821079	Q86VH5	LRRT3_HUMAN	lar (Potential).|LRR 5.		3	GAGAACCATCC	0.488	
-	7	1129	_p.R336C|CTNNA	NM_001127384	NP_001120856	Q9UI47	CTNA3_HUMAN	Potential.	p.R336C(1)	8	CTGGCGAATGG	0.512	
+	10	1997	p.2_Missense_Mu	NM_170744	NP_734465	Q8IZJ1	UNC5B_HUMAN	lasmic (Potential).		3	CCCGGGACACC	0.687	
+	7	883	ense_Mutation_p.	NM_138357	NP_612366	Q8NE86	MCU_HUMAN	rial matrix (Potential).		0	TTTTAGGAATATG	0.328	
-	18	3886	p.S378F|USP54_	NM_152586	NP_689799	Q70EL1	UBP54_HUMAN			6	TATGGGAATCA	0.473	
-	12	2202	G5_uc009xru.1_R	NM_004747	NP_004738	Q8TDM6	DLG5_HUMAN	PDZ 2.		8	CCAGGGACTTC	0.607	
-	8	1022	1P_uc001kbf.2_I	NM_003019	NP_003010	P35247	SFTPD_HUMAN	-type lectin.		1	TGTGGGGTAGG	0.567	
-	5	788		NM_000429	NP_000420	Q00266	METK1_HUMAN			0	AGTCAGGCCGC	0.552	
+	3	371	kce.3_Missense_	NM_032333	NP_115709	Q9BRX8	CJ058_HUMAN			0	TATGGGAAAAA	0.483	
-	6	1427	_p.E77K|MMRN2_	NM_024756	NP_079032	Q9H8L6	MMRN2_HUMAN	Potential.		1	CTCCTCCACCT	0.587	
+	5	561	F1_uc009xua.1_	NM_003972	NP_003963	O14981	BTAF1_HUMAN			3	TTGGCCTTAAT	0.373	
-	29	3143	e_Mutation_p.S99	NM_013451	NP_038479	Q9NZM1	MYOF_HUMAN	lasmic (Potential).		4	CCCAGGATTTG	0.478	
+	6	867	iq.3_Missense_M	NM_001127182	NP_001120654	Q53EZ4	CEP55_HUMAN	tion with TSG101.		0	GTTATCTTCAA	0.328	
+	8	1623	I1_uc001kjd.3_Int	NM_005097	NP_005088	O95970	LGI1_HUMAN	EAR 5.		4	AACATGGAGGA	0.423	
-	1	1509_1510		NR_002319						0	GCCACCCATATG	0.515	
-	12	1599	p.G296E|TCTN3_	NM_015631	NP_056446	Q6NUS6	TECT3_HUMAN	ellular (Potential).		0	GCCTTCCATGA	0.488	
-	15	2202		NM_012465	NP_036597	Q9Y6L7	TLL2_HUMAN	CUB 3.		3	GAAGGGAGATC	0.517	

-	15	2141		NM_012465	NP_036597	Q9Y6L7	TLL2_HUMAN	CUB 3.		3	GATACTCCTTCG	0.527	
+	3	2251	nse_Mutation_p.Q7	NM_021830	NP_068602	Q96RR1	PEO1_HUMAN	SF4 helicase.		1	CACGAGCAGCTG	0.498	
+	6	1553		NM_030912	NP_112174	Q9BZR9	TRIM8_HUMAN			1	GTTCTTCCGTGG	0.647	
+	10	1206	BP2_uc010qrz.1_F	NM_004132	NP_004123	Q14520	HABP2_HUMAN	Peptidase S1.		3	TAAAAACCAGAC	0.303	
+	5	1158	se_Mutation_p.H2	NM_207303	NP_997186	Q5VV63	ATRN1_HUMAN	cellular (Potential).		7	CCAGATCACGGT	0.403	
+	20	3630_3631	se_Mutation_p.G2	NM_207303	NP_997186	Q5VV63	ATRN1_HUMAN	e 2.|Extracellular (Potential		7	CTAAAGGAATAA	0.322	
+	11	1417		NM_001011709	NP_001011709	Q17RR3	LIPR3_HUMAN	PLAT.		1	TGATAAATACATC	0.308	
+	4	5563	se_Mutation_p.V1	NM_206862	NP_996744	O95359	TACC2_HUMAN			10	TCTCCGTTGTG	0.602	
+	52	6662	185_splice|DMBT1	NM_007329	NP_015568	Q9UGM3	DMBT1_HUMAN			7	CTCCTAGGCAGA	0.522	
-	8	1756	p.G194E|CUZD1_	NM_022034	NP_071317	Q86UP6	CUZD1_HUMAN	llular (Potential).|ZP.		2	TAGTGTCCAAATA	0.363	
-	4	1649	_p.H379L|CHST15	NM_015892	NP_056976	Q7LFX5	CHSTF_HUMAN	enal (Potential).		1	AGGCGTGGATG	0.527	
-	1	709	_p.E66K|CHST15	NM_015892	NP_056976	Q7LFX5	CHSTF_HUMAN	lasmic (Potential).		1	AGTTTTCGTTCC	0.463	
+	3	354	CP2_uc001lmh.1_Intron|ZNF511_uc001lmj.1_Missense			Q8NB15	ZN511_HUMAN	C2H2-type 2.		0	TTTGCTCCTTTTG	0.617	
+	16	983	uq.3_Nonsense_M	NM_006757	NP_006748	P45378	TNNT3_HUMAN			1	GCGCTGGAAGTA	0.647	
-	20	3005	p.N999S|TRPM5_	NM_014555	NP_055370	Q9NZQ8	TRPM5_HUMAN	lasmic (Potential).		4	ATCAGGTTGTAG	0.642	
-	6	1908	5_uc010qxr.1_Mis	NM_001130520	NP_001123992	O14628	ZN195_HUMAN			0	TTGTAGGGTTTCT	0.398	
-	7	975		NM_003141	NP_003132	P19474	RO52_HUMAN	B30.2/SPRY.		4	GATGTGGACTG	0.532	
+	1	919_920		NM_001005172	NP_001005172	Q8NGK3	O52K2_HUMAN	lasmic (Potential).		2	TCTTGGGAGTAT	0.485	
+	2	665		NM_152430	NP_689643	Q8TCB6	O51E1_HUMAN	cellular (Potential).		4	GCCGCTCCAATAT	0.537	rs148260821
+	2	797		NM_152430	NP_689643	Q8TCB6	O51E1_HUMAN	Name=5; (Potential).		4	TCATCTCCTTCT	0.498	
-	2	909		NM_030774	NP_110401	Q9H255	O51E2_HUMAN	lasmic (Potential).		5	ACCGTTCGTATT	0.488	
-	2	554		NM_030774	NP_110401	Q9H255	O51E2_HUMAN	Name=3; (Potential).		5	GGGCATGAATAA	0.517	
-	1	1163		NM_001005177	NP_001005177	Q8NGF1	O52R1_HUMAN	lasmic (Potential).		1	CAACATCCTTGG	0.448	
+	1	406		NM_001004753	NP_001004753	Q8NH61	O51F2_HUMAN	lasmic (Potential).		2	TTTGATCGTTTTG	0.463	
+	1	478		NM_001001916	NP_001001916	Q8NH60	O52J3_HUMAN	Name=4; (Potential).		3	ACACTTCCCATG	0.468	
-	2	649	BG2_uc001maj.1_	NM_000559	NP_000550	P69892	HBG2_HUMAN		p.S71F(1)	1	CCAAGGAAGTC	0.532	rs151258456
-	1	778	.1_Intron|HBE1_u	NM_001005567	NP_001005567	Q9H339	O51B5_HUMAN	cellular (Potential).		1	ACGATGAATCA	0.428	
-	1	758	.1_Intron|TRIM22_	NM_001001913	NP_001001913	Q8NH53	O52N1_HUMAN	Name=6; (Potential).		1	ACATAGGTGAGG	0.443	
-	1	685		NM_001004052	NP_001004052	Q96RD2	O52B2_HUMAN	lasmic (Potential).		0	GCAAACGAAACA	0.478	
-	1	25		NM_001004490	NP_001004490	A6NM03	O2AG2_HUMAN	cellular (Potential).		4	GCTTCCCAAGG	0.438	
+	8	2899		NM_176822	NP_789792	Q86W24	NAL14_HUMAN	LRR 5.		8	ATGGTGGAGTAA	0.413	
+	9	3096		NM_176822	NP_789792	Q86W24	NAL14_HUMAN			8	GTCTTTCGGCAT	0.428	
-	18	2326	gf.2_Missense_M	NM_001418	NP_001409	P78344	IF4G2_HUMAN	MI.		2	CAAAGGATGT	0.428	
-	8	643	rcu.1_Missense_	NM_175058	NP_778228	Q6IQ23	PKHA7_HUMAN	PH.		3	CAAGGGGATGC	0.537	
-	5	759	cy.1_Missense_M	NM_000352	NP_000343	Q09428	ABCC8_HUMAN	smic (By similarity).		1	CAGGTCTTGCAG	0.567	
-	2	699		NM_054030	NP_473371	Q96LB1	MRGX2_HUMAN	Name=5; (Potential).		1	GCAGGGCCAGA	0.532	
+	16	4397	on_p.V409M|NAV2	NM_145117	NP_660093	Q8IVL1	NAV2_HUMAN			6	AATTCGGTGGTC	0.527	
+	16	1740	s.1_Missense_Mu	NM_031418	NP_113606	Q9BYT9	ANO3_HUMAN	lasmic (Potential).		4	CACGGGAAAAC	0.398	
-	6	825	_p.E189K|ELF5_u	NM_198381	NP_938195	Q9UKW6	ELF5_HUMAN	ETS.		1	CTTGTTCCCTATC	0.428	
+	9	1219_1220	R5L_uc009ykk.2_	NM_001160167	NP_001153639	Q6MZQ0	PRR5L_HUMAN			1	GGAGGGGGAAG	0.629	
+	9	1326	R5L_uc009ykk.2_	NM_001160167	NP_001153639	Q6MZQ0	PRR5L_HUMAN			1	GCCTGGGGGAG	0.662	
+	2	1109	G1_uc001mwt.2_F	NM_000448	NP_000439	P15918	RAG1_HUMAN	RING-type.		5	TATTGTCCCTCTT	0.498	
+	8	898	18_uc001myg.2_Ir	NM_130783	NP_570139	Q96SJ8	TSN18_HUMAN	lasmic (Potential).		0	CCGGGGCATCC	0.597	
+	8	1667		NM_020229	NP_064614	Q9NQV5	PRD11_HUMAN			1	CTGAGCCCCCCG	0.522	
-	2	376	13_uc009yku.1_5'	NM_020826	NP_065877	Q7L8C5	SYT13_HUMAN	lasmic (Potential).		1	TGGGTCCATAGA	0.532	
+	10	1417	e_Mutation_p.A43	NM_152312	NP_689525	Q8N3Y3	LARG2_HUMAN	enal (Potential).		3	CTTGTGGCCCAG	0.637	
+	9	1764	n.1_Missense_Mu	NM_003682	NP_003673	Q8WXG6	MADD_HUMAN	dDENN.		11	TTTCAAGCTGGC	0.557	

-	18	2705	BL2_uc001ngf.2_F	NM_024783	NP_079059	Q5U5Z8	CBPC2_HUMAN		2	ACCTGGAGCTG	0.458	
-	10	1739	se_Mutation_p.E5	NM_024783	NP_079059	Q5U5Z8	CBPC2_HUMAN		2	TTCTTCAAGAA	0.383	
+	3	491	go.3_Missense_M	NM_002843	NP_002834	Q12913	PTPRJ_HUMAN	ellular (Potential).	8	CTGACCCTTCA	0.423	
+	1	520		NM_001004726	NP_001004726	Q8NH49	OR4X1_HUMAN	ellular (Potential).	3	TGGACCACTAC	0.567	
-	1	358		NM_001005272	NP_001005272	Q8NH83	OR4A5_HUMAN	lasmic (Potential).	3	ATAGCGATCAC	0.468	rs141762692
-	1	844		NM_001004700	NP_001004700	Q6IEV9	OR4CB_HUMAN	Name=7; (Potential).	1	GAGTGGATTGA	0.413	
+	1	656		NM_001004735	NP_001004735	Q8NGL3	OR5DE_HUMAN	Name=5; (Potential).	3	TCACTTCCTATG	0.478	
+	1	823		NM_001001921	NP_001001921	Q8N127	O5AS1_HUMAN	Name=7; (Potential).	5	TGGTGGCAGTG	0.383	
+	1	545		NM_001005200	NP_001005200	Q8N162	OR8H2_HUMAN	ellular (Potential).	2	ACACTTCCCCAA	0.398	
+	1	586		NM_001005200	NP_001005200	Q8N162	OR8H2_HUMAN	ellular (Potential).	2	ACACCGAAATC	0.388	
-	1	767		NM_001005199	NP_001005199	Q8NGG4	OR8H1_HUMAN	Name=6; (Potential).	3	TAAGTAAAAATC	0.358	
+	1	797		NM_001005202	NP_001005202	Q8NH51	OR8K3_HUMAN	ellular (Potential).	4	TCATTCCTTTG	0.423	
+	1	364		NM_001004730	NP_001004730	Q8NGP9	O5AR1_HUMAN	lasmic (Potential).	0	TATGGTCGTTTT	0.512	
+	1	898		NM_001004458	NP_001004458	Q8NH92	OR1S1_HUMAN	Name=7; (Potential).	1	ATAAACCCCTTC	0.453	
-	5	515	mq.2_Missense_	NM_145016	NP_659453	Q8WU03	GLYL2_HUMAN		2	GGTTTTCATGTA	0.388	
-	2	778		NM_000738	NP_000729	P11229	ACM1_HUMAN	lasmic (Potential).	0	TCACGGAGAAG	0.632	
+	9	1764	2A9_uc001nwx.2_	NM_080866	NP_543142	Q8IVM8	S22A9_HUMAN	ical; (Potential).	3	TGCCCTGGATCA	0.502	
+	2	1075		NM_006779	NP_006770	O14613	BORG1_HUMAN		0	AGATCCCCACA	0.657	
+	16	1991		NM_006842	NP_006833	Q13435	SF3B2_HUMAN		3	AAATCCCTGGG	0.498	
-	16	3206_3207		NM_006946	NP_008877	O15020	SPTN2_HUMAN	Spectrin 7.	4	AGCCGGTCTG	0.688	
-	2	313		NM_005995	NP_005986	O75333	TBX10_HUMAN	T-box.	0	TCCTCCCACAG	0.642	
-	13	1707_1708	e_Mutation_p.P51	NM_001876	NP_001867	P50416	CPT1A_HUMAN	lasmic (Potential).	2	GGTACGGAATGT	0.495	rs146533704
+	1	284_285		NM_005553	NP_005544	P26371	KRA59_HUMAN		0	TGGAGGCTGT	0.639	
-	3	477	uq.1_Missense_M	NM_003355	NP_003346	P55851	UCP2_HUMAN	Solcar 1.	0	CAGAGGAAAGG	0.542	
-	10	1584		NM_173582	NP_775853	Q6PCE3	PGM2L_HUMAN		1	AAAAAGGACTT	0.323	
-	6	1172		NM_001039548	NP_001034637	Q6PF15	KLH35_HUMAN	Kelch 6.	0	CCCGCCCGCCA	0.597	
+	1	470_471	.2_Intron|CAPN5_	NM_006189	NP_006180	P47874	OMP_HUMAN		0	GGCCTCCGTGG	0.604	rs2233550
+	32	4557	se_Mutation_p.E1	NM_000260	NP_000251	Q13402	MYO7A_HUMAN	FERM 1.	4	CGCTGGAGAAG	0.592	
-	14	1892	ak.2_Missense_M	NM_001364	NP_001355	Q15700	DLG2_HUMAN		6	GCAGGGATCCG	0.473	
-	3	1252	m.2_Missense_Mu	NM_001143831	NP_001137303	P41594	GRM5_HUMAN	ellular (Potential).	9	GGTTTCGGTGG	0.458	
+	1	699		NM_001008781	NP_001008781	Q8TDW7	FAT3_HUMAN	|Extracellular (Potential).	5	GGTATGATCTG	0.388	
+	1	1525		NM_001008781	NP_001008781	Q8TDW7	FAT3_HUMAN	|Extracellular (Potential).	5	AGGAGAAAATG	0.388	
+	15	10153		NM_001008781	NP_001008781	Q8TDW7	FAT3_HUMAN	(Potential).|Cadherin 31.	5	ATTTTTCCATTGT	0.408	
+	4	467	N5_uc001pfz.2_M	NM_014361	NP_055176	O94779	CNTN5_HUMAN		8	CATCTTCATCTC	0.398	
+	5	777	KIAA1377_uc010r	NM_020802	NP_065853	Q9P2H0	K1377_HUMAN		4	TTCACAGAGCTA	0.318	
+	6	2075	run.1_Missense_	NM_020802	NP_065853	Q9P2H0	K1377_HUMAN		4	GTTTGGAAATC	0.294	
-	4	679	1_uc010ruv.1_Mis	NM_002421	NP_002412	P03956	MMP1_HUMAN	etalloprotease.	4	GATTTCCTCCA	0.438	
-	2	326		NM_002427	NP_002418	P45452	MMP13_HUMAN	switch (By s p.D100N(1)	3	CACATCAGGAA	0.408	rs148152034
+	26	4091	e_Mutation_p.P13	NM_001080463	NP_001073932	Q8NCM8	DYHC2_HUMAN	n (By similarity).	0	ATTCTCCTTATT	0.338	
-	7	1453	hp.2_Missense_M	NM_025208	NP_079484	Q9GZP0	PDGFD_HUMAN		2	TACAATCACATC	0.458	rs146343067
-	6	4283	z.1_Missense_Mu	NM_015065	NP_055880	Q8NEV8	EXPH5_HUMAN		5	GTTTCACTTTGC	0.348	
+	2	348	.1_5'Flank|HSPB2	NM_001541	NP_001532	Q16082	HSPB2_HUMAN		3	TACCCCAGACG	0.657	
+	3	434	se_Mutation_p.P13	NM_207343	NP_997226	Q8ND24	RN214_HUMAN		0	CCATCCAGTCA	0.542	
-	32	5563		NM_020693	NP_065744	Q8TD84	DSCL1_HUMAN	lasmic (Potential).	8	TTCCTTCCTTTG	0.597	
+	8	1012	e_Mutation_p.L21	NM_019894	NP_063947	Q9NRS4	TMPS4_HUMAN	(Potential).|Peptidase S1.	2	GGGTCCTCACG	0.612	
+	7	3865	1281L|MLL_uc001	NM_005933	NP_005924	Q03164	MLL1_HUMAN		25	TGGGCCTGAAT	0.582	
+	7	1215	.2_Missense_Mut	NM_015157	NP_055972	Q86UU1	PHLB1_HUMAN		0	CTGCCCGTTCC	0.637	

+	7	1737	462S|PHLDB1_uc	NM_015157	NP_055972	Q86UU1	PHLB1_HUMAN		0	TTAAGTCCATCT	0.652	
+	8	2200		NM_005422	NP_005413	O75443	TECTA_HUMAN	VWFD 2.	10	CCTCCGAGTTC	0.617	
+	9	2429		NM_005422	NP_005413	O75443	TECTA_HUMAN	VWFD 2.	10	TTTATCGAAACA	0.433	
+	45	6148	_p.S869L|SORL1_	NM_003105	NP_003096	Q92673	SORL_HUMAN	tential).|Fibronectin type-III	15	AGTTTCATTATC	0.249	
-	9	1972	yp.2_Missense_M	NM_006597	NP_006588	P11142	HSP7C_HUMAN		8	AGAGGGAGGAG	0.512	
+	10	1374	D1B_uc010rzx.1_	NM_020716	NP_065767	Q3KR37	GRM1B_HUMAN		1	ACATCCCCACT	0.498	
-	1	899		NM_001005188	NP_001005188	Q8NH79	OR6X1_HUMAN	lasmic (Potential).	3	CCTTTCTTAAG	0.388	
+	1	47		NM_001001965	NP_001001965	Q8NGN0	OR4D5_HUMAN	ellular (Potential).	1	ACTGGGGCTCT	0.418	
+	1	86		NM_001001965	NP_001001965	Q8NGN0	OR4D5_HUMAN	Name=1; (Potential).	1	TCTTCACTGTTTT	0.458	
+	3	237	_p.L10F|VWA5A_	NM_001130142	NP_001123614	O00534	VMA5A_HUMAN	VIT.	2	TCACCCTCCAC	0.448	
+	18	2427	zt.2_Missense_M	NM_001130142	NP_001123614	O00534	VMA5A_HUMAN		2	GTAAGGACTTG	0.562	
-	1	10		NM_001002917	NP_001002917	Q8WZ84	OR8D1_HUMAN	ellular (Potential).	3	AATTTTCCATGG	0.413	
+	5	481_482		NM_017425	NP_059121	Q15506	SP17_HUMAN	IQ.	0	GAAGAGGTTGCT	0.391	
+	13	1404	0sav.1_Missense_	NM_001145290	NP_001138762	Q8TED4	SPX2_HUMAN		2	GCCAGGACGGG	0.622	
+	7	1601	_p.P324S|NTM_u	NM_016522	NP_057606	Q9P121	NTRI_HUMAN		6	CAGGTCCAGGC	0.597	
-	1	122		NM_174927	NP_777587	Q7Z5L4	SPT19_HUMAN		0	AACTGGTTATT	0.433	
-	11	1543	on_p.G334R|SLC	NM_003044	NP_003035	P48065	S6A12_HUMAN	Name=7; (Potential).	1	AAACCCAGCCA	0.502	
+	5	1465_1466	1_Intron|LRTM2_u	NM_001039029	NP_001034118	Q8N967	LRTM2_HUMAN	xtracellular (Potential).	1	TGTAGGGGGAC	0.589	
+	8	1447	A1C_uc001qkn.2	NM_199460	NP_955630	Q13936	CAC1C_HUMAN	cellular (Potential).	11	GGAAGGGACTG	0.517	
+	2	210_211	ee.1_Missense_	NR_027363					0	AAAGCCCCGCT	0.559	
+	4	290	_p.L159F|DYRK4_	NM_003845	NP_003836	Q9NR20	DYRK4_HUMAN		3	CTAAAGCTTTTT	0.517	
+	1	1383		NM_002235	NP_002226	P17658	KCNA6_HUMAN		3	GGCCGGCCAGG	0.617	
+	1	615	k.3_Missense_Mu	NM_002527	NP_002518	P20783	NTF3_HUMAN		1	TGGGGGAGATC	0.522	
-	21	2228		NM_020373	NP_065106	Q9NQ90	ANO2_HUMAN	ellular (Potential).	7	GTTTCGAATGG	0.453	
+	2	1235	_uc001qqx.1_Intr	NM_019858	NP_062832	Q16538	GP162_HUMAN	lasmic (Potential).	3	CCTTGGGTACC	0.687	
-	10	1525		NM_001733	NP_001724	P00736	C1R_HUMAN	eptidase S1.	0	GGGCCCCGCCC	0.627	
-	5	788	quh.2_Missense_	NM_018088	NP_060558	Q86YD7	F90A1_HUMAN		1	TCCCTTCCTTTT	0.552	
-	26	3205	.2_Missense_Mut	NM_002864	NP_002855				5	AGGATCGAGCC	0.488	
-	1	566		NM_023919	NP_076408	Q9NYW3	TA2R7_HUMAN	ellular (Potential).	1	AACTCCAAGTT	0.423	
-	4	943	B4_uc001qzf.1_In	NM_006249	NP_006240	Q04118	PRB3_HUMAN	Pro-rich.	1	GGGGAGGTCTG	0.537	
-	3	285	_p.Q83P|PRB1_u	NM_005039	NP_005030	P04280	PRP1_HUMAN	-P-[PAQ]-Q-[GE]-[GD]- [N	0	CCCCTTGTGGG	0.622	
+	2	1056	raz.2_Missense_M	NM_003979	NP_003970	Q8NFJ5	RAI3_HUMAN	Name=4; (Potential).	0	TTCTGGGTCTG	0.517	
-	13	4359		NM_000834	NP_000825	Q13224	NMDE2_HUMAN	lasmic (Potential).	12	CTGGTCGTCCC	0.612	
-	8	1856		NM_000834	NP_000825	Q13224	NMDE2_HUMAN	ical; (Potential).	12	ATCACCCATAC	0.463	
-	5	793	_p.S49F|SLCO1A	NM_021094	NP_066580	P46721	SO1A2_HUMAN	Name=4; (Potential).	4	TATAGGAAATAC	0.343	
-	10	2696	rjj.1_Missense_M	NM_001002259	NP_001002259	Q6IMN6	CAPR2_HUMAN		2	CGTTGGAATTG	0.388	
-	4	1127_1128		NM_001004329	NP_001004329	Q6ZNG2	DBX2_HUMAN		0	GGCACCTTGCA	0.47	rs149681179
-	7	689	_p.T144I|SLC38A	NM_030674	NP_109599	Q9H2H9	S38A1_HUMAN	lasmic (Potential).	5	CTGTGGTGCCA	0.383	
+	4	753	AM113B_uc001rp	NM_138371	NP_612380	Q96HM7	F113B_HUMAN		5	CCTCCGAAGTG	0.587	
+	4	1128	p.P13S|FAM113B	NM_138371	NP_612380	Q96HM7	F113B_HUMAN		5	TATGGTCCGAAC	0.592	
-	14	1752	p.P387A|RPAP3_	NM_024604	NP_078880	Q9H6T3	RPAP3_HUMAN		1	TGCAGGAATTG	0.403	
-	23	2742	_Missense_Mutat	NM_001098532	NP_001092002	A8K2G5	A8K2G5_HUMAN		4	GACAGGAGGGG	0.413	
-	54	4613	A1_uc009zkw.2_	NM_001844	NP_001835	P02458	CO2A1_HUMAN	lar collagen NC1.	2	CACACCGAATT	0.517	
-	6	1270	p.P355S|ZNF641_	NM_152320	NP_689533	Q96N77	ZN641_HUMAN		2	CTTTGGCACTG	0.592	
-	5	1970	Y6_uc001rsi.3_Mi	NM_015270	NP_056085	O43306	ADCY6_HUMAN	lasmic (Potential).	0	CCTCCGGCAGC	0.552	
-	48	15620		NM_003482	NP_003473	O14686	MLL2_HUMAN	R N-terminal.	41	CCACGGGATAG	0.607	
-	21	5117		NM_003482	NP_003473	O14686	MLL2_HUMAN		41	TGTGGGATTTC	0.637	

+	8	1669	ATS2_uc001ruf.2_	NM_023071	NP_075559	Q86XZ4	SPAS2_HUMAN		1	ATGTTCCCCTCG	0.428	
-	8	1713	NCKAP5L_uc001r	NM_001037806	NP_001032895	Q9HCH0	NCK5L_HUMAN	Pro-rich.	1	GACCCCTTCGG	0.682	
-	3	606		NM_030809	NP_110436	Q9H175	CSRN2_HUMAN		0	AGCTCCGTACA	0.537	
+	10	1380	4A8_uc001ryp.1_	NM_001039960	NP_001035049	Q2Y0W8	S4A8_HUMAN	cellular (Potential).	5	GAGAGTGGGATC	0.493	
+	18	2518	ryo.2_Nonsense_	NM_001039960	NP_001035049	Q2Y0W8	S4A8_HUMAN	ical; (Potential).	5	CCCTGGTGGAC	0.398	
-	2	633		NM_005555	NP_005546	P04259	K2C6B_HUMAN	Coil 1A.|Rod.	2	CAGGGTCCACTT	0.542	
-	1	74		NM_005555	NP_005546	P04259	K2C6B_HUMAN	Head.	2	GGCTCCTGATG	0.632	
-	1	476		NM_015848	NP_056932	Q01546	K22O_HUMAN	Head.	2	caggaccaccaaagct	0.249	
-	4	818		NM_173352	NP_775487	Q8N1N4	K2C78_HUMAN	Coil 1B.|Rod.	2	TCACTTCTTCATT	0.547	
+	8	926	AT2_uc009zms.2_	NM_003578	NP_003569	O75908	SOAT2_HUMAN	ical; (Potential).	1	CCAACACTCATC	0.493	
+	29	3251	p.E600K|NCKAP1	NM_005337	NP_005328	P55160	NCKPL_HUMAN		4	CTCAAGGAATTT	0.418	
-	1	184		NM_001005499	NP_001005499	A6NIJ9	O6C70_HUMAN	lasmic (Potential).	1	AATTACGGAGGA	0.403	
-	7	1002	ion_p.R199H|ARH	NM_032496	NP_115885	Q9BRR9	RHG09_HUMAN		1	GACAGCGGCGA	0.652	rs139154961
+	7	826	sy.1_Missense_Mu	NM_007199	NP_009130	Q9Y616	IRAK3_HUMAN	rotein kinase.	8	ATTTATCCATACA	0.383	
+	3	670	sts.3_Missense_M	NM_006482	NP_006473	Q92630	DYRK2_HUMAN		4	ATCCAGGTTCAA	0.488	rs138020482
+	1	140		NM_000239	NP_000230	P61626	LYSC_HUMAN		0	CCAGAACTCTG	0.468	
+	2	817		NM_014505	NP_055320	Q86W47	KCMB4_HUMAN	cellular (Potential).	0	AGAGAGAAAT	0.328	
-	14	1439	xi.3_Missense_Mu	NM_032606	NP_115995	Q9BXY5	CAYP2_HUMAN		2	TCATCCTCCTGT	0.333	
-	7	992		NM_004950	NP_004941	Q99645	EPYC_HUMAN	LRR 6.	1	TTAATAGGGTTT	0.393	
-	3	235	2_5'Flank|CLLU1_	NM_001025232	NP_001020403	Q5K130	CLU1O_HUMAN		0	GTCACATTTCCTT	0.438	
-	17	3801	1tgp.2_Missense_	NM_015054	NP_055869	A0JNW5	UH1BL_HUMAN		2	ACAACGGACATC	0.338	
+	26	2741	p.P886L|KIAA103	NM_015275	NP_056090	Q2M389	WAHS7_HUMAN		2	AGTATCCTTTTG	0.373	
-	10	2289	se_Mutation_p.H2	NM_012406	NP_036538	Q9UKN5	PRDM4_HUMAN	C2H2-type 2.	2	ACTTGTGGGGCT	0.473	
+	4	1355	mt.2_Missense_M	NM_014653	NP_055468	Q2TBF2	WSCD2_HUMAN	WSC 1.	3	GCGAGGCAGCG	0.692	
-	2	968	M119_uc001tnf.2_	NM_181724	NP_859075	Q4V9L6	TM119_HUMAN	lasmic (Potential).	1	GGGGGGACCCA	0.667	
+	18	1877		NM_001101421	NP_001094891	Q8N1T3	MYO1H_HUMAN		0	CCGAAGGAAAT	0.443	
+	10	1454	p.K380R|CCDC6	NM_152591	NP_689804	Q8NA47	CCD63_HUMAN	Potential.	8	TCAAGAAGATAA	0.502	
+	16	2095		NM_015267	NP_056082	O14529	CUX2_HUMAN		6	GCTCAGACGAC	0.622	
-	16	2186_2187	orf51_uc001tts.2_	NM_001109662	NP_001103132				2	TTAAGGAAGGG	0.396	
+	2	338_339	tux.2_Missense_M	NM_017901	NP_060371	Q9ULQ1	TPC1_HUMAN	lasmic (Potential).	3	CCTGACCTTGGA	0.569	
-	20	3727		NM_000620	NP_000611	P29475	NOS1_HUMAN	-binding FR-type.	7	TCCTACCTGGATT	0.522	
-	2	1188		NM_000620	NP_000611	P29475	NOS1_HUMAN	arity).|PIN (nNOS-inhibiting	7	CAGCCTCCTGCC	0.682	
-	30	3784	T_uc001txj.1_Miss	NM_007174	NP_009105	O14578	CTRO_HUMAN	teraction with Rho/Rac.	10	TCTTTCCGTCGA	0.493	
+	7	1042	D2_uc001udy.1_M	NM_024623	NP_078899	Q6N063	OGFD2_HUMAN		1	AGGAGCCCGCC	0.657	
-	3	363	_p.S75F|PITPNM	NM_020845	NP_065896	Q9BZ72	PITM2_HUMAN		3	GGATGGAGCGG	0.622	
+	7	903	ya.2_Nonsense_M	NM_024809	NP_079085	Q96GX1	TECT2_HUMAN	cellular (Potential).	1	CCAAACAGGAC	0.323	
+	43	7252		NM_207437	NP_997320	Q8IVF4	DYH10_HUMAN		6	CCCATGGAGTAA	0.408	
-	3	1335		NM_133448	NP_597705	Q14C87	T132D_HUMAN	cellular (Potential).	14	TGGCTCGCACG	0.547	rs147819967
+	18	2451	o.2_Intron|GPR13	NM_198827	NP_942122	Q6QNK2	GP133_HUMAN	cellular (Potential).	10	GACCCCCTGCC	0.582	
+	5	761	NF268_uc010tcb.1	NM_003415	NP_003406	Q14587	ZN268_HUMAN	KRAB.	1	GCAGGCCCAAG	0.403	
-	9	1010	dc.1_Missense_Mu	NM_006437	NP_006428	Q9UKK3	PARP4_HUMAN	P alpha-helical.	4	TAGAAGGAGAAT	0.383	
-	1	1359	p.G301E|FAM123	NM_152704	NP_689917	Q8N7J2	F123A_HUMAN		4	CGCCTCCTTGG	0.637	
+	1	1368		NM_001033602	NP_001028774	Q5JR59	MTUS2_HUMAN		0	GGACATCCAGCA	0.507	
+	17	1910	ba.2_Missense_M	NM_130806	NP_570718	Q8WXD0	RXFP2_HUMAN	Name=5; (Potential).	0	TATGTTCTGTTC	0.393	rs139736966
+	61	9385	se_Mutation_p.Y4	NM_023037	NP_075463	Q5TBA9	FRY_HUMAN		7	TACTTATGCCCT	0.522	
+	1	4322		NM_207361	NP_997244	Q5SZK8	FREM2_HUMAN	ar (Potential).|CSPG 9.	11	ACAAATCTTTGG	0.343	
-	10	1233_1234	uyk.2_Missense_	NM_015058	NP_055873	A3KMH1	K0564_HUMAN		6	GCTTGGGACAC	0.366	

+	6	1062	p.Y127H|CYSLTR	NM_020377	NP_065110	Q9NS75	CLTR2_HUMAN	Name=3; (Potential).	2	AGTATTTATTTCC	0.483
-	11	2821_2822	p.H889Y|ATP7B_	NM_000053	NP_000044	P35670	ATP7B_HUMAN	lasmic (Potential).	3	CACGTGGGTAG	0.441
+	5	748	M4_uc001vhk.1_I	NM_006418	NP_006409	Q6UX06	OLFM4_HUMAN	actomedin-like.	1	ATGGTGGTGTG	0.423
-	6	1858	.1_Intron|DACH1_	NM_080759	NP_542937	Q9UI36	DACH1_HUMAN		1	ACCTACGGATTC	0.488
-	15	2292	e_Mutation_p.H61	NM_014953	NP_055768	Q9Y2L1	RRP44_HUMAN		1	CATGTGGAATC	0.318
-	1	1775		NM_052910	NP_443142	Q96PX8	SLIK1_HUMAN	cellular (Potential).	5	CATGATCCTCTT	0.557
-	2	2890	afe.1_Missense_	NM_032229	NP_115605	Q9H5Y7	SLIK6_HUMAN	lasmic (Potential).	3	CTAATACCTTCCT	0.403
+	2	2528	tic.1_Missense_M	NM_015567	NP_056382	O94991	SLIK5_HUMAN	lasmic (Potential).	5	AGAGGGCAACT	0.493
+	3	1004		NM_004466	NP_004457	P78333	GPC5_HUMAN		5	AATGGGACAGA	0.517
-	12	1744	p.R467Q|ABCC4_	NM_005845	NP_005836	O15439	MRP4_HUMAN	C transporter 1.	4	TTTACCCGTGCT	0.493
-	8	1768	nl.2_Missense_M	NM_198968	NP_945319	Q86YF9	DZIP1_HUMAN	Potential.	2	CATCTCCTTGA	0.308
+	13	1113	CA_uc010tiz.1_M	NM_000282	NP_000273	P05165	PCCA_HUMAN	.|Biotin carboxylation.	2	AGCATCCTGTC	0.433
-	39	3489	4A1_uc010agl.2_	NM_001845	NP_001836	P02462	CO4A1_HUMAN	le-helical region.	6	TCCTGGGAGGC	0.498
+	8	782	gr.1_Missense_Mu	NM_003891	NP_003882	P22891	PROZ_HUMAN	eptidase S1.	0	CGGGGGAGAAT	0.567
+	13	2343		NM_017905	NP_060375	Q6UWJ1	TMCO3_HUMAN		0	GTGGAGAGCTG	0.597
+	1	343		NM_001005483	NP_001005483	Q8NGD3	OR4K5_HUMAN	Name=3; (Potential).	2	GTGCTACTTGTT	0.438
+	1	650		NM_001004063	NP_001004063	Q8NGD4	OR4K1_HUMAN	Name=5; (Potential).	3	TTATTTCCTACAC	0.433
+	1	395		NM_001004479	NP_001004479	Q8NGC9	O11H4_HUMAN	lasmic (Potential).	1	TGATCGATACCT	0.468
-	8	966	_p.S241F|HNRN	NM_031314	NP_112604	P07910	HNRPC_HUMAN	Glu-rich (acidic).	0	TCACGGAGCTG	0.488
-	2	213	010tlx.1_Missense	NM_019852	NP_062826	Q86U44	MTA70_HUMAN		2	CAATGCTGCCT	0.468
-	1	238		NM_001005465	NP_001005465	Q8NGC4	O10G3_HUMAN	cellular (Potential).	2	GCGAGGGACAA	0.498
+	6	1225		NM_004995	NP_004986	P50281	MMP14_HUMAN	1.|Extracellular (Potential)	0	TCCGAGGGGAG	0.433
-	6	2591_2592	c010akt.2_5'Flank|	NM_032452	NP_115828	Q96JJ6	JPH4_HUMAN	lasmic (Potential).	2	CTGGGGCCCTC	0.673
+	2	558		NM_203402	NP_981947	A5D6W6	FITM1_HUMAN	cellular (Potential).	0	GCTTCGAGCCA	0.692
+	10	1416	n_p.S345N|GMPR	NM_001002001	NP_001002001	Q9P2T1	GMPR2_HUMAN		3	CTTCAGTGAGG	0.552
+	2	473	RS1_uc001woj.1_	NM_174913	NP_777573	Q86U38	CN021_HUMAN		4	TGTGGCCTGTC	0.488
-	5	749	e_Mutation_p.R21	NM_004131	NP_004122	P10144	GRAB_HUMAN	eptidase S1.	0	AGGCTCGTGGA	0.498
+	3	4102	se_Mutation_p.T1	NM_001173	NP_001025226	Q13017	RHG05_HUMAN	Rho-GAP.	5	AGATACAGGTA	0.353
+	13	4483		NM_004274	NP_004265	Q13023	AKAP6_HUMAN		21	TAAATGGAAAAG	0.368
-	37	6179	LGAPA1_uc010tp	NM_014990	NP_055805	Q6GYQ0	RGPA1_HUMAN	to TCF3/E12 (By similarity	4	AATAAGGACATC	0.343
+	5	3308	a.2_Missense_M	NM_152447	NP_689660	Q96NI6	LRFN5_HUMAN	lasmic (Potential).	8	TTGCTGACTAAT	0.294
+	7	3420	e_Mutation_p.H10	NM_015091	NP_055906	Q9Y4F4	F179B_HUMAN	Ser-rich.	3	ATTTCTCATATTG	0.299
-	1	168		NM_080746	NP_542784	Q96L21	RL10L_HUMAN		1	ATCAGGAACCC	0.542
-	2	945		NM_021136	NP_066959	Q16799	RTN1_HUMAN		4	TCCCTCCACAG	0.448
-	11	2152	H5_uc001xfy.2_3'	NM_139318	NP_647479	Q8NCM2	KCNH5_HUMAN	lasmic (Potential).	9	CACGGGAATGC	0.532
-	4	362	xfz.1_Missense_	NM_139318	NP_647479	Q8NCM2	KCNH5_HUMAN	toplasmic (Potential).	9	AAACAGGGGTT	0.443
+	30	4263	gl.2_Missense_Mu	NM_015180	NP_055995	Q8WXH0	SYNE2_HUMAN	lasmic (Potential).	14	CAGACCTTTCA	0.443
-	3	1123	TB25_uc001xhg.2	NM_006977	NP_008908	P24278	ZBT25_HUMAN		2	ACCCCGGTTGG	0.453
-	15	2980	s.2_Missense_Mu	NM_000347	NP_000338	P11277	SPTB1_HUMAN	Spectrin 7.	11	CCACTACCTTTG	0.612
-	2	2510	e_Mutation_p.E58	NM_183002	NP_892114	P57103	NAC3_HUMAN	|Cytoplasmic (Potential).	7	CCAACTCCCCAT	0.502
-	2	327	2BP_uc010arc.2_	NM_018373	NP_060843	P57105	SYJ2B_HUMAN	toplasmic (Potential).	0	CTCACCGAAAGG	0.542
+	12	1603	N1_uc010ark.2_	NM_000021	NP_000012	P49768	PSN1_HUMAN	with CTNNB1.|Helical; (P	2	CCATCACCTTTG	0.398
-	31	4871		NM_000428	NP_000419	Q14767	LTBP2_HUMAN	alcium-binding (Potential).	2	AGAGACCAGGC	0.473
+	5	2507	M1_uc001xql.3_	NM_019589	NP_062535	P49750	YLPM1_HUMAN		3	CCAAGACCCAG	0.512
-	4	885	se_Mutation_p.E1	NM_199296	NP_954993	Q6H9L7	ISM2_HUMAN		1	tcctcgtcttcctcctttcc	0.284
+	2	2169	td.2_Missense_M	NM_013231	NP_037363	O43155	FLRT2_HUMAN	-III.|Extracellular (Potential	4	TTCAGGAGCGC	0.493
-	18	3259		NM_001080414	NP_001073883	Q9P219	DAPLE_HUMAN	Potential.	3	CACTCGGAGAA	0.622

-	10	1552	N5_uc010aue.2_M	NM_006329	NP_006320	Q9UBX5	FBLN5_HUMAN		6	GGAACGGAGCGT	0.542	
+	7	864	_p.G134R|UBR7_	NM_175748	NP_786924	Q8N806	UBR7_HUMAN		0	GATGATGGATTG	0.393	
-	11	3225	vo.1_Missense_M	NM_001002860	NP_001002860	Q9P203	BTBD7_HUMAN		1	CGAAGGGGAAG	0.493	
+	45	7110	bs.1_Nonsense_	NM_020818	NP_065869	Q9P2D8	UNC79_HUMAN		17	CAAAATCAGAAT	0.493	
-	5	1490	ense_Mutation_p.G	NM_000295	NP_000286	P01009	A1AT_HUMAN		1	ACTTTTCCCATG	0.498	
-	3	862	ydg.2_Missense_	NM_175739	NP_783866	Q86WD7	SPA9_HUMAN		2	GGTGAAAGGGC	0.428	
+	4	1113	ense_Mutation_p.G	NM_001085	NP_001076	P01011	AACT_HUMAN		6	TGTCAGGGATCA	0.507	
+	2	784		NR_015340					2	GGCCTGGGAGAA	0.577	
-	24	5116	p.P1635L|DICER1_	NM_030621	NP_085124	Q9UPY3	DICER_HUMAN		5	CTTGGTGGAATC	0.393	
+	3	741	ense_Mutation_p.W	NM_000623	NP_000614	P30411	BKRB2_HUMAN	Name=4; (Potential).	5	TGATCTGGGGGT	0.607	
+	11	1199	twv.1_Missense_M	NM_032632	NP_116021	P51003	PAPOA_HUMAN		0	ATGTGTCCGTTT	0.408	
-	12	1757		NM_006035	NP_006026	Q9Y5S2	MRCKB_HUMAN	Potential.	11	GCTGTCGCTCGA	0.522	
-	3164								0	CAGCAGGAGGG	0.592	
-	4	423	IIPA1_uc001yve.2_	NM_144599	NP_653200	Q7RTP0	NIPA1_HUMAN	ical; (Potential).	0	CGACGGAGCCT	0.473	
+	1	2276		NM_018958	NP_061831	Q9NZP6	CO002_HUMAN		8	CTCTCCCAAATT	0.468	
-	1	479	89A1_uc010azk.1_	NM_138704	NP_619649	Q96MG7	MAGG1_HUMAN	MAGE.	0	AGGTCGGGGAAG	0.532	
-	21	3722	.2_Missense_Mut	NM_003257	NP_003248	Q07157	ZO1_HUMAN		6	GGACGCGATCTT	0.483	rs35392254
-	9	1199	lissense_Mutation_	NM_139320	NP_647536	Q494W8	CRFM7_HUMAN	ical; (Potential).	1	GATGATCATGGT	0.622	
-	29	3597		NM_014691	NP_055506	O60306	AQR_HUMAN		1	GCTCTGGCTCTC	0.413	
+	20	3485	bi.2_Nonsense_M	NM_003246	NP_003237	P07996	TSP1_HUMAN	SP C-terminal.	6	AGGCTGGAAAGA	0.468	
+	3	1626	bp.1_Missense_M	NM_014952	NP_055767	Q8TBE0	BAHD1_HUMAN		0	CCCGTCCCCCAT	0.657	
+	3	1420		NM_152260	NP_689473	Q8IZ73	RUSD2_HUMAN		1	CCTCAGGAGTTG	0.562	
+	10	1188	e_Mutation_p.T29	NM_001128608	NP_001122080	O60336	MABP1_HUMAN	WD 4.	10	ATGGCACCGTGC	0.592	
-	2	349	uc010bcp.1_RNA	NM_016642	NP_057726	Q9NRC6	SPTN5_HUMAN	Actin-binding.	2	CCGTCTCGTACT	0.622	
-	15	1668		NM_178034	NP_828848	Q86XP0	PA24D_HUMAN		2	CCCTCACCTTCC	0.627	
-	2	1254	n|ZFP106_uc010u	NM_022473	NP_071918	Q9H2Y7	ZF106_HUMAN		3	CTGAAGGAAATT	0.418	
-	2	904	zpx.2_Intron|ZFP1	NM_022473	NP_071918	Q9H2Y7	ZF106_HUMAN		3	ACTGCTCCACTAT	0.473	
-	10	1272	qp.2_Missense_M	NM_173500	NP_775771	Q6IQ55	TTBK2_HUMAN	rotein kinase.	7	AACACGGATGTA	0.378	
-	12	2078	_p.Q649*|TP53BP	NM_005657	NP_005648	Q12888	TP53B_HUMAN		7	CCTCCTGATCTA	0.478	
+	3	282		NM_152448	NP_689661	Q8NHR7	CO043_HUMAN		0	ATTCTTCCTCCTG	0.413	
+	15	1928	e_Mutation_p.E528	NM_017434	NP_059130	Q9NRD9	DUOX1_HUMAN	roxidase activity.|Extracellu	8	AAGAAGGAGATT	0.527	
+	3	211		NM_004212	NP_004203	O43868	S28A2_HUMAN		4	GGGATGGACTGG	0.522	
-	11	1275	_p.S133F|HDC_uc	NM_002112	NP_002103	P19113	DCHS_HUMAN		6	ACCAGAGATTCA	0.418	
-	15	2332	pfi.1_Missense_M	NM_182758	NP_877435	Q3MJ13	WDR72_HUMAN		2	TGCCATCATTTTC	0.408	
+	31	6508	acm.2_Missense_	NM_001080534	NP_001074003	Q8NB66	UN13C_HUMAN		7	TGGTATCCTCTT	0.398	
-	7	948_949		NM_004998	NP_004989	Q12965	MYO1E_HUMAN	osin head-like.	3	CAGAAGGAAGTT	0.441	
-	31	5882		NM_003922	NP_003913	Q15751	HERC1_HUMAN		19	CTCTGCGAAGAA	0.403	
-	10	1281_1282	PX_uc010uiu.1_R	NM_006660	NP_006651	O76031	CLPX_HUMAN		0	TCCACGGAGCTT	0.361	
-	9	2163		NM_003613	NP_003604	O75339	CILP1_HUMAN		7	TCCACAGAGAAC	0.522	
-	22	4148	p.P1300L|DENND	NM_005848	NP_005839	Q7Z401	MYCPP_HUMAN		4	GGCTTAGGAGAA	0.418	
-	10	1295_1296	p.W310*|MEGF11_	NM_032445	NP_115821	A6BM72	MEG11_HUMAN		1	CCAGACCAGCCT	0.584	
+	16	1644	aqw.2_Missense_	NM_145160	NP_660143	Q13163	MP2K5_HUMAN	rotein kinase.	2	CAGGGGAGCAG	0.433	
+	5	705	C49_uc010ukf.1_	NM_017691	NP_060161	Q8IUZ0	LRC49_HUMAN	LRR 2.	1	GGCTTTCGACTC	0.343	
-	4	547	_p.A33T|CIB2_uc	NM_006383	NP_006374	O75838	CIB2_HUMAN	EF-hand 1.	0	ACGCCGCCACGA	0.547	
-	8	1090	umx.1_Missense_	NM_015162	NP_055977	Q96GR2	ACBG1_HUMAN		1	TGGGCCCCCCAC	0.622	
+	12	1711	unn.1_Missense_	NM_018689	NP_061159	Q8WUJ3	K1199_HUMAN		3	TAGACGGCGTGG	0.552	
-	3	348	orf40_uc010uop.1_	NM_001160115	NP_001153587	Q8WUR7	CO040_HUMAN		1	AGATACCGACAG	0.388	

+	7	744	upe.1_Missense_	NM_004213	NP_004204	O00337	S28A1_HUMAN	ical; (Potential).	3	GGTGTCCTTCG	0.582
+	7	1468	p.P433L|AKAP13_	NM_007200	NP_009131	Q12802	AKP13_HUMAN		9	AATGCCCACAG	0.522
-	2	1465		NM_022480	NP_071925	Q9H0H3	ENC2_HUMAN	Kelch 3.	2	TGTTGGCCCCA	0.587
-	2	1138	k.2_RNA|DET1_u	NM_001144074	NP_001137546	Q7L5Y6	DET1_HUMAN		2	TTCGCAGCTGC	0.488
+	12	4846	e_Mutation_p.P14	NM_013227	NP_037359	E7EX88	E7EX88_HUMAN		3	GCTTCCTTCTG	0.507
+	2	191		NM_198526	NP_940928	Q8N1W2	ZN710_HUMAN		1	GGCCGCCGTGC	0.637
+	4	352		NM_001013657	NP_001013679	Q6ZNW5	VTC2_HUMAN		0	AATCTCCCTTTG	0.557
+	16	1951		NM_003870	NP_003861	P46940	IQGA1_HUMAN		8	AGACACCCAAG	0.423
+	5	997	2brb.2_Splice_Site	NM_006011	NP_006002	Q92186	SIA8B_HUMAN		0	CGCGGGTGAGC	0.547
-	2	537	174B_uc002bsl.3_	NM_207446	NP_997329	Q3ZCQ3	F174B_HUMAN	lasmic (Potential).	0	CTGCTGGAGTG	0.473
+	3	425	_5'Flank|uc002bu	NM_173499	NP_775770	Q6RVD6	SPAT8_HUMAN		2	TCACGGAAGGA	0.458
-	16	2326		NM_139057	NP_620688	Q8TE56	ATS17_HUMAN	Spacer.	3	TTCTCCCACAG	0.552
-	3	392	S1_uc002bwh.2_	NM_001040614	NP_001035704	Q8NG48	LINES_HUMAN		0	CTGCTGGGTTG	0.433
-	3	566	M8A_uc002cgv.3_	NM_021259	NP_067082	Q9HCN3	TMM8A_HUMAN	ellular (Potential).	3	GGTGGGAAACG	0.687
+	8	758	va.1_Missense_Mu	NM_003933	NP_003924	O94812	BAIP3_HUMAN	C2 1.	1	TGGACCCCTGC	0.672
+	6	422_423		NM_032520	NP_115909	Q9UJJ9	GNPTG_HUMAN		1	CCTGCCGTTCC	0.683
+	7	1142	|MRPS34_uc002c	NM_001010865	NP_001010865	A4GXA9	EME2_HUMAN		3	CTTCCCCTCCC	0.692
-	2	654_655		NM_001009606	NP_001009606	C9JH64	C9JH64_HUMAN		0	ACGCTCCCCGC	0.663
-	5	736	rz.1_Missense_M	NM_022119	NP_071402	Q9GZN4	BSSP4_HUMAN	eptidase S1.	1	CATGTCCTCAG	0.642
-	2	394		NM_021195	NP_067018	P56747	CLD6_HUMAN	lasmic (Potential).	0	TGGAATCCTTCT	0.612
-	5	1898	ctw.1_Missense_	NM_032805	NP_116194	Q96SZ4	ZSC10_HUMAN		1	CTTCTCCCCTG	0.716
-	10	2126		NM_000243	NP_000234	O15553	MEFV_HUMAN	B30.2/SPRY.	6	CATTTTCCTTCAT	0.537
-	7	2479	C3_uc010bto.1_5'	NM_178844	NP_849172	Q7RTR2	NLRC3_HUMAN		6	CAAGAGGGATC	0.502
-	13	2500_2501	vw.2_Missense_	NM_004380	NP_004371	Q92793	CBP_HUMAN		127	GGAAGGAGAA	0.55
-	8	877	e_Mutation_p.P20	NM_144605	NP_653206	Q8IYM1	SEP12_HUMAN		1	AAAAGGGATTC	0.587
-	22	4303		NM_002705	NP_002696	O60437	PEPL_HUMAN	Potential.	6	TAGCTCCTCCA	0.706
-	13	3694	uyn.1_Missense_	NM_001134407	NP_001127879	Q12879	NMDE1_HUMAN	lasmic (Potential).	45	TACCTAGGGCTC	0.507
-	9	2538	uyn.1_Missense_	NM_001134407	NP_001127879	Q12879	NMDE1_HUMAN	ellular (Potential).	45	GAGGCCGGTCA	0.502
+	11	2093	g.2_Missense_Mu	NM_000246	NP_000237	P33076	C2TA_HUMAN	NACHT.	1	GCCCCCCCGGG	0.682
+	8	1262	C4_uc010uyz.1_5	NM_005236	NP_005227	Q92889	XPF_HUMAN		10	ATGTTCCCAGC	0.428
-	5	1241		NM_001012991	NP_001013009	Q1ED39	CP088_HUMAN	th ZFP106 (By similarity).	0	TGTCAGCCGCC	0.627
-	6	1001		NM_174924	NP_777584	Q8N807	PDILT_HUMAN		1	TGTATTCGATCA	0.443
+	4	545_546	nse_Mutation_p.L	NM_001010845	NP_001010845	Q08AH3	ACS2A_HUMAN		3	TGTGGCCTGCA	0.579
-	4	516_517	_p.L103V|ACSM2	NM_182617	NP_872423	Q68CK6	ACS2B_HUMAN		5	CTGCAGGCCAC	0.569
-	8	1248	SM1_uc010bwg.1	NM_052956	NP_443188	Q08AH1	ACSM1_HUMAN		2	GGGTGGAGTGG	0.537
-	2	432	SM1_uc010bwg.1	NM_052956	NP_443188	Q08AH1	ACSM1_HUMAN		2	CTCAGGAACTC	0.587
+	6	356	_uc010vbj.1_Mis	NM_144672	NP_653273	Q7RTW8	OTOAN_HUMAN		3	AGTTCCGCACT	0.587
+	29	3225	Splice_Site_p.L12	NM_173615	NP_775886	A6NCI4	VWA3A_HUMAN		1	TGCTGGCAAGT	0.517
+	32	3593	se_Mutation_p.S	NM_173615	NP_775886	A6NCI4	VWA3A_HUMAN		1	CCCAATCCTTCA	0.577
+	8	1282	2K_uc002dkh.2_	NM_013302	NP_037434	O00418	EF2K_HUMAN	type protein kinase.	1	GCGTTCCGGCC	0.572
+	15	2763	e_Mutation_p.P57	NM_006910	NP_008841	Q7Z6E9	RBBP6_HUMAN		4	cttcctctccctccgggt	0.308
-	7	1213	_p.L224F|XPO6_u	NM_015171	NP_055986	Q96QU8	XPO6_HUMAN		2	ATCAAGGATGG	0.483
+	4	527	_uc002dsc.2_Miss	NM_014387	NP_055202	O43561	LAT_HUMAN	lasmic (Potential).	0	TTGCCCCCTGG	0.612
+	6	971	.P248L|KIF22_uc	NM_007317	NP_015556	Q14807	KIF22_HUMAN		0	CCTCCCTCGTG	0.582
+	10	1217_1218	tation_p.264_265	NM_002209	NP_002200	P20701	ITAL_HUMAN	Extracellular (Potential).	10	AACATGGAGCTG	0.569
-	8	749	fd.1_Missense_Mu	NM_052874	NP_443106	P61266	STX1B_HUMAN	omology.|Cytoplasmic (Pot	0	CATATCGTGCA	0.562
+	5	543	_p.Q105*|STX4_u	NM_004604	NP_004595	Q12846	STX4_HUMAN	ic (Potential).|Potential.	0	AGCCCCAGAAG	0.418

-	3	2020	ao.2_Missense_M	NM_024706	NP_078982	Q96K58	ZN668_HUMAN	2H2-type 15.	4	CCGGTCAGAGA	0.652	
-	15	2569	fg.1_Missense_M	NM_173502	NP_775773	Q5K4E3	POLS2_HUMAN		1	ATCCCGAGGCC	0.642	
+	14	1524	_p.R276*|FUS_uc	NM_004960	NP_004951	P35637	FUS_HUMAN	Arg/Gly-rich.	958	TATGATCGAGGC	0.612	
+	13	1434	_p.S456F|ITGAX_	NM_000887	NP_000878	P20702	ITAX_HUMAN	Extracellular (Potential).	4	CGGCTCCTACT	0.677	
+	18	2252	bt.2_Missense_M	NM_000887	NP_000878	P20702	ITAX_HUMAN	ellular (Potential).	4	TGACCCCCATT	0.627	
-	20	3057	C12_uc002efa.1_	NM_033226	NP_150229	Q96J65	MRP9_HUMAN	smembrane type-1 2.	3	CAGTGGGAGTC	0.478	
+	7	1047	efx.2_Missense_M	NM_182922	NP_891552	Q7Z4Q2	HEAT3_HUMAN		2	CAAATGAAAGA	0.368	
-	4	530	p.G142E|CES1_u	NM_001025194	NP_001020365	P23141	EST1_HUMAN		0	CCCCTCCGTGG	0.562	
-	2	329	_p.W75*|CES1_u	NM_001025194	NP_001020365	P23141	EST1_HUMAN		0	AGCTCCATGGT	0.537	
-	14	2002		NM_031885	NP_114091	Q9BXC9	BBS2_HUMAN		1	CTCAAAATAGA	0.368	
+	6	747	p.G199E|CPNE2_	NM_152727	NP_689940	Q96FN4	CPNE2_HUMAN	C2 2.	2	CTTTGGGAAGT	0.612	
-	10	1006		NM_001896	NP_001887	P19784	CSK22_HUMAN	rotein kinase.	1	GTTCTCACTATG	0.443	
+	2	232	on.1_Missense_M	NM_001795	NP_001786	P33151	CADH5_HUMAN		6	CAGCAGCAGGT	0.612	
+	4	509	_uc002eqj.2_Miss	NM_005182	NP_005173	P43166	CAH7_HUMAN		0	CTTTTGGGGAG	0.582	
-	8	1191		NM_013304	NP_037436	Q8WTX9	ZDHC1_HUMAN		0	GCTCCCTGTGA	0.632	
+	4	846		NM_000196	NP_000187	P80365	DHI2_HUMAN		0	TCATGGACACA	0.502	
-	1	372	ex.2_Missense_M	NM_022357	NP_071752	Q9H4B8	DPEP3_HUMAN		3	TGAGGCCTGGG	0.711	
-	77	13320	DIN_uc010cfy.2_	NM_032821	NP_116210	Q4G0P3	HYDIN_HUMAN		2	TGAGAGCCCAT	0.438	
-	3	276	nse_Mutation_p.E	NM_032821	NP_116210	Q4G0P3	HYDIN_HUMAN		2	GAACTCTGAGG	0.403	
-	16	2743	_p.R363Q|ADAMT	NM_199355	NP_955387	Q8TE60	ATS18_HUMAN	Spacer.	18	TGCTTCGGGCG	0.502	
+	7	1049		NM_020927	NP_065978	Q9HCJ6	VAT1L_HUMAN		1	TTTTCCCTTTTA	0.507	
+	4	684	_p.E156K|BCMO1	NM_017429	NP_059125	Q9HAY6	BCDO1_HUMAN		0	CCCTGGAGAAG	0.507	
+	25	2856		NM_002661	NP_002652	P16885	PLCG2_HUMAN		8	TTTCAGAGCATC	0.582	
-	23	3651	fhh.2_Missense_	NM_003791	NP_003782	Q14703	MBTP1_HUMAN	asic).|Cytoplasmic (Potent	2	CCGAAGGGGTC	0.627	
-	5	1178		NM_003791	NP_003782	Q14703	MBTP1_HUMAN	ase.|Lumenal (Potential).	2	GTGGGGATGCT	0.453	
+	8	1540	sense_Mutation_p.	NM_001145400	NP_001138872	Q8NCV1	ADAD2_HUMAN	to I editase.	0	CCTTCCGAACCC	0.697	
+	8	720	fhy.2_Missense_M	NM_014861	NP_055676	O75185	AT2C2_HUMAN	lasmic (Potential).	2	TCACGGACCTC	0.532	
+	4	618	_p.P78S|KIAA018	NM_014615	NP_055430	Q14687	GSE1_HUMAN		5	CCTACCCCTTC	0.667	
-	5	858_859	n_p.P7F|NXN_uc	NM_022463	NP_071908	Q6DKJ4	NXN_HUMAN	Thioredoxin.	4	GTAGGGGACGG	0.639	
-	1	859		NM_003553	NP_003544	P30953	OR1E1_HUMAN	Name=7; (Potential).	0	GAAGGGGTTCA	0.448	
+	15	2490	e_Mutation_p.G7	NM_004703	NP_004694	Q15276	RABE1_HUMAN	Potential.	2	AAAAAGGACAG	0.244	
+	11	1509	ron|ALOX12_uc00	NM_000697	NP_000688	P18054	LOX12_HUMAN	ipoxygenase.	1	AAAGGGATGAC	0.592	
-	12	2127	_p.S707F|NEURL	NM_032442	NP_115818	Q96JN8	NEUL4_HUMAN		2	ACGGAGAGCTT	0.612	
+	3	437	11_uc010vtw.1_In	NM_175734	NP_783861	Q0P670	CQ074_HUMAN	Arg-rich.	0	CTTCTTCGCTGT	0.428	
+	27	3685	p.G758S|PFAS_u	NM_012393	NP_036525	O15067	PUR4_HUMAN	midotransferase type-1.	5	AGATGGGCCCT	0.677	
-	15	1563	vf.1_Missense_M	NM_003802	NP_003793	Q9UKX3	MYH13_HUMAN	osin head-like.	6	TGGTTGAAAAA	0.483	
-	5	548		NM_003802	NP_003793	Q9UKX3	MYH13_HUMAN	osin head-like.	6	TGTGGGGCGGG	0.502	
-	37	5480	uc002gml.1_Intron	NM_005963	NP_005954	P12882	MYH1_HUMAN	Potential.	21	CAGGTCCTTCA	0.562	
-	26	3402	_Missense_Mutat	NM_001100112	NP_001093582	Q9UKX2	MYH2_HUMAN	Potential.	14	TGATTTCAAACT	0.328	
-	21	2551		NM_002470	NP_002461	P11055	MYH3_HUMAN		7	TGCTTGACGTTC	0.473	rs121913620
+	17	3183	oo.2_Missense_M	NM_001372	NP_001363	Q9NYC9	DYH9_HUMAN	n (By similarity).	20	CGGAAGAAATT	0.498	
+	20	4199	o.2_Missense_M	NM_001372	NP_001363	Q9NYC9	DYH9_HUMAN	n (By similarity).	20	CTGCAGAATCC	0.617	
-	7	1488	ow.2_Missense_	NM_006470	NP_006461	O95361	TRI16_HUMAN		3	TTTGCGGATGC	0.453	rs146392947
+	65	10914	uc002gsl.2_3'UTR	NM_016239	NP_057323	Q9UKN7	MYO15_HUMAN	Tail.|FERM.	9	CCAGCGAGATC	0.423	
-	2	282	A10_uc002gut.1_	NM_001039999	NP_001035088	A6ND36	FA83G_HUMAN		2	GGCCACCAGGG	0.637	
+	10	1320	_p.P374L|RNF112_	NM_007148	NP_009079	Q7Z5V9	Q7Z5V9_HUMAN		2	AAGCCCTGGTG	0.642	
-	2	135	e_Mutation_p.G2	NM_001042685	NP_001036150	Q3B8N2	LEG9B_HUMAN	Galectin 1.	1	GAGACCCCCTT	0.582	

+	5	604	crt.2_Missense_M	NM_003170	NP_003161	Q7KZ85	SPT6H_HUMAN	Asp/Glu-rich.	3	AGGAGGAGGAA	0.522	
-	1	283	wdi.1_Missense_M	NM_000458	NP_000449	P35680	HNF1B_HUMAN	ation (By similarity).	3	TGGTGACCCCG	0.637	
+	8	1285	tv.2_Missense_Mu	NM_003250	NP_003241	P10827	THA_HUMAN	gand-binding.	0	GCTACGACCCT	0.632	
-	1	301	39_uc010wfm.1_5	NM_213656	NP_998821	Q6A163	K1C39_HUMAN	Head.	0	CTTCACCATACC	0.498	
-	1	363_364		NM_032524	NP_115913	Q9BYR3	KRA44_HUMAN	-C-[GRQVCH]-[SPT]- [VST	0	CACTGGGGCCT	0.658	
-	2	662	T14_uc010cxp.1_M	NM_000526	NP_000517	P02533	K1C14_HUMAN	Coil 1B.|Rod.	1	GGTGCGGAAGT	0.517	
+	14	2444	_p.G472E|WNK4_	NM_032387	NP_115763	Q96J92	WNK4_HUMAN		7	CTCCTGGAACTC	0.577	rs147081637
+	4	2166	_Mutation_p.P684	NM_009590	NP_033720	O75106	AOC2_HUMAN		2	GAGGACCCCTCC	0.572	
-	7	2233	_p.S163F|PLEKH	NM_014798	NP_055613	Q9Y4G2	PKHM1_HUMAN	PH 2.	0	GCAGGGACTCC	0.552	
+	4	341	iky.2_Missense_M	NM_004287	NP_004278	O14653	GOSR2_HUMAN	ic (Potential).|Potential.	2	AGCATCGGCGC	0.542	
+	15	3368	uc002irv.1_Missens	NM_018896	NP_061496	O43497	CAC1G_HUMAN	lasmic (Potential).	1	ACAAGTCCGAAT	0.597	
+	29	4246	sn.2_Missense_Mu	NM_003786	NP_003777	O15438	MRP3_HUMAN	similarity).|ABC transporter	4	CGGCAGCTACT	0.622	
+	10	1351	vpc.1_Missense_M	NM_173503	NP_775774	Q8N7B9	EFCB3_HUMAN		1	GACTCAGGAAGA	0.338	
-	6	1318	_Mutation_p.M398	NM_001100875	NP_001094345	Q8NA82	MARHA_HUMAN		0	TGGCTCCATTGC	0.478	
+	13	1501	_uc010deu.1_Mis	NM_015462	NP_056277	Q9H8H0	NOL11_HUMAN		0	GAATCAGTCACC	0.358	
-	23	3211	ez.2_Missense_Mu	NM_080283	NP_525022	Q8IUA7	ABCA9_HUMAN		6	TTACTTCGGTAC	0.418	
-	20	2808	ez.2_Nonsense_M	NM_080283	NP_525022	Q8IUA7	ABCA9_HUMAN		6	TTTTCTGATATGA	0.368	
-	2	131	plice_Site|ABCA9_	NM_080283	NP_525022	Q8IUA7	ABCA9_HUMAN		6	TGTTTCCTTTAA	0.373	
+	3	1024	_p.S277F|C17orf	NM_017941	NP_060411	Q9BSJ5	CQ080_HUMAN	ellular (Potential).	1	CAGAATCCCTCA	0.423	
+	1	301	_p.G133R|GPRC5	NM_018653	NP_061123	Q9NQ84	GPC5C_HUMAN	Name=2; (Potential).	5	TGCTGGGGACC	0.622	
-	13	1912	.D431N|SLC38A1	NM_001037984	NP_001033073	Q9HBR0	S38AA_HUMAN		2	TCGGTCTTGGC	0.647	
+	5	877_878	_5'Flank|STRA13_	NM_144999	NP_659436	Q96CN5	LRC45_HUMAN		1	ACATCCCTGGAG	0.653	
-	6	1714		NM_130386	NP_569057	Q5KU26	COL12_HUMAN	2.|Extracellular (Potential).	2	TTAGATCCTTTGC	0.701	
-	2	418		NM_014646	NP_055461	Q92539	LPIN2_HUMAN	N-LIP.	2	CTTTGGATCTCA	0.478	
-	4	1194	_p.A345T|ZFP161_	NM_003409	NP_003400	O43829	ZF161_HUMAN	C2H2-type 3.	1	TGGGGCACGG	0.448	
-	1	1717		NM_001080209	NP_001073678	A6NKL6	T200C_HUMAN		0	GAGTCTCGCGTT	0.677	
+	2	1662	NDC2_uc002koh.	NM_001098529	NP_001091999	Q86VQ3	TXND2_HUMAN	eat of Q-P-K-X-G-D-I-P-K-	2	GACATCCCCAAG	0.552	
-	3	542	519_uc002ksr.1_I	NM_145287	NP_660330	Q8TB69	ZN519_HUMAN		0	GACAGAAACTGA	0.284	
+	36	3448	0xal.1_Missense_	NM_001145029	NP_001138501	Q9BXX2	AN30B_HUMAN	Potential.	2	AAAAAGGAAATT	0.303	
+	57	7547	kus.3_Missense_M	NM_198129	NP_937762	Q16787	LAMA3_HUMAN	minin G-like 1.	11	AGTTATGGATCG	0.493	
-	7	4153	plice_Site_p.Q130	NM_015461	NP_056276	Q96K83	ZN521_HUMAN		7	ACATTACCTGCA	0.438	
-	6	833	_p.P200L|SS18_u	NM_001007559	NP_001007560	Q15532	SSXT_HUMAN	Gln-rich.	1884	CTATAGGGAGGA	0.413	
-	5	1003	z.2_Missense_Mu	NM_001650	NP_001641	P55087	AQP4_HUMAN	lasmic (Potential).	0	ATTGGTCTTTCC	0.478	
-	13	2540	n.1_Missense_Mu	NM_001792	NP_001783	P19022	CADH2_HUMAN	(Potential).|Cadherin 5.	4	AGGATGGAAATA	0.463	
-	11	1866	m.2_Missense_Mu	NM_024421	NP_077739	Q08554	DSC1_HUMAN	(Potential).|Cadherin 4.	4	GATTCTCTATCTA	0.318	
-	3	584	_p.L143F|ZNF24_	NM_006965	NP_008896	P17028	ZNF24_HUMAN		0	ACGGAGAGAAA	0.418	rs148053646
+	4	843		NM_015559	NP_056374	Q9Y6X0	SETBP_HUMAN		3	CTTACGAGAGG	0.408	
-	1	631_632	issense_Mutation_	NM_001039360	NP_001034449	A1YPR0	ZBT7C_HUMAN		1	GAAGTCCCTGG	0.574	
+	2	1191	APK4_uc010doz.	NM_002747	NP_002738	P31152	MK04_HUMAN	rotein kinase.	6	GCTCCGAGAGA	0.602	
+	20	3649	p.R849Q|DCC_uc	NM_005215	NP_005206	P43146	DCC_HUMAN	tential).|Fibronectin type-III	17	CTTTCGAATTCA	0.373	
-	18	2137	.1_RNA|uc002lgv.	NM_005603	NP_005594	O43520	AT8B1_HUMAN	lasmic (Potential).	10	AACTCCATCCT	0.363	
+	2	135	10dpv.2_Missense_	NM_003839	NP_003830	Q9Y6Q6	TNR11_HUMAN	ellular (Potential).	3	CTCCTCCATGT	0.473	
-	6	652	_Mutation_p.S209F|SERPINB3_uc010dqa.2_Intron			P48594	SPB4_HUMAN	p.S209Y(1)	3	TGTATGGACTTG	0.373	
+	7	950	n_p.G136E|SERPI	NM_001143818	NP_001137290	P05120	PAI2_HUMAN		2	CAAAGGAAAGT	0.383	
+	12	2464	b.2_Missense_Mu	NM_033646	NP_387450	Q9ULB5	CADH7_HUMAN	lasmic (Potential).	4	TGGGAAAGATTA	0.438	
-	4	1210	m.3_Missense_Mu	NM_006566	NP_006557	Q15762	CD226_HUMAN	ical; (Potential).	0	CCCTCCAGCCA	0.363	
+	2	502		NM_014913	NP_055728	Q6IQ32	ADNP2_HUMAN		8	GGTGCGAAAAA	0.368	

-	2	234		NM_145173	NP_660156	O95057	DIRA1_HUMAN		1	GAAGCGCAGCA	0.557	
-	3	630		NM_030662	NP_109587	P36507	MP2K2_HUMAN	rotein kinase.	0	CGAGTTGCATT	0.612	
+	18	2192	_p.G610E|ANKRD	NM_133475	NP_597732	Q8TF21	ANR24_HUMAN		0	CATGGGGGTGG	0.557	
+	2	66		NM_018074	NP_060544	Q9BW85	CCD94_HUMAN		0	TACTACCCGCC	0.552	
-	2	284	dtv.1_Missense_M	NM_144615	NP_653216	Q96BF3	TMIG2_HUMAN	lar (Potential).|Ig-like.	0	GCAGACCCCCA	0.657	
+	3	524_525		NM_005483	NP_005474	Q13111	CAF1A_HUMAN	1 chromo shadow domain.	2	CCTCTCCCTCCA	0.5	rs150150583
-	22	3830	w.2_Missense_Mu	NM_002850	NP_002841	Q13332	PTPRS_HUMAN	ellular (Potential).	4	GACGCGAGTGC	0.627	
+	18	2500	_p.P815L|SAFB_	NM_002967	NP_002958	Q15424	SAFB1_HUMAN	SAFB2.|Arg-rich.|Gly-rich.	3	TCCTCCCCCCA	0.701	
-	5	1017	mfj.1_Missense_M	NM_003807	NP_003798	O43557	TNF14_HUMAN	ellular (Potential).	1	TCTCCCCAGCC	0.627	
+	26	2509_2510	a.1_Missense_Mu	NM_005428	NP_005419	P15498	VAV_HUMAN	SH3 2.	16	CTCAAGGAGGG	0.569	
+	18	2335	_p.S747F|EMR1_	NM_001974	NP_001965	Q14246	EMR1_HUMAN	Name=5; (Potential).	5	TCAACTCCCTTC	0.323	
+	8	1194	_p.T244S|ZNF557_	NM_001044388	NP_001037853	Q8N988	ZN557_HUMAN	2H2-type 4.	2	GGAAAACCTTC	0.453	
+	7	802	S4_uc002mji.2_5'	NM_024552	NP_078828	Q9HA82	CERS4_HUMAN	TLC.	1	GCTGTGGGCAC	0.572	
-	4	352	n_p.Y80H|MYO1F	NM_012335	NP_036467	O00160	MYO1F_HUMAN	osin head-like.	3	CTCATACTGGG	0.612	
-	61	41292	wj.2_Missense_M	NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	lar (Potential).|SEA 11.	57	CCATCCTTTTC	0.562	
-	21	37694		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	lar (Potential).|SEA 3.	57	TGTTCCTGTCC	0.517	
-	4	31574		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).	57	CAGGCGAAGTG	0.448	
-	3	29368		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	h.|Extracellular (Potential)	57	TGTTTCCACAA	0.488	
-	3	26554		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	h.|Extracellular (Potential)	57	TCATTTCTGCTG	0.507	
-	3	23335		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	h.|Extracellular (Potential)	57	GGGGGGGATAT	0.547	
-	3	19093		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).	57	AGAAGGATGCAT	0.443	
-	3	11488		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	xtracellular (Potential).	57	GAGTTCCTGGG	0.532	
-	1	8251		NM_024690	NP_078966	Q8WXI7	MUC16_HUMAN	h.|Extracell p.E2683K(1)	57	TAGTCTCTGGGA	0.488	
-	1	158		NM_001005192	NP_001005192	Q8NGA0	OR7G1_HUMAN	lasmic (Potential).	2	GGTGGGAGTCA	0.488	
+	1	957		NM_175883	NP_787079	Q96RA2	OR7D2_HUMAN	Name=6; (Potential).	3	GCATTGGGGTC	0.498	
+	1	332		NM_001079935	NP_001073404	Q6IFN5	O7E24_HUMAN	ellular (Potential).	1	TCATCTCCTATG	0.493	
-	10	1276	wr.1_Missense_M	NM_152476	NP_689689	Q96MR9	ZN560_HUMAN	2H2-type 2.	6	TAAAATCTTTTCC	0.393	
-	8	689	dwr.1_Missense_M	NM_152476	NP_689689	Q96MR9	ZN560_HUMAN	KRAB 2.	6	GCCAAGAGATC	0.468	
+	6	933	_Mutation_p.A17	NM_022737	NP_073574	Q96GM1	LPPR2_HUMAN		1	CGTGGCCGCCG	0.701	
-	6	933	mk.1_Missense_M	NM_030824	NP_110451	Q9H7R0	ZN442_HUMAN	KRAB.	4	GTTTTTCATTCA	0.348	
+	1	207	dyz.1_Missense_M	NM_152654	NP_689867	Q8N907	DAND5_HUMAN		1	AGCTTCTGCCC	0.672	
+	3	452	1_uc002mxf.2_In	NM_001031727	NP_001026897	Q9BV20	MTNA_HUMAN		1	CTGCACCGAGG	0.642	
+	3	867_868		NM_173482	NP_775753	Q8IYK2	CC105_HUMAN		1	GTTCTGGAGCAG	0.614	
+	2	133	_Mutation_p.S28	NM_000896	NP_000887	Q08477	CP4F3_HUMAN	ical; (Potential).	3	GGCCTCCTGGC	0.637	
+	8	994_995		NM_023944	NP_076433				7	GGGAAGGCATTG	0.386	
+	1	28		NM_013939	NP_039227	O60403	O10H2_HUMAN	ellular (Potential).	3	GCTGGGGCTAA	0.557	
-	7	901	26_uc002nee.2_I	NM_006387	NP_006378	Q8IWX8	CHERP_HUMAN	CID.	2	TGATGGAGTCA	0.637	
-	22	2901		NM_015692	NP_056507	Q8IZJ3	CPMD8_HUMAN		13	GATTCTCCTCAG	0.562	
-	1	55		NM_138454	NP_612463	Q96CM4	NXNL1_HUMAN	Thioredoxin.	0	ACAGGGAGGCC	0.602	
-	5	454		NM_001080421	NP_001073890	Q9UPW8	UN13A_HUMAN	C2 1.	3	CCACACCTCCA	0.517	
-	8	824	_p.G230E|COMP_	NM_000095	NP_000086	P49747	COMP_HUMAN	EGF-like 4.	0	GGATCCCGTTG	0.706	
-	3	912	e_Mutation_p.P25	NM_014884	NP_055699	Q8IX01	SUGP2_HUMAN		0	CGGTGGGTATTT	0.498	
-	4	1452		NM_021030	NP_066358	P17017	ZNF14_HUMAN	2H2-type 12.	3	GAAGGGAACTT	0.383	
-	4	1562	op.2_Missense_M	NM_033196	NP_149973	O95780	ZN682_HUMAN		2	TGCAGGATTTCT	0.353	
+	3	315	s.1_RNA|ZNF90_	NM_007138	NP_009069	Q03938	ZNF90_HUMAN	KRAB.	2	GCAAGGAAAAA	0.398	
-	4	1600	pc.1_Missense_M	NM_001076675	NP_001070143	Q68DY1	ZN626_HUMAN	ype 12; degenerate.	1	ATTCTTCACATTT	0.388	
-	4	1432	pc.1_Missense_M	NM_001076675	NP_001070143	Q68DY1	ZN626_HUMAN	2H2-type 10.	1	ATTCTTCACATTT	0.388	

-	3	2081		NM_001001411	NP_001001411	Q8N7Q3	ZN676_HUMAN		0	TTTAGGGATTC	0.348	
-	5	1966		NM_001080409	NP_001073878				2	TAAGTTTTGAGG	0.363	
+	4	3694	dd.1_Missense_M	NM_014717	NP_055532	O15090	ZN536_HUMAN		11	AAACCGAACCG	0.567	
-	28	3542		NM_004646	NP_004637	O60500	NPHN_HUMAN	2.|Cytoplasmic (Potential).	5	TACGTTCTTTCT	0.547	
+	8	1431	_Mutation_p.R33	NM_001013659	NP_001013681	Q6ZN11	ZN793_HUMAN	2H2-type 4.	0	TACATCGAAAAA	0.458	
+	5	666	_p.R112C|ZNF540	NM_152606	NP_689819	Q8NDQ6	ZN540_HUMAN		1	CTCTTCGTCTG	0.333	
-	5	2218	hb.1_Missense_M	NM_032689	NP_116078	Q96SK3	ZN607_HUMAN	2H2-type 15.	0	TAAAAGACTTC	0.428	
+	53	8463	_Mutation_p.G277	NM_000540	NP_000531	P21817	RYR1_HUMAN	.|6 X approximate repeats.	12	CCTATGGAGAGA	0.607	
+	73	10827	iv.1_Missense_M	NM_000540	NP_000531	P21817	RYR1_HUMAN		12	AGGCTCCCCGT	0.637	
+	89	12293	p.E4050K|RYR1_	NM_000540	NP_000531	P21817	RYR1_HUMAN		12	ATGTGGAGATG	0.567	
-	6	3019		NM_003890	NP_003881	Q9Y6R7	FCGBP_HUMAN	VWFD 2.	9	AGTTCCCACAG	0.597	
-	3	444	K4_uc002oos.2_	NM_024876	NP_079152	Q96D53	ADCK4_HUMAN		0	GCCCATCCTGGT	0.602	
-	3	374	ib.1_Missense_M	NM_002088	NP_002079	Q16478	GRIK5_HUMAN	ellular (Potential).	0	ACCTCCTTCTC	0.617	
-	3	736	g.1_Intron|PSG3_	NM_021016	NP_066296	Q16557	PSG3_HUMAN	like C2-type 1.	2	AAAGAGGGTCC	0.507	
-	3	685	_Mutation_p.S74	NM_182707	NP_874366	Q9UQ74	PSG8_HUMAN	like C2-type 1.	0	TTTCAGACAAC	0.522	
-	4	894_895	sense_Mutation_p.	NM_006905	NP_008836	P11464	PSG1_HUMAN	like C2-type 2.	2	ATTCTCCCTGGG	0.49	
-	2	526	tion_p.G130R|PS	NM_006905	NP_008836	P11464	PSG1_HUMAN	g-like V-type.	2	TAGTCCCATCAT	0.502	rs34055642
-	4	804_805	ense_Mutation_p.	NM_002782	NP_002773	Q00889	PSG6_HUMAN	like C2-type 2.	2	TTCTCCCTGGG	0.51	
+	6	2489	226_uc010ejg.2_3	NM_001032373	NP_001027545	Q9NYT6	ZN226_HUMAN		0	ATAAATCCTATAA	0.358	
-	4	884	F285_uc010xxa.1	NM_152354	NP_689567	Q96NJ3	ZN285_HUMAN	ype 2; degenerate.	4	TTCTTTCCATACT	0.433	
-	4	707	F285_uc010xxa.	NM_152354	NP_689567	Q96NJ3	ZN285_HUMAN		4	AGTTGGGATGT	0.468	
-	9	1501	0ejp.1_Missense_	NM_001102597	NP_001096067	Q6UY09	CEA20_HUMAN	lasmic (Potential).	2	TCCTCCTTCGG	0.388	
+	7	1636		NM_001042724	NP_001036189	Q92692	PVRL2_HUMAN	lasmic (Potential).	0	AGCTGGAGGCA	0.577	
+	10	1327		NM_006509	NP_006500	Q01201	RELB_HUMAN	RHD.	1	CTCGCGACCAT	0.552	
+	4	300	RS16_uc002pam.	NM_007056	NP_008987	Q8N2M8	CLASR_HUMAN		0	GGATGCCCTGG	0.587	
+	3	242	eb.2_Missense_M	NM_001135113	NP_001128585	Q6UWQ7	IGFL2_HUMAN		0	TCCCCCCTGCA	0.552	
-	2	950	per.3_Missense_	NM_018215	NP_060685	Q86V59	PNML1_HUMAN		0	TGTTGGGGGTC	0.557	
-	3	1080		NM_000960	NP_000951	P43119	PI2R_HUMAN	lasmic (Potential).	0	GGAAAGGGGTG	0.657	
+	6	4412		NM_004491	NP_004482	Q9NRY4	RHG35_HUMAN	Pro-rich.	1	TCAGCCGTCGC	0.677	
-	8	1059	H4_uc002pgb.1_	NM_015168	NP_055983	Q9UPT8	ZC3H4_HUMAN	Gly-rich.	6	GCCCCGACCCA	0.627	
+	4	474		NM_022142	NP_071425	Q96BH3	ESPB1_HUMAN	nectin type-II 2.	0	TCTTCGATGAG	0.517	
-	5	582		NM_019855	NP_062829	Q9NP86	CABP5_HUMAN	EF-hand 4.	1	AGCCTCCCGGA	0.612	
+	9	2085	2D_uc010elx.2_5	NM_000836	NP_000827	O15399	NMDE4_HUMAN	ical; (Potential).	6	TCTTCGCCGTCA	0.587	
+	2	287_288	pjm.2_Missense_	NM_177973	NP_814444	O00204	ST2B1_HUMAN		1	CTACCCCAAGTC	0.644	
+	3	662	0yaf.1_Missense_	NM_033378	NP_203696				0	AGCCTTCCAAGC	0.642	
-	5	938	_Mutation_p.P235L	NM_014037	NP_054756	Q9GZN6	S6A16_HUMAN	ellular (Potential).	4	ATTCAGGATCTG	0.388	
+	7	814	7_uc002pqp.2_5'U	NM_024682	NP_078958	Q9HA65	TBC17_HUMAN		0	CTACTCCACCA	0.692	
-	3	116	_p.P21L|IL4I1_uc	NM_152899	NP_690863	Q96RQ9	OXLA_HUMAN		3	gaggatggggacgag	0.453	
+	5	2132	_p.S632F|ZNF473_	NM_001006656	NP_001006657	Q8WTR7	ZN473_HUMAN		2	GTGCCTCCCTTA	0.478	
-	7	734		NM_152358	NP_689571	Q6UXV1	IZUM2_HUMAN	lasmic (Potential).	0	AGTTTTCGGTTT	0.403	
-	1	271		NM_152358	NP_689571	Q6UXV1	IZUM2_HUMAN	ellular (Potential).	0	AGGCCCCTCCA	0.677	
+	13	1622	p.W533C|MYH14_	NM_024729	NP_079005	Q7Z406	MYH14_HUMAN	osin head-like.	1	CCCTGGACCTT	0.592	
+	26	3412	.A1163V|MYH14_	NM_024729	NP_079005	Q7Z406	MYH14_HUMAN	Potential.	1	TGGGGCCCGGG	0.652	
+	2	56	e_Mutation_p.G11	NM_003121	NP_003112	Q01892	SPIB_HUMAN	AD1 (Acidic).	2	TCGACGGGCCA	0.647	
-	3	249	o.2_Missense_Mu	NM_017509	NP_059979	Q9H2R5	KLK15_HUMAN	eptidase S1.	2	GCTCTCCCAGG	0.622	
-	2	601		NM_002029	NP_002020	P21462	FPR1_HUMAN	ellular (Potential).	3	GTTTTACCAGGT	0.537	
+	6	1703	ya.1_Missense_M	NM_001031721	NP_001026891	Q6PF04	ZN613_HUMAN		1	AGAAACCCTATG	0.418	

+	4	596	dn.1_Missense_M	NM_018260	NP_060730	Q9NV72	ZN701_HUMAN		0	ACCCCGAAGGG	0.413	
-	5	1222	p.R386C|ZNF347_	NM_032584	NP_115973	Q96SE7	ZN347_HUMAN	2H2-type 5.	0	TGAACGAGCTC	0.413	
+	3	1134	.2_Intron|CACNG	NM_145814	NP_665813	Q9BXT2	CCG6_HUMAN	ical; (Potential).	2	TCTCAGGTGAG	0.577	
-	4	473	j.2_RNA|LILRB2_	NM_005874	NP_005865	Q8N423	LIRB2_HUMAN	otential).|Ig-like C2-type 1.	1	TGTAATCCAAGA	0.527	
+	7	1141	18_splice|LILRA1_	NM_006863	NP_006854	O75019	LIRA1_HUMAN		3	CTCCAGGACAG	0.597	
+	16	2261	RB1_uc002qgm.2_	NM_006669	NP_006660	Q8NHL6	LIRB1_HUMAN	lasmic (Potential).	3	CTGTGCCCAGC	0.652	
-	4	1537_1538	p.E488K|NLRP7_	NM_206828	NP_996611	Q8WX94	NALP7_HUMAN	NACHT.	3	GTCCTCCCCCTC	0.574	
-	2	1151	nse_Mutation_p.A	NM_003180	NP_003171	O00445	SYT5_HUMAN	ical; (Potential).	0	CAGGGCCCAGG	0.602	
-	4	504	TPRH_uc002qjs.2_	NM_002842	NP_002833	Q9HD43	PTPRH_HUMAN	III 2.|Extracellular (Potentia	4	CTGGGCCGTCG	0.597	
-	2	361		NM_176820	NP_789790	Q7RTR0	NALP9_HUMAN		7	TTCTCCCATATG	0.373	
+	5	572	P5_uc002qmi.2_Ir	NM_153447	NP_703148	P59047	NALP5_HUMAN		7	AAATTTCACAAG	0.408	
-	7	4220	.S1261F|PEG3_u	NM_001146186	NP_001139658	Q9GZU2	PEG3_HUMAN	2H2-type 9.	12	CGAAAGATTCT	0.468	
+	4	2057		NM_213598	NP_998763	Q08ER8	ZN543_HUMAN		2	GAAGACCTTTTA	0.418	
+	3	1809	_p.P521L|ZNF304_	NM_020657	NP_065708	Q9HCX3	ZN304_HUMAN		1	AAGGCCTTATG	0.488	
+	3	1043		NM_152677	NP_689890	Q8NAM6	ZSCA4_HUMAN	SCAN box.	1	ACTTGGAGAGA	0.413	
+	5	1853		NM_152677	NP_689890	Q8NAM6	ZSCA4_HUMAN	2H2-type 3.	1	GGTCTCATGAG	0.463	
+	3	359	so.2_Missense_M	NM_001009	NP_001000	P46782	RS5_HUMAN		0	GCATGCCTTCG	0.577	
-	3	359		NM_003310	NP_003301	Q53HC9	TSSC1_HUMAN		0	TTTTATTTATAAT	0.413	
+	6	1095		NM_080657	NP_542388	Q8WXG1	RSAD2_HUMAN		0	GGACCCTTCCA	0.383	
+	6	1072	nse_Mutation_p.R	NM_198182	NP_937825	Q9NZI5	GRHL1_HUMAN		2	AAGTTCGAGTA	0.478	
+	8	1041		NM_001034	NP_001025	P31350	RIR2_HUMAN		0	ACAAACCATCG	0.398	
+	9	797	2rat.2_Nonsense_	NM_001039362	NP_001034451	Q8NEY4	VATC2_HUMAN		1	TGTTTCGAAAA	0.517	
-	14	2280	_p.P613S|PUM2_u	NM_015317	NP_056132	Q8TB72	PUM2_HUMAN	ilio 1.|PUM-HD.	1	AGCTGGAGTAG	0.343	
-	26	8008		NM_000384	NP_000375	P04114	APOB_HUMAN		27	CTGATGGAATC	0.413	
-	26	4512		NM_000384	NP_000375	P04114	APOB_HUMAN		27	TGGTCCCCAGG	0.378	
+	12	1641	hv.3_Missense_M	NM_020134	NP_064519	Q9BPU6	DPYL5_HUMAN		2	TGGGGGATGTC	0.567	
-	4	1069	kj.2_Missense_M	NM_144631	NP_653232	Q8N8E2	ZN513_HUMAN		1	GCTGCCCACAG	0.607	
+	27	1876	c.2_Missense_Mu	NM_153021	NP_694566	Q6P1J6	PLB1_HUMAN	ate repeats.|2.|Extracellular	9	CTGTGGTTGTG	0.473	
+	13	2065	_p.E517K|FAM17	NM_199280	NP_954974	Q6ZUX3	F179A_HUMAN		4	CCGAGGAGATC	0.587	
-	7	2357		NM_004304	NP_004295	Q9UM73	ALK_HUMAN	xtracellular (Potential).	1218	GCCATCTTCAA	0.522	
-	36	4070		NM_000379	NP_000370	P47989	XDH_HUMAN		8	CCTCACAGACC	0.498	
-	7	849	ynd.1_Missense_	NM_015475	NP_056290	Q8NCA5	FA98A_HUMAN		1	TTTAGGGGATA	0.403	
-	29	2385	p.W744*|MAP4K3	NM_003618	NP_003609	Q8IVH8	M4K3_HUMAN	CNH.	8	TAAACCATGAA	0.348	
-	2	1930	002rrz.2_Intron|SL	NM_021097	NP_066920	P32418	NAC1_HUMAN	lasmic (Potential).	4	TCTTCTCACTCA	0.507	
-	1	316	HH2_uc002rtf.3_	NM_001101330	NP_001094800				0	AATTATCATTTTT	0.393	
+	4	428	oa.1_Missense_M	NM_022437	NP_071882	Q9H221	ABCG8_HUMAN	er.|Cytoplasmic (Potential).	4	AGCCTCCTTGC	0.607	
-	8	1197_1198	REPL_uc002rui.3_	NM_006036	NP_006027	Q4J6C6	PPCEL_HUMAN		1	CCCAAGGAGGG	0.371	
+	3	755		NM_002158	NP_002149	P32314	FOXN2_HUMAN	Fork-head.	0	ATTTTCCATATTT	0.393	rs147349434
-	27	3073	SME4_uc010fbu.1	NM_014614	NP_055429	Q14997	PSME4_HUMAN	HEAT 2.	5	CCAAGGGAATG	0.338	
-	4	552	.2_Intron|C2orf63_	NM_152385	NP_689598	Q8NHS4	CB063_HUMAN		3	GAATGGATTTG	0.303	
-	11	1751	zj.2_Missense_M	NM_004105	NP_004096	Q12805	FBLN3_HUMAN	nteraction with TIMP3.	6	AAGGTCCCTATA	0.438	
+	6	2109		NM_001080433	NP_001073902	Q96PX6	CC85A_HUMAN		5	AGGTTCGTGTC	0.408	
+	3	461	le.2_Missense_Mu	NM_002664	NP_002655	P08567	PLEK_HUMAN	PH 1.	1	GGCCATTAAAT	0.468	
-	4	828		NM_001024680	NP_001019851	Q5FWF7	FBX48_HUMAN		0	GCATCCATTGG	0.378	
-	3	370		NM_002056	NP_002047	Q06210	GFPT1_HUMAN	midotransferase type-2.	1	ACTTTTCCTTTCT	0.413	
-	10	1907		NM_017880	NP_060350	Q9NWW7	CB042_HUMAN		0	GGGAAGGATAT	0.507	
+	4	626	p.G110E|PCYOX1	NM_016297	NP_057381	Q9UHG3	PCYOX_HUMAN		1	TCTAGGAGGAG	0.403	

+	13	1393	V1B1_uc010fdw.2_	NM_001692	NP_001683	P15313	VATB1_HUMAN		1	GGGAGGAGGCG	0.607	
+	3	2586		NM_001080474	NP_001073943	A6NCI8	CB078_HUMAN		2	TTCTTCTCTGCA	0.403	
+	3	445_446	sense_Mutation_p	NM_001381	NP_001372	Q99704	DOK1_HUMAN		0	ATGCTGGAGAA	0.574	
+	5	875	issense_Mutation_	NM_001381	NP_001372	Q99704	DOK1_HUMAN	Pro-rich.	0	CTGGCCCCCAA	0.627	
+	11	3590		NM_000189	NP_000180	P52789	HXK2_HUMAN	Catalytic.	2	GGAGATGCACA	0.612	
+	13	1908	_p.E635K|CTNNA2	NM_004389	NP_004380	P26232	CTNA2_HUMAN		9	CAGAAGAACTA	0.443	
+	8	1267	HNSL2_uc002sta.	NM_018271	NP_060741	Q86YJ6	THNS2_HUMAN		1	CGGATGAAGCC	0.562	
-	5	633	M131_uc010yvg.1_	NM_015348	NP_056163	Q92545	TM131_HUMAN		6	AACTAGGATTA	0.289	
+	6	699	RPL30_uc002szt.	NM_145213	NP_660214	Q8TCC3	RM30_HUMAN		1	AGATGGTGAGA	0.269	
-	4	471	se_Mutation_p.G1	NM_175735	NP_783862	Q86SG7	LYG2_HUMAN		1	AAGTCCCCTGT	0.517	
+	7	821	vt.1_Missense_M	NM_002518	NP_002509	Q99743	NPAS2_HUMAN		4	TTGAACCCAAAG	0.393	
-	2	494_495		NM_153836	NP_722578	Q8IUH2	CREG2_HUMAN		1	GCAGTCCTTGG	0.51	
+	11	1459	wd.1_Missense_	NM_003855	NP_003846	Q13478	IL18R_HUMAN	oplasmic (Potential).	3	AAAGCCGAAGA	0.348	
-	4	994	_p.G74R|TGFBRA	NM_004257	NP_004248	Q8WUH2	TGFA1_HUMAN		2	AACTCCTTTACT	0.418	
-	16	2320		NM_001144013	NP_001137485	A6NKT7	RGPD3_HUMAN		1	GTTTTCGAGTTC	0.368	
+	6	802		NM_001008743	NP_001008743	Q6IMI6	ST1C3_HUMAN	PAPS.	1	GGAAAGGTAGA	0.403	rs139414825
-	20	3464	_p.W989*|RGPD5_	NM_005054	NP_005045	Q99666	RGPD5_HUMAN	RanBD1 1.	0	CCACATCCATGC	0.438	
+	10	2312	nse_Mutation_p.L	NM_019014	NP_061887	Q9H9Y6	RPA2_HUMAN		1	GATTCTCTTCGT	0.512	
+	3	128		NM_014440	NP_055255	Q9UHA7	IL36A_HUMAN		0	AGTCACTATTG	0.498	
+	12	2525	_uc002tjf.2_Misse	NM_012455	NP_036587	Q8NDX1	PSD4_HUMAN	PH.	2	GCAGGGCATCC	0.612	
+	2	518	PP10_uc002tle.2_	NM_020868	NP_065919	Q8N608	DPP10_HUMAN	KCND2.|Cytoplasmic (Pote	10	GGTAGGAACTG	0.388	
+	20	2158	_p.M563I|DPP10_	NM_020868	NP_065919	Q8N608	DPP10_HUMAN	ellular (Potential).	10	TGCAGGGATGA	0.388	
+	13	4739	t.3_Missense_Mu	NM_005270	NP_005261	P10070	GLI2_HUMAN		13	GAGCTCCATGC	0.642	
-	11	1133	_Mutation_p.V347	NM_014553	NP_055368	Q9NZI6	TF2L1_HUMAN		3	ATCTGGACCAAA	0.557	
-	8	953	0flr.2_Splice_Site_	NM_014553	NP_055368	Q9NZI6	TF2L1_HUMAN		3	ACGTACCCTTC	0.552	
-	2	208	fls.2_Missense_M	NM_032390	NP_115766	Q9BYG3	MK67I_HUMAN		0	CTCCAGGAGTA	0.413	
+	13	1552		NM_001080527	NP_001073996	Q6PIF6	MYO7B_HUMAN	osin head-like.	2	GCTGGCCCTCA	0.602	
+	15	1863		NM_001080527	NP_001073996	Q6PIF6	MYO7B_HUMAN	osin head-like.	2	TGGGCCATGGG	0.552	
-	7	1707	K4_uc010zbg.1_	NM_025052	NP_079328	Q56UN5	YSK4_HUMAN		5	TTAATGGGACCT	0.418	
-	8	3118		NM_002299	NP_002290	P09848	LPH_HUMAN	ntial).|4 X approximate re	13	AGGCAGGATTC	0.488	
+	6	653	f.2_Missense_Mu	NM_006895	NP_008826	P50135	HNMT_HUMAN		1	AAGATGCTCATT	0.353	
-	60	10576		NM_018557	NP_061027	Q9NZR2	LRP1B_HUMAN	ntial).|LDL-receptor class B	50	ATCCATCCATGT	0.294	
+	2	206	_p.D26N|KYNU_u	NM_003937	NP_003928	Q16719	KYNU_HUMAN		2	CAACGGATGAG	0.488	
+	8	830	p.P234S|KYNU_u	NM_003937	NP_003928	Q16719	KYNU_HUMAN		2	AATATTCCTGCC	0.418	
+	2	231	0zbl.1_Missense_	NM_018460	NP_060930	Q53QZ3	RHG15_HUMAN		2	AAATGAGAATCA	0.443	
+	23	2827	5C_uc002twu.1_	NM_004522	NP_004513	O60282	KIF5C_HUMAN		1	AGTTGGACAACG	0.527	
+	2	1843	NT5_uc010zci.1_	NM_014568	NP_055383	Q7Z7M9	GALT5_HUMAN	main A.|Lumenal (Potential	4	ATCAAGGAGATT	0.448	
-	1	515	S1_uc002ubm.2_	NM_016836	NP_058520	P29558	RBMS1_HUMAN		0	CCTTGGCTTGC	0.677	
-	13	2456	.2_Intron|SCN3A_	NM_006922	NP_008853	Q9NY46	SCN3A_HUMAN		10	CCAAGGAAACC	0.488	
+	14	2665	_p.S792F|SCN2A_	NM_001040142	NP_001035232	Q99250	SCN2A_HUMAN	=S2 of repeat II; (Potential	8	TACTGTCTGTTG	0.408	
-	26	4821	uc002udp.2_Intro	NM_002977	NP_002968	Q15858	SCN9A_HUMAN		13	ATCCTTGGATTTT	0.313	
-	15	2703	uc002udp.2_Intro	NM_002977	NP_002968	Q15858	SCN9A_HUMAN	II.	13	ATGGATCCATGG	0.343	
-	14	2235	7A_uc010fpm.1_	NM_002976	NP_002967	Q01118	SCN7A_HUMAN		1	ACCAGGATTGG	0.403	
+	8	2000	udy.2_Missense_	NM_152381	NP_689594	A4UGR9	XIRP2_HUMAN	Xin 4.	14	AACAAGGCCAT	0.438	
+	8	8534	_p.R2664K|XIRP2_	NM_152381	NP_689594	A4UGR9	XIRP2_HUMAN		14	TGAAAGAAAAC	0.383	
+	22	3030	o.1_Missense_Mu	NM_001079818	NP_001073286	P23229	ITA6_HUMAN	ellular (Potential).	2	TGCGGGGGCTG	0.468	
+	9	1227	ej.1_Nonsense_M	NM_145810	NP_665809	Q9BWT1	CDCA7_HUMAN	transcriptional activity.	1	AAACAGGAATTT	0.323	

+	9	1229	ej.1_Missense_Mu	NM_145810	NP_665809	Q9BWT1	CDCA7_HUMAN	transcriptional activity.	1	ACAGGAATTTGA	0.323
-	284	3277_8327	880K|TTN_uc010z	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	CTCCTCCATTAT	0.446
-	284	82243	035E|TTN_uc010z	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	TATTTTCCTGTAT	0.403
-	275	71598	87C|TTN_uc010z	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	TTATACGGAAAA	0.413
-	275	71377	13K|TTN_uc010z	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	CCTGGTCTATCT	0.413
-	200	39408	.1_Missense_Muta	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	TGTCTCCTTTCTT	0.358
-	124	28701	_Intron|TTN_uc0	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	ATTCCTCCTCTG	0.398
-	80	20556	_uc010zfj.1_Intro	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	CATTTCCATCCTG	0.512
-	74	18751	_uc010zfj.1_Intro	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	CAAAAGAAGGT	0.408
-	67	16791	_uc010zfj.1_Intro	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	AGGAGGGAAGC	0.373
-	61	15172	_uc010zfj.1_Intro	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	CAAACGGAGGT	0.443
-	46	11885_1188	G3821S|TTN_uc0	NM_133437	NP_597681	Q8WZ42	TITIN_HUMAN		153	GGGACCCTTTAA	0.46
-	46	13152	N_uc010zfi.1_Intr	NM_133379	NP_596870	Q8WZ42	TITIN_HUMAN		153	GGCTTTGAAAATA	0.408
-	31	7306	TN_uc010zfj.1_Mi	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	CTAAGTCCTTGT	0.428
-	13	2455	une.1_Nonsense_	NM_173648	NP_775919	Q6ZP82	CC141_HUMAN		10	CTGATTGAAACC	0.488
+	3	872_873		NM_194250	NP_919226	Q7Z570	Z804A_HUMAN		11	ACAAAGGGAATT	0.351
-	5	770		NM_182521	NP_872327	Q8NEG5	ZSWM2_HUMAN	ZZ-type.	3	ACTTCCCCTCAAT	0.358
-	5	539		NM_182521	NP_872327	Q8NEG5	ZSWM2_HUMAN	RING-type 1.	3	CACAGCCAAACC	0.274
+	9	809	A1_uc010frw.1_5'	NM_000090	NP_000081	P02461	CO3A1_HUMAN	le-helical region.	13	CTAGGGAGAAT	0.403
+	22	2567	_Mutation_p.R77	NM_001130158	NP_001123630	O43795	MYO1B_HUMAN	IQ 3.	8	TCTGCGGGAAC	0.463
-	43	7902		NM_018897	NP_061720	Q8WXX0	DYH7_HUMAN	k (By similarity).	12	CTACTTGAGATG	0.363
-	41	6983		NM_018897	NP_061720	Q8WXX0	DYH7_HUMAN		12	TACTATCATTCGA	0.383
-	31	5112		NM_018897	NP_061720	Q8WXX0	DYH7_HUMAN	2 (By similarity).	12	CAGCAAGGACCC	0.378
-	22	3992	utl.1_Missense_Mu	NM_020760	NP_065811	Q9P2P5	HECW2_HUMAN	HECT.	18	TCTCTGGATACC	0.358
+	13	1907	p.E519K|SPATS2L	NM_015535	NP_056350	Q9NUQ6	SPS2L_HUMAN		3	CCTCGGAGGCC	0.597
-	14	2055_2056		NM_213589	NP_998754	Q70E73	RAPH1_HUMAN		10	TTGCGGGGATAA	0.342
+	5	4094		NM_020923	NP_065974	Q9HCK1	ZDBF2_HUMAN		3	CCTACAGATTCC	0.393
+	5	659	zjb.1_Missense_M	NM_005048	NP_005039	P49190	PTH2R_HUMAN	Name=1; (Potential).	3	TGTATACCGTTG	0.423
+	8	925	r.2_Missense_Mut	NM_001875	NP_001866	P31327	CPSM_HUMAN	midotransferase type-1.	13	GAGGACCGGGG	0.498
-	32	5060_5061	p.G1296K|ABCA1	NM_173076	NP_775099	Q86UK0	ABCAC_HUMAN		11	GCTCTCCCCCA	0.5
-	8	1397	0zlr.1_Missense_	NM_006216	NP_006207	P07093	GDN_HUMAN		4	CCTGTAGGATTAT	0.418
-	46	5323		NM_000092	NP_000083	P53420	CO4A4_HUMAN	llagen IV NC1.	11	TCGCCTCTTCAG	0.652
+	37	3322	tation_p.G1054R|	NM_000091	NP_000082	Q01955	CO4A3_HUMAN	le-helical region.	3	GATAAGGGAGAG	0.493
+	25	2336	xp.1_Missense_M	NM_001080391	NP_001073860	P23497	SP100_HUMAN		5	TCCCATCCGTGG	0.507
+	1	374	UGT1A9_uc002vu	NM_001072	NP_001063	P19224	UD16_HUMAN		0	ATCTATCCAGTG	0.423
-	2	288	fyp.1_Missense_M	NM_212556	NP_997721	Q6ZVZ8	ASB18_HUMAN		1	CCATTCCATCTC	0.488
+	13	3010		NM_001080504	NP_001073973	Q6ZP01	RBM44_HUMAN		4	GTTTTCCCTTCC	0.413
+	7	1293	_Mutation_p.F14	NM_018226	NP_060696	Q9HAU8	RNPL1_HUMAN		2	GATGACTTTCTC	0.642
+	12	1699		NM_001080437	NP_001073906	Q8TER0	SNED1_HUMAN	EGF-like 7.	2	GCGAGTGCCCG	0.716
-	14	2263	as.2_Missense_M	NM_019609	NP_062555	Q96SM3	CPXM1_HUMAN		4	TCAATCCTTCTGT	0.612
-	7	936	as.2_Missense_M	NM_019609	NP_062555	Q96SM3	CPXM1_HUMAN		4	TCAGAGGATCCC	0.537
-	18	2536	4A11_uc002wih.2_	NM_032034	NP_114423	Q8NBS3	S4A11_HUMAN	bicarbonate transporter).	1	AGTAGTGGATCT	0.617
-	18	1771	md.3_Missense_	NM_019593	NP_062539	Q9NPB8	GPCP1_HUMAN	GDPD.	0	GTATCGGATATTT	0.363
+	2	121	CB1_uc002wmz.1	NM_015192	NP_056007	Q9NQ66	PLCB1_HUMAN		12	GTTACTCCAATTA	0.318
+	5	388	mz.1_Splice_Site_	NM_015192	NP_056007	Q9NQ66	PLCB1_HUMAN		12	TTTCAGGAATG	0.388
-	5	1093	nj.2_Missense_Mu	NM_020341	NP_065074	Q9P286	PAK7_HUMAN	Linker.	23	ACCTCAGAATAG	0.458
+	2	249	_uc010gca.1_Mis	NM_130811	NP_570824	P60880	SNP25_HUMAN	ith CENPF (By similarity).	2	TGGAGGAGATG	0.597

-	18	1838	.H447Y|SEL1L2_	NM_025229	NP_079505	Q5TEA6	SE1L2_HUMAN	(Potential).|Sel1-like 10.	2	CGTTGTGGTATT	0.398	
-	19	2343	ch.1_Missense_M	NM_024704	NP_078980	Q96L93	KI16B_HUMAN	-rich.|Potential.	8	CCAGTTCTTGAA	0.448	
+	22	2757	e_Mutation_p.G87	NM_015585	NP_056400	Q8NHU2	CT026_HUMAN		4	CGCCGGAGTCA	0.652	
+	1	1555		NM_002196	NP_002187	Q01101	INSM1_HUMAN	2H2-type 5.	1	TGTTCCCCTGC	0.657	
+	28	2716	sk.1_Missense_M	NM_012255	NP_036387	Q9H0D6	XRN2_HUMAN		1	TCCTCCCCTTT	0.378	
-	3	813	sm.2_Missense_M	NM_153675	NP_710141	Q9Y261	FOXA2_HUMAN	Fork-head.	4	AGTGGCGGATG	0.617	
+	4	776		NM_033118	NP_149109	Q9H1R3	MYLK2_HUMAN		6	CACCTCGAGGG	0.577	
+	7	762	xb.1_RNA|TTLL9_	NM_001008409	NP_001008409	Q3SXZ7	TTLL9_HUMAN	TTL.	2	GGTAGCCCGGT	0.607	
+	14	1995	se_Mutation_p.G5	NM_032819	NP_116208	Q9BYN7	ZN341_HUMAN	2H2-type 11.	2	ACACAGGCTGC	0.597	
+	17	1874	_p.S520F|ITCH_u	NM_031483	NP_113671	Q96J02	ITCH_HUMAN		6	GGATTCCTTTC	0.403	
-	6	664	S_uc010zup.1_Mi	NM_000178	NP_000169	P48637	GSHB_HUMAN		3	TCCCAGGCTTTG	0.488	
-	4	1551	1_5'Flank|EIF6_uc	NM_178468	NP_848563	Q9BQN1	FA83C_HUMAN		2	GCAGGGGGCTG	0.642	
+	3	240	L_uc002xgw.2_R	NM_022077	NP_071360	Q9NQG1	MANBL_HUMAN		0	CACCTCCGGAG	0.557	
-	11	1841	_p.D500N|TGM2_u	NM_004613	NP_004604	P21980	TGM2_HUMAN		3	GAGGTCCCTCT	0.597	
+	4	392	_p.P48S|L3MBTL_	NM_015478	NP_056293	Q9Y468	LMBL1_HUMAN		0	AGCCCCCGAGC	0.682	
+	4	584	gp.2_Missense_M	NM_001098798	NP_001092268	Q96NM4	TOX2_HUMAN		1	CAGATGGGCAT	0.682	
-	2	1872		NM_020433	NP_065166	Q9BR39	JPH2_HUMAN	ytoplasmic (Potential).	0	TGGCCGTCGGG	0.667	
-	2	1870		NM_020433	NP_065166	Q9BR39	JPH2_HUMAN	ytoplasmic (Potential).	0	GCCGTCGGGCA	0.662	
+	9	1239	p.H362Y|HNF4A_	NM_000457	NP_000448	P41235	HNF4A_HUMAN		3	CACCCCATGCC	0.592	
+	2	427	_p.H124Y|SEMG2_	NM_003008	NP_002999	Q02383	SEMG2_HUMAN	at-rich region.|3-1.	1	CATTTTCACATG	0.398	
+	8	1307		NM_004994	NP_004985	P14780	MMP9_HUMAN		2	GGCCCCCCTTG	0.632	
-	5	1817	_p.E507K|ZNF334_	NM_018102	NP_060572	Q9HCZ1	ZN334_HUMAN	2H2-type 10.	2	TGCATTCATATGG	0.453	
-	5	1232	_p.E312K|ZNF334_	NM_018102	NP_060572	Q9HCZ1	ZN334_HUMAN	2H2-type 5.	2	TGCATTCGTAAG	0.438	
+	34	4740	zyf.1_Missense_M	NM_006420	NP_006411	Q9Y6D5	BIG2_HUMAN		4	TCTAACCCAACA	0.408	
-	2	1107	_Mutation_p.P33	NM_020436	NP_065169	Q9UJQ4	SALL4_HUMAN		2	CTGAGGAAGCA	0.647	
-	2	393	e_Mutation_p.P98	NM_020436	NP_065169	Q9UJQ4	SALL4_HUMAN		2	AGGTGGATTTT	0.537	
-	2	1147		NM_080617	NP_542184	Q9NTU7	CBLN4_HUMAN	C1q.	4	TGAAACTGTAA	0.343	
+	1	832_833		NM_019888	NP_063941	P41968	MC3R_HUMAN	lasmic (Potential).	4	AAGGGGGCAGT	0.609	
+	5	969	xn.1_Missense_M	NM_001033521	NP_001028693	Q05048	CSTF1_HUMAN		1	TGCAATCCTCAA	0.403	
+	6	1507	_Mutation_p.E42	NM_001164116	NP_001157588	Q9NQ75	CASS4_HUMAN	Ser-rich.	3	CGGAGGAGTCA	0.567	
+	8	2816	.R127H|GNAS_uc	NM_080425	NP_536350	P63092	GNAS2_HUMAN	(By similar7)|p.R201L(1)|	292	CTGCCGTGTCC	0.423	rs121913495
+	1	2711		NM_178457	NP_848552	Q5JPB2	ZN831_HUMAN		14	GGCTACCCCAC	0.652	
+	1	3649		NM_178457	NP_848552	Q5JPB2	ZN831_HUMAN		14	GCCTCCGAGAT	0.627	
+	2	3760		NM_178457	NP_848552	Q5JPB2	ZN831_HUMAN		14	TCCCAGGGGTG	0.507	
-	4	329	P2_uc010gju.1_5'	NM_014258	NP_055073	Q9BX26	SYCP2_HUMAN		5	CATTGTGGATAT	0.284	
-	1	192_193		NM_080823	NP_543013	Q9H3Y6	SRMS_HUMAN	SH3.	2	GAAGGGGCTG	0.708	
+	3	523	AM2_uc011acc.1	NM_004540	NP_004531	O15394	NCAM2_HUMAN	1.|Extracellular (Potential).	4	ATATATCGTTGT	0.348	
+	4	909	_p.E86K|JAM2_u	NM_021219	NP_067042	P57087	JAM2_HUMAN	.|Extracellular (Potential).	0	ACCTGGAAGAG	0.478	
-	10	1499	glu.2_Missense_M	NM_020706	NP_065757	O95104	SFR15_HUMAN		0	GAAGTGGAACC	0.373	
+	11	1925		NM_014586	NP_055401	P57058	HUNK_HUMAN		2	CATCCCCGTGC	0.552	
-	4	561	_p.V51M|C21orf59	NM_021254	NP_067077	P57076	CU059_HUMAN		0	CATCACCGCGC	0.498	
-	2	1091	yrw.2_Missense_M	NM_017833	NP_060303	Q9NX36	DJC28_HUMAN		0	TCTCCTTTTGC	0.378	
+	2	847	S6_uc002ytp.2_In	NM_006933	NP_008864	P53794	SC5A3_HUMAN	ellular (Potential).	2	TGAATACTTGT	0.453	
+	2	874	S6_uc002ytp.2_In	NM_006933	NP_008864	P53794	SC5A3_HUMAN	ellular (Potential).	2	CCATAGGATTC	0.448	
-	4	1592	ETD4_uc002yuy.2	NM_017438	NP_059134	Q9NVD3	SETD4_HUMAN	SET.	2	AATAATCATCTGT	0.463	
+	12	1548	aeb.1_Missense_M	NM_005128	NP_005119	Q9Y3R5	DOP2_HUMAN		2	TCATTCCTTTGGT	0.532	
+	6	543_544	e_Mutation_p.L14	NM_001001894	NP_001001894	P53804	TTC3_HUMAN		9	TCATTCCTTATTG	0.337	

+	34	4556	nf.2_Missense_Mu	NM_001001894	NP_001001894	P53804	TTC3_HUMAN		9	ATAATCCTTTTGA	0.308	
-	3	430		NM_005867	NP_005858	P56555	DSCR4_HUMAN		1	GCTTGTCCCTTCT	0.328	
-	26	4996	CAM_uc002yyr.1_F	NM_001389	NP_001380	O60469	DSCAM_HUMAN	tential).|Fibronectin type-III	11	CCAAAGGGCCTG	0.557	
-	24	4602	CAM_uc002yyr.1_F	NM_001389	NP_001380	O60469	DSCAM_HUMAN	III 5.|Extracellular (Potentia	11	TAAGCCGAGGCT	0.428	
+	2	199	)2yzd.1_Missense_	NM_058186	NP_478066	P58499	FAM3B_HUMAN		0	TCGCCTCCTTGTC	0.627	
-	1	137	2yzp.2_Missense_	NM_022115	NP_071398	P57071	PRD15_HUMAN		0	AGCACCGGAAgcc	0.338	
+	2	362		NM_000394	NP_000385	P02489	CRYAA_HUMAN		2	TCCACGGAAAGC	0.647	
-	12	1820		NM_173354	NP_775490	P57059	SIK1_HUMAN		7	TGACAGGGAGCA	0.682	
+	7	679_680	n_p.P46F|RRP1_u	NM_003683	NP_003674	P56182	RRP1_HUMAN		0	TCGACCCCTTCT	0.614	
-	2	259	rf29_uc010gpv.1_5	NM_144991	NP_659428	Q8WU66	TSEAR_HUMAN		0	GGGGGCGGCTA	0.562	rs76207741
+	1	1166	.1_Intron|C21orf29	NM_198687	NP_941960	P60372	KR104_HUMAN	A repeats of C-C-X(3).	0	TCCCTTCCTGCTC	0.711	
+	23	1660_1661	5A1_uc010gqd.1_5	NM_001848	NP_001839	P12109	CO6A1_HUMAN	le-helical region.	1	CCGAGGGCTTCC	0.663	
+	3	588	6A2_uc002zhz.1_I	NM_001849	NP_001840	P12110	CO6A2_HUMAN	I.|Nonhelical region.	8	CAGCCCCTGCG	0.711	
-	10	1101	I.2_Missense_Muta	NM_001001438	NP_001001438	P48449	ERG7_HUMAN		0	TTGATGGTTTTCC	0.602	
+	8	1315	e_p.R285_splice|P	NM_006031	NP_006022	O95613	PCNT_HUMAN		8	TTCTAGGGGCCC	0.52	
+	22	4415	j.2_Missense_Mut	NM_006031	NP_006022	O95613	PCNT_HUMAN	Potential.	8	CCAGATGAAGATT	0.572	
+	34	4219	P2A_uc002zjs.2_M	NM_015151	NP_055966	Q14689	DIP2A_HUMAN		2	GGGTTCGTTTGC	0.458	
-	9	1431	ise_Mutation_p.G1	NM_001136213	NP_001129685	Q6S545	POTEH_HUMAN		1	GTACTTCCGTGCT	0.358	
-	4	1053	ense_Mutation_p.N	NM_001136213	NP_001129685	Q6S545	POTEH_HUMAN	ANK 5.	1	ATTTAAATTTGCTT	0.318	
-	1	703		NM_001005239	NP_001005239	Q8NG94	O11H1_HUMAN	Name=5; (Potential).	0	GGACAAGAGTATA	0.418	
-	7	1071		NM_014433	NP_055248	Q9UHP6	RTDR1_HUMAN		1	GCGGCCCTCGG	0.647	
+	5	555	tw.1_Missense_Mu	NM_004914	NP_004905	O95755	RAB36_HUMAN		2	TTCCCTATAGCCT	0.507	
+	7	1110	y.2_Intron|MMP11_	NM_005940	NP_005931	P24347	MMP11_HUMAN	mopexin-like 2.	3	ctcagtactgggtgtacg	0.453	
+	22	3384_3385	p.P1036L|CABIN1_	NM_012295	NP_036427	Q9Y6J0	CABIN_HUMAN	TPR 5.	5	CTGCCCCAATAG	0.52	
+	12	1508	T1_uc003aav.1_Sp	NM_013430	NP_038347	P19440	GGT1_HUMAN		0	CGGCAGGTGGT	0.637	
+	39	6259	n_p.M1883I|MYO18	NM_032608	NP_115997	Q8IUG5	MY18B_HUMAN	Tail.	12	AAGATGGGGGAC	0.627	
+	4	576		NM_182527	NP_872333	Q86V35	CABP7_HUMAN	lasmic (Potential).	0	AGTGTCCCGTGG	0.637	
-	6	564	aia.2_Missense_M	NM_174975	NP_777635	Q9UDX4	S14L3_HUMAN	CRAL-TRIO.	5	CAGTCCCAGGC	0.517	
+	3	354	oz.3_Missense_Mu	NM_000631	NP_000622	Q15080	NCF4_HUMAN	PX.	1	CTACCGCCGCTA	0.592	
-	2	181	_p.G14R|TMPRSS	NM_153609	NP_705837	Q8IU80	TMPS6_HUMAN	lasmic (Potential).	6	GTCCCCCTGCC	0.657	
+	7	1932	atq.1_Missense_M	NM_001039141	NP_001034230	Q9H2D6	TARA_HUMAN		1	CTGTGCCCAGCC	0.607	
+	9	5253_5254	tu.2_Missense_Mu	NM_001039141	NP_001034230	Q9H2D6	TARA_HUMAN		1	CACCTCCACCCA	0.673	
+	9	1151	k.1_Missense_Mut	NM_006116	NP_006107	Q15750	TAB1_HUMAN	PP2C-like.	1	GCTACCCGCTGC	0.657	
+	28	4765	aye.2_Missense_M	NM_021096	NP_066919	Q9P0X4	CAC1I_HUMAN	4 of repeat IV; (Potential).|I	2	ATGAGGGTTCTGC	0.597	
+	10	1478	aq.1_Missense_M	NM_001469	NP_001460	P12956	XRCC6_HUMAN		5	AAGCTTCGCTTCA	0.448	
-	2	637	naa.2_Missense_M	NM_058238	NP_478679	P56706	WNT7B_HUMAN		1	TCTCGCCGAGG	0.652	
+	19	2442	e_Mutation_p.P41	NM_175607	NP_783200	Q8IWV2	CNTN4_HUMAN	onectin type-III 2.	7	TTCCGGCCCTAC	0.512	
-	8	1239	5RA_uc011asm.1_	NM_000564	NP_000555	Q01344	IL5RA_HUMAN	cellular (Potential).	1	CCTGGGAAACCA	0.478	
+	33	4570	PR1_uc011asu.1_In	NM_001099952	NP_001093422	Q14643	ITPR1_HUMAN	lasmic (Potential).	21	ATCGTTCGCGTGC	0.597	
-	4	721	vi.2_RNA|C3orf31_	NM_138807	NP_620162	Q96BW9	MMP37_HUMAN		0	GTCACAGCACTC	0.448	rs146141760
+	6	936	S254F|PPARG_uc	NM_015869	NP_056953	P37231	PPARG_HUMAN		2	TGAATTCCTTAAT	0.448	
-	27	3691		NM_024923	NP_079199	Q8TEM1	PO210_HUMAN	nenal (Probable).	11	ACGGCATTGCCA	0.617	rs147038229
-	10	1206	P2_uc011avh.1_5'	NM_001080423	NP_001073892	Q9C0E4	GRIP2_HUMAN	PDZ 3.	1	GTGTTCCATGCTC	0.642	
+	1	1095	yk.1_Missense_Mu	NM_152536	NP_689749	Q6ZNL6	FGD5_HUMAN		5	ATTGTCCCTTTTC	0.552	
+	5	535	n_p.V26I|PLCL2_u	NM_001144382	NP_001137854	Q9UPR0	PLCL2_HUMAN	PH.	4	AAAAAGGTTCGCT	0.418	rs141837634
-	1	710	HB_uc003cbm.2_In	NM_144715	NP_653316	Q8N7U6	EFHB_HUMAN		0	CTTTTTCCATTTC	0.507	
-	6	759	ense_Mutation_p.L	NM_003615	NP_003606	Q9Y6M7	S4A7_HUMAN	cellular (Potential).	5	GAACAAGAGGAAT	0.413	

-	9	1661	_p.S184C|OSBPL1	NM_017784	NP_060254	Q9BXB5	OSB10_HUMAN		1	GCAAAGATCGC	0.512
+	12	1648	e_Mutation_p.L46	NM_015442	NP_056257	Q9H9A5	CNOTA_HUMAN		2	ATATGTCTCAGA	0.408
+	7	691	21_uc011axy.1_	NM_016300	NP_057384	Q9UBL0	ARP21_HUMAN		3	ACACGGATTCT	0.388
+	21	2352		NM_002207	NP_002198	Q13797	ITA9_HUMAN	ellular (Potential).	6	TGATGCACGAG	0.562
+	22	3195	e_Mutation_p.M1	NM_007335	NP_031361	Q9Y238	DLEC1_HUMAN		9	GGCATGAAGAA	0.567
-	28	5589	i.2_Missense_Mut	NM_198056	NP_932173	Q14524	SCN5A_HUMAN		9	TTTCTCCCAGA	0.532
-	27	5218		NM_006514	NP_006505	Q9Y5Y9	SCNAA_HUMAN		10	AAAGTCGTCCT	0.493
-	5	1334	cjh.2_Missense_M	NM_033027	NP_149016	Q96S65	CSRN1_HUMAN		5	TGGGTGGGTGG	0.582
+	17	1659	ah.1_Missense_	NM_014016	NP_054735	Q9NTJ5	SAC1_HUMAN		1	AACAACTTTTC	0.343
+	17	1664_1665	ah.1_Missense_	NM_014016	NP_054735	Q9NTJ5	SAC1_HUMAN		1	CTTTTCCGATG	0.342
-	2	455	pu.3_Missense_M	NM_024512	NP_078788	Q9BYS8	LRRC2_HUMAN		1	CACCTCCTTCT	0.458
-	21	4292_4293	3csx.2_Missense_	NM_002673	NP_002664	O43157	PLXB1_HUMAN	r (Potential).|IPT/TIG 3.	5	GGAGGGCAGG	0.574
-	4	980	nse_Mutation_p.	NM_024661	NP_078937	Q96ER9	CCD51_HUMAN		0	ACTACCTGCCT	0.557
-	21	2055	_p.P539S|QARS_u	NM_005051	NP_005042	P47897	SYQ_HUMAN		1	CAAAGGCTGTG	0.567
-	5	445		NM_003280	NP_003271	P63316	TNNC1_HUMAN	EF-hand 4.	0	TGTCTCCGTCC	0.577
-	7	743	v.2_RNA|PBRM1_	NM_181042	NP_060635	Q86U86	PB1_HUMAN	Bromo 2.	140	TGAATACTTTTG	0.318
+	42	5361	_Mutation_p.G17	NM_001128840	NP_001122312	Q01668	CAC1D_HUMAN	lasmic (Potential).	11	AGCAGGAAATT	0.463
-	13	2579	C2_uc003dht.1_	NM_015576	NP_056391	O15083	ERC2_HUMAN	Potential.	2	CTTTTCCAACT	0.443
+	9	1234	66_uc003dhu.2_	NM_001141947	NP_001135419	A2RUB6	CCD66_HUMAN		1	TCTCTCAGTCA	0.443
+	21	3814	f.2_Missense_Mu	NM_001457	NP_001448	O75369	FLNB_HUMAN	with FBLP1.|Filamin 10.	19	ACTTCCCCGCC	0.537
-	3	398	ense_Mutation_p.	NM_004944	NP_004935	Q13609	DNSL3_HUMAN		3	CATATTGTTCTT	0.363
-	24	3674	dqd.2_Missense_	NM_002941	NP_002932	Q9Y6N7	ROBO1_HUMAN	lasmic (Potential).	2	ACTGCCCCGGT	0.418
+	15	2726	A3_uc010hon.1_	NM_005233	NP_005224	P29320	EPHA3_HUMAN	Potential).|Protein kinase.	33	AGGTAATTAAAG	0.478
-	2	567	2_5'UTR|PROS1_	NM_000313	NP_000304	P07225	PROS_HUMAN	Gla.	1	TTTCCGGGTCA	0.388
+	1	331		NM_001005514	NP_001005514	A6NHG9	O5H14_HUMAN	Name=3; (Potential).	1	CCACGGAATGT	0.413
+	1	728		NM_001005515	NP_001005515	A6NDH6	O5H15_HUMAN	Name=6; (Potential).	2	TGGAGCCCATC	0.428
+	3	563		NM_032787	NP_116176	Q96K78	GP128_HUMAN	ellular (Potential).	4	AGATATGGACCA	0.343
-	2	436	2_uc011bhe.1_5'	NM_016247	NP_057331	Q9BZV3	IMPG2_HUMAN	ellular (Potential).	3	GCCTTCTGATT	0.428
+	15	1807	_p.L325F|ZPLD1_	NM_175056	NP_778226	Q8TCW7	ZPLD1_HUMAN	acellular (Potential).	5	CCTTCCTTATG	0.388
+	1	676_677		NM_032600	NP_115989	Q8NEL0	CCD54_HUMAN	Potential.	0	GAACTGGAAATT	0.391
-	38	5513		NM_014981	NP_055796	Q9Y2K3	MYH15_HUMAN	Potential.	7	TACTCCCCATCA	0.468
-	27	3406		NM_014981	NP_055796	Q9Y2K3	MYH15_HUMAN	Potential.	7	CTTCTGAAGCT	0.343
-	6	625		NM_014981	NP_055796	Q9Y2K3	MYH15_HUMAN	osin head-like.	7	AGACTGATTTTC	0.308
+	2	294	x.2_Missense_M	NM_198196	NP_937839	P40200	TACT_HUMAN	Potential).|Ig-like V-type 1.	3	ATGTCAACCTG	0.408
+	12	1510	bhr.1_Missense_	NM_001042575	NP_001036040	Q7RTY8	TMPS7_HUMAN	ntial).|LDL-receptor class	2	CTTTAGGAAAC	0.378
-	2	1458	dzg.2_Missense_	NM_199512	NP_955806	Q76M96	CCD80_HUMAN		2	GGTAAAGATTCT	0.607
-	1	913	F80_uc003ebf.2_	NM_007136	NP_009067	P51504	ZNF80_HUMAN	2H2-type 4.	0	ACACTCGCTGC	0.527
-	2	143		NM_173825	NP_776186	Q5HYI8	RABL3_HUMAN	all GTPase-like.	0	CCACAGTCCAT	0.363
-	14	8470	.D2787N|GOLGB	NM_004487	NP_004478	Q14789	GOGB1_HUMAN	ic (Potential).|Potential.	10	AGCATCTCTCT	0.418
+	6	1064	n_p.S80L|PARP1	NM_001113523	NP_001106995	Q460N3	PAR15_HUMAN	Macro 2.	5	GAAATCAGGTA	0.313
-	10	1313	q.2_Missense_M	NM_053025	NP_444253	Q15746	MYLK_HUMAN		9	TGATGGAGCTG	0.627
+	9	1605	hf.1_Missense_M	NM_001024660	NP_001019831	O60229	KALRN_HUMAN		6	CGAATCCCTCA	0.572
-	3	188	se_Mutation_p.W5	NM_024628	NP_078904	A0AV02	S12A8_HUMAN		0	TCCACCAGGGC	0.572
+	11	1913_1914	M2_uc010hsl.2_	NM_004526	NP_004517	P49736	MCM2_HUMAN	MCM.	4	ACCTCCCTGCA	0.604
-	3	1917	uc003ekl.1_5'Flan	NM_153330	NP_699161	Q8NHS0	DNJB8_HUMAN		0	GAAGGGGCTGT	0.592
-	13	2362_2363		NM_007027	NP_008958	Q92547	TOPB1_HUMAN		7	AACCTTCTTTAG	0.361
-	2	220	.1_Missense_Mut	NM_178554	NP_848649	Q8NBH2	KY_HUMAN		2	GGACTCCATTT	0.388

+	3	650	PHB1_uc011bly.1_	NM_004441	NP_004432	P54762	EPHB1_HUMAN	cellular (Potential).	30	GCAGATGAGAGC	0.493	
+	2	741	2R3A_uc011blz.1_	NM_002718	NP_002709	Q06190	P2R3A_HUMAN		7	ACATCCCTGTGT	0.463	
+	3	471	ne.1_Missense_M	NM_006153	NP_006144	P16333	NCK1_HUMAN	SH3 2.	1	GAGAGAGAGGAT	0.453	
-	4	476	ui.2_Missense_Mu	NM_004766	NP_004757	P35606	COPB2_HUMAN	WD 3.	2	TGCTAGTTAGAAT	0.393	
+	2	690		NM_152616	NP_689829	Q8IWZ5	TRI42_HUMAN	RING-type.	7	CTGTGCGAGAAG	0.602	
+	3	1413		NM_152616	NP_689829	Q8IWZ5	TRI42_HUMAN		7	CAGAAGGAAATT	0.453	
+	3	283	_p.E42K|PLS1_uc	NM_001145319	NP_001138791	Q14651	PLSI_HUMAN	EF-hand 1.	1	TTTAAGGAAGCA	0.368	
+	10	1772	_p.L512F|TRPC1_	NM_003304	NP_003295	P48995	TRPC1_HUMAN	ical; (Potential).	2	TTTCTTCTTGTTT	0.348	
+	15	2226	L590F|P2RY12_uc	NM_053002	NP_443728	Q86YW9	MD12L_HUMAN		7	ATCCTTCTCTATG	0.423	
-	5	5258	_5'Flank|IGSF10_	NM_178822	NP_849144	Q6WRI0	IGS10_HUMAN	-like C2-type 4.	13	ATCTCTTTGGTA	0.493	
-	9	1506	p.G410E|PLCH1_	NM_001130960	NP_001124432	Q4KWH8	PLCH1_HUMAN	PI-PLC X-box.	4	AATATTCCTTTCA	0.438	
-	1	1123	fao.1_Nonsense_	NM_004733	NP_004724	O00400	ACATN_HUMAN	cellular (Potential).	4	GAGGCTGAAACC	0.408	
+	4	1346		NM_001080440	NP_001073909	A6NHN0	OTOL1_HUMAN	C1q.	0	AGATTGGAATG	0.443	
-	7	1215	fk.2_Missense_Mu	NM_005241	NP_005232	Q03112	EVI1_HUMAN		14	CAAAGGAGGCC	0.478	
-	7	1162	fk.2_Missense_Mu	NM_005241	NP_005232	Q03112	EVI1_HUMAN		14	GAAAATCCAGGA	0.473	
-	2	768	COM_uc010hwn.2	NM_004991	NP_004982	Q03112	EVI1_HUMAN		14	CATCCATAACTG	0.393	
+	2	1422	.2_Missense_Mut	NM_005414	NP_005405	P12757	SKIL_HUMAN		3	GGCCACGAACTT	0.443	
+	10	1249		NM_018023	NP_060493	Q9ULM3	YETS2_HUMAN		4	GATGCCCCTCCA	0.488	
-	22	2498	LCN2_uc011brl.1_	NM_004366	NP_004357	P51788	CLCN2_HUMAN	oplasmic (By similarity).	0	GAGCAGGATCAA	0.552	
-	9	1458	p.G376R|MASP1_	NM_001879	NP_001870	P48740	MASP1_HUMAN	Sushi 2.	4	TCAGCCCGTGTT	0.478	rs139378189
-	4	1286	fsg.2_Missense_	NM_018192	NP_060662	Q8IVL5	P3H2_HUMAN		4	GATGGGAGAGA	0.507	
-	30	3634	13A4_uc010hzi.2_	NM_032279	NP_115655	Q4VNC1	AT134_HUMAN	cellular (Potential).	2	ACTCCGGCATGT	0.468	
-	21	2584	13A4_uc011bsr.1_	NM_032279	NP_115655	Q4VNC1	AT134_HUMAN	cellular (Potential).	2	GCCCAGGAGACA	0.428	
+	12	1524	_p.E491K|PDE6B_	NM_000283	NP_000274	P35913	PDE6B_HUMAN		0	AGAAGGAGGAG	0.562	
+	7	489	_p.V49M|TMEM1	NM_032326	NP_115702	Q9BSA9	TM175_HUMAN	ical; (Potential).	0	TTAATGGTGACC	0.542	
-	3	580		NM_177998	NP_819056	Q7RTM1	OTOP1_HUMAN	ical; (Potential).	3	CCCAAAGAAAAT	0.323	
+	5	710	p.S225F|MAN2B2	NM_015274	NP_056089	Q9Y2E5	MA2B2_HUMAN		2	CTTTCTCCAACA	0.537	
-	14	2012_2013	_Mutation_p.A664	NM_198595	NP_940997	Q8N556	AFAP1_HUMAN	Potential.	0	CGCAGGGCCTCT	0.559	
-	10	6730	dr.1_Missense_Mu	NM_148894	NP_683692	Q8NFC6	BOD1L_HUMAN		6	AGGCAAGAGGAC	0.522	
+	37	4781	s.1_Missense_Mut	NM_004787	NP_004778	O94813	SLIT2_HUMAN	CTCK.	11	GTACGAGGTGTG	0.498	
-	10	2062	GC1A_uc003gqt.2	NM_013261	NP_037393	Q9UBK2	PRGC1_HUMAN		8	ATTCTTCCCTCTT	0.468	
-	18	3348		NM_015230	NP_056045	Q8WZ64	ARAP2_HUMAN		3	ATAAGGGAACAA	0.358	
+	7	978	p.V163A|PGM2_u	NM_018290	NP_060760	Q96G03	PGM2_HUMAN		1	AAGGTGTCTTGG	0.363	
-	4	1758	BM47_uc011bys.1_	NM_001098634	NP_001092104	A0AV96	RBM47_HUMAN		3	GGGGTCGCAGG	0.632	
-	6	2160	D4_uc003gwm.2_	NM_207406	NP_997289	Q6ZU67	BEND4_HUMAN		0	TGGGAACTTTTAT	0.517	
-	4	1007	bzc.1_Nonsense_	NM_001114175	NP_001107647	P47869	GBRA2_HUMAN	cellular (Probable).	4	TTAGTCGAAGGA	0.289	
+	6	942	oze.1_Missense_	NM_000812	NP_000803	P18505	GBRB1_HUMAN	cellular (Probable).	2	GACATTGAATTTT	0.373	
+	4	2856	_p.L837F|REST_u	NM_005612	NP_005603	Q13127	REST_HUMAN		9	CAAGTCCTTATT	0.458	
-	5	1205	T2A3_uc010ihp.1_	NM_024743	NP_079019	Q6UWM9	UD2A3_HUMAN	cellular (Potential).	2	ATATGGGAACTC	0.408	
-	1	581	uc003hei.1_Intron	NM_001073	NP_001064	O75310	UDB11_HUMAN		3	AGGAAGGAGGG	0.403	
-	1	80	uc003hei.1_RNA	NM_001073	NP_001064	O75310	UDB11_HUMAN		3	ACTTTTCCACAA	0.453	
-	6	1625	_p.G521E|UGT2A	NM_006798	NP_006789	Q9Y4X1	UD2A1_HUMAN	lasmic (Potential).	1	TTCTTTCCTATCT	0.323	
-	3	300		NM_014243	NP_055058	O15072	ATS3_HUMAN		2	TCTTTTCCAAATG	0.488	
-	29	7073	hgq.2_Missense_	NM_032217	NP_115593	O75179	ANR17_HUMAN		10	CTGAGGGACTT	0.383	
-	4	557	10ijq.1_Missense_	NM_152545	NP_689758	Q0VAM2	RGF1B_HUMAN	rminal Ras-GEF.	0	GGTGAGCCAGA	0.473	
+	4	525	p.G103R|AGPAT9	NM_032717	NP_116106	Q53EU6	GPAT3_HUMAN		1	AGAAGGGATTG	0.443	
-	14	1881	_p.S218F|FAM13	NM_014883	NP_055698	O94988	FA13A_HUMAN		2	ACTTCGGAGACA	0.483	

+	10	1131	p.S286F|BMPR1B	NM_001203	NP_001194	O00238	BMR1B_HUMAN	Potential).|Protein kinase.	8	ATGGTTCCCTTT	0.403	
-	7	775	se_Mutation_p.S1	NM_181887	NP_871616	P61077	UB2D3_HUMAN		0	AAATGGATAAA	0.353	
+	3	1453	T2_uc010ilp.1_Mi	NM_001127208	NP_001120680	Q6N021	TET2_HUMAN	p.S356fs*18(1)	733	AGGTTCCAGCA	0.418	
+	3	2937	T2_uc010ilp.1_Mi	NM_001127208	NP_001120680	Q6N021	TET2_HUMAN	Gln-rich.	733	ACACATCCTGAA	0.373	
+	11	1676	se_Mutation_p.G4	NM_001033047	NP_001028219	Q6UXI9	NPNT_HUMAN	MAM.	1	TGACGGGGCTG	0.602	
-	10	1301	_p.D334N|AGXT2L	NM_031279	NP_112569	Q8TBG4	AT2L1_HUMAN		1	ATGGTCCTTCA	0.468	
+	31	3780	c.1_Missense_Mu	NM_001148	NP_001139	Q01484	ANK2_HUMAN		14	AAGAAGAAAAT	0.423	
-	4	2157		NM_024574	NP_078850	Q8TB73	CD031_HUMAN	nectin type-III 2.	0	AACATCCAGCA	0.388	
+	60	10619	iel.1_Missense_M	NM_015312	NP_056127	Q2LD37	K1109_HUMAN		12	ATCTGCTAGCC	0.408	
+	1	3328		NM_024582	NP_078858	Q6V0I7	FAT4_HUMAN	|Extracellular (Potential).	18	ACTTCGAAGAA	0.388	
+	3	5545	p.1_Missense_Mu	NM_024582	NP_078858	Q6V0I7	FAT4_HUMAN	|Extracellular (Potential).	18	TCTTTTGACATT	0.413	
+	4	5612	.1_Missense_Mu	NM_024582	NP_078858	Q6V0I7	FAT4_HUMAN	|Extracellular (Potential).	18	CTCTGGTGTGA	0.328	
+	13	2703_2704	_p.P788F|PLK4_u	NM_014264	NP_055079	O00444	PLK4_HUMAN		0	CTCCTCCTTCTG	0.347	
-	12	2401		NM_015130	NP_055945	Q6ZT07	TBCD9_HUMAN		1	CTAGGGCCAAC	0.438	
+	2	980	.1_Missense_Mut	NM_022475	NP_071920	Q96QV1	HHIP_HUMAN		6	TGGAGGAAATC	0.398	
+	11	2906		NM_033393	NP_203751	Q9C0D6	FHDC1_HUMAN		2	GAACTCCGTGC	0.711	
-	3	334	x.2_Missense_M	NM_017639	NP_060109	Q6V1P9	PCD23_HUMAN	Cadherin 1.	4	AGGGTCGATCC	0.463	
+	11	2463	se_Mutation_p.P4	NM_000856	NP_000847	Q02108	GCYA3_HUMAN		4	GAACTTCCACCA	0.398	
+	12	1767_1768	p.G462K|GUCY1	NM_000857	NP_000848	Q02153	GCYB1_HUMAN	anylate cyclase.	0	TCATAGGACAGC	0.386	
+	3	431		NM_000824	NP_000815	P48167	GLRB_HUMAN	ellular (Probable).	2	TCAAAGGTTTG	0.333	
+	5	710		NM_000824	NP_000815	P48167	GLRB_HUMAN	ellular (Probable).	2	ATGGAGATGTC	0.308	
-	34	4957_4958	ro.2_Missense_M	NM_017631	NP_060101	Q8IY21	DDX60_HUMAN		3	CAATGGGAGTT	0.327	
-	1	478		NM_006792	NP_006783				0	ACAATCTGCAA	0.443	
-	1	290		NM_006792	NP_006783				0	CGGCAGGAAGA	0.378	
+	5	815	0irr.2_Missense_M	NM_014269	NP_055084	Q9UKF5	ADA29_HUMAN		16	CACCTCCAGGC	0.512	
+	7	1438	3_uc003ive.1_5'F	NM_001080477	NP_001073946	Q9P273	TEN3_HUMAN	ellular (Potential).	0	GAGAGAGCCGG	0.547	
+	25	7178		NM_001080477	NP_001073946	Q9P273	TEN3_HUMAN	ellular (Potential).	0	CCAGCTCCTTTT	0.403	
+	9	1008	_Site_p.I278_splic	NM_021942	NP_068761	Q7Z392	CD041_HUMAN		0	TTGCAGATCTG	0.313	
+	3	753	_p.E170K|ZFP42_	NM_174900	NP_777560	Q96MM3	ZFP42_HUMAN		2	TCGCAGAATTT	0.463	
+	1	450		NM_178556	NP_848651	Q8N9V2	TRIML_HUMAN		4	GGGTGGAAGC	0.622	
+	5	913		NM_052909	NP_443141	Q96PX9	PKH4B_HUMAN		2	TTCATAGTATCTT	0.308	
-	15	1803	.2_RNA|BRD9_u	NM_023924	NP_076413	Q9H8M2	BRD9_HUMAN		0	CGACGGCCGAG	0.657	
-	72	12496	fc.2_Missense_Mu	NM_001369	NP_001360	Q8TE73	DYH5_HUMAN	6 (By similarity).	31	AGGATCGTTGG	0.453	
-	14	1853		NM_001369	NP_001360	Q8TE73	DYH5_HUMAN	n (By similarity).	31	AGCTTTGAAATC	0.393	
+	50	7915	IO_uc003jfg.2_R	NM_007118	NP_009049	O75962	TRIO_HUMAN		18	CACTCCGTTTA	0.448	
+	3	612	d.1_Missense_Mu	NM_004932	NP_004923	P55285	CADH6_HUMAN	(Potential).|Cadherin 1.	7	GAGATGGAGCA	0.393	
-	4	876	_p.P74S|RAD1_u	NM_002853	NP_002844	O60671	RAD1_HUMAN		0	GTCAGGAGACA	0.393	rs79789213
-	10	1740	RLR_uc003jjj.1_In	NM_000949	NP_000940	P16471	PRLR_HUMAN	lasmic (Potential).	3	ATAGGGGATTT	0.493	
-	10	1707	RLR_uc003jjj.1_In	NM_000949	NP_000940	P16471	PRLR_HUMAN	lasmic (Potential).	3	GGGGTCCCAGG	0.507	
+	9	1321	_p.L404F|SPEF2_	NM_024867	NP_079143	Q9C093	SPEF2_HUMAN		4	CAATTCCTTAAA	0.303	
+	8	1337_1338	R_uc011cop.1_R	NM_002185	NP_002176	P16871	IL7RA_HUMAN	lasmic (Potential).	5	CTGCCCCCTCC	0.52	
-	2	188	_Intron|UGT3A2_u	NM_174914	NP_777574	Q3SY77	UD3A2_HUMAN		6	TTCCACCTAGG	0.431	
+	7	1066	FLAM_uc003jle.1_	NM_152403	NP_689616	Q63HQ2	EGFLA_HUMAN		7	GCTATGGACCC	0.483	
+	2	732		NM_000958	NP_000949	P35408	PE2R4_HUMAN	lasmic (Potential).	2	GCGCAAGGAGC	0.622	
+	4	338	7_uc011cpn.1_RN	NM_000587	NP_000578	P10643	CO7_HUMAN	SP type-1 1.	0	TGAACCTACAA	0.473	
-	39	4899	jmi.3_Missense_M	NM_173489	NP_775760	Q7Z745	HTRB2_HUMAN		8	ATACCCCATAG	0.502	
-	17	2767	1_Missense_Muta	NM_000065	NP_000056	P13671	CO6_HUMAN	-binding domain.	7	GGATGAAAGTC	0.428	

+	13	1110	o.2_Missense_Mu	NM_024615	NP_078891	Q8N3A8	PARP8_HUMAN		5	CAGGACGGAATC	0.478
-	19	3130	3jtq.2_RNA|ADAM	NM_197941	NP_922932	Q9UKP5	ATS6_HUMAN	Spacer.	0	AATAGTCCAGGC	0.373
-	16	2786_2787	3jtq.2_RNA|ADAM	NM_197941	NP_922932	Q9UKP5	ATS6_HUMAN		0	TATAACCTTCAG	0.446
+	3	425		NM_006633	NP_006624	Q13576	IQGA2_HUMAN	CH.	7	AGAAGGGCTCC	0.383
+	74	15803	.G2942D|GPR98_	NM_032119	NP_115495	Q8WXG9	GPR98_HUMAN	ellular (Potential).	16	AGAATGGCACAT	0.428
-	12	1887	bi.1_Missense_Mu	NM_000439	NP_000430	P29120	NEC1_HUMAN		2	GTTCTCTCCCC	0.398
-	2	255	na.3_Missense_M	NM_018343	NP_060813	Q9BVS4	RIOK2_HUMAN		1	TATTACAGCCAC	0.358
-	9	1822		NM_180991	NP_851322	Q6ZQN7	SO4C1_HUMAN	Extracellular (Potential).	4	GGATAATAATATG	0.418
+	11	973	MK4_uc010jbv.2_M	NM_001744	NP_001735	Q16566	KCC4_HUMAN	rotein kinase.	5	ACTACATTTCAA	0.423
-	3	1995		NM_020177	NP_064562	Q96JP0	FEM1C_HUMAN		3	TTCCCCTTGGAT	0.388
-	19	2628	3krv.3_Missense_	NM_020796	NP_065847	Q9H2E6	SEM6A_HUMAN	ellular (Potential).	2	TGGCCTTTGAGG	0.537
+	3	485	ksn.2_Missense_	NM_182761	NP_877438	A1A519	F170A_HUMAN		1	GGAACGAGGAG	0.507
+	1	373		NM_177478	NP_803431	Q8N4E7	FTMT_HUMAN	rritin-like diiron.	1	GGGAGGAGACC	0.577
+	4	580	_Intron|SNCAIP_u	NM_005460	NP_005451	Q9Y6H5	SNCAP_HUMAN		2	AGATGGAGTGG	0.557
+	5	1254	_Intron|SNCAIP_	NM_005460	NP_005451	Q9Y6H5	SNCAP_HUMAN	ANK 1.	2	GAAAATGGAAAC	0.438
+	5	1356	_Intron|SNCAIP_	NM_005460	NP_005451	Q9Y6H5	SNCAP_HUMAN	ANK 2.	2	ACACTGAGAAG	0.483
-	50	6851		NM_001999	NP_001990	P35556	FBN2_HUMAN	TB 8.	15	GGGGTCCCCCC	0.458
+	15	2119	X46_uc003kzv.1_	NM_014829	NP_055644	Q7L014	DDX46_HUMAN	case C-terminal.	1	CTTCATGGAGGT	0.353
+	8	1281	p.D200N|TGFBI_u	NM_000358	NP_000349	Q15582	BGH3_HUMAN		4	ATCCCAGACTCA	0.572
-	5	850	LHL3_uc010jem.1_	NM_017415	NP_059111	Q9UH77	KLHL3_HUMAN		0	TCTGCCGAACAT	0.547
-	2	1524	NNA1_uc003ldj.2_	NM_015564	NP_056379	O43300	LRRT2_HUMAN	lar (Potential).|LRRCT.	0	TGAAATCCATGG	0.473
+	5	399	.1_Missense_Mut	NM_006083	NP_006074	Q13123	RED_HUMAN		1	CTAGCAGAGAAG	0.468
+	1	116_117	.2_Intron|PCDHA4	NM_018907	NP_061730	Q9UN74	PCDA4_HUMAN		6	TCCTGGGGAAGC	0.515
+	1	1849	03lhf.2_Intron|PCD	NM_018907	NP_061730	Q9UN74	PCDA4_HUMAN	ellular (Potential).	6	TGCCATGGTCGG	0.667
+	1	190	3lhh.1_Intron|PCD	NM_018910	NP_061733	Q9UN72	PCDA7_HUMAN	|Extracellular (Potential).	4	GCCTGTTCCGG	0.612
+	1	1987	CDHA5_uc003lhk.	NM_018911	NP_061734	Q9Y5H6	PCDA8_HUMAN	|Extracellular (Potential).	2	CCACGGCCACG	0.647
+	1	1993	.2_Intron|PCDHA	NM_018901	NP_061724	Q9Y5I2	PCDAA_HUMAN	(Potential).|Cadherin 6.	5	ACTGTGCTTGTG	0.672
+	1	1760	_Intron|PCDHA8_	NM_018899	NP_061722	Q9Y5I4	PCDC2_HUMAN	|Extracellular (Potential).	4	CCTACTCCCTTC	0.488
+	1	753		NM_013340	NP_037472	Q9Y5F3	PCDB1_HUMAN	|Extracellular (Potential).	0	GCACAGCTCAC	0.592
+	1	1497		NM_013340	NP_037472	Q9Y5F3	PCDB1_HUMAN	|Extracellular (Potential).	0	GCAAAGTCCAT	0.398
+	1	353	HB2_uc003lim.1_	NM_018936	NP_061759	Q9Y5E7	PCDB2_HUMAN	(Potential).|Cadherin 1.	6	CAAAGGAAAA	0.522
+	1	1496	uc003lin.2_RNA	NM_018937	NP_061760	Q9Y5E6	PCDB3_HUMAN	(Potential).|Cadherin 5.	2	ACCTGCCCCTCT	0.667
+	1	454	dah.1_Missense_	NM_018939	NP_061762	Q9Y5E3	PCDB6_HUMAN	|Extracellular (Potential).	1	ATATTTCCTTTG	0.478
+	1	2164	ah.1_Missense_M	NM_018939	NP_061762	Q9Y5E3	PCDB6_HUMAN	lasmic (Potential).	1	TGGGTCGCTAC	0.657
+	1	1804		NM_018940	NP_061763	Q9Y5E2	PCDB7_HUMAN	(Potential).|Cadherin 5.	6	GCAGCGAGGCG	0.706
+	1	1585	B16_uc010jfw.1_	NM_020957	NP_066008	Q9NRJ7	PCDBG_HUMAN	(Potential).|Cadherin 2.	2	TACCGGAAAAC	0.388
+	1	1931	B16_uc010jfw.1_	NM_020957	NP_066008	Q9NRJ7	PCDBG_HUMAN	(Potential).|Cadherin 3.	2	TGGCTCCCTGG	0.488
+	1	337		NM_019119	NP_061992	Q9Y5E1	PCDB9_HUMAN	(Potential).|Cadherin 1.	0	GATGATCCCTTT	0.428
+	1	1129		NM_019119	NP_061992	Q9Y5E1	PCDB9_HUMAN	(Potential).|Cadherin 4.	0	CCGGAGAAAAT	0.388
+	1	511		NM_018930	NP_061753	Q9UN67	PCDBA_HUMAN	(Potential).|Cadherin 1.	2	GATGATCCCTTT	0.418
+	1	2056	dan.1_Missense_	NM_018912	NP_061735	Q9Y5H4	PCDG1_HUMAN	ellular (Potential).	3	CCAACGATTCG	0.692
+	1	666	DHGA2_uc011dac	NM_018915	NP_061738	Q9Y5H1	PCDG2_HUMAN	(Potential).|Cadherin 2.	3	ATGCAGACGTA	0.512
+	1	373	ju.1_Intron|PCDH	NM_018921	NP_061744	Q9Y5G4	PCDG9_HUMAN	|Extracellular (Potential).	0	GTAACTGATATTA	0.478
+	3	886	dbl.1_Missense_M	NM_152550	NP_689763	Q8TEC5	SH3R2_HUMAN	SH3 2.	2	CTCAAGGTAGG	0.512
-	20	3179	jhd.2_Missense_M	NM_002609	NP_002600	P09619	PGFRB_HUMAN	Potential).|Protein kinase.	17	TGGGTAAGGGG	0.582
-	2	405	e_Mutation_p.D40	NM_001146040	NP_001139512	P23415	GLRA1_HUMAN	ellular (Probable).	2	GAAATCCGAGG	0.502
+	4	697	LNT10_uc010jic.2_	NM_198321	NP_938080	Q86SR1	GLT10_HUMAN	main A.|Lumenal (Potential	2	GTGATCGAGGT	0.587

+	1	180		NM_001099293	NP_001092763	Q2VIQ3	KIF4B_HUMAN	inesin-motor.	1	TGAAGGGAATTC	0.592	
+	1	2960		NM_001099293	NP_001092763	Q2VIQ3	KIF4B_HUMAN	RC1 (By similarity).|Potenti	1	CTATACCTTGTC	0.463	
+	33	3818	lws.2_Missense_	NM_001037333	NP_001032410	Q96F07	CYFP2_HUMAN		0	GAAGTCCGTGG	0.522	
-	11	1542	p.R404W|GABRB	NM_021911	NP_068711	P47870	GBRB2_HUMAN	lasmic (Probable).	0	CTTTCCGATACT	0.517	
+	5	1011_1012	_p.P217S|ODZ2_u	NM_001122679	NP_001116151				10	GGATACCCTTTG	0.569	
+	5	650	df.1_Missense_M	NM_006650	NP_006641	Q6PUV4	CPLX2_HUMAN		1	CCATCCCTGCG	0.622	
-	6	1002	Silent_p.L206L|MX	NM_031300	NP_112590	Q9BW11	MAD3_HUMAN		0	ACCCCCAAACA	0.701	
+	5	1242	kz.1_Missense_M	NM_182594	NP_872400	Q8N9F8	ZN454_HUMAN		3	CAGTGGAGAGA	0.388	
+	14	1727	kc.1_Missense_M	NM_025158	NP_079434	Q96T51	RUFY1_HUMAN	Potential.	5	ACTCAGGATGG	0.517	
-	20	2966	mlf.2_Missense_	NM_198868	NP_942568	Q66K14	TBC9B_HUMAN		2	CTCTTCCTGTG	0.498	
-	8	1264	p.A323T|RASGEF	NM_175062	NP_778232	Q8N431	RGF1C_HUMAN	Ras-GEF.	1	CTTGGCCGTCC	0.617	
+	12	1796	q.1_Missense_Mu	NM_004415	NP_004406	P15924	DESP_HUMAN	plakophilin 1 and junction p	9	TGTTCCCTCTGT	0.557	
+	1	266		NM_138574	NP_612641	Q5TGJ6	HDGL1_HUMAN	PWWP.	0	CCCACGAGACG	0.602	
-	1	306		NM_005320	NP_005311	P16402	H13_HUMAN	H15.	1	TGAGGCCAAGC	0.547	
+	11	1565	p.G420E|BTN3A3_	NM_006994	NP_008925	O00478	BT3A3_HUMAN	.|Cytoplasmic (Potential).	0	AGTGGGGATCT	0.498	
-	3	1381		NM_052923	NP_443155	Q6R2W3	SCND3_HUMAN	Potential.	1	TCACTTCCTTTAT	0.353	
+	1	691		NM_030905	NP_112167	O76002	OR2J2_HUMAN	Name=5; (Potential).	0	CAAATGAGCTG	0.478	
+	3	852	_p.R137C|OR2H1	NM_030883	NP_112145	Q9GZK4	OR2H1_HUMAN	lasmic (Potential).	0	ACCCCCGCCTG	0.597	rs141663433
+	7	970		NR_027822					0	GTTCTGGTGTC	0.478	rs145231932
-	4	2060	nrb.3_Missense_	NM_001134870	NP_001128342	Q6NYC8	PHTNS_HUMAN		0	GGCAGGACTCA	0.537	
-	2	262	1_5'Flank|PSORS	NM_014070	NP_054789	Q6UXA7	CF015_HUMAN		0	AGGTGGGAAGC	0.607	
+	2	315_316	_uc003nwb.1_Miss	NM_001003693	NP_001003693	Q5SQ64	LY66F_HUMAN	(Potential).|Ig-like V-type.	2	TACTGGTGCGC	0.569	
-	6	1240	J1_uc010jth.2_No	NM_000434	NP_000425	Q99519	NEUR1_HUMAN		1	ATAGCTGGACTG	0.597	
+	23	3201	_p.E780*|SKIV2L_	NM_006929	NP_008860	Q15477	SKIV2_HUMAN		4	AATGGGGAGAAG	0.577	
+	25	3263	.1_Missense_Mut	NM_007293	NP_009224	P0C0L4	CO4A_HUMAN		0	GTTGTCACGGG	0.622	
-	15	2508	u.1_RNA|NOTCH	NM_004557	NP_004548	Q99466	NOTC4_HUMAN	|Extracellular (Potential).	22	GGCAGGAGAAG	0.632	
-	12	1644	f10_uc011dpx.1_I	NM_006781	NP_006772	Q5SRN2	CF010_HUMAN	Lys-rich.	1	AACTCTCCTTCT	0.244	
-	12	1611	f10_uc011dpx.1_I	NM_006781	NP_006772	Q5SRN2	CF010_HUMAN	Lys-rich.	1	TTAGTACACCTG	0.328	
-	12	1375	px.1_Missense_M	NM_006781	NP_006772	Q5SRN2	CF010_HUMAN		1	GACTCCCTCTTC	0.483	
-	4	767	03obo.1_Intron|uc	NM_002124	NP_002115	P01911	2B1F_HUMAN	ical; (Potential).	1	CCCAAGGAAGA	0.547	
-	46	3631	se_Mutation_p.G1	NM_080680	NP_542411	P13942	COBA2_HUMAN	le-helical region.	5	GTGTCCCTGGG	0.592	
-	6	2099	ation_p.S557F|DA	NM_001350	NP_001341	Q9UER7	DAXX_HUMAN	al (Potential).|Interaction w	23	TTCCGAGATTTT	0.502	
-	6	565	w.3_Missense_M	NM_003322	NP_003313	O00294	TULP1_HUMAN		3	GAGCTTCCTTAT	0.582	
+	76	11600	sense_Mutation_p	NM_001371	NP_001362				21	TGTGGCTGCAG	0.502	
+	77	11830	sense_Mutation_p	NM_001371	NP_001362				21	TATGAAGTTTTT	0.373	
+	91	13985		NM_001371	NP_001362				21	ATTTGACCTTCA	0.473	
+	6	712	h.2_RNA|GLP1R_	NM_002062	NP_002053	P43220	GLP1R_HUMAN	ellular (Potential).	5	GGCTCCTCTCC	0.617	
-	4	627_628	se_Mutation_p.P21	NM_018965	NP_061838	Q9NZC2	TREM2_HUMAN	ical; (Potential).	1	GAGAAGGATGG	0.554	
-	3	613		NM_024807	NP_079083	Q5T2D2	TRML2_HUMAN	ellular (Potential).	2	CAGTTCCACTC	0.527	
+	14	2566		NM_032538	NP_115927	Q5TCY1	TTBK1_HUMAN	-rich.|Potential.	9	ggaagaagaggagg	0.259	
+	7	1103	_Mutation_p.P34	NM_007355	NP_031381	P08238	HS90B_HUMAN		4	GGCTCCCTTTG	0.403	
-	7	918	e_Mutation_p.G21	NM_001098518	NP_001091988	Q8IZF2	GP116_HUMAN	racellular (Potential).	2	AAAATTCCGTAA	0.373	
+	5	689	e_Mutation_p.D16	NM_153839	NP_722581	Q8IZF7	GP111_HUMAN	ellular (Potential).	1	GGTGTTGATGAG	0.398	
+	6	1634	e_Mutation_p.Y47	NM_153839	NP_722581	Q8IZF7	GP111_HUMAN	Name=3; (Potential).	1	ATCCTCTATGGA	0.448	
+	7	2216	_p.T710I|GPR115_	NM_153838	NP_722580	Q8IZF3	GP115_HUMAN	Name=7; (Potential).	8	TTGGAACCATTAT	0.398	
-	61	10807_10808		NM_138694	NP_619639	P08F94	PKHD1_HUMAN	ellular (Potential).	44	TTTCCCCTAAGA	0.431	rs112030234
+	5	1359	k.2_Missense_Mu	NM_001704	NP_001695	O60242	BAI3_HUMAN	.|Extracellular (Potential).	50	CATGTTCGGTTA	0.468	

-	11	1166	COL9A1_uc003pff.	NM_001851	NP_001842	P20849	CO9A1_HUMAN	elical region (COL3).	4	CAATGGAGCCA	0.388
-	8	989	COL9A1_uc003pff	NM_001851	NP_001842	P20849	CO9A1_HUMAN	elical region (COL3).	4	GCCCGGGAGGA	0.607
-	6	725		NM_001563	NP_001554	Q17R60	IMPG1_HUMAN		3	AGTGAGAGGGA	0.398
-	1	44		NM_000863	NP_000854	P28222	5HT1B_HUMAN	llular (By similarity).	0	CGGAGCCCGCG	0.642
-	12	1382	p.G351R|ME1_uc	NM_002395	NP_002386	P48163	MAOX_HUMAN		2	CACGTCCCTACA	0.393
-	4	695_696	bq.1_Missense_M	NM_001080508	NP_001073977	O95935	TBX18_HUMAN	T-box.	5	GTCTCCCCCGAG	0.51
+	3	1119	p.G188E|NT5E_u	NM_002526	NP_002517	P21589	5NTD_HUMAN		4	CCTTAGGGACAA	0.229
-	16	3034	p.W926*|EPHA7_	NM_004440	NP_004431	Q15375	EPHA7_HUMAN	mic (Potential).|SAM.	28	TTGTAGCCATTCT	0.373
-	15	2925	p.R890Q|EPHA7_	NM_004440	NP_004431	Q15375	EPHA7_HUMAN	lasmic (Potential).	28	GGTTTCGAATC	0.408
+	18	2209	0776_uc010kck.2_	NM_015323	NP_056138	O94874	UFL1_HUMAN		1	AAATTCCAGAG	0.368
+	10	1684	go.3_Missense_Mu	NM_021956	NP_068775	Q13002	GRIK2_HUMAN	cellular (Potential).	5	ACATATGAAATTA	0.388
+	12	2023	p.P592S|GRIK2_u	NM_021956	NP_068775	Q13002	GRIK2_HUMAN	lasmic (Potential).	5	TATAATCCACAC	0.398
+	3	788	rw.1_Missense_M	NM_018013	NP_060483	A7XYQ1	SOBP_HUMAN		1	TTTCACCATACA	0.403
-	1	301		NM_007214	NP_009145	Q9UGP8	SEC63_HUMAN	enal (Potential).	2	TTCCCACTGTCA	0.637
+	7	989	ao.1_Missense_M	NM_032131	NP_115507	Q8NEN0	ARMC2_HUMAN	ARM 1.	0	ATACAAGGATTG	0.343
-	6	830	p.G153D|HDAC2_	NM_001527	NP_001518	Q92769	HDAC2_HUMAN	one deacetylase.	4	CAACACCATCA	0.348
-	8	1952		NM_002031	NP_002022	P42685	FRK_HUMAN		6	ATGAAGTTATTTG	0.343
+	6	2899	t.2_Missense_Mut	NM_001080976	NP_001074445	Q9UL01	DSE_HUMAN		1	ATACCAGGTTGTT	0.468
+	11	1245		NM_173560	NP_775831	Q8HWS3	RFX6_HUMAN		3	GCCCAGGTATGT	0.302
+	17	2273		NM_173560	NP_775831	Q8HWS3	RFX6_HUMAN		3	TTTCAAGAGACT	0.547
-	24	2782	ense_Mutation_p.	NM_152730	NP_689943	Q96NH3	BROMI_HUMAN		3	GGATATGATGAA	0.303
+	1	251		NM_001010905	NP_001010905	Q6P5S2	CF058_HUMAN		0	TTGCACCAGATA	0.378
-	23	3630	c.2_Missense_Mu	NM_002844	NP_002835	Q15262	PTPRK_HUMAN	ine-protein phosphatase 1.|	8	CCAGTTCGTCCA	0.383
+	54	7787	ense_Mutation_p.	NM_000426	NP_000417	P24043	LAMA2_HUMAN	minin G-like 3.	10	AGTCCGGCATCA	0.488
-	2	175		NM_001010876	NP_001010876	Q5VVB8	CF191_HUMAN	ical; (Potential).	1	CTCAGGGACACA	0.373
+	5	651	.1_RNA|ENPP3_u	NM_005021	NP_005012	O14638	ENPP3_HUMAN	lar (Potential).|SMB 2.	4	AATTTCGTTGTG	0.378
+	9	1035	o.1_RNA|ENPP3_	NM_005021	NP_005012	O14638	ENPP3_HUMAN	otential).|Phosphodiesteras	4	ATGTATGATGTAA	0.318
+	1	943		NM_053278	NP_444508	Q969N4	TAAR8_HUMAN	lasmic (Potential).	1	TTTTATCCTTGGT	0.333
-	16	2543	_p.S720F|AHI1_uc	NM_001134831	NP_001128303	Q8N157	AHI1_HUMAN	WD 3.	3	ATCATGGAATCAT	0.363
-	4	582	.S108L|BCLAF1_	NM_014739	NP_055554	Q9NYF8	BCLF1_HUMAN		1	AACGTGAACGA	0.468
-	15	2153	gv.2_Missense_Mu	NM_003980	NP_003971	Q14244	MAP7_HUMAN		0	CTGTTCCTCCA	0.358
-	13	2042	gv.2_Missense_Mu	NM_003980	NP_003971	Q14244	MAP7_HUMAN	Potential.	0	TCTTTCTCTCCA	0.542
+	22	3664		NM_020340	NP_065073	Q5TH69	BIG3_HUMAN		2	CATAAGGAAAGA	0.473
-	3	2135	kg.2_Missense_M	NM_002656	NP_002647	Q9UM63	PLAL1_HUMAN		1	CAGGGGATACC	0.602
+	69	9780		NM_007124	NP_009055	P46939	UTRO_HUMAN		5	CTCATCCAGCAG	0.512
-	3	1542	on.3_Missense_M	NM_024963	NP_079239	Q96ME1	FXL18_HUMAN	LRR 8.	3	GGAAGGGCAGG	0.657
+	4	917	_p.T209I|C7orf26_	NM_024067	NP_076972	Q96N11	CG026_HUMAN		1	CCTGACCGAGA	0.587
-	27	2224	p.P386S|COL28A	NM_001037763	NP_001032852	Q2UY09	COSA1_HUMAN		3	AGGGGGGCCAG	0.468
-	9	1335	se_Mutation_p.P1	NM_004956	NP_004947	P50549	ETV1_HUMAN		35	GCAAAGGAGGA	0.478
+	2	866	_uc003stt.3_Splice	NM_001621	NP_001612	P35869	AHR_HUMAN		3	TGATGGTAAGA	0.358
+	22	2966	p.N978K|HDAC9_	NM_058176	NP_478056	Q9UKV0	HDAC9_HUMAN	one deacetylase.	5	GGAAATGAGGT	0.413
-	1	143		NM_001002926	NP_001002926	Q3B726	RPA43_HUMAN		1	CTGTTCACCAGC	0.647
+	15	2906		NM_003777	NP_003768	Q96DT5	DYH11_HUMAN	n (By similarity).	15	TTTAAACCTTCC	0.408
+	21	2628	p.S854L|STK31_	NM_031414	NP_113602	Q9BXU1	STK31_HUMAN	rotein kinase.	9	ATGGATCACTTC	0.353
+	10	1552		NM_002047	NP_002038	P41250	SYG_HUMAN		1	GTTTAGGGTGTG	0.413
+	12	1489		NM_133468	NP_597725	Q8N8U9	BMPER_HUMAN	VWFD.	3	ACCTGGATGGC	0.652
+	6	1024		NM_007252	NP_009183	P78424	PO6F2_HUMAN	Gln-rich.	1	CCAGTCTTCAG	0.517

+	3	559		NM_020192	NP_064577	Q9NRH1	CG036_HUMAN		0	TATGTAGAATGTT	0.393	
-	8	1146	g.1_Missense_Mut	NM_000168	NP_000159	P10071	GLI3_HUMAN		19	GCGCGGAAGAG	0.537	
-	3	140	)3tim.1_RNA|C7orf	NM_018224	NP_060694	Q9GZY4	CG044_HUMAN	ical; (Potential).	1	TGCTCCCAGAG	0.488	
-	1	1		NM_000290	NP_000281	P15259	PGAM2_HUMAN		0	ACGGGGACGGC	0.617	
-	2	981	bw.1_Missense_M	NM_013389	NP_037521	Q9UHC9	NPCL1_HUMAN	lasmic (Potential).	5	GGCGGGGGCCA	0.592	
-	22	3604		NM_138295	NP_612152	Q8TDX9	PK1L1_HUMAN	ular (Potential).|REJ.	11	GTGGGGCTGCA	0.547	
+	5	580_581	_uc011kcg.1_Miss	NM_181597	NP_853628	Q16831	UPP1_HUMAN		0	GATTGCCCCGTC	0.416	
+	17	2749	kyr.2_Missense_M	NM_152701	NP_689914	Q86UQ4	ABCAD_HUMAN		10	ATTTTTGGAGCAC	0.393	
+	23	9342	kys.1_Missense_M	NM_152701	NP_689914	Q86UQ4	ABCAD_HUMAN		10	CCACTCCAAGGT	0.448	rs139183809
-	7	990	p.G233E|ZPBP_uc	NM_007009	NP_008940	Q9BS86	ZPBP1_HUMAN		0	TTCATTCCATATC	0.338	
+	4	1257	e_Mutation_p.H420	NM_182633	NP_872439	Q8N859	ZN713_HUMAN	C2H2-type 5.	2	AAAATCCATACTC	0.393	
-	5	1641		NM_033273	NP_150376	Q96JC4	ZN479_HUMAN	C2H2-type 10.	4	TGAATTCTCTTGT	0.433	
+	4	1206		NM_001159522	NP_001152994	A8MUV8	ZN727_HUMAN	C2H2-type 7.	0	ATTTGTGAAGAAT	0.388	
-	5	1008	_p.E203K|CALN1_	NM_001017440	NP_001017440	Q9BXU9	CABP8_HUMAN	lasmic (Potential).	1	TCTCTTCCTCATT	0.517	
+	2	186		NM_000941	NP_000932	P16435	NCPR_HUMAN		1	TGTTTTCGCTCAT	0.502	
-	10	1977	dy.1_Missense_Mu	NM_012301	NP_036433	Q86UL8	MAGI2_HUMAN		11	GACCATCAGTTGG	0.488	
-	20	15033	ht.1_Missense_Mu	NM_033026	NP_149015	Q9Y6V0	PCLO_HUMAN		7	GCTATGGCAGCC	0.498	
-	7	11487	_p.S3733F|PCLO_u	NM_033026	NP_149015	Q9Y6V0	PCLO_HUMAN		7	CCTGTGGAAATCT	0.443	
-	3	3053	nv.2_Missense_Mu	NM_033026	NP_149015	Q9Y6V0	PCLO_HUMAN	Pro-rich.	7	GAGGAGTTGTAG	0.502	
-	3	2447	nv.2_Missense_Mu	NM_033026	NP_149015	Q9Y6V0	PCLO_HUMAN	Pro-rich.	7	GCTTGGCCTTGG	0.542	
-	2	1064	nv.2_Nonsense_Mu	NM_033026	NP_149015	Q9Y6V0	PCLO_HUMAN	n-rich.|Pro-rich.	7	GACCCTGAATTG	0.473	rs10251512
-	10	1417		NM_006080	NP_006071	Q14563	SEM3A_HUMAN	Sema.	4	GATAAGGCACCCA	0.433	rs139931613
-	29	4211	ic.1_Missense_Mu	NM_000927	NP_000918	P08183	MDR1_HUMAN	otential).|ABC transporter 2	7	AGATGCCTTTCTG	0.443	
+	9	1283	_p.R274Q|RUNDC	NM_138290	NP_612147	Q96NL0	RUN3B_HUMAN		1	TCTTACGACTTCC	0.368	
-	2	234	n_p.Y43*|STEAP4	NM_024636	NP_078912	Q687X5	STEA4_HUMAN		0	AACAGAATAACCA	0.433	
-	22	3580	v.2_Missense_Muta	NM_000466	NP_000457	O43933	PEX1_HUMAN		2	CTCCAGGCAAAT	0.453	
-	5	4383	D9L_uc003umk.1_	NM_152703	NP_689916	Q8IVG5	SAM9L_HUMAN		4	ATGGGGAAAACA	0.393	
+	20	1535	1A2_uc011kib.1_I	NM_000089	NP_000080	P08123	CO1A2_HUMAN		9	CAAAGGAGAGA	0.433	
+	3	1060		NM_002523	NP_002514	P47972	NPTX2_HUMAN	Pentaxin.	3	ATCAACGACAAG	0.667	
-	11	1357	_p.R377K|CYP3A4	NM_017460	NP_059488	P08684	CP3A4_HUMAN		4	TTGTACCTTTCAG	0.502	
+	12	1586	ZAN_uc003uwl.2_F	NM_003386	NP_003377	Q9Y493	ZAN_HUMAN	xtracellular (Potential).	11	TGCGGGGAGTC	0.617	
+	3	4275	C17_uc010lho.1_F	NM_001040105	NP_001035194	Q685J3	MUC17_HUMAN	approximate tandem repea	27	ACGCCGGTAGTC	0.507	
+	3	9154	C17_uc010lho.1_F	NM_001040105	NP_001035194	Q685J3	MUC17_HUMAN	ich.|59 X approximate tand	27	AAGGTACCGGCA	0.507	
+	3	12117	C17_uc010lho.1_F	NM_001040105	NP_001035194	Q685J3	MUC17_HUMAN	cellular (Potential).	27	GGCTGCACTACTT	0.532	
+	4	905	HIT1_uc003uyf.2_F	NM_006349	NP_006340	O43257	ZNHI1_HUMAN	HIT-type.	1	CACTGTGCGCTC	0.662	
+	17	1470	_uc003uyv.2_Splic	NM_001913	NP_001904	P39880	CUX1_HUMAN		8	TGCTAGGACCTC	0.657	
-	8	1086	_Mutation_p.E284I	NM_198999	NP_945350	P58743	S26A5_HUMAN	lasmic (Potential).	1	ATTTCTCTTTAAA	0.448	
-	42	6594	.2_Missense_Muta	NM_005045	NP_005036	P78509	RELN_HUMAN	EGF-like 5.	19	TTGGTTCCATTGA	0.458	
-	13	1631	z.2_Missense_Mut	NM_005045	NP_005036	P78509	RELN_HUMAN		19	CATTTTCATGAGA	0.343	
-	9	998	z.2_Missense_Mut	NM_005045	NP_005036	P78509	RELN_HUMAN		19	TGCTGGGGTCTG	0.323	
+	4	706	D1_uc003vgj.2_M	NM_001007245	NP_001007246	O00458	IFRD1_HUMAN		2	GATTAATTGACCT	0.368	
-	4	3051		NM_002711	NP_002702	Q16821	PPR3A_HUMAN		34	CCTAGAGATTTTT	0.378	
-	1	810		NM_002711	NP_002702	Q16821	PPR3A_HUMAN		34	CACCTTGATTTTA	0.294	
+	17	2472	OXP2_uc011kmu.1	NM_014491	NP_055306	O15409	FOXP2_HUMAN		8	GAATTAGAAGACC	0.438	
+	3	1549_1550	455NL>KF|MET_u	NM_000245	NP_000236	P08581	MET_HUMAN	ular (Potential).|Sema.	159	GCTAATCTTGGG	0.431	
-	5	1351	a.2_Missense_Mu	NM_003391	NP_003382	P09544	WNT2_HUMAN		7	TCTTGGGGGCCT	0.577	
+	14	2074	nq.1_Missense_Mu	NM_000492	NP_000483	P13569	CFTR_HUMAN	lasmic (Potential).	5	GGATGTGATTCTT	0.383	

+	27	4465	q.1_Missense_Mu	NM_000492	NP_000483	P13569	CFTR_HUMAN	lasmic (Potential).		5	CCTCCGACAGG	0.522	rs148783445
-	8	1009	0lkj.2_Missense_M	NM_012338	NP_036470	O95859	TSN12_HUMAN	ellular (Potential).		0	AAAAAGGAATAC	0.398	
-	1	638	PS2_uc010lkq.2_	NM_198085	NP_932351	Q8N7C7	RN148_HUMAN	PA.		0	ACATGGGAAATA	0.448	
-	7	1691	UB_uc010lkt.2_R	NM_178827	NP_849149	Q8NA54	IQUB_HUMAN			4	TGTTTCCCATT	0.343	
+	3	1175	_p.S185F|FSCN3_	NM_020369	NP_065102	Q9NQT6	FSCN3_HUMAN			1	CCTATCCCAGGT	0.498	
+	2	401		NM_014390	NP_055205	Q7KZF4	SND1_HUMAN	TNase-like 1.		3	GAAATCTTGCT	0.582	
+	21	3442	a.3_Missense_Mut	NM_001458	NP_001449	Q14315	FLNC_HUMAN	Filamin 9.		12	GGTAGGCACCC	0.652	
+	21	3834	a.3_Missense_Mut	NM_001458	NP_001449	Q14315	FLNC_HUMAN	Filamin 10.		12	ACGCGGATGGC	0.602	
+	38	6427	a.3_Missense_Mut	NM_001458	NP_001449	Q14315	FLNC_HUMAN	Filamin 19.		12	TGGGGGCTTGG	0.587	
-	28	5101	A4_uc003vqz.3_5	NM_020911	NP_065962	Q9HCM2	PLXA4_HUMAN	lasmic (Potential).		1	CGGATCATGTTT	0.572	
-	22	4373		NM_020911	NP_065962	Q9HCM2	PLXA4_HUMAN	lasmic (Potential).		1	ACGGTCGCGCA	0.577	rs118107843
-	22	4337		NM_020911	NP_065962	Q9HCM2	PLXA4_HUMAN	lasmic (Potential).		1	CGTGCGGATGA	0.602	
-	2	818	p.P197S|PLXNA4	NM_020911	NP_065962	Q9HCM2	PLXA4_HUMAN	lar (Potential).|Sema.		1	GGTGGGAAAAT	0.537	
+	4	1416	CHRM2_uc003vtm	NM_001006630	NP_001006631	P08172	ACM2_HUMAN	smic (By similarity).		5	GCAAAGCCCCC	0.493	
-	8	930	tu.2_Missense_Mu	NM_004717	NP_004708	O75912	DGKI_HUMAN			3	CCAGGGAGCAG	0.488	
-	15	4864_4865	.Q1556*|KIAA154	NM_020910	NP_065961	Q9HCM3	K1549_HUMAN			230	GACCTGGTGTTT	0.554	
+	2	349	rc.1_Missense_M	NM_001008749	NP_001008749	A4D1S5	RAB19_HUMAN	region (By similarity).		0	ACGATTGGAGTG	0.468	
+	3	518	rc.1_Missense_M	NM_001008749	NP_001008749	A4D1S5	RAB19_HUMAN			0	CGAGTCCATCC	0.502	
-	1	570	NND2A_uc003vvw	NM_015689	NP_056504	Q9ULE3	DEN2A_HUMAN			4	CTCGGCCTCGG	0.592	
+	1	947	vz.2_Missense_M	NM_052853	NP_443085	Q7Z695	ADCK2_HUMAN	rotein kinase.		0	GATACCTTGGA	0.562	
-	15	1860		NM_004333	NP_004324	P15056	BRAF_HUMAN	rotein kinas	_R603>I(2)|p.T	18290	GATTTCACTGTA	0.368	
-	11	1461		NM_004333	NP_004324	P15056	BRAF_HUMAN	nilarity).|Pro	p.S467L(1)	18290	CAAATGATCCA	0.383	
+	1	576	852_uc010lnn.2_	NM_001105558	NP_001099028	P0C1S8	WEE2_HUMAN			2	ACCTTGGACTC	0.493	
+	32	3903		NM_004668	NP_004659	O43451	MGA_HUMAN	se.|Lumenal (Potential).		2	TACATGGAGCG	0.562	
-	4	617	TRPV6_uc010lou.	NM_018646	NP_061116	Q9H1D0	TRPV6_HUMAN	ytoplasmic (Potential).		2	GGGCTCGCACC	0.572	rs150734746
-	6	934	bz.2_Missense_M	NM_019841	NP_062815	Q9NQA5	TRPV5_HUMAN	lasmic (Potential).		6	ATGTCCATCGT	0.567	
+	1	82		NM_176881	NP_795362	P59534	T2R39_HUMAN	ellular (Potential).		1	AAAGTGAATTG	0.418	
+	1	701		NM_176881	NP_795362	P59534	T2R39_HUMAN	lasmic (Potential).		1	CCTCTCTCTCA	0.512	
+	20	2461	tc.1_Missense_M	NM_000083	NP_000074	P35523	CLCN1_HUMAN	smic (By similarity).		5	TCCACAGATTTA	0.428	
-	4	910		NM_005232	NP_005223	P21709	EPHA1_HUMAN	ar (Potential).|Cys-rich.		5	TGCTTCGCCAC	0.627	
+	1	575	uc003wda.2_Intro	NM_176883	NP_795364	P59536	T2R41_HUMAN	Name=5; (Potential).		2	CAATTCCTTTTT	0.408	
+	1	350		NM_012369	NP_036501	Q13607	OR2F1_HUMAN	Name=3; (Potential).		3	GTTATTTTTCTCC	0.527	
+	1	777		NM_001005480	NP_001005480	Q6IF42	OR2A2_HUMAN	ellular (Potential).		2	TTACATGGTCCC	0.507	
+	2	680	wek.2_Missense_	NM_005435	NP_005426	Q12774	ARHG5_HUMAN			2	GCGAAGAGCAT	0.502	
+	2	2646	_Mutation_p.P843	NM_005435	NP_005426	Q12774	ARHG5_HUMAN			2	CACTACCCATCA	0.607	
+	6	3732	p.S1205L|ARHGE	NM_005435	NP_005426	Q12774	ARHG5_HUMAN	DH.		2	AACTTCACTCCG	0.507	
+	7	1465		NM_014141	NP_054860	Q9UHC6	CNTP2_HUMAN	1.|Extracellular (Potential).		11	CCTTTGGAGGC	0.378	
+	2	601		NM_145304	NP_660347	Q8WU49	CG033_HUMAN			1	GGGATGGAATT	0.473	
-	4	1709_1710	p.R488C|ZNF786	NM_152411	NP_689624	Q8N393	ZN786_HUMAN	2H2-type 8.		4	CTCACGGAGCTT	0.653	
+	6	1437	p.T217A|ZNF398_	NM_170686	NP_733787	Q8TD17	ZN398_HUMAN	ype 2; degenerate.		1	GCAGCACCTCC	0.567	
-	2	510		NM_015694	NP_056509	Q9ULD5	ZN777_HUMAN			1	GAAGGGAGACT	0.607	
+	10	1655	ga.2_RNA|KRBA1	NM_032534	NP_115923	A5PL33	KRBA1_HUMAN			2	CTCTAGGTCTC	0.607	
+	1	31	467_uc003wgd.2_	NM_198455	NP_940857	A2VEC9	SSPO_HUMAN			0	GGATGGCGTGG	0.647	
+	43	6302		NM_198455	NP_940857	A2VEC9	SSPO_HUMAN	F5/8 type C.		0	CCAGGGGCCCA	0.682	
+	4	998	p.P227L|REPIN1_	NM_013400	NP_037532	Q9BWE0	REPI1_HUMAN			1	CCCTCCCGCCC	0.652	
+	5	1640		NM_175571	NP_783161	Q8ND71	GIMA8_HUMAN			7	TGACAGAAACC	0.498	
+	5	1846		NM_175571	NP_783161	Q8ND71	GIMA8_HUMAN			7	AAAAGGACCCA	0.537	

+	3	296	76B_uc003whv.3_	NM_018487	NP_060957	Q96HP8	T176A_HUMAN	ical; (Potential).	2	TAGGAGGATTTT	0.572
+	9	1299	p.A335T|NOS3_u	NM_000603	NP_000594	P29474	NOS3_HUMAN	ction with NOSIP.	8	TCCCGGCAGTG	0.642
-	3	584		NM_170606	NP_733751	Q8NEZ4	MLL3_HUMAN		63	CAACAGAGACC	0.423
+	1	87	.1_Intron|uc003wlt	NM_024012	NP_076917	P47898	5HT5A_HUMAN	llular (By similarity).	3	ACCTAACCTCCT	0.612
+	2	963		NM_024012	NP_076917	P47898	5HT5A_HUMAN	ame=6; (By similarity).	3	GGATCCCCTTCT	0.592
+	3	216	p.D12N|RNF32_u	NM_030936	NP_112198	Q9H0A6	RNF32_HUMAN		0	AGAAAGATAACT	0.328
-	4	1019_1020	vpe.1_Missense_M	NM_207332	NP_997215	Q86X53	ERIC1_HUMAN	Glu-rich.	2	CTCCTCCCCGG	0.54
-	68	10743	p.F2765L|CSMD1_	NM_033225	NP_150094	Q96PZ7	CSMD1_HUMAN	cellular (Potential).	25	ACCTTGAAAAGT	0.333
-	17	2803	e_Mutation_p.Q19	NM_033225	NP_150094	Q96PZ7	CSMD1_HUMAN	lar (Potential).|CUB 5.	25	CTGTCTGAAATC	0.502
-	2	854		NM_001080826	NP_001074295	Q86YV5	SG223_HUMAN		0	TGGGTGAGCAG	0.682
-	3	1246	v.2_Intron|FAM167	NM_053279	NP_444509	Q96KS9	F167A_HUMAN		0	AACCTCCGAGAG	0.597
-	7	1400	s.2_Missense_Mu	NM_139167	NP_631906	Q96LD1	SGCZ_HUMAN	cellular (Potential).	3	ACCTCCCCTTCT	0.493
+	6	970	C3_uc003wwv.2_	NM_006765	NP_006756	Q13454	TUSC3_HUMAN		3	GTGGACCTCCA	0.378
-	13	1739	xya.1_Nonsense_	NM_004686	NP_004677	Q9Y216	MTMR7_HUMAN	ularin phosphatase.	1	CCACTCCAAAA	0.448
+	7	847	PO7_uc010ltj.1_RN	NM_015024	NP_055839	Q9UIA9	XPO7_HUMAN		5	AGATTCCCACC	0.498
-	2	580		NM_002318	NP_002309	Q9Y4K0	LOXL2_HUMAN	SRCR 1.	3	GGTGCCCCACT	0.657
+	11	1101	se_Mutation_p.E1	NM_014265	NP_055080	Q9UKQ2	ADA28_HUMAN	B.|Extracellular (Potential).	5	CACATGAAATG	0.408
+	6	567	ea.1_Missense_M	NM_003817	NP_003808	Q9H2U9	ADAM7_HUMAN	cellular (Potential).	5	AGGGAGAACAT	0.398
-	13	1348	xek.2_Intron|EBF2	NM_022659	NP_073150	Q9HAK2	COE2_HUMAN		4	TTATTTCCTTGTG	0.473
+	14	2032	YSL2_uc010luk.1_	NM_001386	NP_001377	Q16555	DPYL2_HUMAN		1	GGCGCCCCCCG	0.642
-	2	186		NM_001010906	NP_001010906	Q68CJ6	SLIP_HUMAN		2	GTTACCTGGATG	0.423
-	3	7453		NM_031271	NP_112561	Q9BXT5	TEX15_HUMAN		7	GATCTGGGGAAT	0.413
-	3	270	xns.2_Missense_M	NM_024645	NP_078921	Q9H898	ZMAT4_HUMAN	Matrin-type 1.	3	TCGGACTTTGC	0.473
+	8	1833_1834		NM_178819	NP_848934	Q86UL3	GPAT4_HUMAN		0	GATCGCCACCTG	0.54
-	29	3545	NK1_uc003xoj.2_M	NM_020476	NP_065209	P16157	ANK1_HUMAN		9	TCCAGGAAGGA	0.657
+	3	512	qa.1_Missense_M	NM_001005365	NP_001005365	Q6S8J7	POTEA_HUMAN	ANK 2.	1	GCACTGATCCA	0.393
+	11	1489	p.A465V|MCM4_	NM_182746	NP_877423	P33991	MCM4_HUMAN	MCM.	4	TTCAGCCTTGG	0.373
+	4	407		NM_001007176	NP_001007177	Q8WWR9	PDPFL_HUMAN		0	ATCTGTCTGCTA	0.393
+	4	5198	P1_uc011ldy.1_Intr	NM_006269	NP_006260	P56715	RP1_HUMAN		12	TCTTCTGAACAG	0.413
+	4	5358	P1_uc011ldy.1_Intr	NM_006269	NP_006260	P56715	RP1_HUMAN		12	AGAGGAAGGAG	0.413
+	3	1918		NM_052898	NP_443130	Q5GH76	XKR4_HUMAN		2	ATCTCCTCCAA	0.458
-	3	1742	lyi.2_Missense_Mu	NM_001114635	NP_001108107	Q6DJT9	PLAG1_HUMAN	lack of NLS and KPNA2 int	129	TATAGGGAGGAC	0.453
-	3	571_572		NM_000780	NP_000771	P22680	CP7A1_HUMAN		1	ACATCCCTTCTG	0.46
+	26	3299		NM_024870	NP_079146	Q70Z35	PREX2_HUMAN		17	AGCAGGAGATG	0.383
+	4	760	.1_5'UTR|CRISPL	NM_031461	NP_113649	Q9H336	CRLD1_HUMAN		2	ATAGGCCCCCG	0.363
+	10	4753	.P1501S|ZFHX4_	NM_024721	NP_078997	Q86UP3	ZFHX4_HUMAN		15	CAAGTCCTGTA	0.473
-	6	890		NM_018440	NP_060910	Q9NWQ8	PAG1_HUMAN	lasmic (Potential).	0	TCTGAAGGCTGa	0.418
+	4	459_460	P1_uc010mai.2_5'	NM_007013	NP_008944	Q9H0M0	WWP1_HUMAN	C2.	2	TTCTTCTAATCC	0.332
-	10	1109	aj.2_Nonsense_M	NM_019098	NP_061971	Q9NQW8	CNGB3_HUMAN	cellular (Potential).	3	TTGTTCGAATAA	0.363
+	9	1191	ense_Mutation_p.L	NM_052832	NP_439897	Q8TE54	S26A7_HUMAN	lasmic (Potential).	2	ACATCCTCTCTG	0.438
+	4	554	p.P152S|POP1_u	NM_001145860	NP_001139332	Q99575	POP1_HUMAN		2	GCCTTCCCAGA	0.458
+	13	1978	p.W626*|POP1_u	NM_001145860	NP_001139332	Q99575	POP1_HUMAN		2	GGCTGGGGCAT	0.408
+	2	600	iq.2_Missense_M	NM_001142462	NP_001135934	Q8N2R0	OSR2_HUMAN		1	ATTACTCCTTCCT	0.647
-	16	1945	s.1_Missense_Mu	NM_015902	NP_056986	O95071	UBR5_HUMAN		28	TGCAGGGGTTG	0.383
+	3	753		NM_001100117	NP_001093587	Q9UQ26	RIMS2_HUMAN		15	AAAGTCGATCTC	0.453
+	24	3741	p.G1156D|RIMS2_	NM_014677	NP_055492	Q9UQ26	RIMS2_HUMAN		15	AGATGGTAGCAT	0.493
+	8	1278	nse_Mutation_p.E	NM_012082	NP_036214	Q8WW38	FOG2_HUMAN		5	GAAGCGAACTT	0.498

-	6	1456	no.2_Missense_M	NM_001146	NP_001137	Q15389	ANGP1_HUMAN	ogen C-terminal.	7	CTTCACGATGTT	0.338	
+	2	998		NM_003301	NP_003292	P34981	TRFR_HUMAN	lasmic (Potential).	3	AAATTCCGTGCA	0.438	
+	49	8241		NM_177531	NP_803875	Q86WI1	PKHL1_HUMAN	ellular (Potential).	14	GCCATCTTGAT	0.468	
-	69	10939	nt.2_Missense_Mu	NM_198123	NP_937756	Q7Z407	CSMD3_HUMAN	ellular (Potential).	63	TAAATCCTTGAA	0.353	
-	29	4972	t.2_Missense_Mu	NM_198123	NP_937756	Q7Z407	CSMD3_HUMAN	lar (Potential).|CUB 9.	63	ATGAGGGAAGT	0.373	
-	8	1529	p.R417K|CSMD3_	NM_198123	NP_937756	Q7Z407	CSMD3_HUMAN	ellular (Potential).	63	AATCCTCTAGATT	0.289	
-	6	595	p.S170F|ENPP2_	NM_001040092	NP_001035181	Q13822	ENPP2_HUMAN		7	CCACGGAGAAG	0.373	
+	3	560	DC6_uc011lid.1_I	NM_022783	NP_073620	Q8TB45	DPTOR_HUMAN		0	ACCTTCCCATTG	0.408	
+	10	1107		NM_001039112	NP_001034201	Q2WGJ9	FR1L6_HUMAN	toplasmic (Potential).	11	GTGCTGATCCT	0.502	
+	31	4245	uc003yqy.1_Intron	NM_001039112	NP_001034201	Q2WGJ9	FR1L6_HUMAN	toplasmic (Potential).	11	AGCAAGGGATT	0.488	
-	13	1928	M135B_uc003yva.	NM_015912	NP_056996	Q49AJ0	F135B_HUMAN		9	TCTAATCCATAC	0.448	
+	7	942	nep.2_Missense_	NM_014957	NP_055772	A2RUS2	DEND3_HUMAN	DENN.	1	CCTCGGACTGG	0.542	
+	3	837	.1_3'UTR|LY6K_u	NM_017527	NP_059997	Q17RY6	LY6K_HUMAN	UPAR/Ly6.	1	AGCATGGGTGA	0.547	
+	3	1031_1032	kx.1_Missense_M	NM_198572	NP_940974	Q76KD6	SPERI_HUMAN		2	CAGCCCAGTG	0.396	
-	8	1526	MP1_uc010mhs.1	NM_024896	NP_079172	Q7Z2K6	ERMP1_HUMAN	ical; (Potential).	1	AAACGGAGACA	0.368	
-	20	1970	p.A410V|PTPRD_	NM_002839	NP_002830	P23468	PTPRD_HUMAN	III 2.|Extracellular (Potentia	22	TCGGGGCACTG	0.507	
-	6	1501	se_Mutation_p.G3	NM_017637	NP_060107	Q6ZN30	BNC2_HUMAN	2H2-type 1.	3	AGAGTACCTTTG	0.433	
+	3	403	ite_p.K4_splice|S	NM_003026	NP_003017	Q99962	SH3G2_HUMAN		1	TTTCAGAAAGT	0.383	
-	14	1847	nl.1_Missense_Mu	NM_017645	NP_060115	Q7Z4H7	HAUS6_HUMAN		2	AAATGGATCAC	0.313	
+	18	2446	93S|DENND4C_u	NM_017925	NP_060395	Q5VZ89	DEN4C_HUMAN		2	ATTTTCCTGAG	0.393	
-	1	5395		NM_153809	NP_722516	Q8IZX4	TAF1L_HUMAN		26	CTTCTCCTTCAG	0.473	
+	8	815		NM_012144	NP_036276	Q9UI46	DNAI1_HUMAN		0	TCTTTAGGATCG	0.502	
-	4	1773		NM_003028	NP_003019	Q15464	SHB_HUMAN	with LAT, FAK1, JAK1 and	3	GGACGGCAGG	0.552	
+	1	526	42421_uc004aed.1_RNA						0	AGCCCAATCTG	0.607	rs141617852
+	10	1799	_Mutation_p.A421	NM_006200	NP_006191	Q92824	PCSK5_HUMAN	Catalytic.	3	CCCGTGCGGGA	0.398	
+	14	2426	e_Mutation_p.E63	NM_006200	NP_006191	Q92824	PCSK5_HUMAN		3	GCACAGAGGAT	0.478	
+	19	3029_3030	SK5_uc004akb.2_	NM_006200	NP_006191	Q92824	PCSK5_HUMAN	(Cys-rich motif).	3	AGAATGGATACA	0.426	
+	3	1168	akf.3_Missense_	NM_001490	NP_001481	Q02742	GCNT1_HUMAN	tial).|Catalytic (By similarity	0	GCTTCCTCCAC	0.453	
-	8	4085		NM_015225	NP_056040	Q8WUY3	PRUN2_HUMAN		0	TCCATCGCCAT	0.542	
-	5	692	kn.2_Missense_	NM_015225	NP_056040	Q8WUY3	PRUN2_HUMAN		0	AATTTCCTCCT	0.433	
+	8	870	kq.3_Missense_M	NM_033305	NP_150648	Q96RL7	VP13A_HUMAN		10	TGGTTCGTAAG	0.323	
-	6	692	mr.1_Missense_M	NM_174938	NP_777598	A2A2Y4	FRMD3_HUMAN	FERM.	2	AGGATCGTAAT	0.388	
-	4	1403	_p.T420I|KIF27_u	NM_017576	NP_060046	Q86VH2	KIF27_HUMAN		5	GGAAGGTAAAG	0.448	rs138516740
+	15	2221	p.P575S|PHF2_u	NM_005392	NP_005383	O75151	PHF2_HUMAN		1	AGTTTCCCATC	0.597	
-	1	79	msc.1_Missense_	NM_000197	NP_000188	P37058	DHB3_HUMAN		0	TGTGAGGATGA	0.547	
-	2	252_253	uc004awu.2_5'UT	NM_001333	NP_001324	O60911	CATL2_HUMAN		0	ATTTTGGAACAG	0.431	
+	1	1060		NM_004473	NP_004464	O00358	FOXE1_HUMAN	Fork-head.	0	ACGCGGAGGA	0.647	
-	4	617_618	ion_p.P200L|TRIM	NM_033220	NP_150089	Q14142	TRI14_HUMAN		1	GCACGGGATG	0.594	
+	7	1282	c.2_Missense_Mu	NM_207299	NP_997182	Q8TBJ4	LPPR1_HUMAN		0	ATCCCCGTGGA	0.488	
-	2	1691	bq.1_Missense_M	NM_133445	NP_597702	Q8TCU5	NMD3A_HUMAN	ellular (Potential).	7	TCAGTTCCTCCA	0.512	
+	4	324		NM_001340	NP_001331	Q14093	CYLC2_HUMAN	A repeats of K-K-X.	1	AATTTCTGAGA	0.393	
+	1	578		NM_001004485	NP_001004485	Q8NGS4	O13F1_HUMAN	ellular (Potential).	3	CACCTCCCTGG	0.438	
-	1	842		NM_001001956	NP_001001956	Q8NGT0	O13C9_HUMAN	Name=7; (Potential).	0	AACATGGATATA	0.393	
-	2	167	lwl.1_Missense_	NM_001003936	NP_001003936	Q6A555	TXND8_HUMAN	Thioredoxin.	0	AACAGGAAACA	0.353	
+	12	1267	_p.E357_splice|Z	NM_133374	NP_588615	Q5T7W0	ZN618_HUMAN		0	CAGCGGTGAGT	0.612	
-	13	3005	A_uc004bir.3_Mis	NM_030767	NP_110394	Q7Z591	AKNA_HUMAN		6	CAAAGGGCTGG	0.622	
-	15	4867	C_uc010mvf.2_Int	NM_002160	NP_002151	P24821	TENA_HUMAN	nectin type-III 10.	7	AATCAGTACTAG	0.458	

-	9	1807	p.G569D|ASTN2_	NM_198187	NP_937830	O75129	ASTN2_HUMAN	cellular (Potential).	9	TCATAGCCCCTCT	0.493	
-	8	1654	p.A239V|TRAF1_u	NM_005658	NP_005649	Q13077	TRAF1_HUMAN	MATH.	3	GGAAGGCGTCA	0.602	
-	5	1118	_p.M60I|TRAF1_u	NM_005658	NP_005649	Q13077	TRAF1_HUMAN		3	CTCCTTCATGAA	0.627	
-	1	510_511		NM_012363	NP_036495	Q8NGS0	OR1N1_HUMAN	cellular (Potential).	3	AATTTCCCCAGT	0.5	
+	15	2109	l.3_RNA|RABGAF	NM_012197	NP_036329	Q9Y3P9	RBGP1_HUMAN	ab-GAP TBC.	5	GTGCTCCTTCTC	0.413	
+	52	6966	_p.H2265Y|SPTA	NM_003127	NP_003118	Q13813	SPTA2_HUMAN	Spectrin 23.	10	CGGAGCACAGC	0.632	
+	2	643		NM_006059	NP_006050	Q9Y6N6	LAMC3_HUMAN	ninin N-terminal.	3	CCCCGGCGAGG	0.706	
+	2	870		NM_032536	NP_115925	Q96CW9	NTNG2_HUMAN		0	AGGGCCCCACC	0.617	
-	10	2516	p.R397Q|SETX_uc	NM_015046	NP_055861	Q7Z333	SETX_HUMAN		3	GTTTTTCGTTTTG	0.348	
+	28	4493_4494	TS13_uc004cdz.3	NM_139025	NP_620594	Q76LX8	ATS13_HUMAN	CUB 2.	6	TGGGACCGAGG	0.624	
+	9	1443		NM_000787	NP_000778	P09172	DOPO_HUMAN		4	ACAGTGGTAAGT	0.587	rs75075472
-	15	4295	p.P1322L|CAMSAF	NM_015447	NP_056262	Q5T5Y3	CAMP1_HUMAN		3	AGTATGGGCAGG	0.627	
-	3	443	SEC16A_uc010nb	NM_014866	NP_055681	O15027	SC16A_HUMAN		0	GGCAAGTTGTC	0.567	
-	12	2225	clq.1_Missense_M	NM_013366	NP_037498	Q9UJX6	ANC2_HUMAN		1	GCTCCTCCTCAA	0.662	
-	6	1308	clq.1_Missense_M	NM_013366	NP_037498	Q9UJX6	ANC2_HUMAN		1	TGGAAGGGTCC	0.622	
-	8	1332	v.1_Intron|ENTPD8	NM_001033113	NP_001028285	Q5MY95	ENTP8_HUMAN	cellular (Potential).	1	AGGGCCTCTGG	0.632	
+	2	782	pi.2_Missense_Mu	NM_000451	NP_000442	O15266	SHOX_HUMAN		0	AAGAAGGATTCC	0.617	
+	3	380	_p.G79R|ASMT_u	NM_004043	NP_004034	P46597	HIOM_HUMAN		1	CGAGGGGAGGA	0.493	
+	6	593	p.E150K|ASMT_u	NM_004043	NP_004034	P46597	HIOM_HUMAN		1	GGTCCGAGGGC	0.567	rs147969184
-	5	557	RSD_uc004cra.1_	NM_001669	NP_001660	P51689	ARSD_HUMAN		0	GCAGTGATCCC	0.557	
-	5	3806		NM_015419	NP_056234	Q9NR99	MXRA5_HUMAN		8	CCATTTCCAACT	0.463	
-	2	743	0ndi.2_Missense_	NM_181332	NP_851849	Q8N0W4	NLGNX_HUMAN	cellular (Potential).	4	TGGGGGGTGAG	0.567	
+	3	754		NM_013452	NP_038480	Q9H320	VCX1_HUMAN	of L-S-Q-E-S- [EQ]-V-E-E-	0	AGAGCGAGATG	0.577	
+	4	1637		NM_001649	NP_001640	Q13796	SHRM2_HUMAN		8	AGAGCCCACGCC	0.682	
+	2	1482	d.2_Missense_Mu	NM_138636	NP_619542	Q9NR97	TLR8_HUMAN	cellular (Potential).	7	TTCACCCGTCCT	0.388	
+	2	2823	d.2_Missense_Mu	NM_138636	NP_619542	Q9NR97	TLR8_HUMAN	smic (Potential).|TIR.	7	TAGAGGAGAGG	0.438	
+	5	737	_p.A166V|EGFL6_	NM_015507	NP_056322	Q8IUX8	EGFL6_HUMAN	EGF-like 3.	2	GCCTGGCCCCAA	0.493	
+	9	1212	p.E337K|PHEX_u	NM_000444	NP_000435	P78562	PHEX_HUMAN	cellular (Potential).	3	CCCTCCGAGAAT	0.458	
+	17	1921	p.A573V|PHEX_u	NM_000444	NP_000435	P78562	PHEX_HUMAN	cellular (Potential).	3	ATGGTGCTATAGG	0.323	
+	3	201	se_Mutation_p.E66	NM_016937	NP_058633	P09884	DPOLA_HUMAN		3	TATGAAGAAGTTG	0.443	
-	3	710		NM_025159	NP_079435	Q9HAI6	CX021_HUMAN		1	TCAGAGGGAAAA	0.428	
-	1	1742		NM_203408	NP_981953	Q5JRC9	FA47A_HUMAN		5	GGCTCCGAGAAT	0.522	
+	7	1011		NM_173695	NP_775966	Q8N9S7	CX059_HUMAN		1	GGCATGGACAGA	0.333	
-	4	550	PX_uc011mkh.1_I	NM_006307	NP_006298	P78539	SRPX_HUMAN	Sushi 2.	0	CGCTCCCCTTTC	0.527	
-	19	2489	a.2_RNA|RPGR_u	NM_000328	NP_000319	Q92834	RPGR_HUMAN		1	CCTATGGATTTTA	0.368	
+	3	1187	se_Mutation_p.W3	NM_001097579	NP_001091048	Q9UPC5	GPR34_HUMAN	cellular (Potential).	1	CTACTGGAAAGA	0.343	
-	13	988	p.S208F|GRIPAP1	NM_020137	NP_064522	Q4V328	GRAP1_HUMAN	Potential.	3	GGATGGATACCT	0.512	
-	5	1115	e_Mutation_p.P18	NM_006521	NP_006512	P19532	TFE3_HUMAN		197	GCTGGGGAGCT	0.507	
+	10	1936	0nil.2_Missense_M	NM_033626	NP_296375	Q96HB5	CC120_HUMAN	Pro-rich.	1	TCTCCCGCCGG	0.697	
-	4	491		NM_015698	NP_056513	Q92917	GPKOW_HUMAN		2	GGGGACCGCCT	0.582	
-	9	1380	mmw.1_Missense_	NM_006150	NP_006141	O43900	PRIC3_HUMAN		1	GGACTCTGGGG	0.682	
-	24	3302		NM_001013742	NP_001013764	Q5KSL6	DGKK_HUMAN		2	CGAGCTAAGTGC	0.502	
-	2	224	sw.2_Missense_Mu	NM_015107	NP_055922	Q9UPP1	PHF8_HUMAN	PHD-type.	3	TCACATCGTAAG	0.637	
+	1	222		NM_174912	NP_777572	Q6GMR7	FAAH2_HUMAN	ical; (Potential).	3	TAGTAGGCCGA	0.562	
-	7	867	_p.R267C|MTMR8	NM_017677	NP_060147	Q96EF0	MTMR8_HUMAN	ularin phosphatase.	4	GAAGCGAATGTT	0.488	
-	12	1816	n_p.E523K|LAS1L	NM_031206	NP_112483	Q9Y4W2	LAS1L_HUMAN		4	ttcttcctcctcctcTAC	0.338	
+	2	259	SN_uc010nkp.1_R	NM_002444	NP_002435	P26038	MOES_HUMAN	FERM.	10	GCCATCCAGCCC	0.517	

+	17	2908	kr.2_Missense_Mu	NM_138737	NP_620074	Q9BQS7	HEPH_HUMAN	otential).|Plastocyanin-like	9	CCCAGGATCCA	0.413	
+	3	2950	R_uc011mpf.1_Mi	NM_000044	NP_000035	P10275	ANDR_HUMAN	HIPK3 (By similarity).|Nuc	8	AAAATTGTCCAT	0.333	
+	1	846_847		NM_207320	NP_997203	Q7L8S5	OTU6A_HUMAN	OTU.	2	AACTCCGTGAC	0.678	
+	3	333		NM_198512	NP_940914	Q6ZPD8	DG2L6_HUMAN		1	CCCTATGGAAGT	0.552	
-	1	748		NM_002565	NP_002556	P51582	P2RY4_HUMAN	ellular (Potential).	1	AGGCCGAGTGG	0.572	
+	13	2066	yz.2_Missense_M	NM_005120	NP_005111	Q93074	MED12_HUMAN		4	GAGGGGACCTT	0.537	
+	1	193	|TAF1_uc004dzt.3_	NM_138923	NP_620278	P21675	TAF1_HUMAN	otein kinase 1.	17	TCAATGGAGCC	0.617	
+	6	978	TAF1_uc004dzt.3_	NM_138923	NP_620278	P21675	TAF1_HUMAN	otein kinase 1.	17	GATGATGAAGT	0.423	rs139324935
+	8	1070	RN1_uc011mpt.1_	NM_052957	NP_443189	Q96QF7	ACRC_HUMAN	sp/Ser-rich.	3	TCCCGACGACA	0.493	
-	1	1205	G4_uc004eaj.1_	NM_001024455	NP_001019626	Q5HYW3	RGAG4_HUMAN		3	GAATTCCGACA	0.498	
-	22	2756	_p.E819K|PHKA1_	NM_002637	NP_002628	P46020	KPB1_HUMAN	lin-binding (Potential).	4	AATTTCTCCCA	0.413	
-	21	2538	_p.S746F|PHKA1_	NM_002637	NP_002628	P46020	KPB1_HUMAN		4	GAACAGAGGGA	0.388	
-	21	2534	_p.P745S|PHKA1_	NM_002637	NP_002628	P46020	KPB1_HUMAN		4	AGAGGGAACCT	0.388	
+	1	331		NM_203303	NP_976048	Q8WW36	ZCH13_HUMAN		0	TAAACGAGAGA	0.502	rs142122114
-	9	1788	cr.2_Missense_M	NM_000489	NP_000480	P46100	ATRX_HUMAN		30	GAACAGACACA	0.398	
+	5	1611	w.2_Missense_M	NM_000052	NP_000043	Q04656	ATP7A_HUMAN	lasmic (Potential).	0	GGAAGGAAAGA	0.418	
+	5	380	dm.1_Missense_	NM_152630	NP_689843	Q8NEK8	FA46D_HUMAN		2	TTATAACACTG	0.358	
-	18	1821	p.P582S|RPS6KA	NM_014496	NP_055311	Q9UK32	KS6A6_HUMAN	otein kinase 2.	8	GCATGGAGTTA	0.363	
-	7	806	na.1_Missense_M	NM_003270	NP_003261	O43657	TSN6_HUMAN	lasmic (Potential).	1	GCACGAGAGA	0.388	rs149522304
+	5	733	rh.1_Missense_M	NM_001939	NP_001930	Q13474	DRP2_HUMAN	Spectrin 1.	2	AAAAGGATGAG	0.537	
-	19	2476	ja.3_Missense_M	NM_001099686	NP_001093156	Q9GZY0	NXF2_HUMAN	RRM.	1	GTAGGGCGCAG	0.483	
+	5	3170	.R790K|GPRASP	NM_014710	NP_055525	Q5JY77	GASP1_HUMAN	Glu-rich.	2	GGACAGACTAG	0.512	
+	4	3118	P2_uc004ejm.2_	NM_138437	NP_612446	Q96D09	GASP2_HUMAN		1	TGGTTCTGAAG	0.418	
+	1	745		NM_001031834	NP_001027004	P0C0E4	RB40L_HUMAN		2	TGAATGCCAGGA	0.577	
-	2	356		NM_153448	NP_703149	Q8N693	ESX1_HUMAN		1	CGGCTCCTCCT	0.716	
-	2	218_219		NM_153448	NP_703149	Q8N693	ESX1_HUMAN		1	CTGTTCCGTACT	0.594	rs76590545
-	16	2786	nse_Mutation_p.R	NM_024657	NP_078933	Q8TE76	MORC4_HUMAN	Potential.	1	TGGTTCTTTCC	0.488	
+	4	634	sk.1_Missense_M	NM_182607	NP_872413	Q86XK7	VSIG1_HUMAN	otential).|Ig-like C2-type 2.	2	CTATTTCCCTTT	0.438	
+	7	1165	sk.1_Missense_M	NM_182607	NP_872413	Q86XK7	VSIG1_HUMAN	lasmic (Potential).	2	cccagGATCAGA	0.378	
-	35	3519	sn.1_Missense_M	NM_001847	NP_001838	Q14031	CO4A6_HUMAN	le-helical region.	8	GTTCTCCTCTC	0.493	
-	23	1976	sn.1_Missense_	NM_001847	NP_001838	Q14031	CO4A6_HUMAN	le-helical region.	8	AAGTCCTGGTA	0.547	
-	22	1791	sn.1_Missense_	NM_001847	NP_001838	Q14031	CO4A6_HUMAN	le-helical region.	8	AGCCAGAATCA	0.547	
+	7	588	so.1_Missense_	NM_033380	NP_203699	P29400	CO4A5_HUMAN	le-helical region.	4	CTAGGGAGAAC	0.363	
+	33	3029	_p.K943*|COL4A5	NM_033380	NP_203699	P29400	CO4A5_HUMAN	le-helical region.	4	GTAGTAAAGGA	0.478	
-	4	1315	Y2F_uc011msq.1_	NM_001522	NP_001513	P51841	GUC2F_HUMAN	ellular (Potential).	8	CAACGGTGAAA	0.408	
-	4	1167_1168	_p.A251V|DCX_uc	NM_000555	NP_000546	O43602	DCX_HUMAN	oublecortin 2.	4	CCACAGGCAAT	0.401	
+	14	1926		NM_007231	NP_009162	Q9UN76	S6A14_HUMAN	lasmic (Potential).	3	GGGGTCCATAC	0.403	
-	2	213	LHL13_uc011mtp.	NM_033495	NP_277030	Q9P2N7	KLH13_HUMAN		2	CATTTCGCTGC	0.433	
+	18	2910	ntr.1_Missense_M	NM_019045	NP_061918	Q5JSH3	WDR44_HUMAN		5	AGAGATCGTAAT	0.353	
+	2	270		NM_144658	NP_653259	Q5JSL3	DOC11_HUMAN	tivated CDC42 (By similari	3	CCCAATGGAAGA	0.398	
+	28	3140	qq.2_Missense_	NM_144658	NP_653259	Q5JSL3	DOC11_HUMAN		3	ACTATAGTTTGG	0.408	
+	4	1181	RF3_uc004eqy.2_	NM_001031855	NP_001027026	Q496Y0	LONF3_HUMAN		2	TGAAGGGGGAT	0.532	
-	3	446	sa.1_Missense_M	NM_080632	NP_542199	Q9BZI7	REN3B_HUMAN	C core.|Necessary for inter	3	CTCACCTTTATT	0.358	
+	4	398	n_p.S87L|AKAP14	NM_178813	NP_848928	Q86UN6	AKA28_HUMAN		0	TTTTTCGGTAAG	0.413	
-	12	2297	_p.P744S|ODZ1_u	NM_014253	NP_055068	Q9UKZ4	TEN1_HUMAN	Extracellular (Potential).	23	TCCAGGGCTAC	0.458	
-	1	846		NM_138289	NP_612146	Q8TDG2	ACTT1_HUMAN		5	ACTTCTCTTTGA	0.537	
+	15	1759	r.2_Missense_Mu	NM_000276	NP_000267	Q01968	OCRL_HUMAN		4	CTCTTCCATATT	0.378	

-	4	719	4eux.1_Missense_	NM_001008222	NP_001008223	Q9Y397	ZDHC9_HUMAN	lasmic (Potential).		1	CCTGGGGCACC	0.468	
-	8	1484	e.3_Missense_Mu	NM_001421	NP_001412	Q99607	ELF4_HUMAN			1	ACGGTCCCAATT	0.587	
+	5	1051	4ewb.2_Missense_	NM_144967	NP_659404	Q6ZRI8	RHG36_HUMAN	Rho-GAP.		3	CAAATCCCCCAG	0.458	
-	16	3407	.E1051K|IGSF1_u	NM_001555	NP_001546	Q8N6C5	IGSF1_HUMAN	otential).|Ig-like C2-type 10		5	GAGTTCCAGGG	0.498	
-	1	107	0nrl.1_RNA|MBNL3	NM_018388	NP_060858	Q9NUK0	MBNL3_HUMAN			0	TATCACGAATCAG	0.398	
-	6	2148	wf.1_Missense_Mu	NM_031907	NP_114113	Q9BXU7	UBP26_HUMAN			8	CAAGGGAAGAG	0.378	
-	4	611	ww.1_Missense_M	NM_173470	NP_775741	Q8N4V1	MMGT1_HUMAN	lasmic (Potential).		0	GTATCCGAAGGC	0.358	rs150859420
+	6	6097	.A1731T|GPR112_	NM_153834	NP_722576	Q8IZF6	GP112_HUMAN	cellular (Potential).		12	GTCATGGCAATG	0.423	
+	4	914	EC1_uc010nsl.1_I	NM_005462	NP_005453	O60732	MAGC1_HUMAN			4	TCCACTTTATTGA	0.502	
+	4	1517	EC1_uc010nsl.1_I	NM_005462	NP_005453	O60732	MAGC1_HUMAN			4	CAGATTCCTATGA	0.478	
+	5	398	n.2_Intron|MAGEA	NM_005366	NP_005357	P43364	MAGAB_HUMAN			2	TATTTCCCACAGT	0.532	
+	5	1328_1329	n.2_Intron|MAGEA	NM_005366	NP_005357	P43364	MAGAB_HUMAN	MAGE.		2	TGGGAGGGATCC	0.545	
+	2	988	|GPR50_uc011my	NM_004224	NP_004215	Q13585	MTR1L_HUMAN	Name=7; (Potential).		4	GCCTACTTCAACA	0.502	
-	5	994	4ffl.2_Missense_M	NM_001011543	NP_001011543	P43363	MAGAA_HUMAN	MAGE.		0	CAGTGGGATCCA	0.493	
+	9	1488_1489		NM_018558	NP_061028	Q9UN88	GBRT_HUMAN			3	CCCATGGCCATG	0.55	
+	3	567	e_Mutation_p.R12	NM_005363	NP_005354	P43360	MAGA6_HUMAN	MAGE.		0	AGTATCGAGCCA	0.527	
-	3	1057	AGEA12_uc004fgc	NM_005367	NP_005358	P43365	MAGAC_HUMAN	MAGE.		1	TGTCCTCCCTCC	0.562	
-	5	531	fgr.2_Missense_M	NM_004344	NP_004335	P41208	CETN2_HUMAN	EF-hand 4.		0	GCAGGAACTCTT	0.393	
-	21	5897		NM_005334	NP_005325	P51610	HCFC1_HUMAN			2	CCAGGGACTCG	0.647	
-	9	1978		NM_005334	NP_005325	P51610	HCFC1_HUMAN			2	AGCAGGGACAC	0.607	
-	9	1510	u.1_Nonsense_Mu	NM_001110556	NP_001104026	P21333	FLNA_HUMAN	Filamin 2.		6	GGTCCTGGATCA	0.682	
+	6	1686		NM_017514	NP_059984	P51805	PLXA3_HUMAN	cellular (Potential).		3	CCGGGGACCCG	0.711	
+	10	2196		NM_017514	NP_059984	P51805	PLXA3_HUMAN	cellular (Potential).		3	AGGAGGGCAGG	0.667	
+	21	3855		NM_017514	NP_059984	P51805	PLXA3_HUMAN	ical; (Potential).		3	CGGGGGGTGGC	0.677	
-	10	1724	nzx.1_Frame_Shift	NM_012102	NP_036234	Q9P2R6	RERE_HUMAN	ELM2.	NA	2	CATCTGGAGAA	0.433	
-	13	2591	ne_Shift_Del_p.Q5	NM_003819	NP_003810	Q13310	PABP4_HUMAN	PABC.	NA	0	TTCCTGGGGGG	0.602	
+	1	136_137		NM_001008740	NP_001008740	Q7Z6W1	TMCO2_HUMAN		NA	1	TAGAGTCTCTCT	0.406	
-	2	659_661	h.2_In_Frame_Del	NM_014849	NP_055664	Q7L0J3	SV2A_HUMAN	Interaction w	NA	7	GGAAGTCATCAT	0.542	
+	1	156_161		NM_178354	NP_848131	Q5T754	LCE1F_HUMAN		NA	0	CTGTGGCTCCAG	0.485	
-	7	811	bhj.1_Frame_Shift_	NM_005998	NP_005989	P49368	TCPG_HUMAN		NA	2	TGCATATTTTTTT	0.393	
+	1	259		NM_001004478	NP_001004478	Q8NGY1	O10Z1_HUMAN	cellular (Pote	NA	2	TGGCTGGGGGG	0.552	
+	8	1288_1290	1AP_uc010pks.1_	NM_014697	NP_055512	O75052	CAPON_HUMAN	Poly-Gln.	NA	3	ctcctccagcagcAGC	0.512	
+	4	635_646		NM_001104548	NP_001098018				NA	0	gTagcagcagcagcag	0.283	30217;rs72359595;rs150848171
-	19	2298_2299	p.C122fs|DIP2C_u	NM_014974	NP_055789	Q9Y2E4	DIP2C_HUMAN		NA	7	AACTGCACACAC	0.54	
-	25	4223	.N1311fs|NUP98_	NM_016320	NP_057404	P52948	NUP98_HUMAN		NA	12	GGCTGTTTTTTT	0.512	
-	8	2041_2043	ame_Del_p.D596de	NM_015213	NP_056028	Q6IQ26	DEN5A_HUMAN	Poly-Asp.	NA	1	GTCTTTATCATCAT	0.453	
+	6	1274	plice_Site|AMPD3_	NM_001025389	NP_001020560	Q01432	AMPD3_HUMAN		NA	2	AAAGGTGCGTTA	0.541	
+	3	479	plice|NDUFV1_uc0	NM_007103	NP_009034	P49821	NDUV1_HUMAN		NA	1	TGGCAGGTGTGT	0.599	
-	6	1081_1083	ne_Del_p.D183del	NM_002576	NP_002567	Q13153	PAK1_HUMAN	ction with CF	NA	4	GGGGTAGcatcatca	0.429	
-	4	519_521	.K112del|CHD4_u	NM_001273	NP_001264	Q14839	CHD4_HUMAN	Poly-Lys.	NA	2	CCAAGCTTCTTCT	0.468	
-	12	4127_4129	w.2_In_Frame_De	NM_004719	NP_004710	Q99590	SCAFB_HUMAN	Pro-rich.	NA	0	AGGGGGTGGTG	0.483	
-	6	1097	me_Shift_Del_p.R	NM_198521	NP_940923	Q96LP6	CL042_HUMAN		NA	2	TGGGCGGGGGG	0.587	
+	3	353_355	ne_Del_p.D88del|K	NM_018559	NP_061029	Q8IXQ4	K1704_HUMAN	Poly-Asp.	NA	2	atgatgacgatgatgatg	0.286	rs138421508
-	14	3949_3950	C3H13_uc001vas.	NM_015070	NP_055885	Q5T200	ZC3HD_HUMAN	Potential.	NA	2	gtatctctcctctctctc	0.178	
-	22	3270	hift_Del_p.K282fs|	NM_198968	NP_945319	Q86YF9	DZIP1_HUMAN		NA	2	CCCAGATTTTTTT	0.433	
+	2	609	3C_uc001wss.2_5	NM_014672	NP_055487	O15091	MRRP3_HUMAN		NA	0	TCCTCATTTTTTT	0.423	
+	20	3443_3444	xdq.2_Frame_Shif	NM_002892	NP_002883	P29374	ARI4A_HUMAN		NA	6	GTACAAGAGAGA	0.381	

+	12	1371_1372	.3_In_Frame_Ins_	NM_030943	NP_112205	Q9BXJ7	AMNLS_HUMAN	lasmic (Pote	NA	0	TGTTCGCCGGG	0.713	rs36040113
-	13	1716	bfi.1_Frame_Shift	NM_182758	NP_877435	Q3MJ13	WDR72_HUMAN	WD 8.	NA	2	ACAGGAAAAAG	0.463	
+	2	2259	arh.2_Frame_Shift	NM_015322	NP_056137	Q9UK73	FEM1B_HUMAN	ANK 8.	NA	0	AGTGATTTTTTG	0.463	
+	3	434_436		NM_001030005	NP_001025176	Q8WVH0	CPLX3_HUMAN		NA	0	CACAGAGGAGG	0.616	
+	7	1037_1039	.K238del|UBN1_u	NM_001079514	NP_001072982	Q9NPG3	UBN1_HUMAN	Lys-rich.	NA	2	TAAGGAGAAGAA	0.453	
+	17	1308	ame_Shift_Del_p.G	NM_025187	NP_079463	Q9BSU1	CP070_HUMAN		NA	2	TATGGCCCCCC	0.597	
-	8	826	_p.M262fs|FANCA_	NM_000135	NP_000126	O15360	FANCA_HUMAN		NA	6	CGGCATTTTTC	0.368	
-	15	2000_2002	15_uc002ghy.1_5'	NM_004860	NP_004851	P51116	FXR2_HUMAN	Poly-Arg.	NA	0	GTTACGGCGGC	0.547	
+	8	1209_1211	2gnp.1_In_Frame_	NM_153604	NP_705832	Q8IZQ8	MYCD_HUMAN	Gln-rich.	NA	5	TCAGCcagcagca	0.527	
-	5	1214_1216	Q161del|CXXC1_u	NM_014593	NP_055408	Q9P0U4	CXXC1_HUMAN	CXXC-type.	NA	2	GTTTGATctgctgct	0.468	
+	14	1794	ebw.2_Frame_Shif	NM_015321	NP_056136	Q6UUV9	CRTC1_HUMAN		NA	519	AGAGTCCCCCC	0.617	
+	2	252_254	Deea.2_In_Frame_	NM_005306	NP_005297	O15552	FFAR2_HUMAN	Name=2; (P	NA	1	CCTCCTGCTGC	0.645	
+	3	844_846	2F1_uc010xvw.1_I	NM_052848	NP_443080	Q96F63	CCD97_HUMAN	Potential.	NA	0	AACagcaggaggag	0.384	
+	3	136_138	In_Frame_Del_p.L	NM_001459	NP_001450	P49771	FLT3L_HUMAN		NA	0	CCTCCTGCTGCT	0.621	
-	3	316	_p.P92fs|HS1BP3	NM_022460	NP_071905	Q53T59	H1BP3_HUMAN	PX.	NA	1	GTAGTGGGGGG	0.537	rs77941615
+	7	1476_1477	BL5_uc002rid.2_F	NM_021831	NP_068603	Q8NDL9	CBPC5_HUMAN		NA	2	TACCATCCCCCC	0.515	
+	1	145_146		NM_178457	NP_848552	Q5JPB2	ZN831_HUMAN	Pro-rich.	NA	14	GCCTGGCCCCC	0.728	
-	1	108	rame_Shift_Del_p.	NM_006585	NP_006576	P50990	TCPQ_HUMAN		NA	0	ACGTGAAGCGC	0.627	
-	1	167_168	.1_Intron|C21orf29	NM_198688	NP_941961	P60371	KR106_HUMAN	A repeats o	NA	0	GGGCCGGGGC	0.688	
-	1	498	p.Q122fs|TCF20_	NM_005650	NP_005641	Q9UGU0	TCF20_HUMAN		NA	5	CCCCTGGGGGG	0.567	rs138734341
+	7	1060	IP_uc003ctg.1_Fr	NM_130384	NP_569055	Q8WXE1	ATRIP_HUMAN		NA	1	TGGCACCCCCC	0.537	
-	2	497_499	XP1_uc003dop.2_	NM_032682	NP_116071	Q9H334	FOXP1_HUMAN	Gln-rich.	NA	2	CTGTTGCTGCT	0.586	
-	9	1978_1979	p.N554fs|VEPH1_	NM_024621	NP_078897	Q14D04	MELT_HUMAN		NA	5	CTGAGGTTTTTT	0.396	
+	7	802_803	|EIF4A2_uc011bs	NM_001967	NP_001958	Q14240	IF4A2_HUMAN	case C-term	NA	4	TGTTGAGAGAG	0.351	
+	7	1596_1597	gcg.2_Frame_Shi	NM_021923	NP_068742	Q8N441	FGRL1_HUMAN	ytoplasmic (	NA	0	agacatccacacaca	0.46	
+	1	251_253	hme.2_In_Frame_	NM_004464	NP_004455	P12034	FGF5_HUMAN		NA	2	TCCTTCCTCCT	0.631	
-	3	473_475	1_In_Frame_Del_	NM_016107	NP_057191	Q96KR1	ZFR_HUMAN	Ala-rich.	NA	0	TGGGGGTGGTG	0.483	
+	17	2312_2314	uc003kgi.3_Intron	NM_003248	NP_003239	P35443	TSP4_HUMAN	SP type-3 7	NA	0	GAGTGTGATGAT	0.562	
-	2	321_322	H2AFY_uc003lar.1	NM_138610	NP_613258	O75367	H2AY_HUMAN	istone H2A	NA	0	GTACTTGGGGTG	0.579	
+	5	378_379	k.1_Frame_Shift_	NM_006083	NP_006074	Q13123	RED_HUMAN		NA	1	AAATTGAGAGAG	0.46	
-	17	2665	53_splice|NUP153	NM_005124	NP_005115	P49790	NU153_HUMAN		NA	9	CTTCCTAAAAAA	0.406	27788;rs147103527
+	2	128_130	p.L24del|BTN2A2_	NM_006995	NP_008926	Q8WVV5	BT2A2_HUMAN		NA	0	CAGCCTCcctcctc	0.483	
-	3	688_690	.2_In_Frame_Del_	NM_002586	NP_002577	P40425	PBX2_HUMAN	Poly-Ala.	NA	1	TGCAGCTGCTG	0.616	
+	7	1165	_p.A234fs|FOXP4_	NM_001012426	NP_001012426	Q8IVH2	FOXP4_HUMAN		NA	1	GGGTGCCCCCG	0.682	
-	1	320_322		NM_175747	NP_786923	Q7RTU3	OLIG3_HUMAN	Poly-His.	NA	0	GCTCTCCtggtggt	0.502	
-	11	1417	03qty.3_Frame_S	NM_004562	NP_004553	O60260	PRKN2_HUMAN	ING-type 2	NA	1	TCACCATTTTTTT	0.393	
+	3	679	l_p.A74fs|CCDC1	NM_138771	NP_620126	Q96EE4	CC126_HUMAN		NA	2	GGTGCTTCTAT	0.373	
-	1	725_727	A10_uc003syw.3_	NM_018951	NP_061824	P31260	HXA10_HUMAN	Poly-Gly.	NA	0	TGCGCGCCGCC	0.759	
-	2	1021_1023	.2_In_Frame_Del_	NM_002192	NP_002183	P08476	INHBA_HUMAN		NA	6	ctcctcttctttcttcttctt	0.355	
-	5	1204	.2_Frame_Shift_D	NM_000466	NP_000457	O43933	PEX1_HUMAN		NA	2	ACCTAATTTTTTT	0.353	
-	6	836_838		NM_001080392	NP_001073861	A4D1U4	LCHN_HUMAN	Poly-Cys.	NA	1	GCCAAGCAGCA	0.606	
+	1	528		NM_001001656	NP_001001656	Q8NGU2	OR9A4_HUMAN	ellular (Pote	NA	1	GAACAATTTTTTT	0.383	
-	6	1281		NM_005232	NP_005223	P21709	EPHA1_HUMAN	tential).|Fibr	NA	5	GTGAGCCCCCG	0.617	rs67794922
-	2	530		NM_015694	NP_056509	Q9ULD5	ZN777_HUMAN		NA	1	GTGGTGGGGGG	0.617	
-	14	2088		NM_005502	NP_005493	O95477	ABCA1_HUMAN	Extracellular	NA	17	CGAAGCCCCCC	0.542	
-	6	1155_1156	_p.D59fs|ENG_uc	NM_001114753	NP_001108225	P17813	EGLN_HUMAN	ellular (Pote	NA	0	CGGCATCGAGAT	0.653	
+	5	716_718	04eib.1_In_Frame_	NM_016607	NP_057691	Q9UH62	ARMX3_HUMAN		NA	2	TGGTCTGATGAT	0.448	

+	5	1770_1772	A_uc001bvm.2_3'	NM_001040441	NP_001035531	Q96BR9	ZBT8A_HUMAN	Poly-Glu.	0	TAGTGAAGAAG	0.414	
-	2	279	0oio.1_Frame_Shi	NM_017821	NP_060291	Q9NX52	RHBL2_HUMAN		0	TCTCTCCCCAT	0.502	
+	3	511	u.2_Frame_Shift_	NM_001136493	NP_001129965	Q8NA29	MFS2A_HUMAN		2	ACAGACCCCCT	0.582	
+	1	136_137		NM_001008740	NP_001008740	Q7Z6W1	TMCO2_HUMAN		1	TAGAGTCTCTCT	0.406	
+	15	2422	4A_uc010oki.1_I	NM_014663	NP_055478	O75164	KDM4A_HUMAN	PHD-type 1.	1	GGGGTCCCCCC	0.493	rs141609782
+	18	2455	_Shift_Del_p.P398	NM_015112	NP_055927	Q6P0Q8	MAST2_HUMAN	rotein kinase.	11	GTCCCTTTTTT	0.552	
-	2	136	_p.L34fs|DOCK7_	NM_033407	NP_212132	Q96N67	DOCK7_HUMAN		2	TTTTTGAGCAG	0.393	
-	1	145	way.2_5'Flank|MIE	NM_024763	NP_079039	Q5VTH9	WDR78_HUMAN		2	ACCCCTTTTTT	0.622	
-	1	178_179	wcj.1_Frame_Shi	NM_012152	NP_036284	Q9UBY5	LPAR3_HUMAN	Name=1; (Potential).	5	AATTAGAAAAA	0.401	rs76299065
-	2	3480_3482	ne.1_In_Frame_	NM_007113	NP_009044	Q07283	TRHY_HUMAN	0 AA tandem repeats.	5	CCTTCTCTTCT	0.172	
-	2	1111_1113	wne.1_In_Frame_	NM_007113	NP_009044	Q07283	TRHY_HUMAN	of R-R-E-Q-E-E- E-R-R-E-	5	tcgcgcctctcctcctc	0	rs71757496
+	4	1420_1421	C_uc001fqb.2_In	NM_005973	NP_005964	Q92733	PRCC_HUMAN		27	CTGGTCCCCC	0.53	
+	8	1158	1AP_uc010pks.1_	NM_014697	NP_055512	O75052	CAPON_HUMAN		3	TCGCACCCCCA	0.597	rs146738391
-	2	718	p.V213fs|TNR_uc	NM_003285	NP_003276	Q92752	TENR_HUMAN	Cys-rich.	11	ACACACCCCCC	0.607	
+	17	2127	ps.2_Frame_Shift	NM_001357	NP_001348	Q08211	DHX9_HUMAN	case C-terminal.	2	TGTTGGTTTTTT	0.378	
+	5	828	_uc009wyw.2_Fr	NM_000186	NP_000177	P08603	CFAH_HUMAN	Sushi 3.	6	GATGGTTTTTG	0.343	
+	4	635_646		NM_001104548	NP_001098018				0	Tagcagcagcagca	0.283	30217;rs72359595;rs150848171
-	7	997	0pte.1_Frame_Sh	NM_018252	NP_060722	Q9H813	TM206_HUMAN	ellular (Potential).	1	AGCACTTTTTTT	0.398	
-	4	643	0pty.1_Frame_Shi	NM_005401	NP_005392	Q15678	PTN14_HUMAN	FERM.	5	CACATCTTTTTT	0.423	
+	27	7308	CN_uc001hsp.1_	NM_001098623	NP_001092093	Q5VST9	OBSCN_HUMAN		28	AGGCTGGGGGG	0.662	
-	5	1053		NM_194298	NP_919274	Q7RTY1	MOT9_HUMAN	ellular (Potential).	3	GAGCTATTTTTTT	0.378	
+	2	232	1jsw.2_Frame_S	NM_173473	NP_775744	Q96DE5	APC16_HUMAN		1	ACCTACCCCAA	0.458	
-	7	1352	3fs|APBB1_uc01	NM_001164	NP_001155	O00213	APBB1_HUMAN	PID 1.	2	TACTTCCCCCC	0.582	
+	6	1274	plice_Site|AMPD3_	NM_001025389	NP_001020560	Q01432	AMPD3_HUMAN		2	AAAGGTGCGTT	0.541	
-	9	829_831	A1_uc010rcp.1_	NM_002786	NP_002777	P25786	PSA1_HUMAN		2	AGACACATCATC	0.36	
+	2	423		NM_152316	NP_689529	Q8N8R7	CK046_HUMAN		0	TTAGCCAAAAAA	0.338	
+	6	858_860		NM_024081	NP_076986	Q9BZD6	TMG4_HUMAN	ic (Potential).|Poly-Pro.	0	GTTTCACCACC	0.463	
+	1	241		NM_001005201	NP_001005201	Q8N146	OR8H3_HUMAN	ellular (Potential).	2	ACACCTAAAACC	0.428	
+	5	886	rlo.1_Frame_Shift_	NM_004265	NP_004256	O95864	FADS2_HUMAN	lasmic (Potential).	2	GGCAGCCCATC	0.527	
+	4	544		NM_004585	NP_004576	Q9UL19	TIG3_HUMAN		1	ATACCAAAAAA	0.537	
+	7	810	_5'Flank|C11orf6	NM_006442	NP_006433	Q14919	NC2A_HUMAN	Pro-rich.	0	CAGCGCCCCCG	0.627	
-	22	3672_3674	1qfl.2_In_Frame_	NM_020228	NP_064613	Q9NQV6	PRD10_HUMAN	Poly-Thr.	1	CCGTTGGTGGT	0.547	
-	8	761	N1_uc001rmy.2_	NM_033114	NP_149105	Q8TBF4	ZCRB1_HUMAN		1	TTTCCATTTTTT	0.328	
-	12	4127_4129	w.2_In_Frame_De	NM_004719	NP_004710	Q99590	SCAFB_HUMAN	Pro-rich.	0	AGGGGGTGGTG	0.483	
-	13	4059_4061		NM_003482	NP_003473	O14686	MLL2_HUMAN	Poly-Glu.	41	TTCTTCCTCCT	0.478	
+	2	157	40B_uc001ruq.1_	NM_001031698	NP_001026868	Q6NWY9	PR40B_HUMAN	Pro-rich.	5	GCTATCCCCCC	0.607	
+	6	1083	siz.2_Frame_Shift_	NM_000456	NP_000447	P51687	SUOX_HUMAN	terin domain (By similarity).	0	ACAACTTTCCC	0.527	
+	3	881_882	toc.2_Frame_Shif	NM_001093	NP_001084	O00763	ACACB_HUMAN		8	GCTTTGGGGG	0.574	
+	3	353_355	e_Del_p.D88del|	NM_018559	NP_061029	Q8IXQ4	K1704_HUMAN	Poly-Asp.	2	tgatgacgatgatgat	0.286	rs138421508
+	3	707_710	vbk.2_Frame_Shi	NM_015116	NP_055931	Q9Y2L9	LRCH1_HUMAN	LRR 3.	2	CGCCCTGCCTG	0.436	
+	5	668_670	A|IRF9_uc010alj.2	NM_006084	NP_006075	Q00978	IRF9_HUMAN	Poly-Ser.	1	ATTGGGagcagca	0.448	
-	10	1018	1wmy.1_Frame_S	NM_024658	NP_078934	Q8TEX9	IPO4_HUMAN		1	TGGGGAAAAGG	0.567	
+	2	609	3C_uc001wss.2_5	NM_014672	NP_055487	O15091	MRRP3_HUMAN		0	TCCTCATTTTTTT	0.423	
+	20	3443_3444	xdq.2_Frame_Shi	NM_002892	NP_002883	P29374	ARI4A_HUMAN		6	TACAAGAGAGA	0.381	
-	2	365_367	c010twr.1_Intron|I	NM_020414	NP_065147	Q9GZR7	DDX24_HUMAN	Poly-Glu.	4	TTTCCCTCCTC	0.443	
-	3	684	AA1_uc001ykw.1_	NM_005348	NP_005339	P07900	HS90A_HUMAN		7	CTGCTGAGGAC	0.502	
+	12	1371_1372	.3_In_Frame_Ins_	NM_030943	NP_112205	Q9BXJ7	AMNLS_HUMAN	lasmic (Potential).	0	TGTTCGCCGGG	0.713	rs36040113

-	1	70_72	.2_5'UTR|NIPA1_u	NM_144599	NP_653200	Q7RTP0	NIPA1_HUMAN	ellular (Potential).	0	TCCCCGgccgccg	0.626	
+	5	839	B_uc010ugg.1_5'	NM_004855	NP_004846	Q92521	PIGB_HUMAN		0	TCTTAGTTTTTTT	0.338	
+	6	1825_1827	2afu.2_In_Frame_	NM_017610	NP_060080	Q6ZNA4	RN111_HUMAN	His-rich.	2	TCATCACCACC	0.512	
-	2	378	gx.1_Frame_Shift	NM_000942	NP_000933	P23284	PPIB_HUMAN	e cyclophilin-type.	0	TTTTTGGAACA	0.463	
+	5	794	unn.1_Frame_Sh	NM_018689	NP_061159	Q8WUJ3	K1199_HUMAN		3	AGGCTATTTTTT	0.498	
+	10	1146_1148	ch.2_In_Frame_	NM_014048	NP_054767	Q9ULH7	MKL2_HUMAN		5	GCTCCAGCAGC	0.542	rs146244364
+	11	1356_1358	xy.2_In_Frame_D	NM_000418	NP_000409	P24394	IL4RA_HUMAN	ytoplasmic (Potential).	2	GTGTGAGGAGG	0.591	
+	9	1776	|IL21R_uc002dos.	NM_181078	NP_851564	Q9HBE5	IL21R_HUMAN	lasmic (Potential).	4	AAGGACCCCCC	0.637	
-	2	430	2dxs.2_Frame_Sh	NM_006110	NP_006101	O95400	CD2B2_HUMAN		1	CTGGACCCCCC	0.532	
+	10	1565	10vjk.1_Intron|LR	NM_018296	NP_060766	Q1X8D7	LRC36_HUMAN		0	ACAGTCCCCCC	0.512	
+	12	1273_1274	_Shift_Ins_p.S279	NM_007014	NP_008945	O00308	WWP2_HUMAN		6	TCTTCGAGTGC	0.49	
-	15	2000_2002	15_uc002ghy.1_5'	NM_004860	NP_004851	P51116	FXR2_HUMAN	Poly-Arg.	0	GTTACGGCGGC	0.547	
+	10	1439	6B_uc002gix.2_5'	NM_001080424	NP_001073893	O15054	KDM6B_HUMAN	Pro-rich.	2	CCCGTCCCCCC	0.706	
-	22	2902_2904	.E967del|MYH10_	NM_005964	NP_005955	P35580	MYH10_HUMAN	Potential.	2	TTTCTTTCTTCTT	0.35	
-	1	233_235	dx.3_In_Frame_D	NM_020772	NP_065823	Q7Z417	NUFP2_HUMAN	His-rich.	4	gtgatgatggtggtggt	0.276	rs1054145
-	13	1679	TLL6_uc002ioc.2_	NM_001130918	NP_001124390	Q8N841	TTLL6_HUMAN		0	TTCTTCTTCATT	0.512	
-	5	1187_1189	.1_In_Frame_Del_	NM_007146	NP_009077	Q14119	VEZF1_HUMAN	Poly-Gln.	2	gttgttgttgctgctgctg	0.305	731354;rs73995411
-	2	311_313	_47EE>E|TEX2_u	NM_018469	NP_060939	Q8IWB9	TEX2_HUMAN	Poly-Glu.	1	tcctcctcttcctcctcctc	0.468	
-	3	758	_Shift_Del_p.K109	NM_001098801	NP_001092271	Q96ND0	CR019_HUMAN		2	TCTTCCTTTTTTT	0.433	rs143162930
+	20	1970	xay.1_Frame_Shi	NM_013326	NP_037458	Q96DM3	MIC1_HUMAN	Mic1.	1	TTTTTTGAACAG	0.448	rs80213848
-	5	1214_1216	161del|CXXC1_u	NM_014593	NP_055408	Q9P0U4	CXXC1_HUMAN	CXXC-type.	2	GTTTGATctgctgct	0.468	
+	1	1359		NM_000455	NP_000446	Q15831	STK11_HUMAN	rotein kinaso.?(3)|p.G52_P	266	TCAAGAAGAAG	0.617	
+	2	252_254	eea.2_In_Frame_	NM_005306	NP_005297	O15552	FFAR2_HUMAN	Name=2; (Potential).	1	CCTCCTGCTGC	0.645	
+	18	2356	HG2_uc002olj.2_	NM_022835	NP_073746	Q9H7P9	PKHG2_HUMAN		4	AGTGTCCCCAA	0.577	
+	2	531	k|PPP1R13L_uc0	NM_012099	NP_036231	O15446	RPA34_HUMAN		4	TCTTGTCCCCCC	0.612	
-	20	2714	.1_5'Flank|PLEK	NM_020904	NP_065955	Q9H4M7	PKHA4_HUMAN		3	GATCTGGGGGG	0.687	
-	5	1156_1157	ak.1_Intron|ZNF81	NM_001031665	NP_001026835	Q0VGE8	ZN816_HUMAN	2H2-type 3.	0	ACACTTGTAAGT	0.386	
-	14	1524	rcp.1_Frame_Shif	NM_001142286	NP_001135758	Q96SB8	SMC6_HUMAN	Potential.	6	AAGATATTTTTTT	0.343	
+	3	628_629		NM_002158	NP_002149	P32314	FOXN2_HUMAN		0	ACCCAGAAAAAA	0.431	
+	11	1709	sbz.2_Frame_Shift	NM_015252	NP_056067	Q8NDI1	EHBP1_HUMAN		2	TCACCAAAAACA	0.373	
+	1	96_98	2sda.2_In_Frame_	NM_203437	NP_982261	Q6ULP2	AFTIN_HUMAN		2	AGAGGATGATG	0.409	
-	6	1386	.M392fs|REV1_u	NM_016316	NP_057400	Q9UBZ9	REV1_HUMAN		2	TTTTCATTTTTTT	0.348	
+	1	35		NM_001008743	NP_001008743	Q6IMI6	ST1C3_HUMAN		1	GATGGAAAAAA	0.353	
+	4	610		NM_007115	NP_009046	P98066	TSG6_HUMAN	CUB.	0	TTTTTTAGATTTT	0.408	
-	6	1192_1194	_In_Frame_Del_p	NM_003387	NP_003378	O43516	WIPF1_HUMAN	Pro-rich.	2	TTCTGAGGAGG	0.685	
+	2	422	l_p.N45fs|PPP1R	NM_001080545	NP_001074014	Q8WVI7	PPR1C_HUMAN		0	CATAACCCCCC	0.388	
+	7	2047_2048	p.N645fs|SGOL2_	NM_152524	NP_689737	Q562F6	SGOL2_HUMAN		4	AGGTAATTTTTT	0.337	
-	15	3165	vdt.2_Frame_Shif	NM_152519	NP_689732	A0AUZ9	CB067_HUMAN		3	CACCTATTTTTTT	0.418	
+	4	350	_p.L117fs|RQCD1_	NM_005444	NP_005435	Q92600	RCD1_HUMAN		2	TCCCACTTTTTTT	0.413	
+	19	2288_2290	3_In_Frame_Del_	NM_015575	NP_056390	Q6Y7W6	PERQ2_HUMAN	Gln-rich.	7	TTCCCAGCAGC	0.424	
-	16	2137	p.E637fs|HDLBP_	NM_203346	NP_976221	Q00341	VIGLN_HUMAN	KH 7.	4	AGCTTCGCAGT	0.458	
-	2	297_298		NM_001899	NP_001890	P01036	CYTS_HUMAN		1	AATTCACCCCCC	0.554	rs140501583
-	1	108	rame_Shift_Del_p.	NM_006585	NP_006576	P50990	TCPQ_HUMAN		0	ACGTGAAGCGC	0.627	
+	7	817_819		NM_005049	NP_005040	Q15269	PWP2_HUMAN	Poly-Glu.	1	gaggaagaggaggag	0.527	
-	4	542	l_p.G31fs|TBC1D	NM_031937	NP_114143	Q9BXI6	TB10A_HUMAN	ab-GAP TBC.	1	CGTGGCCCCCC	0.607	
+	3	1161_1181		NM_152243	NP_689449	Q00587	BORG5_HUMAN	of [PT]-[AT]-A- [ENT]-[PT]	0	CCTGCTGCAAA	0.665	0;rs62235033;rs13056859;rs62235034
+	8	2694	Del_p.I807fs|GRM	NM_000844	NP_000835	Q14831	GRM7_HUMAN	Name=6; (Potential).	7	TTCCAATTTTTTT	0.383	

-	23	4302	I1_uc003dmm.2_3	NM_001033057	NP_001028229	Q96QZ7	MAGI1_HUMAN			6	CCCGCTTTTCC	0.587	
-	13	1581_1583	_Frame_Del_p.S1	NM_015541	NP_056356	Q96JA1	LRIG1_HUMAN	tial).|Ig-like C2-type 1.|Poly		5	GGGAGCTGCTG	0.547	
-	2	497_499	XP1_uc003dop.2_	NM_032682	NP_116071	Q9H334	FOXP1_HUMAN	Gln-rich.		2	CTGTTGCTGCT	0.586	
-	7	2698	me_Shift_Del_p.G	NM_199512	NP_955806	Q76M96	CCD80_HUMAN			2	ACACTCCCCCA	0.373	
+	2	249	3ehf.1_Frame_Shi	NM_001024660	NP_001019831	O60229	KALRN_HUMAN	CRAL-TRIO.		6	AAAGGAAAAGG	0.458	
+	4	325	1_Frame_Shift_De	NM_023943	NP_076432	Q6UXF1	TM108_HUMAN			4	CTGCTGATCTT	0.552	
-	9	1978	.N554fs|VEPH1_	NM_024621	NP_078897	Q14D04	MELT_HUMAN			5	CTGAGGTTTTTT	0.393	
+	16	2019	.M503fs|PSMD2_	NM_002808	NP_002799	Q13200	PSMD2_HUMAN			0	GCTATGGGGGA	0.463	
-	2	1425_1426	vp.2_Intron|MUC4_	NM_018406	NP_060876	Q99102	MUC4_HUMAN			0	TTCTTAGAAAAA	0.46	
-	10	1345	p.R276fs|UBXN7_	NM_015562	NP_056377	O94888	UBXN7_HUMAN	UBX.		3	TTCCCTTTTTC	0.308	
+	21	2524_2526	buy.1_In_Frame_	NM_000283	NP_000274	P35913	PDE6B_HUMAN			0	GAGAAGGAGGA	0.562	
+	1	3718_3719		NM_175918	NP_787114	Q8N1N5	CRPAK_HUMAN	7		0	GCTCACGTGCC	0.683	
+	1	3948		NM_175918	NP_787114	Q8N1N5	CRPAK_HUMAN	9		0	GAGTGCCCGCC	0.672	
-	4	678	EL1_uc003gjz.1_3	NM_025196	NP_079472	Q9HAV7	GRPE1_HUMAN			0	CACCACCCCCA	0.537	
-	6	913_914	yl.1_Frame_Shift_	NM_015030	NP_055845	O94915	FRYL_HUMAN			1	CCCTTAGACTTT	0.406	
+	11	2218	D2_uc011cdg.1_Fr	NM_000297	NP_000288	Q13563	PKD2_HUMAN	in.|Cytoplasmic (Potential).		1	AAACTGAAAAAA	0.348	
+	22	2560_2562	cgc.1_In_Frame_	NM_001148	NP_001139	Q01484	ANK2_HUMAN			14	AGGTCACCACC	0.443	
+	8	1369	U_uc011cgq.1_Int	NM_015693	NP_056508	Q9ULD6	PDZD6_HUMAN			1	GGATCATTTTTTT	0.433	
+	15	2957	ve.1_Frame_Shift_	NM_001080477	NP_001073946	Q9P273	TEN3_HUMAN	ellular (Potential).		0	CCACCTTTTTCA	0.408	
-	27	4142_4143	p.G582fs|MYO10_	NM_012334	NP_036466	Q9HD67	MYO10_HUMAN	PH 1.	.S1226fs*25(1	3	GAGGAGCCCCC	0.564	
+	46	8393_8395	E2636del|NIPBL_	NM_133433	NP_597677	Q6KC79	NIPBL_HUMAN			9	TGATGAAGAAG	0.379	
+	3	342		NM_002104	NP_002095	P49863	GRAK_HUMAN	eptidase S1.		0	GAGATCAAAAAA	0.393	
+	14	2276_2277	p.T671fs|BDP1_u	NM_018429	NP_060899	A6H8Y1	BDP1_HUMAN			2	ACTACAGAGAGA	0.302	
+	17	2312_2314	uc003kgi.3_Intron	NM_003248	NP_003239	P35443	TSP4_HUMAN	SP type-3 7.		0	AGTGTGATGAT	0.562	
-	2	321_322	H2AFY_uc003lar.1	NM_138610	NP_613258	O75367	H2AY_HUMAN	istone H2A.		0	TACTTGGGGTG	0.579	
-	8	1002	.K244fs|CDC25C_	NM_001790	NP_001781	P30307	MPIP3_HUMAN			3	AAATACTTTTTTT	0.388	
+	2	128_130	p.L24del|BTN2A2_	NM_006995	NP_008926	Q8WVV5	BT2A2_HUMAN			0	CAGCCTCcctcctc	0.483	
-	1	523_524		NM_052967	NP_443199	P35410	MAS1L_HUMAN	lasmic (Potential).		9	AGAGGACACAC	0.495	
-	20	3367	0jsc.1_Frame_Shi	NM_002714	NP_002705	Q96QC0	PP1RA_HUMAN			4	GGCAGGGGGG	0.572	
+	1	180	nrk.1_Frame_Shift_	NM_178014	NP_821133	P07437	TBB5_HUMAN			1	CGGTGCCAAGG	0.413	
-	10	1618	p.P429fs|BAT3_uc	NM_004639	NP_004630	P46379	BAG6_HUMAN	oximate repeats.|2.|Pro-rich		0	CTGGCGGGGGA	0.627	
+	15	5496	.P1736fs|PHF3_u	NM_015153	NP_055968	Q92576	PHF3_HUMAN	Pro-rich.		5	ATTTTCCCCCAC	0.507	
+	3	679	l_p.A74fs|CCDC12	NM_138771	NP_620126	Q96EE4	CC126_HUMAN			2	GGTGCTTCTAT	0.373	
+	3	358_360	F1_uc011kpa.1_In	NM_005011	NP_005002	Q16656	NRF1_HUMAN	Poly-Ala.		1	GGCCGCTGCTG	0.453	
-	1	103	9B_uc003wig.3_5'I	NM_173681	NP_775952	Q674R7	ATG9B_HUMAN	smic (By similarity).		1	CTTCTCCCCCC	0.642	
+	9	940_941	AM9_uc011lcg.1_R	NM_003816	NP_003807	Q13443	ADAM9_HUMAN	otential).|Peptidase M12B.		2	AGTGGCGGGAA	0.376	
+	6	690_691	_p.L221fs|PREX2_	NM_024870	NP_079146	Q70Z35	PREX2_HUMAN			17	AAGTTAGAAGTT	0.465	rs142449465
+	9	1115	yar.2_Frame_Shift	NM_004133	NP_004124	Q14541	HNF4G_HUMAN			1	CTCCCGGGGGA	0.463	
+	2	694	_p.V167fs|PDP1_u	NM_018444	NP_060914	Q9P0J1	PDP1_HUMAN			4	GGGGGTTTTTG	0.483	
-	1	2929	p.N621fs|RANBP6	NM_012416	NP_036548	O60518	RNBP6_HUMAN	HEAT 7.		3	ATGACATTTTTTT	0.358	
-	11	1166_1168	>P|HNRNPK_uc0	NM_031262	NP_112552	P61978	HNRPK_HUMAN	epeats.|2 X 22 AA approxin		1	TCTAGGTGGTG	0.522	
+	48	6083	_Shift_Del_p.L163	NM_020893	NP_065944					7	TCTTCTCCAGCC	0.522	
+	13	3791_3793		NM_173689	NP_775960	Q5IJ48	CRUM2_HUMAN	ical; (Potential).		1	CCTGCCTCCTC	0.67	
+	13	2206	5fs|DDX3X_uc011	NM_001356	NP_001347	O00571	DDX3X_HUMAN	ecessary for interaction witl		6	AGACCAAAAAG	0.433	
+	5	716_718	04eib.1_In_Frame_	NM_016607	NP_057691	Q9UH62	ARMX3_HUMAN			2	TGGTCTGATGAT	0.448	
-	8	1013	mwc.1_Frame_Shi	NM_024597	NP_078873	Q8IWC1	MA7D3_HUMAN			4	CACCTGGGGGG	0.532	
+	7	512_514	j.1_In_Frame_Del_	NM_007150	NP_009081	O15231	ZN185_HUMAN	Poly-Glu.		3	GACACCgaggagg	0.522	

+	1	1337_1339		NM_207334	NP_997217	Q6ZT52	FA43B_HUMAN		NA	0	gaggacgaggaggag	0.567	
-	11	1675_1676	9wbk.2_Frame_S	NM_030816	NP_110443	Q8N6S4	AN13C_HUMAN		NA	0	GTAGCTTTAAAC	0.361	
+	23	2276_2278	dge.1_In_Frame_	NM_015978	NP_057062	Q59H18	TNI3K_HUMAN	Poly-Ser.	NA	10	TCACCTTCTTC	0.473	
-	25	4510		NM_024408	NP_077719	Q04721	NOTC2_HUMAN	ellular (Pote	NA	27	GTGCTGGGGGG	0.632	
+	7	1724_1726	e_Del_p.E466del|	NM_005807	NP_005798	Q92954	PRG4_HUMAN	epeats of K-	NA	1	ACCAAGGAGCC	0.635	
-	20	2528_2530	E813del|SFMBT2_	NM_001029880	NP_001025051	Q5VUG0	SMBT2_HUMAN		NA	8	GTCTCTCCTCC	0.596	
-	26	3234	p.P1074fs|SMARC	NM_003075	NP_003066	Q8TAQ2	SMRC2_HUMAN	Pro-rich.	NA	6	GTCCAGGGGGG	0.577	
+	16	2686_2688	tbn.1_In_Frame_	NM_004592	NP_004583	Q12872	SFSWA_HUMAN	g/Ser-rich (	NA	0	CACGAGAAGAA	0.493	
+	3	707_710	vbk.2_Frame_Shi	NM_015116	NP_055931	Q9Y2L9	LRCH1_HUMAN	LRR 3.	NA	2	CGCCCTGCCT	0.436	
+	20	3706_3707	.A881fs|LMO7_uc	NM_015842	NP_056667	Q8WWI1	LMO7_HUMAN		NA	5	AGGCAGAGAG	0.386	
-	1	61_63	.2_5'UTR|PGBD4_	NM_020154	NP_064539	Q9NPA0	CO024_HUMAN		NA	0	CGATAGCAGCA	0.665	
+	1	97_98	_p.L13fs|B2M_uc	NM_004048	NP_004039	P61769	B2MG_HUMAN		NA	3	CGCTACTCTCT	0.614	
+	7	4096_4098		NM_015042	NP_055857	O15014	ZN609_HUMAN	Poly-His.	NA	3	CACACACCACC	0.576	
-	22	3911		NM_002705	NP_002696	O60437	PEPL_HUMAN	Potential.	NA	6	ATTTCCTTTTTCA	0.522	
-	8	907_909	p.E75del|MKS1_u	NM_017777	NP_060247	Q9NXB0	MKS1_HUMAN		NA	1	CCCGCTCCTCC	0.532	
+	13	2443		NM_182973	NP_892018	Q7Z410	TMPS9_HUMAN	ellular (Pote	NA	2	AGCTACCAGGT	0.567	
-	5	915	Del_p.Q261fs|ECS	NM_016581	NP_057665	Q9BQ95	ECSIT_HUMAN		NA	1	GGGCTGGGGGG	0.582	
+	13	1487	D1A_uc010xsf.1_	NM_020895	NP_065946	Q96CP6	GRM1A_HUMAN		NA	0	CGCGGCCCCCA	0.692	
+	17	1944_1945	iu.2_Frame_Shift_	NM_000540	NP_000531	P21817	RYR1_HUMAN	mic.|B30.2/	NA	12	CTCCCTGTGTGT	0.53	
-	3	305	NKRD23_uc002s	NM_144994	NP_659431	Q86SG2	ANR23_HUMAN		NA	1	TTCCTGGGGGG	0.527	
+	3	1075_1077	.1_Intron|GZF1_u	NM_022482	NP_071927	Q9H116	GZF1_HUMAN		NA	1	gaggaagaggaggag	0.384	
+	6	641	S1_uc010zte.1_R	NM_021067	NP_066545	Q14691	PSF1_HUMAN		NA	2	CCTATTAAAAAA	0.299	
-	12	5661_5663	.2_In_Frame_Del_	NM_014071	NP_054790	Q14686	NCOA6_HUMAN	.|Gln-rich.|C	NA	7	TCATTtgttgctgctgc	0.498	895426;rs140426729
-	60	8252_8253		NM_005560	NP_005551	O15230	LAMA5_HUMAN	omain II and	NA	3	GGCAGCCCCCC	0.663	
+	2	378_380		NM_033318	NP_201575	Q9H4I9	CV032_HUMAN	sp/Glu-rich	NA	1	AGAGGATGATG	0.478	rs141840500
+	22	3696	p.S679fs|SHANK3	NM_001080420	NP_001073889	F2Z3L0	F2Z3L0_HUMAN		NA	1	ACCAGCAACGG	0.692	
-	3	713_715	bns.1_In_Frame_	NM_015472	NP_056287	Q9GZV5	WWTR1_HUMAN	ential.|Gln-r	NA	4	GTTTCTGCTGC	0.581	
+	1	3808_3809		NM_175918	NP_787114	Q8N1N5	CRPAK_HUMAN	8	NA	0	CTCACATGTGCC	0.683	123539;rs79888804
-	4	1088_1090	y.2_In_Frame_De	NM_001031732	NP_001026902	Q96MU7	YTDC1_HUMAN	Glu-rich.	NA	2	tcttcttcttcctcctcctc	0.202	rs141105019
+	11	1625_1627	lj.2_In_Frame_De	NM_198892	NP_942595	Q9NSY1	BMP2K_HUMAN	Gln/His-rich.	NA	1	cagcagcaccaccac	0.172	
-	2	1076_1078	me_Del_p.P343de	NM_178835	NP_849157	Q17R98	ZN827_HUMAN	Pro-rich.	NA	0	GGGATTgtggtggt	0.35	
-	7	1662	ime.2_Frame_Shi	NM_001009555	NP_001009555	Q5HYK7	SH319_HUMAN	Pro-rich.	NA	2	GAACTGGGGGG	0.557	
-	7	1606_1608	0irc.1_In_Frame_	NM_020870	NP_065921	Q7Z6J0	SH3R1_HUMAN	Poly-Ala.	NA	3	ATTCCAGCAGC	0.601	
+	11	1893		NM_052909	NP_443141	Q96PX9	PKH4B_HUMAN		NA	2	CCCTTGCCCAG	0.662	
+	3	292_299		NM_175921	NP_787117	A6NDU8	CE051_HUMAN		NA	0	AAGAGCTGATTA	0.298	
+	13	2025	f.2_Frame_Shift_	NM_012343	NP_036475	Q13423	NNTM_HUMAN	chondrial ma	NA	3	ACTGACCCCCC	0.463	
+	1	725_727	003kuq.1_5'Flank	NM_001046	NP_001037	P55011	S12A2_HUMAN	ytoplasmic	NA	3	ACTCCGGCGGC	0.65	
+	1	184_185	_uc003nyt.2_5'UT	NM_032454	NP_115830	P49842	STK19_HUMAN		NA	4	CGGGCAAACC	0.634	
-	5	1557_1559	6_377EE>E|DAX	NM_001350	NP_001341	Q9UER7	DAXX_HUMAN	ial.|Necessa	NA	23	tcttcttcttcctcctcctc	0.251	
+	19	4224	1BP1_uc010jvn.2	NM_017754	NP_060224	Q6BDS2	URFB1_HUMAN		NA	3	TGATATCCCCCC	0.517	
-	4	1648	318_uc003ouw.2_	NM_014345	NP_055160	Q5VUA4	ZN318_HUMAN		NA	7	TCGCCTTTTTT	0.493	
-	22	2918	y.3_Frame_Shift_	NM_001144769	NP_001138241	Q03001	DYST_HUMAN	Spectrin 1.	NA	14	TCCACTGCGTCT	0.448	
-	7	1235_1236	edm.1_Frame_Shi	NM_000416	NP_000407	P15260	INGR1_HUMAN	lasmic (Pote	NA	1	AAGAACTCTCT	0.431	
-	2	458		NM_032936	NP_116325	Q9H2L4	TMM60_HUMAN		NA	0	CCAGGCTTTTTT	0.408	
+	8	1031	_p.F215fs|DYNC1	NM_004411	NP_004402	O14576	DC1I1_HUMAN		NA	4	GACATCTTTTTT	0.383	
+	2	163	Shift_Del_p.D13fs	NM_145102	NP_659570	Q9Y2L8	ZKSC5_HUMAN		NA	1	TTAGACCCCCC	0.483	
-	3	838_842	vja.2_Frame_Shift	NM_003391	NP_003382	P09544	WNT2_HUMAN		NA	7	TCTGGCAtcctttcc	0.424	

-	20	2915	_p.P781fs|TNPO3_	NM_012470	NP_036602	Q9Y5L0	TNPO3_HUMAN		NA	5	GTATAGGGGGG	0.483	
+	6	1464	.P226fs|ZNF398_	NM_170686	NP_733787	Q8TD17	ZN398_HUMAN		NA	1	AGACACCCCCC	0.587	
+	1	793_795		NM_138400	NP_612409	Q5C9Z4	NOM1_HUMAN	ization and	NA	0	gaaagtgaggaggag	0.236	
-	3	1464	fs|RAB11FIP1_uc	NM_001002814	NP_001002814	Q6WKZ4	RFIP1_HUMAN		NA	3	GTCCTCCCCCG	0.567	
+	12	1710_1711	.H509fs|ESRP1_	NM_017697	NP_060167	Q6NXG1	ESRP1_HUMAN	RRM 3.	NA	4	TGTCATAAAAAA	0.436	
-	1	315	mcx.1_Frame_Shi	NM_198123	NP_937756	Q7Z407	CSMD3_HUMAN	ical; (Potent	NA	63	GTCAATAAAAA	0.498	
+	3	610_612	ysi.2_In_Frame_D	NM_002467	NP_002458	P01106	MYC_HUMAN	Poly-Gln.	NA	6	CTACCAGCAGC	0.611	rs61752959
+	1	511_513		NM_001013735	NP_001013757	Q5VYV0	FOXB2_HUMAN	Poly-Pro.	NA	0	ccgcccccgccgccg	0.315	
-	8	2229	KNA_uc004bis.3_	NM_030767	NP_110394	Q7Z591	AKNA_HUMAN		NA	6	GGCATGGGGGC	0.577	
-	22	6093	f.2_Frame_Shift_	NM_002160	NP_002151	P24821	TENA_HUMAN	nectin type-	NA	7	TGCCCGGGGGG	0.478	rs148674204
+	2	218_219		NM_001145249	NP_001138721	P0CG42	F157B_HUMAN	Gln-rich.	NA	0	cagcggcggcagcag	0.386	
+	5	716_718	04eib.1_In_Frame_	NM_016607	NP_057691	Q9UH62	ARMX3_HUMAN		NA	2	TGGTCTGATGAT	0.448	
+	3	1864_1866	Q581del|MAMLD1	NM_005491	NP_005482	Q13495	MAMD1_HUMAN	Poly-Gln.	NA	0	Tgcagctgcagcagca	0.488	
-	3	274_276	fen.2_Intron|CD9	NM_031462	NP_113650	Q8TCZ2	C99L2_HUMAN	ar (Potential	NA	3	GGTTGTGGTGG	0.552	
-	8	877_879		NM_001561	NP_001552	Q07011	TNR9_HUMAN	ential).|Inter	p.E250G(1)	4	TCCTCCTTCTTC	0.379	
-	7	868_869	p.F153fs|C1orf201_uc001bjd.2_Frame_Shift_Del_p.F2			Q5TH74	CA201_HUMAN			2	ACGGGAAAAGA	0.455	
-	8	728_730	142del|EYA3_uc0	NM_001990	NP_001981	Q99504	EYA3_HUMAN			3	GCTACTGCTGC	0.404	
-	1	702_704		NM_001080418	NP_001073887	O95886	DLGP3_HUMAN	Poly-His.		3	CGGGACtggtggt	0.537	
+	7	798_799		NM_033055	NP_149044	Q96MC6	HIAT1_HUMAN	lasmic (Potential).		0	TCCAGCTTTTTT	0.386	
+	8	2280	zr.1_Frame_Shift_	NM_004326	NP_004317	O00512	BCL9_HUMAN	y-Pro.|Pro-rich.		6	GAGGACCCCCC	0.582	
+	8	3460	zr.1_Frame_Shift_	NM_004326	NP_004317	O00512	BCL9_HUMAN	Pro-rich.		6	TAAGTCCCCCC	0.622	
-	11	2245_2247	H700del|PBXIP1_	NM_020524	NP_065385	Q96AQ6	PBIP1_HUMAN	His-rich.		1	CCCCGGTGGTG	0.64	rs143592003
-	2	1126	1fpt.1_Frame_Shif	NM_030980	NP_112242	Q9H9L3	I20L2_HUMAN	xonuclease.		2	GTTGAGGGGGG	0.557	
-	1	356_358		NM_030916	NP_112178	Q96NY8	PVRL4_HUMAN			2	CAGTAGCAGCA	0.512	
-	2	1361_1363	.2_Intron|RGL1_u	NM_203454	NP_982279	Q8WW27	ABEC4_HUMAN			0	TCCCTTTCTTCTT	0.419	rs141411396
-	1	89_91		NM_000537	NP_000528	P00797	RENI_HUMAN			4	CCAGAGCAGCA	0.581	917743;rs142739309
-	1	479		NM_032833	NP_116222	Q5SWA1	PR15B_HUMAN			2	GAGGGAAAAAG	0.622	
-	2	253	10pte.1_Frame_S	NM_018252	NP_060722	Q9H813	TM206_HUMAN	lasmic (Potential).		1	CTGCTCGTCTG	0.542	
-	38	5610	xgh.1_Frame_Shi	NM_018072	NP_060542	Q9H583	HEAT1_HUMAN			3	TGTAAGTTTTTTT	0.438	
-	16	6375	1843fs|JMJD1C_u	NM_032776	NP_116165	Q15652	JHD2C_HUMAN			6	TTTACCTTTTTTT	0.373	
-	5	848_849		NM_004969	NP_004960	P14735	IDE_HUMAN			3	CTAAAACACAAA	0.337	
-	7	1155_1156	po.1_Frame_Shif	NM_021828	NP_068600	Q8WWQ2	HPSE2_HUMAN			1	CACTTTCTGAAT	0.465	
+	1	655	_p.I177fs|CNNM2_	NM_017649	NP_060119	Q9H8M5	CNNM2_HUMAN			2	GAGATCAAACC	0.637	
+	21	3110	CS3_uc010qqz.1_	NM_014978	NP_055793	Q9UPU3	SORC3_HUMAN	enal (Potential).		10	ACTTTGGACAG	0.453	
+	3	305	10qsx.1_RNA|FAM	NM_207009	NP_996892	Q8TCE6	FA45A_HUMAN			1	GACTCATTTTTC	0.299	
-	22	2979	01nts.1_Frame_S	NM_153265	NP_694997	Q32P44	EMAL3_HUMAN			1	GGAGGCGGGGG	0.512	
+	4	308	S_uc009yyo.2_R	NM_000317	NP_000308	Q03393	PTPS_HUMAN			0	GATCTCAAAAAA	0.408	
-	22	3672_3674	1qfl.2_In_Frame_	NM_020228	NP_064613	Q9NQV6	PRD10_HUMAN	Poly-Thr.		1	CCGTTGGTGGT	0.547	
-	3	257_259		NM_006248	NP_006239					0	TCCTGGAGGAG	0.601	
+	3	968	1_uc009zmb.1_F	NM_002135	NP_002126	P22736	NR4A1_HUMAN			0	CAGCTGGGGGA	0.632	
+	1	592		NM_001005497	NP_001005497	A6NL08	O6C75_HUMAN	Name=5; (Potential).		3	ATGGCATTTTTTT	0.393	
+	3	344_345	_p.S78fs|RFC3_u	NM_002915	NP_002906	P40938	RFC3_HUMAN			0	TCCATCTAAAAAA	0.267	
-	14	3949_3950	C3H13_uc001vas.	NM_015070	NP_055885	Q5T200	ZC3HD_HUMAN	Potential.		2	gtatctctcctctctctctc	0.178	
+	4	541	1_Frame_Shift_De	NM_144595	NP_653196	Q8ND83	SLAI1_HUMAN			2	TCAGGAAAAAA	0.388	
-	2	2153_2154	p.K560fs|LIG4_uc	NM_002312	NP_002303	P49917	DNLI4_HUMAN			0	TTCCGCTTTTTT	0.386	
-	16	1016	4A1_uc010agl.2_	NM_001845	NP_001836	P02462	CO4A1_HUMAN	le-helical region.		6	ACTCCCTTTTTC	0.398	
-	19	4102_4104	iq.3_In_Frame_D	NM_014977	NP_055792	Q9UKV3	ACINU_HUMAN	sp/Glu/Lys-rich.		4	ctccttttgctcttcttcttct	0.36	

+	16	1812_1813	GS6_uc001xmy.3_	NM_004296	NP_004287	P49758	RGS6_HUMAN	RGS.	3	CATCTACAAGCT	0.49	
+	8	3011_3013	.Q981del|MGA_uc	NM_001080541	NP_001074010	Q8IWI9	MGAP_HUMAN	Gln-rich.	12	GGCACAGCAGC	0.458	
-	4	744_746	2azg.2_In_Frame_	NM_020447	NP_065180	Q5XKK7	CO017_HUMAN		0	CCTCTGCAGATG	0.547	
+	15	1993_1995	.S436del|SLC5A1	NM_052944	NP_443176	Q8WWX8	SC5AB_HUMAN	lasmic (Potential).	2	AGGCCAGCAGC	0.542	
+	3	625	.2_Frame_Shift_D	NM_004937	NP_004928	O60931	CTNS_HUMAN	enal (Potential).	0	TTATCCTTTTTCC	0.393	
+	1	158_160	me_Del_p.K7del|	NM_003457	NP_003448	O43670	ZN207_HUMAN		0	TCGCAAGAAGA	0.542	
-	2	440_442		NM_052850	NP_443082	Q8TAE8	G45IP_HUMAN	y-Gln.|Potential.	2	TCCCGCTGCTG	0.635	
+	7	1022	0xru.1_Frame_Shi	NM_001114093	NP_001107565	Q8ND56	LS14A_HUMAN		1	GTCATCGGGGT	0.438	
+	2	268_269	odk.2_In_Frame_I	NM_001749	NP_001740	P04632	CPNS1_HUMAN	ch (hydrophobic).	0	GGCcgggggcggc	0.322	
-	1	1653_1654	IF3C_uc010ykr.1_	NM_002254	NP_002245	O14782	KIF3C_HUMAN	inesin-motor.	4	GGCATTCCCCCC	0.614	
-	5	1569_1570	sud.1_Frame_Shi	NM_032788	NP_116177	Q96K75	ZN514_HUMAN		0	ATAGGGTTTTTT	0.396	
-	1	128	me_Shift_Del_p.P	NM_001087	NP_001078	Q13685	AAMP_HUMAN		1	CCAGTGGGGGG	0.617	
-	6	760	p.G168fs|DOCK10	NM_014689	NP_055504	Q96BY6	DOC10_HUMAN		2	CTCCACCCCCC	0.498	
+	1	52_54	p.L14del|CHRNG_	NM_005199	NP_005190	P07510	ACHG_HUMAN		0	CCTCCTGCTGC	0.655	
+	19	2288_2290	3_In_Frame_Del_	NM_015575	NP_056390	Q6Y7W6	PERQ2_HUMAN	Gln-rich.	7	TTCCCAGCAGC	0.424	
-	2	743	13A3_uc010gho.1_	NM_033550	NP_291028	Q96S44	PRPK_HUMAN	rotein kinase.	0	TTCCAGGGGGG	0.493	
-	3	428_430	_19DD>D|TFIP11_	NM_012143	NP_036275	Q9UBB9	TFP11_HUMAN	Poly-Asp.	0	GCTCGTCATCAT	0.532	rs145794160
-	13	2272_2274	p.2_In_Frame_Del	NM_001098504	NP_001091974	Q92841	DDX17_HUMAN	Poly-Pro.	4	ggagggggaggagg	0.36	
+	18	4729	ayn.3_Frame_Shif	NM_001162501	NP_001155973	Q9UPQ9	TNR6B_HUMAN		0	GTGCTGGGGGG	0.483	
+	3	244	_p.G43fs|KCTD6_	NM_001128214	NP_001121686	Q8NC69	KCTD6_HUMAN	BTB.	1	TGTTTGGGGGG	0.468	
-	13	1581_1583	_Frame_Del_p.S1	NM_015541	NP_056356	Q96JA1	LRIG1_HUMAN	tial).|Ig-like C2-type 1.|Poly	5	GGGAGCTGCTG	0.547	
-	5	1231		NM_000097	NP_000088	P36551	HEM6_HUMAN		0	CTCCTGGGGGG	0.498	
+	2	1293_1295	y.3_RNA|LNP1_uc	NM_001085451	NP_001078920	A1A4G5	LNP1_HUMAN	Poly-Asp.	0	ACAAAGATGATG	0.507	
+	13	2408	p.K358fs|BBX_uc	NM_001142568	NP_001136040	Q8WY36	BBX_HUMAN	Lys-rich.	4	AATTTGAAAAAA	0.383	
-	15	2113	D11_uc011blr.1_3	NM_032169	NP_115545	Q709F0	ACD11_HUMAN		1	TTACTCCAGGTG	0.353	
-	4	535	N1_uc003euv.1_F	NM_019001	NP_061874	Q8IZH2	XRN1_HUMAN		3	GTCTGTGGAAAT	0.284	
-	3	271_272	.1_Frame_Shift_In	NM_000460	NP_000451	P40225	TPO_HUMAN		1	GACAGCGTTAGC	0.515	
+	1	425_427		NM_020368	NP_065101	Q9NQZ2	SAS10_HUMAN	Glu-rich.	0	gatggcgaggaggag	0.291	
-	3	747_748	_Shift_Ins_p.K74f	NM_003948	NP_003939	Q92772	CDKL2_HUMAN	rotein kinase.	7	ACCATCGTTTTTT	0.322	
+	7	1570	hqa.2_Frame_Shi	NM_080683	NP_542414	Q12923	PTN13_HUMAN		6	ATATATCACACTC	0.443	
+	3	335	C9_uc003ieb.2_F	NM_005033	NP_005024	Q06265	EXOS9_HUMAN	ARE binding.	0	GTATTCTTTTTTT	0.383	
-	17	2126	.2_Frame_Shift_D	NM_144643	NP_653244	Q96NL6	SCLT1_HUMAN	Potential.	5	TTTGGCTTTTTTT	0.353	
-	10	1909	H10_uc011cnu.1_	NM_006727	NP_006718	Q9Y6N8	CAD10_HUMAN	|Extracellular (Potential).	12	AAACTGAAAAAA	0.313	
+	2	418		NM_016048	NP_057132	Q96CN7	ISOC1_HUMAN		0	TATTTTGGGGAT	0.378	
+	9	1679	uc003kwr.3_Intron	NM_003059	NP_003050	Q9H015	S22A4_HUMAN	Name=12; (Potential).	0	TCACCCTTTTTTT	0.418	
+	6	912_914	ame_Del_p.G153d	NM_001903	NP_001894	P35221	CTNA1_HUMAN		11	GGGTGGAGGAG	0.512	
+	3	227	_p.G16fs|TMEM14	NM_016462	NP_057546	Q9P0S9	TM14C_HUMAN	ical; (Potential).	0	GCTTTGGCTACC	0.453	
-	12	1998	nba.2_Frame_Shi	NM_005493	NP_005484	Q96S59	RANB9_HUMAN	action with FMR1.	2	TCAACATTTTTTT	0.378	
-	3	374	_p.P100fs|FAM65B	NM_014722	NP_055537	Q9Y4F9	FA65B_HUMAN	cell filopodia formation.	1	CTCTTTGGGGGG	0.428	
-	1	175_176	1_RNA|HIST1H2A	NM_021058	NP_066402	P06899	H2B1J_HUMAN		0	AACCTTGTACAC	0.54	
+	4	759_761	me_Del_p.Q194de	NM_005007	NP_004998	Q9UBC1	IKBL1_HUMAN		0	GTGCCAGCAGC	0.645	
-	12	1315	009_uc003pkk.2_	NM_014895	NP_055710	Q5TB80	QN1_HUMAN		1	TTGTCAAAAAAA	0.358	
-	10	1313_1314		NM_015718	NP_056533	Q9HBY0	NOX3_HUMAN	ical; (Potential).	1	CAACGCACACAC	0.53	
-	4	864_866		NM_001002926	NP_001002926	Q3B726	RPA43_HUMAN	Lys-rich.	1	GCTTTTTCTTCTT	0.433	
+	11	2523_2524	yh.1_Frame_Shift_	NM_002214	NP_002205	P26012	ITB8_HUMAN	m repeats.|Extracellular (P	3	GGCACGTGTGTG	0.554	
+	3	1631_1632		NM_147128	NP_667339	Q8NHG8	ZNRF2_HUMAN		0	TGAGTAAAGATG	0.356	
-	6	928_930	3tri.2_In_Frame_D	NM_004577	NP_004568	P78330	SERB_HUMAN		2	CAGCAGGAGGA	0.246	

-	2	83_85	_uc010lbj.1_In_Fra	NM_004603	NP_004594	Q16623	STX1A_HUMAN	lasmic (Potential).		0	AGCGACATCATC	0.586	
-	5	964	2_Intron|GPC2_uc	NM_152742	NP_689955	Q8N158	GPC2_HUMAN			2	GGGGACCCCCC	0.642	
+	5	572	ka.2_Frame_Shift_	NM_015908	NP_056992	Q9BXP5	SRRT_HUMAN			2	ATGCTGGGGGG	0.607	
-	4	3398_3401	ame_Shift_Del_p.T	NM_001002814	NP_001002814	Q6WKZ4	RFIP1_HUMAN			3	TGTGGTGAGTGT	0.549	
-	21	1921	lee.1_Frame_Shift	NM_003580	NP_003571	Q92636	FAN_HUMAN	BEACH.		1	TGGTGTCACAAT	0.423	
-	5	987_989		NM_014729	NP_055544	O94900	TOX_HUMAN	lization signal (Potential).		4	GGATCCTTCTTCT	0.453	
-	1	468_469	Flank|COPS5_uc0	NM_006837	NP_006828	Q92905	CSN5_HUMAN			2	TCCTTAGTCCAG	0.545	
+	10	1740	LF1_uc003xyf.2_F	NM_015170	NP_055985	Q8IWU6	SULF1_HUMAN			7	TGTGCCTTTTTTT	0.408	
-	14	1846_1847	p.P525fs|EIF2C2_	NM_012154	NP_036286	Q9UKV8	AGO2_HUMAN	Piwi.		0	CCGGCGGGGGC	0.644	rs148575703
-	2	136_138	_Del_p.24_25AA>A	NM_078480	NP_510965	Q9UHX1	PUF60_HUMAN	homodimerization.		0	caccactgccgccgccg	0.404	
-	1	592	_Shift_Del_p.P12fs	NM_152572	NP_689785	Q96MA6	KAD8_HUMAN		p.E13fs*40(2)	0	CATCTCGGGGGG	0.697	
+	6	1019_1020	Shift_Del_p.Q191f	NM_018360	NP_060830	Q9NUQ3	TXLNG_HUMAN	Potential.		1	ACATCAGAGAGA	0.386	
+	20	2671_2673	p.E837del|CNKSR2	NM_014927	NP_055742	Q8WXI2	CNKR2_HUMAN	ential.|Poly-Glu.		2	gaggaagaggaggag	0.379	
+	8	2280	ozr.1_Frame_Shift_	NM_004326	NP_004317	O00512	BCL9_HUMAN	ly-Pro.|Pro-rich.		6	GAGGACCCCCC	0.582	
-	2	3480_3482	vne.1_In_Frame_D	NM_007113	NP_009044	Q07283	TRHY_HUMAN	30 AA tandem repeats.		5	GCCTTCTCTTCTC	0.172	
+	2	672		NM_001025231	NP_001020402	Q5T749	KPRP_HUMAN	Gln-rich.		5	ACTACACCCCCCA	0.572	
-	21	4220_4223	GON4L_uc001fmb.3	NM_001037533	NP_001032622	Q3T8J9	GON4L_HUMAN			3	AAGACTGTCTGT	0.49	
-	2	1126	1fpt.1_Frame_Shif	NM_030980	NP_112242	Q9H9L3	I20L2_HUMAN	Exonuclease.		2	GTTGAGGGGGG	0.557	
-	6	775	_p.E211fs|CALCOC	NM_020898	NP_065949	Q9P1Z2	CACO1_HUMAN			1	TGATCTCCCCATG	0.527	
+	87	13755_13757		NM_002332	NP_002323	Q07954	LRP1_HUMAN	ical; (Potential).		22	GCTGTTGCTGCTC	0.557	
+	12	2732	oq.2_Frame_Shift_	NM_005269	NP_005260	P08151	GLI1_HUMAN			15	TTGATTCCCCCAC	0.567	
-	21	3042	tbb.1_Frame_Shift	NM_001077261	NP_001070729	Q9Y618	NCOR2_HUMAN			4	ACGATGGGGGG	0.652	rs12321697
+	1	40_42	D1_uc010brm.1_5'	NM_012217	NP_036349	Q9BZJ3	TRYD_HUMAN			0	GAGCCTGCTGCT	0.685	
+	13	3813_3815		NM_014712	NP_055527	O15047	SET1A_HUMAN	Ser-rich.		3	AGctcctcatcctcctcct	0.389	
+	11	2629_2631	02gix.2_In_Frame_	NM_001080424	NP_001073893	O15054	KDM6B_HUMAN	o-rich.|Thr-rich.		2	CGCCGTcaccacca	0.369	
+	7	894		NM_178170	NP_835464	Q86SG6	NEK8_HUMAN			6	AGGTATCCCCCGC	0.617	
+	7	1069	_p.G237fs|AP2B1_	NM_001282	NP_001273	P63010	AP2B1_HUMAN			1	TGTCTGGGGAGC	0.403	
-	3	1648_1650	002sit.3_In_Frame_	NM_015470	NP_056285	Q9BXF6	RFIP5_HUMAN			0	GCCTTGGTGGTC	0.635	
+	6	641	NS1_uc010zte.1_R	NM_021067	NP_066545	Q14691	PSF1_HUMAN			2	CCTATTAAAAAAA	0.299	
-	16	5191_5192	ds.1_Frame_Shift_	NM_033081	NP_149072	Q9BTC0	DIDO1_HUMAN			6	CGGGGCGGGTGC	0.728	
+	5	1304_1306		NM_152612	NP_689825	Q8IYX3	CC116_HUMAN			2	CCCCTGCAGCAG	0.606	
-	7	789_791		NM_016449	NP_057533	Q6PGQ1	CV043_HUMAN	Asp-rich.		1	ACCTGGGcatcatca	0.261	
-	30	4280_4282		NM_002473	NP_002464	P35579	MYH9_HUMAN	Potential.		11	CTTGGCCTCCTCC	0.65	
+	1	221_223		NM_014240	NP_055055	Q9UGP4	LIMD1_HUMAN	tes nuclear export.		1	CCTCCAGCAGCA	0.626	
-	4	1613_1615	40QQ>Q|QRICH1_	NM_198880	NP_942581	Q2TAL8	QRIC1_HUMAN	Gln-rich.		1	CTTGGAgttgctgctgc	0.36	
+	2	1293_1295	y.3_RNA|LNP1_uc	NM_001085451	NP_001078920	A1A4G5	LNP1_HUMAN	Poly-Asp.		0	ACAAAGATGATGA	0.507	
-	13	5978	.N1917fs|GOLGB1	NM_004487	NP_004478	Q14789	GOGB1_HUMAN	ic (Potential).|Potential.		10	AGCTCATTTTTTA	0.358	
+	1	425_427		NM_020368	NP_065101	Q9NQZ2	SAS10_HUMAN	Glu-rich.		0	gatggcgaggaggag	0.291	
+	7	1407	p.G204fs|SLC1A3	NM_004172	NP_004163	P43003	EAA1_HUMAN			0	GTGATTGGGGGG	0.517	
+	11	2401	p.G581fs|LARP1_	NM_033551	NP_291029	Q6PKG0	LARP1_HUMAN			4	ACCCAGGGGGG	0.547	
-	5	372_374	kw.3_In_Frame_De	NM_003322	NP_003313	O00294	TULP1_HUMAN	Poly-Glu.		3	tcctcctcttcctcctcctc	0.389	
-	12	1315	1009_uc003pkk.2_	NM_014895	NP_055710	Q5TB80	QN1_HUMAN			1	TTTGTCAAAAAAA	0.358	
-	17	2245	p.G723fs|ABCB4_	NM_018849	NP_061337	P21439	MDR3_HUMAN	).|ABC transmembrane typ		6	CTGAAGCCCCCC	0.453	
-	15	1860	s|TAF6_uc011kji.1_	NM_139315	NP_647476	P49848	TAF6_HUMAN			2	GTGCTGGGGGG	0.657	
+	14	2288	G247fs|SLC12A9_u	NM_020246	NP_064631	Q9BXP2	S12A9_HUMAN	cellular (Potential).		0	GGGTCTGGGGGC	0.692	
+	3	751	_Shift_Del_p.W155	NM_057168	NP_476509	Q9UBV4	WNT16_HUMAN			5	GCACTGGGGGG	0.532	
-	4	3398_3401	ame_Shift_Del_p.T	NM_001002814	NP_001002814	Q6WKZ4	RFIP1_HUMAN			3	TGTGGTGAGTGT	0.549	

+	1	804_805	1463_uc003xvh.2	NM_152414	NP_689627	Q8NFJ8	BHE22_HUMAN	Gly-rich.	0	cgggaagtggcggcg	0.584	
-	2	P_uc011lwc.1_Intron|IKBKAP_		NM_003640	NP_003631	O95163	ELP1_HUMAN		7	TTCGCATGATGA	0.404	
+	20	4967	1aoj.2_Frame_Shi	NM_015215	NP_056030	Q9Y6Y1	CMTA1_HUMAN	IQ 2.	9	ATGAACAAAAAA	0.473	
-	19	3629_3631	0oag.1_In_Frame_	NM_001009566	NP_001009566	O94985	CSTN1_HUMAN	cidic).|Cytoplasmic (Potenti	1	CTCCCCCTCCTC	0.557	
+	9	1342	BLIM1_uc001axh.	NM_017556	NP_060026	Q8WUP2	FBLI1_HUMAN	nding.|LIM zinc-binding 2.	1	AATTCGCCCCCG	0.488	
-	7	894	1_Intron|MST1P9_	NR_002729					0	CCCCCCGCCCAC	0.657	rs3982176
+	1	528_529	uc001bve.1_RNA	NM_052841	NP_443073	Q96PN8	TSSK3_HUMAN	rotein kinase.	1	ATTTTCCAAAAAA	0.52	
+	15	2319		NM_017629	NP_060099	Q9HCK5	AGO4_HUMAN	Piwi.	1	TGGTGCAAAAAA	0.383	
+	34	4444_4446	.E504del|MACF1_	NM_012090	NP_036222	Q9UPN3	MACF1_HUMAN	Poly-Glu.	16	GTCTGGAGGAG	0.389	
+	10	1573_1575	.L513del|MPL_uc	NM_005373	NP_005364	P40238	TPOR_HUMAN	(Potential).| p.L510P(1)	363	TGGGCCTGCTGC	0.65	
+	12	2824		NM_014652	NP_055467	O94829	IPO13_HUMAN		1	CTTCAGGTGGTG	0.562	
-	4	577	cmv.1_Frame_Shif	NM_020365	NP_065098	Q9NR50	EI2BG_HUMAN		1	ACCTGCTTTTTTT	0.318	
+	18	2455	_Shift_Del_p.P398	NM_015112	NP_055927	Q6P0Q8	MAST2_HUMAN	rotein kinase.	11	CGTCCCTTTTTTT	0.552	
+	1	333_334	1_RNA|PCSK9_uc	NM_174936	NP_777596	Q8NBP7	PCSK9_HUMAN		4	ccgctgccactgctgct	0.574	rs67610340
-	1	1343	_5'Flank|uc010oo	NM_002228	NP_002219	P05412	JUN_HUMAN		0	TTCTTGGGGCA	0.672	
+	15	1294	GIP1_uc001dct.2	NM_032291	NP_115667	Q9BQI5	SGIP1_HUMAN	Pro-rich.	3	ACAGGCCCCCC	0.572	
-	1	145	way.2_5'Flank|MIE	NM_024763	NP_079039	Q5VTH9	WDR78_HUMAN		2	CACCCCTTTTTTT	0.622	
-	5	924_925	IQ3_uc001dfz.3_	NM_001105659	NP_001099129	A6PVS8	LRIQ3_HUMAN		2	CTGCTGTTTTTT	0.327	
-	3	606	IQ3_uc001dfz.3_	NM_001105659	NP_001099129	A6PVS8	LRIQ3_HUMAN	LRRCT.	2	ATATCCTTTTTTA	0.378	
+	23	2276_2278	dge.1_In_Frame_	NM_015978	NP_057062	Q59H18	TNI3K_HUMAN	Poly-Ser.	10	CTCACCTTCTTC	0.473	
+	2	248_249	sw.1_Frame_Shif	NM_003503	NP_003494	O00311	CDC7_HUMAN		5	CTCTTTAAAAAA	0.406	
+	14	1823	dqw.3_Frame_Sh	NM_001114106	NP_001107578	Q8N4M1	CTL3_HUMAN	ical; (Potential).	1	GTAGCTTTTTTT	0.423	
+	5	1085	1dur.2_Frame_Sh	NM_020978	NP_066188	P19961	AMY2B_HUMAN		0	AATGTAAAACTG	0.393	
+	1	654_656	.2_Intron|WNT2B_	NM_024494	NP_078613	Q93097	WNT2B_HUMAN		5	GCTCCTGCTGC	0.744	
-	5	473		NM_005725	NP_005716	O60636	TSN2_HUMAN	ellular (Potential).	0	ATTGCCTTTTCC	0.418	
+	1	33	el_p.F4fs|PSMB4_	NM_002796	NP_002787	P28070	PSB4_HUMAN		2	AAGCGTTTTTG	0.547	
+	2	73_75		NM_173080	NP_775103	Q96PI1	SPRR4_HUMAN	Gln-rich.	0	TCTTCCcagcagca	0.433	
-	2	140_142		NM_001014291	NP_001014313	Q9BYE4	SPR2G_HUMAN		0	TGCACTGCTGC	0.552	
-	3	201		NM_002964	NP_002955	P05109	S10A8_HUMAN	EF-hand 2.	0	GCACCCTTTTTC	0.507	
-	1	422_424	x.1_In_Frame_D	NM_002249	NP_002240	Q9UGI6	KCNN3_HUMAN	Poly-Gln.	1	gctgctgttgctgctgct	0.236	
-	8	668	GPATCH4_uc001f	NM_015590	NP_056405	Q5T3I0	GPTC4_HUMAN	Potential.	1	TTTTTCTTTTTTTT	0.537	
-	4	1309		NM_006617	NP_006608	P48681	NEST_HUMAN	Tail.	6	GGTGTGGGGGG	0.597	
-	6	1404_1406	.V48del|PVRL4_u	NM_030916	NP_112178	Q96NY8	PVRL4_HUMAN	ical; (Potential).	2	ATGAGCACCACC	0.571	
+	3	338_340		NM_001102566	NP_001096036	A6NKN8	PC4L1_HUMAN		0	AGGCGGAGGAG	0.488	
-	6	1020_1021	A11_uc010pmq.1_	NM_178527	NP_848622	Q5TAH2	S9A11_HUMAN		2	AATTTCCAAAAAA	0.282	
+	17	2127	ps.2_Frame_Shift_	NM_001357	NP_001348	Q08211	DHX9_HUMAN	case C-terminal.	2	TGTTGGTTTTTTT	0.378	
+	22	2922_2924		NM_018085	NP_060555	Q96P70	IPO9_HUMAN		2	gaggaagaggaggag	0.33	
+	5	642_643	11A_uc001haf.2_	NM_014827	NP_055642	O75152	ZC11A_HUMAN	3H1-type 1.	2	ACTGCTATTTTTT	0.371	
-	4	1497	C2B_uc001hax.1_	NM_002646	NP_002637	O00750	P3C2B_HUMAN		7	GTGGCAAAATG	0.512	
+	5	701	.2_RNA|CR1L_uc	NM_175710	NP_783641	Q2VPA4	CR1L_HUMAN	Sushi 3.	0	GAGGGAAAAAG	0.507	
+	2	420	_Shift_Del_p.S42fs	NM_016121	NP_057205	Q9Y597	KCTD3_HUMAN	BTB.	3	AGATTCTTTTTTT	0.229	
-	6	886	_Shift_Del_p.K69fs	NM_001031685	NP_001026855	Q13625	ASPP2_HUMAN		3	TCTCACTTTTTTT	0.368	
+	27	7308	CN_uc001hsp.1_	NM_001098623	NP_001092093	Q5VST9	OBSCN_HUMAN		28	AGGCTGGGGGG	0.662	
+	3	1325		NM_021205	NP_067028	Q7L0Q8	RHOU_HUMAN		0	GAAGTCTAAAA	0.458	
+	15	3795	rf18_uc001iik.2_I	NM_017782	NP_060252	Q5VWN6	CJ018_HUMAN		2	CCTTTGAAAAAA	0.413	
+	21	2931		NM_002216	NP_002207	P19823	ITIH2_HUMAN		3	CAGTGGAAAAGG	0.438	
-	14	1771	BL_uc001iqk.2_Int	NM_006393	NP_006384	O76041	NEBL_HUMAN	Nebulin 12.	2	TTTCCCTTTAATT	0.453	

-	17	1780	p.N459fs|MPP7_u	NM_173496	NP_775767	Q5T2T1	MPP7_HUMAN	ylate kinase-like.	1	ACTTTGTTTTTAG	0.363	
-	15	1912	_p.K570fs|FRMPD	NM_001018071	NP_001018081	Q68DX3	FRPD2_HUMAN	FERM.	1	GTGAACTTTTTTT	0.463	
-	12	1806_1808	jh.2_In_Frame_De	NM_138932	NP_620310	Q9NQ94	A1CF_HUMAN		1	Aagcagtagcagcag	0.433	
+	10	3102		NM_032199	NP_115575	Q14865	ARI5B_HUMAN		4	CAGGGAAAAAG	0.607	
+	10	1226_1228	p.Q98del|ZMIZ1_u	NM_020338	NP_065071	Q9ULJ6	ZMIZ1_HUMAN		4	CGGGGCAGCAG	0.65	
+	22	3201	_p.P753fs|ZMIZ1_	NM_020338	NP_065071	Q9ULJ6	ZMIZ1_HUMAN	Pro-rich.	4	CGCCTCCCCCA	0.652	
+	10	1630	STAMBPL1_uc001	NM_020799	NP_065850	Q96FJ0	STALP_HUMAN		1	GCTTGTAAAAAAA	0.423	
+	4	743	c010qnb.1_Intron|	NM_000043	NP_000034	P25445	TNR6_HUMAN	.|Extracellular (Potential).	2	CCAAACTTTTTTT	0.368	
+	11	1237	HECTD2_uc001kh	NM_182765	NP_877497	Q5U5R9	HECD2_HUMAN		1	AGCTGCAAAAAA	0.318	
+	9	6800	001lfz.2_Frame_S	NM_206862	NP_996744	O95359	TACC2_HUMAN		10	AGAGACCCCCC	0.522	
+	16	1588_1589	T1_uc009xzz.1_F	NM_007329	NP_015568	Q9UGM3	DMBT1_HUMAN	SRCR 4.	7	GCCCTGAGGCTG	0.535	
+	48	4948	p.R1649fs|DOCK1_	NM_001380	NP_001371	Q14185	DOCK1_HUMAN		9	AGCCGCCCCCG	0.587	
+	6	663_665	me_Del_p.E180de	NM_020901	NP_065952	Q9P1Y6	PHRF1_HUMAN	Poly-Glu.	0	GAGCGAGGAGG	0.616	
+	1	483	_uc001mam.1_Int	NM_001004750	NP_001004750	Q9H340	O51B6_HUMAN	cellular (Potential).	2	TCGCCTACACTG	0.478	
-	9	829_831	MA1_uc010rcp.1_	NM_002786	NP_002777	P25786	PSA1_HUMAN		2	AGACACATCATC	0.36	
-	3	345	0rew.1_Frame_Shi	NM_001001991	NP_001001991	Q6UXH9	PAMR1_HUMAN		2	AGGTACCCCCC	0.517	
-	8	778		NM_004308	NP_004299	Q07960	RHG01_HUMAN	SH3-binding.	1	GGGCAGGGGGG	0.642	
-	15	2895_2897	229PP>P|FNBP4_	NM_015308	NP_056123	Q8N3X1	FNBP4_HUMAN	Pro-rich.	1	ggtggtggaggagga	0.32	
-	13	2405	P4_uc001ngj.2_F	NM_015308	NP_056123	Q8N3X1	FNBP4_HUMAN		1	GGGCAGGGGGC	0.428	
+	2	222_224	01nkr.1_In_Frame_	NM_000062	NP_000053	P05155	IC1_HUMAN		1	CCTCCTGCTGC	0.709	
-	8	877	1_Frame_Shift_De	NM_015853	NP_056937	Q04323	UBXN1_HUMAN	eraction with BRCA1.	0	TTCCTCCCCACC	0.637	rs111325595
-	12	1894_1896	del|SF1_uc001obc	NM_004630	NP_004621	Q15637	SF01_HUMAN	Pro-rich.	3	GGAGGCTGCTG	0.66	
+	10	3373	1oep.1_Frame_Sh	NM_001099409	NP_001092879	Q8N3D4	EH1L1_HUMAN		1	GCCCTGGTCAG	0.602	
+	4	382	SNX32_uc010rop.1	NM_152760	NP_689973	Q86XE0	SNX32_HUMAN	PX.	0	CAGATCCCCCC	0.612	
-	15	4531	UMA1_uc001orn.	NM_006185	NP_006176	Q14980	NUMA1_HUMAN	Potential.	8	CCCAGCCCCCG	0.622	
+	7	1097	oxb.2_Frame_Shif	NM_032564	NP_115953	Q96PD7	DGAT2_HUMAN	lasmic (Potential).	0	CCTTTGGAGAG	0.527	
-	6	1081_1083	ne_Del_p.D183del	NM_002576	NP_002567	Q13153	PAK1_HUMAN	ction with CRIPAK.	4	GGGGTAGcatcatc	0.429	
+	10	2065_2067	0rsp.1_In_Frame_	NM_020798	NP_065849	Q9P2H5	UBP35_HUMAN		3	CTGTCGCCGCC	0.665	
+	9	4910_4912		NM_001008781	NP_001008781	Q8TDW7	FAT3_HUMAN	.|Extracellular (Potential).	5	GACATGACGACG	0.463	
+	10	1135	_p.H268fs|C11orf5	NM_014039	NP_054758	Q9H0W9	CK054_HUMAN		0	CACTCATTTTTTT	0.378	
-	20	2272_2274	.D667del|MRE11A	NM_005591	NP_005582	P49959	MRE11_HUMAN		5	AAAGGATCATCAT	0.325	
+	1	184		NM_003658	NP_003649	Q9UMQ3	BARX2_HUMAN		0	CCTCTACTCCGT	0.577	
-	27	3275		NM_004963	NP_004954	P25092	GUC2C_HUMAN	lasmic (Potential).	6	TCTGGGTTTTTG	0.428	
-	17	2565	_p.N609fs|NELL2_	NM_001145108	NP_001138580	Q99435	NELL2_HUMAN	VWFC 3.	4	CTGTCATTTTCC	0.323	
-	12	4127_4129	w.2_In_Frame_De	NM_004719	NP_004710	Q99590	SCAFB_HUMAN	Pro-rich.	0	AGGGGGTGGTG	0.483	
-	11	3063_3064	p.E611fs|SFRS2IP	NM_004719	NP_004710	Q99590	SCAFB_HUMAN	Arg-rich.	0	TCCTTTCTCTCT	0.446	
+	2	157	40B_uc001ruq.1_	NM_001031698	NP_001026868	Q6NWY9	PR40B_HUMAN	Pro-rich.	5	AGCTATCCCCCC	0.607	
+	1	298		NM_001005497	NP_001005497	A6NL08	O6C75_HUMAN	Name=3; (Potential).	3	CAGCTATTTTTTT	0.438	
+	30	3307	sjr.2_Frame_Shift_	NM_015292	NP_056107	Q9BSJ8	ESYT1_HUMAN		5	ACCTTTCCCAGG	0.458	
+	23	2669	srr.1_Frame_Shift_	NM_004984	NP_004975	Q12840	KIF5A_HUMAN		3	GACAGTGGGGGG	0.502	
-	3	695_696	rame_Shift_Ins_p.	NM_001478	NP_001469	Q00973	B4GN1_HUMAN	enal (Potential).	0	GGGAGGCCCCC	0.589	
-	9	979_980	.2_5'Flank|CEP29	NM_025114	NP_079390	O15078	CE290_HUMAN	Potential.	7	CTCATAGTTTTTT	0.317	
+	5	577_578	0sye.1_Frame_Sh	NM_152591	NP_689804	Q8NA47	CCD63_HUMAN	Potential.	8	AGATGGAAAAAA	0.416	
-	64	11032_11034		NM_001109662	NP_001103132				2	GGCACAGCAGC	0.64	
-	10	1574		NM_173598	NP_775869	Q6VAB6	KSR2_HUMAN	Pro-rich.	15	AGGGAGGGGGG	0.632	
+	5	848_850		NM_014730	NP_055545	Q14165	MLEC_HUMAN	.|Lumenal (Potential).	1	gaagaggaagaaga	0.404	
+	7	941	F3_uc001uqw.2_	NM_006646	NP_006637	Q9UPY6	WASF3_HUMAN		1	ACTAGGTGTGTG	0.475	

+	10	1588	uqw.2_Frame_Shif	NM_006646	NP_006637	Q9UPY6	WASF3_HUMAN	WH2.	1	:AACTGAAAAAGC	0.507	
+	9	2007	p.K603fs|CKAP2_	NM_001098525	NP_001091995	Q8WWK9	CKAP2_HUMAN		2	GTGTGAAAAAAA	0.318	
-	5	1255		NM_012158	NP_036290	Q9UKT7	FBXL3_HUMAN		0	TCATATAAAAAAA	0.418	
-	38	5521	aev.2_Frame_Shif	NM_015057	NP_055872	O75592	MYCB2_HUMAN		14	AACTGTGGTCAT	0.443	
+	2	950_951	RK5_uc010tic.1_I	NM_015567	NP_056382	O94991	SLIK5_HUMAN	Extracellular (Potential).	5	GCTGATCTCTCT	0.525	
+	5	928	C2_uc001vod.2_F	NM_001144072	NP_001137544	Q8NBM4	UBAC2_HUMAN	ellular (Potential).	1	AGAGTCCAAGTC	0.358	
-	2	2808_2810	6PP>P|SALL2_uc(	NM_005407	NP_005398	Q9Y467	SALL2_HUMAN	Poly-Pro.	3	GTCAGGTGGTG	0.571	rs113881459
-	13	1508	p.Q403fs|RBM23_	NM_001077351	NP_001070819	Q86U06	RBM23_HUMAN		1	GGTCTGGGGGG	0.507	
+	12	1197	E6_uc001wlm.2_F	NM_006032	NP_006023	O95741	CPNE6_HUMAN	VWFA.	3	TCGAATCCCCCC	0.602	
-	5	904	_Shift_Del_p.A188	NM_001099274	NP_001092744	Q9BSI4	TINF2_HUMAN		0	CCAGGCAAGAG	0.517	
-	4	510_511	1xae.2_Frame_Sh	NM_006832	NP_006823	Q96AC1	FERM2_HUMAN		0	CTTCTTCTTTTTT	0.381	
-	18	1872	0apo.2_Frame_Sh	NM_174978	NP_777638	Q08AQ4	Q08AQ4_HUMAN		4	TAGCTCAAAAAA	0.289	
+	4	1996	p.Q522fs|ZBTB1_	NM_001123329	NP_001116801	Q9Y2K1	ZBTB1_HUMAN		1	GTATCCAAAAAAA	0.378	
+	2	1168		NM_018228	NP_060698	Q9H8Y1	VRTN_HUMAN		0	CCACCGGGGGG	0.642	
-	16	2283	GALC_uc010tvy.1_	NM_000153	NP_000144	P54803	GALC_HUMAN		0	ATACCATTTTTTT	0.308	
-	10	982_984	.Q250del|ATXN3_	NM_004993	NP_004984	P54252	ATX3_HUMAN	Poly-Gln.	0	GGTCCCCctgctgct	0.325	474612;rs147904130
+	7	2314_2316	.T650del|RIN3_uc	NM_024832	NP_079108	Q8TB24	RIN3_HUMAN	h RAB5B.|Poly-Thr.|VPS9.	3	CTGGCCACCAC	0.567	
+	6	1030	n.2_RNA|CHGA_u	NM_001275	NP_001266	P10645	CMGA_HUMAN		2	CCCCCACCCGA	0.517	
-	7	2023	wo.1_Frame_Shift_	NM_001002860	NP_001002860	Q9P203	BTBD7_HUMAN		1	CCAGCATTTTTTT	0.383	
-	24	4984	.K1591fs|DICER1_	NM_030621	NP_085124	Q9UPY3	DICER_HUMAN		5	AGGGCCTTTTCC	0.522	
+	31	6475_6476		NM_001376	NP_001367	Q14204	DYHC1_HUMAN		10	TGTGAAGAGAGA	0.46	
+	5	799_800	uc001ymt.2_Frame	NM_001969	NP_001960	P55010	IF5_HUMAN		3	GGATTCATTAAAA	0.406	
-	5	903_905	AKT1_uc001ypm.2_	NM_005163	NP_005154	P31749	AKT1_HUMAN		134	TCCATCTCCTCCT	0.631	
-	8	1515_1517		NM_024490	NP_077816	O60312	AT10A_HUMAN	Cytoplasmic (Potential).	5	CACCACCTCCTC	0.695	
-	14	1621	MTMR10_uc001zf	NM_017762	NP_060232	Q9NXD2	MTMRA_HUMAN	ularin phosphatase.	1	GGTGAGGGGAG	0.473	
-	1	420	uc001zib.2_Frame	NM_133647	NP_598408	Q9UHW9	S12A6_HUMAN	lasmic (Potential).	7	ATCCTGGGGGT	0.498	
+	10	2201	PAK6_uc010bbn.2_	NM_001128628	NP_001122100	Q9NQU5	PAK6_HUMAN	rotein kinase.	8	GTCTCTGGGCAT	0.602	
-	12	2445_2446	p.P771fs|TP53BP	NM_005657	NP_005648	Q12888	TP53B_HUMAN		7	ACTCTGGGAGAT	0.45	
+	8	1883	p.K109fs|TRIM69_	NM_182985	NP_892030	Q86WT6	TRI69_HUMAN	B30.2/SPRY.	0	GACCCTAAAACA	0.448	
+	18	2010_2011		NM_004212	NP_004203	O43868	S28A2_HUMAN		4	ACTGCTGTGGAT	0.421	
-	2	1306		NM_004498	NP_004489	Q9UBC0	HNF6_HUMAN	Homeobox.	0	ACATCTGTGAAG	0.448	
-	11	1368_1369	384fs|ZNF280D_u	NM_017661	NP_060131	Q6N043	Z280D_HUMAN		3	AATTCATGGGGC	0.381	
-	3	347_349	PC5_uc002apt.1_5	NM_006049	NP_006040	O75971	SNPC5_HUMAN	Poly-Glu.	0	tcttcctcttcctcctcctc	0.384	
+	2	929_931	.1_Intron|NOX5_u	NM_145658	NP_663633	Q6UW49	SPESP_HUMAN	Poly-Ala.	0	GCTCTAGCAGCA	0.384	
+	24	2916		NM_003870	NP_003861	P46940	IQGA1_HUMAN		8	CTTACCAAAAAA	0.363	
+	7	1780_1782	.D191del|BLM_uc(	NM_000057	NP_000048	P54132	BLM_HUMAN	Poly-Asp.	6	GACTTTGATGAT	0.374	
-	9	996_998	.E123del|VPS33B_	NM_018668	NP_061138	Q9H267	VP33B_HUMAN		2	CGCCATCCTCCT	0.522	rs147271815
+	1	40_42	01_uc010brm.1_5'	NM_012217	NP_036349	Q9BZJ3	TRYD_HUMAN		0	GAGCCTGCTGC	0.685	
-	7	1227	bsl.1_Frame_Shift	NM_001089	NP_001080	Q99758	ABCA3_HUMAN		16	TCAGGAAAAAGC	0.493	
-	1	929_930	ur.2_3'UTR|TIGD7_	NM_033208	NP_149985	Q6NT04	TIGD7_HUMAN	y similarity).|HTH psq-type.	0	CTTCTTATTTTTT	0.361	
+	3	184_186	f62_uc010vas.1_5	NM_020314	NP_064710	Q7Z3J2	CP062_HUMAN	Ser-rich.	1	CACGTCCTCCT	0.562	
+	22	3160	hift_Del_p.G998fs	NM_007245	NP_009176	Q8WWM7	ATX2L_HUMAN		2	GTCATGGGGGG	0.682	
+	16	2756	ne_Shift_Del_p.F6	NM_006662	NP_006653	Q6ZRS2	SRCAP_HUMAN	ase ATP-binding.	4	ATGCACTTTTTGA	0.512	
+	10	1333_1334	p.C352fs|RSPRY1	NM_133368	NP_588609	Q96DX4	RSPRY_HUMAN	B30.2/SPRY.	1	GCGTTGCACCTT	0.485	
-	13	1866	p.P392fs|FHOD1_	NM_013241	NP_037373	Q9Y613	FHOD1_HUMAN	H1.|Poly-Prp.P585fs*43(1)	3	GGGGAGGGGGG	0.622	
-	3	888_890	jt.1_In_Frame_De	NM_001082486	NP_001075955	Q96AP0	ACD_HUMAN		1	GTCCTGCAGCAG	0.65	
+	16	2002_2004	ne_Del_p.S549del	NM_014329	NP_055144	Q6P2E9	EDC4_HUMAN	Ser-rich.	4	CTCTCCcagcagca	0.453	

+	10	2333	vli.1_Frame_Shift_	NM_001793	NP_001784	P22223	CADH3_HUMAN	(Potential).	p.?(1)	5	AGGCCAAAAAC	0.522	
+	3	992_994		NM_018975	NP_061848	Q9NYB0	TE2IP_HUMAN	Glu-rich (acidic).		1	gaggaggaagaaga	0.369	rs140846731
+	5	718	_p.L86fs|CNTNAP	NM_033401	NP_207837	Q9C0A0	CNTP4_HUMAN	(Potential).|F5/8 type C.		2	CTCCTGATGTT	0.493	
-	6	1365		NM_020310	NP_064706	Q99583	MNT_HUMAN			1	gtggtgctggggggtg	0.353	
-	3	1104_1105	gat.2_Frame_Shif	NM_014519	NP_055334	Q9UNY5	ZN232_HUMAN	SCAN box.		2	CTCTTAGGGTGA	0.55	
-	1	143_145	HX33_uc010clf.2_	NM_020162	NP_064547	Q9H6R0	DHX33_HUMAN			2	CCGGCCTCCTC	0.724	
+	4	597	clt.1_Frame_Shift_	NM_181844	NP_862827	Q8N143	BCL6B_HUMAN	Pro-rich.		1	CAAGGCCCCCC	0.617	
-	7	934	ggo.1_Frame_Shif	NM_020360	NP_065093	Q9NRY6	PLS3_HUMAN	smic (By similarity).		0	CCAGGCCCCCC	0.612	
-	16	2205_2207	ER1_uc010vur.1_	NM_002616	NP_002607	O15534	PER1_HUMAN	binding domain (By simila		9	GTATAGGAGGA	0.586	
+	9	1165_1167	.2_3'UTR|NDEL1_	NM_030808	NP_110435	Q9GZM8	NDEL1_HUMAN	Interaction with NEFL (By		0	CCCGCTCCTCC	0.576	
+	4	797_798	ame_Shift_Del_p.L	NM_153210	NP_694942	Q70EL4	UBP43_HUMAN			5	TTTCCTGTGTGT	0.515	
+	5	454	0crt.2_Frame_Shif	NM_003170	NP_003161	Q7KZ85	SPT6H_HUMAN	sp/Glu-rich.		3	CGTGTCAAAAAA	0.483	
+	12	1137	HOT1_uc002hgx.	NM_018307	NP_060777	Q8IXI2	MIRO1_HUMAN	intermembrane (Potential).		4	ACTACTGAATTA	0.239	
+	1	158_160	me_Del_p.K7del|	NM_003457	NP_003448	O43670	ZN207_HUMAN			0	TCGCAAGAAGA	0.542	
-	3	300	hks.1_Frame_Shi	NM_145898	NP_665905	P55773	CCL23_HUMAN			0	GCACTCGCTGT	0.532	
+	7	712	|STARD3_uc010w	NM_006804	NP_006795	Q14849	STAR3_HUMAN	ytoplasmic (Potential).		0	CCCCTGCTGTT	0.627	
+	10	1737_1738	cyb.1_Frame_Shi	NM_003152	NP_003143	P42229	STA5A_HUMAN			1	ATGAATCCCCCC	0.564	rs146398782
-	22	3004_3005	iff.1_Frame_Shift_	NM_005474	NP_005465	Q9UQL6	HDAC5_HUMAN	ne deacetylase.		1	TCCAATGGGGG	0.609	
+	4	641_642	103_uc002ihp.1_	NM_213607	NP_998772	Q8IW40	CC103_HUMAN			1	GGGCAGAGAG	0.644	
-	8	1173		NM_032043	NP_114432	Q9BX63	FANCJ_HUMAN	ase ATP-binding.		1	TTCTTCCCCAG	0.388	
+	6	911	.2_RNA|DCAF7_u	NM_005828	NP_005819	P61962	DCAF7_HUMAN			1	ACAAGCAGGAC	0.562	
-	11	1158_1160	.2_In_Frame_Del_	NM_017647	NP_060117	Q8IY81	RRMJ3_HUMAN			1	tcctcctcttcctcctcctc	0.463	
+	14	2846_2847	3'UTR|FAM104A_	NM_018714	NP_061184	Q8WTW3	COG1_HUMAN			1	GGTTGTCCCCC	0.584	
+	7	895_897	02jyd.1_In_Frame_	NM_173626	NP_775897	Q86WA9	S2611_HUMAN	ical; (Potential).		0	TGCATGCTGCT	0.675	
-	7	1099_1100	koq.2_Frame_Shi	NM_022068	NP_071351	Q9H5I5	PIEZ2_HUMAN	ical; (Potential).		1	AGCTGGACAG	0.53	
-	4	1755_1756	CO1_uc002kti.1_	NM_052911	NP_443143	Q5FWF5	ESCO1_HUMAN			0	AGTGTTGTGTT	0.436	rs151000067
+	2	125	1_5'Flank|HAUS1_	NM_138443	NP_612452	Q96CS2	HAUS1_HUMAN			1	GTGGTTAAAAAA	0.393	
-	1	700	ift_Del_p.P157fs|	NM_003927	NP_003918	Q9UBB5	MBD2_HUMAN	MBD.		0	ATCCGGGGGG	0.687	
+	8	995	VDR7_uc002lgl.1_	NM_015285	NP_056100	Q9Y4E6	WDR7_HUMAN			3	GGACCGGGGGG	0.418	
-	2	2579		NM_032160	NP_115536	Q8IZU8	DSEL_HUMAN			6	CTCGTCCCCCC	0.458	
-	7	1036_1038	.K72del|GTF2F1_	NM_002096	NP_002087	P35269	T2FA_HUMAN			0	AACCCTTCTTC	0.611	
-	6	1269_1270	xmk.1_Frame_Shi	NM_030824	NP_110451	Q9H7R0	ZN442_HUMAN	2H2-type 2.		4	TAGGCCAAAAAA	0.401	
+	16	3826	.V1000fs|NWD1_uc002nev.3_Frame_Shift_Del_p.V92			Q149M9	NWD1_HUMAN	WD 8.		7	GGCTGTTTTTG	0.552	
-	2	134	Splice_Site|ZNF43	NM_003423	NP_003414	P17038	ZNF43_HUMAN			2	GTCCCTAAAAAA	0.386	
+	11	1438_1440		NM_173479	NP_775750	Q6ZMY6	WDR88_HUMAN	Poly-Ser.		3	ATCGTCATCAT	0.527	
+	2	252_254	eea.2_In_Frame_	NM_005306	NP_005297	O15552	FFAR2_HUMAN	Name=2; (Potential).		1	CCTCCTGCTGC	0.645	
-	18	2238_2240	_5YE>*|CAPN12_	NM_144691	NP_653292	Q6ZSI9	CAN12_HUMAN	|Domain IV.|Potential.		2	TCAGCTCGTAGG	0.581	rs150655757
-	8	1256	1_5'Flank|CAPN1	NM_144691	NP_653292	Q6ZSI9	CAN12_HUMAN	lpain catalytic.		2	TCCTCCTTTTTC	0.652	
-	7	695	|MED29_uc010x	NM_019088	NP_061961	Q8N7H5	PAF1_HUMAN			1	TCTGGCTATCCC	0.502	
+	8	1917	p.S598fs|CEACA	NM_004363	NP_004354	P06731	CEAM5_HUMAN	Ig-like 7.		2	CATTTCCCCCC	0.547	
+	3	1121_1123	002pbp.2_5'Flank|	NM_012099	NP_036231	O15446	RPA34_HUMAN	Poly-Lys.		4	TGCGGAAGAAG	0.581	
+	9	1037_1039	ekw.2_RNA|SAE1	NM_016402	NP_057486	Q9UBE0	SAE1_HUMAN			1	AACAACTTCTTC	0.493	
-	9	974_975	pni.2_Frame_Shift	NM_003598	NP_003589	Q15562	TEAD2_HUMAN	al activation (Potential).		3	GGCATGGGGG	0.564	
-	11	1285_1287	pt.1_RNA|FUZ_u	NM_025129	NP_079405	Q9BT04	FUZZY_HUMAN	Leu-rich.		0	GAGACAGCAGC	0.635	
+	4	817	P62_uc002pqz.2_	NM_012068	NP_036200	Q9Y2D1	ATF5_HUMAN			2	CCTTACCCCCC	0.567	
-	5	1658	2_5'Flank|ZNF577	NM_023074	NP_075562	Q9BS31	ZN649_HUMAN			3	GATTTTCCACCT	0.403	rs61731262
-	3	429		NM_024316	NP_077292	Q96BZ8	LENG1_HUMAN			1	GGGGGCCCCCT	0.642	

+	1	728_730		NM_003108	NP_003099	P35716	SOX11_HUMAN	Poly-Asp.		3	GATGAGgacgacg	0.606	
+	14	2400_2401	rbo.1_Frame_Shi	NM_014668	NP_055483	Q4ZG55	GREB1_HUMAN			1	TGCATTCCCCCC	0.52	
+	18	3087	Shift_Del_p.L563f	NM_014668	NP_055483	Q4ZG55	GREB1_HUMAN			1	ACGCTGGAGAT	0.657	
-	11	1472_1474	1_In_Frame_Del_	NM_015317	NP_056132	Q8TB72	PUM2_HUMAN	Ala-rich.		1	TCCAGCTGCTG	0.424	
-	32	4055_4057	.K543del|OTOF_u	NM_194248	NP_919224	Q9HC10	OTOF_HUMAN	ic (Potential).|Poly-Lys.		7	CAGTGCCcttctt	0.507	
-	3	1787_1788	I291fs|RTN4_uc0	NM_020532	NP_065393	Q9NQC3	RTN4_HUMAN	lasmic (Potential).		3	TCTTCTATTTTTT	0.381	
+	1	96_98	2sda.2_In_Frame_	NM_203437	NP_982261	Q6ULP2	AFTIN_HUMAN			2	AGAGGATGATG	0.409	
+	8	2887		NM_000189	NP_000180	P52789	HXK2_HUMAN	Regulatory.		2	TCTTTGGGGGG	0.547	
-	13	1977	p.K440fs|GGCX_	NM_000821	NP_000812	P38435	VKGC_HUMAN	enal (Potential).		1	TCCACCTTTTCC	0.438	
+	5	1704_1705		NM_001011552	NP_001011552	Q6AI14	SL9A4_HUMAN	ellular (Potential).		3	CCCCTTCTCCAT	0.441	
+	8	824		NM_182640	NP_872578	P82933	RT09_HUMAN			0	TGAATCAAAAAA	0.403	
+	3	766	1C4_uc010ywr.1_	NM_006588	NP_006579	O75897	ST1C4_HUMAN			0	TGTAAGGTAAA	0.378	
+	6	2252_2253	ed.2_Frame_Shift	NM_181453	NP_852118	Q8IWJ2	GCC2_HUMAN	Potential.		1	GTTCAGAAAAAA	0.307	
+	14	3080	fkp.2_Frame_Shif	NM_019014	NP_061887	Q9H9Y6	RPA2_HUMAN			1	ACACCGGGGAA	0.338	
-	12	2147	9A_uc002uds.1_F	NM_002977	NP_002968	Q15858	SCN9A_HUMAN			13	TTGGCTGATGTT	0.557	
-	65	12348		NM_004525	NP_004516	P98164	LRP2_HUMAN	ng (Potential).|Extracellular		29	CATCGTTTTCC	0.438	
+	5	719_721	zej.1_In_Frame_	NM_145810	NP_665809	Q9BWT1	CDCA7_HUMAN			1	CCATGGAGGAG	0.537	
-	277	79729	197fs|TTN_uc010	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN			153	GTTTTCCAGAG	0.393	
-	15	1903	_Shift_Del_p.I1816	NM_152525	NP_689738	Q53TS8	AL2SA_HUMAN			3	TTTTAATTTTTTT	0.323	
+	16	1908	p.L519fs|ATIC_uc	NM_004044	NP_004035	P31939	PUR9_HUMAN			29	GAACTGGGAAT	0.498	
+	1	94_96	I_uc002vsu.3_5'	NM_001631	NP_001622	P09923	PPBI_HUMAN			1	TGGGTGCTGCT	0.66	
+	2	97		NM_054112	NP_473453	Q96PH6	DB118_HUMAN			4	TGGTGAAAAAA	0.398	
+	2	265	IFS1_uc010zvl.1_	NM_080748	NP_542786	P60602	ROMO1_HUMAN	ical; (Potential).		0	GCACCTTTTCC	0.657	
+	5	768_769	p.S71fs|SFRS6_u	NM_006275	NP_006266	Q13247	SRSF6_HUMAN	r-rich (RS domain).		0	CTCGATCTAGAA	0.421	
+	6	686	0zyk.1_Frame_Sh	NM_015266	NP_056081	Q9Y2E8	SL9A8_HUMAN	ical; (Potential).		1	TGCTGTTTTTG	0.383	
-	2	597	Shift_Del_p.Q166f	NM_020436	NP_065169	Q9UJQ4	SALL4_HUMAN			2	GTCCTGGGGGG	0.577	
-	32	3210_3211		NM_014258	NP_055073	Q9BX26	SYCP2_HUMAN			5	TTTATAGTTTTTT	0.327	
+	3	617_619	me_Del_p.A96del|	NM_016434	NP_057518	Q9NZ71	RTEL1_HUMAN	ase ATP-binding.		0	CAACGCTGCTG	0.645	
-	5	1145	_Shift_Del_p.I278	NM_152505	NP_689718	O95447	LCA5L_HUMAN			0	CCTGTATTTTTTT	0.383	
-	3	2043	ne_Shift_Del_p.S	NM_001098402	NP_001091872	Q9ULJ3	ZN295_HUMAN			3	CATGTGAACTA	0.443	
+	11	1360	aex.1_Frame_Shi	NM_004571	NP_004562	P55347	PKNX1_HUMAN			2	CGGGGCCACCC	0.622	
+	6	711_713	15_uc002zsr.2_In	NM_001003891	NP_001003891	Q96RN5	MED15_HUMAN	Poly-Gln.		1	cagctccagcagcag	0.187	
+	8	1169_1171	.Q341del|MED15_	NM_001003891	NP_001003891	Q96RN5	MED15_HUMAN	-rich.|Poly-Gln.		1	AGGTGCAGCAG	0.616	
+	4	415_417	36_uc010gtw.1_I	NM_004914	NP_004905	O95755	RAB36_HUMAN			2	CCAAGGTGGTG	0.586	
-	3	496_498		NM_005877	NP_005868	Q15459	SF3A1_HUMAN	Poly-Gln.		5	TGGTCTGCTGC	0.596	rs141985009
+	6	1651_1652	0gxz.1_Frame_Sh	NM_019008	NP_061881	Q9NQG6	SMC7L_HUMAN			1	GCCAGCTAACC	0.604	
-	5	623	p.P162fs|NAGA_u	NM_000262	NP_000253	P17050	NAGAB_HUMAN			1	TCCTCGGGGGT	0.642	
+	29	2853_2854	CD2_uc003buy.1_	NM_033084	NP_149075	Q9BXW9	FACD2_HUMAN		p.R926fs*6(2)	4	TTTTTCCGAGAG	0.396	
-	11	1376	1axh.1_Frame_S	NM_016141	NP_057225	Q9Y6G9	DC1L1_HUMAN			1	GATCAATTTTTTT	0.398	
+	9	1492	Shift_Del_p.G491	NM_007335	NP_031361	Q9Y238	DLEC1_HUMAN			9	TCATTGGGGGA	0.473	
+	13	3220_3222	|NKTR_uc003clq.	NM_005385	NP_005376	P30414	NKTR_HUMAN			3	TGAAGAGGAGG	0.355	
-	6	513_515	.2_In_Frame_Del	NM_020707	NP_065758	Q9HCP6	HHATL_HUMAN			3	ACCAAGCAGCA	0.621	
+	6	1945	8_splice|ZNF167_	NM_018651	NP_061121	Q9P0L1	ZN167_HUMAN			2	ACTGGTAAGAA	0.448	
-	7	719	3dap.2_Frame_S	NM_006030	NP_006021	Q9NY47	CA2D2_HUMAN	ellular (Potential).		1	TCTGTCCAGTT	0.612	
-	1	499	_5'Flank|NT5DC2_	NM_022908	NP_075059	Q9H857	NT5D2_HUMAN			0	TGCTGTGGTCTT	0.592	
+	21	3869	OBO2_uc011bgk.1	NM_002942	NP_002933	Q9HCK4	ROBO2_HUMAN	lasmic (Potential).		11	TACCTCCCCCC	0.433	
-	5	499	PPA4_uc011bhp.	NM_018189	NP_060659	Q7L190	DPPA4_HUMAN			1	CTTTAATTTTTTT	0.413	

-	7	850	03eal.2_Frame_S	NM_001009899	NP_001009899	Q68DE3	K2018_HUMAN		3	CAATAATTTTTTT	0.373	
+	1	197	TR|HSPBAP1_uc	NM_032839	NP_116228	Q96SL1	DIRC2_HUMAN		0	GGCTCGGGCCT	0.577	
+	2	200_201	_Intron|ABTB1_uc	NM_172027	NP_742024	Q969K4	ABTB1_HUMAN	ANK 2.	0	ACAGCACCCCC	0.624	
+	3	470	NEK11_uc011blk.	NM_024800	NP_079076	Q8NG66	NEK11_HUMAN	rotein kinase.	6	TCAGACAAGAA	0.403	
+	4	288	011bnv.1_Frame_	NM_032025	NP_114414	Q9BY44	EIF2A_HUMAN		0	CCTGGCAACGT	0.398	
+	22	2900	bqm.1_Frame_Shi	NM_014616	NP_055431	Q9Y2G3	AT11B_HUMAN	ical; (Potential).	3	ACAGTATTTTTTT	0.269	
+	10	1570_1572	3fns.2_In_Frame_	NM_198241	NP_937884	Q04637	IF4G1_HUMAN	Poly-Glu.	7	GAAATGgaagaag	0.443	
-	7	1021_1023	A2B_uc010hym.2	NM_004593	NP_004584	P62995	TRA2B_HUMAN	-rich (RS2 domain).	2	CTCTCCAtcctcct	0.32	
+	3	644	tg.2_Frame_Shift_	NM_016531	NP_057615	P57682	KLF3_HUMAN	Pro-rich.	2	ACCGATAAAAAA	0.617	
-	7	944		NM_173536	NP_775807	Q8N1C3	GBRG1_HUMAN	ellular (Probable).	2	AGGTCAAAAAA	0.294	
+	4	418		NM_005212	NP_005203	P07498	CASK_HUMAN		4	GCCATCCCCCC	0.488	
-	3	416_418	.1_5'UTR|NUP54_	NM_017426	NP_059122	Q7Z3B4	NUP54_HUMAN	ch.|9 X 2 AA repeats of F-G	2	AGTTTGCTGCT	0.394	
+	8	1473_1475	.Q217del|PRDM8_	NM_020226	NP_064611	Q9NQV8	PRDM8_HUMAN	-rich.|Poly-Gln.	1	aaagaccagcagcag	0.384	
-	11	1436_1438	hnj.2_In_Frame_D	NM_001077207	NP_001070675	O94979	SC31A_HUMAN	ction with SEC13.	8	ATGGTGCTGCT	0.448	843621;rs140634448
+	8	1279	ike.1_Frame_Shift	NM_001263	NP_001254	Q92903	CDS1_HUMAN		4	TTTGGATTTTTTT	0.308	
-	9	2145_2146	3hqs.3_Frame_Sh	NM_001128310	NP_001121782	Q14515	SPRL1_HUMAN		1	TCCGTAGAGGAA	0.401	
-	1	538_540	C3_uc011cdn.1_I	NM_153757	NP_715638	Q96NT1	NP1L5_HUMAN	Glu-rich.	1	tactcctcttcctcctcctc	0.369	
+	8	1187_1189	p.P363del|NPNT_	NM_001033047	NP_001028219	Q6UXI9	NPNT_HUMAN	Pro-rich.	1	TACTCCACCACC	0.522	
+	4	1196_1198	.E415del|SEC24B	NM_006323	NP_006314	O95487	SC24B_HUMAN	Poly-Glu.	3	gaggaagaggagga	0.369	
+	39	6607	.G123fs|KIAA110	NM_015312	NP_056127	Q2LD37	K1109_HUMAN		12	ACAATGGGGGT	0.438	
+	1	413_414		NM_004575	NP_004566	Q12837	PO4F2_HUMAN		1	CTggtggtggcggcg	0.386	907220;rs72269802
-	5	1095	p.F207fs|LRBA_uc	NM_006726	NP_006717	P50851	LRBA_HUMAN		7	AAAGTTAAAAAA	0.408	
+	5	1107		NM_001873	NP_001864	P16870	CBPE_HUMAN		3	CGCCATTTTCC	0.483	
-	7	919	AH5_uc003jfe.1_	NM_001369	NP_001360	Q8TE73	DYH5_HUMAN	.|Stem (By similarity).	31	AGAGTCTTTTTTT	0.517	
+	2	689_690	jhm.2_Frame_Shif	NM_178140	NP_835260	O15018	PDZD2_HUMAN	PDZ 1.	9	GCGCAGGGGG	0.574	
+	46	8393_8395	E2636del|NIPBL_	NM_133433	NP_597677	Q6KC79	NIPBL_HUMAN		9	TGATGAAGAAG	0.379	
-	3	564	B_uc011cpy.1_Fr	NM_198449	NP_940851	Q6PCB8	EMB_HUMAN	Potential).|Ig-like V-type 1.	0	ACCATCTTTTTTC	0.358	
-	12	2426	03jtq.2_RNA|ADA	NM_197941	NP_922932	Q9UKP5	ATS6_HUMAN	Disintegrin.	0	CTTTTTCAATATT	0.418	
+	8	1149		NM_003248	NP_003239	P35443	TSP4_HUMAN		0	TGGTGCCCCCG	0.562	
+	7	2288	au.2_Frame_Shift_	NM_004385	NP_004376	P13611	CSPG2_HUMAN	minoglycan attachment do	16	TACACCTTTTCC	0.368	
+	13	1510_1512	.E383del|PAM_uc	NM_000919	NP_000910	P19021	AMD_HUMAN	ooxygenase (By similarity)	0	AACGAGAAGAA	0.325	
+	2	237_240	_p.K19fs|AP3S1_	NM_001284	NP_001275	Q92572	AP3S1_HUMAN		0	ATCTAAGAGAGA	0.304	rs80118146
-	1	991_993	Frame_Del_p.E29	NM_020747	NP_065798	Q9ULD9	ZN608_HUMAN	Potential.	6	GGCTCTCCTCC	0.522	
+	10	2028_2030	.MNB1_uc011cxb.	NM_005573	NP_005564	P20700	LMNB1_HUMAN	be involved in chromatin	2	AGAAGAGGAGG	0.325	
+	17	3181	kxh.2_Frame_Shif	NM_005732	NP_005723	Q92878	RAD50_HUMAN	Potential.	4	TCAACAAAAAAA	0.269	
-	4	248		NM_000590	NP_000581	P15248	IL9_HUMAN		0	ATGGTGGTATT	0.388	
+	18	3428	03lft.1_Frame_Shi	NM_020690	NP_065741	Q8IWZ2	Q8IWZ2_HUMAN		6	ATGTTGGAGTT	0.368	
+	1	2394_2395	c003lhc.1_Frame_	NM_018905	NP_061728	Q9Y5H9	PCDA2_HUMAN	ial).|5 X 4 AA repeats of P-	4	GGAGGACCCCC	0.619	
+	1	2373		NM_018930	NP_061753	Q9UN67	PCDBA_HUMAN	lasmic (Potential).	2	GGTCCTTTTCC	0.662	
+	1	2174	.1_Intron|PCDHG	NM_002588	NP_002579	Q9UN70	PCDGK_HUMAN	ellular (Potential).	2	GAGCAGAAAAAA	0.502	
-	16	2249	p.P694fs|DIAPH1_	NM_005219	NP_005210	O60610	DIAP1_HUMAN	FH1.	1	GAGGTGGGGG	0.637	
+	11	2401	p.G581fs|LARP1_	NM_033551	NP_291029	Q6PKG0	LARP1_HUMAN		4	ACCCAGGGGGG	0.547	
-	5	813	ddz.1_Frame_Shi	NM_144726	NP_653327	Q96MT1	RN145_HUMAN		5	CAATTGTCTCC	0.373	
-	2	129	_Frame_Shift_Del_	NM_005520	NP_005511	P31943	HNRH1_HUMAN		0	CCTCTCCACCT	0.567	
-	4	1405_1407	.E433del|TUBB2A	NM_001069	NP_001060	Q13885	TBB2A_HUMAN		1	TCGCCCTCCTC	0.532	
+	4	615	_uc003mwk.2_Intr	NM_001143971	NP_001137443	Q9Y232	CDYL1_HUMAN		0	GAATCCAAAAAC	0.488	
-	12	1998	nba.2_Frame_Shi	NM_005493	NP_005484	Q96S59	RANB9_HUMAN	action with FMR1.	2	TCAACATTTTTTT	0.378	

-	31	3928	Shift_Del_p.A1275f	NM_022113	NP_071396	Q9H1H9	KI13A_HUMAN		4	GGCTGCAATTC	0.423	
+	12	1504	3ncp.1_Frame_Sh	NM_153042	NP_694587	Q8NB78	KDM1B_HUMAN		1	GCTGACTTTTTT	0.463	
-	2	149	rame_Shift_Del_p.	NM_005074	NP_005065	Q14916	NPT1_HUMAN		4	GCTACCTTTTTG	0.403	
-	3	544	BBR1_uc011dlr.1_	NM_001470	NP_001461	Q9UBS5	GABR1_HUMAN	xtracellular (Potential).	7	GCGCTCCCCCC	0.632	
-	7	1054	M26_uc010jry.2_5'	NM_003449	NP_003440	Q12899	TRI26_HUMAN		3	CCGGTCTTTTTT	0.483	
-	20	3367	0jsc.1_Frame_Shi	NM_002714	NP_002705	Q96QC0	PP1RA_HUMAN		4	GGGCAGGGGGG	0.572	
-	19	2712_2714	sc.1_In_Frame_De	NM_002714	NP_002705	Q96QC0	PP1RA_HUMAN	Gly-rich.	4	CGGAATggaggag	0.601	
+	13	1843	ru.2_Intron|DDR1_	NM_013993	NP_054699	Q08345	DDR1_HUMAN	|Cytoplasmic (Potential).	9	CCGGGCCCCCC	0.682	
-	5	1078	uc003ntw.2_Fram	NM_004640	NP_004631	Q13838	DX39B_HUMAN	ase ATP-binding.	0	ACCACCAAAAAA	0.512	
-	22	3361_3362	T3_uc003nvi.3_Fra	NM_004639	NP_004630	P46379	BAG6_HUMAN		0	CTTACTGGGGGG	0.554	
-	2	1369_1371	0jte.2_In_Frame_	NM_005527	NP_005518	P34931	HS71L_HUMAN		6	CGTCCAGCAGCA	0.596	
+	7	739	p.G244fs|SCUBE3	NM_152753	NP_689966	Q8IX30	SCUB3_HUMAN	EGF-like 6.	1	ACAACGGGGGC	0.557	
-	4	1648	318_uc003ouw.2_	NM_014345	NP_055160	Q5VUA4	ZN318_HUMAN		7	GTCGCCTTTTTTC	0.493	
-	10	1967		NM_000255	NP_000246	P22033	MUTA_HUMAN		0	AATACCTTTTTCA	0.368	
+	1	341	v.2_RNA|HCRTR2	NM_001526	NP_001517	O43614	OX2R_HUMAN	cellular (Potential).	6	GGACTCCCCCC	0.567	rs76774128
-	75	13615	.V4380fs|DST_uc	NM_001144769	NP_001138241	Q03001	DYST_HUMAN	Spectrin 15.	14	TTTATTAACGGCT	0.368	
+	7	2884	en.2_Frame_Shift	NM_015153	NP_055968	Q92576	PHF3_HUMAN	TFIIS central.	5	AGAGGAAAAGG	0.279	
+	11	3428	en.2_Frame_Shift_	NM_015153	NP_055968	Q92576	PHF3_HUMAN		5	TTCTCCAAAAAAA	0.358	
-	1	195_197	ob.1_In_Frame_D	NM_145331	NP_663304	O43318	M3K7_HUMAN	Poly-Ser.	6	AGACGAGGAGG	0.655	
+	2	848_849		NM_002356	NP_002347	P29966	MARCS_HUMAN	dulin-binding (PSD).	0	ACCCCGAAAAAA	0.614	
-	2	1019		NM_145176	NP_660159	Q8TD20	GTR12_HUMAN	ical; (Potential).	1	AGTGTTAGTCCTA	0.383	
-	7	1235_1236	edm.1_Frame_Shi	NM_000416	NP_000407	P15260	INGR1_HUMAN	lasmic (Potential).	1	AAGAACTCTCTC	0.431	
-	3	1001	_Shift_Del_p.K141f	NM_031922	NP_114128	Q96D71	REPS1_HUMAN		2	GATCCCTTTTTCA	0.478	
+	6	1390	qqe.2_Frame_Shif	NM_012454	NP_036586	Q8IVF5	TIAM2_HUMAN		4	AAAAGAGGAAAA	0.463	
-	4	366	_p.P87fs|PRKAR1	NM_002735	NP_002726	P31321	KAP1_HUMAN	on and phosphorylation.	0	GGTTCGGGGGG	0.617	
+	8	2004_2005	srz.2_Frame_Shift	NM_014660	NP_055475	O94880	PHF14_HUMAN		3	TTGCAAGAGAGA	0.376	
-	4	864_866		NM_001002926	NP_001002926	Q3B726	RPA43_HUMAN	Lys-rich.	1	GCTTTTTCTTCTT	0.433	
+	5	601_603	0kxo.2_In_Frame_	NM_007252	NP_009183	P78424	PO6F2_HUMAN	Gln-rich.	1	cagctccagcagcagc	0.365	
-	5	540	me_Shift_Del_p.*9	NM_012412	NP_036544	Q71UI9	H2AV_HUMAN		0	CCCTCTAAGCAGT	0.363	
+	17	2184_2185	_p.I601fs|EGFR_u	NM_005228	NP_005219	P00533	EGFR_HUMAN	ical; (Potential).	9571	TCCATCGCCACT	0.619	
-	2	83_85	_uc010lbj.1_In_Fra	NM_004603	NP_004594	Q16623	STX1A_HUMAN	lasmic (Potential).	0	AGCGACATCATCA	0.586	
-	2	458		NM_032936	NP_116325	Q9H2L4	TMM60_HUMAN		0	CCAGGCTTTTTTT	0.408	
+	13	1827_1828	p.F529fs|PHTF2_u	NM_001127357	NP_001120829	Q8N3S3	PHTF2_HUMAN		1	GATTTTCTTTTTTT	0.307	
-	24	15477		NM_033026	NP_149015	Q9Y6V0	PCLO_HUMAN	C2 2.	7	ATCACCTTTTTTT	0.313	
-	6	11286	p.P3666fs|PCLO_u	NM_033026	NP_149015	Q9Y6V0	PCLO_HUMAN		7	CTTGCTGGGGGA	0.473	
+	19	5175_5176	.S1650fs|AKAP9_	NM_005751	NP_005742	Q99996	AKAP9_HUMAN		26	GTTTCAGAGAGA	0.411	
-	15	1860	s|TAF6_uc011kji.1_	NM_139315	NP_647476	P49848	TAF6_HUMAN		2	GTGCTGGGGGG	0.657	
-	1	220_222	p.L22del|ACHE_u	NM_000665	NP_000656	P22303	ACES_HUMAN		2	GCCAGAGGAGG	0.685	
-	20	2704_2705	liz.2_Frame_Shift_	NM_005045	NP_005036	P78509	RELN_HUMAN		19	TCTCTGGGAAGA	0.396	
+	15	2282	p.L359fs|EXOC4_	NM_021807	NP_068579	Q96A65	EXOC4_HUMAN		9	GGATCTCCCCCCA	0.458	rs34608222
-	44	11828	.3_uc003wkx.2_5'F	NM_170606	NP_733751	Q8NEZ4	MLL3_HUMAN		63	TCGTCCTTTTTCC	0.458	
-	3	436		NM_005431	NP_005422	O43543	XRCC2_HUMAN		2	TACACCAAAAAAA	0.393	
-	1	668_673	kwg.1_In_Frame_	NM_175075	NP_778250	Q86YL5	CH042_HUMAN	Poly-Ala.	0	GCCTGggcggcggc	0.65	
+	2	273_275	lank|BMP1_uc003	NM_003018	NP_003009	P11686	PSPC_HUMAN		0	TATCGTGGTGGT	0.601	
+	12	2305_2307	me_Del_p.E38del	NM_000553	NP_000544	Q14191	WRN_HUMAN	Poly-Glu.	7	CTACTAaagaagaa	0.266	
+	13	2412	p.V690fs|UNC5D_	NM_080872	NP_543148	Q6UXZ4	UNC5D_HUMAN	lasmic (Potential).	6	GGCGGTTTTTGC	0.488	
-	16	3521_3523	.E993del|MYST3_u	NM_001099412	NP_001092882	Q92794	MYST3_HUMAN	Poly-Glu.	7	CCGGCTCCTCCT	0.567	

-	5	987_989		NM_014729	NP_055544	O94900	TOX_HUMAN	lization signal (Potential).	4	GATCCTTCTTC	0.453	
-	10	1666_1667	.N420fs|MYBL1_	NM_001080416	NP_001073885	P10243	MYBA_HUMAN	tory domain (By similarity)	3	CAAGTGTTTTTT	0.406	
-	33	5045_5046	.P1006fs|ARFGE	NM_006421	NP_006412	Q9Y6D6	BIG1_HUMAN		8	GAGGTGGGGG	0.421	rs142098461
+	9	1450_1451	RRCC1_uc003ycx	NM_033402	NP_208325	Q9C099	LRCC1_HUMAN	Potential.	0	ACCAAGAGAG	0.267	
-	7	1378	yec.2_Frame_Shif	NM_005941	NP_005932	P51512	MMP16_HUMAN	otential).|Hemopexin-like 1	8	TCGCCAAAACC	0.483	
-	6	1241	yec.2_Frame_Shif	NM_005941	NP_005932	P51512	MMP16_HUMAN	ellular (Potential).	8	CTGTCATTTTTC	0.517	
-	11	1761	p.R469fs|NBN_uc	NM_002485	NP_002476	O60934	NBN_HUMAN		7	TTTCCCTTTTTT	0.323	
-	8	1296	_Shift_Del_p.K377	NM_175634	NP_783552	Q06455	MTG8_HUMAN		16	GCCACCTTTTTT	0.517	
-	45	6393_6394	ks.1_Frame_Shift_	NM_015902	NP_056986	O95071	UBR5_HUMAN		28	CCCTTCTTTTTT	0.381	
-	7	1943	_p.G597fs|LRP12_	NM_013437	NP_038465	Q9Y561	LRP12_HUMAN	lasmic (Potential).	0	AATGACCCAGA	0.438	
-	13	1637_1639	.I506del|TSNARE	NM_145003	NP_659440	Q96NA8	TSNA1_HUMAN	.|Helical; (Potential).	0	TGGCGATGATG	0.414	rs142964918
-	2	331		NM_015117	NP_055932	Q8IXZ2	ZC3H3_HUMAN		1	GCTGGCCCCC	0.632	
-	5	1434		NM_138367	NP_612376	Q9BRH9	ZN251_HUMAN	2H2-type 7.	0	GGAGGAAAAGG	0.458	
-	3	284	l_p.K62fs|KIAA002	NM_014878	NP_055693	Q15397	K0020_HUMAN		1	CACCCTTTTTCC	0.388	
-	4	387	3zjd.2_Frame_Shi	NM_018465	NP_060935	Q9HBL7	CI046_HUMAN	ical; (Potential).	1	AGGCCAAAAAA	0.383	
+	7	1228_1230	03zvr.2_In_Frame_	NM_015297	NP_056112	Q9UPV7	K1045_HUMAN		1	CAGCCAGCAGC	0.596	
-	7	1190_1192	kh.1_5'UTR|VCP_	NM_007126	NP_009057	P55072	TERA_HUMAN		1	GATCAAGAAGA	0.463	
-	2	2007		NM_001206	NP_001197	Q13886	KLF9_HUMAN		0	GCGCCTTTTTC	0.582	
-	26	2978	_p.Y312fs|GOLGA	NM_004486	NP_004477	Q08379	GOGA2_HUMAN		1	CCGGTAAAAAA	0.562	
+	5	629		NM_001807	NP_001798	P19835	CEL_HUMAN		1	CCTTCGGGGGG	0.642	
-	17	2544_2546	841del|RALGDS_	NM_006266	NP_006257	Q12967	GNDS_HUMAN	sociating.|Poly-Glu.	3	CCGGCTCCTCC	0.606	rs35200098
+	10	813	ez.2_Frame_Shift	NM_017588	NP_060058	P61964	WDR5_HUMAN	WD 5.	0	GACAACCCCCC	0.627	
+	1	214_216	p.V11del|MBTPS2	NM_206923	NP_996806	O15391	TYY2_HUMAN		2	TCGCTGGTGGT	0.685	
+	12	1252_1254	L3L_uc004dti.2_R	NM_019067	NP_061940	Q9NVN8	GNL3L_HUMAN		1	TGGGGAAGAAG	0.557	
+	12	1981	|TAF1_uc004dzt.	NM_138923	NP_620278	P21675	TAF1_HUMAN		17	ACATCAAAAAA	0.313	
-	3	4075		NM_001008537	NP_001008537	Q5QGS0	K2022_HUMAN		15	AAGGGTTTTTT	0.403	
-	41	5293	_p.G1347fs|BRW	NM_153252	NP_694984	Q6RI45	BRWD3_HUMAN	Gly-rich.	4	ATCTTCCCCAT	0.259	
-	6	731	p.K154fs|TAF7L_	NM_024885	NP_079161	Q5H9L4	TAF7L_HUMAN		1	CTAACCTTTTTTT	0.363	
+	5	1012_1014	4elx.2_In_Frame_	NM_207318	NP_997201	Q6PEV8	F199X_HUMAN	Ser-rich.	1	GCGCCAGCAGC	0.567	
+	6	604_606	eoz.2_In_Frame_	NM_001128173	NP_001121645	O75914	PAK3_HUMAN	Linker.	10	aagaggaagaagaa	0.325	
+	9	1338		NM_007231	NP_009162	Q9UN76	S6A14_HUMAN	Name=8; (Potential).	3	ATATTATTTTTTT	0.363	
-	2	574_575	P_uc004esg.2_5'	NM_024528	NP_078804	Q8N5F7	NKAP_HUMAN		2	CCAATTCTCTCT	0.317	
-	3	474_475	exp.1_Frame_Shi	NM_021796	NP_068568	Q9HBJ0	PLAC1_HUMAN		1	GGTTTGGGGG	0.51	
+	12	1535	ezk.2_Frame_Shi	NM_006359	NP_006350	Q92581	SL9A6_HUMAN	ical; (Potential).	1	ATTGTGTTTTTTA	0.453	
+	3	1065		NM_001727	NP_001718	P32247	BRS3_HUMAN	ellular (Potential).	1	CCTCTGCCATG	0.468	
+	6	1104_1106	4ezx.2_In_Frame_	NM_001163280	NP_001156752	O43719	HTSF1_HUMAN	Poly-Lys.	3	CTCAAAGAAGA	0.335	
-	11	886_888	.2_In_Frame_Del	NM_031462	NP_113650	Q8TCZ2	C99L2_HUMAN	ic (Potential).|Poly-Pro.	3	TTCGGGCGGCG	0.611	rs7877654
-	19	3629_3631	0oag.1_In_Frame_	NM_001009566	NP_001009566	O94985	CSTN1_HUMAN	idic).|Cytoplasmic (Potent	1	TCCCCCTCCTC	0.557	
-	24	2622	1asb.2_Frame_S	NM_001001998	NP_001001998	Q01780	EXOSX_HUMAN		1	GTTTAATTTTTTT	0.478	
+	11	10149	p.1_Frame_Shift_	NM_015001	NP_055816	Q96T58	MINT_HUMAN	Pro-rich.	15	TACCACCCCCC	0.627	
-	7	894	1_Intron|MST1P9_	NR_002729					0	CCCCCGCCCAC	0.657	rs3982176
+	2	482		NM_032880	NP_116269	Q96ID5	IGS21_HUMAN	Ig-like 1.	4	CCTCTCCCCCC	0.572	
-	3	649	1bfc.2_Frame_Shi	NM_032236	NP_115612	Q86UV5	UBP48_HUMAN		2	CCCACCTTTTTC	0.358	
-	2	275	01btg.1_Frame_S	NM_012392	NP_036524	Q9UBV8	PEF1_HUMAN	m repeat of [AP]-P-G-G-P-	0	GGGGCCCCCG	0.602	
-	9	1711	_Shift_Del_p.Q554	NM_198040	NP_932157	Q8IXK0	PHC2_HUMAN		1	ATTCTGGGGGG	0.587	
-	4	577	mv.1_Frame_Shif	NM_020365	NP_065098	Q9NR50	EI2BG_HUMAN		1	ACCTGCTTTTTTT	0.318	
+	1	333_334	1_RNA|PCSK9_u	NM_174936	NP_777596	Q8NBP7	PCSK9_HUMAN		4	ccgctgccactgctgct	0.574	rs67610340

+	4	624	_p.G138fs|FGGY_u	NM_018291	NP_060761	Q96C11	FGGY_HUMAN		1	ACGTCGGGGGG	0.502	
-	5	924_925	RIQ3_uc001dfz.3_F	NM_001105659	NP_001099129	A6PVS8	LRIQ3_HUMAN		2	CTGCTGTTTTTT	0.327	
+	23	2276_2278	1dge.1_In_Frame_	NM_015978	NP_057062	Q59H18	TNI3K_HUMAN	Poly-Ser.	10	CTCACCTTCTTCT	0.473	
-	9	1732_1734	0ows.1_In_Frame_	NM_015906	NP_056990	Q9UPN9	TRI33_HUMAN	Poly-Thr.	11	TGTTGTGTTGTTC	0.429	
+	8	2428_2429		NM_020440	NP_065173	Q9P2B2	FPRP_HUMAN	6.|Extracellular (Potential).	1	GAAGAGCGACCT	0.584	
-	4	796	epj.2_Frame_Shift_	NM_001461	NP_001452	P49326	FMO5_HUMAN		3	ATCTCCTTTTTCC	0.473	
-	3	270	wmr.1_Frame_Shif	NM_001025603	NP_001020774	P48382	RFX5_HUMAN		1	CACCTGGGGGG	0.557	
-	2	3480_3482	vne.1_In_Frame_D	NM_007113	NP_009044	Q07283	TRHY_HUMAN	30 AA tandem repeats.	5	GCCTTCTCTTCTC	0.172	
-	2	1035_1036	e.1_In_Frame_Ins	NM_007113	NP_009044	Q07283	TRHY_HUMAN	-E-Q-E-E- E-R-R-E-Q-Q-L.	5	gctcgcgcctctcctcctg	0	
-	6	410	ok.2_Frame_Shift_	NM_004515	NP_004506	Q12905	ILF2_HUMAN	DZF.	0	GTCCCCTTTTTAT	0.453	
-	1	422_424	ox.1_In_Frame_De	NM_002249	NP_002240	Q9UGI6	KCNN3_HUMAN	Poly-Gln.	1	gctgctgttgctgctgctg	0.236	
-	4	1309		NM_006617	NP_006608	P48681	NEST_HUMAN	Tail.	6	GGTGTGGGGGG	0.597	
-	6	1404_1406	.V48del|PVRL4_u	NM_030916	NP_112178	Q96NY8	PVRL4_HUMAN	ical; (Potential).	2	ATGAGCACCACC	0.571	
+	3	338_340		NM_001102566	NP_001096036	A6NKN8	PC4L1_HUMAN		0	AGGCGGAGGAG	0.488	
-	12	1922_1924		NM_000069	NP_000060	Q13698	CAC1S_HUMAN	of repeat II; (Potential).|Pol	5	GAAGAGCAGCA	0.562	
+	22	2922_2924		NM_018085	NP_060555	Q96P70	IPO9_HUMAN		2	gaggaagaggaggag	0.33	
+	2	1350_1352		NM_004767	NP_004758	O60883	ETBR2_HUMAN	ic (Potential).|Cys-rich.	2	TCCTGGActgctgct	0.557	
+	5	643	I11A_uc001haf.2_F	NM_014827	NP_055642	O75152	ZC11A_HUMAN	C3H1-type 1.	2	CTGCTATTTTTTT	0.373	
+	1	791_793		NM_000707	NP_000698	P47901	V1BR_HUMAN	Name=5; (Potential).	3	TGCCGGTGACC	0.621	rs150659663
+	3	1066	DYRK3_uc001hei.2	NM_003582	NP_003573	O43781	DYRK3_HUMAN	rotein kinase.	3	CTGATTAAAAAA	0.403	
+	7	1133	_Shift_Del_p.L312f	NM_017898	NP_060368	Q969Z3	MOSC2_HUMAN	MOSC.	0	CTCCACTTTTTGC	0.413	
+	1	255		NM_001004698	NP_001004698	A6NFC9	OR2W5_HUMAN		3	AACCTGGGGGG	0.532	
-	1	235		NM_001004695	NP_001004695	Q8NG76	O2T33_HUMAN	cellular (Potential).	2	CCGCCATTTTGGC	0.577	
+	10	1321_1324	ib.2_Frame_Shift_	NM_001047160	NP_001040625	Q7Z628	ARHG8_HUMAN	PH.	1	GCGGAGCAAGAC	0.525	
+	8	1448_1449	el_p.E431fs|NCOA	NM_001145263	NP_001138735	Q13772	NCOA4_HUMAN		2	GCAGAGTGTGTG	0.485	
-	4	520_521		NM_213606	NP_998771	Q6ZSM3	MOT12_HUMAN	lasmic (Potential).	1	CTCCACAAAAAA	0.361	
+	16	2153_2154		NM_025235	NP_079511	Q9H2K2	TNKS2_HUMAN	ANK 12.	8	CCCTACAAAAAA	0.391	
+	9	1586	p.P323fs|PAX2_uc	NM_003990	NP_003981	Q02962	PAX2_HUMAN		0	ACGTGCCCCCC	0.612	
+	27	4250	_Shift_Del_p.V417	NM_207303	NP_997186	Q5VV63	ATRN1_HUMAN	lasmic (Potential).	7	GAAGTGGGAGC	0.463	
-	3	1541	09xyz.1_Frame_Sh	NM_014904	NP_055719	Q7L804	RFIP2_HUMAN		0	GCTATCTTTTTTT	0.343	
-	8	1956	p.R261fs|CUZD1_	NM_022034	NP_071317	Q86UP6	CUZD1_HUMAN	cellular (Potential).	2	GATCCCTTTTCAG	0.413	
+	19	2126_2128	.Q620del|PTPRE_	NM_006504	NP_006495	P23469	PTPRE_HUMAN	phatase 2.|Cytoplasmic (Po	1	CAGAAGCAGCA	0.65	
+	6	663_665	me_Del_p.E180de	NM_020901	NP_065952	Q9P1Y6	PHRF1_HUMAN	Poly-Glu.	0	GAGCGAGGAGG	0.616	
+	13	1667	RNA|BRSK2_uc00	NM_003957	NP_003948	Q8IWQ3	BRSK2_HUMAN	Pro-rich.	0	AGCAGCCCCCG	0.701	
-	12	2561	ND5A_uc010rbw.1	NM_015213	NP_056028	Q6IQ26	DEN5A_HUMAN		1	CCCATCTTTTCCA	0.517	
-	11	2014	mtf.3_Frame_Shift	NM_001127612	NP_001121084	P26367	PAX6_HUMAN	o/Ser/Thr-rich.	9	ATATGTGGGGGG	0.587	
-	3	345	0rew.1_Frame_Shi	NM_001001991	NP_001001991	Q6UXH9	PAMR1_HUMAN		2	AGGTACCCCCC	0.517	
+	30	3229	GKZ_uc009yky.1_	NM_001105540	NP_001099010	Q13574	DGKZ_HUMAN		3	CTCCAGCCCCCC	0.649	rs3832759
-	1	1385		NM_000741	NP_000732	P08173	ACM4_HUMAN	smic (By similarity).	0	AAGGTCTTTTTAA	0.587	
-	6	909_911	.P302del|CPSF7_	NM_001136040	NP_001129512	Q8N684	CPSF7_HUMAN	Pro-rich.	1	TACCAGGAGGAC	0.611	
+	7	1936_1938	.L366del|SLC22A1	NM_144585	NP_653186	Q96S37	S22AC_HUMAN		1	CGCCCTGCTGC	0.66	
+	4	634	ocu.2_Frame_Shift	NM_003273	NP_003264	O76062	ERG24_HUMAN		1	CACCTGGGGGG	0.587	
+	1	356_358	RFN4_uc001ojq.1_	NM_024036	NP_076941	Q6PJG9	LRFN4_HUMAN		0	CGCTCCTGCTGC	0.719	
+	12	1367	ne_Shift_Del_p.F4	NM_003369	NP_003360	Q9P2Y5	UVRAG_HUMAN		6	ATTTCCTTTTTCC	0.383	
-	22	3331	n.1_RNA|NCAPD3	NM_015261	NP_056076	P42695	CNDD3_HUMAN		5	GACCTGGGGGG	0.522	rs138442478
+	2	451	_Shift_Del_p.S19f	NM_019854	NP_062828	Q9NR22	ANM8_HUMAN		5	GAACAGCCCCCC	0.657	
-	1	80	H1_uc001qzc.2_In	NM_176890	NP_795371	P59544	T2R50_HUMAN	Name=1; (Potential).	2	GAATTGAAAAAAA	0.318	

-	48	7101_7102	zjg.1_Frame_Shift_	NM_002223	NP_002214	Q14571	ITPR2_HUMAN	ical; (Potential).	14	CCCCAGAGAG	0.441	
-	11	2355	p.K703fs|PKP2_u	NM_004572	NP_004563	Q99959	PKP2_HUMAN	ARM 6.	2	GCTGTCTTTTTC	0.473	
-	12	4127_4129	w.2_In_Frame_D	NM_004719	NP_004710	Q99590	SCAFB_HUMAN	Pro-rich.	0	AGGGGGTGGTG	0.483	
-	11	3063_3064	p.E611fs|SFRS2IP	NM_004719	NP_004710	Q99590	SCAFB_HUMAN	Arg-rich.	0	TCCTTTCTCTCT	0.446	
+	2	157	40B_uc001ruq.1_	NM_001031698	NP_001026868	Q6NWY9	PR40B_HUMAN	Pro-rich.	5	AGCTATCCCCCC	0.607	
+	2	245_247	N2_uc009zln.2_5'	NM_001095	NP_001086	P78348	ACCN2_HUMAN	smic (By similarity).	1	GGCCGAGGAGG	0.616	
-	1	170_172	77_uc009zmi.2_5'	NM_175078	NP_778253	Q7Z794	K2C1B_HUMAN	Head.	1	ATATCCACCAC	0.552	rs149726101
-	3	695_696	rame_Shift_Ins_p.	NM_001478	NP_001469	Q00973	B4GN1_HUMAN	enal (Potential).	0	GGGAGGCCCCC	0.589	
+	10	2681	sto.2_Frame_Shift	NM_018448	NP_060918	Q86VP6	CAND1_HUMAN	HEAT 17.	2	TTGCAGGGGGG	0.428	
+	5	706	lice_Site|ZDHHC1	NM_015336	NP_056151	Q8IUH5	ZDH17_HUMAN		0	ACAGGTAAAAA	0.351	rs137909589
-	9	979_980	.2_5'Flank|CEP29	NM_025114	NP_079390	O15078	CE290_HUMAN	Potential.	7	TCATAGTTTTTT	0.317	
+	5	541	ztz.1_Frame_Shift	NM_014503	NP_055318	O75691	UTP20_HUMAN		4	CAGAGTTTTTT	0.398	
+	5	474	PIC_uc010svp.1_	NM_152323	NP_689536	Q8N5J4	SPIC_HUMAN		1	GGGGGAAAAGG	0.393	
+	17	2575_2577		NM_015267	NP_056082	O14529	CUX2_HUMAN	Poly-Ser.	6	GCTGTCCTCCT	0.749	
-	64	11032_11034		NM_001109662	NP_001103132				2	GGCACAGCAGC	0.64	
+	7	941	F3_uc001uqw.2_	NM_006646	NP_006637	Q9UPY6	WASF3_HUMAN		1	ACTAGGTGTGTG	0.475	
+	10	1588	uqw.2_Frame_Shi	NM_006646	NP_006637	Q9UPY6	WASF3_HUMAN	WH2.	1	AACTGAAAAAG	0.507	
-	2	312	tgt.1_Frame_Shift	NM_000053	NP_000044	P35670	ATP7B_HUMAN	lasmic (Potential).	3	AAGGGCCCAGG	0.493	
-	5	1255		NM_012158	NP_036290	Q9UKT7	FBXL3_HUMAN		0	TCATATAAAAAA	0.418	
-	3	1088	BAC2_uc001vod.	NM_005292	NP_005283	Q14330	GPR18_HUMAN	Name=5; (Potential).	0	ATCAAGAAAAAA	0.438	
+	1	678		NM_001004717	NP_001004717	Q8NH43	OR4L1_HUMAN	lasmic (Potential).	5	TGTACCAAAAAA	0.438	
-	20	2986	EP1_uc010tlf.1_R	NM_007110	NP_009041	Q99973	TEP1_HUMAN		5	TAGCTGGGGGG	0.557	
-	19	4208_4209	_uc001wiq.3_Fra	NM_014977	NP_055792	Q9UKV3	ACINU_HUMAN	sp/Glu/Lys-rich.	4	cgctccctttctctctctct	0.436	
+	10	1639	l_p.F369fs|PCK2_	NM_004563	NP_004554	Q16822	PCKGM_HUMAN		1	GGCCCTTTTTT	0.577	
+	3	688_689	rame_Shift_Del_p	NM_014315	NP_055130	Q9Y2U9	KLDC2_HUMAN		1	TGTGCTGTGTG	0.396	
+	20	3442_3443	xdq.2_Frame_Shi	NM_002892	NP_002883	P29374	ARI4A_HUMAN		6	GTACAAGAGAG	0.386	
-	11	2941	H5_uc001xfy.2_3'	NM_139318	NP_647479	Q8NCM2	KCNH5_HUMAN	lasmic (Potential).	9	TATCTGGGGGG	0.383	
+	7	910_912	0ttu.1_In_Frame_	NM_021239	NP_067062	P49756	RBM25_HUMAN		4	CCAGGAAGAAG	0.384	
-	1	1802_1804		NM_006029	NP_006020	Q8ND90	PNMA1_HUMAN	Poly-Glu.	1	GCCTcagcctcctcc	0.256	
-	16	2283	ALC_uc010tvy.1_	NM_000153	NP_000144	P54803	GALC_HUMAN		0	ATACCATTTTTTT	0.308	
-	7	1217_1219	339SS>S|FOXN3_	NM_001085471	NP_001078940	O00409	FOXN3_HUMAN		3	GGCTGAGGAGG	0.65	rs139532153
-	5	903_905	KT1_uc001ypm.2_	NM_005163	NP_005154	P31749	AKT1_HUMAN		134	TCCATCTCCTCC	0.631	
-	7	3802	zpv.2_Frame_Shi	NM_022473	NP_071918	Q9H2Y7	ZF106_HUMAN		3	GTGGGAAAAAG	0.522	
-	15	4136	e_Shift_Del_p.Q1	NM_173500	NP_775771	Q6IQ55	TTBK2_HUMAN		7	CCCTTGGGGGG	0.537	
-	5	646	.T29fs|TEX9_uc00	NM_018365	NP_060835	Q8NEH6	MNS1_HUMAN	ential.|Glu-rich.	1	TCATGGTTTTGG	0.328	
+	6	3071		NM_020778	NP_065829	Q96L96	ALPK3_HUMAN		12	TTCCCAAAAAA	0.537	
+	9	1102		NM_002569	NP_002560	P09958	FURIN_HUMAN		7	GGAACGGGGGC	0.627	
-	7	1108		NM_003223	NP_003214	Q01664	TFAP4_HUMAN		1	TCCTGCTTTTCC	0.667	
+	17	2056	2dan.3_Frame_S	NM_015226	NP_056041	Q2KHT3	CL16A_HUMAN		2	AAGACATTTTTT	0.433	
+	24	3260	2dap.2_Frame_S	NM_015226	NP_056041	Q2KHT3	CL16A_HUMAN		2	CTTGTCCCCCC	0.701	
-	10	895	NTAN1_uc010uzo.	NM_173474	NP_775745	Q96AB6	NTAN1_HUMAN		0	TCTTCATTTTTT	0.383	
+	19	3331	e_Shift_Del_p.D8	NM_006662	NP_006653	Q6ZRS2	SRCAP_HUMAN	Pro-rich.	4	CCTGACCCCCC	0.567	
+	28	3281	ap.1_Frame_Shift_	NM_005353	NP_005344	Q13349	ITAD_HUMAN	ellular (Potential).	1	AGCTTCCAGGA	0.552	
+	9	1264	Shift_Del_p.N290f	NM_133443	NP_597700	Q8TD30	ALAT2_HUMAN		2	GTGAACCCCCC	0.632	
-	1	196	_5'Flank|OGFOD	NM_007006	NP_008937	O43809	CPSF5_HUMAN	ry for RNA-binding.	0	AGTGACCCCCC	0.652	
+	2	113_115	p.E13del|CCDC13	NM_032269	NP_115645	Q8IY82	CC135_HUMAN	Potential.	1	gaaggtggaggagga	0.448	
-	3	888_890	jt.1_In_Frame_De	NM_001082486	NP_001075955	Q96AP0	ACD_HUMAN		1	TCCTGCAGCAG	0.65	

+	8	1053	el_p.W274fs|TSN	NM_018430	NP_060900	Q2TAA8	TXIP1_HUMAN		0	CATCTGGGGGG	0.597	
+	15	2438	38_uc010vmp.1_I	NM_014003	NP_054722	Q92620	PRP16_HUMAN	ase ATP-binding.	1	CTGCCTTTTTG	0.562	
-	2	1059	p.D301fs|MYO18A	NM_078471	NP_510880	Q92614	MY18A_HUMAN	PDZ.	0	GCTGTCCCCTG	0.622	
-	2	759	IP2_uc002hdx.3_I	NM_020772	NP_065823	Q7Z417	NUFP2_HUMAN		4	CTTTCCTTTTTTT	0.388	
-	5	891		NM_139285	NP_644814	Q8NHY3	GA2L2_HUMAN		2	GGGCCGGGGGC	0.597	rs139867246
+	14	4452	rw.3_Frame_Shift_	NM_016507	NP_057591	Q9NYV4	CDK12_HUMAN		19	CAGCGCCCCCA	0.647	
-	6	825_826	2iam.1_Frame_Sh	NM_178126	NP_835227	Q86VR2	F134C_HUMAN		2	CATTGTCTCTCT	0.515	
-	18	1593	_Shift_Del_p.N501	NM_001932	NP_001923	Q13368	MPP3_HUMAN	ylate kinase-like.	2	ACTTTGTTTTTGC	0.443	
-	5	690	43_uc010czw.1_	NM_144609	NP_653210	Q96MW1	CCD43_HUMAN	Potential.	0	GTGTCCTTTTTTT	0.463	
+	4	641_642	103_uc002ihp.1_	NM_213607	NP_998772	Q8IW40	CC103_HUMAN		1	GGGCAGAGAGA	0.644	
-	2	684	_5'Flank|HOXB6_	NM_004502	NP_004493	P09629	HXB7_HUMAN	Homeobox.	0	TTCTCCTTTTTCC	0.473	
-	3	722_723		NM_052855	NP_443087	Q6AI12	ANR40_HUMAN	Pro-rich.	0	TCTGCAGGGGGT	0.574	
-	8	907_909	p.E75del|MKS1_u	NM_017777	NP_060247	Q9NXB0	MKS1_HUMAN		1	CCCGCTCCTCC	0.532	
+	9	1470	lank|ACE_uc010d	NM_000789	NP_000780	P12821	ACE_HUMAN	otential).|Peptidase M2 1.	4	GCGTACCCCCC	0.562	
-	1	452_453	13_uc010wqh.1_5'	NM_006572	NP_006563	Q14344	GNA13_HUMAN		0	TCCTCGCGCGC	0.436	
-	5	1364_1365	C16A6_uc002jha.	NM_004694	NP_004685	O15403	MOT7_HUMAN	ical; (Potential).	0	AAACCCAAAAAA	0.436	
+	4	505_507	10wsa.1_In_Fram	NM_014738	NP_055553	Q12767	K0195_HUMAN	ical; (Potential).	1	GCCGTGCTGCT	0.675	
+	20	2951	195_uc010wsb.1_	NM_014738	NP_055553	Q12767	K0195_HUMAN		1	GAGATCCCCCC	0.612	
-	21	3612	_Shift_Del_p.P415fs|DNAH17_uc002jvs.2_RNA						9	AGGTTGGGGGG	0.582	
+	4	641_643	_Frame_Del_p.E1	NM_032868	NP_116257	Q8N594	MPND_HUMAN	Poly-Glu.	1	atggaagaggaggag	0.532	
-	9	1261_1263	.E147del|GTF2F1_	NM_002096	NP_002087	P35269	T2FA_HUMAN	Glu-rich.	0	TGccttcttctcctcctcc	0.542	
-	1	186	A41_uc010dut.2_	NM_173637	NP_775908	Q8N5S1	S2541_HUMAN	Pro-rich.	0	ggaggttgggggga	0.428	
-	7	1203	e_Shift_Del_p.K3	NM_021155	NP_066978	Q9NNX6	CD209_HUMAN	ellular (Probable).	1	CGGACTTTTTG	0.532	
-	3	567_570	_p.L56fs|FBXL12_	NM_017703	NP_060173	Q9NXK8	FXL12_HUMAN	LRR 2.	2	CGTGCAGGCAG	0.647	rs150413068
-	9	1445_1447	2_In_Frame_Del_	NM_002918	NP_002909	P22670	RFX1_HUMAN	Gly-rich.	2	cctcccccgccgccgc	0.365	
+	2	309		NM_003950	NP_003941	Q96RI0	PAR4_HUMAN		0	GCCTGCCCCCCC	0.667	
-	2	134	Splice_Site|ZNF43	NM_003423	NP_003414	P17038	ZNF43_HUMAN		2	GTCCCTAAAAAA	0.386	
+	2	252_254	eea.2_In_Frame_	NM_005306	NP_005297	O15552	FFAR2_HUMAN	Name=2; (Potential).	1	CCTCCTGCTGC	0.645	
-	9	974_975	pni.2_Frame_Shift_	NM_003598	NP_003589	Q15562	TEAD2_HUMAN	al activation (Potential).	3	GGCATGGGGGC	0.564	
-	11	1285_1287	pt.1_RNA|FUZ_uc	NM_025129	NP_079405	Q9BT04	FUZZY_HUMAN	Leu-rich.	0	GAGACAGCAGC	0.635	
+	12	1412	1_uc002pqa.2_R	NM_017432	NP_059128	Q86YD1	PTOV1_HUMAN	ction with FLOT1.	0	TAGATGGGGGG	0.657	
-	4	864	47_uc002qpm.3_I	NM_017879	NP_060349	Q9BWM5	ZN416_HUMAN		0	GGGTGAAAAAA	0.453	
+	4	717	s|ZIK1_uc002qpi.2	NM_001010879	NP_001010879	Q3SY52	ZIK1_HUMAN		2	CAGTCAAAAAA	0.483	
-	11	1472_1474	1_In_Frame_Del_	NM_015317	NP_056132	Q8TB72	PUM2_HUMAN	Ala-rich.	1	TCCAGCTGCTG	0.424	
-	3	316	_p.P92fs|HS1BP3	NM_022460	NP_071905	Q53T59	H1BP3_HUMAN	PX.	1	GTAGTGGGGGG	0.537	rs77941615
-	20	2931	TF3C2_uc002rju.	NM_001521	NP_001512	Q8WUA4	TF3C2_HUMAN	WD 4.	2	TGACTGCCCCCC	0.537	
+	1	105_107		NM_016441	NP_057525	Q9NZV1	CRIM1_HUMAN		3	TGGGGCTGCTG	0.714	
+	1	96_98	2sda.2_In_Frame_	NM_203437	NP_982261	Q6ULP2	AFTIN_HUMAN		2	AGAGGATGATG	0.409	
-	2	550	l_p.G10fs|MOGS_	NM_006302	NP_006293	Q13724	MOGS_HUMAN	enal (Potential).	0	GGAGTCCCCGG	0.652	
+	6	662	151_splice|SEMA4	NM_004263	NP_004254	O95754	SEM4F_HUMAN		4	CTGCAGGGGGG	0.587	
-	6	747_749	.2_In_Frame_Del_	NM_016079	NP_057163	Q9Y3E7	CHMP3_HUMAN	T-interacting motif.|Interacti	1	CTCTTCCTCCT	0.616	
+	6	2252_2253	ed.2_Frame_Shift_	NM_181453	NP_852118	Q8IWJ2	GCC2_HUMAN	Potential.	1	GTTCAGAAAAAA	0.307	
+	12	2858_2860		NM_198581	NP_940983	P61129	ZC3H6_HUMAN		4	AGGCGATGATG	0.429	
+	5	719_721	zej.1_In_Frame_	NM_145810	NP_665809	Q9BWT1	CDCA7_HUMAN		1	CCATGGAGGAG	0.537	
-	2	852	KL_uc002uod.1_I	NM_002500	NP_002491	Q13562	NDF1_HUMAN		1	CAGGTGGGGGG	0.617	
-	4	1344	PSMD1_uc002vrn.	NM_000867	NP_000858	P41595	5HT2B_HUMAN	smic (By similarity).	0	CCACCTTTTCCC	0.463	rs61731724
+	8	835	Shift_Del_p.H142f	NM_152879	NP_690618	Q16760	DGKD_HUMAN	l-ester/DAG-type 2.	5	AGGTTCACACA	0.562	

-	14	1577	M33_uc002wiu.2_	NM_025220	NP_079496	Q9BZ11	ADA33_HUMAN	r (Potential).|Disintegrin.	4	CGTCTGGGGGA	0.657	
-	7	1256	_Shift_Del_p.K301	NM_001042576	NP_001036041	Q9P2E9	RRBP1_HUMAN	lasmic (Potential).	1	TTGGCCTTTTCT	0.622	
-	1	5735	CE2_uc002yyx.2_I	NM_182832	NP_878252	Q8WY50	PLAC4_HUMAN		0	GTGTCTGGGGT	0.517	rs5019194
-	3	453_455	ne_Del_p.L72del|	NM_194255	NP_919231	P41440	S19A1_HUMAN	ical; (Probable).	0	GGCCCAGCAGC	0.645	
-	5	573	zil.2_Frame_Shift_	NM_001001438	NP_001001438	P48449	ERG7_HUMAN	PFTB 1.	0	CCAACACCCAGA	0.542	
+	6	588_590	015_uc002zsr.2_In	NM_001003891	NP_001003891	Q96RN5	MED15_HUMAN	Poly-Gln.	1	gcagttccagcagcag	0.217	
+	6	711_713	015_uc002zsr.2_In	NM_001003891	NP_001003891	Q96RN5	MED15_HUMAN	Poly-Gln.	1	gcagctccagcagcag	0.187	
-	5	615	me_Shift_Del_p.K	NM_032204	NP_115580	Q9H1I8	ASCC2_HUMAN		0	GTTGCCTTTTCC	0.483	
-	11	1370	uc003ahi.2_Intron|	NM_031937	NP_114143	Q9BXI6	TB10A_HUMAN		1	GGGCTGGGGGC	0.652	
-	3	496_498		NM_005877	NP_005868	Q15459	SF3A1_HUMAN	Poly-Gln.	5	GTGGTCTGCTGC	0.596	rs141985009
+	21	2500	.1_Frame_Shift_D	NM_001007467	NP_001007468	A8K8P3	SFI1_HUMAN		1	GAAGCCAAAAAA	0.512	
+	7	686_688	Del_p.E197del|SH	NM_018957	NP_061830	Q9Y3L3	3BP1_HUMAN	BAR.	1	CTGAAGGAGGA	0.498	
-	5	895_896	2_5'UTR|CYP2D6	NM_000106	NP_000097	Q6NWU0	Q6NWU0_HUMAN		2	GGTCTCGGGGG	0.629	rs72549352
-	1	5454_5456	Q1774del|TCF20_	NM_005650	NP_005641	Q9UGU0	TCF20_HUMAN		5	TCCTTCTGCTGC	0.601	
-	22	3893_3895	3brg.1_In_Frame_	NM_014850	NP_055665	O43295	SRGP2_HUMAN		9	CCGAGCTGCTG	0.739	
-	17	2137	RIP2_uc011avh.1	NM_001080423	NP_001073892	Q9C0E4	GRIP2_HUMAN	PDZ 5.	1	AGTTGTCCAGGC	0.617	
-	3	2472		NM_014831	NP_055646	O15050	TRNK1_HUMAN		2	CACCCGGGGGT	0.483	
-	16	2122	h.2_Frame_Shift_	NM_002343	NP_002334	P02788	TRFL_HUMAN	ansferrin-like 2.	4	GAGCACTTTTTC	0.463	
-	20	3495	s|SCAP_uc003crg.	NM_012235	NP_036367	Q12770	SCAP_HUMAN	milarity).|Cytoplasmic (By s	1	GATGGGTTTTTG	0.607	
+	3	580_581	003cwi.1_Frame_S	NM_173546	NP_775817	Q8IXV7	KLD8B_HUMAN	Kelch 4.	0	TGCTCTGGGGGG	0.609	
+	21	3869	OBO2_uc011bgk.1	NM_002942	NP_002933	Q9HCK4	ROBO2_HUMAN	lasmic (Potential).	11	CTACCTCCCCCC	0.433	
-	7	850	03eal.2_Frame_Sh	NM_001009899	NP_001009899	Q68DE3	K2018_HUMAN		3	CAATAATTTTTTT	0.373	
+	6	776	1bik.1_Frame_Shi	NM_001690	NP_001681	P38606	VATA_HUMAN		3	ATGCCCTTTTTC	0.423	
+	5	2486	edk.2_Frame_Shift	NM_003889	NP_003880	O75469	NR1I2_HUMAN	gand-binding.	2	GCTGCGGGGGG	0.587	
+	8	1209	p.G128fs|PARP15	NM_001113523	NP_001106995	Q460N3	PAR15_HUMAN	Macro 2.	5	GGGGGAAAAGA	0.413	
+	10	1570_1572	3fns.2_In_Frame_	NM_198241	NP_937884	Q04637	IF4G1_HUMAN	Poly-Glu.	7	GAAATGgaagaag	0.443	
-	18	2192	p.E673fs|CLCN2_	NM_004366	NP_004357	P51788	CLCN2_HUMAN	smic (By similarity).	0	GGTCTCCCCCC	0.622	rs143415674
-	12	1572	gmd.2_Frame_Shi	NM_020041	NP_064425	Q9NRM0	GTR9_HUMAN	lasmic (Potential).	3	GTTCTGTTTTTG	0.413	
+	5	567	31fs|ANAPC4_uc0	NM_013367	NP_037499	Q9UJX5	APC4_HUMAN		5	ACTGCCAAAAAA	0.294	
-	7	944		NM_173536	NP_775807	Q8N1C3	GBRG1_HUMAN	ellular (Probable).	2	CAGGTCAAAAAA	0.294	
-	23	3204_3206	ame_Del_p.Q760d	NM_004898	NP_004889	O15516	CLOCK_HUMAN	Gln-rich.	3	gggagctctgctgctgc	0.315	
+	8	1473_1475	.Q217del|PRDM8_	NM_020226	NP_064611	Q9NQV8	PRDM8_HUMAN	-rich.|Poly-Gln.	1	aaagaccagcagcag	0.384	
+	8	1279	ike.1_Frame_Shift	NM_001263	NP_001254	Q92903	CDS1_HUMAN		4	TTTGGATTTTTTT	0.308	
-	1	538_540	C3_uc011cdn.1_I	NM_153757	NP_715638	Q96NT1	NP1L5_HUMAN	Glu-rich.	1	tactcctcttcctcctcctc	0.369	
+	8	1187_1189	p.P363del|NPNT_	NM_001033047	NP_001028219	Q6UXI9	NPNT_HUMAN	Pro-rich.	1	TACTCCACCACC	0.522	
+	39	6607	.G123fs|KIAA110	NM_015312	NP_056127	Q2LD37	K1109_HUMAN		12	ACAATGGGGGT	0.438	
-	3	3529	.N909fs|ANKRD5	NM_020337	NP_065070	Q9ULJ7	ANR50_HUMAN	ANK 19.	1	TGTCCATTTTTGG	0.408	
+	1	413_414		NM_004575	NP_004566	Q12837	PO4F2_HUMAN		1	CTggtggtggcggcg	0.386	907220;rs72269802
-	5	1095	p.F207fs|LRBA_uc	NM_006726	NP_006717	P50851	LRBA_HUMAN		7	AAAGTTAAAAAA	0.408	
+	9	1176		NM_033393	NP_203751	Q9C0D6	FHDC1_HUMAN		2	TCTTTTAGATTAT	0.423	
+	20	3494	p.V972fs|TLL1_uc	NM_012464	NP_036596	O43897	TLL1_HUMAN	CUB 5.	7	CTATGTGGAGCT	0.448	
-	8	993_995	03jcg.2_In_Frame_	NM_030782	NP_110409	Q96KA5	CLP1L_HUMAN	lasmic (Potential).	2	CATGCTCTTCTT	0.537	
+	46	8393_8395	E2636del|NIPBL_	NM_133433	NP_597677	Q6KC79	NIPBL_HUMAN		9	CTGATGAAGAAG	0.379	
-	1	68_70		NM_004465	NP_004456	O15520	FGF10_HUMAN		3	AAAAAGCAGCA	0.537	
-	10	1303	256fs|FAM172A_u	NM_032042	NP_114431	Q8WUF8	F172A_HUMAN		0	GACCCGGGGGC	0.388	rs140492306
+	2	237_240	_p.K19fs|AP3S1_	NM_001284	NP_001275	Q92572	AP3S1_HUMAN		0	ATCTAAGAGAGA	0.304	rs80118146
-	37	5307		NM_001999	NP_001990	P35556	FBN2_HUMAN	TB 6.	15	TGACAGGGGGG	0.507	

+	1	453_455	cyu.1_In_Frame_I	NM_001964	NP_001955	P18146	EGR1_HUMAN	Gly/Ser-rich.		1	cagcaacagcagcag	0.394	
-	3	630	ame_Shift_Del_p.	NM_014790	NP_055605	Q96AA8	JKIP2_HUMAN	Potential.		2	AGCTCCTTCATC	0.532	
-	23	2701_1270	FAT2_uc003lud.3_	NM_001447	NP_001438	Q9NYQ8	FAT2_HUMAN	lasmic (Potential).		6	CTCCAGGGGGA	0.644	
+	5	668_670	mdf.1_In_Frame_	NM_006650	NP_006641	Q6PUV4	CPLX2_HUMAN			1	GGACGAGGAGG	0.645	
+	3	266		NM_002114	NP_002105	P15822	ZEP1_HUMAN			6	AGTTTCAAAAAA	0.259	
+	5	798_799	_uc003nnz.3_Frar	NM_002127	NP_002118	P17693	HLAG_HUMAN	ar (Potential).|Alpha-3.		4	TTCAGACCCCCC	0.54	
-	7	1054	M26_uc010jry.2_5'	NM_003449	NP_003440	Q12899	TRI26_HUMAN			3	CCGGTCTTTTTT	0.483	
+	4	545	_Shift_Del_p.I57fs|	NM_001517	NP_001508	Q92759	TF2H4_HUMAN			3	ACCCCATTTTCC	0.577	
+	5	800	Shift_Del_p.E332f	NM_001710	NP_001701	P00751	CFAB_HUMAN			1	ATCATGAAAATG	0.468	
+	4	1107_1108	jvw.1_Frame_Shif	NM_021922	NP_068741	Q9HB96	FANCE_HUMAN	ction with FANCC.		3	AGGATGCCCCCC	0.54	
+	2	314_316	K13_uc003olt.2_	NM_002754	NP_002745	O15264	MK13_HUMAN	rotein kinase.		3	GGGAGCTGCTG	0.67	
-	6	995		NM_152688	NP_689901	Q5VWX1	KHDR2_HUMAN	Pro-rich.		11	TGGTGCCCCCC	0.542	
-	1	195_197	ob.1_In_Frame_D	NM_145331	NP_663304	O43318	M3K7_HUMAN	Poly-Ser.		6	AGACGAGGAGG	0.655	
-	13	1854	k.2_Frame_Shift_	NM_002037	NP_002028	P06241	FYN_HUMAN	rotein kinase.		7	GGTCCTTTTTCC	0.562	
+	12	1829	Shift_Del_p.K213f	NM_015278	NP_056093	O94885	SASH1_HUMAN			1	TTGGGAAAAAG	0.408	
-	13	2067		NM_032415	NP_115791	Q9BXL7	CAR11_HUMAN			50	GCTCCGGGGGG	0.592	
-	7	678	A1_uc003srq.2_F	NM_022307	NP_071682	Q05084	ICA69_HUMAN	AH.		1	TCAAAGTTTTTTT	0.378	
+	8	2004_2005	srz.2_Frame_Shift	NM_014660	NP_055475	O94880	PHF14_HUMAN			3	TTGCAAGAGAGA	0.376	
-	8	1153	_p.P138fs|ETV1_u	NM_004956	NP_004947	P50549	ETV1_HUMAN			35	GGTGTGGGGGG	0.527	
-	2	279	jxy.1_Frame_Shift	NM_006408	NP_006399	O95994	AGR2_HUMAN			0	TGTCCTTTTTGG	0.493	
-	5	684_685	_Del_p.E93fs|OSB	NM_015550	NP_056365	Q9H4L5	OSBL3_HUMAN	PH.		1	CAGCTTCTCTCT	0.5	
-	1	310_312	ame_Del_p.72_73	NM_005522	NP_005513	P49639	HXA1_HUMAN	Poly-His.		3	ggggtggcgatggtgg	0.527	rs10951154
-	5	936	zm.2_Frame_Shift	NM_175061	NP_778231	Q86VZ6	JAZF1_HUMAN			131	ACACCGGGGGA	0.493	
+	1	403_405	c003tbl.3_5'Flank	NM_002047	NP_002038	P41250	SYG_HUMAN			1	CGCTCTGCTGC	0.749	
+	5	601_603	0kxo.2_In_Frame_	NM_007252	NP_009183	P78424	PO6F2_HUMAN	Gln-rich.		1	cagctccagcagcag	0.365	
+	18	7753	13_uc010kys.1_5	NM_152701	NP_689914	Q86UQ4	ABCAD_HUMAN			10	TACTTTAAAAAAA	0.313	
-	2	83_85	_uc010lbj.1_In_Fr	NM_004603	NP_004594	Q16623	STX1A_HUMAN	lasmic (Potential).		0	AGCGACATCATC	0.586	
-	30	3061	fz.1_Frame_Shift_	NM_005338	NP_005329	O00291	HIP1_HUMAN	I/LWEQ.		8	TAGTGCTTTTTCC	0.507	
-	2	458		NM_032936	NP_116325	Q9H2L4	TMM60_HUMAN			0	CCAGGCTTTTTT	0.408	
+	13	1828	_p.F530fs|PHTF2_	NM_001127357	NP_001120829	Q8N3S3	PHTF2_HUMAN			1	ATTTTCTTTTTTT	0.303	
+	19	5175_5176	.S1650fs|AKAP9_	NM_005751	NP_005742	Q99996	AKAP9_HUMAN			26	GTTTCAGAGAGA	0.411	
-	7	1188	_p.K237fs|CYP51A	NM_000786	NP_000777	Q16850	CP51A_HUMAN			0	ATAACATTTTTTT	0.398	
+	23	4102	LL5_uc010ljf.1_RN	NM_182931	NP_891847	Q8IZD2	MLL5_HUMAN			3	CAAGTGGAAGC	0.473	
+	26	3637	205_uc003vsx.2_5	NM_015135	NP_055950	Q92621	NU205_HUMAN			6	GTTGGATTTTTTT	0.373	
+	3	363	me_Shift_Del_p.E	NM_015917	NP_057001	Q9Y2Q3	GSTK1_HUMAN			0	GCTTGAAAAAG	0.478	
+	2	1926	wjq.1_Frame_Shift	NM_019015	NP_061888	Q9P2E5	CHPF2_HUMAN	enal (Potential).		1	GCAGCGGGGGG	0.632	
-	38	8744	.N1903fs|MLL3_u	NM_170606	NP_733751	Q8NEZ4	MLL3_HUMAN			63	TCATCATTTTTTT	0.378	
-	3	436		NM_005431	NP_005422	O43543	XRCC2_HUMAN			2	TACACCAAAAAA	0.393	
+	12	1730_1731	DR60_uc010lqw.2	NM_018051	NP_060521	Q8WVS4	WDR60_HUMAN		p.G524R(1)	4	TTTGGGAAAAAA	0.332	
+	2	273_275	lank|BMP1_uc003	NM_003018	NP_003009	P11686	PSPC_HUMAN			0	TATCGTGGTGGT	0.601	
+	12	2305_2307	me_Del_p.E38del	NM_000553	NP_000544	Q14191	WRN_HUMAN	Poly-Glu.		7	CTACTAaagaagaa	0.266	
+	10	6850	.I2200fs|ZFHX4_	NM_024721	NP_078997	Q86UP3	ZFHX4_HUMAN			15	CCTCCTATAACGC	0.368	
+	9	1450_1451	RRCC1_uc003ycx	NM_033402	NP_208325	Q9C099	LRCC1_HUMAN	Potential.		0	GACCAAGAGAGA	0.267	
+	4	567		NM_000067	NP_000058	P00918	CAH2_HUMAN			1	GGGGATTTTGGC	0.388	
-	3	492		NM_018710	NP_061180	Q8N4L2	TM55A_HUMAN			0	GGGGGGTTTTTGA	0.393	
-	8	1296	_Shift_Del_p.K377	NM_175634	NP_783552	Q06455	MTG8_HUMAN			16	GCCACCTTTTTTT	0.517	
-	6	468	yhd.2_Frame_Shif	NM_057749	NP_477097	O96020	CCNE2_HUMAN			0	CTCTCCTTTTTTA	0.323	

+	62	12067	yiw.2_Frame_Shift	NM_017890	NP_060360	Q7Z7G8	VP13B_HUMAN			20	AACCTCCCCCC	0.468	
+	6	1430	_p.K118fs|DCAF1	NM_015420	NP_056235	Q9NV06	DCA13_HUMAN	WD 4.		1	CTTTGAAAAAG	0.338	
-	19	1853	.K224fs|ENPP2_u	NM_001040092	NP_001035181	Q13822	ENPP2_HUMAN			7	GACCCTTTTGT	0.358	
+	2	165_166		NM_152412	NP_689625	Q7Z3I7	ZN572_HUMAN			2	AGCAAGAAAAA	0.396	
-	19	4091	Shift_Del_p.N120	NM_015912	NP_056996	Q49AJ0	F135B_HUMAN			9	ACGACGTTTTA	0.428	
-	13	1637_1639	.I506del|TSNARE	NM_145003	NP_659440	Q96NA8	TSNA1_HUMAN	.|Helical; (Potential).		0	TGGCGATGATG	0.414	rs142964918
-	2	529	AX5_uc010mlo.1_	NM_016734	NP_057953	Q02548	PAX5_HUMAN	Paired.	p.?(31)	147	ATTCACAAAAAC	0.522	
-	3	732	nrl.2_Frame_Shift_	NM_000507	NP_000498	P09467	F16P1_HUMAN			0	TGGTTCCAACG	0.398	
+	1	175	10mtn.1_Frame_S	NM_018112	NP_060582	Q9NVV0	TM38B_HUMAN	enal (Potential).		2	TTTCCCTTTTTTG	0.627	
-	22	6093	f.2_Frame_Shift_	NM_002160	NP_002151	P24821	TENA_HUMAN	nectin type-III 15.		7	TGCCCGGGGGG	0.478	rs148674204
+	13	3791_3793		NM_173689	NP_775960	Q5IJ48	CRUM2_HUMAN	ical; (Potential).		1	CCTGCCTCCTC	0.67	
-	11	1559	p.H440fs|FAM129	NM_022833	NP_073744	Q96TA1	NIBL1_HUMAN			0	CTGGTGCAGGA	0.657	
-	26	2978	_p.Y312fs|GOLGA	NM_004486	NP_004477	Q08379	GOGA2_HUMAN			1	CCGGTAAAAAA	0.562	
+	5	629		NM_001807	NP_001798	P19835	CEL_HUMAN			1	CCTTCGGGGGG	0.642	
+	13	2099	9orf86_uc004cjl.1_	NM_024718	NP_078994	Q3YEC7	PARF_HUMAN			0	CCCCACCCCCC	0.652	
+	12	1352_1353	cyn.2_Frame_Shif	NM_003159	NP_003150	O76039	CDKL5_HUMAN			6	GCTTCCTAAATG	0.525	
-	8	951	28fs|DMD_uc010	NM_004006	NP_003997	P11532	DMD_HUMAN	2.|Actin-binding.		6	CTTGGAAGAGT	0.378	
-	1	1710_1712	_p.L12del|PCDH1	NM_020766	NP_001098713	Q8TAB3	PCD19_HUMAN			7	TGGCCAGCAGC	0.665	
-	1	3739_3741		NM_003604	NP_003595	O14654	IRS4_HUMAN			10	GAGTGTCGTCG	0.542	
-	2	574_575	P_uc004esg.2_5'F	NM_024528	NP_078804	Q8N5F7	NKAP_HUMAN			2	CCAATTCTCTCT	0.317	
+	4	726_727	nrd.1_Frame_Shi	NM_021946	NP_068765	Q5H9F3	BCORL_HUMAN	Pro-rich.		7	ATCTGTCCCCCT	0.594	
+	13	5150	evc.1_Frame_Shi	NM_021946	NP_068765	Q5H9F3	BCORL_HUMAN			7	CAGATCCCCCC	0.602	rs137862942
-	11	886_888	.2_In_Frame_Del	NM_031462	NP_113650	Q8TCZ2	C99L2_HUMAN	ic (Potential).|Poly-Pro.		3	TTCGGGCGGCG	0.611	rs7877654
+	3	2011_2012	mu.1_Frame_Shi	NM_006015	NP_006006	O14497	ARI1A_HUMAN		p.Q546*(1)	142	CCCAGAGCCA	0.649	
-	16	1769	cnh.2_Frame_Shi	NM_012222	NP_036354	Q9UIF7	MUTYH_HUMAN			0	GGGGCTTTTTC	0.547	
-	7	758_760	10_uc001emp.3_	NM_001012758	NP_001012776	P0C025	NUD17_HUMAN			0	TTCCATCCTCCT	0.409	
-	1	566_568	1jqs.2_In_Frame_	NM_173555	NP_775826	Q2T9J0	TYSD1_HUMAN			1	AGCTCAGCAGC	0.739	
+	5	471_473	_p.L92del|TSPAN4	NM_003271	NP_003262	O14817	TSN4_HUMAN	ical; (Potential).		1	CTTCCTGCTGC	0.65	rs61867552
+	5	1941_1943	1nno.2_In_Frame_	NM_001142521	NP_001135993	Q96PZ2	F111A_HUMAN			3	TATCATTGAGTT	0.419	
-	3	258_259	_74P>PP|PRB1_u	NM_005039	NP_005030	P04280	PRP1_HUMAN	-P-[PAQ]-Q-[GE]-[GD]- [N		0	TTTCCTGGAGGT	0.619	
-	3	812_814		NM_006248	NP_006239					0	TCCTGGAGGAG	0.606	
-	4	601_603		NM_032656	NP_116045	Q8IY37	DHX37_HUMAN			1	ATTCCGActcctcct	0.601	
+	15	1832	uij.1_Frame_Shift_	NM_004764	NP_004755	Q96J94	PIWL1_HUMAN	ng (By similarity).|Piwi.		2	CCCTACCCCAA	0.453	
-	3	170_172		NM_001025190	NP_001020361	Q96KJ4	MSLNL_HUMAN			4	GTGAAAGCTGT	0.596	rs3765330
-	10	11379_1138	3_uc002fcl.2_Fra	NM_006885	NP_008816	Q15911	ZFHX3_HUMAN			4	AAACTAGGGTGC	0.584	
-	21	2724_2725		NM_002208	NP_002199	P38570	ITAE_HUMAN	ellular (Potential).		4	GTTTCTGGGGT	0.53	
+	2	737	.P226fs|BPTF_uc	NM_182641	NP_872579	Q12830	BPTF_HUMAN			4	TCCCGCCCCTT	0.423	
-	2	202_204		NM_013376	NP_037508	Q9UHV2	SRTD1_HUMAN			0	TCCTTCTCCTCC	0.453	
-	14	2382_2384	H4_uc002pgb.1_I	NM_015168	NP_055983	Q9UPT8	ZC3H4_HUMAN	Potential.		6	CTCTCTCCTCC	0.7	
-	3	1648_1650	02sit.3_In_Frame_	NM_015470	NP_056285	Q9BXF6	RFIP5_HUMAN			0	GCCTTGGTGGT	0.635	
-	24	3343_3344	_p.F771fs|RALGAF	NM_020343	NP_065076	Q2PPJ7	RGPA2_HUMAN			1	GGGAGAAAAAG	0.45	
-	19	1979	kw.2_Frame_Shift_	NM_017886	NP_060356	Q96C45	ULK4_HUMAN			0	GGGTTCTTTTTTT	0.448	
+	1	3375_3376		NM_175918	NP_787114	Q8N1N5	CRPAK_HUMAN	3		0	CTGCTCACACGT	0.708	
+	1	3654_3655		NM_175918	NP_787114	Q8N1N5	CRPAK_HUMAN	6		0	CTGCTCACACGT	0.678	
+	15	2494_2495		NM_001977	NP_001968	Q07075	AMPE_HUMAN	ellular (Potential).		5	TTCAGGAATACT	0.337	
+	3	1067_1068	_p.S44fs|TPBG_u	NM_006670	NP_006661	Q13641	TPBG_HUMAN	ar (Potential).|Ser-rich.		1	tcctcGGCGCCGT	0.55	
-	36	4449_4450	NK1_uc003xoj.2_	NM_020476	NP_065209	P16157	ANK1_HUMAN	ulatory domain.|Death.		9	CGGATGACCCA	0.535	

+	7	1112	mep.2_Splice_Sit	NM_014957	NP_055772	A2RUS2	DEND3_HUMAN			1	AGCAAGGTTAGG	0.559	rs143399544
-	3	523	mvu.1_Frame_Sh	NM_001007551	NP_001007552	Q6NSH3	CT455_HUMAN			0	CCACAGGTGCA	0.443	
-	9	1115_1116	3fs|RBMX_uc004	NM_002139	NP_002130	P38159	HNRPG_HUMAN			1	TAAGATGGCGGG	0.465	
-	1	105_113	52_uc001aii.2_5'	NM_178545	NP_848640	Q8NDY8	TMM52_HUMAN		NA	0	cggcagcggcaggag	0.569	
-	2	317_319	EL1_uc009vlg.1_	NM_033467	NP_258428	Q495T6	MMEL1_HUMAN	type II mem	NA	0	GGTCACcagcagc	0.665	
-	7	901_902	1_Intron|MST1P9_	NR_002729					NA	0	GCCCGCCCCC	0.658	
-	14	3810		NM_001002912	NP_001002912	Q5RHP9	CA173_HUMAN	Glu-rich.	NA	5	CTGCTGGACAG	0.557	
-	2	283_285		NM_052941	NP_443173	Q96PP9	GBP4_HUMAN	Poly-Val.	NA	0	ATGGCCACCAC	0.483	
+	9	1146_1147	.2_Intron|KIAA132	NM_020775	NP_065826	Q6UXG2	K1324_HUMAN	ellular (Pote	NA	5	TTTCTACACACA	0.49	
-	5	580		NM_183058	NP_898881	Q7Z4W2	LYZL2_HUMAN		NA	0	ACAGTCTTTTTT	0.522	
-	3	1279_1281	172PP>P|POLL_u	NM_013274	NP_037406	Q9UGP5	DPOLL_HUMAN		NA	0	GGTGGGAGGAG	0.591	
+	5	471_473	_p.L92del|TSPAN4	NM_003271	NP_003262	O14817	TSN4_HUMAN	ical; (Potent	NA	1	CTTCCTGCTGC	0.65	rs61867552
+	1	800		NM_001004706	NP_001004706	Q8NGI4	OR4DB_HUMAN	ellular (Pote	NA	2	CCCCACAGAAA	0.527	
+	2	598		NM_145719	NP_663771	Q6B0B8	TIGD3_HUMAN		NA	0	TTCATTCCCCCC	0.612	
-	3	539_541		NM_006248	NP_006239				NA	0	GGACTTGTTGT	0.596	
+	2	1283		NM_021191	NP_067014	Q9HD90	NDF4_HUMAN		NA	4	CTGGTACCCCCC	0.468	
+	18	2925_2926		NM_015267	NP_056082	O14529	CUX2_HUMAN	CUT 2.	NA	6	GTGCTGGGCCT	0.629	
-	2	307	|ACAD10_uc001t	NM_006768	NP_006759	Q7Z569	BRAP_HUMAN		NA	1	GTCGTCTTTTTT	0.428	
+	15	1832	uij.1_Frame_Shift	NM_004764	NP_004755	Q96J94	PIWL1_HUMAN	ng (By simil	NA	2	CCCTACCCCAA	0.453	
-	18	1872	apo.2_Frame_Sh	NM_174978	NP_777638	Q08AQ4	Q08AQ4_HUMAN		NA	4	TAGCTCAAAAAA	0.289	
+	9	1035	p.G310fs|EML1_u	NM_004434	NP_004425	O00423	EMAL1_HUMAN		NA	5	AATAGGTTTTTTT	0.428	
-	430								NA	0	TTGCACGTGTCC	0.55	
-	8	1119	LPX_uc010bhg.1_	NM_006660	NP_006651	O76031	CLPX_HUMAN		NA	0	TTGTGCTTTTTC	0.363	
-	1	196	_5'Flank|OGFOD	NM_007006	NP_008937	O43809	CPSF5_HUMAN	ary for RNA-	NA	0	AGTGACCCCCC	0.652	
-	3	888_890	jt.1_In_Frame_De	NM_001082486	NP_001075955	Q96AP0	ACD_HUMAN		NA	1	TCCTGCAGCAG	0.65	
-	10	1370_1372	_363SS>S|RANB	NM_020850	NP_065901	Q6VN20	RBP10_HUMAN	Ser-rich.	NA	1	gaggacgaggaggag	0.414	
+	8	1209_1211	2gnp.1_In_Frame_	NM_153604	NP_705832	Q8IZQ8	MYCD_HUMAN	Gln-rich.	NA	5	CTCAGCcagcagc	0.527	
+	2	737	.P226fs|BPTF_uc	NM_182641	NP_872579	Q12830	BPTF_HUMAN		NA	4	ATCCCGCCCCTT	0.423	
+	1	288		NM_001079935	NP_001073404	Q6IFN5	O7E24_HUMAN	ellular (Pote	NA	1	ACGGTCCCCAA	0.507	
+	6	1151	uc002oyi.2_RNA	NM_013398	NP_037530	Q9NZL3	ZN224_HUMAN		NA	2	CATACGGGGGA	0.428	rs13346417
-	14	2382_2384	H4_uc002pgb.1_I	NM_015168	NP_055983	Q9UPT8	ZC3H4_HUMAN	Potential.	NA	6	GCTCTCTCCTCC	0.7	
+	4	510	hift_Del_p.R102fs	NM_152359	NP_689572	Q8TCG5	CPT1C_HUMAN	intermembr	NA	3	GCTCCGGGGGG	0.672	
-	7	1078	.P143fs|SLC30A3	NM_003459	NP_003450	Q99726	ZNT3_HUMAN	lasmic (Pote	NA	0	ATTGCGGGGGG	0.607	rs146572471
+	5	5867		NM_020923	NP_065974	Q9HCK1	ZDBF2_HUMAN		NA	3	AGGGGAAAAAA	0.413	
-	24	3343_3344	p.F771fs|RALGA	NM_020343	NP_065076	Q2PPJ7	RGPA2_HUMAN		NA	1	AGGGAGAAAAAG	0.45	
-	20	3610_3611	.D1040fs|SFRS15	NM_020706	NP_065757	O95104	SFR15_HUMAN		NA	0	TAGAATCTCTCT	0.525	
-	1	1860_1862		NM_002430	NP_002421	Q10571	MN1_HUMAN	Poly-Gln.	NA	10	tgctggggctgctgctg	0.483	
-	11	3554_3556	.Q639del|SATB1_	NM_002971	NP_002962	Q01826	SATB1_HUMAN	Poly-Gln.	NA	4	GCGGTGCctgctgc	0.468	
+	14	1647	dgm.2_Frame_Shi	NM_006254	NP_006245	Q05655	KPCD_HUMAN	rotein kinas	NA	9	TCAACGGGGGG	0.602	
-	25	4571	e_Site_p.E1361_	NM_053025	NP_444253	Q15746	MYLK_HUMAN		NA	9	GCTCTGGGGGG	0.624	rs41431347
-	3	799_800	80_uc003fda.2_R	NM_173084	NP_775107	Q8IWR1	TRI59_HUMAN	Potential.	NA	0	GGAAACTTTTTT	0.342	
+	7	1210	.G315fs|SAMD7_	NM_182610	NP_872416	Q7Z3H4	SAMD7_HUMAN		NA	1	CAATTGGGGGG	0.378	
+	5	386	_p.K36fs|FXR1_uc	NM_005087	NP_005078	P51114	FXR1_HUMAN		NA	1	ACTGTCAAAAAA	0.333	
+	1	3375_3376		NM_175918	NP_787114	Q8N1N5	CRPAK_HUMAN	3	NA	0	CTGCTCACACGT	0.708	
+	12	1317_1318	gwa.3_Frame_Shi	NM_014988	NP_055803	Q9UPQ0	LIMC1_HUMAN	Potential.	NA	4	AGCGGAGAGAG	0.465	
+	15	2494_2495		NM_001977	NP_001968	Q07075	AMPE_HUMAN	ellular (Pote	NA	5	TTCAGGAATACT	0.337	
+	3	269	A1_uc003jov.2_R	NM_181501	NP_852478	P56199	ITA1_HUMAN	r (Potential).	NA	3	AACCCAAAAAC	0.343	

+	1	616_617		NM_021614	NP_067627	Q9H2S1	KCNN2_HUMAN		NA	2	GCCGCTGCCGCC	0.658	038013;rs34838882
+	1	989	B12_uc011dak.1_	NM_018932	NP_061755	Q9Y5F1	PCDBC_HUMAN	(Potential).	NA	3	AGCCTGGGATT	0.428	
-	2	331_333	e_Del_p.46_47EE	NM_003472	NP_003463	P35659	DEK_HUMAN	-rich (highly	NA	1	ACCTTTTtcctcctc	0.365	
-	2	1324	odz.2_5'Flank|TAF	NM_005453	NP_005444	O15209	ZBT22_HUMAN		NA	1	CAGGACCCCCA	0.597	
-	5	1557_1559	6_377EE>E|DAXX	NM_001350	NP_001341	Q9UER7	DAXX_HUMAN	ial.|Necessa	NA	23	tcttcttcttcctcctcctcc	0.251	
-	3	436	p.Q109fs|SLC26A	NM_052961	NP_443193	Q96RN1	S26A8_HUMAN	ical; (Potent	NA	2	ACCTTGGGGAA	0.418	
+	24	4729	.Y1552fs|CUL9_u	NM_015089	NP_055904	Q8IWT3	CUL9_HUMAN		NA	12	CCAGGTACATTC	0.562	
+	7	581	me_Shift_Del_p.W	NM_005588	NP_005579	Q16819	MEP1A_HUMAN	otential).|M	NA	3	CTGGTGGGACC	0.478	
+	1	570_572		NM_138426	NP_612435	Q86VQ1	GLCI1_HUMAN	Poly-Ser.	NA	0	TCCACTGcctcctcc	0.527	
-	2	83_85	_uc010lbj.1_In_Fr	NM_004603	NP_004594	Q16623	STX1A_HUMAN	lasmic (Pote	NA	0	AGCGACATCATC	0.586	
+	15	1890	bl.1_RNA|LIMK1_	NM_002314	NP_002305	P53667	LIMK1_HUMAN	rotein kinas	NA	3	AACTGCCCCCC	0.657	
+	2	163	Shift_Del_p.D13fs	NM_145102	NP_659570	Q9Y2L8	ZKSC5_HUMAN		NA	1	TTAGACCCCCC	0.483	
+	25	4379	LL5_uc010ljf.1_S	NM_182931	NP_891847	Q8IZD2	MLL5_HUMAN		NA	3	CTCTAGGGGGA	0.463	
+	3	293	PO_uc010lpl.1_Int	NM_198455	NP_940857	A2VEC9	SSPO_HUMAN	EMI.	NA	0	AGGCTGGGGGG	0.622	
-	36	4449_4450	NK1_uc003xoj.2_	NM_020476	NP_065209	P16157	ANK1_HUMAN	ulatory dom	NA	9	ACGGATGACCCA	0.535	
-	4	1442		NM_005328	NP_005319	Q92819	HAS2_HUMAN	lasmic (Pote	NA	15	ATTCTTGATTGTA	0.458	
-	1	20_21	3ziz.1_Frame_Shif	NM_134441	NP_604390	P04090	REL2_HUMAN		NA	0	AGGTGGAAAAAA	0.535	
-	15	2022	c010mjv.2_Frame_	NM_022917	NP_075068	Q9H6R4	NOL6_HUMAN		NA	2	ATCCAGGGGGC	0.512	
-	2	1659_1661	.2_In_Frame_Del_	NM_173691	NP_775962	Q4KMQ1	TPRN_HUMAN	Glu-rich.	NA	0	tcttcctcttcctcctcctc	0.374	
+	15	2792	1mij.1_Frame_Shi	NM_014728	NP_055543	Q14CM0	FRPD4_HUMAN		NA	13	GTGGTGGGGGA	0.572	
-	54	7719_7721	.2_In_Frame_Del_	NM_031407	NP_113584	Q7Z6Z7	HUWE1_HUMAN	p-rich.|Glu-ri	NA	17	cctcatcttcctcctcctc	0.438	
-	15	4609_4611	22EE>E|ATRX_u	NM_000489	NP_000480	P46100	ATRX_HUMAN	Poly-Glu.	NA	30	tcctcctcttcctcctcctc	0.212	
+	4	753	ni.2_Frame_Shift_	NM_014874	NP_055689	O95140	MFN2_HUMAN	lasmic (Pote	NA	1	AGTGGCTTTTTTT	0.537	
+	20	3859_3861	9vwt.2_In_Frame_	NM_002840	NP_002831	P10586	PTPRF_HUMAN	ellular (Pote	NA	10	AGCAGCGGCGG	0.631	
+	7	1141_1142	p.V299fs|SNX7_u	NM_015976	NP_057060	Q9UNH6	SNX7_HUMAN		NA	3	AAAGTTGAAGTT	0.287	
+	9	1376		NM_018420	NP_060890	Q8IZD6	S22AF_HUMAN	ical; (Potent	NA	2	GCCTTTAACATTC	0.473	
+	3	335	ECM1_uc001euu.2	NM_004425	NP_004416	Q16610	ECM1_HUMAN		NA	3	CAGCTCCCCCC	0.587	
+	2	99		NM_178428	NP_848515	Q5TA79	LCE2A_HUMAN	Cys-rich.	NA	0	AAGTGCCCCCC	0.572	rs138365632
+	11	2233	p.D350fs|NPR1_u	NM_000906	NP_000897	P16066	ANPRA_HUMAN	Potential).|F	NA	7	ACCGACCCCCC	0.493	
+	9	2365		NM_021948	NP_068767	Q96GW7	PGCB_HUMAN	EGF-like.	NA	2	GCTATGGGGGG	0.622	
-	4	515	fun.1_Frame_Shif	NM_003564	NP_003555	P37802	TAGL2_HUMAN		NA	0	TCCTTGGATTTC	0.468	
+	7	1327_1328	Ins_p.333_334ins	NM_005807	NP_005798	Q92954	PRG4_HUMAN	-X-P-X-P-T	NA	1	CCACCAAGTCTG	0.658	
+	11	1627	32_splice|SRGAP2	NM_015326	NP_056141	O75044	FNBP2_HUMAN		NA	0	ACACGGTAAGCA	0.441	
-	13	1224	p.L298fs|RGS7_u	NM_002924	NP_002915	P49802	RGS7_HUMAN	rotein gamr	NA	7	GGTGGCAAAAG	0.438	
-	2	211_213	1del|SYT15_uc001	NM_031912	NP_114118	Q9BQS2	SYT15_HUMAN	type III mem	NA	0	TCAACAGCAGC	0.631	
-	13	8094_8095	v.1_Frame_Shift_	NM_002417	NP_002408	P46013	KI67_HUMAN	AA approxir	NA	7	TTCTTTGTGTGT	0.5	
+	16	1890	ren.1_Frame_Shift	NM_024662	NP_078938	Q9H0A0	NAT10_HUMAN		NA	2	GCTCTCCGATGC	0.537	
-	2	331_333		NM_000256	NP_000247	Q14896	MYPC3_HUMAN		NA	3	GACCTTGAGGTC	0.581	
-	1	68		NM_001004471	NP_001004471	Q8NGQ4	O10Q1_HUMAN	ellular (Pote	NA	2	TGGCTGTGGTG	0.512	
-	23	2714_2715	uc.2_Frame_Shift	NM_198334	NP_938148	Q14697	GANAB_HUMAN		NA	5	CCTATTATCACC	0.535	
+	15	2573_2575		NM_015191	NP_056006	Q9H0K1	SIK2_HUMAN		NA	3	AGCTACAGCAGC	0.498	
-	4	792	me_Shift_Del_p.P	NM_003455	NP_003446	O95125	ZN202_HUMAN		NA	1	GCCTTGGTCTCC	0.602	
-	3	441_442	.1_Intron|PRB1_u	NM_005039	NP_005030	P04280	PRP1_HUMAN	-[PAQ]-Q-[G	NA	0	TTTCCTGGAGGT	0.604	
-	3	502_503		NM_006248	NP_006239				NA	0	TTTCCTGGAGGT	0.594	
+	14	1837	00_splice|SLC4A8	NM_001039960	NP_001035049	Q2Y0W8	S4A8_HUMAN		NA	5	GTTTCAGAGACTA	0.448	
+	1	270_271		NM_014212	NP_055027	O43248	HXC11_HUMAN		NA	1	TCCTGCCCCAGG	0.644	
+	7	948_950	.L125del|SLC39A	NM_173596	NP_775867	Q6ZMH5	S39A5_HUMAN	lasmic (Pote	NA	2	TATCCCTGCTGCT	0.635	

+	4	496_497	TSPAN31_uc010s	NM_005981	NP_005972	Q12999	TSN31_HUMAN	cellular (Pote	NA	0	TGGGTCATGAG	0.421	
+	5	1001_1003	vhk.1_In_Frame_	NM_006418	NP_006409	Q6UX06	OLFM4_HUMAN	actomedin-li	NA	1	AGTTTACAACAA	0.433	
+	20	3706_3707	.A881fs|LMO7_uc	NM_015842	NP_056667	Q8WWI1	LMO7_HUMAN		NA	5	GAGGCAGAGAG	0.386	
-	4	459_460	ABCC4_uc001vmf	NM_005845	NP_005836	O15439	MRP4_HUMAN	smembrane	NA	4	atttttCCCAAAAAT	0.337	
-	2	2145		NM_033132	NP_149123	Q96T25	ZIC5_HUMAN		NA	0	TGGCTGGGGGC	0.567	
+	1	690_692		NM_007129	NP_009060	O95409	ZIC2_HUMAN	scriptional a	NA	0	CGCGGCccaccac	0.522	
+	44	4468		NM_001846	NP_001837	P08572	CO4A2_HUMAN	le-helical reg	NA	6	GGAATCCCCCA	0.687	
+	1	1556_1557	PABPN1_uc001wj	NM_004643	NP_004634	Q86U42	PABP2_HUMAN	racts with S	NA	2	GGGAGCCCCCG	0.564	
+	3	506_507	4L2_uc001wlg.3_	NM_198083	NP_932349	D5KJA1	D5KJA1_HUMAN		NA	1	GAAGCCTAATGG	0.53	rs61999853
-	13	3190_3192		NM_001103184	NP_001096654	Q68DA7	FMN1_HUMAN	FH2.	NA	1	TGCACACCACC	0.355	
+	17	1702	65_splice|JMJD7-	NM_001114633	NP_001108105	P0C869	PA24B_HUMAN		NA	1	TGTGTAGACAAG	0.594	
+	9	1421	_Shift_Del_p.P432	NM_024505	NP_078781	Q96PH1	NOX5_HUMAN	smic (Potent	NA	2	GCCCCCTTTTTT	0.537	
-	17	2199	FTUD1_uc002bg	NM_024580	NP_078856	Q7Z2Z2	ETUD1_HUMAN		NA	1	CACCTAACCTTT	0.421	
-	2	158_159	cyh.2_RNA|NAG	NM_016256	NP_057340	Q9UK23	NAGPA_HUMAN	enal (Poten	NA	0	GGAGGCGCGC	0.767	
+	3	184_186	f62_uc010vas.1_	NM_020314	NP_064710	Q7Z3J2	CP062_HUMAN	Ser-rich.	NA	1	CACGTCCTCCT	0.562	
-	16	2205	PS35_uc002eee.	NM_018206	NP_060676	Q96QK1	VPS35_HUMAN		NA	0	AGAGCTTTTTTT	0.368	
+	15	1643_1644	p.L371fs|PLD2_uc	NM_002663	NP_002654	O14939	PLD2_HUMAN	Catalytic.	NA	5	AATCTTATCACC	0.614	
+	11	2629_2631	2gix.2_In_Frame_	NM_001080424	NP_001073893	O15054	KDM6B_HUMAN	-rich.|Thr-ri	NA	2	CGCCGTcaccacca	0.369	
+	1	24_26		NM_001005271	NP_001005271	Q12873	CHD3_HUMAN		NA	1	AGggacgaggagga	0.094	
-	3	355_356		NM_031898	NP_114104	Q9BXF9	TEKT3_HUMAN		NA	2	GACTTTGTAGTA	0.535	
+	5	401	p.L120fs|SLC5A1	NM_001042450	NP_001035915	A0PJK1	SC5AA_HUMAN	ical; (Potent	NA	1	ACCTTACCTGA	0.577	
+	1	443		NM_181710	NP_859061	Q8WWF5	ZNRF4_HUMAN	cellular (Pote	NA	2	GGCGTCCCCCT	0.687	
-	2	120_122		NM_000704	NP_000695	P20648	ATP4A_HUMAN	lasmic (Pote	NA	1	CCCGCCTTCTTC	0.601	
+	5	711	_splice|DMRTC2_	NM_001040283	NP_001035373	Q8IXT2	DMRTD_HUMAN		NA	0	CCCTGGTAAGAT	0.386	
-	2	46_48		NM_000894	NP_000885	P01229	LSHB_HUMAN		NA	0	TGCTCAGCAGC	0.655	
-	22	3498_3500	2psw.1_In_Frame	NM_016148	NP_057232	Q9Y566	SHAN1_HUMAN		NA	2	GGCCTTGATGAT	0.498	
-	3	1626	.2_Intron|ZNF814	NM_001144989	NP_001138461	B7Z6K7	ZN814_HUMAN	2H2-type 9	NA	0	GGCTCCTAAGAT	0.443	
-	1	1978_1980	IF3C_uc010ykr.1_	NM_002254	NP_002245	O14782	KIF3C_HUMAN	-Asn.|Poter	NA	4	CGGTGGTTGTTG	0.621	
-	4	1987	RAB11FIP5_uc002	NM_015470	NP_056285	Q9BXF6	RFIP5_HUMAN		NA	0	CTTTTGGTGTC	0.612	
+	4	698	WBP1_uc002slk.1_	NM_012477	NP_036609	Q96G27	WBP1_HUMAN		NA	0	GAGTGCCCCCC	0.602	
+	3	759_761	2svy.2_In_Frame	NM_001008949	NP_001008949	Q6GPH6	IPIL1_HUMAN	lasmic (Pote	NA	3	CAGTGAGGAGG	0.532	
+	1	590		NM_014213	NP_055028	P28356	HXD9_HUMAN		NA	0	CCCGGCCCCCG	0.597	
-	7	1769_1770	p.G574fs|SPHKA	NM_001142644	NP_001136116	Q2M3C7	SPKAP_HUMAN		NA	10	TCTTTCACCCAG	0.55	
-	8	937_939	zpi.1_In_Frame_D	NM_153269	NP_695001	Q9NUD7	CT096_HUMAN	y-Lys.|Poten	NA	0	TTTTTTTCTTCTT	0.562	
+	7	904	yrl.1_Frame_Shift	NM_000628	NP_000619	Q08334	I10R2_HUMAN	lasmic (Pote	NA	0	CACAGTTTTTG	0.378	
-	9	2028_2030	216HH>H|C21orf5	NM_058180	NP_478060	P58505	CU058_HUMAN	Poly-His.	NA	1	ACAGCAtggtggt	0.631	
-	35	5235		NM_002473	NP_002464	P35579	MYH9_HUMAN	Potential.	NA	11	TCTTTGGCCTG	0.647	
+	18	4729	ayn.3_Frame_Shif	NM_001162501	NP_001155973	Q9UPQ9	TNR6B_HUMAN		NA	0	GTGCTGGGGGG	0.483	
-	11	1200_1202	.1_In_Frame_Del_	NM_139202	NP_631941	Q15049	MLC1_HUMAN	ical; (Potent	NA	1	agcactagcagcagc	0.542	
-	9	669	3bxi.1_Frame_Shi	NM_018306	NP_060776	Q8WWA1	TMM40_HUMAN		NA	0	TCACCTGCGTAA	0.587	
+	3	392	_Shift_Del_p.F74f	NM_207404	NP_997287	Q6ZS27	ZN662_HUMAN	KRAB.	NA	0	GCAGCATTTCCA	0.587	
+	7	802	css.2_Splice_Site	NM_207102	NP_996985	Q6X9E4	FBW12_HUMAN		NA	0	GGTTTCAGGTTG	0.421	
+	7	761	cyk.2_Frame_Shi	NM_004186	NP_004177	Q13275	SEM3F_HUMAN	Sema.	NA	2	CTTCTACCTGG	0.612	
-	17	3301_3302	dic.3_Frame_Shift	NM_015224	NP_056039	Q9UK61	CC063_HUMAN		NA	5	TTGTTGAAGTCA	0.436	
+	21	3869	OBO2_uc011bgk.1	NM_002942	NP_002933	Q9HCK4	ROBO2_HUMAN	lasmic (Pote	NA	11	TACCTCCCCCC	0.433	
-	4	2231		NM_001038705	NP_001033794	Q86SP6	GP149_HUMAN	lasmic (Pote	NA	6	CTCCTGGTAGC	0.423	
+	21	2524_2526	buy.1_In_Frame_	NM_000283	NP_000274	P35913	PDE6B_HUMAN		NA	0	GAGAAGGAGGA	0.562	

+	1	3808_3809		NM_175918	NP_787114	Q8N1N5	CRPAK_HUMAN	8	NA	0	CTCACATGTGC	0.683	123539;rs79888804
+	9	1034_1035	p.S317fs|SLC34A	NM_006424	NP_006415	O95436	NPT2B_HUMAN	ellular (Pot	NA	5	TCCCTCGACTG	0.515	
-	6	908_909	M5_uc010ine.2_I	NM_018699	NP_061169	Q9NQX1	PRDM5_HUMAN	2-type 2; aty	NA	2	TGCACTGAAGA	0.376	
-	21	2813_2814	D8_uc003lcc.1_Int	NM_139199	NP_631938	Q9H0E9	BRD8_HUMAN		NA	1	TAGGTTCTCTCT	0.545	
-	8	986_987	yw.1_Frame_Shif	NM_004134	NP_004125	P38646	GRP75_HUMAN		NA	0	CTCACCTCTCTC	0.431	
-	8	1648_1649	_Ins_p.225_226in	NM_000332	NP_000323	P54253	ATX1_HUMAN		NA	4	TGCTGAGGtgctg	0.366	
-	22	3298_3300	27SS>S|MAP3K5_	NM_005923	NP_005914	Q99683	M3K5_HUMAN		NA	5	CTCACTGCTGC	0.483	
+	16	4100	.S1276fs|ARID1B_	NM_017519	NP_059989	Q8NFD5	ARI1B_HUMAN		NA	2	GCCAGTTACGA	0.502	
+	13	3999	.P4_uc003qrg.2_I	NM_020245	NP_064630	Q9NRJ4	TULP4_HUMAN		NA	1	CCAGACCCCCC	0.657	
+	5	714	K1_uc003uab.2_	NM_002314	NP_002305	P53667	LIMK1_HUMAN	PDZ.	NA	3	ATTGACCCCCC	0.677	rs150491142
-	5	964	2_Intron|GPC2_uc	NM_152742	NP_689955	Q8N158	GPC2_HUMAN		NA	2	GGGGACCCCCC	0.642	
+	4	467		NM_001283	NP_001274	P61966	AP1S1_HUMAN		NA	0	TTGATGGGGGG	0.562	
-	4	481	0lhr.2_Frame_Shi	NM_178176	NP_835470	Q86VF5	MOGT3_HUMAN		NA	2	GATCCGGGGGC	0.582	
+	18	2819	_uc011kkn.1_Intro	NM_181552	NP_853530	P39880	CUX1_HUMAN		NA	8	TCGGTCCCCCC	0.642	
-	5	1108_1109	3uzb.2_Frame_Sh	NM_001146210	NP_001139682	P0CI01	SPDE6_HUMAN		NA	0	CGCTATGACCAT	0.52	
-	3	498		NM_033427	NP_219499	Q8WZ74	CTTB2_HUMAN	Potential.	NA	5	TCTTTTGTCTGC	0.458	
-	2	1009		NM_001098834	NP_001092304	Q14549	GBX1_HUMAN		NA	0	CTTTTCCCCCC	0.577	
-	3	436		NM_005431	NP_005422	O43543	XRCC2_HUMAN		NA	2	TACACCAAAAAA	0.393	
+	12	1380	_p.P415fs|KIAA19	NM_199205	NP_954675	Q8N163	K1967_HUMAN		NA	3	CGGGACCCCCC	0.582	
+	9	2311	el_p.P333fs|AKAP	NM_001136562	NP_001130034	Q9Y2D5	AKAP2_HUMAN	Potential.	NA	6	GGAATCCCCCG	0.512	
+	13	2110_2112	598del|GRIN1_uc	NM_007327	NP_015566	Q05586	NMDZ1_HUMAN	lasmic (Pot	NA	1	CAGCGAGGAGG	0.739	
+	3	1008	me_Shift_Del_p.G	NM_001097579	NP_001091048	Q9UPC5	GPR34_HUMAN	lasmic (Pot	NA	1	AGATTGGGAAG	0.313	
+	5	731	_Site_p.N130_spli	NM_001493	NP_001484	P31150	GDIA_HUMAN		NA	0	TCCTTAGATCTG	0.545	
+	31	5454		NM_017514	NP_059984	P51805	PLXA3_HUMAN	lasmic (Pot	NA	3	GCTCTACATCC	0.587	
-	3	1058	_p.K83fs|RERE_u	NM_012102	NP_036234	Q9P2R6	RERE_HUMAN			2	GAGACTTTTTTT	0.453	
+	4	753	ni.2_Frame_Shift_	NM_014874	NP_055689	O95140	MFN2_HUMAN	lasmic (Potential).		1	GTGGCTTTTTTT	0.537	
+	8	1361_1362	byu.2_Frame_Shi	NM_005095	NP_005086	Q5VZL5	ZMYM4_HUMAN	MYM-type 2.		5	AACTGAAAAAA	0.342	
-	4	1243_1245	IP1_uc010oid.1_R	NM_024700	NP_078976	Q8TAD8	SNIP1_HUMAN	Poly-Glu.		2	TTCTTCCTCCT	0.448	
-	8	1192	1_uc001cyr.1_Int	NM_021080	NP_066566	O75553	DAB1_HUMAN	PID.		3	TGTGCCTTTTTTT	0.393	
+	2	574	GM1_uc010ooz.1	NM_002633	NP_002624	P36871	PGM1_HUMAN			3	ACCCAGGGGGC	0.433	
+	4	780	_p.L168fs|VANGL1	NM_138959	NP_620409	Q8TAA9	VANG1_HUMAN	Name=2; (Potential).		1	GGCACTTTTTTT	0.493	
+	9	3614	Shift_Del_p.L1172	NM_020832	NP_065883	Q8N1G0	ZN687_HUMAN			4	GGGCTGGGGGA	0.622	
+	6	739	B4_uc001eyb.1_3	NM_002796	NP_002787	P28070	PSB4_HUMAN			2	CACCGAAAAAG	0.443	
-	4	633	_Del_p.G127fs|SC	NM_005698	NP_005689	O14828	SCAM3_HUMAN	lasmic (Potential).		3	CTGTGCCCCCC	0.517	
+	8	1428	xcu.1_Frame_Shi	NM_014388	NP_055203	Q68CQ4	DIEXF_HUMAN			0	TGCTTCCCCCC	0.468	
+	20	2533	725fs|MYO3A_uc	NM_017433	NP_059129	Q8NEV4	MYO3A_HUMAN	osin head-like.		18	AATTTCAAAAAA	0.338	
+	1	78_80	xp.1_In_Frame_	NM_014720	NP_055535	Q9H2G2	SLK_HUMAN	Poly-Lys.		8	AGCGAGAAGAA	0.448	
+	14	2026_2027	yv.2_Frame_Shift_	NM_016824	NP_058432	Q9UEY8	ADDG_HUMAN			5	GAACGTAAACA	0.406	rs141186367
-	24	2496_2498	PC3_uc010rhl.1_	NM_000256	NP_000247	Q14896	MYPC3_HUMAN	nectin type-III 1.		3	GTAGCTCTTCTT	0.601	
+	1	94		NM_001004711	NP_001004711	Q8NGE8	OR4D9_HUMAN	Name=1; (Potential).		0	TTCCTGTTTTTG	0.428	
-	12	1314	Splice_Site_p.C3	NM_016931	NP_058627	Q9NPH5	NOX4_HUMAN			2	GACACTAAAAA	0.292	rs56022003
+	10	1135	_p.H268fs|C11orf5	NM_014039	NP_054758	Q9H0W9	CK054_HUMAN			0	CACTCATTTTTT	0.378	
-	7	1531	po.2_Frame_Shif	NM_032725	NP_116114	Q9BRD0	BUD13_HUMAN	Potential.		2	TTACCCTTTTCC	0.448	
+	7	774_776	pqg.2_In_Frame_	NM_001040455	NP_001035545	Q8NBJ9	SIDT2_HUMAN	ellular (Potential).		0	TTATGTGGTGG	0.463	
-	6	2413	zal.2_Frame_Shift_	NM_182557	NP_872363	Q86UU0	BCL9L_HUMAN	teraction with CTNNB1 (By		2	CAGCGGGGGG	0.642	rs147951163
-	7	687		NM_001145018	NP_001138490	Q494R4	CC153_HUMAN			0	ATCCAGGGGGG	0.567	
-	28	4472_4474	F_uc010set.1_Int	NM_000552	NP_000543	P04275	VWF_HUMAN	ite for platelet glycoprotein		12	TGACCTTCTTC	0.611	rs141990425

+	2	157	40B_uc001ruq.1_	NM_001031698	NP_001026868	Q6NWY9	PR40B_HUMAN	Pro-rich.	5	AGCTATCCCCCC	0.607	
-	26	3234	p.P1074fs|SMARC	NM_003075	NP_003066	Q8TAQ2	SMRC2_HUMAN	Pro-rich.	6	GTCCAGGGGGG	0.577	
+	7	948_950	.L125del|SLC39A	NM_173596	NP_775867	Q6ZMH5	S39A5_HUMAN	lasmic (Potential).	2	TATCCCTGCTGC	0.635	
+	1	123_124	_p.A30fs|EP400_	NM_015409	NP_056224	Q96L91	EP400_HUMAN		12	AGCCGGCCCAC	0.649	rs71453134
-	10	1917_1918	p.R637fs|ZC3H13	NM_015070	NP_055885	Q5T200	ZC3HD_HUMAN	Arg/Ser-rich.	2	CAAACCTCTCTC	0.337	
+	3	707_710	vbk.2_Frame_Shi	NM_015116	NP_055931	Q9Y2L9	LRCH1_HUMAN	LRR 3.	2	CCGCCCTGCCT	0.436	
+	6	1323	p.F214fs|CYSLTR	NM_020377	NP_065110	Q9NS75	CLTR2_HUMAN	Name=5; (Potential).	2	CTGCCATTTTTC	0.488	
-	4	579_580	.2_RNA|EBPL_uc	NM_032565	NP_115954	Q9BY08	EBPL_HUMAN	ical; (Potential).	0	ACCGTTAAAAAA	0.48	
-	16	2406	_Shift_Del_p.I648	NM_014953	NP_055768	Q9Y2L1	RRP44_HUMAN		1	CATGAATTTTTTT	0.358	
+	20	3706_3707	.A881fs|LMO7_uc	NM_015842	NP_056667	Q8WWI1	LMO7_HUMAN		5	AGGCAGAGAG	0.386	
+	1	690_692		NM_007129	NP_009060	O95409	ZIC2_HUMAN	scriptional activation or rep	0	CGCGGCccaccac	0.522	
+	14	4097	wwe.3_Frame_Shi	NM_020937	NP_065988	Q8IYD8	FANCM_HUMAN		7	AGTGCAAAAAA	0.328	rs143681767
+	4	371	D12B_uc001wyr.2_	NM_181533	NP_853511	Q7Z5M8	AB12B_HUMAN		1	CTGCCGGGGGG	0.493	
-	14	2876	twc.1_Frame_Shi	NM_007039	NP_008970	Q16825	PTN21_HUMAN		4	GACCAATTTTTT	0.393	
-	3	499	ybp.2_Intron|BTB	NM_001002860	NP_001002860	Q9P203	BTBD7_HUMAN		1	GTTCTCTTTTTT	0.438	
+	8	1064_1066	K_uc001ygg.3_In	NM_001099402	NP_001092872	O75909	CCNK_HUMAN	Poly-Gln.	0	AGCCCAGCAGC	0.621	
+	3	400	IREB2_uc002bdq.	NM_004136	NP_004127	P48200	IREB2_HUMAN		0	TGCCCTTTTTC	0.358	
-	1	253_255	CHRNA3_uc002b	NM_000743	NP_000734	P32297	ACHA3_HUMAN		4	cagagacagcagcag	0.601	rs66793222
-	1	929_930	r.2_3'UTR|TIGD7_	NM_033208	NP_149985	Q6NT04	TIGD7_HUMAN	y similarity).|HTH psq-type.	0	TTCTTATTTTTT	0.361	
+	3	184_186	f62_uc010vas.1_	NM_020314	NP_064710	Q7Z3J2	CP062_HUMAN	Ser-rich.	1	CACGTCCTCCT	0.562	
-	2	423_425	2dxs.2_In_Frame_	NM_006110	NP_006101	O95400	CD2B2_HUMAN		1	CCCCCCATCATC	0.532	
+	10	1762	gjf.2_Frame_Shift_	NM_001005273	NP_001005273	Q12873	CHD3_HUMAN	Chromo 1.	1	TCCCACCCCCC	0.577	
-	5	891		NM_139285	NP_644814	Q8NHY3	GA2L2_HUMAN		2	GGGCCGGGGG	0.597	rs139867246
-	9	1016	18orf34_uc002kx	NM_001105528	NP_001098998	Q5BJE1	CR034_HUMAN	Potential.	1	CCTCCATTTTTTT	0.318	
+	4	443_444	PC2_uc002mix.1_	NM_003083	NP_003074	Q13487	SNPC2_HUMAN		0	TCCAAGCCCCC	0.644	
+	2	813_814		NM_001105570	NP_001099040	A8MXV4	NUD19_HUMAN		0	TTTGCCTCTCTC	0.45	
-	2	120_122		NM_000704	NP_000695	P20648	ATP4A_HUMAN	lasmic (Potential).	1	CCCGCCTTCTTC	0.601	
-	5	492	oeb.3_Frame_Shi	NM_032838	NP_116227	Q969W8	ZN566_HUMAN		0	AATGTCCCCCC	0.393	
+	4	1303_1305	2qlt.2_In_Frame_	NM_007279	NP_009210	P26368	U2AF2_HUMAN		1	CACGAGAAGAA	0.645	
-	2	234_236	HX57_uc002rrg.2_	NM_198963	NP_945314	Q6P158	DHX57_HUMAN	Gly-rich.	3	gccacctccaccacca	0.384	
-	4	737_739	2svr.2_In_Frame_	NM_017849	NP_060319	O75204	TM127_HUMAN		0	TCTTATGCTGCT	0.557	
+	3	759_761	2svy.2_In_Frame_	NM_001008949	NP_001008949	Q6GPH6	IPIL1_HUMAN	lasmic (Potential).	3	CAGTGAGGAGG	0.532	
+	30	4637	Shift_Del_p.K150	NM_018151	NP_060621	Q5UIP0	RIF1_HUMAN		15	AAAATAAAAAAA	0.408	
+	1	982	_uc002ukn.2_Intro	NM_019558	NP_062458	P13378	HXD8_HUMAN	Poly-Pro.	0	ccacctccccCTG	0.502	
-	20	3322		NM_018897	NP_061720	Q8WXX0	DYH7_HUMAN	n (By similarity).	12	TGGACAAAAAAA	0.318	
-	15	1903	_Shift_Del_p.I1816	NM_152525	NP_689738	Q53TS8	AL2SA_HUMAN		3	TTTTAATTTTTTT	0.323	
-	3	493		NM_014617	NP_055432	P11844	CRGA_HUMAN	a crystallin 'Greek key' 4.	0	CTGCACCCCCC	0.532	
-	31	4618_4620	2yzp.2_In_Frame_	NM_022115	NP_071398	P57071	PRD15_HUMAN	Poly-Gln.	0	TACATCTGCTGC	0.611	
-	1	912_914	zma.2_Intron|uc00	NM_031890	NP_114096	Q9BXQ6	CECR6_HUMAN		0	CAGCCCACCAC	0.709	
-	21	3201_3203	1agl.1_In_Frame_	NM_015241	NP_056056	Q7RTP6	MICA3_HUMAN	Glu-rich.	0	GGCGAGGctcctcc	0.453	
+	7	1464	39674_uc003bba.	NM_004599	NP_004590	Q12772	SRBP2_HUMAN	y similarity).|Cytoplasmic (	4	GATGTCCCCCC	0.522	
+	5	477_479		NM_001197	NP_001188	Q13323	BIK_HUMAN	otential).|Helical; (Potentia	0	tgctggcgctgctgctg	0.562	
-	27	3223	t.2_RNA|CLASP2_	NM_015097	NP_055912	B2RTR1	B2RTR1_HUMAN		4	CACCCATTTTTT	0.343	
-	2	2200_2203	_Shift_Del_p.R660	NM_194293	NP_919269	Q702N8	XIRP1_HUMAN	Xin 15.	8	GACGTGTCTGTC	0.618	
+	52	5572		NM_004947	NP_004938	Q8IZD9	DOCK3_HUMAN		0	TGATACCCCCC	0.597	
-	14	3144	dbf.1_Frame_Shift	NM_014703	NP_055518	Q9Y4B6	VPRBP_HUMAN		2	CAGCTGTTTTTT	0.498	
-	5	2710_2711	s_p.K325fs|FILIP	NM_182909	NP_878913	Q4L180	FIL1L_HUMAN	Potential.	1	ATTTAGTTTTTT	0.406	

-	3	713_715	bns.1_In_Frame_	NM_015472	NP_056287	Q9GZV5	WWTR1_HUMAN	ential.|Gln-rich.		4	GTTTCTGCTGC	0.581	
-	28	3481_3482	3A3_uc003ftx.3_5	NM_024524	NP_078800	Q9H7F0	AT133_HUMAN			1	TGACCCAAAAAA	0.381	
+	21	2524_2526	buy.1_In_Frame_	NM_000283	NP_000274	P35913	PDE6B_HUMAN			0	GAGAAGGAGGA	0.562	
+	1	3591_3592		NM_175918	NP_787114	Q8N1N5	CRPAK_HUMAN	5		0	CCTGCTCACAC	0.663	
+	16	2842	853fs|FAM193A_	NM_003704	NP_003695	P78312	F193A_HUMAN			3	CAACCTAAAAAA	0.453	
+	4	1265	1D1_uc010ifd.2_	NM_015173	NP_055988	Q86TI0	TBCD1_HUMAN	PID.		1	ACACCAAAAAA	0.313	
-	61	9721_9722		NM_014991	NP_055806	Q8IZQ1	WDFY3_HUMAN	WD 1.		3	TCTCCCACACAC	0.51	
-	1	538_540	C3_uc011cdn.1_I	NM_153757	NP_715638	Q96NT1	NP1L5_HUMAN	Glu-rich.		1	tactcctcttcctcctcc	0.369	
+	8	1187_1189	p.P363del|NPNT_	NM_001033047	NP_001028219	Q6UXI9	NPNT_HUMAN	Pro-rich.		1	TACTCCACCAC	0.522	
+	3	335	C9_uc003ieb.2_F	NM_005033	NP_005024	Q06265	EXOS9_HUMAN	RE binding.		0	GTATTCTTTTTT	0.383	
+	5	535_536		NM_004477	NP_004468	Q14331	FRG1_HUMAN			0	TGGAAAATATCT	0.361	
+	1	878_879		NM_024563	NP_078839					0	TTTGGGTGTGTG	0.421	
-	4	512_513		NM_001737	NP_001728	P02748	CO9_HUMAN	MACPF.		0	CTGCAGGGGG	0.46	
-	12	2431	03jtq.2_RNA|ADA	NM_197941	NP_922932	Q9UKP5	ATS6_HUMAN	Disintegrin.		0	TACCCCTTTTTC	0.408	
-	2	1109_1111	60DD>D|TAF9_uc	NM_003187	NP_003178	Q16594	TAF9_HUMAN	Poly-Asp.		0	tatcatagtcatcatcat	0.256	
-	8	1648_1649	_Ins_p.225_226in	NM_000332	NP_000323	P54253	ATX1_HUMAN			4	TGCTGAGGtgctg	0.366	
-	5	1078	uc003ntw.2_Fram	NM_004640	NP_004631	Q13838	DX39B_HUMAN	ase ATP-binding.		0	CCACCAAAAAA	0.512	
-	2	1047	Shift_Del_p.G134	NM_033177	NP_149417	O95872	GPAN1_HUMAN	ANK 1.		0	ATATTCCCCCC	0.632	
-	4	1648	318_uc003ouw.2_	NM_014345	NP_055160	Q5VUA4	ZN318_HUMAN			7	TCGCCTTTTTT	0.493	
+	23	2346_2348	ame_Del_p.A667d	NM_018426	NP_060896	Q5T3F8	TM63B_HUMAN			3	CCCACTGCTGC	0.591	
-	14	1681_1682	ame_Shift_Del_p.	NM_001144769	NP_001138241	Q03001	DYST_HUMAN			14	GGCCTTCTCTC	0.441	
+	22	2625_2626	jb.3_Frame_Shift_	NM_003318	NP_003309	P33981	TTK_HUMAN		p.R838fs*4(3)	11	CTTTTGAAAAAA	0.302	
+	3	1448	p.A171fs|TPBG_u	NM_006670	NP_006661	Q13641	TPBG_HUMAN	ellular (Potential).		1	CTCGGCCCCCA	0.647	
-	16	1855	sb.3_Frame_Shif	NM_007214	NP_009145	Q9UGP8	SEC63_HUMAN	ytoplasmic (Potential).		2	GGTTTCTTTTTTT	0.368	
-	1	310_312	ame_Del_p.72_73	NM_005522	NP_005513	P49639	HXA1_HUMAN	Poly-His.		3	ggggtggcgatggtgg	0.527	rs10951154
-	49	7301	toa.1_Intron|PKD1	NM_138295	NP_612152	Q8TDX9	PK1L1_HUMAN	ellular (Potential).		11	CACAGCCCCCA	0.582	
-	2	83_85	_uc010lbj.1_In_Fr	NM_004603	NP_004594	Q16623	STX1A_HUMAN	lasmic (Potential).		0	AGCGACATCATC	0.586	
-	12	2387	_p.G539fs|EPHB4	NM_004444	NP_004435	P54760	EPHB4_HUMAN	Potential).|Protein kinase.		15	AGCCGCCCCCG	0.642	
-	5	745	0lhr.2_Frame_Shif	NM_178176	NP_835470	Q86VF5	MOGT3_HUMAN			2	GCGCACCCCCC	0.677	
-	4	543	3ves.2_Frame_Sh	NM_000111	NP_000102	P40879	S26A3_HUMAN	ical; (Potential).		4	CTGGGAAAAAG	0.448	rs75733585
-	2	110	3vey.2_Frame_Sh	NM_007356	NP_031382	A4D0S4	LAMB4_HUMAN			8	GGTGCAAAAAA	0.308	
-	9	1235_1237		NM_003941	NP_003932	O00401	WASL_HUMAN	Pro-rich.		0	CCTagcaggaggag	0.443	
-	10	1741_1743	3vtb.2_In_Frame_	NM_012450	NP_036582	Q9UKG4	S13A4_HUMAN			0	TTTGGTCTTCTT	0.409	
-	10	976	vue.2_Frame_Shif	NM_001139456	NP_001132928	Q8N434	SVOPL_HUMAN			0	TGAGTCCCCCC	0.557	
-	13	2898		NM_020119	NP_064504	Q7Z2W4	ZCCHV_HUMAN	ARP catalytic.		1	CGACGTTTTTG	0.383	
-	2	227	c003wda.2_5'Flan	NM_005232	NP_005223	P21709	EPHA1_HUMAN	ellular (Potential).		5	CTTTTGGGGGA	0.542	
+	1	162_164	_uc010luh.1_5'UT	NM_004331	NP_004322	O60238	BNI3L_HUMAN			0	CCTGCACAACAA	0.655	
-	7	969_971	|PBK_uc011lap.1_	NM_018492	NP_060962	Q96KB5	TOPK_HUMAN	rotein kinase.		0	TACCTTCATCATC	0.3	rs116080983
+	1	804_805	1463_uc003xvh.2	NM_152414	NP_689627	Q8NFJ8	BHE22_HUMAN	Gly-rich.		0	cgggaagtggcggcg	0.584	
+	10	1740	LF1_uc003xyf.2_F	NM_015170	NP_055985	Q8IWU6	SULF1_HUMAN			7	TGTGCCTTTTTT	0.408	
+	9	1450_1451	RRCC1_uc003ycx	NM_033402	NP_208325	Q9C099	LRCC1_HUMAN	Potential.		0	ACCAAGAGAGA	0.267	
-	8	1394_1396		NM_000498	NP_000489	P19099	C11B2_HUMAN			0	TGGTGCAGCAG	0.685	
+	9	2311	el_p.P333fs|AKAP	NM_001136562	NP_001130034	Q9Y2D5	AKAP2_HUMAN	Potential.		6	GGAATCCCCCG	0.512	
-	15	1633_1635		NM_003086	NP_003077	Q5SXM2	SNPC4_HUMAN			0	CCTCCTCgctgctg	0.473	266724;rs34222232
+	20	2671_2673	.E837del|CNKSR	NM_014927	NP_055742	Q8WXI2	CNKR2_HUMAN	ential.|Poly-Glu.		2	aggaagaggaggag	0.379	
-	10	4018_4020	3_In_Frame_Del_	NM_000489	NP_000480	P46100	ATRX_HUMAN	Poly-Asp.		30	TGTCGTCATCAT	0.379	
+	5	716_718	04eib.1_In_Frame	NM_016607	NP_057691	Q9UH62	ARMX3_HUMAN			2	TGGTCTGATGAT	0.448	

+	7	512_514	j.1_In_Frame_Del_	NM_007150	NP_009081	O15231	ZN185_HUMAN	Poly-Glu.	3	GACACCgaggagg	0.522	
-	14	4550		NM_000132	NP_000123	P00451	FA8_HUMAN	B.	11	AGGTTATTTTTTT	0.413	
-	19	3543_3545	ıg.1_In_Frame_De	NM_001009566	NP_001009566	O94985	CSTN1_HUMAN	cidic).|Cytoplasmic (Potenti	1	tcttcctcttcctcctcctc	0.537	
+	4	817	1aug.1_Frame_Sh	NM_001103170	NP_001096640	Q5VUY0	ADCL3_HUMAN		0	GCTACTGTTTTTT	0.458	rs7513079
-	28	3551_3553	1bab.2_In_Frame_	NM_022089	NP_071372	Q9NQ11	AT132_HUMAN	ical; (Potential).	4	GACCCAGCAGC	0.675	
+	9	1046_1047	/pc.2_Frame_Shift	NM_012387	NP_036519	Q9UM07	PADI4_HUMAN		2	CTGAGGAGGAG	0.55	
-	16	1782_1783	_Ins_p.383_384ins	NM_183008	NP_892120	Q5T124	UBX11_HUMAN	em repeats of P-G-P-G-P-G	1	ccgggaccgggactgg	0.287	rs151149897
+	16	4351_4353	v.1_In_Frame_Del_	NM_006015	NP_006006	O14497	ARI1A_HUMAN	Gln-rich. 334_R1335ins	142	CCCCCCgcagcagc	0.512	
+	1	136_137		NM_001008740	NP_001008740	Q7Z6W1	TMCO2_HUMAN		1	TAGAGTCTCTCT	0.406	
+	20	3859_3861	9vwt.2_In_Frame_	NM_002840	NP_002831	P10586	PTPRF_HUMAN	cellular (Potential).	10	AGCAGCGGCGG	0.631	
+	1	2682_2683		NM_004474	NP_004465	O60548	FOXD2_HUMAN	Fork-head.	0	CAAGATCCCCCG	0.644	
-	2	1873_1875	wne.1_In_Frame_I	NM_007113	NP_009044	Q07283	TRHY_HUMAN	proximate tandem repeats.	5	CCTCCGGCTCCT	0.68	
+	8	1233_1234	9wxs.2_Frame_Sh	NM_000721	NP_000712	Q15878	CAC1E_HUMAN	lasmic (Potential).	6	GCCAAAGAGAGA	0.51	
+	7	922_923		NM_024529	NP_078805	Q6P1J9	CDC73_HUMAN		49	TCAGCAGAGAGA	0.401	356649;rs145694828
+	4	474	hpl.2_Frame_Shift	NM_001136018	NP_001129490	P07099	HYEP_HUMAN		4	GTGAAGCCCCCC	0.627	
-	20	2528_2530	E813del|SFMBT2_	NM_001029880	NP_001025051	Q5VUG0	SMBT2_HUMAN		8	AGTCTCTCCTCCT	0.596	
-	2	551	ame_Shift_Del_p.M	NM_020848	NP_065899	Q9P266	K1462_HUMAN		4	CTTCTTCATCACA	0.557	
+	11	1139	_p.P292fs|NFKB2_	NM_001077494	NP_001070962	Q00653	NFKB2_HUMAN	RHD.	3	CGGACACCCCCC	0.567	
-	16	2264	_p.G617fs|ADAM1	NM_003474	NP_003465	O43184	ADA12_HUMAN	ar (Potential).|Cys-rich.	9	GTGGGTCCCCCG	0.552	
+	1	167_168		NM_001001480	NP_001001480	Q701N2	KRA55_HUMAN		1	ggctgtggaggctgtggg	0.139	rs144216147
-	2	955_957	G2_uc001mak.1_Ir	NM_017481	NP_059509	Q9H347	UBQL3_HUMAN		3	TGGCTGGTGGT	0.537	rs2234451
+	1	268_270		NM_001004460	NP_001004460	Q9H208	O10A2_HUMAN	Name=3; (Potential).	1	TGTATTTCTTCTT	0.517	
-	3	502_503		NM_006248	NP_006239				0	TTTCCTGGAGGT	0.594	
-	12	4127_4129	ɔw.2_In_Frame_De	NM_004719	NP_004710	Q99590	SCAFB_HUMAN	Pro-rich.	0	GAGGGGGTGGTG	0.483	
+	23	5212_5213	scj.2_Frame_Shift_	NM_012291	NP_036423	Q14674	ESPL1_HUMAN		3	GTGACTGTGTGT	0.436	
+	2	164	416_uc010sqx.1_Ir	NM_007264	NP_009195	O15218	GP182_HUMAN	cellular (Potential).	1	GACCTTGGAGAG	0.602	
-	21	3042	tbb.1_Frame_Shift	NM_001077261	NP_001070729	Q9Y618	NCOR2_HUMAN		4	ACGATGGGGGG	0.652	rs12321697
+	1	1529_1531		NM_030979	NP_112241	Q9H361	PABP3_HUMAN		4	GTCctgcagctgctgct	0.414	
+	9	1488	uqw.2_Frame_Shif	NM_006646	NP_006637	Q9UPY6	WASF3_HUMAN		1	CATGGCCCCCA	0.667	
+	4	341		NM_194318	NP_919299	Q6Y288	B3GLT_HUMAN	ıenal (Potential).	2	GCAGTTAAAAAA	0.373	rs141154947
-	1	1241_1243		NM_024496	NP_078772	Q9H1B7	I2BPL_HUMAN	y-Gln.|Potential.	0	gctgctgctgttgctgctg	0.266	rs28718623
+	6	1530	_p.P385fs|RIN3_uc	NM_024832	NP_079108	Q8TB24	RIN3_HUMAN	Pro-rich.	3	GTCCCGCCCCCC	0.622	
-	30	5230_5231	ɔ.K1733fs|SPG11_	NM_025137	NP_079413	Q96JI7	SPTCS_HUMAN	cellular (Potential).	5	ATGGCATTTTTTC	0.391	
+	2	2046_2048	ɔ.L591del|SLC24A1	NM_004727	NP_004718	O60721	NCKX1_HUMAN	ical; (Potential).	0	AGAGCCTGCTGC	0.547	
+	6	864_865	cts.3_Frame_Shift_	NM_004221	NP_004212	P24001	IL32_HUMAN		1	GGGGGACAAGGA	0.574	rs2981599
+	8	1669_1671		NM_139170	NP_631909	Q8IYS4	CP071_HUMAN		1	CAGTGAGGAGGA	0.611	
+	15	1993_1995	ɔ.S436del|SLC5A1	NM_052944	NP_443176	Q8WWX8	SC5AB_HUMAN	lasmic (Potential).	2	AGGCCAGCAGC	0.542	
+	2	594	_p.Y109fs|ADCY7_	NM_001114	NP_001105	P51828	ADCY7_HUMAN	ical; (Potential).	1	TGGGCTATGTGCT	0.642	
+	4	874		NM_000196	NP_000187	P80365	DHI2_HUMAN		0	TCCCTGGGGGG	0.428	
+	16	2021_2023	ne_Del_p.S561del	NM_014329	NP_055144	Q6P2E9	EDC4_HUMAN	Ser-rich.	4	cagcggtagcagcagca	0.458	
-	10	11252_1125	3_uc002fcl.2_In_F	NM_006885	NP_008816	Q15911	ZFHX3_HUMAN	Poly-Gly.	4	GTACGAgccgccgc	0.394	
+	16	1881_1882	/nq.1_Frame_Shift	NM_198390	NP_938204	Q8IY22	CMIP_HUMAN		0	CAACTGCAGATC	0.589	
+	4	1276_1278	SMCR7_uc010vxc	NM_139162	NP_631901	Q96C03	SMCR7_HUMAN		0	GGCGGCTGCTG	0.685	
-	7	830		NM_001008777	NP_001008777	Q5MNV8	FBX47_HUMAN		0	CTCCAGTTTTTGG	0.363	
+	5	1150	P10_uc002hxw.1_5	NM_021939	NP_068758	Q96AY3	FKB10_HUMAN		1	GAGCTCCCCCC	0.632	
-	28	3121_3122	_p.D919fs|EFTUD2	NM_004247	NP_004238	Q15029	U5S1_HUMAN		1	GATCATCGAAGA	0.52	
+	3	312	ıe_Shift_Del_p.P5	NM_003110	NP_003101	Q02086	SP2_HUMAN		0	CTGCTCCCCCAC	0.547	

+	20	2950_2951	195_uc010wsb.1_	NM_014738	NP_055553	Q12767	K0195_HUMAN			1	CGAGATCCCCC	0.614	
+	9	1159	_p.I335fs|EVI5L_u	NM_145245	NP_660288	Q96CN4	EVI5L_HUMAN			1	AGTGATCCCCCA	0.627	
+	5	712	.2_RNA|CARM1_	NM_199141	NP_954592	Q86X55	CARM1_HUMAN			0	GCTCTGGGATC	0.597	
-	1	1072	xoa.1_Frame_Shif	NM_017506	NP_059976	Q15622	OR7A5_HUMAN	Name=7; (Potential).		2	AGCATGGGGGT	0.453	
-	5	1002_1052	uc010xsw.1_5'Fla	NM_033317	NP_201574	Q6E0U4	DMKN_HUMAN	Gly-rich.	S274_S290del	3	gccgccactgctgccgc	0.303	79970;rs144877871;rs147522263;rs140071083;rs13
-	1	207_208	ad.1_Frame_Shif	NM_198538	NP_940940	Q6UWP8	SBSN_HUMAN			1	CCCACCTCTCTC	0.579	
+	7	712_714		NM_001039887	NP_001034976	Q2NL68	CS055_HUMAN	Ser-rich.		1	TCCATCTCCTCC	0.631	
-	9	1206		NM_145296	NP_660339	Q8NFZ8	CADM4_HUMAN	lasmic (Potential).		0	ATGAAGAATTCC	0.577	
+	12	1271_1273	.Q407del|NUCB1_	NM_006184	NP_006175	Q02818	NUCB1_HUMAN	ential.|Poly-Gln.		0	agcggaagcagcag	0.522	
+	4	1303_1305	2qlt.2_In_Frame_	NM_007279	NP_009210	P26368	U2AF2_HUMAN			1	CACGAGAAGAA	0.645	
-	2	234_236	HX57_uc002rrg.2_	NM_198963	NP_945314	Q6P158	DHX57_HUMAN	Gly-rich.		3	gccacctccaccacca	0.384	
+	5	1121_1123	ypt.1_In_Frame_D	NM_014562	NP_055377	P32242	OTX1_HUMAN	His-rich.		2	CTCAGGccaccac	0.537	
-	2	855	GOLN2_uc002spb	NM_006464	NP_006455	O43493	TGON2_HUMAN	l).|10.|14 X 14 AA tandem r		0	TCTTTTGGGGTC	0.572	
-	23	3871		NM_018897	NP_061720	Q8WXX0	DYH7_HUMAN	n (By similarity).		12	CTAATATTTTTTT	0.418	
+	6	915_916	vch.2_Frame_Shi	NM_001142300	NP_001135772	Q8N7R7	CCYL1_HUMAN	clin N-terminal.		0	GTTCTGGGAGC	0.431	
-	3	493		NM_014617	NP_055432	P11844	CRGA_HUMAN	crystallin 'Greek key' 4.		0	CTGCACCCCCC	0.532	
-	11	1963_1964	fwe.1_Frame_Shif	NM_005689	NP_005680	Q9NP58	ABCB6_HUMAN			2	CATGTTCTCCAT	0.49	
+	6	641	S1_uc010zte.1_R	NM_021067	NP_066545	Q14691	PSF1_HUMAN			2	CCTATTAAAAAA	0.299	
+	5	716	_Shift_Del_p.P210	NM_022896	NP_075047	Q9BQK8	LPIN3_HUMAN			4	AGTGGCCCCCC	0.458	
-	3	453_455	ne_Del_p.L72del|	NM_194255	NP_919231	P41440	S19A1_HUMAN	ical; (Probable).		0	GGCCCAGCAGC	0.645	
-	3	428_430	_19DD>D|TFIP11_	NM_012143	NP_036275	Q9UBB9	TFP11_HUMAN	Poly-Asp.		0	GCTCGTCATCAT	0.532	rs145794160
+	4	2301_2318	H_uc003afp.2_5'	NM_021076	NP_066554	P12036	NFH_HUMAN	-S-P-[AEPV]-[EAK]- [AEV		0	AAGTCCCCAGAG	0.55	48451;rs57188573;rs117283469
+	2	372_374	_Intron|LOC3396	NM_004599	NP_004590	Q12772	SRBP2_HUMAN	h.|Cytoplasmic (Potential).		4	agcagtggcagcagca	0.365	
+	1	ranslation_Start_Site|CACNA	NM_001128840	NP_001122312	Q01668	CAC1D_HUMAN			11	tgttcgtGgatgatgatg	0.246	
-	7	1127		NM_013363	NP_037495	Q9UKZ9	PCOC2_HUMAN	NTR.		3	AACAATAATTGC	0.383	
+	21	2524_2526	buy.1_In_Frame_	NM_000283	NP_000274	P35913	PDE6B_HUMAN			0	GAGAAGGAGGA	0.562	
+	4	994_996	.Q279del|MMRN1	NM_007351	NP_031377	Q13201	MMRN1_HUMAN	Poly-Gln.		4	GCTGAGCAGCA	0.448	
+	13	1713_1714	_p.K518fs|PAPD7_	NM_006999	NP_008930	Q5XG87	PAPD7_HUMAN			1	AAAAAACACACA	0.653	
-	3	512_514	0jii.2_In_Frame_D	NM_138379	NP_612388	Q96H15	TIMD4_HUMAN	ar (Potential).|Thr-rich.		2	GGGCTTGTTGT	0.537	
-	2	742	_5'Flank|ATF6B_	NM_022110	NP_071393	Q9UIM3	FKBPL_HUMAN			0	GAGCTCCCCCC	0.587	
+	11	1688	p.H408fs|FOXP4_	NM_001012426	NP_001012426	Q8IVH2	FOXP4_HUMAN			1	GTGCACCCCCC	0.682	
-	17	3632	_Shift_Del_p.P119	NM_014780	NP_055595	Q14999	CUL7_HUMAN			4	CAGGAGGGGGT	0.632	
-	24	2621	pkc.2_Frame_Shi	NM_014841	NP_055656	O60641	AP180_HUMAN			1	AATTCCAAGATC	0.259	
+	6	1344	sna.1_Frame_Shif	NM_001037165	NP_001032242	P85037	FOXK1_HUMAN			2	AGGGCTCCCCCA	0.647	
+	8	2132_2134		NM_138426	NP_612435	Q86VQ1	GLCI1_HUMAN	Poly-Gln.		0	ATCCCAGCAGC	0.562	
-	6	853_854	sxa.1_Frame_Shi	NM_001127453	NP_001120925	O60443	DFNA5_HUMAN			1	GGGGTCCAGGT	0.47	
+	5	601_603	0kxo.2_In_Frame_	NM_007252	NP_009183	P78424	PO6F2_HUMAN	Gln-rich.		1	cagctccagcagcag	0.365	
-	2	382	LM_uc003tka.1_5	NM_013284	NP_037416	Q9NP87	DPOLM_HUMAN	BRCT.		3	GAGCTGGGGGG	0.637	
-	7	981	.K270fs|KRIT1_u	NM_194456	NP_919438	O00522	KRIT1_HUMAN			3	TGCCATTTTTCC	0.338	
-	15	1860	|TAF6_uc011kji.1_	NM_139315	NP_647476	P49848	TAF6_HUMAN			2	GTGCTGGGGGG	0.657	
-	8	1217	y.2_Frame_Shift_	NM_019042	NP_061915	Q96PZ0	PUS7_HUMAN			1	AGTGGGTTTTTT	0.398	
+	1	431_433	IC_uc003vhg.2_5'	NM_199072	NP_951038	Q9P1T7	MDFIC_HUMAN			1	GCggaagaggagga	0.616	
+	1	528		NM_001001656	NP_001001656	Q8NGU2	OR9A4_HUMAN	ellular (Potential).		1	GAACAATTTTTTT	0.383	
+	1	162_164	_uc010luh.1_5'UT	NM_004331	NP_004322	O60238	BNI3L_HUMAN			0	CTGCACAACAA	0.655	
-	11	2018_2019	ls.1_Frame_Shift_	NM_014682	NP_055497	O60284	ST18_HUMAN			5	GATTCGATTTTTT	0.411	
-	6	1265_1266	_Shift_Ins_p.K209	NM_002568	NP_002559	P11940	PABP1_HUMAN	1-binding.|RRM 3.		0	AGCTCCTTTCCG	0.371	rs140822921
-	11	2666_2668		NM_015117	NP_055932	Q8IXZ2	ZC3H3_HUMAN	Poly-Ser.	p.S879F(1)	1	ggggatgaggaggag	0.552	;rs2272753;rs137878905

+	20	2671_2673	.E837del|CNKSR	NM_014927	NP_055742	Q8WXI2	CNKR2_HUMAN	ential.|Poly-Glu.		2	gaggaagaggaggag	0.379	
+	4	621_623	_In_Frame_Del_p	NM_005676	NP_005667	P98175	RBM10_HUMAN	Poly-Arg.		5	CGTAGGCGGCG	0.65	
-	1			NM_018159	NP_060629	Q96G61	NUD11_HUMAN			0	CTCGAGGCAGC	0.584	
+	20	4967	1aoj.2_Frame_Shi	NM_015215	NP_056030	Q9Y6Y1	CMTA1_HUMAN	IQ 2.		9	ATGAACAAAAAA	0.473	
+	1	136_137		NM_001008740	NP_001008740	Q7Z6W1	TMCO2_HUMAN			1	TAGAGTCTCTCT	0.406	
-	1	145	way.2_5'Flank|MIE	NM_024763	NP_079039	Q5VTH9	WDR78_HUMAN			2	ACCCCTTTTTTT	0.622	
+	6	814_816	W3_uc010oqx.1_I	NM_138467	NP_612476	Q6IPR3	TYW3_HUMAN			2	TGAAAATGATGAT	0.33	rs112765232
+	4	581	.2_Intron|CLCA4_	NM_012128	NP_036260	Q14CN2	CLCA4_HUMAN			2	TAAGTCAAAAAA	0.403	
-	3	680_681	_p.R48fs|GBP5_u	NM_052942	NP_443174	Q96PP8	GBP5_HUMAN	(By similarity).		1	CCAGTGCGATAG	0.495	825788;rs61732537
-	2	873	_p.P14fs|SLC16A	NM_003051	NP_003042	P53985	MOT1_HUMAN	lasmic (Potential).		1	CATCTGGGGGG	0.423	
+	9	2365		NM_021948	NP_068767	Q96GW7	PGCB_HUMAN	EGF-like.		2	GCTATGGGGGG	0.622	
+	23	3123	fqk.1_Frame_Shift	NM_001080471	NP_001073940	Q5VY43	PEAR1_HUMAN	Pro-rich.		3	GCCTACCCCCC	0.607	
+	1	259		NM_001004478	NP_001004478	Q8NGY1	O10Z1_HUMAN	ellular (Potential).		2	TGGCTGGGGGG	0.552	
+	17	2658_2659	gqh.2_Frame_Shif	NM_173156	NP_775179	Q92540	SMG7_HUMAN			3	CTCTAGAAAAAA	0.45	
-	2	1361_1363	.2_Intron|RGL1_u	NM_203454	NP_982279	Q8WW27	ABEC4_HUMAN			0	TCCCTTTCTTCTT	0.419	rs141411396
-	3	527	_Shift_Del_p.D63	NM_003929	NP_003920	O14966	RAB7L_HUMAN	(By similarity).		1	AATATCCCACAC	0.393	
+	1	268_270		NM_001004460	NP_001004460	Q9H208	O10A2_HUMAN	Name=3; (Potential).		1	TGTATTTCTTCTT	0.517	
+	2	423		NM_152316	NP_689529	Q8N8R7	CK046_HUMAN			0	TTAGCCAAAAAA	0.338	
+	10	1316	hift_Del_p.W322f	NM_001975	NP_001966	P09104	ENOG_HUMAN			0	TGGCTGGGGGG	0.587	
+	3	524	_uc001qub.1_Intro	NM_016184	NP_057268	Q9UMR7	CLC4A_HUMAN	ellular (Potential).		0	TGTGTGAAAAAA	0.333	
+	10	2681	sto.2_Frame_Shift	NM_018448	NP_060918	Q86VP6	CAND1_HUMAN	HEAT 17.		2	TTGCAGGGGGG	0.428	
+	14	3311	A1091fs|EP400_u	NM_015409	NP_056224	Q96L91	EP400_HUMAN	and RUVBL2.|Helicase AT		12	ATTGCTTTTTTT	0.433	
-	1	1994_1996	o.1_In_Frame_De	NM_183422	NP_904358	Q15714	T22D1_HUMAN	Gln-rich.		0	gttgttgttgctgctgctg	0.409	613609;rs146722477
-	5	1255		NM_012158	NP_036290	Q9UKT7	FBXL3_HUMAN			0	TCATATAAAAAAA	0.418	
-	72	12231	.P3451fs|MYCBP	NM_015057	NP_055872	O75592	MYCB2_HUMAN			14	TGCTGGGGGG	0.433	
+	13	3186	RCC5_uc010tjc.1_	NM_000123	NP_000114	P28715	ERCC5_HUMAN			7	AAAGTGAAAAAA	0.428	
-	30	5230_5231	.K1733fs|SPG11_	NM_025137	NP_079413	Q96JI7	SPTCS_HUMAN	ellular (Potential).		5	ATGGCATTTTTT	0.391	
-	30	7699	fy.1_Frame_Shift_	NM_015263	NP_056078	Q8TDJ6	DMXL2_HUMAN			9	TATCTGAAAAAAA	0.313	
+	6	1825_1827	2afu.2_In_Frame_	NM_017610	NP_060080	Q6ZNA4	RN111_HUMAN	His-rich.		2	ATCATCACCACC	0.512	
+	2	2046_2048	.L591del|SLC24A	NM_004727	NP_004718	O60721	NCKX1_HUMAN	ical; (Potential).		0	GAGCCTGCTGC	0.547	
-	2	435_440	.3_In_Frame_Del_	NM_002693	NP_002684	P54098	DPOG1_HUMAN	Poly-Gln.		2	ctgctgttgctgctgctg	0.466	
-	5	549_551	uc010vct.1_Intron	NM_145659	NP_663634	Q8NEV9	IL27A_HUMAN	Glu-rich.		0	CCCTtcctctcctcctc	0.547	
+	16	2002_2004	ne_Del_p.S549del	NM_014329	NP_055144	Q6P2E9	EDC4_HUMAN	Ser-rich.		4	CTCTCCcagcagca	0.453	
-	4	756	_Shift_Del_p.D67f	NM_006470	NP_006461	O95361	TRI16_HUMAN			3	AGGATCCCCCT	0.567	
-	7	830		NM_001008777	NP_001008777	Q5MNV8	FBX47_HUMAN			0	TCCAGTTTTTGG	0.363	
-	1	262_264		NM_002145	NP_002136	P14652	HXB2_HUMAN			0	CGAAAGGAGGA	0.542	
-	17	2036	K1C_uc010xhq.1_	NM_012398	NP_036530	O60331	PI51C_HUMAN	interaction with TLN2.		4	AGGCCGGGGGG	0.701	
-	1	625_627	xz.1_5'Flank|LGI4	NM_139284	NP_644813	Q8N135	LGI4_HUMAN			1	CAGCCAGCAGC	0.695	
-	5	1002_1052	uc010xsw.1_5'Fla	NM_033317	NP_201574	Q6E0U4	DMKN_HUMAN	Gly-rich.	S274_S290del	3	gccgccactgctgccgc	0.303	79970;rs144877871;rs147522263;rs140071083;rs13
-	9	1206		NM_145296	NP_660339	Q8NFZ8	CADM4_HUMAN	lasmic (Potential).		0	ATGAAGAATTCCT	0.577	
-	14	2382_2384	H4_uc002pgb.1_I	NM_015168	NP_055983	Q9UPT8	ZC3H4_HUMAN	Potential.		6	GCTCTCTCCTCCT	0.7	
-	5	1643	2_5'Flank|ZNF577	NM_023074	NP_075562	Q9BS31	ZN649_HUMAN			3	TGAATCCCCCC	0.448	
-	11	1472_1474	1_In_Frame_Del_	NM_015317	NP_056132	Q8TB72	PUM2_HUMAN	Ala-rich.		1	TCCAGCTGCTG	0.424	
-	3	316	_p.P92fs|HS1BP3	NM_022460	NP_071905	Q53T59	H1BP3_HUMAN	PX.		1	GTAGTGGGGGG	0.537	rs77941615
-	11	2183	113_uc010eyk.1_	NM_001145168	NP_001138640	Q8IZF5	GP113_HUMAN	tracellular (Potential).		4	ACCAACCCCCC	0.612	
-	2	234_236	HX57_uc002rrg.2_	NM_198963	NP_945314	Q6P158	DHX57_HUMAN	Gly-rich.		3	gccacctccaccacca	0.384	
+	5	719_721	zej.1_In_Frame_	NM_145810	NP_665809	Q9BWT1	CDCA7_HUMAN			1	CCATGGAGGAG	0.537	

+	21	2503_2505	Q713del|PTPRA_u	NM_002836	NP_002827	P18433	PTPRA_HUMAN	).|Tyrosine-protein phospha		1	CAGAAGCAGCA	0.621	
+	8	1092	zys.1_Frame_Shif	NM_002827	NP_002818	P18031	PTN1_HUMAN			0	GCATATCCCCC	0.567	
+	19	4651	6A6_uc003eni.3_5	NM_001102608	NP_001096078	A6NMZ7	CO6A6_HUMAN	le-helical region.		8	CCAGGCCCCCC	0.498	rs112135798
-	7	1127		NM_013363	NP_037495	Q9UKZ9	PCOC2_HUMAN	NTR.		3	AACAATAATTGC	0.383	
+	17	2670	e_Shift_Del_p.K85	NM_001002800	NP_001002800	Q9NTJ3	SMC4_HUMAN	Potential.		2	CCTGACAAAAAA	0.323	
-	3	541_543		NM_024524	NP_078800	Q9H7F0	AT133_HUMAN	ical; (Potential).		1	AATAGAGGAGG	0.463	
-	29	6861	3hgq.2_Frame_Sh	NM_032217	NP_115593	O75179	ANR17_HUMAN			10	GGTAAGGGGGC	0.458	
-	3	416_418	.1_5'UTR|NUP54_	NM_017426	NP_059122	Q7Z3B4	NUP54_HUMAN	ch.|9 X 2 AA repeats of F-G		2	AGTTTGCTGCTG	0.394	
+	4	994_996	.Q279del|MMRN1	NM_007351	NP_031377	Q13201	MMRN1_HUMAN	Poly-Gln.		4	GCTGAGCAGCA	0.448	
-	17	2126	.2_Frame_Shift_D	NM_144643	NP_653244	Q96NL6	SCLT1_HUMAN	Potential.		5	TTTGGCTTTTTTT	0.353	
-	9	1430	_p.G258fs|FGG_uc	NM_021870	NP_068656	P02679	FIBG_HUMAN	and Staphylococcus clum		0	TGGCTCCCCCC	0.448	
-	19	3988	_p.E436fs|SORBS	NM_021069	NP_066547	O94875	SRBS2_HUMAN	SH3 3.		1	CGGTTCCCCCC	0.358	
-	12	2431	03jtq.2_RNA|ADAI	NM_197941	NP_922932	Q9UKP5	ATS6_HUMAN	Disintegrin.		0	TACCCCTTTTTC	0.408	
+	9	1679	uc003kwr.3_Intron	NM_003059	NP_003050	Q9H015	S22A4_HUMAN	lame=12; (Potential).		0	TCACCCTTTTTTT	0.418	
+	3	266		NM_002114	NP_002105	P15822	ZEP1_HUMAN			6	AGTTTCAAAAAA	0.259	
+	7	1520		NM_001732	NP_001723	Q13410	BT1A1_HUMAN	lasmic (Potential).		2	CCCATGGGGGA	0.537	
-	2	797_799	l.1_Intron|PSORS	NM_001264	NP_001255	Q15517	CDSN_HUMAN	Ser-rich.		2	TGGTCCACCAC	0.635	
-	11	1174	p.K307fs|CDK19_	NM_015076	NP_055891	Q9BWU1	CDK19_HUMAN			4	GTCACCTTTTTCT	0.358	
+	8	2132_2134		NM_138426	NP_612435	Q86VQ1	GLCI1_HUMAN	Poly-Gln.		0	ATCCCAGCAGC	0.562	
+	8	1031	_p.F215fs|DYNC1	NM_004411	NP_004402	O14576	DC1I1_HUMAN			4	GACATCTTTTTTG	0.383	
-	2	313	Site_p.S68_splice	NM_198990	NP_945341	Q6IQ20	NAPEP_HUMAN			1	AGAACTAAAAAA	0.337	
-	2	110	3vey.2_Frame_Sh	NM_007356	NP_031382	A4D0S4	LAMB4_HUMAN			8	GGTGCAAAAAA	0.308	
-	5	3497_3498		NM_001080826	NP_001074295	Q86YV5	SG223_HUMAN	rotein kinase.		0	cgggagccggggcgg	0.609	rs143409664
+	9	1531_1533	l|CDCA2_uc003xe	NM_152562	NP_689775	Q69YH5	CDCA2_HUMAN			0	CCTCTATGATGAT	0.325	rs116332536
+	12	2305_2307	me_Del_p.E38del	NM_000553	NP_000544	Q14191	WRN_HUMAN	Poly-Glu.		7	CTACTAaagaagaa	0.266	
-	2	1116	10lwe.2_Frame_Sl	NM_023034	NP_075447	Q9BZ95	NSD3_HUMAN			1	TGTTGCTTTTTTT	0.378	
-	45	6393_6394	ks.1_Frame_Shift_	NM_015902	NP_056986	O95071	UBR5_HUMAN			28	CCCTTCTTTTTT	0.381	
+	20	2671_2673	.E837del|CNKSR	NM_014927	NP_055742	Q8WXI2	CNKR2_HUMAN	ential.|Poly-Glu.		2	gaggaagaggaggag	0.379	
+	6	1104_1106	4ezx.2_In_Frame_	NM_001163280	NP_001156752	O43719	HTSF1_HUMAN	Poly-Lys.		3	CTCAAAGAAGA	0.335	
+	1	500	hkw.2_Frame_Shi	NM_025074	NP_079350	Q86XX4	FRAS1_HUMAN	NA	NA	5	AGTATTGCCTCA	0.453	
+	2	203		NM_024869	NP_079145	Q8TAY7	GRPP1_HUMAN		NA	0	GCCCCTCCCTCC	0.617	
-	7	708_709	wdz.2_Frame_Shi	NM_194292	NP_919268	Q6UVJ0	SAS6_HUMAN	Potential.	NA	2	TTCTTGTTTTTT	0.317	
+	6	1846	3'UTR|TCL6_uc00	NM_020554	NP_065579				NA	0	AAGCTGGGGAG	0.557	
-	2	84	2bcu.1_Frame_Sh	NM_032808	NP_116197	Q96FE5	LIGO1_HUMAN		NA	2	TCACGCCCCCC	0.697	
+	1	70	4_uc002mnt.1_Fr	NM_001544	NP_001535	Q14773	ICAM4_HUMAN		NA	1	CTGCTGTTTTTT	0.677	
+	9	1040	Shift_Del_p.P156	NM_014516	NP_055331	O75175	CNOT3_HUMAN		NA	3	TCCCCTCCCAG	0.632	rs36665
-	5	929		NM_176810	NP_789780	Q86W25	NAL13_HUMAN	NACHT.	NA	9	TGGTTGAGACA	0.428	
+	2	688_689	.1_Intron|C21orf29	NM_198689	NP_941962	P60409	KR107_HUMAN	epeats of C-	NA	0	ACCTCCTCCCCC	0.653	
+	1	497_499	uc003tbl.3_5'Flank	NM_002047	NP_002038	P41250	SYG_HUMAN		NA	1	TTGCCCGCCGC	0.729	
-	3	3173	hv.2_Frame_Shift_	NM_033026	NP_149015	Q9Y6V0	PCLO_HUMAN	Pro-rich.	NA	7	TGGGGCCCCTG	0.517	
+	8	1177		NM_002486	NP_002477	Q09161	NCBP1_HUMAN	MIF4G.	NA	1	AATTGAAAAAG	0.373	
-	18	3406		NM_004463	NP_004454	P98174	FGD1_HUMAN	PH 2.	NA	6	GTGATCTTGAAG	0.652	
-	8	1013	mwc.1_Frame_Shi	NM_024597	NP_078873	Q8IWC1	MA7D3_HUMAN		NA	4	CACCTGGGGGG	0.532	
-	19	3629_3631	0oag.1_In_Frame_	NM_001009566	NP_001009566	O94985	CSTN1_HUMAN	cidic).|Cytoplasmic (Potenti		1	TCCCCCTCCTC	0.557	
+	3	1056_1058	obp.1_In_Frame_	NM_015001	NP_055816	Q96T58	MINT_HUMAN	ich.|By similarity.		15	CAATCAGCAGC	0.468	
+	6	814_816	W3_uc010oqx.1_I	NM_138467	NP_612476	Q6IPR3	TYW3_HUMAN			2	TGAAAATGATGA	0.33	rs112765232
-	23	3684	AP29_uc009wdq.1	NM_004815	NP_004806	Q52LW3	RHG29_HUMAN			11	ACTCCTTTTTCC	0.463	

+	8	3460	zr.1_Frame_Shift_	NM_004326	NP_004317	O00512	BCL9_HUMAN	Pro-rich.	6	TAAGTCCCCCC	0.622	
-	18	1926	b.1_Frame_Shift_	NM_001668	NP_001659	P27540	ARNT_HUMAN		9	CGGCCGGGGGG	0.527	
-	2	2734_2736	wne.1_In_Frame_	NM_007113	NP_009044	Q07283	TRHY_HUMAN	0 AA tandem repeats.	5	GTAGCTCCTCC	0.586	rs143222885
-	3	8141_8142		NM_001009931	NP_001009931	Q86YZ3	HORN_HUMAN	29	3	AGTGACCCAAGC	0.579	
+	9	1992	7A3_uc009won.2_	NM_024330	NP_077306	Q5K4L6	S27A3_HUMAN		1	TGCGTCCCCCC	0.617	
+	6	1160	_p.P108fs|TDRD1	NM_001098475	NP_001091945	Q5VZ19	TDR10_HUMAN		1	AAAGGCCCCCC	0.522	
-	13	3761_3762		NM_000130	NP_000121	P12259	FA5_HUMAN	tandem repeats of [TNP]-L	6	GGTCTGGAGAG	0.54	
+	14	1753_1755	0pos.1_In_Frame_	NM_024420	NP_077734	P47712	PA24A_HUMAN	PLA2c.	3	TCCTTTGATGAT	0.433	
-	13	2418_2420	0pty.1_In_Frame_	NM_005401	NP_005392	Q15678	PTN14_HUMAN	Poly-Glu.	5	GGAGCCTCCTC	0.626	
+	20	2516	R_uc010pxx.1_In	NM_000254	NP_000245	Q99707	METH_HUMAN	inding N-terminal.	3	TAAACCAAAAAA	0.279	
-	9	1366	Del_p.I412fs|PAR	NM_019619	NP_062565	Q8TEW0	PARD3_HUMAN		1	TGCCTATTTTTTT	0.433	
+	10	3102		NM_032199	NP_115575	Q14865	ARI5B_HUMAN		4	CAGGGAAAAAG	0.607	
-	19	3018	_p.S792fs|FGFR2_	NM_000141	NP_000132	P21802	FGFR2_HUMAN	lasmic (Potential).	96	TGAAGAACAAG	0.433	
+	25	8653_8655	del|DNHD1_uc00	NM_144666	NP_653267	Q96M86	DNHD1_HUMAN	Glu-rich.	2	AGAGTgaggagg	0.507	
+	1	268_270		NM_001004460	NP_001004460	Q9H208	O10A2_HUMAN	Name=3; (Potential).	1	TGTATTTCTTCTT	0.517	
-	3	345	rew.1_Frame_Shi	NM_001001991	NP_001001991	Q6UXH9	PAMR1_HUMAN		2	AGGTACCCCCC	0.517	
-	38	5650	_uc001ndm.3_Fr	NM_002334	NP_002325	O75096	LRP4_HUMAN	lasmic (Potential).	4	GGAGGCCCCCC	0.562	
-	24	2496_2498	PC3_uc010rhl.1_	NM_000256	NP_000247	Q14896	MYPC3_HUMAN	nectin type-III 1.	3	GTAGCTCTTCTT	0.601	
+	2	352	_Shift_Del_p.P56	NM_006656	NP_006647	A8K327	A8K327_HUMAN		2	TACATACCCCCC	0.567	
+	2	185_187		NM_015516	NP_056331	Q8WUA8	TSK_HUMAN		0	GCCCCTGCTGC	0.616	
+	17	2405_2407	pkl.1_In_Frame_	NM_004398	NP_004389	Q13206	DDX10_HUMAN		4	ATTGGAGtgatgat	0.31	
-	3	382	_p.K73fs|CHD4_u	NM_001273	NP_001264	Q14839	CHD4_HUMAN		2	CCTCCTTTTTTT	0.468	
-	3	441_442	.1_Intron|PRB1_u	NM_005039	NP_005030	P04280	PRP1_HUMAN	-[PAQ]-Q-[GE]-[GD]- [NKS]	0	TTTCCTGGAGGT	0.604	
-	7	1320	hift_Del_p.G270f	NM_001144996	NP_001138468	Q13683	ITA7_HUMAN	Extracellular (Potential).	5	AGTGACCCCCC	0.602	
-	23	3886	N2_uc001tsk.2_	NM_002973	NP_002964	Q99700	ATX2_HUMAN		2	CATGTGGGGTG	0.512	
-	3	359	PS33A_uc001uc	NM_022916	NP_075067	Q96AX1	VP33A_HUMAN		1	TCTGACAAAAAA	0.383	
+	16	2686_2688	tbn.1_In_Frame_	NM_004592	NP_004583	Q12872	SFSWA_HUMAN	g/Ser-rich (RS domain).	0	CACGAGAAGAA	0.493	
+	18	2223	aba.2_Frame_Shif	NM_130806	NP_570718	Q8WXD0	RXFP2_HUMAN	lasmic (Potential).	0	AAAATTAAAAAAA	0.348	
+	9	893	p.A333fs|C13orf3	NM_024808	NP_079084	Q6PGQ7	BORA_HUMAN	Ser-rich.	0	TAGTGCAAAAAA	0.383	
-	3	331	IN_uc010tqp.1_F	NM_182946	NP_891991	Q8N4C6	NIN_HUMAN	EF-hand 2.	6	GCACTGGGGCC	0.587	
+	2	1168		NM_018228	NP_060698	Q9H8Y1	VRTN_HUMAN		0	CCACCGGGGGG	0.642	
-	23	2338	ahb.1_Frame_Shi	NM_020821	NP_065872	Q709C8	VP13C_HUMAN		2	TGTACATTTTTTA	0.328	
+	4	746	qp.2_Frame_Shift_	NM_002434	NP_002425	P29372	3MG_HUMAN		2	GCAGACCCCCC	0.602	
+	3	422_424	PS34_uc002cmo.	NM_001010865	NP_001010865	A4GXA9	EME2_HUMAN		3	GAATTGCTGCT	0.655	
-	2	667_668	_5'Flank|IQCK_uc	NM_001012991	NP_001013009	Q1ED39	CP088_HUMAN	Lys-rich.	0	GGTGGATTTTTT	0.535	
+	17	2641	hift_Del_p.R819fs	NM_173201	NP_775293	O14983	AT2A1_HUMAN	smic (By similarity).	4	GACCGCCCCCC	0.657	
+	30	3476_3478	L1022del|ITGAL_	NM_002209	NP_002200	P20701	ITAL_HUMAN	ical; (Potential).	10	GGGGGCTGCTG	0.601	
+	2	117	fji.2_Frame_Shift_	NM_002163	NP_002154	Q02556	IRF8_HUMAN	phan pentad repeat.	3	TGACAGTAGCAT	0.483	
+	4	1366	SMCR7_uc010vxq	NM_139162	NP_631901	Q96C03	SMCR7_HUMAN		0	CGTCTGGGGGA	0.687	
-	6	2548_2550		NM_139285	NP_644814	Q8NHY3	GA2L2_HUMAN		2	tcctttccttcctcctcctc	0.527	
-	4	1433		NM_032865	NP_116254	Q8IZW8	TENS4_HUMAN		4	GTAAAGGGGGC	0.512	
+	7	954		NM_178160	NP_835454	Q7RTS6	OTOP2_HUMAN	ical; (Potential).	4	AGACCTTTTTT	0.607	
+	6	826	D_uc002kfy.1_5'F	NM_022158	NP_071441	Q9H479	FN3K_HUMAN		0	GGGTTCCCCAG	0.572	
+	8	627	ift_Del_p.G205fs|	NM_006949	NP_008880	Q15833	STXB2_HUMAN		1	AGGGGCCCAGA	0.672	
-	7	1272	e_Shift_Del_p.P3	NM_021155	NP_066978	Q9NNX6	CD209_HUMAN	ellular (Probable).	1	CAGGAGGGGGG	0.498	
-	3	627	_p.K126fs|TRMT1	NM_017722	NP_060192	Q9NXH9	TRM1_HUMAN		2	TCAACCTTTTCC	0.552	
-	1	90_92	EC8_uc002pwu.2_	NM_014442	NP_055257	Q9NYZ4	SIGL8_HUMAN		5	gcaggggcagcagc	0.493	

-	3	1334	NF552_uc010yhg	NM_024762	NP_079038	Q9H707	ZN552_HUMAN	2H2-type 9.		0	CCTAAATTTTTTT	0.413	
-	1	1479_1481		NM_001029883	NP_001025054	A6NGG8	CB071_HUMAN			1	GTCTTCCTCCT	0.542	
+	6	2252_2253	ed.2_Frame_Shift	NM_181453	NP_852118	Q8IWJ2	GCC2_HUMAN	Potential.		1	GTTCAGAAAAAA	0.307	
-	6	926	02tpm.2_Frame_S	NM_031445	NP_113633	Q6DCA0	AMERL_HUMAN	AMMECR1.		1	GACACCTTTTTC	0.388	
-	1	158_159	c002uiq.2_5'Flank	NM_004882	NP_004873	Q86X95	CIR1_HUMAN	action with RBPJ.		1	TTTTTGATATTG	0.505	
-	23	3871		NM_018897	NP_061720	Q8WXX0	DYH7_HUMAN	n (By similarity).		12	CTAATATTTTTTT	0.418	
+	1	164	P2_uc010zju.1_5'	NM_000597	NP_000588	P18065	IBP2_HUMAN			0	ccgccgccgccgctgc	0.337	
-	1	986		NM_012072	NP_036204	Q9NPY3	C1QR1_HUMAN	Extracellular (Potential).		2	GCCATCCCCCC	0.627	
+	2	1083_1085		NM_024893	NP_079169	Q9H7V2	SYNG1_HUMAN	ytoplasmic (Potential).		0	ATGTGGAGGAG	0.547	
-	2	236	2xot.2_Frame_Sh	NM_020398	NP_065131	O95925	EPPI_HUMAN	WAP.	p.C53fs*28(2)	1	TAAACATTTTTTT	0.453	
+	4	301		NM_178456	NP_848551	Q9H1P6	CT085_HUMAN			1	TCCATCCCCCC	0.582	
-	23	2501_2502		NM_014258	NP_055073	Q9BX26	SYCP2_HUMAN			5	TCACCATTTTTT	0.322	
+	9	1213_1223	bp.1_Frame_Shift	NM_001794	NP_001785	P55283	CADH4_HUMAN	|Extracellular (Potential).		6	AGGTCCCCGAA	0.412	
+	4	1162	0gma.2_Frame_S	NM_005534	NP_005525	P38484	INGR2_HUMAN	tential).|Fibronectin type-III		0	ACGGCCTTTTTT	0.458	
+	2	688_689	.1_Intron|C21orf2	NM_198689	NP_941962	P60409	KR107_HUMAN	epeats of C-C-X(3).|16.		0	ACCTCCTCCCC	0.653	
+	38	4673_4675	P2A_uc002zjs.2_	NM_015151	NP_055966	Q14689	DIP2A_HUMAN	Poly-Val.		2	CTGCTGGTGGT	0.596	
-	5	732	ARVCF_uc002zra.	NM_001670	NP_001661	O00192	ARVC_HUMAN			1	CTAGTGGGGGG	0.647	
+	13	1533_1535	aus.2_In_Frame_	NM_012407	NP_036539	Q9NRD5	PICK1_HUMAN	Poly-Glu.		0	GATGGggaggag	0.562	
+	5	477_479		NM_001197	NP_001188	Q13323	BIK_HUMAN	otential).|Helical; (Potenti		0	tgctggcgctgctgctg	0.562	
-	11	1334		NM_173050	NP_766638	Q8IWY4	SCUB1_HUMAN			5	GGCCCGGGGGG	0.647	
+	13	1986_1987	NKTR_uc003clq.1	NM_005385	NP_005376	P30414	NKTR_HUMAN			3	GACAGTCCCCC	0.421	
-	28	3481	3A3_uc003ftx.3_5	NM_024524	NP_078800	Q9H7F0	AT133_HUMAN			1	GACCCAAAAAA	0.383	
-	3	1028	168_uc010iah.2_5	NM_152617	NP_689830	Q8IYW5	RN168_HUMAN	Glu-rich.		0	TTCGCCTTTTTT	0.448	
-	1	340_348		NM_177998	NP_819056	Q7RTM1	OTOP1_HUMAN	ical; (Potential).		3	TCCACAGCAGC	0.727	245977;rs75328065
-	5	763	3hkd.2_Frame_Sh	NM_001042784	NP_001036249	Q5M9N0	CD158_HUMAN			6	CACATATTTTTTT	0.393	
+	1	3100_3102	3igz.2_In_Frame_	NM_032961	NP_116586	Q9P2E7	PCD10_HUMAN	ytoplasmic (Potential).		2	GCCTCTGCTGC	0.581	
+	2	930	on.1_Frame_Shift_	NM_004744	NP_004735	O95237	LRAT_HUMAN	ical; (Potential).		1	GTCTTGGGATT	0.403	
+	12	2085	p.D480fs|TLL1_uc	NM_012464	NP_036596	O43897	TLL1_HUMAN	CUB 2.		7	TATCCTGATGAC	0.423	
+	22	3425_3426	f.2_Frame_Shift_	NM_012343	NP_036475	Q13423	NNTM_HUMAN	chondrial matrix.		3	AATCTTCTACAA	0.426	
+	5	794	3kcy.1_Frame_Shi	NM_001080479	NP_001073948	Q8N1W1	RGNEF_HUMAN			0	TTGTTGGAGGC	0.463	
-	5	537	_p.P109fs|SSBP2_	NM_012446	NP_036578	P81877	SSBP2_HUMAN	Pro-rich.		5	CTCCTGGGGGA	0.458	
+	1	616_617		NM_021614	NP_067627	Q9H2S1	KCNN2_HUMAN			2	CCGCTGCCGCC	0.658	038013;rs34838882
+	6	1394_1395	B1_uc010jdb.1_	NM_005573	NP_005564	P20700	LMNB1_HUMAN	Rod.|Coil 2.		2	GACAAAGAGAG	0.426	
-	15	5611		NM_019105	NP_061978	P22105	TENX_HUMAN	nectin type-III 11.		0	GAGTCAAACTG	0.662	
-	3	1887		NM_019105	NP_061978	P22105	TENX_HUMAN	EGF-like 14.		0	GGCAGCCCCCG	0.692	
+	2	246	oei.2_Frame_Shift	NM_024165	NP_077084	O43189	PHF1_HUMAN			0	CGCAGCCCCCC	0.557	
+	14	2112		NM_001371	NP_001362					21	GATGACCCCCC	0.383	
-	4	1648	318_uc003ouw.2_	NM_014345	NP_055160	Q5VUA4	ZN318_HUMAN			7	TCGCCTTTTTT	0.493	
+	26	3021_3022	p.Q914fs|MYO6_	NM_004999	NP_004990	Q9UM54	MYO6_HUMAN	Potential.		2	TTACAGAAAAAA	0.381	
-	8	1307_1309	1dzv.1_In_Frame_	NM_002042	NP_002033	P24046	GBRR1_HUMAN	ical; (Probable).		1	GAGCAAGAAGA	0.522	
+	1	570_572		NM_138426	NP_612435	Q86VQ1	GLCI1_HUMAN	Poly-Ser.		0	TCCACTGcctcctc	0.527	
+	5	1249	_p.P231fs|DTX2_u	NM_020892	NP_065943	Q86UW9	DTX2_HUMAN			2	CCCCCACACAG	0.657	rs147779783
-	2	390_392	kiw.1_In_Frame_	NM_015545	NP_056360	O75127	PTCD1_HUMAN			1	AACTCTCCTCC	0.606	
+	7	1118_1119	vuy.2_Frame_Shif	NM_016019	NP_057103	Q9Y383	LC7L2_HUMAN	Arg/Ser-rich.		0	GAGAAGAGAG	0.391	
-	2	698	vd.3_Frame_Shift	NM_022740	NP_073577	Q9H2X6	HIPK2_HUMAN	corepression (By similarity)		7	CGCTGTTTTTG	0.577	
+	3	293	PO_uc010lpl.1_Int	NM_198455	NP_940857	A2VEC9	SSPO_HUMAN	EMI.		0	AGGCTGGGGGG	0.622	
-	60	8167	Shift_Del_p.R2704	NM_006904	NP_008835	P78527	PRKDC_HUMAN	KIP-binding.		34	CCAGCCTTTTTT	0.498	

-	11	1327	xzp.2_Frame_Shi	NM_014393	NP_055208	Q9NUL3	STAU2_HUMAN	DRBM 4.	0	CAGCATTTTTTT	0.328	
+	12	1710_1711	.H509fs|ESRP1_	NM_017697	NP_060167	Q6NXG1	ESRP1_HUMAN	RRM 3.	4	TGTCATAAAAAA	0.436	
+	7	2374	zgp.1_Frame_Shi	NM_015158	NP_055973	Q14678	KANK1_HUMAN		4	AGGGTGGAAAT	0.498	
-	5	410		NM_004669	NP_004660	O95833	CLIC3_HUMAN	ST C-terminal.	0	TGGTACAGGGC	0.771	
-	6	1226_1227		NM_005044	NP_005035	P51817	PRKX_HUMAN	rotein kinase.	3	TTCCTAATCGCC	0.426	
+	11	1419	p.Y289fs|MSL3_u	NM_078629	NP_523353	Q8N5Y2	MS3L1_HUMAN		1	AATTACCCCCC	0.458	
+	1	1125		NM_001013736	NP_001013758	Q5HY64	FA47C_HUMAN		3	TGCCTCCCGAG	0.632	
-	14	1420	l.2_5'UTR|BTK_u	NM_000061	NP_000052	Q06187	BTK_HUMAN	ase.|ATP (By similarity).	6	CCAGTCCCCAG	0.438	
-	5	1312	.1_Intron|TEX13A_	NM_031274	NP_112564	Q9BXU3	TX13A_HUMAN	anBP2-type.	2	CCCTTCCCACA	0.478	
-	8	1013	mwc.1_Frame_Shi	NM_024597	NP_078873	Q8IWC1	MA7D3_HUMAN		4	CACCTGGGGGG	0.532	
+	6	1104_1106	4ezx.2_In_Frame_	NM_001163280	NP_001156752	O43719	HTSF1_HUMAN	Poly-Lys.	3	CTCAAAGAAGA	0.335	
+	4	2131_2133	EC1_uc010nsl.1_	NM_005462	NP_005453	O60732	MAGC1_HUMAN		4	GTCCTCTTCAG	0.571	
-	1	159		NM_001009609	NP_001009609	Q5MJ09	SPXN3_HUMAN		2	TCATCATTTTTTT	0.239	
+	10	1280_1282	73_uc009vlk.1_In_	NM_005427	NP_005418	O15350	P73_HUMAN	Poly-Gln.	2	ATCGGCAGCAG	0.606	
-	4	1104	apa.1_Frame_Shi	NM_018948	NP_061821	Q9UJM3	ERRFI_HUMAN		1	ACTCTGGGGGG	0.478	
-	23	3755	E887fs|EIF4G3_u	NM_003760	NP_003751	O43432	IF4G3_HUMAN		1	CTCTTCTTGAG	0.522	
+	12	2906_2908	9vqi.1_In_Frame_	NM_001083621	NP_001077090	Q9NUA8	ZBT40_HUMAN		1	CCCCAAGAAGA	0.517	
-	1	1028		NM_000864	NP_000855	P28221	5HT1D_HUMAN	ame=4; (By similarity).	0	AGAGCGGGGGG	0.597	
+	4	449_450	hift_Del_p.L80fs|	NM_002953	NP_002944	Q15418	KS6A1_HUMAN	otein kinase 1.	1	GGTGCTGAAGA	0.599	
+	7	1951	9vui.2_Frame_Shi	NM_145238	NP_660281	P17040	ZSC20_HUMAN		4	TAGTGCTGAGA	0.582	
+	5	713	oyy.1_Frame_Shif	NM_006099	NP_006090	Q9Y6X2	PIAS3_HUMAN	PINIT.	1	ATTTTCCCCCC	0.463	
-	1	185	CL1_uc001eva.2	NM_021960	NP_068779	Q07820	MCL1_HUMAN		0	GCCGGCCCCCC	0.682	
-	2	1111_1113	wne.1_In_Frame_	NM_007113	NP_009044	Q07283	TRHY_HUMAN	of R-R-E-Q-E-E- E-R-R-E-	5	tcgcgcctctcctcctcc	0	rs71757496
-	3	11637_11638		NM_002016	NP_002007	P20930	FILA_HUMAN	grin 23.|Ser-rich.	16	ACTGTCACTGTC	0.574	
+	14	1756	p.S522fs|UBAP2L	NM_014847	NP_055662	Q14157	UBP2L_HUMAN		2	TCCTTTCTGATT	0.532	
-	7	811	hj.1_Frame_Shift_	NM_005998	NP_005989	P49368	TCPG_HUMAN		2	TGCATATTTTTTT	0.393	
-	11	2418	vsm.2_Frame_Shi	NM_031281	NP_112571	Q96RD9	FCRL5_HUMAN	otential).|Ig-like C2-type 8.	6	GGTGAGGACCG	0.512	
-	7	805	el_p.E178fs|CCD	NM_012337	NP_036469	Q9UL16	CCD19_HUMAN	Potential.	1	TCTGTTCCACAA	0.542	
-	1	507		NM_172000	NP_741997	Q5T9Z0	TEDM1_HUMAN		2	CAGCTCCACCC	0.522	
+	21	3318	grr.1_Frame_Shif	NM_031935	NP_114141	Q96RW7	HMCN1_HUMAN	like C2-type 7.	23	TTCAGCAGGAG	0.453	
+	8	1331_1332	D55_uc009xcf.2_	NM_000574	NP_000565	P08174	DAF_HUMAN	Ser/Thr-rich.	1	CCCAAATAAAGG	0.421	
-	3	2320		NM_002221	NP_002212	P27987	IP3KB_HUMAN		5	ATGACGAAGGG	0.468	
-	10	1052	C13_uc001hug.3_	NM_024525	NP_078801	Q8NBP0	TTC13_HUMAN	TPR 5.	2	CTTTTGAAAGC	0.423	
-	1	63_65	ne_Del_p.C11del|	NM_024525	NP_078801	Q8NBP0	TTC13_HUMAN		2	CCcagaagcagcag	0.557	
+	3	1545	p.K278fs|RPP38_	NM_183005	NP_892117	P78345	RPP38_HUMAN		1	AAAGTAAAAAA	0.358	
+	6	1209		NM_030912	NP_112174	Q9BZR9	TRIM8_HUMAN		1	AGTGTCCCCCT	0.647	
+	12	2642	p.1_Frame_Shift_	NM_014720	NP_055535	Q9H2G2	SLK_HUMAN	Potential.	8	AGAGTAAAAAG	0.348	
-	11	1772	1mda.2_Splice_Si	NM_001164	NP_001155	O00213	APBB1_HUMAN		2	ACATACCAACA	0.483	
-	17	2371	rcv.1_Frame_Shif	NM_175058	NP_778228	Q6IQ23	PKHA7_HUMAN	Potential.	3	CTGTTCCACAT	0.458	
+	3	514	1nqk.2_Frame_S	NM_178031	NP_821174	Q24JP5	T132A_HUMAN	ellular (Potential).	1	GTGGTCCCCCC	0.587	
-	5	6102	AK_uc001ntk.1_I	NM_001620	NP_001611	Q09666	AHNK_HUMAN		19	ACTTTGGGGCC	0.502	
-	3	1341	oop.3_Frame_Sh	NM_001098515	NP_001091985	Q96AM1	MRGRF_HUMAN	lasmic (Potential).	0	TGCTGCCCCCG	0.716	
-	9	1311_1312	_Shift_Del_p.R353fs|CHRDL2_uc001ovj.1_RNA|CHRD			Q6WN34	CRDL2_HUMAN		0	GCAAAGCGACG	0.614	
+	66	10279	Shift_Del_p.I3386	NM_001080463	NP_001073932	Q8NCM8	DYHC2_HUMAN	5 (By similarity).	0	CTTTTATTCCAC	0.358	
-	13	1569	p.Q477fs|TREH_u	NM_007180	NP_009111	O43280	TREA_HUMAN		1	TGACTTCTGCGA	0.607	
+	6	1157		NM_032873	NP_116262	Q8TF42	UBS3B_HUMAN	SH3.	1	CTATACCCCAC	0.552	rs141920402
-	3	350	RP11_uc001qm	NM_020367	NP_065100	Q9NR21	PAR11_HUMAN	WWE.	2	GGGCTCTTTTTA	0.343	

+	11	1217	353fs|DYRK4_uc	NM_003845	NP_003836	Q9NR20	DYRK4_HUMAN	rotein kinase.		3	GGGGGAAAAAA	0.398	
+	2	413_414	23_uc001qrq.2_	NM_001135217	NP_001128689	Q53EV4	LRC23_HUMAN			1	GATCTAGAAGAC	0.322	
+	5	882	6_uc001raa.1_5'	NM_001987	NP_001978	P41212	ETV6_HUMAN			250	CCGGTCCCCCC	0.632	
+	18	1962_1963	BP1_uc001ria.2_	NM_003622	NP_003613	Q86W92	LIPB1_HUMAN			5	GGGGCTTTTTT	0.495	
-	9	944	p.E280fs|SMARC	NM_003075	NP_003066	Q8TAQ2	SMRC2_HUMAN			6	CACCTCATCTG	0.433	
-	2	164_166	p.V29del|STAT2_u	NM_005419	NP_005410	P52630	STAT2_HUMAN			3	ATGTCCACAGG	0.542	
-	1	323_325		NM_139283	NP_644812	Q8NI37	PPTC7_HUMAN	Gly-rich.		0	CGTAGTcgccgcc	0.611	
-	18	2045_2046	_Shift_Del_p.H64	NM_024953	NP_079229	Q14CX7	NAA25_HUMAN			3	TTTCTTATGTTC	0.356	
-	3	558_559	_Shift_Del_p.G99f	NM_032314	NP_115690	Q5HYK3	COQ5_HUMAN			1	GCTTTCCAACCT	0.46	
+	4	502	_uc001tzo.2_RNA	NM_002562	NP_002553	Q99572	P2RX7_HUMAN			5	GTTGTAAAAAG	0.522	
-	4	841	AP1_uc001uep.2_	NM_004642	NP_004633	O14519	CDKA1_HUMAN			0	TTCTGCCAAGC	0.498	
+	6	2495_2496	p.T222fs|ZNF664_	NM_152437	NP_689650	Q8N3J9	ZN664_HUMAN			0	CACACAGGAG	0.515	
+	2	812_813	k|CMTM5_uc010a	NM_022789	NP_073626	Q9H293	IL25_HUMAN			1	TAGCTTGTGTGT	0.604	
-	1	173	1xki.1_Frame_Sh	NM_004926	NP_004917	Q07352	TISB_HUMAN			1	AACTTCGCTCA	0.532	
+	21	3242	0tty.1_Frame_Shi	NM_173462	NP_775733	O95428	PPN_HUMAN			3	CTGCTGGGCCC	0.667	
-	8	1077_1078	9_uc001xrk.2_5'	NM_033116	NP_149107	Q8TD19	NEK9_HUMAN	rotein kinase.		5	TTCCTGAGAAGA	0.396	
-	2	865	c001ynj.1_Frame_	NM_004873	NP_004864	Q9UL15	BAG5_HUMAN	BAG 3.		2	GGTCTCATTGT	0.527	
+	7	1741_1742	p.S557fs|C15orf5	NM_175741	NP_786883	Q86Y26	NUT_HUMAN			30	TTCTTCAGGAAA	0.604	
-	13	1716	bfi.1_Frame_Shift	NM_182758	NP_877435	Q3MJ13	WDR72_HUMAN	WD 8.		2	ACAGGAAAAAG	0.463	
-	2	158_159	cyh.2_RNA|NAG	NM_016256	NP_057340	Q9UK23	NAGPA_HUMAN	enal (Potential).		0	GGAGGCGCGC	0.767	
+	12	1765_1766	p.L545fs|TMC7_u	NM_024847	NP_079123	Q7Z402	TMC7_HUMAN	ellular (Potential).		3	GTCCTGGGGATA	0.49	
+	24	4368		NM_015202	NP_056017	O60303	K0556_HUMAN			8	TCCCTGGAGGG	0.627	
+	1	694	2eca.3_Frame_Sh	NM_001105247	NP_001098717	Q96C12	ARMC5_HUMAN			1	GCAGCGGGGG	0.746	
-	2	214_215	1_5'UTR|SALL1_	NM_002968	NP_002959	Q9NSC2	SALL1_HUMAN			8	CTTCTTGTGGAG	0.485	
+	3	466_467	25_uc002fpc.2_5'	NM_014972	NP_055787	Q9BQ70	TCF25_HUMAN			0	AAGAAGAAAAA	0.406	
+	15	1616	p.F362fs|PLD2_u	NM_002663	NP_002654	O14939	PLD2_HUMAN	Catalytic.		5	TTCTTCTGGCT	0.617	
+	6	794	BG_uc010cmw.2_	NM_001040	NP_001031	P04278	SHBG_HUMAN	minin G-like	p.0?(1)|p.?(1)	0	TCTTTGGACCT	0.567	
+	54	8561_8562		NM_020877	NP_065928	Q9P225	DYH2_HUMAN	4 (By similarity).		13	CCTGATGAATTT	0.51	
-	27	3596_3597	uc002gml.1_Intron	NM_002472	NP_002463	P13535	MYH8_HUMAN	Potential.		11	CTTCTTGTTCAA	0.589	
-	23	2989_2990	.3_Frame_Shift_D	NM_001100112	NP_001093582	Q9UKX2	MYH2_HUMAN	Potential.		14	AGTTCTGAACAT	0.436	
-	33	4838		NM_002470	NP_002461	P11055	MYH3_HUMAN	Potential.		7	CTCTTCAGCTG	0.502	
-	8	974	IGS_uc010wap.1_	NM_005165	NP_005156	P09972	ALDOC_HUMAN			1	TTCTTCGCTCT	0.572	
-	4	1109_1110	EZ6_uc002hdq.1_	NM_178860	NP_849191	Q53EL9	SEZ6_HUMAN	ellular (Potential).		2	TCAGGCCCCC	0.614	
-	6	1221		NM_181534	NP_853512	Q7Z3Z0	K1C25_HUMAN	Rod.|Coil 2.		2	CTCCTATAAGG	0.468	
+	16	2610	AP1_uc010wgs.1	NM_003632	NP_003623	P78357	CNTP1_HUMAN	ellular (Potential).		8	CGCTTCCCCCC	0.567	
-	5	632	ARSD1_uc002icg	NM_025267	NP_079543	Q9BTE6	AASD1_HUMAN			0	CACCTTGATATC	0.512	
+	4	312	rame_Shift_Del_p	NM_144608	NP_653209	Q96MH2	HEXI2_HUMAN			0	CCTCTGGTGCC	0.587	
+	5	1488	_p.I249fs|NFE2L1	NM_003204	NP_003195	Q14494	NF2L1_HUMAN	Glu-rich (acidic).		1	AGCATAACAGA	0.493	
-	4	643_644		NM_005121	NP_005112	Q9UHV7	MED13_HUMAN			2	TCACTGAGAAG	0.361	
-	10	1809_1811	.N582del|UBE2O_	NM_022066	NP_071349	Q9C0C9	UBE2O_HUMAN			5	ACTCGTTGTTG	0.611	
-	16	2567	dw.1_Frame_Shif	NM_004104	NP_004095	P49327	FAS_HUMAN	l transferases (By similarity		1	CAGGTGGGAAC	0.657	
+	13	2103	_uc010xbp.1_Spli	NM_001942	NP_001933	Q02413	DSG1_HUMAN			7	TCAGGTAAGAA	0.284	
-	1	976	Del_p.G320fs|ZBT	NM_001039360	NP_001034449	A1YPR0	ZBT7C_HUMAN	Pro-rich.		1	AGAGGCCCCCC	0.627	rs113275715
+	33	7140	.P2352fs|SPTBN4	NM_020971	NP_066022	Q9H254	SPTN4_HUMAN			5	AGCTTCCCCCA	0.488	
+	14	2665_2666	NRNPUL1_uc002	NM_007040	NP_008971	Q9BUJ2	HNRL1_HUMAN	cessary for interaction with		2	GGTTACAACCCG	0.629	
+	16	2323_2325	T3_uc002qdk.1_	NM_014516	NP_055331	O75175	CNOT3_HUMAN			3	GACACTCTTCTT	0.69	
+	11	1757_1759	me_Del_p.L480del	NM_006669	NP_006660	Q8NHL6	LIRB1_HUMAN	ical; (Potent	p.L479del(1)	3	tcctactgctcctcctcc	0.458	

-	2	269_270	2qwk.2_RNA|uc00	NM_152834	NP_690047	Q96B42	TMM18_HUMAN	ical; (Potential).	1	CACCTAGACACA	0.48	
+	3	545		NM_016441	NP_057525	Q9NZV1	CRIM1_HUMAN		3	CTTTTAGAAGAG	0.48	
-	11	2105_2107	A1L_uc002rwt.2_	NM_000233	NP_000224	P22888	LSHR_HUMAN	lasmic (Potential).	8	GACAACTTCAAG	0.409	
+	1	1649	T10_uc002tex.2_5	NM_023016	NP_075392	Q53LP3	ANR57_HUMAN		0	GGGCAGGGGGG	0.517	
+	12	2021	nt.3_Frame_Shift_	NM_005270	NP_005261	P10070	GLI2_HUMAN		13	GTCCTGCAGCA	0.662	
-	9	1835_1836	uiv.2_Frame_Shif	NM_001033045	NP_001028217	Q7Z3F1	GP155_HUMAN	ical; (Potential).	1	TTATTCCAACAG	0.366	
-	4	1604_1605	_p.E71fs|PDE11A_	NM_016953	NP_058649	Q9HCR9	PDE11_HUMAN	GAF 2.	4	ATGTCCTCTAGG	0.347	
+	48	3839		NM_000090	NP_000081	P02461	CO3A1_HUMAN	lar collagen NC1.	13	AGTCTGTTAATG	0.423	
+	10	1952	uxm.1_Frame_Shi	NM_032974	NP_116756	Q92851	CASPA_HUMAN		6	CTCGACCCCCC	0.572	
+	46	7217	AL1_uc002uzs.3_	NM_001114132	NP_001107604	Q6ZS30	NBEL1_HUMAN		2	AGCCAACCAAAA	0.333	
-	4	763_764	_p.E166fs|FN1_uc	NM_212482	NP_997647	P02751	FINC_HUMAN	-binding 1.|Fibronectin type	13	CACACACTCTAA	0.49	
+	1	602_603		NM_001927	NP_001918	P17661	DESM_HUMAN	Rod.|Coil 1B.	2	ACCAGCGCGC	0.693	rs60538473
-	2	256	119_uc002wvs.2_	NM_153289	NP_695021	Q8N690	DB119_HUMAN		0	GAGGTAGGGCT	0.443	
-	13	1134		NM_080675	NP_542406	Q8TC36	SUN5_HUMAN	SUN.	1	GGGTTCCCCCA	0.587	
-	3	2376_2377	_Shift_Ins_p.K66	NM_015035	NP_055850	Q9H4I2	ZHX3_HUMAN	Homeobox 3.	3	ATTCACTTTTTT	0.5	
+	5	759	_p.T88fs|DBNDD	NM_001048225	NP_001041690				0	ACCAACCCCCC	0.562	
+	4	1167	02xpx.2_Frame_	NM_033421	NP_219489	Q969T3	SNX21_HUMAN		2	CACCACCCCCC	0.617	
+	14	1882_1883		NM_005049	NP_005040	Q15269	PWP2_HUMAN		1	AGATTACAGCCA	0.594	
-	21	3374_3376	agl.1_In_Frame_	NM_015241	NP_056056	Q7RTP6	MICA3_HUMAN	Glu-rich.	0	cgtcatagtcctcctcct	0.33	
-	8	995	_Shift_Del_p.E241	NM_022719	NP_073210	Q96DF8	DGC14_HUMAN		1	AACCTCCCCCC	0.597	
+	7	872	ua.1_Frame_Shift	NM_014291	NP_055106	O75600	KBL_HUMAN		0	TCCCTGCTGCG	0.657	
-	3	292_294	M40_uc003bxi.1_	NM_018306	NP_060776	Q8WWA1	TMM40_HUMAN	Ser-rich.	0	gaggaagaggaggag	0.256	
-	23	2605	.1_Frame_Shift_D	NM_015199	NP_056014	O15084	ANR28_HUMAN		1	CTTTTGAATCTG	0.259	
+	1	158	c010hhd.2_5'UTR	NM_005107	NP_005098	Q9Y2C4	EXOG_HUMAN		0	CTTCGTGGCTG	0.657	
-	3	337_338		NM_000094	NP_000085	Q02388	CO7A1_HUMAN	region (NC1).|VWFA 1.	11	CCCCTTGTAGCT	0.614	
+	49	5198_5199		NM_004947	NP_004938	Q8IZD9	DOCK3_HUMAN		0	CAAGGCTCAGTC	0.55	rs114813991
-	5	1184_1185		NM_000097	NP_000088	P36551	HEM6_HUMAN		0	ATGTAAGAAGGA	0.51	
-	41	5882		NM_014981	NP_055796	Q9Y2K3	MYH15_HUMAN	Potential.	7	CATACCTTTTTCC	0.368	
+	4	1562		NM_139209	NP_631948	Q8WTQ7	GRK7_HUMAN	kinase C-terminal.	5	GGTTCGGGGGG	0.463	
-	2	826	.1_Intron|MED12L	NM_176894	NP_795713	Q9BPV8	P2Y13_HUMAN	Name=6; (Potential).	4	TGGAGCAAAACA	0.353	
+	12	1339_1340	2_Frame_Shift_De	NM_004068	NP_004059	Q96CW1	AP2M1_HUMAN	MHD.	0	CCATTCGCGCCC	0.559	
+	14	2416	711fs|FAM193A_u	NM_003704	NP_003695	P78312	F193A_HUMAN		3	CACCTGCCTCCA	0.627	
+	10	1533_1534	Shift_Ins_p.P205fs	NM_001113361	NP_001106832	Q9P2M4	TBC14_HUMAN	ab-GAP TBC.	2	TGGTCCATATCA	0.416	
-	1	457	uc003hei.1_Intron	NM_001073	NP_001064	O75310	UDB11_HUMAN		3	ATCTGCAAAAA	0.383	
-	1	122_124	20del|NAAA_uc00	NM_014435	NP_055250	Q02083	NAAA_HUMAN		1	CGGCCAGCAGC	0.764	
-	3	2689_2691	ML3_uc011chd.1_I	NM_018717	NP_061187	Q96JK9	MAML3_HUMAN	Gln-rich.	1	GGTGGCGgctgctg	0.419	
-	2	565	e.3_5'Flank|MTRF	NM_024091	NP_076996	Q14CZ7	FAKD3_HUMAN		4	CCATCCTTTTTTT	0.418	
+	1	402		NM_031916	NP_114122	Q96C74	ROP1L_HUMAN		1	CGGGGTAAGCG	0.683	
-	6	1423	3jie.2_Frame_Shif	NM_016180	NP_057264	Q9UMX9	S45A2_HUMAN	Name=10; (Potential).	3	TGAGGTTAAAG	0.527	
+	11	1863	p.E534fs|BDP1_u	NM_018429	NP_060899	A6H8Y1	BDP1_HUMAN		2	TCCACTGAAAAA	0.313	
-	3	913	ame_Shift_Del_p.	NM_014790	NP_055605	Q96AA8	JKIP2_HUMAN	Potential.	2	GATTTTATCTGCT	0.517	
-	13	1336	_p.E355fs|DCTN4_	NM_016221	NP_057305	Q9UJW0	DCTN4_HUMAN		1	ACCCTCCTCAC	0.428	rs139876545
+	11	2401	p.G581fs|LARP1_	NM_033551	NP_291029	Q6PKG0	LARP1_HUMAN		4	ACCCAGGGGGG	0.547	
+	19	2885	_p.S931fs|WWC1_	NM_015238	NP_056053	Q8IX03	KIBRA_HUMAN	ion with histone H3.	5	CTTCTCCCCAG	0.582	
-	16	2462_2464	L795del|FLT4_uc	NM_002020	NP_002011	P35916	VGFR3_HUMAN	ical; (Potential).	15	AGATGAGGAGG	0.581	
+	1	669_670		NM_138574	NP_612641	Q5TGJ6	HDGL1_HUMAN	a-rich.|Glu-rich.	0	gcggagagggcggcg	0.51	
+	51	7150_7151	ey.2_Frame_Shift	NM_002224	NP_002215	Q14573	ITPR3_HUMAN	cellular (Potential).	19	GGGGCTATAAGG	0.559	

+	4	612	jwu.2_Frame_Shif	NM_015050	NP_055865	Q8N1G2	MTR1_HUMAN	G-patch.	5	GGCTTCCAGTC	0.527	
-	6	706	e_Shift_Del_p.L2	NM_145027	NP_659464	Q6ZMV9	KIF6_HUMAN	inesin-motor.	3	TCTCCTAAAAAA	0.398	
+	46	5073	UBR2_uc011dut.1	NM_015255	NP_056070	Q8IWV8	UBR2_HUMAN		4	AGGCTGTTTTTA	0.458	
+	6	1837	vf.1_Frame_Shift_	NM_003131	NP_003122	P11831	SRF_HUMAN		3	GGCGTCCCCCA	0.502	
-	2	110_111	A3_uc010jzq.2_In	NM_000847	NP_000838	Q16772	GSTA3_HUMAN	ST N-terminal.	0	GTCCATTGAAG	0.406	
-	2	4936_4937	.K458fs|CNR1_u	NM_001160260	NP_001153732	P21554	CNR1_HUMAN	lasmic (Potential).	2	GTTACCTTGGC	0.515	
-	2	1027	5_uc003pwh.3_F	NM_153612	NP_705840	Q8IZT8	HS3S5_HUMAN	enal (Potential).	2	TTTTGATTAAAAG	0.423	
-	8	1254_1267	_p.K73fs|HBS1L_u	NM_006620	NP_006611	Q9Y450	HBS1L_HUMAN		2	GGAATGAAGTC	0.364	rs113799065
-	4	366	_p.P87fs|PRKAR1	NM_002735	NP_002726	P31321	KAP1_HUMAN	n and phosphorylation.	0	GGTTCGGGGGG	0.617	
-	2	967_968	11_uc003syy.2_R	NM_005523	NP_005514	P31270	HXA11_HUMAN	Homeobox.	2	TGTTAATTTTTT	0.446	
+	13	1877	1_Splice_Site_p.G	NM_005228	NP_005219	P00533	EGFR_HUMAN		9571	AGGGGTAGGAG	0.517	
-	2	106_107		NR_003949					0	ACCTTCATCCAT	0.505	
-	5	5233	hv.2_Frame_Shift_	NM_033026	NP_149015	Q9Y6V0	PCLO_HUMAN		7	ACTTTTAGTTTC	0.398	
+	5	890_892	_p.L86del|CLDN12	NM_012129	NP_036261	P56749	CLD12_HUMAN	ellular (Potential).	0	CGTGTCCTCCA	0.576	
-	2	390_392	kiw.1_In_Frame_	NM_015545	NP_056360	O75127	PTCD1_HUMAN		1	AACTCTCCTCC	0.606	
+	10	1125_1126	A43_uc003usa.1_	NM_057095	NP_476436	Q9HB55	CP343_HUMAN		2	CCCAATAAGGT	0.495	
-	16	1707	PW1_uc003uus.2_	NM_017984	NP_060454	Q9H0M4	ZCPW1_HUMAN		0	CTTGGTTTTTT	0.478	
-	15	1785	.*336fs|PSMC2_	NM_206884	NP_996767	P58743	S26A5_HUMAN	lasmic (Potential).	1	tcccctACGGTCTC	0.065	
+	11	2589	MET_uc011kni.1_	NM_000245	NP_000236	P08581	MET_HUMAN	r (Potential).|IPT/TIG 3.	159	CTGTTGTACCA	0.408	
+	1	3		NM_001004488	NP_001004488	A4D2G3	O2A25_HUMAN	ellular (Potential).	0	GAAATGGGGGG	0.443	
-	9	1803		NM_004911	NP_004902	P13667	PDIA4_HUMAN	hioredoxin 3.	6	CTCACCTTTTTT	0.612	
+	1	793_795		NM_138400	NP_612409	Q5C9Z4	NOM1_HUMAN	ization and for targeting P	0	gaaagtgaggaggag	0.236	
-	1	1080_1081		NM_000025	NP_000016	P13945	ADRB3_HUMAN	ame=6; (By similarity).	2	GAGACCCAAG	0.589	
+	8	1064	yhu.1_Frame_Shif	NM_014754	NP_055569	P48651	PTSS1_HUMAN	ical; (Potential).	1	AAGTTGGGGTA	0.408	
+	2	176	1_uc010mec.2_F	NM_003882	NP_003873	O95388	WISP1_HUMAN		2	TGGACTTTACC	0.672	
-	3	413	1lkh.1_Frame_Shif	NM_145201	NP_660202	Q6XQN6	PNCB_HUMAN		1	CACCACCAGGA	0.741	
+	11	2242_2243	D7_uc010msp.1_	NM_014290	NP_055105	Q8NHU6	TDRD7_HUMAN		3	TGCCTTGTAAG	0.426	
-	3	1008_1009	axz.2_Frame_Shif	NM_197978	NP_932095	Q9BXL5	HEMGN_HUMAN		1	TTGTATTTTAGG	0.366	
+	1	9		NM_001004457	NP_001004457	Q8NGR9	OR1N2_HUMAN	ellular (Potential).	4	GAAGGTTTTTA	0.274	
-	1	681	2_uc004btl.2_Intro	NM_025072	NP_079348	Q9H7Z7	PGES2_HUMAN	ical; (Potential).	0	GGGCTCCCCCC	0.677	
-	8	993_994	RAPGEF1_uc010	NM_005312	NP_005303	Q13905	RPGF1_HUMAN	H3-binding.	7	TTCTTGGGTGG	0.574	
-	15	3936_3938	C2_uc004dsc.2_3	NM_001111125	NP_001104595	Q5JU85	IQEC2_HUMAN	-rich.|His-rich.	3	GCCAtgatggtggtg	0.586	
+	10	1256_1257	|PIAS3_uc001eod	NM_006099	NP_006090	Q9Y6X2	PIAS3_HUMAN		1	TTCTTAGTTCCT	0.465	
-	1	299	2BE_uc001etc.2_	NM_175065	NP_778235	Q8IUE6	H2A2B_HUMAN		2	TGACACCCCCG	0.557	rs149336231
+	2	672		NM_001025231	NP_001020402	Q5T749	KPRP_HUMAN	Gln-rich.	5	CTACACCCCCC	0.572	
-	11	2245_2247	H700del|PBXIP1_	NM_020524	NP_065385	Q96AQ6	PBIP1_HUMAN	His-rich.	1	CCCCGGTGGTG	0.64	rs143592003
+	7	817	2_Frame_Shift_De	NM_001005388	NP_001005388	O94856	NFASC_HUMAN	otential).|Ig-like C2-type 2.	6	TGCAACCCCCC	0.562	
-	2	1141_1142		NM_004778	NP_004769	Q9Y5Y4	GPR44_HUMAN	lasmic (Potential).	1	GAGGTGCGGC	0.748	rs55642873
-	2	598_600	1orf95_uc001nxs.	NM_001144936	NP_001138408	C9JLR9	CK095_HUMAN	Glu-rich.	0	tcctcttcttcctcctcct	0.532	
-	1	372_374	_p.L35del|LTBP3_	NM_001130144	NP_001123616	Q9NS15	LTBP3_HUMAN	Gly-rich.	3	caggcccagcagcag	0.325	
+	3	321_323	me_Del_p.E98del|	NM_033388	NP_203746	Q8NAA4	A16L2_HUMAN		0	TGGCAGGAGGA	0.591	
+	8	1729	p.H104fs|USPL1_	NM_005800	NP_005791	Q5W0Q7	USPL1_HUMAN		3	TTGCAGCACTAT	0.348	
+	6	2499	10ujg.1_Frame_S	NM_004727	NP_004718	O60721	NCKX1_HUMAN	lasmic (Potential).	0	ATCAGAAGGAG	0.522	
+	2	249	ewp.1_5'Flank|CI	NM_032830	NP_116219	Q969X6	CIR1A_HUMAN	WD 1.	0	TTTCAGGAGAA	0.368	
+	15	2559	H18_uc010chw.2_	NM_144604	NP_653205	Q86VM9	ZCH18_HUMAN		1	CAGCAGGGGGG	0.547	rs139579046
-	32	5122		NM_006445	NP_006436	Q6P2Q9	PRP8_HUMAN	on with pre-mRNA 5' splice	6	ATAGTCCCCCC	0.532	
-	21	2677_2678		NM_002208	NP_002199	P38570	ITAE_HUMAN	ellular (Potential).	4	CGGAGTTAGTTA	0.465	

+	2	303_304	_p.A12fs|EIF5A_u	NM_001970	NP_001961	P63241	IF5A1_HUMAN	OHH-binding.		0	CAGTGCTCAGC	0.525	
+	4	522	72fs|ENGASE_uc	NM_001042573	NP_001036038	Q8NFI3	ENASE_HUMAN		p.P172L(1)	1	CCATTCCCCCA	0.587	
+	2	125	1_5'Flank|HAUS1_	NM_138443	NP_612452	Q96CS2	HAUS1_HUMAN			1	GTGGTTAAAAA	0.393	
-	9	864	_p.R276fs|SEMA6	NM_032108	NP_115484	Q9H3T3	SEM6B_HUMAN	lar (Potential).|Sema.		1	CACGCGGGGGG	0.647	
+	14	2665_2666	NRNPUL1_uc002	NM_007040	NP_008971	Q9BUJ2	HNRL1_HUMAN	cessary for interaction with		2	GGTTACAACCC	0.629	
-	2	459	_Shift_Del_p.Q11	NM_002781	NP_002772	Q15238	PSG5_HUMAN	g-like V-type.		3	ATTCTGGATCA	0.418	
+	2	480	_Shift_Del_p.A14fs	NM_003089	NP_003080	P08621	RU17_HUMAN			0	CTTTGCCCCCC	0.542	
-	1	1911_1913		NM_002152	NP_002143	P23327	SRCH_HUMAN			1	tccagcccctcctcctc	0.409	
+	11	1757_1759	ne_Del_p.L480del	NM_006669	NP_006660	Q8NHL6	LIRB1_HUMAN	ical; (Potent	p.L479del(1)	3	tcctactgctcctcctcc	0.458	
-	3	316	_p.P92fs|HS1BP3	NM_022460	NP_071905	Q53T59	H1BP3_HUMAN	PX.		1	GTAGTGGGGGG	0.537	rs77941615
-	29	5686_5687	fnl.1_Frame_Shift_	NM_018557	NP_061027	Q9NZR2	LRP1B_HUMAN	ellular (Potential).		50	TTTTCATTTCTA	0.302	rs142525375
+	48	3839		NM_000090	NP_000081	P02461	CO3A1_HUMAN	lar collagen NC1.		13	GTCTGTTAATG	0.423	
-	18	3175	108_uc002vjm.3_	NM_194302	NP_919278	Q6ZU64	CC108_HUMAN			4	CTGCTCCAGGT	0.612	
+	15	3131	tm.2_Frame_Shift	NM_181659	NP_858045	Q9Y6Q9	NCOA3_HUMAN	Poly-Gln.		5	TATTGCAACAG	0.428	
-	1	3347_3348		NM_014246	NP_055061	Q9NYQ6	CELR1_HUMAN	(Potential).|Cadherin 9.		11	CTGTTGGACTTG	0.599	
-	7	2103	cbe.2_Frame_Shi	NM_014744	NP_055559	Q92609	TBCD5_HUMAN	ab-GAP TBC.		1	ACCCCTTCATCC	0.378	
+	1	158	c010hhd.2_5'UTR	NM_005107	NP_005098	Q9Y2C4	EXOG_HUMAN			0	CTTCGTGGCTG	0.657	
+	1	3375_3376		NM_175918	NP_787114	Q8N1N5	CRPAK_HUMAN	3		0	CTGCTCACACGT	0.708	
+	10	1533_1534	Shift_Ins_p.P205f	NM_001113361	NP_001106832	Q9P2M4	TBC14_HUMAN	ab-GAP TBC.		2	TGGTCCATATCA	0.416	
-	9	1111	_p.T322fs|RASGE	NM_152545	NP_689758	Q0VAM2	RGF1B_HUMAN	Ras-GEF.		0	CCCAAGTTTTTT	0.383	
-	27	13517	_p.P90fs|FAT1_uc	NM_005245	NP_005236	Q14517	FAT1_HUMAN	lasmic (Potential).		12	GCTGCGGGGAA	0.542	
-	2	624_625	_Shift_Del_p.S47f	NM_006451	NP_006442	Q9H074	PAIP1_HUMAN	eracting motif-2 (PAM2).		1	AGCTTAGACATT	0.46	
+	26	5893	c.3_Frame_Shift_	NM_080686	NP_542417	P48634	PRC2A_HUMAN			0	ACCTACCCCCC	0.522	
+	3	761		NM_003221	NP_003212	Q92481	AP2B_HUMAN			0	GTCATTAAAAAA	0.343	
+	2	172_174	X6AS_uc003uol.2_	NM_005222	NP_005213	P56179	DLX6_HUMAN			2	GGCTCGcaccacc	0.571	
+	1	138	_uc003utj.2_5'Fla	NM_152755	NP_689968	Q8N129	CNPY4_HUMAN			0	TTTTCCTTTTTTT	0.527	
+	4	451	l_p.R104fs|TMEM	NM_153345	NP_699176	Q8IV31	TM139_HUMAN	lasmic (Potential).		0	TGCCGCCCCCA	0.567	
-	7	1685_1687	1kvs.1_In_Frame_	NM_007349	NP_031375	Q6ZW49	PAXI1_HUMAN	Gln-rich.		5	TTTGCATctgctgct	0.227	
-	6	1034	11lir.1_Frame_Shi	NM_014846	NP_055661	Q12768	STRUM_HUMAN			2	CTGGTTGTAAAT	0.388	
+	3	244		NM_183241	NP_899064	Q9BUH6	CI142_HUMAN			0	CATCACCCCCC	0.657	
-	9	1541_1542	nk|ENTPD2_uc0	NM_203468	NP_982293	Q9Y5L3	ENTP2_HUMAN			0	CCCCTAAATGGT	0.416	rs17853460
-	2	1659_1661	.2_In_Frame_Del_	NM_173691	NP_775962	Q4KMQ1	TPRN_HUMAN	Glu-rich.		0	tcttcctcttcctcctcctc	0.374	
-	5	1775_1776	0ndi.2_Frame_Shi	NM_181332	NP_851849	Q8N0W4	NLGNX_HUMAN	ellular (Potential).		4	CAGTCTGTGTA	0.579	
-	11	1496	id.2_Frame_Shift_	NM_006950	NP_008881	P17600	SYN1_HUMAN	Pro-rich linker.		1	GAGCCGGGGGC	0.672	
+	4	763	|TSPY4_uc004frq	NM_001077697	NP_001071165	P0CW01	TSPYA_HUMAN			0	GTATCTGGATTAT	0.493	
-	13	2591	e_Shift_Del_p.Q5	NM_003819	NP_003810	Q13310	PABP4_HUMAN	PABC.	NA	0	TTCCTGGGGGG	0.602	
-	2	393_395	P2_uc001dmy.1_	NM_004120	NP_004111	P32456	GBP2_HUMAN		NA	1	ATCGCCACCAC	0.527	
-	2	2734_2736	wne.1_In_Frame_	NM_007113	NP_009044	Q07283	TRHY_HUMAN	0 AA tande	NA	5	GTAGCTCCTCC	0.586	rs143222885
+	2	1416	_Shift_Del_p.V84f	NM_020318	NP_064714	Q9BXP8	PAPP2_HUMAN		NA	16	CCCGTGGGGGA	0.567	
-	14	2554	29A_uc001grb.1_	NM_052966	NP_443198	Q9BZQ8	NIBAN_HUMAN	Glu-rich.	NA	4	GAAATCCCCCC	0.672	
-	5	1798	AGT_uc009xff.2_F	NM_000029	NP_000020	P01019	ANGT_HUMAN		NA	0	AGCTCAAAAAA	0.562	
+	30	4013_4015	f.2_Intron|CEP164	NM_014956	NP_055771	Q9UPV0	CE164_HUMAN		NA	2	CAGTCGCCGCC	0.67	
-	2	1302	raq.2_Frame_Shift	NM_006143	NP_006134	Q15760	GPR19_HUMAN	lasmic (Pote	NA	1	ACGTAGTTTTTTT	0.398	
+	18	1613	fs|TENC1_uc001s	NM_170754	NP_736610	Q63HR2	TENC1_HUMAN	Pro-rich.	NA	2	GCAGACCCCCC	0.677	rs142183380
-	6	959	p.K272fs|RBM19_	NM_001146699	NP_001140171	Q9Y4C8	RBM19_HUMAN		NA	6	GGTCTCTTTTTC	0.637	
-	15	2654	vfj.2_Frame_Shift_	NM_012141	NP_036273	Q9UL03	INT6_HUMAN		NA	2	TGGTCCTTTTCC	0.398	
+	3	481_483	p.E95del|APBA2_	NM_005503	NP_005494	Q99767	APBA2_HUMAN	Poly-Glu.	NA	0	CCCTGAGGAGG	0.601	

+	11	1617_1622	ove.2_In_Frame_D	NM_005587	NP_005578	Q02078	MEF2A_HUMAN	Gln/Pro-rich	NA	1	GCTTCcagcagcag	0.495	
+	12	3846_3848	ne_Del_p.Q812del|	NM_006599	NP_006590	O94916	NFAT5_HUMAN	Poly-Gln.	NA	0	AATcaacagcagcag	0.389	
+	8	912_914	.L222del|CHRNB1	NM_000747	NP_000738	P11230	ACHB_HUMAN	ical; (Potent	NA	2	GTTCCTGCTGCT	0.498	
-	5	1364	C16A6_uc002jha.	NM_004694	NP_004685	O15403	MOT7_HUMAN	ical; (Potent	NA	0	AAACCCAAAAAAT	0.438	
+	20	2951	0195_uc010wsb.1_	NM_014738	NP_055553	Q12767	K0195_HUMAN		NA	1	CGAGATCCCCCC	0.612	
+	4	988	_5'Flank|ICAM4_uc	NM_000201	NP_000192	P05362	ICAM1_HUMAN	cellular (Pote	NA	1	GTCAGCCCCCG	0.637	
+	20	1991_1993	p.F341del|SLC44A	NM_020428	NP_065161	Q8IWA5	CTL2_HUMAN	cellular (Pote	NA	1	TGGCTTTCTTCT	0.493	
+	6	841	2_Frame_Shift_De	NM_002255	NP_002246	Q99706	KI2L4_HUMAN		NA	1	TGCTCCAAAAAA	0.532	rs66505238
-	4	557	0yoq.1_Splice_Sit	NM_014614	NP_055429	Q14997	PSME4_HUMAN		NA	5	GAACTGGGGGG	0.347	
+	5	1137_1139	ypt.1_In_Frame_D	NM_014562	NP_055377	P32242	OTX1_HUMAN	His-rich.	NA	2	ccaccatcaccaccac	0.542	
+	3	782_783	Intron|TEKT4_uc0	NM_144705	NP_653306	Q8WW24	TEKT4_HUMAN		NA	3	CTCATCCGTACTC	0.663	rs35031477
-	28	4326	zcp.1_Frame_Shift	NM_007366	NP_031392	Q13018	PLA2R_HUMAN	Potential).|C	NA	3	AAAGCCTTTTTTT	0.403	
-	13	1637_1639	ame_Del_p.E417d	NM_001030311	NP_001025482	Q49MI3	CERKL_HUMAN		NA	4	TTTCATCCTCCT	0.369	
-	9	1595	p.K507fs|CLTCL1_	NM_007098	NP_009029	P53675	CLH2_HUMAN	lexible linke	NA	5	GTTACCTTTTTG	0.428	
+	5	1304_1306		NM_152612	NP_689825	Q8IYX3	CC116_HUMAN		NA	2	CCCCTGCAGCAG	0.606	
+	11	1513	.K344fs|CNTN6_u	NM_014461	NP_055276	Q9UQ52	CNTN6_HUMAN	like C2-type	NA	8	CCAGTTAAAAAAA	0.393	
-	6	1160	GOL1_uc003cbx.2	NM_001012410	NP_001012410	Q5FBB7	SGOL1_HUMAN		NA	0	TGTGCATTTTTTT	0.214	
-	2	2200_2203	Shift_Del_p.R660	NM_194293	NP_919269	Q702N8	XIRP1_HUMAN	Xin 15.	NA	8	GACGTGTCTGTC	0.618	
-	7	802_804	3clx.2_In_Frame_D	NM_020707	NP_065758	Q9HCP6	HHATL_HUMAN		NA	3	GCCCGAAGAAG	0.552	
-	20	7299	.A2410fs|CELSR3	NM_001407	NP_001398	Q9NYQ7	CELR3_HUMAN	cellular (Pote	NA	11	ACGGGCCCCCC	0.632	
-	2	758		NM_016206	NP_057290	A8MV65	VGLL3_HUMAN		NA	0	GCCATAGGGGGG	0.512	
-	5	1637	n|FILIP1L_uc010hp	NM_182909	NP_878913	Q4L180	FIL1L_HUMAN	Potential.	NA	1	CCTCCATTTTTAT	0.408	
+	2	398	_p.K62fs|TMEM22	NM_001097600	NP_001091069	Q8TBE7	TMM22_HUMAN		NA	1	GAAATGAAAAAAA	0.413	
-	6	873		NM_014465	NP_055280	O43704	ST1B1_HUMAN		NA	0	TAGTACAAAAAAA	0.348	
+	1	251_253	3hme.2_In_Frame_	NM_004464	NP_004455	P12034	FGF5_HUMAN		NA	2	GTCCTTCCTCCT	0.631	
-	61	9721_9722		NM_014991	NP_055806	Q8IZQ1	WDFY3_HUMAN	WD 1.	NA	3	TCTCCCACACAC	0.51	
+	3	714	TNL8_uc010jll.2_F	NM_001040462	NP_001035552	Q6UX41	BTNL8_HUMAN	2.|Extracellu	NA	2	CTGGTTCCCCCG	0.532	
+	1	209_211	3mtn.2_In_Frame_	NM_001452	NP_001443	Q12947	FOXF2_HUMAN	Poly-Ala.	NA	0	ccgccgcccgccgccg	0.172	rs78728576
+	11	2086	p.F668fs|HSP90A	NM_007355	NP_031381	P08238	HS90B_HUMAN		NA	4	CTGGCTTTTCCC	0.527	
-	8	1483	18_uc010kbq.1_In	NM_001080508	NP_001073977	O95935	TBX18_HUMAN		NA	5	GAGCTGGGGGG	0.537	
+	1	939_941	.G270del|ARID1B_	NM_017519	NP_059989	Q8NFD5	ARI1B_HUMAN	Gly-rich.	NA	2	ggcagcggaggagga	0.158	
+	5	833_835	TTYH3_uc003smc	NM_025250	NP_079526	Q9C0H2	TTYH3_HUMAN	Name=3; (P	NA	0	GGGCCTGCTGCT	0.709	rs146815577
+	11	1744		NM_152744	NP_689957	Q7Z5N4	SDK1_HUMAN	like C2-type	NA	6	GAATCGGGGGG	0.542	
-	1	915_917		NM_033224	NP_150093	Q96QR8	PURB_HUMAN		NA	0	TCTTCGCCGCCC	0.576	
+	2	334	3ule.2_Frame_Shi	NM_005751	NP_005742	Q99996	AKAP9_HUMAN		NA	26	AAGCAGAAAAAAA	0.353	
-	44	11828	.3_uc003wkx.2_5'F	NM_170606	NP_733751	Q8NEZ4	MLL3_HUMAN		NA	63	TCGTCCTTTTTCC	0.458	
-	15	2965	vyy.2_Frame_Shift_	NM_015310	NP_056125	Q9NYI0	PSD3_HUMAN		NA	3	CTTGTCGGGGGG	0.483	rs28651847
+	8	761	.P153fs|EPB49_u	NM_001114136	NP_001107608	Q08495	DEMA_HUMAN		NA	1	CCCAGCCCCCA	0.597	
-	7	735	p.K193fs|PTPLAD	NM_001010915	NP_001010915	Q5VWC8	HACD4_HUMAN	ic (Potential)	NA	1	CATCTTCTTTTTTT	0.368	
-	54	7719_7721	.2_In_Frame_Del_	NM_031407	NP_113584	Q7Z6Z7	HUWE1_HUMAN	p-rich.|Glu-ri	NA	17	cctcatcttcctcctcctc	0.438	
-	10	4018_4020	3_In_Frame_Del_p	NM_000489	NP_000480	P46100	ATRX_HUMAN	Poly-Asp.	NA	30	TGTCGTCATCATC	0.379	
-	4	447	P5_uc001hbv.1_F	NM_005057	NP_005048	Q15291	RBBP5_HUMAN			1	GAAGGGAATCGA	0.453	
+	3	712	2_uc009xch.2_Fra	NM_001877	NP_001868	P20023	CR2_HUMAN	xtracellular (Potential).		8	TGCTGTCCCCCC	0.398	
-	18	2120	uc009xhv.1_Frame_Shift_Del_p.K360fs|PITRM1_uc001			E7ES23	E7ES23_HUMAN			1	GACCGCTTTTTCT	0.478	
+	6	1517_1518		NM_000314	NP_000305	P60484	PTEN_HUMAN	hatase tensi	)|p.D162G(1)|p	2334	AGAGACAAAAAG	0.332	
+	9	1359	Shift_Del_p.F428fs	NM_004055	NP_004046	O15484	CAN5_HUMAN	Domain III.		0	TACATCTTCGAAG	0.308	
+	3	493_494	_p.Q51fs|FGFR1O	NM_015633	NP_056448	Q9NVK5	FGOP2_HUMAN	Potential.		0	GAAATTCAAGAAC	0.282	

+	3	707_710	vbk.2_Frame_Shif	NM_015116	NP_055931	Q9Y2L9	LRCH1_HUMAN	LRR 3.	2	CCGCCCTGCCTG	0.436	
-	1	113_115	01xml.2_In_Frame	NM_033141	NP_149132	P80192	M3K9_HUMAN	ı-rich.|Poly-Glu.	5	GCCGCCGcctcctc	0.68	rs3832971
-	14	1783_1784	0bib.2_Frame_Shif	NM_001004439	NP_001004439	Q9UKX5	ITA11_HUMAN	Extracellular (Potential).	3	CCTCCAGGGGGC	0.574	
+	13	3220_3222	|NKTR_uc003clq.1	NM_005385	NP_005376	P30414	NKTR_HUMAN		3	TGAAGAGGAGGA	0.355	
-	1	538_540	RC3_uc011cdn.1_Ir	NM_153757	NP_715638	Q96NT1	NP1L5_HUMAN	Glu-rich.	1	tactcctcttcctcctcctc	0.369	
+	4	994_996	ı.Q279del|MMRN1	NM_007351	NP_031377	Q13201	MMRN1_HUMAN	Poly-Gln.	4	.GCTGAGCAGCA	0.448	
+	7	1675_1676		NM_001718	NP_001709	P22004	BMP6_HUMAN		3	ATTCTGAAAAAT	0.446	
-	13	3188	p.K631fs|TRERF1	NM_033502	NP_277037	Q96PN7	TREF1_HUMAN	cts with CREBBP.	5	ATGACATTTTAAC	0.517	
-	4	765	.1_Intron|TARP_uc003tgf.1_RNA|TARP_uc003tgj.1_RN			A2JGV3	A2JGV3_HUMAN		0	CCTTGATTTTTTT	0.264	
-	2	317_319	EL1_uc009vlg.1_F	NM_033467	NP_258428	Q495T6	MMEL1_HUMAN	type II membrane protein;	0	GGTCACcagcagca	0.665	
-	8	1405_1406		NR_026567					0	ggcggcggcagcTGC	0.653	78439;rs67547754
-	9	1126_1131	1_Intron|MST1P9_	NR_002729					0	CCAGCGCTGGCA	0.704	
+	7	1510_1511	os.1_Frame_Shift_	NM_001134673	NP_001128145	Q12857	NFIA_HUMAN		2	TCCCTGGGAACG	0.554	
+	9	1992	27A3_uc009won.2_	NM_024330	NP_077306	Q5K4L6	S27A3_HUMAN		1	TGCGTCCCCCCC	0.617	
+	3	619	p.S161fs|HAX1_uc	NM_006118	NP_006109	O00165	HAX1_HUMAN	d in HCLS1 binding.	0	GTGAATCCCCCA	0.532	
-	2	718	p.V213fs|TNR_uc	NM_003285	NP_003276	Q92752	TENR_HUMAN	Cys-rich.	11	ACACACCCCCCC	0.607	
+	7	2540	Shift_Del_p.T737fs	NM_005807	NP_005798	Q92954	PRG4_HUMAN	K-X-P-X-P-T-T-X.|56; appro	1	CAACTACCCCCA	0.592	
-	3	615_616		NM_022735	NP_073572	Q9H3P7	GCP60_HUMAN	tential.|Glu-rich.	0	CTTCACCTTTTTT	0.411	
-	5	1984_1986	.E107del|PSD_uc	NM_002779	NP_002770	A5PKW4	PSD1_HUMAN	Poly-Glu.	3	CTCTGCCTCCTC	0.66	
-	2	586_588	ıme_Del_p.E162de	NM_001164	NP_001155	O00213	APBB1_HUMAN	Glu-rich. p.E162K(1)	2	catcatcatcctcctcctc	0.404	rs145320037
+	1	268_270		NM_001004460	NP_001004460	Q9H208	O10A2_HUMAN	Name=3; (Potential).	1	.TGTATTTCTTCTT	0.517	
-	10	1315	ı.Q434fs|PLEKHA7	NM_175058	NP_778228	Q6IQ23	PKHA7_HUMAN		3	CACCTGGGCCA	0.537	
-	14	1235	_Shift_Del_p.E357f	NM_005709	NP_005700	Q9Y6N9	USH1C_HUMAN	Potential.	1	AGTCTTCTTCCCA	0.498	
-	1	355		NM_001005284	NP_001005284	Q8NGQ1	OR9G4_HUMAN	Name=3; (Potential).	3	CACAGGAAAAAA	0.473	
-	9	1377	ntt.1_Frame_Shift_	NM_153265	NP_694997	Q32P44	EMAL3_HUMAN	WD 2.	1	GAAGGCCCCCA	0.592	
+	10	2065_2067	0rsp.1_In_Frame_	NM_020798	NP_065849	Q9P2H5	UBP35_HUMAN		3	CTGTCGCCGCCC	0.665	
+	6	1228		NM_004268	NP_004259	Q9NVC6	MED17_HUMAN		1	TTCAAATTAAATC	0.418	
-	4	670	F9B_uc001qgy.1_5	NM_014987	NP_055802	Q9UPX0	TUTLB_HUMAN	xtracellular (Potential).	0	GTACTGGGGGG	0.572	
-	3	812_814		NM_006248	NP_006239				0	TCCTGGAGGAGC	0.606	
+	88	13864		NM_002332	NP_002323	Q07954	LRP1_HUMAN	Interaction with MAFB (By s	22	GAACGTGGAGATT	0.567	
+	3	444	10srs.1_Frame_Sh	NM_001146258	NP_001139730	Q8TBX8	PI42C_HUMAN	PIPK.	3	TATTGTCCCCAGC	0.388	
+	3	552_553		NM_012240	NP_036372	Q9Y6E7	SIRT4_HUMAN	etylase sirtuin-type.	0	CTCCCCGGGGGC	0.579	
+	11	1513	1_5'UTR|DNAH10	NM_207437	NP_997320	Q8IVF4	DYH10_HUMAN	n (By similarity).	6	GTGACGGGGGA	0.478	rs148982654
+	46	8279_8281	00_uc001ujm.2_In	NM_015409	NP_056224	Q96L91	EP400_HUMAN	ith ZNF42 (By similarity).	12	aacagACGACGAC	0.34	
-	23	3282	f.1_RNA|TEP1_uc	NM_007110	NP_009041	Q99973	TEP1_HUMAN		5	GCCACACCCCCC	0.587	
+	6	1186	Shift_Del_p.E307fs	NM_015589	NP_056404	Q9UPU9	SMAG1_HUMAN		0	ATCGAGGGGGGC	0.637	rs137951039
-	65	12542_12543		NM_003922	NP_003913	Q15751	HERC1_HUMAN	RCC1 10.	19	CTCCTTGTAAGG	0.465	
-	11	1628_1630	AH3_uc002die.2_Ir	NM_017539	NP_060009	Q8TD57	DYH3_HUMAN	n (By similarity).	18	CGATCAGCAGCA	0.498	
-	2	210	199_uc002hba.2_5	NM_015584	NP_056399	Q9Y2S7	PDIP2_HUMAN		0	GGCTTTGCCACC	0.762	rs113730440
-	5	891		NM_139285	NP_644814	Q8NHY3	GA2L2_HUMAN		2	GGGCCGGGGGC	0.597	rs139867246
+	1	118	c002ibf.3_5'Flank|F	NM_005854	NP_005845	O60895	RAMP2_HUMAN		0	TAGGACCCGAGT	0.791	
-	3	1258	_p.G91fs|CA10_uc	NM_020178	NP_064563	Q9NS85	CAH10_HUMAN		2	TCCTGCCCCCCC	0.493	
-	2	452_455	.2_5'UTR|TIMP2_u	NM_003255	NP_003246	P16035	TIMP2_HUMAN	NTR.	2	TCTCACTGACCG	0.51	
+	12	6027	xq.2_Frame_Shift_	NM_030632	NP_085135	Q9C0F0	ASXL3_HUMAN		3	TGTTATCCCCCA	0.413	
-	5	640		NM_020714	NP_065765	Q9ULM2	ZN490_HUMAN	C2H2-type 1.	0	TATTAAGGGAGAC	0.433	
-	2	120_122		NM_000704	NP_000695	P20648	ATP4A_HUMAN	lasmic (Potential).	1	CCCGCCTTCTTC	0.601	
+	4	656_658	E183del|KLC3_uc	NM_177417	NP_803136	Q6P597	KLC3_HUMAN	Poly-Glu.	1	CAGCGAGGAGG	0.645	

-	11	1735		NM_021733	NP_068379	Q9UJT2	TSKS_HUMAN		2	TGCCTCCCCCC	0.552	
+	10	1050		NM_033068	NP_149059	Q9BZG2	PPAT_HUMAN	ellular (Potential).	0	AGCCTCCCCGG	0.682	
-	5	1962		NM_014650	NP_055465	O94892	ZN432_HUMAN	2H2-type 13.	3	AAGCCTTTTCC	0.398	
-	1	206		NM_176820	NP_789790	Q7RTR0	NALP9_HUMAN	DAPIN.	7	TTTGTCCAGCA	0.468	
-	8	1077	jy.1_Frame_Shift_	NM_015317	NP_056132	Q8TB72	PUM2_HUMAN	Ala-rich.	1	ATACACCCCCC	0.507	
+	37	5895	w.2_Frame_Shift_	NM_004341	NP_004332	P27708	PYR1_HUMAN	Linker.	10	CTGCACCCCCA	0.622	
+	2	1350_1352	.1_Intron|KIF3B_u	NM_004798	NP_004789	O15066	KIF3B_HUMAN	y-Glu.|Potential.	5	GGggaagaggagg	0.433	
-	1	912_914	zma.2_Intron|uc00	NM_031890	NP_114096	Q9BXQ6	CECR6_HUMAN		0	CAGCCCACCAC	0.709	
-	1	2553_2554		NM_002430	NP_002421	Q10571	MN1_HUMAN	Poly-Gln.	10	tgctgctgttgctgctgc	0.391	rs34890218
+	13	1587	p.T420fs|MTMR3_	NM_021090	NP_066576	Q13615	MTMR3_HUMAN	ularin phosphatase.	5	CCGCACCCCCC	0.547	
+	2	1890	.3_Intron|SYNGR	NM_006116	NP_006107	Q15750	TAB1_HUMAN		1	TGGGACCCCCC	0.592	
-	7	1050_1052	gye.1_In_Frame_	NM_020831	NP_065882	Q969V6	MKL1_HUMAN	Gln-rich.	5	GTGGTGCTGCT	0.66	
-	6	1160	GOL1_uc003cbx.	NM_001012410	NP_001012410	Q5FBB7	SGOL1_HUMAN		0	TGTGCATTTTTTT	0.214	
+	19	1660	yp.1_Frame_Shift	NM_005108	NP_005099	O75191	XYLB_HUMAN		1	CTTCTCCCCCA	0.502	
+	1	261		NM_004617	NP_004608	P48230	T4S4_HUMAN	ical; (Potential).	0	TGCCTGGGGGG	0.537	
+	42	6369_6371	bnz.1_In_Frame_	NM_053002	NP_443728	Q86YW9	MD12L_HUMAN	Gln-rich.	7	GACCCAGCAGC	0.527	
+	1	251_253	hme.2_In_Frame_	NM_004464	NP_004455	P12034	FGF5_HUMAN		2	TCCTTCCTCCT	0.631	
-	13	1850	t.1_Frame_Shift_	NM_000204	NP_000195	P05156	CFAI_HUMAN	eptidase S1.	0	GTTTTCCCCCC	0.463	rs7437875
+	15	2297_2299	RF2_uc011ctn.1_	NM_006909	NP_008840	O14827	RGRF2_HUMAN		12	AGTCCCACCAC	0.562	
+	1	41_46	CDHGB2_uc003lj	NM_003736	NP_003727	Q9UN71	PCDGG_HUMAN		0	GGCTGCCAGTG	0.617	
-	2	779	jgi.1_Frame_Shift	NM_001127496	NP_001120968	Q9C004	SPY4_HUMAN	ys-rich.|SPR.	2	CGTCCGGGGGG	0.607	
+	4	387_388	3_uc003owo.2_In	NM_153246	NP_694978	Q8N319	CF223_HUMAN	Ala-rich.	0	AGAGCGCgcggc	0.639	rs72369323
-	12	2478	OL12A1_uc003ph	NM_004370	NP_004361	Q99715	COCA1_HUMAN	nectin type-III 4.	9	TGGGTGGGGTG	0.413	
+	9	1421	3tvz.2_Frame_Sh	NM_022479	NP_071924	Q6IS24	GLTL3_HUMAN	ectin.|Lumenal (Potential).	7	CAAGGCAAAAG	0.542	
+	4	1128	uve.1_Frame_Shi	NM_173564	NP_775835	Q6ZVC0	CG051_HUMAN	Pro-rich.	1	GAAATCCCCCC	0.682	
+	8	1077_1079	xa.2_In_Frame_D	NM_015908	NP_056992	Q9BXP5	SRRT_HUMAN	Glu-rich.	2	GAGCAGGAGGA	0.596	
+	6	972	ce_Site_p.Q108_s	NM_014491	NP_055306	O15409	FOXP2_HUMAN		8	TGATACcagcagca	0.414	rs111544687
-	6	468	yhd.2_Frame_Shif	NM_057749	NP_477097	O96020	CCNE2_HUMAN		0	CTCTCCTTTTTT	0.323	
-	3	2403		NM_001017969	NP_001017969	Q5HYC2	K2026_HUMAN	Lys-rich.	3	TTTTGCTTTTTTT	0.323	
+	3	2665	USC2_uc003zwx.	NM_014806	NP_055621	Q8N2Y8	RUSC2_HUMAN		1	CCCCTCCCCCA	0.667	
+	15	2792	1mij.1_Frame_Shi	NM_014728	NP_055543	Q14CM0	FRPD4_HUMAN		13	GTGGTGGGGGA	0.572	
+	1	1263_1265		NM_004455	NP_004446	Q92935	EXTL1_HUMAN	enal (Potential).	1	CCTGCCTCCTC	0.606	
+	14	1261	p.I350fs|RPS6KA	NM_002953	NP_002944	Q15418	KS6A1_HUMAN	kinase C-terminal.	1	GGCATCCCCCC	0.672	
+	23	3277		NM_015284	NP_056099	Q5T011	SZT2_HUMAN		0	GCCTGCCCCGC	0.602	
+	2	99		NM_178428	NP_848515	Q5TA79	LCE2A_HUMAN	Cys-rich.	0	AAGTGCCCCCC	0.572	rs138365632
-	9	1705		NM_020699	NP_065750	Q8WXI9	P66B_HUMAN		0	GTAGTGGGGGA	0.498	
-	10	1559	ne_Shift_Del_p.P4	NM_183001	NP_892113	P29353	SHC1_HUMAN	ro-rich.|CH1.	2	GGATTGGGGGG	0.567	
-	11	1713	fmd.3_Frame_Shi	NM_001037533	NP_001032622	Q3T8J9	GON4L_HUMAN	Asp-rich.	3	TAAGTCCCCCC	0.423	
+	1	267_268	_5'Flank|EFCAB2_	NR_026586		Q5VUJ9	EFCB2_HUMAN		0	ACAGGGCGCGC	0.777	rs10536649
+	1	666	IN_uc009xti.2_5'F	NM_000314	NP_000305	P60484	PTEN_HUMAN		2334	CGGCGGCTGGC	0.505	rs71022512
+	1	51_53		NM_178537	NP_848632	Q76KP1	B4GN4_HUMAN	type II membrane protein;	1	AGATGAAgctgctg	0.429	
-	4	1598_1600	.2_Intron|C11orf95	NM_001144936	NP_001138408	C9JLR9	CK095_HUMAN	-rich.|Glu-rich.	0	CACCCCActcctcct	0.547	
+	5	1036	_Shift_Del_p.A243	NM_020155	NP_064540	Q96N19	G137A_HUMAN	ellular (Potential).	1	CTTGGCCCCCC	0.637	
-	1	189		NM_003793	NP_003784	Q9UBX1	CATF_HUMAN		0	GGCGGCCCCCA	0.781	
+	1	55_56		NM_021046	NP_066384	O75690	KRA58_HUMAN		0	TCTGGAGGCTG	0.649	379698;rs72145325
+	6	1228		NM_004268	NP_004259	Q9NVC6	MED17_HUMAN		1	TTCAAATTAAAT	0.418	
-	2	672	.2_Intron|EFS_uc	NM_005864	NP_005855	O43281	EFS_HUMAN	SH3.	1	CTCCTGGGGGG	0.627	

+	9	5934		NM_025081	NP_079357	Q9P2P1	NYNRI_HUMAN		3	AAGCTGGGGTG	0.597	
-	5	903_905	KT1_uc001ypm.2_	NM_005163	NP_005154	P31749	AKT1_HUMAN		134	TCCATCTCCTCC	0.631	
-	1	196	_5'Flank|OGFOD	NM_007006	NP_008937	O43809	CPSF5_HUMAN	ry for RNA-binding.	0	AGTGACCCCCC	0.652	
-	9	1687	2gai.1_Frame_Shi	NM_015099	NP_055914	O94983	CMTA2_HUMAN		1	CAGCTGGGGGG	0.562	rs149765180
+	1	267	.1_5'UTR|WNK4_	NM_032387	NP_115763	Q96J92	WNK4_HUMAN		7	CCGGACCCCCC	0.716	
-	2	452_455	.2_5'UTR|TIMP2_	NM_003255	NP_003246	P16035	TIMP2_HUMAN	NTR.	2	TCTCACTGACCG	0.51	
+	4	1882_1883	_Shift_Del_p.H604	NM_144566	NP_653167	Q9H0M5	ZN700_HUMAN	2H2-type 13.	0	GACTCACACTG	0.47	
+	8	2673_2674	2phi.3_Frame_Sh	NM_015711	NP_056526	Q9NZM4	GSCR1_HUMAN		3	CCAGGCCCCC	0.723	
-	1	437_439	2xys.2_Intron|PME	NM_020182	NP_064567	Q969W9	PMEPA_HUMAN	ellular (Potential).	1	GCTgcccggcggcg	0.369	
-	1	2553_2554		NM_002430	NP_002421	Q10571	MN1_HUMAN	Poly-Gln.	10	tgctgctgttgctgctgc	0.391	rs34890218
+	3	439	2_uc003adw.1_5'	NM_172002	NP_741999	Q8IWL3	HSC20_HUMAN	J.	1	CCTGGCCCCC	0.493	
+	13	1587	p.T420fs|MTMR3_	NM_021090	NP_066576	Q13615	MTMR3_HUMAN	ularin phosphatase.	5	CCGCACCCCCC	0.547	
-	6	6180	.P1795fs|C22orf3	NM_173566	NP_775837	Q5THK1	PR14L_HUMAN		0	GTTCTGGGGGG	0.532	
-	7	1050_1052	gye.1_In_Frame_	NM_020831	NP_065882	Q969V6	MKL1_HUMAN	Gln-rich.	5	GTGGTGCTGCT	0.66	
-	1	200_202		NM_183357	NP_899200	O95622	ADCY5_HUMAN	lasmic (Potential).	4	AGGCGCTGCTG	0.734	
-	1	200_202		NM_002994	NP_002985	P42830	CXCL5_HUMAN		0	GCGTCAGCAGC	0.7	rs139966143
+	1	184_185	_uc003nyt.2_5'UT	NM_032454	NP_115830	P49842	STK19_HUMAN		4	CGGGCAAACC	0.634	
+	14	1595	p.S529fs|SCUBE	NM_152753	NP_689966	Q8IX30	SCUB3_HUMAN		1	TGACTCCTCTC	0.612	
+	7	1611		NM_004053	NP_004044	Q13895	BYST_HUMAN		0	GCAGTCCCCCG	0.582	
+	1	499_501	_Del_p.17_18LL>	NM_006586	NP_006577	Q9BT09	CNPY3_HUMAN		1	CTTCCCTtgctgctg	0.606	
+	4	387_388	3_uc003owo.2_In	NM_153246	NP_694978	Q8N319	CF223_HUMAN	Ala-rich.	0	AGAGCGCgcggc	0.639	rs72369323
-	2	872		NM_014452	NP_055267	O75509	TNR21_HUMAN	(Potential).|TNFR-Cys 3.	0	CGTATGGGGGG	0.557	
+	16	2396		NM_002047	NP_002038	P41250	SYG_HUMAN		1	CAAGACCCCCC	0.502	
+	10	1401_1402	G2_uc010lgy.2_I	NM_006076	NP_006067	O95081	AGFG2_HUMAN	Pro-rich.	1	GCTGTTCCCCC	0.594	
+	8	1077_1079	xa.2_In_Frame_D	NM_015908	NP_056992	Q9BXP5	SRRT_HUMAN	Glu-rich.	2	GAGCAGGAGGA	0.596	
+	10	1861	oa.3_Frame_Shift_	NM_001458	NP_001449	Q14315	FLNC_HUMAN	Filamin 3.	12	CACGTGGGGCG	0.652	
+	14	4653	wem.2_Frame_S	NM_005435	NP_005426	Q12774	ARHG5_HUMAN		2	AGACTCCCCCC	0.557	
+	6	1464	.P226fs|ZNF398_	NM_170686	NP_733787	Q8TD17	ZN398_HUMAN		1	AGACACCCCCC	0.587	
+	8	1236	p.P314fs|NOS3_u	NM_000603	NP_000594	P29474	NOS3_HUMAN	ction with NOSIP.	8	AGGTGCCCCTG	0.647	
-	2	129	hift_Del_p.N23fs|	NM_004935	NP_004926	Q00535	CDK5_HUMAN	rotein kinase.	2	CCCGGTTTTTG	0.582	
-	3	346	M1_uc003xkx.2_R	NM_014462	NP_055277	O15116	LSM1_HUMAN		0	TTTTGCCCACAT	0.393	
-	3	618	_p.A59fs|TPD52_u	NM_001025252	NP_001020423	P55327	TPD52_HUMAN	Potential.	1	TCTTTTGCTGCT	0.408	
-	16	2344	n|DDX58_uc011l	NM_014314	NP_055129	O95786	DDX58_HUMAN		4	CTGCCTATTAGA	0.315	
-	10	1827_1829	mc.3_In_Frame_	NM_006521	NP_006512	P19532	TFE3_HUMAN		197	ACCCCCTCCTC	0.66	
+	20	4967	1aoj.2_Frame_Shi	NM_015215	NP_056030	Q9Y6Y1	CMTA1_HUMAN	IQ 2.	9	TGAACAAAAAA	0.473	
-	5	1096	AGBL4_uc001crv.	NM_024603	NP_078879	Q7L4P6	BEND5_HUMAN	BEN.	1	TCTTTCTTTTTTT	0.463	
+	2	301_302	_Ins_p.48_49ins	NM_030965	NP_112227	Q9BVH7	SIA7E_HUMAN	.|Lumenal (Potential).	2	agcagcagcagcagc	0.594	rs62637703
+	8	2280	zr.1_Frame_Shift_	NM_004326	NP_004317	O00512	BCL9_HUMAN	y-Pro.|Pro-rich.	6	GAGGACCCCCC	0.582	
+	6	739	B4_uc001eyb.1_3	NM_002796	NP_002787	P28070	PSB4_HUMAN		2	CACCGAAAAAG	0.443	
-	2	3390_3392	ne.1_In_Frame_	NM_007113	NP_009044	Q07283	TRHY_HUMAN	0 AA tandem repeats.	5	ggcgccttctcttctccc	0.241	
-	2	1111_1113	wne.1_In_Frame_	NM_007113	NP_009044	Q07283	TRHY_HUMAN	of R-R-E-Q-E-E- E-R-R-E-	5	tcgcgcctctcctcctcc	0	rs71757496
-	3	5776_5777	uc001ezv.2_Intron	NM_001014342	NP_001014364	Q5D862	FILA2_HUMAN		17	TTGGCTGTGTGT	0.515	rs140875805
-	8	2374_2376	1ffo.2_In_Frame_	NM_002249	NP_002240	Q9UGI6	KCNN3_HUMAN	Poly-Gln.	1	AGGAGCTGCTG	0.64	
-	1	422_424	ox.1_In_Frame_De	NM_002249	NP_002240	Q9UGI6	KCNN3_HUMAN	Poly-Gln.	1	gctgctgttgctgctgct	0.236	
-	11	2245_2247	H700del|PBXIP1_	NM_020524	NP_065385	Q96AQ6	PBIP1_HUMAN	His-rich.	1	CCCCGGTGGTG	0.64	rs143592003
-	1	313_314	_Shift_Ins_p.P31	NM_183001	NP_892113	P29353	SHC1_HUMAN		2	TCCTCCGGGGG	0.619	rs115641580
+	9	2365		NM_021948	NP_068767	Q96GW7	PGCB_HUMAN	EGF-like.	2	GCTATGGGGGG	0.622	

-	4	1309		NM_006617	NP_006608	P48681	NEST_HUMAN	Tail.	6	GGTGTGGGGGG	0.597	
+	1	259		NM_001004478	NP_001004478	Q8NGY1	O10Z1_HUMAN	cellular (Potential).	2	TGGCTGGGGGG	0.552	
-	6	1357_1359	p.V32del|PVRL4_	NM_030916	NP_112178	Q96NY8	PVRL4_HUMAN	ical; (Potential).	2	ACACCCACCAC	0.606	
+	3	338_340		NM_001102566	NP_001096036	A6NKN8	PC4L1_HUMAN		0	AGGCGGAGGAG	0.488	
+	20	6213	PA2_uc009www.2_	NM_020318	NP_064714	Q9BXP8	PAPP2_HUMAN	Sushi 5.	16	GTAATCCCCCC	0.468	
+	8	1233_1234	9wxs.2_Frame_Sh	NM_000721	NP_000712	Q15878	CAC1E_HUMAN	lasmic (Potential).	6	CCAAAGAGAGA	0.51	
+	7	1843_1845	e_Del_p.K506del|	NM_005807	NP_005798	Q92954	PRG4_HUMAN	8 AA repeats of K-X-P-X-P	1	CACCAAGAAGC	0.65	
-	1	1610		NM_032833	NP_116222	Q5SWA1	PR15B_HUMAN		2	ACTACACTTATTC	0.458	
+	4	635_646		NM_001104548	NP_001098018				0	gTagcagcagcagcag	0.283	30217;rs72359595;rs150848171
-	13	2418_2420	0pty.1_In_Frame_	NM_005401	NP_005392	Q15678	PTN14_HUMAN	Poly-Glu.	5	GGAGCCTCCTC	0.626	
+	28	5556_5557	m.2_Frame_Shift_	NM_198551	NP_940953	Q5JRA6	MIA3_HUMAN	ytoplasmic (Potential).	5	CTTGGCCCAAGA	0.545	
-	5	1798	AGT_uc009xff.2_F	NM_000029	NP_000020	P01019	ANGT_HUMAN		0	AAGCTCAAAAAA	0.562	
+	3	629_631	ame_Del_p.S197de	NM_032429	NP_115805	Q9BRK4	LZTS2_HUMAN	ntrosomal localization (By s	4	GGCCCTGcctcctc	0.557	
-	4	533		NM_001080998	NP_001074467	Q96QU4	FRG2B_HUMAN		0	CCGAGACCTATG	0.557	
+	1	735_736		NM_001127389	NP_001120861	F5GZ66	F5GZ66_HUMAN		0	GGGCCAGGCAC	0.708	rs138894859
+	3	548_550	rlo.1_In_Frame_D	NM_004265	NP_004256	O95864	FADS2_HUMAN	ical; (Potential).	2	TTCTTCCTCCT	0.537	
+	8	941	1oxd.2_Splice_Sit	NM_003369	NP_003360	Q9P2Y5	UVRAG_HUMAN		6	ATTTAGAAAAAA	0.302	
-	8	1187_1189	CADM1_uc001ppj.	NM_014333	NP_055148	Q9BY67	CADM1_HUMAN	cellular (Potential).	2	gtaaggatggtggtggt	0.266	
-	1	355	AFX_uc001pvh.1_F	NM_002105	NP_002096	P16104	H2AX_HUMAN		0	CTTGTTGAGCTC	0.672	rs141798641
-	3	539_541		NM_006248	NP_006239				0	GGACTTGTTGT	0.596	
-	3	314_315		NM_006248	NP_006239				0	GGAGGTGGGG	0.614	
-	2	1302	raq.2_Frame_Shift	NM_006143	NP_006134	Q15760	GPR19_HUMAN	lasmic (Potential).	1	ACGTAGTTTTTTT	0.398	
-	12	1271_1273	DM2_uc001sns.2_	NM_014925	NP_055740	Q9Y2K5	R3HD2_HUMAN	Gln-rich.	2	AGGAAGTtgctgct	0.488	
+	1	1317_1319	.E437del|EP400_	NM_015409	NP_056224	Q96L91	EP400_HUMAN	Poly-Glu.	12	gaagaagaggagga	0.286	rs62635809
+	46	8261_8262	0_uc001ujm.2_In_	NM_015409	NP_056224	Q96L91	EP400_HUMAN	ith ZNF42 (By similarity).	12	agcagcaacagcagc	0.327	rs111782215
-	1	410	uc001uxv.1_Intron	NM_032138	NP_115514	Q8WVZ9	KBTB7_HUMAN		1	CCGTGAAAAAG	0.632	
-	1	1994_1996	o.1_In_Frame_De	NM_183422	NP_904358	Q15714	T22D1_HUMAN	Gln-rich.	0	gttgttgttgctgctgctg	0.409	613609;rs146722477
+	22	2792	nh.2_Frame_Shift	NM_005766	NP_005757	Q9Y4F1	FARP1_HUMAN	PH 1.	2	CGAGTGGGGGG	0.617	
-	1	1123		NM_001080396	NP_001073865	B1AL88	F155A_HUMAN		1	CCCGTCCCCCC	0.607	
-	1	772_774		NM_001080396	NP_001073865	B1AL88	F155A_HUMAN	Poly-Gln.	1	cgctgcctctgctgctgc	0.404	
+	2	348	s|APEX1_uc001v	NM_001641	NP_001632	P27695	APEX1_HUMAN	iation with rRNA, endoribo	4	GTGGGAAAAAG	0.557	
-	2	306	EXOC5_uc010trh.	NM_006544	NP_006535	O00471	EXOC5_HUMAN		3	GACGTTCAATAT	0.333	
-	13	2476_2478	0twc.1_In_Frame_	NM_007039	NP_008970	Q16825	PTN21_HUMAN	Poly-Glu.	4	CTCGTCCTCCT	0.704	
-	7	2023	wo.1_Frame_Shift_	NM_001002860	NP_001002860	Q9P203	BTBD7_HUMAN		1	CCAGCATTTTTTT	0.383	
-	6	1584	jo.2_Frame_Shift_	NM_170675	NP_733775	O14770	MEIS2_HUMAN		2	TGGGCATTTTCC	0.478	
-	69	13096		NM_003922	NP_003913	Q15751	HERC1_HUMAN	C1 14.|WD 11.	19	ATTGCTCCCCCA	0.438	
-	3	553_555	20GG>G|KIAA043	NM_014647	NP_055462	Q9Y4F3	LKAP_HUMAN	Poly-Gly.	0	ACCGCCACCAC	0.532	
-	2	667	_5'Flank|IQCK_uc	NM_001012991	NP_001013009	Q1ED39	CP088_HUMAN	Lys-rich.	0	GGTGGATTTTTT	0.532	
+	9	1622_1633	C100132247_uc	NM_001135865	NP_001129337	A8MRT5	K220L_HUMAN	Pro-rich.	0	TCCACCCTCAGC	0.571	
+	13	3813_3815		NM_014712	NP_055527	O15047	SET1A_HUMAN	Ser-rich.	3	Gctcctcatcctcctcct	0.389	
+	2	113_115	p.E13del|CCDC13	NM_032269	NP_115645	Q8IY82	CC135_HUMAN	Potential.	1	gaaggtggaggagga	0.448	
-	3	888_890	jt.1_In_Frame_De	NM_001082486	NP_001075955	Q96AP0	ACD_HUMAN		1	TCCTGCAGCAG	0.65	
-	14	2504	_p.F283fs|ADAMT	NM_199355	NP_955387	Q8TE60	ATS18_HUMAN	Cys-rich. p.A696fs*18(2)	18	CATTGCAAAAAA	0.403	
+	3	433	l_p.T16fs|KIAA01	NM_014615	NP_055430	Q14687	GSE1_HUMAN		5	CAGCACCCCCC	0.687	
-	5	772		NM_015982	NP_057066	Q9Y2T7	YBOX2_HUMAN	quired for mRNA-binding.	0	AGGCCGGGGGC	0.622	
+	8	912_914	.L222del|CHRNB1	NM_000747	NP_000738	P11230	ACHB_HUMAN	ical; (Potential).	2	GTTCCTGCTGCT	0.498	
+	11	2629_2631	2gix.2_In_Frame_	NM_001080424	NP_001073893	O15054	KDM6B_HUMAN	-rich.|Thr-rich.	2	CGCCGTcaccacca	0.369	

+	10	1762	gjf.2_Frame_Shift_	NM_001005273	NP_001005273	Q12873	CHD3_HUMAN	Chromo 1.	1	TCCCACCCCCC	0.577	
+	2	137	R11_uc002ixg.1_	NM_018304	NP_060774	Q96HE9	PRR11_HUMAN		2	TTATTCAAAAAA	0.348	
-	19	3481	p.V1052fs|USP36_	NM_025090	NP_079366	Q9P275	UBP36_HUMAN		5	TGACTGACCGC	0.567	
+	11	1445_1447		NM_015897	NP_056981	Q8N2W9	PIAS4_HUMAN	Glu-rich (acidic).	1	gaggatgaggagga	0.552	
-	6	1132_1134		NM_005934	NP_005925	Q03111	ENL_HUMAN	Poly-Ser.	1	GAGAAGGAGGA	0.65	
-	2	440_442		NM_052850	NP_443082	Q8TAE8	G45IP_HUMAN	y-Gln.|Potential.	2	TCCCGCTGCTG	0.635	
-	3	909	_Shift_Del_p.I255f	NM_014884	NP_055699	Q8IX01	SUGP2_HUMAN		0	TGGGTATTTTTT	0.502	
-	2	120_122		NM_000704	NP_000695	P20648	ATP4A_HUMAN	lasmic (Potential).	1	CCGCCTTCTTC	0.601	
+	10	765		NM_015302	NP_056117	O94927	HAUS5_HUMAN		0	AACCACCCCCC	0.642	
-	2	231	1_Frame_Shift_D	NM_006905	NP_008836	P11464	PSG1_HUMAN		2	GTGGTGGGCAG	0.493	rs77328225
-	9	974_975	pni.2_Frame_Shift	NM_003598	NP_003589	Q15562	TEAD2_HUMAN	al activation (Potential).	3	GGCATGGGGG	0.564	
+	11	1757_1759	ne_Del_p.L480del	NM_006669	NP_006660	Q8NHL6	LIRB1_HUMAN	ical; (Potent p.L479del(1)	3	tcctactgctcctcctcc	0.458	
+	1	230	.2_Intron|SPTBN1	NR_002229					0	GCCACAAAAAA	0.537	
-	4	737_739	02svr.2_In_Frame_	NM_017849	NP_060319	O75204	TM127_HUMAN		0	CTTATGCTGCTG	0.557	
+	8	1145	2_Intron|ANKRD3	NM_001164315	NP_001157787	A6QL64	AN36A_HUMAN		0	ACAGGTATTTTG	0.302	
+	10	1092		NM_182640	NP_872578	P82933	RT09_HUMAN		0	AGGCTGGAGCA	0.562	
+	9	1518	20A1_uc002uzy.3_	NM_177538	NP_803882	Q6UW02	CP20A_HUMAN		0	AAGTTCAAAAAA	0.348	
+	1	182_184	P_uc002vsr.2_5'F	NM_001632	NP_001623	P05187	PPB1_HUMAN		1	CCCTGCAtgctgct	0.542	
+	2	175_177		NM_022134	NP_071417	Q9H3Q3	G3ST2_HUMAN	type II membrane protein;	0	GGTCATCCTCCT	0.631	
-	14	2158	_p.K662fs|ZMYN	NM_012408	NP_036540	Q9ULU4	PKCB1_HUMAN		5	TTGGGCTTTTTT	0.488	
-	1	737	e_Shift_Del_p.K2	NM_080618	NP_542185	Q8NI51	CTCFL_HUMAN		4	AGGCCTTTTTC	0.502	
-	11	905	PTE_uc002yir.1_	NM_199261	NP_954870	P56180	TPTE_HUMAN	ical; (Potential).	5	ATGTCAAAAAAA	0.299	
+	4	1162	0gma.2_Frame_S	NM_005534	NP_005525	P38484	INGR2_HUMAN	tential).|Fibronectin type-III	0	ACGGCCTTTTTT	0.458	
-	2	1210	2yrw.2_Frame_Sh	NM_017833	NP_060303	Q9NX36	DJC28_HUMAN		0	ATTCTGGTTGG	0.393	
-	1	5854	E2_uc002yyx.2_I	NM_182832	NP_878252	Q8WY50	PLAC4_HUMAN		0	gagggtatccagggtg	0.159	
-	8	995	_Shift_Del_p.E241	NM_022719	NP_073210	Q96DF8	DGC14_HUMAN		1	AACCTCCCCCC	0.597	
-	30	4280_4282		NM_002473	NP_002464	P35579	MYH9_HUMAN	Potential.	11	TTGGCCTCCTC	0.65	
-	1	5454_5456	1774del|TCF20_	NM_005650	NP_005641	Q9UGU0	TCF20_HUMAN		5	CCTTCTGCTGC	0.601	
+	4	842	pk.1_Frame_Shift	NM_178329	NP_847899	P51677	CCR3_HUMAN	ellular (Potential).	8	CTGGGTTTTTG	0.488	
+	6	9506		NM_003458	NP_003449	Q9UPA5	BSN_HUMAN		8	CACCCTTTTTC	0.607	
-	6	1104_1105	2A1_uc011blv.1_	NM_005630	NP_005621	Q92959	SO2A1_HUMAN	Name=6; (Potential).	1	GGAAGAAAAAA	0.49	rs141736851
+	21	2524_2526	buy.1_In_Frame_	NM_000283	NP_000274	P35913	PDE6B_HUMAN		0	GAGAAGGAGGA	0.562	
-	17	2126	.2_Frame_Shift_D	NM_144643	NP_653244	Q96NL6	SCLT1_HUMAN	Potential.	5	TTGGCTTTTTTT	0.353	
+	6	626_627		NM_004477	NP_004468	Q14331	FRG1_HUMAN		0	TAGGGGAAAATG	0.351	
-	3	318		NM_032286	NP_115662	Q9BTT4	MED10_HUMAN		1	TGCTCATTTTTAG	0.418	
-	11	1838_1839	.1_Frame_Shift_	NM_000065	NP_000056	P13671	CO6_HUMAN	EGF-like.	7	CTCTGACACACA	0.475	
-	4	1093	kin.2_Frame_Shi	NM_001884	NP_001875	P10915	HPLN1_HUMAN	Link 2.	5	TTATGCTTTTTAT	0.493	
-	1	479_480		NM_001085377	NP_001078846	P23508	CRCM_HUMAN		1	ctgccgctgccgccgc	0.391	
+	4	1770	lnn.1_Frame_Shi	NM_020768	NP_065819	Q68DU8	KCD16_HUMAN		4	GCAGCAAAAAA	0.468	
-	8	1648_1649	_Ins_p.225_226in	NM_000332	NP_000323	P54253	ATX1_HUMAN		4	TGCTGAGGtgctg	0.366	
+	14	2219_2221	AT2_uc003nvc.3_	NM_080686	NP_542417	P48634	PRC2A_HUMAN	X 57 AA type A repeats.	0	TCCTGAagcagca	0.453	
+	8	1034_1035	1dpb.1_Frame_Shift_Ins_p.V276fs			P08686	CP21A_HUMAN		0	CCGTGGTTTTTT	0.614	
+	6	808	10khi.2_Frame_S	NM_014721	NP_055536	O75167	PHAR2_HUMAN		2	TCATTCAAAAAA	0.398	
-	10	1313_1314		NM_015718	NP_056533	Q9HBY0	NOX3_HUMAN	ical; (Potential).	1	CAACGCACACA	0.53	
-	4	864_866		NM_001002926	NP_001002926	Q3B726	RPA43_HUMAN	Lys-rich.	1	GCTTTTTCTTCT	0.433	
+	11	3191_3192	_800insS|POM121_	NM_172020	NP_742017	Q96HA1	P121A_HUMAN	side (Potential).	0	TGTCTTCTTCGG	0.663	686669;rs67569765
-	2	390_392	kiw.1_In_Frame_	NM_015545	NP_056360	O75127	PTCD1_HUMAN		1	AACTCTCCTCC	0.606	

-	5	964	2_Intron|GPC2_uc	NM_152742	NP_689955	Q8N158	GPC2_HUMAN		2	GGGGACCCCCC	0.642	
+	6	972	ce_Site_p.Q108_s	NM_014491	NP_055306	O15409	FOXP2_HUMAN		8	TGATACcagcagca	0.414	rs111544687
-	9	1235_1237		NM_003941	NP_003932	O00401	WASL_HUMAN	Pro-rich.	0	CCTagcaggaggag	0.443	
+	7	1118_1119	vuy.2_Frame_Shif	NM_016019	NP_057103	Q9Y383	LC7L2_HUMAN	Arg/Ser-rich.	0	AGAGAAGAGAGA	0.391	
+	1	528		NM_001001656	NP_001001656	Q8NGU2	OR9A4_HUMAN	ellular (Potential).	1	GAACAATTTTTT	0.383	
-	2	129	hift_Del_p.N23fs|	NM_004935	NP_004926	Q00535	CDK5_HUMAN	rotein kinase.	2	TCCCGGTTTTTG	0.582	
+	5	504	PB49_uc011kyu.1	NM_001114136	NP_001107608	Q08495	DEMA_HUMAN		1	CACATCCCCCC	0.602	
+	2	273_275	lank|BMP1_uc003	NM_003018	NP_003009	P11686	PSPC_HUMAN		0	TATCGTGGTGG	0.601	
+	13	1644	p.P503fs|KIAA196	NM_199205	NP_954675	Q8N163	K1967_HUMAN		3	CTCCACCCCCC	0.572	
+	34	7676_7678		NM_017780	NP_060250	Q9P2D1	CHD7_HUMAN	ential.|Poly-Arg.	9	CAGCGGAGGAG	0.512	
+	2	604		NM_004770	NP_004761	Q92953	KCNB2_HUMAN	lasmic (Potential).	7	AGGCTCCCCG	0.502	
-	13	1637_1639	.I506del|TSNARE	NM_145003	NP_659440	Q96NA8	TSNA1_HUMAN	.|Helical; (Potential).	0	TGGCGATGATG	0.414	rs142964918
-	2	1659_1661	.2_In_Frame_Del_	NM_173691	NP_775962	Q4KMQ1	TPRN_HUMAN	Glu-rich.	0	tcttcctcttcctcctcctc	0.374	
-	8	1013	mwc.1_Frame_Shi	NM_024597	NP_078873	Q8IWC1	MA7D3_HUMAN		4	CACCTGGGGGG	0.532	
+	4	1735_1737	EC1_uc010nsl.1_I	NM_005462	NP_005453	O60732	MAGC1_HUMAN		4	TGAGCTCCTCC	0.473	rs144357389
+	4	2131_2133	EC1_uc010nsl.1_I	NM_005462	NP_005453	O60732	MAGC1_HUMAN		4	GTCCTCTTCAG	0.571	
+	11	9934_9935	bp.1_Frame_Shift_	NM_015001	NP_055816	Q96T58	MINT_HUMAN	Pro-rich.	15	Tgcccccacccccac	0.416	
-	7	967	F1_uc010oce.1_I	NM_017940	NP_060410	Q3BBV0	NBPF1_HUMAN		0	CAGCTGGGGGC	0.488	
-	13	2591	e_Shift_Del_p.Q5	NM_003819	NP_003810	Q13310	PABP4_HUMAN	PABC.	0	TTCCTGGGGGG	0.602	
+	2	301_302	_Ins_p.48_49ins	NM_030965	NP_112227	Q9BVH7	SIA7E_HUMAN	.|Lumenal (Potential).	2	agcagcagcagcagc	0.594	rs62637703
-	6	852		NM_206996	NP_996879	Q6Q759	SPG17_HUMAN		6	TGCCAGGTGTG	0.423	
-	34	7254_7255		NM_024408	NP_077719	Q04721	NOTC2_HUMAN	lasmic (Potential).	27	GGCCCGCAAC	0.629	
+	6	700	hift_Del_p.F167fs|	NM_004425	NP_004416	Q16610	ECM1_HUMAN	roximate repeats.|1.	3	GGCTTCCCCCC	0.602	
-	25	3397	p.Q18fs|NUP210L	NM_207308	NP_997191	Q5VU65	P210L_HUMAN		11	GGGCTGGGGGC	0.458	
-	1	422_424	x.1_In_Frame_D	NM_002249	NP_002240	Q9UGI6	KCNN3_HUMAN	Poly-Gln.	1	gctgctgttgctgctgct	0.236	
+	1	259		NM_001004478	NP_001004478	Q8NGY1	O10Z1_HUMAN	ellular (Potential).	2	TGGCTGGGGGG	0.552	
+	2	652_654		NM_004983	NP_004974	Q92806	IRK9_HUMAN	me=M2; (By similarity).	2	ATCGTGCTGCT	0.64	
+	56	8916		NM_031935	NP_114141	Q96RW7	HMCN1_HUMAN	ike C2-type 27.	23	TTTATCCAGTG	0.463	
+	4	635_646		NM_001104548	NP_001098018				0	Tagcagcagcagca	0.283	30217;rs72359595;rs150848171
+	4	1558	fd.1_Frame_Shift_	NM_014777	NP_055592	Q14146	URB2_HUMAN		3	GTTTTGGGGGT	0.567	
+	5	2472		NM_000740	NP_000731	P20309	ACM3_HUMAN	smic (By similarity).	5	GTGACAAAAAA	0.502	
+	1	153_154		NM_001004688	NP_001004688	Q96R28	OR2M2_HUMAN	lasmic (Potential).	4	TACCTGGACACC	0.53	
-	20	2528_2530	E813del|SFMBT2_	NM_001029880	NP_001025051	Q5VUG0	SMBT2_HUMAN		8	AGTCTCTCCTCC	0.596	
-	9	1622_1624	_RNA|uc001ive.1_	NM_018109	NP_060579	Q9NVV4	PAPD1_HUMAN		1	TGATGTCCTCCT	0.507	
-	2	1199	p.F229fs|CHST15_	NM_015892	NP_056976	Q7LFX5	CHSTF_HUMAN	enal (Potential).	1	CGTCGAAGGTG	0.647	
-	2	598_600	1orf95_uc001nxs.	NM_001144936	NP_001138408	C9JLR9	CK095_HUMAN	Glu-rich.	0	tcctcttcttcctcctcctc	0.532	
+	2	185_187		NM_015516	NP_056331	Q8WUA8	TSK_HUMAN		0	GCCCCTGCTGC	0.616	
-	3	369	_p.P46fs|PRDM1	NM_020228	NP_064613	Q9NQV6	PRD10_HUMAN		1	GCTGTGGGGGG	0.547	
+	9	608_610	1ruq.1_In_Frame_	NM_001031698	NP_001026868	Q6NWY9	PR40B_HUMAN		5	GAAACAGCAGC	0.64	
+	1	546	1_Intron|GEFT_uc	NM_182947	NP_891992	Q86VW2	ARHGP_HUMAN		0	CGCCCGGGGGG	0.607	
+	17	2575_2577		NM_015267	NP_056082	O14529	CUX2_HUMAN	Poly-Ser.	6	GCTGTCCTCCT	0.749	
-	13	2476_2478	0twc.1_In_Frame_	NM_007039	NP_008970	Q16825	PTN21_HUMAN	Poly-Glu.	4	CTCGTCCTCCT	0.704	
-	8	942	C2_uc001zbl.1_5'	NM_004667	NP_004658	O95714	HERC2_HUMAN		13	ATGCTTCCTGGC	0.592	
+	12	2039	bbi.2_Frame_Shif	NM_003246	NP_003237	P07996	TSP1_HUMAN	lcium-binding (Potential).	6	CCCTGCCCCCC	0.572	
-	1	694		NM_203349	NP_976224	Q6S5L8	SHC4_HUMAN	CH2.	5	CATGCGGGGGA	0.627	
-	5	1150_1151	uoe.1_Frame_Shif	NM_001079533	NP_001073001	Q9BZB8	CPEB1_HUMAN		2	CTGGCCTCTCT	0.579	
-	2	292_294	02cpi.1_In_Frame_	NM_182563	NP_872369	Q6PL45	CP079_HUMAN	.|Helical; (Potential).	1	Ccagcaccagcagca	0.562	

-	3	385_387	P2_uc010byn.2_Ir	NM_024816	NP_079092	Q9H5N1	RABE2_HUMAN	y-Gln.|Potential.	3	AGTCCTGCTGC	0.527	
+	10	1584	10vjk.1_Intron|LRI	NM_018296	NP_060766	Q1X8D7	LRC36_HUMAN		0	CAGAACCCCCC	0.527	
-	3	888_890	jt.1_In_Frame_De	NM_001082486	NP_001075955	Q96AP0	ACD_HUMAN		1	TCCTGCAGCAG	0.65	
+	3	433	l_p.T16fs|KIAA018	NM_014615	NP_055430	Q14687	GSE1_HUMAN		5	CAGCACCCCCC	0.687	
-	16	2618	vsf.1_Frame_Shift	NM_014389	NP_055204	Q8IZL8	PELP1_HUMAN	Pro-rich.	2	TGGCAGGGGGG	0.617	
-	1	338_340	P1_uc010vsf.1_5'l	NM_014389	NP_055204	Q8IZL8	PELP1_HUMAN		2	TCTCCAGCAGC	0.695	
-	1	143_145	HX33_uc010clf.2_	NM_020162	NP_064547	Q9H6R0	DHX33_HUMAN		2	CCGGCCTCCTC	0.724	
-	7	934	ggo.1_Frame_Shif	NM_020360	NP_065093	Q9NRY6	PLS3_HUMAN	smic (By similarity).	0	CCAGGCCCCCC	0.612	
+	1	24_26		NM_001005271	NP_001005271	Q12873	CHD3_HUMAN		1	AGggacgaggagga	0.094	
-	1	233_235	dx.3_In_Frame_De	NM_020772	NP_065823	Q7Z417	NUFP2_HUMAN	His-rich.	4	ggtgatgatggtggtggt	0.276	rs1054145
-	5	975		NM_012285	NP_036417	Q9UQ05	KCNH4_HUMAN	lasmic (Potential).	1	CGAGACCCCCC	0.607	
+	4	505_507	10wsa.1_In_Frame	NM_014738	NP_055553	Q12767	K0195_HUMAN	ical; (Potential).	1	GCCGTGCTGCT	0.675	
-	5	1361_1363		NM_003655	NP_003646	O00257	CBX4_HUMAN	Interaction with BMI1.	2	GACGGCgtggtgg	0.507	rs3833850
-	2	117	N5_uc002mat.1_In	NM_052972	NP_443204	P02750	A2GL_HUMAN		1	GGTGACCCCCC	0.597	
-	1	186	A41_uc010dut.2_	NM_173637	NP_775908	Q8N5S1	S2541_HUMAN	Pro-rich.	0	ggaggttgggggga	0.428	
+	5	714	2mgp.2_Frame_S	NM_020533	NP_065394	Q9GZU1	MCLN1_HUMAN		1	TGGATCCCCCC	0.637	rs145706318
-	20	2254		NM_012335	NP_036467	O00160	MYO1F_HUMAN	IQ.	3	TCTCCTCGTACTT	0.637	
-	1	207_208	oad.1_Frame_Shif	NM_198538	NP_940940	Q6UWP8	SBSN_HUMAN		1	CCCACCTCTCTC	0.579	
+	9	1289		NM_005178	NP_005169	P20749	BCL3_HUMAN	Pro/Ser-rich.	2	AGTCTCCCCCC	0.498	
+	13	1642	16_uc010xxh.1_5'I	NM_006509	NP_006500	Q01201	RELB_HUMAN		1	TGCTGCCCCCG	0.697	
-	1	1911_1913		NM_002152	NP_002143	P23327	SRCH_HUMAN		1	tccagcccctcctcctc	0.409	
+	6	694	uc002pqp.2_5'UTI	NM_024682	NP_078958	Q9HA65	TBC17_HUMAN		0	GGACTCCCGCC	0.627	
+	1	69_71	010yct.1_In_Frame	NM_014441	NP_055256	Q9Y336	SIGL9_HUMAN		1	GACATGCTGCT	0.611	
+	12	1349	RE_uc002rlt.2_Fra	NM_199194	NP_954664	Q9NXR7	BRE_HUMAN	UEV-like 2.	3	GGCCCAAAAAA	0.448	
+	1	1958_1959		NM_000189	NP_000180	P52789	HXK2_HUMAN	Hydrophobic.	2	CTTCTTCACGGA	0.653	
+	2	175_177		NM_022134	NP_071417	Q9H3Q3	G3ST2_HUMAN	type II membrane protein;	0	GGTCATCCTCCT	0.631	
+	6	588_590	015_uc002zsr.2_In	NM_001003891	NP_001003891	Q96RN5	MED15_HUMAN	Poly-Gln.	1	gcagttccagcagcag	0.217	
-	53	6184	p.D376fs|PI4KA_u	NM_058004	NP_477352	P42356	PI4KA_HUMAN	PI3K/PI4K.	4	CCGTGTCCAACA	0.617	
-	3	428_430	_19DD>D|TFIP11_	NM_012143	NP_036275	Q9UBB9	TFP11_HUMAN	Poly-Asp.	0	GCTCGTCATCAT	0.532	rs145794160
+	5	474	2_3'UTR|POLR2F_	NM_021974	NP_068809	P61218	RPAB2_HUMAN		1	AGACTGGGGGG	0.512	
+	14	1647	dgm.2_Frame_Shif	NM_006254	NP_006245	Q05655	KPCD_HUMAN	rotein kinase.	9	TCAACGGGGGG	0.602	
+	21	2524_2526	buy.1_In_Frame_	NM_000283	NP_000274	P35913	PDE6B_HUMAN		0	GAGAAGGAGGA	0.562	
+	1	3191_3192		NM_175918	NP_787114	Q8N1N5	CRPAK_HUMAN		0	CCTGCTCATGTG	0.644	
+	1	3654_3655		NM_175918	NP_787114	Q8N1N5	CRPAK_HUMAN	6	0	CTGCTCACACGT	0.678	
-	7	944		NM_173536	NP_775807	Q8N1C3	GBRG1_HUMAN	ellular (Probable).	2	AGGTCAAAAAA	0.294	
+	2	205	3ifb.2_Frame_Shif	NM_199327	NP_955359	O43609	SPY1_HUMAN		3	AAATCAACATGC	0.428	
+	14	1615	S14_uc003mgi.2_	NM_006480	NP_006471	O43566	RGS14_HUMAN		1	AGCGTCCCCCA	0.577	
-	8	1648_1649	_Ins_p.225_226in	NM_000332	NP_000323	P54253	ATX1_HUMAN		4	TGCTGAGGtgctgc	0.366	
-	3	1001	_Shift_Del_p.K141	NM_031922	NP_114128	Q96D71	REPS1_HUMAN		2	GATCCCTTTTTCA	0.478	
+	9	3522_3524	2_3'UTR|GRM1_uc	NM_000838	NP_000829	Q13255	GRM1_HUMAN	|Cytoplasmic (Potential).	19	TCTCCAGCAGC	0.66	
+	13	1711	ze.1_Frame_Shift_	NM_031414	NP_113602	Q9BXU1	STK31_HUMAN		9	CGCAATGGATAA	0.363	
-	1	310_312	ame_Del_p.72_73	NM_005522	NP_005513	P49639	HXA1_HUMAN	Poly-His.	3	ggggtggcgatggtgg	0.527	rs10951154
+	1	539_540	.1_5'Flank|ZCWP	NM_019606	NP_062552	Q7L2J0	MEPCE_HUMAN	Gly-rich.	1	CACCTGGGGGC	0.693	
+	6	972	ce_Site_p.Q108_s	NM_014491	NP_055306	O15409	FOXP2_HUMAN		8	TGATACcagcagca	0.414	rs111544687
-	12	1351_1352	koj.1_Frame_Shift	NM_018077	NP_060547	Q9NW13	RBM28_HUMAN	RRM 3.	2	AACCTTGAGCTG	0.45	
+	1	528		NM_001001656	NP_001001656	Q8NGU2	OR9A4_HUMAN	ellular (Potential).	1	GAACAATTTTTTT	0.383	
-	7	1282_1284	1kvs.1_In_Frame_	NM_007349	NP_031375	Q6ZW49	PAXI1_HUMAN	Gln-rich.	5	ACCGGGtgctgctg	0.369	

+	11	2081_2082	kvv.1_Frame_Shift	NM_053043	NP_444271	Q96EV2	RBM33_HUMAN	Pro-rich.		1	CTGCCCACACAC	0.53	
+	1	210	_p.P59fs|NEFM_u	NM_005382	NP_005373	P07197	NFM_HUMAN	Head.		1	GCCCCGCGCCT	0.706	
-	9	1219		NM_152413	NP_689626	Q8NHS2	AATC2_HUMAN			1	GTTCTTGGGAT	0.468	
+	4	327_328	_p.L53fs|SDCBP_	NM_005625	NP_005616	O00560	SDCB1_HUMAN			0	GGGCTGAGTTTA	0.342	
+	34	7676_7678		NM_017780	NP_060250	Q9P2D1	CHD7_HUMAN	ential.|Poly-Arg.		9	CAGCGGAGGAG	0.512	
+	11	9751_9753		NM_024721	NP_078997	Q86UP3	ZFHX4_HUMAN	Pro-rich.		15	ctccaccacctcctcctc	0.379	
-	13	1637_1639	.I506del|TSNARE	NM_145003	NP_659440	Q96NA8	TSNA1_HUMAN	.|Helical; (Potential).		0	GTGGCGATGATG	0.414	rs142964918
-	11	2666_2668		NM_015117	NP_055932	Q8IXZ2	ZC3H3_HUMAN	Poly-Ser.	p.S879F(1)	1	aggggatgaggaggag	0.552	;rs2272753;rs137878905
+	3	411	zay.2_Frame_Shift	NM_001916	NP_001907	P08574	CY1_HUMAN	ytochrome c.		0	CGCCTCCTGCC	0.602	
-	4	3699		NM_001145196	NP_001138668	Q5VVP1	F75A6_HUMAN			0	GGCATGGTGCG	0.493	
+	3	1021_1023	bag.1_In_Frame_	NM_006981	NP_008912	Q92570	NR4A3_HUMAN	Poly-His.		173	tcaccatcaccaccacc	0.483	
-	8	1013	mwc.1_Frame_Shi	NM_024597	NP_078873	Q8IWC1	MA7D3_HUMAN			4	CACCTGGGGGG	0.532	
-	28	4158	c001ayw.2_5'Flan	NM_017940	NP_060410	Q3BBV0	NBPF1_HUMAN	NBPF 7.		0	AGAAAAGCCAAC	0.433	
+	1	1263_1265		NM_004455	NP_004446	Q92935	EXTL1_HUMAN	enal (Potential).		1	GCCTGCCTCCTC	0.606	
-	4	983	sd.2_Frame_Shift_	NM_014654	NP_055469	O75056	SDC3_HUMAN	ellular (Potential).		2	CTGGGCCCCCC	0.607	
+	2	278	D1_uc001cab.2_F	NM_018067	NP_060537	Q3KQU3	MA7D1_HUMAN	Pro-rich.		5	CAGGACCCCCC	0.612	rs145462639
+	7	799		NM_033055	NP_149044	Q96MC6	HIAT1_HUMAN	lasmic (Potential).		0	TCCAGCTTTTTTT	0.388	
-	4	296_297		NM_001010979	NP_001010979	Q5VU69	CA189_HUMAN			0	CATCTGATTTAG	0.475	
-	2	1126	1fpt.1_Frame_Shif	NM_030980	NP_112242	Q9H9L3	I20L2_HUMAN	Exonuclease.		2	GTTGAGGGGGG	0.557	
+	105	16580	grs.1_Frame_Shift	NM_031935	NP_114141	Q96RW7	HMCN1_HUMAN	alcium-binding (Potential).		23	ACCTTTGGAAGT	0.398	
-	21	3806	_Shift_Del_p.A955	NM_003607	NP_003598	Q5VT25	MRCKA_HUMAN			11	AAATGCCAAGA	0.338	
+	10	3102		NM_032199	NP_115575	Q14865	ARI5B_HUMAN			4	CAGGGAAAAAG	0.607	
+	2	234_235	sz.2_5'UTR|LDB3_	NM_007078	NP_009009	O75112	LDB3_HUMAN	PDZ.		1	TCAAGTCTGCCA	0.614	
+	1	842	E3B_uc010rcr.1_Fr	NM_000922	NP_000913	Q13370	PDE3B_HUMAN	ical; (Potential).		0	TTACCTGGGGGA	0.731	
+	6	878	nse.1_Frame_Shif	NM_001127392	NP_001120864	Q9Y2G1	MRF_HUMAN	DT80.|Pro-rich.		1	TGAATCCCCCCC	0.637	
-	4	752	ame_Shift_Del_p.	NM_001077241	NP_001070709	Q8N413	S2545_HUMAN	e=3; (Potential).|Solcar 2.		0	AGGAACCCCCC	0.657	
+	5	700_701	V1_uc001omk.3_F	NM_007103	NP_009034	P49821	NDUV1_HUMAN			1	TGATTGGCAAGA	0.569	
-	3	310	_5'UTR|C15orf52_	NM_207380	NP_997263	Q6ZUT6	CO052_HUMAN			1	GCCATCCCCCC	0.647	
-	36	6678	-4310|MI0015840_	NM_016642	NP_057726	Q9NRC6	SPTN5_HUMAN	Spectrin 18.		2	GCCATCAGCAG	0.682	
+	7	1780_1782	.D191del|BLM_uc	NM_000057	NP_000048	P54132	BLM_HUMAN	Poly-Asp.		6	GACTTTGATGAT	0.374	
-	3	494	X33_uc002gcb.2_	NM_020162	NP_064547	Q9H6R0	DHX33_HUMAN	ase ATP-binding.		2	CTGGTGTCTTCT	0.363	
-	1	175_177	2hdx.3_In_Frame_	NM_020772	NP_065823	Q7Z417	NUFP2_HUMAN	His-rich.		4	gtggtgcggctgctgctg	0.251	
+	4	370	STXBP4_uc010dc	NM_178509	NP_848604	Q6ZWJ1	STXB4_HUMAN	PDZ.		1	TTCCTGGAGGA	0.383	
+	3	285_286	_Shift_Ins_p.I60fs	NM_018696	NP_061166	Q9H777	RNZ1_HUMAN			0	CTTCATCACACA	0.411	
+	6	1225	SMAD4_uc002lfb.	NM_005359	NP_005350	Q13485	SMAD4_HUMAN		p.0?(35)|p.?(2)	369	ATACTGGGGGG	0.443	
-	4	734_735	xhl.1_Frame_Shift_	NM_031304	NP_112594	Q9BU89	DOHH_HUMAN	T-like PBS-type 3.		0	CCAGGGCGGCC	0.723	
-	8	1079_1081	26_uc002nee.2_I	NM_006387	NP_006378	Q8IWX8	CHERP_HUMAN	Gln-rich.		2	gctgctgttgctgctgctg	0.552	
+	23	5029_5030	0egx.2_Frame_Sh	NM_020971	NP_066022	Q9H254	SPTN4_HUMAN	Spectrin 14.		5	TGAGGACAAGGG	0.708	
-	2	1150_1151		NM_152600	NP_689813	Q8NAF0	ZN579_HUMAN	Gly-rich.		0	TTCTGCCCTTCT	0.574	478862;rs144853314
+	7	1477	BL5_uc002rid.2_F	NM_021831	NP_068603	Q8NDL9	CBPC5_HUMAN			2	ACCATCCCCCC	0.512	
-	9	1691	_uc002rjw.1_Frame	NM_001521	NP_001512	Q8WUA4	TF3C2_HUMAN			2	CAAGGCCCCAG	0.597	
+	6	2201	ed.2_Frame_Shift_	NM_181453	NP_852118	Q8IWJ2	GCC2_HUMAN	Potential.		1	GAAGTATTGTCA	0.333	
+	27	3301	0zgs.1_Frame_Sh	NM_001080539	NP_001074008	Q8NCX0	CC150_HUMAN			0	CTTCTGGGGAA	0.423	
+	17	2335	M8_uc010fyj.2_In	NM_024080	NP_076985	Q7Z2W7	TRPM8_HUMAN	Name=3; (Potential).		4	CCACACCCCCC	0.577	
+	4	1167	02xpx.2_Frame_	NM_033421	NP_219489	Q969T3	SNX21_HUMAN			2	CACCACCCCCC	0.617	
+	1	237_239	PB_uc002xvh.2_	NM_005194	NP_005185	P17676	CEBPB_HUMAN	r Lys-174 sumoylation.		0	CCCTGCCGCCG	0.65	
-	2	208	zzv.1_Frame_Shi	NM_016045	NP_057129	Q9Y3B1	SLMO2_HUMAN	RELI/MSF1.		1	CACTTGGGTTC	0.453	

+	5	751	p.F183fs|SLC17A	NM_022082	NP_071365	Q9BYT1	S17A9_HUMAN	ical; (Potential).		2	CTATTTCTCCGGC	0.642	
+	2	256		NM_172201	NP_751951	Q9Y6J6	KCNE2_HUMAN			0	TCCAAGCCAAAG	0.458	
-	4	571_573	j.1_RNA|PTTG1IP_	NM_004339	NP_004330	P53801	PTTG_HUMAN	Cytoplasmic (Potential).		1	TCCTGCAGCAGC	0.616	
+	2	378_380		NM_033318	NP_201575	Q9H4I9	CV032_HUMAN	Asp/Glu-rich.		1	CAGAGGATGATG	0.478	rs141840500
-	2	498_500	odm.1_In_Frame_I	NM_173467	NP_775738	Q8IVS2	FABD_HUMAN			1	GAATCCAGCAGC	0.532	
-	1	2125_2126	3cuf.1_Frame_Shif	NM_001407	NP_001398	Q9NYQ7	CELR3_HUMAN	r (Potential).|Cadherin 3.		11	GCATACTCTCTC	0.589	
-	7	1792	edn.2_Frame_Shi	NM_001146156	NP_001139628	P49841	GSK3B_HUMAN	rotein kinase.		2	ACCTTGATTATTT	0.254	
-	7	2209_2211	1blc.1_In_Frame_	NM_001017395	NP_001017395	O94876	TMCC1_HUMAN	Potential.		1	CCACCTGCTGC	0.581	
+	7	1596_1597	gcg.2_Frame_Shif	NM_021923	NP_068742	Q8N441	FGRL1_HUMAN	ytoplasmic (Potential).		0	agacatccacacacac	0.46	
+	1	3991_3992		NM_175918	NP_787114	Q8N1N5	CRPAK_HUMAN			0	CTGCTCACACGT	0.658	
-	15	1909	.N566fs|PROM1_	NM_006017	NP_006008	O43490	PROM1_HUMAN	cellular (Potential).		7	CCTCTATTTTTTT	0.428	
-	15	2846_2847	cah.1_Frame_Shif	NM_004439	NP_004430	P54756	EPHA5_HUMAN	Potential).|Protein kinase.		24	CATCTTGATTGG	0.401	
+	3	948	rf35_uc003jqy.2_F	NM_153706	NP_714917	Q8NE22	CE035_HUMAN			1	GGATATCAAAAGT	0.373	
+	5	378_379	k.1_Frame_Shift_I	NM_006083	NP_006074	Q13123	RED_HUMAN			1	AAATTGAGAGAG	0.46	
+	1	1027		NM_018938	NP_061761	Q9Y5E5	PCDB4_HUMAN	|Extracellular (Potential).		3	GACAATCCCCCAC	0.443	
-	2	570_572	0jgi.1_In_Frame_I	NM_001127496	NP_001120968	Q9C004	SPY4_HUMAN	Poly-Ser.		2	GATGTGCTGCTC	0.66	
+	15	2605_2606	3lny.2_Frame_Shif	NM_018989	NP_061862	Q9P2N5	RBM27_HUMAN	Potential.		3	GTGCTTAAAAAA	0.351	
+	10	987	134_uc003rdd.2_F	NM_024909	NP_079185	Q5SQI0	ATAT_HUMAN			0	ACCCTGGGGGC	0.602	
-	3	1236_1237	me_Shift_Del_p.Y	NM_001350	NP_001341	Q9UER7	DAXX_HUMAN			23	TGGCCTATAGTC	0.525	
-	2	168	.2_5'UTR|SRPK1_	NM_003137	NP_003128	Q96SB4	SRPK1_HUMAN			1	GGCCTTGGTCCT	0.547	
-	27	8038_8040		NM_001080495	NP_001073964	O15417	TNC18_HUMAN	Ser-rich.		0	tgccactactgctgctgc	0.483	
-	2	601_602		NM_022728	NP_073565	Q96NK8	NDF6_HUMAN	lization signal (Potential).		2	GTTGTCTTTTTT	0.396	
+	3	358_359	MK1_uc003uab.2_F	NM_002314	NP_002305	P53667	LIMK1_HUMAN	I zinc-binding 1.		3	ACTATGAGAAGG	0.614	
+	6	569_571	RIP1_uc011kkq.1_	NM_024653	NP_078929	Q9H875	PKRI1_HUMAN	Poly-Glu.		1	AACAGAGGAGG	0.567	
-	20	2915	_p.P781fs|TNPO3	NM_012470	NP_036602	Q9Y5L0	TNPO3_HUMAN			5	GTATAGGGGGG	0.483	
-	60	8167	Shift_Del_p.R2704	NM_006904	NP_008835	P78527	PRKDC_HUMAN	KIP-binding.		34	CCAGCCTTTTTT	0.498	
-	14	1846	p.P525fs|EIF2C2_	NM_012154	NP_036286	Q9UKV8	AGO2_HUMAN	Piwi.		0	CCGGCGGGGGG	0.647	rs148575703
-	5	474	p.A146fs|TSTA3_	NM_003313	NP_003304	Q13630	FCL_HUMAN			1	CTCTTGGCATAC	0.672	
+	1	475_476	msh.2_Frame_Shif	NM_014282	NP_055097	Q5JVS0	HABP4_HUMAN			1	GCCCCGGGGGC	0.782	
+	14	1354_1356		NM_015354	NP_056169	Q5SRE5	NU188_HUMAN			7	CTTCTCTCCCCAC	0.483	
+	6	1104_1106	4ezx.2_In_Frame_	NM_001163280	NP_001156752	O43719	HTSF1_HUMAN	Poly-Lys.		3	CTCAAAGAAGA	0.335	
-	4	1161		NM_005334	NP_005325	P51610	HCFC1_HUMAN			2	ATTGTCTTTTTCG	0.582	
-	8	877_879		NM_001561	NP_001552	Q07011	TNR9_HUMAN	ential).|Intera	p.E250G(1)	4	TCCTCCTTCTTCT	0.379	
+	11	2611_2612	bp.1_Frame_Shift	NM_015001	NP_055816	Q96T58	MINT_HUMAN	Arg-rich.		15	GAGTGGAGAGAC	0.431	
-	2	497_498	t.1_RNA|FUCA1_	NM_000147	NP_000138	P04066	FUCO_HUMAN			1	CAGTTCCAAGAC	0.51	
+	1	1263_1265		NM_004455	NP_004446	Q92935	EXTL1_HUMAN	enal (Potential).		1	GCCTGCCTCCTC	0.606	
+	34	4444_4446	.E504del|MACF1_	NM_012090	NP_036222	Q9UPN3	MACF1_HUMAN	Poly-Glu.		16	GTCTGGAGGAG	0.389	
+	18	2455	_Shift_Del_p.P398	NM_015112	NP_055927	Q6P0Q8	MAST2_HUMAN	rotein kinase.		11	CGTCCCTTTTTTT	0.552	
-	1	145	way.2_5'Flank|MIE	NM_024763	NP_079039	Q5VTH9	WDR78_HUMAN			2	CACCCCTTTTTTT	0.622	
-	7	727	1dfs.2_Frame_Shif	NM_203350	NP_976225	O95218	ZRAB2_HUMAN	equired for nuclear targeting		2	CTTGAGGGGGA	0.383	
-	2	1873_1875	wne.1_In_Frame_I	NM_007113	NP_009044	Q07283	TRHY_HUMAN	proximate tandem repeats.		5	CCTCCGGCTCCT	0.68	
-	3	928_931		NM_001122965	NP_001116437	Q6XPR3	RPTN_HUMAN	Gln-rich.		0	GCCTTGTCTGTC	0.49	
-	3	5776_5777	uc001ezv.2_Intron	NM_001014342	NP_001014364	Q5D862	FILA2_HUMAN			17	TTGGCTGTGTGT	0.515	rs140875805
-	2	1126	1fpt.1_Frame_Shif	NM_030980	NP_112242	Q9H9L3	I20L2_HUMAN	Exonuclease.		2	GTTGAGGGGGG	0.557	
+	1	903_904	uc001fso.1_RNA	NM_001004472	NP_001004472	Q8NGX6	O10R2_HUMAN	Name=7; (Potential).		3	GATTGTCACTCCA	0.416	
+	3	338_340		NM_001102566	NP_001096036	A6NKN8	PC4L1_HUMAN			0	AGGCGGAGGAG	0.488	
+	7	1574_1576	ne_Del_p.T418del|	NM_005807	NP_005798	Q92954	PRG4_HUMAN	ats of K-X-P-X-P-T-T-X.|21		1	TGCACCCACCAC	0.645	

-	32	4715_4717	Del_p.1437_1438F	NM_033056	NP_149045	Q96QU1	PCD15_HUMAN	Cytoplasmic (Potential).	13	Tggcggaggcggcgg	0.438	rs12246234
+	2	234_235	sz.2_5'UTR|LDB3_	NM_007078	NP_009009	O75112	LDB3_HUMAN	PDZ.	1	TCAAGTCTGCCA	0.614	
+	7	559	Shift_Del_p.K28fs|I	NM_018063	NP_060533	Q9NRZ9	HELLS_HUMAN		2	GTGGCTAAAAAA	0.214	
+	1	758		NM_001127389	NP_001120861	F5GZ66	F5GZ66_HUMAN		0	TGGCAGGGCGC	0.736	
+	1	268_270		NM_001004460	NP_001004460	Q9H208	O10A2_HUMAN	Name=3; (Potential).	1	TGTATTTCTTCTT	0.517	
+	3	514	01nqk.2_Frame_Sl	NM_178031	NP_821174	Q24JP5	T132A_HUMAN	cellular (Potential).	1	GTGGTCCCCCC	0.587	
-	2	285_286	.2_Splice_Site|STX	NM_003164	NP_003155	Q13190	STX5_HUMAN	lasmic (Potential).	2	GTCACTGGGGG	0.629	
+	17	3442_3444	rpn.1_In_Frame_D	NM_012308	NP_036440	Q9Y2K7	KDM2A_HUMAN		9	gaggaagaggaggag	0.473	
-	3	626_628		NM_006248	NP_006239				0	TCCTGGAGGAG	0.591	
-	3	319_320		NM_006248	NP_006239				0	TTTCCTGGAGGT	0.614	
-	3	314_315		NM_006248	NP_006239				0	GGAGGTGGGG	0.614	
-	3	189_191		NM_006248	NP_006239				0	GAGGAGATGGG	0.557	
+	10	1001_1002	e_Shift_Ins_p.I294	NM_003667	NP_003658	O75473	LGR5_HUMAN	lar (Potential).|LRR 11.	9	CACAAATAACTGA	0.356	
-	16	2240	teh.1_Frame_Shift	NM_004734	NP_004725	O15075	DCLK1_HUMAN		9	TGTGTTGAAATG	0.373	
-	1	772_774		NM_001080396	NP_001073865	B1AL88	F155A_HUMAN	Poly-Gln.	1	cgctgcctctgctgctgc	0.404	
+	2	678_680	1_Intron|NAA30_u	NM_001011713	NP_001011713	Q147X3	NAA30_HUMAN		1	GAGCAGGAGGA	0.675	
-	6	961_963	.E208del|BEGAIN_	NM_001159531	NP_001153003	Q9BUH8	BEGIN_HUMAN		0	CTCGGCCTCCTC	0.724	
+	3	434_436		NM_001030005	NP_001025176	Q8WVH0	CPLX3_HUMAN		0	CACAGAGGAGG	0.616	
-	2	158_159	2cyh.2_RNA|NAGF	NM_016256	NP_057340	Q9UK23	NAGPA_HUMAN	nenal (Potential).	0	GGAGGCGCGC	0.767	
+	3	433	l_p.T16fs|KIAA018	NM_014615	NP_055430	Q14687	GSE1_HUMAN		5	CAGCACCCCCC	0.687	
+	4	370	STXBP4_uc010dc	NM_178509	NP_848604	Q6ZWJ1	STXB4_HUMAN	PDZ.	1	TTCCTGGAGGA	0.383	
-	8	1079_1081	026_uc002nee.2_I	NM_006387	NP_006378	Q8IWX8	CHERP_HUMAN	Gln-rich.	2	gctgctgttgctgctgctg	0.552	
-	9	974_975	pni.2_Frame_Shift_	NM_003598	NP_003589	Q15562	TEAD2_HUMAN	nal activation (Potential).	3	AGGCATGGGGG	0.564	
-	2	1150_1151		NM_152600	NP_689813	Q8NAF0	ZN579_HUMAN	Gly-rich.	0	TTCTGCCCTTCT	0.574	478862;rs144853314
+	19	2288_2290	3_In_Frame_Del_	NM_015575	NP_056390	Q6Y7W6	PERQ2_HUMAN	Gln-rich.	7	TTCCCAGCAGCA	0.424	
+	4	1167	002xpx.2_Frame_S	NM_033421	NP_219489	Q969T3	SNX21_HUMAN		2	ACACCACCCCCC	0.617	
-	3	332_333		NM_020820	NP_065871	Q8TCU6	PREX1_HUMAN	DH.	6	GTCTTCGATGTT	0.48	rs141887028
+	17	2126		NM_017895	NP_060365	Q96GQ7	DDX27_HUMAN		2	GATGCCAAAAAA	0.488	
-	2	208	0zzv.1_Frame_Shi	NM_016045	NP_057129	Q9Y3B1	SLMO2_HUMAN	PRELI/MSF1.	1	ACACTTGGGTTCA	0.453	
-	9	2380	adl.1_Frame_Shift_	NM_003253	NP_003244	Q13009	TIAM1_HUMAN		10	CCTTTTGGGGTTT	0.507	
-	4	571_573	j.1_RNA|PTTG1IP_	NM_004339	NP_004330	P53801	PTTG_HUMAN	Cytoplasmic (Potential).	1	TCCTGCAGCAG	0.616	
+	38	4673_4675	P2A_uc002zjs.2_I	NM_015151	NP_055966	Q14689	DIP2A_HUMAN	Poly-Val.	2	CTGCTGGTGGT	0.596	
+	6	711_713	015_uc002zsr.2_In	NM_001003891	NP_001003891	Q96RN5	MED15_HUMAN	Poly-Gln.	1	gcagctccagcagcag	0.187	
-	3	428_430	_19DD>D|TFIP11_	NM_012143	NP_036275	Q9UBB9	TFP11_HUMAN	Poly-Asp.	0	GCTCGTCATCAT	0.532	rs145794160
+	2	378_380		NM_033318	NP_201575	Q9H4I9	CV032_HUMAN	Asp/Glu-rich.	1	CAGAGGATGATGA	0.478	rs141840500
+	2	2642_2643	WDR6_uc010hkn.2	NM_018031	NP_060501	Q9NNW5	WDR6_HUMAN		1	GTCTGCGGGGG	0.639	
+	13	2407_2408	p.L357fs|BBX_uc0	NM_001142568	NP_001136040	Q8WY36	BBX_HUMAN	Lys-rich.	4	GAATTTGAAAAAA	0.381	
-	7	2209_2211	1blc.1_In_Frame_	NM_001017395	NP_001017395	O94876	TMCC1_HUMAN	Potential.	1	ACCACCTGCTGC	0.581	
+	21	2524_2526	1buy.1_In_Frame_	NM_000283	NP_000274	P35913	PDE6B_HUMAN		0	GAGAAGGAGGA	0.562	
+	7	528_529	_p.C62fs|TMEM17	NM_032326	NP_115702	Q9BSA9	TM175_HUMAN	ical; (Potential).	0	TGTTCTGTGTGT	0.406	
+	1	3718_3719		NM_175918	NP_787114	Q8N1N5	CRPAK_HUMAN	7	0	GCTCACGTGCC	0.683	
+	1	3991_3992		NM_175918	NP_787114	Q8N1N5	CRPAK_HUMAN		0	CTGCTCACACGT	0.658	
+	9	1377	p.L385fs|C4orf23_	NM_152544	NP_689757	Q8IYL2	TRM44_HUMAN		0	AAGCAATTAAACA	0.493	
-	10	5094_5095	0idr.1_Frame_Shift_	NM_148894	NP_683692	Q8NFC6	BOD1L_HUMAN		6	TTCTTCAGAGCC	0.406	
+	11	1711	gnl.1_Frame_Shift_	NM_182485	NP_872291	Q7Z5Q1	CPEB2_HUMAN		1	GCTCCCTTTTTTT	0.443	
+	4	1023	tg.2_Frame_Shift_	NM_016531	NP_057615	P57682	KLF3_HUMAN	Pro-rich.	2	TTGTTGCAAGAG	0.453	
+	8	1054	03hhu.2_RNA|uc0	NM_001144978	NP_001138450	Q9H903	MTD2L_HUMAN		2	GCAGCTAAAAAA	0.378	

+	4	994_996	.Q279del|MMRN1_	NM_007351	NP_031377	Q13201	MMRN1_HUMAN	Poly-Gln.	4	GCTGAGCAGCA	0.448	
+	3	335	C9_uc003ieb.2_F	NM_005033	NP_005024	Q06265	EXOS9_HUMAN	RE binding.	0	GTATTCTTTTTTT	0.383	
+	1	3100_3102	3igz.2_In_Frame_	NM_032961	NP_116586	Q9P2E7	PCD10_HUMAN	ytoplasmic (Potential).	2	GCCTCTGCTGCT	0.581	
+	2	759_761		NM_004575	NP_004566	Q12837	PO4F2_HUMAN	Poly-His.	1	GGCACGcaccacc	0.552	
+	9	1679	uc003kwr.3_Intron	NM_003059	NP_003050	Q9H015	S22A4_HUMAN	lame=12; (Potential).	0	TCACCCTTTTTTT	0.418	
+	23	3406	NJ2_uc003qqz.1_	NM_003898	NP_003889	O15056	SYNJ2_HUMAN	atalytic (By similarity).	1	AGAGACCCCCC	0.637	
+	6	690	JN1_uc003sjf.2_F	NM_001130965	NP_001124437	O94901	SUN1_HUMAN	Nuclear.	0	CGCGGCCCCCG	0.557	
+	8	2132_2134		NM_138426	NP_612435	Q86VQ1	GLCI1_HUMAN	Poly-Gln.	0	ATCCCAGCAGC	0.562	
-	1	310_312	ame_Del_p.72_73	NM_005522	NP_005513	P49639	HXA1_HUMAN	Poly-His.	3	ggggtggcgatggtgg	0.527	rs10951154
+	5	601_603	0kxo.2_In_Frame_	NM_007252	NP_009183	P78424	PO6F2_HUMAN	Gln-rich.	1	cagctccagcagcagc	0.365	
+	19	5175_5176	.S1650fs|AKAP9_	NM_005751	NP_005742	Q99996	AKAP9_HUMAN		26	GTTTCAGAGAGA	0.411	
-	5	5440	D9L_uc003umk.1_	NM_152703	NP_689916	Q8IVG5	SAM9L_HUMAN		4	GAGTTGTTTTTTT	0.408	
+	14	1294_1295	_p.Q359fs|CCDC1	NM_017667	NP_060137	Q96JG6	CC132_HUMAN		0	TATGGCAGGTTT	0.272	rs140810598
-	5	964	2_Intron|GPC2_uc	NM_152742	NP_689955	Q8N158	GPC2_HUMAN		2	GGGGACCCCCC	0.642	
+	6	569_571	IP1_uc011kkq.1_	NM_024653	NP_078929	Q9H875	PKRI1_HUMAN	Poly-Glu.	1	AACAGAGGAGG	0.567	
-	7	1282_1284	1kvs.1_In_Frame_	NM_007349	NP_031375	Q6ZW49	PAXI1_HUMAN	Gln-rich.	5	ACCGGGtgctgct	0.369	
-	9	2677_2679	wwl.1_In_Frame_	NM_182643	NP_872584	Q96QB1	RHG07_HUMAN	Poly-Ser.	7	ACTGGCTGCTG	0.621	rs137989738
-	60	8167	Shift_Del_p.R2704	NM_006904	NP_008835	P78527	PRKDC_HUMAN	KIP-binding.	34	CCAGCCTTTTTT	0.498	
-	9	2947_2949	R2_uc004ari.1_Int	NM_004560	NP_004551	Q01974	ROR2_HUMAN	lasmic (Potential).	20	AGCCTTCCTCCT	0.645	
+	3	630		NM_021619	NP_067632	Q9H4Q4	PRD12_HUMAN		0	TTGAGGTGTGT	0.594	
+	11	1816_1818	zv.2_In_Frame_D	NM_005157	NP_005148	P00519	ABL1_HUMAN	n signal 1 (Potential).|Poly-	817	GATCAAGAAGA	0.616	
+	5	1490	_p.I228fs|NHS_uc	NM_198270	NP_938011	Q6T4R5	NHS_HUMAN		7	GGTATCCCCAG	0.418	
-	2	264	_Intron|ACOT9_uc	NM_001033583	NP_001028755	Q9Y305	ACOT9_HUMAN		3	TGCTTGCCTTC	0.438	
+	1	385_386		NM_022076	NP_071359	Q9H596	DUS21_HUMAN	ient for mitochondrial local	2	TTTTTTGACCCC	0.54	
-	3	268	lice_Site|ZNF630_	NM_001037735	NP_001032824	Q2M218	ZN630_HUMAN		2	GTTCCTATAACA	0.465	
-	1			NM_018159	NP_060629	Q96G61	NUD11_HUMAN		0	CTCGAGGCAGC	0.584	
-	54	7719_7721	.2_In_Frame_Del_	NM_031407	NP_113584	Q7Z6Z7	HUWE1_HUMAN	p-rich.|Glu-rich.	17	cctcatcttcctcctcctc	0.438	
+	2	92	HEPH_uc010nkr.2	NM_138737	NP_620074	Q9BQS7	HEPH_HUMAN		9	CCTCTGGGCTC	0.527	
+	12	1981	|TAF1_uc004dzt.	NM_138923	NP_620278	P21675	TAF1_HUMAN		17	ACATCAAAAAAA	0.313	
+	5	716_718	04eib.1_In_Frame	NM_016607	NP_057691	Q9UH62	ARMX3_HUMAN		2	TGGTCTGATGAT	0.448	
+	4	1067_1069	1mrt.1_In_Frame_	NM_001142526	NP_001135998	Q6PI77	BHLH9_HUMAN	Poly-Glu.	2	GGCTGAGGAGG	0.488	
-	4	413	D7_uc011muy.1_	NM_194277	NP_919253	Q6ZUT3	FRMD7_HUMAN	FERM.	1	ATTTCACCATAA	0.323	
+	6	1104_1106	4ezx.2_In_Frame_	NM_001163280	NP_001156752	O43719	HTSF1_HUMAN	Poly-Lys.	3	CTCAAAGAAGA	0.335	
-	4	396_398	_In_Frame_Del_p.	NM_001042663	NP_001036128	O94827	PKHG5_HUMAN	Poly-Glu.	1	AGCTCTCCTCC	0.631	
-	4	449_450	aog.2_Frame_Shi	NM_018198	NP_060668	Q9NVH1	DJC11_HUMAN		2	TCTCTTCTCTCT	0.505	
+	4	381_383		NM_004781	NP_004772	Q15836	VAMP3_HUMAN	IV membrane protein; (Po	0	TATCTTCATCAT	0.365	
-	7	1113	ba.1_Frame_Shif	NM_000831	NP_000822	Q13003	GRIK3_HUMAN	ellular (Potential).	7	TCGTACAGTAA	0.647	
-	4	577_578	cmv.1_Frame_Shif	NM_020365	NP_065098	Q9NR50	EI2BG_HUMAN		1	ACCTGCTTTTTT	0.317	rs148977100
+	13	1428	ddf.2_Frame_Shif	NM_001077700	NP_001071168	Q8N108	MIER1_HUMAN		1	CCCCTCCCCCA	0.383	
-	5	924_925	IQ3_uc001dfz.3_	NM_001105659	NP_001099129	A6PVS8	LRIQ3_HUMAN		2	CTGCTGTTTTTT	0.327	
+	23	2276_2278	1dge.1_In_Frame_	NM_015978	NP_057062	Q59H18	TNI3K_HUMAN	Poly-Ser.	10	TCACCTTCTTCT	0.473	
-	3	841		NM_003921	NP_003912	O95999	BCL10_HUMAN	CARD.	2	TGAGTATTTTTTT	0.343	
+	4	327_329	326_uc009wda.1_	NM_182976	NP_892021	Q5BKZ1	ZN326_HUMAN	l activation (By similarity).|	1	CACAGTGGTGG	0.409	
-	9	1232	Shift_Del_p.M408	NM_005665	NP_005656	O60447	EVI5_HUMAN	Interaction with alpha-tubul	2	TTTTCATTTTTTT	0.318	
-	64	5252	G1657fs|COL11A1	NM_001854	NP_001845	P12107	COBA1_HUMAN	lar collagen NC1.	12	TCTCACCACCA	0.378	
-	9	1607	0ovy.1_Frame_Sh	NM_004696	NP_004687	O15374	MOT5_HUMAN	ical; (Potential).	3	GGTACAAAAAAA	0.388	
+	32	3100_3101	e_Shift_Ins_p.R96	NM_003176	NP_003167	Q15431	SYCP1_HUMAN	Lys-rich (basic).	1	GGATAGAAAAAA	0.356	

+	3	513_515	nj.2_Intron|HFE2_	NM_213653	NP_998818	Q6ZVN8	RGMC_HUMAN	Poly-Gly.	1	CTTCGAGGAGG	0.626	
+	6	910	09wlw.2_Frame_S	NM_019032	NP_061905	Q6UY14	ATL4_HUMAN		2	CCCATCCCCCC	0.622	rs145240194
-	1	643_645	.E61del|MCL1_uc	NM_021960	NP_068779	Q07820	MCL1_HUMAN	PEST-like.	0	CTCGTCCTCCT	0.635	
-	2	1111_1113	wne.1_In_Frame_	NM_007113	NP_009044	Q07283	TRHY_HUMAN	of R-R-E-Q-E-E- E-R-R-E-	5	tcgcgcctctcctcctcc	0	rs71757496
-	2	245	R2A_uc001fbf.2_I	NM_001017418	NP_001017418	P35325	SPR2B_HUMAN		0	AGGGTGGGGAA	0.567	
-	2	985	2_Frame_Shift_De	NM_001111	NP_001102	P55265	DSRAD_HUMAN		6	TGTCTGGTCTT	0.493	
-	4	1309		NM_006617	NP_006608	P48681	NEST_HUMAN	Tail.	6	GGTGTGGGGGG	0.597	
+	3	338_340		NM_001102566	NP_001096036	A6NKN8	PC4L1_HUMAN		0	AGGCGGAGGAG	0.488	
+	17	2363_2365	2F1_uc010plh.1_I	NM_002697	NP_002688	P14859	PO2F1_HUMAN		5	TGCGTCCACCAC	0.601	
+	7	1724_1726	e_Del_p.E466del|	NM_005807	NP_005798	Q92954	PRG4_HUMAN	epeats of K-X-P-X-P-T-T-X	1	ACCAAGGAGCC	0.635	
+	10	1834	p.C507fs|PKP1_uc	NM_000299	NP_000290	Q13835	PKP1_HUMAN	ARM 6.	2	TGACTGCCCCC	0.572	
-	1	89_91		NM_000537	NP_000528	P00797	RENI_HUMAN		4	CCAGAGCAGCA	0.581	917743;rs142739309
-	1	895		NM_203376	NP_976310	Q6P7N7	TMM81_HUMAN	lasmic (Potential).	0	GCAGGCCCCCC	0.537	
+	4	635_646		NM_001104548	NP_001098018				0	Tagcagcagcagca	0.283	30217;rs72359595;rs150848171
+	2	420	Shift_Del_p.S42fs	NM_016121	NP_057205	Q9Y597	KCTD3_HUMAN	BTB.	3	AGATTCTTTTTTT	0.229	
+	4	3146_3147	ea.1_Frame_Shift_	NM_198551	NP_940953	Q5JRA6	MIA3_HUMAN	ellular (Potential).	5	ACCACCTCTAGA	0.545	
+	3	384_386	tron|FAM177B_uc	NM_207468	NP_997351	A6PVY3	F177B_HUMAN	Poly-Glu.	1	GCACAgaggagga	0.36	
+	5	775	_p.*180fs|FBXO28	NM_015176	NP_055991	Q9NVF7	FBX28_HUMAN		5	AGCCCTAACAA	0.423	
+	27	7308	CN_uc001hsp.1_	NM_001098623	NP_001092093	Q5VST9	OBSCN_HUMAN		28	AGGCTGGGGGG	0.662	
-	1	2019_2020		NM_175876	NP_787072	Q8IYI6	EXOC8_HUMAN		1	GCTCTCCAAAA	0.455	
+	3	710	hvy.1_Frame_Shi	NM_173508	NP_775779	Q8IY50	S35F3_HUMAN	ical; (Potential).	2	TTCTTTGGACAC	0.413	
+	20	2516	R_uc010pxx.1_In	NM_000254	NP_000245	Q99707	METH_HUMAN	inding N-terminal.	3	TAAACCAAAAAA	0.279	
+	99	14329	yb.1_Frame_Shift_	NM_001035	NP_001026	Q92736	RYR2_HUMAN	lame=M7; (Potential).	33	ACAACTTTTTTT	0.403	
+	3	422_423	pzb.1_Frame_Shi	NM_001001957	NP_001001957	Q7Z3T1	OR2W3_HUMAN	lasmic (Potential).	3	GGCTGGACCC	0.594	
+	1	246	L13_uc001ids.2_I	NM_001004686	NP_001004686	Q8NH16	OR2L2_HUMAN	lasmic (Potential).	3	TTTTTGGACAT	0.363	
+	1	595	L13_uc001ids.2_I	NM_001004687	NP_001004687	Q8NG85	OR2L3_HUMAN	Name=5; (Potential).	0	ACAGTGTTTTTG	0.488	rs60743763
-	1	707		NM_001004693	NP_001004693	Q8NGZ9	O2T10_HUMAN	lasmic (Potential).	1	AAGGCCTTTTTC	0.478	
+	5	471_473	_p.L92del|TSPAN4	NM_003271	NP_003262	O14817	TSN4_HUMAN	ical; (Potential).	1	CTTCCTGCTGC	0.65	rs61867552
-	25	4223	.N1311fs|NUP98_	NM_016320	NP_057404	P52948	NUP98_HUMAN		12	GGCTGTTTTTT	0.512	
-	1	429	5_uc001mbq.1_I	NM_001005168	NP_001005168	Q6IFG1	O52E8_HUMAN	lasmic (Potential).	2	TTGCTGGTGAG	0.512	
+	1	310_312		NM_178168	NP_835462	Q9H207	O10A5_HUMAN	Name=3; (Potential).	3	TGTATTTCTTCTT	0.517	
+	9	842	rck.1_Frame_Shift	NM_018222	NP_060692	Q9NVD7	PARVA_HUMAN	CH 2.	3	TGGTGAAAAAG	0.522	
+	1	525		NM_001003750	NP_001003750	Q8N0Y5	OR8I2_HUMAN	ellular (Potential).	1	CAATCATTTTTTT	0.443	rs112181516
+	1	62_64	0rld.1_In_Frame_	NM_001079807	NP_001073275				2	AGTGGCTGCTG	0.567	
+	3	548_550	rlo.1_In_Frame_	NM_004265	NP_004256	O95864	FADS2_HUMAN	ical; (Potential).	2	TTCTTCCTCCT	0.537	
+	2	185_187		NM_015516	NP_056331	Q8WUA8	TSK_HUMAN		0	GCCCCTGCTGC	0.616	
-	2	682		NM_004549	NP_004540	O95298	NDUC2_HUMAN	ical; (Potential).	0	CCAGCAAAAAAA	0.358	
-	2	60	ntron|CASP5_uc0	NM_004347	NP_004338	P51878	CASP5_HUMAN		3	TACGCCTTTTTTT	0.388	
-	8	1187_1189	CADM1_uc001ppj.	NM_014333	NP_055148	Q9BY67	CADM1_HUMAN	ellular (Potential).	2	gtaaggatggtggtggt	0.266	
-	4	537_539	.D104del|IFT46_u	NM_020153	NP_064538	Q9NQC8	IFT46_HUMAN	-rich (highly acidic).	0	GCTCTTCATCAT	0.419	
+	9	1502_1504		NM_005188	NP_005179	P22681	CBL_HUMAN	Glu-rich (acl(1)|p.E366_K	149	AAATTATGATGAT	0.473	
+	16	2803		NM_005188	NP_005179	P22681	CBL_HUMAN	n with CD2AP.|UBA.	149	ATGGCCAAAAAC	0.507	
-	3	319_320		NM_006248	NP_006239				0	TTTCCTGGAGGT	0.614	
-	3	314_315		NM_006248	NP_006239				0	GGAGGTGGGG	0.614	
-	18	2595	1rlx.2_Frame_Shif	NM_017641	NP_060111	Q7Z4S6	KI21A_HUMAN		7	GGTTTCTTTTTTG	0.323	
-	6	782	_p.K63fs|RPAP3_u	NM_024604	NP_078880	Q9H6T3	RPAP3_HUMAN	TPR 4.	1	AATACCTTTTTTG	0.363	
+	9	664	1ruq.1_Frame_Sh	NM_001031698	NP_001026868	Q6NWY9	PR40B_HUMAN		5	CCTGACCCCCC	0.637	

+	3	427_428	_Shift_Del_p.G91f	NM_173602	NP_775873	Q9P265	DIP2B_HUMAN		6	ATCTGGGGGAG	0.48	
-	1	193		NM_175068	NP_778238	Q86Y46	K2C73_HUMAN	lead.|Gly-rich.	6	GGGCACCCCCC	0.637	
+	1	298		NM_001005497	NP_001005497	A6NL08	O6C75_HUMAN	Name=3; (Potential).	3	CAGCTATTTTTT	0.438	
+	5	442_443	_Shift_Del_p.L74f	NM_001089704	NP_001083173	P61224	RAP1B_HUMAN		0	GATTTACAAGAC	0.327	
-	25	3416	SBNO1_uc010taq	NM_018183	NP_060653	A3KN83	SBNO1_HUMAN		9	TTCCATTTTTTT	0.388	
-	8	694	2_uc001ume.2_I	NM_199254	NP_954863	Q6XPS3	TPTE2_HUMAN	ical; (Potential).	0	ATGTCAAAAAA	0.303	
-	9	1177_1178	p.I309fs|DIAPH3_	NM_001042517	NP_001035982	Q9NSV4	DIAP3_HUMAN	GBD/FH3.	2	TGTCAATTTTTT	0.322	
+	20	3706_3707	.A881fs|LMO7_uc	NM_015842	NP_056667	Q8WWI1	LMO7_HUMAN		5	AGGCAGAGAG	0.386	
-	15	2201_2202	_p.K703fs|RBM26_	NM_022118	NP_071401	Q5T8P6	RBM26_HUMAN	Potential.	1	TTACCTGTTTTTT	0.332	
+	16	4738_4740	1xmv.2_In_Frame	NM_015556	NP_056371	O43166	SI1L1_HUMAN	Ser-rich.	4	tcctcctcttcctcctcctc	0.468	
-	2	400	2ctw.1_Intron|ZS	NM_032805	NP_116194	Q96SZ4	ZSC10_HUMAN	Pro-rich.	1	TGGCTGGGGAC	0.582	
-	7	1766		NM_000243	NP_000234	O15553	MEFV_HUMAN		6	CATCTACCTGA	0.502	
+	7	1037_1039	.K238del|UBN1_u	NM_001079514	NP_001072982	Q9NPG3	UBN1_HUMAN	Lys-rich.	2	TAAGGAGAAGAA	0.453	
-	11	1628_1630	H3_uc002die.2_I	NM_017539	NP_060009	Q8TD57	DYH3_HUMAN	n (By similarity).	18	CGATCAGCAGC	0.498	
+	9	3655	.K928fs|TNRC6A_	NM_014494	NP_055309	Q8NDV7	TNR6A_HUMAN	ction with EIF2C1 and EIF	2	GTGGCAAAAAA	0.224	
+	25	5954	_Shift_Del_p.P16	NM_006662	NP_006653	Q6ZRS2	SRCAP_HUMAN	Pro-rich.	4	CTGGTCCCCCC	0.612	
+	13	3813_3815		NM_014712	NP_055527	O15047	SET1A_HUMAN	Ser-rich.	3	Gctcctcatcctcctcct	0.389	
+	3	278_280	vho.1_In_Frame_	NM_020312	NP_064708	O75208	COQ9_HUMAN		1	CGGCGAGGAGG	0.576	rs149029279
-	14	1166_1168	h.2_In_Frame_Del	NM_001297	NP_001288	Q14028	CNGB1_HUMAN	ytoplasmic (Potential).	4	tcctcctcttcctcctcctc	0.414	
-	6	1372_1373	XOC3L_uc002ery.	NM_178516	NP_848611	Q86VI1	EX3L1_HUMAN		0	TGCCTCCAGCTG	0.545	
+	15	2170_2172	.E413del|SLC9A	NM_004594	NP_004585	Q14940	SL9A5_HUMAN		2	GTCTGAGGAGG	0.571	
+	3	433	_p.T16fs|KIAA01	NM_014615	NP_055430	Q14687	GSE1_HUMAN		5	CAGCACCCCCC	0.687	
-	10	1079_1081	63EE>E|C17orf85	NM_001114118	NP_001107590	Q53F19	CQ085_HUMAN	Glu-rich.	1	tcttcctcttcctcctcctc	0.379	
+	6	719	_p.N140fs|MYOCD	NM_153604	NP_705832	Q8IZQ8	MYCD_HUMAN		5	GGTAACCAGGT	0.468	
+	9	1291	_p.L457fs|SLC13	NM_003984	NP_003975	Q13183	S13A2_HUMAN		0	CTCCTCGACTG	0.562	
+	3	202_204	10crt.2_In_Frame_	NM_003170	NP_003161	Q7KZ85	SPT6H_HUMAN	sp/Glu-rich.	3	AGATGAGGAGG	0.453	
+	34	4663_4665	0crt.2_In_Frame_	NM_003170	NP_003161	Q7KZ85	SPT6H_HUMAN	Poly-Ser.	3	CCCTAGCAGCA	0.537	
-	1	40_41		NM_031960	NP_114166	Q9BYQ9	KRA48_HUMAN		0	TGACCATGGTGT	0.55	
-	2	516_517		NM_004645	NP_004636	P38432	COIL_HUMAN		1	CTCTTGTTTTTT	0.366	
-	33	4884	yn.1_Frame_Shift_	NM_032582	NP_115971	Q8NFA0	UBP32_HUMAN		5	TTTGGGTTTTTG	0.423	
+	9	1570_1571	NF236_uc002lmk.	NM_007345	NP_031371	Q9UL36	ZN236_HUMAN		4	AAAAAGAAAAAA	0.381	
-	11	1320_1321	nfg.1_Frame_Shift	NM_033417	NP_219485	Q9BT25	HAUS8_HUMAN		0	TGAACGAGAGAG	0.495	
+	17	1944_1945	iu.2_Frame_Shift_	NM_000540	NP_000531	P21817	RYR1_HUMAN	smic.|B30.2/SPRY 1.	12	CTCCCTGTGTGT	0.53	
-	6	1386	PSG1_uc002our.1	NM_006905	NP_008836	P11464	PSG1_HUMAN		2	ggaactgtccagtctac	0	
-	1	1886		NM_032040	NP_114429	Q9H0W5	CCDC8_HUMAN		3	GCCCCTGCCCTC	0.627	
-	9	2408_2410	0xyr.1_In_Frame_	NM_015063	NP_055878	Q9UPR5	NAC2_HUMAN	lasmic (Potential).	4	ACCCGTCCTCCT	0.616	
-	6	547_548	2pkf.2_Frame_Sh	NM_001130915	NP_001124387	Q6ZN01	MASTR_HUMAN	Pro-rich.	1	TTGTGTGGGGGG	0.569	
+	9	1040	Shift_Del_p.P156	NM_014516	NP_055331	O75175	CNOT3_HUMAN		3	TCCCCTCCCAG	0.632	rs36665
-	2	333_335	qdo.2_In_Frame_	NM_001145303	NP_001138775	Q7Z404	TMC4_HUMAN	xtracellular (Potential).	1	TCCATCCTCCT	0.645	
+	11	1043_1044	V1C2_uc002rat.2_	NM_001039362	NP_001034451	Q8NEY4	VATC2_HUMAN		1	CCGACAGAGAGA	0.604	
+	9	1268	_p.T214fs|RASGR	NM_170672	NP_733772	Q8IV61	GRP3_HUMAN	Ras-GEF.	5	ACCAACCCCCC	0.428	
-	4	557	0yoq.1_Splice_Sit	NM_014614	NP_055429	Q14997	PSME4_HUMAN		5	GAACTGGGGGG	0.347	
+	1	96_98	2sda.2_In_Frame_	NM_203437	NP_982261	Q6ULP2	AFTIN_HUMAN		2	CAGAGGATGATG	0.409	
-	5	659_660	sud.1_Frame_Shif	NM_032788	NP_116177	Q96K75	ZN514_HUMAN		0	TACCTGGAATAA	0.381	
+	8	1145	2_Intron|ANKRD3	NM_001164315	NP_001157787	A6QL64	AN36A_HUMAN		0	ACAGGTATTTTG	0.302	
+	8	1227		NM_152945	NP_694453	Q8IUH3	RBM45_HUMAN		0	TCATGCAAAAAA	0.353	
-	2	611_612	2upb.2_Frame_Sh	NM_013436	NP_038464	Q9Y2A7	NCKP1_HUMAN		2	TTGTTGCGGGTT	0.371	

+	7	2036	p.L641fs|SGOL2_	NM_152524	NP_689737	Q562F6	SGOL2_HUMAN		4	TGGCCTAAAAAA	0.333	
+	17	2334_2335	PM8_uc010fyj.2_In	NM_024080	NP_076985	Q7Z2W7	TRPM8_HUMAN	Name=3; (Potential).	4	GCCACACCCCC	0.574	
+	2	175_177		NM_022134	NP_071417	Q9H3Q3	G3ST2_HUMAN	type II membrane protein;	0	GGTCATCCTCCT	0.631	
-	14	1294	L1L2_uc010zrl.1_	NM_025229	NP_079505	Q5TEA6	SE1L2_HUMAN	r (Potential).|Sel1-like 7.	2	CCACCCTTTTTC	0.393	
+	10	1729	zwj.1_Frame_Shif	NM_002466	NP_002457	P10244	MYBB_HUMAN		5	TTGTAACCCCAG	0.622	
+	20	3995_3997	tm.2_In_Frame_D	NM_181659	NP_858045	Q9Y6Q9	NCOA3_HUMAN	n.|Acetyltransferase.	5	cagcagcaacagcaa	0.31	;rs11472494;rs112826888
-	1	737	e_Shift_Del_p.K2	NM_080618	NP_542185	Q8NI51	CTCFL_HUMAN		4	CAGGCCTTTTTC	0.502	
-	11	905	PTE_uc002yir.1_	NM_199261	NP_954870	P56180	TPTE_HUMAN	ical; (Potential).	5	AATGTCAAAAAA	0.299	
-	7	2832		NM_007038	NP_008969	Q9UNA0	ATS5_HUMAN	Cys-rich.	4	CACTTCCCCCG	0.493	
-	3	428_430	_19DD>D|TFIP11_	NM_012143	NP_036275	Q9UBB9	TFP11_HUMAN	Poly-Asp.	0	GCTCGTCATCAT	0.532	rs145794160
-	1	2553_2554		NM_002430	NP_002421	Q10571	MN1_HUMAN	Poly-Gln.	10	ctgctgctgttgctgctgc	0.391	rs34890218
-	1	130	_RNA|INPP5J_uc	NM_080430	NP_536355	Q8WWX9	SELM_HUMAN		0	AGTGGCGGCTG	0.701	
+	7	686_688	Del_p.E197del|SH	NM_018957	NP_061830	Q9Y3L3	3BP1_HUMAN	BAR.	1	CTGAAGGAGGA	0.498	
+	7	1953_1961	atq.1_In_Frame_D	NM_001039141	NP_001034230	Q9H2D6	TARA_HUMAN		1	GCCTCCAGAAC	0.589	
+	2	1850	.3_Intron|SYNGR	NM_006116	NP_006107	Q15750	TAB1_HUMAN		1	CCTCTCCCCCA	0.612	
-	4	1073	Shift_Del_p.D212f	NM_001001331	NP_001001331	Q01814	AT2B2_HUMAN	lasmic (Potential).	6	CTATGTCCCCAA	0.587	
+	1	263_265	bwl.1_In_Frame_	NM_133625	NP_598328	Q92777	SYN2_HUMAN		2	CAGCAAGCGCC	0.345	272937;rs74800608
-	1	205_207	g.1_In_Frame_De	NM_004628	NP_004619	Q01831	XPC_HUMAN	lu.|Glu-rich (acidic).	3	CTCACCCTCCTC	0.734	rs72561774
-	19	1979_1980	kw.2_Frame_Shift	NM_017886	NP_060356	Q96C45	ULK4_HUMAN		0	GGGTTCTTTTTT	0.45	
+	13	1986_1987	NKTR_uc003clq.1	NM_005385	NP_005376	P30414	NKTR_HUMAN		3	GACAGTCCCCC	0.421	
+	72	11844	ddv.2_Frame_Shif	NM_015512	NP_056327	Q9P2D7	DYH1_HUMAN		3	GTTCCTGGACGA	0.602	
+	14	1647	dgm.2_Frame_Shif	NM_006254	NP_006245	Q05655	KPCD_HUMAN	rotein kinase.	9	TCAACGGGGGG	0.602	
-	16	3037_3039	C2_uc003dhq.1_R	NM_015576	NP_056391	O15083	ERC2_HUMAN	Poly-His.	2	gtggtgatggtggtggt	0.389	
-	13	1581_1583	_Frame_Del_p.S1	NM_015541	NP_056356	Q96JA1	LRIG1_HUMAN	tial).|Ig-like C2-type 1.|Poly	5	GGGAGCTGCTG	0.547	
-	3	457_458	717_uc003dpw.3_	NM_001128223	NP_001121695	C9JSV9	C9JSV9_HUMAN		0	TACAGGGTCCTC	0.51	rs76346895
-	7	2209_2211	1blc.1_In_Frame_	NM_001017395	NP_001017395	O94876	TMCC1_HUMAN	Potential.	1	CCACCTGCTGC	0.581	
-	6	2336	|ATP2C1_uc003e	NM_014065	NP_054784	Q2TB18	ASTE1_HUMAN		0	TCTGCCTTTTTT	0.403	
+	4	1562		NM_139209	NP_631948	Q8WTQ7	GRK7_HUMAN	kinase C-terminal.	5	GGTTCGGGGGG	0.463	
-	6	783	RL_uc003fme.2_In	NM_018622	NP_061092	Q9H300	PARL_HUMAN	intermembrane (Potential).	0	GCTCTTGACCCA	0.418	
+	1	3715_3716		NM_175918	NP_787114	Q8N1N5	CRPAK_HUMAN	7	0	CCTGCTCACGTC	0.693	rs144861850
+	1	3718_3719		NM_175918	NP_787114	Q8N1N5	CRPAK_HUMAN	7	0	GCTCACGTGCCC	0.683	
+	1	3991_3992		NM_175918	NP_787114	Q8N1N5	CRPAK_HUMAN		0	CTGCTCACACGT	0.658	
-	5	1026_1028		NM_000730	NP_000721	P32238	CCKAR_HUMAN	lasmic (Potential).	4	GGCCCTGCTGC	0.606	
-	9	1294_1295	hba.1_Frame_Shi	NM_004898	NP_004889	O15516	CLOCK_HUMAN	PAS 1.	3	ATTGCTAAAAAA	0.287	
+	4	994_996	.Q279del|MMRN1	NM_007351	NP_031377	Q13201	MMRN1_HUMAN	Poly-Gln.	4	GCTGAGCAGCA	0.448	
+	22	2560_2562	cgc.1_In_Frame_	NM_001148	NP_001139	Q01484	ANK2_HUMAN		14	GAGGTCACCACC	0.443	
+	32	3975	Shift_Del_p.T468f	NM_001148	NP_001139	Q01484	ANK2_HUMAN		14	CCTTTACAACAAA	0.378	
-	18	1757	ijz.3_Frame_Shift	NM_001102653	NP_001096123	Q01804	OTUD4_HUMAN		3	GTTGGTCCAAAA	0.478	
-	5	1095	p.F207fs|LRBA_u	NM_006726	NP_006717	P50851	LRBA_HUMAN		7	AAAGTTAAAAAA	0.408	
+	9	624_625	jqh.3_Frame_Shif	NM_001136034	NP_001129506	Q9NQI0	DDX4_HUMAN	Gly-rich.	2	TTGGTTCTAGAA	0.342	
-	2	1109_1111	60DD>D|TAF9_uc	NM_003187	NP_003178	Q16594	TAF9_HUMAN	Poly-Asp.	0	tatcatagtcatcatcat	0.256	
+	17	2312_2314	uc003kgi.3_Intron	NM_003248	NP_003239	P35443	TSP4_HUMAN	TSP type-3 7.	0	GAGTGTGATGAT	0.562	
-	1	189_191	lwl.2_In_Frame_D	NM_032782	NP_116171	Q8TDQ0	HAVR2_HUMAN		0	TAGTAGCAGCA	0.291	
+	13	4948	nfs.1_Frame_Shift_	NM_022455	NP_071900	Q96L73	NSD1_HUMAN	PHD-type 2.	3	GATGTTAAAAGG	0.423	
+	11	1475	mkl.2_Frame_Shif	NM_001746	NP_001737	P27824	CALX_HUMAN	nenal (Potential).	0	CTGACATTTTTTT	0.423	
-	1	357	Shift_Del_p.P20fs	NM_175062	NP_778232	Q8N431	RGF1C_HUMAN		1	TCGGTGGGGGG	0.652	
-	8	1068_1069	wm.2_Frame_Shi	NM_006638	NP_006629	O75818	RPP40_HUMAN		0	TGATTATTAAAAA	0.356	

-	8	1612_1613	_Ins_p.214_214Q	NM_000332	NP_000323	P54253	ATX1_HUMAN	Poly-Gln.	4	tgctgctgctgctgctga	0.381	806515;rs66949327
-	8	1604_1606	me_Del_p.H211de	NM_000332	NP_000323	P54253	ATX1_HUMAN	Poly-Gln.	4	ctgctgctgatgctgat	0.384	rs59310777
-	3	444	p.M121fs|SLC17A2_uc003nfl.2_Frame_Shift_Del_p.M1			O00624	NPT3_HUMAN		1	CAAGCATTTTTT	0.453	
-	3	544	BR1_uc011dlr.1_	NM_001470	NP_001461	Q9UBS5	GABR1_HUMAN	xtracellular (Potential).	7	GCGCTCCCCCC	0.632	
+	7	1303_1304	tron|LOC285830_	NM_001098479	NP_001091949	P30511	HLAF_HUMAN		0	ATCTTGTTTTTT	0.535	
+	7	1034		NR_027822					0	GAGTCATTTTTC	0.488	
+	5	704_705	p.S170fs|RING1_	NM_002931	NP_002922	Q06587	RING1_HUMAN	iptional repression (By sim	2	TGAGTGGGGG	0.619	
+	8	1146_1148	n.1_RNA|UHRF1	NM_017754	NP_060224	Q6BDS2	URFB1_HUMAN		3	GCAACAGCAGC	0.552	
+	14	3278_3279	.H1068fs|CUL9_u	NM_015089	NP_055904	Q8IWT3	CUL9_HUMAN		12	GATGCATAAGG	0.52	
+	1	73	dwh.1_Frame_Sh	NM_005588	NP_005579	Q16819	MEP1A_HUMAN		3	ATTCTCTTTTTTA	0.388	rs146460388
+	2	226		NM_014051	NP_054770	Q9Y6G1	TM14A_HUMAN	ical; (Potential).	0	GAAGCATTTTTG	0.433	
-	5	501		NM_145740	NP_665683	P08263	GSTA1_HUMAN	ST C-terminal.	1	TAGCGATTTTTT	0.433	
-	2	453		NM_001003760	NP_001003760	Q9H511	KLH31_HUMAN	BTB.	1	GGGTCTTTTTTT	0.423	
+	26	3021_3022	p.Q914fs|MYO6_	NM_004999	NP_004990	Q9UM54	MYO6_HUMAN	Potential.	2	TTACAGAAAAAA	0.381	
-	13	1115	.2_Frame_Shift_	NM_020320	NP_064716	Q5T160	SYRM_HUMAN		3	AAATGCTTTTTTT	0.333	
+	9	3522_3524	_3'UTR|GRM1_u	NM_000838	NP_000829	Q13255	GRM1_HUMAN	|Cytoplasmic (Potential).	19	TCTCCAGCAGC	0.66	
+	11	970	p.L246fs|IQCE_uc	NM_152558	NP_689771	Q6IPM2	IQCE_HUMAN	Potential.	0	CGTCTCCAGAC	0.473	rs7786703
+	6	694_695	p.L112fs|ZDHHC4	NM_001134388	NP_001127860	Q9NPG8	ZDHC4_HUMAN	ical; (Potential).	2	AACCTGTTTTTT	0.45	
+	8	2004_2005	srz.2_Frame_Shift	NM_014660	NP_055475	O94880	PHF14_HUMAN		3	TTGCAAGAGAGA	0.376	
+	9	1209	_Shift_Del_p.K304	NM_016447	NP_057531	Q9NZW5	MPP6_HUMAN		0	GTAGCAAAAAAA	0.299	
-	21	2723	ite_p.N737_splic	NM_015550	NP_056365	Q9H4L5	OSBL3_HUMAN		1	TAGGATCTAAGA	0.366	
+	1	403_405	c003tbl.3_5'Flank	NM_002047	NP_002038	P41250	SYG_HUMAN		1	CGCTCTGCTGC	0.749	
+	3	337	rf16_uc011kaf.1_I	NM_006658	NP_006649	O96001	GSUB_HUMAN		3	AGACCAAAAAA	0.438	
+	3	559	l_p.I179fs|FKBP9	NM_007270	NP_009201	O95302	FKBP9_HUMAN	se FKBP-type 1.	14	TGTGATCCCCCC	0.443	
+	3	342	_uc011kby.1_Intro	NM_002541	NP_002532	Q02218	ODO1_HUMAN		2	GGACATTTTTTT	0.577	
+	18	7513_7514	13_uc010kys.1_5	NM_152701	NP_689914	Q86UQ4	ABCAD_HUMAN		10	CTCTTAGAAATG	0.421	
+	3	211	trb.2_Frame_Shif	NM_015969	NP_057053	Q9Y2R5	RT17_HUMAN		0	CAGTTGGGGAT	0.438	
+	5	1249	p.P231fs|DTX2_u	NM_020892	NP_065943	Q86UW9	DTX2_HUMAN		2	CCCCCACACAG	0.657	rs147779783
-	10	1091_1092	p.S339fs|ABCB4_	NM_018849	NP_061337	P21439	MDR3_HUMAN	).|ABC transmembrane typ	6	GGATTGAAAAAA	0.347	
-	5	1204	.2_Frame_Shift_D	NM_000466	NP_000457	O43933	PEX1_HUMAN		2	ACCTAATTTTTTT	0.353	
-	16	1707	PW1_uc003uus.2_	NM_017984	NP_060454	Q9H0M4	ZCPW1_HUMAN		0	CTTGGTTTTTTG	0.478	
-	12	1337_1338	_Shift_Ins_p.F243	NM_017984	NP_060454	Q9H0M4	ZCPW1_HUMAN	PWWP.	0	TTCTCCAAAAAA	0.48	
+	8	1077_1079	xa.2_In_Frame_D	NM_015908	NP_056992	Q9BXP5	SRRT_HUMAN	Glu-rich.	2	GAGCAGGAGGA	0.596	
+	12	2008	ljj.1_Frame_Shift_	NM_021930	NP_068749	Q6NUQ1	RINT1_HUMAN	INT1/TIP20.	4	GTCTTTGATGAC	0.398	
-	20	2915	_p.P781fs|TNPO3	NM_012470	NP_036602	Q9Y5L0	TNPO3_HUMAN		5	GTATAGGGGGG	0.483	
+	11	2081_2082	kvv.1_Frame_Shif	NM_053043	NP_444271	Q96EV2	RBM33_HUMAN	Pro-rich.	1	CTGCCCACACAC	0.53	
-	15	2035		NM_001010906	NP_001010906	Q68CJ6	SLIP_HUMAN		2	AGGAAATTTTTTT	0.453	
-	2	417	166_uc003xhu.2_	NM_016127	NP_057211	Q96BY9	TMM66_HUMAN		0	CTTTTGGGGTAT	0.458	
-	16	3521_3523	.E993del|MYST3_	NM_001099412	NP_001092882	Q92794	MYST3_HUMAN	Poly-Glu.	7	CCGGCTCCTCC	0.567	
-	7	1563	xon.3_Frame_Shif	NM_001099412	NP_001092882	Q92794	MYST3_HUMAN	tion with RUNX1-1.	7	ACCTGTTTTTTG	0.398	
+	12	1709_1710	p.R537fs|POP1_u	NM_001145860	NP_001139332	Q99575	POP1_HUMAN		2	AAGTTAGACAGC	0.406	
-	6	1215		NM_001385	NP_001376	Q14117	DPYS_HUMAN		2	CACGCCTTTTTC	0.478	
+	3	444_445	lim.1_Frame_Shif	NM_005005	NP_004996	Q9Y6M9	NDUB9_HUMAN		2	CTTTGCCAAGAG	0.465	
-	15	2303	mdt.2_Frame_Shif	NM_004519	NP_004510	O43525	KCNQ3_HUMAN		5	GTTCCGGGGGG	0.547	
+	23	3289_3290	.A1064fs|SMARC	NM_003070	NP_003061	P51531	SMCA2_HUMAN	case C-terminal.	3	TGAGAGCGACTA	0.441	
+	13	2110_2112	598del|GRIN1_u	NM_007327	NP_015566	Q05586	NMDZ1_HUMAN	lasmic (Potential).	1	CAGCGAGGAGG	0.739	
-	6	2189	RHGAP6_uc004c	NM_013427	NP_038286	O43182	RHG06_HUMAN	Rho-GAP.	2	ACTCTCTTTTTTG	0.368	

+	8	1061	FD1_uc004cvs.3	NM_003611	NP_003602	O75665	OFD1_HUMAN	Potential.	0	GAAGCAAAAAA	0.299	
+	16	2457	1_uc010nen.2_F	NM_003611	NP_003602	O75665	OFD1_HUMAN	nteraction with SDCCAG8.	0	TCTCTGAGCAG	0.537	
+	1	1497_1499		NM_001136234	NP_001129706				1	gctgctattgctgctgct	0.202	
-	18	2564_2566	sw.2_In_Frame_	NM_015107	NP_055922	Q9UPP1	PHF8_HUMAN		3	CGTTCTCCTCC	0.591	
+	5	716_718	04eib.1_In_Frame	NM_016607	NP_057691	Q9UH62	ARMX3_HUMAN		2	GGTCTGATGAT	0.448	
-	3	652_653	9B_uc004eli.1_In	NM_016370	NP_057454	Q9NP90	RAB9B_HUMAN		3	TGTTACCCAGAA	0.45	
-	1	1805_1806		NM_003604	NP_003595	O14654	IRS4_HUMAN		10	CCTTTGCCCCC	0.545	
-	2	203	_p.R4fs|CXorf56_	NM_022101	NP_071384	Q9H5V9	CX056_HUMAN		0	GTCCCGGGGC	0.463	
-	13	1536_1537	evh.2_Frame_Shi	NM_004208	NP_004199	O95831	AIFM1_HUMAN	xidoreductase (By similarit	5	TGGTGCTCTACC	0.431	
-	1	159		NM_001009609	NP_001009609	Q5MJ09	SPXN3_HUMAN		2	TCATCATTTTTTT	0.239	
-	1	825		NM_001009615	NP_001009615	Q5MJ10	SPXN2_HUMAN		1	TCATCATTTTTTT	0.239	
+	3	1556_1558	Q477del|MAMLD1	NM_005491	NP_005482	Q13495	MAMD1_HUMAN	Poly-Gln.	0	cagcaacagcagca	0.433	
+	3	1864_1866	Q581del|MAMLD1	NM_005491	NP_005482	Q13495	MAMD1_HUMAN	Poly-Gln.	0	Tgcagctgcagcagca	0.488	
+	5	666_668	HMGB3_uc004fer	NM_005342	NP_005333	O15347	HMGB3_HUMAN	Glu-rich (acidic).	0	gaagaagaggagga	0.281	
+	9	1017_1019		NM_173493	NP_775764	Q8IV76	PASD1_HUMAN	Poly-Ala.	3	TGAACCCgctgctg	0.355	
-	14	4550		NM_000132	NP_000123	P00451	FA8_HUMAN	B.	11	AGGTTATTTTTTT	0.413	
-	35	4931	bm.1_Frame_Shift	NM_020765	NP_065816	Q5T4S7	UBR4_HUMAN		25	CTCTTCCACCG	0.507	
-	9	1622_1624	_RNA|uc001ive.1_	NM_018109	NP_060579	Q9NVV4	PAPD1_HUMAN		1	TGATGTCCTCCT	0.507	
+	4	1819_1821	qvt.1_In_Frame_	NM_138329	NP_612202	P59044	NALP6_HUMAN	Poly-Glu.	2	GCCAGAGGAGG	0.67	
-	2	955_957	2_uc001mak.1_In	NM_017481	NP_059509	Q9H347	UBQL3_HUMAN		3	TGGCTGGTGGT	0.537	rs2234451
+	9	1630		NM_006108	NP_006099	Q9HCB6	SPON1_HUMAN		0	ATGAGGTGTGTG	0.594	
-	2	369	.1_5'UTR|RIN1_u	NM_004292	NP_004283	Q13671	RIN1_HUMAN	SH2.	3	GCATGTGCAGT	0.726	
-	1	174_176	RNA|MMP1_uc01	NM_002421	NP_002412	P03956	MMP1_HUMAN		4	AGAACAGCAGC	0.498	
-	2	308_322	prt.1_5'UTR|TMP	NM_001077263	NP_001070731	Q9BYE2	TMPSD_HUMAN	-A-[GLQR].|Cytoplasmic (	1	GGAGATGCCCG	0.67	
-	4	372	_p.E78fs|RERG_u	NM_032918	NP_116307	Q96A58	RERG_HUMAN		1	GCCTTCCCCCC	0.458	
+	23	5212_5213	cj.2_Frame_Shift_	NM_012291	NP_036423	Q14674	ESPL1_HUMAN		3	GTGACTGTGTG	0.436	
+	1	298		NM_001005518	NP_001005518	A6NJZ3	O6C65_HUMAN	Name=3; (Potential).	0	CAAGTATTTTTT	0.358	
-	19	2421	.R523fs|R3HDM2	NM_014925	NP_055740	Q9Y2K5	R3HD2_HUMAN		2	AGGCCGGGGG	0.557	
-	1	39	uc001srx.2_Intron	NM_001099676	NP_001093146	Q8IXR9	CL056_HUMAN		0	CTGTTCCTGCG	0.716	
+	35	4504		NM_014503	NP_055318	O75691	UTP20_HUMAN		4	GTTCGCTTTGAG	0.333	
+	12	1457_1459	me_Del_p.Q445d	NM_001143779	NP_001137251	Q8WYA0	IFT81_HUMAN	Potential.	1	TATTCAACAACA	0.345	
+	7	941	F3_uc001uqw.2_	NM_006646	NP_006637	Q9UPY6	WASF3_HUMAN		1	ACTAGGTGTGTG	0.475	
-	2	2237	_Shift_Del_p.N674	NM_001040108	NP_001035197	Q9UHC1	MLH3_HUMAN		2	CTGCAATTTTTT	0.348	
+	10	1130	op.1_Frame_Shift	NM_001080464	NP_001073933	Q86U10	LPP60_HUMAN		0	CCTTCGGGGGG	0.682	
+	8	3011_3013	.Q981del|MGA_uc	NM_001080541	NP_001074010	Q8IWI9	MGAP_HUMAN	Gln-rich.	12	GGCACAGCAGC	0.458	
+	4	1969	592_uc010upb.1_	NM_014630	NP_055445	Q92610	ZN592_HUMAN		6	AGGTGAAAAAG	0.577	
+	19	3331	e_Shift_Del_p.D8	NM_006662	NP_006653	Q6ZRS2	SRCAP_HUMAN	Pro-rich.	4	CCTGACCCCCC	0.567	
+	5	636	fs|RNF167_uc002	NM_015528	NP_056343	Q9H6Y7	RN167_HUMAN	PA.	0	CACCACCCCCA	0.537	
+	10	2188_2189	gjr.2_Frame_Shift	NM_053051	NP_444279	Q8N137	CNTRB_HUMAN	d for centrosome localizati	2	CTCGGAGAGAG	0.579	
-	4	595_607	_Shift_Del_p.P13f	NM_006470	NP_006461	O95361	TRI16_HUMAN		3	CAGTGGCCCTG	0.629	
+	1	158_160	me_Del_p.K7del|	NM_003457	NP_003448	O43670	ZN207_HUMAN		0	TCGCAAGAAGA	0.542	
-	21	4684_4686	12EE>E|BZRAP1	NM_004758	NP_004749	O95153	RIMB1_HUMAN	Poly-Glu.	3	Gctcctcttcctcctcct	0.468	
-	14	1600_1602	jca.2_In_Frame_	NM_017647	NP_060117	Q8IY81	RRMJ3_HUMAN		1	GGATTCTCCTCC	0.537	
-	7	1257_1277	el_p.SGPSGPS2	NM_015476	NP_056291	Q68CL5	TPGS2_HUMAN		1	GACCGGAGGGT	0.552	805698;rs117567703
-	1	468_470	2utd.1_In_Frame	NM_016192	NP_057276	Q9UIK5	TEFF2_HUMAN		5	ACGGGCAGCAG	0.601	
-	1	224_226	g.1_In_Frame_De	NM_001485	NP_001476	P52951	GBX2_HUMAN	Poly-Pro.	0	AGCGCGggcggcg	0.626	
+	2	1350_1352	.1_Intron|KIF3B_u	NM_004798	NP_004789	O15066	KIF3B_HUMAN	y-Glu.|Potential.	5	GGggaagaggagga	0.433	

-	21	3201_3203	1agl.1_In_Frame_	NM_015241	NP_056056	Q7RTP6	MICA3_HUMAN	Glu-rich.	0	GGCGAGGctcctcc	0.453	
+	6	591		NM_000496	NP_000487	P43320	CRBB2_HUMAN	a crystallin 'Greek key' 4.	0	CCCTCACCCCCA	0.647	
-	3	496_498		NM_005877	NP_005868	Q15459	SF3A1_HUMAN	Poly-Gln.	5	GTGGTCTGCTGC	0.596	rs141985009
+	13	1533_1535	aus.2_In_Frame_I	NM_012407	NP_036539	Q9NRD5	PICK1_HUMAN	Poly-Glu.	0	AGATGGggaggag	0.562	
+	3	406_408	me_Del_p.E76del|	NM_012324	NP_036456	Q13387	JIP2_HUMAN	'Glu-rich (acidic).	3	gaggaagaggaggag	0.483	
+	8	2694	Del_p.I807fs|GRM	NM_000844	NP_000835	Q14831	GRM7_HUMAN	Name=6; (Potential).	7	TTCCAATTTTTTT	0.383	
-	1	205_207	/g.1_In_Frame_De	NM_004628	NP_004619	Q01831	XPC_HUMAN	lu.|Glu-rich (acidic).	3	CTCACCCTCCTC	0.734	rs72561774
+	13	1544	e_Shift_Del_p.T254	NM_000249	NP_000240	P40692	MLH1_HUMAN	action with ET495A(1)|p.0?(	77	CTTGTACCCCCC	0.473	
+	7	1229		NM_017875	NP_060345	Q96DW6	S2538_HUMAN	Solcar 3.	0	TGGCATCCCCCG	0.488	
-	6	513_515	x.2_In_Frame_Del	NM_020707	NP_065758	Q9HCP6	HHATL_HUMAN		3	GACCAAGCAGCA	0.621	
+	1	221_223		NM_014240	NP_055055	Q9UGP4	LIMD1_HUMAN	tes nuclear export.	1	CCTCCAGCAGCA	0.626	
-	3	456_458	ame_Del_p.L89de	NM_147129	NP_667340	Q60I27	AL2CL_HUMAN		5	CCTCGCAGCAG	0.611	
-	14	3144	dbf.1_Frame_Shift	NM_014703	NP_055518	Q9Y4B6	VPRBP_HUMAN		2	CAGCTGTTTTTT	0.498	
+	11	1711	gnl.1_Frame_Shift_	NM_182485	NP_872291	Q7Z5Q1	CPEB2_HUMAN		1	GCTCCCTTTTTTT	0.443	
-	7	944		NM_173536	NP_775807	Q8N1C3	GBRG1_HUMAN	cellular (Probable).	2	CAGGTCAAAAAA	0.294	
-	25	3483	I1107fs|SEC31A_	NM_001077207	NP_001070675	O94979	SC31A_HUMAN	ction with PDCD6.	8	TGGTAATTTTTTT	0.388	
+	44	7494_7503	p.V418fs|KIAA1109	NM_015312	NP_056127	Q2LD37	K1109_HUMAN		12	TGGATTCAGACA	0.386	
+	2	574	3jhm.2_Frame_Shi	NM_178140	NP_835260	O15018	PDZD2_HUMAN		9	TCACAGCCCCCC	0.587	
+	8	2216	p.F486fs|JARID2_	NM_004973	NP_004964	Q92833	JARD2_HUMAN	ARID.	4	GCCTGCTTTTTCC	0.493	
-	8	1420	_Shift_Del_p.P150f	NM_000332	NP_000323	P54253	ATX1_HUMAN		4	CGGTTGGGGGG	0.632	
+	3	631	rame_Shift_Del_p.T	NM_002121	NP_002112	P04440	DPB1_HUMAN	-type.|Extracellular (Potenti	1	AATGACCCCCCA	0.562	
+	15	1702	e_Shift_Del_p.P45	NM_024165	NP_077084	O43189	PHF1_HUMAN		0	AAGTGCCCCCCA	0.532	
+	6	808	10khi.2_Frame_Sh	NM_014721	NP_055536	O75167	PHAR2_HUMAN		2	TCATTCAAAAAAA	0.398	
+	9	3522_3524	2_3'UTR|GRM1_uc	NM_000838	NP_000829	Q13255	GRM1_HUMAN	|Cytoplasmic (Potential).	19	CTCTCCAGCAGCA	0.66	
+	8	2132_2134		NM_138426	NP_612435	Q86VQ1	GLCI1_HUMAN	Poly-Gln.	0	CATCCCAGCAGCA	0.562	
+	8	2004_2005	srz.2_Frame_Shift	NM_014660	NP_055475	O94880	PHF14_HUMAN		3	TTGCAAGAGAGA	0.376	
+	15	1878	bl.1_RNA|LIMK1_	NM_002314	NP_002305	P53667	LIMK1_HUMAN	rotein kinase.	3	CTACTGCCCCCC	0.647	
-	3	284	l_p.K62fs|KIAA002	NM_014878	NP_055693	Q15397	K0020_HUMAN		1	ACACCCTTTTTCC	0.388	
-	3	2403_2404		NM_001017969	NP_001017969	Q5HYC2	K2026_HUMAN	Lys-rich.	3	GTTTTGCTTTTTT	0.327	
-	4	473		NM_001561	NP_001552	Q07011	TNR9_HUMAN	(Potential).|TNFR-Cys 3.	4	CGTACCTTTTTTT	0.413	rs9657965
-	3	882_883	_p.E24fs|RERE_uc	NM_012102	NP_036234	Q9P2R6	RERE_HUMAN		2	GTCTCTTTTCtctct	0.342	
-	2	283_284		NM_004102	NP_004093	P05413	FABPH_HUMAN		1	GCTGTTGTCTCA	0.475	
-	7	1080	am.1_Frame_Shift	NM_002227	NP_002218	P23458	JAK1_HUMAN	FERM.	61	TTTTGTCAAAGTT	0.393	
+	10	2124	ova.1_Frame_Shif	NM_001144937	NP_001138409	Q5VTL7	FNDC7_HUMAN	onectin type-III 8.	2	CTGTCCAAAAAA	0.363	
-	2	3480_3482	vne.1_In_Frame_D	NM_007113	NP_009044	Q07283	TRHY_HUMAN	30 AA tandem repeats.	5	GCCTTCTCTTCTC	0.172	
-	2	1203_1204	ie.1_In_Frame_Ins	NM_007113	NP_009044	Q07283	TRHY_HUMAN	repeats of R-R-E-Q-Q-L.|2	5	ctcgcgcctcagctgctg	0.094	
-	3	1792_1795		NM_001122965	NP_001116437	Q6XPR3	RPTN_HUMAN	Gln-rich.	0	GCCTTGTCTGTC	0.466	
+	17	2363_2365	J2F1_uc010plh.1_I	NM_002697	NP_002688	P14859	PO2F1_HUMAN		5	TGCGTCCACCAC	0.601	
+	14	5165	PA2_uc009www.2_	NM_020318	NP_064714	Q9BXP8	PAPP2_HUMAN		16	ATGTCCTTTTCCA	0.483	
+	7	1574_1576	ne_Del_p.T418del|	NM_005807	NP_005798	Q92954	PRG4_HUMAN	ats of K-X-P-X-P-T-T-X.|21	1	TGCACCCACCAC	0.645	
-	1	774_775		NM_001004734	NP_001004734	A6ND48	O14I1_HUMAN	Name=6; (Potential).	0	TGGTCCTAAGGC	0.47	
-	10	4927	_Shift_Del_p.Q136	NM_032776	NP_116165	Q15652	JHD2C_HUMAN		6	TGGTTGACTTGT	0.398	
-	20	2483	1jxl.1_Frame_Shift	NM_001161352	NP_001154824	Q12791	KCMA1_HUMAN	lasmic (Potential).	3	CGTTGCTTTTTTT	0.502	
+	25	3716	_p.D924fs|ZMIZ1_u	NM_020338	NP_065071	Q9ULJ6	ZMIZ1_HUMAN		4	CTGGACCCCCCC	0.557	
-	9	1499_1501	XM2_uc001lhj.2_F	NM_198148	NP_937791	Q8N436	CPXM2_HUMAN	Poly-Leu.	2	TGCACCAGCAGCA	0.626	
-	3	564		NM_002032	NP_002023	P02794	FRIH_HUMAN	rritin-like diiron.	1	TTCACATTTTTTT	0.423	
+	22	2658	l_5'Flank|PACS1_	NM_006842	NP_006833	Q13435	SF3B2_HUMAN		3	TACAGCAAAAAAA	0.512	

+	7	644_645	CS_uc001ois.2_RN	NM_005125	NP_005116	O14618	CCS_HUMAN	xide dismutase-like.		0	TTATTGATGAGG	0.574	
-	5	674_675		NM_002426	NP_002417	P39900	MMP12_HUMAN			0	CAAGTGGTGCC	0.416	192524;rs33924686
-	1	327_328	H1_uc001qzc.2_In	NM_176885	NP_795366	P59538	T2R31_HUMAN	ellular (Potential).		0	GACATTATAAGC	0.381	
-	3	258_259	_74P>PP|PRB1_u	NM_005039	NP_005030	P04280	PRP1_HUMAN	-P-[PAQ]-Q-[GE]-[GD]- [NK		0	TTTCCTGGAGGT	0.619	
-	3	502_503		NM_006248	NP_006239					0	TTTCCTGGAGGT	0.594	
-	2	1302	raq.2_Frame_Shift	NM_006143	NP_006134	Q15760	GPR19_HUMAN	lasmic (Potential).		1	ACGTAGTTTTTT	0.398	
-	11	1445	p.L408fs|KIAA052	NM_014802	NP_055617	Q86YS7	K0528_HUMAN			4	AGCCTAATGCT	0.353	
+	3	227	nk|MARS_uc001s	NM_004990	NP_004981	P56192	SYMC_HUMAN			5	CAGATATTTTTT	0.488	
-	14	2248	p.K669fs|MDM1_u	NM_017440	NP_059136	Q8TC05	MDM1_HUMAN			5	CTTTTCTTAGCT	0.408	
-	19	3106	zux.1_Frame_Shift	NM_014706	NP_055521	Q15020	SART3_HUMAN			1	AGCTTGGCAAA	0.627	
+	4	646_648	p.L194del|TPCN1_	NM_017901	NP_060371	Q9ULQ1	TPC1_HUMAN	=S1 of repeat I; (Potential).		3	GGCCCTGCTGC	0.64	
+	16	2686_2688	tbn.1_In_Frame_	NM_004592	NP_004583	Q12872	SFSWA_HUMAN	g/Ser-rich (RS domain).		0	CACGAGAAGAA	0.493	
-	34	4381_4382	_p.V250fs|POLE_u	NM_006231	NP_006222	Q07864	DPOE1_HUMAN			8	TTGACCACACAC	0.604	
-	1	321	_5'Flank|KIAA170	NM_012345	NP_036477	Q9UHK0	NUFP1_HUMAN	Pro-rich.		0	GCGTCGAAGGG	0.627	
-	11	2278_2279	p.R758fs|ZC3H13	NM_015070	NP_055885	Q5T200	ZC3HD_HUMAN	lu-rich.|Potential.		2	tctctctccctctctctctc	0.153	
-	9	1177_1178	p.I309fs|DIAPH3_	NM_001042517	NP_001035982	Q9NSV4	DIAP3_HUMAN	GBD/FH3.		2	TGTCAATTTTTT	0.322	
-	2	1567_1569	orf43_uc010tud.1_	NM_194278	NP_919254	Q6PJG2	CN043_HUMAN	-rich.|Gln-rich.		5	GGgctgcctgctgctg	0.473	
-	24	6379_6380	fy.1_Frame_Shift_	NM_015263	NP_056078	Q8TDJ6	DMXL2_HUMAN			9	CAGTCATAAGGA	0.371	
+	7	4096_4098		NM_015042	NP_055857	O15014	ZN609_HUMAN	Poly-His.		3	CACACACCACC	0.576	
+	7	861	IS3L_uc002apq.2_	NM_001143688	NP_001137160	Q8TF46	DI3L1_HUMAN			2	GGGATGAAGGC	0.483	
-	5	697_698	002atw.1_Frame_	NM_182471	NP_872271	P14618	KPYM_HUMAN			1	CTCGTCACACTT	0.51	
+	5	1216_1217		NM_000761	NP_000752	P05177	CP1A2_HUMAN			4	CCCTTCACCATC	0.629	
+	3	434_436		NM_001030005	NP_001025176	Q8WVH0	CPLX3_HUMAN			0	CACAGAGGAGG	0.616	
-	11	4245		NM_001116	NP_001107	O60503	ADCY9_HUMAN	lasmic (Potential).		6	CATCTGGCCTTT	0.577	
-	3	178	_p.F47fs|GLYR1_u	NM_032569	NP_115958	Q49A26	GLYR1_HUMAN	PWWP.		0	TGTTCCAAAAAA	0.433	
-	19	2594_2595	_p.S358fs|ARHGA	NM_001006634	NP_001006635	Q68EM7	RHG17_HUMAN			0	ATCTTGGAAGCT	0.505	
+	4	3080	8R_uc010byg.1_F	NM_018690	NP_061160	Q0VD83	APOBR_HUMAN			0	CCCCCAACCCT	0.677	
+	13	3813_3815		NM_014712	NP_055527	O15047	SET1A_HUMAN	Ser-rich.		3	Gctcctcatcctcctcct	0.389	
+	12	2232_2234	gpz.2_In_Frame_	NM_016113	NP_057197	Q9Y5S1	TRPV2_HUMAN	ical; (Potential).		1	ATGGTGCTGCT	0.596	
-	8	926_927	p.S305fs|MYO1D_	NM_015194	NP_056009	O94832	MYO1D_HUMAN	osin head-like.		3	TTAGTAGAGAGC	0.426	
-	3	566	hjz.1_RNA|MMP2	NM_024302	NP_077278	Q9H239	MMP28_HUMAN			1	CTCAGCCCAGG	0.572	
+	2	497	_p.F113fs|KLHL10_	NM_152467	NP_689680	Q6JEL2	KLH10_HUMAN			4	GACCAGTTTAAC	0.483	
+	20	6727_6729	.T2353del|BPTF_	NM_182641	NP_872579	Q12830	BPTF_HUMAN	Thr-rich.		4	CCAGCACCACC	0.542	rs143937013
+	9	1438_1439	2jgl.2_Frame_Shift	NM_002266	NP_002257	P52292	IMA2_HUMAN	ARM 9.		2	CCAAGATTATTC	0.366	
+	6	895_896		NM_152721	NP_689934	Q6PKX4	DOK6_HUMAN	RS-type PTB.		3	CATGAAAGATTA	0.45	
-	5	1002_1052	uc010xsw.1_5'Fla	NM_033317	NP_201574	Q6E0U4	DMKN_HUMAN	Gly-rich.	S274_S290del	3	gccgccactgctgccgc	0.303	79970;rs144877871;rs147522263;rs140071083;rs13
-	5	1929	xwy.1_Frame_Shif	NM_001083335	NP_001076804	Q9UJU3	ZF112_HUMAN			5	TTTTTCTCCAGT	0.463	
+	7	954_955	pfy.2_Frame_Shift	NM_002517	NP_002508	Q99742	NPAS1_HUMAN			0	GAAATCCACGCT	0.604	
+	3	136_138	In_Frame_Del_p.L	NM_001459	NP_001450	P49771	FLT3L_HUMAN			0	CCTCCTGCTGCT	0.621	
-	7	1721_1722	p.R435fs|ZNF160_	NM_001102603	NP_001096073	Q9HCG1	ZN160_HUMAN	2H2-type 7.		1	ATTGTACCTAAA	0.426	rs145975178
-	4	719	do.2_Frame_Shift	NM_001145303	NP_001138775	Q7Z404	TMC4_HUMAN	lasmic (Potential).		1	GGCCTGGGGGA	0.647	
-	3	316	_p.P92fs|HS1BP3	NM_022460	NP_071905	Q53T59	H1BP3_HUMAN	PX.		1	GTAGTGGGGGG	0.537	rs77941615
-	67	7984		NM_014709	NP_055524	Q70CQ2	UBP34_HUMAN			19	TGCCAGTTTATTT	0.413	
+	3	1397_1398		NM_001011552	NP_001011552	Q6AI14	SL9A4_HUMAN	ame=I/M7; (Potential).		3	TGTCTTACTTAG	0.406	
+	8	2074	02udy.2_Frame_S	NM_152381	NP_689594	A4UGR9	XIRP2_HUMAN			14	TAACTGGGGGG	0.418	
-	15	1867	HD1_uc010gft.1_	NM_015474	NP_056289	Q9Y3Z3	SAMH1_HUMAN			0	GGCTTGGTGAA	0.383	
-	11	905	PTE_uc002yir.1_	NM_199261	NP_954870	P56180	TPTE_HUMAN	ical; (Potential).		5	ATGTCAAAAAA	0.299	

-	1	1882_1884		NM_002430	NP_002421	Q10571	MN1_HUMAN			10	CACACCAtgctgctg	0.463	
+	13	1587	p.T420fs|MTMR3_	NM_021090	NP_066576	Q13615	MTMR3_HUMAN	ularin phosphatase.		5	ACCGCACCCCCC	0.547	
+	7	1953_1961	atq.1_In_Frame_D	NM_001039141	NP_001034230	Q9H2D6	TARA_HUMAN			1	GCCTCCAGAAC	0.589	
-	13	1723_1724	GRIP2_uc011avh.	NM_001080423	NP_001073892	Q9C0E4	GRIP2_HUMAN	PDZ 4.	p.A478T(1)	1	CGGTGGCGAAGA	0.678	rs61731933
+	3	622		NM_005513	NP_005504	P29083	T2EA_HUMAN			1	ATGCCCAAAAAA	0.418	
+	1	3006_3007		NM_175918	NP_787114	Q8N1N5	CRPAK_HUMAN			0	CTGCTCACACGT	0.465	
+	1	3808_3809		NM_175918	NP_787114	Q8N1N5	CRPAK_HUMAN	8		0	CTCACATGTGCC	0.683	123539;rs79888804
+	1	3836_3837		NM_175918	NP_787114	Q8N1N5	CRPAK_HUMAN			0	CTGCTCACACGT	0.683	
+	1	3897_3898		NM_175918	NP_787114	Q8N1N5	CRPAK_HUMAN			0	CCTGCTCACGTC	0.663	
+	1	4086_4087		NM_175918	NP_787114	Q8N1N5	CRPAK_HUMAN	eraction with PAK1.		0	CTGCTCACACGT	0.639	
+	2	203_205		NM_002111	NP_002102	P42858	HD_HUMAN			4	TCCTTCcagcagca	0.335	rs10618869
+	2	790	iov.2_Frame_Shift	NM_005900	NP_005891	Q15797	SMAD1_HUMAN	MH1.		1	ATCCCTACCACTA	0.438	
-	1	1032_1034	rj.2_5'Flank|NBLA	NM_021973	NP_068808	P61296	HAND2_HUMAN	Poly-Ala.		1	gcggctggcggcggcg	0.473	
+	21	2550_2551	p.F793fs|TNPO1_	NM_002270	NP_002261	Q92973	TNPO1_HUMAN			7	CAGTTTATAAGA	0.366	
+	19	3557	R98_uc003kjt.2_5'U	NM_032119	NP_115495	Q8WXG9	GPR98_HUMAN	cellular (Potential).		16	TATCTTGGCAGC	0.378	
+	4	322	uc003kqe.1_Intron|REEP5_uc011cvx.1_Intron|REEP5_			P09132	SRP19_HUMAN			0	GCGGTGCTGGC	0.363	
+	9	1679	uc003kwr.3_Intron	NM_003059	NP_003050	Q9H015	S22A4_HUMAN	Name=12; (Potential).		0	TCACCCTTTTTTT	0.418	
-	2	238_239	me_Shift_Del_p.E2	NM_007054	NP_008985	Q9Y496	KIF3A_HUMAN	Kinesin-motor.		1	TGATTTCTCTCT	0.411	
+	10	2092	p.G568fs|RREB1_	NM_001003698	NP_001003698	Q92766	RREB1_HUMAN			11	AGTCCGGGACC	0.711	
+	8	2004_2005	srz.2_Frame_Shift	NM_014660	NP_055475	O94880	PHF14_HUMAN			3	TTGCAAGAGAGA	0.376	
+	4	952_953		NM_001159279	NP_001152751					2	AGCCGCTCAACA	0.416	
+	4	1034_1036		NM_001159279	NP_001152751					2	GCCGCTCTTCAA	0.419	
-	20	2915	_p.P781fs|TNPO3	NM_012470	NP_036602	Q9Y5L0	TNPO3_HUMAN			5	GTATAGGGGGG	0.483	
+	1	528		NM_001001656	NP_001001656	Q8NGU2	OR9A4_HUMAN	cellular (Potential).		1	GAACAATTTTTTT	0.383	
+	21	2194	l_uc003xjw.2_Spli	NM_001031836	NP_001027006	A8MYU2	KCNU1_HUMAN			1	TCCTTAGAAACG	0.46	
+	10	1740	LF1_uc003xyf.2_F	NM_015170	NP_055985	Q8IWU6	SULF1_HUMAN			7	TGTGCCTTTTTTT	0.408	
-	2	284		NM_001033723	NP_001028895	Q6ZNC4	ZN704_HUMAN			0	GAGACATTTTTTT	0.423	
-	10	1506	p.R384fs|NBN_uc	NM_002485	NP_002476	O60934	NBN_HUMAN	r localization signal.		7	CAGACCTTTTTTT	0.338	
-	10	978_979	yhd.2_Frame_Shif	NM_057749	NP_477097	O96020	CCNE2_HUMAN			0	TGGAACTCTAAT	0.376	
-	3	534_536	f.2_Intron|TP53IN	NM_033285	NP_150601	Q96A56	T53I1_HUMAN	Glu-rich.		0	CCTCCTCTTCTT	0.458	
-	3	991	3yjk.1_Splice_Site	NM_015435	NP_056250	Q9NV58	RN19A_HUMAN			4	CTTCTTACCCACA	0.338	
-	6	1215		NM_001385	NP_001376	Q14117	DPYS_HUMAN			2	CACGCCTTTTTC	0.478	
+	12	1287	_p.L350fs|HEATR7	NM_032450	NP_115826	Q8NDA8	HTR7A_HUMAN	HEAT 3.		0	CGCCTACTGGC	0.592	rs144186714
+	4	766_768	Q238del|SMARCA	NM_003070	NP_003061	P51531	SMCA2_HUMAN	Poly-Gln.		3	cagcaacagcagcag	0.271	070757;rs62639301
-	5	724_726	e_Del_p.152_153	NM_004529	NP_004520	P42568	AF9_HUMAN	Poly-Ser.		3	tgctgctactgctgctgct	0.148	
-	2	902	awg.2_Frame_Shi	NM_153695	NP_710162	Q7RTV3	ZN367_HUMAN	C2H2-type 1.		0	AGCCTGGAGCG	0.353	
+	23	2412	_Shift_Del_p.P365	NM_020893	NP_065944					7	CTCCTGCCCCCC	0.507	
-	39	9961_9962	nty.2_Frame_Shift	NM_153366	NP_699197	Q4LDE5	SVEP1_HUMAN	Sushi 30.		7	CCCTTCTGCACA	0.386	
+	6	785	p.E225fs|NUP214	NM_005085	NP_005076	P35658	NU214_HUMAN			16	GCAGGAAAAAA	0.363	
+	42	6348_6350	4dza.2_In_Frame_	NM_005120	NP_005111	Q93074	MED12_HUMAN	Gln-rich.		4	TACCTGagcagcag	0.281	
+	3	306	uc011msx.1_5'UTR|ALG13_uc011msz.1_Frame_Shift_D			Q9NP73	ALG13_HUMAN			1	CTCTGGAAAAAG	0.388	
-	3	866_868	v.2_In_Frame_Del	NM_003588	NP_003579	Q13620	CUL4B_HUMAN	Ser-rich.		3	GAAGATgaggagga	0.424	
-	1	729	uc004fbf.1_RNA	NM_004065	NP_004056	P51861	CDR1_HUMAN	pproximate repeats.|1.		0	TGTCTTCCAGTAA	0.433	
+	4	381_383		NM_004781	NP_004772	Q15836	VAMP3_HUMAN	e IV membrane protein; (Pc		0	TATCTTCATCATC	0.365	
-	3	882_883	_p.E24fs|RERE_u	NM_012102	NP_036234	Q9P2R6	RERE_HUMAN			2	TCTCTTTTCtctct	0.342	
+	4	817	1aug.1_Frame_Sh	NM_001103170	NP_001096640	Q5VUY0	ADCL3_HUMAN			0	GCTACTGTTTTTT	0.458	rs7513079
+	5	613_615		NM_152493	NP_689706	Q5T0B9	ZN362_HUMAN			0	CACACCCACCAC	0.675	

+	34	4444_4446	.E504del|MACF1_	NM_012090	NP_036222	Q9UPN3	MACF1_HUMAN	Poly-Glu.	16	GTCTGGAGGAG	0.389	
+	7	1426_1427	me_Shift_Del_p.H	NM_005012	NP_005003	Q01973	ROR1_HUMAN	xtracellular (Potential).	19	ATCCCCACACAC	0.554	
+	2	248_249	sw.1_Frame_Shif	NM_003503	NP_003494	O00311	CDC7_HUMAN		5	CTCTTTAAAAAA	0.406	
+	12	2267_2269	.S575del|BRDT_u	NM_207189	NP_997072	Q58F21	BRDT_HUMAN	Ser-rich.	4	AGTGAGagcagca	0.35	
-	59	4728	K1482fs|COL11A1	NM_001854	NP_001845	P12107	COBA1_HUMAN	le-helical region.	12	GTCACCTTTTTC	0.403	
-	3	5776_5777	uc001ezv.2_Intron	NM_001014342	NP_001014364	Q5D862	FILA2_HUMAN		17	TTGGCTGTGTGT	0.515	rs140875805
+	2	99		NM_178428	NP_848515	Q5TA79	LCE2A_HUMAN	Cys-rich.	0	AAGTGCCCCCC	0.572	rs138365632
-	6	1404_1406	.V48del|PVRL4_u	NM_030916	NP_112178	Q96NY8	PVRL4_HUMAN	ical; (Potential).	2	TGAGCACCACC	0.571	
-	6	1357_1359	p.V32del|PVRL4_	NM_030916	NP_112178	Q96NY8	PVRL4_HUMAN	ical; (Potential).	2	ACACCCACCAC	0.606	
+	17	2363_2365	2F1_uc010plh.1_	NM_002697	NP_002688	P14859	PO2F1_HUMAN		5	GCGTCCACCAC	0.601	
+	3	348_349	D1_uc010pli.1_In	NM_052862	NP_443094	Q6JBY9	CPZIP_HUMAN		5	CCTGTTCCCCCC	0.554	rs144007158
-	4	615	LUL_uc001gpc.1	NM_001033056	NP_001028228	P15104	GLNA_HUMAN		0	CTCCTGCTCCAT	0.522	
+	7	1327_1328	_Ins_p.333_334ins	NM_005807	NP_005798	Q92954	PRG4_HUMAN	-X-P-X-P-T-T-X.|11; appro	1	CCACCAAGTCTG	0.658	
+	7	1574_1576	e_Del_p.T418del|	NM_005807	NP_005798	Q92954	PRG4_HUMAN	ats of K-X-P-X-P-T-T-X.|21	1	GCACCCACCAC	0.645	
+	7	1586_1588	e_Del_p.E420del|	NM_005807	NP_005798	Q92954	PRG4_HUMAN	ats of K-X-P-X-P-T-T-X.|22	1	ACCAAGGAGCC	0.64	
-	3	472_474	ame_Del_p.K93de	NM_001136504	NP_001129976	Q8N9I0	SYT2_HUMAN	lasmic (Potential).	3	ctccttcttgttcttcttct	0.483	
-	3	588		NM_003395	NP_003386	O14904	WNT9A_HUMAN	p.C168fs*6(1)	2	CGCAGCCCCCC	0.627	
+	9	1195_1196	p.Y273fs|CDH23_	NM_022124	NP_071407	Q9H251	CAD23_HUMAN	|Extracellular (Potential).	11	TGGCTACACCAT	0.594	
+	11	1237	ECTD2_uc001kh	NM_182765	NP_877497	Q5U5R9	HECD2_HUMAN		1	GCTGCAAAAAA	0.318	
+	16	2167		NM_014633	NP_055448	Q6PD62	CTR9_HUMAN	TPR 14.	2	CCAAGTAAGAG	0.403	
-	4	616	BTBD10_uc010rcr	NM_032320	NP_115696	Q9BSF8	BTBDA_HUMAN	Ser-rich.	0	CCATTTGGGGAT	0.433	
-	5	674_675		NM_002426	NP_002417	P39900	MMP12_HUMAN		0	CAAGTGGTGCC	0.416	192524;rs33924686
+	9	1502_1504		NM_005188	NP_005179	P22681	CBL_HUMAN	Glu-rich (acel(1)|p.E366_K	149	AAATTATGATGAT	0.473	
-	2	1302	raq.2_Frame_Shift	NM_006143	NP_006134	Q15760	GPR19_HUMAN	lasmic (Potential).	1	ACGTAGTTTTTT	0.398	
-	7	1152_1153		NM_024829	NP_079105	Q6P4A8	PLBL1_HUMAN		0	CCATCATATTGG	0.441	
-	12	4127_4129	w.2_In_Frame_De	NM_004719	NP_004710	Q99590	SCAFB_HUMAN	Pro-rich.	0	AGGGGGTGGTG	0.483	
+	3	227	nk|MARS_uc001s	NM_004990	NP_004981	P56192	SYMC_HUMAN		5	CAGATATTTTTT	0.488	
+	4	646_648	p.L194del|TPCN1_	NM_017901	NP_060371	Q9ULQ1	TPC1_HUMAN	=S1 of repeat I; (Potential).	3	GGCCCTGCTGC	0.64	
+	16	2686_2688	tbn.1_In_Frame_	NM_004592	NP_004583	Q12872	SFSWA_HUMAN	g/Ser-rich (RS domain).	0	CACGAGAAGAA	0.493	
-	34	4381_4382	_p.V250fs|POLE_	NM_006231	NP_006222	Q07864	DPOE1_HUMAN		8	TTGACCACACAC	0.604	
-	20	2640_2641	vme.2_Frame_Shi	NM_005845	NP_005836	O15439	MRP4_HUMAN	|ABC transmembrane type	4	AATCTAAAAACG	0.406	
+	2	666_667	1_Intron|RNASE7_	NM_032572	NP_115961	Q9H1E1	RNAS7_HUMAN		1	AGCCTCCCCAGA	0.505	
-	3	294	32fs|RBM23_uc0	NM_001077351	NP_001070819	Q86U06	RBM23_HUMAN		1	TAATCCTTTTTAA	0.483	
+	13	2290_2291	M_uc001wwe.3_F	NM_020937	NP_065988	Q8IYD8	FANCM_HUMAN		7	ATCAACTCTCTC	0.347	
+	1	809_811	06del|FAM63B_uc	NM_001040450	NP_001035540	Q8NBR6	FA63B_HUMAN		1	CCCTGAGGAGG	0.621	
+	7	4096_4098		NM_015042	NP_055857	O15014	ZN609_HUMAN	Poly-His.	3	CACACACCACC	0.576	
+	8	4222		NM_015042	NP_055857	O15014	ZN609_HUMAN		3	ACCCACCCCCC	0.338	
-	5	728	LPX_uc010bhg.1_	NM_006660	NP_006651	O76031	CLPX_HUMAN		0	AATGATGTCTGC	0.343	
-	6	1160_1162	188LL>L|PARP16	NM_017851	NP_060321	Q8N5Y8	PAR16_HUMAN	(Potential).|Poly-Leu.	2	TATGAGCAGCA	0.488	
-	11	1628_1630	H3_uc002die.2_I	NM_017539	NP_060009	Q8TD57	DYH3_HUMAN	n (By similarity).	18	CGATCAGCAGC	0.498	
+	5	400_402	6A_uc010bxs.2_	NM_014494	NP_055309	Q8NDV7	TNR6A_HUMAN	Gln-rich.	2	cagccacagcagcag	0.241	
-	12	1595	hift_Del_p.A445fs|	NM_024816	NP_079092	Q9H5N1	RABE2_HUMAN	Potential.	3	GCTCTGCCTGC	0.672	
+	5	540	_p.P104fs|STX4_u	NM_004604	NP_004595	Q12846	STX4_HUMAN	ic (Potential).|Potential.	0	TAGAGCCCCAG	0.423	
+	5	1317_1319	hx.2_In_Frame_D	NM_024335	NP_077311	P78412	IRX6_HUMAN		6	gaggaagaggagga	0.493	
+	12	2232_2234	gpz.2_In_Frame_	NM_016113	NP_057197	Q9Y5S1	TRPV2_HUMAN	ical; (Potential).	1	ATGGTGCTGCT	0.596	
+	5	825		NM_001070	NP_001061	P23258	TBG1_HUMAN	TP (Potential).	1	TTGCTGGGGGG	0.507	
+	3	443_445	wla.1_In_Frame_	NM_018129	NP_060599	Q9NVS9	PNPO_HUMAN		0	ATGTTGCTGCT	0.498	

-	2	1371_1372		NM_004645	NP_004636	P38432	COIL_HUMAN	repeats of S-L-P-A.	1	ATAGTAGATGAA	0.411	
+	2	1067	N_uc002jqo.2_5'	NM_003857	NP_003848	O43603	GALR2_HUMAN	lasmic (Potential).	0	GGGCACCCACA	0.726	
-	20	3375_3378		NM_005406	NP_005397	Q13464	ROCK1_HUMAN	Glu-rich.	5	TAAAGTATTTATT	0.309	
+	6	895_896		NM_152721	NP_689934	Q6PKX4	DOK6_HUMAN	S-type PTB.	3	CATGAAAGATTA	0.45	
+	20	2554		NM_014975	NP_055790	Q9Y2H9	MAST1_HUMAN		7	CAGCGCCCCCC	0.721	
-	2	202_204		NM_013376	NP_037508	Q9UHV2	SRTD1_HUMAN		0	TCCTTCTCCTCC	0.453	
-	5	1929	xwy.1_Frame_Shif	NM_001083335	NP_001076804	Q9UJU3	ZF112_HUMAN		5	TTTTTCTCCAGT	0.463	
-	9	974_975	pni.2_Frame_Shift	NM_003598	NP_003589	Q15562	TEAD2_HUMAN	al activation (Potential).	3	GGCATGGGGG	0.564	
+	3	136_138	In_Frame_Del_p.L	NM_001459	NP_001450	P49771	FLT3L_HUMAN		0	CCTCCTGCTGC	0.621	
-	2	333_335	qdo.2_In_Frame_	NM_001145303	NP_001138775	Q7Z404	TMC4_HUMAN	xtracellular (Potential).	1	TCCATCCTCCT	0.645	
-	7	765	2qxs.2_Frame_Sh	NM_002936	NP_002927	O60930	RNH1_HUMAN	RNase H.	1	TTCTTCCAACC	0.403	
-	2	234_236	HX57_uc002rrg.2_	NM_198963	NP_945314	Q6P158	DHX57_HUMAN	Gly-rich.	3	gccacctccaccacca	0.384	
-	4	575_576	_p.P21fs|ST3GAL	NM_003896	NP_003887	Q9UNP4	SIAT9_HUMAN	enal (Potential).	0	TCTTTGGGGGC	0.505	
+	23	3012_3013		NM_001080527	NP_001073996	Q6PIF6	MYO7B_HUMAN		2	CCAGCCACACA	0.574	
+	8	2074	02udy.2_Frame_S	NM_152381	NP_689594	A4UGR9	XIRP2_HUMAN		14	TAACTGGGGGG	0.418	
-	205	40489	fi.1_Frame_Shift_	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		153	GCCTTGGATAG	0.428	
-	7	1855	_p.P346fs|SATB2_	NM_015265	NP_056080	Q9UPW6	SATB2_HUMAN		1	GCTCTGGGGAT	0.542	
+	1	209_211	Translation_Start_	NM_005759	NP_005750	Q9NYB9	ABI2_HUMAN		0	CTGTATgaggagg	0.601	
-	4	1070_1071		NM_000214	NP_000205	P78504	JAG1_HUMAN	ular (Potential).|DSL.	9	AGGTCACGCG	0.52	
-	12	5661_5663	.2_In_Frame_Del_	NM_014071	NP_054790	Q14686	NCOA6_HUMAN	.|Gln-rich.|CREBBP-bindin	7	TCATTtgttgctgctgc	0.498	895426;rs140426729
-	4	1934_1936	1aaq.1_In_Frame_	NM_017798	NP_060268	Q9BYJ9	YTHD1_HUMAN		2	ACCACCTCCTC	0.557	
-	11	905	PTE_uc002yir.1_	NM_199261	NP_954870	P56180	TPTE_HUMAN	ical; (Potential).	5	ATGTCAAAAAA	0.299	
-	1	48_50		NM_181610	NP_853641	Q3LI73	KR194_HUMAN		2	AAAGCCTCCAC	0.557	
+	4	1162	0gma.2_Frame_S	NM_005534	NP_005525	P38484	INGR2_HUMAN	tential).|Fibronectin type-III	0	ACGGCCTTTTTT	0.458	
+	11	1903_1905	1A_uc002ywl.2_3	NM_001396	NP_001387	Q13627	DYR1A_HUMAN	Poly-His.	4	tcaccatcaccaccac	0.384	
-	2	475	70_uc002zxr.1_5'	NM_021916	NP_068735	Q9UC06	ZNF70_HUMAN		2	TTGCTGGGGGA	0.448	
+	7	1953_1961	atq.1_In_Frame_D	NM_001039141	NP_001034230	Q9H2D6	TARA_HUMAN		1	GCCTCCAGAAC	0.589	
-	10	2571_2573	E>E|RANGAP1_	NM_002883	NP_002874	P46060	RAGP1_HUMAN	cidic).|Asp/Glu-rich (highly	0	tcttctccttcctcctcctc	0.266	
+	1		ranslation_Start_Site|CACNA1	NM_001128840	NP_001122312	Q01668	CAC1D_HUMAN		11	tgttcgtGgatgatgatg	0.246	
-	38	5712_5713	.Q1866fs|ADAMT	NM_182920	NP_891550	Q9P2N4	ATS9_HUMAN	GON.	4	TCCCTTGTGATA	0.401	
-	4	757	3dmh.1_Frame_S	NM_182920	NP_891550	Q9P2N4	ATS9_HUMAN		4	ATTTTCTTGCT	0.388	
+	10	1609	_p.S482fs|MITF_u	NM_198159	NP_937802	O75030	MITF_HUMAN		2	AGTGTCCCCCG	0.527	
-	2	584_586		NM_016206	NP_057290	A8MV65	VGLL3_HUMAN		0	TGGtctttctcctcctc	0.394	
-	7	2209_2211	1blc.1_In_Frame_	NM_001017395	NP_001017395	O94876	TMCC1_HUMAN	Potential.	1	CCACCTGCTGC	0.581	
+	1	3775_3776		NM_175918	NP_787114	Q8N1N5	CRPAK_HUMAN	8	0	CCTGCTCACGT	0.688	
+	1	3808_3809		NM_175918	NP_787114	Q8N1N5	CRPAK_HUMAN	8	0	CTCACATGTGCC	0.683	123539;rs79888804
+	1	3897_3898		NM_175918	NP_787114	Q8N1N5	CRPAK_HUMAN		0	CCTGCTCACGT	0.663	
+	1	4086_4087		NM_175918	NP_787114	Q8N1N5	CRPAK_HUMAN	raction with PAK1.	0	CTGCTCACACG	0.639	
+	2	865	l_p.L108fs|RUFY3	NM_014961	NP_055776	Q7L099	RUFY3_HUMAN		0	AACCTGGGGAG	0.478	
+	4	994_996	.Q279del|MMRN1	NM_007351	NP_031377	Q13201	MMRN1_HUMAN	Poly-Gln.	4	GCTGAGCAGCA	0.448	
+	1	413_414		NM_004575	NP_004566	Q12837	PO4F2_HUMAN		1	CTggtggtggcggcg	0.386	907220;rs72269802
-	41	6826	p.I766fs|LRBA_uc	NM_006726	NP_006717	P50851	LRBA_HUMAN		7	GGTCGATTTTTT	0.453	rs34237929
-	4	411		NM_017631	NP_060101	Q8IY21	DDX60_HUMAN		3	TCAATCAAAAAA	0.308	
-	10	1909	10_uc011cnu.1_	NM_006727	NP_006718	Q9Y6N8	CAD10_HUMAN	|Extracellular (Potential).	12	AAACTGAAAAAA	0.313	
-	3	512_514	0jii.2_In_Frame_D	NM_138379	NP_612388	Q96H15	TIMD4_HUMAN	ar (Potential).|Thr-rich.	2	GGGCTTGTTGT	0.537	
-	4	349_350	BC1D7_uc003nac	NM_016495	NP_057579	Q9P0N9	TBCD7_HUMAN	ab-GAP TBC.	1	GACATCCAAGTA	0.475	
-	4	884	_p.K228fs|NUP153	NM_005124	NP_005115	P49790	NU153_HUMAN		9	TGCTGGTTTTTT	0.413	

+	2	128_130	p.L24del|BTN2A2_	NM_006995	NP_008926	Q8WVV5	BT2A2_HUMAN			0	CAGCCTCcctcctc	0.483	
+	7	1095	S1A_uc011dst.1_5	NM_015245	NP_056060	Q92625	ANS1A_HUMAN			4	ATAAAACCCCCC	0.418	
-	1	210_212		NM_024807	NP_079083	Q5T2D2	TRML2_HUMAN			2	GCCACAGCAGC	0.631	
+	6	926_928	.C204del|MDFI_u	NM_005586	NP_005577	Q99750	MDFI_HUMAN	Cys-rich.		0	GCCTCTGCTGC	0.655	
+	22	2625_2626	jb.3_Frame_Shift_	NM_003318	NP_003309	P33981	TTK_HUMAN		p.R838fs*4(3)	11	CTTTTGAAAAAA	0.302	
-	12	1315	009_uc003pkk.2_	NM_014895	NP_055710	Q5TB80	QN1_HUMAN			1	TTGTCAAAAAAA	0.358	
+	6	690	JN1_uc003sjf.2_F	NM_001130965	NP_001124437	O94901	SUN1_HUMAN	Nuclear.		0	CGCGGCCCCCG	0.557	
+	22	3420	so.2_Frame_Shift_	NM_152744	NP_689957	Q7Z5N4	SDK1_HUMAN	nectin type-III 5.		6	CAGGCTATGACG	0.577	
+	3	425_426	wp.1_Frame_Shift_	NM_032172	NP_115548	Q9H9J4	UBP42_HUMAN			5	TTGTCTTAAGTG	0.446	
-	2	967_968	A11_uc003syy.2_R	NM_005523	NP_005514	P31270	HXA11_HUMAN	Homeobox.		2	CTGTTAATTTTTT	0.446	
+	4	952_953		NM_001159279	NP_001152751					2	AGCCGCTCAACA	0.416	
+	4	475	STAG3_uc011kjk.1	NM_012447	NP_036579	Q9UJ98	STAG3_HUMAN			8	AGCCGCCAAAA	0.458	
-	20	2915	_p.P781fs|TNPO3_	NM_012470	NP_036602	Q9Y5L0	TNPO3_HUMAN			5	GTATAGGGGGG	0.483	
-	3	579	P6_uc010lmv.2_In	NM_145808	NP_665807	Q538Z0	LUZP6_HUMAN			0	GACAGCAGACA	0.338	
+	1	528		NM_001001656	NP_001001656	Q8NGU2	OR9A4_HUMAN	cellular (Potential).		1	GAACAATTTTTTT	0.383	
-	60	8167	Shift_Del_p.R2704	NM_006904	NP_008835	P78527	PRKDC_HUMAN	KIP-binding.		34	CCAGCCTTTTTT	0.498	
-	11	2018_2019	ls.1_Frame_Shift_	NM_014682	NP_055497	O60284	ST18_HUMAN			5	GATTCGATTTTTT	0.411	
-	10	1666_1667	.N420fs|MYBL1_u	NM_001080416	NP_001073885	P10243	MYBA_HUMAN	atory domain (By similarity)		3	CAAGTGTTTTTT	0.406	
+	10	1740	LF1_uc003xyf.2_F	NM_015170	NP_055985	Q8IWU6	SULF1_HUMAN			7	TGTGCCTTTTTT	0.408	
+	2	604		NM_004770	NP_004761	Q92953	KCNB2_HUMAN	lasmic (Potential).		7	AGGCTCCCCCG	0.502	
-	10	1506	p.R384fs|NBN_uc	NM_002485	NP_002476	O60934	NBN_HUMAN	r localization signal.		7	CAGACCTTTTTTT	0.338	
+	8	954	_Shift_Del_p.L262	NM_001359	NP_001350	Q16698	DECR_HUMAN			0	CGCCTGGGGAC	0.413	
-	1	150	.2_5'UTR|RUNX1	NM_175634	NP_783552	Q06455	MTG8_HUMAN			16	GTTCCCTTTTTC	0.343	
-	3	534_536	f.2_Intron|TP53IN	NM_033285	NP_150601	Q96A56	T53I1_HUMAN	Glu-rich.		0	CCTCCTCTTCTT	0.458	
+	8	1488_1489	lhs.1_Frame_Shift_	NM_012082	NP_036214	Q8WW38	FOG2_HUMAN			5	ATATTGGGCCTT	0.436	
+	25	3326	3yoy.2_Frame_Sh	NM_021110	NP_066933	Q05707	COEA1_HUMAN			12	ATTCCACCAGCA	0.388	
+	3	610_612	ysi.2_In_Frame_D	NM_002467	NP_002458	P01106	MYC_HUMAN	Poly-Gln.		6	CTACCAGCAGC	0.611	rs61752959
-	30	4625	ae.1_Splice_Site_	NM_201380	NP_958782	Q15149	PLEC_HUMAN			9	CTGTACCTCCTC	0.621	
+	10	3752_3754	.1_In_Frame_Del_	NM_015158	NP_055973	Q14678	KANK1_HUMAN			4	AGAAGAGGAGG	0.463	
+	4	766_768	Q238del|SMARCA	NM_003070	NP_003061	P51531	SMCA2_HUMAN	Poly-Gln.		3	cagcaacagcagcag	0.271	070757;rs62639301
+	25	4030	Shift_Del_p.G127	NM_020829	NP_065880	Q4ADV7	RIC1_HUMAN			0	GAAGTTGGAAGC	0.547	
-	5	724_726	e_Del_p.152_153	NM_004529	NP_004520	P42568	AF9_HUMAN	Poly-Ser.		3	tgctgctactgctgctgc	0.148	
+	2	218_219		NM_001145249	NP_001138721	P0CG42	F157B_HUMAN	Gln-rich.		0	cagcggcggcagcag	0.386	
+	20	2671_2673	.E837del|CNKSR2	NM_014927	NP_055742	Q8WXI2	CNKR2_HUMAN	ential.|Poly-Glu.		2	gaggaagaggaggag	0.379	
-	18	2564_2566	sw.2_In_Frame_D	NM_015107	NP_055922	Q9UPP1	PHF8_HUMAN			3	GCGTTCTCCTCC	0.591	
-	31	7024_7026	27EE>E|ATRX_u	NM_000489	NP_000480	P46100	ATRX_HUMAN	Poly-Glu.		30	TCAACTCTTCTT	0.369	
+	24	2831_2833	me_Del_p.P867del|ALG13_uc011mta.1_Intron|ALG13_			Q9NP73	ALG13_HUMAN	Pro-rich.		1	accaccacctcctcct	0.197	rs13440710
-	25	5169	.A1708fs|ODZ1_u	NM_014253	NP_055068	Q9UKZ4	TEN1_HUMAN	cellular (Potential).		23	CTAGTTGCCGTC	0.438	
-	8	1013	mwc.1_Frame_Shi	NM_024597	NP_078873	Q8IWC1	MA7D3_HUMAN			4	CACCTGGGGGG	0.532	
+	6	1104_1106	4ezx.2_In_Frame_	NM_001163280	NP_001156752	O43719	HTSF1_HUMAN	Poly-Lys.		3	CTCAAAGAAGA	0.335	
-	1	825		NM_001009615	NP_001009615	Q5MJ10	SPXN2_HUMAN			1	TCATCATTTTTTT	0.239	
+	2	215		NM_017514	NP_059984	P51805	PLXA3_HUMAN			3	GCCGTGGGGGG	0.682	
-	7	811_812	1_Intron|MST1P9_	NR_002729					NA	0	GGTACGCCGCG	0.649	
+	23	2276_2278	dge.1_In_Frame_	NM_015978	NP_057062	Q59H18	TNI3K_HUMAN	Poly-Ser.	NA	10	CTCACCTTCTTC	0.473	
-	9	1732_1734	ows.1_In_Frame_	NM_015906	NP_056990	Q9UPN9	TRI33_HUMAN	Poly-Thr.	NA	11	TGTTGTGTTGTT	0.429	
-	1	2523		NM_021794	NP_068566	Q9UKF2	ADA30_HUMAN	lasmic (Pote	NA	3	GGTTACTTTTTTT	0.358	
-	2	2734_2736	wne.1_In_Frame_	NM_007113	NP_009044	Q07283	TRHY_HUMAN	30 AA tande	NA	5	TGTAGCTCCTCC	0.586	rs143222885

+	4	1420_1421	C_uc001fqb.2_In	NM_005973	NP_005964	Q92733	PRCC_HUMAN		NA	27	CCTGGTCCCCC	0.53	
-	15	2113	Shift_Del_p.V623f	NM_001135050	NP_001128522	Q9P2J2	TUTLA_HUMAN	III 2.|Extrace	NA	5	GAGTACCCCCC	0.672	
-	4	570_571	tron|NR1I3_uc001	NM_001077480	NP_001070948	Q14994	NR1I3_HUMAN		NA	2	TGTGGCGGGTGT	0.564	rs139473535
+	8	1233_1234	9wxs.2_Frame_Sh	NM_000721	NP_000712	Q15878	CAC1E_HUMAN	lasmic (Pote	NA	6	GCCAAAGAGAGA	0.51	
-	19	9119	.K1369fs|ASPM_	NM_018136	NP_060606	Q8IZT6	ASPM_HUMAN	IQ 35.|IQ 34	NA	6	TTTCACTTTACA	0.313	
-	5	1798	AGT_uc009xff.2_F	NM_000029	NP_000020	P01019	ANGT_HUMAN		NA	0	AAGCTCAAAAAA	0.562	
+	30	3927	.1_Intron|MYO3A_	NM_017433	NP_059129	Q8NEV4	MYO3A_HUMAN		NA	18	GACTCCAAAAAA	0.403	
-	32	4715_4717	Del_p.1437_1438P	NM_033056	NP_149045	Q96QU1	PCD15_HUMAN	Cytoplasmic	NA	13	Tggcggaggcggcgg	0.438	rs12246234
+	4	743	c010qnb.1_Intron|	NM_000043	NP_000034	P25445	TNR6_HUMAN	.|Extracellula	NA	2	CCAAACTTTTTTT	0.368	
+	8	1043		NM_000392	NP_000383	Q92887	MRP2_HUMAN	smic (By sin	NA	1	GGACCAAAAAA	0.403	
+	19	2126_2128	.Q620del|PTPRE_	NM_006504	NP_006495	P23469	PTPRE_HUMAN	phatase 2.|C	NA	1	GCAGAAGCAGCA	0.65	
+	2	1024_1053	_uc001ltv.2_In_Fra	NR_021489					NA	0	GAGCCACAGCCC	0.657	4;rs36134435;rs61869706
+	10	1289	pkl.1_Splice_Site_	NM_004398	NP_004389	Q13206	DDX10_HUMAN		NA	4	TTGTTTAGGTACA	0.353	rs150843730
+	16	2803		NM_005188	NP_005179	P22681	CBL_HUMAN	on with CD2	NA	149	ATGGCCAAAAAC	0.507	
-	3	539_541		NM_006248	NP_006239				NA	0	GGGACTTGTTGT	0.596	
+	87	13755_13757		NM_002332	NP_002323	Q07954	LRP1_HUMAN	ical; (Potent	NA	22	GCTGTTGCTGCT	0.557	
+	8	893	pq.2_Frame_Shift_	NM_005269	NP_005260	P08151	GLI1_HUMAN	C2H2-type 2	NA	15	CCACTGGGGGG	0.597	
+	16	2686_2688	0tbn.1_In_Frame_	NM_004592	NP_004583	Q12872	SFSWA_HUMAN	rg/Ser-rich (	NA	0	CCACGAGAAGAA	0.493	
+	1	123_124	s_p.A30fs|EP400_	NM_015409	NP_056224	Q96L91	EP400_HUMAN		NA	12	AGCCGGCCCAC	0.649	rs71453134
-	34	4381_4382	_p.V250fs|POLE_	NM_006231	NP_006222	Q07864	DPOE1_HUMAN		NA	8	TTGACCACACAC	0.604	
-	1	1123		NM_001080396	NP_001073865	B1AL88	F155A_HUMAN		NA	1	CCCGTCCCCCC	0.607	
+	1	568_570	10_uc001whe.2_5'	NM_014045	NP_054764	Q7Z4F1	LRP10_HUMAN		NA	1	GCCACCCTCCTC	0.67	
-	18	1872	0apo.2_Frame_Sh	NM_174978	NP_777638	Q08AQ4	Q08AQ4_HUMAN		NA	4	TAGCTCAAAAAA	0.289	
-	2	1567_1569	orf43_uc010tud.1_	NM_194278	NP_919254	Q6PJG2	CN043_HUMAN	o-rich.|Gln-ri	NA	5	AGGgctgcctgctgctg	0.473	
-	6	961_963	.E208del|BEGAIN_	NM_001159531	NP_001153003	Q9BUH8	BEGIN_HUMAN		NA	0	CTCGGCCTCCTC	0.724	
+	4	2193_2194		NM_015042	NP_055857	O15014	ZN609_HUMAN	Poly-Lys.	NA	3	AAAGACAAAAAA	0.49	
+	7	2928_2930	10ujg.1_In_Frame_	NM_004727	NP_004718	O60721	NCKX1_HUMAN	ic (Potential)	NA	0	gaggaagaggaggag	0.281	
+	6	864_865	cts.3_Frame_Shift_	NM_004221	NP_004212	P24001	IL32_HUMAN		NA	1	GGGGGACAAGGA	0.574	rs2981599
+	12	3846_3848	ne_Del_p.Q812del|	NM_006599	NP_006590	O94916	NFAT5_HUMAN	Poly-Gln.	NA	0	TAATcaacagcagcag	0.389	
-	10	10282_10284	_In_Frame_Del_p	NM_006885	NP_008816	Q15911	ZFHX3_HUMAN	Poly-Gln.	NA	4	cctgtggttgctgctgctg	0.522	
-	9	3770	2fnc.1_Frame_Shi	NM_013275	NP_037407	Q6UB99	ANR11_HUMAN	Lys-rich.	NA	6	GTCATCTTTTTTT	0.468	
-	10	1079_1081	_63EE>E|C17orf85	NM_001114118	NP_001107590	Q53F19	CQ085_HUMAN	Glu-rich.	NA	1	tcttcctcttcctcctcctc	0.379	
+	11	2629_2631	02gix.2_In_Frame_	NM_001080424	NP_001073893	O15054	KDM6B_HUMAN	o-rich.|Thr-ri	NA	2	CGCCGTcaccacca	0.369	
+	34	4663_4665	0crt.2_In_Frame_	NM_003170	NP_003161	Q7KZ85	SPT6H_HUMAN	Poly-Ser.	NA	3	CCCCTAGCAGCAC	0.537	
-	2	287		NM_033060	NP_149049	Q9BYQ7	KRA41_HUMAN		NA	0	GCTGGGGTGGCA	0.646	9;rs483893;rs2320229;rs79048996;rs2320230
-	7	527	_Del_p.P94fs|ETV4	NM_001986	NP_001977	P43268	ETV4_HUMAN		NA	7	TGTCTGGGGGG	0.577	
+	7	711	10xia.1_Frame_Sh	NM_170678	NP_733778	Q9NPI5	NRK2_HUMAN		NA	2	CCTGATCCCCCC	0.587	
-	11	1320_1321	nfg.1_Frame_Shift_	NM_033417	NP_219485	Q9BT25	HAUS8_HUMAN		NA	0	TGAACGAGAGAG	0.495	
-	2	134	Splice_Site|ZNF43	NM_003423	NP_003414	P17038	ZNF43_HUMAN		NA	2	GTCCCTAAAAAA	0.386	
-	7	4346_4348	Del_p.1220_1221E	NM_181882	NP_870998	Q9BXM0	PRAX_HUMAN	Poly-Glu.	NA	2	TGCcctcttcctcctcc	0.606	
+	11	1043_1044	V1C2_uc002rat.2_	NM_001039362	NP_001034451	Q8NEY4	VATC2_HUMAN		NA	1	CCGACAGAGAGA	0.604	
+	12	2379		NM_003048	NP_003039	Q9UBY0	SL9A2_HUMAN	lasmic (Pote	NA	8	CCAGCACCCCCC	0.527	
+	12	1452_1453	p.V341fs|DCAF17_	NM_025000	NP_079276	Q5H9S7	DCA17_HUMAN		NA	0	GGGTGGTAAAAA	0.371	
-	1	139	c002uml.2_RNA|F	NM_181342	NP_851939	Q9Y680	FKBP7_HUMAN		NA	0	GCATGGTTTTTGC	0.522	
-	56	13909	N_uc010zfj.1_Intr	NM_133378	NP_596869	Q8WZ42	TITIN_HUMAN		NA	153	GCATCATTTTTGG	0.408	
-	29	3477_3478	vul.2_Frame_Shift	NM_018218	NP_060688	Q9NVE5	UBP40_HUMAN		NA	3	AATCTTGTTTTTTT	0.317	
+	2	175_177		NM_022134	NP_071417	Q9H3Q3	G3ST2_HUMAN	type II mem	NA	0	GGTCATCCTCCT	0.631	

+	7	739	PL2_uc011aah.1_F	NM_144498	NP_653081	Q9H1P3	OSBL2_HUMAN		NA	2	TCACCACCCCCC	0.463	rs79735057
+	4	1162	0gma.2_Frame_S	NM_005534	NP_005525	P38484	INGR2_HUMAN	tential).|Fibr	NA	0	ACGGCCTTTTTT	0.458	
-	22	3016_3018	aph.1_In_Frame_D	NM_002473	NP_002464	P35579	MYH9_HUMAN	Potential.	NA	11	CAGCGCTCCTCC	0.665	
-	7	1050_1052	gye.1_In_Frame_D	NM_020831	NP_065882	Q969V6	MKL1_HUMAN	Gln-rich.	NA	5	GTGGTGCTGCTC	0.66	
+	2	372_374	_Intron|LOC33967	NM_004599	NP_004590	Q12772	SRBP2_HUMAN	ch.|Cytoplasi	NA	4	agcagtggcagcagca	0.365	
+	5	477_479		NM_001197	NP_001188	Q13323	BIK_HUMAN	Potential).|He	NA	0	ctgctggcgctgctgctg	0.562	
-	19	1979	kw.2_Frame_Shift_	NM_017886	NP_060356	Q96C45	ULK4_HUMAN		NA	0	GGGTTCTTTTTTT	0.448	
+	14	1647	dgm.2_Frame_Shif	NM_006254	NP_006245	Q05655	KPCD_HUMAN	rotein kinase	NA	9	TCAACGGGGGG	0.602	
-	5	499	DPPA4_uc011bhp.1	NM_018189	NP_060659	Q7L190	DPPA4_HUMAN		NA	1	CTTTAATTTTTTT	0.413	
+	7	796	XTELC1_uc011bja.	NM_152305	NP_689518	Q8NBL1	PGLT1_HUMAN		NA	0	ACACCAAAAACC	0.408	
+	4	1562		NM_139209	NP_631948	Q8WTQ7	GRK7_HUMAN	kinase C-ter	NA	5	GGTTCGGGGGG	0.463	
+	29	4276_4278	a.1_Intron|P2RY12	NM_053002	NP_443728	Q86YW9	MD12L_HUMAN		NA	7	ATGGTTGGTGGC	0.527	
+	1	59_61	0icw.2_In_Frame_	NM_001528	NP_001519	Q04756	HGFA_HUMAN		NA	2	CCCCTTCCTCCT	0.729	
-	3	304	G78fs|ADH1A_uc0	NM_000667	NP_000658	P07327	ADH1A_HUMAN		NA	2	CCTTCTCCAACA	0.473	
-	3	299	0ilr.2_Frame_Shift	NM_020395	NP_065128	Q96CB8	INT12_HUMAN		NA	0	GCTTTCAAAAAAA	0.383	
+	3	351		NM_006583	NP_006574	O14718	OPSX_HUMAN	Name=3; (P	NA	1	TGAATATTTTTTT	0.393	
-	1	1220		NM_152402	NP_689615	Q8N609	TR1L1_HUMAN	lasmic (Pote	NA	1	CTGTTCTTTTTTT	0.383	
-	2	1076_1078	me_Del_p.P343de	NM_178835	NP_849157	Q17R98	ZN827_HUMAN	Pro-rich.	NA	0	AGGGATTgtggtggt	0.35	
+	6	626_627		NM_004477	NP_004468	Q14331	FRG1_HUMAN		NA	0	TAGGGGAAAATG	0.351	
-	7	919	AH5_uc003jfe.1_F	NM_001369	NP_001360	Q8TE73	DYH5_HUMAN	.|Stem (By s	NA	31	AGAGTCTTTTTTT	0.517	
+	1	453_455	cyu.1_In_Frame_I	NM_001964	NP_001955	P18146	EGR1_HUMAN	Gly/Ser-rich	NA	1	cagcaacagcagcag	0.394	
+	26	4712	n.1_Frame_Shift_D	NM_020690	NP_065741	Q8IWZ2	Q8IWZ2_HUMAN		NA	6	TTGGGAAAAAAA	0.423	
+	11	2401	p.G581fs|LARP1_	NM_033551	NP_291029	Q6PKG0	LARP1_HUMAN		NA	4	ACCCAGGGGGG	0.547	
-	1	506_508	c003mnq.2_5'Flan	NM_032765	NP_116154	Q96A61	TRI52_HUMAN	Glu-rich.	NA	0	GCTtcctcgtcctcctcct	0.404	rs146030758
-	1	523_524		NM_052967	NP_443199	P35410	MAS1L_HUMAN	lasmic (Pote	NA	9	AGAGGACACACA	0.495	
+	9	1106_1107	vc.3_Frame_Shift_	NM_080686	NP_542417	P48634	PRC2A_HUMAN	57 AA type A	NA	0	TGTGGCGGGCCC	0.495	rs147717718
+	3	406_408	p.Q71del|RUNX2_	NM_001024630	NP_001019801	Q13950	RUNX2_HUMAN	Poly-Gln.	NA	3	cagcaacagcagcag	0.276	
+	15	2788	p.K847fs|GRIK2_u	NM_021956	NP_068775	Q13002	GRIK2_HUMAN	lasmic (Pote	NA	5	AATCCAAAAAAA	0.348	
+	2	688		NM_198570	NP_940972	Q2TAL6	VWC2_HUMAN		NA	0	CCGGGCCAGGA	0.716	
-	7	1188	p.K237fs|CYP51A	NM_000786	NP_000777	Q16850	CP51A_HUMAN		NA	0	ATAACATTTTTTT	0.398	
-	9	2023_2025		NM_022574	NP_072096	O75420	PERQ1_HUMAN	Poly-Glu.	NA	2	AAGGTTCCTCCT	0.675	rs142340746
+	8	1077_1079	xa.2_In_Frame_D	NM_015908	NP_056992	Q9BXP5	SRRT_HUMAN	Glu-rich.	NA	2	GAGCAGGAGGA	0.596	
+	1	528		NM_001001656	NP_001001656	Q8NGU2	OR9A4_HUMAN	cellular (Pote	NA	1	GAACAATTTTTTT	0.383	
+	1	_Intron|uc010loj.1_Intron|uc003wad.2_Intron|uc003wag.1_Intron|TRY6_uc011ksn.1_Intron|uc003wan.1_Intron|uc0							NA	0	GCTGGCGAGTTT	0.535	
-	60	8167	Shift_Del_p.R2704	NM_006904	NP_008835	P78527	PRKDC_HUMAN	KIP-binding.	NA	34	CCAGCCTTTTTTT	0.498	
+	3	780_781		NM_014943	NP_055758	Q9Y6X8	ZHX2_HUMAN		NA	2	CAGTCCAAAAAA	0.49	
+	5	332	_Intron|ARHGAP6	NM_001142	NP_001133	Q99217	AMELX_HUMAN		NA	0	GTGGTGCCAGC	0.617	
-	18	2564_2566	dsw.2_In_Frame_D	NM_015107	NP_055922	Q9UPP1	PHF8_HUMAN		NA	3	GCGTTCTCCTCCT	0.591	
+	12	1981	n|TAF1_uc004dzt.3	NM_138923	NP_620278	P21675	TAF1_HUMAN		NA	17	CACATCAAAAAAA	0.313	
-	15	4609_4611	422EE>E|ATRX_uc	NM_000489	NP_000480	P46100	ATRX_HUMAN	Poly-Glu.	NA	30	tcctcctcttcctcctcctc	0.212	
-	1	1805_1806		NM_003604	NP_003595	O14654	IRS4_HUMAN		NA	10	CCTTTGCCCCCC	0.545	
-	14	2723	p.A823fs|IGSF1_u	NM_001555	NP_001546	Q8N6C5	IGSF1_HUMAN	Potential).|Ig-	NA	5	CACTGGCCCCCG	0.488	
-	3	645	exp.1_Frame_Shift	NM_021796	NP_068568	Q9HBJ0	PLAC1_HUMAN		NA	1	GGGACTTTTGGC	0.527	
-	1	159		NM_001009609	NP_001009609	Q5MJ09	SPXN3_HUMAN		NA	2	TCATCATTTTTTT	0.239	
+	3	1864_1866	Q581del|MAMLD1	NM_005491	NP_005482	Q13495	MAMD1_HUMAN	Poly-Gln.	NA	0	Tgcagctgcagcagca	0.488	
-	8	877_879		NM_001561	NP_001552	Q07011	TNR9_HUMAN	ential).|Intera	p.E250G(1)	4	TCCTCCTTCTTCT	0.379	
+	10	1424	vni.2_Splice_Site_	NM_014874	NP_055689	O95140	MFN2_HUMAN			1	CTCCTAGGGGGC	0.48	

+	11	10149	p.1_Frame_Shift_	NM_015001	NP_055816	Q96T58	MINT_HUMAN	Pro-rich.	15	TACCACCCCCC	0.627	
-	6	632	ble.3_Frame_Shif	NM_000437	NP_000428	Q99487	PAFA2_HUMAN		2	CTTCTGGGGCC	0.498	
+	14	1261	p.I350fs|RPS6KA	NM_002953	NP_002944	Q15418	KS6A1_HUMAN	kinase C-terminal.	1	GGCATCCCCCC	0.672	
+	20	6238_6239	_p.L801fs|ARID1	NM_006015	NP_006006	O14497	ARI1A_HUMAN		142	ATCCTAGAGGAC	0.535	
-	9	1564_1565	vup.2_Frame_Shif	NM_007167	NP_009098	O95789	ZMYM6_HUMAN		3	CCTTGTAAAAAA	0.351	
+	6	520_521	_RNA|ST3GAL3_	NM_006279	NP_006270	Q11203	SIAT6_HUMAN	enal (Potential).	3	CCTTTCGCAAGT	0.515	
+	13	1543_1544	TA1_uc001djy.1_	NM_001081472	NP_001074941				1	GCACAGAAAAA	0.228	
+	4	327_329	326_uc009wda.1_	NM_182976	NP_892021	Q5BKZ1	ZN326_HUMAN	l activation (By similarity).|	1	CACAGTGGTGG	0.409	
+	6	1737	p.S374fs|PRPF38	NM_018061	NP_060531	Q5VTL8	PR38B_HUMAN		0	AAATCAAAAAAA	0.343	
+	21	3910	.1_3'UTR|MAGI3_	NM_001142782	NP_001136254	Q5TCQ9	MAGI3_HUMAN		6	TCCTCTAAAAAA	0.453	
-	9	1732_1734	ows.1_In_Frame_	NM_015906	NP_056990	Q9UPN9	TRI33_HUMAN	Poly-Thr.	11	TGTTGTGTTGTT	0.429	
-	5	848_849	ehg.2_Frame_Shif	NM_017686	NP_060156	Q9NXN4	GDAP2_HUMAN	Macro.	2	TGCTATGTGTGT	0.292	
+	8	2280	zr.1_Frame_Shift_	NM_004326	NP_004317	O00512	BCL9_HUMAN	y-Pro.|Pro-rich.	6	GAGGACCCCCC	0.582	
-	2	4365_4366	.1_In_Frame_Ins_	NM_007113	NP_009044	Q07283	TRHY_HUMAN	proximate tandem repeats.	5	CTGGCGCAGCT	0.559	
-	2	1035_1036	e.1_In_Frame_Ins	NM_007113	NP_009044	Q07283	TRHY_HUMAN	-E-Q-E-E- E-R-R-E-Q-Q-L	5	ctcgcgcctctcctcctg	0	
+	4	1420_1421	C_uc001fqb.2_In	NM_005973	NP_005964	Q92733	PRCC_HUMAN		27	CCTGGTCCCCC	0.53	
+	8	1233_1234	9wxs.2_Frame_Sh	NM_000721	NP_000712	Q15878	CAC1E_HUMAN	lasmic (Potential).	6	CCAAAGAGAGA	0.51	
+	9	1102_1103	qh.2_Frame_Shif	NM_173156	NP_775179	Q92540	SMG7_HUMAN		3	GCTATGTTGGAC	0.391	
-	15	1913	EM3_uc010pom.	NM_025191	NP_079467	Q9BZQ6	EDEM3_HUMAN		1	CCACATTTTTCA	0.363	
+	7	1256_1258	e_Del_p.E310del	NM_005807	NP_005798	Q92954	PRG4_HUMAN	ats of K-X-P-X-P-T-T-X.|8.	1	ACCAAGGAGCC	0.65	rs139084037
+	7	1327_1328	_Ins_p.333_334ins	NM_005807	NP_005798	Q92954	PRG4_HUMAN	-X-P-X-P-T-T-X.|11; appro	1	CCACCAAGTCTG	0.658	
+	7	1633_1634	_Ins_p.435_436ins	NM_005807	NP_005798	Q92954	PRG4_HUMAN	-X-P-X-P-T-T-X.|24; appro	1	CCACCAAGTCTG	0.639	
-	2	850	1hha.3_Frame_Sh	NM_025179	NP_079455	O75051	PLXA2_HUMAN		3	CTGCTGGGGGG	0.652	
+	18	2704	ub.1_Frame_Shif	NM_016121	NP_057205	Q9Y597	KCTD3_HUMAN		3	GGCATAAAAAA	0.418	
-	61	12429		NM_206933	NP_996816	O75445	USH2A_HUMAN	II 25.|Extracellular (Potenti	26	ACGGTAGGGCT	0.423	
+	4	474	hpl.2_Frame_Shift	NM_001136018	NP_001129490	P07099	HYEP_HUMAN		4	TGAAGCCCCCC	0.627	
+	4	883	.1_Intron|ZNF678_	NM_178549	NP_848644	F5GXA7	F5GXA7_HUMAN		1	AGAAACCCTAC	0.363	
-	8	852_853	p.Q174fs|RGS7_	NM_002924	NP_002915	P49802	RGS7_HUMAN		7	CTTTGCTTGTGC	0.441	
-	1	679	N3_uc001hzb.2_In	NM_001821	NP_001812	P26374	RAE2_HUMAN		6	TCCTCTACATCA	0.358	
-	1	1608	KG1_uc001jjn.2_I	NM_015235	NP_056050	Q9H0L4	CSTFT_HUMAN	peats of G-[AT]-G-[MI]- Q.|	1	tgtatgcctgctccctgc	0.214	
-	22	4568_4569	.S605fs|USP54_u	NM_152586	NP_689799	Q70EL1	UBP54_HUMAN		6	CCCTTGGGAAG	0.52	
-	5	914	plice_Site_p.Q1	NM_000770	NP_000761	P10632	CP2C8_HUMAN		0	ATCTTACCTGCT	0.368	
-	9	1499_1501	XM2_uc001lhj.2_	NM_198148	NP_937791	Q8N436	CPXM2_HUMAN	Poly-Leu.	2	GCACCAGCAGC	0.626	
+	10	2005		NM_007183	NP_009114	Q9Y446	PKP3_HUMAN		1	TGGGCGGGGGT	0.682	
+	2	1024_1053	_uc001ltv.2_In_Fr	NR_021489					0	AGCCACAGCCC	0.657	4;rs36134435;rs61869706
-	1	194		NM_001005160	NP_001005160	Q9H2C5	O52A5_HUMAN	Name=2; (Potential).	4	ATGGCCAAAAAA	0.383	
-	5	1326	p.V323fs|FAM160	NM_001098794	NP_001092264	Q8N612	F16A2_HUMAN		2	ATCAACCAACTG	0.542	
-	4	465	yii.2_Splice_Site_	NM_018362	NP_060832	Q9NUP9	LIN7C_HUMAN		0	TCCTTACCACTC	0.404	
-	6	1027	p.P341fs|CPSF7_	NM_001136040	NP_001129512	Q8N684	CPSF7_HUMAN	Pro-rich.	1	TTGGTGGGGGG	0.557	
+	5	419	nyx.2_Frame_Shif	NM_003377	NP_003368	P49765	VEGFB_HUMAN		0	GACCTAAAAAA	0.388	
+	15	1523	p.L384fs|TPCN2_	NM_139075	NP_620714	Q8NHX9	TPC2_HUMAN	S2 of repeat II; (Potential).	0	ATCCTGGGGGT	0.637	
+	1	521	1_Intron|PIWIL4_u	NM_002033	NP_002024	P22083	FUT4_HUMAN	lasmic (Potential).	1	ATTCTGGGACC	0.741	
-	5	674_675		NM_002426	NP_002417	P39900	MMP12_HUMAN		0	CAAGTGGTGCC	0.416	192524;rs33924686
+	3	358	uc001qmv.2_5'UT	NM_001130862	NP_001124334	Q96B01	R51A1_HUMAN		0	CCCCTAAAAAA	0.348	rs34810644
+	5	2042_2043	rx.1_Frame_Shift_	NM_001007026	NP_001007027	P54259	ATN1_HUMAN		6	TTTCCCACCGGT	0.619	
-	1	33		NM_023921	NP_076410	Q9NYW0	T2R10_HUMAN	Name=1; (Potential).	0	ACAACAAAAATG	0.378	
-	3	441_442	.1_Intron|PRB1_u	NM_005039	NP_005030	P04280	PRP1_HUMAN	-[PAQ]-Q-[GE]-[GD]- [NKS]	0	TTTCCTGGAGGT	0.604	

-	3	258_259	_74P>PP|PRB1_u	NM_005039	NP_005030	P04280	PRP1_HUMAN	-P-[PAQ]-Q-[GE]-[GD]- [N	0	TTTCCTGGAGGT	0.619	
-	3	502_503		NM_006248	NP_006239				0	TTTCCTGGAGGT	0.594	
-	3	257_259		NM_006248	NP_006239				0	TCCTGGAGGAG	0.601	
-	6	542	_Shift_Del_p.A150f	NM_004447	NP_004438	Q12929	EPS8_HUMAN		4	CAGTGCAAGAA	0.388	
+	4	669	|FAR2_uc009zjm.	NM_018099	NP_060569	Q96K12	FACR2_HUMAN		0	GAGCCAAAAAA	0.388	
+	31	4582_4583	_p.F325fs|LRRK2_	NM_198578	NP_940980	Q5S007	LRRK2_HUMAN	Roc.	24	CACTTTGTGAAT	0.441	
+	10	1054_1055	e_Shift_Del_p.V3	NM_006431	NP_006422	P78371	TCPB_HUMAN		3	GGTGTGGAACG	0.351	
+	8	1314	C3_uc009zsm.2_	NM_181783	NP_861448	Q6ZXV5	TMTC3_HUMAN	ical; (Potential).	1	CGAACCTTTTTT	0.303	
+	16	1595_1596	p.H504fs|KIAA103	NM_015275	NP_056090	Q2M389	WAHS7_HUMAN		2	TTCACATATAAC	0.332	
-	3	263		NM_005719	NP_005710	O15145	ARPC3_HUMAN		1	TCATAGTTTTTGA	0.244	
-	34	4381_4382	_p.V250fs|POLE_	NM_006231	NP_006222	Q07864	DPOE1_HUMAN		8	TTGACCACACAC	0.604	
-	2	595_596	RPC4_uc010abw.	NM_016179	NP_057263	Q9UBN4	TRPC4_HUMAN	l).|Multimerization domain	6	ACTAGGTTTTTT	0.297	
+	9	2007	_p.K603fs|CKAP2_	NM_001098525	NP_001091995	Q8WWK9	CKAP2_HUMAN		2	GTGTGAAAAAA	0.318	
+	20	3706_3707	.A881fs|LMO7_uc	NM_015842	NP_056667	Q8WWI1	LMO7_HUMAN		5	GAGGCAGAGAG	0.386	
-	58	9857_9858	aev.2_Frame_Shi	NM_015057	NP_055872	O75592	MYCB2_HUMAN		14	AAGTGCTTCCTC	0.465	
-	1	825	P1_uc001vni.2_I	NM_178861	NP_849192	Q8IZP6	R113B_HUMAN	RING-type.	3	CTGGGTTTTGG	0.567	
-	1	1123		NM_001080396	NP_001073865	B1AL88	F155A_HUMAN		1	CCCGTCCCCCC	0.607	
+	1	96_97		NM_172194	NP_751944	Q8NH05	OR4Q3_HUMAN	Name=1; (Potential).	3	TTTTTGTTTTTT	0.381	
+	1	568_570	0_uc001whe.2_5'	NM_014045	NP_054764	Q7Z4F1	LRP10_HUMAN		1	CCACCCTCCTC	0.67	
-	2	421_422	.1_Frame_Shift_I	NM_017917	NP_060387	Q969Q6	P2R3C_HUMAN		1	GTTCACTTTTTT	0.262	
-	8	1800	mk.2_Frame_Shi	NM_033141	NP_149132	P80192	M3K9_HUMAN		5	CCTGGCCCCCA	0.493	
+	13	3597	te_p.S940_splice|	NM_014982	NP_055797	Q96RV3	PCX1_HUMAN		1	TTTTTAGAGTGT	0.312	rs79889635
+	12	1357_1358	tts.1_Frame_Shift	NM_015604	NP_056419	Q8WV16	DCAF4_HUMAN	WD 1.	3	ATCCTCCAAGAT	0.545	rs148311071
+	1	707	_5'Flank|TMED8_	NM_001010860	NP_001010860	Q9P1V8	SAM15_HUMAN		0	GATGACCAAAC	0.478	
-	5	633_635	.3_In_Frame_Del_	NM_005065	NP_005056	Q9UBV2	SE1L1_HUMAN	action with ERLEC1, OS9 a	1	AGCCTCTTCTT	0.345	
-	1	115_116		NM_001080490	NP_001073959	Q3MJ16	PA24E_HUMAN		0	ACTGGCCCCC	0.594	746726;rs72237204
-	2	1779	on|ZFP106_uc010	NM_022473	NP_071918	Q9H2Y7	ZF106_HUMAN		3	AGGGGAAAAAA	0.393	
+	12	1375_1377		NM_007347	NP_031373	Q9UPM8	AP4E1_HUMAN		0	TTATTCAGACAAT	0.365	
+	4	1018		NM_015554	NP_056369	O94923	GLCE_HUMAN	enal (Potential).	2	GCTGATAAGTCT	0.403	
+	9	2591	_p.Q769fs|PML_uc	NM_033238	NP_150241	P29590	PML_HUMAN		5	CGGCAGGGGGG	0.647	
-	3	247_248	G4_uc010bkn.2_	NM_138573	NP_612640	Q8WWG1	NRG4_HUMAN	r (Potential).|EGF-like.	0	ACAAAGCCCCC	0.381	
+	5	1049	HD1_uc010ble.2_	NM_001013619	NP_001013641	A2RU49	AGPD1_HUMAN		0	AGTCGTTTTTG	0.458	
+	6	864_865	ts.3_Frame_Shift_	NM_004221	NP_004212	P24001	IL32_HUMAN		1	GGGGACAAGG	0.574	rs2981599
-	3	512	_5'Flank|ATP6V0	NM_001138	NP_001129	O00253	AGRP_HUMAN		0	CCTCTGCCAAG	0.607	
-	10	0282_1028	_In_Frame_Del_p	NM_006885	NP_008816	Q15911	ZFHX3_HUMAN	Poly-Gln.	4	cctgtggttgctgctgct	0.522	
-	14	2504	_p.F283fs|ADAMT	NM_199355	NP_955387	Q8TE60	ATS18_HUMAN	Cys-rich. p.A696fs*18(2)	18	CATTGCAAAAAA	0.403	
+	2	617		NM_001406	NP_001397	Q15768	EFNB3_HUMAN	ellular (Potential).	1	TCCTCTCCTAAT	0.627	
-	36	5385		NM_003802	NP_003793	Q9UKX3	MYH13_HUMAN		6	GAGCTCACATCC	0.436	rs112383245
+	34	4663_4665	0crt.2_In_Frame_	NM_003170	NP_003161	Q7KZ85	SPT6H_HUMAN	Poly-Ser.	3	CCCTAGCAGCA	0.537	
-	2	287		NM_033060	NP_149049	Q9BYQ7	KRA41_HUMAN		0	GCTGGGGTGGC	0.646	9;rs483893;rs2320229;rs79048996;rs2320230
-	2	522_524	DC_uc002hze.3_	NM_032484	NP_115873	Q8N2G8	GHDC_HUMAN		0	ATGTTGgcagcag	0.502	
-	2	973	_Shift_Del_p.G170	NM_001145365	NP_001138837	Q9Y2D9	ZN652_HUMAN	Glu-rich.	1	TTCTCTCCATAGT	0.473	
+	4	505_507	10wsa.1_In_Fram	NM_014738	NP_055553	Q12767	K0195_HUMAN	ical; (Potential).	1	GCCGTGCTGCT	0.675	
-	4	1782		NM_052947	NP_443179	Q86TB3	ALPK2_HUMAN		14	AGTCCTTTCCCC	0.522	
+	3	617	G_uc010drr.2_Fr	NM_001728	NP_001719	P35613	BASI_HUMAN	Potential).|Ig-like C2-type.	0	CTGAAGGGGGG	0.617	
+	6	896	_Shift_Del_p.D19	NM_012218	NP_036350	Q12906	ILF3_HUMAN	DZF.	3	AACGACCCCCC	0.502	
+	3	316	s.1_RNA|ZNF90_	NM_007138	NP_009069	Q03938	ZNF90_HUMAN	KRAB.	2	GCAAGGAAAAAA	0.393	

+	6	1442_1443	714_uc010ecp.1_F	NM_182515	NP_872321	Q96N38	ZN714_HUMAN	C2H2-type 9.		0	ATAAGATGATTCA	0.356	
+	5	839_840		NM_018025	NP_060495	Q9BRR8	GPTC1_HUMAN	G-patch.		1	CGAGTAAAGAGA	0.361	
-	5	1009_1020	c002nzv.2_5'Flank	NM_033317	NP_201574	Q6E0U4	DMKN_HUMAN	Gly-rich.	S274_S290del	3	gccgccactgctgctgc	0.241	522263;rs140071083;rs138902616;rs113540509
+	7	712_714		NM_001039887	NP_001034976	Q2NL68	CS055_HUMAN	Ser-rich.		1	TCCATCTCCTCC	0.631	
+	17	1944_1945	piu.2_Frame_Shift_	NM_000540	NP_000531	P21817	RYR1_HUMAN	smic.|B30.2/SPRY 1.		12	CTCCCTGTGTGT	0.53	
+	7	1250	oxp.3_Frame_Shi	NM_181845	NP_862828	Q8N7M2	ZN283_HUMAN	C2H2-type 5.		0	AAGGCCTTTTTTT	0.408	
-	4	318_319	e_Shift_Del_p.S6	NM_000234	NP_000225	P18858	DNLI1_HUMAN			3	CCCTTCGCTGCC	0.584	rs149883221
+	3	612	RT_uc002pof.1_5'U	NM_001136019	NP_001129491	P55899	FCGRN_HUMAN	ar (Potential).|Alpha-1.		1	GCCCCGGGGAC	0.652	rs11551281
+	3	238	808_uc002pzq.2_	NM_001039886	NP_001034975	Q8N4W9	ZN808_HUMAN			0	CTTCCTCAGGTG	0.378	
+	11	1043_1044	V1C2_uc002rat.2_	NM_001039362	NP_001034451	Q8NEY4	VATC2_HUMAN			1	CCGACAGAGAGA	0.604	
-	1	1479_1481		NM_001029883	NP_001025054	A6NGG8	CB071_HUMAN			1	GTCTTCCTCCTC	0.542	
+	12	2379		NM_003048	NP_003039	Q9UBY0	SL9A2_HUMAN	lasmic (Potential).		8	CAGCACCCCCC	0.527	
+	21	2570	GKD_uc010fyh.1_F	NM_152879	NP_690618	Q16760	DGKD_HUMAN			5	CTTCTGGGGGG	0.582	
+	8	1134	gal.1_Frame_Shift_	NM_198994	NP_945345	O95932	TGM3L_HUMAN			4	TGCCACCCCCCA	0.582	
+	9	1585	wil.2_Frame_Shift_	NM_139321	NP_647537	O75882	ATRN_HUMAN	ar (Potential).|Kelch 3.		2	TGCAAGGGGGT	0.502	
+	30	4617	GAPB_uc002xiy.1_	NM_020336	NP_065069	Q86X10	RLGPB_HUMAN			2	TACAGTCCCCCC	0.428	
+	1	368_369	xjf.2_In_Frame_In	NM_030919	NP_112181	Q9H4H8	FA83D_HUMAN			3	GGAGGGCgcggc	0.619	
-	7	859_860		NM_020820	NP_065871	Q8TCU6	PREX1_HUMAN	PH.		6	GATCTTTAACAAA	0.545	
-	2	2489_2490	xus.1_Frame_Shif	NM_004975	NP_004966	Q14721	KCNB1_HUMAN	lasmic (Potential).		2	GCTTTTGGGGG	0.545	
-	12	2865_2866		NM_003185	NP_003176	O00268	TAF4_HUMAN			3	CCTCTGCTTTTC	0.525	rs138584893
+	4	334	l_p.T11fs|KCNJ15_	NM_002243	NP_002234	Q99712	IRK15_HUMAN	smic (By similarity).		6	CAGCACCCCCC	0.522	
-	42	7065	goc.1_Frame_Shi	NM_018963	NP_061836	Q9NSI6	BRWD1_HUMAN			4	CCCCTTAAAAAA	0.323	
+	5	602	.S140fs|DIP2A_uc	NM_015151	NP_055966	Q14689	DIP2A_HUMAN			2	CTGCCTCAGAAG	0.592	
+	2	884	KL_uc002ztg.1_R	NM_005207	NP_005198	P46109	CRKL_HUMAN	SH3 1.		0	TAACCTGGAATAT	0.433	
-	7	789_791		NM_016449	NP_057533	Q6PGQ1	CV043_HUMAN	Asp-rich.		1	CCTGGGcatcatc	0.261	
+	8	1121_1122	.3_RNA|NF2_uc0	NM_000268	NP_000259	P35240	MERL_HUMAN	FERM.	_E270del(1)|p	728	CAGAATAAAAAG	0.48	
-	27	3737_3738		NM_002473	NP_002464	P35579	MYH9_HUMAN	Potential.		11	ATGTTCACCTCC	0.614	
-	22	3016_3018	aph.1_In_Frame_	NM_002473	NP_002464	P35579	MYH9_HUMAN	Potential.		11	CAGCGCTCCTCC	0.665	
+	3	268	3L_uc011ann.1_Fr	NM_016091	NP_057175	Q9Y262	EIF3L_HUMAN			1	TCCACAAAACTC	0.443	
+	2	378_380		NM_033318	NP_201575	Q9H4I9	CV032_HUMAN	Asp/Glu-rich.		1	CAGAGGATGATG	0.478	rs141840500
-	1	871_873	.S246del|TCF20_	NM_005650	NP_005641	Q9UGU0	TCF20_HUMAN	Ser-rich.		5	AAGGGAaggagga	0.438	
-	7	1008_1009	3_uc011apq.1_Fra	NM_032311	NP_115687	Q9BY77	PDIP3_HUMAN	RRM.		0	GGCCCCACACAC	0.559	
+	4	644_646	hce.1_5'Flank|BH	NM_003670	NP_003661	O14503	BHE40_HUMAN			1	TGATCAGCAGCA	0.438	rs147291233
+	16	2116		NM_014296	NP_055111	Q9Y6W3	CAN7_HUMAN	Domain III.		1	GATGGGAAAAAA	0.289	
-	16	3037_3039	C2_uc003dhq.1_R	NM_015576	NP_056391	O15083	ERC2_HUMAN	Poly-His.		2	ggtggtgatggtggtgg	0.389	
-	16	4234_4236	eed.2_In_Frame_	NM_199420	NP_955452	O75417	DPOLQ_HUMAN			11	CACTCCTTCTGAA	0.448	
+	6	1298	me_Shift_Del_p.I1	NM_017554	NP_060024	Q460N5	PAR14_HUMAN			6	CACCATAAAAAAT	0.398	
-	3	790_791	Shift_Del_p.S205f	NM_003925	NP_003916	O95243	MBD4_HUMAN			2	AAGTTAGAGAGT	0.416	
+	11	1582_1583	l_p.L332fs|CEP63_	NM_025180	NP_079456	Q96MT8	CEP63_HUMAN	Potential.		1	AGAACTGAAGAG	0.351	
+	29	4276_4278	a.1_Intron|P2RY12	NM_053002	NP_443728	Q86YW9	MD12L_HUMAN			7	TGGTTGGTGGC	0.527	
+	2	800	fgv.2_Frame_Shift_	NM_005414	NP_005405	P12757	SKIL_HUMAN			3	CCAGCGAAAAAA	0.438	
-	2	5329	C4_uc003fvp.2_Int	NM_018406	NP_060876	Q99102	MUC4_HUMAN			0	GCTGAGGAAGT	0.567	
+	1	3006_3007		NM_175918	NP_787114	Q8N1N5	CRPAK_HUMAN			0	CTGCTCACACGT	0.465	
+	1	3102_3103		NM_175918	NP_787114	Q8N1N5	CRPAK_HUMAN	1		0	CACACATGCCCA	0.644	rs144787346
+	1	3344_3345		NM_175918	NP_787114	Q8N1N5	CRPAK_HUMAN			0	CTGCTCACACGT	0.693	
+	1	4053_4054		NM_175918	NP_787114	Q8N1N5	CRPAK_HUMAN			0	CTGCTCACACAC	0.658	
+	17	3256_3257	ifd.2_Frame_Shift	NM_015173	NP_055988	Q86TI0	TBCD1_HUMAN	ab-GAP TBC.		1	TTCCTCACCATG	0.535	

-	5	391	et.3_Frame_Shift_	NM_001891	NP_001882	P05814	CASB_HUMAN			0	GGGTCAAAAAA	0.473	
+	4	994_996	.Q279del|MMRN1_	NM_007351	NP_031377	Q13201	MMRN1_HUMAN	Poly-Gln.		4	GCTGAGCAGCA	0.448	
-	3	2265	L3_uc011chd.1_I	NM_018717	NP_061187	Q96JK9	MAML3_HUMAN			1	tgctgttgctgctgctgc	0.263	
+	17	2312_2314	uc003kgi.3_Intron	NM_003248	NP_003239	P35443	TSP4_HUMAN	SP type-3 7.		0	AGTGTGATGAT	0.562	
+	4	1030_1031		NM_002439	NP_002430	P20585	MSH3_HUMAN	ction with EXO1.		4	TCTTTGGGGAA	0.347	
+	15	2297_2299	RF2_uc011ctn.1_	NM_006909	NP_008840	O14827	RGRF2_HUMAN			12	AGTCCCACCAC	0.562	
+	21	2611_2613	36_uc010jbu.2_I	NM_139281	NP_644810	Q8NI36	WDR36_HUMAN			2	ACTTGAAGAAG	0.251	
+	6	912_914	me_Del_p.G153d	NM_001903	NP_001894	P35221	CTNA1_HUMAN			11	GGGTGGAGGAG	0.512	
+	6	1328	_p.A223fs|LARP1_	NM_033551	NP_291029	Q6PKG0	LARP1_HUMAN			4	CGTGGCCCCCC	0.642	
+	4	629_630		NM_145049	NP_659486	Q8WVY7	UBCP1_HUMAN			1	GATATTGAAGAT	0.312	
+	5	996		NM_003862	NP_003853	O76093	FGF18_HUMAN			0	GGCTTCACCAA	0.607	
+	5	1860	nfs.1_Frame_Shift_	NM_022455	NP_071900	Q96L73	NSD1_HUMAN			3	TGTGGAAAAAA	0.423	
-	4	1510_1512	_Frame_Del_p.E3	NM_178012	NP_821080	Q9BVA1	TBB2B_HUMAN			1	TCGCCCTCCTC	0.65	
-	14	1681_1682	me_Shift_Del_p.	NM_001144769	NP_001138241	Q03001	DYST_HUMAN			14	GGCCTTCTCTC	0.441	
-	2	894		NM_002031	NP_002022	P42685	FRK_HUMAN	SH2.		6	TTCTCCTTTTTG	0.398	
-	2	894	PRH_uc003qlg.1_	NM_001042683	NP_001036148	Q149N8	SHPRH_HUMAN		p.E166fs*7(1)	3	GGTTCTTTTTT	0.363	
+	26	3025_3026	me_Shift_Ins_p.D	NM_015440	NP_056255	Q6UB35	C1TM_HUMAN	hydrofolate synthetase.		4	CCTGACAAAAAA	0.48	
-	12	1527_1528	egw.1_5'Flank|W	NM_018288	NP_060758	Q8WUB8	PHF10_HUMAN			1	GTGTTGGGGG	0.391	
+	2	1295	rame_Shift_Del_p.	NM_001098201	NP_001091671	Q99527	GPER_HUMAN	ellular (Potential).		1	GCCCACCCCCT	0.627	
+	8	2004_2005	srz.2_Frame_Shift_	NM_014660	NP_055475	O94880	PHF14_HUMAN			3	TTGCAAGAGAGA	0.376	
-	4	706	_p.F63fs|TRA2A_	NM_013293	NP_037425	Q13595	TRA2A_HUMAN	RRM.		1	TACACAAAAGC	0.368	
+	3	342	_uc011kby.1_Intro	NM_002541	NP_002532	Q02218	ODO1_HUMAN			2	GGACATTTTTTT	0.577	
+	4	952_953		NM_001159279	NP_001152751					2	AGCCGCTCAACA	0.416	
+	4	1034_1036		NM_001159279	NP_001152751					2	CCGCTCTTCAA	0.419	
-	7	1188	_p.K237fs|CYP51A	NM_000786	NP_000777	Q16850	CP51A_HUMAN			0	ATAACATTTTTTT	0.398	
-	21	3334	y.2_Frame_Shift_	NM_000466	NP_000457	O43933	PEX1_HUMAN			2	ACAGACTTAGGT	0.373	
+	72	11555_1155	P_uc003upr.2_Fr	NM_003496	NP_003487	Q9Y4A5	TRRAP_HUMAN	PI3K/PI4K.		37	TGGCACAAAAAA	0.55	
-	2	390_392	kiw.1_In_Frame_	NM_015545	NP_056360	O75127	PTCD1_HUMAN			1	AAACTCTCCTCC	0.606	
-	13	2332	ir-25|MI0000082_	NM_005916	NP_005907	P33993	MCM7_HUMAN	ction with ATRIP.		0	GATAGCCAGCA	0.547	
+	1	924_926	.1_5'Flank|ZCWP	NM_019606	NP_062552	Q7L2J0	MEPCE_HUMAN			1	CCACCAGCAGC	0.65	
+	4	467		NM_001283	NP_001274	P61966	AP1S1_HUMAN			0	TTGATGGGGGG	0.562	
+	5	743	_p.E17fs|CBLL1_	NM_024814	NP_079090	Q75N03	HAKAI_HUMAN	RING-type.		5	ACATGAAAAAAA	0.269	
-	4	1558_1559		NM_033427	NP_219499	Q8WZ74	CTTB2_HUMAN	Pro-rich.		5	GTATTCCGAGCT	0.535	
+	4	1161	HRM2_uc003vtm	NM_001006630	NP_001006631	P08172	ACM2_HUMAN	llular (By similarity).		5	ATTCAGTTTTTTT	0.498	
-	10	1269		NM_004333	NP_004324	P15056	BRAF_HUMAN			18290	AGGCAGGGGGG	0.428	
+	1	528		NM_001001656	NP_001001656	Q8NGU2	OR9A4_HUMAN	ellular (Potential).		1	GAACAATTTTTTT	0.383	
-	9	2677_2679	wwl.1_In_Frame_	NM_182643	NP_872584	Q96QB1	RHG07_HUMAN	Poly-Ser.		7	ACTGGCTGCTG	0.621	rs137989738
-	60	8167	Shift_Del_p.R2704	NM_006904	NP_008835	P78527	PRKDC_HUMAN	KIP-binding.		34	CCAGCCTTTTTT	0.498	
-	4	555_556	xyp.2_Frame_Shi	NM_016027	NP_057111	Q53H82	LACB2_HUMAN			1	CCTCTTCTAAGA	0.371	
-	2	284		NM_001033723	NP_001028895	Q6ZNC4	ZN704_HUMAN			0	GAGACATTTTTTT	0.423	
-	5	730_731		NM_018710	NP_061180	Q8N4L2	TM55A_HUMAN			0	AGTGTTGAACC	0.317	
+	12	1711	.K510fs|ESRP1_	NM_017697	NP_060167	Q6NXG1	ESRP1_HUMAN	RRM 3.		4	TGTCATAAAAAA	0.438	
-	38	5023	s.1_Frame_Shift_	NM_015902	NP_056986	O95071	UBR5_HUMAN			28	AATCATCTTCAG	0.353	
-	56	8985	ynt.2_Frame_Shift	NM_198123	NP_937756	Q7Z407	CSMD3_HUMAN	r (Potential).|Sushi 20.		63	TCTTTTAGAATTG	0.303	
+	3	780_781		NM_014943	NP_055758	Q9Y6X8	ZHX2_HUMAN			2	CAGTCCAAAAAA	0.49	
-	13	1698	D2_uc003yqi.3_R	NM_014109	NP_054828	Q6PL18	ATAD2_HUMAN			2	TTCGTCAAAAAA	0.413	
+	14	2027	uc003yqx.1_Intron	NM_001039112	NP_001034201	Q2WGJ9	FR1L6_HUMAN			11	CCTGGTAGGTG	0.488	

-	32	9448_9450	zae.1_In_Frame_D	NM_201380	NP_958782	Q15149	PLEC_HUMAN	Globular 2.		9	GATCTTGATGATC	0.616	
-	10	1683	nc.3_Frame_Shift_	NM_006521	NP_006512	P19532	TFE3_HUMAN			197	GCAGGTCCCCCC	0.647	
-	18	2564_2566	dsw.2_In_Frame_D	NM_015107	NP_055922	Q9UPP1	PHF8_HUMAN			3	GCGTTCTCCTCC	0.591	
+	1	595		NM_015686	NP_056501	O75949	F155B_HUMAN			2	TCCGCCAAAAAA	0.592	
+	16	2323	s|OGT_uc004eac.2	NM_181672	NP_858058	O15294	OGT1_HUMAN			5	CCACACTTTTTT	0.398	
-	3	364		NM_001006938	NP_001006939	Q6IPX3	TCAL6_HUMAN	Glu-rich.		1	CCCTGCTTTTCCT	0.418	
+	3	1003_1004	msr.1_Frame_Shif	NM_020769	NP_065820	Q8NET4	RGAG1_HUMAN			4	CCTCTGGAGAGA	0.5	
+	3	421	euc.2_Frame_Shi	NM_006603	NP_006594	Q8N3U4	STAG2_HUMAN			5	GATTTTGAAGATA	0.308	
+	15	8000	nsb.1_Frame_Shift	NM_153834	NP_722576	Q8IZF6	GP112_HUMAN	cellular (Potential).		12	GCTGCGGGGGG	0.532	
+	4	1210_1212	EC1_uc010nsl.1_I	NM_005462	NP_005453	O60732	MAGC1_HUMAN			4	GTGAGCTCCTCC	0.483	660605;rs141900922
+	7	512_514	j.1_In_Frame_Del_	NM_007150	NP_009081	O15231	ZN185_HUMAN	Poly-Glu.		3	GACACCgaggagg	0.522	
-	23	3222	P1038fs|L1CAM_u	NM_000425	NP_000416	P32004	L1CAM_HUMAN	III 5.|Extracellular (Potentia		9	CTCCTTGGGGAC	0.587	
-	14	3808_3809		NM_000132	NP_000123	P00451	FA8_HUMAN	B.		11	CCTGAATTTTTT	0.327	
+	3	2072	omu.1_Frame_Shif	NM_006015	NP_006006	O14497	ARI1A_HUMAN	Poly-Gln.	NA	142	CCTCAGCAGCCA	0.637	
-	4	361_362	ogr.1_Frame_Shift_	NM_006912	NP_008843	Q92963	RIT1_HUMAN		NA	1	TGATCTTATAAGC	0.371	
+	5	534_535	1_5'Flank|MBD6_u	NM_052897	NP_443129	Q96DN6	MBD6_HUMAN		NA	4	ACCACCGGCGGA	0.579	
-	38	5554	taq.2_Frame_Shif	NM_025114	NP_079390	O15078	CE290_HUMAN	Potential.	NA	7	TTCTCCTTCAAGC	0.313	
-	5	538_539	1wmy.1_5'UTR|IPC	NM_024658	NP_078934	Q8TEX9	IPO4_HUMAN		NA	1	GGTACCTCTCTC	0.559	
-	4	1894_1896	1ygb.2_In_Frame_	NM_138576	NP_612808	Q9C0K0	BC11B_HUMAN	Glu-rich.	NA	10	GTAGCAGctcctcct	0.517	
+	15	1583	0bnd.2_Frame_Sh	NM_002605	NP_002596	O60658	PDE8A_HUMAN		NA	4	TTTCAACAAAAAC	0.303	
+	13	1393	vv.1_Frame_Shift_	NM_000548	NP_000539	P49815	TSC2_HUMAN		NA	10	CTCCTATAGAGCG	0.602	rs45493394
+	5	712	0vnq.1_Splice_Site	NM_198390	NP_938204	Q8IY22	CMIP_HUMAN		NA	0	CCTTTAGAACAC	0.446	
+	10	1094	_Shift_Del_p.L266f	NM_001130021	NP_001123493	Q93050	VPP1_HUMAN	lasmic (Pote	NA	1	GAACCTGTGCAA	0.527	
+	3	1547	C1_uc002kae.2_5	NM_001080519	NP_001073988	Q9P281	BAHC1_HUMAN		NA	1	GGAAGGCCCCCC	0.652	
-	4	1505	2B_uc010dsw.1_I	NM_198532	NP_940934	Q6ZS72	CS035_HUMAN		NA	1	CAGCGCCAGGG	0.682	
-	12	1196_1197	p.G413fs|STAP2_u	NM_001013841	NP_001013863	Q9UGK3	STAP2_HUMAN		NA	1	TCCTGCCCAAGC	0.337	
-	11	1313_1315		NM_001080421	NP_001073890	Q9UPW8	UN13A_HUMAN	-rich.|Poten	NA	3	TCAGGCAcctcctcc	0.433	
+	11	1633_1634	p.T424fs|KIRREL2	NM_199180	NP_954649	Q6UWL6	KIRR2_HUMAN	5.|Extracellu	NA	3	GGGGACCCAGGA	0.668	
+	18	5228		NM_015073	NP_055888	O60292	SI1L3_HUMAN		NA	2	GCTCTTCACCAG	0.756	
-	8	1171_1172	02utu.2_Frame_Sh	NM_012086	NP_036218	Q9Y5Q9	TF3C3_HUMAN	TPR 6.	NA	7	CTGAAGTTTTTT	0.337	
-	23	3555	E513fs|CADPS_uc	NM_003716	NP_003707	Q9ULU8	CAPS1_HUMAN	nteraction wi	NA	3	CAGATCTTCTGAG	0.488	
+	4	1374_1375		NM_021620	NP_067633	Q9H4Q3	PRD13_HUMAN		NA	0	TGGGGACccgccg	0.505	
-	4	773_774	3H_uc010mfk.1_5	NM_198488	NP_940890	Q6ZRV2	FA83H_HUMAN		NA	3	CAGTCCACCAGC	0.658	
+	14	1705	C22_uc004dnc.1_	NM_014008	NP_054727	O60826	CCD22_HUMAN	Potential.	NA	1	TTGTCTGATACGA	0.567	
+	8	892_893	afx.2_Frame_Shif	NM_031921	NP_114127	Q5T9A4	ATD3B_HUMAN			0	CTCAGCCAAGAA	0.683	
+	6	1188	uc001gof.1_Intron	NM_033343	NP_203129	Q969G2	LHX4_HUMAN			1	TGCCATCCCACG	0.562	
+	3	638	GBD2_uc009xhd.2	NM_170725	NP_733843	Q6P3X8	PGBD2_HUMAN			1	ATCGTTATGCTTG	0.378	
+	15	2195	AT_uc001jhy.1_Fr	NM_020549	NP_065574	P28329	CLAT_HUMAN			3	GTGCCTGCTACAA	0.522	
+	23	3324	_p.P794fs|ZMIZ1_	NM_020338	NP_065071	Q9ULJ6	ZMIZ1_HUMAN	Pro-rich.		4	ACGGGCCCCCC	0.597	
+	2	1449	kvi.1_5'Flank|FBXL	NM_024326	NP_077302	Q9H469	FXL15_HUMAN	F-box.		1	CGGCTGCAGCGC	0.711	
-	2	955_957	G2_uc001mak.1_Ir	NM_017481	NP_059509	Q9H347	UBQL3_HUMAN			3	TGGCTGGTGGT	0.537	rs2234451
-	7	1231_1232	.1_Intron|AMBRA1	NM_017749	NP_060219	Q9C0C7	AMRA1_HUMAN			3	GCTGTCGGAGCC	0.629	
-	27	3487	ndj.1_Frame_Shif	NM_001008938	NP_001008938	Q14008	CKAP5_HUMAN			2	TTGGCCTTTTTTC	0.323	
+	4	544		NM_004585	NP_004576	Q9UL19	TIG3_HUMAN			1	GATACCAAAAAAA	0.537	
+	5	419	nyx.2_Frame_Shif	NM_003377	NP_003368	P49765	VEGFB_HUMAN			0	GACCTAAAAAAA	0.388	
-	30	5914	_p.K42fs|ODZ4_uc	NM_001098816	NP_001092286	Q6N022	TEN4_HUMAN	cellular (Potential).		4	CTGCTCTTTGCGG	0.672	
-	1	420_422		NM_007037	NP_008968	Q9UP79	ATS8_HUMAN			1	gccagcggcagcagca	0.374	548872;rs11222097

-	11	1272_1273	052_uc001qiu.1_F	NM_134424	NP_602296	P43351	RAD52_HUMAN		1	GAGGTCCCAAGA	0.465	
-	3	297	tcr.1_Frame_Shift	NM_022459	NP_071904	Q9C0E2	XPO4_HUMAN		3	GCTACCTTTTTC	0.433	
+	1	31_33	RG2_uc010tll.1_In	NM_138331	NP_612204	Q8TDE3	RNAS8_HUMAN		0	CCCCCTGCTGC	0.557	
-	11	2887	IH5_uc001xfy.2_3'	NM_139318	NP_647479	Q8NCM2	KCNH5_HUMAN	nbly) (By similarity).|Cytopla	9	GTACGCTTTTTC	0.473	
-	36	6843	FYVE26_uc001xkl	NM_015346	NP_056161	Q68DK2	ZFY26_HUMAN		11	TACTTTCCCCAG	0.433	
-	21	6718	auf.1_Frame_Shift	NM_004239	NP_004230	Q15643	TRIPB_HUMAN		13	TGCTTTAAAAGG	0.423	
-	4	1894_1896	1ygb.2_In_Frame_	NM_138576	NP_612808	Q9C0K0	BC11B_HUMAN	Glu-rich.	10	GTAGCAGctcctct	0.517	
+	11	1696_1698	1znc.2_In_Frame_	NM_181642	NP_857593	O43278	SPIT1_HUMAN		1	CGGACACCACC	0.586	
-	65	8481_8482	N1_uc010beo.1_R	NM_000138	NP_000129	P35555	FBN1_HUMAN		3	ATCTTACACTCG	0.51	
-	14	1841_1842	p.M465fs|SCAPEF	NM_020843	NP_065894	Q9BY12	SCAPE_HUMAN	Glu-rich.	3	TTCTTCCATCAT	0.371	
+	19	2026	POLR3E_uc002dk	NM_018119	NP_060589	Q9NVU0	RPC5_HUMAN		2	AGTTTCCCCCC	0.562	
+	4	271	Shift_Del_p.R87fs|	NM_005796	NP_005787	P61970	NTF2_HUMAN		0	CTTGTAGAGCCT	0.554	rs111772962
-	7	934	ggo.1_Frame_Shif	NM_020360	NP_065093	Q9NRY6	PLS3_HUMAN	smic (By similarity).	0	CCAGGCCCCCC	0.612	
-	14	1854	itf.2_Frame_Shift_	NM_001130528	NP_001124000	O60271	JIP4_HUMAN		5	TTGACCTTTTTTT	0.323	
-	6	1372_1373	xmk.1_Frame_Shi	NM_030824	NP_110451	Q9H7R0	ZN442_HUMAN	2H2-type 3.	4	TCATGTCTTAGA	0.401	
+	1	303		NM_002446	NP_002437	Q02779	M3K10_HUMAN	Poly-Glu.	6	GAGGAGGGGGC	0.667	
-	5	1643	2_5'Flank|ZNF577	NM_023074	NP_075562	Q9BS31	ZN649_HUMAN		3	TGAATCCCCCC	0.448	
-	11	2354	_Shift_Del_p.P507	NM_015025	NP_055840	Q9UL68	MYT1L_HUMAN	2HC-type 2.	6	CACCCGGGGGT	0.502	rs114191331
-	3	1031		NM_012344	NP_036476	O95665	NTR2_HUMAN	ellular (Potential).	0	CAGTACATGAG	0.597	
-	5	632	.1_Intron|MRPL30	NM_138798	NP_620153	Q8WV92	MITD1_HUMAN		2	ATTTCTCGGTCAT	0.289	rs141265262
-	13	2241	zlm.1_Frame_Shif	NM_004438	NP_004429	P54764	EPHA4_HUMAN	e.|Cytoplasmic (Potential).	12	TTCATCCCAGA	0.453	
+	1	776_805	n_Frame_Del_p.V	NM_053277	NP_444507	Q96NY7	CLIC6_HUMAN	- [VIM]-[DEQ]-A-[EAG]-[G	2	GGGGGTCCCG	0.761	358718;rs13049745;rs13048804
+	7	2100_2108	atq.1_In_Frame_D	NM_001039141	NP_001034230	Q9H2D6	TARA_HUMAN		1	GCCTCCAGAAC	0.579	
-	27	3223	t.2_RNA|CLASP2_	NM_015097	NP_055912	B2RTR1	B2RTR1_HUMAN		4	CACCCATTTTTT	0.343	
+	23	3432	_Shift_Del_p.S114	NM_007335	NP_031361	Q9Y238	DLEC1_HUMAN		9	GGGAGCCCCCA	0.552	
-	20	3118	dlm.2_Frame_Shif	NM_003716	NP_003707	Q9ULU8	CAPS1_HUMAN	ction with DRD2.	3	CATGCTCCACCA	0.448	
+	1	3808_3809		NM_175918	NP_787114	Q8N1N5	CRPAK_HUMAN	8	0	CTCACATGTGC	0.683	123539;rs79888804
+	4	416		NM_144725	NP_653326	Q6PF05	TT23L_HUMAN		1	ATTTTGGGGAC	0.453	
-	6	1240	ame_Shift_Del_p.F	NM_173488	NP_775759	Q86UG4	SO6A1_HUMAN	lasmic (Potential).	7	GCTGTCAAAAAA	0.299	
+	32	7837_7838	jcl.1_Frame_Shift_	NM_005509	NP_005500	Q9Y485	DMXL1_HUMAN		2	TATATCGCAAGT	0.441	
+	14	1795_1796		NM_018214	NP_060684	Q9BTT6	LRRC1_HUMAN	Potential.	1	GGACTGGACTCA	0.465	
+	4	1374_1375		NM_021620	NP_067633	Q9H4Q3	PRD13_HUMAN		0	TGGGGACccgcc	0.505	
-	7	1235_1236	edm.1_Frame_Shi	NM_000416	NP_000407	P15260	INGR1_HUMAN	lasmic (Potential).	1	AAGAACTCTCT	0.431	
+	6	808	10khi.2_Frame_Sh	NM_014721	NP_055536	O75167	PHAR2_HUMAN		2	TCATTCAAAAAA	0.398	
+	8	1473_1474	qvr.2_Frame_Shi	NM_018974	NP_061847	Q86WB7	UN93A_HUMAN		0	GGAGTCCAAGA	0.545	
+	13	1827_1828	p.F529fs|PHTF2_	NM_001127357	NP_001120829	Q8N3S3	PHTF2_HUMAN		1	GATTTTCTTTTTT	0.307	
+	2	1645	p.L520fs|PIK3CG_	NM_002649	NP_002640	P48736	PK3CG_HUMAN		38	TCTTCTGGACAA	0.537	
+	6	972	ce_Site_p.Q108_s	NM_014491	NP_055306	O15409	FOXP2_HUMAN		8	TGATACcagcagca	0.414	rs111544687
+	8	921	lar.1_Frame_Shift	NM_018091	NP_060561	Q9H9T3	ELP3_HUMAN		0	AGACACCAACA	0.463	
-	11	1327	xzp.2_Frame_Shi	NM_014393	NP_055208	Q9NUL3	STAU2_HUMAN	DRBM 4.	0	GCAGCATTTTTTT	0.328	
-	5	1330		NM_002546	NP_002537	O00300	TR11B_HUMAN	Death 2.	2	TCGCCATTTTTTA	0.458	
+	4	1521	hift_Del_p.D285fs	NM_181872	NP_870987	Q9Y5R5	DMRT2_HUMAN		0	ATTGTTGACACG	0.532	
+	9	7065	_p.C2167fs|ZNF46	NM_021224	NP_067047	Q96JM2	ZN462_HUMAN	2H2-type 24.	5	CTCTCTGCCTCT	0.532	
+	5	602	uc010ncd.1_RNA|C9orf173_uc011mev.1_Intron|C9orf1			Q8N7X2	CI173_HUMAN		1	GCCACACCCACC	0.682	
-	4	675		NM_000216	NP_000207	P23352	KALM_HUMAN	WAP.	4	AGTCTTGGGTAC	0.507	
-	7	878_879	NRNP40_uc010og	NM_004814	NP_004805	Q96DI7	SNR40_HUMAN		0	TTTCCTTGAAATA	0.391	
-	3	127	AD1_uc010ooa.1_	NM_001010978	NP_001010978	Q5T700	LRAD1_HUMAN		3	GCAGGCCCCGC	0.672	

+	2	248_249	sw.1_Frame_Shif	NM_003503	NP_003494	O00311	CDC7_HUMAN		5	CTCTTTAAAAAA	0.406	
+	31	8393_8394		NM_001408	NP_001399	Q9HCU4	CELR2_HUMAN	lasmic (Potential).	8	GTACTCCCAAGG	0.594	
+	9	905	1_splice|FAM40A	NM_033088	NP_149079	Q5VSL9	FA40A_HUMAN		4	TGATGCAGTGCA	0.564	
-	2	1361_1363	.2_Intron|RGL1_u	NM_203454	NP_982279	Q8WW27	ABEC4_HUMAN		0	TCCCTTTCTTCTT	0.419	rs141411396
-	38	5610	xgh.1_Frame_Shi	NM_018072	NP_060542	Q9H583	HEAT1_HUMAN		3	TGTAAGTTTTTTT	0.438	
-	14	1762	p.S486fs|FOLH1_	NM_004476	NP_004467	Q04609	FOLH1_HUMAN	.|Extracellular (Probable).	3	AAGGACTTTTTT	0.353	
+	6	694_695		NM_014224	NP_055039	P00790	PEPA_HUMAN		1	ATGACAAGAGTG	0.505	
-	2	362_364	_p.P33del|PDE2A	NM_002599	NP_002590	O00408	PDE2A_HUMAN		4	GGCTGCGGCGG	0.724	
-	39	11819_11827		NM_003482	NP_003473	O14686	MLL2_HUMAN	ential.|Gln-rich.	41	ctgctgttgttgaagctgc	0.014	rs112586166
+	2	226	el_p.S9fs|ACAD10	NM_025247	NP_079523	Q6JQN1	ACD10_HUMAN		2	CCAGTCCCCCC	0.617	
+	3	344_345	_p.S78fs|RFC3_u	NM_002915	NP_002906	P40938	RFC3_HUMAN		0	CCATCTAAAAAA	0.267	
+	20	3443_3444	xdq.2_Frame_Shif	NM_002892	NP_002883	P29374	ARI4A_HUMAN		6	TACAAGAGAGA	0.381	
-	1	985	1_Intron|TMEM30	NM_001017970	NP_001017970	Q3MIR4	CC50B_HUMAN		0	ACACTGGGCCC	0.697	
-	18	2031		NM_178034	NP_828848	Q86XP0	PA24D_HUMAN	PLA2c.	2	GTCCACCAGGC	0.642	
-	7	1499_1501	il.1_In_Frame_De	NM_005078	NP_005069	Q04726	TLE3_HUMAN	Gln-rich.	2	TGGAGCTGCTG	0.665	
-	1	293_295	_Del_p.15_16GG	NM_002094	NP_002085	P15170	ERF3A_HUMAN		3	ctgctcccgccgccgc	0.34	
+	3	715	1_uc002ebo.2_5'	NM_001008274	NP_001008275	Q6ZMU5	TRI72_HUMAN		0	TGGAGGTGAGG	0.599	
+	10	815_816	fof.2_Frame_Shift	NM_052988	NP_443714	Q15131	CDK10_HUMAN	rotein kinase.	1	GCACGCCCAGT	0.47	
-	9	1040_1041	cjf.2_Intron|PRD	NM_001098173	NP_001091643	Q9NQW5	PRDM7_HUMAN	SET.	1	TCTATAGAAGAT	0.535	
-	4	502_503	fs|TP53_uc010cni	NM_001126112	NP_001119584	P04637	P53_HUMAN	y similarity).W91fs*13(1)|p	22245	CCCTGGTAGGT	0.639	
-	2	260	_p.G55fs|MYH10_	NM_005964	NP_005955	P35580	MYH10_HUMAN	osin head-like.	2	TCATCTCCCCGT	0.443	
-	1	174	10_uc010cqw.1_	NM_007202	NP_009133	O43572	AKA10_HUMAN		1	GGTGCGGGGGG	0.746	
+	2	177	15_uc002hed.1_5	NM_138349	NP_612358	Q8NBR0	P5I13_HUMAN	ellular (Potential).	0	CTCCGCAGGTA	0.662	
-	2	588		NM_020805	NP_065856	Q9P2G3	KLH14_HUMAN	BTB.	1	CGAGAGGGGGG	0.527	
-	8	855		NM_005570	NP_005561	P49257	LMAN1_HUMAN		1	TGGGCTTTTTT	0.294	
+	7	897	10xeo.1_Frame_S	NM_080474	NP_536722	Q96P63	SPB12_HUMAN		0	TCCTTCCCCCG	0.448	
+	1	120_121	ebv.2_Frame_Shi	NM_015321	NP_056136	Q6UUV9	CRTC1_HUMAN		519	ATTCAGCGAGA	0.545	
-	6	472	_p.P16fs|C19orf47	NM_178830	NP_849152	Q8N9M1	CS047_HUMAN		2	CGCCTGGGGGG	0.612	
-	13	1476	rcp.1_Frame_Shif	NM_001142286	NP_001135758	Q96SB8	SMC6_HUMAN	Potential.	6	CTACCTTTTTTT	0.294	
+	17	0335_1033	sjg.2_In_Frame_D	NM_015120	NP_055935	Q8TCU4	ALMS1_HUMAN		9	CCAGTGCTGCT	0.414	
-	1	263_265	c002std.1_5'Flan	NM_004836	NP_004827	Q9NZJ5	E2AK3_HUMAN		3	AGCCCcagcagca	0.32	rs72416210
+	8	7114_7116	rame_Del_p.P219	NM_152381	NP_689594	A4UGR9	XIRP2_HUMAN	Pro-rich.	14	GCCGCCTCCTC	0.468	
+	9	1518	20A1_uc002uzy.3_	NM_177538	NP_803882	Q6UW02	CP20A_HUMAN		0	AAGTTCAAAAAA	0.348	
+	2	555_556	_p.M83fs|DSTN_u	NM_006870	NP_006861	P60981	DEST_HUMAN	ADF-H.	2	TTGATGTTTTTT	0.356	
+	2	1083_1085		NM_024893	NP_079169	Q9H7V2	SYNG1_HUMAN	ytoplasmic (Potential).	0	ATGTGGAGGAG	0.547	
+	1	216	GR_uc002yxz.2_	NM_007341	NP_031367	P55822	SH3BG_HUMAN		0	GTGTTGGGGGG	0.552	
+	35	4221	_Del_p.G1165fs|SL	NM_130444	NP_569711	P39060	COIA1_HUMAN	lical region 9 (COL9).	1	CCCGGCCCCCC	0.736	
+	39	5384	R1_uc011asu.1_I	NM_001099952	NP_001093422	Q14643	ITPR1_HUMAN	lasmic (Potential).	21	GACCCTGAGGG	0.413	
-	1	102	el_p.R3fs|NCKIPS	NM_016453	NP_057537	Q9NZQ3	SPN90_HUMAN	SH3.	0	GCGCGCGGTAC	0.741	
-	1	82	hsi.1_Frame_Shi	NM_144639	NP_653240	Q96N76	HUTU_HUMAN		1	TCTCTGGGAGG	0.682	
+	6	1112_1114	esi.3_In_Frame_	NM_012219	NP_036351	O14807	RASM_HUMAN	Poly-Lys.	4	AGCCAGAAGAA	0.522	
-	20	3897_3898		NM_001184	NP_001175	Q13535	ATR_HUMAN		20	ATTCTGGATGAT	0.287	
-	6	1009		NM_013363	NP_037495	Q9UKZ9	PCOC2_HUMAN		3	GGCAGTTTTTTT	0.383	
+	4	868_869		NM_207352	NP_997235	Q6ZWL3	CP4V2_HUMAN		0	AACTGCTTTTTT	0.322	
+	1	177_178		NM_001080478	NP_001073947	A6NHZ5	LR14B_HUMAN		1	GTGACGCGCG	0.703	
-	3	473_475	1_In_Frame_Del_	NM_016107	NP_057191	Q96KR1	ZFR_HUMAN	Ala-rich.	0	TGGGGGTGGTG	0.483	
-	1	479_480		NM_001085377	NP_001078846	P23508	CRCM_HUMAN		1	ctgccgctgccgccgc	0.391	

-	1	991_993	Frame_Del_p.E29	NM_020747	NP_065798	Q9ULD9	ZN608_HUMAN	Potential.		6	TGGCTCTCCTCC	0.522	
-	5	741		NM_005649	NP_005640	O60765	Z354A_HUMAN			3	TCTCTGGGAAG	0.358	
-	4	239	P1_uc003okw.3_Ir	NM_003322	NP_003313	O00294	TULP1_HUMAN			3	GGTCTGGGGAA	0.721	
-	16	1855	osb.3_Frame_Shift	NM_007214	NP_009145	Q9UGP8	SEC63_HUMAN	Cytoplasmic (Potential).		2	GGTTTCTTTTTTT	0.368	
+	5	1958	0kee.2_Frame_Shi	NM_001010892	NP_001010892	Q5TD94	RSH4A_HUMAN			0	AATATACCCCCCT	0.378	
+	2	681		NM_001128636	NP_001122108					0	CTACATCGAGGA	0.637	
-	5	1204	v.2_Frame_Shift_D	NM_000466	NP_000457	O43933	PEX1_HUMAN			2	ACCTAATTTTTTT	0.353	
+	7	1118_1119	vuy.2_Frame_Shift	NM_016019	NP_057103	Q9Y383	LC7L2_HUMAN	Arg/Ser-rich.		0	AGAGAAGAGAGA	0.391	
-	38	8609	p.K1858fs|MLL3_u	NM_170606	NP_733751	Q8NEZ4	MLL3_HUMAN		p.K2797fs*26(1	63	TGTTCCTTTTTTT	0.348	
+	3	299_300	.72fs|ADAM28_uc	NM_014265	NP_055080	Q9UKQ2	ADA28_HUMAN			5	TATTTGAAAAAA	0.332	
-	3	534_536	nf.2_Intron|TP53IN	NM_033285	NP_150601	Q96A56	T53I1_HUMAN	Glu-rich.		0	CCTCCTCTTCTT	0.458	
-	2	136	26fs|CPSF3L_uc0	NM_017871	NP_060341	Q5TA45	INT11_HUMAN			0	ATTCTTGCCCGC	0.652	
-	5	596_597	chg.2_Frame_Shif	NM_014947	NP_055762	Q9UPW0	FOXJ3_HUMAN	Fork-head.		2	TTTTTGGGTGAG	0.381	
-	22	3517	olg.1_Frame_Shift	NM_003738	NP_003729	Q9Y6C5	PTC2_HUMAN	lasmic (Potential).		18	AGGCAGGGGGG	0.657	
+	29	4304	l.1_Frame_Shift_D	NM_000642	NP_000633	P35573	GDE_HUMAN	-glucanotransferase.		3	TTATCCAAAAAA	0.323	
-	3	1569_1570		NM_001008536	NP_001008536	Q5QJ38	TCHL1_HUMAN			2	GTGCTAAATCTT	0.5	
-	3	2327_2328		NM_001122965	NP_001116437	Q6XPR3	RPTN_HUMAN	Gln-rich.		0	TCTCTGATGGCT	0.52	
-	8	1048	ne_Shift_Del_p.R2	NM_025191	NP_079467	Q9BZQ6	EDEM3_HUMAN			1	GCTGTCTTTTTTC	0.313	
+	7	1633_1634	_Ins_p.435_436ins	NM_005807	NP_005798	Q92954	PRG4_HUMAN	K-X-P-X-P-T-T-X.|24; appro		1	CCACCAAGTCTG	0.639	
+	22	2922_2924		NM_018085	NP_060555	Q96P70	IPO9_HUMAN			2	gaggaagaggaggag	0.33	
+	2	208	_p.V29fs|TBCE_uc	NM_003193	NP_003184	Q15813	TBCE_HUMAN	CAP-Gly.		0	GTGTTGTCCCT	0.308	
-	22	3166_3167	9xgh.1_Frame_Sh	NM_018072	NP_060542	Q9H583	HEAT1_HUMAN			3	TTTGCTATATAAC	0.347	
+	20	5628	_p.A1148fs|KIAA1	NM_019590	NP_062536	Q5T5P2	SKT_HUMAN			7	CGGGGCCCCAC	0.612	
+	1	296_298		NM_199461	NP_955631	Q8WY41	NANO1_HUMAN			0	GGAACGGCGGC	0.562	
-	7	1352	33fs|APBB1_uc010	NM_001164	NP_001155	O00213	APBB1_HUMAN	PID 1.		2	TTACTTCCCCCCA	0.582	
-	4	1327	_Intron|KBTBD4_u	NM_016506	NP_057590	Q9NVX7	KBTB4_HUMAN	Kelch 4.		2	TCTCCTCCCCCC	0.517	
-	15	2895_2897	229PP>P|FNBP4_	NM_015308	NP_056123	Q8N3X1	FNBP4_HUMAN	Pro-rich.		1	ggtggtggaggaggag	0.32	
-	1	325_330	j.2_5'UTR|FNBP4_	NM_015308	NP_056123	Q8N3X1	FNBP4_HUMAN			1	CGCGGTGGTGGT	0.748	rs59413596
-	3	257_259		NM_006248	NP_006239					0	TCCTGGAGGAG	0.601	
-	20	2758	p.W621fs|GRIP1_u	NM_021150	NP_066973	Q9Y3R0	GRIP1_HUMAN			2	TTGAGACCAGAA	0.468	
-	2	1245_1246	SP6_uc001taz.2_Ir	NM_001946	NP_001937	Q16828	DUS6_HUMAN	-protein phosphatase.		0	TTTGCTTGTATTT	0.465	
+	5	1001_1003	1vhk.1_In_Frame_	NM_006418	NP_006409	Q6UX06	OLFM4_HUMAN	actomedin-like.		1	AGTTTACAACAA	0.433	
-	23	3282	f.1_RNA|TEP1_uc	NM_007110	NP_009041	Q99973	TEP1_HUMAN			5	GCCACACCCCCC	0.587	
+	1	238_239		NM_001001912	NP_001001912	Q8NGC2	OR4E2_HUMAN	cellular (Potential).		4	TGCCTAAGATGT	0.441	
-	4	507	_p.Q63fs|MAP4K5	NM_006575	NP_006566	Q9Y4K4	M4K5_HUMAN	rotein kinase.		1	CTTGTTGAATCAA	0.289	
-	8	2219	two.1_Frame_Shif	NM_001002860	NP_001002860	Q9P203	BTBD7_HUMAN			1	GCTGCTGATCTG	0.438	
+	9	1762_1764	n_Frame_Del_p.Q2	NM_006291	NP_006282	Q03169	TNAP2_HUMAN			1	GCCGAGCAGCA	0.626	
+	8	3011_3013	.Q981del|MGA_uc	NM_001080541	NP_001074010	Q8IWI9	MGAP_HUMAN	Gln-rich.		12	GGCACAGCAGC	0.458	
+	3	438_439	2bdz.2_Frame_Sh	NM_000745	NP_000736	P30532	ACHA5_HUMAN	cellular (Potential).		3	CAGTTAATGACA	0.267	
+	6	1090	p.Q172fs|CHD2_u	NM_001271	NP_001262	O14647	CHD2_HUMAN			2	CAGAACAAAAAA	0.418	
-	8	1385_1387	ARF1_uc002fta.1_I	NM_003693	NP_003684	Q14162	SREC_HUMAN	lasmic (Potential).		1	GGCCCAGCAGC	0.67	
-	16	2618	vsf.1_Frame_Shift	NM_014389	NP_055204	Q8IZL8	PELP1_HUMAN	Pro-rich.		2	TGGCAGGGGGG	0.617	
+	10	1188	yss.1_Frame_Shift_	NM_053013	NP_443739	P13929	ENOB_HUMAN			1	TGGCTGGGGGG	0.567	
-	4	502_503	fs|TP53_uc010cni	NM_001126112	NP_001119584	P04637	P53_HUMAN	y similarity).W91fs*13(1)|p.		22245	CCCTGGTAGGTT	0.639	
+	11	2629_2631	02gix.2_In_Frame_	NM_001080424	NP_001073893	O15054	KDM6B_HUMAN	o-rich.|Thr-rich.		2	CGCCGTcaccacca	0.369	
-	1	42_44		NM_018143	NP_060613	Q9NVR0	KLH11_HUMAN			0	Agccgcggccgccgcc	0.537	
-	9	1623_1625		NM_133373	NP_588614	Q8N3E9	PLCD3_HUMAN			3	cctcgtcatcctcctcctc	0.527	

-	9	1430		NM_032043	NP_114432	Q9BX63	FANCJ_HUMAN	ase ATP-binding.		1	TTCCTTATATTAT	0.398	
+	5	423_426	wpe.1_Frame_Shi	NM_025185	NP_079461	Q9HCD6	TANC2_HUMAN			2	CACTCTGACTAG	0.466	
+	9	1449	Flank|ACE_uc010	NM_000789	NP_000780	P12821	ACE_HUMAN	Potential).|Peptidase M2 1.		4	GCGCTGGGGG	0.532	
-	21	3612	_Shift_Del_p.P415fs|DNAH17_uc002jvs.2_RNA							9	AGGTTGGGGGG	0.582	
-	16	2743_2744	Shift_Ins_p.Q418f	NM_025090	NP_079366	Q9P275	UBP36_HUMAN			5	GGGCTCTGGG	0.634	
+	5	489		NM_032482	NP_115871	Q8TEK3	DOT1L_HUMAN			4	GAGATCAAGAT	0.622	
+	14	2041		NM_000453	NP_000444	Q92911	SC5A5_HUMAN	lasmic (Potential).		4	GTGGTGGGACC	0.597	
+	2	648_650	egn.1_In_Frame_	NM_003407	NP_003398	P26651	TTP_HUMAN	P-P-P-P-G.		1	ACCTCACCACC	0.685	
-	5	1989_1991	2omv.2_In_Frame	NM_001005851	NP_001005851	Q9Y6R6	Z780B_HUMAN	2H2-type 18.		2	TTACATTTAAATG	0.414	
+	7	900	_uc002pqp.2_5'U	NM_024682	NP_078958	Q9HA65	TBC17_HUMAN			0	ACCTTCCCCCG	0.537	
-	3	425	18_splice|PTPRH_	NM_002842	NP_002833	Q9HD43	PTPRH_HUMAN			4	CTCTTACCTGT	0.473	
+	12	2844		NM_001011552	NP_001011552	Q6AI14	SL9A4_HUMAN	lasmic (Potential).		3	TGCTCCAAAAAA	0.473	
-	11	1630	zgu.1_Frame_Shi	NM_012086	NP_036218	Q9Y5Q9	TF3C3_HUMAN	TPR 9.		7	TGGTTCCAGAG	0.473	
-	1	157_158		NM_003284	NP_003275	P09430	STP1_HUMAN			0	GTCATCGCCCC	0.55	
+	2	889_890	Shift_Del_p.D180f	NM_022720	NP_073557	Q8WYQ5	DGCR8_HUMAN	nd retention.|Necessary for		0	TGCTGATAAGAA	0.515	
-	4	542	l_p.G31fs|TBC1D	NM_031937	NP_114143	Q9BXI6	TB10A_HUMAN	ab-GAP TBC.		1	CGTGGCCCCCC	0.607	
-	11	1334		NM_173050	NP_766638	Q8IWY4	SCUB1_HUMAN			5	GGCCCGGGGG	0.647	
+	6	1060	p.C217fs|ABHD6_	NM_020676	NP_065727	Q9BV23	ABHD6_HUMAN	lasmic (Potential).		2	AGCTCTGCTCCT	0.577	
-	5	1253_1254		NM_000097	NP_000088	P36551	HEM6_HUMAN			0	CTTCTGAGCTGC	0.495	
-	29	3946		NM_014981	NP_055796	Q9Y2K3	MYH15_HUMAN			7	TTACTTACCACTC	0.468	
+	6	1112_1114	esi.3_In_Frame_	NM_012219	NP_036351	O14807	RASM_HUMAN	Poly-Lys.		4	AGCCAGAAGAA	0.522	
+	1	355_357		NM_000297	NP_000288	Q13563	PKD2_HUMAN	ytoplasmic (Potential).		1	AGGCCgaggagg	0.498	
-	1	372_374	'Flank|CXXC4_uc	NM_025212	NP_079488	Q9H2H0	CXXC4_HUMAN	Poly-Ser.		1	GGACGAGGAGG	0.606	rs146939312
-	17	2126	.2_Frame_Shift_D	NM_144643	NP_653244	Q96NL6	SCLT1_HUMAN	Potential.		5	TTTGGCTTTTTTT	0.353	
+	4	576	Shift_Del_p.P167f	NM_003687	NP_003678	P50479	PDLI4_HUMAN			2	CTCCACCCCCC	0.592	
+	4	1418_1419	y.1_RNA|TXNDC1	NM_024715	NP_078991	Q96J42	TXD15_HUMAN	(Potential).|Thioredoxin.		2	GCCTTTCTACCA	0.351	
+	1	404	c003lhh.1_Intron|	NM_018909	NP_061732	Q9UN73	PCDA6_HUMAN	|Extracellular (Potential).		2	GGACATTAACG	0.587	
+	5	1152	_uc011dmz.1_Fra	NM_020442	NP_065175	Q5ST30	SYVM_HUMAN			4	TGCGTGGGGAT	0.473	
-	23	1745	p.G102fs|COL9A1	NM_001851	NP_001842	P20849	CO9A1_HUMAN	lical region (COL2).		4	GGAGACCAGGA	0.428	
-	85	14337		NM_014611	NP_055426	Q9NU22	MDN1_HUMAN			10	AAGCTCCCCAT	0.358	
+	6	690	N1_uc003sjf.2_F	NM_001130965	NP_001124437	O94901	SUN1_HUMAN	Nuclear.		0	CGCGGCCCCCG	0.557	
-	1	616_618	1_uc010lqq.1_5'F	NM_005515	NP_005506	P50219	MNX1_HUMAN	Poly-Gly.		0	gcccgtgccgccgcc	0.537	
-	3	534_536	f.2_Intron|TP53IN	NM_033285	NP_150601	Q96A56	T53I1_HUMAN	Glu-rich.		0	CTCCTCTTCTT	0.458	
+	7	921_923	zay.2_In_Frame_	NM_001916	NP_001907	P08574	CY1_HUMAN	rs to the membrane; (Pote		0	ATGTTGATGAT	0.581	
-	5	955	p.P227fs|ELAVL2_	NM_004432	NP_004423	Q12926	ELAV2_HUMAN			3	GTCCTGGATAC	0.478	
-	7	2587	IGO_uc003zwf.2_	NM_032634	NP_116023	Q8TEQ8	PIGO_HUMAN			3	GAGACGGGGGG	0.662	rs148341577
+	20	2842_2844	44_uc010mwo.1_	NM_001161808	NP_001155280	Q7Z7M1	GP144_HUMAN	lasmic (Potential).		0	TCTTTCTGCCCC	0.645	
-	2	1154	PS1_uc011mac.1_	NM_012098	NP_036230	Q9UKU9	ANGL2_HUMAN			0	GCAGCGGGGG	0.637	
-	2	826_828	rf69_uc004cgy.2_	NM_152833	NP_690046					0	GGCCCAGCAGC	0.685	
+	12	1735_1736	.G228fs|GYG2_u	NM_003918	NP_003909	O15488	GLYG2_HUMAN			2	CATGGGGAAGG	0.564	
+	2	113_114	_p.L36fs|TARS2_	NM_025150	NP_079426	Q9BW92	SYTM_HUMAN		NA	1	AGCGGCTTGGC	0.51	
+	8	2096_2097	glg.2_Frame_Shif	NM_021165	NP_066988	Q9C0B6	FAM5B_HUMAN		NA	6	TGGGGGCAGCC	0.564	394323;rs150183035
+	5	471_473	_p.L92del|TSPAN4	NM_003271	NP_003262	O14817	TSN4_HUMAN	ical; (Potent	NA	1	CTTCCTGCTGC	0.65	rs61867552
+	3	771	N10_uc010did.1_	NM_031945	NP_114151	Q9H1Z9	TSN10_HUMAN		NA	1	ACTTTAACTAAC	0.637	rs137956393
+	2	475_499	td.2_Frame_Shift_	NM_001130072	NP_001123544	Q9Y6I3	EPN1_HUMAN	ENTH.	NA	0	CCTACAACGTT	0.569	
-	2	300	.2_Frame_Shift_D	NM_006698	NP_006689	P62952	BLCAP_HUMAN	ical; (Potent	NA	0	GAGCAGGTAGA	0.557	
-	4	298_301	_5'Flank|PHF7_u	NM_004656	NP_004647	Q92560	BAP1_HUMAN		NA	65	TAGAGACCTTTC	0.51	

+	3	618	t_Del_p.T206fs|HL	NM_002116	NP_002107	P30443	1A01_HUMAN	ar (Potential	NA	2	CGCACGGGTAC	0.637	rs115073453
+	2	676_705	_In_Frame_Del_p.	NM_153362	NP_699193	Q8N3Z0	PRS35_HUMAN	Peptidase S1	NA	1	AAAGGACTATGT	0.47	739716;rs151268050
+	39	7196_7230	ZAN_uc010lhh.2_F	NM_003386	NP_003377	Q9Y493	ZAN_HUMAN	Extracellular	NA	11	CGCTTGCAAGGC	0.506	029369;rs112538235;rs59541653
-	4	396_398	_In_Frame_Del_p.	NM_001042663	NP_001036128	O94827	PKHG5_HUMAN	Poly-Glu.		1	GAGCTCTCCTCC	0.631	
+	20	4967	1aoj.2_Frame_Shif	NM_015215	NP_056030	Q9Y6Y1	CMTA1_HUMAN	IQ 2.		9	ATGAACAAAAAAA	0.473	
+	8	5315	.2_Intron|PRDM2_	NM_012231	NP_036363	Q13029	PRDM2_HUMAN			1	CCTCCCAAAAAAA	0.463	rs141416335
-	7	901_902	1_Intron|MST1P9_	NR_002729						0	CGCCCGCCCCCC	0.658	
-	7	811_812	1_Intron|MST1P9_	NR_002729						0	GGTACGCCGCGC	0.649	
+	12	2906_2908	9vqi.1_In_Frame_	NM_001083621	NP_001077090	Q9NUA8	ZBT40_HUMAN			1	CCCCCAAGAAGA	0.517	
+	16	4351_4353	v.1_In_Frame_Del	NM_006015	NP_006006	O14497	ARI1A_HUMAN	Gln-rich.	334_R1335ins	142	CCCCCCgcagcag	0.512	
-	6	1559_1561	S4_uc010ofy.1_3'	NM_005626	NP_005617	Q08170	SRSF4_HUMAN	r-rich (RS domain).		0	TCTTCCTTCTTC	0.325	rs138237342
+	1	136_137		NM_001008740	NP_001008740	Q7Z6W1	TMCO2_HUMAN			1	TAGAGTCTCTCT	0.406	
+	2	155_156	n|CCDC30_uc010c	NM_001080850	NP_001074319	Q5VVM6	CCD30_HUMAN			0	TCAAAAGAGAGA	0.356	
-	4	577	cmv.1_Frame_Shif	NM_020365	NP_065098	Q9NR50	EI2BG_HUMAN			1	ACCTGCTTTTTTT	0.318	
-	6	1430_1431	s.3_Frame_Shift_	NM_005897	NP_005888	Q9Y573	IPP_HUMAN	Kelch 2.		1	CCATAACACACA	0.317	
-	5	1172	s.3_Frame_Shift_	NM_005897	NP_005888	Q9Y573	IPP_HUMAN	Kelch 1.		1	AGCGACCCCCC	0.428	
-	4	444	_p.S134fs|LRRC41	NM_006369	NP_006360	Q15345	LRC41_HUMAN			4	CATGGGAAAAAA	0.483	
-	5	1096_1097	AGBL4_uc001crv.	NM_024603	NP_078879	Q7L4P6	BEND5_HUMAN	BEN.		1	ATCTTTCTTTTTT	0.46	
-	5	924_925	RIQ3_uc001dfz.3_	NM_001105659	NP_001099129	A6PVS8	LRIQ3_HUMAN			2	CTGCTGTTTTTTT	0.327	
+	23	2276_2278	1dge.1_In_Frame_	NM_015978	NP_057062	Q59H18	TNI3K_HUMAN	Poly-Ser.		10	CTCACCTTCTTCT	0.473	
-	3	1621_1622	CBL2_uc001dmr.2	NM_001162536	NP_001156008	Q96E39	RBMXL_HUMAN	Ser-rich.		0	TAAGATGGCGGG	0.475	
-	3	717	CCBL2_uc001dmr.	NM_001162536	NP_001156008	Q96E39	RBMXL_HUMAN			0	CAACCATTTTTTT	0.498	rs78548172
-	9	1232	Shift_Del_p.M408	NM_005665	NP_005656	O60447	EVI5_HUMAN	Interaction with alpha-tubul		2	TTTTCATTTTTTT	0.318	
+	9	1146_1147	.2_Intron|KIAA132	NM_020775	NP_065826	Q6UXG2	K1324_HUMAN	cellular (Potential).		5	TTTCTACACACA	0.49	
-	7	777	_p.K153fs|GSTM3_	NM_000849	NP_000840	P21266	GSTM3_HUMAN	ST C-terminal.		0	CCTACCTTTTCCC	0.438	
-	3	1756_1759		NM_001122965	NP_001116437	Q6XPR3	RPTN_HUMAN	Gln-rich.		0	GCCTTGTCTGTC	0.485	
-	27	9178_9179	|ASH1L_uc001fkt.	NM_018489	NP_060959	Q9NR48	ASH1L_HUMAN			11	CCTCTGTTTTTTT	0.52	
-	12	1570_1571	0907_uc009wrk.1_	NM_014949	NP_055764	Q7Z7F0	K0907_HUMAN			0	TGTCCCTCTCTC	0.396	
-	5	1175	MF1_uc010pjl.1_Ir	NM_003037	NP_003028	Q13291	SLAF1_HUMAN	(Potential).|Ig-like V-type.		2	TAAGGCTTTTTTT	0.433	
-	6	1404_1406	.V48del|PVRL4_u	NM_030916	NP_112178	Q96NY8	PVRL4_HUMAN	ical; (Potential).		2	ATGAGCACCACC	0.571	
+	17	2363_2365	J2F1_uc010plh.1_I	NM_002697	NP_002688	P14859	PO2F1_HUMAN			5	TGCGTCCACCAC	0.601	
+	8	1233_1234	9wxs.2_Frame_Sh	NM_000721	NP_000712	Q15878	CAC1E_HUMAN	lasmic (Potential).		6	GCCAAAGAGAGA	0.51	
-	2	1361_1363	.2_Intron|RGL1_u	NM_203454	NP_982279	Q8WW27	ABEC4_HUMAN			0	TCCCTTTCTTCTT	0.419	rs141411396
+	7	1724_1726	ne_Del_p.E466del|	NM_005807	NP_005798	Q92954	PRG4_HUMAN	epeats of K-X-P-X-P-T-T-X		1	ACCAAGGAGCC	0.635	
+	22	2922_2924		NM_018085	NP_060555	Q96P70	IPO9_HUMAN			2	gaggaagaggaggag	0.33	
-	24	2573_2575		NM_014698	NP_055513	O94886	TM63A_HUMAN			2	AGGTCTGCTGCT	0.626	
-	32	4715_4717	Del_p.1437_1438F	NM_033056	NP_149045	Q96QU1	PCD15_HUMAN	Cytoplasmic (Potential).		13	Tggcggaggcggcgg	0.438	rs12246234
-	37	12084_1208	K3_uc010qih.1_In	NM_020987	NP_066267	Q12955	ANK3_HUMAN	Thr-rich.		19	ggtggcagtggtggtgg	0.32	
+	4	743	c010qnb.1_Intron|	NM_000043	NP_000034	P25445	TNR6_HUMAN	.|Extracellular (Potential).		2	CCAAACTTTTTTT	0.368	
-	2	431	0qot.1_Frame_Shi	NM_020123	NP_064508	Q9HD45	TM9S3_HUMAN			0	TGATACTTTTTTT	0.363	
+	1	753_754	y.2_Intron|DHDPS	NM_001009997	NP_001009997	Q5T681	CJ062_HUMAN	His-rich.		0	GCCAATCACACA	0.545	
+	1	735_736		NM_001127389	NP_001120861	F5GZ66	F5GZ66_HUMAN			0	GGGCCAGGCAC	0.708	rs138894859
+	1	758		NM_001127389	NP_001120861	F5GZ66	F5GZ66_HUMAN			0	TGGCAGGGCGC	0.736	
+	5	471_473	_p.L92del|TSPAN4	NM_003271	NP_003262	O14817	TSN4_HUMAN	ical; (Potential).		1	CTTCCTGCTGCT	0.65	rs61867552
+	1	310_312		NM_178168	NP_835462	Q9H207	O10A5_HUMAN	Name=3; (Potential).		3	TGTATTTCTTCTT	0.517	
+	4	544		NM_004585	NP_004576	Q9UL19	TIG3_HUMAN			1	GATACCAAAAAAA	0.537	
+	5	419	nyx.2_Frame_Shif	NM_003377	NP_003368	P49765	VEGFB_HUMAN			0	GACCTAAAAAAA	0.388	

+	12	1367	ne_Shift_Del_p.F4	NM_003369	NP_003360	Q9P2Y5	UVRAG_HUMAN		6	ATTTCCTTTTTCC	0.383	
+	3	285	zaa.1_Frame_Shi	NM_000073	NP_000064	P09693	CD3G_HUMAN	ılar (Potential).|Ig-like.	0	GAAGATAAAAAA	0.403	
+	3	2334_2335	.L_uc001psz.1_Fra	NM_005933	NP_005924	Q03164	MLL1_HUMAN		25	CTCTCACCCCCC	0.45	
+	7	1559_1560	K1_uc009zbp.2_F	NM_001114122	NP_001107594	O14757	CHK1_HUMAN	rotein kinase.	6	GGAAAGAAAAAA	0.361	rs35817404
-	4	560	010sbo.1_5'Flank|	NM_003139	NP_003130	P08240	SRPR_HUMAN		0	GCCCCCTTTTTTT	0.438	
-	22	3672_3674	1qfl.2_In_Frame_D	NM_020228	NP_064613	Q9NQV6	PRD10_HUMAN	Poly-Thr.	1	CCGTTGGTGGT	0.547	
+	13	1588	.1_3'UTR|GLB1L3	NM_001080407	NP_001073876	Q8NCI6	GLBL3_HUMAN		1	GTGTATCCCCCC	0.602	
+	4	775	ame_Shift_Del_p.A	NM_001135217	NP_001128689	Q53EV4	LRC23_HUMAN	LRR 2.	1	GAAGTGCCCAGA	0.488	
-	3	539_541		NM_006248	NP_006239				0	GGACTTGTTGT	0.596	
-	2	149_151	5'UTR|CASC1_uc	NM_001082973	NP_001076442	Q6TDU7	CASC1_HUMAN	Glu-rich.	2	CGTCTCTCCTCC	0.365	
-	11	3063_3064	p.E611fs|SFRS2IP	NM_004719	NP_004710	Q99590	SCAFB_HUMAN	Arg-rich.	0	TCCTTTCTCTCT	0.446	
-	9	1884_1886	k|CCNT1_uc009z	NM_001240	NP_001231	O60563	CCNT1_HUMAN	His-rich.	6	TGATTATGATGAT	0.443	
+	1	306_308		NM_001005280	NP_001005280	Q8NGE5	O10A7_HUMAN	Name=3; (Potential).	4	ATGTACTTCTTC	0.414	
+	9	1779_1780	sjd.1_Frame_Shift	NM_022465	NP_071910	Q9H2S9	IKZF4_HUMAN	2H2-type 5.	1	TTCCTGGACCAC	0.574	
-	3	695_696	rame_Shift_Ins_p.	NM_001478	NP_001469	Q00973	B4GN1_HUMAN	ıenal (Potential).	0	GGGAGGCCCCC	0.589	
-	6	409_410		NM_002442	NP_002433	O43347	MSI1H_HUMAN	RRM 2.	3	CGACAGCCCCCC	0.564	
-	5	489_491	tyt.2_In_Frame_D	NM_015918	NP_057002	Q969H6	POP5_HUMAN		0	CCTGACTCCTCC	0.517	
-	25	3416	SBNO1_uc010taq	NM_018183	NP_060653	A3KN83	SBNO1_HUMAN		9	CTTCCATTTTTTT	0.388	
-	34	4381_4382	_p.V250fs|POLE_u	NM_006231	NP_006222	Q07864	DPOE1_HUMAN		8	TTGACCACACAC	0.604	
-	1	1994_1996	o.1_In_Frame_De	NM_183422	NP_904358	Q15714	T22D1_HUMAN	Gln-rich.	0	gttgttgttgctgctgctg	0.409	613609;rs146722477
-	10	1917_1918	p.R637fs|ZC3H13	NM_015070	NP_055885	Q5T200	ZC3HD_HUMAN	Arg/Ser-rich.	2	CAAACCTCTCTC	0.337	
+	3	707_710	vbk.2_Frame_Shif	NM_015116	NP_055931	Q9Y2L9	LRCH1_HUMAN	LRR 3.	2	CCGCCCTGCCTG	0.436	
+	1	690_692		NM_007129	NP_009060	O95409	ZIC2_HUMAN	scriptional activation or rep	0	CGCGGCccaccac	0.522	
+	1	568_570	l0_uc001whe.2_5'	NM_014045	NP_054764	Q7Z4F1	LRP10_HUMAN		1	GCCACCCTCCTC	0.67	
-	6	2422	.A167fs|JPH4_uc	NM_032452	NP_115828	Q96JJ6	JPH4_HUMAN	lasmic (Potєp.A502fs*12(1)	2	GCCTGCCCCCC	0.687	rs144738828
+	5	648	me_Shift_Del_p.E	NM_002791	NP_002782	P60900	PSA6_HUMAN		0	TCCTTGAAAAAA	0.403	
-	11	2527		NM_018353	NP_060823	Q6P0N0	M18BP_HUMAN		0	TGGGACTTTTTTT	0.373	
+	1	839	1_Intron|RPL36AL	NM_002408	NP_002399	Q10469	MGAT2_HUMAN	ıenal (Potential).	0	CTGGGCCCCCC	0.602	
+	13	2141	CH_uc010tsb.1_F	NM_006255	NP_006246	P24723	KPCL_HUMAN	rotein kinase.	6	ACATCCTTTTTTT	0.522	
+	16	4738_4740	1xmv.2_In_Frame	NM_015556	NP_056371	O43166	SI1L1_HUMAN	Ser-rich.	4	tcctcctcttcctcctcctc	0.468	
-	1	61_63	.2_5'UTR|PGBD4_	NM_020154	NP_064539	Q9NPA0	CO024_HUMAN		0	CGATAGCAGCAC	0.665	
-	3	310	_5'UTR|C15orf52_	NM_207380	NP_997263	Q6ZUT6	CO052_HUMAN		1	GCCATCCCCCC	0.647	
-	15	2082_2083	p.E647fs|SLTM_uc	NM_024755	NP_079031	Q9NWH9	SLTM_HUMAN	lu-rich.|Potential.	1	AGGCGCTCTCTC	0.475	
+	6	1825_1827	2afu.2_In_Frame_	NM_017610	NP_060080	Q6ZNA4	RN111_HUMAN	His-rich.	2	TCATCACCACCA	0.512	
+	7	4096_4098		NM_015042	NP_055857	O15014	ZN609_HUMAN	Poly-His.	3	CACACACCACCA	0.576	
+	2	2046_2048	.L591del|SLC24A	NM_004727	NP_004718	O60721	NCKX1_HUMAN	ical; (Potential).	0	GAGCCTGCTGC	0.547	
+	3	434_436		NM_001030005	NP_001025176	Q8WVH0	CPLX3_HUMAN		0	CACAGAGGAGG	0.616	
+	7	1037_1039	.K238del|UBN1_u	NM_001079514	NP_001072982	Q9NPG3	UBN1_HUMAN	Lys-rich.	2	TAAGGAGAAGAA	0.453	
-	3	553_555	20GG>G|KIAA043	NM_014647	NP_055462	Q9Y4F3	LKAP_HUMAN	Poly-Gly.	0	ACCGCCACCAC	0.532	
+	9	960_962	ne_Del_p.E294del	NM_001099661	NP_001093131	B5ME19	B5ME19_HUMAN		0	GGATGAGGAGG	0.562	
+	30	3476_3478	L1022del|ITGAL_u	NM_002209	NP_002200	P20701	ITAL_HUMAN	ical; (Potential).	10	GGGGGCTGCTG	0.601	
+	25	6010_6011	_Shift_Ins_p.Q16	NM_006662	NP_006653	Q6ZRS2	SRCAP_HUMAN	Pro-rich.	4	CGCCAGCCCCCC	0.569	
-	8	897_898	ge.1_Frame_Shift	NM_013263	NP_037395	Q9NPI1	BRD7_HUMAN		0	GAGTCCTCTCTC	0.47	
+	3	278_280	vho.1_In_Frame_	NM_020312	NP_064708	O75208	COQ9_HUMAN		1	CGGCGAGGAGG	0.576	rs149029279
+	2	250	.2_Frame_Shift_D	NM_016951	NP_058647	Q9UBR5	CKLF_HUMAN	MARVEL.	0	ATGACCTTTTTTA	0.318	
+	5	2064_2065	02ewd.2_Frame_	NM_133458	NP_597715	Q8TF47	ZFP90_HUMAN	2H2-type 12.	1	CTTCCGAAAAAA	0.411	
-	6	583_585		NM_014062	NP_054781	Q9ULX3	NOB1_HUMAN	Poly-Glu.	0	TTTCTTCCTCCTC	0.522	

-	14	2504	_p.F283fs|ADAMT	NM_199355	NP_955387	Q8TE60	ATS18_HUMAN	Cys-rich.	p.A696fs*18(2)	18	CATTGCAAAAA	0.403	
-	13	1822	me_Shift_Del_p.K	NM_002532	NP_002523	Q99567	NUP88_HUMAN	Potential.		1	TGTTTCTTTTTTT	0.363	
-	15	2000_2002	15_uc002ghy.1_5'	NM_004860	NP_004851	P51116	FXR2_HUMAN	Poly-Arg.		0	GTTACGGCGGC	0.547	
+	34	4663_4665	0crt.2_In_Frame_	NM_003170	NP_003161	Q7KZ85	SPT6H_HUMAN	Poly-Ser.		3	CCCTAGCAGCA	0.537	
+	37	5115	crt.2_Frame_Shift	NM_003170	NP_003161	Q7KZ85	SPT6H_HUMAN			3	TGGGGAAAAAT	0.567	
-	12	1542	hift_Del_p.G471fs|	NM_001256	NP_001247	P30260	CDC27_HUMAN			5	AAATAACCTTTC	0.368	
-	14	1854	itf.2_Frame_Shift_	NM_001130528	NP_001124000	O60271	JIP4_HUMAN			5	TTGACCTTTTTT	0.323	
-	21	4684_4686	12EE>E|BZRAP1	NM_004758	NP_004749	O95153	RIMB1_HUMAN	Poly-Glu.		3	AGctcctcttcctcctcct	0.468	
-	14	1600_1602	jca.2_In_Frame_	NM_017647	NP_060117	Q8IY81	RRMJ3_HUMAN			1	GGATTCTCCTCC	0.537	
+	20	6727_6729	.T2353del|BPTF_	NM_182641	NP_872579	Q12830	BPTF_HUMAN	Thr-rich.		4	GCCAGCACCACC	0.542	rs143937013
+	9	1570_1571	NF236_uc002lmk.	NM_007345	NP_031371	Q9UL36	ZN236_HUMAN			4	AAAAAGAAAAAA	0.381	
-	9	1668_1669	orf29_uc002lyi.3_	NM_001080543	NP_001074012	Q8WUQ7	CS029_HUMAN			0	GCACCGCCTCGC	0.748	
+	20	2639	ne_Shift_Del_p.F8	NM_001005361	NP_001005361	P50570	DYN2_HUMAN	Pro-rich.		6	CTCTTCCCAGC	0.667	
-	4	860	63_uc002mtq.2_	NM_145276	NP_660319	Q8TA94	ZN563_HUMAN	2H2-type 3.		0	GGGCCAAAAAA	0.393	
-	8	1079_1081	26_uc002nee.2_I	NM_006387	NP_006378	Q8IWX8	CHERP_HUMAN	Gln-rich.		2	gctgctgttgctgctgct	0.552	
+	1	111_113		NM_021175	NP_066998	P81172	HEPC_HUMAN			1	CCTGCTCCTCC	0.64	
+	7	712_714		NM_001039887	NP_001034976	Q2NL68	CS055_HUMAN	Ser-rich.		1	TCCATCTCCTCC	0.631	
-	1	177_179	m.2_In_Frame_D	NM_014400	NP_055215	O95274	LYPD3_HUMAN			1	GCGAAGCAGCA	0.675	rs141441894
-	6	2275_2277	2pdl.2_In_Frame_	NM_030785	NP_110412	Q9H0K4	RSH6A_HUMAN	Glu-rich.		2	ctcctcgccctcctcctc	0.409	
-	6	2257_2259	2pdl.2_In_Frame_	NM_030785	NP_110412	Q9H0K4	RSH6A_HUMAN	Glu-rich.		2	ctcctcgccctcctcctc	0.438	rs62639328
-	9	2408_2410	0xyr.1_In_Frame_	NM_015063	NP_055878	Q9UPR5	NAC2_HUMAN	lasmic (Potential).		4	ACCCGTCCTCCT	0.616	
-	4	572_574		NM_018263	NP_060733	Q76L83	ASXL2_HUMAN	Ser-rich.		1	ATCACTGCTGC	0.463	
-	2	234_236	HX57_uc002rrg.2_	NM_198963	NP_945314	Q6P158	DHX57_HUMAN	Gly-rich.		3	gccacctccaccacca	0.384	
-	4	557	0yoq.1_Splice_Sit	NM_014614	NP_055429	Q14997	PSME4_HUMAN			5	GAACTGGGGG	0.347	
-	16	2711	p.K327fs|MTIF2_	NM_001005369	NP_001005369	P46199	IF2M_HUMAN			1	TTTAAATTTTTTT	0.378	
+	3	460	_p.K41fs|UGP2_u	NM_006759	NP_006750	Q16851	UGPA_HUMAN			0	ACACCAAAAAA	0.358	
-	4	737_739	02svr.2_In_Frame_	NM_017849	NP_060319	O75204	TM127_HUMAN			0	CTTATGCTGCT	0.557	
+	3	759_761	02svy.2_In_Frame	NM_001008949	NP_001008949	Q6GPH6	IPIL1_HUMAN	lasmic (Potential).		3	CAGTGAGGAGG	0.532	
+	3	146_148		NM_014440	NP_055255	Q9UHA7	IL36A_HUMAN			0	TCATGCCGACAT	0.512	
-	7	936	uc002tnj.1_Intron	NM_032390	NP_115766	Q9BYG3	MK67I_HUMAN			0	TTCGTCTTTTTTT	0.294	
-	28	4326_4327	zcp.1_Frame_Shif	NM_007366	NP_031392	Q13018	PLA2R_HUMAN	Potential).|C-type lectin 8.		3	AAAGCCTTTTTT	0.401	
+	12	1368	B_uc002ufz.2_Fra	NM_138995	NP_620482	Q8WXR4	MYO3B_HUMAN	osin head-like.		19	TCCAATCCCCCC	0.463	
+	8	1227		NM_152945	NP_694453	Q8IUH3	RBM45_HUMAN			0	CATGCAAAAAA	0.353	
+	17	1951_1952	p.R523fs|ITGAV_u	NM_002210	NP_002201	P06756	ITAV_HUMAN	ellular (Potential).		4	TTTCAAGGGGGG	0.431	
+	7	931	.1_Frame_Shift_D	NM_000578	NP_000569	P49279	NRAM1_HUMAN	ical; (Potential).		4	GGAAGCTTTTTT	0.418	
+	19	2288_2290	3_In_Frame_Del_	NM_015575	NP_056390	Q6Y7W6	PERQ2_HUMAN	Gln-rich.		7	TTCCCAGCAGC	0.424	
+	2	175_177		NM_022134	NP_071417	Q9H3Q3	G3ST2_HUMAN	type II membrane protein;		0	GGTCATCCTCCT	0.631	
+	3	173_174	j.1_RNA|FRG1B_uc010gdr.1_RNA|FRG1B_uc010ztk.1_5'UTR							0	TAGGGGAAAATG	0.322	
-	12	5661_5663	.2_In_Frame_Del_	NM_014071	NP_054790	Q14686	NCOA6_HUMAN	.|Gln-rich.|CREBBP-binding		7	TCATTtgttgctgctgc	0.498	895426;rs140426729
-	2	2489_2490	xus.1_Frame_Shif	NM_004975	NP_004966	Q14721	KCNB1_HUMAN	lasmic (Potential).		2	GCTTTTGGGGG	0.545	
-	4	1934_1936	1aaq.1_In_Frame_	NM_017798	NP_060268	Q9BYJ9	YTHD1_HUMAN			2	ACCACCTCCTC	0.557	
-	11	905	PTE_uc002yir.1_	NM_199261	NP_954870	P56180	TPTE_HUMAN	ical; (Potential).		5	ATGTCAAAAAA	0.299	
-	3	302	_p.Q71fs|C21orf91	NM_001100420	NP_001093890	Q9NYK6	EURL_HUMAN			1	AACCCTGGTTTG	0.353	
-	20	3323_3325	.Q944del|SFRS15	NM_020706	NP_065757	O95104	SFR15_HUMAN	Poly-Gln.		0	GGTGgtggctgctgc	0.291	
-	3	496_498		NM_005877	NP_005868	Q15459	SF3A1_HUMAN	Poly-Gln.		5	TGGTCTGCTGC	0.596	rs141985009
-	30	4280_4282		NM_002473	NP_002464	P35579	MYH9_HUMAN	Potential.		11	TTGGCCTCCTC	0.65	
+	3	1161_1181		NM_152243	NP_689449	Q00587	BORG5_HUMAN	of [PT]-[AT]-A- [ENT]-[PT]		0	CCTGCTGCAAA	0.665	0;rs62235033;rs13056859;rs62235034

-	1	1016_1017	P3_uc011aoy.1_5	NM_145174	NP_660157	Q7Z6W7	DNJB7_HUMAN	Poly-Lys.	1	CGCTTCTTTTTT	0.381	
-	10	2571_2573	E>E|RANGAP1_	NM_002883	NP_002874	P46060	RAGP1_HUMAN	cidic).|Asp/Glu-rich (highly	0	tcttctccttcctcctcct	0.266	
+	2	372_374	_Intron|LOC33967	NM_004599	NP_004590	Q12772	SRBP2_HUMAN	h.|Cytoplasmic (Potential).	4	gcagtggcagcagca	0.365	
-	10	1116	p.N255fs|ARFGAP	NM_014570	NP_055385	Q9NP61	ARFG3_HUMAN		1	TCAACATTTTTTT	0.224	
+	2	818_820	tr.1_In_Frame_Del	NM_014760	NP_055575	Q93075	TATD2_HUMAN		2	AATAACTCCTCC	0.635	
+	13	2715	NKTR_uc003clq.1	NM_005385	NP_005376	P30414	NKTR_HUMAN		3	TCATTCAAAAAA	0.373	
-	2	303	el_p.K44fs|ANO10	NM_018075	NP_060545	Q9NW15	ANO10_HUMAN	lasmic (Potential).	2	TCCATCTTTTTTT	0.408	
-	7	2318_2319	bf.1_Frame_Shift	NM_002375	NP_002366	P27816	MAP4_HUMAN		3	CTTTTTGTGTTT	0.455	
+	11	2031	p.R565fs|ALAS1_	NM_000688	NP_000679	P13196	HEM1_HUMAN		3	GCCCCGGGGAG	0.517	rs139914359
+	2	1293_1295	y.3_RNA|LNP1_uc	NM_001085451	NP_001078920	A1A4G5	LNP1_HUMAN	Poly-Asp.	0	ACAAAGATGATG	0.507	
+	3	425_426	2_uc003eeo.2_In	NM_018456	NP_060926	Q96CJ1	EAF2_HUMAN		0	CACTGTAAAAAA	0.243	
+	42	6369_6371	bnz.1_In_Frame_	NM_053002	NP_443728	Q86YW9	MD12L_HUMAN	Gln-rich.	7	GACCCAGCAGC	0.527	
-	2	132_134	ame_Del_p.T35de	NM_024947	NP_079223	Q8NDX5	PHC3_HUMAN	Poly-Thr.	2	Agtggtgatggtggtgg	0.424	
+	5	690	_p.S38fs|FETUB_	NM_014375	NP_055190	Q9UGM5	FETUB_HUMAN		2	AGTTTCAAAAAA	0.418	
-	3	1028	168_uc010iah.2_5	NM_152617	NP_689830	Q8IYW5	RN168_HUMAN	Glu-rich.	0	TTCGCCTTTTTT	0.448	
+	1	3159_3160		NM_175918	NP_787114	Q8N1N5	CRPAK_HUMAN		0	CTGCTCACACA	0.634	
+	1	3283_3284		NM_175918	NP_787114	Q8N1N5	CRPAK_HUMAN	2	0	CCTGCTCACGT	0.668	rs79704405
-	15	1909	.N566fs|PROM1_	NM_006017	NP_006008	O43490	PROM1_HUMAN	ellular (Potential).	7	CCTCTATTTTTTT	0.428	
+	4	1003	tg.2_Frame_Shift_	NM_016531	NP_057615	P57682	KLF3_HUMAN	Pro-rich.	2	AGTGTCCCCCC	0.423	
+	16	1633_1634	el_p.R448fs|FIP1L	NM_030917	NP_112179	Q6UN15	FIP1_HUMAN	ction with CPSF1 and CST	2	CACCAGAGAGA	0.292	
-	8	1472	_p.L340fs|AASDH_	NM_181806	NP_861522	Q4L235	ACSF4_HUMAN		4	GTCCCAAAAAA	0.363	rs148777026
+	4	994_996	.Q279del|MMRN1_	NM_007351	NP_031377	Q13201	MMRN1_HUMAN	Poly-Gln.	4	GCTGAGCAGCA	0.448	
+	3	335	C9_uc003ieb.2_F	NM_005033	NP_005024	Q06265	EXOS9_HUMAN	RE binding.	0	GTATTCTTTTTTT	0.383	
-	8	596_598	3ijz.3_In_Frame_	NM_001102653	NP_001096123	Q01804	OTUD4_HUMAN		3	ACATCAGCAGC	0.34	
-	41	6826	p.I766fs|LRBA_uc	NM_006726	NP_006717	P50851	LRBA_HUMAN		7	GGTCGATTTTTTT	0.453	rs34237929
+	13	1713_1714	_p.K518fs|PAPD7_	NM_006999	NP_008930	Q5XG87	PAPD7_HUMAN		1	AAAAAACACACA	0.653	
-	14	2587_2589	D2_uc011cmz.1_	NM_001332	NP_001323	Q9UQB3	CTND2_HUMAN	Poly-Lys.	8	TCTTTTTCTTCTT	0.502	
-	77	13500	jfc.2_Frame_Shift_	NM_001369	NP_001360	Q8TE73	DYH5_HUMAN		31	GGGTTAAAAAA	0.423	
-	10	1909	H10_uc011cnu.1_	NM_006727	NP_006718	Q9Y6N8	CAD10_HUMAN	|Extracellular (Potential).	12	AAACTGAAAAAA	0.313	
-	11	1838_1839	.1_Frame_Shift_	NM_000065	NP_000056	P13671	CO6_HUMAN	EGF-like.	7	CTCTGACACACA	0.475	
-	2	1109_1111	60DD>D|TAF9_uc	NM_003187	NP_003178	Q16594	TAF9_HUMAN	Poly-Asp.	0	tatcatagtcatcatcat	0.256	
+	17	2312_2314	uc003kgi.3_Intron	NM_003248	NP_003239	P35443	TSP4_HUMAN	SP type-3 7.	0	GAGTGTGATGAT	0.562	
+	7	1394		NM_002439	NP_002430	P20585	MSH3_HUMAN		4	GGGACAAAAAA	0.348	
+	2	237_240	_p.K19fs|AP3S1_	NM_001284	NP_001275	Q92572	AP3S1_HUMAN		0	ATCTAAGAGAGA	0.304	rs80118146
+	1	1731_1743	uc003lin.2_5'Flank	NM_018937	NP_061760	Q9Y5E6	PCDB3_HUMAN	(Potential).|Cadherin 6.	2	CGGGCGGCTGA	0.709	
-	3	512_514	0jii.2_In_Frame_D	NM_138379	NP_612388	Q96H15	TIMD4_HUMAN	ar (Potential).|Thr-rich.	2	GGGCTTGTTGT	0.537	
-	3	567	ddz.1_Frame_Shif	NM_144726	NP_653327	Q96MT1	RN145_HUMAN	ical; (Potential).	5	GCAGTCAAAAAA	0.343	
+	11	1475	mkl.2_Frame_Shif	NM_001746	NP_001737	P27824	CALX_HUMAN	enal (Potential).	0	CTGACATTTTTTT	0.423	
+	18	2852	xq.1_Frame_Shift_	NM_004415	NP_004406	P15924	DESP_HUMAN	ular 1.|Spectrin 2.	9	CGGTGAAAAG	0.493	
+	2	128_130	p.L24del|BTN2A2_	NM_006995	NP_008926	Q8WVV5	BT2A2_HUMAN		0	CAGCCTCcctcctc	0.483	
+	1	72_74	2A3_uc011dkm.1_RNA						0	GCCTCCCTCCTC	0.586	rs113134648
+	3	618	_Del_p.T206fs|HL	NM_002116	NP_002107	P30443	1A01_HUMAN	ar (Potential).|Alpha-2.	2	CGCACGGGTAC	0.637	rs115073453
+	26	5893	c.3_Frame_Shift_	NM_080686	NP_542417	P48634	PRC2A_HUMAN		0	ACCTACCCCCC	0.522	
-	4	658	p.P115fs|BAT3_uc	NM_004639	NP_004630	P46379	BAG6_HUMAN		0	TACCAGGGGGG	0.592	
-	2	742	_5'Flank|ATF6B_	NM_022110	NP_071393	Q9UIM3	FKBPL_HUMAN		0	GAGCTCCCCCC	0.587	
-	2	290	KBP5_uc003oky.2	NM_001145776	NP_001139248	Q13451	FKBP5_HUMAN		1	CTGTCTTTTTTG	0.468	rs143557566
-	4	1648	318_uc003ouw.2_	NM_014345	NP_055160	Q5VUA4	ZN318_HUMAN		7	TCGCCTTTTTT	0.493	

+	16	2191		NM_012120	NP_036252	Q9Y5K6	CD2AP_HUMAN	Potential.		2	GATGTGAAAAAA	0.388	
-	12	1315	009_uc003pkk.2_	NM_014895	NP_055710	Q5TB80	QN1_HUMAN			1	TTGTCAAAAAAA	0.358	
+	9	3522_3524	2_3'UTR|GRM1_u	NM_000838	NP_000829	Q13255	GRM1_HUMAN	|Cytoplasmic (Potential).		19	TCTCCAGCAGC	0.66	
-	3	360	P1_uc010ksc.2_I	NM_001031617	NP_001026788	Q49B96	COX19_HUMAN			0	AATTCATTTTTTT	0.463	rs75087611
+	3	337	rf16_uc011kaf.1_I	NM_006658	NP_006649	O96001	GSUB_HUMAN			3	AGACCAAAAAA	0.438	
+	5	601_603	0kxo.2_In_Frame_	NM_007252	NP_009183	P78424	PO6F2_HUMAN	Gln-rich.		1	cagctccagcagcag	0.365	
+	3	342	_uc011kby.1_Intro	NM_002541	NP_002532	Q02218	ODO1_HUMAN			2	GGACATTTTTTT	0.577	
+	5	1249	_p.P231fs|DTX2_u	NM_020892	NP_065943	Q86UW9	DTX2_HUMAN			2	CCCCCACACAG	0.657	rs147779783
-	7	1188	_p.K237fs|CYP51A	NM_000786	NP_000777	Q16850	CP51A_HUMAN			0	ATAACATTTTTTT	0.398	
-	3	436		NM_005431	NP_005422	O43543	XRCC2_HUMAN			2	TACACCAAAAAA	0.393	
+	2	273_275	lank|BMP1_uc003	NM_003018	NP_003009	P11686	PSPC_HUMAN			0	TATCGTGGTGG	0.601	
-	15	2035		NM_001010906	NP_001010906	Q68CJ6	SLIP_HUMAN			2	AGGAAATTTTTT	0.453	
-	16	3521_3523	.E993del|MYST3_	NM_001099412	NP_001092882	Q92794	MYST3_HUMAN	Poly-Glu.		7	CCGGCTCCTCC	0.567	
-	3	971_972	_Shift_Ins_p.E111	NM_002568	NP_002559	P11940	PABP1_HUMAN	RRM 2.		0	ATTTTTTCAATA	0.337	
-	3	363_367	yqd.2_Frame_Shi	NM_032847	NP_116236	Q96K31	CH076_HUMAN			2	CAGCGCCTCCA	0.424	
-	6	524_525	3yqt.2_Frame_Shi	NM_004306	NP_004297	P27216	ANX13_HUMAN	Annexin 2.		3	CCAGGATTTTTT	0.411	
-	30	4625	ae.1_Splice_Site_	NM_201380	NP_958782	Q15149	PLEC_HUMAN			9	TGTACCTCCTC	0.621	
-	5	724_726	e_Del_p.152_153	NM_004529	NP_004520	P42568	AF9_HUMAN	Poly-Ser.		3	tgctgctactgctgctgc	0.148	
-	1	2084	uc003zrh.1_RNA	NM_153809	NP_722516	Q8IZX4	TAF1L_HUMAN		p.K665fs*4(2)	26	TTGGCCTTTTTTT	0.478	
-	14	2236_2237	e_Shift_Ins_p.N28	NM_007126	NP_009057	P55072	TERA_HUMAN			1	GAACACATTTTTT	0.515	
-	12	1637		NM_006289	NP_006280	Q9Y490	TLN1_HUMAN	vith LAYN (By similarity).		13	TCGTACTTTTTGG	0.498	
-	3	128_129	_Shift_Ins_p.K34f	NM_016390	NP_057474	Q5T280	CI114_HUMAN			0	CTTCCATTTTTT	0.525	
+	24	2526	bwu.2_Frame_Shi	NM_015354	NP_056169	Q5SRE5	NU188_HUMAN			7	GGTGTCCCCCC	0.473	
+	5	647	ddo.2_Frame_Shif	NM_000950	NP_000941	O14668	TMG1_HUMAN	ic (Potential).|Poly-Pro.		2	CCCCACCCCCC	0.488	
-	18	2564_2566	sw.2_In_Frame_	NM_015107	NP_055922	Q9UPP1	PHF8_HUMAN			3	GCGTTCTCCTCC	0.591	
-	1	1805_1806		NM_003604	NP_003595	O14654	IRS4_HUMAN			10	CCTTTGCCCCCC	0.545	
+	2	310_311	_5'Flank|LOC100	NM_001152	NP_001143	P05141	ADT2_HUMAN	Solcar 1.		1	GGAGCAGGGAG	0.49	rs113356560
+	4	1735_1737	EC1_uc010nsl.1_	NM_005462	NP_005453	O60732	MAGC1_HUMAN			4	TGAGCTCCTCC	0.473	rs144357389
-	1	159		NM_001009609	NP_001009609	Q5MJ09	SPXN3_HUMAN			2	TCATCATTTTTTT	0.239	
+	20	4967	1aoj.2_Frame_Shi	NM_015215	NP_056030	Q9Y6Y1	CMTA1_HUMAN	IQ 2.		9	ATGAACAAAAAA	0.473	
-	4	473		NM_001561	NP_001552	Q07011	TNR9_HUMAN	(Potential).|TNFR-Cys 3.		4	CGTACCTTTTTTT	0.413	rs9657965
+	8	5315	.2_Intron|PRDM2_	NM_012231	NP_036363	Q13029	PRDM2_HUMAN			1	CTCCCAAAAAA	0.463	rs141416335
-	7	811_812	1_Intron|MST1P9_	NR_002729						0	GGTACGCCGCG	0.649	
+	12	2906_2908	9vqi.1_In_Frame_	NM_001083621	NP_001077090	Q9NUA8	ZBT40_HUMAN			1	CCCCAAGAAGA	0.517	
+	2	155_156	|CCDC30_uc010c	NM_001080850	NP_001074319	Q5VVM6	CCD30_HUMAN			0	TCAAAAGAGAGA	0.356	
-	5	924_925	IQ3_uc001dfz.3_	NM_001105659	NP_001099129	A6PVS8	LRIQ3_HUMAN			2	CTGCTGTTTTTT	0.327	
-	3	841		NM_003921	NP_003912	O95999	BCL10_HUMAN	CARD.		2	TGAGTATTTTTTT	0.343	
-	11	1958_1959	3_uc001dmu.2_F	NM_018284	NP_060754	Q9H0R5	GBP3_HUMAN	Potential.		2	TCTTGGTTTTTT	0.371	
-	9	1232	Shift_Del_p.M408	NM_005665	NP_005656	O60447	EVI5_HUMAN	Interaction with alpha-tubul		2	TTTTCATTTTTTT	0.318	
-	9	1732_1734	ows.1_In_Frame_	NM_015906	NP_056990	Q9UPN9	TRI33_HUMAN	Poly-Thr.		11	TGTTGTGTTGTT	0.429	
-	4	601	160_uc001eom.1_	NM_007053	NP_008984	O95971	BY55_HUMAN			0	TGGAGAAAAAAT	0.498	
+	8	2280	zr.1_Frame_Shift_	NM_004326	NP_004317	O00512	BCL9_HUMAN	y-Pro.|Pro-rich.		6	GAGGACCCCCC	0.582	
+	14	2499	Shift_Del_p.G778	NM_019032	NP_061905	Q6UY14	ATL4_HUMAN	SP type-1 2.		2	AATTTGGGGGG	0.692	rs149280379
-	3	1792_1795		NM_001122965	NP_001116437	Q6XPR3	RPTN_HUMAN	Gln-rich.		0	GCCTTGTCTGTC	0.466	
-	3	1756_1759		NM_001122965	NP_001116437	Q6XPR3	RPTN_HUMAN	Gln-rich.		0	GCCTTGTCTGTC	0.485	
-	3	1720_1723		NM_001122965	NP_001116437	Q6XPR3	RPTN_HUMAN	Gln-rich.		0	GCCTTGTCTGTC	0.505	
+	11	2233	_p.D350fs|NPR1_u	NM_000906	NP_000897	P16066	ANPRA_HUMAN	Potential).|Protein kinase.		7	ACCGACCCCCC	0.493	

-	12	1570_1571	0907_uc009wrk.1_	NM_014949	NP_055764	Q7Z7F0	K0907_HUMAN		0	TGTCCCTCTCTC	0.396	
-	5	1175	MF1_uc010pjl.1_Ir	NM_003037	NP_003028	Q13291	SLAF1_HUMAN	(Potential).|Ig-like V-type.	2	TAAGGCTTTTTT	0.433	
-	6	1404_1406	.V48del|PVRL4_u	NM_030916	NP_112178	Q96NY8	PVRL4_HUMAN	ical; (Potential).	2	ATGAGCACCACC	0.571	
+	3	338_340		NM_001102566	NP_001096036	A6NKN8	PC4L1_HUMAN		0	AGGCGGAGGAG	0.488	
-	12	2285	ng.3_Frame_Shift_	NM_007314	NP_009298	P42684	ABL2_HUMAN		14	CGTTTGGGGGG	0.502	rs138240636
-	2	1361_1363	.2_Intron|RGL1_u	NM_203454	NP_982279	Q8WW27	ABEC4_HUMAN		0	TCCCTTTCTTCTT	0.419	rs141411396
+	7	1574_1576	ne_Del_p.T418del|	NM_005807	NP_005798	Q92954	PRG4_HUMAN	ats of K-X-P-X-P-T-T-X.|21	1	GCACCCACCAC	0.645	
-	6	886	_Shift_Del_p.K69fs	NM_001031685	NP_001026855	Q13625	ASPP2_HUMAN		3	TCTCACTTTTTTT	0.368	
-	19	2548		NM_001081	NP_001072	O60494	CUBN_HUMAN	CUB 4.	19	TTAGGAAAAAAA	0.413	
-	15	1912_1913	_p.K570fs|FRMPD	NM_001018071	NP_001018081	Q68DX3	FRPD2_HUMAN	FERM.	1	GTGAACTTTTTT	0.465	
+	2	237		NM_001080512	NP_001073981	Q9H694	BICC1_HUMAN		4	AAAAGGTAAGTT	0.388	
-	4	784	01jod.1_Frame_S	NM_017987	NP_060457	Q8WXA3	RUFY2_HUMAN	RUN.	1	GGCCATTTTTTT	0.398	
-	2	431	0qot.1_Frame_Shi	NM_020123	NP_064508	Q9HD45	TM9S3_HUMAN		0	TGATACTTTTTTT	0.363	
+	3	629_631	ame_Del_p.S197d	NM_032429	NP_115805	Q9BRK4	LZTS2_HUMAN	ntrosomal localization (By	4	GGCCCTGcctcctc	0.557	
-	2	955_957	2_uc001mak.1_Ir	NM_017481	NP_059509	Q9H347	UBQL3_HUMAN		3	TGGCTGGTGGT	0.537	rs2234451
-	8	920		NM_006292	NP_006283	Q99816	TS101_HUMAN	Potential.	0	TGACCCTTTTTC	0.438	
-	4	391	eo.1_Frame_Shift_	NM_015957	NP_057041	Q96GX9	MTNB_HUMAN		0	ACTGGCTTTTTT	0.343	
-	3	345	rew.1_Frame_Shi	NM_001001991	NP_001001991	Q6UXH9	PAMR1_HUMAN		2	AGGTACCCCCC	0.517	
+	7	728	CS_uc010rfn.1_3	NM_001127219	NP_001120691	Q96QU6	1A1L1_HUMAN		4	CTTACTATGGCG	0.577	
+	2	185_187		NM_015516	NP_056331	Q8WUA8	TSK_HUMAN		0	GCCCCTGCTGC	0.616	
-	3	483	AF1D_uc001pdz.2	NM_024116	NP_077021	Q9H5J8	TAF1D_HUMAN		0	TTTTTCTTTTTTT	0.348	
+	3	285	zaa.1_Frame_Shi	NM_000073	NP_000064	P09693	CD3G_HUMAN	lar (Potential).|Ig-like.	0	GAAGATAAAAAA	0.403	
+	9	1502_1504		NM_005188	NP_005179	P22681	CBL_HUMAN	Glu-rich (acel(1)|p.E366_K	149	AAATTATGATGAT	0.473	
-	4	1425	sap.1_Frame_Shi	NM_024631	NP_078907	Q6P1R3	CK061_HUMAN		0	TGGGTTCTATTT	0.488	
+	7	1559_1560	K1_uc009zbp.2_F	NM_001114122	NP_001107594	O14757	CHK1_HUMAN	rotein kinase.	6	GGAAAGAAAAAA	0.361	rs35817404
-	4	560	010sbo.1_5'Flank|	NM_003139	NP_003130	P08240	SRPR_HUMAN		0	GCCCCCTTTTTTT	0.438	
-	3	258_259	_74P>PP|PRB1_u	NM_005039	NP_005030	P04280	PRP1_HUMAN	-P-[PAQ]-Q-[GE]-[GD]- [N	0	TTTCCTGGAGGT	0.619	
-	11	3063_3064	p.E611fs|SFRS2IP	NM_004719	NP_004710	Q99590	SCAFB_HUMAN	Arg-rich.	0	TCCTTTCTCTCT	0.446	
-	9	1884_1886	k|CCNT1_uc009z	NM_001240	NP_001231	O60563	CCNT1_HUMAN	His-rich.	6	TGATTATGATGAT	0.443	
-	9	1781_1782	v.1_In_Frame_Ins_	NM_006121	NP_006112	P04264	K2C1_HUMAN	y/Ser-rich.|Tail.	2	ctgccatggccgccgc	0.084	
+	1	306_308		NM_001005280	NP_001005280	Q8NGE5	O10A7_HUMAN	Name=3; (Potential).	4	ATGTACTTCTTC	0.414	
+	5	734	sjr.2_Frame_Shift_	NM_015292	NP_056107	Q9BSJ8	ESYT1_HUMAN		5	GAAATATTTTTGC	0.478	
-	12	1669	p.P480fs|UHRF1B	NM_015054	NP_055869	A0JNW5	UH1BL_HUMAN		2	CTTTTGGGGGA	0.348	
-	25	3416	SBNO1_uc010taq	NM_018183	NP_060653	A3KN83	SBNO1_HUMAN		9	TTCCATTTTTTT	0.388	
-	34	4381_4382	_p.V250fs|POLE_u	NM_006231	NP_006222	Q07864	DPOE1_HUMAN		8	TTGACCACACAC	0.604	
-	10	3917	I963fs|SACS_uc0	NM_014363	NP_055178	Q9NZJ4	SACS_HUMAN		12	CTTCAATTTTTTT	0.383	
+	3	707_710	vbk.2_Frame_Shi	NM_015116	NP_055931	Q9Y2L9	LRCH1_HUMAN	LRR 3.	2	CGCCCTGCCTG	0.436	
-	29	3774	BCC4_uc010afk.2	NM_005845	NP_005836	O15439	MRP4_HUMAN	C transporter 2.	4	CCGGATTTTTTT	0.378	
+	1	568_570	0_uc001whe.2_5'	NM_014045	NP_054764	Q7Z4F1	LRP10_HUMAN		1	CCACCCTCCTC	0.67	
-	11	2527		NM_018353	NP_060823	Q6P0N0	M18BP_HUMAN		0	TGGGACTTTTTTT	0.373	
+	1	839	1_Intron|RPL36AL	NM_002408	NP_002399	Q10469	MGAT2_HUMAN	enal (Potential).	0	CTGGGCCCCCC	0.602	
-	1	61_63	.2_5'UTR|PGBD4_	NM_020154	NP_064539	Q9NPA0	CO024_HUMAN		0	CGATAGCAGCA	0.665	
-	15	2082_2083	p.E647fs|SLTM_u	NM_024755	NP_079031	Q9NWH9	SLTM_HUMAN	lu-rich.|Potential.	1	AGGCGCTCTCTC	0.475	
+	3	434_436		NM_001030005	NP_001025176	Q8WVH0	CPLX3_HUMAN		0	CACAGAGGAGG	0.616	
-	1	929	r.2_3'UTR|TIGD7_	NM_033208	NP_149985	Q6NT04	TIGD7_HUMAN	y similarity).|HTH psq-type.	0	TTCTTATTTTTTT	0.358	
-	3	972_973		NM_001012991	NP_001013009	Q1ED39	CP088_HUMAN	th ZFP106 (By similarity).	0	GTTGCCTTTTTT	0.564	
+	9	960_962	ne_Del_p.E294del	NM_001099661	NP_001093131	B5ME19	B5ME19_HUMAN		0	GGATGAGGAGG	0.562	

+	30	3476_3478	L1022del|ITGAL_	NM_002209	NP_002200	P20701	ITAL_HUMAN	ical; (Potential).	10	GGGGGCTGCTG	0.601	
+	25	6010_6011	_Shift_Ins_p.Q16	NM_006662	NP_006653	Q6ZRS2	SRCAP_HUMAN	Pro-rich.	4	GCCAGCCCCC	0.569	
-	8	897_898	ge.1_Frame_Shift	NM_013263	NP_037395	Q9NPI1	BRD7_HUMAN		0	GAGTCCTCTCT	0.47	
+	5	1317_1319	hx.2_In_Frame_D	NM_024335	NP_077311	P78412	IRX6_HUMAN		6	gaggaagaggagga	0.493	
+	6	773_774	p.Y208fs|CPNE2_	NM_152727	NP_689940	Q96FN4	CPNE2_HUMAN	C2 2.	2	AGTTTTATAAGC	0.599	
-	3	393	IAPIN1_uc010cda	NM_020313	NP_064709	Q6FI81	CPIN1_HUMAN		0	CTGTGCAGAGT	0.473	
+	3	278_280	vho.1_In_Frame_	NM_020312	NP_064708	O75208	COQ9_HUMAN		1	CGGCGAGGAGG	0.576	rs149029279
+	15	2170_2172	.E413del|SLC9A	NM_004594	NP_004585	Q14940	SL9A5_HUMAN		2	GTCTGAGGAGG	0.571	
+	3	433	_p.T16fs|KIAA01	NM_014615	NP_055430	Q14687	GSE1_HUMAN		5	CAGCACCCCCC	0.687	
-	15	2000_2002	15_uc002ghy.1_5'	NM_004860	NP_004851	P51116	FXR2_HUMAN	Poly-Arg.	0	GTTACGGCGGC	0.547	
+	10	2188_2189	2gjr.2_Frame_Shif	NM_053051	NP_444279	Q8N137	CNTRB_HUMAN	d for centrosome localizat	2	CTCGGAGAGAG	0.579	
+	6	2233	_p.L615fs|CYTSB_	NM_001033553	NP_001028725	Q5M775	CYTSB_HUMAN	Potential.	0	AAGCTGGAGGA	0.478	
+	34	4663_4665	0crt.2_In_Frame_	NM_003170	NP_003161	Q7KZ85	SPT6H_HUMAN	Poly-Ser.	3	CCCTAGCAGCA	0.537	
-	15	2756	bh.1_Frame_Shift	NM_033389	NP_203747	Q76I76	SSH2_HUMAN		2	GTTCTGGGGGG	0.483	
-	8	2163_2164	p.S622fs|GPATCH	NM_001002909	NP_001002909	Q9UKJ3	GPTC8_HUMAN	Lys-rich.	4	GCCTTAGAGCTT	0.45	
-	5	690	43_uc010czw.1_	NM_144609	NP_653210	Q96MW1	CCD43_HUMAN	Potential.	0	GTGTCCTTTTTT	0.463	
+	5	488_489	ilh.2_Frame_Shift_	NM_001002841	NP_001002841	P12829	MYL4_HUMAN		2	ATCCTGCAGCA	0.53	
-	4	843	X11_uc010wnf.1_	NM_004375	NP_004366	Q9Y6N1	COX11_HUMAN	Potential).|Mitochondrial m	1	GCTTCAAAAAA	0.353	
+	6	1129	02jlp.2_Frame_Sh	NM_004252	NP_004243	O14745	NHRF1_HUMAN		0	GACAGCCCCCC	0.597	
-	8	1079_1081	26_uc002nee.2_I	NM_006387	NP_006378	Q8IWX8	CHERP_HUMAN	Gln-rich.	2	gctgctgttgctgctgct	0.552	
+	7	1022	0xru.1_Frame_Sh	NM_001114093	NP_001107565	Q8ND56	LS14A_HUMAN		1	GTCATCGGGGT	0.438	
+	1	111_113		NM_021175	NP_066998	P81172	HEPC_HUMAN		1	CCTGCTCCTCC	0.64	
-	1	177_179	m.2_In_Frame_D	NM_014400	NP_055215	O95274	LYPD3_HUMAN		1	GCGAAGCAGCA	0.675	rs141441894
-	2	1402_1404	2per.3_In_Frame_	NM_018215	NP_060685	Q86V59	PNML1_HUMAN		0	CTCACCTTCTTC	0.562	
-	4	572_574		NM_018263	NP_060733	Q76L83	ASXL2_HUMAN	Ser-rich.	1	ATCACTGCTGC	0.463	
-	15	2287_2289		NM_014709	NP_055524	Q70CQ2	UBP34_HUMAN		19	gtggtgatggtggtgg	0.281	
+	30	3643_3645	k.2_In_Frame_De	NM_003494	NP_003485	O75923	DYSF_HUMAN	ic (Potential).|Arg-rich.	7	CCTTCCGCCGC	0.655	
+	3	759_761	02svy.2_In_Frame	NM_001008949	NP_001008949	Q6GPH6	IPIL1_HUMAN	lasmic (Potential).	3	CAGTGAGGAGG	0.532	
+	5	1001	_Shift_Del_p.T237	NM_022826	NP_073737	Q9H992	MARH7_HUMAN	Ser-rich.	0	ATCTACTTTTTTT	0.393	
-	7	1432	Shift_Del_p.K210	NM_004490	NP_004481	Q14449	GRB14_HUMAN	PH.	7	TCCATGTTTTTT	0.373	
+	8	1227		NM_152945	NP_694453	Q8IUH3	RBM45_HUMAN		0	CATGCAAAAAA	0.353	
+	4	842		NM_019048	NP_061921	Q9NWL6	ASND1_HUMAN	midotransferase type-2.	3	TAGGGATTTTTTT	0.393	
+	9	1518	20A1_uc002uzy.3_	NM_177538	NP_803882	Q6UW02	CP20A_HUMAN		0	AAGTTCAAAAAA	0.348	
+	4	350	_p.L117fs|RQCD1_	NM_005444	NP_005435	Q92600	RCD1_HUMAN		2	TCCCACTTTTTT	0.413	
+	2	364_365	s_p.I20fs|DSTN_	NM_006870	NP_006861	P60981	DEST_HUMAN	ADF-H.	2	CTGTCATTTTTT	0.386	
+	3	173_174	j.1_RNA|FRG1B_uc010gdr.1_RNA|FRG1B_uc010ztk.1_5'UTR						0	TAGGGGAAAATG	0.322	
-	2	797	002wwn.2_Frame_	NM_138578	NP_612815	Q07817	B2CL1_HUMAN	BH1.	2	AGGAGAAAAAG	0.542	
+	3	213		NM_033118	NP_149109	Q9H1R3	MYLK2_HUMAN		6	CCTGGCCCCCC	0.587	
-	8	665	gju.1_Frame_Shif	NM_014258	NP_055073	Q9BX26	SYCP2_HUMAN		5	CATTCATTTTTTT	0.289	
-	20	3323_3325	.Q944del|SFRS15	NM_020706	NP_065757	O95104	SFR15_HUMAN	Poly-Gln.	0	GGTGgtggctgctgc	0.291	
-	5	757		NM_144659	NP_653260	Q9NV44	CU077_HUMAN		0	AGACACCCCCC	0.478	
+	4	1162	0gma.2_Frame_S	NM_005534	NP_005525	P38484	INGR2_HUMAN	tential).|Fibronectin type-III	0	ACGGCCTTTTTT	0.458	
+	33	3643	_p.K1180fs|TTC3_	NM_001001894	NP_001001894	P53804	TTC3_HUMAN	Lys-rich (basic).	9	CTCAAGAAAAAA	0.383	
-	3	496_498		NM_005877	NP_005868	Q15459	SF3A1_HUMAN	Poly-Gln.	5	TGGTCTGCTGC	0.596	rs141985009
+	3	1161_1181		NM_152243	NP_689449	Q00587	BORG5_HUMAN	of [PT]-[AT]-A- [ENT]-[PT]	0	CCTGCTGCAAA	0.665	0;rs62235033;rs13056859;rs62235034
-	10	2571_2573	E>E|RANGAP1_	NM_002883	NP_002874	P46060	RAGP1_HUMAN	cidic).|Asp/Glu-rich (highly	0	tcttctccttcctcctcct	0.266	
-	10	1116	p.N255fs|ARFGAP	NM_014570	NP_055385	Q9NP61	ARFG3_HUMAN		1	TCAACATTTTTTT	0.224	

-	9	2343	_uc010has.1_RNA	NM_020461	NP_065194	Q96RT7	GCP6_HUMAN			4	CACCCGGGGGC	0.597	
+	11	1513	.K344fs|CNTN6_	NM_014461	NP_055276	Q9UQ52	CNTN6_HUMAN	like C2-type 5.		8	CAGTTAAAAAA	0.393	
+	13	1986_1987	NKTR_uc003clq.1	NM_005385	NP_005376	P30414	NKTR_HUMAN			3	GACAGTCCCCC	0.421	
-	2	303	el_p.K44fs|ANO10	NM_018075	NP_060545	Q9NW15	ANO10_HUMAN	lasmic (Potential).		2	TCCATCTTTTTT	0.408	
+	5	867		NM_016006	NP_057090	Q8WTS1	ABHD5_HUMAN			1	ACTGTAATGTG	0.299	
-	25	4571	e_Site_p.E1361_	NM_053025	NP_444253	Q15746	MYLK_HUMAN			9	GCTCTGGGGG	0.624	rs41431347
-	25	4273		NM_007027	NP_008958	Q92547	TOPB1_HUMAN			7	GCTGGATTTTTT	0.343	
-	8	1759_1761	91DD>D|DBR1_u	NM_016216	NP_057300	Q9UK59	DBR1_HUMAN			0	TGCATCGTCAT	0.251	0114751;rs2622736
+	42	6369_6371	bnz.1_In_Frame_	NM_053002	NP_443728	Q86YW9	MD12L_HUMAN	Gln-rich.		7	GACCCAGCAGC	0.527	
-	2	132_134	ame_Del_p.T35de	NM_024947	NP_079223	Q8NDX5	PHC3_HUMAN	Poly-Thr.		2	Agtggtgatggtggtgg	0.424	
-	2	355	fme.2_Frame_Shif	NM_018622	NP_061092	Q9H300	PARL_HUMAN	rial matrix (Potential).		0	GGTTTATGAGA	0.418	
+	5	690	_p.S38fs|FETUB_	NM_014375	NP_055190	Q9UGM5	FETUB_HUMAN			2	AGTTTCAAAAAA	0.418	
-	15	1909	.N566fs|PROM1_	NM_006017	NP_006008	O43490	PROM1_HUMAN	ellular (Potential).		7	CCTCTATTTTTTT	0.428	
+	16	1633_1634	el_p.R448fs|FIP1L	NM_030917	NP_112179	Q6UN15	FIP1_HUMAN	action with CPSF1 and CS		2	CACCAGAGAGA	0.292	
-	10	1336	ft.1_Frame_Shift_	NM_000204	NP_000195	P05156	CFAI_HUMAN	eptidase S1.		0	AGCAGTCAGAAT	0.418	
+	6	700	SC9_uc003ieb.2_	NM_005033	NP_005024	Q06265	EXOS9_HUMAN	RE binding.		0	TTTGCCTTTTTCC	0.358	
-	14	1840	iii.2_Frame_Shift_	NM_001130675	NP_001124147	O14967	CLGN_HUMAN	lasmic (Potential).		3	TTTTGCTTTTTTT	0.378	
-	8	596_598	3ijz.3_In_Frame_	NM_001102653	NP_001096123	Q01804	OTUD4_HUMAN			3	ACATCAGCAGC	0.34	
-	4	702_704	B2_uc003itb.2_In	NM_001130689	NP_001124161	P26583	HMGB2_HUMAN	Glu-rich (acidic).		0	tcttcttcttcctcctcctc	0.286	
-	14	2587_2589	D2_uc011cmz.1_	NM_001332	NP_001323	Q9UQB3	CTND2_HUMAN	Poly-Lys.		8	TCTTTTTCTTCTT	0.502	
-	27	4142_4143	p.G582fs|MYO10_	NM_012334	NP_036466	Q9HD67	MYO10_HUMAN	PH 1.	.S1226fs*25(	3	GAGGAGCCCCC	0.564	
-	10	1909	10_uc011cnu.1_	NM_006727	NP_006718	Q9Y6N8	CAD10_HUMAN	|Extracellular (Potential).		12	AAACTGAAAAAA	0.313	
+	17	2312_2314	uc003kgi.3_Intron	NM_003248	NP_003239	P35443	TSP4_HUMAN	SP type-3 7.		0	GAGTGTGATGAT	0.562	
+	7	1394		NM_002439	NP_002430	P20585	MSH3_HUMAN			4	GGGACAAAAAAA	0.348	
+	2	237_240	_p.K19fs|AP3S1_	NM_001284	NP_001275	Q92572	AP3S1_HUMAN			0	ATCTAAGAGAGA	0.304	rs80118146
-	1	991_993	Frame_Del_p.E29	NM_020747	NP_065798	Q9ULD9	ZN608_HUMAN	Potential.		6	GGCTCTCCTCC	0.522	
-	22	3471	_Shift_Del_p.R109	NM_016340	NP_057424	Q8TEU7	RPGF6_HUMAN			3	GTGCCCTTTTTT	0.453	
+	9	1679	uc003kwr.3_Intron	NM_003059	NP_003050	Q9H015	S22A4_HUMAN	ame=12; (Potential).		0	TCACCCTTTTTTT	0.418	
+	5	378_379	k.1_Frame_Shift_	NM_006083	NP_006074	Q13123	RED_HUMAN			1	AAATTGAGAGAG	0.46	
-	3	1571	p.P485fs|PCDH1_	NM_002587	NP_002578	Q08174	PCDH1_HUMAN	(Potential).|Cadherin 4.		5	AGAGTGGGGGG	0.532	
+	6	1327_1328	_p.A223fs|LARP1_	NM_033551	NP_291029	Q6PKG0	LARP1_HUMAN			4	CGTGGCCCCC	0.644	
+	5	351	3lvz.3_Frame_Shi	NM_014180	NP_054899	Q9NWU5	RM22_HUMAN			0	ATGACAAAAAAG	0.378	
+	2	128_130	p.L24del|BTN2A2_	NM_006995	NP_008926	Q8WVV5	BT2A2_HUMAN			0	CAGCCTCcctcctc	0.483	
+	1	72_74	2A3_uc011dkm.1_RNA							0	CCTCCCTCCTC	0.586	rs113134648
+	3	618	_Del_p.T206fs|HL	NM_002116	NP_002107	P30443	1A01_HUMAN	ar (Potential).|Alpha-2.		2	CGCACGGGTAC	0.637	rs115073453
+	26	5893	c.3_Frame_Shift_	NM_080686	NP_542417	P48634	PRC2A_HUMAN			0	ACCTACCCCCC	0.522	
-	20	3156	vi.3_Frame_Shift_	NM_004639	NP_004630	P46379	BAG6_HUMAN			0	TACCTGGGGGG	0.532	
+	7	1416	drf.1_Frame_Shift_	NM_002263	NP_002254	Q9BW19	KIFC1_HUMAN	inesin-motor.		0	CTGCCGGGGGA	0.652	rs116903030
-	4	1648	318_uc003ouw.2_	NM_014345	NP_055160	Q5VUA4	ZN318_HUMAN			7	TCGCCTTTTTT	0.493	
+	11	1515	_p.K287fs|C6orf1	NM_001031743	NP_001026913	Q8IYR0	CF165_HUMAN			1	AGGCCAAAAAA	0.269	
+	14	3679	.T1136fs|ARID1B_	NM_017519	NP_059989	Q8NFD5	ARI1B_HUMAN			2	ACAGACCCCCC	0.547	
+	3	945	g.2_Frame_Shift_	NM_006775	NP_006766	Q96PU8	QKI_HUMAN	KH.		2	GGGATAAAAAA	0.363	
-	3	360	P1_uc010ksc.2_I	NM_001031617	NP_001026788	Q49B96	COX19_HUMAN			0	AATTCATTTTTTT	0.463	rs75087611
+	8	2132_2134		NM_138426	NP_612435	Q86VQ1	GLCI1_HUMAN	Poly-Gln.		0	ATCCCAGCAGC	0.562	
+	3	337	rf16_uc011kaf.1_I	NM_006658	NP_006649	O96001	GSUB_HUMAN			3	AGACCAAAAAA	0.438	
+	3	342	_uc011kby.1_Intro	NM_002541	NP_002532	Q02218	ODO1_HUMAN			2	GGACATTTTTTT	0.577	
+	5	1249	_p.P231fs|DTX2_u	NM_020892	NP_065943	Q86UW9	DTX2_HUMAN			2	CCCCCACACAG	0.657	rs147779783

-	2	458		NM_032936	NP_116325	Q9H2L4	TMM60_HUMAN			0	CCAGGCTTTTTT	0.408	
+	13	1828	_p.F530fs|PHTF2_	NM_001127357	NP_001120829	Q8N3S3	PHTF2_HUMAN			1	ATTTTCTTTTTTT	0.303	
-	2	1795	hv.2_Frame_Shift_	NM_033026	NP_149015	Q9Y6V0	PCLO_HUMAN	n approximate repeats of P		7	GGCTGTTGAGA	0.607	
-	5	585		NM_018843	NP_061331	Q8TBP6	S2540_HUMAN	Solcar 1.		1	CTTCTTATACCA	0.323	
-	7	1188	_p.K237fs|CYP51A	NM_000786	NP_000777	Q16850	CP51A_HUMAN			0	ATAACATTTTTTT	0.398	
+	14	1294_1295	_p.Q359fs|CCDC1	NM_017667	NP_060137	Q96JG6	CC132_HUMAN			0	TATGGCAGGTTT	0.272	rs140810598
-	2	390_392	kiw.1_In_Frame_	NM_015545	NP_056360	O75127	PTCD1_HUMAN			1	AACTCTCCTCC	0.606	
-	5	964	2_Intron|GPC2_uc	NM_152742	NP_689955	Q8N158	GPC2_HUMAN			2	GGGGACCCCCC	0.642	
-	6	841	lix.2_Frame_Shift_	NM_014377	NP_055192	Q99543	DNJC2_HUMAN	ZRF1-UBD.		1	GGAACATTTTTT	0.234	
-	2	110	3vey.2_Frame_Sh	NM_007356	NP_031382	A4D0S4	LAMB4_HUMAN			8	GGTGCAAAAAA	0.308	
+	1	528		NM_001001656	NP_001001656	Q8NGU2	OR9A4_HUMAN	ellular (Potential).		1	GAACAATTTTTT	0.383	
-	3	341		NM_001103176	NP_001096646	Q3B7I2	CNPY1_HUMAN			0	CTCCTGGGCGA	0.443	
-	4	4130_4131		NM_178857	NP_849188	Q8IWN7	RP1L1_HUMAN			8	ATTGCACCTCTT	0.297	
-	9	1257	119fs|MTMR7_uc	NM_004686	NP_004677	Q9Y216	MTMR7_HUMAN	se.|Substrate binding (By s		1	GCCATCAGAAC	0.552	
-	15	2035		NM_001010906	NP_001010906	Q68CJ6	SLIP_HUMAN			2	AGGAAATTTTTT	0.453	
-	9	1343_1344		NM_152413	NP_689626	Q8NHS2	AATC2_HUMAN			1	TCAGTGTTTTTT	0.371	
+	9	940_941	M9_uc011lcg.1_R	NM_003816	NP_003807	Q13443	ADAM9_HUMAN	otential).|Peptidase M12B.		2	AGTGGCGGGAA	0.376	
-	60	8167	Shift_Del_p.R2704	NM_006904	NP_008835	P78527	PRKDC_HUMAN	KIP-binding.		34	CCAGCCTTTTTT	0.498	
+	4	614		NM_000067	NP_000058	P00918	CAH2_HUMAN			1	TAGGTATTTTTTT	0.388	
-	3	534_536	f.2_Intron|TP53IN	NM_033285	NP_150601	Q96A56	T53I1_HUMAN	Glu-rich.		0	CCTCCTCTTCTT	0.458	
-	8	1503	_Shift_Del_p.K28	NM_002568	NP_002559	P11940	PABP1_HUMAN	RRM 4.		0	AACCCTTTGCT	0.383	rs112966887
-	3	363_367	yqd.2_Frame_Shi	NM_032847	NP_116236	Q96K31	CH076_HUMAN			2	CAGCGCCTCCA	0.424	
-	13	1637_1639	.I506del|TSNARE	NM_145003	NP_659440	Q96NA8	TSNA1_HUMAN	.|Helical; (Potential).		0	TGGCGATGATG	0.414	rs142964918
-	5	724_726	e_Del_p.152_153	NM_004529	NP_004520	P42568	AF9_HUMAN	Poly-Ser.		3	tgctgctactgctgctgc	0.148	
-	2	633		NM_005384	NP_005375	Q16649	NFIL3_HUMAN	Basic motif.		0	CCGCCTTTTTTC	0.423	
-	4	884_886	Del_p.E251del|EC	NM_001393	NP_001384	O94769	ECM2_HUMAN	Poly-Glu.		2	cctcctcatcctcctcct	0.399	rs137929518
-	3	128_129	_Shift_Ins_p.K34f	NM_016390	NP_057474	Q5T280	CI114_HUMAN			0	CTTCCATTTTTT	0.525	
+	6	1019_1020	Shift_Del_p.Q191f	NM_018360	NP_060830	Q9NUQ3	TXLNG_HUMAN	Potential.		1	ACATCAGAGAGA	0.386	
+	5	647	ddo.2_Frame_Shif	NM_000950	NP_000941	O14668	TMG1_HUMAN	ic (Potential).|Poly-Pro.		2	CCCCACCCCCC	0.488	
-	18	2564_2566	sw.2_In_Frame_	NM_015107	NP_055922	Q9UPP1	PHF8_HUMAN			3	CGTTCTCCTCC	0.591	
-	6	725	_p.L144fs|OPHN1_	NM_002547	NP_002538	O60890	OPHN1_HUMAN			2	TCCAGTAAAGAA	0.413	
-	38	4617_4618	e_Shift_Del_p.L11	NM_153252	NP_694984	Q6RI45	BRWD3_HUMAN			4	TTCTTAGACGTT	0.361	
+	5	716_718	04eib.1_In_Frame_	NM_016607	NP_057691	Q9UH62	ARMX3_HUMAN			2	TGGTCTGATGAT	0.448	
-	3	383	_Shift_Del_p.K95f	NM_002814	NP_002805	O75832	PSD10_HUMAN	n with RELA.|ANK 3.		1	GCACCTTTTCC	0.453	
+	2	310_311	_5'Flank|LOC100	NM_001152	NP_001143	P05141	ADT2_HUMAN	Solcar 1.		1	GAGCAGGGAG	0.49	rs113356560
+	6	1104_1106	4ezx.2_In_Frame_	NM_001163280	NP_001156752	O43719	HTSF1_HUMAN	Poly-Lys.		3	CTCAAAGAAGA	0.335	
+	4	1210_1212	EC1_uc010nsl.1_	NM_005462	NP_005453	O60732	MAGC1_HUMAN			4	TGAGCTCCTCC	0.483	660605;rs141900922
-	2	1111_1113	wne.1_In_Frame_	NM_007113	NP_009044	Q07283	TRHY_HUMAN	of R-R-E-Q	NA	5	tcgcgcctctcctcctcc	0	rs71757496
+	7	1104	ucl.1_Frame_Shift	NM_001211	NP_001202	O60566	BUB1B_HUMAN		NA	4	TAGCACCCCCC	0.478	
+	3	3566	n.1_Frame_Shift_	NM_030665	NP_109590	Q7Z5J4	RAI1_HUMAN		NA	2	CAGGGCCCCCC	0.697	
-	2	210	199_uc002hba.2_	NM_015584	NP_056399	Q9Y2S7	PDIP2_HUMAN		NA	0	GGCTTTGCCACC	0.762	rs113730440
-	16	2136	_Shift_Del_p.H700	NM_032108	NP_115484	Q9H3T3	SEM6B_HUMAN	lasmic (Pote	NA	1	GTCGTGGGGCC	0.701	
-	2	1021_1023	.2_In_Frame_Del_	NM_002192	NP_002183	P08476	INHBA_HUMAN		NA	6	ctcctcttctttcttcttcttc	0.355	
+	9	2353_2354	hift_Ins_p.H537fs	NM_015570	NP_056385	Q8WXX7	AUTS2_HUMAN	His-rich.	NA	3	caccagcacacgcacc	0.51	
+	14	1576_1588	.W382fs|POMT1_	NM_007171	NP_009102	Q9Y6A1	POMT1_HUMAN	MIR 3.	NA	1	AAGACCATCCT	0.451	
-	2	1659_1661	.2_In_Frame_Del_	NM_173691	NP_775962	Q4KMQ1	TPRN_HUMAN	Glu-rich.	NA	0	tcttcctcttcctcctcctc	0.374	
-	1	702_704		NM_001080418	NP_001073887	O95886	DLGP3_HUMAN	Poly-His.	NA	3	CCGGGACtggtggt	0.537	

-	4	1248_1250	IP1_uc010oid.1_R	NM_024700	NP_078976	Q8TAD8	SNIP1_HUMAN	Poly-Glu.	NA	2	AGACACTTCTTC	0.453	
-	3	841		NM_003921	NP_003912	O95999	BCL10_HUMAN	CARD.	NA	2	TGAGTATTTTTTT	0.343	
-	9	1232	Shift_Del_p.M408	NM_005665	NP_005656	O60447	EVI5_HUMAN	Interaction w	NA	2	TTTTCATTTTTTT	0.318	
-	59	4728	K1482fs|COL11A1	NM_001854	NP_001845	P12107	COBA1_HUMAN	le-helical reg	NA	12	GTCACCTTTTTC	0.403	
+	2	267_269	.E40del|HAX1_uc	NM_006118	NP_006109	O00165	HAX1_HUMAN	ed for localiz	NA	0	TGAGGAAGAAG	0.522	rs11556342
+	4	474	hpl.2_Frame_Shift	NM_001136018	NP_001129490	P07099	HYEP_HUMAN		NA	4	TGAAGCCCCCC	0.627	
-	2	955_957	2_uc001mak.1_Ir	NM_017481	NP_059509	Q9H347	UBQL3_HUMAN		NA	3	TGGCTGGTGGT	0.537	rs2234451
-	4	499_501	p.D92del|IFT46_u	NM_020153	NP_064538	Q9NQC8	IFT46_HUMAN	-rich (highly	NA	0	CAGATGAatcatcat	0.424	
-	11	3063_3064	p.E611fs|SFRS2IP	NM_004719	NP_004710	Q99590	SCAFB_HUMAN	Arg-rich.	NA	0	TCCTTTCTCTCT	0.446	
+	7	948_950	.L125del|SLC39A	NM_173596	NP_775867	Q6ZMH5	S39A5_HUMAN	lasmic (Pote	NA	2	TATCCCTGCTGC	0.635	
+	8	1314	C3_uc009zsm.2_	NM_181783	NP_861448	Q6ZXV5	TMTC3_HUMAN	ical; (Potent	NA	1	CGAACCTTTTTT	0.303	
+	18	2223	aba.2_Frame_Shif	NM_130806	NP_570718	Q8WXD0	RXFP2_HUMAN	lasmic (Pote	NA	0	AAAATTAAAAAAA	0.348	
+	1	314_316	1vbk.2_In_Frame_	NM_015116	NP_055931	Q9Y2L9	LRCH1_HUMAN	His-rich.	NA	2	TCATCCccaccacc	0.409	
+	3	707_710	vbk.2_Frame_Shi	NM_015116	NP_055931	Q9Y2L9	LRCH1_HUMAN	LRR 3.	NA	2	CCGCCCTGCCTG	0.436	
+	16	4738_4740	1xmv.2_In_Frame	NM_015556	NP_056371	O43166	SI1L1_HUMAN	Ser-rich.	NA	4	tcctcctcttcctcctcctc	0.468	
-	2	1567_1569	orf43_uc010tud.1_	NM_194278	NP_919254	Q6PJG2	CN043_HUMAN	-rich.|Gln-ri	NA	5	GGgctgcctgctgctg	0.473	
-	3	499	ybp.2_Intron|BTB	NM_001002860	NP_001002860	Q9P203	BTBD7_HUMAN		NA	1	GTTCTCTTTTTTT	0.438	
-	9	996_998	.E123del|VPS33B_	NM_018668	NP_061138	Q9H267	VP33B_HUMAN		NA	2	GCCATCCTCCT	0.522	rs147271815
+	13	3813_3815		NM_014712	NP_055527	O15047	SET1A_HUMAN	Ser-rich.	NA	3	Gctcctcatcctcctcct	0.389	
-	10	1079_1081	63EE>E|C17orf85	NM_001114118	NP_001107590	Q53F19	CQ085_HUMAN	Glu-rich.	NA	1	tcttcctcttcctcctcctc	0.379	
-	1	71	ank|SDF2_uc002h	NM_006923	NP_008854	Q99470	SDF2_HUMAN		NA	0	CACAAACCCCCC	0.582	
+	1	158_160	me_Del_p.K7del|	NM_003457	NP_003448	O43670	ZN207_HUMAN		NA	0	TCGCAAGAAGA	0.542	
-	6	825_826	2iam.1_Frame_Sh	NM_178126	NP_835227	Q86VR2	F134C_HUMAN		NA	2	CATTGTCTCTCT	0.515	
-	9	1623_1625		NM_133373	NP_588614	Q8N3E9	PLCD3_HUMAN		NA	3	cctcgtcatcctcctcctc	0.527	
+	1	140_142		NM_003811	NP_003802	P41273	TNFL9_HUMAN	r for type II	NA	1	TCGCGGGgctgctg	0.66	
+	11	1321	xom.1_Frame_Shi	NM_000896	NP_000887	Q08477	CP4F3_HUMAN		NA	3	TCAGTGTTTTTGC	0.622	
+	16	3826	.V1000fs|NWD1_uc002nev.3_Frame_Shift_Del_p.V92			Q149M9	NWD1_HUMAN	WD 8.	NA	7	CGGCTGTTTTTG	0.552	
+	2	252_254	eea.2_In_Frame_	NM_005306	NP_005297	O15552	FFAR2_HUMAN	Name=2; (P	NA	1	CCTCCTGCTGC	0.645	
-	15	2287_2289		NM_014709	NP_055524	Q70CQ2	UBP34_HUMAN		NA	19	gtggtgatggtggtggt	0.281	
-	14	2158	_p.K662fs|ZMYND	NM_012408	NP_036540	Q9ULU4	PKCB1_HUMAN		NA	5	TTGGGCTTTTTT	0.488	
-	32	3210_3211		NM_014258	NP_055073	Q9BX26	SYCP2_HUMAN		NA	5	TTTATAGTTTTTT	0.327	
-	7	789_791		NM_016449	NP_057533	Q6PGQ1	CV043_HUMAN	Asp-rich.	NA	1	CCTGGGcatcatc	0.261	
+	7	600	p.S151fs|APPL1_	NM_012096	NP_036228	Q9UKG1	DP13A_HUMAN	for RAB5A	NA	1	TTTATCAAAAAA	0.299	
-	8	1092	py.2_Frame_Shift_	NM_004454	NP_004445	P41161	ETV5_HUMAN		NA	5	GTGCTGGGGGC	0.547	
-	3	541_543		NM_024524	NP_078800	Q9H7F0	AT133_HUMAN	ical; (Potent	NA	1	AATAGAGGAGG	0.463	
+	11	1711	nl.1_Frame_Shift_	NM_182485	NP_872291	Q7Z5Q1	CPEB2_HUMAN		NA	1	CTCCCTTTTTTT	0.443	
-	13	2807_2809	11ckv.1_In_Frame	NM_021069	NP_066547	O94875	SRBS2_HUMAN	His-rich.	NA	1	Aggtggcggtggtggt	0.384	
+	13	1713_1714	_p.K518fs|PAPD7_	NM_006999	NP_008930	Q5XG87	PAPD7_HUMAN		NA	1	AAAAAACACACA	0.653	
+	10	2300	p.K601fs|NIPBL_u	NM_133433	NP_597677	Q6KC79	NIPBL_HUMAN		NA	9	ACACCTAAAAAA	0.353	
-	2	331_333	e_Del_p.46_47EE	NM_003472	NP_003463	P35659	DEK_HUMAN	-rich (highly	NA	1	ACCTTTTtcctcctc	0.365	
+	8	1034_1035	1dpb.1_Frame_Shift_Ins_p.V276fs			P08686	CP21A_HUMAN		NA	0	CCGTGGTTTTTT	0.614	
-	3	477	LC17A5_uc011dy	NM_012434	NP_036566	Q9NRA2	S17A5_HUMAN	ical; (Potent	NA	6	GCCATAAAAAAA	0.423	
-	3	577_578	11ebw.1_Frame_S	NM_033515	NP_277050	Q8N392	RHG18_HUMAN		NA	3	TGTTTGTTTTTT	0.421	
+	11	1744		NM_152744	NP_689957	Q7Z5N4	SDK1_HUMAN	like C2-type	NA	6	GAATCGGGGGG	0.542	
-	2	601_602		NM_022728	NP_073565	Q96NK8	NDF6_HUMAN	lization sign	NA	2	GTTGTCTTTTTT	0.396	
-	2	1021_1023	.2_In_Frame_Del_	NM_002192	NP_002183	P08476	INHBA_HUMAN		NA	6	ctcctcttctttcttcttctt	0.355	
+	9	1443	3tvz.2_Frame_Sh	NM_022479	NP_071924	Q6IS24	GLTL3_HUMAN	ectin.|Lumer	NA	7	GACCAGGGGCC	0.532	

-	2	83_85	_uc010lbj.1_In_Fr	NM_004603	NP_004594	Q16623	STX1A_HUMAN	lasmic (Pot	NA	0	AGCGACATCATC	0.586	
+	1	1295_1297	.1_5'Flank|ZCWP	NM_019606	NP_062552	Q7L2J0	MEPCE_HUMAN		NA	1	GCCGCCACCAC	0.581	rs71555278
+	8	1077_1079	xa.2_In_Frame_D	NM_015908	NP_056992	Q9BXP5	SRRT_HUMAN	Glu-rich.	NA	2	GAGCAGGAGGA	0.596	
+	4	1653_1654	_Intron|FBXL13_	NM_001031692	NP_001026862	Q8N6Y2	LRC17_HUMAN		NA	1	AATGGGAAAAA	0.337	
-	3	838_842	vja.2_Frame_Shift	NM_003391	NP_003382	P09544	WNT2_HUMAN		NA	7	TCTGGCAtcctttcc	0.424	
+	6	1464	.P226fs|ZNF398_	NM_170686	NP_733787	Q8TD17	ZN398_HUMAN		NA	1	AGACACCCCCC	0.587	
-	2	129	hift_Del_p.N23fs|	NM_004935	NP_004926	Q00535	CDK5_HUMAN	rotein kinas	NA	2	CCCGGTTTTTG	0.582	
+	1	793_795		NM_138400	NP_612409	Q5C9Z4	NOM1_HUMAN	ization and	NA	0	gaaagtgaggaggag	0.236	
+	12	1731	DR60_uc010lqw.2	NM_018051	NP_060521	Q8WVS4	WDR60_HUMAN		NA	4	TTGGGAAAAAA	0.328	
-	16	3521_3523	.E993del|MYST3_	NM_001099412	NP_001092882	Q92794	MYST3_HUMAN	Poly-Glu.	NA	7	CCGGCTCCTCC	0.567	
+	10	1740	LF1_uc003xyf.2_F	NM_015170	NP_055985	Q8IWU6	SULF1_HUMAN		NA	7	TGTGCCTTTTTT	0.408	
+	27	3072_3073	gr.1_RNA|INTS8_	NM_017864	NP_060334	Q75QN2	INT8_HUMAN		NA	0	AGAAGGAAAAA	0.332	
+	2	1053	3zvv.2_Frame_Shi	NM_203299	NP_976044	Q5VYM1	CI131_HUMAN		NA	0	TGCCACCCCCC	0.527	
-	2	633		NM_005384	NP_005375	Q16649	NFIL3_HUMAN	Basic motif.	NA	0	CCGCCTTTTTC	0.423	
+	14	1576_1588	.W382fs|POMT1_	NM_007171	NP_009102	Q9Y6A1	POMT1_HUMAN	MIR 3.	NA	1	AAGACCATCCT	0.451	
-	1	160_162	z.2_In_Frame_D	NM_020871	NP_065922	Q5VUJ6	LRCH2_HUMAN	Gly-rich.	NA	1	AGGGTCccgccgc	0.34	rs111707157
-	2	574_575	P_uc004esg.2_5'	NM_024528	NP_078804	Q8N5F7	NKAP_HUMAN		NA	2	CCAATTCTCTCT	0.317	
+	2	555	cr.2_Frame_Shift_	NM_002025	NP_002016	P51816	AFF2_HUMAN		NA	5	CACTTAAAAAAA	0.378	
-	4	1243_1245	IP1_uc010oid.1_R	NM_024700	NP_078976	Q8TAD8	SNIP1_HUMAN	Poly-Glu.		2	TTCTTCCTCCT	0.448	
+	3	634	ne_Shift_Del_p.Y4	NM_003672	NP_003663	Q9UNH5	CC14A_HUMAN	A.		1	GTTTCTATGCAG	0.284	
-	4	796	pj.2_Frame_Shift_	NM_001461	NP_001452	P49326	FMO5_HUMAN			3	TCTCCTTTTTCC	0.473	
-	2	4369_4370	.1_In_Frame_Ins_	NM_007113	NP_009044	Q07283	TRHY_HUMAN	proximate tandem repeats.		5	CTCCTGGCGC	0.564	
-	2	3480_3482	ne.1_In_Frame_	NM_007113	NP_009044	Q07283	TRHY_HUMAN	0 AA tandem repeats.		5	CCTTCTCTTCT	0.172	
+	20	6213	A2_uc009www.2_	NM_020318	NP_064714	Q9BXP8	PAPP2_HUMAN	Sushi 5.		16	GTAATCCCCCC	0.468	
+	7	1345	_p.K95fs|FAM5B_	NM_021165	NP_066988	Q9C0B6	FAM5B_HUMAN			6	TGCTGAAAAGG	0.592	
-	1	369	K2_uc010pqs.1_F	NM_018208	NP_060678	Q9NVF9	EKI2_HUMAN			2	AGGTGAAAGGA	0.672	
-	15	2268		NM_001618	NP_001609	P09874	PARP1_HUMAN	P alpha-helical.		10	AGCTTCCCCAA	0.597	
+	1	408	L13_uc001ids.2_I	NM_001004686	NP_001004686	Q8NH16	OR2L2_HUMAN	Name=3; (Potential).		3	TTCTTGACTTTA	0.308	
+	5	1149	ZNF365_uc001jlz.	NM_014951	NP_055766	Q70YC4	TALAN_HUMAN			2	ACCTGAAAAAG	0.567	
-	4	1313	p.S264fs|FAM53B_	NM_014661	NP_055476	Q14153	FA53B_HUMAN			2	GCGGGAAAGGC	0.572	
-	25	4223	.N1311fs|NUP98_	NM_016320	NP_057404	P52948	NUP98_HUMAN			12	GGCTGTTTTTT	0.512	
-	2	491_492		NM_003737	NP_003728	Q96JQ0	PCD16_HUMAN			5	agcagcagcagcagc	0.52	
+	1	84_85	rf80_uc001ojh.2_	NM_024650	NP_078926	Q8N6T0	CK080_HUMAN			0	AGGAGGGggcgg	0.569	
+	5	552	rf54_uc001peh.2_	NM_014039	NP_054758	Q9H0W9	CK054_HUMAN			0	TAAACCAAAAAA	0.353	
+	3	1103		NM_018039	NP_060509	Q6B0I6	KDM4D_HUMAN	Poly-Lys.		0	TACCATAAAAAAA	0.453	
-	17	3723_3726	vv.1_Frame_Shift_	NM_002519	NP_002510	Q14207	NPAT_HUMAN			2	TTTTGGTCATTT	0.358	
-	10	1165	_p.G89fs|TMPRSS	NM_030770	NP_110397	Q9H3S3	TMPS5_HUMAN	.|Extracellular (Potential).		1	TGTGGCCCCAG	0.652	
-	4	745_747	.1_Intron|PRB1_u	NM_005039	NP_005030	P04280	PRP1_HUMAN	-P-[PAQ]-Q-[GE]-[GD]- [N		0	TCCTGGAGGAG	0.611	
-	4	562_564	.1_Intron|PRB1_u	NM_005039	NP_005030	P04280	PRP1_HUMAN	[PAQ]-Q-[GE]-[GD]- [NKS]-		0	TCCTGGAGGAG	0.606	
-	3	441_442	.1_Intron|PRB1_u	NM_005039	NP_005030	P04280	PRP1_HUMAN	-[PAQ]-Q-[GE]-[GD]- [NKS]		0	TTTCCTGGAGGT	0.604	
-	3	626_628		NM_006248	NP_006239					0	TCCTGGAGGAG	0.591	
-	2	149_151	5'UTR|CASC1_uc	NM_001082973	NP_001076442	Q6TDU7	CASC1_HUMAN	Glu-rich.		2	GTCTCTCCTCC	0.365	
-	8	3259_3261	224YQ>*|NCKAP5	NM_001037806	NP_001032895	Q9HCH0	NCK5L_HUMAN			1	ACCTTGGTACA	0.66	
+	1	298		NM_001005497	NP_001005497	A6NL08	O6C75_HUMAN	Name=3; (Potential).		3	CAGCTATTTTTT	0.438	
+	3	227	nk|MARS_uc001s	NM_004990	NP_004981	P56192	SYMC_HUMAN			5	CAGATATTTTTT	0.488	
-	13	2872		NM_024312	NP_077288	Q3T906	GNPTA_HUMAN			2	AAATACTTTTTTT	0.353	
-	9	807	e_Shift_Del_p.Q5	NM_138341	NP_612350	Q8NCL8	TM116_HUMAN			1	AGTTTTGGAAAC	0.368	

-	8	694	E2_uc001ume.2_Ir	NM_199254	NP_954863	Q6XPS3	TPTE2_HUMAN	ical; (Potential).		0	AATGTCAAAAAAA	0.303	
+	18	2222_2223	aba.2_Frame_Shi	NM_130806	NP_570718	Q8WXD0	RXFP2_HUMAN	lasmic (Potential).		0	AAAATTAAAAAAA	0.351	
+	2	318		NM_015678	NP_056493	Q8NFP9	NBEA_HUMAN			11	cggcaccgggggcag	0.557	
-	29	3774	BCC4_uc010afk.2	NM_005845	NP_005836	O15439	MRP4_HUMAN	C transporter 2.		4	CCCGGATTTTTTT	0.378	
+	1	371	M_uc010agc.2_In	NM_000123	NP_000114	P28715	ERCC5_HUMAN			7	AATCTATAAAACT	0.428	
-	2	376	1wrg.1_5'UTR|HE	NM_015473	NP_056288	Q86XA9	HTR5A_HUMAN			1	ACTTTCTTTAGCT	0.373	
+	2	609	3C_uc001wss.2_5	NM_014672	NP_055487	O15091	MRRP3_HUMAN			0	TCCTCATTTTTTT	0.423	
-	16	3454	cvw.2_Frame_Shi	NM_004380	NP_004371	Q92793	CBP_HUMAN		p.I1084fs*15(1	127	GCCTACTTTTTTT	0.398	
+	7	1037_1039	.K238del|UBN1_u	NM_001079514	NP_001072982	Q9NPG3	UBN1_HUMAN	Lys-rich.		2	TAAGGAGAAGAA	0.453	
-	6	570_571	dxx.2_5'UTR|SEP	NM_052838	NP_443070	Q8WYJ6	SEPT1_HUMAN			1	TGGATGTTCTTC	0.594	
+	3	278_280	vho.1_In_Frame_	NM_020312	NP_064708	O75208	COQ9_HUMAN			1	CGGCGAGGAGG	0.576	rs149029279
+	8	752	.A123fs|LGALS9_	NM_009587	NP_033665	O00182	LEG9_HUMAN			0	ACTCCCGCCATC	0.587	
-	14	1854	itf.2_Frame_Shift_	NM_001130528	NP_001124000	O60271	JIP4_HUMAN			5	TTGACCTTTTTTT	0.323	
+	1	434	1D_uc010ddm.1_	NM_003620	NP_003611	O15297	PPM1D_HUMAN	with CHEK1.|PP2C-like.		1	GGTGGCAGCCC	0.522	
+	1	455_457	E138del|BPTF_uc	NM_182641	NP_872579	Q12830	BPTF_HUMAN			4	GAGAGCgaggagg	0.384	
-	20	2662	1_uc002jzo.1_Fra	NM_014984	NP_055799	Q9UPN4	AZI1_HUMAN			4	GCCTCAGCTCT	0.662	
-	8	855		NM_005570	NP_005561	P49257	LMAN1_HUMAN			1	GTGGGCTTTTTTT	0.294	
-	5	625_626	Shift_Del_p.A42fs	NM_016368	NP_057452	Q9NPH2	INO1_HUMAN			2	TTGTCCGCGCG	0.644	
-	6	472	_p.P16fs|C19orf47	NM_178830	NP_849152	Q8N9M1	CS047_HUMAN			2	CGCCTGGGGGG	0.612	
-	1			NM_002516	NP_002507	Q9UNW9	NOVA2_HUMAN			0	CTCCATGGGGG	0.401	
+	2	1058		NM_002030	NP_002021	P25089	FPR3_HUMAN	Name=7; (Potential).		6	TTGGCCTTTTTTA	0.428	
-	32	4507		NM_004850	NP_004841	O75116	ROCK2_HUMAN			4	GAGCTGGGGG	0.438	
-	2	718	2rqx.2_Splice_Site	NM_138394	NP_612403	Q8WVV9	HNRLL_HUMAN			1	ATCCTTACCATAT	0.408	
+	1	202	fez.1_Frame_Shift	NM_144993	NP_659430	O43151	TET3_HUMAN			0	GTGGCCTTTTCG	0.607	
-	2	111	r.2_Intron|DOK1_	NM_032603	NP_115992	P58215	LOXL3_HUMAN			0	AGCAGCCCCCA	0.557	
-	27	5465	uc002udp.2_Intron	NM_002977	NP_002968	Q15858	SCN9A_HUMAN	IV.		13	ATGAACTTTTTTT	0.423	
+	8	1077_1079	AJC10_uc002uoz.	NM_018981	NP_061854	Q8IXB1	DJC10_HUMAN	hioredoxin 1.		4	CAGATCAAAGGA	0.32	
-	6	598_600	gdo.1_In_Frame_	NM_025176	NP_079452	Q9Y2I6	NINL_HUMAN			5	GGTCTGCAGCTG	0.429	
-	15	1983	e|RBL1_uc002xgj.	NM_002895	NP_002886	P28749	RBL1_HUMAN			10	GCATATCtaaaaaa	0.282	
+	1	368_369	xjf.2_In_Frame_In	NM_030919	NP_112181	Q9H4H8	FA83D_HUMAN			3	GGAGGGCgcggc	0.619	
+	16	2099	T10_uc010hfv.1_	NM_015442	NP_056257	Q9H9A5	CNOTA_HUMAN			2	AGGATCAGACA	0.368	
+	13	3220_3222	|NKTR_uc003clq.	NM_005385	NP_005376	P30414	NKTR_HUMAN			3	TGAAGAGGAGG	0.355	
-	2	584_586		NM_016206	NP_057290	A8MV65	VGLL3_HUMAN			0	TGGtctttctcctcctc	0.394	
-	4	709	me_Shift_Del_p.A	NM_178824	NP_849146	Q8IV35	WDR49_HUMAN			3	CATTGCCAACA	0.408	
-	2	5455	C4_uc003fvp.2_In	NM_018406	NP_060876	Q99102	MUC4_HUMAN			0	ACAGGAAGAGG	0.587	
-	2	2132	vp.2_Intron|MUC4	NM_018406	NP_060876	Q99102	MUC4_HUMAN			0	CTGTTGTTTTTG	0.547	
-	3	1028	168_uc010iah.2_5	NM_152617	NP_689830	Q8IYW5	RN168_HUMAN	Glu-rich.		0	TTCGCCTTTTTTC	0.448	
-	2	838_839	uc003hei.1_Intron	NM_001073	NP_001064	O75310	UDB11_HUMAN			3	CTCCAACAAAAT	0.391	
+	1	71		NM_001133	NP_001124	P43652	AFAM_HUMAN			3	TTCTTGTTTTTTT	0.313	rs145217978
+	5	949_950	p.Y271fs|ADAMT	NM_139056	NP_620687	Q8TE57	ATS16_HUMAN			8	GATGAGTATAAGT	0.48	
+	13	1510_1512	.E383del|PAM_uc	NM_000919	NP_000910	P19021	AMD_HUMAN	ooxygenase (By similarity)		0	AACGAGAAGAA	0.325	
-	1	94_96	29506_uc010jfe.2_	NM_016459	NP_057543	Q8WU39	PERP1_HUMAN			0	GGCTCCcagcagca	0.527	
-	7	1054	M26_uc010jry.2_5	NM_003449	NP_003440	Q12899	TRI26_HUMAN			3	CCGGTCTTTTTTT	0.483	
+	1	184_185	_uc003nyt.2_5'UT	NM_032454	NP_115830	P49842	STK19_HUMAN			4	GCGGGCAAACC	0.634	
-	5	1557_1559	6_377EE>E|DAX	NM_001350	NP_001341	Q9UER7	DAXX_HUMAN	ial.|Necessary for interactio		23	tcttcttcttcctcctcctc	0.251	
-	1	195_197	ob.1_In_Frame_D	NM_145331	NP_663304	O43318	M3K7_HUMAN	Poly-Ser.		6	AGACGAGGAGG	0.655	
+	2	481		NM_001198	NP_001189	O75626	PRDM1_HUMAN		p.?(1)	56	GCATCCTTACCA	0.498	

+	3	337	rf16_uc011kaf.1_I	NM_006658	NP_006649	O96001	GSUB_HUMAN		3	AGACCAAAAAA	0.438	
-	2	382	LM_uc003tka.1_5	NM_013284	NP_037416	Q9NP87	DPOLM_HUMAN	BRCT.	3	GAGCTGGGGGG	0.637	
-	2	458		NM_032936	NP_116325	Q9H2L4	TMM60_HUMAN		0	CCAGGCTTTTTT	0.408	
-	7	12205	p.P3972fs|PCLO_	NM_033026	NP_149015	Q9Y6V0	PCLO_HUMAN		7	TATCTTGGGCTC	0.423	
+	3	535	hift_Del_p.V114fs	NM_000602	NP_000593	P05121	PAI1_HUMAN		3	CTGGTCCAGGG	0.567	
-	20	2915	_p.P781fs|TNPO3	NM_012470	NP_036602	Q9Y5L0	TNPO3_HUMAN		5	GTATAGGGGGG	0.483	
-	5	4079_4081		NM_001080826	NP_001074295	Q86YV5	SG223_HUMAN		0	AAACTTCATCAT	0.675	
+	3	299_300	.72fs|ADAM28_uc	NM_014265	NP_055080	Q9UKQ2	ADA28_HUMAN		5	TATTTGAAAAAA	0.332	
+	19	2164	ame_Shift_Del_p.I	NM_052832	NP_439897	Q8TE54	S26A7_HUMAN	toplasmic (Potential).	2	AACCAATTTTTT	0.343	
-	23	3681_3682	.K981fs|RGS22_	NM_015668	NP_056483	Q8NE09	RGS22_HUMAN	Potential.	7	TGCCAATTTTTT	0.312	rs7841915
-	5	777_778	p.G144fs|CRAT_u	NM_000755	NP_000746	P43155	CACP_HUMAN		1	TGGCTTCCCCC	0.609	
+	4	514	uc004bxn.1_Intron	NM_178001	NP_821068	Q15257	PTPA_HUMAN		3	aaaggagcaggctgc	0.154	
+	1	788	ix.1_Frame_Shift_	NM_198270	NP_938011	Q6T4R5	NHS_HUMAN		7	CTCTTCCAGGA	0.692	
-	1	573_574	33A_uc004efr.1_5	NM_004538	NP_004529	Q99457	NP1L3_HUMAN		2	CGGGGCCCGC	0.386	
+	4	1067_1069	1mrt.1_In_Frame_	NM_001142526	NP_001135998	Q6PI77	BHLH9_HUMAN	Poly-Glu.	2	GGCTGAGGAGG	0.488	
+	3	557_558	ekm.2_Frame_Sh	NM_024863	NP_079139	Q96EI5	TCAL4_HUMAN	Glu-rich.	0	gaggatcagagagag	0.144	
+	17	2287	p.A621fs|SCNN1	NM_002978	NP_002969				0	CTTCTGCCCTC	0.701	
-	23	2999_3000	vqd.2_Frame_Shif	NM_005529	NP_005520	P98160	PGBM_HUMAN	inin IV type A 2.	9	AGGGTCCAGATA	0.396	
-	17	2052	wdz.2_Frame_Shif	NM_194292	NP_919268	Q6UVJ0	SAS6_HUMAN		2	GGTTTGGAAGA	0.388	
+	10	2124	ova.1_Frame_Shif	NM_001144937	NP_001138409	Q5VTL7	FNDC7_HUMAN	nectin type-III 8.	2	TGTCCAAAAAA	0.363	
+	7	1724_1726	e_Del_p.E466del|	NM_005807	NP_005798	Q92954	PRG4_HUMAN	epeats of K-X-P-X-P-T-T-X	1	ACCAAGGAGCC	0.635	
-	4	459_460	mp.3_Frame_Shi	NM_138789	NP_620144	Q8WWB5	PIHD2_HUMAN		1	AACTGATTTTTT	0.376	
-	7	2967	_Shift_Del_p.Q25	NM_014758	NP_055573	Q92543	SNX19_HUMAN		4	GTCTTGGGCTG	0.562	
-	20	2170	_5'Flank|DDX12_	NM_004400	NP_004391				0	GGGCAGGATGT	0.572	
-	4	745_747	.1_Intron|PRB1_u	NM_005039	NP_005030	P04280	PRP1_HUMAN	-P-[PAQ]-Q-[GE]-[GD]- [N	0	TCCTGGAGGAG	0.611	
-	3	441_442	.1_Intron|PRB1_u	NM_005039	NP_005030	P04280	PRP1_HUMAN	-[PAQ]-Q-[GE]-[GD]- [NKS]	0	TTTCCTGGAGGT	0.604	
-	4	372	_p.E78fs|RERG_u	NM_032918	NP_116307	Q96A58	RERG_HUMAN		1	GCCTTCCCCCC	0.458	
+	4	1266	xex.3_Frame_Shi	NM_021003	NP_066283	P35813	PPM1A_HUMAN		1	GATTTTGATCTG	0.403	
-	4	714	1xqc.2_Frame_Sh	NM_001039479	NP_001034568	O15033	K0317_HUMAN	Filamin.	5	ACCTCATAGGGG	0.557	
+	1	1107_1108	_5'Flank|TMED8_	NM_001010860	NP_001010860	Q9P1V8	SAM15_HUMAN		0	AATGAGAAAAAA	0.386	1283439;rs4903576
+	13	1457_1459	atj.2_In_Frame_D	NM_198309	NP_938051	Q8TAM2	TTC8_HUMAN	TPR 7.	0	TGGTCAACAAC	0.537	
-	1	65	rf102_uc001xyj.1_	NM_017970	NP_060440	Q9H7Z3	CN102_HUMAN		3	AGCCTCACTAA	0.627	
+	6	2496	.Q354fs|NFAT5_u	NM_006599	NP_006590	O94916	NFAT5_HUMAN	RHD.	0	CACTGCAAACA	0.378	
+	6	508_509	p.W26fs|STXBP4_	NM_178509	NP_848604	Q6ZWJ1	STXB4_HUMAN	PDZ.	1	CTGCTTGGGAG	0.337	
-	4	506	_p.N137fs|EXOC7	NM_001145297	NP_001138769	Q9UPT5	EXOC7_HUMAN		0	ACTTTGTTGAG	0.542	
-	2	1458		NM_005760	NP_005751	Q03701	CEBPZ_HUMAN		1	AACATCTTTTTTT	0.368	
-	9	1986		NM_022168	NP_071451	Q9BYX4	IFIH1_HUMAN		1	ATTACCTTTTTTT	0.328	
+	18	2301	.F610fs|OSBPL6_	NM_032523	NP_115912	Q9BZF3	OSBL6_HUMAN		1	TATTTCAGAGC	0.453	
-	17	2265	_p.S623fs|TNS1_u	NM_022648	NP_072174	Q9HBL0	TENS1_HUMAN		4	TTCCGAAAAGG	0.587	
+	4	350	_p.L117fs|RQCD1_	NM_005444	NP_005435	Q92600	RCD1_HUMAN		2	TCCCACTTTTTT	0.413	
-	5	552_553	.2_5'UTR|C20orf1	NM_001009984	NP_001009984	Q5TEA3	CT194_HUMAN		0	ACCTTGGGAGCT	0.436	
+	8	1224	_Shift_Del_p.G299	NM_022098	NP_071381	Q9NQH7	XPP3_HUMAN		0	TCCCTGGGACA	0.473	
-	5	1900	3fs|TUBGCP6_uc	NM_020461	NP_065194	Q96RT7	GCP6_HUMAN		4	TCTTGAAGAGA	0.622	
+	1	3897_3898		NM_175918	NP_787114	Q8N1N5	CRPAK_HUMAN		0	CCTGCTCACGT	0.663	
+	1	3958_3959		NM_175918	NP_787114	Q8N1N5	CRPAK_HUMAN	9	0	CTGCTCACACA	0.668	
-	7	944		NM_173536	NP_775807	Q8N1C3	GBRG1_HUMAN	ellular (Probable).	2	CAGGTCAAAAAA	0.294	
+	8	715_716		NM_015325	NP_056140	Q9Y2F5	K0947_HUMAN	Potential.	2	AGGAATTTAAGA	0.406	

-	1	929_931	l_Intron|HNRNPA(	NM_006805	NP_006796	Q13151	ROA0_HUMAN	Gly-rich.		0	gttgtaaccgccgccgc	0.261	
+	2	128_130	p.L24del|BTN2A2_	NM_006995	NP_008926	Q8WVV5	BT2A2_HUMAN			0	CAGCCTCcctcctc(	0.483	
-	1	349_351	10kcc.2_Translati(	NM_021244	NP_067067	Q9NQL2	RRAGD_HUMAN			3	CCAGctcatcctcctc(	0.493	
+	11	1314_1315	MPCB_uc010liv.2_	NM_004279	NP_004270	O75439	MPPB_HUMAN			4	AAATGTTATGCTA	0.347	
+	11	2081_2082	kvv.1_Frame_Shift	NM_053043	NP_444271	Q96EV2	RBM33_HUMAN	Pro-rich.		1	CTGCCCACACAC	0.53	
-	1	1746	p.E227fs|RANBP6	NM_012416	NP_036548	O60518	RNBP6_HUMAN		p.E579K(1)	3	ATTTTTCCTTCCC	0.393	
-	13	2033_2034	p.P587fs|MAP3K6	NM_004672	NP_004663	O95382	M3K6_HUMAN		NA	9	TGAGCCGGGGG(	0.663	793155;rs139401154
+	3	249	C1_uc010ohe.1_5	NM_004964	NP_004955	Q13547	HDAC1_HUMAN	one deacetyl	NA	3	TGCTGAGGAGAT(	0.458	
+	9	1706	01dur.2_Frame_Sh	NM_020978	NP_066188	P19961	AMY2B_HUMAN		NA	0	CAGTTTCAAAAT(	0.333	
+	10	1080_1081		NM_001010883	NP_001010883	Q5T8I3	F102B_HUMAN		NA	1	GTCCTGGGGGA	0.302	
-	4	848	0pbv.1_Frame_Sh	NM_030920	NP_112182	Q9BTT0	AN32E_HUMAN	n (highly acic	NA	0	CTCCTCTTCAGA	0.393	
-	13	1089	p.A298fs|ILF2_uc(	NM_004515	NP_004506	Q12905	ILF2_HUMAN	DZF.	NA	0	ACAGCTGGCATC	0.463	
+	14	1753_1755	0pos.1_In_Frame_	NM_024420	NP_077734	P47712	PA24A_HUMAN	PLA2c.	NA	3	TCCTTTGATGAT(	0.433	
-	17	3001	p.E871fs|LAMB3_	NM_001017402	NP_001017402	Q13751	LAMB3_HUMAN	nain I.|Poter	NA	6	GGTCTCCAAGC(	0.582	
-	4	784	01jod.1_Frame_S	NM_017987	NP_060457	Q8WXA3	RUFY2_HUMAN	RUN.	NA	1	CGGCCATTTTTTT	0.398	
+	7	1229	KZ_uc001nck.1_5'U	NM_001105540	NP_001099010	Q13574	DGKZ_HUMAN	l-ester/DAG	NA	3	CGACGCCAGGA	0.642	
-	1	174_176	RNA|MMP1_uc01	NM_002421	NP_002412	P03956	MMP1_HUMAN		NA	4	AGAACAGCAGC	0.498	
+	1	422		NM_175854	NP_787050	Q58A45	PAN3_HUMAN	olyadenylat(	NA	1	GCTCTGGCTGG	0.746	
+	1	310		NM_021999	NP_068839	Q9Y287	ITM2B_HUMAN	lasmic (Pote	NA	0	ATCATCCCCCC(	0.721	
-	7	1217_1219	339SS>S|FOXN3_	NM_001085471	NP_001078940	O00409	FOXN3_HUMAN		NA	3	GGCTGAGGAGG	0.65	rs139532153
-	7	2023	wo.1_Frame_Shift_	NM_001002860	NP_001002860	Q9P203	BTBD7_HUMAN		NA	1	CCAGCATTTTTTT	0.383	
-	1	346	.1_Intron|SEPHS2	NM_012248	NP_036380	Q99611	SPS2_HUMAN		NA	2	CCTTCATGCCG(	0.726	
+	2	473_475	CD1_uc002gco.2_	NM_015253	NP_056068	Q658N2	WSCD1_HUMAN	ical; (Potent	NA	0	GCAGCCTGCTGC	0.68	
+	15	2007_2009	me_Del_p.P190de	NM_005892	NP_005883	O95466	FMNL_HUMAN	Pro-rich.	NA	1	GGTgcctccgccgcc	0.3	
-	14	2528	AP3K14_uc002iiu.	NM_003954	NP_003945	Q99558	M3K14_HUMAN		NA	8	TGTCATCCGACA(	0.582	
+	25	3766	E_uc010wpj.1_Fra	NM_000789	NP_000780	P12821	ACE_HUMAN	cellular (Pote	NA	4	GGCCTGGACCT	0.612	
+	11	1514_1515		NM_001001664	NP_001001664	Q6IQ16	SPOPL_HUMAN		NA	3	CCTTTCGAGCA(	0.421	
-	1	1023_1024	THBD_uc002wsu.1	NM_000361	NP_000352	P07204	TRBM_HUMAN	Extracellula	NA	0	TCGTTGCAGGA(	0.713	rs151272584
+	7	1073	).Q177fs|DOK5_u(	NM_018431	NP_060901	Q9P104	DOK5_HUMAN		NA	1	GCTTGCAAGGT	0.667	
+	28	5463	jj.2_Frame_Shift_	NM_006031	NP_006022	O95613	PCNT_HUMAN	Potential.	NA	8	GTGGGCAGGCC	0.706	
+	7	1806_1817	tq.1_In_Frame_D	NM_001039141	NP_001034230	Q9H2D6	TARA_HUMAN		NA	1	CCTCCAGAACCT	0.599	
+	7	1953_1961	atq.1_In_Frame_D	NM_001039141	NP_001034230	Q9H2D6	TARA_HUMAN		NA	1	GCCTCCAGAAC(	0.589	
-	10	1116	p.N255fs|ARFGAP	NM_014570	NP_055385	Q9NP61	ARFG3_HUMAN		NA	1	TCAACATTTTTTT	0.224	
-	4	998	0htg.2_Frame_Shi	NM_001017395	NP_001017395	O94876	TMCC1_HUMAN		NA	1	TAGCAGAGCTG(	0.438	
+	1	185	Jiar.2_Frame_Shift_	NM_033029	NP_149018	Q96KR4	LMLN_HUMAN		NA	1	TCTACTCCCGTC	0.687	
+	1	3897_3898		NM_175918	NP_787114	Q8N1N5	CRPAK_HUMAN		NA	0	CCTGCTCACGT(	0.663	
+	5	786_787	_p.V207fs|WFS1_	NM_001145853	NP_001139325	O76024	WFS1_HUMAN		NA	2	CCAGGTCAACGA	0.649	
-	6	1359_1360		NM_001237	NP_001228	P20248	CCNA2_HUMAN		NA	1	CTGATGGCAAAT	0.391	
-	16	2171	p.P668fs|DIAPH1_	NM_005219	NP_005210	O60610	DIAP1_HUMAN	FH1.	NA	1	GAGGTGGGGGG	0.612	
+	6	824	LHDC3_uc003otn.	NM_057161	NP_476502	Q9BQ90	KLDC3_HUMAN	Kelch 4.	NA	1	GAGTCTTTGACA	0.567	
-	2	394	G5_uc003prg.2_5'U	NM_004849	NP_004840	Q9H1Y0	ATG5_HUMAN		NA	1	ATTCGTCCAAAC(	0.383	
-	3	371_372	BCL7B_uc003tyg.1	NM_001707	NP_001698	Q9BQE9	BCL7B_HUMAN		NA	1	GAATTCAAGAAG	0.366	
-	2	609_611	e_Del_p.34_35SI>	NM_006379	NP_006370	Q99985	SEM3C_HUMAN		NA	1	ACAGATAGAACA	0.355	
-	37	4148	_p.S200fs|DOCK4_	NM_014705	NP_055520	Q8N1I0	DOCK4_HUMAN	DHR-2.	NA	4	CATCTTGCTCAG(	0.443	
+	2	644	nh.1_Frame_Shift_	NM_000245	NP_000236	P08581	MET_HUMAN	ılar (Potentia	NA	159	ACTGCTGACATA(	0.522	
+	4	582_583	).1_RNA|IDO2_uc(	NM_194294	NP_919270	Q6ZQW0	I23O2_HUMAN		NA	2	GAGAGGCGCAG(	0.624	
+	10	1740	LF1_uc003xyf.2_F	NM_015170	NP_055985	Q8IWU6	SULF1_HUMAN		NA	7	TGTGCCTTTTTTT	0.408	

-	13	1698	D2_uc003yqi.3_RI	NM_014109	NP_054828	Q6PL18	ATAD2_HUMAN		NA	2	TTCGTCAAAAAA	0.413	
-	2	154	3yqt.2_Frame_Shi	NM_004306	NP_004297	P27216	ANX13_HUMAN	Annexin 1.	NA	3	TCCTTTGCAGGC	0.408	
+	3	610_612	ysi.2_In_Frame_D	NM_002467	NP_002458	P01106	MYC_HUMAN	Poly-Gln.	NA	6	CTACCAGCAGC	0.611	rs61752959
-	11	3440	24_uc010mkb.2_Ir	NM_194313	NP_919289	Q5T7B8	KIF24_HUMAN		NA	1	TTGCTGAAGAC	0.582	
-	9	948	p.Q220fs|ALDH1A	NM_000689	NP_000680	P00352	AL1A1_HUMAN		NA	4	GCCCTGGTGGT	0.368	
-	2	1659_1661	.2_In_Frame_Del_	NM_173691	NP_775962	Q4KMQ1	TPRN_HUMAN	Glu-rich.	NA	0	tcttcctcttcctcctcctc	0.374	
+	15	2470	cyn.2_Frame_Shif	NM_003159	NP_003150	O76039	CDKL5_HUMAN		NA	6	TTCTCTACCATCA	0.373	
+	2	1213_1215	nqm.1_In_Frame_	NM_006777	NP_006768	Q86T24	KAISO_HUMAN		NA	3	TGAAGAGGAGG	0.433	
+	4	877_878		NM_024082	NP_076987	Q9BZD7	TMG3_HUMAN	lasmic (Pote	NA	4	CAGTCGGGGG	0.673	rs139807152
+	3	432_433	HACTR4_uc001b	NM_001048183	NP_001041648	Q8IZ21	PHAR4_HUMAN			0	TGGAGGAAAAA	0.391	
+	7	1426_1427	me_Shift_Del_p.H	NM_005012	NP_005003	Q01973	ROR1_HUMAN	xtracellular (Potential).		19	ATCCCCACACAC	0.554	
+	10	2124	ova.1_Frame_Shif	NM_001144937	NP_001138409	Q5VTL7	FNDC7_HUMAN	nectin type-III 8.		2	TGTCCAAAAAA	0.363	
+	3	278	j.2_Intron|S100A1	NM_006271	NP_006262	P23297	S10A1_HUMAN	EF-hand 2.		0	GCTGTGGACAA	0.557	
-	5	1175	MF1_uc010pjl.1_Ir	NM_003037	NP_003028	Q13291	SLAF1_HUMAN	(Potential).|Ig-like V-type.		2	TAAGGCTTTTTT	0.433	
+	7	1748_1750	e_Del_p.E474del|	NM_005807	NP_005798	Q92954	PRG4_HUMAN	ats of K-X-P-X-P-T-T-X.|29		1	CCCAAGGAGCC	0.635	
+	5	637	_p.G173fs|CTSE_	NM_001910	NP_001901	P14091	CATE_HUMAN			1	CCAGGCCAGAC	0.542	
-	4	784	01jod.1_Frame_S	NM_017987	NP_060457	Q8WXA3	RUFY2_HUMAN	RUN.		1	GGCCATTTTTTT	0.398	
-	1	106_108	L1_uc001mns.2_	NM_138421	NP_612430	Q96ER3	SAAL1_HUMAN			0	GCCACCTCCTC	0.67	
+	3	548_550	rlo.1_In_Frame_D	NM_004265	NP_004256	O95864	FADS2_HUMAN	ical; (Potential).		2	TTCTTCCTCCT	0.537	
-	9	1657_1659	_554PP>P|IFFO1	NM_080730	NP_542768	Q0D2I5	IFFO1_HUMAN	Poly-Pro.		0	GCTTGGCGGCG	0.601	rs144019095
-	1	174		NM_032656	NP_116045	Q8IY37	DHX37_HUMAN			1	GGCTCGGGGGG	0.711	
-	2	1785_1786	p.S437fs|LIG4_uc	NM_002312	NP_002303	P49917	DNLI4_HUMAN			0	AACACGAGAGA	0.48	
+	2	503		NM_020857	NP_065908	Q9P253	VPS18_HUMAN			3	TTCCGAGCGCA	0.507	
-	1	348_353	174B_uc002bsl.3_	NM_207446	NP_997329	Q3ZCQ3	F174B_HUMAN	ellular (Potential).		0	TGTTGGAGCTGG	0.578	56278;rs111725167
+	1	96_98	2sda.2_In_Frame_	NM_203437	NP_982261	Q6ULP2	AFTIN_HUMAN			2	AGAGGATGATG	0.409	
-	12	1561_1562	df.1_Frame_Shift_	NM_004525	NP_004516	P98164	LRP2_HUMAN	s B 1.|Extracellular (Potenti		29	CAACTGAAAAAA	0.317	
-	6	791	RKAG3_uc010fvy	NM_017431	NP_059127	Q9UGI9	AAKG3_HUMAN	CBS 1.		2	CACCAGGGGGG	0.652	
+	1	228_230		NM_138983	NP_620450	Q8TAK6	OLIG1_HUMAN	Ser-rich.		1	AGCCGCcctcctc	0.552	
-	1	1016_1017	P3_uc011aoy.1_5	NM_145174	NP_660157	Q7Z6W7	DNJB7_HUMAN	Poly-Lys.		1	CGCTTCTTTTTT	0.381	
+	7	1464	39674_uc003bba.	NM_004599	NP_004590	Q12772	SRBP2_HUMAN	y similarity).|Cytoplasmic (		4	GATGTCCCCCC	0.522	
-	1	668_670	79QQ>Q|TCF20_	NM_005650	NP_005641	Q9UGU0	TCF20_HUMAN	Poly-Gln.		5	GACTTGCTGCT	0.571	
-	10	1116	p.N255fs|ARFGAP	NM_014570	NP_055385	Q9NP61	ARFG3_HUMAN			1	TCAACATTTTTTT	0.224	
-	2	451	05fs|NCEH1_uc0	NM_001146276	NP_001139748	Q6PIU2	NCEH1_HUMAN	enal (Potential).		0	ACGCGCTTTTTT	0.507	
-	8	1472	_p.L340fs|AASDH_	NM_181806	NP_861522	Q4L235	ACSF4_HUMAN			4	GTCCCAAAAAA	0.363	rs148777026
-	1	169	NO_uc003jpv.2_R	NM_021147	NP_066970	P22674	CCNO_HUMAN			0	GGACAGGGGGT	0.716	
-	6	830	53_splice|DEPDC	NM_018369	NP_060839	Q8WUY9	DEP1B_HUMAN			1	GTACTTACAATT	0.351	
+	7	1394		NM_002439	NP_002430	P20585	MSH3_HUMAN			4	GGGACAAAAAA	0.348	
+	6	1327_1328	_p.A223fs|LARP1_	NM_033551	NP_291029	Q6PKG0	LARP1_HUMAN			4	CGTGGCCCCC	0.644	
-	2	222	fs|MIR1236_hsa-m	NM_002904	NP_002895	P18615	NELFE_HUMAN			0	AGTCCGGGGG	0.547	
+	7	1137	3pxy.1_Frame_Shi	NM_001029858	NP_001025029	Q5T1Q4	S35F1_HUMAN	ical; (Potential).		1	TTCAGTCAACCT	0.473	
+	30	5366		NM_003777	NP_003768	Q96DT5	DYH11_HUMAN	n (By similarity).		15	TTCCATAAAAAC	0.338	
+	7	1038	64fs|EGFR_uc010	NM_005228	NP_005219	P00533	EGFR_HUMAN	.|Extracellul	V30_R297>G(	9571	ACCTGCCCCCC	0.582	
-	5	1204	.2_Frame_Shift_D	NM_000466	NP_000457	O43933	PEX1_HUMAN			2	ACCTAATTTTTTT	0.353	
-	12	1587		NM_144651	NP_653252	A1KZ92	PXDNL_HUMAN	like C2-type 3.		2	TTTTCACCCCCA	0.453	
+	10	1740	LF1_uc003xyf.2_F	NM_015170	NP_055985	Q8IWU6	SULF1_HUMAN			7	TGTGCCTTTTTT	0.408	
-	2	284		NM_001033723	NP_001028895	Q6ZNC4	ZN704_HUMAN			0	GAGACATTTTTTT	0.423	
-	3	1842	_p.K471fs|ZHX1_	NM_007222	NP_009153	Q9UKY1	ZHX1_HUMAN	uired for interaction with NF		1	TTTGTCTTTTTTG	0.393	

-	13	1698	D2_uc003yqi.3_RI	NM_014109	NP_054828	Q6PL18	ATAD2_HUMAN		2	TTCGTCAAAAAA	0.413	
+	3	610_612	ysi.2_In_Frame_D	NM_002467	NP_002458	P01106	MYC_HUMAN	Poly-Gln.	6	CTACCAGCAGC	0.611	rs61752959
+	20	2671_2673	.E837del|CNKSR	NM_014927	NP_055742	Q8WXI2	CNKR2_HUMAN	ential.|Poly-Glu.	2	gaggaagaggaggag	0.379	
+	4	756		NM_001136273	NP_001129745	A6NM28	ZFP92_HUMAN	C2H2-type 4.	0	CTCCTGGAGCA	0.697	
-	4	396_398	_In_Frame_Del_p.	NM_001042663	NP_001036128	O94827	PKHG5_HUMAN	Poly-Glu.	1	GAGCTCTCCTCC	0.631	
-	7	901_902	1_Intron|MST1P9_	NR_002729					0	CGCCCGCCCCC	0.658	
-	6	1559_1561	S4_uc010ofy.1_3'	NM_005626	NP_005617	Q08170	SRSF4_HUMAN	r-rich (RS domain).	0	TCTTCCTTCTTC	0.325	rs138237342
+	1	136_137		NM_001008740	NP_001008740	Q7Z6W1	TMCO2_HUMAN		1	TAGAGTCTCTCT	0.406	
+	4	1436_1453		NM_000098	NP_000089	P23786	CPT2_HUMAN	ial matrix (By similarity).	0	TAGTGGCAATGA	0.546	rs142790440
-	12	1182_1183		NM_015306	NP_056121	Q9UPU5	UBP24_HUMAN		13	CTGATCTGAATT	0.337	
-	2	1873_1875	wne.1_In_Frame_I	NM_007113	NP_009044	Q07283	TRHY_HUMAN	roximate tandem repeats.	5	CCTCCGGCTCCT	0.68	
-	1	422_424	ox.1_In_Frame_De	NM_002249	NP_002240	Q9UGI6	KCNN3_HUMAN	Poly-Gln.	1	gctgctgttgctgctgctg	0.236	
-	12	1570_1571	0907_uc009wrk.1_	NM_014949	NP_055764	Q7Z7F0	K0907_HUMAN		0	TGTCCCTCTCTC	0.396	
+	4	635_646		NM_001104548	NP_001098018				0	gTagcagcagcagcag	0.283	30217;rs72359595;rs150848171
-	24	2573_2575		NM_014698	NP_055513	O94886	TM63A_HUMAN		2	AGGTCTGCTGC	0.626	
-	5	1798	AGT_uc009xff.2_F	NM_000029	NP_000020	P01019	ANGT_HUMAN		0	AAGCTCAAAAAA	0.562	
-	9	1499_1501	XM2_uc001lhj.2_F	NM_198148	NP_937791	Q8N436	CPXM2_HUMAN	Poly-Leu.	2	GCACCAGCAGC	0.626	
-	3	345	0rew.1_Frame_Shi	NM_001001991	NP_001001991	Q6UXH9	PAMR1_HUMAN		2	AGGTACCCCCC	0.517	
-	2	584	hift_Del_p.L154fs|	NM_016506	NP_057590	Q9NVX7	KBTB4_HUMAN		2	GGGCCAAAAAC	0.517	
-	2	285_286	.2_Splice_Site|ST	NM_003164	NP_003155	Q13190	STX5_HUMAN	lasmic (Potential).	2	GTCACTGGGGG	0.629	
-	9	1226	DDX6_uc001puc.2	NM_004397	NP_004388	P26196	DDX6_HUMAN		1	AATTCTGGGGGG	0.426	
+	7	1559_1560	K1_uc009zbp.2_F	NM_001114122	NP_001107594	O14757	CHK1_HUMAN	rotein kinase.	6	GGAAAGAAAAAA	0.361	rs35817404
-	3	539_541		NM_006248	NP_006239				0	GGACTTGTTGT	0.596	
-	12	4127_4129	w.2_In_Frame_De	NM_004719	NP_004710	Q99590	SCAFB_HUMAN	Pro-rich.	0	AGGGGGTGGTG	0.483	
-	8	775	me_Shift_Del_p.I2	NM_153694	NP_710161	Q8IZU3	SYCP3_HUMAN	tential.|Gln-rich.	0	TCATAATTTTTTT	0.259	
-	34	4381_4382	p.V250fs|POLE_u	NM_006231	NP_006222	Q07864	DPOE1_HUMAN		8	TTGACCACACAC	0.604	
+	1	1529_1531		NM_030979	NP_112241	Q9H361	PABP3_HUMAN		4	GTCctgcagctgctgct	0.414	
-	23	3282	f.1_RNA|TEP1_uc	NM_007110	NP_009041	Q99973	TEP1_HUMAN		5	CCACACCCCCC	0.587	
+	2	348	s|APEX1_uc001vx	NM_001641	NP_001632	P27695	APEX1_HUMAN	iation with rRNA, endoribo	4	GTGGGAAAAAG	0.557	
+	1	568_570	l0_uc001whe.2_5'	NM_014045	NP_054764	Q7Z4F1	LRP10_HUMAN		1	CCACCCTCCTC	0.67	
+	5	647_648	me_Shift_Ins_p.E	NM_002791	NP_002782	P60900	PSA6_HUMAN		0	TCCTTGAAAAAA	0.406	
-	11	2527		NM_018353	NP_060823	Q6P0N0	M18BP_HUMAN		0	TGGGACTTTTTTT	0.373	
+	7	4096_4098		NM_015042	NP_055857	O15014	ZN609_HUMAN	Poly-His.	3	CACACACCACC	0.576	
+	2	2046_2048	.L591del|SLC24A	NM_004727	NP_004718	O60721	NCKX1_HUMAN	ical; (Potential).	0	AGAGCCTGCTGC	0.547	
+	2	1053	on|APOB48R_uc0	NM_018690	NP_061160	Q0VD83	APOBR_HUMAN		0	CTCAGGAGGGG	0.705	365499;rs67465726;rs71657822;rs441214
+	9	960_962	ne_Del_p.E294del	NM_001099661	NP_001093131	B5ME19	B5ME19_HUMAN		0	GGATGAGGAGG	0.562	
+	13	3813_3815		NM_014712	NP_055527	O15047	SET1A_HUMAN	Ser-rich.	3	AGctcctcatcctcctcct	0.389	
+	15	2170_2172	.E413del|SLC9A5	NM_004594	NP_004585	Q14940	SL9A5_HUMAN		2	GTCTGAGGAGG	0.571	
+	10	1188	ss.1_Frame_Shift_	NM_053013	NP_443739	P13929	ENOB_HUMAN		1	TGGCTGGGGGG	0.567	
+	11	2629_2634	2gix.2_In_Frame_I	NM_001080424	NP_001073893	O15054	KDM6B_HUMAN	o-rich.|Thr-rich.	2	GCCGTcaccaccac	0.364	
+	12	2232_2234	gpz.2_In_Frame_	NM_016113	NP_057197	Q9Y5S1	TRPV2_HUMAN	ical; (Potential).	1	CATGGTGCTGCT	0.596	
+	14	4391	rw.3_Frame_Shift_	NM_016507	NP_057591	Q9NYV4	CDK12_HUMAN	Poly-Pro.	19	CTGAGCCCCCC	0.562	
-	1	96_98	_5'Flank|TMEM99	NM_000421	NP_000412	P13645	K1C10_HUMAN	lead.|Gly-rich.	0	cctccacatcctcctcctc	0.409	
-	1	279_280		NM_033188	NP_149445	Q9BYR2	KRA45_HUMAN	-C-[GRQVCHIEK]- [SPTR]	0	ggtggtctggcagcag	0.139	265645;rs146438235
+	15	2006_2007	_Ins_p.190_191in	NM_005892	NP_005883	O95466	FMNL_HUMAN	Pro-rich.	1	CGGTgcctccgccgc	0.292	
+	11	1588	l0wku.1_Splice_Si	NM_006310	NP_006301	P55786	PSA_HUMAN		0	ATAAGGTAAAAAA	0.337	rs142614305
-	5	1214_1216	Q161del|CXXC1_u	NM_014593	NP_055408	Q9P0U4	CXXC1_HUMAN	CXXC-type.	2	GTTTGATctgctgctg	0.468	

+	4	651	I120fs|LDLR_uc01	NM_000527	NP_000518	P01130	LDLR_HUMAN	s A 4.|Extracellular (Potenti		4	TGCATCCCCCA	0.642	
+	1	111_113		NM_021175	NP_066998	P81172	HEPC_HUMAN			1	CCTGCTCCTCC	0.64	
+	2	648_650	egn.1_In_Frame_	NM_003407	NP_003398	P26651	TTP_HUMAN	P-P-P-P-G.		1	ACCTCACCACC	0.685	
-	1	177_179	wm.2_In_Frame_D	NM_014400	NP_055215	O95274	LYPD3_HUMAN			1	GCGAAGCAGCA	0.675	rs141441894
-	9	2408_2410	0xyr.1_In_Frame_	NM_015063	NP_055878	Q9UPR5	NAC2_HUMAN	lasmic (Potential).		4	ACCCGTCCTCCT	0.616	
-	2	333_335	qdo.2_In_Frame_	NM_001145303	NP_001138775	Q7Z404	TMC4_HUMAN	xtracellular (Potential).		1	TCCATCCTCCT	0.645	
-	10	1701_1703	10erj.2_RNA|LILR	NM_005874	NP_005865	Q8N423	LIRB2_HUMAN	ical; (Potential).		1	gaggaagaggaggag	0.488	
+	11	1757_1759	me_Del_p.L480del	NM_006669	NP_006660	Q8NHL6	LIRB1_HUMAN	ical; (Potent	p.L479del(1)	3	Atcctactgctcctcctcc	0.458	
-	2	1150_1151		NM_152600	NP_689813	Q8NAF0	ZN579_HUMAN	Gly-rich.		0	TTCTGCCCTTCT	0.574	478862;rs144853314
-	1	1479_1481		NM_001029883	NP_001025054	A6NGG8	CB071_HUMAN			1	GTCTTCCTCCT	0.542	
+	3	759_761	02svy.2_In_Frame	NM_001008949	NP_001008949	Q6GPH6	IPIL1_HUMAN	lasmic (Potential).		3	CAGTGAGGAGG	0.532	
+	7	1430_1431	2tic.1_Frame_Shi	NM_005415	NP_005406	Q8WUM9	S20A1_HUMAN	lasmic (Potential).		2	CTCCAGAGAGA	0.515	
+	36	4261	tpr.2_Splice_Site_	NM_020120	NP_064505	Q9NYU2	UGGG1_HUMAN			1	TCAGGTAGGCC	0.376	
-	12	5661_5663	.2_In_Frame_Del_	NM_014071	NP_054790	Q14686	NCOA6_HUMAN	.|Gln-rich.|CREBBP-bindin		7	TCATTtgttgctgctgc	0.498	895426;rs140426729
-	20	3323_3325	.Q944del|SFRS15	NM_020706	NP_065757	O95104	SFR15_HUMAN	Poly-Gln.		0	GGTGgtggctgctgc	0.291	
+	7	1737_1739	3atq.1_In_Frame_	NM_001039141	NP_001034230	Q9H2D6	TARA_HUMAN			1	AGAGCCTCCTC	0.601	
+	7	2031_2033	3atq.1_In_Frame_	NM_001039141	NP_001034230	Q9H2D6	TARA_HUMAN			1	AGAGCCTCCTC	0.596	
-	10	2571_2573	E>E|RANGAP1_	NM_002883	NP_002874	P46060	RAGP1_HUMAN	cidic).|Asp/Glu-rich (highly		0	tcttctccttcctcctcctc	0.266	
-	1	205_207	g.1_In_Frame_De	NM_004628	NP_004619	Q01831	XPC_HUMAN	lu.|Glu-rich (acidic).		3	TCACCCTCCTC	0.734	rs72561774
-	4	1615_1616	40Q>QQ|QRICH1	NM_198880	NP_942581	Q2TAL8	QRIC1_HUMAN	Gln-rich.		1	CTTGGAgttgctgct	0.361	
+	21	3869	OBO2_uc011bgk.1	NM_002942	NP_002933	Q9HCK4	ROBO2_HUMAN	lasmic (Potential).		11	TACCTCCCCCC	0.433	
+	2	1293_1295	y.3_RNA|LNP1_uc	NM_001085451	NP_001078920	A1A4G5	LNP1_HUMAN	Poly-Asp.		0	ACAAAGATGATG	0.507	
+	1	3561_3562		NM_175918	NP_787114	Q8N1N5	CRPAK_HUMAN	5		0	CTGCTCACACGT	0.658	
+	1	4053_4054		NM_175918	NP_787114	Q8N1N5	CRPAK_HUMAN			0	CTGCTCACACAC	0.658	
-	15	1909	.N566fs|PROM1_	NM_006017	NP_006008	O43490	PROM1_HUMAN	ellular (Potential).		7	CCTCTATTTTTTT	0.428	
+	4	994_996	.Q279del|MMRN1	NM_007351	NP_031377	Q13201	MMRN1_HUMAN	Poly-Gln.		4	GCTGAGCAGCA	0.448	
+	3	351		NM_006583	NP_006574	O14718	OPSX_HUMAN	Name=3; (Potential).		1	TGAATATTTTTTT	0.393	
+	15	2059_2060	_p.T567fs|SDHA_u	NM_004168	NP_004159	P31040	DHSA_HUMAN			0	AAAACTTTGAAC	0.431	rs112307877
+	7	1303_1304	tron|LOC285830_	NM_001098479	NP_001091949	P30511	HLAF_HUMAN			0	ATCTTGTTTTTT	0.535	
-	2	531_533	rb.3_In_Frame_De	NM_001134870	NP_001128342	Q6NYC8	PHTNS_HUMAN	Poly-Gln.		0	GTtgttgttgctgctgct	0.547	
-	2	1592_1593	odz.2_5'Flank|TAF	NM_005453	NP_005444	O15209	ZBT22_HUMAN			1	CCGTCCCCACT	0.629	
-	40	6082_6083		NM_014611	NP_055426	Q9NU22	MDN1_HUMAN			10	CTCACCTTTTTT	0.401	
-	1	195_197	ob.1_In_Frame_	NM_145331	NP_663304	O43318	M3K7_HUMAN	Poly-Ser.		6	AGACGAGGAGG	0.655	
-	1	310_312	ame_Del_p.72_73	NM_005522	NP_005513	P49639	HXA1_HUMAN	Poly-His.		3	ggggtggcgatggtgg	0.527	rs10951154
+	1	403_405	c003tbl.3_5'Flank	NM_002047	NP_002038	P41250	SYG_HUMAN			1	CGCTCTGCTGC	0.749	
+	5	1249	_p.P231fs|DTX2_u	NM_020892	NP_065943	Q86UW9	DTX2_HUMAN			2	CCCCCACACAG	0.657	rs147779783
+	1	478_480	3ugm.2_5'Flank|u	NM_198467	NP_940869	Q6PCB5	RSBNL_HUMAN	Poly-Ala.		1	CTGCCCGCCGC	0.685	
-	9	1592	p.G185fs|MCM7_u	NM_005916	NP_005907	P33993	MCM7_HUMAN	MCM.		0	CCACACCCCCG	0.502	
+	3	9487_9489	C17_uc010lho.1_	NM_001040105	NP_001035194	Q685J3	MUC17_HUMAN	ch.|59 X approximate tand		27	TTCATCTCCTAC	0.493	
+	3	9663_9664	C17_uc010lho.1_	NM_001040105	NP_001035194	Q685J3	MUC17_HUMAN	ch.|59 X approximate tand		27	CTTCATCTACAA	0.5	
-	15	1999_2001	.1_In_Frame_Del	NM_015356	NP_056171	Q14160	SCRIB_HUMAN	to adherens junction and		5	taccctcttcctcctcctc	0.478	
+	10	3752_3754	.1_In_Frame_Del_	NM_015158	NP_055973	Q14678	KANK1_HUMAN			4	AGAAGAGGAGG	0.463	
-	1	2084	uc003zrh.1_RNA	NM_153809	NP_722516	Q8IZX4	TAF1L_HUMAN		p.K665fs*4(2)	26	TTGGCCTTTTTTT	0.478	
+	3	1021_1023	bag.1_In_Frame_	NM_006981	NP_008912	Q92570	NR4A3_HUMAN	Poly-His.		173	tcaccatcaccaccacc	0.483	
+	3	630		NM_021619	NP_067632	Q9H4Q4	PRD12_HUMAN			0	TTGAGGTGTGT	0.594	
+	5	629		NM_001807	NP_001798	P19835	CEL_HUMAN			1	CCTTCGGGGGG	0.642	
+	3	392	mkk.1_Frame_Sh	NM_004615	NP_004606	P41732	TSN7_HUMAN	ical; (Potential).		1	CATTTCAGGGT	0.423	

-	18	2564_2566	sw.2_In_Frame_D	NM_015107	NP_055922	Q9UPP1	PHF8_HUMAN		3	CGTTCTCCTCC	0.591	
+	4	1067_1069	1mrt.1_In_Frame_	NM_001142526	NP_001135998	Q6PI77	BHLH9_HUMAN	Poly-Glu.	2	GGCTGAGGAGG	0.488	
+	5	1012_1014	4elx.2_In_Frame_	NM_207318	NP_997201	Q6PEV8	F199X_HUMAN	Ser-rich.	1	GCGCCAGCAGC	0.567	
+	2	310_311	_5'Flank|LOC100	NM_001152	NP_001143	P05141	ADT2_HUMAN	Solcar 1.	1	GGAGCAGGGAG	0.49	rs113356560
-	3	274_276	fen.2_Intron|CD9	NM_031462	NP_113650	Q8TCZ2	C99L2_HUMAN	ar (Potential).|Poly-Thr.	3	GGTTGTGGTGG	0.552	
-	4	451_460	_p.A166fs|BCAP31	NM_001139441	NP_001132913	P51572	BAP31_HUMAN	enal (Potential).	0	TTCCTCTGGGCA	0.552	
-	2	90	ame.2_Frame_Shi	NM_000983	NP_000974	P35268	RL22_HUMAN		0	TGCTTCTTTTTTT	0.398	
-	4	396_398	_In_Frame_Del_p.	NM_001042663	NP_001036128	O94827	PKHG5_HUMAN	Poly-Glu.	1	AGCTCTCCTCC	0.631	
+	4	817	1aug.1_Frame_Sh	NM_001103170	NP_001096640	Q5VUY0	ADCL3_HUMAN		0	CTACTGTTTTTT	0.458	rs7513079
-	7	901_902	1_Intron|MST1P9_	NR_002729					0	GCCCGCCCCC	0.658	
+	14	1261	_p.I350fs|RPS6KA	NM_002953	NP_002944	Q15418	KS6A1_HUMAN	kinase C-terminal.	1	GGCATCCCCCC	0.672	
+	3	699_701		NM_018053	NP_060523	Q9H6D3	XKR8_HUMAN	ical; (Potential).	0	GAACCTGCTGC	0.665	
-	6	1559_1561	S4_uc010ofy.1_3'	NM_005626	NP_005617	Q08170	SRSF4_HUMAN	r-rich (RS domain).	0	TCTTCCTTCTTC	0.325	rs138237342
-	6	1205	S4_uc010ofy.1_3'	NM_005626	NP_005617	Q08170	SRSF4_HUMAN	r-rich (RS domain).	0	TGTTTTGGATCTT	0.443	
-	4	520	_p.M98fs|ZMYM6_	NM_007167	NP_009098	O95789	ZMYM6_HUMAN		3	AAGCATTTTTTT	0.453	
+	8	1361_1362	byu.2_Frame_Shi	NM_005095	NP_005086	Q5VZL5	ZMYM4_HUMAN	MYM-type 2.	5	AACTGAAAAAA	0.342	
-	3	179	1_5'UTR|INPP5B_	NM_005540	NP_005531	P32019	I5P2_HUMAN		1	GCTGTCCCCCT	0.687	
+	1	136_137		NM_001008740	NP_001008740	Q7Z6W1	TMCO2_HUMAN		1	TAGAGTCTCTCT	0.406	
-	4	379	|STIL_uc001crd.1	NM_003035	NP_003026	Q15468	STIL_HUMAN		3	GACGAATTTTTT	0.303	rs144192357
+	4	1436_1453		NM_000098	NP_000089	P23786	CPT2_HUMAN	ial matrix (By similarity).	0	TAGTGGCAATGA	0.546	rs142790440
-	12	1182_1183		NM_015306	NP_056121	Q9UPU5	UBP24_HUMAN		13	CTGATCTGAATT	0.337	
+	23	2276_2278	dge.1_In_Frame_	NM_015978	NP_057062	Q59H18	TNI3K_HUMAN	Poly-Ser.	10	TCACCTTCTTC	0.473	
-	3	841		NM_003921	NP_003912	O95999	BCL10_HUMAN	CARD.	2	TGAGTATTTTTTT	0.343	
+	2	248_249	sw.1_Frame_Shif	NM_003503	NP_003494	O00311	CDC7_HUMAN		5	CTCTTTAAAAAA	0.406	
-	10	3781_3783	gq.1_In_Frame_D	NM_001007237	NP_001007238	O75054	IGSF3_HUMAN	8.|Extracellular (Potential).	2	TGTTGGgtcgtcgt	0.478	rs55719879
-	1	2523		NM_021794	NP_068566	Q9UKF2	ADA30_HUMAN	lasmic (Potential).	3	GGTTACTTTTTTT	0.358	
+	3	190	0oyd.1_Intron|NB	NM_001037675	NP_001032764	Q3BBV1	NBPFK_HUMAN		0	CCTCAAAGAGAT	0.47	
+	3	513_515	nj.2_Intron|HFE2_	NM_213653	NP_998818	Q6ZVN8	RGMC_HUMAN	Poly-Gly.	1	CTTCGAGGAGG	0.626	
+	14	2499	_Shift_Del_p.G778	NM_019032	NP_061905	Q6UY14	ATL4_HUMAN	TSP type-1 2.	2	AATTTGGGGGG	0.692	rs149280379
-	1	643_645	.E61del|MCL1_uc	NM_021960	NP_068779	Q07820	MCL1_HUMAN	PEST-like.	0	CTCGTCCTCCT	0.635	
-	2	2734_2736	wne.1_In_Frame_	NM_007113	NP_009044	Q07283	TRHY_HUMAN	30 AA tandem repeats.	5	GTAGCTCCTCC	0.586	rs143222885
+	1	171_176		NM_178356	NP_848133	Q5TA78	LCE4A_HUMAN	Cys-rich.	0	GGCTGTGGTTG	0.578	269814;rs74871420;rs79268808
+	9	1991_1992	7A3_uc009won.2_	NM_024330	NP_077306	Q5K4L6	S27A3_HUMAN		1	TGCGTCCCCCC	0.619	
-	12	1570_1571	0907_uc009wrk.1_	NM_014949	NP_055764	Q7Z7F0	K0907_HUMAN		0	TGTCCCTCTCTC	0.396	
-	2	1126	1fpt.1_Frame_Shi	NM_030980	NP_112242	Q9H9L3	I20L2_HUMAN	Exonuclease.	2	GTTGAGGGGGG	0.557	
-	1	400	uc001fxm.2_5'UTR	NM_001025598	NP_001020769	Q7Z6I6	RHG30_HUMAN		3	CACCCAAAAAC	0.632	
-	6	1404_1406	.V48del|PVRL4_u	NM_030916	NP_112178	Q96NY8	PVRL4_HUMAN	ical; (Potential).	2	TGAGCACCACC	0.571	
-	6	1357_1359	p.V32del|PVRL4_	NM_030916	NP_112178	Q96NY8	PVRL4_HUMAN	ical; (Potential).	2	ACACCCACCAC	0.606	
-	6	1125_1127		NM_005814	NP_005805	Q99795	GPA33_HUMAN	c (Potential).|Poly-Cys.	0	CTCGGCAGCAG	0.567	
-	5	1433	.K421fs|C1orf114_	NM_021179	NP_067002	Q5TID7	CA114_HUMAN		0	TCGTGCTTTTTTT	0.363	
+	20	6213	A2_uc009www.2_	NM_020318	NP_064714	Q9BXP8	PAPP2_HUMAN	Sushi 5.	16	GTAATCCCCCC	0.468	
+	8	1233_1234	9wxs.2_Frame_Sh	NM_000721	NP_000712	Q15878	CAC1E_HUMAN	lasmic (Potential).	6	CCAAAGAGAGA	0.51	
-	2	1361_1363	.2_Intron|RGL1_u	NM_203454	NP_982279	Q8WW27	ABEC4_HUMAN		0	TCCCTTTCTTCTT	0.419	rs141411396
+	14	4052	Q1250fs|CAMSA	NM_203459	NP_982284	Q08AD1	CAMP2_HUMAN		4	TAAAACAAAAAA	0.368	
+	22	2922_2924		NM_018085	NP_060555	Q96P70	IPO9_HUMAN		2	gaggaagaggagga	0.33	
+	4	635_646		NM_001104548	NP_001098018				0	Tagcagcagcagca	0.283	30217;rs72359595;rs150848171
-	20	2967_2969	31QQ>Q|INTS7_	NM_015434	NP_056249	Q9NVH2	INT7_HUMAN	Gln-rich.	0	GCGTTGCTGCT	0.443	

-	24	2573_2575		NM_014698	NP_055513	O94886	TM63A_HUMAN		2	AGGTCTGCTGC	0.626	
-	5	1798	AGT_uc009xff.2_F	NM_000029	NP_000020	P01019	ANGT_HUMAN		0	AAGCTCAAAAAA	0.562	
+	14	1271	p.T389fs|KMO_uc	NM_003679	NP_003670	O15229	KMO_HUMAN	ical; (Potential).	2	GGTCACTTTTTC	0.348	
-	37	2102_1210	K3_uc010qih.1_In	NM_020987	NP_066267	Q12955	ANK3_HUMAN	Thr-rich.	19	ggtggtagtggtggtgg	0.291	
+	25	3716	_p.D924fs|ZMIZ1_	NM_020338	NP_065071	Q9ULJ6	ZMIZ1_HUMAN		4	CTGGACCCCCC	0.557	
-	3	1355	kgo.1_Frame_Shif	NM_148977	NP_683878	Q8TE04	PANK1_HUMAN		0	TACGGCTTTTTT	0.438	
+	14	2864	43_uc010qpu.1_I	NM_017893	NP_060363	Q9NTN9	SEM4G_HUMAN	lasmic (Potential).	1	CCTGGAAAAAA	0.562	
+	3	629_631	ame_Del_p.S197d	NM_032429	NP_115805	Q9BRK4	LZTS2_HUMAN	ntrosomal localization (By	4	GGCCCTGcctcctc	0.557	
+	9	6800	001lfz.2_Frame_S	NM_206862	NP_996744	O95359	TACC2_HUMAN		10	AGAGACCCCCC	0.522	
-	9	1499_1501	XM2_uc001lhj.2_F	NM_198148	NP_937791	Q8N436	CPXM2_HUMAN	Poly-Leu.	2	GCACCAGCAGC	0.626	
+	1	735_736		NM_001127389	NP_001120861	F5GZ66	F5GZ66_HUMAN		0	GGGCCAGGCAC	0.708	rs138894859
+	5	471_473	_p.L92del|TSPAN4	NM_003271	NP_003262	O14817	TSN4_HUMAN	ical; (Potential).	1	CTTCCTGCTGCT	0.65	rs61867552
+	1	310_312		NM_178168	NP_835462	Q9H207	O10A5_HUMAN	Name=3; (Potential).	3	TGTATTTCTTCTT	0.517	
+	1	268_270		NM_001004460	NP_001004460	Q9H208	O10A2_HUMAN	Name=3; (Potential).	1	TGTATTTCTTCTT	0.517	
+	2	423		NM_152316	NP_689529	Q8N8R7	CK046_HUMAN		0	TTAGCCAAAAAA	0.338	
+	1	525		NM_001003750	NP_001003750	Q8N0Y5	OR8I2_HUMAN	cellular (Potential).	1	CAATCATTTTTTT	0.443	rs112181516
+	3	548_550	rlo.1_In_Frame_D	NM_004265	NP_004256	O95864	FADS2_HUMAN	ical; (Potential).	2	GTTCTTCCTCCT	0.537	
+	4	543_544		NM_004585	NP_004576	Q9UL19	TIG3_HUMAN		1	GATACCAAAAAA	0.54	rs74932327
-	5	412_414	_uc001ocz.1_5'Fl	NM_001997	NP_001988	P35544	UBIM_HUMAN		0	ACCTGTCTTCTT	0.542	rs1065065
+	17	3442_3444	rpn.1_In_Frame_D	NM_012308	NP_036440	Q9Y2K7	KDM2A_HUMAN		9	gaggaagaggaggag	0.473	
+	3	321_323	me_Del_p.E98del|	NM_033388	NP_203746	Q8NAA4	A16L2_HUMAN		0	TGGCAGGAGGA	0.591	
+	9	1297	me_Shift_Del_p.S	NM_020193	NP_064578	Q7Z589	EMSY_HUMAN	nteraction with BRCA2.	6	TTCCTTCCCCCA	0.408	
-	5	675		NM_002426	NP_002417	P39900	MMP12_HUMAN		0	AACAAGTGGTG	0.416	197361;rs35342965
+	17	2405_2407	pkl.1_In_Frame_D	NM_004398	NP_004389	Q13206	DDX10_HUMAN		4	ATTGGAGtgatgat	0.31	
+	7	1559_1560	K1_uc009zbp.2_F	NM_001114122	NP_001107594	O14757	CHK1_HUMAN	rotein kinase.	6	GGAAAGAAAAAA	0.361	rs35817404
-	22	3672_3674	1qfl.2_In_Frame_D	NM_020228	NP_064613	Q9NQV6	PRD10_HUMAN	Poly-Thr.	1	CCGTTGGTGGT	0.547	
+	3	1265	DC5_uc009zjj.2_F	NM_020782	NP_065833	Q9P2K6	KLDC5_HUMAN	Kelch 5.	2	ATCGTGGGGGG	0.592	rs145908611
+	4	669	|FAR2_uc009zjm.2	NM_018099	NP_060569	Q96K12	FACR2_HUMAN		0	GGAGCCAAAAAA	0.388	
+	4	1243_1245		NM_018169	NP_060639	Q9HCM1	CL035_HUMAN		2	AAAGACCTCCTC	0.414	rs79406084
-	14	2006_2008	21A_uc001rlz.2_I	NM_017641	NP_060111	Q7Z4S6	KI21A_HUMAN		7	TGTCAtcttcctcctcc	0.281	
+	1	371_373	ANO6_uc010slf.1_	NM_001025356	NP_001020527	Q4KMQ2	ANO6_HUMAN	lasmic (Potential).	2	AAATGGAGGAG	0.626	
-	12	4127_4129	w.2_In_Frame_De	NM_004719	NP_004710	Q99590	SCAFB_HUMAN	Pro-rich.	0	AGGGGGTGGTG	0.483	
-	11	3063_3064	p.E611fs|SFRS2IP	NM_004719	NP_004710	Q99590	SCAFB_HUMAN	Arg-rich.	0	TCCTTTCTCTCT	0.446	
+	2	157	40B_uc001ruq.1_F	NM_001031698	NP_001026868	Q6NWY9	PR40B_HUMAN	Pro-rich.	5	AGCTATCCCCCC	0.607	
+	13	1098	c001sbo.1_Frame	NM_170754	NP_736610	Q63HR2	TENC1_HUMAN	2 tensin-type.	2	GGCTTCCAGCC	0.572	
+	4	553_555	zmy.1_In_Frame_	NM_020547	NP_065434	Q16671	AMHR2_HUMAN	ical; (Potential).	2	CCTCCTGCTGC	0.591	
+	1	306_308		NM_001005280	NP_001005280	Q8NGE5	O10A7_HUMAN	Name=3; (Potential).	4	ATGTACTTCTTC	0.414	
+	7	948_950	.L125del|SLC39A	NM_173596	NP_775867	Q6ZMH5	S39A5_HUMAN	lasmic (Potential).	2	ATCCCTGCTGCT	0.635	
-	3	467_469	GOLGA2B_uc001	NM_017600	NP_060070				0	GGCACCTCCTC	0.635	
+	17	2575_2577		NM_015267	NP_056082	O14529	CUX2_HUMAN	Poly-Ser.	6	GCTGTCCTCCT	0.749	
-	26	3014_3016		NM_006836	NP_006827	Q92616	GCN1L_HUMAN		4	ATCCACTCCTCC	0.631	
-	25	3416	SBNO1_uc010taq	NM_018183	NP_060653	A3KN83	SBNO1_HUMAN		9	TTCCATTTTTTT	0.388	
-	21	3042	tbb.1_Frame_Shif	NM_001077261	NP_001070729	Q9Y618	NCOR2_HUMAN		4	ACGATGGGGGG	0.652	rs12321697
+	46	8261_8262	0_uc001ujm.2_In	NM_015409	NP_056224	Q96L91	EP400_HUMAN	ith ZNF42 (By similarity).	12	agcagcaacagcagc	0.327	rs111782215
-	34	4381_4382	_p.V250fs|POLE_	NM_006231	NP_006222	Q07864	DPOE1_HUMAN		8	TTGACCACACAC	0.604	
-	8	694	2_uc001ume.2_Ir	NM_199254	NP_954863	Q6XPS3	TPTE2_HUMAN	ical; (Potential).	0	AATGTCAAAAAA	0.303	
+	1	1529_1531		NM_030979	NP_112241	Q9H361	PABP3_HUMAN		4	TCctgcagctgctgct	0.414	

+	12	1143_1145	.Q376del|CDK8_u	NM_001260	NP_001251	P49336	CDK8_HUMAN	Poly-Gln.	5	GAACCAGCAGC	0.463	
+	7	941	F3_uc001uqw.2_I	NM_006646	NP_006637	Q9UPY6	WASF3_HUMAN		1	ACTAGGTGTGTG	0.475	
+	18	2223	aba.2_Frame_Shif	NM_130806	NP_570718	Q8WXD0	RXFP2_HUMAN	lasmic (Potential).	0	AAAATTAAAAAAA	0.348	
-	14	3949_3950	C3H13_uc001vas.	NM_015070	NP_055885	Q5T200	ZC3HD_HUMAN	Potential.	2	gtatctctcctctctctctc	0.178	
+	3	707_710	vbk.2_Frame_Shif	NM_015116	NP_055931	Q9Y2L9	LRCH1_HUMAN	LRR 3.	2	CCGCCCTGCCTG	0.436	
-	15	2201_2202	_p.K703fs|RBM26_	NM_022118	NP_071401	Q5T8P6	RBM26_HUMAN	Potential.	1	TTACCTGTTTTTT	0.332	
+	7	1388_1390	Site|TOX4_uc010t	NM_014828	NP_055643	O94842	TOX4_HUMAN	ro-rich.|Poly-Ala.	1	AGCAGCTGCTG	0.581	
+	1	568_570	10_uc001whe.2_5'	NM_014045	NP_054764	Q7Z4F1	LRP10_HUMAN		1	CCACCCTCCTC	0.67	
+	5	668_670	A|IRF9_uc010alj.2	NM_006084	NP_006075	Q00978	IRF9_HUMAN	Poly-Ser.	1	ATTGGGagcagca	0.448	
+	11	1225_1226	G2E3_uc010tpf.1_	NM_017769	NP_060239	Q7L622	G2E3_HUMAN		3	CAAATTAAAAAA	0.272	
+	2	505	_Shift_Del_p.F28f	NM_005930	NP_005921	O15320	CTGE5_HUMAN		0	GTTCTCTTTTTTT	0.373	rs75842899
-	11	2527		NM_018353	NP_060823	Q6P0N0	M18BP_HUMAN		0	TGGGACTTTTTTT	0.373	
+	16	1934	_p.D676fs|PLEKH	NM_015549	NP_056364	A1L390	PKHG3_HUMAN		1	ATGGACCCCCC	0.612	
-	2	1567_1569	rf43_uc010tud.1_	NM_194278	NP_919254	Q6PJG2	CN043_HUMAN	-rich.|Gln-rich.	5	GGgctgcctgctgctg	0.473	
+	2	1168		NM_018228	NP_060698	Q9H8Y1	VRTN_HUMAN		0	CCACCGGGGGG	0.642	
-	2	1971	_Shift_Del_p.K585	NM_001040108	NP_001035197	Q9UHC1	MLH3_HUMAN		2	AGATTCTTTTTTT	0.358	
-	13	2476_2478	0twc.1_In_Frame_	NM_007039	NP_008970	Q16825	PTN21_HUMAN	Poly-Glu.	4	CTCGTCCTCCT	0.704	
+	13	1457_1459	atj.2_In_Frame_D	NM_198309	NP_938051	Q8TAM2	TTC8_HUMAN	TPR 7.	0	TGGTCAACAAC	0.537	
-	10	982_984	.Q250del|ATXN3_	NM_004993	NP_004984	P54252	ATX3_HUMAN	Poly-Gln.	0	GTCCCCctgctgct	0.325	74612;rs147904130
+	1	607_609		NM_003403	NP_003394	P25490	TYY1_HUMAN	Glu-rich (acidic).	0	gtgggcgaggaggag	0.34	
-	3	310	_5'UTR|C15orf52_	NM_207380	NP_997263	Q6ZUT6	CO052_HUMAN		1	GCCATCCCCCC	0.647	
-	2	1779	on|ZFP106_uc010	NM_022473	NP_071918	Q9H2Y7	ZF106_HUMAN		3	AGGGGAAAAAA	0.393	
+	10	1137	p.Q215fs|ADAL_u	NM_001159280	NP_001152752	Q6DHV7	ADAL_HUMAN		0	AAACCAAAAAA	0.453	
+	11	1380	_Shift_Del_p.L380	NM_014444	NP_055259	Q9UGJ1	GCP4_HUMAN		3	ATGTTGAAAAC	0.428	
-	17	3106	.K1025fs|SPG11_	NM_025137	NP_079413	Q96JI7	SPTCS_HUMAN	ellular (Potential).	5	TAACTCTTTTTTT	0.328	
+	7	4096_4098		NM_015042	NP_055857	O15014	ZN609_HUMAN	Poly-His.	3	CACACACCACC	0.576	
-	6	580	0bhb.2_Frame_Sh	NM_001127889	NP_001121361	Q9NZD8	SPG21_HUMAN		0	GAACTATTTTTTT	0.378	
+	2	2046_2048	.L591del|SLC24A	NM_004727	NP_004718	O60721	NCKX1_HUMAN	ical; (Potential).	0	GAGCCTGCTGC	0.547	
+	7	1140_1142	ame_Del_p.L345d	NM_024505	NP_078781	Q96PH1	NOX5_HUMAN	doreductase.|Helical; (Pote	2	CGCTCTGCTGC	0.626	
-	8	1968_1970	pw.1_In_Frame_D	NM_198525	NP_940927	Q2M1P5	KIF7_HUMAN	Poly-Glu.	3	TGGGCGGctcctcc	0.567	
+	6	919_920	hift_Ins_p.S249fs	NM_021168	NP_066991	Q96S21	RB40C_HUMAN		0	CCAGAGCCCCC	0.678	
-	10	895	NTAN1_uc010uzo.	NM_173474	NP_775745	Q96AB6	NTAN1_HUMAN		0	TCTTCATTTTTTT	0.383	
+	3	184_186	f62_uc010vas.1_	NM_020314	NP_064710	Q7Z3J2	CP062_HUMAN	Ser-rich.	1	CACGTCCTCCT	0.562	
-	2	667_668	_5'Flank|IQCK_uc	NM_001012991	NP_001013009	Q1ED39	CP088_HUMAN	Lys-rich.	0	GGTGGATTTTTT	0.535	
-	11	1628_1630	H3_uc002die.2_Ir	NM_017539	NP_060009	Q8TD57	DYH3_HUMAN	n (By similarity).	18	CGATCAGCAGC	0.498	
+	11	1356_1358	xy.2_In_Frame_D	NM_000418	NP_000409	P24394	IL4RA_HUMAN	ytoplasmic (Potential).	2	GTGTGAGGAGG	0.591	
+	9	960_962	ne_Del_p.E294del	NM_001099661	NP_001093131	B5ME19	B5ME19_HUMAN		0	GGATGAGGAGG	0.562	
+	17	2641	hift_Del_p.R819fs	NM_173201	NP_775293	O14983	AT2A1_HUMAN	smic (By similarity).	4	GACCGCCCCCC	0.657	
+	30	3476_3478	L1022del|ITGAL_	NM_002209	NP_002200	P20701	ITAL_HUMAN	ical; (Potential).	10	GGGGGCTGCTG	0.601	
+	13	3813_3815		NM_014712	NP_055527	O15047	SET1A_HUMAN	Ser-rich.	3	Gctcctcatcctcctcct	0.389	
-	2	749_751	ne_Del_p.Q143de	NM_002968	NP_002959	Q9NSC2	SALL1_HUMAN	Poly-Gln.	8	TGGATCTGCTGC	0.562	
+	3	278_280	0vho.1_In_Frame_	NM_020312	NP_064708	O75208	COQ9_HUMAN		1	CGGCGAGGAGG	0.576	rs149029279
+	15	2170_2172	.E413del|SLC9A5	NM_004594	NP_004585	Q14940	SL9A5_HUMAN		2	GTCTGAGGAGG	0.571	
+	3	1005	.2_Intron|MARVEL	NM_052858	NP_443090	Q96A59	MALD3_HUMAN	.|Helical; (Potential).	1	ATCGCGGGGGG	0.582	rs150498655
-	10	10282_1028	_In_Frame_Del_p	NM_006885	NP_008816	Q15911	ZFHX3_HUMAN	Poly-Gln.	4	cctgtggttgctgctgct	0.522	
+	11	2629_2634	2gix.2_In_Frame_	NM_001080424	NP_001073893	O15054	KDM6B_HUMAN	-rich.|Thr-rich.	2	GCCGTcaccaccac	0.364	
+	13	2245_2247	.K762del|CHD3_u	NM_001005273	NP_001005273	Q12873	CHD3_HUMAN	Poly-Lys.	1	AGTATAAGAAGA	0.488	

+	12	2232_2234	gpz.2_In_Frame_	NM_016113	NP_057197	Q9Y5S1	TRPV2_HUMAN	ical; (Potential).	1	ATGGTGCTGCT	0.596	
+	2	393_395		NM_018019	NP_060489	Q9NWA0	MED9_HUMAN	Potential.	0	CGAACAGCAGC	0.581	
-	1	233_235	dx.3_In_Frame_D	NM_020772	NP_065823	Q7Z417	NUFP2_HUMAN	His-rich.	4	gtgatgatggtggtggt	0.276	rs1054145
+	14	4391	rw.3_Frame_Shift_	NM_016507	NP_057591	Q9NYV4	CDK12_HUMAN	Poly-Pro.	19	CTGAGCCCCCC	0.562	
-	1	96_98	_5'Flank|TMEM9	NM_000421	NP_000412	P13645	K1C10_HUMAN	ead.|Gly-rich.	0	ctccacatcctcctcct	0.409	
-	1	279_280		NM_033188	NP_149445	Q9BYR2	KRA45_HUMAN	-C-[GRQVCHIEK]- [SPTR]	0	ggtggtctggcagcag	0.139	265645;rs146438235
-	9	1271	hzi.3_Frame_Shif	NM_012448	NP_036580	P51692	STA5B_HUMAN		6	CACCTGGGGGG	0.577	rs144993426
-	12	1542	hift_Del_p.G471fs|	NM_001256	NP_001247	P30260	CDC27_HUMAN		5	AAATAACCTTTC	0.368	
+	11	1588	0wku.1_Splice_Si	NM_006310	NP_006301	P55786	PSA_HUMAN		0	TAAGGTAAAAA	0.337	rs142614305
-	1	262_264		NM_002145	NP_002136	P14652	HXB2_HUMAN		0	CGAAAGGAGGA	0.542	
-	21	4684_4686	12EE>E|BZRAP1	NM_004758	NP_004749	O95153	RIMB1_HUMAN	Poly-Glu.	3	Gctcctcttcctcctcc	0.468	
-	6	506	_Shift_Del_p.N94f	NM_138619	NP_619525	Q9NZ52	GGA3_HUMAN	RF1 (in long isoform).	2	CAGGGTTTTTG	0.542	
+	9	844_846	02lhb.2_In_Fram	NM_001144967	NP_001138439	Q96PU5	NED4L_HUMAN	WW 1.	4	AACTTCCTCCT	0.498	
-	6	1132_1134		NM_005934	NP_005925	Q03111	ENL_HUMAN	Poly-Ser.	1	GAGAAGGAGGA	0.65	
-	11	1320_1321	nfg.1_Frame_Shift	NM_033417	NP_219485	Q9BT25	HAUS8_HUMAN		0	TGAACGAGAGAG	0.495	
-	13	1932_1934	O8_uc010eap.2_	NM_020959	NP_066010	Q9HCE9	ANO8_HUMAN	ytoplasmic (Potential).	3	cctcctcgtcctcctcc	0.197	
-	2	165_166	2nhx.1_Frame_Sh	NM_005535	NP_005526	P42701	I12R1_HUMAN	ellular (Potential).	1	TATGGCGGGTC	0.564	978336;rs113524129
+	7	1022	0xru.1_Frame_Shi	NM_001114093	NP_001107565	Q8ND56	LS14A_HUMAN		1	GTCATCGGGGT	0.438	
+	1	111_113		NM_021175	NP_066998	P81172	HEPC_HUMAN		1	CCTGCTCCTCC	0.64	
-	5	751_753	|ZNF569_uc002o	NM_152484	NP_689697	Q5MCW4	ZN569_HUMAN	KRAB.	3	ATGGTTCTTCT	0.433	
+	8	1049_1051	ne_Del_p.K267de	NM_174905	NP_777565	Q17RN3	FA98C_HUMAN		1	TCGCAAGAAGA	0.606	
+	2	648_650	egn.1_In_Frame_	NM_003407	NP_003398	P26651	TTP_HUMAN	P-P-P-P-G.	1	ACCTCACCACC	0.685	
-	2	202_204		NM_013376	NP_037508	Q9UHV2	SRTD1_HUMAN		0	TCCTTCTCCTCC	0.453	
-	1	177_179	m.2_In_Frame_D	NM_014400	NP_055215	O95274	LYPD3_HUMAN		1	GCGAAGCAGCA	0.675	rs141441894
+	17	1960	pba.1_Frame_Shift_Del_p.P679fs			Q96L34	MARK4_HUMAN		3	AACCGCCCCCC	0.642	
-	6	2257_2259	2pdl.2_In_Frame_	NM_030785	NP_110412	Q9H0K4	RSH6A_HUMAN	Glu-rich.	2	ctcctcgccctcctcctc	0.438	rs62639328
-	2	1402_1404	2per.3_In_Frame_	NM_018215	NP_060685	Q86V59	PNML1_HUMAN		0	CTCACCTTCTTC	0.562	
-	9	2408_2410	0xyr.1_In_Frame_	NM_015063	NP_055878	Q9UPR5	NAC2_HUMAN	lasmic (Potential).	4	CCCGTCCTCCT	0.616	
-	2	333_335	qdo.2_In_Frame_	NM_001145303	NP_001138775	Q7Z404	TMC4_HUMAN	xtracellular (Potential).	1	TCCATCCTCCT	0.645	
-	10	1701_1703	10erj.2_RNA|LILR	NM_005874	NP_005865	Q8N423	LIRB2_HUMAN	ical; (Potential).	1	aggaagaggaggag	0.488	
+	11	1757_1759	ne_Del_p.L480del	NM_006669	NP_006660	Q8NHL6	LIRB1_HUMAN	ical; (Potent p.L479del(1)	3	tcctactgctcctcctcc	0.458	
-	1	1479_1481		NM_001029883	NP_001025054	A6NGG8	CB071_HUMAN		1	GTCTTCCTCCT	0.542	
-	2	234_236	HX57_uc002rrg.2_	NM_198963	NP_945314	Q6P158	DHX57_HUMAN	Gly-rich.	3	gccacctccaccacca	0.384	
-	12	1400		NM_014709	NP_055524	Q70CQ2	UBP34_HUMAN		19	GTGTCTAAAAAA	0.342	
+	1	96_98	2sda.2_In_Frame_	NM_203437	NP_982261	Q6ULP2	AFTIN_HUMAN		2	AGAGGATGATG	0.409	
-	3	1648_1650	02sit.3_In_Frame	NM_015470	NP_056285	Q9BXF6	RFIP5_HUMAN		0	GCCTTGGTGGT	0.635	
+	1	147_152	2sjf.1_In_Frame_	NM_015120	NP_055935	Q8TCU4	ALMS1_HUMAN	Glu-rich.	9	AGCTggaggagg	0.403	rs72319667
-	4	737_739	02svr.2_In_Frame_	NM_017849	NP_060319	O75204	TM127_HUMAN		0	CTTATGCTGCT	0.557	
+	3	759_761	02svy.2_In_Frame	NM_001008949	NP_001008949	Q6GPH6	IPIL1_HUMAN	lasmic (Potential).	3	CAGTGAGGAGG	0.532	
-	6	1386	.M392fs|REV1_u	NM_016316	NP_057400	Q9UBZ9	REV1_HUMAN		2	TTTTCATTTTTTT	0.348	
+	6	2252_2253	ed.2_Frame_Shift	NM_181453	NP_852118	Q8IWJ2	GCC2_HUMAN	Potential.	1	GTTCAGAAAAAA	0.307	
-	7	738_740	tfo.3_In_Frame_	NM_207181	NP_997064	O15259	NPHP1_HUMAN	Glu-rich.	2	TTGGCCTTCTTC	0.404	
+	7	1430_1431	2tic.1_Frame_Shi	NM_005415	NP_005406	Q8WUM9	S20A1_HUMAN	lasmic (Potential).	2	CTCCAGAGAGA	0.515	
+	36	4261	tpr.2_Splice_Site_	NM_020120	NP_064505	Q9NYU2	UGGG1_HUMAN		1	TCAGGTAGGCC	0.376	
+	13	1538	1_uc002txn.2_Fr	NM_018151	NP_060621	Q5UIP0	RIF1_HUMAN		15	CCTTCCTTTTTTT	0.343	
-	28	4326_4327	zcp.1_Frame_Shif	NM_007366	NP_031392	Q13018	PLA2R_HUMAN	Potential).|C-type lectin 8.	3	AAAGCCTTTTTT	0.401	
+	2	422	l_p.N45fs|PPP1R	NM_001080545	NP_001074014	Q8WVI7	PPR1C_HUMAN		0	CATAACCCCCC	0.388	

+	7	931	.1_Frame_Shift_D	NM_000578	NP_000569	P49279	NRAM1_HUMAN	ical; (Potential).	4	GGAAGCTTTTTTT	0.418	
-	12	1511	p.F418fs|DOCK10	NM_014689	NP_055504	Q96BY6	DOC10_HUMAN		2	ACTCACAAAAAA	0.398	
-	29	3477_3478	vul.2_Frame_Shift	NM_018218	NP_060688	Q9NVE5	UBP40_HUMAN		3	AATCTTGTTTTTT	0.317	
+	2	175_177		NM_022134	NP_071417	Q9H3Q3	G3ST2_HUMAN	type II membrane protein;	0	GGTCATCCTCCT	0.631	
+	2	85_86	tj.1_RNA|FRG1B_uc010gdr.1_RNA|FRG1B_uc010ztk.1_Intron						0	ATGGAAAATATCT	0.342	
-	12	5661_5663	.2_In_Frame_Del_	NM_014071	NP_054790	Q14686	NCOA6_HUMAN	.|Gln-rich.|CREBBP-binding	7	TCATTtgttgctgctgc	0.498	895426;rs140426729
-	2	2489_2490	xus.1_Frame_Shif	NM_004975	NP_004966	Q14721	KCNB1_HUMAN	lasmic (Potential).	2	GCTTTTGGGGG	0.545	
-	1	737	ne_Shift_Del_p.K2	NM_080618	NP_542185	Q8NI51	CTCFL_HUMAN		4	CAGGCCTTTTTCC	0.502	
+	30	1616	2ydn.2_Frame_Sh	NM_001853	NP_001844	Q14050	CO9A3_HUMAN	ical region 3 (NC3).	0	AAATTGCACAGTT	0.552	
-	20	3323_3325	.Q944del|SFRS15	NM_020706	NP_065757	O95104	SFR15_HUMAN	Poly-Gln.	0	GGTGgtggctgctgc	0.291	
-	1	167_168	.1_Intron|C21orf29	NM_198688	NP_941961	P60371	KR106_HUMAN	A repeats of C-C-X(3).	0	GGGGCCGGGGC	0.688	
-	24	5314	|MCM3AP_uc002z	NM_003906	NP_003897	O60318	MCM3A_HUMAN		5	AAGCCGGGGGG	0.527	
-	7	789_791		NM_016449	NP_057533	Q6PGQ1	CV043_HUMAN	Asp-rich.	1	ACCTGGGcatcatca	0.261	
-	30	4280_4282		NM_002473	NP_002464	P35579	MYH9_HUMAN	Potential.	11	CTTGGCCTCCTCC	0.65	
+	7	2031_2033	3atq.1_In_Frame_	NM_001039141	NP_001034230	Q9H2D6	TARA_HUMAN		1	CAGAGCCTCCTCT	0.596	
-	12	2566	gye.1_Frame_Shift	NM_020831	NP_065882	Q969V6	MKL1_HUMAN	Pro-rich.	5	TGCCAGGGGGG	0.612	
-	10	2571_2573	EE>E|RANGAP1_u	NM_002883	NP_002874	P46060	RAGP1_HUMAN	cidic).|Asp/Glu-rich (highly	0	tcttctccttcctcctcctc	0.266	
-	1	871_873	.S246del|TCF20_u	NM_005650	NP_005641	Q9UGU0	TCF20_HUMAN	Ser-rich.	5	AAGGGAaggagga	0.438	
-	1	668_670	79QQ>Q|TCF20_u	NM_005650	NP_005641	Q9UGU0	TCF20_HUMAN	Poly-Gln.	5	GGACTTGCTGCT	0.571	
+	5	477_479		NM_001197	NP_001188	Q13323	BIK_HUMAN	Potential).|Helical; (Potentia	0	ctgctggcgctgctgctg	0.562	
+	8	2694	Del_p.I807fs|GRM	NM_000844	NP_000835	Q14831	GRM7_HUMAN	Name=6; (Potential).	7	TTCCAATTTTTTT	0.383	
-	1	205_207	vg.1_In_Frame_De	NM_004628	NP_004619	Q01831	XPC_HUMAN	lu.|Glu-rich (acidic).	3	CTCACCCTCCTC	0.734	rs72561774
+	2	804		NM_003884	NP_003875	Q92831	KAT2B_HUMAN		3	CCACTCCCCCA	0.448	
-	27	3223	t.2_RNA|CLASP2_	NM_015097	NP_055912	B2RTR1	B2RTR1_HUMAN		4	CACCCATTTTTTT	0.343	
+	5	750	p.F199fs|PDCD6I	NM_013374	NP_037506	Q8WUM4	PDC6I_HUMAN	with CHMP4A, CHMP4B a	2	GAAGTATTTTTTT	0.368	
+	13	1544	_Shift_Del_p.T25	NM_000249	NP_000240	P40692	MLH1_HUMAN	action with ET495A(1)|p.0?(	77	CTTGTACCCCCCC	0.473	
-	7	802_804	3clx.2_In_Frame_	NM_020707	NP_065758	Q9HCP6	HHATL_HUMAN		3	GCCCGAAGAAG	0.552	
-	14	1709_1710	3csi.1_Frame_Shif	NM_001789	NP_001780	P30304	MPIP1_HUMAN	Rhodanese.	5	GGCGATCTCTCT	0.515	
-	4	1615_1616	40Q>QQ|QRICH1	NM_198880	NP_942581	Q2TAL8	QRIC1_HUMAN	Gln-rich.	1	CTTGGAgttgctgct	0.361	
-	18	2397_2399	cwp.2_In_Frame_	NM_003363	NP_003354	Q13107	UBP4_HUMAN		4	TGTGGTCTTCTT	0.532	
+	3	1740_1742		NM_004393	NP_004384	Q14118	DAG1_HUMAN	.|Mucin-like domain.	2	GACTCCACCAC	0.581	
-	11	1563	ame_Shift_Del_p.L	NM_032682	NP_116071	Q9H334	FOXP1_HUMAN		2	AGTCAGGGGGG	0.572	
-	2	497_499	XP1_uc003dop.2_	NM_032682	NP_116071	Q9H334	FOXP1_HUMAN	Gln-rich.	2	CCTGTTGCTGCT	0.586	
-	2	584_586		NM_016206	NP_057290	A8MV65	VGLL3_HUMAN		0	TGGtctttctcctcctcc	0.394	
+	18	2116	p.K632fs|TBC1D2	NM_018309	NP_060779	Q9NUY8	TBC23_HUMAN		2	ACATCCAAAAAAA	0.353	
+	2	1293_1295	y.3_RNA|LNP1_uc	NM_001085451	NP_001078920	A1A4G5	LNP1_HUMAN	Poly-Asp.	0	ACAAAGATGATG	0.507	
-	10	1345_1348	LC9A10_uc010hq	NM_183061	NP_898884	Q4G0N8	S9A10_HUMAN	ical; (Potential).	5	TTAGGCATCCCC	0.377	170229;rs141074336
-	7	850	03eal.2_Frame_S	NM_001009899	NP_001009899	Q68DE3	K2018_HUMAN		3	CAATAATTTTTTT	0.373	
-	9	2364	bjg.1_Frame_Shif	NM_153002	NP_694547	Q8NFN8	GP156_HUMAN	lasmic (Potential).	2	GCCAGCCCCCC	0.552	
+	12	4015	_Shift_Del_p.E10	NM_017554	NP_060024	Q460N5	PAR14_HUMAN	Macro 3.	6	AGTGTGAAAAAA	0.423	
-	7	2240	.2_Intron|ZXDC_u	NM_025112	NP_079388	Q2QGD7	ZXDC_HUMAN		1	CTCTGCTTTTTTT	0.522	
-	4	1041_1043	tg.2_In_Frame_De	NM_001017395	NP_001017395	O94876	TMCC1_HUMAN		1	AGACATgcagcagc	0.404	
-	8	1759_1761	91DD>D|DBR1_u	NM_016216	NP_057300	Q9UK59	DBR1_HUMAN		0	CTGCATCGTCAT	0.251	0114751;rs2622736
+	5	386	p.K36fs|FXR1_uc	NM_005087	NP_005078	P51114	FXR1_HUMAN		1	ACTGTCAAAAAA	0.333	
-	3	541_543		NM_024524	NP_078800	Q9H7F0	AT133_HUMAN	ical; (Potential).	1	AATAGAGGAGG	0.463	
-	12	2438	1_Frame_Shift_De	NM_005781	NP_005772	Q07912	ACK1_HUMAN	ed for interaction with NED	10	CGGGCGGGGGG	0.726	
+	1	3561_3562		NM_175918	NP_787114	Q8N1N5	CRPAK_HUMAN	5	0	CTGCTCACACGT	0.658	

+	1	4117_4118		NM_175918	NP_787114	Q8N1N5	CRPAK_HUMAN	eraction with PAK1.	0	CTGCTCACACAC	0.639	
+	8	1111	gp.1_Frame_Shift_	NM_182982	NP_892027	P32298	GRK4_HUMAN	rotein kinase.	1	AGCTACAAAAAA	0.393	
-	1	340_348		NM_177998	NP_819056	Q7RTM1	OTOP1_HUMAN	ical; (Potential).	3	ATCCACAGCAGC	0.727	245977;rs75328065
-	7	900_902	.K136del|LYAR_uc	NM_001145725	NP_001139197	Q9NX58	LYAR_HUMAN	Lys-rich.	0	CGCTGCTTCTTC	0.601	
-	15	1909	.N566fs|PROM1_	NM_006017	NP_006008	O43490	PROM1_HUMAN	cellular (Potential).	7	CCTCTATTTTTTT	0.428	
-	7	944		NM_173536	NP_775807	Q8N1C3	GBRG1_HUMAN	cellular (Probable).	2	CAGGTCAAAAAA	0.294	
+	8	2988_2990	1bzz.1_In_Frame_	NM_020722	NP_065773	Q6ZU35	K1211_HUMAN	Poly-Lys.	2	AGAACAGAAGAA	0.567	
+	1	425_427		NM_020368	NP_065101	Q9NQZ2	SAS10_HUMAN	Glu-rich.	0	gatggcgaggaggag	0.291	
-	25	3483	I1107fs|SEC31A_	NM_001077207	NP_001070675	O94979	SC31A_HUMAN	ction with PDCD6.	8	TGGTAATTTTTTT	0.388	
-	11	1548	hnj.2_Frame_Shift_	NM_001077207	NP_001070675	O94979	SC31A_HUMAN	ction with SEC13.	8	CATCAATTTTTTT	0.353	
-	61	9721_9722		NM_014991	NP_055806	Q8IZQ1	WDFY3_HUMAN	WD 1.	3	TCTCCCACACAC	0.51	
-	1	591_593	C3_uc011cdn.1_I	NM_153757	NP_715638	Q96NT1	NP1L5_HUMAN	Glu-rich.	1	GCCGCAGcctcctc	0.389	
+	3	351		NM_006583	NP_006574	O14718	OPSX_HUMAN	Name=3; (Potential).	1	TGAATATTTTTTT	0.393	
+	10	2336_2338	V692del|GAB1_uc	NM_002039	NP_002030	Q13480	GAB1_HUMAN		4	GATTATGTTGTT	0.458	
-	8	596_598	3ijz.3_In_Frame_	NM_001102653	NP_001096123	Q01804	OTUD4_HUMAN		3	ACATCAGCAGCA	0.34	
+	15	2059_2060	_p.T567fs|SDHA_u	NM_004168	NP_004159	P31040	DHSA_HUMAN		0	AAAACTTTGAAC	0.431	rs112307877
+	13	1713_1714	_p.K518fs|PAPD7_	NM_006999	NP_008930	Q5XG87	PAPD7_HUMAN		1	AAAAAACACACA	0.653	
+	13	2025	f.2_Frame_Shift_	NM_012343	NP_036475	Q13423	NNTM_HUMAN	chondrial matrix.	3	CACTGACCCCCC	0.463	
-	3	349		NM_003664	NP_003655	O00203	AP3B1_HUMAN		1	GATGCATTTTTC	0.294	
+	3	1200_1201	TNFAIP8_uc011cw	NM_014350	NP_055165	O95379	TFIP8_HUMAN		1	CTGCCTTGTATAA	0.376	
-	12	1247	H7A1_uc003kty.2_	NM_001182	NP_001173	P49419	AL7A1_HUMAN		3	TAGGCCTTTTTA	0.383	
+	1	725_727	c003kuq.1_5'Flank	NM_001046	NP_001037	P55011	S12A2_HUMAN	ytoplasmic (Potential).	3	ACTCCGGCGGC	0.65	
-	22	3471	_Shift_Del_p.R109	NM_016340	NP_057424	Q8TEU7	RPGF6_HUMAN		3	GTGCCCTTTTTT	0.453	
-	16	2124_2125	_Shift_Ins_p.S640f	NM_016340	NP_057424	Q8TEU7	RPGF6_HUMAN		3	CGATTACTTTTTT	0.366	
+	9	1679	uc003kwr.3_Intron	NM_003059	NP_003050	Q9H015	S22A4_HUMAN	Name=12; (Potential).	0	TCACCCTTTTTTT	0.418	
+	5	378_379	k.1_Frame_Shift_	NM_006083	NP_006074	Q13123	RED_HUMAN		1	AAATTGAGAGAG	0.46	
+	4	1770	lnn.1_Frame_Shif	NM_020768	NP_065819	Q68DU8	KCD16_HUMAN		4	GCAGCAAAAAA	0.468	
-	19	2076	lbr.1_Frame_Shift_	NM_020117	NP_064502	Q9P2J5	SYLC_HUMAN		0	AAGTTACCCCCC	0.453	
-	1	189_191	lwl.2_In_Frame_D	NM_032782	NP_116171	Q8TDQ0	HAVR2_HUMAN		0	TAGTAGCAGCAC	0.291	
+	2	364_366	3mxm.1_Translati	NM_031480	NP_113668	Q9BRS2	RIOK1_HUMAN		4	agggttatgacgatgatg	0.3	rs2274212
+	8	2216	p.F486fs|JARID2_	NM_004973	NP_004964	Q92833	JARD2_HUMAN	ARID.	4	GCCTGCTTTTTC	0.493	
-	2	1369_1371	0jte.2_In_Frame_	NM_005527	NP_005518	P34931	HS71L_HUMAN		6	CGTCCAGCAGC	0.596	
+	1	184_185	_uc003nyt.2_5'UT	NM_032454	NP_115830	P49842	STK19_HUMAN		4	GCGGGCAAACC	0.634	
+	15	3067_3069	.H937del|SYNGA	NM_006772	NP_006763	Q96PV0	SYGP1_HUMAN		4	CTCccatcaccacca	0.547	
-	5	372_374	w.3_In_Frame_De	NM_003322	NP_003313	O00294	TULP1_HUMAN	Poly-Glu.	3	tcctcctcttcctcctcctc	0.389	
+	6	926_928	.C204del|MDFI_u	NM_005586	NP_005577	Q99750	MDFI_HUMAN	Cys-rich.	0	GCCTCTGCTGC	0.655	
-	8	1307_1309	1dzv.1_In_Frame_	NM_002042	NP_002033	P24046	GBRR1_HUMAN	ical; (Probable).	1	GAGCAAGAAGA	0.522	
-	7	875_877	1dzx.1_In_Frame_	NM_002043	NP_002034	P28476	GBRR2_HUMAN	ical; (Potential).	0	GAGCAAGAAGA	0.517	
-	13	5977	.P1807fs|REV3L_	NM_002912	NP_002903	O60673	DPOLZ_HUMAN	teraction with MAD2L2.	6	TACTTGGGGGG	0.428	
+	2	498	uc003qid.1_5'Flan	NM_015439	NP_056254	Q8IWP9	CC28A_HUMAN		0	AATGCCAAAAAA	0.413	
+	26	3025_3026	me_Shift_Ins_p.D	NM_015440	NP_056255	Q6UB35	C1TM_HUMAN	hydrofolate synthetase.	4	CCTGACAAAAAA	0.48	
+	3	945	g.2_Frame_Shift_	NM_006775	NP_006766	Q96PU8	QKI_HUMAN	KH.	2	AGGGATAAAAAA	0.363	
-	15	2268_2270		NM_032415	NP_115791	Q9BXL7	CAR11_HUMAN		50	GGTGGGAGGAG	0.616	
+	8	2004_2005	srz.2_Frame_Shift_	NM_014660	NP_055475	O94880	PHF14_HUMAN		3	TTGCAAGAGAGA	0.376	
-	1	310_312	ame_Del_p.72_73	NM_005522	NP_005513	P49639	HXA1_HUMAN	Poly-His.	3	ggggtggcgatggtgg	0.527	rs10951154
-	2	601		NM_022728	NP_073565	Q96NK8	NDF6_HUMAN	lization signal (Potential).	2	GTTGTCTTTTTTT	0.398	
+	5	601_603	0kxo.2_In_Frame_	NM_007252	NP_009183	P78424	PO6F2_HUMAN	Gln-rich.	1	cagctccagcagcag	0.365	

+	21	3700_3702	.K708del|AEBP1_	NM_001129	NP_001120	Q8IUX7	AEBP1_HUMAN	y).|Glu-rich.|Interaction wit	0	aggaggagaaagag	0.458	rs13928
-	2	83_85	_uc010lbj.1_In_Fr	NM_004603	NP_004594	Q16623	STX1A_HUMAN	lasmic (Potential).	0	AGCGACATCATC	0.586	
+	5	714	K1_uc003uab.2_	NM_002314	NP_002305	P53667	LIMK1_HUMAN	PDZ.	3	ATTGACCCCCC	0.677	rs150491142
+	5	1249	_p.P231fs|DTX2_u	NM_020892	NP_065943	Q86UW9	DTX2_HUMAN		2	CCCCCACACAG	0.657	rs147779783
-	2	458		NM_032936	NP_116325	Q9H2L4	TMM60_HUMAN		0	CCAGGCTTTTTT	0.408	
-	11	1360	_p.F440fs|SEMA3	NM_152754	NP_689967	O95025	SEM3D_HUMAN	Sema.	5	CTCTTGAACGTT	0.438	
+	19	5175_5176	.S1650fs|AKAP9_	NM_005751	NP_005742	Q99996	AKAP9_HUMAN		26	GTTTCAGAGAGA	0.411	
+	46	11454	.M3366fs|AKAP9_	NM_005751	NP_005742	Q99996	AKAP9_HUMAN		26	CGGATGGGGGG	0.537	rs143306820
+	1	137_138	_uc003utj.2_5'Fla	NM_152755	NP_689968	Q8N129	CNPY4_HUMAN		0	TTTTCCTTTTTTT	0.525	
+	4	574	|AGFG2_uc010lgy	NM_006076	NP_006067	O95081	AGFG2_HUMAN	Arf-GAP.	1	TATGTCCCCCC	0.517	
+	1	1875_1876		NM_012281	NP_036413	Q9NZV8	KCND2_HUMAN	r; Name=Segment S4; (Po	5	AGTTTTCCCGCC	0.52	rs143247237
-	20	2915	_p.P781fs|TNPO3	NM_012470	NP_036602	Q9Y5L0	TNPO3_HUMAN		5	GTATAGGGGGG	0.483	
+	1	528		NM_001001656	NP_001001656	Q8NGU2	OR9A4_HUMAN	ellular (Potential).	1	GAACAATTTTTTT	0.383	
-	5	4079_4081		NM_001080826	NP_001074295	Q86YV5	SG223_HUMAN		0	AAACTTCATCAT	0.675	
-	9	2293	wl.1_Frame_Shif	NM_182643	NP_872584	Q96QB1	RHG07_HUMAN		7	AGTCCGGGGGG	0.652	
+	8	1102_1104	_uc003www.2_In_	NM_006765	NP_006756	Q13454	TUSC3_HUMAN		3	TTCTTCTAAATG	0.384	
-	15	2035		NM_001010906	NP_001010906	Q68CJ6	SLIP_HUMAN		2	AGGAAATTTTTTT	0.453	
-	16	3521_3523	.E993del|MYST3_	NM_001099412	NP_001092882	Q92794	MYST3_HUMAN	Poly-Glu.	7	CCGGCTCCTCC	0.567	
-	60	8167	Shift_Del_p.R2704	NM_006904	NP_008835	P78527	PRKDC_HUMAN	KIP-binding.	34	CCAGCCTTTTTT	0.498	
-	10	1666_1667	.N420fs|MYBL1_	NM_001080416	NP_001073885	P10243	MYBA_HUMAN	atory domain (By similarity)	3	CAAGTGTTTTTT	0.406	
+	10	1740	LF1_uc003xyf.2_	NM_015170	NP_055985	Q8IWU6	SULF1_HUMAN		7	TGTGCCTTTTTT	0.408	
-	10	1506	p.R384fs|NBN_uc	NM_002485	NP_002476	O60934	NBN_HUMAN	r localization signal.	7	AGACCTTTTTTT	0.338	
-	6	1215		NM_001385	NP_001376	Q14117	DPYS_HUMAN		2	ACGCCTTTTTC	0.478	
+	14	1975	_Splice_Site|WDR	NM_145647	NP_663622	Q96DN5	WDR67_HUMAN		1	TTACAGTTTTTT	0.322	
-	13	1698	D2_uc003yqi.3_R	NM_014109	NP_054828	Q6PL18	ATAD2_HUMAN		2	TTCGTCAAAAAA	0.413	
-	14	1846	p.P525fs|EIF2C2_	NM_012154	NP_036286	Q9UKV8	AGO2_HUMAN	Piwi.	0	CGGCGGGGGG	0.647	rs148575703
-	13	1637_1639	.I506del|TSNARE	NM_145003	NP_659440	Q96NA8	TSNA1_HUMAN	.|Helical; (Potential).	0	TGGCGATGATG	0.414	rs142964918
+	10	3752_3754	.1_In_Frame_Del_	NM_015158	NP_055973	Q14678	KANK1_HUMAN		4	AGAAGAGGAGG	0.463	
-	1	2929	p.N621fs|RANBP	NM_012416	NP_036548	O60518	RNBP6_HUMAN	HEAT 7.	3	ATGACATTTTTTT	0.358	
-	1	2084	uc003zrh.1_RNA	NM_153809	NP_722516	Q8IZX4	TAF1L_HUMAN	p.K665fs*4(2)	26	TTGGCCTTTTTTT	0.478	
-	11	2102	24_uc010mkb.2_I	NM_194313	NP_919289	Q5T7B8	KIF24_HUMAN		1	TCTGGCTTTTTTT	0.527	
+	1	417_419	8376_uc003zys.1_	NM_001039792	NP_001034881	Q6UXD1	HRCT1_HUMAN	His-rich.	0	acccccaccgccacca	0.389	rs138232567
-	9	2947_2949	R2_uc004ari.1_In	NM_004560	NP_004551	Q01974	ROR2_HUMAN	lasmic (Potential).	20	AGCCTTCCTCCT	0.645	
-	2	367_369	A_uc004axs.3_R	NM_000380	NP_000371	P23025	XPA_HUMAN	EP164 and required for U	1	TTCTGTTCTTCTT	0.34	
+	3	1021_1023	bag.1_In_Frame_	NM_006981	NP_008912	Q92570	NR4A3_HUMAN	Poly-His.	173	tcaccatcaccaccac	0.483	
-	22	6093	f.2_Frame_Shift_	NM_002160	NP_002151	P24821	TENA_HUMAN	nectin type-III 15.	7	TGCCCGGGGGG	0.478	rs148674204
-	3	762_764	.L221del|ASTN2_	NM_198187	NP_937830	O75129	ASTN2_HUMAN	ical; (Potential).	9	ACACCAGCAGC	0.601	
-	3	561_562		NM_016322	NP_057406	P61106	RAB14_HUMAN		0	CTTACATTTTTT	0.292	
+	6	826_828	4blo.2_In_Frame_	NM_032552	NP_115941	Q5VWQ8	DAB2P_HUMAN	C2.	2	CGACAAGAAGA	0.601	
+	3	630		NM_021619	NP_067632	Q9H4Q4	PRD12_HUMAN		0	TTGAGGTGTGT	0.594	
+	13	2110_2112	598del|GRIN1_u	NM_007327	NP_015566	Q05586	NMDZ1_HUMAN	lasmic (Potential).	1	CAGCGAGGAGG	0.739	
-	3	1135_1137	4dsc.2_In_Frame_	NM_001111125	NP_001104595	Q5JU85	IQEC2_HUMAN	Poly-Glu.	3	TTTATCTCCTCC	0.635	
-	18	2564_2566	sw.2_In_Frame_	NM_015107	NP_055922	Q9UPP1	PHF8_HUMAN		3	CGTTCTCCTCC	0.591	
-	1	1019_1021	1mqj.1_In_Frame	NM_021963	NP_068798	Q9ULW6	NP1L2_HUMAN	u-rich (acidic).	1	AATGTCGtcctcct	0.33	
+	5	716_718	04eib.1_In_Frame	NM_016607	NP_057691	Q9UH62	ARMX3_HUMAN		2	TGGTCTGATGAT	0.448	
+	4	1067_1069	1mrt.1_In_Frame_	NM_001142526	NP_001135998	Q6PI77	BHLH9_HUMAN	Poly-Glu.	2	GGCTGAGGAGG	0.488	
+	9	1337_1338		NM_007231	NP_009162	Q9UN76	S6A14_HUMAN	Name=8; (Potential).	3	CATATTATTTTTT	0.361	

+	2	310_311	_5'Flank|LOC100	NM_001152	NP_001143	P05141	ADT2_HUMAN	Solcar 1.	1	GAGCAGGGAG	0.49	rs113356560
+	2	339_340	nqm.1_Frame_Sh	NM_006777	NP_006768	Q86T24	KAISO_HUMAN	y similarity).|Interaction wit	3	GTTATTGTGGAA	0.45	
-	3	866_868	v.2_In_Frame_Del	NM_003588	NP_003579	Q13620	CUL4B_HUMAN	Ser-rich.	3	GAAGATgaggagg	0.424	
-	6	1931	mvf.1_Frame_Shif	NM_031907	NP_114113	Q9BXU7	UBP26_HUMAN	p.G488fs*6(2)|p.F487	8	GCTCCAAAAAA	0.383	
-	3	474	exp.1_Frame_Shi	NM_021796	NP_068568	Q9HBJ0	PLAC1_HUMAN		1	GGTTTGGGGGG	0.507	
+	4	1210_1212	EC1_uc010nsl.1_	NM_005462	NP_005453	O60732	MAGC1_HUMAN		4	TGAGCTCCTCC	0.483	660605;rs141900922
+	3	1556_1558	Q477del|MAMLD1	NM_005491	NP_005482	Q13495	MAMD1_HUMAN	Poly-Gln.	0	cagcaacagcagca	0.433	
-	3	274_276	fen.2_Intron|CD9	NM_031462	NP_113650	Q8TCZ2	C99L2_HUMAN	ar (Potential).|Poly-Thr.	3	GGTTGTGGTGG	0.552	
+	7	512_514	j.1_In_Frame_Del	NM_007150	NP_009081	O15231	ZN185_HUMAN	Poly-Glu.	3	GACACCgaggagg	0.522	
-	4	451_460	_p.A166fs|BCAP31	NM_001139441	NP_001132913	P51572	BAP31_HUMAN	enal (Potential).	0	TCCTCTGGGCA	0.552	
-	14	4550		NM_000132	NP_000123	P00451	FA8_HUMAN	B.	11	AGGTTATTTTTTT	0.413	
-	6	4241_4243	vsz.1_In_Frame_	NM_001029882	NP_001025053	Q5TGY3	AHDC1_HUMAN		1	GCTGGAaggagga	0.596	
+	4	654_655	.R144fs|THRAP3	NM_005119	NP_005110	Q9Y2W1	TR150_HUMAN	-rich.|Ser-rich.	9	ATTCTAGAAACT	0.535	
+	7	1426_1427	me_Shift_Del_p.H	NM_005012	NP_005003	Q01973	ROR1_HUMAN	xtracellular (Potential).	19	ATCCCCACACAC	0.554	
+	7	1343_1345	e_Del_p.P339del|	NM_005807	NP_005798	Q92954	PRG4_HUMAN	-X-P-X-P-T-T-X.|11; appro	1	ACCACTCCCAA	0.655	
-	20	2967_2969	31QQ>Q|INTS7_	NM_015434	NP_056249	Q9NVH2	INT7_HUMAN	Gln-rich.	0	GCGTTGCTGCT	0.443	
+	2	983_984		NM_014053	NP_054772	Q9Y5Y0	FLVC1_HUMAN		0	CCCAACACACA	0.361	
+	3	629_631	ame_Del_p.S197d	NM_032429	NP_115805	Q9BRK4	LZTS2_HUMAN	ntrosomal localization (By	4	GGCCCTGcctcctc	0.557	
+	1	758		NM_001127389	NP_001120861	F5GZ66	F5GZ66_HUMAN		0	TGGCAGGGCGC	0.736	
+	5	886	rlo.1_Frame_Shift_	NM_004265	NP_004256	O95864	FADS2_HUMAN	lasmic (Potential).	2	GGCAGCCCATC	0.527	
-	5	1096		NM_001039548	NP_001034637	Q6PF15	KLH35_HUMAN	Kelch 5.	0	TGCCTCCCCCC	0.562	
-	3	539_541		NM_006248	NP_006239				0	GGACTTGTTGT	0.596	
-	2	665	1_splice|DACH1_	NM_080759	NP_542937	Q9UI36	DACH1_HUMAN		1	ccgctgccgccgccgc	0.262	
-	2	57	6_uc010tpm.1_5'	NM_152233	NP_689419	Q9UNH7	SNX6_HUMAN		0	GTCCAGGCCTT	0.592	
+	13	2290_2291	M_uc001wwe.3_F	NM_020937	NP_065988	Q8IYD8	FANCM_HUMAN		7	ATCAACTCTCTC	0.347	
-	18	1872	apo.2_Frame_Sh	NM_174978	NP_777638	Q08AQ4	Q08AQ4_HUMAN		4	TAGCTCAAAAAA	0.289	
+	9	960_962	ne_Del_p.E294del	NM_001099661	NP_001093131	B5ME19	B5ME19_HUMAN		0	GGATGAGGAGG	0.562	
-	2	423_425	2dxs.2_In_Frame_	NM_006110	NP_006101	O95400	CD2B2_HUMAN		1	CCCCCCATCATC	0.532	
-	5	412	2lbq.3_Frame_Shi	NM_024430	NP_077748	Q9H939	PPIP2_HUMAN	Potential.	1	ATTCTTCCATCTT	0.378	
+	9	977	l_p.S299fs|SPPL2	NM_152988	NP_694533	Q8TCT7	PSL1_HUMAN	ical; (Potential).	0	CTGCTCCTGGC	0.697	
+	7	641_642	E1_uc010eal.1_In	NM_018467	NP_060937	Q9NZ43	USE1_HUMAN	ic (Potential).|Potential.	0	agtgtcatcaagaagg	0.262	
-	1	1479_1481		NM_001029883	NP_001025054	A6NGG8	CB071_HUMAN		1	GTCTTCCTCCT	0.542	
+	2	483	AP25_uc002sev.2	NM_001007231	NP_001007232	P42331	RHG25_HUMAN		4	GTCCACCCCCA	0.592	
+	8	1145	2_Intron|ANKRD3	NM_001164315	NP_001157787	A6QL64	AN36A_HUMAN		0	ACAGGTATTTTG	0.302	
+	2	495	.1_Intron|CD28_u	NM_006139	NP_006130	P10747	CD28_HUMAN	(Potential).|Ig-like V-type.	0	TTGGGCAATGA	0.403	
-	1	5854	E2_uc002yyx.2_I	NM_182832	NP_878252	Q8WY50	PLAC4_HUMAN		0	gagggtatccagggtg	0.159	
-	1	80_82	15_uc011akw.1_5	NM_001017981	NP_001017981	Q9Y6U7	RN215_HUMAN	ical; (Potential).	1	gcaggggcagcagca	0.266	
-	1	1195	_p.A311fs|MST1R_	NM_002447	NP_002438	Q04912	RON_HUMAN	lar (Potential).|Sema.	6	TGGGGCCCCCC	0.667	
+	2	1293_1295	y.3_RNA|LNP1_uc	NM_001085451	NP_001078920	A1A4G5	LNP1_HUMAN	Poly-Asp.	0	ACAAAGATGATG	0.507	
+	12	1247	p.Q316fs|ACTL6A	NM_004301	NP_004292	O96019	ACL6A_HUMAN		1	AATACAGAGTTTT	0.353	
+	1	3102_3103		NM_175918	NP_787114	Q8N1N5	CRPAK_HUMAN	1	0	CACACATGCCCA	0.644	rs144787346
+	1	3804_3805		NM_175918	NP_787114	Q8N1N5	CRPAK_HUMAN	8	0	CCTGCTCACATG	0.693	
-	16	3651	lps.2_RNA|SH3T	NM_024577	NP_078853	Q8TF17	S3TC2_HUMAN	TPR 7.	2	GGCCACCAGCT	0.453	
-	25	3048_3049	jg.2_Frame_Shift_	NM_003062	NP_003053	O75094	SLIT3_HUMAN	LRRCT 4.	4	CTCCTTGTACCC	0.639	
+	1	1337_1338		NM_001453	NP_001444	Q12948	FOXC1_HUMAN		1	TGAGTCAcggcgg	0.54	
+	2	364_366	3mxm.1_Translati	NM_031480	NP_113668	Q9BRS2	RIOK1_HUMAN		4	agggttatgacgatgat	0.3	rs2274212
-	8	1612_1613	_Ins_p.214_214Q	NM_000332	NP_000323	P54253	ATX1_HUMAN	Poly-Gln.	4	tgctgctgctgctgctg	0.381	806515;rs66949327

-	8	1604_1606	me_Del_p.H211de	NM_000332	NP_000323	P54253	ATX1_HUMAN	Poly-Gln.		4	gctgctgctgatgctgat	0.384	rs59310777
-	19	2712_2714	c.1_In_Frame_De	NM_002714	NP_002705	Q96QC0	PP1RA_HUMAN	Gly-rich.		4	CGGAATggaggag	0.601	
+	13	1843	ru.2_Intron|DDR1_	NM_013993	NP_054699	Q08345	DDR1_HUMAN	|Cytoplasmic (Potential).		9	CCGGGCCCCC	0.682	
+	1	284	3nyf.2_Frame_Sh	NM_001710	NP_001701	P00751	CFAB_HUMAN			1	TGGTTCTTTTTTG	0.582	
-	5	372_374	w.3_In_Frame_De	NM_003322	NP_003313	O00294	TULP1_HUMAN	Poly-Glu.		3	tcctcctcttcctcctcctc	0.389	
+	24	2661		NM_015050	NP_055865	Q8N1G2	MTR1_HUMAN	tion with POLR2A.		5	GGAGTGGGGGG	0.572	
+	6	926_928	.C204del|MDFI_u	NM_005586	NP_005577	Q99750	MDFI_HUMAN	Cys-rich.		0	GCCTCTGCTGC	0.655	
+	14	2482_2484		NM_032538	NP_115927	Q5TCY1	TTBK1_HUMAN	-rich.|Potential.		9	gaggaagaggagga	0.291	
-	6	2278_2279		NM_014452	NP_055267	O75509	TNR21_HUMAN	lasmic (Potential).		0	CTCTTCAATCAC	0.52	
+	2	1016		NM_004770	NP_004761	Q92953	KCNB2_HUMAN	lasmic (Potential).		7	ATCATCAAAAAAA	0.448	
+	10	1284_1286	bhp.2_In_Frame_	NM_152786	NP_689999	Q8TAL5	CI043_HUMAN	Gln-rich.		0	gcagcggcagcagca	0.438	
-	3	1637_1638	vf.2_Frame_Shift_	NM_002160	NP_002151	P24821	TENA_HUMAN	EGF-like 9.		7	CTCATCACACAC	0.579	
+	3	627	H2_uc010okk.1_I	NM_001384	NP_001375	Q9BQC3	DPH2_HUMAN		NA	1	CCAGACCCCAA	0.602	
+	1	758		NM_001127389	NP_001120861	F5GZ66	F5GZ66_HUMAN		NA	0	TGGCAGGGCGC	0.736	
-	3	539_541		NM_006248	NP_006239				NA	0	GGACTTGTTGT	0.596	
+	87	3755_13757		NM_002332	NP_002323	Q07954	LRP1_HUMAN	ical; (Potent	NA	22	CTGTTGCTGCT	0.557	
-	1	1385_1387		NM_024496	NP_078772	Q9H1B7	I2BPL_HUMAN	Poly-Ala.	NA	0	ACCgcagcggcggc	0.581	
-	5	891	n|DYX1C1_uc002	NM_130810	NP_570722	Q8WXU2	DYXC1_HUMAN		NA	1	tctctctgaattttttttgc	0.045	
-	1	253_255	CHRNA3_uc002b	NM_000743	NP_000734	P32297	ACHA3_HUMAN		NA	4	cagagacagcagcag	0.601	rs66793222
-	9	1952	a.3_RNA|CCDC14	NM_182568	NP_872374				NA	2	TTGTTCATCAGC	0.406	rs66528329
+	3	759_761	2svy.2_In_Frame	NM_001008949	NP_001008949	Q6GPH6	IPIL1_HUMAN	lasmic (Pot	NA	3	CAGTGAGGAGG	0.532	
+	5	757	ow.2_Frame_Shift	NM_020194	NP_064579	Q9GZY8	MFF_HUMAN	lasmic (Pot	NA	1	GCACTGAAAAC	0.393	
-	7	1050_1052	gye.1_In_Frame_	NM_020831	NP_065882	Q969V6	MKL1_HUMAN	Gln-rich.	NA	5	GTGGTGCTGCT	0.66	
-	1	135	.1_Intron|LOC400	NM_018280	NP_060750	Q9NV39	CV026_HUMAN	Pro-rich.	NA	0	GGTTGGGGGG	0.751	
+	2	1293_1295	y.3_RNA|LNP1_uc	NM_001085451	NP_001078920	A1A4G5	LNP1_HUMAN	Poly-Asp.	NA	0	ACAAAGATGATG	0.507	
+	12	1247	p.Q316fs|ACTL6A	NM_004301	NP_004292	O96019	ACL6A_HUMAN		NA	1	ATACAGAGTTTT	0.353	
+	1	3102_3103		NM_175918	NP_787114	Q8N1N5	CRPAK_HUMAN	1	NA	0	CACACATGCCCA	0.644	rs144787346
+	1	1337_1338		NM_001453	NP_001444	Q12948	FOXC1_HUMAN		NA	1	TGAGTCAcggcgg	0.54	
+	2	364_366	3mxm.1_Translati	NM_031480	NP_113668	Q9BRS2	RIOK1_HUMAN		NA	4	agggttatgacgatgatg	0.3	rs2274212
+	6	926_928	.C204del|MDFI_u	NM_005586	NP_005577	Q99750	MDFI_HUMAN	Cys-rich.	NA	0	GCCTCTGCTGC	0.655	
+	12	2906_2908	9vqi.1_In_Frame_	NM_001083621	NP_001077090	Q9NUA8	ZBT40_HUMAN			1	CCCCAAGAAGA	0.517	
+	3	433	HACTR4_uc001b	NM_001048183	NP_001041648	Q8IZ21	PHAR4_HUMAN			0	GGAGGAAAAAA	0.393	
+	3	513_515	nj.2_Intron|HFE2_	NM_213653	NP_998818	Q6ZVN8	RGMC_HUMAN	Poly-Gly.		1	CTTCGAGGAGG	0.626	
+	2	1178	ftp.3_Frame_Shift_	NM_002036	NP_002027	Q16570	DUFFY_HUMAN	lasmic (Potential).		2	CACCCGCACCC	0.582	
-	6	746	141_uc009yga.1_	NM_016422	NP_057506	Q8WVD5	RN141_HUMAN			0	TCATTTGCTCCA	0.428	
+	7	1028	121_uc001orb.2_	NM_018320	NP_060790	Q9H920	RN121_HUMAN	G-type; atypical.		0	TGTGTGGGCAG	0.502	
-	3	539_541		NM_006248	NP_006239					0	GGACTTGTTGT	0.596	
-	1	61_63	.2_5'UTR|PGBD4_	NM_020154	NP_064539	Q9NPA0	CO024_HUMAN			0	CGATAGCAGCA	0.665	
+	6	1090	p.Q172fs|CHD2_	NM_001271	NP_001262	O14647	CHD2_HUMAN			2	AGAACAAAAAA	0.418	
-	5	1214_1216	161del|CXXC1_u	NM_014593	NP_055408	Q9P0U4	CXXC1_HUMAN	CXXC-type.		2	GTTTGATctgctgct	0.468	
-	67	2634_12635		NM_004525	NP_004516	P98164	LRP2_HUMAN	ellular (Potential).		29	GCATTACGTATT	0.47	rs150382715
+	4	301		NM_178456	NP_848551	Q9H1P6	CT085_HUMAN			1	TCCATCCCCCC	0.582	
-	1	5854	E2_uc002yyx.2_I	NM_182832	NP_878252	Q8WY50	PLAC4_HUMAN			0	gagggtatccagggtga	0.159	
+	7	1737_1739	3atq.1_In_Frame_	NM_001039141	NP_001034230	Q9H2D6	TARA_HUMAN			1	AGAGCCTCCTC	0.601	
+	4	287_289	03ckr.2_In_Frame	NM_001904	NP_001895	P35222	CTNB1_HUMAN	_Y142>V(1)|p.A20_L148d		3166	GCTCCTTCTCT	0.502	rs121913407
+	1	3561_3562		NM_175918	NP_787114	Q8N1N5	CRPAK_HUMAN	5		0	CTGCTCACACGT	0.658	
-	6	585_592		NM_152680	NP_689893	Q6P9G4	TM154_HUMAN	lasmic (Potential).		0	TCAAAGTCGGCT	0.409	

+	3	500	.T70fs|PHF3_uc01	NM_015153	NP_055968	Q92576	PHF3_HUMAN		5	TAACACAAAAAA	0.383	
-	2	171	|CDCA7L_uc003s	NM_018719	NP_061189	Q96GN5	CDA7L_HUMAN		0	GGCGTTAAAGAT	0.468	
+	3	9487_9489	C17_uc010lho.1_F	NM_001040105	NP_001035194	Q685J3	MUC17_HUMAN	ich.|59 X approximate tand	27	TTCATCTCCTAC	0.493	
-	5	1878	g.2_RNA|CSGALN	NM_001130518	NP_001123990	Q8TDX6	CGAT1_HUMAN	enal (Potential).	3	CACCCTTTTTG	0.433	
-	16	3521_3523	.E993del|MYST3_	NM_001099412	NP_001092882	Q92794	MYST3_HUMAN	Poly-Glu.	7	CCGGCTCCTCC	0.567	
+	12	2906_2908	9vqi.1_In_Frame_	NM_001083621	NP_001077090	Q9NUA8	ZBT40_HUMAN		1	CCCCAAGAAGA	0.517	
+	6	796	zqm.1_Frame_Shi	NM_007235	NP_009166	O43592	XPOT_HUMAN	an, nuclear localization an	2	CCCAAGTTTTTT	0.443	
-	3	1787	.I291fs|RTN4_uc0	NM_020532	NP_065393	Q9NQC3	RTN4_HUMAN	lasmic (Potential).	3	CTTCTATTTTTTT	0.378	
-	10	1758	160_uc010gll.1_F	NM_015565	NP_056380	O94822	LTN1_HUMAN		0	TTACCATTTTTTT	0.378	
-	1	5854	E2_uc002yyx.2_I	NM_182832	NP_878252	Q8WY50	PLAC4_HUMAN		0	gagggtatccagggtg	0.159	
-	30	4280_4282		NM_002473	NP_002464	P35579	MYH9_HUMAN	Potential.	11	TTGGCCTCCTC	0.65	
+	7	1737_1739	3atq.1_In_Frame_	NM_001039141	NP_001034230	Q9H2D6	TARA_HUMAN		1	AGAGCCTCCTC	0.601	
+	4	287_289	03ckr.2_In_Frame	NM_001904	NP_001895	P35222	CTNB1_HUMAN	_Y142>V(1)|p.A20_L148d	3166	GCTCCTTCTCT	0.502	rs121913407
-	6	585_592		NM_152680	NP_689893	Q6P9G4	TM154_HUMAN	lasmic (Potential).	0	TCAAAGTCGGCT	0.409	
+	9	1208_1209	_Shift_Ins_p.S303f	NM_016447	NP_057531	Q9NZW5	MPP6_HUMAN		0	AGTAGCAAAAAA	0.302	
+	3	9487_9489	C17_uc010lho.1_F	NM_001040105	NP_001035194	Q685J3	MUC17_HUMAN	ich.|59 X approximate tand	27	TTCATCTCCTAC	0.493	
-	1	549		NM_020710	NP_065761	Q8N1G4	LRC47_HUMAN	LRR 4.	2	CGGGGCGAAAG	0.692	
-	4	449_450	aog.2_Frame_Shi	NM_018198	NP_060668	Q9NVH1	DJC11_HUMAN		2	TCTCTTCTCTCT	0.505	
+	3	513_515	nj.2_Intron|HFE2_	NM_213653	NP_998818	Q6ZVN8	RGMC_HUMAN	Poly-Gly.	1	CTTCGAGGAGG	0.626	
-	3	393	lank|POLR3C_uc	NM_006468	NP_006459	Q9BUI4	RPC3_HUMAN		1	TGCACTGGGCTT	0.468	
+	7	866	_Shift_Del_p.C51f	NM_001080471	NP_001073940	Q5VY43	PEAR1_HUMAN	EGF-like 2.	3	AGCTGCCCCCC	0.612	rs77456537
-	6	1357_1359	p.V32del|PVRL4_	NM_030916	NP_112178	Q96NY8	PVRL4_HUMAN	ical; (Potential).	2	ACACCCACCAC	0.606	
+	3	338_340		NM_001102566	NP_001096036	A6NKN8	PC4L1_HUMAN		0	AGGCGGAGGAG	0.488	
+	17	2363_2365	2F1_uc010plh.1_	NM_002697	NP_002688	P14859	PO2F1_HUMAN		5	TGCGTCCACCAC	0.601	
-	12	1603	L3_uc001ggt.2_In	NM_181093	NP_851607	Q8IZE3	PACE1_HUMAN		2	TGCCAGAAAAGA	0.413	
+	10	1695	p.Q317fs|KLHL20_	NM_014458	NP_055273	Q9Y2M5	KLH20_HUMAN	Kelch 4.	1	GTATATCAGGAC	0.507	
+	22	6427	A2_uc009www.2_	NM_020318	NP_064714	Q9BXP8	PAPP2_HUMAN		16	ATGACGGGGGA	0.532	
+	1	611_613		NM_005298	NP_005289	O00155	GPR25_HUMAN	=5; (Potential).|Poly-Leu.	1	AGCTTGCTGCT	0.724	
+	13	2034	0ptd.1_Frame_Sh	NM_006243	NP_006234	Q15172	2A5A_HUMAN		1	CCGAATAAAAAA	0.328	rs71759537
-	3	1355	kgo.1_Frame_Shi	NM_148977	NP_683878	Q8TE04	PANK1_HUMAN		0	TACGGCTTTTTT	0.438	
-	13	4574	av.1_Frame_Shift_	NM_002417	NP_002408	P46013	KI67_HUMAN	approximate repeats.|4.	7	TGGGCCTTTTCC	0.488	
+	9	1225	el_p.A352fs|TNN	NM_138567	NP_612634	Q8NBV8	SYT8_HUMAN	lasmic (Potential).	1	CCACGCCCGGC	0.756	
+	6	839	9ykr.2_Frame_Shi	NM_001031854	NP_001027025	Q4AC99	1A1L2_HUMAN		5	TTCCTGGTCCC	0.537	
+	11	1217	oks.2_Frame_Shi	NM_004584	NP_004575	Q99638	RAD9A_HUMAN	r interaction with ABL1.	0	ACGCTCCCCCC	0.612	
+	9	928_929	58fs|TCIRG1_uc0	NM_006019	NP_006010	Q13488	VPP3_HUMAN	lasmic (Potential).	1	GGAGACAGAG	0.708	
+	8	1369_1389		NM_025004	NP_079280	Q0P6D6	CCD15_HUMAN		2	CAGAAGGCCAG	0.475	
+	16	2686_2688	tbn.1_In_Frame_	NM_004592	NP_004583	Q12872	SFSWA_HUMAN	g/Ser-rich (RS domain).	0	CACGAGAAGAA	0.493	
-	5	538_539	wmy.1_5'UTR|IPC	NM_024658	NP_078934	Q8TEX9	IPO4_HUMAN		1	GGTACCTCTCTC	0.559	
-	3	462_463	10asg.1_RNA|TME	NM_006827	NP_006818	P49755	TMEDA_HUMAN	l (Potential).|GOLD.	0	TTTTTCGCCTCC	0.485	
-	22	5408	.F1728fs|DMXL2_	NM_015263	NP_056078	Q8TDJ6	DMXL2_HUMAN		9	GCAAGAAAAAA	0.348	
+	1	150	CTP2_uc010bok.	NM_018349	NP_060819	Q6DN12	MCTP2_HUMAN		3	AGGTGAAAAAG	0.532	
-	2	1377_1378	.p.G470fs|IGFALS_	NM_004970	NP_004961	P35858	ALS_HUMAN		0	GCCAGCCCCC	0.678	
-	7	1266	bsl.1_Frame_Shift	NM_001089	NP_001080	Q99758	ABCA3_HUMAN		16	GCGGGAAAAGG	0.527	
+	9	1085		NM_006612	NP_006603	O43896	KIF1C_HUMAN	inesin-motor.	2	AGTGAGCGAGC	0.617	
+	8	1209_1211	2gnp.1_In_Frame_	NM_153604	NP_705832	Q8IZQ8	MYCD_HUMAN	Gln-rich.	5	CTCAGCcagcagc	0.527	
-	15	2100_2101	.A154fs|TOP3A_	NM_004618	NP_004609	Q13472	TOP3A_HUMAN		3	TTCTTTGCTTTA	0.248	
+	12	1003	wjd.1_Frame_Shi	NM_002390	NP_002381	O75078	ADA11_HUMAN	otential).|Peptidase M12B.	1	AGGACCTTCCAG	0.697	

-	7	1092		NM_080284	NP_525023	Q8N139	ABCA6_HUMAN	ical; (Potential).		7	CCATATAAAAAAA	0.308	
-	13	3301_3302	N2C_uc010wrh.1_	NM_000835	NP_000826	Q14957	NMDE3_HUMAN	lasmic (Potential).		4	CCTCCAGCTCCG	0.762	495021;rs67510083
-	2	402	_Shift_Del_p.G102	NM_001930	NP_001921	P49366	DHYS_HUMAN			1	GTATATCCCAGG	0.577	
-	1	142_143		NM_013940	NP_039228	Q9Y4A9	O10H1_HUMAN	cellular (Potential).		0	AAGACAGAGAA	0.574	rs147833765
-	2	412_413	owf.3_Frame_Shift	NM_002784	NP_002775	Q00887	PSG9_HUMAN	g-like V-type.		2	GGGATGCGTTG	0.406	
-	4	491	_Shift_Del_p.L127	NM_006840	NP_006831	O75023	LIRB5_HUMAN	Potential).|Ig-like C2-type 2.		2	AGGGCTAAAAGA	0.547	
-	3	1648_1650	02sit.3_In_Frame	NM_015470	NP_056285	Q9BXF6	RFIP5_HUMAN			0	GCCTTGGTGGT	0.635	
+	8	1227		NM_152945	NP_694453	Q8IUH3	RBM45_HUMAN			0	TCATGCAAAAAA	0.353	
+	1	209_211	Translation_Start_	NM_005759	NP_005750	Q9NYB9	ABI2_HUMAN			0	CTGTATgaggagga	0.601	
-	21	3762_3763	Shift_Del_p.Q881fs	NM_025176	NP_079452	Q9Y2I6	NINL_HUMAN	Potential.		5	GGTCTTGACTTT	0.569	
-	23	2501		NM_014258	NP_055073	Q9BX26	SYCP2_HUMAN			5	TCACCATTTTTTT	0.323	
-	20	3610_3611	.D1040fs|SFRS15	NM_020706	NP_065757	O95104	SFR15_HUMAN			0	TAGAATCTCTCT	0.525	
+	5	1336_1337	p.E279fs|HMGXB	NM_001003681	NP_001003681	Q9UGU5	HMGX4_HUMAN			2	CATAGTGAaaaaa	0.406	rs76572304
-	6	579_580	eo.2_Frame_Shift_	NM_005677	NP_005668	Q9Y215	COLQ_HUMAN	ollagen-like 1.		0	TCCTTCAGGGCC	0.584	
-	7	850	03eal.2_Frame_Sl	NM_001009899	NP_001009899	Q68DE3	K2018_HUMAN			3	CAATAATTTTTTT	0.373	
-	9	2364	bjg.1_Frame_Shif	NM_153002	NP_694547	Q8NFN8	GP156_HUMAN	lasmic (Potential).		2	GCCAGCCCCCC	0.552	
+	9	1470	10hrm.2_Frame_	NM_032839	NP_116228	Q96SL1	DIRC2_HUMAN	ical; (Potential).		0	TGTCTTGGTTCA	0.458	
-	1	150_152	94A_uc003eyh.2_	NM_152394	NP_689607	Q7L0X2	F194A_HUMAN	Glu-rich.		3	ccacctcttcctcctcctc	0.232	
-	2	132_134	ame_Del_p.T35de	NM_024947	NP_079223	Q8NDX5	PHC3_HUMAN	Poly-Thr.		2	Agtggtgatggtggtgg	0.424	
-	1	218	_p.P13fs|EMCN_u	NM_016242	NP_057326	Q9ULC0	MUCEN_HUMAN			0	AATACTGGGCAG	0.458	
+	3	351		NM_006583	NP_006574	O14718	OPSX_HUMAN	Name=3; (Potential).		1	TGAATATTTTTTT	0.393	
+	13	2105	lny.2_Frame_Shift	NM_018989	NP_061862	Q9P2N5	RBM27_HUMAN	RRM.		3	TATCTTACCAATG	0.378	
-	9	1715_1716	3loh.3_Frame_Shi	NM_004576	NP_004567	Q00005	2ABB_HUMAN			2	CGCTTGCCCCCC	0.5	
-	39	4906	.S1566fs|KIF13A_	NM_022113	NP_071396	Q9H1H9	KI13A_HUMAN			4	TGTGGGAAAAGT	0.522	
+	7	1303_1304	tron|LOC285830_	NM_001098479	NP_001091949	P30511	HLAF_HUMAN			0	GATCTTGTTTTTT	0.535	
-	4	649	_p.Q229fs|CCHCR	NM_019052	NP_061925	Q8TD31	CCHCR_HUMAN	Potential.		1	GCTCTTGGTGCA	0.557	
-	2	1782_1783	0jte.2_Frame_Shift	NM_005527	NP_005518	P34931	HS71L_HUMAN			6	CCTCTGGACCTC	0.446	
+	4	418	T1_uc003oag.2_5'	NM_006913	NP_008844	Q99942	RNF5_HUMAN			0	CCCCGCCCCCA	0.522	
-	61	11385_11386		NM_138694	NP_619639	P08F94	PKHD1_HUMAN	cellular (Potential).		44	AACATTCTCTAG	0.406	
-	8	1152	p.K221fs|ICK_uc0	NM_016513	NP_057597	Q9UPZ9	ICK_HUMAN	rotein kinase.		5	ATTACCTTTTTTG	0.502	
+	8	2132_2134		NM_138426	NP_612435	Q86VQ1	GLCI1_HUMAN	Poly-Gln.		0	CATCCCAGCAGC	0.562	
+	5	601_603	0kxo.2_In_Frame_	NM_007252	NP_009183	P78424	PO6F2_HUMAN	Gln-rich.		1	cagctccagcagcag	0.365	
+	15	1890	bl.1_RNA|LIMK1_	NM_002314	NP_002305	P53667	LIMK1_HUMAN	rotein kinase.		3	AACTGCCCCCC	0.657	
-	18	3149_3151		NM_022574	NP_072096	O75420	PERQ1_HUMAN			2	CCTCCTGCTGCT	0.65	
-	12	2387	_p.G539fs|EPHB4	NM_004444	NP_004435	P54760	EPHB4_HUMAN	Potential).|Protein kinase.		15	AGCCGCCCCCG	0.642	
-	4	2096		NM_002711	NP_002702	Q16821	PPR3A_HUMAN			34	TATCTCTTTTTCC	0.393	
+	7	1118_1119	vuy.2_Frame_Shift	NM_016019	NP_057103	Q9Y383	LC7L2_HUMAN	Arg/Ser-rich.		0	AGAGAAGAGAGA	0.391	
+	1	528		NM_001001656	NP_001001656	Q8NGU2	OR9A4_HUMAN	cellular (Potential).		1	GAACAATTTTTTT	0.383	
+	8	1621		NM_014141	NP_054860	Q9UHC6	CNTP2_HUMAN	cellular (Potential).		11	CTTGTGTGGAA	0.438	
+	57	8246		NM_198455	NP_940857	A2VEC9	SSPO_HUMAN	TSP type-1 6.		0	AGCCTGGGGGG	0.667	
-	6	524_525	3yqt.2_Frame_Shi	NM_004306	NP_004297	P27216	ANX13_HUMAN	Annexin 2.		3	CCAGGATTTTTT	0.411	
-	4	505_506	.1_RNA|FLJ43860	NM_207414	NP_997297	Q6ZUA9	Q6ZUA9_HUMAN			0	GGAACTTGTGCC	0.594	
+	22	3293	D1_uc010nen.2_F	NM_003611	NP_003602	O75665	OFD1_HUMAN	nteraction with SDCCAG8.		0	GAGCTCAAAAAA	0.348	
-	3	1261_1262	1_uc011moi.1_5'F	NM_004463	NP_004454	P98174	FGD1_HUMAN	ng (Potential).|Pro-rich.		6	TCCAGTGGGGG	0.658	
-	3	361	KF5_uc004eij.1_R	NM_032946	NP_116564	Q9H1B4	NXF5_HUMAN			1	GCCTCATTTTTCT	0.368	
-	3	564		NM_001013403	NP_001013421	Q5JRM2	CX066_HUMAN	lasmic (Potential).		0	GTGCCTTTTCCA	0.413	
-	6	1404_1406	.V48del|PVRL4_u	NM_030916	NP_112178	Q96NY8	PVRL4_HUMAN	ical; (Potent	NA	2	ATGAGCACCACC	0.571	

-	12	1603	L3_uc001ggt.2_In	NM_181093	NP_851607	Q8IZE3	PACE1_HUMAN		NA	2	TGCCAGAAAAGA	0.413	
+	8	1369_1389		NM_025004	NP_079280	Q0P6D6	CCD15_HUMAN		NA	2	CAGAAGGCCAG	0.475	
+	16	2686_2688	tbn.1_In_Frame_	NM_004592	NP_004583	Q12872	SFSWA_HUMAN	g/Ser-rich (	NA	0	CACGAGAAGAA	0.493	
+	12	931	10cke.2_Frame_S	NM_015085	NP_055900	Q684P5	RPGP2_HUMAN	Rap-GAP.	NA	1	GGAACAATGAG	0.473	
-	1	142_143		NM_013940	NP_039228	Q9Y4A9	O10H1_HUMAN	ellular (Pot	NA	0	AAGACAGAGAA	0.574	rs147833765
-	1	725	xz.1_5'Flank|LGI4_	NM_139284	NP_644813	Q8N135	LGI4_HUMAN		NA	1	GGTCCGGGGAG	0.662	
-	1	207_208	ad.1_Frame_Shif	NM_198538	NP_940940	Q6UWP8	SBSN_HUMAN		NA	1	CCCACCTCTCTC	0.579	
-	2	412_413	wf.3_Frame_Shift	NM_002784	NP_002775	Q00887	PSG9_HUMAN	g-like V-type	NA	2	GGGATGCGTTG	0.406	
-	4	491	_Shift_Del_p.L127	NM_006840	NP_006831	O75023	LIRB5_HUMAN	otential).|Ig	NA	2	GGGCTAAAAGA	0.547	
-	2	132_134	ame_Del_p.T35d	NM_024947	NP_079223	Q8NDX5	PHC3_HUMAN	Poly-Thr.	NA	2	Agtggtgatggtggtgg	0.424	
-	5	1565	1ebt.1_Frame_Shi	NM_001010923	NP_001010923	Q8N1K5	THMS1_HUMAN	CABIT 2.	NA	4	GAGGATTTTTC	0.453	